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Supplementary information

In utero origin of myelofibrosis presenting in adult monozygotic twins

Supplementary Information

Supplement to: Sousos N. et al. *In utero* origin of myelofibrosis presenting in adult monozygotic twins.

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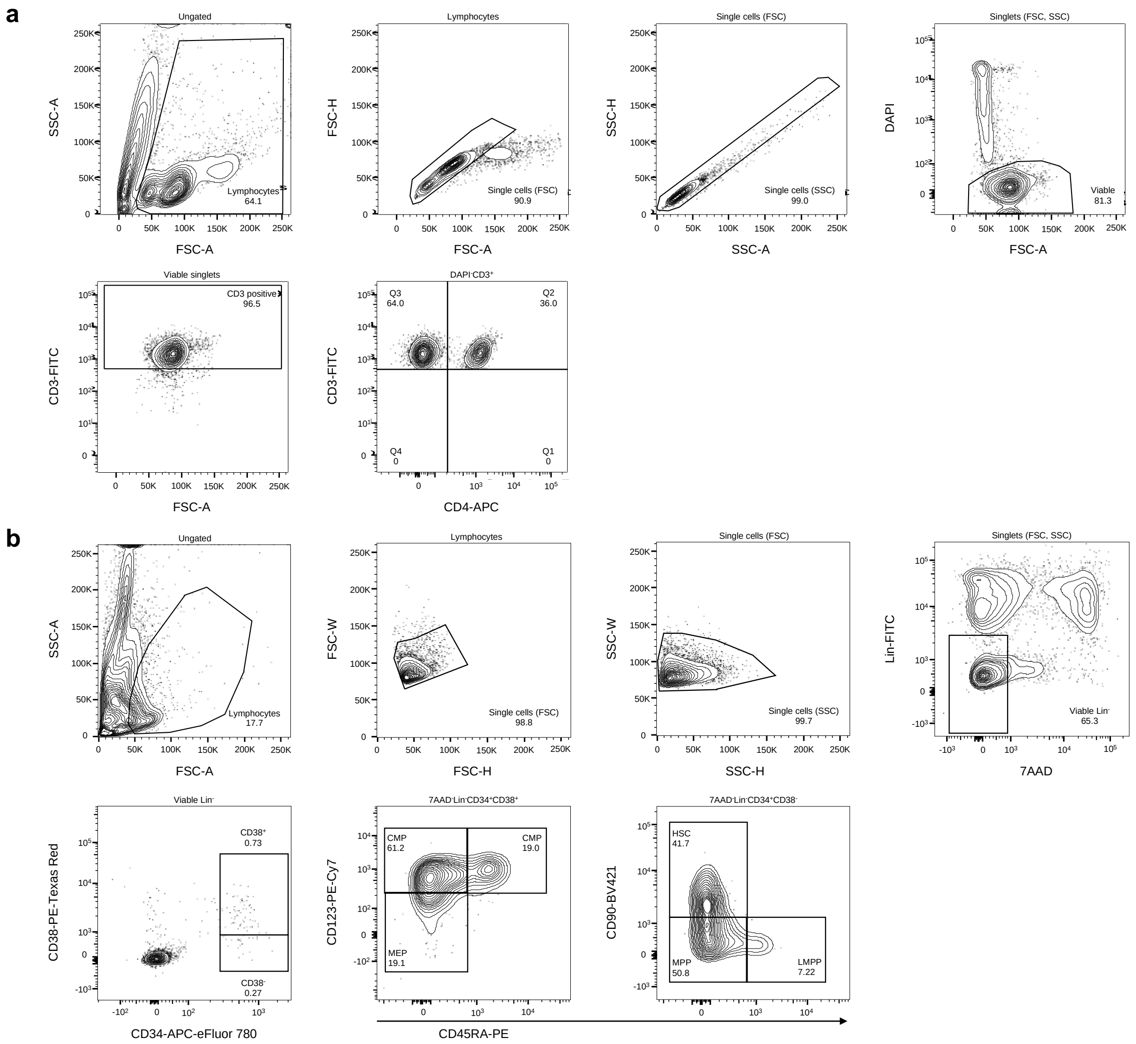
Supplementary Figure 1. Gating strategy for (a) T cell flow cytometry analysis and (b) HSPC index sorting

CMP, common myeloid progenitor; Lin, Lineage; MEP, megakaryocyte-erythroid progenitor; GMP, granulocyte macrophage progenitor; HSC, hematopoietic stem cell; MPP, multi-potent progenitor; LMPP, lymphoid-primed multi-potent progenitor.



Supplementary Table 1. Catalogue of somatic substitutions and indels in twin A and twin B

Individual	Chr	Pos	Ref	Alt	Mutation_ type	Annotation	Gene	Existing_ variation
Twin_A	1	7048875	C	T	Substitution	intron_variant	*CAMTA1*	rs190299624
Twin_A	1	7276191	T	TA	Insertion	intron_variant	*CAMTA1*	rs34532883
Twin_A	1	7932734	TAC	T	Deletion	intron_variant	*TNFRSF9*	rs3841802
Twin_A	1	17778871	G	A	Substitution	intron_variant	*ACTL8*	-
Twin_A	1	19011134	G	A	Substitution	regulatory_region_variant	-	-
Twin_A	1	24201443	G	A	Substitution	intron_variant	*LINC02800*	-
Twin_A	1	25634524	A	G	Substitution	intron_variant	*MAN1C1*	-
Twin_A	1	26355029	G	A	Substitution	upstream_gene_variant	*CRYBG2*	-
Twin_A	1	32905284	G	GT	Insertion	upstream_gene_variant	*TMEM54*	rs201477428
Twin_A	1	36908778	GGT	G	Deletion	intron_variant	*GRIK3*	rs56228690
Twin_A	1	53327841	CA	C	Deletion	frameshift_variant	*LRP8*	rs761955852
Twin_A	1	54128162	C	CT	Insertion	downstream_gene_variant	*CDCP2*	rs35156752
Twin_A	1	58795504	G	GA	Insertion	intron_variant	*LINC01135*	rs773735239
Twin_A	1	58846527	T	C	Substitution	intron_variant	*LINC01135*	rs1310251048
Twin_A	1	62922910	C	A	Substitution	intergenic_variant	-	-
Twin_A	1	81244570	C	T	Substitution	intergenic_variant	-	-
Twin_A	1	82141981	T	TA	Insertion	intergenic_variant	-	rs1036875026
Twin_A	1	91064439	G	T	Substitution	intergenic_variant	-	rs556744289
Twin_A	1	91598893	G	A	Substitution	upstream_gene_variant	*AL714022.1*	-
Twin_A	1	93828702	C	CT	Insertion	intron_variant	*BCAR3*	rs969811086
Twin_A	1	106288464	G	T	Substitution	intergenic_variant	-	rs183684643
Twin_A	1	111854251	A	G	Substitution	intron_variant	*KCND3*	-
Twin_A	1	112723366	C	A	Substitution	intron_variant	*TAFA3*	-
Twin_A	1	117227167	C	T	Substitution	intergenic_variant	-	rs1249405708
Twin_A	1	122502993	T	A	Substitution	intergenic_variant	-	rs1271741426
Twin_A	1	123009960	C	A	Substitution	intergenic_variant	-	rs1355262045
Twin_A	1	144518342	G	A	Substitution	intergenic_variant	-	rs1289463903
Twin_A	1	152011365	A	G	Substitution	intron_variant	*AL450992.1*	-
Twin_A	1	152568644	A	G	Substitution	upstream_gene_variant	*LCE3E*	-
Twin_A	1	155136742	C	CA	Insertion	intron_variant	*SLC50A1*	rs879631277
Twin_A	1	155442289	T	TA	Insertion	intron_variant	*ASH1L*	rs1016155747
Twin_A	1	155643901	C	T	Substitution	intron_variant	*AL353807.3*	-
Twin_A	1	164325871	G	A	Substitution	intergenic_variant	-	-
Twin_A	1	167888410	A	AT	Insertion	intron_variant	*ADCY10*	rs930197268
Twin_A	1	172874706	T	C	Substitution	intron_variant	*AL031599.1*	-
Twin_A	1	173897024	T	A	Substitution	3_prime_UTR_variant	*ZBTB37*	rs1000471968
Twin_A	1	178136491	C	T	Substitution	intron_variant	*RASAL2*	-

Twin_A	1	182688357	GCT	G	Deletion	upstream_gene_variant	*RGS8*	rs57313959
Twin_A	1	182732230	TTC	T	Deletion	upstream_gene_variant	*AL353778.1*	rs1191757083
Twin_A	1	185587702	C	A	Substitution	intron_variant	*LINC01350*	-
Twin_A	1	185717034	C	T	Substitution	regulatory_region_variant	-	rs74766303
Twin_A	1	188790583	C	T	Substitution	intergenic_variant	-	-
Twin_A	1	190678569	TGTTG	T	Deletion	intron_variant	*LINC01720*	-
Twin_A	1	191116119	T	TTA	Insertion	intron_variant	*AL138927.1*	rs386354456
Twin_A	1	191963370	T	TC	Insertion	intron_variant	*LINC02770*	-
Twin_A	1	196771008	G	T	Substitution	upstream_gene_variant	*CFHR3*	-
Twin_A	1	199078846	G	GA	Insertion	downstream_gene_variant	*LINC01221*	rs914403440
Twin_A	1	213790163	G	T	Substitution	intron_variant	*AC096639.1*	-
Twin_A	1	218758531	G	A	Substitution	intergenic_variant	-	-
Twin_A	1	237523679	G	A	Substitution	intron_variant	*RYR2*	rs1165384474
Twin_A	1	238480115	T	C	Substitution	downstream_gene_variant	*LINC01139*	rs1384492382
Twin_A	1	240415525	T	TATA	Insertion	intron_variant	*FMN2*	rs202218606
Twin_A	1	243567256	GC	G	Deletion	intron_variant	*AKT3*	-
Twin_A	2	184966	A	T	Substitution	intergenic_variant	-	-
Twin_A	2	2982012	G	A	Substitution	intron_variant	*LINC01250*	rs1038718094
Twin_A	2	5026216	TA	T	Deletion	intergenic_variant	-	rs1002511716
Twin_A	2	11568288	G	A	Substitution	intron_variant	*GREB1*	rs1225502656
Twin_A	2	12436887	T	G	Substitution	intron_variant	*MIR3681HG*	-
Twin_A	2	13111603	C	A	Substitution	intron_variant	*AC093912.1*	-
Twin_A	2	17632861	A	C	Substitution	intron_variant	*VSNL1*	-
Twin_A	2	19486986	C	CT	Insertion	intron_variant	*LINC01808*	rs796988189
Twin_A	2	24266260	C	T	Substitution	intron_variant	*ITSN2*	-
Twin_A	2	25819904	C	CTTAT	Insertion	intron_variant	*ASXL2*	rs879625913
Twin_A	2	29907671	C	G	Substitution	downstream_gene_variant	*AC106870.1*	rs1275974026
Twin_A	2	31671794	C	T	Substitution	intergenic_variant	-	rs936962348
Twin_A	2	32351096	CT	C	Deletion	intergenic_variant	-	rs747843331
Twin_A	2	35209815	A	G	Substitution	intergenic_variant	-	-
Twin_A	2	38570879	C	CA	Insertion	intron_variant	*HNRNPLL*	rs796515789
Twin_A	2	49012790	C	T	Substitution	intron_variant	*FSHR*	rs1051686975
Twin_A	2	54291307	G	A	Substitution	intron_variant	*ACYP2*	-
Twin_A	2	62581105	A	G	Substitution	intron_variant	*AC092155.1*	rs1357993052
Twin_A	2	64592352	T	TA	Insertion	3_prime_UTR_variant	*AFTPH*	rs879897290
Twin_A	2	66088937	C	T	Substitution	downstream_gene_variant	*AC007389.1*	-
Twin_A	2	78204244	C	A	Substitution	intron_variant	*AC012494.1*	-
Twin_A	2	78265814	T	C	Substitution	intron_variant	*AC012494.1*	-
Twin_A	2	79075253	T	TA	Insertion	intergenic_variant	-	rs200270320
Twin_A	2	83704515	C	T	Substitution	intergenic_variant	-	-
Twin_A	2	86143605	A	AT	Insertion	downstream_gene_variant	*PTCD3*	rs952364218
Twin_A	2	86786422	C	T	Substitution	intron_variant	*CD8A*	-

Twin_A	2	87046122	A	C	Substitution	intron_variant	*ANAPC1P2*	rs79742084
Twin_A	2	89100821	C	G	Substitution	upstream_gene_variant	*IGKV1*	-
Twin_A	2	90026936	G	A	Substitution	downstream_gene_variant	*IGKV6D*	rs568946974
Twin_A	2	93865725	G	C	Substitution	intergenic_variant	-	-
Twin_A	2	98022727	T	TTG	Insertion	regulatory_region_variant	-	rs371216469
Twin_A	2	105464070	C	CA	Insertion	intergenic_variant	-	rs1161295349
Twin_A	2	107747999	TAC	T	Deletion	intron_variant	*LINC01885*	rs146173650
Twin_A	2	113030007	C	T	Substitution	intron_variant	*IL36B*	rs771673800
Twin_A	2	115188061	AAG	A	Deletion	intron_variant	*DPP10*	rs59672278
Twin_A	2	118358987	C	T	Substitution	intergenic_variant	-	-
Twin_A	2	119522301	G	GA	Insertion	intron_variant	*SCTR*	rs797004076
Twin_A	2	122548088	A	G	Substitution	intron_variant	*AC011246.1*	rs893268258
Twin_A	2	124139117	G	GT	Insertion	downstream_gene_variant	*CNTNAP5*	rs1052761072
Twin_A	2	126462653	G	A	Substitution	intergenic_variant	-	rs147150064
Twin_A	2	126802154	C	T	Substitution	regulatory_region_variant	-	rs1390212792
Twin_A	2	130631605	G	T	Substitution	intron_variant	*POTEJ*	-
Twin_A	2	135703624	G	GT	Insertion	intron_variant	*R3HDM1*	rs1194873094
Twin_A	2	139236448	C	A	Substitution	intergenic_variant	-	-
Twin_A	2	140606025	AAG	A	Deletion	intron_variant	*LRP1B*	rs541895855
Twin_A	2	142582383	T	C	Substitution	regulatory_region_variant	-	-
Twin_A	2	145569408	G	A	Substitution	non_coding_transcript_ exon_variant	*AC092484.1*	-
Twin_A	2	145603291	G	A	Substitution	non_coding_transcript_ exon_variant	*AC079163.1*	rs373802799
Twin_A	2	148242718	A	T	Substitution	intron_variant	*MBD5*	-
Twin_A	2	153181357	C	CA	Insertion	intron_variant	*AC011901.1*	rs34588886
Twin_A	2	153730111	G	GA	Insertion	intergenic_variant	-	rs929649211
Twin_A	2	154639539	G	A	Substitution	intergenic_variant	-	-
Twin_A	2	162949464	C	G	Substitution	intergenic_variant	-	-
Twin_A	2	163100502	C	A	Substitution	intergenic_variant	-	-
Twin_A	2	167809460	T	G	Substitution	intergenic_variant	-	-
Twin_A	2	174496556	C	A	Substitution	intergenic_variant	-	-
Twin_A	2	175727129	G	T	Substitution	intergenic_variant	-	rs182157918
Twin_A	2	181542157	CAGTG	C	Deletion	intron_variant	*CERKL*	-
Twin_A	2	183736872	T	C	Substitution	intergenic_variant	-	-
Twin_A	2	193562677	CGT	C	Deletion	intergenic_variant	-	rs59053823
Twin_A	2	194108461	C	CT	Insertion	intergenic_variant	-	rs879718049
Twin_A	2	196497946	T	C	Substitution	intron_variant	*HECW2*	-
Twin_A	2	199505098	A	G	Substitution	intergenic_variant	-	-
Twin_A	2	199984230	A	G	Substitution	intron_variant	*MAIP1*	-
Twin_A	2	200975338	A	T	Substitution	downstream_gene_variant	*FAM126B*	-
Twin_A	2	202920157	C	CT	Insertion	intron_variant	*CARF*	rs969806621
Twin_A	2	217649629	G	C	Substitution	intron_variant	*DIRC3*	-
Twin_A	2	218749467	C	CT	Insertion	intron_variant	*TTLL4*	rs368058156

Twin_A	2	221924308	A	G	Substitution	intergenic_variant	-	-
Twin_A	2	227692889	T	C	Substitution	intron_variant	*SLC19A3*	-
Twin_A	2	228021121	C	T	Substitution	intron_variant	*SPHKAP*	rs531054237
Twin_A	2	234919271	G	GT	Insertion	intergenic_variant	-	rs893811865
Twin_A	2	235048421	C	A	Substitution	intron_variant	*SH3BP4*	-
Twin_A	2	235142193	T	C	Substitution	downstream_gene_variant	*CEP19P1*	rs953123210
Twin_A	2	236024598	A	G	Substitution	intron_variant	*AGAP1*	-
Twin_A	2	236165626	A	C	Substitution	3_prime_UTR_variant	*GBX2*	-
Twin_A	2	240285993	G	A	Substitution	upstream_gene_variant	*U3*	rs79159698
Twin_A	2	240487775	C	T	Substitution	intron_variant	*ANKMY1*	-
Twin_A	3	1259968	A	G	Substitution	intron_variant	*CNTN6*	-
Twin_A	3	6904723	G	GT	Insertion	intron_variant	*GRM7*	rs143641576
Twin_A	3	9646697	T	A	Substitution	upstream_gene_variant	*MTMR14*	rs1001727401
Twin_A	3	26440532	A	T	Substitution	intergenic_variant	-	-
Twin_A	3	29763656	A	C	Substitution	intron_variant	*RBMS3*	-
Twin_A	3	32019778	T	C	Substitution	intron_variant	*OSBPL10*	rs545152631
Twin_A	3	32526653	CCA	C	Deletion	3_prime_UTR_variant	*DYNC1LI1*	rs3836420
Twin_A	3	40432373	TGA	T	Deletion	downstream_gene_variant	*ENTPD3*	rs142976010
Twin_A	3	42455599	G	T	Substitution	intergenic_variant	-	-
Twin_A	3	59893891	T	C	Substitution	intron_variant	*FHIT*	-
Twin_A	3	65074311	C	T	Substitution	intergenic_variant	-	-
Twin_A	3	71644657	A	T	Substitution	intron_variant	*AC097634.4*	rs11925350
Twin_A	3	72405852	G	A	Substitution	intron_variant	*RYBP*	-
Twin_A	3	74296285	G	A	Substitution	intron_variant	*CNTN3*	rs74970959
Twin_A	3	74299076	G	A	Substitution	intron_variant	*CNTN3*	rs149006907
Twin_A	3	74980380	T	A	Substitution	regulatory_region_variant	-	-
Twin_A	3	75692610	CTTA	C	Deletion	intron_variant	*ZNF717*	rs140744949
Twin_A	3	76086971	T	C	Substitution	intron_variant	*ROBO2*	-
Twin_A	3	80858231	C	T	Substitution	intergenic_variant	-	rs982669611
Twin_A	3	86921756	A	G	Substitution	intron_variant	*VGLL3*	-
Twin_A	3	90430217	C	G	Substitution	intergenic_variant	-	-
Twin_A	3	90965981	A	G	Substitution	intergenic_variant	-	rs1304555355
Twin_A	3	95430870	C	T	Substitution	intergenic_variant	-	rs562186321
Twin_A	3	103475498	G	A	Substitution	intergenic_variant	-	-
Twin_A	3	107699193	C	T	Substitution	intron_variant	*BBX*	-
Twin_A	3	117666302	C	CT	Insertion	intergenic_variant	-	rs560342962
Twin_A	3	118298534	T	C	Substitution	intron_variant	*AC068633.1*	-
Twin_A	3	124027883	G	A	Substitution	intergenic_variant	-	-
Twin_A	3	125726439	G	A	Substitution	downstream_gene_variant	*OR7E93P*	rs147522636
Twin_A	3	126102405	G	A	Substitution	downstream_gene_variant	*ALDH1L1*	rs1348872806
Twin_A	3	147257030	A	G	Substitution	intron_variant	*AC092957.1*	-
Twin_A	3	148087688	G	GT	Insertion	intron_variant	*LINC02032*	rs35840438

Twin_A	3	152974761	T	C	Substitution	intergenic_variant	-	rs137865769
Twin_A	3	153068733	G	A	Substitution	downstream_gene_variant	*HMGN2P13*	-
Twin_A	3	153706759	T	G	Substitution	intron_variant	*LINC02006*	-
Twin_A	3	156297775	C	T	Substitution	intron_variant	*KCNAB1*	rs370869760
Twin_A	3	160115640	G	A	Substitution	intron_variant	*IL12A-AS1*	rs985125306
Twin_A	3	165572607	C	T	Substitution	intron_variant	*LINC01322*	-
Twin_A	3	168769424	G	A	Substitution	intron_variant	*EGFEM1P*	rs536413401
Twin_A	3	168769557	T	C	Substitution	intron_variant	*EGFEM1P*	rs575522209
Twin_A	3	183534087	TTACTTTTAAAGTACTTTAAAAGTACTTTACTTTTAAAGTACTTTG	T	Deletion	intron_variant	*KLHL6*	rs1193720974
Twin_A	3	187366417	G	A	Substitution	upstream_gene_variant	*RTP4*	-
Twin_A	4	3011910	G	A	Substitution	intron_variant	*GRK4*	rs1056281673
Twin_A	4	5718308	T	A	Substitution	intron_variant	*EVC*	-
Twin_A	4	15955763	G	C	Substitution	downstream_gene_variant	*FGFBP2*	-
Twin_A	4	17001308	C	T	Substitution	intron_variant	*AC106894.1*	rs1437750527
Twin_A	4	17415320	G	A	Substitution	intergenic_variant	-	-
Twin_A	4	22103283	A	G	Substitution	intron_variant	*AC096719.1*	-
Twin_A	4	26343555	G	GT	Insertion	intron_variant	*RBPJ*	rs150586776
Twin_A	4	26935882	A	G	Substitution	intron_variant	*STIM2*	rs1392350220
Twin_A	4	31169536	C	A	Substitution	upstream_gene_variant	*LINC02497*	-
Twin_A	4	35852584	CAG	C	Deletion	intergenic_variant	-	rs150417183
Twin_A	4	38452605	G	A	Substitution	non_coding_transcript_ exon_variant	*LINC01258*	rs527412993
Twin_A	4	44413264	T	G	Substitution	intron_variant	*KCTD8*	-
Twin_A	4	52545084	CCTCT	C	Deletion	intron_variant	*AC097522.2*	rs748919064
Twin_A	4	54682436	C	CT	Insertion	intron_variant	*KIT*	rs368264394
Twin_A	4	55961258	A	G	Substitution	intron_variant	*CEP135*	-
Twin_A	4	61895466	AAAT	A	Deletion	upstream_gene_variant	*ADGRL3*	rs10603633
Twin_A	4	63566747	C	T	Substitution	intergenic_variant	-	-
Twin_A	4	66771456	G	C	Substitution	intergenic_variant	-	-
Twin_A	4	69630424	C	T	Substitution	intron_variant	*UGT2A1*	-
Twin_A	4	74248292	T	C	Substitution	intron_variant	*MTHFD2L*	-
Twin_A	4	74655308	C	T	Substitution	regulatory_region_variant	-	rs781899546
Twin_A	4	74668604	C	CT	Insertion	regulatory_region_variant	-	rs1418001328
Twin_A	4	76432023	G	T	Substitution	upstream_gene_variant	*SHROOM3*	-
Twin_A	4	82531664	A	G	Substitution	intron_variant	*TMEM150C*	-
Twin_A	4	105234449	TA	T	Deletion	frameshift_variant	*TET2*	-
Twin_A	4	106394908	AAT	A	Deletion	intergenic_variant	-	rs140334876
Twin_A	4	109876682	A	G	Substitution	downstream_gene_variant	*LRIT3*	-
Twin_A	4	110522189	C	CT	Insertion	intron_variant	*ENPEP*	rs539673220
Twin_A	4	111359412	C	T	Substitution	intergenic_variant	-	-
Twin_A	4	113822564	A	AT	Insertion	regulatory_region_variant	-	rs34730469

