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Unravelling the cellular origin and clinical prognostic markers of infant B-cell acute lymphoblastic leukemia using genome-wide analysis

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ABSTRACT

B-cell acute lymphoblastic leukemia is the commonest childhood cancer. In infants, B-cell acute lymphoblastic leukemia remains fatal, especially in patients with t(4;11), present in ~80% of cases. The pathogenesis of t(4;11)/KMT2A-AFF1+ (MLL-AF4+) infant B-cell acute lymphoblastic leukemia remains difficult to model, and the pathogenic contribution in cancer of the reciprocal fusions resulting from derivative translocated-chromosomes remains obscure. Here, a “multi-layered” genome-wide analyses and validation was performed on a total of 124 *de novo* infant B-cell acute lymphoblastic leukemias uniformly diagnosed/treated according to Interfant99/06 protocol. These patients showed the most silent mutational landscape reported so far for any sequenced pediatric cancer. Recurrent mutations were exclusively found in *K- and N-RAS*, and were subclonal and frequently lost at relapse, despite a larger number of non-recurrent/non-silent mutations. Unlike non-MLL-rearranged B-cell acute lymphoblastic leukemias, B-cell receptor repertoire analysis revealed minor, non-expanded B-cell clones in t(4;11)+ infant B-cell acute lymphoblastic leukemia, and RNA-sequencing showed transcriptomic similarities between t(4;11)+ infant B-cell acute lymphoblastic leukemias and the most immature human fetal liver hematopoietic stem/progenitor cells, confirming a “pre-VDJ” fetal cellular origin for both t(4;11) and RAS^{mut}. The reciprocal fusion *AF4-MLL* was expressed in only 45% (19/43) of the t(4;11)+ patients, and HOXA cluster genes are exclusively expressed in *AF4-MLL*-expressing patients. Importantly, *AF4-MLL/HOXA*-expressing patients had a significantly better 4-year event-free survival (62.4% vs 11.7%, p=0.001), and overall-survival (73.7 versus 25.2%, p=0.016). AF4-MLL expression retained its prognostic significance when analyzed in a Cox model adjusting for risk stratification according to Interfant-06 protocol based on age at diagnosis, WBC count and Prednisone response. This study has clinical implications in disease outcome and diagnostic risk-stratification of t(4;11)+ infant B-cell acute lymphoblastic leukemia.

INTRODUCTION

B-cell precursor acute lymphoblastic leukemia (BCP-ALL) is the most frequent cancer in children.[1] Current 5-year survival rates in pediatric BCP-ALL approach 90%. However, BCP-ALL in infants (iBCP-ALL; <1 year of age) remains clinically challenging with an aggressive early clinical presentation in uniquely vulnerable hosts.[2] Approximately 80% of iBCP-ALLs are diagnosed with chromosomal rearrangements involving the mixed-lineage leukemia (*KMTA2*, also called *MLL*) gene, located on 11q23[3–5], which confers a dismal prognosis especially in patients carrying the t(4;11)/KMT2A-AFF1+ (MLL-AF4+).[6–8]

MLL is a H3K4 histone methyltransferase (HMT) required for normal hematopoiesis and *HOX* gene expression.[9,10] Leukemia transformation by *MLL* fusions requires the recruitment of the H3K79 HMT Dot1L to the MLL transcriptional complex.[11,12] Indeed, an H3K79 methylation profile defines both mouse and human t(4;11)/MLL-AF4+ BCP-ALL.[13] Importantly, *MLL* rearrangements (*MLL*r) occur prenatally during embryonic/fetal hematopoiesis, and the concordance rate for iBCP-ALL in identical twins with a monochorionic placenta is close to 100%.[14–17] This, coupled to the extremely short latency, suggests that MLL fusions might be sufficient for leukemogenesis.[4] Accordingly, genome-wide studies using both SNP arrays and whole-genome sequencing revealed that *MLL*r iBCP-ALL has a very low frequency of somatic mutations with the predominant clone carrying ~1.3 non-silent mutations and 1 copy number alteration (CNA).[18–20] Although these studies were performed at low coverage sequencing they reinforce that *MLL*r iBCP-ALL requires few additional mutations to induce full transformation. In contrast, MLL-AF4-induced leukemogenesis has proven difficult to model.[4,9] With the exception of a recent work by Lin et al[21,22] who fused human MLL to murine Af4, creating an artificial leukemogenic human-mouse chimeric fusion, current murine and humanized models of MLL-AF4+ BCP-ALL do not faithfully recapitulate the disease pathogenesis/phenotype, suggesting that MLL-AF4 *per se* is insufficient to initiate leukemogenesis.[23–28]

The few mutations and CNAs present in *MLL*r iBCP-ALL seem subclonal and not always retained at relapse.[20] Intratumor heterogeneity drives clonal evolution in response to microenvironmental cues and cytotoxic treatment and therefore recurrent mutations at diagnosis and relapse may be found in minor but clinically relevant subclones.[29] Here we aimed to address the clinical relevance of subclonal mutations and gene expression signatures in a large cohort of iBCP-ALL. For this, we performed deeper exome sequencing along with whole-genome DNA and RNA-sequencing on a large cohort of 50 MLLr and non-MLL iBCP-ALL patients uniformly treated and followed up according to the Interfant treatment protocol.[30] Similar to Anderson AK *et al* [20], we report a silent mutational landscape in iBCP-ALL irrespective of the *MLL* rearrangement/status. However, strikingly our genome-wide DNA and RNA analysis reveals new, clinically relevant information about disease outcome and cell-of-origin for t(4;11) and RAS mutations.

METHODS

Patients

Bone Marrow (BM) or peripheral blood (PB) samples from 124 infants (<12 months old) diagnosed with either pro-B or pre-B cell ALL were used in this study. The discovery patient cohort was composed by 42 *de novo* samples: 27 with the t(4;11) encoding for MLL-AF4, 5 with the t(9;11) encoding for KMT2A-MLLT3 (MLL-AF9) and 10 without *MLL*r (non-MLL B-other BCP-ALL without numerical or structural chromosomal abnormality reported at diagnosis). Additionally, for eight MLL-AF4+ iBCP-ALL patients matched diagnostic-relapse samples were available allowing for longitudinal studies. *MLL* rearrangements were confirmed by fluorescence in-situ hybridization (FISH).[31,32] For validation, an additional patient cohort comprising 43 MLL-AF4+, 11 MLL-AF9+, and 28 non-MLL iBCP-ALL cases were used. All patients were enrolled in the interfant99 treatment study. BM samples were collected at Erasmus MC-Sophia Children's Hospital (Rotterdam, The Netherlands), Armand Trousseau Hospital (Paris, France), and San Gerardo Pediatric Hospital (Monza, Italy). Complete remission BM samples were available for all patients. **Table S1** list the clinical and genetic features of patients. As control for the RNA-sequencing (RNA-seq) studies, CD34+CD19+ healthy B-cell progenitors were FACS-purified from 22-week-old human fetal livers (FL) as previously described.[32] FL HSPCs were processed and FACS-purified from second trimester human FL as previously described[33]. Briefly, cells were processed and stained for flow cytometry with up to ten fluorophore-conjugated monoclonal antibody (mAb). [antibodies (clone): CD34PECy7 (8G12), CD45RA FITC (HI100), CD19APC (HIB19), CD123PE (9F5), CD90 PECy5 (5E10), CD38 Pacific Blue (HIT2), lineage cocktail APC (CD2 (RPA-2.10)/ CD3 (OKT3)/ CD14 (61D3)/ CD16 (CB16)/ CD19 (HIB19)/ CD56 (TULY56)/ CD235a (HIR2)]. FACS was performed using a BD FACSAria II (Becton Dickinson). Gates were set with unstained and fluorescence minus one controls, on viable cells. Data were analyzed on FlowJo software (Tree Star). Gating strategies are as described in the results section. The study was approved by the Barcelona Clinic Hospital (2013/8529) and Hammersmith and Queen Charlotte's Hospital (04/Q0406/145) Research Ethics Committee.

Statistical Analysis

For quantitative variables, one-tailed t-test was used to identify significant differences between groups. For qualitative variables, Fisher exact test was used in order to identify significant differences between patient groups. Software for analysis of mutations and gene expression have their own statistical models explained in detailed in the references. Where multiple tests were performed the significance is shown corrected for multi-test. Mutation allele frequency evolution was plotted with the R package distribution Fishplot. Patterns Fisher's exact test was used to assess the association between clinical characteristics and presence of RAS mutations or AF4-MLL expression. Event-free survival (EFS) was defined as time from diagnosis to first event, i.e. resistance, relapse, death from any cause, or second malignant neoplasm. Observation periods were censored at time of last contact when no events were reported. EFS curves were estimated with the Kaplan-Meier method and standard errors (SE) were calculated according to Greenwood. Differences in EFS and OS between groups were compared with the log-rank test. Analysis of prognostic relevance of AF4-MLL/HOXA-expression in combination with risk stratification according to Interfant-06 protocol (based on age at diagnosis, WBC count and Prednisone response) was performed with the Cox model and the Wald test. All tests were two sided. Analysis was performed using SAS 9.2.

DNA, RNA and BCR (VDJ) repertoiregenome-wide analyses and data analysis

Preparation and analysis of all DNA and RNA genome-wide high-throughput sequencing is detailed in Online Methods (**Suppl Methods**) and in **Figure S1** and **Table S2**.

RESULTS

Diagnostic iBCP-ALL shows a silent mutational landscape irrespective of *MLL* gene status.

WES and WGS analysis reported a silent mutational landscape in the three iBCP-ALL subtypes here studied: MLL-AF4+, MLL-AF9+ and non-MLL (n=42 patients, **Table S1**). Our study revealed an average of 1 genomic rearrangement and 2,5 non-silent SNVs, 2-fold higher than that reported by Andersson AK *et al*[20], likely reflecting the 3-fold larger sequencing coverage (**Figure 1a, Figure S1 and Table S3**). All mutations found at diagnosis were validated using orthogonal methods. This mutational frequency is the lowest described for any other pediatric tumor type according to recent reports[34] (**Figure S2**). Intriguingly, one third of the mutations validated showed a mutant allele frequency (MAF) <20% indicating that iBCP-ALL contains genetically different intratumoral subclones despite its genomic stability, likely explaining the higher mutational load than that reported by Andersson AK *et al* [20] (**Figure 1a and Table S3**). Despite of the paucity of mutations, ~80% of the validated protein-coding mutations (90/116) are predicted to produce deleterious effects on the protein (**Figure S3a**) which might support a strong selective pressure in iBCP-ALL. To gain insights into the molecular mechanisms underlying the accumulation of mutations, we analysed the enrichment of specific mutational signatures as described in Alexandrov et al[35]. We identified in the MLL-AF4+ iBCP-ALL subgroup a significant enrichment of signature 1 characterized by the accumulation of C>T/G>A transitions, linked to a spontaneous deamination of 5-methylcytosine (**Figure S3b,c**).[35] This mutational signature has also been described in other pediatric tumors, suggesting that iBCP-ALL is not subjected to a specific mutational signature.

We also determined the molecular breakpoint of all MLLr at the base-pair level. In t(4;11)/MLL-AF4+ iBCP-ALL, the *AF4* breakpoints were almost invariably localizing within intron 3 whereas *MLL* breakpoints were found between introns 9 and 11 (**Table S4**).[3] We found WGS reads compatible with an AF4-MLL reciprocal rearrangement in all samples (**Figure S4**). AF4-MLL genomic breakpoints were validated by PCR-capillary sequencing and they were located nearby MLL-AF4 breakpoint, confirming a reciprocal chromosomal translocation.

RAS-PI3K is the only recurrently mutated pathway in iBCP-ALL with NRAS mutations being significantly more frequent in t(4;11)+ patients

Despite the low number of mutations found per sample, 38% of the sequenced iBCP-ALL patients displayed activating/gain-of-function mutations in either *KRAS* or *NRAS*. Additional mutations in other genes members of the RAS-PI3K pathway such as *FGFR4*, *JAK2*, *PTPN11*, *SETD2*, or *FLT3* were also identified (**Figure 1b**). To further validate the unique recurrence of *KRAS* and *NRAS* mutations, we performed targeted sequencing of these mutations in a large additional infant patient validation cohort (n=82) and confirmed that 34% of the iBCP-ALLs cases carry mutations in either *KRAS* or *NRAS* [36](**Figure 2a**). Interestingly, the overall frequency of RAS mutations slightly differed between the different cytogenetic subgroups of iBCP-ALL, with the MLL-AF4+ subgroup showing the highest frequency (42%) and the MLL-AF9+ subgroup the lowest (19%). This difference was basically attributed to the frequency of *NRAS* mutations, which was 6-fold more common in the MLL-AF4+ subgroup (32% vs 6%, Fisher exact test p=0.01) (**Figure 2a,b**).

Surprisingly, we observed that many iBCP-ALL patients had mutations in both *KRAS* and *NRAS*, or more than one (different) mutation in the same gene (**Figure 2a,c**). To further analyse the biological contribution of *KRAS* and *NRAS* mutations, we calculated the MAF of individual mutations and observed that the majority of patients who contain a single *RAS* mutation (either *KRAS* or *NRAS*) had MAF scores between 0.20 and 0.45, suggesting that the mutation is present in a major leukemic subclone (p=0.0025). By contrast, those patients harbouring ≥2 RAS mutations display MAF scores between 1% and 20%, compatible with these RAS mutations being in distinct and smaller leukemic subclones. We then analysed the impact of RAS mutations on disease outcome and found no clinical correlation of RAS mutations with either clinical outcome (OS, EFS, CNS) or diagnostic parameters (gender, age, % of blasts and WBCs) (**Figure S5**).

Evidence of clone selection and genomic instability at relapse

Paired diagnostic-relapse samples were available in eight MLL-AF4+ iBCP-ALL patients, permitting for longitudinal studies. WES revealed an 8-fold increase in the number of somatic non-synonymous mutations at relapse (19.5 mutations/patient, range:1-434, paired t-test p=0.03; **Figures 3a,b and Table S3**). We performed orthogonal validation for 160 random mutations, and 90% and 75% of mutations with MAF>15% and <15%, respectively, were confirmed (data not shown). Similarly to diagnosis, the majority of the somatic mutations found at relapse had MAFs commonly <30%, suggesting the existence of multiple leukemic subclones (**Figure 3a**). Importantly, none of the new *de novo* somatic mutations found at relapse were found in more than one patient, likely reflecting an intrinsic genomic instability of leukemic clones surviving induction/consolidation chemotherapy. This is further reflected by a significant enrichment of signature 6 associated with defective DNA mismatch repair, including higher number of small indels, observed in MLL-AF4+ patients at relapse (**Figure S6a**).

To delineate the evolutionary clonal structure from diagnosis to relapse, we performed high-coverage targeted sequencing on the identified mutations in paired diagnostic-remission-relapse samples.[37] Importantly, the main leukemic clone at relapse was always present at diagnosis although in some cases with a very low MAF, suggesting a chemotherapy-induced clonal pressure selecting for resistant/adapted leukemic subclones (**Figure 3c**). Interestingly, we found a correlation between the number of mutations and time-to-relapse in MLL-AF4+ patients, with a trend towards a higher mutational load in late relapses. (**Figure S6b**). We next analysed the clonal evolution of *RAS*-mutated leukemic clones at relapse. We found that the contribution of the *RAS* mutations varied among patients: one third of the iBCP-ALL patients had *RAS*-mutated clones at relapse (MA4_20 and MA4_22 increased the size of the *RAS*-mutated initial clone and in MA4_14 a *de novo* RAS mutations emerged), whereas it was lost in two thirds of the patients (MA4_17, MA4_18, MA4_23, MA4_24)(**Figure 3d**). This indicates that infants with MLL-AF4+ BCP-ALL relapse irrespective of the status of *KRAS* and *NRAS*. Thus, subclones carrying *KRAS* mutations do not exert an advantage over non-mutated clones, despite representing a recurrent genetic insult at diagnosis. Hence, this would argue against a leukemia-initiating role for RAS mutations.[38] Alternatively, RAS mutations might indeed be leukemogenic drivers, but the treatment-induced genetic instability observed at relapse may compensate *de novo* RAS mutations, acting as new leukemia drivers cooperating with MLL-AF4 during relapse.

HOXA cluster genes are only expressed in t(4;11)+ patients expressing the reciprocal fusion *AF4-MLL* which determines clinical outcome

To gain insights into the mechanisms underlying leukemogenesis in these mutationally silent *MLL*r and *MLL* germline iBCP-ALL patients, we performed RNA-Seq in the patient discovery cohort (n=42) using FL-derived CD34+CD19+ healthy B-cell progenitors as controls, as these cells most likely represent the healthy counterparts of the leukemic blast stalled at the pro/pre-B differentiation stage. We first surveyed the expression of the genes previously reported to be specific to either *MLL*r iBCP-ALL or specifically to MLL-AF4+ iBCP-ALL[39]. RNA Seq profiling confirmed that these genes segregate patients according to the molecular subtype, MLL-AF4+, MLL-AF9+ and MLL germline (**Figure S7**). We also observed, at diagnosis, a strong upregulation of the MLL target genes *FLT3* [40], *MEIS1, PROM1* and *HOXA* genes in many of our *MLL*r iBCP-ALL samples but not in *MLL* germline samples (t-test, $p<0.05$, **Figure 4a**), thus validating our RNA-seq approach.

Strikingly, the reciprocal AF4-MLL fusion gene was discernibly expressed in 19/43 (45%) of the t(4;11)+ infant BCP-ALL samples, and its expression was always maintained at relapse (data not shown). We then compared the genes differentially expressed between AF4-MLL-expressing and non-expressing t(4;11)+ patients and found a striking positive correlation between the expression of *HOXA* gene cluster and the overexpression of the reciprocal AF4-MLL fusion (t-test, p=0.002, **Figure 4b**). These AF4-MLL/HOXA-expressing patients (n=19) had a significantly better prognosis than those lacking AF4-MLL/HOXA expression (n=24). Four-year EFS and OS was 62.4% (SE, 11.3%) versus 11.7% (SE, 10.2%) (p=0.001, **Figure 4c**), and 73.7% (SE, 10.1%) versus 25.2% (SE, 10.3%) (p=0.016, **Figure 4d**), respectively. When “AF4-MLL expression” was analyzed in a Cox model adjusting for risk stratification (medium risk or high risk according to Interfant-06 protocol based on age at diagnosis, WBC count and Prednisone response), it retained its prognostic significance with an hazard ratio for patients lacking AF4-MLL expression of 3.42 (95%CI 1.35-8.63, p=0.01) compared to those expressing AF4-MLL/HOXA, while risk group was not significant (the hazard ratio of high risk versus medium risk was 1.34 [95%CI 0.59-3.03, p=0.49]). This is the first report showing that AF4-MLL overexpression correlates very well with transcriptional deregulation of HOXA gene cluster in iBCP-ALL and that the co-expression of *AF4-MLL* and HOXA cluster identifies a subgroup of t(4;11)+ iBCP-ALL with a way more favourable clinical outcome

We next explored new molecular pathways involved in the pathogenesis of iBCP-ALL, by performing an unbiased transcriptional analysis of the RNA-Seq data from the iBCP-ALL patients. We found deregulated expression in a total of 3905 genes, of which 2575 (66%) were upregulated and 1330 (34%) downregulated as compared with healthy FL-derived B-cell progenitors, illustrating the global transcriptional activation nature of *MLL* fusions (**Figure S8**).[25,41] Furthermore, a significant upregulation of genes involved in the control of cell growth including the CDK inhibitors *P21, P16, P19, P27* and components of the TGF-β pathway such as *TGFB1, SMADs and ACVR1B* was observed in iBCP-ALLs (**Figure 4d and Figure S9**). By contrast, iBCP-ALLs showed a robust downregulation of genes involved in DNA integrity checkpoints such as *CHEK1*, *CHEK2*, *ATM*, *ATR and RAD17*, and in double-strand break repair genes including *ERCC4*, *BRCA1, POLA1* and *RAD51* (**Figure 4e and Figure S9**). These transcriptional changes were validated by RT-qPCR (n=10 patients/group, **Figure S10**). Deregulation of DNA integrity checkpoints and DSB repair genes may well contribute to the genomic instability observed at relapse, and might explain the enrichment in C>T/G>A transitions, associated with the spontaneous deamination of 5-methylcytosine (**Figure S3, S6**).

By using FL-derived normal B-cell progenitors as controls, one could state differences between leukemic blasts and their normal counterparts but it does not allow to define transcriptomic differences within the iBCP-ALL cytogenetic groups. We have then analysed the RNA-seq data comparing the genes differentially expressed in MLL-AF4+ *versus* MLL-AF9+ and MLLwt iBCP-ALL patients, without considering normal B-cell progenitors as controls. A Gene Ontology analysis (GSEA) performed with the genes differentially expressed revealed that MLL-AF4+ patients show, as compared to both MLL-AF9+ and MLLwt patients, a significant upregulation of genes associated to cellular catabolism, coupled to a significant downregulation of negative regulators of PI3-MAPK pathway, as well as of genes involved in lymphoid differentiation and RNApol II transcriptional regulation (**Figure 5**). This suggests, respectively, a metabolic change in MLL-AF4+ cells towards a rapid energy generation while reinforcing the basal hyperactivation of the PI3-MAPK pathway by RAS mutations (**Figures 1,2**), a poorly differentiated cellular origin of t(4;11), and an impairment of the normal function of AF4, a key component of the RNApol II transcription complex.

Deep-sequencing analysis of B-cell Receptor (BCR) repertoires suggest a HSC/early pre-VDJ progenitor as the cell-of-origin for t(4;11) and RAS mutations.

We next analysed BCR repertoires to gain insights into the immunoglobulin heavy chain (IgH) rearrangement clonal composition of paired DX-REL samples from t(4;11)+ iBCP-ALL (n=4 pairs). BCRs are generated through DNA recombination during B-cell differentiation and represent unique markers for each B-cell clone. Because the BCR sequence provides a molecular tag for each B-cell clone high-throughput sequencing of BCR provides a detailed analysis of the B-cell populations dynamics and clone tracking.[42,43] BCR sequencing was therefore performed to address whether i) t(4;11)+ iBCP-ALL cells expressed fully rearranged B-cell receptors from which increased levels of B-cell clonal expansion may be observed and ii) to determine if there are detectable levels of B-cell clonal persistence over time indicative of B-cell clonal survival. BCR sequencing was performed on t(4;11)/MLL-AF4+ iBCP-ALL PB samples (blasts>98%) using a PCR-based method[37] with additional incorporation of unique molecular barcodes, allowing for accurate quantitation of relative B-cell clone frequency. After BCR sequence filtering, each sample yielded between 1,583-46,863 BCRs (1,213-38,426 unique BCRs) (**Table S5**).

We firstly delineated the relative clonality of these patients, and found that the BCR repertoires from t(4;11)+ patients did not exhibit significantly expanded VDJ rearranged B-cell clones (**Figure 6a**) either at diagnosis or relapse compared to healthy PB samples (**Figure 6b**). This is in contrast to non-MLL BCP-ALL patients (n=5) including 3 t(1;19)/TCF3-PBX1+ (EF2-PBX1+) patients, one t(12;21)/ETV6-RUNX1+ (TEL-AML1+) and one t(9;22)/BCR-ABL1+, which were all found significantly clonal, with large B-cell clones comprising ~3-40% of total BCRs (**Figure 6b-c**).[37] Given the persistence of both t(4;11) and RAS mutations in MLL-AF4+ iBCP-ALL, the lack of B-cell clonal expansion or persistence supports the model that t(4;11)/MLL-AF4+ iBCP-ALL malignant cells are developmentally stalled at pro-B stage, and that the cellular origin of such genomic drivers has to be a pre-VDJ stem/progenitor cells.

Finally, in order to understand whether the fetal cell-of-origin in iBCP-ALL lies upstream of committed B progenitors, we compared the transcriptome of iBCP-ALL blasts (n=42) with that of highly purified human FL HSPC populations (n=3-7 for each population) (**Figure 7a,b, Table S6)** by RNA-sequencing. In keeping with the results of the BCR analysis, our principal component analysis (PCA) revealed a gene expression signature for primitive Lin-CD34+CD38-CD19- FL HSPCs (HSC, MPP and LMPP; which lie upstream of B progenitors) very similar to t(4;11)+ iBCP-ALL, while FL-committed B progenitors (CBP) clustered as a transcriptionally different entity (**Figure 7c)**.

DISCUSSION

We set out to perform multi-layered sequencing on a large cohort iBCP-ALL patients, all enrolled in the international, collaborative Interfant treatment protocol. The fact that all patients were identically treated provides legitimacy and confidence in potential correlations of clinical value. Our study revealed an average of 2,5 non-silent SNVs, 2-fold higher than that reported by Andersson AK *et al*[20], likely reflecting the 3-fold larger sequencing coverage. This silent mutational landscape, even in non-MLL iBCP-ALLs, likely reflects the very young age of these patients, reinforcing the notion that infant cancer is a developmental disease with no enough time to develop somatic mutations. We also found the only recurrent, but subclonal, mutations to occur in the *KRAS* and *NRAS* genes (gain-of-function mutations), although the frequency of subclonal *NRAS* mutations are significantly higher in t(4;11)+ patients. In line with our previous work we found no recurrent mutations in the *FLT3* gene.[40]

Analysis of clonal evolution of *RAS*-mutated clones from diagnosis-to-relapse revealed that one third of the patients still carry *RAS* mutations at relapse, whereas the other two thirds of relapses have lost the diagnostic *RAS* mutation. This is in accordance with recently published data by Trentin *et al.*[36], and suggest that in some patients the therapy is able to eliminate the *RAS*-mutated clone, while in other patients the *RAS* mutation seems to confer chemo-resistance, allowing these clones to evade treatment[44]. Intriguingly, ~25% of the patients carry more than one *RAS*-mutated clone at diagnosis, indicating a selection bias towards mutations in the *RAS* genes, or activated RAS pathways during leukemic transformation. From this perspective, the occurrence of patients carrying multiple distinct clones with activated RAS pathways may point to convergent evolution of clones capable of controlling the proliferation rate. However, arguing against this is the substantial representation of patients not carrying *RAS* mutations at all. Hence, the role of *RAS* mutations in t(4;11)+ iBCP-ALL remains obscure, and the available data suggests that RAS pathway mutations are unlikely leukemia-initiating lesion. Indeed, Tamai *et al.*[45] showed that leukemogenesis of transgenic mice expressing human MLL-AF4 could be significantly accelerated by *KRAS* mutations. However, although activated *KRAS* did cooperate with MLL-AF4 in human cord blood (CB)-derived CD34+ hematopoietic stem/progenitors to promote extramedullary infiltration and CNS infiltration it failed to initiate leukemia in engrafted mice.[27] Importantly, we report a lack of correlation between RAS status and parameters associated to diagnostic or disease outcome such as OS, EFS, CNS, gender, % of blasts, WBCs and age, further supporting that RAS mutations are not leukemia-initiating/propagating lesions.

Clearly, this brings us back to the central question of whether or not MLL-AF4 by itself is sufficient to initiate BCP-ALL in humans. The silent mutational landscape herein observed and by others[20], certainly votes in favor of MLL-AF4+ iBCP-ALL being initiated by a single "big-bang" transformation hit, probably in a short-lived but highly proliferative prenatal B-cell progenitor.[4] This hypothesis is supported by recent work from Lin *et al.*, who indeed demonstrated that enforced expression of a fusion transcript consisting of human MLL and murine Af4 in CB-derived CD34$^+$ HSCPs is sufficient to induce pro-B ALL in xenografted immunodeficient mice.[21,22] Yet, similar results using a human MLL-AF4 transcript remain to be established.

Although MLL-AF4 by itself may be sufficient to induce BCP-ALL without significant contributions of cooperative genetic lesions, the contribution of the *MLL-AF4* and RAS mutations to leukemogenesis should take into account the nature of both the fetal target cell for transformation and the leukemia initiating cell, according to the increasingly accepted stochastic stem cell model of B-ALL.[46,47] Here, we employed high-throughput BCR-sequencing of the IgH locus to delineate the dynamics-clonality of B-cell populations in diagnosis-relapsed pairs of t(4;11)/MLL-AF4+ iBCP-ALL. While E2A-PBX1+, TEL-AML1+ and BCR-ABL1+ pediatric patients were all significantly clonal, with a major VDJ rearranged B-cell IgH clone comprising up to 40% of total BCRs, MLL-AF4+ iBCP-ALL infants exhibited a BCR repertoire composed of thousands of minor, non-expanded VDJ rearranged IgH B-cell clones. Because MLL fusions are clonal and RAS mutations are found in clones of relative big size, this suggests that MLL fusions +/- RAS mutations are likely to originate in primitive fetal progenitors that have a germline or an incompletely rearranged (DJ) IgH locus.[48] Indeed, an unsupervised comparison of the transcriptome of FL HSPC populations and iBCP-ALL blasts suggests that while the gene expression of primitive FL HSPCs (Lin-CD38-CD34+CD19- populations) is similar to iBCP-ALL, FL B progenitors (CD34+CD19+) are transcriptionally distinct. Our data elegantly reinforces previous FISH observations suggesting that a primitive "pre-VDJ" stem/progenitor (perhaps CD34+CD19-) may represent the cell wherein both t(4;11) and RAS mutations arise.[14,31,49]

Cooperative leukemogenic events in iBCP-ALL may need to be sought beyond genetic insults; for instance, epigenetic and transcriptomic deregulation. MLL-AF4 might only induce BCP-ALL in cells that meet certain epigenetic and transcriptomic make-up criteria, either influenced by certain micro-environmental cues, or characteristic to the cell-of-origin.[31] Indeed, lesions such as RAS mutations may contribute to disease pathogenesis only against certain intrinsic epigenetic or transcriptomic backgrounds present in the cell in which the *MLL* translocations occurred[50,51]. This is supported by the limited impact of RAS mutations in transcriptomic signatures associated with leukemia origin, development and pathogenesis, although this may be likely due to the subclonal nature of *RAS* mutations.[38] However, in line with the reported contribution of RAS mutations in extramedullary infiltration of MLLr BCP-ALL blasts[27], RAS-mutated patients displayed a transcriptomic signature associated to migration.

The functional and molecular contribution of the reciprocal fusion genes resulting from the derivative translocated chromosomes remains obscure in cancer. The AF4-MLL genomic fusion was previously detected in 80-85% of t(4;11) patients.[5,52] Our "multi-layered Omics" approach allowed for the exact characterization of the t(4;11) molecular DNA/RNA breakpoints and the identification of those patients expressing the reciprocal AF4-MLL fusion. We now report that the AF4-MLL reciprocal fusion is expressed in only 50% of the t(4;11)+ iBCP-ALL patients. Strikingly, there was a previously unrecognized and very significant positive correlation between the upregulation of the *HOXA* gene cluster and the expression of AF4-MLL. Of note, a recent study showed that approximately half of t(4;11) patients do not have an activated HOXA signature.[44,53,54] Furthermore, in the recent MLL-Af4-induced B-ALL xenograft model MLL-Af4 failed to bind to HOXA genes and therefore HOXA gene expression was not upregulated.[21] This is experimentally supported by ChIP-seq analysis performed in human embryonic stem cells transduced with MLL-AF4, AF4-MLL or both showing a significant enrichment of H3K79 methylated regions specifically associated with *HOX-A* cluster genes in double fusion-expressing hematopoietic derivatives, establishing a functional and molecular cooperation between MLL-AF4 and AF4-MLL fusions during human hematopoietic development (data not shown). Strikingly, AF4-MLL-expressing patients displayed 5-fold higher EFS and a 3-fold higher OS than t(4;11)+ iBCP-ALL patients lacking AF4-MLL expression which is in line with previous reports suggesting that high HOXA gene expression is associated with improved survival and lower risk of relapse.[22,39] Because the expression of AF4-MLL is not analyzed in routine molecular diagnosis, our "multi-layered Omics" approach was critical to unravel the association between AF4-MLL and HOXA expression, thus identifying a novel subgroup of t(4;11)+ iBCP-ALL with better clinical outcome. Very important for the diagnostic routine/clinical practice is that when the expression of AF4-MLL was evaluated in a Cox model adjusting for risk stratification (medium risk or high risk according to Interfant-06 protocol), it retained its prognostic significance.

Mechanistically, AF4-MLL contains the SET domain disrupted from its "specification domain", the N-terminal portion of MLL, which binds to MEN1 and LEDGF thus shaping the gene targeting module of the MLL gene. When AF4-MLL is expressed, the N-terminal portion is substituted by the AF4 N-terminus (AF4N) which is the crucial domain to bind to and strongly activate RNA polymerase II (RNAP II) for transcriptional elongation. Thus, expression of A4M-MLL may induce robust RNAP II-dependent gene transcription by overwriting the elongation control process in a dominant fashion.[55–58] We hypothesize that a likely function of AF4-MLL could be to prepare the ground for MLL-AF4 or other transcription factors to skew normal and leukemic hematopoietic cell fate decisions. This also explains why MLL-AF4 but not AF4-MLL seems to be necessary in 100% of patients.

Despite being a developmental cancer, infant BCP-ALL patients did not show a reactivation of pluripotent or embryonic-like gene expression signatures as revealed by RNA-seq. Additional research is required to decipher the nature of the insults initiating *MLL*r iBCP-ALL, as so far we can only speculate on the data currently available. Whole genome pyrosequencing will likely provide unique insights into the DNA methylome landscape of this mutational silent iBCP-ALL. This study has clinical implications in the diagnostic risk-stratification of t(4;11)+ iBCP-ALL.

AUTHOR CONTRIBUTIONS

A.A-D., R.B-R: designed and performed experiments, analysed data and wrote the manuscript. C.B, P.S., T.M., C.R., A.R, and M.G.V: designed and performed experiments and analysed data. R.W.S., M.B., G.C., P.B., P.S., M.G.V, P.D.L, I.R, and R.P.: provided leukemic samples and clinical data. I.V. and P.M.: conceived the study, designed experiments, analysed data and wrote the manuscript.

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CONFLICT OF INTEREST DISCLOSURE

The authors have nothing to disclose.

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LEGENDS TO FIGURES

Figure 1. Somatic mutations detected by WES in the discovery cohort of iBCP-ALL. (A) Total number of mutations identified in each individual patient. Total number of non-synonymous mutations (yellow area, right Y axis) and MAF for each mutation (individual dots, left Y axis) are represented. **(B)** Oncodrive software identified PI3k-RAS pathway as the only recurrently mutated pathway in iBCP-ALL. Distribution of mutations in genes of the PI3k-RAS pathway is shown for all patients within the three BCP-ALL subgroups (n=42 patients, 27 t(4;11)+, 5 t(9;11)+ and 10 MLLwt).

Figure 2. Frequent somatic mutations in *RA*S genes in both discovery and validation cohorts. (A) Specific *KRAS* and *NRAS* mutations recurrently found for each patient by high coverage targeted sequencing. **(B)** Proportion of patients with mutations in *KRAS* (brown), *NRAS* (yellow) or both (grey) within the three iBCP-ALL subgroups. **(C)** MAF of *KRAS* (brown squares) or *NRAS* (yellow circles) mutations in each individual patient. Discovery cohort, n=42; validation cohort, n=82.

Figure 3. Clonal evolution and genomic instability at relapse. (A) Total number of mutations identified for each patient in paired diagnostic-relapse samples. Total number of non-synonymous mutations (yellow area, right Y axis) and MAF for each mutation (individual dots, left Y axis) are represented in paired diagnostic and relapsed (R) samples. **(B)** Circus plot representation of the total number of mutations identified at diagnosis and relapse for a representative patient (MA4_17). Genomic rearrangements are represented with lines connecting both breakpoints. Copy number alterations (blue=gains, red=losses) are represented in the outer grey circle. Somatic mutations (both SNVs and indels) are depicted in the centre of the circle and the affected gene is indicated. **C)** Graphic representation of clonal evolution in paired diagnostic (DX)-relapsed (RL) samples. The number of unique somatic mutations called at diagnosis (orange), relapse (yellow) or shared between DX and REL

(red) are indicated. Bigger gene's name indicate higher MAFs for the mu*tati*ons shared at DX and REL. **(D)** Dynamics of RAS-mutated clones identified as MAF in matched DX-Remission-REL trios (n=8).

Figure 4. Transcriptional signature of iBCP-ALL samples. (A) Heatmap representing *FLT3, PROM1, MEIS1* and *HOXA* gene expression according to the BCP-ALL cytogenetic group and *RAS* mutations. **(B)** *Top panel*, heatmap showing HOXA cluster gene expression according to the expression of the reciprocal fusion *AF4-MLL*. Bottom *panel*, qPCR validating high expression of HOXA cluster genes in t(4;11) iBCP-ALL patients expressing *AF4-MLL*. **(C,D)** 4 year EFS **(C)** and OS **(D)** Kaplan-Meyer curves for t(4;11) iBCP-ALL patients according to *AF4-MLL* expression, n=43 t(4;11)+ patients. **(E)** Heatmap representation of selected genes for the signalling pathways most significantly deregulated. Right panels represent positive pathway enrichment called by GSEA software. n=42 patients, 27 t(4;11)+, 5 t(9;11)+ and 10 MLLwt.

Figure 5. Specific transcriptional differences between MLL-AF4+ and MLL-AF9+ or MLLwt iBCP-ALL patients. Here, FL-derived CD34+CD19+ progenitors were not included as normalizers in the analysis in order to avoid potential bias. A GSEA analysis was performed with the genes differentially expressed between MLL-AF4+ patients and MLL-AF9+ or MLLwt patients. MLL-AF4+ iBCP-ALL patients showed a significant overexpression of genes associated to cellular catabolism, coupled to a significant downregulation of negative regulators of PI3-MAPK pathway, as well as of genes involved in lymphoid differentiation and RNApol II transcriptional regulation as compared to both MLL-AF9+ and MLLwt iBCP-ALL patients. Bottom panels represent positive pathway enrichment called by GSEA software. n=42 patients, 27 t(4;11)+, 5 t(9;11)+ and 10 MLLwt.

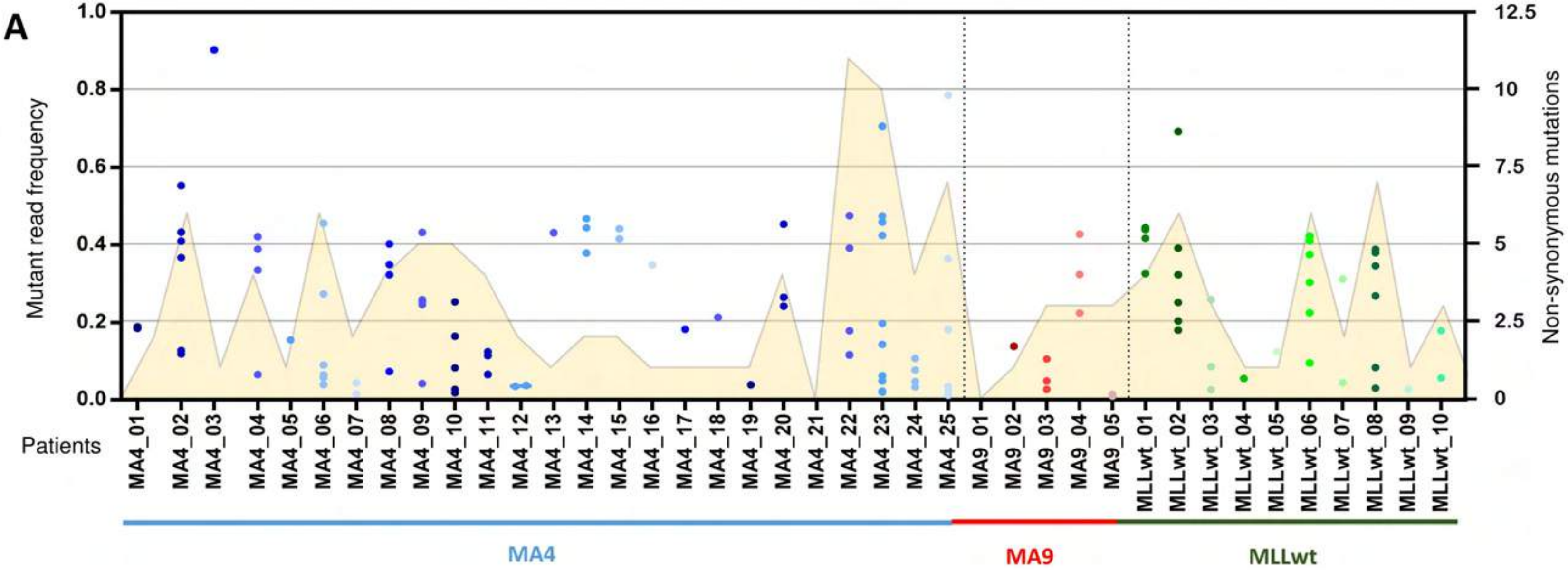
Figure 6. Analysis of BCR repertoires suggest a HSC/early pre-VDJ progenitor as the cell-of-origin for t(4;11)/MLL-AF4+ iBCP-ALL. (A) Cloud-plots of BCR repertoires from two representative t(4;11)+ BCP-ALL infants depicting the existence of many minor non-expanded B-cell clones either at diagnosis or relapse. Each vertex represents a unique BCR sequence, and relative vertex size is

proportional to the number of identical reads. **(B)** Largest BCR clone size in t(4;11)+ iBCP-ALL, healthy individuals and non-t(4;11)+ pediatric BCP-ALL. **(C)** Cloud-plots of BCR repertoires of representative t(1;19)/E2A-PBX1+, t(12;21)/TEL-AML1+ and t(9;22)/BCR-ABL+ patients showing high clonality of B-cell clones. BCP-ALL patients BCR-sequenced were: n=4 MLL-AF4+ diagnostic-relapse pairs, n=3 E2A-PBX1+, n=1 TEL-AML1+ and n=1 BCR-ABL+.

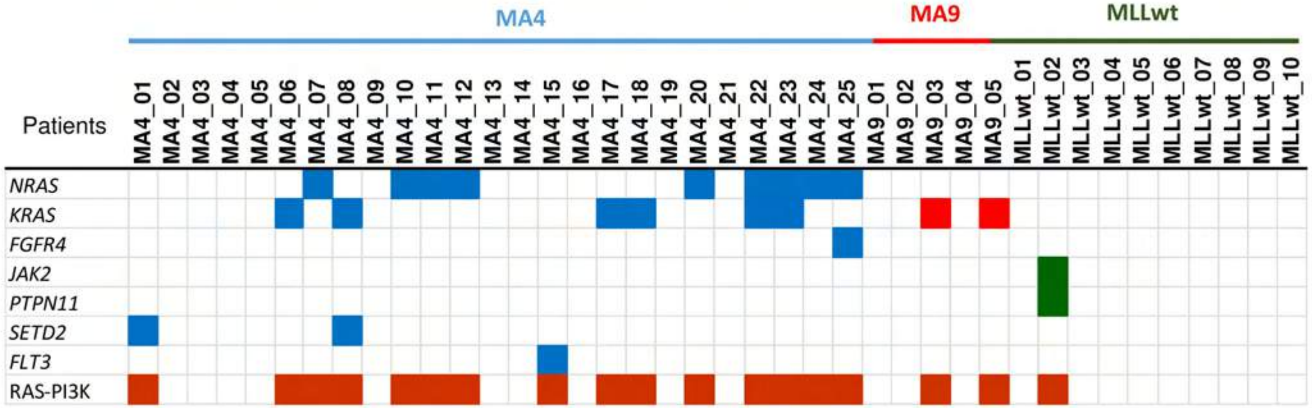
Figure 7. Comparison of the transcriptome of human fetal CD34+ HSPC populations to iBCP-ALL. (A) Schematic representation of B-cell development in human FL showing immunophenotypic definitions for HSC (hematopoietic stem cell), MPP (multipotent progenitor), LMPP (lymphoid-primed multipotent progenitor), CBP (committed B progenitor) and B cells. The onset and expected patterns of IgH rearrangements[59,60] are depicted as red arrows. **(B)** Sorting strategy for FL HSPC populations by FACS. Sort gates for each population are depicted in representative flow plots on the left. Purity of sorted populations is depicted on the right demonstrating >95% purity. (Lin, Lineage cocktail). **(C)** Principal component analysis of gene expression of iBCP-ALL samples (n=42) and FL HSPC populations (n=3-7) using the top 1000 variably expressed genes by RNA-sequencing. FL HSPC as in (A); MAF4, MLL-AF4+ iBCP-ALL; MA9, MLL-AF9+ iBCP-ALL; MLLwt, MLL wild type iBCP-ALL.

Agraz-Doblas et al. Fig. 1

A



B



Patients	MA4_01	MA4_02	MA4_03	MA4_04	MA4_05	MA4_06	MA4_07	MA4_08	MA4_09	MA4_10	MA4_11	MA4_12	MA4_13	MA4_14	MA4_15	MA4_16	MA4_17	MA4_18	MA4_19	MA4_20	MA4_21	MA4_22	MA4_23	MA4_24	MA4_25	MA9_01	MA9_02	MA9_03	MA9_04	MA9_05	MLLwt_01	MLLwt_02	MLLwt_03	MLLwt_04	MLLwt_05	MLLwt_06	MLLwt_07	MLLwt_08	MLLwt_09	MLLwt_10
NRAS							🟦			🟦	🟦	🟦								🟦		🟦	🟦	🟦	🟦															
KRAS						🟦		🟦									🟦	🟦				🟦	🟦					🟥		🟥										
FGFR4																									🟦															
JAK2																																🟩								
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SETD2	🟦							🟦																																
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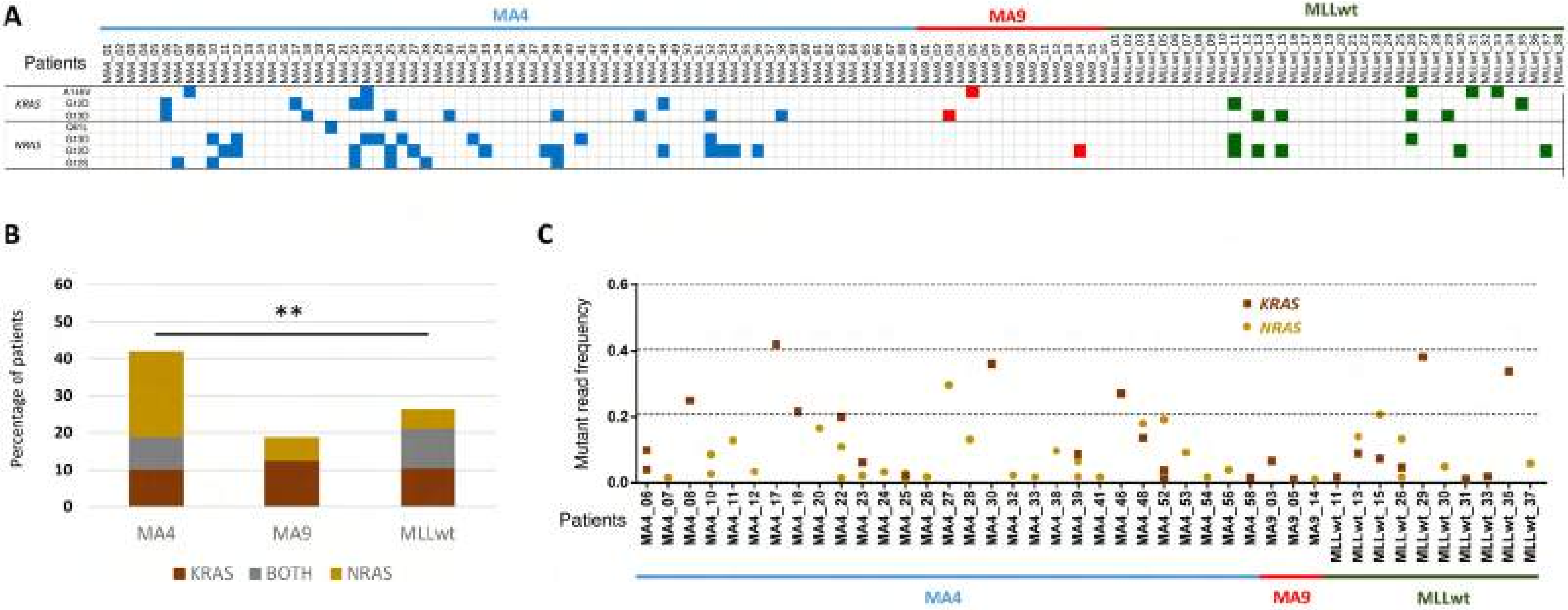
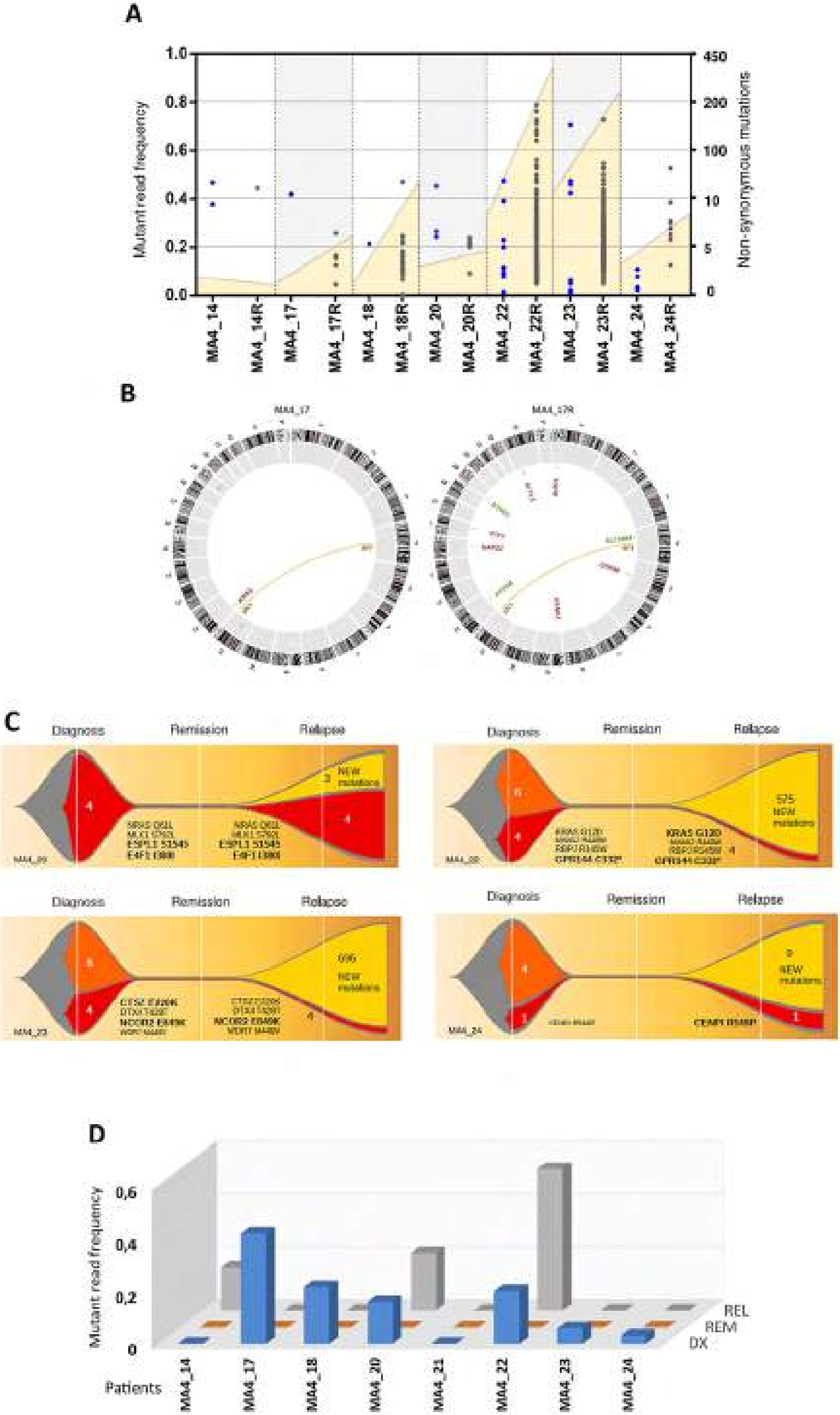
RAS-PI3K	🟧					🟧	🟧	🟧		🟧	🟧	🟧			🟧		🟧	🟧		🟧		🟧	🟧	🟧	🟧			🟧		🟧		🟧								

Agraz-Doblas et al. Fig. 2



Agraz-Doblas et al. Fig. 3



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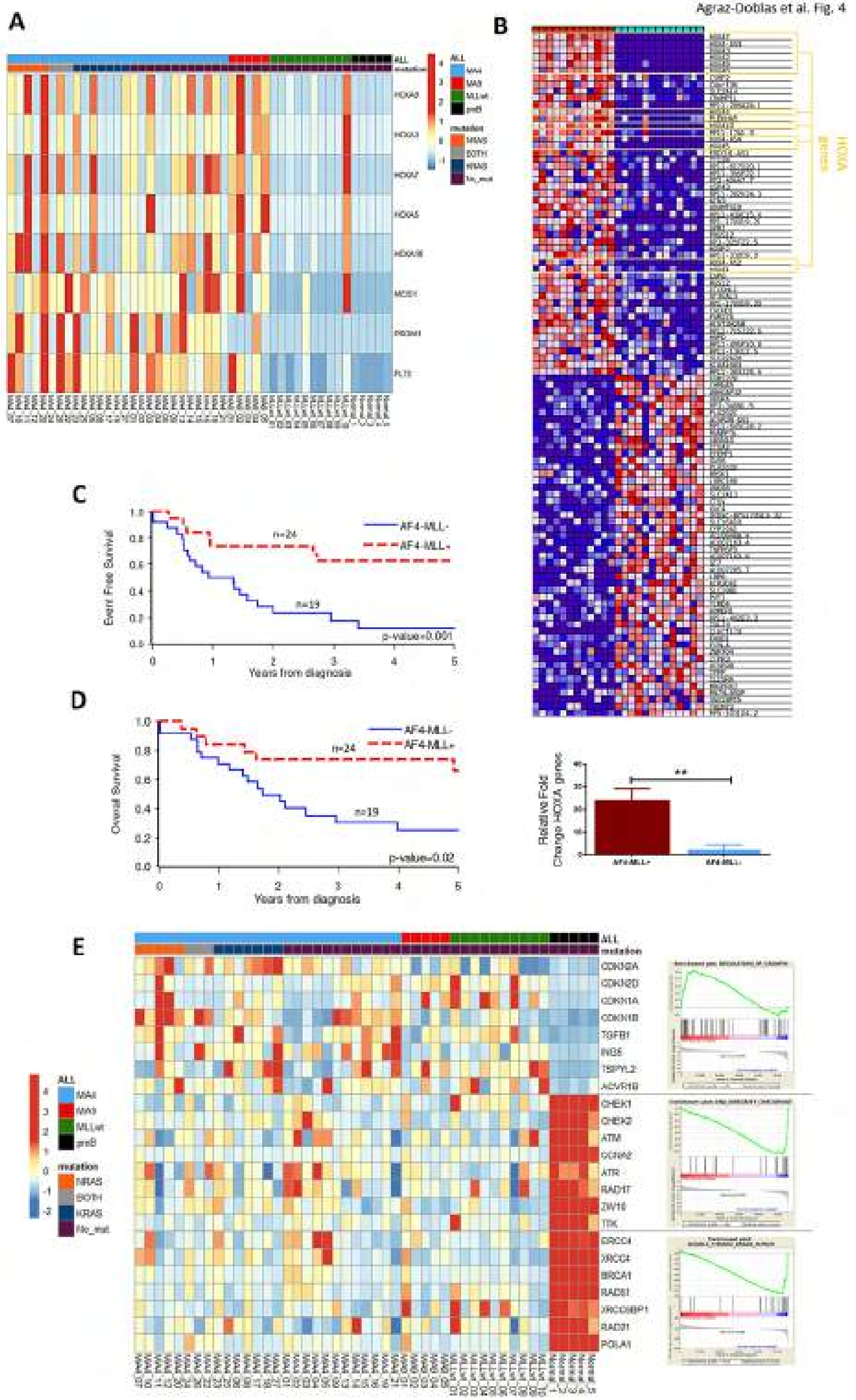

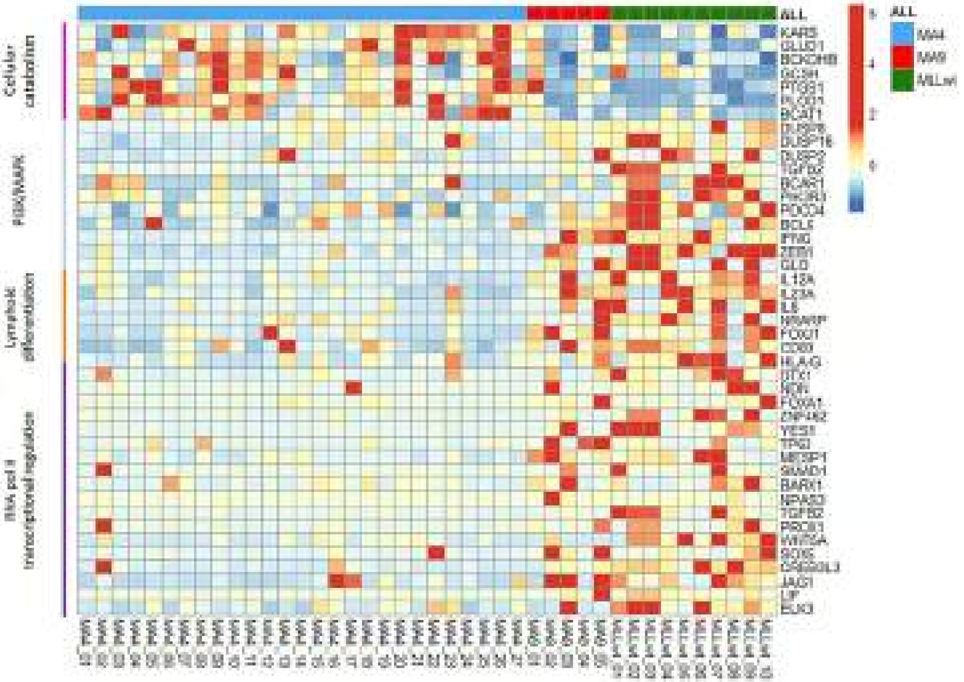
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BCL6
IFNG
ZEB1
GLI3
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IL23A
IL6
NRARP
FOXJ1
CD83
HLA-G
DTX1
NOR
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SOX5
CREB3L3
JAG1
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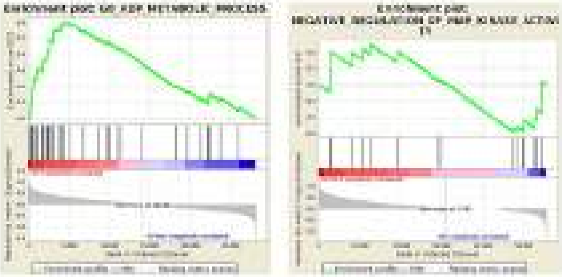
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Enrichment plot:
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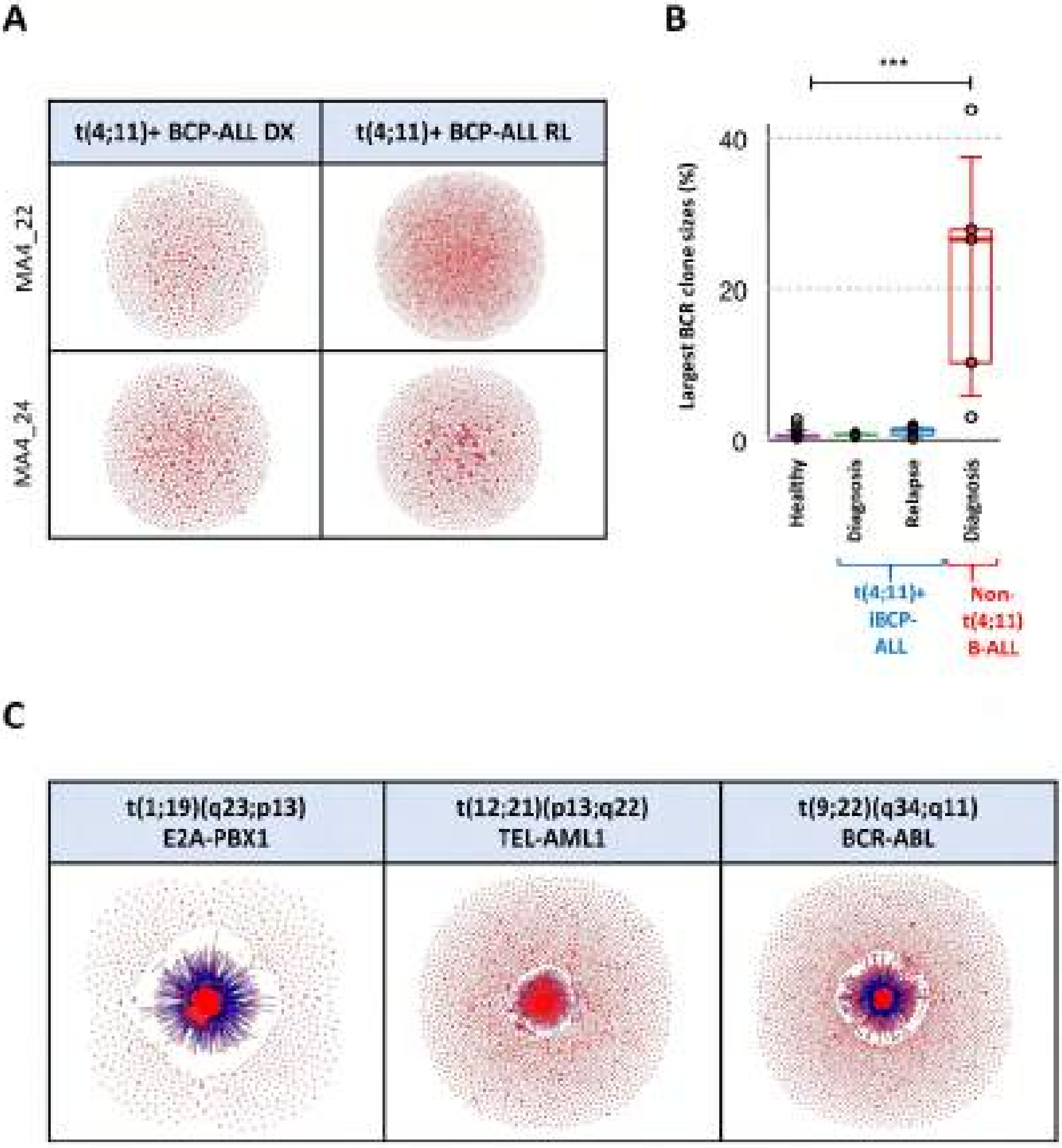
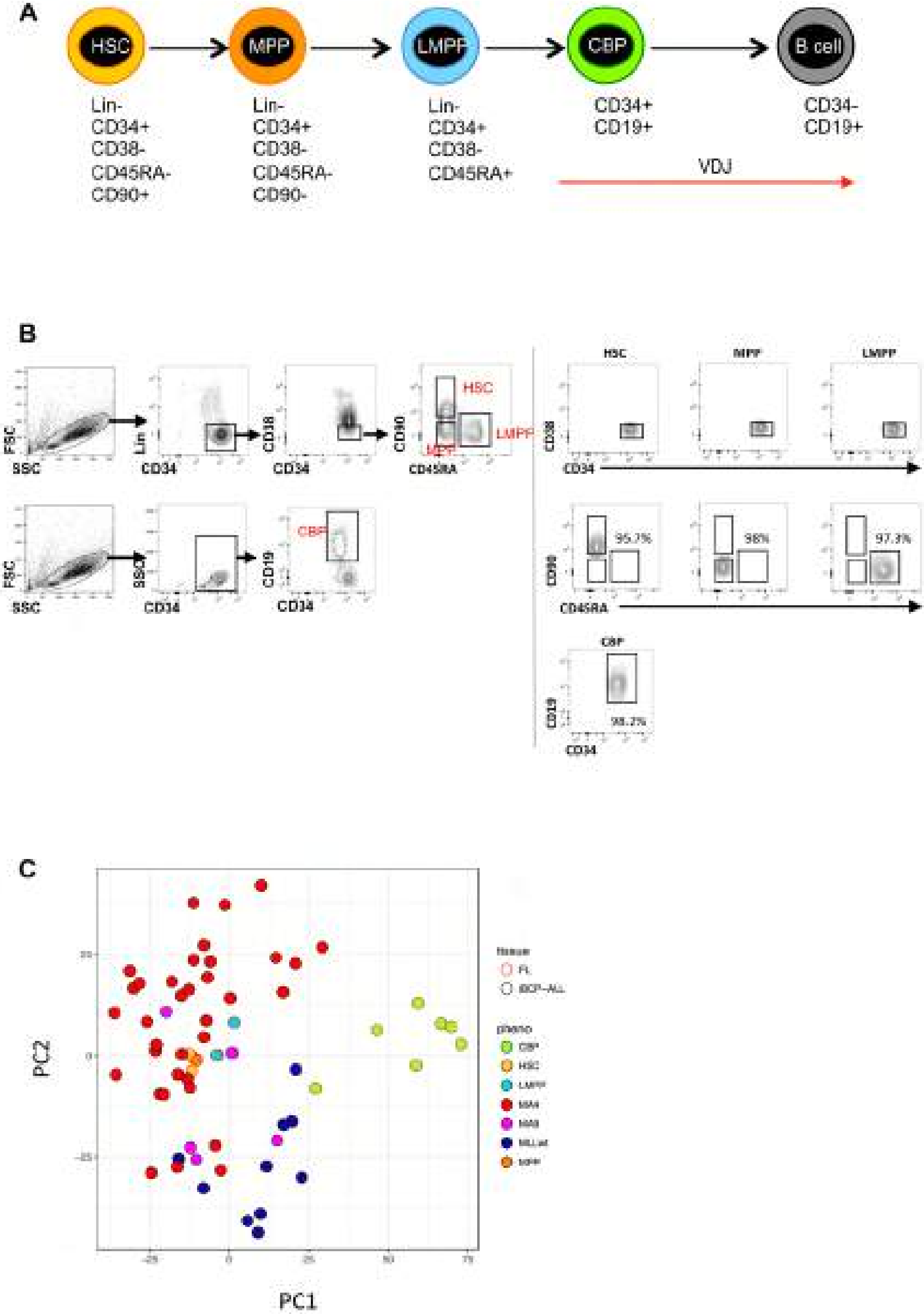
Rank in Ordered Dataset
Enrichment profile
Hits
Ranking metric scores

Agraz-Doblas et al. Fig. 6

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MA4
MA9
MLLot
MPP

Whole-exome sequencing (WES) and mutational analysis

For the discovery cohort (n=50, 42 diagnostics and 8 matching relapses), paired-end whole exome sequencing (WES) was performed on DNA extracted from FACS-purified CD34+CD19+ blasts (purity>95%) at diagnosis. For eight MLL-AF4+ iBCP-ALL patients, DNA was also collected at relapse. Two samples were discarded due to discordant diagnostic-remission SNP genotyping due to previous allogenic stem cell transplantation. We used DNA from patients at complete molecular remission to discriminate somatic from germline mutations. The Agilent Human All Exon 50 Mb v5 Kit was used for the exon-enriched genomic library generation following the manufacturer's instructions. Each library was sequenced on an Illumina HiSeq 2500 instrument using HiSeq PE Cluster Kitv3 with a 2x101 paired-end protocol. Raw sequence (100X coverage, **Figure S1**) data fastq files were subjected to quality control using FastQC v0.11.2 and mapped to the human genome (hg19) using BWA 0.7.3.[1] We used Picard 1.61 to fix-clean the alignment and to mark PCR duplicates reads, and GATK v2.2.8 to perform local realignment around small insertions and deletions (indels).[2] Paired tumor/normal bam files were used to identify putative somatic single nucleotide variants (SNVs) with our in-house written RAMSES[3] algorithm selecting mutations with a confidence score >4 and mutational frequency >0.01. We used PINDEL to detect indels.[4] A minimum of 5 independent reads of the indel and no evidence of it in the control DNA was required to report the indel. Potential germline variants were flagged away using 1000 Genomes mutation database. Functional consequence of mutations was annotated using Ensembl database v73 through the Perl API.[5] We run OncodriveFM software[6] to detect genes with evidence of selective pressure from the analysis. Gene ontology analysis was performed using GOrilla.[7]

Copy number variations (CNVs) were identified by analysing the difference in read depth for each genomic segment between tumoral and matching normal DNA using CopywriteR software.[8]

Confidence for a CNV segment boundary was determined using a series of criteria including length of flanking segments, difference of copy number between neighbouring segments, presence of sequence gaps on the reference genome and the presence of evidence of CNV in the matching germline sample. Regions of loss-of-heterozygosity were estimated using Control-Freec software with a minimal coverage per position of 5 and minimal quality per position of 10.[9] For validation of somatic mutations, DNA was whole-genome amplified using Repli-g Mini kit (Qiagen) and PCR fragments containing the potential mutation were generated for the diagnostic, control and relapsed samples using the FastStart High Fidelity PCR System® (Roche) and ultrasequenced at 30000X in a MiSeq (Illumina). CNV mutations were validated by qPCR using Luminaris Color HiGreen PCR Master Mix (Thermo Fisher).

Whole-genome sequencing (WGS)

Whole-genome sequencing (WGS) was performed in all patients of the discovery cohort (n=50). Briefly short-insert paired-end libraries were prepared with a PCR-free protocol. TruSeq™DNA Sample Preparation Kit v2 (Illumina) and the KAPA Library Preparation kit (Kapa Biosystems) were used with modifications. In brief, 0.5-1.0 µg of genomic DNA was sheared on a Covaris™ instrument, and DNA fragments of 220-550bp were selected using AMPure XP beads (Agencourt, Beckman Coulter). Fragmented DNA was end-repaired, adenylated and ligated to Illumina specific indexed paired-end adaptors. Libraries were sequenced using the TruSeq SBS Kitv3-HS (Illumina) in 2x76 bp protocol on a HiSeq 2500 instrument (Illumina). A minimum of 70 million reads were generated for each sample (**Figure S1**). Sequence data was mapped as described above. Structural variations including inter-chromosomal translocations, intra-chromosomal translocations, inversions, deletions, duplications and insertions were identified with Delly[10] using the default parameters and annotated using Ensembl perl API.[5] Thirty low-coverage sequenced normal genomes from the 1000 Genomes

Project database were used to filter potential false positives. Structural variations were PCR-validated using primers spanning the breakpoint. Sanger sequencing of the PCR products was performed to detect the breakpoint at the base pair level.

RNA-sequencing (RNA-Seq)

RNA-seq was performed in all patients of the discovery cohort at diagnosis (n=42). The RNASeq libraries were prepared from total RNA using the TruSeq™ RNA Sample Prep Kit v2 (Illumina), and were sequenced on HiSeq2500 platform (Illumina) in paired-end mode with a read length of 2x76bp using the TruSeq SBS Kit v3 (**Figure S1**). We generated a mean of 40 million paired-end reads per sample that were aligned to the human genome (hg19) using Tophat.[11] All predicted transcripts were analysed *in-silico* and those missing start or stop codon were filtered out. Differentially expressed genes (DEG) were identified using HTSeq and DESeq.[12,13] Differential expression of RNA transcript levels was performed with R packages and a minimum of 3 counts for a gene in more than two independent samples were required. A fold change >2 with a q-value<0.05 were used to call DEG. Signalling pathway enrichment was analysed using the Gene Set Enrichment Analysis (GSEA) tool.[14] For RNA-Sequencing of FL HSPCs, 100 cells from each subpopulation were FACS-sorted, followed by RNA extraction and amplification, and cDNA library preparation using Nextera Index kit as per protocol. Indexed cDNA libraries were sequenced using Illumina HiSeq2500 to generate 100 and 150bp paired-end reads, yielding >30 million reads per sample. For comparison of FL HSPCs and iBCP-ALL RNASeq data, all FASTQ files were mapped to GRCh38 of the human genome and counted using STAR v2.4.2a[2] and featureCounts v1.5.5-p12.[15,16] Downstream analysis was performed in R (3.4.3) with Limma[17] after accounting for batch effects. To validate RNA-Seq data, reverse transcription was performed using the PrimeScript cDNA Synthesis kit® (Takara) and the mRNA expression of a selected group of genes was performed by qRT-PCR using Luminaris Color

HiGreen qPCR Master Mix with the StepOnePlus RT-PCR system. Relative expression was calculated using the CT method ($2^{-\Delta CT}$). Sequencing data is publicly available at the European Nucleotide Archive under the accession number PRJEB23605.

Sequencing and analysis of B-cell receptor (BCR) VDJ repertoires

Analysis of BCR repertories was performed as previously described in detail[18], using standard BIOMED-2primers in n=4 t(4;11)/MLL-AF4+ diagnostic-relapse pairs, n=3 t(1;19)/E2A-PBX1+, n=1 t(12;21)/TEL-AML1+ and n=1 t(9;22)/BCR-ABL+.[19] Briefly, reverse transcription was performed and the cDNA was cleaned-up with Agencourt AMPure XP beads and PCR amplified with V-gene multiplex primer mix and 3' universal reverse primer using KAPA protocol. Primers are provided in **Table S2**. Libraries were prepared using Illumina protocols and sequenced using 300bp paired-ended MiSeq. Raw MiSeq reads were filtered for base quality (median Phred score>32) using QUASR (http://sourceforge.net/projects/quasr/).[20] MiSeq forward and reverse reads were merged together if they contained identical overlapping region of >50bp, or otherwise discarded. Universal barcoded regions were identified in reads and orientated to read from V-primer to constant region primer. The barcoded region within each primer was identified and checked for conserved bases. Primers and constant regions were trimmed from each sequence, and sequences were retained only if there was >80% per base sequence similarity between all sequences obtained with the same barcode, otherwise discarded. Sequences were trimmed to give only the region of the sequence corresponding to the variable (V-D-J) regions. Sequences without complete reading frames and non-Ig sequences were removed and only reads with significant similarity to reference IgH and J genes from the IMGT database were retained using BLAST[21] and not shared between unrelated individuals (public BCRs). The network generation algorithm and network properties were calculated as in Bashford-Rogers *et al.*[22] Each vertex represents a unique sequence, where relative vertex size is proportional to the number of identical reads. Edges join vertices that differ by single nucleotide non-indel differences and clusters are collections of related, connected vertices.

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2013;368(1614):20120205–20120205.

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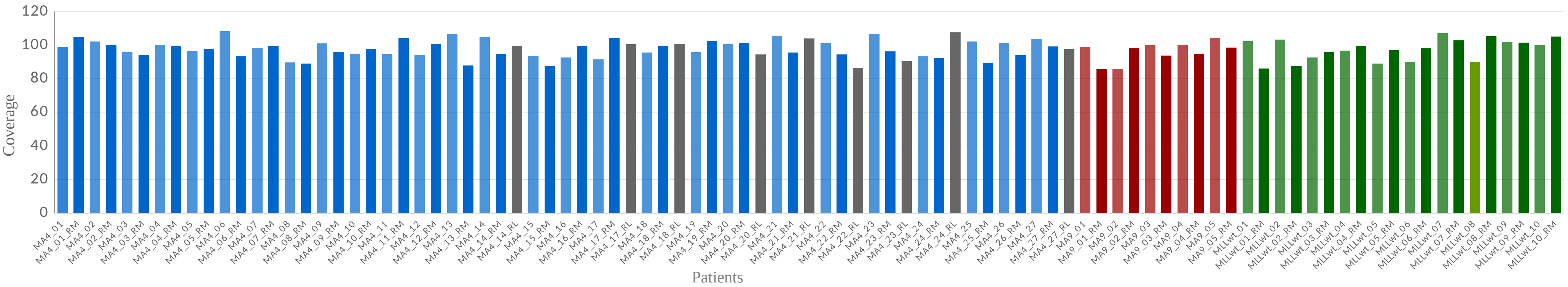
Supplementary Figures

Table of Contents

Suppl. Figure 1. Summary of coverage and number of reads.

(A) Coverage per patient for whole-exome sequencing. (B) Number of reads generated in RNA sequencing. (C)Number of reads generated in whole-genome sequencing. Samples are grouped according to the specific MLL translocation (MLL-AF4 in blue, MLL-AF9 in red and MLLwt in green). Black bars represent the reference control samples ($CD34^+$ $CD19^+$ B-cell progenitors) in RNAseq. In exome-data experiment, for each patient the sequencing data generated at diagnosis (light color) and remission samples (dark color) are shown. Relapses are indicated in grey. Orange areas in (C) represent the number of PCR duplicates.

