Supplementary

Table S1 Target-captured region for fusion gene detection

Gene	Target region*	Design remarks
ABL1	chr9:130713831-130887725	Whole gene
ABL2	chr1:179099277-179229734	Whole gene
BCL2	chr18:63123296-63320178	Whole gene
BCL9	chr1:147541362-147626269	Whole gene
BCR	chr22:23179654-23318087	Whole gene
CDKN2A	chr9:21967702-21995351	Whole gene
CDKN2B	chr9:22002853-22009413	Whole gene
CRLF2	chrX:1187499-1212800	Whole gene
CSF1R	chr5:150053241-150113422	Whole gene
DUX4	chr4:190173724-190185992	Whole gene
EBF1	chr5:158695865-159099830	Whole gene
EPOR	chr19:11377155-11384392	Whole gene
ERG	chr21:38367211-38661830	Whole gene
ETV6	chr12:11649804-11895452	Whole gene
FLT3	chr13:28003224-28100642	Whole gene
HNRNPUL1	chr19:41262426-41307742	Whole gene
IKZF1	chr7:50304033-50405151	Whole gene
IL7R	chr5:35852645-35879653	Whole gene
JAK2	chr9:4984983-5128233	Whole gene
KMT2A	chr11:118436440-118526882	Whole gene
MEF2D	chr1:156463671-156500892	Whole gene
MYC	chr8:127732884-127741484	Whole gene + 2.5 kb upstream
NUTM1	chr15:34343265-34357787	Whole gene
P2RY8	chrX:1462522-1537194	Whole gene
PAX5	chr9:36833225-37034529	Whole gene
PBX1	chr1:164555534-164899346	Whole gene
PDGFRB	chr5:150113787-150155922	Whole gene
RUNX1	chr21:34787751-35049348	Whole gene
TCF3	chr19:1609240-1652655	Whole gene
TP53	chr17:7661729-7687600	Whole gene
ZNF384	chr12:6666427-6689622	Whole gene

*, hg38 coordinate.

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Table S2 Somatic point mutations identified on the exome

UPN	Gene	Reference	Nucleotide change	Effect	Amino acid change	VAF
1	*AGRN*	NM_001305275	c.1177+3G>C	splice site	(exon 6)	0.17
1	*FAM110B*	NM_147189	c.772C>T	missense	p.R258W	0.34
1	*GLIS3*	NM_152629	c.1926C>T	silent	p.T642T	0.39
1	*MAGI1*	NM_001033057	c.2819C>T	missense	p.T940M	0.33
1	*MAP3K10*	NM_002446	c.1971C>T	silent	p.S657S	0.16
1	*SERPINI1*	NM_001122752	c.125A>G	missense	p.E42G	0.44
1	*TRDN*	NM_001251987	c.1285C>T	nonsense	p.R429*	0.42
1	*ZNF148*	NM_021964	c.1979G>A	missense	p.R660Q	0.14
1	*ZNF552*	NM_024762	c.129G>T	silent	p.T43T	0.37
2	*EYS*	NM_001142800	c.2883C>T	silent	p.P961P	0.26
2	*SLC35E2*	NM_182838	c.784A>G	missense	p.M262V	0.59
2	**WHSC1*	NM_001042424	c.3295G>A	missense	p.E1099K	0.14
2	*ZNF506*	NM_001145404	c.677G>A	missense	p.R226K	0.16
7	*AIPL1*	NM_001033055	c.201C>T	silent	p.F67F	0.44
7	*DBH*	NM_000787	c.958_959insGGGGTCC	frameshift	S325Rfs*254	0.40
7	*IGFN1*	NM_001164586	c.1767C>T	silent	p.D589D	0.35
7	*MYO15A*	NM_016239	c.7520C>G	missense	p.P2507R	0.54
7	*OVCH1*	NM_183378	c.1593G>T	missense	p.L531F	0.25
7	*RNF150*	NM_020724	c.718G>T	missense	p.A240S	0.22
7	*SMC5*	NM_015110	c.340G>A	missense	p.V114M	0.51
7	*ZNF273*	NM_021148	c.1644C>T	silent	p.D548D	0.12
8	*CASC5*	NM_144508	c.628G>A	missense	p.E210K	0.44
8	*CFAP74*	NM_001304360	c.3451G>A	missense	p.A1151T	0.44
8	*KAT6B*	NM_001256468	c.3252C>T	silent	p.T1084T	0.42
8	*MCPH1*	NM_024596	c.1875_1876insGG	frameshift	p.F627Afs*12	0.47
8	**PAX5*	NM_016734	c.A397C	missense	p.S133R	0.10
8	*XKR4*	NM_052898	c.976G>A	missense	p.V326I	0.39
9	*BICC1*	NM_001080512	c.2124C>T	silent	p.A708A	0.21
9	*CSNK1A1*	NM_001271742	c.25G>A	missense	p.E9K	0.46
9	*ELF1*	NM_001145353	c.142dupT	frameshift	p.Y48Lfs*12	0.24
9	*FBXL18*	NM_024963	c.742C>T	missense	p.R248W	0.40
9	*GATB*	NM_004564	c.1651C>T	silent	p.L551L	0.41
9	*LRFN1*	NM_020862	c.245G>A	missense	p.R82H	0.54
9	*OLFML2B*	NM_001297713	c.969C>T	silent	p.S323S	0.93
9	*RPH3A*	NM_014954	c.1759A>G	missense	p.K587E	0.16
9	*SLC6A1*	NM_003042	c.846C>T	silent	p.S282S	0.11
9	*SMIM24*	NM_001136503	c.132C>A	silent	p.I44I	0.32
9	*TCTN2*	NM_001143850	c.1350C>T	silent	p.N450N	0.19
9	*UGT2B4*	NM_001297615	c.495A>G	silent	p.K165K	0.41
10	**KRAS*	NM_004985	c.35G>T	missense	p.G12V	0.06
10	*MZF1*	NM_003422	c.1987C>T	missense	p.R663W	0.11
10	*NLGN3*	NM_001166660	c.1377G>A	silent	p.S459S	0.47
10	*NOTCH2*	NM_024408	c.2546_2547delAA	frameshift	p.K849Rfs*6	0.38
10	**NRAS*	NM_002524	c.34G>A	missense	p.G12S	0.09
10	*RASSF9*	NM_005447	c.380G>A	missense	p.R127Q	0.12
10	*RBPMS*	NM_001008710	c.111T>C	silent	p.P37P	0.26
10	*REV1*	NM_001037872	c.1583C>A	missense	p.A528D	0.38
10	**WT1*	NM_000378	c.1091C>A	nonsense	p.S364*	0.39
11	*AKIP1*	NM_001206647	c.-6-5C>G	splice site	(exon 2)	0.52
11	*CACNA1B*	NM_000718	c.159G>A	silent	p.A53A	0.23
11	*CEND1*	NM_016564	c.421G>T	missense	p.G141C	0.42
11	*DHX34*	NM_014681	c.3410_3411insCT	frameshift	p.H1138Sfs*19	0.53
11	**ETV6*	NM_001987	c.771dupC	frameshift	p.R259Pfs*41	0.39
11	**IL7R*	NM_002185	c.760_761insAAA	in-frame	p.A254delinsET	0.42
11	*KANK2*	NM_015493	c.362A>G	missense	p.N121S	0.59
11	*MDGA1*	NM_153487	c.741C>T	silent	p.N247N	0.62
11	*NLGN3*	NM_018977	c.501C>T	silent	p.D167D	0.31
11	*NLRC5*	NM_032206	c.1210_1211insCC	frameshift	p. V405Rfs*32	0.66
11	**NOTCH1*	NM_017617	c.4719_4720insGGT	in-frame	p.L1574delinsGL	0.17
11	*OGFR*	NM_007346	c.1468_1469insCT	frameshift	p.H490Pfs*225	0.29
11	*PCDH7*	NM_001173523	c.2833C>A	missense	p.Q945K	0.44
11	*SATB1*	NM_001131010	c.454_455insAAGATAACCGGA	in-frame	p.T152delinsKDNRT	0.44
11	*ZSCAN5A*	NM_024303	c.1389C>T	silent	p.S463S	0.52
12	*ABCA6*	NM_080284	c.1529C>T	missense	p.T510M	0.23
12	*ABHD4*	NM_022060	c.579C>T	silent	p.A193A	0.31
12	*ADAMTS2*	NM_014244	c.2140G>A	missense	p.V714M	0.29
12	*AFF1*	NM_001313960	c.735A>C	missense	p.K245N	0.37
12	*ALPI*	NM_001631	c.1383C>T	silent	p.R461R	0.37
12	*BAIAP2L1*	NM_018842	c.276+4C>T	splice site	(exon 4)	0.41
12	*CCT5*	NM_012073	c.873+1G>C	splice site	(exon 6)	0.23

