| Pluripotent cells | → | Primary mediastinal non seminomatous germ cell tumor
Teratoma | → | Melanocytic Neuroectodermal Tumor (MNT) | → | Anaplastic MNT |

Malignant transformation   Anaplastic transformation

Somatic mutations acquisition   *Additional somatic mutation events*   *Genetic instability*
Other genetic alterations   *Cytotoxic chemotherapy selection*   *Chemotherapy induced cytotoxicity*

Supplemental Figure 1. Hypothetical tumoral evolution

Non-seminomatous germ cell tumors could originate from pluripotent cells that have acquired various genetic alterations and somatic mutations. These tumors may contain a teratomatous component which is selected by chemotherapy. In our study, the teratomatous component is at the origin of the malignant transformation called MNT. This MNT component then underwent an anaplastic transformation potentially due to genetic instability and chemotherapy induced cytotoxicity

Table S1

VAF Teratoma (%)	VAF MNT (%)	VAF Melanoma (%)	rSID	CHROM	POS	REF	ALT	Consequence	SYMBOL	HGVSp_Short	SIFT	PolyPhen
21.43				1	880153	A	G	missense_variant	NOC2L	p.L724P	tolerated(0.07)	benign(0.028)
10.87			rs368105340	1	2415897	C	T	missense_variant	PLCH2	p.T78M	deleterious(0)	probably_damaging(1)
		10.94	rs754535443	1	3511965	G	A	missense_variant	MEGF6	p.R105W	deleterious(0)	probably_damaging(0.997)
		10.64	rs770807708	1	3551815	G	A	missense_variant	WRAP73	p.T216M	deleterious(0.01)	possibly_damaging(0.771)
18.75				1	6662703	G	T	missense_variant	KLHL21	p.P59T	tolerated(0.4)	benign(0)
9.26			rs753954585	1	7723485	G	A	missense_variant	CAMTA1	p.R293Q	tolerated(0.06)	probably_damaging(0.999)
9.84			rs1441919068	1	7863905	G	A	missense_variant	PER3	p.R377Q	deleterious(0.03)	possibly_damaging(0.911)
11.76			rs777216395	1	15546088	G	A	missense_variant	TMEM51	p.R204Q	deleterious(0.01)	probably_damaging(1)
33.33	12.77		rs770113993	1	16070906	T	G	missense_variant	TMEM82	p.H196Q	tolerated(0.13)	benign(0.003)
	11.76		rs768703816	1	16752062	C	T	missense_variant	SPATA21	p.R149Q	tolerated(0.9)	benign(0.007)
8.77			rs1304791222	1	17965150	C	T	missense_variant	ARHGEF10L	p.R416C	deleterious(0.02)	probably_damaging(1)
17.5				1	19983522	A	C	missense_variant	NBL1	p.H184P	tolerated_low_confidence(0.09)	benign(0)
7.81			rs752798095	1	20412693	G	A	missense_variant	PLA2G5	p.R53Q	deleterious(0)	benign(0.003)
9.09			rs764850346	1	22446934	C	T	missense_variant	WNT4	p.R222Q	tolerated(0.26)	probably_damaging(0.966)
		17.28		1	24771708	A	G	missense_variant	NIPAL3	p.E41G	deleterious(0.01)	probably_damaging(1)
	11.36		rs200432041	1	26612475	G	A	stop_gained	UBXN11	p.Q85*		
14.29			rs1322153609	1	27320495	G	A	stop_gained	TRNP1	p.W73*		
	22.73			1	33237116	A	G	missense_variant	KIAA1522	p.E720G	deleterious(0)	possibly_damaging(0.745)
8.47			rs779682329	1	38304324	C	T	missense_variant	MTF1	p.R251Q	deleterious(0)	probably_damaging(1)
12.24			rs1344281914	1	40768856	C	T	missense_variant&splice_region_variant	COL9A2	p.G517D	deleterious(0)	probably_damaging(1)
11.11			rs373328524	1	43738443	A	G	missense_variant	TMEM125	p.D17A	tolerated(0.06)	benign(0.013)
	10.81		rs960864289	1	44605340	T	C	missense_variant	KLF18	p.E655G	tolerated(1)	unknown(0)
9.43			rs1032104702	1	44680499	G	A	missense_variant	DMAP1	p.G108R	deleterious(0)	probably_damaging(1)
10.53			rs377701856	1	46746902	G	A	missense_variant	LRRC41	p.R551W	deleterious(0.01)	probably_damaging(0.999)
		22.5	rs1569885226	1	54060359	T	G	missense_variant	GLIS1	p.T73P	deleterious_low_confidence(0.05)	benign(0.167)
	29.07			1	55625349	C	G	missense_variant	USP24	p.D335H	tolerated(0.06)	benign(0.894)
	11.9			1	109815303	T	A	missense_variant	CELSR2	p.L2699Q	tolerated(0.32)	possibly_damaging(0.718)
	12.5			1	111726120	G	A	missense_variant	CEPT1	p.D348N	deleterious(0)	probably_damaging(1)
	10			1	117663726	A	C	missense_variant	TRIM45	p.L33W	deleterious(0.03)	possibly_damaging(0.782)
11.54			rs753171524	1	150523468	AT	A	frameshift_variant	AL356356.1	p.I133X		
17.31				1	150529196	G	C	missense_variant	ADAMTSL4	p.R559P	deleterious(0)	probably_damaging(1)
	10.2			1	151785790	G	A	missense_variant	RORC	p.R367W	deleterious(0)	probably_damaging(1)
	10.42			1	152080708	C	T	missense_variant	TCHH	p.R1662H	deleterious_low_confidence(0)	probably_damaging(0.954)
	20			1	153724757	C	A	missense_variant&splice_region_variant	INTS3	p.F244L	deleterious(0.01)	possibly_damaging(0.954)
		12.5	COSM1334916;rs759081520	1	156642803	TG	T	frameshift_variant	NES	p.P392X		
10.42			rs755958507	1	156946840	C	T	missense_variant	ARHGEF11	p.E173K	deleterious(0.04)	possibly_damaging(0.705)
	11.48		rs749910003	1	160808755	C	T	missense_variant	CD244	p.R155K	tolerated(0.24)	benign(0.093)
	10.71		rs409763	1	161483723	G	A	splice_donor_variant	FCGR2A			
17.24			rs376915775	1	167815318	C	T	missense_variant	ADCY10	p.R782Q	tolerated(0.41)	benign(0.196)
	10.2		rs951414940	1	186158808	T	C	missense_variant	HMCN1	p.F5569S	deleterious(0)	probably_damaging(0.999)
10.14			rs750268281	1	202394768	G	A	missense_variant	PPP1R12B	p.G206R	deleterious(0.02)	probably_damaging(0.999)
8.47			rs765881137	1	205628612	C	T	missense_variant	SLC45A3	p.R471H	tolerated(0.54)	benign(0.005)
10			rs1366967873	1	207307917	G	A	missense_variant	C4BPA	p.R418Q	tolerated(0.28)	probably_damaging(0.978)
	11.9			1	212981098	C	T	missense_variant	TATDN3	p.H170Y	deleterious(0)	probably_damaging(1)
11.11				1	213031991	G	A	missense_variant	FLVCR1	p.G66E	tolerated_low_confidence(0.24)	benign(0.01)
11.32				1	226923907	A	C	missense_variant	ITPKB	p.L418R	deleterious_low_confidence(0.02)	possibly_damaging(0.578)
		13.89	rs1572079552	1	227170611	A	C	missense_variant	ADCK3	p.D319A	tolerated(0.11)	benign(0.387)
8.77			rs750686607	1	227192791	G	A	missense_variant	CDC42BPA	p.R1654W	deleterious_low_confidence(0)	probably_damaging(1)
14.71			rs780444152	1	228528934	G	A	missense_variant	OBSCN	p.V5946M	deleterious(0.02)	probably_damaging(1)
8.77			rs745612968	1	236341829	C	T	stop_gained	GPR137B	p.R194*		
13.33			rs746058779	1	247264178	C	T	missense_variant	ZNF669	p.R298Q	deleterious(0.02)	possibly_damaging(0.566)
9.8			rs755429246	2	3727534	C	T	missense_variant	ALLC	p.T83M	tolerated(0.08)	possibly_damaging(0.951)
	8.2		rs781120730	2	10583681	C	A	missense_variant	ODC1	p.G201C	deleterious(0.09)	probably_damaging(0.997)
27.91	15.62	22.31		2	11335131	G	A	missense_variant	ROCK2	p.L1157F	deleterious(0)	probably_damaging(0.999)
		12.5		2	27458489	A	G	missense_variant	CAD	p.Y1352C	deleterious(0.03)	probably_damaging(1)
		30.77	rs1553315333	2	32341231	G	A	missense_variant	SPAST	p.A350T	tolerated(0.74)	benign(0)