Twin_A	4	115289705	A	T	Substitution	intergenic_variant	-	rs201585293
Twin_A	4	119833655	A	T	Substitution	intergenic_variant	-	-
Twin_A	4	122600220	C	T	Substitution	intergenic_variant	-	-
Twin_A	4	124416683	A	AT	Insertion	intergenic_variant	-	rs112541914
Twin_A	4	134850961	G	A	Substitution	intergenic_variant	-	-
Twin_A	4	145648023	AT	A	Deletion	upstream_gene_variant	*MMAA*	rs771723312
Twin_A	4	160621868	A	G	Substitution	intergenic_variant	-	-
Twin_A	4	161252551	T	C	Substitution	regulatory_region_variant	-	-
Twin_A	4	161288198	G	GA	Insertion	intergenic_variant	-	rs969053461
Twin_A	4	162816440	T	C	Substitution	intron_variant	*AC021134.1*	-
Twin_A	4	180265089	G	A	Substitution	intergenic_variant	-	-
Twin_A	4	180667100	G	A	Substitution	regulatory_region_variant	-	rs563546983
Twin_A	4	182387149	G	A	Substitution	intron_variant	*TENM3*	rs983423020
Twin_A	4	183453115	T	C	Substitution	downstream_gene_variant	*CDKN2AIP*	-
Twin_A	4	185461063	T	C	Substitution	missense_variant	*CCDC110*	rs773624975
Twin_A	4	186034311	C	T	Substitution	intergenic_variant	-	rs199807699
Twin_A	4	187661068	G	T	Substitution	downstream_gene_variant	*AC097521.1*	-
Twin_A	4	188628950	T	TA	Insertion	intron_variant	*LINC01060*	-
Twin_A	4	105259633*	G	A	Substitution	missense_variant	*TET2*	rs1456238164
Twin_A	5	2114089	AT	A	Deletion	intron_variant	*AC124852.1*	rs374364105
Twin_A	5	4579966	C	T	Substitution	intron_variant	*AC106799.2*	-
Twin_A	5	6643035	G	GT	Insertion	intron_variant	*SRD5A1*	rs35377021
Twin_A	5	7817145	G	GA	Insertion	intron_variant	*ADCY2*	rs57771304
Twin_A	5	7987372	C	T	Substitution	intergenic_variant	-	rs1320304875
Twin_A	5	10921181	G	GT	Insertion	intergenic_variant	-	rs60156777
Twin_A	5	10937820	A	G	Substitution	intergenic_variant	-	rs561589454
Twin_A	5	12387040	G	A	Substitution	intergenic_variant	-	-
Twin_A	5	18474168	C	T	Substitution	intergenic_variant	-	-
Twin_A	5	24399357	G	A	Substitution	intergenic_variant	-	rs868374455
Twin_A	5	33779372	G	A	Substitution	intron_variant	*ADAMTS12*	-
Twin_A	5	35831884	C	T	Substitution	upstream_gene_variant	*AC137810.1*	-
Twin_A	5	36636178	G	T	Substitution	intron_variant	*SLC1A3*	-
Twin_A	5	41753270	TAC	T	Deletion	intron_variant	*OXCT1*	rs36095905
Twin_A	5	52121218	T	G	Substitution	intergenic_variant	-	rs111904173
Twin_A	5	56387833	C	T	Substitution	intergenic_variant	-	-
Twin_A	5	58833324	TCA	T	Deletion	intron_variant	*RAB3C*	rs571940681
Twin_A	5	58833331	C	T	Substitution	intron_variant	*RAB3C*	rs199895867
Twin_A	5	63548792	G	C	Substitution	intergenic_variant	-	-
Twin_A	5	69055388	A	T	Substitution	intergenic_variant	-	-
Twin_A	5	73740730	C	T	Substitution	intron_variant	*ARHGEF28*	rs934596518
Twin_A	5	75285945	G	T	Substitution	intergenic_variant	-	-
Twin_A	5	78363812	A	AT	Insertion	upstream_gene_variant	*SCAMP1*	rs566623870

Twin_A	5	79269736	A	AT	Insertion	intron_variant	*JMY*	rs905517032
Twin_A	5	80583714	T	TGC	Insertion	intergenic_variant	-	rs113455475
Twin_A	5	81377269	G	A	Substitution	intron_variant	*ACOT12*	-
Twin_A	5	82451636	A	G	Substitution	intergenic_variant	-	-
Twin_A	5	85688616	C	T	Substitution	intergenic_variant	-	-
Twin_A	5	86606508	G	GT	Insertion	intergenic_variant	-	rs1353717748
Twin_A	5	91742536	G	C	Substitution	intron_variant	*AC093298.2*	-
Twin_A	5	93374643	C	T	Substitution	intron_variant	*NR2F1*	rs529601636
Twin_A	5	95231337	GAT	G	Deletion	intron_variant	*MCTP1*	rs138755290
Twin_A	5	95701747	A	G	Substitution	upstream_gene_variant	*SPATA9*	-
Twin_A	5	97765568	G	A	Substitution	intergenic_variant	-	-
Twin_A	5	100034257	G	A	Substitution	intergenic_variant	-	-
Twin_A	5	100071988	T	A	Substitution	upstream_gene_variant	*AC092278.1*	rs78484001
Twin_A	5	100155088	G	GT	Insertion	downstream_gene_variant	*RNU6*	rs5869895
Twin_A	5	100295778	C	T	Substitution	intergenic_variant	-	-
Twin_A	5	105654988	C	T	Substitution	intergenic_variant	-	rs1173103088
Twin_A	5	105941453	T	G	Substitution	intergenic_variant	-	-
Twin_A	5	111449354	A	G	Substitution	intron_variant	*CAMK4*	-
Twin_A	5	115666098	C	T	Substitution	regulatory_region_variant	-	-
Twin_A	5	116208129	T	C	Substitution	intron_variant	*COMMD10*	-
Twin_A	5	116797618	T	TA	Insertion	intergenic_variant	-	rs370022009
Twin_A	5	123223704	C	A	Substitution	intergenic_variant	-	-
Twin_A	5	130388901	G	A	Substitution	upstream_gene_variant	*RNU7*	rs1308696583
Twin_A	5	131362688	C	T	Substitution	intron_variant	*CDC42SE2*	-
Twin_A	5	131622186	T	TA	Insertion	intron_variant	*RAPGEF6*	rs368148920
Twin_A	5	142866780	T	G	Substitution	intron_variant	*ARHGAP26*	-
Twin_A	5	147611565	T	C	Substitution	intron_variant	*JAKMIP2*	-
Twin_A	5	152460283	G	A	Substitution	intron_variant	*AC008571.2*	-
Twin_A	5	155157242	C	T	Substitution	intron_variant	*AC010476.2*	rs950323196
Twin_A	5	162912266	C	A	Substitution	intron_variant	*AC113414.1*	-
Twin_A	5	163087087	G	GA	Insertion	intron_variant	*AC113414.1*	rs979728237
Twin_A	5	166031221	GTAGA	G	Deletion	upstream_gene_variant	*RPL7P20*	-
Twin_A	6	7238595	C	CT	Insertion	intron_variant	*RREB1*	rs796560101
Twin_A	6	8925748	C	T	Substitution	intron_variant	*HULC*	-
Twin_A	6	9330828	G	A	Substitution	intergenic_variant	-	-
Twin_A	6	15203913	A	AT	Insertion	intergenic_variant	-	rs1241556169
Twin_A	6	16644979	C	T	Substitution	intron_variant	*ATXN1*	-
Twin_A	6	19952193	G	A	Substitution	intergenic_variant	-	rs779233914
Twin_A	6	31570888	C	T	Substitution	upstream_gene_variant	*LTA*	rs956044849
Twin_A	6	36883002	G	T	Substitution	upstream_gene_variant	*C6orf89*	-
Twin_A	6	40639879	ACT	A	Deletion	intergenic_variant	-	rs35021402
Twin_A	6	40934220	G	A	Substitution	intergenic_variant	-	-

Twin_A	6	46776061	TA	T	Deletion	intergenic_variant	-	-
Twin_A	6	46995372	G	GT	Insertion	downstream_gene_variant	*ADGRF1*	rs142966227
Twin_A	6	58029106	G	A	Substitution	intron_variant	*AL445250.1*	rs1539609
Twin_A	6	60497665	T	C	Substitution	intron_variant	*AC244258.1*	-
Twin_A	6	62533854	G	A	Substitution	intergenic_variant	-	rs1050425018
Twin_A	6	70161977	C	A	Substitution	intron_variant	*COL19A1*	rs754784425
Twin_A	6	71671466	A	T	Substitution	intergenic_variant	-	-
Twin_A	6	80070589	C	T	Substitution	upstream_gene_variant	*AL591135.1*	rs113123867
Twin_A	6	90318383	C	CT	Insertion	upstream_gene_variant	*AL132996.1*	rs1230991775
Twin_A	6	93048770	T	TA	Insertion	regulatory_region_variant	-	rs1214397059
Twin_A	6	93696846	GTC	G	Deletion	intergenic_variant	-	rs142217537
Twin_A	6	95778674	T	A	Substitution	intergenic_variant	-	-
Twin_A	6	97233067	G	GA	Insertion	intron_variant	*MMS22L*	rs573093148
Twin_A	6	103570525	T	TTA	Insertion	intergenic_variant	-	rs533182054
Twin_A	6	111252036	C	T	Substitution	intron_variant	*AL360227.1*	-
Twin_A	6	117652832	G	A	Substitution	intergenic_variant	-	-
Twin_A	6	119799146	C	CT	Insertion	intergenic_variant	-	rs1218766914
Twin_A	6	119917789	C	G	Substitution	intergenic_variant	-	-
Twin_A	6	123368975	C	G	Substitution	intron_variant	*TRDN*	-
Twin_A	6	124380080	A	T	Substitution	intron_variant	*NKAIN2*	-
Twin_A	6	126389883	T	C	Substitution	intron_variant	*AL356534.1*	-
Twin_A	6	131059163	G	A	Substitution	intron_variant	*EPB41L2*	-
Twin_A	6	131399570	C	G	Substitution	intergenic_variant	-	-
Twin_A	6	134069108	C	T	Substitution	intergenic_variant	-	rs187112667
Twin_A	6	140986451	A	C	Substitution	intergenic_variant	-	-
Twin_A	6	145547033	T	G	Substitution	intron_variant	*EPM2A*	-
Twin_A	6	159660393	C	T	Substitution	intron_variant	*AL078604.4*	rs769079326
Twin_A	6	159881330	C	CAT	Insertion	intergenic_variant	-	rs10672852
Twin_A	6	166093829	G	T	Substitution	upstream_gene_variant	*AL627443.3*	-
Twin_A	6	166187121	G	GA	Insertion	intergenic_variant	-	-
Twin_A	7	4979367	T	C	Substitution	intron_variant	*RNF216P1*	rs868499198
Twin_A	7	5000741	A	G	Substitution	downstream_gene_variant	*RNF216P1*	rs1338617888
Twin_A	7	7056369	G	A	Substitution	intron_variant	*AC079804.3*	-
Twin_A	7	9227657	G	A	Substitution	regulatory_region_variant	-	rs999966239
Twin_A	7	21817695	A	AT	Insertion	intron_variant	*DNAH11*	rs201247500
Twin_A	7	30831221	C	T	Substitution	intron_variant	*MINDY4*	-
Twin_A	7	36071829	A	G	Substitution	intergenic_variant	-	rs757946495
Twin_A	7	38945518	G	GA	Insertion	intergenic_variant	-	rs796386392
Twin_A	7	41732610	A	G	Substitution	intron_variant	*INHBA*	-
Twin_A	7	43378810	C	CA	Insertion	intron_variant	*HECW1*	rs202007736
Twin_A	7	44090851	C	T	Substitution	intergenic_variant	-	-
Twin_A	7	44510030	T	A	Substitution	downstream_gene_variant	*NPC1L1*	-

Twin_A	7	49269510	AT	A	Deletion	intergenic_variant	-	rs1265301921
Twin_A	7	49269512	A	C	Substitution	intergenic_variant	-	rs984581632
Twin_A	7	53068163	G	A	Substitution	intergenic_variant	-	rs935736922
Twin_A	7	53091502	C	T	Substitution	intergenic_variant	-	-
Twin_A	7	53364914	G	A	Substitution	upstream_gene_variant	*RNU1*	rs34714639
Twin_A	7	54587046	C	A	Substitution	intergenic_variant	-	-
Twin_A	7	62529040	C	T	Substitution	intergenic_variant	-	rs555323358
Twin_A	7	64713934	GTATT	G	Deletion	downstream_gene_variant	*ZNF107*	rs369110012
Twin_A	7	67857057	G	A	Substitution	intergenic_variant	-	rs1319269938
Twin_A	7	68076463	CAT	C	Deletion	intergenic_variant	-	rs139100940
Twin_A	7	69630257	A	G	Substitution	intron_variant	*AUTS2*	-
Twin_A	7	73627805	C	T	Substitution	upstream_gene_variant	*MLXIPL*	-
Twin_A	7	81046412	CT	C	Deletion	intergenic_variant	-	rs1381425510
Twin_A	7	88505688	G	A	Substitution	intron_variant	*AC002069.2*	-
Twin_A	7	89031211	GTA	G	Deletion	intron_variant	*ZNF804B*	-
Twin_A	7	90565456	G	GT	Insertion	intron_variant	*CDK14*	rs373870738
Twin_A	7	95205017	CCA	C	Deletion	intron_variant	*PPP1R9A*	rs143843788
Twin_A	7	95298520	G	C	Substitution	3_prime_UTR_variant	*PON1*	-
Twin_A	7	96055652	T	TA	Insertion	intron_variant	*DYNC1I1*	rs11374590
Twin_A	7	98561959	C	A	Substitution	intergenic_variant	-	-
Twin_A	7	102065090	G	GT	Insertion	intron_variant	*CUX1*	rs562493293
Twin_A	7	109185877	G	A	Substitution	intergenic_variant	-	rs1228545900
Twin_A	7	110615318	C	T	Substitution	intergenic_variant	-	-
Twin_A	7	122016458	C	A	Substitution	intron_variant	*PTPRZ1*	-
Twin_A	7	124142825	C	T	Substitution	intron_variant	*AC006148.1*	-
Twin_A	7	128429252	C	CT	Insertion	downstream_gene_variant	*AC010655.1*	rs56056515
Twin_A	7	129776973	A	G	Substitution	upstream_gene_variant	*MIR96*	rs1401666012
Twin_A	7	137296579	A	G	Substitution	intron_variant	*PTN*	-
Twin_A	7	139519359	T	TA	Insertion	upstream_gene_variant	*CLEC2L*	rs1220935636
Twin_A	7	149998259	A	G	Substitution	upstream_gene_variant	*AC092681.2*	rs2969815
Twin_A	7	153528906	T	C	Substitution	intergenic_variant	-	-
Twin_A	7	154611485	A	G	Substitution	intron_variant	*DPP6*	-
Twin_A	8	503037	C	T	Substitution	intron_variant	*TDRP*	rs1166917437
Twin_A	8	13876611	G	GA	Insertion	regulatory_region_variant	-	rs34968549
Twin_A	8	17691704	G	GT	Insertion	intron_variant	*MTUS1*	rs200014137
Twin_A	8	19550828	C	T	Substitution	intron_variant	*CSGALNACT1*	-
Twin_A	8	25892225	T	C	Substitution	intron_variant	*EBF2*	-
Twin_A	8	30978684	T	C	Substitution	downstream_gene_variant	*AC008066.1*	-
Twin_A	8	36379501	CAT	C	Deletion	intron_variant	*AC090809.1*	rs148082032
Twin_A	8	36570758	T	A	Substitution	intron_variant	*AC090809.1*	-
Twin_A	8	39656195	G	GA	Insertion	intron_variant	*ADAM18*	rs201971418
Twin_A	8	48680993	A	G	Substitution	intron_variant	*AC022915.2*	-

Twin_A	8	51711248	T	C	Substitution	intron_variant	*PXDNL*	COSV62492491
Twin_A	8	53511516	G	GA	Insertion	downstream_gene_variant	*AC022034.1*	rs535409810
Twin_A	8	61457436	G	A	Substitution	intron_variant	*CLVS1*	-
Twin_A	8	63967261	A	AT	Insertion	intron_variant	*LINC01414*	rs5891933
Twin_A	8	64128898	G	A	Substitution	intron_variant	*LINC01414*	rs545104948
Twin_A	8	65916408	G	A	Substitution	intergenic_variant	-	-
Twin_A	8	68253460	T	TA	Insertion	regulatory_region_variant	-	rs1000407340
Twin_A	8	72453042	C	T	Substitution	intergenic_variant	-	rs1051744174
Twin_A	8	77781391	C	CT	Insertion	intergenic_variant	-	rs1198479285
Twin_A	8	83358311	GGCTACAGACAAACCTTCAATGGA	G	Deletion	intergenic_variant	-	-
Twin_A	8	86318421	G	GA	Insertion	intron_variant	*SLC7A13*	rs34723665
Twin_A	8	88356215	C	A	Substitution	intron_variant	*AC090578.1*	-
Twin_A	8	95037819	G	GA	Insertion	intron_variant	*NDUFAF6*	rs59511473
Twin_A	8	104362862	A	G	Substitution	intron_variant	*DPYS*	rs555618444
Twin_A	8	108043942	A	T	Substitution	intron_variant	*RSPO2*	-
Twin_A	8	115536798	G	GT	Insertion	intron_variant	*TRPS1*	rs900943605
Twin_A	8	117615713	ATCT	A	Deletion	regulatory_region_variant	-	-
Twin_A	8	124975564	C	G	Substitution	intron_variant	*ZNF572*	-
Twin_A	8	129273738	G	GT	Insertion	intron_variant	*CCDC26*	rs891751618
Twin_A	8	129372882	C	CA	Insertion	intron_variant	*CCDC26*	rs560030895
Twin_A	8	129733477	G	A	Substitution	downstream_gene_variant	*MTRF1LP2*	-
Twin_A	8	132428552	CAG	C	Deletion	intron_variant	*KCNQ3*	rs201318711
Twin_A	8	134856654	C	G	Substitution	intron_variant	*AC103764.1*	rs1321197388
Twin_A	8	135261370	G	C	Substitution	intron_variant	*LINC01591*	-
Twin_A	8	137128263	C	T	Substitution	intergenic_variant	-	rs1053069745
Twin_A	8	138139847	C	T	Substitution	intron_variant	*FAM135B*	rs947110030
Twin_A	8	143051626	G	A	Substitution	intron_variant	*C8orf31*	-
Twin_A	9	50071	AT	A	Deletion	intron_variant	*WASHC1*	-
Twin_A	9	395970	T	G	Substitution	intron_variant	*DOCK8*	-
Twin_A	9	1822815	C	T	Substitution	intergenic_variant	-	-
Twin_A	9	4316936	C	T	Substitution	intron_variant	*GLIS3*	-
Twin_A	9	5368234	T	C	Substitution	intron_variant	*PLGRKT*	-
Twin_A	9	14104419	G	GT	Insertion	intron_variant	*NFIB*	rs945961609
Twin_A	9	17180226	GT	G	Deletion	intron_variant	*CNTLN*	rs1264390576
Twin_A	9	19348792	G	GA	Insertion	intron_variant	*DENND4C*	rs367658826
Twin_A	9	23699353	A	G	Substitution	intron_variant	*ELAVL2*	rs568285627
Twin_A	9	24066549	G	A	Substitution	upstream_gene_variant	*AL513317.1*	rs895109680
Twin_A	9	28150104	C	A	Substitution	intron_variant	*LINGO2*	-
Twin_A	9	31556284	G	A	Substitution	intergenic_variant	-	rs12347583
Twin_A	9	39080916	C	T	Substitution	intron_variant	*CNTNAP3*	rs369395719
Twin_A	9	41655135	C	T	Substitution	upstream_gene_variant	*AL591926.2*	rs1226839471

Twin_A	9	45155466	G	C	Substitution	intergenic_variant	-	rs1476645657
Twin_A	9	61566797	T	C	Substitution	intergenic_variant	-	-
Twin_A	9	73087756	A	G	Substitution	intergenic_variant	-	-
Twin_A	9	77004114	C	A	Substitution	intergenic_variant	-	-
Twin_A	9	81050746	G	A	Substitution	intergenic_variant	-	rs764741538
Twin_A	9	82371224	C	T	Substitution	intron_variant	*AL162726.3*	-
Twin_A	9	83484424	C	CT	Insertion	intron_variant	*FRMD3*	-
Twin_A	9	84858874	G	GA	Insertion	intron_variant	*NTRK2*	rs965433677
Twin_A	9	87748283	T	TA	Insertion	regulatory_region_variant	-	rs143725130
Twin_A	9	88768716	G	A	Substitution	intron_variant	*AL390791.1*	rs548341913
Twin_A	9	96382496	C	CTA	Insertion	intron_variant	*SLC35D2*	rs142809659
Twin_A	9	101191229	G	A	Substitution	intron_variant	*PLPPR1*	-
Twin_A	9	101784275	G	A	Substitution	intergenic_variant	-	-
Twin_A	9	102487319	C	T	Substitution	intergenic_variant	-	rs1189198082
Twin_A	9	111554985	G	T	Substitution	3_prime_UTR_variant	*ZNF483*	rs1039810650
Twin_A	9	118247951	T	C	Substitution	intergenic_variant	-	-
Twin_A	9	120700338	T	A	Substitution	intron_variant	*MEGF9*	-
Twin_A	9	122872477	T	C	Substitution	downstream_gene_variant	*RC3H2*	rs996687988
Twin_A	9	125539853	T	TA	Insertion	intron_variant	*MAPKAP1*	rs201724260
Twin_A	9	127663224	C	G	Substitution	missense_variant	*STXBP1*	-
Twin_A	9	131190221	A	T	Substitution	intron_variant	*NUP214*	-
Twin_A	9	134828811	CCA	C	Deletion	intron_variant	*COL5A1*	rs906680873
Twin_A	9	136468856	C	CT	Insertion	intron_variant	*SEC16A*	-
Twin_A	10	4183898	A	G	Substitution	regulatory_region_variant	-	-
Twin_A	10	9239651	C	CT	Insertion	intergenic_variant	-	rs963757968
Twin_A	10	10849842	T	A	Substitution	intron_variant	*CELF2*	rs1365457744
Twin_A	10	11168124	TTC	T	Deletion	intron_variant	*CELF2*	-
Twin_A	10	15299120	C	T	Substitution	intron_variant	*FAM171A1*	rs558867054
Twin_A	10	18976904	C	T	Substitution	intergenic_variant	-	rs181225799
Twin_A	10	23617158	C	CAT	Insertion	intergenic_variant	-	rs144728449
Twin_A	10	23958376	G	A	Substitution	intron_variant	*KIAA1217*	-
Twin_A	10	27864409	G	GA	Insertion	intron_variant	*ARMC4*	rs998440262
Twin_A	10	34892061	G	T	Substitution	intergenic_variant	-	-
Twin_A	10	47221434	C	T	Substitution	intergenic_variant	-	-
Twin_A	10	54174376	C	CA	Insertion	intron_variant	*PCDH15*	rs112450699
Twin_A	10	56140794	C	CAT	Insertion	intergenic_variant	-	rs999676086
Twin_A	10	56950504	A	T	Substitution	intergenic_variant	-	-
Twin_A	10	60147699	C	G	Substitution	intron_variant	*ANK3*	-
Twin_A	10	62705771	AAT	A	Deletion	intron_variant	*AC067751.1*	rs10573238
Twin_A	10	64210270	G	T	Substitution	intron_variant	*AC013287.1*	rs75029261
Twin_A	10	67571470	TA	T	Deletion	intron_variant	*CTNNA3*	-
Twin_A	10	70021310	G	GA	Insertion	upstream_gene_variant	*LINC02636*	rs944814046

Twin_A	10	75905930	G	GT	Insertion	intron_variant	*LRMDA*	rs5786198
Twin_A	10	78393818	G	A	Substitution	intron_variant	*AC012560.1*	-
Twin_A	10	83188578	G	A	Substitution	intergenic_variant	-	rs778523013
Twin_A	10	83492892	C	T	Substitution	intergenic_variant	-	-
Twin_A	10	93187731	G	A	Substitution	intergenic_variant	-	-
Twin_A	10	94576898	A	AT	Insertion	intron_variant	*HELLS*	rs540746312
Twin_A	10	94950682	A	G	Substitution	intron_variant	*CYP2C9*	rs907386662
Twin_A	10	103273122	G	A	Substitution	upstream_gene_variant	*INA*	rs1286474689
Twin_A	10	109091857	G	A	Substitution	intergenic_variant	-	rs954171718
Twin_A	10	111830308	A	G	Substitution	intron_variant	*AL136119.1*	rs1430607514
Twin_A	10	113814958	A	G	Substitution	intergenic_variant	-	-
Twin_A	10	115169017	CTT	C	Deletion	intron_variant	*ATRNL1*	rs71010011
Twin_A	10	115409272	G	A	Substitution	intron_variant	*ATRNL1*	-
Twin_A	10	116526803	T	C	Substitution	intergenic_variant	-	-
Twin_A	10	120224348	T	TA	Insertion	intergenic_variant	-	-
Twin_A	10	121613197	T	C	Substitution	downstream_gene_variant	*AC009988.1*	-
Twin_A	10	122518538	G	A	Substitution	downstream_gene_variant	*HTRA1*	rs568255913
Twin_A	10	124140841	T	C	Substitution	intergenic_variant	-	rs1455378017
Twin_A	10	124588678	T	G	Substitution	intron_variant	*LHPP*	-
Twin_A	11	6802600	C	T	Substitution	upstream_gene_variant	*OR6A2*	rs745932107
Twin_A	11	12635917	G	A	Substitution	intron_variant	*AC107881.1*	rs1470450176
Twin_A	11	17634218	C	T	Substitution	stop_gained	*OTOG*	rs866476223
Twin_A	11	18214790	G	A	Substitution	downstream_gene_variant	*SLC25A51P4*	-
Twin_A	11	25629284	G	T	Substitution	upstream_gene_variant	*AC100770.1*	-
Twin_A	11	27431935	C	T	Substitution	intron_variant	*LGR4*	rs187542892
Twin_A	11	29268317	G	GTA	Insertion	downstream_gene_variant	*AC090791.1*	rs57529313
Twin_A	11	30414572	A	AT	Insertion	intron_variant	*MPPED2*	rs574457624
Twin_A	11	34947336	TAC	T	Deletion	intron_variant	*PDHX*	rs201136678
Twin_A	11	40970112	A	T	Substitution	intron_variant	*LRRC4C*	-
Twin_A	11	42181489	A	AT	Insertion	downstream_gene_variant	*LINC02740*	rs1268779757
Twin_A	11	42992114	T	A	Substitution	intergenic_variant	-	-
Twin_A	11	49443145	TATC	T	Deletion	intergenic_variant	-	rs1327126227
Twin_A	11	59547928	A	G	Substitution	intron_variant	*AP003778.1*	-
Twin_A	11	62907973	C	T	Substitution	downstream_gene_variant	*M1*	-
Twin_A	11	69424352	G	A	Substitution	upstream_gene_variant	*AP000439.2*	-
Twin_A	11	70172132	A	G	Substitution	intron_variant	*ANO1*	rs11235475
Twin_A	11	71917009	GTTA	G	Deletion	downstream_gene_variant	*AP002495.1*	rs550657033
Twin_A	11	72630002	T	A	Substitution	intron_variant	*PDE2A*	rs956005801
Twin_A	11	78991748	C	T	Substitution	intron_variant	*TENM4*	-
Twin_A	11	83859358	A	G	Substitution	intron_variant	*DLG2*	-
Twin_A	11	83984865	G	A	Substitution	intron_variant	*DLG2*	rs2514172
Twin_A	11	87084313	C	CT	Insertion	intron_variant	*TMEM135*	rs5793234

