Supplementary file 2. All molecular aberrations detected in plasma cell-free DNA samples from patients with advanced cancers

Full ID	Patient ID	Gene	Annotation Impact	HGVSc	HGVSp	cosmic count	dbSNP	SNP_KEY	SAMPLE SNP KEY	VAF
65_bl-2	65	KRAS	MODERATE	c.34G>C	p.Gly12Arg	3755	FALSE	chr12:25398285:C:G	6:chr12:25398285:C:G	0.088195
65_bl-2	65	RET	MODERATE	c.1778G>A	p.Gly593Glu	1	FALSE	chr10:43609022:G:A	6:chr10:43609022:G:A	0.002729
65_bl-2	65	TP53	HIGH	c.439C>T; c.520C>T; c.799C>T; c.916C>T	p.Arg147*; p.Arg174*; p.Arg267*; p.Arg306*	167	FALSE	chr17:7577022:G:A	6:chr17:7577022:G:A	0.121813
65_bl-2	65	BRAF	HIGH	c.1906C>T	p.Gln636*	2	FALSE	chr7:140449173:G:A	6:chr7:140449173:G:A	0.002685
11_c3-1	11	ERBB2	MODERATE; MODIFIER	c.1179C>A; c.1224C>A; c.1269C>A; n.1593C>A	p.Ser393Arg; p.Ser408Arg; p.Ser423Arg;	1	FALSE	chr17:37871745:C:A	7:chr17:37871745:C:A	0.001237
11_c3-1	11	EPHA3	HIGH	c.1515C>A	p.Tyr505*	0	FALSE	chr3:89448551:C:A	7:chr3:89448551:C:A	0.001867
11_c3-1	11	ERBB2; MIEN1; MIR4728	MODIFIER; MODERATE	c.*174C>A; c.3505C>A; c.3550C>A; c.3595C>A; n.3919C>A; c.*388G>T; n.*67C>A	; p.Pro1169Thr; p.Pro1184Thr; p.Pro1199Thr	2	FALSE	chr17:37884124:C:A	7:chr17:37884124:C:A	0.001227

11_c3-1	11	FGFR1; LETM2	MODERATE; MODIFIER	c.1834G>A; c.1840G>A; c.2077G>A; c.2101G>A; c.2107G>A; c.2200G>A; c.*1406C>T; c.*1423C>T; c.*1553C>T; c.*1567C>T; c.*1638C>T	p.Gly612Ser; p.Gly614Ser; p.Gly693Ser; p.Gly701Ser; p.Gly703Ser; p.Gly734Ser;	2	FALSE	chr8:38271749:C:T	7:chr8:38271749:C:T	0.001281
11_c3-1	11	NF1	MODERATE	c.2695T>G	p.Leu899Val	3	FALSE	chr17:29556328:T:G	7:chr17:29556328:T:G	0.012256
11_c3-1	11	FGFR1	MODIFIER; MODERATE	c.-85G>T; c.107G>T; c.8G>T	; p.Ser36Ile; p.Ser3Ile	1	FALSE	chr8:38314957:C:A	7:chr8:38314957:C:A	0.001045
11_c3-1	11	KIT	MODERATE	c.1726C>T; c.1738C>T	p.His576Tyr; p.His580Tyr	2	FALSE	chr4:55593672:C:T	7:chr4:55593672:C:T	0.001021
11_c3-1	11	KRAS	MODERATE	c.35G>T	p.Gly12Val	11213	FALSE	chr12:25398284:C:A	7:chr12:25398284:C:A	0.003529
11_c3-1	11	NF1	MODERATE	c.1382G>A	p.Arg461Gln	1	FALSE	chr17:29533379:G:A	7:chr17:29533379:G:A	0.00146
11_c3-1	11	PIK3CA	MODERATE	c.478C>A	p.His160Asn	1	FALSE	chr3:178917603:C:A	7:chr3:178917603:C:A	0.001075
11_c3-1	11	PTEN	MODERATE	c.421C>A	p.His141Asn	2	FALSE	chr10:89692937:C:A	7:chr10:89692937:C:A	0.00163
11_c3-1	11	CTNNB1	MODERATE	c.98C>A	p.Ser33Tyr	0	FALSE	chr3:41266101:C:A	7:chr3:41266101:C:A	0.001064
11_c3-1	11	HOXD-AS2; HOXD8	MODIFIER; MODERATE	n.*692G>T; c.-123-62C>A; c.368C>A	; p.Pro123His	0	FALSE	chr2:176995462:C:A	7:chr2:176995462:C:A	0.002334
11_c3-1	11	PTEN	MODERATE	c.443C>A	p.Ala148Glu	1	FALSE	chr10:89692959:C:A	7:chr10:89692959:C:A	0.00121
11_c3-1	11	PTEN	HIGH	c.633C>A	p.Cys211*	2	FALSE	chr10:89712015:C:A	7:chr10:89712015:C:A	0.002981

11_c3-1	11	CTNNB1	MODERATE	c.884C>A	p.Ala295Asp	0	FALSE	chr3:41267300:C:A	7:chr3:41267300:C:A	0.00174
11_c3-1	11	TP53	MODERATE	c.392G>T; c.473G>T; c.752G>T; c.869G>T	p.Arg131Leu; p.Arg158Leu; p.Arg251Leu; p.Arg290Leu	20	FALSE	chr17:7577069:C:A	7:chr17:7577069:C:A	0.0011
11_c3-1	11	NF1	MODERATE	c.1319G>A	p.Arg440Gln	1	FALSE	chr17:29533316:G:A	7:chr17:29533316:G:A	0.001113
11_c3-1	11	TP53	MODERATE	c.128G>A; c.407G>A; c.47G>A; c.524G>A	p.Arg43His; p.Arg136His; p.Arg16His; p.Arg175His	979	FALSE	chr17:7578406:C:T	7:chr17:7578406:C:T	0.001319
11_c3-1	11	CTNNB1	HIGH	c.999C>A	p.Tyr333*	0	FALSE	chr3:41268761:C:A	7:chr3:41268761:C:A	0.000966
11_c3-1	11	CTNNB1	MODERATE	c.125C>A	p.Thr42Lys	0	FALSE	chr3:41266128:C:A	7:chr3:41266128:C:A	0.001046
11_c3-1	11	ALK	MODERATE	c.3271G>A	p.Asp1091Asn	3	FALSE	chr2:29446296:C:T	7:chr2:29446296:C:T	0.000964
11_c3-1	11	EPHA3	MODERATE	c.2317G>A	p.Asp773Asn	0	FALSE	chr3:89480480:G:A	7:chr3:89480480:G:A	0.001142
11_c3-1	11	HGF	MODERATE	c.5G>T	p.Trp2Leu	0	FALSE	chr7:81399283:C:A	7:chr7:81399283:C:A	0.001131
44_c2-1	44	EGFR; EGFR-AS1	LOW; MODIFIER	c.2472C>A; n.-1G>T	p.Gly824Gly;	1	FALSE	chr7:55259414:C:A	8:chr7:55259414:C:A	0.001873
44_c2-1	44	CTNNB1	MODERATE	c.157G>A	p.Glu53Lys	0	FALSE	chr3:41266160:G:A	8:chr3:41266160:G:A	0.00213
44_c2-1	44	TP53	MODIFIER; MODERATE	c.-5G>T; c.356G>T; c.473G>T; c.77G>T	; p.Arg119Leu; p.Arg158Leu; p.Arg26Leu	80	FALSE	chr17:7578457:C:A	8:chr17:7578457:C:A	0.001393
44_c2-1	44	KIT	LOW	c.1869G>A; c.1881G>A	p.Pro623Pro; p.Pro627Pro	1	FALSE	chr4:55594178:G:A	8:chr4:55594178:G:A	0.002324
44_c2-1	44	CTNNB1	MODERATE	c.91C>A	p.Leu31Met	0	FALSE	chr3:41266094:C:A	8:chr3:41266094:C:A	0.001689
44_c2-1	44	HGF	MODERATE	c.655G>T; c.670G>T	p.Asp219Tyr; p.Asp224Tyr	0	FALSE	chr7:81374392:C:A	8:chr7:81374392:C:A	0.001101

44_c2-1	44	TP53	MODERATE	c.128G>T; c.209G>T; c.488G>T; c.605G>T	p.Arg43Leu; p.Arg70Leu; p.Arg163Leu; p.Arg202Leu	4	FALSE	chr17:7578244:C:A	8:chr17:7578244:C:A	0.001235
44_c2-1	44	NF1	MODERATE	c.1319G>A	p.Arg440Gln	1	FALSE	chr17:29533316:G:A	8:chr17:29533316:G:A	0.001198
44_c2-1	44	PTEN	MODERATE	c.325G>A	p.Asp109Asn	2	FALSE	chr10:89692841:G:A	8:chr10:89692841:G:A	0.001214
44_c2-1	44	HGF	MODERATE	c.1057G>T; c.1072G>T	p.Asp353Tyr; p.Asp358Tyr	0	FALSE	chr7:81355302:C:A	8:chr7:81355302:C:A	0.001198
44_c2-1	44	TP53	MODERATE; MODIFIER	c.208G>A; c.91G>A; c.-279G>A; c.-360G>A	p.Ala70Thr; p.Ala31Thr;	1	FALSE	chr17:7579479:C:T	8:chr17:7579479:C:T	0.001708
44_c2-1	44	MET	MODERATE	c.2980G>A; c.3034G>A	p.Glu994Lys; p.Glu1012Lys	1	FALSE	chr7:116411995:G:A	8:chr7:116411995:G:A	0.001113
44_c2-1	44	TP53	MODERATE; MODIFIER	c.128C>T; c.245C>T; c.-279C>T; c.-360C>T	p.Pro43Leu; p.Pro82Leu;	6	FALSE	chr17:7579442:G:A	8:chr17:7579442:G:A	0.001584
44_c2-1	44	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2576C>A; n.-1G>T	p.Ala859Asp;	1	FALSE	chr7:55259518:C:A	8:chr7:55259518:C:A	0.001377
44_c2-1	44	KIT	MODERATE	c.235C>A	p.Gln79Lys	2	FALSE	chr4:55561845:C:A	8:chr4:55561845:C:A	0.001116
44_c2-1	44	CTNNB1	MODERATE	c.1456C>T	p.Arg486Cys	0	FALSE	chr3:41275290:C:T	8:chr3:41275290:C:T	0.001052
44_c2-1	44	CTNNB1	MODERATE	c.1972G>T	p.Val658Phe	0	FALSE	chr3:41278096:G:T	8:chr3:41278096:G:T	0.001159
44_c2-1	44	MET	MODERATE	c.3443G>A; c.3497G>A	p.Arg1148Gln; p.Arg1166Gln	4	FALSE	chr7:116418932:G:A	8:chr7:116418932:G:A	0.001198
44_c2-1	44	EPHA3	MODERATE	c.1082T>C	p.Ile361Thr	0	FALSE	chr3:89391016:T:C	8:chr3:89391016:T:C	0.00111

44_c2-1	44	TP53	MODERATE	c.341G>A; c.422G>A; c.701G>A; c.818G>A	p.Arg114His; p.Arg141His; p.Arg234His; p.Arg273His	647	TRUE	chr17:7577120:C:T	8:chr17:7577120:C:T	0.006757
44_c2-1	44	PTEN	HIGH	c.720C>A	p.Tyr240*	3	FALSE	chr10:89717695:C:A	8:chr10:89717695:C:A	0.001898
44_c2-1	44	TP53	MODERATE	c.128G>T; c.407G>T; c.47G>T; c.524G>T	p.Arg43Leu; p.Arg136Leu; p.Arg16Leu; p.Arg175Leu	979	FALSE	chr17:7578406:C:A	8:chr17:7578406:C:A	0.001421
44_c2-1	44	DDR2	MODERATE	c.1598C>A	p.Thr533Lys	1	FALSE	chr1:162741907:C:A	8:chr1:162741907:C:A	0.001252
44_c2-1	44	NF1	MODERATE	c.2695T>G	p.Leu899Val	3	FALSE	chr17:29556328:T:G	8:chr17:29556328:T:G	0.018454
44_c2-1	44	CTNNB1	MODERATE	c.1604G>A	p.Arg535Gln	0	FALSE	chr3:41275709:G:A	8:chr3:41275709:G:A	0.001234
44_c2-1	44	RET	MODERATE	c.1690A>C	p.Thr564Pro	1	FALSE	chr10:43608342:A:C	8:chr10:43608342:A:C	0.009753
44_c2-1	44	BRAF	HIGH	c.925G>T	p.Glu309*	1	FALSE	chr7:140500217:C:A	8:chr7:140500217:C:A	0.001485
44_c2-1	44	TP53	MODERATE	c.248G>T; c.329G>T; c.608G>T; c.725G>T	p.Cys83Phe; p.Cys110Phe; p.Cys203Phe; p.Cys242Phe	72	FALSE	chr17:7577556:C:A	8:chr17:7577556:C:A	0.001926
44_c2-1	44	DDR2	MODERATE	c.1195C>T	p.Arg399Trp	1	FALSE	chr1:162737051:C:T	8:chr1:162737051:C:T	0.001023
63_bl-2	63	TP53	MODERATE	c.167G>T; c.248G>T; c.527G>T; c.644G>T	p.Ser56Ile; p.Ser83Ile; p.Ser176Ile; p.Ser215Ile	20	FALSE	chr17:7578205:C:A	9:chr17:7578205:C:A	0.001855
63_bl-2	63	PIK3CA	MODERATE	c.478C>A	p.His160Asn	1	FALSE	chr3:178917603:C:A	9:chr3:178917603:C:A	0.001929
63_bl-2	63	NF1	MODERATE	c.2695T>G	p.Leu899Val	3	FALSE	chr17:29556328:T:G	9:chr17:29556328:T:G	0.016008
63_bl-2	63	PIK3CA	MODERATE	c.278G>A	p.Arg93Gln	13	FALSE	chr3:178916891:G:A	9:chr3:178916891:G:A	0.201667

63_bl-2	63	EGFR	MODERATE	c.445C>T	p.Arg149Trp	1	FALSE	chr7:55214319:C:T	9:chr7:55214319:C:T	0.002265
63_bl-2	63	HGF	HIGH	c.1268G>A; c.1283G>A	p.Trp423*; p.Trp428*	0	FALSE	chr7:81346670:C:T	9:chr7:81346670:C:T	0.207129
63_bl-2	63	TP53	MODERATE	c.128G>T; c.209G>T; c.488G>T; c.605G>T	p.Arg43Leu; p.Arg70Leu; p.Arg163Leu; p.Arg202Leu	4	FALSE	chr17:7578244:C:A	9:chr17:7578244:C:A	0.001768
63_bl-2	63	RET	MODERATE	c.2236C>A	p.Leu746Met	1	FALSE	chr10:43612131:C:A	9:chr10:43612131:C:A	0.001797
63_bl-2	63	AKT1	MODERATE	c.1099C>T	p.Arg367Cys	1	FALSE	chr14:105239288:G:A	9:chr14:105239288:G:A	0.002195
63_bl-2	63	NF1	MODERATE	c.5420G>A; c.5483G>A	p.Arg1807Gln; p.Arg1828Gln	2	FALSE	chr17:29654731:G:A	9:chr17:29654731:G:A	0.0016
63_bl-2	63	DDR2	MODERATE	c.313C>A	p.Arg105Ser	2	FALSE	chr1:162724541:C:A	9:chr1:162724541:C:A	0.002373
63_bl-2	63	CTNNB1	MODERATE	c.884C>A	p.Ala295Asp	0	FALSE	chr3:41267300:C:A	9:chr3:41267300:C:A	0.002119
63_bl-2	63	MET	MODERATE	c.959C>T	p.Ala320Val	1	FALSE	chr7:116340097:C:T	9:chr7:116340097:C:T	0.001679
63_bl-2	63	CTNNB1	MODERATE	c.91C>A	p.Leu31Met	0	FALSE	chr3:41266094:C:A	9:chr3:41266094:C:A	0.001914
63_bl-2	63	KRAS	MODERATE	c.35G>T	p.Gly12Val	11213	FALSE	chr12:25398284:C:A	9:chr12:25398284:C:A	0.209607
63_bl-2	63	NF1	MODERATE	c.1319G>A	p.Arg440Gln	1	FALSE	chr17:29533316:G:A	9:chr17:29533316:G:A	0.004926
63_bl-2	63	AKT3	MODERATE	c.425G>T	p.Arg142Ile	0	FALSE	chr1:243809199:C:A	9:chr1:243809199:C:A	0.002558
63_bl-2	63	ERBB2; MIEN1; MIR4728	MODERATE; MODIFIER	c.3025G>A; c.3070G>A; c.3115G>A; n.3439G>A; c.*388C>T; n.*67G>A	p.Ala1009Thr; p.Ala1024Thr; p.Ala1039Thr;	2	FALSE	chr17:37883212:G:A	9:chr17:37883212:G:A	0.005602

63_bl-2	63	TP53	MODIFIER; MODERATE	c.-9G>T; c.352G>T; c.469G>T; c.73G>T	; p.Val118Phe; p.Val157Phe; p.Val25Phe	169	FALSE	chr17:7578461:C:A	9:chr17:7578461:C:A	0.002407
63_bl-2	63	RET	HIGH	c.1827C>A	p.Cys609*	1	FALSE	chr10:43609071:C:A	9:chr10:43609071:C:A	0.002227
63_bl-2	63	KRAS	HIGH	c.292G>T	p.Glu98*	1	FALSE	chr12:25378706:C:A	9:chr12:25378706:C:A	0.002237
63_bl-2	63	RET	MODERATE	c.1690A>C	p.Thr564Pro	1	FALSE	chr10:43608342:A:C	9:chr10:43608342:A:C	0.008491
63_bl-2	63	CTNNB1	MODERATE	c.96C>A	p.Asp32Glu	0	FALSE	chr3:41266099:C:A	9:chr3:41266099:C:A	0.001955
63_bl-2	63	ALK	MODERATE	c.3824G>T	p.Arg1275Leu	79	FALSE	chr2:29432664:C:A	9:chr2:29432664:C:A	0.001953
63_bl-2	63	EPHA3	HIGH	c.1153C>T	p.Arg385*	0	FALSE	chr3:89391087:C:T	9:chr3:89391087:C:T	0.001704
63_bl-2	63	PTEN	MODERATE	c.424C>T	p.Arg142Trp	6	FALSE	chr10:89692940:C:T	9:chr10:89692940:C:T	0.001857
63_bl-2	63	KIT	MODERATE	c.2579C>T; c.2591C>T	p.Ser860Phe; p.Ser864Phe	2	FALSE	chr4:55602770:C:T	9:chr4:55602770:C:T	0.002473
63_bl-2	63	CTNNB1	MODERATE	c.125C>A	p.Thr42Lys	0	FALSE	chr3:41266128:C:A	9:chr3:41266128:C:A	0.003876
63_bl-2	63	EPHA3	MODERATE	c.1132C>A	p.Pro378Thr	0	FALSE	chr3:89391066:C:A	9:chr3:89391066:C:A	0.001649
63_bl-2	63	PTEN	MODERATE	c.389G>A	p.Arg130Gln	89	FALSE	chr10:89692905:G:A	9:chr10:89692905:G:A	0.001689
63_bl-2	63	PIK3CA	MODERATE	c.3140A>T	p.His1047Leu	1717	FALSE	chr3:178952085:A:T	9:chr3:178952085:A:T	0.219809
63_bl-2	63	TP53	MODIFIER; MODERATE	c.-5G>T; c.356G>T; c.473G>T; c.77G>T	; p.Arg119Leu; p.Arg158Leu; p.Arg26Leu	80	FALSE	chr17:7578457:C:A	9:chr17:7578457:C:A	0.002466
25_c5-1	25	RET	MODERATE	c.1444C>T	p.His482Tyr	1	FALSE	chr10:43606835:C:T	10:chr10:43606835:C:T	0.002035
25_c5-1	25	MAP2K1	MODERATE	c.371C>T	p.Pro124Leu	1	FALSE	chr15:66729163:C:T	10:chr15:66729163:C:T	0.001916
25_c5-1	25	BRAF	MODERATE	c.1799T>A	p.Val600Glu	23024	FALSE	chr7:140453136:A:T	10:chr7:140453136:A:T	0.005476

25_c5-1	25	NF1	MODERATE	c.3407G>A	p.Arg1136Gln	2	FALSE	chr17:29559810:G:A	10:chr17:29559810:G:A	0.002215
25_c5-1	25	TP53	MODERATE; MODIFIER	c.140C>T; c.257C>T; c.-279C>T; c.-360C>T	p.Ala47Val; p.Ala86Val;	1	FALSE	chr17:7579430:G:A	10:chr17:7579430:G:A	0.002695
25_c5-1	25	MET	MODERATE	c.1690G>A	p.Ala564Thr	1	FALSE	chr7:116381068:G:A	10:chr7:116381068:G:A	0.002169
25_c5-1	25	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2305G>A; n.1257C>T	p.Val769Met;	3	FALSE	chr7:55249007:G:A	10:chr7:55249007:G:A	0.001967
25_c5-1	25	NF1	MODIFIER; HIGH	c.*2165G>A; c.2088G>A	; p.Trp696*	1	FALSE	chr17:29553539:G:A	10:chr17:29553539:G:A	0.002195
25_c5-1	25	BRAF	MODERATE	c.386C>T	p.Ser129Leu	2	FALSE	chr7:140534527:G:A	10:chr7:140534527:G:A	0.002381
25_c5-1	25	PIK3R1	MODERATE	c.1096G>A; c.1186G>A; c.1996G>A; c.907G>A	p.Glu366Lys; p.Glu396Lys; p.Glu666Lys; p.Glu303Lys	2	FALSE	chr5:67593250:G:A	10:chr5:67593250:G:A	0.002755
25_c5-1	25	TP53	MODIFIER; MODERATE	c.-3G>T; c.358G>T; c.475G>T; c.79G>T	; p.Ala120Ser; p.Ala159Ser; p.Ala27Ser	23	FALSE	chr17:7578455:C:A	10:chr17:7578455:C:A	0.002252
25_c5-1	25	RET	MODERATE	c.1379A>T	p.Asp460Val	1	FALSE	chr10:43606770:A:T	10:chr10:43606770:A:T	0.001944
26_c1d1-1	26	DDR2	MODERATE	c.2255G>A	p.Arg752His	1	FALSE	chr1:162746132:G:A	11:chr1:162746132:G:A	0.001385
26_c1d1-1	26	NF1	MODERATE	c.4030G>A	p.Glu1344Lys	2	FALSE	chr17:29576057:G:A	11:chr17:29576057:G:A	0.001661
26_c1d1-1	26	EPHA3	HIGH	c.318C>A	p.Cys106*	0	FALSE	chr3:89259174:C:A	11:chr3:89259174:C:A	0.001775
26_c1d1-1	26	KIT	MODERATE	c.235C>A	p.Gln79Lys	2	FALSE	chr4:55561845:C:A	11:chr4:55561845:C:A	0.002389
26_c1d1-1	26	ALK	MODERATE	c.4255G>A	p.Glu1419Lys	1	FALSE	chr2:29416698:C:T	11:chr2:29416698:C:T	0.001452

26_c1d1-1	26	TP53	MODERATE; MODIFIER	c.100G>T; c.217G>T; c.-279G>T; c.-360G>T	p.Val34Leu; p.Val73Leu;	5	FALSE	chr17:7579470:C:A	11:chr17:7579470:C:A	0.002181
26_c1d1-1	26	PIK3CA	MODERATE	c.277C>T	p.Arg93Trp	24	FALSE	chr3:178916890:C:T	11:chr3:178916890:C:T	0.001653
26_c1d1-1	26	CWH43	MODERATE	c.1741C>T; c.1822C>T	p.His581Tyr; p.His608Tyr	0	FALSE	chr4:49046821:C:T	11:chr4:49046821:C:T	0.001617
26_c1d1-1	26	HGF	MODERATE	c.1307G>A; c.1322G>A	p.Arg436Gln; p.Arg441Gln	0	FALSE	chr7:81346631:C:T	11:chr7:81346631:C:T	0.001781
26_c1d1-1	26	EGFR	MODERATE	c.787A>C	p.Thr263Pro	6	FALSE	chr7:55221743:A:C	11:chr7:55221743:A:C	0.001712
26_c1d1-1	26	CTNNB1	MODERATE	c.157G>A	p.Glu53Lys	0	FALSE	chr3:41266160:G:A	11:chr3:41266160:G:A	0.001496
26_c1d1-1	26	ALK	MODERATE	c.4280C>T	p.Ser1427Phe	2	FALSE	chr2:29416673:G:A	11:chr2:29416673:G:A	0.001464
26_c1d1-1	26	CTNNB1	MODERATE	c.122C>A	p.Thr41Asn	0	FALSE	chr3:41266125:C:A	11:chr3:41266125:C:A	0.002295
26_c1d1-1	26	BRAF	MODERATE	c.1799T>A	p.Val600Glu	23024	FALSE	chr7:140453136:A:T	11:chr7:140453136:A:T	0.04721
26_c1d1-1	26	TP53	MODERATE	c.110G>A; c.191G>A; c.470G>A; c.587G>A	p.Arg37Gln; p.Arg64Gln; p.Arg157Gln; p.Arg196Gln	19	FALSE	chr17:7578262:C:T	11:chr17:7578262:C:T	0.001862
26_c1d1-1	26	PTEN	MODERATE	c.392C>A	p.Thr131Asn	2	FALSE	chr10:89692908:C:A	11:chr10:89692908:C:A	0.002475
64_bl-2	64	KRAS	HIGH	c.292G>T	p.Glu98*	1	FALSE	chr12:25378706:C:A	12:chr12:25378706:C:A	0.002837
64_bl-2	64	KRAS	MODERATE	c.181C>A	p.Gln61Lys	40	FALSE	chr12:25380277:G:T	12:chr12:25380277:G:T	0.002894
64_bl-2	64	TP53	MODIFIER; HIGH	c.*131C>T; c.*43C>T; c.1024C>T; c.547C>T; c.628C>T; c.907C>T	; p.Arg342*; p.Arg183*; p.Arg210*; p.Arg303*	111	FALSE	chr17:7574003:G:A	12:chr17:7574003:G:A	0.004944

64_bl-2	64	DDR2	MODERATE	c.1598C>A	p.Thr533Lys	1	FALSE	chr1:162741907:C:A	12:chr1:162741907:C:A	0.002706
64_bl-2	64	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2591C>A; n.-1G>T	p.Ala864Glu;	2	FALSE	chr7:55259533:C:A	12:chr7:55259533:C:A	0.002985
64_bl-2	64	MAP2K1	MODERATE	c.198C>A	p.Asp66Glu	4	FALSE	chr15:66727482:C:A	12:chr15:66727482:C:A	0.003619
64_bl-2	64	TP53	MODERATE	c.364G>T; c.445G>T; c.724G>T; c.841G>T	p.Asp122Tyr; p.Asp149Tyr; p.Asp242Tyr; p.Asp281Tyr	28	FALSE	chr17:7577097:C:A	12:chr17:7577097:C:A	0.002915
64_bl-2	64	ALK	HIGH	c.1846G>T	p.Gly616*	1	FALSE	chr2:29498334:C:A	12:chr2:29498334:C:A	0.002564
64_bl-2	64	TP53	MODIFIER; MODERATE	c.-3G>T; c.358G>T; c.475G>T; c.79G>T	; p.Ala120Ser; p.Ala159Ser; p.Ala27Ser	23	FALSE	chr17:7578455:C:A	12:chr17:7578455:C:A	0.003058
64_bl-2	64	EGFR; EGFR-AS1	LOW; MODIFIER	c.2472C>A; n.-1G>T	p.Gly824Gly;	1	FALSE	chr7:55259414:C:A	12:chr7:55259414:C:A	0.006048
64_bl-2	64	HOXD-AS2; HOXD8	MODIFIER; MODERATE	n.*692G>T; c.22C>A; c.574C>A	; p.Gln8Lys; p.Gln192Lys	0	FALSE	chr2:176995668:C:A	12:chr2:176995668:C:A	0.003295
68_bl-2	68	EGFR	MODERATE	c.738C>A	p.Ser246Arg	2	FALSE	chr7:55220348:C:A	13:chr7:55220348:C:A	0.001883
68_bl-2	68	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2572C>A; n.-1G>T	p.Leu858Met;	8	FALSE	chr7:55259514:C:A	13:chr7:55259514:C:A	0.002562
68_bl-2	68	ALK	MODERATE	c.886G>A	p.Glu296Lys	1	FALSE	chr2:29917782:C:T	13:chr2:29917782:C:T	0.001386
68_bl-2	68	TP53	MODERATE	c.178C>T; c.259C>T; c.538C>T; c.655C>T	p.Pro60Ser; p.Pro87Ser; p.Pro180Ser; p.Pro219Ser	4	FALSE	chr17:7578194:G:A	13:chr17:7578194:G:A	0.003487
68_bl-2	68	NF1	MODERATE	c.2695T>G	p.Leu899Val	3	FALSE	chr17:29556328:T:G	13:chr17:29556328:T:G	0.020218
68_bl-2	68	PIK3CA	MODERATE	c.518C>A	p.Ser173Tyr	1	FALSE	chr3:178917643:C:A	13:chr3:178917643:C:A	0.001376
68_bl-2	68	ALK	MODERATE	c.1588G>A	p.Glu530Lys	1	FALSE	chr2:29541229:C:T	13:chr2:29541229:C:T	0.002095

68_bl-2	68	GNA11	MODERATE	c.440G>A	p.Arg147His	1	FALSE	chr19:3113446:G:A	13:chr19:3113446:G:A	0.001791
68_bl-2	68	ALK	MODERATE	c.3184A>G	p.Lys1062Glu	1	FALSE	chr2:29446383:T:C	13:chr2:29446383:T:C	0.001296
68_bl-2	68	RET	MODERATE	c.1696C>A	p.Pro566Thr	1	FALSE	chr10:43608348:C:A	13:chr10:43608348:C:A	0.001434
68_bl-2	68	EGFR; EGFR-AS1	LOW; MODIFIER	c.2472C>A; n.-1G>T	p.Gly824Gly;	1	FALSE	chr7:55259414:C:A	13:chr7:55259414:C:A	0.002581
68_bl-2	68	BRAF	MODERATE	c.1202C>T	p.Thr401Ile	1	FALSE	chr7:140482933:G:A	13:chr7:140482933:G:A	0.001949
68_bl-2	68	CWH43	MODERATE	c.1601A>G; c.1682A>G	p.Gln534Arg; p.Gln561Arg	0	FALSE	chr4:49040076:A:G	13:chr4:49040076:A:G	0.001775
68_bl-2	68	TP53	MODERATE	c.269G>T; c.350G>T; c.629G>T; c.746G>T	p.Arg90Met; p.Arg117Met; p.Arg210Met; p.Arg249Met	36	FALSE	chr17:7577535:C:A	13:chr17:7577535:C:A	0.066898
68_bl-2	68	TP53	MODERATE	c.270G>T; c.351G>T; c.630G>T; c.747G>T	p.Arg90Ser; p.Arg117Ser; p.Arg210Ser; p.Arg249Ser	318	FALSE	chr17:7577534:C:A	13:chr17:7577534:C:A	0.068063
68_bl-2	68	DDR2	MODERATE	c.700G>A	p.Asp234Asn	1	FALSE	chr1:162729614:G:A	13:chr1:162729614:G:A	0.001453
68_bl-2	68	PTEN	MODERATE	c.452C>A	p.Ala151Asp	1	FALSE	chr10:89692968:C:A	13:chr10:89692968:C:A	0.001781
68_bl-2	68	PTEN	HIGH	c.633C>A	p.Cys211*	2	FALSE	chr10:89712015:C:A	13:chr10:89712015:C:A	0.002066
68_bl-2	68	FGFR1	MODIFIER; MODERATE	c.-85G>T; c.107G>T; c.8G>T	; p.Ser36Ile; p.Ser3Ile	1	FALSE	chr8:38314957:C:A	13:chr8:38314957:C:A	0.002072
68_bl-2	68	EGFR	MODERATE	c.755G>A	p.Arg252His	3	FALSE	chr7:55221711:G:A	13:chr7:55221711:G:A	0.00161
68_bl-2	68	PIK3CA	MODERATE	c.1624G>A	p.Glu542Lys	777	FALSE	chr3:178936082:G:A	13:chr3:178936082:G:A	0.029542
68_bl-2	68	PTEN	HIGH	c.720C>A	p.Tyr240*	3	FALSE	chr10:89717695:C:A	13:chr10:89717695:C:A	0.001786
68_bl-2	68	KIT	MODERATE	c.1888C>T; c.1900C>T	p.Arg630Trp; p.Arg634Trp	2	FALSE	chr4:55594197:C:T	13:chr4:55594197:C:T	0.001521

68_bl-2	68	KLLN; PTEN	MODIFIER; LOW	c.-951G>T; c.78C>A	; p.Thr26Thr	2	FALSE	chr10:89624304:C:A	13:chr10:89624304:C:A	0.002653
68_bl-2	68	CTNNB1	MODERATE	c.125C>A	p.Thr42Lys	0	FALSE	chr3:41266128:C:A	13:chr3:41266128:C:A	0.001674
66_bl-2	66	MITF	MODIFIER; MODERATE	c.-53+197C>A; c.104+24188C>A; c.48C>A	; p.Phe16Leu	0	FALSE	chr3:69813040:C:A	14:chr3:69813040:C:A	0.001151
66_bl-2	66	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2350T>C; n.1212A>G	p.Ser784Pro;	4	FALSE	chr7:55249052:T:C	14:chr7:55249052:T:C	0.000979
66_bl-2	66	NF1	HIGH	c.1307C>A	p.Ser436*	1	FALSE	chr17:29533304:C:A	14:chr17:29533304:C:A	0.001188
66_bl-2	66	CTNNB1	MODERATE	c.96C>A	p.Asp32Glu	0	FALSE	chr3:41266099:C:A	14:chr3:41266099:C:A	0.001868
66_bl-2	66	TP53	MODIFIER; MODERATE	c.-74G>A; c.287G>A; c.404G>A; c.8G>A	; p.Cys96Tyr; p.Cys135Tyr; p.Cys3Tyr	59	FALSE	chr17:7578526:C:T	14:chr17:7578526:C:T	0.50272
66_bl-2	66	KIT	MODERATE	c.1493G>A	p.Gly498Asp	1	FALSE	chr4:55592169:G:A	14:chr4:55592169:G:A	0.001373
66_bl-2	66	MAP2K1	MODERATE	c.379G>A	p.Val127Met	1	FALSE	chr15:66729171:G:A	14:chr15:66729171:G:A	0.000865
66_bl-2	66	EPHA3	MODERATE	c.1812C>A	p.Asp604Glu	0	FALSE	chr3:89462340:C:A	14:chr3:89462340:C:A	0.001063
66_bl-2	66	EGFR; EGFR-AS1	LOW; MODIFIER	c.2472C>A; n.-1G>T	p.Gly824Gly;	1	FALSE	chr7:55259414:C:A	14:chr7:55259414:C:A	0.002423
66_bl-2	66	MAP2K1	MODERATE	c.198C>A	p.Asp66Glu	4	FALSE	chr15:66727482:C:A	14:chr15:66727482:C:A	0.001076
66_bl-2	66	EPHA3	MODERATE	c.2662C>A	p.Leu888Met	0	FALSE	chr3:89499492:C:A	14:chr3:89499492:C:A	0.001015
66_bl-2	66	TP53	MODERATE	c.400G>T; c.481G>T; c.760G>T; c.877G>T	p.Gly134Trp; p.Gly161Trp; p.Gly254Trp; p.Gly293Trp	4	FALSE	chr17:7577061:C:A	14:chr17:7577061:C:A	0.001017
66_bl-2	66	DDR2	MODERATE	c.1598C>A	p.Thr533Lys	1	FALSE	chr1:162741907:C:A	14:chr1:162741907:C:A	0.001288
66_bl-2	66	AKT1	MODERATE	c.340G>C	p.Glu114Gln	1	FALSE	chr14:105242084:C:G	14:chr14:105242084:C:G	0.001875

66_bl-2	66	FGFR1	MODIFIER; MODERATE	c.-85G>T; c.107G>T; c.8G>T	; p.Ser36Ile; p.Ser3Ile	1	FALSE	chr8:38314957:C:A	14:chr8:38314957:C:A	0.001205
66_bl-2	66	TP53	MODIFIER; MODERATE	c.-5G>T; c.356G>T; c.473G>T; c.77G>T	; p.Arg119Leu; p.Arg158Leu; p.Arg26Leu	80	FALSE	chr17:7578457:C:A	14:chr17:7578457:C:A	0.0013
66_bl-2	66	MET	MODERATE	c.3973G>A; c.4027G>A	p.Glu1325Lys; p.Glu1343Lys	1	FALSE	chr7:116435978:G:A	14:chr7:116435978:G:A	0.001017
66_bl-2	66	HOXD-AS2; HOXD8	MODIFIER; MODERATE	n.*692G>T; c.22C>A; c.574C>A	; p.Gln8Lys; p.Gln192Lys	0	FALSE	chr2:176995668:C:A	14:chr2:176995668:C:A	0.001512
66_bl-2	66	PIK3R1	MODERATE	c.629C>A	p.Ala210Asp	1	FALSE	chr5:67575556:C:A	14:chr5:67575556:C:A	0.001559
66_bl-2	66	HOXD-AS2; HOXD8	MODIFIER; MODERATE	n.*692G>T; c.-123-62C>A; c.368C>A	; p.Pro123His	0	FALSE	chr2:176995462:C:A	14:chr2:176995462:C:A	0.001986
66_bl-2	66	TP53	MODIFIER; MODERATE	c.-9G>T; c.352G>T; c.469G>T; c.73G>T	; p.Val118Phe; p.Val157Phe; p.Val25Phe	169	FALSE	chr17:7578461:C:A	14:chr17:7578461:C:A	0.001283
66_bl-2	66	CTNNB1	MODERATE	c.91C>A	p.Leu31Met	0	FALSE	chr3:41266094:C:A	14:chr3:41266094:C:A	0.002477
66_bl-2	66	TP53	MODERATE	c.358G>T; c.439G>T; c.718G>T; c.835G>T	p.Gly120Trp; p.Gly147Trp; p.Gly240Trp; p.Gly279Trp	7	FALSE	chr17:7577103:C:A	14:chr17:7577103:C:A	0.001103
66_bl-2	66	DDR2	MODERATE	c.313C>A	p.Arg105Ser	2	FALSE	chr1:162724541:C:A	14:chr1:162724541:C:A	0.000988
66_bl-2	66	CTNNB1	MODERATE	c.86C>A	p.Ser29Tyr	0	FALSE	chr3:41266089:C:A	14:chr3:41266089:C:A	0.00126
66_bl-2	66	TP53	HIGH	c.319G>T; c.400G>T; c.679G>T; c.796G>T	p.Gly107*; p.Gly134*; p.Gly227*; p.Gly266*	38	FALSE	chr17:7577142:C:A	14:chr17:7577142:C:A	0.00148

66_bl-2	66	ALK	MODERATE	c.536G>A	p.Arg179His	1	FALSE	chr2:30142990:C:T	14:chr2:30142990:C:T	0.00091
66_bl-2	66	TP53	HIGH	c.142G>T; c.421G>T; c.538G>T; c.61G>T	p.Glu48*; p.Glu141*; p.Glu180*; p.Glu21*	14	FALSE	chr17:7578392:C:A	14:chr17:7578392:C:A	0.001144
66_bl-2	66	NRAS	MODERATE	c.394G>A	p.Glu132Lys	2	FALSE	chr1:115252246:C:T	14:chr1:115252246:C:T	0.001142
66_bl-2	66	EPHA3	MODERATE	c.1234G>A	p.Val412Ile	0	FALSE	chr3:89391168:G:A	14:chr3:89391168:G:A	0.000982
66_bl-2	66	RET	MODERATE	c.1385C>T	p.Ser462Leu	1	FALSE	chr10:43606776:C:T	14:chr10:43606776:C:T	0.000963
66_bl-2	66	EPHA3	HIGH	c.1515C>A	p.Tyr505*	0	FALSE	chr3:89448551:C:A	14:chr3:89448551:C:A	0.001265
66_bl-2	66	PTEN	MODERATE	c.443C>A	p.Ala148Glu	1	FALSE	chr10:89692959:C:A	14:chr10:89692959:C:A	0.001353
66_bl-2	66	TP53	MODIFIER; MODERATE	c.-3G>T; c.358G>T; c.475G>T; c.79G>T	; p.Ala120Ser; p.Ala159Ser; p.Ala27Ser	23	FALSE	chr17:7578455:C:A	14:chr17:7578455:C:A	0.001285
66_bl-2	66	CTNNB1	MODERATE	c.497T>G	p.Val166Gly	0	FALSE	chr3:41266826:T:G	14:chr3:41266826:T:G	0.001951
66_bl-2	66	FGFR1	MODERATE	c.488G>T; c.494G>T; c.737G>T; c.755G>T; c.761G>T; c.854G>T	p.Arg163Leu; p.Arg165Leu; p.Arg246Leu; p.Arg252Leu; p.Arg254Leu; p.Arg285Leu	1	FALSE	chr8:38282202:C:A	14:chr8:38282202:C:A	0.001665
66_bl-2	66	RPL19	MODERATE	c.452G>A	p.Arg151His	0	FALSE	chr17:37360425:G:A	14:chr17:37360425:G:A	0.001206
66_bl-2	66	RET	MODERATE	c.2038G>A	p.Ala680Thr	1	FALSE	chr10:43610086:G:A	14:chr10:43610086:G:A	0.000959
66_bl-2	66	AKT3	HIGH	c.289G>T	p.Glu97*	0	FALSE	chr1:243809335:C:A	14:chr1:243809335:C:A	0.001262
66_bl-2	66	RET	MODERATE	c.1690A>C	p.Thr564Pro	1	FALSE	chr10:43608342:A:C	14:chr10:43608342:A:C	0.011146
66_bl-2	66	GNA11	MODERATE	c.1030G>A	p.Val344Met	1	FALSE	chr19:3121127:G:A	14:chr19:3121127:G:A	0.001149

66_bl-2	66	NF1	MODERATE	c.2695T>G	p.Leu899Val	3	FALSE	chr17:29556328:T:G	14:chr17:29556328:T:G	0.008636
66_bl-2	66	BRAF	MODERATE	c.1799T>A	p.Val600Glu	23024	FALSE	chr7:140453136:A:T	14:chr7:140453136:A:T	0.332435
66_bl-2	66	AKT3	MODERATE	c.44G>T	p.Arg15Met	0	FALSE	chr1:244006429:C:A	14:chr1:244006429:C:A	0.001328
66_bl-2	66	NF1	MODERATE	c.7367C>A; c.7430C>A	p.Pro2456His; p.Pro2477His	1	FALSE	chr17:29677309:C:A	14:chr17:29677309:C:A	0.001587
51_bl-1	51	EGFR	MODERATE	c.719G>A	p.Cys240Tyr	1	FALSE	chr7:55220329:G:A	15:chr7:55220329:G:A	0.001436
51_bl-1	51	TP53	MODERATE	c.438G>T; c.519G>T; c.798G>T; c.915G>T	p.Lys146Asn; p.Lys173Asn; p.Lys266Asn; p.Lys305Asn	3	FALSE	chr17:7577023:C:A	15:chr17:7577023:C:A	0.001428
51_bl-1	51	ERBB2; MIEN1; MIR4728	MODERATE; MODIFIER	c.2720A>G; c.2765A>G; c.2810A>G; n.3134A>G; c.*388T>C; n.-1A>G	p.Lys907Arg; p.Lys922Arg; p.Lys937Arg; 	1	FALSE	chr17:37882044:A:G	15:chr17:37882044:A:G	0.001756
51_bl-1	51	KRAS	MODERATE	c.35G>A	p.Gly12Asp	11213	FALSE	chr12:25398284:C:T	15:chr12:25398284:C:T	0.015695
51_bl-1	51	TP53	MODERATE	c.353G>T; c.434G>T; c.713G>T; c.830G>T	p.Cys118Phe; p.Cys145Phe; p.Cys238Phe; p.Cys277Phe	22	FALSE	chr17:7577108:C:A	15:chr17:7577108:C:A	0.001635
51_bl-1	51	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2410G>A; n.1152C>T	p.Glu804Lys; 	2	FALSE	chr7:55249112:G:A	15:chr7:55249112:G:A	0.001346
51_bl-1	51	TP53	MODERATE; MODIFIER	c.100G>T; c.217G>T; c.-279G>T; c.-360G>T	p.Val34Leu; p.Val73Leu; 	5	FALSE	chr17:7579470:C:A	15:chr17:7579470:C:A	0.001747
51_bl-1	51	RET	MODERATE	c.1867G>A	p.Glu623Lys	1	FALSE	chr10:43609111:G:A	15:chr10:43609111:G:A	0.001077

51_bl-1	51	DDR2	MODERATE	c.1598C>A	p.Thr533Lys	1	FALSE	chr1:162741907:C:A	15:chr1:162741907:C:A	0.001508
51_bl-1	51	PTEN	MODERATE	c.361G>A	p.Ala121Thr	3	FALSE	chr10:89692877:G:A	15:chr10:89692877:G:A	0.002066
51_bl-1	51	CTNNB1	MODERATE	c.884C>A	p.Ala295Asp	0	FALSE	chr3:41267300:C:A	15:chr3:41267300:C:A	0.001855
51_bl-1	51	TP53	MODERATE	c.265C>T; c.346C>T; c.625C>T; c.742C>T	p.Arg89Trp; p.Arg116Trp; p.Arg209Trp; p.Arg248Trp	559	FALSE	chr17:7577539:G:A	15:chr17:7577539:G:A	0.006677
51_bl-1	51	EGFR	MODERATE	c.1159C>A	p.Leu387Met	1	FALSE	chr7:55224477:C:A	15:chr7:55224477:C:A	0.001931
51_bl-1	51	NF1	MODERATE	c.2695T>G	p.Leu899Val	3	FALSE	chr17:29556328:T:G	15:chr17:29556328:T:G	0.011466
51_bl-1	51	EGFR	MODERATE	c.3289G>A	p.Val1097Ile	1	FALSE	chr7:55272966:G:A	15:chr7:55272966:G:A	0.001561
51_bl-1	51	EVI2A; NF1	MODIFIER; MODERATE	c.-266G>A; c.-338G>A; c.5020C>T; c.5083C>T	; p.Arg1674Trp; p.Arg1695Trp	1	FALSE	chr17:29653085:C:T	15:chr17:29653085:C:T	0.001396
51_bl-1	51	EGFR	MODERATE	c.940G>A	p.Asp314Asn	1	FALSE	chr7:55223573:G:A	15:chr7:55223573:G:A	0.001296
51_bl-1	51	MET	MODERATE	c.1640G>A	p.Arg547Gln	1	FALSE	chr7:116381018:G:A	15:chr7:116381018:G:A	0.001296
51_t2c1-1	51	TP53	MODIFIER; MODERATE	c.-3G>T; c.358G>T; c.475G>T; c.79G>T	; p.Ala120Ser; p.Ala159Ser; p.Ala27Ser	23	FALSE	chr17:7578455:C:A	16:chr17:7578455:C:A	0.002962
51_t2c1-1	51	CTNNB1	MODERATE	c.884C>A	p.Ala295Asp	0	FALSE	chr3:41267300:C:A	16:chr3:41267300:C:A	0.001647
51_t2c1-1	51	KIT	HIGH	c.1698C>A; c.1710C>A	p.Tyr566*; p.Tyr570*	2	FALSE	chr4:55593644:C:A	16:chr4:55593644:C:A	0.001553
51_t2c1-1	51	AKT3	MODERATE	c.197G>T	p.Arg66Leu	0	FALSE	chr1:243828161:C:A	16:chr1:243828161:C:A	0.001256
51_t2c1-1	51	NF1	MODERATE	c.3559C>A	p.Leu1187Ile	1	FALSE	chr17:29560082:C:A	16:chr17:29560082:C:A	0.001367

51_t2c1-1	51	TP53	MODERATE; MODIFIER	c.140C>T; c.23C>T; c.-279C>T; c.-360C>T	p.Pro47Leu; p.Pro8Leu;	2	FALSE	chr17:7579547:G:A	16:chr17:7579547:G:A	0.002237
51_t2c1-1	51	DDR2	MODERATE	c.1963G>A	p.Glu655Lys	1	FALSE	chr1:162745548:G:A	16:chr1:162745548:G:A	0.001908
51_t2c1-1	51	KIT	MODERATE	c.2825G>A; c.2837G>A	p.Arg942Gln; p.Arg946Gln	1	FALSE	chr4:55604629:G:A	16:chr4:55604629:G:A	0.001421
51_t2c1-1	51	RET	MODERATE	c.1531G>A	p.Glu511Lys	1	FALSE	chr10:43607555:G:A	16:chr10:43607555:G:A	0.001198
51_t2c1-1	51	BRAF	MODERATE	c.2285C>T	p.Ala762Val	2	FALSE	chr7:140434413:G:A	16:chr7:140434413:G:A	0.001068
51_t2c1-1	51	NF1	MODERATE	c.6405C>A; c.6468C>A	p.Phe2135Leu; p.Phe2156Leu	1	FALSE	chr17:29664426:C:A	16:chr17:29664426:C:A	0.002835
51_t2c1-1	51	BRAF	MODERATE	c.2223G>T	p.Glu741Asp	1	FALSE	chr7:140434475:C:A	16:chr7:140434475:C:A	0.001224
51_t2c1-1	51	PIK3CA	HIGH	c.241G>T	p.Glu81*	38	FALSE	chr3:178916854:G:T	16:chr3:178916854:G:T	0.001293
51_t2c1-1	51	PTEN	MODERATE	c.442G>A	p.Ala148Thr	2	FALSE	chr10:89692958:G:A	16:chr10:89692958:G:A	0.002865
51_t2c1-1	51	DDR2	MODERATE	c.2516G>A	p.Arg839His	3	FALSE	chr1:162749984:G:A	16:chr1:162749984:G:A	0.0012
51_t2c1-1	51	DDR2	MODERATE	c.313C>A	p.Arg105Ser	2	FALSE	chr1:162724541:C:A	16:chr1:162724541:C:A	0.001767
51_t2c1-1	51	FGFR1	MODIFIER; MODERATE	c.-63G>T; c.129G>T; c.30G>T	; p.Trp43Cys; p.Trp10Cys	1	FALSE	chr8:38314935:C:A	16:chr8:38314935:C:A	0.001567
51_t2c1-1	51	EGFR; EGFR-AS1	MODIFIER; MODERATE	c.*2364T>C; c.2240T>C; n.*2821A>G	; p.Leu747Ser	13	FALSE	chr7:55242470:T:C	16:chr7:55242470:T:C	0.001117
51_t2c1-1	51	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2350T>C; n.1212A>G	p.Ser784Pro;	4	FALSE	chr7:55249052:T:C	16:chr7:55249052:T:C	0.001225
51_t2c1-1	51	TP53	MODERATE	c.126G>T; c.207G>T; c.486G>T; c.603G>T	p.Leu42Phe; p.Leu69Phe; p.Leu162Phe; p.Leu201Phe	4	FALSE	chr17:7578246:C:A	16:chr17:7578246:C:A	0.001577

51_t2c1-1	51	RET	MODERATE	c.1349G>A	p.Ser450Asn	1	FALSE	chr10:43606740:G:A	16:chr10:43606740:G:A	0.001127
51_t2c1-1	51	CTNNB1	MODERATE	c.1456C>T	p.Arg486Cys	0	FALSE	chr3:41275290:C:T	16:chr3:41275290:C:T	0.001253
51_t2c1-1	51	MET	HIGH	c.1249C>T	p.Arg417*	1	FALSE	chr7:116371770:C:T	16:chr7:116371770:C:T	0.000976
51_t2c1-1	51	TP53	MODERATE	c.265C>T; c.346C>T; c.625C>T; c.742C>T	p.Arg89Trp; p.Arg116Trp; p.Arg209Trp; p.Arg248Trp	559	FALSE	chr17:7577539:G:A	16:chr17:7577539:G:A	0.339193
51_t2c1-1	51	CTNNB1	MODERATE	c.125C>A	p.Thr42Lys	0	FALSE	chr3:41266128:C:A	16:chr3:41266128:C:A	0.00219
51_t2c1-1	51	DDR2	MODERATE	c.1598C>A	p.Thr533Lys	1	FALSE	chr1:162741907:C:A	16:chr1:162741907:C:A	0.001505
51_t2c1-1	51	NF1	MODERATE	c.5494A>G; c.5557A>G	p.Thr1832Ala; p.Thr1853Ala	1	FALSE	chr17:29654805:A:G	16:chr17:29654805:A:G	0.001367
51_t2c1-1	51	PIK3CA	MODERATE	c.3044C>A	p.Ser1015Tyr	3	FALSE	chr3:178951989:C:A	16:chr3:178951989:C:A	0.001157
51_t2c1-1	51	CTNNB1	MODERATE	c.419T>C	p.Ile140Thr	0	FALSE	chr3:41266622:T:C	16:chr3:41266622:T:C	0.001258
51_t2c1-1	51	EPHA3	MODERATE	c.1132C>A	p.Pro378Thr	0	FALSE	chr3:89391066:C:A	16:chr3:89391066:C:A	0.001289
51_t2c1-1	51	FGFR1	MODIFIER; MODERATE	c.-85G>T; c.107G>T; c.8G>T	; p.Ser36Ile; p.Ser3Ile	1	FALSE	chr8:38314957:C:A	16:chr8:38314957:C:A	0.002494
51_t2c1-1	51	EPHA3	MODERATE	c.497C>A	p.Thr166Asn	0	FALSE	chr3:89259353:C:A	16:chr3:89259353:C:A	0.001255
51_t2c1-1	51	ROS1	MODERATE	c.5651G>T	p.Arg1884Ile	1	FALSE	chr6:117642548:C:A	16:chr6:117642548:C:A	0.001561
51_t2c1-1	51	TP53	MODIFIER; MODERATE	c.-5G>T; c.356G>T; c.473G>T; c.77G>T	; p.Arg119Leu; p.Arg158Leu; p.Arg26Leu	80	FALSE	chr17:7578457:C:A	16:chr17:7578457:C:A	0.002033

51_t2c1-1	51	TP53	MODIFIER; HIGH	c.*143G>T; c.*55G>T; c.1036G>T; c.559G>T; c.640G>T; c.919G>T	; p.Glu346*; p.Glu187*; p.Glu214*; p.Glu307*	4	FALSE	chr17:7573991:C:A	16:chr17:7573991:C:A	0.002534
51_t2c1-1	51	ALK	MODERATE	c.874C>T	p.Arg292Cys	1	FALSE	chr2:29917794:G:A	16:chr2:29917794:G:A	0.00127
51_t2c1-1	51	NF1	MODERATE	c.2695T>G	p.Leu899Val	3	FALSE	chr17:29556328:T:G	16:chr17:29556328:T:G	0.017995
51_t2c1-1	51	HGF	MODERATE	c.5G>T	p.Trp2Leu	0	FALSE	chr7:81399283:C:A	16:chr7:81399283:C:A	0.001383
51_t2c1-1	51	KRAS	MODERATE	c.35G>A	p.Gly12Asp	11213	FALSE	chr12:25398284:C:T	16:chr12:25398284:C:T	0.403834
51_t2c1-1	51	TP53	HIGH; MODIFIER	c.166G>T; c.49G>T; c.-279G>T; c.-360G>T	p.Glu56*; p.Glu17*;	6	FALSE	chr17:7579521:C:A	16:chr17:7579521:C:A	0.002326
51_t2c1-1	51	TP53	MODIFIER; MODERATE	c.*137A>G; c.*225A>G; c.1001A>G; c.1118A>G; c.641A>G; c.722A>G	; p.Lys334Arg; p.Lys373Arg; p.Lys214Arg; p.Lys241Arg	1	FALSE	chr17:7572991:T:C	16:chr17:7572991:T:C	0.01072
51_t2c1-1	51	EGFR	MODERATE	c.940G>A	p.Asp314Asn	1	FALSE	chr7:55223573:G:A	16:chr7:55223573:G:A	0.001194
51_t2c1-1	51	GNA11	MODERATE	c.805G>A	p.Val269Ile	1	FALSE	chr19:3119273:G:A	16:chr19:3119273:G:A	0.001603
51_t2c1-1	51	RET	MODERATE	c.1690A>C	p.Thr564Pro	1	FALSE	chr10:43608342:A:C	16:chr10:43608342:A:C	0.006527
51_t2c1-1	51	EGFR	MODERATE	c.866C>A	p.Ala289Asp	34	FALSE	chr7:55221822:C:A	16:chr7:55221822:C:A	0.00155
51_t2c1-1	51	NF1	MODERATE	c.3748C>T	p.Arg1250Trp	1	FALSE	chr17:29562668:C:T	16:chr17:29562668:C:T	0.001214

51_c2-1	51	TP53	MODERATE	c.265C>T; c.346C>T; c.625C>T; c.742C>T	p.Arg89Trp; p.Arg116Trp; p.Arg209Trp; p.Arg248Trp	559	FALSE	chr17:7577539:G:A	17:chr17:7577539:G:A	0.132686
51_c2-1	51	TP53	MODERATE; MODIFIER	c.145G>A; c.28G>A; c.-279G>A; c.-360G>A	p.Asp49Asn; p.Asp10Asn;	4	FALSE	chr17:7579542:C:T	17:chr17:7579542:C:T	0.006897
51_c2-1	51	PTEN	MODERATE	c.829A>T	p.Thr277Ser	1	FALSE	chr10:89720678:A:T	17:chr10:89720678:A:T	0.007874
51_c2-1	51	KRAS	MODERATE	c.35G>A	p.Gly12Asp	11213	FALSE	chr12:25398284:C:T	17:chr12:25398284:C:T	0.180288
51_c3-1	51	PTEN	MODERATE	c.443C>A	p.Ala148Glu	1	FALSE	chr10:89692959:C:A	18:chr10:89692959:C:A	0.003371
51_c3-1	51	RET	MODERATE	c.1900T>G	p.Cys634Gly	13	FALSE	chr10:43609948:T:G	18:chr10:43609948:T:G	0.001813
51_c3-1	51	TP53	MODERATE	c.248G>T; c.329G>T; c.608G>T; c.725G>T	p.Cys83Phe; p.Cys110Phe; p.Cys203Phe; p.Cys242Phe	72	FALSE	chr17:7577556:C:A	18:chr17:7577556:C:A	0.001862
51_c3-1	51	NF1	MODERATE	c.2695T>G	p.Leu899Val	3	FALSE	chr17:29556328:T:G	18:chr17:29556328:T:G	0.015625
51_c3-1	51	TP53	MODIFIER; MODERATE	c.*137A>G; c.*225A>G; c.1001A>G; c.1118A>G; c.641A>G; c.722A>G	; p.Lys334Arg; p.Lys373Arg; p.Lys214Arg; p.Lys241Arg	1	FALSE	chr17:7572991:T:C	18:chr17:7572991:T:C	0.005579
51_c3-1	51	TP53	MODERATE	c.265C>T; c.346C>T; c.625C>T; c.742C>T	p.Arg89Trp; p.Arg116Trp; p.Arg209Trp; p.Arg248Trp	559	FALSE	chr17:7577539:G:A	18:chr17:7577539:G:A	0.107317

51_c3-1	51	PIK3R1	MODERATE	c.1096G>A; c.1186G>A; c.1996G>A; c.907G>A	p.Glu366Lys; p.Glu396Lys; p.Glu666Lys; p.Glu303Lys	2	FALSE	chr5:67593250:G:A	18:chr5:67593250:G:A	0.001671
51_c3-1	51	TP53	MODIFIER; LOW	c.-100C>T; c.-19C>T; c.261C>T; c.378C>T	; p.Tyr87Tyr; p.Tyr126Tyr	5	FALSE	chr17:7578552:G:A	18:chr17:7578552:G:A	0.001781
51_c3-1	51	FGFR1	MODIFIER; MODERATE	c.-85G>T; c.107G>T; c.8G>T	; p.Ser36Ile; p.Ser3Ile	1	FALSE	chr8:38314957:C:A	18:chr8:38314957:C:A	0.001704
51_c3-1	51	DDR2	MODERATE	c.1418G>A	p.Arg473His	2	FALSE	chr1:162740216:G:A	18:chr1:162740216:G:A	0.002138
51_c3-1	51	TP53	MODERATE	c.298G>T; c.379G>T; c.658G>T; c.775G>T	p.Asp100Tyr; p.Asp127Tyr; p.Asp220Tyr; p.Asp259Tyr	23	FALSE	chr17:7577506:C:A	18:chr17:7577506:C:A	0.002083
51_c3-1	51	CWH43	MODERATE	c.415G>A; c.496G>A	p.Asp139Asn; p.Asp166Asn	0	FALSE	chr4:48994092:G:A	18:chr4:48994092:G:A	0.002079
51_c3-1	51	KRAS	MODERATE	c.35G>A	p.Gly12Asp	11213	FALSE	chr12:25398284:C:T	18:chr12:25398284:C:T	0.191297
51_c3-1	51	TP53	MODERATE; MODIFIER	c.115G>T; c.232G>T; c.-279G>T; c.-360G>T	p.Ala39Ser; p.Ala78Ser;	1	FALSE	chr17:7579455:C:A	18:chr17:7579455:C:A	0.004444
51_c3-1	51	DDR2	MODERATE	c.313C>A	p.Arg105Ser	2	FALSE	chr1:162724541:C:A	18:chr1:162724541:C:A	0.001317
51_c3-1	51	RET	MODERATE	c.1838C>T	p.Pro613Leu	1	FALSE	chr10:43609082:C:T	18:chr10:43609082:C:T	0.001509
51_c3-1	51	PIK3R1	MODERATE	c.514G>A	p.Val172Met	1	FALSE	chr5:67575441:G:A	18:chr5:67575441:G:A	0.001892

51_c3-1	51	GAPDH; IFFO1; NCAPD2	MODERATE; MODIFIER	c.113G>C; c.239G>C; c.*1743C>G; c.*1746C>G; c.*1770C>G; n.*2798C>G; c.*4252G>C	p.Arg38Pro; p.Arg80Pro;	0	FALSE	chr12:6646088:G:C	18:chr12:6646088:G:C	0.002389
51_c3-1	51	PIK3CA	MODERATE	c.478C>A	p.His160Asn	1	FALSE	chr3:178917603:C:A	18:chr3:178917603:C:A	0.001563
51_c3-1	51	RET	MODERATE	c.1690A>C	p.Thr564Pro	1	FALSE	chr10:43608342:A:C	18:chr10:43608342:A:C	0.007736
51_c3-1	51	CTNNB1	HIGH	c.283C>T	p.Arg95*	0	FALSE	chr3:41266486:C:T	18:chr3:41266486:C:T	0.001433
51_c3-1	51	CTNNB1	MODERATE	c.67A>G	p.Ser23Gly	0	FALSE	chr3:41266070:A:G	18:chr3:41266070:A:G	0.001676
51_c3-1	51	TP53	MODIFIER; MODERATE	c.-9G>T; c.352G>T; c.469G>T; c.73G>T	; p.Val118Phe; p.Val157Phe; p.Val25Phe	169	FALSE	chr17:7578461:C:A	18:chr17:7578461:C:A	0.002822
51_c3-1	51	HGF	MODERATE	c.5G>T	p.Trp2Leu	0	FALSE	chr7:81399283:C:A	18:chr7:81399283:C:A	0.001552
51_c4-1	51	RPL19	MODERATE	c.452G>A	p.Arg151His	0	FALSE	chr17:37360425:G:A	19:chr17:37360425:G:A	0.001754
51_c4-1	51	RET	MODERATE	c.1385C>T	p.Ser462Leu	1	FALSE	chr10:43606776:C:T	19:chr10:43606776:C:T	0.00122
51_c4-1	51	BRAF	MODERATE	c.1394C>T	p.Ser465Phe	1	FALSE	chr7:140481414:G:A	19:chr7:140481414:G:A	0.001291
51_c4-1	51	EGFR	MODIFIER; MODERATE	c.*2133G>A; c.*2364G>A; c.2030G>A	; p.Arg677His	5	FALSE	chr7:55240786:G:A	19:chr7:55240786:G:A	0.003783
51_c4-1	51	DDR2	MODERATE	c.1195C>T	p.Arg399Trp	1	FALSE	chr1:162737051:C:T	19:chr1:162737051:C:T	0.001252
51_c4-1	51	DDR2	MODERATE	c.1418G>A	p.Arg473His	2	FALSE	chr1:162740216:G:A	19:chr1:162740216:G:A	0.001322
51_c4-1	51	DDR2	MODERATE	c.313C>A	p.Arg105Ser	2	FALSE	chr1:162724541:C:A	19:chr1:162724541:C:A	0.001264

51_c4-1	51	NF1	MODERATE	c.2695T>G	p.Leu899Val	3	FALSE	chr17:29556328:T:G	19:chr17:29556328:T:G	0.009155
51_c4-1	51	EPHA3	MODERATE	c.1132C>A	p.Pro378Thr	0	FALSE	chr3:89391066:C:A	19:chr3:89391066:C:A	0.001309
51_c4-1	51	BRAF	MODERATE	c.2285C>A	p.Ala762Glu	2	FALSE	chr7:140434413:G:T	19:chr7:140434413:G:T	0.001133
51_c4-1	51	RET	MODERATE	c.1574G>A	p.Arg525Gln	1	FALSE	chr10:43607598:G:A	19:chr10:43607598:G:A	0.001281
51_c4-1	51	PHLPP1	MODERATE	c.2303C>A	p.Ser768Tyr	0	FALSE	chr18:60563103:C:A	19:chr18:60563103:C:A	0.00188
51_c4-1	51	EGFR	MODERATE	c.755G>A	p.Arg252His	3	FALSE	chr7:55221711:G:A	19:chr7:55221711:G:A	0.002185
51_c4-1	51	PTEN	MODERATE	c.443C>A	p.Ala148Glu	1	FALSE	chr10:89692959:C:A	19:chr10:89692959:C:A	0.002667
51_c4-1	51	TP53	MODIFIER; MODERATE	c.-5G>T; c.356G>T; c.473G>T; c.77G>T	; p.Arg119Leu; p.Arg158Leu; p.Arg26Leu	80	FALSE	chr17:7578457:C:A	19:chr17:7578457:C:A	0.002358
51_c4-1	51	MET	MODERATE	c.3217C>T; c.3271C>T	p.Pro1073Ser; p.Pro1091Ser	1	FALSE	chr7:116415123:C:T	19:chr7:116415123:C:T	0.001425
51_c4-1	51	KIT	MODERATE	c.1485C>A	p.Asn495Lys	1	FALSE	chr4:55592161:C:A	19:chr4:55592161:C:A	0.001699
51_c4-1	51	PIK3CA	MODERATE	c.1412C>T	p.Pro471Leu	4	FALSE	chr3:178928226:C:T	19:chr3:178928226:C:T	0.001498
51_c4-1	51	PTEN	MODERATE	c.133G>A	p.Val45Ile	1	FALSE	chr10:89653835:G:A	19:chr10:89653835:G:A	0.002445
51_c4-1	51	TP53	MODIFIER; MODERATE	c.*137A>G; c.*225A>G; c.1001A>G; c.1118A>G; c.641A>G; c.722A>G	; p.Lys334Arg; p.Lys373Arg; p.Lys214Arg; p.Lys241Arg	1	FALSE	chr17:7572991:T:C	19:chr17:7572991:T:C	0.00436
51_c4-1	51	PIK3R1	MODERATE	c.1096G>A; c.1186G>A; c.1996G>A; c.907G>A	p.Glu366Lys; p.Glu396Lys; p.Glu666Lys; p.Glu303Lys	2	FALSE	chr5:67593250:G:A	19:chr5:67593250:G:A	0.001549

51_c4-1	51	DDR2	MODERATE	c.691C>A	p.Gln231Lys	1	FALSE	chr1:162729605:C:A	19:chr1:162729605:C:A	0.001471
51_c4-1	51	PIK3CA	MODERATE	c.1070G>A	p.Arg357Gln	2	FALSE	chr3:178922301:G:A	19:chr3:178922301:G:A	0.001665
51_c4-1	51	ERBB2	MODERATE; MODIFIER	c.1594C>T; c.1639C>T; c.1684C>T; n.2008C>T	p.Pro532Ser; p.Pro547Ser; p.Pro562Ser;	1	FALSE	chr17:37872805:C:T	19:chr17:37872805:C:T	0.001305
51_c4-1	51	EGFR	MODERATE	c.1168C>A	p.Gln390Lys	1	FALSE	chr7:55224486:C:A	19:chr7:55224486:C:A	0.001295
51_c4-1	51	HGF	HIGH	c.1993G>T; c.2008G>T	p.Glu665*; p.Glu670*	0	FALSE	chr7:81334708:C:A	19:chr7:81334708:C:A	0.002125
51_c4-1	51	CTNNB1	MODERATE	c.91C>A	p.Leu31Met	0	FALSE	chr3:41266094:C:A	19:chr3:41266094:C:A	0.002264
51_c4-1	51	PIK3CA	MODERATE	c.2594G>A	p.Gly865Asp	1	FALSE	chr3:178947158:G:A	19:chr3:178947158:G:A	0.001391
51_c4-1	51	KRAS	MODERATE	c.35G>A	p.Gly12Asp	11213	FALSE	chr12:25398284:C:T	19:chr12:25398284:C:T	0.342124
51_c4-1	51	CTNNB1	HIGH	c.999C>A	p.Tyr333*	0	FALSE	chr3:41268761:C:A	19:chr3:41268761:C:A	0.001311
51_c4-1	51	RET	MODERATE	c.1690A>C	p.Thr564Pro	1	FALSE	chr10:43608342:A:C	19:chr10:43608342:A:C	0.004892
51_c4-1	51	TP53	MODERATE	c.265C>T; c.346C>T; c.625C>T; c.742C>T	p.Arg89Trp; p.Arg116Trp; p.Arg209Trp; p.Arg248Trp	559	FALSE	chr17:7577539:G:A	19:chr17:7577539:G:A	0.260179
51_c4-1	51	AKT3	MODERATE	c.825G>T	p.Glu275Asp	0	FALSE	chr1:243727145:C:A	19:chr1:243727145:C:A	0.001726
51_c4-1	51	HGF	MODERATE	c.490G>T; c.505G>T	p.Gly164Cys; p.Gly169Cys	0	FALSE	chr7:81381556:C:A	19:chr7:81381556:C:A	0.001541
51_c4-1	51	PIK3R1	HIGH	c.1224C>A; c.135C>A; c.324C>A; c.414C>A	p.Tyr408*; p.Tyr45*; p.Tyr108*; p.Tyr138*	1	FALSE	chr5:67589236:C:A	19:chr5:67589236:C:A	0.001452
51_c4-1	51	CTNNB1	LOW	c.1956G>A	p.Ala652Ala	0	FALSE	chr3:41278080:G:A	19:chr3:41278080:G:A	0.001457

25_c1-1	25	TP53	MODIFIER; MODERATE	c.-2A>G; c.-83A>G; c.278A>G; c.395A>G	; p.Lys93Arg; p.Lys132Arg	42	FALSE	chr17:7578535:T:C	20:chr17:7578535:T:C	0.003339
25_c1-1	25	TP53	MODERATE	c.355C>T; c.436C>T; c.715C>T; c.832C>T	p.Pro119Ser; p.Pro146Ser; p.Pro239Ser; p.Pro278Ser	59	FALSE	chr17:7577106:G:A	20:chr17:7577106:G:A	0.008214
25_t2c2-2	25	PTEN	MODERATE	c.402G>A	p.Met134Ile	2	FALSE	chr10:89692918:G:A	21:chr10:89692918:G:A	0.001901
25_t2c2-2	25	EGFR	MODERATE	c.865G>A	p.Ala289Thr	10	FALSE	chr7:55221821:G:A	21:chr7:55221821:G:A	0.002028
25_t2c2-2	25	TP53	MODERATE; MODIFIER	c.115G>T; c.232G>T; c.-279G>T; c.-360G>T	p.Ala39Ser; p.Ala78Ser;	1	FALSE	chr17:7579455:C:A	21:chr17:7579455:C:A	0.002478
25_t2c2-2	25	NF1	MODERATE	c.6166G>A; c.6229G>A	p.Asp2056Asn; p.Asp2077Asn	1	FALSE	chr17:29663734:G:A	21:chr17:29663734:G:A	0.001894
25_t2c2-2	25	PTEN	MODERATE	c.389G>A	p.Arg130Gln	89	FALSE	chr10:89692905:G:A	21:chr10:89692905:G:A	0.001927
25_t2c2-2	25	CTNNB1	MODERATE	c.86C>A	p.Ser29Tyr	0	FALSE	chr3:41266089:C:A	21:chr3:41266089:C:A	0.001903
25_t2c2-2	25	TP53	MODIFIER; MODERATE	c.-3G>T; c.358G>T; c.475G>T; c.79G>T	; p.Ala120Ser; p.Ala159Ser; p.Ala27Ser	23	FALSE	chr17:7578455:C:A	21:chr17:7578455:C:A	0.002137
25_t2c2-2	25	PTEN	HIGH	c.720C>A	p.Tyr240*	3	FALSE	chr10:89717695:C:A	21:chr10:89717695:C:A	0.003195
25_t2c2-2	25	DDR2	MODERATE	c.313C>A	p.Arg105Ser	2	FALSE	chr1:162724541:C:A	21:chr1:162724541:C:A	0.00186
25_t2c2-2	25	CTNNB1	MODERATE	c.884C>A	p.Ala295Asp	0	FALSE	chr3:41267300:C:A	21:chr3:41267300:C:A	0.003839
25_t2c2-2	25	TP53	MODERATE	c.353G>T; c.434G>T; c.713G>T; c.830G>T	p.Cys118Phe; p.Cys145Phe; p.Cys238Phe; p.Cys277Phe	22	FALSE	chr17:7577108:C:A	21:chr17:7577108:C:A	0.003268

25_t2c2-2	25	TP53	LOW; MODIFIER; MODERATE	c.-51G>A; c.310G>A; c.31G>A; c.427G>A	; p.Val104Met; p.Val11Met; p.Val143Met	24	FALSE	chr17:7578503:C:T	21:chr17:7578503:C:T	0.001936
25_t2c2-2	25	HGF	MODERATE	c.1612G>T; c.1627G>T	p.Asp538Tyr; p.Asp543Tyr	0	FALSE	chr7:81335733:C:A	21:chr7:81335733:C:A	0.002077
25_t2c2-2	25	KIT	MODERATE	c.106C>A	p.Pro36Thr	1	FALSE	chr4:55561716:C:A	21:chr4:55561716:C:A	0.001808
25_t2c2-2	25	EGFR	MODERATE	c.3287C>T	p.Ser1096Phe	1	FALSE	chr7:55272964:C:T	21:chr7:55272964:C:T	0.002151
25_t2c2-2	25	RET	MODERATE	c.1690A>C	p.Thr564Pro	1	FALSE	chr10:43608342:A:C	21:chr10:43608342:A:C	0.009018
25_t2c2-2	25	KIT	MODERATE	c.391G>A	p.Asp131Asn	1	FALSE	chr4:55564503:G:A	21:chr4:55564503:G:A	0.001898
26_c3-b	26	EGFR	MODERATE	c.738C>A	p.Ser246Arg	2	FALSE	chr7:55220348:C:A	22:chr7:55220348:C:A	0.001824
26_c3-b	26	TP53	MODERATE	c.10T>A; c.370T>A; c.487T>A; c.91T>A	p.Tyr4Asn; p.Tyr124Asn; p.Tyr163Asn; p.Tyr31Asn	23	FALSE	chr17:7578443:A:T	22:chr17:7578443:A:T	0.001971
26_c3-b	26	PIK3CA	MODERATE	c.1645G>A	p.Asp549Asn	4	FALSE	chr3:178936103:G:A	22:chr3:178936103:G:A	0.001163
26_c3-b	26	PHLPP1	MODERATE	c.2303C>A	p.Ser768Tyr	0	FALSE	chr18:60563103:C:A	22:chr18:60563103:C:A	0.001739
26_c3-b	26	KIT	MODERATE	c.2197G>A; c.2209G>A	p.Asp733Asn; p.Asp737Asn	2	FALSE	chr4:55597561:G:A	22:chr4:55597561:G:A	0.001008
26_c3-b	26	RET	MODERATE	c.1580A>G	p.Glu527Gly	1	FALSE	chr10:43607604:A:G	22:chr10:43607604:A:G	0.002878
26_c3-b	26	CSDE1; NRAS	MODIFIER; MODERATE	c.*2430G>T; c.*2523G>T; c.*2817G>T; c.*2910G>T; c.*2964G>T; c.*3057G>T; c.38G>T	; p.Gly13Val	238	FALSE	chr1:115258744:C:A	22:chr1:115258744:C:A	0.001125

26_c3-b	26	FGFR1	MODERATE	c.1060C>T; c.1066C>T; c.1303C>T; c.1327C>T; c.1333C>T; c.1426C>T	p.Arg354Trp; p.Arg356Trp; p.Arg435Trp; p.Arg443Trp; p.Arg445Trp; p.Arg476Trp	2	FALSE	chr8:38275843:G:A	22:chr8:38275843:G:A	0.001018
26_c3-b	26	CTNNB1	MODERATE	c.1972G>T	p.Val658Phe	0	FALSE	chr3:41278096:G:T	22:chr3:41278096:G:T	0.001039
26_c3-b	26	KIT	MODERATE	c.1485C>A	p.Asn495Lys	1	FALSE	chr4:55592161:C:A	22:chr4:55592161:C:A	0.001241
26_c3-b	26	KRAS	HIGH	c.64C>T	p.Gln22*	15	FALSE	chr12:25398255:G:A	22:chr12:25398255:G:A	0.001044
26_c3-b	26	HOXD-AS2; HOXD8	MODIFIER; MODERATE	n.*692G>T; c.22C>A; c.574C>A	; p.Gln8Lys; p.Gln192Lys	0	FALSE	chr2:176995668:C:A	22:chr2:176995668:C:A	0.002447
26_c3-b	26	FGFR1	MODERATE	c.487C>T; c.493C>T; c.736C>T; c.754C>T; c.760C>T; c.853C>T	p.Arg163Trp; p.Arg165Trp; p.Arg246Trp; p.Arg252Trp; p.Arg254Trp; p.Arg285Trp	1	FALSE	chr8:38282203:G:A	22:chr8:38282203:G:A	0.00158
26_c3-b	26	TP53	MODERATE; MODIFIER	c.115G>T; c.232G>T; c.-279G>T; c.-360G>T	p.Ala39Ser; p.Ala78Ser;	1	FALSE	chr17:7579455:C:A	22:chr17:7579455:C:A	0.001397
26_c3-b	26	GNA11	MODERATE	c.625C>A	p.Gln209Lys	3	FALSE	chr19:3118941:C:A	22:chr19:3118941:C:A	0.001592
26_c3-b	26	TP53	MODERATE	c.265C>T; c.346C>T; c.625C>T; c.742C>T	p.Arg89Trp; p.Arg116Trp; p.Arg209Trp; p.Arg248Trp	559	FALSE	chr17:7577539:G:A	22:chr17:7577539:G:A	0.001093
26_c3-b	26	MET	MODERATE	c.143C>T	p.Ala48Val	1	FALSE	chr7:116339281:C:T	22:chr7:116339281:C:T	0.000947

26_c3-b	26	HOXD-AS2; HOXD8	MODIFIER; MODERATE	n.*692C>T; c.260G>A; c.809G>A; c.812G>A	; p.Gly87Glu; p.Gly270Glu; p.Gly271Glu	0	FALSE	chr2:176996279:G:A	22:chr2:176996279:G:A	0.001019
26_c3-b	26	KLLN; PTEN	MODIFIER; LOW	c.-951G>T; c.78C>A	; p.Thr26Thr	2	FALSE	chr10:89624304:C:A	22:chr10:89624304:C:A	0.001585
26_c3-b	26	GNA11	MODERATE	c.997G>A	p.Asp333Asn	1	FALSE	chr19:3121094:G:A	22:chr19:3121094:G:A	0.001065
26_c3-b	26	NF1	MODERATE	c.4462C>T; c.4525C>T	p.Arg1488Cys; p.Arg1509Cys	1	FALSE	chr17:29587481:C:T	22:chr17:29587481:C:T	0.001072
26_c3-b	26	PTEN	HIGH	c.688G>T	p.Gly230*	2	FALSE	chr10:89717663:G:T	22:chr10:89717663:G:T	0.001097
26_c3-b	26	PIK3CA	MODERATE	c.478C>A	p.His160Asn	1	FALSE	chr3:178917603:C:A	22:chr3:178917603:C:A	0.001159
26_c3-b	26	KIT	MODERATE	c.1648G>A; c.1660G>A	p.Glu550Lys; p.Glu554Lys	3	FALSE	chr4:55593594:G:A	22:chr4:55593594:G:A	0.00115
26_c3-b	26	ERBB2; MIEN1; MIR4728	MODIFIER; MODERATE	c.3160-319G>A; c.3145G>A; c.3190G>A; c.3235G>A; n.3559G>A; c.*388C>T; n.*67G>A	; p.Glu1049Lys; p.Glu1064Lys; p.Glu1079Lys	1	FALSE	chr17:37883623:G:A	22:chr17:37883623:G:A	0.001411
26_c3-b	26	EPHA3	MODERATE	c.1132C>A	p.Pro378Thr	0	FALSE	chr3:89391066:C:A	22:chr3:89391066:C:A	0.001308
26_c3-b	26	RET	MODERATE	c.2161C>T	p.Arg721Trp	1	FALSE	chr10:43612056:C:T	22:chr10:43612056:C:T	0.001546
26_c3-b	26	EGFR	MODIFIER; MODERATE	c.*1464C>A; c.1310C>A	; p.Ser437Tyr	1	FALSE	chr7:55227843:C:A	22:chr7:55227843:C:A	0.001172
26_c3-b	26	TP53	MODERATE	c.232A>G; c.313A>G; c.592A>G; c.709A>G	p.Met78Val; p.Met105Val; p.Met198Val; p.Met237Val	10	FALSE	chr17:7577572:T:C	22:chr17:7577572:T:C	0.001025