Table S2 (*continued*)

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Table S2 (*continued*)

UPN	Gene	Reference	Nucleotide change	Effect	Amino acid change	VAF
12	*CNGB1*	NM_001286130	c.3584C>T	missense	p.P1195L	0.33
12	*CYSLTR2*	NM_001308471	c.269C>T	missense	p.T90M	0.29
12	*EIF2AK1*	NM_001134335	c.1231C>T	missense	p.P411S	0.42
12	*ENDOG*	NM_004435	c.576C>T	silent	p.N192N	0.38
12	*FARP1*	NM_001001715	c.354G>A	silent	p.A118A	0.19
12	*GATA3*	NM_001002295	c.520G>A	missense	p.G174S	0.37
12	*GLI3*	NM_000168	c.2718C>T	silent	p.S906S	0.38
12	*GPAM*	NM_001244949	c.952C>T	missense	p.R318C	0.18
12	*GRM6*	NM_000843	c.1780G>A	missense	p.V594M	0.32
12	*IRX1*	NM_024337	c.1194C>T	silent	p.H398H	0.21
12	**KMT2D*	NM_003482	c.12022_12036del	in-frame	p.4008_4012del	0.32
12	**KMT2D*	NM_003482	c.12015_12018delAAGA	frameshift	p.L4006Nfs*15	0.44
12	*LOC389199*	NM_203423	c.205G>A	missense	p.G69R	0.27
12	*MMAA*	NM_172250	c.1206C>T	silent	p.S402S	0.35
12	*MUC16*	NM_024690	c.23043G>A	silent	p.V7681V	0.37
12	*MYH4*	NM_017533	c.3301G>A	missense	p.E1101K	0.40
12	*MYH7*	NM_000257	c.1401C>A	silent	p.I467I	0.23
12	**NRAS*	NM_002524	c.38G>A	missense	p.G13D	0.45
12	*OR2L2*	NM_001004686	c.778C>T	missense	p.R260C	0.28
12	*OR5D14*	NM_001004735	c.808C>T	missense	p.R270W	0.28
12	*OVCH1*	NM_183378	c.2220G>A	silent	p.G740G	0.40
12	*RUNX1T1*	NM_175636	c.1389C>T	silent	p.D463D	0.21
12	*SLC45A4*	NM_001080431	c.234C>T	silent	p.G78G	0.27
12	*SYPL2*	NM_001040709	c.55-4G>A	splice site	(exon 2)	0.51
12	*TENM2*	NM_001080428	c.3278C>T	missense	p.T1093M	0.19
12	*TENM4*	NM_001098816	c.4682G>A	missense	p.R1561Q	0.33
12	*TSNARE1*	NM_001291931	c.92C>T	missense	p.T31I	0.28
12	*TTN*	NM_003319	c.48275G>A	missense	p.R16092Q	0.42
12	*VPS18*	NM_020857	c.1176A>G	silent	p.Q392Q	0.41
12	*ZNF503*	NM_032772	c.1704C>T	silent	p.A568A	0.34
13	*APBA3*	NM_004886	c.869C>G	missense	p.A290G	0.39
13	**BCORL1*	NM_001184772	c.2896G>T	nonsense	p.E966*	0.10
13	*CHSY1*	NM_014918	c.1650T>G	missense	p.F550L	0.20
13	**CSF3R*	NM_000760	c.1853C>T	missense	p.T618I	0.16
13	*CYFIP1*	NM_001033028	c.1882C>G	missense	p.L628V	0.35
13	*DFFB*	NM_001282669	c.431C>T	missense	p.A144V	0.48
13	*DLG2*	NM_001142702	c.752C>T	missense	p.A251V	0.30
13	*EPHA2*	NM_004431	c.1855A>T	missense	p.I619F	0.38
13	*FOXO3*	NM_001455	c.700T>G	missense	p.W234G	0.44
13	*FREM1*	NM_144966	c.1309T>A	missense	p.F437I	0.11
13	*GALNT9*	NM_021808	c.380G>T	missense	p.C127F	0.52
13	*GYS2*	NM_021957	c.719A>T	missense	p.H240L	0.41
13	*HAS3*	NM_001199280	c.121C>T	missense	p.H41Y	0.13
13	*IGF2BP1*	NM_001160423	c.600C>T	silent	p.A200A	0.33
13	*PRDM5*	NM_018699	c.723T>C	silent	p.S241S	0.24
13	*SCN1A*	NM_001165963	c.5612T>G	missense	p.F1871C	0.16
13	*SP7*	NM_152860	c.1253C>T	missense	p.A418V	0.38
13	*SPATA19*	NM_001291992	c.14C>A	missense	p.T5K	0.41
13	*ST18*	NM_014682	c.2371G>A	missense	p.G791R	0.38
13	*TNC*	NM_002160	c.324C>T	silent	p.R108R	0.25
13	*UROD*	NM_000374	c.994C>T	missense	p.R332C	0.35
13	*ZEB2*	NM_001171653	c.3041A>G	missense	p.H1014R	0.26
13	*ZNF536*	NM_014717	c.2288C>G	missense	p.S763C	0.26
16	*C3orf70*	NM_001025266	c.606G>A	silent	p.S202S	0.45
16	*COL18A1*	NM_030582	c.2445C>T	silent	p.P815P	0.48
16	*DAZAP1*	NM_018959	c.1216C>T	nonsense	p.R406*	0.54
16	*PIWIL1*	NM_001190971	c.1028T>A	nonsense	p.L343*	0.34
16	*PNPLA5*	NM_001177675	c.282C>T	silent	p.N94N	0.51
16	*SIN3B*	NM_015260	c.2711_2712insG	frameshift	p.D904Efs*32	0.44
17	*ARHGEF26*	NM_001251962	c.328C>T	missense	p.R110W	0.16
17	**ARID1A*	NM_006015	c.4906delC	frameshift	p.R1636Gfs*18	0.45
17	*CWH43*	NM_001286791	c.789C>T	silent	p.F263F	0.38
17	*ERN2*	NM_001308220	c.654G>A	silent	p.T218T	0.45
17	*FAT2*	NM_001447	c.7808C>T	missense	p.P2603L	0.13
17	*GRIK1*	NM_000830	c.280C>T	missense	p.R94W	0.53
17	*HOXA13*	NM_000522	c.1032T>C	silent	p.N344N	0.47
17	*HPGDS*	NM_014485	c.301T>C	missense	p.C101R	0.12
17	*MAP2*	NM_002374	c.2713C>T	nonsense	p.R905*	0.43
17	*MXRA5*	NM_015419	c.444C>T	silent	p.N148N	0.35
17	*MYBPC1*	NM_001254722	c.1197A>G	silent	p.K399K	0.37

Table S2 (*continued*)

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Table S2 (*continued*)

