	Chr	Pos	Ref	Alt	Qual	dbSNP	Type	Gene	Mutation
756	1	9018318	C	T	1822.19	.	Substitutio	SLC2A7	c.494G>A_
760	1	9040089	C	G	792.19	.	Substitutio	SLC2A5	c.672G>C_
910	1	11027518	G	C	1379.19	.	Substitutio	MASP2	c.1428C>
1809	1	17283051	C	G	1788.19	.	Substitutio	PADI3	c.1967C>
2393	1	24089566	C	G	522.19	.	Substitutio	MYOM3	c.1586G>
2920	1	32226498	G	A	410.19	.	Substitutio	EIF3I	c.496G>A_
3074	1	35451769	C	T	753.19	.	Substitutio	KIAA0319L	c.1921G>
3305	1	39684155	G	C	1018.19	.	Substitutio	HPCAL4	c.163-3C>
3378	1	40463038	C	G	2886.19	.	Substitutio	ZFP69B	c.1054C>
3571	1	43578894	C	T	719.19	.	Substitutio	PTPRF	c.653C>T_
3668	1	44757552	C	G	1025.19	.	Substitutio	KIF2C	c.816-4C>
3742	1	45614322	C	T	911.19	.	Substitutio	NASP	c.1622C>T
3744	1	45615469	C	G	1427.19	.	Substitutio	NASP	c.1828C>
4097	1	53461648	G	A	1533.19	.	Substitutio	DMRTB1	c.750+3G>
4339	1	61406561	G	C	12.55	.	Substitutio	NFIA	c.199-1G>
5110	1	88983707	T	C	57.2	rs1126362	Substitutio	RBMXL1	c.120A>G_
6633	1	1.5E+08	C	T	247.19	.	Substitutio	PRPF3	c.277-7C>
6926	1	1.52E+08	C	T	368.23	rs7687917	Substitutio	HRNR	c.5144G>
6927	1	1.52E+08	C	T	163.28	rs8001828	Substitutio	HRNR	c.5107G>
7278	1	1.55E+08	G	C	1293.19	.	Substitutio	PBXIP1	c.1133C>
7781	1	1.6E+08	C	T	462.19	.	Substitutio	C1orf204	c.332+1G>
8370	1	1.68E+08	C	A	1577.19	.	Substitutio	GPR161	c.1321G>T
8434	1	1.69E+08	G	A	226.19	.	Substitutio	CCDC181	c.1243C>T
8442	1	1.7E+08	C	T	868.19	.	Substitutio	F5	c.6528+4G
8755	1	1.78E+08	G	A	159.19	.	Substitutio	SEC16B	c.2267C>T
8796	1	1.79E+08	G	A	505.19	.	Substitutio	RALGPS2	c.73G>A_
8797	1	1.79E+08	G	C	590.19	.	Substitutio	RALGPS2	c.102G>C_
8798	1	1.79E+08	G	A	871.19	.	Substitutio	RALGPS2	c.151G>A_
8935	1	1.8E+08	C	G	896.19	.	Substitutio	CEP350	c.5278C>
9125	1	1.83E+08	C	T	673.19	.	Substitutio	LAMC1	c.3728C>T
9581	1	2.01E+08	C	G	461.19	.	Substitutio	LAD1	c.1570G>
9582	1	2.01E+08	C	G	474.19	rs1408085	Substitutio	LAD1	c.1398G>
10455	1	2.11E+08	G	T	542.19	.	Substitutio	RCOR3	c.136G>T_
10597	1	2.13E+08	C	T	674.19	.	Substitutio	RPS6KC1	c.388C>T_
10812	1	2.21E+08	C	T	4168.19	.	Substitutio	HLX	c.1324C>T
10940	1	2.24E+08	G	A	698.19	.	Substitutio	DEGS1	c.415G>A_
10994	1	2.25E+08	G	C	974.19	.	Substitutio	DNAH14	c.5247G>
11084	1	2.26E+08	C	T	734.19	.	Substitutio	PARP1	c.853G>A_
11110	1	2.27E+08	C	G	2071.19	.	Substitutio	ADCK3	c.1452C>
11430	1	2.31E+08	C	G	666.19	.	Substitutio	TRIM67	c.1772C>
11456	1	2.31E+08	G	A	1669.19	.	Substitutio	EXOC8	c.43C>T_p
11587	1	2.35E+08	G	T	444.19	.	Substitutio	TBCE	c.1114G>T
11616	1	2.36E+08	C	T	3036.19	.	Substitutio	LYST	c.1373G>
11875	1	2.4E+08	G	A	54.19	.	Substitutio	FMN2	c.3970G>
11953	1	2.43E+08	C	T	1077.19	.	Substitutio	CEP170	c.3208G>
12064	1	2.47E+08	C	G	875.19	.	Substitutio	AHCTF1	c.6397G>
12344	1	2.49E+08	A	G	121.19	rs2005549	Substitutio	OR2T29	c.215T>C_
12830	2	10046183	G	A	1243.19	.	Substitutio	KLF11	c.25G>A_
12831	2	10046228	G	A	1043.19	.	Substitutio	KLF11	c.70G>A_
12832	2	10047939	G	A	1680.19	.	Substitutio	KLF11	c.551G>A_
13060	2	19946549	G	C	1676.19	.	Substitutio	WDR35	c.1579C>
13507	2	27523348	C	T	906.19	.	Substitutio	GCKR	c.1787C>T
13705	2	32063834	G	A	389.19	.	Substitutio	SPAST	c.3G>A_p.
14299	2	47570232	C	T	1212.19	.	Substitutio	KCNK12	c.100G>A_

14443	2	55222251	C	T	1767.19	.	Substitutio	CLHC1	c.161G>A_
14701	2	64989686	C	T	1174.19	.	Substitutio	SLC1A4	c.43C>T_p
14817	2	68464869	C	T	1050.19	.	Substitutio	FBXO48	c.277G>A_
14818	2	68464947	C	G	1457.19	.	Substitutio	FBXO48	c.199G>C_
15533	2	95149730	C	G	1120.19	.	Substitutio	ZNF514	c.755G>C_
15651	2	96808699	C	T	1444.19	.	Substitutio	CNNM4	c.2087C>T
15969	2	1.02E+08	G	A	1126.19	rs5661653	Substitutio	IL1R2	c.586G>A_
16333	2	1.13E+08	C	T	623.19	.	Substitutio	SLC20A1	c.800C>T_
16619	2	1.2E+08	CT	C	122.69	.	Deletion	PTPN4	c.1981-3de
16828	2	1.28E+08	G	C	57.19	rs6173201	Substitutio	HS6ST1	c.187C>G_
17154	2	1.35E+08	C	T	1164.19	.	Substitutio	RAB3GAP	c.352C>T_
17422	2	1.52E+08	G	T	692.19	.	Substitutio	CACNB4	c.959C>A_
17527	2	1.58E+08	C	T	447.19	.	Substitutio	UPP2	c.695C>T_
17579	2	1.59E+08	TA	T	24.16	.	Deletion	WDSUB1	c.1274-3de
17753	2	1.66E+08	C	T	918.19	.	Substitutio	SCN9A	c.3325G>A
17754	2	1.66E+08	C	G	706.19	.	Substitutio	SCN9A	c.2944G>C
18055	2	1.72E+08	G	A	596.19	.	Substitutio	ITGA6	c.724G>A_
18220	2	1.76E+08	G	A	665.19	.	Substitutio	HOXD9	c.706G>A_
18382	2	1.79E+08	C	T	1207.19	.	Substitutio	TTN	c.53086G>
18388	2	1.79E+08	C	T	1100.19	.	Substitutio	TTN	c.24739G>
18566	2	1.86E+08	G	C	1600.19	.	Substitutio	FSIP2	c.11833G>
18723	2	1.91E+08	G	T	164.19	.	Substitutio	TMEM194	c.33C>A_p
18728	2	1.91E+08	C	T	544.19	.	Substitutio	NAB1	c.1247C>T
18840	2	1.96E+08	C	T	644.19	.	Substitutio	HECW2	c.250G>A_
18911	2	1.99E+08	G	C	920.19	.	Substitutio	SATB2	c.1942C>G
19104	2	2.03E+08	G	C	432.19	.	Substitutio	NBEAL1	c.3265G>C
19221	2	2.06E+08	C	G	2015.19	.	Substitutio	ZDBF2	c.5251C>G
19814	2	2.2E+08	C	T	1597.19	.	Substitutio	CHPF	c.661G>A_
19917	2	2.23E+08	A	C	1335.19	.	Substitutio	ACSL3	c.1107A>C
19995	2	2.27E+08	G	A	1538.19	.	Substitutio	IRS1	c.1154C>T
20039	2	2.27E+08	G	C	610.19	.	Substitutio	COL4A3	c.2866G>C
20309	2	2.33E+08	G	C	2820.19	.	Substitutio	NEU2	c.1126G>C
20328	2	2.33E+08	G	A	1489.19	.	Substitutio	SAG	c.75+3G>A
21409	3	10104536	C	T	1486.19	.	Substitutio	FANCD2O	c.239G>A_
21563	3	13571205	G	A	926.19	.	Substitutio	FBLN2	c.850G>A_
21748	3	16598119	C	G	186.19	.	Substitutio	DAZL	c.210G>C_
22196	3	38598981	C	T	750.19	rs1994731	Substitutio	SCN5A	c.1960G>A
22502	3	44629488	G	C	637.19	.	Substitutio	ZNF197	c.334G>C_
22884	3	48918497	C	A	1656.19	.	Substitutio	ARIH2OS	c.653G>T_
23429	3	56648839	G	C	200.19	.	Substitutio	FAM208A	c.1496C>G
23507	3	58408950	G	C	1399.19	.	Substitutio	PXK	c.1257G>C
23574	3	62281569	G	A	351.19	.	Substitutio	PTPRG	c.3685G>A
23652	3	64647944	C	T	469.19	.	Substitutio	ADAMTS9	c.1622G>A
25190	3	1.2E+08	G	T	523.19	.	Substitutio	NR1I2	c.519+5G>
25436	3	1.24E+08	C	T	902.19	.	Substitutio	MYLK	c.121G>A_
25813	3	1.29E+08	G	C	868.19	.	Substitutio	KIAA1257	c.809-3C>
25814	3	1.29E+08	G	C	423.19	.	Substitutio	EFCC1	c.4G>C_p.
25816	3	1.29E+08	G	C	817.19	.	Substitutio	EFCC1	c.25G>C_p
26296	3	1.41E+08	G	C	1504.19	.	Substitutio	PXYLP1	c.1216G>C
26305	3	1.42E+08	C	T	1967.19	.	Substitutio	RASA2	c.1034C>T
26404	3	1.49E+08	G	A	327.19	.	Substitutio	HPS3	c.211G>A_
26859	3	1.68E+08	G	C	404.19	.	Substitutio	WDR49	c.1413C>G
27464	3	1.87E+08	G	T	1324.19	.	Substitutio	MASP1	c.1787C>A
27654	3	1.93E+08	G	A	531.19	rs3731850	Substitutio	MB21D2	c.451C>T_
28822	4	3316685	C	G	1926.19	.	Substitutio	RGS12	c.515C>G_

