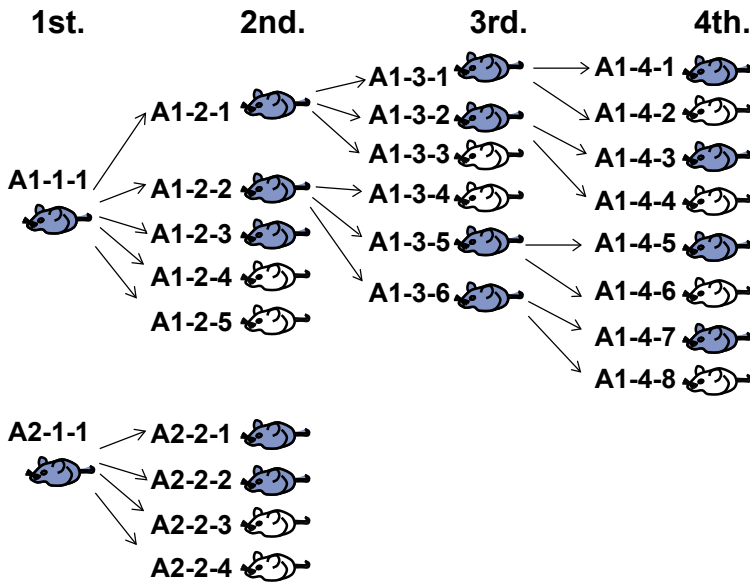


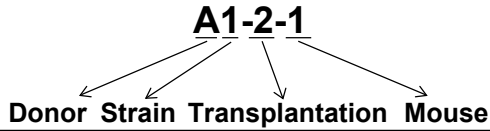
# Supplementary Figure 1

## Donor A

### Transplantation

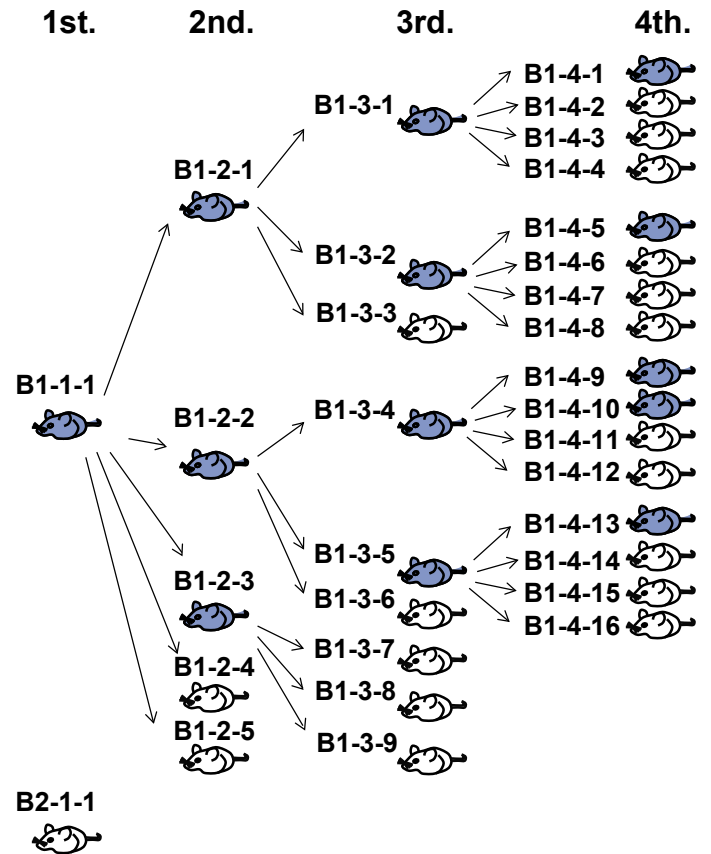


### Annotation



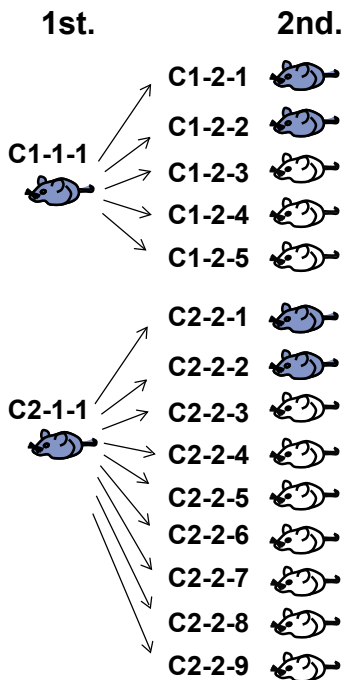
## Donor B

### Transplantation



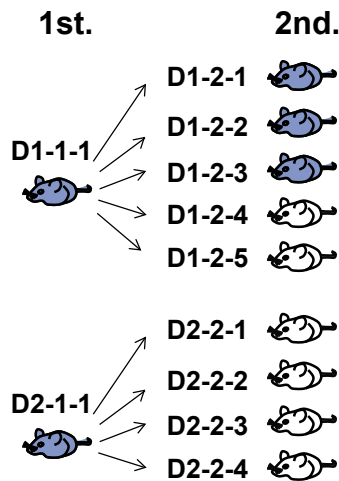
## Donor C

### Transplantation



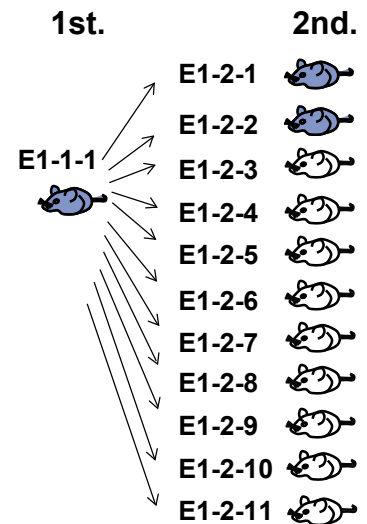
## Donor D

### Transplantation



## Donor E

### Transplantation



→

Transplantation  
(N=96)

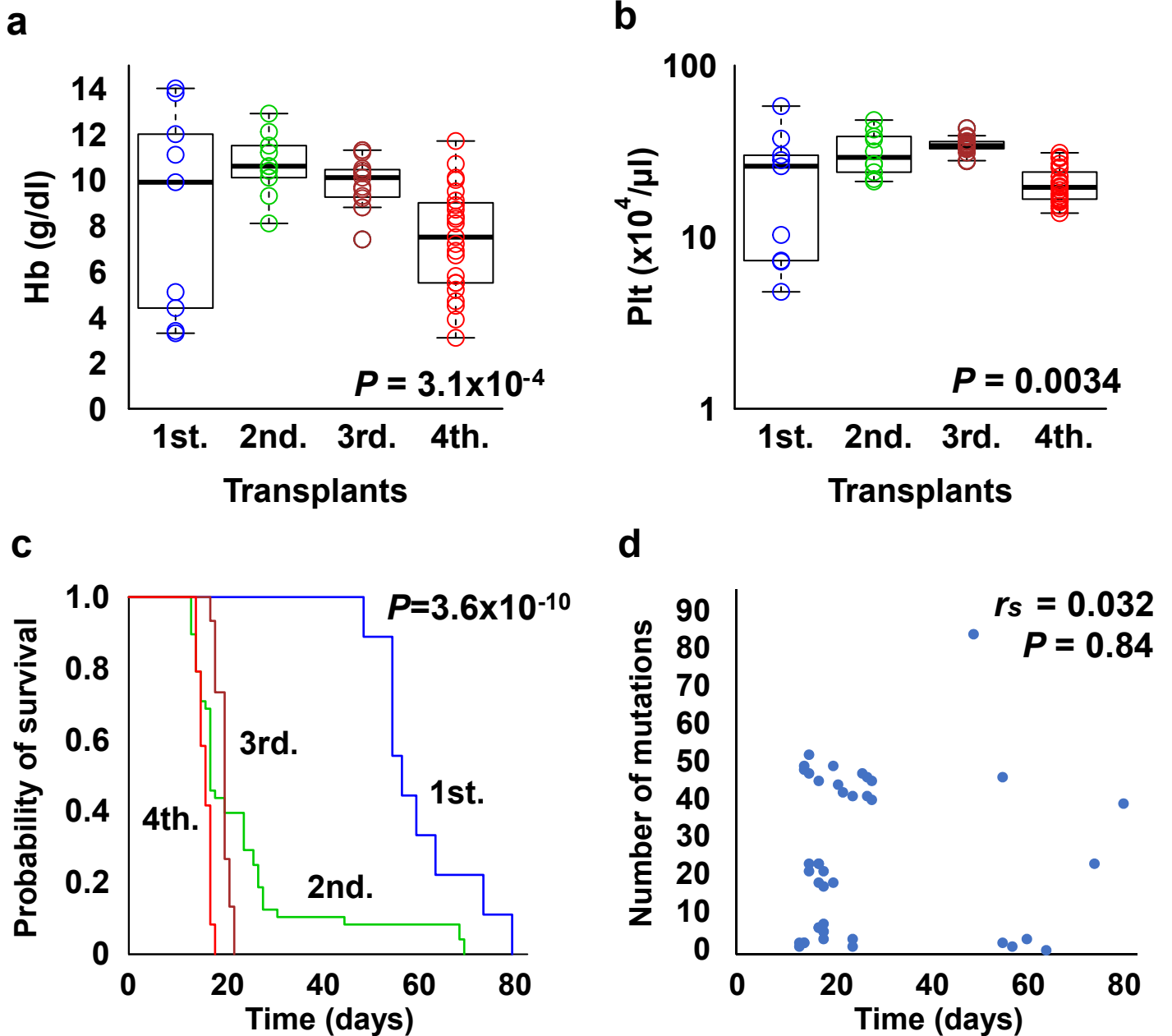
1st. (n= 9)  
 2nd. (n=48)  
 3rd. (n=15)  
 4th. (n=24)

→

Sequenced  
(n=42)

**Supplementary Figure 1. Transplantation of mouse *MLL/AF9* acute myeloid leukemia (*MLL/AF9*-AML).** Serial transplantation of mouse *MLL/AF9*-AML was performed in C57BL/6 mice (N=96). Blue mice were analyzed by whole exome sequencing but white ones were not.

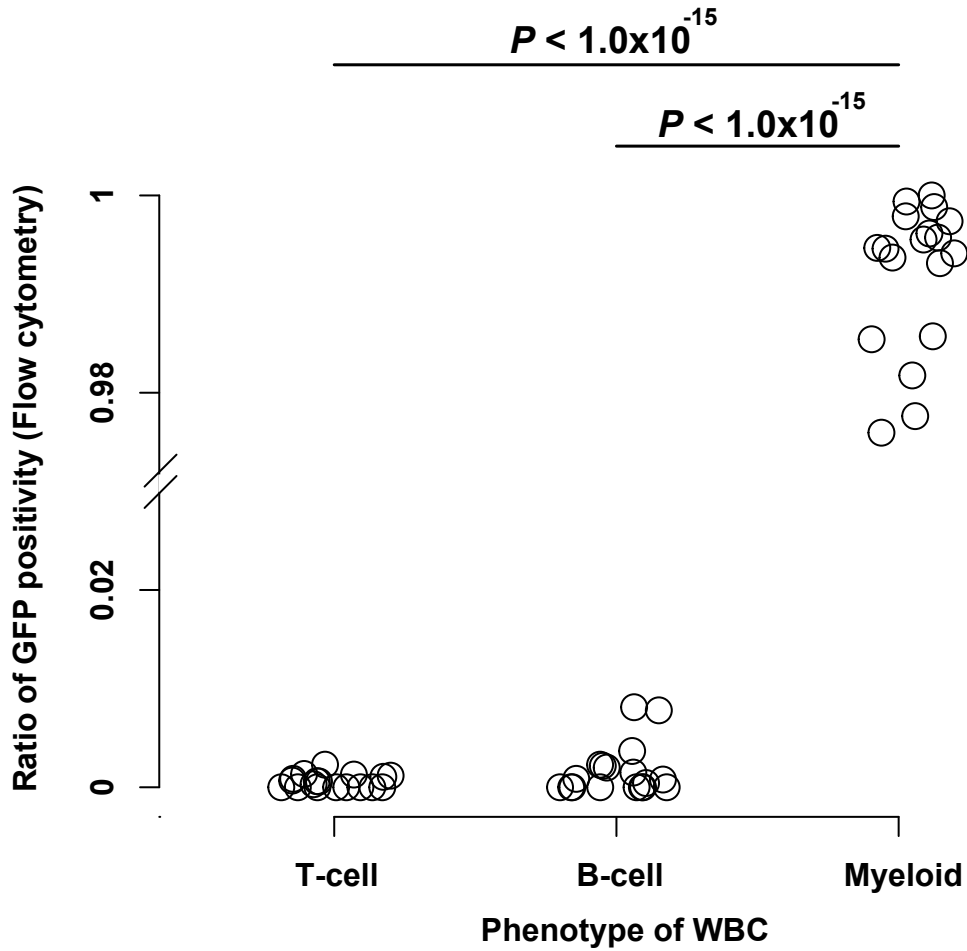
## Supplementary Figure 2



### Supplementary Figure 2. Blood counts, relapse time, and number of mutations during serial transplantation of mouse *MLL/AF9* acute myeloid leukemia.

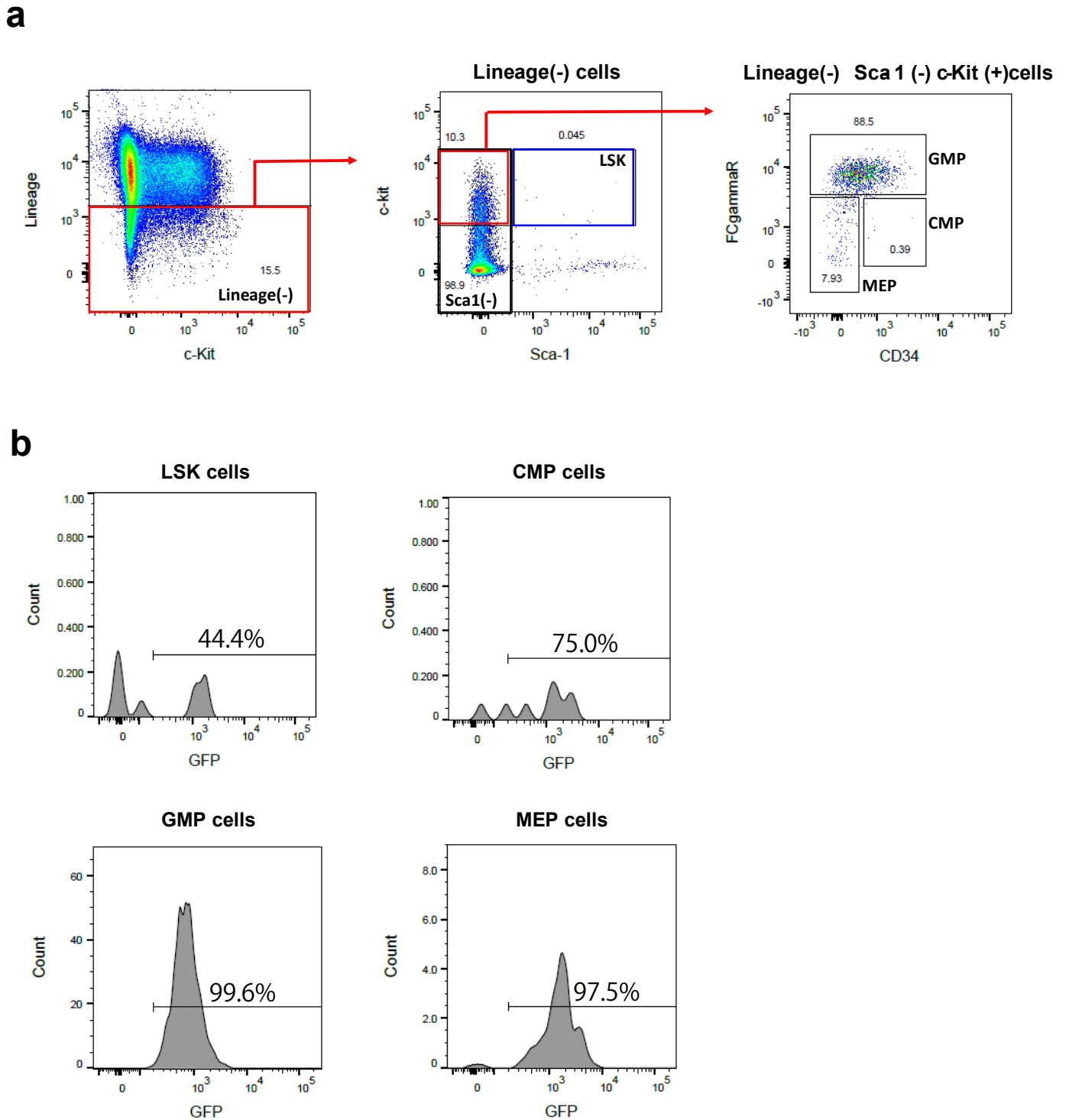
Hemoglobin levels (Hb) (a) and platelet counts (Plt) (b) were measured on day 14 after transplantation. Trends of changes in the blood counts (a, b) and time to leukemia onset after transplantation (c) were assessed by the Jonckheere-Terpstra test. The correlation between number of mutations and time of leukemia onset was assessed by Spearman's rank correlation coefficient (d).

### Supplementary Figure 3



**Supplementary Figure 3. Phenotype of WBC in peripheral blood in *MLL/AF9*-AML mouse model.** In serial transplantation of mouse *MLL/AF9* acute myeloid leukemia, GFP positivity was examined by flowcytometry in T-cell, B-cell, and myeloid populations.

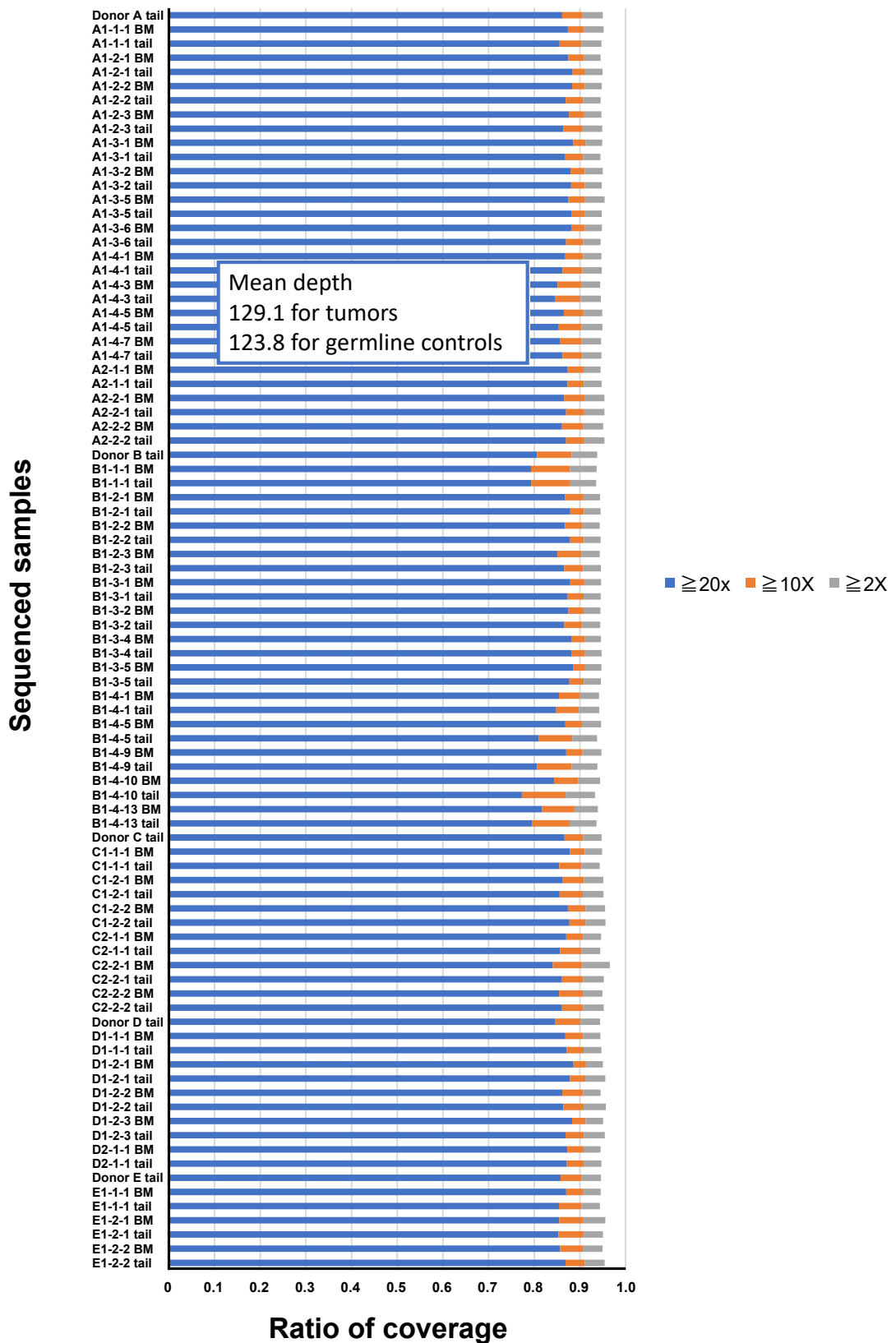
# Supplementary Figure 4



## Supplementary Figure 4. Phenotype of mouse *MLL/AF9* acute myeloid leukemia.

Phenotype of mouse *MLL/AF9* acute myeloid leukemia cells was examined by flowcytometry using fluorescence-conjugated anti-lineage, Sca1, c-Kit, FcR gamma II/III, and CD34 antibodies (a). GFP positivity was measured in LSK, CMP, GMP, and MEP populations by flowcytometry (b). Representative results were shown in the second transplantation.