26_c3-b	26	PTEN	MODERATE	c.729C>A	p.Phe243Leu	1	FALSE	chr10:89717704:C:A	22:chr10:89717704:C:A	0.001294
26_c3-b	26	TP53	MODERATE; MODIFIER	c.140C>T; c.257C>T; c.-279C>T; c.-360C>T	p.Ala47Val; p.Ala86Val;	1	FALSE	chr17:7579430:G:A	22:chr17:7579430:G:A	0.001356
26_c3-b	26	ALK	MODERATE	c.1588G>A	p.Glu530Lys	1	FALSE	chr2:29541229:C:T	22:chr2:29541229:C:T	0.001122
26_c3-b	26	TP53	MODIFIER; MODERATE	c.-3G>A; c.358G>A; c.475G>A; c.79G>A	; p.Ala120Thr; p.Ala159Thr; p.Ala27Thr	23	FALSE	chr17:7578455:C:T	22:chr17:7578455:C:T	0.001295
26_c3-b	26	TP53	MODERATE	c.340C>T; c.421C>T; c.700C>T; c.817C>T	p.Arg114Cys; p.Arg141Cys; p.Arg234Cys; p.Arg273Cys	601	FALSE	chr17:7577121:G:A	22:chr17:7577121:G:A	0.001723
26_c3-b	26	TP53	MODERATE; MODIFIER	c.206C>T; c.89C>T; c.-279C>T; c.-360C>T	p.Ala69Val; p.Ala30Val;	3	FALSE	chr17:7579481:G:A	22:chr17:7579481:G:A	0.001485
26_c3-b	26	KRAS	MODERATE	c.182A>T	p.Gln61Leu	92	FALSE	chr12:25380276:T:A	22:chr12:25380276:T:A	0.266735
26_c3-b	26	PIK3CA	MODERATE	c.1345C>A	p.Pro449Thr	3	FALSE	chr3:178928067:C:A	22:chr3:178928067:C:A	0.001285
26_c3-b	26	FGFR1	MODERATE	c.488G>T; c.494G>T; c.737G>T; c.755G>T; c.761G>T; c.854G>T	p.Arg163Leu; p.Arg165Leu; p.Arg246Leu; p.Arg252Leu; p.Arg254Leu; p.Arg285Leu	1	FALSE	chr8:38282202:C:A	22:chr8:38282202:C:A	0.001053
26_c3-b	26	HOXD-AS2; HOXD8	MODIFIER; MODERATE	n.*692C>T; c.304G>A; c.853G>A; c.856G>A	; p.Glu102Lys; p.Glu285Lys; p.Glu286Lys	0	FALSE	chr2:176996323:G:A	22:chr2:176996323:G:A	0.001553

26_c3-b	26	HGF	MODERATE	c.1057G>T; c.1072G>T	p.Asp353Tyr; p.Asp358Tyr	0	FALSE	chr7:81355302:C:A	22:chr7:81355302:C:A	0.001096
26_c3-b	26	HGF	MODERATE	c.908G>T; c.923G>T	p.Gly303Val; p.Gly308Val	0	FALSE	chr7:81359038:C:A	22:chr7:81359038:C:A	0.000966
26_c3-b	26	KIT	MODERATE	c.1465G>A	p.Val489Ile	1	FALSE	chr4:55592141:G:A	22:chr4:55592141:G:A	0.001167
26_c3-b	26	TP53	MODIFIER; MODERATE	c.*168A>G; c.*80A>G; c.1061A>G; c.584A>G; c.665A>G; c.944A>G	; p.Gln354Arg; p.Gln195Arg; p.Gln222Arg; p.Gln315Arg	2	FALSE	chr17:7573966:T:C	22:chr17:7573966:T:C	0.000961
26_c3-b	26	RET	MODERATE	c.1538C>T	p.Ala513Val	1	FALSE	chr10:43607562:C:T	22:chr10:43607562:C:T	0.001037
26_c3-b	26	CWH43	MODERATE	c.1813G>A; c.1894G>A	p.Glu605Lys; p.Glu632Lys	0	FALSE	chr4:49052739:G:A	22:chr4:49052739:G:A	0.001058
26_c3-b	26	PTEN	MODERATE	c.731C>A	p.Pro244His	2	FALSE	chr10:89717706:C:A	22:chr10:89717706:C:A	0.00128
26_c3-b	26	HGF	MODERATE	c.767G>A; c.782G>A	p.Arg256His; p.Arg261His	0	FALSE	chr7:81372752:C:T	22:chr7:81372752:C:T	0.001111
26_c3-b	26	DDR2	MODERATE	c.313C>A	p.Arg105Ser	2	FALSE	chr1:162724541:C:A	22:chr1:162724541:C:A	0.001316
26_c3-b	26	TP53	MODERATE	c.110G>A; c.191G>A; c.470G>A; c.587G>A	p.Arg37Gln; p.Arg64Gln; p.Arg157Gln; p.Arg196Gln	19	FALSE	chr17:7578262:C:T	22:chr17:7578262:C:T	0.001061
26_c3-b	26	CTNNB1	MODERATE	c.2129G>A	p.Arg710His	0	FALSE	chr3:41279559:G:A	22:chr3:41279559:G:A	0.001389
26_c3-b	26	TP53	MODERATE	c.245C>T; c.326C>T; c.605C>T; c.722C>T	p.Ser82Phe; p.Ser109Phe; p.Ser202Phe; p.Ser241Phe	91	FALSE	chr17:7577559:G:A	22:chr17:7577559:G:A	0.004199
26_c3-b	26	AKT1	MODERATE	c.104T>C	p.Phe35Ser	1	FALSE	chr14:105246496:A:G	22:chr14:105246496:A:G	0.00102

26_c3-b	26	CWH43	MODERATE	c.1535G>A; c.1616G>A	p.Gly512Asp; p.Gly539Asp	0	FALSE	chr4:49034690:G:A	22:chr4:49034690:G:A	0.001102
26_c3-b	26	GNA11	MODERATE	c.1030G>A	p.Val344Met	1	FALSE	chr19:3121127:G:A	22:chr19:3121127:G:A	0.003165
26_c3-b	26	MET	MODERATE	c.608C>A	p.Ser203Tyr	1	FALSE	chr7:116339746:C:A	22:chr7:116339746:C:A	0.001943
26_c3-b	26	EPHA3	HIGH	c.1515C>A	p.Tyr505*	0	FALSE	chr3:89448551:C:A	22:chr3:89448551:C:A	0.003636
26_c3-b	26	PHLPP1	MODERATE	c.2452G>A	p.Val818Ile	0	FALSE	chr18:60570204:G:A	22:chr18:60570204:G:A	0.001043
26_c3-b	26	AKT3	MODERATE	c.899C>T	p.Ala300Val	0	FALSE	chr1:243727071:G:A	22:chr1:243727071:G:A	0.000974
26_c3-b	26	PIK3CA	MODERATE	c.1633G>A	p.Glu545Lys	1189	FALSE	chr3:178936091:G:A	22:chr3:178936091:G:A	0.013812
26_c3-b	26	CTNNB1	MODERATE	c.1004A>C	p.Lys335Thr	0	FALSE	chr3:41268766:A:C	22:chr3:41268766:A:C	0.038366
26_c3-b	26	GAPDH; IFFO1	MODERATE; MODIFIER	c.503C>T; c.629C>T; c.*1743G>A; c.*1746G>A; c.*1770G>A; n.*2798G>A	p.Ser168Phe; p.Ser210Phe;	0	FALSE	chr12:6646853:C:T	22:chr12:6646853:C:T	0.001184
26_c3-b	26	PTEN	MODERATE	c.443C>A	p.Ala148Glu	1	FALSE	chr10:89692959:C:A	22:chr10:89692959:C:A	0.002078
26_c3-b	26	TP53	MODERATE	c.293T>C; c.374T>C; c.653T>C; c.770T>C	p.Leu98Pro; p.Leu125Pro; p.Leu218Pro; p.Leu257Pro	11	FALSE	chr17:7577511:A:G	22:chr17:7577511:A:G	0.001141
26_c3-b	26	PHLPP1	MODERATE	c.3604C>T	p.Arg1202Cys	0	FALSE	chr18:60639790:C:T	22:chr18:60639790:C:T	0.001046
26_c3-b	26	TP53	MODERATE; MODIFIER	c.100G>T; c.217G>T; c.-279G>T; c.-360G>T	p.Val34Leu; p.Val73Leu;	5	FALSE	chr17:7579470:C:A	22:chr17:7579470:C:A	0.001415
26_c3-b	26	CTNNB1	MODERATE	c.96C>A	p.Asp32Glu	0	FALSE	chr3:41266099:C:A	22:chr3:41266099:C:A	0.001019

26_c3-b	26	NF1	MODERATE	c.5878A>G; c.5941A>G	p.Met1960Val; p.Met1981Val	1	FALSE	chr17:29661984:A:G	22:chr17:29661984:A:G	0.001293
26_c3-b	26	NF1	MODERATE	c.2695T>G	p.Leu899Val	3	FALSE	chr17:29556328:T:G	22:chr17:29556328:T:G	0.020174
26_c3-b	26	MET	HIGH	c.3508C>T; c.3562C>T	p.Arg1170*; p.Arg1188*	4	FALSE	chr7:116418997:C:T	22:chr7:116418997:C:T	0.001012
26_c3-b	26	CTNNB1	MODERATE	c.451C>T	p.Arg151Cys	0	FALSE	chr3:41266654:C:T	22:chr3:41266654:C:T	0.001024
26_c3-b	26	KRAS	MODERATE	c.204G>T	p.Arg68Ser	1	FALSE	chr12:25380254:C:A	22:chr12:25380254:C:A	0.001053
26_c3-b	26	FGFR1	MODIFIER; MODERATE	c.-32G>A; c.160G>A; c.61G>A	; p.Ala54Thr; p.Ala21Thr	2	FALSE	chr8:38314904:C:T	22:chr8:38314904:C:T	0.001089
26_c3-b	26	MAP2K1	MODERATE	c.198C>A	p.Asp66Glu	4	FALSE	chr15:66727482:C:A	22:chr15:66727482:C:A	0.001905
26_c3-b	26	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2356G>A; n.1206C>T	p.Val786Met;	6	FALSE	chr7:55249058:G:A	22:chr7:55249058:G:A	0.001496
26_c3-b	26	TP53	MODERATE	c.128G>T; c.407G>T; c.47G>T; c.524G>T	p.Arg43Leu; p.Arg136Leu; p.Arg16Leu; p.Arg175Leu	979	FALSE	chr17:7578406:C:A	22:chr17:7578406:C:A	0.001241
26_c3-b	26	CTNNB1	MODERATE	c.125C>A	p.Thr42Lys	0	FALSE	chr3:41266128:C:A	22:chr3:41266128:C:A	0.001007
26_c3-b	26	CTNNB1	MODERATE	c.1147T>G	p.Trp383Gly	0	FALSE	chr3:41274897:T:G	22:chr3:41274897:T:G	0.003283
26_c3-b	26	CTNNB1	MODERATE	c.122C>A	p.Thr41Asn	0	FALSE	chr3:41266125:C:A	22:chr3:41266125:C:A	0.001517
26_c3-b	26	RET	MODERATE	c.1690A>C	p.Thr564Pro	1	FALSE	chr10:43608342:A:C	22:chr10:43608342:A:C	0.009174
26_c3-b	26	CTNNB1	MODERATE	c.884C>A	p.Ala295Asp	0	FALSE	chr3:41267300:C:A	22:chr3:41267300:C:A	0.001276
26_c3-b	26	TP53	MODERATE; MODIFIER	c.208G>A; c.91G>A; c.-279G>A; c.-360G>A	p.Ala70Thr; p.Ala31Thr;	1	FALSE	chr17:7579479:C:T	22:chr17:7579479:C:T	0.002254
26_c3-b	26	EGFR	MODERATE	c.844G>A	p.Glu282Lys	1	FALSE	chr7:55221800:G:A	22:chr7:55221800:G:A	0.001005

26_c3-b	26	TP53	MODERATE	c.350C>T; c.431C>T; c.710C>T; c.827C>T	p.Ala117Val; p.Ala144Val; p.Ala237Val; p.Ala276Val	10	FALSE	chr17:7577111:G:A	22:chr17:7577111:G:A	0.001145
26_c3-b	26	TP53	MODERATE	c.15G>T; c.375G>T; c.492G>T; c.96G>T	p.Lys5Asn; p.Lys125Asn; p.Lys164Asn; p.Lys32Asn	6	FALSE	chr17:7578438:C:A	22:chr17:7578438:C:A	0.001286
25_c3-2	25	NF1	MODERATE	c.2695T>G	p.Leu899Val	3	FALSE	chr17:29556328:T:G	26:chr17:29556328:T:G	0.029268
25_c4-1	25	PTEN	HIGH	c.720C>A	p.Tyr240*	3	FALSE	chr10:89717695:C:A	27:chr10:89717695:C:A	0.001413
25_c4-1	25	PTEN	MODERATE	c.923G>A	p.Arg308His	1	FALSE	chr10:89720772:G:A	27:chr10:89720772:G:A	0.001889
25_c4-1	25	RET	MODERATE	c.1991C>A	p.Ala664Asp	2	FALSE	chr10:43610039:C:A	27:chr10:43610039:C:A	0.001136
25_c4-1	25	BRAF	MODERATE	c.1202C>T	p.Thr401Ile	1	FALSE	chr7:140482933:G:A	27:chr7:140482933:G:A	0.002028
25_c4-1	25	PTEN	HIGH	c.688G>T	p.Gly230*	2	FALSE	chr10:89717663:G:T	27:chr10:89717663:G:T	0.001937
25_c4-1	25	PIK3CA	MODERATE	c.518C>A	p.Ser173Tyr	1	FALSE	chr3:178917643:C:A	27:chr3:178917643:C:A	0.001329
25_c4-1	25	PIK3CA	MODERATE	c.1615C>A	p.Pro539Thr	3	FALSE	chr3:178936073:C:A	27:chr3:178936073:C:A	0.001507
25_c4-1	25	ERBB2; MIEN1; MIR4728	MODIFIER; MODERATE	c.3160-213A>G; c.3251A>G; c.3296A>G; c.3341A>G; n.3665A>G; c.*388T>C; n.*67A>G	; p.Glu1084Gly; p.Glu1099Gly; p.Glu1114Gly	1	FALSE	chr17:37883729:A:G	27:chr17:37883729:A:G	0.001559
25_c4-1	25	FGFR1	MODIFIER; MODERATE	c.-85G>T; c.107G>T; c.8G>T	; p.Ser36Ile; p.Ser3Ile	1	FALSE	chr8:38314957:C:A	27:chr8:38314957:C:A	0.00122

25_c4-1	25	TP53	MODERATE	c.248G>T; c.329G>T; c.608G>T; c.725G>T	p.Cys83Phe; p.Cys110Phe; p.Cys203Phe; p.Cys242Phe	72	FALSE	chr17:7577556:C:A	27:chr17:7577556:C:A	0.001406
25_c4-1	25	RET	MODERATE	c.1349G>A	p.Ser450Asn	1	FALSE	chr10:43606740:G:A	27:chr10:43606740:G:A	0.001159
25_c4-1	25	BRAF	MODERATE	c.1799T>A	p.Val600Glu	23024	FALSE	chr7:140453136:A:T	27:chr7:140453136:A:T	0.002937
25_c4-1	25	MITF	MODIFIER; MODERATE	c.-53+197C>A; c.104+24188C>A; c.48C>A	; p.Phe16Leu	0	FALSE	chr3:69813040:C:A	27:chr3:69813040:C:A	0.001358
25_c4-1	25	PIK3CA	MODERATE	c.478C>A	p.His160Asn	1	FALSE	chr3:178917603:C:A	27:chr3:178917603:C:A	0.001299
25_c4-1	25	CTNNB1	MODERATE	c.1972G>T	p.Val658Phe	0	FALSE	chr3:41278096:G:T	27:chr3:41278096:G:T	0.002926
25_c4-1	25	NF1	MODERATE	c.5426G>A; c.5489G>A	p.Arg1809His; p.Arg1830His	1	FALSE	chr17:29654737:G:A	27:chr17:29654737:G:A	0.0011
25_c4-1	25	PHLPP1	MODERATE	c.1971C>A	p.Phe657Leu	0	FALSE	chr18:60527739:C:A	27:chr18:60527739:C:A	0.00188
25_c4-1	25	BRAF	MODERATE	c.1099C>T	p.Pro367Ser	1	FALSE	chr7:140494149:G:A	27:chr7:140494149:G:A	0.00146
25_c4-1	25	CTNNB1	MODERATE	c.91C>A	p.Leu31Met	0	FALSE	chr3:41266094:C:A	27:chr3:41266094:C:A	0.001456
25_c4-1	25	PTEN	HIGH	c.633C>A	p.Cys211*	2	FALSE	chr10:89712015:C:A	27:chr10:89712015:C:A	0.002762
25_c4-1	25	PHLPP1	MODERATE	c.2303C>A	p.Ser768Tyr	0	FALSE	chr18:60563103:C:A	27:chr18:60563103:C:A	0.002187
25_c4-1	25	PIK3CA	MODERATE	c.3001C>A	p.Leu1001Ile	3	FALSE	chr3:178951946:C:A	27:chr3:178951946:C:A	0.00135
25_c4-1	25	HGF	MODERATE	c.767G>A; c.782G>A	p.Arg256His; p.Arg261His	0	FALSE	chr7:81372752:C:T	27:chr7:81372752:C:T	0.001581
25_c4-1	25	EPHA3	MODERATE	c.1280C>T	p.Ala427Val	0	FALSE	chr3:89391214:C:T	27:chr3:89391214:C:T	0.001585
25_c4-1	25	CWH43	MODERATE	c.1535G>A; c.1616G>A	p.Gly512Asp; p.Gly539Asp	0	FALSE	chr4:49034690:G:A	27:chr4:49034690:G:A	0.001371
25_c4-1	25	CTNNB1	MODERATE	c.134C>A	p.Ser45Tyr	0	FALSE	chr3:41266137:C:A	27:chr3:41266137:C:A	0.002075

25_c4-1	25	RET	MODERATE	c.1690A>C	p.Thr564Pro	1	FALSE	chr10:43608342:A:C	27:chr10:43608342:A:C	0.019155
25_c4-1	25	HOXD-AS2; HOXD8	MODIFIER; MODERATE	n.*692G>T; c.22C>A; c.574C>A	; p.Gln8Lys; p.Gln192Lys	0	FALSE	chr2:176995668:C:A	27:chr2:176995668:C:A	0.002935
25_c4-1	25	NF1	MODERATE	c.2695T>G	p.Leu899Val	3	FALSE	chr17:29556328:T:G	27:chr17:29556328:T:G	0.040855
25_c4-1	25	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2606A>G; n.-1T>C	p.Tyr869Cys;	1	FALSE	chr7:55259548:A:G	27:chr7:55259548:A:G	0.001929
25_c4-1	25	TP53	MODIFIER; HIGH	c.*143G>T; c.*55G>T; c.1036G>T; c.559G>T; c.640G>T; c.919G>T	; p.Glu346*; p.Glu187*; p.Glu214*; p.Glu307*	4	FALSE	chr17:7573991:C:A	27:chr17:7573991:C:A	0.001203
25_c4-1	25	TP53	MODERATE	c.121G>T; c.400G>T; c.40G>T; c.517G>T	p.Val41Leu; p.Val134Leu; p.Val14Leu; p.Val173Leu	55	FALSE	chr17:7578413:C:A	27:chr17:7578413:C:A	0.001642
25_c4-1	25	NF1	MODERATE	c.3917G>A	p.Arg1306Gln	2	FALSE	chr17:29562982:G:A	27:chr17:29562982:G:A	0.001585
25_c4-1	25	AKT3	MODERATE	c.1100G>A	p.Arg367Gln	0	FALSE	chr1:243716094:C:T	27:chr1:243716094:C:T	0.001437
25_c4-1	25	FGFR1	MODERATE	c.359C>T; c.365C>T; c.608C>T; c.626C>T; c.632C>T; c.725C>T	p.Ala120Val; p.Ala122Val; p.Ala203Val; p.Ala209Val; p.Ala211Val; p.Ala242Val	1	FALSE	chr8:38283753:G:A	27:chr8:38283753:G:A	0.001394
25_c4-1	25	CTNNB1	MODERATE	c.884C>A	p.Ala295Asp	0	FALSE	chr3:41267300:C:A	27:chr3:41267300:C:A	0.001592
25_c4-1	25	DDR2	MODERATE	c.313C>A	p.Arg105Ser	2	FALSE	chr1:162724541:C:A	27:chr1:162724541:C:A	0.001826

25_c4-1	25	TP53	MODERATE	c.355C>T; c.436C>T; c.715C>T; c.832C>T	p.Pro119Ser; p.Pro146Ser; p.Pro239Ser; p.Pro278Ser	59	FALSE	chr17:7577106:G:A	27:chr17:7577106:G:A	0.00293
25_c4-1	25	TP53	MODERATE; MODIFIER	c.115G>T; c.232G>T; c.-279G>T; c.-360G>T	p.Ala39Ser; p.Ala78Ser;	1	FALSE	chr17:7579455:C:A	27:chr17:7579455:C:A	0.003457
25_c4-1	25	AKT3	MODERATE	c.825G>T	p.Glu275Asp	0	FALSE	chr1:243727145:C:A	27:chr1:243727145:C:A	0.002655
25_c4-1	25	BRAF	MODERATE	c.436C>T	p.Arg146Trp	1	FALSE	chr7:140534477:G:A	27:chr7:140534477:G:A	0.001296
25_c4-1	25	GNA11	MODERATE	c.440G>A	p.Arg147His	1	FALSE	chr19:3113446:G:A	27:chr19:3113446:G:A	0.00214
25_c4-1	25	PTEN	MODERATE	c.443C>A	p.Ala148Glu	1	FALSE	chr10:89692959:C:A	27:chr10:89692959:C:A	0.001695
25_c4-1	25	ERBB2	MODERATE; MODIFIER	c.560G>A; c.605G>A; c.650G>A; n.974G>A	p.Arg187His; p.Arg202His; p.Arg217His;	1	FALSE	chr17:37866345:G:A	27:chr17:37866345:G:A	0.00128
25_c4-1	25	ALK	HIGH	c.4414G>T	p.Glu1472*	1	FALSE	chr2:29416539:C:A	27:chr2:29416539:C:A	0.001074
25_c4-1	25	NF1	MODERATE	c.7583C>T; c.7646C>T	p.Ser2528Leu; p.Ser2549Leu	3	FALSE	chr17:29683508:C:T	27:chr17:29683508:C:T	0.001379
25_c4-1	25	KIT	MODERATE	c.1485C>A	p.Asn495Lys	1	FALSE	chr4:55592161:C:A	27:chr4:55592161:C:A	0.003049
25_c4-1	25	TP53	MODERATE	c.392G>A; c.473G>A; c.752G>A; c.869G>A	p.Arg131His; p.Arg158His; p.Arg251His; p.Arg290His	20	FALSE	chr17:7577069:C:T	27:chr17:7577069:C:T	0.001429
25_c4-1	25	EPHA3	MODERATE	c.237C>A	p.Asn79Lys	0	FALSE	chr3:89259093:C:A	27:chr3:89259093:C:A	0.001376
25_c4-1	25	CTNNB1	MODERATE	c.861C>A	p.Asn287Lys	0	FALSE	chr3:41267277:C:A	27:chr3:41267277:C:A	0.001483

25_c4-1	25	EGFR	MODIFIER; MODERATE	c.*1464G>A; c.1606G>A	; p.Val536Met	1	FALSE	chr7:55229299:G:A	27:chr7:55229299:G:A	0.002143
25_c4-1	25	NF1	MODERATE	c.6405C>A; c.6468C>A	p.Phe2135Leu; p.Phe2156Leu	1	FALSE	chr17:29664426:C:A	27:chr17:29664426:C:A	0.001499
26_c5-1	26	KRAS	MODERATE	c.182A>T	p.Gln61Leu	92	FALSE	chr12:25380276:T:A	28:chr12:25380276:T:A	0.130112
26_c5-1	26	CTNNB1	MODERATE	c.1004A>C	p.Lys335Thr	0	FALSE	chr3:41268766:A:C	28:chr3:41268766:A:C	0.021552
26_c5-1	26	PTEN	MODERATE	c.815A>C	p.His272Pro	2	FALSE	chr10:89720664:A:C	28:chr10:89720664:A:C	0.00369
26_c5-1	26	NF1	MODERATE	c.7718G>A; c.7781G>A	p.Arg2573His; p.Arg2594His	3	FALSE	chr17:29684020:G:A	28:chr17:29684020:G:A	0.001592
26_c5-1	26	NF1	MODERATE	c.2695T>G	p.Leu899Val	3	FALSE	chr17:29556328:T:G	28:chr17:29556328:T:G	0.02828
26_c5-1	26	EPHA3	MODERATE	c.1132C>A	p.Pro378Thr	0	FALSE	chr3:89391066:C:A	28:chr3:89391066:C:A	0.001376
26_c5-1	26	DDR2	MODERATE	c.1598C>A	p.Thr533Lys	1	FALSE	chr1:162741907:C:A	28:chr1:162741907:C:A	0.001511
26_c5-1	26	PIK3CA	MODERATE	c.518C>A	p.Ser173Tyr	1	FALSE	chr3:178917643:C:A	28:chr3:178917643:C:A	0.001802
26_c5-1	26	TP53	MODIFIER; MODERATE	c.-13G>T; c.105G>T; c.-279G>T; c.-360G>T	; p.Leu35Phe	2	FALSE	chr17:7579582:C:A	28:chr17:7579582:C:A	0.001923
26_c5-1	26	RET	MODERATE	c.1690A>C	p.Thr564Pro	1	FALSE	chr10:43608342:A:C	28:chr10:43608342:A:C	0.009375
26_c5-1	26	PIK3CA	MODERATE	c.1633G>A	p.Glu545Lys	1189	FALSE	chr3:178936091:G:A	28:chr3:178936091:G:A	0.006431
26_c5-1	26	TP53	MODERATE	c.368G>T; c.449G>T; c.728G>T; c.845G>T	p.Arg123Leu; p.Arg150Leu; p.Arg243Leu; p.Arg282Leu	26	FALSE	chr17:7577093:C:A	28:chr17:7577093:C:A	0.001606
26_c5-1	26	PIK3CA	MODERATE	c.1645G>A	p.Asp549Asn	4	FALSE	chr3:178936103:G:A	28:chr3:178936103:G:A	0.001726

26_c5-1	26	TP53	HIGH; MODIFIER	c.184G>T; c.67G>T; c.-279G>T; c.-360G>T	p.Glu62*; p.Glu23*;	8	FALSE	chr17:7579503:C:A	28:chr17:7579503:C:A	0.002125
26_c5-1	26	EPHA3	MODERATE	c.1142G>A	p.Arg381His	0	FALSE	chr3:89391076:G:A	28:chr3:89391076:G:A	0.001383
26_c5-1	26	TP53	MODERATE	c.245C>T; c.326C>T; c.605C>T; c.722C>T	p.Ser82Phe; p.Ser109Phe; p.Ser202Phe; p.Ser241Phe	91	FALSE	chr17:7577559:G:A	28:chr17:7577559:G:A	0.002125
26_c5-1	26	TP53	MODERATE	c.341G>A; c.422G>A; c.701G>A; c.818G>A	p.Arg114His; p.Arg141His; p.Arg234His; p.Arg273His	647	TRUE	chr17:7577120:C:T	28:chr17:7577120:C:T	0.001676
26_c5-1	26	KIT	MODERATE	c.1469A>G	p.Glu490Gly	1	FALSE	chr4:55592145:A:G	28:chr4:55592145:A:G	0.001605
26_c5-1	26	EGFR	MODIFIER; HIGH	c.*2364G>A; c.2193G>A	; p.Trp731*	2	FALSE	chr7:55242423:G:A	28:chr7:55242423:G:A	0.001458
26_c5-1	26	CTNNB1	MODERATE	c.122C>A	p.Thr41Asn	0	FALSE	chr3:41266125:C:A	28:chr3:41266125:C:A	0.00219
26_c5-1	26	TP53	MODERATE	c.224A>G; c.305A>G; c.584A>G; c.701A>G	p.Tyr75Cys; p.Tyr102Cys; p.Tyr195Cys; p.Tyr234Cys	94	FALSE	chr17:7577580:T:C	28:chr17:7577580:T:C	0.002022
26_c5-1	26	NF1	MODIFIER; HIGH	c.*2165G>A; c.2087G>A	; p.Trp696*	2	FALSE	chr17:29553538:G:A	28:chr17:29553538:G:A	0.001463
26_c5-1	26	PIK3R1	MODERATE	c.1702C>A; c.613C>A; c.802C>A; c.892C>A	p.Pro568Thr; p.Pro205Thr; p.Pro268Thr; p.Pro298Thr	1	FALSE	chr5:67591109:C:A	28:chr5:67591109:C:A	0.0016

26_c5-1	26	TP53	MODIFIER; MODERATE	c.-3G>T; c.358G>T; c.475G>T; c.79G>T	; p.Ala120Ser; p.Ala159Ser; p.Ala27Ser	23	FALSE	chr17:7578455:C:A	28:chr17:7578455:C:A	0.001805
26_c5-1	26	ALK	MODERATE	c.3394G>A	p.Glu1132Lys	1	FALSE	chr2:29445439:C:T	28:chr2:29445439:C:T	0.001825
26_c5-1	26	TP53	MODIFIER; MODERATE	c.-9G>T; c.352G>T; c.469G>T; c.73G>T	; p.Val118Phe; p.Val157Phe; p.Val25Phe	169	FALSE	chr17:7578461:C:A	28:chr17:7578461:C:A	0.0036
25_t2c4-1	25	CTNNB1	MODERATE	c.122C>A	p.Thr41Asn	0	FALSE	chr3:41266125:C:A	29:chr3:41266125:C:A	0.001034
25_t2c4-1	25	GNA11	MODERATE	c.997G>A	p.Asp333Asn	1	FALSE	chr19:3121094:G:A	29:chr19:3121094:G:A	0.001013
25_t2c4-1	25	PTEN	MODERATE	c.611C>A	p.Pro204Gln	3	FALSE	chr10:89711993:C:A	29:chr10:89711993:C:A	0.001096
25_t2c4-1	25	CTNNB1	MODERATE	c.86C>A	p.Ser29Tyr	0	FALSE	chr3:41266089:C:A	29:chr3:41266089:C:A	0.001638
25_t2c4-1	25	CTNNB1	MODERATE	c.96C>A	p.Asp32Glu	0	FALSE	chr3:41266099:C:A	29:chr3:41266099:C:A	0.002128
25_t2c4-1	25	TP53	MODERATE	c.355C>T; c.436C>T; c.715C>T; c.832C>T	p.Pro119Ser; p.Pro146Ser; p.Pro239Ser; p.Pro278Ser	59	FALSE	chr17:7577106:G:A	29:chr17:7577106:G:A	0.001559
25_t2c4-1	25	BRAF	MODERATE	c.1330C>T	p.Arg444Trp	5	FALSE	chr7:140481478:G:A	29:chr7:140481478:G:A	0.001557
25_t2c4-1	25	NF1	HIGH	c.5817C>A; c.5880C>A	p.Cys1939*; p.Cys1960*	1	FALSE	chr17:29661923:C:A	29:chr17:29661923:C:A	0.002596
25_t2c4-1	25	EPHA3	MODERATE	c.1379C>A	p.Pro460His	0	FALSE	chr3:89445059:C:A	29:chr3:89445059:C:A	0.001722
25_t2c4-1	25	NF1	MODERATE	c.2695T>G	p.Leu899Val	3	FALSE	chr17:29556328:T:G	29:chr17:29556328:T:G	0.056907

25_t2c4-1	25	ERBB2; MIEN1; MIR4728	MODERATE; MODIFIER	c.2236G>A; c.2281G>A; c.2326G>A; n.2650G>A; c.*388C>T; n.-1G>A	p.Gly746Ser; p.Gly761Ser; p.Gly776Ser;	5	FALSE	chr17:37880997:G:A	29:chr17:37880997:G:A	0.001078
25_t2c4-1	25	MAP2K1	MODERATE	c.198C>A	p.Asp66Glu	4	FALSE	chr15:66727482:C:A	29:chr15:66727482:C:A	0.002346
25_t2c4-1	25	PHLPP1	MODERATE	c.2303C>A	p.Ser768Tyr	0	FALSE	chr18:60563103:C:A	29:chr18:60563103:C:A	0.0016
25_t2c4-1	25	EGFR	MODIFIER; MODERATE	c.*2133G>A; c.*2364G>A; c.2030G>A	; p.Arg677His	5	FALSE	chr7:55240786:G:A	29:chr7:55240786:G:A	0.001992
25_t2c4-1	25	BRAF	MODERATE	c.2223G>T	p.Glu741Asp	1	FALSE	chr7:140434475:C:A	29:chr7:140434475:C:A	0.000882
25_t2c4-1	25	RET	MODERATE	c.1690A>C	p.Thr564Pro	1	FALSE	chr10:43608342:A:C	29:chr10:43608342:A:C	0.015748
25_t2c4-1	25	BRAF	MODERATE	c.1799T>A	p.Val600Glu	23024	FALSE	chr7:140453136:A:T	29:chr7:140453136:A:T	0.002697
25_t2c4-1	25	CTNNB1	MODERATE	c.98C>A	p.Ser33Tyr	0	FALSE	chr3:41266101:C:A	29:chr3:41266101:C:A	0.001047
25_t2c4-1	25	PIK3CA	MODERATE	c.518C>A	p.Ser173Tyr	1	FALSE	chr3:178917643:C:A	29:chr3:178917643:C:A	0.001033
25_t2c4-1	25	PIK3R1	HIGH	c.1077C>A; c.1167C>A; c.1977C>A; c.888C>A	p.Cys359*; p.Cys389*; p.Cys659*; p.Cys296*	1	FALSE	chr5:67592161:C:A	29:chr5:67592161:C:A	0.001161
25_t2c4-1	25	PTEN	HIGH	c.720C>A	p.Tyr240*	3	FALSE	chr10:89717695:C:A	29:chr10:89717695:C:A	0.00213
25_t2c4-1	25	NF1	MODERATE	c.169G>A	p.Gly57Ser	1	FALSE	chr17:29483109:G:A	29:chr17:29483109:G:A	0.001011
25_t2c4-1	25	ALK	HIGH	c.4414G>T	p.Glu1472*	1	FALSE	chr2:29416539:C:A	29:chr2:29416539:C:A	0.000861
25_t2c4-1	25	MET	HIGH	c.1639C>T	p.Arg547*	2	FALSE	chr7:116381017:C:T	29:chr7:116381017:C:T	0.000834
25_t2c4-1	25	PIK3CA	MODERATE	c.112C>A	p.Arg38Ser	9	FALSE	chr3:178916725:C:A	29:chr3:178916725:C:A	0.001657

25_t2c4-1	25	CTNNB1	MODERATE	c.884C>A	p.Ala295Asp	0	FALSE	chr3:41267300:C:A	29:chr3:41267300:C:A	0.00115
25_t2c4-1	25	KIT	MODERATE	c.235C>A	p.Gln79Lys	2	FALSE	chr4:55561845:C:A	29:chr4:55561845:C:A	0.000872
25_t2c4-1	25	KRAS	HIGH	c.292G>T	p.Glu98*	1	FALSE	chr12:25378706:C:A	29:chr12:25378706:C:A	0.001285
25_t2c4-1	25	FGFR1	MODIFIER; MODERATE	c.-85G>T; c.107G>T; c.8G>T	; p.Ser36Ile; p.Ser3Ile	1	FALSE	chr8:38314957:C:A	29:chr8:38314957:C:A	0.001919
25_t2c4-1	25	BRAF	MODERATE	c.1391G>T	p.Gly464Val	9	FALSE	chr7:140481417:C:A	29:chr7:140481417:C:A	0.001032
25_t2c4-1	25	CTNNB1	MODERATE	c.861C>A	p.Asn287Lys	0	FALSE	chr3:41267277:C:A	29:chr3:41267277:C:A	0.002259
25_t2c4-1	25	ALK	MODERATE	c.2653G>T	p.Asp885Tyr	2	FALSE	chr2:29451912:C:A	29:chr2:29451912:C:A	0.001356
25_t2c4-1	25	PIK3R1	MODERATE	c.825C>A	p.Phe275Leu	1	FALSE	chr5:67576546:C:A	29:chr5:67576546:C:A	0.001095
25_t2c4-1	25	HGF	HIGH	c.1993G>T; c.2008G>T	p.Glu665*; p.Glu670*	0	FALSE	chr7:81334708:C:A	29:chr7:81334708:C:A	0.001131
25_t2c4-1	25	MET	MODERATE	c.1234C>T	p.Arg412Cys	1	FALSE	chr7:116371755:C:T	29:chr7:116371755:C:T	0.00144
25_t2c4-1	25	DDR2	MODERATE	c.1234C>A	p.Leu412Ile	1	FALSE	chr1:162737090:C:A	29:chr1:162737090:C:A	0.0014
25_t2c4-1	25	HOXD-AS2; HOXD8	MODIFIER; MODERATE	n.*692G>T; c.22C>A; c.574C>A	; p.Gln8Lys; p.Gln192Lys	0	FALSE	chr2:176995668:C:A	29:chr2:176995668:C:A	0.002201
25_t2c4-1	25	CTNNB1	MODERATE	c.1127G>A	p.Arg376His	0	FALSE	chr3:41274877:G:A	29:chr3:41274877:G:A	0.000975
25_t2c4-1	25	PIK3CA	MODERATE	c.1255C>A	p.His419Asn	1	FALSE	chr3:178927977:C:A	29:chr3:178927977:C:A	0.001776
25_t2c4-1	25	TP53	HIGH	c.115G>T; c.196G>T; c.475G>T; c.592G>T	p.Glu39*; p.Glu66*; p.Glu159*; p.Glu198*	30	FALSE	chr17:7578257:C:A	29:chr17:7578257:C:A	0.001389

25_t2c4-1	25	ERBB2; MIEN1; MIR4728	MODIFIER; MODERATE	c.3160-213A>G; c.3251A>G; c.3296A>G; c.3341A>G; n.3665A>G; c.*388T>C; n.*67A>G	; p.Glu1084Gly; p.Glu1099Gly; p.Glu1114Gly	1	FALSE	chr17:37883729:A:G	29:chr17:37883729:A:G	0.001274
25_t2c4-1	25	TP53	MODERATE; MODIFIER	c.225G>T; c.342G>T; c.-279G>T; c.-360G>T	p.Leu75Phe; p.Leu114Phe;	2	FALSE	chr17:7579345:C:A	29:chr17:7579345:C:A	0.001096
25_t2c4-1	25	TP53	MODERATE	c.371G>T; c.452G>T; c.731G>T; c.848G>T	p.Arg124Leu; p.Arg151Leu; p.Arg244Leu; p.Arg283Leu	24	FALSE	chr17:7577090:C:A	29:chr17:7577090:C:A	0.00106
25_t2c4-1	25	ZNF716	MODERATE	c.260C>A	p.Pro87Gln	0	FALSE	chr7:57522872:C:A	29:chr7:57522872:C:A	0.00104
25_t2c4-1	25	RET	MODERATE	c.2038G>A	p.Ala680Thr	1	FALSE	chr10:43610086:G:A	29:chr10:43610086:G:A	0.001905
25_t2c4-1	25	PIK3R1	MODERATE	c.1064T>C; c.1253T>C; c.1343T>C; c.2153T>C	p.Val355Ala; p.Val418Ala; p.Val448Ala; p.Val718Ala	1	FALSE	chr5:67593407:T:C	29:chr5:67593407:T:C	0.0008
25_t2c4-1	25	HGF	MODERATE	c.5G>T	p.Trp2Leu	0	FALSE	chr7:81399283:C:A	29:chr7:81399283:C:A	0.002647
25_t2c4-1	25	AKT3	MODERATE	c.825G>T	p.Glu275Asp	0	FALSE	chr1:243727145:C:A	29:chr1:243727145:C:A	0.001297
25_t2c4-1	25	MAP2K1	MODERATE	c.323G>A	p.Arg108Gln	1	FALSE	chr15:66729115:G:A	29:chr15:66729115:G:A	0.001034
25_t2c4-1	25	CTNNB1	MODERATE	c.134C>A	p.Ser45Tyr	0	FALSE	chr3:41266137:C:A	29:chr3:41266137:C:A	0.001496
25_t2c4-1	25	NF1	MODERATE	c.2573C>A	p.Ser858Tyr	1	FALSE	chr17:29556206:C:A	29:chr17:29556206:C:A	0.000944
61_c2-1	61	PTEN	MODERATE	c.731C>A	p.Pro244His	2	FALSE	chr10:89717706:C:A	30:chr10:89717706:C:A	0.002155

61_c2-1	61	CTNNB1	MODERATE	c.861C>A	p.Asn287Lys	0	FALSE	chr3:41267277:C:A	30:chr3:41267277:C:A	0.001932
61_c2-1	61	KLLN; PTEN	MODIFIER; MODERATE	c.-951C>A; c.44G>T	; p.Arg15Ile	3	FALSE	chr10:89624270:G:T	30:chr10:89624270:G:T	0.002347
61_c2-1	61	RET	MODERATE	c.1690A>C	p.Thr564Pro	1	FALSE	chr10:43608342:A:C	30:chr10:43608342:A:C	0.009184
61_c2-1	61	PTEN	MODERATE	c.320A>C	p.Asp107Ala	2	FALSE	chr10:89692836:A:C	30:chr10:89692836:A:C	0.002157
61_c2-1	61	CTNNB1	MODERATE	c.134C>A	p.Ser45Tyr	0	FALSE	chr3:41266137:C:A	30:chr3:41266137:C:A	0.001706
61_c2-1	61	NF1	MODERATE	c.2695T>G	p.Leu899Val	3	FALSE	chr17:29556328:T:G	30:chr17:29556328:T:G	0.03428
61_c2-1	61	HOXD-AS2; HOXD8	MODIFIER; MODERATE	n.*692G>T; c.22C>A; c.574C>A	; p.Gln8Lys; p.Gln192Lys	0	FALSE	chr2:176995668:C:A	30:chr2:176995668:C:A	0.002706
61_c2-1	61	ERBB2; MIEN1; MIR4728	MODERATE; MODIFIER	c.2597G>A; c.2642G>A; c.2687G>A; n.3011G>A; c.*388C>T; n.-1G>A	p.Arg866His; p.Arg881His; p.Arg896His;	2	FALSE	chr17:37881617:G:A	30:chr17:37881617:G:A	0.004008
69_c3-1	69	DDR2	MODERATE	c.700G>A	p.Asp234Asn	1	FALSE	chr1:162729614:G:A	33:chr1:162729614:G:A	0.001503
69_c3-1	69	NF1	MODERATE	c.2695T>G	p.Leu899Val	3	FALSE	chr17:29556328:T:G	33:chr17:29556328:T:G	0.041384
69_c3-1	69	BRAF	MODERATE	c.1799T>A	p.Val600Glu	23024	FALSE	chr7:140453136:A:T	33:chr7:140453136:A:T	0.047383
69_c3-1	69	PTEN	MODERATE	c.283C>T	p.Pro95Ser	3	FALSE	chr10:89692799:C:T	33:chr10:89692799:C:T	0.018644

69_c3-1	69	FGFR1; LETM2	MODERATE; MODIFIER	c.1777T>G; c.1783T>G; c.2020T>G; c.2044T>G; c.2050T>G; c.2143T>G; c.*1406A>C; c.*1423A>C; c.*1553A>C; c.*1567A>C; c.*1638A>C	p.Trp593Gly; p.Trp595Gly; p.Trp674Gly; p.Trp682Gly; p.Trp684Gly; p.Trp715Gly;	1	FALSE	chr8:38271806:A:C	33:chr8:38271806:A:C	0.00282
69_c3-1	69	TP53	HIGH; MODIFIER	c.181C>T; c.298C>T; c.-279C>T; c.-360C>T	p.Gln61*; p.Gln100*;	16	FALSE	chr17:7579389:G:A	33:chr17:7579389:G:A	0.025692
69_c3-1	69	ERBB2; MIEN1; MIR4728	MODERATE; MODIFIER	c.2720A>G; c.2765A>G; c.2810A>G; n.3134A>G; c.*388T>C; n.-1A>G	p.Lys907Arg; p.Lys922Arg; p.Lys937Arg;	1	FALSE	chr17:37882044:A:G	33:chr17:37882044:A:G	0.002625
69_c3-1	69	ALK	MODERATE	c.3718T>G	p.Leu1240Val	2	FALSE	chr2:29436875:A:C	33:chr2:29436875:A:C	0.001565
69_c3-1	69	EPHA3	MODERATE	c.2002C>A	p.Leu668Met	0	FALSE	chr3:89468468:C:A	33:chr3:89468468:C:A	0.001556
69_c3-1	69	CTNNB1	MODERATE	c.125C>A	p.Thr42Lys	0	FALSE	chr3:41266128:C:A	33:chr3:41266128:C:A	0.001422
69_c3-1	69	HGF	MODERATE	c.6G>T	p.Trp2Cys	0	FALSE	chr7:81399282:C:A	33:chr7:81399282:C:A	0.001652
69_c3-1	69	DDR2	MODERATE	c.313C>A	p.Arg105Ser	2	FALSE	chr1:162724541:C:A	33:chr1:162724541:C:A	0.001438

69_c3-1	69	ERBB2	MODERATE; MODIFIER	c.632C>T; c.677C>T; c.722C>T; n.1046C>T	p.Ala211Val; p.Ala226Val; p.Ala241Val;	2	FALSE	chr17:37866417:C:T	33:chr17:37866417:C:T	0.001461
69_c3-1	69	ALG10	MODERATE	c.217A>G	p.Ile73Val	0	FALSE	chr12:34176942:A:G	33:chr12:34176942:A:G	0.002126
69_c3-1	69	PIK3CA	MODERATE	c.178C>A	p.Gln60Lys	1	FALSE	chr3:178916791:C:A	33:chr3:178916791:C:A	0.001272
69_c3-1	69	EGFR	MODIFIER; MODERATE	c.*1464C>A; c.1476C>A	; p.Ser492Arg	4	FALSE	chr7:55228009:C:A	33:chr7:55228009:C:A	0.002306
69_c3-1	69	GNA11	MODERATE	c.440G>A	p.Arg147His	1	FALSE	chr19:3113446:G:A	33:chr19:3113446:G:A	0.001515
69_c3-1	69	PTEN	MODERATE	c.443C>A	p.Ala148Glu	1	FALSE	chr10:89692959:C:A	33:chr10:89692959:C:A	0.001761
69_c3-1	69	KIT	MODERATE	c.1493G>A	p.Gly498Asp	1	FALSE	chr4:55592169:G:A	33:chr4:55592169:G:A	0.001646
69_c3-1	69	FGFR1	MODIFIER; MODERATE	c.-63G>T; c.129G>T; c.30G>T	; p.Trp43Cys; p.Trp10Cys	1	FALSE	chr8:38314935:C:A	33:chr8:38314935:C:A	0.001296
69_c3-1	69	KIT	MODERATE	c.2374A>G; c.2386A>G	p.Arg792Gly; p.Arg796Gly	3	FALSE	chr4:55599260:A:G	33:chr4:55599260:A:G	0.001843
69_c3-1	69	RET	MODERATE	c.1690A>C	p.Thr564Pro	1	FALSE	chr10:43608342:A:C	33:chr10:43608342:A:C	0.004894
73_c2-1	73	KIT	MODERATE	c.1978G>A; c.1990G>A	p.Gly660Arg; p.Gly664Arg	1	FALSE	chr4:55594287:G:A	34:chr4:55594287:G:A	0.002714
73_c2-1	73	TP53	MODIFIER; MODERATE	c.-13G>T; c.105G>T; c.-279G>T; c.-360G>T	; p.Leu35Phe	2	FALSE	chr17:7579582:C:A	34:chr17:7579582:C:A	0.003442
73_c2-1	73	PIK3CA	MODERATE	c.365G>A	p.Gly122Asp	2	FALSE	chr3:178917490:G:A	34:chr3:178917490:G:A	0.003077
73_c2-1	73	CTNNB1	MODERATE	c.1166C>T	p.Ser389Leu	0	FALSE	chr3:41274916:C:T	34:chr3:41274916:C:T	0.002433
73_c2-1	73	CTNNB1	MODERATE	c.1564G>A	p.Ala522Thr	0	FALSE	chr3:41275669:G:A	34:chr3:41275669:G:A	0.002656
73_c2-1	73	PIK3CA	MODERATE	c.1645G>A	p.Asp549Asn	4	FALSE	chr3:178936103:G:A	34:chr3:178936103:G:A	0.002937

73_c2-1	73	TP53	MODERATE	c.116A>G; c.35A>G; c.395A>G; c.512A>G	p.Glu39Gly; p.Glu12Gly; p.Glu132Gly; p.Glu171Gly	3	FALSE	chr17:7578418:T:C	34:chr17:7578418:T:C	0.00458
73_c2-1	73	ROS1	MODERATE	c.5391G>T	p.Gln1797His	1	FALSE	chr6:117647553:C:A	34:chr6:117647553:C:A	0.002581
73_c2-1	73	DDR2	MODERATE	c.263A>G	p.Gln88Arg	1	FALSE	chr1:162724491:A:G	34:chr1:162724491:A:G	0.00299
73_c2-1	73	DDR2	MODERATE	c.1598C>A	p.Thr533Lys	1	FALSE	chr1:162741907:C:A	34:chr1:162741907:C:A	0.002646
73_c2-1	73	TP53	MODIFIER; MODERATE	c.-30A>G; c.331A>G; c.448A>G; c.52A>G	; p.Thr111Ala; p.Thr150Ala; p.Thr18Ala	1	FALSE	chr17:7578482:T:C	34:chr17:7578482:T:C	0.003063
73_c2-1	73	NF1	MODERATE	c.2695T>G	p.Leu899Val	3	FALSE	chr17:29556328:T:G	34:chr17:29556328:T:G	0.050536
73_c2-1	73	ALK	MODERATE	c.3911G>A	p.Gly1304Glu	1	FALSE	chr2:29430064:C:T	34:chr2:29430064:C:T	0.003472
73_bl-1	73	TP53	MODIFIER; MODERATE	c.*122G>A; c.*34G>A; c.1015G>A; c.538G>A; c.619G>A; c.898G>A	; p.Glu339Lys; p.Glu180Lys; p.Glu207Lys; p.Glu300Lys	18	FALSE	chr17:7574012:C:T	45:chr17:7574012:C:T	0.001408
73_bl-1	73	EGFR	MODERATE	c.3235G>A	p.Glu1079Lys	1	FALSE	chr7:55270282:G:A	45:chr7:55270282:G:A	0.001569
73_bl-1	73	TP53	MODERATE	c.152C>T; c.431C>T; c.548C>T; c.71C>T	p.Ser51Leu; p.Ser144Leu; p.Ser183Leu; p.Ser24Leu	26	FALSE	chr17:7578382:G:A	45:chr17:7578382:G:A	0.002306
73_bl-1	73	PIK3CA	MODERATE	c.1633G>A	p.Glu545Lys	1189	FALSE	chr3:178936091:G:A	45:chr3:178936091:G:A	0.001808
73_bl-1	73	EPHA3	MODERATE	c.1123C>T	p.Pro375Ser	0	FALSE	chr3:89391057:C:T	45:chr3:89391057:C:T	0.001481

73_bl-1	73	CWH43	MODERATE	c.112G>A; c.31G>A	p.Glu38Lys; p.Glu11Lys	0	FALSE	chr4:48990562:G:A	45:chr4:48990562:G:A	0.001641
73_bl-1	73	NF1	MODERATE	c.5602G>A; c.5665G>A	p.Glu1868Lys; p.Glu1889Lys	1	FALSE	chr17:29657369:G:A	45:chr17:29657369:G:A	0.00188
73_bl-1	73	PIK3R1	MODERATE	c.1147G>A; c.1237G>A; c.2047G>A; c.958G>A	p.Glu383Lys; p.Glu413Lys; p.Glu683Lys; p.Glu320Lys	2	FALSE	chr5:67593301:G:A	45:chr5:67593301:G:A	0.001526
73_bl-1	73	BRAF	MODERATE	c.1405G>A	p.Gly469Arg	11	FALSE	chr7:140481403:C:T	45:chr7:140481403:C:T	0.001992
73_bl-1	73	NF1	MODERATE	c.7733C>T; c.7796C>T	p.Ser2578Phe; p.Ser2599Phe	1	FALSE	chr17:29684035:C:T	45:chr17:29684035:C:T	0.001652
73_bl-1	73	HGF	HIGH	c.1230G>A; c.1245G>A	p.Trp410*; p.Trp415*	0	FALSE	chr7:81350087:C:T	45:chr7:81350087:C:T	0.001963
73_bl-1	73	BRAF	MODERATE	c.305C>T	p.Ser102Phe	1	FALSE	chr7:140534608:G:A	45:chr7:140534608:G:A	0.001608
73_bl-1	73	PIK3CA	MODERATE	c.3052G>A	p.Asp1018Asn	4	FALSE	chr3:178951997:G:A	45:chr3:178951997:G:A	0.001579
73_bl-1	73	PIK3CA	MODERATE	c.115G>A	p.Glu39Lys	7	FALSE	chr3:178916728:G:A	45:chr3:178916728:G:A	0.001549
73_bl-1	73	PTEN	MODERATE	c.389G>A	p.Arg130Gln	89	FALSE	chr10:89692905:G:A	45:chr10:89692905:G:A	0.00173
73_bl-1	73	BRAF	MODERATE	c.1406G>A	p.Gly469Glu	38	FALSE	chr7:140481402:C:T	45:chr7:140481402:C:T	0.003033
73_bl-1	73	CWH43	MODERATE	c.731C>T; c.812C>T	p.Ser244Leu; p.Ser271Leu	0	FALSE	chr4:49005761:C:T	45:chr4:49005761:C:T	0.001696
73_bl-1	73	PTEN	HIGH	c.733C>T	p.Gln245*	10	FALSE	chr10:89717708:C:T	45:chr10:89717708:C:T	0.001984
73_bl-1	73	BRAF	HIGH	c.1906C>T	p.Gln636*	2	FALSE	chr7:140449173:G:A	45:chr7:140449173:G:A	0.001965
73_bl-1	73	ALK	MODERATE	c.2024C>T	p.Pro675Leu	1	FALSE	chr2:29497982:G:A	45:chr2:29497982:G:A	0.002191
73_bl-1	73	BRAF	MODERATE	c.1345G>A	p.Asp449Asn	1	FALSE	chr7:140481463:C:T	45:chr7:140481463:C:T	0.001711
73_bl-1	73	NF1	MODERATE	c.8070G>T; c.8133G>T	p.Leu2690Phe; p.Leu2711Phe	1	FALSE	chr17:29686006:G:T	45:chr17:29686006:G:T	0.009074

73_bl-1	73	HOXD-AS2; HOXD8	MODIFIER; MODERATE	n.*692C>T; c.304G>A; c.853G>A; c.856G>A	; p.Glu102Lys; p.Glu285Lys; p.Glu286Lys	0	FALSE	chr2:176996323:G:A	45:chr2:176996323:G:A	0.001544
73_bl-1	73	TP53	MODERATE	c.257G>A; c.338G>A; c.617G>A; c.734G>A	p.Gly86Asp; p.Gly113Asp; p.Gly206Asp; p.Gly245Asp	126	FALSE	chr17:7577547:C:T	45:chr17:7577547:C:T	0.001661
73_bl-1	73	TP53	MODIFIER; MODERATE	c.-9G>T; c.352G>T; c.469G>T; c.73G>T	; p.Val118Phe; p.Val157Phe; p.Val25Phe	169	FALSE	chr17:7578461:C:A	45:chr17:7578461:C:A	0.001753
73_bl-1	73	KIT	MODERATE	c.217G>A	p.Glu73Lys	1	FALSE	chr4:55561827:G:A	45:chr4:55561827:G:A	0.001474
73_bl-1	73	EPHA3	MODERATE	c.1142G>A	p.Arg381His	0	FALSE	chr3:89391076:G:A	45:chr3:89391076:G:A	0.00149
73_bl-1	73	NF1	MODERATE	c.5294C>T; c.5357C>T	p.Ser1765Leu; p.Ser1786Leu	1	FALSE	chr17:29654605:C:T	45:chr17:29654605:C:T	0.001616
73_bl-1	73	EGFR	MODERATE	c.719G>A	p.Cys240Tyr	1	FALSE	chr7:55220329:G:A	45:chr7:55220329:G:A	0.002392
73_bl-1	73	NF1	MODERATE	c.2614G>A	p.Glu872Lys	1	FALSE	chr17:29556247:G:A	45:chr17:29556247:G:A	0.002299
73_bl-1	73	CTNNB1	MODERATE	c.163G>A	p.Glu55Lys	0	FALSE	chr3:41266166:G:A	45:chr3:41266166:G:A	0.001591
73_bl-1	73	BRAF	MODERATE	c.1385G>A	p.Arg462Lys	2	FALSE	chr7:140481423:C:T	45:chr7:140481423:C:T	0.002742
73_bl-1	73	CTNNB1	MODERATE	c.96C>A	p.Asp32Glu	0	FALSE	chr3:41266099:C:A	45:chr3:41266099:C:A	0.001721
73_bl-1	73	KLLN; PTEN	MODIFIER; MODERATE	c.-951C>T; c.32G>A	; p.Arg11Lys	1	FALSE	chr10:89624258:G:A	45:chr10:89624258:G:A	0.002786
73_bl-1	73	NF1	HIGH	c.5817C>A; c.5880C>A	p.Cys1939*; p.Cys1960*	1	FALSE	chr17:29661923:C:A	45:chr17:29661923:C:A	0.002445
73_bl-1	73	ALK	MODERATE	c.4280C>T	p.Ser1427Phe	2	FALSE	chr2:29416673:G:A	45:chr2:29416673:G:A	0.001969
73_bl-1	73	EPHA3	HIGH	c.406C>T	p.Arg136*	0	FALSE	chr3:89259262:C:T	45:chr3:89259262:C:T	0.001667

73_bl-1	73	EGFR	MODERATE	c.844G>A	p.Glu282Lys	1	FALSE	chr7:55221800:G:A	45:chr7:55221800:G:A	0.001457
73_bl-1	73	NF1	HIGH	c.1105C>T	p.Gln369*	2	FALSE	chr17:29528097:C:T	45:chr17:29528097:C:T	0.004535
73_bl-1	73	GAPDH; IFFO1	MODERATE; MODIFIER	c.503C>T; c.629C>T; c.*1743G>A; c.*1746G>A; c.*1770G>A; n.*2798G>A	p.Ser168Phe; p.Ser210Phe;	0	FALSE	chr12:6646853:C:T	45:chr12:6646853:C:T	0.002028
73_bl-1	73	PTEN	HIGH	c.511C>T	p.Gln171*	13	FALSE	chr10:89711893:C:T	45:chr10:89711893:C:T	0.002132
73_bl-1	73	EPHA3	MODERATE	c.311G>A	p.Arg104Gln	0	FALSE	chr3:89259167:G:A	45:chr3:89259167:G:A	0.001627
73_bl-1	73	HGF	HIGH	c.526C>T; c.541C>T	p.Arg176*; p.Arg181*	0	FALSE	chr7:81381520:G:A	45:chr7:81381520:G:A	0.001552
73_bl-1	73	MET	MODERATE	c.2980G>A; c.3034G>A	p.Glu994Lys; p.Glu1012Lys	1	FALSE	chr7:116411995:G:A	45:chr7:116411995:G:A	0.00172
73_bl-1	73	TP53	MODERATE; MODIFIER	c.254G>A; c.371G>A; c.-279G>A; c.-360G>A	p.Cys85Tyr; p.Cys124Tyr;	3	FALSE	chr17:7579316:C:T	45:chr17:7579316:C:T	0.001805
73_bl-1	73	CWH43	MODERATE	c.415G>A; c.496G>A	p.Asp139Asn; p.Asp166Asn	0	FALSE	chr4:48994092:G:A	45:chr4:48994092:G:A	0.002215
73_bl-1	73	CTNNB1	MODERATE	c.125C>A	p.Thr42Lys	0	FALSE	chr3:41266128:C:A	45:chr3:41266128:C:A	0.001661
73_bl-1	73	PIK3CA	MODERATE	c.277C>T	p.Arg93Trp	24	FALSE	chr3:178916890:C:T	45:chr3:178916890:C:T	0.0016
73_bl-1	73	NF1	MODIFIER; HIGH	c.*2165G>A; c.2088G>A	; p.Trp696*	1	FALSE	chr17:29553539:G:A	45:chr17:29553539:G:A	0.001726
73_bl-1	73	PIK3CA	MODERATE	c.56G>A	p.Arg19Lys	1	FALSE	chr3:178916669:G:A	45:chr3:178916669:G:A	0.001581
73_bl-1	73	PTEN	MODERATE	c.424C>T	p.Arg142Trp	6	FALSE	chr10:89692940:C:T	45:chr10:89692940:C:T	0.001779
73_bl-1	73	EPHA3	MODERATE	c.1916G>A	p.Arg639His	0	FALSE	chr3:89468382:G:A	45:chr3:89468382:G:A	0.002225

73_bl-1	73	CTNNB1	MODERATE	c.160G>A	p.Glu54Lys	0	FALSE	chr3:41266163:G:A	45:chr3:41266163:G:A	0.001584
49_c4-1	49	TP53	MODIFIER; MODERATE	c.-3G>T; c.358G>T; c.475G>T; c.79G>T	; p.Ala120Ser; p.Ala159Ser; p.Ala27Ser	23	FALSE	chr17:7578455:C:A	46:chr17:7578455:C:A	0.002209
49_c4-1	49	EGFR	MODERATE	c.1159C>A	p.Leu387Met	1	FALSE	chr7:55224477:C:A	46:chr7:55224477:C:A	0.000884
49_c4-1	49	PIK3R1	MODERATE	c.902G>A	p.Arg301Gln	2	FALSE	chr5:67576820:G:A	46:chr5:67576820:G:A	0.001051
49_c4-1	49	BRAF	MODERATE	c.1202C>T	p.Thr401Ile	1	FALSE	chr7:140482933:G:A	46:chr7:140482933:G:A	0.00136
49_c4-1	49	ALK	MODERATE	c.3455T>C	p.Leu1152Pro	1	FALSE	chr2:29445270:A:G	46:chr2:29445270:A:G	0.001611
49_c4-1	49	NF1	HIGH	c.5817C>A; c.5880C>A	p.Cys1939*; p.Cys1960*	1	FALSE	chr17:29661923:C:A	46:chr17:29661923:C:A	0.001206
49_c4-1	49	ROS1	MODERATE	c.5651G>T	p.Arg1884Ile	1	FALSE	chr6:117642548:C:A	46:chr6:117642548:C:A	0.001009
49_c4-1	49	FGFR1	MODIFIER; MODERATE	c.92-1373C>T; c.208C>T; c.232C>T; c.331C>T	; p.Arg70Cys; p.Arg78Cys; p.Arg111Cys	1	FALSE	chr8:38287326:G:A	46:chr8:38287326:G:A	0.000926
49_c4-1	49	TP53	MODIFIER; MODERATE	c.-9G>T; c.352G>T; c.469G>T; c.73G>T	; p.Val118Phe; p.Val157Phe; p.Val25Phe	169	FALSE	chr17:7578461:C:A	46:chr17:7578461:C:A	0.002775
49_c4-1	49	DDR2	MODERATE	c.313C>A	p.Arg105Ser	2	FALSE	chr1:162724541:C:A	46:chr1:162724541:C:A	0.002226
49_c4-1	49	CWH43	MODERATE	c.1972G>A; c.2053G>A	p.Glu658Lys; p.Glu685Lys	0	FALSE	chr4:49063860:G:A	46:chr4:49063860:G:A	0.001064
49_c4-1	49	TP53	HIGH	c.109C>T; c.190C>T; c.469C>T; c.586C>T	p.Arg37*; p.Arg64*; p.Arg157*; p.Arg196*	191	FALSE	chr17:7578263:G:A	46:chr17:7578263:G:A	0.000844
49_c4-1	49	KRAS	HIGH	c.292G>T	p.Glu98*	1	FALSE	chr12:25378706:C:A	46:chr12:25378706:C:A	0.001139

49_c4-1	49	PIK3CA	MODERATE	c.478C>A	p.His160Asn	1	FALSE	chr3:178917603:C:A	46:chr3:178917603:C:A	0.002195
49_c4-1	49	TP53	MODERATE	c.234G>T; c.315G>T; c.594G>T; c.711G>T	p.Met78Ile; p.Met105Ile; p.Met198Ile; p.Met237Ile	81	FALSE	chr17:7577570:C:A	46:chr17:7577570:C:A	0.001465
49_c4-1	49	PTEN	MODERATE	c.729C>A	p.Phe243Leu	1	FALSE	chr10:89717704:C:A	46:chr10:89717704:C:A	0.000996
49_c4-1	49	TP53	MODERATE	c.127C>T; c.208C>T; c.487C>T; c.604C>T	p.Arg43Cys; p.Arg70Cys; p.Arg163Cys; p.Arg202Cys	6	FALSE	chr17:7578245:G:A	46:chr17:7578245:G:A	0.000853
49_c4-1	49	ALK	MODERATE	c.4192C>T	p.Pro1398Ser	1	FALSE	chr2:29416761:G:A	46:chr2:29416761:G:A	0.001008
49_c4-1	49	FGFR1	MODIFIER; MODERATE	c.-85G>T; c.107G>T; c.8G>T	; p.Ser36Ile; p.Ser3Ile	1	FALSE	chr8:38314957:C:A	46:chr8:38314957:C:A	0.000898
49_c4-1	49	MET	MODERATE	c.1640G>A	p.Arg547Gln	1	FALSE	chr7:116381018:G:A	46:chr7:116381018:G:A	0.000835
49_c4-1	49	MET	MODERATE	c.487T>C	p.Ser163Pro	1	FALSE	chr7:116339625:T:C	46:chr7:116339625:T:C	0.001178
49_c4-1	49	ERBB2	MODERATE; MODIFIER	c.322C>T; c.367C>T; c.412C>T; n.736C>T	p.Arg108Trp; p.Arg123Trp; p.Arg138Trp;	1	FALSE	chr17:37864760:C:T	46:chr17:37864760:C:T	0.000804
49_c4-1	49	HGF	MODERATE	c.808G>T; c.823G>T	p.Asp270Tyr; p.Asp275Tyr	0	FALSE	chr7:81372711:C:A	46:chr7:81372711:C:A	0.001049
49_c4-1	49	NF1	MODERATE	c.4321C>T; c.4384C>T	p.Arg1441Trp; p.Arg1462Trp	1	FALSE	chr17:29586101:C:T	46:chr17:29586101:C:T	0.000937
49_c4-1	49	BRAF	MODERATE	c.386C>T	p.Ser129Leu	2	FALSE	chr7:140534527:G:A	46:chr7:140534527:G:A	0.000802
49_c4-1	49	PTEN	MODERATE	c.392C>A	p.Thr131Asn	2	FALSE	chr10:89692908:C:A	46:chr10:89692908:C:A	0.001783
49_c4-1	49	HGF	MODERATE	c.5G>T	p.Trp2Leu	0	FALSE	chr7:81399283:C:A	46:chr7:81399283:C:A	0.000977

49_c4-1	49	RET	MODERATE	c.1799G>A	p.Arg600Gln	1	FALSE	chr10:43609043:G:A	46:chr10:43609043:G:A	0.001303
49_c4-1	49	CTNNB1	MODERATE	c.884C>A	p.Ala295Asp	0	FALSE	chr3:41267300:C:A	46:chr3:41267300:C:A	0.001897
49_c4-1	49	KIT	MODERATE	c.1485C>A	p.Asn495Lys	1	FALSE	chr4:55592161:C:A	46:chr4:55592161:C:A	0.001007
49_c4-1	49	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2527G>A; n.-1C>T	p.Val843Ile;	6	FALSE	chr7:55259469:G:A	46:chr7:55259469:G:A	0.001217
49_c4-1	49	ALK	MODERATE	c.619G>A	p.Ala207Thr	1	FALSE	chr2:30142907:C:T	46:chr2:30142907:C:T	0.00144
49_c4-1	49	AKT3	MODERATE	c.44G>T	p.Arg15Met	0	FALSE	chr1:244006429:C:A	46:chr1:244006429:C:A	0.001088
49_c4-1	49	KRAS	MODERATE	c.35G>A	p.Gly12Asp	11213	FALSE	chr12:25398284:C:T	46:chr12:25398284:C:T	0.001416
49_c4-1	49	KRAS	MODERATE	c.218G>T	p.Arg73Met	1	FALSE	chr12:25380240:C:A	46:chr12:25380240:C:A	0.000878
49_c4-1	49	TP53	MODIFIER; MODERATE	c.-17G>T; c.344G>T; c.461G>T; c.65G>T	; p.Gly115Val; p.Gly154Val; p.Gly22Val	39	FALSE	chr17:7578469:C:A	46:chr17:7578469:C:A	0.001117
49_c4-1	49	FGFR1	MODERATE	c.1013C>T; c.1019C>T; c.1112C>T; c.746C>T; c.752C>T; c.995C>T	p.Thr338Met; p.Thr340Met; p.Thr371Met; p.Thr249Met; p.Thr251Met; p.Thr332Met	2	FALSE	chr8:38279377:G:A	46:chr8:38279377:G:A	0.001534
49_c4-1	49	CTNNB1	MODERATE	c.1972G>T	p.Val658Phe	0	FALSE	chr3:41278096:G:T	46:chr3:41278096:G:T	0.002271
49_c4-1	49	FGFR1	MODERATE	c.475C>T; c.481C>T; c.724C>T; c.742C>T; c.748C>T; c.841C>T	p.Arg159Trp; p.Arg161Trp; p.Arg242Trp; p.Arg248Trp; p.Arg250Trp; p.Arg281Trp	2	FALSE	chr8:38282215:G:A	46:chr8:38282215:G:A	0.000904
49_c4-1	49	EPHA3	MODERATE	c.237C>A	p.Asn79Lys	0	FALSE	chr3:89259093:C:A	46:chr3:89259093:C:A	0.001363

49_c4-1	49	PTEN	MODERATE	c.443C>A	p.Ala148Glu	1	FALSE	chr10:89692959:C:A	46:chr10:89692959:C:A	0.001013
49_c4-1	49	TP53	MODERATE; MODIFIER	c.134C>T; c.251C>T; c.-279C>T; c.-360C>T	p.Ala45Val; p.Ala84Val;	4	FALSE	chr17:7579436:G:A	46:chr17:7579436:G:A	0.00126
49_c4-1	49	EPHA3	MODERATE	c.934C>T	p.Arg312Trp	0	FALSE	chr3:89390185:C:T	46:chr3:89390185:C:T	0.000909
49_c4-1	49	PTEN	HIGH	c.720C>A	p.Tyr240*	3	FALSE	chr10:89717695:C:A	46:chr10:89717695:C:A	0.000971
49_c4-1	49	TP53	HIGH	c.439C>T; c.520C>T; c.799C>T; c.916C>T	p.Arg147*; p.Arg174*; p.Arg267*; p.Arg306*	167	FALSE	chr17:7577022:G:A	46:chr17:7577022:G:A	0.000886
49_c4-1	49	PIK3CA	MODERATE	c.518C>A	p.Ser173Tyr	1	FALSE	chr3:178917643:C:A	46:chr3:178917643:C:A	0.001351
49_c4-1	49	EGFR	MODERATE	c.442G>A	p.Val148Met	1	FALSE	chr7:55214316:G:A	46:chr7:55214316:G:A	0.001807
68_c3-2	68	RAC1	MODERATE	c.203G>A	p.Arg68His	0	FALSE	chr7:6431650:G:A	47:chr7:6431650:G:A	0.001008
68_c3-2	68	TP53	LOW; MODIFIER; MODERATE	c.-6C>T; c.355C>T; c.472C>T; c.76C>T	; p.Arg119Cys; p.Arg158Cys; p.Arg26Cys	17	FALSE	chr17:7578458:G:A	47:chr17:7578458:G:A	0.002717
68_c3-2	68	EGFR	MODERATE	c.3352G>A	p.Ala1118Thr	3	FALSE	chr7:55273029:G:A	47:chr7:55273029:G:A	0.000809
68_c3-2	68	TP53	MODERATE	c.338T>A; c.419T>A; c.698T>A; c.815T>A	p.Val113Glu; p.Val140Glu; p.Val233Glu; p.Val272Glu	9	FALSE	chr17:7577123:A:T	47:chr17:7577123:A:T	0.001151
68_c3-2	68	TP53	MODIFIER; MODERATE	c.-3G>T; c.358G>T; c.475G>T; c.79G>T	; p.Ala120Ser; p.Ala159Ser; p.Ala27Ser	23	FALSE	chr17:7578455:C:A	47:chr17:7578455:C:A	0.001335
68_c3-2	68	PTEN	MODERATE	c.421C>A	p.His141Asn	2	FALSE	chr10:89692937:C:A	47:chr10:89692937:C:A	0.001013

68_c3-2	68	TP53	MODERATE	c.119T>G; c.38T>G; c.398T>G; c.515T>G	p.Val40Gly; p.Val13Gly; p.Val133Gly; p.Val172Gly	12	FALSE	chr17:7578415:A:C	47:chr17:7578415:A:C	0.001283
68_c3-2	68	PIK3CA	MODERATE	c.178C>A	p.Gln60Lys	1	FALSE	chr3:178916791:C:A	47:chr3:178916791:C:A	0.000727
68_c3-2	68	PTEN	MODERATE	c.506C>A	p.Pro169His	1	FALSE	chr10:89711888:C:A	47:chr10:89711888:C:A	0.00111
68_c3-2	68	TP53	MODERATE	c.128G>A; c.407G>A; c.47G>A; c.524G>A	p.Arg43His; p.Arg136His; p.Arg16His; p.Arg175His	979	FALSE	chr17:7578406:C:T	47:chr17:7578406:C:T	0.001262
68_c3-2	68	CTNNB1	MODERATE	c.134C>A	p.Ser45Tyr	0	FALSE	chr3:41266137:C:A	47:chr3:41266137:C:A	0.001453
68_c3-2	68	EPHA3	HIGH	c.1515C>A	p.Tyr505*	0	FALSE	chr3:89448551:C:A	47:chr3:89448551:C:A	0.001684
68_c3-2	68	PIK3R1	MODERATE	c.1145C>T; c.1235C>T; c.2045C>T; c.956C>T	p.Ala382Val; p.Ala412Val; p.Ala682Val; p.Ala319Val	2	FALSE	chr5:67593299:C:T	47:chr5:67593299:C:T	0.001158
68_c3-2	68	PIK3CA	MODERATE	c.1624G>A	p.Glu542Lys	777	FALSE	chr3:178936082:G:A	47:chr3:178936082:G:A	0.026203
68_c3-2	68	BRAF	MODERATE	c.2044C>T	p.Arg682Trp	1	FALSE	chr7:140439695:G:A	47:chr7:140439695:G:A	0.000962
68_c3-2	68	EPHA3	MODERATE	c.497C>A	p.Thr166Asn	0	FALSE	chr3:89259353:C:A	47:chr3:89259353:C:A	0.000827
68_c3-2	68	HGF	MODERATE	c.527G>A; c.542G>A	p.Arg176Gln; p.Arg181Gln	0	FALSE	chr7:81381519:C:T	47:chr7:81381519:C:T	0.000894
68_c3-2	68	DDR2	MODERATE	c.1418G>A	p.Arg473His	2	FALSE	chr1:162740216:G:A	47:chr1:162740216:G:A	0.000927

68_c3-2	68	FGFR1	MODERATE	c.488G>T; c.494G>T; c.737G>T; c.755G>T; c.761G>T; c.854G>T	p.Arg163Leu; p.Arg165Leu; p.Arg246Leu; p.Arg252Leu; p.Arg254Leu; p.Arg285Leu	1	FALSE	chr8:38282202:C:A	47:chr8:38282202:C:A	0.000896
68_c3-2	68	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2572C>A; n.-1G>T	p.Leu858Met;	8	FALSE	chr7:55259514:C:A	47:chr7:55259514:C:A	0.001157
68_c3-2	68	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2568T>G; n.-1A>C	p.Phe856Leu;	1	FALSE	chr7:55259510:T:G	47:chr7:55259510:T:G	0.001737
68_c3-2	68	PIK3CA	MODERATE	c.3180C>A	p.His1060Gln	2	FALSE	chr3:178952125:C:A	47:chr3:178952125:C:A	0.00067
68_c3-2	68	CTNNB1	MODERATE	c.884C>A	p.Ala295Asp	0	FALSE	chr3:41267300:C:A	47:chr3:41267300:C:A	0.002155
68_c3-2	68	EGFR	MODIFIER; MODERATE	c.*2133G>A; c.*2364G>A; c.2030G>A	; p.Arg677His	5	FALSE	chr7:55240786:G:A	47:chr7:55240786:G:A	0.002114
68_c3-2	68	MET	HIGH	c.2552C>A; c.2606C>A	p.Ser851*; p.Ser869*	1	FALSE	chr7:116403291:C:A	47:chr7:116403291:C:A	0.000962
68_c3-2	68	RET	MODERATE	c.1690A>C	p.Thr564Pro	1	FALSE	chr10:43608342:A:C	47:chr10:43608342:A:C	0.008138
68_c3-2	68	PTEN	MODERATE	c.392C>A	p.Thr131Asn	2	FALSE	chr10:89692908:C:A	47:chr10:89692908:C:A	0.001403
68_c3-2	68	EPHA3	MODERATE	c.2648G>A	p.Arg883Gln	0	FALSE	chr3:89499478:G:A	47:chr3:89499478:G:A	0.001486
68_c3-2	68	PTEN	HIGH	c.720C>A	p.Tyr240*	3	FALSE	chr10:89717695:C:A	47:chr10:89717695:C:A	0.002081
68_c3-2	68	EGFR	MODERATE	c.406C>A	p.Pro136Thr	1	FALSE	chr7:55211163:C:A	47:chr7:55211163:C:A	0.001587
68_c3-2	68	TP53	MODERATE	c.127C>T; c.208C>T; c.487C>T; c.604C>T	p.Arg43Cys; p.Arg70Cys; p.Arg163Cys; p.Arg202Cys	6	FALSE	chr17:7578245:G:A	47:chr17:7578245:G:A	0.00144
68_c3-2	68	ALK	MODERATE	c.3455T>C	p.Leu1152Pro	1	FALSE	chr2:29445270:A:G	47:chr2:29445270:A:G	0.002836

68_c3-2	68	RET	MODERATE	c.2116G>A	p.Val706Met	2	FALSE	chr10:43610164:G:A	47:chr10:43610164:G:A	0.000808
68_c3-2	68	CTNNB1	MODERATE	c.96C>A	p.Asp32Glu	0	FALSE	chr3:41266099:C:A	47:chr3:41266099:C:A	0.00155
68_c3-2	68	CTNNB1	MODERATE	c.110C>A	p.Ser37Tyr	0	FALSE	chr3:41266113:C:A	47:chr3:41266113:C:A	0.001015
68_c3-2	68	DDR2	MODERATE	c.1963G>A	p.Glu655Lys	1	FALSE	chr1:162745548:G:A	47:chr1:162745548:G:A	0.001328
68_c3-2	68	NF1	MODERATE	c.3559C>A	p.Leu1187Ile	1	FALSE	chr17:29560082:C:A	47:chr17:29560082:C:A	0.000966
68_c3-2	68	PTEN	MODERATE	c.443C>A	p.Ala148Glu	1	FALSE	chr10:89692959:C:A	47:chr10:89692959:C:A	0.001801
68_c3-2	68	MAP2K1	MODERATE	c.316G>A	p.Ala106Thr	1	FALSE	chr15:66729108:G:A	47:chr15:66729108:G:A	0.000983
68_c3-2	68	KIT	MODERATE	c.605T>C	p.Leu202Pro	1	FALSE	chr4:55564717:T:C	47:chr4:55564717:T:C	0.001056
68_c3-2	68	PIK3CA	MODERATE	c.223C>A	p.Gln75Lys	1	FALSE	chr3:178916836:C:A	47:chr3:178916836:C:A	0.000719
68_c3-2	68	TP53	MODERATE	c.269G>T; c.350G>T; c.629G>T; c.746G>T	p.Arg90Met; p.Arg117Met; p.Arg210Met; p.Arg249Met	36	FALSE	chr17:7577535:C:A	47:chr17:7577535:C:A	0.057018
68_c3-2	68	TP53	MODERATE	c.234G>T; c.315G>T; c.594G>T; c.711G>T	p.Met78Ile; p.Met105Ile; p.Met198Ile; p.Met237Ile	81	FALSE	chr17:7577570:C:A	47:chr17:7577570:C:A	0.001182
68_c3-2	68	CTNNB1	MODERATE	c.125C>A	p.Thr42Lys	0	FALSE	chr3:41266128:C:A	47:chr3:41266128:C:A	0.001977
68_c3-2	68	EGFR	MODERATE	c.971G>A	p.Arg324His	3	FALSE	chr7:55223604:G:A	47:chr7:55223604:G:A	0.001635
68_c3-2	68	HOXD-AS2; HOXD8	MODIFIER; MODERATE	n.*692G>T; c.105C>A; c.654C>A; c.657C>A	; p.Asn35Lys; p.Asn218Lys; p.Asn219Lys	0	FALSE	chr2:176996124:C:A	47:chr2:176996124:C:A	0.001446

68_c3-2	68	TP53	MODERATE	c.270G>T; c.351G>T; c.630G>T; c.747G>T	p.Arg90Ser; p.Arg117Ser; p.Arg210Ser; p.Arg249Ser	318	FALSE	chr17:7577534:C:A	47:chr17:7577534:C:A	0.056911
68_c3-2	68	KIT	MODERATE	c.2854C>T; c.2866C>T	p.Arg952Trp; p.Arg956Trp	3	FALSE	chr4:55604658:C:T	47:chr4:55604658:C:T	0.001826
68_c3-2	68	NF1	MODERATE	c.5458C>A; c.5521C>A	p.Gln1820Lys; p.Gln1841Lys	3	FALSE	chr17:29654769:C:A	47:chr17:29654769:C:A	0.000823
68_c3-2	68	KIT	MODERATE	c.148G>A	p.Val50Met	4	FALSE	chr4:55561758:G:A	47:chr4:55561758:G:A	0.000827
68_c3-2	68	PIK3CA	MODERATE	c.518C>A	p.Ser173Tyr	1	FALSE	chr3:178917643:C:A	47:chr3:178917643:C:A	0.001328
68_c3-2	68	CTNNB1	MODERATE	c.1346G>A	p.Arg449His	0	FALSE	chr3:41275180:G:A	47:chr3:41275180:G:A	0.001248
68_c3-2	68	TP53	MODERATE	c.178C>T; c.259C>T; c.538C>T; c.655C>T	p.Pro60Ser; p.Pro87Ser; p.Pro180Ser; p.Pro219Ser	4	FALSE	chr17:7578194:G:A	47:chr17:7578194:G:A	0.005546
68_c3-2	68	HGF	HIGH	c.1993G>T; c.2008G>T	p.Glu665*; p.Glu670*	0	FALSE	chr7:81334708:C:A	47:chr7:81334708:C:A	0.001585
68_c3-2	68	PIK3CA	MODERATE	c.1255C>A	p.His419Asn	1	FALSE	chr3:178927977:C:A	47:chr3:178927977:C:A	0.001513
68_c3-2	68	KIT	MODERATE	c.1156G>A	p.Glu386Lys	1	FALSE	chr4:55575630:G:A	47:chr4:55575630:G:A	0.000948
68_c3-2	68	NF1	MODERATE	c.6405C>A; c.6468C>A	p.Phe2135Leu; p.Phe2156Leu	1	FALSE	chr17:29664426:C:A	47:chr17:29664426:C:A	0.001044
75_c3-1	75	RET	MODERATE	c.1771G>A	p.Val591Ile	1	FALSE	chr10:43609015:G:A	48:chr10:43609015:G:A	0.002088
75_c3-1	75	PTEN	MODERATE	c.443C>A	p.Ala148Glu	1	FALSE	chr10:89692959:C:A	48:chr10:89692959:C:A	0.002242
75_c3-1	75	TP53	MODERATE	c.136C>T; c.415C>T; c.532C>T; c.55C>T	p.His46Tyr; p.His139Tyr; p.His178Tyr; p.His19Tyr	7	FALSE	chr17:7578398:G:A	48:chr17:7578398:G:A	0.001729