	8.77		rs375243952	2	40342494	G	A	missense_variant	SLC8A1	p.R941W	deleterious(0.02)	probably_damaging(1)
			rs745357489	2	46605084	C	T	missense_variant	EPAS1	p.P434L	deleterious(0.05)	probably_damaging(0.959)
	11.36		rs762456312	2	47136177	G	A	missense_variant	MCFD2	p.T45I	tolerated(0.71)	benign(0.063)
	10.2		rs780627523	2	61021162	G	A	missense_variant	PAPOLG	p.V609I	tolerated_low_confidence(0.36)	benign(0.204)
	15.15			2	71740861	A	G	missense_variant	DYSF	p.E158G	tolerated(0.16)	benign(0)
12.24			rs781690577	2	75720439	C	T	missense_variant	EVA1A	p.E128K	deleterious(0)	probably_damaging(1)
20				2	80530156	C	G	missense_variant	LRRTM1	p.L283F	deleterious(0.04)	benign(0.288)
	8.2		rs773439589	2	85059231	G	A	missense_variant	TRABD2A	p.R295W	deleterious(0)	probably_damaging(1)
		12.75		2	95818950	G	T	missense_variant	ZNF514	p.Q17K	tolerated(0.53)	probably_damaging(0.959)
12				2	120003197	G	A	missense_variant	STEAP3	p.S42Y	tolerated(0.07)	probably_damaging(0.959)
13.51				2	129076029	C	G	missense_variant	HS6ST1	p.G37R	tolerated(0.07)	possibly_damaging(0.856)
22.22			rs780375294	2	131520201	T	C	missense_variant	AMER3	p.S186P	tolerated(0.1)	benign(0)
	10.39		rs777487694	2	131981309	A	G	missense_variant	POTEE	p.H221R	tolerated_low_confidence(0.37)	unknown(0)
7.94				2	158114652	G	A	missense_variant	GALNT5	p.V20I	tolerated(0.24)	benign(0)
	18.52		rs149332956	2	160901608	G	A	missense_variant	PLA2R1	p.S57L	tolerated(0.08)	possibly_damaging(0.84)
13.51			rs761002539	2	163055267	C	T	missense_variant&splice_region_variant	FAP	p.G468S	deleterious(0)	probably_damaging(1)
	12.82		rs189583381	2	175213406	C	T	missense_variant	CIR1	p.R391Q	tolerated_low_confidence(0.14)	possibly_damaging(0.899)
10.2			rs371621174	2	179485685	G	A	missense_variant	TTN	p.R6345W	deleterious(0)	probably_damaging(0.964)
15.15				2	190719625	G	T	stop_gained	PMS1	p.E328*		
		12.2		2	212286781	G	A	missense_variant	ERBB4	p.A972V	tolerated(0.16)	benign(0.046)
	14.29		rs778972713	2	217297475	G	A	missense_variant	SMARCAL1	p.A457T	tolerated(0.06)	benign(0)
	10		rs147774381	2	219143769	G	A	missense_variant&NMD_transcript_variant	TMBIM1	p.R117C	deleterious_low_confidence(0.03)	possibly_damaging(0.944)
8.33				2	233323413	G	A	missense_variant	ALPI	p.V419M	tolerated(0.17)	benign(0.427)
		10.42	rs1318022705	2	233709254	C	A	missense_variant	GIGYF2	p.T1092K	tolerated(0.74)	benign(0)
17.5				2	234372894	T	G	missense_variant	DGKD	p.W1091G	tolerated(0.08)	benign(0.104)
	17.24		rs201684914	2	237405855	G	A	missense_variant&NMD_transcript_variant	IQCA1	p.T96M	deleterious(0)	possibly_damaging(0.538)
13.89			rs146267919	2	241569925	G	A	missense_variant	GPR35	p.V186M	deleterious(0)	probably_damaging(0.99)
30.77				2	242066568	C	G	missense_variant	PASK	p.A588P	deleterious(0)	benign(0.001)
17.78				2	242066573	A	G	missense_variant	PASK	p.L586P	deleterious(0)	benign(0)
	10.61			3	9825821	G	A	missense_variant	TADA3	p.R333C	tolerated(0.05)	probably_damaging(0.999)
22.22			rs760248534	3	10353776	G	A	missense_variant	SEC13	p.S111L	deleterious(0.05)	probably_damaging(1)
10.71			rs201215546	3	38151709	G	A	missense_variant	DLEC1	p.R1127H	deleterious(0)	possibly_damaging(0.673)
12.82				3	38793819	A	T	missense_variant	SCN11A	p.L549H	deleterious(0.25)	probably_damaging(0.802)
	10.87		rs951508265	3	38913730	C	T	missense_variant	SCN11A	p.R1150Q	deleterious(0)	probably_damaging(1)
16.67			rs199566978	3	39184844	C	T	missense_variant	CSRNP1	p.R491Q	tolerated(1)	benign(0)
	11.36			3	40231706	T	G	missense_variant	MYRIP	p.S473A	tolerated(0.1)	benign(0.625)
11.11			rs752967293	3	43388929	G	A	missense_variant	SNRK	p.R393Q	deleterious(0.04)	probably_damaging(0.997)
	10		rs1401363614	3	44283817	C	T	missense_variant	TOPAZ1	p.P91L	tolerated(0.07)	benign(0.022)
13.33				3	44959626	G	A	missense_variant	ZDHHC3	p.R117C	deleterious(0)	probably_damaging(1)
	12.5			3	47032980	G	C	missense_variant	NBEAL2	p.D243H	deleterious(0.03)	probably_damaging(0.998)
12.82			rs761187184	3	47165718	C	A	missense_variant&NMD_transcript_variant	SETD2	p.R8S	deleterious(0)	probably_damaging(1)
16.07				3	47452746	G	A	missense_variant	PTPN23	p.R1153Q	tolerated(0.24)	probably_damaging(0.998)
13.95				3	48336687	G	A	missense_variant	NME6	p.A91V	deleterious(0)	probably_damaging(0.99)
19.23				3	49690007	T	A	missense_variant	BSN	p.S1006R	deleterious(0)	probably_damaging(1)
36.36	20			3	49690741	G	A	missense_variant	BSN	p.S1251N	tolerated(0.21)	benign(0)
	8.77		rs200436621	3	52544491	G	A	missense_variant	STAB1	p.D919N		benign(0.134)
10			rs201719784	3	52551609	G	A	missense_variant	STAB1	p.R1536Q	tolerated(0.17)	benign(0.003)
8.93			rs778999330	3	52850985	C	T	missense_variant	ITIH4	p.A796T	deleterious(0.03)	probably_damaging(0.987)
	13.95			3	64133025	G	T	missense_variant	PRICKLE2	p.L381M	deleterious(0.04)	probably_damaging(0.993)
13.16				3	100096610	T	A	missense_variant	TOMM70A	p.N344I	tolerated(0.15)	possibly_damaging(0.754)
10.64			rs143771376	3	114018527	G	A	missense_variant	TIGIT	p.V159M	tolerated(0.25)	benign(0.005)
		13.46		3	118621525	A	T	missense_variant	IGSF11	p.S379T	tolerated(0.25)	benign(0.241)
25.68	8.57	23.53		3	121238847	A	G	missense_variant	POLQ	p.S447P	deleterious(0)	possibly_damaging(0.921)
12				3	122598147	T	G	missense_variant	DIRC2	p.C453W	deleterious(0.03)	probably_damaging(0.999)
12.82				3	126154476	A	G	missense_variant	CCDC37	p.Q568R	deleterious(0.03)	probably_damaging(1)
	20.69			3	133306742	AT	A	frameshift_variant	CDV3	p.D210X		
	10.2		rs1232069643	3	133969478	A	C	missense_variant	RYK	p.L6R	deleterious_low_confidence(0)	benign(0)
15.25				3	150128564	GG	CC	missense_variant	TSC22D2	p.G476A	tolerated(0.9)	benign(0.073)
16			rs1258941709	3	158428663	C	A	missense_variant	RARRES1	p.K133N	tolerated(0.12)	possibly_damaging(0.93)
	9.09	13.41	rs140056427	3	169801806	C	T	missense_variant	GPR160	p.R16C	tolerated(0.17)	possibly_damaging(0.688)
	10		rs773581866	3	170723825	G	A	stop_gained	SLC2A2	p.R228*		
7.59			rs945466107	3	178962429	C	T	missense_variant	KCNMB3	p.D105N	deleterious(0.02)	benign(0.503)
10.59	10.14		rs747366842	3	195510052	G	C	missense_variant&NMD_transcript_variant	MUC4	p.H1133Q	tolerated_low_confidence(0.19)	possibly_damaging(0.663)
		20		4	661649	T	C	missense_variant	PDE6B	p.F786S	deleterious(0)	probably_damaging(0.981)
16.67				4	1343508	C	CTG	frameshift_variant	UVSSA	p.L99LX		
7.14			rs370127436	4	1980581	C	T	missense_variant	WHSC1	p.P696L	tolerated_low_confidence(0.23)	benign(0)
10			rs781477850	4	3134403	G	A	missense_variant	HTT	p.R784H	tolerated(0.06)	benign(0.163)
22.22		36.3		4	24810351	G	T	missense_variant	CCDC149	p.S417Y	deleterious_low_confidence(0.01)	possibly_damaging(0.812)