A



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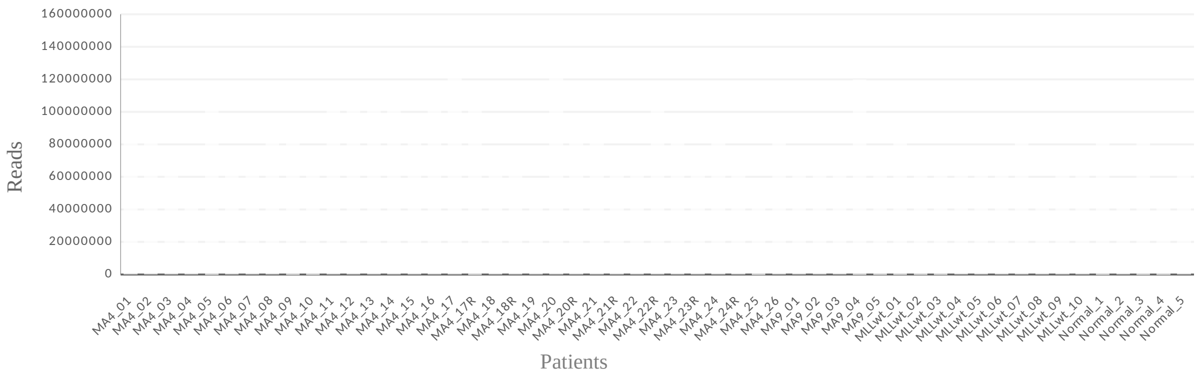

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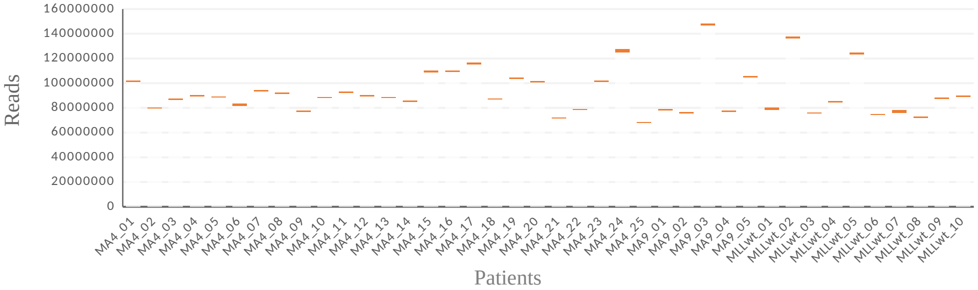
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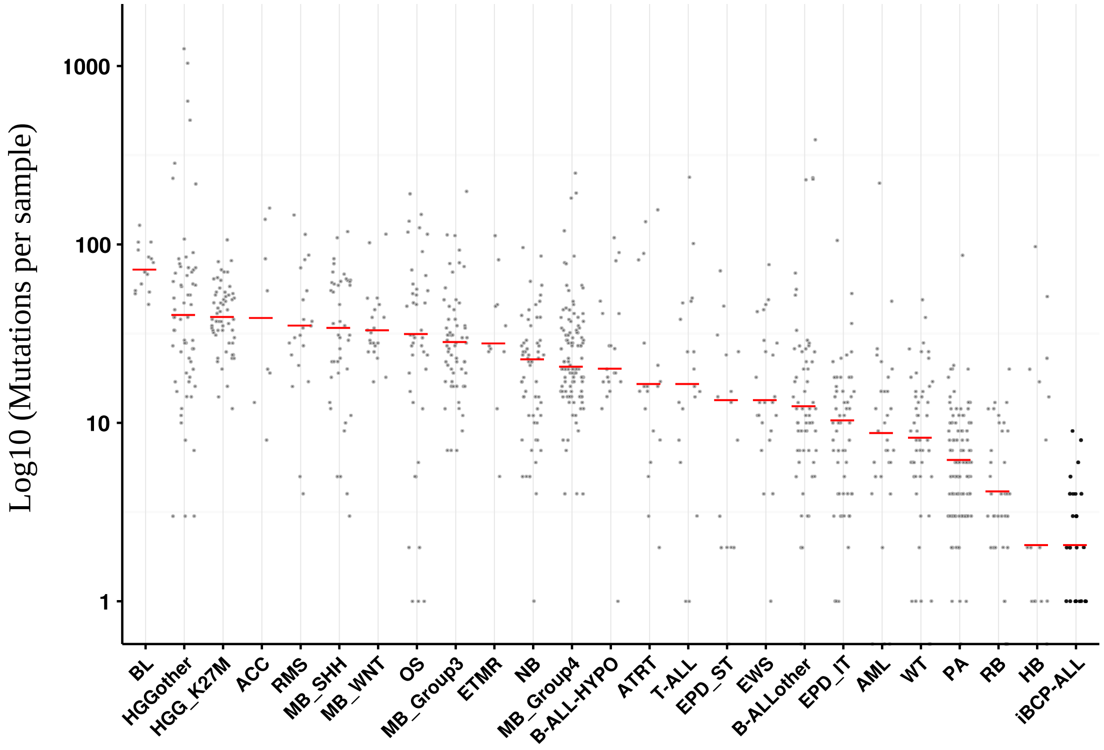
MLLwt_10
Patients

Suppl. Figure 2. Mutational load in childhood cancers.

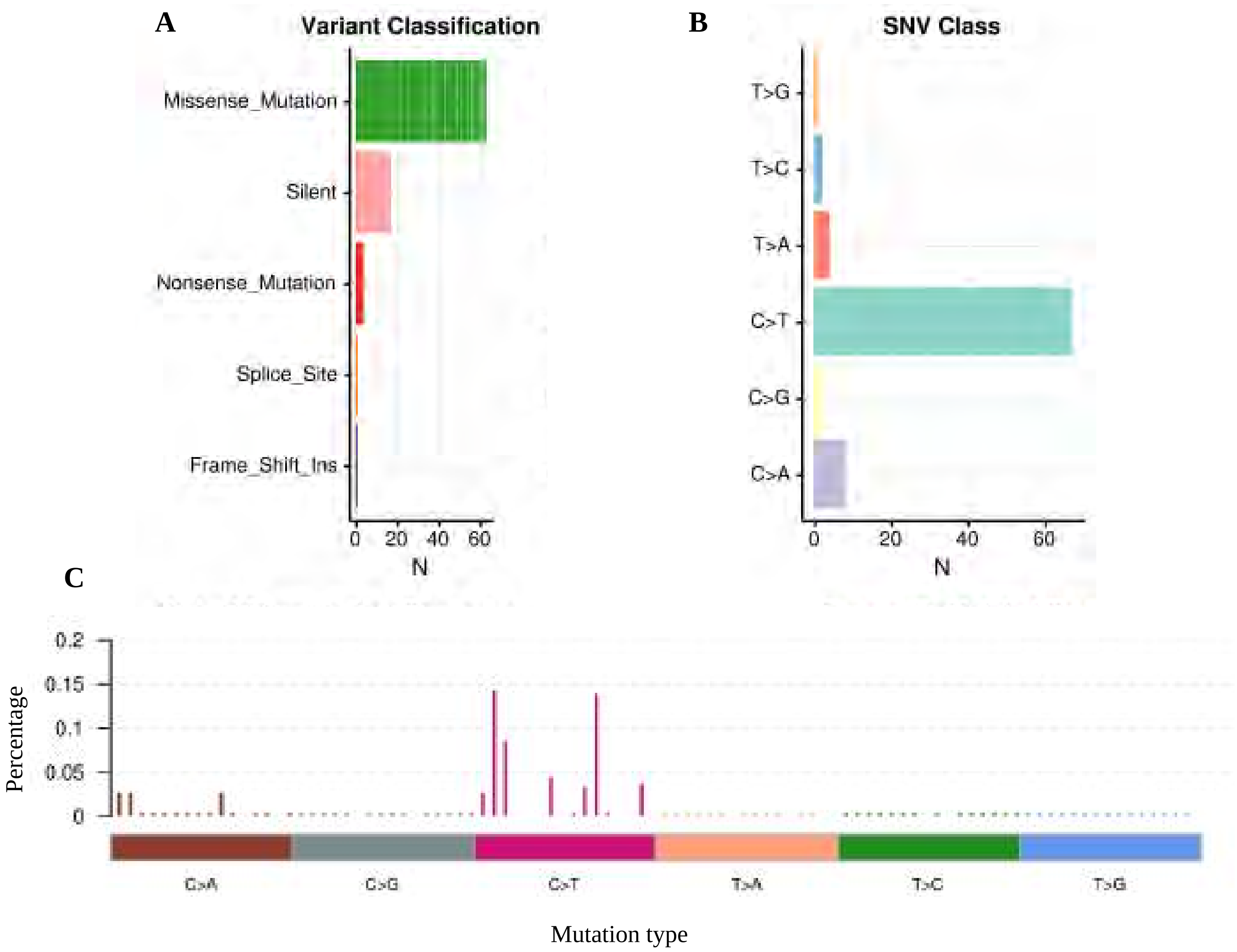
Comparison of the mutational load across 24 different cancer cohorts (Grobner SN *et al*, Nature, 2018) revealing that iBCP-ALL represents the cancer type with the most stable genome (2.5 mutations per genome). Burkitt's lymphoma (BL) is the highest mutated childhood cancer with an average of 70 mutations per genome.



BL	Burkitt's Lymphoma
HGG	High grade glioma
ACC	Adrenocortical carcinoma
RMS	Rhabdomyosarcoma
MB	Medulloblastoma
OS	Osteosarcoma
ETMR	Embryomal tumor with multilayered rosettes
NB	Neuroblastoma
B-ALL-Hypo	Hypodiploide B-ALL
ATRT	Atypical teratoid rhabdoid tumor
T-ALL	T cell ALL
EPD	Ependynoma infratentorial
EWS	Ewing's sarcoma
B-ALL other	B-other ALL (absence of numeric/structural chromosomal abnormalities)
AML	Acute Myeloid Leukemia
WT	Wilms tumor
PA	Policytic astrocytoma
RB	Retinoblastoma
HB	Hepatoblastoma

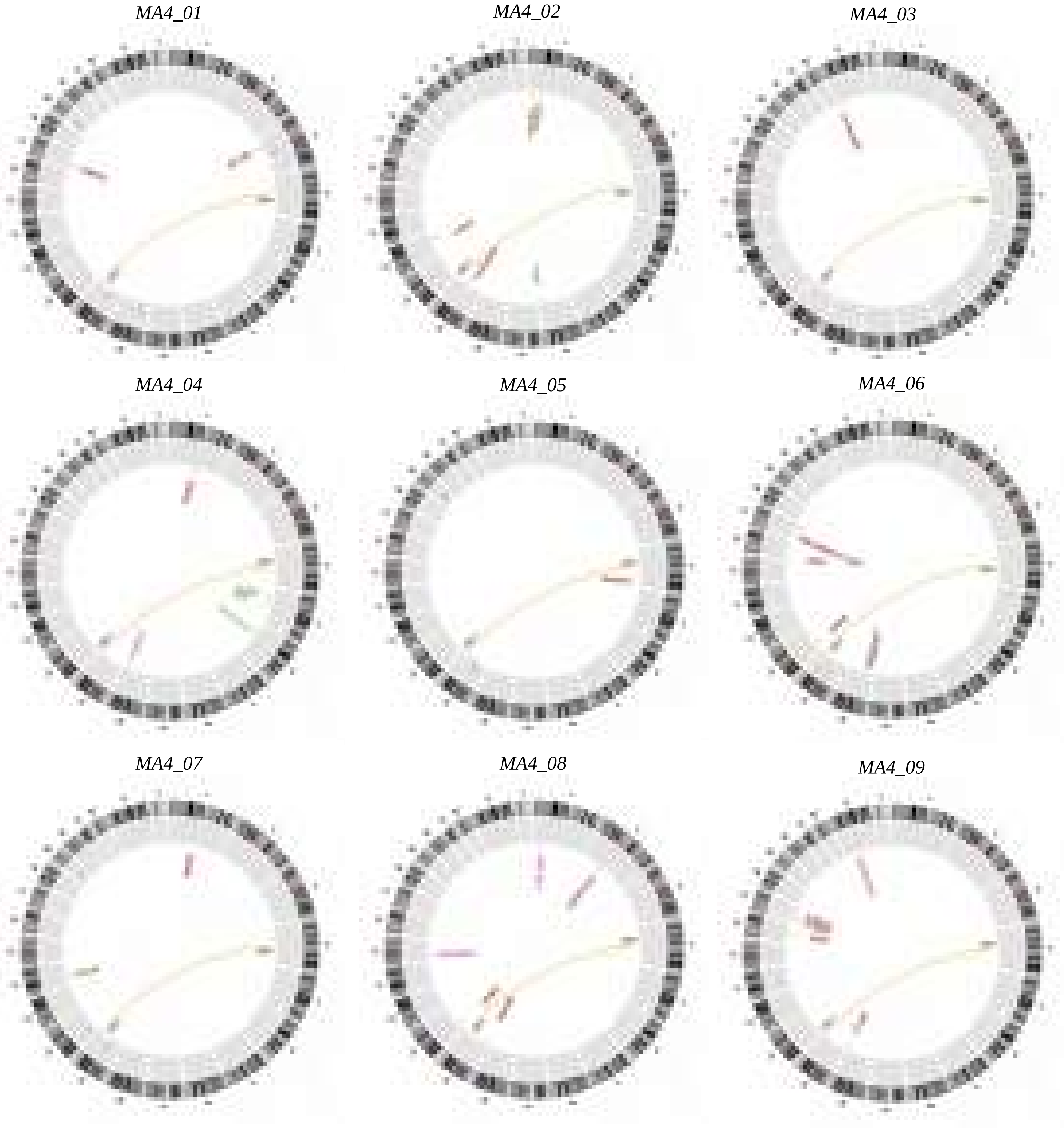
Suppl. Figure 3. Summary of functional and molecular distribution of mutations and mutational signature analysis in the MLL-AF4 subgroup.

A) Distribution of mutations by functional consequence. B) Distribution of mutations according to the specific base mutation. C) Significant enrichment score of signature 1 in diagnosis according to the mutational signatures described by Alexandrov et al. (Alexandrov LB, Nik-Zainal S, Wedge DC, et al. Signatures of mutational processes in human cancer. *Nature*. 2013;500:415–21.) based on 7000 cancer genomes. This signature is associated with a spontaneous deamination of 5-methylcytosine and very few indels. In addition, this signature is associated with a small number of insertions and delections.



Suppl. Figure 4. Circos plots of MLLr at diagnosis.

Representation of the total number of mutations identified at diagnosis for each patient. Copy number alterations (blue:gains, red:losses) are represented in the outer grey circle. Gene mutations (both SNVs and indels) are represented in the centre of the circle next to the name of the gene affected. Genomic chromosomal rearrangements are represented with orange lines connecting both breakpoints. Gene symbols: Red=Missense mutations; Green=Silent mutations; Purple=Nonsence,stop-lost/splice-site. Brown=*MLL* and *AF4*.



MA4_01 *MA4_02* *MA4_03*

MA4_04 *MA4_05* *MA4_06*

MA4_07 *MA4_08* *MA4_09*

MA4_10

MA4_11

MA4_12

MA4_13

MA4_14

MA4_15

MA4_16

MA4_17

MA4_18

MA4_19

MA4_20

MA4_21

MA4_22

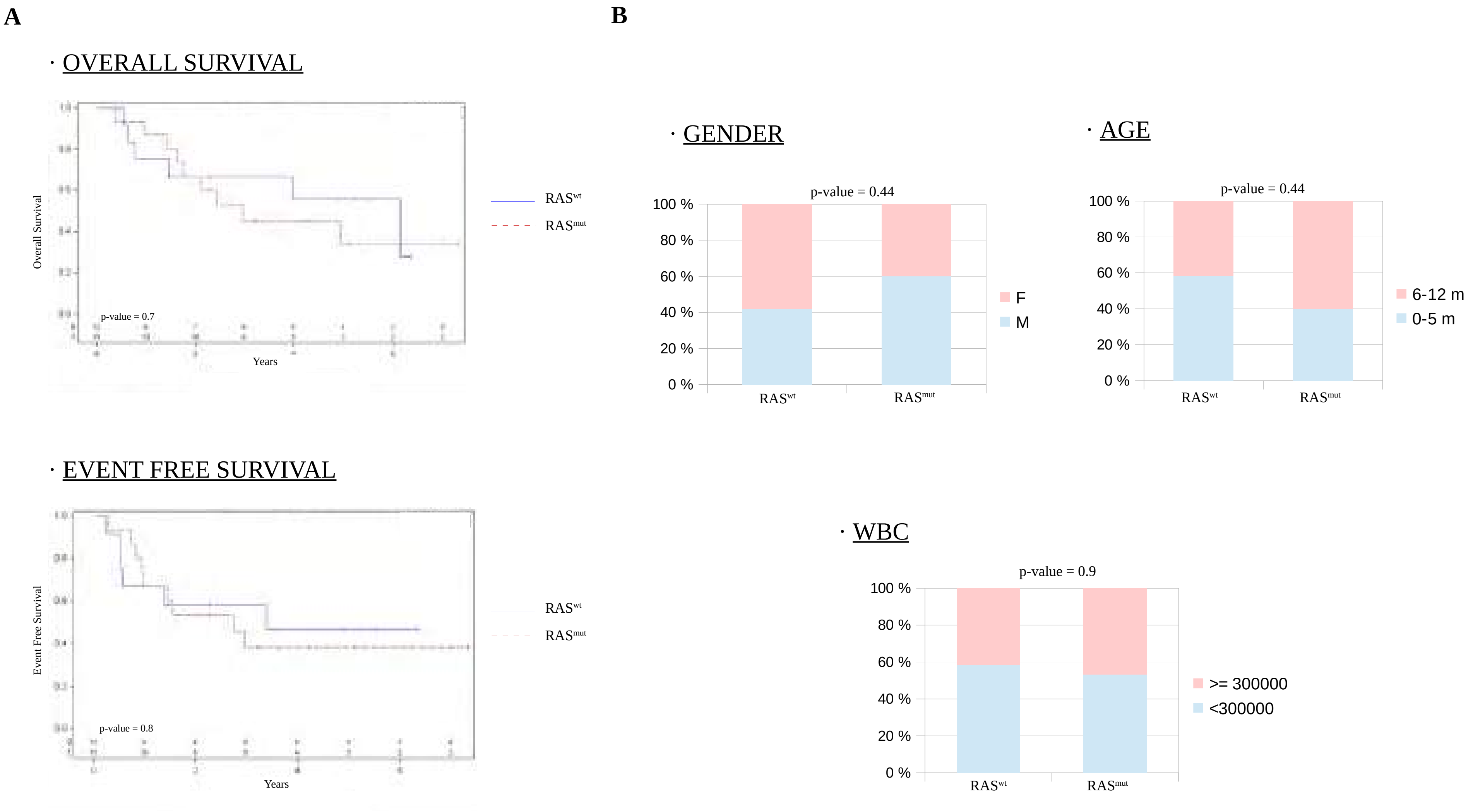
MA4_23

MA4_24

MA4_25

Suppl. Figure 5. Clinical correlation between the presence of RAS mutations and disease outcome.

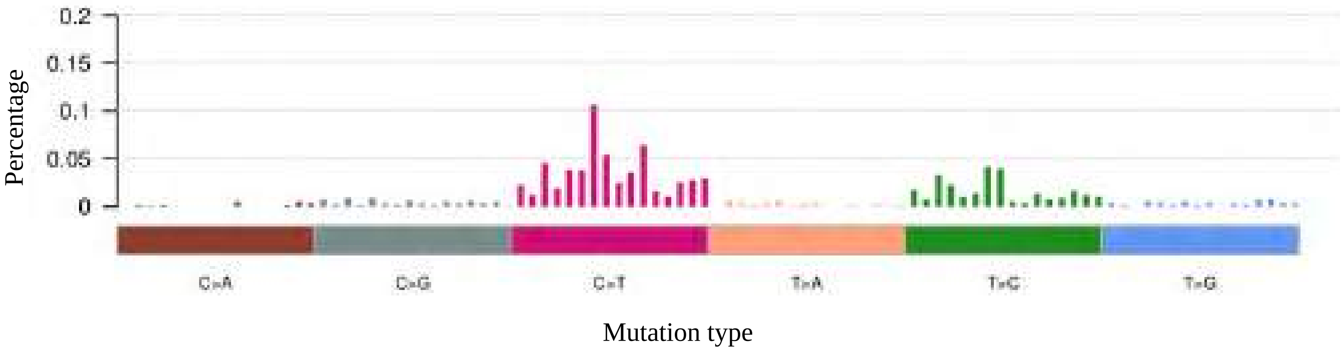
(A) Kaplan-Meier plots for overall survival (top panel) and disease free survival (botom panel). (B) The presence of mutated RAS has no impact on gender, patient age, white blood cells (WBC)/blasts counts.



Suppl. Figure 6. Genomic instability at relapse.

A) Mutational signature analysis in the MLL-AF4 subgroup at relapse. Significant enrichment score in signature 6 in relapses according to the mutational signatures described by Alexandrov et al. (Alexandrov LB, Nik-Zainal S, Wedge DC, et al. Signatures of mutational processes in human cancer. *Nature*. 2013;500:415–21.) based on 7000 cancer genomes. This signature is associated with defective DNA mismatch repair found in unstable tumours and with high number of small (shorter than 3 bp) insertions and deletions.
B) Correlation between the number of mutations and time-to-relpase for the n=8 MLL-AF4+ relapses.

A



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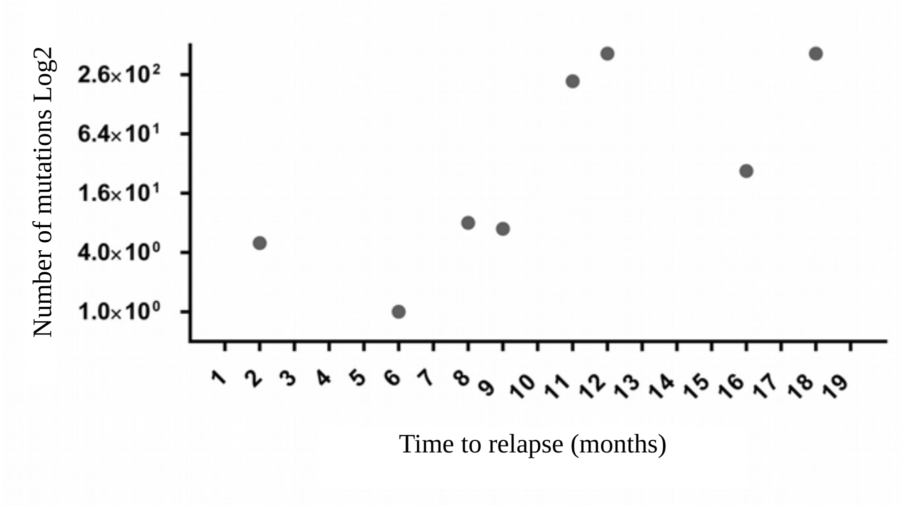
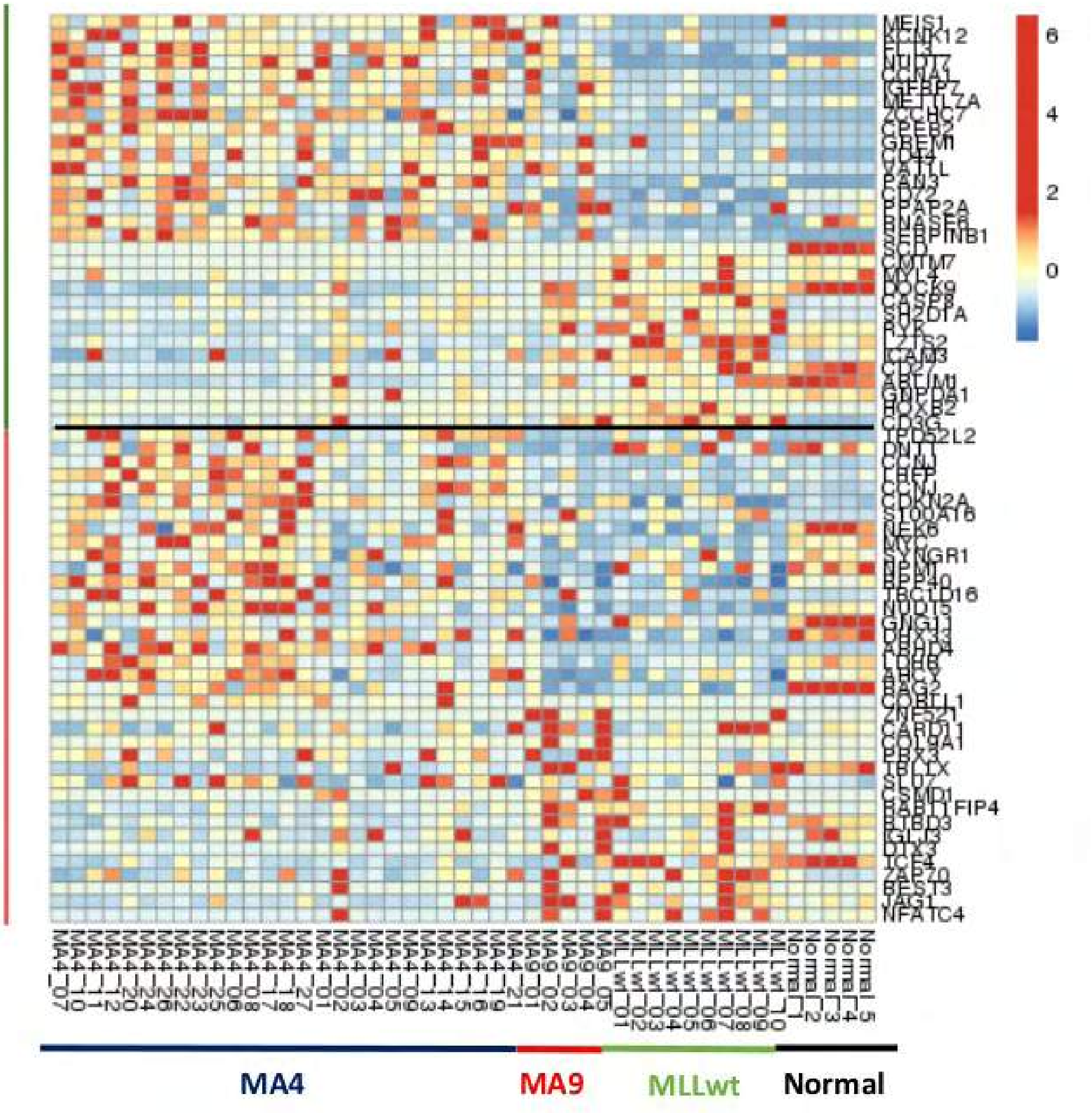


Suppl. Figure 7. RNA-Seq expression of genes previously reported to define a MLLr or MLL-AF4+ BCP-ALL (Ronald W. Stam *et al*, Blood, 2010).

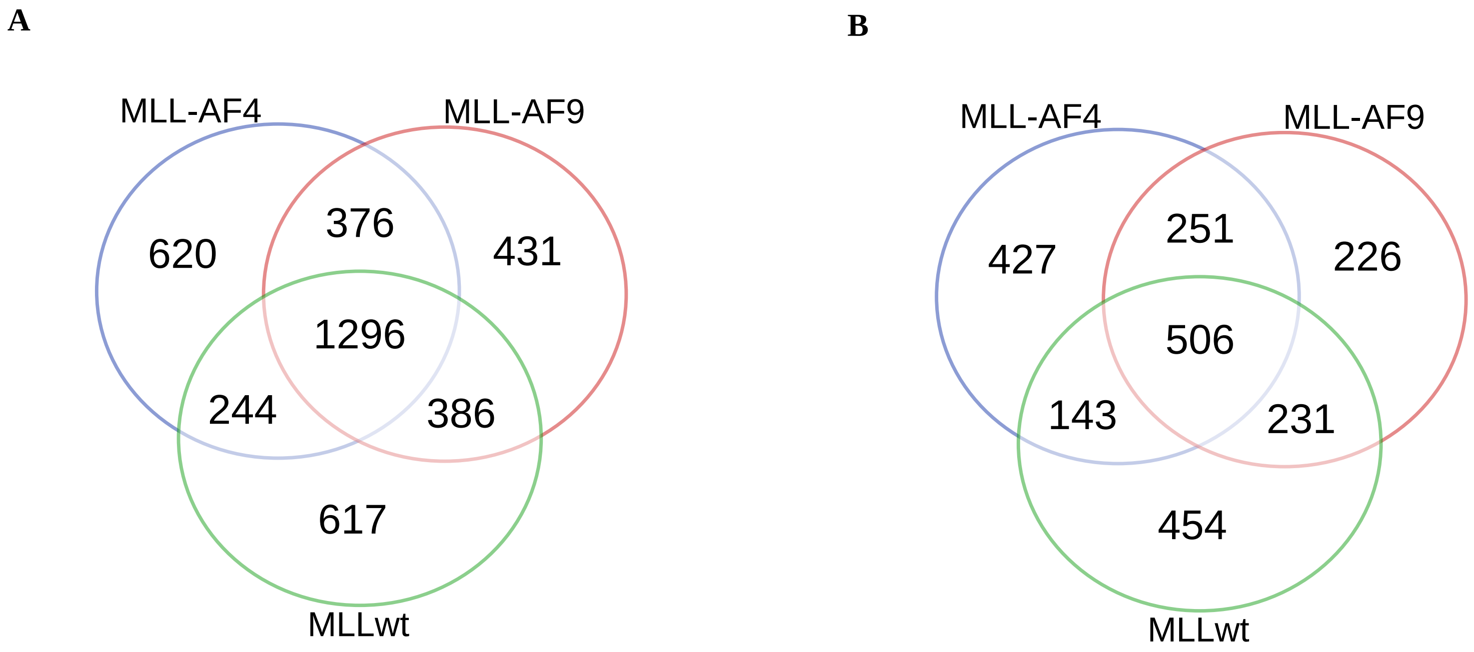


Gene expression associated to MLLr infant BCP-ALL

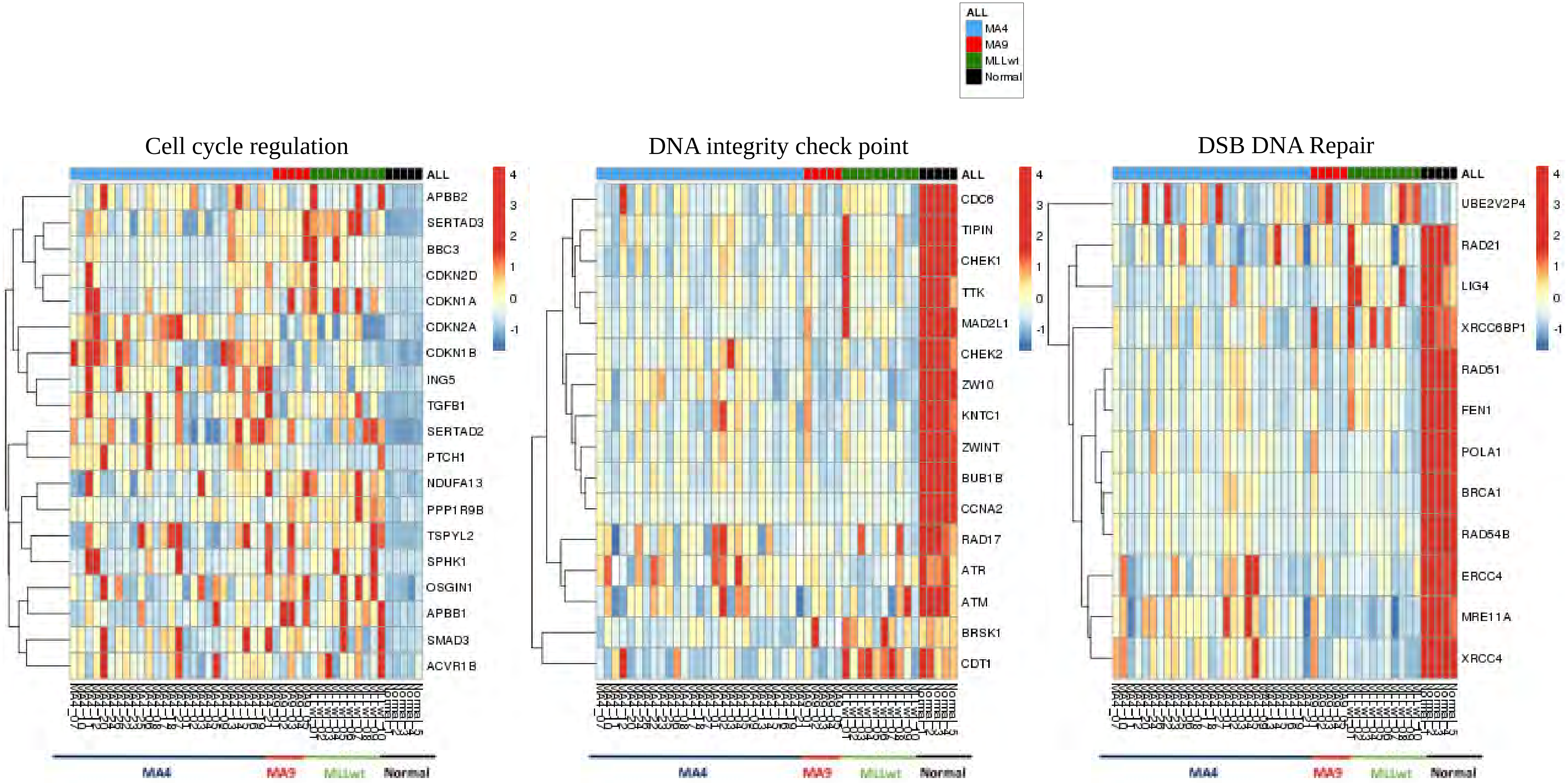
Gene expression associated to infant MLL-AF4+ BCP-ALL

Suppl. Figure 8. Venn Diagram of global transcriptional activation nature of MLL fusions.

Number of upregulated (A) and downregulated (B) genes in each group studied by RNAseq.

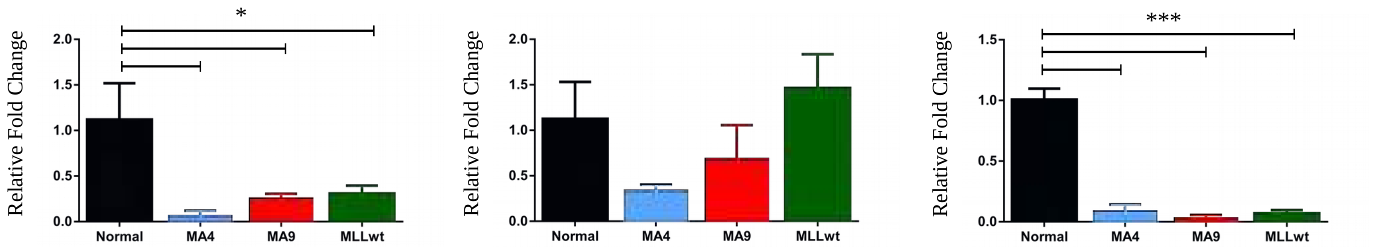


Suppl. Figure 9. Heatmap representation of the most significant deregulated pathways identified by GSEA in the three infant iBCP-ALL subgroups as compared to normal FL-derived B-cell progenitors.

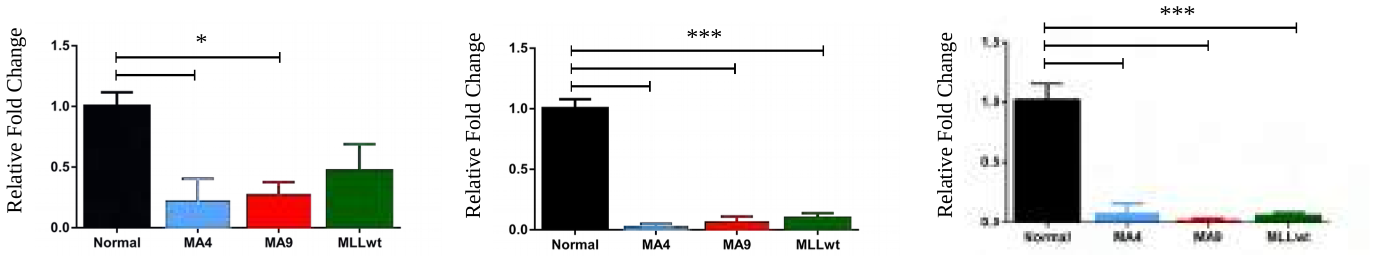


Suppl. Figure 10. qRT-PCR validation of the indicated genes observed in our RNA-Seq.

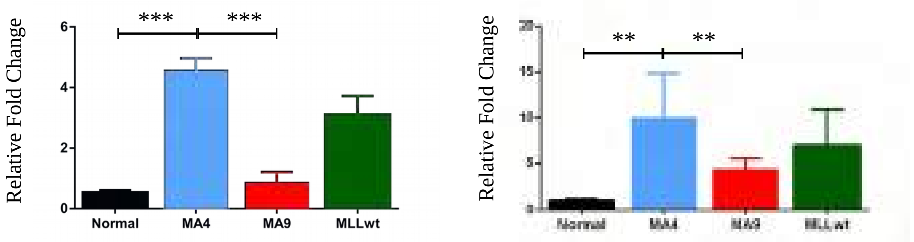
Bars represente average of relative fold-change and standard desviation in three independent replicates. *p<0,05, ** p<0.01 y *** p<0.001



ATR *CEBPG* *CCNA*



CHECK1 *RAD51* *BRCA1*



TGFB1 *CDKN1A*

Supplementary Tables

Suppl. Table 1. Clinical and genetic characteristics of the 42 iBCP-ALL used in the discovery cohort. * months #PB: Peripheral blood, BM: Bone marrow.

Cases ID	Hospital	Age*	Gender	MLLr	Specimen#	% Blast	Relapse
MA4_01	Paris	6 m	M	MLL-AF4	PB	90	NO
MA4_02	Paris	12 m	M	MLL-AF4	BM	92	NO
MA4_03	Paris	5 m	M	MLL-AF4	PB	96	NO
MA4_04	Paris	7 m	M	MLL-AF4	PB	99	NO
MA4_05	Paris	4.5 m	F	MLL-AF4	PB	93	NO
MA4_06	Erasmus	6.4 m	F	MLL-AF4	BM	90	NO
MA4_07	Erasmus	3.1 m	F	MLL-AF4	PB	92	NO
MA4_08	Erasmus	2.5 m	M	MLL-AF4	BM	97	NO
MA4_09	Erasmus	8.7 m	F	MLL-AF4	PB	90	NO
MA4_10	Erasmus	10.3 m	F	MLL-AF4	PB	94	NO
MA4_11	Erasmus	10.1 m	F	MLL-AF4	BM	98	NO
MA4_12	Erasmus	8.8 m	M	MLL-AF4	BM	94	NO
MA4_13	Erasmus	3.6 m	M	MLL-AF4	PB	97	NO
MA4_14	Erasmus	0.1 m	F	MLL-AF4	BM	96	YES
MA4_15	Erasmus	4.2 m	F	MLL-AF4	PB	92	NO
MA4_16	Erasmus	6.5 m	F	MLL-AF4	BM	92	NO
MA4_17	Erasmus	5.6 m	M	MLL-AF4	PB	94	YES
MA4_18	Monza	6.3 m	F	MLL-AF4	BM	99	YES
MA4_19	Monza	2.5 m	M	MLL-AF4	BM	88	NO
MA4_20	Monza	4.2 m	M	MLL-AF4	BM	100	YES
MA4_21	Monza	6 m	F	MLL-AF4	BM	98	YES
MA4_22	Monza	8 m	M	MLL-AF4	BM	98	YES
MA4_23	Monza	7.5 m	M	MLL-AF4	BM	87	YES
MA4_24	Monza	0.8 m	M	MLL-AF4	BM	Unknown	YES
MA4_25	Monza	3.1 m	M	MLL-AF4	BM	100	NO
MA4_26	Erasmus	7.2 m	M	MLL-AF4	PB	96	NO
MA4_27	Erasmus	6.4 m	M	MLL-AF4	BM	92	YES
MA9_01	Erasmus	3 m	F	MLL-AF9	PB	93	NO
MA9_02	Erasmus	2.6 m	F	MLL-AF9	PB	98	NO
MA9_03	Erasmus	11.2 m	F	MLL-AF9	PB	90	NO
MA9_04	Erasmus	11.4 m	F	MLL-AF9	BM	90	NO
MA9_05	Erasmus	0.4 m	F	MLL-AF9	PB	90	NO
MLLwt_01	Erasmus	11.3 m	F	MLLwt	BM	93	NO
MLLwt_02	Erasmus	11.3 m	M	MLLwt	BM	90	NO
MLLwt_03	Erasmus	0.4 m	F	MLLwt	PB	98	NO
MLLwt_04	Erasmus	11.7 m	M	MLLwt	PB	93	NO
MLLwt_05	Erasmus	3.3 m	M	MLLwt	BM	98	NO
MLLwt_06	Erasmus	9 m	F	MLLwt	BM	97	NO
MLLwt_07	Erasmus	7.4 m	F	MLLwt	PB	99	NO
MLLwt_08	Erasmus	8.5 m	M	MLLwt	PB	94	NO
MLLwt_09	Erasmus	11.7 m	M	MLLwt	BM	98	NO
MLLwt_10	Erasmus	4.2 m	M	MLLwt	PB	95	NO

Suppl. Table 2. Primers used for analysis of BCR repertories.

Oligo Name	Sequence 5’ to 3’
VH1-FR1-HUMAN_BIOMED	GGCCTCAGTGAAGGTCTCCTGCAAG
VH2-FR1_HUMAN_BIOMED	GTCTGGTCCTACGCTGGTGAAACCC
VH3-FR1_HUMAN_BIOMED	CTGGGGGGTCCCTGAGACTCTCCTG
VH4-FR1_HUMAN_BIOMED	CTTCGGAGACCCTGTCCCTCACCTG
VH5-FR1_HUMAN_BIOMED	CGGGGAGTCTCTGAAGATCTCCTGT
VH6-FR1_HUMAN_BIOMED	TCGCAGACCCTCTCACTCACCTGTG
BC_IgHJ_HUMAN_BIOMED	TGTCCAGCACGCTTCAGGCTNNNNTNNNNTNNNNCTTACCTGAGGAGACGGTGACC
CNU_S	TGTCCAGCACGCTTCAGGCT

Suppl. Table 4. MLL translocation breakpoints.

Genomic breakpoints determined by WGS at the base pair level in the MLL-AF4 and MLL-AF9 translocations

Cases ID	MLL exon/intron	AF4 exon/intron	Breakpoint
MA4_01	Exon 10	Intron 3	*Chr4:88004655-Chr11:118355607
MA4_03	Intron 10	Intron 3	Chr11:118359080-Chr4:87975057 *Chr4:87975036-Chr11:118358981
MA4_04	Intron 10	Intron 3	Chr11:118358194-Chr4:87992124 *Chr4:87989772-Chr11:118358572
MA4_08	Intron 10	Intron 3	Chr11:118359048-Chr4: 87977078
MA4_09	Exon 8	Intron 3	Chr11:118353327-Chr4:87975144
MA4_10	Intron 8	Intron 3	Chr11:118355109-Chr4:87976002
MA4_13	Exon 9	Before exon 1 (reverse)	*Chr4:87854734-Chr11:118354941
MA4_15	Intron 9	Intron 3	*Chr4:87995770-Chr11:118355672
MA4_16	Intron 8 (reverse)	Intron 3 (reverse)	*Chr4:87974323-Chr11:118354668
MA4_19	Intron 10	Intron 3	Chr11:118358319-Chr4:87988309 *Chr4:87988383-Chr11:118358153
MA4_21	Intron 10	Intron 3	Chr11:118357172-Chr4:87997625
MA4_22	Exon 11	Intron 4 (reverse)	*Chr4:88010955-Chr11:118359356
MA4_23	Intron 8	Intron 3	Chr11: 118353991-Chr4:87998295 *Chr4:87998749-Chr11:118353750
MA4_26	Intron 10	Intron 3	*Chr4:87998602-Chr11:118359398

Cases ID	MLL exon/intron	MLLT3 exon/intron	Breakpoint
MA9_02	Intron 9	Intron 4	Chr11:118355190-Chr9:20441134
MA9_04	Intron 10	Intron 5 (reverse)	*Chr9:20369705-Chr11: 118355611
MA9_05	Intron 10	Intron 5	Chr11:118358294-Chr9:20403549

* reverse

Sample	Chrom	Position	Ref_base	Mut_base	Variant Allele Freq	Gene_ID	Transcript_ID	c.Annot	p.Annot	Consequence
MA4_01	Chr17	15134242	G	A	0.188959285	PMP22	ENST00000395938_r73	c.475 C>T	p.R159C	MISSENSE
MA4_01	Chr3	47144912	A	T	0.184537246	SETD2	ENST00000409792_r73	c.4841 T>A	p.I1614K	MISSENSE
MA4_02	Chr1	29602226	C	T	0.118736142	PTPRU	ENST00000345512_r73	c.1411 C>T	p.R471C	MISSENSE
MA4_02	Chr1	52442655	G	A	0.366571019	RAB3B	ENST00000371655_r73	c.135 C>T	p.D45D	SILENT
MA4_02	Chr11	67265042	G	A	0.43257233	PITPNM1	ENST00000534749_r73	c.1891 C>T	p.R631C	MISSENSE
MA4_02	Chr13	76415945	C	T	0.409429001	LMO7	ENST00000341547_r73	c.3011 C>T	p.P1004L	MISSENSE
MA4_02	Chr8	144993489	G	A	0.552685248	PLEC	ENST00000345136_r73	c.10500 C>T	p.R3500R	SILENT
MA4_02	ChrX	44942756	-	CAGG	0.127366057	KDM6A	ENST00000377967_r73	c.3336 ->CAGG	p.V1112fs*40	FRAMESHIFT
MA4_03	ChrX	11196264	C	T	0.902975312	ARHGAP6	ENST00000380736_r73	c.976 G>A	p.V326M	MISSENSE
MA4_04	Chr1	119466114	G	A	0.388781998	TBX15	ENST00000207157_r73	c.488 C>T	p.T163M	MISSENSE
MA4_04	Chr10	124351862	C	T	0.334958854	DMBT1	ENST00000368909_r73	c.2251 C>T	p.R751*	NONSENSE
MA4_04	Chr5	54529067	T	G	0.421348315	CCNO	ENST00000282572_r73	c.285 A>C	p.L95L	SILENT
MA4_04	Chr5	76028542	C	T	0.06541033	F2R	ENST00000319211_r73	c.492 C>T	p.S164S	SILENT
MA4_05	Chr4	170028169	T	C	0.155313712	SH3RF1	ENST00000284637_r73	c.2327 A>G	p.D776G	MISSENSE
MA4_06	Chr10	22826203	G	A	0.057377049	PIP4K2A	ENST00000376573_r73	c.1148 C>T	p.A383V	MISSENSE
MA4_06	Chr16	943056	C	T	0.455605039	LMF1	ENST00000262301_r73	c.680 G>A	p.R227Q	MISSENSE
MA4_06	Chr17	26910871	G	A	0.273290703	RP11-192H23.4	ENST00000531839_r73	c.761 C>T	p.T254M	MISSENSE
MA4_06	Chr17	66878843	C	T	0.064910079	ABCA8	ENST00000269080_r73	c.3605 G>A	p.S1202N	MISSENSE
MA4_06	Chr12	25398284	C	A	0.097262667	KRAS	ENST00000311936_r73	c.35 G>T	p.G12V	MISSENSE
MA4_06	Chr12	25398281	C	T	0.04127907	KRAS	ENST00000311936_r73	c.38 G>A	p.G13D	MISSENSE
MA4_07	Chr14	38060843	G	A	0.044476206	FOXA1	ENST00000250448_r73	c.1146 C>T	p.H382H	SILENT
MA4_07	Chr1	115258748	C	T	0.015116414	NRAS	ENST00000369535_r73	c.34 G>A	p.G12S	MISSENSE
MA4_08	Chr1	32157115	T	A	0.073264246	COL16A1	ENST00000373672_r73	Exon 19 - 2 A>T	-	ESSENTIAL_SPLICE
MA4_08	Chr11	3723715	G	A	0.323017992	NUP98	ENST00000324932_r73	c.3490 C>T	p.P1164S	MISSENSE
MA4_08	Chr12	25378561	G	A	0.348619422	KRAS	ENST00000311936_r73	c.437 C>T	p.A146V	MISSENSE
MA4_08	Chr2	99438545	C	T	0.402624515	KIAA1211L	ENST00000397899_r73	c.2191 G>A	p.G731R	MISSENSE
MA4_09	Chr1	156640767	C	T	0.432276908	NES	ENST00000368223_r73	c.3213 G>A	p.V1071V	SILENT
MA4_09	Chr10	134622358	C	T	0.24640952	TTC40	ENST00000368586_r73	c.7715 G>A	p.R2572Q	MISSENSE
MA4_09	Chr16	85942669	G	C	0.042319508	IRF8	ENST00000268638_r73	c.248 G>C	p.R83P	MISSENSE
MA4_09	Chr17	33875517	C	T	0.254864556	SLFN14	ENST00000415846_r73	c.2480 G>A	p.R827H	MISSENSE
MA4_09	Chr17	29196542	G	A	0.258426966	ATAD5	ENST00000321990_r73	c.3485 G>A	p.R1162H	MISSENSE
MA4_10	Chr11	113700009	A	T	0.25327096	USP28	ENST00000003302_r73	c.969 T>A	p.Y323*	NONSENSE
MA4_10	Chr18	63527018	G	A	0.164255091	CDH7	ENST00000323011_r73	c.1569 G>A	p.T523T	SILENT
MA4_10	Chr1	115258747	C	T	0.018408166	NRAS	ENST00000369535_r73	c.35 G>A	p.G12D	MISSENSE
MA4_10	Chr1	115258744	C	T	0.027023838	NRAS	ENST00000369535_r73	c.38 G>A	p.G13D	MISSENSE
MA4_10	Chr1	115258748	C	T	0.082718744	NRAS	ENST00000369535_r73	c.34 G>A	p.G12S	MISSENSE

MA4_11	Chr11	117329595	G	A	0.065889916	DSCAML1	ENST00000321322_r73	c.3623 C>T	p.T1208M	MISSENSE
MA4_11	Chr4	30724484	G	A	0.114128216	PCDH7	ENST00000361762_r73	c.1440 G>A	p.Q480Q	SILENT
MA4_11	ChrX	122800961	G	A	0.1242656	THOC2	ENST00000355725_r73	c.1186 C>T	p.R396*	NONSENSE
MA4_11	Chr1	115258747	C	T	0.130104615	NRAS	ENST00000369535_r73	c.35 G>A	p.G12D	MISSENSE
MA4_12	Chr1	115258747	C	T	0.03465982	NRAS	ENST00000369535_r73	c.35 G>A	p.G12D	MISSENSE
MA4_12	Chr1	115258744	C	T	0.037227214	NRAS	ENST00000369535_r73	c.38 G>A	p.G13D	MISSENSE
MA4_13	Chr1	77093213	G	A	0.431059092	ST6GALNAC3	ENST00000328299_r73	c.700 G>A	p.V234I	MISSENSE
MA4_14	Chr1	12183370	G	A	0.378454145	TNFRSF8	ENST00000263932_r73	c.976 G>A	p.A326T	MISSENSE
MA4_14	ChrX	153582588	C	T	0.467612001	FLNA	ENST00000360319_r73	c.5464 G>A	p.V1822M	MISSENSE
MA4_14R	Chr1	115258748	C	T	0.443557526	NRAS	ENST00000369535_r73	c.34 G>A	p.G12S	MISSENSE
MA4_15	ChrX	32503115	A	G	0.41562785	DMD	ENST00000378677_r73	c.2712 T>C	p.D904D	SILENT
MA4_15	Chr13	28602340	G	T	0.441176471	FLT3	ENST00000241453_r73	c.2028 C>A	p.N676K	MISSENSE
MA4_16	Chr20	62493709	C	T	0.348211355	ABHD16B	ENST00000369916_r73	c.816 C>T	p.F272F	SILENT
MA4_17	Chr12	25398284	C	A	0.41875	KRAS	ENST00000311936_r73	c.35 G>T	p.G12V	MISSENSE
MA4_17R	Chr1	26670871	G	T	0.153743711	AIM1L	ENST00000374207_r73	c.313 C>A	p.L105M	MISSENSE
MA4_17R	Chr12	70965002	T	A	0.139347021	PTPRB	ENST00000334414_r73	c.3174 A>T	p.S1058S	SILENT
MA4_17R	Chr15	60747314	G	C	0.124878397	NARG2	ENST00000261520_r73	c.831 C>G	p.H277Q	MISSENSE
MA4_17R	Chr16	67228769	G	A	0.159920574	E2F4	ENST00000379378_r73	c.694 G>A	p.A232T	MISSENSE
MA4_17R	Chr19	1987165	C	T	0.171126761	BTBD2	ENST00000255608_r73	c.1269 G>A	p.Q423Q	SILENT
MA4_17R	Chr4	48490578	C	T	0.179612163	SLC10A4	ENST00000273861_r73	c.936 C>T	p.Y312Y	SILENT
MA4_17R	Chr5	90144542	G	A	0.167889439	GPR98	ENST00000405460_r73	c.17108 G>A	p.R5703H	MISSENSE
MA4_17R	ChrX	37979633	G	C	0.257247584	SYTL5	ENST00000297875_r73	c.1619 G>C	p.G540A	MISSENSE
MA4_17R	Chr9	732503	G	A	0.045454546	KANK1	ENST00000382303_r73	c.3131 G>A	p.R1044Q	MISSENSE
MA4_18	Chr12	25398281	C	T	0.212984055	KRAS	ENST00000311936_r73	c.38 G>A	p.G13D	MISSENSE
MA4_18R	Chr10	50315892	G	A	0.137142857	VSTM4	ENST00000332853_r73	c.204 C>T	p.F68F	SILENT
MA4_18R	Chr10	61898828	C	T	0.084442696	ANK3	ENST00000280772_r73	c.2632 G>A	p.G878R	MISSENSE
MA4_18R	Chr11	65628573	G	A	0.166583665	MUS81	ENST00000308110_r73	c.265 G>A	p.G89S	MISSENSE
MA4_18R	Chr11	73074260	C	G	0.183411215	ARHGEF17	ENST00000263674_r73	c.5006 C>G	p.T1669S	MISSENSE
MA4_18R	Chr11	108593986	G	A	0.146759388	DDX10	ENST00000322536_r73	c.1762 G>A	p.D588N	MISSENSE
MA4_18R	Chr14	75375610	C	G	0.068568233	RPS6KL1	ENST00000555647_r73	c.1386 G>C	p.T462T	SILENT
MA4_18R	Chr15	79296469	G	A	0.151010002	RASGRF1	ENST00000558480_r73	c.2124 C>T	p.Y708Y	SILENT
MA4_18R	Chr16	71065790	G	C	0.086487782	HYDIN	ENST00000393567_r73	c.2560 C>G	p.P854A	MISSENSE
MA4_18R	Chr17	10541516	G	C	0.13260947	MYH3	ENST00000583535_r73	c.3573 C>G	p.A1191A	SILENT
MA4_18R	Chr18	74587457	C	G	0.181245626	ZNF236	ENST00000253159_r73	c.671 C>G	p.P224R	MISSENSE
MA4_18R	Chr19	9070839	C	T	0.172091641	MUC16	ENST00000397910_r73	c.16607 G>A	p.R5536Q	MISSENSE
MA4_18R	Chr19	13409769	C	T	0.001333088	CACNA1A	ENST00000360228_r73	c.2678 G>A	p.R893Q	MISSENSE
MA4_18R	Chr2	69556824	C	G	0.131769029	GFPT1	ENST00000361060_r73	c.1535 G>C	p.R512P	MISSENSE

MA4_18R	Chr2	219893011	G	A	0.002873563	CCDC108	ENST00000341552_r73	c.1763 C>T	p.T588M	MISSENSE
MA4_18R	Chr20	36374918	C	T	0.174187651	CTNNBL1	ENST00000361383_r73	c.375 C>T	p.H125H	SILENT
MA4_18R	Chr22	43901486	G	A	0.181884817	MPPED1	ENST00000417669_r73	c.971 G>A	p.R324Q	MISSENSE
MA4_18R	Chr3	48681041	G	C	0.207036615	CELSR3	ENST00000164024_r73	c.8235 C>G	p.V2745V	SILENT
MA4_18R	Chr3	62502298	C	T	0.139903995	CADPS	ENST00000383710_r73	c.2414 G>A	p.R805Q	MISSENSE
MA4_18R	Chr9	139404399	C	T	0.24613351	NOTCH1	ENST00000277541_r73	c.2755 G>A	p.G919R	MISSENSE
MA4_18R	Chr3	138187036	G	C	0.160185368	ESYT3	ENST00000389567_r73	c.1308 G>C	p.E436D	MISSENSE
MA4_18R	Chr10	95069922	C	T	0.159251197	MYOF	ENST00000358334_r73	c.5963 G>A	p.R1988Q	MISSENSE
MA4_18R	Chr6	143093951	C	T	0.178131544	HIVEP2	ENST00000367604_r73	c.1925 G>A	p.R642Q	MISSENSE
MA4_18R	Chr16	30410163	G	A	0.162408063	ZNF48	ENST00000320159_r73	c.1592 G>A	p.R531Q	MISSENSE
MA4_18R	Chr11	17742858	G	A	0.065334358	MYOD1	ENST00000250003_r73	c.766 G>A	p.V256M	MISSENSE
MA4_18R	Chr13	80055428	C	T	0.097651422	NDFIP2	ENST00000218652_r73	c.90 C>T	p.T30T	SILENT
MA4_18R	Chr19	17439019	C	T	0.148471616	ANO8	ENST00000159087_r73	c.2178 G>A	p.S726S	SILENT
MA4_18R	Chr4	110448484	G	A	0.131083481	SEC24B	ENST00000399100_r73	c.2867 G>A	p.R956Q	MISSENSE
MA4_18R	Chr6	96034806	G	A	0.097014925	MANEA	ENST00000358812_r73	c.491 G>A	p.R164Q	MISSENSE
MA4_18R	Chr6	154414520	C	T	0.117647059	OPRM1	ENST00000229768_r73	c.1280 C>T	p.S427L	MISSENSE
MA4_18R	Chr7	97937061	G	A	0.14	BAIAP2L1	ENST00000005260_r73	c.1103 C>T	p.T368M	MISSENSE
MA4_18R	Chr7	100634393	T	G	0.24	MUC12	ENST00000536621_r73	c.549 T>G	p.S183R	MISSENSE
MA4_18R	Chr7	103216088	C	G	0.215384615	RELN	ENST00000428762_r73	c.4210 G>C	p.D1404H	MISSENSE
MA4_18R	Chr8	110587801	G	A	0.116129032	SYBU	ENST00000533895_r73	c.1323 C>T	p.F441F	SILENT
MA4_18R	Chr8	121209184	T	A	0.205714286	COL14A1	ENST00000297848_r73	c.591 T>A	p.I197I	SILENT
MA4_18R	Chr9	15657131	A	G	0.470588235	CCDC171	ENST00000380701_r73	c.829 A>G	p.T277A	MISSENSE
MA4_18R	Chr9	117846595	G	C	0.110294118	TNC	ENST00000350763_r73	c.2024 C>G	p.T675R	MISSENSE
MA4_18R	Chr9	122011276	T	A	0.163043478	DBC1	ENST00000265922_r73	c.371 A>T	p.K124M	MISSENSE
MA4_18R	ChrX	54117762	G	A	0.104477612	FAM120C	ENST00000375180_r73	c.2410 C>T	p.R804*	NONSENSE
MA4_18R	ChrX	71876082	C	T	0.221698113	PHKA1	ENST00000373542_r73	c.929 G>A	p.R310H	MISSENSE
MA4_18R	ChrX	152827614	G	A	0.105263158	ATP2B3	ENST00000349466_r73	c.3073 G>A	p.G1025R	MISSENSE
MA4_18R	Chr3	32571050	T	-	0.135135135	DYNC1LI1	ENST00000273130_r73	c.1288 A>-	p.I430fs*5	FRAMESHIFT
MA4_19	Chr22	22712553	G	A	0.039168111	IGLV1-47	ENST00000390294_r73	c.296 G>A	p.R99Q	MISSENSE
MA4_20	Chr1	115256529	T	A	0.264634839	NRAS	ENST00000369535_r73	c.182 A>T	p.Q61L	MISSENSE
MA4_20	Chr16	2283522	C	T	0.452965621	E4F1	ENST00000301727_r73	c.1140 C>T	p.I380I	SILENT
MA4_20	Chr22	40807815	G	A	0.241766284	MKL1	ENST00000355630_r73	c.2375 C>T	p.S792L	MISSENSE
MA4_20	Chr12	53682409	GCCCAT	-	0.453414352	ESPL1	ENST00000552462_r73	c.4634 GCCCAT>-	p.S1545 SPC>S	MISSENSE
MA4_20R	Chr1	115256529	T	A	0.201530891	NRAS	ENST00000369535_r73	c.182 A>T	p.Q61L	MISSENSE
MA4_20R	Chr10	24889767	C	T	0.069881598	ARHGAP21	ENST00000396432_r73	c.2940 G>A	p.T980T	SILENT
MA4_20R	Chr11	108380476	C	G	0.09033675	EXPH5	ENST00000265843_r73	c.5758 G>C	p.G1920R	MISSENSE
MA4_20R	Chr16	2283522	C	T	0.229450857	E4F1	ENST00000301727_r73	c.1140 C>T	p.I380I	SILENT

MA4_20R	Chr17	7577121	G	A	0.211493113	TP53	ENST00000269305_r73	c.817 C>T	p.R273C	MISSENSE
MA4_20R	Chr22	40807815	G	A	0.237129485	MKL1	ENST00000355630_r73	c.2375 C>T	p.S792L	MISSENSE
MA4_20R	Chr12	53682409	GCCCAT	-	0.220722509	ESPL1	ENST00000552462_r73	c.4634 GCCCAT>-	p.S1545 SPC>S	MISSENSE
MA4_21	Chr11	70332174	T	G	0.186440678	SHANK2	ENST00000409161_r73	c.2436 A>C	p.T812T	SILENT
MA4_21	Chr5	139422532	-	GCTGCTGCT	0.391304348	NRG2	ENST00000361474_r73	c.123 ->AGCAGCAGC	p.S41 S>RAAA	MISSENSE
MA4_22	Chr9	127216294	C	A	0.475362319	GPR144	ENST00000334810_r73	c.996 C>A	p.C332*	NONSENSE
MA4_22	Chr12	23818481	C	T	0.178747941	SOX5	ENST00000546136_r73	c.789 G>A	p.P263P	SILENT
MA4_22	Chr15	75114997	C	T	0.116832958	LMAN1L	ENST00000309664_r73	c.1146 C>T	p.V382V	SILENT
MA4_22	Chr10	48428949	C	T	0.391472285	GDF10	ENST00000224605_r73	c.937 G>A	p.A313T	MISSENSE
MA4_22	Chr1	31836903	G	T	0.078651685	ZCCHC17	ENST00000344147_r73	c.589 G>T	p.D197Y	MISSENSE
MA4_22	Chr16	46993000	C	T	0.115942029	DNAJA2	ENST00000317089_r73	c.962 G>A	p.R321H	MISSENSE
MA4_22	Chr1	115258747	C	T	0.109902848	NRAS	ENST00000369535_r73	c.35 G>A	p.G12D	MISSENSE
MA4_22	Chr1	115258744	C	T	0.013689556	NRAS	ENST00000369535_r73	c.38 G>A	p.G13D	MISSENSE
MA4_22	Chr12	25398284	C	A	0.199459703	KRAS	ENST00000311936_r73	c.35 G>A	p.G12D	MISSENSE
MA4_22	Chr4	26422290	C	T	0.228111724	RBPJ	ENST00000345843_r73	c.433 C>T	p.R145W	MISSENSE
MA4_22	Chr11	95825853	G	A	0.091054045	MAML2	ENST00000524717_r73	c.1342 C>T	p.R448W	MISSENSE
MA4_22R	Chr13	52549042	G	A	0.34623323	ATP7B	ENST00000242839_r73	c.314 C>T	p.S105L	MISSENSE
MA4_22R	Chr18	42531586	G	A	0.377956481	SETBP1	ENST00000282030_r73	c.2281 G>A	p.V761M	MISSENSE
MA4_22R	Chr16	16173246	G	A	0.763759526	ABCC1	ENST00000399410_r73	c.2026 G>A	p.V676M	MISSENSE
MA4_22R	Chr16	76555115	C	T	0.138461539	CNTNAP4	ENST00000478060_r73	c.2225 C>T	p.A742V	MISSENSE
MA4_22R	Chr16	81078294	G	A	0.376859504	ATMIN	ENST00000299575_r73	c.2191 G>A	p.V731M	MISSENSE
MA4_22R	Chr6	96997360	G	A	0.402628435	UFL1	ENST00000369278_r73	c.1593 G>A	p.T531T	SILENT
MA4_22R	Chr3	137988903	G	A	0.271493213	ARMC8	ENST00000481646_r73	c.1366 G>A	p.V456I	MISSENSE
MA4_22R	Chr3	142277509	G	C	0.068720379	ATR	ENST00000350721_r73	c.1842 C>G	p.A614A	SILENT
MA4_22R	Chr9	124632975	C	T	0.417341041	TTLL11	ENST00000321582_r73	c.1804 G>A	p.E602K	MISSENSE
MA4_22R	Chr12	20801787	A	C	0.076212471	PDE3A	ENST00000359062_r73	c.2731 A>C	p.K911Q	MISSENSE
MA4_22R	Chr12	21795009	G	C	0.300685136	LDHB	ENST00000396076_r73	c.472 C>G	p.R158G	MISSENSE
MA4_22R	Chr12	76740737	C	T	0.246085011	BBS10	ENST00000393262_r73	c.1028 G>A	p.R343Q	MISSENSE
MA4_22R	Chr11	95825853	G	A	0.131651985	MAML2	ENST00000524717_r73	c.1342 C>T	p.R448W	MISSENSE
MA4_22R	Chr15	68695329	C	T	0.400844406	ITGA11	ENST00000315757_r73	c.92 G>A	p.R31Q	MISSENSE
MA4_22R	Chr15	98513945	G	A	0.296703297	ARRDC4	ENST00000268042_r73	c.1172 G>A	p.R391Q	MISSENSE
MA4_22R	Chr8	144994538	G	A	0.094175286	PLEC	ENST00000345136_r73	c.9451 C>T	p.R3151C	MISSENSE
MA4_22R	Chr4	26422290	C	T	0.229225636	RBPJ	ENST00000345843_r73	c.433 C>T	p.R145W	MISSENSE
MA4_22R	Chr4	77036593	C	T	0.685747664	NUP54	ENST00000264883_r73	c.1450 G>A	p.D484N	MISSENSE
MA4_22R	Chr4	88986625	G	A	0.366681825	PKD2	ENST00000237596_r73	c.2218 G>A	p.E740K	MISSENSE
MA4_22R	Chr10	70105604	G	A	0.2566146	RUFY2	ENST00000388768_r73	c.1847 C>T	p.P616L	MISSENSE
MA4_22R	Chr5	50091171	G	A	0.331018519	PARP8	ENST00000505697_r73	c.1348 G>A	p.A450T	MISSENSE

MA4_22R	Chr7	131825491	C	T	0.248064138	PLXNA4	ENST00000359827_r73	c.5305 G>A	p.A1769T	MISSENSE
MA4_22R	Chr7	150553626	C	T	0.278790389	AOC1	ENST00000493429_r73	c.68 C>T	p.P23L	MISSENSE
MA4_22R	Chr17	7577539	G	A	0.788971717	TP53	ENST00000269305_r73	c.742 C>T	p.R248W	MISSENSE
MA4_22R	Chr17	27185635	G	A	0.409534128	ERAL1	ENST00000254928_r73	c.753 G>A	p.T251T	SILENT
MA4_22R	Chr1	15987008	G	A	0.344632768	RSC1A1	ENST00000345034_r73	c.645 G>A	p.T215T	SILENT
MA4_22R	Chr1	223177194	G	A	0.365754813	DISP1	ENST00000284476_r73	c.2455 G>A	p.A819T	MISSENSE
MA4_22R	Chr1	15987008	G	A	0.344632768	DDI2	ENST00000480945_r73	c.1923 G>A	-	UTR
MA4_22R	Chr7	131825491	C	T	0.248064138	PLXNA4	ENST00000359827_r73	c.5546 C>T	p.A1849V	MISSENSE
MA4_22R	Chr12	25398284	C	A	0.538461538	KRAS	ENST00000311936_r73	c.437 C>T	p.A146V	MISSENSE
MA4_22R	Chr9	127216294	C	A	0.472222222	GPR144	ENST00000334810_r73	c.996 C>A	p.C332*	NONSENSE
MA4_22R	Chr11	899385	C	T	0.051546392	CHID1	ENST00000323578_r73	c.563 G>A	p.G188D	MISSENSE
MA4_22R	Chr11	3727740	G	C	0.051724138	NUP98	ENST00000324932_r73	c.2860 C>G	p.Q954E	MISSENSE
MA4_22R	Chr11	3756473	C	T	0.076086957	NUP98	ENST00000324932_r73	c.1490 G>A	p.G497E	MISSENSE
MA4_22R	Chr11	5067819	C	T	0.070588235	OR52J3	ENST00000380370_r73	c.64 C>T	p.L22L	SILENT
MA4_22R	Chr11	5444297	G	A	0.06043956	OR51Q1	ENST00000300778_r73	c.867 G>A	p.M289I	MISSENSE
MA4_22R	Chr11	5565853	C	T	0.303571429	OR52H1	ENST00000322653_r73	c.901 G>A	p.G301R	MISSENSE
MA4_22R	Chr11	5809210	C	T	0.059701493	OR52N1	ENST00000317078_r73	c.837 G>A	p.M279I	MISSENSE
MA4_22R	Chr11	8941004	G	A	0.291139241	AKIP1	ENST00000299576_r73	c.529 G>A	p.V177M	MISSENSE
MA4_22R	Chr11	9735099	C	G	0.050420168	SWAP70	ENST00000318950_r73	c.327 C>G	p.L109L	SILENT
MA4_22R	Chr11	32975682	G	A	0.322033898	QSER1	ENST00000399302_r73	c.4070 G>A	p.R1357H	MISSENSE
MA4_22R	Chr11	33090290	G	A	0.064516129	TCP11L1	ENST00000334274_r73	c.1212 G>A	p.V404V	SILENT
MA4_22R	Chr11	36248802	G	A	0.238938053	LDLRAD3	ENST00000315571_r73	c.622 G>A	p.V208M	MISSENSE
MA4_22R	Chr11	46388273	C	T	0.098765432	DGKZ	ENST00000454345_r73	c.467 C>T	p.P156L	MISSENSE
MA4_22R	Chr11	46724646	C	A	0.136363636	ZNF408	ENST00000311764_r73	c.505 C>A	p.L169M	MISSENSE
MA4_22R	Chr11	47446685	G	C	0.125	PSMC3	ENST00000298852_r73	c.272 C>G	p.S91C	MISSENSE
MA4_22R	Chr11	56409825	C	G	0.051502146	OR5AP2	ENST00000302981_r73	c.91 G>C	p.G31R	MISSENSE
MA4_22R	Chr11	57564307	G	A	0.066115703	CTNND1	ENST00000524630_r73	c.799 G>A	p.G267R	MISSENSE
MA4_22R	Chr11	60506408	G	A	0.052631579	MS4A18	ENST00000529108_r73	c.205 G>A	p.A69T	MISSENSE
MA4_22R	Chr11	62362542	C	A	0.114754098	MTA2	ENST00000278823_r73	c.1484 G>T	p.C495F	MISSENSE
MA4_22R	Chr11	64507168	G	T	0.105882353	RASGRP2	ENST00000394432_r73	c.636 C>A	p.L212L	SILENT
MA4_22R	Chr11	64697810	G	A	0.469387755	PPP2R5B	ENST00000164133_r73	c.739 G>A	p.E247K	MISSENSE
MA4_22R	Chr11	66190332	C	T	0.065789474	NPAS4	ENST00000311034_r73	c.618 C>T	p.G206G	SILENT
MA4_22R	Chr1	238045782	C	T	0.066115703	ZP4	ENST00000366570_r73	c.1563 G>A	p.L521L	SILENT
MA4_22R	Chr1	241755414	G	A	0.087912088	KMO	ENST00000366559_r73	c.1420 G>A	p.V474M	MISSENSE
MA4_22R	Chr1	242030233	G	C	0.248554913	EXO1	ENST00000366548_r73	c.1143 G>C	p.S381S	SILENT
MA4_22R	Chr13	25274920	C	T	0.051546392	ATP12A	ENST00000381946_r73	c.1741 C>T	p.P581S	MISSENSE
MA4_22R	Chr13	25363493	G	C	0.394736842	RNF17	ENST00000255324_r73	c.791 G>C	p.R264P	MISSENSE

MA4_22R	Chr13	28498569	C	T	0.133333333	PDX1	ENST00000381033_r73	c.583 C>T	p.Q195*	NONSENSE
MA4_22R	Chr13	33016677	C	T	0.062893082	N4BP2L2	ENST00000399396_r73	c.1997 G>A	p.R666K	MISSENSE
MA4_22R	Chr13	39424199	G	A	0.180722892	FREM2	ENST00000280481_r73	c.6404 G>A	p.R2135Q	MISSENSE
MA4_22R	Chr13	39597187	A	T	0.05106383	PROSER1	ENST00000352251_r73	Exon 8 2 T>A	-	ESSENTIAL_SPLICE
MA4_22R	Chr13	46544580	C	T	0.051948052	ZC3H13	ENST00000282007_r73	c.2489 G>A	p.G830E	MISSENSE
MA4_22R	Chr13	50059823	C	T	0.055813954	SETDB2	ENST00000317257_r73	c.1576 C>T	p.R526*	NONSENSE
MA4_22R	Chr13	79191089	G	A	0.051136364	RNF219	ENST00000282003_r73	c.807 C>T	p.S269S	SILENT
MA4_22R	Chr13	80911657	C	T	0.105263158	SPRY2	ENST00000377102_r73	c.184 G>A	p.V62I	MISSENSE
MA4_22R	Chr13	103317148	C	T	0.376146789	TPP2	ENST00000376065_r73	c.3205 C>T	p.R1069*	NONSENSE
MA4_22R	Chr13	103388797	C	T	0.050724638	CCDC168	ENST00000322527_r73	c.363 G>A	p.E121E	SILENT
MA4_22R	Chr13	103710650	C	T	0.2	SLC10A2	ENST00000245312_r73	c.460 G>A	p.D154N	MISSENSE
MA4_22R	Chr13	110436664	G	A	0.057142857	IRS2	ENST00000375856_r73	c.1737 C>T	p.T579T	SILENT
MA4_22R	Chr13	111927085	A	T	0.057692308	ARHGEF7	ENST00000317133_r73	c.1220 A>T	p.H407L	MISSENSE
MA4_22R	Chr16	1536065	C	T	0.050847458	PTX4	ENST00000293922_r73	c.1297 G>A	p.E433K	MISSENSE
MA4_22R	Chr16	2293382	G	A	0.060240964	ECI1	ENST00000301729_r73	c.500 C>T	p.A167V	MISSENSE
MA4_22R	Chr16	3493148	C	T	0.1	ZNF597	ENST00000301744_r73	c.6 G>A	p.A2A	SILENT
MA4_22R	Chr16	4033331	C	T	0.069565217	ADCY9	ENST00000294016_r73	c.2421 G>A	p.L807L	SILENT
MA4_22R	Chr18	5397114	C	G	0.059259259	EPB41L3	ENST00000341928_r73	c.2784 G>C	p.E928D	MISSENSE
MA4_22R	Chr18	9221872	A	G	0.054054054	ANKRD12	ENST00000262126_r73	c.818 A>G	p.H273R	MISSENSE
MA4_22R	Chr18	21152144	C	T	0.05	NPC1	ENST00000269228_r73	c.181 G>A	p.E61K	MISSENSE
MA4_22R	Chr18	34349352	G	A	0.105769231	FHOD3	ENST00000257209_r73	c.4200 G>A	p.P1400P	SILENT
MA4_22R	Chr18	34740289	G	A	0.089108911	KIAA1328	ENST00000280020_r73	c.1359 G>A	p.M453I	MISSENSE
MA4_22R	Chr18	47796189	C	A	0.108695652	MBD1	ENST00000353909_r73	Exon 16 - 1 G>T	-	ESSENTIAL_SPLICE
MA4_22R	Chr18	59774078	C	T	0.058333333	PIGN	ENST00000357637_r73	c.1711 G>A	p.G571R	MISSENSE
MA4_22R	Chr18	60036630	G	A	0.28	TNFRSF11A	ENST00000586569_r73	c.1480 G>A	p.E494K	MISSENSE
MA4_22R	Chr18	70209141	G	A	0.284090909	CBLN2	ENST00000585159_r73	c.255 C>T	p.S85S	SILENT
MA4_22R	Chr16	11845214	C	T	0.068965517	ZC3H7A	ENST00000396516_r73	c.2875 G>A	p.D959N	MISSENSE
MA4_22R	Chr16	15692718	C	A	0.11627907	KIAA0430	ENST00000396368_r73	c.4977 G>T	p.E1659D	MISSENSE
MA4_22R	Chr16	20335355	G	A	0.25	GP2	ENST00000302555_r73	c.318 C>T	p.T106T	SILENT
MA4_22R	Chr16	20362003	G	A	0.059701493	UMOD	ENST00000570689_r73	c.57 C>T	p.I19I	SILENT
MA4_22R	Chr16	22092160	G	C	0.058823529	C16orf52	ENST00000542527_r73	c.463 G>C	p.V155L	MISSENSE
MA4_22R	Chr16	30020553	G	A	0.098765432	DOC2A	ENST00000350119_r73	c.387 C>T	p.V129V	SILENT
MA4_22R	Chr16	31336632	G	A	75	ITGAM	ENST00000287497_r73	c.2412 G>A	p.V804V	SILENT
MA4_22R	Chr16	53358011	G	A	0.169811321	CHD9	ENST00000566029_r73	c.7850 G>A	p.R2617Q	MISSENSE
MA4_22R	Chr16	69177089	G	A	0.056818182	CIRH1A	ENST00000314423_r73	c.535 G>A	p.V179I	MISSENSE
MA4_22R	Chr16	70843889	G	A	0.086956522	HYDIN	ENST00000393567_r73	c.14680 C>T	p.Q4894*	NONSENSE
MA4_22R	Chr16	75575261	C	T	0.112676056	TMEM231	ENST00000258173_r73	c.757 G>A	p.V253M	MISSENSE