Twin_A	11	89364256	TTC	T	Deletion	intron_variant	*NOX4*	-
Twin_A	11	91531418	GTC	G	Deletion	intergenic_variant	-	rs57259378
Twin_A	11	92625315	G	A	Substitution	intron_variant	*FAT3*	rs1044839433
Twin_A	11	93542010	C	T	Substitution	intron_variant	*SMCO4*	rs1238441458
Twin_A	11	93572399	A	T	Substitution	regulatory_region_variant	-	-
Twin_A	11	96395662	G	GA	Insertion	downstream_gene_variant	*JRKL*	rs1197147759
Twin_A	11	98979001	G	GCA	Insertion	intergenic_variant	-	rs5793962
Twin_A	11	99123208	G	GT	Insertion	downstream_gene_variant	*RN7SKP53*	rs370959291
Twin_A	11	105917523	A	G	Substitution	intron_variant	*GRIA4*	-
Twin_A	11	112108171	G	T	Substitution	intron_variant	*AP002884.2*	-
Twin_A	11	118973448	G	T	Substitution	intron_variant	*FOXR1*	-
Twin_A	11	121731425	T	C	Substitution	intron_variant	*AP001977.1*	-
Twin_A	11	130155838	CA	C	Deletion	upstream_gene_variant	*ST14*	rs71061368
Twin_A	11	133629356	A	T	Substitution	intergenic_variant	-	-
Twin_A	12	8992708	A	AT	Insertion	intron_variant	*KLRG1*	rs1011939413
Twin_A	12	14002642	GTA	G	Deletion	intergenic_variant	-	rs767637242
Twin_A	12	27135862	C	A	Substitution	intron_variant	*AC092747.1*	-
Twin_A	12	33793906	A	G	Substitution	intergenic_variant	-	rs1160899620
Twin_A	12	37544249	GGT	G	Deletion	intergenic_variant	-	rs139856566
Twin_A	12	39556427	T	A	Substitution	intron_variant	*ABCD2*	-
Twin_A	12	45801804	CAG	C	Deletion	intron_variant	*ARID2*	rs200185178
Twin_A	12	47093368	A	AT	Insertion	intron_variant	*PCED1B*	rs142397807
Twin_A	12	54193118	A	G	Substitution	upstream_gene_variant	*SMUG1*	-
Twin_A	12	55987166	G	GT	Insertion	intron_variant	*RAB5B*	rs34223637
Twin_A	12	61094238	T	C	Substitution	intergenic_variant	-	rs795318
Twin_A	12	61096059	C	T	Substitution	intergenic_variant	-	-
Twin_A	12	63499491	A	T	Substitution	intergenic_variant	-	rs367633111
Twin_A	12	67241412	G	GA	Insertion	intergenic_variant	-	rs570864048
Twin_A	12	80465550	CA	C	Deletion	intron_variant	*PTPRQ*	rs1565723030
Twin_A	12	96021004	T	A	Substitution	intron_variant	*LTA4H*	-
Twin_A	12	99195605	T	C	Substitution	intron_variant	*ANKS1B*	-
Twin_A	12	99570645	C	CA	Insertion	intron_variant	*ANKS1B*	rs34453262
Twin_A	12	100385137	A	T	Substitution	intron_variant	*SLC17A8*	rs564312355
Twin_A	12	101478301	G	A	Substitution	intron_variant	*SPIC*	-
Twin_A	12	111703138	A	G	Substitution	intron_variant	*ACAD10*	-
Twin_A	12	112201473	G	GA	Insertion	intron_variant	*HECTD4*	rs59104653
Twin_A	12	117866839	T	TA	Insertion	intron_variant	*KSR2*	rs34463256
Twin_A	12	120238552	T	A	Substitution	intron_variant	*PXN*	-
Twin_A	12	129194036	A	G	Substitution	intron_variant	*TMEM132D*	-
Twin_A	12	129699976	C	T	Substitution	missense_variant	*TMEM132D*	COSV70606773
Twin_A	12	130201343	C	T	Substitution	intergenic_variant	-	rs752475595
Twin_A	12	131372998	C	T	Substitution	downstream_gene_variant	*AC140118.1*	rs1044089851

Twin_A	12	131449745	T	TTATATATATATA	Insertion	intron_variant	*AC073578.2*	rs60625980
Twin_A	12	131913217	G	T	Substitution	synonymous_variant	*ULK1*	COSV58854885
Twin_A	12	132658754	CG	C	Deletion	intron_variant	*POLE*	-
Twin_A	13	16312671	T	G	Substitution	intergenic_variant	-	rs1452678559
Twin_A	13	19458900	T	C	Substitution	intron_variant	*TPTE2*	-
Twin_A	13	21198801	T	A	Substitution	regulatory_region_variant	-	-
Twin_A	13	21198803	G	T	Substitution	regulatory_region_variant	-	-
Twin_A	13	22486341	G	A	Substitution	intergenic_variant	-	-
Twin_A	13	24407230	C	T	Substitution	upstream_gene_variant	*TPTE2P6*	-
Twin_A	13	27747684	T	C	Substitution	downstream_gene_variant	*POLR1D*	rs530116991
Twin_A	13	33789922	C	T	Substitution	regulatory_region_variant	-	-
Twin_A	13	35458160	C	G	Substitution	intron_variant	*NBEA*	-
Twin_A	13	40248330	G	A	Substitution	intron_variant	*LINC00598*	rs570712758
Twin_A	13	44807574	G	A	Substitution	intron_variant	*LINC00330*	-
Twin_A	13	51185115	A	T	Substitution	intron_variant	*C13orf42*	rs982603544
Twin_A	13	54356322	T	A	Substitution	regulatory_region_variant	-	-
Twin_A	13	57950093	C	T	Substitution	intergenic_variant	-	-
Twin_A	13	60127004	G	A	Substitution	intron_variant	*DIAPH3*	-
Twin_A	13	61979712	AT	A	Deletion	intergenic_variant	-	-
Twin_A	13	86387551	T	TA	Insertion	intergenic_variant	-	rs578195336
Twin_A	13	95408931	G	T	Substitution	intergenic_variant	-	-
Twin_A	13	97673189	G	A	Substitution	downstream_gene_variant	*AL359502.1*	rs1006927199
Twin_A	13	100032713	C	CA	Insertion	upstream_gene_variant	*NDUFA12P1*	rs914603334
Twin_A	13	110038016	G	GCA	Insertion	intron_variant	*AL390755.1*	rs34470615
Twin_A	13	112177050	A	T	Substitution	intergenic_variant	-	-
Twin_A	13	112393758	C	T	Substitution	intron_variant	*SPACA7*	-
Twin_A	14	27812525	AAG	A	Deletion	intron_variant	*AL390334.1*	rs368944583
Twin_A	14	27980040	G	A	Substitution	intergenic_variant	-	-
Twin_A	14	29729980	G	A	Substitution	intron_variant	*PRKD1*	rs536812458
Twin_A	14	30110595	C	CT	Insertion	intron_variant	*PRKD1*	rs1412349193
Twin_A	14	37141508	T	TA	Insertion	intron_variant	*SLC25A21*	rs533050099
Twin_A	14	39514017	ATATC	A	Deletion	downstream_gene_variant	*AL049828.1*	rs78432958
Twin_A	14	58577605	T	A	Substitution	intergenic_variant	-	-
Twin_A	14	59907903	T	C	Substitution	intergenic_variant	-	-
Twin_A	14	59942776	C	CT	Insertion	intron_variant	*LRRC9*	rs1440781193
Twin_A	14	61869166	A	G	Substitution	intron_variant	*SYT16*	-
Twin_A	14	81424362	TG	T	Deletion	intron_variant	*STON2*	-
Twin_A	14	87211954	G	GA	Insertion	regulatory_region_variant	-	-
Twin_A	15	17735761	T	G	Substitution	intergenic_variant	-	rs1425932497
Twin_A	15	24574554	C	A	Substitution	non_coding_transcript_ exon_variant	*PWRN1*	-
Twin_A	15	25170693	A	G	Substitution	upstream_gene_variant	*SNORD115*	-

Twin_A	15	27699074	C	T	Substitution	intergenic_variant	-	rs979345355
Twin_A	15	27798227	G	A	Substitution	intron_variant	*OCA2*	rs575593376
Twin_A	15	56330772	G	GA	Insertion	intron_variant	*TEX9*	rs202192979
Twin_A	15	58918915	C	CT	Insertion	intron_variant	*SLTM*	rs566389959
Twin_A	15	60956234	G	GT	Insertion	intron_variant	*RORA*	rs796500717
Twin_A	15	63420915	CAT	C	Deletion	intron_variant	*LINC02568*	rs142303229
Twin_A	15	69253960	G	A	Substitution	intron_variant	*GLCE*	-
Twin_A	15	80950475	T	A	Substitution	3_prime_UTR_variant	*CEMIP*	-
Twin_A	15	83158851	C	CT	Insertion	intron_variant	*HDGFL3*	rs554737989
Twin_A	15	96972773	A	G	Substitution	intergenic_variant	-	-
Twin_A	15	99025033	T	A	Substitution	intron_variant	*AC036108.1*	-
Twin_A	16	3192939	A	AT	Insertion	intron_variant	*AJ003147.2*	-
Twin_A	16	7113874	T	C	Substitution	intron_variant	*RBFOX1*	-
Twin_A	16	7450654	G	A	Substitution	intron_variant	*RBFOX1*	rs146577787
Twin_A	16	7806761	G	A	Substitution	intergenic_variant	-	rs752635066
Twin_A	16	8247620	G	A	Substitution	intergenic_variant	-	rs942245726
Twin_A	16	8372617	C	T	Substitution	intron_variant	*AC018767.1*	rs909464601
Twin_A	16	11338624	C	CT	Insertion	intron_variant	*RMI2*	rs377660326
Twin_A	16	13671261	G	A	Substitution	intergenic_variant	-	rs544425045
Twin_A	16	22306291	C	T	Substitution	intron_variant	*POLR3E*	-
Twin_A	16	25681378	C	T	Substitution	intergenic_variant	-	-
Twin_A	16	34085953	C	T	Substitution	regulatory_region_variant	-	rs759751179
Twin_A	16	35232723	C	A	Substitution	intron_variant	*AC023824.3*	-
Twin_A	16	35736091	G	A	Substitution	downstream_gene_variant	*RNA5SP407*	rs1168416095
Twin_A	16	47099927	C	T	Substitution	intron_variant	*NETO2*	-
Twin_A	16	47823047	C	A	Substitution	intron_variant	*LINC02133*	-
Twin_A	16	48066801	G	T	Substitution	intergenic_variant	-	-
Twin_A	16	49303993	C	T	Substitution	intron_variant	*AC007614.1*	-
Twin_A	16	49413774	A	C	Substitution	regulatory_region_variant	-	-
Twin_A	16	51823583	C	T	Substitution	intergenic_variant	-	-
Twin_A	16	52276870	G	A	Substitution	intron_variant	*CASC22*	-
Twin_A	16	52638073	C	T	Substitution	intron_variant	*CASC16*	rs995891657
Twin_A	16	61886296	T	TA	Insertion	intron_variant	*CDH8*	rs535315018
Twin_A	16	64432341	G	GT	Insertion	intron_variant	*AC092131.1*	rs901796829
Twin_A	16	64614439	G	A	Substitution	intergenic_variant	-	-
Twin_A	16	64919655	T	A	Substitution	intergenic_variant	-	-
Twin_A	16	66602481	T	TA	Insertion	upstream_gene_variant	*CMTM3*	rs145668319
Twin_A	16	67608941	A	G	Substitution	intron_variant	*CTCF*	rs892105462
Twin_A	16	71030715	G	C	Substitution	intron_variant	*HYDIN*	rs12102892
Twin_A	16	72362589	G	T	Substitution	intron_variant	*LINC01572*	-
Twin_A	16	74358477	G	GTGTGTGTGTA	Insertion	intron_variant	*AC009053.1*	rs1355695440
Twin_A	16	77781037	CAGG	C	Deletion	regulatory_region_variant	-	rs145741815

Twin_A	16	83070380	C	T	Substitution	intron_variant	*CDH13*	-
Twin_A	16	85313584	C	A	Substitution	intron_variant	*GSE1*	rs1483404740
Twin_A	16	86284090	G	A	Substitution	intron_variant	*LINC01081*	-
Twin_A	17	578020	G	C	Substitution	intron_variant	*VPS53*	-
Twin_A	17	2793153	AT	A	Deletion	upstream_gene_variant	*RAP1GAP2*	rs200252910
Twin_A	17	8040550	GA	G	Deletion	intron_variant	*ALOX15B*	rs57248868
Twin_A	17	8080028	C	T	Substitution	non_coding_transcript_ exon_variant	*AC129492.1*	-
Twin_A	17	9019997	A	G	Substitution	upstream_gene_variant	*NTN1*	-
Twin_A	17	9546387	TA	T	Deletion	intron_variant	*STX8*	rs56901611
Twin_A	17	14728731	G	A	Substitution	intron_variant	*AC013248.1*	-
Twin_A	17	15719138	C	CA	Insertion	3_prime_UTR_variant	*ZNF286A*	rs372793188
Twin_A	17	32918315	T	G	Substitution	regulatory_region_variant	-	-
Twin_A	17	34590397	T	C	Substitution	intron_variant	*TMEM132E*	rs1390883369
Twin_A	17	34849723	CACA	C	Deletion	intron_variant	*AC022903.1*	rs952016458
Twin_A	17	41287213	A	G	Substitution	regulatory_region_variant	-	-
Twin_A	17	48780087	G	GA	Insertion	intron_variant	*TTLL6*	rs371091415
Twin_A	17	63184014	C	CA	Insertion	intron_variant	*TANC2*	rs570141267
Twin_A	17	64353316	C	T	Substitution	intron_variant	*PECAM1*	rs879198491
Twin_A	17	66569297	G	A	Substitution	intron_variant	*PRKCA*	rs540966408
Twin_A	17	72065475	G	A	Substitution	intron_variant	*AC007461.1*	-
Twin_A	17	72109757	C	T	Substitution	intron_variant, non_coding_transcript_variant	*SOX9-AS1*	-
Twin_A	17	73729002	C	G	Substitution	intergenic_variant	-	-
Twin_A	17	78164605	G	A	Substitution	upstream_gene_variant	*SYNGR2*	-
Twin_A	17	79118078	G	A	Substitution	intron_variant	*RBFOX3*	rs560513487
Twin_A	17	82853402	C	CT	Insertion	intron_variant	*TBCD*	-
Twin_A	18	9601220	A	G	Substitution	intron_variant	*PPP4R1*	rs982592192
Twin_A	18	14227264	CAA	C	Deletion	intron_variant	*ANKRD20A5P*	rs200661335
Twin_A	18	20189631	G	A	Substitution	intergenic_variant	-	rs1337042912
Twin_A	18	20830406	G	A	Substitution	intergenic_variant	-	-
Twin_A	18	27867692	T	C	Substitution	intergenic_variant	-	-
Twin_A	18	29896712	C	T	Substitution	intergenic_variant	-	-
Twin_A	18	32161626	G	T	Substitution	intron_variant	*GAREM1*	-
Twin_A	18	32191812	T	C	Substitution	intron_variant	*MEP1B*	-
Twin_A	18	33837694	C	A	Substitution	regulatory_region_variant	-	-
Twin_A	18	34514791	G	A	Substitution	intron_variant	*DTNA*	-
Twin_A	18	41122265	A	G	Substitution	intergenic_variant	-	-
Twin_A	18	50652311	G	A	Substitution	intron_variant	*MAPK4*	-
Twin_A	18	51531692	G	A	Substitution	intron_variant	*LINC01630*	-
Twin_A	18	52758063	C	T	Substitution	intron_variant	*DCC*	rs75634824
Twin_A	18	53231840	T	C	Substitution	intron_variant	*DCC*	rs1236652956
Twin_A	18	56463814	T	TA	Insertion	intergenic_variant	-	rs139733893
Twin_A	18	57470379	T	C	Substitution	intron_variant	*ONECUT2*	-

Twin_A	18	63454630	A	AT	Insertion	regulatory_region_variant	-	rs900204433
Twin_A	18	68909930	A	T	Substitution	intron_variant	*CCDC102B*	-
Twin_A	18	70340966	C	G	Substitution	upstream_gene_variant	*LIVAR*	-
Twin_A	18	75784106	G	A	Substitution	intergenic_variant	-	-
Twin_A	18	76850613	G	GT	Insertion	intron_variant	*ZNF236*	-
Twin_A	19	3661315	C	A	Substitution	intron_variant	*PIP5K1C*	-
Twin_A	19	7346680	T	C	Substitution	upstream_gene_variant	*AC119396.1*	-
Twin_A	19	10065329	CAA	C	Deletion	intron_variant	*C3P1*	-
Twin_A	19	12943750	AGCAGAGGCTTAAGGAGGAGGAAGAAGACAAGAAACGCAAAGAGGAGGAGGAG	A	Deletion	frameshift_variant	*CALR*	rs1555760738
Twin_A	19	14455965	T	TA	Insertion	intron_variant	*PKN1*	rs540413655
Twin_A	19	15471572	G	C	Substitution	intron_variant	*PGLYRP2*	-
Twin_A	19	16234332	C	T	Substitution	intron_variant	*AP1M1*	rs1266106157
Twin_A	19	22883084	C	T	Substitution	regulatory_region_variant	-	-
Twin_A	19	22892036	CT	C	Deletion	intergenic_variant	-	rs59650600
Twin_A	19	27404653	C	G	Substitution	intergenic_variant	-	-
Twin_A	19	27753864	G	T	Substitution	downstream_gene_variant	*AC006504.1*	-
Twin_A	19	28326785	C	T	Substitution	intron_variant	*AC005580.1*	rs1436772262
Twin_A	19	28434046	C	T	Substitution	upstream_gene_variant	*AC005307.1*	rs1029855214
Twin_A	19	40522348	A	T	Substitution	intron_variant	*SPTBN4*	rs1434639441
Twin_A	19	44493750	T	TCTCTCTTG	Insertion	intron_variant	*ZNF180*	rs1258057463
Twin_A	19	48040435	C	A	Substitution	intron_variant	*CABP5*	-
Twin_A	19	54956200	CAAGG	C	Deletion	intron_variant	*NLRP7*	rs752034667
Twin_A	19	55462076	G	GGA	Insertion	upstream_gene_variant	*ISOC2*	-
Twin_A	20	4322280	G	GT	Insertion	regulatory_region_variant	-	rs921737367
Twin_A	20	13915926	C	G	Substitution	intron_variant	*SEL1L2*	rs1392345509
Twin_A	20	24530811	G	GT	Insertion	intron_variant	*SYNDIG1*	rs374193810
Twin_A	20	28628245	A	G	Substitution	intergenic_variant	-	rs879967418
Twin_A	20	39766967	C	T	Substitution	intron_variant	*AL118523.1*	rs1468797562
Twin_A	20	42620323	G	C	Substitution	intron_variant	*PTPRT*	-
Twin_A	20	44696207	C	A	Substitution	upstream_gene_variant	*AL139352.1*	-
Twin_A	20	45737606	A	T	Substitution	intergenic_variant	-	-
Twin_A	20	51168664	C	A	Substitution	intergenic_variant	-	-
Twin_A	20	53076039	C	T	Substitution	intron_variant	*TSHZ2*	rs559693937
Twin_A	20	55145960	T	C	Substitution	intergenic_variant	-	-
Twin_A	20	55476594	G	A	Substitution	intron_variant	*LINC01440*	rs910371781
Twin_A	20	57038323	C	T	Substitution	intergenic_variant	-	-
Twin_A	21	10536357	C	T	Substitution	intron_variant	*TPTE*	-
Twin_A	21	18807398	GCA	G	Deletion	intergenic_variant	-	rs56088107
Twin_A	21	24361606	G	GT	Insertion	intron_variant	*LINC01684*	rs564109768

Twin_A	21	25056551	G	A	Substitution	intron_variant	*AP000235.1*	rs529745996
Twin_A	21	25235168	GTTT	G	Deletion	intron_variant	*AP001341.1*	-
Twin_A	21	26121394	C	CT	Insertion	intron_variant	*APP*	rs147930861
Twin_A	21	27842645	T	C	Substitution	intergenic_variant	-	-
Twin_A	21	28932587	T	C	Substitution	synonymous_variant	*LTN1*	-
Twin_A	21	31309695	A	G	Substitution	intron_variant	*TIAM1*	-
Twin_A	21	32999596	A	T	Substitution	intron_variant	*AP000282.1*	rs1265368759
Twin_A	21	35313715	G	A	Substitution	intron_variant	*RUNX1*	rs1050527217
Twin_A	21	35666262	C	T	Substitution	intron_variant	*RUNX1*	-
Twin_A	21	37443516	T	G	Substitution	intron_variant	*DYRK1A*	rs575428175
Twin_A	21	41859981	G	T	Substitution	intron_variant	*PRDM15*	-
Twin_A	21	42078747	A	G	Substitution	intron_variant	*UMODL1*	-
Twin_A	22	12521506	A	T	Substitution	intergenic_variant	-	rs1476432335
Twin_A	22	15748369	C	T	Substitution	downstream_gene_variant	*GRAMD4P2*	rs529661114
Twin_A	22	16418819	G	A	Substitution	intergenic_variant	-	rs73387994
Twin_A	22	20582589	G	A	Substitution	intron_variant	*MED15*	rs765884898
Twin_A	22	30118881	G	A	Substitution	intron_variant	*HORMAD2*	-
Twin_A	22	33353441	A	G	Substitution	intron_variant	*LARGE1*	rs1007665809
Twin_A	22	34641670	G	A	Substitution	non_coding_transcript_ exon_variant	*AL021877.2*	rs765266284
Twin_A	22	37322215	G	A	Substitution	intergenic_variant	-	rs898967364
Twin_A	22	44313831	C	T	Substitution	upstream_gene_variant	*SHISAL1*	-
Twin_A	22	45732457	C	CA	Insertion	intron_variant	*ATXN10*	rs971974596
Twin_A	22	50478755	C	G	Substitution	upstream_gene_variant	*SBF1*	-
Twin_A	X	1688073	G	A	Substitution	intergenic_variant	-	rs1402629241
Twin_A	X	3810086	TAC	T	Deletion	intergenic_variant	-	rs768564761
Twin_A	X	9793750	C	CT	Insertion	intron_variant	*SHROOM2*	rs368389307
Twin_A	X	10753565	T	TG	Insertion	intron_variant	*MID1*	rs745425008
Twin_A	X	20062481	T	TA	Insertion	intron_variant	*MAP7D2*	rs141341947
Twin_A	X	21515041	T	TA	Insertion	intron_variant	*CNKSR2*	rs111880925
Twin_A	X	26568200	C	T	Substitution	intron_variant	*VENTXP1*	rs760685569
Twin_A	X	35432699	T	C	Substitution	intergenic_variant	-	-
Twin_A	X	41283486	G	T	Substitution	intergenic_variant	-	-
Twin_A	X	43355581	AAG	A	Deletion	intron_variant	*AL023574.1*	rs747346757
Twin_A	X	48123449	G	A	Substitution	downstream_gene_variant	*SSX6P*	rs1311655959
Twin_A	X	53838712	T	TTTTTTC	Insertion	intergenic_variant	-	rs1491090843
Twin_A	X	56963616	T	TCA	Insertion	intron_variant	*SPIN3*	rs367803469
Twin_A	X	64210261	C	CA	Insertion	upstream_gene_variant	*AMER1*	rs1361525685
Twin_A	X	66930421	A	T	Substitution	intergenic_variant	-	-
Twin_A	X	69456838	G	GT	Insertion	intergenic_variant	-	rs367604349
Twin_A	X	73938408	AAAAT	A	Deletion	downstream_gene_variant	*FTX*	rs1467359046
Twin_A	X	74173149	C	CA	Insertion	upstream_gene_variant	*ATP5MDP1*	rs1215712048
Twin_A	X	80107643	A	T	Substitution	intergenic_variant	-	-