32.43	24.64			4	4228424	TT	CC	missense_variant	OTOP1	p.K56R	deleterious(0)	probably_damaging(0.989)
		20.71	rs147627339	4	55948198	G	A	missense_variant	KDR	p.T1258M	deleterious(0)	benign(0)
17.78			rs201914215	4	70066424	T	C	missense_variant	UGT2B11	p.I442V	tolerated(0.27)	benign(0)
	13.89			4	73944478	T	C	missense_variant	ANKRD17	p.E2179G	deleterious_low_confidence(0)	
		18.67		4	80992806	G	GA	frameshift_variant&splice_region_variant	ANTXR2	p.S52FX		
13.89				4	88035579	C	T	missense_variant	AFF1	p.P525S	tolerated(0.07)	probably_damaging(0.957)
11.11				4	89018681	G	T	missense_variant	ABCG2	p.A524E	tolerated(0.01)	probably_damaging(0.936)
		8.05	rs1222965404	4	90169749	T	C	missense_variant	GPRIN3	p.T505A	tolerated(0.49)	benign(0.003)
	13.22			4	103501757	G	T	missense_variant	NFKB1	p.G266W	deleterious(0)	probably_damaging(1)
		17.07	rs77618489	4	103826685	T	A	stop_gained	SLC9B1	p.K440*		
16.13				4	119689452	C	A	missense_variant	SEC24D	p.L352F	deleterious(0)	possibly_damaging(0.681)
10			rs141970683	4	120488257	C	T	missense_variant	PDE5A	p.G250S	tolerated(0.49)	probably_damaging(0.777)
11.36			rs138835887	4	164394415	C	T	missense_variant	TKTL2	p.E158K	deleterious(0.01)	probably_damaging(1)
10			rs982730698	4	190864421	AT	A	frameshift_variant	FRG1	p.I43X		
	12.5			5	6491457	G	A	missense_variant	UBE2QL1	p.G161S	deleterious(0)	probably_damaging(1)
12.82		10	rs1579737436	5	42808388	T	G	missense_variant	SEPP1	p.D23G	tolerated(1)	benign(0)
	17.24			5	42808433	G	A	missense_variant	SEPP1	p.A8V	tolerated(0.12)	benign(0.022)
9.8			rs756935198	5	60831346	C	T	missense_variant	ZSWIM6	p.R761W	deleterious(0)	probably_damaging(1)
	14.71		rs754098115	5	70308523	T	C	missense_variant	NAIP	p.S74G	deleterious(0.1)	probably_damaging(0.801)
	14.71			5	70308528	G	A	missense_variant	NAIP	p.P72L	deleterious(0.17)	probably_damaging(0.676)
		25		5	70852736	T	A	missense_variant	BDP1	p.N2408K	tolerated(0.05)	benign(0.074)
12.77			rs767928406	5	126755885	G	A	missense_variant	MEGF10	p.E526K	deleterious(0.02)	possibly_damaging(0.801)
8.45				5	141039458	G	A	missense_variant	ARAP3	p.T1052M	deleterious(0)	probably_damaging(1)
	14.29		rs149514957	5	145393493	C	T	missense_variant	SH3RF2	p.R310W	deleterious(0)	probably_damaging(1)
	10.53			5	145886636	C	T	stop_gained	TCERG1	p.R926*		
		10.45	rs746300490	5	147861098	CT	C	frameshift_variant	HTR4	p.K390X		
12.28	10.17		rs201960506	5	150502549	C	T	missense_variant	ANXA6	p.D388N	tolerated(0.16)	benign(0.087)
		11.76	rs963142407	5	151784218	G	A	missense_variant	NMUR2	p.R153C	deleterious(0)	probably_damaging(1)
	11.76			5	154173387	T	G	missense_variant	LARP1	p.V222G	tolerated(0.32)	benign(0.027)
	9.8		rs1370186359	5	171510041	C	T	missense_variant	STK10	p.R578Q	tolerated(0.05)	benign(0)
	8		rs758448625	5	176296722	G	A	missense_variant	UNC5A	p.G243R	deleterious(0.01)	probably_damaging(0.999)
15.15				5	176318405	GG	CC	missense_variant	HK3	p.S81W	tolerated(0.95)	benign(0)
		10.14	rs777334601	5	180058713	C	T	missense_variant	FLT4	p.D42N	deleterious(0.01)	possibly_damaging(0.999)
12.73				5	180631713	T	G	missense_variant	TRIM7	p.H133P	deleterious(0)	probably_damaging(0.984)
17.39				5	180631723	G	T	missense_variant	TRIM7	p.C130S	deleterious(0)	probably_damaging(0.904)
	13.95		rs374957295	6	5369126	C	T	missense_variant	FARS2	p.T108L	deleterious(0)	probably_damaging(0.82)
15.04		11.35	rs781453322	6	10697597	C	T	missense_variant	PAK1IP1	p.T42I	deleterious(0.05)	benign(0.388)
9.8				6	24278352	C	T	missense_variant	DCDC2	p.V283M	deleterious(0.23)	probably_damaging(0.993)
		15.48		6	30708995	C	T	missense_variant	FLOT1	p.R109K	deleterious(0)	possibly_damaging(0.955)
15				6	31842596	G	T	missense_variant	SLC44A4	p.P124T	tolerated(0.08)	benign(0)
		13.41		6	33168107	C	A	missense_variant	RXRB	p.R36L	deleterious_low_confidence(0)	probably_damaging(0.993)
13.51			rs765836408	6	39846200	C	T	missense_variant	DAAM2	p.R461C	deleterious(0.05)	probably_damaging(1)
10			rs539287481	6	41250408	G	A	missense_variant	TREM1	p.T44M	deleterious(0.01)	benign(0.001)
14.29				6	56504246	A	G	splice_donor_variant	DST			

Table S1

VAF Teratoma (%)	VAF MNT (%)	VAF Melanoma (%)	rSID	CHROM	POS	REF	ALT	Consequence	SYMBOL	HGVSp_Short	SIFT	PolyPhen
11.86				6	64288830	C	T	missense_variant	PTP4A1	p.P76S	deleterious(0)	probably_damaging(0.968)
	10.53			6	76595777	C	T	stop_gained	MYO6	p.R825*		
	10.87		rs369773005	6	83905582	G	A	missense_variant	RWDD2A	p.R157Q	deleterious(0.01)	probably_damaging(1)
14.29				6	107955855	G	C	missense_variant	SOBP	p.G603R	deleterious_low_confidence(0.04)	probably_damaging(1)
12.5			rs567601349	6	125283914	C	G	missense_variant	RNF217	p.P75R	deleterious_low_confidence(0.04)	benign(0.117)
		11.36		6	150001575	C	A	missense_variant	LATS1	p.A677S	tolerated(0.09)	benign(0.374)
		33.33		6	161157958	CG	AC	missense_variant	PLG	p.P574H	deleterious(0.02)	probably_damaging(1)
	12.5		rs757360452	6	161508894	C	T	missense_variant	MAP3K4	p.R911C	tolerated(0.1)	benign(0.006)
11.54				6	165715287	T	G	missense_variant	C6orf118	p.E175A	tolerated(0.02)	probably_damaging(1)
	12.62			6	166779550	C	A	missense_variant	MPC1	p.V73L	deleterious(0.01)	probably_damaging(0.997)
12.5				7	1594924	G	A	missense_variant	TMEM184A	p.A66V	deleterious(0)	probably_damaging(0.994)
17.02			rs2963556	7	33014363	A	G	missense_variant	FKBP9	p.N119S	tolerated(1)	benign(0)
12			rs532143087	7	43484441	G	A	missense_variant	HECW1	p.R557Q	tolerated_low_confidence(0.06)	probably_damaging(1)
10.42			rs1252894599	7	43548590	C	T	missense_variant	HECW1	p.R1297W	deleterious(0)	probably_damaging(1)
	13.64		rs548117828	7	50468251	G	A	missense_variant	IKZF1	p.G496S	deleterious(0)	probably_damaging(1)
11.54			rs754843005	7	66410129	C	T	missense_variant	TMEM248	p.P109L	tolerated(0.66)	benign(0.049)
	10.64			7	77398024	G	T	missense_variant	RSBN1L	p.R510L	deleterious(0.04)	probably_damaging(1)
	10.64		rs373775990	7	92734891	G	A	missense_variant	SAMD9	p.R174C	deleterious(0.05)	benign(0.26)
	8.11			7	95775900	C	G	missense_variant	SLC25A13	p.V474L	tolerated(0.53)	benign(0.003)
	13.46			7	97482424	G	C	missense_variant	ASNS	p.T475S	tolerated(0.86)	benign(0)
	15.91		rs1200135918	7	97823658	C	T	missense_variant	LMTK2	p.S1294L	deleterious(0)	probably_damaging(1)
10.58				7	98579527	C	T	missense_variant	TRRAP	p.R2899C	deleterious(0)	probably_damaging(1)
12.5			rs780018734	7	100189485	G	A	missense_variant	FBXO24	p.R173Q	deleterious_low_confidence(0.01)	probably_damaging(1)
	12.5			7	100463889	T	G	missense_variant	SLC12A9	p.W803G	deleterious(0.02)	probably_damaging(0.998)
10.71			rs771305881	7	100777032	G	A	missense_variant	SERPINE1	p.G253R	deleterious(0.01)	probably_damaging(0.997)