UPN	Gene	Reference	Nucleotide change	Effect	Amino acid change	VAF
17	*PER2*	NM_022817	c.433G>A	missense	p.V145M	0.47
17	*SORCS3*	NM_014978	c.983G>A	missense	p.R328Q	0.42
19	*AGRN*	NM_198576	c.2796C>T	silent	p.N932N	0.27
19	*APOA4*	NM_000482	c.386G>A	missense	p.R129Q	0.15
19	*ASB7*	NM_024708	c.784C>T	nonsense	p.R262*	0.31
19	*C11orf85*	NM_001037225	c.93G>C	missense	p.K31N	0.41
19	*CCDC33*	NM_182791	c.753G>C	missense	p.L251F	0.42
19	*CCDC91*	NM_018318	c.925-4G>C	splice site	(exon 10)	0.58
19	*IL18*	NM_001243211	c.523G>C	missense	p.E175Q	0.58
19	*INTU*	NM_015693	c.1276G>C	missense	p.E426Q	0.50
19	*LGI2*	NM_018176	c.414-4C>G	splice site	(exon 5)	0.40
19	*LOXL1*	NM_005576	c.1158G>C	missense	p.Q386H	0.39
19	*MYO16*	NM_001198950	c.3486C>G	silent	p.L1162L	0.40
19	*PPL*	NM_002705	c.4669G>C	missense	p.E1557Q	0.37
19	*PRSS23*	NM_001293179	c.658C>T	nonsense	p.Q220*	0.32
19	*UBA2*	NM_005499	c.349G>A	missense	p.D117N	0.26
19	*ZNF526*	NM_001314033	c.492T>C	silent	p.L164L	0.47
19	*ZNF880*	NM_001145434	c.80C>T	missense	p.A27V	0.29
20	*BOD1*	NM_001159651	c.315G>A	silent	p.T105T	0.11
20	*BOD1*	NM_001159651	c.343C>T	silent	p.L115L	0.11
20	*BOD1*	NM_001159651	c.330G>A	silent	p.Q110Q	0.11
20	*PCDHB11*	NM_018931	c.1487T>C	missense	p.L496P	0.15
20	*PTPRJ*	NM_001098503	c.722A>G	missense	p.E241G	0.33
21	*GAL3ST1*	NM_004861	c.837C>T	silent	p.N279N	0.57
21	**SETD2*	NM_014159	c.1717_1720delTTCT	frameshift	p.F573Vfs*5	0.18
22	*C4B*	NM_001002029	c.3214C>T	missense	p.R1072W	0.15
22	*POTEE*	NM_001083538	c.2738A>C	missense	p.K913T	0.13
24	*ALDOB*	NM_000035	c.385G>T	missense	p.D129Y	0.44
24	*ANKRD2*	NM_001129981	c.888C>T	silent	p.H296H	0.65
24	*EXTL3*	NM_001440	c.839G>A	missense	p.R280H	0.38
24	*HMCN1*	NM_031935	c.11378G>A	missense	p.R3793H	0.43
24	*KIF5C*	NM_004522	c.566C>A	missense	p.A189E	0.35
24	*RGAG4*	NM_001024455	c.1462T>C	missense	p.Y488H	0.96
24	*RYR2*	NM_001035	c.14137G>A	missense	p.V4713I	0.31
24	*SEMA4F*	NM_001271661	c.374G>A	missense	p.R125Q	0.52
24	**TP53*	NM_001126115	c.460G>A	missense	p.E154K	0.36
25	*ADAMTS12*	NM_030955	c.4046C>T	missense	p.A1349V	0.23
25	*CCSER1*	NM_001145065	c.2297G>A	missense	p.R766H	0.45
25	*CYR61*	NM_001554	c.213C>A	missense	p.D71E	0.44
25	*DGKD*	NM_003648	c.1977G>A	silent	p.P659P	0.98
25	*DNAH8*	NM_001206927	c.9080G>A	missense	p.R3027Q	0.31
25	*ERC2*	NM_015576	c.1376C>T	missense	p.T459I	0.66
25	*FAM120C*	NM_017848	c.2770G>A	missense	p.V924I	0.31
25	*FSIP2*	NM_173651	c.3637G>A	missense	p.V1213I	0.35
25	**IKZF1*	NM_001291840	c.830C>T	missense	p.S277L	0.46
25	*KCNA10*	NM_005549	c.724C>T	missense	p.R242W	0.48
25	**KRAS*	NM_004985	c.38G>A	missense	p.G13D	0.52
25	*KRTAP5-3*	NM_001012708	c.528C>T	silent	p.C176C	0.22
25	*MST1L*	NM_001271733	c.1377T>C	silent	p.C459C	0.34
25	*NBPF1*	NM_017940	c.2667-3delC	splice site	(exon 25)	0.14
25	*PDLIM5*	NM_001256428	c.75G>A	silent	p.S25S	0.45
25	*PITX1*	NM_002653	c.434G>A	missense	p.R145H	0.51
25	*SEC61A2*	NM_001142628	c.298A>T	missense	p.I100F	0.34
25	*SNAP25*	NM_003081	c.13G>A	missense	p.A5T	0.20
25	*TBC1D30*	NM_015279	c.223G>A	missense	p.D75N	0.52
25	*USP17L20*	NM_001256861	c.860C>T	missense	p.T287I	0.12
26	**JAK2*	NM_004972	c.2047A>G	missense	p.R683G	0.23
26	*KAT6A*	NM_001305878	c.368G>A	missense	p.R123H	0.15
26	*PTGES2*	NM_025072	c.560C>T	missense	p.T187I	0.73
26	*RFPL4A*	NM_001145014	c.388C>T	nonsense	p.Q130*	0.15
26	*SRL*	NM_001098814	c.75T>C	silent	p.D25D	0.42
26	*TEKT4*	NM_001286559	c.456A>G	silent	p.K152K	0.15
26	*TPM1*	NM_001018008	c.144C>T	silent	p.D48D	0.33
27	*CHMP4C*	NM_152284	c.344C>T	missense	p.A115V	0.30
27	*CMYA5*	NM_153610	c.895G>A	missense	p.V299I	0.56
27	*LAMB1*	NM_002291	c.936C>A	nonsense	p.C312*	0.48
27	*MUC4*	NM_018406	c.11523T>G	silent	p.L3841L	0.16
27	*NEIL1*	NM_001256552	c.876G>A	silent	p.P292P	0.50
27	*NKD1*	NM_033119	c.835G>A	missense	p.V279M	0.29
27	*OBSCN*	NM_001271223	c.14091G>A	silent	p.V4697V	0.42

Table S2 (*continued*)

https://dx.doi.org/10.21037/tp-22-512

Table S2 (*continued*)

UPN	Gene	Reference	Nucleotide change	Effect	Amino acid change	VAF
27	**PAX5*	NM_016734	c.C101G	missense	p.P34R	0.34
27	*SALL2*	NM_005407	c.2606C>T	missense	p.P869L	0.27
27	*TANC2*	NM_025185	c.4863C>T	silent	p.A1621A	0.33
28	*CLCN6*	NM_001256959	c.818G>A	missense	p.R273H	0.22
28	*HYDIN*	NM_001198542	c.2350T>C	missense	p.S784P	0.16
28	**IKZF1*	NM_001220768	c.265G>T	nonsense	p.G89*	0.77
28	*LUZP1*	NM_001142546	c.2401T>C	missense	p.S801P	0.44
28	*MGAM*	NM_004668	c.1841C>T	missense	p.T614I	0.39
28	*PGGT1B*	NM_005023	c.1025C>T	missense	p.P342L	0.42
28	*WASF3*	NM_006646	c.691G>A	missense	p.E231K	0.49
30	*DDX11*	NM_001257144	c.1221C>A	missense	p.S407R	0.11
30	*DLK1*	NM_003836	c.712G>A	missense	p.E238K	0.46
30	*FARP1*	NM_001286839	c.2093G>A	missense	p.R698Q	0.28
30	*FMO1*	NM_001282692	c.724C>T	missense	p.R242C	0.10
30	**KRAS*	NM_004985	c.38G>A	missense	p.G13D	0.21
30	*NARS*	NM_004539	c.279G>T	missense	p.K93N	0.34
30	*NEBL*	NM_006393	c.430G>C	missense	p.E144Q	0.25
30	**NRAS*	NM_002524	c.35G>C	missense	p.G12A	0.07
30	*RPTOR*	NM_001163034	c.420C>T	silent	p.N140N	0.18
30	*SDK1*	NM_152744	c.1345C>T	missense	p.R449C	0.25
30	*ZNF208*	NM_007153	c.3480G>T	missense	p.K1160N	0.37
31	*ACAN*	NM_001135	c.823C>T	missense	p.R275W	0.61
31	*ADGRV1*	NM_032119	c.9314G>A	missense	p.R3105Q	0.45
31	*ATP12A*	NM_001185085	c.563G>A	missense	p.R188Q	0.36
31	*BIN3*	NM_018688	c.260C>T	missense	p.T87M	0.10
31	*C6*	NM_000065	c.2222C>T	missense	p.P741L	0.44
31	*CYP4F22*	NM_173483	c.889G>T	missense	p.A297S	0.42
31	*DNAH3*	NM_017539	c.1912T>C	missense	p.F638L	0.44
31	*DSE*	NM_001080976	c.449C>T	missense	p.P150L	0.45
31	*FBN1*	NM_000138	c.3026C>T	missense	p.P1009L	0.49
31	*FLNC*	NM_001127487	c.6708C>A	silent	p.G2236G	0.41
31	*HEATR1*	NM_018072	c.5259C>T	silent	p.S1753S	0.46
31	*IFNL2*	NM_172138	c.359T>G	missense	p.V120G	0.29
31	*KCNA10*	NM_005549	c.640G>A	missense	p.A214T	0.33
31	*KMT5A*	NM_020382	c.42_47delGGCGGC	in-frame	p.14_16del	1.00
31	*LAMA1*	NM_005559	c.4723G>A	missense	p.V1575I	0.53
31	*MB21D1*	NM_138441	c.162C>T	silent	p.A54A	0.44
31	*NOL4L*	NM_080616	c.180G>A	silent	p.T60T	0.48
31	**NOTCH1*	NM_017617	c.7205_7206insGGGCGCTT	frameshift	p.I2402Mfs*23	0.39
31	*NPFFR2*	NM_004885	c.55G>A	missense	p.V19I	0.38
31	*NUP205*	NM_015135	c.4600C>T	missense	p.R1534C	0.43
31	*NWD1*	NM_001007525	c.865C>A	missense	p.Q289K	0.47
31	*OTX2*	NM_001270525	c.500C>T	missense	p.P167L	0.59
31	*OXGR1*	NM_080818	c.803G>A	missense	p.R268H	0.40
31	*POFUT2*	NM_015227	c.301C>T	missense	p.R101W	0.43
31	*ROR1*	NM_001083592	c.554G>T	missense	p.R185L	0.50
31	**RUNX1*	NM_001001890	c.415C>T	nonsense	p.R139*	0.53
31	**SUZ12*	NM_015355	c.856C>T	nonsense	p.R286*	0.43
31	**SUZ12*	NM_015355	c.758G>C	missense	p.R253T	0.44
31	*TLL1*	NM_001204760	c.1085C>A	missense	p.S362Y	0.49
31	*TMEM132D*	NM_133448	c.242C>A	nonsense	p.S81*	0.53
38	*ANKFN1*	NM_153228	c.1170T>C	silent	p.G390G	0.23
38	**FLT3*	NM_004119	c.2503G>T	missense	p.D835Y	0.25
38	**MYC*	NM_002467	c.218C>A	missense	p.T73N	0.27
38	*TECTA*	NM_005422	c.1332C>T	silent	p.Y444Y	0.16
39	*DYNAP*	NM_001307955	c.218T>C	missense	p.M73T	0.19
40	*CHRM2*	NM_001006629	c.1070A>T	missense	p.K357M	0.32
40	*CNBP*	NM_001127192	c.237C>T	silent	p.C79C	0.43
40	*ERG*	NM_001136155	c.278_279insTGCGGG	in-frame	p.A93delinsAAG	0.30
40	*FAM229A*	NM_001167676	c.282-1insATTTCCCCA	splice site	(exon 3)	0.42
40	*FAM57A*	NM_024792	c.660C>G	missense	p.F220L	0.39
40	*GCLC*	NM_001498	c.447-1G>C	splice site	(exon 4)	0.55
40	*IRF5*	NM_001098629	c.490C>T	nonsense	p.Q164*	0.54
40	*KIF2B*	NM_032559	c.338C>T	missense	p.T113M	0.45
40	*KLHL18*	NM_025010	c.394C>T	nonsense	p.R132*	0.15
40	*PABPN1*	NM_004643	c.866G>A	missense	p.R289Q	0.49
40	*PAK7*	NM_177990	c.1463G>A	missense	p.R488Q	0.32
40	*TNPO3*	NM_001191028	c.1870-1G>T	splice site	(exon 16)	0.34
40	*TNPO3*	NM_001191028	c.138C>A	silent	p.I46I	0.38
40	**U2AF1*	NM_001025203	c.101C>T	missense	p.S34F	0.37