75_c3-1	75	EGFR	MODIFIER; MODERATE	c.*2364C>T; c.2174C>T	; p.Thr725Met	2	FALSE	chr7:55241726:C:T	48:chr7:55241726:C:T	0.001706
75_c3-1	75	PIK3CA	MODERATE	c.473C>T	p.Ser158Leu	1	FALSE	chr3:178917598:C:T	48:chr3:178917598:C:T	0.002028
75_c3-1	75	TP53	MODIFIER; MODERATE	c.-3G>T; c.358G>T; c.475G>T; c.79G>T	; p.Ala120Ser; p.Ala159Ser; p.Ala27Ser	23	FALSE	chr17:7578455:C:A	48:chr17:7578455:C:A	0.001825
75_c3-1	75	RET	MODERATE	c.1690A>C	p.Thr564Pro	1	FALSE	chr10:43608342:A:C	48:chr10:43608342:A:C	0.003058
75_c3-1	75	AKT1	MODERATE	c.1108C>T	p.Arg370Cys	1	FALSE	chr14:105239279:G:A	48:chr14:105239279:G:A	0.001696
75_c3-1	75	DDR2	MODERATE	c.664G>A	p.Gly222Arg	2	FALSE	chr1:162725552:G:A	48:chr1:162725552:G:A	0.001818
75_c3-1	75	PIK3R1	MODERATE	c.1709T>C; c.620T>C; c.809T>C; c.899T>C	p.Leu570Pro; p.Leu207Pro; p.Leu270Pro; p.Leu300Pro	2	FALSE	chr5:67591116:T:C	48:chr5:67591116:T:C	0.00198
75_c3-1	75	TP53	MODERATE	c.364G>A; c.481G>A; c.4G>A; c.85G>A	p.Ala122Thr; p.Ala161Thr; p.Ala2Thr; p.Ala29Thr	53	FALSE	chr17:7578449:C:T	48:chr17:7578449:C:T	0.00185
75_c3-1	75	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2300C>T; n.1262G>A	p.Ala767Val;	5	FALSE	chr7:55249002:C:T	48:chr7:55249002:C:T	0.001311
75_c3-1	75	PIK3CA	MODERATE	c.1255C>A	p.His419Asn	1	FALSE	chr3:178927977:C:A	48:chr3:178927977:C:A	0.003759
75_c3-1	75	KIT	MODERATE	c.1156G>A	p.Glu386Lys	1	FALSE	chr4:55575630:G:A	48:chr4:55575630:G:A	0.003322
75_c3-1	75	TP53	MODERATE	c.497G>T; c.578G>T; c.857G>T; c.974G>T	p.Gly166Val; p.Gly193Val; p.Gly286Val; p.Gly325Val	1	FALSE	chr17:7576872:C:A	48:chr17:7576872:C:A	0.001878
75_c3-1	75	PIK3CA	MODERATE	c.518C>A	p.Ser173Tyr	1	FALSE	chr3:178917643:C:A	48:chr3:178917643:C:A	0.00191
75_c3-1	75	HRAS; LRRC56	MODERATE; MODIFIER	c.175G>A; c.-506C>T	p.Ala59Thr;	2	FALSE	chr11:533881:C:T	48:chr11:533881:C:T	0.001691

75_c3-1	75	EGFR	MODIFIER; MODERATE	c.*1464C>A; c.1476C>A	; p.Ser492Arg	4	FALSE	chr7:55228009:C:A	48:chr7:55228009:C:A	0.002035
62_c2-2	62	PTEN	MODERATE	c.443C>A	p.Ala148Glu	1	FALSE	chr10:89692959:C:A	50:chr10:89692959:C:A	0.001718
62_c2-2	62	TP53	MODERATE	c.126G>T; c.207G>T; c.486G>T; c.603G>T	p.Leu42Phe; p.Leu69Phe; p.Leu162Phe; p.Leu201Phe	4	FALSE	chr17:7578246:C:A	50:chr17:7578246:C:A	0.000876
62_c2-2	62	ALK	MODERATE	c.2431G>A	p.Val811Met	2	FALSE	chr2:29456487:C:T	50:chr2:29456487:C:T	0.001757
62_c2-2	62	CTNNB1	MODERATE	c.125C>A	p.Thr42Lys	0	FALSE	chr3:41266128:C:A	50:chr3:41266128:C:A	0.002102
62_c2-2	62	EGFR; EGFR-AS1	LOW; MODIFIER	c.2472C>A; n.-1G>T	p.Gly824Gly;	1	FALSE	chr7:55259414:C:A	50:chr7:55259414:C:A	0.00225
62_c2-2	62	TP53	MODIFIER; HIGH	c.-104A>G; c.-23A>G; c.259-2A>G; c.376-2A>G		19	FALSE	chr17:7578556:T:C	50:chr17:7578556:T:C	0.001131
62_c2-2	62	ROS1	MODERATE	c.5412G>T	p.Lys1804Asn	1	FALSE	chr6:117647532:C:A	50:chr6:117647532:C:A	0.001919
62_c2-2	62	RET	MODERATE	c.2236C>A	p.Leu746Met	1	FALSE	chr10:43612131:C:A	50:chr10:43612131:C:A	0.001064
62_c2-2	62	BRAF	MODERATE	c.1796C>T	p.Thr599Ile	4	FALSE	chr7:140453139:G:A	50:chr7:140453139:G:A	0.000978
62_c2-2	62	TP53	MODIFIER; MODERATE	c.*137A>G; c.*225A>G; c.1001A>G; c.1118A>G; c.641A>G; c.722A>G	; p.Lys334Arg; p.Lys373Arg; p.Lys214Arg; p.Lys241Arg	1	FALSE	chr17:7572991:T:C	50:chr17:7572991:T:C	0.005036
62_c2-2	62	TP53	MODERATE; MODIFIER	c.115G>T; c.232G>T; c.-279G>T; c.-360G>T	p.Ala39Ser; p.Ala78Ser;	1	FALSE	chr17:7579455:C:A	50:chr17:7579455:C:A	0.001595

62_c2-2	62	CTNNB1	MODERATE	c.884C>A	p.Ala295Asp	0	FALSE	chr3:41267300:C:A	50:chr3:41267300:C:A	0.001765
62_c2-2	62	NF1	HIGH	c.1318C>T	p.Arg440*	10	FALSE	chr17:29533315:C:T	50:chr17:29533315:C:T	0.001024
62_c2-2	62	TP53	MODIFIER; MODERATE	c.-5G>T; c.356G>T; c.473G>T; c.77G>T	; p.Arg119Leu; p.Arg158Leu; p.Arg26Leu	80	FALSE	chr17:7578457:C:A	50:chr17:7578457:C:A	0.001543
62_c2-2	62	KIT	MODERATE	c.235C>A	p.Gln79Lys	2	FALSE	chr4:55561845:C:A	50:chr4:55561845:C:A	0.001669
62_c2-2	62	ALK	MODERATE	c.1307C>T	p.Ala436Val	1	FALSE	chr2:29551323:G:A	50:chr2:29551323:G:A	0.000915
62_c2-2	62	TP53	MODERATE	c.126G>T; c.405G>T; c.45G>T; c.522G>T	p.Arg42Ser; p.Arg135Ser; p.Arg15Ser; p.Arg174Ser	2	FALSE	chr17:7578408:C:A	50:chr17:7578408:C:A	0.001818
62_c2-2	62	HGF	HIGH	c.1993G>T; c.2008G>T	p.Glu665*; p.Glu670*	0	FALSE	chr7:81334708:C:A	50:chr7:81334708:C:A	0.002377
62_c2-2	62	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2612C>T; n.-1G>A	p.Ala871Val;	3	FALSE	chr7:55259554:C:T	50:chr7:55259554:C:T	0.001726
62_c2-2	62	EPHA3	MODERATE	c.497C>A	p.Thr166Asn	0	FALSE	chr3:89259353:C:A	50:chr3:89259353:C:A	0.00111
62_c2-2	62	ALK	MODERATE	c.1359G>T	p.Gln453His	1	FALSE	chr2:29551271:C:A	50:chr2:29551271:C:A	0.000942
62_c2-2	62	CSDE1; NRAS	MODIFIER; HIGH	c.*2430G>T; c.*2523G>T; c.*2817G>T; c.*2910G>T; c.*2964G>T; c.*3057G>T; c.187G>T	; p.Glu63*	1	FALSE	chr1:115256524:C:A	50:chr1:115256524:C:A	0.001017
62_c2-2	62	CTNNB1	MODERATE	c.86C>A	p.Ser29Tyr	0	FALSE	chr3:41266089:C:A	50:chr3:41266089:C:A	0.001468

62_c2-2	62	FGFR1	MODERATE	c.1013C>T; c.1019C>T; c.1112C>T; c.746C>T; c.752C>T; c.995C>T	p.Thr338Met; p.Thr340Met; p.Thr371Met; p.Thr249Met; p.Thr251Met; p.Thr332Met	2	FALSE	chr8:38279377:G:A	50:chr8:38279377:G:A	0.001646
62_c2-2	62	MET	MODERATE	c.1690G>A	p.Ala564Thr	1	FALSE	chr7:116381068:G:A	50:chr7:116381068:G:A	0.001252
62_c2-2	62	CSDE1; NRAS	MODIFIER; MODERATE	c.*2430A>G; c.*2523A>G; c.*2817A>G; c.*2910A>G; c.*2964A>G; c.*3057A>G; c.182A>G	; p.Gln61Arg	1103	FALSE	chr1:115256529:T:C	50:chr1:115256529:T:C	0.507299
62_c2-2	62	DDR2	MODERATE	c.313C>A	p.Arg105Ser	2	FALSE	chr1:162724541:C:A	50:chr1:162724541:C:A	0.001437
62_c2-2	62	CWH43	MODERATE	c.209C>T; c.290C>T	p.Ala70Val; p.Ala97Val	0	FALSE	chr4:48993525:C:T	50:chr4:48993525:C:T	0.001102
62_c2-2	62	RPL19	MODERATE	c.452G>A	p.Arg151His	0	FALSE	chr17:37360425:G:A	50:chr17:37360425:G:A	0.001188
62_c2-2	62	EPHA3	MODERATE	c.1132C>A	p.Pro378Thr	0	FALSE	chr3:89391066:C:A	50:chr3:89391066:C:A	0.000453
62_c2-2	62	RET	MODERATE	c.1665C>A	p.Phe555Leu	1	FALSE	chr10:43608317:C:A	50:chr10:43608317:C:A	0.001236
62_c2-2	62	TP53	MODERATE	c.367C>T; c.448C>T; c.727C>T; c.844C>T	p.Arg123Trp; p.Arg150Trp; p.Arg243Trp; p.Arg282Trp	479	FALSE	chr17:7577094:G:A	50:chr17:7577094:G:A	0.00105
62_c2-2	62	PTEN	MODERATE	c.392C>A	p.Thr131Asn	2	FALSE	chr10:89692908:C:A	50:chr10:89692908:C:A	0.001397
62_c2-2	62	KIT	MODERATE	c.2869G>A; c.2881G>A	p.Gly957Ser; p.Gly961Ser	2	FALSE	chr4:55604673:G:A	50:chr4:55604673:G:A	0.000883

62_c2-2	62	PIK3CA	MODERATE	c.518C>A	p.Ser173Tyr	1	FALSE	chr3:178917643:C:A	50:chr3:178917643:C:A	0.001014
62_c2-2	62	DDR2	MODERATE	c.1963G>A	p.Glu655Lys	1	FALSE	chr1:162745548:G:A	50:chr1:162745548:G:A	0.001898
62_c2-2	62	EPHA3	MODERATE	c.1280C>T	p.Ala427Val	0	FALSE	chr3:89391214:C:T	50:chr3:89391214:C:T	0.000501
62_c2-2	62	ERBB2	MODERATE; MODIFIER	c.560G>A; c.605G>A; c.650G>A; n.974G>A	p.Arg187His; p.Arg202His; p.Arg217His;	1	FALSE	chr17:37866345:G:A	50:chr17:37866345:G:A	0.001711
62_c2-2	62	RET	MODERATE	c.1690A>C	p.Thr564Pro	1	FALSE	chr10:43608342:A:C	50:chr10:43608342:A:C	0.002279
62_c2-2	62	PIK3CA	MODERATE	c.193G>A	p.Glu65Lys	1	FALSE	chr3:178916806:G:A	50:chr3:178916806:G:A	0.000882
62_c2-2	62	TP53	MODERATE	c.364G>T; c.445G>T; c.724G>T; c.841G>T	p.Asp122Tyr; p.Asp149Tyr; p.Asp242Tyr; p.Asp281Tyr	28	FALSE	chr17:7577097:C:A	50:chr17:7577097:C:A	0.001587
62_c2-2	62	DDR2	MODERATE	c.691C>A	p.Gln231Lys	1	FALSE	chr1:162729605:C:A	50:chr1:162729605:C:A	0.001705
62_c2-2	62	EPHA3	MODERATE	c.1234G>A	p.Val412Ile	0	FALSE	chr3:89391168:G:A	50:chr3:89391168:G:A	0.000465
62_c2-2	62	PIK3CA	MODERATE	c.3180C>A	p.His1060Gln	2	FALSE	chr3:178952125:C:A	50:chr3:178952125:C:A	0.000762
62_c2-2	62	PIK3CA	HIGH	c.3152G>A	p.Trp1051*	3	FALSE	chr3:178952097:G:A	50:chr3:178952097:G:A	0.000808
62_c2-2	62	PTEN	MODERATE	c.377C>A	p.Ala126Asp	4	FALSE	chr10:89692893:C:A	50:chr10:89692893:C:A	0.00094
62_c2-2	62	ALK	MODERATE	c.4409C>T	p.Ala1470Val	1	FALSE	chr2:29416544:G:A	50:chr2:29416544:G:A	0.000856
62_c2-2	62	KIT	MODERATE	c.2197G>A; c.2209G>A	p.Asp733Asn; p.Asp737Asn	2	FALSE	chr4:55597561:G:A	50:chr4:55597561:G:A	0.00085
62_c2-2	62	PIK3CA	MODERATE	c.478C>A	p.His160Asn	1	FALSE	chr3:178917603:C:A	50:chr3:178917603:C:A	0.000954
62_c2-2	62	EPHA3	HIGH	c.1515C>A	p.Tyr505*	0	FALSE	chr3:89448551:C:A	50:chr3:89448551:C:A	0.001103

62_c2-2		62	TP53	MODERATE	c.340C>T; c.421C>T; c.700C>T; c.817C>T	p.Arg114Cys; p.Arg141Cys; p.Arg234Cys; p.Arg273Cys	601	FALSE	chr17:7577121:G:A	50:chr17:7577121:G:A	0.001004
62_c2-2		62	CWH43	MODERATE	c.1372G>A; c.1453G>A	p.Glu458Lys; p.Glu485Lys	0	FALSE	chr4:49032922:G:A	50:chr4:49032922:G:A	0.001183
62_c2-2		62	EGFR; EGFR-AS1	MODIFIER; MODERATE	c.*2364C>T; c.2258C>T; n.*2821G>A	; p.Pro753Leu	3	FALSE	chr7:55242488:C:T	50:chr7:55242488:C:T	0.001399
62_c2-2		62	TP53	MODERATE	c.125G>A; c.404G>A; c.44G>A; c.521G>A	p.Arg42Lys; p.Arg135Lys; p.Arg15Lys; p.Arg174Lys	5	FALSE	chr17:7578409:C:T	50:chr17:7578409:C:T	0.001823
62_c2-2		62	EGFR	HIGH	c.211C>T	p.Gln71*	1	FALSE	chr7:55210101:C:T	50:chr7:55210101:C:T	0.000986
82_c2-b		82	PIK3CA	MODERATE	c.478C>A	p.His160Asn	1	FALSE	chr3:178917603:C:A	51:chr3:178917603:C:A	0.001855
82_c2-b		82	MET	HIGH	c.1619G>A	p.Trp540*	1	FALSE	chr7:116380997:G:A	51:chr7:116380997:G:A	0.001022
82_c2-b		82	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2353A>C; n.1209T>G	p.Thr785Pro;	1	FALSE	chr7:55249055:A:C	51:chr7:55249055:A:C	0.001043
82_c2-b		82	TP53	MODIFIER; MODERATE	c.-5G>T; c.356G>T; c.473G>T; c.77G>T	; p.Arg119Leu; p.Arg158Leu; p.Arg26Leu	80	FALSE	chr17:7578457:C:A	51:chr17:7578457:C:A	0.001623
82_c2-b		82	NF1	MODERATE	c.2695T>G	p.Leu899Val	3	FALSE	chr17:29556328:T:G	51:chr17:29556328:T:G	0.013265
82_c2-b		82	PTEN	MODERATE	c.443C>A	p.Ala148Glu	1	FALSE	chr10:89692959:C:A	51:chr10:89692959:C:A	0.001356

82_c2-b	82	TP53	MODIFIER; MODERATE	c.*137A>G; c.*225A>G; c.1001A>G; c.1118A>G; c.641A>G; c.722A>G	; p.Lys334Arg; p.Lys373Arg; p.Lys214Arg; p.Lys241Arg	1	FALSE	chr17:7572991:T:C	51:chr17:7572991:T:C	0.003941
82_c2-b	82	FGFR1	MODERATE	c.359C>T; c.365C>T; c.608C>T; c.626C>T; c.632C>T; c.725C>T	p.Ala120Val; p.Ala122Val; p.Ala203Val; p.Ala209Val; p.Ala211Val; p.Ala242Val	1	FALSE	chr8:38283753:G:A	51:chr8:38283753:G:A	0.001173
82_c2-b	82	MET	MODERATE	c.608C>A	p.Ser203Tyr	1	FALSE	chr7:116339746:C:A	51:chr7:116339746:C:A	0.000935
82_c2-b	82	CTNNB1	MODERATE	c.70C>T	p.His24Tyr	0	FALSE	chr3:41266073:C:T	51:chr3:41266073:C:T	0.001229
82_c2-b	82	MET	MODERATE	c.487T>C	p.Ser163Pro	1	FALSE	chr7:116339625:T:C	51:chr7:116339625:T:C	0.000867
82_c2-b	82	HGF	MODERATE	c.1324G>T; c.1339G>T	p.Ala442Ser; p.Ala447Ser	0	FALSE	chr7:81346614:C:A	51:chr7:81346614:C:A	0.001317
82_c2-b	82	FGFR1	MODERATE	c.488G>T; c.494G>T; c.737G>T; c.755G>T; c.761G>T; c.854G>T	p.Arg163Leu; p.Arg165Leu; p.Arg246Leu; p.Arg252Leu; p.Arg254Leu; p.Arg285Leu	1	FALSE	chr8:38282202:C:A	51:chr8:38282202:C:A	0.001087
82_c2-b	82	CTNNB1	MODERATE	c.884C>A	p.Ala295Asp	0	FALSE	chr3:41267300:C:A	51:chr3:41267300:C:A	0.001253
82_c2-b	82	MAP2K1	MODERATE	c.198C>A	p.Asp66Glu	4	FALSE	chr15:66727482:C:A	51:chr15:66727482:C:A	0.001042
82_c2-b	82	HRAS; LRRC56	MODERATE; MODIFIER	c.351G>T; c.-506C>A	p.Lys117Asn;	3	FALSE	chr11:533552:C:A	51:chr11:533552:C:A	0.00142
82_c2-b	82	PIK3CA	MODERATE	c.263G>A	p.Arg88Gln	97	FALSE	chr3:178916876:G:A	51:chr3:178916876:G:A	0.000835

82_c2-b	82	TP53	MODERATE	c.337G>A; c.418G>A; c.697G>A; c.814G>A	p.Val113Met; p.Val140Met; p.Val233Met; p.Val272Met	85	FALSE	chr17:7577124:C:T	51:chr17:7577124:C:T	0.018543
82_c2-b	82	HOXD-AS2; HOXD8	MODIFIER; MODERATE	n.*692G>T; c.22C>A; c.574C>A	; p.Gln8Lys; p.Gln192Lys	0	FALSE	chr2:176995668:C:A	51:chr2:176995668:C:A	0.001838
82_c2-b	82	PTEN	MODERATE	c.392C>A	p.Thr131Asn	2	FALSE	chr10:89692908:C:A	51:chr10:89692908:C:A	0.001121
82_c2-b	82	GAPDH; IFFO1	MODERATE; MODIFIER	c.773G>A; c.899G>A; c.*1743C>T; c.*1746C>T; c.*1770C>T; n.*2798C>T	p.Gly258Asp; p.Gly300Asp; ;	0	FALSE	chr12:6647123:G:A	51:chr12:6647123:G:A	0.001326
82_c2-b	82	BRAF	MODERATE	c.1405G>A	p.Gly469Arg	11	FALSE	chr7:140481403:C:T	51:chr7:140481403:C:T	0.001164
82_c2-b	82	TP53	HIGH	c.109C>T; c.190C>T; c.469C>T; c.586C>T	p.Arg37*; p.Arg64*; p.Arg157*; p.Arg196*	191	FALSE	chr17:7578263:G:A	51:chr17:7578263:G:A	0.093786
82_c2-b	82	PIK3CA	MODERATE	c.1633G>A	p.Glu545Lys	1189	FALSE	chr3:178936091:G:A	51:chr3:178936091:G:A	0.078626
82_c2-b	82	TP53	MODIFIER; MODERATE	c.-3G>T; c.358G>T; c.475G>T; c.79G>T	; p.Ala120Ser; p.Ala159Ser; p.Ala27Ser	23	FALSE	chr17:7578455:C:A	51:chr17:7578455:C:A	0.001599
82_c2-b	82	PTEN	MODERATE	c.407G>A	p.Cys136Tyr	14	FALSE	chr10:89692923:G:A	51:chr10:89692923:G:A	0.001116
82_c2-b	82	TP53	MODERATE; MODIFIER	c.115G>T; c.232G>T; c.-279G>T; c.-360G>T	p.Ala39Ser; p.Ala78Ser;	1	FALSE	chr17:7579455:C:A	51:chr17:7579455:C:A	0.00173

82_c2-b	82	FGFR1	MODERATE	c.1048G>A; c.1066G>A; c.1072G>A; c.1165G>A; c.799G>A; c.805G>A	p.Val350Ile; p.Val356Ile; p.Val358Ile; p.Val389Ile; p.Val267Ile; p.Val269Ile	1	FALSE	chr8:38279324:C:T	51:chr8:38279324:C:T	0.001496
82_c2-b	82	MET	HIGH	c.1249C>T	p.Arg417*	1	FALSE	chr7:116371770:C:T	51:chr7:116371770:C:T	0.001504
82_c2-b	82	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2305G>A; n.1257C>T	p.Val769Met;	3	FALSE	chr7:55249007:G:A	51:chr7:55249007:G:A	0.00094
82_c2-b	82	KIT	MODERATE	c.1485C>A	p.Asn495Lys	1	FALSE	chr4:55592161:C:A	51:chr4:55592161:C:A	0.001263
82_c2-b	82	TP53	MODERATE	c.142G>T; c.223G>T; c.502G>T; c.619G>T	p.Asp48Tyr; p.Asp75Tyr; p.Asp168Tyr; p.Asp207Tyr	1	FALSE	chr17:7578230:C:A	51:chr17:7578230:C:A	0.001206
82_c2-b	82	CTNNB1	MODERATE	c.110C>A	p.Ser37Tyr	0	FALSE	chr3:41266113:C:A	51:chr3:41266113:C:A	0.001176
82_c2-b	82	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2386G>A; n.1176C>T	p.Gly796Ser;	3	FALSE	chr7:55249088:G:A	51:chr7:55249088:G:A	0.001044
82_c2-b	82	PTEN	HIGH	c.720C>A	p.Tyr240*	3	FALSE	chr10:89717695:C:A	51:chr10:89717695:C:A	0.001808
82_c2-b	82	ROS1	MODERATE	c.5412G>T	p.Lys1804Asn	1	FALSE	chr6:117647532:C:A	51:chr6:117647532:C:A	0.001422
82_c2-b	82	RET	MODERATE	c.1690A>C	p.Thr564Pro	1	FALSE	chr10:43608342:A:C	51:chr10:43608342:A:C	0.008677
82_c2-b	82	EGFR; EGFR-AS1	MODIFIER; MODERATE	c.*2364G>A; c.2227G>A; n.*2821C>T	; p.Ala743Thr	3	FALSE	chr7:55242457:G:A	51:chr7:55242457:G:A	0.001071
82_c2-b	82	DDR2	MODERATE	c.907C>A	p.Gln303Lys	1	FALSE	chr1:162731052:C:A	51:chr1:162731052:C:A	0.000876
82_c2-b	82	CWH43	MODERATE	c.1495G>A; c.1576G>A	p.Glu499Lys; p.Glu526Lys	0	FALSE	chr4:49034650:G:A	51:chr4:49034650:G:A	0.001174

48_c2-1	48	NF1	MODERATE	c.8170G>A; c.8233G>A	p.Gly2724Arg; p.Gly2745Arg	2	FALSE	chr17:29687577:G:A	52:chr17:29687577:G:A	0.002096
48_c2-1	48	PHLPP1	MODERATE	c.2197G>A	p.Val733Ile	0	FALSE	chr18:60562374:G:A	52:chr18:60562374:G:A	0.002384
48_c2-1	48	PTEN	MODERATE	c.421C>A	p.His141Asn	2	FALSE	chr10:89692937:C:A	52:chr10:89692937:C:A	0.003233
48_c2-1	48	TP53	MODERATE	c.367C>T; c.448C>T; c.727C>T; c.844C>T	p.Arg123Trp; p.Arg150Trp; p.Arg243Trp; p.Arg282Trp	479	FALSE	chr17:7577094:G:A	52:chr17:7577094:G:A	0.002304
48_c2-1	48	TP53	MODERATE	c.110G>A; c.191G>A; c.470G>A; c.587G>A	p.Arg37Gln; p.Arg64Gln; p.Arg157Gln; p.Arg196Gln	19	FALSE	chr17:7578262:C:T	52:chr17:7578262:C:T	0.002128
48_c2-1	48	NF1	MODERATE	c.2695T>G	p.Leu899Val	3	FALSE	chr17:29556328:T:G	52:chr17:29556328:T:G	0.012461
48_c2-1	48	PTEN	HIGH	c.633C>A	p.Cys211*	2	FALSE	chr10:89712015:C:A	52:chr10:89712015:C:A	0.003049
48_c2-1	48	TP53	MODIFIER; MODERATE	c.*137A>G; c.*225A>G; c.1001A>G; c.1118A>G; c.641A>G; c.722A>G	; p.Lys334Arg; p.Lys373Arg; p.Lys214Arg; p.Lys241Arg	1	FALSE	chr17:7572991:T:C	52:chr17:7572991:T:C	0.003436
48_c2-1	48	CTNNB1	MODERATE	c.884C>A	p.Ala295Asp	0	FALSE	chr3:41267300:C:A	52:chr3:41267300:C:A	0.002451
48_c2-1	48	PHLPP1	MODERATE	c.2956G>A	p.Asp986Asn	0	FALSE	chr18:60587343:G:A	52:chr18:60587343:G:A	0.002601
48_c2-1	48	CTNNB1	MODERATE	c.1345C>T	p.Arg449Cys	0	FALSE	chr3:41275179:C:T	52:chr3:41275179:C:T	0.001942
48_c2-1	48	HOXD-AS2; HOXD8	MODIFIER; MODERATE	n.*692G>T; c.22C>A; c.574C>A	; p.Gln8Lys; p.Gln192Lys	0	FALSE	chr2:176995668:C:A	52:chr2:176995668:C:A	0.003367
48_c2-1	48	MET	HIGH	c.1639C>T	p.Arg547*	2	FALSE	chr7:116381017:C:T	52:chr7:116381017:C:T	0.003141

48_c2-1	48	PTEN	MODERATE	c.392C>A	p.Thr131Asn	2	FALSE	chr10:89692908:C:A	52:chr10:89692908:C:A	0.003135
48_c2-1	48	NF1	MODERATE	c.3559C>A	p.Leu1187Ile	1	FALSE	chr17:29560082:C:A	52:chr17:29560082:C:A	0.002174
48_c3-2	48	TP53	MODERATE	c.146G>T; c.425G>T; c.542G>T; c.65G>T	p.Arg49Leu; p.Arg142Leu; p.Arg181Leu; p.Arg22Leu	25	FALSE	chr17:7578388:C:A	53:chr17:7578388:C:A	0.001614
48_c3-2	48	MET	MODERATE	c.1627G>A	p.Asp543Asn	1	FALSE	chr7:116381005:G:A	53:chr7:116381005:G:A	0.001417
48_c3-2	48	HGF	HIGH	c.526C>T; c.541C>T	p.Arg176*; p.Arg181*	0	FALSE	chr7:81381520:G:A	53:chr7:81381520:G:A	0.001461
48_c3-2	48	NF1	MODERATE	c.8070G>T; c.8133G>T	p.Leu2690Phe; p.Leu2711Phe	1	FALSE	chr17:29686006:G:T	53:chr17:29686006:G:T	0.004027
48_c3-2	48	MET	MODERATE	c.3973G>A; c.4027G>A	p.Glu1325Lys; p.Glu1343Lys	1	FALSE	chr7:116435978:G:A	53:chr7:116435978:G:A	0.001529
48_c3-2	48	CTNNB1	MODERATE	c.91C>A	p.Leu31Met	0	FALSE	chr3:41266094:C:A	53:chr3:41266094:C:A	0.001529
48_c3-2	48	EGFR	MODERATE	c.3352G>A	p.Ala1118Thr	3	FALSE	chr7:55273029:G:A	53:chr7:55273029:G:A	0.001422
48_c3-2	48	RET	MODERATE	c.1690A>C	p.Thr564Pro	1	FALSE	chr10:43608342:A:C	53:chr10:43608342:A:C	0.006339
48_c3-2	48	NF1	MODERATE	c.2695T>G	p.Leu899Val	3	FALSE	chr17:29556328:T:G	53:chr17:29556328:T:G	0.006456
48_c3-2	48	AKT1	MODERATE	c.1112C>T	p.Thr371Met	1	FALSE	chr14:105239275:G:A	53:chr14:105239275:G:A	0.001852
48_c3-2	48	DDR2	MODERATE	c.1418G>A	p.Arg473His	2	FALSE	chr1:162740216:G:A	53:chr1:162740216:G:A	0.001415
48_c3-2	48	TP53	MODIFIER; MODERATE	c.*160G>T; c.*72G>T; c.1053G>T; c.576G>T; c.657G>T; c.936G>T	; p.Lys351Asn; p.Lys192Asn; p.Lys219Asn; p.Lys312Asn	1	FALSE	chr17:7573974:C:A	53:chr17:7573974:C:A	0.001406
48_c3-2	48	CWH43	HIGH	c.1250G>A; c.1331G>A	p.Trp417*; p.Trp444*	0	FALSE	chr4:49030710:G:A	53:chr4:49030710:G:A	0.001536

48_c3-2	48	BRAF	MODERATE	c.1397G>T	p.Gly466Val	18	FALSE	chr7:140481411:C:A	53:chr7:140481411:C:A	0.001425
48_c3-2	48	DDR2	MODERATE	c.313C>A	p.Arg105Ser	2	FALSE	chr1:162724541:C:A	53:chr1:162724541:C:A	0.002102
48_c3-2	48	CTNNB1	MODERATE	c.1346G>A	p.Arg449His	0	FALSE	chr3:41275180:G:A	53:chr3:41275180:G:A	0.001298
48_c3-2	48	HGF	MODERATE	c.1172G>A; c.1187G>A	p.Gly391Asp; p.Gly396Asp	0	FALSE	chr7:81350145:C:T	53:chr7:81350145:C:T	0.001498
48_c3-2	48	ERBB2; MIEN1; MIR4728	MODERATE; MODIFIER	c.2720A>G; c.2765A>G; c.2810A>G; n.3134A>G; c.*388T>C; n.-1A>G	p.Lys907Arg; p.Lys922Arg; p.Lys937Arg;	1	FALSE	chr17:37882044:A:G	53:chr17:37882044:A:G	0.001963
48_c3-2	48	KRAS	MODERATE	c.204G>T	p.Arg68Ser	1	FALSE	chr12:25380254:C:A	53:chr12:25380254:C:A	0.001479
48_c3-2	48	PIK3CA	MODERATE	c.518C>A	p.Ser173Tyr	1	FALSE	chr3:178917643:C:A	53:chr3:178917643:C:A	0.001563
48_c3-2	48	CTNNB1	MODERATE	c.1166C>T	p.Ser389Leu	0	FALSE	chr3:41274916:C:T	53:chr3:41274916:C:T	0.001227
48_c3-2	48	TP53	HIGH; MODIFIER	c.184G>T; c.67G>T; c.-279G>T; c.-360G>T	p.Glu62*; p.Glu23*;	8	FALSE	chr17:7579503:C:A	53:chr17:7579503:C:A	0.005076
48_c3-2	48	KRAS	MODERATE	c.34G>T	p.Gly12Cys	3755	FALSE	chr12:25398285:C:A	53:chr12:25398285:C:A	0.002373
71_bl-1	71	PIK3R1	MODERATE	c.1702C>A; c.613C>A; c.802C>A; c.892C>A	p.Pro568Thr; p.Pro205Thr; p.Pro268Thr; p.Pro298Thr	1	FALSE	chr5:67591109:C:A	54:chr5:67591109:C:A	0.000597
71_bl-1	71	MET	HIGH	c.1619G>A	p.Trp540*	1	FALSE	chr7:116380997:G:A	54:chr7:116380997:G:A	0.000539
71_bl-1	71	PIK3CA	MODERATE	c.2102A>C	p.His701Pro	6	FALSE	chr3:178938860:A:C	54:chr3:178938860:A:C	0.000644

71_bl-1	71	TP53	MODERATE	c.144G>T; c.423G>T; c.540G>T; c.63G>T	p.Glu48Asp; p.Glu141Asp; p.Glu180Asp; p.Glu21Asp	5	FALSE	chr17:7578390:C:A	54:chr17:7578390:C:A	0.001031
71_bl-1	71	MET	HIGH	c.1639C>T	p.Arg547*	2	FALSE	chr7:116381017:C:T	54:chr7:116381017:C:T	0.000795
71_bl-1	71	RPL19	MODERATE	c.452G>A	p.Arg151His	0	FALSE	chr17:37360425:G:A	54:chr17:37360425:G:A	0.001145
71_bl-1	71	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2568T>G; n.-1A>C	p.Phe856Leu;	1	FALSE	chr7:55259510:T:G	54:chr7:55259510:T:G	0.000661
71_bl-1	71	FGFR1	MODERATE	c.1121C>T; c.1139C>T; c.1145C>T; c.1238C>T; c.872C>T; c.878C>T	p.Thr374Ile; p.Thr380Ile; p.Thr382Ile; p.Thr413Ile; p.Thr291Ile; p.Thr293Ile	1	FALSE	chr8:38277190:G:A	54:chr8:38277190:G:A	0.000623
71_bl-1	71	RET	HIGH	c.1827C>A	p.Cys609*	1	FALSE	chr10:43609071:C:A	54:chr10:43609071:C:A	0.000718
71_bl-1	71	NF1	MODERATE	c.6031G>A; c.6094G>A	p.Ala2011Thr; p.Ala2032Thr	1	FALSE	chr17:29663438:G:A	54:chr17:29663438:G:A	0.0006
71_bl-1	71	TP53	MODERATE; MODIFIER	c.119C>T; c.236C>T; c.-279C>T; c.-360C>T	p.Ala40Val; p.Ala79Val;	2	FALSE	chr17:7579451:G:A	54:chr17:7579451:G:A	0.000883
71_bl-1	71	TP53	MODERATE	c.353G>T; c.434G>T; c.713G>T; c.830G>T	p.Cys118Phe; p.Cys145Phe; p.Cys238Phe; p.Cys277Phe	22	FALSE	chr17:7577108:C:A	54:chr17:7577108:C:A	0.000741

71_bl-1	71	TP53	MODIFIER; MODERATE	c.*137A>G; c.*225A>G; c.1001A>G; c.1118A>G; c.641A>G; c.722A>G	; p.Lys334Arg; p.Lys373Arg; p.Lys214Arg; p.Lys241Arg	1	FALSE	chr17:7572991:T:C	54:chr17:7572991:T:C	0.003673
71_bl-1	71	CTNNB1	HIGH	c.999C>A	p.Tyr333*	0	FALSE	chr3:41268761:C:A	54:chr3:41268761:C:A	0.000533
71_bl-1	71	EPHA3	MODERATE	c.497C>A	p.Thr166Asn	0	FALSE	chr3:89259353:C:A	54:chr3:89259353:C:A	0.000842
71_bl-1	71	EGFR	MODERATE	c.755G>A	p.Arg252His	3	FALSE	chr7:55221711:G:A	54:chr7:55221711:G:A	0.001019
71_bl-1	71	MITF	MODIFIER; MODERATE	c.-53+197C>A; c.104+24188C>A; c.48C>A	; p.Phe16Leu	0	FALSE	chr3:69813040:C:A	54:chr3:69813040:C:A	0.000824
71_bl-1	71	TP53	MODERATE; MODIFIER	c.140C>T; c.23C>T; c.-279C>T; c.-360C>T	p.Pro47Leu; p.Pro8Leu;	2	FALSE	chr17:7579547:G:A	54:chr17:7579547:G:A	0.000938
71_bl-1	71	KRAS	MODERATE	c.108A>G	p.Ile36Met	1	FALSE	chr12:25398211:T:C	54:chr12:25398211:T:C	0.000744
71_bl-1	71	TP53	MODERATE	c.341G>A; c.422G>A; c.701G>A; c.818G>A	p.Arg114His; p.Arg141His; p.Arg234His; p.Arg273His	647	TRUE	chr17:7577120:C:T	54:chr17:7577120:C:T	0.001478
71_bl-1	71	ERBB2; MIEN1; MIR4728	MODERATE; MODIFIER	c.2720A>G; c.2765A>G; c.2810A>G; n.3134A>G; c.*388T>C; n.-1A>G	p.Lys907Arg; p.Lys922Arg; p.Lys937Arg;	1	FALSE	chr17:37882044:A:G	54:chr17:37882044:A:G	0.001537
71_bl-1	71	NF1	MODERATE	c.2695T>G	p.Leu899Val	3	FALSE	chr17:29556328:T:G	54:chr17:29556328:T:G	0.006883

71_bl-1	71	FGFR1	MODERATE	c.475C>T; c.481C>T; c.724C>T; c.742C>T; c.748C>T; c.841C>T	p.Arg159Trp; p.Arg161Trp; p.Arg242Trp; p.Arg248Trp; p.Arg250Trp; p.Arg281Trp	2	FALSE	chr8:38282215:G:A	54:chr8:38282215:G:A	0.000591
71_bl-1	71	PTEN	MODERATE	c.392C>A	p.Thr131Asn	2	FALSE	chr10:89692908:C:A	54:chr10:89692908:C:A	0.000644
71_bl-1	71	TP53	MODIFIER; MODERATE	c.-3G>T; c.358G>T; c.475G>T; c.79G>T	; p.Ala120Ser; p.Ala159Ser; p.Ala27Ser	23	FALSE	chr17:7578455:C:A	54:chr17:7578455:C:A	0.001283
71_bl-1	71	PIK3CA	MODERATE	c.3180C>A	p.His1060Gln	2	FALSE	chr3:178952125:C:A	54:chr3:178952125:C:A	0.00077
71_bl-1	71	DDR2	MODERATE	c.1418G>A	p.Arg473His	2	FALSE	chr1:162740216:G:A	54:chr1:162740216:G:A	0.000866
71_bl-1	71	KIT	MODERATE	c.1485C>A	p.Asn495Lys	1	FALSE	chr4:55592161:C:A	54:chr4:55592161:C:A	0.000677
71_bl-1	71	PTEN	HIGH	c.720C>A	p.Tyr240*	3	FALSE	chr10:89717695:C:A	54:chr10:89717695:C:A	0.000656
71_bl-1	71	CTNNB1	MODERATE	c.953G>A	p.Ser318Asn	0	FALSE	chr3:41268715:G:A	54:chr3:41268715:G:A	0.000643
71_bl-1	71	EGFR	MODERATE	c.719G>A	p.Cys240Tyr	1	FALSE	chr7:55220329:G:A	54:chr7:55220329:G:A	0.000617
71_bl-1	71	TP53	MODERATE; MODIFIER	c.257C>T; c.374C>T; c.-279C>T; c.-360C>T	p.Thr86Met; p.Thr125Met;	18	FALSE	chr17:7579313:G:A	54:chr17:7579313:G:A	0.000804
71_bl-1	71	MAP2K1	MODERATE	c.198C>A	p.Asp66Glu	4	FALSE	chr15:66727482:C:A	54:chr15:66727482:C:A	0.001386
71_bl-1	71	CTNNB1	MODERATE	c.125C>A	p.Thr42Lys	0	FALSE	chr3:41266128:C:A	54:chr3:41266128:C:A	0.000926
71_bl-1	71	TP53	MODERATE	c.164G>T; c.443G>T; c.560G>T; c.83G>T	p.Gly55Val; p.Gly148Val; p.Gly187Val; p.Gly28Val	7	FALSE	chr17:7578289:C:A	54:chr17:7578289:C:A	0.000626

71_bl-1	71	RET	MODERATE	c.1690A>C	p.Thr564Pro	1	FALSE	chr10:43608342:A:C	54:chr10:43608342:A:C	0.003811
71_bl-1	71	ALK	MODERATE	c.206G>A	p.Arg69Gln	2	FALSE	chr2:30143320:C:T	54:chr2:30143320:C:T	0.000891
71_bl-1	71	CTNNB1	MODERATE	c.91C>A	p.Leu31Met	0	FALSE	chr3:41266094:C:A	54:chr3:41266094:C:A	0.000632
71_bl-1	71	NF1	HIGH	c.5817C>A; c.5880C>A	p.Cys1939*; p.Cys1960*	1	FALSE	chr17:29661923:C:A	54:chr17:29661923:C:A	0.001314
71_bl-1	71	DDR2	MODERATE	c.2255G>A	p.Arg752His	1	FALSE	chr1:162746132:G:A	54:chr1:162746132:G:A	0.000513
71_bl-1	71	ALK	MODERATE	c.617C>T	p.Ala206Val	2	FALSE	chr2:30142909:G:A	54:chr2:30142909:G:A	0.001092
71_bl-1	71	FGFR1	MODERATE	c.1070G>T; c.1076G>T; c.1313G>T; c.1337G>T; c.1343G>T; c.1436G>T	p.Arg357Leu; p.Arg359Leu; p.Arg438Leu; p.Arg446Leu; p.Arg448Leu; p.Arg479Leu	1	FALSE	chr8:38275833:C:A	54:chr8:38275833:C:A	0.000485
71_bl-1	71	KIT	MODERATE	c.365G>A	p.Arg122His	1	FALSE	chr4:55564477:G:A	54:chr4:55564477:G:A	0.001271
71_bl-1	71	DDR2	MODERATE	c.313C>A	p.Arg105Ser	2	FALSE	chr1:162724541:C:A	54:chr1:162724541:C:A	0.001468
71_bl-1	71	KIT	MODERATE	c.2570A>G; c.2582A>G	p.Glu857Gly; p.Glu861Gly	3	FALSE	chr4:55602761:A:G	54:chr4:55602761:A:G	0.001053
71_bl-1	71	TP53	MODIFIER; MODERATE	c.-29C>T; c.332C>T; c.449C>T; c.53C>T	; p.Thr111Ile; p.Thr150Ile; p.Thr18Ile	4	FALSE	chr17:7578481:G:A	54:chr17:7578481:G:A	0.000895
71_bl-1	71	AKT1	MODERATE	c.745C>T	p.Arg249Trp	1	FALSE	chr14:105239875:G:A	54:chr14:105239875:G:A	0.000629
71_bl-1	71	PIK3R1	MODERATE	c.629C>A	p.Ala210Asp	1	FALSE	chr5:67575556:C:A	54:chr5:67575556:C:A	0.000785
71_bl-1	71	PIK3CA	MODERATE	c.1615C>A	p.Pro539Thr	3	FALSE	chr3:178936073:C:A	54:chr3:178936073:C:A	0.000632

71_bl-1	71	TP53	MODERATE; MODIFIER	c.124G>T; c.7G>T; c.-279G>T; c.-360G>T	p.Asp42Tyr; p.Asp3Tyr;	1	FALSE	chr17:7579563:C:A	54:chr17:7579563:C:A	0.000994
71_bl-1	71	FGFR1	MODIFIER; MODERATE	c.92-1469C>T; c.112C>T; c.136C>T; c.235C>T	; p.His38Tyr; p.His46Tyr; p.His79Tyr	1	FALSE	chr8:38287422:G:A	54:chr8:38287422:G:A	0.000696
71_bl-1	71	MET	MODERATE	c.3509G>A; c.3563G>A	p.Arg1170Gln; p.Arg1188Gln	1	FALSE	chr7:116418998:G:A	54:chr7:116418998:G:A	0.001178
71_bl-1	71	KIT	MODERATE	c.235C>A	p.Gln79Lys	2	FALSE	chr4:55561845:C:A	54:chr4:55561845:C:A	0.00051
71_bl-1	71	DDR2	MODERATE	c.1963G>A	p.Glu655Lys	1	FALSE	chr1:162745548:G:A	54:chr1:162745548:G:A	0.001717
71_bl-1	71	BRAF	MODERATE	c.338G>T	p.Ser113Ile	1	FALSE	chr7:140534575:C:A	54:chr7:140534575:C:A	0.000824
71_bl-1	71	NF1	MODERATE	c.2659G>A	p.Ala887Thr	1	FALSE	chr17:29556292:G:A	54:chr17:29556292:G:A	0.000545
71_bl-1	71	ALK	MODERATE	c.3455T>C	p.Leu1152Pro	1	FALSE	chr2:29445270:A:G	54:chr2:29445270:A:G	0.001436
71_bl-1	71	AKT3	MODERATE	c.825G>T	p.Glu275Asp	0	FALSE	chr1:243727145:C:A	54:chr1:243727145:C:A	0.000828
71_bl-1	71	MITF	MODERATE	c.157A>C; c.265A>C; c.310A>C; c.313A>C	p.Thr53Pro; p.Thr89Pro; p.Thr104Pro; p.Thr105Pro	0	FALSE	chr3:69928493:A:C	54:chr3:69928493:A:C	0.000835
71_bl-1	71	PTEN	MODERATE	c.443C>A	p.Ala148Glu	1	FALSE	chr10:89692959:C:A	54:chr10:89692959:C:A	0.000781
71_bl-1	71	TP53	MODERATE	c.270G>T; c.351G>T; c.630G>T; c.747G>T	p.Arg90Ser; p.Arg117Ser; p.Arg210Ser; p.Arg249Ser	318	FALSE	chr17:7577534:C:A	54:chr17:7577534:C:A	0.004719
71_bl-1	71	FGFR1	MODIFIER; MODERATE	c.-85G>T; c.107G>T; c.8G>T	; p.Ser36Ile; p.Ser3Ile	1	FALSE	chr8:38314957:C:A	54:chr8:38314957:C:A	0.000548

70_bl-1	70	ALK	MODERATE	c.1753G>A	p.Ala585Thr	3	FALSE	chr2:29519818:C:T	55:chr2:29519818:C:T	0.0013
70_bl-1	70	TP53	MODIFIER; MODERATE	c.*117G>T; c.*29G>T; c.1010G>T; c.533G>T; c.614G>T; c.893G>T	; p.Arg337Leu; p.Arg178Leu; p.Arg205Leu; p.Arg298Leu	21	FALSE	chr17:7574017:C:A	55:chr17:7574017:C:A	0.792332
70_bl-1	70	HGF	MODERATE	c.5G>T	p.Trp2Leu	0	FALSE	chr7:81399283:C:A	55:chr7:81399283:C:A	0.002835
70_bl-1	70	TP53	MODERATE; HIGH	c.363G>T; c.480G>T; c.84G>T; c.3G>T	p.Met121Ile; p.Met160Ile; p.Met28Ile; p.Met1?	4	FALSE	chr17:7578450:C:A	55:chr17:7578450:C:A	0.002294
70_bl-1	70	BRAF	HIGH	c.532C>T	p.Arg178*	1	FALSE	chr7:140508768:G:A	55:chr7:140508768:G:A	0.000705
70_bl-1	70	NF1	MODERATE	c.3559C>A	p.Leu1187Ile	1	FALSE	chr17:29560082:C:A	55:chr17:29560082:C:A	0.001367
70_bl-1	70	PIK3CA	MODERATE	c.3180C>A	p.His1060Gln	2	FALSE	chr3:178952125:C:A	55:chr3:178952125:C:A	0.000872
70_bl-1	70	GAPDH; IFFO1	MODERATE; MODIFIER	c.591C>A; c.717C>A; c.*1743G>T; c.*1746G>T; c.*1770G>T; n.*2798G>T	p.Asn197Lys; p.Asn239Lys;	0	FALSE	chr12:6646941:C:A	55:chr12:6646941:C:A	0.001117
70_bl-1	70	ERBB2	MODERATE; MODIFIER	c.379C>T; c.424C>T; c.469C>T; n.793C>T	p.Arg127Trp; p.Arg142Trp; p.Arg157Trp;	1	FALSE	chr17:37865600:C:T	55:chr17:37865600:C:T	0.00109
70_bl-1	70	PTEN	MODERATE	c.743C>A	p.Pro248His	4	FALSE	chr10:89717718:C:A	55:chr10:89717718:C:A	0.003093
70_bl-1	70	NF1	HIGH	c.5294C>A; c.5357C>A	p.Ser1765*; p.Ser1786*	1	FALSE	chr17:29654605:C:A	55:chr17:29654605:C:A	0.001049

70_bl-1	70	PTEN	MODERATE	c.443C>A	p.Ala148Glu	1	FALSE	chr10:89692959:C:A	55:chr10:89692959:C:A	0.002107
70_bl-1	70	MET	MODERATE	c.3973G>A; c.4027G>A	p.Glu1325Lys; p.Glu1343Lys	1	FALSE	chr7:116435978:G:A	55:chr7:116435978:G:A	0.000841
70_bl-1	70	BRAF	MODERATE	c.1796C>T	p.Thr599Ile	4	FALSE	chr7:140453139:G:A	55:chr7:140453139:G:A	0.000866
70_bl-1	70	NF1	LOW	c.1641G>A	p.Glu547Glu	1	FALSE	chr17:29546136:G:A	55:chr17:29546136:G:A	0.001358
70_bl-1	70	PIK3CA	MODERATE	c.3076C>A	p.Leu1026Ile	1	FALSE	chr3:178952021:C:A	55:chr3:178952021:C:A	0.000821
70_bl-1	70	CTNNB1	MODERATE	c.884C>A	p.Ala295Asp	0	FALSE	chr3:41267300:C:A	55:chr3:41267300:C:A	0.002946
70_bl-1	70	FGFR1	MODERATE	c.1060C>T; c.1066C>T; c.1303C>T; c.1327C>T; c.1333C>T; c.1426C>T	p.Arg354Trp; p.Arg356Trp; p.Arg435Trp; p.Arg443Trp; p.Arg445Trp; p.Arg476Trp	2	FALSE	chr8:38275843:G:A	55:chr8:38275843:G:A	0.001817
70_bl-1	70	EGFR	MODIFIER; MODERATE	c.*2364C>T; c.2165C>T	; p.Ala722Val	2	FALSE	chr7:55241717:C:T	55:chr7:55241717:C:T	0.001451
70_bl-1	70	PTEN	MODERATE	c.392C>A	p.Thr131Asn	2	FALSE	chr10:89692908:C:A	55:chr10:89692908:C:A	0.001656
70_bl-1	70	HGF	MODERATE	c.2157G>T; c.2172G>T	p.Lys719Asn; p.Lys724Asn	0	FALSE	chr7:81331912:C:A	55:chr7:81331912:C:A	0.001585
70_bl-1	70	PTEN	MODERATE	c.729C>A	p.Phe243Leu	1	FALSE	chr10:89717704:C:A	55:chr10:89717704:C:A	0.002049
70_bl-1	70	TP53	MODERATE	c.105G>T; c.24G>T; c.384G>T; c.501G>T	p.Gln35His; p.Gln8His; p.Gln128His; p.Gln167His	3	FALSE	chr17:7578429:C:A	55:chr17:7578429:C:A	0.002039
70_bl-1	70	TP53	MODERATE	c.121G>T; c.400G>T; c.40G>T; c.517G>T	p.Val41Leu; p.Val134Leu; p.Val14Leu; p.Val173Leu	55	FALSE	chr17:7578413:C:A	55:chr17:7578413:C:A	0.001942

70_bl-1	70	NF1	HIGH	c.5817C>A; c.5880C>A	p.Cys1939*; p.Cys1960*	1	FALSE	chr17:29661923:C:A	55:chr17:29661923:C:A	0.001698
70_bl-1	70	NF1	MODERATE	c.7405G>A; c.7468G>A	p.Glu2469Lys; p.Glu2490Lys	1	FALSE	chr17:29679285:G:A	55:chr17:29679285:G:A	0.002016
70_bl-1	70	ALK	MODERATE	c.741G>T	p.Trp247Cys	1	FALSE	chr2:29940490:C:A	55:chr2:29940490:C:A	0.001552
70_bl-1	70	KRAS	HIGH	c.292G>T	p.Glu98*	1	FALSE	chr12:25378706:C:A	55:chr12:25378706:C:A	0.0025
70_bl-1	70	NF1	MODERATE	c.2695T>G	p.Leu899Val	3	FALSE	chr17:29556328:T:G	55:chr17:29556328:T:G	0.013536
70_bl-1	70	TP53	HIGH; MODIFIER	c.184G>T; c.67G>T; c.-279G>T; c.-360G>T	p.Glu62*; p.Glu23*;	8	FALSE	chr17:7579503:C:A	55:chr17:7579503:C:A	0.004386
70_bl-1	70	ROS1	MODERATE	c.5185G>T	p.Val1729Leu	1	FALSE	chr6:117658398:C:A	55:chr6:117658398:C:A	0.001228
70_bl-1	70	HGF	HIGH	c.1993G>T; c.2008G>T	p.Glu665*; p.Glu670*	0	FALSE	chr7:81334708:C:A	55:chr7:81334708:C:A	0.0027
70_bl-1	70	DDR2	MODERATE	c.313C>A	p.Arg105Ser	2	FALSE	chr1:162724541:C:A	55:chr1:162724541:C:A	0.002484
70_bl-1	70	DDR2	MODERATE	c.1963G>A	p.Glu655Lys	1	FALSE	chr1:162745548:G:A	55:chr1:162745548:G:A	0.002401
70_bl-1	70	TP53	MODERATE	c.131G>A; c.410G>A; c.50G>A; c.527G>A	p.Cys44Tyr; p.Cys137Tyr; p.Cys17Tyr; p.Cys176Tyr	143	FALSE	chr17:7578403:C:T	55:chr17:7578403:C:T	0.00189
70_bl-1	70	TP53	MODIFIER; MODERATE	c.-9G>T; c.352G>T; c.469G>T; c.73G>T	; p.Val118Phe; p.Val157Phe; p.Val25Phe	169	FALSE	chr17:7578461:C:A	55:chr17:7578461:C:A	0.00358
70_bl-1	70	ERBB2	MODERATE; MODIFIER	c.1180G>A; c.1225G>A; c.1270G>A; n.1594G>A	p.Val394Ile; p.Val409Ile; p.Val424Ile;	1	FALSE	chr17:37871746:G:A	55:chr17:37871746:G:A	0.001316

70_bl-1	70	FGFR1	MODIFIER; MODERATE	c.-85G>T; c.107G>T; c.8G>T	; p.Ser36Ile; p.Ser3Ile	1	FALSE	chr8:38314957:C:A	55:chr8:38314957:C:A	0.003112
70_bl-1	70	ERBB2; MIEN1; MIR4728	MODIFIER; MODERATE	c.*174C>A; c.3505C>A; c.3550C>A; c.3595C>A; n.3919C>A; c.*388G>T; n.*67C>A	; p.Pro1169Thr; p.Pro1184Thr; p.Pro1199Thr	2	FALSE	chr17:37884124:C:A	55:chr17:37884124:C:A	0.001096
70_bl-1	70	ALK	HIGH	c.4414G>T	p.Glu1472*	1	FALSE	chr2:29416539:C:A	55:chr2:29416539:C:A	0.001114
70_bl-1	70	MET	MODERATE	c.470A>G	p.Glu157Gly	1	FALSE	chr7:116339608:A:G	55:chr7:116339608:A:G	0.000697
5_pro-2	5	KLLN; PTEN	MODIFIER; MODERATE	c.-951C>T; c.32G>A	; p.Arg11Lys	1	FALSE	chr10:89624258:G:A	56:chr10:89624258:G:A	0.003559
5_pro-2	5	SMO	MODERATE	c.1045A>C	p.Thr349Pro	0	FALSE	chr7:128846115:A:C	56:chr7:128846115:A:C	0.002717
5_pro-2	5	TP53	MODERATE	c.110G>A; c.191G>A; c.470G>A; c.587G>A	p.Arg37Gln; p.Arg64Gln; p.Arg157Gln; p.Arg196Gln	19	FALSE	chr17:7578262:C:T	56:chr17:7578262:C:T	0.004505
5_pro-2	5	TP53	MODERATE	c.256G>C; c.337G>C; c.616G>C; c.733G>C	p.Gly86Arg; p.Gly113Arg; p.Gly206Arg; p.Gly245Arg	361	FALSE	chr17:7577548:C:G	56:chr17:7577548:C:G	0.004021
5_pro-2	5	ATM	HIGH	c.4852C>T	p.Arg1618*	0	FALSE	chr11:108165729:C:T	56:chr11:108165729:C:T	0.002751
5_pro-2	5	MIR4673; NOTCH1	MODIFIER; MODERATE	n.-1C>T; c.368C>T	; p.Thr123Met	0	FALSE	chr9:139418204:G:A	56:chr9:139418204:G:A	0.003795
5_pro-2	5	PDGFRA	MODERATE	c.2152C>T	p.Arg718Trp	1	FALSE	chr4:55144678:C:T	56:chr4:55144678:C:T	0.002797

4_bl-b	4	FGFR1; LETM2	MODERATE; MODIFIER	c.2126C>T; c.2132C>T; c.2369C>T; c.2393C>T; c.2399C>T; c.2492C>T; c.*1406G>A; c.*1423G>A; c.*1553G>A; c.*1567G>A; c.*1638G>A	p.Pro709Leu; p.Pro711Leu; p.Pro790Leu; p.Pro798Leu; p.Pro800Leu; p.Pro831Leu;	1	FALSE	chr8:38271216:G:A	57:chr8:38271216:G:A	0.001404
4_bl-b	4	KRAS	MODERATE	c.182A>G	p.Gln61Arg	92	FALSE	chr12:25380276:T:C	57:chr12:25380276:T:C	0.106092
4_bl-b	4	FGFR3	MODIFIER; MODERATE	c.931-417C>A; c.1153C>A; c.1159C>A	; p.Leu385Met; p.Leu387Met	1	FALSE	chr4:1806134:C:A	57:chr4:1806134:C:A	0.00158
4_bl-b	4	PDGFRA	MODERATE	c.1516C>A	p.Leu506Ile	2	FALSE	chr4:55139855:C:A	57:chr4:55139855:C:A	0.001264
4_bl-b	4	IDH1	MODERATE	c.299G>T	p.Arg100Leu	5	FALSE	chr2:209113208:C:A	57:chr2:209113208:C:A	0.001389
4_bl-b	4	TP53	MODERATE	c.113C>T; c.32C>T; c.392C>T; c.509C>T	p.Thr38Met; p.Thr11Met; p.Thr131Met; p.Thr170Met	8	FALSE	chr17:7578421:G:A	57:chr17:7578421:G:A	0.001503
4_bl-b	4	MAP2K1	MODERATE	c.602G>A	p.Arg201His	2	FALSE	chr15:66774126:G:A	57:chr15:66774126:G:A	0.001565
4_bl-b	4	PDGFRA	MODERATE	c.401C>T	p.Thr134Met	3	FALSE	chr4:55129867:C:T	57:chr4:55129867:C:T	0.001255
4_bl-b	4	PIK3CA	MODERATE	c.241G>A	p.Glu81Lys	38	FALSE	chr3:178916854:G:A	57:chr3:178916854:G:A	0.001296
4_bl-b	4	TP53	MODERATE	c.266G>A; c.347G>A; c.626G>A; c.743G>A	p.Arg89Gln; p.Arg116Gln; p.Arg209Gln; p.Arg248Gln	673	FALSE	chr17:7577538:C:T	57:chr17:7577538:C:T	0.001983

4_bl-b	4	AKT1	MODERATE	c.49G>A	p.Glu17Lys	287	FALSE	chr14:105246551:C:T	57:chr14:105246551:C:T	0.092537
4_bl-b	4	CTNNB1	MODERATE	c.91C>A	p.Leu31Met	0	FALSE	chr3:41266094:C:A	57:chr3:41266094:C:A	0.001322
4_bl-b	4	DDR2	MODERATE	c.2516G>A	p.Arg839His	3	FALSE	chr1:162749984:G:A	57:chr1:162749984:G:A	0.001259
4_bl-b	4	CDKN2A; CDKN2B-AS1	MODERATE; MODIFIER	c.22A>G; n.-1T>C	p.Thr8Ala;	1	FALSE	chr9:21994309:T:C	57:chr9:21994309:T:C	0.00578
4_bl-b	4	TP53	MODERATE	c.236G>A; c.317G>A; c.596G>A; c.713G>A	p.Cys79Tyr; p.Cys106Tyr; p.Cys199Tyr; p.Cys238Tyr	74	FALSE	chr17:7577568:C:T	57:chr17:7577568:C:T	0.001254
4_bl-b	4	FBXW7	MODERATE	c.1078G>T; c.1318G>T; c.964G>T	p.Asp360Tyr; p.Asp440Tyr; p.Asp322Tyr	0	FALSE	chr4:153249460:C:A	57:chr4:153249460:C:A	0.002075
4_bl-b	4	TP53	MODERATE	c.103C>T; c.184C>T; c.463C>T; c.580C>T	p.Leu35Phe; p.Leu62Phe; p.Leu155Phe; p.Leu194Phe	22	FALSE	chr17:7578269:G:A	57:chr17:7578269:G:A	0.001491
4_bl-b	4	GNA11	MODERATE	c.196G>A	p.Gly66Ser	2	FALSE	chr19:3110206:G:A	57:chr19:3110206:G:A	0.00154
4_bl-b	4	NOTCH1	MODERATE	c.5885G>A	p.Arg1962His	0	FALSE	chr9:139395053:C:T	57:chr9:139395053:C:T	0.001601
4_bl-b	4	C9orf53; CDKN2A	MODIFIER; MODERATE	n.*616C>G; c.*140G>C; c.217G>C; c.260G>C	; p.Ala73Pro; p.Arg87Pro	1	FALSE	chr9:21971141:C:G	57:chr9:21971141:C:G	0.018732
4_bl-b	4	ERBB2; MIEN1; MIR4728	MODIFIER; MODERATE	c.3160-213A>G; c.3251A>G; c.3296A>G; c.3341A>G; n.3665A>G; c.*388T>C; n.*67A>G	; p.Glu1084Gly; p.Glu1099Gly; p.Glu1114Gly	1	FALSE	chr17:37883729:A:G	57:chr17:37883729:A:G	0.001494

4_bl-b	4	CTNNB1	MODERATE	c.1723G>A	p.Gly575Arg	0	FALSE	chr3:41277254:G:A	57:chr3:41277254:G:A	0.001674
4_bl-b	4	KDR	HIGH	c.823C>T	p.Arg275*	3	FALSE	chr4:55979624:G:A	57:chr4:55979624:G:A	0.001358
4_bl-b	4	NTRK1	MODERATE	c.804C>G; c.894C>G	p.His268Gln; p.His298Gln	1	FALSE	chr1:156843468:C:G	57:chr1:156843468:C:G	0.00321
4_bl-b	4	TP53	MODERATE	c.152C>T; c.431C>T; c.548C>T; c.71C>T	p.Ser51Leu; p.Ser144Leu; p.Ser183Leu; p.Ser24Leu	26	FALSE	chr17:7578382:G:A	57:chr17:7578382:G:A	0.001403
7_bl-1	7	CTNNB1	MODERATE	c.98C>A	p.Ser33Tyr	0	FALSE	chr3:41266101:C:A	58:chr3:41266101:C:A	0.002051
7_bl-1	7	FBXW7	MODERATE	c.1444G>T; c.1558G>T; c.1798G>T	p.Asp482Tyr; p.Asp520Tyr; p.Asp600Tyr	0	FALSE	chr4:153245393:C:A	58:chr4:153245393:C:A	0.002169
7_bl-1	7	ERBB2; MIEN1; MIR4728	MODIFIER; MODERATE	c.3160-213A>G; c.3251A>G; c.3296A>G; c.3341A>G; n.3665A>G; c.*388T>C; n.*67A>G	; p.Glu1084Gly; p.Glu1099Gly; p.Glu1114Gly	1	FALSE	chr17:37883729:A:G	58:chr17:37883729:A:G	0.002421
7_bl-1	7	KIT	MODERATE	c.1156G>A	p.Glu386Lys	1	FALSE	chr4:55575630:G:A	58:chr4:55575630:G:A	0.003916
7_bl-1	7	ATM	MODERATE	c.6200C>A	p.Ala2067Asp	0	FALSE	chr11:108188101:C:A	58:chr11:108188101:C:A	0.003012
7_bl-1	7	FBXW7	MODERATE	c.182G>A; c.296G>A; c.536G>A	p.Arg61His; p.Arg99His; p.Arg179His	0	FALSE	chr4:153271242:C:T	58:chr4:153271242:C:T	0.00216
7_bl-1	7	RET	MODERATE	c.1690A>C	p.Thr564Pro	1	FALSE	chr10:43608342:A:C	58:chr10:43608342:A:C	0.002191
7_bl-1	7	MAP2K1	MODERATE	c.140G>A	p.Arg47Gln	4	FALSE	chr15:66727424:G:A	58:chr15:66727424:G:A	0.002222
7_bl-1	7	BRAF	MODERATE	c.1799T>A	p.Val600Glu	23024	FALSE	chr7:140453136:A:T	58:chr7:140453136:A:T	0.004338

7_bl-1	7	FOXL2; FOXL2NB; LINC01391	MODERATE; MODIFIER	c.282T>A; c.-132A>T; n.-1T>A	p.Asn94Lys;	0	FALSE	chr3:138665283:A:T	58:chr3:138665283:A:T	0.008969
7_bl-1	7	NTRK2	MODERATE	c.1960C>A; c.2008C>A	p.Leu654Met; p.Leu670Met	0	FALSE	chr9:87570268:C:A	58:chr9:87570268:C:A	0.002326
7_bl-1	7	SMO	MODERATE	c.1045A>C	p.Thr349Pro	0	FALSE	chr7:128846115:A:C	58:chr7:128846115:A:C	0.003378
7_bl-1	7	KDR	MODERATE	c.2323G>A	p.Ala775Thr	1	FALSE	chr4:55964914:C:T	58:chr4:55964914:C:T	0.002058
7_bl-1	7	TP53	MODERATE; MODIFIER	c.115G>T; c.232G>T; c.-279G>T; c.-360G>T	p.Ala39Ser; p.Ala78Ser;	1	FALSE	chr17:7579455:C:A	58:chr17:7579455:C:A	0.002516
11_bl-1	11	DDR2	MODERATE	c.313C>A	p.Arg105Ser	2	FALSE	chr1:162724541:C:A	59:chr1:162724541:C:A	0.001259
11_bl-1	11	PDGFRA	MODERATE	c.685G>A	p.Glu229Lys	3	FALSE	chr4:55131142:G:A	59:chr4:55131142:G:A	0.001235
11_bl-1	11	AKT3	MODERATE	c.425G>T	p.Arg142Ile	0	FALSE	chr1:243809199:C:A	59:chr1:243809199:C:A	0.001538
11_bl-1	11	INSRR; NTRK1	MODIFIER; MODERATE	c.3397+13C>T; c.28G>A	; p.Ala10Thr	1	FALSE	chr1:156811891:G:A	59:chr1:156811891:G:A	0.001133
11_bl-1	11	GNA11	MODERATE	c.440G>A	p.Arg147His	1	FALSE	chr19:3113446:G:A	59:chr19:3113446:G:A	0.001405
11_bl-1	11	RET	MODERATE	c.1690A>C	p.Thr564Pro	1	FALSE	chr10:43608342:A:C	59:chr10:43608342:A:C	0.002639
11_bl-1	11	SMO	MODERATE	c.1045A>C	p.Thr349Pro	0	FALSE	chr7:128846115:A:C	59:chr7:128846115:A:C	0.002572
11_bl-1	11	TSC2	MODERATE	c.1099C>T	p.Arg367Trp	0	FALSE	chr16:2110794:C:T	59:chr16:2110794:C:T	0.001509
11_bl-1	11	MIR4673; NOTCH1	MODIFIER; MODERATE	n.*59G>T; c.1286G>T	; p.Cys429Phe	0	FALSE	chr9:139412359:C:A	59:chr9:139412359:C:A	0.001905
11_bl-1	11	DDR2	MODERATE	c.1598C>A	p.Thr533Lys	1	FALSE	chr1:162741907:C:A	59:chr1:162741907:C:A	0.001395
11_bl-1	11	BRAF	MODERATE	c.1593G>T	p.Trp531Cys	1	FALSE	chr7:140476813:C:A	59:chr7:140476813:C:A	0.001098
11_bl-1	11	MIR4674; MIR4674HG; NOTCH1	MODIFIER; MODERATE	n.*87G>T; n.-1C>A; c.62G>T	; p.Gly21Val	0	FALSE	chr9:139438554:C:A	59:chr9:139438554:C:A	0.002387

11_bl-1	11	NTRK1	MODERATE	c.1411C>T; c.1501C>T; c.1519C>T	p.Arg471Cys; p.Arg501Cys; p.Arg507Cys	1	FALSE	chr1:156845889:C:T	59:chr1:156845889:C:T	0.001576
11_bl-1	11	FBXW7	HIGH	c.357G>A; c.471G>A; c.711G>A	p.Trp119*; p.Trp157*; p.Trp237*	0	FALSE	chr4:153268097:C:T	59:chr4:153268097:C:T	0.001468
11_bl-1	11	PKD1; TSC2	MODIFIER; MODERATE	c.*13118G>A; c.*13121G>A; c.3935C>T; c.4067C>T; c.4136C>T	; p.Ser1312Leu; p.Ser1356Leu; p.Ser1379Leu	0	FALSE	chr16:2134359:C:T	59:chr16:2134359:C:T	0.00127
11_bl-1	11	KRAS	MODERATE	c.182A>G	p.Gln61Arg	92	FALSE	chr12:25380276:T:C	59:chr12:25380276:T:C	0.002459
11_bl-1	11	EVI2A; NF1	MODIFIER; MODERATE	c.-266G>A; c.-338G>A; c.5020C>T; c.5083C>T	; p.Arg1674Trp; p.Arg1695Trp	1	FALSE	chr17:29653085:C:T	59:chr17:29653085:C:T	0.001164
11_bl-1	11	EGFR	MODIFIER; MODERATE	c.*2133G>A; c.*2364G>A; c.2030G>A	; p.Arg677His	5	FALSE	chr7:55240786:G:A	59:chr7:55240786:G:A	0.001921
11_bl-1	11	TSC2	MODERATE	c.1610G>A	p.Arg537His	0	FALSE	chr16:2115530:G:A	59:chr16:2115530:G:A	0.001254
11_bl-1	11	HRAS; LRRC56	MODERATE; MODIFIER	c.368G>A; c.-506C>T	p.Arg123His;	2	FALSE	chr11:533535:C:T	59:chr11:533535:C:T	0.00144
11_bl-1	11	TSC2	MODERATE	c.1503C>A	p.Asp501Glu	0	FALSE	chr16:2114332:C:A	59:chr16:2114332:C:A	0.001498
11_bl-1	11	AKT1	MODERATE	c.49G>A	p.Glu17Lys	287	FALSE	chr14:105246551:C:T	59:chr14:105246551:C:T	0.0015
11_bl-1	11	NTRK2	MODERATE	c.1960C>A; c.2008C>A	p.Leu654Met; p.Leu670Met	0	FALSE	chr9:87570268:C:A	59:chr9:87570268:C:A	0.001567

11_bl-1	11	MITF	MODERATE	c.1091G>A; c.1136G>A; c.1139G>A; c.650G>A; c.818G>A; c.836G>A; c.983G>A	p.Arg364Gln; p.Arg379Gln; p.Arg380Gln; p.Arg217Gln; p.Arg273Gln; p.Arg279Gln; p.Arg328Gln	0	FALSE	chr3:70008549:G:A	59:chr3:70008549:G:A	0.001339
11_bl-1	11	MAP2K1	MODERATE	c.379G>A	p.Val127Met	1	FALSE	chr15:66729171:G:A	59:chr15:66729171:G:A	0.001729
11_bl-1	11	PDGFRA	MODERATE	c.1526C>A	p.Ala509Asp	1	FALSE	chr4:55139865:C:A	59:chr4:55139865:C:A	0.001222
11_bl-1	11	CTNNB1	MODERATE	c.96C>A	p.Asp32Glu	0	FALSE	chr3:41266099:C:A	59:chr3:41266099:C:A	0.001812
11_bl-1	11	C9orf53; CDKN2A	MODIFIER; MODERATE; LOW	n.*616T>G; c.*120A>C; c.197A>C; c.240A>C	; p.His66Pro; p.Pro80Pro	1	FALSE	chr9:21971161:T:G	59:chr9:21971161:T:G	0.018743
11_bl-1	11	PIK3CA	MODERATE	c.1255C>A	p.His419Asn	1	FALSE	chr3:178927977:C:A	59:chr3:178927977:C:A	0.002035
11_bl-1	11	KIT	MODERATE	c.682G>A	p.Glu228Lys	1	FALSE	chr4:55565858:G:A	59:chr4:55565858:G:A	0.001401
11_bl-1	11	NTRK2	MODERATE	c.770C>T	p.Ser257Phe	0	FALSE	chr9:87339188:C:T	59:chr9:87339188:C:T	0.001245
11_bl-1	11	CWH43	MODERATE	c.569C>T; c.650C>T	p.Ser190Phe; p.Ser217Phe	0	FALSE	chr4:48996774:C:T	59:chr4:48996774:C:T	0.001329
11_bl-1	11	C9orf53; CDKN2A	MODIFIER; MODERATE	n.*616C>T; c.*245G>A; c.322G>A; c.365G>A	; p.Asp108Asn; p.Arg122Gln	14	FALSE	chr9:21971036:C:T	59:chr9:21971036:C:T	0.001333

11_bl-1	11	FGFR2	MODIFIER; MODERATE	c.1087+1267C>T; c.749-2096C>T; c.820+1267C>T; c.939+2564C>T; c.643C>T; c.721C>T; c.988C>T; n.1438C>T	; p.Arg215Trp; p.Arg241Trp; p.Arg330Trp	2	FALSE	chr10:123276929:G:A	59:chr10:123276929:G:A	0.00206
11_bl-1	11	CDKN2A	MODIFIER; MODERATE	c.194-3568A>C; c.52A>C	; p.Thr18Pro	1	FALSE	chr9:21974775:T:G	59:chr9:21974775:T:G	0.004307
11_bl-1	11	TP53	MODERATE	c.116A>G; c.35A>G; c.395A>G; c.512A>G	p.Glu39Gly; p.Glu12Gly; p.Glu132Gly; p.Glu171Gly	3	FALSE	chr17:7578418:T:C	59:chr17:7578418:T:C	0.001503
11_bl-1	11	NOTCH1	MODERATE	c.4828G>A	p.Ala1610Thr	0	FALSE	chr9:139399315:C:T	59:chr9:139399315:C:T	0.001553
11_bl-1	11	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2527G>A; n.-1C>T	p.Val843Ile;	6	FALSE	chr7:55259469:G:A	59:chr7:55259469:G:A	0.00144
11_bl-1	11	ESR1	MODERATE	c.929C>T; c.932C>T; c.938C>T	p.Thr310Met; p.Thr311Met; p.Thr313Met	0	FALSE	chr6:152265479:C:T	59:chr6:152265479:C:T	0.001171
11_bl-1	11	ATM	MODERATE	c.1237C>A	p.Leu413Ile	0	FALSE	chr11:108121429:C:A	59:chr11:108121429:C:A	0.002269
11_bl-1	11	NF1	MODERATE	c.1657C>T	p.His553Tyr	1	FALSE	chr17:29548883:C:T	59:chr17:29548883:C:T	0.001476
11_bl-1	11	MAP2K1	MODERATE	c.198C>A	p.Asp66Glu	4	FALSE	chr15:66727482:C:A	59:chr15:66727482:C:A	0.001364
11_c4-b	11	IDH1	MODERATE	c.299G>T	p.Arg100Leu	5	FALSE	chr2:209113208:C:A	60:chr2:209113208:C:A	0.001825
11_c4-b	11	SMO	MODERATE	c.1045A>C	p.Thr349Pro	0	FALSE	chr7:128846115:A:C	60:chr7:128846115:A:C	0.004613
11_c4-b	11	PTEN	MODERATE	c.392C>A	p.Thr131Asn	2	FALSE	chr10:89692908:C:A	60:chr10:89692908:C:A	0.002504
11_c4-b	11	FLT3	MODERATE	c.393G>C	p.Leu131Phe	0	FALSE	chr13:28631575:C:G	60:chr13:28631575:C:G	0.001642

11_c4-b	11	KRAS	MODERATE	c.35G>T	p.Gly12Val	11213	FALSE	chr12:25398284:C:A	60:chr12:25398284:C:A	0.002852
11_c4-b	11	CDH1	MODERATE	c.2204C>T	p.Ala735Val	0	FALSE	chr16:68862116:C:T	60:chr16:68862116:C:T	0.001869
11_c4-b	11	PIK3R1	HIGH	c.1224C>A; c.135C>A; c.324C>A; c.414C>A	p.Tyr408*; p.Tyr45*; p.Tyr108*; p.Tyr138*	1	FALSE	chr5:67589236:C:A	60:chr5:67589236:C:A	0.001671
11_c4-b	11	HOXD-AS2; HOXD8	MODIFIER; MODERATE	n.*692G>T; c.105C>A; c.654C>A; c.657C>A	; p.Asn35Lys; p.Asn218Lys; p.Asn219Lys	0	FALSE	chr2:176996124:C:A	60:chr2:176996124:C:A	0.001586
11_c4-b	11	FGFR4	MODIFIER; MODERATE	c.1098-65G>A; c.1251+10G>A; c.1067G>A	; p.Arg356His	1	FALSE	chr5:176520342:G:A	60:chr5:176520342:G:A	0.001631
11_c4-b	11	PDGFRA	MODERATE	c.364C>A	p.Pro122Thr	1	FALSE	chr4:55127576:C:A	60:chr4:55127576:C:A	0.002451
11_c4-b	11	FBXW7	HIGH	c.1069G>T; c.1309G>T; c.955G>T	p.Gly357*; p.Gly437*; p.Gly319*	0	FALSE	chr4:153249469:C:A	60:chr4:153249469:C:A	0.001698
11_c4-b	11	ALK	MODERATE	c.1359G>T	p.Gln453His	1	FALSE	chr2:29551271:C:A	60:chr2:29551271:C:A	0.001556
11_c4-b	11	KDR	MODERATE	c.583G>T	p.Ala195Ser	1	FALSE	chr4:55981116:C:A	60:chr4:55981116:C:A	0.003053
11_c4-b	11	NOTCH1	MODERATE	c.4391G>T	p.Ser1464Ile	0	FALSE	chr9:139399957:C:A	60:chr9:139399957:C:A	0.001984
11_c4-b	11	ATM	HIGH	c.2558C>A	p.Ser853*	0	FALSE	chr11:108137989:C:A	60:chr11:108137989:C:A	0.001447
11_c4-b	11	FBXW7	MODERATE	c.1204G>T; c.1318G>T; c.1558G>T	p.Asp402Tyr; p.Asp440Tyr; p.Asp520Tyr	0	FALSE	chr4:153247244:C:A	60:chr4:153247244:C:A	0.001658
11_c4-b	11	DDR2	MODERATE	c.313C>A	p.Arg105Ser	2	FALSE	chr1:162724541:C:A	60:chr1:162724541:C:A	0.002575
11_c4-b	11	NTRK2	MODERATE	c.770C>T	p.Ser257Phe	0	FALSE	chr9:87339188:C:T	60:chr9:87339188:C:T	0.001502