MA4_22R	Chr16	79245676	G	A	0.0625	WWOX	ENST00000566780_r73	c.1228 G>A	p.G410S	MISSENSE
MA4_22R	Chr16	84473064	G	C	0.283783784	ATP2C2	ENST00000262429_r73	c.1143 G>C	p.T381T	SILENT
MA4_22R	Chr16	88747917	G	A	0.066666667	SNAI3	ENST00000332281_r73	c.282 C>T	p.D94D	SILENT
MA4_22R	Chr16	89787187	G	A	0.192307692	VPS9D1	ENST00000389386_r73	c.83 C>T	p.T28I	MISSENSE
MA4_22R	Chr6	8015908	C	T	0.050847458	BLOC1S5	ENST00000397457_r73	c.538 G>A	p.D180N	MISSENSE
MA4_22R	Chr6	16306741	G	A	0.051813472	ATXN1	ENST00000244769_r73	c.2267 C>T	p.P756L	MISSENSE
MA4_22R	Chr6	22292797	G	C	0.204081633	PRL	ENST00000306482_r73	c.282 C>G	p.P94P	SILENT
MA4_22R	Chr6	29455181	T	C	0.058252427	MAS1L	ENST00000377127_r73	c.499 A>G	p.I167V	MISSENSE
MA4_22R	Chr6	43322744	C	T	0.097560976	ZNF318	ENST00000361428_r73	c.2328 G>A	p.P776P	SILENT
MA4_22R	Chr6	49518654	C	T	0.339622642	C6orf141	ENST00000414696_r73	c.149 C>T	p.A50V	MISSENSE
MA4_22R	Chr6	72975190	G	T	0.14	RIMS1	ENST00000521978_r73	c.3292 G>T	p.D1098Y	MISSENSE
MA4_22R	Chr6	76660399	G	A	0.053763441	IMPG1	ENST00000369950_r73	c.1704 C>T	p.P568P	SILENT
MA4_22R	Chr6	102376485	G	A	0.057553957	GRIK2	ENST00000421544_r73	c.2063 G>A	p.G688D	MISSENSE
MA4_22R	Chr6	109274465	G	A	0.068627451	ARMC2	ENST00000392644_r73	c.1826 G>A	p.R609H	MISSENSE
MA4_22R	Chr6	112461037	G	A	0.062015504	LAMA4	ENST00000230538_r73	c.3027 C>T	p.A1009A	SILENT
MA4_22R	Chr6	117859847	G	A	0.071942446	DCBLD1	ENST00000296955_r73	c.825 G>A	p.S275S	SILENT
MA4_22R	Chr6	131481326	C	A	0.111111111	AKAP7	ENST00000431975_r73	c.279 C>A	p.I93I	SILENT
MA4_22R	Chr6	131927620	C	T	0.061946903	MED23	ENST00000354577_r73	c.1384 G>A	p.E462K	MISSENSE
MA4_22R	Chr6	139488186	G	A	0.067961165	HECA	ENST00000367658_r73	c.1037 G>A	p.R346Q	MISSENSE
MA4_22R	Chr6	147704066	G	A	0.088235294	STXBP5	ENST00000367481_r73	c.3238 G>A	p.G1080S	MISSENSE
MA4_22R	Chr6	148865271	G	A	0.259541985	SASH1	ENST00000367467_r73	c.2665 G>A	p.D889N	MISSENSE
MA4_22R	Chr6	151694763	C	G	0.3125	ZBTB2	ENST00000325144_r73	c.10 G>C	p.A4P	MISSENSE
MA4_22R	Chr6	155450464	A	T	0.061068702	TIAM2	ENST00000461783_r73	c.107 A>T	p.H36L	MISSENSE
MA4_22R	Chr6	161016412	G	A	0.052132701	LPA	ENST00000316300_r73	c.3443 C>T	p.P1148L	MISSENSE
MA4_22R	Chr6	165844942	C	G	0.052631579	PDE10A	ENST00000539869_r73	c.712 G>C	p.A238P	MISSENSE
MA4_22R	ChrX	15593791	C	T	0.077777778	ACE2	ENST00000252519_r73	c.1440 G>A	p.M480I	MISSENSE
MA4_22R	ChrX	16627715	G	T	0.135135135	CTPS2	ENST00000359276_r73	c.1640 C>A	p.A547E	MISSENSE
MA4_22R	ChrX	18622441	G	A	0.144927536	CDKL5	ENST00000379996_r73	c.1397 G>A	p.R466Q	MISSENSE
MA4_22R	ChrX	29301132	G	T	0.153061225	IL1RAPL1	ENST00000378993_r73	c.160 G>T	p.A54S	MISSENSE
MA4_22R	ChrX	46747095	A	T	0.102040816	CXorf31	ENST00000377879_r73	c.170 T>A	p.V57E	MISSENSE
MA4_22R	ChrX	48666668	C	A	0.123595506	HDAC6	ENST00000334136_r73	c.741 C>A	p.V247V	SILENT
MA4_22R	ChrX	54950100	G	T	0.101694915	TRO	ENST00000173898_r73	c.1135 G>T	p.E379*	NONSENSE
MA4_22R	ChrX	54960268	G	A	0.710526316	PFKFB1	ENST00000375006_r73	c.1342 C>T	p.R448W	MISSENSE
MA4_22R	ChrX	55047547	G	A	0.269230769	ALAS2	ENST00000396198_r73	c.537 C>T	p.S179S	SILENT
MA4_22R	ChrX	57021244	C	T	0.417582418	SPIN3	ENST00000374919_r73	c.137 G>A	p.R46Q	MISSENSE
MA4_22R	ChrX	63411097	G	T	0.125	AMER1	ENST00000330258_r73	c.2070 C>A	p.S690R	MISSENSE
MA4_22R	ChrX	69507161	C	T	0.727272727	PDZD11	ENST00000239666_r73	c.353 G>A	p.R118H	MISSENSE

MA4_22R	ChrX	70316558	G	A	0.1	FOXO4	ENST00000374259_r73	c.180 G>A	p.T60T	SILENT
MA4_22R	ChrX	76890137	G	T	0.112781955	ATRX	ENST00000373344_r73	c.4757 C>A	p.P1586Q	MISSENSE
MA4_22R	Chr3	11059024	G	A	0.072289157	SLC6A1	ENST00000287766_r73	c.127 G>A	p.D43N	MISSENSE
MA4_22R	Chr3	14508035	C	T	0.064220184	SLC6A6	ENST00000454876_r73	c.744 C>T	p.F248F	SILENT
MA4_22R	Chr3	19959819	C	T	0.057142857	EFHB	ENST00000295824_r73	c.1082 G>A	p.R361Q	MISSENSE
MA4_22R	Chr3	23250290	G	C	0.052631579	UBE2E2	ENST00000425792_r73	c.100 G>C	p.E34Q	MISSENSE
MA4_22R	Chr3	28365666	C	T	0.061068702	AZI2	ENST00000479665_r73	c.1046 G>A	p.W349*	NONSENSE
MA4_22R	Chr3	31710219	C	T	0.056701031	OSBPL10	ENST00000396556_r73	c.2011 G>A	p.E671K	MISSENSE
MA4_22R	Chr3	32726979	G	A	0.056603774	CNOT10	ENST00000331889_r73	Exon 1 5 G>A	-	ESSENTIAL_SPLICE
MA4_22R	ChrX	96013231	C	T	0.05019305	DIAPH2	ENST00000373049_r73	c.421 C>T	p.Q141*	NONSENSE
MA4_22R	ChrX	105167153	A	T	0.096491228	NRK	ENST00000243300_r73	c.2654 A>T	p.Y885F	MISSENSE
MA4_22R	ChrX	105179175	C	T	0.08045977	NRK	ENST00000243300_r73	c.3513 C>T	p.F1171F	SILENT
MA4_22R	ChrX	106844025	C	A	0.152173913	FRMPD3	ENST00000439554_r73	c.2699 C>A	p.S900*	NONSENSE
MA4_22R	ChrX	119670796	G	T	0.103448276	CUL4B	ENST00000371322_r73	c.2032 C>A	p.H678N	MISSENSE
MA4_22R	ChrX	132161058	G	C	0.074766355	USP26	ENST00000370832_r73	c.1191 C>G	p.N397K	MISSENSE
MA4_22R	ChrX	140993500	G	A	0.062015504	MAGEC1	ENST00000285879_r73	c.310 G>A	p.E104K	MISSENSE
MA4_22R	ChrX	148797302	C	T	0.125	MAGEA11	ENST00000355220_r73	c.231 C>T	p.P77P	SILENT
MA4_22R	ChrX	150573396	G	T	0.103448276	VMA21	ENST00000330374_r73	c.172 G>T	p.G58W	MISSENSE
MA4_22R	ChrX	153171301	C	A	0.133333333	AVPR2	ENST00000358927_r73	c.341 C>A	p.A114D	MISSENSE
MA4_22R	Chr3	38318437	C	T	0.060606061	SLC22A13	ENST00000311856_r73	c.1381 C>T	p.R461W	MISSENSE
MA4_22R	Chr3	39228715	G	C	0.050761421	XIRP1	ENST00000396251_r73	c.2222 C>G	p.A741G	MISSENSE
MA4_22R	Chr3	44762890	G	C	0.32173913	ZNF502	ENST00000436624_r73	c.581 G>C	p.R194P	MISSENSE
MA4_22R	Chr3	49679891	G	C	0.070422535	BSN	ENST00000296452_r73	c.824 G>C	p.G275A	MISSENSE
MA4_22R	Chr3	49698362	C	T	0.345864662	BSN	ENST00000296452_r73	c.9084 C>T	p.P3028P	SILENT
MA4_22R	Chr3	50220929	C	T	0.0625	SEMA3F	ENST00000002829_r73	c.1165 C>T	p.H389Y	MISSENSE
MA4_22R	Chr3	50418192	G	A	0.433333333	CACNA2D2	ENST00000424201_r73	c.829 C>T	p.R277*	NONSENSE
MA4_22R	Chr3	51663360	C	T	0.231527094	RAD54L2	ENST00000409535_r73	c.352 C>T	p.R118W	MISSENSE
MA4_22R	Chr3	61975389	G	A	0.051724138	PTPRG	ENST00000474889_r73	c.281 G>A	p.R94H	MISSENSE
MA4_22R	Chr3	62189178	C	T	0.067484663	PTPRG	ENST00000474889_r73	c.1709 C>T	p.P570L	MISSENSE
MA4_22R	Chr3	64589638	A	T	0.06097561	ADAMTS9	ENST00000498707_r73	c.3707 T>A	p.V1236E	MISSENSE
MA4_22R	Chr3	89521697	C	T	0.050314465	EPHA3	ENST00000336596_r73	c.2774 C>T	p.T925I	MISSENSE
MA4_22R	Chr3	107799004	G	A	0.063583815	CD47	ENST00000355354_r73	c.234 C>T	p.P78P	SILENT
MA4_22R	Chr3	107799088	G	A	0.058139535	CD47	ENST00000355354_r73	c.150 C>T	p.N50N	SILENT
MA4_22R	Chr3	119666194	C	T	0.277227723	GSK3B	ENST00000264235_r73	c.287 G>A	p.R96Q	MISSENSE
MA4_22R	Chr3	122259629	C	T	0.054945055	PARP9	ENST00000477522_r73	c.1455 G>A	p.M485I	MISSENSE
MA4_22R	Chr3	128345586	C	T	0.051724138	RPN1	ENST00000296255_r73	c.1126 G>A	p.E376K	MISSENSE
MA4_22R	Chr3	130162344	C	T	0.055555556	COL6A5	ENST00000312481_r73	c.6512 C>T	p.P2171L	MISSENSE

MA4_22R	Chr3	130318627	C	T	0.06741573	COL6A6	ENST00000358511_r73	c.4626 C>T	p.P1542P	SILENT
MA4_22R	Chr3	138762690	C	T	0.305785124	PRR23C	ENST00000413199_r73	c.773 G>A	p.R258H	MISSENSE
MA4_22R	Chr3	142031593	T	A	0.058333333	XRN1	ENST00000264951_r73	c.4665 A>T	p.I1555I	SILENT
MA4_22R	Chr3	142537239	T	A	0.061728395	PCOLCE2	ENST00000295992_r73	c.1186 A>T	p.I396F	MISSENSE
MA4_22R	Chr3	142741745	C	T	0.068181818	U2SURP	ENST00000473835_r73	c.1069 C>T	p.P357S	MISSENSE
MA4_22R	Chr3	142741765	A	T	0.088235294	U2SURP	ENST00000473835_r73	c.1089 A>T	p.I363I	SILENT
MA4_22R	Chr3	160233267	C	T	0.065934066	KPNA4	ENST00000334256_r73	c.1005 G>A	p.L335L	SILENT
MA4_22R	Chr3	164714347	C	T	0.08411215	SI	ENST00000264382_r73	c.4668 G>A	p.R1556R	SILENT
MA4_22R	Chr3	183907373	C	T	0.068965517	ABCF3	ENST00000429586_r73	c.1142 C>T	p.S381F	MISSENSE
MA4_22R	Chr3	191098013	G	A	0.09009009	CCDC50	ENST00000392455_r73	c.514 G>A	p.E172K	MISSENSE
MA4_22R	Chr3	195487888	C	T	0.063157895	MUC4	ENST00000349607_r73	c.1854 G>A	p.W618*	NONSENSE
MA4_22R	Chr3	196054298	G	A	0.103896104	TM4SF19	ENST00000442633_r73	c.164 C>T	p.A55V	MISSENSE
MA4_22R	Chr3	196215543	G	A	0.059405941	RNF168	ENST00000318037_r73	c.313 C>T	p.Q105*	NONSENSE
MA4_22R	Chr9	742270	G	A	0.059259259	KANK1	ENST00000382303_r73	c.3762 G>A	p.L1254L	SILENT
MA4_22R	Chr9	8319853	C	T	0.361111111	PTPRD	ENST00000381196_r73	c.5648 G>A	p.R1883Q	MISSENSE
MA4_22R	Chr9	17415795	C	T	0.147058824	CNTLN	ENST00000380647_r73	c.2806 C>T	p.H936Y	MISSENSE
MA4_22R	Chr9	37442512	G	A	0.056910569	ZBTB5	ENST00000307750_r73	c.37 C>T	p.Q13*	NONSENSE
MA4_22R	Chr9	72472880	G	C	0.058558559	C9orf135	ENST00000377197_r73	c.436 G>C	p.D146H	MISSENSE
MA4_22R	Chr9	84268926	G	A	0.18	TLE1	ENST00000376499_r73	c.260 C>T	p.T87M	MISSENSE
MA4_22R	Chr9	100862295	C	T	0.059259259	TRIM14	ENST00000375098_r73	c.455 G>A	p.R152K	MISSENSE
MA4_22R	Chr9	101812146	C	T	0.06185567	COL15A1	ENST00000375001_r73	c.2873 C>T	p.P958L	MISSENSE
MA4_22R	Chr9	102861104	G	A	0.056074766	ERP44	ENST00000262455_r73	c.19 C>T	p.L7L	SILENT
MA4_22R	Chr9	111965991	G	A	0.062962963	EPB41L4B	ENST00000374566_r73	c.1898 C>T	p.P633L	MISSENSE
MA4_22R	Chr9	112200416	C	T	0.273381295	PTPN3	ENST00000374541_r73	c.565 G>A	p.E189K	MISSENSE
MA4_22R	Chr9	113265477	G	C	0.052173913	SVEP1	ENST00000401783_r73	c.1324 C>G	p.R442G	MISSENSE
MA4_22R	Chr9	126139223	C	T	0.315789474	CRB2	ENST00000373631_r73	c.3740 C>T	p.A1247V	MISSENSE
MA4_22R	Chr12	2926453	G	A	0.173913044	ITFG2	ENST00000228799_r73	c.161 G>A	p.R54Q	MISSENSE
MA4_22R	Chr12	7469851	G	A	0.162337662	ACSM4	ENST00000399422_r73	c.739 G>A	p.G247S	MISSENSE
MA4_22R	Chr12	11138988	A	T	0.164874552	TAS2R50	ENST00000506868_r73	c.472 T>A	p.Y158N	MISSENSE
MA4_22R	Chr12	23699323	C	T	0.064102564	SOX5	ENST00000546136_r73	c.1485 G>A	p.L495L	SILENT
MA4_22R	Chr12	32137414	G	A	0.050420168	KIAA1551	ENST00000312561_r73	c.3525 G>A	p.L1175L	SILENT
MA4_22R	Chr12	49434127	C	T	0.066666667	KMT2D	ENST00000301067_r73	c.7426 G>A	p.E2476K	MISSENSE
MA4_22R	Chr12	49580433	G	A	0.068376068	TUBA1A	ENST00000301071_r73	c.187 C>T	p.P63S	MISSENSE
MA4_22R	Chr12	51213482	G	T	0.142857143	ATF1	ENST00000262053_r73	c.736 G>T	p.A246S	MISSENSE
MA4_22R	Chr12	53432146	G	A	0.063157895	EIF4B	ENST00000262056_r73	c.1527 G>A	p.G509G	SILENT
MA4_22R	Chr12	53701467	G	A	0.072289157	AAAS	ENST00000209873_r73	c.1447 C>T	p.P483S	MISSENSE
MA4_22R	Chr12	54757225	T	A	0.053435115	GPR84	ENST00000267015_r73	c.411 A>T	p.I137I	SILENT

MA4_22R	Chr12	55846797	C	T	0.052173913	OR6C2	ENST00000322678_r73	c.800 C>T	p.A267V	MISSENSE
MA4_22R	Chr12	56119655	C	T	0.068965517	CD63	ENST00000546939_r73	c.347 G>A	p.W116*	NONSENSE
MA4_22R	Chr9	130475050	G	C	0.063291139	C9orf117	ENST00000373295_r73	c.1200 G>C	p.M400I	MISSENSE
MA4_22R	Chr9	130550582	C	A	0.102941177	CDK9	ENST00000373264_r73	c.522 C>A	p.F174L	MISSENSE
MA4_22R	Chr9	130914258	C	T	0.060606061	LCN2	ENST00000373017_r73	c.429 C>T	p.F143F	SILENT
MA4_22R	Chr12	59272846	G	A	0.098214286	LRIG3	ENST00000379141_r73	c.1663 C>T	p.R555*	NONSENSE
MA4_22R	Chr12	72023451	C	T	0.233870968	ZFC3H1	ENST00000378743_r73	c.3764 G>A	p.R1255Q	MISSENSE
MA4_22R	Chr12	88479826	G	T	0.120481928	CEP290	ENST00000552810_r73	c.4427 C>A	p.S1476*	NONSENSE
MA4_22R	Chr12	96273421	C	T	0.357142857	CCDC38	ENST00000344280_r73	Exon 12 1 G>A	-	ESSENTIAL_SPLICE
MA4_22R	Chr12	110820648	C	G	0.068376068	ANAPC7	ENST00000455511_r73	c.1037 G>C	p.G346A	MISSENSE
MA4_22R	Chr12	114374833	C	T	0.052631579	RBM19	ENST00000545145_r73	c.2047 G>A	p.D683N	MISSENSE
MA4_22R	Chr12	118298167	C	T	0.209302326	KSR2	ENST00000339824_r73	c.250 G>A	p.A84T	MISSENSE
MA4_22R	Chr12	121858394	C	T	0.073529412	RNF34	ENST00000361234_r73	c.741 C>T	p.S247S	SILENT
MA4_22R	Chr12	123782540	C	T	0.057553957	SBNO1	ENST00000602750_r73	c.4021 G>A	p.G1341R	MISSENSE
MA4_22R	Chr12	133389991	G	A	0.103448276	GOLGA3	ENST00000450791_r73	c.421 C>T	p.P141S	MISSENSE
MA4_22R	Chr14	23884667	G	T	0.133333333	MYH7	ENST00000355349_r73	c.5206 C>A	p.Q1736K	MISSENSE
MA4_22R	Chr14	36988571	G	A	0.14	NKX2-1	ENST00000354822_r73	c.82 C>T	p.R28C	MISSENSE
MA4_22R	Chr14	45633567	G	T	0.190476191	FANCM	ENST00000267430_r73	c.1587 G>T	p.V529V	SILENT
MA4_22R	Chr14	50666444	G	C	0.056179775	SOS2	ENST00000216373_r73	c.475 C>G	p.Q159E	MISSENSE
MA4_22R	Chr14	64520254	C	T	0.054945055	SYNE2	ENST00000344113_r73	c.9623 C>T	p.A3208V	MISSENSE
MA4_22R	Chr14	64892545	G	T	0.101449275	MTHFD1	ENST00000555709_r73	c.953 G>T	p.S318I	MISSENSE
MA4_22R	Chr14	70839817	C	T	0.294736842	SYNJ2BP	ENST00000256366_r73	c.329 G>A	p.R110Q	MISSENSE
MA4_22R	Chr14	75290989	G	A	0.056338028	YLPM1	ENST00000325680_r73	c.6142 G>A	p.D2048N	MISSENSE
MA4_22R	Chr14	77793187	C	T	0.072463768	GSTZ1	ENST00000216465_r73	c.74 C>T	p.A25V	MISSENSE
MA4_22R	Chr14	92790184	C	T	0.25	SLC24A4	ENST00000531433_r73	c.10 C>T	p.R4C	MISSENSE
MA4_22R	Chr14	94088559	C	T	0.166666667	UNC79	ENST00000256339_r73	c.4449 C>T	p.S1483S	SILENT
MA4_22R	Chr14	94395244	G	C	0.52631579	FAM181A	ENST00000557719_r73	c.613 G>C	p.V205L	MISSENSE
MA4_22R	Chr14	100193004	C	T	0.36	CYP46A1	ENST00000261835_r73	c.1443 C>T	p.P481P	SILENT
MA4_22R	Chr14	102027983	G	A	0.275	DIO3	ENST00000510508_r73	c.150 G>A	p.P50P	SILENT
MA4_22R	Chr14	104639754	C	T	0.294736842	KIF26A	ENST00000423312_r73	c.1771 C>T	p.R591*	NONSENSE
MA4_22R	Chr14	106967286	C	T	0.063218391	IGHV1-46	ENST00000390622_r73	c.114 G>A	p.K38K	SILENT
MA4_22R	Chr15	37390309	G	A	0.159090909	MEIS2	ENST00000338564_r73	c.104 C>T	p.P35L	MISSENSE
MA4_22R	Chr15	48056943	C	T	0.214285714	SEMA6D	ENST00000558014_r73	c.1206 C>T	p.A402A	SILENT
MA4_22R	Chr15	48826377	G	C	0.237410072	FBN1	ENST00000316623_r73	c.762 C>G	p.P254P	SILENT
MA4_22R	Chr15	49309166	G	A	0.06763285	SECISBP2L	ENST00000559471_r73	c.1298 C>T	p.P433L	MISSENSE
MA4_22R	Chr15	56435072	C	T	0.085271318	RFX7	ENST00000559847_r73	c.14 G>A	p.R5Q	MISSENSE
MA4_22R	Chr15	56974447	C	T	0.138888889	ZNF280D	ENST00000559237_r73	Exon 9 5 G>A	-	ESSENTIAL_SPLICE

MA4_22R	Chr15	63991133	C	T	0.068181818	HERC1	ENST00000443617_r73	c.4699 G>A	p.D1567N	MISSENSE
MA4_22R	Chr15	64427004	G	A	0.366666667	SNX1	ENST00000261889_r73	c.1363 G>A	p.E455K	MISSENSE
MA4_22R	Chr15	65255961	C	A	0.166666667	SPG21	ENST00000204566_r73	c.927 G>T	p.*309Y	STOP-LOST
MA4_22R	Chr15	65822990	G	C	0.071428571	PTPLAD1	ENST00000261875_r73	c.21 G>C	p.T7T	SILENT
MA4_22R	Chr15	66206091	G	A	0.212121212	MEGF11	ENST00000409699_r73	c.2694 C>T	p.T898T	SILENT
MA4_22R	Chr15	67681345	G	A	0.078947368	IQCH	ENST00000335894_r73	Exon 12 1 G>A	-	ESSENTIAL_SPLICE
MA4_22R	Chr11	71715718	G	T	0.146341463	NUMA1	ENST00000393695_r73	c.5974 C>A	p.L1992I	MISSENSE
MA4_22R	Chr11	82443907	C	T	0.169491525	FAM181B	ENST00000329203_r73	c.865 G>A	p.V289M	MISSENSE
MA4_22R	Chr11	82893483	G	T	0.11627907	PCF11	ENST00000298281_r73	c.4366 G>T	p.E1456*	NONSENSE
MA4_22R	Chr11	85623719	C	T	0.055900621	CCDC83	ENST00000280245_r73	c.822 C>T	p.T274T	SILENT
MA4_22R	Chr11	110450184	G	T	0.108910891	ARHGAP20	ENST00000260283_r73	c.3486 C>A	p.S1162R	MISSENSE
MA4_22R	Chr11	116707031	C	T	0.0625	APOA1	ENST00000375320_r73	c.297 G>A	p.L99L	SILENT
MA4_22R	Chr11	117985906	C	T	0.058394161	TMPRSS4	ENST00000534111_r73	c.1057 C>T	p.R353W	MISSENSE
MA4_22R	Chr11	120176362	G	A	0.285714286	POU2F3	ENST00000260264_r73	c.643 G>A	p.G215R	MISSENSE
MA4_22R	Chr11	126110873	G	A	0.051851852	FAM118B	ENST00000533050_r73	c.273 G>A	p.Q91Q	SILENT
MA4_22R	Chr11	129727330	C	T	0.555555556	TMEM45B	ENST00000281441_r73	c.693 C>T	p.A231A	SILENT
MA4_22R	Chr21	27462366	G	A	0.64	APP	ENST00000346798_r73	c.248 C>T	p.T83I	MISSENSE
MA4_22R	Chr21	41684028	T	A	0.081967213	DSCAM	ENST00000400454_r73	c.2042 A>T	p.Q681L	MISSENSE
MA4_22R	Chr21	43531640	C	T	0.055214724	UMODL1	ENST00000400427_r73	c.2092 C>T	p.P698S	MISSENSE
MA4_22R	Chr21	45089798	G	A	0.1	RRP1B	ENST00000340648_r73	c.164 G>A	p.W55*	NONSENSE
MA4_22R	Chr21	45563146	T	A	0.106796117	C21orf33	ENST00000291577_r73	c.581 T>A	p.V194E	MISSENSE
MA4_22R	Chr21	47531483	C	T	0.227027027	COL6A2	ENST00000300527_r73	c.93 C>T	p.T31T	SILENT
MA4_22R	Chr7	1785228	C	T	0.24516129	ELFN1	ENST00000424383_r73	c.996 C>T	p.T332T	SILENT
MA4_22R	Chr15	74336773	G	A	0.075757576	PML	ENST00000268058_r73	c.2073 G>A	p.L691L	SILENT
MA4_22R	Chr15	75499024	C	T	0.060150376	C15orf39	ENST00000360639_r73	c.635 C>T	p.P212L	MISSENSE
MA4_22R	Chr15	76587987	G	A	0.061728395	ETFA	ENST00000557943_r73	c.131 C>T	p.A44V	MISSENSE
MA4_22R	Chr15	84651111	G	A	0.051470588	ADAMTSL3	ENST00000286744_r73	c.2731 G>A	p.E911K	MISSENSE
MA4_22R	Chr15	89444866	C	T	0.097087379	MFGE8	ENST00000268151_r73	c.786 G>A	p.W262*	NONSENSE
MA4_22R	Chr15	91303904	C	T	0.051282051	BLM	ENST00000355112_r73	c.1301 C>T	p.S434L	MISSENSE
MA4_22R	Chr15	99701968	G	A	0.0625	TTC23	ENST00000394132_r73	c.970 C>T	p.L324L	SILENT
MA4_22R	Chr20	2097332	G	T	0.170731707	STK35	ENST00000381482_r73	c.913 G>T	p.A305S	MISSENSE
MA4_22R	Chr20	2321189	G	A	0.055555556	TGM3	ENST00000381458_r73	c.2044 G>A	p.A682T	MISSENSE
MA4_22R	Chr20	2841651	C	T	0.055045872	VPS16	ENST00000380445_r73	c.666 C>T	p.F222F	SILENT
MA4_22R	Chr20	3759095	C	T	0.067567568	SPEF1	ENST00000379756_r73	c.576 G>A	p.E192E	SILENT
MA4_22R	Chr20	5166403	G	A	0.051020408	CDS2	ENST00000460006_r73	Exon 9 - 1 G>A	-	ESSENTIAL_SPLICE
MA4_22R	Chr20	16387048	C	T	0.053475936	KIF16B	ENST00000354981_r73	c.1666 G>A	p.E556K	MISSENSE
MA4_22R	Chr20	25002122	G	A	0.607843137	ACSS1	ENST00000323482_r73	c.1011 C>T	p.I337I	SILENT

MA4_22R	Chr20	31044159	G	C	0.065789474	C20orf112	ENST00000359676_r73	c.149 C>G	p.S50C	MISSENSE
MA4_22R	Chr20	33519918	G	T	0.101010101	GSS	ENST00000216951_r73	c.853 C>A	p.L285M	MISSENSE
MA4_22R	Chr20	35125427	C	G	0.095238095	DLGAP4	ENST00000373913_r73	c.1968 C>G	p.P656P	SILENT
MA4_22R	Chr20	37137733	A	T	0.066455696	RALGAPB	ENST00000262879_r73	c.754 A>T	p.T252S	MISSENSE
MA4_22R	Chr20	37137734	C	T	0.052307692	RALGAPB	ENST00000262879_r73	c.755 C>T	p.T252I	MISSENSE
MA4_22R	Chr20	42907808	G	A	0.115789474	GDAP1L1	ENST00000342560_r73	c.972 G>A	p.S324S	SILENT
MA4_22R	Chr20	44180783	C	T	0.051792829	WFDC8	ENST00000357199_r73	c.608 G>A	p.R203H	MISSENSE
MA4_22R	Chr20	44515285	C	A	0.101123596	SPATA25	ENST00000372519_r73	c.555 G>T	p.M185I	MISSENSE
MA4_22R	Chr20	45174777	C	A	0.111111111	OCSTAMP	ENST00000279028_r73	c.236 G>T	p.G79V	MISSENSE
MA4_22R	Chr20	45192082	C	T	0.054945055	SLC13A3	ENST00000279027_r73	c.1603 G>A	p.A535T	MISSENSE
MA4_22R	Chr20	46279756	C	T	0.72	NCOA3	ENST00000372004_r73	c.3670 C>T	p.Q1224*	NONSENSE
MA4_22R	Chr20	52774123	G	A	0.057971015	CYP24A1	ENST00000216862_r73	c.1238 C>T	p.T413I	MISSENSE
MA4_22R	Chr20	57466842	G	T	0.103448276	GNAS	ENST00000371095_r73	c.61 G>T	p.E21*	NONSENSE
MA4_22R	Chr20	58567563	G	A	0.363013699	CDH26	ENST00000348616_r73	c.1414 G>A	p.A472T	MISSENSE
MA4_22R	Chr20	61537367	G	A	0.082352941	DIDO1	ENST00000395343_r73	c.1460 C>T	p.A487V	MISSENSE
MA4_22R	Chr4	677412	C	T	0.103896104	MFSD7	ENST00000322224_r73	c.979 G>A	p.V327M	MISSENSE
MA4_22R	Chr4	737326	G	A	0.06185567	PCGF3	ENST00000362003_r73	c.327 G>A	p.K109K	SILENT
MA4_22R	Chr4	3184176	C	A	0.101694915	HTT	ENST00000355072_r73	c.4845 C>A	p.L1615L	SILENT
MA4_22R	Chr4	6325146	C	T	0.053846154	PPP2R2C	ENST00000335585_r73	c.1227 G>A	p.L409L	SILENT
MA4_22R	Chr8	8749575	G	A	0.066037736	MFHAS1	ENST00000276282_r73	c.994 C>T	p.R332C	MISSENSE
MA4_22R	Chr8	12879165	C	T	0.06884058	KIAA1456	ENST00000524591_r73	c.977 C>T	p.A326V	MISSENSE
MA4_22R	Chr8	25191643	A	C	0.240963855	DOCK5	ENST00000276440_r73	c.2123 A>C	p.K708T	MISSENSE
MA4_22R	Chr8	28991612	G	C	0.082352941	KIF13B	ENST00000524189_r73	c.2729 C>G	p.S910C	MISSENSE
MA4_22R	Chr8	33310939	C	T	0.223880597	FUT10	ENST00000327671_r73	c.171 G>A	p.T57T	SILENT
MA4_22R	Chr8	38684879	C	T	0.057377049	TACC1	ENST00000520615_r73	c.1061 C>T	p.S354L	MISSENSE
MA4_22R	Chr8	40683102	G	T	0.12962963	ZMAT4	ENST00000315769_r73	c.94 C>A	p.H32N	MISSENSE
MA4_22R	Chr8	57354239	G	A	0.088328076	PENK	ENST00000314922_r73	c.396 C>T	p.L132L	SILENT
MA4_22R	Chr8	61767063	C	T	0.06097561	CHD7	ENST00000423902_r73	c.6917 C>T	p.A2306V	MISSENSE
MA4_22R	Chr8	67507825	G	T	0.103896104	MYBL1	ENST00000522677_r73	c.680 C>A	p.P227H	MISSENSE
MA4_22R	Chr8	94746016	G	A	0.271676301	RBM12B	ENST00000399300_r73	c.2623 C>T	p.P875S	MISSENSE
MA4_22R	Chr8	107726089	C	T	0.065573771	OXR1	ENST00000531443_r73	c.1832 C>T	p.P611L	MISSENSE
MA4_22R	Chr8	125094647	C	T	0.285714286	FER1L6	ENST00000522917_r73	c.4339 C>T	p.R1447C	MISSENSE
MA4_22R	Chr8	143618426	G	A	0.4375	BAI1	ENST00000517894_r73	c.3649 G>A	p.G1217S	MISSENSE
MA4_22R	Chr10	14991042	C	G	0.109090909	DCLRE1C	ENST00000378278_r73	c.154 G>C	p.E52Q	MISSENSE
MA4_22R	Chr10	20335922	C	G	0.054421769	PLXDC2	ENST00000377252_r73	c.449 C>G	p.S150C	MISSENSE
MA4_22R	Chr10	38246468	C	T	0.4	ZNF25	ENST00000302609_r73	c.22 G>A	p.V8M	MISSENSE
MA4_22R	Chr10	46967641	C	G	0.121875	SYT15	ENST00000503753_r73	c.436 G>C	p.G146R	MISSENSE

MA4_22R	Chr4	7043158	C	T	0.054901961	CCDC96	ENST00000310085_r73	c.1508 G>A	p.G503D	MISSENSE
MA4_22R	Chr4	20599961	G	A	0.222222222	SLIT2	ENST00000504154_r73	c.3635 G>A	p.R1212Q	MISSENSE
MA4_22R	Chr4	25418062	A	T	0.05982906	ANAPC4	ENST00000315368_r73	c.1917 A>T	p.L639F	MISSENSE
MA4_22R	Chr4	39515714	C	T	0.0875	UGDH	ENST00000316423_r73	c.253 G>A	p.V85I	MISSENSE
MA4_22R	Chr4	48517088	C	T	0.063063063	FRYL	ENST00000503238_r73	c.7894 G>A	p.E2632K	MISSENSE
MA4_22R	Chr4	53610954	C	T	0.051724138	ERVMER34-1	ENST00000443173_r73	c.734 G>A	p.R245H	MISSENSE
MA4_22R	Chr4	54348015	C	T	0.054545455	LNX1	ENST00000306888_r73	c.1069 G>A	p.E357K	MISSENSE
MA4_22R	Chr4	56322146	C	T	0.097222222	CLOCK	ENST00000309964_r73	c.900 G>A	p.L300L	SILENT
MA4_22R	Chr4	57798031	C	G	0.055214724	REST	ENST00000309042_r73	c.3007 C>G	p.Q1003E	MISSENSE
MA4_22R	Chr4	70078419	C	A	0.127272727	UGT2B11	ENST00000446444_r73	c.742 G>T	p.E248*	NONSENSE
MA4_22R	Chr4	70723328	T	G	0.307692308	SULT1E1	ENST00000226444_r73	c.35 A>C	p.E12A	MISSENSE
MA4_22R	Chr4	71701903	A	T	0.245901639	GRSF1	ENST00000254799_r73	c.486 T>A	p.T162T	SILENT
MA4_22R	Chr4	85656218	G	T	0.102040816	WDFY3	ENST00000295888_r73	c.6971 C>A	p.T2324K	MISSENSE
MA4_22R	Chr4	88987031	G	A	0.058139535	PKD2	ENST00000237596_r73	c.2358 G>A	p.R786R	SILENT
MA4_22R	Chr4	90856145	A	T	0.058536585	MMRN1	ENST00000394980_r73	c.1314 A>T	p.A438A	SILENT
MA4_22R	Chr4	100532313	C	T	0.321428571	MTTP	ENST00000265517_r73	c.1783 C>T	p.R595*	NONSENSE
MA4_22R	Chr4	110670734	A	G	0.072072072	CFI	ENST00000394634_r73	c.965 T>C	p.L322S	MISSENSE
MA4_22R	Chr4	113541204	C	T	0.061728395	C4orf21	ENST00000505019_r73	c.305 G>A	p.G102D	MISSENSE
MA4_22R	Chr4	123280818	T	A	0.065217391	KIAA1109	ENST00000264501_r73	c.14742 T>A	p.Y4914*	NONSENSE
MA4_22R	Chr4	124323268	G	A	0.111111111	SPRY1	ENST00000339241_r73	c.522 G>A	p.L174L	SILENT
MA4_22R	Chr4	129812279	G	A	0.060606061	SCLT1	ENST00000281142_r73	c.1843 C>T	p.R615*	NONSENSE
MA4_22R	Chr4	148595015	T	A	0.050761421	PRMT10	ENST00000322396_r73	c.349 A>T	p.R117W	MISSENSE
MA4_22R	Chr4	148653548	C	T	0.060301508	ARHGAP10	ENST00000336498_r73	c.96 C>T	p.T32T	SILENT
MA4_22R	Chr4	153247366	C	T	0.351851852	FBXW7	ENST00000281708_r73	c.1436 G>A	p.R479Q	MISSENSE
MA4_22R	Chr4	186560180	G	A	0.076923077	SORBS2	ENST00000437304_r73	c.1231 C>T	p.P411S	MISSENSE
MA4_22R	Chr10	50151445	A	T	0.070422535	WDFY4	ENST00000325239_r73	c.7700 A>T	p.Y2567F	MISSENSE
MA4_22R	Chr10	65379496	C	G	0.057777778	REEP3	ENST00000373758_r73	c.647 C>G	p.T216R	MISSENSE
MA4_22R	Chr10	69961725	C	G	0.053097345	MYPN	ENST00000358913_r73	c.3633 C>G	p.T1211T	SILENT
MA4_22R	Chr10	70243256	C	T	0.051282051	SLC25A16	ENST00000265870_r73	c.932 G>A	p.C311Y	MISSENSE
MA4_22R	Chr10	74953307	C	G	0.344262295	FAM149B1	ENST00000242505_r73	c.498 C>G	p.S166S	SILENT
MA4_22R	Chr10	75283499	A	T	0.054945055	USP54	ENST00000339859_r73	c.2204 T>A	p.I735K	MISSENSE
MA4_22R	Chr10	88703086	G	A	0.059782609	MMRN2	ENST00000372027_r73	c.1455 C>T	p.L485L	SILENT
MA4_22R	Chr10	96341107	G	T	0.11627907	HELLS	ENST00000348459_r73	c.1057 G>T	p.V353L	MISSENSE
MA4_22R	Chr10	101590588	G	A	0.06741573	ABCC2	ENST00000370449_r73	c.2863 G>A	p.E955K	MISSENSE
MA4_22R	Chr10	102763678	C	T	0.179775281	LZTS2	ENST00000370223_r73	c.823 C>T	p.R275W	MISSENSE
MA4_22R	Chr10	105798871	C	T	0.25	COL17A1	ENST00000353479_r73	c.2905 G>A	p.G969S	MISSENSE
MA4_22R	Chr10	111881968	G	A	0.052287582	ADD3	ENST00000360162_r73	c.1061 G>A	p.G354E	MISSENSE

MA4_22R	Chr10	124895854	T	C	0.05982906	HMX3	ENST00000357878_r73	c.288 T>C	p.F96F	SILENT
MA4_22R	Chr10	129913861	C	T	0.194331984	MKI67	ENST00000368654_r73	c.811 G>A	p.A271T	MISSENSE
MA4_22R	Chr10	131958338	G	T	0.108695652	GLRX3	ENST00000331244_r73	Exon 3 5 G>T	-	ESSENTIAL_SPLICE
MA4_22R	Chr19	1005543	C	T	0.415384615	GRIN3B	ENST00000234389_r73	c.2043 C>T	p.H681H	SILENT
MA4_22R	Chr19	2114166	C	T	0.053811659	AP3D1	ENST00000355272_r73	c.2559 G>A	p.E853E	SILENT
MA4_22R	Chr19	2291521	C	T	0.096774194	LINGO3	ENST00000585527_r73	c.255 G>A	p.L85L	SILENT
MA4_22R	Chr19	3542962	C	T	0.063829787	MFSD12	ENST00000398558_r73	c.1434 G>A	p.W478*	NONSENSE
MA4_22R	Chr19	5211657	G	C	0.05	PTPRS	ENST00000587303_r73	c.5178 C>G	p.P1726P	SILENT
MA4_22R	Chr19	11976988	C	G	0.056603774	ZNF439	ENST00000304030_r73	c.17 C>G	p.P6R	MISSENSE
MA4_22R	Chr19	14066781	G	A	0.25	DCAF15	ENST00000254337_r73	c.424 G>A	p.V142I	MISSENSE
MA4_22R	Chr19	16957871	G	A	0.073684211	SIN3B	ENST00000379803_r73	c.673 G>A	p.E225K	MISSENSE
MA4_22R	Chr19	19751255	C	T	0.068376068	GMIP	ENST00000203556_r73	c.364 G>A	p.E122K	MISSENSE
MA4_22R	Chr19	33600873	G	A	0.085714286	GPATCH1	ENST00000170564_r73	c.1536 G>A	p.K512K	SILENT
MA4_22R	Chr19	35610320	G	T	0.139534884	FXYD3	ENST00000604404_r73	c.40 G>T	p.G14C	MISSENSE
MA4_22R	Chr19	37240210	G	C	0.059405941	ZNF850	ENST00000591344_r73	c.1732 C>G	p.Q578E	MISSENSE
MA4_22R	Chr19	39364604	G	A	0.102941177	RINL	ENST00000591812_r73	c.235 C>T	p.P79S	MISSENSE
MA4_22R	Chr19	40842060	T	A	0.058823529	C19orf47	ENST00000582783_r73	c.290 A>T	p.D97V	MISSENSE
MA4_22R	Chr19	41779891	C	T	0.432432432	HNRNPUL1	ENST00000595018_r73	c.277 C>T	p.R93C	MISSENSE
MA4_22R	Chr19	46417691	C	T	0.087301587	NANOS2	ENST00000341294_r73	c.261 G>A	p.V87V	SILENT
MA4_22R	Chr19	48801484	C	A	0.110091743	CCDC114	ENST00000315396_r73	c.1243 G>T	p.E415*	NONSENSE
MA4_22R	Chr19	55994493	G	A	0.085714286	ZNF628	ENST00000598519_r73	c.1933 G>A	p.A645T	MISSENSE
MA4_22R	Chr19	56243463	C	T	0.081395349	NLRP9	ENST00000332836_r73	c.1734 G>A	p.L578L	SILENT
MA4_22R	Chr19	58989159	G	T	0.101265823	ZNF446	ENST00000594369_r73	c.498 G>T	p.V166V	SILENT
MA4_22R	Chr5	1280309	G	A	0.30075188	TERT	ENST00000310581_r73	c.1914 C>T	p.Y638Y	SILENT
MA4_22R	Chr5	31318018	C	T	0.19	CDH6	ENST00000265071_r73	c.1869 C>T	p.I623I	SILENT
MA4_22R	Chr5	41911179	G	A	0.097560976	C5orf51	ENST00000381647_r73	c.384 G>A	p.L128L	SILENT
MA4_22R	Chr5	53815413	G	A	0.051136364	SNX18	ENST00000343017_r73	c.1631 G>A	p.W544*	NONSENSE
MA4_22R	Chr5	64492932	G	A	0.052173913	ADAMTS6	ENST00000381055_r73	c.2622 C>T	p.S874S	SILENT
MA4_22R	Chr5	74026094	G	A	0.2125	GFM2	ENST00000296805_r73	c.1717 C>T	p.R573C	MISSENSE
MA4_22R	Chr5	75914346	G	A	0.05	F2RL2	ENST00000296641_r73	c.186 C>T	p.A62A	SILENT
MA4_22R	Chr5	96341909	A	T	0.096774194	LNPEP	ENST00000231368_r73	c.1918 A>T	p.K640*	NONSENSE
MA4_22R	Chr5	118483009	C	G	0.052631579	DMXL1	ENST00000311085_r73	c.2755 C>G	p.P919A	MISSENSE
MA4_22R	Chr5	124036904	G	C	0.052083333	ZNF608	ENST00000306315_r73	c.965 C>G	p.P322R	MISSENSE
MA4_22R	Chr5	137727662	G	A	0.052631579	KDM3B	ENST00000314358_r73	c.2341 G>A	p.A781T	MISSENSE
MA4_22R	Chr5	140176813	G	A	0.128205128	PCDHA2	ENST00000526136_r73	c.2264 G>A	p.R755Q	MISSENSE
MA4_22R	Chr5	140215289	G	A	0.339622642	PCDHA7	ENST00000525929_r73	c.1321 G>A	p.V441M	MISSENSE
MA4_22R	Chr5	140750726	G	A	0.051546392	PCDHGB3	ENST00000576222_r73	c.765 G>A	p.L255L	SILENT

MA4_22R	Chr5	148407426	C	T	0.090909091	SH3TC2	ENST00000515425_r73	c.1869 G>A	p.G623G	SILENT
MA4_22R	Chr5	149417020	G	C	0.285714286	HMGXB3	ENST00000502717_r73	c.2343 G>C	p.V781V	SILENT
MA4_22R	Chr5	149495412	G	T	0.12962963	PDGFRB	ENST00000261799_r73	c.3235 C>A	p.Q1079K	MISSENSE
MA4_22R	Chr5	157053387	A	T	0.067961165	SOX30	ENST00000265007_r73	c.2223 T>A	p.S741R	MISSENSE
MA4_22R	Chr5	170827164	G	A	0.075268817	NPM1	ENST00000517671_r73	c.532 G>A	p.D178N	MISSENSE
MA4_22R	Chr5	176823783	G	A	0.051546392	SLC34A1	ENST00000324417_r73	c.1224 G>A	p.V408V	SILENT
MA4_22R	Chr5	176827505	G	A	0.063829787	PFN3	ENST00000358571_r73	c.73 C>T	p.H25Y	MISSENSE
MA4_22R	Chr5	180552290	C	T	0.050505051	OR2V1	ENST00000329365_r73	c.15 G>A	p.V5V	SILENT
MA4_22R	Chr7	44714066	G	A	0.114754098	OGDH	ENST00000443864_r73	c.845 G>A	p.G282D	MISSENSE
MA4_22R	Chr7	48314009	C	T	0.063157895	ABCA13	ENST00000435803_r73	c.4746 C>T	p.A1582A	SILENT
MA4_22R	Chr7	56119600	T	A	0.078651685	CCT6A	ENST00000275603_r73	c.59 T>A	p.L20Q	MISSENSE
MA4_22R	Chr7	72718795	G	A	0.113636364	NSUN5	ENST00000428206_r73	c.590 C>T	p.A197V	MISSENSE
MA4_22R	Chr7	75051365	G	A	0.161290323	POM121C	ENST00000453279_r73	c.2170 C>T	p.P724S	MISSENSE
MA4_22R	Chr7	76952988	C	T	0.052238806	GSAP	ENST00000257626_r73	c.1899 G>A	p.M633I	MISSENSE
MA4_22R	Chr7	81964550	T	C	0.095238095	CACNA2D1	ENST00000356860_r73	c.195 A>G	p.Q65Q	SILENT
MA4_22R	Chr7	83634702	C	T	0.115853659	SEMA3A	ENST00000265362_r73	c.1313 G>A	p.R438Q	MISSENSE
MA4_22R	Chr7	86823157	G	A	0.05	DMTF1	ENST00000331242_r73	c.1767 G>A	p.L589L	SILENT
MA4_22R	Chr7	87195400	C	T	0.05	ABCB1	ENST00000265724_r73	c.688 G>A	p.A230T	MISSENSE
MA4_22R	Chr7	89856763	C	G	0.25	STEAP2	ENST00000287908_r73	c.971 C>G	p.P324R	MISSENSE
MA4_22R	Chr7	93055777	G	T	0.10619469	CALCR	ENST00000394441_r73	c.1316 C>A	p.P439Q	MISSENSE
MA4_22R	Chr7	97847329	G	T	0.107142857	TECPR1	ENST00000447648_r73	c.3183 C>A	p.I1061I	SILENT
MA4_22R	Chr7	98957229	C	T	0.077586207	ARPC1A	ENST00000262942_r73	c.851 C>T	p.S284F	MISSENSE
MA4_22R	Chr7	99711864	T	A	0.074324324	TAF6	ENST00000437822_r73	c.80 A>T	p.H27L	MISSENSE
MA4_22R	Chr7	121651144	C	T	0.06918239	PTPRZ1	ENST00000393386_r73	c.2044 C>T	p.R682C	MISSENSE
MA4_22R	Chr7	124503458	C	T	0.052083333	POT1	ENST00000357628_r73	c.492 G>A	p.L164L	SILENT
MA4_22R	Chr7	128415200	T	A	0.1	OPN1SW	ENST00000249389_r73	c.361 A>T	p.T121S	MISSENSE
MA4_22R	Chr7	132973690	G	T	0.108695652	EXOC4	ENST00000393161_r73	c.291 G>T	p.L97L	SILENT
MA4_22R	Chr7	144095425	G	T	0.103092784	NOBOX	ENST00000483238_r73	c.1628 C>A	p.P543Q	MISSENSE
MA4_22R	Chr7	150779363	C	T	0.053571429	TMUB1	ENST00000297533_r73	c.288 G>A	p.P96P	SILENT
MA4_22R	Chr2	9580763	C	A	0.111111111	CPSF3	ENST00000238112_r73	c.904 C>A	p.P302T	MISSENSE
MA4_22R	Chr2	15644291	T	A	0.059288538	NBAS	ENST00000281513_r73	c.932 A>T	p.Y311F	MISSENSE
MA4_22R	Chr2	23785338	C	T	0.5	KLHL29	ENST00000486442_r73	c.272 C>T	p.A91V	MISSENSE
MA4_22R	Chr2	31570446	G	A	0.538461539	XDH	ENST00000379416_r73	c.3218 C>T	p.P1073L	MISSENSE
MA4_22R	Chr2	32828115	G	T	0.13559322	BIRC6	ENST00000421745_r73	c.14035 G>T	p.E4679*	NONSENSE
MA4_22R	Chr2	43924331	C	T	0.055555556	PLEKHH2	ENST00000282406_r73	c.524 C>T	p.S175F	MISSENSE
MA4_22R	Chr2	48602394	C	T	0.057471264	FOXN2	ENST00000340553_r73	c.1108 C>T	p.Q370*	NONSENSE
MA4_22R	Chr2	49295382	G	A	0.095238095	FSHR	ENST00000406846_r73	c.200 C>T	p.S67L	MISSENSE

MA4_22R	Chr2	54148234	C	T	0.678571429	PSME4	ENST00000404125_r73	c.2054 G>A	p.R685Q	MISSENSE
MA4_22R	Chr2	55096480	G	T	0.115384615	EML6	ENST00000356458_r73	c.2214 G>T	p.V738V	SILENT
MA4_22R	Chr2	55566693	G	C	0.10619469	CCDC88A	ENST00000336838_r73	c.1425 C>G	p.T475T	SILENT
MA4_22R	Chr2	56145080	G	C	0.054545455	EFEMP1	ENST00000394555_r73	c.237 C>G	p.V79V	SILENT
MA4_22R	Chr2	61541776	C	T	0.054794521	USP34	ENST00000398571_r73	c.3486 G>A	p.M1162I	MISSENSE
MA4_22R	Chr2	70486562	G	T	0.106382979	PCYOX1	ENST00000433351_r73	c.183 G>T	p.V61V	SILENT
MA4_22R	Chr2	71631089	A	T	0.05511811	ZNF638	ENST00000264447_r73	c.2919 A>T	p.S973S	SILENT
MA4_22R	Chr2	73989867	G	T	0.118644068	DUSP11	ENST00000272444_r73	c.1055 C>A	p.A352E	MISSENSE
MA4_22R	Chr2	74709640	G	A	0.068181818	CCDC142	ENST00000290418_r73	c.325 C>T	p.R109*	NONSENSE
MA4_22R	Chr2	74902895	C	T	0.059405941	SEMA4F	ENST00000357877_r73	c.1502 C>T	p.S501F	MISSENSE
MA4_22R	Chr2	84774741	G	A	0.056962025	DNAH6	ENST00000237449_r73	Exon 6 5 G>A	-	ESSENTIAL_SPLICE
MA4_22R	Chr2	86847448	C	T	0.049586777	CHMP3	ENST00000439940_r73	Exon 3 5 G>A	-	ESSENTIAL_SPLICE
MA4_22R	Chr2	86847448	C	T	0.049586777	RNF103-CHMP3	ENST00000604011_r73	Exon 3 5 G>A	-	ESSENTIAL_SPLICE
MA4_22R	Chr2	86847448	C	T	0.049586777	RNF103	ENST00000237455_r73	Exon 2 5 G>A	-	ESSENTIAL_SPLICE
MA4_22R	Chr2	86847448	C	T	0.049586777	CHMP3	ENST00000439940_r73	Exon 3 5 G>A	-	ESSENTIAL_SPLICE
MA4_22R	Chr2	87017571	C	T	0.265151515	CD8A	ENST00000352580_r73	c.283 G>A	p.G95R	MISSENSE
MA4_22R	Chr2	88387471	C	T	0.386363636	SMYD1	ENST00000419482_r73	c.405 C>T	p.H135H	SILENT
MA4_22R	Chr2	102793049	C	T	0.248275862	IL1R1	ENST00000410023_r73	c.1540 C>T	p.R514C	MISSENSE
MA4_22R	Chr2	105473338	G	A	0.294797688	POU3F3	ENST00000361360_r73	c.1370 G>A	p.R457Q	MISSENSE
MA4_22R	Chr2	128339485	G	A	0.27027027	MYO7B	ENST00000409816_r73	c.1100 G>A	p.R367Q	MISSENSE
MA4_22R	Chr2	130910208	G	T	0.12195122	SMPD4	ENST00000351288_r73	c.2434 C>A	p.L812M	MISSENSE
MA4_22R	Chr2	133618104	G	A	0.050632911	NCKAP5	ENST00000409261_r73	c.768 C>T	p.F256F	SILENT
MA4_22R	Chr2	135308203	C	T	0.317460318	TMEM163	ENST00000281924_r73	c.396 G>A	p.S132S	SILENT
MA4_22R	Chr2	160801458	G	A	0.079096045	PLA2R1	ENST00000283243_r73	c.4103 C>T	p.P1368L	MISSENSE
MA4_22R	Chr2	162280208	G	A	0.34	TBR1	ENST00000389554_r73	c.1519 G>A	p.A507T	MISSENSE
MA4_22R	Chr2	167108340	C	T	0.061728395	SCN9A	ENST00000409672_r73	c.3374 G>A	p.G1125E	MISSENSE
MA4_22R	Chr2	171055777	C	T	0.061068702	MYO3B	ENST00000409044_r73	c.62 C>T	p.P21L	MISSENSE
MA4_22R	Chr2	179429213	G	A	0.314285714	TTN	ENST00000342992_r73	c.73942 C>T	p.R24648C	MISSENSE
MA4_22R	Chr2	179480116	G	A	0.067039106	TTN	ENST00000342992_r73	c.40852 C>T	p.R13618C	MISSENSE
MA4_22R	Chr2	190436555	T	G	0.055555556	SLC40A1	ENST00000261024_r73	c.400 A>C	p.I134L	MISSENSE
MA4_22R	Chr2	192255067	C	T	0.05952381	MYO1B	ENST00000339514_r73	c.1831 C>T	p.L611L	SILENT
MA4_22R	Chr2	198570371	C	T	0.056074766	MARS2	ENST00000282276_r73	c.242 C>T	p.P81L	MISSENSE
MA4_22R	Chr2	202248908	C	T	0.256281407	TRAK2	ENST00000332624_r73	c.1995 G>A	p.S665S	SILENT
MA4_22R	Chr2	204009852	G	A	0.06993007	NBEAL1	ENST00000449802_r73	c.5186 G>A	p.R1729Q	MISSENSE
MA4_22R	Chr2	206588620	G	A	0.063063063	NRP2	ENST00000360409_r73	c.776 G>A	p.G259D	MISSENSE
MA4_22R	Chr2	210561752	C	T	0.103448276	MAP2	ENST00000360351_r73	c.4499 C>T	p.S1500F	MISSENSE
MA4_22R	Chr2	215976355	G	T	0.108695652	ABCA12	ENST00000272895_r73	c.128 C>A	p.T43N	MISSENSE

MA4_22R	Chr2	219487531	G	A	0.057692308	PLCD4	ENST00000450993_r73	c.702 G>A	p.E234E	SILENT
MA4_22R	Chr2	220112400	G	A	0.284671533	STK16	ENST00000409638_r73	c.578 G>A	p.R193Q	MISSENSE
MA4_22R	Chr2	220478944	C	A	0.157894737	STK11IP	ENST00000295641_r73	c.2811 C>A	p.V937V	SILENT
MA4_22R	Chr2	223478577	A	T	0.081081081	FARSB	ENST00000281828_r73	c.1415 T>A	p.L472Q	MISSENSE
MA4_22R	Chr17	3030327	C	G	0.112359551	OR1G1	ENST00000328890_r73	c.519 G>C	p.E173D	MISSENSE
MA4_22R	Chr17	5358516	C	T	0.076271186	DHX33	ENST00000225296_r73	c.1111 G>A	p.D371N	MISSENSE
MA4_22R	Chr17	10317560	C	T	0.054054054	MYH8	ENST00000403437_r73	c.957 G>A	p.G319G	SILENT
MA4_22R	Chr17	10451131	G	A	0.051851852	MYH2	ENST00000245503_r73	c.107 C>T	p.T36I	MISSENSE
MA4_22R	Chr17	19186759	C	T	0.05027933	EPN2	ENST00000314728_r73	c.327 C>T	p.F109F	SILENT
MA4_22R	Chr17	28384857	T	A	0.050314465	EFCAB5	ENST00000536908_r73	c.2361 T>A	p.F787L	MISSENSE
MA4_22R	Chr17	31355390	C	T	0.342857143	ASIC2	ENST00000225823_r73	c.1008 G>A	p.P336P	SILENT
MA4_22R	Chr17	34867273	G	A	0.101449275	MYO19	ENST00000431794_r73	c.916 C>T	p.L306F	MISSENSE
MA4_22R	Chr17	35880734	C	G	0.071428571	SYNRG	ENST00000339208_r73	c.3684 G>C	p.L1228L	SILENT
MA4_22R	Chr17	38711651	C	T	0.076923077	CCR7	ENST00000246657_r73	c.480 G>A	p.Q160Q	SILENT
MA4_22R	Chr17	38927490	T	A	0.071428571	KRT26	ENST00000335552_r73	Exon 2 - 2 A>T	-	ESSENTIAL_SPLICE
MA4_22R	Chr17	39975865	G	A	0.074534162	FKBP10	ENST00000321562_r73	c.1001 G>A	p.C334Y	MISSENSE
MA4_22R	Chr17	39992198	C	T	0.066037736	NT5C3B	ENST00000435506_r73	c.24 G>A	p.L8L	SILENT
MA4_22R	Chr2	239353004	C	T	0.068181818	ASB1	ENST00000264607_r73	c.516 C>T	p.V172V	SILENT
MA4_22R	Chr2	241817491	G	T	0.103092784	AGXT	ENST00000307503_r73	c.995 G>T	p.W332L	MISSENSE
MA4_22R	Chr17	41598785	G	T	0.150943396	DHX8	ENST00000262415_r73	c.3115 G>T	p.E1039*	NONSENSE
MA4_22R	Chr17	44109023	G	A	0.115942029	KANSL1	ENST00000574590_r73	c.3137 C>T	p.P1046L	MISSENSE
MA4_22R	Chr17	46628451	T	C	0.666666667	HOXB3	ENST00000470495_r73	c.541 A>G	p.S181G	MISSENSE
MA4_22R	Chr17	48245917	G	A	0.074766355	SGCA	ENST00000344627_r73	c.568 G>A	p.E190K	MISSENSE
MA4_22R	Chr17	57644084	C	A	0.14893617	DHX40	ENST00000251241_r73	c.209 C>A	p.S70*	NONSENSE
MA4_22R	Chr17	58286188	G	A	0.064220184	USP32	ENST00000300896_r73	c.2600 C>T	p.A867V	MISSENSE
MA4_22R	Chr17	63537574	G	A	0.12244898	AXIN2	ENST00000307078_r73	c.1058 C>T	p.P353L	MISSENSE
MA4_22R	Chr17	73488684	C	T	0.059602649	KIAA0195	ENST00000314256_r73	c.1726 C>T	p.Q576*	NONSENSE
MA4_22R	Chr17	73520492	G	A	0.071428571	TSEN54	ENST00000333213_r73	c.1580 G>A	p.*527*	SILENT
MA4_22R	Chr17	74283314	C	T	0.073770492	QRICH2	ENST00000262765_r73	c.3472 G>A	p.E1158K	MISSENSE
MA4_22R	Chr17	74865120	C	T	0.0625	MGAT5B	ENST00000301618_r73	c.9 C>T	p.T3T	SILENT
MA4_22R	Chr22	17669257	C	T	0.058252427	CECR1	ENST00000399839_r73	c.1053 G>A	p.L351L	SILENT
MA4_22R	Chr22	21119138	T	A	0.063063063	PI4KA	ENST00000255882_r73	c.2675 A>T	p.Y892F	MISSENSE
MA4_22R	Chr22	30925111	C	T	0.058823529	SEC14L6	ENST00000402034_r73	c.627 G>A	p.M209I	MISSENSE
MA4_22R	Chr1	1007257	G	A	0.271428571	RNF223	ENST00000453464_r73	c.690 C>T	p.P230P	SILENT
MA4_22R	Chr1	1168143	G	A	0.483516484	B3GALT6	ENST00000379198_r73	c.485 G>A	p.R162Q	MISSENSE
MA4_22R	Chr1	1960665	C	A	0.101010101	GABRD	ENST00000378585_r73	c.807 C>A	p.F269L	MISSENSE
MA4_22R	Chr1	3683892	G	A	0.068181818	CCDC27	ENST00000294600_r73	c.1626 G>A	p.L542L	SILENT

MA4_22R	Chr1	4772148	G	A	0.561403509	AJAP1	ENST00000378190_r73	c.218 G>A	p.R73Q	MISSENSE
MA4_22R	Chr1	6531080	G	A	0.403508772	PLEKHG5	ENST00000377748_r73	c.1593 C>T	p.R531R	SILENT
MA4_22R	Chr1	11589887	C	T	0.195121951	PTCHD2	ENST00000294484_r73	c.2973 C>T	p.C991C	SILENT
MA4_22R	Chr1	17396656	T	A	0.064102564	PADI2	ENST00000375486_r73	c.1691 A>T	p.Q564L	MISSENSE
MA4_22R	Chr1	24408594	C	T	0.265306122	MYOM3	ENST00000374434_r73	c.2177 G>A	p.R726H	MISSENSE
MA4_22R	Chr22	40042742	C	T	0.077419355	CACNA1I	ENST00000404898_r73	c.1318 C>T	p.Q440*	NONSENSE
MA4_22R	Chr22	50714157	C	T	0.089552239	PLXNB2	ENST00000449103_r73	c.5493 G>A	p.L1831L	SILENT
MA4_22R	Chr22	50714157	C	T	0.089552239	AL022328.1	ENST00000595015_r73	c.55 C>T	p.Q19*	NONSENSE
MA4_22R	Chr1	156509684	G	A	0.051094891	IQGAP3	ENST00000361170_r73	c.2838 C>T	p.S946S	SILENT
MA4_22R	Chr1	158326365	C	T	0.113402062	CD1E	ENST00000368167_r73	c.982 C>T	p.R328W	MISSENSE
MA4_22R	Chr1	158450438	G	A	0.333333333	OR10R2	ENST00000368152_r73	c.771 G>A	p.A257A	SILENT
MA4_22R	Chr1	161165409	C	A	0.108910891	ADAMTS4	ENST00000367996_r73	c.1107 G>T	p.M369I	MISSENSE
MA4_22R	Chr1	162567643	G	A	0.058823529	UAP1	ENST00000367926_r73	c.1420 G>A	p.G474R	MISSENSE
MA4_22R	Chr1	169292461	C	T	0.096491228	NME7	ENST00000472647_r73	c.64 G>A	p.E22K	MISSENSE
MA4_22R	Chr1	169493034	C	T	0.063380282	F5	ENST00000367797_r73	Exon 20 5 G>A	-	ESSENTIAL_SPLICE
MA4_22R	Chr1	172543102	C	A	0.111111111	SUCO	ENST00000263688_r73	c.1121 C>A	p.S374Y	MISSENSE
MA4_22R	Chr1	177245460	C	T	0.053763441	FAM5B	ENST00000361539_r73	c.902 C>T	p.P301L	MISSENSE
MA4_22R	Chr1	179562979	A	G	0.389380531	TDRD5	ENST00000367614_r73	c.617 A>G	p.E206G	MISSENSE
MA4_22R	Chr1	180885344	G	A	0.070175439	KIAA1614	ENST00000367588_r73	c.105 G>A	p.V35V	SILENT
MA4_22R	Chr1	184764692	C	T	0.061643836	FAM129A	ENST00000367511_r73	c.2206 G>A	p.G736R	MISSENSE
MA4_22R	Chr1	190234153	G	A	0.420634921	FAM5C	ENST00000367462_r73	c.460 C>T	p.R154W	MISSENSE
MA4_22R	Chr1	205033551	G	A	0.064516129	CNTN2	ENST00000331830_r73	c.1342 G>A	p.A448T	MISSENSE
MA4_22R	Chr1	223803625	C	T	0.058823529	CAPN8	ENST00000366872_r73	c.1342 G>A	p.G448R	MISSENSE
MA4_22R	Chr1	226127230	G	T	0.135135135	LEFTY2	ENST00000366820_r73	c.568 C>A	p.L190M	MISSENSE
MA4_22R	Chr1	228506816	C	T	0.2125	OBSCN	ENST00000284548_r73	c.14363 C>T	p.T4788M	MISSENSE
MA4_22R	Chr1	232650601	C	G	0.053691275	SIPA1L2	ENST00000366630_r73	c.485 G>C	p.S162T	MISSENSE
MA4_22R	Chr1	232943422	A	T	0.05952381	MAP10	ENST00000418460_r73	c.2653 A>T	p.K885*	NONSENSE
MA4_22R	Chr1	235887462	C	T	0.060240964	LYST	ENST00000389794_r73	c.9181 G>A	p.E3061K	MISSENSE
MA4_22R	Chr11	15199983	GG	-	0.123076923	INSC	ENST00000379554_r73	c.710 GG>-	p.R237fs*10	FRAMESHIFT
MA4_22R	Chr7	26237308	G	-	0.180124224	HNRNPA2B1	ENST00000354667_r73	c.87 C>-	p.S29fs*9	FRAMESHIFT
MA4_22R	Chr7	100001318	G	-	0.185185185	ZCWPW1	ENST00000398027_r73	c.1409 C>-	p.T470fs*41	FRAMESHIFT
MA4_22R	Chr2	43924491	G	-	0.113207547	PLEKHH2	ENST00000282406_r73	c.684 G>-	p.M228fs*16	FRAMESHIFT
MA4_22R	Chr2	73430157	GC	-	0.133333333	NOTO	ENST00000398468_r73	c.363 GC>-	p.L121fs*32	FRAMESHIFT
MA4_22R	Chr2	71160044	T	-	0.125	VAX2	ENST00000234392_r73	c.583 T>-	p.P195fs*9	FRAMESHIFT
MA4_22R	Chr2	113588969	TC	-	0.107142857	IL1B	ENST00000263341_r73	c.496 GA>-	p.E166fs*3	FRAMESHIFT
MA4_22R	Chr2	201399723	TTC	-	0.148148148	SGOL2	ENST00000357799_r73	c.138 TTC>-	p.N46 NS>N	MISSENSE
MA4_22R	Chr2	220412717	CC	-	0.142857143	TMEM198	ENST00000344458_r73	c.656 CC>-	p.A219fs*22	FRAMESHIFT

MA4_22R	Chr2	222291323	AC	-	0.101694915	EPHA4	ENST00000409938_r73	c.2706 GT>-	p.L902fs*7	FRAMESHIFT
MA4_22R	Chr2	238662045	G	-	0.117647059	LRRFIP1	ENST00000308482_r73	c.961 G>-	p.D321fs*3	FRAMESHIFT
MA4_22R	Chr1	22970558	GCT	-	0.176470588	C1QC	ENST00000374640_r73	c.42 GCT>-	p.K14 KL>K	MISSENSE
MA4_22R	Chr1	31899598	C	-	0.102040816	SERINC2	ENST00000373710_r73	c.735 C>-	p.G245fs*112	FRAMESHIFT
MA4_22R	Chr1	150469354	A	-	0.133333333	TARS2	ENST00000369064_r73	c.990 A>-	p.R330fs*6	FRAMESHIFT
MA4_22R	Chr16	22019647	G	-	0.230769231	C16orf52	ENST00000542527_r73	c.25 G>-	p.G9fs*71	FRAMESHIFT
MA4_22R	Chr16	67680870	GC	-	0.117647059	RLTPR	ENST00000334583_r73	c.605 GC>-	p.G202fs*30	FRAMESHIFT
MA4_22R	Chr16	68026446	T	-	0.142857143	DPEP2	ENST00000393847_r73	c.357 A>-	p.L119fs*51	FRAMESHIFT
MA4_22R	Chr13	51929241	T	-	0.107526882	SERPINE3	ENST00000521255_r73	c.962 T>-	p.L321fs*9	FRAMESHIFT
MA4_22R	Chr6	38743571	G	-	0.148148148	DNAH8	ENST00000449981_r73	c.1806 G>-	p.L602fs*6	FRAMESHIFT
MA4_22R	ChrX	13792720	TG	-	0.107142857	GPM6B	ENST00000454189_r73	c.683 CA>-	p.T228fs*2	FRAMESHIFT
MA4_22R	ChrX	47918404	C	-	0.125	ZNF630	ENST00000409324_r73	c.1427 G>-	p.G476fs*59	FRAMESHIFT
MA4_22R	ChrX	50654097	C	-	0.153846154	BMP15	ENST00000252677_r73	c.314 C>-	p.A105fs*26	FRAMESHIFT
MA4_22R	ChrX	53588762	CC	-	0.12	HUWE1	ENST00000342160_r73	c.7461 GG>-	p.R2487fs*3	FRAMESHIFT
MA4_22R	ChrX	99941061	T	-	0.1	SYTL4	ENST00000372989_r73	c.1375 A>-	p.G459fs*45	FRAMESHIFT
MA4_22R	ChrX	104728339	C	-	0.127659575	IL1RAPL2	ENST00000372582_r73	c.732 C>-	p.F244fs*10	FRAMESHIFT
MA4_22R	ChrX	106229235	T	-	0.113207547	MORC4	ENST00000355610_r73	c.504 A>-	p.I168fs*11	FRAMESHIFT
MA4_22R	ChrX	117695409	TA	-	0.121212121	DOCK11	ENST00000276202_r73	c.622 TA>-	p.Y208fs*1	FRAMESHIFT
MA4_22R	ChrX	131211974	CA	-	0.126984127	FRMD7	ENST00000298542_r73	c.2070 TG>-	p.D690fs*11	FRAMESHIFT
MA4_22R	Chr3	9989580	CG	-	0.153846154	PRRT3	ENST00000295984_r73	c.1276 CG>-	p.R426fs*225	FRAMESHIFT
MA4_22R	Chr3	11372865	GCCGGGA	-	0.100628931	ATG7	ENST00000446450_r73	c.613 GCCGGGA>-	p.P205fs*420	FRAMESHIFT
MA4_22R	Chr3	52538052	GC	-	0.106666667	STAB1	ENST00000321725_r73	c.1031 GC>-	p.C344fs*1	FRAMESHIFT
MA4_22R	Chr9	38068159	AG	-	0.115384615	RP11-613M10.9	ENST00000540557_r73	c.483 CT>-	p.L161fs*84	FRAMESHIFT
MA4_22R	Chr9	38068159	AG	-	0.115384615	SHB	ENST00000377707_r73	c.483 CT>-	p.L161fs*84	FRAMESHIFT
MA4_22R	Chr9	140329682	A	-	0.115384615	ENTPD8	ENST00000344119_r73	c.1159 T>-	p.W387fs*23	FRAMESHIFT
MA4_22R	Chr12	33592372	A	-	0.123076923	SYT10	ENST00000228567_r73	c.86 T>-	p.V29fs*29	FRAMESHIFT
MA4_22R	Chr12	64062132	G	-	0.113207547	DPY19L2	ENST00000324472_r73	c.42 C>-	p.S14fs*20	FRAMESHIFT
MA4_22R	Chr12	102591411	T	-	0.115384615	PMCH	ENST00000329406_r73	c.138 A>-	p.K46fs*29	FRAMESHIFT
MA4_22R	Chr12	108133240	C	-	0.125	PRDM4	ENST00000228437_r73	c.2013 G>-	p.E671fs*42	FRAMESHIFT
MA4_22R	Chr12	121678328	-	TT	0.12195122	CAMKK2	ENST00000392474_r73	c.1614 ->AA	p.K538fs*7	FRAMESHIFT
MA4_22R	Chr14	95909596	C	-	0.103896104	SYNE3	ENST00000334258_r73	c.1807 G>-	p.A603fs*64	FRAMESHIFT
MA4_22R	Chr15	42164605	TGGT	-	0.117647059	SPTBN5	ENST00000320955_r73	c.5057 ACCA>-	p.D1686fs*44	FRAMESHIFT
MA4_22R	Chr4	6037696	CT	-	0.111111111	JAKMIP1	ENST00000409021_r73	c.2313 AG>-	p.R771fs*72	FRAMESHIFT
MA4_22R	Chr19	10096537	G	-	0.166666667	COL5A3	ENST00000264828_r73	c.2387 C>-	p.P796fs*19	FRAMESHIFT
MA4_22R	Chr19	17337584	G	-	0.24	OCEL1	ENST00000215061_r73	c.152 G>-	p.C51fs*106	FRAMESHIFT
MA4_22R	Chr19	56154064	T	-	0.166666667	ZNF580	ENST00000325333_r73	c.190 T>-	p.T64fs*127	FRAMESHIFT
MA4_22R	Chr10	33017914	A	-	0.181818182	C10orf68	ENST00000302316_r73	c.689 A>-	p.E230fs*8	FRAMESHIFT