Table S2 (*continued*)

https://dx.doi.org/10.21037/tp-22-512

Table S2 (*continued*)

UPN	Gene	Reference	Nucleotide change	Effect	Amino acid change	VAF
40	*ZNF462*	NM_021224	c.676C>T	missense	p.R226C	0.48
40	*ZNF770*	NM_014106	c.2024_2031delACTTTAAA	frameshift	p.H675Rfs*18	0.26
41	**BRAF*	NM_004333	c.1803A>T	missense	p.K601N	0.33
41	*CCDC120*	NM_001163321	c.1640G>A	missense	p.R547H	0.26
41	*CCDC88C*	NM_001080414	c.4808G>A	missense	p.S1603N	0.55
41	*FAM47A*	NM_203408	c.1494T>A	silent	p.T498T	0.17
41	*GNB1*	NM_001282539	c.239T>A	missense	p.I80N	0.24
41	*HS3ST6*	NM_001009606	c.860C>A	missense	p.P287H	0.25
41	**KRAS*	NM_004985	c.436G>A	missense	p.A146T	0.16
41	*MTOR*	NM_004958	c.4377_4378insTCC	in-frame	p.L1460delinsSL	0.25
41	*MUC4*	NM_018406	c.10400C>A	missense	p.T3467K	0.10
41	*MUC4*	NM_018406	c.10387T>A	missense	p.S3463T	0.11
41	*MYO9A*	NM_006901	c.455G>A	missense	p.C152Y	0.15
41	**PAX5*	NM_016734	c.T404C	missense	p.I135T	0.80
41	*PLEKHG2*	NM_022835	c.1099G>A	missense	p.V367M	0.35
41	*RAI2*	NM_021785	c.328G>A	missense	p.A110T	0.39
41	*TBX22*	NM_001303475	c.48G>A	silent	p.K16K	0.45
41	*TDRD9*	NM_153046	c.936T>A	silent	p.I312I	0.39
41	**XBP1*	NM_005080	c.581dupT	frameshift	p.L194Ffs*190	0.38
41	*XIRP2*	NM_001199144	c.9224G>A	missense	p.R3075H	0.41
42	**CEBPA*	NM_001285829	c.579_580insCAG	in-frame	p.K194delinsQK	0.41
42	**CEBPA*	NM_004364	c.78delC	frameshift	p.S27Afs*133	0.47
42	*CREB5*	NM_001011666	c.417G>A	silent	p.P139P	0.42
42	*TAF1L*	NM_153809	c.1975C>G	missense	p.L659V	0.41
42	**WT1*	NM_001198552	c.458_459insGTACGGTCGGC	frameshift	p.S154Yfs*70	0.27
42	**WT1*	NM_001198552	c.539dupA	frameshift	p.M181Dfs*9	0.40
43	*ACTR8*	NM_022899	c.937G>C	missense	p.D313H	0.31
43	*CCDC40*	NM_001243342	c.2895A>G	silent	p.A965A	0.12
43	*COBLL1*	NM_001278461	c.1860T>C	silent	p.H620H	0.30
43	*ESYT3*	NM_031913	c.2201C>G	missense	p.S734C	0.37
43	*EYA1*	NM_172059	c.1302C>T	silent	p.A434A	0.33
43	*HAPLN4*	NM_023002	c.1069C>T	missense	p.R357W	0.29
43	*KCNB2*	NM_004770	c.155C>T	missense	p.T52M	0.31
43	*SLTM*	NM_001013843	c.400G>A	missense	p.E134K	0.57
43	**WHSC1*	NM_001042424	c.3295G>A	missense	p.E1099K	0.41
44	*ACACB*	NM_001093	c.3105G>A	silent	p.P1035P	0.53
44	*AKNAD1*	NM_152763	c.866C>T	missense	p.S289F	0.28
44	*ARNT2*	NM_014862	c.379G>A	missense	p.A127T	0.41
44	*CDH12*	NM_001317227	c.2068C>T	missense	p.R690C	0.52
44	*CDH2*	NM_001308176	c.1625C>T	missense	p.A542V	0.54
44	**CDKN2A*	NM_000077	c.181_182insCGG	in-frame	p.E61delinsAE	0.48
44	**CDKN2A*	NM_000077	c.172_173insT	frameshift	p.R58Lfs*62	0.54
44	**CHD4*	NM_001297553	c.3259G>A	missense	p.E1087K	0.53
44	*CTNND2*	NM_001288716	c.1792C>T	nonsense	p.R598*	0.41
44	*CYFIP1*	NM_014608	c.351T>A	silent	p.P117P	0.50
44	*PCDH11X*	NM_001168362	c.3833A>C	missense	p.D1278A	0.27
44	*PCDH15*	NM_001142765	c.3320T>C	missense	p.V1107A	0.27
44	*RAPH1*	NM_203365	c.329G>A	missense	p.R110H	0.29
44	*STRA6*	NM_001142617	c.1963C>T	missense	p.R655C	0.40
44	*TMEM11*	NM_003876	c.240C>T	silent	p.C80C	0.42
44	*TTN*	NM_133378	c.27338A>G	missense	p.H9113R	0.26
44	*UNC80*	NM_032504	c.3333C>A	missense	p.D1111E	0.36
44	*USP54*	NM_152586	c.602G>A	missense	p.R201Q	0.25
44	*ZNF275*	NM_001080485	c.637G>T	nonsense	p.E213*	0.22
46	*C17orf74*	NM_175734	c.573G>A	silent	p.L191L	0.41
46	*CPXM2*	NM_198148	c.1697G>A	missense	p.R566Q	0.45
46	*CRAMP1*	NM_020825	c.2627G>A	missense	p.R876Q	0.33
46	*DNAH8*	NM_001206927	c.8324G>A	missense	p.G2775E	0.42
46	*EGFR*	NM_005228	c.1939G>A	missense	p.A647T	0.39
46	*GDNF*	NM_000514	c.100delG	frameshift	p. E34Kfs*14	0.51
46	*HRNR*	NM_001009931	c.6330C>T	silent	p.H2110H	0.28
46	*NELL1*	NM_001288713	c.75C>T	silent	p.P25P	0.35
46	*PDE2A*	NM_001243784	c.2553-5C>T	splice site	(exon 31)	0.67
46	**PTEN*	NM_000314	c.697_699delinsTA	frameshift	p.R233Yfs*23	0.54
47	*ADAM21*	NM_003813	c.1252G>T	nonsense	p.E418*	0.32
47	**IKZF3*	NM_001257408	c.162_163insGAATA	frameshift	p. D55Efs*2	0.23
47	*KCNH5*	NM_139318	c.605C>T	missense	p.T202M	0.61
47	*KCTD4*	NM_198404	c.569C>T	missense	p.S190L	0.48
47	*OR5M10*	NM_001004741	c.516T>G	silent	p.L172L	0.44
47	*STEAP3*	NM_138637	c.1272G>A	silent	p.P424P	0.45