11_c4-b	11	TSC1	HIGH	c.496G>T; c.649G>T	p.Glu166*; p.Glu217*	0	FALSE	chr9:135797220:C:A	60:chr9:135797220:C:A	0.003911
11_c4-b	11	CDH1	MODERATE	c.294C>A	p.Phe98Leu	0	FALSE	chr16:68835703:C:A	60:chr16:68835703:C:A	0.001992
11_c4-b	11	KDR	MODERATE	c.2323G>T	p.Ala775Ser	1	FALSE	chr4:55964914:C:A	60:chr4:55964914:C:A	0.006071
11_c4-b	11	ALK	MODERATE	c.871C>T	p.Arg291Cys	3	FALSE	chr2:29917797:G:A	60:chr2:29917797:G:A	0.001663
11_c4-b	11	FGFR3	MODERATE	c.905G>A	p.Gly302Asp	1	FALSE	chr4:1803727:G:A	60:chr4:1803727:G:A	0.003953
11_c4-b	11	CTNNB1	MODERATE	c.884C>A	p.Ala295Asp	0	FALSE	chr3:41267300:C:A	60:chr3:41267300:C:A	0.004077
11_c4-b	11	FBXW7	MODERATE	c.1039C>T; c.1153C>T; c.1393C>T	p.Arg347Cys; p.Arg385Cys; p.Arg465Cys	0	FALSE	chr4:153249385:G:A	60:chr4:153249385:G:A	0.001784
11_c4-b	11	CDKN2A	MODIFIER; MODERATE	c.194-3568A>C; c.52A>C	; p.Thr18Pro	1	FALSE	chr9:21974775:T:G	60:chr9:21974775:T:G	0.003708
11_c4-b	11	FGFR2	MODIFIER; MODERATE	c.110-14054G>T; c.110-934G>T; n.757-14054G>T; c.301G>T	; p.Asp101Tyr	3	FALSE	chr10:123325027:C:A	60:chr10:123325027:C:A	0.001708
11_c4-b	11	HGF	MODERATE	c.5G>T	p.Trp2Leu	0	FALSE	chr7:81399283:C:A	60:chr7:81399283:C:A	0.00202
11_c4-b	11	RET	MODERATE	c.1690A>C	p.Thr564Pro	1	FALSE	chr10:43608342:A:C	60:chr10:43608342:A:C	0.005505
11_c4-b	11	ATM	MODERATE	c.2930G>A	p.Cys977Tyr	0	FALSE	chr11:108141986:G:A	60:chr11:108141986:G:A	0.001522
11_c4-b	11	PTEN	HIGH	c.640C>T	p.Gln214*	12	FALSE	chr10:89717615:C:T	60:chr10:89717615:C:T	0.001821
11_c4-b	11	NOTCH1	MODERATE	c.3635G>A	p.Gly1212Asp	0	FALSE	chr9:139401765:C:T	60:chr9:139401765:C:T	0.0025
11_c4-b	11	DDR2	MODERATE	c.185G>A	p.Arg62Lys	1	FALSE	chr1:162722987:G:A	60:chr1:162722987:G:A	0.001883
11_c4-b	11	IGF1R	MODERATE	c.3905T>C; c.3908T>C	p.Val1302Ala; p.Val1303Ala	0	FALSE	chr15:99500475:T:C	60:chr15:99500475:T:C	0.003071
11_c4-b	11	TSC2	MODERATE	c.1654G>A	p.Ala552Thr	0	FALSE	chr16:2115574:G:A	60:chr16:2115574:G:A	0.002291

11_c4-b	11	TP53	MODERATE	c.128G>A; c.407G>A; c.47G>A; c.524G>A	p.Arg43His; p.Arg136His; p.Arg16His; p.Arg175His	979	FALSE	chr17:7578406:C:T	60:chr17:7578406:C:T	0.002336
11_c4-b	11	CDKN2A	MODIFIER; MODERATE	c.194-3521G>T; c.99G>T	; p.Glu33Asp	1	FALSE	chr9:21974728:C:A	60:chr9:21974728:C:A	0.002457
11_c4-b	11	CTNNB1	MODERATE	c.595G>A	p.Val199Ile	0	FALSE	chr3:41266924:G:A	60:chr3:41266924:G:A	0.001714
11_c4-b	11	AKT3	MODERATE	c.1100G>A	p.Arg367Gln	0	FALSE	chr1:243716094:C:T	60:chr1:243716094:C:T	0.001847
11_c4-b	11	NTRK3	MODERATE	c.1351C>T; c.1375C>T	p.Arg451Trp; p.Arg459Trp	0	FALSE	chr15:88669523:G:A	60:chr15:88669523:G:A	0.001818
11_c4-b	11	NOTCH1	MODERATE	c.4918G>A	p.Ala1640Thr	0	FALSE	chr9:139399225:C:T	60:chr9:139399225:C:T	0.002442
11_c4-b	11	EGFR	MODERATE	c.445C>T	p.Arg149Trp	1	FALSE	chr7:55214319:C:T	60:chr7:55214319:C:T	0.002112
25_pro-b	25	ALK	MODERATE	c.4280C>T	p.Ser1427Phe	2	FALSE	chr2:29416673:G:A	63:chr2:29416673:G:A	0.001437
25_pro-b	25	IDH1	MODERATE	c.299G>T	p.Arg100Leu	5	FALSE	chr2:209113208:C:A	63:chr2:209113208:C:A	0.001676
25_pro-b	25	NTRK2	MODERATE	c.1822G>A; c.1870G>A	p.Val608Met; p.Val624Met	0	FALSE	chr9:87563482:G:A	63:chr9:87563482:G:A	0.001625
25_pro-b	25	KRAS	HIGH	c.292G>T	p.Glu98*	1	FALSE	chr12:25378706:C:A	63:chr12:25378706:C:A	0.001932
25_pro-b	25	CACNB1; RPL19	MODIFIER; MODERATE	c.-209C>T; c.82G>A	; p.Glu28Lys	0	FALSE	chr17:37357542:G:A	63:chr17:37357542:G:A	0.001873
25_pro-b	25	IGF1R	MODERATE	c.3905T>C; c.3908T>C	p.Val1302Ala; p.Val1303Ala	0	FALSE	chr15:99500475:T:C	63:chr15:99500475:T:C	0.001817
25_pro-b	25	MET	MODERATE	c.2335G>A; c.2389G>A	p.Val779Met; p.Val797Met	1	FALSE	chr7:116399515:G:A	63:chr7:116399515:G:A	0.001516
25_pro-b	25	C9orf53; CDKN2A	MODIFIER; MODERATE	n.*616C>G; c.*140G>C; c.217G>C; c.260G>C	; p.Ala73Pro; p.Arg87Pro	1	FALSE	chr9:21971141:C:G	63:chr9:21971141:C:G	0.011382
25_pro-b	25	PIK3CA	MODERATE	c.3068G>A	p.Arg1023Gln	4	FALSE	chr3:178952013:G:A	63:chr3:178952013:G:A	0.001538

25_pro-b	25	KIT	MODERATE	c.1726C>T; c.1738C>T	p.His576Tyr; p.His580Tyr	2	FALSE	chr4:55593672:C:T	63:chr4:55593672:C:T	0.001589
25_pro-b	25	MET	MODERATE	c.487T>C	p.Ser163Pro	1	FALSE	chr7:116339625:T:C	63:chr7:116339625:T:C	0.003867
38_pro-b	38	MET	HIGH	c.1639C>T	p.Arg547*	2	FALSE	chr7:116381017:C:T	65:chr7:116381017:C:T	0.001029
38_pro-b	38	TP53	HIGH; MODIFIER	c.151G>T; c.34G>T; c.-279G>T; c.-360G>T	p.Glu51*; p.Glu12*;	10	FALSE	chr17:7579536:C:A	65:chr17:7579536:C:A	0.001686
38_pro-b	38	SMO	MODERATE	c.1045A>C	p.Thr349Pro	0	FALSE	chr7:128846115:A:C	65:chr7:128846115:A:C	0.001195
38_pro-b	38	C9orf53; CDKN2A	MODIFIER; MODERATE	n.*616C>G; c.*140G>C; c.217G>C; c.260G>C	; p.Ala73Pro; p.Arg87Pro	1	FALSE	chr9:21971141:C:G	65:chr9:21971141:C:G	0.01487
38_pro-b	38	PTEN	MODERATE	c.421C>A	p.His141Asn	2	FALSE	chr10:89692937:C:A	65:chr10:89692937:C:A	0.001506
38_pro-b	38	NTRK1	MODERATE	c.2028C>A; c.2118C>A; c.2136C>A	p.Ser676Arg; p.Ser706Arg; p.Ser712Arg	1	FALSE	chr1:156849880:C:A	65:chr1:156849880:C:A	0.001349
38_pro-b	38	NTRK1	MODERATE	c.184G>A; c.274G>A	p.Glu62Lys; p.Glu92Lys	1	FALSE	chr1:156834207:G:A	65:chr1:156834207:G:A	0.001524
38_pro-b	38	ATM	MODERATE	c.7328G>A	p.Arg2443Gln	0	FALSE	chr11:108200961:G:A	65:chr11:108200961:G:A	0.001158
38_pro-b	38	NF1	HIGH	c.5294C>A; c.5357C>A	p.Ser1765*; p.Ser1786*	1	FALSE	chr17:29654605:C:A	65:chr17:29654605:C:A	0.000995
38_pro-b	38	TP53	MODERATE	c.128G>A; c.407G>A; c.47G>A; c.524G>A	p.Arg43His; p.Arg136His; p.Arg16His; p.Arg175His	979	FALSE	chr17:7578406:C:T	65:chr17:7578406:C:T	0.001542
38_pro-b	38	NOTCH1	MODERATE	c.2528A>G	p.Glu843Gly	0	FALSE	chr9:139405663:T:C	65:chr9:139405663:T:C	0.229068
38_pro-b	38	PIK3CA	MODERATE	c.1633G>A	p.Glu545Lys	1189	FALSE	chr3:178936091:G:A	65:chr3:178936091:G:A	0.203255

38_pro-b	38	HOXD-AS2; HOXD8	MODIFIER; MODERATE	n.*692G>T; c.105C>A; c.654C>A; c.657C>A	; p.Asn35Lys; p.Asn218Lys; p.Asn219Lys	0	FALSE	chr2:176996124:C:A	65:chr2:176996124:C:A	0.001396
38_pro-b	38	HRAS; LRRC56	MODERATE; MODIFIER	c.175G>A; c.-506C>T	p.Ala59Thr;	2	FALSE	chr11:533881:C:T	65:chr11:533881:C:T	0.001458
38_pro-b	38	EPHA3	HIGH	c.406C>T	p.Arg136*	0	FALSE	chr3:89259262:C:T	65:chr3:89259262:C:T	0.001091
38_pro-b	38	ALK	MODERATE	c.2629G>T	p.Ala877Ser	1	FALSE	chr2:29455173:C:A	65:chr2:29455173:C:A	0.001507
38_pro-b	38	IGF1R	MODERATE	c.3934T>C; c.3937T>C	p.Ser1312Pro; p.Ser1313Pro	0	FALSE	chr15:99500504:T:C	65:chr15:99500504:T:C	0.001303
38_pro-b	38	DDR2	MODERATE	c.313C>A	p.Arg105Ser	2	FALSE	chr1:162724541:C:A	65:chr1:162724541:C:A	0.000749
38_pro-b	38	TP53	MODIFIER; MODERATE	c.*137A>G; c.*225A>G; c.1001A>G; c.1118A>G; c.641A>G; c.722A>G	; p.Lys334Arg; p.Lys373Arg; p.Lys214Arg; p.Lys241Arg	1	FALSE	chr17:7572991:T:C	65:chr17:7572991:T:C	0.00496
38_pro-b	38	TP53	MODERATE	c.337G>A; c.418G>A; c.697G>A; c.814G>A	p.Val113Met; p.Val140Met; p.Val233Met; p.Val272Met	85	FALSE	chr17:7577124:C:T	65:chr17:7577124:C:T	0.00816
38_pro-b	38	MIR4673; NOTCH1	MODIFIER; MODERATE	n.*59G>A; c.1024G>A	; p.Ala342Thr	0	FALSE	chr9:139413118:C:T	65:chr9:139413118:C:T	0.001669
38_pro-b	38	FGFR1	MODERATE	c.487C>T; c.493C>T; c.736C>T; c.754C>T; c.760C>T; c.853C>T	p.Arg163Trp; p.Arg165Trp; p.Arg246Trp; p.Arg252Trp; p.Arg254Trp; p.Arg285Trp	1	FALSE	chr8:38282203:G:A	65:chr8:38282203:G:A	0.001896

38_pro-b	38	TP53	HIGH	c.109C>T; c.190C>T; c.469C>T; c.586C>T	p.Arg37*; p.Arg64*; p.Arg157*; p.Arg196*	191	FALSE	chr17:7578263:G:A	65:chr17:7578263:G:A	0.251568
38_pro-b	38	PIK3CA	MODERATE	c.308A>G	p.Glu103Gly	2	FALSE	chr3:178916921:A:G	65:chr3:178916921:A:G	0.000844
38_pro-b	38	KDR	HIGH	c.2830C>T	p.Arg944*	1	FALSE	chr4:55961110:G:A	65:chr4:55961110:G:A	0.001408
38_pro-b	38	TP53	MODERATE	c.116A>G; c.35A>G; c.395A>G; c.512A>G	p.Glu39Gly; p.Glu12Gly; p.Glu132Gly; p.Glu171Gly	3	FALSE	chr17:7578418:T:C	65:chr17:7578418:T:C	0.001517
38_pro-b	38	TP53	MODIFIER; MODERATE	c.*135A>G; c.*47A>G; c.1028A>G; c.551A>G; c.632A>G; c.911A>G	; p.Glu343Gly; p.Glu184Gly; p.Glu211Gly; p.Glu304Gly	1	FALSE	chr17:7573999:T:C	65:chr17:7573999:T:C	0.001239
38_pro-b	38	NTRK1	MODERATE	c.1669C>T; c.1759C>T; c.1777C>T	p.Arg557Trp; p.Arg587Trp; p.Arg593Trp	1	FALSE	chr1:156846336:C:T	65:chr1:156846336:C:T	0.001122
38_pro-b	38	CDH1	MODERATE	c.2074G>A	p.Ala692Thr	0	FALSE	chr16:68857439:G:A	65:chr16:68857439:G:A	0.00118
61_c3-b	61	BRAF	MODERATE	c.1799T>A	p.Val600Glu	23024	FALSE	chr7:140453136:A:T	68:chr7:140453136:A:T	0.261006
61_c3-b	61	TP53	HIGH; MODIFIER	c.181C>T; c.298C>T; c.-279C>T; c.-360C>T	p.Gln61*; p.Gln100*;	16	FALSE	chr17:7579389:G:A	68:chr17:7579389:G:A	0.025597
61_c3-b	61	PTEN	MODERATE	c.284C>T	p.Pro95Leu	5	FALSE	chr10:89692800:C:T	68:chr10:89692800:C:T	0.003252
61_c3-b	61	FLT3	MODERATE	c.2464G>A	p.Gly822Arg	0	FALSE	chr13:28592681:C:T	68:chr13:28592681:C:T	0.002587

61_c3-b	61	TP53	MODERATE	c.130T>C; c.409T>C; c.49T>C; c.526T>C	p.Cys44Arg; p.Cys137Arg; p.Cys17Arg; p.Cys176Arg	15	FALSE	chr17:7578404:A:G	68:chr17:7578404:A:G	0.003077
61_c3-b	61	ERBB2	MODERATE; MODIFIER	c.560G>A; c.605G>A; c.650G>A; n.974G>A	p.Arg187His; p.Arg202His; p.Arg217His;	1	FALSE	chr17:37866345:G:A	68:chr17:37866345:G:A	0.002717
61_c3-b	61	RET	MODERATE	c.1690A>C	p.Thr564Pro	1	FALSE	chr10:43608342:A:C	68:chr10:43608342:A:C	0.004969
61_c3-b	61	HGF	MODERATE	c.973G>A; c.988G>A	p.Asp325Asn; p.Asp330Asn	0	FALSE	chr7:81358973:C:T	68:chr7:81358973:C:T	0.002584
61_c3-b	61	CDKN2A	MODIFIER; MODERATE	c.194-3568A>C; c.52A>C	; p.Thr18Pro	1	FALSE	chr9:21974775:T:G	68:chr9:21974775:T:G	0.013333
61_c3-b	61	SMO	MODERATE	c.1045A>C	p.Thr349Pro	0	FALSE	chr7:128846115:A:C	68:chr7:128846115:A:C	0.012032
61_c3-b	61	NF1	MODERATE	c.2695T>G	p.Leu899Val	3	FALSE	chr17:29556328:T:G	68:chr17:29556328:T:G	0.002869
61_c3-b	61	FBXW7	HIGH	c.1027G>T; c.1267G>T; c.913G>T	p.Gly343*; p.Gly423*; p.Gly305*	0	FALSE	chr4:153249511:C:A	68:chr4:153249511:C:A	0.002894
61_c3-b	61	PTEN	MODERATE	c.283C>T	p.Pro95Ser	3	FALSE	chr10:89692799:C:T	68:chr10:89692799:C:T	0.01626
62_c3-b	62	KDR	MODERATE	c.2915C>T	p.Ser972Leu	1	FALSE	chr4:55961025:G:A	69:chr4:55961025:G:A	0.000461
62_c3-b	62	TP53	MODERATE	c.383A>G; c.464A>G; c.743A>G; c.860A>G	p.Glu128Gly; p.Glu155Gly; p.Glu248Gly; p.Glu287Gly	2	FALSE	chr17:7577078:T:C	69:chr17:7577078:T:C	0.000551
62_c3-b	62	ESR1	MODERATE	c.1003C>A; c.1006C>A; c.1012C>A	p.Pro335Thr; p.Pro336Thr; p.Pro338Thr	0	FALSE	chr6:152265553:C:A	69:chr6:152265553:C:A	0.000792

62_c3-b	62	TP53	MODERATE; MODIFIER	c.236C>T; c.353C>T; c.-279C>T; c.-360C>T	p.Thr79Ile; p.Thr118Ile;	4	FALSE	chr17:7579334:G:A	69:chr17:7579334:G:A	0.000871
62_c3-b	62	EPHA3	MODERATE	c.2641C>A	p.Leu881Ile	0	FALSE	chr3:89499471:C:A	69:chr3:89499471:C:A	0.000301
62_c3-b	62	BRAF	MODERATE	c.1363G>A	p.Gly455Arg	1	FALSE	chr7:140481445:C:T	69:chr7:140481445:C:T	0.000421
62_c3-b	62	ALK	MODERATE	c.619G>A	p.Ala207Thr	1	FALSE	chr2:30142907:C:T	69:chr2:30142907:C:T	0.00081
62_c3-b	62	NOTCH1	MODERATE	c.4733T>G	p.Val1578Gly	0	FALSE	chr9:139399410:A:C	69:chr9:139399410:A:C	0.001691
62_c3-b	62	ATM	MODERATE	c.6503C>T	p.Ser2168Leu	0	FALSE	chr11:108192078:C:T	69:chr11:108192078:C:T	0.000545
62_c3-b	62	TP53	MODERATE	c.367C>T; c.448C>T; c.727C>T; c.844C>T	p.Arg123Trp; p.Arg150Trp; p.Arg243Trp; p.Arg282Trp	479	FALSE	chr17:7577094:G:A	69:chr17:7577094:G:A	0.000843
62_c3-b	62	ALK	MODERATE	c.4435G>A	p.Ala1479Thr	1	FALSE	chr2:29416518:C:T	69:chr2:29416518:C:T	0.000413
62_c3-b	62	ATM	HIGH	c.8545C>T	p.Arg2849*	0	FALSE	chr11:108216596:C:T	69:chr11:108216596:C:T	0.00044
62_c3-b	62	IGF1R	MODERATE	c.3934T>C; c.3937T>C	p.Ser1312Pro; p.Ser1313Pro	0	FALSE	chr15:99500504:T:C	69:chr15:99500504:T:C	0.013181
62_c3-b	62	FGFR3	MODERATE	c.1183G>A; c.1519G>A; c.1525G>A	p.Val395Met; p.Val507Met; p.Val509Met	1	FALSE	chr4:1807188:G:A	69:chr4:1807188:G:A	0.001457
62_c3-b	62	TSC1	MODERATE	c.1964G>A; c.2114G>A; c.2117G>A	p.Arg655His; p.Arg705His; p.Arg706His	0	FALSE	chr9:135779129:C:T	69:chr9:135779129:C:T	0.000481

62_c3-b	62	TP53	MODIFIER; MODERATE	c.*117G>A; c.*29G>A; c.1010G>A; c.533G>A; c.614G>A; c.893G>A	; p.Arg337His; p.Arg178His; p.Arg205His; p.Arg298His	21	FALSE	chr17:7574017:C:T	69:chr17:7574017:C:T	0.000445
62_c3-b	62	STK11	MODERATE	c.1100C>T	p.Thr367Met	1	FALSE	chr19:1223163:C:T	69:chr19:1223163:C:T	0.001206
62_c3-b	62	SMO	MODERATE	c.869G>A	p.Arg290His	0	FALSE	chr7:128845572:G:A	69:chr7:128845572:G:A	0.000551
62_c3-b	62	ERBB2	MODERATE; MODIFIER	c.1042C>T; c.1087C>T; c.1132C>T; n.1456C>T	p.Pro348Ser; p.Pro363Ser; p.Pro378Ser;	1	FALSE	chr17:37868685:C:T	69:chr17:37868685:C:T	0.000466
62_c3-b	62	TP53	MODIFIER; MODERATE	c.-3G>T; c.358G>T; c.475G>T; c.79G>T	; p.Ala120Ser; p.Ala159Ser; p.Ala27Ser	23	FALSE	chr17:7578455:C:A	69:chr17:7578455:C:A	0.00077
62_c3-b	62	AKT3	HIGH	c.109G>T	p.Gly37*	0	FALSE	chr1:243858956:C:A	69:chr1:243858956:C:A	0.00078
62_c3-b	62	MET	MODERATE	c.1024C>A	p.Leu342Ile	1	FALSE	chr7:116340162:C:A	69:chr7:116340162:C:A	0.000451
62_c3-b	62	HGF	HIGH	c.1993G>T; c.2008G>T	p.Glu665*; p.Glu670*	0	FALSE	chr7:81334708:C:A	69:chr7:81334708:C:A	0.00056
62_c3-b	62	KIT	MODERATE	c.1673A>G; c.1685A>G	p.Glu558Gly; p.Glu562Gly	2	FALSE	chr4:55593619:A:G	69:chr4:55593619:A:G	0.000549
62_c3-b	62	KIT	MODERATE	c.1485C>A	p.Asn495Lys	1	FALSE	chr4:55592161:C:A	69:chr4:55592161:C:A	0.00091
62_c3-b	62	CTNNB1	MODERATE	c.2217G>A	p.Met739Ile	0	FALSE	chr3:41280704:G:A	69:chr3:41280704:G:A	0.000536
62_c3-b	62	CDH1	MODERATE	c.1223C>A	p.Ala408Glu	0	FALSE	chr16:68847301:C:A	69:chr16:68847301:C:A	0.000756
62_c3-b	62	PHLPP1	HIGH	c.2179C>T	p.Arg727*	0	FALSE	chr18:60562356:C:T	69:chr18:60562356:C:T	0.000568
62_c3-b	62	NF1	HIGH	c.1307C>A	p.Ser436*	1	FALSE	chr17:29533304:C:A	69:chr17:29533304:C:A	0.000513

62_c3-b	62	NOTCH1	HIGH	c.3880G>T	p.Glu1294*	0	FALSE	chr9:139401189:C:A	69:chr9:139401189:C:A	0.000543
62_c3-b	62	NTRK2	MODERATE	c.412C>A	p.Leu138Ile	0	FALSE	chr9:87322811:C:A	69:chr9:87322811:C:A	0.000633
62_c3-b	62	DDR2	MODERATE	c.1598C>A	p.Thr533Lys	1	FALSE	chr1:162741907:C:A	69:chr1:162741907:C:A	0.000716
62_c3-b	62	PTEN	HIGH	c.633C>A	p.Cys211*	2	FALSE	chr10:89712015:C:A	69:chr10:89712015:C:A	0.000595
62_c3-b	62	PIK3R1	HIGH	c.1494C>A; c.405C>A; c.594C>A; c.684C>A	p.Cys498*; p.Cys135*; p.Cys198*; p.Cys228*	1	FALSE	chr5:67590432:C:A	69:chr5:67590432:C:A	0.000436
62_c3-b	62	RET	MODERATE	c.1907C>T	p.Thr636Met	1	FALSE	chr10:43609955:C:T	69:chr10:43609955:C:T	0.000806
62_c3-b	62	BRAF	MODERATE	c.2012G>A	p.Arg671Gln	1	FALSE	chr7:140439727:C:T	69:chr7:140439727:C:T	0.000608
62_c3-b	62	KDR	MODERATE	c.2309G>T	p.Gly770Val	1	FALSE	chr4:55964928:C:A	69:chr4:55964928:C:A	0.001223
62_c3-b	62	GAPDH; IFFO1; NCAPD2	MODERATE; MODIFIER	c.187G>A; c.61G>A; c.*1743C>T; c.*1746C>T; c.*1770C>T; n.*2798C>T; c.*4252G>A	p.Glu63Lys; p.Glu21Lys;	0	FALSE	chr12:6645907:G:A	69:chr12:6645907:G:A	0.00068
62_c3-b	62	FGFR3	MODERATE	c.1162G>A; c.1498G>A; c.1504G>A	p.Ala388Thr; p.Ala500Thr; p.Ala502Thr	1	FALSE	chr4:1807167:G:A	69:chr4:1807167:G:A	0.001041
62_c3-b	62	FBXW7	MODERATE	c.1444G>T; c.1558G>T; c.1798G>T	p.Asp482Tyr; p.Asp520Tyr; p.Asp600Tyr	0	FALSE	chr4:153245393:C:A	69:chr4:153245393:C:A	0.001035
62_c3-b	62	BRAF	MODERATE	c.1796C>T	p.Thr599Ile	4	FALSE	chr7:140453139:G:A	69:chr7:140453139:G:A	0.000458
62_c3-b	62	TSC2	MODERATE	c.1819G>A	p.Ala607Thr	0	FALSE	chr16:2120559:G:A	69:chr16:2120559:G:A	0.000451

62_c3-b	62	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2305G>A; n.1257C>T	p.Val769Met;	3	FALSE	chr7:55249007:G:A	69:chr7:55249007:G:A	0.00044
62_c3-b	62	TP53	MODERATE; HIGH	c.363G>T; c.480G>T; c.84G>T; c.3G>T	p.Met121Ile; p.Met160Ile; p.Met28Ile; p.Met1?	4	FALSE	chr17:7578450:C:A	69:chr17:7578450:C:A	0.000775
62_c3-b	62	MIR4673; NOTCH1	MODIFIER; MODERATE	n.*59G>T; c.1433G>T	; p.Cys478Phe	0	FALSE	chr9:139412212:C:A	69:chr9:139412212:C:A	0.000744
62_c3-b	62	KIT	MODERATE	c.154G>A	p.Asp52Asn	7	FALSE	chr4:55561764:G:A	69:chr4:55561764:G:A	0.000436
62_c3-b	62	DDR2	MODERATE	c.313C>A	p.Arg105Ser	2	FALSE	chr1:162724541:C:A	69:chr1:162724541:C:A	0.001202
62_c3-b	62	NF1	MODERATE	c.2695T>G	p.Leu899Val	3	FALSE	chr17:29556328:T:G	69:chr17:29556328:T:G	0.014532
62_c3-b	62	TP53	MODERATE	c.387T>A; c.468T>A; c.747T>A; c.864T>A	p.Asn129Lys; p.Asn156Lys; p.Asn249Lys; p.Asn288Lys	2	FALSE	chr17:7577074:A:T	69:chr17:7577074:A:T	0.000543
62_c3-b	62	TSC2	MODERATE	c.2702G>A	p.Arg901His	0	FALSE	chr16:2126131:G:A	69:chr16:2126131:G:A	0.000904
62_c3-b	62	TP53	MODIFIER; MODERATE	c.-30A>G; c.331A>G; c.448A>G; c.52A>G	; p.Thr111Ala; p.Thr150Ala; p.Thr18Ala	1	FALSE	chr17:7578482:T:C	69:chr17:7578482:T:C	0.000846
62_c3-b	62	ALK	MODERATE	c.4192C>T	p.Pro1398Ser	1	FALSE	chr2:29416761:G:A	69:chr2:29416761:G:A	0.000514
62_c3-b	62	FGFR1	MODERATE	c.488G>T; c.494G>T; c.737G>T; c.755G>T; c.761G>T; c.854G>T	p.Arg163Leu; p.Arg165Leu; p.Arg246Leu; p.Arg252Leu; p.Arg254Leu; p.Arg285Leu	1	FALSE	chr8:38282202:C:A	69:chr8:38282202:C:A	0.000859
62_c3-b	62	KDR	MODERATE	c.2323G>T	p.Ala775Ser	1	FALSE	chr4:55964914:C:A	69:chr4:55964914:C:A	0.004656

62_c3-b	62	NF1	HIGH	c.3049C>T	p.Gln1017*	2	FALSE	chr17:29557336:C:T	69:chr17:29557336:C:T	0.000432
62_c3-b	62	MET	MODERATE	c.959C>T	p.Ala320Val	1	FALSE	chr7:116340097:C:T	69:chr7:116340097:C:T	0.000432
62_c3-b	62	TP53	MODERATE; MODIFIER	c.104C>T; c.221C>T; c.-279C>T; c.-360C>T	p.Ala35Val; p.Ala74Val;	1	FALSE	chr17:7579466:G:A	69:chr17:7579466:G:A	0.000951
62_c3-b	62	TP53	MODIFIER; MODERATE	c.-9G>T; c.352G>T; c.469G>T; c.73G>T	; p.Val118Phe; p.Val157Phe; p.Val25Phe	169	FALSE	chr17:7578461:C:A	69:chr17:7578461:C:A	0.001593
62_c3-b	62	CDH1	MODERATE	c.1528G>A	p.Ala510Thr	0	FALSE	chr16:68849625:G:A	69:chr16:68849625:G:A	0.000446
62_c3-b	62	C9orf53; CDKN2A	MODIFIER; MODERATE	n.*616G>A; c.*324C>T; c.*45C>T; c.401C>T	; p.Ala134Val	1	FALSE	chr9:21970957:G:A	69:chr9:21970957:G:A	0.000715
62_c3-b	62	RET	MODERATE	c.1531G>A	p.Glu511Lys	1	FALSE	chr10:43607555:G:A	69:chr10:43607555:G:A	0.000853
62_c3-b	62	PDGFRA	MODERATE	c.418G>A	p.Val140Met	2	FALSE	chr4:55129884:G:A	69:chr4:55129884:G:A	0.000471
62_c3-b	62	ALK	MODERATE	c.874C>T	p.Arg292Cys	1	FALSE	chr2:29917794:G:A	69:chr2:29917794:G:A	0.000492
62_c3-b	62	TP53	MODERATE	c.126G>T; c.405G>T; c.45G>T; c.522G>T	p.Arg42Ser; p.Arg135Ser; p.Arg15Ser; p.Arg174Ser	2	FALSE	chr17:7578408:C:A	69:chr17:7578408:C:A	0.001264
62_c3-b	62	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2324G>A; n.1238C>T	p.Cys775Tyr;	2	FALSE	chr7:55249026:G:A	69:chr7:55249026:G:A	0.000497
62_c3-b	62	HOXD-AS2; HOXD8	MODIFIER; MODERATE	n.*692C>T; c.304G>A; c.853G>A; c.856G>A	; p.Glu102Lys; p.Glu285Lys; p.Glu286Lys	0	FALSE	chr2:176996323:G:A	69:chr2:176996323:G:A	0.000381

62_c3-b	62	TSC1	MODERATE	c.2751G>T; c.2901G>T; c.2904G>T	p.Arg917Ser; p.Arg967Ser; p.Arg968Ser	0	FALSE	chr9:135772642:C:A	69:chr9:135772642:C:A	0.000489
62_c3-b	62	FGFR3	MODIFIER; MODERATE	c.931-398C>A; c.1172C>A; c.1178C>A	; p.Ala391Glu; p.Ala393Glu	34	FALSE	chr4:1806153:C:A	69:chr4:1806153:C:A	0.001206
62_c3-b	62	CDH1	MODERATE	c.760G>A	p.Asp254Asn	0	FALSE	chr16:68844172:G:A	69:chr16:68844172:G:A	0.000465
62_c3-b	62	CTNNB1	MODERATE	c.96C>A	p.Asp32Glu	0	FALSE	chr3:41266099:C:A	69:chr3:41266099:C:A	0.001557
62_c3-b	62	CDH1	MODERATE	c.2074G>A	p.Ala692Thr	0	FALSE	chr16:68857439:G:A	69:chr16:68857439:G:A	0.000751
62_c3-b	62	TP53	MODERATE	c.335A>G; c.416A>G; c.695A>G; c.812A>G	p.Glu112Gly; p.Glu139Gly; p.Glu232Gly; p.Glu271Gly	8	FALSE	chr17:7577126:T:C	69:chr17:7577126:T:C	0.000551
62_c3-b	62	NF1	HIGH	c.5817C>A; c.5880C>A	p.Cys1939*; p.Cys1960*	1	FALSE	chr17:29661923:C:A	69:chr17:29661923:C:A	0.000907
62_c3-b	62	IGF1R	MODERATE	c.3637C>A; c.3640C>A	p.Gln1213Lys; p.Gln1214Lys	0	FALSE	chr15:99491855:C:A	69:chr15:99491855:C:A	0.000521
62_c3-b	62	AR	MODERATE	c.2324G>A; c.728G>A	p.Arg775His; p.Arg243His	0	FALSE	chrX:66941680:G:A	69:chrX:66941680:G:A	0.001015
62_c3-b	62	PIK3CA	MODERATE	c.1636C>A	p.Gln546Lys	127	FALSE	chr3:178936094:C:A	69:chr3:178936094:C:A	0.000467
62_c3-b	62	NF1	MODERATE	c.6943G>A; c.7006G>A	p.Ala2315Thr; p.Ala2336Thr	2	FALSE	chr17:29667607:G:A	69:chr17:29667607:G:A	0.00044
62_c3-b	62	EPHA3	MODERATE	c.1616G>A	p.Ser539Asn	0	FALSE	chr3:89456440:G:A	69:chr3:89456440:G:A	0.000291
62_c3-b	62	PTEN	MODERATE	c.389G>A	p.Arg130Gln	89	FALSE	chr10:89692905:G:A	69:chr10:89692905:G:A	0.000755
62_c3-b	62	CDH1	MODERATE	c.2246G>A	p.Arg749Gln	0	FALSE	chr16:68862158:G:A	69:chr16:68862158:G:A	0.000578
62_c3-b	62	KIT	MODERATE	c.2071G>A; c.2083G>A	p.Glu691Lys; p.Glu695Lys	1	FALSE	chr4:55595593:G:A	69:chr4:55595593:G:A	0.000442

62_c3-b	62	BRAF	MODERATE	c.1331G>A	p.Arg444Gln	2	FALSE	chr7:140481477:C:T	69:chr7:140481477:C:T	0.00043
62_c3-b	62	NF1	HIGH	c.5294C>A; c.5357C>A	p.Ser1765*; p.Ser1786*	1	FALSE	chr17:29654605:C:A	69:chr17:29654605:C:A	0.000435
62_c3-b	62	SMO	MODERATE	c.1045A>C	p.Thr349Pro	0	FALSE	chr7:128846115:A:C	69:chr7:128846115:A:C	0.01241
62_c3-b	62	CDH1	MODERATE	c.779C>A	p.Pro260His	0	FALSE	chr16:68844191:C:A	69:chr16:68844191:C:A	0.000462
62_c3-b	62	FGFR1	MODERATE	c.1060C>T; c.1066C>T; c.1303C>T; c.1327C>T; c.1333C>T; c.1426C>T	p.Arg354Trp; p.Arg356Trp; p.Arg435Trp; p.Arg443Trp; p.Arg445Trp; p.Arg476Trp	2	FALSE	chr8:38275843:G:A	69:chr8:38275843:G:A	0.000424
62_c3-b	62	KDR	MODERATE	c.869G>T	p.Ser290Ile	1	FALSE	chr4:55979578:C:A	69:chr4:55979578:C:A	0.000447
62_c3-b	62	PTEN	MODERATE	c.829A>T	p.Thr277Ser	1	FALSE	chr10:89720678:A:T	69:chr10:89720678:A:T	0.003363
62_c3-b	62	FGFR4	MODERATE	c.1978G>A; c.2062G>A; c.2182G>A	p.Ala660Thr; p.Ala688Thr; p.Ala728Thr	1	FALSE	chr5:176524321:G:A	69:chr5:176524321:G:A	0.00092
62_c3-b	62	CWH43	MODERATE	c.328C>T; c.409C>T	p.Arg110Cys; p.Arg137Cys	0	FALSE	chr4:48994005:C:T	69:chr4:48994005:C:T	0.000733
62_c3-b	62	PIK3CA	MODERATE	c.1727C>A	p.Ser576Tyr	1	FALSE	chr3:178937046:C:A	69:chr3:178937046:C:A	0.000484
62_c3-b	62	NOTCH1	MODERATE	c.4918G>A	p.Ala1640Thr	0	FALSE	chr9:139399225:C:T	69:chr9:139399225:C:T	0.000713
62_c3-b	62	FGFR1	MODIFIER; MODERATE	c.-85G>T; c.107G>T; c.8G>T	; p.Ser36Ile; p.Ser3Ile	1	FALSE	chr8:38314957:C:A	69:chr8:38314957:C:A	0.001166
62_c3-b	62	NTRK1	MODERATE	c.1738G>A; c.1828G>A; c.1846G>A	p.Asp580Asn; p.Asp610Asn; p.Asp616Asn	1	FALSE	chr1:156848954:G:A	69:chr1:156848954:G:A	0.000545
62_c3-b	62	DDR2	MODERATE	c.2560G>A	p.Asp854Asn	3	FALSE	chr1:162750028:G:A	69:chr1:162750028:G:A	0.00031

62_c3-b	62	MET	MODERATE	c.1132G>A	p.Val378Ile	1	FALSE	chr7:116340270:G:A	69:chr7:116340270:G:A	0.000413
62_c3-b	62	VHL	MODIFIER; MODERATE	c.341-3249C>A; c.365C>A	; p.Ala122Glu	0	FALSE	chr3:10188222:C:A	69:chr3:10188222:C:A	0.000551
62_c3-b	62	PDGFRA	MODERATE	c.2824T>C	p.Ser942Pro	1	FALSE	chr4:55155225:T:C	69:chr4:55155225:T:C	0.000758
62_c3-b	62	FLT3	MODERATE	c.2464G>A	p.Gly822Arg	0	FALSE	chr13:28592681:C:T	69:chr13:28592681:C:T	0.00071
62_c3-b	62	FBXW7	MODERATE	c.1069G>A; c.1309G>A; c.955G>A	p.Gly357Arg; p.Gly437Arg; p.Gly319Arg	0	FALSE	chr4:153249469:C:T	69:chr4:153249469:C:T	0.00049
62_c3-b	62	CTNNB1	MODERATE	c.1000G>A	p.Glu334Lys	0	FALSE	chr3:41268762:G:A	69:chr3:41268762:G:A	0.000454
62_c3-b	62	CTNNB1	MODERATE	c.110C>A	p.Ser37Tyr	0	FALSE	chr3:41266113:C:A	69:chr3:41266113:C:A	0.001236
62_c3-b	62	PTEN	MODERATE	c.700C>T	p.Arg234Trp	4	FALSE	chr10:89717675:C:T	69:chr10:89717675:C:T	0.000446
62_c3-b	62	ATM	MODERATE	c.8981A>G	p.Asn2994Ser	0	FALSE	chr11:108235939:A:G	69:chr11:108235939:A:G	0.00051
62_c3-b	62	PTEN	MODERATE	c.421C>A	p.His141Asn	2	FALSE	chr10:89692937:C:A	69:chr10:89692937:C:A	0.000875
62_c3-b	62	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2527G>A; n.-1C>T	p.Val843Ile;	6	FALSE	chr7:55259469:G:A	69:chr7:55259469:G:A	0.000572
62_c3-b	62	CDKN2B; CDKN2B-AS1	MODIFIER; MODERATE	c.*199C>T; c.313C>T; n.371+10930G>A	; p.Arg105Trp	0	FALSE	chr9:22006090:G:A	69:chr9:22006090:G:A	0.000729
62_c3-b	62	KIT	MODERATE	c.389A>G	p.Asn130Ser	3	FALSE	chr4:55564501:A:G	69:chr4:55564501:A:G	0.000507
62_c3-b	62	PIK3CA	MODERATE	c.1022C>T	p.Ala341Val	2	FALSE	chr3:178921540:C:T	69:chr3:178921540:C:T	0.000457
62_c3-b	62	PDGFRA	MODERATE	c.1526C>A	p.Ala509Asp	1	FALSE	chr4:55139865:C:A	69:chr4:55139865:C:A	0.000894
62_c3-b	62	FGFR2	MODIFIER; HIGH	n.936C>T; c.289C>T; c.367C>T; c.634C>T	; p.Gln97*; p.Gln123*; p.Gln212*	2	FALSE	chr10:123298220:G:A	69:chr10:123298220:G:A	0.000699

62_c3-b	62	TP53	MODERATE	c.371G>A; c.452G>A; c.731G>A; c.848G>A	p.Arg124His; p.Arg151His; p.Arg244His; p.Arg283His	24	FALSE	chr17:7577090:C:T	69:chr17:7577090:C:T	0.000844
62_c3-b	62	MAP2K1	MODERATE	c.198C>A	p.Asp66Glu	4	FALSE	chr15:66727482:C:A	69:chr15:66727482:C:A	0.000859
62_c3-b	62	EGFR	MODERATE	c.818C>A	p.Thr273Asn	1	FALSE	chr7:55221774:C:A	69:chr7:55221774:C:A	0.000546
62_c3-b	62	EGFR; EGFR-AS1	LOW; MODIFIER	c.2472C>A; n.-1G>T	p.Gly824Gly;	1	FALSE	chr7:55259414:C:A	69:chr7:55259414:C:A	0.002774
62_c3-b	62	TSC1	MODERATE	c.437G>T; c.590G>T	p.Cys146Phe; p.Cys197Phe	0	FALSE	chr9:135797279:C:A	69:chr9:135797279:C:A	0.000519
62_c3-b	62	C9orf53; CDKN2A	MODIFIER; MODERATE; LOW	n.*616T>C; c.*246A>G; c.323A>G; c.366A>G	; p.Asp108Gly; p.Arg122Arg	2	FALSE	chr9:21971035:T:C	69:chr9:21971035:T:C	0.000721
62_c3-b	62	TSC1	HIGH	c.1921C>T; c.2071C>T; c.2074C>T	p.Arg641*; p.Arg691*; p.Arg692*	0	FALSE	chr9:135779172:G:A	69:chr9:135779172:G:A	0.000495
62_c3-b	62	PDGFRA	MODERATE	c.1202C>A	p.Ala401Asp	1	FALSE	chr4:55136880:C:A	69:chr4:55136880:C:A	0.000582
62_c3-b	62	TP53	MODERATE	c.364G>T; c.445G>T; c.724G>T; c.841G>T	p.Asp122Tyr; p.Asp149Tyr; p.Asp242Tyr; p.Asp281Tyr	28	FALSE	chr17:7577097:C:A	69:chr17:7577097:C:A	0.00085
62_c3-b	62	FLT3	HIGH	c.1243G>T	p.Glu415*	0	FALSE	chr13:28611388:C:A	69:chr13:28611388:C:A	0.000558
62_c3-b	62	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2548C>A; n.-1G>T	p.His850Asn;	1	FALSE	chr7:55259490:C:A	69:chr7:55259490:C:A	0.000875
62_c3-b	62	ATM	HIGH	c.8284C>T	p.Gln2762*	0	FALSE	chr11:108213964:C:T	69:chr11:108213964:C:T	0.000539
62_c3-b	62	NF1	MODERATE	c.5420G>A; c.5483G>A	p.Arg1807Gln; p.Arg1828Gln	2	FALSE	chr17:29654731:G:A	69:chr17:29654731:G:A	0.000366
62_c3-b	62	KIT	MODERATE	c.734C>T	p.Thr245Met	1	FALSE	chr4:55565910:C:T	69:chr4:55565910:C:T	0.000457

62_c3-b	62	PIK3R1	MODERATE	c.1046G>A; c.1136G>A; c.1946G>A; c.857G>A	p.Arg349Gln; p.Arg379Gln; p.Arg649Gln; p.Arg286Gln	4	FALSE	chr5:67592130:G:A	69:chr5:67592130:G:A	0.000974
62_c3-b	62	FBXW7	MODERATE	c.1039C>T; c.1153C>T; c.1393C>T	p.Arg347Cys; p.Arg385Cys; p.Arg465Cys	0	FALSE	chr4:153249385:G:A	69:chr4:153249385:G:A	0.000735
62_c3-b	62	KRAS	HIGH	c.292G>T	p.Glu98*	1	FALSE	chr12:25378706:C:A	69:chr12:25378706:C:A	0.000554
62_c3-b	62	CDH1	MODERATE	c.1676G>A	p.Ser559Asn	0	FALSE	chr16:68853293:G:A	69:chr16:68853293:G:A	0.00073
62_c3-b	62	TSC1	MODERATE	c.530G>A; c.683G>A	p.Arg177Gln; p.Arg228Gln	0	FALSE	chr9:135796804:C:T	69:chr9:135796804:C:T	0.000519
62_c3-b	62	EGFR	MODERATE	c.608G>A	p.Gly203Glu	1	FALSE	chr7:55219035:G:A	69:chr7:55219035:G:A	0.000582
62_c3-b	62	ERBB2; MIEN1; MIR4728	MODERATE; MODIFIER	c.2236G>A; c.2281G>A; c.2326G>A; n.2650G>A; c.*388C>T; n.-1G>A	p.Gly746Ser; p.Gly761Ser; p.Gly776Ser;	5	FALSE	chr17:37880997:G:A	69:chr17:37880997:G:A	0.000883
62_c3-b	62	TP53	MODERATE	c.125G>A; c.404G>A; c.44G>A; c.521G>A	p.Arg42Lys; p.Arg135Lys; p.Arg15Lys; p.Arg174Lys	5	FALSE	chr17:7578409:C:T	69:chr17:7578409:C:T	0.001266
62_c3-b	62	FGFR2	MODIFIER; MODERATE	c.110-14053A>G; c.110-933A>G; n.757-14053A>G; c.302A>G	; p.Asp101Gly	1	FALSE	chr10:123325026:T:C	69:chr10:123325026:T:C	0.000733
62_c3-b	62	EPHA3	MODERATE	c.2306G>A	p.Arg769His	0	FALSE	chr3:89480469:G:A	69:chr3:89480469:G:A	0.000293
62_c3-b	62	TSC1	MODERATE	c.416G>A; c.569G>A	p.Arg139His; p.Arg190His	0	FALSE	chr9:135797300:C:T	69:chr9:135797300:C:T	0.000498

62_c3-b	62	CDH1	MODERATE	c.1711G>A	p.Gly571Ser	0	FALSE	chr16:68853328:G:A	69:chr16:68853328:G:A	0.00062
62_c3-b	62	IGF1R	MODERATE	c.3821G>A; c.3824G>A	p.Arg1274Gln; p.Arg1275Gln	0	FALSE	chr15:99500391:G:A	69:chr15:99500391:G:A	0.000556
62_c3-b	62	RET	MODERATE	c.2038G>A	p.Ala680Thr	1	FALSE	chr10:43610086:G:A	69:chr10:43610086:G:A	0.000448
62_c3-b	62	TP53	MODERATE; MODIFIER	c.206C>T; c.89C>T; c.-279C>T; c.-360C>T	p.Ala69Val; p.Ala30Val;	3	FALSE	chr17:7579481:G:A	69:chr17:7579481:G:A	0.000916
62_c3-b	62	KIT	MODERATE	c.235C>A	p.Gln79Lys	2	FALSE	chr4:55561845:C:A	69:chr4:55561845:C:A	0.001822
62_c3-b	62	NF1	MODERATE	c.1319G>A	p.Arg440Gln	1	FALSE	chr17:29533316:G:A	69:chr17:29533316:G:A	0.000517
62_c3-b	62	NF1	MODERATE	c.5426G>A; c.5489G>A	p.Arg1809His; p.Arg1830His	1	FALSE	chr17:29654737:G:A	69:chr17:29654737:G:A	0.00053
62_c3-b	62	C9orf53; CDKN2A	MODIFIER; MODERATE	n.*616G>A; c.*218C>T; c.295C>T; c.338C>T	; p.Arg99Trp; p.Pro113Leu	2	FALSE	chr9:21971063:G:A	69:chr9:21971063:G:A	0.000691
62_c3-b	62	BRAF	MODERATE	c.914C>T	p.Ala305Val	2	FALSE	chr7:140500228:G:A	69:chr7:140500228:G:A	0.000491
62_c3-b	62	TP53	MODERATE	c.128G>T; c.407G>T; c.47G>T; c.524G>T	p.Arg43Leu; p.Arg136Leu; p.Arg16Leu; p.Arg175Leu	979	FALSE	chr17:7578406:C:A	69:chr17:7578406:C:A	0.000636
62_c3-b	62	NTRK2	MODERATE	c.413T>C	p.Leu138Pro	0	FALSE	chr9:87322812:T:C	69:chr9:87322812:T:C	0.000639
62_c3-b	62	CTNNB1	MODERATE	c.125C>A	p.Thr42Lys	0	FALSE	chr3:41266128:C:A	69:chr3:41266128:C:A	0.0009
62_c3-b	62	PDGFRA	MODERATE	c.2485G>A	p.Gly829Arg	1	FALSE	chr4:55152053:G:A	69:chr4:55152053:G:A	0.000547
62_c3-b	62	MET	MODERATE	c.1690G>A	p.Ala564Thr	1	FALSE	chr7:116381068:G:A	69:chr7:116381068:G:A	0.000683

62_c3-b	62	TP53	MODERATE	c.128G>T; c.209G>T; c.488G>T; c.605G>T	p.Arg43Leu; p.Arg70Leu; p.Arg163Leu; p.Arg202Leu	4	FALSE	chr17:7578244:C:A	69:chr17:7578244:C:A	0.000893
62_c3-b	62	EGFR	MODERATE	c.787A>G	p.Thr263Ala	6	FALSE	chr7:55221743:A:G	69:chr7:55221743:A:G	0.000561
62_c3-b	62	NTRK2	MODERATE	c.1408G>A; c.1456G>A	p.Val470Ile; p.Val486Ile	0	FALSE	chr9:87482169:G:A	69:chr9:87482169:G:A	0.000413
62_c3-b	62	PIK3CA	MODERATE	c.1255C>A	p.His419Asn	1	FALSE	chr3:178927977:C:A	69:chr3:178927977:C:A	0.002193
62_c3-b	62	FGFR1	MODERATE	c.487C>T; c.493C>T; c.736C>T; c.754C>T; c.760C>T; c.853C>T	p.Arg163Trp; p.Arg165Trp; p.Arg246Trp; p.Arg252Trp; p.Arg254Trp; p.Arg285Trp	1	FALSE	chr8:38282203:G:A	69:chr8:38282203:G:A	0.000861
62_c3-b	62	FGFR3	MODIFIER; MODERATE	c.931-308G>A; c.1262G>A; c.1268G>A	; p.Arg421Gln; p.Arg423Gln	1	FALSE	chr4:1806243:G:A	69:chr4:1806243:G:A	0.001049
62_c3-b	62	PIK3CA	MODERATE	c.3180C>A	p.His1060Gln	2	FALSE	chr3:178952125:C:A	69:chr3:178952125:C:A	0.000553
62_c3-b	62	ATM	MODERATE	c.5713T>C	p.Ser1905Pro	0	FALSE	chr11:108178662:T:C	69:chr11:108178662:T:C	0.000444
62_c3-b	62	CDKN2A	MODIFIER; MODERATE	c.194-3568A>C; c.52A>C	; p.Thr18Pro	1	FALSE	chr9:21974775:T:G	69:chr9:21974775:T:G	0.006079
62_c3-b	62	NOTCH1	MODERATE	c.5885G>A	p.Arg1962His	0	FALSE	chr9:139395053:C:T	69:chr9:139395053:C:T	0.000928
62_c3-b	62	GNA11	MODERATE	c.1030G>A	p.Val344Met	1	FALSE	chr19:3121127:G:A	69:chr19:3121127:G:A	0.000749
62_c3-b	62	KDR	MODERATE	c.115G>T	p.Asp39Tyr	1	FALSE	chr4:55987310:C:A	69:chr4:55987310:C:A	0.000405
62_c3-b	62	CTNNB1	MODERATE	c.953G>A	p.Ser318Asn	0	FALSE	chr3:41268715:G:A	69:chr3:41268715:G:A	0.000605
62_c3-b	62	KDR	MODERATE	c.583G>T	p.Ala195Ser	1	FALSE	chr4:55981116:C:A	69:chr4:55981116:C:A	0.000386

62_c3-b	62	TP53	MODERATE	c.181T>C; c.262T>C; c.541T>C; c.658T>C	p.Tyr61His; p.Tyr88His; p.Tyr181His; p.Tyr220His	16	FALSE	chr17:7578191:A:G	69:chr17:7578191:A:G	0.000805
62_c3-b	62	EPHA3	HIGH	c.1515C>A	p.Tyr505*	0	FALSE	chr3:89448551:C:A	69:chr3:89448551:C:A	0.000669
62_c3-b	62	EGFR	MODERATE	c.3289G>A	p.Val1097Ile	1	FALSE	chr7:55272966:G:A	69:chr7:55272966:G:A	0.000731
62_c3-b	62	ATM	HIGH	c.2558C>A	p.Ser853*	0	FALSE	chr11:108137989:C:A	69:chr11:108137989:C:A	0.000804
62_c3-b	62	NF1	MODERATE	c.7747C>T; c.7810C>T	p.Leu2583Phe; p.Leu2604Phe	1	FALSE	chr17:29684049:C:T	69:chr17:29684049:C:T	0.000446
62_c3-b	62	EPHA3	MODERATE	c.1234G>A	p.Val412Ile	0	FALSE	chr3:89391168:G:A	69:chr3:89391168:G:A	0.000685
62_c3-b	62	KDR	HIGH	c.2830C>T	p.Arg944*	1	FALSE	chr4:55961110:G:A	69:chr4:55961110:G:A	0.000552
62_c3-b	62	FGFR3	MODERATE	c.1177G>A; c.1513G>A; c.1519G>A	p.Val393Ile; p.Val505Ile; p.Val507Ile	1	FALSE	chr4:1807182:G:A	69:chr4:1807182:G:A	0.00197
62_c3-b	62	TP53	MODIFIER; MODERATE	c.-61G>T; c.21G>T; c.300G>T; c.417G>T	; p.Lys7Asn; p.Lys100Asn; p.Lys139Asn	7	FALSE	chr17:7578513:C:A	69:chr17:7578513:C:A	0.000745
62_c3-b	62	HRAS; LRRC56	MODERATE; MODIFIER	c.183G>T; c.-506C>A	p.Gln61His;	15	FALSE	chr11:533873:C:A	69:chr11:533873:C:A	0.000527
62_c3-b	62	CWH43	MODERATE	c.1532C>T; c.1613C>T	p.Ser511Leu; p.Ser538Leu	0	FALSE	chr4:49034687:C:T	69:chr4:49034687:C:T	0.000469
62_c3-b	62	ATM	MODERATE	c.6154G>A	p.Glu2052Lys	0	FALSE	chr11:108186796:G:A	69:chr11:108186796:G:A	0.000426
62_c3-b	62	FBXW7	MODERATE	c.1204G>T; c.1318G>T; c.1558G>T	p.Asp402Tyr; p.Asp440Tyr; p.Asp520Tyr	0	FALSE	chr4:153247244:C:A	69:chr4:153247244:C:A	0.000466
62_c3-b	62	RET	MODERATE	c.1690A>C	p.Thr564Pro	1	FALSE	chr10:43608342:A:C	69:chr10:43608342:A:C	0.009893

62_c3-b	62	FBXW7	MODERATE	c.1040G>T; c.1154G>T; c.1394G>T	p.Arg347Leu; p.Arg385Leu; p.Arg465Leu	0	FALSE	chr4:153249384:C:A	69:chr4:153249384:C:A	0.000736
62_c3-b	62	NOTCH1	MODERATE	c.3859C>T	p.Arg1287Cys	0	FALSE	chr9:139401210:G:A	69:chr9:139401210:G:A	0.000556
62_c3-b	62	CSDE1; NRAS	MODIFIER; MODERATE	c.*2430A>G; c.*2523A>G; c.*2817A>G; c.*2910A>G; c.*2964A>G; c.*3057A>G; c.182A>G	; p.Gln61Arg	1103	FALSE	chr1:115256529:T:C	69:chr1:115256529:T:C	0.324876
62_c3-b	62	GAPDH; IFFO1; NCAPD2	MODERATE; MODIFIER	c.148G>A; c.274G>A; c.*1743C>T; c.*1746C>T; c.*1770C>T; n.*2798C>T; c.*4252G>A	p.Ala50Thr; p.Ala92Thr;	0	FALSE	chr12:6646123:G:A	69:chr12:6646123:G:A	0.000762
62_c3-b	62	GNA11	MODERATE	c.1052T>C	p.Leu351Pro	1	FALSE	chr19:3121149:T:C	69:chr19:3121149:T:C	0.000578
62_c3-b	62	TP53	MODIFIER; MODERATE	c.*137A>G; c.*225A>G; c.1001A>G; c.1118A>G; c.641A>G; c.722A>G	; p.Lys334Arg; p.Lys373Arg; p.Lys214Arg; p.Lys241Arg	1	FALSE	chr17:7572991:T:C	69:chr17:7572991:T:C	0.00148
62_c3-b	62	IGF1R	MODERATE	c.3905T>C; c.3908T>C	p.Val1302Ala; p.Val1303Ala	0	FALSE	chr15:99500475:T:C	69:chr15:99500475:T:C	0.004827
62_c3-b	62	FGFR4	MODIFIER; MODERATE	c.1058-174G>A; c.1078G>A	; p.Ala360Thr	1	FALSE	chr5:176520159:G:A	69:chr5:176520159:G:A	0.000657

62_c3-b	62	NTRK1	MODERATE	c.1940T>G; c.2030T>G; c.2048T>G	p.Val647Gly; p.Val677Gly; p.Val683Gly	2	FALSE	chr1:156849792:T:G	69:chr1:156849792:T:G	0.013151
62_c3-b	62	ERBB2; MIEN1; MIR4728	MODERATE; MODIFIER	c.2261G>A; c.2306G>A; c.2351G>A; n.2675G>A; c.*388C>T; n.-1G>A	p.Arg754His; p.Arg769His; p.Arg784His;	1	FALSE	chr17:37881022:G:A	69:chr17:37881022:G:A	0.000515
62_c3-b	62	TP53	MODERATE	c.145G>T; c.226G>T; c.505G>T; c.622G>T	p.Asp49Tyr; p.Asp76Tyr; p.Asp169Tyr; p.Asp208Tyr	2	FALSE	chr17:7578227:C:A	69:chr17:7578227:C:A	0.000483
62_c3-b	62	PDGFRA	MODERATE	c.1876G>A	p.Val626Met	1	FALSE	chr4:55143644:G:A	69:chr4:55143644:G:A	0.000823
62_c3-b	62	ATM	MODERATE	c.3925G>A	p.Ala1309Thr	0	FALSE	chr11:108155132:G:A	69:chr11:108155132:G:A	0.000416
62_c3-b	62	EPHA3	MODERATE	c.1760A>T	p.His587Leu	0	FALSE	chr3:89457279:A:T	69:chr3:89457279:A:T	0.000425
62_c3-b	62	HGF	MODERATE	c.1255C>T; c.1270C>T	p.Arg419Cys; p.Arg424Cys	0	FALSE	chr7:81350062:G:A	69:chr7:81350062:G:A	0.000572
62_c3-b	62	EPHA3	MODERATE	c.1535G>A	p.Arg512Gln	0	FALSE	chr3:89448571:G:A	69:chr3:89448571:G:A	0.000654
62_c3-b	62	EPHA3	MODERATE	c.237C>A	p.Asn79Lys	0	FALSE	chr3:89259093:C:A	69:chr3:89259093:C:A	0.00072
62_c3-b	62	NTRK2	MODERATE	c.1628A>G; c.1676A>G	p.Glu543Gly; p.Glu559Gly	0	FALSE	chr9:87549119:A:G	69:chr9:87549119:A:G	0.000899
62_c3-b	62	MET	HIGH	c.1619G>A	p.Trp540*	1	FALSE	chr7:116380997:G:A	69:chr7:116380997:G:A	0.000736
62_c3-b	62	NF1	MODERATE	c.1681T>C	p.Trp561Arg	1	FALSE	chr17:29548907:T:C	69:chr17:29548907:T:C	0.000505
62_c3-b	62	DDR2	MODERATE	c.257T>C	p.Phe86Ser	1	FALSE	chr1:162724485:T:C	69:chr1:162724485:T:C	0.000425
62_c3-b	62	PIK3CA	MODERATE	c.1093G>A	p.Glu365Lys	6	FALSE	chr3:178922324:G:A	69:chr3:178922324:G:A	0.000467

62_c3-b	62	HGF	MODERATE	c.2157G>T; c.2172G>T	p.Lys719Asn; p.Lys724Asn	0	FALSE	chr7:81331912:C:A	69:chr7:81331912:C:A	0.000629
62_c3-b	62	NF1	MODERATE	c.8070G>T; c.8133G>T	p.Leu2690Phe; p.Leu2711Phe	1	FALSE	chr17:29686006:G:T	69:chr17:29686006:G:T	0.006913
62_c3-b	62	PTEN	MODERATE	c.392C>A	p.Thr131Asn	2	FALSE	chr10:89692908:C:A	69:chr10:89692908:C:A	0.001004
62_c3-b	62	VHL	MODIFIER; MODERATE	c.341-3184G>A; c.430G>A	; p.Gly144Arg	0	FALSE	chr3:10188287:G:A	69:chr3:10188287:G:A	0.000586
62_c3-b	62	NOTCH1	MODERATE	c.5033T>A	p.Leu1678Gln	0	FALSE	chr9:139397768:A:T	69:chr9:139397768:A:T	0.000982
62_c3-b	62	EPHA3	MODERATE	c.2734A>G	p.Thr912Ala	0	FALSE	chr3:89521657:A:G	69:chr3:89521657:A:G	0.000484
62_c3-b	62	ATM	MODERATE	c.1634C>A	p.Ala545Glu	0	FALSE	chr11:108122590:C:A	69:chr11:108122590:C:A	0.000456
62_c3-b	62	PTEN	MODERATE	c.443C>A	p.Ala148Glu	1	FALSE	chr10:89692959:C:A	69:chr10:89692959:C:A	0.001923
62_c3-b	62	APC	MODERATE	c.1771G>A; c.1825G>A	p.Val591Ile; p.Val609Ile	0	FALSE	chr5:112170729:G:A	69:chr5:112170729:G:A	0.000822
62_c3-b	62	PTEN	MODERATE	c.361G>A	p.Ala121Thr	3	FALSE	chr10:89692877:G:A	69:chr10:89692877:G:A	0.00077
62_c3-b	62	C9orf53; CDKN2A	MODIFIER; MODERATE; LOW	n.*616T>G; c.*120A>C; c.197A>C; c.240A>C	; p.His66Pro; p.Pro80Pro	1	FALSE	chr9:21971161:T:G	69:chr9:21971161:T:G	0.025143
62_c3-b	62	GNA11	MODERATE	c.440G>A	p.Arg147His	1	FALSE	chr19:3113446:G:A	69:chr19:3113446:G:A	0.000962
62_c3-b	62	NRAS	MODERATE	c.490C>T	p.Arg164Cys	1	FALSE	chr1:115251236:G:A	69:chr1:115251236:G:A	0.000408
62_c3-b	62	CTNNB1	MODERATE	c.1346G>A	p.Arg449His	0	FALSE	chr3:41275180:G:A	69:chr3:41275180:G:A	0.00086
62_c3-b	62	BRAF	MODERATE	c.1813A>G	p.Ser605Gly	4	FALSE	chr7:140453122:T:C	69:chr7:140453122:T:C	0.000468
62_c3-b	62	NTRK1	MODERATE	c.1768C>A; c.1858C>A; c.1876C>A	p.Gln590Lys; p.Gln620Lys; p.Gln626Lys	1	FALSE	chr1:156848984:C:A	69:chr1:156848984:C:A	0.000529

62_c3-b	62	PIK3R1	MODERATE	c.1540C>T; c.451C>T; c.640C>T; c.730C>T	p.Arg514Cys; p.Arg151Cys; p.Arg214Cys; p.Arg244Cys	2	FALSE	chr5:67590478:C:T	69:chr5:67590478:C:T	0.000525
62_c3-b	62	PIK3R1	MODERATE	c.1082G>A; c.1271G>A; c.1361G>A; c.2171G>A	p.Arg361Gln; p.Arg424Gln; p.Arg454Gln; p.Arg724Gln	1	FALSE	chr5:67593425:G:A	69:chr5:67593425:G:A	0.000344
62_c3-b	62	NF1	MODERATE	c.2617C>T	p.Arg873Cys	1	FALSE	chr17:29556250:C:T	69:chr17:29556250:C:T	0.000389
62_c3-b	62	EPHA3	MODERATE	c.2821G>A	p.Asp941Asn	0	FALSE	chr3:89521744:G:A	69:chr3:89521744:G:A	0.000508
62_c3-b	62	ESR1	HIGH	c.469C>T	p.Arg157*	0	FALSE	chr6:152163748:C:T	69:chr6:152163748:C:T	0.000596
62_c3-b	62	ATM	MODERATE	c.412G>A	p.Gly138Arg	0	FALSE	chr11:108106477:G:A	69:chr11:108106477:G:A	0.000776
62_c3-b	62	TP53	MODERATE	c.131G>A; c.410G>A; c.50G>A; c.527G>A	p.Cys44Tyr; p.Cys137Tyr; p.Cys17Tyr; p.Cys176Tyr	143	FALSE	chr17:7578403:C:T	69:chr17:7578403:C:T	0.000629
62_c3-b	62	KDR	MODERATE	c.2497C>T	p.Arg833Trp	1	FALSE	chr4:55964316:G:A	69:chr4:55964316:G:A	0.000472
62_c3-b	62	TSC1	MODERATE	c.365C>T; c.518C>T	p.Ala122Val; p.Ala173Val	0	FALSE	chr9:135797351:G:A	69:chr9:135797351:G:A	0.001037
62_c3-b	62	IGF1R	MODERATE	c.2824G>A; c.2827G>A	p.Ala942Thr; p.Ala943Thr	0	FALSE	chr15:99472831:G:A	69:chr15:99472831:G:A	0.000422
62_c3-b	62	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2568T>G; n.-1A>C	p.Phe856Leu;	1	FALSE	chr7:55259510:T:G	69:chr7:55259510:T:G	0.001438
62_c3-b	62	KIT	MODERATE	c.1486G>A	p.Asp496Asn	1	FALSE	chr4:55592162:G:A	69:chr4:55592162:G:A	0.00061
62_c3-b	62	TSC2	MODERATE	c.673G>A	p.Val225Met	0	FALSE	chr16:2106669:G:A	69:chr16:2106669:G:A	0.000578
62_c3-b	62	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2576C>A; n.-1G>T	p.Ala859Asp;	1	FALSE	chr7:55259518:C:A	69:chr7:55259518:C:A	0.000599

70_c4-b	70	FBXW7	MODERATE	c.232A>T; c.346A>T; c.586A>T	p.Thr78Ser; p.Thr116Ser; p.Thr196Ser	0	FALSE	chr4:153268222:T:A	70:chr4:153268222:T:A	0.013396
70_c4-b	70	NTRK1	MODERATE	c.1940T>G; c.2030T>G; c.2048T>G	p.Val647Gly; p.Val677Gly; p.Val683Gly	2	FALSE	chr1:156849792:T:G	70:chr1:156849792:T:G	0.01291
70_c4-b	70	PIK3CA	MODERATE	c.1255C>A	p.His419Asn	1	FALSE	chr3:178927977:C:A	70:chr3:178927977:C:A	0.002215
70_c4-b	70	ROS1	MODERATE	c.5651G>A	p.Arg1884Lys	1	FALSE	chr6:117642548:C:T	70:chr6:117642548:C:T	0.001304
70_c4-b	70	KIT	MODERATE	c.2398C>T; c.2410C>T	p.Arg800Trp; p.Arg804Trp	4	FALSE	chr4:55599284:C:T	70:chr4:55599284:C:T	0.001926
70_c4-b	70	CTNNB1	MODERATE	c.1564G>A	p.Ala522Thr	0	FALSE	chr3:41275669:G:A	70:chr3:41275669:G:A	0.001207
70_c4-b	70	NOTCH1	MODERATE	c.3374C>T	p.Ala1125Val	0	FALSE	chr9:139402543:G:A	70:chr9:139402543:G:A	0.002639
70_c4-b	70	TP53	MODIFIER; MODERATE	c.-3G>T; c.358G>T; c.475G>T; c.79G>T	; p.Ala120Ser; p.Ala159Ser; p.Ala27Ser	23	FALSE	chr17:7578455:C:A	70:chr17:7578455:C:A	0.001339
70_c4-b	70	NF1	HIGH	c.1007G>A	p.Trp336*	1	FALSE	chr17:29527558:G:A	70:chr17:29527558:G:A	0.001174
70_c4-b	70	IGF1R	MODERATE	c.3905T>C; c.3908T>C	p.Val1302Ala; p.Val1303Ala	0	FALSE	chr15:99500475:T:C	70:chr15:99500475:T:C	0.002436
70_c4-b	70	IGF1R	MODERATE	c.3934T>C; c.3937T>C	p.Ser1312Pro; p.Ser1313Pro	0	FALSE	chr15:99500504:T:C	70:chr15:99500504:T:C	0.018076
70_c4-b	70	TP53	MODIFIER; MODERATE	c.*137A>G; c.*225A>G; c.1001A>G; c.1118A>G; c.641A>G; c.722A>G	; p.Lys334Arg; p.Lys373Arg; p.Lys214Arg; p.Lys241Arg	1	FALSE	chr17:7572991:T:C	70:chr17:7572991:T:C	0.0016

70_c4-b	70	CDKN2B; CDKN2B-AS1	MODIFIER; MODERATE	c.*253C>T; c.367C>T; n.371+10876G>A	; p.Arg123Trp	0	FALSE	chr9:22006036:G:A	70:chr9:22006036:G:A	0.001565
70_c4-b	70	SMO	MODERATE	c.1045A>C	p.Thr349Pro	0	FALSE	chr7:128846115:A:C	70:chr7:128846115:A:C	0.009793
70_c4-b	70	GNA11	MODERATE	c.1052T>C	p.Leu351Pro	1	FALSE	chr19:3121149:T:C	70:chr19:3121149:T:C	0.001961
70_c4-b	70	NTRK1	MODERATE	c.1853G>A; c.1943G>A; c.1961G>A	p.Arg618His; p.Arg648His; p.Arg654His	3	FALSE	chr1:156849069:G:A	70:chr1:156849069:G:A	0.001343
70_c4-b	70	PTEN	MODERATE	c.518G>A	p.Arg173His	27	FALSE	chr10:89711900:G:A	70:chr10:89711900:G:A	0.001289
70_c4-b	70	PTEN	MODERATE	c.443C>A	p.Ala148Glu	1	FALSE	chr10:89692959:C:A	70:chr10:89692959:C:A	0.001438
70_c4-b	70	ERBB2; MIEN1; MIR4728	MODERATE; MODIFIER	c.3025G>A; c.3070G>A; c.3115G>A; n.3439G>A; c.*388C>T; n.*67G>A	p.Ala1009Thr; p.Ala1024Thr; p.Ala1039Thr;	2	FALSE	chr17:37883212:G:A	70:chr17:37883212:G:A	0.003208
70_c4-b	70	C9orf53; CDKN2A	MODIFIER; MODERATE; LOW	n.*616T>G; c.*120A>C; c.197A>C; c.240A>C	; p.His66Pro; p.Pro80Pro	1	FALSE	chr9:21971161:T:G	70:chr9:21971161:T:G	0.018773
70_c4-b	70	NOTCH1	MODERATE	c.4984C>T	p.Arg1662Trp	0	FALSE	chr9:139399159:G:A	70:chr9:139399159:G:A	0.002973
70_c4-b	70	APC	MODERATE	c.1733C>T; c.1787C>T	p.Ser578Leu; p.Ser596Leu	0	FALSE	chr5:112170691:C:T	70:chr5:112170691:C:T	0.001178
70_c4-b	70	NF1	MODERATE	c.8070G>T; c.8133G>T	p.Leu2690Phe; p.Leu2711Phe	1	FALSE	chr17:29686006:G:T	70:chr17:29686006:G:T	0.011964
70_c4-b	70	ATM	MODERATE	c.6280G>A	p.Glu2094Lys	0	FALSE	chr11:108188181:G:A	70:chr11:108188181:G:A	0.001009
70_c4-b	70	ATM	MODERATE	c.5639C>G	p.Thr1880Arg	0	FALSE	chr11:108175544:C:G	70:chr11:108175544:C:G	0.005829

70_c4-b	70	GAPDH; IFFO1; NCAPD2	MODERATE; MODIFIER	c.148G>A; c.274G>A; c.*1743C>T; c.*1746C>T; c.*1770C>T; n.*2798C>T; c.*4252G>A	p.Ala50Thr; p.Ala92Thr;	0	FALSE	chr12:6646123:G:A	70:chr12:6646123:G:A	0.001466
70_c4-b	70	RET	MODERATE	c.1690A>C	p.Thr564Pro	1	FALSE	chr10:43608342:A:C	70:chr10:43608342:A:C	0.012326
70_c4-b	70	RET	MODERATE	c.1907C>T	p.Thr636Met	1	FALSE	chr10:43609955:C:T	70:chr10:43609955:C:T	0.00092
70_c4-b	70	NF1	MODERATE	c.2695T>G	p.Leu899Val	3	FALSE	chr17:29556328:T:G	70:chr17:29556328:T:G	0.012698
70_c4-b	70	FGFR3	MODERATE	c.599G>A	p.Arg200His	1	FALSE	chr4:1803247:G:A	70:chr4:1803247:G:A	0.001778
70_c4-b	70	NTRK2	MODERATE	c.2017G>A; c.2065G>A	p.Val673Met; p.Val689Met	0	FALSE	chr9:87570325:G:A	70:chr9:87570325:G:A	0.00119
70_c4-b	70	KDR	MODERATE	c.2323G>T	p.Ala775Ser	1	FALSE	chr4:55964914:C:A	70:chr4:55964914:C:A	0.002884
70_c4-b	70	NTRK3	HIGH	c.1348C>T; c.1372C>T	p.Arg450*; p.Arg458*	0	FALSE	chr15:88669526:G:A	70:chr15:88669526:G:A	0.001086
70_c4-b	70	STK11	MODERATE	c.622G>A	p.Asp208Asn	1	FALSE	chr19:1220604:G:A	70:chr19:1220604:G:A	0.002114
70_c4-b	70	FBXW7	MODERATE	c.182G>A; c.296G>A; c.536G>A	p.Arg61His; p.Arg99His; p.Arg179His	0	FALSE	chr4:153271242:C:T	70:chr4:153271242:C:T	0.0013
70_c4-b	70	NTRK1	MODERATE	c.1768C>A; c.1858C>A; c.1876C>A	p.Gln590Lys; p.Gln620Lys; p.Gln626Lys	1	FALSE	chr1:156848984:C:A	70:chr1:156848984:C:A	0.001178
70_c4-b	70	NOTCH1	MODERATE	c.6088T>C	p.Ser2030Pro	0	FALSE	chr9:139393443:A:G	70:chr9:139393443:A:G	0.001431

70_c4-b	70	TP53	MODIFIER; MODERATE	c.*117G>T; c.*29G>T; c.1010G>T; c.533G>T; c.614G>T; c.893G>T	; p.Arg337Leu; p.Arg178Leu; p.Arg205Leu; p.Arg298Leu	21	FALSE	chr17:7574017:C:A	70:chr17:7574017:C:A	0.006176
70_c4-b	70	MAP2K2	MODERATE	c.196G>A	p.Glu66Lys	0	FALSE	chr19:4117524:C:T	70:chr19:4117524:C:T	0.001491
70_c4-b	70	C9orf53; CDKN2A	MODIFIER; MODERATE	n.*616C>G; c.*140G>C; c.217G>C; c.260G>C	; p.Ala73Pro; p.Arg87Pro	1	FALSE	chr9:21971141:C:G	70:chr9:21971141:C:G	0.015278
70_c4-b	70	DDR2	MODERATE	c.1135A>C	p.Thr379Pro	1	FALSE	chr1:162735826:A:C	70:chr1:162735826:A:C	0.001565
70_c4-b	70	CTNNB1	MODERATE	c.122C>A	p.Thr41Asn	0	FALSE	chr3:41266125:C:A	70:chr3:41266125:C:A	0.001085
83_bl-b	83	CTNNB1	MODERATE	c.861C>A	p.Asn287Lys	0	FALSE	chr3:41267277:C:A	71:chr3:41267277:C:A	0.001309
83_bl-b	83	EPHA3	MODERATE	c.1234G>A	p.Val412Ile	0	FALSE	chr3:89391168:G:A	71:chr3:89391168:G:A	0.001283
83_bl-b	83	STK11	MODERATE	c.941C>A	p.Pro314His	2	FALSE	chr19:1223004:C:A	71:chr19:1223004:C:A	0.001718
83_bl-b	83	MAP2K1	MODERATE	c.379G>A	p.Val127Met	1	FALSE	chr15:66729171:G:A	71:chr15:66729171:G:A	0.001864
83_bl-b	83	CDH1	MODERATE	c.1223C>A	p.Ala408Glu	0	FALSE	chr16:68847301:C:A	71:chr16:68847301:C:A	0.001119
83_bl-b	83	HGF	MODERATE	c.1678C>T; c.1693C>T	p.Leu560Phe; p.Leu565Phe	0	FALSE	chr7:81335667:G:A	71:chr7:81335667:G:A	0.001205
83_bl-b	83	NTRK1	MODERATE	c.1039C>T; c.949C>T	p.Arg347Cys; p.Arg317Cys	1	FALSE	chr1:156843613:C:T	71:chr1:156843613:C:T	0.001883
83_bl-b	83	EGFR	MODERATE	c.442G>A	p.Val148Met	1	FALSE	chr7:55214316:G:A	71:chr7:55214316:G:A	0.001453
83_bl-b	83	KRAS	MODERATE	c.35G>A	p.Gly12Asp	11213	FALSE	chr12:25398284:C:T	71:chr12:25398284:C:T	0.002646
83_bl-b	83	IGF1R	MODERATE	c.2380C>T	p.Arg794Trp	0	FALSE	chr15:99465555:C:T	71:chr15:99465555:C:T	0.001193

83_bl-b	83	FBXW7	MODERATE	c.232A>T; c.346A>T; c.586A>T	p.Thr78Ser; p.Thr116Ser; p.Thr196Ser	0	FALSE	chr4:153268222:T:A	71:chr4:153268222:T:A	0.004085
83_bl-b	83	FBXW7	MODERATE	c.1082G>A; c.1196G>A; c.1436G>A	p.Arg361Gln; p.Arg399Gln; p.Arg479Gln	0	FALSE	chr4:153247366:C:T	71:chr4:153247366:C:T	0.001224
83_bl-b	83	KDR	MODERATE	c.2323G>T	p.Ala775Ser	1	FALSE	chr4:55964914:C:A	71:chr4:55964914:C:A	0.001824
83_bl-b	83	TP53	MODERATE	c.236G>A; c.317G>A; c.596G>A; c.713G>A	p.Cys79Tyr; p.Cys106Tyr; p.Cys199Tyr; p.Cys238Tyr	74	FALSE	chr17:7577568:C:T	71:chr17:7577568:C:T	0.003446
83_bl-b	83	NF1	MODERATE	c.2695T>G	p.Leu899Val	3	FALSE	chr17:29556328:T:G	71:chr17:29556328:T:G	0.008075
83_bl-b	83	TP53	MODERATE	c.364G>T; c.445G>T; c.724G>T; c.841G>T	p.Asp122Tyr; p.Asp149Tyr; p.Asp242Tyr; p.Asp281Tyr	28	FALSE	chr17:7577097:C:A	71:chr17:7577097:C:A	0.001376
83_bl-b	83	SMO	MODERATE	c.1045A>C	p.Thr349Pro	0	FALSE	chr7:128846115:A:C	71:chr7:128846115:A:C	0.009726
83_bl-b	83	TP53	MODIFIER; MODERATE	c.-3G>T; c.358G>T; c.475G>T; c.79G>T	; p.Ala120Ser; p.Ala159Ser; p.Ala27Ser	23	FALSE	chr17:7578455:C:A	71:chr17:7578455:C:A	0.001543
83_bl-b	83	TP53	MODERATE	c.341G>A; c.422G>A; c.701G>A; c.818G>A	p.Arg114His; p.Arg141His; p.Arg234His; p.Arg273His	647	TRUE	chr17:7577120:C:T	71:chr17:7577120:C:T	0.001386
83_bl-b	83	IGF1R	MODERATE	c.3934T>C; c.3937T>C	p.Ser1312Pro; p.Ser1313Pro	0	FALSE	chr15:99500504:T:C	71:chr15:99500504:T:C	0.007077
83_bl-b	83	APC	MODERATE	c.1771G>A; c.1825G>A	p.Val591Ile; p.Val609Ile	0	FALSE	chr5:112170729:G:A	71:chr5:112170729:G:A	0.484169

83_bl-b	83	IGF1R	MODERATE	c.3905T>C; c.3908T>C	p.Val1302Ala; p.Val1303Ala	0	FALSE	chr15:99500475:T:C	71:chr15:99500475:T:C	0.002259
83_bl-b	83	NOTCH1	MODERATE	c.5011G>A	p.Val1671Ile	0	FALSE	chr9:139399132:C:T	71:chr9:139399132:C:T	0.509142
83_bl-b	83	RET	MODERATE	c.1690A>C	p.Thr564Pro	1	FALSE	chr10:43608342:A:C	71:chr10:43608342:A:C	0.00836
83_bl-b	83	TSC1	MODERATE	c.2677G>A; c.2827G>A; c.2830G>A	p.Ala893Thr; p.Ala943Thr; p.Ala944Thr	0	FALSE	chr9:135772716:C:T	71:chr9:135772716:C:T	0.001258
83_bl-b	83	PTEN	MODERATE	c.443C>A	p.Ala148Glu	1	FALSE	chr10:89692959:C:A	71:chr10:89692959:C:A	0.001553
83_bl-b	83	NF1	MODERATE	c.3790G>A	p.Glu1264Lys	1	FALSE	chr17:29562710:G:A	71:chr17:29562710:G:A	0.001234
83_bl-b	83	ALK	MODERATE	c.4409C>T	p.Ala1470Val	1	FALSE	chr2:29416544:G:A	71:chr2:29416544:G:A	0.00107
83_bl-b	83	KDR	MODERATE	c.1405G>A	p.Glu469Lys	3	FALSE	chr4:55973911:C:T	71:chr4:55973911:C:T	0.002907
83_bl-b	83	NTRK1	MODERATE	c.1940T>G; c.2030T>G; c.2048T>G	p.Val647Gly; p.Val677Gly; p.Val683Gly	2	FALSE	chr1:156849792:T:G	71:chr1:156849792:T:G	0.016582
78_bl-b	78	DDR2	MODERATE	c.1135A>C	p.Thr379Pro	1	FALSE	chr1:162735826:A:C	76:chr1:162735826:A:C	0.001765
78_bl-b	78	KIT	MODERATE	c.2197G>A; c.2209G>A	p.Asp733Asn; p.Asp737Asn	2	FALSE	chr4:55597561:G:A	76:chr4:55597561:G:A	0.001071
78_bl-b	78	ATM	HIGH	c.4396C>T	p.Arg1466*	0	FALSE	chr11:108160488:C:T	76:chr11:108160488:C:T	0.001258
78_bl-b	78	PTEN	MODERATE	c.829A>T	p.Thr277Ser	1	FALSE	chr10:89720678:A:T	76:chr10:89720678:A:T	0.007788
78_bl-b	78	NF1	MODERATE	c.8070G>T; c.8133G>T	p.Leu2690Phe; p.Leu2711Phe	1	FALSE	chr17:29686006:G:T	76:chr17:29686006:G:T	0.0366
78_bl-b	78	KDR	MODERATE	c.2497C>T	p.Arg833Trp	1	FALSE	chr4:55964316:G:A	76:chr4:55964316:G:A	0.001315
78_bl-b	78	ATM	MODERATE	c.8762C>T	p.Thr2921Met	0	FALSE	chr11:108224583:C:T	76:chr11:108224583:C:T	0.001828
78_bl-b	78	STK11	MODERATE	c.628T>C	p.Cys210Arg	1	FALSE	chr19:1220610:T:C	76:chr19:1220610:T:C	0.002137