MA4_22R	Chr5	61833074	A	-	0.136986301	IPO11	ENST00000325324_r73	c.2208 A>-	p.L736fs*23	FRAMESHIFT
MA4_22R	Chr5	72183033	A	-	0.117647059	TNPO1	ENST00000337273_r73	c.1287 A>-	p.L429fs*12	FRAMESHIFT
MA4_22R	Chr5	98109796	TC	-	0.130434783	RGMB	ENST00000308234_r73	c.145 TC>-	p.S49fs*10	FRAMESHIFT
MA4_23	Chr18	43311053	C	T	0.143349807	SLC14A1	ENST00000321925_r73	c.225 C>T	p.P75P	SILENT
MA4_23	Chr19	6374247	C	G	0.474226804	ALKBH7	ENST00000245812_r73	c.238 C>G	p.R80G	MISSENSE
MA4_23	Chr19	40900136	G	A	0.705932932	PRX	ENST00000324001_r73	c.4123 C>T	p.R1375W	MISSENSE
MA4_23	Chr6	63921655	T	C	0.006410997	FKBP1C	ENST00000370659_r73	c.194 T>C	p.V65A	MISSENSE
MA4_23	Chr7	100275000	G	A	0.049090909	GNB2	ENST00000303210_r73	c.229 G>A	p.G77R	MISSENSE
MA4_23	Chr20	57571837	C	T	0.4588161	CTSZ	ENST00000217131_r73	c.658 G>A	p.E220K	MISSENSE
MA4_23	Chr1	115258747	C	T	0.06218555	NRAS	ENST00000311936_r73	c.35 G>A	p.G12D	MISSENSE
MA4_23	Chr12	25398284	C	A	0.0203125	KRAS	ENST00000311936_r73	c.437 C>T	p.A146V	MISSENSE
MA4_23	Chr12	25378561	G	A	0.02244898	KRAS	ENST00000369535_r73	c.35 G>A	p.G12D	MISSENSE
MA4_23	Chr12	124856830	C	T	0.424094635	NCOR2	ENST00000405201_r73	c.2545 G>A	p.E849K	MISSENSE
MA4_23	Chr11	58959633	G	A	0.19753824	DTX4	ENST00000227451_r73	c.1284 G>A	p.T428T	SILENT
MA4_23	Chr18	54362417	A	G	0.011690047	WDR7	ENST00000357574_r73	c.1345 A>G	p.M449V	MISSENSE
MA4_23R	Chr1	152188413	C	T	0.134920635	HRNR	ENST00000368801_r73	c.5692 G>A	p.E1898K	MISSENSE
MA4_23R	Chr11	58959633	G	A	0.194152547	DTX4	ENST00000227451_r73	c.1284 G>A	p.T428T	SILENT
MA4_23R	Chr12	124856830	C	T	0.418136171	NCOR2	ENST00000405201_r73	c.2545 G>A	p.E849K	MISSENSE
MA4_23R	Chr13	28597490	C	T	0.186016213	FLT3	ENST00000241453_r73	c.2415 G>A	p.K805K	SILENT
MA4_23R	Chr15	41989003	G	C	0.170652877	MGA	ENST00000566586_r73	c.1795 G>C	p.V599L	MISSENSE
MA4_23R	Chr16	70883694	G	A	0.092937092	HYDIN	ENST00000393567_r73	c.12808 C>T	p.H4270Y	MISSENSE
MA4_23R	Chr16	70937582	G	A	0.094841213	HYDIN	ENST00000393567_r73	c.8795 C>T	p.P2932L	MISSENSE
MA4_23R	Chr18	54362417	A	G	0.181823661	WDR7	ENST00000357574_r73	c.1345 A>G	p.M449V	MISSENSE
MA4_23R	Chr20	17950950	G	A	0.171070534	MGME1	ENST00000377710_r73	c.448 G>A	p.E150K	MISSENSE
MA4_23R	Chr3	49756522	C	T	0.236234458	AMIGO3	ENST00000320431_r73	c.377 G>A	p.R126H	MISSENSE
MA4_23R	Chr3	133368471	A	G	0.219197759	TOPBP1	ENST00000260810_r73	c.1260 T>C	p.H420H	SILENT
MA4_23R	Chr4	10445952	T	C	0.201005025	ZNF518B	ENST00000326756_r73	c.2001 A>G	p.R667R	SILENT
MA4_23R	Chr4	16077351	T	C	0.186183079	PROM1	ENST00000505450_r73	c.179 A>G	p.H60R	MISSENSE
MA4_23R	Chr6	114270153	T	C	0.17850901	HDAC2	ENST00000519065_r73	c.831 A>G	p.L277L	SILENT
MA4_23R	Chr6	117128289	G	C	0.185470706	GPRC6A	ENST00000310357_r73	c.579 C>G	p.F193L	MISSENSE
MA4_23R	Chr8	144994337	G	A	0.235934664	PLEC	ENST00000345136_r73	c.9652 C>T	p.R3218W	MISSENSE
MA4_23R	ChrX	24741351	C	T	0.258435032	POLA1	ENST00000379059_r73	c.1149 C>T	p.I383I	SILENT
MA4_23R	ChrX	35938045	C	T	0.540260608	CXorf22	ENST00000297866_r73	c.129 C>T	p.I43I	SILENT
MA4_23R	ChrX	35969297	G	A	0.528962956	CXorf22	ENST00000297866_r73	c.706 G>A	p.V236M	MISSENSE
MA4_23R	ChrX	44171953	T	C	0.385125184	EFHC2	ENST00000420999_r73	c.92 A>G	p.N31S	MISSENSE
MA4_23R	ChrX	48847497	T	C	0.530505952	GRIPAP1	ENST00000376441_r73	c.483 A>G	p.E161E	SILENT
MA4_23R	ChrX	139038443	G	A	0.254189944	CXorf66	ENST00000370540_r73	c.698 C>T	p.P233L	MISSENSE

MA4_23R	Chr1	152278814	C	T	0.209754681	FLG	ENST00000368799_r73	c.8548 G>A	p.G2850S	MISSENSE
MA4_23R	Chr6	32191659	-	AGC	0.070879242	NOTCH4	ENST00000375023_r73	c.47 ->GCT	p.L16 L>RL	MISSENSE
MA4_23R	ChrX	12937804	C	T	0.532887403	TLR8	ENST00000218032_r73	c.645 C>T	p.H215H	SILENT
MA4_23R	ChrX	12939112	G	C	0.546212396	TLR8	ENST00000218032_r73	c.1953 G>C	p.L651L	SILENT
MA4_23R	ChrX	22291732	C	T	0.553430079	ZNF645	ENST00000323684_r73	c.624 C>T	p.I208I	SILENT
MA4_23R	ChrX	36403036	A	G	0.286539082	CXorf30	ENST00000378657_r73	c.1817 A>G	p.H606R	MISSENSE
MA4_23R	ChrX	135430044	T	C	0.283352557	GPR112	ENST00000394143_r73	c.4179 T>C	p.T1393T	SILENT
MA4_23R	ChrX	16168677	T	C	0.551388889	GRPR	ENST00000380289_r73	c.663 T>C	p.I221I	SILENT
MA4_23R	Chr18	43311053	C	T	0.196078431	SLC14A1	ENST00000321925_r73	c.225 C>T	p.P75P	SILENT
MA4_23R	Chr20	57571837	C	T	0.2951875	CTSZ	ENST00000217131_r73	c.658 G>A	p.E220K	MISSENSE
MA4_23R	ChrX	135430483	T	C	0.26859095	GPR112	ENST00000394143_r73	c.4618 T>C	p.S1540P	MISSENSE
MA4_23R	Chr1	985377	C	T	0.130434783	AGRN	ENST00000379370_r73	c.4839 C>T	p.C1613C	SILENT
MA4_23R	Chr1	989216	C	T	0.290322581	AGRN	ENST00000379370_r73	c.5735 C>T	p.A1912V	MISSENSE
MA4_23R	Chr1	1217690	C	T	0.177777778	SCNN1D	ENST00000379116_r73	c.346 C>T	p.R116W	MISSENSE
MA4_23R	Chr1	2451298	G	A	0.171875	PANK4	ENST00000378466_r73	c.795 C>T	p.L265L	SILENT
MA4_23R	Chr1	11733905	C	T	0.147286822	FBXO6	ENST00000376753_r73	c.879 C>T	p.F293F	SILENT
MA4_23R	Chr1	12248855	G	C	0.248554913	TNFRSF1B	ENST00000376259_r73	c.81 G>C	p.V27V	SILENT
MA4_23R	Chr1	16353911	A	G	0.143884892	CLCNKA	ENST00000375692_r73	c.762 A>G	p.A254A	SILENT
MA4_23R	Chr1	16535487	G	C	0.184210526	ARHGEF19	ENST00000270747_r73	c.63 C>G	p.H21Q	MISSENSE
MA4_23R	Chr1	17603340	C	T	0.163265306	PADI3	ENST00000375460_r73	c.1524 C>T	p.H508H	SILENT
MA4_23R	Chr1	22202483	G	A	0.118811881	HSPG2	ENST00000374695_r73	c.3056 C>T	p.P1019L	MISSENSE
MA4_23R	Chr1	22307376	C	T	0.409090909	CELA3B	ENST00000337107_r73	c.189 C>T	p.I63I	SILENT
MA4_23R	Chr1	25883695	C	T	0.183908046	LDLRAP1	ENST00000374338_r73	c.396 C>T	p.I132I	SILENT
MA4_23R	Chr1	26665873	C	G	0.234042553	AIM1L	ENST00000527815_r73	c.630 G>C	p.K210N	MISSENSE
MA4_23R	Chr1	28206363	G	C	0.285714286	THEMIS2	ENST00000373925_r73	c.444 G>C	p.L148L	SILENT
MA4_23R	Chr1	29475296	G	A	0.196969697	SRSF4	ENST00000373795_r73	c.1111 C>T	p.R371C	MISSENSE
MA4_23R	Chr1	32740366	G	A	0.151515152	LCK	ENST00000336890_r73	c.134 G>A	p.R45Q	MISSENSE
MA4_23R	Chr1	41475187	A	G	0.292307692	CTPS1	ENST00000372621_r73	c.1617 A>G	p.P539P	SILENT
MA4_23R	Chr1	45228266	A	T	0.28125	KIF2C	ENST00000372224_r73	c.1907 A>T	p.E636V	MISSENSE
MA4_23R	Chr1	53569148	C	T	0.096774194	SLC1A7	ENST00000371494_r73	c.567 G>A	p.E189E	SILENT
MA4_23R	Chr1	54060404	G	A	0.288888889	GLIS1	ENST00000312233_r73	c.172 C>T	p.P58S	MISSENSE
MA4_23R	Chr1	79121172	C	T	0.225806452	IFI44	ENST00000370747_r73	c.816 C>T	p.N272N	SILENT
MA4_23R	Chr1	91967341	A	G	0.149350649	CDC7	ENST00000234626_r73	c.68 A>G	p.Q23R	MISSENSE
MA4_23R	Chr1	108697684	C	T	0.152091255	SLC25A24	ENST00000565488_r73	c.743 G>A	p.R248H	MISSENSE
MA4_23R	Chr1	109808448	A	G	0.177419355	CELSR2	ENST00000271332_r73	c.5819 A>G	p.D1940G	MISSENSE
MA4_23R	Chr1	114226447	A	G	0.181818182	MAGI3	ENST00000307546_r73	c.4257 A>G	p.V1419V	SILENT
MA4_23R	Chr1	117120150	G	A	0.136363636	IGSF3	ENST00000369486_r73	c.3369 C>T	p.D1123D	SILENT

MA4_23R	Chr1	143767466	G	A	0.086206897	PPIAL4G	ENST00000419275_r73	c.383 C>T	p.A128V	MISSENSE
MA4_23R	Chr1	144921924	G	A	0.080745342	PDE4DIP	ENST00000313382_r73	c.1303 C>T	p.L435L	SILENT
MA4_23R	Chr1	151810935	G	C	0.14	C2CD4D	ENST00000454109_r73	c.531 C>G	p.A177A	SILENT
MA4_23R	Chr1	152187589	G	A	0.201117318	HRNR	ENST00000368801_r73	c.6516 C>T	p.H2172H	SILENT
MA4_23R	Chr1	152187628	A	G	0.090909091	HRNR	ENST00000368801_r73	c.6477 T>C	p.Y2159Y	SILENT
MA4_23R	Chr1	152188999	G	A	0.120967742	HRNR	ENST00000368801_r73	c.5106 C>T	p.H1702H	SILENT
MA4_23R	Chr1	152190835	G	A	0.258064516	HRNR	ENST00000368801_r73	c.3270 C>T	p.G1090G	SILENT
MA4_23R	Chr1	152190945	C	T	0.407407407	HRNR	ENST00000368801_r73	c.3160 G>A	p.E1054K	MISSENSE
MA4_23R	Chr1	152276699	A	G	0.162962963	FLG	ENST00000368799_r73	c.10663 T>C	p.W3555R	MISSENSE
MA4_23R	Chr1	153967598	G	A	0.20661157	NUP210L	ENST00000368559_r73	c.5445 C>T	p.L1815L	SILENT
MA4_23R	Chr1	155004236	G	A	0.175	DCST2	ENST00000368424_r73	c.553 C>T	p.R185W	MISSENSE
MA4_23R	Chr1	155152310	C	T	0.090909091	TRIM46	ENST00000368382_r73	c.1419 C>T	p.P473P	SILENT
MA4_23R	Chr1	156518453	G	A	0.181818182	IQGAP3	ENST00000361170_r73	c.1913 C>T	p.A638V	MISSENSE
MA4_23R	Chr1	161642985	G	A	0.20754717	FCGR2B	ENST00000236937_r73	c.612 G>A	p.L204L	SILENT
MA4_23R	Chr1	165638548	C	T	0.144329897	ALDH9A1	ENST00000354775_r73	c.1070 G>A	p.R357Q	MISSENSE
MA4_23R	Chr1	166961966	T	C	0.15	MAEL	ENST00000367872_r73	c.369 T>C	p.H123H	SILENT
MA4_23R	Chr1	167962499	G	T	0.140186916	DCAF6	ENST00000367843_r73	c.724 G>T	p.A242S	MISSENSE
MA4_23R	Chr1	192778206	A	G	0.315789474	RGS2	ENST00000235382_r73	c.5 A>G	p.Q2R	MISSENSE
MA4_23R	Chr1	193119478	C	T	0.175257732	CDC73	ENST00000367435_r73	c.873 C>T	p.N291N	SILENT
MA4_23R	Chr1	200613610	T	C	0.12345679	DDX59	ENST00000331314_r73	c.1632 A>G	p.T544T	SILENT
MA4_23R	Chr1	203141167	C	T	0.180327869	MYBPH	ENST00000255416_r73	c.510 G>A	p.E170E	SILENT
MA4_23R	Chr1	207263734	A	T	0.24	C4BPB	ENST00000367078_r73	c.140 A>T	p.Y47F	MISSENSE
MA4_23R	Chr1	209805977	C	T	0.181818182	LAMB3	ENST00000356082_r73	c.773 G>A	p.R258H	MISSENSE
MA4_23R	Chr1	222802152	A	G	0.194444444	MIA3	ENST00000344922_r73	c.1590 A>G	p.G530G	SILENT
MA4_23R	Chr1	247587870	G	A	0.217948718	NLRP3	ENST00000391828_r73	c.1125 G>A	p.E375E	SILENT
MA4_23R	Chr1	247719734	C	T	0.151515152	GCSAML	ENST00000366488_r73	c.55 C>T	p.P19S	MISSENSE
MA4_23R	Chr1	248202474	A	G	0.113861386	OR2L2	ENST00000366479_r73	c.905 A>G	p.Q302R	MISSENSE
MA4_23R	Chr1	248616776	C	T	0.164285714	OR2T2	ENST00000342927_r73	c.678 C>T	p.V226V	SILENT
MA4_23R	Chr10	3141522	G	A	0.333333333	PFKP	ENST00000381125_r73	c.242 G>A	p.S81N	MISSENSE
MA4_23R	Chr10	3143135	G	A	175	PFKP	ENST00000381075_r73	c.183 G>A	p.R61R	SILENT
MA4_23R	Chr10	13672334	A	G	0.106122449	PRPF18	ENST00000378572_r73	c.1023 A>G	p.A341A	SILENT
MA4_23R	Chr10	13672334	A	G	0.106122449	RP11-295P9.3	ENST00000595538_r73	c.98 A>G	p.A33G	MISSENSE
MA4_23R	Chr10	13699231	C	T	0.230769231	FRMD4A	ENST00000357447_r73	c.2358 G>A	p.R786R	SILENT
MA4_23R	Chr10	13702435	C	T	0.183673469	FRMD4A	ENST00000357447_r73	c.1779 G>A	p.Q593Q	SILENT
MA4_23R	Chr10	23319653	T	C	0.135021097	ARMC3	ENST00000298032_r73	c.2174 T>C	p.M725T	MISSENSE
MA4_23R	Chr10	24762184	G	A	0.178947368	KIAA1217	ENST00000376462_r73	c.634 G>A	p.G212R	MISSENSE
MA4_23R	Chr10	32097609	G	A	0.222222222	ARHGAP12	ENST00000311380_r73	c.2178 C>T	p.D726D	SILENT

MA4_23R	Chr10	50667225	C	G	0.157303371	ERCC6	ENST00000355832_r73	c.4118 G>C	p.R1373T	MISSENSE
MA4_23R	Chr10	61835633	G	A	0.182795699	ANK3	ENST00000280772_r73	c.5006 C>T	p.P1669L	MISSENSE
MA4_23R	Chr10	69299372	T	G	0.223214286	CTNNA3	ENST00000433211_r73	c.348 A>C	p.P116P	SILENT
MA4_23R	Chr10	79781312	G	A	0.27027027	POLR3A	ENST00000372371_r73	c.1177 C>T	p.P393S	MISSENSE
MA4_23R	Chr10	82013319	T	G	0.223076923	AL359195.1	ENST00000356374_r73	c.837 T>G	p.F279L	MISSENSE
MA4_23R	Chr10	94223726	A	G	0.196969697	IDE	ENST00000265986_r73	c.2523 T>C	p.N841N	SILENT
MA4_23R	Chr10	105178380	G	A	0.222222222	PDCD11	ENST00000369797_r73	c.2095 G>A	p.E699K	MISSENSE
MA4_23R	Chr10	106075269	G	A	0.25	ITPRIP	ENST00000337478_r73	c.541 C>T	p.R181W	MISSENSE
MA4_23R	Chr10	116853561	G	A	0.23943662	ATRNL1	ENST00000355044_r73	c.52 G>A	p.G18R	MISSENSE
MA4_23R	Chr10	134218641	C	T	0.28	PWWP2B	ENST00000305233_r73	c.637 C>T	p.R213C	MISSENSE
MA4_23R	Chr10	134622089	A	G	0.164705882	TTC40	ENST00000368586_r73	c.7984 T>C	p.W2662R	MISSENSE
MA4_23R	Chr11	5537147	C	G	0.194029851	UBQLNL	ENST00000380184_r73	c.525 G>C	p.M175I	MISSENSE
MA4_23R	Chr11	16838719	C	T	0.16025641	PLEKHA7	ENST00000355661_r73	c.1494 G>A	p.A498A	SILENT
MA4_23R	Chr11	45672170	G	A	0.266055046	CHST1	ENST00000308064_r73	c.304 C>T	p.P102S	MISSENSE
MA4_23R	Chr11	46907712	A	G	0.172839506	LRP4	ENST00000378623_r73	c.2436 T>C	p.D812D	SILENT
MA4_23R	Chr11	55541614	G	T	0.166666667	OR5D13	ENST00000361760_r73	c.701 G>T	p.S234I	MISSENSE
MA4_23R	Chr11	55872749	C	T	0.151394422	OR8H2	ENST00000313503_r73	c.231 C>T	p.V77V	SILENT
MA4_23R	Chr11	57147126	G	A	0.173553719	PRG3	ENST00000287143_r73	c.216 C>T	p.N72N	SILENT
MA4_23R	Chr11	60610065	G	A	0.342342342	CCDC86	ENST00000227520_r73	c.468 G>A	p.P156P	SILENT
MA4_23R	Chr11	62286188	G	A	0.156862745	AHNAK	ENST00000378024_r73	c.15701 C>T	p.P5234L	MISSENSE
MA4_23R	Chr11	62656046	A	C	0.176056338	SLC3A2	ENST00000377890_r73	c.1774 A>C	p.K592Q	MISSENSE
MA4_23R	Chr11	64577243	G	A	0.181818182	MEN1	ENST00000377326_r73	c.339 C>T	p.S113S	SILENT
MA4_23R	Chr11	65359552	A	G	0.141791045	EHBP1L1	ENST00000309295_r73	c.4463 A>G	p.K1488R	MISSENSE
MA4_23R	Chr11	65359552	A	G	0.141791045	AP001362.1	ENST00000597463_r73	c.268 T>C	p.L90L	SILENT
MA4_23R	Chr11	67209515	C	T	0.240963855	CORO1B	ENST00000341356_r73	c.246 G>A	p.T82T	SILENT
MA4_23R	Chr11	73007938	C	T	0.166666667	P2RY6	ENST00000540342_r73	c.375 C>T	p.Y125Y	SILENT
MA4_23R	Chr11	89133530	A	G	0.149122807	NOX4	ENST00000343727_r73	c.792 T>C	p.S264S	SILENT
MA4_23R	Chr11	102482626	T	G	0.174825175	MMP20	ENST00000260228_r73	c.383 A>C	p.K128T	MISSENSE
MA4_23R	Chr11	120980048	C	T	0.191011236	TECTA	ENST00000392793_r73	c.327 C>T	p.G109G	SILENT
MA4_23R	Chr11	120984338	A	G	0.107692308	TECTA	ENST00000392793_r73	c.701 A>G	p.Q234R	MISSENSE
MA4_23R	Chr11	121008285	C	T	0.163793103	TECTA	ENST00000392793_r73	c.3097 C>T	p.R1033W	MISSENSE
MA4_23R	Chr11	121489544	C	T	0.153846154	SORL1	ENST00000260197_r73	c.5666 C>T	p.T1889I	MISSENSE
MA4_23R	Chr11	123753959	G	A	0.157894737	TMEM225	ENST00000375026_r73	c.564 C>T	p.I188I	SILENT
MA4_23R	Chr11	124267056	G	A	0.227799228	OR8B3	ENST00000354597_r73	c.192 C>T	p.F64F	SILENT
MA4_23R	Chr11	128638142	C	T	0.139784946	FLI1	ENST00000429175_r73	c.360 C>T	p.N120N	SILENT
MA4_23R	Chr12	332338	G	A	0.2	SLC6A13	ENST00000343164_r73	c.1374 C>T	p.F458F	SILENT
MA4_23R	Chr12	674540	T	C	0.270833333	NINJ2	ENST00000305108_r73	c.428 A>G	p.K143R	MISSENSE

MA4_23R	Chr12	6640519	G	A	0.260869565	NCAPD2	ENST00000315579_r73	c.4147 G>A	p.E1383K	MISSENSE
MA4_23R	Chr12	7637940	T	C	0.130434783	CD163	ENST00000359156_r73	c.2531 A>G	p.N844S	MISSENSE
MA4_23R	Chr12	11546192	G	A	0.279069767	PRB2	ENST00000389362_r73	c.820 C>T	p.P274S	MISSENSE
MA4_23R	Chr12	51693021	C	T	0.225352113	BIN2	ENST00000267012_r73	c.568 G>A	p.E190K	MISSENSE
MA4_23R	Chr12	52585534	C	T	0.148148148	KRT80	ENST00000313234_r73	c.153 G>A	p.S51S	SILENT
MA4_23R	Chr12	53004526	C	T	0.213333333	KRT73	ENST00000305748_r73	c.1204 G>A	p.A402T	MISSENSE
MA4_23R	Chr12	53200921	C	G	0.179104478	KRT4	ENST00000551956_r73	c.1495 G>C	p.G499R	MISSENSE
MA4_23R	Chr12	53591607	C	T	0.166666667	ITGB7	ENST00000267082_r73	c.330 G>A	p.P110P	SILENT
MA4_23R	Chr12	56748273	G	A	0.175438597	STAT2	ENST00000314128_r73	c.759 C>T	p.H253H	SILENT
MA4_23R	Chr12	58174038	G	C	0.206896552	METTL21B	ENST00000300209_r73	c.290 G>C	p.G97A	MISSENSE
MA4_23R	Chr12	80855816	T	C	0.12962963	PTPRQ	ENST00000266688_r73	c.533 T>C	p.V178A	MISSENSE
MA4_23R	Chr12	95604081	G	A	0.186915888	FGD6	ENST00000343958_r73	c.979 C>T	p.R327C	MISSENSE
MA4_23R	Chr12	101603543	G	A	0.226086957	SLC5A8	ENST00000536262_r73	c.84 C>T	p.I28I	SILENT
MA4_23R	Chr12	106995090	C	T	0.25	RFX4	ENST00000357881_r73	c.36 C>T	p.G12G	SILENT
MA4_23R	Chr12	107713087	C	T	0.175438597	BTBD11	ENST00000280758_r73	c.370 C>T	p.L124L	SILENT
MA4_23R	Chr12	109994854	C	T	0.163636364	MMAB	ENST00000545712_r73	c.732 G>A	p.S244S	SILENT
MA4_23R	Chr12	129308324	C	T	0.191919192	SLC15A4	ENST00000266771_r73	c.165 G>A	p.T55T	SILENT
MA4_23R	Chr12	133634950	A	G	0.172839506	ZNF84	ENST00000539354_r73	c.1649 A>G	p.K550R	MISSENSE
MA4_23R	Chr13	29600208	G	A	0.209876543	MTUS2	ENST00000431530_r73	c.1403 G>A	p.R468Q	MISSENSE
MA4_23R	Chr13	39424254	T	C	0.152173913	FREM2	ENST00000280481_r73	c.6459 T>C	p.T2153T	SILENT
MA4_23R	Chr13	77581658	G	A	0.213483146	FBXL3	ENST00000355619_r73	c.909 C>T	p.F303F	SILENT
MA4_23R	Chr13	96530055	T	C	0.155279503	UGGT2	ENST00000376747_r73	c.3284 A>G	p.Q1095R	MISSENSE
MA4_23R	Chr13	102250542	C	T	0.197916667	ITGBL1	ENST00000376180_r73	c.908 C>T	p.A303V	MISSENSE
MA4_23R	Chr13	103438592	T	C	0.201183432	KDELC1	ENST00000376004_r73	c.1481 A>G	p.H494R	MISSENSE
MA4_23R	Chr14	20404080	T	C	0.148825065	OR4K1	ENST00000285600_r73	c.255 T>C	p.F85F	SILENT
MA4_23R	Chr14	23549380	G	A	0.257575758	ACIN1	ENST00000262710_r73	c.1338 C>T	p.P446P	SILENT
MA4_23R	Chr14	23566949	C	T	0.121212121	C14orf119	ENST00000319074_r73	c.82 C>T	p.P28S	MISSENSE
MA4_23R	Chr14	23861839	G	C	0.190909091	MYH6	ENST00000356287_r73	c.3274 C>G	p.Q1092E	MISSENSE
MA4_23R	Chr14	24769809	G	A	0.194029851	NOP9	ENST00000267425_r73	c.443 G>A	p.S148N	MISSENSE
MA4_23R	Chr14	24911441	G	C	0.183098592	SDR39U1	ENST00000399395_r73	c.149 C>G	p.P50R	MISSENSE
MA4_23R	Chr14	45711535	T	G	0.124223603	MIS18BP1	ENST00000310806_r73	c.845 A>C	p.N282T	MISSENSE
MA4_23R	Chr14	52527005	T	C	0.277777778	NID2	ENST00000216286_r73	c.604 A>G	p.N202D	MISSENSE
MA4_23R	Chr14	57858186	G	A	0.235294118	NAA30	ENST00000556492_r73	c.511 G>A	p.E171K	MISSENSE
MA4_23R	Chr14	59939804	G	A	0.173469388	L3HYPDH	ENST00000247194_r73	c.944 C>T	p.A315V	MISSENSE
MA4_23R	Chr14	63735877	C	T	0.279069767	RHOJ	ENST00000316754_r73	c.228 C>T	p.T76T	SILENT
MA4_23R	Chr14	64488055	A	G	0.161290323	SYNE2	ENST00000344113_r73	c.5174 A>G	p.N1725S	MISSENSE
MA4_23R	Chr14	64954574	G	C	0.161290323	ZBTB25	ENST00000261683_r73	c.375 C>G	p.S125S	SILENT

MA4_23R	Chr14	91113353	G	A	0.25	TTC7B	ENST00000328459_r73	c.1532 C>T	p.S511L	MISSENSE
MA4_23R	Chr14	100934449	G	A	0.154761905	WDR25	ENST00000554998_r73	c.914 G>A	p.R305Q	MISSENSE
MA4_23R	Chr14	105174236	T	C	0.214285714	INF2	ENST00000330634_r73	c.1632 T>C	p.H544H	SILENT
MA4_23R	Chr14	105407977	A	G	0.245283019	AHNAK2	ENST00000333244_r73	c.13811 T>C	p.M4604T	MISSENSE
MA4_23R	Chr14	105411286	G	A	0.125	AHNAK2	ENST00000333244_r73	c.10502 C>T	p.P3501L	MISSENSE
MA4_23R	Chr14	105411287	G	A	0.125	AHNAK2	ENST00000333244_r73	c.10501 C>T	p.P3501S	MISSENSE
MA4_23R	Chr14	106829985	G	A	0.18	IGHV4-34	ENST00000390616_r73	c.61 C>T	p.P21S	MISSENSE
MA4_23R	Chr14	107083424	T	C	0.402173913	IGHV4-59	ENST00000455737_r73	c.180 A>G	p.P60P	SILENT
MA4_23R	Chr14	107179058	G	A	0.133333333	IGHV2-70	ENST00000390634_r73	c.119 C>T	p.T40I	MISSENSE
MA4_23R	Chr15	23006346	T	C	0.270833333	NIPA2	ENST00000337451_r73	c.958 A>G	p.M320V	MISSENSE
MA4_23R	Chr15	30659641	C	T	0.212121212	CHRFAM7A	ENST00000299847_r73	c.700 G>A	p.G234R	MISSENSE
MA4_23R	Chr15	35274130	G	C	0.203703704	ZNF770	ENST00000356321_r73	c.1506 C>G	p.P502P	SILENT
MA4_23R	Chr15	41961191	T	C	0.210884354	MGA	ENST00000566586_r73	c.99 T>C	p.N33N	SILENT
MA4_23R	Chr15	42148796	T	A	0.169491525	SPTBN5	ENST00000320955_r73	c.8809 A>T	p.N2937Y	MISSENSE
MA4_23R	Chr15	43290373	A	G	0.095890411	UBR1	ENST00000290650_r73	c.3750 T>C	p.H1250H	SILENT
MA4_23R	Chr15	48779352	C	T	0.262820513	FBN1	ENST00000316623_r73	c.3509 G>A	p.R1170H	MISSENSE
MA4_23R	Chr15	51830647	T	C	0.303030303	DMXL2	ENST00000251076_r73	c.1108 A>G	p.I370V	MISSENSE
MA4_23R	Chr15	63597969	C	T	0.164705882	APH1B	ENST00000261879_r73	c.763 C>T	p.R255C	MISSENSE
MA4_23R	Chr15	64008623	A	C	0.156862745	HERC1	ENST00000443617_r73	c.4028 T>G	p.F1343C	MISSENSE
MA4_23R	Chr15	73615695	C	T	0.186440678	HCN4	ENST00000261917_r73	c.2739 G>A	p.A913A	SILENT
MA4_23R	Chr15	74277048	C	T	0.202380952	STOML1	ENST00000564777_r73	c.802 G>A	p.V268I	MISSENSE
MA4_23R	Chr15	78393899	A	G	0.146067416	SH2D7	ENST00000328828_r73	c.1304 A>G	p.K435R	MISSENSE
MA4_23R	Chr15	78474907	G	A	0.133333333	ACSBG1	ENST00000258873_r73	c.795 C>T	p.D265D	SILENT
MA4_23R	Chr15	96877696	G	A	0.185185185	NR2F2	ENST00000421109_r73	c.435 G>A	p.S145S	SILENT
MA4_23R	Chr16	334920	C	T	0.164634146	PDIA2	ENST00000219406_r73	c.583 C>T	p.Q195*	NONSENSE
MA4_23R	Chr16	420061	T	G	0.202380952	MRPL28	ENST00000199706_r73	c.158 A>C	p.N53T	MISSENSE
MA4_23R	Chr16	630878	C	T	0.239130435	PIGQ	ENST00000409527_r73	c.1437 C>T	p.A479A	SILENT
MA4_23R	Chr16	1748888	G	A	0.194444444	HN1L	ENST00000248098_r73	c.462 G>A	p.Q154Q	SILENT
MA4_23R	Chr16	1837741	C	T	0.219178082	NUBP2	ENST00000262302_r73	c.398 C>T	p.T133M	MISSENSE
MA4_23R	Chr16	1841153	G	A	0.1	IGFALS	ENST00000215539_r73	c.1266 C>T	p.L422L	SILENT
MA4_23R	Chr16	2140954	G	A	0.190476191	PKD1	ENST00000262304_r73	c.11934 C>T	p.D3978D	SILENT
MA4_23R	Chr16	2287651	G	A	0.162361624	DNASE1L2	ENST00000564065_r73	Exon 4 1 G>A	-	ESSENTIAL_SPLICE
MA4_23R	Chr16	2571122	A	G	0.150943396	ATP6C	ENST00000569317_r73	c.217 A>G	p.K73E	MISSENSE
MA4_23R	Chr16	2571122	A	G	0.150943396	AMDHD2	ENST00000302956_r73	c.358 A>G	p.K120E	MISSENSE
MA4_23R	Chr16	2816359	C	T	0.151260504	SRRM2	ENST00000301740_r73	c.5830 C>T	p.R1944C	MISSENSE
MA4_23R	Chr16	3487431	G	C	0.184397163	ZNF597	ENST00000301744_r73	c.268 C>G	p.P90A	MISSENSE
MA4_23R	Chr16	11001797	C	T	0.12345679	CIITA	ENST00000324288_r73	c.2448 C>T	p.A816A	SILENT

MA4_23R	Chr16	21213488	C	T	0.193181818	ZP2	ENST00000574002_r73	c.1224 G>A	p.E408E	SILENT
MA4_23R	Chr16	22144284	C	A	0.223880597	VWA3A	ENST00000389398_r73	c.1936 C>A	p.L646I	MISSENSE
MA4_23R	Chr16	22182168	C	T	0.173913044	SDR42E2	ENST00000602312_r73	c.307 C>T	p.R103W	MISSENSE
MA4_23R	Chr16	22201561	A	G	0.28358209	SDR42E2	ENST00000602312_r73	c.1014 A>G	p.L338L	SILENT
MA4_23R	Chr16	22826046	T	G	0.191304348	HS3ST2	ENST00000261374_r73	c.115 T>G	p.C39G	MISSENSE
MA4_23R	Chr16	29063529	C	T	0.379310345	CTB-134H23.2	ENST00000424293_r73	c.779 C>T	p.S260F	MISSENSE
MA4_23R	Chr16	29708436	C	T	0.134615385	QPRT	ENST00000395384_r73	c.669 C>T	p.N223N	SILENT
MA4_23R	Chr16	30975492	C	T	0.166666667	SETD1A	ENST00000262519_r73	c.717 C>T	p.N239N	SILENT
MA4_23R	Chr16	46766304	C	T	0.164179105	MYLK3	ENST00000394809_r73	c.1278 G>A	p.T426T	SILENT
MA4_23R	Chr16	57101678	T	A	0.17948718	NLRC5	ENST00000262510_r73	c.4437 T>A	p.D1479E	MISSENSE
MA4_23R	Chr16	72164240	G	C	0.274193548	PMFBP1	ENST00000237353_r73	c.1654 C>G	p.L552V	MISSENSE
MA4_23R	Chr16	72170469	G	A	0.213483146	PMFBP1	ENST00000237353_r73	c.1081 C>T	p.R361W	MISSENSE
MA4_23R	Chr16	72821625	C	T	0.229166667	ZFHX3	ENST00000268489_r73	c.10550 G>A	p.G3517D	MISSENSE
MA4_23R	Chr16	80583473	C	T	0.19205298	DYNLRB2	ENST00000305904_r73	c.172 C>T	p.R58C	MISSENSE
MA4_23R	Chr16	87344867	G	A	0.154639175	C16orf95	ENST00000567970_r73	c.366 C>T	p.T122T	SILENT
MA4_23R	Chr17	2291323	C	T	0.168539326	MNT	ENST00000174618_r73	c.828 G>A	p.K276K	SILENT
MA4_23R	Chr17	2605278	G	A	0.190476191	CLUH	ENST00000570628_r73	c.435 C>T	p.S145S	SILENT
MA4_23R	Chr17	4689601	A	G	0.137096774	VMO1	ENST00000441199_r73	c.47 T>C	p.L16P	MISSENSE
MA4_23R	Chr17	8146306	T	C	0.215686275	CTC1	ENST00000315684_r73	c.194 A>G	p.Y65C	MISSENSE
MA4_23R	Chr17	15477417	A	G	0.196428571	RP11-385D13.1	ENST00000455584_r73	c.2858 T>C	p.L953P	MISSENSE
MA4_23R	Chr17	18566585	G	A	0.164021164	ZNF286B	ENST00000545289_r73	c.234 C>T	p.S78S	SILENT
MA4_23R	Chr17	20354923	G	A	0.225806452	LGALS9B	ENST00000324290_r73	c.792 C>T	p.I264I	SILENT
MA4_23R	Chr17	21319267	C	T	0.072519084	KCNJ12	ENST00000583088_r73	c.613 C>T	p.R205C	MISSENSE
MA4_23R	Chr17	31087609	G	A	0.185185185	MYO1D	ENST00000318217_r73	c.1072 C>T	p.R358C	MISSENSE
MA4_23R	Chr17	34432664	T	A	0.176100629	CCL4	ENST00000250151_r73	c.238 T>A	p.S80T	MISSENSE
MA4_23R	Chr17	38191515	A	G	0.213333333	MED24	ENST00000356271_r73	c.375 T>C	p.S125S	SILENT
MA4_23R	Chr17	42335379	G	A	0.149253731	SLC4A1	ENST00000262418_r73	c.1257 C>T	p.P419P	SILENT
MA4_23R	Chr17	45016025	C	T	0.05	GOSR2	ENST00000393456_r73	c.538 C>T	p.R180W	MISSENSE
MA4_23R	Chr17	45016025	C	T	0.05	RP11-156P1.2	ENST00000571841_r73	c.538 C>T	p.R180W	MISSENSE
MA4_23R	Chr17	58503639	C	G	0.205882353	C17orf64	ENST00000269127_r73	c.271 C>G	p.H91D	MISSENSE
MA4_23R	Chr17	72349656	C	T	0.178010471	KIF19	ENST00000389916_r73	c.2244 C>T	p.G748G	SILENT
MA4_23R	Chr17	73830182	C	T	0.188679245	UNC13D	ENST00000207549_r73	c.2341 G>A	p.V781I	MISSENSE
MA4_23R	Chr17	74005802	C	T	0.185714286	EVPL	ENST00000301607_r73	c.3484 G>A	p.E1162K	MISSENSE
MA4_23R	Chr17	76482177	G	A	0.210526316	DNAH17	ENST00000585328_r73	c.7125 C>T	p.I2375I	SILENT
MA4_23R	Chr17	77769143	C	T	0.309859155	CBX8	ENST00000269385_r73	c.461 G>A	p.R154Q	MISSENSE
MA4_23R	Chr17	80206865	G	A	0.2	CSNK1D	ENST00000314028_r73	c.1083 C>T	p.S361S	SILENT
MA4_23R	Chr18	6999496	G	A	0.218181818	LAMA1	ENST00000389658_r73	c.4611 C>T	p.L1537L	SILENT

MA4_23R	Chr18	9204535	A	G	0.22818792	ANKRD12	ENST00000262126_r73	c.297 A>G	p.T99T	SILENT
MA4_23R	Chr18	10485561	G	A	0.179310345	APCDD1	ENST00000355285_r73	c.877 G>A	p.G293R	MISSENSE
MA4_23R	Chr18	13029750	A	G	0.168316832	CEP192	ENST00000506447_r73	c.1139 A>G	p.N380S	MISSENSE
MA4_23R	Chr18	34298589	C	T	0.185483871	FHOD3	ENST00000257209_r73	c.2803 C>T	p.L935L	SILENT
MA4_23R	Chr18	46343626	A	G	0.183673469	CTIF	ENST00000256413_r73	c.1406 A>G	p.Q469R	MISSENSE
MA4_23R	Chr18	57013161	T	A	0.326530612	LMAN1	ENST00000251047_r73	c.945 A>T	p.Q315H	MISSENSE
MA4_23R	Chr19	687035	T	A	0.174193548	PRSS57	ENST00000329267_r73	c.535 A>T	p.K179*	NONSENSE
MA4_23R	Chr19	1010673	G	A	0.255319149	TMEM259	ENST00000356663_r73	c.1539 C>T	p.P513P	SILENT
MA4_23R	Chr19	3942175	C	T	0.179104478	NMRK2	ENST00000168977_r73	c.597 C>T	p.A199A	SILENT
MA4_23R	Chr19	6183185	C	A	0.211864407	ACSBG2	ENST00000591403_r73	c.1224 C>A	p.F408L	MISSENSE
MA4_23R	Chr19	11508199	C	T	0.164556962	RGL3	ENST00000380456_r73	c.1821 G>A	p.P607P	SILENT
MA4_23R	Chr19	11512897	C	T	0.2	RGL3	ENST00000380456_r73	c.1356 G>A	p.R452R	SILENT
MA4_23R	Chr19	11618630	G	A	0.20952381	ECSIT	ENST00000270517_r73	c.832 C>T	p.R278C	MISSENSE
MA4_23R	Chr19	12984928	C	T	0.234567901	MAST1	ENST00000251472_r73	c.3957 C>T	p.G1319G	SILENT
MA4_23R	Chr19	13218667	G	A	0.226890756	TRMT1	ENST00000221504_r73	c.1317 C>T	p.A439A	SILENT
MA4_23R	Chr19	16962292	A	G	0.222222222	SIN3B	ENST00000379803_r73	c.796 A>G	p.S266G	MISSENSE
MA4_23R	Chr19	19038597	C	T	0.191489362	DDX49	ENST00000247003_r73	c.1125 C>T	p.S375S	SILENT
MA4_23R	Chr19	20989454	T	C	0.212765957	ZNF66	ENST00000344519_r73	c.1048 T>C	p.F350L	MISSENSE
MA4_23R	Chr19	21300018	G	A	0.164948454	ZNF714	ENST00000596143_r73	c.548 G>A	p.R183Q	MISSENSE
MA4_23R	Chr19	22271303	C	T	0.206896552	ZNF257	ENST00000594947_r73	c.751 C>T	p.H251Y	MISSENSE
MA4_23R	Chr19	35173717	T	A	0.135294118	ZNF302	ENST00000457781_r73	c.45 T>A	p.H15Q	MISSENSE
MA4_23R	Chr19	39281364	G	A	0.208333333	LGALS7B	ENST00000314980_r73	c.131 G>A	p.G44D	MISSENSE
MA4_23R	Chr19	39880149	C	T	0.213333333	PAF1	ENST00000221265_r73	c.330 G>A	p.E110E	SILENT
MA4_23R	Chr19	40900136	G	A	0.225352113	PRX	ENST00000324001_r73	c.4123 C>T	p.R1375W	MISSENSE
MA4_23R	Chr19	46915525	C	T	0.25	CCDC8	ENST00000307522_r73	c.543 G>A	p.E181E	SILENT
MA4_23R	Chr19	49116359	T	C	0.148648649	FAM83E	ENST00000263266_r73	c.271 A>G	p.T91A	MISSENSE
MA4_23R	Chr19	49206550	G	A	0.175438597	FUT2	ENST00000425340_r73	c.337 G>A	p.V113M	MISSENSE
MA4_23R	Chr19	54697199	A	G	0.296296296	TSEN34	ENST00000302937_r73	c.915 A>G	p.Q305Q	SILENT
MA4_23R	Chr19	54723078	G	A	0.134020619	LILRB3	ENST00000391750_r73	c.1346 C>T	p.S449L	MISSENSE
MA4_23R	Chr19	55237603	G	A	0.201680672	KIR3DL3	ENST00000291860_r73	c.155 G>A	p.R52H	MISSENSE
MA4_23R	Chr19	55241172	A	C	0.128654971	KIR3DL3	ENST00000291860_r73	c.869 A>C	p.N290T	MISSENSE
MA4_23R	Chr19	55246812	G	C	0.223880597	KIR3DL3	ENST00000291860_r73	c.1042 G>C	p.A348P	MISSENSE
MA4_23R	Chr19	55247449	A	T	0.217105263	KIR3DL3	ENST00000291860_r73	c.1119 A>T	p.E373D	MISSENSE
MA4_23R	Chr19	55255361	G	A	0.134502924	KIR2DL3	ENST00000342376_r73	c.489 G>A	p.E163E	SILENT
MA4_23R	Chr19	55317439	C	T	0.254237288	KIR2DL4	ENST00000359085_r73	c.395 C>T	p.P132L	MISSENSE
MA4_23R	Chr19	55333275	G	T	0.150684932	KIR3DL1	ENST00000391728_r73	c.911 G>T	p.W304L	MISSENSE
MA4_23R	Chr19	55363504	G	A	0.24822695	KIR3DL2	ENST00000326321_r73	c.122 G>A	p.R41Q	MISSENSE

MA4_23R	Chr19	58117099	G	C	0.2	ZNF530	ENST00000332854_r73	c.206 G>C	p.S69T	MISSENSE
MA4_23R	Chr2	21258553	T	A	0.25	APOB	ENST00000233242_r73	c.721 A>T	p.S241C	MISSENSE
MA4_23R	Chr2	27303740	C	T	0.176470588	EMILIN1	ENST00000380320_r73	c.431 C>T	p.P144L	MISSENSE
MA4_23R	Chr2	28843469	T	C	0.157142857	PLB1	ENST00000327757_r73	c.3386 T>C	p.I1129T	MISSENSE
MA4_23R	Chr2	29274749	C	T	0.162601626	FAM179A	ENST00000379558_r73	c.2850 C>T	p.R950R	SILENT
MA4_23R	Chr2	29416768	G	A	0.198412698	ALK	ENST00000389048_r73	c.4185 C>T	p.T1395T	SILENT
MA4_23R	Chr2	47202156	C	T	0.274509804	TTC7A	ENST00000319190_r73	c.562 C>T	p.R188C	MISSENSE
MA4_23R	Chr2	61331001	G	A	0.146153846	KIAA1841	ENST00000402291_r73	c.1379 G>A	p.R460K	MISSENSE
MA4_23R	Chr2	65300035	T	G	0.175879397	CEP68	ENST00000377990_r73	c.1805 T>G	p.F602C	MISSENSE
MA4_23R	Chr2	71206851	G	A	0.172413793	ANKRD53	ENST00000272421_r73	c.478 G>A	p.V160I	MISSENSE
MA4_23R	Chr2	74699368	G	A	0.159763314	MRPL53	ENST00000258105_r73	c.217 C>T	p.R73C	MISSENSE
MA4_23R	Chr2	85780132	C	T	0.21969697	GGCX	ENST00000233838_r73	c.1217 G>A	p.R406H	MISSENSE
MA4_23R	Chr2	90121841	C	A	0.155339806	IGKV1D-17	ENST00000483379_r73	c.59 C>A	p.A20D	MISSENSE
MA4_23R	Chr2	111551680	A	G	0.157894737	ACOXL	ENST00000439055_r73	c.274 A>G	p.M92V	MISSENSE
MA4_23R	Chr2	112578860	G	A	0.25	ANAPC1	ENST00000341068_r73	c.3162 C>T	p.Y1054Y	SILENT
MA4_23R	Chr2	127816628	C	T	0.1875	BIN1	ENST00000357970_r73	c.961 G>A	p.G321R	MISSENSE
MA4_23R	Chr2	133542131	A	T	0.157232704	NCKAP5	ENST00000409261_r73	c.2253 T>A	p.V751V	SILENT
MA4_23R	Chr2	150427678	T	C	0.256410256	MMADHC	ENST00000303319_r73	c.617 A>G	p.N206S	MISSENSE
MA4_23R	Chr2	152320764	A	G	0.163043478	RIF1	ENST00000444746_r73	c.4730 A>G	p.N1577S	MISSENSE
MA4_23R	Chr2	165772426	C	T	0.177339902	SLC38A11	ENST00000303735_r73	c.441 G>A	p.G147G	SILENT
MA4_23R	Chr2	179397368	G	A	0.18627451	TTN	ENST00000342992_r73	c.96270 C>T	p.I32090I	SILENT
MA4_23R	Chr2	207003230	C	T	0.164835165	NDUFS1	ENST00000233190_r73	c.1371 G>A	p.S457S	SILENT
MA4_23R	Chr2	209358019	C	T	0.238095238	PTH2R	ENST00000272847_r73	c.1288 C>T	p.R430W	MISSENSE
MA4_23R	Chr2	211018503	T	C	0.180257511	KANSL1L	ENST00000281772_r73	c.804 A>G	p.Q268Q	SILENT
MA4_23R	Chr2	219414580	C	T	0.094017094	USP37	ENST00000258399_r73	c.381 G>A	p.R127R	SILENT
MA4_23R	Chr2	220161758	C	T	0.237288136	PTPRN	ENST00000409251_r73	c.2098 G>A	p.A700T	MISSENSE
MA4_23R	Chr2	220493959	G	A	0.346938776	SLC4A3	ENST00000358055_r73	c.311 G>A	p.R104Q	MISSENSE
MA4_23R	Chr2	225661080	A	C	0.211640212	DOCK10	ENST00000258390_r73	c.4891 T>G	p.S1631A	MISSENSE
MA4_23R	Chr2	228855865	G	A	0.196581197	SPHKAP	ENST00000392056_r73	c.4810 C>T	p.P1604S	MISSENSE
MA4_23R	Chr2	230723502	T	C	0.141025641	TRIP12	ENST00000283943_r73	c.887 A>G	p.Q296R	MISSENSE
MA4_23R	Chr2	233413012	G	A	0.409090909	TIGD1	ENST00000408957_r73	c.1581 C>T	p.I527I	SILENT
MA4_23R	Chr2	238449108	G	T	0.394736842	MLPH	ENST00000264605_r73	c.1222 G>T	p.A408S	MISSENSE
MA4_23R	Chr2	242371116	T	C	0.173913044	FARP2	ENST00000264042_r73	c.794 T>C	p.F265S	MISSENSE
MA4_23R	Chr20	633682	T	C	0.243902439	SRXN1	ENST00000381962_r73	c.148 A>G	p.I50V	MISSENSE
MA4_23R	Chr20	3687772	C	T	0.273972603	SIGLEC1	ENST00000344754_r73	c.4 G>A	p.G2S	MISSENSE
MA4_23R	Chr20	13280052	G	A	0.106382979	ISM1	ENST00000262487_r73	c.1341 G>A	p.E447E	SILENT
MA4_23R	Chr20	33875140	C	T	0.136752137	FAM83C	ENST00000374408_r73	c.1442 G>A	p.G481D	MISSENSE

MA4_23R	Chr20	39831546	C	T	0.188571429	ZHX3	ENST00000309060_r73	c.2011 G>A	p.E671K	MISSENSE
MA4_23R	Chr20	43727834	C	T	0.337209302	KCNS1	ENST00000306117_r73	c.44 G>A	p.R15Q	MISSENSE
MA4_23R	Chr20	57246312	A	C	0.112244898	STX16	ENST00000355957_r73	c.700 A>C	p.N234H	MISSENSE
MA4_23R	Chr20	57246312	A	C	0.112244898	STX16-NPEPL1	ENST00000530122_r73	c.751 A>C	p.N251H	MISSENSE
MA4_23R	Chr20	57571837	C	T	0.284023669	CTSZ	ENST00000217131_r73	c.658 G>A	p.E220K	MISSENSE
MA4_23R	Chr20	61459319	C	T	0.213483146	COL9A3	ENST00000343916_r73	c.891 C>T	p.S297S	SILENT
MA4_23R	Chr20	62195536	G	A	0.188679245	HELZ2	ENST00000427522_r73	c.2932 C>T	p.R978W	MISSENSE
MA4_23R	Chr21	30380903	G	A	0.142857143	RWDD2B	ENST00000493196_r73	c.107 C>T	p.A36V	MISSENSE
MA4_23R	Chr21	34837660	A	G	0.202898551	TMEM50B	ENST00000420455_r73	c.269 T>C	p.L90S	MISSENSE
MA4_23R	Chr21	34922515	G	A	0.194444444	SON	ENST00000356577_r73	c.978 G>A	p.M326I	MISSENSE
MA4_23R	Chr21	40552338	T	G	0.139705882	PSMG1	ENST00000331573_r73	c.266 A>C	p.N89T	MISSENSE
MA4_23R	Chr21	43240044	G	A	0.191489362	PRDM15	ENST00000398548_r73	c.2265 C>T	p.H755H	SILENT
MA4_23R	Chr22	23523753	C	T	0.195121951	BCR	ENST00000305877_r73	c.606 C>T	p.S202S	SILENT
MA4_23R	Chr22	29876996	G	A	0.25	NEFH	ENST00000310624_r73	c.745 G>A	p.G249S	MISSENSE
MA4_23R	Chr22	32909761	C	G	0.223529412	SYN3	ENST00000358763_r73	c.1661 G>C	p.R554P	MISSENSE
MA4_23R	Chr22	37414181	A	G	0.461538462	TST	ENST00000403892_r73	c.593 T>C	p.V198A	MISSENSE
MA4_23R	Chr22	37890166	C	A	0.166666667	CARD10	ENST00000403299_r73	c.2403 G>T	p.R801R	SILENT
MA4_23R	Chr22	38211281	C	G	0.235294118	GCAT	ENST00000323205_r73	c.803 C>G	p.T268R	MISSENSE
MA4_23R	Chr22	39621819	G	A	0.1875	PDGFB	ENST00000331163_r73	c.635 C>T	p.T212M	MISSENSE
MA4_23R	Chr22	39917587	C	T	0.205882353	ATF4	ENST00000404241_r73	c.137 C>T	p.P46L	MISSENSE
MA4_23R	Chr22	45255677	A	G	0.166666667	PRR5-ARHGAP8	ENST00000361473_r73	c.1337 A>G	p.Y446C	MISSENSE
MA4_23R	Chr22	45255677	A	G	0.166666667	ARHGAP8	ENST00000389774_r73	c.1037 A>G	p.Y346C	MISSENSE
MA4_23R	Chr22	46658198	A	G	0.253012048	PKDREJ	ENST00000253255_r73	c.1022 T>C	p.L341P	MISSENSE
MA4_23R	Chr22	50885863	C	T	0.212765957	SBF1	ENST00000380817_r73	c.5471 G>A	p.R1824H	MISSENSE
MA4_23R	Chr3	16358506	A	G	0.08974359	RFTN1	ENST00000334133_r73	c.1566 T>C	p.P522P	SILENT
MA4_23R	Chr3	32995349	C	T	0.192090396	CCR4	ENST00000330953_r73	c.435 C>T	p.S145S	SILENT
MA4_23R	Chr3	40557438	G	A	0.196969697	ZNF620	ENST00000314529_r73	c.353 G>A	p.G118D	MISSENSE
MA4_23R	Chr3	46008939	G	A	0.192307692	FYCO1	ENST00000296137_r73	c.1887 C>T	p.V629V	SILENT
MA4_23R	Chr3	49060313	C	T	0.25974026	NDUFAF3	ENST00000326912_r73	c.171 C>T	p.I57I	SILENT
MA4_23R	Chr3	49837207	C	T	0.192771084	CDHR4	ENST00000412678_r73	c.39 G>A	p.P13P	SILENT
MA4_23R	Chr3	49850929	A	G	0.25	UBA7	ENST00000333486_r73	c.208 T>C	p.S70P	MISSENSE
MA4_23R	Chr3	52283025	C	T	0.175572519	PPM1M	ENST00000409502_r73	c.396 C>T	p.L132L	SILENT
MA4_23R	Chr3	52398913	A	G	0.154589372	DNAH1	ENST00000420323_r73	c.5396 A>G	p.K1799R	MISSENSE
MA4_23R	Chr3	52661351	G	A	0.235294118	PBRM1	ENST00000394830_r73	c.1479 C>T	p.I493I	SILENT
MA4_23R	Chr3	52858459	G	A	0.264285714	ITIH4	ENST00000266041_r73	c.999 C>T	p.N333N	SILENT
MA4_23R	Chr3	101571742	C	G	0.192546584	NFKBIZ	ENST00000394054_r73	c.173 C>G	p.T58R	MISSENSE
MA4_23R	Chr3	108781994	C	T	0.151898734	MORC1	ENST00000232603_r73	Exon 10 5 G>A	-	ESSENTIAL_SPLICE

MA4_23R	Chr3	122420142	G	A	0.220994475	PARP14	ENST00000474629_r73	c.2741 G>A	p.R914Q	MISSENSE
MA4_23R	Chr3	132196983	G	A	0.16	DNAJC13	ENST00000260818_r73	c.2708 G>A	p.R903K	MISSENSE
MA4_23R	Chr3	145782480	A	G	0.227272727	AC107021.1	ENST00000422482_r73	c.101 A>G	p.H34R	MISSENSE
MA4_23R	Chr3	150834162	A	G	0.183206107	MED12L	ENST00000474524_r73	c.137 A>G	p.N46S	MISSENSE
MA4_23R	Chr3	169485469	G	A	0.189655172	ACTRT3	ENST00000330368_r73	c.870 C>T	p.F290F	SILENT
MA4_23R	Chr3	184071136	G	A	0.227722772	CLCN2	ENST00000265593_r73	c.1930 C>T	p.R644C	MISSENSE
MA4_23R	Chr3	184101429	C	T	0.243243243	CHRD	ENST00000204604_r73	c.1439 C>T	p.T480M	MISSENSE
MA4_23R	Chr3	193081090	C	T	0.1875	ATP13A5	ENST00000342358_r73	c.319 G>A	p.E107K	MISSENSE
MA4_23R	Chr4	1388564	T	C	0.272727273	CRIPAK	ENST00000324803_r73	c.265 T>C	p.C89R	MISSENSE
MA4_23R	Chr4	6303769	G	A	0.201970443	WFS1	ENST00000503569_r73	c.2247 G>A	p.T749T	SILENT
MA4_23R	Chr4	17841383	A	G	0.210526316	NCAPG	ENST00000251496_r73	c.2551 A>G	p.T851A	MISSENSE
MA4_23R	Chr4	40339286	C	G	0.157894737	CHRNA9	ENST00000310169_r73	c.270 C>G	p.A90A	SILENT
MA4_23R	Chr4	48844693	A	T	0.235294118	OCIAD1	ENST00000264312_r73	c.180 A>T	p.G60G	SILENT
MA4_23R	Chr4	56847506	A	G	0.227722772	CEP135	ENST00000257287_r73	c.1740 A>G	p.R580R	SILENT
MA4_23R	Chr4	70146902	T	C	0.4375	UGT2B28	ENST00000335568_r73	c.684 T>C	p.D228D	SILENT
MA4_23R	Chr4	89300241	C	A	0.404761905	HERC6	ENST00000380265_r73	c.168 C>A	p.G56G	SILENT
MA4_23R	Chr4	91230194	A	C	0.230769231	CCSER1	ENST00000509176_r73	c.759 A>C	p.T253T	SILENT
MA4_23R	Chr4	106190798	G	A	0.101941748	TET2	ENST00000380013_r73	c.4076 G>A	p.R1359H	MISSENSE
MA4_23R	Chr4	122062982	G	A	0.189189189	TNIP3	ENST00000057513_r73	c.874 C>T	p.R292W	MISSENSE
MA4_23R	Chr4	141446698	T	G	0.177514793	ELMOD2	ENST00000323570_r73	c.116 T>G	p.V39G	MISSENSE
MA4_23R	Chr4	144922436	T	G	0.063926941	GYPB	ENST00000502664_r73	c.38 A>C	p.E13A	MISSENSE
MA4_23R	Chr4	154626370	C	T	0.173913044	TLR2	ENST00000260010_r73	c.2311 C>T	p.R771W	MISSENSE
MA4_23R	Chr4	155490820	A	G	0.216216216	FGB	ENST00000302068_r73	c.1113 A>G	p.S371S	SILENT
MA4_23R	Chr5	428022	C	T	0.176470588	AHRR	ENST00000505113_r73	c.821 C>T	p.A274V	MISSENSE
MA4_23R	Chr5	1087084	G	A	0.135483871	SLC12A7	ENST00000264930_r73	c.609 C>T	p.L203L	SILENT
MA4_23R	Chr5	1217004	G	A	0.174603175	SLC6A19	ENST00000304460_r73	c.1117 G>A	p.A373T	MISSENSE
MA4_23R	Chr5	13717485	G	A	0.145833333	DNAH5	ENST00000265104_r73	c.12644 C>T	p.A4215V	MISSENSE
MA4_23R	Chr5	32058127	C	T	0.126213592	PDZD2	ENST00000438447_r73	c.2118 C>T	p.S706S	SILENT
MA4_23R	Chr5	93966286	G	A	0.142857143	ANKRD32	ENST00000265140_r73	c.269 G>A	p.W90*	NONSENSE
MA4_23R	Chr5	107717088	C	T	0.217391304	FBXL17	ENST00000542267_r73	c.305 G>A	p.R102Q	MISSENSE
MA4_23R	Chr5	126755873	G	A	0.098591549	MEGF10	ENST00000503335_r73	c.1564 G>A	p.G522R	MISSENSE
MA4_23R	Chr5	131008132	T	C	0.179661017	FNIP1	ENST00000307968_r73	c.1921 A>G	p.K641E	MISSENSE
MA4_23R	Chr5	131329826	C	G	0.189473684	ACSL6	ENST00000379264_r73	c.168 G>C	p.V56V	SILENT
MA4_23R	Chr5	132150837	C	G	0.140186916	SOWAHA	ENST00000378693_r73	c.1524 C>G	p.A508A	SILENT
MA4_23R	Chr5	133473774	G	A	0.307692308	TCF7	ENST00000342854_r73	c.466 G>A	p.G156S	MISSENSE
MA4_23R	Chr5	138260288	C	T	0.297297297	CTNNA1	ENST00000302763_r73	c.1636 C>T	p.R546*	NONSENSE
MA4_23R	Chr5	139060486	G	A	0.159763314	CXXC5	ENST00000302517_r73	c.378 G>A	p.A126A	SILENT

MA4_23R	Chr5	139714273	A	G	0.156028369	HBEGF	ENST00000230990_r73	c.615 T>C	p.T205T	SILENT
MA4_23R	Chr5	145843260	T	C	0.131428571	TCERG1	ENST00000296702_r73	c.1039 T>C	p.S347P	MISSENSE
MA4_23R	Chr5	149578896	C	T	0.164179105	SLC6A7	ENST00000230671_r73	c.690 C>T	p.L230L	SILENT
MA4_23R	Chr5	162939175	A	G	0.205882353	MAT2B	ENST00000280969_r73	c.198 A>G	p.A66A	SILENT
MA4_23R	Chr5	167630831	A	C	0.183673469	TENM2	ENST00000518659_r73	c.3568 A>C	p.K1190Q	MISSENSE
MA4_23R	Chr5	171509391	C	T	0.104651163	STK10	ENST00000176763_r73	c.1928 G>A	p.R643H	MISSENSE
MA4_23R	Chr5	174869692	G	C	0.192307692	DRD1	ENST00000393752_r73	c.411 C>G	p.P137P	SILENT
MA4_23R	Chr5	176832999	T	C	0.113636364	F12	ENST00000253496_r73	c.179 A>G	p.K60R	MISSENSE
MA4_23R	Chr5	178358521	G	T	0.161290323	ZFP2	ENST00000361362_r73	c.207 G>T	p.M69I	MISSENSE
MA4_23R	Chr5	179260201	G	A	0.176470588	SQSTM1	ENST00000389805_r73	c.924 G>A	p.A308A	SILENT
MA4_23R	Chr6	656694	G	C	0.182926829	HUS1B	ENST00000380907_r73	c.251 C>G	p.A84G	MISSENSE
MA4_23R	Chr6	10634514	C	T	0.202702703	GCNT6	ENST00000379591_r73	c.357 C>T	p.A119A	SILENT
MA4_23R	Chr6	26156843	G	A	0.210526316	HIST1H1E	ENST00000304218_r73	c.225 G>A	p.K75K	SILENT
MA4_23R	Chr6	31779134	T	C	0.205479452	HSPA1L	ENST00000375654_r73	c.616 A>G	p.T206A	MISSENSE
MA4_23R	Chr6	32905086	G	A	0.168316832	HLA-DMB	ENST00000418107_r73	c.485 C>T	p.A162V	MISSENSE
MA4_23R	Chr6	34208668	C	T	0.227272727	HMGA1	ENST00000311487_r73	c.111 C>T	p.P37P	SILENT
MA4_23R	Chr6	35262346	G	A	0.132075472	ZNF76	ENST00000373953_r73	c.1608 G>A	p.Q536Q	SILENT
MA4_23R	Chr6	41754576	C	T	0.202380952	PRICKLE4	ENST00000335515_r73	c.864 C>T	p.L288L	SILENT
MA4_23R	Chr6	42072274	C	T	0.193548387	C6orf132	ENST00000341865_r73	c.3376 G>A	p.A1126T	MISSENSE
MA4_23R	Chr6	51889823	G	A	0.191358025	PKHD1	ENST00000371117_r73	c.4785 C>T	p.G1595G	SILENT
MA4_23R	Chr6	54804720	C	T	0.223776224	FAM83B	ENST00000306858_r73	c.951 C>T	p.S317S	SILENT
MA4_23R	Chr6	84871572	G	A	0.24137931	KIAA1009	ENST00000403245_r73	c.2569 C>T	p.R857C	MISSENSE
MA4_23R	Chr6	109764598	A	T	0.2734375	SMPD2	ENST00000258052_r73	c.858 A>T	p.P286P	SILENT
MA4_23R	Chr6	126080448	T	C	0.136363636	HEY2	ENST00000368364_r73	c.514 T>C	p.S172P	MISSENSE
MA4_23R	Chr6	131919806	G	A	0.174757282	MED23	ENST00000354577_r73	c.2334 C>T	p.N778N	SILENT
MA4_23R	Chr6	137479526	G	A	0.220779221	IL22RA2	ENST00000349184_r73	c.155 C>T	p.A52V	MISSENSE
MA4_23R	Chr6	142539730	G	A	0.197802198	VTA1	ENST00000367630_r73	c.874 G>A	p.V292I	MISSENSE
MA4_23R	Chr6	154481128	C	T	0.2	IPCEF1	ENST00000265198_r73	c.1149 G>A	p.P383P	SILENT
MA4_23R	Chr7	4722377	G	A	0.36	FOXK1	ENST00000328914_r73	c.438 G>A	p.R146R	SILENT
MA4_23R	Chr7	4824597	C	T	0.219512195	AP5Z1	ENST00000348624_r73	c.849 C>T	p.A283A	SILENT
MA4_23R	Chr7	5434174	C	G	0.166666667	TNRC18	ENST00000430969_r73	c.240 G>C	p.S80S	SILENT
MA4_23R	Chr7	21893969	G	C	0.259615385	DNAH11	ENST00000409508_r73	c.11098 G>C	p.E3700Q	MISSENSE
MA4_23R	Chr7	26192248	G	A	0.390243902	NFE2L3	ENST00000056233_r73	c.130 G>A	p.D44N	MISSENSE
MA4_23R	Chr7	26224382	C	T	0.066371681	NFE2L3	ENST00000056233_r73	c.1064 C>T	p.T355I	MISSENSE
MA4_23R	Chr7	47409029	G	A	0.261904762	TNS3	ENST00000311160_r73	c.1214 C>T	p.T405M	MISSENSE
MA4_23R	Chr7	48314389	T	C	0.266666667	ABCA13	ENST00000435803_r73	c.5126 T>C	p.L1709P	MISSENSE
MA4_23R	Chr7	100356262	G	C	0.142857143	ZAN	ENST00000349350_r73	c.3560 G>C	p.G1187A	MISSENSE

MA4_23R	Chr7	100643477	A	C	0.074829932	MUC12	ENST00000536621_r73	c.9633 A>C	p.S3211S	SILENT
MA4_23R	Chr7	100645731	G	A	0.111111111	MUC12	ENST00000536621_r73	c.11887 G>A	p.E3963K	MISSENSE
MA4_23R	Chr7	100855576	G	A	0.171428571	PLOD3	ENST00000223127_r73	c.1085 C>T	p.P362L	MISSENSE
MA4_23R	Chr7	117243823	C	T	0.167567568	CFTR	ENST00000003084_r73	c.2895 C>T	p.N965N	SILENT
MA4_23R	Chr7	121944279	G	A	0.159624413	FEZF1	ENST00000442488_r73	c.213 C>T	p.I71I	SILENT
MA4_23R	Chr7	139257887	C	T	0.163265306	HIPK2	ENST00000406875_r73	c.3383 G>A	p.R1128H	MISSENSE
MA4_23R	Chr7	140287517	G	A	0.189873418	DENND2A	ENST00000275884_r73	c.1059 C>T	p.Y353Y	SILENT
MA4_23R	Chr7	148904547	A	G	0.14516129	ZNF282	ENST00000262085_r73	c.817 A>G	p.M273V	MISSENSE
MA4_23R	Chr7	150713295	G	C	0.17948718	ATG9B	ENST00000377974_r73	c.2546 C>G	p.P849R	MISSENSE
MA4_23R	Chr7	150716160	T	C	0.158878505	ATG9B	ENST00000377974_r73	c.1265 A>G	p.Y422C	MISSENSE
MA4_23R	Chr8	8185328	C	T	0.220183486	SGK223	ENST00000520004_r73	c.2964 G>A	p.S988S	SILENT
MA4_23R	Chr8	8235510	G	C	0.151898734	SGK223	ENST00000520004_r73	c.409 C>G	p.R137G	MISSENSE
MA4_23R	Chr8	8560176	G	A	0.212121212	CLDN23	ENST00000519106_r73	c.268 G>A	p.A90T	MISSENSE
MA4_23R	Chr8	9009379	G	A	0.25	RP11-10A14.4	ENST00000518496_r73	c.21 G>A	p.K7K	SILENT
MA4_23R	Chr8	11659451	G	C	0.428571429	RP11-297N6.4	ENST00000533405_r73	c.146 C>G	p.A49G	MISSENSE
MA4_23R	Chr8	12957678	C	T	0.174863388	DLC1	ENST00000276297_r73	c.2168 G>A	p.R723H	MISSENSE
MA4_23R	Chr8	22548277	C	T	0.137931035	EGR3	ENST00000317216_r73	c.873 G>A	p.E291E	SILENT
MA4_23R	Chr8	28671031	A	C	0.189393939	INTS9	ENST00000521022_r73	c.587 T>G	p.L196R	MISSENSE
MA4_23R	Chr8	28929820	A	C	0.17948718	KIF13B	ENST00000524189_r73	c.4535 T>G	p.M1512R	MISSENSE
MA4_23R	Chr8	68028331	C	T	0.269662921	CSPP1	ENST00000262210_r73	c.1455 C>T	p.S485S	SILENT
MA4_23R	Chr8	98656775	C	T	0.225806452	MTDH	ENST00000336273_r73	c.41 C>T	p.A14V	MISSENSE
MA4_23R	Chr8	103372358	G	A	0.181818182	UBR5	ENST00000520539_r73	c.327 C>T	p.D109D	SILENT
MA4_23R	Chr8	110302077	A	T	0.183206107	NUDCD1	ENST00000239690_r73	c.726 T>A	p.N242K	MISSENSE
MA4_23R	Chr8	126052103	T	C	0.242105263	KIAA0196	ENST00000318410_r73	c.2888 A>G	p.N963S	MISSENSE
MA4_23R	Chr8	144332046	G	A	0.107142857	ZFP41	ENST00000520584_r73	c.33 G>A	p.T11T	SILENT
MA4_23R	Chr8	144332046	G	A	0.107142857	ZFP41	ENST00000522452_r73	c.33 G>A	p.T11T	SILENT
MA4_23R	Chr8	144810572	G	A	0.150684932	FAM83H	ENST00000388913_r73	c.1059 C>T	p.A353A	SILENT
MA4_23R	Chr8	145748360	G	C	0.195402299	LRRC24	ENST00000529415_r73	c.1041 C>G	p.A347A	SILENT
MA4_23R	Chr9	6012864	C	T	0.073033708	RANBP6	ENST00000259569_r73	c.2744 G>A	p.R915Q	MISSENSE
MA4_23R	Chr9	19409094	G	C	0.191489362	ACER2	ENST00000340967_r73	c.12 G>C	p.P4P	SILENT
MA4_23R	Chr9	34690000	C	T	0.166666667	CCL19	ENST00000311925_r73	c.203 G>A	p.R68H	MISSENSE
MA4_23R	Chr9	34993437	G	A	0.178571429	DNAJB5	ENST00000453597_r73	c.549 G>A	p.E183E	SILENT
MA4_23R	Chr9	79635269	C	T	0.410958904	FOXB2	ENST00000376708_r73	c.699 C>T	p.A233A	SILENT
MA4_23R	Chr9	95177598	T	C	0.140625	OMD	ENST00000375550_r73	c.1102 A>G	p.T368A	MISSENSE
MA4_23R	Chr9	96860820	G	A	0.152777778	PTPDC1	ENST00000375360_r73	c.1810 G>A	p.V604I	MISSENSE
MA4_23R	Chr9	100112770	C	T	0.186046512	CCDC180	ENST00000529487_r73	c.3067 C>T	p.R1023W	MISSENSE
MA4_23R	Chr9	121930252	C	T	0.308411215	DBC1	ENST00000265922_r73	c.1396 G>A	p.V466M	MISSENSE