Table S2 (*continued*)

https://dx.doi.org/10.21037/tp-22-512

Table S2 (*continued*)

UPN	Gene	Reference	Nucleotide change	Effect	Amino acid change	VAF
48	*DMRTB1*	NM_033067	c.751_751delG	frameshift	p.V251Cfs*59	0.40
48	*FAT3*	NM_001008781	c.1670G>T	missense	p.R557L	0.35
48	*GIMD1*	NM_001195138	c.249G>A	silent	p.L83L	0.42
48	*LCE1E*	NM_178353	c.174C>A	silent	p.G58G	0.12
48	*LMNTD1*	NM_001145728	c.33G>C	silent	p.S11S	0.43
48	*MDGA2*	NM_001113498	c.1229C>T	missense	p.T410M	0.49
48	**WT1*	NM_001198552	c.134_144delGTGAGCAGCAG	frameshift	p.G45Vfs*32	0.74
48	*ZNFX1*	NM_021035	c.1461T>G	missense	p.N487K	0.10
49	*CORO2B*	NM_001190456	c.807G>C	silent	p.L269L	0.47
49	*CPAMD8*	NM_015692	c.3697C>T	missense	p.R1233C	0.17
49	*F11*	NM_000128	c.1679G>T	missense	p.C560F	0.35
49	*FAM188B*	NM_032222	c.1143G>A	silent	p.E381E	0.34
49	*FGFR1*	NM_001174066	c.1091G>A	missense	p.G364E	0.42
49	*NCAPH*	NM_001281712	c.1443G>A	silent	p.G481G	0.44
49	**NRAS*	NM_002524	c.38G>A	missense	p.G13D	0.21
49	*OR10K1*	NM_001004473	c.847C>T	missense	p.P283S	0.44
49	*OR11H2*	NM_001197287	c.827G>T	missense	p.S276I	0.19
49	*OSBPL11*	NM_022776	c.1984A>T	nonsense	p.R662*	0.42
49	*PMS2*	NM_000535	c.1146T>C	silent	p.G382G	0.18
49	*RASGRP2*	NM_001098670	c.1075G>A	missense	p.D359N	0.47
49	*SCN1A*	NM_001165963	c.1285C>T	nonsense	p.Q429*	0.13
49	*SLC7A7*	NM_001126105	c.248C>T	missense	p.S83F	0.18
49	*SPATA6*	NM_001286239	c.942G>A	silent	p.S314S	0.47
51	*AMDHD1*	NM_152435	c.798G>A	silent	p.P266P	0.44
51	*CSMD3*	NM_052900	c.6917A>G	missense	p.D2306G	0.37
51	*DOK3*	NM_001144876	c.406G>C	missense	p.G136R	0.41
51	*SMAD9*	NM_001127217	c.185C>T	missense	p.P62L	0.40
51	*UNC13C*	NM_001080534	c.3409G>A	missense	p.E1137K	0.35
51	*ZNF181*	NM_001029997	c.1352A>C	missense	p.H451P	0.15
53	*AASDH*	NM_001286668	c.974C>G	missense	p.A325G	0.26
53	*BLM*	NM_000057	c.872_873insTGA	in-frame	p.F291delinsFD	0.47
53	*CACNA1B*	NM_000718	c.2944C>T	missense	p.R982W	0.39
53	*CACNA1G*	NM_001256332	c.3317G>A	missense	p.R1106Q	0.40
53	*DSG3*	NM_001944	c.276C>T	silent	p.I92I	0.37
53	*GRIK4*	NM_001282470	c.1396C>T	missense	p.R466C	0.63
53	*GRIN2B*	NM_000834	c.3957G>A	silent	p.P1319P	0.43
53	*KCTD14*	NM_023930	c.89C>T	missense	p.T30M	0.43
53	*LOC100129307*	NM_001310140	c.717C>G	silent	p.V239V	0.25
53	*LY6D*	NM_003695	c.319G>A	missense	p.A107T	0.39
53	*MBTPS1*	NM_003791	c.569C>T	missense	p.P190L	0.13
53	*PRAMEF1*	NM_023013	c.558C>G	silent	p.V186V	0.16
53	*PRAMEF1*	NM_023013	c.560A>G	missense	p.N187S	0.16
53	*PTPRF*	NM_002840	c.1962C>T	silent	p.R654R	0.35
53	*QRFPR*	NM_198179	c.157G>A	missense	p.V53M	0.36
53	*SOX3*	NM_005634	c.527A>C	missense	p.D176A	0.29
53	*STX11*	NM_003764	c.338C>T	missense	p.A113V	0.24
53	*VSX2*	NM_182894	c.810C>T	silent	p.P270P	0.43
56	*FAM135A*	NM_001162529	c.923C>T	missense	p.A308V	0.25
56	*FGD1*	NM_004463	c.2697G>C	missense	p.W899C	0.20
56	*FGD2*	NM_173558	c.368T>C	missense	p.L123P	0.31
56	*LANCL3*	NM_001170331	c.1028T>C	missense	p.V343A	0.36
56	*MYO9B*	NM_001130065	c.5433G>A	silent	p.L1811L	0.46
56	*NETO1*	NM_001201465	c.620G>A	missense	p.R207Q	0.31
56	*OR12D2*	NM_013936	c.109G>T	missense	p.V37L	0.33
56	*PCDHGA12*	NM_003735	c.1437C>T	silent	p.P479P	0.44
56	**PTPN11*	NM_002834	c.218C>T	missense	p.T73I	0.53
56	**WHSC1*	NM_001042424	c.3448A>G	missense	p.T1150A	0.26
56	*ZNF41*	NM_007130	c.550C>A	missense	p.P184T	0.21
57	*HIST1H2AG*	NM_021064	c.72C>G	silent	p.L24L	0.28
57	**KRAS*	NM_004985	c.38G>A	missense	p.G13D	0.06
57	*MUC4*	NM_018406	c.10707T>G	silent	p.L3569L	0.10
57	*NLGN1*	NM_014932	c.1052G>A	missense	p.R351Q	0.43
57	**NRAS*	NM_002524	c.181C>A	missense	p.Q61K	0.34
57	*NUDT15*	NM_001304745	c.279T>C	silent	p.V93V	0.37
57	*OR8D1*	NM_001002917	c.379T>C	missense	p.C127R	0.30
57	*SERPINB11*	NM_001291279	c.269C>T	missense	p.S90L	0.30
57	*TBC1D30*	NM_015279	c.1920G>A	silent	p.P640P	0.28
57	*TNXB*	NM_019105	c.5495C>T	missense	p.P1832L	0.29
58	*ANKRD27*	NM_032139	c.3098C>T	missense	p.P1033L	0.40
58	*CWC27*	NM_001297645	c.1113G>A	silent	p.T371T	0.36

Table S2 (*continued*)

https://dx.doi.org/10.21037/tp-22-512

Table S2 (*continued*)