		11.25		7	106508784	G	T	missense_variant	PIK3CG	p.D260Y	deleterious(0.03)	benign(0.006)
	9.43		rs139376972	7	122787316	G	A	missense_variant	SLC13A1	p.R237C	tolerated(1)	benign(0)
	11.76		rs773076395	7	127326707	G	A	missense_variant	SND1	p.R40H	tolerated(0.08)	benign(0.322)
		15.22		7	128506626	A	C	missense_variant	LOC100130705	p.T55P	tolerated(0.12)	benign(0.007)
12.77	10			7	138946169	AT	A	frameshift_variant	UBN2	p.C277X		
	11.11		rs185106716	7	143632716	C	T	stop_gained	OR2F2	p.R131*		
8.47			rs766657533	7	148767951	G	A	missense_variant	ZNF786	p.A552V	tolerated(0.28)	benign(0.307)
14.29			rs749339029	8	22105750	G	A	missense_variant	POLR3D	p.E149K	deleterious(0.01)	probably_damaging(1)
9.43				8	22273704	T	A	missense_variant	SLC39A14	p.L353Q	deleterious(0)	probably_damaging(1)
12.5				8	22273713	G	A	missense_variant	SLC39A14	p.G356D	deleterious(0)	probably_damaging(1)
10.17			rs149217492	8	22887166	G	A	missense_variant	TNFRSF10B	p.R145W	deleterious(0)	probably_damaging(0.972)
	10			8	25136134	A	G	missense_variant	DOCK5	p.T92A	deleterious(0.04)	benign(0.191)
		11.67	rs755674364	8	101730335	C	A	missense_variant	PABPC1	p.G123C	deleterious(0)	probably_damaging(1)
		11.27		8	143960542	G	A	stop_gained	CYP11B1	p.Q101*		
	9.84		rs782384815	8	144888639	G	A	missense_variant	SCRIB	p.R762W	deleterious(0)	probably_damaging(1)
	10.71			8	144990883	G	A	missense_variant	PLEC	p.S4506L	deleterious(0)	probably_damaging(1)
	8.2		rs374435478	8	145114633	G	A	missense_variant	OPLAH	p.R78C	deleterious(0)	probably_damaging(1)
		28.57	rs376030025	8	145727095	G	C	missense_variant	PPP1R16A	p.A466P	deleterious(0)	probably_damaging(1)
	7.35			9	16435990	G	A	stop_gained	BNC2	p.R700*		
12.5			rs370842526	9	18905872	G	C	missense_variant	ADAMTSL1	p.Q349H	tolerated(0.11)	probably_damaging(0.989)
	7.69			9	32634482	G	A	stop_gained	TAF1L	p.R366*		
		19.57	rs200731425	9	33798543	A	G	missense_variant	PRSS3	p.K186E	tolerated(1)	benign(0)
15				9	34623680	C	T	missense_variant	ARID3C	p.E203K	deleterious(0)	benign(0.315)
13.51			rs751290466	9	35059646	A	AT	frameshift_variant	VCP	p.N616KX		
	10.91		rs778023792	9	90745053	G	A	missense_variant	SPATA31C2	p.H967Y	tolerated(0.26)	benign(0.167)
25			rs368250201	9	97522657	C	T	missense_variant	C9orf3	p.R198C	tolerated(0.14)	benign(0)
		10.2		9	98691105	C	A	missense_variant	ERCC6L2	p.F581L	deleterious(0)	probably_damaging(0.999)
	10.42		rs759572823	9	100193272	C	T	missense_variant	TDRD7	p.R89C	tolerated(0.1)	benign(0.003)
21.74			rs753099999	9	117240876	C	T	missense_variant	DFNB31	p.R265Q	tolerated(0.08)	benign(0.009)
		20.51	rs758518892	9	121930001	G	C	missense_variant	BRINP1	p.C549W	deleterious(0)	probably_damaging(0.995)
9.68				9	131339180	G	C	missense_variant	SPTAN1	p.A244P	deleterious(0)	probably_damaging(0.999)
	12.5			9	133327700	T	A	missense_variant	ASS1	p.Y29N	deleterious(0)	probably_damaging(0.998)
9.43				9	136030674	G	A	missense_variant	GBGT1	p.T96I	tolerated_low_confidence(0.08)	benign(0.003)
8.33			rs75461307	9	136208483	C	T	missense_variant	MED22	p.D159N	tolerated_low_confidence(0.36)	possibly_damaging(0.804)
	12		rs148803403	9	136277935	C	T	missense_variant	REXO4	p.V227I	tolerated(0.51)	benign(0)
9.21			rs372292949	9	136535814	G	A	missense_variant	SARDH	p.A224V	deleterious(0.03)	possibly_damaging(0.917)
		23.64		9	138714186	T	A	missense_variant	CAMSAP1	p.Q496L	tolerated(0.09)	probably_damaging(1)
	9.26		rs779497777	9	140137961	G	A	missense_variant	TUBB4B	p.E431K	tolerated_low_confidence(0.14)	benign(0.065)
	10		rs139912371	10	1151084	C	T	missense_variant	WDR37	p.T327M	deleterious(0)	probably_damaging(1)
10				10	27702612	T	G	missense_variant	PTCHD3	p.T190P	tolerated(0.29)	benign(0.044)
9.8				10	35477188	G	A	missense_variant	CREM	p.G206E	deleterious(0)	probably_damaging(0.998)
13.64			rs121909283	10	72195155	C	T	missense_variant	NODAL	p.G260R	deleterious(0)	probably_damaging(1)
11.36			rs377111967	10	75185914	G	A	missense_variant	MSS51	p.R242W	deleterious(0)	possibly_damaging(0.655)
10.64				10	75227398	G	A	stop_gained	PPP3CB	p.R341*		
		14.58		10	85953339	C	T	missense_variant	CDHR1	p.P49S	deleterious(0.03)	benign(0.378)
	10.91			10	88704976	T	A	missense_variant	MMRN2	p.E150D	deleterious(0.07)	benign(0.251)
	10.64			10	89268219	G	A	missense_variant	MINPP1	p.G255E	deleterious(0)	probably_damaging(1)
	8.77		rs978681231	10	99656729	C	T	missense_variant	CRTAC1	p.G385R	tolerated(0.22)	probably_damaging(0.991)
	9.84		rs749797221	10	102795321	G	A	missense_variant	SFXN3	p.A81T	deleterious(0.01)	probably_damaging(1)
12.2			rs150975627	10	115664694	C	T	missense_variant	XPNPEP1	p.N628K	tolerated(0.3)	benign(0)
8.47			rs777887330	10	120801889	G	A	missense_variant	EIF3A	p.P1048L	deleterious(0.04)	benign(0.001)
	7.35			10	121203154	C	T	missense_variant	GRK5	p.R281C	deleterious(0)	probably_damaging(1)
	11.11		rs557203104	10	124089074	GG	AA	missense_variant	BTBD16	p.G331N	tolerated(0.12)	probably_damaging(0.665)
	12.82			10	127265416	C	T	missense_variant	TEX36	p.G98R	tolerated(0.77)	benign(0.001)
8.7		17.91		10	134218818	C	T	missense_variant	PWWP2B	p.R272C	deleterious(0)	probably_damaging(1)
10.42				10	135097484	G	A	missense_variant	TUBGCP2	p.R683W	deleterious(0)	probably_damaging(0.999)
10.42			rs768965722	11	403259	G	A	missense_variant	PKP3	p.R640H	deleterious(0.04)	probably_damaging(0.999)
	13.33		rs1395404818	11	619049	G	T	missense_variant	CDHR5	p.P504T	deleterious(0)	probably_damaging(0.985)
12.31				11	626928	G	A	missense_variant	SCT	p.R45W	deleterious(0.01)	benign(0.211)
	17.65			11	639956	G	C	missense_variant	DRD4	p.R236P	tolerated(0.08)	benign(0.001)
8.96			rs147542803	11	10514915	C	T	missense_variant	AMPD3	p.A320V	deleterious(0.01)	probably_damaging(1)
6.33			rs746245139	11	46329469	C	T	missense_variant	CREB3L1	p.S145L	tolerated(0.07)	possibly_damaging(0.682)
		17.07		11	46717544	C	T	missense_variant	ARHGAP1	p.M38I	tolerated(0.32)	benign(0.003)
	10			11	48267445	G	A	missense_variant	OR4Q2	p.A264T	tolerated(0.11)	probably_damaging(0.529)
11.11			rs761076139	11	63676695	G	A	missense_variant	MARK2	p.E776K	deleterious(0)	probably_damaging(0.994)
	11.63		rs1203009966	11	64876776	C	T	missense_variant	RASGRP2	p.R550H	deleterious(0)	probably_damaging(0.999)
8.82			rs1205283058	11	64876776	C	T	missense_variant	VPS51	p.R490C	deleterious(0)	probably_damaging(1)
26.32			rs1205283058	11	65000776	T	C	non_coding_transcript_exon_variant	SLC22A20			
	18.75		rs1039859068	11	65633833	C	T	missense_variant	CTSF	p.R217Q	tolerated(0.3)	possibly_damaging(0.769)
	13.64		rs571184986	11	68377484	G	A	missense_variant	PPP6R3	p.E775K	tolerated(0.2)	probably_damaging(0.998)