MA4_23R	Chr9	125486542	A	G	0.123167155	OR1L4	ENST00000259466_r73	c.274 A>G	p.I92V	MISSENSE
MA4_23R	Chr9	131768786	G	A	0.154929578	NUP188	ENST00000372577_r73	c.5079 G>A	p.T1693T	SILENT
MA4_23R	Chr9	137711997	G	A	0.171974522	COL5A1	ENST00000371817_r73	c.4482 G>A	p.P1494P	SILENT
MA4_23R	Chr9	139636334	G	A	0.166666667	LCN10	ENST00000497771_r73	c.256 C>T	p.R86W	MISSENSE
MA4_23R	Chr9	139935576	C	T	0.175675676	NPDC1	ENST00000371601_r73	c.323 G>A	p.R108Q	MISSENSE
MA4_23R	ChrX	2777948	A	T	0.186813187	GYG2	ENST00000398806_r73	c.679 A>T	p.N227Y	MISSENSE
MA4_23R	ChrX	2825403	A	G	0.175572519	ARSD	ENST00000381154_r73	c.1691 T>C	p.M564T	MISSENSE
MA4_23R	ChrX	2836037	G	C	0.223684211	ARSD	ENST00000381154_r73	c.671 C>G	p.S224C	MISSENSE
MA4_23R	ChrX	2951348	A	G	0.4	ARSH	ENST00000381130_r73	c.1611 A>G	p.P537P	SILENT
MA4_23R	ChrX	3002687	A	G	0.382978723	ARSF	ENST00000381127_r73	c.810 A>G	p.E270E	SILENT
MA4_23R	ChrX	3228411	G	A	0.755555556	MXRA5	ENST00000217939_r73	c.7833 C>T	p.A2611A	SILENT
MA4_23R	ChrX	3228891	A	G	0.471428571	MXRA5	ENST00000217939_r73	c.7353 T>C	p.T2451T	SILENT
MA4_23R	ChrX	3235724	C	T	0.727272727	MXRA5	ENST00000217939_r73	c.5998 G>A	p.G2000S	MISSENSE
MA4_23R	ChrX	3239545	C	T	0.523809524	MXRA5	ENST00000217939_r73	c.4181 G>A	p.G1394D	MISSENSE
MA4_23R	ChrX	3240343	G	A	0.546875	MXRA5	ENST00000217939_r73	c.3383 C>T	p.A1128V	MISSENSE
MA4_23R	ChrX	3241050	G	A	0.642857143	MXRA5	ENST00000217939_r73	c.2676 C>T	p.S892S	SILENT
MA4_23R	ChrX	3241256	T	C	0.338235294	MXRA5	ENST00000217939_r73	c.2470 A>G	p.I824V	MISSENSE
MA4_23R	ChrX	3241317	T	C	0.37704918	MXRA5	ENST00000217939_r73	c.2409 A>G	p.P803P	SILENT
MA4_23R	ChrX	3241791	G	A	0.471698113	MXRA5	ENST00000217939_r73	c.1935 C>T	p.D645D	SILENT
MA4_23R	ChrX	3592725	G	A	0.492753623	PRKX	ENST00000262848_r73	c.249 C>T	p.P83P	SILENT
MA4_23R	ChrX	3631167	A	G	0.45945946	PRKX	ENST00000262848_r73	c.128 T>C	p.V43A	MISSENSE
MA4_23R	ChrX	7889828	C	T	0.306122449	PNPLA4	ENST00000381042_r73	c.337 G>A	p.V113I	MISSENSE
MA4_23R	ChrX	10180554	G	A	0.333333333	CLCN4	ENST00000380833_r73	c.1437 G>A	p.A479A	SILENT
MA4_23R	ChrX	12937513	C	T	0.253424658	TLR8	ENST00000218032_r73	c.354 C>T	p.D118D	SILENT
MA4_23R	ChrX	16168467	T	C	0.647058824	GRPR	ENST00000380289_r73	c.453 T>C	p.S151S	SILENT
MA4_23R	ChrX	16627756	C	T	0.346153846	CTPS2	ENST00000359276_r73	c.1599 G>A	p.P533P	SILENT
MA4_23R	ChrX	16859628	G	A	0.517241379	TXLNG	ENST00000380122_r73	c.1326 G>A	p.Q442Q	SILENT
MA4_23R	ChrX	21508666	A	G	0.193277311	CNKSR2	ENST00000279451_r73	c.651 A>G	p.Q217Q	SILENT
MA4_23R	ChrX	21861434	A	G	0.28	MBTPS2	ENST00000379484_r73	c.222 A>G	p.Q74Q	SILENT
MA4_23R	ChrX	23019346	G	T	0.339285714	DDX53	ENST00000327968_r73	c.1172 G>T	p.R391M	MISSENSE
MA4_23R	ChrX	23933852	G	A	0.3125	CXorf58	ENST00000379211_r73	c.252 G>A	p.V84V	SILENT
MA4_23R	ChrX	24608284	A	G	0.223880597	PCYT1B	ENST00000379145_r73	c.288 T>C	p.S96S	SILENT
MA4_23R	ChrX	26157792	C	T	0.560606061	MAGEB18	ENST00000325250_r73	c.690 C>T	p.A230A	SILENT
MA4_23R	ChrX	27999146	C	T	0.302013423	DCAF8L1	ENST00000441525_r73	c.306 G>A	p.E102E	SILENT
MA4_23R	ChrX	30254361	G	A	0.375	MAGEB3	ENST00000378986_r73	c.320 G>A	p.R107H	MISSENSE
MA4_23R	ChrX	30254530	A	G	0.186440678	MAGEB3	ENST00000378986_r73	c.489 A>G	p.V163V	SILENT
MA4_23R	ChrX	30326983	C	T	0.328767123	NR0B1	ENST00000378970_r73	c.498 G>A	p.R166R	SILENT

MA4_23R	ChrX	31496426	T	C	0.234848485	DMD	ENST00000378677_r73	c.8722 A>G	p.N2908D	MISSENSE
MA4_23R	ChrX	31496431	T	A	0.2421875	DMD	ENST00000378677_r73	c.8717 A>T	p.E2906V	MISSENSE
MA4_23R	ChrX	31697636	A	G	0.27972028	DMD	ENST00000378677_r73	c.7716 T>C	p.N2572N	SILENT
MA4_23R	ChrX	31893307	T	G	0.310344828	DMD	ENST00000378677_r73	c.7084 A>C	p.K2362Q	MISSENSE
MA4_23R	ChrX	32235149	G	A	0.222222222	DMD	ENST00000378677_r73	c.6310 C>T	p.R2104C	MISSENSE
MA4_23R	ChrX	32380996	C	T	0.330275229	DMD	ENST00000378677_r73	c.5222 G>A	p.R1741H	MISSENSE
MA4_23R	ChrX	35988996	T	C	0.4	CXorf22	ENST00000297866_r73	c.1926 T>C	p.L642L	SILENT
MA4_23R	ChrX	35993454	C	T	0.612903226	CXorf22	ENST00000297866_r73	c.2445 C>T	p.D815D	SILENT
MA4_23R	ChrX	36007464	A	T	0.333333333	CXorf22	ENST00000297866_r73	c.2742 A>T	p.E914D	MISSENSE
MA4_23R	ChrX	36368166	G	A	0.304347826	CXorf30	ENST00000378657_r73	c.955 G>A	p.D319N	MISSENSE
MA4_23R	ChrX	36371719	T	A	0.479591837	CXorf30	ENST00000378657_r73	c.1112 T>A	p.F371Y	MISSENSE
MA4_23R	ChrX	36385156	A	G	0.216374269	CXorf30	ENST00000378657_r73	c.1437 A>G	p.E479E	SILENT
MA4_23R	ChrX	37028127	A	G	0.322580645	FAM47C	ENST00000358047_r73	c.1644 A>G	p.P548P	SILENT
MA4_23R	ChrX	37029254	A	C	0.323076923	FAM47C	ENST00000358047_r73	c.2771 A>C	p.N924T	MISSENSE
MA4_23R	ChrX	39932907	T	C	0.201438849	BCOR	ENST00000397354_r73	c.1692 A>G	p.A564A	SILENT
MA4_23R	ChrX	40513785	C	T	0.183673469	MED14	ENST00000324817_r73	c.4122 G>A	p.S1374S	SILENT
MA4_23R	ChrX	40573157	G	A	0.296875	MED14	ENST00000324817_r73	c.525 C>T	p.D175D	SILENT
MA4_23R	ChrX	43603391	T	C	0.606060606	MAOA	ENST00000338702_r73	c.1410 T>C	p.D470D	SILENT
MA4_23R	ChrX	44401295	T	G	0.119047619	FUNDC1	ENST00000378045_r73	c.81 A>C	p.A27A	SILENT
MA4_23R	ChrX	47343254	C	T	0.284482759	CXorf24	ENST00000357412_r73	c.251 C>T	p.T84I	MISSENSE
MA4_23R	ChrX	47444985	T	C	0.351851852	TIMP1	ENST00000218388_r73	c.372 T>C	p.F124F	SILENT
MA4_23R	ChrX	47483800	G	A	0.327272727	CFP	ENST00000396992_r73	c.1284 C>T	p.N428N	SILENT
MA4_23R	ChrX	47918205	G	A	0.666666667	ZNF630	ENST00000409324_r73	c.1626 C>T	p.P542P	SILENT
MA4_23R	ChrX	48418126	A	G	0.271186441	TBC1D25	ENST00000376771_r73	c.830 A>G	p.N277S	MISSENSE
MA4_23R	ChrX	48418659	G	A	0.377192983	TBC1D25	ENST00000376771_r73	c.1363 G>A	p.A455T	MISSENSE
MA4_23R	ChrX	48751289	G	A	0.394736842	TIMM17B	ENST00000376582_r73	c.324 C>T	p.G108G	SILENT
MA4_23R	ChrX	48888074	T	C	0.538461539	TFE3	ENST00000315869_r73	c.1323 A>G	p.V441V	SILENT
MA4_23R	ChrX	53457622	T	C	0.176470588	RIBC1	ENST00000375327_r73	c.942 T>C	p.T314T	SILENT
MA4_23R	ChrX	54836361	A	G	0.2	MAGED2	ENST00000375068_r73	c.252 A>G	p.S84S	SILENT
MA4_23R	ChrX	54836505	A	G	0.188235294	MAGED2	ENST00000375068_r73	c.396 A>G	p.T132T	SILENT
MA4_23R	ChrX	54838077	C	T	0.23255814	MAGED2	ENST00000375068_r73	c.981 C>T	p.S327S	SILENT
MA4_23R	ChrX	67937976	G	A	0.295081967	STARD8	ENST00000374599_r73	c.1220 G>A	p.R407Q	MISSENSE
MA4_23R	ChrX	68381912	G	A	0.493670886	PJA1	ENST00000374583_r73	c.1170 C>T	p.G390G	SILENT
MA4_23R	ChrX	70597546	C	G	0.204081633	TAF1	ENST00000373790_r73	c.805 C>G	p.L269V	MISSENSE
MA4_23R	ChrX	70787856	T	C	0.268965517	OGT	ENST00000373719_r73	c.2856 T>C	p.A952A	SILENT
MA4_23R	ChrX	71350133	T	G	0.279411765	RGAG4	ENST00000479991_r73	c.1258 A>C	p.S420R	MISSENSE
MA4_23R	ChrX	71360204	A	G	0.242424242	NHSL2	ENST00000373677_r73	c.1708 A>G	p.R570G	MISSENSE

MA4_23R	ChrX	73524557	A	G	0.333333333	ZCCHC13	ENST00000339534_r73	c.456 A>G	p.L152L	SILENT
MA4_23R	ChrX	77913569	G	A	0.292134832	ZCCHC5	ENST00000321110_r73	c.349 C>T	p.P117S	MISSENSE
MA4_23R	ChrX	78216024	A	C	0.22	P2RY10	ENST00000171757_r73	c.7 A>C	p.N3H	MISSENSE
MA4_23R	ChrX	79281202	G	A	0.368421053	TBX22	ENST00000373296_r73	c.559 G>A	p.E187K	MISSENSE
MA4_23R	ChrX	83723541	A	G	0.283018868	HDX	ENST00000297977_r73	c.1190 T>C	p.F397S	MISSENSE
MA4_23R	ChrX	85219021	T	C	0.174757282	CHM	ENST00000357749_r73	c.351 A>G	p.A117A	SILENT
MA4_23R	ChrX	86887244	C	T	0.25	KLHL4	ENST00000373119_r73	c.1359 C>T	p.T453T	SILENT
MA4_23R	ChrX	88008807	G	A	0.285714286	CPXCR1	ENST00000276127_r73	c.392 G>A	p.R131H	MISSENSE
MA4_23R	ChrX	89177673	G	A	0.279069767	TGIF2LX	ENST00000283891_r73	c.589 G>A	p.V197I	MISSENSE
MA4_23R	ChrX	99890204	C	T	0.295454546	TSPAN6	ENST00000373020_r73	c.322 G>A	p.A108T	MISSENSE
MA4_23R	ChrX	100749588	A	C	0.325	ARMCX4	ENST00000423738_r73	c.6012 A>C	p.Q2004H	MISSENSE
MA4_23R	ChrX	100808222	C	T	0.214876033	ARMCX1	ENST00000372829_r73	c.309 C>T	p.G103G	SILENT
MA4_23R	ChrX	103042882	T	C	0.263157895	PLP1	ENST00000303958_r73	c.609 T>C	p.D203D	SILENT
MA4_23R	ChrX	103294760	C	T	0.462686567	H2BFM	ENST00000355016_r73	c.217 C>T	p.Q73*	NONSENSE
MA4_23R	ChrX	104992963	T	C	0.26984127	IL1RAPL2	ENST00000372582_r73	c.1059 T>C	p.Y353Y	SILENT
MA4_23R	ChrX	105152282	G	A	0.333333333	NRK	ENST00000243300_r73	c.1072 G>A	p.V358M	MISSENSE
MA4_23R	ChrX	105449445	T	A	0.284210526	MUM1L1	ENST00000357175_r73	c.20 T>A	p.L7Q	MISSENSE
MA4_23R	ChrX	105449709	G	A	0.324786325	MUM1L1	ENST00000357175_r73	c.284 G>A	p.G95D	MISSENSE
MA4_23R	ChrX	111698613	T	C	0.279411765	ZCCHC16	ENST00000340433_r73	c.657 T>C	p.H219H	SILENT
MA4_23R	ChrX	111914244	A	G	0.272727273	LHFPL1	ENST00000371968_r73	c.375 T>C	p.F125F	SILENT
MA4_23R	ChrX	114398338	T	G	0.213333333	LRCH2	ENST00000317135_r73	c.1364 A>C	p.K455T	MISSENSE
MA4_23R	ChrX	114541176	G	A	0.5	LUZP4	ENST00000371920_r73	c.749 G>A	p.R250K	MISSENSE
MA4_23R	ChrX	117528142	C	T	0.26056338	WDR44	ENST00000254029_r73	c.951 C>T	p.T317T	SILENT
MA4_23R	ChrX	118108785	T	C	0.225806452	LONRF3	ENST00000365713_r73	c.42 T>C	p.A14A	SILENT
MA4_23R	ChrX	118587003	C	T	0.206666667	SLC25A43	ENST00000217909_r73	c.1001 C>T	p.P334L	MISSENSE
MA4_23R	ChrX	118604436	T	C	0.565217391	SLC25A5	ENST00000317881_r73	c.699 T>C	p.T233T	SILENT
MA4_23R	ChrX	118678364	G	A	0.454545455	CXorf56	ENST00000486230_r73	c.375 C>T	p.G125G	SILENT
MA4_23R	ChrX	122537277	T	C	0.571428571	GRIA3	ENST00000371251_r73	c.1200 T>C	p.N400N	SILENT
MA4_23R	ChrX	123034511	A	C	0.5	XIAP	ENST00000371199_r73	c.1268 A>C	p.Q423P	MISSENSE
MA4_23R	ChrX	123540315	G	T	0.75	TENM1	ENST00000371130_r73	c.4986 C>A	p.T1662T	SILENT
MA4_23R	ChrX	125954964	C	G	0.172413793	CXorf64	ENST00000371125_r73	c.343 C>G	p.L115V	MISSENSE
MA4_23R	ChrX	128880614	T	C	0.529411765	XPNPEP2	ENST00000371106_r73	c.447 T>C	p.P149P	SILENT
MA4_23R	ChrX	129201179	C	T	0.152542373	ELF4	ENST00000335997_r73	c.1509 G>A	p.T503T	SILENT
MA4_23R	ChrX	129283520	A	G	0.222222222	AIFM1	ENST00000416073_r73	c.273 T>C	p.D91D	SILENT
MA4_23R	ChrX	129349295	T	G	0.265306122	ZNF280C	ENST00000370978_r73	c.1851 A>C	p.G617G	SILENT
MA4_23R	ChrX	129518646	A	G	0.244897959	GPR119	ENST00000276218_r73	c.776 T>C	p.V259A	MISSENSE
MA4_23R	ChrX	130408745	G	A	0.273972603	IGSF1	ENST00000370910_r73	c.3552 C>T	p.V1184V	SILENT

MA4_23R	ChrX	130409217	C	G	0.333333333	IGSF1	ENST00000370910_r73	c.3201 G>C	p.M1067I	MISSENSE
MA4_23R	ChrX	131212512	A	G	0.288288288	FRMD7	ENST00000298542_r73	c.1533 T>C	p.I511I	SILENT
MA4_23R	ChrX	131212944	A	G	0.236111111	FRMD7	ENST00000298542_r73	c.1101 T>C	p.N367N	SILENT
MA4_23R	ChrX	132161159	G	A	0.212389381	USP26	ENST00000370832_r73	c.1090 C>T	p.L364F	MISSENSE
MA4_23R	ChrX	132161673	C	T	0.253164557	USP26	ENST00000370832_r73	c.576 G>A	p.E192E	SILENT
MA4_23R	ChrX	133963268	C	T	0.251968504	FAM122C	ENST00000370785_r73	c.202 C>T	p.P68S	MISSENSE
MA4_23R	ChrX	134185997	T	A	0.405405405	FAM127B	ENST00000370775_r73	c.142 A>T	p.S48C	MISSENSE
MA4_23R	ChrX	134990000	C	T	0.283333333	SAGE1	ENST00000370709_r73	c.1159 C>T	p.H387Y	MISSENSE
MA4_23R	ChrX	134991078	A	G	0.20625	SAGE1	ENST00000370709_r73	c.1497 A>G	p.Q499Q	SILENT
MA4_23R	ChrX	134994005	T	C	0.35483871	SAGE1	ENST00000370709_r73	c.2414 T>C	p.L805S	MISSENSE
MA4_23R	ChrX	135426693	A	G	0.189655172	GPR112	ENST00000394143_r73	c.828 A>G	p.I276M	MISSENSE
MA4_23R	ChrX	135431236	T	C	0.297435897	GPR112	ENST00000394143_r73	c.5371 T>C	p.F1791L	MISSENSE
MA4_23R	ChrX	135431358	C	T	0.277777778	GPR112	ENST00000394143_r73	c.5493 C>T	p.P1831P	SILENT
MA4_23R	ChrX	135480126	T	C	0.37037037	GPR112	ENST00000394143_r73	c.8271 T>C	p.F2757F	SILENT
MA4_23R	ChrX	135496398	G	A	0.26519337	GPR112	ENST00000394143_r73	c.9117 G>A	p.T3039T	SILENT
MA4_23R	ChrX	138679712	T	A	0.17948718	MCF2	ENST00000520602_r73	c.2142 A>T	p.G714G	SILENT
MA4_23R	ChrX	142795225	G	A	0.230769231	SPANXN2	ENST00000370498_r73	c.453 C>T	p.D151D	SILENT
MA4_23R	ChrX	149013097	G	A	0.173913044	MAGEA8	ENST00000286482_r73	c.51 G>A	p.Q17Q	SILENT
MA4_23R	ChrX	149680554	C	T	0.289156627	MAMLD1	ENST00000432680_r73	c.2208 C>T	p.S736S	SILENT
MA4_23R	ChrX	150348610	C	T	0.220183486	GPR50	ENST00000218316_r73	c.555 C>T	p.N185N	SILENT
MA4_23R	ChrX	150817094	C	G	0.242105263	PASD1	ENST00000370357_r73	c.637 C>G	p.Q213E	MISSENSE
MA4_23R	ChrX	150840916	C	T	0.510638298	PASD1	ENST00000370357_r73	c.1699 C>T	p.L567L	SILENT
MA4_23R	ChrX	150911107	G	A	0.375	CNGA2	ENST00000329903_r73	c.582 G>A	p.L194L	SILENT
MA4_23R	ChrX	151092220	A	G	0.242424242	MAGEA4	ENST00000370340_r73	c.84 A>G	p.A28A	SILENT
MA4_23R	ChrX	151899913	T	C	0.227722772	MAGEA12	ENST00000357916_r73	c.888 A>G	p.G296G	SILENT
MA4_23R	ChrX	152106638	C	T	0.230769231	ZNF185	ENST00000370268_r73	c.1139 C>T	p.S380F	MISSENSE
MA4_23R	ChrX	152751497	G	A	0.3	U82695.9	ENST00000428676_r73	c.140 G>A	p.R47H	MISSENSE
MA4_23R	ChrX	153039502	G	C	0.304347826	PLXNB3	ENST00000361971_r73	c.3468 G>C	p.E1156D	MISSENSE
MA4_23R	ChrX	153041544	T	C	0.186046512	PLXNB3	ENST00000361971_r73	c.4604 T>C	p.M1535T	MISSENSE
MA4_23R	ChrX	153046686	C	T	0.1875	SRPK3	ENST00000370104_r73	c.75 C>T	p.C25C	SILENT
MA4_23R	ChrX	153070999	G	A	0.28125	PDZD4	ENST00000164640_r73	c.612 C>T	p.N204N	SILENT
MA4_23R	ChrX	153132228	G	A	0.276923077	L1CAM	ENST00000370060_r73	c.2307 C>T	p.S769S	SILENT
MA4_23R	ChrX	153172059	C	T	0.212962963	AVPR2	ENST00000358927_r73	c.993 C>T	p.S331S	SILENT
MA4_23R	ChrX	153421912	T	C	0.216216216	OPN1LW	ENST00000369951_r73	c.888 T>C	p.G296G	SILENT
MA4_23R	ChrX	153540977	A	G	0.25	TKTL1	ENST00000369915_r73	c.717 A>G	p.E239E	SILENT
MA4_23R	ChrX	153581932	A	G	0.36	FLNA	ENST00000360319_r73	c.5826 T>C	p.A1942A	SILENT
MA4_23R	ChrX	153667176	T	C	0.271186441	GDI1	ENST00000447750_r73	c.219 T>C	p.N73N	SILENT

MA4_23R	ChrX	153760953	C	T	0.298850575	G6PD	ENST00000393562_r73	c.1206 G>A	p.Q402Q	SILENT
MA4_23R	ChrX	153880569	A	G	0.363636364	CTAG2	ENST00000247306_r73	c.606 T>C	p.N202N	SILENT
MA4_23R	ChrX	153880634	C	G	0.391304348	CTAG2	ENST00000247306_r73	c.541 G>C	p.G181R	MISSENSE
MA4_23R	ChrX	153880830	A	C	0.297709924	CTAG2	ENST00000247306_r73	c.345 T>G	p.P115P	SILENT
MA4_23R	ChrX	153881525	G	C	0.267441861	CTAG2	ENST00000247306_r73	c.265 C>G	p.Q89E	MISSENSE
MA4_23R	Chr11	209895	CCC	-	0.107142857	RIC8A	ENST00000325207_r73	c.621 CCC>-	p.N207 NP>N	MISSENSE
MA4_23R	Chr11	17352478	ACA	-	0.166666667	NUCB2	ENST00000529010_r73	c.1203 ACA>-	p.L401 LQ>L	MISSENSE
MA4_23R	Chr11	4592707	-	AC	0.151162791	C11orf40	ENST00000307616_r73	c.600 ->GT	p.C200fs*12	FRAMESHIFT
MA4_23R	Chr11	5172796	-	C	0.192592593	OR52A1	ENST00000380367_r73	c.804 ->G	p.G268fs*14	FRAMESHIFT
MA4_23R	Chr11	71850157	-	TA	0.112033195	FOLR3	ENST00000542161_r73	c.313 ->TA	p.*105fs*73	FRAMESHIFT
MA4_23R	Chr11	73020376	-	CTC	0.125	ARHGEF17	ENST00000263674_r73	c.693 ->CTC	p.C231 C>CS	MISSENSE
MA4_23R	Chr11	94153333	-	ATC	0.142857143	MRE11A	ENST00000323929_r73	c.2085 ->GAT	p.D695 D>EI	MISSENSE
MA4_23R	Chr7	137612914	TGG	-	0.4375	CREB3L2	ENST00000330387_r73	c.299 CCA>-	p.T100 TS>S	MISSENSE
MA4_23R	Chr7	12391269	-	A	0.2	VWDE	ENST00000275358_r73	c.3816 ->T	p.N1272fs*2	FRAMESHIFT
MA4_23R	Chr17	38858135	A	-	0.180851064	KRT24	ENST00000264651_r73	c.666 T>-	p.N222fs*11	FRAMESHIFT
MA4_23R	Chr17	72957963	T	-	0.3125	HID1	ENST00000425042_r73	Exon 6 + 5 A>-	-	ESSENTIAL_SPLICE
MA4_23R	Chr17	79219501	ATG	-	0.260273973	SLC38A10	ENST00000374759_r73	c.3213 CAT>-	p.I1071 II>I	MISSENSE
MA4_23R	Chr2	3749152	GAA	-	0.176470588	ALLC	ENST00000252505_r73	c.901 GAA>-	p.E301Del(E)	MISSENSE
MA4_23R	Chr2	112843593	TTGATAT	-	0.222222222	TMEM87B	ENST00000283206_r73	c.850 TTGATAT>-	p.L284fs*4	FRAMESHIFT
MA4_23R	Chr2	238244864	GCA	-	0.171052632	COL6A3	ENST00000295550_r73	c.8877 TGC>-	p.A2959 AA>A	MISSENSE
MA4_23R	Chr2	71801335	-	AGGCGG	0.109090909	DYSF	ENST00000409762_r73	c.3233 ->AGGCGG	p.Q1078 Q>QAE	MISSENSE
MA4_23R	Chr2	170387133	-	T	0.181818182	FASTKD1	ENST00000453153_r73	c.2406 ->A	p.K802fs*18	FRAMESHIFT
MA4_23R	Chr2	172967129	-	GCT	0.122222222	DLX2	ENST00000234198_r73	c.138 ->AGC	p.S46 S>RA	MISSENSE
MA4_23R	Chr2	234113397	-	TG	0.181818182	INPP5D	ENST00000491070_r73	c.110 ->TG	p.I37fs*90	FRAMESHIFT
MA4_23R	Chr2	234429740	-	TTC	0.271186441	USP40	ENST00000450966_r73	c.2255 ->GAA	p.K752 K>RK	MISSENSE
MA4_23R	Chr22	38119755	CAA	-	0.157894737	TRIOBP	ENST00000406386_r73	c.1192 CAA>-	p.Q398Del(Q)	MISSENSE
MA4_23R	Chr22	36587846	-	CT	0.120171674	APOL4	ENST00000404685_r73	c.331 ->AG	p.V111fs*242	FRAMESHIFT
MA4_23R	Chr1	9304979	CCCAGGCA	-	0.178571429	H6PD	ENST00000377403_r73	Exon 2 - 5 CCCAGGCA>-	-	ESSENTIAL_SPLICE
MA4_23R	Chr1	36643701	AGA	-	0.333333333	MAP7D1	ENST00000373151_r73	c.1607 AGA>-	p.E536 EK>E	MISSENSE
MA4_23R	Chr1	45974801	CCCGCC	-	0.158273381	MMACHC	ENST00000401061_r73	c.763 CCCGCC>-	p.P255Del(PA)	MISSENSE
MA4_23R	Chr1	153907279	CTGCTGCTG	-	0.102040816	DENND4B	ENST00000361217_r73	c.2722 CAGCAGCAG>-	p.Q908Del(QQQ)	MISSENSE
MA4_23R	Chr1	154542837	ACA	-	0.145833333	CHRNB2	ENST00000368476_r73	c.359 ACA>-	p.Y120 YN>Y	MISSENSE
MA4_23R	Chr1	156354348	C	-	0.184210526	RHBG	ENST00000368249_r73	c.1265 C>-	p.S422fs*38	FRAMESHIFT
MA4_23R	Chr1	206239432	AAT	-	0.183823529	C1orf186	ENST00000331555_r73	c.464 ATT>-	p.Y155 YF>F	MISSENSE
MA4_23R	Chr1	23966895	-	AAG	0.275362319	MDS2	ENST00000374555_r73	c.279 ->AAG	p.V93 V>VR	MISSENSE
MA4_23R	Chr1	85598680	-	A	0.110236221	WDR63	ENST00000294664_r73	c.2675 ->A	p.*892fs*1	FRAMESHIFT
MA4_23R	Chr1	153907279	-	CTG	0.102040816	DENND4B	ENST00000361217_r73	c.2730 ->CAG	p.Q910 Q>HR	MISSENSE

MA4_23R	Chr1	234744946	-	GCT	0.205882353	IRF2BP2	ENST00000366610_r73	c.295 ->AGC	p.L99Ins(S)	MISSENSE
MA4_23R	Chr1	248059780	-	A	0.136363636	OR2W3	ENST00000360358_r73	c.892 ->A	p.K298fs*19	FRAMESHIFT
MA4_23R	Chr18	60646248	CAG	-	0.129533679	PHLPP1	ENST00000262719_r73	c.4738 CAG>-	p.Q1580Del(Q)	MISSENSE
MA4_23R	Chr16	3406757	T	-	0.175257732	OR2C1	ENST00000304936_r73	c.817 T>-	p.F273fs*13	FRAMESHIFT
MA4_23R	Chr16	7760847	AAA	-	0.238095238	RBFOX1	ENST00000550418_r73	Exon 16 + 5 AAA>-	-	ESSENTIAL_SPLICE
MA4_23R	Chr16	67859708	AGG	-	0.125	TSNAXIP1	ENST00000388833_r73	c.791 AGG>-	p.Q264 QE>Q	MISSENSE
MA4_23R	Chr16	336889	-	A	0.190476191	PDIA2	ENST00000219406_r73	c.1477 ->A	p.N493fs*64	FRAMESHIFT
MA4_23R	Chr13	61102576	ATA	-	0.133640553	TDRD3	ENST00000377894_r73	c.938 ATA>-	p.D313 DN>D	MISSENSE
MA4_23R	Chr13	77532065	CAGAGGTAG	-	0.207317073	IRG1	ENST00000377462_r73	c.1391 CAGAGGTAG>-	p.P464 PEVA>P	MISSENSE
MA4_23R	Chr6	168314998	G	-	0.108108108	MLLT4	ENST00000392108_r73	Exon 16 + 5 G>-	-	ESSENTIAL_SPLICE
MA4_23R	ChrX	135474445	GAT	-	0.266666667	GPR112	ENST00000394143_r73	c.7966 GAT>-	p.D2656Del(D)	MISSENSE
MA4_23R	ChrX	36162685	-	TG	0.30952381	CHDC2	ENST00000378660_r73	c.1268 ->TG	p.L423fs*2	FRAMESHIFT
MA4_23R	ChrX	112022298	-	AGG	0.177777778	AMOT	ENST00000304758_r73	c.1857 ->CCT	p.P619 P>PL	MISSENSE
MA4_23R	Chr3	124482495	TTGTTGAAC	-	0.144578313	ITGB5	ENST00000296181_r73	c.2367 GTTCAACAA>-	p.K789 KFNK>K	MISSENSE
MA4_23R	Chr3	56650055	-	CTC	0.188679245	CCDC66	ENST00000394672_r73	c.1817 ->CTC	p.S606 S>SP	MISSENSE
MA4_23R	Chr3	122459291	-	AGA	0.111111111	HSPBAP1	ENST00000306103_r73	c.1368 ->TCT	p.P456 P>PL	MISSENSE
MA4_23R	Chr9	139235482	C	-	0.159090909	GPSM1	ENST00000392945_r73	c.1239 C>-	p.L413fs*57	FRAMESHIFT
MA4_23R	Chr9	80881428	-	GGG	0.153333333	CEP78	ENST00000415759_r73	c.1871 ->GGG	p.P624 P>RA	MISSENSE
MA4_23R	Chr9	125391771	-	A	0.255813954	OR1B1	ENST00000304833_r73	c.44 ->T	p.L15fs*9	FRAMESHIFT
MA4_23R	Chr12	27849503	A	-	0.2	REP15	ENST00000310791_r73	c.8 A>-	p.Q3fs*9	FRAMESHIFT
MA4_23R	Chr12	72070506	GTT	-	0.101449275	THAP2	ENST00000308086_r73	c.305 GTT>-	p.S102 SC>S	MISSENSE
MA4_23R	Chr12	2062324	-	TGC	0.104477612	DCP1B	ENST00000280665_r73	c.782 ->GCA	p.Q261 Q>RK	MISSENSE
MA4_23R	Chr20	25457050	CTCCCA	-	0.161764706	NINL	ENST00000278886_r73	c.2872 TGGGAG>-	p.W958Del(WE)	MISSENSE
MA4_23R	Chr14	94410276	A	-	0.32	RP11-131H24.4	ENST00000557646_r73	c.167 A>-	p.Q56fs*8	FRAMESHIFT
MA4_23R	Chr14	105352885	GCAGGA	-	0.215686275	CEP170B	ENST00000556508_r73	c.2099 GCAGGA>-	p.R700 RRS>R	MISSENSE
MA4_23R	Chr14	23548788	-	GTGAAT	0.123076923	ACIN1	ENST00000262710_r73	c.1930 ->ATTCAC	p.R644Ins(IH)	MISSENSE
MA4_23R	Chr15	43579798	C	-	0.121827411	TGM7	ENST00000452443_r73	c.628 G>-	p.A210fs*17	FRAMESHIFT
MA4_23R	Chr15	41099900	-	GGGGC	0.153846154	ZFYVE19	ENST00000355341_r73	c.113 ->GGGGC	p.W38fs*73	FRAMESHIFT
MA4_23R	Chr8	75664695	A	-	0.143646409	RP11-758M4.1	ENST00000523442_r73	c.248 A>-	p.H83fs*24	FRAMESHIFT
MA4_23R	Chr8	145740367	A	-	0.111111111	RECQL4	ENST00000428558_r73	c.1573 T>-	p.C525fs*33	FRAMESHIFT
MA4_23R	Chr8	72755648	-	T	0.166666667	RP11-383H13.1	ENST00000537896_r73	c.12 ->T	p.T4fs*16	FRAMESHIFT
MA4_23R	Chr4	177106010	TCTC	-	0.158227848	SPATA4	ENST00000280191_r73	c.836 GAGA>-	p.R279fs*4	FRAMESHIFT
MA4_23R	Chr19	8389893	TCC	-	0.13592233	KANK3	ENST00000330915_r73	c.2022 GGA>-	p.E674 ED>D	MISSENSE
MA4_23R	Chr19	11558341	GAG	-	0.1875	PRKCSH	ENST00000591462_r73	c.937 GAG>-	p.E313Del(E)	MISSENSE
MA4_23R	Chr19	23927742	CA	-	0.119047619	ZNF681	ENST00000402377_r73	c.609 TG>-	p.C203fs*5	FRAMESHIFT
MA4_23R	Chr19	37879853	TGTGCA	-	0.125748503	ZNF527	ENST00000436120_r73	c.902 TGTGCA>-	p.P301 PYA>PYA	MISSENSE
MA4_23R	Chr19	54973989	CCT	-	0.172413793	LENG9	ENST00000333834_r73	c.785 AGG>-	p.E262 EA>A	MISSENSE

MA4_23R	Chr19	34263201	-	AGC	0.13	CHST8	ENST00000438847_r73	c.508 ->AGC	p.S170Ins(S)	MISSENSE
MA4_23R	Chr19	46265048	-	TCCAGC	0.128205128	AC074212.3	ENST00000457052_r73	c.1357 ->TCCAGC	p.S453Ins(SS)	MISSENSE
MA4_23R	Chr19	55790887	-	GCCGCCGCC	0.112359551	HSPBP1	ENST00000255631_r73	c.90 ->GGCGGCGGC	p.G30 G>GAAA	MISSENSE
MA4_23R	Chr19	56244722	-	T	0.143884892	NLRP9	ENST00000332836_r73	c.475 ->A	p.T159fs*31	FRAMESHIFT
MA4_23R	Chr10	21435341	CACT	-	0.133640553	C10orf113	ENST00000534331_r73	c.94 AGTG>-	p.S32fs*5	FRAMESHIFT
MA4_23R	Chr10	22498485	-	AGA	0.251231527	EBLN1	ENST00000422359_r73	c.428 ->TCT	p.L143 L>LL	MISSENSE
MA4_23R	Chr10	27702257	-	C	0.121052632	PTCHD3	ENST00000438700_r73	c.923 ->G	p.G308fs*27	FRAMESHIFT
MA4_23R	Chr10	32740799	-	T	0.183486239	CCDC7	ENST00000277657_r73	c.229 ->T	p.L77fs*6	FRAMESHIFT
MA4_23R	Chr5	7867478	ATA	-	0.147368421	FASTKD3	ENST00000264669_r73	c.717 TAT>-	p.I239 II>I	MISSENSE
MA4_23R	Chr5	74491716	TCA	-	0.14	ANKRD31	ENST00000506364_r73	c.755 TGA>-	p.M252 MN>N	MISSENSE
MA4_23R	Chr5	111755670	G	-	0.132653061	FLJ11235	ENST00000600409_r73	c.376 G>-	p.G126fs*173	FRAMESHIFT
MA4_23R	Chr5	180687429	TCT	-	0.233502538	TRIM52	ENST00000327767_r73	c.384 AGA>-	p.E128 EE>E	MISSENSE
MA4_24	Chr2	130832835	C	T	0.107142857	POTEF	ENST00000409914_r73	c.2210 G>A	p.R737H	MISSENSE
MA4_24	Chr1	203134484	G	T	0.076923077	ADORA1	ENST00000309502_r73	c.437 G>T	p.W146L	MISSENSE
MA4_24	Chr9	138377427	C	T	0.04787234	PPP1R26	ENST00000605286_r73	c.1071 C>T	p.S357S	SILENT
MA4_24	Chr1	115258748	C	T	0.033224146	NRAS	ENST00000369535_r73	c.34 G>A	p.G12S	MISSENSE
MA4_24	ChrX	100400133	G	C	0.022727273	CENPI	ENST00000372927_r73	c.1646 G>C	p.R549P	MISSENSE
MA4_24R	Chr21	22849652	G	A	0.30781759	NCAM2	ENST00000400546_r73	c.1937 G>A	p.G646E	MISSENSE
MA4_24R	Chr1	186014936	G	A	0.251021166	HMCN1	ENST00000271588_r73	c.6421 G>A	p.G2141S	MISSENSE
MA4_24R	Chr6	152420061	A	G	0.386363636	ESR1	ENST00000338799_r73	c.1748 A>G	p.Y583C	MISSENSE
MA4_24R	ChrX	100400133	G	C	0.52644041	CENPI	ENST00000372927_r73	c.1646 G>C	p.R549P	MISSENSE
MA4_24R	Chr14	64954616	T	A	0.31037692	ZBTB25	ENST00000261683_r73	c.333 A>T	p.A111A	SILENT
MA4_24R	Chr8	37702629	C	G	0.3010279	BRF2	ENST00000220659_r73	c.639 G>C	p.E213D	MISSENSE
MA4_24R	Chr9	126783462	C	T	0.231441048	LHX2	ENST00000373615_r73	c.812 C>T	p.T271M	MISSENSE
MA4_24R	Chr8	26240718	G	A	0.299591837	BNIP3L	ENST00000380629_r73	c.72 G>A	p.Q24Q	SILENT
MA4_24R	Chr12	53298699	G	A	0.277777778	KRT8	ENST00000552551_r73	c.67 C>T	p.R23C	MISSENSE
MA4_24R	ChrX	100745623	G	-	0.125	ARMCX4	ENST00000423738_r73	c.2047 G>-	p.D683fs*262	FRAMESHIFT
MA4_25	Chr22	31495066	C	T	0.181305399	SMTN	ENST00000358743_r73	c.2352 C>T	p.R784R	SILENT
MA4_25	Chr12	25398284	C	T	0.182159147	KRAS	ENST00000311936_r73	c.35 G>A	p.G12D	MISSENSE
MA4_25	Chr4	100574475	G	A	0.363435173	RP11-766F14.2	ENST00000511828_r73	c.1331 C>T	p.T444M	MISSENSE
MA4_25	Chr5	176517475	G	A	0.785784993	FGFR4	ENST00000292408_r73	c.176 G>A	p.R59Q	MISSENSE
MA4_25	Chr1	115258747	C	T	0.011875955	NRAS	ENST00000369535_r73	c.35 G>A	p.G12D	MISSENSE
MA4_25	Chr1	115258748	C	T	0.03457938	NRAS	ENST00000369535_r73	c.34 G>A	p.G12S	MISSENSE
MA4_25	Chr12	25398281	C	T	0.02281746	KRAS	ENST00000311936_r73	c.38 G>A	p.G13D	MISSENSE
MA9_02	Chr8	142204230	G	A	0.138424043	DENND3	ENST00000262585_r73	c.3495 G>A	p.A1165A	SILENT
MA9_05	Chr12	25378561	G	A	0.010122395	KRAS	ENST00000369535_r73	c.35 G>A	p.G12D	MISSENSE
MA9_05	Chr3	78684959	G	A	0.013206336	ROBO1	ENST00000464233_r73	c.3337 C>T	p.Q1113*	NONSENSE

MA9_05	Chr3	165547388	C	T	0.014514278	BCHE	ENST00000264381_r73	c.1434 G>A	p.L478L	SILENT
MA9_03	Chr2	228563984	G	A	0.048889717	SLC19A3	ENST00000425817_r73	c.447 C>T	p.A149A	SILENT
MA9_03	Chr1	79002226	C	T	0.105546838	PTGFR	ENST00000370758_r73	c.934 C>T	p.L312F	MISSENSE
MA9_03	Chr12	25398281	C	T	0.026697105	KRAS	ENST00000311936_r73	c.38 G>A	p.G13D	MISSENSE
MA9_04	Chr2	189868770	G	C	0.223776224	COL3A1	ENST00000304636_r73	c.2724 G>C	p.A908A	SILENT
MA9_04	Chr12	104092949	C	T	0.42753908	STAB2	ENST00000388887_r73	c.3658 C>T	p.R1220C	MISSENSE
MA9_04	Chr8	113702206	A	G	0.323759791	CSMD3	ENST00000343508_r73	c.1926 T>C	p.N642N	SILENT
MLLwt_01	Chr17	7577094	-	CCT	0.326332017	TP53	ENST00000269305_r73	c.844 ->AGG	p.R282Ins(R)	MISSENSE
MLLwt_01	Chr8	12595499	C	T	0.444754464	LONRF1	ENST00000398246_r73	Exon 4 5 G>A	-	ESSENTIAL_SPLICE
MLLwt_01	Chr1	38341371	G	A	0.417063492	INPP5B	ENST00000373024_r73	c.1695 C>T	p.D565D	SILENT
MLLwt_01	Chr14	68270920	G	A	0.439142317	ZFYVE26	ENST00000347230_r73	c.1333 C>T	p.L445F	MISSENSE
MLLwt_02	Chr8	2820915	C	T	0.692964304	CSMD1	ENST00000537824_r73	c.9283 G>A	p.V3095M	MISSENSE
MLLwt_02	Chr9	5078360	A	G	0.322690992	JAK2	ENST00000381652_r73	c.2047 A>G	p.R683G	MISSENSE
MLLwt_02	Chr3	32933224	G	A	0.391132723	TRIM71	ENST00000383763_r73	c.2528 G>A	p.R843H	MISSENSE
MLLwt_02	Chr4	81865980	G	A	0.251284104	C4orf22	ENST00000358105_r73	c.493 G>A	p.A165T	MISSENSE
MLLwt_02	Chr9	139278036	C	T	0.203371398	SNAPC4	ENST00000298532_r73	c.1585 G>A	p.G529S	MISSENSE
MLLwt_02	Chr1	216462698	G	T	0.180441281	USH2A	ENST00000307340_r73	c.1895 C>A	p.P632H	MISSENSE
MLLwt_03	Chr9	95237025	-	TCATCATCA	0.026448196	ASPN	ENST00000375544_r73	c.155 ->TGATGATGA	p.E52 E>VMMK	MISSENSE
MLLwt_03	Chr11	1266996	T	C	0.258956916	MUC5B	ENST00000529681_r73	c.8886 T>C	p.R2962R	SILENT
MLLwt_03	Chr12	112888162	G	C	0.0860887	PTPN11	ENST00000392597_r73	c.178 G>C	p.G60R	MISSENSE
MLLwt_04	Chr16	58076166	G	A	0.055459184	MMP15	ENST00000219271_r73	c.1196 G>A	p.R399H	MISSENSE
MLLwt_05	Chr3	10953794	C	T	0.124726845	SLC6A11	ENST00000254488_r73	c.911 C>T	p.T304M	MISSENSE
MLLwt_06	Chr7	4800821	C	T	0.375	FOXK1	ENST00000328914_r73	c.1823 C>T	p.T608I	MISSENSE
MLLwt_06	Chr6	20124710	G	A	0.410250182	MBOAT1	ENST00000324607_r73	c.836 C>T	p.P279L	MISSENSE
MLLwt_06	Chr6	27100393	A	T	0.224532225	HIST1H2BJ	ENST00000607124_r73	c.137 T>A	p.L46Q	MISSENSE
MLLwt_06	Chr20	60791797	C	G	0.422680412	HRH3	ENST00000340177_r73	c.603 G>C	p.T201T	SILENT
MLLwt_06	Chr1	86289382	G	T	0.303030303	COL24A1	ENST00000370571_r73	c.3721 C>A	p.Q1241K	MISSENSE
MLLwt_06	Chr4	169433068	G	C	0.095695971	PALLD	ENST00000261509_r73	c.413 G>C	p.R138P	MISSENSE
MLLwt_07	Chr7	100643824	C	T	0.044602273	MUC12	ENST00000536621_r73	c.9980 C>T	p.T3327M	MISSENSE
MLLwt_07	Chr12	112230482	G	A	0.312261781	ALDH2	ENST00000416293_r73	c.838 G>A	p.V280M	MISSENSE
MLLwt_08	Chr16	737085	C	T	0.379388448	WDR24	ENST00000293883_r73	c.991 G>A	p.A331T	MISSENSE
MLLwt_08	Chr11	1017828	G	A	0.083926755	MUC6	ENST00000421673_r73	c.4973 C>T	p.T1658M	MISSENSE
MLLwt_08	Chr17	4643865	C	T	0.346	ZMYND15	ENST00000433935_r73	c.22 C>T	p.R8W	MISSENSE
MLLwt_08	Chr10	15719628	G	A	0.388174807	ITGA8	ENST00000378076_r73	c.639 C>T	p.D213D	SILENT
MLLwt_08	Chr6	38905788	C	T	0.268558952	DNAH8	ENST00000449981_r73	c.11602 C>T	p.R3868*	NONSENSE
MLLwt_08	Chr2	43452533	-	AG	0.346	ZFP36L2	ENST00000282388_r73	c.410 ->CT	p.L137fs*51	FRAMESHIFT
MLLwt_08	Chr20	62599293	G	A	0.030521212	ZNF512B	ENST00000369888_r73	c.11 C>T	p.P4L	MISSENSE

MLLwt_09	Chr12	25398281	C	T	0.026697105	KRAS	ENST00000311936_r73	c.38 G>A	p.G13D	MISSENSE
MLLwt_10	Chr16	29830928	G	A	0.057032224	PAGR1	ENST00000320330_r73	c.618 G>A	p.S206S	SILENT
MLLwt_10	Chr1	156761566	C	T	0.178651281	PRCC	ENST00000271526_r73	c.1161 C>T	p.S387S	SILENT

Suppl. Table 5. Read counts per sample used for analysis of BCR repertories.

Sample (RNA)	Total number of BCRs capture	Number of unique BCRs captured
MA4_18	12795	10328
MA4_18R	1583	1213
MA4_20	13464	8456
MA4_20R	29747	25759
MA4_21	26731	20934
MA4_21R	2620	1784
MA4_22	13862	9506
MA4_22R	46863	38426
MA4_23	11129	5217
MA4_23R	2543	1777
MA4_24	17511	9927
MA4_24R	24313	18482
MA4_27	7157	5232
MA4_27R	8129	6112

Suppl. Table 6. Top 100 genes determining PC1 and PC2 separation in Figure 6C.

PC1:

Gene stable ID	Gene name	Gene type	Chromosome
ENSG00000007062	PROM1	protein_coding	4
ENSG00000011600	TYROBP	protein_coding	19
ENSG00000024526	DEPDC1	protein_coding	1
ENSG00000030419	IKZF2	protein_coding	2
ENSG00000035499	DEPDC1B	protein_coding	5
ENSG00000066279	ASPM	protein_coding	1
ENSG00000072571	HMMR	protein_coding	5
ENSG00000075426	FOSL2	protein_coding	2
ENSG00000077152	UBE2T	protein_coding	1
ENSG00000087074	PPP1R15A	protein_coding	19
ENSG00000090382	LYZ	protein_coding	12
ENSG00000092621	PHGDH	protein_coding	1
ENSG00000100097	LGALS1	protein_coding	22
ENSG00000100721	TCL1A	protein_coding	14
ENSG00000101003	GINS1	protein_coding	20
ENSG00000102760	RGCC	protein_coding	13
ENSG00000105011	ASF1B	protein_coding	19
ENSG00000106004	HOXA5	protein_coding	7
ENSG00000107447	DNTT	protein_coding	10
ENSG00000110777	POU2AF1	protein_coding	11
ENSG00000111247	RAD51AP1	protein_coding	12
ENSG00000112984	KIF20A	protein_coding	5
ENSG00000117399	CDC20	protein_coding	1
ENSG00000117724	CENPF	protein_coding	1
ENSG00000119138	KLF9	protein_coding	9
ENSG00000119508	NR4A3	protein_coding	9
ENSG00000123358	NR4A1	protein_coding	12
ENSG00000124785	NRN1	protein_coding	6
ENSG00000125740	FOSB	protein_coding	19
ENSG00000125869	LAMP5	protein_coding	20
ENSG00000126787	DLGAP5	protein_coding	14
ENSG00000127528	KLF2	protein_coding	19
ENSG00000128218	VPREB3	protein_coding	22
ENSG00000128322	IGLL1	protein_coding	22
ENSG00000129173	E2F8	protein_coding	11
ENSG00000131016	AKAP12	protein_coding	6
ENSG00000131747	TOP2A	protein_coding	17
ENSG00000132465	JCHAIN	protein_coding	4
ENSG00000133101	CCNA1	protein_coding	13
ENSG00000135069	PSAT1	protein_coding	9
ENSG00000135144	DTX1	protein_coding	12
ENSG00000135604	STX11	protein_coding	6
ENSG00000136826	KLF4	protein_coding	9
ENSG00000137804	NUSAP1	protein_coding	15
ENSG00000137812	KNL1	protein_coding	15
ENSG00000138160	KIF11	protein_coding	10
ENSG00000138180	CEP55	protein_coding	10
ENSG00000142178	SIK1	protein_coding	21

ENSG00000143228	NUF2	protein_coding	1
ENSG00000143507	DUSP10	protein_coding	1
ENSG00000148773	MKI67	protein_coding	10
ENSG00000152253	SPC25	protein_coding	2
ENSG00000153234	NR4A2	protein_coding	2
ENSG00000156738	MS4A1	protein_coding	11
ENSG00000157514	TSC22D3	protein_coding	X
ENSG00000161835	GRASP	protein_coding	12
ENSG00000163808	KIF15	protein_coding	3
ENSG00000164929	BAALC	protein_coding	8
ENSG00000165030	NFIL3	protein_coding	9
ENSG00000166349	RAG1	protein_coding	11
ENSG00000168078	PBK	protein_coding	8
ENSG00000169397	RNASE3	protein_coding	14
ENSG00000169429	CXCL8	protein_coding	4
ENSG00000169575	VPREB1	protein_coding	22
ENSG00000170293	CMTM8	protein_coding	3
ENSG00000170312	CDK1	protein_coding	10
ENSG00000171246	NPTX1	protein_coding	17
ENSG00000174123	TLR10	protein_coding	4
ENSG00000174500	GCSAM	protein_coding	3
ENSG00000175097	RAG2	protein_coding	11
ENSG00000178999	AURKB	protein_coding	17
ENSG00000185028	LRRC14B	protein_coding	5
ENSG00000185275	CD24P4	processed_pseudogene	Y
ENSG00000188536	HBA2	protein_coding	16
ENSG00000189057	FAM111B	protein_coding	11
ENSG00000189283	FHIT	protein_coding	3
ENSG00000196549	MME	protein_coding	3
ENSG00000197747	S100A10	protein_coding	1
ENSG00000199568	RNU5A-1	snRNA	15
ENSG00000199899	RF00019	misc_RNA	12
ENSG00000200169	RNU5D-1	snRNA	1
ENSG00000206047	DEFA1	protein_coding	8
ENSG00000206172	HBA1	protein_coding	16
ENSG00000206828	RF00003	snRNA	1
ENSG00000211904	IGHJ2	IG_J_gene	14
ENSG00000211905	IGHJ1	IG_J_gene	14
ENSG00000211966	IGHV5-51	IG_V_gene	14
ENSG00000211978	IGHV5-78	IG_V_pseudogene	14
ENSG00000227507	LTB	protein_coding	6
ENSG00000230945	LINC01507	lincRNA	9
ENSG00000236597	IGHD7-27	IG_D_gene	14
ENSG00000237547	IGHJ2P	IG_J_pseudogene	14
ENSG00000242887	IGHJ3	IG_J_gene	14
ENSG00000244734	HBB	protein_coding	11
ENSG00000253983	AC087627.1	antisense	8
ENSG00000261434	AC021087.3	sense_overlapping	5
ENSG00000265929	MIR5195	miRNA	14
ENSG00000270640	AC104695.3	sense_intronic	2
ENSG00000272398	CD24	protein_coding	6
ENSG00000275993	SIK1B	protein_coding	21

PC2:

Gene stable ID	Gene name	Gene type	Chromosome
ENSG00000117318	ID3	protein_coding	1
ENSG00000119535	CSF3R	protein_coding	1
ENSG00000133048	CHI3L1	protein_coding	1
ENSG00000143546	S100A8	protein_coding	1
ENSG00000150681	RGS18	protein_coding	1
ENSG00000158825	CDA	protein_coding	1
ENSG00000159339	PADI4	protein_coding	1
ENSG00000162747	FCGR3B	protein_coding	1
ENSG00000163154	TNFAIP8L2	protein_coding	1
ENSG00000163220	S100A9	protein_coding	1
ENSG00000163221	S100A12	protein_coding	1
ENSG00000163563	MNDA	protein_coding	1
ENSG00000186891	TNFRSF18	protein_coding	1
ENSG00000235492	LINC01221	lincRNA	1
ENSG00000275538	RNVU1-19	snRNA	1
ENSG00000158050	DUSP2	protein_coding	2
ENSG00000188011	RTP5	protein_coding	2
ENSG00000189292	ALKAL2	protein_coding	2
ENSG00000204099	NEU4	protein_coding	2
ENSG00000012223	LTF	protein_coding	3
ENSG00000073792	IGF2BP2	protein_coding	3
ENSG00000164047	CAMP	protein_coding	3
ENSG00000168334	XIRP1	protein_coding	3
ENSG00000274840	AC132807.2	lincRNA	3
ENSG00000163993	S100P	protein_coding	4
ENSG00000038427	VCAN	protein_coding	5
ENSG00000072571	HMMR	protein_coding	5
ENSG00000160883	HK3	protein_coding	5
ENSG00000168671	UGT3A2	protein_coding	5
ENSG00000182578	CSF1R	protein_coding	5
ENSG00000096006	CRISP3	protein_coding	6
ENSG00000112299	VNN1	protein_coding	6
ENSG00000198719	DLL1	protein_coding	6
ENSG00000232891	AL450344.3	sense_intronic	6
ENSG00000105967	TFEC	protein_coding	7
ENSG00000211688	TRGJP2	TR_J_gene	7
ENSG00000164821	DEFA4	protein_coding	8
ENSG00000165071	TMEM71	protein_coding	8
ENSG00000206047	DEFA1	protein_coding	8
ENSG00000239839	DEFA3	protein_coding	8
ENSG00000240247	DEFA1B	protein_coding	8
ENSG00000271938	AC103724.4	lincRNA	8
ENSG00000119508	NR4A3	protein_coding	9
ENSG00000148346	LCN2	protein_coding	9
ENSG00000229314	ORM1	protein_coding	9
ENSG00000266017	MIR4477B	miRNA	9
ENSG00000118113	MMP8	protein_coding	11
ENSG00000134827	TCN1	protein_coding	11
ENSG00000149516	MS4A3	protein_coding	11
ENSG00000156575	PRG3	protein_coding	11
ENSG00000184545	DUSP8	protein_coding	11

ENSG00000090382	LYZ	protein_coding	12
ENSG00000121316	PLBD1	protein_coding	12
ENSG00000123358	NR4A1	protein_coding	12
ENSG00000123405	NFE2	protein_coding	12
ENSG00000161835	GRASP	protein_coding	12
ENSG00000257883	AC125603.2	lincRNA	12
ENSG00000102524	TNFSF13B	protein_coding	13
ENSG00000102837	OLFM4	protein_coding	13
ENSG00000122025	FLT3	protein_coding	13
ENSG00000100439	ABHD4	protein_coding	14
ENSG00000100448	CTSG	protein_coding	14
ENSG00000100504	PYGL	protein_coding	14
ENSG00000126787	DLGAP5	protein_coding	14
ENSG00000136315	AL355922.1	lincRNA	14
ENSG00000169385	RNASE2	protein_coding	14
ENSG00000169397	RNASE3	protein_coding	14
ENSG00000169413	RNASE6	protein_coding	14
ENSG00000104043	ATP8B4	protein_coding	15
ENSG00000173546	CSPG4	protein_coding	15
ENSG00000270789	AC135983.5	processed_pseudogene	15
ENSG00000171724	VAT1L	protein_coding	16
ENSG00000188536	HBA2	protein_coding	16
ENSG00000206053	JPT2	protein_coding	16
ENSG00000005381	MPO	protein_coding	17
ENSG00000121053	EPX	protein_coding	17
ENSG00000131747	TOP2A	protein_coding	17
ENSG00000008438	PGLYRP1	protein_coding	19
ENSG00000099860	GADD45B	protein_coding	19
ENSG00000104918	RETN	protein_coding	19
ENSG00000105205	CLC	protein_coding	19
ENSG00000124469	CEACAM8	protein_coding	19
ENSG00000125740	FOSB	protein_coding	19
ENSG00000126266	FFAR1	protein_coding	19
ENSG00000170909	OSCAR	protein_coding	19
ENSG00000171051	FPR1	protein_coding	19
ENSG00000172232	AZU1	protein_coding	19
ENSG00000196415	PRTN3	protein_coding	19
ENSG00000197561	ELANE	protein_coding	19
ENSG00000087586	AURKA	protein_coding	20
ENSG00000100985	MMP9	protein_coding	20
ENSG00000101347	SAMHD1	protein_coding	20
ENSG00000101425	BPI	protein_coding	20
ENSG00000124107	SLPI	protein_coding	20
ENSG00000125810	CD93	protein_coding	20
ENSG00000125869	LAMP5	protein_coding	20
ENSG00000225988	LAMP5-AS1	antisense	20
ENSG00000165168	CYBB	protein_coding	X
ENSG00000274536	AL034397.3	antisense	X
ENSG00000129824	RPS4Y1	protein_coding	Y

Supplementary Tables

Suppl. Table 1. Clinical and genetic characteristics of the 42 iBCP-ALL used in the discovery cohort. * months #PB: Peripheral blood, BM: Bone marrow.

Cases ID	Hospital	Age*	Gender	MLLr	Specimen[#]	% Blast	Relapse
MA4_01	Paris	6 m	M	MLL-AF4	PB	90	NO
MA4_02	Paris	12 m	M	MLL-AF4	BM	92	NO
MA4_03	Paris	5 m	M	MLL-AF4	PB	96	NO
MA4_04	Paris	7 m	M	MLL-AF4	PB	99	NO
MA4_05	Paris	4.5 m	F	MLL-AF4	PB	93	NO
MA4_06	Erasmus	6.4 m	F	MLL-AF4	BM	90	NO
MA4_07	Erasmus	3.1 m	F	MLL-AF4	PB	92	NO
MA4_08	Erasmus	2.5 m	M	MLL-AF4	BM	97	NO
MA4_09	Erasmus	8.7 m	F	MLL-AF4	PB	90	NO
MA4_10	Erasmus	10.3 m	F	MLL-AF4	PB	94	NO
MA4_11	Erasmus	10.1 m	F	MLL-AF4	BM	98	NO
MA4_12	Erasmus	8.8 m	M	MLL-AF4	BM	94	NO
MA4_13	Erasmus	3.6 m	M	MLL-AF4	PB	97	NO
MA4_14	Erasmus	0.1 m	F	MLL-AF4	BM	96	YES
MA4_15	Erasmus	4.2 m	F	MLL-AF4	PB	92	NO
MA4_16	Erasmus	6.5 m	F	MLL-AF4	BM	92	NO
MA4_17	Erasmus	5.6 m	M	MLL-AF4	PB	94	YES
MA4_18	Monza	6.3 m	F	MLL-AF4	BM	99	YES
MA4_19	Monza	2.5 m	M	MLL-AF4	BM	88	NO
MA4_20	Monza	4.2 m	M	MLL-AF4	BM	100	YES
MA4_21	Monza	6 m	F	MLL-AF4	BM	98	YES
MA4_22	Monza	8 m	M	MLL-AF4	BM	98	YES
MA4_23	Monza	7.5 m	M	MLL-AF4	BM	87	YES
MA4_24	Monza	0.8 m	M	MLL-AF4	BM	Unknown	YES
MA4_25	Monza	3.1 m	M	MLL-AF4	BM	100	NO
MA4_26	Erasmus	7.2 m	M	MLL-AF4	PB	96	NO
MA4_27	Erasmus	6.4 m	M	MLL-AF4	BM	92	YES
MA9_01	Erasmus	3 m	F	MLL-AF9	PB	93	NO
MA9_02	Erasmus	2.6 m	F	MLL-AF9	PB	98	NO
MA9_03	Erasmus	11.2 m	F	MLL-AF9	PB	90	NO
MA9_04	Erasmus	11.4 m	F	MLL-AF9	BM	90	NO
MA9_05	Erasmus	0.4 m	F	MLL-AF9	PB	90	NO
MLLwt_01	Erasmus	11.3 m	F	MLLwt	BM	93	NO
MLLwt_02	Erasmus	11.3 m	M	MLLwt	BM	90	NO
MLLwt_03	Erasmus	0.4 m	F	MLLwt	PB	98	NO
MLLwt_04	Erasmus	11.7 m	M	MLLwt	PB	93	NO
MLLwt_05	Erasmus	3.3 m	M	MLLwt	BM	98	NO
MLLwt_06	Erasmus	9 m	F	MLLwt	BM	97	NO
MLLwt_07	Erasmus	7.4 m	F	MLLwt	PB	99	NO
MLLwt_08	Erasmus	8.5 m	M	MLLwt	PB	94	NO
MLLwt_09	Erasmus	11.7 m	M	MLLwt	BM	98	NO
MLLwt_10	Erasmus	4.2 m	M	MLLwt	PB	95	NO

Suppl. Table 2. Primers used for analysis of BCR repertories.

Oligo Name	Sequence 5’ to 3’
VH1-FR1-HUMAN_BIOMED	GGCCTCAGTGAAGGTCTCCTGCAAG
VH2-FR1_HUMAN_BIOMED	GTCTGGTCCTACGCTGGTGAAACCC
VH3-FR1_HUMAN_BIOMED	CTGGGGGGTCCCTGAGACTCTCCTG
VH4-FR1_HUMAN_BIOMED	CTTCGGAGACCCTGTCCCTCACCTG
VH5-FR1_HUMAN_BIOMED	CGGGGAGTCTCTGAAGATCTCCTGT
VH6-FR1_HUMAN_BIOMED	TCGCAGACCCTCTCACTCACCTGTG
BC_IgHJ_HUMAN_BIOMED	TGTCCAGCACGCTTCAGGCTNNNNTNNNNTNNNNCTTACCTGAGGAGACGGTGACC
CNU_S	TGTCCAGCACGCTTCAGGCT

Suppl. Table 4. MLL translocation breakpoints.

Genomic breakpoints determined by WGS at the base pair level in the MLL-AF4 and MLL-AF9 translocations

Cases ID	MLL exon/intron	AF4 exon/intron	Breakpoint
MA4_01	Exon 10	Intron 3	*Chr4:88004655-Chr11:118355607
MA4_03	Intron 10	Intron 3	Chr11:118359080-Chr4:87975057 *Chr4:87975036-Chr11:118358981
MA4_04	Intron 10	Intron 3	Chr11:118358194-Chr4:87992124 *Chr4:87989772-Chr11:118358572
MA4_08	Intron 10	Intron 3	Chr11:118359048-Chr4: 87977078
MA4_09	Exon 8	Intron 3	Chr11:118353327-Chr4:87975144
MA4_10	Intron 8	Intron 3	Chr11:118355109-Chr4:87976002
MA4_13	Exon 9	Before exon 1 (reverse)	*Chr4:87854734-Chr11:118354941
MA4_15	Intron 9	Intron 3	*Chr4:87995770-Chr11:118355672
MA4_16	Intron 8 (reverse)	Intron 3 (reverse)	*Chr4:87974323-Chr11:118354668
MA4_19	Intron 10	Intron 3	Chr11:118358319-Chr4:87988309 *Chr4:87988383-Chr11:118358153
MA4_21	Intron 10	Intron 3	Chr11:118357172-Chr4:87997625
MA4_22	Exon 11	Intron 4 (reverse)	*Chr4:88010955-Chr11:118359356
MA4_23	Intron 8	Intron 3	Chr11: 118353991-Chr4:87998295 *Chr4:87998749-Chr11:118353750
MA4_26	Intron 10	Intron 3	*Chr4:87998602-Chr11:118359398

Cases ID	MLL exon/intron	MLLT3 exon/intron	Breakpoint
MA9_02	Intron 9	Intron 4	Chr11:118355190-Chr9:20441134
MA9_04	Intron 10	Intron 5 (reverse)	*Chr9:20369705-Chr11: 118355611
MA9_05	Intron 10	Intron 5	Chr11:118358294-Chr9:20403549

* reverse

Suppl. Table 5. Read counts per sample used for analysis of BCR repertories.

Sample (RNA)	Total number of BCRs capture	Number of unique BCRs captured
MA4_18	12795	10328
MA4_18R	1583	1213
MA4_20	13464	8456
MA4_20R	29747	25759
MA4_21	26731	20934
MA4_21R	2620	1784
MA4_22	13862	9506
MA4_22R	46863	38426
MA4_23	11129	5217
MA4_23R	2543	1777
MA4_24	17511	9927
MA4_24R	24313	18482
MA4_27	7157	5232
MA4_27R	8129	6112

Suppl. Table 6. Top 100 genes determining PC1 and PC2 separation in Figure 6C.

PC1:

Gene stable ID	Gene name	Gene type	Chromosome
ENSG00000007062	PROM1	protein_coding	4
ENSG00000011600	TYROBP	protein_coding	19
ENSG00000024526	DEPDC1	protein_coding	1
ENSG00000030419	IKZF2	protein_coding	2
ENSG00000035499	DEPDC1B	protein_coding	5
ENSG00000066279	ASPM	protein_coding	1
ENSG00000072571	HMMR	protein_coding	5
ENSG00000075426	FOSL2	protein_coding	2
ENSG00000077152	UBE2T	protein_coding	1
ENSG00000087074	PPP1R15A	protein_coding	19
ENSG00000090382	LYZ	protein_coding	12
ENSG00000092621	PHGDH	protein_coding	1
ENSG00000100097	LGALS1	protein_coding	22
ENSG00000100721	TCL1A	protein_coding	14
ENSG00000101003	GINS1	protein_coding	20
ENSG00000102760	RGCC	protein_coding	13
ENSG00000105011	ASF1B	protein_coding	19
ENSG00000106004	HOXA5	protein_coding	7
ENSG00000107447	DNTT	protein_coding	10
ENSG00000110777	POU2AF1	protein_coding	11
ENSG00000111247	RAD51AP1	protein_coding	12
ENSG00000112984	KIF20A	protein_coding	5
ENSG00000117399	CDC20	protein_coding	1
ENSG00000117724	CENPF	protein_coding	1
ENSG00000119138	KLF9	protein_coding	9
ENSG00000119508	NR4A3	protein_coding	9
ENSG00000123358	NR4A1	protein_coding	12
ENSG00000124785	NRN1	protein_coding	6
ENSG00000125740	FOSB	protein_coding	19
ENSG00000125869	LAMP5	protein_coding	20
ENSG00000126787	DLGAP5	protein_coding	14
ENSG00000127528	KLF2	protein_coding	19
ENSG00000128218	VPREB3	protein_coding	22
ENSG00000128322	IGLL1	protein_coding	22
ENSG00000129173	E2F8	protein_coding	11
ENSG00000131016	AKAP12	protein_coding	6
ENSG00000131747	TOP2A	protein_coding	17
ENSG00000132465	JCHAIN	protein_coding	4
ENSG00000133101	CCNA1	protein_coding	13
ENSG00000135069	PSAT1	protein_coding	9
ENSG00000135144	DTX1	protein_coding	12
ENSG00000135604	STX11	protein_coding	6
ENSG00000136826	KLF4	protein_coding	9
ENSG00000137804	NUSAP1	protein_coding	15
ENSG00000137812	KNL1	protein_coding	15
ENSG00000138160	KIF11	protein_coding	10
ENSG00000138180	CEP55	protein_coding	10
ENSG00000142178	SIK1	protein_coding	21

ENSG00000143228	NUF2	protein_coding	1
ENSG00000143507	DUSP10	protein_coding	1
ENSG00000148773	MKI67	protein_coding	10
ENSG00000152253	SPC25	protein_coding	2
ENSG00000153234	NR4A2	protein_coding	2
ENSG00000156738	MS4A1	protein_coding	11
ENSG00000157514	TSC22D3	protein_coding	X
ENSG00000161835	GRASP	protein_coding	12
ENSG00000163808	KIF15	protein_coding	3
ENSG00000164929	BAALC	protein_coding	8
ENSG00000165030	NFIL3	protein_coding	9
ENSG00000166349	RAG1	protein_coding	11
ENSG00000168078	PBK	protein_coding	8
ENSG00000169397	RNASE3	protein_coding	14
ENSG00000169429	CXCL8	protein_coding	4
ENSG00000169575	VPREB1	protein_coding	22
ENSG00000170293	CMTM8	protein_coding	3
ENSG00000170312	CDK1	protein_coding	10
ENSG00000171246	NPTX1	protein_coding	17
ENSG00000174123	TLR10	protein_coding	4
ENSG00000174500	GCSAM	protein_coding	3
ENSG00000175097	RAG2	protein_coding	11
ENSG00000178999	AURKB	protein_coding	17
ENSG00000185028	LRRC14B	protein_coding	5
ENSG00000185275	CD24P4	processed_pseudogene	Y
ENSG00000188536	HBA2	protein_coding	16
ENSG00000189057	FAM111B	protein_coding	11
ENSG00000189283	FHIT	protein_coding	3
ENSG00000196549	MME	protein_coding	3
ENSG00000197747	S100A10	protein_coding	1
ENSG00000199568	RNU5A-1	snRNA	15
ENSG00000199899	RF00019	misc_RNA	12
ENSG00000200169	RNU5D-1	snRNA	1
ENSG00000206047	DEFA1	protein_coding	8
ENSG00000206172	HBA1	protein_coding	16
ENSG00000206828	RF00003	snRNA	1
ENSG00000211904	IGHJ2	IG_J_gene	14
ENSG00000211905	IGHJ1	IG_J_gene	14
ENSG00000211966	IGHV5-51	IG_V_gene	14
ENSG00000211978	IGHV5-78	IG_V_pseudogene	14
ENSG00000227507	LTB	protein_coding	6
ENSG00000230945	LINC01507	lincRNA	9
ENSG00000236597	IGHD7-27	IG_D_gene	14
ENSG00000237547	IGHJ2P	IG_J_pseudogene	14
ENSG00000242887	IGHJ3	IG_J_gene	14
ENSG00000244734	HBB	protein_coding	11
ENSG00000253983	AC087627.1	antisense	8
ENSG00000261434	AC021087.3	sense_overlapping	5
ENSG00000265929	MIR5195	miRNA	14
ENSG00000270640	AC104695.3	sense_intronic	2
ENSG00000272398	CD24	protein_coding	6
ENSG00000275993	SIK1B	protein_coding	21

PC2:

Gene stable ID	Gene name	Gene type	Chromosome
ENSG00000117318	ID3	protein_coding	1
ENSG00000119535	CSF3R	protein_coding	1
ENSG00000133048	CHI3L1	protein_coding	1
ENSG00000143546	S100A8	protein_coding	1
ENSG00000150681	RGS18	protein_coding	1
ENSG00000158825	CDA	protein_coding	1
ENSG00000159339	PADI4	protein_coding	1
ENSG00000162747	FCGR3B	protein_coding	1
ENSG00000163154	TNFAIP8L2	protein_coding	1
ENSG00000163220	S100A9	protein_coding	1
ENSG00000163221	S100A12	protein_coding	1
ENSG00000163563	MNDA	protein_coding	1
ENSG00000186891	TNFRSF18	protein_coding	1
ENSG00000235492	LINC01221	lincRNA	1
ENSG00000275538	RNVU1-19	snRNA	1
ENSG00000158050	DUSP2	protein_coding	2
ENSG00000188011	RTP5	protein_coding	2
ENSG00000189292	ALKAL2	protein_coding	2
ENSG00000204099	NEU4	protein_coding	2
ENSG00000012223	LTF	protein_coding	3
ENSG00000073792	IGF2BP2	protein_coding	3
ENSG00000164047	CAMP	protein_coding	3
ENSG00000168334	XIRP1	protein_coding	3
ENSG00000274840	AC132807.2	lincRNA	3
ENSG00000163993	S100P	protein_coding	4
ENSG00000038427	VCAN	protein_coding	5
ENSG00000072571	HMMR	protein_coding	5
ENSG00000160883	HK3	protein_coding	5
ENSG00000168671	UGT3A2	protein_coding	5
ENSG00000182578	CSF1R	protein_coding	5
ENSG00000096006	CRISP3	protein_coding	6
ENSG00000112299	VNN1	protein_coding	6
ENSG00000198719	DLL1	protein_coding	6
ENSG00000232891	AL450344.3	sense_intronic	6
ENSG00000105967	TFEC	protein_coding	7
ENSG00000211688	TRGJP2	TR_J_gene	7
ENSG00000164821	DEFA4	protein_coding	8
ENSG00000165071	TMEM71	protein_coding	8
ENSG00000206047	DEFA1	protein_coding	8
ENSG00000239839	DEFA3	protein_coding	8
ENSG00000240247	DEFA1B	protein_coding	8
ENSG00000271938	AC103724.4	lincRNA	8
ENSG00000119508	NR4A3	protein_coding	9
ENSG00000148346	LCN2	protein_coding	9
ENSG00000229314	ORM1	protein_coding	9
ENSG00000266017	MIR4477B	miRNA	9
ENSG00000118113	MMP8	protein_coding	11
ENSG00000134827	TCN1	protein_coding	11
ENSG00000149516	MS4A3	protein_coding	11
ENSG00000156575	PRG3	protein_coding	11
ENSG00000184545	DUSP8	protein_coding	11

ENSG00000090382	LYZ	protein_coding	12
ENSG00000121316	PLBD1	protein_coding	12
ENSG00000123358	NR4A1	protein_coding	12
ENSG00000123405	NFE2	protein_coding	12
ENSG00000161835	GRASP	protein_coding	12
ENSG00000257883	AC125603.2	lincRNA	12
ENSG00000102524	TNFSF13B	protein_coding	13
ENSG00000102837	OLFM4	protein_coding	13
ENSG00000122025	FLT3	protein_coding	13
ENSG00000100439	ABHD4	protein_coding	14
ENSG00000100448	CTSG	protein_coding	14
ENSG00000100504	PYGL	protein_coding	14
ENSG00000126787	DLGAP5	protein_coding	14
ENSG00000136315	AL355922.1	lincRNA	14
ENSG00000169385	RNASE2	protein_coding	14
ENSG00000169397	RNASE3	protein_coding	14
ENSG00000169413	RNASE6	protein_coding	14
ENSG00000104043	ATP8B4	protein_coding	15
ENSG00000173546	CSPG4	protein_coding	15
ENSG00000270789	AC135983.5	processed_pseudogene	15
ENSG00000171724	VAT1L	protein_coding	16
ENSG00000188536	HBA2	protein_coding	16
ENSG00000206053	JPT2	protein_coding	16
ENSG00000005381	MPO	protein_coding	17
ENSG00000121053	EPX	protein_coding	17
ENSG00000131747	TOP2A	protein_coding	17
ENSG00000008438	PGLYRP1	protein_coding	19
ENSG00000099860	GADD45B	protein_coding	19
ENSG00000104918	RETN	protein_coding	19
ENSG00000105205	CLC	protein_coding	19
ENSG00000124469	CEACAM8	protein_coding	19
ENSG00000125740	FOSB	protein_coding	19
ENSG00000126266	FFAR1	protein_coding	19
ENSG00000170909	OSCAR	protein_coding	19
ENSG00000171051	FPR1	protein_coding	19
ENSG00000172232	AZU1	protein_coding	19
ENSG00000196415	PRTN3	protein_coding	19
ENSG00000197561	ELANE	protein_coding	19
ENSG00000087586	AURKA	protein_coding	20
ENSG00000100985	MMP9	protein_coding	20
ENSG00000101347	SAMHD1	protein_coding	20
ENSG00000101425	BPI	protein_coding	20
ENSG00000124107	SLPI	protein_coding	20
ENSG00000125810	CD93	protein_coding	20
ENSG00000125869	LAMP5	protein_coding	20
ENSG00000225988	LAMP5-AS1	antisense	20
ENSG00000165168	CYBB	protein_coding	X
ENSG00000274536	AL034397.3	antisense	X
ENSG00000129824	RPS4Y1	protein_coding	Y