Twin_A	X	102759593	AAC	A	Deletion	intergenic_variant	-	rs4009667
Twin_A	X	105950823	CAG	C	Deletion	intron_variant	*NRK*	rs746466025
Twin_A	X	113523343	C	G	Substitution	downstream_gene_variant	*AC233289.1*	-
Twin_A	X	114062259	G	GT	Insertion	upstream_gene_variant	*XACT*	rs1357977704
Twin_A	X	115465393	T	C	Substitution	intergenic_variant	-	-
Twin_A	X	119227169	C	CA	Insertion	upstream_gene_variant	*AC004835.2*	rs11420910
Twin_A	X	130938304	T	C	Substitution	intergenic_variant	-	-
Twin_A	X	142708225	C	A	Substitution	intron_variant	*AL031073.2*	-
Twin_A	X	144608023	C	T	Substitution	intergenic_variant	-	-
Twin_A	Y	12123479	G	GA	Insertion	intron_variant	*GYG2P1*	rs113188804
Twin_A	Y	20863824	C	T	Substitution	downstream_gene_variant	*GAPDHP17*	-
Twin_B	1	1948293	G	A	Substitution	intron_variant	*CFAP74*	-
Twin_B	1	5360980	A	G	Substitution	intergenic_variant	-	-
Twin_B	1	7752725	A	G	Substitution	intron_variant	*CAMTA1*	rs1558304741
Twin_B	1	8034377	T	C	Substitution	intron_variant	*AL034417.2*	-
Twin_B	1	12823937	C	T	Substitution	downstream_gene_variant	*PRAMEF11*	-
Twin_B	1	16874999	G	T	Substitution	downstream_gene_variant	*BX284668.2*	rs6586499
Twin_B	1	21195179	C	T	Substitution	TF_binding_site_variant	*AL023574.1*	rs1040263005
Twin_B	1	28903853	G	GT	Insertion	intron_variant	*EPB41*	rs776964978
Twin_B	1	30198944	G	A	Substitution	intergenic_variant	-	rs959100631
Twin_B	1	46567799	T	A	Substitution	downstream_gene_variant	*MKNK1*	-
Twin_B	1	46733432	G	A	Substitution	intergenic_variant	-	rs910046833
Twin_B	1	46925759	G	C	Substitution	downstream_gene_variant	*CYP4A11*	-
Twin_B	1	47112037	C	T	Substitution	intron_variant	*CYP4Z1*	rs764020558
Twin_B	1	49651607	C	T	Substitution	intron_variant	*AGBL4*	-
Twin_B	1	52446089	C	T	Substitution	downstream_gene_variant	*TUT4*	-
Twin_B	1	55508033	CA	C	Deletion	intron_variant	*AL603840.1*	-
Twin_B	1	57203495	C	T	Substitution	intron_variant	*DAB1*	-
Twin_B	1	68690432	C	T	Substitution	intron_variant	*AL033530.1*	rs1263200065
Twin_B	1	90494264	G	A	Substitution	intergenic_variant	-	-
Twin_B	1	104033383	A	G	Substitution	intergenic_variant	-	-
Twin_B	1	110190300	G	C	Substitution	intron_variant	*SLC6A17*	-
Twin_B	1	110738023	A	G	Substitution	intergenic_variant	-	-
Twin_B	1	114307529	G	C	Substitution	intergenic_variant	-	-
Twin_B	1	115892616	C	T	Substitution	intergenic_variant	-	rs1302223823
Twin_B	1	143898748	G	A	Substitution	downstream_gene_variant	*H3*	-
Twin_B	1	147277076	C	A	Substitution	downstream_gene_variant	*CHD1L*	-
Twin_B	1	157062690	T	C	Substitution	upstream_gene_variant	*SMU1P1*	-
Twin_B	1	158329018	G	A	Substitution	splice_region_variant	*CD1B*	-
Twin_B	1	159742120	G	T	Substitution	intergenic_variant	-	-
Twin_B	1	165976313	A	G	Substitution	intergenic_variant	-	-
Twin_B	1	166242296	C	T	Substitution	intron_variant	*AL596087.2*	-

Twin_B	1	166972081	G	A	Substitution	intron_variant	*ILDR2*	rs747200728
Twin_B	1	170852137	G	C	Substitution	intron_variant	*BX284613.2*	-
Twin_B	1	175165067	G	T	Substitution	intron_variant	*KIAA0040*	-
Twin_B	1	176214397	G	A	Substitution	intron_variant	*AL591043.2*	-
Twin_B	1	177128801	C	A	Substitution	intron_variant	*ASTN1*	-
Twin_B	1	187326523	G	A	Substitution	intron_variant	*LINC01036*	-
Twin_B	1	190010459	C	T	Substitution	intergenic_variant	-	rs574701171
Twin_B	1	192061801	C	A	Substitution	intergenic_variant	-	-
Twin_B	1	194370180	G	A	Substitution	intergenic_variant	-	rs568526830
Twin_B	1	194805882	A	T	Substitution	intron_variant	*AL353072.2*	rs529354380
Twin_B	1	197898293	C	A	Substitution	upstream_gene_variant	*C1orf53*	-
Twin_B	1	211364253	C	T	Substitution	downstream_gene_variant	*TRAF5*	-
Twin_B	1	213739818	C	T	Substitution	intron_variant	*AC096639.1*	rs751851426
Twin_B	1	216808720	G	A	Substitution	intron_variant	*ESRRG*	-
Twin_B	1	226114304	T	TTA	Insertion	intergenic_variant	-	rs1263797763
Twin_B	1	228759153	C	T	Substitution	intergenic_variant	-	-
Twin_B	1	231661954	G	T	Substitution	intron_variant	*DISC1*	-
Twin_B	1	237523679	G	A	Substitution	intron_variant	*RYR2*	rs1165384474
Twin_B	1	239287292	C	T	Substitution	intergenic_variant	-	-
Twin_B	1	239790569	T	G	Substitution	intron_variant	*CHRM3*	-
Twin_B	2	3059701	C	T	Substitution	intron_variant	*LINC01250*	rs902349418
Twin_B	2	5809965	G	A	Substitution	downstream_gene_variant	*LINC01810*	-
Twin_B	2	7937210	A	T	Substitution	intron_variant	*LINC00298*	-
Twin_B	2	14870316	G	A	Substitution	intron_variant	*AC068286.2*	-
Twin_B	2	17702798	C	A	Substitution	downstream_gene_variant	*SMC6*	rs956379181
Twin_B	2	17816780	A	G	Substitution	missense_variant	*MSGN1*	-
Twin_B	2	21701231	C	T	Substitution	intron_variant	*AC018742.1*	-
Twin_B	2	22021980	T	C	Substitution	intron_variant	*AC096570.1*	-
Twin_B	2	22585137	GT	G	Deletion	intergenic_variant	-	-
Twin_B	2	22585139	T	A	Substitution	intergenic_variant	-	-
Twin_B	2	22619775	C	T	Substitution	intergenic_variant	-	rs540314768
Twin_B	2	22994571	A	G	Substitution	intergenic_variant	-	rs1455047191
Twin_B	2	24019295	T	C	Substitution	downstream_gene_variant	*MFSD2B*	-
Twin_B	2	27314362	G	A	Substitution	downstream_gene_variant	*MPV17*	-
Twin_B	2	28287298	T	A	Substitution	intron_variant	*BABAM2*	-
Twin_B	2	29298533	A	G	Substitution	intron_variant	*ALK*	-
Twin_B	2	30708062	G	A	Substitution	intergenic_variant	-	rs1306752997
Twin_B	2	33204005	TG	T	Deletion	intron_variant	*LTBP1*	-
Twin_B	2	34609950	A	G	Substitution	intron_variant	*LINC01320*	-
Twin_B	2	35621513	C	T	Substitution	intergenic_variant	-	rs185192135
Twin_B	2	39543295	C	T	Substitution	intron_variant	*MAP4K3*	-
Twin_B	2	41851787	C	T	Substitution	regulatory_region_variant	-	-

Twin_B	2	52199227	T	C	Substitution	intron_variant	*AC007402.1*	-
Twin_B	2	55637956	C	T	Substitution	intron_variant	*PNPT1*	rs931753562
Twin_B	2	55778474	G	A	Substitution	intergenic_variant	-	rs1269019834
Twin_B	2	59742006	A	T	Substitution	intron_variant	*AC007100.1*	-
Twin_B	2	65862748	C	T	Substitution	intron_variant	*AC007389.1*	-
Twin_B	2	67673061	AGC	A	Deletion	intron_variant	*AC007422.1*	rs142178881
Twin_B	2	72017331	C	T	Substitution	intergenic_variant	-	-
Twin_B	2	76343534	G	A	Substitution	intron_variant	*AC073091.1*	-
Twin_B	2	77138659	C	T	Substitution	intron_variant	*LRRTM4*	-
Twin_B	2	77305966	T	C	Substitution	intron_variant	*LRRTM4*	rs1354282051
Twin_B	2	79741961	T	A	Substitution	intron_variant	*CTNNA2*	-
Twin_B	2	84976628	T	A	Substitution	intron_variant	*KCMF1*	rs1459851336
Twin_B	2	89011497	G	A	Substitution	upstream_gene_variant	*IGKV1*	rs1327184549
Twin_B	2	92889972	CAT	C	Deletion	intergenic_variant	-	rs1381310181
Twin_B	2	94087365	T	C	Substitution	intergenic_variant	-	rs1304472866
Twin_B	2	100572501	T	C	Substitution	downstream_gene_variant	*PDCL3*	-
Twin_B	2	103642003	G	A	Substitution	intergenic_variant	-	-
Twin_B	2	104572208	AC	A	Deletion	intergenic_variant	-	rs1234997111
Twin_B	2	110152812	G	A	Substitution	intron_variant	*NPHP1*	-
Twin_B	2	112972342	G	A	Substitution	regulatory_region_variant	-	-
Twin_B	2	113360949	C	G	Substitution	intron_variant	*AC016745.1*	-
Twin_B	2	114347202	C	G	Substitution	intergenic_variant	-	-
Twin_B	2	122468457	C	T	Substitution	intron_variant	*AC011246.1*	-
Twin_B	2	124707645	G	T	Substitution	intron_variant	*CNTNAP5*	-
Twin_B	2	125662877	G	T	Substitution	upstream_gene_variant	*AC097499.2*	-
Twin_B	2	130970780	G	C	Substitution	intron_variant	*ARHGEF4*	-
Twin_B	2	136809746	AG	A	Deletion	intron_variant	*THSD7B*	-
Twin_B	2	139199861	C	T	Substitution	intergenic_variant	-	rs9646664
Twin_B	2	139215973	T	A	Substitution	intergenic_variant	-	-
Twin_B	2	139897503	C	CTT	Insertion	intergenic_variant	-	-
Twin_B	2	140219327	G	T	Substitution	downstream_gene_variant	*MTND1P27*	-
Twin_B	2	142622241	G	A	Substitution	intergenic_variant	-	-
Twin_B	2	147580489	T	C	Substitution	intergenic_variant	-	-
Twin_B	2	156625930	G	A	Substitution	intergenic_variant	-	rs919742480
Twin_B	2	156749565	A	G	Substitution	intergenic_variant	-	-
Twin_B	2	157345619	GTGGAAAAGAAGCTGCTGGGATCTACTTACC	G	Deletion	intergenic_variant	-	-
Twin_B	2	158735231	G	A	Substitution	intron_variant	*AC005042.1*	-
Twin_B	2	166646939	T	TC	Insertion	intergenic_variant	-	rs397801435
Twin_B	2	168435246	A	T	Substitution	intergenic_variant	-	rs13393085
Twin_B	2	181754253	G	A	Substitution	intergenic_variant	-	rs928244754
Twin_B	2	186809029	C	A	Substitution	intergenic_variant	-	-

Twin_B	2	187978655	C	T	Substitution	intron_variant	*LINC01090*	-
Twin_B	2	190310023	C	T	Substitution	intron_variant	*HIBCH*	rs1380735746
Twin_B	2	191398351	T	G	Substitution	intron_variant	*MYO1B*	-
Twin_B	2	197588962	G	A	Substitution	intron_variant	*RFTN2*	-
Twin_B	2	202594928	C	T	Substitution	intergenic_variant	-	rs987671953
Twin_B	2	202941148	T	C	Substitution	intron_variant	*CARF*	-
Twin_B	2	214886582	T	G	Substitution	intron_variant	*SNHG31*	-
Twin_B	2	215762883	A	C	Substitution	intron_variant	*LINC00607*	-
Twin_B	2	220248897	TTCTC	T	Deletion	intron_variant	*AC019211.1*	-
Twin_B	2	222991555	T	C	Substitution	intergenic_variant	-	-
Twin_B	2	226321782	C	T	Substitution	intergenic_variant	-	-
Twin_B	2	228241318	G	A	Substitution	intergenic_variant	-	rs746719263
Twin_B	2	236024598	A	G	Substitution	intron_variant	*AGAP1*	-
Twin_B	2	238340846	T	G	Substitution	intron_variant	*TRAF3IP1*	rs200969651
Twin_B	2	238788248	G	A	Substitution	downstream_gene_variant	*AC145625.1*	-
Twin_B	3	4096954	C	T	Substitution	intron_variant	*SUMF1*	rs993902730
Twin_B	3	6268058	G	C	Substitution	intron_variant	*AC026167.1*	-
Twin_B	3	8179865	C	T	Substitution	intron_variant	*LMCD1*	-
Twin_B	3	8330619	T	A	Substitution	intron_variant	*LMCD1*	-
Twin_B	3	8749340	G	C	Substitution	downstream_gene_variant	*CAV3*	-
Twin_B	3	8766880	C	G	Substitution	downstream_gene_variant	*OXTR*	-
Twin_B	3	8800977	A	G	Substitution	intron_variant	*RAD18*	-
Twin_B	3	9646697	T	A	Substitution	regulatory_region_variant	-	rs1001727401
Twin_B	3	39756857	A	T	Substitution	intergenic_variant	-	rs950684554
Twin_B	3	50879771	C	G	Substitution	intron_variant	*DOCK3*	-
Twin_B	3	52975648	C	A	Substitution	intron_variant	*SFMBT1*	-
Twin_B	3	54092594	G	A	Substitution	intron_variant	*AC115282.1*	-
Twin_B	3	57095586	C	T	Substitution	3_prime_UTR_variant	*IL17RD*	rs1428340204
Twin_B	3	59401686	C	T	Substitution	intron_variant	*AC126121.3*	-
Twin_B	3	62217141	G	T	Substitution	downstream_gene_variant	*PTPRG*	-
Twin_B	3	66880474	C	T	Substitution	intergenic_variant	-	rs1357891267
Twin_B	3	74463202	G	A	Substitution	intron_variant	*CNTN3*	-
Twin_B	3	80315771	G	C	Substitution	intergenic_variant	-	-
Twin_B	3	84248079	T	A	Substitution	intergenic_variant	-	rs543628716
Twin_B	3	84322937	C	A	Substitution	intergenic_variant	-	rs912367414
Twin_B	3	89748810	A	C	Substitution	intergenic_variant	-	-
Twin_B	3	95223077	C	T	Substitution	intergenic_variant	-	-
Twin_B	3	96820605	G	A	Substitution	intron_variant	*EPHA6*	-
Twin_B	3	99124717	G	C	Substitution	intergenic_variant	-	rs868051607
Twin_B	3	101873401	C	A	Substitution	regulatory_region_variant	-	-
Twin_B	3	107880323	C	T	Substitution	intron_variant	*LINC00635*	-
Twin_B	3	111393544	T	G	Substitution	intron_variant	*CD96*	-

Twin_B	3	120551312	G	T	Substitution	intergenic_variant	-	-
Twin_B	3	124318634	C	T	Substitution	intron_variant	*KALRN*	-
Twin_B	3	127184194	T	A	Substitution	intron_variant	*AC112482.2*	-
Twin_B	3	145553273	C	T	Substitution	intergenic_variant	-	rs181820859
Twin_B	3	146968300	C	A	Substitution	intron_variant	*AC092957.1*	-
Twin_B	3	148123392	C	T	Substitution	intron_variant	*AC092958.2*	rs893487280
Twin_B	3	150872501	C	T	Substitution	intron_variant	*MINDY4B*	-
Twin_B	3	152516100	G	A	Substitution	intergenic_variant	-	-
Twin_B	3	157178549	C	G	Substitution	downstream_gene_variant	*AC092944.1*	-
Twin_B	3	169022850	C	A	Substitution	intron_variant	*LINC01997*	-
Twin_B	3	179003062	C	T	Substitution	intron_variant	*ZMAT3*	-
Twin_B	3	182077482	T	A	Substitution	intergenic_variant	-	-
Twin_B	3	187366417	G	A	Substitution	upstream_gene_variant	*RTP4*	-
Twin_B	3	192580552	T	A	Substitution	intron_variant	*FGF12*	-
Twin_B	3	197965767	A	G	Substitution	intron_variant	*LMLN*	-
Twin_B	4	1811861	C	T	Substitution	3_prime_UTR_variant	*LETM1*	-
Twin_B	4	6451943	C	A	Substitution	intron_variant	*PPP2R2C*	-
Twin_B	4	12745680	C	T	Substitution	intergenic_variant	-	rs1006183911
Twin_B	4	16908350	G	T	Substitution	intergenic_variant	-	rs750655685
Twin_B	4	26875683	C	G	Substitution	intron_variant	*STIM2*	-
Twin_B	4	27652841	G	A	Substitution	intergenic_variant	-	rs1037907678
Twin_B	4	33615886	T	A	Substitution	intron_variant	*AC079772.1*	-
Twin_B	4	37418639	A	T	Substitution	intron_variant	*NWD2*	rs543621535
Twin_B	4	39429436	G	A	Substitution	intron_variant	*KLB*	-
Twin_B	4	46668719	G	C	Substitution	intergenic_variant	-	-
Twin_B	4	47220483	T	C	Substitution	intron_variant	*GABRB1*	-
Twin_B	4	49731501	T	C	Substitution	intergenic_variant	-	rs1458775311
Twin_B	4	52190355	A	G	Substitution	intergenic_variant	-	-
Twin_B	4	57634212	TG	T	Deletion	intron_variant	*AC093725.2*	-
Twin_B	4	57634214	TG	T	Deletion	intron_variant	*AC093725.2*	-
Twin_B	4	60517882	C	T	Substitution	intergenic_variant	-	-
Twin_B	4	64216296	A	G	Substitution	intergenic_variant	-	rs562121918
Twin_B	4	64665477	T	A	Substitution	intergenic_variant	-	-
Twin_B	4	67380380	G	A	Substitution	intergenic_variant	-	rs551895523
Twin_B	4	70520668	A	T	Substitution	intron_variant	*AMTN*	-
Twin_B	4	71648848	A	G	Substitution	intergenic_variant	-	rs1040824596
Twin_B	4	76047967	G	A	Substitution	intron_variant	*ART3*	-
Twin_B	4	86440642	A	G	Substitution	intron_variant	*MAPK10*	-
Twin_B	4	88387262	T	C	Substitution	upstream_gene_variant	*HERC6*	-
Twin_B	4	108394132	G	A	Substitution	intergenic_variant	-	-
Twin_B	4	115259241	A	T	Substitution	intergenic_variant	-	-
Twin_B	4	117969239	T	C	Substitution	intergenic_variant	-	rs71627746

Twin_B	4	119161162	A	C	Substitution	intron_variant	*MYOZ2*	-
Twin_B	4	120599980	G	A	Substitution	intergenic_variant	-	-
Twin_B	4	125617334	A	T	Substitution	intergenic_variant	-	-
Twin_B	4	126647636	A	G	Substitution	intron_variant	*AC097528.1*	-
Twin_B	4	127771889	A	G	Substitution	intron_variant	*SLC25A31*	rs1201508233
Twin_B	4	140154007	T	G	Substitution	5_prime_UTR_variant	*MAML3*	-
Twin_B	4	144879760	C	T	Substitution	downstream_gene_variant	*AC109811.1*	-
Twin_B	4	147616580	G	C	Substitution	intron_variant	*AC093835.1*	-
Twin_B	4	152098840	G	A	Substitution	intron_variant	*LINC02273*	-
Twin_B	4	161716379	T	C	Substitution	intron_variant	*FSTL5*	-
Twin_B	4	166613505	T	C	Substitution	intergenic_variant	-	-
Twin_B	4	168686621	G	A	Substitution	intron_variant	*PALLD*	rs1030969924
Twin_B	4	174170616	G	A	Substitution	intron_variant	*LINC02268*	rs1241611683
Twin_B	4	179639868	C	T	Substitution	intergenic_variant	-	-
Twin_B	4	180135661	C	A	Substitution	intergenic_variant	-	-
Twin_B	4	184638048	T	C	Substitution	intron_variant	*CASP3*	-
Twin_B	4	187716917	C	T	Substitution	downstream_gene_variant	*AC097521.1*	rs1306869395
Twin_B	5	4311163	C	T	Substitution	intergenic_variant	-	rs755225209
Twin_B	5	4490226	G	A	Substitution	intron_variant	*AC106799.2*	-
Twin_B	5	5721155	C	A	Substitution	intergenic_variant	-	rs1404060316
Twin_B	5	7425190	G	A	Substitution	intron_variant	*ADCY2*	-
Twin_B	5	9500811	T	C	Substitution	intron_variant	*SEMA5A*	-
Twin_B	5	11361065	G	A	Substitution	downstream_gene_variant	*CTNND2*	-
Twin_B	5	18474168	C	T	Substitution	intergenic_variant	-	-
Twin_B	5	19703201	C	T	Substitution	intron_variant	*CDH18*	-
Twin_B	5	29927998	G	A	Substitution	intergenic_variant	-	rs910971117
Twin_B	5	30228903	G	A	Substitution	intergenic_variant	-	-
Twin_B	5	32183802	G	A	Substitution	intergenic_variant	-	rs1321151704
Twin_B	5	35163531	G	A	Substitution	intron_variant	*PRLR*	-
Twin_B	5	41232152	T	G	Substitution	intron_variant	*C6*	-
Twin_B	5	41663190	G	A	Substitution	intergenic_variant	-	-
Twin_B	5	42222760	G	A	Substitution	intergenic_variant	-	-
Twin_B	5	45194560	C	T	Substitution	intergenic_variant	-	rs550304760
Twin_B	5	47101412	G	A	Substitution	intergenic_variant	-	rs1255895881
Twin_B	5	50007872	T	C	Substitution	intergenic_variant	-	-
Twin_B	5	53160317	A	G	Substitution	intergenic_variant	-	-
Twin_B	5	59291742	T	G	Substitution	intron_variant	*PDE4D*	rs57801368
Twin_B	5	63614795	GAC	G	Deletion	intergenic_variant	-	rs1396639575
Twin_B	5	72404389	A	G	Substitution	intergenic_variant	-	-
Twin_B	5	84595108	T	C	Substitution	intergenic_variant	-	rs1003756160
Twin_B	5	85129366	T	C	Substitution	intergenic_variant	-	-
Twin_B	5	93483038	G	A	Substitution	intron_variant	*NR2F1*	rs918359530

Twin_B	5	105561137	C	T	Substitution	intergenic_variant	-	-
Twin_B	5	106685060	G	A	Substitution	intergenic_variant	-	-
Twin_B	5	110479443	C	T	Substitution	intron_variant	*TMEM232*	-
Twin_B	5	119572129	C	T	Substitution	intron_variant	*HSD17B4*	-
Twin_B	5	122619069	G	A	Substitution	intergenic_variant	-	-
Twin_B	5	130265666	C	T	Substitution	intergenic_variant	-	rs62391477
Twin_B	5	134868896	C	T	Substitution	intergenic_variant	-	rs910097048
Twin_B	5	137416371	G	C	Substitution	intron_variant	*SPOCK1*	-
Twin_B	5	140836906	A	G	Substitution	3_prime_UTR_variant	*PCDHA7*	-
Twin_B	5	147046232	G	T	Substitution	intron_variant	*PPP2R2B*	-
Twin_B	5	155317926	G	T	Substitution	intergenic_variant	-	-
Twin_B	5	157005759	C	A	Substitution	intergenic_variant	-	-
Twin_B	5	158293742	G	A	Substitution	intergenic_variant	-	-
Twin_B	5	159980907	T	C	Substitution	intergenic_variant	-	-
Twin_B	5	161395724	G	A	Substitution	intron_variant	*GABRB2*	-
Twin_B	5	161830310	G	T	Substitution	intergenic_variant	-	-
Twin_B	5	166256348	G	A	Substitution	intergenic_variant	-	-
Twin_B	5	175182485	G	A	Substitution	intergenic_variant	-	-
Twin_B	5	178484296	T	G	Substitution	intron_variant	*COL23A1*	-
Twin_B	6	1850433	CT	C	Deletion	intron_variant	*GMDS*	-
Twin_B	6	18553216	G	T	Substitution	intron_variant	*MIR548A1HG*	-
Twin_B	6	20182475	T	G	Substitution	intron_variant	*MBOAT1*	-
Twin_B	6	23725753	C	T	Substitution	intergenic_variant	-	-
Twin_B	6	23820823	AG	A	Deletion	intergenic_variant	-	-
Twin_B	6	32530993	T	C	Substitution	regulatory_region_variant	-	rs74714255
Twin_B	6	33355096	C	T	Substitution	intergenic_variant	-	-
Twin_B	6	40322738	T	C	Substitution	intergenic_variant	-	-
Twin_B	6	45795560	T	G	Substitution	intergenic_variant	-	-
Twin_B	6	49245413	G	A	Substitution	intergenic_variant	-	-
Twin_B	6	49866189	C	T	Substitution	intron_variant	*CRISP1*	-
Twin_B	6	50314470	C	T	Substitution	intergenic_variant	-	rs192304872
Twin_B	6	68164502	G	A	Substitution	intergenic_variant	-	rs539171573
Twin_B	6	73054903	C	A	Substitution	intron_variant	*KCNQ5*	-
Twin_B	6	77608472	C	G	Substitution	intergenic_variant	-	rs145374562
Twin_B	6	78332113	A	G	Substitution	intergenic_variant	-	-
Twin_B	6	80558206	T	C	Substitution	upstream_gene_variant	*AL590824.1*	-
Twin_B	6	95406340	C	T	Substitution	intergenic_variant	-	rs548629996
Twin_B	6	101437584	G	A	Substitution	intron_variant	*GRIK2*	rs1368442237
Twin_B	6	102787939	T	A	Substitution	intergenic_variant	-	-
Twin_B	6	105574693	A	C	Substitution	intron_variant	*AL096794.1*	-
Twin_B	6	110560428	G	A	Substitution	downstream_gene_variant	*AL512430.3*	-
Twin_B	6	115939145	A	G	Substitution	3_prime_UTR_variant	*FRK*	-