7.81				11	70007339	A	G	missense_variant	ANO1	p.N493D	tolerated(0.09)	possibly_damaging(0.469)
9.09			rs183610034	11	77781037	C	T	missense_variant	NDUFC2	p.R119H	deleterious(0)	benign(0.213)
13.33				11	86665931	A	T	missense_variant	FZD4	p.L66Q	deleterious(0)	probably_damaging(0.971)
		18.89		11	92577163	G	T	stop_gained	FAT3	p.E3544*		
9.09				11	118629536	C	T	missense_variant	DDX6	p.A314T	tolerated(0.05)	probably_damaging(0.993)
	11.11		rs771967603	11	119061042	AG	A	frameshift_variant	CCDC153	p.P200X		
14.29		10.08	rs199970781	11	123894602	A	C	missense_variant	OR10G9	p.K295Q	deleterious(0.02)	benign(0.265)
		15.15	rs779611109	11	125817742	G	A	missense_variant	VSIG10L2	p.V82I		
8.33			rs1273194927	11	129996703	G	A	missense_variant	APLP2	p.R400Q	deleterious(0)	probably_damaging(0.997)
16.67			rs1293235453	11	130781542	C	T	missense_variant	SNX19	p.R600Q	deleterious(0)	probably_damaging(1)
10				12	662815	G	A	missense_variant	B4GALNT3	p.D576N	deleterious(0.21)	benign(0.386)
	11.76			12	968512	AA	TT	missense_variant	WNK1	p.K501I	deleterious(0)	probably_damaging(0.997)
	11.86		rs1379873399	12	6334637	G	A	missense_variant	CD9	p.D38N	deleterious(0.01)	probably_damaging(1)
	10		rs374216855	12	6566838	G	A	missense_variant	TAPBPL	p.E278K	deleterious(0)	probably_damaging(1)
	10.39			12	10565202	A	G	missense_variant	KLRC3	p.I23T	deleterious_low_confidence(0.01)	benign(0.039)
	11.11		rs539707080	12	11545900	T	G	missense_variant	PRB2	p.Q371P	tolerated_low_confidence(0.65)	benign(0)
	14.58		rs766060662	12	13716136	C	T	missense_variant	GRIN2B	p.L1346K	tolerated(0.18)	possibly_damaging(0.597)
10				12	18576877	A	C	splice_acceptor_variant	PIK3C2G			
	10.91		rs764046781	12	22797153	C	T	missense_variant	ETNK1	p.S231L	deleterious(0)	benign(0.264)
11.32	10.07	38.04	COSM1360847;COSM27159	12	25380271	C	T	missense_variant	KRAS	p.E63K	deleterious(0)	probably_damaging(0.993)
	10.17		rs71434326	12	40882710	G	A	missense_variant	MUC19	p.A5319T		
	7.94		rs145821678	12	44537360	G	A	missense_variant	TMEM117	p.R148Q	tolerated(0.11)	probably_damaging(0.999)
10.71			rs121912882	12	48373317	G	A	missense_variant	COL2A1	p.R835C	deleterious(0)	probably_damaging(0.999)
	13.51			12	48477396	G	C	missense_variant	SENP1	p.R177Q	tolerated(0.06)	probably_damaging(0.992)
	10			12	49228116	C	T	missense_variant	DDX23	p.R516H	tolerated(0.17)	probably_damaging(1)
	9.8		rs780474358	12	50191090	G	A	missense_variant	NCKAP5L	p.R185W	deleterious(0)	probably_damaging(0.996)
		10.67		12	50746915	GA	G	frameshift_variant	FAM186A	p.L1233X		
35.48	12.96			12	54675886	C	T	missense_variant	HNRNPA1	p.P98S	deleterious(0.04)	probably_damaging(0.965)
13.51			rs1325310132	12	56995829	C	T	missense_variant	BAZ2A	p.R1161Q	tolerated(0.12)	benign(0)
12.5				12	57920432	G	A	missense_variant	MBD6	p.G502R	deleterious_low_confidence(0)	benign(0)
15.79		19.35		12	57920442	C	G	missense_variant	MBD6	p.P505R	deleterious_low_confidence(0)	probably_damaging(0.998)
	10.87			12	57921744	C	G	missense_variant	MBD6	p.P784A	tolerated_low_confidence(0.13)	benign(0.202)
22.45			rs747887445	12	58100652	A	C	missense_variant	OS9	p.H230P	deleterious(0)	probably_damaging(0.999)
16.67			rs138728046	12	58204726	G	A	stop_gained	AVIL	p.R199*		
8.57			rs761266832	12	70704726	C	T	missense_variant	CNOT2	p.D34N	deleterious_low_confidence(0.04)	possibly_damaging(0.553)
	9.26		rs149558160	12	107393778	C	T	missense_variant	CRY1	p.R256Q	deleterious(0)	probably_damaging(0.997)
11.11			rs767230315	12	112184069	C	T	missense_variant	ACAD10	p.T746M	tolerated(0.43)	benign(0.009)
	10.87			12	112669480	C	T	missense_variant	HECTD4	p.A1841T	deleterious(0)	probably_damaging(0.999)
12.82			rs779192016	12	113812337	G	A	missense_variant	PLBD2	p.S201N	tolerated(0.56)	benign(0.17)
10.71				12	117672473	GT	AA	missense_variant	NOS1	p.N1044I	deleterious(0)	probably_damaging(1)
24				12	121712209	A	T	missense_variant	CAMKK2	p.S41T	deleterious_low_confidence(0.01)	possibly_damaging(0.89)
11.76			rs756695315	12	123341599	C	T	missense_variant	HIP1R	p.T551M	deleterious(0)	possibly_damaging(0.646)
37.5			rs61940805	12	126137053	A	G	missense_variant	TMEM132B	p.T656A	tolerated(0.14)	benign(0.208)
		17.02		13	27216444	TT	AA	missense_variant	WASF3	p.L13K	deleterious(0)	probably_damaging(0.999)
16			rs771122221	13	41705572	C	T	missense_variant	KBTBD6	p.C359Y	tolerated(0.97)	benign(0)
9.09			rs370360481	13	42385463	G	A	missense_variant	VWA8	p.A654V	deleterious(0)	benign(0)
	10.87		rs371060996	13	50134166	G	A	missense_variant	RCBTB1	p.T111M	deleterious(0.04)	probably_damaging(0.984)
		31.07		13	51363787	C	CT	frameshift_variant	FAM124A	p.S3925X		
14.71			rs199616382	14	21501986	C	T	stop_gained	RP11-998D10.1	p.R108*		
	14.29		rs373719056	14	37754558	C	T	missense_variant	MIPOL1	p.R177C	deleterious(0)	probably_damaging(1)
11.9			rs149705965	14	57070588	C	T	missense_variant	TMEM260	p.R134C	deleterious(0)	probably_damaging(1)
15.38				14	61190087	C	G	missense_variant	SIX4	p.A36P	tolerated_low_confidence(0.19)	benign(0.17)
9.43				14	61746821	C	T	missense_variant	TMEM30B	p.D349N	tolerated_low_confidence(0.3)	possibly_damaging(0.727)
	11.11			14	65209071	A	T	missense_variant	PLEKHG3	p.R890W	deleterious(0)	probably_damaging(1)
	10.87			14	65209077	G	T	missense_variant	PLEKHG3	p.P892S	deleterious(0.15)	probably_damaging(1)
		8.79		14	68272216	G	T	missense_variant	ZFYVE26	p.S379R	deleterious(0)	probably_damaging(1)
12.5			rs764251926	14	74759528	C	T	missense_variant	ABCD4	p.V183I	tolerated(0.81)	benign(0)
	10.71		rs770999611	14	78392249	G	A	missense_variant	ADCK1	p.R384Q	deleterious(0)	probably_damaging(1)
6.17			rs1408576877	14	89016725	G	A	missense_variant	PTPN21	p.R13W	deleterious(0)	probably_damaging(1)
		24	rs374851347	14	89148283	C	T	stop_gained	EML5	p.W987*		
11.63				14	94394894	G	A	missense_variant	FAM181A	p.S150T	tolerated(0.36)	
11.63			rs768758518	14	94754861	C	T	missense_variant	SERPINA10	p.E252K	deleterious(0.03)	benign(0.086)
	12.82		rs763948380	14	99665423	G	A	missense_variant	SETD3	p.R460C	deleterious(0)	probably_damaging(1)
	11.36		rs756353033	14	105211201	G	A	missense_variant	ADSSL1	p.G376S	deleterious(0)	probably_damaging(0.999)
10.34			rs201179900	14	105352753	C	T	missense_variant	CEP170B	p.P726L	tolerated(0.16)	probably_damaging(0.995)
8.77			rs1203995382	15	22997855	G	A	missense_variant	CYFIP1	p.R1034Q	tolerated(0.17)	probably_damaging(0.995)
		21.74	rs112738749	15	23685206	C	G	missense_variant	GOLGA6L2	p.A806P	deleterious_low_confidence(0)	unknown(0)
10.29		10.64		15	64385892	CT	C	frameshift_variant	FAM96A	p.G25X		
		10.64		15	74622585	T	C	missense_variant	CCDC33	p.L42P	deleterious(0.03)	benign(0)