31987	4	1.09E+08	TA	T	20.19	rs3395872	Deletion	ETNPPL	c.928-5del
32174	4	1.18E+08	G	A	1413.19	.	Substitutio	NDST3	c.133G>A_
32474	4	1.29E+08	C	T	1648.19	.	Substitutio	JADE1	c.110C>T_
32881	4	1.51E+08	C	G	180.19	.	Substitutio	SH3D19	c.694+3G>
33181	4	1.63E+08	C	G	1797.19	.	Substitutio	NPY5R	c.913C>G_
33600	4	1.83E+08	G	A	1604.19	.	Substitutio	CDKN2AIF	c.272+7G>
34775	5	32087680	C	T	931.19	.	Substitutio	PDZD2	c.4232C>T
34994	5	37226404	G	A	854.19	.	Substitutio	C5orf42	c.2191C>T
35102	5	41012588	C	T	741.19	.	Substitutio	MROH2B	c.3130G>A
35465	5	56923959	C	G	750.19	.	Substitutio	MIER3	c.1005G>C
36922	5	1.16E+08	C	T	1886.19	.	Substitutio	TMED7-TI	c.527G>A_
37632	5	1.39E+08	C	T	622.19	rs3757318	Substitutio	ECSCR	c.157+3G>
37885	5	1.41E+08	A	G	18.25	.	Substitutio	PCDHB11	c.479A>G_
37886	5	1.41E+08	C	A	18.25	.	Substitutio	PCDHB11	c.482C>A_
38667	5	1.57E+08	C	T	602.19	rs1381397	Substitutio	HAVCR2	c.890G>A_
39109	5	1.74E+08	C	T	1169.19	.	Substitutio	BOD1	c.142G>A_
39155	5	1.75E+08	G	T	1411.19	.	Substitutio	DRD1	c.167C>A_
39252	5	1.77E+08	G	A	1651.19	.	Substitutio	RNF44	c.944C>T_
39794	5	1.81E+08	C	T	1491.19	.	Substitutio	FLT4	c.214G>A_
39982	6	2623466	C	G	800.19	.	Substitutio	C6orf195	c.357G>C_
40464	6	11005562	G	T	790.19	.	Substitutio	ELOVL2	c.68-3C>A
40526	6	12120295	C	T	2680.19	.	Substitutio	HIVEP1	c.500C>T_
40726	6	20126524	G	A	2054.19	rs1422552	Substitutio	MBOAT1	c.707C>T_
40916	6	25495160	C	A	1657.19	.	Substitutio	LRRC16A	c.1270C>A
41067	6	27132411	C	T	1411.19	.	Substitutio	HIST1H2B	c.340G>A_
41174	6	28435508	C	T	784.19	.	Substitutio	ZSCAN23	c.508G>A_
41712	6	30137328	G	A	290.19	.	Substitutio	TRIM40	c.292G>A_
42025	6	31144729	C	A	866.19	.	Substitutio	CCHCR1	c.2125G>T
42201	6	31271082	G	C	21.22	rs4155561	Substitutio	HLA-C	c.610C>G_
42202	6	31271089	C	G	30.19	rs1741367	Substitutio	HLA-C	c.603G>C_
42540	6	31529914	G	C	553.19	.	Substitutio	MCCD1	c.339G>C_
42593	6	31625595	G	A	1218.19	.	Substitutio	PRRC2A	c.743G>A_
42722	6	31880184	G	T	699.19	.	Substitutio	EHMT2	c.3533C>A
42749	6	31970204	C	G	1869.19	.	Substitutio	DXO	c.949-1G>
42998	6	32517756	C	CA	46.15	.	Insertion	HLA-DRB5	c.788-5du
42999	6	32517758	G	A	55.19	.	Substitutio	HLA-DRB5	c.788-6C>
43243	6	32580273	G	A	54.23	rs2873225	Substitutio	HLA-DRB1	c.764-3C>
43244	6	32580276	A	G	54.23	rs2873225	Substitutio	HLA-DRB1	c.764-6T>
44015	6	32745200	C	T	56.19	rs2007452	Substitutio	HLA-DQA2	c.124C>T_
44259	6	33205046	G	A	1431.19	.	Substitutio	HSD17B8	c.197G>A_
44915	6	43013339	C	G	680.19	.	Substitutio	MEA1	c.79G>C_
44927	6	43173853	G	C	1630.19	.	Substitutio	SRF	c.520G>C_
45285	6	53009574	G	C	346.19	.	Substitutio	ICK	c.1493-7C
45596	6	73428785	G	A	306.19	.	Substitutio	MB21D1	c.1141C>T
46394	6	1.08E+08	G	A	1037.19	.	Substitutio	SEC63	c.394C>T_
46475	6	1.09E+08	C	T	1439.19	rs1118923	Substitutio	SMPD2	c.492-7C>
47302	6	1.38E+08	C	T	1482.19	.	Substitutio	NHSL1	c.2386G>A
47347	6	1.42E+08	C	G	415.19	.	Substitutio	NMBR	c.711G>C_
47723	6	1.52E+08	C	A	502.19	.	Substitutio	SYNE1	c.22233G>
47766	6	1.53E+08	C	T	651.19	.	Substitutio	VIP	c.108-3C>
47802	6	1.54E+08	C	G	213.19	.	Substitutio	CNKSR3	c.834G>C_
48509	6	1.7E+08	G	C	1551.19	.	Substitutio	C6orf120	c.496G>C_
49553	7	22194009	G	A	1522.19	.	Substitutio	RAPGEF5	c.1021C>T
49763	7	27792066	C	T	849.19	.	Substitutio	TAX1BP1	c.1099C>T
50984	7	56021092	C	T	573.19	.	Substitutio	PSPH	c.121G>A_