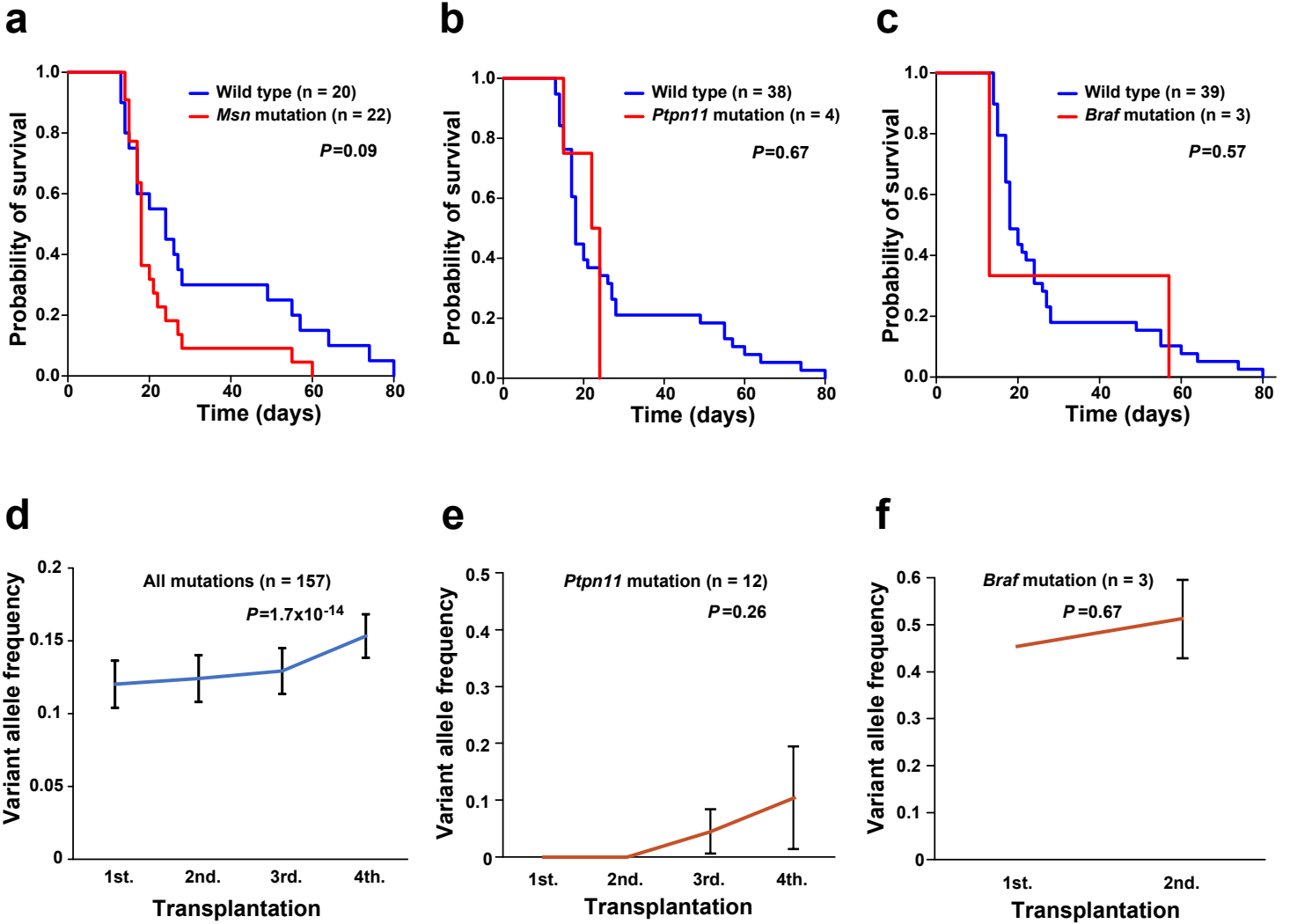
# Supplementary Figure 5



## Supplementary Figure 5. Mean coverage of whole exome sequencing.

The coverage of the targeted region is plotted for 42 paired tumor/germline samples from transplanted mice and germline samples from 5 donor mice. The mean depth for all tumor (bone marrow: BM) and germline (tail) samples is also indicated.

# Supplementary Figure 6

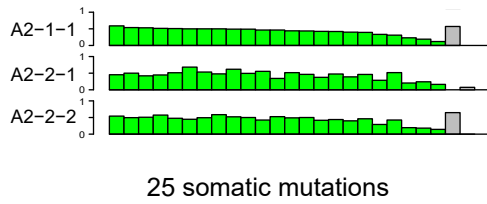
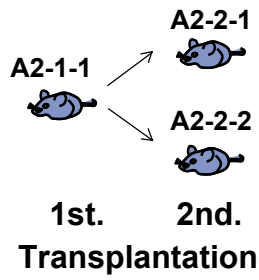


## Supplementary Figure 6. Prognostic impact and allelic burden of identified mutations.

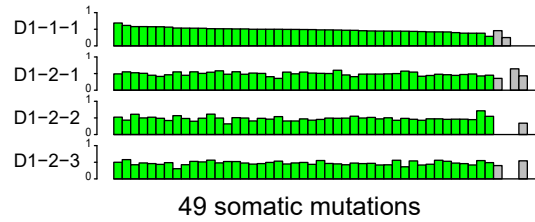
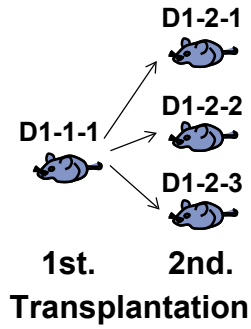
(a-c) Comparison of leukemia-onset time between cases with and without mutations in *Msn* (a), *Ptpn11* (b), and *Braf* (c). (d-f) Assessment of trend in variant allele frequencies of all mutations (d), *Ptpn11* (e), and *Braf* (f).

# Supplementary Figure 7

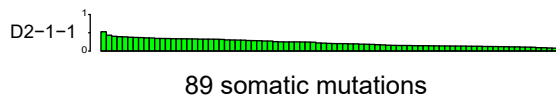
**a**



**b**



**c**



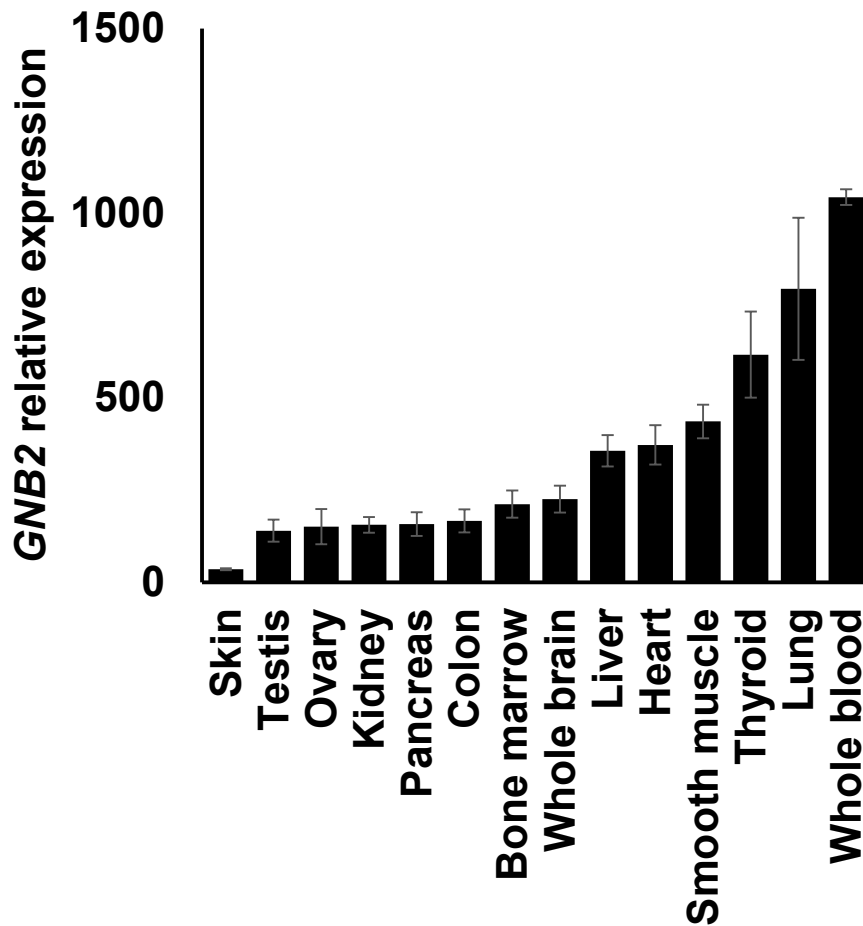
Shared mutation

Private mutation

## Supplementary Figure 7. Landscape of somatic mutations in transplantation model of mouse *MLL/AF9*-AML.

Upper panels show mice analyzed by WES in strain A2 (a), D1 (b), and D2 (c). Lower panels demonstrate landscape and number of somatic mutations in each strain. Green and gray indicate shared and private mutations, respectively.

## Supplementary Figure 8

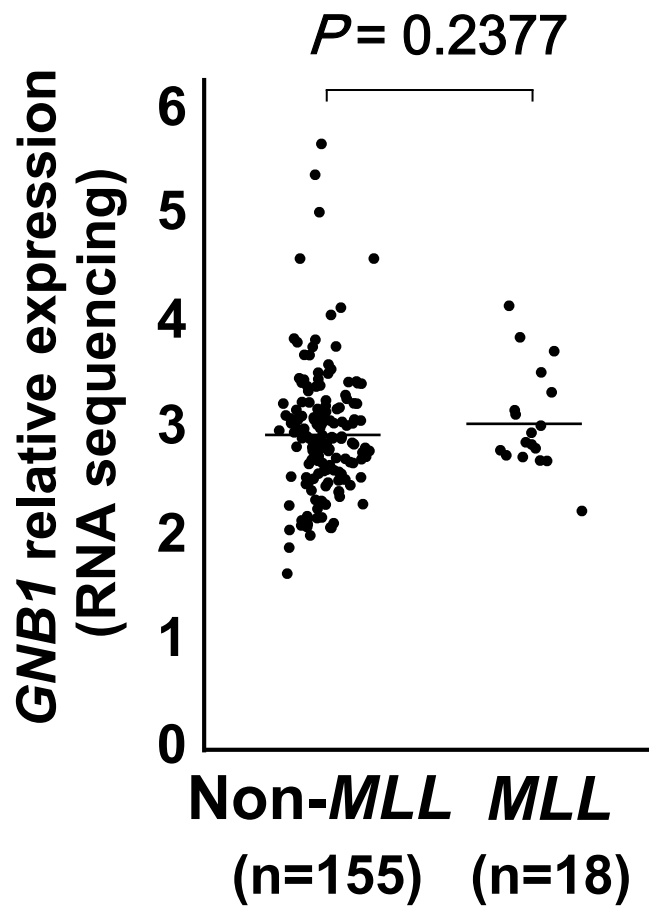


### Supplementary Figure 8. *GNB2* relative expression in human normal tissues.

Relative expressions of *GNB2* mRNA in various human normal tissues were extracted from the global gene expression data set analyzed by GeneAtlas U133A expression array, which was downloaded from BioGPS (<http://biogps.org/>).



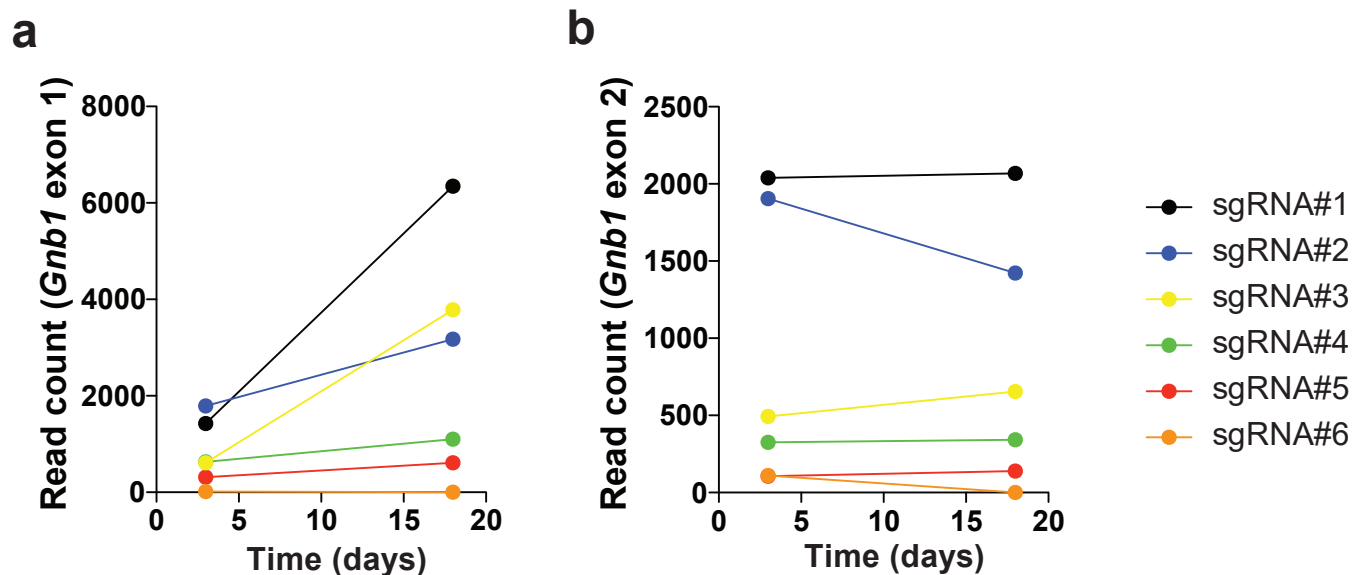
## Supplementary Figure 9



**Supplementary Figure 9. *GNB1* relative expression in human *MLL*-AML.**

*GNB1* relative expression in human AML with and without *MLL*-fusion gene (RNA sequencing).

## Supplementary Figure 10



### Supplementary Figure 10. Impact of depletion of *Gnb1* in mouse *MLL/AF9* acute myeloid leukemia.

By genome-wide CRISPR-Cas9 screens, read counts of six sgRNAs targeting per exon (exon 1 (a) and 2 (b)) in *Gnb1* were measured after a 16-day incubation period to confirm potential oncogenic function of *Gnb1* in *MLL*-AML.

**Supplementary Table 1. Primer sets for real time RT-PCR**

<b>Primer annotation</b>	<b>Primer sequence</b>
<b><i>GNB2</i></b> (NM_005273)	
Forward primer	TGAATCCGACATCAATGCAG
Reverse primer	TCAGAGCCGGTGGTGAAG
<b><i>Gnb2</i></b> (NM_010312)	
Forward primer	GGCAAAAATCTATGCCATGC
Reverse primer	TGATGAGCTTTCCGTCCTG
<b><i>Gnb1</i></b> (NM_001160017)	
Forward primer	CCAGTTCTGGAGACACCACAT
Reverse primer	GGAGCAAGAGACAGGCTCA
<b><i>18S</i></b>	
Forward primer	GTAACCCGTTGAACCCATT
Reverse primer	CCATCCAATCGGTAGTAGCG

**Supplementary Table 2. Targeted sequences of shRNA for *GNB2* knockdown**

Target gene	shRNA #	Targeted sequence
<i>GNB2</i>	#2	CCTGGATGACAACCAAATCAT
<i>GNB2</i>	#5	CGACGACTTCAACTGCAACAT
<i>GNB2</i>	#6	GCCAATTCCAACCTGTAAAA
Scramble	-	CCTAAGGTTAAGTCGCCCTCG

Effect of shRNA #6 was shown in **Figure 8a-c**. Results of #2 and #5 were not shown.

Supplementary Table 3. Somatic mutations identified by whole exome sequencing in mouse *MLL/AF9* leukemic cells (n = 42).