78_bl-b	78	KDR	MODERATE	c.2323G>T	p.Ala775Ser	1	FALSE	chr4:55964914:C:A	76:chr4:55964914:C:A	0.005521
78_bl-b	78	NTRK1	MODERATE	c.2028C>A; c.2118C>A; c.2136C>A	p.Ser676Arg; p.Ser706Arg; p.Ser712Arg	1	FALSE	chr1:156849880:C:A	76:chr1:156849880:C:A	0.002885
78_bl-b	78	SMO	MODERATE	c.1045A>C	p.Thr349Pro	0	FALSE	chr7:128846115:A:C	76:chr7:128846115:A:C	0.021753
78_bl-b	78	BRAF	MODERATE	c.1799T>A	p.Val600Glu	23024	FALSE	chr7:140453136:A:T	76:chr7:140453136:A:T	0.001814
78_bl-b	78	MAP2K1	MODERATE	c.198C>A	p.Asp66Glu	4	FALSE	chr15:66727482:C:A	76:chr15:66727482:C:A	0.00156
78_bl-b	78	CTNNB1	MODERATE	c.125C>A	p.Thr42Lys	0	FALSE	chr3:41266128:C:A	76:chr3:41266128:C:A	0.001248
78_bl-b	78	PTEN	HIGH	c.1038C>A	p.Tyr346*	1	FALSE	chr10:89725055:C:A	76:chr10:89725055:C:A	0.001808
78_bl-b	78	CTNNB1	HIGH	c.999C>A	p.Tyr333*	0	FALSE	chr3:41268761:C:A	76:chr3:41268761:C:A	0.001161
78_bl-b	78	IGF1R	MODERATE	c.3934T>C; c.3937T>C	p.Ser1312Pro; p.Ser1313Pro	0	FALSE	chr15:99500504:T:C	76:chr15:99500504:T:C	0.014015
78_bl-b	78	HGF	MODERATE	c.518G>A; c.533G>A	p.Arg173Gln; p.Arg178Gln	0	FALSE	chr7:81381528:C:T	76:chr7:81381528:C:T	0.001246
78_bl-b	78	PIK3CA	MODERATE	c.1255C>A	p.His419Asn	1	FALSE	chr3:178927977:C:A	76:chr3:178927977:C:A	0.002165
78_bl-b	78	DEAR; FBXW7	MODIFIER; MODERATE	n.-1A>G; c.526T>C; c.640T>C; c.880T>C	; p.Ser176Pro; p.Ser214Pro; p.Ser294Pro	0	FALSE	chr4:153253853:A:G	76:chr4:153253853:A:G	0.001652
78_bl-b	78	PDGFRA	MODERATE	c.1516C>A	p.Leu506Ile	2	FALSE	chr4:55139855:C:A	76:chr4:55139855:C:A	0.002037
78_bl-b	78	NRAS	MODERATE	c.394G>A	p.Glu132Lys	2	FALSE	chr1:115252246:C:T	76:chr1:115252246:C:T	0.001097
78_bl-b	78	PTEN	MODERATE	c.389G>A	p.Arg130Gln	89	FALSE	chr10:89692905:G:A	76:chr10:89692905:G:A	0.00122
78_bl-b	78	CWH43	MODERATE	c.209C>T; c.290C>T	p.Ala70Val; p.Ala97Val	0	FALSE	chr4:48993525:C:T	76:chr4:48993525:C:T	0.001229

78_bl-b	78	NTRK1	MODERATE	c.1940T>G; c.2030T>G; c.2048T>G	p.Val647Gly; p.Val677Gly; p.Val683Gly	2	FALSE	chr1:156849792:T:G	76:chr1:156849792:T:G	0.02139
78_bl-b	78	APC	HIGH	c.1228G>T; c.1282G>T	p.Glu410*; p.Glu428*	0	FALSE	chr5:112155011:G:T	76:chr5:112155011:G:T	0.002766
78_bl-b	78	C9orf53; CDKN2A	MODIFIER; MODERATE; LOW	n.*616T>G; c.*120A>C; c.197A>C; c.240A>C	; p.His66Pro; p.Pro80Pro	1	FALSE	chr9:21971161:T:G	76:chr9:21971161:T:G	0.015385
78_bl-b	78	FGFR3	MODERATE	c.1543G>A; c.1879G>A; c.1885G>A	p.Glu515Lys; p.Glu627Lys; p.Glu629Lys	1	FALSE	chr4:1807820:G:A	76:chr4:1807820:G:A	0.001732
78_bl-b	78	C9orf53; CDKN2A	MODIFIER; MODERATE	n.*616C>G; c.*140G>C; c.217G>C; c.260G>C	; p.Ala73Pro; p.Arg87Pro	1	FALSE	chr9:21971141:C:G	76:chr9:21971141:C:G	0.007321
78_bl-b	78	NTHL1; TSC2	MODIFIER; MODERATE	c.-20G>A; c.175C>T	; p.Arg59Trp	0	FALSE	chr16:2100437:C:T	76:chr16:2100437:C:T	0.001399
78_bl-b	78	EGFR	MODERATE	c.442G>A	p.Val148Met	1	FALSE	chr7:55214316:G:A	76:chr7:55214316:G:A	0.001459
78_bl-b	78	CDH1	MODERATE	c.2246G>A	p.Arg749Gln	0	FALSE	chr16:68862158:G:A	76:chr16:68862158:G:A	0.001331
78_bl-b	78	CTNNB1	MODERATE	c.1972G>T	p.Val658Phe	0	FALSE	chr3:41278096:G:T	76:chr3:41278096:G:T	0.00194
78_bl-b	78	AKT1	MODERATE	c.194C>T	p.Thr65Met	1	FALSE	chr14:105243089:G:A	76:chr14:105243089:G:A	0.001741
78_bl-b	78	FOXL2; FOXL2NB; LINC01391	MODERATE; MODIFIER	c.205G>A; c.-132C>T; n.-1G>A	p.Glu69Lys;	0	FALSE	chr3:138665360:C:T	76:chr3:138665360:C:T	0.001522
78_bl-b	78	APC	HIGH	c.1733C>A; c.1787C>A	p.Ser578*; p.Ser596*	0	FALSE	chr5:112170691:C:A	76:chr5:112170691:C:A	0.001277
78_bl-b	78	RET	MODERATE	c.1690A>C	p.Thr564Pro	1	FALSE	chr10:43608342:A:C	76:chr10:43608342:A:C	0.010237
78_bl-b	78	NOTCH1	MODERATE	c.2282C>A	p.Pro761His	0	FALSE	chr9:139407915:G:T	76:chr9:139407915:G:T	0.00161

78_bl-b	78	PTEN	MODERATE	c.1007A>T	p.Tyr336Phe	1	FALSE	chr10:89720856:A:T	76:chr10:89720856:A:T	0.003593
78_bl-b	78	BRAF	MODERATE	c.812G>A	p.Arg271His	1	FALSE	chr7:140501260:C:T	76:chr7:140501260:C:T	0.002009
80_bl-b	80	EPHA3	MODERATE	c.2530C>T	p.Pro844Ser	0	FALSE	chr3:89499360:C:T	77:chr3:89499360:C:T	0.001862
80_bl-b	80	NF1	MODERATE	c.5458C>A; c.5521C>A	p.Gln1820Lys; p.Gln1841Lys	3	FALSE	chr17:29654769:C:A	77:chr17:29654769:C:A	0.00091
80_bl-b	80	IGF1R	MODERATE	c.3934T>C; c.3937T>C	p.Ser1312Pro; p.Ser1313Pro	0	FALSE	chr15:99500504:T:C	77:chr15:99500504:T:C	0.029893
80_bl-b	80	PIK3R1	HIGH	c.1714C>T; c.625C>T; c.814C>T; c.904C>T	p.Gln572*; p.Gln209*; p.Gln272*; p.Gln302*	2	FALSE	chr5:67591121:C:T	77:chr5:67591121:C:T	0.000912
80_bl-b	80	FGFR4	MODIFIER; MODERATE	c.1098-65G>A; c.1251+10G>A; c.1067G>A	; p.Arg356His	1	FALSE	chr5:176520342:G:A	77:chr5:176520342:G:A	0.000882
80_bl-b	80	ATM	HIGH	c.6311G>A	p.Trp2104*	0	FALSE	chr11:108188212:G:A	77:chr11:108188212:G:A	0.001047
80_bl-b	80	PTEN	MODERATE	c.284C>T	p.Pro95Leu	5	FALSE	chr10:89692800:C:T	77:chr10:89692800:C:T	0.001037
80_bl-b	80	BRAF	MODERATE	c.1799T>A	p.Val600Glu	23024	FALSE	chr7:140453136:A:T	77:chr7:140453136:A:T	0.089187
80_bl-b	80	ESR1	MODERATE	c.1297C>T; c.1300C>T; c.1306C>T	p.Arg433Trp; p.Arg434Trp; p.Arg436Trp	0	FALSE	chr6:152382190:C:T	77:chr6:152382190:C:T	0.000962
80_bl-b	80	IGF1R	MODERATE	c.3905T>C; c.3908T>C	p.Val1302Ala; p.Val1303Ala	0	FALSE	chr15:99500475:T:C	77:chr15:99500475:T:C	0.004785
80_bl-b	80	ALG10	MODERATE	c.217A>G	p.Ile73Val	0	FALSE	chr12:34176942:A:G	77:chr12:34176942:A:G	0.000846
80_bl-b	80	GNA11	MODERATE	c.805G>A	p.Val269Ile	1	FALSE	chr19:3119273:G:A	77:chr19:3119273:G:A	0.001005
80_bl-b	80	SMO	MODERATE	c.413G>A	p.Arg138Gln	0	FALSE	chr7:128843306:G:A	77:chr7:128843306:G:A	0.000996
80_bl-b	80	NF1	MODERATE	c.8070G>T; c.8133G>T	p.Leu2690Phe; p.Leu2711Phe	1	FALSE	chr17:29686006:G:T	77:chr17:29686006:G:T	0.035133

80_bl-b	80	MIR4673; NOTCH1	MODIFIER; MODERATE	n.*59A>G; c.890A>G	; p.Asp297Gly	0	FALSE	chr9:139413252:T:C	77:chr9:139413252:T:C	0.002425
80_bl-b	80	FGFR3	MODIFIER; MODERATE	c.931-398C>A; c.1172C>A; c.1178C>A	; p.Ala391Glu; p.Ala393Glu	34	FALSE	chr4:1806153:C:A	77:chr4:1806153:C:A	0.003524
80_bl-b	80	ATM	HIGH	c.5188C>T	p.Arg1730*	0	FALSE	chr11:108172385:C:T	77:chr11:108172385:C:T	0.001374
80_bl-b	80	NTRK1	MODERATE	c.804C>G; c.894C>G	p.His268Gln; p.His298Gln	1	FALSE	chr1:156843468:C:G	77:chr1:156843468:C:G	0.002113
80_bl-b	80	NF1	MODERATE	c.6500C>T; c.6563C>T	p.Ser2167Phe; p.Ser2188Phe	1	FALSE	chr17:29664521:C:T	77:chr17:29664521:C:T	0.001012
80_bl-b	80	NTRK1	MODERATE	c.1940T>G; c.2030T>G; c.2048T>G	p.Val647Gly; p.Val677Gly; p.Val683Gly	2	FALSE	chr1:156849792:T:G	77:chr1:156849792:T:G	0.03006
80_bl-b	80	ALK	MODERATE	c.1049C>T	p.Ser350Leu	1	FALSE	chr2:29754886:G:A	77:chr2:29754886:G:A	0.001066
80_bl-b	80	MIR4673; NOTCH1	MODIFIER; MODERATE	n.*59C>T; c.1510C>T	; p.Arg504Cys	0	FALSE	chr9:139411769:G:A	77:chr9:139411769:G:A	0.001795
80_bl-b	80	ATM	MODERATE	c.8180T>C	p.Val2727Ala	0	FALSE	chr11:108206600:T:C	77:chr11:108206600:T:C	0.000923
80_bl-b	80	PDGFRA	MODERATE	c.452G>A	p.Arg151His	2	FALSE	chr4:55129918:G:A	77:chr4:55129918:G:A	0.000999
80_bl-b	80	MET	MODERATE	c.487T>C	p.Ser163Pro	1	FALSE	chr7:116339625:T:C	77:chr7:116339625:T:C	0.001569
80_bl-b	80	KDR	MODERATE	c.2323G>T	p.Ala775Ser	1	FALSE	chr4:55964914:C:A	77:chr4:55964914:C:A	0.003846
80_bl-b	80	PTEN	MODERATE	c.494G>A	p.Gly165Glu	7	FALSE	chr10:89711876:G:A	77:chr10:89711876:G:A	0.001363
80_bl-b	80	ATM	MODERATE	c.8762C>T	p.Thr2921Met	0	FALSE	chr11:108224583:C:T	77:chr11:108224583:C:T	0.000947
80_bl-b	80	NF1	MODERATE	c.5425C>T; c.5488C>T	p.Arg1809Cys; p.Arg1830Cys	4	FALSE	chr17:29654736:C:T	77:chr17:29654736:C:T	0.000849

80_bl-b	80	EVI2A; NF1	MODIFIER; MODERATE	c.-266C>T; c.-338C>T; c.4882G>A; c.4945G>A	; p.Gly1628Arg; p.Gly1649Arg	1	FALSE	chr17:29652947:G:A	77:chr17:29652947:G:A	0.000823
80_bl-b	80	TP53	MODERATE	c.119T>G; c.38T>G; c.398T>G; c.515T>G	p.Val40Gly; p.Val13Gly; p.Val133Gly; p.Val172Gly	12	FALSE	chr17:7578415:A:C	77:chr17:7578415:A:C	0.001153
80_bl-b	80	KIT	MODERATE	c.1485C>A	p.Asn495Lys	1	FALSE	chr4:55592161:C:A	77:chr4:55592161:C:A	0.000962
80_bl-b	80	FGFR4	MODERATE	c.976G>A	p.Glu326Lys	1	FALSE	chr5:176519704:G:A	77:chr5:176519704:G:A	0.001033
80_bl-b	80	TP53	MODIFIER; MODERATE	c.-17C>T; c.101C>T; c.-279C>T; c.-360C>T	; p.Pro34Leu	2	FALSE	chr17:7579586:G:A	77:chr17:7579586:G:A	0.001265
80_bl-b	80	TP53	MODERATE	c.304A>G; c.385A>G; c.664A>G; c.781A>G	p.Ser102Gly; p.Ser129Gly; p.Ser222Gly; p.Ser261Gly	3	FALSE	chr17:7577500:T:C	77:chr17:7577500:T:C	0.001186
80_bl-b	80	PTEN	MODERATE	c.829A>T	p.Thr277Ser	1	FALSE	chr10:89720678:A:T	77:chr10:89720678:A:T	0.004454
80_bl-b	80	KIT	MODERATE	c.1460G>A	p.Gly487Asp	1	FALSE	chr4:55592136:G:A	77:chr4:55592136:G:A	0.000915
80_bl-b	80	KDR	MODERATE	c.241G>A	p.Asp81Asn	2	FALSE	chr4:55984888:C:T	77:chr4:55984888:C:T	0.001509
80_bl-b	80	TP53	MODERATE; MODIFIER	c.211C>T; c.328C>T; c.-279C>T; c.-360C>T	p.Arg71Cys; p.Arg110Cys;	6	FALSE	chr17:7579359:G:A	77:chr17:7579359:G:A	0.017553
80_bl-b	80	NF1	MODERATE	c.2695T>G	p.Leu899Val	3	FALSE	chr17:29556328:T:G	77:chr17:29556328:T:G	0.006217
80_bl-b	80	ALK	MODERATE	c.562C>T	p.Arg188Cys	2	FALSE	chr2:30142964:G:A	77:chr2:30142964:G:A	0.001277
80_bl-b	80	PTEN	MODERATE	c.392C>A	p.Thr131Asn	2	FALSE	chr10:89692908:C:A	77:chr10:89692908:C:A	0.001401

80_bl-b	80	FGFR1	MODERATE	c.1060C>T; c.1066C>T; c.1303C>T; c.1327C>T; c.1333C>T; c.1426C>T	p.Arg354Trp; p.Arg356Trp; p.Arg435Trp; p.Arg443Trp; p.Arg445Trp; p.Arg476Trp	2	FALSE	chr8:38275843:G:A	77:chr8:38275843:G:A	0.001176
80_bl-b	80	HGF	MODERATE	c.737C>T; c.752C>T	p.Pro246Leu; p.Pro251Leu	0	FALSE	chr7:81372782:G:A	77:chr7:81372782:G:A	0.001108
80_bl-b	80	RET	MODERATE	c.1690A>C	p.Thr564Pro	1	FALSE	chr10:43608342:A:C	77:chr10:43608342:A:C	0.005363
80_bl-b	80	FBXW7	MODERATE	c.1078G>T; c.1318G>T; c.964G>T	p.Asp360Tyr; p.Asp440Tyr; p.Asp322Tyr	0	FALSE	chr4:153249460:C:A	77:chr4:153249460:C:A	0.001998
80_bl-b	80	CTNNB1	MODERATE	c.1972G>T	p.Val658Phe	0	FALSE	chr3:41278096:G:T	77:chr3:41278096:G:T	0.001931
80_bl-b	80	RET	MODERATE	c.1907C>T	p.Thr636Met	1	FALSE	chr10:43609955:C:T	77:chr10:43609955:C:T	0.000813
80_bl-b	80	FBXW7	MODERATE	c.1444G>T; c.1558G>T; c.1798G>T	p.Asp482Tyr; p.Asp520Tyr; p.Asp600Tyr	0	FALSE	chr4:153245393:C:A	77:chr4:153245393:C:A	0.000982
80_bl-b	80	MAP2K1	MODERATE	c.198C>A	p.Asp66Glu	4	FALSE	chr15:66727482:C:A	77:chr15:66727482:C:A	0.001863
80_bl-b	80	TP53	MODERATE	c.355C>T; c.436C>T; c.715C>T; c.832C>T	p.Pro119Ser; p.Pro146Ser; p.Pro239Ser; p.Pro278Ser	59	FALSE	chr17:7577106:G:A	77:chr17:7577106:G:A	0.050592
80_bl-b	80	EGFR; EGFR-AS1	LOW; MODIFIER	c.2284-6C>T; n.1284G>A		1	FALSE	chr7:55248980:C:T	77:chr7:55248980:C:T	0.000828
80_bl-b	80	FLT3	MODERATE	c.2822C>T	p.Ser941Leu	0	FALSE	chr13:28588626:G:A	77:chr13:28588626:G:A	0.000845
80_bl-b	80	TSC2	MODERATE	c.1864C>T	p.Arg622Trp	0	FALSE	chr16:2121535:C:T	77:chr16:2121535:C:T	0.00125
80_bl-b	80	NTRK2	MODERATE	c.1981G>A; c.2029G>A	p.Ala661Thr; p.Ala677Thr	0	FALSE	chr9:87570289:G:A	77:chr9:87570289:G:A	0.001011

80_bl-b	80	FOXL2; FOXL2NB; LINC01391	MODERATE; MODIFIER	c.282T>A; c.-132A>T; n.-1T>A	p.Asn94Lys;	0	FALSE	chr3:138665283:A:T	77:chr3:138665283:A:T	0.012156
82_bl-b	82	C9orf53; CDKN2A	MODIFIER; MODERATE; LOW	n.*616T>G; c.*120A>C; c.197A>C; c.240A>C	; p.His66Pro; p.Pro80Pro	1	FALSE	chr9:21971161:T:G	78:chr9:21971161:T:G	0.031847
82_bl-b	82	CTNNB1	MODERATE	c.1972G>T	p.Val658Phe	0	FALSE	chr3:41278096:G:T	78:chr3:41278096:G:T	0.002745
82_bl-b	82	ATM	MODERATE	c.2075G>A	p.Arg692His	0	FALSE	chr11:108124717:G:A	78:chr11:108124717:G:A	0.000942
82_bl-b	82	EGFR	MODIFIER; MODERATE	c.*1464C>A; c.1476C>A	; p.Ser492Arg	4	FALSE	chr7:55228009:C:A	78:chr7:55228009:C:A	0.001368
82_bl-b	82	NF1	MODERATE	c.7718G>A; c.7781G>A	p.Arg2573His; p.Arg2594His	3	FALSE	chr17:29684020:G:A	78:chr17:29684020:G:A	0.001129
82_bl-b	82	KIT	MODERATE	c.273C>A	p.Asn91Lys	1	FALSE	chr4:55561883:C:A	78:chr4:55561883:C:A	0.001006
82_bl-b	82	NOTCH1	MODERATE	c.4391G>T	p.Ser1464Ile	0	FALSE	chr9:139399957:C:A	78:chr9:139399957:C:A	0.0013
82_bl-b	82	PIK3CA	MODERATE	c.1357G>C	p.Glu453Gln	20	FALSE	chr3:178928079:G:C	78:chr3:178928079:G:C	0.024103
82_bl-b	82	KRAS	MODERATE	c.25G>T	p.Val9Phe	3	FALSE	chr12:25398294:C:A	78:chr12:25398294:C:A	0.001183
82_bl-b	82	IGF1R	MODERATE	c.3934T>C; c.3937T>C	p.Ser1312Pro; p.Ser1313Pro	0	FALSE	chr15:99500504:T:C	78:chr15:99500504:T:C	0.038274
82_bl-b	82	CWH43	MODERATE	c.1407C>A; c.1488C>A	p.Ser469Arg; p.Ser496Arg	0	FALSE	chr4:49032957:C:A	78:chr4:49032957:C:A	0.002813
82_bl-b	82	EPHA3	HIGH	c.1515C>A	p.Tyr505*	0	FALSE	chr3:89448551:C:A	78:chr3:89448551:C:A	0.001877
82_bl-b	82	FBXW7	MODERATE	c.1186G>T; c.1300G>T; c.1540G>T	p.Val396Phe; p.Val434Phe; p.Val514Phe	0	FALSE	chr4:153247262:C:A	78:chr4:153247262:C:A	0.00153
82_bl-b	82	ALK	MODERATE	c.3700G>A	p.Ala1234Thr	1	FALSE	chr2:29436893:C:T	78:chr2:29436893:C:T	0.001384
82_bl-b	82	CDH1	MODERATE	c.184G>A	p.Gly62Ser	0	FALSE	chr16:68835593:G:A	78:chr16:68835593:G:A	0.001062

82_bl-b	82	C9orf53; CDKN2A	MODIFIER; MODERATE	n.*616G>A; c.*314C>T; c.*35C>T; c.391C>T	; p.Arg131Cys	2	FALSE	chr9:21970967:G:A	78:chr9:21970967:G:A	0.001512
82_bl-b	82	ALK	MODERATE	c.2629G>T	p.Ala877Ser	1	FALSE	chr2:29455173:C:A	78:chr2:29455173:C:A	0.002815
82_bl-b	82	NTRK1	MODERATE	c.1738G>A; c.1828G>A; c.1846G>A	p.Asp580Asn; p.Asp610Asn; p.Asp616Asn	1	FALSE	chr1:156848954:G:A	78:chr1:156848954:G:A	0.001552
82_bl-b	82	EGFR	MODERATE	c.627A>C	p.Lys209Asn	1	FALSE	chr7:55219054:A:C	78:chr7:55219054:A:C	0.001762
82_bl-b	82	BRAF	MODERATE	c.1796C>T	p.Thr599Ile	4	FALSE	chr7:140453139:G:A	78:chr7:140453139:G:A	0.001157
82_bl-b	82	SMO	MODERATE	c.1045A>C	p.Thr349Pro	0	FALSE	chr7:128846115:A:C	78:chr7:128846115:A:C	0.015826
82_bl-b	82	ATM	MODERATE	c.6751C>A	p.Leu2251Ile	0	FALSE	chr11:108196215:C:A	78:chr11:108196215:C:A	0.002582
82_bl-b	82	TP53	MODIFIER; MODERATE	c.-3G>T; c.358G>T; c.475G>T; c.79G>T	; p.Ala120Ser; p.Ala159Ser; p.Ala27Ser	23	FALSE	chr17:7578455:C:A	78:chr17:7578455:C:A	0.002144
82_bl-b	82	NTRK2	MODERATE	c.1984G>A; c.2032G>A	p.Ala662Thr; p.Ala678Thr	0	FALSE	chr9:87570292:G:A	78:chr9:87570292:G:A	0.001471
82_bl-b	82	KDR	MODERATE	c.2309G>T	p.Gly770Val	1	FALSE	chr4:55964928:C:A	78:chr4:55964928:C:A	0.001191
82_bl-b	82	EPHA3	MODERATE	c.715C>A	p.Pro239Thr	0	FALSE	chr3:89259571:C:A	78:chr3:89259571:C:A	0.001137
82_bl-b	82	MAP2K1	MODERATE	c.198C>A	p.Asp66Glu	4	FALSE	chr15:66727482:C:A	78:chr15:66727482:C:A	0.001992
82_bl-b	82	IDH2	MODERATE	c.136G>T; c.370G>T; c.526G>T	p.Gly46Cys; p.Gly124Cys; p.Gly176Cys	1	FALSE	chr15:90631827:C:A	78:chr15:90631827:C:A	0.00157
82_bl-b	82	FGFR3	MODERATE	c.905G>A	p.Gly302Asp	1	FALSE	chr4:1803727:G:A	78:chr4:1803727:G:A	0.002334

82_bl-b	82	FGFR2	MODIFIER; MODERATE	c.749-4686G>T; c.568G>T; c.646G>T; c.913G>T; n.1215G>T	; p.Gly190Trp; p.Gly216Trp; p.Gly305Trp	3	FALSE	chr10:123279519:C:A	78:chr10:123279519:C:A	0.002174
82_bl-b	82	ATM	MODERATE	c.6371A>G	p.Tyr2124Cys	0	FALSE	chr11:108190704:A:G	78:chr11:108190704:A:G	0.001381
82_bl-b	82	EPHA3	MODERATE	c.237C>A	p.Asn79Lys	0	FALSE	chr3:89259093:C:A	78:chr3:89259093:C:A	8.00E-04
82_bl-b	82	PIK3CA	MODERATE	c.3044C>A	p.Ser1015Tyr	3	FALSE	chr3:178951989:C:A	78:chr3:178951989:C:A	0.0007
82_bl-b	82	ATM	MODERATE	c.5639C>G	p.Thr1880Arg	0	FALSE	chr11:108175544:C:G	78:chr11:108175544:C:G	0.013492
82_bl-b	82	TP53	MODERATE	c.371G>T; c.452G>T; c.731G>T; c.848G>T	p.Arg124Leu; p.Arg151Leu; p.Arg244Leu; p.Arg283Leu	24	FALSE	chr17:7577090:C:A	78:chr17:7577090:C:A	0.001442
82_bl-b	82	DDR2	HIGH	c.2125C>T	p.Arg709*	4	FALSE	chr1:162746002:C:T	78:chr1:162746002:C:T	0.000949
82_bl-b	82	NF1	MODERATE	c.6314T>C; c.6377T>C	p.Val2105Ala; p.Val2126Ala	2	FALSE	chr17:29663882:T:C	78:chr17:29663882:T:C	0.001002
82_bl-b	82	ESR1	MODERATE	c.1003C>A; c.1006C>A; c.1012C>A	p.Pro335Thr; p.Pro336Thr; p.Pro338Thr	0	FALSE	chr6:152265553:C:A	78:chr6:152265553:C:A	0.001125
82_bl-b	82	DDR2	MODERATE	c.313C>A	p.Arg105Ser	2	FALSE	chr1:162724541:C:A	78:chr1:162724541:C:A	0.001802
82_bl-b	82	EGFR	MODERATE	c.866C>A	p.Ala289Asp	34	FALSE	chr7:55221822:C:A	78:chr7:55221822:C:A	0.001432

82_bl-b	82	FGFR2	MODERATE; MODIFIER	c.1260G>T; c.1263G>T; c.1266G>T; c.1275G>T; c.1344G>T; c.1347G>T; c.1611G>T; c.1614G>T; n.2061G>T	p.Met420Ile; p.Met421Ile; p.Met422Ile; p.Met425Ile; p.Met448Ile; p.Met449Ile; p.Met537Ile; p.Met538Ile;	1	FALSE	chr10:123258070:C:A	78:chr10:123258070:C:A	0.002278
82_bl-b	82	KDR	MODERATE	c.2323G>T	p.Ala775Ser	1	FALSE	chr4:55964914:C:A	78:chr4:55964914:C:A	0.010962
82_bl-b	82	MET	HIGH	c.1639C>T	p.Arg547*	2	FALSE	chr7:116381017:C:T	78:chr7:116381017:C:T	0.001217
82_bl-b	82	FLT3	MODERATE	c.1361C>T	p.Ser454Leu	0	FALSE	chr13:28610129:G:A	78:chr13:28610129:G:A	0.000628
82_bl-b	82	TP53	MODERATE	c.128G>T; c.209G>T; c.488G>T; c.605G>T	p.Arg43Leu; p.Arg70Leu; p.Arg163Leu; p.Arg202Leu	4	FALSE	chr17:7578244:C:A	78:chr17:7578244:C:A	0.001657
82_bl-b	82	NOTCH1	MODERATE	c.2860T>C	p.Cys954Arg	0	FALSE	chr9:139404294:A:G	78:chr9:139404294:A:G	0.001685
82_bl-b	82	KIT	MODERATE	c.839C>T	p.Ala280Val	1	FALSE	chr4:55569972:C:T	78:chr4:55569972:C:T	0.001092
82_bl-b	82	EGFR	MODIFIER; MODERATE	c.*1464G>A; c.1606G>A	; p.Val536Met	1	FALSE	chr7:55229299:G:A	78:chr7:55229299:G:A	0.001546
82_bl-b	82	ERBB2; MIEN1; MIR4728	MODERATE; MODIFIER	c.3025G>A; c.3070G>A; c.3115G>A; n.3439G>A; c.*388C>T; n.*67G>A	p.Ala1009Thr; p.Ala1024Thr; p.Ala1039Thr;	2	FALSE	chr17:37883212:G:A	78:chr17:37883212:G:A	0.003593
82_bl-b	82	PIK3CA	MODERATE	c.892C>A	p.Pro298Thr	1	FALSE	chr3:178921410:C:A	78:chr3:178921410:C:A	0.000924

82_bl-b	82	PTEN	MODERATE	c.392C>A	p.Thr131Asn	2	FALSE	chr10:89692908:C:A	78:chr10:89692908:C:A	0.001778
82_bl-b	82	KIT	MODERATE	c.1485C>A	p.Asn495Lys	1	FALSE	chr4:55592161:C:A	78:chr4:55592161:C:A	0.00157
82_bl-b	82	APC	HIGH	c.1733C>A; c.1787C>A	p.Ser578*; p.Ser596*	0	FALSE	chr5:112170691:C:A	78:chr5:112170691:C:A	0.002013
82_bl-b	82	PDGFRA	MODERATE	c.1114G>A	p.Glu372Lys	2	FALSE	chr4:55133901:G:A	78:chr4:55133901:G:A	0.001063
82_bl-b	82	ROS1	HIGH	c.5332G>T	p.Gly1778*	1	FALSE	chr6:117650526:C:A	78:chr6:117650526:C:A	0.000946
82_bl-b	82	PIK3CA	MODERATE	c.35G>A	p.Gly12Asp	5	FALSE	chr3:178916648:G:A	78:chr3:178916648:G:A	0.000755
82_bl-b	82	NF1	MODERATE	c.2695T>G	p.Leu899Val	3	FALSE	chr17:29556328:T:G	78:chr17:29556328:T:G	0.017956
82_bl-b	82	MIR1225; PKD1; TSC2	MODIFIER; MODERATE	n.*90C>T; c.*13118C>T; c.*13121C>T; c.4954G>A; c.5086G>A; c.5155G>A	; p.Ala1652Thr; p.Ala1696Thr; p.Ala1719Thr	0	FALSE	chr16:2138135:G:A	78:chr16:2138135:G:A	0.001327
82_bl-b	82	RET	MODERATE	c.1690A>C	p.Thr564Pro	1	FALSE	chr10:43608342:A:C	78:chr10:43608342:A:C	0.009373
82_bl-b	82	MAP2K2	MODERATE	c.281C>T	p.Ser94Leu	0	FALSE	chr19:4117439:G:A	78:chr19:4117439:G:A	0.005348
82_bl-b	82	FGFR1; LETM2	MODERATE; MODIFIER	c.1777T>G; c.1783T>G; c.2020T>G; c.2044T>G; c.2050T>G; c.2143T>G; c.*1406A>C; c.*1423A>C; c.*1553A>C; c.*1567A>C; c.*1638A>C	p.Trp593Gly; p.Trp595Gly; p.Trp674Gly; p.Trp682Gly; p.Trp684Gly; p.Trp715Gly;	1	FALSE	chr8:38271806:A:C	78:chr8:38271806:A:C	0.012953

82_bl-b	82	EPHA3	MODERATE	c.676G>A	p.Val226Ile	0	FALSE	chr3:89259532:G:A	78:chr3:89259532:G:A	0.000691
82_bl-b	82	TP53	MODERATE	c.265C>T; c.346C>T; c.625C>T; c.742C>T	p.Arg89Trp; p.Arg116Trp; p.Arg209Trp; p.Arg248Trp	559	FALSE	chr17:7577539:G:A	78:chr17:7577539:G:A	0.549505
82_bl-b	82	EVI2A; NF1	MODIFIER; MODERATE	c.-266C>T; c.-338C>T; c.4882G>A; c.4945G>A	; p.Gly1628Arg; p.Gly1649Arg	1	FALSE	chr17:29652947:G:A	78:chr17:29652947:G:A	0.000832
82_bl-b	82	NF1	MODERATE	c.8070G>T; c.8133G>T	p.Leu2690Phe; p.Leu2711Phe	1	FALSE	chr17:29686006:G:T	78:chr17:29686006:G:T	0.024707
82_bl-b	82	FGFR1	MODERATE	c.359C>T; c.365C>T; c.608C>T; c.626C>T; c.632C>T; c.725C>T	p.Ala120Val; p.Ala122Val; p.Ala203Val; p.Ala209Val; p.Ala211Val; p.Ala242Val	1	FALSE	chr8:38283753:G:A	78:chr8:38283753:G:A	0.001572
82_bl-b	82	NF1	MODERATE	c.4463G>A; c.4526G>A	p.Arg1488His; p.Arg1509His	1	FALSE	chr17:29587482:G:A	78:chr17:29587482:G:A	0.001008
82_bl-b	82	TP53	HIGH	c.415G>T; c.496G>T; c.775G>T; c.892G>T	p.Glu139*; p.Glu166*; p.Glu259*; p.Glu298*	50	FALSE	chr17:7577046:C:A	78:chr17:7577046:C:A	0.001327
82_bl-b	82	KRAS	MODERATE	c.35G>A	p.Gly12Asp	11213	FALSE	chr12:25398284:C:T	78:chr12:25398284:C:T	0.455943
82_bl-b	82	TSC2	MODERATE	c.866C>T	p.Ala289Val	0	FALSE	chr16:2108765:C:T	78:chr16:2108765:C:T	0.001352
82_bl-b	82	DDR2	MODERATE	c.2516G>A	p.Arg839His	3	FALSE	chr1:162749984:G:A	78:chr1:162749984:G:A	0.00114
82_bl-b	82	EGFR	MODERATE	c.1168C>A	p.Gln390Lys	1	FALSE	chr7:55224486:C:A	78:chr7:55224486:C:A	0.001115

82_bl-b	82	IGF1R	MODERATE	c.3905T>C; c.3908T>C	p.Val1302Ala; p.Val1303Ala	0	FALSE	chr15:99500475:T:C	78:chr15:99500475:T:C	0.010212
82_bl-b	82	FBXW7	HIGH	c.1177C>T; c.823C>T; c.937C>T	p.Arg393*; p.Arg275*; p.Arg313*	0	FALSE	chr4:153250883:G:A	78:chr4:153250883:G:A	0.001327
82_bl-b	82	IDH1	MODERATE	c.299G>T	p.Arg100Leu	5	FALSE	chr2:209113208:C:A	78:chr2:209113208:C:A	0.001187
82_bl-b	82	NTRK2	MODERATE	c.1981G>A; c.2029G>A	p.Ala661Thr; p.Ala677Thr	0	FALSE	chr9:87570289:G:A	78:chr9:87570289:G:A	0.001475
82_bl-b	82	DDR2	MODERATE	c.1598C>A	p.Thr533Lys	1	FALSE	chr1:162741907:C:A	78:chr1:162741907:C:A	0.001567
82_bl-b	82	ALK	MODERATE	c.3521T>C	p.Phe1174Ser	9	FALSE	chr2:29443696:A:G	78:chr2:29443696:A:G	0.001546
82_bl-b	82	NF1	HIGH	c.5817C>A; c.5880C>A	p.Cys1939*; p.Cys1960*	1	FALSE	chr17:29661923:C:A	78:chr17:29661923:C:A	0.002302
82_bl-b	82	EPHA3	MODERATE	c.1234G>A	p.Val412Ile	0	FALSE	chr3:89391168:G:A	78:chr3:89391168:G:A	0.000876
82_bl-b	82	NTRK1	MODERATE	c.1940T>G; c.2030T>G; c.2048T>G	p.Val647Gly; p.Val677Gly; p.Val683Gly	2	FALSE	chr1:156849792:T:G	78:chr1:156849792:T:G	0.023381
82_bl-b	82	SMO	MODERATE	c.1193G>A	p.Arg398Gln	0	FALSE	chr7:128846357:G:A	78:chr7:128846357:G:A	0.001085
82_bl-b	82	FBXW7	HIGH	c.1027G>T; c.1267G>T; c.913G>T	p.Gly343*; p.Gly423*; p.Gly305*	0	FALSE	chr4:153249511:C:A	78:chr4:153249511:C:A	0.001676
82_bl-b	82	PDGFRA	MODERATE	c.3078C>A	p.Asp1026Glu	1	FALSE	chr4:55156677:C:A	78:chr4:55156677:C:A	0.001202
82_bl-b	82	PIK3CA	MODERATE	c.1634A>C	p.Glu545Ala	132	FALSE	chr3:178936092:A:C	78:chr3:178936092:A:C	0.009385
82_bl-b	82	NOTCH1	MODERATE	c.4252G>A	p.Ala1418Thr	0	FALSE	chr9:139400096:C:T	78:chr9:139400096:C:T	0.002227
25_t2c5-1	25	BRAF	MODERATE	c.1799T>A	p.Val600Glu	23024	FALSE	chr7:140453136:A:T	79:chr7:140453136:A:T	0.019929
25_t2c5-1	25	NTRK1	MODERATE	c.1975C>T; c.2065C>T; c.2083C>T	p.Pro659Ser; p.Pro689Ser; p.Pro695Ser	2	FALSE	chr1:156849827:C:T	79:chr1:156849827:C:T	0.002602

25_t2c5-1	25	CDH1	MODERATE	c.2156C>T	p.Ala719Val	0	FALSE	chr16:68857521:C:T	79:chr16:68857521:C:T	0.001329
25_t2c5-1	25	NOTCH1	MODERATE	c.3407G>T	p.Gly1136Val	0	FALSE	chr9:139402510:C:A	79:chr9:139402510:C:A	0.001665
25_t2c5-1	25	ATM	MODERATE	c.8762C>T	p.Thr2921Met	0	FALSE	chr11:108224583:C:T	79:chr11:108224583:C:T	0.002721
25_t2c5-1	25	CTNNB1	MODERATE	c.884C>A	p.Ala295Asp	0	FALSE	chr3:41267300:C:A	79:chr3:41267300:C:A	0.002778
25_t2c5-1	25	EGFR	MODERATE	c.719G>A	p.Cys240Tyr	1	FALSE	chr7:55220329:G:A	79:chr7:55220329:G:A	0.001421
25_t2c5-1	25	NOTCH1	MODERATE	c.6121G>T	p.Val2041Leu	0	FALSE	chr9:139393410:C:A	79:chr9:139393410:C:A	0.001723
25_t2c5-1	25	PDGFRA	MODERATE	c.364C>A	p.Pro122Thr	1	FALSE	chr4:55127576:C:A	79:chr4:55127576:C:A	0.002502
25_t2c5-1	25	VHL	MODIFIER; MODERATE	c.341-3238G>A; c.376G>A	; p.Asp126Asn	0	FALSE	chr3:10188233:G:A	79:chr3:10188233:G:A	0.0013
25_t2c5-1	25	C9orf53; CDKN2A	MODIFIER; LOW	n.*616C>A; c.*328G>T; c.*49G>T; c.405G>T	; p.Gly135Gly	1	FALSE	chr9:21970953:C:A	79:chr9:21970953:C:A	0.00158
25_t2c5-1	25	CTNNB1	MODERATE	c.91C>A	p.Leu31Met	0	FALSE	chr3:41266094:C:A	79:chr3:41266094:C:A	0.001975
25_t2c5-1	25	FGFR1; LETM2	MODERATE; MODIFIER	c.1927C>T; c.1933C>T; c.2170C>T; c.2194C>T; c.2200C>T; c.2293C>T; c.*1406G>A; c.*1423G>A; c.*1553G>A; c.*1567G>A; c.*1638G>A	p.Arg643Trp; p.Arg645Trp; p.Arg724Trp; p.Arg732Trp; p.Arg734Trp; p.Arg765Trp;	1	FALSE	chr8:38271528:G:A	79:chr8:38271528:G:A	0.002004
25_t2c5-1	25	IGF1R	MODERATE	c.880G>A	p.Glu294Lys	0	FALSE	chr15:99434793:G:A	79:chr15:99434793:G:A	0.001438

25_t2c5-1	25	ALK	HIGH	c.4414G>T	p.Glu1472*	1	FALSE	chr2:29416539:C:A	79:chr2:29416539:C:A	0.001177
25_t2c5-1	25	PTEN	MODERATE	c.421C>A	p.His141Asn	2	FALSE	chr10:89692937:C:A	79:chr10:89692937:C:A	0.001367
25_t2c5-1	25	TP53	MODERATE	c.105G>T; c.24G>T; c.384G>T; c.501G>T	p.Gln35His; p.Gln8His; p.Gln128His; p.Gln167His	3	FALSE	chr17:7578429:C:A	79:chr17:7578429:C:A	0.002117
25_t2c5-1	25	RET	MODERATE	c.1696C>A	p.Pro566Thr	1	FALSE	chr10:43608348:C:A	79:chr10:43608348:C:A	0.001271
25_t2c5-1	25	MIR4673; NOTCH1	MODIFIER; MODERATE	n.-1G>T; c.221G>T	; p.Cys74Phe	0	FALSE	chr9:139418351:C:A	79:chr9:139418351:C:A	0.003003
25_t2c5-1	25	TP53	MODERATE	c.355C>T; c.436C>T; c.715C>T; c.832C>T	p.Pro119Ser; p.Pro146Ser; p.Pro239Ser; p.Pro278Ser	59	FALSE	chr17:7577106:G:A	79:chr17:7577106:G:A	0.010021
25_t2c5-1	25	MAP2K1	MODERATE	c.198C>A	p.Asp66Glu	4	FALSE	chr15:66727482:C:A	79:chr15:66727482:C:A	0.00147
25_t2c5-1	25	NF1	MODERATE	c.7733C>T; c.7796C>T	p.Ser2578Phe; p.Ser2599Phe	1	FALSE	chr17:29684035:C:T	79:chr17:29684035:C:T	0.001416
25_t2c5-1	25	TP53	MODERATE	c.234G>T; c.315G>T; c.594G>T; c.711G>T	p.Met78Ile; p.Met105Ile; p.Met198Ile; p.Met237Ile	81	FALSE	chr17:7577570:C:A	79:chr17:7577570:C:A	0.001206
25_t2c5-1	25	IGF1R	MODERATE	c.3905T>C; c.3908T>C	p.Val1302Ala; p.Val1303Ala	0	FALSE	chr15:99500475:T:C	79:chr15:99500475:T:C	0.004237
25_t2c5-1	25	EGFR	MODERATE	c.406C>A	p.Pro136Thr	1	FALSE	chr7:55211163:C:A	79:chr7:55211163:C:A	0.00277
25_t2c5-1	25	EGFR	MODIFIER; MODERATE	c.*2364G>A; c.2161G>A	; p.Gly721Ser	5	FALSE	chr7:55241713:G:A	79:chr7:55241713:G:A	0.00139
25_t2c5-1	25	FGFR1	MODIFIER; MODERATE	c.-85G>T; c.107G>T; c.8G>T	; p.Ser36Ile; p.Ser3Ile	1	FALSE	chr8:38314957:C:A	79:chr8:38314957:C:A	0.001263
25_t2c5-1	25	EGFR	MODIFIER; MODERATE	c.*1464C>T; c.1279C>T	; p.Arg427Cys	2	FALSE	chr7:55225427:C:T	79:chr7:55225427:C:T	0.001334

25_t2c5-1	25	TP53	LOW; MODIFIER; MODERATE	c.-18G>T; c.343G>T; c.460G>T; c.64G>T	; p.Gly115Cys; p.Gly154Cys; p.Gly22Cys	9	FALSE	chr17:7578470:C:A	79:chr17:7578470:C:A	0.001441
25_t2c5-1	25	NOTCH1	MODERATE	c.5347C>T	p.Arg1783Trp	0	FALSE	chr9:139396761:G:A	79:chr9:139396761:G:A	0.00197
25_t2c5-1	25	PIK3R1	HIGH	c.901C>T	p.Arg301*	1	FALSE	chr5:67576819:C:T	79:chr5:67576819:C:T	0.001366
25_t2c5-1	25	TP53	MODERATE; MODIFIER	c.211C>T; c.328C>T; c.-279C>T; c.-360C>T	p.Arg71Cys; p.Arg110Cys;	6	FALSE	chr17:7579359:G:A	79:chr17:7579359:G:A	0.005857
25_t2c5-1	25	HGF	HIGH	c.1582C>T; c.1597C>T	p.Arg528*; p.Arg533*	0	FALSE	chr7:81336625:G:A	79:chr7:81336625:G:A	0.001584
25_t2c5-1	25	TSC1	HIGH	c.496G>T; c.649G>T	p.Glu166*; p.Glu217*	0	FALSE	chr9:135797220:C:A	79:chr9:135797220:C:A	0.003006
25_t2c5-1	25	TSC2	MODERATE	c.3289G>A; c.3421G>A	p.Ala1097Thr; p.Ala1141Thr	0	FALSE	chr16:2130189:G:A	79:chr16:2130189:G:A	0.001762
25_t2c5-1	25	NOTCH1	MODERATE	c.3859C>T	p.Arg1287Cys	0	FALSE	chr9:139401210:G:A	79:chr9:139401210:G:A	0.001506
25_t2c5-1	25	C9orf53; CDKN2A	MODIFIER; MODERATE; LOW	n.*616T>G; c.*120A>C; c.197A>C; c.240A>C	; p.His66Pro; p.Pro80Pro	1	FALSE	chr9:21971161:T:G	79:chr9:21971161:T:G	0.029312
25_t2c5-1	25	ERBB2; MIEN1; MIR4728	MODERATE; MODIFIER	c.3025G>A; c.3070G>A; c.3115G>A; n.3439G>A; c.*388C>T; n.*67G>A	p.Ala1009Thr; p.Ala1024Thr; p.Ala1039Thr;	2	FALSE	chr17:37883212:G:A	79:chr17:37883212:G:A	0.001754
25_t2c5-1	25	IDH1	MODERATE	c.395G>A	p.Arg132His	4157	FALSE	chr2:209113112:C:T	79:chr2:209113112:C:T	0.002186

25_t2c5-1	25	TP53	MODIFIER; MODERATE	c.-13G>T; c.105G>T; c.-279G>T; c.-360G>T	; p.Leu35Phe	2	FALSE	chr17:7579582:C:A	79:chr17:7579582:C:A	0.001549
25_t2c5-1	25	KRAS	MODERATE	c.204G>T	p.Arg68Ser	1	FALSE	chr12:25380254:C:A	79:chr12:25380254:C:A	0.002011
25_t2c5-1	25	NTRK3	MODERATE	c.1071G>T	p.Glu357Asp	0	FALSE	chr15:88678465:C:A	79:chr15:88678465:C:A	0.001365
25_t2c5-1	25	APC	MODERATE	c.1171C>A; c.1225C>A	p.Leu391Ile; p.Leu409Ile	0	FALSE	chr5:112154954:C:A	79:chr5:112154954:C:A	0.0013
25_t2c5-1	25	SMO	MODERATE	c.961G>A	p.Val321Met	0	FALSE	chr7:128846031:G:A	79:chr7:128846031:G:A	0.001296
25_t2c5-1	25	TP53	MODERATE	c.352T>G; c.433T>G; c.712T>G; c.829T>G	p.Cys118Gly; p.Cys145Gly; p.Cys238Gly; p.Cys277Gly	5	FALSE	chr17:7577109:A:C	79:chr17:7577109:A:C	0.002216
25_t2c5-1	25	APC	MODERATE	c.703G>A; c.757G>A	p.Gly235Ser; p.Gly253Ser	0	FALSE	chr5:112137003:G:A	79:chr5:112137003:G:A	0.001343
25_t2c5-1	25	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2591C>T; n.-1G>A	p.Ala864Val;	2	FALSE	chr7:55259533:C:T	79:chr7:55259533:C:T	0.002357
25_t3c2-1	25	ATM	MODERATE	c.7183G>A	p.Asp2395Asn	0	FALSE	chr11:108199841:G:A	80:chr11:108199841:G:A	0.001127
25_t3c2-1	25	FGFR2	MODIFIER; MODERATE	c.749-4686G>A; c.568G>A; c.646G>A; c.913G>A; n.1215G>A	; p.Gly190Arg; p.Gly216Arg; p.Gly305Arg	3	FALSE	chr10:123279519:C:T	80:chr10:123279519:C:T	0.001265
25_t3c2-1	25	CDH1	MODERATE	c.1489G>A	p.Glu497Lys	0	FALSE	chr16:68849586:G:A	80:chr16:68849586:G:A	0.001064
25_t3c2-1	25	KLLN; PTEN	MODIFIER; MODERATE	c.-951C>T; c.59G>A	; p.Gly20Glu	1	FALSE	chr10:89624285:G:A	80:chr10:89624285:G:A	0.001496
25_t3c2-1	25	IDH2	LOW; MODIFIER	c.-4G>T; c.-17-2860G>T; c.153G>T	; p.Val51Val	1	FALSE	chr15:90634839:C:A	80:chr15:90634839:C:A	0.001418

25_t3c2-1	25	PTEN	MODERATE	c.443C>A	p.Ala148Glu	1	FALSE	chr10:89692959:C:A	80:chr10:89692959:C:A	0.002517
25_t3c2-1	25	FBXW7	MODERATE	c.1078G>T; c.1318G>T; c.964G>T	p.Asp360Tyr; p.Asp440Tyr; p.Asp322Tyr	0	FALSE	chr4:153249460:C:A	80:chr4:153249460:C:A	0.001638
25_t3c2-1	25	FGFR3	MODERATE	c.905G>A	p.Gly302Asp	1	FALSE	chr4:1803727:G:A	80:chr4:1803727:G:A	0.001375
25_t3c2-1	25	TP53	MODERATE	c.242G>T; c.323G>T; c.602G>T; c.719G>T	p.Ser81Ile; p.Ser108Ile; p.Ser201Ile; p.Ser240Ile	6	FALSE	chr17:7577562:C:A	80:chr17:7577562:C:A	0.001583
25_t3c2-1	25	KIT	MODERATE	c.1156G>A	p.Glu386Lys	1	FALSE	chr4:55575630:G:A	80:chr4:55575630:G:A	0.001149
25_t3c2-1	25	CDH1	MODERATE	c.1468G>A	p.Glu490Lys	0	FALSE	chr16:68849565:G:A	80:chr16:68849565:G:A	0.001079
25_t3c2-1	25	FBXW7	MODERATE	c.1204G>T; c.1318G>T; c.1558G>T	p.Asp402Tyr; p.Asp440Tyr; p.Asp520Tyr	0	FALSE	chr4:153247244:C:A	80:chr4:153247244:C:A	0.000986
25_t3c2-1	25	PIK3R1	LOW; MODIFIER	c.1017G>A; c.117G>A; c.207G>A; c.-233G>A	p.Ser339Ser; p.Ser39Ser; p.Ser69Ser;	1	FALSE	chr5:67588187:G:A	80:chr5:67588187:G:A	0.001176
25_t3c2-1	25	KIT	MODERATE	c.273C>A	p.Asn91Lys	1	FALSE	chr4:55561883:C:A	80:chr4:55561883:C:A	0.001024
25_t3c2-1	25	CTNNB1	MODERATE	c.98C>A	p.Ser33Tyr	0	FALSE	chr3:41266101:C:A	80:chr3:41266101:C:A	0.001027
25_t3c2-1	25	BRAF	MODERATE	c.1799T>A	p.Val600Glu	23024	FALSE	chr7:140453136:A:T	80:chr7:140453136:A:T	0.012353
25_t3c2-1	25	MIR4674; MIR4674HG; NOTCH1	MODIFIER; MODERATE	n.*87G>T; n.-1C>A; c.62G>T	; p.Gly21Val	0	FALSE	chr9:139438554:C:A	80:chr9:139438554:C:A	0.003226
25_t3c2-1	25	NF1	MODERATE	c.3559C>A	p.Leu1187Ile	1	FALSE	chr17:29560082:C:A	80:chr17:29560082:C:A	0.00111

25_t3c2-1	25	TP53	MODIFIER; MODERATE	c.*137A>G; c.*225A>G; c.1001A>G; c.1118A>G; c.641A>G; c.722A>G	; p.Lys334Arg; p.Lys373Arg; p.Lys214Arg; p.Lys241Arg	1	FALSE	chr17:7572991:T:C	80:chr17:7572991:T:C	0.00613
25_t3c2-1	25	ALK	MODERATE	c.741G>T	p.Trp247Cys	1	FALSE	chr2:29940490:C:A	80:chr2:29940490:C:A	0.001016
25_t3c2-1	25	MIR4673; NOTCH1	MODIFIER; MODERATE	n.*59G>T; c.1343G>T	; p.Arg448Leu	0	FALSE	chr9:139412302:C:A	80:chr9:139412302:C:A	0.001664
25_t3c2-1	25	SMO	MODERATE	c.517C>A	p.Arg173Ser	0	FALSE	chr7:128843410:C:A	80:chr7:128843410:C:A	0.001244
25_t3c2-1	25	TP53	MODERATE	c.248G>A; c.329G>A; c.608G>A; c.725G>A	p.Cys83Tyr; p.Cys110Tyr; p.Cys203Tyr; p.Cys242Tyr	72	FALSE	chr17:7577556:C:T	80:chr17:7577556:C:T	0.001037
25_t3c2-1	25	ATM	MODERATE	c.3070G>A	p.Ala1024Thr	0	FALSE	chr11:108142126:G:A	80:chr11:108142126:G:A	0.00137
25_t3c2-1	25	SMO	MODERATE	c.1691A>G	p.Lys564Arg	0	FALSE	chr7:128850844:A:G	80:chr7:128850844:A:G	0.001622
25_t3c2-1	25	PTEN	MODERATE	c.1041C>A	p.Phe347Leu	1	FALSE	chr10:89725058:C:A	80:chr10:89725058:C:A	0.001542
25_t3c2-1	25	TP53	MODERATE	c.359G>T; c.440G>T; c.719G>T; c.836G>T	p.Gly120Val; p.Gly147Val; p.Gly240Val; p.Gly279Val	37	FALSE	chr17:7577102:C:A	80:chr17:7577102:C:A	0.001066
25_t3c2-1	25	TP53	MODERATE	c.261G>A; c.342G>A; c.621G>A; c.738G>A	p.Met87Ile; p.Met114Ile; p.Met207Ile; p.Met246Ile	21	FALSE	chr17:7577543:C:T	80:chr17:7577543:C:T	0.001096

25_t3c2-1	25	FGFR2	MODIFIER; MODERATE	c.749-4842C>T; c.412C>T; c.490C>T; c.757C>T; n.1059C>T	; p.Pro138Ser; p.Pro164Ser; p.Pro253Ser	1	FALSE	chr10:123279675:G:A	80:chr10:123279675:G:A	0.001373
25_t3c2-1	25	NOTCH1	HIGH	c.5110G>T	p.Gly1704*	0	FALSE	chr9:139397691:C:A	80:chr9:139397691:C:A	0.00207
25_t3c2-1	25	ATM	MODERATE	c.1237C>A	p.Leu413Ile	0	FALSE	chr11:108121429:C:A	80:chr11:108121429:C:A	0.002326
25_t3c2-1	25	TP53	MODERATE; MODIFIER	c.211C>T; c.328C>T; c.-279C>T; c.-360C>T	p.Arg71Cys; p.Arg110Cys;	6	FALSE	chr17:7579359:G:A	80:chr17:7579359:G:A	0.002571
25_t3c2-1	25	NTRK1	MODERATE	c.804C>G; c.894C>G	p.His268Gln; p.His298Gln	1	FALSE	chr1:156843468:C:G	80:chr1:156843468:C:G	0.002155
25_t3c2-1	25	C9orf53; CDKN2A	MODIFIER; MODERATE; LOW	n.*616T>G; c.*120A>C; c.197A>C; c.240A>C	; p.His66Pro; p.Pro80Pro	1	FALSE	chr9:21971161:T:G	80:chr9:21971161:T:G	0.028971
25_t3c2-1	25	PTEN	MODERATE	c.729C>A	p.Phe243Leu	1	FALSE	chr10:89717704:C:A	80:chr10:89717704:C:A	0.001858
25_t3c2-1	25	SMO	MODERATE	c.1045A>C	p.Thr349Pro	0	FALSE	chr7:128846115:A:C	80:chr7:128846115:A:C	0.002197
25_t3c2-1	25	FGFR4	MODERATE	c.1444G>A; c.1528G>A; c.1648G>A	p.Val482Met; p.Val510Met; p.Val550Met	2	FALSE	chr5:176522551:G:A	80:chr5:176522551:G:A	0.001502
25_t3c2-1	25	C9orf53; CDKN2A	MODIFIER; MODERATE	n.*616T>C; c.*77A>G; c.154A>G; c.197A>G	; p.Met52Val; p.His66Arg	1	FALSE	chr9:21971204:T:C	80:chr9:21971204:T:C	0.001765

25_t3c2-1	25	TP53	MODIFIER; MODERATE	c.-11G>T; c.350G>T; c.467G>T; c.71G>T	; p.Arg117Leu; p.Arg156Leu; p.Arg24Leu	26	FALSE	chr17:7578463:C:A	80:chr17:7578463:C:A	0.00129
25_t3c2-1	25	MIR4673; NOTCH1	MODIFIER; MODERATE	n.*59G>T; c.1286G>T	; p.Cys429Phe	0	FALSE	chr9:139412359:C:A	80:chr9:139412359:C:A	0.002486
25_t3c2-1	25	CTNNB1	MODERATE	c.2212G>A	p.Glu738Lys	0	FALSE	chr3:41280699:G:A	80:chr3:41280699:G:A	0.001027
25_t3c2-1	25	IGF1R	MODERATE	c.3905T>C; c.3908T>C	p.Val1302Ala; p.Val1303Ala	0	FALSE	chr15:99500475:T:C	80:chr15:99500475:T:C	0.002495
25_t3c2-1	25	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2356G>A; n.1206C>T	p.Val786Met;	6	FALSE	chr7:55249058:G:A	80:chr7:55249058:G:A	0.001185
25_t3c2-1	25	IGF1R	MODERATE	c.1172G>A	p.Arg391His	0	FALSE	chr15:99442775:G:A	80:chr15:99442775:G:A	0.001202
25_t3c2-1	25	ERBB2; MIEN1; MIR4728	MODIFIER; MODERATE	c.3160-213A>G; c.3251A>G; c.3296A>G; c.3341A>G; n.3665A>G; c.*388T>C; n.*67A>G	; p.Glu1084Gly; p.Glu1099Gly; p.Glu1114Gly	1	FALSE	chr17:37883729:A:G	80:chr17:37883729:A:G	0.001315
25_t3c2-1	25	NTRK1	MODERATE	c.1478G>A; c.1568G>A; c.1586G>A	p.Cys493Tyr; p.Cys523Tyr; p.Cys529Tyr	1	FALSE	chr1:156845956:G:A	80:chr1:156845956:G:A	0.001907
25_t3c2-1	25	DDR2	MODERATE	c.2141G>A	p.Arg714Gln	1	FALSE	chr1:162746018:G:A	80:chr1:162746018:G:A	0.001079
25_t3c2-1	25	PIK3CA	MODERATE	c.1022C>T	p.Ala341Val	2	FALSE	chr3:178921540:C:T	80:chr3:178921540:C:T	0.001298
25_t3c2-1	25	TP53	MODERATE	c.355C>T; c.436C>T; c.715C>T; c.832C>T	p.Pro119Ser; p.Pro146Ser; p.Pro239Ser; p.Pro278Ser	59	FALSE	chr17:7577106:G:A	80:chr17:7577106:G:A	0.006601
25_t3c2-1	25	PDGFRA	MODERATE	c.827C>T	p.Thr276Met	1	FALSE	chr4:55133523:C:T	80:chr4:55133523:C:T	0.001787

25_t3c2-1	25	FGFR3	MODERATE	c.1526G>A; c.1862G>A; c.1868G>A	p.Arg509His; p.Arg621His; p.Arg623His	2	FALSE	chr4:1807803:G:A	80:chr4:1807803:G:A	0.002226
25_t3c2-1	25	DDR2	MODERATE	c.1022G>A	p.Arg341Gln	1	FALSE	chr1:162731167:G:A	80:chr1:162731167:G:A	0.000953
25_t3c2-1	25	ALK	MODERATE	c.4192C>T	p.Pro1398Ser	1	FALSE	chr2:29416761:G:A	80:chr2:29416761:G:A	0.001866
25_t3c2-1	25	IGF1R	MODERATE	c.3799G>A; c.3802G>A	p.Glu1267Lys; p.Glu1268Lys	0	FALSE	chr15:99500369:G:A	80:chr15:99500369:G:A	0.001184
25_t3c2-1	25	TP53	MODERATE; MODIFIER	c.230C>T; c.347C>T; c.-279C>T; c.-360C>T	p.Ser77Phe; p.Ser116Phe;	1	FALSE	chr17:7579340:G:A	80:chr17:7579340:G:A	0.001181
25_t3c2-1	25	FBXW7	MODERATE	c.1084G>T; c.1198G>T; c.1438G>T	p.Asp362Tyr; p.Asp400Tyr; p.Asp480Tyr	0	FALSE	chr4:153247364:C:A	80:chr4:153247364:C:A	0.000907
25_t3c2-1	25	EGFR	MODERATE	c.1159C>G	p.Leu387Val	1	FALSE	chr7:55224477:C:G	80:chr7:55224477:C:G	0.002895
25_t3c2-1	25	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2602G>A; n.-1C>T	p.Glu868Lys;	2	FALSE	chr7:55259544:G:A	80:chr7:55259544:G:A	0.001437
25_t3c2-1	25	EGFR	MODERATE	c.932G>A	p.Cys311Tyr	1	FALSE	chr7:55223565:G:A	80:chr7:55223565:G:A	0.001135
25_t3c2-1	25	CTNNB1	MODERATE	c.96C>A	p.Asp32Glu	0	FALSE	chr3:41266099:C:A	80:chr3:41266099:C:A	0.001044
25_t3c2-1	25	PTEN	MODERATE	c.409G>A	p.Ala137Thr	1	FALSE	chr10:89692925:G:A	80:chr10:89692925:G:A	0.001072
25_t3c2-1	25	PHLPP1	MODERATE	c.2452G>A	p.Val818Ile	0	FALSE	chr18:60570204:G:A	80:chr18:60570204:G:A	0.001046
25_t3c2-1	25	TP53	MODERATE; MODIFIER	c.115G>T; c.232G>T; c.-279G>T; c.-360G>T	p.Ala39Ser; p.Ala78Ser;	1	FALSE	chr17:7579455:C:A	80:chr17:7579455:C:A	0.001376
25_t3c2-1	25	PDGFRA	MODERATE	c.1516C>A	p.Leu506Ile	2	FALSE	chr4:55139855:C:A	80:chr4:55139855:C:A	0.001085

25_t3c2-1	25	TP53	MODIFIER; MODERATE	c.-5G>T; c.356G>T; c.473G>T; c.77G>T	; p.Arg119Leu; p.Arg158Leu; p.Arg26Leu	80	FALSE	chr17:7578457:C:A	80:chr17:7578457:C:A	0.001948
25_t3c2-1	25	TSC2	HIGH	c.3280C>T; c.3412C>T	p.Arg1094*; p.Arg1138*	0	FALSE	chr16:2130180:C:T	80:chr16:2130180:C:T	0.001507
25_t3c2-1	25	NTRK2	MODERATE	c.1318C>A; c.1357C>A	p.Leu440Met; p.Leu453Met	0	FALSE	chr9:87366961:C:A	80:chr9:87366961:C:A	0.001099
25_t3c2-1	25	ESR1	MODERATE	c.932C>T; c.935C>T; c.941C>T	p.Ala311Val; p.Ala312Val; p.Ala314Val	0	FALSE	chr6:152265482:C:T	80:chr6:152265482:C:T	0.001047
25_t3c2-1	25	HOXD-AS2; HOXD8	MODIFIER; MODERATE	n.*692C>T; c.304G>A; c.853G>A; c.856G>A	; p.Glu102Lys; p.Glu285Lys; p.Glu286Lys	0	FALSE	chr2:176996323:G:A	80:chr2:176996323:G:A	0.001024
25_t3c2-1	25	IGF1R	MODERATE	c.3637C>A; c.3640C>A	p.Gln1213Lys; p.Gln1214Lys	0	FALSE	chr15:99491855:C:A	80:chr15:99491855:C:A	0.001752
25_t3c2-1	25	CDH1	MODERATE	c.671G>A	p.Arg224His	0	FALSE	chr16:68842735:G:A	80:chr16:68842735:G:A	0.001256
25_t3c2-1	25	ATM	MODERATE	c.7328G>A	p.Arg2443Gln	0	FALSE	chr11:108200961:G:A	80:chr11:108200961:G:A	0.002211
25_t3c2-1	25	CTNNB1	MODERATE	c.643G>A	p.Ala215Thr	0	FALSE	chr3:41266972:G:A	80:chr3:41266972:G:A	0.000973
25_t3c2-1	25	DDR2	MODERATE	c.1598C>A	p.Thr533Lys	1	FALSE	chr1:162741907:C:A	80:chr1:162741907:C:A	0.001273
25_t3c2-1	25	ATM	MODERATE	c.8762C>T	p.Thr2921Met	0	FALSE	chr11:108224583:C:T	80:chr11:108224583:C:T	0.002729
25_t3c2-1	25	NTRK3	MODERATE	c.333G>T	p.Lys111Asn	0	FALSE	chr15:88726711:C:A	80:chr15:88726711:C:A	0.002813
25_t3c2-1	25	GNA11	MODERATE	c.1052T>C	p.Leu351Pro	1	FALSE	chr19:3121149:T:C	80:chr19:3121149:T:C	0.001323
25_t3c2-1	25	NTRK1	MODERATE	c.1967G>A; c.2057G>A; c.2075G>A	p.Arg656His; p.Arg686His; p.Arg692His	1	FALSE	chr1:156849819:G:A	80:chr1:156849819:G:A	0.002366

25_t3c2-1	25	FGFR1	MODERATE	c.487C>T; c.493C>T; c.736C>T; c.754C>T; c.760C>T; c.853C>T	p.Arg163Trp; p.Arg165Trp; p.Arg246Trp; p.Arg252Trp; p.Arg254Trp; p.Arg285Trp	1	FALSE	chr8:38282203:G:A	80:chr8:38282203:G:A	0.0012
25_t3c2-1	25	SMO	MODERATE	c.869G>A	p.Arg290His	0	FALSE	chr7:128845572:G:A	80:chr7:128845572:G:A	0.001066
25_t3c2-1	25	ATM	HIGH	c.2558C>A	p.Ser853*	0	FALSE	chr11:108137989:C:A	80:chr11:108137989:C:A	0.001036
49_c8-1	49	PDGFRA	MODERATE	c.1516C>A	p.Leu506Ile	2	FALSE	chr4:55139855:C:A	81:chr4:55139855:C:A	0.001546
49_c8-1	49	NOTCH1	MODERATE	c.6019G>A	p.Val2007Met	0	FALSE	chr9:139393627:C:T	81:chr9:139393627:C:T	0.001625
49_c8-1	49	ATM	HIGH	c.2156C>A	p.Ser719*	0	FALSE	chr11:108126973:C:A	81:chr11:108126973:C:A	0.001468
49_c8-1	49	FBXW7	MODERATE	c.1186G>T; c.1300G>T; c.1540G>T	p.Val396Phe; p.Val434Phe; p.Val514Phe	0	FALSE	chr4:153247262:C:A	81:chr4:153247262:C:A	0.001392
49_c8-1	49	TP53	MODIFIER; MODERATE	c.*137A>G; c.*225A>G; c.1001A>G; c.1118A>G; c.641A>G; c.722A>G	; p.Lys334Arg; p.Lys373Arg; p.Lys214Arg; p.Lys241Arg	1	FALSE	chr17:7572991:T:C	81:chr17:7572991:T:C	0.006283
49_c8-1	49	CTNNB1	HIGH	c.283C>T	p.Arg95*	0	FALSE	chr3:41266486:C:T	81:chr3:41266486:C:T	0.001533
49_c8-1	49	STK11	HIGH	c.996G>A	p.Trp332*	2	FALSE	chr19:1223059:G:A	81:chr19:1223059:G:A	0.001762
49_c8-1	49	TSC2	MODIFIER; MODERATE	c.2837+1108G>A; c.2933G>A	; p.Arg978His	0	FALSE	chr16:2127694:G:A	81:chr16:2127694:G:A	0.001541
49_c8-1	49	EGFR	MODIFIER; MODERATE	c.*1464C>A; c.1476C>A	; p.Ser492Arg	4	FALSE	chr7:55228009:C:A	81:chr7:55228009:C:A	0.001397

49_c8-1	49	PTEN	MODERATE	c.454C>A	p.Leu152Ile	1	FALSE	chr10:89692970:C:A	81:chr10:89692970:C:A	0.001582
49_c8-1	49	IGF1R	MODERATE	c.1511G>A	p.Arg504His	0	FALSE	chr15:99454592:G:A	81:chr15:99454592:G:A	0.001404
49_c8-1	49	KDR	MODERATE	c.491G>T	p.Arg164Ile	1	FALSE	chr4:55981208:C:A	81:chr4:55981208:C:A	0.001639
49_c8-1	49	NF1	MODERATE	c.3917G>A	p.Arg1306Gln	2	FALSE	chr17:29562982:G:A	81:chr17:29562982:G:A	0.001018
49_c8-1	49	IGF1R	MODERATE	c.2380C>T	p.Arg794Trp	0	FALSE	chr15:99465555:C:T	81:chr15:99465555:C:T	0.001305
49_c8-1	49	APC	HIGH	c.793C>T; c.847C>T	p.Arg265*; p.Arg283*	0	FALSE	chr5:112151204:C:T	81:chr5:112151204:C:T	0.001626
49_c8-1	49	FGFR1	MODERATE	c.475C>T; c.481C>T; c.724C>T; c.742C>T; c.748C>T; c.841C>T	p.Arg159Trp; p.Arg161Trp; p.Arg242Trp; p.Arg248Trp; p.Arg250Trp; p.Arg281Trp	2	FALSE	chr8:38282215:G:A	81:chr8:38282215:G:A	0.001591
49_c8-1	49	RET	MODERATE	c.2116G>A	p.Val706Met	2	FALSE	chr10:43610164:G:A	81:chr10:43610164:G:A	0.001232
49_c8-1	49	ATM	MODERATE	c.6200C>A	p.Ala2067Asp	0	FALSE	chr11:108188101:C:A	81:chr11:108188101:C:A	0.003018
49_c8-1	49	KDR	MODERATE	c.1699G>A	p.Val567Met	1	FALSE	chr4:55971098:C:T	81:chr4:55971098:C:T	0.001289
49_c8-1	49	C9orf53; CDKN2A	MODIFIER; MODERATE; LOW	n.*616T>G; c.*120A>C; c.197A>C; c.240A>C	; p.His66Pro; p.Pro80Pro	1	FALSE	chr9:21971161:T:G	81:chr9:21971161:T:G	0.031888
49_c8-1	49	ATM	HIGH	c.7792C>T	p.Arg2598*	0	FALSE	chr11:108203492:C:T	81:chr11:108203492:C:T	0.00203
49_c8-1	49	NTRK1	MODERATE	c.266G>A; c.356G>A	p.Arg89His; p.Arg119His	1	FALSE	chr1:156834588:G:A	81:chr1:156834588:G:A	0.001848

49_c8-1	49	FGFR1	MODERATE	c.1013C>T; c.1019C>T; c.1112C>T; c.746C>T; c.752C>T; c.995C>T	p.Thr338Met; p.Thr340Met; p.Thr371Met; p.Thr249Met; p.Thr251Met; p.Thr332Met	2	FALSE	chr8:38279377:G:A	81:chr8:38279377:G:A	0.001642
49_c8-1	49	CSDE1; NRAS	MODIFIER; HIGH	c.*2430G>T; c.*2523G>T; c.*2817G>T; c.*2910G>T; c.*2964G>T; c.*3057G>T; c.187G>T	; p.Glu63*	1	FALSE	chr1:115256524:C:A	81:chr1:115256524:C:A	0.001857
49_c8-1	49	FBXW7	MODERATE	c.1444G>T; c.1558G>T; c.1798G>T	p.Asp482Tyr; p.Asp520Tyr; p.Asp600Tyr	0	FALSE	chr4:153245393:C:A	81:chr4:153245393:C:A	0.00148
49_c8-1	49	CTNNB1	MODERATE	c.96C>A	p.Asp32Glu	0	FALSE	chr3:41266099:C:A	81:chr3:41266099:C:A	0.001398
49_c8-1	49	TP53	MODIFIER; MODERATE	c.-5G>T; c.356G>T; c.473G>T; c.77G>T	; p.Arg119Leu; p.Arg158Leu; p.Arg26Leu	80	FALSE	chr17:7578457:C:A	81:chr17:7578457:C:A	0.001616
49_c8-1	49	EGFR	MODERATE	c.1789G>A	p.Ala597Thr	1	FALSE	chr7:55233039:G:A	81:chr7:55233039:G:A	0.002581
49_c8-1	49	ATM	MODERATE	c.8228C>T	p.Thr2743Met	0	FALSE	chr11:108206648:C:T	81:chr11:108206648:C:T	0.001336
49_c8-1	49	FGFR3	MODIFIER; MODERATE	c.931-398C>A; c.1172C>A; c.1178C>A	; p.Ala391Glu; p.Ala393Glu	34	FALSE	chr4:1806153:C:A	81:chr4:1806153:C:A	0.002941
49_c8-1	49	MET	MODERATE	c.3583C>A; c.3637C>A	p.Leu1195Ile; p.Leu1213Ile	1	FALSE	chr7:116422102:C:A	81:chr7:116422102:C:A	0.001479
49_c8-1	49	NOTCH1	MODERATE	c.5720C>T	p.Pro1907Leu	0	FALSE	chr9:139395218:G:A	81:chr9:139395218:G:A	0.001957

49_c8-1	49	KDR	MODERATE	c.2309G>T	p.Gly770Val	1	FALSE	chr4:55964928:C:A	81:chr4:55964928:C:A	0.001362
49_c8-1	49	KDR	MODERATE	c.3449G>T	p.Arg1150Ile	1	FALSE	chr4:55955096:C:A	81:chr4:55955096:C:A	0.001397
49_c8-1	49	FGFR3	MODERATE	c.1586A>G; c.1922A>G; c.1928A>G	p.Asp529Gly; p.Asp641Gly; p.Asp643Gly	1	FALSE	chr4:1807863:A:G	81:chr4:1807863:A:G	0.002788
49_c8-1	49	TP53	MODERATE; MODIFIER	c.137C>T; c.254C>T; c.-279C>T; c.-360C>T	p.Pro46Leu; p.Pro85Leu;	1	FALSE	chr17:7579433:G:A	81:chr17:7579433:G:A	0.001761
49_c8-1	49	CTNNB1	MODERATE	c.98C>A	p.Ser33Tyr	0	FALSE	chr3:41266101:C:A	81:chr3:41266101:C:A	0.001377
49_c8-1	49	NOTCH1	MODERATE	c.2644G>A	p.Ala882Thr	0	FALSE	chr9:139405201:C:T	81:chr9:139405201:C:T	0.002066
49_c8-1	49	FBXW7	HIGH	c.1069G>T; c.1309G>T; c.955G>T	p.Gly357*; p.Gly437*; p.Gly319*	0	FALSE	chr4:153249469:C:A	81:chr4:153249469:C:A	0.001453
49_c8-1	49	FBXW7	HIGH	c.1027G>T; c.1267G>T; c.913G>T	p.Gly343*; p.Gly423*; p.Gly305*	0	FALSE	chr4:153249511:C:A	81:chr4:153249511:C:A	0.001565
49_c8-1	49	NOTCH1	MODERATE	c.2860T>C	p.Cys954Arg	0	FALSE	chr9:139404294:A:G	81:chr9:139404294:A:G	0.001685
49_c8-1	49	TP53	MODIFIER; MODERATE	c.-9G>T; c.352G>T; c.469G>T; c.73G>T	; p.Val118Phe; p.Val157Phe; p.Val25Phe	169	FALSE	chr17:7578461:C:A	81:chr17:7578461:C:A	0.00237
49_c8-1	49	KDR	MODERATE	c.3311C>T	p.Ser1104Phe	1	FALSE	chr4:55955634:G:A	81:chr4:55955634:G:A	0.001395
49_c8-1	49	NTRK3	MODERATE	c.1463C>T; c.1487C>T	p.Ala488Val; p.Ala496Val	0	FALSE	chr15:88576186:G:A	81:chr15:88576186:G:A	0.002828
49_c8-1	49	NOTCH1	MODERATE	c.2528A>G	p.Glu843Gly	0	FALSE	chr9:139405663:T:C	81:chr9:139405663:T:C	0.238698

49_c8-1	49	FBXW7	MODERATE	c.232A>T; c.346A>T; c.586A>T	p.Thr78Ser; p.Thr116Ser; p.Thr196Ser	0	FALSE	chr4:153268222:T:A	81:chr4:153268222:T:A	0.00194
49_c8-1	49	PDGFRA	MODERATE	c.1495G>A	p.Val499Met	2	FALSE	chr4:55139834:G:A	81:chr4:55139834:G:A	0.002234
49_c8-1	49	MIR4674; MIR4674HG; NOTCH1	MODIFIER; MODERATE	n.*87G>T; n.-1C>A; c.62G>T	; p.Gly21Val	0	FALSE	chr9:139438554:C:A	81:chr9:139438554:C:A	0.002837
49_c8-1	49	EGFR	MODERATE	c.1774G>A	p.Val592Ile	1	FALSE	chr7:55233024:G:A	81:chr7:55233024:G:A	0.002418
49_c8-1	49	FBXW7	MODERATE	c.1088C>T; c.1202C>T; c.1442C>T	p.Ala363Val; p.Ala401Val; p.Ala481Val	0	FALSE	chr4:153247360:G:A	81:chr4:153247360:G:A	0.001267
49_c8-1	49	EGFR; EGFR-AS1	LOW; MODIFIER	c.2472C>A; n.-1G>T	p.Gly824Gly;	1	FALSE	chr7:55259414:C:A	81:chr7:55259414:C:A	0.002008
49_c8-1	49	TSC2	MODERATE	c.1381G>A	p.Val461Met	0	FALSE	chr16:2112992:G:A	81:chr16:2112992:G:A	0.001664
49_c8-1	49	IDH2	LOW; MODIFIER	c.-4G>T; c.-17-2860G>T; c.153G>T	; p.Val51Val	1	FALSE	chr15:90634839:C:A	81:chr15:90634839:C:A	0.002899
49_c8-1	49	PTEN	MODERATE	c.923G>A	p.Arg308His	1	FALSE	chr10:89720772:G:A	81:chr10:89720772:G:A	0.001812
49_c8-1	49	NTRK2	MODERATE	c.1960C>A; c.2008C>A	p.Leu654Met; p.Leu670Met	0	FALSE	chr9:87570268:C:A	81:chr9:87570268:C:A	0.002318
49_c8-1	49	EGFR	MODERATE	c.1841G>A	p.Gly614Asp	1	FALSE	chr7:55233091:G:A	81:chr7:55233091:G:A	0.00369
49_c8-1	49	PDGFRA	MODERATE	c.1526C>A	p.Ala509Asp	1	FALSE	chr4:55139865:C:A	81:chr4:55139865:C:A	0.003051
49_c8-1	49	FGFR4	MODIFIER; MODERATE	c.1058-174G>A; c.1078G>A	; p.Ala360Thr	1	FALSE	chr5:176520159:G:A	81:chr5:176520159:G:A	0.00144
49_c8-1	49	IDH1	MODERATE	c.395G>A	p.Arg132His	4157	FALSE	chr2:209113112:C:T	81:chr2:209113112:C:T	0.002484
49_c8-1	49	ATM	MODERATE	c.7328G>A	p.Arg2443Gln	0	FALSE	chr11:108200961:G:A	81:chr11:108200961:G:A	0.001499
49_c8-1	49	KIT	MODERATE	c.2329G>A; c.2341G>A	p.Ala777Thr; p.Ala781Thr	1	FALSE	chr4:55598144:G:A	81:chr4:55598144:G:A	0.001828