Sample	Chrom	Position	Ref_base	Mut_base	Variant Allele Freq	Gene_ID	Transcript_ID	c.Annot	p.Annot	Consequence
MA4_01	Chr17	15134242	G	A	0.188959285	PMP22	ENST00000395938_r73	c.475 C>T	p.R159C	MISSENSE
MA4_01	Chr3	47144912	A	T	0.184537246	SETD2	ENST00000409792_r73	c.4841 T>A	p.I1614K	MISSENSE
MA4_02	Chr1	29602226	C	T	0.118736142	PTPRU	ENST00000345512_r73	c.1411 C>T	p.R471C	MISSENSE
MA4_02	Chr1	52442655	G	A	0.366571019	RAB3B	ENST00000371655_r73	c.135 C>T	p.D45D	SILENT
MA4_02	Chr11	67265042	G	A	0.43257233	PITPNM1	ENST00000534749_r73	c.1891 C>T	p.R631C	MISSENSE
MA4_02	Chr13	76415945	C	T	0.409429001	LMO7	ENST00000341547_r73	c.3011 C>T	p.P1004L	MISSENSE
MA4_02	Chr8	144993489	G	A	0.552685248	PLEC	ENST00000345136_r73	c.10500 C>T	p.R3500R	SILENT
MA4_02	ChrX	44942756	-	CAGG	0.127366057	KDM6A	ENST00000377967_r73	c.3336 ->CAGG	p.V1112fs*40	FRAMESHIFT
MA4_03	ChrX	11196264	C	T	0.902975312	ARHGAP6	ENST00000380736_r73	c.976 G>A	p.V326M	MISSENSE
MA4_04	Chr1	119466114	G	A	0.388781998	TBX15	ENST00000207157_r73	c.488 C>T	p.T163M	MISSENSE
MA4_04	Chr10	124351862	C	T	0.334958854	DMBT1	ENST00000368909_r73	c.2251 C>T	p.R751*	NONSENSE
MA4_04	Chr5	54529067	T	G	0.421348315	CCNO	ENST00000282572_r73	c.285 A>C	p.L95L	SILENT
MA4_04	Chr5	76028542	C	T	0.06541033	F2R	ENST00000319211_r73	c.492 C>T	p.S164S	SILENT
MA4_05	Chr4	170028169	T	C	0.155313712	SH3RF1	ENST00000284637_r73	c.2327 A>G	p.D776G	MISSENSE
MA4_06	Chr10	22826203	G	A	0.057377049	PIP4K2A	ENST00000376573_r73	c.1148 C>T	p.A383V	MISSENSE
MA4_06	Chr16	943056	C	T	0.455605039	LMF1	ENST00000262301_r73	c.680 G>A	p.R227Q	MISSENSE
MA4_06	Chr17	26910871	G	A	0.273290703	RP11-192H23.4	ENST00000531839_r73	c.761 C>T	p.T254M	MISSENSE
MA4_06	Chr17	66878843	C	T	0.064910079	ABCA8	ENST00000269080_r73	c.3605 G>A	p.S1202N	MISSENSE
MA4_06	Chr12	25398284	C	A	0.097262667	KRAS	ENST00000311936_r73	c.35 G>T	p.G12V	MISSENSE
MA4_06	Chr12	25398281	C	T	0.04127907	KRAS	ENST00000311936_r73	c.38 G>A	p.G13D	MISSENSE
MA4_07	Chr14	38060843	G	A	0.044476206	FOXA1	ENST00000250448_r73	c.1146 C>T	p.H382H	SILENT
MA4_07	Chr1	115258748	C	T	0.015116414	NRAS	ENST00000369535_r73	c.34 G>A	p.G12S	MISSENSE
MA4_08	Chr1	32157115	T	A	0.073264246	COL16A1	ENST00000373672_r73	Exon 19 - 2 A>T	-	ESSENTIAL_SPLICE
MA4_08	Chr11	3723715	G	A	0.323017992	NUP98	ENST00000324932_r73	c.3490 C>T	p.P1164S	MISSENSE
MA4_08	Chr12	25378561	G	A	0.348619422	KRAS	ENST00000311936_r73	c.437 C>T	p.A146V	MISSENSE
MA4_08	Chr2	99438545	C	T	0.402624515	KIAA1211L	ENST00000397899_r73	c.2191 G>A	p.G731R	MISSENSE
MA4_09	Chr1	156640767	C	T	0.432276908	NES	ENST00000368223_r73	c.3213 G>A	p.V1071V	SILENT
MA4_09	Chr10	134622358	C	T	0.24640952	TTC40	ENST00000368586_r73	c.7715 G>A	p.R2572Q	MISSENSE
MA4_09	Chr16	85942669	G	C	0.042319508	IRF8	ENST00000268638_r73	c.248 G>C	p.R83P	MISSENSE
MA4_09	Chr17	33875517	C	T	0.254864556	SLFN14	ENST00000415846_r73	c.2480 G>A	p.R827H	MISSENSE
MA4_09	Chr17	29196542	G	A	0.258426966	ATAD5	ENST00000321990_r73	c.3485 G>A	p.R1162H	MISSENSE
MA4_10	Chr11	113700009	A	T	0.25327096	USP28	ENST00000003302_r73	c.969 T>A	p.Y323*	NONSENSE
MA4_10	Chr18	63527018	G	A	0.164255091	CDH7	ENST00000323011_r73	c.1569 G>A	p.T523T	SILENT
MA4_10	Chr1	115258747	C	T	0.018408166	NRAS	ENST00000369535_r73	c.35 G>A	p.G12D	MISSENSE
MA4_10	Chr1	115258744	C	T	0.027023838	NRAS	ENST00000369535_r73	c.38 G>A	p.G13D	MISSENSE
MA4_10	Chr1	115258748	C	T	0.082718744	NRAS	ENST00000369535_r73	c.34 G>A	p.G12S	MISSENSE

MA4_11	Chr11	117329595	G	A	0.065889916	DSCAML1	ENST00000321322_r73	c.3623 C>T	p.T1208M	MISSENSE
MA4_11	Chr4	30724484	G	A	0.114128216	PCDH7	ENST00000361762_r73	c.1440 G>A	p.Q480Q	SILENT
MA4_11	ChrX	122800961	G	A	0.1242656	THOC2	ENST00000355725_r73	c.1186 C>T	p.R396*	NONSENSE
MA4_11	Chr1	115258747	C	T	0.130104615	NRAS	ENST00000369535_r73	c.35 G>A	p.G12D	MISSENSE
MA4_12	Chr1	115258747	C	T	0.03465982	NRAS	ENST00000369535_r73	c.35 G>A	p.G12D	MISSENSE
MA4_12	Chr1	115258744	C	T	0.037227214	NRAS	ENST00000369535_r73	c.38 G>A	p.G13D	MISSENSE
MA4_13	Chr1	77093213	G	A	0.431059092	ST6GALNAC3	ENST00000328299_r73	c.700 G>A	p.V234I	MISSENSE
MA4_14	Chr1	12183370	G	A	0.378454145	TNFRSF8	ENST00000263932_r73	c.976 G>A	p.A326T	MISSENSE
MA4_14	ChrX	153582588	C	T	0.467612001	FLNA	ENST00000360319_r73	c.5464 G>A	p.V1822M	MISSENSE
MA4_14R	Chr1	115258748	C	T	0.443557526	NRAS	ENST00000369535_r73	c.34 G>A	p.G12S	MISSENSE
MA4_15	ChrX	32503115	A	G	0.41562785	DMD	ENST00000378677_r73	c.2712 T>C	p.D904D	SILENT
MA4_15	Chr13	28602340	G	T	0.441176471	FLT3	ENST00000241453_r73	c.2028 C>A	p.N676K	MISSENSE
MA4_16	Chr20	62493709	C	T	0.348211355	ABHD16B	ENST00000369916_r73	c.816 C>T	p.F272F	SILENT
MA4_17	Chr12	25398284	C	A	0.41875	KRAS	ENST00000311936_r73	c.35 G>T	p.G12V	MISSENSE
MA4_17R	Chr1	26670871	G	T	0.153743711	AIM1L	ENST00000374207_r73	c.313 C>A	p.L105M	MISSENSE
MA4_17R	Chr12	70965002	T	A	0.139347021	PTPRB	ENST00000334414_r73	c.3174 A>T	p.S1058S	SILENT
MA4_17R	Chr15	60747314	G	C	0.124878397	NARG2	ENST00000261520_r73	c.831 C>G	p.H277Q	MISSENSE
MA4_17R	Chr16	67228769	G	A	0.159920574	E2F4	ENST00000379378_r73	c.694 G>A	p.A232T	MISSENSE
MA4_17R	Chr19	1987165	C	T	0.171126761	BTBD2	ENST00000255608_r73	c.1269 G>A	p.Q423Q	SILENT
MA4_17R	Chr4	48490578	C	T	0.179612163	SLC10A4	ENST00000273861_r73	c.936 C>T	p.Y312Y	SILENT
MA4_17R	Chr5	90144542	G	A	0.167889439	GPR98	ENST00000405460_r73	c.17108 G>A	p.R5703H	MISSENSE
MA4_17R	ChrX	37979633	G	C	0.257247584	SYTL5	ENST00000297875_r73	c.1619 G>C	p.G540A	MISSENSE
MA4_17R	Chr9	732503	G	A	0.045454546	KANK1	ENST00000382303_r73	c.3131 G>A	p.R1044Q	MISSENSE
MA4_18	Chr12	25398281	C	T	0.212984055	KRAS	ENST00000311936_r73	c.38 G>A	p.G13D	MISSENSE
MA4_18R	Chr10	50315892	G	A	0.137142857	VSTM4	ENST00000332853_r73	c.204 C>T	p.F68F	SILENT
MA4_18R	Chr10	61898828	C	T	0.084442696	ANK3	ENST00000280772_r73	c.2632 G>A	p.G878R	MISSENSE
MA4_18R	Chr11	65628573	G	A	0.166583665	MUS81	ENST00000308110_r73	c.265 G>A	p.G89S	MISSENSE
MA4_18R	Chr11	73074260	C	G	0.183411215	ARHGEF17	ENST00000263674_r73	c.5006 C>G	p.T1669S	MISSENSE
MA4_18R	Chr11	108593986	G	A	0.146759388	DDX10	ENST00000322536_r73	c.1762 G>A	p.D588N	MISSENSE
MA4_18R	Chr14	75375610	C	G	0.068568233	RPS6KL1	ENST00000555647_r73	c.1386 G>C	p.T462T	SILENT
MA4_18R	Chr15	79296469	G	A	0.151010002	RASGRF1	ENST00000558480_r73	c.2124 C>T	p.Y708Y	SILENT
MA4_18R	Chr16	71065790	G	C	0.086487782	HYDIN	ENST00000393567_r73	c.2560 C>G	p.P854A	MISSENSE
MA4_18R	Chr17	10541516	G	C	0.13260947	MYH3	ENST00000583535_r73	c.3573 C>G	p.A1191A	SILENT
MA4_18R	Chr18	74587457	C	G	0.181245626	ZNF236	ENST00000253159_r73	c.671 C>G	p.P224R	MISSENSE
MA4_18R	Chr19	9070839	C	T	0.172091641	MUC16	ENST00000397910_r73	c.16607 G>A	p.R5536Q	MISSENSE
MA4_18R	Chr19	13409769	C	T	0.001333088	CACNA1A	ENST00000360228_r73	c.2678 G>A	p.R893Q	MISSENSE
MA4_18R	Chr2	69556824	C	G	0.131769029	GFPT1	ENST00000361060_r73	c.1535 G>C	p.R512P	MISSENSE

MA4_18R	Chr2	219893011	G	A	0.002873563	CCDC108	ENST00000341552_r73	c.1763 C>T	p.T588M	MISSENSE
MA4_18R	Chr20	36374918	C	T	0.174187651	CTNNBL1	ENST00000361383_r73	c.375 C>T	p.H125H	SILENT
MA4_18R	Chr22	43901486	G	A	0.181884817	MPPED1	ENST00000417669_r73	c.971 G>A	p.R324Q	MISSENSE
MA4_18R	Chr3	48681041	G	C	0.207036615	CELSR3	ENST00000164024_r73	c.8235 C>G	p.V2745V	SILENT
MA4_18R	Chr3	62502298	C	T	0.139903995	CADPS	ENST00000383710_r73	c.2414 G>A	p.R805Q	MISSENSE
MA4_18R	Chr9	139404399	C	T	0.24613351	NOTCH1	ENST00000277541_r73	c.2755 G>A	p.G919R	MISSENSE
MA4_18R	Chr3	138187036	G	C	0.160185368	ESYT3	ENST00000389567_r73	c.1308 G>C	p.E436D	MISSENSE
MA4_18R	Chr10	95069922	C	T	0.159251197	MYOF	ENST00000358334_r73	c.5963 G>A	p.R1988Q	MISSENSE
MA4_18R	Chr6	143093951	C	T	0.178131544	HIVEP2	ENST00000367604_r73	c.1925 G>A	p.R642Q	MISSENSE
MA4_18R	Chr16	30410163	G	A	0.162408063	ZNF48	ENST00000320159_r73	c.1592 G>A	p.R531Q	MISSENSE
MA4_18R	Chr11	17742858	G	A	0.065334358	MYOD1	ENST00000250003_r73	c.766 G>A	p.V256M	MISSENSE
MA4_18R	Chr13	80055428	C	T	0.097651422	NDFIP2	ENST00000218652_r73	c.90 C>T	p.T30T	SILENT
MA4_18R	Chr19	17439019	C	T	0.148471616	ANO8	ENST00000159087_r73	c.2178 G>A	p.S726S	SILENT
MA4_18R	Chr4	110448484	G	A	0.131083481	SEC24B	ENST00000399100_r73	c.2867 G>A	p.R956Q	MISSENSE
MA4_18R	Chr6	96034806	G	A	0.097014925	MANEA	ENST00000358812_r73	c.491 G>A	p.R164Q	MISSENSE
MA4_18R	Chr6	154414520	C	T	0.117647059	OPRM1	ENST00000229768_r73	c.1280 C>T	p.S427L	MISSENSE
MA4_18R	Chr7	97937061	G	A	0.14	BAIAP2L1	ENST00000005260_r73	c.1103 C>T	p.T368M	MISSENSE
MA4_18R	Chr7	100634393	T	G	0.24	MUC12	ENST00000536621_r73	c.549 T>G	p.S183R	MISSENSE
MA4_18R	Chr7	103216088	C	G	0.215384615	RELN	ENST00000428762_r73	c.4210 G>C	p.D1404H	MISSENSE
MA4_18R	Chr8	110587801	G	A	0.116129032	SYBU	ENST00000533895_r73	c.1323 C>T	p.F441F	SILENT
MA4_18R	Chr8	121209184	T	A	0.205714286	COL14A1	ENST00000297848_r73	c.591 T>A	p.I197I	SILENT
MA4_18R	Chr9	15657131	A	G	0.470588235	CCDC171	ENST00000380701_r73	c.829 A>G	p.T277A	MISSENSE
MA4_18R	Chr9	117846595	G	C	0.110294118	TNC	ENST00000350763_r73	c.2024 C>G	p.T675R	MISSENSE
MA4_18R	Chr9	122011276	T	A	0.163043478	DBC1	ENST00000265922_r73	c.371 A>T	p.K124M	MISSENSE
MA4_18R	ChrX	54117762	G	A	0.104477612	FAM120C	ENST00000375180_r73	c.2410 C>T	p.R804*	NONSENSE
MA4_18R	ChrX	71876082	C	T	0.221698113	PHKA1	ENST00000373542_r73	c.929 G>A	p.R310H	MISSENSE
MA4_18R	ChrX	152827614	G	A	0.105263158	ATP2B3	ENST00000349466_r73	c.3073 G>A	p.G1025R	MISSENSE
MA4_18R	Chr3	32571050	T	-	0.135135135	DYNC1LI1	ENST00000273130_r73	c.1288 A>-	p.I430fs*5	FRAMESHIFT
MA4_19	Chr22	22712553	G	A	0.039168111	IGLV1-47	ENST00000390294_r73	c.296 G>A	p.R99Q	MISSENSE
MA4_20	Chr1	115256529	T	A	0.264634839	NRAS	ENST00000369535_r73	c.182 A>T	p.Q61L	MISSENSE
MA4_20	Chr16	2283522	C	T	0.452965621	E4F1	ENST00000301727_r73	c.1140 C>T	p.I380I	SILENT
MA4_20	Chr22	40807815	G	A	0.241766284	MKL1	ENST00000355630_r73	c.2375 C>T	p.S792L	MISSENSE
MA4_20	Chr12	53682409	GCCCAT	-	0.453414352	ESPL1	ENST00000552462_r73	c.4634 GCCCAT>-	p.S1545 SPC>S	MISSENSE
MA4_20R	Chr1	115256529	T	A	0.201530891	NRAS	ENST00000369535_r73	c.182 A>T	p.Q61L	MISSENSE
MA4_20R	Chr10	24889767	C	T	0.069881598	ARHGAP21	ENST00000396432_r73	c.2940 G>A	p.T980T	SILENT
MA4_20R	Chr11	108380476	C	G	0.09033675	EXPH5	ENST00000265843_r73	c.5758 G>C	p.G1920R	MISSENSE
MA4_20R	Chr16	2283522	C	T	0.229450857	E4F1	ENST00000301727_r73	c.1140 C>T	p.I380I	SILENT

MA4_20R	Chr17	7577121	G	A	0.211493113	TP53	ENST00000269305_r73	c.817 C>T	p.R273C	MISSENSE
MA4_20R	Chr22	40807815	G	A	0.237129485	MKL1	ENST00000355630_r73	c.2375 C>T	p.S792L	MISSENSE
MA4_20R	Chr12	53682409	GCCCAT	-	0.220722509	ESPL1	ENST00000552462_r73	c.4634 GCCCAT>-	p.S1545 SPC>S	MISSENSE
MA4_21	Chr11	70332174	T	G	0.186440678	SHANK2	ENST00000409161_r73	c.2436 A>C	p.T812T	SILENT
MA4_21	Chr5	139422532	-	GCTGCTGCT	0.391304348	NRG2	ENST00000361474_r73	c.123 ->AGCAGCAGC	p.S41 S>RAAA	MISSENSE
MA4_22	Chr9	127216294	C	A	0.475362319	GPR144	ENST00000334810_r73	c.996 C>A	p.C332*	NONSENSE
MA4_22	Chr12	23818481	C	T	0.178747941	SOX5	ENST00000546136_r73	c.789 G>A	p.P263P	SILENT
MA4_22	Chr15	75114997	C	T	0.116832958	LMAN1L	ENST00000309664_r73	c.1146 C>T	p.V382V	SILENT
MA4_22	Chr10	48428949	C	T	0.391472285	GDF10	ENST00000224605_r73	c.937 G>A	p.A313T	MISSENSE
MA4_22	Chr1	31836903	G	T	0.078651685	ZCCHC17	ENST00000344147_r73	c.589 G>T	p.D197Y	MISSENSE
MA4_22	Chr16	46993000	C	T	0.115942029	DNAJA2	ENST00000317089_r73	c.962 G>A	p.R321H	MISSENSE
MA4_22	Chr1	115258747	C	T	0.109902848	NRAS	ENST00000369535_r73	c.35 G>A	p.G12D	MISSENSE
MA4_22	Chr1	115258744	C	T	0.013689556	NRAS	ENST00000369535_r73	c.38 G>A	p.G13D	MISSENSE
MA4_22	Chr12	25398284	C	A	0.199459703	KRAS	ENST00000311936_r73	c.35 G>A	p.G12D	MISSENSE
MA4_22	Chr4	26422290	C	T	0.228111724	RBPJ	ENST00000345843_r73	c.433 C>T	p.R145W	MISSENSE
MA4_22	Chr11	95825853	G	A	0.091054045	MAML2	ENST00000524717_r73	c.1342 C>T	p.R448W	MISSENSE
MA4_22R	Chr13	52549042	G	A	0.34623323	ATP7B	ENST00000242839_r73	c.314 C>T	p.S105L	MISSENSE
MA4_22R	Chr18	42531586	G	A	0.377956481	SETBP1	ENST00000282030_r73	c.2281 G>A	p.V761M	MISSENSE
MA4_22R	Chr16	16173246	G	A	0.763759526	ABCC1	ENST00000399410_r73	c.2026 G>A	p.V676M	MISSENSE
MA4_22R	Chr16	76555115	C	T	0.138461539	CNTNAP4	ENST00000478060_r73	c.2225 C>T	p.A742V	MISSENSE
MA4_22R	Chr16	81078294	G	A	0.376859504	ATMIN	ENST00000299575_r73	c.2191 G>A	p.V731M	MISSENSE
MA4_22R	Chr6	96997360	G	A	0.402628435	UFL1	ENST00000369278_r73	c.1593 G>A	p.T531T	SILENT
MA4_22R	Chr3	137988903	G	A	0.271493213	ARMC8	ENST00000481646_r73	c.1366 G>A	p.V456I	MISSENSE
MA4_22R	Chr3	142277509	G	C	0.068720379	ATR	ENST00000350721_r73	c.1842 C>G	p.A614A	SILENT
MA4_22R	Chr9	124632975	C	T	0.417341041	TTLL11	ENST00000321582_r73	c.1804 G>A	p.E602K	MISSENSE
MA4_22R	Chr12	20801787	A	C	0.076212471	PDE3A	ENST00000359062_r73	c.2731 A>C	p.K911Q	MISSENSE
MA4_22R	Chr12	21795009	G	C	0.300685136	LDHB	ENST00000396076_r73	c.472 C>G	p.R158G	MISSENSE
MA4_22R	Chr12	76740737	C	T	0.246085011	BBS10	ENST00000393262_r73	c.1028 G>A	p.R343Q	MISSENSE
MA4_22R	Chr11	95825853	G	A	0.131651985	MAML2	ENST00000524717_r73	c.1342 C>T	p.R448W	MISSENSE
MA4_22R	Chr15	68695329	C	T	0.400844406	ITGA11	ENST00000315757_r73	c.92 G>A	p.R31Q	MISSENSE
MA4_22R	Chr15	98513945	G	A	0.296703297	ARRDC4	ENST00000268042_r73	c.1172 G>A	p.R391Q	MISSENSE
MA4_22R	Chr8	144994538	G	A	0.094175286	PLEC	ENST00000345136_r73	c.9451 C>T	p.R3151C	MISSENSE
MA4_22R	Chr4	26422290	C	T	0.229225636	RBPJ	ENST00000345843_r73	c.433 C>T	p.R145W	MISSENSE
MA4_22R	Chr4	77036593	C	T	0.685747664	NUP54	ENST00000264883_r73	c.1450 G>A	p.D484N	MISSENSE
MA4_22R	Chr4	88986625	G	A	0.366681825	PKD2	ENST00000237596_r73	c.2218 G>A	p.E740K	MISSENSE
MA4_22R	Chr10	70105604	G	A	0.2566146	RUFY2	ENST00000388768_r73	c.1847 C>T	p.P616L	MISSENSE
MA4_22R	Chr5	50091171	G	A	0.331018519	PARP8	ENST00000505697_r73	c.1348 G>A	p.A450T	MISSENSE

MA4_22R	Chr7	131825491	C	T	0.248064138	PLXNA4	ENST00000359827_r73	c.5305 G>A	p.A1769T	MISSENSE
MA4_22R	Chr7	150553626	C	T	0.278790389	AOC1	ENST00000493429_r73	c.68 C>T	p.P23L	MISSENSE
MA4_22R	Chr17	7577539	G	A	0.788971717	TP53	ENST00000269305_r73	c.742 C>T	p.R248W	MISSENSE
MA4_22R	Chr17	27185635	G	A	0.409534128	ERAL1	ENST00000254928_r73	c.753 G>A	p.T251T	SILENT
MA4_22R	Chr1	15987008	G	A	0.344632768	RSC1A1	ENST00000345034_r73	c.645 G>A	p.T215T	SILENT
MA4_22R	Chr1	223177194	G	A	0.365754813	DISP1	ENST00000284476_r73	c.2455 G>A	p.A819T	MISSENSE
MA4_22R	Chr1	15987008	G	A	0.344632768	DDI2	ENST00000480945_r73	c.1923 G>A	-	UTR
MA4_22R	Chr7	131825491	C	T	0.248064138	PLXNA4	ENST00000359827_r73	c.5546 C>T	p.A1849V	MISSENSE
MA4_22R	Chr12	25398284	C	A	0.538461538	KRAS	ENST00000311936_r73	c.437 C>T	p.A146V	MISSENSE
MA4_22R	Chr9	127216294	C	A	0.472222222	GPR144	ENST00000334810_r73	c.996 C>A	p.C332*	NONSENSE
MA4_22R	Chr11	899385	C	T	0.051546392	CHID1	ENST00000323578_r73	c.563 G>A	p.G188D	MISSENSE
MA4_22R	Chr11	3727740	G	C	0.051724138	NUP98	ENST00000324932_r73	c.2860 C>G	p.Q954E	MISSENSE
MA4_22R	Chr11	3756473	C	T	0.076086957	NUP98	ENST00000324932_r73	c.1490 G>A	p.G497E	MISSENSE
MA4_22R	Chr11	5067819	C	T	0.070588235	OR52J3	ENST00000380370_r73	c.64 C>T	p.L22L	SILENT
MA4_22R	Chr11	5444297	G	A	0.06043956	OR51Q1	ENST00000300778_r73	c.867 G>A	p.M289I	MISSENSE
MA4_22R	Chr11	5565853	C	T	0.303571429	OR52H1	ENST00000322653_r73	c.901 G>A	p.G301R	MISSENSE
MA4_22R	Chr11	5809210	C	T	0.059701493	OR52N1	ENST00000317078_r73	c.837 G>A	p.M279I	MISSENSE
MA4_22R	Chr11	8941004	G	A	0.291139241	AKIP1	ENST00000299576_r73	c.529 G>A	p.V177M	MISSENSE
MA4_22R	Chr11	9735099	C	G	0.050420168	SWAP70	ENST00000318950_r73	c.327 C>G	p.L109L	SILENT
MA4_22R	Chr11	32975682	G	A	0.322033898	QSER1	ENST00000399302_r73	c.4070 G>A	p.R1357H	MISSENSE
MA4_22R	Chr11	33090290	G	A	0.064516129	TCP11L1	ENST00000334274_r73	c.1212 G>A	p.V404V	SILENT
MA4_22R	Chr11	36248802	G	A	0.238938053	LDLRAD3	ENST00000315571_r73	c.622 G>A	p.V208M	MISSENSE
MA4_22R	Chr11	46388273	C	T	0.098765432	DGKZ	ENST00000454345_r73	c.467 C>T	p.P156L	MISSENSE
MA4_22R	Chr11	46724646	C	A	0.136363636	ZNF408	ENST00000311764_r73	c.505 C>A	p.L169M	MISSENSE
MA4_22R	Chr11	47446685	G	C	0.125	PSMC3	ENST00000298852_r73	c.272 C>G	p.S91C	MISSENSE
MA4_22R	Chr11	56409825	C	G	0.051502146	OR5AP2	ENST00000302981_r73	c.91 G>C	p.G31R	MISSENSE
MA4_22R	Chr11	57564307	G	A	0.066115703	CTNND1	ENST00000524630_r73	c.799 G>A	p.G267R	MISSENSE
MA4_22R	Chr11	60506408	G	A	0.052631579	MS4A18	ENST00000529108_r73	c.205 G>A	p.A69T	MISSENSE
MA4_22R	Chr11	62362542	C	A	0.114754098	MTA2	ENST00000278823_r73	c.1484 G>T	p.C495F	MISSENSE
MA4_22R	Chr11	64507168	G	T	0.105882353	RASGRP2	ENST00000394432_r73	c.636 C>A	p.L212L	SILENT
MA4_22R	Chr11	64697810	G	A	0.469387755	PPP2R5B	ENST00000164133_r73	c.739 G>A	p.E247K	MISSENSE
MA4_22R	Chr11	66190332	C	T	0.065789474	NPAS4	ENST00000311034_r73	c.618 C>T	p.G206G	SILENT
MA4_22R	Chr1	238045782	C	T	0.066115703	ZP4	ENST00000366570_r73	c.1563 G>A	p.L521L	SILENT
MA4_22R	Chr1	241755414	G	A	0.087912088	KMO	ENST00000366559_r73	c.1420 G>A	p.V474M	MISSENSE
MA4_22R	Chr1	242030233	G	C	0.248554913	EXO1	ENST00000366548_r73	c.1143 G>C	p.S381S	SILENT
MA4_22R	Chr13	25274920	C	T	0.051546392	ATP12A	ENST00000381946_r73	c.1741 C>T	p.P581S	MISSENSE
MA4_22R	Chr13	25363493	G	C	0.394736842	RNF17	ENST00000255324_r73	c.791 G>C	p.R264P	MISSENSE

MA4_22R	Chr13	28498569	C	T	0.133333333	PDX1	ENST00000381033_r73	c.583 C>T	p.Q195*	NONSENSE
MA4_22R	Chr13	33016677	C	T	0.062893082	N4BP2L2	ENST00000399396_r73	c.1997 G>A	p.R666K	MISSENSE
MA4_22R	Chr13	39424199	G	A	0.180722892	FREM2	ENST00000280481_r73	c.6404 G>A	p.R2135Q	MISSENSE
MA4_22R	Chr13	39597187	A	T	0.05106383	PROSER1	ENST00000352251_r73	Exon 8 2 T>A	-	ESSENTIAL_SPLICE
MA4_22R	Chr13	46544580	C	T	0.051948052	ZC3H13	ENST00000282007_r73	c.2489 G>A	p.G830E	MISSENSE
MA4_22R	Chr13	50059823	C	T	0.055813954	SETDB2	ENST00000317257_r73	c.1576 C>T	p.R526*	NONSENSE
MA4_22R	Chr13	79191089	G	A	0.051136364	RNF219	ENST00000282003_r73	c.807 C>T	p.S269S	SILENT
MA4_22R	Chr13	80911657	C	T	0.105263158	SPRY2	ENST00000377102_r73	c.184 G>A	p.V62I	MISSENSE
MA4_22R	Chr13	103317148	C	T	0.376146789	TPP2	ENST00000376065_r73	c.3205 C>T	p.R1069*	NONSENSE
MA4_22R	Chr13	103388797	C	T	0.050724638	CCDC168	ENST00000322527_r73	c.363 G>A	p.E121E	SILENT
MA4_22R	Chr13	103710650	C	T	0.2	SLC10A2	ENST00000245312_r73	c.460 G>A	p.D154N	MISSENSE
MA4_22R	Chr13	110436664	G	A	0.057142857	IRS2	ENST00000375856_r73	c.1737 C>T	p.T579T	SILENT
MA4_22R	Chr13	111927085	A	T	0.057692308	ARHGEF7	ENST00000317133_r73	c.1220 A>T	p.H407L	MISSENSE
MA4_22R	Chr16	1536065	C	T	0.050847458	PTX4	ENST00000293922_r73	c.1297 G>A	p.E433K	MISSENSE
MA4_22R	Chr16	2293382	G	A	0.060240964	ECI1	ENST00000301729_r73	c.500 C>T	p.A167V	MISSENSE
MA4_22R	Chr16	3493148	C	T	0.1	ZNF597	ENST00000301744_r73	c.6 G>A	p.A2A	SILENT
MA4_22R	Chr16	4033331	C	T	0.069565217	ADCY9	ENST00000294016_r73	c.2421 G>A	p.L807L	SILENT
MA4_22R	Chr18	5397114	C	G	0.059259259	EPB41L3	ENST00000341928_r73	c.2784 G>C	p.E928D	MISSENSE
MA4_22R	Chr18	9221872	A	G	0.054054054	ANKRD12	ENST00000262126_r73	c.818 A>G	p.H273R	MISSENSE
MA4_22R	Chr18	21152144	C	T	0.05	NPC1	ENST00000269228_r73	c.181 G>A	p.E61K	MISSENSE
MA4_22R	Chr18	34349352	G	A	0.105769231	FHOD3	ENST00000257209_r73	c.4200 G>A	p.P1400P	SILENT
MA4_22R	Chr18	34740289	G	A	0.089108911	KIAA1328	ENST00000280020_r73	c.1359 G>A	p.M453I	MISSENSE
MA4_22R	Chr18	47796189	C	A	0.108695652	MBD1	ENST00000353909_r73	Exon 16 - 1 G>T	-	ESSENTIAL_SPLICE
MA4_22R	Chr18	59774078	C	T	0.058333333	PIGN	ENST00000357637_r73	c.1711 G>A	p.G571R	MISSENSE
MA4_22R	Chr18	60036630	G	A	0.28	TNFRSF11A	ENST00000586569_r73	c.1480 G>A	p.E494K	MISSENSE
MA4_22R	Chr18	70209141	G	A	0.284090909	CBLN2	ENST00000585159_r73	c.255 C>T	p.S85S	SILENT
MA4_22R	Chr16	11845214	C	T	0.068965517	ZC3H7A	ENST00000396516_r73	c.2875 G>A	p.D959N	MISSENSE
MA4_22R	Chr16	15692718	C	A	0.11627907	KIAA0430	ENST00000396368_r73	c.4977 G>T	p.E1659D	MISSENSE
MA4_22R	Chr16	20335355	G	A	0.25	GP2	ENST00000302555_r73	c.318 C>T	p.T106T	SILENT
MA4_22R	Chr16	20362003	G	A	0.059701493	UMOD	ENST00000570689_r73	c.57 C>T	p.I19I	SILENT
MA4_22R	Chr16	22092160	G	C	0.058823529	C16orf52	ENST00000542527_r73	c.463 G>C	p.V155L	MISSENSE
MA4_22R	Chr16	30020553	G	A	0.098765432	DOC2A	ENST00000350119_r73	c.387 C>T	p.V129V	SILENT
MA4_22R	Chr16	31336632	G	A	75	ITGAM	ENST00000287497_r73	c.2412 G>A	p.V804V	SILENT
MA4_22R	Chr16	53358011	G	A	0.169811321	CHD9	ENST00000566029_r73	c.7850 G>A	p.R2617Q	MISSENSE
MA4_22R	Chr16	69177089	G	A	0.056818182	CIRH1A	ENST00000314423_r73	c.535 G>A	p.V179I	MISSENSE
MA4_22R	Chr16	70843889	G	A	0.086956522	HYDIN	ENST00000393567_r73	c.14680 C>T	p.Q4894*	NONSENSE
MA4_22R	Chr16	75575261	C	T	0.112676056	TMEM231	ENST00000258173_r73	c.757 G>A	p.V253M	MISSENSE

MA4_22R	Chr16	79245676	G	A	0.0625	WWOX	ENST00000566780_r73	c.1228 G>A	p.G410S	MISSENSE
MA4_22R	Chr16	84473064	G	C	0.283783784	ATP2C2	ENST00000262429_r73	c.1143 G>C	p.T381T	SILENT
MA4_22R	Chr16	88747917	G	A	0.066666667	SNAI3	ENST00000332281_r73	c.282 C>T	p.D94D	SILENT
MA4_22R	Chr16	89787187	G	A	0.192307692	VPS9D1	ENST00000389386_r73	c.83 C>T	p.T28I	MISSENSE
MA4_22R	Chr6	8015908	C	T	0.050847458	BLOC1S5	ENST00000397457_r73	c.538 G>A	p.D180N	MISSENSE
MA4_22R	Chr6	16306741	G	A	0.051813472	ATXN1	ENST00000244769_r73	c.2267 C>T	p.P756L	MISSENSE
MA4_22R	Chr6	22292797	G	C	0.204081633	PRL	ENST00000306482_r73	c.282 C>G	p.P94P	SILENT
MA4_22R	Chr6	29455181	T	C	0.058252427	MAS1L	ENST00000377127_r73	c.499 A>G	p.I167V	MISSENSE
MA4_22R	Chr6	43322744	C	T	0.097560976	ZNF318	ENST00000361428_r73	c.2328 G>A	p.P776P	SILENT
MA4_22R	Chr6	49518654	C	T	0.339622642	C6orf141	ENST00000414696_r73	c.149 C>T	p.A50V	MISSENSE
MA4_22R	Chr6	72975190	G	T	0.14	RIMS1	ENST00000521978_r73	c.3292 G>T	p.D1098Y	MISSENSE
MA4_22R	Chr6	76660399	G	A	0.053763441	IMPG1	ENST00000369950_r73	c.1704 C>T	p.P568P	SILENT
MA4_22R	Chr6	102376485	G	A	0.057553957	GRIK2	ENST00000421544_r73	c.2063 G>A	p.G688D	MISSENSE
MA4_22R	Chr6	109274465	G	A	0.068627451	ARMC2	ENST00000392644_r73	c.1826 G>A	p.R609H	MISSENSE
MA4_22R	Chr6	112461037	G	A	0.062015504	LAMA4	ENST00000230538_r73	c.3027 C>T	p.A1009A	SILENT
MA4_22R	Chr6	117859847	G	A	0.071942446	DCBLD1	ENST00000296955_r73	c.825 G>A	p.S275S	SILENT
MA4_22R	Chr6	131481326	C	A	0.111111111	AKAP7	ENST00000431975_r73	c.279 C>A	p.I93I	SILENT
MA4_22R	Chr6	131927620	C	T	0.061946903	MED23	ENST00000354577_r73	c.1384 G>A	p.E462K	MISSENSE
MA4_22R	Chr6	139488186	G	A	0.067961165	HECA	ENST00000367658_r73	c.1037 G>A	p.R346Q	MISSENSE
MA4_22R	Chr6	147704066	G	A	0.088235294	STXBP5	ENST00000367481_r73	c.3238 G>A	p.G1080S	MISSENSE
MA4_22R	Chr6	148865271	G	A	0.259541985	SASH1	ENST00000367467_r73	c.2665 G>A	p.D889N	MISSENSE
MA4_22R	Chr6	151694763	C	G	0.3125	ZBTB2	ENST00000325144_r73	c.10 G>C	p.A4P	MISSENSE
MA4_22R	Chr6	155450464	A	T	0.061068702	TIAM2	ENST00000461783_r73	c.107 A>T	p.H36L	MISSENSE
MA4_22R	Chr6	161016412	G	A	0.052132701	LPA	ENST00000316300_r73	c.3443 C>T	p.P1148L	MISSENSE
MA4_22R	Chr6	165844942	C	G	0.052631579	PDE10A	ENST00000539869_r73	c.712 G>C	p.A238P	MISSENSE
MA4_22R	ChrX	15593791	C	T	0.077777778	ACE2	ENST00000252519_r73	c.1440 G>A	p.M480I	MISSENSE
MA4_22R	ChrX	16627715	G	T	0.135135135	CTPS2	ENST00000359276_r73	c.1640 C>A	p.A547E	MISSENSE
MA4_22R	ChrX	18622441	G	A	0.144927536	CDKL5	ENST00000379996_r73	c.1397 G>A	p.R466Q	MISSENSE
MA4_22R	ChrX	29301132	G	T	0.153061225	IL1RAPL1	ENST00000378993_r73	c.160 G>T	p.A54S	MISSENSE
MA4_22R	ChrX	46747095	A	T	0.102040816	CXorf31	ENST00000377879_r73	c.170 T>A	p.V57E	MISSENSE
MA4_22R	ChrX	48666668	C	A	0.123595506	HDAC6	ENST00000334136_r73	c.741 C>A	p.V247V	SILENT
MA4_22R	ChrX	54950100	G	T	0.101694915	TRO	ENST00000173898_r73	c.1135 G>T	p.E379*	NONSENSE
MA4_22R	ChrX	54960268	G	A	0.710526316	PFKFB1	ENST00000375006_r73	c.1342 C>T	p.R448W	MISSENSE
MA4_22R	ChrX	55047547	G	A	0.269230769	ALAS2	ENST00000396198_r73	c.537 C>T	p.S179S	SILENT
MA4_22R	ChrX	57021244	C	T	0.417582418	SPIN3	ENST00000374919_r73	c.137 G>A	p.R46Q	MISSENSE
MA4_22R	ChrX	63411097	G	T	0.125	AMER1	ENST00000330258_r73	c.2070 C>A	p.S690R	MISSENSE
MA4_22R	ChrX	69507161	C	T	0.727272727	PDZD11	ENST00000239666_r73	c.353 G>A	p.R118H	MISSENSE

MA4_22R	ChrX	70316558	G	A	0.1	FOXO4	ENST00000374259_r73	c.180 G>A	p.T60T	SILENT
MA4_22R	ChrX	76890137	G	T	0.112781955	ATRX	ENST00000373344_r73	c.4757 C>A	p.P1586Q	MISSENSE
MA4_22R	Chr3	11059024	G	A	0.072289157	SLC6A1	ENST00000287766_r73	c.127 G>A	p.D43N	MISSENSE
MA4_22R	Chr3	14508035	C	T	0.064220184	SLC6A6	ENST00000454876_r73	c.744 C>T	p.F248F	SILENT
MA4_22R	Chr3	19959819	C	T	0.057142857	EFHB	ENST00000295824_r73	c.1082 G>A	p.R361Q	MISSENSE
MA4_22R	Chr3	23250290	G	C	0.052631579	UBE2E2	ENST00000425792_r73	c.100 G>C	p.E34Q	MISSENSE
MA4_22R	Chr3	28365666	C	T	0.061068702	AZI2	ENST00000479665_r73	c.1046 G>A	p.W349*	NONSENSE
MA4_22R	Chr3	31710219	C	T	0.056701031	OSBPL10	ENST00000396556_r73	c.2011 G>A	p.E671K	MISSENSE
MA4_22R	Chr3	32726979	G	A	0.056603774	CNOT10	ENST00000331889_r73	Exon 1 5 G>A	-	ESSENTIAL_SPLICE
MA4_22R	ChrX	96013231	C	T	0.05019305	DIAPH2	ENST00000373049_r73	c.421 C>T	p.Q141*	NONSENSE
MA4_22R	ChrX	105167153	A	T	0.096491228	NRK	ENST00000243300_r73	c.2654 A>T	p.Y885F	MISSENSE
MA4_22R	ChrX	105179175	C	T	0.08045977	NRK	ENST00000243300_r73	c.3513 C>T	p.F1171F	SILENT
MA4_22R	ChrX	106844025	C	A	0.152173913	FRMPD3	ENST00000439554_r73	c.2699 C>A	p.S900*	NONSENSE
MA4_22R	ChrX	119670796	G	T	0.103448276	CUL4B	ENST00000371322_r73	c.2032 C>A	p.H678N	MISSENSE
MA4_22R	ChrX	132161058	G	C	0.074766355	USP26	ENST00000370832_r73	c.1191 C>G	p.N397K	MISSENSE
MA4_22R	ChrX	140993500	G	A	0.062015504	MAGEC1	ENST00000285879_r73	c.310 G>A	p.E104K	MISSENSE
MA4_22R	ChrX	148797302	C	T	0.125	MAGEA11	ENST00000355220_r73	c.231 C>T	p.P77P	SILENT
MA4_22R	ChrX	150573396	G	T	0.103448276	VMA21	ENST00000330374_r73	c.172 G>T	p.G58W	MISSENSE
MA4_22R	ChrX	153171301	C	A	0.133333333	AVPR2	ENST00000358927_r73	c.341 C>A	p.A114D	MISSENSE
MA4_22R	Chr3	38318437	C	T	0.060606061	SLC22A13	ENST00000311856_r73	c.1381 C>T	p.R461W	MISSENSE
MA4_22R	Chr3	39228715	G	C	0.050761421	XIRP1	ENST00000396251_r73	c.2222 C>G	p.A741G	MISSENSE
MA4_22R	Chr3	44762890	G	C	0.32173913	ZNF502	ENST00000436624_r73	c.581 G>C	p.R194P	MISSENSE
MA4_22R	Chr3	49679891	G	C	0.070422535	BSN	ENST00000296452_r73	c.824 G>C	p.G275A	MISSENSE
MA4_22R	Chr3	49698362	C	T	0.345864662	BSN	ENST00000296452_r73	c.9084 C>T	p.P3028P	SILENT
MA4_22R	Chr3	50220929	C	T	0.0625	SEMA3F	ENST00000002829_r73	c.1165 C>T	p.H389Y	MISSENSE
MA4_22R	Chr3	50418192	G	A	0.433333333	CACNA2D2	ENST00000424201_r73	c.829 C>T	p.R277*	NONSENSE
MA4_22R	Chr3	51663360	C	T	0.231527094	RAD54L2	ENST00000409535_r73	c.352 C>T	p.R118W	MISSENSE
MA4_22R	Chr3	61975389	G	A	0.051724138	PTPRG	ENST00000474889_r73	c.281 G>A	p.R94H	MISSENSE
MA4_22R	Chr3	62189178	C	T	0.067484663	PTPRG	ENST00000474889_r73	c.1709 C>T	p.P570L	MISSENSE
MA4_22R	Chr3	64589638	A	T	0.06097561	ADAMTS9	ENST00000498707_r73	c.3707 T>A	p.V1236E	MISSENSE
MA4_22R	Chr3	89521697	C	T	0.050314465	EPHA3	ENST00000336596_r73	c.2774 C>T	p.T925I	MISSENSE
MA4_22R	Chr3	107799004	G	A	0.063583815	CD47	ENST00000355354_r73	c.234 C>T	p.P78P	SILENT
MA4_22R	Chr3	107799088	G	A	0.058139535	CD47	ENST00000355354_r73	c.150 C>T	p.N50N	SILENT
MA4_22R	Chr3	119666194	C	T	0.277227723	GSK3B	ENST00000264235_r73	c.287 G>A	p.R96Q	MISSENSE
MA4_22R	Chr3	122259629	C	T	0.054945055	PARP9	ENST00000477522_r73	c.1455 G>A	p.M485I	MISSENSE
MA4_22R	Chr3	128345586	C	T	0.051724138	RPN1	ENST00000296255_r73	c.1126 G>A	p.E376K	MISSENSE
MA4_22R	Chr3	130162344	C	T	0.055555556	COL6A5	ENST00000312481_r73	c.6512 C>T	p.P2171L	MISSENSE

MA4_22R	Chr3	130318627	C	T	0.06741573	COL6A6	ENST00000358511_r73	c.4626 C>T	p.P1542P	SILENT
MA4_22R	Chr3	138762690	C	T	0.305785124	PRR23C	ENST00000413199_r73	c.773 G>A	p.R258H	MISSENSE
MA4_22R	Chr3	142031593	T	A	0.058333333	XRN1	ENST00000264951_r73	c.4665 A>T	p.I1555I	SILENT
MA4_22R	Chr3	142537239	T	A	0.061728395	PCOLCE2	ENST00000295992_r73	c.1186 A>T	p.I396F	MISSENSE
MA4_22R	Chr3	142741745	C	T	0.068181818	U2SURP	ENST00000473835_r73	c.1069 C>T	p.P357S	MISSENSE
MA4_22R	Chr3	142741765	A	T	0.088235294	U2SURP	ENST00000473835_r73	c.1089 A>T	p.I363I	SILENT
MA4_22R	Chr3	160233267	C	T	0.065934066	KPNA4	ENST00000334256_r73	c.1005 G>A	p.L335L	SILENT
MA4_22R	Chr3	164714347	C	T	0.08411215	SI	ENST00000264382_r73	c.4668 G>A	p.R1556R	SILENT
MA4_22R	Chr3	183907373	C	T	0.068965517	ABCF3	ENST00000429586_r73	c.1142 C>T	p.S381F	MISSENSE
MA4_22R	Chr3	191098013	G	A	0.09009009	CCDC50	ENST00000392455_r73	c.514 G>A	p.E172K	MISSENSE
MA4_22R	Chr3	195487888	C	T	0.063157895	MUC4	ENST00000349607_r73	c.1854 G>A	p.W618*	NONSENSE
MA4_22R	Chr3	196054298	G	A	0.103896104	TM4SF19	ENST00000442633_r73	c.164 C>T	p.A55V	MISSENSE
MA4_22R	Chr3	196215543	G	A	0.059405941	RNF168	ENST00000318037_r73	c.313 C>T	p.Q105*	NONSENSE
MA4_22R	Chr9	742270	G	A	0.059259259	KANK1	ENST00000382303_r73	c.3762 G>A	p.L1254L	SILENT
MA4_22R	Chr9	8319853	C	T	0.361111111	PTPRD	ENST00000381196_r73	c.5648 G>A	p.R1883Q	MISSENSE
MA4_22R	Chr9	17415795	C	T	0.147058824	CNTLN	ENST00000380647_r73	c.2806 C>T	p.H936Y	MISSENSE
MA4_22R	Chr9	37442512	G	A	0.056910569	ZBTB5	ENST00000307750_r73	c.37 C>T	p.Q13*	NONSENSE
MA4_22R	Chr9	72472880	G	C	0.058558559	C9orf135	ENST00000377197_r73	c.436 G>C	p.D146H	MISSENSE
MA4_22R	Chr9	84268926	G	A	0.18	TLE1	ENST00000376499_r73	c.260 C>T	p.T87M	MISSENSE
MA4_22R	Chr9	100862295	C	T	0.059259259	TRIM14	ENST00000375098_r73	c.455 G>A	p.R152K	MISSENSE
MA4_22R	Chr9	101812146	C	T	0.06185567	COL15A1	ENST00000375001_r73	c.2873 C>T	p.P958L	MISSENSE
MA4_22R	Chr9	102861104	G	A	0.056074766	ERP44	ENST00000262455_r73	c.19 C>T	p.L7L	SILENT
MA4_22R	Chr9	111965991	G	A	0.062962963	EPB41L4B	ENST00000374566_r73	c.1898 C>T	p.P633L	MISSENSE
MA4_22R	Chr9	112200416	C	T	0.273381295	PTPN3	ENST00000374541_r73	c.565 G>A	p.E189K	MISSENSE
MA4_22R	Chr9	113265477	G	C	0.052173913	SVEP1	ENST00000401783_r73	c.1324 C>G	p.R442G	MISSENSE
MA4_22R	Chr9	126139223	C	T	0.315789474	CRB2	ENST00000373631_r73	c.3740 C>T	p.A1247V	MISSENSE
MA4_22R	Chr12	2926453	G	A	0.173913044	ITFG2	ENST00000228799_r73	c.161 G>A	p.R54Q	MISSENSE
MA4_22R	Chr12	7469851	G	A	0.162337662	ACSM4	ENST00000399422_r73	c.739 G>A	p.G247S	MISSENSE
MA4_22R	Chr12	11138988	A	T	0.164874552	TAS2R50	ENST00000506868_r73	c.472 T>A	p.Y158N	MISSENSE
MA4_22R	Chr12	23699323	C	T	0.064102564	SOX5	ENST00000546136_r73	c.1485 G>A	p.L495L	SILENT
MA4_22R	Chr12	32137414	G	A	0.050420168	KIAA1551	ENST00000312561_r73	c.3525 G>A	p.L1175L	SILENT
MA4_22R	Chr12	49434127	C	T	0.066666667	KMT2D	ENST00000301067_r73	c.7426 G>A	p.E2476K	MISSENSE
MA4_22R	Chr12	49580433	G	A	0.068376068	TUBA1A	ENST00000301071_r73	c.187 C>T	p.P63S	MISSENSE
MA4_22R	Chr12	51213482	G	T	0.142857143	ATF1	ENST00000262053_r73	c.736 G>T	p.A246S	MISSENSE
MA4_22R	Chr12	53432146	G	A	0.063157895	EIF4B	ENST00000262056_r73	c.1527 G>A	p.G509G	SILENT
MA4_22R	Chr12	53701467	G	A	0.072289157	AAAS	ENST00000209873_r73	c.1447 C>T	p.P483S	MISSENSE
MA4_22R	Chr12	54757225	T	A	0.053435115	GPR84	ENST00000267015_r73	c.411 A>T	p.I137I	SILENT

MA4_22R	Chr12	55846797	C	T	0.052173913	OR6C2	ENST00000322678_r73	c.800 C>T	p.A267V	MISSENSE
MA4_22R	Chr12	56119655	C	T	0.068965517	CD63	ENST00000546939_r73	c.347 G>A	p.W116*	NONSENSE
MA4_22R	Chr9	130475050	G	C	0.063291139	C9orf117	ENST00000373295_r73	c.1200 G>C	p.M400I	MISSENSE
MA4_22R	Chr9	130550582	C	A	0.102941177	CDK9	ENST00000373264_r73	c.522 C>A	p.F174L	MISSENSE
MA4_22R	Chr9	130914258	C	T	0.060606061	LCN2	ENST00000373017_r73	c.429 C>T	p.F143F	SILENT
MA4_22R	Chr12	59272846	G	A	0.098214286	LRIG3	ENST00000379141_r73	c.1663 C>T	p.R555*	NONSENSE
MA4_22R	Chr12	72023451	C	T	0.233870968	ZFC3H1	ENST00000378743_r73	c.3764 G>A	p.R1255Q	MISSENSE
MA4_22R	Chr12	88479826	G	T	0.120481928	CEP290	ENST00000552810_r73	c.4427 C>A	p.S1476*	NONSENSE
MA4_22R	Chr12	96273421	C	T	0.357142857	CCDC38	ENST00000344280_r73	Exon 12 1 G>A	-	ESSENTIAL_SPLICE
MA4_22R	Chr12	110820648	C	G	0.068376068	ANAPC7	ENST00000455511_r73	c.1037 G>C	p.G346A	MISSENSE
MA4_22R	Chr12	114374833	C	T	0.052631579	RBM19	ENST00000545145_r73	c.2047 G>A	p.D683N	MISSENSE
MA4_22R	Chr12	118298167	C	T	0.209302326	KSR2	ENST00000339824_r73	c.250 G>A	p.A84T	MISSENSE
MA4_22R	Chr12	121858394	C	T	0.073529412	RNF34	ENST00000361234_r73	c.741 C>T	p.S247S	SILENT
MA4_22R	Chr12	123782540	C	T	0.057553957	SBNO1	ENST00000602750_r73	c.4021 G>A	p.G1341R	MISSENSE
MA4_22R	Chr12	133389991	G	A	0.103448276	GOLGA3	ENST00000450791_r73	c.421 C>T	p.P141S	MISSENSE
MA4_22R	Chr14	23884667	G	T	0.133333333	MYH7	ENST00000355349_r73	c.5206 C>A	p.Q1736K	MISSENSE
MA4_22R	Chr14	36988571	G	A	0.14	NKX2-1	ENST00000354822_r73	c.82 C>T	p.R28C	MISSENSE
MA4_22R	Chr14	45633567	G	T	0.190476191	FANCM	ENST00000267430_r73	c.1587 G>T	p.V529V	SILENT
MA4_22R	Chr14	50666444	G	C	0.056179775	SOS2	ENST00000216373_r73	c.475 C>G	p.Q159E	MISSENSE
MA4_22R	Chr14	64520254	C	T	0.054945055	SYNE2	ENST00000344113_r73	c.9623 C>T	p.A3208V	MISSENSE
MA4_22R	Chr14	64892545	G	T	0.101449275	MTHFD1	ENST00000555709_r73	c.953 G>T	p.S318I	MISSENSE
MA4_22R	Chr14	70839817	C	T	0.294736842	SYNJ2BP	ENST00000256366_r73	c.329 G>A	p.R110Q	MISSENSE
MA4_22R	Chr14	75290989	G	A	0.056338028	YLPM1	ENST00000325680_r73	c.6142 G>A	p.D2048N	MISSENSE
MA4_22R	Chr14	77793187	C	T	0.072463768	GSTZ1	ENST00000216465_r73	c.74 C>T	p.A25V	MISSENSE
MA4_22R	Chr14	92790184	C	T	0.25	SLC24A4	ENST00000531433_r73	c.10 C>T	p.R4C	MISSENSE
MA4_22R	Chr14	94088559	C	T	0.166666667	UNC79	ENST00000256339_r73	c.4449 C>T	p.S1483S	SILENT
MA4_22R	Chr14	94395244	G	C	0.52631579	FAM181A	ENST00000557719_r73	c.613 G>C	p.V205L	MISSENSE
MA4_22R	Chr14	100193004	C	T	0.36	CYP46A1	ENST00000261835_r73	c.1443 C>T	p.P481P	SILENT
MA4_22R	Chr14	102027983	G	A	0.275	DIO3	ENST00000510508_r73	c.150 G>A	p.P50P	SILENT
MA4_22R	Chr14	104639754	C	T	0.294736842	KIF26A	ENST00000423312_r73	c.1771 C>T	p.R591*	NONSENSE
MA4_22R	Chr14	106967286	C	T	0.063218391	IGHV1-46	ENST00000390622_r73	c.114 G>A	p.K38K	SILENT
MA4_22R	Chr15	37390309	G	A	0.159090909	MEIS2	ENST00000338564_r73	c.104 C>T	p.P35L	MISSENSE
MA4_22R	Chr15	48056943	C	T	0.214285714	SEMA6D	ENST00000558014_r73	c.1206 C>T	p.A402A	SILENT
MA4_22R	Chr15	48826377	G	C	0.237410072	FBN1	ENST00000316623_r73	c.762 C>G	p.P254P	SILENT
MA4_22R	Chr15	49309166	G	A	0.06763285	SECISBP2L	ENST00000559471_r73	c.1298 C>T	p.P433L	MISSENSE
MA4_22R	Chr15	56435072	C	T	0.085271318	RFX7	ENST00000559847_r73	c.14 G>A	p.R5Q	MISSENSE
MA4_22R	Chr15	56974447	C	T	0.138888889	ZNF280D	ENST00000559237_r73	Exon 9 5 G>A	-	ESSENTIAL_SPLICE

MA4_22R	Chr15	63991133	C	T	0.068181818	HERC1	ENST00000443617_r73	c.4699 G>A	p.D1567N	MISSENSE
MA4_22R	Chr15	64427004	G	A	0.366666667	SNX1	ENST00000261889_r73	c.1363 G>A	p.E455K	MISSENSE
MA4_22R	Chr15	65255961	C	A	0.166666667	SPG21	ENST00000204566_r73	c.927 G>T	p.*309Y	STOP-LOST
MA4_22R	Chr15	65822990	G	C	0.071428571	PTPLAD1	ENST00000261875_r73	c.21 G>C	p.T7T	SILENT
MA4_22R	Chr15	66206091	G	A	0.212121212	MEGF11	ENST00000409699_r73	c.2694 C>T	p.T898T	SILENT
MA4_22R	Chr15	67681345	G	A	0.078947368	IQCH	ENST00000335894_r73	Exon 12 1 G>A	-	ESSENTIAL_SPLICE
MA4_22R	Chr11	71715718	G	T	0.146341463	NUMA1	ENST00000393695_r73	c.5974 C>A	p.L1992I	MISSENSE
MA4_22R	Chr11	82443907	C	T	0.169491525	FAM181B	ENST00000329203_r73	c.865 G>A	p.V289M	MISSENSE
MA4_22R	Chr11	82893483	G	T	0.11627907	PCF11	ENST00000298281_r73	c.4366 G>T	p.E1456*	NONSENSE
MA4_22R	Chr11	85623719	C	T	0.055900621	CCDC83	ENST00000280245_r73	c.822 C>T	p.T274T	SILENT
MA4_22R	Chr11	110450184	G	T	0.108910891	ARHGAP20	ENST00000260283_r73	c.3486 C>A	p.S1162R	MISSENSE
MA4_22R	Chr11	116707031	C	T	0.0625	APOA1	ENST00000375320_r73	c.297 G>A	p.L99L	SILENT
MA4_22R	Chr11	117985906	C	T	0.058394161	TMPRSS4	ENST00000534111_r73	c.1057 C>T	p.R353W	MISSENSE
MA4_22R	Chr11	120176362	G	A	0.285714286	POU2F3	ENST00000260264_r73	c.643 G>A	p.G215R	MISSENSE
MA4_22R	Chr11	126110873	G	A	0.051851852	FAM118B	ENST00000533050_r73	c.273 G>A	p.Q91Q	SILENT
MA4_22R	Chr11	129727330	C	T	0.555555556	TMEM45B	ENST00000281441_r73	c.693 C>T	p.A231A	SILENT
MA4_22R	Chr21	27462366	G	A	0.64	APP	ENST00000346798_r73	c.248 C>T	p.T83I	MISSENSE
MA4_22R	Chr21	41684028	T	A	0.081967213	DSCAM	ENST00000400454_r73	c.2042 A>T	p.Q681L	MISSENSE
MA4_22R	Chr21	43531640	C	T	0.055214724	UMODL1	ENST00000400427_r73	c.2092 C>T	p.P698S	MISSENSE
MA4_22R	Chr21	45089798	G	A	0.1	RRP1B	ENST00000340648_r73	c.164 G>A	p.W55*	NONSENSE
MA4_22R	Chr21	45563146	T	A	0.106796117	C21orf33	ENST00000291577_r73	c.581 T>A	p.V194E	MISSENSE
MA4_22R	Chr21	47531483	C	T	0.227027027	COL6A2	ENST00000300527_r73	c.93 C>T	p.T31T	SILENT
MA4_22R	Chr7	1785228	C	T	0.24516129	ELFN1	ENST00000424383_r73	c.996 C>T	p.T332T	SILENT
MA4_22R	Chr15	74336773	G	A	0.075757576	PML	ENST00000268058_r73	c.2073 G>A	p.L691L	SILENT
MA4_22R	Chr15	75499024	C	T	0.060150376	C15orf39	ENST00000360639_r73	c.635 C>T	p.P212L	MISSENSE
MA4_22R	Chr15	76587987	G	A	0.061728395	ETFA	ENST00000557943_r73	c.131 C>T	p.A44V	MISSENSE
MA4_22R	Chr15	84651111	G	A	0.051470588	ADAMTSL3	ENST00000286744_r73	c.2731 G>A	p.E911K	MISSENSE
MA4_22R	Chr15	89444866	C	T	0.097087379	MFGE8	ENST00000268151_r73	c.786 G>A	p.W262*	NONSENSE
MA4_22R	Chr15	91303904	C	T	0.051282051	BLM	ENST00000355112_r73	c.1301 C>T	p.S434L	MISSENSE
MA4_22R	Chr15	99701968	G	A	0.0625	TTC23	ENST00000394132_r73	c.970 C>T	p.L324L	SILENT
MA4_22R	Chr20	2097332	G	T	0.170731707	STK35	ENST00000381482_r73	c.913 G>T	p.A305S	MISSENSE
MA4_22R	Chr20	2321189	G	A	0.055555556	TGM3	ENST00000381458_r73	c.2044 G>A	p.A682T	MISSENSE
MA4_22R	Chr20	2841651	C	T	0.055045872	VPS16	ENST00000380445_r73	c.666 C>T	p.F222F	SILENT
MA4_22R	Chr20	3759095	C	T	0.067567568	SPEF1	ENST00000379756_r73	c.576 G>A	p.E192E	SILENT
MA4_22R	Chr20	5166403	G	A	0.051020408	CDS2	ENST00000460006_r73	Exon 9 - 1 G>A	-	ESSENTIAL_SPLICE
MA4_22R	Chr20	16387048	C	T	0.053475936	KIF16B	ENST00000354981_r73	c.1666 G>A	p.E556K	MISSENSE
MA4_22R	Chr20	25002122	G	A	0.607843137	ACSS1	ENST00000323482_r73	c.1011 C>T	p.I337I	SILENT

MA4_22R	Chr20	31044159	G	C	0.065789474	C20orf112	ENST00000359676_r73	c.149 C>G	p.S50C	MISSENSE
MA4_22R	Chr20	33519918	G	T	0.101010101	GSS	ENST00000216951_r73	c.853 C>A	p.L285M	MISSENSE
MA4_22R	Chr20	35125427	C	G	0.095238095	DLGAP4	ENST00000373913_r73	c.1968 C>G	p.P656P	SILENT
MA4_22R	Chr20	37137733	A	T	0.066455696	RALGAPB	ENST00000262879_r73	c.754 A>T	p.T252S	MISSENSE
MA4_22R	Chr20	37137734	C	T	0.052307692	RALGAPB	ENST00000262879_r73	c.755 C>T	p.T252I	MISSENSE
MA4_22R	Chr20	42907808	G	A	0.115789474	GDAP1L1	ENST00000342560_r73	c.972 G>A	p.S324S	SILENT
MA4_22R	Chr20	44180783	C	T	0.051792829	WFDC8	ENST00000357199_r73	c.608 G>A	p.R203H	MISSENSE
MA4_22R	Chr20	44515285	C	A	0.101123596	SPATA25	ENST00000372519_r73	c.555 G>T	p.M185I	MISSENSE
MA4_22R	Chr20	45174777	C	A	0.111111111	OCSTAMP	ENST00000279028_r73	c.236 G>T	p.G79V	MISSENSE
MA4_22R	Chr20	45192082	C	T	0.054945055	SLC13A3	ENST00000279027_r73	c.1603 G>A	p.A535T	MISSENSE
MA4_22R	Chr20	46279756	C	T	0.72	NCOA3	ENST00000372004_r73	c.3670 C>T	p.Q1224*	NONSENSE
MA4_22R	Chr20	52774123	G	A	0.057971015	CYP24A1	ENST00000216862_r73	c.1238 C>T	p.T413I	MISSENSE
MA4_22R	Chr20	57466842	G	T	0.103448276	GNAS	ENST00000371095_r73	c.61 G>T	p.E21*	NONSENSE
MA4_22R	Chr20	58567563	G	A	0.363013699	CDH26	ENST00000348616_r73	c.1414 G>A	p.A472T	MISSENSE
MA4_22R	Chr20	61537367	G	A	0.082352941	DIDO1	ENST00000395343_r73	c.1460 C>T	p.A487V	MISSENSE
MA4_22R	Chr4	677412	C	T	0.103896104	MFSD7	ENST00000322224_r73	c.979 G>A	p.V327M	MISSENSE
MA4_22R	Chr4	737326	G	A	0.06185567	PCGF3	ENST00000362003_r73	c.327 G>A	p.K109K	SILENT
MA4_22R	Chr4	3184176	C	A	0.101694915	HTT	ENST00000355072_r73	c.4845 C>A	p.L1615L	SILENT
MA4_22R	Chr4	6325146	C	T	0.053846154	PPP2R2C	ENST00000335585_r73	c.1227 G>A	p.L409L	SILENT
MA4_22R	Chr8	8749575	G	A	0.066037736	MFHAS1	ENST00000276282_r73	c.994 C>T	p.R332C	MISSENSE
MA4_22R	Chr8	12879165	C	T	0.06884058	KIAA1456	ENST00000524591_r73	c.977 C>T	p.A326V	MISSENSE
MA4_22R	Chr8	25191643	A	C	0.240963855	DOCK5	ENST00000276440_r73	c.2123 A>C	p.K708T	MISSENSE
MA4_22R	Chr8	28991612	G	C	0.082352941	KIF13B	ENST00000524189_r73	c.2729 C>G	p.S910C	MISSENSE
MA4_22R	Chr8	33310939	C	T	0.223880597	FUT10	ENST00000327671_r73	c.171 G>A	p.T57T	SILENT
MA4_22R	Chr8	38684879	C	T	0.057377049	TACC1	ENST00000520615_r73	c.1061 C>T	p.S354L	MISSENSE
MA4_22R	Chr8	40683102	G	T	0.12962963	ZMAT4	ENST00000315769_r73	c.94 C>A	p.H32N	MISSENSE
MA4_22R	Chr8	57354239	G	A	0.088328076	PENK	ENST00000314922_r73	c.396 C>T	p.L132L	SILENT
MA4_22R	Chr8	61767063	C	T	0.06097561	CHD7	ENST00000423902_r73	c.6917 C>T	p.A2306V	MISSENSE
MA4_22R	Chr8	67507825	G	T	0.103896104	MYBL1	ENST00000522677_r73	c.680 C>A	p.P227H	MISSENSE
MA4_22R	Chr8	94746016	G	A	0.271676301	RBM12B	ENST00000399300_r73	c.2623 C>T	p.P875S	MISSENSE
MA4_22R	Chr8	107726089	C	T	0.065573771	OXR1	ENST00000531443_r73	c.1832 C>T	p.P611L	MISSENSE
MA4_22R	Chr8	125094647	C	T	0.285714286	FER1L6	ENST00000522917_r73	c.4339 C>T	p.R1447C	MISSENSE
MA4_22R	Chr8	143618426	G	A	0.4375	BAI1	ENST00000517894_r73	c.3649 G>A	p.G1217S	MISSENSE
MA4_22R	Chr10	14991042	C	G	0.109090909	DCLRE1C	ENST00000378278_r73	c.154 G>C	p.E52Q	MISSENSE
MA4_22R	Chr10	20335922	C	G	0.054421769	PLXDC2	ENST00000377252_r73	c.449 C>G	p.S150C	MISSENSE
MA4_22R	Chr10	38246468	C	T	0.4	ZNF25	ENST00000302609_r73	c.22 G>A	p.V8M	MISSENSE
MA4_22R	Chr10	46967641	C	G	0.121875	SYT15	ENST00000503753_r73	c.436 G>C	p.G146R	MISSENSE

MA4_22R	Chr4	7043158	C	T	0.054901961	CCDC96	ENST00000310085_r73	c.1508 G>A	p.G503D	MISSENSE
MA4_22R	Chr4	20599961	G	A	0.222222222	SLIT2	ENST00000504154_r73	c.3635 G>A	p.R1212Q	MISSENSE
MA4_22R	Chr4	25418062	A	T	0.05982906	ANAPC4	ENST00000315368_r73	c.1917 A>T	p.L639F	MISSENSE
MA4_22R	Chr4	39515714	C	T	0.0875	UGDH	ENST00000316423_r73	c.253 G>A	p.V85I	MISSENSE
MA4_22R	Chr4	48517088	C	T	0.063063063	FRYL	ENST00000503238_r73	c.7894 G>A	p.E2632K	MISSENSE
MA4_22R	Chr4	53610954	C	T	0.051724138	ERVMER34-1	ENST00000443173_r73	c.734 G>A	p.R245H	MISSENSE
MA4_22R	Chr4	54348015	C	T	0.054545455	LNX1	ENST00000306888_r73	c.1069 G>A	p.E357K	MISSENSE
MA4_22R	Chr4	56322146	C	T	0.097222222	CLOCK	ENST00000309964_r73	c.900 G>A	p.L300L	SILENT
MA4_22R	Chr4	57798031	C	G	0.055214724	REST	ENST00000309042_r73	c.3007 C>G	p.Q1003E	MISSENSE
MA4_22R	Chr4	70078419	C	A	0.127272727	UGT2B11	ENST00000446444_r73	c.742 G>T	p.E248*	NONSENSE
MA4_22R	Chr4	70723328	T	G	0.307692308	SULT1E1	ENST00000226444_r73	c.35 A>C	p.E12A	MISSENSE
MA4_22R	Chr4	71701903	A	T	0.245901639	GRSF1	ENST00000254799_r73	c.486 T>A	p.T162T	SILENT
MA4_22R	Chr4	85656218	G	T	0.102040816	WDFY3	ENST00000295888_r73	c.6971 C>A	p.T2324K	MISSENSE
MA4_22R	Chr4	88987031	G	A	0.058139535	PKD2	ENST00000237596_r73	c.2358 G>A	p.R786R	SILENT
MA4_22R	Chr4	90856145	A	T	0.058536585	MMRN1	ENST00000394980_r73	c.1314 A>T	p.A438A	SILENT
MA4_22R	Chr4	100532313	C	T	0.321428571	MTTP	ENST00000265517_r73	c.1783 C>T	p.R595*	NONSENSE
MA4_22R	Chr4	110670734	A	G	0.072072072	CFI	ENST00000394634_r73	c.965 T>C	p.L322S	MISSENSE
MA4_22R	Chr4	113541204	C	T	0.061728395	C4orf21	ENST00000505019_r73	c.305 G>A	p.G102D	MISSENSE
MA4_22R	Chr4	123280818	T	A	0.065217391	KIAA1109	ENST00000264501_r73	c.14742 T>A	p.Y4914*	NONSENSE
MA4_22R	Chr4	124323268	G	A	0.111111111	SPRY1	ENST00000339241_r73	c.522 G>A	p.L174L	SILENT
MA4_22R	Chr4	129812279	G	A	0.060606061	SCLT1	ENST00000281142_r73	c.1843 C>T	p.R615*	NONSENSE
MA4_22R	Chr4	148595015	T	A	0.050761421	PRMT10	ENST00000322396_r73	c.349 A>T	p.R117W	MISSENSE
MA4_22R	Chr4	148653548	C	T	0.060301508	ARHGAP10	ENST00000336498_r73	c.96 C>T	p.T32T	SILENT
MA4_22R	Chr4	153247366	C	T	0.351851852	FBXW7	ENST00000281708_r73	c.1436 G>A	p.R479Q	MISSENSE
MA4_22R	Chr4	186560180	G	A	0.076923077	SORBS2	ENST00000437304_r73	c.1231 C>T	p.P411S	MISSENSE
MA4_22R	Chr10	50151445	A	T	0.070422535	WDFY4	ENST00000325239_r73	c.7700 A>T	p.Y2567F	MISSENSE
MA4_22R	Chr10	65379496	C	G	0.057777778	REEP3	ENST00000373758_r73	c.647 C>G	p.T216R	MISSENSE
MA4_22R	Chr10	69961725	C	G	0.053097345	MYPN	ENST00000358913_r73	c.3633 C>G	p.T1211T	SILENT
MA4_22R	Chr10	70243256	C	T	0.051282051	SLC25A16	ENST00000265870_r73	c.932 G>A	p.C311Y	MISSENSE
MA4_22R	Chr10	74953307	C	G	0.344262295	FAM149B1	ENST00000242505_r73	c.498 C>G	p.S166S	SILENT
MA4_22R	Chr10	75283499	A	T	0.054945055	USP54	ENST00000339859_r73	c.2204 T>A	p.I735K	MISSENSE
MA4_22R	Chr10	88703086	G	A	0.059782609	MMRN2	ENST00000372027_r73	c.1455 C>T	p.L485L	SILENT
MA4_22R	Chr10	96341107	G	T	0.11627907	HELLS	ENST00000348459_r73	c.1057 G>T	p.V353L	MISSENSE
MA4_22R	Chr10	101590588	G	A	0.06741573	ABCC2	ENST00000370449_r73	c.2863 G>A	p.E955K	MISSENSE
MA4_22R	Chr10	102763678	C	T	0.179775281	LZTS2	ENST00000370223_r73	c.823 C>T	p.R275W	MISSENSE
MA4_22R	Chr10	105798871	C	T	0.25	COL17A1	ENST00000353479_r73	c.2905 G>A	p.G969S	MISSENSE
MA4_22R	Chr10	111881968	G	A	0.052287582	ADD3	ENST00000360162_r73	c.1061 G>A	p.G354E	MISSENSE

MA4_22R	Chr10	124895854	T	C	0.05982906	HMX3	ENST00000357878_r73	c.288 T>C	p.F96F	SILENT
MA4_22R	Chr10	129913861	C	T	0.194331984	MKI67	ENST00000368654_r73	c.811 G>A	p.A271T	MISSENSE
MA4_22R	Chr10	131958338	G	T	0.108695652	GLRX3	ENST00000331244_r73	Exon 3 5 G>T	-	ESSENTIAL_SPLICE
MA4_22R	Chr19	1005543	C	T	0.415384615	GRIN3B	ENST00000234389_r73	c.2043 C>T	p.H681H	SILENT
MA4_22R	Chr19	2114166	C	T	0.053811659	AP3D1	ENST00000355272_r73	c.2559 G>A	p.E853E	SILENT
MA4_22R	Chr19	2291521	C	T	0.096774194	LINGO3	ENST00000585527_r73	c.255 G>A	p.L85L	SILENT
MA4_22R	Chr19	3542962	C	T	0.063829787	MFSD12	ENST00000398558_r73	c.1434 G>A	p.W478*	NONSENSE
MA4_22R	Chr19	5211657	G	C	0.05	PTPRS	ENST00000587303_r73	c.5178 C>G	p.P1726P	SILENT
MA4_22R	Chr19	11976988	C	G	0.056603774	ZNF439	ENST00000304030_r73	c.17 C>G	p.P6R	MISSENSE
MA4_22R	Chr19	14066781	G	A	0.25	DCAF15	ENST00000254337_r73	c.424 G>A	p.V142I	MISSENSE
MA4_22R	Chr19	16957871	G	A	0.073684211	SIN3B	ENST00000379803_r73	c.673 G>A	p.E225K	MISSENSE
MA4_22R	Chr19	19751255	C	T	0.068376068	GMIP	ENST00000203556_r73	c.364 G>A	p.E122K	MISSENSE
MA4_22R	Chr19	33600873	G	A	0.085714286	GPATCH1	ENST00000170564_r73	c.1536 G>A	p.K512K	SILENT
MA4_22R	Chr19	35610320	G	T	0.139534884	FXYD3	ENST00000604404_r73	c.40 G>T	p.G14C	MISSENSE
MA4_22R	Chr19	37240210	G	C	0.059405941	ZNF850	ENST00000591344_r73	c.1732 C>G	p.Q578E	MISSENSE
MA4_22R	Chr19	39364604	G	A	0.102941177	RINL	ENST00000591812_r73	c.235 C>T	p.P79S	MISSENSE
MA4_22R	Chr19	40842060	T	A	0.058823529	C19orf47	ENST00000582783_r73	c.290 A>T	p.D97V	MISSENSE
MA4_22R	Chr19	41779891	C	T	0.432432432	HNRNPUL1	ENST00000595018_r73	c.277 C>T	p.R93C	MISSENSE
MA4_22R	Chr19	46417691	C	T	0.087301587	NANOS2	ENST00000341294_r73	c.261 G>A	p.V87V	SILENT
MA4_22R	Chr19	48801484	C	A	0.110091743	CCDC114	ENST00000315396_r73	c.1243 G>T	p.E415*	NONSENSE
MA4_22R	Chr19	55994493	G	A	0.085714286	ZNF628	ENST00000598519_r73	c.1933 G>A	p.A645T	MISSENSE
MA4_22R	Chr19	56243463	C	T	0.081395349	NLRP9	ENST00000332836_r73	c.1734 G>A	p.L578L	SILENT
MA4_22R	Chr19	58989159	G	T	0.101265823	ZNF446	ENST00000594369_r73	c.498 G>T	p.V166V	SILENT
MA4_22R	Chr5	1280309	G	A	0.30075188	TERT	ENST00000310581_r73	c.1914 C>T	p.Y638Y	SILENT
MA4_22R	Chr5	31318018	C	T	0.19	CDH6	ENST00000265071_r73	c.1869 C>T	p.I623I	SILENT
MA4_22R	Chr5	41911179	G	A	0.097560976	C5orf51	ENST00000381647_r73	c.384 G>A	p.L128L	SILENT
MA4_22R	Chr5	53815413	G	A	0.051136364	SNX18	ENST00000343017_r73	c.1631 G>A	p.W544*	NONSENSE
MA4_22R	Chr5	64492932	G	A	0.052173913	ADAMTS6	ENST00000381055_r73	c.2622 C>T	p.S874S	SILENT
MA4_22R	Chr5	74026094	G	A	0.2125	GFM2	ENST00000296805_r73	c.1717 C>T	p.R573C	MISSENSE
MA4_22R	Chr5	75914346	G	A	0.05	F2RL2	ENST00000296641_r73	c.186 C>T	p.A62A	SILENT
MA4_22R	Chr5	96341909	A	T	0.096774194	LNPEP	ENST00000231368_r73	c.1918 A>T	p.K640*	NONSENSE
MA4_22R	Chr5	118483009	C	G	0.052631579	DMXL1	ENST00000311085_r73	c.2755 C>G	p.P919A	MISSENSE
MA4_22R	Chr5	124036904	G	C	0.052083333	ZNF608	ENST00000306315_r73	c.965 C>G	p.P322R	MISSENSE
MA4_22R	Chr5	137727662	G	A	0.052631579	KDM3B	ENST00000314358_r73	c.2341 G>A	p.A781T	MISSENSE
MA4_22R	Chr5	140176813	G	A	0.128205128	PCDHA2	ENST00000526136_r73	c.2264 G>A	p.R755Q	MISSENSE
MA4_22R	Chr5	140215289	G	A	0.339622642	PCDHA7	ENST00000525929_r73	c.1321 G>A	p.V441M	MISSENSE
MA4_22R	Chr5	140750726	G	A	0.051546392	PCDHGB3	ENST00000576222_r73	c.765 G>A	p.L255L	SILENT