Strain	Mouse	Chromosome	Start	End	Reference	Alteration	Gene	Mutation type	Accession number	Nucleotide	Amino acid	Variant allele frequency
A1	A1-1-1	chr1	110925165	110925165	G	A	Cdh19	Missense	NM_001081386	c.C1039T	p.H347Y	0.302
A1	A1-1-1	chr1	88215102	88215102	G	A	Ugt1a1	Missense	NM_201645	c.G929A	p.G310E	0.099
A1	A1-1-1	chr1	63309706	63309706	G	A	Zdbf2	Missense	NM_001267872	c.G7243A	p.A2415T	0.095
A1	A1-1-1	chr2	93696152	93696152	G	A	Ext2	Missense	NM_010163	c.C2138T	p.P713L	0.517
A1	A1-1-1	chr2	155421512	155421512	G	A	Ncoa6	Missense	NM_019825	c.C1001T	p.P334L	0.593
A1	A1-1-1	chr2	124664020	124664020	G	A	Sema6d	Splice site	NM_199241	c.1934-1G>A	NA	0.426
A1	A1-1-1	chr2	59838975	59838975	G	A	Tanc1	Missense	NM_198294	c.G3803A	p.G1268E	0.452
A1	A1-1-1	chr3	106149750	106149750	T	C	Chi3l3	Missense	NM_009892	c.A877G	p.K293E	0.266
A1	A1-1-1	chr4	63225586	63225586	T	G	Col27a1	Missense	NM_025685	c.T1510G	p.L504V	0.461
A1	A1-1-1	chr5	120609628	120609628	G	A	1110008J03Rik	Missense	NM_029096	c.C604T	p.P202S	0.491
A1	A1-1-1	chr5	14539711	14539711	C	T	Pclo	Missense	NM_011995	c.C2024T	p.A675V	0.321
A1	A1-1-1	chr6	38196439	38196439	G	A	D630045J12Rik	Missense	NM_194061	c.C793T	p.L265F	0.448
A1	A1-1-1	chr6	85337030	85337030	G	A	Rab11fip5	Missense	NM_001003955	c.C3950T	p.P1317L	0.416
A1	A1-1-1	chr7	128133275	128133275	T	C	Itgax	Missense	NM_021334	c.T572C	p.L191P	0.435
A1	A1-1-1	chr7	102752989	102752989	T	A	Olfir560	Missense	NM_147113	c.A939T	p.E313D	0.554
A1	A1-1-1	chr7	25081644	25081644	C	T	Zfp574	Missense	NM_001168506	c.C2090T	p.P697L	0.506
A1	A1-1-1	chr8	27154308	27154308	G	A	Rab11fip1	Missense	NM_001080813	c.C1448T	p.P483L	0.544
A1	A1-1-1	chr9	14572677	14572677	C	T	Amotl1	Missense	NM_001081395	c.G1589A	p.R530Q	0.382
A1	A1-1-1	chr9	54335830	54335830	T	A	Gldn	Nonsense	NM_177350	c.T1095A	p.Y365X	0.488
A1	A1-1-1	chr10	11295240	11295240	T	G	Fbxo30	Missense	NM_027968	c.T2061G	p.F687L	0.515
A1	A1-1-1	chr10	129912132	129912132	C	T	Olfir816	Missense	NM_146672	c.G145A	p.V49M	0.525
A1	A1-1-1	chr10	94794675	94794675	C	A	Plxnc1	Nonsense	NM_018797	c.G4456T	p.E1486X	0.5
A1	A1-1-1	chr10	51723856	51723856	C	T	Rfx6	Missense	NM_001159389	c.C1799T	p.P600L	0.552
A1	A1-1-1	chr10	26245602	26245602	T	C	Samd3	Missense	NM_001115154	c.T616C	p.F206L	0.456
A1	A1-1-1	chr10	33200204	33200204	C	A	Trdn	Missense	NM_029726	c.C829A	p.H277N	0.5
A1	A1-1-1	chr11	120273314	120273314	G	A	Bahcc1	Splice site	NM_198423	c.2228-1G>A	NA	0.48
A1	A1-1-1	chr11	106813834	106813834	G	A	Cep95	Missense	NM_177088	c.G1514A	p.R505K	0.439
A1	A1-1-1	chr11	54916905	54916905	G	A	Tnfp1	Missense	NM_021327	c.C1709T	p.A570V	0.505
A1	A1-1-1	chr13	73268858	73268858	G	A	Irx4	Missense	NM_018885	c.G1372A	p.G458S	0.517
A1	A1-1-1	chr14	37057443	37057443	A	T	Lrit1	Missense	NM_146245	c.A332T	p.E111V	0.44
A1	A1-1-1	chr14	79770248	79770248	C	T	Pcdh8	Missense	NM_021543	c.G874A	p.E292K	0.504
A1	A1-1-1	chr14	57643200	57643200	G	A	Xpo4	Missense	NM_020506	c.C199T	p.L67F	0.319
A1	A1-1-1	chr15	76106727	76106727	C	T	Eppk1	Missense	NM_144848	c.G5953A	p.G1985S	0.397
A1	A1-1-1	chr15	52335160	52335160	G	T	Slc30a8	Missense	NM_172816	c.G1000T	p.A334S	0.429
A1	A1-1-1	chr17	65256583	65256583	C	T	Tmem232	Missense	NM_001008973	c.G1814A	p.R605Q	0.583
A1	A1-1-1	chr18	34863349	34863349	G	T	Egr1	Missense	NM_007913	c.G1183T	p.A395S	0.565
A1	A1-1-1	chr19	29717713	29717713	G	A	9930021J03Rik	Missense	NM_172836	c.C4580T	p.P1527L	0.424
A1	A1-1-1	chr19	54047310	54047310	G	A	Adra2a	Missense	NM_007417	c.G1096A	p.E366K	0.503
A1	A1-1-1	chrX	94538510	94538510	T	C	Maged1	Splice site	NM_019791	c.1414-2A>G	NA	0.434
A1	A1-1-1	chrX	139824102	139824102	C	T	Morc4	Missense	NM_001193309	c.G2213A	p.G738E	0.444
A1	A1-2-1	chr1	110925165	110925165	G	A	Cdh19	Missense	NM_001081386	c.C1039T	p.H347Y	0.489
A1	A1-2-1	chr2	93696152	93696152	G	A	Ext2	Missense	NM_010163	c.C2138T	p.P713L	0.449
A1	A1-2-1	chr2	155421512	155421512	G	A	Ncoa6	Missense	NM_019825	c.C1001T	p.P334L	0.516
A1	A1-2-1	chr2	124664020	124664020	G	A	Sema6d	Splice site	NM_199241	c.1934-1G>A	NA	0.486
A1	A1-2-1	chr2	59838975	59838975	G	A	Tanc1	Missense	NM_198294	c.G3803A	p.G1268E	0.303
A1	A1-2-1	chr3	106149750	106149750	T	C	Chi3l3	Missense	NM_009892	c.A877G	p.K293E	0.193
A1	A1-2-1	chr3	158161735	158161735	C	T	Lrrc7	Missense	NM_001081358	c.G2368A	p.A790T	0.086
A1	A1-2-1	chr4	63225586	63225586	T	G	Col27a1	Missense	NM_025685	c.T1510G	p.L504V	0.557
A1	A1-2-1	chr4	113177004	113177004	G	A	Skint6	Nonsense	NM_001103199	c.C925T	p.Q309X	0.537
A1	A1-2-1	chr5	120609628	120609628	G	A	1110008J03Rik	Missense	NM_029096	c.C604T	p.P202S	0.552
A1	A1-2-1	chr5	35043862	35043880	G	-	Hgfac	Nonsense	NM_019447	c.628_646del	p.G211X	0.242
A1	A1-2-1	chr6	38196439	38196439	G	A	D630045J12Rik	Missense	NM_194061	c.C793T	p.L265F	0.493
A1	A1-2-1	chr6	85337030	85337030	G	A	Rab11fip5	Missense	NM_001003955	c.C3950T	p.P1317L	0.5
A1	A1-2-1	chr7	128133275	128133275	T	C	Itgax	Missense	NM_021334	c.T572C	p.L191P	0.545
A1	A1-2-1	chr7	102752989	102752989	T	A	Olfir560	Missense	NM_147113	c.A939T	p.E313D	0.366
A1	A1-2-1	chr7	25081644	25081644	C	T	Zfp574	Missense	NM_001168506	c.C2090T	p.P697L	0.482
A1	A1-2-1	chr8	27154308	27154308	G	A	Rab11fip1	Missense	NM_001080813	c.C1448T	p.P483L	0.489
A1	A1-2-1	chr9	14572677	14572677	C	T	Amotl1	Missense	NM_001081395	c.G1589A	p.R530Q	0.089
A1	A1-2-1	chr9	54335830	54335830	T	A	Gldn	Nonsense	NM_177350	c.T1095A	p.Y365X	0.404
A1	A1-2-1	chr10	11295240	11295240	T	G	Fbxo30	Missense	NM_027968	c.T2061G	p.F687L	0.447
A1	A1-2-1	chr10	129912132	129912132	C	T	Olfir816	Missense	NM_146672	c.G145A	p.V49M	0.514
A1	A1-2-1	chr10	94794675	94794675	C	A	Plxnc1	Nonsense	NM_018797	c.G4456T	p.E1486X	0.574
A1	A1-2-1	chr10	51723856	51723856	C	T	Rfx6	Missense	NM_001159389	c.C1799T	p.P600L	0.423
A1	A1-2-1	chr10	26245602	26245602	T	C	Samd3	Missense	NM_001115154	c.T616C	p.F206L	0.473
A1	A1-2-1	chr10	33200204	33200204	C	A	Trdn	Missense	NM_029726	c.C829A	p.H277N	0.5
A1	A1-2-1	chr11	120273314	120273314	G	A	Bahcc1	Splice site	NM_198423	c.2228-1G>A	NA	0.483
A1	A1-2-1	chr11	106813834	106813834	G	A	Cep95	Missense	NM_177088	c.G1514A	p.R505K	0.585
A1	A1-2-1	chr11	54916905	54916905	G	A	Tnfp1	Missense	NM_021327	c.C1709T	p.A570V	0.494
A1	A1-2-1	chr13	73268858	73268858	G	A	Irx4	Missense	NM_018885	c.G1372A	p.G458S	0.498
A1	A1-2-1	chr14	37057443	37057443	A	T	Lrit1	Missense	NM_146245	c.A332T	p.E111V	0.482
A1	A1-2-1	chr14	79770248	79770248	C	T	Pcdh8	Missense	NM_021543	c.G874A	p.E292K	0.527
A1	A1-2-1	chr14	57643200	57643200	G	A	Xpo4	Missense	NM_020506	c.C199T	p.L67F	0.528
A1	A1-2-1	chr15	76106727	76106727	C	T	Eppk1	Missense	NM_144848	c.G5953A	p.G1985S	0.475
A1	A1-2-1	chr15	52335160	52335160	G	T	Slc30a8	Missense	NM_172816	c.G1000T	p.A334S	0.5
A1	A1-2-1	chr15	89116046	89116046	C	T	Tubgcp6	Missense	NM_001163319	c.G1115A	p.R372Q	0.07
A1	A1-2-1	chr17	65256583	65256583	C	T	Tmem232	Missense	NM_001008973	c.G1814A	p.R605Q	0.462
A1	A1-2-1	chr18	34863349	34863349	G	T	Egr1	Missense	NM_007913	c.G1183T	p.A395S	0.526
A1	A1-2-1	chr19	29717713	29717713	G	A	9930021J03Rik	Missense	NM_172836	c.C4580T	p.P1527L	0.497
A1	A1-2-1	chr19	54047310	54047310	G	A	Adra2a	Missense	NM_007417	c.G1096A	p.E366K	0.483
A1	A1-2-1	chrX	94538510	94538510	T	C	Maged1	Splice site	NM_019791	c.1414-2A>G	NA	0.431
A1	A1-2-1	chrX	139824102	139824102	C	T	Morc4	Missense	NM_001193309	c.G2213A	p.G738E	0.481
A1	A1-2-1	chrX	96160175	96160175	C	T	Msn	Missense	NM_010833	c.C883T	p.R295C	0.405
A1	A1-2-2	chr1	110925165	110925165	G	A	Cdh19	Missense	NM_001081386	c.C1039T	p.H347Y	0.478
A1	A1-2-2	chr2	93696152	93696152	G	A	Ext2	Missense	NM_010163	c.C2138T	p.P713L	0.495
A1	A1-2-2	chr2	155421512	155421512	G	A	Ncoa6	Missense	NM_019825	c.C1001T	p.P334L	0.5
A1	A1-2-2	chr2	124664020	124664020	G	A	Sema6d	Splice site	NM_199241	c.1934-1G>A	NA	0.456
A1	A1-2-2	chr2	59838975	59838975	G	A	Tanc1	Missense	NM_198294	c.G3803A	p.G1268E	0.5
A1	A1-2-2	chr3	106149750	106149750	T	C	Chi3l3	Missense	NM_009892	c.A877G	p.K293E	0.207
A1	A1-2-2	chr4	63225586	63225586	T	G	Col27a1	Missense	NM_025685	c.T1510G	p.L504V	0.52
A1	A1-2-2	chr5	120609628	120609628	G	A	1110008J03Rik	Missense	NM_029096	c.C604T	p.P202S	0.485
A1	A1-2-2	chr5	35043862	35043880	G	-	Hgfac	Nonsense	NM_019447	c.628_646del	p.G211X	0.314
A1	A1-2-2	chr5	14539711	14539711	C	T	Pclo	Missense	NM_011995	c.C2024T	p.A675V	0.11
A1	A1-2-2	chr6	38196439	38196439	G	A	D630045J12Rik	Missense	NM_194061	c.C793T	p.L265F	0.514
A1	A1-2-2	chr6	85337030	85337030	G	A	Rab11fip5	Missense	NM_001003955	c.C3950T	p.P1317L	0.393
A1	A1-2-2	chr7	128133275	128133275	T	C	Itgax	Missense	NM_021334	c.T572C	p.L191P	0.497
A1	A1-2-2	chr7	102752989	102752989	T	A	Olfir560	Missense	NM_147113	c.A939T	p.E313D	0.483
A1	A1-2-2	chr7	25081644	25081644	C	T	Zfp574	Missense	NM_001168506	c.C2090T	p.P697L	0.502

A1	A1-2-2	chrX	96160175	96160175	C	T	Msn	Missense	NM_010833	c.C883T	p.R295C	0.351
A1	A1-2-3	chr1	110925165	110925165	G	A	Cdh19	Missense	NM_001081386	c.C1039T	p.H347Y	0.591
A1	A1-2-3	chr1	63309706	63309706	G	A	Zdbf2	Missense	NM_001267872	c.G7243A	p.A2415T	0.102
A1	A1-2-3	chr2	93696152	93696152	G	A	Ext2	Missense	NM_010163	c.C2138T	p.P713L	0.418
A1	A1-2-3	chr2	155421512	155421512	G	A	Ncoa6	Missense	NM_019825	c.C1001T	p.P334L	0.355
A1	A1-2-3	chr2	124664020	124664020	G	A	Sema6d	Splice site	NM_199241	c.1934-1G>A	NA	0.431
A1	A1-2-3	chr2	59838975	59838975	G	A	Tanc1	Missense	NM_198294	c.G3803A	p.G1268E	0.514
A1	A1-2-3	chr3	106149750	106149750	T	C	Chi3l3	Missense	NM_009892	c.A877G	p.K293E	0.254
A1	A1-2-3	chr4	63225586	63225586	T	G	Col27a1	Missense	NM_025685	c.T1510G	p.L504V	0.538
A1	A1-2-3	chr4	113177004	113177004	G	A	Skint6	Nonsense	NM_001103199	c.C925T	p.Q309X	0.415
A1	A1-2-3	chr5	120609628	120609628	G	A	1110008J03Rik	Missense	NM_029096	c.C604T	p.P202S	0.479
A1	A1-2-3	chr5	35043862	35043880	GTGGGCGACCACTGGGCC	-	Hgfac	Nonsense	NM_019447	c.G28_646del	p.G211X	0.077
A1	A1-2-3	chr5	14539711	14539711	C	T	Pclo	Missense	NM_011995	c.C2024T	p.A675V	0.195
A1	A1-2-3	chr6	38196439	38196439	G	A	D630045J12Rik	Missense	NM_194061	c.C793T	p.L265F	0.459
A1	A1-2-3	chr6	85337030	85337030	G	A	Rab11fip5	Missense	NM_001003955	c.C3950T	p.P1317L	0.42
A1	A1-2-3	chr7	128133275	128133275	T	C	Ilgax	Missense	NM_021334	c.T572C	p.L191P	0.441
A1	A1-2-3	chr7	102752989	102752989	T	A	Olfir560	Missense	NM_147113	c.A939T	p.E313D	0.52
A1	A1-2-3	chr7	25081644	25081644	C	T	Zfp574	Missense	NM_001168506	c.C2090T	p.P697L	0.438
A1	A1-2-3	chr8	27154308	27154308	G	A	Rab11fip1	Missense	NM_001080813	c.C1448T	p.P483L	0.549
A1	A1-2-3	chr9	14572677	14572677	C	T	Amotl1	Missense	NM_001081395	c.G1589A	p.R530Q	0.305
A1	A1-2-3	chr9	54335830	54335830	T	A	Gldn	Nonsense	NM_177350	c.T1095A	p.Y365X	0.43
A1	A1-2-3	chr10	11295240	11295240	T	G	Fbxo30	Missense	NM_027968	c.T2061G	p.F687L	0.302
A1	A1-2-3	chr10	129912132	129912132	C	T	Olfir816	Missense	NM_146672	c.G145A	p.V49M	0.438
A1	A1-2-3	chr10	94794675	94794675	C	A	Plxnc1	Nonsense	NM_018797	c.G4456T	p.E1486X	0.52
A1	A1-2-3	chr10	51723856	51723856	C	T	Rfx6	Missense	NM_001159389	c.C1799T	p.P600L	0.51
A1	A1-2-3	chr10	26245602	26245602	T	C	Samd3	Missense	NM_001115154	c.T616C	p.F206L	0.533
A1	A1-2-3	chr10	33200204	33200204	C	A	Trdn	Missense	NM_029726	c.C829A	p.H277N	0.457
A1	A1-2-3	chr11	120273314	120273314	G	A	Bahcc1	Splice site	NM_198423	c.2228-1G>A	NA	0.484
A1	A1-2-3	chr11	106813834	106813834	G	A	Cep95	Missense	NM_177088	c.G1514A	p.R505K	0.452
A1	A1-2-3	chr11	54916905	54916905	G	A	Tnip1	Missense	NM_021327	c.C1709T	p.A570V	0.508
A1	A1-2-3	chr13	73268858	73268858	G	A	Irx4	Missense	NM_018885	c.G1372A	p.G458S	0.465
A1	A1-2-3	chr14	37057443	37057443	A	T	Lrit1	Missense	NM_146245	c.A332T	p.E111V	0.524
A1	A1-2-3	chr14	79770248	79770248	C	T	Pcdh8	Missense	NM_021543	c.G874A	p.E292K	0.532
A1	A1-2-3	chr14	57643200	57643200	G	A	Xpo4	Missense	NM_020506	c.C199T	p.L67F	0.5
A1	A1-2-3	chr15	76106727	76106727	C	T	Eppk1	Missense	NM_144848	c.G5953A	p.G1985S	0.487
A1	A1-2-3	chr15	52335160	52335160	G	T	Slc30a8	Missense	NM_172816	c.G1000T	p.A334S	0.514
A1	A1-2-3	chr17	65256583	65256583	C	T	Tmem232	Missense	NM_001008973	c.G1814A	p.R605Q	0.406
A1	A1-2-3	chr18	34863349	34863349	G	T	Egr1	Missense	NM_007913	c.G1183T	p.A395S	0.483
A1	A1-2-3	chr19	29717713	29717713	G	A	9930021J03Rik	Missense	NM_172836	c.C4580T	p.P1527L	0.455
A1	A1-2-3	chr19	54047310	54047310	G	A	Adra2a	Missense	NM_007417	c.G1096A	p.E366K	0.459
A1	A1-2-3	chrX	94538510	94538510	T	C	Maged1	Splice site	NM_019791	c.1414-2A>G	NA	0.463
A1	A1-2-3	chrX	139824102	139824102	C	T	Morc4	Missense	NM_001193309	c.G2213A	p.G738E	0.517
A1	A1-2-3	chrX	96160175	96160175	C	T	Msn	Missense	NM_010833	c.C883T	p.R295C	0.151
A1	A1-3-1	chr1	154472253	154472253	G	A	Cacna1e	Nonsense	NM_009782	c.C2761T	p.R921X	0.175
A1	A1-3-1	chr1	110925165	110925165	G	A	Cdh19	Missense	NM_001081386	c.C1039T	p.H347Y	0.475
A1	A1-3-1	chr2	93696152	93696152	G	A	Ext2	Missense	NM_010163	c.C2138T	p.P713L	0.354
A1	A1-3-1	chr2	40596939	40596939	C	T	Lrp1b	Missense	NM_053011	c.G13795A	p.A4599T	0.239
A1	A1-3-1	chr2	155421512	155421512	G	A	Ncoa6	Missense	NM_019825	c.C1001T	p.P334L	0.385
A1	A1-3-1	chr2	124664020	124664020	G	A	Sema6d	Splice site	NM_199241	c.1934-1G>A	NA	0.549
A1	A1-3-1	chr2	59838975	59838975	G	A	Tanc1	Missense	NM_198294	c.G3803A	p.G1268E	0.429
A1	A1-3-1	chr3	106149750	106149750	T	C	Chi3l3	Missense	NM_009892	c.A877G	p.K293E	0.246
A1	A1-3-1	chr4	63225586	63225586	T	G	Col27a1	Missense	NM_025685	c.T1510G	p.L504V	0.446
A1	A1-3-1	chr5	120609628	120609628	G	A	1110008J03Rik	Missense	NM_029096	c.C604T	p.P202S	0.479
A1	A1-3-1	chr6	38196439	38196439	G	A	D630045J12Rik	Missense	NM_194061	c.C793T	p.L265F	0.527
A1	A1-3-1	chr6	85337030	85337030	G	A	Rab11fip5	Missense	NM_001003955	c.C3950T	p.P1317L	0.639
A1	A1-3-1	chr7	128133275	128133275	T	C	Ilgax	Missense	NM_021334	c.T572C	p.L191P	0.492
A1	A1-3-1	chr7	102752989	102752989	T	A	Olfir560	Missense	NM_147113	c.A939T	p.E313D	0.533
A1	A1-3-1	chr7	25081644	25081644	C	T	Zfp574	Missense	NM_001168506	c.C2090T	p.P697L	0.52
A1	A1-3-1	chr8	94941666	94941666	C	T	Gpr114	Missense	NM_001145972	c.C1358T	p.A453V	0.133
A1	A1-3-1	chr8	27154308	27154308	G	A	Rab11fip1	Missense	NM_001080813	c.C1448T	p.P483L	0.458
A1	A1-3-1	chr9	14572677	14572677	C	T	Amotl1	Missense	NM_001081395	c.G1589A	p.R530Q	0.202
A1	A1-3-1	chr9	62432454	62432454	G	A	Coro2b	Missense	NM_175484	c.C386T	p.A129V	0.107
A1	A1-3-1	chr9	54335830	54335830	T	A	Gldn	Nonsense	NM_177350	c.T1095A	p.Y365X	0.417
A1	A1-3-1	chr10	11295240	11295240	T	G	Fbxo30	Missense	NM_027968	c.T2061G	p.F687L	0.483
A1	A1-3-1	chr10	129912132	129912132	C	T	Olfir816	Missense	NM_146672	c.G145A	p.V49M	0.389
A1	A1-3-1	chr10	94794675	94794675	C	A	Plxnc1	Nonsense	NM_018797	c.G4456T	p.E1486X	0.536
A1	A1-3-1	chr10	51723856	51723856	C	T	Rfx6	Missense	NM_001159389	c.C1799T	p.P600L	0.438
A1	A1-3-1	chr10	26245602	26245602	T	C	Samd3	Missense	NM_001115154	c.T616C	p.F206L	0.558
A1	A1-3-1	chr10	33200204	33200204	C	A	Trdn	Missense	NM_029726	c.C829A	p.H277N	0.533
A1	A1-3-1	chr11	120273314	120273314	G	A	Bahcc1	Splice site	NM_198423	c.2228-1G>A	NA	0.476
A1	A1-3-1	chr11	106813834	106813834	G	A	Cep95	Missense	NM_177088	c.G1514A	p.R505K	0.438
A1	A1-3-1	chr11	73847215	73847216	TC	AT	Olfir393	Missense	NM_147008	c.GA908_909AT	p.R303N	0.151
A1	A1-3-1	chr11	54916905	54916905	G	A	Tnip1	Missense	NM_021327	c.C1709T	p.A570V	0.47
A1	A1-3-1	chr13	73268858	73268858	G	A	Irx4	Missense	NM_018885	c.G1372A	p.G458S	0.531
A1	A1-3-1	chr14	49774037	49774037	G	C	3632451O06Rik	Missense	NM_026142	c.C212G	p.T71S	0.136
A1	A1-3-1	chr14	37057443	37057443	A	T	Lrit1	Missense	NM_146245	c.A332T	p.E111V	0.451
A1	A1-3-1	chr14	79770248	79770248	C	T	Pcdh8	Missense	NM_021543	c.G874A	p.E292K	0.529
A1	A1-3-1	chr14	70440016	70440016	G	A	Polr3d	Missense	NM_001164082	c.C919T	p.R307W	0.292
A1	A1-3-1	chr14	57643200	57643200	G	A	Xpo4	Missense	NM_020506	c.C199T	p.L67F	0.42
A1	A1-3-1	chr14	55063007	55063007	C	T	Zfhx2	Missense	NM_001039198	c.G7286A	p.S2429N	0.216
A1	A1-3-1	chr15	76106727	76106727	C	T	Eppk1	Missense	NM_144848	c.G5953A	p.G1985S	0.489
A1	A1-3-1	chr15	52335160	52335160	G	T	Slc30a8	Missense	NM_172816	c.G1000T	p.A334S	0.479
A1	A1-3-1	chr17	65256583	65256583	C	T	Tmem232	Missense	NM_001008973	c.G1814A	p.R605Q	0.452
A1	A1-3-1	chr18	34863349	34863349	G	T	Egr1	Missense	NM_007913	c.G1183T	p.A395S	0.522
A1	A1-3-1	chr19	29717713	29717713	G	A	9930021J03Rik	Missense	NM_172836	c.C4580T	p.P1527L	0.455
A1	A1-3-1	chr19	54047310	54047310	G	A	Adra2a	Missense	NM_007417	c.G1096A	p.E366K	0.501
A1	A1-3-1	chrX	94538510	94538510	T	C	Maged1	Splice site	NM_019791	c.1414-2A>G	NA	0.326
A1	A1-3-1	chrX	139824102	139824102	C	T	Morc4	Missense	NM_001193309	c.G2213A	p.G738E	0.466
A1	A1-3-1	chrX	96160175	96160175	C	T	Msn	Missense	NM_010833	c.C883T	p.R295C	0.105
A1	A1-3-2	chr1	154472253	154472253	G	A	Cacna1e	Nonsense	NM_009782	c.C2761T	p.R921X	0.175
A1	A1-3-2	chr1	110925165	110925165	G	A	Cdh19	Missense	NM_001081386	c.C1039T	p.H347Y	0.508
A1	A1-3-2	chr1	88215102	88215102	G	A	Ugt1a1	Missense	NM_201645	c.G929A	p.G310E	0.078
A1	A1-3-2	chr2	93696152	93696152	G	A	Ext2	Missense	NM_010163	c.C2138T	p.P713L	0.416
A1	A1-3-2	chr2	151970755	151970755	G	A	Fam110a	Missense	NM_028666	c.C94T	p.P32S	0.17
A1	A1-3-2	chr2	40596939	40596939	C	T	Lrp1b	Missense	NM_053011	c.G13795A	p.A4599T	0.129
A1	A1-3-2	chr2	155421512	155421512	G	A	Ncoa6	Missense	NM_019825	c.C1001T	p.P334L	0.5
A1	A1-3-2	chr2	124664020	124664020	G	A	Sema6d	Splice site	NM_199241	c.1934-1G>A	NA	0.536
A1	A1-3-2	chr2	59838975	59838975	G	A	Tanc1	Missense	NM_198294	c.G3803A	p.G1268E	0.478
A1	A1-3-2	chr3	106149750	106149750	T							