		10	rs762588978	15	74622586	G	A	missense_variant	CCDC33	p.R43Q	deleterious(0.05)	possibly_damaging(0.732)
		18.97	rs200437529	15	89400137	A	G	missense_variant	ACAN	p.T1441A	tolerated(0.41)	benign(0.23)
10.87				15	90610455	C	T	missense_variant	ZNF710	p.S29F	deleterious_low_confidence(0)	probably_damaging(0.998)

VAF Teratoma (%)	VAF MNT (%)	VAF Melanoma (%)	rSID	CHROM	POS	REF	ALT	Consequence	SYMBOL	HGVSp_Short	SIFT	PolyPhen
	10.42		rs1023592505	15	90628058	C	T	missense_variant	IDH2	p.G421S	deleterious_low_confidence(0.01)	probably_damaging(1)
	11.49		.	15	93524121	G	A	missense_variant	CHD2	p.G985R	deleterious(0.01)	probably_damaging(0.994)
17.5				16	1435260	C	G	missense_variant	UNKL	p.A402P	deleterious(0.01)	probably_damaging(0.009)
7.58			rs780635813	16	1719068	C	T	missense_variant	CRAMP1L	p.P509L	deleterious(0.01)	probably_damaging(1)
		15.79	rs1034055795	16	2018522	G	A	missense_variant	RNF151	p.A111T	tolerated(0.35)	possibly_damaging(0.485)
12			rs143442513	16	2282198	G	A	missense_variant	E4F1	p.V148M	deleterious(0.01)	probably_damaging(1)
	31.58		rs369048340	16	2349500	C	T	missense_variant	ABCA3	p.V549I	tolerated(0.18)	benign(0.284)
21.21			rs1035056179	16	2983478	A	C	missense_variant	FLYWCH1	p.T382P	deleterious_low_confidence(0)	possibly_damaging(0.948)
8.62			rs768816607	16	3606957	G	A	missense_variant	NLRC3	p.A713V	tolerated(0.11)	probably_damaging(0.995)
	13.33			16	3651040	A	G	missense_variant	SLX4	p.L368P	deleterious(0)	probably_damaging(1)
11.63			rs1401593486	16	3778563	C	T	missense_variant	CREBBP	p.G2162E	deleterious_low_confidence(0)	possibly_damaging(0.9)
	17.95		rs767541693	16	3808047	G	T	missense_variant&splice_region_variant	CREBBP	p.D1124E	deleterious(0)	possibly_damaging(0.915)
	9.26			16	4563005	G	A	missense_variant	CDIP1	p.T101M	tolerated(0.14)	benign(0.04)
11.63			rs370228529	16	4933630	G	A	missense_variant	PPL	p.R1676C	deleterious(0)	probably_damaging(1)
	11.9		rs201222846	16	17228388	G	A	missense_variant	XYLT1	p.R657C	deleterious(0)	probably_damaging(1)
9.26			rs1198488974	16	18853724	C	T	missense_variant	SMG1	p.R2091H	tolerated(0.37)	benign(0.015)
11.63			rs200495483	16	19883969	C	T	missense_variant	GPRC5B	p.A67T	tolerated(0.3)	probably_damaging(0.98)
	8.33		rs369137473	16	20497980	G	A	missense_variant	ACSM2A	p.G572R	tolerated(0.27)	benign(0.081)
	10.64		rs150949875	16	23383109	C	T	missense_variant	SCNN1B	p.R398C	deleterious(0)	probably_damaging(1)
	10.34			16	27549562	G	A	missense_variant	GTF3C1	p.R183W	deleterious(0)	probably_damaging(1)
9.26			rs749404725	16	27777751	C	T	missense_variant	KIAA0556	p.R1311C	deleterious(0)	probably_damaging(1)
11.11			rs143560174	16	30018536	C	T	missense_variant	DOC2A	p.R14H	deleterious_low_confidence(0)	unknown(0)
	10.64			16	30531196	G	A	stop_gained	ZNF768	p.R89*		
9.8			rs75918054	16	31089651	G	A	missense_variant	ZNF646	p.R669Q	tolerated(0.21)	possibly_damaging(0.831)
10.87				16	31276745	T	A	missense_variant	ITGAM	p.V55E	tolerated(1)	benign(0.015)
	13.16		rs1257023502	16	55575826	G	A	missense_variant	LPCAT2	p.R168Q	deleterious_low_confidence(0)	unknown(0)
10.2			rs1257988371	16	55880488	G	A	missense_variant	CES5A	p.R535W	deleterious(0)	probably_damaging(0.999)
10.53			rs1460745902	16	56503928	C	T	missense_variant	OGFOD1	p.T305M	deleterious(0.05)	probably_damaging(0.785)
30.3				16	56782200	AA	TT	missense_variant	NUP93	p.E14V	deleterious(0)	probably_damaging(0.935)
	15.38		rs1340092292	16	57974199	G	A	missense_variant	CNGB1	p.S383L	tolerated_low_confidence(0.13)	benign(0.088)
	16.22			16	67516705	T	C	missense_variant	AGRP	p.D78G	tolerated(1)	
15.38			rs779606514	16	81183412	T	C	missense_variant	PKD1L2	p.S1546G	deleterious(0.03)	benign(0.337)
11.48				16	84531062	T	C	missense_variant	TLDC1	p.N12S	tolerated_low_confidence(0.07)	benign(0.006)
	11.63		rs776801976	16	88725117	C	T	missense_variant	MVD	p.D28N	tolerated(0.14)	benign(0.09)
12.9			rs1323835920	16	90086234	A	G	missense_variant&NMD_transcript_variant	DBNDD1	p.V19A		unknown(0)
	11.11		rs767109499	17	3978671	G	A	missense_variant	ZZEF1	p.T1096M	deleterious(0.04)	probably_damaging(0.999)
8.93			rs757825581	17	5268516	G	A	missense_variant	RABEP1	p.E590K	deleterious(0.05)	benign(0.044)
		12.63	COSM983903;rs769406740	17	7164213	C	T	missense_variant	CLDN7	p.A97T		unknown(0)
10.42			rs375375075	17	7293739	G	A	stop_gained	TMEM256-PLSCR3	p.R285*		
44.83	32	42.86	rs1567551073	17	7578183	CG	G	frameshift_variant	TP53	p.P222X		
	10.61			17	8064837	C	G	missense_variant	VAMP2	p.M96I	deleterious(0.05)	benign(0.045)
20				17	8742966	A	T	missense_variant	PIK3R6	p.L21H	deleterious(0)	probably_damaging(1)
19.23				17	8742972	C	G	missense_variant	PIK3R6	p.R19P	deleterious(0)	probably_damaging(1)
	12.5			17	16055259	C	T	splice_donor_variant	NCOR1			
	15.38		rs372588990	17	17896113	C	T	missense_variant	LRRC48	p.T160M	deleterious(0.01)	possibly_damaging(0.765)
16.67			rs751392060	17	18874526	G	A	missense_variant	SLC5A10	p.D198N	deleterious(0.01)	probably_damaging(1)
8.33			rs376516509	17	25950493	G	A	missense_variant	KSR1	p.R72Q	tolerated(0.45)	possibly_damaging(0.663)
		17.86		17	27024999	G	A	missense_variant	SUPT6H	p.E1467K	tolerated(0.45)	benign(0.021)
17.65				17	30325720	G	A	missense_variant	SUZ12	p.V640I	deleterious(0.11)	possibly_damaging(0.78)
		17.39		17	33805097	G	C	missense_variant	SLFN12L	p.P401A	deleterious(0.02)	possibly_damaging(0.517)
	12.24		rs1194456402	17	37351199	G	A	stop_gained	CACNB1	p.R37*		
	9.8		rs373489642	17	38126842	G	A	missense_variant	GSDMA	p.R167Q	tolerated(0.22)	benign(0.233)
10.29			rs201060748	17	39406130	G	A	missense_variant	KRTAP9-4	p.R53H	tolerated(0.15)	benign
	11.11		rs768412142	17	41165100	C	T	stop_gained	IFI35	p.R53*		
13.73			rs1276320435	17	45890676	C	T	missense_variant	OSBPL7	p.E565K	deleterious(0)	probably_damaging(1)
	14.29		rs375207701	17	46607028	G	A	missense_variant	HOXB1	p.R263*		
	10.2		rs999916427	17	48653148	T	C	missense_variant	CACNA1G	p.V462A	tolerated(0.13)	benign(0)
8.77			rs1223463280	17	60447683	G	A	missense_variant&splice_region_variant	EFCAB3	p.G12R	deleterious_low_confidence(0.04)	probably_damaging(0.957)
10.87				17	60755982	G	A	missense_variant	MRC2	p.A724T	tolerated(0.34)	possibly_damaging(0.58)
7.94			rs763689978	17	72245199	C	T	missense_variant	TTYH2	p.T285M	deleterious(0)	probably_damaging(1)
10.42				17	73316559	A	C	missense_variant	GRB2	p.F141V	tolerated(0.57)	benign(0)
	11.86		rs1294999297	17	73872359	G	C	stop_gained	TRIM47	p.S329*		
15.62			rs200342777	17	73915929	G	A	missense_variant	FBF1	p.S638L	tolerated(0.06)	possibly_damaging(0.58)
	8.33		rs760704583	17	74536288	G	A	missense_variant	PRCD	p.R22Q	tolerated_low_confidence(0.13)	benign(0.168)