51665	7	76281518	G	C	123.19	.	Substitutio	SRRM3	c.1086G>
51838	7	82915772	C	T	653.19	.	Substitutio	PCLO	c.2374G>
51900	7	87545910	C	T	1298.19	.	Substitutio	ABCB1	c.1840G>
52138	7	94411033	GT	G	88.15	rs3558740	Deletion	COL1A2	c.1252-7de
52741	7	1.01E+08	C	T	57.87	.	Substitutio	MUC3A	c.3584C>T
52744	7	1.01E+08	C	T	28.45	.	Substitutio	MUC3A	c.3599C>T
53745	7	1.18E+08	C	A	53.19	rs4727853	Substitutio	CFTR	c.1251C>
54041	7	1.29E+08	C	T	2131.19	.	Substitutio	TNPO3	c.43G>A_
54426	7	1.39E+08	G	A	376.19	.	Substitutio	KIAA1549	c.98C>T_p
54982	7	1.43E+08	G	A	918.19	.	Substitutio	PIP	c.95+3G>
55453	7	1.52E+08	G	C	1358.19	.	Substitutio	KMT2C	c.14461-3
55822	8	245496	C	G	1226.19	.	Substitutio	ZNF596	c.649C>G_
56689	8	17544492	G	T	1302.19	.	Substitutio	SLC7A2	c.538G>T_
56848	8	20211224	C	G	1471.19	.	Substitutio	ATP6V1B2	c.511C>G_
57255	8	27422313	G	A	1318.19	.	Substitutio	PTK2B	c.481G>A_
58056	8	58496828	G	C	892.19	.	Substitutio	CYP7A1	c.684C>G_
58389	8	76704305	C	G	1464.19	.	Substitutio	ZFHX4	c.217C>G_
58544	8	86556270	C	T	1139.19	.	Substitutio	CPNE3	c.1423C>T
59115	8	1.08E+08	G	A	430.19	.	Substitutio	EIF3E	c.188C>T_
59126	8	1.09E+08	G	C	1973.19	.	Substitutio	PKHD1L1	c.8310G>
59127	8	1.09E+08	G	A	2096.19	rs2676017	Substitutio	PKHD1L1	c.8377G>
59128	8	1.1E+08	C	T	449.19	.	Substitutio	PKHD1L1	c.12223C>
60253	8	1.44E+08	G	A	1391.19	rs5689420	Substitutio	TONSL	c.2623C>T
60308	8	1.45E+08	C	G	1525.19	.	Substitutio	RECQL4	c.2467G>
60591	9	5922523	C	G	530.19	.	Substitutio	KIAA2026	c.3383G>
60717	9	13175787	C	G	577.19	.	Substitutio	MPDZ	c.3020G>
60844	9	17464481	CT	C	12.4	.	Deletion	CNTLN	c.3405-5de
61166	9	33313717	G	C	782.19	.	Substitutio	NFX1	c.1512G>
61293	9	34512111	C	T	494.19	.	Substitutio	DNAI1	c.1314C>T
61382	9	35385757	C	T	628.19	.	Substitutio	UNC13B	c.1423C>T
61431	9	35801067	C	T	583.19	.	Substitutio	NPR2	c.1352-3C
61706	9	41938378	C	A	109.23	.	Substitutio	CNTNAP3	c.1821G>T
62216	9	76502496	G	A	865.19	.	Substitutio	GCNT1	c.115G>A_
62271	9	77339509	A	T	27.29	.	Substitutio	VPS13A	c.6379-7A
62543	9	89045816	C	G	1106.19	.	Substitutio	SHC3	c.1131G>
62648	9	92416628	C	T	475.19	.	Substitutio	OMD	c.931G>A_
62764	9	95111478	C	G	958.19	.	Substitutio	FANCC	c.1314G>
62852	9	97693658	G	A	150.19	.	Substitutio	XPA	c.274C>T_
62936	9	99968415	AT	A	30.21	rs3686506	Deletion	STX17	c.670-5del
63121	9	1.06E+08	C	G	602.19	.	Substitutio	FKTN	c.352C>G_
63277	9	1.1E+08	C	G	1530.19	.	Substitutio	SVEP1	c.6091G>
63463	9	1.13E+08	G	C	347.19	.	Substitutio	PRPF4	c.634G>C_
63998	9	1.25E+08	C	T	849.19	.	Substitutio	MAPKAP1	c.685G>A_
64966	9	1.36E+08	G	A	1685.19	rs1995734	Substitutio	LCN1	c.386G>A_
66201	10	15782222	G	C	283.19	.	Substitutio	FAM188A	c.1121C>G
66353	10	20176998	G	C	617.19	.	Substitutio	PLXDC2	c.737-1G>
67040	10	43386956	G	A	990.19	.	Substitutio	HNRNPF	c.929C>T_
67237	10	47351181	G	C	1304.19	.	Substitutio	RBP3	c.2697G>
67377	10	49708509	G	C	1325.19	.	Substitutio	C10orf53	c.366G>C_
68114	10	73765528	C	A	798.19	.	Substitutio	SEC24C	c.1305C>
68422	10	84213351	G	C	746.19	.	Substitutio	CDHR1	c.2040+3G
68658	10	89443777	C	G	952.19	.	Substitutio	SLC16A12	c.283G>C_
69036	10	97650995	C	G	393.19	.	Substitutio	PI4K2A	c.490C>G_
69480	10	1.05E+08	C	T	282.19	.	Substitutio	SORCS3	c.3533C>T
69765	10	1.17E+08	G	C	977.19	.	Substitutio	ENO4	c.1222G>

69784	10	1.17E+08	G	C	2915.19	.	Substitutio	KCNK18	c.955G>C_
70133	10	1.25E+08	G	C	1499.19	.	Substitutio	ZRANB1	c.195G>C_
70556	10	1.33E+08	G	A	334.19	.	Substitutio	UTF1	c.583G>A_
70786	11	373831	G	T	1422.19	.	Substitutio	B4GALNT	c.783+3G>
70787	11	375532	G	A	1166.19	.	Substitutio	B4GALNT	c.850+5G>
70789	11	376297	G	C	1347.19	.	Substitutio	B4GALNT	c.1243G>C
72118	11	6239403	G	C	1625.19	.	Substitutio	CNGA4	c.82G>C_
72566	11	9420501	G	A	272.19	.	Substitutio	IPO7	c.817G>A_
72574	11	9577203	C	T	663.19	.	Substitutio	WEE1	c.1081C>T
73077	11	20103722	C	A	1664.19	.	Substitutio	NAV2	c.6651C>A
73612	11	36592989	C	G	1156.19	.	Substitutio	RAG2	c.1180G>C
73613	11	36593112	C	T	1292.19	.	Substitutio	RAG2	c.1057G>A
73636	11	43444125	G	C	1820.19	.	Substitutio	TTC17	c.2752G>C
73823	11	46875902	C	G	1489.19	.	Substitutio	LRP4	c.3601G>C
73862	11	47245789	C	T	1168.19	.	Substitutio	ACP2	c.343G>A_
73869	11	47267981	G	A	790.19	.	Substitutio	NR1H3	c.1057G>A
74402	11	56743060	T	C	1482.19	.	Substitutio	OR9G4	c.752A>G_
74872	11	61962736	G	C	2778.19	.	Substitutio	BEST1	c.1582G>C
75123	11	64315797	G	A	168.19	rs2013363	Substitutio	ESRRA	c.1100G>A
75125	11	64315818	G	A	123.19	rs1508483	Substitutio	ESRRA	c.1121G>A
75126	11	64315821	G	T	87.19	rs2019713	Substitutio	ESRRA	c.1124G>T
75127	11	64315823	CGGG	C	75.15	.	Deletion	ESRRA	c.1127_11
75130	11	64315848	T	C	69.19	rs2010729	Substitutio	ESRRA	c.1151T>C
75131	11	64315856	C	T	75.19	rs7920458	Substitutio	ESRRA	c.1159C>T
75804	11	70326604	C	T	842.19	.	Substitutio	PPFIA1	c.716C>T_
77181	11	1.07E+08	C	G	1002.19	.	Substitutio	CWF19L2	c.1936G>C
77187	11	1.07E+08	G	T	786.19	.	Substitutio	CWF19L2	c.707C>A_
77255	11	1.08E+08	G	C	129.19	.	Substitutio	ATM	c.5415G>C
77748	11	1.19E+08	C	T	688.19	.	Substitutio	PHLDB1	c.1739C>T
78574	11	1.3E+08	G	C	490.19	.	Substitutio	NFRKB	c.196C>G_
81299	12	42313917	C	T	511.19	.	Substitutio	ZCRB1	c.280G>A_
81614	12	49043139	C	T	361.19	.	Substitutio	KMT2D	c.5581G>A
81632	12	49186409	A	G	158.19	rs5877844	Substitutio	TUBA1A	c.428T>C_
81633	12	49186412	T	C	161.19	.	Substitutio	TUBA1A	c.425A>G_
81889	12	51702800	G	A	1007.19	.	Substitutio	SCN8A	c.1020G>A
81971	12	52315327	C	G	1018.19	.	Substitutio	KRT83	c.1279G>C
82416	12	55574714	C	G	1386.19	.	Substitutio	OR2AP1	c.300C>G_
82589	12	57187259	C	G	590.19	.	Substitutio	LRP1	c.6842-8C
82655	12	57571324	G	A	528.19	.	Substitutio	KIF5A	c.1030G>A
83744	12	95670124	C	G	734.19	.	Substitutio	NTN4	c.1422G>C
83936	12	1.03E+08	C	T	1248.19	.	Substitutio	PAH	c.334G>A_
84407	12	1.1E+08	G	C	1246.19	.	Substitutio	IFT81	c.166G>C_
84981	12	1.22E+08	G	A	545.19	.	Substitutio	PSMD9	c.472G>A_
86928	13	35159904	G	A	999.19	.	Substitutio	NBEA	c.3733G>A
87299	13	45015531	G	A	1427.19	.	Substitutio	GPALPP1	c.130G>A_
87410	13	48473359	G	A	173.19	rs5877788	Substitutio	RB1	c.2490-1G
87639	13	59983875	G	C	167.19	.	Substitutio	DIAPH3	c.585C>G_
87870	13	77761053	C	T	534.19	rs5447492	Substitutio	SLAIN1	c.443C>T_
87878	13	78615900	C	T	1377.19	.	Substitutio	RNF219	c.1861G>A
87908	13	79405744	C	T	1799.19	.	Substitutio	RBM26	c.31G>A_
88197	13	1.03E+08	C	T	1071.19	.	Substitutio	CCDC168	c.6745G>A
89640	14	31069839	C	G	626.19	.	Substitutio	AP4S1	c.139-4C>
89854	14	37591910	C	T	1241.19	.	Substitutio	FOXA1	c.874G>A_
90091	14	50771439	G	C	1182.19	.	Substitutio	NIN	c.1011C>G
91833	14	91458830	C	T	869.19	.	Substitutio	SMEK1	c.1714G>A