49_c8-1	49	EPHA3	MODERATE	c.1379C>A	p.Pro460His	0	FALSE	chr3:89445059:C:A	81:chr3:89445059:C:A	0.00165
49_c8-1	49	CTNNB1	MODERATE	c.1723G>A	p.Gly575Arg	0	FALSE	chr3:41277254:G:A	81:chr3:41277254:G:A	0.002018
49_c8-1	49	KIT	MODERATE	c.1485C>A	p.Asn495Lys	1	FALSE	chr4:55592161:C:A	81:chr4:55592161:C:A	0.001538
49_c8-1	49	EPHA3	HIGH	c.2757G>A	p.Trp919*	0	FALSE	chr3:89521680:G:A	81:chr3:89521680:G:A	0.001376
49_c8-1	49	TP53	LOW; MODIFIER; MODERATE	c.-6C>T; c.355C>T; c.472C>T; c.76C>T	; p.Arg119Cys; p.Arg158Cys; p.Arg26Cys	17	FALSE	chr17:7578458:G:A	81:chr17:7578458:G:A	0.001606
49_c8-1	49	NOTCH1	MODERATE	c.3407G>T	p.Gly1136Val	0	FALSE	chr9:139402510:C:A	81:chr9:139402510:C:A	0.002806
49_c8-1	49	KRAS	HIGH	c.292G>T	p.Glu98*	1	FALSE	chr12:25378706:C:A	81:chr12:25378706:C:A	0.001833
49_c8-1	49	CDH1	MODERATE	c.294C>A	p.Phe98Leu	0	FALSE	chr16:68835703:C:A	81:chr16:68835703:C:A	0.00148
49_c8-1	49	IGF1R	MODERATE	c.167A>G	p.Glu56Gly	0	FALSE	chr15:99250863:A:G	81:chr15:99250863:A:G	0.002143
49_c8-1	49	MET	MODERATE	c.608C>A	p.Ser203Tyr	1	FALSE	chr7:116339746:C:A	81:chr7:116339746:C:A	0.001383
82_c3-1	82	NOTCH1	MODERATE	c.6019G>A	p.Val2007Met	0	FALSE	chr9:139393627:C:T	82:chr9:139393627:C:T	0.002978
82_c3-1	82	PIK3CA	MODERATE	c.1645G>A	p.Asp549Asn	4	FALSE	chr3:178936103:G:A	82:chr3:178936103:G:A	0.001829
82_c3-1	82	ALK	MODERATE	c.2629G>T	p.Ala877Ser	1	FALSE	chr2:29455173:C:A	82:chr2:29455173:C:A	0.001619
82_c3-1	82	FBXW7	HIGH	c.1027G>T; c.1267G>T; c.913G>T	p.Gly343*; p.Gly423*; p.Gly305*	0	FALSE	chr4:153249511:C:A	82:chr4:153249511:C:A	0.002408
82_c3-1	82	TP53	MODERATE	c.134C>A; c.413C>A; c.530C>A; c.53C>A	p.Pro45His; p.Pro138His; p.Pro177His; p.Pro18His	20	FALSE	chr17:7578400:G:T	82:chr17:7578400:G:T	0.002481
82_c3-1	82	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2327G>A; n.1235C>T	p.Arg776His;	7	FALSE	chr7:55249029:G:A	82:chr7:55249029:G:A	0.001464

82_c3-1	82	MET	MODERATE	c.1450C>A	p.His484Asn	1	FALSE	chr7:116380061:C:A	82:chr7:116380061:C:A	0.001232
82_c3-1	82	NTRK2	MODERATE	c.250G>A	p.Glu84Lys	0	FALSE	chr9:87317111:G:A	82:chr9:87317111:G:A	0.001275
82_c3-1	82	FGFR3	MODERATE	c.1162G>A; c.1498G>A; c.1504G>A	p.Ala388Thr; p.Ala500Thr; p.Ala502Thr	1	FALSE	chr4:1807167:G:A	82:chr4:1807167:G:A	0.001898
82_c3-1	82	FGFR2	MODERATE; MODIFIER	c.1357G>C; c.1360G>C; c.1363G>C; c.1372G>C; c.1441G>C; c.1444G>C; c.1708G>C; c.1711G>C; n.2158G>C	p.Gly453Arg; p.Gly454Arg; p.Gly455Arg; p.Gly458Arg; p.Gly481Arg; p.Gly482Arg; p.Gly570Arg; p.Gly571Arg;	1	FALSE	chr10:123256201:C:G	82:chr10:123256201:C:G	0.001786
82_c3-1	82	PIK3CA	MODERATE	c.892C>A	p.Pro298Thr	1	FALSE	chr3:178921410:C:A	82:chr3:178921410:C:A	0.001144
82_c3-1	82	TP53	MODIFIER; MODERATE	c.-3G>T; c.358G>T; c.475G>T; c.79G>T	; p.Ala120Ser; p.Ala159Ser; p.Ala27Ser	23	FALSE	chr17:7578455:C:A	82:chr17:7578455:C:A	0.003436
82_c3-1	82	ATM	MODERATE	c.6200C>A	p.Ala2067Asp	0	FALSE	chr11:108188101:C:A	82:chr11:108188101:C:A	0.003018
82_c3-1	82	TSC2	MODERATE	c.1654G>A	p.Ala552Thr	0	FALSE	chr16:2115574:G:A	82:chr16:2115574:G:A	0.002876
82_c3-1	82	FBXW7	MODERATE	c.1384C>T; c.1498C>T; c.1738C>T	p.His462Tyr; p.His500Tyr; p.His580Tyr	0	FALSE	chr4:153245453:G:A	82:chr4:153245453:G:A	0.001494
82_c3-1	82	MIR4674; MIR4674HG; NOTCH1	MODIFIER; MODERATE	n.*87G>T; n.-1C>A; c.62G>T	; p.Gly21Val	0	FALSE	chr9:139438554:C:A	82:chr9:139438554:C:A	0.004104
82_c3-1	82	CDKN2A	MODIFIER; MODERATE	c.194-3571G>A; c.49G>A	; p.Ala17Thr	1	FALSE	chr9:21974778:C:T	82:chr9:21974778:C:T	0.00188

82_c3-1	82	EGFR	MODERATE	c.493C>T	p.Arg165Trp	1	FALSE	chr7:55214367:C:T	82:chr7:55214367:C:T	0.001579
82_c3-1	82	RPL19	MODERATE	c.320G>A	p.Arg107Lys	0	FALSE	chr17:37359326:G:A	82:chr17:37359326:G:A	0.001148
82_c3-1	82	FBXW7	HIGH	c.1057G>T; c.1171G>T; c.1411G>T	p.Glu353*; p.Glu391*; p.Glu471*	0	FALSE	chr4:153249367:C:A	82:chr4:153249367:C:A	0.001505
82_c3-1	82	EPHA3	MODERATE	c.1543G>A	p.Ala515Thr	0	FALSE	chr3:89448579:G:A	82:chr3:89448579:G:A	0.003035
82_c3-1	82	CTNNB1	MODERATE	c.86C>A	p.Ser29Tyr	0	FALSE	chr3:41266089:C:A	82:chr3:41266089:C:A	0.001488
82_c3-1	82	FGFR2	MODERATE; MODIFIER	c.1859G>T; c.1862G>T; c.1865G>T; c.1874G>T; c.1943G>T; c.1946G>T; c.2210G>T; c.2213G>T; n.2660G>T	p.Arg620Met; p.Arg621Met; p.Arg622Met; p.Arg625Met; p.Arg648Met; p.Arg649Met; p.Arg737Met; p.Arg738Met;	1	FALSE	chr10:123243303:C:A	82:chr10:123243303:C:A	0.001641
82_c3-1	82	ERBB2; MIEN1; MIR4728	MODERATE; MODIFIER	c.2720A>G; c.2765A>G; c.2810A>G; n.3134A>G; c.*388T>C; n.-1A>G	p.Lys907Arg; p.Lys922Arg; p.Lys937Arg;	1	FALSE	chr17:37882044:A:G	82:chr17:37882044:A:G	0.001516
82_c3-1	82	FOXL2; FOXL2NB; LINC01391	MODERATE; MODIFIER	c.433C>T; c.-132G>A; n.-1C>T	p.Arg145Cys;	0	FALSE	chr3:138665132:G:A	82:chr3:138665132:G:A	0.002903
82_c3-1	82	FLT3	MODERATE	c.2669C>T	p.Pro890Leu	0	FALSE	chr13:28589378:G:A	82:chr13:28589378:G:A	0.001508
82_c3-1	82	PTEN	HIGH	c.633C>A	p.Cys211*	2	FALSE	chr10:89712015:C:A	82:chr10:89712015:C:A	0.004049
82_c3-1	82	STK11	LOW	c.462C>T	p.His154His	1	FALSE	chr19:1219410:C:T	82:chr19:1219410:C:T	0.002445

82_c3-1	82	APC	MODERATE	c.1864C>T; c.1918C>T	p.Arg622Trp; p.Arg640Trp	0	FALSE	chr5:112170822:C:T	82:chr5:112170822:C:T	0.001386
82_c3-1	82	FGFR1	MODERATE	c.292C>T; c.298C>T; c.541C>T; c.559C>T; c.565C>T; c.658C>T	p.Arg98Cys; p.Arg100Cys; p.Arg181Cys; p.Arg187Cys; p.Arg189Cys; p.Arg220Cys	1	FALSE	chr8:38285495:G:A	82:chr8:38285495:G:A	0.001411
82_c3-1	82	PIK3CA	MODERATE	c.35G>A	p.Gly12Asp	5	FALSE	chr3:178916648:G:A	82:chr3:178916648:G:A	0.000948
82_c3-1	82	FLT3	MODERATE	c.2546G>A	p.Arg849His	0	FALSE	chr13:28589834:C:T	82:chr13:28589834:C:T	0.002774
82_c3-1	82	CTNNB1	MODERATE	c.884C>A	p.Ala295Asp	0	FALSE	chr3:41267300:C:A	82:chr3:41267300:C:A	0.001627
82_c3-1	82	PIK3CA	MODERATE	c.1633G>A	p.Glu545Lys	1189	FALSE	chr3:178936091:G:A	82:chr3:178936091:G:A	0.114121
82_c3-1	82	KDR	MODERATE	c.2158C>T	p.Arg720Trp	1	FALSE	chr4:55968172:G:A	82:chr4:55968172:G:A	0.001334
82_c3-1	82	TP53	MODERATE	c.337G>A; c.418G>A; c.697G>A; c.814G>A	p.Val113Met; p.Val140Met; p.Val233Met; p.Val272Met	85	FALSE	chr17:7577124:C:T	82:chr17:7577124:C:T	0.013261
82_c3-1	82	PIK3CA	MODERATE	c.3001C>A	p.Leu1001Ile	3	FALSE	chr3:178951946:C:A	82:chr3:178951946:C:A	0.001029
82_c3-1	82	PIK3CA	MODERATE	c.518C>A	p.Ser173Tyr	1	FALSE	chr3:178917643:C:A	82:chr3:178917643:C:A	0.001097
82_c3-1	82	TP53	MODIFIER; HIGH	c.*113G>T; c.*25G>T; c.1006G>T; c.529G>T; c.610G>T; c.889G>T	; p.Glu336*; p.Glu177*; p.Glu204*; p.Glu297*	7	FALSE	chr17:7574021:C:A	82:chr17:7574021:C:A	0.001396

82_c3-1	82	TP53	LOW; MODIFIER; MODERATE	c.-6C>T; c.355C>T; c.472C>T; c.76C>T	; p.Arg119Cys; p.Arg158Cys; p.Arg26Cys	17	FALSE	chr17:7578458:G:A	82:chr17:7578458:G:A	0.001744
82_c3-1	82	TP53	MODIFIER; MODERATE	c.*137A>G; c.*225A>G; c.1001A>G; c.1118A>G; c.641A>G; c.722A>G	; p.Lys334Arg; p.Lys373Arg; p.Lys214Arg; p.Lys241Arg	1	FALSE	chr17:7572991:T:C	82:chr17:7572991:T:C	0.002384
82_c3-1	82	PTEN	HIGH	c.1003C>T	p.Arg335*	27	FALSE	chr10:89720852:C:T	82:chr10:89720852:C:T	0.002551
82_c3-1	82	TP53	HIGH	c.109C>T; c.190C>T; c.469C>T; c.586C>T	p.Arg37*; p.Arg64*; p.Arg157*; p.Arg196*	191	FALSE	chr17:7578263:G:A	82:chr17:7578263:G:A	0.134467
82_c3-1	82	BRAF	MODERATE	c.1385G>T	p.Arg462Ile	2	FALSE	chr7:140481423:C:A	82:chr7:140481423:C:A	0.001286
82_c3-1	82	AR	MODERATE	c.1847G>A; c.251G>A	p.Arg616His; p.Arg84His	0	FALSE	chrX:66905930:G:A	82:chrX:66905930:G:A	0.001509
82_c3-1	82	NF1	MODERATE	c.7381G>A; c.7444G>A	p.Asp2461Asn; p.Asp2482Asn	1	FALSE	chr17:29677323:G:A	82:chr17:29677323:G:A	0.001656
82_c3-1	82	AR	MODERATE	c.1846C>T; c.250C>T	p.Arg616Cys; p.Arg84Cys	0	FALSE	chrX:66905929:C:T	82:chrX:66905929:C:T	0.001511
82_c3-1	82	PIK3R1	MODERATE	c.1082G>A; c.1271G>A; c.1361G>A; c.2171G>A	p.Arg361Gln; p.Arg424Gln; p.Arg454Gln; p.Arg724Gln	1	FALSE	chr5:67593425:G:A	82:chr5:67593425:G:A	0.001805
82_c3-1	82	ATM	MODERATE	c.8558C>T	p.Thr2853Met	0	FALSE	chr11:108216609:C:T	82:chr11:108216609:C:T	0.001529
82_c3-1	82	TP53	MODERATE; MODIFIER	c.158C>T; c.275C>T; c.-279C>T; c.-360C>T	p.Pro53Leu; p.Pro92Leu;	1	FALSE	chr17:7579412:G:A	82:chr17:7579412:G:A	0.001848

82_c3-1	82	ALK	MODERATE	c.1669C>T	p.Arg557Cys	1	FALSE	chr2:29519902:G:A	82:chr2:29519902:G:A	0.001291
82_c3-1	82	STK11	MODERATE	c.488G>A	p.Gly163Asp	1	FALSE	chr19:1220395:G:A	82:chr19:1220395:G:A	0.002554
82_c3-1	82	FBXW7	MODERATE	c.289G>A; c.403G>A; c.643G>A	p.Ala97Thr; p.Ala135Thr; p.Ala215Thr	0	FALSE	chr4:153268165:C:T	82:chr4:153268165:C:T	0.001078
82_c3-1	82	TP53	MODERATE; MODIFIER	c.115G>T; c.232G>T; c.-279G>T; c.-360G>T	p.Ala39Ser; p.Ala78Ser;	1	FALSE	chr17:7579455:C:A	82:chr17:7579455:C:A	0.001808
82_c3-1	82	GNA11	MODERATE	c.440G>A	p.Arg147His	1	FALSE	chr19:3113446:G:A	82:chr19:3113446:G:A	0.001617
82_c3-1	82	NOTCH1	MODERATE	c.5885G>A	p.Arg1962His	0	FALSE	chr9:139395053:C:T	82:chr9:139395053:C:T	0.002679
77_c2-2	77	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2356G>A; n.1206C>T	p.Val786Met;	6	FALSE	chr7:55249058:G:A	83:chr7:55249058:G:A	0.001064
77_c2-2	77	NOTCH1	MODERATE	c.4549G>A	p.Asp1517Asn	0	FALSE	chr9:139399799:C:T	83:chr9:139399799:C:T	0.001116
77_c2-2	77	FLT3	HIGH	c.2749G>T	p.Glu917*	0	FALSE	chr13:28589298:C:A	83:chr13:28589298:C:A	0.001133
77_c2-2	77	PDGFRA	MODERATE	c.1526C>A	p.Ala509Asp	1	FALSE	chr4:55139865:C:A	83:chr4:55139865:C:A	0.001783
77_c2-2	77	EGFR	MODERATE	c.940G>A	p.Asp314Asn	1	FALSE	chr7:55223573:G:A	83:chr7:55223573:G:A	0.001015
77_c2-2	77	FGFR2	MODERATE; MODIFIER	c.1397G>T; c.1400G>T; c.1403G>T; c.1412G>T; c.1481G>T; c.1484G>T; c.1748G>T; c.1751G>T; n.2198G>T	p.Gly466Val; p.Gly467Val; p.Gly468Val; p.Gly471Val; p.Gly494Val; p.Gly495Val; p.Gly583Val; p.Gly584Val;	1	FALSE	chr10:123256161:C:A	83:chr10:123256161:C:A	0.001886
77_c2-2	77	RET	MODERATE	c.1907C>T	p.Thr636Met	1	FALSE	chr10:43609955:C:T	83:chr10:43609955:C:T	0.001337

77_c2-2	77	IGF1R	MODERATE	c.3905T>C; c.3908T>C	p.Val1302Ala; p.Val1303Ala	0	FALSE	chr15:99500475:T:C	83:chr15:99500475:T:C	0.001785
77_c2-2	77	IGF1R	MODERATE	c.2824G>A; c.2827G>A	p.Ala942Thr; p.Ala943Thr	0	FALSE	chr15:99472831:G:A	83:chr15:99472831:G:A	0.001001
77_c2-2	77	NF1	MODERATE	c.2695T>G	p.Leu899Val	3	FALSE	chr17:29556328:T:G	83:chr17:29556328:T:G	0.001531
77_c2-2	77	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2350T>C; n.1212A>G	p.Ser784Pro;	4	FALSE	chr7:55249052:T:C	83:chr7:55249052:T:C	0.001636
77_c2-2	77	NTHL1; TSC2	MODIFIER; MODERATE	c.-20C>T; c.170G>A	; p.Arg57His	0	FALSE	chr16:2100432:G:A	83:chr16:2100432:G:A	0.001124
77_c2-2	77	DDR2	MODERATE	c.1433G>A	p.Arg478His	1	FALSE	chr1:162740231:G:A	83:chr1:162740231:G:A	0.001086
77_c2-2	77	NTRK1	MODERATE	c.804C>G; c.894C>G	p.His268Gln; p.His298Gln	1	FALSE	chr1:156843468:C:G	83:chr1:156843468:C:G	0.001322
77_c2-2	77	NOTCH1	MODERATE	c.2588G>T	p.Gly863Val	0	FALSE	chr9:139405257:C:A	83:chr9:139405257:C:A	0.002265
77_c2-2	77	FGFR1	MODERATE	c.488G>T; c.494G>T; c.737G>T; c.755G>T; c.761G>T; c.854G>T	p.Arg163Leu; p.Arg165Leu; p.Arg246Leu; p.Arg252Leu; p.Arg254Leu; p.Arg285Leu	1	FALSE	chr8:38282202:C:A	83:chr8:38282202:C:A	0.001159
77_c2-2	77	BRAF	MODERATE	c.1781A>G	p.Asp594Gly	59	FALSE	chr7:140453154:T:C	83:chr7:140453154:T:C	0.001121
77_c2-2	77	ROS1	MODERATE	c.5185G>T	p.Val1729Leu	1	FALSE	chr6:117658398:C:A	83:chr6:117658398:C:A	0.001124
77_c2-2	77	CDH1	MODERATE	c.221G>A	p.Arg74Gln	0	FALSE	chr16:68835630:G:A	83:chr16:68835630:G:A	0.000951
77_c2-2	77	PDGFRA	MODERATE	c.340G>A	p.Gly114Ser	1	FALSE	chr4:55127552:G:A	83:chr4:55127552:G:A	0.001157
77_c2-2	77	KIT	MODERATE	c.365G>A	p.Arg122His	1	FALSE	chr4:55564477:G:A	83:chr4:55564477:G:A	0.001078
77_c2-2	77	PHLPP1	MODERATE	c.1971C>A	p.Phe657Leu	0	FALSE	chr18:60527739:C:A	83:chr18:60527739:C:A	0.001372
77_c2-2	77	APC	HIGH	c.1733C>A; c.1787C>A	p.Ser578*; p.Ser596*	0	FALSE	chr5:112170691:C:A	83:chr5:112170691:C:A	0.001734

77_c2-2	77	CTNNB1	MODERATE	c.98C>A	p.Ser33Tyr	0	FALSE	chr3:41266101:C:A	83:chr3:41266101:C:A	0.001558
77_c2-2	77	PIK3CA	MODERATE	c.49C>T	p.Pro17Ser	1	FALSE	chr3:178916662:C:T	83:chr3:178916662:C:T	0.000978
77_c2-2	77	C9orf53; CDKN2A	MODIFIER; MODERATE; LOW	n.*616T>G; c.*120A>C; c.197A>C; c.240A>C	; p.His66Pro; p.Pro80Pro	1	FALSE	chr9:21971161:T:G	83:chr9:21971161:T:G	0.018298
77_c2-2	77	TSC1	MODERATE	c.2751G>T; c.2901G>T; c.2904G>T	p.Arg917Ser; p.Arg967Ser; p.Arg968Ser	0	FALSE	chr9:135772642:C:A	83:chr9:135772642:C:A	0.001605
77_c2-2	77	CTNNB1	MODERATE	c.91C>A	p.Leu31Met	0	FALSE	chr3:41266094:C:A	83:chr3:41266094:C:A	0.002093
77_c2-2	77	MIR4673; NOTCH1	MODIFIER; MODERATE	n.*59G>T; c.1343G>T	; p.Arg448Leu	0	FALSE	chr9:139412302:C:A	83:chr9:139412302:C:A	0.001652
77_c2-2	77	TSC2	MODERATE	c.1832G>A	p.Arg611Gln	0	FALSE	chr16:2120572:G:A	83:chr16:2120572:G:A	0.001712
77_c2-2	77	KIT	MODERATE	c.1485C>A	p.Asn495Lys	1	FALSE	chr4:55592161:C:A	83:chr4:55592161:C:A	0.001172
77_c2-2	77	NTRK3	MODERATE	c.1071G>T	p.Glu357Asp	0	FALSE	chr15:88678465:C:A	83:chr15:88678465:C:A	0.001147
77_c2-2	77	NTRK3	MODERATE	c.1459G>T; c.1483G>T	p.Asp487Tyr; p.Asp495Tyr	0	FALSE	chr15:88576190:C:A	83:chr15:88576190:C:A	0.002981
77_c2-2	77	AR	MODERATE	c.2360G>A; c.764G>A	p.Arg787Gln; p.Arg255Gln	0	FALSE	chrX:66941716:G:A	83:chrX:66941716:G:A	0.002698
77_c2-2	77	KDR	MODERATE	c.2075G>T	p.Gly692Val	1	FALSE	chr4:55968588:C:A	83:chr4:55968588:C:A	0.001378
77_c2-2	77	C9orf53; CDKN2A	MODIFIER; MODERATE; LOW	n.*616C>A; c.*183G>T; c.260G>T; c.303G>T	; p.Arg87Leu; p.Pro101Pro	2	FALSE	chr9:21971098:C:A	83:chr9:21971098:C:A	0.001146
77_c2-2	77	EPHA3	MODERATE	c.380C>A	p.Ser127Tyr	0	FALSE	chr3:89259236:C:A	83:chr3:89259236:C:A	0.001206
77_c2-2	77	ATM	MODERATE	c.2075G>A	p.Arg692His	0	FALSE	chr11:108124717:G:A	83:chr11:108124717:G:A	0.00206

77_c2-2	77	RET	MODERATE	c.1991C>A	p.Ala664Asp	2	FALSE	chr10:43610039:C:A	83:chr10:43610039:C:A	0.001494
77_c2-2	77	TP53	MODIFIER; MODERATE	c.*137A>G; c.*225A>G; c.1001A>G; c.1118A>G; c.641A>G; c.722A>G	; p.Lys334Arg; p.Lys373Arg; p.Lys214Arg; p.Lys241Arg	1	FALSE	chr17:7572991:T:C	83:chr17:7572991:T:C	0.002479
77_c2-2	77	IDH2	MODERATE	c.128A>C; c.362A>C; c.518A>C	p.His43Pro; p.His121Pro; p.His173Pro	1	FALSE	chr15:90631835:T:G	83:chr15:90631835:T:G	0.001907
77_c2-2	77	GNA11	MODERATE	c.1030G>A	p.Val344Met	1	FALSE	chr19:3121127:G:A	83:chr19:3121127:G:A	0.001605
77_c2-2	77	NF1	HIGH	c.5817C>A; c.5880C>A	p.Cys1939*; p.Cys1960*	1	FALSE	chr17:29661923:C:A	83:chr17:29661923:C:A	0.001459
77_c2-2	77	DDR2	MODERATE	c.1418G>A	p.Arg473His	2	FALSE	chr1:162740216:G:A	83:chr1:162740216:G:A	0.00102
77_c2-2	77	SMO	MODERATE	c.869G>A	p.Arg290His	0	FALSE	chr7:128845572:G:A	83:chr7:128845572:G:A	0.001017
77_c2-2	77	MET	MODERATE	c.608C>A	p.Ser203Tyr	1	FALSE	chr7:116339746:C:A	83:chr7:116339746:C:A	0.001508
77_c2-2	77	TP53	MODERATE	c.257G>A; c.338G>A; c.617G>A; c.734G>A	p.Gly86Asp; p.Gly113Asp; p.Gly206Asp; p.Gly245Asp	126	FALSE	chr17:7577547:C:T	83:chr17:7577547:C:T	0.001731
77_c2-2	77	ERBB2	MODIFIER; MODERATE	c.*2388C>T; c.1841C>T; c.1886C>T; c.1931C>T; n.2255C>T	; p.Ala614Val; p.Ala629Val; p.Ala644Val	1	FALSE	chr17:37876072:C:T	83:chr17:37876072:C:T	0.001541
77_c2-2	77	PIK3CA	MODERATE	c.112C>A	p.Arg38Ser	9	FALSE	chr3:178916725:C:A	83:chr3:178916725:C:A	0.000939
77_c2-2	77	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2300C>T; n.1262G>A	p.Ala767Val;	5	FALSE	chr7:55249002:C:T	83:chr7:55249002:C:T	0.0009

77_c2-2	77	NTRK3	MODERATE	c.1966G>T; c.1990G>T	p.Ala656Ser; p.Ala664Ser	0	FALSE	chr15:88472565:C:A	83:chr15:88472565:C:A	0.001108
77_c2-2	77	KIT	MODERATE	c.235C>A	p.Gln79Lys	2	FALSE	chr4:55561845:C:A	83:chr4:55561845:C:A	0.001458
77_c2-2	77	PTEN	HIGH	c.688G>T	p.Gly230*	2	FALSE	chr10:89717663:G:T	83:chr10:89717663:G:T	0.001036
77_c2-2	77	MAP2K1	MODERATE	c.722C>A	p.Ser241Tyr	2	FALSE	chr15:66777356:C:A	83:chr15:66777356:C:A	0.001324
77_c2-2	77	KDR	MODERATE	c.583G>T	p.Ala195Ser	1	FALSE	chr4:55981116:C:A	83:chr4:55981116:C:A	0.001063
77_c2-2	77	FBXW7	HIGH	c.1027G>T; c.1267G>T; c.913G>T	p.Gly343*; p.Gly423*; p.Gly305*	0	FALSE	chr4:153249511:C:A	83:chr4:153249511:C:A	0.001315
77_c2-2	77	MET	HIGH	c.1619G>A	p.Trp540*	1	FALSE	chr7:116380997:G:A	83:chr7:116380997:G:A	0.000922
77_c2-2	77	ALK	MODERATE	c.932G>T	p.Arg311Leu	3	FALSE	chr2:29917736:C:A	83:chr2:29917736:C:A	0.001108
77_c2-2	77	FGFR2	MODERATE; MODIFIER	c.1002G>T; c.1071G>T; c.1074G>T; c.1338G>T; c.1341G>T; c.987G>T; c.990G>T; c.993G>T; n.1788G>T	p.Arg334Ser; p.Arg357Ser; p.Arg358Ser; p.Arg446Ser; p.Arg447Ser; p.Arg329Ser; p.Arg330Ser; p.Arg331Ser;	1	FALSE	chr10:123263405:C:A	83:chr10:123263405:C:A	0.001994
77_c2-2	77	TSC2	MODERATE	c.1923C>A	p.Ser641Arg	0	FALSE	chr16:2121594:C:A	83:chr16:2121594:C:A	0.00111
77_c2-2	77	TP53	MODERATE; HIGH	c.363G>T; c.480G>T; c.84G>T; c.3G>T	p.Met121Ile; p.Met160Ile; p.Met28Ile; p.Met1?	4	FALSE	chr17:7578450:C:A	83:chr17:7578450:C:A	0.001392

77_c2-2	77	TP53	HIGH	c.183T>A; c.264T>A; c.543T>A; c.660T>A	p.Tyr61*; p.Tyr88*; p.Tyr181*; p.Tyr220*	3	FALSE	chr17:7578189:A:T	83:chr17:7578189:A:T	0.001325
77_c2-2	77	TSC2	MODERATE	c.1654G>A	p.Ala552Thr	0	FALSE	chr16:2115574:G:A	83:chr16:2115574:G:A	0.002452
77_c2-2	77	NTRK1	MODERATE	c.2028C>A; c.2118C>A; c.2136C>A	p.Ser676Arg; p.Ser706Arg; p.Ser712Arg	1	FALSE	chr1:156849880:C:A	83:chr1:156849880:C:A	0.002349
77_c2-2	77	NF1	MODERATE	c.3610C>T	p.Arg1204Trp	2	FALSE	chr17:29560133:C:T	83:chr17:29560133:C:T	0.001062
77_c2-2	77	NOTCH1	MODERATE	c.6121G>T	p.Val2041Leu	0	FALSE	chr9:139393410:C:A	83:chr9:139393410:C:A	0.001542
77_c2-2	77	PTEN	HIGH	c.138C>A	p.Tyr46*	2	FALSE	chr10:89653840:C:A	83:chr10:89653840:C:A	0.00111
77_c2-2	77	FGFR4	MODERATE	c.461G>A	p.Arg154His	3	FALSE	chr5:176517963:G:A	83:chr5:176517963:G:A	0.001926
77_c2-2	77	FBXW7	MODERATE	c.1444G>T; c.1558G>T; c.1798G>T	p.Asp482Tyr; p.Asp520Tyr; p.Asp600Tyr	0	FALSE	chr4:153245393:C:A	83:chr4:153245393:C:A	0.001127
77_c2-2	77	PTEN	MODERATE	c.729C>A	p.Phe243Leu	1	FALSE	chr10:89717704:C:A	83:chr10:89717704:C:A	0.001832
77_c2-2	77	C9orf53; CDKN2A	MODIFIER; MODERATE	n.*616G>A; c.*318C>T; c.*39C>T; c.395C>T	; p.Ala132Val	1	FALSE	chr9:21970963:G:A	83:chr9:21970963:G:A	0.001723
77_c2-2	77	TP53	MODIFIER; MODERATE	c.-5G>T; c.356G>T; c.473G>T; c.77G>T	; p.Arg119Leu; p.Arg158Leu; p.Arg26Leu	80	FALSE	chr17:7578457:C:A	83:chr17:7578457:C:A	0.002094
77_c2-2	77	NTRK1	MODERATE	c.1751G>A; c.1841G>A; c.1859G>A	p.Gly584Asp; p.Gly614Asp; p.Gly620Asp	1	FALSE	chr1:156848967:G:A	83:chr1:156848967:G:A	0.001195
77_c2-2	77	IGF1R	MODERATE	c.1732G>A	p.Ala578Thr	0	FALSE	chr15:99456415:G:A	83:chr15:99456415:G:A	0.001067

77_c2-2	77	TP53	MODERATE	c.350C>T; c.431C>T; c.710C>T; c.827C>T	p.Ala117Val; p.Ala144Val; p.Ala237Val; p.Ala276Val	10	FALSE	chr17:7577111:G:A	83:chr17:7577111:G:A	0.001241
77_c2-2	77	C9orf53; CDKN2A	MODIFIER; MODERATE; LOW	n.*616G>A; c.*228C>T; c.305C>T; c.348C>T	; p.Ala102Val; p.Gly116Gly	5	FALSE	chr9:21971053:G:A	83:chr9:21971053:G:A	0.001063
77_c2-2	77	ATM	MODERATE	c.7949A>C	p.Asp2650Ala	0	FALSE	chr11:108204634:A:C	83:chr11:108204634:A:C	0.001163
77_c2-2	77	PTEN	MODERATE	c.421C>A	p.His141Asn	2	FALSE	chr10:89692937:C:A	83:chr10:89692937:C:A	0.00114
77_c2-2	77	ATM	MODERATE	c.1634C>A	p.Ala545Glu	0	FALSE	chr11:108122590:C:A	83:chr11:108122590:C:A	0.001199
77_c2-2	77	HGF	MODERATE	c.1172G>A; c.1187G>A	p.Gly391Asp; p.Gly396Asp	0	FALSE	chr7:81350145:C:T	83:chr7:81350145:C:T	0.001651
77_c2-2	77	GNA11	MODERATE	c.440G>A	p.Arg147His	1	FALSE	chr19:3113446:G:A	83:chr19:3113446:G:A	0.001212
77_c2-2	77	ALK	MODERATE	c.871C>T	p.Arg291Cys	3	FALSE	chr2:29917797:G:A	83:chr2:29917797:G:A	0.001004
77_c2-2	77	PHLPP1	MODERATE	c.2452G>A	p.Val818Ile	0	FALSE	chr18:60570204:G:A	83:chr18:60570204:G:A	0.001108
77_c2-2	77	PIK3CA	MODERATE	c.2452C>T	p.Arg818Cys	2	FALSE	chr3:178943785:C:T	83:chr3:178943785:C:T	0.001194
77_c2-2	77	FGFR2	MODERATE; MODIFIER	c.1591G>A; c.1594G>A; c.1597G>A; c.1606G>A; c.1675G>A; c.1678G>A; c.1942G>A; c.1945G>A; n.2392G>A	p.Ala531Thr; p.Ala532Thr; p.Ala533Thr; p.Ala536Thr; p.Ala559Thr; p.Ala560Thr; p.Ala648Thr; p.Ala649Thr;	3	FALSE	chr10:123247549:C:T	83:chr10:123247549:C:T	0.001229

77_c2-2	77	ERBB2	MODERATE; MODIFIER	c.632C>T; c.677C>T; c.722C>T; n.1046C>T	p.Ala211Val; p.Ala226Val; p.Ala241Val;	2	FALSE	chr17:37866417:C:T	83:chr17:37866417:C:T	0.001076
77_c2-2	77	ATM	HIGH	c.2558C>A	p.Ser853*	0	FALSE	chr11:108137989:C:A	83:chr11:108137989:C:A	0.001536
77_c2-2	77	FBXW7	MODERATE	c.1028G>T; c.1268G>T; c.914G>T	p.Gly343Val; p.Gly423Val; p.Gly305Val	0	FALSE	chr4:153249510:C:A	83:chr4:153249510:C:A	0.00198
77_c2-2	77	TSC2	MODERATE	c.781C>T	p.Arg261Trp	0	FALSE	chr16:2107112:C:T	83:chr16:2107112:C:T	0.002627
77_c2-2	77	KDR	MODERATE	c.3449G>T	p.Arg1150Ile	1	FALSE	chr4:55955096:C:A	83:chr4:55955096:C:A	0.001039
77_c2-2	77	NTRK1	MODERATE	c.1039C>T; c.949C>T	p.Arg347Cys; p.Arg317Cys	1	FALSE	chr1:156843613:C:T	83:chr1:156843613:C:T	0.001048
77_c2-2	77	RET	MODERATE	c.1690A>C	p.Thr564Pro	1	FALSE	chr10:43608342:A:C	83:chr10:43608342:A:C	0.001692
77_c2-2	77	INSRR; NTRK1	LOW	c.3397+8G>T; c.33C>A	; p.Pro11Pro	1	FALSE	chr1:156811896:C:A	83:chr1:156811896:C:A	0.001082
77_c2-2	77	EGFR	MODERATE	c.1159C>G	p.Leu387Val	1	FALSE	chr7:55224477:C:G	83:chr7:55224477:C:G	0.001031
77_c2-2	77	PTEN	HIGH	c.720C>A	p.Tyr240*	3	FALSE	chr10:89717695:C:A	83:chr10:89717695:C:A	0.002309
77_c2-2	77	HGF	HIGH	c.1993G>T; c.2008G>T	p.Glu665*; p.Glu670*	0	FALSE	chr7:81334708:C:A	83:chr7:81334708:C:A	0.001836
77_c2-2	77	TP53	MODERATE	c.116A>G; c.35A>G; c.395A>G; c.512A>G	p.Glu39Gly; p.Glu12Gly; p.Glu132Gly; p.Glu171Gly	3	FALSE	chr17:7578418:T:C	83:chr17:7578418:T:C	0.001932
77_c2-2	77	NOTCH1	MODERATE	c.2644G>A	p.Ala882Thr	0	FALSE	chr9:139405201:C:T	83:chr9:139405201:C:T	0.001404
77_c2-2	77	KRAS	MODERATE	c.38G>T	p.Gly13Val	4010	FALSE	chr12:25398281:C:A	83:chr12:25398281:C:A	0.001155

77_c2-2	77	GAPDH; IFFO1; NCAPD2	MODERATE; MODIFIER	c.157G>A; c.283G>A; c.*1743C>T; c.*1746C>T; c.*1770C>T; n.*2798C>T; c.*4252G>A	p.Val53Ile; p.Val95Ile;	0	FALSE	chr12:6646132:G:A	83:chr12:6646132:G:A	0.001438
77_c2-2	77	MIR4673; NOTCH1	MODIFIER; MODERATE	n.-1G>T; c.221G>T	; p.Cys74Phe	0	FALSE	chr9:139418351:C:A	83:chr9:139418351:C:A	0.002773
77_c2-2	77	MITF	MODIFIER; MODERATE	c.-53+197C>A; c.104+24188C>A; c.48C>A	; p.Phe16Leu	0	FALSE	chr3:69813040:C:A	83:chr3:69813040:C:A	0.001011
77_c2-2	77	HGF	MODERATE	c.5G>T	p.Trp2Leu	0	FALSE	chr7:81399283:C:A	83:chr7:81399283:C:A	0.001255
77_c2-2	77	EGFR	MODIFIER; MODERATE	c.*2364C>T; c.2174C>T	; p.Thr725Met	2	FALSE	chr7:55241726:C:T	83:chr7:55241726:C:T	0.001291
77_c2-2	77	FBXW7	MODERATE	c.182G>A; c.296G>A; c.536G>A	p.Arg61His; p.Arg99His; p.Arg179His	0	FALSE	chr4:153271242:C:T	83:chr4:153271242:C:T	0.001214
77_c2-2	77	NF1	MODERATE	c.3559C>A	p.Leu1187Ile	1	FALSE	chr17:29560082:C:A	83:chr17:29560082:C:A	0.001096
77_c2-2	77	CTNNB1	MODERATE	c.861C>A	p.Asn287Lys	0	FALSE	chr3:41267277:C:A	83:chr3:41267277:C:A	0.001744
77_c2-2	77	TP53	MODIFIER; MODERATE	c.-1G>T; c.-82G>T; c.279G>T; c.396G>T	; p.Lys93Asn; p.Lys132Asn	34	FALSE	chr17:7578534:C:A	83:chr17:7578534:C:A	0.001255
77_c2-2	77	MIR4673; NOTCH1	MODIFIER; MODERATE	n.*59G>A; c.1775G>A	; p.Arg592His	0	FALSE	chr9:139410063:C:T	83:chr9:139410063:C:T	0.001512
77_c2-2	77	PTEN	MODERATE	c.392C>A	p.Thr131Asn	2	FALSE	chr10:89692908:C:A	83:chr10:89692908:C:A	0.001082
77_c2-2	77	IGF1R	MODERATE	c.3934T>C; c.3937T>C	p.Ser1312Pro; p.Ser1313Pro	0	FALSE	chr15:99500504:T:C	83:chr15:99500504:T:C	0.004023

77_c2-2	77	DDR2	MODERATE	c.313C>A	p.Arg105Ser	2	FALSE	chr1:162724541:C:A	83:chr1:162724541:C:A	0.001052
77_c2-2	77	FGFR1	MODIFIER; MODERATE	c.-32G>A; c.160G>A; c.61G>A	; p.Ala54Thr; p.Ala21Thr	2	FALSE	chr8:38314904:C:T	83:chr8:38314904:C:T	0.000979
77_c2-2	77	ALK	MODERATE	c.4192C>T	p.Pro1398Ser	1	FALSE	chr2:29416761:G:A	83:chr2:29416761:G:A	0.001176
77_c2-2	77	PIK3CA	MODERATE	c.3044C>A	p.Ser1015Tyr	3	FALSE	chr3:178951989:C:A	83:chr3:178951989:C:A	0.000969
77_c2-2	77	IDH2	MODIFIER; HIGH	c.-3G>T; c.-17-2859G>T; c.154G>T	; p.Glu52*	1	FALSE	chr15:90634838:C:A	83:chr15:90634838:C:A	0.001637
77_c2-2	77	EGFR; EGFR-AS1	LOW; MODIFIER	c.2472C>A; n.-1G>T	p.Gly824Gly;	1	FALSE	chr7:55259414:C:A	83:chr7:55259414:C:A	0.001614
77_c2-2	77	NF1	MODERATE	c.335A>G	p.Gln112Arg	1	FALSE	chr17:29490250:A:G	83:chr17:29490250:A:G	0.002119
77_c2-2	77	PIK3CA	MODERATE	c.1633G>A	p.Glu545Lys	1189	FALSE	chr3:178936091:G:A	83:chr3:178936091:G:A	0.006366
77_c2-2	77	FGFR3	MODIFIER; MODERATE	c.931-374G>A; c.1196G>A; c.1202G>A	; p.Arg399His; p.Arg401His	1	FALSE	chr4:1806177:G:A	83:chr4:1806177:G:A	0.001579
77_c2-2	77	HRAS; LRRC56	MODERATE; MODIFIER	c.383G>T; c.-506C>A	p.Arg128Leu;	1	FALSE	chr11:533520:C:A	83:chr11:533520:C:A	0.001258
77_c2-2	77	TP53	MODERATE; MODIFIER	c.100G>T; c.217G>T; c.-279G>T; c.-360G>T	p.Val34Leu; p.Val73Leu;	5	FALSE	chr17:7579470:C:A	83:chr17:7579470:C:A	0.001522
77_c2-2	77	AKT3	HIGH	c.109G>T	p.Gly37*	0	FALSE	chr1:243858956:C:A	83:chr1:243858956:C:A	0.001132
77_c2-2	77	ERBB2; MIEN1; MIR4728	MODERATE; MODIFIER	c.2720A>G; c.2765A>G; c.2810A>G; n.3134A>G; c.*388T>C; n.-1A>G	p.Lys907Arg; p.Lys922Arg; p.Lys937Arg;	1	FALSE	chr17:37882044:A:G	83:chr17:37882044:A:G	0.00292
77_c2-2	77	BRAF	MODERATE	c.1391G>T	p.Gly464Val	9	FALSE	chr7:140481417:C:A	83:chr7:140481417:C:A	0.001139

77_c2-2	77	GAPDH; IFFO1	MODERATE; MODIFIER	c.683T>C; c.809T>C; c.*1743A>G; c.*1746A>G; c.*1770A>G; n.*2798A>G	p.Leu228Pro; p.Leu270Pro;	0	FALSE	chr12:6647033:T:C	83:chr12:6647033:T:C	0.001263
77_c2-2	77	TP53	MODIFIER; MODERATE	c.*145T>C; c.*233T>C; c.1009T>C; c.1126T>C; c.649T>C; c.730T>C	; p.Ser337Pro; p.Ser376Pro; p.Ser217Pro; p.Ser244Pro	2	FALSE	chr17:7572983:A:G	83:chr17:7572983:A:G	0.001654
77_c2-2	77	RET	MODERATE	c.2116G>A	p.Val706Met	2	FALSE	chr10:43610164:G:A	83:chr10:43610164:G:A	0.000914
77_c2-2	77	ATM	MODERATE	c.4315C>A	p.Leu1439Ile	0	FALSE	chr11:108160407:C:A	83:chr11:108160407:C:A	0.001151
77_c2-2	77	FBXW7	HIGH	c.1057G>T; c.1171G>T; c.1411G>T	p.Glu353*; p.Glu391*; p.Glu471*	0	FALSE	chr4:153249367:C:A	83:chr4:153249367:C:A	0.002241
77_c2-2	77	NOTCH1	MODERATE	c.4571C>T	p.Ala1524Val	0	FALSE	chr9:139399777:G:A	83:chr9:139399777:G:A	0.001284
77_c2-2	77	NF1	MODERATE	c.1496T>C	p.Leu499Pro	1	FALSE	chr17:29541572:T:C	83:chr17:29541572:T:C	0.001122
77_c2-2	77	NOTCH1	MODERATE	c.3407G>T	p.Gly1136Val	0	FALSE	chr9:139402510:C:A	83:chr9:139402510:C:A	0.001465
77_c2-2	77	CTNNB1	MODERATE	c.110C>A	p.Ser37Tyr	0	FALSE	chr3:41266113:C:A	83:chr3:41266113:C:A	0.002083
77_c2-2	77	EGFR	MODERATE	c.719G>A	p.Cys240Tyr	1	FALSE	chr7:55220329:G:A	83:chr7:55220329:G:A	0.001214
77_c2-2	77	FBXW7	MODERATE	c.1078G>T; c.1318G>T; c.964G>T	p.Asp360Tyr; p.Asp440Tyr; p.Asp322Tyr	0	FALSE	chr4:153249460:C:A	83:chr4:153249460:C:A	0.001144
77_c2-2	77	NTRK3	MODERATE	c.698G>T	p.Gly233Val	0	FALSE	chr15:88679765:C:A	83:chr15:88679765:C:A	0.001237
77_c2-2	77	ALG10	MODERATE	c.272G>A	p.Cys91Tyr	0	FALSE	chr12:34176997:G:A	83:chr12:34176997:G:A	0.001546

77_c2-2	77	FBXW7	MODERATE	c.1204G>T; c.1318G>T; c.1558G>T	p.Asp402Tyr; p.Asp440Tyr; p.Asp520Tyr	0	FALSE	chr4:153247244:C:A	83:chr4:153247244:C:A	0.001115
77_c2-2	77	EPHA3	MODERATE	c.237C>A	p.Asn79Lys	0	FALSE	chr3:89259093:C:A	83:chr3:89259093:C:A	0.001043
77_c2-2	77	DDR2	MODERATE	c.691C>A	p.Gln231Lys	1	FALSE	chr1:162729605:C:A	83:chr1:162729605:C:A	0.00114
77_c2-2	77	FGFR4	MODIFIER; MODERATE	c.1098-65G>A; c.1251+10G>A; c.1067G>A	; p.Arg356His	1	FALSE	chr5:176520342:G:A	83:chr5:176520342:G:A	0.001425
77_c2-2	77	FGFR3	MODIFIER; MODERATE	c.931-398C>A; c.1172C>A; c.1178C>A	; p.Ala391Glu; p.Ala393Glu	34	FALSE	chr4:1806153:C:A	83:chr4:1806153:C:A	0.005952
77_c2-2	77	FGFR1	MODERATE	c.1453C>T; c.1459C>T; c.1696C>T; c.1720C>T; c.1726C>T; c.1819C>T	p.Arg485Trp; p.Arg487Trp; p.Arg566Trp; p.Arg574Trp; p.Arg576Trp; p.Arg607Trp	1	FALSE	chr8:38273516:G:A	83:chr8:38273516:G:A	0.002037
77_c2-2	77	KDR	MODERATE	c.491G>T	p.Arg164Ile	1	FALSE	chr4:55981208:C:A	83:chr4:55981208:C:A	0.00183
80_c3-1	80	CWH43	MODERATE	c.1407C>A; c.1488C>A	p.Ser469Arg; p.Ser496Arg	0	FALSE	chr4:49032957:C:A	84:chr4:49032957:C:A	0.004577
80_c3-1	80	C9orf53; CDKN2A	MODIFIER; MODERATE	n.*616C>G; c.*140G>C; c.217G>C; c.260G>C	; p.Ala73Pro; p.Arg87Pro	1	FALSE	chr9:21971141:C:G	84:chr9:21971141:C:G	0.058252
80_c3-1	80	IGF1R	MODERATE	c.3934T>C; c.3937T>C	p.Ser1312Pro; p.Ser1313Pro	0	FALSE	chr15:99500504:T:C	84:chr15:99500504:T:C	0.026005

80_c3-1	80	TP53	MODIFIER; MODERATE	c.*137A>G; c.*225A>G; c.1001A>G; c.1118A>G; c.641A>G; c.722A>G	; p.Lys334Arg; p.Lys373Arg; p.Lys214Arg; p.Lys241Arg	1	FALSE	chr17:7572991:T:C	84:chr17:7572991:T:C	0.00722
80_c3-1	80	C9orf53; CDKN2A	MODIFIER; MODERATE; LOW	n.*616T>G; c.*120A>C; c.197A>C; c.240A>C	; p.His66Pro; p.Pro80Pro	1	FALSE	chr9:21971161:T:G	84:chr9:21971161:T:G	0.021645
80_c3-1	80	VHL	MODIFIER; MODERATE	c.341-3270A>C; c.344A>C	; p.His115Pro	0	FALSE	chr3:10188201:A:C	84:chr3:10188201:A:C	0.004751
80_c3-1	80	CTNNB1	MODERATE	c.1972G>T	p.Val658Phe	0	FALSE	chr3:41278096:G:T	84:chr3:41278096:G:T	0.004376
80_c3-1	80	PIK3CA	MODERATE	c.892C>T	p.Pro298Ser	1	FALSE	chr3:178921410:C:T	84:chr3:178921410:C:T	0.004264
80_c3-1	80	ERBB2; MIEN1; MIR4728	MODIFIER; MODERATE	c.3160-213A>G; c.3251A>G; c.3296A>G; c.3341A>G; n.3665A>G; c.*388T>C; n.*67A>G	; p.Glu1084Gly; p.Glu1099Gly; p.Glu1114Gly	1	FALSE	chr17:37883729:A:G	84:chr17:37883729:A:G	0.004673
80_c3-1	80	PIK3CA	MODERATE	c.1235G>A	p.Arg412Gln	1	FALSE	chr3:178927472:G:A	84:chr3:178927472:G:A	0.004535
80_c3-1	80	NTRK1	MODERATE	c.1940T>G; c.2030T>G; c.2048T>G	p.Val647Gly; p.Val677Gly; p.Val683Gly	2	FALSE	chr1:156849792:T:G	84:chr1:156849792:T:G	0.023333
86_c1w2-1	86	IGF1R	MODERATE	c.3934T>C; c.3937T>C	p.Ser1312Pro; p.Ser1313Pro	0	FALSE	chr15:99500504:T:C	85:chr15:99500504:T:C	0.021231

86_c1w2-1	86	TP53	MODIFIER; HIGH	c.-55C>A; c.27C>A; c.306C>A; c.423C>A	; p.Cys9*; p.Cys102*; p.Cys141*	13	FALSE	chr17:7578507:G:T	85:chr17:7578507:G:T	0.283654
86_c1w2-1	86	EPHA3	MODERATE	c.2275G>T	p.Val759Leu	0	FALSE	chr3:89480438:G:T	85:chr3:89480438:G:T	0.020833
86_c1w2-1	86	CDH1	HIGH	c.1595G>A	p.Trp532*	0	FALSE	chr16:68853212:G:A	85:chr16:68853212:G:A	0.019802
86_c1w2-1	86	TP53	MODIFIER; MODERATE	c.-3G>T; c.358G>T; c.475G>T; c.79G>T	; p.Ala120Ser; p.Ala159Ser; p.Ala27Ser	23	FALSE	chr17:7578455:C:A	85:chr17:7578455:C:A	0.006472
86_c1w2-1	86	NTRK1	MODERATE	c.1940T>G; c.2030T>G; c.2048T>G	p.Val647Gly; p.Val677Gly; p.Val683Gly	2	FALSE	chr1:156849792:T:G	85:chr1:156849792:T:G	0.02381
86_c1w2-1	86	TP53	MODIFIER; MODERATE	c.*148A>C; c.*236A>C; c.1012A>C; c.1129A>C; c.652A>C; c.733A>C	; p.Thr338Pro; p.Thr377Pro; p.Thr218Pro; p.Thr245Pro	2	FALSE	chr17:7572980:T:G	85:chr17:7572980:T:G	0.232558
86_c1w2-1	86	CDKN2A	MODIFIER; MODERATE	c.194-3568A>C; c.52A>C	; p.Thr18Pro	1	FALSE	chr9:21974775:T:G	85:chr9:21974775:T:G	0.012903
86_c1w2-1	86	MITF	MODERATE	c.127A>C; c.235A>C; c.280A>C; c.283A>C	p.Thr43Pro; p.Thr79Pro; p.Thr94Pro; p.Thr95Pro	0	FALSE	chr3:69928463:A:C	85:chr3:69928463:A:C	0.043478
86_c1w2-1	86	CDKN2A	MODIFIER; MODERATE	c.194-3570C>G; c.50C>G	; p.Ala17Gly	1	FALSE	chr9:21974777:G:C	85:chr9:21974777:G:C	0.013423
86_c1w2-1	86	C9orf53; CDKN2A	MODIFIER; MODERATE	n.*616C>G; c.*140G>C; c.217G>C; c.260G>C	; p.Ala73Pro; p.Arg87Pro	1	FALSE	chr9:21971141:C:G	85:chr9:21971141:C:G	0.059055

86_c1w2-1	86	ERBB2; MIEN1; MIR4728	MODERATE; MODIFIER	c.2600G>A; c.2645G>A; c.2690G>A; n.3014G>A; c.*388C>T; n.-1G>A	p.Arg867Gln; p.Arg882Gln; p.Arg897Gln;	2	FALSE	chr17:37881620:G:A	85:chr17:37881620:G:A	0.007752
86_c2-1	86	KRAS	MODERATE	c.35G>C	p.Gly12Ala	11213	FALSE	chr12:25398284:C:G	86:chr12:25398284:C:G	0.053333
86_c2-1	86	FGFR3	MODERATE	c.743G>A	p.Arg248His	2	FALSE	chr4:1803565:G:A	86:chr4:1803565:G:A	0.00722
86_c2-1	86	CTNNB1	MODERATE	c.1972G>T	p.Val658Phe	0	FALSE	chr3:41278096:G:T	86:chr3:41278096:G:T	0.003906
86_c2-1	86	TP53	MODIFIER; MODERATE	c.*137A>G; c.*225A>G; c.1001A>G; c.1118A>G; c.641A>G; c.722A>G	; p.Lys334Arg; p.Lys373Arg; p.Lys214Arg; p.Lys241Arg	1	FALSE	chr17:7572991:T:C	86:chr17:7572991:T:C	0.012048
86_c2-1	86	TP53	MODIFIER; MODERATE	c.-14C>G; c.347C>G; c.464C>G; c.68C>G	; p.Thr116Ser; p.Thr155Ser; p.Thr23Ser	27	FALSE	chr17:7578466:G:C	86:chr17:7578466:G:C	0.008214
86_c2-1	86	RET	MODERATE	c.1690A>C	p.Thr564Pro	1	FALSE	chr10:43608342:A:C	86:chr10:43608342:A:C	0.004
86_c2-1	86	C9orf53; CDKN2A	MODIFIER; MODERATE; LOW	n.*616T>G; c.*120A>C; c.197A>C; c.240A>C	; p.His66Pro; p.Pro80Pro	1	FALSE	chr9:21971161:T:G	86:chr9:21971161:T:G	0.029674
86_c2-1	86	C9orf53; CDKN2A	MODIFIER; MODERATE	n.*616C>G; c.*140G>C; c.217G>C; c.260G>C	; p.Ala73Pro; p.Arg87Pro	1	FALSE	chr9:21971141:C:G	86:chr9:21971141:C:G	0.046931
86_c2-1	86	IGF1R	MODERATE	c.3934T>C; c.3937T>C	p.Ser1312Pro; p.Ser1313Pro	0	FALSE	chr15:99500504:T:C	86:chr15:99500504:T:C	0.012526

86_c2-1	86	TP53	MODIFIER; MODERATE	c.-15A>C; c.346A>C; c.463A>C; c.67A>C	; p.Thr116Pro; p.Thr155Pro; p.Thr23Pro	17	FALSE	chr17:7578467:T:G	86:chr17:7578467:T:G	0.008421
86_c2-1	86	NTHL1; TSC2	MODIFIER; MODERATE	c.-20G>A; c.175C>T	; p.Arg59Trp	0	FALSE	chr16:2100437:C:T	86:chr16:2100437:C:T	0.007859
73_c4-1	73	CDH1	HIGH	c.763C>T	p.Gln255*	0	FALSE	chr16:68844175:C:T	88:chr16:68844175:C:T	0.001558
73_c4-1	73	IGF1R	MODERATE	c.3934T>C; c.3937T>C	p.Ser1312Pro; p.Ser1313Pro	0	FALSE	chr15:99500504:T:C	88:chr15:99500504:T:C	0.005982
73_c4-1	73	MAP2K1	MODERATE	c.198C>A	p.Asp66Glu	4	FALSE	chr15:66727482:C:A	88:chr15:66727482:C:A	0.001885
73_c4-1	73	HGF	HIGH	c.1993G>T; c.2008G>T	p.Glu665*; p.Glu670*	0	FALSE	chr7:81334708:C:A	88:chr7:81334708:C:A	0.001883
73_c4-1	73	NOTCH1	MODERATE	c.6121G>T	p.Val2041Leu	0	FALSE	chr9:139393410:C:A	88:chr9:139393410:C:A	0.002439
73_c4-1	73	NOTCH1	MODERATE	c.4825G>T	p.Asp1609Tyr	0	FALSE	chr9:139399318:C:A	88:chr9:139399318:C:A	0.003405
73_c4-1	73	NTRK2	MODERATE	c.1318C>A; c.1357C>A	p.Leu440Met; p.Leu453Met	0	FALSE	chr9:87366961:C:A	88:chr9:87366961:C:A	0.001756
73_c4-1	73	IDH2	MODERATE	c.124A>G; c.358A>G; c.514A>G	p.Arg42Gly; p.Arg120Gly; p.Arg172Gly	19	FALSE	chr15:90631839:T:C	88:chr15:90631839:T:C	0.00191
73_c4-1	73	NTRK3	MODERATE	c.1071G>T	p.Glu357Asp	0	FALSE	chr15:88678465:C:A	88:chr15:88678465:C:A	0.001787
73_c4-1	73	NF1	HIGH	c.5401C>T; c.5464C>T	p.Gln1801*; p.Gln1822*	1	FALSE	chr17:29654712:C:T	88:chr17:29654712:C:T	0.00166
73_c4-1	73	HRAS; LRRC56	MODERATE; MODIFIER	c.351G>T; c.-506C>A	p.Lys117Asn;	3	FALSE	chr11:533552:C:A	88:chr11:533552:C:A	0.003135
73_c4-1	73	PTEN	MODERATE	c.404T>C	p.Ile135Thr	4	FALSE	chr10:89692920:T:C	88:chr10:89692920:T:C	0.001712
73_c4-1	73	PDGFRA	MODERATE	c.1499G>A	p.Arg500Gln	1	FALSE	chr4:55139838:G:A	88:chr4:55139838:G:A	0.00177
73_c4-1	73	AKT1	MODERATE	c.932G>A	p.Gly311Asp	1	FALSE	chr14:105239613:C:T	88:chr14:105239613:C:T	0.002703
73_c4-1	73	IGF1R	MODERATE	c.2425G>A	p.Glu809Lys	0	FALSE	chr15:99465600:G:A	88:chr15:99465600:G:A	0.00191

73_c4-1	73	C9orf53; CDKN2A	MODIFIER; MODERATE	n.*616C>A; c.*20G>T; c.*299G>T; c.376G>T	; p.Val126Phe	2	FALSE	chr9:21970982:C:A	88:chr9:21970982:C:A	0.002141
73_c4-1	73	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2492G>A; n.-1C>T	p.Arg831His;	4	FALSE	chr7:55259434:G:A	88:chr7:55259434:G:A	0.003083
73_c4-1	73	CTNNB1	MODERATE	c.134C>A	p.Ser45Tyr	0	FALSE	chr3:41266137:C:A	88:chr3:41266137:C:A	0.001667
73_c4-1	73	TP53	MODIFIER; MODERATE	c.*137A>G; c.*225A>G; c.1001A>G; c.1118A>G; c.641A>G; c.722A>G	; p.Lys334Arg; p.Lys373Arg; p.Lys214Arg; p.Lys241Arg	1	FALSE	chr17:7572991:T:C	88:chr17:7572991:T:C	0.002833
73_c4-1	73	MIR4673; NOTCH1	MODIFIER; MODERATE	n.*59A>C; c.1195A>C	; p.Thr399Pro	0	FALSE	chr9:139412649:T:G	88:chr9:139412649:T:G	0.00601
73_c4-1	73	SMO	MODERATE	c.1045A>C	p.Thr349Pro	0	FALSE	chr7:128846115:A:C	88:chr7:128846115:A:C	0.006228
73_c4-1	73	C9orf53; CDKN2A	MODIFIER; MODERATE	n.*616C>A; c.*266G>T; c.343G>T; c.386G>T	; p.Val115Leu; p.Arg129Leu	4	FALSE	chr9:21971015:C:A	88:chr9:21971015:C:A	0.002191
73_c4-1	73	KIT	MODERATE	c.1485C>A	p.Asn495Lys	1	FALSE	chr4:55592161:C:A	88:chr4:55592161:C:A	0.001859
73_c4-1	73	TSC2	MODERATE	c.1381G>A	p.Val461Met	0	FALSE	chr16:2112992:G:A	88:chr16:2112992:G:A	0.00226
73_c4-1	73	TP53	MODERATE	c.200G>A; c.281G>A; c.560G>A; c.677G>A	p.Gly67Asp; p.Gly94Asp; p.Gly187Asp; p.Gly226Asp	5	FALSE	chr17:7577604:C:T	88:chr17:7577604:C:T	0.001671
73_c4-1	73	HRAS; LRRC56	MODERATE; MODIFIER	c.305G>T; c.-506C>A	p.Arg102Leu;	1	FALSE	chr11:533598:C:A	88:chr11:533598:C:A	0.002548

73_c4-1	73	FBXW7	MODERATE	c.1028G>T; c.1268G>T; c.914G>T	p.Gly343Val; p.Gly423Val; p.Gly305Val	0	FALSE	chr4:153249510:C:A	88:chr4:153249510:C:A	0.001864
73_c4-1	73	CDH1	MODERATE	c.671G>A	p.Arg224His	0	FALSE	chr16:68842735:G:A	88:chr16:68842735:G:A	0.003027
73_c4-1	73	PDGFRA	MODERATE	c.1198G>A	p.Asp400Asn	1	FALSE	chr4:55136876:G:A	88:chr4:55136876:G:A	0.001567
73_c4-1	73	NF1	MODERATE	c.2573C>A	p.Ser858Tyr	1	FALSE	chr17:29556206:C:A	88:chr17:29556206:C:A	0.001881
73_c4-1	73	ATM	MODERATE	c.1237C>A	p.Leu413Ile	0	FALSE	chr11:108121429:C:A	88:chr11:108121429:C:A	0.00207
73_c4-1	73	FBXW7	MODERATE	c.1178G>A; c.824G>A; c.938G>A	p.Arg393Gln; p.Arg275Gln; p.Arg313Gln	0	FALSE	chr4:153250882:C:T	88:chr4:153250882:C:T	0.001715
73_c4-1	73	FGFR1	MODIFIER; MODERATE	c.-85G>T; c.107G>T; c.8G>T	; p.Ser36Ile; p.Ser3Ile	1	FALSE	chr8:38314957:C:A	88:chr8:38314957:C:A	0.00173
73_c4-1	73	ALK	MODERATE	c.2077C>T	p.Pro693Ser	1	FALSE	chr2:29474098:G:A	88:chr2:29474098:G:A	0.00202
73_c4-1	73	FGFR1	MODERATE	c.1033T>A; c.1051T>A; c.1057T>A; c.1150T>A; c.784T>A; c.790T>A	p.Ser345Thr; p.Ser351Thr; p.Ser353Thr; p.Ser384Thr; p.Ser262Thr; p.Ser264Thr	1	FALSE	chr8:38279339:A:T	88:chr8:38279339:A:T	0.002033
73_c4-1	73	HRAS; LRRC56	HIGH; MODIFIER	c.403C>T; c.-506G>A	p.Arg135*;	1	FALSE	chr11:533500:G:A	88:chr11:533500:G:A	0.002053
73_c4-1	73	TP53	MODIFIER; MODERATE	c.-36G>T; c.325G>T; c.442G>T; c.46G>T	; p.Asp109Tyr; p.Asp148Tyr; p.Asp16Tyr	5	FALSE	chr17:7578488:C:A	88:chr17:7578488:C:A	0.002137
73_c4-1	73	KDR	MODERATE	c.1051C>T	p.Pro351Ser	1	FALSE	chr4:55976861:G:A	88:chr4:55976861:G:A	0.001225
73_c4-1	73	CTNNB1	MODERATE	c.861C>A	p.Asn287Lys	0	FALSE	chr3:41267277:C:A	88:chr3:41267277:C:A	0.001807

73_c4-1	73	NTRK3	MODERATE	c.2110G>T; c.2134G>T; c.2176G>T	p.Val704Leu; p.Val712Leu; p.Val726Leu	0	FALSE	chr15:88423659:C:A	88:chr15:88423659:C:A	0.004115
73_c4-1	73	ALK	MODERATE	c.4192C>T	p.Pro1398Ser	1	FALSE	chr2:29416761:G:A	88:chr2:29416761:G:A	0.001969
73_c4-1	73	TP53	MODIFIER; MODERATE	c.-3G>T; c.358G>T; c.475G>T; c.79G>T	; p.Ala120Ser; p.Ala159Ser; p.Ala27Ser	23	FALSE	chr17:7578455:C:A	88:chr17:7578455:C:A	0.002
73_c4-1	73	PIK3CA	MODERATE	c.1727C>A	p.Ser576Tyr	1	FALSE	chr3:178937046:C:A	88:chr3:178937046:C:A	0.001932
73_c4-1	73	MITF	MODERATE	c.157A>C; c.265A>C; c.310A>C; c.313A>C	p.Thr53Pro; p.Thr89Pro; p.Thr104Pro; p.Thr105Pro	0	FALSE	chr3:69928493:A:C	88:chr3:69928493:A:C	0.001759
73_c4-1	73	ERBB2; MIEN1; MIR4728	MODERATE; MODIFIER	c.2261G>A; c.2306G>A; c.2351G>A; n.2675G>A; c.*388C>T; n.-1G>A	p.Arg754His; p.Arg769His; p.Arg784His;	1	FALSE	chr17:37881022:G:A	88:chr17:37881022:G:A	0.001616
73_c4-1	73	NTRK1	MODERATE	c.415G>A; c.505G>A	p.Gly139Arg; p.Gly169Arg	1	FALSE	chr1:156837972:G:A	88:chr1:156837972:G:A	0.001944
73_c4-1	73	TP53	MODERATE	c.261G>T; c.342G>T; c.621G>T; c.738G>T	p.Met87Ile; p.Met114Ile; p.Met207Ile; p.Met246Ile	21	FALSE	chr17:7577543:C:A	88:chr17:7577543:C:A	0.002613
73_c4-1	73	ATM	MODERATE	c.1009C>T	p.Arg337Cys	0	FALSE	chr11:108117798:C:T	88:chr11:108117798:C:T	0.001592
94_bl-1	94	C9orf53; CDKN2A	MODIFIER; MODERATE	n.*616C>T; c.*176G>A; c.253G>A; c.296G>A	; p.Ala85Thr; p.Arg99His	1	FALSE	chr9:21971105:C:T	89:chr9:21971105:C:T	0.005405

94_bl-1	94	PIK3CA	MODERATE	c.1624G>A	p.Glu542Lys	777	FALSE	chr3:178936082:G:A	89:chr3:178936082:G:A	0.003906
94_bl-1	94	NTRK1	MODERATE	c.1940T>G; c.2030T>G; c.2048T>G	p.Val647Gly; p.Val677Gly; p.Val683Gly	2	FALSE	chr1:156849792:T:G	89:chr1:156849792:T:G	0.003663
94_bl-1	94	ERBB2; MIEN1; MIR4728	MODERATE; MODIFIER	c.2239G>C; c.2284G>C; c.2329G>C; n.2653G>C; c.*388C>G; n.-1G>C	p.Val747Leu; p.Val762Leu; p.Val777Leu;	9	FALSE	chr17:37881000:G:C	89:chr17:37881000:G:C	0.155689
94_bl-1	94	RET	MODERATE	c.1690A>C	p.Thr564Pro	1	FALSE	chr10:43608342:A:C	89:chr10:43608342:A:C	0.006614
94_bl-1	94	NTRK1	MODERATE	c.804C>G; c.894C>G	p.His268Gln; p.His298Gln	1	FALSE	chr1:156843468:C:G	89:chr1:156843468:C:G	0.004651
94_bl-1	94	TP53	MODIFIER; HIGH	c.*113G>T; c.*25G>T; c.1006G>T; c.529G>T; c.610G>T; c.889G>T	; p.Glu336*; p.Glu177*; p.Glu204*; p.Glu297*	7	FALSE	chr17:7574021:C:A	89:chr17:7574021:C:A	0.002381
94_bl-1	94	TP53	MODERATE	c.137A>C; c.416A>C; c.533A>C; c.56A>C	p.His46Pro; p.His139Pro; p.His178Pro; p.His19Pro	10	FALSE	chr17:7578397:T:G	89:chr17:7578397:T:G	0.002301
94_bl-1	94	PIK3CA	MODERATE	c.2078G>A	p.Arg693His	1	FALSE	chr3:178938836:G:A	89:chr3:178938836:G:A	0.002581
94_bl-1	94	IGF1R	MODERATE	c.3934T>C; c.3937T>C	p.Ser1312Pro; p.Ser1313Pro	0	FALSE	chr15:99500504:T:C	89:chr15:99500504:T:C	0.003466
94_bl-1	94	ALG10	MODERATE	c.217A>G	p.Ile73Val	0	FALSE	chr12:34176942:A:G	89:chr12:34176942:A:G	0.002053
94_bl-1	94	NOTCH1	MODERATE	c.3407G>T	p.Gly1136Val	0	FALSE	chr9:139402510:C:A	89:chr9:139402510:C:A	0.003552

94_bl-1	94	PDGFRA	MODERATE	c.1516C>A	p.Leu506Ile	2	FALSE	chr4:55139855:C:A	89:chr4:55139855:C:A	0.001951
94_bl-1	94	ATM	MODERATE	c.2803A>G	p.Thr935Ala	0	FALSE	chr11:108139301:A:G	89:chr11:108139301:A:G	0.003958
94_bl-1	94	FBXW7	MODERATE	c.1078G>T; c.1318G>T; c.964G>T	p.Asp360Tyr; p.Asp440Tyr; p.Asp322Tyr	0	FALSE	chr4:153249460:C:A	89:chr4:153249460:C:A	0.005495
94_bl-1	94	IGF1R	MODERATE	c.167A>G	p.Glu56Gly	0	FALSE	chr15:99250863:A:G	89:chr15:99250863:A:G	0.001741
94_bl-1	94	ERBB2; MIR4728	MODERATE; LOW; MODIFIER	c.2215G>C; c.2260G>C; c.2305G>C; n.2629G>C; n.-1G>C	p.Asp739His; p.Asp754His; p.Asp769His;	5	FALSE	chr17:37880261:G:C	89:chr17:37880261:G:C	0.195479
94_bl-1	94	IDH1	MODERATE	c.395G>T	p.Arg132Leu	4157	FALSE	chr2:209113112:C:A	89:chr2:209113112:C:A	0.003937
94_bl-1	94	FGFR1	MODERATE	c.475C>T; c.481C>T; c.724C>T; c.742C>T; c.748C>T; c.841C>T	p.Arg159Trp; p.Arg161Trp; p.Arg242Trp; p.Arg248Trp; p.Arg250Trp; p.Arg281Trp	2	FALSE	chr8:38282215:G:A	89:chr8:38282215:G:A	0.001086
94_bl-1	94	IGF1R	MODERATE	c.676G>A	p.Glu226Lys	0	FALSE	chr15:99434589:G:A	89:chr15:99434589:G:A	0.00216
94_bl-1	94	TP53	MODERATE	c.361A>G; c.442A>G; c.721A>G; c.838A>G	p.Arg121Gly; p.Arg148Gly; p.Arg241Gly; p.Arg280Gly	24	FALSE	chr17:7577100:T:C	89:chr17:7577100:T:C	0.002384
94_bl-1	94	RET	MODERATE	c.1778G>A	p.Gly593Glu	1	FALSE	chr10:43609022:G:A	89:chr10:43609022:G:A	0.003221
94_bl-1	94	TSC1	MODERATE	c.2677G>A; c.2827G>A; c.2830G>A	p.Ala893Thr; p.Ala943Thr; p.Ala944Thr	0	FALSE	chr9:135772716:C:T	89:chr9:135772716:C:T	0.002907
94_bl-1	94	KDR	MODERATE	c.1699G>A	p.Val567Met	1	FALSE	chr4:55971098:C:T	89:chr4:55971098:C:T	0.00199

94_bl-1	94	NF1	HIGH	c.4537C>T; c.4600C>T	p.Arg1513*; p.Arg1534*	9	FALSE	chr17:29588751:C:T	89:chr17:29588751:C:T	0.002574
95_c1d1-1	95	SMO	MODERATE	c.1045A>C	p.Thr349Pro	0	FALSE	chr7:128846115:A:C	90:chr7:128846115:A:C	0.00779
95_c1d1-1	95	FGFR4	MODIFIER; MODERATE	c.1098-65G>A; c.1251+10G>A; c.1067G>A	; p.Arg356His	1	FALSE	chr5:176520342:G:A	90:chr5:176520342:G:A	0.002086
95_c1d1-1	95	TP53	MODERATE	c.128G>A; c.407G>A; c.47G>A; c.524G>A	p.Arg43His; p.Arg136His; p.Arg16His; p.Arg175His	979	FALSE	chr17:7578406:C:T	90:chr17:7578406:C:T	0.002191
95_c1d1-1	95	ROS1	MODERATE	c.5412G>T	p.Lys1804Asn	1	FALSE	chr6:117647532:C:A	90:chr6:117647532:C:A	0.003222
95_c1d1-1	95	BRAF	MODERATE	c.914C>T	p.Ala305Val	2	FALSE	chr7:140500228:G:A	90:chr7:140500228:G:A	0.002242
95_c1d1-1	95	EGFR	MODERATE	c.445C>T	p.Arg149Trp	1	FALSE	chr7:55214319:C:T	90:chr7:55214319:C:T	0.002167
95_c1d1-1	95	TP53	MODERATE; MODIFIER	c.225G>T; c.342G>T; c.-279G>T; c.-360G>T	p.Leu75Phe; p.Leu114Phe;	2	FALSE	chr17:7579345:C:A	90:chr17:7579345:C:A	0.002012
95_c1d1-1	95	ERBB2; MIR4728	MODERATE; MODIFIER	c.2211C>G; c.2256C>G; c.2301C>G; n.2625C>G; n.-1C>G	p.Ile737Met; p.Ile752Met; p.Ile767Met;	6	FALSE	chr17:37880257:C:G	90:chr17:37880257:C:G	0.002157
95_c1d1-1	95	MIR4673; NOTCH1	MODIFIER; MODERATE	n.*59A>C; c.1195A>C	; p.Thr399Pro	0	FALSE	chr9:139412649:T:G	90:chr9:139412649:T:G	0.006553
95_c1d1-1	95	EGFR	MODERATE	c.1039G>A	p.Asp347Asn	1	FALSE	chr7:55224258:G:A	90:chr7:55224258:G:A	0.00227
95_c1d1-1	95	STK11	MODERATE	c.622G>A	p.Asp208Asn	1	FALSE	chr19:1220604:G:A	90:chr19:1220604:G:A	0.003012
95_c1d1-1	95	CDKN2A	MODIFIER; MODERATE	c.194-3568A>C; c.52A>C	; p.Thr18Pro	1	FALSE	chr9:21974775:T:G	90:chr9:21974775:T:G	0.004392

95_c1d1-1	95	MIR4673; NOTCH1	MODIFIER; MODERATE	n.*59G>T; c.1286G>T	; p.Cys429Phe	0	FALSE	chr9:139412359:C:A	90:chr9:139412359:C:A	0.004695
95_c1d1-1	95	CWH43	MODERATE	c.737C>T; c.818C>T	p.Ala246Val; p.Ala273Val	0	FALSE	chr4:49005767:C:T	90:chr4:49005767:C:T	0.001949
95_c1d1-1	95	ERBB2; MIEN1; MIR4728	MODERATE; MODIFIER	c.2239G>C; c.2284G>C; c.2329G>C; n.2653G>C; c.*388C>G; n.-1G>C	p.Val747Leu; p.Val762Leu; p.Val777Leu;	9	FALSE	chr17:37881000:G:C	90:chr17:37881000:G:C	0.014418
95_c1d1-1	95	PTEN	MODERATE	c.274G>T	p.Asp92Tyr	3	FALSE	chr10:89692790:G:T	90:chr10:89692790:G:T	0.002564
95_c1d1-1	95	NTRK3	HIGH	c.1768G>T; c.1792G>T	p.Glu590*; p.Glu598*	0	FALSE	chr15:88476340:C:A	90:chr15:88476340:C:A	0.002594
95_c1d1-1	95	PIK3CA	MODERATE	c.1633G>C	p.Glu545Gln	1189	FALSE	chr3:178936091:G:C	90:chr3:178936091:G:C	0.003254
95_c1d1-1	95	C9orf53; CDKN2A	MODIFIER; MODERATE	n.*616C>G; c.*140G>C; c.217G>C; c.260G>C	; ; p.Ala73Pro; p.Arg87Pro	1	FALSE	chr9:21971141:C:G	90:chr9:21971141:C:G	0.019856
95_c1d1-1	95	TP53	HIGH	c.439C>T; c.520C>T; c.799C>T; c.916C>T	p.Arg147*; p.Arg174*; p.Arg267*; p.Arg306*	167	FALSE	chr17:7577022:G:A	90:chr17:7577022:G:A	0.002183
95_c1d1-1	95	TP53	MODIFIER; MODERATE	c.-89T>C; c.-8T>C; c.272T>C; c.389T>C	; p.Leu91Pro; p.Leu130Pro	8	FALSE	chr17:7578541:A:G	90:chr17:7578541:A:G	0.002451
95_c1d1-1	95	ERBB2; MIR4728	MODERATE; LOW; MODIFIER	c.2215G>C; c.2260G>C; c.2305G>C; n.2629G>C; n.-1G>C	p.Asp739His; p.Asp754His; p.Asp769His;	5	FALSE	chr17:37880261:G:C	90:chr17:37880261:G:C	0.045055
95_c1d1-1	95	CTNNB1	MODERATE	c.91C>A	p.Leu31Met	0	FALSE	chr3:41266094:C:A	90:chr3:41266094:C:A	0.0022

95_c1d1-1	95	RET	MODERATE	c.1690A>C	p.Thr564Pro	1	FALSE	chr10:43608342:A:C	90:chr10:43608342:A:C	0.005482
95_c1d1-1	95	TP53	MODIFIER; MODERATE	c.-5G>T; c.356G>T; c.473G>T; c.77G>T	; p.Arg119Leu; p.Arg158Leu; p.Arg26Leu	80	FALSE	chr17:7578457:C:A	90:chr17:7578457:C:A	0.003817
95_c1d1-1	95	KIT	MODERATE	c.365G>A	p.Arg122His	1	FALSE	chr4:55564477:G:A	90:chr4:55564477:G:A	0.001925
95_c1d1-1	95	IGF1R	MODERATE	c.2824G>A; c.2827G>A	p.Ala942Thr; p.Ala943Thr	0	FALSE	chr15:99472831:G:A	90:chr15:99472831:G:A	0.001876
95_c1d1-1	95	ATM	MODERATE	c.2611G>A	p.Glu871Lys	0	FALSE	chr11:108138042:G:A	90:chr11:108138042:G:A	0.002134
95_c1d1-1	95	IDH2; ZNF710	MODERATE; MODIFIER	c.1091C>T; c.1247C>T; c.857C>T; c.*2147G>A	p.Ala364Val; p.Ala416Val; p.Ala286Val;	1	FALSE	chr15:90628072:G:A	90:chr15:90628072:G:A	0.002092
78_c4-1	78	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2568T>G; n.-1A>C	p.Phe856Leu;	1	FALSE	chr7:55259510:T:G	95:chr7:55259510:T:G	0.008584
78_c4-1	78	IGF1R	MODERATE	c.3905T>C; c.3908T>C	p.Val1302Ala; p.Val1303Ala	0	FALSE	chr15:99500475:T:C	95:chr15:99500475:T:C	0.00885
78_c4-1	78	BRAF	MODERATE	c.2223G>T	p.Glu741Asp	1	FALSE	chr7:140434475:C:A	95:chr7:140434475:C:A	0.009146
78_c4-1	78	FGFR1; LETM2	MODERATE; MODIFIER	c.1927C>T; c.1933C>T; c.2170C>T; c.2194C>T; c.2200C>T; c.2293C>T; c.*1406G>A; c.*1423G>A; c.*1553G>A; c.*1567G>A; c.*1638G>A	p.Arg643Trp; p.Arg645Trp; p.Arg724Trp; p.Arg732Trp; p.Arg734Trp; p.Arg765Trp;	1	FALSE	chr8:38271528:G:A	95:chr8:38271528:G:A	0.010256