A1	A1-3-2	chr14	37057443	37057443	A	T	Lrit1	Missense	NM_146245	c.A332T	p.E111V	0.394	
A1	A1-3-2	chr14	79770248	79770248	C	T	Pcdh8	Missense	NM_021543	c.G874A	p.E292K	0.532	
A1	A1-3-2	chr14	70440016	70440016	G	A	Poir3d	Missense	NM_001164082	c.C919T	p.R307W	0.138	
A1	A1-3-2	chr14	57643200	57643200	G	A	Xpo4	Missense	NM_020506	c.C199T	p.L67F	0.538	
A1	A1-3-2	chr14	55063007	55063007	C	T	Zfhx2	Missense	NM_001039198	c.G7286A	p.S2429N	0.169	
A1	A1-3-2	chr15	76106727	76106727	C	T	Eppk1	Missense	NM_144848	c.G5953A	p.G1985S	0.47	
A1	A1-3-2	chr15	52335160	52335160	G	T	Slc30a8	Missense	NM_172816	c.G1000T	p.A334S	0.458	
A1	A1-3-2	chr16	16673840	16673840	A	C	Olfir19	Missense	NM_146335	c.T140G	p.I47S	0.084	
A1	A1-3-2	chr17	65256583	65256583	C	T	Tmem232	Missense	NM_001008973	c.G1814A	p.R605Q	0.409	
A1	A1-3-2	chr18	61849326	61849326	C	T	Abli3	Missense	NM_001164491	c.G547A	p.V183I	0.107	
A1	A1-3-2	chr18	34863349	34863349	G	T	Egr1	Missense	NM_007913	c.G1183T	p.A395S	0.511	
A1	A1-3-2	chr19	29717713	29717713	G	A	9930021J03Rik	Missense	NM_172836	c.C4580T	p.P1527L	0.512	
A1	A1-3-2	chr19	54047310	54047310	G	A	Adra2a	Missense	NM_007417	c.G1096A	p.E366K	0.47	
A1	A1-3-2	chrX	94538510	94538510	T	C	Maged1	Splice site	NM_019791	c.1414-2A>G	NA	0.414	
A1	A1-3-2	chrX	139824102	139824102	C	T	Morc4	Missense	NM_001193309	c.G2213A	p.G738E	0.556	
A1	A1-3-5	chr1	110925165	110925165	G	A	Cdh19	Missense	NM_001081386	c.C1039T	p.H347Y	0.361	
A1	A1-3-5	chr2	93696152	93696152	G	A	Ext2	Missense	NM_010163	c.C2138T	p.P713L	0.447	
A1	A1-3-5	chr2	155421512	155421512	G	A	Ncoa6	Missense	NM_019825	c.C1001T	p.P334L	0.376	
A1	A1-3-5	chr2	124664020	124664020	G	A	Sema6d	Splice site	NM_199241	c.1934-1G>A	NA	0.551	
A1	A1-3-5	chr2	59838975	59838975	G	A	Tanc1	Missense	NM_198294	c.G3803A	p.G1268E	0.526	
A1	A1-3-5	chr3	106149750	106149750	T	C	Chi3l3	Missense	NM_009892	c.A877G	p.K293E	0.28	
A1	A1-3-5	chr4	63225586	63225586	T	G	Col27a1	Missense	NM_025685	c.T1510G	p.L504V	0.447	
A1	A1-3-5	chr5	120609628	120609628	G	A	1110008J03Rik	Missense	NM_029096	c.C604T	p.P202S	0.481	
A1	A1-3-5	chr5	35043862	35043880	G	GTGGGCGACCACTGGGCC	-	Hgfac	Nonsense	NM_019447	c.628_646del	p.G211X	0.102
A1	A1-3-5	chr6	38196439	38196439	G	A	D630045J12Rik	Missense	NM_194061	c.C793T	p.L265F	0.449	
A1	A1-3-5	chr6	60988306	60988306	A	C	Mmrn1	Missense	NM_027613	c.A3320C	p.N1107T	0.094	
A1	A1-3-5	chr6	85337030	85337030	G	A	Rab11fp5	Missense	NM_001003955	c.C3950T	p.P1317L	0.5	
A1	A1-3-5	chr7	128133275	128133275	T	C	Itgax	Missense	NM_021334	c.T572C	p.L191P	0.438	
A1	A1-3-5	chr7	102752989	102752989	T	A	Olfir560	Missense	NM_147113	c.A939T	p.E313D	0.584	
A1	A1-3-5	chr7	25081644	25081644	C	T	Zfp574	Missense	NM_001168506	c.C2090T	p.P697L	0.464	
A1	A1-3-5	chr8	27154308	27154308	G	A	Rab11fp1	Missense	NM_001080813	c.C1448T	p.P483L	0.432	
A1	A1-3-5	chr9	14572677	14572677	C	T	Amotl1	Missense	NM_001081395	c.G1589A	p.R530Q	0.318	
A1	A1-3-5	chr9	54335830	54335830	T	A	Gldn	Nonsense	NM_177350	c.T1095A	p.Y365X	0.541	
A1	A1-3-5	chr10	11295240	11295240	T	G	Fbxo30	Missense	NM_027968	c.T2061G	p.F687L	0.444	
A1	A1-3-5	chr10	129912132	129912132	C	T	Olfir816	Missense	NM_146672	c.G145A	p.V49M	0.524	
A1	A1-3-5	chr10	94794675	94794675	C	A	Plxnc1	Nonsense	NM_018797	c.G4456T	p.E1486X	0.481	
A1	A1-3-5	chr10	51723856	51723856	C	T	Rfx6	Missense	NM_001159389	c.C1799T	p.P600L	0.508	
A1	A1-3-5	chr10	26245602	26245602	T	C	Samd3	Missense	NM_001115154	c.T616C	p.F206L	0.673	
A1	A1-3-5	chr10	33200204	33200204	C	A	Trdn	Missense	NM_029726	c.C829A	p.H277N	0.484	
A1	A1-3-5	chr11	120273314	120273314	G	A	Bahcc1	Splice site	NM_198423	c.2228-1G>A	NA	0.448	
A1	A1-3-5	chr11	106813834	106813834	G	A	Cep95	Missense	NM_177088	c.G1514A	p.R505K	0.387	
A1	A1-3-5	chr11	54916905	54916905	G	A	Tnlp1	Missense	NM_021327	c.C1709T	p.A570V	0.479	
A1	A1-3-5	chr13	58382465	58382465	G	A	2210016F16Rik	Missense	NM_027335	c.C730T	p.L244F	0.138	
A1	A1-3-5	chr13	73268858	73268858	G	A	Irx4	Missense	NM_018885	c.G1372A	p.G458S	0.432	
A1	A1-3-5	chr14	123980462	123980462	A	G	Fg14	Missense	NM_010201	c.T628C	p.S210P	0.119	
A1	A1-3-5	chr14	37057443	37057443	A	T	Lrit1	Missense	NM_146245	c.A332T	p.E111V	0.45	
A1	A1-3-5	chr14	79770248	79770248	C	T	Pcdh8	Missense	NM_021543	c.G874A	p.E292K	0.518	
A1	A1-3-5	chr14	57643200	57643200	G	A	Xpo4	Missense	NM_020506	c.C199T	p.L67F	0.609	
A1	A1-3-5	chr15	76106727	76106727	C	T	Eppk1	Missense	NM_144848	c.G5953A	p.G1985S	0.489	
A1	A1-3-5	chr15	83119999	83119999	G	A	Rrp7a	Missense	NM_029101	c.C235T	p.L79F	0.147	
A1	A1-3-5	chr15	101039945	101039945	G	A	Scn8a	Missense	NM_001077499	c.G5194A	p.G1732R	0.1	
A1	A1-3-5	chr15	52335160	52335160	G	T	Slc30a8	Missense	NM_172816	c.G1000T	p.A334S	0.415	
A1	A1-3-5	chr17	65256583	65256583	C	T	Tmem232	Missense	NM_001008973	c.G1814A	p.R605Q	0.529	
A1	A1-3-5	chr18	34863349	34863349	G	T	Egr1	Missense	NM_007913	c.G1183T	p.A395S	0.493	
A1	A1-3-5	chr19	29717713	29717713	G	A	9930021J03Rik	Missense	NM_172836	c.C4580T	p.P1527L	0.505	
A1	A1-3-5	chr19	54047310	54047310	G	A	Adra2a	Missense	NM_007417	c.G1096A	p.E366K	0.471	
A1	A1-3-5	chrX	94538510	94538510	T	C	Maged1	Splice site	NM_019791	c.1414-2A>G	NA	0.56	
A1	A1-3-5	chrX	139824102	139824102	C	T	Morc4	Missense	NM_001193309	c.G2213A	p.G738E	0.534	
A1	A1-3-5	chrX	96160175	96160175	C	T	Msn	Missense	NM_010833	c.C883T	p.R295C	0.2	
A1	A1-3-5	chrX	37217843	37217843	C	T	Rhox1	Missense	NM_001025084	c.G388A	p.E130K	0.082	
A1	A1-3-6	chr1	110925165	110925165	G	A	Cdh19	Missense	NM_001081386	c.C1039T	p.H347Y	0.489	
A1	A1-3-6	chr2	93696152	93696152	G	A	Ext2	Missense	NM_010163	c.C2138T	p.P713L	0.333	
A1	A1-3-6	chr2	155421512	155421512	G	A	Ncoa6	Missense	NM_019825	c.C1001T	p.P334L	0.464	
A1	A1-3-6	chr2	124664020	124664020	G	A	Sema6d	Splice site	NM_199241	c.1934-1G>A	NA	0.619	
A1	A1-3-6	chr2	59838975	59838975	G	A	Tanc1	Missense	NM_198294	c.G3803A	p.G1268E	0.372	
A1	A1-3-6	chr3	106149750	106149750	T	C	Chi3l3	Missense	NM_009892	c.A877G	p.K293E	0.263	
A1	A1-3-6	chr3	5401735	5401735	A	G	Zfhx4	Missense	NM_030708	c.A6952G	p.S2318G	0.162	
A1	A1-3-6	chr4	63225586	63225586	T	G	Col27a1	Missense	NM_025685	c.T1510G	p.L504V	0.451	
A1	A1-3-6	chr5	120609628	120609628	G	A	1110008J03Rik	Missense	NM_029096	c.C604T	p.P202S	0.487	
A1	A1-3-6	chr5	35043862	35043880	G	GTGGGCGACCACTGGGCC	-	Hgfac	Nonsense	NM_019447	c.628_646del	p.G211X	0.099
A1	A1-3-6	chr5	14539711	14539711	C	G	Pclo	Missense	NM_011995	c.C2024T	p.A675V	0.074	
A1	A1-3-6	chr5	121168003	121168003	C	T	Ptpn11	Missense	NM_011202	c.G178A	p.G60R	0.18	
A1	A1-3-6	chr6	38196439	38196439	G	A	D630045J12Rik	Missense	NM_194061	c.C793T	p.L265F	0.507	
A1	A1-3-6	chr6	85337030	85337030	G	A	Rab11fp5	Missense	NM_001003955	c.C3950T	p.P1317L	0.517	
A1	A1-3-6	chr7	128133275	128133275	T	C	Itgax	Missense	NM_021334	c.T572C	p.L191P	0.467	
A1	A1-3-6	chr7	102752989	102752989	T	A	Olfir560	Missense	NM_147113	c.A939T	p.E313D	0.529	
A1	A1-3-6	chr7	25081644	25081644	C	T	Zfp574	Missense	NM_001168506	c.C2090T	p.P697L	0.474	
A1	A1-3-6	chr8	27154308	27154308	G	A	Rab11fp1	Missense	NM_001080813	c.C1448T	p.P483L	0.438	
A1	A1-3-6	chr9	14572677	14572677	C	T	Amotl1	Missense	NM_001081395	c.G1589A	p.R530Q	0.289	
A1	A1-3-6	chr9	5959858	5959858	G	T	Fat3	Missense	NM_001080814	c.C11236A	p.Q3746K	0.137	
A1	A1-3-6	chr9	54335830	54335830	T	A	Gldn	Nonsense	NM_177350	c.T1095A	p.Y365X	0.485	
A1	A1-3-6	chr10	11295240	11295240	T	G	Fbxo30	Missense	NM_027968	c.T2061G	p.F687L	0.483	
A1	A1-3-6	chr10	129912132	129912132	C	T	Olfir816	Missense	NM_146672	c.G145A	p.V49M	0.471	
A1	A1-3-6	chr10	94794675	94794675	C	A	Plxnc1	Nonsense	NM_018797	c.G4456T	p.E1486X	0.515	
A1	A1-3-6	chr10	51723856	51723856	C	T	Rfx6	Missense	NM_001159389	c.C1799T	p.P600L	0.528	
A1	A1-3-6	chr10	26245602	26245602	T	C	Samd3	Missense	NM_001115154	c.T616C	p.F206L	0.382	
A1	A1-3-6	chr10	33200204	33200204	C	A	Trdn	Missense	NM_029726	c.C829A	p.H277N	0.478	
A1	A1-3-6	chr11	120273314	120273314	G	A	Bahcc1	Splice site	NM_198423	c.2228-1G>A	NA	0.531	
A1	A1-3-6	chr11	106813834	106813834	G	A	Cep95	Missense	NM_177088	c.G1514A	p.R505K	0.571	
A1	A1-3-6	chr11	54916905	54916905	G	A	Tnlp1	Missense	NM_021327	c.C1709T	p.A570V	0.476	
A1	A1-3-6	chr13	73268858	73268858	G	A	Irx4	Missense	NM_018885	c.G1372A	p.G458S	0.523	
A1	A1-3-6	chr14	37057443	37057443	A	T	Lrit1	Missense	NM_146245	c.A332T	p.E111V	0.546	
A1	A1-3-6	chr14	79770248	79770248	C	T	Pcdh8	Missense	NM_021543	c.G874A	p.E292K	0.543	
A1	A1-3-6	chr14	57643200	57643200	G	A	Xpo4	Missense	NM_020506	c.C199T	p.L67F	0.525	
A1	A1-3-6	chr15	76106727	76106727	C	T	Eppk1	Missense	NM_144848	c.G5953A	p.G1985S	0.445	
A1	A1-3-6	chr15	52335160	52335160	G	T	Slc30a8	Missense	NM_172816	c.G1000T	p.A334S	0.523	
A1	A1-3-6	chr17	65256583	65256583	C	T	Tmem232	Missense	NM_001008973	c.G1814A	p.R605Q	0.591	
A1	A1-3-6	chr18	34863349	34863349	G	T	Egr1	Missense	NM_007913	c.G1183T	p.A395S	0.5	
A1	A1-3-6	chr19	29717713	29									