92555	14	1.03E+08	C	G	907.19	.	Substitutio	CDC42BP	c.1491G>C
92556	14	1.03E+08	C	G	3535.19	.	Substitutio	CDC42BP	c.1351G>C
93987	15	33788385	G	T	2817.19	.	Substitutio	RYR3	c.9757G>T
97135	15	89116426	G	C	1110.19	.	Substitutio	ABHD2	c.99G>C_p
98781	16	2764585	G	C	1074.19	.	Substitutio	SRRM2	c.4057G>C
99112	16	4727113	T	C	505.19	rs3705516	Substitutio	ANKS3	c.235A>G_
99685	16	15068234	C	A	287.19	.	Substitutio	RRN3	c.1389G>T
100215	16	27463582	C	G	2042.19	.	Substitutio	GTF3C1	c.5808G>C
100246	16	28496179	G	A	651.19	.	Substitutio	APOBR	c.1138G>A
100345	16	29804841	G	A	220.19	rs3692971	Substitutio	KIF22	c.1543G>A
100891	16	53826005	G	C	1199.19	.	Substitutio	FTO	c.265G>C_
101560	16	68738336	CCT	C	2916.15	.	Deletion	CDH1	c.89_90del
102750	16	87403029	G	A	1890.19	rs3719257	Substitutio	MAP1LC3	c.310G>A_
103192	16	89898647	G	A	2124.19	rs1164843	Substitutio	TCF25	c.408G>A_
103248	16	90094032	A	C	182.41	.	Substitutio	TUBB8P7	c.10A>C_p
103585	17	2701491	C	T	2792.19	.	Substitutio	CLUH	c.660G>A_
103806	17	4242281	C	G	193.19	.	Substitutio	ANKFY1	c.304G>C_
103969	17	5034364	G	A	1116.19	.	Substitutio	SLC52A1	c.131-6C>
104327	17	7674946	GA	G	1502.15	.	Deletion	TP53	c.107delT
105735	17	30442361	G	A	274.19	.	Substitutio	CPD	c.2284G>A
105782	17	31258365	C	T	1674.19	.	Substitutio	NF1	c.4132C>T
105833	17	31966130	C	CT	147.5	rs3978018	Insertion	SUZ12	c.456-3dup
105987	17	35422236	C	T	941.19	.	Substitutio	SLFN12	c.793G>A_
106302	17	39723557	C	T	1362.19	.	Substitutio	ERBB2	c.1277C>T
106347	17	40035180	C	G	1295.19	.	Substitutio	MED24	c.457G>C_
106416	17	40834673	C	G	1745.19	.	Substitutio	TMEM99	c.157C>G_
106546	17	41350612	G	T	220.19	.	Substitutio	KRT33A	c.156C>A_
106773	17	42570133	G	A	642.19	.	Substitutio	MLX	c.628G>A_
106809	17	42839327	G	A	288.19	.	Substitutio	PSME3	c.631G>A_
107113	17	45245018	C	A	2090.19	.	Substitutio	FMNL1	c.2638C>A
107837	17	58206293	G	C	3138.19	.	Substitutio	MKS1	c.1548C>G
107884	17	59211420	G	A	1320.19	.	Substitutio	SMG8	c.1369G>A
107912	17	59910559	C	G	657.19	.	Substitutio	RPS6KB1	c.142-3C>
107914	17	59962962	C	T	1258.19	.	Substitutio	RNFT1	c.379G>A_
107915	17	59963263	C	G	570.19	.	Substitutio	RNFT1	c.78G>C_p
107968	17	61683652	AATAG	A	693.15	.	Deletion	BRIP1	c.3390_33
108056	17	63822006	G	A	1393.19	.	Substitutio	FTSJ3	c.1453C>T
108075	17	63957312	C	T	1838.19	.	Substitutio	SCN4A	c.2226G>A
108192	17	67347350	C	T	1665.19	.	Substitutio	PSMD12	c.646G>A_
108313	17	70175391	G	A	1748.19	.	Substitutio	KCNJ2	c.352G>A_
108419	17	73447749	C	T	874.19	.	Substitutio	SDK2	c.480-1G>
108513	17	74704787	G	C	2192.19	.	Substitutio	CD300LF	c.73C>G_p
109508	17	81252500	C	G	1829.19	.	Substitutio	SLC38A10	c.1640G>C
109509	17	81253124	C	A	794.19	.	Substitutio	SLC38A10	c.1405G>T
109676	17	82084663	C	T	1218.19	.	Substitutio	FASN	c.4618G>A
109750	17	82415451	C	T	1426.19	.	Substitutio	OGFOD3	c.251G>A_
109751	17	82415488	C	G	1328.19	.	Substitutio	OGFOD3	c.214G>C_
109752	17	82415582	C	G	830.19	.	Substitutio	OGFOD3	c.120G>C_
110735	18	23568939	C	G	276.19	.	Substitutio	NPC1	c.347G>C_
111921	18	68836860	G	A	1364.19	.	Substitutio	CCDC102	c.97G>A_p
112462	19	899677	C	G	564.19	.	Substitutio	R3HDM4	c.508G>C_
112599	19	1073988	C	T	696.19	.	Substitutio	HMHA1	c.845C>T_
112602	19	1074198	C	A	1488.19	.	Substitutio	HMHA1	c.966C>A_
112635	19	1117507	G	C	752.19	.	Substitutio	SBNO2	c.1528-8C>
112840	19	2290252	C	T	1229.19	.	Substitutio	LINGO3	c.1525G>A

113275	19	4684692	G	A	1588.19	rs3693043	Substitutio	DPP9	c.2149C>T
113283	19	4793182	C	G	634.19	.	Substitutio	FEM1A	c.1328C>G
113455	19	6374926	G	A	383.19	.	Substitutio	ALKBH7	c.436G>A_
113841	19	8882357	T	G	16.29	.	Substitutio	MUC16	c.41726A>
113842	19	8882365	A	G	24.2	.	Substitutio	MUC16	c.41718T>
113843	19	8882372	C	G	36.19	.	Substitutio	MUC16	c.41717-6
113899	19	8892955	C	G	943.19	.	Substitutio	MUC16	c.40009G>
114185	19	10986282	G	A	2314.19	.	Substitutio	SMARCA4	c.449G>A_
114395	19	12628250	G	C	1725.19	.	Substitutio	ZNF791	c.721G>C_
114426	19	12933564	G	A	873.19	.	Substitutio	FARSA	c.133C>T_
115133	19	17649539	C	G	1820.19	.	Substitutio	UNC13A	c.1488G>C
115740	19	22758375	C	T	266.19	.	Substitutio	ZNF99	c.1261G>A
116116	19	34454426	CT	C	17.23	.	Deletion	UBA2	c.1133-6de
116556	19	38374713	C	G	990.19	.	Substitutio	PSMD8	c.112C>G_
116697	19	39314064	C	T	2128.19	.	Substitutio	LRFN1	c.1273G>A
116821	19	39971220	C	G	1191.19	.	Substitutio	PSMC4	c.18C>G_p
116903	19	40613073	G	A	1701.19	.	Substitutio	LTBP4	c.2509G>A
117105	19	42199680	C	T	1616.19	.	Substitutio	DEDD2	c.739G>A_
117121	19	42294012	C	T	1861.19	.	Substitutio	CIC	c.6836C>T
117412	19	44066195	C	G	658.19	.	Substitutio	ZNF223	c.367C>G_
117448	19	44157289	G	C	524.19	.	Substitutio	ZNF234	c.1273G>C
117697	19	46376458	G	C	2578.19	.	Substitutio	PPP5C	c.517G>C_
117814	19	47456970	C	T	1450.19	.	Substitutio	SLC8A2	c.568G>A_
119794	19	54939737	G	T	260.19	.	Substitutio	NLRP7	c.1082C>A
119795	19	54939872	G	A	992.19	.	Substitutio	NLRP7	c.947C>T_
119996	19	55678638	C	T	1589.19	.	Substitutio	EPN1	c.11C>T_p
120098	19	56384763	C	G	390.19	.	Substitutio	ZNF582	c.654G>C_
120216	19	57443564	C	A	1217.19	.	Substitutio	ZNF749	c.416C>A_
120218	19	57443826	C	A	1014.19	.	Substitutio	ZNF749	c.678C>A_
120220	19	57444181	C	T	927.19	.	Substitutio	ZNF749	c.1033C>T
120221	19	57445234	C	T	540.19	.	Substitutio	ZNF749	c.2086C>T
120222	19	57445397	C	T	2397.19	.	Substitutio	ZNF749	c.2249C>T
120228	19	57455861	G	A	662.19	.	Substitutio	VN1R1	c.626C>T_
120229	19	57455977	G	T	742.19	.	Substitutio	VN1R1	c.510C>A_
120445	19	58088799	G	C	1448.19	.	Substitutio	ZSCAN18	c.610C>G_
120580	19	58562101	G	A	686.19	.	Substitutio	MZF1	c.2176C>T
120621	20	298007	G	A	949.19	.	Substitutio	ZCCHC3	c.421G>A_
120865	20	3122367	C	T	1527.19	.	Substitutio	UBOX5	c.272G>A_
121295	20	17436826	G	C	1224.19	.	Substitutio	PCSK2	c.828G>C_
122155	20	36548031	G	A	531.19	.	Substitutio	MYL9	c.185-1G>
122265	20	38525441	G	A	1766.19	.	Substitutio	RALGAPB	c.1825G>A
123235	20	62656851	C	T	2050.19	.	Substitutio	SLCO4A1	c.397C>T_
123377	20	63313883	G	A	1528.19	rs3701513	Substitutio	COL20A1	c.2350G>A
124069	21	32325356	G	A	1019.19	.	Substitutio	URB1	c.4994C>T
125042	21	44773637	C	T	1024.19	.	Substitutio	UBE2G2	c.295G>A_
125364	21	46558394	G	C	767.19	.	Substitutio	DIP2A	c.3957+1G
126177	22	22195973	C	T	1641.19	.	Substitutio	IGLV6-57	c.50C>T_p
127919	22	38089553	G	A	123.19	.	Substitutio	BAIAP2L2	c.734C>T_
128335	22	42128812	A	G	44.19	rs1995351	Substitutio	CYP2D6	c.638T>C_
128337	22	42128818	T	TC	65.15	.	Insertion	CYP2D6	c.631dupG
129418	23	3311198	C	T	1838.19	.	Substitutio	MXRA5	c.7005G>A
129609	23	12716331	T	A	1567.19	.	Substitutio	FRMPD4	c.1752T>A
129813	23	23001186	G	A	1067.19	.	Substitutio	DDX53	c.1129G>A
129903	23	30846641	C	T	404.19	.	Substitutio	TAB3	c.1714G>A
129994	23	40697186	G	A	686.19	.	Substitutio	MED14	c.1491-3C>