Twin_B	6	132482937	C	T	Substitution	intron_variant	*STX7*	-
Twin_B	6	133738256	C	A	Substitution	intron_variant	*TARID*	-
Twin_B	6	153868755	C	A	Substitution	intergenic_variant	-	-
Twin_B	6	155942473	C	T	Substitution	intron_variant	*AL589693.1*	rs1029874863
Twin_B	6	157796066	T	G	Substitution	intron_variant	*SNX9*	-
Twin_B	6	160228462	G	T	Substitution	intron_variant	*SLC22A2*	-
Twin_B	6	160512492	C	T	Substitution	intron_variant	*LPAL2*	rs573849624
Twin_B	6	163903570	G	A	Substitution	intergenic_variant	-	rs138646256
Twin_B	6	164337205	G	A	Substitution	intergenic_variant	-	rs1395517073
Twin_B	6	170147589	C	A	Substitution	downstream_gene_variant	*AL596442.4*	-
Twin_B	7	4358841	C	T	Substitution	intergenic_variant	-	rs746784235
Twin_B	7	7383076	A	T	Substitution	intron_variant	*COL28A1*	-
Twin_B	7	9012014	G	A	Substitution	intergenic_variant	-	-
Twin_B	7	10181486	C	T	Substitution	intergenic_variant	-	-
Twin_B	7	20905885	C	G	Substitution	intron_variant	*LINC01162*	-
Twin_B	7	26002719	G	A	Substitution	intergenic_variant	-	-
Twin_B	7	27125974	G	A	Substitution	downstream_gene_variant	*AC004080.6*	-
Twin_B	7	30124532	G	T	Substitution	downstream_gene_variant	*AC007036.5*	-
Twin_B	7	33443171	A	T	Substitution	intron_variant	*BBS9*	-
Twin_B	7	33920177	G	A	Substitution	intron_variant	*BMPER*	-
Twin_B	7	34052098	C	T	Substitution	intron_variant	*BMPER*	-
Twin_B	7	43433707	A	C	Substitution	intron_variant	*HECW1*	-
Twin_B	7	44053423	G	A	Substitution	downstream_gene_variant	*DBNL*	rs1254859423
Twin_B	7	45053757	A	G	Substitution	intron_variant	*CCM2*	-
Twin_B	7	45393430	C	G	Substitution	upstream_gene_variant	*ELK1P1*	-
Twin_B	7	48916465	T	C	Substitution	upstream_gene_variant	*CDC14C*	rs1245635730
Twin_B	7	54587046	C	A	Substitution	intergenic_variant	-	-
Twin_B	7	57036330	G	A	Substitution	intergenic_variant	-	rs368641980
Twin_B	7	60485855	A	C	Substitution	intergenic_variant	-	rs1335884497
Twin_B	7	60938781	CA	C	Deletion	intergenic_variant	-	rs1250869720
Twin_B	7	61436516	T	A	Substitution	intergenic_variant	-	rs1169588355
Twin_B	7	61970818	T	C	Substitution	intergenic_variant	-	rs1283251044
Twin_B	7	62882059	A	C	Substitution	intergenic_variant	-	rs112905112
Twin_B	7	62882071	C	A	Substitution	intergenic_variant	-	rs1395947656
Twin_B	7	65034946	G	A	Substitution	upstream_gene_variant	*AC073210.2*	rs954732530
Twin_B	7	65590326	T	C	Substitution	intergenic_variant	-	-
Twin_B	7	67521209	C	T	Substitution	intergenic_variant	-	rs183903994
Twin_B	7	71219697	C	T	Substitution	intron_variant	*GALNT17*	-
Twin_B	7	71503989	G	A	Substitution	intron_variant	*GALNT17*	-
Twin_B	7	73980208	CAA	C	Deletion	intergenic_variant	-	rs60681274
Twin_B	7	75784737	G	A	Substitution	intron_variant	*CCL26*	-
Twin_B	7	86130259	T	G	Substitution	intergenic_variant	-	-

Twin_B	7	102788991	TATG	T	Deletion	downstream_gene_variant	*FAM185A*	rs1163997473
Twin_B	7	108865841	G	A	Substitution	intergenic_variant	-	-
Twin_B	7	111235913	G	A	Substitution	intron_variant	*IMMP2L*	-
Twin_B	7	116155279	G	C	Substitution	intron_variant	*TFEC*	-
Twin_B	7	134178896	G	A	Substitution	intron_variant	*LRGUK*	-
Twin_B	7	137739877	G	T	Substitution	intron_variant	*DGKI*	rs190071670
Twin_B	7	142637901	C	A	Substitution	downstream_gene_variant	*TRBV21*	-
Twin_B	7	146668441	T	TGG	Insertion	intron_variant	*CNTNAP2*	rs35693921
Twin_B	7	150085019	G	A	Substitution	intergenic_variant	-	rs1461424202
Twin_B	7	152410761	T	C	Substitution	intron_variant	*KMT2C*	rs80138121
Twin_B	7	156931430	C	T	Substitution	intergenic_variant	-	-
Twin_B	8	924933	C	T	Substitution	intron_variant	*DLGAP2*	-
Twin_B	8	3391860	G	T	Substitution	intron_variant	*CSMD1*	-
Twin_B	8	4997791	G	A	Substitution	regulatory_region_variant	-	-
Twin_B	8	5826762	C	T	Substitution	intergenic_variant	-	-
Twin_B	8	19798556	G	T	Substitution	intergenic_variant	-	-
Twin_B	8	20863668	T	A	Substitution	intergenic_variant	-	-
Twin_B	8	25151260	C	A	Substitution	intergenic_variant	-	-
Twin_B	8	26940513	G	A	Substitution	intergenic_variant	-	-
Twin_B	8	32400294	G	T	Substitution	intron_variant	*NRG1*	-
Twin_B	8	32524703	G	A	Substitution	intron_variant	*NRG1*	-
Twin_B	8	34194743	G	C	Substitution	intron_variant	*AC087855.2*	-
Twin_B	8	41188472	A	T	Substitution	intergenic_variant	-	-
Twin_B	8	43877252	G	GT	Insertion	intergenic_variant	-	-
Twin_B	8	44701946	T	G	Substitution	intergenic_variant	-	rs1325351437
Twin_B	8	46315152	G	A	Substitution	intergenic_variant	-	-
Twin_B	8	49102414	A	C	Substitution	intron_variant	*AC044893.1*	-
Twin_B	8	50264084	A	G	Substitution	intron_variant	*SNTG1*	-
Twin_B	8	51178687	G	A	Substitution	intergenic_variant	-	rs1207366775
Twin_B	8	53427578	TAC	T	Deletion	intron_variant	*AC022034.3*	-
Twin_B	8	57557945	G	A	Substitution	intron_variant	*AC090796.1*	-
Twin_B	8	58506466	G	T	Substitution	downstream_gene_variant	*PPIAP85*	rs973571307
Twin_B	8	59792693	T	A	Substitution	intergenic_variant	-	-
Twin_B	8	64469993	C	A	Substitution	intergenic_variant	-	-
Twin_B	8	69896186	C	A	Substitution	intergenic_variant	-	rs1204844083
Twin_B	8	70358021	AGCCTG	A	Deletion	downstream_gene_variant	*RNY3P14*	-
Twin_B	8	71477385	T	C	Substitution	intron_variant	*EYA1*	-
Twin_B	8	78483436	T	C	Substitution	intron_variant	*PKIA*	-
Twin_B	8	81785469	A	G	Substitution	intergenic_variant	-	rs1439987215
Twin_B	8	82359769	T	C	Substitution	intron_variant	*AC060765.2*	-
Twin_B	8	84130068	C	T	Substitution	intron_variant	*AC015522.1*	rs114417960
Twin_B	8	87159687	A	T	Substitution	intron_variant	*CNBD1*	-

Twin_B	8	87159688	G	A	Substitution	intron_variant	*CNBD1*	-
Twin_B	8	98496864	T	C	Substitution	intron_variant	*STK3*	rs1015493993
Twin_B	8	98657310	C	T	Substitution	intron_variant	*STK3*	-
Twin_B	8	100119116	G	A	Substitution	intron_variant	*RGS22*	-
Twin_B	8	109438926	A	G	Substitution	missense_variant	*PKHD1L1*	-
Twin_B	8	109534244	C	T	Substitution	3_prime_UTR_variant	*PKHD1L1*	rs539684370
Twin_B	8	111647834	G	C	Substitution	intron_variant	*LINC02237*	-
Twin_B	8	111905799	G	A	Substitution	intergenic_variant	-	rs1453724199
Twin_B	8	113516282	C	A	Substitution	intergenic_variant	-	-
Twin_B	8	114563854	C	T	Substitution	intergenic_variant	-	-
Twin_B	8	116551195	C	T	Substitution	intergenic_variant	-	-
Twin_B	8	122234933	G	A	Substitution	intergenic_variant	-	rs1423584842
Twin_B	8	126381321	C	T	Substitution	intergenic_variant	-	rs1433139292
Twin_B	8	131552936	T	A	Substitution	intergenic_variant	-	-
Twin_B	8	133562727	G	A	Substitution	downstream_gene_variant	*ST3GAL1*	-
Twin_B	8	136497219	A	G	Substitution	intron_variant	*LINC02055*	-
Twin_B	8	139066773	G	A	Substitution	intergenic_variant	-	-
Twin_B	9	595757	G	A	Substitution	intron_variant	*KANK1*	rs1028227944
Twin_B	9	5583708	G	A	Substitution	intron_variant	*AL162253.2*	-
Twin_B	9	9208774	T	C	Substitution	intron_variant	*PTPRD*	-
Twin_B	9	10229559	G	A	Substitution	intron_variant	*PTPRD*	-
Twin_B	9	12626664	C	T	Substitution	intergenic_variant	-	-
Twin_B	9	12964481	A	T	Substitution	intron_variant	*AL161449.2*	rs1563767337
Twin_B	9	21096138	A	G	Substitution	intergenic_variant	-	rs896126975
Twin_B	9	23036773	C	T	Substitution	intron_variant	*AL391117.1*	-
Twin_B	9	24723875	G	T	Substitution	intergenic_variant	-	-
Twin_B	9	24924904	G	A	Substitution	intergenic_variant	-	rs193241464
Twin_B	9	38292964	C	T	Substitution	intergenic_variant	-	-
Twin_B	9	38995507	T	C	Substitution	intron_variant	*AL953883.1*	rs1422022710
Twin_B	9	42290039	T	A	Substitution	intron_variant	*AL445584.2*	rs1211321020
Twin_B	9	42760705	C	T	Substitution	intron_variant	*BX664718.2*	rs56025544
Twin_B	9	42945900	G	A	Substitution	intron_variant	*ANKRD20A7P*	-
Twin_B	9	65672213	T	C	Substitution	intron_variant	*CBWD5*	rs796503817
Twin_B	9	66779265	C	T	Substitution	intergenic_variant	-	rs1271105675
Twin_B	9	67205531	TG	T	Deletion	intron_variant	*AL162233.1*	rs368975415
Twin_B	9	73452437	GTTTC	G	Deletion	intergenic_variant	-	-
Twin_B	9	74317541	T	C	Substitution	intergenic_variant	-	-
Twin_B	9	77105186	C	T	Substitution	intergenic_variant	-	rs538603299
Twin_B	9	87267784	G	A	Substitution	intergenic_variant	-	rs1328259639
Twin_B	9	88848472	C	A	Substitution	intergenic_variant	-	-
Twin_B	9	95722226	G	T	Substitution	intergenic_variant	-	-
Twin_B	9	98676266	A	T	Substitution	intron_variant	*GABBR2*	-

Twin_B	9	102339974	A	G	Substitution	intergenic_variant	-	-
Twin_B	9	102993672	C	A	Substitution	upstream_gene_variant	*CYLC2*	-
Twin_B	9	103368304	G	A	Substitution	intron_variant	*AL390962.1*	-
Twin_B	9	104257777	G	T	Substitution	intergenic_variant	-	-
Twin_B	9	104331598	T	G	Substitution	upstream_gene_variant	*AL512646.1*	-
Twin_B	9	105298502	A	G	Substitution	intron_variant	*SLC44A1*	-
Twin_B	9	118261593	G	A	Substitution	intergenic_variant	-	rs1353495123
Twin_B	9	124851965	C	T	Substitution	upstream_gene_variant	*WDR38*	rs962035631
Twin_B	9	127439569	C	T	Substitution	intron_variant	*ZNF79*	-
Twin_B	9	130429019	C	T	Substitution	intron_variant	*HMCN2*	rs554518691
Twin_B	9	131860557	T	A	Substitution	missense_variant	*MED27*	-
Twin_B	9	134007274	C	T	Substitution	intergenic_variant	-	-
Twin_B	9	135090386	T	G	Substitution	intron_variant	*OLFM1*	rs56337838
Twin_B	10	1176537	C	T	Substitution	downstream_gene_variant	*ADARB2*	rs757910551
Twin_B	10	9492286	A	C	Substitution	intergenic_variant	-	rs148903298
Twin_B	10	10933457	T	A	Substitution	downstream_gene_variant	*LINC00710*	-
Twin_B	10	12067169	A	G	Substitution	upstream_gene_variant	*DHTKD1*	rs1055077923
Twin_B	10	14501740	C	A	Substitution	intergenic_variant	-	-
Twin_B	10	19776842	A	T	Substitution	intron_variant	*MALRD1*	-
Twin_B	10	24984824	G	A	Substitution	missense_variant	*ENKUR*	rs200773323
Twin_B	10	30158617	C	A	Substitution	intergenic_variant	-	-
Twin_B	10	33849532	T	C	Substitution	intergenic_variant	-	-
Twin_B	10	37826153	C	T	Substitution	downstream_gene_variant	*ZNF248*	-
Twin_B	10	42358812	A	G	Substitution	intron_variant	*BX322639.1*	-
Twin_B	10	46311814	C	A	Substitution	downstream_gene_variant	*ANTXRL*	-
Twin_B	10	54568022	G	T	Substitution	intron_variant	*PCDH15*	-
Twin_B	10	65525504	T	C	Substitution	intergenic_variant	-	-
Twin_B	10	73104873	G	A	Substitution	upstream_gene_variant	*AL731563.3*	-
Twin_B	10	75129152	A	T	Substitution	downstream_gene_variant	*RPS26P42*	rs1477868012
Twin_B	10	82739562	G	A	Substitution	intron_variant	*NRG3*	-
Twin_B	10	86750662	C	A	Substitution	non_coding_transcript_ exon_variant	*AC067750.1*	-
Twin_B	10	88654107	TA	T	Deletion	intergenic_variant	-	rs200426640
Twin_B	10	90700494	C	T	Substitution	intergenic_variant	-	-
Twin_B	10	92770872	T	A	Substitution	intergenic_variant	-	-
Twin_B	10	93234495	G	T	Substitution	intergenic_variant	-	rs184258432
Twin_B	10	102661031	C	T	Substitution	downstream_gene_variant	*TRIM8*	-
Twin_B	10	103273122	G	A	Substitution	TF_binding_site_variant	*INA*	rs1286474689
Twin_B	10	110609195	T	A	Substitution	downstream_gene_variant	*SMC3*	-
Twin_B	10	115355253	A	G	Substitution	intron_variant	*ATRNL1*	-
Twin_B	10	116513252	G	A	Substitution	intergenic_variant	-	-
Twin_B	10	118845653	C	T	Substitution	intron_variant	*AL157388.1*	-
Twin_B	10	121236516	G	A	Substitution	intergenic_variant	-	rs75201857

Twin_B	10	125904313	C	T	Substitution	intron_variant	*FANK1*	rs571397776
Twin_B	10	131096200	G	A	Substitution	downstream_gene_variant	*TCERG1L*	-
Twin_B	10	132055519	G	A	Substitution	intron_variant	*JAKMIP3*	rs11813033
Twin_B	11	2172588	G	A	Substitution	upstream_gene_variant	*MIR4686*	rs970284747
Twin_B	11	4222159	G	A	Substitution	intergenic_variant	-	rs78524524
Twin_B	11	4861410	G	A	Substitution	intron_variant	*MMP26*	-
Twin_B	11	5952018	A	G	Substitution	downstream_gene_variant	*OR56A3*	-
Twin_B	11	8836985	G	A	Substitution	intron_variant	*DENND2B*	-
Twin_B	11	11456484	C	T	Substitution	intron_variant	*GALNT18*	-
Twin_B	11	19063121	G	A	Substitution	upstream_gene_variant	*MRGPRX2*	-
Twin_B	11	20315541	A	G	Substitution	intergenic_variant	-	-
Twin_B	11	20325176	G	T	Substitution	intergenic_variant	-	-
Twin_B	11	36738318	A	G	Substitution	intergenic_variant	-	rs1297968115
Twin_B	11	36973840	G	A	Substitution	intergenic_variant	-	rs983687999
Twin_B	11	42300900	G	A	Substitution	intergenic_variant	-	rs915445215
Twin_B	11	42391773	A	G	Substitution	intergenic_variant	-	-
Twin_B	11	44879657	AG	A	Deletion	intron_variant	*TSPAN18*	-
Twin_B	11	54940328	C	A	Substitution	intergenic_variant	-	-
Twin_B	11	55783372	G	A	Substitution	upstream_gene_variant	*OR5D15P*	rs566667825
Twin_B	11	81625515	T	C	Substitution	intergenic_variant	-	rs1018593916
Twin_B	11	82290505	C	T	Substitution	intron_variant	*MIR4300HG*	rs181088482
Twin_B	11	82375060	A	T	Substitution	intron_variant	*MIR4300HG*	-
Twin_B	11	83760647	C	A	Substitution	intron_variant	*DLG2*	-
Twin_B	11	88442713	G	T	Substitution	intergenic_variant	-	-
Twin_B	11	91384045	G	T	Substitution	downstream_gene_variant	*AP002791.1*	-
Twin_B	11	93116767	C	A	Substitution	intergenic_variant	-	-
Twin_B	11	93907782	C	T	Substitution	intergenic_variant	-	rs1382214357
Twin_B	11	103587114	C	G	Substitution	intergenic_variant	-	rs1026010882
Twin_B	11	107071946	A	G	Substitution	intergenic_variant	-	-
Twin_B	11	112616847	C	T	Substitution	intron_variant	*LINC02763*	rs920020081
Twin_B	11	114708783	G	A	Substitution	downstream_gene_variant	*NXPE2*	-
Twin_B	11	114958122	G	T	Substitution	intergenic_variant	-	-
Twin_B	11	117410900	C	A	Substitution	downstream_gene_variant	*CEP164*	-
Twin_B	11	122025753	C	T	Substitution	downstream_gene_variant	*MIR100HG*	-
Twin_B	11	122979808	C	A	Substitution	intron_variant	*BSX*	-
Twin_B	11	124291010	G	A	Substitution	intergenic_variant	-	-
Twin_B	11	128554716	C	T	Substitution	intron_variant	*ETS1*	rs78814353
Twin_B	11	132785635	G	A	Substitution	intron_variant	*OPCML*	-
Twin_B	11	133338345	C	T	Substitution	intron_variant	*OPCML*	rs907145809
Twin_B	11	133761282	T	A	Substitution	intergenic_variant	-	-
Twin_B	12	6117683	C	T	Substitution	downstream_gene_variant	*VWF*	rs546633664
Twin_B	12	6307820	C	T	Substitution	regulatory_region_variant	-	rs1256264888

Twin_B	12	6520513	G	A	Substitution	downstream_gene_variant	*NCAPD2*	-
Twin_B	12	6789295	C	T	Substitution	intron_variant	*CD4*	-
Twin_B	12	8205043	GC	G	Deletion	downstream_gene_variant	*FAM66C*	rs144267844
Twin_B	12	9683004	G	A	Substitution	downstream_gene_variant	*CLEC2D*	rs188982524
Twin_B	12	11785599	A	G	Substitution	intron_variant	*ETV6*	rs778627490
Twin_B	12	18037838	C	T	Substitution	intergenic_variant	-	-
Twin_B	12	20532321	G	A	Substitution	intron_variant	*PDE3A*	-
Twin_B	12	24620263	G	A	Substitution	intergenic_variant	-	-
Twin_B	12	25350278	C	T	Substitution	intergenic_variant	-	rs944670622
Twin_B	12	26030102	G	A	Substitution	intron_variant	*RASSF8*	rs771217533
Twin_B	12	32986809	G	A	Substitution	non_coding_transcript_ exon_variant	*AC087311.1*	-
Twin_B	12	34148556	C	T	Substitution	upstream_gene_variant	*AC140847.1*	rs1252261441
Twin_B	12	35988466	T	C	Substitution	intergenic_variant	-	rs1164988538
Twin_B	12	38746830	T	C	Substitution	intron_variant	*CPNE8*	-
Twin_B	12	43641305	G	A	Substitution	intergenic_variant	-	rs568390024
Twin_B	12	46321777	C	T	Substitution	intergenic_variant	-	rs150303645
Twin_B	12	50558428	A	T	Substitution	intron_variant	*DIP2B*	-
Twin_B	12	61470230	G	C	Substitution	intergenic_variant	-	rs1421114192
Twin_B	12	68411586	C	A	Substitution	intron_variant	*LINC02384*	-
Twin_B	12	77504158	G	A	Substitution	intron_variant	*NAV3*	rs991324887
Twin_B	12	78382902	C	T	Substitution	intron_variant	*AC128707.1*	-
Twin_B	12	79065377	C	T	Substitution	intron_variant	*SYT1*	rs993033305
Twin_B	12	80780558	A	T	Substitution	intergenic_variant	-	-
Twin_B	12	83300749	C	T	Substitution	intergenic_variant	-	rs538003003
Twin_B	12	84484910	G	A	Substitution	intergenic_variant	-	-
Twin_B	12	86386833	C	A	Substitution	intron_variant	*MGAT4C*	-
Twin_B	12	87232193	G	A	Substitution	intergenic_variant	-	-
Twin_B	12	87810848	T	G	Substitution	intergenic_variant	-	-
Twin_B	12	88071791	G	A	Substitution	missense_variant	*CEP290*	rs761572735
Twin_B	12	90780665	C	T	Substitution	intron_variant	*AC112481.2*	-
Twin_B	12	95719552	T	C	Substitution	intron_variant	*NTN4*	COSV59220221
Twin_B	12	96233025	A	G	Substitution	intron_variant	*ELK3*	-
Twin_B	12	100396583	T	A	Substitution	intron_variant	*SLC17A8*	rs1220972791
Twin_B	12	105124962	C	T	Substitution	intron_variant	*WASHC4*	-
Twin_B	12	109600533	C	G	Substitution	downstream_gene_variant	*MVK*	-
Twin_B	12	113992218	G	A	Substitution	intergenic_variant	-	-
Twin_B	12	114026760	G	A	Substitution	intergenic_variant	-	rs142779521
Twin_B	12	115283072	C	A	Substitution	intergenic_variant	-	-
Twin_B	12	116627058	G	C	Substitution	intergenic_variant	-	-
Twin_B	12	121968151	A	T	Substitution	missense_variant	*CFAP251*	-
Twin_B	12	126210035	C	T	Substitution	intron_variant	*AC007368.1*	-
Twin_B	12	128451756	C	T	Substitution	intron_variant	*TMEM132C*	-

Twin_B	12	129158414	A	G	Substitution	intron_variant	*TMEM132D*	-
Twin_B	12	129545572	G	A	Substitution	intron_variant	*TMEM132D*	rs548980444
Twin_B	12	132821132	C	T	Substitution	downstream_gene_variant	*CHFR*	rs981825385
Twin_B	13	16017183	C	T	Substitution	intergenic_variant	-	rs1346805079
Twin_B	13	16661736	C	A	Substitution	intergenic_variant	-	rs1306983302
Twin_B	13	17304667	T	A	Substitution	intergenic_variant	-	rs1456450575
Twin_B	13	17466593	C	T	Substitution	intergenic_variant	-	rs1444264382
Twin_B	13	34712768	G	A	Substitution	intergenic_variant	-	rs956638263
Twin_B	13	37492154	T	A	Substitution	intergenic_variant	-	rs5028161
Twin_B	13	51338069	C	T	Substitution	intron_variant	*SERPINE3*	rs943522065
Twin_B	13	57247644	C	T	Substitution	intergenic_variant	-	rs1015436925
Twin_B	13	64005202	A	C	Substitution	intron_variant	*LINC00355*	-
Twin_B	13	66744717	G	A	Substitution	intron_variant	*PCDH9*	rs1436271609
Twin_B	13	68771491	A	G	Substitution	intergenic_variant	-	-
Twin_B	13	81289794	T	C	Substitution	intron_variant	*AL353633.1*	rs1481888041
Twin_B	13	92237367	G	A	Substitution	downstream_gene_variant	*AL157815.1*	rs1265338638
Twin_B	13	95505939	C	G	Substitution	intron_variant	*CLDN10*	-
Twin_B	13	106932614	C	T	Substitution	intergenic_variant	-	-
Twin_B	13	109688927	C	T	Substitution	intron_variant	*AL163541.1*	-
Twin_B	13	112351281	G	A	Substitution	intergenic_variant	-	rs115643630
Twin_B	13	112451541	C	T	Substitution	intergenic_variant	-	rs1471601068
Twin_B	14	25383375	A	AT	Insertion	intergenic_variant	-	rs1443265250
Twin_B	14	28045753	A	G	Substitution	intergenic_variant	-	rs1373127559
Twin_B	14	28160448	C	G	Substitution	intergenic_variant	-	-
Twin_B	14	28481339	C	T	Substitution	intergenic_variant	-	rs987212689
Twin_B	14	28933071	A	T	Substitution	downstream_gene_variant	*LINC02327*	-
Twin_B	14	34755189	T	C	Substitution	downstream_gene_variant	*BAZ1A*	-
Twin_B	14	39719161	C	T	Substitution	intron_variant	*AL049828.1*	-
Twin_B	14	39760915	GC	G	Deletion	intron_variant	*AL049828.1*	-
Twin_B	14	40646136	G	C	Substitution	intron_variant	*AL390800.1*	-
Twin_B	14	42163357	C	T	Substitution	intergenic_variant	-	-
Twin_B	14	44806590	C	A	Substitution	intergenic_variant	-	-
Twin_B	14	45687961	C	A	Substitution	intergenic_variant	-	-
Twin_B	14	49208635	C	T	Substitution	intergenic_variant	-	-
Twin_B	14	52546562	G	A	Substitution	intron_variant	*TXNDC16*	-
Twin_B	14	55273174	G	GTT	Insertion	intron_variant	*FBXO34*	-
Twin_B	14	62950522	C	T	Substitution	missense_variant	*KCNH5*	rs587777164, CM1310653, COSV59758318, COSV59758899
Twin_B	14	76286201	T	G	Substitution	downstream_gene_variant	*AC016526.3*	-
Twin_B	14	87098315	C	T	Substitution	intergenic_variant	-	-
Twin_B	14	94965692	G	C	Substitution	upstream_gene_variant	*LINC02279*	-
Twin_B	14	96647102	C	T	Substitution	intergenic_variant	-	-