94_c2-1	94	TP53	MODIFIER; HIGH	c.-55C>A; c.27C>A; c.306C>A; c.423C>A	; p.Cys9*; p.Cys102*; p.Cys141*	13	FALSE	chr17:7578507:G:T	96:chr17:7578507:G:T	0.103053
94_c2-1	94	C9orf53; CDKN2A	MODIFIER; MODERATE; LOW	n.*616G>A; c.*228C>T; c.305C>T; c.348C>T	; p.Ala102Val; p.Gly116Gly	5	FALSE	chr9:21971053:G:A	96:chr9:21971053:G:A	0.004405
51_t2c2-1	51	NTRK3	MODERATE	c.1393G>T; c.1417G>T	p.Gly465Cys; p.Gly473Cys	0	FALSE	chr15:88576256:C:A	99:chr15:88576256:C:A	0.001439
51_t2c2-1	51	GAPDH; IFFO1	MODERATE; MODIFIER	c.591C>A; c.717C>A; c.*1743G>T; c.*1746G>T; c.*1770G>T; n.*2798G>T	p.Asn197Lys; p.Asn239Lys;	0	FALSE	chr12:6646941:C:A	99:chr12:6646941:C:A	0.000501
51_t2c2-1	51	NOTCH1	MODERATE	c.5806G>A	p.Ala1936Thr	0	FALSE	chr9:139395132:C:T	99:chr9:139395132:C:T	0.000821
51_t2c2-1	51	FGFR1	MODERATE	c.488G>T; c.494G>T; c.737G>T; c.755G>T; c.761G>T; c.854G>T	p.Arg163Leu; p.Arg165Leu; p.Arg246Leu; p.Arg252Leu; p.Arg254Leu; p.Arg285Leu	1	FALSE	chr8:38282202:C:A	99:chr8:38282202:C:A	0.000925
51_t2c2-1	51	CDH1	MODERATE	c.856G>A	p.Ala286Thr	0	FALSE	chr16:68845610:G:A	99:chr16:68845610:G:A	0.00065
51_t2c2-1	51	TSC2	HIGH	c.690C>A	p.Cys230*	0	FALSE	chr16:2106686:C:A	99:chr16:2106686:C:A	0.000479
51_t2c2-1	51	FGFR3	MODERATE	c.1183G>A; c.1519G>A; c.1525G>A	p.Val395Met; p.Val507Met; p.Val509Met	1	FALSE	chr4:1807188:G:A	99:chr4:1807188:G:A	0.000754

51_t2c2-1	51	TP53	MODIFIER; HIGH	c.*143G>T; c.*55G>T; c.1036G>T; c.559G>T; c.640G>T; c.919G>T	; p.Glu346*; p.Glu187*; p.Glu214*; p.Glu307*	4	FALSE	chr17:7573991:C:A	99:chr17:7573991:C:A	0.00132
51_t2c2-1	51	PTEN	HIGH	c.720C>A	p.Tyr240*	3	FALSE	chr10:89717695:C:A	99:chr10:89717695:C:A	0.002786
51_t2c2-1	51	PDGFRA	MODERATE	c.1495G>A	p.Val499Met	2	FALSE	chr4:55139834:G:A	99:chr4:55139834:G:A	0.00115
51_t2c2-1	51	NOTCH1	MODERATE	c.3407G>T	p.Gly1136Val	0	FALSE	chr9:139402510:C:A	99:chr9:139402510:C:A	0.001135
51_t2c2-1	51	CDKN2A	MODIFIER; MODERATE	c.194-3567C>T; c.53C>T	; p.Thr18Met	1	FALSE	chr9:21974774:G:A	99:chr9:21974774:G:A	0.001184
51_t2c2-1	51	CDKN2B; CDKN2B-AS1	MODIFIER; MODERATE	c.*221G>T; c.335G>T; n.371+10908C>A	; p.Trp112Leu	0	FALSE	chr9:22006068:C:A	99:chr9:22006068:C:A	0.000607
51_t2c2-1	51	RET	MODERATE	c.1667C>A	p.Ser556Tyr	1	FALSE	chr10:43608319:C:A	99:chr10:43608319:C:A	0.000559
51_t2c2-1	51	EGFR	MODERATE	c.664C>T	p.Arg222Cys	8	FALSE	chr7:55220274:C:T	99:chr7:55220274:C:T	0.000917
51_t2c2-1	51	TP53	MODERATE	c.350C>T; c.431C>T; c.710C>T; c.827C>T	p.Ala117Val; p.Ala144Val; p.Ala237Val; p.Ala276Val	10	FALSE	chr17:7577111:G:A	99:chr17:7577111:G:A	0.001076
51_t2c2-1	51	FGFR4	MODERATE	c.1274G>A; c.1358G>A; c.1478G>A	p.Arg425Gln; p.Arg453Gln; p.Arg493Gln	2	FALSE	chr5:176520735:G:A	99:chr5:176520735:G:A	0.000556
51_t2c2-1	51	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2572C>A; n.-1G>T	p.Leu858Met;	8	FALSE	chr7:55259514:C:A	99:chr7:55259514:C:A	0.000536
51_t2c2-1	51	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2441T>C; n.1121A>G	p.Leu814Pro;	4	FALSE	chr7:55249143:T:C	99:chr7:55249143:T:C	0.000974
51_t2c2-1	51	EGFR	MODERATE	c.3025G>A	p.Asp1009Asn	1	FALSE	chr7:55268959:G:A	99:chr7:55268959:G:A	0.000808

51_t2c2-1	51	MIR4673; NOTCH1	MODIFIER; MODERATE	n.*59A>G; c.890A>G	; p.Asp297Gly	0	FALSE	chr9:139413252:T:C	99:chr9:139413252:T:C	0.004591
51_t2c2-1	51	ALK	MODERATE	c.536G>A	p.Arg179His	1	FALSE	chr2:30142990:C:T	99:chr2:30142990:C:T	0.000434
51_t2c2-1	51	TP53	MODIFIER; MODERATE	c.-66G>T; c.16G>T; c.295G>T; c.412G>T	; p.Ala6Ser; p.Ala99Ser; p.Ala138Ser	17	FALSE	chr17:7578518:C:A	99:chr17:7578518:C:A	0.000776
51_t2c2-1	51	ATM	MODERATE	c.6751C>A	p.Leu2251Ile	0	FALSE	chr11:108196215:C:A	99:chr11:108196215:C:A	0.003617
51_t2c2-1	51	NTRK2	MODERATE	c.1960C>A; c.2008C>A	p.Leu654Met; p.Leu670Met	0	FALSE	chr9:87570268:C:A	99:chr9:87570268:C:A	0.001461
51_t2c2-1	51	C9orf53; CDKN2A	MODIFIER; MODERATE	n.*616C>A; c.*187G>T; c.264G>T; c.307G>T	; p.Glu88Asp; p.Gly103Trp	6	FALSE	chr9:21971094:C:A	99:chr9:21971094:C:A	0.000589
51_t2c2-1	51	TP53	MODIFIER; MODERATE	c.-3G>T; c.358G>T; c.475G>T; c.79G>T	; p.Ala120Ser; p.Ala159Ser; p.Ala27Ser	23	FALSE	chr17:7578455:C:A	99:chr17:7578455:C:A	0.001239
51_t2c2-1	51	TSC1	HIGH	c.367G>T; c.520G>T	p.Glu123*; p.Glu174*	0	FALSE	chr9:135797349:C:A	99:chr9:135797349:C:A	0.000809
51_t2c2-1	51	NTRK1	MODERATE	c.804C>G; c.894C>G	p.His268Gln; p.His298Gln	1	FALSE	chr1:156843468:C:G	99:chr1:156843468:C:G	0.001021
51_t2c2-1	51	ATM	MODERATE	c.2542G>A	p.Glu848Lys	0	FALSE	chr11:108137973:G:A	99:chr11:108137973:G:A	0.002478
51_t2c2-1	51	TP53	MODERATE; HIGH	c.363G>T; c.480G>T; c.84G>T; c.3G>T	p.Met121Ile; p.Met160Ile; p.Met28Ile; p.Met1?	4	FALSE	chr17:7578450:C:A	99:chr17:7578450:C:A	0.000834
51_t2c2-1	51	TP53	MODERATE	c.362G>T; c.443G>T; c.722G>T; c.839G>T	p.Arg121Ile; p.Arg148Ile; p.Arg241Ile; p.Arg280Ile	64	FALSE	chr17:7577099:C:A	99:chr17:7577099:C:A	0.000697

51_t2c2-1	51	MIR4673; NOTCH1	MODIFIER; MODERATE	n.*59G>A; c.1775G>A	; p.Arg592His	0	FALSE	chr9:139410063:C:T	99:chr9:139410063:C:T	0.000667
51_t2c2-1	51	SMO	MODERATE	c.1640G>A	p.Arg547His	0	FALSE	chr7:128850377:G:A	99:chr7:128850377:G:A	0.000844
51_t2c2-1	51	HGF	MODERATE	c.685C>T; c.700C>T	p.Arg229Cys; p.Arg234Cys	0	FALSE	chr7:81374362:G:A	99:chr7:81374362:G:A	0.000852
51_t2c2-1	51	FGFR3	MODIFIER; MODERATE	c.931-417C>A; c.1153C>A; c.1159C>A	; p.Leu385Met; p.Leu387Met	1	FALSE	chr4:1806134:C:A	99:chr4:1806134:C:A	0.001367
51_t2c2-1	51	MIR4673; NOTCH1	MODIFIER; MODERATE	n.*59G>T; c.778G>T	; p.Asp260Tyr	0	FALSE	chr9:139413982:C:A	99:chr9:139413982:C:A	0.000846
51_t2c2-1	51	C9orf53; CDKN2A	MODIFIER; MODERATE	n.*616C>A; c.*269G>T; c.346G>T; c.389G>T	; p.Asp116Tyr; p.Gly130Val	3	FALSE	chr9:21971012:C:A	99:chr9:21971012:C:A	0.000571
51_t2c2-1	51	ERBB2; MIEN1; MIR4728	MODIFIER; HIGH	n.3151C>T; c.2737C>T; c.2782C>T; c.2827C>T; c.*388G>A; n.-1C>T	; p.Gln913*; p.Gln928*; p.Gln943*	1	FALSE	chr17:37882061:C:T	99:chr17:37882061:C:T	0.000707
51_t2c2-1	51	IGF1R	MODERATE	c.2824G>A; c.2827G>A	p.Ala942Thr; p.Ala943Thr	0	FALSE	chr15:99472831:G:A	99:chr15:99472831:G:A	0.000756
51_t2c2-1	51	ALK	MODERATE	c.584C>T	p.Ala195Val	1	FALSE	chr2:30142942:G:A	99:chr2:30142942:G:A	0.000617
51_t2c2-1	51	MET	MODERATE	c.2908C>A; c.2962C>A	p.Arg970Ser; p.Arg988Ser	6	FALSE	chr7:116411923:C:A	99:chr7:116411923:C:A	0.001138
51_t2c2-1	51	ALK	MODERATE	c.1049C>T	p.Ser350Leu	1	FALSE	chr2:29754886:G:A	99:chr2:29754886:G:A	0.000629
51_t2c2-1	51	TSC2	MODERATE	c.1610G>A	p.Arg537His	0	FALSE	chr16:2115530:G:A	99:chr16:2115530:G:A	0.000652

51_t2c2-1	51	IDH2	MODERATE	c.317C>T; c.473C>T; c.83C>T	p.Pro106Leu; p.Pro158Leu; p.Pro28Leu	2	FALSE	chr15:90631880:G:A	99:chr15:90631880:G:A	0.000766
51_t2c2-1	51	CDH1	HIGH	c.1596G>A	p.Trp532*	0	FALSE	chr16:68853213:G:A	99:chr16:68853213:G:A	0.00058
51_t2c2-1	51	TP53	MODIFIER; MODERATE	c.-11G>T; c.350G>T; c.467G>T; c.71G>T	; p.Arg117Leu; p.Arg156Leu; p.Arg24Leu	26	FALSE	chr17:7578463:C:A	99:chr17:7578463:C:A	0.001247
51_t2c2-1	51	EGFR	MODERATE	c.932G>A	p.Cys311Tyr	1	FALSE	chr7:55223565:G:A	99:chr7:55223565:G:A	0.000409
51_t2c2-1	51	EPHA3	HIGH	c.1114C>T	p.Gln372*	0	FALSE	chr3:89391048:C:T	99:chr3:89391048:C:T	0.000626
51_t2c2-1	51	CTNNB1	MODERATE	c.131C>A	p.Pro44His	0	FALSE	chr3:41266134:C:A	99:chr3:41266134:C:A	0.001119
51_t2c2-1	51	FGFR1	MODIFIER; MODERATE	c.-85G>T; c.107G>T; c.8G>T	; p.Ser36Ile; p.Ser3Ile	1	FALSE	chr8:38314957:C:A	99:chr8:38314957:C:A	0.001303
51_t2c2-1	51	FGFR1	MODERATE	c.475C>T; c.481C>T; c.724C>T; c.742C>T; c.748C>T; c.841C>T	p.Arg159Trp; p.Arg161Trp; p.Arg242Trp; p.Arg248Trp; p.Arg250Trp; p.Arg281Trp	2	FALSE	chr8:38282215:G:A	99:chr8:38282215:G:A	0.001018
51_t2c2-1	51	NTRK1	MODERATE	c.1007C>A; c.917C>A	p.Ala336Glu; p.Ala306Glu	3	FALSE	chr1:156843581:C:A	99:chr1:156843581:C:A	0.000788
51_t2c2-1	51	PDGFRA	HIGH	c.2540C>A	p.Ser847*	1	FALSE	chr4:55152108:C:A	99:chr4:55152108:C:A	0.000813
51_t2c2-1	51	TP53	MODERATE; MODIFIER	c.239C>T; c.356C>T; c.-279C>T; c.-360C>T	p.Ala80Val; p.Ala119Val;	1	FALSE	chr17:7579331:G:A	99:chr17:7579331:G:A	0.000653
51_t2c2-1	51	STK11	MODERATE	c.479T>C	p.Leu160Pro	1	FALSE	chr19:1220386:T:C	99:chr19:1220386:T:C	0.001052
51_t2c2-1	51	GNA11	MODERATE	c.1030G>A	p.Val344Met	1	FALSE	chr19:3121127:G:A	99:chr19:3121127:G:A	0.000789

51_t2c2-1	51	PIK3R1	MODERATE	c.1030G>T; c.1120G>T; c.1930G>T; c.841G>T	p.Gly344Cys; p.Gly374Cys; p.Gly644Cys; p.Gly281Cys	1	FALSE	chr5:67592114:G:T	99:chr5:67592114:G:T	0.000652
51_t2c2-1	51	KIT	MODERATE	c.235C>A	p.Gln79Lys	2	FALSE	chr4:55561845:C:A	99:chr4:55561845:C:A	0.002139
51_t2c2-1	51	FGFR3	MODIFIER; MODERATE	c.931-308G>A; c.1262G>A; c.1268G>A	; p.Arg421Gln; p.Arg423Gln	1	FALSE	chr4:1806243:G:A	99:chr4:1806243:G:A	0.000852
51_t2c2-1	51	MAP2K1	MODERATE	c.371C>T	p.Pro124Leu	1	FALSE	chr15:66729163:C:T	99:chr15:66729163:C:T	0.001046
51_t2c2-1	51	EPHA3	MODERATE	c.1280C>T	p.Ala427Val	0	FALSE	chr3:89391214:C:T	99:chr3:89391214:C:T	0.001038
51_t2c2-1	51	BRAF	HIGH	c.37G>T	p.Glu13*	2	FALSE	chr7:140624467:C:A	99:chr7:140624467:C:A	0.001005
51_t2c2-1	51	IDH1	MODERATE	c.299G>T	p.Arg100Leu	5	FALSE	chr2:209113208:C:A	99:chr2:209113208:C:A	0.001382
51_t2c2-1	51	FGFR3	MODERATE	c.1162G>A; c.1498G>A; c.1504G>A	p.Ala388Thr; p.Ala500Thr; p.Ala502Thr	1	FALSE	chr4:1807167:G:A	99:chr4:1807167:G:A	0.002761
51_t2c2-1	51	KIT	MODERATE	c.1403C>T	p.Pro468Leu	2	FALSE	chr4:55592079:C:T	99:chr4:55592079:C:T	0.000757
51_t2c2-1	51	PDGFRA	MODERATE	c.1526C>A	p.Ala509Asp	1	FALSE	chr4:55139865:C:A	99:chr4:55139865:C:A	0.001491
51_t2c2-1	51	EGFR	MODIFIER; MODERATE	c.*1464C>T; c.1279C>T	; p.Arg427Cys	2	FALSE	chr7:55225427:C:T	99:chr7:55225427:C:T	0.00052
51_t2c2-1	51	DDR2	MODERATE	c.1598C>A	p.Thr533Lys	1	FALSE	chr1:162741907:C:A	99:chr1:162741907:C:A	0.002294
51_t2c2-1	51	MIR4674; MIR4674HG; NOTCH1	MODIFIER; MODERATE	n.*87G>T; n.-1C>A; c.62G>T	; p.Gly21Val	0	FALSE	chr9:139438554:C:A	99:chr9:139438554:C:A	0.003177
51_t2c2-1	51	TSC2	HIGH	c.3280C>T; c.3412C>T	p.Arg1094*; p.Arg1138*	0	FALSE	chr16:2130180:C:T	99:chr16:2130180:C:T	0.000616

51_t2c2-1	51	FGFR3	MODERATE	c.1177G>A; c.1513G>A; c.1519G>A	p.Val393Ile; p.Val505Ile; p.Val507Ile	1	FALSE	chr4:1807182:G:A	99:chr4:1807182:G:A	0.000756
51_t2c2-1	51	NTHL1; TSC2	MODIFIER; MODERATE	c.-20C>T; c.170G>A	; p.Arg57His	0	FALSE	chr16:2100432:G:A	99:chr16:2100432:G:A	0.000962
51_t2c2-1	51	CTNNB1	MODERATE	c.2217G>A	p.Met739Ile	0	FALSE	chr3:41280704:G:A	99:chr3:41280704:G:A	0.000852
51_t2c2-1	51	TSC2	MODERATE	c.1654G>A	p.Ala552Thr	0	FALSE	chr16:2115574:G:A	99:chr16:2115574:G:A	0.000725
51_t2c2-1	51	HGF	MODERATE	c.767G>A; c.782G>A	p.Arg256His; p.Arg261His	0	FALSE	chr7:81372752:C:T	99:chr7:81372752:C:T	0.000531
51_t2c2-1	51	CDKN2B; CDKN2B-AS1	MODIFIER; MODERATE	c.*253C>T; c.367C>T; n.371+10876G>A	; p.Arg123Trp	0	FALSE	chr9:22006036:G:A	99:chr9:22006036:G:A	0.000928
51_t2c2-1	51	NF1	MODERATE	c.5420G>A; c.5483G>A	p.Arg1807Gln; p.Arg1828Gln	2	FALSE	chr17:29654731:G:A	99:chr17:29654731:G:A	0.00049
51_t2c2-1	51	PHLPP1	MODERATE	c.3298G>A	p.Glu1100Lys	0	FALSE	chr18:60612478:G:A	99:chr18:60612478:G:A	0.000666
51_t2c2-1	51	BRAF	MODERATE	c.2223G>T	p.Glu741Asp	1	FALSE	chr7:140434475:C:A	99:chr7:140434475:C:A	0.000523
51_t2c2-1	51	MAP2K1	MODERATE	c.198C>A	p.Asp66Glu	4	FALSE	chr15:66727482:C:A	99:chr15:66727482:C:A	0.002366
51_t2c2-1	51	SMO	MODERATE	c.869G>A	p.Arg290His	0	FALSE	chr7:128845572:G:A	99:chr7:128845572:G:A	0.001016
51_t2c2-1	51	EGFR	MODERATE	c.1774G>A	p.Val592Ile	1	FALSE	chr7:55233024:G:A	99:chr7:55233024:G:A	0.000831
51_t2c2-1	51	NOTCH1	MODERATE	c.5885G>A	p.Arg1962His	0	FALSE	chr9:139395053:C:T	99:chr9:139395053:C:T	0.000802
51_t2c2-1	51	EPHA3	MODERATE	c.2275G>T	p.Val759Leu	0	FALSE	chr3:89480438:G:T	99:chr3:89480438:G:T	0.00084
51_t2c2-1	51	PDGFRA	MODERATE	c.94C>A	p.Pro32Thr	1	FALSE	chr4:55127306:C:A	99:chr4:55127306:C:A	0.000646
51_t2c2-1	51	TSC2	MODERATE	c.2513G>A	p.Ser838Asn	0	FALSE	chr16:2124358:G:A	99:chr16:2124358:G:A	0.000729
51_t2c2-1	51	CTNNB1	LOW	c.15T>C	p.Ala5Ala	0	FALSE	chr3:41266018:T:C	99:chr3:41266018:T:C	0.001181

51_t2c2-1	51	NF1	MODERATE	c.6405C>A; c.6468C>A	p.Phe2135Leu; p.Phe2156Leu	1	FALSE	chr17:29664426:C:A	99:chr17:29664426:C:A	0.001091
51_t2c2-1	51	EPHA3	HIGH	c.2757G>A	p.Trp919*	0	FALSE	chr3:89521680:G:A	99:chr3:89521680:G:A	0.000694
51_t2c2-1	51	NOTCH1	MODERATE	c.5192C>T	p.Pro1731Leu	0	FALSE	chr9:139396916:G:A	99:chr9:139396916:G:A	0.003731
51_t2c2-1	51	RET	MODERATE	c.2116G>A	p.Val706Met	2	FALSE	chr10:43610164:G:A	99:chr10:43610164:G:A	0.00039
51_t2c2-1	51	TSC2	MODERATE	c.2702G>A	p.Arg901His	0	FALSE	chr16:2126131:G:A	99:chr16:2126131:G:A	0.000502
51_t2c2-1	51	MIR4673; NOTCH1	MODIFIER; MODERATE	n.*59G>T; c.1039G>T	; p.Gly347Cys	0	FALSE	chr9:139413103:C:A	99:chr9:139413103:C:A	0.001035
51_t2c2-1	51	FGFR1	MODERATE	c.1013C>T; c.1019C>T; c.1112C>T; c.746C>T; c.752C>T; c.995C>T	p.Thr338Met; p.Thr340Met; p.Thr371Met; p.Thr249Met; p.Thr251Met; p.Thr332Met	2	FALSE	chr8:38279377:G:A	99:chr8:38279377:G:A	0.0018
51_t2c2-1	51	CTNNB1	MODERATE	c.122C>A	p.Thr41Asn	0	FALSE	chr3:41266125:C:A	99:chr3:41266125:C:A	0.001418
51_t2c2-1	51	PDGFRA	MODERATE	c.1471G>A	p.Ala491Thr	1	FALSE	chr4:55139810:G:A	99:chr4:55139810:G:A	0.000553
51_t2c2-1	51	EPHA3	MODERATE	c.1180G>A	p.Val394Met	0	FALSE	chr3:89391114:G:A	99:chr3:89391114:G:A	0.000526
51_t2c2-1	51	CDKN2A	MODIFIER; MODERATE	c.194-3519C>T; c.101C>T	; p.Ala34Val	2	FALSE	chr9:21974726:G:A	99:chr9:21974726:G:A	0.000548
51_t2c2-1	51	PIK3CA	MODERATE	c.2727C>A	p.Phe909Leu	1	FALSE	chr3:178947852:C:A	99:chr3:178947852:C:A	0.002401
51_t2c2-1	51	TP53	HIGH	c.16C>T; c.376C>T; c.493C>T; c.97C>T	p.Gln6*; p.Gln126*; p.Gln165*; p.Gln33*	33	FALSE	chr17:7578437:G:A	99:chr17:7578437:G:A	0.000793
51_t2c2-1	51	DDR2	MODERATE	c.2002C>T	p.Arg668Cys	2	FALSE	chr1:162745587:C:T	99:chr1:162745587:C:T	0.000565
51_t2c2-1	51	NTRK2	MODERATE	c.220G>A	p.Ala74Thr	0	FALSE	chr9:87317081:G:A	99:chr9:87317081:G:A	0.001159

51_t2c2-1	51	ERBB2; MIEN1; MIR4728	MODERATE; MODIFIER	c.2236G>A; c.2281G>A; c.2326G>A; n.2650G>A; c.*388C>T; n.-1G>A	p.Gly746Ser; p.Gly761Ser; p.Gly776Ser;	5	FALSE	chr17:37880997:G:A	99:chr17:37880997:G:A	0.000529
51_t2c2-1	51	EGFR	MODIFIER; MODERATE	c.*2364G>A; c.2104G>A	; p.Ala702Thr	2	FALSE	chr7:55241656:G:A	99:chr7:55241656:G:A	0.000469
51_t2c2-1	51	TP53	MODERATE	c.234G>T; c.315G>T; c.594G>T; c.711G>T	p.Met78Ile; p.Met105Ile; p.Met198Ile; p.Met237Ile	81	FALSE	chr17:7577570:C:A	99:chr17:7577570:C:A	0.000693
51_t2c2-1	51	NTRK1	MODERATE	c.1669C>T; c.1759C>T; c.1777C>T	p.Arg557Trp; p.Arg587Trp; p.Arg593Trp	1	FALSE	chr1:156846336:C:T	99:chr1:156846336:C:T	0.000576
51_t2c2-1	51	EGFR	MODERATE	c.442G>A	p.Val148Met	1	FALSE	chr7:55214316:G:A	99:chr7:55214316:G:A	0.000591
51_t2c2-1	51	TP53	MODERATE; MODIFIER	c.132G>T; c.15G>T; c.-279G>T; c.-360G>T	p.Met44Ile; p.Met5Ile;	1	FALSE	chr17:7579555:C:A	99:chr17:7579555:C:A	0.001034
51_t2c2-1	51	TSC1	MODERATE	c.2751G>T; c.2901G>T; c.2904G>T	p.Arg917Ser; p.Arg967Ser; p.Arg968Ser	0	FALSE	chr9:135772642:C:A	99:chr9:135772642:C:A	0.002556
51_t2c2-1	51	EPHA3	MODERATE	c.237C>A	p.Asn79Lys	0	FALSE	chr3:89259093:C:A	99:chr3:89259093:C:A	0.000771
51_t2c2-1	51	ALK	MODERATE	c.641G>A	p.Arg214His	1	FALSE	chr2:30142885:C:T	99:chr2:30142885:C:T	0.001283
51_t2c2-1	51	IGF1R	MODERATE	c.1940G>A	p.Arg647His	0	FALSE	chr15:99459304:G:A	99:chr15:99459304:G:A	0.000566
51_t2c2-1	51	INSRR; NTRK1	MODERATE	c.3385G>T; c.53C>A	p.Val1129Phe; p.Thr18Lys	1	FALSE	chr1:156811916:C:A	99:chr1:156811916:C:A	0.000709

51_t2c2-1	51	CDKN2A	MODIFIER; MODERATE	c.194-3471A>G; c.149A>G	; p.Gln50Arg	2	FALSE	chr9:21974678:T:C	99:chr9:21974678:T:C	0.000525
51_t2c2-1	51	EGFR	MODIFIER; MODERATE	c.*2133G>A; c.*2364G>A; c.2030G>A	; p.Arg677His	5	FALSE	chr7:55240786:G:A	99:chr7:55240786:G:A	0.001411
51_t2c2-1	51	DDR2	MODERATE	c.1418G>A	p.Arg473His	2	FALSE	chr1:162740216:G:A	99:chr1:162740216:G:A	0.000559
51_t2c2-1	51	C9orf53; CDKN2A	MODIFIER; MODERATE; LOW	n.*616G>A; c.*180C>T; c.257C>T; c.300C>T	; p.Ala86Val; p.Cys100Cys	1	FALSE	chr9:21971101:G:A	99:chr9:21971101:G:A	0.000596
51_t2c2-1	51	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2356G>A; n.1206C>T	p.Val786Met;	6	FALSE	chr7:55249058:G:A	99:chr7:55249058:G:A	0.000652
51_t2c2-1	51	PDGFRA	MODERATE	c.1202C>A	p.Ala401Asp	1	FALSE	chr4:55136880:C:A	99:chr4:55136880:C:A	0.002535
51_t2c2-1	51	TSC2	MODERATE	c.781C>T	p.Arg261Trp	0	FALSE	chr16:2107112:C:T	99:chr16:2107112:C:T	0.000919
51_t2c2-1	51	NOTCH1	MODERATE	c.2524G>T	p.Gly842Trp	0	FALSE	chr9:139405667:C:A	99:chr9:139405667:C:A	0.000807
51_t2c2-1	51	CDKN2A	MODIFIER; MODERATE	c.194-3610G>T; c.10G>T	; p.Ala4Ser	1	FALSE	chr9:21974817:C:A	99:chr9:21974817:C:A	0.001667
51_t2c2-1	51	MIR4673; NOTCH1	MODIFIER; MODERATE	n.*59G>T; c.1451G>T	; p.Gly484Val	0	FALSE	chr9:139411828:C:A	99:chr9:139411828:C:A	0.001002
51_t2c2-1	51	BRAF	MODERATE	c.1202C>T	p.Thr401Ile	1	FALSE	chr7:140482933:G:A	99:chr7:140482933:G:A	0.000932
51_t2c2-1	51	CTNNB1	MODERATE	c.86C>A	p.Ser29Tyr	0	FALSE	chr3:41266089:C:A	99:chr3:41266089:C:A	0.000718
51_t2c2-1	51	KDR	MODERATE	c.1876A>G	p.Ile626Val	1	FALSE	chr4:55970921:T:C	99:chr4:55970921:T:C	0.000778
51_t2c2-1	51	HRAS; LRRC56	MODERATE; MODIFIER	c.183G>T; c.-506C>A	p.Gln61His;	15	FALSE	chr11:533873:C:A	99:chr11:533873:C:A	0.000538
51_t2c2-1	51	EGFR	MODERATE	c.594C>A	p.Ser198Arg	3	FALSE	chr7:55219021:C:A	99:chr7:55219021:C:A	0.000567
51_t2c2-1	51	EPHA3	MODERATE	c.2662C>A	p.Leu888Met	0	FALSE	chr3:89499492:C:A	99:chr3:89499492:C:A	0.001022
51_t2c2-1	51	CDKN2A	MODIFIER; HIGH	c.194-3544G>T; c.76G>T	; p.Glu26*	2	FALSE	chr9:21974751:C:A	99:chr9:21974751:C:A	0.000579

51_t2c2-1	51	TP53	MODIFIER; HIGH	c.*122G>T; c.*34G>T; c.1015G>T; c.538G>T; c.619G>T; c.898G>T	; p.Glu339*; p.Glu180*; p.Glu207*; p.Glu300*	18	FALSE	chr17:7574012:C:A	99:chr17:7574012:C:A	0.000855
51_t2c2-1	51	NOTCH1	MODERATE	c.4391G>T	p.Ser1464Ile	0	FALSE	chr9:139399957:C:A	99:chr9:139399957:C:A	0.000596
51_t2c2-1	51	MIR4673; NOTCH1	MODIFIER; MODERATE	n.-1G>T; c.221G>T	; p.Cys74Phe	0	FALSE	chr9:139418351:C:A	99:chr9:139418351:C:A	0.001295
51_t2c2-1	51	IGF1R	MODERATE	c.880G>A	p.Glu294Lys	0	FALSE	chr15:99434793:G:A	99:chr15:99434793:G:A	0.001397
51_t2c2-1	51	CTNNB1	MODERATE	c.96C>A	p.Asp32Glu	0	FALSE	chr3:41266099:C:A	99:chr3:41266099:C:A	0.000673
51_t2c2-1	51	DDR2	MODERATE	c.2038C>T	p.Arg680Cys	1	FALSE	chr1:162745623:C:T	99:chr1:162745623:C:T	0.000504
51_t2c2-1	51	NTRK1	MODERATE	c.1709C>A; c.1799C>A; c.1817C>A	p.Pro570His; p.Pro600His; p.Pro606His	1	FALSE	chr1:156848925:C:A	99:chr1:156848925:C:A	0.00048
51_t2c2-1	51	AKT3	MODERATE	c.425G>T	p.Arg142Ile	0	FALSE	chr1:243809199:C:A	99:chr1:243809199:C:A	0.004228
51_t2c2-1	51	MIR4673; NOTCH1	MODIFIER; MODERATE	n.*59G>T; c.1433G>T	; p.Cys478Phe	0	FALSE	chr9:139412212:C:A	99:chr9:139412212:C:A	0.00072
51_t2c2-1	51	TSC1	MODERATE	c.1433C>T; c.1583C>T; c.1586C>T	p.Ala478Val; p.Ala528Val; p.Ala529Val	0	FALSE	chr9:135781379:G:A	99:chr9:135781379:G:A	0.000482
51_t2c2-1	51	NOTCH1	MODERATE	c.4987C>T	p.Arg1663Trp	0	FALSE	chr9:139399156:G:A	99:chr9:139399156:G:A	0.001068
51_t2c2-1	51	EGFR; EGFR-AS1	LOW; MODIFIER	c.2472C>A; n.-1G>T	p.Gly824Gly;	1	FALSE	chr7:55259414:C:A	99:chr7:55259414:C:A	0.000701

51_t2c2-1	51	FGFR1	MODERATE	c.1060C>T; c.1066C>T; c.1303C>T; c.1327C>T; c.1333C>T; c.1426C>T	p.Arg354Trp; p.Arg356Trp; p.Arg435Trp; p.Arg443Trp; p.Arg445Trp; p.Arg476Trp	2	FALSE	chr8:38275843:G:A	99:chr8:38275843:G:A	0.000568
51_t2c2-1	51	C9orf53; CDKN2A	MODIFIER; MODERATE; LOW	n.*616C>A; c.*262G>T; c.382G>T; c.339G>T	; p.Ala128Ser; p.Leu113Leu	1	FALSE	chr9:21971019:C:A	99:chr9:21971019:C:A	0.000571
51_t2c2-1	51	TP53	MODERATE	c.117G>T; c.36G>T; c.396G>T; c.513G>T	p.Glu39Asp; p.Glu12Asp; p.Glu132Asp; p.Glu171Asp	2	FALSE	chr17:7578417:C:A	99:chr17:7578417:C:A	0.000762
51_t2c2-1	51	ALK	MODERATE	c.1316G>T	p.Ser439Ile	1	FALSE	chr2:29551314:C:A	99:chr2:29551314:C:A	0.000684
51_t2c2-1	51	C9orf53; CDKN2A	MODIFIER; MODERATE; LOW	n.*616T>G; c.*120A>C; c.197A>C; c.240A>C	; p.His66Pro; p.Pro80Pro	1	FALSE	chr9:21971161:T:G	99:chr9:21971161:T:G	0.003639
51_t2c2-1	51	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2387G>A; n.1175C>T	p.Gly796Asp;	3	FALSE	chr7:55249089:G:A	99:chr7:55249089:G:A	0.000443
51_t2c2-1	51	CWH43	MODERATE	c.782G>A; c.863G>A	p.Cys261Tyr; p.Cys288Tyr	0	FALSE	chr4:49005812:G:A	99:chr4:49005812:G:A	0.00056
51_t2c2-1	51	CTNNB1	MODERATE	c.643G>A	p.Ala215Thr	0	FALSE	chr3:41266972:G:A	99:chr3:41266972:G:A	0.000632
51_t2c2-1	51	CTNNB1	MODERATE	c.861C>A	p.Asn287Lys	0	FALSE	chr3:41267277:C:A	99:chr3:41267277:C:A	0.004673
51_t2c2-1	51	EGFR	MODERATE	c.445C>T	p.Arg149Trp	1	FALSE	chr7:55214319:C:T	99:chr7:55214319:C:T	0.000579
51_t2c2-1	51	NTRK2	MODERATE	c.2023C>T; c.2071C>T	p.Arg675Cys; p.Arg691Cys	0	FALSE	chr9:87570331:C:T	99:chr9:87570331:C:T	0.000677

51_t2c2-1	51	NOTCH1	MODERATE	c.6019G>A	p.Val2007Met	0	FALSE	chr9:139393627:C:T	99:chr9:139393627:C:T	0.000546
51_t2c2-1	51	STK11	MODERATE	c.644G>A	p.Gly215Asp	1	FALSE	chr19:1220626:G:A	99:chr19:1220626:G:A	0.000754
51_t2c2-1	51	ERBB2; MIEN1; MIR4728	MODERATE; MODIFIER	c.3025G>A; c.3070G>A; c.3115G>A; n.3439G>A; c.*388C>T; n.*67G>A	p.Ala1009Thr; p.Ala1024Thr; p.Ala1039Thr;	2	FALSE	chr17:37883212:G:A	99:chr17:37883212:G:A	0.001907
51_t2c2-1	51	AKT1	MODERATE	c.1112C>T	p.Thr371Met	1	FALSE	chr14:105239275:G:A	99:chr14:105239275:G:A	0.001068
51_t2c2-1	51	NOTCH1	HIGH	c.2155G>T	p.Glu719*	0	FALSE	chr9:139409014:C:A	99:chr9:139409014:C:A	0.001402
51_t2c2-1	51	C9orf53; CDKN2A	MODIFIER; MODERATE; LOW	n.*616G>A; c.*217C>T; c.337C>T; c.294C>T	; p.Pro113Ser; p.His98His	1	FALSE	chr9:21971064:G:A	99:chr9:21971064:G:A	0.000547
51_t2c2-1	51	TP53	MODERATE	c.144G>T; c.423G>T; c.540G>T; c.63G>T	p.Glu48Asp; p.Glu141Asp; p.Glu180Asp; p.Glu21Asp	5	FALSE	chr17:7578390:C:A	99:chr17:7578390:C:A	0.001361
51_t2c2-1	51	TP53	MODERATE; MODIFIER	c.100G>T; c.217G>T; c.-279G>T; c.-360G>T	p.Val34Leu; p.Val73Leu;	5	FALSE	chr17:7579470:C:A	99:chr17:7579470:C:A	0.001608
51_t2c2-1	51	RET	MODERATE	c.1867G>A	p.Glu623Lys	1	FALSE	chr10:43609111:G:A	99:chr10:43609111:G:A	0.000714
51_t2c2-1	51	TP53	LOW; MODIFIER; MODERATE	c.-6C>T; c.355C>T; c.472C>T; c.76C>T	; p.Arg119Cys; p.Arg158Cys; p.Arg26Cys	17	FALSE	chr17:7578458:G:A	99:chr17:7578458:G:A	0.001268
51_t2c2-1	51	GNA11	MODERATE	c.88C>T	p.Arg30Trp	1	FALSE	chr19:3094737:C:T	99:chr19:3094737:C:T	0.000913
51_t2c2-1	51	NOTCH1	MODERATE	c.5272C>A	p.Arg1758Ser	0	FALSE	chr9:139396836:G:T	99:chr9:139396836:G:T	0.000898

51_t2c2-1	51	ALK	MODERATE	c.2629G>T	p.Ala877Ser	1	FALSE	chr2:29455173:C:A	99:chr2:29455173:C:A	0.000658
51_t2c2-1	51	TP53	MODERATE; MODIFIER	c.236C>T; c.353C>T; c.-279C>T; c.-360C>T	p.Thr79Ile; p.Thr118Ile;	4	FALSE	chr17:7579334:G:A	99:chr17:7579334:G:A	0.000652
51_t2c2-1	51	TSC2	MODIFIER; MODERATE	c.2837+1108G>A; c.2933G>A	; p.Arg978His	0	FALSE	chr16:2127694:G:A	99:chr16:2127694:G:A	0.001109
51_t2c2-1	51	ERBB2	MODERATE; MODIFIER	c.517C>T; c.562C>T; c.607C>T; n.931C>T	p.Arg173Cys; p.Arg188Cys; p.Arg203Cys;	1	FALSE	chr17:37866098:C:T	99:chr17:37866098:C:T	0.000504
51_t2c2-1	51	VHL	MODIFIER; MODERATE	c.341-3257C>A; c.357C>A	; p.Phe119Leu	0	FALSE	chr3:10188214:C:A	99:chr3:10188214:C:A	0.000647
51_t2c2-1	51	NTRK1	MODERATE	c.1937G>A; c.2027G>A; c.2045G>A	p.Arg646His; p.Arg676His; p.Arg682His	1	FALSE	chr1:156849153:G:A	99:chr1:156849153:G:A	0.000565
51_t2c2-1	51	ESR1	MODERATE	c.929C>T; c.932C>T; c.938C>T	p.Thr310Met; p.Thr311Met; p.Thr313Met	0	FALSE	chr6:152265479:C:T	99:chr6:152265479:C:T	0.000449
51_t2c2-1	51	KIT	MODERATE	c.1778C>A; c.1790C>A	p.Ala593Asp; p.Ala597Asp	1	FALSE	chr4:55594004:C:A	99:chr4:55594004:C:A	0.000686
51_t2c2-1	51	FGFR2	MODIFIER; MODERATE	c.749-4847G>T; c.407G>T; c.485G>T; c.752G>T; n.1054G>T	; p.Arg136Leu; p.Arg162Leu; p.Arg251Leu	2	FALSE	chr10:123279680:C:A	99:chr10:123279680:C:A	0.00061
51_t2c2-1	51	AKT1	MODERATE	c.361C>T	p.Arg121Trp	2	FALSE	chr14:105242063:G:A	99:chr14:105242063:G:A	0.000494
51_t2c2-1	51	CTNNB1	MODERATE	c.134C>A	p.Ser45Tyr	0	FALSE	chr3:41266137:C:A	99:chr3:41266137:C:A	0.001117

51_t2c2-1	51	TP53	HIGH	c.142G>T; c.421G>T; c.538G>T; c.61G>T	p.Glu48*; p.Glu141*; p.Glu180*; p.Glu21*	14	FALSE	chr17:7578392:C:A	99:chr17:7578392:C:A	0.000677
51_t2c2-1	51	PIK3R1	MODERATE	c.1147G>A; c.1237G>A; c.2047G>A; c.958G>A	p.Glu383Lys; p.Glu413Lys; p.Glu683Lys; p.Glu320Lys	2	FALSE	chr5:67593301:G:A	99:chr5:67593301:G:A	0.000582
51_t2c2-1	51	FGFR2	MODERATE; MODIFIER	c.148C>T; c.226C>T; c.493C>T; n.795C>T	p.Arg50Trp; p.Arg76Trp; p.Arg165Trp;	1	FALSE	chr10:123310935:G:A	99:chr10:123310935:G:A	0.000667
51_t2c2-1	51	RET	MODERATE	c.1665C>A	p.Phe555Leu	1	FALSE	chr10:43608317:C:A	99:chr10:43608317:C:A	0.000569
51_t2c2-1	51	PIK3CA	MODERATE	c.478C>A	p.His160Asn	1	FALSE	chr3:178917603:C:A	99:chr3:178917603:C:A	0.003373
51_t2c2-1	51	KDR	MODERATE	c.3449G>T	p.Arg1150Ile	1	FALSE	chr4:55955096:C:A	99:chr4:55955096:C:A	0.001101
51_t2c2-1	51	PIK3R1	HIGH	c.484C>T	p.Arg162*	3	FALSE	chr5:67569823:C:T	99:chr5:67569823:C:T	0.000939
51_t2c2-1	51	PDGFRA	MODERATE	c.3078C>A	p.Asp1026Glu	1	FALSE	chr4:55156677:C:A	99:chr4:55156677:C:A	0.000509
51_t2c2-1	51	NTRK1	MODERATE	c.1478G>A; c.1568G>A; c.1586G>A	p.Cys493Tyr; p.Cys523Tyr; p.Cys529Tyr	1	FALSE	chr1:156845956:G:A	99:chr1:156845956:G:A	0.000926
51_t2c2-1	51	TP53	MODERATE	c.15G>T; c.375G>T; c.492G>T; c.96G>T	p.Lys5Asn; p.Lys125Asn; p.Lys164Asn; p.Lys32Asn	6	FALSE	chr17:7578438:C:A	99:chr17:7578438:C:A	0.000797
51_t2c2-1	51	TP53	MODIFIER; HIGH	c.-48C>T; c.313C>T; c.34C>T; c.430C>T	; p.Gln105*; p.Gln12*; p.Gln144*	42	FALSE	chr17:7578500:G:A	99:chr17:7578500:G:A	0.001986
51_t2c2-1	51	DDR2	MODERATE	c.1963G>A	p.Glu655Lys	1	FALSE	chr1:162745548:G:A	99:chr1:162745548:G:A	0.000824

51_t2c2-1	51	PDGFRA	MODERATE	c.1516C>A	p.Leu506Ile	2	FALSE	chr4:55139855:C:A	99:chr4:55139855:C:A	0.001213
51_t2c2-1	51	PDGFRA	MODERATE	c.1406T>C	p.Val469Ala	1	FALSE	chr4:55139745:T:C	99:chr4:55139745:T:C	0.00065
51_t2c2-1	51	AKT3	MODERATE	c.1056G>T	p.Glu352Asp	0	FALSE	chr1:243716138:C:A	99:chr1:243716138:C:A	0.002367
51_t2c2-1	51	EGFR	MODIFIER; HIGH	c.*1464C>T; c.1591C>T	; p.Arg531*	1	FALSE	chr7:55229284:C:T	99:chr7:55229284:C:T	0.000475
51_t2c2-1	51	MIR4673; NOTCH1	MODIFIER; HIGH	n.*59C>T; c.1324C>T	; p.Gln442*	0	FALSE	chr9:139412321:G:A	99:chr9:139412321:G:A	0.000981
51_t2c2-1	51	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2336G>A; n.1226C>T	p.Gly779Asp;	2	FALSE	chr7:55249038:G:A	99:chr7:55249038:G:A	0.000931
51_t2c2-1	51	NOTCH1	MODERATE	c.4045G>T	p.Ala1349Ser	0	FALSE	chr9:139400303:C:A	99:chr9:139400303:C:A	0.000765
51_t2c2-1	51	VHL	MODIFIER; MODERATE	c.341-3231T>C; c.383T>C	; p.Leu128Pro	0	FALSE	chr3:10188240:T:C	99:chr3:10188240:T:C	0.000718
51_t2c2-1	51	FGFR4	HIGH	c.1041G>A	p.Trp347*	1	FALSE	chr5:176519769:G:A	99:chr5:176519769:G:A	0.001042
51_t2c2-1	51	TP53	MODIFIER; MODERATE	c.-5G>T; c.356G>T; c.473G>T; c.77G>T	; p.Arg119Leu; p.Arg158Leu; p.Arg26Leu	80	FALSE	chr17:7578457:C:A	99:chr17:7578457:C:A	0.000841
51_t2c2-1	51	HOXD-AS2; HOXD8	MODIFIER; MODERATE	n.*692C>T; c.-123-30G>A; c.400G>A	; p.Ala134Thr	0	FALSE	chr2:176995494:G:A	99:chr2:176995494:G:A	0.00106
51_t2c2-1	51	BRAF	HIGH	c.925G>T	p.Glu309*	1	FALSE	chr7:140500217:C:A	99:chr7:140500217:C:A	0.00088
51_t2c2-1	51	ATM	MODERATE	c.6200C>A	p.Ala2067Asp	0	FALSE	chr11:108188101:C:A	99:chr11:108188101:C:A	0.003442
51_t2c2-1	51	C9orf53; CDKN2A	MODIFIER; MODERATE; LOW	n.*616A>G; c.*111T>C; c.188T>C; c.231T>C	; p.Leu63Pro; p.Ala77Ala	2	FALSE	chr9:21971170:A:G	99:chr9:21971170:A:G	0.000758
51_t2c2-1	51	NOTCH1	MODERATE	c.5720C>T	p.Pro1907Leu	0	FALSE	chr9:139395218:G:A	99:chr9:139395218:G:A	0.000887

51_t2c2-1	51	CDKN2A	MODIFIER; HIGH	c.194-3523G>T; c.97G>T	; p.Glu33*	3	FALSE	chr9:21974730:C:A	99:chr9:21974730:C:A	0.000829
51_t2c2-1	51	C9orf53; CDKN2A	MODIFIER; MODERATE	n.*616C>G; c.*140G>C; c.217G>C; c.260G>C	; p.Ala73Pro; p.Arg87Pro	1	FALSE	chr9:21971141:C:G	99:chr9:21971141:C:G	0.024716
51_t2c2-1	51	C9orf53; CDKN2A	MODIFIER; MODERATE	n.*616C>A; c.*266G>T; c.343G>T; c.386G>T	; p.Val115Leu; p.Arg129Leu	4	FALSE	chr9:21971015:C:A	99:chr9:21971015:C:A	0.000561
51_t2c2-1	51	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2432C>T; n.1130G>A	p.Ser811Phe;	1	FALSE	chr7:55249134:C:T	99:chr7:55249134:C:T	0.0005
51_t2c2-1	51	NOTCH1	MODERATE	c.5777G>A	p.Arg1926His	0	FALSE	chr9:139395161:C:T	99:chr9:139395161:C:T	0.001166
51_t2c2-1	51	TP53	MODERATE; MODIFIER	c.188C>T; c.305C>T; c.-279C>T; c.-360C>T	p.Thr63Ile; p.Thr102Ile;	7	FALSE	chr17:7579382:G:A	99:chr17:7579382:G:A	0.00121
51_t2c2-1	51	EPHA3	MODERATE	c.1132C>A	p.Pro378Thr	0	FALSE	chr3:89391066:C:A	99:chr3:89391066:C:A	0.001417
51_t2c2-1	51	C9orf53; CDKN2A	MODIFIER; MODERATE; LOW	n.*616A>G; c.*261T>C; c.338T>C; c.381T>C	; p.Leu113Pro; p.Ser127Ser	1	FALSE	chr9:21971020:A:G	99:chr9:21971020:A:G	0.000582
51_t2c2-1	51	FGFR3	MODERATE	c.1552G>A; c.1888G>A; c.1894G>A	p.Val518Met; p.Val630Met; p.Val632Met	1	FALSE	chr4:1807829:G:A	99:chr4:1807829:G:A	0.000845
51_t2c2-1	51	SMO	MODERATE	c.628G>A	p.Val210Met	0	FALSE	chr7:128845134:G:A	99:chr7:128845134:G:A	0.0009
51_t2c2-1	51	KDR	MODERATE	c.2323G>T	p.Ala775Ser	1	FALSE	chr4:55964914:C:A	99:chr4:55964914:C:A	0.002418
51_t2c2-1	51	CTNNB1	LOW	c.1956G>A	p.Ala652Ala	0	FALSE	chr3:41278080:G:A	99:chr3:41278080:G:A	0.000835
51_t2c2-1	51	RET	MODERATE	c.1574G>A	p.Arg525Gln	1	FALSE	chr10:43607598:G:A	99:chr10:43607598:G:A	0.000434

51_t2c2-1	51	KDR	MODERATE	c.3433G>A	p.Gly1145Arg	4	FALSE	chr4:55955112:C:T	99:chr4:55955112:C:T	0.000595
51_t2c2-1	51	NTRK2	MODERATE	c.1925G>A; c.1973G>A	p.Gly642Asp; p.Gly658Asp	0	FALSE	chr9:87570233:G:A	99:chr9:87570233:G:A	0.000663
51_t2c2-1	51	IDH1	MODERATE	c.766G>T	p.Ala256Ser	2	FALSE	chr2:209106802:C:A	99:chr2:209106802:C:A	0.000583
51_t2c2-1	51	ERBB2; MIEN1; MIR4728	MODERATE; MODIFIER	c.2600G>A; c.2645G>A; c.2690G>A; n.3014G>A; c.*388C>T; n.-1G>A	p.Arg867Gln; p.Arg882Gln; p.Arg897Gln;	2	FALSE	chr17:37881620:G:A	99:chr17:37881620:G:A	0.000664
51_t2c2-1	51	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2381C>A; n.1181G>T	p.Pro794His;	1	FALSE	chr7:55249083:C:A	99:chr7:55249083:C:A	0.000668
51_t2c2-1	51	MAP2K1	MODERATE	c.316G>A	p.Ala106Thr	1	FALSE	chr15:66729108:G:A	99:chr15:66729108:G:A	0.001675
51_t2c2-1	51	PHLPP1	HIGH	c.2179C>T	p.Arg727*	0	FALSE	chr18:60562356:C:T	99:chr18:60562356:C:T	0.000536
51_t2c2-1	51	HGF	MODERATE	c.490G>T; c.505G>T	p.Gly164Cys; p.Gly169Cys	0	FALSE	chr7:81381556:C:A	99:chr7:81381556:C:A	0.000848
51_t2c2-1	51	PIK3R1	MODERATE	c.825C>A	p.Phe275Leu	1	FALSE	chr5:67576546:C:A	99:chr5:67576546:C:A	0.003851
51_t2c2-1	51	TP53	MODERATE	c.438G>T; c.519G>T; c.798G>T; c.915G>T	p.Lys146Asn; p.Lys173Asn; p.Lys266Asn; p.Lys305Asn	3	FALSE	chr17:7577023:C:A	99:chr17:7577023:C:A	0.001169
51_t2c2-1	51	TP53	MODIFIER; MODERATE	c.*137A>G; c.*225A>G; c.1001A>G; c.1118A>G; c.641A>G; c.722A>G	; p.Lys334Arg; p.Lys373Arg; p.Lys214Arg; p.Lys241Arg	1	FALSE	chr17:7572991:T:C	99:chr17:7572991:T:C	0.001818
51_t2c2-1	51	ZNF716	MODERATE	c.32G>A	p.Arg11Gln	0	FALSE	chr7:57510026:G:A	99:chr7:57510026:G:A	0.000586

51_t2c2-1	51	VHL	MODIFIER; MODERATE	c.341-3270A>C; c.344A>C	; p.His115Pro	0	FALSE	chr3:10188201:A:C	99:chr3:10188201:A:C	0.001037
51_t2c2-1	51	KRAS	MODERATE	c.35G>A	p.Gly12Asp	11213	FALSE	chr12:25398284:C:T	99:chr12:25398284:C:T	0.42663
51_t2c2-1	51	PIK3R1	MODERATE	c.1082G>A; c.1271G>A; c.1361G>A; c.2171G>A	p.Arg361Gln; p.Arg424Gln; p.Arg454Gln; p.Arg724Gln	1	FALSE	chr5:67593425:G:A	99:chr5:67593425:G:A	0.000748
51_t2c2-1	51	BRAF	MODERATE	c.146A>T	p.Asn49Ile	1	FALSE	chr7:140550005:T:A	99:chr7:140550005:T:A	0.00311
51_t2c2-1	51	EPHA3	HIGH	c.318C>A	p.Cys106*	0	FALSE	chr3:89259174:C:A	99:chr3:89259174:C:A	0.001121
51_t2c2-1	51	NTRK1	MODERATE	c.1751G>A; c.1841G>A; c.1859G>A	p.Gly584Asp; p.Gly614Asp; p.Gly620Asp	1	FALSE	chr1:156848967:G:A	99:chr1:156848967:G:A	0.001007
51_t2c2-1	51	SMO	MODERATE	c.1193G>A	p.Arg398Gln	0	FALSE	chr7:128846357:G:A	99:chr7:128846357:G:A	0.000448
51_t2c2-1	51	DDR2	MODERATE	c.2255G>A	p.Arg752His	1	FALSE	chr1:162746132:G:A	99:chr1:162746132:G:A	0.000664
51_t2c2-1	51	CDKN2B; CDKN2B-AS1	MODERATE; MODIFIER	c.19G>T; n.371+13774C>A	p.Gly7Cys;	0	FALSE	chr9:22008934:C:A	99:chr9:22008934:C:A	0.000713
51_t2c2-1	51	EPHA3	HIGH	c.1515C>A	p.Tyr505*	0	FALSE	chr3:89448551:C:A	99:chr3:89448551:C:A	0.000855
51_t2c2-1	51	FGFR4	MODIFIER; MODERATE	c.1098-65G>A; c.1251+10G>A; c.1067G>A	; p.Arg356His	1	FALSE	chr5:176520342:G:A	99:chr5:176520342:G:A	0.001187
51_t2c2-1	51	SMO	HIGH	c.871C>T	p.Arg291*	0	FALSE	chr7:128845574:C:T	99:chr7:128845574:C:T	0.000407
51_t2c2-1	51	TP53	MODERATE; MODIFIER	c.167C>T; c.284C>T; c.-279C>T; c.-360C>T	p.Ser56Phe; p.Ser95Phe;	3	FALSE	chr17:7579403:G:A	99:chr17:7579403:G:A	0.000904
51_t2c2-1	51	CTNNB1	MODERATE	c.91C>A	p.Leu31Met	0	FALSE	chr3:41266094:C:A	99:chr3:41266094:C:A	0.001718

51_t2c2-1	51	IGF1R	MODERATE	c.3613G>A; c.3616G>A	p.Ala1205Thr; p.Ala1206Thr	0	FALSE	chr15:99491831:G:A	99:chr15:99491831:G:A	0.001294
51_t2c2-1	51	NOTCH1	MODERATE	c.2806G>T	p.Gly936Cys	0	FALSE	chr9:139404348:C:A	99:chr9:139404348:C:A	0.000541
51_t2c2-1	51	ERBB2; MIEN1; MIR4728	MODERATE; MODIFIER	c.2597G>A; c.2642G>A; c.2687G>A; n.3011G>A; c.*388C>T; n.-1G>A	p.Arg866His; p.Arg881His; p.Arg896His;	2	FALSE	chr17:37881617:G:A	99:chr17:37881617:G:A	0.000664
51_t2c2-1	51	TSC2	MODERATE	c.3514C>A; c.3646C>A	p.Leu1172Ile; p.Leu1216Ile	0	FALSE	chr16:2131631:C:A	99:chr16:2131631:C:A	0.001194
51_t2c2-1	51	STK11	HIGH	c.996G>A	p.Trp332*	2	FALSE	chr19:1223059:G:A	99:chr19:1223059:G:A	0.001038
51_t2c2-1	51	NOTCH1	MODERATE	c.4984C>T	p.Arg1662Trp	0	FALSE	chr9:139399159:G:A	99:chr9:139399159:G:A	0.000704
51_t2c2-1	51	KRAS	HIGH	c.292G>T	p.Glu98*	1	FALSE	chr12:25378706:C:A	99:chr12:25378706:C:A	0.002821
51_t2c2-1	51	FGFR2	MODIFIER; MODERATE	c.749-4686G>T; c.568G>T; c.646G>T; c.913G>T; n.1215G>T	; p.Gly190Trp; p.Gly216Trp; p.Gly305Trp	3	FALSE	chr10:123279519:C:A	99:chr10:123279519:C:A	0.00067
51_t2c2-1	51	CTNNB1	MODERATE	c.98C>A	p.Ser33Tyr	0	FALSE	chr3:41266101:C:A	99:chr3:41266101:C:A	0.003012
51_t2c2-1	51	FLT3	HIGH	c.610G>T	p.Glu204*	0	FALSE	chr13:28626686:C:A	99:chr13:28626686:C:A	0.000666
51_t2c2-1	51	MIR4673; NOTCH1	MODIFIER; HIGH	n.-1G>T; c.574G>T	; p.Gly192*	0	FALSE	chr9:139417470:C:A	99:chr9:139417470:C:A	0.000726

51_t2c2-1	51	TP53	MODIFIER; HIGH	c.*152G>T; c.*64G>T; c.1045G>T; c.568G>T; c.649G>T; c.928G>T	; p.Glu349*; p.Glu190*; p.Glu217*; p.Glu310*	13	FALSE	chr17:7573982:C:A	99:chr17:7573982:C:A	0.000765
51_t2c2-1	51	C9orf53; CDKN2A	MODIFIER; MODERATE; LOW	n.*616C>A; c.*189G>T; c.266G>T; c.309G>T	; p.Gly89Val; p.Gly103Gly	3	FALSE	chr9:21971092:C:A	99:chr9:21971092:C:A	0.000584
51_t2c2-1	51	APC	MODERATE	c.1771G>A; c.1825G>A	p.Val591Ile; p.Val609Ile	0	FALSE	chr5:112170729:G:A	99:chr5:112170729:G:A	0.002183
51_t2c2-1	51	TP53	MODERATE; MODIFIER	c.170C>T; c.287C>T; c.-279C>T; c.-360C>T	p.Ser57Phe; p.Ser96Phe;	3	FALSE	chr17:7579400:G:A	99:chr17:7579400:G:A	0.000881
51_t2c2-1	51	EGFR	MODERATE	c.755G>A	p.Arg252His	3	FALSE	chr7:55221711:G:A	99:chr7:55221711:G:A	0.000553
51_t2c2-1	51	IDH2	MODIFIER; MODERATE	c.-13G>T; c.-17-2869G>T; c.144G>T	; p.Lys48Asn	2	FALSE	chr15:90634848:C:A	99:chr15:90634848:C:A	0.001337
51_t2c2-1	51	MET	MODERATE	c.3731A>G; c.3785A>G	p.Lys1244Arg; p.Lys1262Arg	3	FALSE	chr7:116423456:A:G	99:chr7:116423456:A:G	0.001998
51_t2c2-1	51	TP53	HIGH	c.379G>T; c.460G>T; c.739G>T; c.856G>T	p.Glu127*; p.Glu154*; p.Glu247*; p.Glu286*	82	FALSE	chr17:7577082:C:A	99:chr17:7577082:C:A	0.000702
51_t2c2-1	51	PTEN	MODERATE	c.914G>A	p.Ser305Asn	1	FALSE	chr10:89720763:G:A	99:chr10:89720763:G:A	0.008368

51_t2c2-1	51	C9orf53; CDKN2A	MODIFIER; HIGH; LOW	n.*616G>A; c.*142C>T; c.262C>T; c.219C>T	; p.Arg88*; p.Ala73Ala	1	FALSE	chr9:21971139:G:A	99:chr9:21971139:G:A	0.000788
51_t2c2-1	51	CTNNB1	MODERATE	c.125C>A	p.Thr42Lys	0	FALSE	chr3:41266128:C:A	99:chr3:41266128:C:A	0.001074
51_t2c2-1	51	C9orf53; CDKN2A	MODIFIER; MODERATE; LOW	n.*616C>T; c.*258G>A; c.335G>A; c.378G>A	; p.Arg112His; p.Pro126Pro	1	FALSE	chr9:21971023:C:T	99:chr9:21971023:C:T	0.000864
51_t2c2-1	51	INSRR; NTRK1	MODIFIER; MODERATE	c.3397+28C>T; c.13G>A	; p.Ala5Thr	3	FALSE	chr1:156811876:G:A	99:chr1:156811876:G:A	0.000722
51_t2c2-1	51	APC	HIGH	c.350C>A; c.380C>A	p.Ser117*; p.Ser127*	0	FALSE	chr5:112103015:C:A	99:chr5:112103015:C:A	0.002235
51_t2c2-1	51	FBXW7	MODERATE	c.314G>T; c.428G>T; c.668G>T	p.Arg105Leu; p.Arg143Leu; p.Arg223Leu	0	FALSE	chr4:153268140:C:A	99:chr4:153268140:C:A	0.000488
51_t2c2-1	51	NTRK1	MODERATE	c.1813C>A; c.1903C>A; c.1921C>A	p.Leu605Met; p.Leu635Met; p.Leu641Met	1	FALSE	chr1:156849029:C:A	99:chr1:156849029:C:A	0.000991
51_t2c2-1	51	RET	MODERATE	c.1901G>A	p.Cys634Tyr	7	FALSE	chr10:43609949:G:A	99:chr10:43609949:G:A	0.000417
51_t2c2-1	51	TP53	MODERATE	c.265C>T; c.346C>T; c.625C>T; c.742C>T	p.Arg89Trp; p.Arg116Trp; p.Arg209Trp; p.Arg248Trp	559	FALSE	chr17:7577539:G:A	99:chr17:7577539:G:A	0.385237
51_t2c2-1	51	NTRK1	MODERATE	c.2028C>A; c.2118C>A; c.2136C>A	p.Ser676Arg; p.Ser706Arg; p.Ser712Arg	1	FALSE	chr1:156849880:C:A	99:chr1:156849880:C:A	0.000716
51_t2c2-1	51	FGFR3	MODIFIER; MODERATE	c.931-374G>A; c.1196G>A; c.1202G>A	; p.Arg399His; p.Arg401His	1	FALSE	chr4:1806177:G:A	99:chr4:1806177:G:A	0.000813

51_t2c2-1	51	NTRK3	HIGH	c.1768G>T; c.1792G>T	p.Glu590*; p.Glu598*	0	FALSE	chr15:88476340:C:A	99:chr15:88476340:C:A	0.001029
51_t2c2-1	51	ERBB2	MODERATE; MODIFIER	c.841T>A; c.886T>A; c.931T>A; n.1255T>A	p.Cys281Ser; p.Cys296Ser; p.Cys311Ser;	1	FALSE	chr17:37868210:T:A	99:chr17:37868210:T:A	0.000481
51_t2c2-1	51	MIR4673; NOTCH1	MODIFIER; MODERATE	n.*59G>T; c.1343G>T	; p.Arg448Leu	0	FALSE	chr9:139412302:C:A	99:chr9:139412302:C:A	0.001473
51_t2c2-1	51	C9orf53; CDKN2A	MODIFIER; MODERATE	n.*616G>A; c.*218C>T; c.295C>T; c.338C>T	; p.Arg99Trp; p.Pro113Leu	2	FALSE	chr9:21971063:G:A	99:chr9:21971063:G:A	0.000819
51_t2c2-1	51	RET	MODERATE	c.1892A>G	p.Asp631Gly	3	FALSE	chr10:43609940:A:G	99:chr10:43609940:A:G	0.000424
51_t2c2-1	51	C9orf53; CDKN2A	MODIFIER; MODERATE	n.*616G>T; c.*263C>A; c.340C>A; c.383C>A	; p.Pro114Thr; p.Ala128Asp	2	TRUE	chr9:21971018:G:T	99:chr9:21971018:G:T	0.000564
51_t2c2-1	51	TP53	MODERATE	c.370C>T; c.451C>T; c.730C>T; c.847C>T	p.Arg124Cys; p.Arg151Cys; p.Arg244Cys; p.Arg283Cys	19	FALSE	chr17:7577091:G:A	99:chr17:7577091:G:A	0.000682
51_t2c2-1	51	C9orf53; CDKN2A	MODIFIER; MODERATE	n.*616G>A; c.*318C>T; c.*39C>T; c.395C>T	; p.Ala132Val	1	FALSE	chr9:21970963:G:A	99:chr9:21970963:G:A	0.00057
51_t2c2-1	51	GAPDH; IFFO1	MODERATE; MODIFIER	c.217G>A; c.343G>A; c.*1743C>T; c.*1746C>T; c.*1770C>T; n.*2798C>T	p.Gly73Arg; p.Gly115Arg;	0	FALSE	chr12:6646282:G:A	99:chr12:6646282:G:A	0.00052

51_t2c2-1	51	ESR1	HIGH	c.1426C>T; c.1429C>T; c.1435C>T	p.Arg476*; p.Arg477*; p.Arg479*	0	FALSE	chr6:152415579:C:T	99:chr6:152415579:C:T	0.000965
51_t2c2-1	51	NOTCH1	HIGH	c.6022G>T	p.Glu2008*	0	FALSE	chr9:139393624:C:A	99:chr9:139393624:C:A	0.000546
51_t2c2-1	51	ALK	MODERATE	c.4192C>T	p.Pro1398Ser	1	FALSE	chr2:29416761:G:A	99:chr2:29416761:G:A	0.001806
51_t2c2-1	51	IDH1	MODERATE	c.974C>T	p.Thr325Met	2	FALSE	chr2:209104604:G:A	99:chr2:209104604:G:A	0.000671
51_t2c2-1	51	NOTCH1	MODERATE	c.5347C>T	p.Arg1783Trp	0	FALSE	chr9:139396761:G:A	99:chr9:139396761:G:A	0.000655
51_t2c2-1	51	ALK	MODERATE	c.2258G>T	p.Arg753Leu	1	FALSE	chr2:29462643:C:A	99:chr2:29462643:C:A	0.000536
51_t2c2-1	51	TP53	MODERATE	c.364G>T; c.445G>T; c.724G>T; c.841G>T	p.Asp122Tyr; p.Asp149Tyr; p.Asp242Tyr; p.Asp281Tyr	28	FALSE	chr17:7577097:C:A	99:chr17:7577097:C:A	0.00069
51_t2c2-1	51	NOTCH1	HIGH	c.3250G>T	p.Glu1084*	0	FALSE	chr9:139402759:C:A	99:chr9:139402759:C:A	0.000888
51_t2c2-1	51	HGF	MODERATE	c.5G>T	p.Trp2Leu	0	FALSE	chr7:81399283:C:A	99:chr7:81399283:C:A	0.001828
51_t2c2-1	51	SMO	HIGH	c.1191C>A	p.Tyr397*	0	FALSE	chr7:128846355:C:A	99:chr7:128846355:C:A	0.000672
51_t2c2-1	51	MITF	MODERATE	c.250C>T; c.358C>T; c.403C>T; c.406C>T; c.85C>T	p.Arg84Trp; p.Arg120Trp; p.Arg135Trp; p.Arg136Trp; p.Arg29Trp	0	FALSE	chr3:69987024:C:T	99:chr3:69987024:C:T	0.00061
51_t2c2-1	51	ERBB2; MIEN1; MIR4728	MODIFIER; MODERATE	c.3160-213A>G; c.3251A>G; c.3296A>G; c.3341A>G; n.3665A>G; c.*388T>C; n.*67A>G	; p.Glu1084Gly; p.Glu1099Gly; p.Glu1114Gly	1	FALSE	chr17:37883729:A:G	99:chr17:37883729:A:G	0.00093

51_t2c2-1	51	NTRK2	MODERATE	c.1023G>A; c.1062G>A	p.Met341Ile; p.Met354Ile	0	FALSE	chr9:87342777:G:A	99:chr9:87342777:G:A	0.001359
51_t2c2-1	51	FGFR3	MODIFIER; MODERATE	c.931-398C>A; c.1172C>A; c.1178C>A	; p.Ala391Glu; p.Ala393Glu	34	FALSE	chr4:1806153:C:A	99:chr4:1806153:C:A	0.001756
51_t2c2-1	51	CDH1	MODERATE	c.1204G>A	p.Asp402Asn	0	FALSE	chr16:68847282:G:A	99:chr16:68847282:G:A	0.00066
51_t2c2-1	51	RET	MODERATE	c.1349G>A	p.Ser450Asn	1	FALSE	chr10:43606740:G:A	99:chr10:43606740:G:A	0.000455
51_t2c2-1	51	NF1	MODERATE	c.5458C>A; c.5521C>A	p.Gln1820Lys; p.Gln1841Lys	3	FALSE	chr17:29654769:C:A	99:chr17:29654769:C:A	0.000533
51_t2c2-1	51	RET	MODERATE	c.1991C>A	p.Ala664Asp	2	FALSE	chr10:43610039:C:A	99:chr10:43610039:C:A	0.000799
51_t2c2-1	51	TSC2	MODERATE	c.1381G>A	p.Val461Met	0	FALSE	chr16:2112992:G:A	99:chr16:2112992:G:A	0.000543
51_t2c2-1	51	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2576C>A; n.-1G>T	p.Ala859Asp;	1	FALSE	chr7:55259518:C:A	99:chr7:55259518:C:A	0.000806
51_t2c2-1	51	INSRR; NTRK1	MODERATE; LOW	c.3356G>T; c.82C>A	p.Arg1119Leu; p.Arg28Arg	1	FALSE	chr1:156811945:C:A	99:chr1:156811945:C:A	0.000797
100_bl-1	100	KRAS	MODERATE	c.436G>A	p.Ala146Thr	118	FALSE	chr12:25378562:C:T	100:chr12:25378562:C:T	0.054945
100_bl-1	100	BRAF	MODERATE	c.1780G>A	p.Asp594Asn	20	FALSE	chr7:140453155:C:T	100:chr7:140453155:C:T	0.081897
100_bl-1	100	RET	MODERATE	c.1942G>A	p.Val648Ile	2	FALSE	chr10:43609990:G:A	100:chr10:43609990:G:A	0.086066
100_bl-1	100	EGFR	MODERATE	c.1159C>G	p.Leu387Val	1	FALSE	chr7:55224477:C:G	100:chr7:55224477:C:G	0.011494
100_bl-1	100	AKT3	HIGH	c.196C>T	p.Arg66*	0	FALSE	chr1:243828162:G:A	100:chr1:243828162:G:A	0.105932

52_bl-2	52	FGFR2	MODERATE; MODIFIER	c.1394C>T; c.1397C>T; c.1400C>T; c.1409C>T; c.1478C>T; c.1481C>T; c.1745C>T; c.1748C>T; n.2195C>T	p.Pro465Leu; p.Pro466Leu; p.Pro467Leu; p.Pro470Leu; p.Pro493Leu; p.Pro494Leu; p.Pro582Leu; p.Pro583Leu;	2	FALSE	chr10:123256164:G:A	101:chr10:123256164:G:A	0.003268
52_bl-2	52	KRAS	MODERATE	c.34G>T	p.Gly12Cys	3755	FALSE	chr12:25398285:C:A	101:chr12:25398285:C:A	0.005263
52_bl-2	52	CDKN2A	MODIFIER; MODERATE	c.194-3568A>C; c.52A>C	; p.Thr18Pro	1	FALSE	chr9:21974775:T:G	101:chr9:21974775:T:G	0.004739
52_bl-2	52	TSC2	MODERATE	c.667G>A	p.Asp223Asn	0	FALSE	chr16:2106663:G:A	101:chr16:2106663:G:A	0.003361
52_bl-2	52	TP53	MODIFIER; MODERATE	c.*144A>G; c.*56A>G; c.1037A>G; c.560A>G; c.641A>G; c.920A>G	; p.Glu346Gly; p.Glu187Gly; p.Glu214Gly; p.Glu307Gly	1	FALSE	chr17:7573990:T:C	101:chr17:7573990:T:C	0.003077
52_bl-2	52	NTRK3	MODERATE	c.506G>A	p.Arg169His	0	FALSE	chr15:88680751:C:T	101:chr15:88680751:C:T	0.00313
52_bl-2	52	GNA11	MODERATE	c.440G>A	p.Arg147His	1	FALSE	chr19:3113446:G:A	101:chr19:3113446:G:A	0.002954
102_bl-1	102	NTRK1	MODERATE	c.804C>G; c.894C>G	p.His268Gln; p.His298Gln	1	FALSE	chr1:156843468:C:G	102:chr1:156843468:C:G	0.002663
102_bl-1	102	SMO	MODERATE	c.1684C>T	p.Arg562Trp	0	FALSE	chr7:128850837:C:T	102:chr7:128850837:C:T	0.000998
102_bl-1	102	KDR	MODERATE	c.1028C>T	p.Thr343Met	3	FALSE	chr4:55976884:G:A	102:chr4:55976884:G:A	0.000706
102_bl-1	102	NTRK3	MODERATE	c.1420C>T; c.1444C>T	p.His474Tyr; p.His482Tyr	0	FALSE	chr15:88576229:G:A	102:chr15:88576229:G:A	0.001498

102_bl-1	102	NTRK3	MODERATE	c.2009G>A; c.2033G>A	p.Arg670Gln; p.Arg678Gln	0	FALSE	chr15:88472522:C:T	102:chr15:88472522:C:T	0.00116
102_bl-1	102	PIK3CA	MODERATE	c.3154A>G	p.Thr1052Ala	3	FALSE	chr3:178952099:A:G	102:chr3:178952099:A:G	0.001238
102_bl-1	102	FGFR1	MODERATE	c.487C>T; c.493C>T; c.736C>T; c.754C>T; c.760C>T; c.853C>T	p.Arg163Trp; p.Arg165Trp; p.Arg246Trp; p.Arg252Trp; p.Arg254Trp; p.Arg285Trp	1	FALSE	chr8:38282203:G:A	102:chr8:38282203:G:A	0.001206
102_bl-1	102	CDH1	MODERATE	c.1297G>A	p.Asp433Asn	0	FALSE	chr16:68847375:G:A	102:chr16:68847375:G:A	0.001126
102_bl-1	102	KDR	MODERATE	c.3455C>T	p.Thr1152Met	1	FALSE	chr4:55955090:G:A	102:chr4:55955090:G:A	0.001027
102_bl-1	102	MET	MODERATE	c.959C>T	p.Ala320Val	1	FALSE	chr7:116340097:C:T	102:chr7:116340097:C:T	0.001149
102_bl-1	102	ALK	MODERATE	c.446C>T	p.Ala149Val	1	FALSE	chr2:30143080:G:A	102:chr2:30143080:G:A	0.001826
102_bl-1	102	ERBB2	MODERATE; MODIFIER	c.1031C>T; c.1076C>T; c.986C>T; n.1400C>T	p.Ala344Val; p.Ala359Val; p.Ala329Val;	1	FALSE	chr17:37868629:C:T	102:chr17:37868629:C:T	0.001003
102_bl-1	102	IGF1R	MODERATE	c.3934T>C; c.3937T>C	p.Ser1312Pro; p.Ser1313Pro	0	FALSE	chr15:99500504:T:C	102:chr15:99500504:T:C	0.005088
102_bl-1	102	TP53	MODERATE	c.143A>G; c.422A>G; c.539A>G; c.62A>G	p.Glu48Gly; p.Glu141Gly; p.Glu180Gly; p.Glu21Gly	1	FALSE	chr17:7578391:T:C	102:chr17:7578391:T:C	0.001817
102_bl-1	102	INSRR; NTRK1	MODIFIER; MODERATE	c.3397+13C>T; c.28G>A	; p.Ala10Thr	1	FALSE	chr1:156811891:G:A	102:chr1:156811891:G:A	0.000857

102_bl-1	102	FGFR1	MODERATE	c.359C>T; c.365C>T; c.608C>T; c.626C>T; c.632C>T; c.725C>T	p.Ala120Val; p.Ala122Val; p.Ala203Val; p.Ala209Val; p.Ala211Val; p.Ala242Val	1	FALSE	chr8:38283753:G:A	102:chr8:38283753:G:A	0.001334
102_bl-1	102	FBXW7	MODERATE	c.1159C>T; c.1273C>T; c.1513C>T	p.Arg387Cys; p.Arg425Cys; p.Arg505Cys	0	FALSE	chr4:153247289:G:A	102:chr4:153247289:G:A	0.001085
102_bl-1	102	MET	MODERATE	c.1406G>A	p.Arg469Gln	2	FALSE	chr7:116380017:G:A	102:chr7:116380017:G:A	0.001865
102_bl-1	102	TP53	MODIFIER; HIGH	c.*158A>T; c.*70A>T; c.1051A>T; c.574A>T; c.655A>T; c.934A>T	; p.Lys351*; p.Lys192*; p.Lys219*; p.Lys312*	2	FALSE	chr17:7573976:T:A	102:chr17:7573976:T:A	0.001112
102_bl-1	102	KRAS	MODERATE	c.34G>T	p.Gly12Cys	3755	FALSE	chr12:25398285:C:A	102:chr12:25398285:C:A	0.30802
102_bl-1	102	KDR	MODERATE	c.2003C>T	p.Thr668Met	1	FALSE	chr4:55968660:G:A	102:chr4:55968660:G:A	0.001529
102_bl-1	102	IGF1R	MODERATE	c.3005G>A; c.3008G>A	p.Arg1002Gln; p.Arg1003Gln	0	FALSE	chr15:99478104:G:A	102:chr15:99478104:G:A	0.001153
102_bl-1	102	CTNNB1	MODERATE	c.497T>G	p.Val166Gly	0	FALSE	chr3:41266826:T:G	102:chr3:41266826:T:G	0.001637
102_bl-1	102	NOTCH1	MODERATE	c.5987C>T	p.Thr1996Met	0	FALSE	chr9:139393659:G:A	102:chr9:139393659:G:A	0.001204
102_bl-1	102	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2393T>C; n.1169A>G	p.Leu798Pro;	3	FALSE	chr7:55249095:T:C	102:chr7:55249095:T:C	0.00168
102_bl-1	102	C9orf53; CDKN2A	MODIFIER; MODERATE; LOW	n.*616T>G; c.*120A>C; c.197A>C; c.240A>C	; p.His66Pro; p.Pro80Pro	1	FALSE	chr9:21971161:T:G	102:chr9:21971161:T:G	0.034707

102_bl-1	102	EGFR	MODIFIER; MODERATE	c.*2364C>T; c.2165C>T	; p.Ala722Val	2	FALSE	chr7:55241717:C:T	102:chr7:55241717:C:T	0.001215
102_bl-1	102	TP53	MODIFIER; MODERATE	c.*137A>G; c.*225A>G; c.1001A>G; c.1118A>G; c.641A>G; c.722A>G	; p.Lys334Arg; p.Lys373Arg; p.Lys214Arg; p.Lys241Arg	1	FALSE	chr17:7572991:T:C	102:chr17:7572991:T:C	0.003546
102_bl-1	102	DDR2	MODERATE	c.2002C>T	p.Arg668Cys	2	FALSE	chr1:162745587:C:T	102:chr1:162745587:C:T	0.000854
102_bl-1	102	MITF	MODIFIER; MODERATE	c.93+115G>A; c.208G>A; c.373G>A; c.481G>A; c.526G>A; c.529G>A	; p.Ala70Thr; p.Ala125Thr; p.Ala161Thr; p.Ala176Thr; p.Ala177Thr	0	FALSE	chr3:69987147:G:A	102:chr3:69987147:G:A	0.00154
102_bl-1	102	ROS1	HIGH	c.5728C>T	p.Arg1910*	1	FALSE	chr6:117642471:G:A	102:chr6:117642471:G:A	0.001426
102_bl-1	102	TP53	MODERATE	c.242G>T; c.323G>T; c.602G>T; c.719G>T	p.Ser81Ile; p.Ser108Ile; p.Ser201Ile; p.Ser240Ile	6	FALSE	chr17:7577562:C:A	102:chr17:7577562:C:A	0.001646
102_bl-1	102	CDH1	MODERATE	c.1423G>A	p.Val475Met	0	FALSE	chr16:68849520:G:A	102:chr16:68849520:G:A	0.001189
102_bl-1	102	MET	MODERATE	c.487T>C	p.Ser163Pro	1	FALSE	chr7:116339625:T:C	102:chr7:116339625:T:C	0.002125

102_bl-1	102	FGFR1; LETM2	LOW; MODIFIER	c.2022G>A; c.2028G>A; c.2265G>A; c.2289G>A; c.2295G>A; c.2388G>A; c.*1406C>T; c.*1423C>T; c.*1553C>T; c.*1567C>T; c.*1638C>T	p.Glu674Glu; p.Glu676Glu; p.Glu755Glu; p.Glu763Glu; p.Glu765Glu; p.Glu796Glu;	1	FALSE	chr8:38271320:C:T	102:chr8:38271320:C:T	0.001813
102_bl-1	102	PDGFRA	MODERATE	c.827C>T	p.Thr276Met	1	FALSE	chr4:55133523:C:T	102:chr4:55133523:C:T	0.001314
102_bl-1	102	DDR2	MODERATE	c.700G>A	p.Asp234Asn	1	FALSE	chr1:162729614:G:A	102:chr1:162729614:G:A	0.000988
102_bl-1	102	AKT1	MODERATE	c.286C>T	p.Arg96Trp	1	FALSE	chr14:105242997:G:A	102:chr14:105242997:G:A	0.001377
102_bl-1	102	KIT	HIGH	c.2476C>T; c.2488C>T	p.Arg826*; p.Arg830*	2	FALSE	chr4:55602667:C:T	102:chr4:55602667:C:T	0.001186
42_bl-2	42	KIT	MODERATE	c.1632A>T; c.1644A>T	p.Leu544Phe; p.Leu548Phe	1	FALSE	chr4:55593487:A:T	103:chr4:55593487:A:T	0.004219
42_bl-2	42	NTRK3	MODERATE	c.2138G>A; c.2162G>A; c.2204G>A	p.Arg713His; p.Arg721His; p.Arg735His	0	FALSE	chr15:88423631:C:T	103:chr15:88423631:C:T	0.003759
42_bl-2	42	FBXW7	MODERATE	c.232A>T; c.346A>T; c.586A>T	p.Thr78Ser; p.Thr116Ser; p.Thr196Ser	0	FALSE	chr4:153268222:T:A	103:chr4:153268222:T:A	0.001794
42_bl-2	42	CDKN2A	MODIFIER; MODERATE	c.194-3568A>C; c.52A>C	; p.Thr18Pro	1	FALSE	chr9:21974775:T:G	103:chr9:21974775:T:G	0.00545
42_bl-2	42	KRAS	MODERATE	c.35G>A	p.Gly12Asp	11213	FALSE	chr12:25398284:C:T	103:chr12:25398284:C:T	0.113276
42_bl-2	42	TSC2	MODERATE	c.781C>T	p.Arg261Trp	0	FALSE	chr16:2107112:C:T	103:chr16:2107112:C:T	0.002899