130004	23	41148376	G	A	368.19	.	Substitution	USP9X	c.1427G>A
130231	23	48975303	G	C	948.19	.	Substitution	GRIPAP1	c.2192C>G
130499	23	69506075	G	A	1598.19	.	Substitution	FAM155B	c.793G>A_
130806	23	1.01E+08	C	T	3446.19	.	Substitution	CSTF2	c.50C>T_p
131006	23	1.16E+08	G	C	1042.19	.	Substitution	PLS3	c.1467G>C
131065	23	1.19E+08	G	T	203.19	.	Substitution	SLC25A5	c.361G>T_
131068	23	1.19E+08	G	A	84.19	rs2005503	Substitution	SLC25A5	c.413G>A_
131071	23	1.19E+08	G	A	75.19	rs2010502	Substitution	SLC25A5	c.446G>A_
131072	23	1.19E+08	CT	C	66.15	.	Deletion	SLC25A5	c.450delT
131073	23	1.19E+08	G	A	42.19	rs1996788	Substitution	SLC25A5	c.472G>A_
131355	23	1.4E+08	G	C	425.19	.	Substitution	MCF2	c.1544-6C>
131463	23	1.46E+08	C	A	1661.19	.	Substitution	SLITRK2	c.2402C>A

Class	normGeno	normAlt	normTot	tumorGenc	tumorAlt	tumorTot	Somatic	captureKit	normClass
NSY	C/C	0	171	C/T	63	86	TRUE	1	R/R
NSY	C/C	0	94	C/G	26	44	TRUE	1	R/R
NSY	G/G	0	111	G/C	45	64	TRUE	1	R/R
NSY	C/C	0	180	C/G	64	97	TRUE	1	R/R
NSY	C/C	0	49	C/G	18	24	TRUE	1	R/R
NSY	G/G	0	88	G/A	16	25	TRUE	0	R/R
NSY	C/C	0	49	C/T	25	39	TRUE	0	R/R
SS	G/G	0	103	G/C	33	46	TRUE	1	R/R
NSY	C/C	0	305	C/G	95	163	TRUE	1	R/R
NSY	C/C	0	103	C/T	24	38	TRUE	1	R/R
SS	C/C	0	80	C/G	35	50	TRUE	1	R/R
NSY	C/C	0	83	C/T	29	38	TRUE	1	R/R
EE	C/C	0	107	C/G	47	76	TRUE	0	R/R
SS	G/G	0	129	G/A	53	72	TRUE	1	R/R
ESS	G/G	1	16	G/C	2	16	TRUE	0	R/R
NSY	T/T	1	23	T/C	3	16	TRUE	0	R/R
SS	C/C	0	25	C/T	13	53	TRUE	1	R/R
NSY	C/C	2	26	C/T	21	56	TRUE	0	R/R
NSY	C/C	2	25	C/T	11	38	TRUE	0	R/R
NSY	G/G	0	230	G/C	72	376	TRUE	1	R/R
ESS	C/C	0	55	C/T	23	96	TRUE	1	R/R
SG	C/C	0	142	C/A	68	259	TRUE	1	R/R
SG	G/G	0	40	G/A	11	53	TRUE	1	R/R
SS	C/C	0	204	C/T	51	298	TRUE	1	R/R
NSY	G/G	0	45	G/A	14	95	TRUE	1	R/R
NSY	G/G	0	115	G/A	32	171	TRUE	1	R/R
NSY	G/G	0	160	G/C	40	249	TRUE	1	R/R
NSY	G/G	0	195	G/A	59	349	TRUE	1	R/R
NSY	C/C	0	98	C/G	46	207	TRUE	1	R/R
NSY	C/C	0	74	C/T	37	132	TRUE	1	R/R
NSY	C/C	0	55	C/G	25	102	TRUE	1	R/R
NSY	C/C	0	34	C/G	19	81	TRUE	1	R/R
SG	G/G	0	68	G/T	29	121	TRUE	0	R/R
SG	C/C	0	82	C/T	33	150	TRUE	1	R/R
NSY	C/C	0	221	C/T	157	344	TRUE	1	R/R
NSY	G/G	1	163	G/A	44	243	TRUE	1	R/R
NSY	G/G	0	104	G/C	50	181	TRUE	1	R/R
NSY	C/C	0	152	C/T	42	198	TRUE	1	R/R
NSY	C/C	0	267	C/G	101	413	TRUE	1	R/R
NSY	C/C	0	88	C/G	34	122	TRUE	1	R/R
NSY	G/G	0	313	G/A	100	528	TRUE	1	R/R
SG	G/G	0	53	G/T	19	71	TRUE	0	R/R
NSY	C/C	0	182	C/T	115	308	TRUE	1	R/R
NSY	G/G	0	22	G/A	5	35	TRUE	0	R/R
NSY	C/C	0	59	C/T	45	106	TRUE	1	R/R
NSY	C/C	0	85	C/G	42	153	TRUE	1	R/R
NSY	A/A	1	21	A/G	9	45	TRUE	0	R/R
NSY	G/G	0	159	G/A	51	148	TRUE	1	R/R
NSY	G/G	0	156	G/A	47	137	TRUE	1	R/R
NSY	G/G	0	226	G/A	72	228	TRUE	1	R/R
NSY	G/G	0	115	G/C	61	122	TRUE	1	R/R
NSY	C/C	0	102	C/T	36	91	TRUE	1	R/R
IM	G/G	0	48	G/A	16	43	TRUE	1	R/R
NSY	C/C	0	143	C/T	49	110	TRUE	1	R/R

NSY	C/C	0	205	C/T	65	178	TRUE	0	R/R
SG	C/C	0	110	C/T	41	102	TRUE	1	R/R
NSY	C/C	0	155	C/T	40	85	TRUE	1	R/R
NSY	C/C	0	160	C/G	51	130	TRUE	1	R/R
NSY	C/C	0	118	C/G	43	106	TRUE	1	R/R
NSY	C/C	0	135	C/T	56	125	TRUE	1	R/R
NSY	G/G	0	84	G/A	43	98	TRUE	1	R/R
NSY	C/C	0	67	C/T	26	63	TRUE	0	R/R
SS	CT/CT	2	19	CT/C	9	19	TRUE	1	R/R
NSY	G/G	2	97	G/C	9	66	TRUE	1	R/R
SG	C/C	0	130	C/T	45	136	TRUE	1	R/R
NSY	G/G	0	74	G/T	29	64	TRUE	1	R/R
NSY	C/C	0	57	C/T	19	47	TRUE	1	R/R
SS	TA/TA	1	31	TA/T	5	24	TRUE	1	R/R
NSY	C/C	0	86	C/T	34	87	TRUE	0	R/R
NSY	C/C	0	64	C/G	29	90	TRUE	1	R/R
NSY	G/G	0	115	G/A	27	101	TRUE	1	R/R
NSY	G/G	0	92	G/A	26	78	TRUE	1	R/R
NSY	C/C	0	185	C/T	54	157	TRUE	1	R/R
NSY	C/C	0	111	C/T	41	111	TRUE	1	R/R
NSY	G/G	0	144	G/C	58	132	TRUE	1	R/R
NSY	G/G	0	34	G/T	9	29	TRUE	1	R/R
NSY	C/C	0	79	C/T	22	60	TRUE	1	R/R
NSY	C/C	1	76	C/T	26	66	TRUE	1	R/R
NSY	G/G	0	105	G/C	36	97	TRUE	1	R/R
NSY	G/G	0	46	G/C	17	45	TRUE	1	R/R
NSY	C/C	0	245	C/G	80	201	TRUE	1	R/R
NSY	C/C	0	200	C/T	64	165	TRUE	1	R/R
NSY	A/A	0	164	A/C	55	138	TRUE	1	R/R
NSY	G/G	0	218	G/A	58	179	TRUE	1	R/R
NSY	G/G	0	59	G/C	20	49	TRUE	1	R/R
NSY	G/G	0	376	G/C	119	309	TRUE	1	R/R
SS	G/G	0	139	G/A	55	112	TRUE	1	R/R
NSY	C/C	0	123	C/T	61	147	TRUE	1	R/R
NSY	G/G	0	159	G/A	40	107	TRUE	1	R/R
NSY	C/C	0	22	C/G	7	18	TRUE	0	R/R
NSY	C/C	0	68	C/T	33	92	TRUE	1	R/R
NSY	G/G	0	38	G/C	27	78	TRUE	1	R/R
NSY	C/C	0	157	C/A	62	135	TRUE	1	R/R
NSY	G/G	0	32	G/C	9	30	TRUE	1	R/R
NSY	G/G	0	111	G/C	51	107	TRUE	1	R/R
NSY	G/G	0	35	G/A	15	46	TRUE	1	R/R
NSY	C/C	0	67	C/T	22	71	TRUE	1	R/R
SS5	G/G	0	35	G/T	19	38	TRUE	1	R/R
NSY	C/C	0	95	C/T	35	82	TRUE	1	R/R
SS	G/G	0	117	G/C	35	116	TRUE	1	R/R
NSY	G/G	0	44	G/C	13	37	TRUE	1	R/R
NSY	G/G	0	56	G/C	24	60	TRUE	1	R/R
NSY	G/G	0	130	G/C	56	145	TRUE	1	R/R
NSY	C/C	0	151	C/T	74	188	TRUE	1	R/R
NSY	G/G	0	47	G/A	12	36	TRUE	1	R/R
NSY	G/G	0	79	G/C	19	60	TRUE	1	R/R
NSY	G/G	0	224	G/T	55	192	TRUE	1	R/R
NSY	G/G	0	62	G/A	21	57	TRUE	1	R/R
SG	C/C	0	219	C/G	69	126	TRUE	1	R/R