10.91			rs370495709	17	76236014	G	A	missense_variant	TMEM235	p.E382K	tolerated_low_confidence(0.19)	benign(0.227)
10.42			rs757161991	17	76526516	C	T	missense_variant	DNAH17	p.D1065N	tolerated(0.1)	benign(0.07)
13.51			rs749901447	17	79031687	C	T	missense_variant	BAIAP2	p.T46M	deleterious(0.02)	probably_damaging(1)
11.76				17	79100339	G	A	missense_variant	AATK	p.R215W	deleterious(0)	probably_damaging(1)
		21.05	rs774275112	18	5291149	C	T	missense_variant	ZBTB14	p.R353K	deleterious(0.01)	possibly_damaging(0.941)
	10.42		rs745969754	18	7080343	G	A	missense_variant	LAMA1	p.R59W	deleterious(0.02)	probably_damaging(0.937)
10			rs745694128	18	10698994	C	T	missense_variant	PIEZO2	p.R2095Q	tolerated(0.07)	probably_damaging(1)
12.2				18	19070185	C	T	missense_variant	GREB1L	p.A859V	deleterious(0)	probably_damaging(1)
	10.87		rs769397614	18	33059306	C	T	missense_variant	INO80C	p.A113T	tolerated(0.17)	possibly_damaging(0.933)
9.43			rs756508090	18	44140082	C	T	missense_variant	LOXHD1	p.V731M	deleterious(0.05)	possibly_damaging(0.791)
11.36			rs1319522958	18	56171336	G	A	missense_variant	ALPK2	p.P2025L	deleterious(0)	benign(0)
8.2			rs768439708	19	643410	C	T	stop_gained&splice_region_variant	FGF22	p.R66*		
10			rs375772213	19	861703	C	T	missense_variant	CFD	p.S121L	deleterious(0.05)	probably_damaging(0.984)
9.09			rs759410596	19	994035	C	T	missense_variant	WDR18	p.S368L	tolerated(0.27)	benign(0.001)
16.13			rs200886519	19	3196270	G	A	missense_variant	NCLN	p.V204M	deleterious(0.01)	probably_damaging(0.97)
	10		rs758119857	19	3613334	G	A	missense_variant	CACTIN	p.P435L	tolerated(0.07)	benign(0.223)
7.94			rs1334513817	19	3618903	G	A	missense_variant	CACTIN	p.R310C	deleterious(0)	probably_damaging(0.952)
10.87				19	4054369	G	A	missense_variant	ZBTB7A	p.P288S	deleterious(0.01)	possibly_damaging(0.845)
	9.43		rs768236560	19	4254455	G	A	missense_variant	CCDC94	p.R125Q	tolerated(0.17)	benign(0.131)
25.71	20.59	16.67	rs1555674896	19	4499647	G	A	missense_variant	HDGFRP2	p.E579K	tolerated(0.35)	unknown(0)
	12.5		rs746370938	19	5679653	C	T	missense_variant	C19orf70	p.A51T	deleterious(0.02)	probably_damaging(1)
	9.26		rs1189018419	19	5790273	C	T	missense_variant	DUS3L	p.E58K	deleterious(0.32)	benign(0.005)
8.33				19	6418060	G	A	missense_variant	KHSRP	p.R304W	deleterious(0)	probably_damaging(1)
	11.9		rs143346745	19	7692212	G	A	stop_gained	XAB2	p.R147*		
	10		rs1056634030	19	9089312	C	G	missense_variant	MUC16	p.P835A	tolerated_low_confidence(0.08)	possibly_damaging(0.794)
14.29				19	10081306	C	T	missense_variant	COL5A3	p.G1310S	deleterious(0)	probably_damaging(1)
22.73				19	10081102	C	CT	frameshift_variant	COL5A3	p.G1058EX		
	11.11		rs368092939	19	10431342	C	T	missense_variant	RAVER1	p.D604N	deleterious(0.01)	possibly_damaging(0.649)
10			rs150808873	19	10662902	C	T	missense_variant	ATG4D	p.R382C	deleterious(0)	probably_damaging(1)
11.36			rs770755291	19	14910637	G	GA	frameshift_variant	OR7C1	p.F104FX		
	11.36			19	16908608	G	A	missense_variant	NWD1	p.D989N	deleterious(0.04)	probably_damaging(1)
		8.62		19	17015094	G	A	missense_variant	CPAMD8	p.P1445L	deleterious(0)	probably_damaging(0.999)
9.09			rs765297024	19	17452313	C	T	missense_variant	GTPBP3	p.P427L	deleterious(0)	probably_damaging(0.999)
	11.9		rs750633279	19	19655888	G	A	missense_variant	CILP2	p.R845H	deleterious(0)	probably_damaging(0.998)
10.42				19	22124140	C	T	missense_variant	ZNF208	p.E105K	tolerated_low_confidence(0.95)	unknown(0)
	10.81			19	35232061	C	A	missense_variant	ZNF181	p.H303N	deleterious(0)	probably_damaging(0.998)
	9.33			19	35940743	C	G	missense_variant	FFAR2	p.P43A	deleterious(0)	probably_damaging(0.992)
7.23			rs1165005487	19	36210811	C	T	missense_variant	KMT2B	p.R189W	deleterious_low_confidence(0)	probably_damaging(1)
	9.46		rs1402350378	19	36388578	G	A	missense_variant	NFKBID	p.P146L	tolerated(0.89)	benign(0)
	10.42		rs948675160	19	36388627	C	T	missense_variant	NFKBID	p.E130K	tolerated(0.14)	probably_damaging(0.987)
	25			19	36497486	A	T	missense_variant	SYNE4	p.W236R	deleterious(0.05)	possibly_damaging(0.901)
	11.11			19	38964329	A	G	missense_variant	RYR1	p.T1360A	tolerated(0.79)	benign(0.043)
11.54			rs575947922	19	40728306	C	T	missense_variant	CNTD2	p.A131T	deleterious(0)	probably_damaging(1)
9.86			rs886042356	19	41925120	C	T	missense_variant	BCKDHA	p.R189C	deleterious(0.01)	probably_damaging(1)
16				19	44223040	G	A	stop_gained	IRGC	p.W110*		
8.93			rs777898158	19	45899860	C	T	missense_variant	PPP1R13L	p.G219R	deleterious_low_confidence(0)	probably_damaging(0.999)
8.97			rs370742577	19	48863379	C	T	missense_variant	TMEM143	p.V107M	tolerated(0.07)	probably_damaging(0.997)
12.2				19	49232678	A	C	missense_variant	RASIP1	p.V450G	deleterious(0)	probably_damaging(0.895)
16.13				19	49658478	G	A	missense_variant	HRC	p.P6L	deleterious(0)	probably_damaging(0.964)
10.42			rs372510933	19	50099706	G	A	missense_variant	PRR12	p.R705H	deleterious(0)	probably_damaging(0.999)
11.54				19	50391777	A	AC	frameshift_variant	TBC1D7	p.T615TX		
	12.82		rs145414197	19	53572897	C	T	missense_variant	ZNF160	p.R297H	tolerated(0.14)	benign(0.067)
	14.29			19	57722922	A	G	missense_variant	ZNF264	p.K153E	tolerated(0.13)	benign(0.067)
12			rs1410174208	20	2637177	C	T	stop_gained	NOP56	p.R381*		
	10	7.59		20	5556089	C	T	missense_variant	GPCPD1	p.R324Q	deleterious(0)	probably_damaging(1)
	12.82			20	31381401	G	A	missense_variant&splice_region_variant	DNMT3B	p.E376Q	tolerated(0.08)	benign(0)
8.06			rs766976346	20	32232435	G	A	missense_variant	CBFA2T2	p.D591N	deleterious_low_confidence(0)	probably_damaging(1)
11.76			rs141372100	20	33447395	G	A	missense_variant	GGT7	p.R289W	deleterious(0)	probably_damaging(0.995)
			rs994772771	20	60847197	C	T	missense_variant	OSBPL2	p.T92M	deleterious(0)	probably_damaging(1)
	10.42			20	60885573	A	T	missense_variant	LAMA5	p.L3501Q	deleterious(0)	probably_damaging(0.964)
12.82				20	60926976	G	G	missense_variant	LAMA5	p.V283L	deleterious(0.02)	probably_damaging(0.964)
10.87				20	62194395	A	C	missense_variant	HELZ2	p.V1358G	deleterious(0)	benign(0.317)
	12.86			20	62572521	G	T	missense_variant	UCKL1	p.P316Q	tolerated_low_confidence(0.46)	probably_damaging(0.988)
	10.53		rs763982889	21	37734524	C	T	missense_variant&splice_region_variant	MORC3	p.R484W	deleterious(0)	probably_damaging(0.978)
10.64				21	43299246	G	C	missense_variant	PRDM15	p.R36G	deleterious_low_confidence(0.05)	benign(0)
	18.92			21	43319284	T	C	missense_variant	C2CD2	p.D428G	tolerated(0.18)	benign(0.006)
8.77				21	47421908	C	T	stop_gained	COL6A1	p.Q664*		
21.74				22	17600628	T	G	missense_variant	CECR6	p.S464R	tolerated(0.06)	possibly_damaging(0.681)