A1	A1-4-1	chr8	27154308	27154308	G	A	Rab11fp1	Missense	NM_001080813	c.C1448T	p.P483L	0.356
A1	A1-4-1	chr9	14572677	14572677	C	T	Amotl1	Missense	NM_001081395	c.G1589A	p.R530Q	0.427
A1	A1-4-1	chr9	62432454	62432454	G	A	Coro2b	Missense	NM_175484	c.C386T	p.A129V	0.198
A1	A1-4-1	chr9	54335830	54335830	T	A	Gldn	Nonsense	NM_177350	c.T1095A	p.Y365X	0.495
A1	A1-4-1	chr10	11295240	11295240	T	G	Fbxo30	Missense	NM_027968	c.T2061G	p.F687L	0.678
A1	A1-4-1	chr10	129912132	129912132	C	T	Olfir816	Missense	NM_146672	c.G145A	p.V49M	0.531
A1	A1-4-1	chr10	94794675	94794675	C	A	Plxnc1	Nonsense	NM_018797	c.G4456T	p.E1486X	0.578
A1	A1-4-1	chr10	51723856	51723856	C	T	Rfx6	Missense	NM_001159389	c.C1799T	p.P600L	0.566
A1	A1-4-1	chr10	26245602	26245602	T	C	Samd3	Missense	NM_001115154	c.T616C	p.F206L	0.411
A1	A1-4-1	chr10	33200204	33200204	C	A	Trdn	Missense	NM_029726	c.C829A	p.H277N	0.584
A1	A1-4-1	chr11	120273314	120273314	G	A	Bahcc1	Splice site	NM_198423	c.2228-1G>A	NA	0.54
A1	A1-4-1	chr11	106813834	106813834	G	A	Cep95	Missense	NM_177088	c.G1514A	p.R505K	0.571
A1	A1-4-1	chr11	73847215	73847216	TC	AT	Olfir393	Missense	NM_147008	c.GA908_909AT	p.R303N	0.21
A1	A1-4-1	chr11	54916905	54916905	G	A	Tnip1	Missense	NM_021327	c.C1709T	p.A570V	0.47
A1	A1-4-1	chr13	73268858	73268858	G	A	Irx4	Missense	NM_018885	c.G1372A	p.G458S	0.566
A1	A1-4-1	chr14	37057443	37057443	A	T	Lrit1	Missense	NM_146245	c.A332T	p.E111V	0.446
A1	A1-4-1	chr14	79770248	79770248	C	T	Pcdh8	Missense	NM_021543	c.G874A	p.E292K	0.534
A1	A1-4-1	chr14	70440016	70440016	G	A	Polr3d	Missense	NM_001164082	c.C919T	p.R307W	0.115
A1	A1-4-1	chr14	57643200	57643200	G	A	Xpo4	Missense	NM_020506	c.C199T	p.L67F	0.645
A1	A1-4-1	chr14	55063007	55063007	C	T	Zfx2	Missense	NM_001039198	c.G7286A	p.S2429N	0.156
A1	A1-4-1	chr15	76106727	76106727	C	T	Eppk1	Missense	NM_144848	c.G5953A	p.G1985S	0.457
A1	A1-4-1	chr15	52335160	52335160	G	T	Slc30a8	Missense	NM_172816	c.G1000T	p.A334S	0.368
A1	A1-4-1	chr17	65256583	65256583	C	T	Tmem232	Missense	NM_001008973	c.G1814A	p.R605Q	0.475
A1	A1-4-1	chr18	61849326	61849326	C	T	Ablim3	Missense	NM_001164491	c.G547A	p.V183I	0.105
A1	A1-4-1	chr18	34863349	34863349	G	T	Egr1	Missense	NM_007913	c.G1183T	p.A395S	0.468
A1	A1-4-1	chr19	29717713	29717713	G	A	9930021J03Rik	Missense	NM_172836	c.C4580T	p.P1527L	0.518
A1	A1-4-1	chr19	54047310	54047310	G	A	Adra2a	Missense	NM_007417	c.G1096A	p.E366K	0.493
A1	A1-4-1	chrX	94538510	94538510	T	C	Maged1	Splice site	NM_019791	c.1414-2A>G	NA	0.42
A1	A1-4-1	chrX	139824102	139824102	C	T	Morc4	Missense	NM_001193309	c.G2213A	p.G738E	0.46
A1	A1-4-3	chr1	154472253	154472253	G	A	Cacna1e	Nonsense	NM_009782	c.C2761T	p.R921X	0.144
A1	A1-4-3	chr1	110925165	110925165	G	A	Cdh19	Missense	NM_001081386	c.C1039T	p.H347Y	0.579
A1	A1-4-3	chr1	88215102	88215102	G	A	Ugt1a1	Missense	NM_201645	c.G929A	p.G310E	0.074
A1	A1-4-3	chr2	93696152	93696152	G	A	Ext2	Missense	NM_010163	c.C2138T	p.P713L	0.443
A1	A1-4-3	chr2	151970755	151970755	G	A	Fam110a	Missense	NM_028666	c.C94T	p.P32S	0.282
A1	A1-4-3	chr2	40596939	40596939	C	T	Lrp1b	Missense	NM_053011	c.G13795A	p.A4599T	0.102
A1	A1-4-3	chr2	155421512	155421512	G	A	Ncoa6	Missense	NM_019825	c.C1001T	p.P334L	0.456
A1	A1-4-3	chr2	38740483	38740483	G	A	Nr6a1	Missense	NM_001159548	c.C595T	p.P199S	0.123
A1	A1-4-3	chr2	59838975	59838975	G	A	Tanc1	Missense	NM_198294	c.G3803A	p.G1268E	0.541
A1	A1-4-3	chr3	106149750	106149750	T	C	Chi3l3	Missense	NM_009892	c.A877G	p.K293E	0.281
A1	A1-4-3	chr4	63225586	63225586	T	G	Col27a1	Missense	NM_025685	c.T1510G	p.L504V	0.494
A1	A1-4-3	chr4	56790899	56790899	C	A	Ikbkap	Missense	NM_026079	c.G853T	p.D285Y	0.255
A1	A1-4-3	chr5	120609628	120609628	G	A	1110008J03Rik	Missense	NM_029096	c.C604T	p.P202S	0.469
A1	A1-4-3	chr6	38196439	38196439	G	A	D630045J12Rik	Missense	NM_194061	c.C793T	p.L265F	0.434
A1	A1-4-3	chr6	85337030	85337030	G	A	Rab11fp5	Missense	NM_001003955	c.C3950T	p.P1317L	0.609
A1	A1-4-3	chr6	83151912	83151912	G	A	Rtkn	Missense	NM_001136227	c.G1387A	p.A463T	0.147
A1	A1-4-3	chr7	128133275	128133275	T	C	Itgax	Missense	NM_021334	c.T572C	p.L191P	0.49
A1	A1-4-3	chr7	102752989	102752989	T	A	Olfir560	Missense	NM_147113	c.A939T	p.E313D	0.597
A1	A1-4-3	chr7	25081644	25081644	C	T	Zfp574	Missense	NM_001168506	c.C2090T	p.P697L	0.495
A1	A1-4-3	chr8	94941666	94941666	C	T	Gpr114	Missense	NM_001145972	c.C1358T	p.A453V	0.118
A1	A1-4-3	chr8	27154308	27154308	G	A	Rab11fp1	Missense	NM_001080813	c.C1448T	p.P483L	0.494
A1	A1-4-3	chr9	14572677	14572677	C	T	Amotl1	Missense	NM_001081395	c.G1589A	p.R530Q	0.333
A1	A1-4-3	chr9	54335830	54335830	T	A	Gldn	Nonsense	NM_177350	c.T1095A	p.Y365X	0.391
A1	A1-4-3	chr9	44388846	44388846	C	T	Hyou1	Missense	NM_021395	c.C2431T	p.R811W	0.094
A1	A1-4-3	chr10	11295240	11295240	T	G	Fbxo30	Missense	NM_027968	c.T2061G	p.F687L	0.66
A1	A1-4-3	chr10	79755182	79755182	G	A	Fgf22	Missense	NM_023304	c.G64A	p.G22R	0.137
A1	A1-4-3	chr10	129912132	129912132	C	T	Olfir816	Missense	NM_146672	c.G145A	p.V49M	0.375
A1	A1-4-3	chr10	94794675	94794675	C	A	Plxnc1	Nonsense	NM_018797	c.G4456T	p.E1486X	0.463
A1	A1-4-3	chr10	51723856	51723856	C	T	Rfx6	Missense	NM_001159389	c.C1799T	p.P600L	0.422
A1	A1-4-3	chr10	26245602	26245602	T	C	Samd3	Missense	NM_001115154	c.T616C	p.F206L	0.476
A1	A1-4-3	chr10	33200204	33200204	C	A	Trdn	Missense	NM_029726	c.C829A	p.H277N	0.444
A1	A1-4-3	chr11	120273314	120273314	G	A	Bahcc1	Splice site	NM_198423	c.2228-1G>A	NA	0.533
A1	A1-4-3	chr11	106813834	106813834	G	A	Cep95	Missense	NM_177088	c.G1514A	p.R505K	0.476
A1	A1-4-3	chr11	54916905	54916905	G	A	Tnip1	Missense	NM_021327	c.C1709T	p.A570V	0.475
A1	A1-4-3	chr12	104864940	104864940	C	G	Clmn	Missense	NM_053155	c.G12C	p.Q4H	0.114
A1	A1-4-3	chr13	73268858	73268858	G	A	Irx4	Missense	NM_018885	c.G1372A	p.G458S	0.464
A1	A1-4-3	chr14	37057443	37057443	A	T	Lrit1	Missense	NM_146245	c.A332T	p.E111V	0.5
A1	A1-4-3	chr14	79770248	79770248	C	T	Pcdh8	Missense	NM_021543	c.G874A	p.E292K	0.515
A1	A1-4-3	chr14	57643200	57643200	G	A	Xpo4	Missense	NM_020506	c.C199T	p.L67F	0.591
A1	A1-4-3	chr14	55063007	55063007	C	T	Zfx2	Missense	NM_001039198	c.G7286A	p.S2429N	0.116
A1	A1-4-3	chr15	76106727	76106727	C	T	Eppk1	Missense	NM_144848	c.G5953A	p.G1985S	0.418
A1	A1-4-3	chr15	52335160	52335160	G	T	Slc30a8	Missense	NM_172816	c.G1000T	p.A334S	0.489
A1	A1-4-3	chr17	65256583	65256583	C	T	Tmem232	Missense	NM_001008973	c.G1814A	p.R605Q	0.375
A1	A1-4-3	chr18	61849326	61849326	C	T	Ablim3	Missense	NM_001164491	c.G547A	p.V183I	0.137
A1	A1-4-3	chr18	34863349	34863349	G	T	Egr1	Missense	NM_007913	c.G1183T	p.A395S	0.497
A1	A1-4-3	chr19	29717713	29717713	G	A	9930021J03Rik	Missense	NM_172836	c.C4580T	p.P1527L	0.464
A1	A1-4-3	chr19	54047310	54047310	G	A	Adra2a	Missense	NM_007417	c.G1096A	p.E366K	0.425
A1	A1-4-3	chrX	94538510	94538510	T	C	Maged1	Splice site	NM_019791	c.1414-2A>G	NA	0.458
A1	A1-4-3	chrX	139824102	139824102	C	T	Morc4	Missense	NM_001193309	c.G2213A	p.G738E	0.556
A1	A1-4-5	chr1	110925165	110925165	G	A	Cdh19	Missense	NM_001081386	c.C1039T	p.H347Y	0.471
A1	A1-4-5	chr2	154202621	154202621	G	A	Bpifb1	Missense	NM_001012392	c.G7A	p.G3S	0.391
A1	A1-4-5	chr2	93696152	93696152	G	A	Ext2	Missense	NM_010163	c.C2138T	p.P713L	0.445
A1	A1-4-5	chr2	155421512	155421512	G	A	Ncoa6	Missense	NM_019825	c.C1001T	p.P334L	0.459
A1	A1-4-5	chr2	87418099	87418099	C	T	Olfir1123	Missense	NM_146350	c.C50T	p.S17L	0.34
A1	A1-4-5	chr2	124664020	124664020	G	A	Sema6d	Splice site	NM_199241	c.1934-1G>A	NA	0.465
A1	A1-4-5	chr2	59838975	59838975	G	A	Tanc1	Missense	NM_198294	c.G3803A	p.G1268E	0.333
A1	A1-4-5	chr3	106149750	106149750	T	C	Chi3l3	Missense	NM_009892	c.A877G	p.K293E	0.232
A1	A1-4-5	chr4	63225586	63225586	T	G	Col27a1	Missense	NM_025685	c.T1510G	p.L504V	0.39
A1	A1-4-5	chr5	120609628	120609628	G	A	1110008J03Rik	Missense	NM_029096	c.C604T	p.P202S	0.509
A1	A1-4-5	chr5	114064898	114064898	C	T	Svop	Nonsense	NM_026805	c.G252A	p.W84X	0.083
A1	A1-4-5	chr5	137403232	137403232	G	C	Zan	Missense	NM_011741	c.C12224G	p.A4075G	0.126
A1	A1-4-5	chr6	38196439	38196439	G	A	D630045J12Rik	Missense	NM_194061	c.C793T	p.L265F	0.411
A1	A1-4-5	chr6	85337030	85337030	G	A	Rab11fp5	Missense	NM_001003955	c.C3950T	p.P1317L	0.514
A1	A1-4-5	chr7	119575707	119575707	G	A	Acsm2	Missense	NM_001177978	c.G694A	p.E232K	0.204
A1	A1-4-5	chr7	128133275	128133275	T	C	Itgax	Missense	NM_021334	c.T572C	p.L191P	0.408
A1	A1-4-5	chr7	102752989	102752989	T	A	Olfir560	Missense	NM_147113	c.A939T	p.E313D	0.43
A1	A1-4-5	chr7	25081644	25081644	C	T	Zfp574	Missense	NM_001168506	c.C2090T	p.P697L	0.498
A1	A1-4-5	chr8	27154308	27154308	G	A	Rab11fp1	Missense	NM_001080813	c.C1448T	p.P483L	0.425
A1	A1-4-5	chr9	14572677	14572677	C	T	Amotl1	Missense	NM_001081395	c.G1589A	p.R530Q	0.344
A1	A1-4-5	chr9	54335830	54335830	T	A	Gldn					



A1	A1-4-5	chr19	29717713	29717713	G	A	9930021J03Rik	Missense	NM_172836	c.C4580T	p.P1527L	0.427
A1	A1-4-5	chr19	54047310	54047310	G	A	Adra2a	Missense	NM_007417	c.G1096A	p.E366K	0.477
A1	A1-4-5	chrX	94538510	94538510	T	C	Maged1	Splice site	NM_019791	c.1414-2A>G	NA	0.432
A1	A1-4-5	chrX	139824102	139824102	C	T	Morc4	Missense	NM_001193309	c.G2213A	p.G738E	0.673
A1	A1-4-5	chrX	96160175	96160175	C	T	Msn	Missense	NM_010833	c.C883T	p.R295C	0.07
A1	A1-4-5	chrX	37217843	37217843	C	T	Rhox1	Missense	NM_001025084	c.G388A	p.E130K	0.294
A1	A1-4-5	chrX	42211151	42211151	G	T	Stag2	Missense	NM_001077712	c.G197T	p.G66V	0.3
A1	A1-4-7	chr1	110925165	110925165	G	A	Cdh19	Missense	NM_001081386	c.C1039T	p.H347Y	0.559
A1	A1-4-7	chr2	93696152	93696152	G	A	Ext2	Missense	NM_010163	c.C2138T	p.P713L	0.384
A1	A1-4-7	chr2	155421512	155421512	G	A	Ncoa6	Missense	NM_019825	c.C1001T	p.P334L	0.5
A1	A1-4-7	chr2	101641954	101641954	C	T	Rag1	Missense	NM_009019	c.G2842A	p.E948K	0.169
A1	A1-4-7	chr2	124664020	124664020	G	A	Sema6d	Splice site	NM_199241	c.1934-1G>A	NA	0.643
A1	A1-4-7	chr2	59838975	59838975	G	A	Tanc1	Missense	NM_198294	c.G3803A	p.G1268E	0.455
A1	A1-4-7	chr3	106149750	106149750	T	C	Chi3l3	Missense	NM_009892	c.A877G	p.K293E	0.252
A1	A1-4-7	chr3	5401735	5401735	A	G	Zfx4	Missense	NM_030708	c.A6952G	p.S2318G	0.411
A1	A1-4-7	chr4	63225586	63225586	T	G	Col27a1	Missense	NM_025685	c.T1510G	p.L504V	0.519
A1	A1-4-7	chr4	28947638	28947638	C	T	Epha7	Missense	NM_010141	c.C1909T	p.R637C	0.276
A1	A1-4-7	chr5	120609628	120609628	G	A	1110008J03Rik	Missense	NM_029096	c.C604T	p.P202S	0.512
A1	A1-4-7	chr5	35042599	35042599	C	T	Hgfac	Missense	NM_019447	c.C323T	p.P108L	0.133
A1	A1-4-7	chr5	121168003	121168003	C	T	Ptpn11	Missense	NM_011202	c.G178A	p.G60R	0.417
A1	A1-4-7	chr6	38196439	38196439	G	A	D630045J12Rik	Missense	NM_194061	c.C793T	p.L265F	0.527
A1	A1-4-7	chr6	85337030	85337030	G	A	Rab11fp5	Missense	NM_001003955	c.C3950T	p.P1317L	0.397
A1	A1-4-7	chr7	82574004	82574004	G	A	Adamtsl3	Missense	NM_001190374	c.G2992A	p.G998S	0.129
A1	A1-4-7	chr7	128133275	128133275	T	C	Itgax	Missense	NM_021334	c.T572C	p.L191P	0.566
A1	A1-4-7	chr7	102752989	102752989	T	A	Olfir560	Missense	NM_147113	c.A939T	p.E313D	0.612
A1	A1-4-7	chr7	25081644	25081644	C	T	Zfp574	Missense	NM_001168506	c.C2090T	p.P697L	0.464
A1	A1-4-7	chr8	27154308	27154308	G	A	Rab11fp1	Missense	NM_001080813	c.C1448T	p.P483L	0.439
A1	A1-4-7	chr9	14572677	14572677	C	T	Amtl1	Missense	NM_001081395	c.G1589A	p.R530Q	0.292
A1	A1-4-7	chr9	15959858	15959858	G	T	Fat3	Missense	NM_001080814	c.C11236A	p.Q3746K	0.469
A1	A1-4-7	chr9	54335830	54335830	T	A	Gldn	Nonsense	NM_177350	c.T1095A	p.Y365X	0.595
A1	A1-4-7	chr10	11295240	11295240	T	G	Fbxo30	Missense	NM_027968	c.T2061G	p.F687L	0.419
A1	A1-4-7	chr10	129912132	129912132	C	T	Olfir816	Missense	NM_146672	c.G145A	p.V49M	0.455
A1	A1-4-7	chr10	94794675	94794675	C	A	Plxnc1	Nonsense	NM_018797	c.G4456T	p.E1486X	0.495
A1	A1-4-7	chr10	51723856	51723856	C	T	Rfx6	Missense	NM_001159389	c.C1799T	p.P600L	0.447
A1	A1-4-7	chr10	26245602	26245602	T	C	Samd3	Missense	NM_001115154	c.T616C	p.F206L	0.667
A1	A1-4-7	chr10	33200204	33200204	C	A	Trdn	Missense	NM_029726	c.C829A	p.H277N	0.491
A1	A1-4-7	chr11	120273314	120273314	G	A	Bahcc1	Splice site	NM_198423	c.2228-1G>A	NA	0.556
A1	A1-4-7	chr11	106813834	106813834	G	A	Cep95	Missense	NM_177088	c.G1514A	p.R505K	0.667
A1	A1-4-7	chr11	54916905	54916905	G	A	Tnfp1	Missense	NM_021327	c.C1709T	p.A570V	0.489
A1	A1-4-7	chr11	51070644	51070644	C	T	Zfp354a	Missense	NM_009329	c.C1678T	p.L560F	0.091
A1	A1-4-7	chr13	73268858	73268858	G	A	Irx4	Missense	NM_018885	c.G1372A	p.G458S	0.453
A1	A1-4-7	chr14	37057443	37057443	A	T	Lrit1	Missense	NM_146245	c.A332T	p.E111V	0.525
A1	A1-4-7	chr14	79770248	79770248	C	T	Pcdh8	Missense	NM_021543	c.G874A	p.E292K	0.522
A1	A1-4-7	chr14	57643200	57643200	G	A	Xpo4	Missense	NM_020506	c.C199T	p.L67F	0.407
A1	A1-4-7	chr15	76106727	76106727	C	T	Eppk1	Missense	NM_144848	c.G5953A	p.G1985S	0.508
A1	A1-4-7	chr15	52335160	52335160	G	T	Slc30a8	Missense	NM_172816	c.G1000T	p.A334S	0.519
A1	A1-4-7	chr16	33196120	33196120	C	T	Osbpl11	Missense	NM_176840	c.C244T	p.L82F	0.196
A1	A1-4-7	chr17	65256583	65256583	C	T	Tmem232	Missense	NM_001008973	c.G1814A	p.R605Q	0.448
A1	A1-4-7	chr18	34863349	34863349	G	T	Egr1	Missense	NM_007913	c.G1183T	p.A395S	0.509
A1	A1-4-7	chr19	29717713	29717713	G	A	9930021J03Rik	Missense	NM_172836	c.C4580T	p.P1527L	0.424
A1	A1-4-7	chr19	54047310	54047310	G	A	Adra2a	Missense	NM_007417	c.G1096A	p.E366K	0.494
A1	A1-4-7	chrX	134806689	134806690	AG	GA	Armcx2	Missense	NM_001166397	c.CT193_194TC	p.L65S	0.175
A1	A1-4-7	chrX	94538510	94538510	T	C	Maged1	Splice site	NM_019791	c.1414-2A>G	NA	0.425
A1	A1-4-7	chrX	139824102	139824102	C	T	Morc4	Missense	NM_001193309	c.G2213A	p.G738E	0.462
A1	A1-4-7	chrX	89405846	89405846	C	T	Pet2	Missense	NM_008821	c.G676A	p.V226I	0.081
A2	A2-1-1	chr2	35354896	35354896	T	A	4930568D16Rik	Missense	NM_029463	c.A443T	p.K148I	0.589
A2	A2-1-1	chr2	88411871	88411871	T	A	Olfir1180	Missense	NM_146918	c.A786T	p.E262D	0.44
A2	A2-1-1	chr2	153243656	153243656	C	T	Pofut1	Missense	NM_080463	c.C158T	p.A53V	0.531
A2	A2-1-1	chr3	131293658	131293658	C	T	Cyp2u1	Missense	NM_027816	c.G1273A	p.G425S	0.4
A2	A2-1-1	chr4	135750763	135750763	G	A	Il22ra1	Missense	NM_178257	c.G1144A	p.G382R	0.5
A2	A2-1-1	chr6	23115156	23115156	C	T	Aass	Splice site	NM_013930	c.473-1G>A	NA	0.571
A2	A2-1-1	chr6	83652425	83652425	C	T	Clec4f	Missense	NM_016751	c.G1150A	p.E384K	0.538
A2	A2-1-1	chr6	140593564	140593577	TGTCCTCTCTCTCT	-	Plekha5	Frameshift deletion	NM_144920	c.3725_3738del	p.L1242fs	0.118
A2	A2-1-1	chr6	47820441	47820441	T	C	Zfp786	Missense	NM_177882	c.A1562G	p.E521G	0.436
A2	A2-1-1	chr7	119595998	119595998	G	A	Acsm2	Missense	NM_001177978	c.G1732A	p.G578R	0.5
A2	A2-1-1	chr7	130503754	130503754	G	A	Ate1	Nonsense	NM_001136054	c.C904T	p.Q302X	0.31
A2	A2-1-1	chr7	81974048	81974048	G	A	Bnc1	Missense	NM_007562	c.C1430T	p.P477L	0.42
A2	A2-1-1	chr9	78414233	78414233	G	A	Ddx43	Missense	NM_001191044	c.G1183A	p.E395K	0.464
A2	A2-1-1	chr9	44263885	44263885	G	A	Nlrx1	Missense	NM_001163742	c.C593T	p.S198F	0.508
A2	A2-1-1	chr10	56162043	56162043	A	C	D630037F22Rik	Missense	NM_001033385	c.T1897G	p.L633V	0.393
A2	A2-1-1	chr10	51590152	51590152	G	A	Fam162b	Missense	NM_029894	c.C175T	p.P59S	0.514
A2	A2-1-1	chr11	87871456	87871456	G	A	Epx	Missense	NM_007946	c.C968T	p.A323V	0.189
A2	A2-1-1	chr11	69400041	69400041	C	T	Kdm6b	Missense	NM_001017426	c.G4801A	p.E1601K	0.49
A2	A2-1-1	chr15	94283837	94283837	T	-	Adamts20	Frameshift deletion	NM_177431	c.4974delA	p.K1658fs	0.333
A2	A2-1-1	chr15	98544040	98544040	G	A	Ccnt1	Missense	NM_009833	c.C1346T	p.P449L	0.464
A2	A2-1-1	chr18	60270062	60270062	G	A	Gm4841	Missense	NM_001034859	c.C958T	p.L320F	0.491
A2	A2-1-1	chr19	47665872	47665872	C	T	Col17a1	Missense	NM_007732	c.G1945A	p.E649K	0.5
A2	A2-1-1	chr19	33168452	33168452	G	T	Rnls	Missense	NM_001167818	c.C620A	p.P207Q	0.424
A2	A2-1-1	chrX	6083060	6083060	A	C	AU022751	Missense	NM_001166433	c.T263G	p.L88R	0.23
A2	A2-2-1	chr2	35354896	35354896	T	A	4930568D16Rik	Missense	NM_029463	c.A443T	p.K148I	0.453
A2	A2-2-1	chr2	88411871	88411871	T	A	Olfir1180	Missense	NM_146918	c.A786T	p.E262D	0.516
A2	A2-2-1	chr2	153243656	153243656	C	T	Pofut1	Missense	NM_080463	c.C158T	p.A53V	0.42
A2	A2-2-1	chr3	131293658	131293658	C	T	Cyp2u1	Missense	NM_027816	c.G1273A	p.G425S	0.389
A2	A2-2-1	chr4	135750763	135750763	G	A	Il22ra1	Missense	NM_178257	c.G1144A	p.G382R	0.534
A2	A2-2-1	chr6	83652425	83652425	C	T	Clec4f	Missense	NM_016751	c.G1150A	p.E384K	0.5
A2	A2-2-1	chr6	140593564	140593577	TGTCCTCTCTCTCT	-	Plekha5	Frameshift deletion	NM_144920	c.3725_3738del	p.L1242fs	0.163
A2	A2-2-1	chr6	48835525	48835525	T	A	Tmem176b	Missense	NM_001164208	c.C505T	p.P169S	0.074
A2	A2-2-1	chr6	47820441	47820441	G	C	Zfp786	Missense	NM_177882	c.A1562G	p.E521G	0.464
A2	A2-2-1	chr7	119595998	119595998	G	A	Acsm2	Missense	NM_001177978	c.G1732A	p.G578R	0.682
A2	A2-2-1	chr7	130503754	130503754	G	A	Ate1	Nonsense	NM_001136054	c.C904T	p.Q302X	0.517
A2	A2-2-1	chr7	81974048	81974048	G	A	Bnc1	Missense	NM_007562	c.C1430T	p.P477L	0.475
A2	A2-2-1	chr9	78414233	78414233	G	A	Ddx43	Missense	NM_001191044	c.G1183A	p.E395K	0.342
A2	A2-2-1	chr9	44263885	44263885	G	A	Nlrx1	Missense	NM_001163742	c.C593T	p.S198F	0.513
A2	A2-2-1	chr10	56162043	56162043	A	C	D630037F22Rik	Missense	NM_001033385	c.T1897G	p.L633V	0.462
A2	A2-2-1	chr10	51590152	51590152	G	A	Fam162b	Missense	NM_029894	c.C175T	p.P59S	0.446
A2	A2-2-1	chr11	87871456	87871456	G	A	Epx	Missense	NM_007946	c.C968T	p.A323V	0.241
A2	A2-2-1	chr11	69400041	69400041	C	T	Kdm6b	Missense	NM_001017426	c.G4801A	p.E1601K	0.494
A2	A2-2-1	chr15	94283837	94283837	T	-	Adamts20	Frameshift deletion	NM_177431	c.4974delA	p.K1658fs	0.286
A2	A2-2-1	chr15	98544									