SS	TA/TA	1	29	TA/T	5	23	TRUE	1	R/R
NSY	G/G	0	159	G/A	50	87	TRUE	1	R/R
NSY	C/C	0	141	C/T	66	141	TRUE	1	R/R
SS	C/C	0	38	C/G	8	27	TRUE	1	R/R
NSY	C/C	0	130	C/G	51	150	TRUE	1	R/R
SS	G/G	0	160	G/A	64	139	TRUE	1	R/R
NSY	C/C	0	154	C/T	38	114	TRUE	1	R/R
SG	G/G	0	77	G/A	32	61	TRUE	1	R/R
NSY	C/C	1	96	C/T	27	73	TRUE	1	R/R
NSY	C/C	0	64	C/G	26	74	TRUE	1	R/R
NSY	C/C	0	239	C/T	82	267	TRUE	1	R/R
SS	C/C	0	172	C/T	29	95	TRUE	1	R/R
NSY	A/A	1	38	A/G	4	44	TRUE	0	R/R
NSY	C/C	1	37	C/A	4	42	TRUE	0	R/R
NSY	C/C	0	56	C/T	22	55	TRUE	0	R/R
NSY	C/C	0	107	C/T	46	102	TRUE	1	R/R
NSY	G/G	0	197	G/T	58	164	TRUE	1	R/R
NSY	G/G	0	171	G/A	65	161	TRUE	1	R/R
NSY	C/C	0	105	C/T	54	125	TRUE	1	R/R
NSY	C/C	0	80	C/G	30	66	TRUE	1	R/R
SS	G/G	0	65	G/T	34	89	TRUE	0	R/R
NSY	C/C	0	236	C/T	96	220	TRUE	1	R/R
NSY	G/G	0	191	G/A	78	164	TRUE	1	R/R
NSY	C/C	0	194	C/A	75	213	TRUE	1	R/R
NSY	C/C	0	175	C/T	57	167	TRUE	1	R/R
NSY	C/C	0	118	C/T	33	93	TRUE	1	R/R
NSY	G/G	0	65	G/A	14	49	TRUE	1	R/R
SG	C/C	0	113	C/A	36	82	TRUE	1	R/R
NSY	G/G	2	123	G/C	7	86	TRUE	0	R/R
NSY	C/C	2	124	C/G	7	82	TRUE	0	R/R
NSY	G/G	0	61	G/C	24	62	TRUE	1	R/R
NSY	G/G	0	173	G/A	54	154	TRUE	1	R/R
SG	G/G	0	119	G/T	31	87	TRUE	1	R/R
ESS	C/C	0	159	C/G	70	166	TRUE	1	R/R
SS	C/C	1	39	C/CA	4	25	TRUE	1	R/R
SS	G/G	1	39	G/A	2	23	TRUE	1	R/R
SS	G/G	1	22	G/A	3	17	TRUE	1	R/R
SS	A/A	1	20	A/G	3	16	TRUE	1	R/R
NSY	C/C	2	80	C/T	8	80	TRUE	1	R/R
NSY	G/G	1	155	G/A	52	117	TRUE	1	R/R
NSY	C/C	2	74	C/G	26	77	TRUE	1	R/R
NSY	G/G	0	163	G/C	62	150	TRUE	1	R/R
SS	G/G	0	82	G/C	16	77	TRUE	0	R/R
NSY	G/G	0	38	G/A	13	34	TRUE	1	R/R
NSY	G/G	1	182	G/A	48	157	TRUE	1	R/R
SS	C/C	0	118	C/T	55	114	TRUE	1	R/R
NSY	C/C	0	166	C/T	60	149	TRUE	1	R/R
NSY	C/C	0	47	C/G	18	51	TRUE	1	R/R
NSY	C/C	0	77	C/A	20	64	TRUE	0	R/R
SS	C/C	0	63	C/T	27	71	TRUE	1	R/R
NSY	C/C	0	20	C/G	9	20	TRUE	1	R/R
NSY	G/G	0	152	G/C	55	146	TRUE	1	R/R
SG	G/G	0	167	G/A	66	177	TRUE	1	R/R
NSY	C/C	0	61	C/T	37	96	TRUE	1	R/R
NSY	C/C	0	296	C/T	47	278	TRUE	1	R/R

NSY	G/G	0	51	G/C	7	26	TRUE	1	R/R
NSY	C/C	0	82	C/T	27	73	TRUE	1	R/R
NSY	C/C	0	133	C/T	53	140	TRUE	1	R/R
SS	GT/GT	2	27	GT/G	10	39	TRUE	1	R/R
NSY	C/C	2	30	C/T	3	28	TRUE	0	R/R
NSY	C/C	1	17	C/T	3	26	TRUE	0	R/R
NSY	C/C	2	39	C/A	8	45	TRUE	1	R/R
NSY	C/C	0	253	C/T	91	223	TRUE	1	R/R
NSY	G/G	0	34	G/A	16	40	TRUE	0	R/R
SS	G/G	0	119	G/A	38	102	TRUE	1	R/R
SS	G/G	0	142	G/C	59	148	TRUE	1	R/R
NSY	C/C	0	132	C/G	44	117	TRUE	1	R/R
SG	G/G	0	155	G/T	52	152	TRUE	1	R/R
NSY	C/C	0	134	C/G	55	148	TRUE	1	R/R
NSY	G/G	0	175	G/A	51	128	TRUE	1	R/R
NSY	G/G	0	99	G/C	38	112	TRUE	1	R/R
NSY	C/C	0	161	C/G	62	165	TRUE	1	R/R
NSY	C/C	0	98	C/T	41	95	TRUE	1	R/R
NSY	G/G	0	54	G/A	17	55	TRUE	0	R/R
NSY	G/G	0	155	G/C	70	170	TRUE	1	R/R
NSY	G/G	0	183	G/A	80	187	TRUE	1	R/R
NSY	C/C	0	47	C/T	16	45	TRUE	1	R/R
SG	G/G	0	185	G/A	61	176	TRUE	1	R/R
NSY	C/C	0	209	C/G	59	157	TRUE	1	R/R
NSY	C/C	0	62	C/G	21	58	TRUE	1	R/R
NSY	C/C	0	83	C/G	25	69	TRUE	1	R/R
SS	CT/CT	0	22	CT/C	4	31	TRUE	1	R/R
NSY	G/G	0	132	G/C	34	126	TRUE	1	R/R
EE	C/C	0	77	C/T	23	74	TRUE	1	R/R
SG	C/C	0	56	C/T	28	78	TRUE	1	R/R
SS	C/C	0	56	C/T	23	50	TRUE	1	R/R
NSY	C/C	1	17	C/A	7	19	TRUE	0	R/R
NSY	G/G	0	150	G/A	36	124	TRUE	1	R/R
SS	A/A	1	21	A/T	3	16	TRUE	1	R/R
NSY	C/C	0	153	C/G	43	105	TRUE	1	R/R
NSY	C/C	0	65	C/T	20	49	TRUE	1	R/R
NSY	C/C	0	135	C/G	40	121	TRUE	1	R/R
NSY	G/G	0	24	G/A	7	19	TRUE	1	R/R
SS	AT/AT	2	24	AT/A	6	30	TRUE	1	R/R
NSY	C/C	0	117	C/G	30	115	TRUE	1	R/R
NSY	C/C	1	180	C/G	56	165	TRUE	1	R/R
NSY	G/G	0	54	G/C	16	40	TRUE	1	R/R
NSY	C/C	0	152	C/T	37	97	TRUE	1	R/R
NSY	G/G	0	231	G/A	73	164	TRUE	1	R/R
NSY	G/G	0	34	G/C	12	27	TRUE	1	R/R
ESS	G/G	0	38	G/C	22	48	TRUE	1	R/R
NSY	G/G	0	96	G/A	36	104	TRUE	1	R/R
NSY	G/G	0	145	G/C	56	163	TRUE	1	R/R
NSY	G/G	0	107	G/C	46	120	TRUE	1	R/R
NSY	C/C	0	103	C/A	35	100	TRUE	1	R/R
SS	G/G	0	87	G/C	31	84	TRUE	1	R/R
NSY	C/C	0	141	C/G	44	126	TRUE	1	R/R
NSY	C/C	0	68	C/G	18	58	TRUE	1	R/R
NSY	C/C	0	49	C/T	12	32	TRUE	1	R/R
NSY	G/G	0	85	G/C	36	83	TRUE	1	R/R