Twin_B	14	98254213	A	T	Substitution	intergenic_variant	-	rs200791071
Twin_B	14	99920248	A	G	Substitution	downstream_gene_variant	*EML1*	-
Twin_B	15	17031425	C	T	Substitution	intergenic_variant	-	rs988560630
Twin_B	15	24913380	C	T	Substitution	downstream_gene_variant	*AC090983.2*	rs995136908
Twin_B	15	25046210	A	G	Substitution	downstream_gene_variant	*SNHG14*	-
Twin_B	15	26017195	A	G	Substitution	intron_variant	*LINC02346*	-
Twin_B	15	40140978	A	G	Substitution	intergenic_variant	-	-
Twin_B	15	45848202	CAAA	C	Deletion	intron_variant	*AC068722.1*	rs1232293898
Twin_B	15	48080087	A	G	Substitution	intergenic_variant	-	-
Twin_B	15	48928081	AG	A	Deletion	intron_variant	*SHC4*	-
Twin_B	15	60120205	G	A	Substitution	regulatory_region_variant	-	-
Twin_B	15	60352764	T	C	Substitution	downstream_gene_variant	*ANXA2*	rs1242885715
Twin_B	15	71202412	A	G	Substitution	intron_variant	*THSD4*	-
Twin_B	15	72502854	C	T	Substitution	intron_variant	*ARIH1*	rs1435288541
Twin_B	15	77267388	A	G	Substitution	intron_variant	*PEAK1*	-
Twin_B	15	79562906	G	A	Substitution	upstream_gene_variant	*AC023968.2*	-
Twin_B	15	80681168	T	A	Substitution	intron_variant	*ABHD17C*	-
Twin_B	15	83132180	G	C	Substitution	3_prime_UTR_variant	*HDGFL3*	-
Twin_B	15	87983261	T	A	Substitution	intron_variant	*NTRK3*	-
Twin_B	15	95004101	T	C	Substitution	intron_variant	*AC087633.2*	-
Twin_B	16	737082	C	G	Substitution	downstream_gene_variant	*CIAO3*	-
Twin_B	16	1550273	G	A	Substitution	downstream_gene_variant	*AL031719.2*	-
Twin_B	16	5534803	T	C	Substitution	intron_variant	*RBFOX1*	-
Twin_B	16	9532674	G	T	Substitution	intergenic_variant	-	rs1341344135
Twin_B	16	18537225	T	TAG	Insertion	downstream_gene_variant	*AC136618.2*	-
Twin_B	16	19362955	T	G	Substitution	intron_variant	*AC130456.2*	rs140765053
Twin_B	16	20424714	G	A	Substitution	TF_binding_site_variant	*ACSM5*	-
Twin_B	16	22677228	G	A	Substitution	intergenic_variant	-	-
Twin_B	16	32008073	G	A	Substitution	downstream_gene_variant	*AC142381.3*	-
Twin_B	16	35787574	T	C	Substitution	upstream_gene_variant	*AC106785.2*	rs1243395959
Twin_B	16	36133454	G	A	Substitution	intergenic_variant	-	-
Twin_B	16	50321074	G	A	Substitution	downstream_gene_variant	*ADCY7*	rs372755442
Twin_B	16	51336582	G	A	Substitution	intron_variant	*AC087564.1*	rs1461056097
Twin_B	16	54256124	G	C	Substitution	intron_variant	*LINC02169*	-
Twin_B	16	57821035	G	A	Substitution	downstream_gene_variant	*AC092118.1*	-
Twin_B	16	64699930	G	A	Substitution	intergenic_variant	-	-
Twin_B	16	65902588	C	T	Substitution	intergenic_variant	-	rs115844235
Twin_B	16	67105628	T	A	Substitution	downstream_gene_variant	*CBFB*	rs1349050758
Twin_B	16	67608941	A	G	Substitution	intron_variant	*CTCF*	rs892105462
Twin_B	16	68548732	C	G	Substitution	intron_variant	*ZFP90*	rs564497116
Twin_B	16	69148663	G	A	Substitution	intron_variant	*UTP4*	rs1469117705
Twin_B	16	70802883	G	T	Substitution	3_prime_UTR_variant	*HYDIN*	-

Twin_B	16	73552032	A	T	Substitution	intron_variant	*ZFHX3*	rs562962066
Twin_B	16	77256710	G	T	Substitution	intron_variant	*ADAMTS18*	-
Twin_B	16	77493285	T	C	Substitution	intergenic_variant	-	-
Twin_B	16	82066056	G	T	Substitution	intron_variant	*HSD17B2*	-
Twin_B	16	82874338	C	T	Substitution	intron_variant	*CDH13*	-
Twin_B	16	85313584	C	A	Substitution	downstream_gene_variant	*AC092275.1*	rs1483404740
Twin_B	17	4511744	T	G	Substitution	intron_variant	*SPNS2*	-
Twin_B	17	4976602	G	T	Substitution	downstream_gene_variant	*AC004771.1*	-
Twin_B	17	9021059	G	T	Substitution	regulatory_region_variant	-	-
Twin_B	17	10363095	A	T	Substitution	intron_variant	*MYH13*	-
Twin_B	17	10978272	C	T	Substitution	intergenic_variant	-	-
Twin_B	17	14670774	C	A	Substitution	intergenic_variant	-	-
Twin_B	17	18385438	G	A	Substitution	downstream_gene_variant	*AL353997.5*	rs1682277
Twin_B	17	27983490	G	A	Substitution	intron_variant	*LINC01992*	rs778201958
Twin_B	17	30755275	A	C	Substitution	intron_variant	*SUZ12P1*	-
Twin_B	17	31863521	T	A	Substitution	splice_region_variant	*UTP6*	rs78181996
Twin_B	17	34811921	G	A	Substitution	intergenic_variant	-	rs1011328968
Twin_B	17	40381174	C	T	Substitution	non_coding_transcript_ exon_variant	*AC080112.2*	-
Twin_B	17	41094327	C	T	Substitution	downstream_gene_variant	*AC100808.1*	-
Twin_B	17	41488518	C	T	Substitution	intron_variant	*KRT36*	-
Twin_B	17	41662731	C	G	Substitution	TF_binding_site_variant	*AC130686.1*	-
Twin_B	17	52148573	C	T	Substitution	intron_variant	*CA10*	-
Twin_B	17	52202053	T	G	Substitution	intergenic_variant	-	-
Twin_B	17	56525449	C	T	Substitution	intergenic_variant	-	-
Twin_B	17	59529075	G	A	Substitution	upstream_gene_variant	*LINC01476*	-
Twin_B	17	63728030	A	G	Substitution	intron_variant	*STRADA*	-
Twin_B	17	64448232	C	A	Substitution	upstream_gene_variant	*MILR1*	-
Twin_B	17	74236263	A	G	Substitution	intron_variant	*TTYH2*	rs1373649197
Twin_B	17	74482732	T	C	Substitution	intron_variant	*CD300A*	rs9900660
Twin_B	17	79561251	G	A	Substitution	intergenic_variant	-	rs924318212
Twin_B	18	524695	A	T	Substitution	intergenic_variant	-	-
Twin_B	18	924915	C	G	Substitution	downstream_gene_variant	*LINC01904*	-
Twin_B	18	8101586	A	C	Substitution	intron_variant	*PTPRM*	-
Twin_B	18	14702966	G	A	Substitution	intron_variant	*MODIFIER*	rs1201652554
Twin_B	18	14791710	G	A	Substitution	intron_variant	*ANKRD30B*	-
Twin_B	18	15293364	T	C	Substitution	intergenic_variant	-	-
Twin_B	18	20715870	G	A	Substitution	intergenic_variant	-	rs1457573477
Twin_B	18	27402273	G	A	Substitution	downstream_gene_variant	*AC068408.1*	rs1054519887
Twin_B	18	29688544	T	C	Substitution	intergenic_variant	-	rs147589821
Twin_B	18	29768107	G	A	Substitution	intergenic_variant	-	rs1280023452
Twin_B	18	30770852	G	A	Substitution	intergenic_variant	-	rs554280292
Twin_B	18	32293060	C	T	Substitution	downstream_gene_variant	*AC015563.2*	-

Twin_B	18	33117524	G	A	Substitution	intron_variant	*CCDC178*	rs138071520
Twin_B	18	33505461	T	C	Substitution	intergenic_variant	-	-
Twin_B	18	43720938	CA	C	Deletion	intergenic_variant	-	-
Twin_B	18	52406485	T	C	Substitution	intron_variant	*DCC*	-
Twin_B	18	56544081	T	C	Substitution	intergenic_variant	-	rs1341586653
Twin_B	18	58043724	G	A	Substitution	regulatory_region_variant	-	-
Twin_B	18	61155354	C	T	Substitution	intergenic_variant	-	-
Twin_B	18	61706959	G	A	Substitution	intron_variant	*AC105094.2*	-
Twin_B	18	62562373	C	A	Substitution	downstream_gene_variant	*ZCCHC2*	-
Twin_B	18	63887009	AG	A	Deletion	intron_variant	*SERPINB2*	-
Twin_B	18	67455918	G	A	Substitution	intergenic_variant	-	-
Twin_B	18	74237595	C	T	Substitution	intron_variant	*AC090398.1*	-
Twin_B	18	75984267	C	G	Substitution	intergenic_variant	-	-
Twin_B	19	8086471	T	A	Substitution	downstream_gene_variant	*FBN3*	rs113759974
Twin_B	19	8183739	C	A	Substitution	intergenic_variant	-	rs946588717
Twin_B	19	12943750	AGCAGAGGCTTAAGGAGGAGGAAGAAGACAAGAAACGCAAAGAGGAGGAGGAG	A	Deletion	frameshift_variant	*CALR*	rs1555760738
Twin_B	19	16774565	G	A	Substitution	intron_variant	*NWD1*	rs577537244
Twin_B	19	17247444	C	A	Substitution	downstream_gene_variant	*USHBP1*	-
Twin_B	19	19549515	C	T	Substitution	downstream_gene_variant	*CILP2*	-
Twin_B	19	22564447	G	A	Substitution	intergenic_variant	-	rs146882932
Twin_B	19	22624713	TG	T	Deletion	downstream_gene_variant	*AC011467.2*	rs1285085532
Twin_B	19	27496424	T	C	Substitution	intergenic_variant	-	rs1568343244
Twin_B	19	28110861	A	C	Substitution	intron_variant	*AC010511.1*	-
Twin_B	19	31656627	G	A	Substitution	upstream_gene_variant	*RNA5SP471*	-
Twin_B	19	31931918	G	C	Substitution	intron_variant	*LINC01837*	-
Twin_B	19	38958665	C	G	Substitution	intron_variant	*FBXO17*	-
Twin_B	19	41492820	G	A	Substitution	downstream_gene_variant	*PCAT19*	-
Twin_B	19	47920579	G	A	Substitution	TF_binding_site_variant	-	rs367708441
Twin_B	19	53377680	A	G	Substitution	downstream_gene_variant	*ZNF525*	-
Twin_B	19	55277604	C	G	Substitution	downstream_gene_variant	*HSPBP1*	-
Twin_B	20	173236	G	A	Substitution	intergenic_variant	-	rs1034386228
Twin_B	20	1061518	G	A	Substitution	intron_variant	*AL110114.1*	-
Twin_B	20	12995529	T	C	Substitution	intron_variant	*LINC01723*	rs1438512520
Twin_B	20	14336990	T	C	Substitution	intron_variant	*FLRT3*	-
Twin_B	20	21629260	C	T	Substitution	intron_variant	*LINC01726*	rs540343176
Twin_B	20	22689135	A	T	Substitution	intron_variant	*AL158175.1*	-
Twin_B	20	28497717	AG	A	Deletion	intergenic_variant	-	rs1434446279
Twin_B	20	29525288	A	AC	Insertion	intergenic_variant	-	rs1188254666
Twin_B	20	30212896	T	G	Substitution	downstream_gene_variant	*CFTRP3*	-

Twin_B	20	30755746	C	T	Substitution	intergenic_variant	-	-
Twin_B	20	39854921	G	A	Substitution	intergenic_variant	-	rs1346211420
Twin_B	20	48547263	G	A	Substitution	intergenic_variant	-	-
Twin_B	20	50715766	T	A	Substitution	intergenic_variant	-	-
Twin_B	20	50895064	C	T	Substitution	intron_variant	*ADNP*	-
Twin_B	20	52629042	C	G	Substitution	intron_variant	*LINC01524*	-
Twin_B	20	64283610	C	G	Substitution	intron_variant	*PCMTD2*	rs1428268334
Twin_B	21	8020747	T	A	Substitution	intergenic_variant	-	rs1443418402
Twin_B	21	9928024	G	A	Substitution	intergenic_variant	-	rs1342179447
Twin_B	21	14455201	C	A	Substitution	intergenic_variant	-	-
Twin_B	21	24993236	A	G	Substitution	intron_variant	*LINC01692*	-
Twin_B	21	36182754	A	G	Substitution	intron_variant	*DOP1B*	-
Twin_B	21	40180743	A	T	Substitution	intron_variant	*DSCAM*	-
Twin_B	21	40558302	G	T	Substitution	intron_variant	*DSCAM*	-
Twin_B	21	46037210	G	A	Substitution	non_coding_transcript_ exon_variant	*AP001476.1*	-
Twin_B	22	11356944	CT	C	Deletion	intergenic_variant	-	rs1322963034
Twin_B	22	16847213	CTTAA	C	Deletion	downstream_gene_variant	*AC007064.4*	-
Twin_B	22	28259506	G	A	Substitution	intron_variant	*TTC28*	-
Twin_B	22	30635421	T	C	Substitution	TF_binding_site_variant	-	-
Twin_B	22	32657960	T	G	Substitution	intron_variant	*SYN3*	-
Twin_B	22	34618472	G	A	Substitution	intergenic_variant	-	rs867876389
Twin_B	22	34793591	T	C	Substitution	intron_variant	*LINC02885*	-
Twin_B	22	36709756	C	T	Substitution	intron_variant	*AL049749.1*	rs567131721
Twin_B	22	37961231	A	G	Substitution	intron_variant	*POLR2F*	-
Twin_B	22	42966759	C	A	Substitution	intron_variant	*PACSIN2*	-
Twin_B	22	43588922	C	T	Substitution	intron_variant	*EFCAB6*	rs567321760
Twin_B	22	48568894	G	C	Substitution	intron_variant	*TAFA5*	-
Twin_B	X	1604020	G	T	Substitution	downstream_gene_variant	*AKAP17A*	rs560737268
Twin_B	X	12284898	G	A	Substitution	intron_variant	*FRMPD4*	COSV66220435
Twin_B	X	17501537	C	A	Substitution	intron_variant	*NHS*	-
Twin_B	X	19248964	C	A	Substitution	intergenic_variant	-	-
Twin_B	X	24411967	C	T	Substitution	intergenic_variant	-	-
Twin_B	X	35556794	T	C	Substitution	intergenic_variant	-	-
Twin_B	X	35907670	T	C	Substitution	intergenic_variant	-	-
Twin_B	X	62714059	C	T	Substitution	intergenic_variant	-	rs143334744
Twin_B	X	70098264	T	A	Substitution	intergenic_variant	-	-
Twin_B	X	73335262	T	C	Substitution	intergenic_variant	-	-
Twin_B	X	78738428	T	A	Substitution	intergenic_variant	-	-
Twin_B	X	80869548	G	C	Substitution	intergenic_variant	-	-
Twin_B	X	87003014	A	G	Substitution	intergenic_variant	-	-
Twin_B	X	92949595	G	A	Substitution	intergenic_variant	-	-
Twin_B	X	107445958	C	T	Substitution	intergenic_variant	-	rs1441643081

Twin_B	X	108369773	T	A	Substitution	intron_variant	*COL4A6*	-
Twin_B	X	113433231	T	G	Substitution	intergenic_variant	-	-
Twin_B	X	115105220	C	T	Substitution	intergenic_variant	-	-
Twin_B	X	117525429	C	A	Substitution	intergenic_variant	-	-

Note: Gene annotation not provided for intergenic variants, regulatory region variants and TF binding site variants. Catalogue corresponds to the high-confidence call set prior to vafCorrect genotyping and filtering (see Methods - *Variant calling*). Gene names are provided in italics in accordance with the current HUGO Gene Nomenclature Committee (HGNC) guidelines.[50]
*An additional variant from the myeloid-gene panel is also included for Twin A (marked with an asterisk). This is a variant detected in the targeted myeloid-gene panel sequencing but with no high-confidence support from whole genome sequencing data; therefore, it was excluded from the downstream analysis.

Supplementary Table 2. Catalogue of somatic structural variants in twin A and twin B

Individual	SV_class	SV_length	Chr1	Pos1	Chr2	Pos2
Twin_A	tandem_duplication	165127	11	54384289	11	54549416
Twin_A	tandem_duplication	71117	12	11054568	12	11125685
Twin_A	tandem_duplication	75902	20	23727447	20	23803349
Twin_A	translocation	.	6	[chr6:50867003[G	12	[chr12:93869517[C
Twin_A	translocation	.	3	]chr3:11573465]A	15	T[chr15:78040845[
Twin_B	tandem_duplication	272076	11	26184499	11	26456575
Twin_B	deletion	397816	11	48727000	11	55124816
Twin_B	translocation	.	6	[chr6:43581762[C	19	[chr19:41643986[C
Twin_B	deletion	604488	2	92998101	1	93602589
Twin_B	translocation	.	5	G]chr5:248313]	5	T]chr5:1579393]

Supplementary Table 3. Summary of somatic mutations shared between twin A and twin B

#	Chr	Pos	Ref	Alt	Mutation_type	Annotation	Shared_annotation	Gene	Existing_variation	CCF_in_Twin_A	CCF_in_Twin_B	Used_in_Validation
1	1	237523679	G	A	Substitution	intron_variant	High-confidence call set; vafCorrect genotyping	*RYR2*	rs1165384474	0.93	0.54	Yes
2	2	236024598	A	G	Substitution	intron_variant	High-confidence call set; vafCorrect genotyping	*AGAP1*	-	1.05	0.99	Yes
3	3	9646697	T	A	Substitution	upstream_gene_variant	High-confidence call set; vafCorrect genotyping	*MTMR14*	rs1001727401	0.93	1.06	No
4	3	187366417	G	A	Substitution	upstream_gene_variant	High-confidence call set; vafCorrect genotyping	*RTP4*	-	1.01	1.16	Yes
5	5	18474168	C	T	Substitution	intergenic_variant	High-confidence call set; vafCorrect genotyping	-	-	1.17	0.92	No
6	7	54587046	C	A	Substitution	intergenic_variant	High-confidence call set; vafCorrect genotyping	-	-	0.89	0.37	No
7	10	103273122	G	A	Substitution	upstream_gene_variant	High-confidence call set	*INA*	rs1286474689	0.39	0.57	No
8	16	67608941	A	G	Substitution	intron_variant	High-confidence call set	*CTCF*	rs892105462	0.97	0.25	No
9	16	85313584	C	A	Substitution	downstream_gene_variant	High-confidence call set; vafCorrect genotyping	*AC092275.1*	rs1483404740	1.03	1.01	Yes
10	19	12943750	AGCAGAGGCTTAGGAGGAGGAAGAAGACAAGAAACGCAAAGAGGAGGAGGAG	A	Deletion	frameshift_variant	High-confidence call set	*CALR*	rs1555760738	0.69*	1.07	Yes
11	18	9601220	A	G	Substitution	intron_variant	vafCorrect genotyping	*PPP4R1*	rs982592192, COSV53280449	0.49	0.33	No
12	2	93865725	G	C	Substitution	intergenic_variant	vafCorrect genotyping	-	-	2	1.4	No
13	4	119161162	A	C	Substitution	intron_variant	vafCorrect genotyping	*MYOZ2*	-	0.75	0.2	No
14	4	16908350	G	T	Substitution	intergenic_variant; regulatory_region_variant	vafCorrect genotyping	-	rs750655685	0.79	1.06	No
15	5	130265666	C	T	Substitution	intergenic_variant	vafCorrect genotyping	-	rs62391477	0.61	0.68	No
16	7	71219697	C	T	Substitution	intron_variant	vafCorrect genotyping	*GALNT17*	-	0.77	0.82	No
17	1	93828702	C	CT	Insertion	intron_variant; regulatory_region_variant	vafCorrect genotyping	*BCAR3*	rs969811086	0.654	0.31	No
18	2	193562677	CGT	C	Deletion	intergenic_variant	vafCorrect genotyping	-	rs59053823	0.53	0.26	No
19	4	26343555	G	GT	Insertion	upstream_gene_variant	vafCorrect genotyping	*RBPJ*	rs969811086	0.43	0.26	No
20	4	61895466	AAAT	A	Deletion	upstream_gene_variant	vafCorrect genotyping	*ADGRL3*	rs969811086	0.62	0.26	No
21	6	7238595	C	CT	Insertion	intron_variant	vafCorrect genotyping	*RREB1*	rs796560101	0.41	0.28	No
22	7	43378810	C	CA	Insertion	intron_variant	vafCorrect genotyping	*HECW1*	rs202007736	0.5	0.23	No
23	8	17691704	G	GT	Insertion	regulatory_region_variant	vafCorrect genotyping	-	rs200014137	0.3	0.32	No
24	9	67205531	TG	T	Deletion	intron_variant	vafCorrect genotyping	*CNTNAP3P2*	rs368975415	0.3	0.5	No

Note: Gene annotation not provided for intergenic variants. CCF, cancer cell fraction, i.e., estimate of the fraction of tumor cells that carry the mutation. Somatic shared variants from the 'High-confidence call set' are reported in both Twin A and Twin B in Supplementary Table 1. Somatic shared variants identified after vafCorrect genotyping are reported in either Twin A or Twin B in Supplementary Table 1 (see Methods - *Variant calling* and *Mutation clustering*). Gene names are provided in italics in accordance with the current HUGO Gene Nomenclature Committee (HGNC) guidelines.[50] *95% confidence interval for *CALR* CCF: 0.42-1.

Supplementary Table 4. Summary of non-silent coding variants in twin A and twin B

Individual	**Chr**	**Pos**	**Ref**	**Alt**	**Mutation_type**	**Annotation**	**Impact**	**Gene**	**Existing_variation**	**Clinical_significance**	**CADD_PHRED**
Twin_A	1	53327841	CA	C	Deletion	frameshift_variant	HIGH	*LRP8*	rs761955852, COSV60099910	-	22
Twin_A	4	105234449	TA	T	Deletion	frameshift_variant	HIGH	*TET2*	-	-	-
Twin_A	4	105259633*	G	A	Substitution	missense_variant	MODERATE	*TET2*	COSV54404036	pathogenic	27.2
Twin_A	11	17634218	C	T	Substitution	stop_gained	HIGH	*OTOG*	rs866476223	pathogenic	40
Twin_A	19	12943750	AGCAGAGGCTTAAGGAGGAGGAAGAAGACAAGAAACGCAAAGAGGAGGAGGAG	A	Deletion	frameshift_variant	HIGH	*CALR*	rs1555760738	pathogenic	35
Twin_B	9	131860557	T	A	Substitution	missense_variant	MODERATE	*MED27*			31
Twin_B	10	24984824	G	A	Substitution	missense_variant	MODERATE	*ENKUR*	rs200773323, COSV58633510	-	25.9
Twin_B	12	88071791	G	A	Substitution	missense_variant	MODERATE	*CEP290*	rs761572735	-	25.1
Twin_B	14	62950522	C	T	Substitution	missense_variant	MODERATE	*KCNH5*	rs587777164, CM1310653, COSV59758318, COSV59758899	uncertain_significance, pathogenic	28
Twin_B	19	12943750	AGCAGAGGCTTAAGGAGGAGGAAGAAGACAAGAAACGCAAAGAGGAGGAGGAG	A	Deletion	frameshift_variant	HIGH	*CALR*	rs1555760738	pathogenic	35

Note: Gene names are provided in italics in accordance with the current HUGO Gene Nomenclature Committee (HGNC) guidelines.[50] *An additional variant from the myeloid-gene panel is also included for Twin A (marked with an asterisk). This is a variant detected in the targeted myeloid-gene panel sequencing but with no high-confidence support from whole genome sequencing data; therefore, it was excluded from the downstream analysis.