A2	A2-2-2	chr19	47665872	47665872	C	T	Col17a1	Missense	NM_007732	c.G1945A	p.E649K	0.586
A2	A2-2-2	chr19	33168452	33168452	G	T	Rnl5	Missense	NM_001167818	c.C620A	p.P207Q	0.417
A2	A2-2-2	chrX	6083060	6083060	A	C	AU022751	Missense	NM_001166433	c.T263G	p.L88R	0.195
B1	B1-1-1	chr3	92868846	92868846	C	A	2310050C09Rik	Nonsense	NM_025621	c.G529T	p.G177X	0.118
B1	B1-1-1	chr11	43776006	43776006	A	G	Adra1b	Missense	NM_007416	c.T1403C	p.L468P	0.38
B1	B1-1-1	chr14	102981774	102981774	C	T	Kctd12	Missense	NM_177715	c.G667A	p.G223R	0.315
B1	B1-1-1	chrX	96160175	96160175	C	T	Msn	Missense	NM_010833	c.C883T	p.R295C	0.477
B1	B1-2-1	chr11	43776006	43776006	A	G	Adra1b	Missense	NM_007416	c.T1403C	p.L468P	0.277
B1	B1-2-1	chr11	70318181	70318181	A	C	Alox12e	Missense	NM_145684	c.T1238G	p.I413S	0.138
B1	B1-2-1	chr14	102981774	102981774	C	T	Kctd12	Missense	NM_177715	c.G667A	p.G223R	0.282
B1	B1-2-1	chrX	96160175	96160175	C	T	Msn	Missense	NM_010833	c.C883T	p.R295C	0.451
B1	B1-2-2	chr1	71047666	71047666	T	G	Bard1	Missense	NM_007525	c.A1748C	p.K583T	0.194
B1	B1-2-2	chr3	92868846	92868846	C	A	2310050C09Rik	Nonsense	NM_025621	c.G529T	p.G177X	0.092
B1	B1-2-2	chr5	137529884	137529884	C	T	Gnb2	Missense	NM_010312	c.G229A	p.G77R	0.11
B1	B1-2-2	chr11	43776006	43776006	A	G	Adra1b	Missense	NM_007416	c.T1403C	p.L468P	0.321
B1	B1-2-2	chr11	70318181	70318181	A	C	Alox12e	Missense	NM_145684	c.T1238G	p.I413S	0.133
B1	B1-2-2	chr14	102981774	102981774	C	T	Kctd12	Missense	NM_177715	c.G667A	p.G223R	0.314
B1	B1-2-2	chrX	96160175	96160175	C	T	Msn	Missense	NM_010833	c.C883T	p.R295C	0.367
B1	B1-2-3	chr1	71047666	71047666	T	G	Bard1	Missense	NM_007525	c.A1748C	p.K583T	0.526
B1	B1-2-3	chr3	92868846	92868846	C	A	2310050C09Rik	Nonsense	NM_025621	c.G529T	p.G177X	0.162
B1	B1-2-3	chr5	137529884	137529884	C	T	Gnb2	Missense	NM_010312	c.G229A	p.G77R	0.165
B1	B1-2-3	chr11	43776006	43776006	A	G	Adra1b	Missense	NM_007416	c.T1403C	p.L468P	0.311
B1	B1-2-3	chr11	70318181	70318181	A	C	Alox12e	Missense	NM_145684	c.T1238G	p.I413S	0.155
B1	B1-2-3	chr14	102981774	102981774	C	T	Kctd12	Missense	NM_177715	c.G667A	p.G223R	0.301
B1	B1-2-3	chrX	96160175	96160175	C	T	Msn	Missense	NM_010833	c.C883T	p.R295C	0.428
B1	B1-3-1	chr5	137529884	137529884	C	T	Gnb2	Missense	NM_010312	c.G229A	p.G77R	0.397
B1	B1-3-1	chr7	79098085	79098085	A	C	Acan	Missense	NM_007424	c.A2603C	p.E868A	0.091
B1	B1-3-1	chr11	43776006	43776006	A	G	Adra1b	Missense	NM_007416	c.T1403C	p.L468P	0.224
B1	B1-3-1	chr14	102981774	102981774	C	T	Kctd12	Missense	NM_177715	c.G667A	p.G223R	0.213
B1	B1-3-1	chrX	96160175	96160175	C	T	Msn	Missense	NM_010833	c.C883T	p.R295C	0.408
B1	B1-3-1	chrX	64272307	64272307	C	A	Slitr4	Missense	NM_178740	c.G753T	p.R251S	0.12
B1	B1-3-2	chr1	71047666	71047666	T	G	Bard1	Missense	NM_007525	c.A1748C	p.K583T	0.158
B1	B1-3-2	chr5	137529884	137529884	C	T	Gnb2	Missense	NM_010312	c.G229A	p.G77R	0.432
B1	B1-3-2	chr11	43776006	43776006	A	G	Adra1b	Missense	NM_007416	c.T1403C	p.L468P	0.198
B1	B1-3-2	chr14	102981774	102981774	C	T	Kctd12	Missense	NM_177715	c.G667A	p.G223R	0.166
B1	B1-3-2	chr14	76134837	76134837	C	T	Nufip1	Nonsense	NM_013745	c.C1390T	p.R464X	0.07
B1	B1-3-2	chrX	96160175	96160175	C	T	Msn	Missense	NM_010833	c.C883T	p.R295C	0.269
B1	B1-3-4	chr1	71047666	71047666	T	G	Bard1	Missense	NM_007525	c.A1748C	p.K583T	0.367
B1	B1-3-4	chr2	74705975	74705975	A	T	Hoxd8	Missense	NM_008276	c.A428T	p.Q143L	0.104
B1	B1-3-4	chr2	59842945	59842945	G	A	Tanc1	Missense	NM_198294	c.G4393A	p.E1465K	0.112
B1	B1-3-4	chr4	115920216	115920216	T	A	Dmbx1	Missense	NM_001025567	c.A434T	p.E145V	0.094
B1	B1-3-4	chr4	120097199	120097199	T	G	Hivep3	Missense	NM_010657	c.T2711G	p.F904C	0.173
B1	B1-3-4	chr4	81335755	81335755	C	T	Mpdz	Missense	NM_010820	c.G3139A	p.E1047K	0.1
B1	B1-3-4	chr5	90474665	90474665	A	G	Alb	Missense	NM_009654	c.A1751G	p.K584R	0.076
B1	B1-3-4	chr5	137529884	137529884	C	T	Gnb2	Missense	NM_010312	c.G229A	p.G77R	0.229
B1	B1-3-4	chr8	110415777	110415777	G	A	Hydin	Missense	NM_172916	c.G2287A	p.E763K	0.167
B1	B1-3-4	chr11	43776006	43776006	A	G	Adra1b	Missense	NM_007416	c.T1403C	p.L468P	0.222
B1	B1-3-4	chr11	69744685	69744685	G	A	Polr2a	Missense	NM_009089	c.C1583T	p.P528L	0.09
B1	B1-3-4	chr13	104375757	104375757	G	A	Adamts6	Missense	NM_001081020	c.G1486A	p.A496T	0.213
B1	B1-3-4	chr14	102981774	102981774	C	T	Kctd12	Missense	NM_177715	c.G667A	p.G223R	0.277
B1	B1-3-4	chr14	75525901	75525901	C	A	Siah3	Missense	NM_001128093	c.C591A	p.F197L	0.153
B1	B1-3-4	chr15	66919401	66919401	G	A	Wisp1	Missense	NM_018865	c.G1051A	p.D351N	0.087
B1	B1-3-4	chr17	31105597	31105597	C	T	Abcg1	Missense	NM_009593	c.C815T	p.T272I	0.074
B1	B1-3-4	chrX	105875297	105875297	T	G	Atrx	Missense	NM_009530	c.A2936C	p.K979T	0.098
B1	B1-3-4	chrX	96160175	96160175	C	T	Msn	Missense	NM_010833	c.C883T	p.R295C	0.242
B1	B1-3-4	chrX	64272307	64272307	C	A	Slitr4	Missense	NM_178740	c.G753T	p.R251S	0.116
B1	B1-3-5	chr2	74705975	74705975	A	T	Hoxd8	Missense	NM_008276	c.A428T	p.Q143L	0.092
B1	B1-3-5	chr5	137529884	137529884	C	T	Gnb2	Missense	NM_010312	c.G229A	p.G77R	0.363
B1	B1-3-5	chr9	45752068	45752068	C	T	Dscam1	Missense	NM_001081270	c.C5588T	p.S1863F	0.097
B1	B1-3-5	chr11	43776006	43776006	A	G	Adra1b	Missense	NM_007416	c.T1403C	p.L468P	0.225
B1	B1-3-5	chr14	102981774	102981774	C	T	Kctd12	Missense	NM_177715	c.G667A	p.G223R	0.221
B1	B1-3-5	chr17	31105597	31105597	C	T	Abcg1	Missense	NM_009593	c.C815T	p.T272I	0.076
B1	B1-3-5	chrX	96160175	96160175	C	T	Msn	Missense	NM_010833	c.C883T	p.R295C	0.259
B1	B1-3-5	chrX	64272307	64272307	C	A	Slitr4	Missense	NM_178740	c.G753T	p.R251S	0.094
B1	B1-4-1	chr1	71047666	71047666	T	G	Bard1	Missense	NM_007525	c.A1748C	p.K583T	0.241
B1	B1-4-1	chr1	34278049	34278049	A	T	Dst	Missense	NM_001276764	c.A20481T	p.E6827D	0.145
B1	B1-4-1	chr3	62493796	62493796	G	A	Dhx36	Nonsense	NM_028136	c.C1048T	p.R350X	0.135
B1	B1-4-1	chr3	92028012	92028012	C	T	Pglyrp3	Missense	NM_207247	c.C568T	p.R190W	0.3
B1	B1-4-1	chr5	137529884	137529884	C	T	Gnb2	Missense	NM_010312	c.G229A	p.G77R	0.771
B1	B1-4-1	chr6	13836698	13836698	C	T	Gpr85	Missense	NM_145066	c.G206A	p.R69K	0.08
B1	B1-4-1	chr6	121358699	121358699	C	G	Slc6a12	Missense	NM_133661	c.C987G	p.C329W	0.154
B1	B1-4-1	chr7	140297699	140297699	C	T	5830411N06Rik	Missense	NM_001128146	c.C2671T	p.L891F	0.079
B1	B1-4-1	chr9	108084849	108084849	G	A	Mst1	Missense	NM_008243	c.G2065A	p.V689M	0.155
B1	B1-4-1	chr10	94181503	94181503	C	T	Nr2c1	Missense	NM_011629	c.C1102T	p.P368S	0.08
B1	B1-4-1	chr11	43776006	43776006	A	G	Adra1b	Missense	NM_007416	c.T1403C	p.L468P	0.141
B1	B1-4-1	chr12	76575914	76575914	C	T	Plekhg3	Missense	NM_153804	c.C1930T	p.P644S	0.078
B1	B1-4-1	chr13	93677100	93677100	G	A	Dmgdh	Missense	NM_028772	c.G152A	p.G51D	0.135
B1	B1-4-1	chr14	102981774	102981774	C	T	Kctd12	Missense	NM_177715	c.G667A	p.G223R	0.137
B1	B1-4-1	chr14	76134837	76134837	C	T	Nufip1	Nonsense	NM_013745	c.C1390T	p.R464X	0.083
B1	B1-4-1	chr18	20536959	20536959	G	A	Dsg3	Missense	NM_030596	c.G2029A	p.E677K	0.157
B1	B1-4-1	chr19	37685837	37685837	C	T	Cyp26c1	Missense	NM_001105201	c.C158T	p.S53F	0.077
B1	B1-4-1	chrX	96160175	96160175	C	T	Msn	Missense	NM_010833	c.C883T	p.R295C	0.116
B1	B1-4-5	chr1	172239796	172239796	C	T	Atp1a4	Missense	NM_013734	c.G1768A	p.E590K	0.161
B1	B1-4-5	chr1	171237964	171237964	G	A	Ndufs2	Nonsense	NM_153064	c.C967T	p.R323X	0.11
B1	B1-4-5	chr2	65022586	65022586	G	A	Grb14	Missense	NM_016719	c.C59T	p.S20L	0.159
B1	B1-4-5	chr3	62493796	62493796	G	A	Dhx36	Nonsense	NM_028136	c.C1048T	p.R350X	0.137
B1	B1-4-5	chr5	137529884	137529884	C	T	Gnb2	Missense	NM_010312	c.G229A	p.G77R	0.718
B1	B1-4-5	chr5	142776308	142776308	G	A	Tnrc18	Missense	NM_001122730	c.C2110T	p.L704F	0.071
B1	B1-4-5	chr6	121358699	121358699	C	G	Slc6a12	Missense	NM_133661	c.C987G	p.C329W	0.183
B1	B1-4-5	chr7	6277419	6277419	G	A	Gm6792	Splice site	NM_001177416	c.277-1G>A	NA	0.114
B1	B1-4-5	chr7	104704475	104704475	G	A	Olfir663	Missense	NM_001011757	c.G907A	p.E303K	0.133
B1	B1-4-5	chr8	4210997	4210997	G	A	BC068157	Missense	NM_207203	c.C2819T	p.S940F	0.083
B1	B1-4-5	chr9	4299348	4299348	G	A	Aasdhppt	Missense	NM_026276	c.C715T	p.H239Y	0.091
B1	B1-4-5	chr9	108084849	108084849	G	A	Mst1	Missense	NM_008243	c.G2065A	p.V689M	0.121
B1	B1-4-5	chr11	43776006	43776006	A	G	Adra1b	Missense	NM_007416	c.T1403C	p.L468P	0.107
B1	B1-4-5	chr11	12249810	12249810	G	A	Cobl	Missense	NM_172496	c.C3836T	p.P1279L	0.087
B1	B1-4-5	chr13	93677100	93677100	G	A	Dmgdh	Missense	NM_028772	c.G152A	p.G51D	0.166
B1	B1-4-5	chr13	64921751	64921751	T	A	Spata31	Missense	NM_030047	c.T1712A	p.M571K	0.079
B1	B1-4-5	chr14	76134837	76134837	C	T	Nufip1	Nonsense	NM_013745	c.C1390T	p.R464X	0.174
B1	B1-4-5	chr17	37151568	37151568	G	A	Olfir93	Missense	NM_			