UPN	Gene	Reference	Nucleotide change	Effect	Amino acid change	VAF
58	*EAF2*	NM_018456	c.106+1delGTG	splice site	(exon 1)	0.22
58	*FER1L6*	NM_001039112	c.2718C>T	silent	p.D906D	0.24
58	*HTR3A*	NM_213621	c.1129G>A	missense	p.V377M	0.39
58	*MEF2A*	NM_001130928	c.1087dupC	frameshift	p.Q365Afs*20	0.46
58	*MTERF1*	NM_001301134	c.233A>T	missense	p.H78L	0.38
58	**NRAS*	NM_002524	c.38G>A	missense	p.G13D	0.33
58	*ORMDL1*	NM_001128150	c.344dupT	frameshift	p. Y116Lfs*5	0.35
58	*PLCG1*	NM_002660	c.2231_2232insCCGACC	in-frame	p.H744delinsHRP	0.17
58	*SETBP1*	NM_001130110	c.170C>T	missense	p.P57L	0.39
58	*SHANK2*	NM_133266	c.2099G>A	missense	p.R700Q	0.42
58	*TMEM132E*	NM_001304438	c.1257C>T	silent	p.G419G	0.50
58	*VGF*	NM_003378	c.1250A>G	missense	p.D417G	0.18
58	*XPR1*	NM_001135669	c.1769G>A	missense	p.R590H	0.20
58	*ZNF541*	NM_001277075	c.3158+1G>A	splice site	(exon 8)	0.36
59	*PCDH8*	NM_002590	c.2833C>A	missense	p.Q945K	0.12
59	**WT1*	NM_000378	c.1091C>A	nonsense	p.S364*	0.51
61	*DST*	NM_015548	c.9237A>G	silent	p.T3079T	0.25
61	*FAM81A*	NM_152450	c.1075C>T	nonsense	p.Q359*	0.25
61	*GRM8*	NM_000845	c.2186G>A	missense	p.R729Q	0.46
61	*HNRNPM*	NM_001297418	c.880_921del	in-frame	p.294_307del	0.23
61	*ITPRIP*	NM_001272012	c.166G>T	nonsense	p.E56*	0.30
61	*KRI1*	NM_023008	c.1600G>A	missense	p.V534M	0.16
61	*LOC100129697*	NM_001290330	c.912C>T	silent	p.H304H	0.12
61	*LOC100129697*	NM_001290330	c.915A>G	silent	p.R305R	0.13
61	*LY75-CD302*	NM_001198759	c.757G>C	missense	p.D253H	0.18
61	*MACC1*	NM_182762	c.636C>T	silent	p.V212V	0.20
61	*PRR32*	NM_001122716	c.403G>C	missense	p.G135R	0.48
61	*SALL1*	NM_001127892	c.384C>A	silent	p.A128A	0.30
61	*SPATA7*	NM_001040428	c.1423C>G	missense	p.Q475E	0.19
61	*TUBA3C*	NM_006001	c.727C>T	nonsense	p.R243*	0.37
61	*WNK2*	NM_001282394	c.2463G>A	silent	p.P821P	0.13
61	*ZMYM2*	NM_001190965	c.566C>A	missense	p.T189N	0.19
62	*C15orf59*	NM_001039614	c.62A>G	missense	p.E21G	0.11
62	*FAM83H*	NM_198488	c.1918G>A	missense	p.V640I	0.54
62	*RBBP6*	NM_006910	c.1918G>A	missense	p.E640K	0.17
64	*ABHD2*	NM_152924	c.207G>A	silent	p.P69P	0.45
64	*CLDN18*	NM_001002026	c.216G>T	silent	p.L72L	0.43
64	*HMBOX1*	NM_001135726	c.325C>T	missense	p.P109S	0.63
64	*IGSF22*	NM_173588	c.315C>T	silent	p.G105G	0.36
64	*KCNH8*	NM_144633	c.1125C>T	silent	p.Y375Y	0.39
64	**KRAS*	NM_004985	c.35G>T	missense	p.G12V	0.36
64	*LRIG3*	NM_001136051	c.1963G>A	missense	p.V655I	0.33
64	*LZTS1*	NM_021020	c.825C>T	silent	p.G275G	0.37
64	*NCOA1*	NM_003743	c.809_810insTAAAATCATC	frameshift	p.S274*	0.44
64	*PTCHD1*	NM_173495	c.1417G>A	missense	p.E473K	0.32
64	*QPCTL*	NM_001163377	c.709_710insTCC	in-frame	p.F237delinsFL	0.42
64	*RGPD3*	NM_001144013	c.3683C>T	missense	p.A1228V	0.42
65	**NRAS*	NM_002524	c.38G>A	missense	p.G13D	0.32
65	*RNF39*	NM_025236	c.1187T>C	missense	p.L396P	0.22
66	*ASTN1*	NM_001286164	c.3249C>T	silent	p.D1083D	0.29
66	*DAAM2*	NM_001201427	c.388G>T	missense	p.V130L	0.27
66	*EFEMP1*	NM_001039349	c.159C>T	silent	p.D53D	0.31
66	*KCNU1*	NM_001031836	c.39C>T	silent	p.D13D	0.34
66	*OR2M3*	NM_001004689	c.107C>T	missense	p.S36L	0.33
66	*PDZRN3*	NM_001303139	c.459C>T	silent	p.N153N	0.37
66	*SPIN3*	NM_001010862	c.48G>A	silent	p.T16T	0.35
66	*SPTAN1*	NM_001130438	c.2943G>A	silent	p.K981K	0.25
67	*ABCC8*	NM_000352	c.4504T>C	missense	p.F1502L	0.36
67	*ABCC8*	NM_000352	c.4525G>T	missense	p.A1509S	0.36
67	*MTCH2*	NM_001317232	c.710T>C	missense	p.V237A	0.37
67	*MTCH2*	NM_001317232	c.683T>C	missense	p.F228S	0.42
67	*ZNF732*	NM_001137608	c.1080C>G	silent	p.P360P	0.43
68	*ADCY5*	NM_001199642	c.102C>G	silent	p.L34L	0.21
68	*AP5Z1*	NM_014855	c.970-4G>A	splice site	(exon 9)	0.24
68	*CCNA1*	NM_001111045	c.79G>A	missense	p.G27R	0.25
68	*CD109*	NM_001159588	c.2493C>T	silent	p.I831I	0.12
68	*COL19A1*	NM_001858	c.2553C>T	silent	p.G851G	0.40
68	*COL6A3*	NM_057166	c.5203C>T	nonsense	p.R1735*	0.18
68	*DNAH7*	NM_018897	c.10602G>C	missense	p.Q3534H	0.21
68	*FRMPD4*	NM_014728	c.3714G>A	silent	p.P1238P	0.74

Table S2 (*continued*)

https://dx.doi.org/10.21037/tp-22-512

Table S2 (*continued*)