MA4_22R	Chr5	148407426	C	T	0.090909091	SH3TC2	ENST00000515425_r73	c.1869 G>A	p.G623G	SILENT
MA4_22R	Chr5	149417020	G	C	0.285714286	HMGXB3	ENST00000502717_r73	c.2343 G>C	p.V781V	SILENT
MA4_22R	Chr5	149495412	G	T	0.12962963	PDGFRB	ENST00000261799_r73	c.3235 C>A	p.Q1079K	MISSENSE
MA4_22R	Chr5	157053387	A	T	0.067961165	SOX30	ENST00000265007_r73	c.2223 T>A	p.S741R	MISSENSE
MA4_22R	Chr5	170827164	G	A	0.075268817	NPM1	ENST00000517671_r73	c.532 G>A	p.D178N	MISSENSE
MA4_22R	Chr5	176823783	G	A	0.051546392	SLC34A1	ENST00000324417_r73	c.1224 G>A	p.V408V	SILENT
MA4_22R	Chr5	176827505	G	A	0.063829787	PFN3	ENST00000358571_r73	c.73 C>T	p.H25Y	MISSENSE
MA4_22R	Chr5	180552290	C	T	0.050505051	OR2V1	ENST00000329365_r73	c.15 G>A	p.V5V	SILENT
MA4_22R	Chr7	44714066	G	A	0.114754098	OGDH	ENST00000443864_r73	c.845 G>A	p.G282D	MISSENSE
MA4_22R	Chr7	48314009	C	T	0.063157895	ABCA13	ENST00000435803_r73	c.4746 C>T	p.A1582A	SILENT
MA4_22R	Chr7	56119600	T	A	0.078651685	CCT6A	ENST00000275603_r73	c.59 T>A	p.L20Q	MISSENSE
MA4_22R	Chr7	72718795	G	A	0.113636364	NSUN5	ENST00000428206_r73	c.590 C>T	p.A197V	MISSENSE
MA4_22R	Chr7	75051365	G	A	0.161290323	POM121C	ENST00000453279_r73	c.2170 C>T	p.P724S	MISSENSE
MA4_22R	Chr7	76952988	C	T	0.052238806	GSAP	ENST00000257626_r73	c.1899 G>A	p.M633I	MISSENSE
MA4_22R	Chr7	81964550	T	C	0.095238095	CACNA2D1	ENST00000356860_r73	c.195 A>G	p.Q65Q	SILENT
MA4_22R	Chr7	83634702	C	T	0.115853659	SEMA3A	ENST00000265362_r73	c.1313 G>A	p.R438Q	MISSENSE
MA4_22R	Chr7	86823157	G	A	0.05	DMTF1	ENST00000331242_r73	c.1767 G>A	p.L589L	SILENT
MA4_22R	Chr7	87195400	C	T	0.05	ABCB1	ENST00000265724_r73	c.688 G>A	p.A230T	MISSENSE
MA4_22R	Chr7	89856763	C	G	0.25	STEAP2	ENST00000287908_r73	c.971 C>G	p.P324R	MISSENSE
MA4_22R	Chr7	93055777	G	T	0.10619469	CALCR	ENST00000394441_r73	c.1316 C>A	p.P439Q	MISSENSE
MA4_22R	Chr7	97847329	G	T	0.107142857	TECPR1	ENST00000447648_r73	c.3183 C>A	p.I1061I	SILENT
MA4_22R	Chr7	98957229	C	T	0.077586207	ARPC1A	ENST00000262942_r73	c.851 C>T	p.S284F	MISSENSE
MA4_22R	Chr7	99711864	T	A	0.074324324	TAF6	ENST00000437822_r73	c.80 A>T	p.H27L	MISSENSE
MA4_22R	Chr7	121651144	C	T	0.06918239	PTPRZ1	ENST00000393386_r73	c.2044 C>T	p.R682C	MISSENSE
MA4_22R	Chr7	124503458	C	T	0.052083333	POT1	ENST00000357628_r73	c.492 G>A	p.L164L	SILENT
MA4_22R	Chr7	128415200	T	A	0.1	OPN1SW	ENST00000249389_r73	c.361 A>T	p.T121S	MISSENSE
MA4_22R	Chr7	132973690	G	T	0.108695652	EXOC4	ENST00000393161_r73	c.291 G>T	p.L97L	SILENT
MA4_22R	Chr7	144095425	G	T	0.103092784	NOBOX	ENST00000483238_r73	c.1628 C>A	p.P543Q	MISSENSE
MA4_22R	Chr7	150779363	C	T	0.053571429	TMUB1	ENST00000297533_r73	c.288 G>A	p.P96P	SILENT
MA4_22R	Chr2	9580763	C	A	0.111111111	CPSF3	ENST00000238112_r73	c.904 C>A	p.P302T	MISSENSE
MA4_22R	Chr2	15644291	T	A	0.059288538	NBAS	ENST00000281513_r73	c.932 A>T	p.Y311F	MISSENSE
MA4_22R	Chr2	23785338	C	T	0.5	KLHL29	ENST00000486442_r73	c.272 C>T	p.A91V	MISSENSE
MA4_22R	Chr2	31570446	G	A	0.538461539	XDH	ENST00000379416_r73	c.3218 C>T	p.P1073L	MISSENSE
MA4_22R	Chr2	32828115	G	T	0.13559322	BIRC6	ENST00000421745_r73	c.14035 G>T	p.E4679*	NONSENSE
MA4_22R	Chr2	43924331	C	T	0.055555556	PLEKHH2	ENST00000282406_r73	c.524 C>T	p.S175F	MISSENSE
MA4_22R	Chr2	48602394	C	T	0.057471264	FOXN2	ENST00000340553_r73	c.1108 C>T	p.Q370*	NONSENSE
MA4_22R	Chr2	49295382	G	A	0.095238095	FSHR	ENST00000406846_r73	c.200 C>T	p.S67L	MISSENSE

MA4_22R	Chr2	54148234	C	T	0.678571429	PSME4	ENST00000404125_r73	c.2054 G>A	p.R685Q	MISSENSE
MA4_22R	Chr2	55096480	G	T	0.115384615	EML6	ENST00000356458_r73	c.2214 G>T	p.V738V	SILENT
MA4_22R	Chr2	55566693	G	C	0.10619469	CCDC88A	ENST00000336838_r73	c.1425 C>G	p.T475T	SILENT
MA4_22R	Chr2	56145080	G	C	0.054545455	EFEMP1	ENST00000394555_r73	c.237 C>G	p.V79V	SILENT
MA4_22R	Chr2	61541776	C	T	0.054794521	USP34	ENST00000398571_r73	c.3486 G>A	p.M1162I	MISSENSE
MA4_22R	Chr2	70486562	G	T	0.106382979	PCYOX1	ENST00000433351_r73	c.183 G>T	p.V61V	SILENT
MA4_22R	Chr2	71631089	A	T	0.05511811	ZNF638	ENST00000264447_r73	c.2919 A>T	p.S973S	SILENT
MA4_22R	Chr2	73989867	G	T	0.118644068	DUSP11	ENST00000272444_r73	c.1055 C>A	p.A352E	MISSENSE
MA4_22R	Chr2	74709640	G	A	0.068181818	CCDC142	ENST00000290418_r73	c.325 C>T	p.R109*	NONSENSE
MA4_22R	Chr2	74902895	C	T	0.059405941	SEMA4F	ENST00000357877_r73	c.1502 C>T	p.S501F	MISSENSE
MA4_22R	Chr2	84774741	G	A	0.056962025	DNAH6	ENST00000237449_r73	Exon 6 5 G>A	-	ESSENTIAL_SPLICE
MA4_22R	Chr2	86847448	C	T	0.049586777	CHMP3	ENST00000439940_r73	Exon 3 5 G>A	-	ESSENTIAL_SPLICE
MA4_22R	Chr2	86847448	C	T	0.049586777	RNF103-CHMP3	ENST00000604011_r73	Exon 3 5 G>A	-	ESSENTIAL_SPLICE
MA4_22R	Chr2	86847448	C	T	0.049586777	RNF103	ENST00000237455_r73	Exon 2 5 G>A	-	ESSENTIAL_SPLICE
MA4_22R	Chr2	86847448	C	T	0.049586777	CHMP3	ENST00000439940_r73	Exon 3 5 G>A	-	ESSENTIAL_SPLICE
MA4_22R	Chr2	87017571	C	T	0.265151515	CD8A	ENST00000352580_r73	c.283 G>A	p.G95R	MISSENSE
MA4_22R	Chr2	88387471	C	T	0.386363636	SMYD1	ENST00000419482_r73	c.405 C>T	p.H135H	SILENT
MA4_22R	Chr2	102793049	C	T	0.248275862	IL1R1	ENST00000410023_r73	c.1540 C>T	p.R514C	MISSENSE
MA4_22R	Chr2	105473338	G	A	0.294797688	POU3F3	ENST00000361360_r73	c.1370 G>A	p.R457Q	MISSENSE
MA4_22R	Chr2	128339485	G	A	0.27027027	MYO7B	ENST00000409816_r73	c.1100 G>A	p.R367Q	MISSENSE
MA4_22R	Chr2	130910208	G	T	0.12195122	SMPD4	ENST00000351288_r73	c.2434 C>A	p.L812M	MISSENSE
MA4_22R	Chr2	133618104	G	A	0.050632911	NCKAP5	ENST00000409261_r73	c.768 C>T	p.F256F	SILENT
MA4_22R	Chr2	135308203	C	T	0.317460318	TMEM163	ENST00000281924_r73	c.396 G>A	p.S132S	SILENT
MA4_22R	Chr2	160801458	G	A	0.079096045	PLA2R1	ENST00000283243_r73	c.4103 C>T	p.P1368L	MISSENSE
MA4_22R	Chr2	162280208	G	A	0.34	TBR1	ENST00000389554_r73	c.1519 G>A	p.A507T	MISSENSE
MA4_22R	Chr2	167108340	C	T	0.061728395	SCN9A	ENST00000409672_r73	c.3374 G>A	p.G1125E	MISSENSE
MA4_22R	Chr2	171055777	C	T	0.061068702	MYO3B	ENST00000409044_r73	c.62 C>T	p.P21L	MISSENSE
MA4_22R	Chr2	179429213	G	A	0.314285714	TTN	ENST00000342992_r73	c.73942 C>T	p.R24648C	MISSENSE
MA4_22R	Chr2	179480116	G	A	0.067039106	TTN	ENST00000342992_r73	c.40852 C>T	p.R13618C	MISSENSE
MA4_22R	Chr2	190436555	T	G	0.055555556	SLC40A1	ENST00000261024_r73	c.400 A>C	p.I134L	MISSENSE
MA4_22R	Chr2	192255067	C	T	0.05952381	MYO1B	ENST00000339514_r73	c.1831 C>T	p.L611L	SILENT
MA4_22R	Chr2	198570371	C	T	0.056074766	MARS2	ENST00000282276_r73	c.242 C>T	p.P81L	MISSENSE
MA4_22R	Chr2	202248908	C	T	0.256281407	TRAK2	ENST00000332624_r73	c.1995 G>A	p.S665S	SILENT
MA4_22R	Chr2	204009852	G	A	0.06993007	NBEAL1	ENST00000449802_r73	c.5186 G>A	p.R1729Q	MISSENSE
MA4_22R	Chr2	206588620	G	A	0.063063063	NRP2	ENST00000360409_r73	c.776 G>A	p.G259D	MISSENSE
MA4_22R	Chr2	210561752	C	T	0.103448276	MAP2	ENST00000360351_r73	c.4499 C>T	p.S1500F	MISSENSE
MA4_22R	Chr2	215976355	G	T	0.108695652	ABCA12	ENST00000272895_r73	c.128 C>A	p.T43N	MISSENSE

MA4_22R	Chr2	219487531	G	A	0.057692308	PLCD4	ENST00000450993_r73	c.702 G>A	p.E234E	SILENT
MA4_22R	Chr2	220112400	G	A	0.284671533	STK16	ENST00000409638_r73	c.578 G>A	p.R193Q	MISSENSE
MA4_22R	Chr2	220478944	C	A	0.157894737	STK11IP	ENST00000295641_r73	c.2811 C>A	p.V937V	SILENT
MA4_22R	Chr2	223478577	A	T	0.081081081	FARSB	ENST00000281828_r73	c.1415 T>A	p.L472Q	MISSENSE
MA4_22R	Chr17	3030327	C	G	0.112359551	OR1G1	ENST00000328890_r73	c.519 G>C	p.E173D	MISSENSE
MA4_22R	Chr17	5358516	C	T	0.076271186	DHX33	ENST00000225296_r73	c.1111 G>A	p.D371N	MISSENSE
MA4_22R	Chr17	10317560	C	T	0.054054054	MYH8	ENST00000403437_r73	c.957 G>A	p.G319G	SILENT
MA4_22R	Chr17	10451131	G	A	0.051851852	MYH2	ENST00000245503_r73	c.107 C>T	p.T36I	MISSENSE
MA4_22R	Chr17	19186759	C	T	0.05027933	EPN2	ENST00000314728_r73	c.327 C>T	p.F109F	SILENT
MA4_22R	Chr17	28384857	T	A	0.050314465	EFCAB5	ENST00000536908_r73	c.2361 T>A	p.F787L	MISSENSE
MA4_22R	Chr17	31355390	C	T	0.342857143	ASIC2	ENST00000225823_r73	c.1008 G>A	p.P336P	SILENT
MA4_22R	Chr17	34867273	G	A	0.101449275	MYO19	ENST00000431794_r73	c.916 C>T	p.L306F	MISSENSE
MA4_22R	Chr17	35880734	C	G	0.071428571	SYNRG	ENST00000339208_r73	c.3684 G>C	p.L1228L	SILENT
MA4_22R	Chr17	38711651	C	T	0.076923077	CCR7	ENST00000246657_r73	c.480 G>A	p.Q160Q	SILENT
MA4_22R	Chr17	38927490	T	A	0.071428571	KRT26	ENST00000335552_r73	Exon 2 - 2 A>T	-	ESSENTIAL_SPLICE
MA4_22R	Chr17	39975865	G	A	0.074534162	FKBP10	ENST00000321562_r73	c.1001 G>A	p.C334Y	MISSENSE
MA4_22R	Chr17	39992198	C	T	0.066037736	NT5C3B	ENST00000435506_r73	c.24 G>A	p.L8L	SILENT
MA4_22R	Chr2	239353004	C	T	0.068181818	ASB1	ENST00000264607_r73	c.516 C>T	p.V172V	SILENT
MA4_22R	Chr2	241817491	G	T	0.103092784	AGXT	ENST00000307503_r73	c.995 G>T	p.W332L	MISSENSE
MA4_22R	Chr17	41598785	G	T	0.150943396	DHX8	ENST00000262415_r73	c.3115 G>T	p.E1039*	NONSENSE
MA4_22R	Chr17	44109023	G	A	0.115942029	KANSL1	ENST00000574590_r73	c.3137 C>T	p.P1046L	MISSENSE
MA4_22R	Chr17	46628451	T	C	0.666666667	HOXB3	ENST00000470495_r73	c.541 A>G	p.S181G	MISSENSE
MA4_22R	Chr17	48245917	G	A	0.074766355	SGCA	ENST00000344627_r73	c.568 G>A	p.E190K	MISSENSE
MA4_22R	Chr17	57644084	C	A	0.14893617	DHX40	ENST00000251241_r73	c.209 C>A	p.S70*	NONSENSE
MA4_22R	Chr17	58286188	G	A	0.064220184	USP32	ENST00000300896_r73	c.2600 C>T	p.A867V	MISSENSE
MA4_22R	Chr17	63537574	G	A	0.12244898	AXIN2	ENST00000307078_r73	c.1058 C>T	p.P353L	MISSENSE
MA4_22R	Chr17	73488684	C	T	0.059602649	KIAA0195	ENST00000314256_r73	c.1726 C>T	p.Q576*	NONSENSE
MA4_22R	Chr17	73520492	G	A	0.071428571	TSEN54	ENST00000333213_r73	c.1580 G>A	p.*527*	SILENT
MA4_22R	Chr17	74283314	C	T	0.073770492	QRICH2	ENST00000262765_r73	c.3472 G>A	p.E1158K	MISSENSE
MA4_22R	Chr17	74865120	C	T	0.0625	MGAT5B	ENST00000301618_r73	c.9 C>T	p.T3T	SILENT
MA4_22R	Chr22	17669257	C	T	0.058252427	CECR1	ENST00000399839_r73	c.1053 G>A	p.L351L	SILENT
MA4_22R	Chr22	21119138	T	A	0.063063063	PI4KA	ENST00000255882_r73	c.2675 A>T	p.Y892F	MISSENSE
MA4_22R	Chr22	30925111	C	T	0.058823529	SEC14L6	ENST00000402034_r73	c.627 G>A	p.M209I	MISSENSE
MA4_22R	Chr1	1007257	G	A	0.271428571	RNF223	ENST00000453464_r73	c.690 C>T	p.P230P	SILENT
MA4_22R	Chr1	1168143	G	A	0.483516484	B3GALT6	ENST00000379198_r73	c.485 G>A	p.R162Q	MISSENSE
MA4_22R	Chr1	1960665	C	A	0.101010101	GABRD	ENST00000378585_r73	c.807 C>A	p.F269L	MISSENSE
MA4_22R	Chr1	3683892	G	A	0.068181818	CCDC27	ENST00000294600_r73	c.1626 G>A	p.L542L	SILENT

MA4_22R	Chr1	4772148	G	A	0.561403509	AJAP1	ENST00000378190_r73	c.218 G>A	p.R73Q	MISSENSE
MA4_22R	Chr1	6531080	G	A	0.403508772	PLEKHG5	ENST00000377748_r73	c.1593 C>T	p.R531R	SILENT
MA4_22R	Chr1	11589887	C	T	0.195121951	PTCHD2	ENST00000294484_r73	c.2973 C>T	p.C991C	SILENT
MA4_22R	Chr1	17396656	T	A	0.064102564	PADI2	ENST00000375486_r73	c.1691 A>T	p.Q564L	MISSENSE
MA4_22R	Chr1	24408594	C	T	0.265306122	MYOM3	ENST00000374434_r73	c.2177 G>A	p.R726H	MISSENSE
MA4_22R	Chr22	40042742	C	T	0.077419355	CACNA1I	ENST00000404898_r73	c.1318 C>T	p.Q440*	NONSENSE
MA4_22R	Chr22	50714157	C	T	0.089552239	PLXNB2	ENST00000449103_r73	c.5493 G>A	p.L1831L	SILENT
MA4_22R	Chr22	50714157	C	T	0.089552239	AL022328.1	ENST00000595015_r73	c.55 C>T	p.Q19*	NONSENSE
MA4_22R	Chr1	156509684	G	A	0.051094891	IQGAP3	ENST00000361170_r73	c.2838 C>T	p.S946S	SILENT
MA4_22R	Chr1	158326365	C	T	0.113402062	CD1E	ENST00000368167_r73	c.982 C>T	p.R328W	MISSENSE
MA4_22R	Chr1	158450438	G	A	0.333333333	OR10R2	ENST00000368152_r73	c.771 G>A	p.A257A	SILENT
MA4_22R	Chr1	161165409	C	A	0.108910891	ADAMTS4	ENST00000367996_r73	c.1107 G>T	p.M369I	MISSENSE
MA4_22R	Chr1	162567643	G	A	0.058823529	UAP1	ENST00000367926_r73	c.1420 G>A	p.G474R	MISSENSE
MA4_22R	Chr1	169292461	C	T	0.096491228	NME7	ENST00000472647_r73	c.64 G>A	p.E22K	MISSENSE
MA4_22R	Chr1	169493034	C	T	0.063380282	F5	ENST00000367797_r73	Exon 20 5 G>A	-	ESSENTIAL_SPLICE
MA4_22R	Chr1	172543102	C	A	0.111111111	SUCO	ENST00000263688_r73	c.1121 C>A	p.S374Y	MISSENSE
MA4_22R	Chr1	177245460	C	T	0.053763441	FAM5B	ENST00000361539_r73	c.902 C>T	p.P301L	MISSENSE
MA4_22R	Chr1	179562979	A	G	0.389380531	TDRD5	ENST00000367614_r73	c.617 A>G	p.E206G	MISSENSE
MA4_22R	Chr1	180885344	G	A	0.070175439	KIAA1614	ENST00000367588_r73	c.105 G>A	p.V35V	SILENT
MA4_22R	Chr1	184764692	C	T	0.061643836	FAM129A	ENST00000367511_r73	c.2206 G>A	p.G736R	MISSENSE
MA4_22R	Chr1	190234153	G	A	0.420634921	FAM5C	ENST00000367462_r73	c.460 C>T	p.R154W	MISSENSE
MA4_22R	Chr1	205033551	G	A	0.064516129	CNTN2	ENST00000331830_r73	c.1342 G>A	p.A448T	MISSENSE
MA4_22R	Chr1	223803625	C	T	0.058823529	CAPN8	ENST00000366872_r73	c.1342 G>A	p.G448R	MISSENSE
MA4_22R	Chr1	226127230	G	T	0.135135135	LEFTY2	ENST00000366820_r73	c.568 C>A	p.L190M	MISSENSE
MA4_22R	Chr1	228506816	C	T	0.2125	OBSCN	ENST00000284548_r73	c.14363 C>T	p.T4788M	MISSENSE
MA4_22R	Chr1	232650601	C	G	0.053691275	SIPA1L2	ENST00000366630_r73	c.485 G>C	p.S162T	MISSENSE
MA4_22R	Chr1	232943422	A	T	0.05952381	MAP10	ENST00000418460_r73	c.2653 A>T	p.K885*	NONSENSE
MA4_22R	Chr1	235887462	C	T	0.060240964	LYST	ENST00000389794_r73	c.9181 G>A	p.E3061K	MISSENSE
MA4_22R	Chr11	15199983	GG	-	0.123076923	INSC	ENST00000379554_r73	c.710 GG>-	p.R237fs*10	FRAMESHIFT
MA4_22R	Chr7	26237308	G	-	0.180124224	HNRNPA2B1	ENST00000354667_r73	c.87 C>-	p.S29fs*9	FRAMESHIFT
MA4_22R	Chr7	100001318	G	-	0.185185185	ZCWPW1	ENST00000398027_r73	c.1409 C>-	p.T470fs*41	FRAMESHIFT
MA4_22R	Chr2	43924491	G	-	0.113207547	PLEKHH2	ENST00000282406_r73	c.684 G>-	p.M228fs*16	FRAMESHIFT
MA4_22R	Chr2	73430157	GC	-	0.133333333	NOTO	ENST00000398468_r73	c.363 GC>-	p.L121fs*32	FRAMESHIFT
MA4_22R	Chr2	71160044	T	-	0.125	VAX2	ENST00000234392_r73	c.583 T>-	p.P195fs*9	FRAMESHIFT
MA4_22R	Chr2	113588969	TC	-	0.107142857	IL1B	ENST00000263341_r73	c.496 GA>-	p.E166fs*3	FRAMESHIFT
MA4_22R	Chr2	201399723	TTC	-	0.148148148	SGOL2	ENST00000357799_r73	c.138 TTC>-	p.N46 NS>N	MISSENSE
MA4_22R	Chr2	220412717	CC	-	0.142857143	TMEM198	ENST00000344458_r73	c.656 CC>-	p.A219fs*22	FRAMESHIFT

MA4_22R	Chr2	222291323	AC	-	0.101694915	EPHA4	ENST00000409938_r73	c.2706 GT>-	p.L902fs*7	FRAMESHIFT
MA4_22R	Chr2	238662045	G	-	0.117647059	LRRFIP1	ENST00000308482_r73	c.961 G>-	p.D321fs*3	FRAMESHIFT
MA4_22R	Chr1	22970558	GCT	-	0.176470588	C1QC	ENST00000374640_r73	c.42 GCT>-	p.K14 KL>K	MISSENSE
MA4_22R	Chr1	31899598	C	-	0.102040816	SERINC2	ENST00000373710_r73	c.735 C>-	p.G245fs*112	FRAMESHIFT
MA4_22R	Chr1	150469354	A	-	0.133333333	TARS2	ENST00000369064_r73	c.990 A>-	p.R330fs*6	FRAMESHIFT
MA4_22R	Chr16	22019647	G	-	0.230769231	C16orf52	ENST00000542527_r73	c.25 G>-	p.G9fs*71	FRAMESHIFT
MA4_22R	Chr16	67680870	GC	-	0.117647059	RLTPR	ENST00000334583_r73	c.605 GC>-	p.G202fs*30	FRAMESHIFT
MA4_22R	Chr16	68026446	T	-	0.142857143	DPEP2	ENST00000393847_r73	c.357 A>-	p.L119fs*51	FRAMESHIFT
MA4_22R	Chr13	51929241	T	-	0.107526882	SERPINE3	ENST00000521255_r73	c.962 T>-	p.L321fs*9	FRAMESHIFT
MA4_22R	Chr6	38743571	G	-	0.148148148	DNAH8	ENST00000449981_r73	c.1806 G>-	p.L602fs*6	FRAMESHIFT
MA4_22R	ChrX	13792720	TG	-	0.107142857	GPM6B	ENST00000454189_r73	c.683 CA>-	p.T228fs*2	FRAMESHIFT
MA4_22R	ChrX	47918404	C	-	0.125	ZNF630	ENST00000409324_r73	c.1427 G>-	p.G476fs*59	FRAMESHIFT
MA4_22R	ChrX	50654097	C	-	0.153846154	BMP15	ENST00000252677_r73	c.314 C>-	p.A105fs*26	FRAMESHIFT
MA4_22R	ChrX	53588762	CC	-	0.12	HUWE1	ENST00000342160_r73	c.7461 GG>-	p.R2487fs*3	FRAMESHIFT
MA4_22R	ChrX	99941061	T	-	0.1	SYTL4	ENST00000372989_r73	c.1375 A>-	p.G459fs*45	FRAMESHIFT
MA4_22R	ChrX	104728339	C	-	0.127659575	IL1RAPL2	ENST00000372582_r73	c.732 C>-	p.F244fs*10	FRAMESHIFT
MA4_22R	ChrX	106229235	T	-	0.113207547	MORC4	ENST00000355610_r73	c.504 A>-	p.I168fs*11	FRAMESHIFT
MA4_22R	ChrX	117695409	TA	-	0.121212121	DOCK11	ENST00000276202_r73	c.622 TA>-	p.Y208fs*1	FRAMESHIFT
MA4_22R	ChrX	131211974	CA	-	0.126984127	FRMD7	ENST00000298542_r73	c.2070 TG>-	p.D690fs*11	FRAMESHIFT
MA4_22R	Chr3	9989580	CG	-	0.153846154	PRRT3	ENST00000295984_r73	c.1276 CG>-	p.R426fs*225	FRAMESHIFT
MA4_22R	Chr3	11372865	GCCGGGA	-	0.100628931	ATG7	ENST00000446450_r73	c.613 GCCGGGA>-	p.P205fs*420	FRAMESHIFT
MA4_22R	Chr3	52538052	GC	-	0.106666667	STAB1	ENST00000321725_r73	c.1031 GC>-	p.C344fs*1	FRAMESHIFT
MA4_22R	Chr9	38068159	AG	-	0.115384615	RP11-613M10.9	ENST00000540557_r73	c.483 CT>-	p.L161fs*84	FRAMESHIFT
MA4_22R	Chr9	38068159	AG	-	0.115384615	SHB	ENST00000377707_r73	c.483 CT>-	p.L161fs*84	FRAMESHIFT
MA4_22R	Chr9	140329682	A	-	0.115384615	ENTPD8	ENST00000344119_r73	c.1159 T>-	p.W387fs*23	FRAMESHIFT
MA4_22R	Chr12	33592372	A	-	0.123076923	SYT10	ENST00000228567_r73	c.86 T>-	p.V29fs*29	FRAMESHIFT
MA4_22R	Chr12	64062132	G	-	0.113207547	DPY19L2	ENST00000324472_r73	c.42 C>-	p.S14fs*20	FRAMESHIFT
MA4_22R	Chr12	102591411	T	-	0.115384615	PMCH	ENST00000329406_r73	c.138 A>-	p.K46fs*29	FRAMESHIFT
MA4_22R	Chr12	108133240	C	-	0.125	PRDM4	ENST00000228437_r73	c.2013 G>-	p.E671fs*42	FRAMESHIFT
MA4_22R	Chr12	121678328	-	TT	0.12195122	CAMKK2	ENST00000392474_r73	c.1614 ->AA	p.K538fs*7	FRAMESHIFT
MA4_22R	Chr14	95909596	C	-	0.103896104	SYNE3	ENST00000334258_r73	c.1807 G>-	p.A603fs*64	FRAMESHIFT
MA4_22R	Chr15	42164605	TGGT	-	0.117647059	SPTBN5	ENST00000320955_r73	c.5057 ACCA>-	p.D1686fs*44	FRAMESHIFT
MA4_22R	Chr4	6037696	CT	-	0.111111111	JAKMIP1	ENST00000409021_r73	c.2313 AG>-	p.R771fs*72	FRAMESHIFT
MA4_22R	Chr19	10096537	G	-	0.166666667	COL5A3	ENST00000264828_r73	c.2387 C>-	p.P796fs*19	FRAMESHIFT
MA4_22R	Chr19	17337584	G	-	0.24	OCEL1	ENST00000215061_r73	c.152 G>-	p.C51fs*106	FRAMESHIFT
MA4_22R	Chr19	56154064	T	-	0.166666667	ZNF580	ENST00000325333_r73	c.190 T>-	p.T64fs*127	FRAMESHIFT
MA4_22R	Chr10	33017914	A	-	0.181818182	C10orf68	ENST00000302316_r73	c.689 A>-	p.E230fs*8	FRAMESHIFT

MA4_22R	Chr5	61833074	A	-	0.136986301	IPO11	ENST00000325324_r73	c.2208 A>-	p.L736fs*23	FRAMESHIFT
MA4_22R	Chr5	72183033	A	-	0.117647059	TNPO1	ENST00000337273_r73	c.1287 A>-	p.L429fs*12	FRAMESHIFT
MA4_22R	Chr5	98109796	TC	-	0.130434783	RGMB	ENST00000308234_r73	c.145 TC>-	p.S49fs*10	FRAMESHIFT
MA4_23	Chr18	43311053	C	T	0.143349807	SLC14A1	ENST00000321925_r73	c.225 C>T	p.P75P	SILENT
MA4_23	Chr19	6374247	C	G	0.474226804	ALKBH7	ENST00000245812_r73	c.238 C>G	p.R80G	MISSENSE
MA4_23	Chr19	40900136	G	A	0.705932932	PRX	ENST00000324001_r73	c.4123 C>T	p.R1375W	MISSENSE
MA4_23	Chr6	63921655	T	C	0.006410997	FKBP1C	ENST00000370659_r73	c.194 T>C	p.V65A	MISSENSE
MA4_23	Chr7	100275000	G	A	0.049090909	GNB2	ENST00000303210_r73	c.229 G>A	p.G77R	MISSENSE
MA4_23	Chr20	57571837	C	T	0.4588161	CTSZ	ENST00000217131_r73	c.658 G>A	p.E220K	MISSENSE
MA4_23	Chr1	115258747	C	T	0.06218555	NRAS	ENST00000311936_r73	c.35 G>A	p.G12D	MISSENSE
MA4_23	Chr12	25398284	C	A	0.0203125	KRAS	ENST00000311936_r73	c.437 C>T	p.A146V	MISSENSE
MA4_23	Chr12	25378561	G	A	0.02244898	KRAS	ENST00000369535_r73	c.35 G>A	p.G12D	MISSENSE
MA4_23	Chr12	124856830	C	T	0.424094635	NCOR2	ENST00000405201_r73	c.2545 G>A	p.E849K	MISSENSE
MA4_23	Chr11	58959633	G	A	0.19753824	DTX4	ENST00000227451_r73	c.1284 G>A	p.T428T	SILENT
MA4_23	Chr18	54362417	A	G	0.011690047	WDR7	ENST00000357574_r73	c.1345 A>G	p.M449V	MISSENSE
MA4_23R	Chr1	152188413	C	T	0.134920635	HRNR	ENST00000368801_r73	c.5692 G>A	p.E1898K	MISSENSE
MA4_23R	Chr11	58959633	G	A	0.194152547	DTX4	ENST00000227451_r73	c.1284 G>A	p.T428T	SILENT
MA4_23R	Chr12	124856830	C	T	0.418136171	NCOR2	ENST00000405201_r73	c.2545 G>A	p.E849K	MISSENSE
MA4_23R	Chr13	28597490	C	T	0.186016213	FLT3	ENST00000241453_r73	c.2415 G>A	p.K805K	SILENT
MA4_23R	Chr15	41989003	G	C	0.170652877	MGA	ENST00000566586_r73	c.1795 G>C	p.V599L	MISSENSE
MA4_23R	Chr16	70883694	G	A	0.092937092	HYDIN	ENST00000393567_r73	c.12808 C>T	p.H4270Y	MISSENSE
MA4_23R	Chr16	70937582	G	A	0.094841213	HYDIN	ENST00000393567_r73	c.8795 C>T	p.P2932L	MISSENSE
MA4_23R	Chr18	54362417	A	G	0.181823661	WDR7	ENST00000357574_r73	c.1345 A>G	p.M449V	MISSENSE
MA4_23R	Chr20	17950950	G	A	0.171070534	MGME1	ENST00000377710_r73	c.448 G>A	p.E150K	MISSENSE
MA4_23R	Chr3	49756522	C	T	0.236234458	AMIGO3	ENST00000320431_r73	c.377 G>A	p.R126H	MISSENSE
MA4_23R	Chr3	133368471	A	G	0.219197759	TOPBP1	ENST00000260810_r73	c.1260 T>C	p.H420H	SILENT
MA4_23R	Chr4	10445952	T	C	0.201005025	ZNF518B	ENST00000326756_r73	c.2001 A>G	p.R667R	SILENT
MA4_23R	Chr4	16077351	T	C	0.186183079	PROM1	ENST00000505450_r73	c.179 A>G	p.H60R	MISSENSE
MA4_23R	Chr6	114270153	T	C	0.17850901	HDAC2	ENST00000519065_r73	c.831 A>G	p.L277L	SILENT
MA4_23R	Chr6	117128289	G	C	0.185470706	GPRC6A	ENST00000310357_r73	c.579 C>G	p.F193L	MISSENSE
MA4_23R	Chr8	144994337	G	A	0.235934664	PLEC	ENST00000345136_r73	c.9652 C>T	p.R3218W	MISSENSE
MA4_23R	ChrX	24741351	C	T	0.258435032	POLA1	ENST00000379059_r73	c.1149 C>T	p.I383I	SILENT
MA4_23R	ChrX	35938045	C	T	0.540260608	CXorf22	ENST00000297866_r73	c.129 C>T	p.I43I	SILENT
MA4_23R	ChrX	35969297	G	A	0.528962956	CXorf22	ENST00000297866_r73	c.706 G>A	p.V236M	MISSENSE
MA4_23R	ChrX	44171953	T	C	0.385125184	EFHC2	ENST00000420999_r73	c.92 A>G	p.N31S	MISSENSE
MA4_23R	ChrX	48847497	T	C	0.530505952	GRIPAP1	ENST00000376441_r73	c.483 A>G	p.E161E	SILENT
MA4_23R	ChrX	139038443	G	A	0.254189944	CXorf66	ENST00000370540_r73	c.698 C>T	p.P233L	MISSENSE

MA4_23R	Chr1	152278814	C	T	0.209754681	FLG	ENST00000368799_r73	c.8548 G>A	p.G2850S	MISSENSE
MA4_23R	Chr6	32191659	-	AGC	0.070879242	NOTCH4	ENST00000375023_r73	c.47 ->GCT	p.L16 L>RL	MISSENSE
MA4_23R	ChrX	12937804	C	T	0.532887403	TLR8	ENST00000218032_r73	c.645 C>T	p.H215H	SILENT
MA4_23R	ChrX	12939112	G	C	0.546212396	TLR8	ENST00000218032_r73	c.1953 G>C	p.L651L	SILENT
MA4_23R	ChrX	22291732	C	T	0.553430079	ZNF645	ENST00000323684_r73	c.624 C>T	p.I208I	SILENT
MA4_23R	ChrX	36403036	A	G	0.286539082	CXorf30	ENST00000378657_r73	c.1817 A>G	p.H606R	MISSENSE
MA4_23R	ChrX	135430044	T	C	0.283352557	GPR112	ENST00000394143_r73	c.4179 T>C	p.T1393T	SILENT
MA4_23R	ChrX	16168677	T	C	0.551388889	GRPR	ENST00000380289_r73	c.663 T>C	p.I221I	SILENT
MA4_23R	Chr18	43311053	C	T	0.196078431	SLC14A1	ENST00000321925_r73	c.225 C>T	p.P75P	SILENT
MA4_23R	Chr20	57571837	C	T	0.2951875	CTSZ	ENST00000217131_r73	c.658 G>A	p.E220K	MISSENSE
MA4_23R	ChrX	135430483	T	C	0.26859095	GPR112	ENST00000394143_r73	c.4618 T>C	p.S1540P	MISSENSE
MA4_23R	Chr1	985377	C	T	0.130434783	AGRN	ENST00000379370_r73	c.4839 C>T	p.C1613C	SILENT
MA4_23R	Chr1	989216	C	T	0.290322581	AGRN	ENST00000379370_r73	c.5735 C>T	p.A1912V	MISSENSE
MA4_23R	Chr1	1217690	C	T	0.177777778	SCNN1D	ENST00000379116_r73	c.346 C>T	p.R116W	MISSENSE
MA4_23R	Chr1	2451298	G	A	0.171875	PANK4	ENST00000378466_r73	c.795 C>T	p.L265L	SILENT
MA4_23R	Chr1	11733905	C	T	0.147286822	FBXO6	ENST00000376753_r73	c.879 C>T	p.F293F	SILENT
MA4_23R	Chr1	12248855	G	C	0.248554913	TNFRSF1B	ENST00000376259_r73	c.81 G>C	p.V27V	SILENT
MA4_23R	Chr1	16353911	A	G	0.143884892	CLCNKA	ENST00000375692_r73	c.762 A>G	p.A254A	SILENT
MA4_23R	Chr1	16535487	G	C	0.184210526	ARHGEF19	ENST00000270747_r73	c.63 C>G	p.H21Q	MISSENSE
MA4_23R	Chr1	17603340	C	T	0.163265306	PADI3	ENST00000375460_r73	c.1524 C>T	p.H508H	SILENT
MA4_23R	Chr1	22202483	G	A	0.118811881	HSPG2	ENST00000374695_r73	c.3056 C>T	p.P1019L	MISSENSE
MA4_23R	Chr1	22307376	C	T	0.409090909	CELA3B	ENST00000337107_r73	c.189 C>T	p.I63I	SILENT
MA4_23R	Chr1	25883695	C	T	0.183908046	LDLRAP1	ENST00000374338_r73	c.396 C>T	p.I132I	SILENT
MA4_23R	Chr1	26665873	C	G	0.234042553	AIM1L	ENST00000527815_r73	c.630 G>C	p.K210N	MISSENSE
MA4_23R	Chr1	28206363	G	C	0.285714286	THEMIS2	ENST00000373925_r73	c.444 G>C	p.L148L	SILENT
MA4_23R	Chr1	29475296	G	A	0.196969697	SRSF4	ENST00000373795_r73	c.1111 C>T	p.R371C	MISSENSE
MA4_23R	Chr1	32740366	G	A	0.151515152	LCK	ENST00000336890_r73	c.134 G>A	p.R45Q	MISSENSE
MA4_23R	Chr1	41475187	A	G	0.292307692	CTPS1	ENST00000372621_r73	c.1617 A>G	p.P539P	SILENT
MA4_23R	Chr1	45228266	A	T	0.28125	KIF2C	ENST00000372224_r73	c.1907 A>T	p.E636V	MISSENSE
MA4_23R	Chr1	53569148	C	T	0.096774194	SLC1A7	ENST00000371494_r73	c.567 G>A	p.E189E	SILENT
MA4_23R	Chr1	54060404	G	A	0.288888889	GLIS1	ENST00000312233_r73	c.172 C>T	p.P58S	MISSENSE
MA4_23R	Chr1	79121172	C	T	0.225806452	IFI44	ENST00000370747_r73	c.816 C>T	p.N272N	SILENT
MA4_23R	Chr1	91967341	A	G	0.149350649	CDC7	ENST00000234626_r73	c.68 A>G	p.Q23R	MISSENSE
MA4_23R	Chr1	108697684	C	T	0.152091255	SLC25A24	ENST00000565488_r73	c.743 G>A	p.R248H	MISSENSE
MA4_23R	Chr1	109808448	A	G	0.177419355	CELSR2	ENST00000271332_r73	c.5819 A>G	p.D1940G	MISSENSE
MA4_23R	Chr1	114226447	A	G	0.181818182	MAGI3	ENST00000307546_r73	c.4257 A>G	p.V1419V	SILENT
MA4_23R	Chr1	117120150	G	A	0.136363636	IGSF3	ENST00000369486_r73	c.3369 C>T	p.D1123D	SILENT

MA4_23R	Chr1	143767466	G	A	0.086206897	PPIAL4G	ENST00000419275_r73	c.383 C>T	p.A128V	MISSENSE
MA4_23R	Chr1	144921924	G	A	0.080745342	PDE4DIP	ENST00000313382_r73	c.1303 C>T	p.L435L	SILENT
MA4_23R	Chr1	151810935	G	C	0.14	C2CD4D	ENST00000454109_r73	c.531 C>G	p.A177A	SILENT
MA4_23R	Chr1	152187589	G	A	0.201117318	HRNR	ENST00000368801_r73	c.6516 C>T	p.H2172H	SILENT
MA4_23R	Chr1	152187628	A	G	0.090909091	HRNR	ENST00000368801_r73	c.6477 T>C	p.Y2159Y	SILENT
MA4_23R	Chr1	152188999	G	A	0.120967742	HRNR	ENST00000368801_r73	c.5106 C>T	p.H1702H	SILENT
MA4_23R	Chr1	152190835	G	A	0.258064516	HRNR	ENST00000368801_r73	c.3270 C>T	p.G1090G	SILENT
MA4_23R	Chr1	152190945	C	T	0.407407407	HRNR	ENST00000368801_r73	c.3160 G>A	p.E1054K	MISSENSE
MA4_23R	Chr1	152276699	A	G	0.162962963	FLG	ENST00000368799_r73	c.10663 T>C	p.W3555R	MISSENSE
MA4_23R	Chr1	153967598	G	A	0.20661157	NUP210L	ENST00000368559_r73	c.5445 C>T	p.L1815L	SILENT
MA4_23R	Chr1	155004236	G	A	0.175	DCST2	ENST00000368424_r73	c.553 C>T	p.R185W	MISSENSE
MA4_23R	Chr1	155152310	C	T	0.090909091	TRIM46	ENST00000368382_r73	c.1419 C>T	p.P473P	SILENT
MA4_23R	Chr1	156518453	G	A	0.181818182	IQGAP3	ENST00000361170_r73	c.1913 C>T	p.A638V	MISSENSE
MA4_23R	Chr1	161642985	G	A	0.20754717	FCGR2B	ENST00000236937_r73	c.612 G>A	p.L204L	SILENT
MA4_23R	Chr1	165638548	C	T	0.144329897	ALDH9A1	ENST00000354775_r73	c.1070 G>A	p.R357Q	MISSENSE
MA4_23R	Chr1	166961966	T	C	0.15	MAEL	ENST00000367872_r73	c.369 T>C	p.H123H	SILENT
MA4_23R	Chr1	167962499	G	T	0.140186916	DCAF6	ENST00000367843_r73	c.724 G>T	p.A242S	MISSENSE
MA4_23R	Chr1	192778206	A	G	0.315789474	RGS2	ENST00000235382_r73	c.5 A>G	p.Q2R	MISSENSE
MA4_23R	Chr1	193119478	C	T	0.175257732	CDC73	ENST00000367435_r73	c.873 C>T	p.N291N	SILENT
MA4_23R	Chr1	200613610	T	C	0.12345679	DDX59	ENST00000331314_r73	c.1632 A>G	p.T544T	SILENT
MA4_23R	Chr1	203141167	C	T	0.180327869	MYBPH	ENST00000255416_r73	c.510 G>A	p.E170E	SILENT
MA4_23R	Chr1	207263734	A	T	0.24	C4BPB	ENST00000367078_r73	c.140 A>T	p.Y47F	MISSENSE
MA4_23R	Chr1	209805977	C	T	0.181818182	LAMB3	ENST00000356082_r73	c.773 G>A	p.R258H	MISSENSE
MA4_23R	Chr1	222802152	A	G	0.194444444	MIA3	ENST00000344922_r73	c.1590 A>G	p.G530G	SILENT
MA4_23R	Chr1	247587870	G	A	0.217948718	NLRP3	ENST00000391828_r73	c.1125 G>A	p.E375E	SILENT
MA4_23R	Chr1	247719734	C	T	0.151515152	GCSAML	ENST00000366488_r73	c.55 C>T	p.P19S	MISSENSE
MA4_23R	Chr1	248202474	A	G	0.113861386	OR2L2	ENST00000366479_r73	c.905 A>G	p.Q302R	MISSENSE
MA4_23R	Chr1	248616776	C	T	0.164285714	OR2T2	ENST00000342927_r73	c.678 C>T	p.V226V	SILENT
MA4_23R	Chr10	3141522	G	A	0.333333333	PFKP	ENST00000381125_r73	c.242 G>A	p.S81N	MISSENSE
MA4_23R	Chr10	3143135	G	A	175	PFKP	ENST00000381075_r73	c.183 G>A	p.R61R	SILENT
MA4_23R	Chr10	13672334	A	G	0.106122449	PRPF18	ENST00000378572_r73	c.1023 A>G	p.A341A	SILENT
MA4_23R	Chr10	13672334	A	G	0.106122449	RP11-295P9.3	ENST00000595538_r73	c.98 A>G	p.A33G	MISSENSE
MA4_23R	Chr10	13699231	C	T	0.230769231	FRMD4A	ENST00000357447_r73	c.2358 G>A	p.R786R	SILENT
MA4_23R	Chr10	13702435	C	T	0.183673469	FRMD4A	ENST00000357447_r73	c.1779 G>A	p.Q593Q	SILENT
MA4_23R	Chr10	23319653	T	C	0.135021097	ARMC3	ENST00000298032_r73	c.2174 T>C	p.M725T	MISSENSE
MA4_23R	Chr10	24762184	G	A	0.178947368	KIAA1217	ENST00000376462_r73	c.634 G>A	p.G212R	MISSENSE
MA4_23R	Chr10	32097609	G	A	0.222222222	ARHGAP12	ENST00000311380_r73	c.2178 C>T	p.D726D	SILENT

MA4_23R	Chr10	50667225	C	G	0.157303371	ERCC6	ENST00000355832_r73	c.4118 G>C	p.R1373T	MISSENSE
MA4_23R	Chr10	61835633	G	A	0.182795699	ANK3	ENST00000280772_r73	c.5006 C>T	p.P1669L	MISSENSE
MA4_23R	Chr10	69299372	T	G	0.223214286	CTNNA3	ENST00000433211_r73	c.348 A>C	p.P116P	SILENT
MA4_23R	Chr10	79781312	G	A	0.27027027	POLR3A	ENST00000372371_r73	c.1177 C>T	p.P393S	MISSENSE
MA4_23R	Chr10	82013319	T	G	0.223076923	AL359195.1	ENST00000356374_r73	c.837 T>G	p.F279L	MISSENSE
MA4_23R	Chr10	94223726	A	G	0.196969697	IDE	ENST00000265986_r73	c.2523 T>C	p.N841N	SILENT
MA4_23R	Chr10	105178380	G	A	0.222222222	PDCD11	ENST00000369797_r73	c.2095 G>A	p.E699K	MISSENSE
MA4_23R	Chr10	106075269	G	A	0.25	ITPRIP	ENST00000337478_r73	c.541 C>T	p.R181W	MISSENSE
MA4_23R	Chr10	116853561	G	A	0.23943662	ATRNL1	ENST00000355044_r73	c.52 G>A	p.G18R	MISSENSE
MA4_23R	Chr10	134218641	C	T	0.28	PWWP2B	ENST00000305233_r73	c.637 C>T	p.R213C	MISSENSE
MA4_23R	Chr10	134622089	A	G	0.164705882	TTC40	ENST00000368586_r73	c.7984 T>C	p.W2662R	MISSENSE
MA4_23R	Chr11	5537147	C	G	0.194029851	UBQLNL	ENST00000380184_r73	c.525 G>C	p.M175I	MISSENSE
MA4_23R	Chr11	16838719	C	T	0.16025641	PLEKHA7	ENST00000355661_r73	c.1494 G>A	p.A498A	SILENT
MA4_23R	Chr11	45672170	G	A	0.266055046	CHST1	ENST00000308064_r73	c.304 C>T	p.P102S	MISSENSE
MA4_23R	Chr11	46907712	A	G	0.172839506	LRP4	ENST00000378623_r73	c.2436 T>C	p.D812D	SILENT
MA4_23R	Chr11	55541614	G	T	0.166666667	OR5D13	ENST00000361760_r73	c.701 G>T	p.S234I	MISSENSE
MA4_23R	Chr11	55872749	C	T	0.151394422	OR8H2	ENST00000313503_r73	c.231 C>T	p.V77V	SILENT
MA4_23R	Chr11	57147126	G	A	0.173553719	PRG3	ENST00000287143_r73	c.216 C>T	p.N72N	SILENT
MA4_23R	Chr11	60610065	G	A	0.342342342	CCDC86	ENST00000227520_r73	c.468 G>A	p.P156P	SILENT
MA4_23R	Chr11	62286188	G	A	0.156862745	AHNAK	ENST00000378024_r73	c.15701 C>T	p.P5234L	MISSENSE
MA4_23R	Chr11	62656046	A	C	0.176056338	SLC3A2	ENST00000377890_r73	c.1774 A>C	p.K592Q	MISSENSE
MA4_23R	Chr11	64577243	G	A	0.181818182	MEN1	ENST00000377326_r73	c.339 C>T	p.S113S	SILENT
MA4_23R	Chr11	65359552	A	G	0.141791045	EHBP1L1	ENST00000309295_r73	c.4463 A>G	p.K1488R	MISSENSE
MA4_23R	Chr11	65359552	A	G	0.141791045	AP001362.1	ENST00000597463_r73	c.268 T>C	p.L90L	SILENT
MA4_23R	Chr11	67209515	C	T	0.240963855	CORO1B	ENST00000341356_r73	c.246 G>A	p.T82T	SILENT
MA4_23R	Chr11	73007938	C	T	0.166666667	P2RY6	ENST00000540342_r73	c.375 C>T	p.Y125Y	SILENT
MA4_23R	Chr11	89133530	A	G	0.149122807	NOX4	ENST00000343727_r73	c.792 T>C	p.S264S	SILENT
MA4_23R	Chr11	102482626	T	G	0.174825175	MMP20	ENST00000260228_r73	c.383 A>C	p.K128T	MISSENSE
MA4_23R	Chr11	120980048	C	T	0.191011236	TECTA	ENST00000392793_r73	c.327 C>T	p.G109G	SILENT
MA4_23R	Chr11	120984338	A	G	0.107692308	TECTA	ENST00000392793_r73	c.701 A>G	p.Q234R	MISSENSE
MA4_23R	Chr11	121008285	C	T	0.163793103	TECTA	ENST00000392793_r73	c.3097 C>T	p.R1033W	MISSENSE
MA4_23R	Chr11	121489544	C	T	0.153846154	SORL1	ENST00000260197_r73	c.5666 C>T	p.T1889I	MISSENSE
MA4_23R	Chr11	123753959	G	A	0.157894737	TMEM225	ENST00000375026_r73	c.564 C>T	p.I188I	SILENT
MA4_23R	Chr11	124267056	G	A	0.227799228	OR8B3	ENST00000354597_r73	c.192 C>T	p.F64F	SILENT
MA4_23R	Chr11	128638142	C	T	0.139784946	FLI1	ENST00000429175_r73	c.360 C>T	p.N120N	SILENT
MA4_23R	Chr12	332338	G	A	0.2	SLC6A13	ENST00000343164_r73	c.1374 C>T	p.F458F	SILENT
MA4_23R	Chr12	674540	T	C	0.270833333	NINJ2	ENST00000305108_r73	c.428 A>G	p.K143R	MISSENSE

MA4_23R	Chr12	6640519	G	A	0.260869565	NCAPD2	ENST00000315579_r73	c.4147 G>A	p.E1383K	MISSENSE
MA4_23R	Chr12	7637940	T	C	0.130434783	CD163	ENST00000359156_r73	c.2531 A>G	p.N844S	MISSENSE
MA4_23R	Chr12	11546192	G	A	0.279069767	PRB2	ENST00000389362_r73	c.820 C>T	p.P274S	MISSENSE
MA4_23R	Chr12	51693021	C	T	0.225352113	BIN2	ENST00000267012_r73	c.568 G>A	p.E190K	MISSENSE
MA4_23R	Chr12	52585534	C	T	0.148148148	KRT80	ENST00000313234_r73	c.153 G>A	p.S51S	SILENT
MA4_23R	Chr12	53004526	C	T	0.213333333	KRT73	ENST00000305748_r73	c.1204 G>A	p.A402T	MISSENSE
MA4_23R	Chr12	53200921	C	G	0.179104478	KRT4	ENST00000551956_r73	c.1495 G>C	p.G499R	MISSENSE
MA4_23R	Chr12	53591607	C	T	0.166666667	ITGB7	ENST00000267082_r73	c.330 G>A	p.P110P	SILENT
MA4_23R	Chr12	56748273	G	A	0.175438597	STAT2	ENST00000314128_r73	c.759 C>T	p.H253H	SILENT
MA4_23R	Chr12	58174038	G	C	0.206896552	METTL21B	ENST00000300209_r73	c.290 G>C	p.G97A	MISSENSE
MA4_23R	Chr12	80855816	T	C	0.12962963	PTPRQ	ENST00000266688_r73	c.533 T>C	p.V178A	MISSENSE
MA4_23R	Chr12	95604081	G	A	0.186915888	FGD6	ENST00000343958_r73	c.979 C>T	p.R327C	MISSENSE
MA4_23R	Chr12	101603543	G	A	0.226086957	SLC5A8	ENST00000536262_r73	c.84 C>T	p.I28I	SILENT
MA4_23R	Chr12	106995090	C	T	0.25	RFX4	ENST00000357881_r73	c.36 C>T	p.G12G	SILENT
MA4_23R	Chr12	107713087	C	T	0.175438597	BTBD11	ENST00000280758_r73	c.370 C>T	p.L124L	SILENT
MA4_23R	Chr12	109994854	C	T	0.163636364	MMAB	ENST00000545712_r73	c.732 G>A	p.S244S	SILENT
MA4_23R	Chr12	129308324	C	T	0.191919192	SLC15A4	ENST00000266771_r73	c.165 G>A	p.T55T	SILENT
MA4_23R	Chr12	133634950	A	G	0.172839506	ZNF84	ENST00000539354_r73	c.1649 A>G	p.K550R	MISSENSE
MA4_23R	Chr13	29600208	G	A	0.209876543	MTUS2	ENST00000431530_r73	c.1403 G>A	p.R468Q	MISSENSE
MA4_23R	Chr13	39424254	T	C	0.152173913	FREM2	ENST00000280481_r73	c.6459 T>C	p.T2153T	SILENT
MA4_23R	Chr13	77581658	G	A	0.213483146	FBXL3	ENST00000355619_r73	c.909 C>T	p.F303F	SILENT
MA4_23R	Chr13	96530055	T	C	0.155279503	UGGT2	ENST00000376747_r73	c.3284 A>G	p.Q1095R	MISSENSE
MA4_23R	Chr13	102250542	C	T	0.197916667	ITGBL1	ENST00000376180_r73	c.908 C>T	p.A303V	MISSENSE
MA4_23R	Chr13	103438592	T	C	0.201183432	KDELC1	ENST00000376004_r73	c.1481 A>G	p.H494R	MISSENSE
MA4_23R	Chr14	20404080	T	C	0.148825065	OR4K1	ENST00000285600_r73	c.255 T>C	p.F85F	SILENT
MA4_23R	Chr14	23549380	G	A	0.257575758	ACIN1	ENST00000262710_r73	c.1338 C>T	p.P446P	SILENT
MA4_23R	Chr14	23566949	C	T	0.121212121	C14orf119	ENST00000319074_r73	c.82 C>T	p.P28S	MISSENSE
MA4_23R	Chr14	23861839	G	C	0.190909091	MYH6	ENST00000356287_r73	c.3274 C>G	p.Q1092E	MISSENSE
MA4_23R	Chr14	24769809	G	A	0.194029851	NOP9	ENST00000267425_r73	c.443 G>A	p.S148N	MISSENSE
MA4_23R	Chr14	24911441	G	C	0.183098592	SDR39U1	ENST00000399395_r73	c.149 C>G	p.P50R	MISSENSE
MA4_23R	Chr14	45711535	T	G	0.124223603	MIS18BP1	ENST00000310806_r73	c.845 A>C	p.N282T	MISSENSE
MA4_23R	Chr14	52527005	T	C	0.277777778	NID2	ENST00000216286_r73	c.604 A>G	p.N202D	MISSENSE
MA4_23R	Chr14	57858186	G	A	0.235294118	NAA30	ENST00000556492_r73	c.511 G>A	p.E171K	MISSENSE
MA4_23R	Chr14	59939804	G	A	0.173469388	L3HYPDH	ENST00000247194_r73	c.944 C>T	p.A315V	MISSENSE
MA4_23R	Chr14	63735877	C	T	0.279069767	RHOJ	ENST00000316754_r73	c.228 C>T	p.T76T	SILENT
MA4_23R	Chr14	64488055	A	G	0.161290323	SYNE2	ENST00000344113_r73	c.5174 A>G	p.N1725S	MISSENSE
MA4_23R	Chr14	64954574	G	C	0.161290323	ZBTB25	ENST00000261683_r73	c.375 C>G	p.S125S	SILENT

MA4_23R	Chr14	91113353	G	A	0.25	TTC7B	ENST00000328459_r73	c.1532 C>T	p.S511L	MISSENSE
MA4_23R	Chr14	100934449	G	A	0.154761905	WDR25	ENST00000554998_r73	c.914 G>A	p.R305Q	MISSENSE
MA4_23R	Chr14	105174236	T	C	0.214285714	INF2	ENST00000330634_r73	c.1632 T>C	p.H544H	SILENT
MA4_23R	Chr14	105407977	A	G	0.245283019	AHNAK2	ENST00000333244_r73	c.13811 T>C	p.M4604T	MISSENSE
MA4_23R	Chr14	105411286	G	A	0.125	AHNAK2	ENST00000333244_r73	c.10502 C>T	p.P3501L	MISSENSE
MA4_23R	Chr14	105411287	G	A	0.125	AHNAK2	ENST00000333244_r73	c.10501 C>T	p.P3501S	MISSENSE
MA4_23R	Chr14	106829985	G	A	0.18	IGHV4-34	ENST00000390616_r73	c.61 C>T	p.P21S	MISSENSE
MA4_23R	Chr14	107083424	T	C	0.402173913	IGHV4-59	ENST00000455737_r73	c.180 A>G	p.P60P	SILENT
MA4_23R	Chr14	107179058	G	A	0.133333333	IGHV2-70	ENST00000390634_r73	c.119 C>T	p.T40I	MISSENSE
MA4_23R	Chr15	23006346	T	C	0.270833333	NIPA2	ENST00000337451_r73	c.958 A>G	p.M320V	MISSENSE
MA4_23R	Chr15	30659641	C	T	0.212121212	CHRFAM7A	ENST00000299847_r73	c.700 G>A	p.G234R	MISSENSE
MA4_23R	Chr15	35274130	G	C	0.203703704	ZNF770	ENST00000356321_r73	c.1506 C>G	p.P502P	SILENT
MA4_23R	Chr15	41961191	T	C	0.210884354	MGA	ENST00000566586_r73	c.99 T>C	p.N33N	SILENT
MA4_23R	Chr15	42148796	T	A	0.169491525	SPTBN5	ENST00000320955_r73	c.8809 A>T	p.N2937Y	MISSENSE
MA4_23R	Chr15	43290373	A	G	0.095890411	UBR1	ENST00000290650_r73	c.3750 T>C	p.H1250H	SILENT
MA4_23R	Chr15	48779352	C	T	0.262820513	FBN1	ENST00000316623_r73	c.3509 G>A	p.R1170H	MISSENSE
MA4_23R	Chr15	51830647	T	C	0.303030303	DMXL2	ENST00000251076_r73	c.1108 A>G	p.I370V	MISSENSE
MA4_23R	Chr15	63597969	C	T	0.164705882	APH1B	ENST00000261879_r73	c.763 C>T	p.R255C	MISSENSE
MA4_23R	Chr15	64008623	A	C	0.156862745	HERC1	ENST00000443617_r73	c.4028 T>G	p.F1343C	MISSENSE
MA4_23R	Chr15	73615695	C	T	0.186440678	HCN4	ENST00000261917_r73	c.2739 G>A	p.A913A	SILENT
MA4_23R	Chr15	74277048	C	T	0.202380952	STOML1	ENST00000564777_r73	c.802 G>A	p.V268I	MISSENSE
MA4_23R	Chr15	78393899	A	G	0.146067416	SH2D7	ENST00000328828_r73	c.1304 A>G	p.K435R	MISSENSE
MA4_23R	Chr15	78474907	G	A	0.133333333	ACSBG1	ENST00000258873_r73	c.795 C>T	p.D265D	SILENT
MA4_23R	Chr15	96877696	G	A	0.185185185	NR2F2	ENST00000421109_r73	c.435 G>A	p.S145S	SILENT
MA4_23R	Chr16	334920	C	T	0.164634146	PDIA2	ENST00000219406_r73	c.583 C>T	p.Q195*	NONSENSE
MA4_23R	Chr16	420061	T	G	0.202380952	MRPL28	ENST00000199706_r73	c.158 A>C	p.N53T	MISSENSE
MA4_23R	Chr16	630878	C	T	0.239130435	PIGQ	ENST00000409527_r73	c.1437 C>T	p.A479A	SILENT
MA4_23R	Chr16	1748888	G	A	0.194444444	HN1L	ENST00000248098_r73	c.462 G>A	p.Q154Q	SILENT
MA4_23R	Chr16	1837741	C	T	0.219178082	NUBP2	ENST00000262302_r73	c.398 C>T	p.T133M	MISSENSE
MA4_23R	Chr16	1841153	G	A	0.1	IGFALS	ENST00000215539_r73	c.1266 C>T	p.L422L	SILENT
MA4_23R	Chr16	2140954	G	A	0.190476191	PKD1	ENST00000262304_r73	c.11934 C>T	p.D3978D	SILENT
MA4_23R	Chr16	2287651	G	A	0.162361624	DNASE1L2	ENST00000564065_r73	Exon 4 1 G>A	-	ESSENTIAL_SPLICE
MA4_23R	Chr16	2571122	A	G	0.150943396	ATP6C	ENST00000569317_r73	c.217 A>G	p.K73E	MISSENSE
MA4_23R	Chr16	2571122	A	G	0.150943396	AMDHD2	ENST00000302956_r73	c.358 A>G	p.K120E	MISSENSE
MA4_23R	Chr16	2816359	C	T	0.151260504	SRRM2	ENST00000301740_r73	c.5830 C>T	p.R1944C	MISSENSE
MA4_23R	Chr16	3487431	G	C	0.184397163	ZNF597	ENST00000301744_r73	c.268 C>G	p.P90A	MISSENSE
MA4_23R	Chr16	11001797	C	T	0.12345679	CIITA	ENST00000324288_r73	c.2448 C>T	p.A816A	SILENT

MA4_23R	Chr16	21213488	C	T	0.193181818	ZP2	ENST00000574002_r73	c.1224 G>A	p.E408E	SILENT
MA4_23R	Chr16	22144284	C	A	0.223880597	VWA3A	ENST00000389398_r73	c.1936 C>A	p.L646I	MISSENSE
MA4_23R	Chr16	22182168	C	T	0.173913044	SDR42E2	ENST00000602312_r73	c.307 C>T	p.R103W	MISSENSE
MA4_23R	Chr16	22201561	A	G	0.28358209	SDR42E2	ENST00000602312_r73	c.1014 A>G	p.L338L	SILENT
MA4_23R	Chr16	22826046	T	G	0.191304348	HS3ST2	ENST00000261374_r73	c.115 T>G	p.C39G	MISSENSE
MA4_23R	Chr16	29063529	C	T	0.379310345	CTB-134H23.2	ENST00000424293_r73	c.779 C>T	p.S260F	MISSENSE
MA4_23R	Chr16	29708436	C	T	0.134615385	QPRT	ENST00000395384_r73	c.669 C>T	p.N223N	SILENT
MA4_23R	Chr16	30975492	C	T	0.166666667	SETD1A	ENST00000262519_r73	c.717 C>T	p.N239N	SILENT
MA4_23R	Chr16	46766304	C	T	0.164179105	MYLK3	ENST00000394809_r73	c.1278 G>A	p.T426T	SILENT
MA4_23R	Chr16	57101678	T	A	0.17948718	NLRC5	ENST00000262510_r73	c.4437 T>A	p.D1479E	MISSENSE
MA4_23R	Chr16	72164240	G	C	0.274193548	PMFBP1	ENST00000237353_r73	c.1654 C>G	p.L552V	MISSENSE
MA4_23R	Chr16	72170469	G	A	0.213483146	PMFBP1	ENST00000237353_r73	c.1081 C>T	p.R361W	MISSENSE
MA4_23R	Chr16	72821625	C	T	0.229166667	ZFHX3	ENST00000268489_r73	c.10550 G>A	p.G3517D	MISSENSE
MA4_23R	Chr16	80583473	C	T	0.19205298	DYNLRB2	ENST00000305904_r73	c.172 C>T	p.R58C	MISSENSE
MA4_23R	Chr16	87344867	G	A	0.154639175	C16orf95	ENST00000567970_r73	c.366 C>T	p.T122T	SILENT
MA4_23R	Chr17	2291323	C	T	0.168539326	MNT	ENST00000174618_r73	c.828 G>A	p.K276K	SILENT
MA4_23R	Chr17	2605278	G	A	0.190476191	CLUH	ENST00000570628_r73	c.435 C>T	p.S145S	SILENT
MA4_23R	Chr17	4689601	A	G	0.137096774	VMO1	ENST00000441199_r73	c.47 T>C	p.L16P	MISSENSE
MA4_23R	Chr17	8146306	T	C	0.215686275	CTC1	ENST00000315684_r73	c.194 A>G	p.Y65C	MISSENSE
MA4_23R	Chr17	15477417	A	G	0.196428571	RP11-385D13.1	ENST00000455584_r73	c.2858 T>C	p.L953P	MISSENSE
MA4_23R	Chr17	18566585	G	A	0.164021164	ZNF286B	ENST00000545289_r73	c.234 C>T	p.S78S	SILENT
MA4_23R	Chr17	20354923	G	A	0.225806452	LGALS9B	ENST00000324290_r73	c.792 C>T	p.I264I	SILENT
MA4_23R	Chr17	21319267	C	T	0.072519084	KCNJ12	ENST00000583088_r73	c.613 C>T	p.R205C	MISSENSE
MA4_23R	Chr17	31087609	G	A	0.185185185	MYO1D	ENST00000318217_r73	c.1072 C>T	p.R358C	MISSENSE
MA4_23R	Chr17	34432664	T	A	0.176100629	CCL4	ENST00000250151_r73	c.238 T>A	p.S80T	MISSENSE
MA4_23R	Chr17	38191515	A	G	0.213333333	MED24	ENST00000356271_r73	c.375 T>C	p.S125S	SILENT
MA4_23R	Chr17	42335379	G	A	0.149253731	SLC4A1	ENST00000262418_r73	c.1257 C>T	p.P419P	SILENT
MA4_23R	Chr17	45016025	C	T	0.05	GOSR2	ENST00000393456_r73	c.538 C>T	p.R180W	MISSENSE
MA4_23R	Chr17	45016025	C	T	0.05	RP11-156P1.2	ENST00000571841_r73	c.538 C>T	p.R180W	MISSENSE
MA4_23R	Chr17	58503639	C	G	0.205882353	C17orf64	ENST00000269127_r73	c.271 C>G	p.H91D	MISSENSE
MA4_23R	Chr17	72349656	C	T	0.178010471	KIF19	ENST00000389916_r73	c.2244 C>T	p.G748G	SILENT
MA4_23R	Chr17	73830182	C	T	0.188679245	UNC13D	ENST00000207549_r73	c.2341 G>A	p.V781I	MISSENSE
MA4_23R	Chr17	74005802	C	T	0.185714286	EVPL	ENST00000301607_r73	c.3484 G>A	p.E1162K	MISSENSE
MA4_23R	Chr17	76482177	G	A	0.210526316	DNAH17	ENST00000585328_r73	c.7125 C>T	p.I2375I	SILENT
MA4_23R	Chr17	77769143	C	T	0.309859155	CBX8	ENST00000269385_r73	c.461 G>A	p.R154Q	MISSENSE
MA4_23R	Chr17	80206865	G	A	0.2	CSNK1D	ENST00000314028_r73	c.1083 C>T	p.S361S	SILENT
MA4_23R	Chr18	6999496	G	A	0.218181818	LAMA1	ENST00000389658_r73	c.4611 C>T	p.L1537L	SILENT

MA4_23R	Chr18	9204535	A	G	0.22818792	ANKRD12	ENST00000262126_r73	c.297 A>G	p.T99T	SILENT
MA4_23R	Chr18	10485561	G	A	0.179310345	APCDD1	ENST00000355285_r73	c.877 G>A	p.G293R	MISSENSE
MA4_23R	Chr18	13029750	A	G	0.168316832	CEP192	ENST00000506447_r73	c.1139 A>G	p.N380S	MISSENSE
MA4_23R	Chr18	34298589	C	T	0.185483871	FHOD3	ENST00000257209_r73	c.2803 C>T	p.L935L	SILENT
MA4_23R	Chr18	46343626	A	G	0.183673469	CTIF	ENST00000256413_r73	c.1406 A>G	p.Q469R	MISSENSE
MA4_23R	Chr18	57013161	T	A	0.326530612	LMAN1	ENST00000251047_r73	c.945 A>T	p.Q315H	MISSENSE
MA4_23R	Chr19	687035	T	A	0.174193548	PRSS57	ENST00000329267_r73	c.535 A>T	p.K179*	NONSENSE
MA4_23R	Chr19	1010673	G	A	0.255319149	TMEM259	ENST00000356663_r73	c.1539 C>T	p.P513P	SILENT
MA4_23R	Chr19	3942175	C	T	0.179104478	NMRK2	ENST00000168977_r73	c.597 C>T	p.A199A	SILENT
MA4_23R	Chr19	6183185	C	A	0.211864407	ACSBG2	ENST00000591403_r73	c.1224 C>A	p.F408L	MISSENSE
MA4_23R	Chr19	11508199	C	T	0.164556962	RGL3	ENST00000380456_r73	c.1821 G>A	p.P607P	SILENT
MA4_23R	Chr19	11512897	C	T	0.2	RGL3	ENST00000380456_r73	c.1356 G>A	p.R452R	SILENT
MA4_23R	Chr19	11618630	G	A	0.20952381	ECSIT	ENST00000270517_r73	c.832 C>T	p.R278C	MISSENSE
MA4_23R	Chr19	12984928	C	T	0.234567901	MAST1	ENST00000251472_r73	c.3957 C>T	p.G1319G	SILENT
MA4_23R	Chr19	13218667	G	A	0.226890756	TRMT1	ENST00000221504_r73	c.1317 C>T	p.A439A	SILENT
MA4_23R	Chr19	16962292	A	G	0.222222222	SIN3B	ENST00000379803_r73	c.796 A>G	p.S266G	MISSENSE
MA4_23R	Chr19	19038597	C	T	0.191489362	DDX49	ENST00000247003_r73	c.1125 C>T	p.S375S	SILENT
MA4_23R	Chr19	20989454	T	C	0.212765957	ZNF66	ENST00000344519_r73	c.1048 T>C	p.F350L	MISSENSE
MA4_23R	Chr19	21300018	G	A	0.164948454	ZNF714	ENST00000596143_r73	c.548 G>A	p.R183Q	MISSENSE
MA4_23R	Chr19	22271303	C	T	0.206896552	ZNF257	ENST00000594947_r73	c.751 C>T	p.H251Y	MISSENSE
MA4_23R	Chr19	35173717	T	A	0.135294118	ZNF302	ENST00000457781_r73	c.45 T>A	p.H15Q	MISSENSE
MA4_23R	Chr19	39281364	G	A	0.208333333	LGALS7B	ENST00000314980_r73	c.131 G>A	p.G44D	MISSENSE
MA4_23R	Chr19	39880149	C	T	0.213333333	PAF1	ENST00000221265_r73	c.330 G>A	p.E110E	SILENT
MA4_23R	Chr19	40900136	G	A	0.225352113	PRX	ENST00000324001_r73	c.4123 C>T	p.R1375W	MISSENSE
MA4_23R	Chr19	46915525	C	T	0.25	CCDC8	ENST00000307522_r73	c.543 G>A	p.E181E	SILENT
MA4_23R	Chr19	49116359	T	C	0.148648649	FAM83E	ENST00000263266_r73	c.271 A>G	p.T91A	MISSENSE
MA4_23R	Chr19	49206550	G	A	0.175438597	FUT2	ENST00000425340_r73	c.337 G>A	p.V113M	MISSENSE
MA4_23R	Chr19	54697199	A	G	0.296296296	TSEN34	ENST00000302937_r73	c.915 A>G	p.Q305Q	SILENT
MA4_23R	Chr19	54723078	G	A	0.134020619	LILRB3	ENST00000391750_r73	c.1346 C>T	p.S449L	MISSENSE
MA4_23R	Chr19	55237603	G	A	0.201680672	KIR3DL3	ENST00000291860_r73	c.155 G>A	p.R52H	MISSENSE
MA4_23R	Chr19	55241172	A	C	0.128654971	KIR3DL3	ENST00000291860_r73	c.869 A>C	p.N290T	MISSENSE
MA4_23R	Chr19	55246812	G	C	0.223880597	KIR3DL3	ENST00000291860_r73	c.1042 G>C	p.A348P	MISSENSE
MA4_23R	Chr19	55247449	A	T	0.217105263	KIR3DL3	ENST00000291860_r73	c.1119 A>T	p.E373D	MISSENSE
MA4_23R	Chr19	55255361	G	A	0.134502924	KIR2DL3	ENST00000342376_r73	c.489 G>A	p.E163E	SILENT
MA4_23R	Chr19	55317439	C	T	0.254237288	KIR2DL4	ENST00000359085_r73	c.395 C>T	p.P132L	MISSENSE
MA4_23R	Chr19	55333275	G	T	0.150684932	KIR3DL1	ENST00000391728_r73	c.911 G>T	p.W304L	MISSENSE
MA4_23R	Chr19	55363504	G	A	0.24822695	KIR3DL2	ENST00000326321_r73	c.122 G>A	p.R41Q	MISSENSE