B1	B1-4-9	chrX	96160175	96160175	C	T	Msn	Missense	NM_010833	c.C883T	p.R295C	0.126
B1	B1-4-10	chr2	74705975	74705975	A	T	Hoxd8	Missense	NM_008276	c.A428T	p.Q143L	0.206
B1	B1-4-10	chr2	59842945	59842945	G	A	Tanc1	Missense	NM_198294	c.G4393A	p.E1465K	0.203
B1	B1-4-10	chr4	115920216	115920216	T	A	Dmbx1	Missense	NM_001025567	c.A434T	p.E145V	0.227
B1	B1-4-10	chr4	120097199	120097199	T	G	Hivep3	Missense	NM_010657	c.T2711G	p.F904C	0.228
B1	B1-4-10	chr4	81335755	81335755	C	T	Mpdz	Missense	NM_010820	c.G3139A	p.E1047K	0.293
B1	B1-4-10	chr5	90474665	90474665	A	G	Alb	Missense	NM_009654	c.A1751G	p.K584R	0.194
B1	B1-4-10	chr5	137529884	137529884	C	T	Gnb2	Missense	NM_010312	c.G229A	p.G77R	0.145
B1	B1-4-10	chr7	105144072	105144072	T	G	Olfir683	Missense	NM_147045	c.A238C	p.I80L	0.346
B1	B1-4-10	chr8	80496720	80496720	C	T	Gypa	Missense	NM_010369	c.C124T	p.L42F	0.22
B1	B1-4-10	chr8	110415777	110415777	G	A	Hydin	Missense	NM_172916	c.G2287A	p.E763K	0.209
B1	B1-4-10	chr9	45752068	45752068	C	T	Dscam11	Missense	NM_001081270	c.C5588T	p.S1863F	0.218
B1	B1-4-10	chr9	62696892	62696892	G	C	Itga11	Missense	NM_176922	c.G61C	p.D21H	0.203
B1	B1-4-10	chr11	43776006	43776006	A	G	Adra1b	Missense	NM_007416	c.T1403C	p.L468P	0.193
B1	B1-4-10	chr11	69744685	69744685	G	A	Polr2a	Missense	NM_009089	c.C1583T	p.P528L	0.17
B1	B1-4-10	chr12	73941721	73941721	T	G	Hif1a	Missense	NM_010431	c.T1567G	p.F523V	0.164
B1	B1-4-10	chr14	102981774	102981774	C	T	Kctd12	Missense	NM_177715	c.G667A	p.G223R	0.177
B1	B1-4-10	chr14	75525901	75525901	C	A	Siah3	Missense	NM_001128093	c.C591A	p.F197L	0.15
B1	B1-4-10	chr15	66919401	66919401	G	A	Wispl	Missense	NM_018865	c.G1051A	p.D351N	0.232
B1	B1-4-10	chr17	31105597	31105597	C	T	Abcg1	Missense	NM_009593	c.C815T	p.T272I	0.255
B1	B1-4-10	chr19	58733459	58733459	T	G	Pnliprp1	Missense	NM_018874	c.T569G	p.I190S	0.352
B1	B1-4-10	chrX	105875297	105875297	T	G	Atrx	Missense	NM_009530	c.A2936C	p.K979T	0.191
B1	B1-4-10	chrX	96160175	96160175	C	T	Msn	Missense	NM_010833	c.C883T	p.R295C	0.126
B1	B1-4-13	chr2	155276972	155276972	G	A	Map1lc3a	Missense	NM_025735	c.G55A	p.E19K	0.093
B1	B1-4-13	chr2	126829167	126829167	T	A	Trpm7	Missense	NM_021450	c.A1894T	p.M632L	0.231
B1	B1-4-13	chr4	115920216	115920216	T	A	Dmbx1	Missense	NM_001025567	c.A434T	p.E145V	0.122
B1	B1-4-13	chr4	120097199	120097199	T	T	Hivep3	Missense	NM_010657	c.T2711G	p.F904C	0.091
B1	B1-4-13	chr4	141683988	141683988	G	G	Rsc1a1	Missense	NM_023544	c.C1612A	p.P538T	0.093
B1	B1-4-13	chr5	90474665	90474665	A	G	Alb	Missense	NM_009654	c.A1751G	p.K584R	0.105
B1	B1-4-13	chr5	114263107	114263107	G	A	Foxn4	Missense	NM_148935	c.C134T	p.S45L	0.102
B1	B1-4-13	chr5	137529884	137529884	C	T	Gnb2	Missense	NM_010312	c.G229A	p.G77R	0.591
B1	B1-4-13	chr8	110415777	110415777	G	A	Hydin	Missense	NM_172916	c.G2287A	p.E763K	0.114
B1	B1-4-13	chr9	92343681	92343681	C	T	1700057G04Rik	Missense	NM_001033184	c.C55T	p.H19Y	0.167
B1	B1-4-13	chr9	62696892	62696892	G	C	Itga11	Missense	NM_176922	c.G61C	p.D21H	0.1
B1	B1-4-13	chr11	43776006	43776006	A	G	Adra1b	Missense	NM_007416	c.T1403C	p.L468P	0.092
B1	B1-4-13	chr11	55532341	55532341	G	A	Gira1	Nonsense	NM_020492	c.C640T	p.Q214X	0.112
B1	B1-4-13	chr11	103208861	103208861	C	T	Spata32	Missense	NM_177801	c.G817A	p.D273N	0.125
B1	B1-4-13	chr14	70638916	70638916	G	C	Fgf17	Missense	NM_008004	c.C136G	p.Q46E	0.09
B1	B1-4-13	chr14	102981774	102981774	C	T	Kctd12	Missense	NM_177715	c.G667A	p.G223R	0.099
B1	B1-4-13	chr15	66919401	66919401	G	A	Wispl	Missense	NM_018865	c.G1051A	p.D351N	0.194
B1	B1-4-13	chr16	93810163	93810163	C	T	Dopey2	Missense	NM_027293	c.C6704T	p.S2235F	0.083
B1	B1-4-13	chr18	82986882	82986882	C	A	Zfp516	Missense	NM_001177464	c.C1910A	p.S637Y	0.089
B1	B1-4-13	chr19	58733459	58733459	T	G	Pnliprp1	Missense	NM_018874	c.T569G	p.I190S	0.22
B1	B1-4-13	chrX	105875297	105875297	T	G	Atrx	Missense	NM_009530	c.A2936C	p.K979T	0.105
B1	B1-4-13	chrX	96160175	96160175	C	T	Msn	Missense	NM_010833	c.C883T	p.R295C	0.124
C1	C1-1-1	chr8	110858656	110858656	G	A	Cog4	Missense	NM_133973	c.G952A	p.V318I	0.533
C1	C1-2-1	chr5	121168003	121168003	C	T	Ptpn11	Missense	NM_011202	c.G178A	p.G60R	0.276
C1	C1-2-1	chr8	110858656	110858656	G	A	Cog4	Missense	NM_133973	c.G952A	p.V318I	0.585
C1	C1-2-2	chr2	173568941	173568941	G	A	Ankrd60	Missense	NM_027303	c.C785T	p.T262M	0.085
C1	C1-2-2	chr5	122457255	122457255	C	T	Atp2a2	Missense	NM_001110140	c.G3031A	p.A1011T	0.077
C1	C1-2-2	chr5	121168003	121168003	C	T	Ptpn11	Missense	NM_011202	c.G178A	p.G60R	0.323
C1	C1-2-2	chr8	110858656	110858656	G	A	Cog4	Missense	NM_133973	c.G952A	p.V318I	0.456
C2	C2-1-1	chr6	39627783	39627783	A	T	Braf	Missense	NM_139294	c.T1910A	p.V637E	0.453
C2	C2-1-1	chr7	57408803	57408803	G	A	Gabra5	Missense	NM_176942	c.C1196T	p.A399V	0.439
C2	C2-2-1	chr2	25295931	25295931	A	C	Grin1	Missense	NM_008169	c.T2450G	p.F817C	0.078
C2	C2-2-1	chr6	39627783	39627783	A	T	Braf	Missense	NM_139294	c.T1910A	p.V637E	0.394
C2	C2-2-1	chr7	57408803	57408803	G	A	Gabra5	Missense	NM_176942	c.C1196T	p.A399V	0.524
C2	C2-2-2	chr6	39627783	39627783	A	T	Braf	Missense	NM_139294	c.T1910A	p.V637E	0.63
C2	C2-2-2	chr7	57408803	57408803	G	A	Gabra5	Missense	NM_176942	c.C1196T	p.A399V	0.423
D1	D1-1-1	chr1	43742308	43742308	G	A	1500015O10Rik	Missense	NM_024283	c.G349A	p.D117N	0.575
D1	D1-1-1	chr1	58233915	58233915	G	A	Aox4	Missense	NM_023631	c.G988A	p.E330K	0.381
D1	D1-1-1	chr1	160577443	160577443	T	A	Gpr52	Missense	NM_001146330	c.A311T	p.Y104F	0.58
D1	D1-1-1	chr2	83879660	83879660	A	G	Fam171b	Missense	NM_175514	c.A1675G	p.R559G	0.481
D1	D1-1-1	chr2	41449323	41449323	T	A	Lrp1b	Missense	NM_053011	c.A2507T	p.N836I	0.5
D1	D1-1-1	chr2	87753589	87753589	C	T	Olfir1141	Missense	NM_146637	c.G403A	p.D135N	0.496
D1	D1-1-1	chr3	87975556	87975556	A	G	Nes	Missense	NM_016701	c.A1121G	p.K374R	0.5
D1	D1-1-1	chr3	102941078	102941078	A	G	Nr1h5	Missense	NM_198658	c.T1310C	p.L437P	0.442
D1	D1-1-1	chr3	109827654	109827654	C	T	Ntng1	Missense	NM_030699	c.G1363A	p.G455R	0.514
D1	D1-1-1	chr3	129811729	129811729	G	A	Rrh	Missense	NM_009102	c.C602T	p.P201L	0.422
D1	D1-1-1	chr3	5412423	5412423	G	A	Zfhx4	Missense	NM_030708	c.G10022A	p.S3341N	0.481
D1	D1-1-1	chr4	101814920	101814920	C	T	Lepr	Missense	NM_146146	c.C3140T	p.S1047L	0.47
D1	D1-1-1	chr4	43101826	43101826	T	A	Unc13b	Nonsense	NM_021468	c.T420A	p.Y140X	0.517
D1	D1-1-1	chr5	101814467	101814467	C	T	Cds1	Missense	NM_173370	c.C947T	p.S316F	0.436
D1	D1-1-1	chr5	4757484	4757484	C	T	Fzd1	Missense	NM_021457	c.G97A	p.G33R	0.419
D1	D1-1-1	chr5	106845458	106845458	C	T	Hfm1	Missense	NM_177873	c.G3898A	p.D1300N	0.468
D1	D1-1-1	chr5	33668158	33668158	C	T	Tacc3	Missense	NM_001040435	c.C1231T	p.L411F	0.5
D1	D1-1-1	chr6	142449487	142449487	A	T	Gys2	Missense	NM_145572	c.T1251A	p.N417K	0.446
D1	D1-1-1	chr7	103451408	103451408	G	A	Olfir606	Missense	NM_147094	c.G70A	p.E24K	0.286
D1	D1-1-1	chr7	35584548	35584548	C	A	Rgs9bp	Missense	NM_145840	c.G673T	p.V225L	0.51
D1	D1-1-1	chr8	25739570	25739570	C	T	Dhd2	Missense	NM_028102	c.G1141A	p.A381T	0.25
D1	D1-1-1	chr8	33572140	33572140	C	T	Tex15	Missense	NM_031374	c.C1597T	p.L533F	0.5
D1	D1-1-1	chr9	43279886	43279886	G	A	De30033O11Rik	Missense	NM_001243261	c.G348A	p.M116I	0.688
D1	D1-1-1	chr9	3634462	3634462	G	A	Gucy1a2	Missense	NM_001033322	c.G505A	p.E169K	0.382
D1	D1-1-1	chr9	38403692	38403692	G	T	Olfir147	Nonsense	NM_146869	c.G817T	p.G273X	0.399
D1	D1-1-1	chr9	78313067	78313067	G	A	Omt2a	Missense	NM_001164523	c.C49T	p.L17F	0.449
D1	D1-1-1	chr9	48832304	48832304	G	A	Zbtb16	Missense	NM_001033324	c.C707T	p.P236L	0.564
D1	D1-1-1	chr10	89714952	89714952	G	A	Actr6	Missense	NM_025914	c.C979T	p.P327S	0.615
D1	D1-1-1	chr10	128953950	128953950	C	A	Itga7	Missense	NM_008398	c.C3059A	p.P1020Q	0.534
D1	D1-1-1	chr10	88548796	88548796	G	A	Mybpc1	Missense	NM_001252372	c.C1625T	p.P542L	0.49
D1	D1-1-1	chr11	85178450	85178450	G	A	1700125H20Rik	Missense	NM_028589	c.G623A	p.G208E	0.532
D1	D1-1-1	chr11	75432578	75432578	C	T	Serpinf2	Missense	NM_008878	c.G1301A	p.R434K	0.421
D1	D1-1-1	chr12	3367043	3367043	C	T	Kif3c	Missense	NM_008445	c.C1063T	p.L355F	0.515
D1	D1-1-1	chr12	69722113	69722113	A	T	L2hgdh	Missense	NM_145443	c.T224A	p.L75H	0.537
D1	D1-1-1	chr13	92752398	92752398	G	A	Thbs4	Missense	NM_011582	c.C2786T	p.S929F	0.381
D1	D1-1-1	chr14	28522675	28522675	C	T	Wnt5a	Missense	NM_001256224	c.C818T	p.S273F	0.456
D1	D1-1-1	chr15	20666089	20666089	C	T	Acot10	Missense	NM_022816	c.G565A	p.D189N	0.43
D1	D1-1-1	chr15	98594461	98594461	G	A	Adcy2	Missense	NM_007405	c.C2921T	p.S974L	0.53
D1	D1-1-1	chr17	36128961	36128961	C	T	Gm7030	Missense	NM_001177467	c.G280A	p.E94K	0.458
D1	D1-1-1	chr17	71504803	71504803	A	C	Ndc80	Missense	NM_023294	c.T1427G	p.L476R	0.58
D1	D1-1-1	chr18	38254491	3825449								