NSY	G/G	0	304	G/C	108	261	TRUE	1	R/R
NSY	G/G	0	167	G/C	61	181	TRUE	1	R/R
NSY	G/G	0	40	G/A	16	36	TRUE	1	R/R
SS	G/G	0	270	G/T	63	182	TRUE	1	R/R
SS5	G/G	0	173	G/A	47	114	TRUE	1	R/R
NSY	G/G	0	194	G/C	53	128	TRUE	1	R/R
NSY	G/G	0	215	G/C	71	202	TRUE	1	R/R
NSY	G/G	0	29	G/A	11	25	TRUE	1	R/R
SG	C/C	0	75	C/T	26	58	TRUE	1	R/R
EE	C/C	0	201	C/A	68	168	TRUE	1	R/R
NSY	C/C	0	125	C/G	43	126	TRUE	1	R/R
NSY	C/C	0	104	C/T	46	126	TRUE	1	R/R
NSY	G/G	0	175	G/C	73	146	TRUE	1	R/R
NSY	C/C	0	133	C/G	59	154	TRUE	1	R/R
NSY	C/C	2	121	C/T	51	127	TRUE	1	R/R
NSY	G/G	0	78	G/A	32	79	TRUE	1	R/R
NSY	T/T	0	102	T/C	55	122	TRUE	1	R/R
NSY	G/G	0	333	G/C	107	290	TRUE	1	R/R
NSY	G/G	0	48	G/A	8	47	TRUE	1	R/R
NSY	G/G	0	38	G/A	6	36	TRUE	1	R/R
NSY	G/G	0	34	G/T	5	34	TRUE	1	R/R
IF	CGGG/CG	0	34	CGGG/C	5	35	TRUE	1	R/R
NSY	T/T	0	20	T/C	4	25	TRUE	1	R/R
NSY	C/C	0	15	C/T	4	24	TRUE	1	R/R
NSY	C/C	0	45	C/T	30	68	TRUE	1	R/R
NSY	C/C	0	153	C/G	39	108	TRUE	1	R/R
NSY	G/G	0	155	G/T	38	141	TRUE	1	R/R
NSY	G/G	0	55	G/C	9	45	TRUE	1	R/R
NSY	C/C	0	118	C/T	32	91	TRUE	1	R/R
NSY	G/G	0	57	G/C	21	49	TRUE	1	R/R
NSY	C/C	1	46	C/T	23	73	TRUE	1	R/R
NSY	C/C	0	115	C/T	20	61	TRUE	1	R/R
NSY	A/A	1	36	A/G	6	28	TRUE	1	R/R
NSY	T/T	2	38	T/C	7	29	TRUE	1	R/R
NSY	G/G	0	178	G/A	49	189	TRUE	1	R/R
NSY	C/C	0	110	C/G	42	94	TRUE	1	R/R
NSY	C/C	0	134	C/G	49	136	TRUE	1	R/R
SS	C/C	0	99	C/G	30	121	TRUE	1	R/R
NSY	G/G	0	60	G/A	22	56	TRUE	1	R/R
NSY	C/C	0	43	C/G	25	32	TRUE	1	R/R
NSY	C/C	0	89	C/T	43	55	TRUE	1	R/R
NSY	G/G	0	174	G/C	44	76	TRUE	1	R/R
NSY	G/G	0	67	G/A	22	34	TRUE	1	R/R
NSY	G/G	0	119	G/A	42	101	TRUE	1	R/R
NSY	G/G	0	139	G/A	61	161	TRUE	1	R/R
ESS	G/G	0	23	G/A	7	23	TRUE	1	R/R
NSY	G/G	0	31	G/C	10	33	TRUE	1	R/R
NSY	C/C	0	64	C/T	22	62	TRUE	1	R/R
NSY	C/C	0	144	C/T	55	133	TRUE	1	R/R
NSY	C/C	0	292	C/T	79	202	TRUE	1	R/R
NSY	C/C	0	168	C/T	45	144	TRUE	1	R/R
SS	C/C	0	44	C/G	21	45	TRUE	1	R/R
NSY	C/C	0	145	C/T	47	67	TRUE	1	R/R
NSY	G/G	0	104	G/C	45	64	TRUE	1	R/R
NSY	C/C	0	27	C/T	29	39	TRUE	0	R/R

NSY	C/C	0	58	C/G	27	32	TRUE	1	R/R
NSY	C/C	0	151	C/G	118	149	TRUE	1	R/R
NSY	G/G	0	302	G/T	102	162	TRUE	1	R/R
NSY	G/G	0	158	G/C	36	71	TRUE	1	R/R
NSY	G/G	0	115	G/C	43	116	TRUE	1	R/R
NSY	T/T	0	54	T/C	22	68	TRUE	1	R/R
NSY	C/C	0	26	C/A	13	22	TRUE	1	R/R
NSY	C/C	0	180	C/G	80	162	TRUE	1	R/R
NSY	G/G	1	95	G/A	28	77	TRUE	1	R/R
NSY	G/G	0	44	G/A	11	43	TRUE	1	R/R
NSY	G/G	0	118	G/C	43	65	TRUE	1	R/R
FS	CCT/CCT	0	361	CCT/C	74	111	TRUE	1	R/R
NSY	G/G	0	183	G/A	67	104	TRUE	0	R/R
EE	G/G	0	223	G/A	79	119	TRUE	1	R/R
NSY	A/A	2	30	A/C	6	20	TRUE	0	R/R
NSY	C/C	0	302	C/T	107	157	TRUE	1	R/R
NSY	C/C	0	21	C/G	7	15	TRUE	0	R/R
SS	G/G	0	137	G/A	42	61	TRUE	1	R/R
FS	GA/GA	0	137	GA/G	45	67	TRUE	1	R/R
NSY	G/G	0	71	G/A	13	46	TRUE	1	R/R
SG	C/C	0	193	C/T	72	177	TRUE	1	R/R
SS	C/C	2	21	C/CT	12	19	TRUE	0	R/R
NSY	C/C	0	89	C/T	34	67	TRUE	1	R/R
NSY	C/C	0	114	C/T	55	103	TRUE	1	R/R
NSY	C/C	0	130	C/G	50	110	TRUE	1	R/R
NSY	C/C	0	136	C/G	66	143	TRUE	1	R/R
NSY	G/G	0	21	G/T	9	27	TRUE	0	R/R
NSY	G/G	0	65	G/A	31	74	TRUE	1	R/R
NSY	G/G	0	41	G/A	11	31	TRUE	1	R/R
NSY	C/C	0	196	C/A	79	171	TRUE	1	R/R
NSY	G/G	0	361	G/C	124	340	TRUE	1	R/R
NSY	G/G	0	158	G/A	55	143	TRUE	1	R/R
SS	C/C	0	44	C/G	26	56	TRUE	1	R/R
NSY	C/C	0	183	C/T	58	143	TRUE	1	R/R
NSY	C/C	0	41	C/G	23	62	TRUE	1	R/R
FS	AATAG/AA	0	49	AATAG/A	20	56	TRUE	1	R/R
SG	G/G	0	150	G/A	63	166	TRUE	1	R/R
SG	C/C	0	229	C/T	74	205	TRUE	1	R/R
NSY	C/C	0	132	C/T	59	128	TRUE	1	R/R
NSY	G/G	0	135	G/A	67	125	TRUE	1	R/R
ESS	C/C	0	81	C/T	34	86	TRUE	1	R/R
NSY	G/G	0	252	G/C	86	254	TRUE	1	R/R
NSY	C/C	0	241	C/G	71	224	TRUE	1	R/R
SG	C/C	0	101	C/A	38	95	TRUE	1	R/R
NSY	C/C	0	147	C/T	51	138	TRUE	1	R/R
NSY	C/C	1	190	C/T	57	147	TRUE	1	R/R
NSY	C/C	0	185	C/G	53	135	TRUE	1	R/R
NSY	C/C	0	102	C/G	36	90	TRUE	1	R/R
NSY	C/C	0	48	C/G	11	22	TRUE	1	R/R
NSY	G/G	0	231	G/A	56	152	TRUE	1	R/R
NSY	C/C	0	59	C/G	24	58	TRUE	1	R/R
NSY	C/C	0	102	C/T	30	62	TRUE	1	R/R
SG	C/C	0	168	C/A	42	104	TRUE	1	R/R
SS	G/G	0	76	G/C	31	76	TRUE	0	R/R
NSY	C/C	0	158	C/T	51	131	TRUE	1	R/R

NSY	G/G	0	220	G/A	67	184	TRUE	1	R/R
NSY	C/C	0	72	C/G	24	48	TRUE	1	R/R
NSY	G/G	0	61	G/A	18	58	TRUE	1	R/R
NSY	T/T	1	29	T/G	3	39	TRUE	0	R/R
EE	A/A	1	28	A/G	4	41	TRUE	0	R/R
SS	C/C	1	26	C/G	4	38	TRUE	0	R/R
NSY	C/C	0	115	C/G	40	106	TRUE	1	R/R
NSY	G/G	0	208	G/A	92	204	TRUE	1	R/R
NSY	G/G	0	204	G/C	69	223	TRUE	1	R/R
SG	G/G	0	66	G/A	37	82	TRUE	1	R/R
NSY	C/C	0	217	C/G	72	186	TRUE	1	R/R
NSY	C/C	0	48	C/T	12	44	TRUE	0	R/R
SS	CT/CT	1	29	CT/C	6	35	TRUE	1	R/R
NSY	C/C	0	105	C/G	37	81	TRUE	1	R/R
NSY	C/C	0	187	C/T	57	152	TRUE	1	R/R
NSY	C/C	0	115	C/G	46	110	TRUE	1	R/R
NSY	G/G	0	269	G/A	79	200	TRUE	1	R/R
NSY	C/C	0	307	C/T	75	211	TRUE	1	R/R
NSY	C/C	1	221	C/T	74	170	TRUE	1	R/R
NSY	C/C	0	128	C/G	26	83	TRUE	1	R/R
NSY	G/G	0	103	G/C	25	76	TRUE	1	R/R
NSY	G/G	0	344	G/C	107	289	TRUE	1	R/R
NSY	C/C	0	172	C/T	61	144	TRUE	1	R/R
SG	G/G	0	44	G/T	11	33	TRUE	0	R/R
NSY	G/G	0	115	G/A	37	90	TRUE	1	R/R
NSY	C/C	0	195	C/T	65	191	TRUE	1	R/R
NSY	C/C	0	40	C/G	14	37	TRUE	1	R/R
SG	C/C	0	145	C/A	50	119	TRUE	1	R/R
NSY	C/C	0	106	C/A	44	104	TRUE	1	R/R
SG	C/C	0	208	C/T	33	166	TRUE	1	R/R
NSY	C/C	1	113	C/T	24	81	TRUE	1	R/R
NSY	C/C	1	212	C/T	93	196	TRUE	1	R/R
NSY	G/G	0	116	G/A	29	77	TRUE	1	R/R
NSY	G/G	0	113	G/T	33	95	TRUE	1	R/R
NSY	G/G	0	127	G/C	58	138	TRUE	1	R/R
SG	G/G	0	90	G/A	30	79	TRUE	1	R/R
NSY	G/G	0	69	G/A	36	81	TRUE	1	R/R
NSY	C/C	0	173	C/T	57	158	TRUE	1	R/R
NSY	G/G	0	111	G/C	44	115	TRUE	1	R/R
ESS	G/G	0	45	G/A	21	63	TRUE	0	R/R
NSY	G/G	0	206	G/A	73	178	TRUE	1	R/R
NSY	C/C	0	192	C/T	80	182	TRUE	1	R/R
NSY	G/G	0	157	G/A	72	165	TRUE	1	R/R
NSY	G/G	0	94	G/A	45	106	TRUE	1	R/R
NSY	C/C	0	118	C/T	43	118	TRUE	1	R/R
ESS	G/G	0	123	G/C	30	87	TRUE	1	R/R
NSY	C/C	0	177	C/T	62	103	TRUE	1	R/R
NSY	G/G	0	25	G/A	7	18	TRUE	1	R/R
NSY	A/A	1	81	A/G	4	43	TRUE	1	R/R
FS	T/T	1	81	T/TC	5	47	TRUE	1	R/R
NSY	C/C	0	219	C/T	75	197	TRUE	1	R/R
NSY	T/T	0	136	T/A	57	128	TRUE	1	R/R
NSY	G/G	0	86	G/A	38	90	TRUE	1	R/R
NSY	C/C	0	63	C/T	18	58	TRUE	1	R/R
SS	G/G	0	39	G/A	26	47	TRUE	1	R/R