UPN	Gene	Reference	Nucleotide change	Effect	Amino acid change	VAF
68	*GCDH*	NM_000159	c.1138G>A	missense	p.D380N	0.19
68	*KATNA1*	NM_001204076	c.892G>C	missense	p.E298Q	0.21
68	*KIAA2022*	NM_001008537	c.1837G>C	missense	p.E613Q	0.40
68	*KLF1*	NM_006563	c.193G>A	missense	p.D65N	0.20
68	*KSR1*	NM_014238	c.1833C>T	silent	p.I611I	0.16
68	*MYCT1*	NM_025107	c.426C>G	silent	p.L142L	0.23
68	*NOL4*	NM_001198549	c.1022C>T	missense	p.S341F	0.17
68	*OR51I2*	NM_001004754	c.552G>A	missense	p.M184I	0.12
68	*PDS5B*	NM_015032	c.4151C>T	missense	p.P1384L	0.25
68	*PRKD1*	NM_002742	c.418G>C	missense	p.E140Q	0.21
68	*RUNX3*	NM_004350	c.879C>T	silent	p.S293S	0.30
68	*SI*	NM_001041	c.317G>C	missense	p.C106S	0.19
68	*SLITRK4*	NM_001184749	c.1133A>G	missense	p.N378S	0.18
68	*SORBS2*	NM_001145674	c.1122C>G	missense	p.I374M	0.13
68	*SPIRE1*	NM_001128627	c.1711T>G	missense	p.C571G	0.15
68	*STRADB*	NM_001206864	c.7C>G	missense	p.L3V	0.27
68	*SYCE2*	NM_001105578	c.273C>G	silent	p.L91L	0.15
68	*TINF2*	NM_001099274	c.1222G>C	missense	p.E408Q	0.19
68	*TTN*	NM_133379	c.13795G>A	missense	p.E4599K	0.21
68	*TTN*	NM_133379	c.13427G>C	missense	p.R4476T	0.21
68	*TTN*	NM_001256850	c.1100C>G	missense	p.S367C	0.24
68	*VPS13D*	NM_015378	c.2401G>A	missense	p.E801K	0.28
68	*VWF*	NM_000552	c.1616C>T	missense	p.S539F	0.11
68	*VWF*	NM_000552	c.1920C>A	silent	p.V640V	0.22
68	*ZNF709*	NM_152601	c.1249G>C	missense	p.E417Q	0.14
69	*BAIAP2L1*	NM_018842	c.666G>A	silent	p.L222L	0.46
69	*DCPS*	NM_014026	c.454C>T	nonsense	p.R152*	0.47
69	*DDX54*	NM_001111322	c.1283G>A	missense	p.R428H	0.43
69	*FAT3*	NM_001008781	c.12541C>T	missense	p.R4181C	0.50
69	*HIST2H2AB*	NM_175065	c.45C>A	silent	p.A15A	0.16
69	*RNF224*	NM_001190228	c.119G>A	missense	p.R40H	0.55
69	*SNHG32*	NM_001040438	c.163dupA	frameshift	p.N55Kfs*20	0.62
69	*SPEG*	NM_005876	c.578C>T	missense	p.T193M	0.57
69	*UBC*	NM_021009	c.632_633insAGGT	nonsense	p.Y211*	0.43
70	**FLT3*	NM_004119	c.1987A>C	missense	p.K663Q	0.25
70	*GABRB3*	NM_001191320	c.567T>G	silent	p.A189A	0.18
70	*GATAD2A*	NM_001300946	c.948G>C	silent	p.G316G	0.26
70	*IFI16*	NM_001206567	c.169C>T	nonsense	p.R57*	0.14
70	**IKZF1*	NM_001291840	c.424A>G	missense	p.N142D	0.17
70	*IWS1*	NM_017969	c.422G>A	missense	p.G141E	0.27
70	*KRT14*	NM_000526	c.978C>T	silent	p.S326S	0.34
70	*NCAM1*	NM_001076682	c.1810+1G>A	splice site	(exon 15)	0.12
70	**NRAS*	NM_002524	c.38G>A	missense	p.G13D	0.21
70	*OR13C8*	NM_001004483	c.762C>G	silent	p.T254T	0.19
70	*TJP1*	NM_003257	c.831C>T	silent	p.S277S	0.42
70	*UTY*	NM_001258265	c.233A>G	missense	p.Y78C	0.45
70	**WHSC1*	NM_001042424	c.3295G>A	missense	p.E1099K	0.13
73	*ALKBH7*	NM_032306	c.650C>T	missense	p.P217L	0.46
73	*ARHGEF33*	NM_001145451	c.1860C>T	silent	p.G620G	0.56
73	*C9orf170*	NM_001001709	c.340G>A	missense	p.V114M	0.55
73	*DHRS7C*	NM_001105571	c.454T>A	missense	p.F152I	0.24
73	*FABP1*	NM_001443	c.124G>A	missense	p.V42M	0.26
73	*FAM47A*	NM_203408	c.1616G>A	missense	p.R539Q	0.42
73	*HLA-DQA2*	NM_020056	c.208C>A	missense	p.Q70K	0.17
73	**IKZF3*	NM_001257408	c.96_99delCAAA	frameshift	p.K33Lfs*20	0.30
73	*ITGA2B*	NM_000419	c.1097G>A	missense	p.R366Q	0.39
73	*MUC17*	NM_001040105	c.3480T>C	silent	p.T1160T	0.40
73	*MUC4*	NM_018406	c.4530T>G	silent	p.P1510P	0.42
73	*NBEA*	NM_001204197	c.899G>A	missense	p.R300Q	0.27
73	*NOTCH3*	NM_000435	c.4884C>T	silent	p.D1628D	0.49
73	**NRAS*	NM_002524	c.38G>A	missense	p.G13D	0.43
73	*OR10Q1*	NM_001004471	c.290C>T	missense	p.S97L	0.45
73	*POM121L12*	NM_182595	c.475C>T	missense	p.R159C	0.45
73	*PRAMEF4*	NM_001009611	c.457G>A	missense	p.V153I	0.95
73	*PTPRT*	NM_007050	c.2679C>T	silent	p.Y893Y	0.32
73	*QRFPR*	NM_198179	c.732G>A	silent	p.K244K	0.23
73	*WNK3*	NM_020922	c.3812G>A	missense	p.R1271H	0.54
73	*WNT7A*	NM_004625	c.700G>A	missense	p.E234K	0.24
73	*ZNF804B*	NM_181646	c.1613C>T	missense	p.T538M	0.46
74	**NRAS*	NM_002524	c.38G>A	missense	p.G13D	0.37

Table S2 (*continued*)

https://dx.doi.org/10.21037/tp-22-512

Table S2 (*continued*)

UPN	Gene	Reference	Nucleotide change	Effect	Amino acid change	VAF
74	*VWA2*	NM_001272046	c.1369_1370insCC	frameshift	p.E458Pfs*22	0.39
75	*DYNAP*	NM_001307955	c.218T>C	missense	p.M73T	0.17
75	**NRAS*	NM_002524	c.183A>T	missense	p.Q61H	0.16
75	*POTEH*	NM_001136213	c.484_510del	in-frame	p.162_170del	0.40
76	*DHX38*	NM_014003	c.1051C>T	missense	p.R351W	0.48
76	*FAM84A*	NM_145175	c.414C>T	silent	p.P138P	0.44
76	*HFE*	NM_000410	c.173T>A	missense	p.F58Y	0.39
76	**NRAS*	NM_002524	c.35G>C	missense	p.G12A	0.20
76	*PGLYRP2*	NM_052890	c.697C>T	nonsense	p.R233*	0.32
76	*REPIN1*	NM_014374	c.969C>T	silent	p.A323A	0.67
76	*SPATA31E1*	NM_178828	c.3234G>A	silent	p.A1078A	0.36
76	*UBE2J1*	NM_016021	c.660delT	frameshift	p.A221Lfs*24	0.40
80	*ACSS3*	NM_024560	c.1783G>T	missense	p.G595C	0.45
80	*DUS3L*	NM_020175	c.849G>T	silent	p.G283G	0.38
80	*FAM205A*	NM_001141917	c.3797C>T	missense	p.T1266M	0.45
80	*FRMPD3*	NM_032428	c.2344C>A	missense	p.P782T	0.35
80	*GNAS*	NM_016592	c.258C>T	silent	p.H86H	0.45
80	**JAK2*	NM_004972	c.2047A>G	missense	p.R683G	0.34
80	*NLGN1*	NM_014932	c.1171G>T	nonsense	p.E391*	0.52
80	**NRAS*	NM_002524	c.201_202insGGAACC	in-frame	p.R68delinsGTR	0.33
80	*OR51E1*	NM_152430	c.813C>A	missense	p.D271E	0.39
80	*PALD1*	NM_014431	c.1687C>T	missense	p.R563W	0.38
80	*PCDHGA1*	NM_018912	c.1910C>T	missense	p.A637V	0.44
80	*PRSS54*	NM_001080492	c.63C>T	silent	p.L21L	0.51
80	*PSG9*	NM_001301707	c.549C>T	silent	p.N183N	0.44
80	*RBM45*	NM_152945	c.744G>A	silent	p.L248L	0.53
80	*TNR*	NM_003285	c.2935G>A	missense	p.E979K	0.39
80	*TRPM8*	NM_024080	c.2946G>A	silent	p.T982T	0.49
80	*TTN*	NM_003319	c.48729A>T	silent	p.P16243P	0.13
80	*ZMYM1*	NM_001289089	c.1437C>T	silent	p.H479H	0.46
80	*ZNF385D*	NM_024697	c.605G>A	missense	p.R202Q	0.36
82	*CTBP2*	NM_022802	c.2272G>T	nonsense	p.E758*	0.14
82	*SORL1*	NM_003105	c.5828C>T	missense	p.T1943M	0.20
84	*ACE*	NM_000789	c.1143G>A	silent	p.T381T	0.31
84	**ARID5B*	NM_032199	c.137dupG	frameshift	p. C46Wfs*29	0.41
84	*BRINP3*	NM_001317188	c.14C>A	missense	p.P5H	0.52
84	*C22orf29*	NM_024627	c.209G>A	missense	p.G70D	0.32
84	*CSMD3*	NM_052900	c.8558C>A	missense	p.T2853K	0.56
84	*EEF1A2*	NM_001958	c.912C>T	silent	p.P304P	0.41
84	**FLT3*	NM_004119	c.2039C>T	missense	p.A680V	0.48
84	*INADL*	NM_176877	c.1952G>A	missense	p.R651H	0.54
84	*KIR3DL3*	NM_153443	c.620C>T	missense	p.S207L	0.44
84	*LAS1L*	NM_001170650	c.317C>T	missense	p.P106L	0.32
84	*MPDZ*	NM_001261406	c.3382C>T	nonsense	p.R1128*	0.38
84	**PTPN11*	NM_002834	c.226G>A	missense	p.E76K	0.41
84	*RFC5*	NM_001206801	c.772G>A	missense	p.D258N	0.38
84	*RIPK4*	NM_020639	c.1855G>A	missense	p.V619M	0.24
84	*RPS6KA2*	NM_021135	c.1441T>G	missense	p.F481V	0.29
84	*SNX29*	NM_032167	c.2320G>A	missense	p.D774N	0.41
84	*UBE3C*	NM_014671	c.1552G>A	missense	p.E518K	0.50
84	*ZNF626*	NM_001076675	c.1046C>A	missense	p.A349D	0.13
85	*ADAMTS8*	NM_007037	c.1730C>T	missense	p.T577M	0.42
85	*ANKRD45*	NM_198493	c.311A>G	missense	p.N104S	0.54
85	*ASZ1*	NM_001301821	c.101C>T	missense	p.S34F	0.54
85	*CUL4A*	NM_001278513	c.1732-2A>G	splice site	(exon 19)	0.62
85	*FSIP2*	NM_173651	c.14275T>C	missense	p.S4759P	0.55
85	*KMT2D*	NM_003482	c.16599G>A	silent	p.R5533R	0.57
85	**NOTCH1*	NM_017617	c.7020dupC	frameshift	p.S2341Lfs*13	0.51
85	**RPL10*	NM_001256580	c.184C>A	missense	p.R62S	0.95
85	*TAL1*	NM_001290406	c.86G>A	missense	p.R29Q	0.48
85	*TBC1D10A*	NM_001204240	c.1449_1463del	in-frame	p.483_488delKDSAP	0.46
85	*THBS1*	NM_003246	c.2115C>T	silent	p.C705C	0.50
85	*TRMT5*	NM_020810	c.1118G>C	missense	p.G373A	0.51
87	*CHRM2*	NM_001006629	c.99C>T	silent	p.L33L	0.36
87	*DPYSL4*	NM_006426	c.747G>A	silent	p.P249P	0.47
87	*HBB*	NM_000518	c.76G>C	missense	p.G26R	0.11
87	*HBB*	NM_000518	c.84C>A	silent	p.A28A	0.14
87	**KRAS*	NM_004985	c.35G>T	missense	p.G12V	0.04
89	*CKAP5*	NM_001008938	c.2688G>A	silent	p.P896P	0.45
89	*GRHL3*	NM_001195010	c.1095C>T	silent	p.D365D	0.39