D1	D1-2-1	chr7	108346731	108346732	AT	TA	Olf493	Missense	NM_146310	c.AT248_249TA	p.N83I	0.643
D1	D1-2-1	chr7	103451408	103451408	G	A	Olf606	Missense	NM_147094	c.G70A	p.E24K	0.451
D1	D1-2-1	chr7	35584548	35584548	C	A	Rgs9bp	Missense	NM_145840	c.G673T	p.V225L	0.48
D1	D1-2-1	chr8	104931069	104931069	T	C	Ces2e	Missense	NM_172759	c.T919C	p.F307L	0.433
D1	D1-2-1	chr8	33572140	33572140	C	T	Tex15	Missense	NM_031374	c.C1597T	p.L533F	0.356
D1	D1-2-1	chr9	43279886	43279886	G	A	D630033O11Rik	Missense	NM_001243261	c.G348A	p.M116I	0.491
D1	D1-2-1	chr9	3634462	3634462	G	A	Gucy1a2	Missense	NM_001033322	c.G505A	p.E169K	0.473
D1	D1-2-1	chr9	38403692	38403692	G	T	Olf147	Nonsense	NM_146869	c.G817T	p.G273X	0.446
D1	D1-2-1	chr9	78313067	78313067	G	A	Omt2a	Missense	NM_001164523	c.C49T	p.L17F	0.485
D1	D1-2-1	chr9	48832304	48832304	G	A	Zbtb16	Missense	NM_001033324	c.C707T	p.P236L	0.464
D1	D1-2-1	chr10	89714952	89714952	G	A	Actr6	Missense	NM_025914	c.C979T	p.P327S	0.552
D1	D1-2-1	chr10	128953950	128953950	C	A	Itga7	Missense	NM_008398	c.C3059A	p.P1020Q	0.449
D1	D1-2-1	chr10	88548796	88548796	G	A	Mybpc1	Missense	NM_001252372	c.C1625T	p.P542L	0.515
D1	D1-2-1	chr11	85178450	85178450	G	A	1700125H20Rik	Missense	NM_028589	c.G623A	p.G208E	0.553
D1	D1-2-1	chr11	75432578	75432578	C	T	Serpinf2	Missense	NM_008878	c.G1301A	p.R434K	0.48
D1	D1-2-1	chr12	3367043	3367043	C	T	Kif3c	Missense	NM_008445	c.C1063T	p.L355F	0.583
D1	D1-2-1	chr12	69722113	69722113	A	T	L2hgdh	Missense	NM_145443	c.T224A	p.L75H	0.551
D1	D1-2-1	chr13	92752398	92752398	G	A	Thbs4	Missense	NM_011582	c.C2786T	p.S929F	0.488
D1	D1-2-1	chr14	28522675	28522675	C	T	Wnt5a	Missense	NM_001256224	c.C818T	p.S273F	0.484
D1	D1-2-1	chr15	20666089	20666089	C	T	Acot10	Missense	NM_022816	c.G565A	p.D189N	0.42
D1	D1-2-1	chr15	98594461	98594461	G	A	Adcy6	Missense	NM_007405	c.C2921T	p.S974L	0.506
D1	D1-2-1	chr17	36128961	36128961	C	T	Gm7030	Missense	NM_001177467	c.G280A	p.E94K	0.356
D1	D1-2-1	chr17	71504803	71504803	A	C	Ndc80	Missense	NM_023294	c.T1427G	p.L476R	0.525
D1	D1-2-1	chr18	38254491	38254491	C	T	0610009O20Rik	Missense	NM_024179	c.C682T	p.L228F	0.492
D1	D1-2-1	chr18	7129517	7129517	T	A	Armc4	Missense	NM_001081393	c.A2660T	p.N887I	0.5
D1	D1-2-1	chr19	36057177	36057177	C	A	Htr7	Missense	NM_008315	c.G77T	p.R26L	0.555
D1	D1-2-1	chrX	100573860	100573860	G	A	Awat1	Nonsense	NM_001081136	c.G215A	p.W72X	0.6
D1	D1-2-1	chrX	129972594	129972594	C	T	Diap2	Missense	NM_172493	c.C2038T	p.P680S	0.493
D1	D1-2-1	chrX	152209512	152209512	C	T	Iqsec2	Missense	NM_001114664	c.C2144T	p.S715F	0.545
D1	D1-2-1	chrX	66654019	66654019	G	A	Slitr2	Missense	NM_001161431	c.G115A	p.E39K	0.45
D1	D1-2-2	chr1	43742308	43742308	G	A	1500015O10Rik	Missense	NM_024283	c.G349A	p.D117N	0.489
D1	D1-2-2	chr1	58233915	58233915	G	A	Aox4	Missense	NM_023631	c.G988A	p.E330K	0.714
D1	D1-2-2	chr1	160577443	160577443	T	A	Gpr52	Missense	NM_001146330	c.A311T	p.Y104F	0.5
D1	D1-2-2	chr2	83879660	83879660	A	G	Fam171b	Missense	NM_175514	c.A1675G	p.R559G	0.495
D1	D1-2-2	chr2	41449323	41449323	T	A	Lrp1b	Missense	NM_053011	c.A2507T	p.N836I	0.409
D1	D1-2-2	chr2	87753589	87753589	C	T	Olf1141	Missense	NM_146637	c.G403A	p.D135N	0.408
D1	D1-2-2	chr3	87975556	87975556	A	G	Nes	Missense	NM_016701	c.A1121G	p.K374R	0.488
D1	D1-2-2	chr3	102941078	102941078	A	G	Nr1h5	Missense	NM_198658	c.T1310C	p.L437P	0.486
D1	D1-2-2	chr3	109827654	109827654	C	T	Ntn1	Missense	NM_030699	c.G1363A	p.G455R	0.321
D1	D1-2-2	chr3	129811729	129811729	G	A	Rrh	Missense	NM_009102	c.C602T	p.P201L	0.473
D1	D1-2-2	chr3	5412423	5412423	G	A	Zfhx4	Missense	NM_030708	c.G10022A	p.S3341N	0.455
D1	D1-2-2	chr4	101814920	101814920	C	T	Lepr	Missense	NM_146146	c.C3140T	p.S1047L	0.494
D1	D1-2-2	chr4	43101826	43101826	T	A	Unc13b	Nonsense	NM_021468	c.T420A	p.Y140X	0.613
D1	D1-2-2	chr5	101814467	101814467	C	T	Cds1	Missense	NM_173370	c.C947T	p.S316F	0.459
D1	D1-2-2	chr5	4757484	4757484	C	T	Fzd1	Missense	NM_021457	c.G97A	p.G33R	0.457
D1	D1-2-2	chr5	106845458	106845458	C	T	Hfm1	Missense	NM_177873	c.G3898A	p.D1300N	0.551
D1	D1-2-2	chr5	33668158	33668158	C	T	Tacc3	Missense	NM_001040435	c.C1231T	p.L411F	0.463
D1	D1-2-2	chr6	142449487	142449487	A	T	Gys2	Missense	NM_145572	c.T1251A	p.N417K	0.471
D1	D1-2-2	chr7	103451408	103451408	G	A	Olf606	Missense	NM_147094	c.G70A	p.E24K	0.548
D1	D1-2-2	chr7	35584548	35584548	C	A	Rgs9bp	Missense	NM_145840	c.G673T	p.V225L	0.497
D1	D1-2-2	chr8	104931069	104931069	T	C	Ces2e	Missense	NM_172759	c.T919C	p.F307L	0.342
D1	D1-2-2	chr8	33572140	33572140	C	T	Tex15	Missense	NM_031374	c.C1597T	p.L533F	0.539
D1	D1-2-2	chr9	43279886	43279886	G	A	D630033O11Rik	Missense	NM_001243261	c.G348A	p.M116I	0.523
D1	D1-2-2	chr9	3634462	3634462	G	A	Gucy1a2	Missense	NM_001033322	c.G505A	p.E169K	0.462
D1	D1-2-2	chr9	38403692	38403692	G	T	Olf147	Nonsense	NM_146869	c.G817T	p.G273X	0.463
D1	D1-2-2	chr9	78313067	78313067	G	A	Omt2a	Missense	NM_001164523	c.C49T	p.L17F	0.515
D1	D1-2-2	chr9	48832304	48832304	G	A	Zbtb16	Missense	NM_001033324	c.C707T	p.P236L	0.422
D1	D1-2-2	chr10	89714952	89714952	G	A	Actr6	Missense	NM_025914	c.C979T	p.P327S	0.433
D1	D1-2-2	chr10	128953950	128953950	C	A	Itga7	Missense	NM_008398	c.C3059A	p.P1020Q	0.483
D1	D1-2-2	chr10	88548796	88548796	G	A	Mybpc1	Missense	NM_001252372	c.C1625T	p.P542L	0.432
D1	D1-2-2	chr11	85178450	85178450	G	A	1700125H20Rik	Missense	NM_028589	c.G623A	p.G208E	0.4
D1	D1-2-2	chr11	75432578	75432578	C	T	Serpinf2	Missense	NM_008878	c.G1301A	p.R434K	0.473
D1	D1-2-2	chr12	3367043	3367043	C	T	Kif3c	Missense	NM_008445	c.C1063T	p.L355F	0.496
D1	D1-2-2	chr12	69722113	69722113	A	T	L2hgdh	Missense	NM_145443	c.T224A	p.L75H	0.568
D1	D1-2-2	chr13	92752398	92752398	G	A	Thbs4	Missense	NM_011582	c.C2786T	p.S929F	0.449
D1	D1-2-2	chr14	28522675	28522675	C	T	Wnt5a	Missense	NM_001256224	c.C818T	p.S273F	0.497
D1	D1-2-2	chr15	20666089	20666089	C	T	Acot10	Missense	NM_022816	c.G565A	p.D189N	0.429
D1	D1-2-2	chr15	98594461	98594461	G	A	Adcy6	Missense	NM_007405	c.C2921T	p.S974L	0.491
D1	D1-2-2	chr17	71504803	71504803	A	C	Ndc80	Missense	NM_023294	c.T1427G	p.L476R	0.61
D1	D1-2-2	chr18	38254491	38254491	C	T	0610009O20Rik	Missense	NM_024179	c.C682T	p.L228F	0.504
D1	D1-2-2	chr18	7129517	7129517	T	A	Armc4	Missense	NM_001081393	c.A2660T	p.N887I	0.429
D1	D1-2-2	chr19	36057177	36057177	C	A	Htr7	Missense	NM_008315	c.G77T	p.R26L	0.508
D1	D1-2-2	chrX	100573860	100573860	G	A	Awat1	Nonsense	NM_001081136	c.G215A	p.W72X	0.489
D1	D1-2-2	chrX	129972594	129972594	C	T	Diap2	Missense	NM_172493	c.C2038T	p.P680S	0.408
D1	D1-2-2	chrX	152209512	152209512	C	T	Iqsec2	Missense	NM_001114664	c.C2144T	p.S715F	0.471
D1	D1-2-2	chrX	66654019	66654019	G	A	Slitr2	Missense	NM_001161431	c.G115A	p.E39K	0.521
D1	D1-2-3	chr1	43742308	43742308	G	A	1500015O10Rik	Missense	NM_024283	c.G349A	p.D117N	0.436
D1	D1-2-3	chr1	58233915	58233915	G	A	Aox4	Missense	NM_023631	c.G988A	p.E330K	0.55
D1	D1-2-3	chr1	160577443	160577443	T	A	Gpr52	Missense	NM_001146330	c.A311T	p.Y104F	0.479
D1	D1-2-3	chr2	83879660	83879660	A	G	Fam171b	Missense	NM_175514	c.A1675G	p.R559G	0.464
D1	D1-2-3	chr2	41449323	41449323	T	A	Lrp1b	Missense	NM_053011	c.A2507T	p.N836I	0.444
D1	D1-2-3	chr2	87753589	87753589	C	T	Olf1141	Missense	NM_146637	c.G403A	p.D135N	0.448
D1	D1-2-3	chr3	87975556	87975556	A	G	Nes	Missense	NM_016701	c.A1121G	p.K374R	0.46
D1	D1-2-3	chr3	102941078	102941078	A	G	Nr1h5	Missense	NM_198658	c.T1310C	p.L437P	0.364
D1	D1-2-3	chr3	109827654	109827654	C	T	Ntn1	Missense	NM_030699	c.G1363A	p.G455R	0.522
D1	D1-2-3	chr3	129811729	129811729	G	A	Rrh	Missense	NM_009102	c.C602T	p.P201L	0.44
D1	D1-2-3	chr3	5412423	5412423	G	A	Zfhx4	Missense	NM_030708	c.G10022A	p.S3341N	0.552
D1	D1-2-3	chr4	101814920	101814920	C	T	Lepr	Missense	NM_146146	c.C3140T	p.S1047L	0.425
D1	D1-2-3	chr4	43101826	43101826	T	A	Unc13b	Nonsense	NM_021468	c.T420A	p.Y140X	0.563
D1	D1-2-3	chr5	101814467	101814467	C	T	Cds1	Missense	NM_173370	c.C947T	p.S316F	0.54
D1	D1-2-3	chr5	4757484	4757484	C	T	Fzd1	Missense	NM_021457	c.G97A	p.G33R	0.529
D1	D1-2-3	chr5	106845458	106845458	C	T	Hfm1	Missense	NM_177873	c.G3898A	p.D1300N	0.475
D1	D1-2-3	chr5	33668158	33668158	C	T	Tacc3	Missense	NM_001040435	c.C1231T	p.L411F	0.495
D1	D1-2-3	chr6	142449487	142449487	A	T	Gys2	Missense	NM_145572	c.T1251A	p.N417K	0.418
D1	D1-2-3	chr7	103451408	103451408	G	A	Olf606	Missense	NM_147094	c.G70A	p.E24K	0.489
D1	D1-2-3	chr7	35584548	35584548	C	A	Rgs9bp	Missense	NM_145840	c.G673T	p.V225L	0.477
D1	D1-2-3	chr8	104931069	104931069	T	C	Ces2e	Missense	NM_172759	c.T919C	p.F307L	0.543
D1	D1-2-3	chr8	33572140	33572140	C	T	Tex15	Missense	NM_031374	c.C1597T	p.L533F	0.533
D1	D1-2-3	chr9	43279886	43279886	G	A	D630033O11Rik	Missense	NM_001243261	c.G348A	p.M116I	0.5
D1	D1-2-3	chr9										

D2	D2-1-1	chr1	133329529	133329529	C	T	Kiss1	Missense	NM_178260	c.C265T	p.P89S	0.331
D2	D2-1-1	chr1	157175868	157175868	T	G	Rasal2	Missense	NM_177644	c.A1274C	p.K425T	0.143
D2	D2-1-1	chr1	131977494	131977494	G	A	Slc45a3	Missense	NM_001177628	c.G254A	p.R85Q	0.136
D2	D2-1-1	chr1	75532637	75532637	C	A	Stk11ip	Nonsense	NM_027886	c.C2298A	p.C766X	0.132
D2	D2-1-1	chr2	154368820	154368820	G	A	Cdk5rap1	Missense	NM_025876	c.C397T	p.L133F	0.114
D2	D2-1-1	chr2	153622686	153622686	G	A	Comm7	Missense	NM_133850	c.C301T	p.L101F	0.104
D2	D2-1-1	chr2	165292083	165292083	G	A	Elmo2	Missense	NM_207705	c.C1984T	p.L662F	0.298
D2	D2-1-1	chr2	167983186	167983186	C	T	Fam65c	Missense	NM_001080708	c.G2402A	p.G801E	0.137
D2	D2-1-1	chr2	132915191	132915191	C	T	Fermt1	Missense	NM_198029	c.G1718A	p.R573K	0.118
D2	D2-1-1	chr2	71841706	71841706	C	T	Itga6	Missense	NM_008397	c.C2465T	p.S822F	0.342
D2	D2-1-1	chr2	155622647	155622647	G	A	Myh7b	Missense	NM_001085378	c.G1903A	p.E635K	0.174
D2	D2-1-1	chr2	86988709	86988709	G	A	Olf1101	Missense	NM_146591	c.C466T	p.H156Y	0.092
D2	D2-1-1	chr2	153865380	153865380	C	T	Sun5	Missense	NM_029599	c.G377A	p.G126E	0.242
D2	D2-1-1	chr2	26916799	26916799	C	T	Surf2	Missense	NM_013678	c.C173T	p.S58F	0.124
D2	D2-1-1	chr2	21213075	21213075	G	A	Thns1	Missense	NM_177588	c.G1639A	p.G547R	0.361
D2	D2-1-1	chr3	89033297	89033297	C	T	Ash11	Missense	NM_138679	c.C6127T	p.P2043S	0.324
D2	D2-1-1	chr3	84474415	84474415	G	A	Fhdc1	Missense	NM_001033301	c.C226T	p.P76S	0.131
D2	D2-1-1	chr3	107105483	107105483	A	G	Kcna2	Missense	NM_008417	c.A1379G	p.E460G	0.335
D2	D2-1-1	chr3	36671189	36671189	C	T	Trpc3	Missense	NM_019510	c.G637A	p.D213N	0.326
D2	D2-1-1	chr3	152368254	152368254	C	T	Usp33	Missense	NM_133247	c.C736T	p.R246C	0.222
D2	D2-1-1	chr4	41499553	41499553	G	T	AI464131	Missense	NM_001085515	c.C76A	p.L26I	0.403
D2	D2-1-1	chr4	141308592	141308592	C	T	Epha2	Missense	NM_010139	c.C338T	p.S113L	0.147
D2	D2-1-1	chr4	130718248	130718248	C	T	Pum1	Missense	NM_030722	c.C527T	p.A176V	0.079
D2	D2-1-1	chr4	129080462	129080462	C	T	Rnf19b	Missense	NM_029219	c.C1514T	p.P505L	0.248
D2	D2-1-1	chr4	129294260	129294260	G	A	Sync	Missense	NM_023485	c.G1084A	p.E362K	0.303
D2	D2-1-1	chr4	120931266	120931266	G	A	Zfp69	Missense	NM_001005788	c.C851T	p.P284L	0.25
D2	D2-1-1	chr5	92941071	92941071	C	T	Shroom3	Missense	NM_015756	c.C1679T	p.S560L	0.274
D2	D2-1-1	chr5	137463449	137463449	G	C	Zan	Missense	NM_011741	c.C3467G	p.S1156C	0.141
D2	D2-1-1	chr6	146952391	146952391	C	T	1700034J05Rik	Nonsense	NM_028509	c.G767A	p.W256X	0.125
D2	D2-1-1	chr6	125463701	125463701	T	A	Cd9	Missense	NM_007657	c.A326T	p.Y109F	0.114
D2	D2-1-1	chr6	136043944	136043944	G	A	Grin2b	Missense	NM_008171	c.C358T	p.L120F	0.197
D2	D2-1-1	chr6	141817717	141817717	C	T	Slco1a4	Splice site	NM_030687	c.1271+1G>A	NA	0.131
D2	D2-1-1	chr6	108144689	108144689	G	A	Sumf1	Missense	NM_145937	c.C850T	p.P284S	0.188
D2	D2-1-1	chr7	126582813	126582813	G	A	Cln3	Missense	NM_009907	c.C76T	p.P26S	0.09
D2	D2-1-1	chr7	119916240	119916240	C	A	Lym1	Missense	NM_029610	c.C352A	p.H118N	0.209
D2	D2-1-1	chr7	141866900	141866900	G	T	Muc5b	Missense	NM_028801	c.G12503T	p.C4168F	0.285
D2	D2-1-1	chr7	45054552	45054552	C	T	Prrg2	Missense	NM_022999	c.G545A	p.G182E	0.14
D2	D2-1-1	chr8	95242266	95242266	G	A	Cngb1	Missense	NM_001195413	c.C3613T	p.L1205F	0.288
D2	D2-1-1	chr8	27199371	27199371	G	A	Got11	Missense	NM_029674	c.C659T	p.S220F	0.203
D2	D2-1-1	chr9	49419478	49419478	C	T	Ank1	Missense	NM_172922	c.G762A	p.M254I	0.151
D2	D2-1-1	chr9	46242403	46242403	G	A	Apoa4	Missense	NM_007468	c.G301A	p.E101K	0.275
D2	D2-1-1	chr9	45854694	45854694	G	A	Bace1	Missense	NM_011792	c.G418A	p.E140K	0.388
D2	D2-1-1	chr9	108190201	108190201	C	T	Bsn	Missense	NM_007567	c.G58A	p.G20S	0.168
D2	D2-1-1	chr9	108829695	108829695	C	T	Celsr3	Missense	NM_080437	c.C3376T	p.R1126C	0.152
D2	D2-1-1	chr9	58199740	58199740	G	A	Islr2	Missense	NM_001161541	c.C236T	p.S79L	0.335
D2	D2-1-1	chr9	66970932	66970932	G	A	Lactb	Missense	NM_030717	c.C614T	p.S205F	0.258
D2	D2-1-1	chr9	7447297	7447297	G	T	Mmp3	Missense	NM_010809	c.G386T	p.R129I	0.325
D2	D2-1-1	chr9	38855552	38855552	G	A	Olf26	Missense	NM_146783	c.G489A	p.M163I	0.25
D2	D2-1-1	chr9	110861292	110861292	C	A	Prss50	Missense	NM_146227	c.C502A	p.L168I	0.146
D2	D2-1-1	chr9	107752115	107752115	G	A	Rbm5	Missense	NM_148930	c.C1037T	p.T346I	0.196
D2	D2-1-1	chr9	44683054	44683054	G	A	Treh	Missense	NM_021481	c.G614A	p.G205E	0.246
D2	D2-1-1	chr10	80341782	80341782	G	A	Adamts15	Missense	NM_001113548	c.C1045T	p.P349S	0.147
D2	D2-1-1	chr10	127193169	127193169	G	A	Dtx3	Missense	NM_030714	c.C190T	p.P64S	0.186
D2	D2-1-1	chr10	127370372	127370372	G	A	Inhbc	Missense	NM_010565	c.C25T	p.L9F	0.139
D2	D2-1-1	chr10	7801956	7801956	G	T	Ppil4	Missense	NM_026141	c.G790T	p.G264W	0.3
D2	D2-1-1	chr10	89776005	89776005	C	T	Uhrf1bp11	Missense	NM_029166	c.C313T	p.P105S	0.378
D2	D2-1-1	chr11	5130674	5130674	G	A	Emid1	Missense	NM_080595	c.C775T	p.P259S	0.12
D2	D2-1-1	chr11	97334964	97334964	G	A	Gpr179	Nonsense	NM_001081220	c.C6364T	p.Q2122X	0.372
D2	D2-1-1	chr11	100145811	100145811	C	T	Krt19	Missense	NM_008471	c.G49A	p.G17S	0.528
D2	D2-1-1	chr11	86286608	86286608	G	A	Med13	Missense	NM_001080931	c.C4661T	p.S1554L	0.202
D2	D2-1-1	chr11	78015583	78015583	A	T	Phf12	Missense	NM_174852	c.A922T	p.M308L	0.136
D2	D2-1-1	chr11	20314058	20314058	C	T	Slc1a4	Missense	NM_018861	c.G658A	p.G220R	0.109
D2	D2-1-1	chr12	80759527	80759527	C	T	Ccdc177	Splice site	NM_001008423	c.-28-1G>A	NA	0.282
D2	D2-1-1	chr12	104101802	104101802	C	T	Serpina5	Missense	NM_172953	c.C121T	p.P41S	0.155
D2	D2-1-1	chr12	75899152	75899152	A	T	Syne2	Missense	NM_001005510	c.A997T	p.S333C	0.344
D2	D2-1-1	chr13	61353808	61353809	AT	TA	Cts7	Missense	NM_019539	c.AT876_877TA	p.KY292_2930.152	
D2	D2-1-1	chr13	112626334	112626334	G	T	Ddx4	Missense	NM_001145885	c.C487A	p.L163I	0.337
D2	D2-1-1	chr13	21468185	21468185	G	T	Nkapl	Missense	NM_025719	c.C257A	p.S86Y	0.182
D2	D2-1-1	chr14	35569565	35569565	C	T	Grid1	Nonsense	NM_008166	c.C2428T	p.R810X	0.345
D2	D2-1-1	chr14	50892697	50892697	-	G	Klhl33	Frameshift insertion	NM_001166651	c.559_560insC	p.D187fs	0.123
D2	D2-1-1	chr14	50361709	50361709	G	A	Tlr11	Missense	NM_205819	c.G1151A	p.G384E	0.204
D2	D2-1-1	chr15	39842076	39842076	G	A	Dpys	Missense	NM_022722	c.C640T	p.P214S	0.434
D2	D2-1-1	chr15	85821661	85821661	G	T	Pkdrej	Missense	NM_011105	c.C73A	p.P25T	0.159
D2	D2-1-1	chr16	8600949	8600950	CC	TT	Abat	Missense	NM_172961	c.CC406_407TT	p.P136L	0.107
D2	D2-1-1	chr16	90951887	90951887	G	A	Synj1	Missense	NM_001164483	c.C3280T	p.P1094S	0.326
D2	D2-1-1	chr17	35637937	35637937	C	T	Dpcr1	Missense	NM_001033366	c.G769A	p.E257K	0.216
D2	D2-1-1	chr17	56394823	56394823	C	T	Kdm4b	Missense	NM_172132	c.C1831T	p.P611S	0.252
D2	D2-1-1	chr17	14955115	14955115	T	A	Phf10	Missense	NM_024250	c.A458T	p.Y153F	0.392
D2	D2-1-1	chr18	61220938	61220938	C	T	Pde6a	Missense	NM_146086	c.C334T	p.L112F	0.333
D2	D2-1-1	chr19	47648228	47648228	C	T	Col17a1	Splice site	NM_007732	c.3977-1G>A	NA	0.318
D2	D2-1-1	chr19	44532612	44532612	C	T	Sec31b	Nonsense	NM_001033343	c.G864A	p.W288X	0.357
D2	D2-1-1	chrX	112243346	112243346	G	T	4933403O08Rik	Nonsense	NM_001177389	c.G808T	p.G270X	0.368
D2	D2-1-1	chrX	20517159	20517159	C	T	Phf16	Missense	NM_199317	c.C1735T	p.P579S	0.305
D2	D2-1-1	chrX	150398538	150398538	G	A	Tmem29	Missense	NM_001164683	c.C256T	p.P86S	0.084
E1	E1-1-1	chr15	35073217	35073217	G	A	Stk3	Missense	NM_019635	c.C356T	p.T119I	0.385
E1	E1-1-1	chrX	96160175	96160175	C	T	Msn	Missense	NM_010833	c.C883T	p.R295C	0.331
E1	E1-1-1	chrX	162784385	162784385	T	G	Txlng	Missense	NM_178935	c.A1089C	p.E363D	0.386
E1	E1-2-1	chr14	73322031	73322031	C	T	Rb1	Missense	NM_009029	c.G232A	p.V78M	0.188
E1	E1-2-1	chrX	96160175	96160175	C	T	Msn	Missense	NM_010833	c.C883T	p.R295C	0.49
E1	E1-2-1	chrX	162784385	162784385	T	G	Txlng	Missense	NM_178935	c.A1089C	p.E363D	0.414
E1	E1-2-2	chr15	35073217	35073217	G	A	Stk3	Missense	NM_019635	c.C356T	p.T119I	0.475
E1	E1-2-2	chrX	96160175	96160175	C	T	Msn	Missense	NM_010833	c.C883T	p.R295C	0.61
E1	E1-2-2	chrX	162784385	162784385	T	G	Txlng	Missense	NM_178935	c.A1089C	p.E363D	0.515

Abbreviations: NA, not applicable.