Supplementary Table 5. Data for time to the most recent common ancestor (MRCA) estimation

(a) Using N[C>T]pG mutation count data

	mean	**se_mean**	**SD**	**95%_CI_lower_ confidence _limit**	**95%_CI_upper_ confidence _limit**	**n_eff**	**Rhat**
t_{MRCA}	0.95	0.00	0.54	0.20	2.25	287761.60	1.0000
t[1]	2.80	0.00	0.15	2.453	2.99	211004.80	1.0000
t[2]	31.87	0.01	3.37	25.329	38.16	188785.40	1.0000
rate	36.69	0.00	1.93	32.035	39.30	294264.00	1.0000
lp__	732.06	0.01	1.64	727.945	734.12	106813.70	1.0000

Bridge sampling estimate of the log marginal likelihood: -10.93478; Relative Mean-Squared Error: 1.756122e-06.

(b) Using lineage-restricted SNV count data

	mean	**se_mean**	**SD**	**95%_CI_lower_ confidence _limit**	**95%_CI_upper_ confidence _limit**	**n_eff**	**Rhat**
t_{MRCA}	2.16	0.00	0.98	0.61	4.37	78069.74	1.0000
t[1]	4.12	0.01	2.06	2.427	9.95	44277.66	1.0001
t[2]	25.22	0.03	7.53	9.059	36.49	51312.44	1.0000
rate	24.97	0.03	7.50	8.952	36.41	51542.02	1.0000
lp__	644.68	0.01	1.65	640.584	646.79	77872.47	1.0001

Bridge sampling estimate of the log marginal likelihood: -9.01966; Relative Mean-Squared Error: 9.335533e-06.

Note: t_{MRCA} is an estimate of time (years) between fertilization and the branch point of MPN lineages in twin A and B. t[1] and t[2] are estimates of the time (years) to the MRCA of cells in twin A and twin B. lp__ corresponds to the logarithm of the (unnormalized) posterior density as calculated by Stan. n_eff is a crude measure of effective sample size and 'Rhat' is the potential scale reduction factor on split chains (Rhat=1 at convergence). se_mean is the estimated standard error of the mean of the simulations. rate is the (a) N[C>T]pG (b) clonal mutation rate per genome per year. SNV, single-nucleotide variant.

Supplementary Table 6. Summary of the shared somatic variants and unique somatic variants for each twin, used in whole genome sequencing validation at the single-cell level

Variant studied	Chr	Pos	Ref	Alt	Mutation_type	Annotation	Nearest_gene	Existing_variation	VAF_Twin_A	VAF_Twin_B
somatic_shared	19	12943750	AGCAGAGGCTTAAGGAGGAGGAAGAAGACAAGAAACGCAAAGAGGAGGAGGAG	A	Deletion	frameshift_variant	*CALR*	rs1555760738	_	_
somatic_shared_1	1	237523679	G	A	Substitution	intron_variant	*RYR2*	rs1165384474	0.32	
somatic_shared_2	2	236024598	A	G	Substitution	intron_variant	*AGAP1*	-	0.41	
somatic_shared_3	3	187366417	G	A	Substitution	upstream_gene_variant		-	0.39	
somatic_shared_4	16	85313584	C	A	Substitution	downstream_gene_variant	*AC092275.1*	rs1483404740	0.36	
somatic_unique_Twin_A_1	10	18976904	C	T	Substitution	Intergenic_variant		rs181225799	0.31	NA
somatic_unique_Twin_A_2	11	78991748	C	T	Substitution	intron_variant	*TENM4*	.	0.29	NA
somatic_unique_Twin_B_1	7	116155279	G	C	Substitution	intergenic_variant		rs1461424202	NA	0.19
somatic_unique_Twin_B_2	8	20863668	T	A	Substitution	intergenic_variant		-	NA	0.23

Note: Gene names are provided in italics in accordance with the current HUGO Gene Nomenclature Committee (HGNC) guidelines.[50] VAF, variant allele frequency.

Supplementary Table 7. Overview of patient clinical information for the JAK2V617F-mutant myeloproliferative neoplasm cohort

Sample	**Gender**	**MPN Dx**	**Age at Dx (years)**	**Driver mutation**	**Driver mutation VAF at Dx (%)**	**BMAT**	**Cytogenetics**	**NGS myeloid-gene panel**	***JAK2V617F* detection on DBS (Y/N)**
DBS_1	Female	SM	31.9	*KITD816V*	NK	SM	NA	Nil else	N
DBS_2	Male	PV	28.9	*JAK2V617F*	16.0	NA	NA	NA	N
DBS_3	Female	PV	32.7	*JAK2V617F*	65.0	PV	Normal; 46,XX[20]	Nil else	N
DBS_4	Male	PV	34.1	*JAK2V617F*	28.0	NA	NA	Nil else	Y

Note: Gene names are provided in italics in accordance with the current HUGO Gene Nomenclature Committee (HGNC) guidelines.[50] BMAT, bone marrow aspirate and trephine; DBS, neonatal dried blood spot; Dx, diagnosis; MPN, myeloproliferative neoplasm; NGS, next-generation sequencing; NK, not known; PV, polycythemia vera; SM, systemic mastocytosis; VAF, variant allele frequency.

Supplementary Table 8. Flow cytometry and cell sorting panels used in granulocyte, T cell and HSPC analysis and sorting

(a) Granulocyte panel

Antigen	Clone	Conjugate	Dilution	Company	Catalogue_number
CD3	SK7	FITC	5:100	BD Biosciences§	345763
CD34	4HI1	APC-eFluor® 780	2:100	eBioscience™#	47-0349-42
CD71	M-A712	Alexa Fluor® 700	5:100	BD Biosciences§	563769
CD19	HIB19	V450	5:100	BD Biosciences§	560354
7AAD (7-Aminoactinomycin D)			1:100*	Cayman Chemical†	11397
CD11b	ICRF44	APC	5:100	eBioscience™#	17-0118-42
CD14	61D3	APC	5:100	eBioscience™#	17-0149-42
CD33	WM53	PE	5:100	BioLegend‡	303404

(b) T cell panel

Antigen	Clone	Conjugate	Dilution	Company	Catalogue_number
CD3	SK7	FITC	5:100	BD Biosciences§	345763
CD4	SK3	APC	5:100	BD Pharmingen™§	565994
DAPI (4',6-Diamidino-2-Phenylindole, Dilactate)			1:100*	Invitrogen™#	D3571
CD19	HIB19	APC-Cyanine7	5:100	BioLegend‡	302218
CD11b	ICRF44	PE-Cyanine5	5:100	BioLegend‡	301308
CD14	61D3	PE-Cyanine5	5:100	eBioscience™#	15-0149-42

(c) HSPC panel

Antigen	Clone	Conjugate	Dilution	Company	Catalogue_number
CD34	4HI1	APC-eFluor® 780	0.66:100	eBioscience™#	47-0349-42
CD38	HIT2	PE-Texas Red®	4.66:100	Invitrogen™#	MHCD3817
CD45RA	HI100	PE	0.66:100	BioLegend‡	304108
CD90	5E10	Brilliant Violet 421™	3.33:100	BioLegend‡	328122
CD123	6H6	PE-Cyanine7	1.66:100	BioLegend‡	306010
7AAD (7-Aminoactinomycin D)			1:100*	Cayman Chemical†	11397
Lineage mix			21.66:100		
CD8a^	RPA-T8	FITC	1:100 of Lineage mix	BioLegend‡	301006
CD10^	HI10a	FITC	3.33:100 of Lineage mix	BioLegend‡	312208
CD20^	2H7	FITC	0.66:100 of Lineage mix	BioLegend‡	302304
CD66b^	G10F5	FITC	6.66:100 of Lineage mix	BioLegend‡	305104
CD127^	eBioRDR5	FITC	3.33:100 of Lineage mix	eBioscience™#	11-1278-52
Human Hematopoietic Lineage Cocktail (CD2, CD3, CD14, CD16, CD56, CD235a) ^	RPA-2.10, OKT3, 61D3, CB16, HIB19, TULY56, HIR2	FITC	6.66:100 of Lineage mix	eBioscience™#	22-7778-72

*Viability stains were previously diluted 1:200 for 7-AAD and 1:100 for DAPI from their 5mg/ml stock solutions. ^Lineage mix. §Becton, Dickinson and Company, Franklin Lakes, US-NJ; #Thermo Fisher Scientific Inc., Waltham, US-MA; †Cayman Chemical Company, Ann Arbor, US-MI; ‡BioLegend, San Diego, US-CA. HSPC, hematopoietic stem and progenitor cell.

Supplementary Table 9. Catalogue of oligonucleotides used in the polymerase chain reaction assays

Target nucleotide(s)	Nearest gene	Forward_primer_sequence (5' → 3')	Reverse_primer_sequence (5' → 3')	Probe_sequence	Product size (bp)	Company
chr19:12943750-1294801	*CALR*	GCAGCAGAGAAACAAATG	GCCTCTCTACAGCTCGTCCTT		207	Invitrogen™
chr4:105234449	*TET2*	ACGTAACTTCGGGGTAAGCC	TCCACGGAAGAGGCAGAAAC		291	Invitrogen™
chr4:105259633	*TET2*	tgtgtggttatgccacagctt	acatcaggaagtaaacaaacCTCT		312	Invitrogen™
chr1:237523679	*RYR2*	ccagctgggagagaatatttgtga	ggagctgctaaaggttattctgc		1300	Invitrogen™
chr2:236024598	*AGAP1*	ttgtccttttccccagaccc	catgaatccgggctgtcaaac		259	Invitrogen™
chr3:187366417	_	gaatttaagccccaggaggaca	ccagtgtcagaggaaccgtag		268	Invitrogen™
chr16:85313584	*AC092275.1*	tccagcgtgattccgtgttt	ttctgaccgcccagactttg		346	Invitrogen™
chr10:18976904	_	aactcaacccttgtccccatc	cttttccctcccactgacaca		213	Invitrogen™
chr11:78991748	*TENM4*	gcacttgttgaatgcttgtgc	ggtctgggcccacatttctt		390	Invitrogen™
chr7:116155279	_	ttctagcccctgctatgcac	ggcccaatggcacagtaaga		452	Invitrogen™
chr8:20863668	_	gccttcgattggggctgttta	aaggggttctcttccagcaaa		441	Invitrogen™
chr9:5073770	*JAK2*	aggcttacacaggggtttcc	ttgtttgggcattgtaaccttc		505	Life Technologies™
chr9:5073770	*JAK2*	GCTTTCTCACAAGCATTTG	gcattagaaagcctgtagtttta		84	Thermo Fisher Scientific
chr9:5073770(G)	*JAK2*			[HEX]TCGTCTCCACAGACACATACTCCATGAGACGA[BHQ1]		Merck
chr9:5073770(T)	*JAK2*			[6FAM]TCGTCTCCACAGAAACATACTCCATGAGACGA[BHQ1]		Merck

Note: All target coordinates according to the Genome Reference Consortium Human Build 38 (GRCh38). All primers were checked against RefSeq and human genome assembly databases using NCBI Primer-BLAST® (National Library of Medicine, Bethesda, US-MD) as well as SnapGene® Viewer, v5.3 (GSL Biotech LLC, Chicago, US-IL). The ddPCR assay probes were labelled with HEX and FAM for wild-type *JAK2* and the NM_004972.3[JAK2]:c.1849G>T p.V617F, respectively. Gene names are provided in italics in accordance with the current HUGO Gene Nomenclature Committee guidelines.[50] Uppercase letters are used for exonic regions, while lowercase letters represent intronic regions. Invitrogen™, Life Technologies™, Thermo Fisher Scientific: Thermo Fisher Scientific, Waltham, US-MA; Merck: Merck Group, Darmstadt, DE. ddPCR, droplet digital polymerase chain reaction.

Supplementary Table 10. Catalogue of the genes targeted in the next-generation sequencing panel

Gene	**RefSeq_accession_number**
ABL1	NM_005157; NM_007313
ANKRD26	NM_001256053; NM_014915
ASXL1	NM_015338
ATRX	NM_000489
BCOR	NM_001123383; NM_017745
BCORL1	NM_021946; NM_001184772
BRAF	NM_004333
BRCC3	NM_024332
CALR	NM_004343
CBL	NM_005188
CBLB	NM_170662
CBLC	NM_012116
CDKN2A	NM_001195132; NM_000077; NM_058195
CEBPA	NM_004364
CHEK2	NM_001005735; NM_007194
CSF3R	NM_156039
CUX1	NM_001202543; NM_181552
DDX41	NM_016222
DNMT3A	NM_022552; NM_175629
ETV6	NM_001987
EZH2	NM_004456
FBXW7	NM_033632; NM_018315
FLT3	NM_004119
GATA1	NM_002049
GATA2	NM_032638; NM_001145661
GNAS	NM_000516; NM_001077490
HRAS	NM_005343; NM_001130442
IDH1	NM_005896; NM_001282386; NM_001282387
IDH2	NM_002168
IKZF1	NM_001220765; NM_006060
JAK2	NM_004972; NM_001322194; NM_001322195; NM_001322196
JAK3	NM_000215
KDM6A	NM_021140
KIT	NM_000222
KRAS	NM_033360
KMT2A	NM_001197104; NM_005933
MPL	NM_005373
MYD88	NM_001172567

NF1	NM_000267
NFE2	NM_001136023; NM_001261461; NM_006163
NOTCH1	NM_017617
NPM1	NM_002520; NM_001355006
NRAS	NM_002524
PDGFRA	NM_006206
PHF6	NM_032458; NM_001015877
PPM1D	NM_003620
PTEN	NM_000314
PTPN11	NM_002834
RAD21	NM_006265
RUNX1	NM_001754
SETBP1	NM_015559
SETD2	NM_014159
SETDB1	NM_001145415
SF3B1	NM_012433
SH2B3	NM_005475
SMC1A	NM_006306
SMC3	NM_005445
SRSF2	NM_001195427; NM_003016
STAG1	NM_005862
STAG2	NM_001042749; NM_006603; NM_001282418
STAT3	NM_139276
STAT5B	NM_012448
TET2	NM_001127208
TP53	NM_000546; NM_001126112
U2AF1	NM_001025203
WT1	NM_024426
ZRSR2	NM_005089

Note: Gene names are provided in italics in accordance with the current HUGO Gene Nomenclature Committee (HGNC) guidelines.[50]

Supplementary Table 11. Summary of multidimensional mutation clustering

(a) Summary of mutation assignments

Cluster_no	**CCF_in_Twin_A**	**CCF_in_Twin_B**	**Estimated_no_of_mutations**	**No_of_mutations_assigned**
1	0.000	0.315	452.348	452
2	0.359	0.000	425.794	426
3	0.898	1.003	9.859	10

(b) Individual mutation assignments

Most_likely_cluster	**Chr**	**Mutation_start**	**Twin_A_Subclonal_Fraction**	**Twin_B_Subclonal_Fraction**
1	1	104033383	0.000	0.300
2	1	106288464	0.254	0.000
1	1	110190300	0.000	0.674
1	1	110738023	0.000	0.434
2	1	111854251	0.167	0.000
2	1	112723366	0.444	0.000
1	1	114307529	0.000	0.271
1	1	12823937	0.000	0.271
1	1	143898748	0.000	0.643
1	1	147277076	0.000	0.362
2	1	152011365	0.291	0.000
2	1	152568644	0.444	0.000
2	1	155442289	0.342	0.044
2	1	155643901	0.838	0.000
1	1	157062690	0.000	0.251
1	1	158329018	0.000	0.643
1	1	159742120	0.000	0.334
2	1	164325871	0.392	0.000
1	1	165976313	0.000	0.181
1	1	166242296	0.000	0.322
2	1	172874706	0.296	0.000
2	1	173897024	0.272	0.000
1	1	175165067	0.000	0.241
1	1	176214397	0.000	0.470
1	1	177128801	0.000	0.478
2	1	17778871	0.190	0.000
2	1	178136491	0.747	0.000
2	1	185587702	0.644	0.000
2	1	185717034	0.533	0.000
1	1	187326523	0.000	0.217
2	1	188790583	0.491	0.000
1	1	190010459	0.000	0.507

2	1	19011134	0.508	0.000
2	1	190678569	0.503	0.000
2	1	191963370	0.471	0.000
1	1	194805882	0.000	0.329
1	1	1948293	0.000	0.592
2	1	196771008	0.667	0.000
2	1	199078846	0.368	0.101
1	1	211364253	0.000	0.247
1	1	21195179	0.000	0.931
1	1	216808720	0.000	0.310
2	1	218758531	0.410	0.000
1	1	228759153	0.000	0.724
1	1	231661954	0.000	0.310
1	1	239287292	0.000	0.140
1	1	239790569	0.000	0.354
3	1	54128162	0.966	0.909
1	1	57203495	0.000	0.322
2	1	58846527	0.500	0.000
1	1	68690432	0.000	0.869
2	1	81244570	0.339	0.000
2	1	82141981	0.267	0.043
1	1	90494264	0.000	0.661
2	1	91064439	1.191	0.000
2	1	91598893	0.410	0.000
2	1	93828702	0.654	0.310
1	2	103642003	0.000	0.194
1	2	104572208	0.000	0.078
2	2	105464070	0.291	0.000
1	2	110152812	0.000	0.350
1	2	112972342	0.000	0.212
2	2	113030007	0.632	0.000
1	2	113360949	0.000	0.000
1	2	114347202	0.000	0.000
2	2	11568288	0.182	0.263
1	2	122468457	0.000	0.000
2	2	122548088	0.333	0.496
2	2	124139117	0.288	0.000
2	2	12436887	0.381	0.207
1	2	124707645	0.000	0.000
1	2	125662877	0.000	0.217
2	2	126802154	0.453	0.000
2	2	13111603	0.427	0.000

2	2	135703624	0.308	0.217
1	2	136809746	0.000	0.601
1	2	139215973	0.000	0.651
2	2	139236448	0.356	0.290
1	2	139897503	0.000	0.000
2	2	140606025	0.522	0.000
2	2	142582383	0.140	0.362
1	2	142622241	0.000	0.142
2	2	145569408	0.381	0.217
2	2	145603291	0.200	0.371
1	2	147580489	0.000	0.000
2	2	148242718	0.444	0.496
1	2	14870316	0.000	0.000
2	2	153181357	0.533	0.383
1	2	156749565	0.000	0.231
1	2	158735231	0.000	0.000
2	2	163100502	0.395	0.054
2	2	167809460	0.281	0.416
2	2	174496556	0.471	0.000
2	2	175727129	0.556	0.000
2	2	17632861	0.054	0.000
1	2	17816780	0.000	0.189
2	2	181542157	0.222	0.000
1	2	181754253	0.000	0.290
2	2	184966	0.519	0.000
1	2	186809029	0.000	0.000
1	2	187978655	0.000	0.434
1	2	190310023	0.000	0.290
2	2	193562677	0.533	0.117
2	2	19486986	0.494	0.000
2	2	196497946	0.344	0.000
1	2	197588962	0.000	0.354
2	2	199505098	0.296	0.449
2	2	199984230	0.317	0.000
2	2	200975338	0.333	0.434
1	2	202941148	0.000	0.000
1	2	214886582	0.000	0.695
1	2	215762883	0.000	0.062
1	2	21701231	0.000	0.000
2	2	217649629	0.533	0.620
1	2	22021980	0.000	0.000
1	2	220248897	0.000	0.455

2	2	221924308	0.406	0.248
1	2	222991555	0.000	0.197
1	2	22585137	0.000	0.465
1	2	22585139	0.000	0.571
1	2	226321782	0.000	0.000
2	2	227692889	0.325	0.000
1	2	22994571	0.000	0.462
2	2	235048421	0.421	0.395
2	2	235142193	0.133	0.347
3	2	236024598	1.259	0.597
2	2	236165626	0.417	0.494
1	2	238340846	0.000	0.265
1	2	238788248	0.000	0.000
1	2	24019295	0.000	0.000
2	2	24266260	0.533	0.176
2	2	25819904	0.351	0.698
1	2	27314362	0.000	0.300
1	2	28287298	0.000	0.000
1	2	29298533	0.000	0.000
2	2	2982012	0.444	0.000
2	2	29907671	0.184	0.400
2	2	31671794	0.320	0.000
1	2	33204005	0.000	0.000
1	2	34609950	0.000	0.229
2	2	35209815	0.222	0.261
1	2	39543295	0.000	0.000
1	2	41851787	0.000	0.338
2	2	5026216	0.454	0.000
1	2	5809965	0.000	0.000
1	2	76343534	0.000	0.000
1	2	77138659	0.000	0.000
1	2	77305966	0.000	0.000
2	2	78265814	0.356	0.000
1	2	7937210	0.000	0.106
1	2	79741961	0.000	0.000
1	2	84976628	0.000	0.606
2	2	90026936	0.866	0.362
2	2	98022727	0.364	0.302
1	3	101873401	0.000	0.000
2	3	103475498	0.808	0.253
2	3	107699193	0.571	0.511
1	3	107880323	0.000	0.000

1	3	111393544	0.000	0.371
2	3	118298534	0.296	0.000
1	3	120551312	0.000	0.494
1	3	124318634	0.000	0.000
2	3	1259968	0.390	0.308
2	3	126102405	0.356	0.368
1	3	127184194	0.000	0.064
1	3	146968300	0.000	0.000
1	3	148123392	0.000	0.465
1	3	150872501	0.000	0.352
1	3	152516100	0.000	0.000
2	3	152974761	0.392	0.111
2	3	153068733	0.491	0.339
2	3	153706759	0.340	0.217
1	3	157178549	0.000	0.390
2	3	160115640	0.578	0.310
1	3	169022850	0.000	0.225
1	3	182077482	0.000	0.334
3	3	187366417	1.333	0.000
1	3	192580552	0.000	0.000
1	3	197965767	0.000	0.000
2	3	26440532	0.267	0.000
2	3	29763656	0.216	0.339
2	3	32019778	0.342	0.420
2	3	32526653	0.610	0.000
1	3	39756857	0.000	0.229
1	3	50879771	0.000	0.000
1	3	52975648	0.000	0.140
1	3	54092594	0.000	0.000
1	3	57095586	0.000	0.140
1	3	59401686	0.000	0.000
2	3	59893891	0.242	0.000
1	3	62217141	0.000	0.000
1	3	6268058	0.000	0.310
2	3	65074311	0.702	0.310
2	3	72405852	0.566	0.434
1	3	74463202	0.000	0.000
2	3	74980380	0.229	0.376
2	3	76086971	0.305	0.597
2	3	80858231	0.508	0.326
1	3	8179865	0.000	0.661
1	3	8330619	0.000	0.000

1	3	84248079	0.000	0.241
2	3	86921756	0.218	0.133
1	3	8749340	0.000	0.170
1	3	8766880	0.000	0.724
1	3	8800977	0.000	0.181
1	3	89748810	0.000	0.449
2	3	90430217	0.821	0.496
1	3	95223077	0.000	0.526
3	3	9646697	0.948	0.000
1	3	96820605	0.000	0.207
2	4	105234449	0.190	0.000
2	4	106394908	0.444	0.414
1	4	108394132	0.000	0.424
2	4	109876682	0.533	0.000
2	4	111359412	0.600	0.300
1	4	115259241	0.000	0.000
2	4	119161162	0.747	0.000
2	4	119833655	0.389	0.000
1	4	120599980	0.000	0.000
2	4	122600220	0.519	0.000
1	4	125617334	0.000	0.000
1	4	126647636	0.000	0.000
1	4	127771889	0.000	0.000
2	4	134850961	0.381	0.434
1	4	140154007	0.000	0.000
1	4	144879760	0.000	0.000
1	4	147616580	0.000	0.000
1	4	152098840	0.000	0.000
2	4	160621868	0.410	0.554
2	4	161252551	0.163	0.521
2	4	161288198	0.397	0.362
1	4	161716379	0.000	0.059
2	4	162816440	0.549	0.280
1	4	166613505	0.000	0.000
3	4	16908350	0.789	0.651
1	4	174170616	0.000	0.167
1	4	179639868	0.000	0.171
1	4	180135661	0.000	0.261
2	4	180265089	0.455	0.056
2	4	183453115	0.089	0.390
1	4	184638048	0.000	0.000
2	4	187661068	0.099	0.155

2	4	188628950	0.516	0.334
2	4	22103283	0.284	0.150
2	4	26343555	0.432	0.404
1	4	26875683	0.000	0.070
2	4	26935882	0.144	0.217
2	4	3011910	0.381	0.271
2	4	31169536	0.323	0.163
1	4	33615886	0.000	0.170
2	4	35852584	0.316	0.383
1	4	37418639	0.000	0.271
1	4	39429436	0.000	0.434
2	4	44413264	0.296	0.000
1	4	46668719	0.000	0.402
1	4	47220483	0.000	0.000
1	4	52190355	0.000	0.235
2	4	52545084	0.491	0.630
2	4	5718308	0.310	0.000
2	4	61895466	0.615	0.000
1	4	64216296	0.000	0.352
1	4	6451943	0.000	0.339
1	4	64665477	0.000	0.668
2	4	69630424	0.373	0.000
1	4	70520668	0.000	0.258
1	4	71648848	0.000	0.000
2	4	74668604	0.505	0.034
1	4	76047967	0.000	0.000
2	4	82531664	0.237	0.000
1	4	86440642	0.000	0.000
1	4	88387262	0.000	0.000
2	5	100034257	0.381	0.000
2	5	100071988	0.274	0.265
2	5	100155088	0.471	0.000
2	5	100295778	0.649	0.000
1	5	105561137	0.000	0.323
2	5	105941453	0.296	0.286
1	5	106685060	0.116	0.189
2	5	10937820	0.360	0.053
1	5	110479443	0.000	0.000
2	5	111449354	0.323	0.679
1	5	11361065	0.000	0.000
2	5	115666098	0.308	0.177
2	5	116208129	0.276	0.300