SG	G/G	0	28	G/A	14	34	TRUE	0	R/R
NSY	G/G	0	65	G/C	35	82	TRUE	0	R/R
NSY	G/G	0	220	G/A	56	78	TRUE	1	R/R
NSY	C/C	0	377	C/T	129	206	TRUE	1	R/R
NSY	G/G	0	99	G/C	35	49	TRUE	1	R/R
NSY	G/G	0	73	G/T	9	53	TRUE	1	R/R
NSY	G/G	1	58	G/A	5	36	TRUE	1	R/R
NSY	G/G	1	41	G/A	5	37	TRUE	0	R/R
FS	CT/CT	1	40	CT/C	5	37	TRUE	0	R/R
NSY	G/G	1	41	G/A	3	35	TRUE	0	R/R
SS	G/G	0	55	G/C	15	19	TRUE	1	R/R
NSY	C/C	0	193	C/A	56	86	TRUE	1	R/R

tumorClass	normHet	tumorHet	covFilter	strandFilter	LOH	SNVFilter	INDELFilter
R/A	0	0.732558	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.590909	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.703125	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.659794	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.75	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.64	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.641026	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.717391	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.582822	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.631579	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.7	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.763158	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.618421	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.736111	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0.0625	0.125	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0.043478	0.1875	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.245283	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0.076923	0.375	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0.08	0.289474	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.191489	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.239583	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.262548	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.207547	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.171141	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.147368	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.187135	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.160643	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.169054	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.222222	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.280303	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.245098	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.234568	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.239669	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.22	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.456395	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0.006135	0.18107	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.276243	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.212121	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.244552	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.278689	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.189394	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.267606	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.373377	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.142857	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.424528	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.27451	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0.047619	0.2	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.344595	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.343066	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.315789	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.5	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.395604	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.372093	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.445455	TRUE	TRUE	FALSE	TRUE	FALSE

R/A	0	0.365169	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.401961	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.470588	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.392308	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.40566	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.448	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.438776	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.412698	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0.105263	0.473684	TRUE	TRUE	FALSE	FALSE	TRUE
R/A	0.020619	0.136364	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.330882	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.453125	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.404255	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0.032258	0.208333	TRUE	TRUE	FALSE	FALSE	TRUE
R/A	0	0.390805	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.322222	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.267327	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.333333	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.343949	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.369369	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.439394	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.310345	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.366667	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0.013158	0.393939	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.371134	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.377778	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.39801	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.387879	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.398551	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.324022	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.408163	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.385113	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.491071	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.414966	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.373832	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.388889	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.358696	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.346154	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.459259	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.3	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.476636	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.326087	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.309859	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.5	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.426829	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.301724	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.351351	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.4	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.386207	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.393617	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.333333	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.316667	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.286458	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.368421	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.547619	TRUE	TRUE	FALSE	TRUE	FALSE

R/A	0.034483	0.217391	TRUE	TRUE	FALSE	FALSE	TRUE
R/A	0	0.574713	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.468085	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.296296	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.34	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.460432	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.333333	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.52459	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0.010417	0.369863	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.351351	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.307116	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.305263	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0.026316	0.090909	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0.027027	0.095238	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.4	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.45098	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.353659	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.403727	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.432	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.454545	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.382022	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.436364	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.47561	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.352113	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.341317	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.354839	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.285714	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.439024	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0.01626	0.081395	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0.016129	0.085366	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.387097	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.350649	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.356322	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.421687	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0.025641	0.16	TRUE	TRUE	FALSE	FALSE	TRUE
R/A	0.025641	0.086957	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0.045455	0.176471	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0.05	0.1875	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0.025	0.1	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0.006452	0.444444	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0.027027	0.337662	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.413333	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.207792	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.382353	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0.005495	0.305732	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.482456	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.402685	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.352941	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.3125	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.380282	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.45	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.376712	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.372881	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.385417	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.169065	TRUE	TRUE	FALSE	TRUE	FALSE

R/A	0	0.269231	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.369863	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.378571	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0.074074	0.25641	TRUE	TRUE	FALSE	FALSE	TRUE
R/A	0.066667	0.107143	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0.058824	0.115385	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0.051282	0.177778	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.408072	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.4	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.372549	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.398649	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.376068	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.342105	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.371622	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.398438	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.339286	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.375758	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.431579	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.309091	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.411765	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.427807	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.355556	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.346591	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.375796	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.362069	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.362319	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.129032	TRUE	TRUE	FALSE	FALSE	TRUE
R/A	0	0.269841	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.310811	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.358974	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.46	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0.058824	0.368421	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.290323	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0.047619	0.1875	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.409524	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.408163	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.330579	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.368421	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0.083333	0.2	TRUE	TRUE	FALSE	FALSE	TRUE
R/A	0	0.26087	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0.005556	0.339394	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.4	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.381443	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.445122	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.444444	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.458333	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.346154	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.343558	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.383333	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.35	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.369048	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.349206	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.310345	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.375	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.433735	TRUE	TRUE	FALSE	TRUE	FALSE

R/A	0	0.413793	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.337017	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.444444	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.346154	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.412281	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.414063	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.351485	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.44	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.448276	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.404762	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.34127	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.365079	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.5	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.383117	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0.016529	0.401575	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.405063	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.45082	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.368966	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.170213	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.166667	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.147059	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.142857	TRUE	TRUE	FALSE	FALSE	TRUE
R/A	0	0.16	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.166667	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.441176	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.361111	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.269504	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.2	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.351648	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.428571	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0.021739	0.315068	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.327869	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0.027778	0.214286	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0.052632	0.241379	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.259259	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.446809	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.360294	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.247934	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.392857	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.78125	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.781818	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.578947	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.647059	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.415842	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.378882	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.304348	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.30303	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.354839	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.413534	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.391089	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.3125	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.466667	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.701493	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.703125	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.74359	TRUE	TRUE	FALSE	TRUE	FALSE

R/A	0	0.84375	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.791946	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.62963	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.507042	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.37069	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.323529	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.590909	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.493827	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0.010526	0.363636	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.255814	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.661538	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.666667	TRUE	TRUE	FALSE	FALSE	TRUE
R/A	0	0.644231	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.663866	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0.066667	0.3	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.681529	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.466667	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.688525	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.671642	TRUE	TRUE	FALSE	FALSE	TRUE
R/A	0	0.282609	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.40678	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0.095238	0.631579	TRUE	TRUE	FALSE	FALSE	TRUE
R/A	0	0.507463	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.533981	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.454545	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.461538	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.333333	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.418919	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.354839	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.461988	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.364706	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.384615	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.464286	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.405594	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.370968	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.357143	TRUE	TRUE	FALSE	FALSE	TRUE
R/A	0	0.379518	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.360976	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.460938	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.536	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.395349	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.338583	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.316964	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.4	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.369565	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0.005263	0.387755	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.392593	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.4	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.5	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.368421	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.413793	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.483871	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.403846	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.407895	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.389313	TRUE	TRUE	FALSE	TRUE	FALSE

R/A	0	0.36413	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.5	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.310345	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0.034483	0.076923	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0.035714	0.097561	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0.038462	0.105263	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.377358	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.45098	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.309417	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.45122	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.387097	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.272727	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0.034483	0.171429	TRUE	TRUE	FALSE	FALSE	TRUE
R/A	0	0.45679	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.375	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.418182	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.395	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.35545	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0.004525	0.435294	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.313253	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.328947	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.370242	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.423611	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.333333	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.411111	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.340314	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.378378	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.420168	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.423077	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.198795	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0.00885	0.296296	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0.004717	0.47449	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.376623	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.347368	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.42029	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.379747	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.444444	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.360759	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.382609	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.333333	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.410112	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.43956	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.436364	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.424528	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.364407	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.344828	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.601942	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.388889	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0.012346	0.093023	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0.012346	0.106383	TRUE	TRUE	FALSE	FALSE	TRUE
R/A	0	0.380711	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.445313	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.422222	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.310345	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.553191	TRUE	TRUE	FALSE	TRUE	FALSE

R/A	0	0.411765	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.426829	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.717949	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.626214	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.714286	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.169811	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0.017241	0.138889	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0.02439	0.135135	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0.025	0.135135	TRUE	TRUE	FALSE	FALSE	TRUE
R/A	0.02439	0.085714	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.789474	TRUE	TRUE	FALSE	TRUE	FALSE
R/A	0	0.651163	TRUE	TRUE	FALSE	TRUE	FALSE