	13.89		rs1195659276	22	20759722	G	A	missense_variant	ZNF74	p.G139S	deleterious_low_confidence(0)	probably_damaging(0.957)
	11.9		rs372979261	22	20819206	C	T	missense_variant	KLHL22	p.V351I	tolerated(0.1)	probably_damaging(0.957)
	10.53			22	21800907	C	T	missense_variant	HIC2	p.R575C	deleterious(0)	benign(0.12)
		35.29	rs769371624	22	23077461	C	T	missense_variant	IGLV1-18	p.P80S	tolerated_low_confidence(0.25)	benign(0.026)
12			rs41277283	22	23154645	C	T	stop_gained	IGLV3-10	p.R72*		
	20			22	23956321	C	T	splice_donor_variant	C22orf43			
12.5			rs899565528	X	45574145	A	G	missense_variant	NUP50	p.T123A	tolerated(0.54)	benign(0)
	10.42		rs772293670	X	7066150	G	A	missense_variant	HDHD1	p.A2V	tolerated(0.17)	benign(0.001)
10.94				X	15790687	G	A	missense_variant	CA5B	p.R72C	tolerated(0.71)	benign(0)
	15.15		rs144980753	X	18342162	G	A	missense_variant	SCML2	p.R72C	tolerated(0.09)	benign(0.11)
26.32				X	24859804	C	G	missense_variant	POLA1	p.H125D	deleterious(0.41)	probably_damaging(1)
20.83				X	24859809	A	T	missense_variant	POLA1	p.K1253N	deleterious(0)	benign(0.048)
47.92	42.5	47.46		X	37028566	C	A	missense_variant	FAM47C	p.P695T	tolerated(0.07)	possibly_damaging(0.721)
	15.79		rs782680032	X	48123289	G	A	missense_variant	SSX1	p.D135N	tolerated(0.43)	probably_damaging(0.897)
10.64				X	49065814	G	A	missense_variant	CACNA1F	p.R1621W		probably_damaging(1)
		29.41		X	49070342	C	G	missense_variant	CACNA1F	p.W1243C		probably_damaging(1)
	12.2			X	71681921	C	T	missense_variant	HDAC8	p.R222Q	deleterious(0)	probably_damaging(1)
9.09			rs61754467	X	73812036	G	A	missense_variant	RLIM	p.R372W	deleterious(0)	probably_damaging(1)
	11.76			X	75649806	G	A	missense_variant	MAGEE1	p.V495I	deleterious(0)	probably_damaging(1)
13.89				X	103903678	T	C	splice_donor_variant	IL1RAPL2			
	11.9			X	134166480	T	A	missense_variant	FAM127A	p.W23R	tolerated(0.26)	probably_damaging(0.98)
	10.42			X	135455125	A	C	missense_variant	GPR112	p.T2358P	tolerated(0.17)	probably_damaging(0.997)
	11.9			X	150345312	T	C	missense_variant	GPR50	p.V40A	tolerated(0.1)	benign(0.053)
8.33				X	153578199	G	A	missense_variant	FLNA	p.A2417V	deleterious(0)	probably_damaging(0.997)

Table S2

Gene	Weighted score	Gene	Weighted score	Gene	Weighted score	Gene	Weighted score	Gene	Weighted score	Gene	Weighted score
PIK3R6	1	VPS51	1	IGLV3-10	1	IL1RAPL2	1	SOBP	1	SNRK	2
GGT7	1	MRC2	1	FRG1	1	IRGC	1	ABCG2	1	OSBPL7	2
TRRAP	1	MEGF10	1	DIRC2	1	DOC2A	1	TMEM260	1	SENP1	2
FZD4	1	CNOT2	1	FBXO24	1	TMEM256-PLSCR3	1	AFF1	1	MMRN2	2
TKTL2	1	KLHL21	1	PMS1	1	VCP	1	PKD1L2	1	CILP2	2
OR7C1	1	ZDHHC3	1	TRNP1	1	SLC22A20	1	PPP1R12B	1	POLA1	2
PKP3	1	TNFRSF10B	1	C4BPA	1	FAM181A	1	DDX6	1	GPR160	2
PLCH2	1	DST	1	COL5A3	1	NHLRC2	1	CCDC37	1	PRCD	2
NUP50	1	NDUFC2	1	TTN	1	COL2A1	1	PWWP2B	1	KLF18	2
TREM1	1	PTP4A1	1	SERPINE1	1	ARHGEF11	1	GPRC5B	1	SMARCAL1	2
ZBTB7A	1	NMUR2	1	WDR18	1	RP11-998D10.1	1	GALNT5	1	LAMA5	2
ZSWIM6	1	PIK3R6	1	RLIM	1	E4F1	1	HECW1	1	CBFA2T2	2
KCNMB3	1	BSN	1	CYFIP1	1	CACNA1F	1	GPR35	1	SEC24D	2
PER3	1	HS6ST1	1	PASK	1	OS9	1	FLYWCH1	1	RYK	2
MSS51	1	EPAS1	1	APLP2	1	CAMKK2	1	ATG4D	1	NCOR1	2
SNX19	1	KIAA0556	1	EVA1A	1	OBSCN	1	CNTD2	1	NAIP	2
SLC39A14	1	ITIH4	1	NCLN	1	SIX4	1	NODAL	1	XYLT1	2
MBD6	1	CAMTA1	1	SLC39A14	1	TMEM30B	1	HTT	1	C2CD2	2
TMEM132B	1	FBF1	1	DCDC2	1	TMEM184A	1	NOC2L	1	SCN11A	2
FLNA	1	PPP3CB	1	NUP93	1	DAAM2	1	TMEM125	1	TUBB4B	2
ANO1	1	UVSSA	1	TMEM51	1	PRR12	1	UNKL	1	MYO6	2
DBNDD1	1	COL6A1	1	ALPI	1	HECW1	1	CREB3L1	1	FAM127A	2
GBGT1	1	ACAD10	1	TLDC1	1	ADAMTSL4	1	TOMM70A	1	SEPP1	2
SERPINA10	1	GPR137B	1	TIGIT	1	VWA8	1	LOXHD1	1	CRY1	2
PTPN21	1	WHSC1	1	ZNF646	1	EFCAB3	1	FAP	1	INTS3	2
SPTAN1	1	KRTAP9-4	1	STAB1	1	AMPD3	1	B4GALNT3	1	LMTK2	2
BCKDHA	1	ZNF786	1	TUBGCP2	1	SLC5A10	1	TTYH2	1	ODC1	2
SUZ12	1	RASIP1	1	SLC44A4	1	ITGAM	1	SMG1	1	NFKBID	2
CDC42BPA	1	CREM	1	OGFOD1	1	MARK2	1	PRDM15	1	ARHGEF10L	2
HK3	1	CREBBP	1	CECR6	1	NOP56	1	BTBD16	2	DYSF	2
MED22	1	TBC1D17	1	CEP170B	1	KHSRP	1	LAMA1	2	SETD3	2
TRIM7	1	GRB2	1	XPNPEP1	1	FKBP9	1	SETD2	2	CACNB1	2
PIEZO2	1	ZNF710	1	HIP1R	1	SCT	1	CEPT1	2	ARHGAP1	2
AMER3	1	MTF1	1	ZNF669	1	CES5A	1	ZNF74	2	LRRC48	2
GREB1L	1	ZNF208	1	ALLC	1	NLRC3	1	ETNK1	2	PPP6R3	2
KBTBD6	1	ABCD4	1	FGF22	1	ARID3C	1	HOXB1	2	SLC13A1	2
HELZ2	1	CFD	1	BAZ2A	1	C6orf118	1	AATK	2	ZNF768	2
TMEM248	1	STEAP3	1	NOS1	1	RABEP1	1	NBEAL2	2	STK10	2
AVIL	1	LAMA5	1	PIK3C2G	1	DFNB31	1	HECTD4	2	GTF3C1	2
ARAP3	1	WNT4	1	RNF217	1	TMEM143	1	OR4X2	2	MAGEE1	2
HRC	1	CRAMP1L	1	LRRTM1	1	PLBD2	1	GRIN2B	2	ZZEF1	2
NME6	1	KSR1	1	FLVCR1	1	CSRNP1	1	NCKAP5L	2	GRK5	2
PTCHD3	1	C9orf3	1	COL9A2	1	SARDH	1	CACTIN	2	MINPP1	2
PPP1R13L	1	TRIM7	1	ITPKB	1	UGT2B11	1	MYRIP	2	TMEM117	2
PASK	1	CA5B	1	OSBPL2	1	PPL	1	PRICKLE2	2	SLC45A3	2
TSC22D2	1	COL5A3	1	GTPBP3	1	ALPK2	1	SEC13	2	INO80C	2

Gene	Weighted score	Gene	Weighted score	Gene	Weighted score	Gene	Weighted score	Gene	Weighted score
DOCK5	2	ADCK1	2	OR2F2	2	GOLGA6L2	3	FLOT1	3
HIC2	2	WRAP73	2	PRB2	2	GLIS1	3	RNF151	3
PLA2R1	2	SLC2A2	2	HDAC8	2	IGLV2-18	3	HTR4	3
CRTAC1	2	ACAN	2	CTSF	2	USP24	3	ZFYVE26	3
CACTIN	2	TRIM47	2	KLHL22	2	PPP1R16A	3	SUPT6H	3
RSBN1L	2	TCHH	2	CCDC94	2	SLC9B1	3	CAD	3
CDIP1	2	UNC5A	2	LRRC41	2	ZNF514	3	CCDC33	3
TCERG1	2	SSX1	2	SCNN1B	2	CDHR5	3	EML5	3
DRD4	2	PLEC	2	TADA3	2	CHD2	3	CYP11B1	3
SPATA21	2	GPR112	2	XAB2	2	KDR	3	ERCC6L2	3
KIAA1522	2	POLA1	2	MUC19	2	LATS1	3	POTEE	3
TMBIM1	2	DLEC1	2	MAP3K4	2	FAM124A	3	BDP1	3
FLT4	2	GPR50	2	ACSM2A	2	NES	3	NFKB1	3
DNAH17	2	UBE2QL1	2	RYR1	2	CD244	3	CAMSAP1	3
SCML2	2	CD9	2	C19orf70	2	BNC2	3	CLDN7	3
BRINP1	2	AL356356.1	2	RAVER1	2	CREBBP	3	OTOP1	3
STAB1	2	ASS1	2	RORC	2	WASF3	3	FAM96A	3
ADSSL1	2	GPCPD1	2	MIR4426	2	PLG	3	MUC4	3
MCFD2	2	VSIG10L2	2	IDH2	2	MPC1	3	TMEM82	3
SND1	2	NBL1	2	TAPBPL	2	SLFN12L	3	MBD6	3
SYNE4	2	SH3RF2	2	IKZF1	2	DNMT3B	3	UBN2	3
UBXN11	2	TATDN3	2	EIF3A	2	IGSF11	3	BSN	3
CACNA1G	2	ADAMTSL1	2	ANXA6	2	SPAST	3	RARRES1	4
IFI35	2	TMEM235	2	VAMP2	2	ANTXR2	3	CCDC149	4
SCN10A	2	PLEKHG3	2	MBD6	2	TEX36	3	PAK1IP1	4
MVD	2	SLC12A9	2	PAPOLG	2	NIPAL3	3	HNRNPA1	4
SLX4	2	UCKL1	2	RASGRP2	2	LOC100130705	3	SEPP1	5
TAF1L	2	CCDC153	2	IQCA1	2	MUC16	3	OR10G9	5
DUS3L	2	MIPOL1	2	BAIAP2	2	CACNA1F	3	HDGFRP2	6
TOPAZ1	2	C22orf43	2	DDX23	2	ZNF181	3	TP53	6
HMCN1	2	AGRP	2	NWD1	2	ADCK3	3	FAM47C	6
PDE5A	2	FCGR2A	2	ASNS	2	SPATA31C2	3	KRAS	6
PLEKHG3	2	ZNF264	2	POLR3D	2	PABPC1	3	ROCK2	6
KLRC3	2	CNGB1	2	SAMD9	2	RXRB	3	POLQ	6
GSDMA	2	MORC3	2	CIR1	2	CPAMD8	3		
NAIP	2	TRABD2A	2	SLC25A13	2	FAM186A	3		
ABCA3	2	ADCY10	2	TRIM45	2	GPRIN3	3		
DGKD	2	HDHD1	2	WDR37	2	FAT3	3		
ANKRD17	2	MUC19	2	LPCAT2	2	FFAR2	3		
SCRIB	2	REXO4	2	ZNF160	2	PIK3CG	3		
OPLAH	2	PLA2G5	2	DMAP1	2	CDHR1	3		
CELSR2	2	TDRD7	2	FARS2	2	LARP1	3		
MEGF6	2	RWDD2A	2	NFKBID	2	ERBB4	3		
PTPN23	2	WNK1	2	SFXN3	2	PRSS3	3		
SLC8A1	2	CDV3	2	PDE6B	3	CCDC33	3		
RCBTB1	2	KMT2B	2	GIGYF2	3	ZBTB14	3		