2	5	116797618	0.340	0.000
1	5	122619069	0.000	0.592
2	5	123223704	0.278	0.217
2	5	12387040	0.471	0.000
2	5	131362688	0.310	0.000
2	5	131622186	0.437	0.000
1	5	137416371	0.000	0.000
1	5	140836906	0.000	0.407
1	5	147046232	0.000	0.814
2	5	147611565	0.058	0.000
2	5	152460283	0.260	0.395
2	5	155157242	0.547	0.973
1	5	155317926	0.000	0.000
1	5	157005759	0.000	1.025
1	5	159980907	0.000	0.000
1	5	161395724	0.000	0.532
1	5	161830310	0.000	0.323
2	5	162912266	0.267	0.461
2	5	163087087	0.333	0.362
2	5	166031221	0.284	0.000
1	5	175182485	0.000	0.217
1	5	178484296	0.000	0.334
3	5	18474168	0.889	0.000
1	5	19703201	0.000	0.000
2	5	2114089	0.561	0.223
1	5	30228903	0.000	0.159
1	5	32183802	0.000	0.362
2	5	33779372	0.342	0.189
1	5	35163531	0.000	0.000
2	5	35831884	0.909	0.370
2	5	36636178	0.516	0.543
1	5	41232152	0.000	0.322
1	5	41663190	0.000	0.000
1	5	42222760	0.000	0.197
1	5	45194560	0.000	0.296
2	5	4579966	0.545	0.000
1	5	53160317	0.000	0.310
2	5	56387833	0.368	0.271
1	5	5721155	0.000	0.407
2	5	63548792	0.577	0.000
2	5	6643035	0.421	0.000
2	5	69055388	0.372	0.263

1	5	72404389	0.000	0.000
1	5	7425190	0.000	0.000
2	5	75285945	0.513	0.078
2	5	7817145	0.327	0.000
2	5	79269736	0.533	0.271
2	5	81377269	0.424	0.310
1	5	85129366	0.000	0.235
2	5	85688616	0.741	0.000
2	5	91742536	0.593	0.000
1	5	9500811	0.000	0.000
2	5	95231337	0.392	0.000
2	5	95701747	0.715	0.280
2	5	97765568	0.201	0.000
1	6	101437584	0.000	0.094
1	6	102787939	0.000	0.000
2	6	103570525	0.381	0.362
1	6	105574693	0.000	0.629
1	6	110560428	0.000	0.362
2	6	111252036	0.485	0.000
1	6	115939145	0.000	0.620
2	6	117652832	0.181	0.255
2	6	123368975	0.092	0.000
2	6	124380080	0.800	0.000
2	6	126389883	0.086	0.519
2	6	131059163	0.351	0.000
2	6	131399570	0.406	0.372
1	6	132482937	0.000	0.064
2	6	145547033	0.410	0.062
1	6	153868755	0.000	0.329
1	6	155942473	0.000	0.000
1	6	1850433	0.000	1.067
1	6	18553216	0.000	0.000
1	6	20182475	0.000	0.223
1	6	23725753	0.000	0.643
1	6	23820823	0.000	0.000
1	6	33355096	0.000	0.197
1	6	40322738	0.000	0.103
2	6	40934220	0.638	0.000
1	6	45795560	0.000	0.362
2	6	46776061	0.232	0.000
2	6	46995372	0.406	0.827
1	6	49245413	0.000	0.000

1	6	49866189	0.000	0.280
2	6	60497665	0.208	0.000
2	6	62533854	0.585	0.445
2	6	70161977	0.558	0.000
2	6	71671466	0.067	0.322
2	6	7238595	0.415	0.000
1	6	73054903	0.000	0.362
1	6	78332113	0.000	0.526
1	6	80558206	0.000	0.543
2	6	9330828	0.267	0.109
2	6	93696846	0.310	0.290
2	6	95778674	0.274	0.326
1	7	10181486	0.000	0.000
2	7	102065090	0.301	0.452
1	7	108865841	0.000	0.255
2	7	110615318	0.464	0.000
1	7	111235913	0.000	0.318
1	7	116155279	0.000	0.000
2	7	122016458	0.381	0.043
2	7	124142825	0.323	0.000
1	7	134178896	0.000	0.322
2	7	137296579	0.417	0.386
1	7	137739877	0.000	0.000
2	7	139519359	0.211	0.000
1	7	142637901	0.000	0.099
2	7	153528906	0.424	0.758
2	7	154611485	0.305	0.383
2	7	156931430	0.184	0.000
1	7	20905885	0.000	0.266
1	7	26002719	0.000	0.161
1	7	27125974	0.000	0.000
1	7	30124532	0.000	0.192
2	7	30831221	0.261	0.000
1	7	33443171	0.000	0.000
1	7	33920177	0.000	0.661
2	7	41732610	0.434	0.000
2	7	43378810	0.503	0.362
1	7	43433707	0.000	0.000
1	7	4358841	0.000	0.558
1	7	44053423	0.000	0.164
2	7	44090851	0.261	0.000
1	7	45053757	0.000	0.000

1	7	48916465	0.000	0.000
2	7	49269510	0.296	0.000
2	7	49269512	0.296	0.000
2	7	4979367	0.308	0.255
2	7	53091502	0.627	0.000
2	7	54587046	0.978	0.494
2	7	60485855	0.229	0.000
1	7	65590326	0.000	0.300
1	7	67521209	0.000	0.371
2	7	69630257	0.305	0.472
2	7	7056369	0.352	0.259
3	7	71219697	0.770	0.000
1	7	71503989	0.000	0.000
1	7	7383076	0.000	0.496
1	7	75784737	0.000	0.000
1	7	86130259	0.000	0.000
2	7	88505688	0.372	0.000
2	7	90565456	0.232	0.465
2	7	9227657	0.571	0.302
2	7	95205017	0.547	0.461
2	7	95298520	0.314	0.528
2	7	96055652	0.296	0.000
2	7	98561959	0.421	0.181
2	8	104362862	0.444	0.606
2	8	108043942	0.356	0.000
1	8	111647834	0.000	0.101
1	8	114563854	0.000	0.535
1	8	116551195	0.000	0.451
2	8	117615713	0.480	0.388
1	8	122234933	0.000	0.000
2	8	124975564	0.065	0.478
2	8	129273738	0.281	0.000
2	8	129372882	0.567	0.049
2	8	129733477	0.261	1.022
1	8	131552936	0.000	0.000
1	8	133562727	0.000	0.418
2	8	135261370	0.549	0.543
1	8	136497219	0.000	0.225
2	8	17691704	0.296	0.000
2	8	19550828	0.480	0.000
1	8	19798556	0.000	0.310
1	8	20863668	0.000	0.148

1	8	25151260	0.000	0.247
2	8	25892225	0.325	0.000
1	8	26940513	0.000	0.000
2	8	30978684	0.424	0.000
1	8	32400294	0.000	0.231
1	8	32524703	0.000	0.148
1	8	3391860	0.000	0.000
1	8	34194743	0.000	0.517
2	8	36379501	0.351	0.326
2	8	36570758	0.444	0.000
1	8	41188472	0.000	0.362
1	8	43877252	0.000	0.310
1	8	46315152	0.000	0.352
2	8	48680993	0.711	0.159
1	8	49102414	0.000	0.000
1	8	4997791	0.000	0.248
1	8	50264084	0.000	0.362
2	8	51711248	0.388	0.207
1	8	53427578	0.000	0.348
1	8	57557945	0.000	0.000
1	8	5826762	0.000	0.225
1	8	58506466	0.000	0.000
1	8	59792693	0.000	0.163
2	8	63967261	0.327	0.585
1	8	64469993	0.000	0.418
1	8	924933	0.000	0.090
1	8	98657310	0.000	0.000
2	9	101191229	0.218	1.048
1	9	10229559	0.000	0.000
1	9	102339974	0.000	0.000
2	9	102487319	0.690	0.290
1	9	102993672	0.000	0.434
1	9	103368304	0.000	0.560
1	9	104257777	0.000	0.163
1	9	104331598	0.000	0.000
1	9	105298502	0.000	0.000
2	9	111554985	0.274	0.189
2	9	118247951	0.086	0.000
1	9	118261593	0.000	0.117
2	9	120700338	0.604	0.000
2	9	122872477	0.491	0.139
1	9	124851965	0.000	0.000

2	9	125539853	0.254	0.000
1	9	12626664	0.000	0.000
2	9	127663224	0.174	0.000
1	9	12964481	0.000	0.000
2	9	131190221	0.698	0.255
1	9	131860557	0.000	0.000
2	9	14104419	0.519	0.323
2	9	1822815	0.511	0.630
2	9	19348792	0.410	0.114
1	9	21096138	0.000	0.965
1	9	23036773	0.000	0.819
2	9	23699353	0.250	0.000
1	9	24723875	0.000	0.372
1	9	24924904	0.000	0.000
2	9	28150104	0.235	0.217
1	9	38292964	0.000	0.000
2	9	395970	0.404	0.420
1	9	42290039	0.000	0.136
2	9	4316936	0.622	0.000
2	9	50071	0.143	0.000
1	9	5583708	0.000	0.338
1	9	595757	0.000	0.374
2	9	61566797	0.401	0.000
2	9	73087756	0.610	0.000
1	9	73452437	0.000	0.310
1	9	74317541	0.000	0.068
2	9	77004114	0.808	0.000
2	9	83484424	0.322	0.724
2	9	84858874	0.267	0.452
1	9	88848472	0.000	0.000
1	9	9208774	0.000	0.000
1	9	95722226	0.000	0.489
1	9	98676266	0.000	0.869
1	10	102661031	0.000	0.370
2	10	10849842	0.410	0.362
2	10	109091857	0.485	0.278
1	10	10933457	0.000	0.000
1	10	110609195	0.000	0.000
2	10	11168124	0.625	0.000
2	10	111830308	0.267	0.374
2	10	113814958	0.638	0.000
1	10	115355253	0.000	0.514

2	10	115409272	1.091	0.374
1	10	116513252	0.000	1.357
2	10	116526803	0.400	0.507
1	10	118845653	0.000	0.286
3	10	120224348	2.256	0.000
2	10	12067169	0.356	0.000
2	10	121613197	0.519	0.000
2	10	124588678	0.278	0.159
1	10	131096200	0.000	0.334
1	10	132055519	0.000	0.235
1	10	14501740	0.000	0.286
1	10	19776842	0.000	0.452
2	10	23617158	0.464	0.543
2	10	23958376	0.281	0.472
1	10	24984824	0.000	0.000
2	10	27864409	0.460	0.286
1	10	30158617	0.000	0.483
1	10	33849532	0.000	0.000
2	10	34892061	0.213	0.000
1	10	37826153	0.000	0.505
2	10	4183898	0.406	0.000
1	10	42358812	0.000	0.000
1	10	46311814	0.000	0.000
2	10	47221434	0.370	0.302
2	10	54174376	0.403	0.334
1	10	54568022	0.000	0.280
2	10	56140794	0.267	0.000
2	10	56950504	0.556	0.278
2	10	60147699	0.278	0.047
2	10	62705771	0.747	0.380
2	10	64210270	0.491	0.318
1	10	65525504	0.000	0.000
2	10	67571470	0.403	0.152
2	10	70021310	0.320	1.018
1	10	73104873	0.000	0.475
1	10	75129152	0.000	0.000
2	10	75905930	0.523	0.150
2	10	78393818	0.344	0.235
2	10	83492892	0.544	0.000
1	10	86750662	0.000	0.000
1	10	90700494	0.000	0.575
2	10	9239651	0.325	0.225

1	10	92770872	0.000	0.000
2	10	93187731	0.741	0.724
1	10	93234495	0.000	0.000
2	10	94576898	0.508	0.434
2	10	94950682	0.186	0.193
1	11	103587114	0.000	0.204
2	11	105917523	0.083	0.000
1	11	107071946	0.000	0.579
1	11	11456484	0.000	0.283
1	11	114708783	0.000	0.248
1	11	114958122	0.000	0.290
1	11	117410900	0.000	0.000
2	11	118973448	0.421	0.000
2	11	121731425	0.356	0.066
1	11	122025753	0.000	0.639
1	11	122979808	0.000	0.000
1	11	124291010	0.000	0.251
1	11	132785635	0.000	1.062
1	11	133338345	0.000	0.374
1	11	133761282	0.000	0.620
2	11	17634218	0.640	0.235
2	11	18214790	0.680	0.000
1	11	19063121	0.000	0.000
1	11	20315541	0.000	0.620
1	11	20325176	0.000	0.000
2	11	25629284	0.533	0.000
2	11	29268317	0.348	0.000
2	11	30414572	0.434	0.255
1	11	36738318	0.000	0.181
2	11	40970112	0.271	0.000
2	11	42181489	0.444	0.000
2	11	4222159	0.148	0.000
1	11	42391773	0.000	0.383
2	11	42992114	0.276	0.109
1	11	44879657	0.000	0.414
2	11	49443145	0.457	0.271
2	11	59547928	0.148	0.000
2	11	62907973	0.696	0.310
2	11	6802600	0.600	0.526
2	11	69424352	0.430	0.181
2	11	70172132	0.556	0.000
2	11	71917009	0.406	0.000

2	11	78991748	0.696	0.255
1	11	81625515	0.000	0.121
1	11	82375060	0.000	0.704
1	11	83760647	0.000	0.646
2	11	83859358	0.242	0.000
1	11	8836985	0.000	0.263
1	11	88442713	0.000	0.056
2	11	89364256	0.314	0.056
1	11	91384045	0.000	0.461
2	11	92625315	0.296	0.000
1	11	93116767	0.000	0.334
2	11	93572399	0.583	0.117
2	11	98979001	0.355	0.000
2	11	99123208	0.441	0.000
1	12	100396583	0.000	0.114
2	12	101478301	0.317	0.000
1	12	105124962	0.000	0.247
1	12	109600533	0.000	0.000
2	12	111703138	0.356	0.517
2	12	112201473	0.978	0.000
1	12	113992218	0.000	0.362
1	12	114026760	0.000	0.000
1	12	115283072	0.000	0.557
1	12	126210035	0.000	0.000
1	12	128451756	0.000	0.000
1	12	129158414	0.000	0.101
2	12	129194036	0.260	0.743
2	12	129699976	0.533	0.000
2	12	130201343	0.571	0.000
2	12	132658754	0.387	0.000
1	12	18037838	0.000	0.114
1	12	20532321	0.000	0.334
2	12	27135862	0.333	0.229
1	12	32986809	0.000	0.111
2	12	37544249	0.533	0.000
1	12	38746830	0.000	0.000
2	12	39556427	0.474	0.000
2	12	45801804	0.271	0.399
2	12	47093368	0.444	0.226
2	12	54193118	0.274	0.124
2	12	61096059	0.390	0.310
2	12	6117683	0.107	0.514

1	12	61470230	0.000	0.000
1	12	6307820	0.000	0.000
2	12	67241412	0.303	0.000
1	12	6789295	0.000	0.217
1	12	77504158	0.000	0.145
1	12	78382902	0.000	0.814
1	12	79065377	0.000	0.404
2	12	80465550	0.209	0.041
1	12	80780558	0.000	0.263
1	12	8205043	0.000	0.894
1	12	84484910	0.000	0.000
1	12	87232193	0.000	0.698
1	12	87810848	0.000	0.000
1	12	88071791	0.000	0.000
1	12	90780665	0.000	0.911
1	12	95719552	0.000	0.213
2	12	96021004	0.222	0.931
1	12	96233025	0.000	0.746
2	12	99195605	0.356	0.000
1	13	106932614	0.000	0.217
1	13	109688927	0.000	0.000
2	13	112177050	0.588	0.241
1	13	112351281	0.000	0.000
2	13	19458900	0.200	0.181
2	13	21198801	0.296	0.000
2	13	21198803	0.505	0.277
2	13	22486341	0.667	0.202
2	13	24407230	0.424	0.000
2	13	35458160	0.800	0.106
2	13	44807574	0.290	0.000
2	13	51185115	0.274	0.000
1	13	51338069	0.000	0.181
2	13	54356322	0.222	0.000
2	13	57950093	0.923	0.000
2	13	60127004	0.889	0.181
2	13	61979712	0.208	0.070
1	13	64005202	0.000	0.000
1	13	68771491	0.000	0.000
1	13	81289794	0.000	0.310
2	13	86387551	0.333	0.633
1	13	95505939	0.000	0.000
2	14	81424362	0.598	0.383

1	14	87098315	0.000	0.668
2	14	87211954	0.390	0.000
1	14	94965692	0.000	0.271
1	14	96647102	0.000	0.000
1	14	99920248	0.000	0.000
1	15	25046210	0.000	0.000
2	15	25170693	0.248	0.000
1	15	26017195	0.000	0.000
1	15	45848202	0.000	0.000
1	15	48080087	0.000	0.302
1	15	48928081	0.000	0.000
2	15	56330772	0.406	0.310
1	15	60120205	0.000	0.174
1	15	60352764	0.000	0.281
2	15	60956234	0.327	0.343
2	15	63420915	0.325	0.582
1	15	72502854	0.000	0.691
1	15	77267388	0.000	0.420
1	15	80681168	0.000	0.226
2	15	80950475	0.497	0.045
1	15	83132180	0.000	0.000
2	15	83158851	0.344	0.161
1	15	87983261	0.000	0.000
1	15	95004101	0.000	0.000
2	15	96972773	0.390	0.207
2	15	99025033	0.323	0.326
1	16	1550273	0.000	0.000
1	16	18537225	0.000	0.000
1	16	20424714	0.000	0.000
2	16	22306291	0.600	0.000
1	16	22677228	0.000	0.283
2	16	25681378	0.232	0.290
2	16	3192939	0.311	0.475
2	16	34085953	0.946	0.350
2	16	35232723	0.570	0.000
2	16	47099927	0.325	0.000
2	16	47823047	0.174	0.000
2	16	48066801	0.622	0.592
1	16	50321074	0.000	0.062
2	16	51823583	0.213	0.760
2	16	52276870	0.261	0.000
1	16	5534803	0.000	0.434

1	16	57821035	0.000	0.402
2	16	61886296	0.230	0.000
2	16	64432341	0.232	0.000
2	16	64614439	0.427	0.452
1	16	64699930	0.000	0.000
2	16	64919655	0.174	0.391
2	16	66602481	0.250	0.046
1	16	67105628	0.000	0.465
2	16	67608941	0.081	0.000
1	16	69148663	0.000	0.000
1	16	70802883	0.000	0.395
2	16	71030715	0.254	0.345
2	16	7113874	0.195	0.395
2	16	72362589	0.505	0.434
2	16	7450654	0.857	0.286
1	16	77256710	0.000	0.000
1	16	77493285	0.000	0.362
2	16	77781037	0.370	0.287
1	16	82066056	0.000	0.000
1	16	82874338	0.000	0.229
2	16	83070380	0.667	0.109
3	16	85313584	0.912	0.981
2	16	86284090	0.194	0.334
1	16	9532674	0.000	0.000
1	17	10363095	0.000	0.212
1	17	10978272	0.000	0.241
1	17	14670774	0.000	0.000
2	17	14728731	0.267	0.000
1	17	30755275	0.000	0.000
1	17	31863521	0.000	0.000
2	17	32918315	0.686	0.225
2	17	34590397	0.722	0.307
1	17	34811921	0.000	0.060
2	17	34849723	0.247	0.362
1	17	40381174	0.000	0.000
1	17	41094327	0.000	0.000
2	17	41287213	0.348	0.822
1	17	41488518	0.000	0.347
1	17	41662731	0.000	0.271
1	17	4511744	0.000	0.248
2	17	48780087	0.567	0.543
1	17	4976602	0.000	0.000

1	17	52148573	0.000	0.000
2	17	52202053	0.092	0.000
1	17	59529075	0.000	0.000
1	17	63728030	0.000	0.000
1	17	64448232	0.000	0.000
2	17	72065475	0.566	0.000
2	17	73729002	0.296	0.000
1	17	74236263	0.000	0.000
2	17	78164605	0.333	0.420
2	17	8080028	0.364	0.388
2	17	82853402	0.427	0.322
2	17	9019997	0.310	0.000
1	17	9021059	0.000	0.271
1	18	14791710	0.000	0.000
1	18	15293364	0.000	0.112
2	18	27867692	0.577	0.000
2	18	29896712	0.351	0.000
2	18	50652311	0.242	0.339
2	18	51531692	0.296	0.197
1	18	524695	0.000	0.000
2	18	52758063	0.718	0.395
1	18	56544081	0.000	0.319
2	18	57470379	0.404	0.000
1	18	58043724	0.000	0.452
1	18	61155354	0.000	0.271
1	18	61706959	0.000	0.217
2	18	63454630	0.271	0.000
1	18	63887009	0.000	0.334
1	18	67455918	0.000	0.000
2	18	68909930	0.325	0.345
2	18	70340966	0.496	0.263
1	18	74237595	0.000	0.370
2	18	75784106	0.496	0.724
1	18	75984267	0.000	0.000
1	18	8101586	0.000	0.000
1	18	924915	0.000	0.445
2	18	9601220	0.491	0.566
2	19	10065329	0.571	0.494
3	19	12943750	0.687	0.000
2	19	16234332	0.424	0.193
1	19	19549515	0.000	0.901
1	19	22624713	0.000	0.136

2	19	22883084	0.982	0.000
2	19	22892036	0.649	0.246
1	19	27496424	0.000	0.651
2	19	27753864	0.333	0.672
1	19	28110861	0.000	0.457
2	19	28326785	0.821	0.197
1	19	31656627	0.000	0.062
2	19	3661315	0.410	0.343
1	19	38958665	0.000	0.519
2	19	40522348	0.250	0.452
1	19	41492820	0.000	0.000
2	19	48040435	0.415	0.300
1	19	53377680	0.000	0.524
2	19	7346680	0.325	0.000
1	19	8086471	0.000	0.987
1	20	12995529	0.000	0.414
2	20	13915926	0.323	0.543
1	20	14336990	0.000	0.334
1	20	21629260	0.000	0.383
1	20	22689135	0.000	0.000
2	20	28497717	0.125	0.000
2	20	39766967	0.260	0.434
1	20	39854921	0.000	0.000
2	20	44696207	0.430	0.000
2	20	45737606	0.213	0.293
1	20	48547263	0.000	0.045
1	20	50715766	0.000	0.404
1	20	50895064	0.000	0.000
1	20	52629042	0.000	0.223
2	20	53076039	0.513	0.000
2	20	55145960	0.533	0.271
1	20	64283610	0.000	0.000
2	21	10536357	0.362	0.000
1	21	24993236	0.000	0.079
2	21	25235168	0.667	0.132
2	21	26121394	0.397	0.378
2	21	27842645	0.286	0.000
2	21	28932587	0.260	0.899
2	21	31309695	0.186	0.449
2	21	32999596	0.267	0.000
2	21	35666262	0.496	0.475
1	21	36182754	0.000	0.000

2	21	37443516	0.063	0.157
1	21	40180743	0.000	0.000
1	21	40558302	0.000	0.000
2	21	42078747	0.119	0.259
1	21	46037210	0.000	0.511
1	22	11356944	0.075	0.000
2	22	20582589	1.143	0.000
1	22	32657960	0.000	0.326
2	22	33353441	0.260	0.286
1	22	34793591	0.000	0.000
2	22	37322215	0.360	0.000
1	22	37961231	0.000	0.000
1	22	42966759	0.000	0.170
2	22	44313831	0.545	0.452
2	22	45732457	0.278	0.703
1	22	48568894	0.000	0.302

Note: Results from multidimensional Bayesian Dirichlet Process-based mutation clustering. Columns *CCF_in_Twin_A* and *CCF_in_Twin_B* show for each cluster in each twin the proportion of tumour cells that the cluster represents. CCF, cancer cell fraction.

Supplementary Table 12. Additional candidate cancer genes

Gene			
ABL2	*EP300*	*MKL1*	*RAD21*
AFF3	*ERCC2*	*MLL*	*RB1*
APC	*ETV6*	*MLL2*	*RET*
AR	*EZH2*	*MLL3*	*RUNX1*
ARID2	*FBXW7*	*MLL5*	*SDHAF2*
ASXL1	*FLT3*	*MPL*	*SF1*
ATE1	*FOXP1*	*MYC*	*SF3A1*
ATM	*GATA2*	*MYD88*	*SF3B1*
ATRX	*GNAS*	*MYO5A*	*SH2B3*
BCOR	*GNB1*	*NF1*	*SRSF2*
BRAF	*IDH1*	*NOTCH1*	*STAG2*
CALR	*IDH2*	*NPM1*	*STAT3*
CBL	*IKZF1*	*NRAS*	*TET2*
CBLB	*JAK2*	*PABPC1*	*TMEM127*
CDKN2A	*KDM5A*	*PHF6*	*TP53*
CEBPA	*KDM5C*	*PPARG*	*TP63*
CHEK2	*KDM6A*	*PPM1D*	*U2AF1*
CREBBP	*KIT*	*PRPF40B*	*WT1*
CUX1	*KMT2C*	*PTEN*	*ZRSR2*
DNM2	*KRAS*	*PTPN11*	
DNMT3A	*LZTR1*	*PTPRD*	

Note: Additional gene list for putative driver mutation analyses. Curated list based on literature support for genes associated with blood cancer risk of biology.[44-46] Gene names are listed in alphabetical order and provided in italics in accordance with the current HUGO Gene Nomenclature Committee (HGNC) guidelines.[50]

APPENDIX A. Reporting Summary