MA4_23R	Chr19	58117099	G	C	0.2	ZNF530	ENST00000332854_r73	c.206 G>C	p.S69T	MISSENSE
MA4_23R	Chr2	21258553	T	A	0.25	APOB	ENST00000233242_r73	c.721 A>T	p.S241C	MISSENSE
MA4_23R	Chr2	27303740	C	T	0.176470588	EMILIN1	ENST00000380320_r73	c.431 C>T	p.P144L	MISSENSE
MA4_23R	Chr2	28843469	T	C	0.157142857	PLB1	ENST00000327757_r73	c.3386 T>C	p.I1129T	MISSENSE
MA4_23R	Chr2	29274749	C	T	0.162601626	FAM179A	ENST00000379558_r73	c.2850 C>T	p.R950R	SILENT
MA4_23R	Chr2	29416768	G	A	0.198412698	ALK	ENST00000389048_r73	c.4185 C>T	p.T1395T	SILENT
MA4_23R	Chr2	47202156	C	T	0.274509804	TTC7A	ENST00000319190_r73	c.562 C>T	p.R188C	MISSENSE
MA4_23R	Chr2	61331001	G	A	0.146153846	KIAA1841	ENST00000402291_r73	c.1379 G>A	p.R460K	MISSENSE
MA4_23R	Chr2	65300035	T	G	0.175879397	CEP68	ENST00000377990_r73	c.1805 T>G	p.F602C	MISSENSE
MA4_23R	Chr2	71206851	G	A	0.172413793	ANKRD53	ENST00000272421_r73	c.478 G>A	p.V160I	MISSENSE
MA4_23R	Chr2	74699368	G	A	0.159763314	MRPL53	ENST00000258105_r73	c.217 C>T	p.R73C	MISSENSE
MA4_23R	Chr2	85780132	C	T	0.21969697	GGCX	ENST00000233838_r73	c.1217 G>A	p.R406H	MISSENSE
MA4_23R	Chr2	90121841	C	A	0.155339806	IGKV1D-17	ENST00000483379_r73	c.59 C>A	p.A20D	MISSENSE
MA4_23R	Chr2	111551680	A	G	0.157894737	ACOXL	ENST00000439055_r73	c.274 A>G	p.M92V	MISSENSE
MA4_23R	Chr2	112578860	G	A	0.25	ANAPC1	ENST00000341068_r73	c.3162 C>T	p.Y1054Y	SILENT
MA4_23R	Chr2	127816628	C	T	0.1875	BIN1	ENST00000357970_r73	c.961 G>A	p.G321R	MISSENSE
MA4_23R	Chr2	133542131	A	T	0.157232704	NCKAP5	ENST00000409261_r73	c.2253 T>A	p.V751V	SILENT
MA4_23R	Chr2	150427678	T	C	0.256410256	MMADHC	ENST00000303319_r73	c.617 A>G	p.N206S	MISSENSE
MA4_23R	Chr2	152320764	A	G	0.163043478	RIF1	ENST00000444746_r73	c.4730 A>G	p.N1577S	MISSENSE
MA4_23R	Chr2	165772426	C	T	0.177339902	SLC38A11	ENST00000303735_r73	c.441 G>A	p.G147G	SILENT
MA4_23R	Chr2	179397368	G	A	0.18627451	TTN	ENST00000342992_r73	c.96270 C>T	p.I32090I	SILENT
MA4_23R	Chr2	207003230	C	T	0.164835165	NDUFS1	ENST00000233190_r73	c.1371 G>A	p.S457S	SILENT
MA4_23R	Chr2	209358019	C	T	0.238095238	PTH2R	ENST00000272847_r73	c.1288 C>T	p.R430W	MISSENSE
MA4_23R	Chr2	211018503	T	C	0.180257511	KANSL1L	ENST00000281772_r73	c.804 A>G	p.Q268Q	SILENT
MA4_23R	Chr2	219414580	C	T	0.094017094	USP37	ENST00000258399_r73	c.381 G>A	p.R127R	SILENT
MA4_23R	Chr2	220161758	C	T	0.237288136	PTPRN	ENST00000409251_r73	c.2098 G>A	p.A700T	MISSENSE
MA4_23R	Chr2	220493959	G	A	0.346938776	SLC4A3	ENST00000358055_r73	c.311 G>A	p.R104Q	MISSENSE
MA4_23R	Chr2	225661080	A	C	0.211640212	DOCK10	ENST00000258390_r73	c.4891 T>G	p.S1631A	MISSENSE
MA4_23R	Chr2	228855865	G	A	0.196581197	SPHKAP	ENST00000392056_r73	c.4810 C>T	p.P1604S	MISSENSE
MA4_23R	Chr2	230723502	T	C	0.141025641	TRIP12	ENST00000283943_r73	c.887 A>G	p.Q296R	MISSENSE
MA4_23R	Chr2	233413012	G	A	0.409090909	TIGD1	ENST00000408957_r73	c.1581 C>T	p.I527I	SILENT
MA4_23R	Chr2	238449108	G	T	0.394736842	MLPH	ENST00000264605_r73	c.1222 G>T	p.A408S	MISSENSE
MA4_23R	Chr2	242371116	T	C	0.173913044	FARP2	ENST00000264042_r73	c.794 T>C	p.F265S	MISSENSE
MA4_23R	Chr20	633682	T	C	0.243902439	SRXN1	ENST00000381962_r73	c.148 A>G	p.I50V	MISSENSE
MA4_23R	Chr20	3687772	C	T	0.273972603	SIGLEC1	ENST00000344754_r73	c.4 G>A	p.G2S	MISSENSE
MA4_23R	Chr20	13280052	G	A	0.106382979	ISM1	ENST00000262487_r73	c.1341 G>A	p.E447E	SILENT
MA4_23R	Chr20	33875140	C	T	0.136752137	FAM83C	ENST00000374408_r73	c.1442 G>A	p.G481D	MISSENSE

MA4_23R	Chr20	39831546	C	T	0.188571429	ZHX3	ENST00000309060_r73	c.2011 G>A	p.E671K	MISSENSE
MA4_23R	Chr20	43727834	C	T	0.337209302	KCNS1	ENST00000306117_r73	c.44 G>A	p.R15Q	MISSENSE
MA4_23R	Chr20	57246312	A	C	0.112244898	STX16	ENST00000355957_r73	c.700 A>C	p.N234H	MISSENSE
MA4_23R	Chr20	57246312	A	C	0.112244898	STX16-NPEPL1	ENST00000530122_r73	c.751 A>C	p.N251H	MISSENSE
MA4_23R	Chr20	57571837	C	T	0.284023669	CTSZ	ENST00000217131_r73	c.658 G>A	p.E220K	MISSENSE
MA4_23R	Chr20	61459319	C	T	0.213483146	COL9A3	ENST00000343916_r73	c.891 C>T	p.S297S	SILENT
MA4_23R	Chr20	62195536	G	A	0.188679245	HELZ2	ENST00000427522_r73	c.2932 C>T	p.R978W	MISSENSE
MA4_23R	Chr21	30380903	G	A	0.142857143	RWDD2B	ENST00000493196_r73	c.107 C>T	p.A36V	MISSENSE
MA4_23R	Chr21	34837660	A	G	0.202898551	TMEM50B	ENST00000420455_r73	c.269 T>C	p.L90S	MISSENSE
MA4_23R	Chr21	34922515	G	A	0.194444444	SON	ENST00000356577_r73	c.978 G>A	p.M326I	MISSENSE
MA4_23R	Chr21	40552338	T	G	0.139705882	PSMG1	ENST00000331573_r73	c.266 A>C	p.N89T	MISSENSE
MA4_23R	Chr21	43240044	G	A	0.191489362	PRDM15	ENST00000398548_r73	c.2265 C>T	p.H755H	SILENT
MA4_23R	Chr22	23523753	C	T	0.195121951	BCR	ENST00000305877_r73	c.606 C>T	p.S202S	SILENT
MA4_23R	Chr22	29876996	G	A	0.25	NEFH	ENST00000310624_r73	c.745 G>A	p.G249S	MISSENSE
MA4_23R	Chr22	32909761	C	G	0.223529412	SYN3	ENST00000358763_r73	c.1661 G>C	p.R554P	MISSENSE
MA4_23R	Chr22	37414181	A	G	0.461538462	TST	ENST00000403892_r73	c.593 T>C	p.V198A	MISSENSE
MA4_23R	Chr22	37890166	C	A	0.166666667	CARD10	ENST00000403299_r73	c.2403 G>T	p.R801R	SILENT
MA4_23R	Chr22	38211281	C	G	0.235294118	GCAT	ENST00000323205_r73	c.803 C>G	p.T268R	MISSENSE
MA4_23R	Chr22	39621819	G	A	0.1875	PDGFB	ENST00000331163_r73	c.635 C>T	p.T212M	MISSENSE
MA4_23R	Chr22	39917587	C	T	0.205882353	ATF4	ENST00000404241_r73	c.137 C>T	p.P46L	MISSENSE
MA4_23R	Chr22	45255677	A	G	0.166666667	PRR5-ARHGAP8	ENST00000361473_r73	c.1337 A>G	p.Y446C	MISSENSE
MA4_23R	Chr22	45255677	A	G	0.166666667	ARHGAP8	ENST00000389774_r73	c.1037 A>G	p.Y346C	MISSENSE
MA4_23R	Chr22	46658198	A	G	0.253012048	PKDREJ	ENST00000253255_r73	c.1022 T>C	p.L341P	MISSENSE
MA4_23R	Chr22	50885863	C	T	0.212765957	SBF1	ENST00000380817_r73	c.5471 G>A	p.R1824H	MISSENSE
MA4_23R	Chr3	16358506	A	G	0.08974359	RFTN1	ENST00000334133_r73	c.1566 T>C	p.P522P	SILENT
MA4_23R	Chr3	32995349	C	T	0.192090396	CCR4	ENST00000330953_r73	c.435 C>T	p.S145S	SILENT
MA4_23R	Chr3	40557438	G	A	0.196969697	ZNF620	ENST00000314529_r73	c.353 G>A	p.G118D	MISSENSE
MA4_23R	Chr3	46008939	G	A	0.192307692	FYCO1	ENST00000296137_r73	c.1887 C>T	p.V629V	SILENT
MA4_23R	Chr3	49060313	C	T	0.25974026	NDUFAF3	ENST00000326912_r73	c.171 C>T	p.I57I	SILENT
MA4_23R	Chr3	49837207	C	T	0.192771084	CDHR4	ENST00000412678_r73	c.39 G>A	p.P13P	SILENT
MA4_23R	Chr3	49850929	A	G	0.25	UBA7	ENST00000333486_r73	c.208 T>C	p.S70P	MISSENSE
MA4_23R	Chr3	52283025	C	T	0.175572519	PPM1M	ENST00000409502_r73	c.396 C>T	p.L132L	SILENT
MA4_23R	Chr3	52398913	A	G	0.154589372	DNAH1	ENST00000420323_r73	c.5396 A>G	p.K1799R	MISSENSE
MA4_23R	Chr3	52661351	G	A	0.235294118	PBRM1	ENST00000394830_r73	c.1479 C>T	p.I493I	SILENT
MA4_23R	Chr3	52858459	G	A	0.264285714	ITIH4	ENST00000266041_r73	c.999 C>T	p.N333N	SILENT
MA4_23R	Chr3	101571742	C	G	0.192546584	NFKBIZ	ENST00000394054_r73	c.173 C>G	p.T58R	MISSENSE
MA4_23R	Chr3	108781994	C	T	0.151898734	MORC1	ENST00000232603_r73	Exon 10 5 G>A	-	ESSENTIAL_SPLICE

MA4_23R	Chr3	122420142	G	A	0.220994475	PARP14	ENST00000474629_r73	c.2741 G>A	p.R914Q	MISSENSE
MA4_23R	Chr3	132196983	G	A	0.16	DNAJC13	ENST00000260818_r73	c.2708 G>A	p.R903K	MISSENSE
MA4_23R	Chr3	145782480	A	G	0.227272727	AC107021.1	ENST00000422482_r73	c.101 A>G	p.H34R	MISSENSE
MA4_23R	Chr3	150834162	A	G	0.183206107	MED12L	ENST00000474524_r73	c.137 A>G	p.N46S	MISSENSE
MA4_23R	Chr3	169485469	G	A	0.189655172	ACTRT3	ENST00000330368_r73	c.870 C>T	p.F290F	SILENT
MA4_23R	Chr3	184071136	G	A	0.227722772	CLCN2	ENST00000265593_r73	c.1930 C>T	p.R644C	MISSENSE
MA4_23R	Chr3	184101429	C	T	0.243243243	CHRD	ENST00000204604_r73	c.1439 C>T	p.T480M	MISSENSE
MA4_23R	Chr3	193081090	C	T	0.1875	ATP13A5	ENST00000342358_r73	c.319 G>A	p.E107K	MISSENSE
MA4_23R	Chr4	1388564	T	C	0.272727273	CRIPAK	ENST00000324803_r73	c.265 T>C	p.C89R	MISSENSE
MA4_23R	Chr4	6303769	G	A	0.201970443	WFS1	ENST00000503569_r73	c.2247 G>A	p.T749T	SILENT
MA4_23R	Chr4	17841383	A	G	0.210526316	NCAPG	ENST00000251496_r73	c.2551 A>G	p.T851A	MISSENSE
MA4_23R	Chr4	40339286	C	G	0.157894737	CHRNA9	ENST00000310169_r73	c.270 C>G	p.A90A	SILENT
MA4_23R	Chr4	48844693	A	T	0.235294118	OCIAD1	ENST00000264312_r73	c.180 A>T	p.G60G	SILENT
MA4_23R	Chr4	56847506	A	G	0.227722772	CEP135	ENST00000257287_r73	c.1740 A>G	p.R580R	SILENT
MA4_23R	Chr4	70146902	T	C	0.4375	UGT2B28	ENST00000335568_r73	c.684 T>C	p.D228D	SILENT
MA4_23R	Chr4	89300241	C	A	0.404761905	HERC6	ENST00000380265_r73	c.168 C>A	p.G56G	SILENT
MA4_23R	Chr4	91230194	A	C	0.230769231	CCSER1	ENST00000509176_r73	c.759 A>C	p.T253T	SILENT
MA4_23R	Chr4	106190798	G	A	0.101941748	TET2	ENST00000380013_r73	c.4076 G>A	p.R1359H	MISSENSE
MA4_23R	Chr4	122062982	G	A	0.189189189	TNIP3	ENST00000057513_r73	c.874 C>T	p.R292W	MISSENSE
MA4_23R	Chr4	141446698	T	G	0.177514793	ELMOD2	ENST00000323570_r73	c.116 T>G	p.V39G	MISSENSE
MA4_23R	Chr4	144922436	T	G	0.063926941	GYPB	ENST00000502664_r73	c.38 A>C	p.E13A	MISSENSE
MA4_23R	Chr4	154626370	C	T	0.173913044	TLR2	ENST00000260010_r73	c.2311 C>T	p.R771W	MISSENSE
MA4_23R	Chr4	155490820	A	G	0.216216216	FGB	ENST00000302068_r73	c.1113 A>G	p.S371S	SILENT
MA4_23R	Chr5	428022	C	T	0.176470588	AHRR	ENST00000505113_r73	c.821 C>T	p.A274V	MISSENSE
MA4_23R	Chr5	1087084	G	A	0.135483871	SLC12A7	ENST00000264930_r73	c.609 C>T	p.L203L	SILENT
MA4_23R	Chr5	1217004	G	A	0.174603175	SLC6A19	ENST00000304460_r73	c.1117 G>A	p.A373T	MISSENSE
MA4_23R	Chr5	13717485	G	A	0.145833333	DNAH5	ENST00000265104_r73	c.12644 C>T	p.A4215V	MISSENSE
MA4_23R	Chr5	32058127	C	T	0.126213592	PDZD2	ENST00000438447_r73	c.2118 C>T	p.S706S	SILENT
MA4_23R	Chr5	93966286	G	A	0.142857143	ANKRD32	ENST00000265140_r73	c.269 G>A	p.W90*	NONSENSE
MA4_23R	Chr5	107717088	C	T	0.217391304	FBXL17	ENST00000542267_r73	c.305 G>A	p.R102Q	MISSENSE
MA4_23R	Chr5	126755873	G	A	0.098591549	MEGF10	ENST00000503335_r73	c.1564 G>A	p.G522R	MISSENSE
MA4_23R	Chr5	131008132	T	C	0.179661017	FNIP1	ENST00000307968_r73	c.1921 A>G	p.K641E	MISSENSE
MA4_23R	Chr5	131329826	C	G	0.189473684	ACSL6	ENST00000379264_r73	c.168 G>C	p.V56V	SILENT
MA4_23R	Chr5	132150837	C	G	0.140186916	SOWAHA	ENST00000378693_r73	c.1524 C>G	p.A508A	SILENT
MA4_23R	Chr5	133473774	G	A	0.307692308	TCF7	ENST00000342854_r73	c.466 G>A	p.G156S	MISSENSE
MA4_23R	Chr5	138260288	C	T	0.297297297	CTNNA1	ENST00000302763_r73	c.1636 C>T	p.R546*	NONSENSE
MA4_23R	Chr5	139060486	G	A	0.159763314	CXXC5	ENST00000302517_r73	c.378 G>A	p.A126A	SILENT

MA4_23R	Chr5	139714273	A	G	0.156028369	HBEGF	ENST00000230990_r73	c.615 T>C	p.T205T	SILENT
MA4_23R	Chr5	145843260	T	C	0.131428571	TCERG1	ENST00000296702_r73	c.1039 T>C	p.S347P	MISSENSE
MA4_23R	Chr5	149578896	C	T	0.164179105	SLC6A7	ENST00000230671_r73	c.690 C>T	p.L230L	SILENT
MA4_23R	Chr5	162939175	A	G	0.205882353	MAT2B	ENST00000280969_r73	c.198 A>G	p.A66A	SILENT
MA4_23R	Chr5	167630831	A	C	0.183673469	TENM2	ENST00000518659_r73	c.3568 A>C	p.K1190Q	MISSENSE
MA4_23R	Chr5	171509391	C	T	0.104651163	STK10	ENST00000176763_r73	c.1928 G>A	p.R643H	MISSENSE
MA4_23R	Chr5	174869692	G	C	0.192307692	DRD1	ENST00000393752_r73	c.411 C>G	p.P137P	SILENT
MA4_23R	Chr5	176832999	T	C	0.113636364	F12	ENST00000253496_r73	c.179 A>G	p.K60R	MISSENSE
MA4_23R	Chr5	178358521	G	T	0.161290323	ZFP2	ENST00000361362_r73	c.207 G>T	p.M69I	MISSENSE
MA4_23R	Chr5	179260201	G	A	0.176470588	SQSTM1	ENST00000389805_r73	c.924 G>A	p.A308A	SILENT
MA4_23R	Chr6	656694	G	C	0.182926829	HUS1B	ENST00000380907_r73	c.251 C>G	p.A84G	MISSENSE
MA4_23R	Chr6	10634514	C	T	0.202702703	GCNT6	ENST00000379591_r73	c.357 C>T	p.A119A	SILENT
MA4_23R	Chr6	26156843	G	A	0.210526316	HIST1H1E	ENST00000304218_r73	c.225 G>A	p.K75K	SILENT
MA4_23R	Chr6	31779134	T	C	0.205479452	HSPA1L	ENST00000375654_r73	c.616 A>G	p.T206A	MISSENSE
MA4_23R	Chr6	32905086	G	A	0.168316832	HLA-DMB	ENST00000418107_r73	c.485 C>T	p.A162V	MISSENSE
MA4_23R	Chr6	34208668	C	T	0.227272727	HMGA1	ENST00000311487_r73	c.111 C>T	p.P37P	SILENT
MA4_23R	Chr6	35262346	G	A	0.132075472	ZNF76	ENST00000373953_r73	c.1608 G>A	p.Q536Q	SILENT
MA4_23R	Chr6	41754576	C	T	0.202380952	PRICKLE4	ENST00000335515_r73	c.864 C>T	p.L288L	SILENT
MA4_23R	Chr6	42072274	C	T	0.193548387	C6orf132	ENST00000341865_r73	c.3376 G>A	p.A1126T	MISSENSE
MA4_23R	Chr6	51889823	G	A	0.191358025	PKHD1	ENST00000371117_r73	c.4785 C>T	p.G1595G	SILENT
MA4_23R	Chr6	54804720	C	T	0.223776224	FAM83B	ENST00000306858_r73	c.951 C>T	p.S317S	SILENT
MA4_23R	Chr6	84871572	G	A	0.24137931	KIAA1009	ENST00000403245_r73	c.2569 C>T	p.R857C	MISSENSE
MA4_23R	Chr6	109764598	A	T	0.2734375	SMPD2	ENST00000258052_r73	c.858 A>T	p.P286P	SILENT
MA4_23R	Chr6	126080448	T	C	0.136363636	HEY2	ENST00000368364_r73	c.514 T>C	p.S172P	MISSENSE
MA4_23R	Chr6	131919806	G	A	0.174757282	MED23	ENST00000354577_r73	c.2334 C>T	p.N778N	SILENT
MA4_23R	Chr6	137479526	G	A	0.220779221	IL22RA2	ENST00000349184_r73	c.155 C>T	p.A52V	MISSENSE
MA4_23R	Chr6	142539730	G	A	0.197802198	VTA1	ENST00000367630_r73	c.874 G>A	p.V292I	MISSENSE
MA4_23R	Chr6	154481128	C	T	0.2	IPCEF1	ENST00000265198_r73	c.1149 G>A	p.P383P	SILENT
MA4_23R	Chr7	4722377	G	A	0.36	FOXK1	ENST00000328914_r73	c.438 G>A	p.R146R	SILENT
MA4_23R	Chr7	4824597	C	T	0.219512195	AP5Z1	ENST00000348624_r73	c.849 C>T	p.A283A	SILENT
MA4_23R	Chr7	5434174	C	G	0.166666667	TNRC18	ENST00000430969_r73	c.240 G>C	p.S80S	SILENT
MA4_23R	Chr7	21893969	G	C	0.259615385	DNAH11	ENST00000409508_r73	c.11098 G>C	p.E3700Q	MISSENSE
MA4_23R	Chr7	26192248	G	A	0.390243902	NFE2L3	ENST00000056233_r73	c.130 G>A	p.D44N	MISSENSE
MA4_23R	Chr7	26224382	C	T	0.066371681	NFE2L3	ENST00000056233_r73	c.1064 C>T	p.T355I	MISSENSE
MA4_23R	Chr7	47409029	G	A	0.261904762	TNS3	ENST00000311160_r73	c.1214 C>T	p.T405M	MISSENSE
MA4_23R	Chr7	48314389	T	C	0.266666667	ABCA13	ENST00000435803_r73	c.5126 T>C	p.L1709P	MISSENSE
MA4_23R	Chr7	100356262	G	C	0.142857143	ZAN	ENST00000349350_r73	c.3560 G>C	p.G1187A	MISSENSE

MA4_23R	Chr7	100643477	A	C	0.074829932	MUC12	ENST00000536621_r73	c.9633 A>C	p.S3211S	SILENT
MA4_23R	Chr7	100645731	G	A	0.111111111	MUC12	ENST00000536621_r73	c.11887 G>A	p.E3963K	MISSENSE
MA4_23R	Chr7	100855576	G	A	0.171428571	PLOD3	ENST00000223127_r73	c.1085 C>T	p.P362L	MISSENSE
MA4_23R	Chr7	117243823	C	T	0.167567568	CFTR	ENST00000003084_r73	c.2895 C>T	p.N965N	SILENT
MA4_23R	Chr7	121944279	G	A	0.159624413	FEZF1	ENST00000442488_r73	c.213 C>T	p.I71I	SILENT
MA4_23R	Chr7	139257887	C	T	0.163265306	HIPK2	ENST00000406875_r73	c.3383 G>A	p.R1128H	MISSENSE
MA4_23R	Chr7	140287517	G	A	0.189873418	DENND2A	ENST00000275884_r73	c.1059 C>T	p.Y353Y	SILENT
MA4_23R	Chr7	148904547	A	G	0.14516129	ZNF282	ENST00000262085_r73	c.817 A>G	p.M273V	MISSENSE
MA4_23R	Chr7	150713295	G	C	0.17948718	ATG9B	ENST00000377974_r73	c.2546 C>G	p.P849R	MISSENSE
MA4_23R	Chr7	150716160	T	C	0.158878505	ATG9B	ENST00000377974_r73	c.1265 A>G	p.Y422C	MISSENSE
MA4_23R	Chr8	8185328	C	T	0.220183486	SGK223	ENST00000520004_r73	c.2964 G>A	p.S988S	SILENT
MA4_23R	Chr8	8235510	G	C	0.151898734	SGK223	ENST00000520004_r73	c.409 C>G	p.R137G	MISSENSE
MA4_23R	Chr8	8560176	G	A	0.212121212	CLDN23	ENST00000519106_r73	c.268 G>A	p.A90T	MISSENSE
MA4_23R	Chr8	9009379	G	A	0.25	RP11-10A14.4	ENST00000518496_r73	c.21 G>A	p.K7K	SILENT
MA4_23R	Chr8	11659451	G	C	0.428571429	RP11-297N6.4	ENST00000533405_r73	c.146 C>G	p.A49G	MISSENSE
MA4_23R	Chr8	12957678	C	T	0.174863388	DLC1	ENST00000276297_r73	c.2168 G>A	p.R723H	MISSENSE
MA4_23R	Chr8	22548277	C	T	0.137931035	EGR3	ENST00000317216_r73	c.873 G>A	p.E291E	SILENT
MA4_23R	Chr8	28671031	A	C	0.189393939	INTS9	ENST00000521022_r73	c.587 T>G	p.L196R	MISSENSE
MA4_23R	Chr8	28929820	A	C	0.17948718	KIF13B	ENST00000524189_r73	c.4535 T>G	p.M1512R	MISSENSE
MA4_23R	Chr8	68028331	C	T	0.269662921	CSPP1	ENST00000262210_r73	c.1455 C>T	p.S485S	SILENT
MA4_23R	Chr8	98656775	C	T	0.225806452	MTDH	ENST00000336273_r73	c.41 C>T	p.A14V	MISSENSE
MA4_23R	Chr8	103372358	G	A	0.181818182	UBR5	ENST00000520539_r73	c.327 C>T	p.D109D	SILENT
MA4_23R	Chr8	110302077	A	T	0.183206107	NUDCD1	ENST00000239690_r73	c.726 T>A	p.N242K	MISSENSE
MA4_23R	Chr8	126052103	T	C	0.242105263	KIAA0196	ENST00000318410_r73	c.2888 A>G	p.N963S	MISSENSE
MA4_23R	Chr8	144332046	G	A	0.107142857	ZFP41	ENST00000520584_r73	c.33 G>A	p.T11T	SILENT
MA4_23R	Chr8	144332046	G	A	0.107142857	ZFP41	ENST00000522452_r73	c.33 G>A	p.T11T	SILENT
MA4_23R	Chr8	144810572	G	A	0.150684932	FAM83H	ENST00000388913_r73	c.1059 C>T	p.A353A	SILENT
MA4_23R	Chr8	145748360	G	C	0.195402299	LRRC24	ENST00000529415_r73	c.1041 C>G	p.A347A	SILENT
MA4_23R	Chr9	6012864	C	T	0.073033708	RANBP6	ENST00000259569_r73	c.2744 G>A	p.R915Q	MISSENSE
MA4_23R	Chr9	19409094	G	C	0.191489362	ACER2	ENST00000340967_r73	c.12 G>C	p.P4P	SILENT
MA4_23R	Chr9	34690000	C	T	0.166666667	CCL19	ENST00000311925_r73	c.203 G>A	p.R68H	MISSENSE
MA4_23R	Chr9	34993437	G	A	0.178571429	DNAJB5	ENST00000453597_r73	c.549 G>A	p.E183E	SILENT
MA4_23R	Chr9	79635269	C	T	0.410958904	FOXB2	ENST00000376708_r73	c.699 C>T	p.A233A	SILENT
MA4_23R	Chr9	95177598	T	C	0.140625	OMD	ENST00000375550_r73	c.1102 A>G	p.T368A	MISSENSE
MA4_23R	Chr9	96860820	G	A	0.152777778	PTPDC1	ENST00000375360_r73	c.1810 G>A	p.V604I	MISSENSE
MA4_23R	Chr9	100112770	C	T	0.186046512	CCDC180	ENST00000529487_r73	c.3067 C>T	p.R1023W	MISSENSE
MA4_23R	Chr9	121930252	C	T	0.308411215	DBC1	ENST00000265922_r73	c.1396 G>A	p.V466M	MISSENSE

MA4_23R	Chr9	125486542	A	G	0.123167155	OR1L4	ENST00000259466_r73	c.274 A>G	p.I92V	MISSENSE
MA4_23R	Chr9	131768786	G	A	0.154929578	NUP188	ENST00000372577_r73	c.5079 G>A	p.T1693T	SILENT
MA4_23R	Chr9	137711997	G	A	0.171974522	COL5A1	ENST00000371817_r73	c.4482 G>A	p.P1494P	SILENT
MA4_23R	Chr9	139636334	G	A	0.166666667	LCN10	ENST00000497771_r73	c.256 C>T	p.R86W	MISSENSE
MA4_23R	Chr9	139935576	C	T	0.175675676	NPDC1	ENST00000371601_r73	c.323 G>A	p.R108Q	MISSENSE
MA4_23R	ChrX	2777948	A	T	0.186813187	GYG2	ENST00000398806_r73	c.679 A>T	p.N227Y	MISSENSE
MA4_23R	ChrX	2825403	A	G	0.175572519	ARSD	ENST00000381154_r73	c.1691 T>C	p.M564T	MISSENSE
MA4_23R	ChrX	2836037	G	C	0.223684211	ARSD	ENST00000381154_r73	c.671 C>G	p.S224C	MISSENSE
MA4_23R	ChrX	2951348	A	G	0.4	ARSH	ENST00000381130_r73	c.1611 A>G	p.P537P	SILENT
MA4_23R	ChrX	3002687	A	G	0.382978723	ARSF	ENST00000381127_r73	c.810 A>G	p.E270E	SILENT
MA4_23R	ChrX	3228411	G	A	0.755555556	MXRA5	ENST00000217939_r73	c.7833 C>T	p.A2611A	SILENT
MA4_23R	ChrX	3228891	A	G	0.471428571	MXRA5	ENST00000217939_r73	c.7353 T>C	p.T2451T	SILENT
MA4_23R	ChrX	3235724	C	T	0.727272727	MXRA5	ENST00000217939_r73	c.5998 G>A	p.G2000S	MISSENSE
MA4_23R	ChrX	3239545	C	T	0.523809524	MXRA5	ENST00000217939_r73	c.4181 G>A	p.G1394D	MISSENSE
MA4_23R	ChrX	3240343	G	A	0.546875	MXRA5	ENST00000217939_r73	c.3383 C>T	p.A1128V	MISSENSE
MA4_23R	ChrX	3241050	G	A	0.642857143	MXRA5	ENST00000217939_r73	c.2676 C>T	p.S892S	SILENT
MA4_23R	ChrX	3241256	T	C	0.338235294	MXRA5	ENST00000217939_r73	c.2470 A>G	p.I824V	MISSENSE
MA4_23R	ChrX	3241317	T	C	0.37704918	MXRA5	ENST00000217939_r73	c.2409 A>G	p.P803P	SILENT
MA4_23R	ChrX	3241791	G	A	0.471698113	MXRA5	ENST00000217939_r73	c.1935 C>T	p.D645D	SILENT
MA4_23R	ChrX	3592725	G	A	0.492753623	PRKX	ENST00000262848_r73	c.249 C>T	p.P83P	SILENT
MA4_23R	ChrX	3631167	A	G	0.45945946	PRKX	ENST00000262848_r73	c.128 T>C	p.V43A	MISSENSE
MA4_23R	ChrX	7889828	C	T	0.306122449	PNPLA4	ENST00000381042_r73	c.337 G>A	p.V113I	MISSENSE
MA4_23R	ChrX	10180554	G	A	0.333333333	CLCN4	ENST00000380833_r73	c.1437 G>A	p.A479A	SILENT
MA4_23R	ChrX	12937513	C	T	0.253424658	TLR8	ENST00000218032_r73	c.354 C>T	p.D118D	SILENT
MA4_23R	ChrX	16168467	T	C	0.647058824	GRPR	ENST00000380289_r73	c.453 T>C	p.S151S	SILENT
MA4_23R	ChrX	16627756	C	T	0.346153846	CTPS2	ENST00000359276_r73	c.1599 G>A	p.P533P	SILENT
MA4_23R	ChrX	16859628	G	A	0.517241379	TXLNG	ENST00000380122_r73	c.1326 G>A	p.Q442Q	SILENT
MA4_23R	ChrX	21508666	A	G	0.193277311	CNKSR2	ENST00000279451_r73	c.651 A>G	p.Q217Q	SILENT
MA4_23R	ChrX	21861434	A	G	0.28	MBTPS2	ENST00000379484_r73	c.222 A>G	p.Q74Q	SILENT
MA4_23R	ChrX	23019346	G	T	0.339285714	DDX53	ENST00000327968_r73	c.1172 G>T	p.R391M	MISSENSE
MA4_23R	ChrX	23933852	G	A	0.3125	CXorf58	ENST00000379211_r73	c.252 G>A	p.V84V	SILENT
MA4_23R	ChrX	24608284	A	G	0.223880597	PCYT1B	ENST00000379145_r73	c.288 T>C	p.S96S	SILENT
MA4_23R	ChrX	26157792	C	T	0.560606061	MAGEB18	ENST00000325250_r73	c.690 C>T	p.A230A	SILENT
MA4_23R	ChrX	27999146	C	T	0.302013423	DCAF8L1	ENST00000441525_r73	c.306 G>A	p.E102E	SILENT
MA4_23R	ChrX	30254361	G	A	0.375	MAGEB3	ENST00000378986_r73	c.320 G>A	p.R107H	MISSENSE
MA4_23R	ChrX	30254530	A	G	0.186440678	MAGEB3	ENST00000378986_r73	c.489 A>G	p.V163V	SILENT
MA4_23R	ChrX	30326983	C	T	0.328767123	NR0B1	ENST00000378970_r73	c.498 G>A	p.R166R	SILENT

MA4_23R	ChrX	31496426	T	C	0.234848485	DMD	ENST00000378677_r73	c.8722 A>G	p.N2908D	MISSENSE
MA4_23R	ChrX	31496431	T	A	0.2421875	DMD	ENST00000378677_r73	c.8717 A>T	p.E2906V	MISSENSE
MA4_23R	ChrX	31697636	A	G	0.27972028	DMD	ENST00000378677_r73	c.7716 T>C	p.N2572N	SILENT
MA4_23R	ChrX	31893307	T	G	0.310344828	DMD	ENST00000378677_r73	c.7084 A>C	p.K2362Q	MISSENSE
MA4_23R	ChrX	32235149	G	A	0.222222222	DMD	ENST00000378677_r73	c.6310 C>T	p.R2104C	MISSENSE
MA4_23R	ChrX	32380996	C	T	0.330275229	DMD	ENST00000378677_r73	c.5222 G>A	p.R1741H	MISSENSE
MA4_23R	ChrX	35988996	T	C	0.4	CXorf22	ENST00000297866_r73	c.1926 T>C	p.L642L	SILENT
MA4_23R	ChrX	35993454	C	T	0.612903226	CXorf22	ENST00000297866_r73	c.2445 C>T	p.D815D	SILENT
MA4_23R	ChrX	36007464	A	T	0.333333333	CXorf22	ENST00000297866_r73	c.2742 A>T	p.E914D	MISSENSE
MA4_23R	ChrX	36368166	G	A	0.304347826	CXorf30	ENST00000378657_r73	c.955 G>A	p.D319N	MISSENSE
MA4_23R	ChrX	36371719	T	A	0.479591837	CXorf30	ENST00000378657_r73	c.1112 T>A	p.F371Y	MISSENSE
MA4_23R	ChrX	36385156	A	G	0.216374269	CXorf30	ENST00000378657_r73	c.1437 A>G	p.E479E	SILENT
MA4_23R	ChrX	37028127	A	G	0.322580645	FAM47C	ENST00000358047_r73	c.1644 A>G	p.P548P	SILENT
MA4_23R	ChrX	37029254	A	C	0.323076923	FAM47C	ENST00000358047_r73	c.2771 A>C	p.N924T	MISSENSE
MA4_23R	ChrX	39932907	T	C	0.201438849	BCOR	ENST00000397354_r73	c.1692 A>G	p.A564A	SILENT
MA4_23R	ChrX	40513785	C	T	0.183673469	MED14	ENST00000324817_r73	c.4122 G>A	p.S1374S	SILENT
MA4_23R	ChrX	40573157	G	A	0.296875	MED14	ENST00000324817_r73	c.525 C>T	p.D175D	SILENT
MA4_23R	ChrX	43603391	T	C	0.606060606	MAOA	ENST00000338702_r73	c.1410 T>C	p.D470D	SILENT
MA4_23R	ChrX	44401295	T	G	0.119047619	FUNDC1	ENST00000378045_r73	c.81 A>C	p.A27A	SILENT
MA4_23R	ChrX	47343254	C	T	0.284482759	CXorf24	ENST00000357412_r73	c.251 C>T	p.T84I	MISSENSE
MA4_23R	ChrX	47444985	T	C	0.351851852	TIMP1	ENST00000218388_r73	c.372 T>C	p.F124F	SILENT
MA4_23R	ChrX	47483800	G	A	0.327272727	CFP	ENST00000396992_r73	c.1284 C>T	p.N428N	SILENT
MA4_23R	ChrX	47918205	G	A	0.666666667	ZNF630	ENST00000409324_r73	c.1626 C>T	p.P542P	SILENT
MA4_23R	ChrX	48418126	A	G	0.271186441	TBC1D25	ENST00000376771_r73	c.830 A>G	p.N277S	MISSENSE
MA4_23R	ChrX	48418659	G	A	0.377192983	TBC1D25	ENST00000376771_r73	c.1363 G>A	p.A455T	MISSENSE
MA4_23R	ChrX	48751289	G	A	0.394736842	TIMM17B	ENST00000376582_r73	c.324 C>T	p.G108G	SILENT
MA4_23R	ChrX	48888074	T	C	0.538461539	TFE3	ENST00000315869_r73	c.1323 A>G	p.V441V	SILENT
MA4_23R	ChrX	53457622	T	C	0.176470588	RIBC1	ENST00000375327_r73	c.942 T>C	p.T314T	SILENT
MA4_23R	ChrX	54836361	A	G	0.2	MAGED2	ENST00000375068_r73	c.252 A>G	p.S84S	SILENT
MA4_23R	ChrX	54836505	A	G	0.188235294	MAGED2	ENST00000375068_r73	c.396 A>G	p.T132T	SILENT
MA4_23R	ChrX	54838077	C	T	0.23255814	MAGED2	ENST00000375068_r73	c.981 C>T	p.S327S	SILENT
MA4_23R	ChrX	67937976	G	A	0.295081967	STARD8	ENST00000374599_r73	c.1220 G>A	p.R407Q	MISSENSE
MA4_23R	ChrX	68381912	G	A	0.493670886	PJA1	ENST00000374583_r73	c.1170 C>T	p.G390G	SILENT
MA4_23R	ChrX	70597546	C	G	0.204081633	TAF1	ENST00000373790_r73	c.805 C>G	p.L269V	MISSENSE
MA4_23R	ChrX	70787856	T	C	0.268965517	OGT	ENST00000373719_r73	c.2856 T>C	p.A952A	SILENT
MA4_23R	ChrX	71350133	T	G	0.279411765	RGAG4	ENST00000479991_r73	c.1258 A>C	p.S420R	MISSENSE
MA4_23R	ChrX	71360204	A	G	0.242424242	NHSL2	ENST00000373677_r73	c.1708 A>G	p.R570G	MISSENSE

MA4_23R	ChrX	73524557	A	G	0.333333333	ZCCHC13	ENST00000339534_r73	c.456 A>G	p.L152L	SILENT
MA4_23R	ChrX	77913569	G	A	0.292134832	ZCCHC5	ENST00000321110_r73	c.349 C>T	p.P117S	MISSENSE
MA4_23R	ChrX	78216024	A	C	0.22	P2RY10	ENST00000171757_r73	c.7 A>C	p.N3H	MISSENSE
MA4_23R	ChrX	79281202	G	A	0.368421053	TBX22	ENST00000373296_r73	c.559 G>A	p.E187K	MISSENSE
MA4_23R	ChrX	83723541	A	G	0.283018868	HDX	ENST00000297977_r73	c.1190 T>C	p.F397S	MISSENSE
MA4_23R	ChrX	85219021	T	C	0.174757282	CHM	ENST00000357749_r73	c.351 A>G	p.A117A	SILENT
MA4_23R	ChrX	86887244	C	T	0.25	KLHL4	ENST00000373119_r73	c.1359 C>T	p.T453T	SILENT
MA4_23R	ChrX	88008807	G	A	0.285714286	CPXCR1	ENST00000276127_r73	c.392 G>A	p.R131H	MISSENSE
MA4_23R	ChrX	89177673	G	A	0.279069767	TGIF2LX	ENST00000283891_r73	c.589 G>A	p.V197I	MISSENSE
MA4_23R	ChrX	99890204	C	T	0.295454546	TSPAN6	ENST00000373020_r73	c.322 G>A	p.A108T	MISSENSE
MA4_23R	ChrX	100749588	A	C	0.325	ARMCX4	ENST00000423738_r73	c.6012 A>C	p.Q2004H	MISSENSE
MA4_23R	ChrX	100808222	C	T	0.214876033	ARMCX1	ENST00000372829_r73	c.309 C>T	p.G103G	SILENT
MA4_23R	ChrX	103042882	T	C	0.263157895	PLP1	ENST00000303958_r73	c.609 T>C	p.D203D	SILENT
MA4_23R	ChrX	103294760	C	T	0.462686567	H2BFM	ENST00000355016_r73	c.217 C>T	p.Q73*	NONSENSE
MA4_23R	ChrX	104992963	T	C	0.26984127	IL1RAPL2	ENST00000372582_r73	c.1059 T>C	p.Y353Y	SILENT
MA4_23R	ChrX	105152282	G	A	0.333333333	NRK	ENST00000243300_r73	c.1072 G>A	p.V358M	MISSENSE
MA4_23R	ChrX	105449445	T	A	0.284210526	MUM1L1	ENST00000357175_r73	c.20 T>A	p.L7Q	MISSENSE
MA4_23R	ChrX	105449709	G	A	0.324786325	MUM1L1	ENST00000357175_r73	c.284 G>A	p.G95D	MISSENSE
MA4_23R	ChrX	111698613	T	C	0.279411765	ZCCHC16	ENST00000340433_r73	c.657 T>C	p.H219H	SILENT
MA4_23R	ChrX	111914244	A	G	0.272727273	LHFPL1	ENST00000371968_r73	c.375 T>C	p.F125F	SILENT
MA4_23R	ChrX	114398338	T	G	0.213333333	LRCH2	ENST00000317135_r73	c.1364 A>C	p.K455T	MISSENSE
MA4_23R	ChrX	114541176	G	A	0.5	LUZP4	ENST00000371920_r73	c.749 G>A	p.R250K	MISSENSE
MA4_23R	ChrX	117528142	C	T	0.26056338	WDR44	ENST00000254029_r73	c.951 C>T	p.T317T	SILENT
MA4_23R	ChrX	118108785	T	C	0.225806452	LONRF3	ENST00000365713_r73	c.42 T>C	p.A14A	SILENT
MA4_23R	ChrX	118587003	C	T	0.206666667	SLC25A43	ENST00000217909_r73	c.1001 C>T	p.P334L	MISSENSE
MA4_23R	ChrX	118604436	T	C	0.565217391	SLC25A5	ENST00000317881_r73	c.699 T>C	p.T233T	SILENT
MA4_23R	ChrX	118678364	G	A	0.454545455	CXorf56	ENST00000486230_r73	c.375 C>T	p.G125G	SILENT
MA4_23R	ChrX	122537277	T	C	0.571428571	GRIA3	ENST00000371251_r73	c.1200 T>C	p.N400N	SILENT
MA4_23R	ChrX	123034511	A	C	0.5	XIAP	ENST00000371199_r73	c.1268 A>C	p.Q423P	MISSENSE
MA4_23R	ChrX	123540315	G	T	0.75	TENM1	ENST00000371130_r73	c.4986 C>A	p.T1662T	SILENT
MA4_23R	ChrX	125954964	C	G	0.172413793	CXorf64	ENST00000371125_r73	c.343 C>G	p.L115V	MISSENSE
MA4_23R	ChrX	128880614	T	C	0.529411765	XPNPEP2	ENST00000371106_r73	c.447 T>C	p.P149P	SILENT
MA4_23R	ChrX	129201179	C	T	0.152542373	ELF4	ENST00000335997_r73	c.1509 G>A	p.T503T	SILENT
MA4_23R	ChrX	129283520	A	G	0.222222222	AIFM1	ENST00000416073_r73	c.273 T>C	p.D91D	SILENT
MA4_23R	ChrX	129349295	T	G	0.265306122	ZNF280C	ENST00000370978_r73	c.1851 A>C	p.G617G	SILENT
MA4_23R	ChrX	129518646	A	G	0.244897959	GPR119	ENST00000276218_r73	c.776 T>C	p.V259A	MISSENSE
MA4_23R	ChrX	130408745	G	A	0.273972603	IGSF1	ENST00000370910_r73	c.3552 C>T	p.V1184V	SILENT

MA4_23R	ChrX	130409217	C	G	0.333333333	IGSF1	ENST00000370910_r73	c.3201 G>C	p.M1067I	MISSENSE
MA4_23R	ChrX	131212512	A	G	0.288288288	FRMD7	ENST00000298542_r73	c.1533 T>C	p.I511I	SILENT
MA4_23R	ChrX	131212944	A	G	0.236111111	FRMD7	ENST00000298542_r73	c.1101 T>C	p.N367N	SILENT
MA4_23R	ChrX	132161159	G	A	0.212389381	USP26	ENST00000370832_r73	c.1090 C>T	p.L364F	MISSENSE
MA4_23R	ChrX	132161673	C	T	0.253164557	USP26	ENST00000370832_r73	c.576 G>A	p.E192E	SILENT
MA4_23R	ChrX	133963268	C	T	0.251968504	FAM122C	ENST00000370785_r73	c.202 C>T	p.P68S	MISSENSE
MA4_23R	ChrX	134185997	T	A	0.405405405	FAM127B	ENST00000370775_r73	c.142 A>T	p.S48C	MISSENSE
MA4_23R	ChrX	134990000	C	T	0.283333333	SAGE1	ENST00000370709_r73	c.1159 C>T	p.H387Y	MISSENSE
MA4_23R	ChrX	134991078	A	G	0.20625	SAGE1	ENST00000370709_r73	c.1497 A>G	p.Q499Q	SILENT
MA4_23R	ChrX	134994005	T	C	0.35483871	SAGE1	ENST00000370709_r73	c.2414 T>C	p.L805S	MISSENSE
MA4_23R	ChrX	135426693	A	G	0.189655172	GPR112	ENST00000394143_r73	c.828 A>G	p.I276M	MISSENSE
MA4_23R	ChrX	135431236	T	C	0.297435897	GPR112	ENST00000394143_r73	c.5371 T>C	p.F1791L	MISSENSE
MA4_23R	ChrX	135431358	C	T	0.277777778	GPR112	ENST00000394143_r73	c.5493 C>T	p.P1831P	SILENT
MA4_23R	ChrX	135480126	T	C	0.37037037	GPR112	ENST00000394143_r73	c.8271 T>C	p.F2757F	SILENT
MA4_23R	ChrX	135496398	G	A	0.26519337	GPR112	ENST00000394143_r73	c.9117 G>A	p.T3039T	SILENT
MA4_23R	ChrX	138679712	T	A	0.17948718	MCF2	ENST00000520602_r73	c.2142 A>T	p.G714G	SILENT
MA4_23R	ChrX	142795225	G	A	0.230769231	SPANXN2	ENST00000370498_r73	c.453 C>T	p.D151D	SILENT
MA4_23R	ChrX	149013097	G	A	0.173913044	MAGEA8	ENST00000286482_r73	c.51 G>A	p.Q17Q	SILENT
MA4_23R	ChrX	149680554	C	T	0.289156627	MAMLD1	ENST00000432680_r73	c.2208 C>T	p.S736S	SILENT
MA4_23R	ChrX	150348610	C	T	0.220183486	GPR50	ENST00000218316_r73	c.555 C>T	p.N185N	SILENT
MA4_23R	ChrX	150817094	C	G	0.242105263	PASD1	ENST00000370357_r73	c.637 C>G	p.Q213E	MISSENSE
MA4_23R	ChrX	150840916	C	T	0.510638298	PASD1	ENST00000370357_r73	c.1699 C>T	p.L567L	SILENT
MA4_23R	ChrX	150911107	G	A	0.375	CNGA2	ENST00000329903_r73	c.582 G>A	p.L194L	SILENT
MA4_23R	ChrX	151092220	A	G	0.242424242	MAGEA4	ENST00000370340_r73	c.84 A>G	p.A28A	SILENT
MA4_23R	ChrX	151899913	T	C	0.227722772	MAGEA12	ENST00000357916_r73	c.888 A>G	p.G296G	SILENT
MA4_23R	ChrX	152106638	C	T	0.230769231	ZNF185	ENST00000370268_r73	c.1139 C>T	p.S380F	MISSENSE
MA4_23R	ChrX	152751497	G	A	0.3	U82695.9	ENST00000428676_r73	c.140 G>A	p.R47H	MISSENSE
MA4_23R	ChrX	153039502	G	C	0.304347826	PLXNB3	ENST00000361971_r73	c.3468 G>C	p.E1156D	MISSENSE
MA4_23R	ChrX	153041544	T	C	0.186046512	PLXNB3	ENST00000361971_r73	c.4604 T>C	p.M1535T	MISSENSE
MA4_23R	ChrX	153046686	C	T	0.1875	SRPK3	ENST00000370104_r73	c.75 C>T	p.C25C	SILENT
MA4_23R	ChrX	153070999	G	A	0.28125	PDZD4	ENST00000164640_r73	c.612 C>T	p.N204N	SILENT
MA4_23R	ChrX	153132228	G	A	0.276923077	L1CAM	ENST00000370060_r73	c.2307 C>T	p.S769S	SILENT
MA4_23R	ChrX	153172059	C	T	0.212962963	AVPR2	ENST00000358927_r73	c.993 C>T	p.S331S	SILENT
MA4_23R	ChrX	153421912	T	C	0.216216216	OPN1LW	ENST00000369951_r73	c.888 T>C	p.G296G	SILENT
MA4_23R	ChrX	153540977	A	G	0.25	TKTL1	ENST00000369915_r73	c.717 A>G	p.E239E	SILENT
MA4_23R	ChrX	153581932	A	G	0.36	FLNA	ENST00000360319_r73	c.5826 T>C	p.A1942A	SILENT
MA4_23R	ChrX	153667176	T	C	0.271186441	GDI1	ENST00000447750_r73	c.219 T>C	p.N73N	SILENT

MA4_23R	ChrX	153760953	C	T	0.298850575	G6PD	ENST00000393562_r73	c.1206 G>A	p.Q402Q	SILENT
MA4_23R	ChrX	153880569	A	G	0.363636364	CTAG2	ENST00000247306_r73	c.606 T>C	p.N202N	SILENT
MA4_23R	ChrX	153880634	C	G	0.391304348	CTAG2	ENST00000247306_r73	c.541 G>C	p.G181R	MISSENSE
MA4_23R	ChrX	153880830	A	C	0.297709924	CTAG2	ENST00000247306_r73	c.345 T>G	p.P115P	SILENT
MA4_23R	ChrX	153881525	G	C	0.267441861	CTAG2	ENST00000247306_r73	c.265 C>G	p.Q89E	MISSENSE
MA4_23R	Chr11	209895	CCC	-	0.107142857	RIC8A	ENST00000325207_r73	c.621 CCC>-	p.N207 NP>N	MISSENSE
MA4_23R	Chr11	17352478	ACA	-	0.166666667	NUCB2	ENST00000529010_r73	c.1203 ACA>-	p.L401 LQ>L	MISSENSE
MA4_23R	Chr11	4592707	-	AC	0.151162791	C11orf40	ENST00000307616_r73	c.600 ->GT	p.C200fs*12	FRAMESHIFT
MA4_23R	Chr11	5172796	-	C	0.192592593	OR52A1	ENST00000380367_r73	c.804 ->G	p.G268fs*14	FRAMESHIFT
MA4_23R	Chr11	71850157	-	TA	0.112033195	FOLR3	ENST00000542161_r73	c.313 ->TA	p.*105fs*73	FRAMESHIFT
MA4_23R	Chr11	73020376	-	CTC	0.125	ARHGEF17	ENST00000263674_r73	c.693 ->CTC	p.C231 C>CS	MISSENSE
MA4_23R	Chr11	94153333	-	ATC	0.142857143	MRE11A	ENST00000323929_r73	c.2085 ->GAT	p.D695 D>EI	MISSENSE
MA4_23R	Chr7	137612914	TGG	-	0.4375	CREB3L2	ENST00000330387_r73	c.299 CCA>-	p.T100 TS>S	MISSENSE
MA4_23R	Chr7	12391269	-	A	0.2	VWDE	ENST00000275358_r73	c.3816 ->T	p.N1272fs*2	FRAMESHIFT
MA4_23R	Chr17	38858135	A	-	0.180851064	KRT24	ENST00000264651_r73	c.666 T>-	p.N222fs*11	FRAMESHIFT
MA4_23R	Chr17	72957963	T	-	0.3125	HID1	ENST00000425042_r73	Exon 6 + 5 A>-	-	ESSENTIAL_SPLICE
MA4_23R	Chr17	79219501	ATG	-	0.260273973	SLC38A10	ENST00000374759_r73	c.3213 CAT>-	p.I1071 II>I	MISSENSE
MA4_23R	Chr2	3749152	GAA	-	0.176470588	ALLC	ENST00000252505_r73	c.901 GAA>-	p.E301Del(E)	MISSENSE
MA4_23R	Chr2	112843593	TTGATAT	-	0.222222222	TMEM87B	ENST00000283206_r73	c.850 TTGATAT>-	p.L284fs*4	FRAMESHIFT
MA4_23R	Chr2	238244864	GCA	-	0.171052632	COL6A3	ENST00000295550_r73	c.8877 TGC>-	p.A2959 AA>A	MISSENSE
MA4_23R	Chr2	71801335	-	AGGCGG	0.109090909	DYSF	ENST00000409762_r73	c.3233 ->AGGCGG	p.Q1078 Q>QAE	MISSENSE
MA4_23R	Chr2	170387133	-	T	0.181818182	FASTKD1	ENST00000453153_r73	c.2406 ->A	p.K802fs*18	FRAMESHIFT
MA4_23R	Chr2	172967129	-	GCT	0.122222222	DLX2	ENST00000234198_r73	c.138 ->AGC	p.S46 S>RA	MISSENSE
MA4_23R	Chr2	234113397	-	TG	0.181818182	INPP5D	ENST00000491070_r73	c.110 ->TG	p.I37fs*90	FRAMESHIFT
MA4_23R	Chr2	234429740	-	TTC	0.271186441	USP40	ENST00000450966_r73	c.2255 ->GAA	p.K752 K>RK	MISSENSE
MA4_23R	Chr22	38119755	CAA	-	0.157894737	TRIOBP	ENST00000406386_r73	c.1192 CAA>-	p.Q398Del(Q)	MISSENSE
MA4_23R	Chr22	36587846	-	CT	0.120171674	APOL4	ENST00000404685_r73	c.331 ->AG	p.V111fs*242	FRAMESHIFT
MA4_23R	Chr1	9304979	CCCAGGCA	-	0.178571429	H6PD	ENST00000377403_r73	Exon 2 - 5 CCCAGGCA>-	-	ESSENTIAL_SPLICE
MA4_23R	Chr1	36643701	AGA	-	0.333333333	MAP7D1	ENST00000373151_r73	c.1607 AGA>-	p.E536 EK>E	MISSENSE
MA4_23R	Chr1	45974801	CCCGCC	-	0.158273381	MMACHC	ENST00000401061_r73	c.763 CCCGCC>-	p.P255Del(PA)	MISSENSE
MA4_23R	Chr1	153907279	CTGCTGCTG	-	0.102040816	DENND4B	ENST00000361217_r73	c.2722 CAGCAGCAG>-	p.Q908Del(QQQ)	MISSENSE
MA4_23R	Chr1	154542837	ACA	-	0.145833333	CHRNB2	ENST00000368476_r73	c.359 ACA>-	p.Y120 YN>Y	MISSENSE
MA4_23R	Chr1	156354348	C	-	0.184210526	RHBG	ENST00000368249_r73	c.1265 C>-	p.S422fs*38	FRAMESHIFT
MA4_23R	Chr1	206239432	AAT	-	0.183823529	C1orf186	ENST00000331555_r73	c.464 ATT>-	p.Y155 YF>F	MISSENSE
MA4_23R	Chr1	23966895	-	AAG	0.275362319	MDS2	ENST00000374555_r73	c.279 ->AAG	p.V93 V>VR	MISSENSE
MA4_23R	Chr1	85598680	-	A	0.110236221	WDR63	ENST00000294664_r73	c.2675 ->A	p.*892fs*1	FRAMESHIFT
MA4_23R	Chr1	153907279	-	CTG	0.102040816	DENND4B	ENST00000361217_r73	c.2730 ->CAG	p.Q910 Q>HR	MISSENSE

MA4_23R	Chr1	234744946	-	GCT	0.205882353	IRF2BP2	ENST00000366610_r73	c.295 ->AGC	p.L99Ins(S)	MISSENSE
MA4_23R	Chr1	248059780	-	A	0.136363636	OR2W3	ENST00000360358_r73	c.892 ->A	p.K298fs*19	FRAMESHIFT
MA4_23R	Chr18	60646248	CAG	-	0.129533679	PHLPP1	ENST00000262719_r73	c.4738 CAG>-	p.Q1580Del(Q)	MISSENSE
MA4_23R	Chr16	3406757	T	-	0.175257732	OR2C1	ENST00000304936_r73	c.817 T>-	p.F273fs*13	FRAMESHIFT
MA4_23R	Chr16	7760847	AAA	-	0.238095238	RBFOX1	ENST00000550418_r73	Exon 16 + 5 AAA>-	-	ESSENTIAL_SPLICE
MA4_23R	Chr16	67859708	AGG	-	0.125	TSNAXIP1	ENST00000388833_r73	c.791 AGG>-	p.Q264 QE>Q	MISSENSE
MA4_23R	Chr16	336889	-	A	0.190476191	PDIA2	ENST00000219406_r73	c.1477 ->A	p.N493fs*64	FRAMESHIFT
MA4_23R	Chr13	61102576	ATA	-	0.133640553	TDRD3	ENST00000377894_r73	c.938 ATA>-	p.D313 DN>D	MISSENSE
MA4_23R	Chr13	77532065	CAGAGGTAG	-	0.207317073	IRG1	ENST00000377462_r73	c.1391 CAGAGGTAG>-	p.P464 PEVA>P	MISSENSE
MA4_23R	Chr6	168314998	G	-	0.108108108	MLLT4	ENST00000392108_r73	Exon 16 + 5 G>-	-	ESSENTIAL_SPLICE
MA4_23R	ChrX	135474445	GAT	-	0.266666667	GPR112	ENST00000394143_r73	c.7966 GAT>-	p.D2656Del(D)	MISSENSE
MA4_23R	ChrX	36162685	-	TG	0.30952381	CHDC2	ENST00000378660_r73	c.1268 ->TG	p.L423fs*2	FRAMESHIFT
MA4_23R	ChrX	112022298	-	AGG	0.177777778	AMOT	ENST00000304758_r73	c.1857 ->CCT	p.P619 P>PL	MISSENSE
MA4_23R	Chr3	124482495	TTGTTGAAC	-	0.144578313	ITGB5	ENST00000296181_r73	c.2367 GTTCAACAA>-	p.K789 KFNK>K	MISSENSE
MA4_23R	Chr3	56650055	-	CTC	0.188679245	CCDC66	ENST00000394672_r73	c.1817 ->CTC	p.S606 S>SP	MISSENSE
MA4_23R	Chr3	122459291	-	AGA	0.111111111	HSPBAP1	ENST00000306103_r73	c.1368 ->TCT	p.P456 P>PL	MISSENSE
MA4_23R	Chr9	139235482	C	-	0.159090909	GPSM1	ENST00000392945_r73	c.1239 C>-	p.L413fs*57	FRAMESHIFT
MA4_23R	Chr9	80881428	-	GGG	0.153333333	CEP78	ENST00000415759_r73	c.1871 ->GGG	p.P624 P>RA	MISSENSE
MA4_23R	Chr9	125391771	-	A	0.255813954	OR1B1	ENST00000304833_r73	c.44 ->T	p.L15fs*9	FRAMESHIFT
MA4_23R	Chr12	27849503	A	-	0.2	REP15	ENST00000310791_r73	c.8 A>-	p.Q3fs*9	FRAMESHIFT
MA4_23R	Chr12	72070506	GTT	-	0.101449275	THAP2	ENST00000308086_r73	c.305 GTT>-	p.S102 SC>S	MISSENSE
MA4_23R	Chr12	2062324	-	TGC	0.104477612	DCP1B	ENST00000280665_r73	c.782 ->GCA	p.Q261 Q>RK	MISSENSE
MA4_23R	Chr20	25457050	CTCCCA	-	0.161764706	NINL	ENST00000278886_r73	c.2872 TGGGAG>-	p.W958Del(WE)	MISSENSE
MA4_23R	Chr14	94410276	A	-	0.32	RP11-131H24.4	ENST00000557646_r73	c.167 A>-	p.Q56fs*8	FRAMESHIFT
MA4_23R	Chr14	105352885	GCAGGA	-	0.215686275	CEP170B	ENST00000556508_r73	c.2099 GCAGGA>-	p.R700 RRS>R	MISSENSE
MA4_23R	Chr14	23548788	-	GTGAAT	0.123076923	ACIN1	ENST00000262710_r73	c.1930 ->ATTCAC	p.R644Ins(IH)	MISSENSE
MA4_23R	Chr15	43579798	C	-	0.121827411	TGM7	ENST00000452443_r73	c.628 G>-	p.A210fs*17	FRAMESHIFT
MA4_23R	Chr15	41099900	-	GGGGC	0.153846154	ZFYVE19	ENST00000355341_r73	c.113 ->GGGGC	p.W38fs*73	FRAMESHIFT
MA4_23R	Chr8	75664695	A	-	0.143646409	RP11-758M4.1	ENST00000523442_r73	c.248 A>-	p.H83fs*24	FRAMESHIFT
MA4_23R	Chr8	145740367	A	-	0.111111111	RECQL4	ENST00000428558_r73	c.1573 T>-	p.C525fs*33	FRAMESHIFT
MA4_23R	Chr8	72755648	-	T	0.166666667	RP11-383H13.1	ENST00000537896_r73	c.12 ->T	p.T4fs*16	FRAMESHIFT
MA4_23R	Chr4	177106010	TCTC	-	0.158227848	SPATA4	ENST00000280191_r73	c.836 GAGA>-	p.R279fs*4	FRAMESHIFT
MA4_23R	Chr19	8389893	TCC	-	0.13592233	KANK3	ENST00000330915_r73	c.2022 GGA>-	p.E674 ED>D	MISSENSE
MA4_23R	Chr19	11558341	GAG	-	0.1875	PRKCSH	ENST00000591462_r73	c.937 GAG>-	p.E313Del(E)	MISSENSE
MA4_23R	Chr19	23927742	CA	-	0.119047619	ZNF681	ENST00000402377_r73	c.609 TG>-	p.C203fs*5	FRAMESHIFT
MA4_23R	Chr19	37879853	TGTGCA	-	0.125748503	ZNF527	ENST00000436120_r73	c.902 TGTGCA>-	p.P301 PYA>PYA	MISSENSE
MA4_23R	Chr19	54973989	CCT	-	0.172413793	LENG9	ENST00000333834_r73	c.785 AGG>-	p.E262 EA>A	MISSENSE

MA4_23R	Chr19	34263201	-	AGC	0.13	CHST8	ENST00000438847_r73	c.508 ->AGC	p.S170Ins(S)	MISSENSE
MA4_23R	Chr19	46265048	-	TCCAGC	0.128205128	AC074212.3	ENST00000457052_r73	c.1357 ->TCCAGC	p.S453Ins(SS)	MISSENSE
MA4_23R	Chr19	55790887	-	GCCGCCGCC	0.112359551	HSPBP1	ENST00000255631_r73	c.90 ->GGCGGCGGC	p.G30 G>GAAA	MISSENSE
MA4_23R	Chr19	56244722	-	T	0.143884892	NLRP9	ENST00000332836_r73	c.475 ->A	p.T159fs*31	FRAMESHIFT
MA4_23R	Chr10	21435341	CACT	-	0.133640553	C10orf113	ENST00000534331_r73	c.94 AGTG>-	p.S32fs*5	FRAMESHIFT
MA4_23R	Chr10	22498485	-	AGA	0.251231527	EBLN1	ENST00000422359_r73	c.428 ->TCT	p.L143 L>LL	MISSENSE
MA4_23R	Chr10	27702257	-	C	0.121052632	PTCHD3	ENST00000438700_r73	c.923 ->G	p.G308fs*27	FRAMESHIFT
MA4_23R	Chr10	32740799	-	T	0.183486239	CCDC7	ENST00000277657_r73	c.229 ->T	p.L77fs*6	FRAMESHIFT
MA4_23R	Chr5	7867478	ATA	-	0.147368421	FASTKD3	ENST00000264669_r73	c.717 TAT>-	p.I239 II>I	MISSENSE
MA4_23R	Chr5	74491716	TCA	-	0.14	ANKRD31	ENST00000506364_r73	c.755 TGA>-	p.M252 MN>N	MISSENSE
MA4_23R	Chr5	111755670	G	-	0.132653061	FLJ11235	ENST00000600409_r73	c.376 G>-	p.G126fs*173	FRAMESHIFT
MA4_23R	Chr5	180687429	TCT	-	0.233502538	TRIM52	ENST00000327767_r73	c.384 AGA>-	p.E128 EE>E	MISSENSE
MA4_24	Chr2	130832835	C	T	0.107142857	POTEF	ENST00000409914_r73	c.2210 G>A	p.R737H	MISSENSE
MA4_24	Chr1	203134484	G	T	0.076923077	ADORA1	ENST00000309502_r73	c.437 G>T	p.W146L	MISSENSE
MA4_24	Chr9	138377427	C	T	0.04787234	PPP1R26	ENST00000605286_r73	c.1071 C>T	p.S357S	SILENT
MA4_24	Chr1	115258748	C	T	0.033224146	NRAS	ENST00000369535_r73	c.34 G>A	p.G12S	MISSENSE
MA4_24	ChrX	100400133	G	C	0.022727273	CENPI	ENST00000372927_r73	c.1646 G>C	p.R549P	MISSENSE
MA4_24R	Chr21	22849652	G	A	0.30781759	NCAM2	ENST00000400546_r73	c.1937 G>A	p.G646E	MISSENSE
MA4_24R	Chr1	186014936	G	A	0.251021166	HMCN1	ENST00000271588_r73	c.6421 G>A	p.G2141S	MISSENSE
MA4_24R	Chr6	152420061	A	G	0.386363636	ESR1	ENST00000338799_r73	c.1748 A>G	p.Y583C	MISSENSE
MA4_24R	ChrX	100400133	G	C	0.52644041	CENPI	ENST00000372927_r73	c.1646 G>C	p.R549P	MISSENSE
MA4_24R	Chr14	64954616	T	A	0.31037692	ZBTB25	ENST00000261683_r73	c.333 A>T	p.A111A	SILENT
MA4_24R	Chr8	37702629	C	G	0.3010279	BRF2	ENST00000220659_r73	c.639 G>C	p.E213D	MISSENSE
MA4_24R	Chr9	126783462	C	T	0.231441048	LHX2	ENST00000373615_r73	c.812 C>T	p.T271M	MISSENSE
MA4_24R	Chr8	26240718	G	A	0.299591837	BNIP3L	ENST00000380629_r73	c.72 G>A	p.Q24Q	SILENT
MA4_24R	Chr12	53298699	G	A	0.277777778	KRT8	ENST00000552551_r73	c.67 C>T	p.R23C	MISSENSE
MA4_24R	ChrX	100745623	G	-	0.125	ARMCX4	ENST00000423738_r73	c.2047 G>-	p.D683fs*262	FRAMESHIFT
MA4_25	Chr22	31495066	C	T	0.181305399	SMTN	ENST00000358743_r73	c.2352 C>T	p.R784R	SILENT
MA4_25	Chr12	25398284	C	T	0.182159147	KRAS	ENST00000311936_r73	c.35 G>A	p.G12D	MISSENSE
MA4_25	Chr4	100574475	G	A	0.363435173	RP11-766F14.2	ENST00000511828_r73	c.1331 C>T	p.T444M	MISSENSE
MA4_25	Chr5	176517475	G	A	0.785784993	FGFR4	ENST00000292408_r73	c.176 G>A	p.R59Q	MISSENSE
MA4_25	Chr1	115258747	C	T	0.011875955	NRAS	ENST00000369535_r73	c.35 G>A	p.G12D	MISSENSE
MA4_25	Chr1	115258748	C	T	0.03457938	NRAS	ENST00000369535_r73	c.34 G>A	p.G12S	MISSENSE
MA4_25	Chr12	25398281	C	T	0.02281746	KRAS	ENST00000311936_r73	c.38 G>A	p.G13D	MISSENSE
MA9_02	Chr8	142204230	G	A	0.138424043	DENND3	ENST00000262585_r73	c.3495 G>A	p.A1165A	SILENT
MA9_05	Chr12	25378561	G	A	0.010122395	KRAS	ENST00000369535_r73	c.35 G>A	p.G12D	MISSENSE
MA9_05	Chr3	78684959	G	A	0.013206336	ROBO1	ENST00000464233_r73	c.3337 C>T	p.Q1113*	NONSENSE

MA9_05	Chr3	165547388	C	T	0.014514278	BCHE	ENST00000264381_r73	c.1434 G>A	p.L478L	SILENT
MA9_03	Chr2	228563984	G	A	0.048889717	SLC19A3	ENST00000425817_r73	c.447 C>T	p.A149A	SILENT
MA9_03	Chr1	79002226	C	T	0.105546838	PTGFR	ENST00000370758_r73	c.934 C>T	p.L312F	MISSENSE
MA9_03	Chr12	25398281	C	T	0.026697105	KRAS	ENST00000311936_r73	c.38 G>A	p.G13D	MISSENSE
MA9_04	Chr2	189868770	G	C	0.223776224	COL3A1	ENST00000304636_r73	c.2724 G>C	p.A908A	SILENT
MA9_04	Chr12	104092949	C	T	0.42753908	STAB2	ENST00000388887_r73	c.3658 C>T	p.R1220C	MISSENSE
MA9_04	Chr8	113702206	A	G	0.323759791	CSMD3	ENST00000343508_r73	c.1926 T>C	p.N642N	SILENT
MLLwt_01	Chr17	7577094	-	CCT	0.326332017	TP53	ENST00000269305_r73	c.844 ->AGG	p.R282Ins(R)	MISSENSE
MLLwt_01	Chr8	12595499	C	T	0.444754464	LONRF1	ENST00000398246_r73	Exon 4 5 G>A	-	ESSENTIAL_SPLICE
MLLwt_01	Chr1	38341371	G	A	0.417063492	INPP5B	ENST00000373024_r73	c.1695 C>T	p.D565D	SILENT
MLLwt_01	Chr14	68270920	G	A	0.439142317	ZFYVE26	ENST00000347230_r73	c.1333 C>T	p.L445F	MISSENSE
MLLwt_02	Chr8	2820915	C	T	0.692964304	CSMD1	ENST00000537824_r73	c.9283 G>A	p.V3095M	MISSENSE
MLLwt_02	Chr9	5078360	A	G	0.322690992	JAK2	ENST00000381652_r73	c.2047 A>G	p.R683G	MISSENSE
MLLwt_02	Chr3	32933224	G	A	0.391132723	TRIM71	ENST00000383763_r73	c.2528 G>A	p.R843H	MISSENSE
MLLwt_02	Chr4	81865980	G	A	0.251284104	C4orf22	ENST00000358105_r73	c.493 G>A	p.A165T	MISSENSE
MLLwt_02	Chr9	139278036	C	T	0.203371398	SNAPC4	ENST00000298532_r73	c.1585 G>A	p.G529S	MISSENSE
MLLwt_02	Chr1	216462698	G	T	0.180441281	USH2A	ENST00000307340_r73	c.1895 C>A	p.P632H	MISSENSE
MLLwt_03	Chr9	95237025	-	TCATCATCA	0.026448196	ASPN	ENST00000375544_r73	c.155 ->TGATGATGA	p.E52 E>VMMK	MISSENSE
MLLwt_03	Chr11	1266996	T	C	0.258956916	MUC5B	ENST00000529681_r73	c.8886 T>C	p.R2962R	SILENT
MLLwt_03	Chr12	112888162	G	C	0.0860887	PTPN11	ENST00000392597_r73	c.178 G>C	p.G60R	MISSENSE
MLLwt_04	Chr16	58076166	G	A	0.055459184	MMP15	ENST00000219271_r73	c.1196 G>A	p.R399H	MISSENSE
MLLwt_05	Chr3	10953794	C	T	0.124726845	SLC6A11	ENST00000254488_r73	c.911 C>T	p.T304M	MISSENSE
MLLwt_06	Chr7	4800821	C	T	0.375	FOXK1	ENST00000328914_r73	c.1823 C>T	p.T608I	MISSENSE
MLLwt_06	Chr6	20124710	G	A	0.410250182	MBOAT1	ENST00000324607_r73	c.836 C>T	p.P279L	MISSENSE
MLLwt_06	Chr6	27100393	A	T	0.224532225	HIST1H2BJ	ENST00000607124_r73	c.137 T>A	p.L46Q	MISSENSE
MLLwt_06	Chr20	60791797	C	G	0.422680412	HRH3	ENST00000340177_r73	c.603 G>C	p.T201T	SILENT
MLLwt_06	Chr1	86289382	G	T	0.303030303	COL24A1	ENST00000370571_r73	c.3721 C>A	p.Q1241K	MISSENSE
MLLwt_06	Chr4	169433068	G	C	0.095695971	PALLD	ENST00000261509_r73	c.413 G>C	p.R138P	MISSENSE
MLLwt_07	Chr7	100643824	C	T	0.044602273	MUC12	ENST00000536621_r73	c.9980 C>T	p.T3327M	MISSENSE
MLLwt_07	Chr12	112230482	G	A	0.312261781	ALDH2	ENST00000416293_r73	c.838 G>A	p.V280M	MISSENSE
MLLwt_08	Chr16	737085	C	T	0.379388448	WDR24	ENST00000293883_r73	c.991 G>A	p.A331T	MISSENSE
MLLwt_08	Chr11	1017828	G	A	0.083926755	MUC6	ENST00000421673_r73	c.4973 C>T	p.T1658M	MISSENSE
MLLwt_08	Chr17	4643865	C	T	0.346	ZMYND15	ENST00000433935_r73	c.22 C>T	p.R8W	MISSENSE
MLLwt_08	Chr10	15719628	G	A	0.388174807	ITGA8	ENST00000378076_r73	c.639 C>T	p.D213D	SILENT
MLLwt_08	Chr6	38905788	C	T	0.268558952	DNAH8	ENST00000449981_r73	c.11602 C>T	p.R3868*	NONSENSE
MLLwt_08	Chr2	43452533	-	AG	0.346	ZFP36L2	ENST00000282388_r73	c.410 ->CT	p.L137fs*51	FRAMESHIFT
MLLwt_08	Chr20	62599293	G	A	0.030521212	ZNF512B	ENST00000369888_r73	c.11 C>T	p.P4L	MISSENSE

MLLwt_09	Chr12	25398281	C	T	0.026697105	KRAS	ENST00000311936_r73	c.38 G>A	p.G13D	MISSENSE
MLLwt_10	Chr16	29830928	G	A	0.057032224	PAGR1	ENST00000320330_r73	c.618 G>A	p.S206S	SILENT
MLLwt_10	Chr1	156761566	C	T	0.178651281	PRCC	ENST00000271526_r73	c.1161 C>T	p.S387S	SILENT