Table S2 (*continued*)

https://dx.doi.org/10.21037/tp-22-512

Table S2 (*continued*)

UPN	Gene	Reference	Nucleotide change	Effect	Amino acid change	VAF
93	*FBXL8*	NM_018378	c.937T>G	missense	p.S313A	0.96
93	*IRS1*	NM_005544	c.1021T>C	missense	p.S341P	0.67
93	*KRTAP10-2*	NM_198693	c.233C>T	missense	p.S78L	0.37
93	*MTUS1*	NM_001001924	c.2216A>T	missense	p.N739I	0.32
93	*SHISA7*	NM_001145176	c.568T>C	missense	p.C190R	0.63
93	*SRRM3*	NM_001291831	c.1161G>C	silent	p.R387R	1.00
93	*ZFHX4*	NM_024721	c.1870T>C	missense	p.S624P	0.53
93	*ZXDB*	NM_007157	c.732G>A	silent	p.A244A	1.00
94	**FLT3*	NM_004119	c.2503G>T	missense	p.D835Y	0.63
94	*MBLAC2*	NM_203406	c.568G>A	missense	p.V190I	0.59
94	*SKAP1*	NM_001075099	c.286G>A	missense	p.E96K	0.80
95	*APBB3*	NM_006051	c.1157A>G	missense	p.D386G	0.43
95	*DOCK5*	NM_024940	c.343C>T	missense	p.R115C	0.50
95	*DPH7*	NM_138778	c.741C>A	missense	p.S247R	0.47
95	*PIR*	NM_001018109	c.284C>T	missense	p.A95V	0.57
95	*ZHX1*	NM_001017926	c.581A>C	missense	p.K194T	0.48
99	*ATP11C*	NM_001010986	c.2788G>T	nonsense	p.E930*	0.88
99	*MYH7*	NM_000257	c.1324C>T	missense	p.R442C	0.37
99	*ROR1*	NM_005012	c.1387-3C>-	splice site	(exon 9)	0.51
101	*APOBEC3F*	NM_001006666	c.280G>A	missense	p.A94T	0.35
101	*CDC27*	NM_001114091	c.172T>C	missense	p.Y58H	0.56
101	*FAH*	NM_000137	c.782C>T	missense	p.P261L	0.50
101	*NHSL1*	NM_020464	c.2022G>T	missense	p.K674N	0.60
101	*ROBO3*	NM_022370	c.3412C>T	nonsense	p.R1138*	0.47
101	*UBE2D3*	NM_181893	c.406T>C	missense	p.Y136H	0.67

*, possible driver mutations. UPN, unique patient number; VAF, variant allele frequency.

Table S3 Fusion genes

UPN	Fusion gene	Breakpoint 1*	Breakpoint 2*
1	ETV6-RUNX1	chr12:12034688	chr21:36335734
19	ETV6-RUNX1	chr12:12037335	chr21:36297114
40	ETV6-RUNX1	chr12:12030912	chr21:36417670
43	ETV6-RUNX1	chr12:12034273	chr21:36260162
58	ETV6-RUNX1	chr12:12031200	chr21:36402962
61	ETV6-RUNX1	chr12:12023334	chr21:36419079
62	ETV6-RUNX1	chr12:12035898	chr21:36308613
68	ETV6-RUNX1	chr12:12035211	chr21:36265114
95	ETV6-RUNX1	chr12:12035696	chr21:36265894
2	TCF3-PBX1	chr1:164682489	chr19:1618817
7	TCF3-PBX1	chr1:164658024	chr19:1617928
9	TCF3-PBX1	chr1:164695245	chr19:1616862
20	TCF3-PBX1	chr1:164680606	chr19:1617927
21	TCF3-PBX1	chr1:164659227	chr19:1617944
27	TCF3-PBX1	chr1:164657580	chr19:1617931
47	TCF3-PBX1	chr1:164756478	chr19:1617932
87	TCF3-PBX1	chr1:164752679	chr19:1617071
89	TCF3-PBX1	chr1:164754008	chr19:1617926
92	TCF3-PBX1	chr1:164756367	chr19:1617926
93	TCF3-PBX1	chr1:164654805	chr19:1617931
26	P2RY8-CRLF2	chrX:1333754	chrX:1654735
80	P2RY8-CRLF2	chrX:1335073	chrX:1654734
101	P2RY8-CRLF2	chrX:1335077	chrX:1654914
28	BCR-ABL1	chr9:133678974	chr22:23577185
66	TCF3-HLF	chr17:53397769	chr19:1618340
17	MEF2D-BCL9	chr1:147095613	chr1:156445440
75	BCL2/IGH	chr14:106330842	chr18:60793550
99	PML-RARA	chr15:74326125	chr17:38494349

*, hg19 coordinate.

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Table S4 B-ALL cases without known causative mutations

UPN	Method	Somatic point mutations on exome	Tumor content	Tumor contamination in germline samples	CNV	SV
65	WES	2	0.64	0.32	No significant finding	No significant finding
98	WGS	0	N/A	N/A	No significant finding	No significant finding

B-ALL, B-cell precursor acute lymphoblastic leukemia; UPN, unique patient number; CNV, copy number variations; SV, structural variations; WES, whole-exome sequencing + targeted sequencing; WGS, whole-genome sequencing; N/A, not available.

Table S5 B-ALL classification and concomitant somatic mutations including RAS signaling pathway mutations

Subtype	No. of patients	Percentages (%)	Average number of somatic mutations	RAS signaling pathway mutations	
				Number of cases	Number of mutated genes
HHD	12	24.5	14	9 [2]*	4 KRAS
					5 NRAS
					2 PTPN11
TCF3-PBX1	11	22.4	5.6	1	1 KRAS
ETV6-RUNX1	9	18.4	13.7	1	1 NRAS
PAX5alt	4	8.1	12	1 [1]*	1 KRAS
					1 BRAF
P2RY8-CRLF2	3	6.1	10.7	1	1 NRAS
del(11)(q23)	2	4.1	9	0	0
iAMP21	1	2	23	0	0
MEF2D-BCL9	1	2	13	0	0
BCR-ABL1	1	2	7	0	0
TCF3-HLF	1	2	8	0	0
Ph-like (FLT3)	1	2	13	1	1 NRAS
BCL2/IGH	1	2	3	1	1 NRAS
B-other-ALL	2	4.1	3	1	1 NRAS

*, number of cases with double mutations. B-ALL, B-cell precursor acute lymphoblastic leukemia; HHD, high hyperdiploidy.

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