42_bl-2	42	TP53	MODIFIER; HIGH	c.*158A>T; c.*70A>T; c.1051A>T; c.574A>T; c.655A>T; c.934A>T	; p.Lys351*; p.Lys192*; p.Lys219*; p.Lys312*	2	FALSE	chr17:7573976:T:A	103:chr17:7573976:T:A	0.075334
42_bl-2	42	ROS1	MODERATE	c.5651G>A	p.Arg1884Lys	1	FALSE	chr6:117642548:C:T	103:chr6:117642548:C:T	0.002967
42_bl-2	42	MITF	MODERATE	c.157A>C; c.265A>C; c.310A>C; c.313A>C	p.Thr53Pro; p.Thr89Pro; p.Thr104Pro; p.Thr105Pro	0	FALSE	chr3:69928493:A:C	103:chr3:69928493:A:C	0.002045
42_bl-2	42	TP53	MODIFIER; HIGH	c.-41G>A; c.320G>A; c.41G>A; c.437G>A	; p.Trp107*; p.Trp14*; p.Trp146*	47	FALSE	chr17:7578493:C:T	103:chr17:7578493:C:T	0.025271
42_bl-2	42	NF1	MODERATE	c.5426G>A; c.5489G>A	p.Arg1809His; p.Arg1830His	1	FALSE	chr17:29654737:G:A	103:chr17:29654737:G:A	0.002237
42_bl-2	42	RET	MODERATE	c.1852T>C	p.Cys618Arg	2	FALSE	chr10:43609096:T:C	103:chr10:43609096:T:C	0.00344
106_c2-1	106	KRAS	MODERATE	c.35G>A	p.Gly12Asp	11213	FALSE	chr12:25398284:C:T	109:chr12:25398284:C:T	0.004728
106_c2-1	106	NTRK1	MODERATE	c.1738G>A; c.1828G>A; c.1846G>A	p.Asp580Asn; p.Asp610Asn; p.Asp616Asn	1	FALSE	chr1:156848954:G:A	109:chr1:156848954:G:A	0.006006
106_c2-1	106	PDGFRA	MODERATE	c.1288G>A	p.Gly430Arg	2	FALSE	chr4:55138611:G:A	109:chr4:55138611:G:A	0.004938
106_c2-1	106	FLT3	MODERATE	c.2440G>A	p.Ala814Thr	0	FALSE	chr13:28592705:C:T	109:chr13:28592705:C:T	0.006135
106_c2-1	106	C9orf53; CDKN2A	MODIFIER; MODERATE	n.*616C>G; c.*140G>C; c.217G>C; c.260G>C	; p.Ala73Pro; p.Arg87Pro	1	FALSE	chr9:21971141:C:G	109:chr9:21971141:C:G	0.029762

106_c2-1	106	IGF1R	MODERATE	c.3526C>T; c.3529C>T	p.Arg1176Cys; p.Arg1177Cys	0	FALSE	chr15:99486223:C:T	109:chr15:99486223:C:T	0.00551
106_c2-1	106	PDGFRA	MODERATE	c.2914A>G	p.Ser972Gly	1	FALSE	chr4:55156513:A:G	109:chr4:55156513:A:G	0.004608
106_c2-1	106	C9orf53; CDKN2A	MODIFIER; MODERATE; LOW	n.*616C>T; c.*258G>A; c.335G>A; c.378G>A	; p.Arg112His; p.Pro126Pro	1	FALSE	chr9:21971023:C:T	109:chr9:21971023:C:T	0.007143
106_c2-1	106	KDR	MODERATE	c.2323G>T	p.Ala775Ser	1	FALSE	chr4:55964914:C:A	109:chr4:55964914:C:A	0.004556
106_c2-1	106	ALK	MODERATE	c.1588G>A	p.Glu530Lys	1	FALSE	chr2:29541229:C:T	109:chr2:29541229:C:T	0.005682
49_c12-1	49	KIT	MODERATE	c.2197G>A; c.2209G>A	p.Asp733Asn; p.Asp737Asn	2	FALSE	chr4:55597561:G:A	110:chr4:55597561:G:A	0.001705
49_c12-1	49	NTRK3	HIGH	c.1348C>T; c.1372C>T	p.Arg450*; p.Arg458*	0	FALSE	chr15:88669526:G:A	110:chr15:88669526:G:A	0.001823
49_c12-1	49	RET	MODERATE	c.1690A>C	p.Thr564Pro	1	FALSE	chr10:43608342:A:C	110:chr10:43608342:A:C	0.007524
49_c12-1	49	CDH1	MODERATE	c.2074G>A	p.Ala692Thr	0	FALSE	chr16:68857439:G:A	110:chr16:68857439:G:A	0.001166
49_c12-1	49	CDH1	MODERATE	c.871G>A	p.Asp291Asn	0	FALSE	chr16:68845625:G:A	110:chr16:68845625:G:A	0.001267
49_c12-1	49	SMO	MODERATE	c.1045A>C	p.Thr349Pro	0	FALSE	chr7:128846115:A:C	110:chr7:128846115:A:C	0.009294
49_c12-1	49	CTNNB1	MODERATE	c.164A>G	p.Glu55Gly	0	FALSE	chr3:41266167:A:G	110:chr3:41266167:A:G	0.00121
49_c12-1	49	MET	MODERATE	c.487T>C	p.Ser163Pro	1	FALSE	chr7:116339625:T:C	110:chr7:116339625:T:C	0.002268
49_c12-1	49	NTRK1	MODERATE	c.1940T>G; c.2030T>G; c.2048T>G	p.Val647Gly; p.Val677Gly; p.Val683Gly	2	FALSE	chr1:156849792:T:G	110:chr1:156849792:T:G	0.006403
49_c12-1	49	HRAS; LRRC56	MODERATE; MODIFIER	c.368G>A; c.-506C>T	p.Arg123His;	2	FALSE	chr11:533535:C:T	110:chr11:533535:C:T	0.001383

49_c12-1	49	FGFR1	MODERATE	c.475C>T; c.481C>T; c.724C>T; c.742C>T; c.748C>T; c.841C>T	p.Arg159Trp; p.Arg161Trp; p.Arg242Trp; p.Arg248Trp; p.Arg250Trp; p.Arg281Trp	2	FALSE	chr8:38282215:G:A	110:chr8:38282215:G:A	0.001245
49_c12-1	49	NOTCH1	MODERATE	c.5819G>A	p.Arg1940His	0	FALSE	chr9:139395119:C:T	110:chr9:139395119:C:T	0.001623
49_c12-1	49	KDR	MODERATE	c.3091G>A	p.Ala1031Thr	1	FALSE	chr4:55956224:C:T	110:chr4:55956224:C:T	0.001292
49_c12-1	49	EGFR	HIGH	c.3202C>T	p.Arg1068*	1	FALSE	chr7:55270249:C:T	110:chr7:55270249:C:T	0.001183
49_c12-1	49	DDR2	MODERATE	c.1022G>A	p.Arg341Gln	1	FALSE	chr1:162731167:G:A	110:chr1:162731167:G:A	0.001505
49_c12-1	49	FBXW7	HIGH	c.1480C>T; c.1594C>T; c.1834C>T	p.Gln494*; p.Gln532*; p.Gln612*	0	FALSE	chr4:153245357:G:A	110:chr4:153245357:G:A	0.001958
49_c12-1	49	C9orf53; CDKN2A	MODIFIER; MODERATE; LOW	n.*616T>G; c.*120A>C; c.197A>C; c.240A>C	; p.His66Pro; p.Pro80Pro	1	FALSE	chr9:21971161:T:G	110:chr9:21971161:T:G	0.023102
49_c12-1	49	NOTCH1	MODERATE	c.4252G>A	p.Ala1418Thr	0	FALSE	chr9:139400096:C:T	110:chr9:139400096:C:T	0.001556
49_c12-1	49	PIK3R1	MODERATE	c.1145C>T; c.1235C>T; c.2045C>T; c.956C>T	p.Ala382Val; p.Ala412Val; p.Ala682Val; p.Ala319Val	2	FALSE	chr5:67593299:C:T	110:chr5:67593299:C:T	0.001119
49_c12-1	49	PIK3CA	MODERATE	c.1634A>C	p.Glu545Ala	132	FALSE	chr3:178936092:A:C	110:chr3:178936092:A:C	0.001235
49_c12-1	49	NF1	MODERATE	c.5624C>T; c.5687C>T	p.Ser1875Leu; p.Ser1896Leu	1	FALSE	chr17:29657391:C:T	110:chr17:29657391:C:T	0.001328

49_c12-1	49	ERBB2; MIEN1; MIR4728	MODIFIER; MODERATE	c.3160-213A>G; c.3251A>G; c.3296A>G; c.3341A>G; n.3665A>G; c.*388T>C; n.*67A>G	; p.Glu1084Gly; p.Glu1099Gly; p.Glu1114Gly	1	FALSE	chr17:37883729:A:G	110:chr17:37883729:A:G	0.001974
49_c12-1	49	KIT	MODERATE	c.1486G>A	p.Asp496Asn	1	FALSE	chr4:55592162:G:A	110:chr4:55592162:G:A	0.001344
49_c12-1	49	CDH1	MODERATE	c.937G>A	p.Asp313Asn	0	FALSE	chr16:68845691:G:A	110:chr16:68845691:G:A	0.001245
49_c12-1	49	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2305G>A; n.1257C>T	p.Val769Met;	3	FALSE	chr7:55249007:G:A	110:chr7:55249007:G:A	0.001074
49_c12-1	49	CTNNB1	MODERATE	c.1345C>T	p.Arg449Cys	0	FALSE	chr3:41275179:C:T	110:chr3:41275179:C:T	0.001131
49_c12-1	49	ERBB2; MIEN1; MIR4728	MODERATE; MODIFIER	c.3025G>A; c.3070G>A; c.3115G>A; n.3439G>A; c.*388C>T; n.*67G>A	p.Ala1009Thr; p.Ala1024Thr; p.Ala1039Thr;	2	FALSE	chr17:37883212:G:A	110:chr17:37883212:G:A	0.001403
49_c12-1	49	IGF1R	MODERATE	c.3934T>C; c.3937T>C	p.Ser1312Pro; p.Ser1313Pro	0	FALSE	chr15:99500504:T:C	110:chr15:99500504:T:C	0.004624
49_c12-1	49	ATM	MODERATE	c.7949A>C	p.Asp2650Ala	0	FALSE	chr11:108204634:A:C	110:chr11:108204634:A:C	0.00127
49_c12-1	49	NRAS	MODERATE	c.394G>A	p.Glu132Lys	2	FALSE	chr1:115252246:C:T	110:chr1:115252246:C:T	0.001157
49_c12-1	49	NTHL1; TSC2	MODIFIER; MODERATE	c.-20C>T; c.170G>A	; p.Arg57His	0	FALSE	chr16:2100432:G:A	110:chr16:2100432:G:A	0.001316
49_c12-1	49	CDKN2A	MODIFIER; MODERATE	c.194-3567C>T; c.53C>T	; p.Thr18Met	1	FALSE	chr9:21974774:G:A	110:chr9:21974774:G:A	0.001603
49_c12-1	49	KRAS	MODERATE	c.35G>A	p.Gly12Asp	11213	FALSE	chr12:25398284:C:T	110:chr12:25398284:C:T	0.00404
49_c12-1	49	ROS1	MODERATE	c.5651G>A	p.Arg1884Lys	1	FALSE	chr6:117642548:C:T	110:chr6:117642548:C:T	0.001418

49_c12-1	49	C9orf53; CDKN2A	MODIFIER; MODERATE	n.*616C>G; c.*140G>C; c.217G>C; c.260G>C	; p.Ala73Pro; p.Arg87Pro	1	FALSE	chr9:21971141:C:G	110:chr9:21971141:C:G	0.011858
49_c12-1	49	TSC2	MODERATE	c.1610G>A	p.Arg537His	0	FALSE	chr16:2115530:G:A	110:chr16:2115530:G:A	0.001718
49_c12-1	49	NF1	MODERATE	c.4463G>A; c.4526G>A	p.Arg1488His; p.Arg1509His	1	FALSE	chr17:29587482:G:A	110:chr17:29587482:G:A	0.001204
49_c12-1	49	CDKN2A	MODIFIER; MODERATE	c.194-3568A>C; c.52A>C	; p.Thr18Pro	1	FALSE	chr9:21974775:T:G	110:chr9:21974775:T:G	0.00817
49_c12-1	49	AKT3	MODERATE	c.899C>T	p.Ala300Val	0	FALSE	chr1:243727071:G:A	110:chr1:243727071:G:A	0.001196
49_c12-1	49	C9orf53; CDKN2A	MODIFIER; MODERATE	n.*616G>A; c.*324C>T; c.*45C>T; c.401C>T	; p.Ala134Val	1	FALSE	chr9:21970957:G:A	110:chr9:21970957:G:A	0.00143
49_c12-1	49	ROS1	MODERATE	c.5920G>A	p.Glu1974Lys	1	FALSE	chr6:117641051:C:T	110:chr6:117641051:C:T	0.001294
49_c12-1	49	KDR	MODERATE	c.2323G>T	p.Ala775Ser	1	FALSE	chr4:55964914:C:A	110:chr4:55964914:C:A	0.001179
49_c12-1	49	DDR2	MODERATE	c.1418G>A	p.Arg473His	2	FALSE	chr1:162740216:G:A	110:chr1:162740216:G:A	0.001054
49_c12-1	49	TSC2	MODERATE	c.1654G>A	p.Ala552Thr	0	FALSE	chr16:2115574:G:A	110:chr16:2115574:G:A	0.001869
49_c12-1	49	PHLPP1	MODERATE	c.2452G>A	p.Val818Ile	0	FALSE	chr18:60570204:G:A	110:chr18:60570204:G:A	0.001859
86_c3-1	86	RET	MODERATE	c.1444C>T	p.His482Tyr	1	FALSE	chr10:43606835:C:T	113:chr10:43606835:C:T	0.000361
86_c3-1	86	SMO	MODERATE	c.1234C>T	p.Leu412Phe	0	FALSE	chr7:128846398:C:T	113:chr7:128846398:C:T	0.000501
86_c3-1	86	NTHL1; TSC2	MODIFIER; MODERATE	c.-20C>T; c.170G>A	; p.Arg57His	0	FALSE	chr16:2100432:G:A	113:chr16:2100432:G:A	0.001354

86_c3-1	86	FGFR1	MODERATE	c.1150C>T; c.1156C>T; c.1393C>T; c.1417C>T; c.1423C>T; c.1516C>T	p.Arg384Trp; p.Arg386Trp; p.Arg465Trp; p.Arg473Trp; p.Arg475Trp; p.Arg506Trp	1	FALSE	chr8:38275753:G:A	113:chr8:38275753:G:A	0.000299
86_c3-1	86	MET	MODERATE	c.3748A>G; c.3802A>G	p.Met1250Val; p.Met1268Val	1	FALSE	chr7:116423473:A:G	113:chr7:116423473:A:G	0.00037
86_c3-1	86	TP53	MODERATE	c.421C>T; c.502C>T; c.781C>T; c.898C>T	p.Pro141Ser; p.Pro168Ser; p.Pro261Ser; p.Pro300Ser	3	FALSE	chr17:7577040:G:A	113:chr17:7577040:G:A	0.000508
86_c3-1	86	EGFR	MODIFIER; HIGH	c.*2133C>T; c.*2364C>T; c.2005C>T	; p.Arg669*	1	FALSE	chr7:55240761:C:T	113:chr7:55240761:C:T	0.000781
86_c3-1	86	TP53	MODIFIER; MODERATE	c.-5G>T; c.356G>T; c.473G>T; c.77G>T	; p.Arg119Leu; p.Arg158Leu; p.Arg26Leu	80	FALSE	chr17:7578457:C:A	113:chr17:7578457:C:A	0.00036
86_c3-1	86	ATM	MODERATE	c.8228C>T	p.Thr2743Met	0	FALSE	chr11:108206648:C:T	113:chr11:108206648:C:T	0.000371
86_c3-1	86	BRAF	HIGH	c.1525C>T	p.Arg509*	1	FALSE	chr7:140476881:G:A	113:chr7:140476881:G:A	0.000622
86_c3-1	86	TP53	MODIFIER; MODERATE	c.-26C>T; c.335C>T; c.452C>T; c.56C>T	; p.Pro112Leu; p.Pro151Leu; p.Pro19Leu	30	FALSE	chr17:7578478:G:A	113:chr17:7578478:G:A	0.000371
86_c3-1	86	NF1	LOW	c.2850G>A	p.Gln950Gln	1	FALSE	chr17:29556483:G:A	113:chr17:29556483:G:A	0.000828
86_c3-1	86	NF1	MODERATE	c.6943G>A; c.7006G>A	p.Ala2315Thr; p.Ala2336Thr	2	FALSE	chr17:29667607:G:A	113:chr17:29667607:G:A	0.000956

86_c3-1	86	FBXW7	MODERATE	c.1088C>T; c.1202C>T; c.1442C>T	p.Ala363Val; p.Ala401Val; p.Ala481Val	0	FALSE	chr4:153247360:G:A	113:chr4:153247360:G:A	0.000467
86_c3-1	86	MIR4673; NOTCH1	MODIFIER; HIGH	n.*59C>T; c.1828C>T	; p.Gln610*	0	FALSE	chr9:139410010:G:A	113:chr9:139410010:G:A	0.000715
86_c3-1	86	TP53	MODERATE; MODIFIER	c.236C>T; c.353C>T; c.-279C>T; c.-360C>T	p.Thr79Ile; p.Thr118Ile;	4	FALSE	chr17:7579334:G:A	113:chr17:7579334:G:A	0.000366
86_c3-1	86	PIK3CA	MODERATE	c.365G>A	p.Gly122Asp	2	FALSE	chr3:178917490:G:A	113:chr3:178917490:G:A	0.00045
86_c3-1	86	CTNNB1	MODERATE	c.1972G>T	p.Val658Phe	0	FALSE	chr3:41278096:G:T	113:chr3:41278096:G:T	0.002389
86_c3-1	86	MITF	MODIFIER; MODERATE	c.93+115G>A; c.208G>A; c.373G>A; c.481G>A; c.526G>A; c.529G>A	; p.Ala70Thr; p.Ala125Thr; p.Ala161Thr; p.Ala176Thr; p.Ala177Thr	0	FALSE	chr3:69987147:G:A	113:chr3:69987147:G:A	0.000715
86_c3-1	86	FGFR1	MODIFIER; MODERATE	c.92-1367C>T; c.214C>T; c.238C>T; c.337C>T	; p.Arg72Cys; p.Arg80Cys; p.Arg113Cys	1	FALSE	chr8:38287320:G:A	113:chr8:38287320:G:A	0.00022
86_c3-1	86	C9orf53; CDKN2A	MODIFIER; MODERATE; LOW	n.*616G>A; c.*217C>T; c.337C>T; c.294C>T	; p.Pro113Ser; p.His98His	1	FALSE	chr9:21971064:G:A	113:chr9:21971064:G:A	0.00062
86_c3-1	86	CDH1	MODERATE	c.2053G>A	p.Val685Met	0	FALSE	chr16:68857418:G:A	113:chr16:68857418:G:A	0.000355
86_c3-1	86	NOTCH1	MODERATE	c.4718C>T	p.Thr1573Met	0	FALSE	chr9:139399425:G:A	113:chr9:139399425:G:A	0.000446
86_c3-1	86	AKT3	MODERATE	c.899C>T	p.Ala300Val	0	FALSE	chr1:243727071:G:A	113:chr1:243727071:G:A	0.000399

86_c3-1	86	TP53	MODIFIER; MODERATE	c.-29C>T; c.332C>T; c.449C>T; c.53C>T	; p.Thr111Ile; p.Thr150Ile; p.Thr18Ile	4	FALSE	chr17:7578481:G:A	113:chr17:7578481:G:A	0.000563
86_c3-1	86	ERBB2	MODERATE; MODIFIER	c.1628C>T; c.1673C>T; c.1718C>T; n.2042C>T	p.Ser543Leu; p.Ser558Leu; p.Ser573Leu;	1	FALSE	chr17:37872839:C:T	113:chr17:37872839:C:T	0.001217
86_c3-1	86	HGF	MODERATE	c.1172G>A; c.1187G>A	p.Gly391Asp; p.Gly396Asp	0	FALSE	chr7:81350145:C:T	113:chr7:81350145:C:T	0.000497
86_c3-1	86	NTRK1	MODERATE	c.1975C>T; c.2065C>T; c.2083C>T	p.Pro659Ser; p.Pro689Ser; p.Pro695Ser	2	FALSE	chr1:156849827:C:T	113:chr1:156849827:C:T	0.00048
86_c3-1	86	SMO	MODERATE	c.1082A>C	p.His361Pro	0	FALSE	chr7:128846152:A:C	113:chr7:128846152:A:C	0.000347
86_c3-1	86	EGFR	MODERATE	c.755G>A	p.Arg252His	3	FALSE	chr7:55221711:G:A	113:chr7:55221711:G:A	0.000804
86_c3-1	86	EPHA3	MODERATE	c.1543G>A	p.Ala515Thr	0	FALSE	chr3:89448579:G:A	113:chr3:89448579:G:A	0.000497
86_c3-1	86	PDGFRA	MODERATE	c.1198G>A	p.Asp400Asn	1	FALSE	chr4:55136876:G:A	113:chr4:55136876:G:A	0.000343
86_c3-1	86	KIT	MODERATE	c.2825G>A; c.2837G>A	p.Arg942Gln; p.Arg946Gln	1	FALSE	chr4:55604629:G:A	113:chr4:55604629:G:A	0.000551
86_c3-1	86	FGFR1	MODIFIER; MODERATE	c.-34C>T; c.158C>T; c.59C>T	; p.Thr53Ile; p.Thr20Ile	1	FALSE	chr8:38314906:G:A	113:chr8:38314906:G:A	0.000156
86_c3-1	86	TP53	MODERATE; MODIFIER	c.148C>T; c.265C>T; c.-279C>T; c.-360C>T	p.Pro50Ser; p.Pro89Ser;	3	FALSE	chr17:7579422:G:A	113:chr17:7579422:G:A	0.000472
86_c3-1	86	EGFR	MODIFIER; MODERATE	c.*2364G>A; c.2104G>A	; p.Ala702Thr	2	FALSE	chr7:55241656:G:A	113:chr7:55241656:G:A	0.000368
86_c3-1	86	RET	MODERATE	c.1690A>C	p.Thr564Pro	1	FALSE	chr10:43608342:A:C	113:chr10:43608342:A:C	0.011107
86_c3-1	86	SMO	HIGH	c.767G>A	p.Trp256*	0	FALSE	chr7:128845470:G:A	113:chr7:128845470:G:A	0.000306

86_c3-1	86	PIK3R1	HIGH	c.901C>T	p.Arg301*	1	FALSE	chr5:67576819:C:T	113:chr5:67576819:C:T	0.00043
86_c3-1	86	EGFR	MODIFIER; MODERATE	c.*1464G>A; c.1606G>A	; p.Val536Met	1	FALSE	chr7:55229299:G:A	113:chr7:55229299:G:A	0.000362
86_c3-1	86	TP53	MODERATE; MODIFIER	c.257C>T; c.374C>T; c.-279C>T; c.-360C>T	p.Thr86Met; p.Thr125Met;	18	FALSE	chr17:7579313:G:A	113:chr17:7579313:G:A	0.000609
86_c3-1	86	FGFR1; LETM2	MODERATE; MODIFIER	c.1927C>T; c.1933C>T; c.2170C>T; c.2194C>T; c.2200C>T; c.2293C>T; c.*1406G>A; c.*1423G>A; c.*1553G>A; c.*1567G>A; c.*1638G>A	p.Arg643Trp; p.Arg645Trp; p.Arg724Trp; p.Arg732Trp; p.Arg734Trp; p.Arg765Trp;	1	FALSE	chr8:38271528:G:A	113:chr8:38271528:G:A	0.000482
86_c3-1	86	ALK	MODERATE	c.536G>A	p.Arg179His	1	FALSE	chr2:30142990:C:T	113:chr2:30142990:C:T	0.000316
86_c3-1	86	ATM	HIGH	c.748C>T	p.Arg250*	0	FALSE	chr11:108115600:C:T	113:chr11:108115600:C:T	0.000388
86_c3-1	86	TP53	MODERATE	c.352T>G; c.433T>G; c.712T>G; c.829T>G	p.Cys118Gly; p.Cys145Gly; p.Cys238Gly; p.Cys277Gly	5	FALSE	chr17:7577109:A:C	113:chr17:7577109:A:C	0.000533
86_c3-1	86	CDKN2A	MODIFIER; MODERATE	c.194-3570C>G; c.50C>G	; p.Ala17Gly	1	FALSE	chr9:21974777:G:C	113:chr9:21974777:G:C	0.00182
86_c3-1	86	NOTCH1	MODERATE	c.5837G>A	p.Arg1946His	0	FALSE	chr9:139395101:C:T	113:chr9:139395101:C:T	0.000763
86_c3-1	86	CTNNB1	MODERATE	c.1406G>A	p.Arg469His	0	FALSE	chr3:41275240:G:A	113:chr3:41275240:G:A	0.000309

86_c3-1	86	MAP2K1	MODERATE	c.146G>A	p.Arg49His	1	FALSE	chr15:66727430:G:A	113:chr15:66727430:G:A	0.000386
86_c3-1	86	RET	MODERATE	c.1942G>A	p.Val648Ile	2	FALSE	chr10:43609990:G:A	113:chr10:43609990:G:A	0.000295
86_c3-1	86	PIK3CA	MODERATE	c.1357G>A	p.Glu453Lys	20	FALSE	chr3:178928079:G:A	113:chr3:178928079:G:A	0.000417
86_c3-1	86	EGFR	MODERATE	c.977G>A	p.Cys326Tyr	1	FALSE	chr7:55223610:G:A	113:chr7:55223610:G:A	0.000421
86_c3-1	86	TP53	MODERATE; MODIFIER	c.214C>T; c.97C>T; c.-279C>T; c.-360C>T	p.Pro72Ser; p.Pro33Ser;	3	FALSE	chr17:7579473:G:A	113:chr17:7579473:G:A	0.000449
86_c3-1	86	DDR2	MODERATE	c.700G>A	p.Asp234Asn	1	FALSE	chr1:162729614:G:A	113:chr1:162729614:G:A	0.000576
86_c3-1	86	NTRK3	MODERATE	c.1528C>T; c.1552C>T	p.Arg510Cys; p.Arg518Cys	0	FALSE	chr15:88576121:G:A	113:chr15:88576121:G:A	0.000387
86_c3-1	86	TP53	MODIFIER; MODERATE	c.-3G>A; c.358G>A; c.475G>A; c.79G>A	; p.Ala120Thr; p.Ala159Thr; p.Ala27Thr	23	FALSE	chr17:7578455:C:T	113:chr17:7578455:C:T	0.000533
86_c3-1	86	CWH43	MODERATE	c.782G>A; c.863G>A	p.Cys261Tyr; p.Cys288Tyr	0	FALSE	chr4:49005812:G:A	113:chr4:49005812:G:A	0.000359
86_c3-1	86	ATM	MODERATE	c.1048G>A	p.Ala350Thr	0	FALSE	chr11:108117837:G:A	113:chr11:108117837:G:A	0.000418
86_c3-1	86	PIK3CA	MODERATE	c.3129G>T	p.Met1043Ile	45	FALSE	chr3:178952074:G:T	113:chr3:178952074:G:T	0.003729
86_c3-1	86	MET	MODERATE	c.142G>A	p.Ala48Thr	1	FALSE	chr7:116339280:G:A	113:chr7:116339280:G:A	0.000485
86_c3-1	86	MET	HIGH	c.1619G>A	p.Trp540*	1	FALSE	chr7:116380997:G:A	113:chr7:116380997:G:A	0.000809
86_c3-1	86	ALK	MODERATE	c.4523G>A	p.Gly1508Asp	1	FALSE	chr2:29416430:C:T	113:chr2:29416430:C:T	0.000309
86_c3-1	86	ALK	MODERATE	c.3592C>T	p.Leu1198Phe	1	FALSE	chr2:29443625:G:A	113:chr2:29443625:G:A	0.000846

86_c3-1	86	FGFR2	MODERATE; MODIFIER	c.148C>T; c.226C>T; c.493C>T; n.795C>T	p.Arg50Trp; p.Arg76Trp; p.Arg165Trp;	1	FALSE	chr10:123310935:G:A	113:chr10:123310935:G:A	0.000615
86_c3-1	86	PIK3CA	MODERATE	c.3030G>A	p.Met1010Ile	1	FALSE	chr3:178951975:G:A	113:chr3:178951975:G:A	0.000504
86_c3-1	86	C9orf53; CDKN2A	MODIFIER; MODERATE; LOW	n.*616G>A; c.*223C>T; c.343C>T; c.300C>T	; p.Arg115Trp; p.Ala100Ala	1	FALSE	chr9:21971058:G:A	113:chr9:21971058:G:A	0.000416
86_c3-1	86	PKD1; TSC2	MODIFIER; MODERATE	c.*13118A>C; c.*13121A>C; c.4080T>G; c.4212T>G; c.4281T>G	; p.Ser1360Arg; p.Ser1404Arg; p.Ser1427Arg	0	FALSE	chr16:2134504:T:G	113:chr16:2134504:T:G	0.001604
86_c3-1	86	FGFR1	MODERATE	c.1060C>T; c.1066C>T; c.1303C>T; c.1327C>T; c.1333C>T; c.1426C>T	p.Arg354Trp; p.Arg356Trp; p.Arg435Trp; p.Arg443Trp; p.Arg445Trp; p.Arg476Trp	2	FALSE	chr8:38275843:G:A	113:chr8:38275843:G:A	0.000483
86_c3-1	86	C9orf53; CDKN2A	MODIFIER; MODERATE	n.*616A>C; c.*137T>G; c.214T>G; c.257T>G	; p.Cys72Gly; p.Leu86Arg	1	FALSE	chr9:21971144:A:C	113:chr9:21971144:A:C	0.000768
86_c3-1	86	TP53	MODERATE	c.335A>G; c.416A>G; c.695A>G; c.812A>G	p.Glu112Gly; p.Glu139Gly; p.Glu232Gly; p.Glu271Gly	8	FALSE	chr17:7577126:T:C	113:chr17:7577126:T:C	0.001805
86_c3-1	86	NOTCH1	MODERATE	c.3631C>T	p.Arg1211Trp	0	FALSE	chr9:139401769:G:A	113:chr9:139401769:G:A	0.000738
86_c3-1	86	CTNNB1	LOW	c.1956G>A	p.Ala652Ala	0	FALSE	chr3:41278080:G:A	113:chr3:41278080:G:A	0.000392

86_c3-1	86	IGF1R	MODERATE	c.2035G>A	p.Asp679Asn	0	FALSE	chr15:99459939:G:A	113:chr15:99459939:G:A	0.000459
86_c3-1	86	FGFR4	MODIFIER; MODERATE	c.1098-65G>A; c.1251+10G>A; c.1067G>A	; p.Arg356His	1	FALSE	chr5:176520342:G:A	113:chr5:176520342:G:A	0.000782
86_c3-1	86	FGFR1	LOW; MODIFIER; MODERATE	c.-25C>T; c.167C>T; c.68C>T	; p.Pro56Leu; p.Pro23Leu	1	FALSE	chr8:38314897:G:A	113:chr8:38314897:G:A	0.000165
86_c3-1	86	FGFR1	MODIFIER; MODERATE	c.92-1373C>T; c.208C>T; c.232C>T; c.331C>T	; p.Arg70Cys; p.Arg78Cys; p.Arg111Cys	1	FALSE	chr8:38287326:G:A	113:chr8:38287326:G:A	0.000223
86_c3-1	86	ALK	MODERATE	c.872G>A	p.Arg291His	1	FALSE	chr2:29917796:C:T	113:chr2:29917796:C:T	0.000481
86_c3-1	86	ERBB2; MIEN1; MIR4728	MODERATE; MODIFIER	c.2597G>A; c.2642G>A; c.2687G>A; n.3011G>A; c.*388C>T; n.-1G>A	p.Arg866His; p.Arg881His; p.Arg896His;	2	FALSE	chr17:37881617:G:A	113:chr17:37881617:G:A	0.000498
86_c3-1	86	EGFR	MODERATE	c.445C>T	p.Arg149Trp	1	FALSE	chr7:55214319:C:T	113:chr7:55214319:C:T	0.00042
86_c3-1	86	TP53	MODERATE	c.176T>G; c.257T>G; c.536T>G; c.653T>G	p.Val59Gly; p.Val86Gly; p.Val179Gly; p.Val218Gly	8	FALSE	chr17:7578196:A:C	113:chr17:7578196:A:C	0.00081
86_c3-1	86	CTNNB1	MODERATE	c.1604G>A	p.Arg535Gln	0	FALSE	chr3:41275709:G:A	113:chr3:41275709:G:A	0.000576
86_c3-1	86	MET	HIGH	c.2387C>A; c.2441C>A	p.Ser796*; p.Ser814*	1	FALSE	chr7:116403126:C:A	113:chr7:116403126:C:A	0.000351
86_c3-1	86	ATM	MODERATE	c.8558C>T	p.Thr2853Met	0	FALSE	chr11:108216609:C:T	113:chr11:108216609:C:T	0.0004

86_c3-1	86	FGFR3	MODIFIER; MODERATE	c.931-398C>T; c.1172C>T; c.1178C>T	; p.Ala391Val; p.Ala393Val	34	FALSE	chr4:1806153:C:T	113:chr4:1806153:C:T	0.000481
86_c3-1	86	EGFR	MODERATE	c.3025G>A	p.Asp1009Asn	1	FALSE	chr7:55268959:G:A	113:chr7:55268959:G:A	0.000385
86_c3-1	86	IGF1R	MODERATE	c.3430G>A; c.3433G>A	p.Glu1144Lys; p.Glu1145Lys	0	FALSE	chr15:99482565:G:A	113:chr15:99482565:G:A	0.000393
86_c3-1	86	TSC2	MODERATE	c.3032G>A; c.3164G>A	p.Gly1011Asp; p.Gly1055Asp	0	FALSE	chr16:2129309:G:A	113:chr16:2129309:G:A	0.000571
86_c3-1	86	EGFR	MODERATE	c.406C>A	p.Pro136Thr	1	FALSE	chr7:55211163:C:A	113:chr7:55211163:C:A	0.000502
86_c3-1	86	PIK3CA	MODERATE	c.333G>T	p.Lys111Asn	9	FALSE	chr3:178916946:G:T	113:chr3:178916946:G:T	0.004431
86_c3-1	86	CDH1	MODERATE	c.1204G>A	p.Asp402Asn	0	FALSE	chr16:68847282:G:A	113:chr16:68847282:G:A	0.000592
86_c3-1	86	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2515G>A; n.-1C>T	p.Ala839Thr;	4	FALSE	chr7:55259457:G:A	113:chr7:55259457:G:A	0.000408
86_c3-1	86	VHL	MODIFIER; MODERATE	c.341-3202C>T; c.412C>T	; p.Pro138Ser	0	FALSE	chr3:10188269:C:T	113:chr3:10188269:C:T	0.000389
86_c3-1	86	FGFR1	MODERATE	c.359C>T; c.365C>T; c.608C>T; c.626C>T; c.632C>T; c.725C>T	p.Ala120Val; p.Ala122Val; p.Ala203Val; p.Ala209Val; p.Ala211Val; p.Ala242Val	1	FALSE	chr8:38283753:G:A	113:chr8:38283753:G:A	0.000332
86_c3-1	86	CTNNB1	MODERATE	c.497T>G	p.Val166Gly	0	FALSE	chr3:41266826:T:G	113:chr3:41266826:T:G	0.000937
86_c3-1	86	KDR	MODERATE	c.2866C>T	p.Pro956Ser	1	FALSE	chr4:55961074:G:A	113:chr4:55961074:G:A	0.000365
86_c3-1	86	ATM	HIGH	c.6100C>T	p.Arg2034*	0	FALSE	chr11:108186742:C:T	113:chr11:108186742:C:T	0.00053
86_c3-1	86	SMO	MODERATE	c.469G>A	p.Val157Met	0	FALSE	chr7:128843362:G:A	113:chr7:128843362:G:A	0.000448
86_c3-1	86	APC	MODIFIER; MODERATE	c.676-8832G>A; c.647G>A	; p.Arg216Gln	0	FALSE	chr5:112128144:G:A	113:chr5:112128144:G:A	0.000448

86_c3-1	86	GAPDH; IFFO1; NCAPD2	MODERATE; MODIFIER	c.157G>A; c.283G>A; c.*1743C>T; c.*1746C>T; c.*1770C>T; n.*2798C>T; c.*4252G>A	p.Val53Ile; p.Val95Ile;	0	FALSE	chr12:6646132:G:A	113:chr12:6646132:G:A	0.000324
86_c3-1	86	PDGFRA	MODERATE	c.1495G>A	p.Val499Met	2	FALSE	chr4:55139834:G:A	113:chr4:55139834:G:A	0.00093
86_c3-1	86	EGFR	MODERATE	c.1159C>A	p.Leu387Met	1	FALSE	chr7:55224477:C:A	113:chr7:55224477:C:A	0.000381
86_c3-1	86	MET	MODERATE	c.487T>C	p.Ser163Pro	1	FALSE	chr7:116339625:T:C	113:chr7:116339625:T:C	0.004306
86_c3-1	86	SMO	MODERATE	c.1640G>A	p.Arg547His	0	FALSE	chr7:128850377:G:A	113:chr7:128850377:G:A	0.000653
86_c3-1	86	ALK	MODERATE	c.446C>T	p.Ala149Val	1	FALSE	chr2:30143080:G:A	113:chr2:30143080:G:A	0.000538
86_c3-1	86	IDH2; ZNF710	MODERATE; MODIFIER	c.1108G>A; c.718G>A; c.952G>A; c.*2147C>T	p.Ala370Thr; p.Ala240Thr; p.Ala318Thr;	1	FALSE	chr15:90628303:C:T	113:chr15:90628303:C:T	0.000453
86_c3-1	86	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2518G>A; n.-1C>T	p.Ala840Thr;	2	FALSE	chr7:55259460:G:A	113:chr7:55259460:G:A	0.000407
86_c3-1	86	TP53	MODERATE	c.137A>C; c.416A>C; c.533A>C; c.56A>C	p.His46Pro; p.His139Pro; p.His178Pro; p.His19Pro	10	FALSE	chr17:7578397:T:G	113:chr17:7578397:T:G	0.002984
86_c3-1	86	TP53	MODIFIER; MODERATE	c.*109G>A; c.*197G>A; c.1090G>A; c.613G>A; c.694G>A; c.973G>A	; p.Ala364Thr; p.Ala205Thr; p.Ala232Thr; p.Ala325Thr	1	FALSE	chr17:7573937:C:T	113:chr17:7573937:C:T	0.000494

86_c3-1	86	GNA11	MODERATE	c.1052T>C	p.Leu351Pro	1	FALSE	chr19:3121149:T:C	113:chr19:3121149:T:C	0.000962
86_c3-1	86	KIT	MODERATE	c.1403C>T	p.Pro468Leu	2	FALSE	chr4:55592079:C:T	113:chr4:55592079:C:T	0.000342
86_c3-1	86	KDR	MODERATE	c.2315C>T	p.Ala772Val	1	FALSE	chr4:55964922:G:A	113:chr4:55964922:G:A	0.000578
86_c3-1	86	FGFR3	MODERATE	c.1162G>A; c.1498G>A; c.1504G>A	p.Ala388Thr; p.Ala500Thr; p.Ala502Thr	1	FALSE	chr4:1807167:G:A	113:chr4:1807167:G:A	0.000443
86_c3-1	86	NF1	MODERATE	c.4321C>T; c.4384C>T	p.Arg1441Trp; p.Arg1462Trp	1	FALSE	chr17:29586101:C:T	113:chr17:29586101:C:T	0.000432
86_c3-1	86	PIK3CA	MODERATE	c.3012G>A	p.Met1004Ile	8	FALSE	chr3:178951957:G:A	113:chr3:178951957:G:A	0.000342
86_c3-1	86	KRAS	MODERATE	c.35G>A	p.Gly12Asp	11213	FALSE	chr12:25398284:C:T	113:chr12:25398284:C:T	0.000358
86_c3-1	86	FGFR2	MODIFIER; MODERATE	c.939+4740G>A; c.1165G>A; c.1168G>A; c.820G>A; c.829G>A; c.898G>A; c.901G>A; n.1615G>A	; p.Ala389Thr; p.Ala390Thr; p.Ala274Thr; p.Ala277Thr; p.Ala300Thr; p.Ala301Thr	1	FALSE	chr10:123274753:C:T	113:chr10:123274753:C:T	0.000336
86_c3-1	86	EGFR	MODIFIER; MODERATE	c.*2364G>A; c.2156G>A	; p.Gly719Asp	51	FALSE	chr7:55241708:G:A	113:chr7:55241708:G:A	0.000388
86_c3-1	86	BRAF	MODERATE	c.1061G>A	p.Arg354Gln	3	FALSE	chr7:140494187:C:T	113:chr7:140494187:C:T	0.000439
86_c3-1	86	IGF1R	MODERATE	c.2824G>A; c.2827G>A	p.Ala942Thr; p.Ala943Thr	0	FALSE	chr15:99472831:G:A	113:chr15:99472831:G:A	0.000742
86_c3-1	86	TP53	MODERATE; MODIFIER	c.134C>T; c.251C>T; c.-279C>T; c.-360C>T	p.Ala45Val; p.Ala84Val;	4	FALSE	chr17:7579436:G:A	113:chr17:7579436:G:A	0.0007
86_c3-1	86	TSC2	MODERATE	c.673G>A	p.Val225Met	0	FALSE	chr16:2106669:G:A	113:chr16:2106669:G:A	0.000499

86_c3-1	86	NTRK3	MODIFIER; MODERATE	c.1205-1502C>T; c.1211C>T	; p.Thr404Met	0	FALSE	chr15:88671959:G:A	113:chr15:88671959:G:A	0.000393
86_c3-1	86	PHLPP1	MODERATE	c.3499G>A	p.Ala1167Thr	0	FALSE	chr18:60630644:G:A	113:chr18:60630644:G:A	0.000459
86_c3-1	86	HRAS; LRRC56	MODERATE; MODIFIER	c.248C>T; c.-506G>A	p.Ala83Val;	1	FALSE	chr11:533808:G:A	113:chr11:533808:G:A	0.000913
86_c3-1	86	FGFR3; LETM1	MODERATE; MODIFIER	c.1808A>T; c.2144A>T; c.2150A>T; c.*2517T>A	p.Lys603Met; p.Lys715Met; p.Lys717Met;	1	FALSE	chr4:1808386:A:T	113:chr4:1808386:A:T	0.000557
86_c3-1	86	FGFR1	MODIFIER; MODERATE	c.92-1469C>T; c.112C>T; c.136C>T; c.235C>T	; p.His38Tyr; p.His46Tyr; p.His79Tyr	1	FALSE	chr8:38287422:G:A	113:chr8:38287422:G:A	0.000278
86_c3-1	86	CDH1	MODERATE	c.394G>A	p.Val132Ile	0	FALSE	chr16:68842333:G:A	113:chr16:68842333:G:A	0.000377
86_c3-1	86	ERBB2; MIEN1; MIR4728	MODIFIER; MODERATE	c.3160-213A>G; c.3251A>G; c.3296A>G; c.3341A>G; n.3665A>G; c.*388T>C; n.*67A>G	; p.Glu1084Gly; p.Glu1099Gly; p.Glu1114Gly	1	FALSE	chr17:37883729:A:G	113:chr17:37883729:A:G	0.001338
86_c3-1	86	CTNNB1	MODERATE	c.86C>A	p.Ser29Tyr	0	FALSE	chr3:41266089:C:A	113:chr3:41266089:C:A	0.000387
86_c3-1	86	STK11	MODERATE	c.1105C>T	p.Pro369Ser	1	FALSE	chr19:1223168:C:T	113:chr19:1223168:C:T	0.000545
86_c3-1	86	PIK3CA	MODERATE	c.1633G>A	p.Glu545Lys	1189	FALSE	chr3:178936091:G:A	113:chr3:178936091:G:A	0.012058
86_c3-1	86	EGFR	MODIFIER; MODERATE	c.*1464G>A; c.1321G>A	; p.Val441Ile	1	FALSE	chr7:55227854:G:A	113:chr7:55227854:G:A	0.000412
86_c3-1	86	HGF	HIGH	c.1582C>T; c.1597C>T	p.Arg528*; p.Arg533*	0	FALSE	chr7:81336625:G:A	113:chr7:81336625:G:A	0.000577

86_c3-1	86	NF1	HIGH	c.3916C>T	p.Arg1306*	8	FALSE	chr17:29562981:C:T	113:chr17:29562981:C:T	0.000359
86_c3-1	86	FGFR2	MODERATE; MODIFIER	c.263G>A; c.341G>A; c.608G>A; n.910G>A	p.Arg88His; p.Arg114His; p.Arg203His;	2	FALSE	chr10:123310820:C:T	113:chr10:123310820:C:T	0.001122
86_c3-1	86	ERBB2	MODERATE; MODIFIER	c.632C>T; c.677C>T; c.722C>T; n.1046C>T	p.Ala211Val; p.Ala226Val; p.Ala241Val;	2	FALSE	chr17:37866417:C:T	113:chr17:37866417:C:T	0.000487
86_c3-1	86	NF1	MODERATE	c.2740C>T	p.Arg914Trp	1	FALSE	chr17:29556373:C:T	113:chr17:29556373:C:T	0.000517
86_c3-1	86	TSC1	MODERATE	c.388C>T; c.541C>T	p.His130Tyr; p.His181Tyr	0	FALSE	chr9:135797328:G:A	113:chr9:135797328:G:A	0.000501
86_c3-1	86	FBXW7	MODERATE	c.1160G>A; c.1274G>A; c.1514G>A	p.Arg387His; p.Arg425His; p.Arg505His	0	FALSE	chr4:153247288:C:T	113:chr4:153247288:C:T	0.001032
86_c3-1	86	KIT	MODERATE	c.506G>A	p.Gly169Asp	1	FALSE	chr4:55564618:G:A	113:chr4:55564618:G:A	0.00034
86_c3-1	86	MIR4673; NOTCH1	MODIFIER; MODERATE	n.-1C>T; c.392C>T	; p.Pro131Leu	0	FALSE	chr9:139418180:G:A	113:chr9:139418180:G:A	0.00053
86_c3-1	86	SMO	MODERATE	c.961G>A	p.Val321Met	0	FALSE	chr7:128846031:G:A	113:chr7:128846031:G:A	0.000284
86_c3-1	86	KDR	MODERATE	c.1193T>C	p.Val398Ala	1	FALSE	chr4:55976632:A:G	113:chr4:55976632:A:G	0.000577
86_c3-1	86	DDR2	MODERATE	c.2141G>A	p.Arg714Gln	1	FALSE	chr1:162746018:G:A	113:chr1:162746018:G:A	0.000495
86_c3-1	86	CTNNB1	MODERATE	c.91C>A	p.Leu31Met	0	FALSE	chr3:41266094:C:A	113:chr3:41266094:C:A	0.00038
86_c3-1	86	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2305G>A; n.1257C>T	p.Val769Met;	3	FALSE	chr7:55249007:G:A	113:chr7:55249007:G:A	0.000579
86_c3-1	86	NF1	MODERATE	c.103A>G	p.Ser35Gly	1	FALSE	chr17:29483043:A:G	113:chr17:29483043:A:G	0.000432
86_c3-1	86	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2612C>T; n.-1G>A	p.Ala871Val;	3	FALSE	chr7:55259554:C:T	113:chr7:55259554:C:T	0.000549

86_c3-1	86	FGFR1	MODERATE	c.292C>T; c.298C>T; c.541C>T; c.559C>T; c.565C>T; c.658C>T	p.Arg98Cys; p.Arg100Cys; p.Arg181Cys; p.Arg187Cys; p.Arg189Cys; p.Arg220Cys	1	FALSE	chr8:38285495:G:A	113:chr8:38285495:G:A	0.00063
86_c3-1	86	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2327G>A; n.1235C>T	p.Arg776His;	7	FALSE	chr7:55249029:G:A	113:chr7:55249029:G:A	0.000495
86_c3-1	86	CTNNB1	MODERATE	c.125C>T	p.Thr42Ile	0	FALSE	chr3:41266128:C:T	113:chr3:41266128:C:T	0.000377
86_c3-1	86	FGFR4	MODERATE	c.1745G>A; c.1829G>A; c.1949G>A	p.Arg582His; p.Arg610His; p.Arg650His	1	FALSE	chr5:176523292:G:A	113:chr5:176523292:G:A	0.001006
86_c3-1	86	FGFR1	MODERATE	c.475C>T; c.481C>T; c.724C>T; c.742C>T; c.748C>T; c.841C>T	p.Arg159Trp; p.Arg161Trp; p.Arg242Trp; p.Arg248Trp; p.Arg250Trp; p.Arg281Trp	2	FALSE	chr8:38282215:G:A	113:chr8:38282215:G:A	0.000639
86_c3-1	86	ALK	HIGH	c.4414G>T	p.Glu1472*	1	FALSE	chr2:29416539:C:A	113:chr2:29416539:C:A	0.000288
86_c3-1	86	CDH1	MODERATE	c.1901C>T	p.Ala634Val	0	FALSE	chr16:68856093:C:T	113:chr16:68856093:C:T	0.000474
86_c3-1	86	DDR2	MODERATE	c.1624G>A	p.Ala542Thr	1	FALSE	chr1:162741933:G:A	113:chr1:162741933:G:A	0.000504
86_c3-1	86	EGFR	MODERATE	c.1789G>A	p.Ala597Thr	1	FALSE	chr7:55233039:G:A	113:chr7:55233039:G:A	0.000999
86_c3-1	86	ATM	MODERATE	c.5833G>A	p.Ala1945Thr	0	FALSE	chr11:108180957:G:A	113:chr11:108180957:G:A	0.000386
86_c3-1	86	CDKN2A	MODIFIER; MODERATE	c.194-3567C>T; c.53C>T	; p.Thr18Met	1	FALSE	chr9:21974774:G:A	113:chr9:21974774:G:A	0.000505
86_c3-1	86	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2575G>A; n.-1C>T	p.Ala859Thr;	4	FALSE	chr7:55259517:G:A	113:chr7:55259517:G:A	0.000617
86_c3-1	86	NOTCH1	MODERATE	c.5098G>A	p.Ala1700Thr	0	FALSE	chr9:139397703:C:T	113:chr9:139397703:C:T	0.000493

86_c3-1	86	TP53	MODERATE	c.350C>T; c.431C>T; c.710C>T; c.827C>T	p.Ala117Val; p.Ala144Val; p.Ala237Val; p.Ala276Val	10	FALSE	chr17:7577111:G:A	113:chr17:7577111:G:A	0.000354
86_c3-1	86	TP53	HIGH	c.160C>T; c.241C>T; c.520C>T; c.637C>T	p.Arg54*; p.Arg81*; p.Arg174*; p.Arg213*	291	FALSE	chr17:7578212:G:A	113:chr17:7578212:G:A	0.000482
86_c3-1	86	ALK	MODERATE	c.617C>T	p.Ala206Val	2	FALSE	chr2:30142909:G:A	113:chr2:30142909:G:A	0.000415
86_c3-1	86	NRAS	MODERATE	c.394G>A	p.Glu132Lys	2	FALSE	chr1:115252246:C:T	113:chr1:115252246:C:T	0.000368
86_c3-1	86	SMO	MODERATE	c.1193G>A	p.Arg398Gln	0	FALSE	chr7:128846357:G:A	113:chr7:128846357:G:A	0.000291
86_c3-1	86	TP53	MODERATE	c.323G>T; c.404G>T; c.683G>T; c.800G>T	p.Arg108Leu; p.Arg135Leu; p.Arg228Leu; p.Arg267Leu	18	FALSE	chr17:7577138:C:A	113:chr17:7577138:C:A	0.000402
86_c3-1	86	CTNNB1	MODERATE	c.59C>T	p.Ala20Val	0	FALSE	chr3:41266062:C:T	113:chr3:41266062:C:T	0.000788
86_c3-1	86	ALK	MODERATE	c.3626G>A	p.Arg1209Gln	2	FALSE	chr2:29443591:C:T	113:chr2:29443591:C:T	0.000501
86_c3-1	86	TP53	MODERATE; MODIFIER	c.206C>T; c.89C>T; c.-279C>T; c.-360C>T	p.Ala69Val; p.Ala30Val;	3	FALSE	chr17:7579481:G:A	113:chr17:7579481:G:A	0.000446
86_c3-1	86	PDGFRA	MODERATE	c.1013A>G	p.Glu338Gly	2	FALSE	chr4:55133800:A:G	113:chr4:55133800:A:G	0.000429
86_c3-1	86	VHL	MODIFIER; MODERATE	c.341-3270A>C; c.344A>C	; p.His115Pro	0	FALSE	chr3:10188201:A:C	113:chr3:10188201:A:C	0.002153
86_c3-1	86	APC	MODERATE	c.1198G>A; c.1252G>A	p.Glu400Lys; p.Glu418Lys	0	FALSE	chr5:112154981:G:A	113:chr5:112154981:G:A	0.000356
86_c3-1	86	ALK	MODERATE	c.584C>T	p.Ala195Val	1	FALSE	chr2:30142942:G:A	113:chr2:30142942:G:A	0.000617

86_c3-1	86	ERBB2; MIR4728	MODERATE; MODIFIER	c.2211C>G; c.2256C>G; c.2301C>G; n.2625C>G; n.-1C>G	p.Ile737Met; p.Ile752Met; p.Ile767Met;	6	FALSE	chr17:37880257:C:G	113:chr17:37880257:C:G	0.020701
86_c3-1	86	RPL19	MODERATE	c.406C>T	p.Arg136Trp	0	FALSE	chr17:37360379:C:T	113:chr17:37360379:C:T	0.000543
86_c3-1	86	ATM	MODERATE	c.1619G>A	p.Cys540Tyr	0	FALSE	chr11:108122575:G:A	113:chr11:108122575:G:A	0.000405
86_c3-1	86	MAP2K2	MODERATE	c.169T>C	p.Phe57Leu	0	FALSE	chr19:4117551:A:G	113:chr19:4117551:A:G	0.000487
86_c3-1	86	CTNNB1	MODERATE	c.1346G>A	p.Arg449His	0	FALSE	chr3:41275180:G:A	113:chr3:41275180:G:A	0.000305
86_c3-1	86	ERBB2; MIEN1; MIR4728	MODERATE; MODIFIER	c.3025G>A; c.3070G>A; c.3115G>A; n.3439G>A; c.*388C>T; n.*67G>A	p.Ala1009Thr; p.Ala1024Thr; p.Ala1039Thr;	2	FALSE	chr17:37883212:G:A	113:chr17:37883212:G:A	0.001036
86_c3-1	86	PIK3R1	MODERATE	c.514G>A	p.Val172Met	1	FALSE	chr5:67575441:G:A	113:chr5:67575441:G:A	0.000477
86_c3-1	86	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2614G>A; n.-1C>T	p.Glu872Lys;	1	FALSE	chr7:55259556:G:A	113:chr7:55259556:G:A	0.000562
86_c3-1	86	SMO	MODERATE	c.628G>A	p.Val210Met	0	FALSE	chr7:128845134:G:A	113:chr7:128845134:G:A	0.000358
86_c3-1	86	MAP2K1	MODERATE	c.361T>A	p.Cys121Ser	4	FALSE	chr15:66729153:T:A	113:chr15:66729153:T:A	0.000479
86_c3-1	86	MAP2K1	MODERATE	c.379G>A	p.Val127Met	1	FALSE	chr15:66729171:G:A	113:chr15:66729171:G:A	0.000452
86_c3-1	86	NF1	MODERATE	c.8170G>A; c.8233G>A	p.Gly2724Arg; p.Gly2745Arg	2	FALSE	chr17:29687577:G:A	113:chr17:29687577:G:A	0.000373
86_c3-1	86	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2591C>T; n.-1G>A	p.Ala864Val;	2	FALSE	chr7:55259533:C:T	113:chr7:55259533:C:T	0.000651

86_c3-1	86	ERBB2	MODERATE; MODIFIER	c.1306G>A; c.1351G>A; c.1396G>A; n.1720G>A	p.Ala436Thr; p.Ala451Thr; p.Ala466Thr;	1	FALSE	chr17:37872075:G:A	113:chr17:37872075:G:A	0.000341
86_c3-1	86	CDH1	MODERATE	c.2204C>T	p.Ala735Val	0	FALSE	chr16:68862116:C:T	113:chr16:68862116:C:T	0.00033
86_c3-1	86	EPHA3	MODERATE	c.1516G>A	p.Val506Ile	0	FALSE	chr3:89448552:G:A	113:chr3:89448552:G:A	0.000517
86_c3-1	86	EGFR	MODERATE	c.866C>T	p.Ala289Val	34	FALSE	chr7:55221822:C:T	113:chr7:55221822:C:T	0.000399
86_c3-1	86	FGFR1	MODERATE	c.1013C>T; c.1019C>T; c.1112C>T; c.746C>T; c.752C>T; c.995C>T	p.Thr338Met; p.Thr340Met; p.Thr371Met; p.Thr249Met; p.Thr251Met; p.Thr332Met	2	FALSE	chr8:38279377:G:A	113:chr8:38279377:G:A	0.000584
86_c3-1	86	AKT1	MODERATE	c.238T>C	p.Trp80Arg	2	FALSE	chr14:105243045:A:G	113:chr14:105243045:A:G	0.000448
86_c3-1	86	FGFR3	MODERATE	c.905G>A	p.Gly302Asp	1	FALSE	chr4:1803727:G:A	113:chr4:1803727:G:A	0.000865
86_c3-1	86	RET	MODERATE	c.2267C>T	p.Ala756Val	1	FALSE	chr10:43612162:C:T	113:chr10:43612162:C:T	0.00044
86_c3-1	86	INSRR; NTRK1	MODIFIER; MODERATE	c.3397+13C>T; c.28G>A	; p.Ala10Thr	1	FALSE	chr1:156811891:G:A	113:chr1:156811891:G:A	0.000327
86_c3-1	86	KIT	MODERATE	c.2651G>A; c.2663G>A	p.Arg884Gln; p.Arg888Gln	3	FALSE	chr4:55602953:G:A	113:chr4:55602953:G:A	0.000315
86_c3-1	86	KDR	MODERATE	c.2323G>T	p.Ala775Ser	1	FALSE	chr4:55964914:C:A	113:chr4:55964914:C:A	0.004261

86_c3-1	86	FGFR1; LETM2	MODERATE; MODIFIER	c.1777T>G; c.1783T>G; c.2020T>G; c.2044T>G; c.2050T>G; c.2143T>G; c.*1406A>C; c.*1423A>C; c.*1553A>C; c.*1567A>C; c.*1638A>C	p.Trp593Gly; p.Trp595Gly; p.Trp674Gly; p.Trp682Gly; p.Trp684Gly; p.Trp715Gly;	1	FALSE	chr8:38271806:A:C	113:chr8:38271806:A:C	0.001329
86_c3-1	86	PIK3CA	MODERATE	c.2078G>A	p.Arg693His	1	FALSE	chr3:178938836:G:A	113:chr3:178938836:G:A	0.000921
86_c3-1	86	ALK	MODERATE	c.3599C>T	p.Ala1200Val	2	FALSE	chr2:29443618:G:A	113:chr2:29443618:G:A	0.000429
86_c3-1	86	C9orf53; CDKN2A	MODIFIER; MODERATE	n.*616C>G; c.*140G>C; c.217G>C; c.260G>C	; p.Ala73Pro; p.Arg87Pro	1	FALSE	chr9:21971141:C:G	113:chr9:21971141:C:G	0.01012
86_c3-1	86	IGF1R	MODERATE	c.3905T>C; c.3908T>C	p.Val1302Ala; p.Val1303Ala	0	FALSE	chr15:99500475:T:C	113:chr15:99500475:T:C	0.005192
86_c3-1	86	EGFR	MODERATE	c.1774G>A	p.Val592Ile	1	FALSE	chr7:55233024:G:A	113:chr7:55233024:G:A	0.000472
86_c3-1	86	PIK3CA	MODERATE	c.1531G>A	p.Ala511Thr	1	FALSE	chr3:178928345:G:A	113:chr3:178928345:G:A	0.000456
86_c3-1	86	FGFR1	MODERATE	c.1424A>G; c.1430A>G; c.1667A>G; c.1691A>G; c.1697A>G; c.1790A>G	p.Lys475Arg; p.Lys477Arg; p.Lys556Arg; p.Lys564Arg; p.Lys566Arg; p.Lys597Arg	1	FALSE	chr8:38273545:T:C	113:chr8:38273545:T:C	0.000639

86_c3-1	86	ERBB2; MIEN1; MIR4728	MODERATE; MODIFIER	c.2600G>A; c.2645G>A; c.2690G>A; n.3014G>A; c.*388C>T; n.-1G>A	p.Arg867Gln; p.Arg882Gln; p.Arg897Gln;	2	FALSE	chr17:37881620:G:A	113:chr17:37881620:G:A	0.000496
86_c3-1	86	MET	MODERATE	c.3973G>A; c.4027G>A	p.Glu1325Lys; p.Glu1343Lys	1	FALSE	chr7:116435978:G:A	113:chr7:116435978:G:A	0.00035
86_c3-1	86	C9orf53; CDKN2A	MODIFIER; MODERATE	n.*616G>A; c.*324C>T; c.*45C>T; c.401C>T	; p.Ala134Val	1	FALSE	chr9:21970957:G:A	113:chr9:21970957:G:A	0.000459
86_c3-1	86	CTNNB1	MODERATE	c.643G>A	p.Ala215Thr	0	FALSE	chr3:41266972:G:A	113:chr3:41266972:G:A	0.000492
86_c3-1	86	MIR4673; NOTCH1	MODIFIER; MODERATE	n.*59C>T; c.1057C>T	; p.Arg353Cys	0	FALSE	chr9:139413085:G:A	113:chr9:139413085:G:A	0.000538
86_c3-1	86	MITF	MODIFIER; MODERATE	c.93+143C>T; c.236C>T; c.401C>T; c.509C>T; c.554C>T; c.557C>T	; p.Thr79Met; p.Thr134Met; p.Thr170Met; p.Thr185Met; p.Thr186Met	0	FALSE	chr3:69987175:C:T	113:chr3:69987175:C:T	0.000469
86_c3-1	86	KLLN; PTEN	MODIFIER; MODERATE	c.-951T>C; c.20A>G	; p.Glu7Gly	1	FALSE	chr10:89624246:A:G	113:chr10:89624246:A:G	0.000524
86_c3-1	86	C9orf53; CDKN2A	MODIFIER; MODERATE; LOW	n.*616T>G; c.*120A>C; c.197A>C; c.240A>C	; p.His66Pro; p.Pro80Pro	1	FALSE	chr9:21971161:T:G	113:chr9:21971161:T:G	0.02448
86_c3-1	86	PIK3R1	MODERATE	c.553G>A	p.Ala185Thr	1	FALSE	chr5:67575480:G:A	113:chr5:67575480:G:A	0.00039
86_c3-1	86	EPHA3	MODERATE	c.485T>C	p.Leu162Pro	0	FALSE	chr3:89259341:T:C	113:chr3:89259341:T:C	0.000518
86_c3-1	86	FBXW7	HIGH	c.310C>T; c.424C>T; c.664C>T	p.Arg104*; p.Arg142*; p.Arg222*	0	FALSE	chr4:153268144:G:A	113:chr4:153268144:G:A	0.000351

86_c3-1	86	INSRR; NTRK1	MODIFIER; MODERATE	c.3397+28C>T; c.13G>A	; p.Ala5Thr	3	FALSE	chr1:156811876:G:A	113:chr1:156811876:G:A	0.000343
86_c3-1	86	ERBB2; MIEN1; MIR4728	MODERATE; MODIFIER	c.2261G>A; c.2306G>A; c.2351G>A; n.2675G>A; c.*388C>T; n.-1G>A	p.Arg754His; p.Arg769His; p.Arg784His;	1	FALSE	chr17:37881022:G:A	113:chr17:37881022:G:A	0.000345
86_c3-1	86	TSC2	MODERATE	c.2152C>T	p.Arg718Cys	0	FALSE	chr16:2122296:C:T	113:chr16:2122296:C:T	0.00033
86_c3-1	86	IDH1	MODERATE	c.941G>A	p.Arg314His	1	FALSE	chr2:209104637:C:T	113:chr2:209104637:C:T	0.000368
86_c3-1	86	EGFR	MODIFIER; MODERATE	c.*1464C>A; c.1621C>A	; p.Leu541Ile	1	FALSE	chr7:55229314:C:A	113:chr7:55229314:C:A	0.000416
86_c3-1	86	ESR1	MODERATE	c.932C>T; c.935C>T; c.941C>T	p.Ala311Val; p.Ala312Val; p.Ala314Val	0	FALSE	chr6:152265482:C:T	113:chr6:152265482:C:T	0.000615
86_c3-1	86	FGFR4	MODIFIER; MODERATE	c.1058-174G>A; c.1078G>A	; p.Ala360Thr	1	FALSE	chr5:176520159:G:A	113:chr5:176520159:G:A	0.000759
86_c3-1	86	FGFR3	MODERATE	c.1526G>A; c.1862G>A; c.1868G>A	p.Arg509His; p.Arg621His; p.Arg623His	2	FALSE	chr4:1807803:G:A	113:chr4:1807803:G:A	0.000868
86_c3-1	86	NTRK3	MODERATE	c.995C>T	p.Thr332Met	0	FALSE	chr15:88678541:G:A	113:chr15:88678541:G:A	0.000356
86_c3-1	86	FBXW7	MODERATE	c.1183A>G; c.1297A>G; c.1537A>G	p.Arg395Gly; p.Arg433Gly; p.Arg513Gly	0	FALSE	chr4:153247265:T:C	113:chr4:153247265:T:C	0.001693
86_c3-1	86	PKD1; TSC2	MODIFIER; MODERATE	c.*13118C>T; c.*13121C>T; c.4192G>A; c.4324G>A; c.4393G>A	; p.Asp1398Asn; p.Asp1442Asn; p.Asp1465Asn	0	FALSE	chr16:2134616:G:A	113:chr16:2134616:G:A	0.000306
86_c3-1	86	KIT	MODERATE	c.682G>A	p.Glu228Lys	1	FALSE	chr4:55565858:G:A	113:chr4:55565858:G:A	0.000585

86_c3-1	86	CWH43	MODERATE	c.1535G>A; c.1616G>A	p.Gly512Asp; p.Gly539Asp	0	FALSE	chr4:49034690:G:A	113:chr4:49034690:G:A	0.000553
86_c3-1	86	NRAS	MODERATE	c.490C>T	p.Arg164Cys	1	FALSE	chr1:115251236:G:A	113:chr1:115251236:G:A	0.000395
86_c3-1	86	C9orf53; CDKN2A	MODIFIER; MODERATE	n.*616C>T; c.*176G>A; c.253G>A; c.296G>A	; p.Ala85Thr; p.Arg99His	1	FALSE	chr9:21971105:C:T	113:chr9:21971105:C:T	0.000463
86_c3-1	86	EGFR	MODERATE	c.185T>C	p.Leu62Pro	7	FALSE	chr7:55210075:T:C	113:chr7:55210075:T:C	0.000395
86_c3-1	86	ALK	MODERATE	c.1316G>T	p.Ser439Ile	1	FALSE	chr2:29551314:C:A	113:chr2:29551314:C:A	0.000323
86_c3-1	86	NOTCH1	MODERATE	c.4571C>T	p.Ala1524Val	0	FALSE	chr9:139399777:G:A	113:chr9:139399777:G:A	0.000987
86_c3-1	86	CDH1	MODERATE	c.1058A>G	p.Glu353Gly	0	FALSE	chr16:68846087:A:G	113:chr16:68846087:A:G	0.000808
86_c3-1	86	AR	MODERATE	c.2131A>G; c.535A>G	p.Arg711Gly; p.Arg179Gly	0	FALSE	chrX:66931489:A:G	113:chrX:66931489:A:G	0.00037
86_c3-1	86	RET	MODERATE	c.2038G>A	p.Ala680Thr	1	FALSE	chr10:43610086:G:A	113:chr10:43610086:G:A	0.00043
86_c3-1	86	HOXD-AS2; HOXD8	MODIFIER; HIGH	n.*692G>A; c.-99C>T; c.454C>T	; p.Gln152*	0	FALSE	chr2:176995548:C:T	113:chr2:176995548:C:T	0.000407
86_c3-1	86	TP53	MODIFIER; MODERATE	c.-57T>C; c.25T>C; c.304T>C; c.421T>C	; p.Cys9Arg; p.Cys102Arg; p.Cys141Arg	23	FALSE	chr17:7578509:A:G	113:chr17:7578509:A:G	0.000371
86_c3-1	86	NOTCH1	MODERATE	c.5885G>A	p.Arg1962His	0	FALSE	chr9:139395053:C:T	113:chr9:139395053:C:T	0.000785
86_c3-1	86	FGFR3	MODIFIER; MODERATE	c.931-308G>A; c.1262G>A; c.1268G>A	; p.Arg421Gln; p.Arg423Gln	1	FALSE	chr4:1806243:G:A	113:chr4:1806243:G:A	0.000401
86_c3-1	86	KIT	MODERATE	c.25G>A	p.Asp9Asn	1	FALSE	chr4:55524206:G:A	113:chr4:55524206:G:A	0.000368

86_c3-1	86	ERBB2; MIEN1; MIR4728	MODERATE; MODIFIER	c.2720A>G; c.2765A>G; c.2810A>G; n.3134A>G; c.*388T>C; n.-1A>G	p.Lys907Arg; p.Lys922Arg; p.Lys937Arg;	1	FALSE	chr17:37882044:A:G	113:chr17:37882044:A:G	0.000565
86_c3-1	86	KIT	MODERATE	c.1835C>T; c.1847C>T	p.Ala612Val; p.Ala616Val	1	FALSE	chr4:55594061:C:T	113:chr4:55594061:C:T	0.000519
86_c3-1	86	NF1	MODERATE	c.5582G>A; c.5645G>A	p.Cys1861Tyr; p.Cys1882Tyr	1	FALSE	chr17:29657349:G:A	113:chr17:29657349:G:A	0.000597
86_c3-1	86	TP53	MODERATE	c.127C>T; c.406C>T; c.46C>T; c.523C>T	p.Arg43Cys; p.Arg136Cys; p.Arg16Cys; p.Arg175Cys	20	FALSE	chr17:7578407:G:A	113:chr17:7578407:G:A	0.000325
86_c3-1	86	FLT3	MODERATE	c.2039C>T	p.Ala680Val	0	FALSE	chr13:28602329:G:A	113:chr13:28602329:G:A	0.000584
86_c3-1	86	NF1	MODERATE	c.2695T>G	p.Leu899Val	3	FALSE	chr17:29556328:T:G	113:chr17:29556328:T:G	0.003988
86_c3-1	86	TP53	MODIFIER; MODERATE	c.-11C>T; c.-92C>T; c.269C>T; c.386C>T	; p.Ala90Val; p.Ala129Val	2	FALSE	chr17:7578544:G:A	113:chr17:7578544:G:A	0.000352
86_c3-1	86	NF1	MODERATE	c.2659G>A	p.Ala887Thr	1	FALSE	chr17:29556292:G:A	113:chr17:29556292:G:A	0.000678
86_c3-1	86	VHL	MODIFIER; MODERATE	c.341-3226G>A; c.388G>A	; p.Val130Ile	0	FALSE	chr3:10188245:G:A	113:chr3:10188245:G:A	0.000367
86_c3-1	86	GAPDH; IFFO1	MODERATE; MODIFIER	c.773G>A; c.899G>A; c.*1743C>T; c.*1746C>T; c.*1770C>T; n.*2798C>T	p.Gly258Asp; p.Gly300Asp;	0	FALSE	chr12:6647123:G:A	113:chr12:6647123:G:A	0.000319
86_c3-1	86	PTEN	MODERATE	c.698G>A	p.Arg233Gln	2	FALSE	chr10:89717673:G:A	113:chr10:89717673:G:A	0.0004

86_c3-1	86	EPHA3	MODERATE	c.1535G>A	p.Arg512Gln	0	FALSE	chr3:89448571:G:A	113:chr3:89448571:G:A	0.000499
86_c3-1	86	TSC2	MODERATE	c.2807G>A	p.Arg936Gln	0	FALSE	chr16:2126556:G:A	113:chr16:2126556:G:A	0.000576
86_c3-1	86	ALK	MODERATE	c.4192C>T	p.Pro1398Ser	1	FALSE	chr2:29416761:G:A	113:chr2:29416761:G:A	0.000603
86_c3-1	86	SMO	MODERATE	c.983G>A	p.Gly328Asp	0	FALSE	chr7:128846053:G:A	113:chr7:128846053:G:A	0.000269
86_c3-1	86	PHLPP1	MODERATE	c.2197G>A	p.Val733Ile	0	FALSE	chr18:60562374:G:A	113:chr18:60562374:G:A	0.000416
86_c3-1	86	NTRK1	MODERATE	c.835C>T; c.925C>T	p.Pro279Ser; p.Pro309Ser	1	FALSE	chr1:156843499:C:T	113:chr1:156843499:C:T	0.000364
86_c3-1	86	TSC2	MODERATE	c.2513G>A	p.Ser838Asn	0	FALSE	chr16:2124358:G:A	113:chr16:2124358:G:A	0.000531
86_c3-1	86	ERBB2	MODERATE; MODIFIER	c.839C>T; c.884C>T; c.929C>T; n.1253C>T	p.Ser280Phe; p.Ser295Phe; p.Ser310Phe;	28	FALSE	chr17:37868208:C:T	113:chr17:37868208:C:T	0.008383
86_c3-1	86	PIK3CA	MODERATE	c.277C>T	p.Arg93Trp	24	FALSE	chr3:178916890:C:T	113:chr3:178916890:C:T	0.000348
86_c3-1	86	KDR	HIGH	c.3064C>T	p.Arg1022*	3	FALSE	chr4:55958789:G:A	113:chr4:55958789:G:A	0.000359
86_c3-1	86	TP53	MODERATE	c.340C>T; c.421C>T; c.700C>T; c.817C>T	p.Arg114Cys; p.Arg141Cys; p.Arg234Cys; p.Arg273Cys	601	FALSE	chr17:7577121:G:A	113:chr17:7577121:G:A	0.000704
86_c3-1	86	ALK	MODERATE	c.874C>T	p.Arg292Cys	1	FALSE	chr2:29917794:G:A	113:chr2:29917794:G:A	0.000478
86_c3-1	86	NTRK1	MODERATE	c.415G>A; c.505G>A	p.Gly139Arg; p.Gly169Arg	1	FALSE	chr1:156837972:G:A	113:chr1:156837972:G:A	0.000488
86_c3-1	86	TP53	MODERATE; MODIFIER	c.179C>T; c.296C>T; c.-279C>T; c.-360C>T	p.Ser60Phe; p.Ser99Phe;	3	FALSE	chr17:7579391:G:A	113:chr17:7579391:G:A	0.000466

86_c3-1	86	TP53	MODERATE	c.109A>G; c.28A>G; c.388A>G; c.505A>G	p.Met37Val; p.Met10Val; p.Met130Val; p.Met169Val	3	FALSE	chr17:7578425:T:C	113:chr17:7578425:T:C	0.000333
86_c3-1	86	FOXL2; FOXL2NB; LINC01391	MODERATE; MODIFIER	c.282T>A; c.-132A>T; n.-1T>A	p.Asn94Lys;	0	FALSE	chr3:138665283:A:T	113:chr3:138665283:A:T	0.012394
86_c3-1	86	PTEN	MODERATE	c.914G>A	p.Ser305Asn	1	FALSE	chr10:89720763:G:A	113:chr10:89720763:G:A	0.000545
86_c3-1	86	TSC2	MODERATE	c.1099C>T	p.Arg367Trp	0	FALSE	chr16:2110794:C:T	113:chr16:2110794:C:T	0.000423
86_c3-1	86	ATM	HIGH	c.2413C>T	p.Arg805*	0	FALSE	chr11:108129749:C:T	113:chr11:108129749:C:T	0.000369
86_c3-1	86	PIK3CA	HIGH	c.3152G>A	p.Trp1051*	3	FALSE	chr3:178952097:G:A	113:chr3:178952097:G:A	0.000343
86_c3-1	86	FBXW7	MODERATE	c.1082G>A; c.1196G>A; c.1436G>A	p.Arg361Gln; p.Arg399Gln; p.Arg479Gln	0	FALSE	chr4:153247366:C:T	113:chr4:153247366:C:T	0.000304
86_c3-1	86	FGFR2	MODERATE; MODIFIER	c.1073A>G; c.1076A>G; c.1079A>G; c.1088A>G; c.1157A>G; c.1160A>G; c.1424A>G; c.1427A>G; n.1874A>G	p.Glu358Gly; p.Glu359Gly; p.Glu360Gly; p.Glu363Gly; p.Glu386Gly; p.Glu387Gly; p.Glu475Gly; p.Glu476Gly;	2	FALSE	chr10:123263319:T:C	113:chr10:123263319:T:C	0.000668
86_c3-1	86	CTNNB1	MODERATE	c.1564G>A	p.Ala522Thr	0	FALSE	chr3:41275669:G:A	113:chr3:41275669:G:A	0.000591
86_c3-1	86	MET	MODERATE	c.1132G>A	p.Val378Ile	1	FALSE	chr7:116340270:G:A	113:chr7:116340270:G:A	0.000518
86_c3-1	86	PIK3CA	MODERATE	c.2176G>A	p.Glu726Lys	26	FALSE	chr3:178938934:G:A	113:chr3:178938934:G:A	0.005826
86_c3-1	86	APC	MODERATE	c.941G>A; c.995G>A	p.Arg314Gln; p.Arg332Gln	0	FALSE	chr5:112154724:G:A	113:chr5:112154724:G:A	0.000594

86_c3-1	86	PIK3CA	MODERATE	c.3034G>A	p.Glu1012Lys	2	FALSE	chr3:178951979:G:A	113:chr3:178951979:G:A	0.000328
86_c3-1	86	PKD1; TSC2	MODIFIER; MODERATE	c.*13118C>T; c.*13121C>T; c.4280G>A; c.4412G>A; c.4481G>A	; p.Gly1427Asp; p.Gly1471Asp; p.Gly1494Asp	0	FALSE	chr16:2134704:G:A	113:chr16:2134704:G:A	0.000474
86_c3-1	86	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2390G>A; n.1172C>T	p.Cys797Tyr;	3	FALSE	chr7:55249092:G:A	113:chr7:55249092:G:A	0.000353
86_c3-1	86	EGFR	MODERATE	c.967G>A	p.Val323Ile	2	FALSE	chr7:55223600:G:A	113:chr7:55223600:G:A	0.000394
86_c3-1	86	KIT	MODERATE	c.2854C>T; c.2866C>T	p.Arg952Trp; p.Arg956Trp	3	FALSE	chr4:55604658:C:T	113:chr4:55604658:C:T	0.000694
86_c3-1	86	ALK	MODERATE	c.1753G>A	p.Ala585Thr	3	FALSE	chr2:29519818:C:T	113:chr2:29519818:C:T	0.000319
86_c3-1	86	PIK3R1	MODERATE	c.1168T>C; c.1258T>C; c.2068T>C; c.979T>C	p.Ser390Pro; p.Ser420Pro; p.Ser690Pro; p.Ser327Pro	2	FALSE	chr5:67593322:T:C	113:chr5:67593322:T:C	0.000598
86_c3-1	86	TSC1	MODERATE	c.1823C>T; c.1973C>T; c.1976C>T	p.Ala608Val; p.Ala658Val; p.Ala659Val	0	FALSE	chr9:135780989:G:A	113:chr9:135780989:G:A	0.000505
86_c3-1	86	TP53	MODERATE	c.266G>A; c.347G>A; c.626G>A; c.743G>A	p.Arg89Gln; p.Arg116Gln; p.Arg209Gln; p.Arg248Gln	673	FALSE	chr17:7577538:C:T	113:chr17:7577538:C:T	0.000558
86_c3-1	86	TP53	MODERATE; MODIFIER	c.140C>T; c.23C>T; c.-279C>T; c.-360C>T	p.Pro47Leu; p.Pro8Leu;	2	FALSE	chr17:7579547:G:A	113:chr17:7579547:G:A	0.000407
86_c3-1	86	PIK3CA	MODERATE	c.1625A>G	p.Glu542Gly	14	FALSE	chr3:178936083:A:G	113:chr3:178936083:A:G	0.000399

86_c3-1	86	TP53	MODERATE	c.242G>T; c.323G>T; c.602G>T; c.719G>T	p.Ser81Ile; p.Ser108Ile; p.Ser201Ile; p.Ser240Ile	6	FALSE	chr17:7577562:C:A	113:chr17:7577562:C:A	0.000372
86_c3-1	86	ERBB2; MIEN1; MIR4728	MODERATE; MODIFIER	c.2239G>C; c.2284G>C; c.2329G>C; n.2653G>C; c.*388C>G; n.-1G>C	p.Val747Leu; p.Val762Leu; p.Val777Leu;	9	FALSE	chr17:37881000:G:C	113:chr17:37881000:G:C	0.030645
86_c3-1	86	TP53	MODERATE	c.365C>T; c.482C>T; c.5C>T; c.86C>T	p.Ala122Val; p.Ala161Val; p.Ala2Val; p.Ala29Val	9	FALSE	chr17:7578448:G:A	113:chr17:7578448:G:A	0.000359
86_c3-1	86	NOTCH1	MODERATE	c.3374C>T	p.Ala1125Val	0	FALSE	chr9:139402543:G:A	113:chr9:139402543:G:A	0.000548
86_c3-1	86	FGFR1	MODERATE	c.476G>A; c.482G>A; c.725G>A; c.743G>A; c.749G>A; c.842G>A	p.Arg159Gln; p.Arg161Gln; p.Arg242Gln; p.Arg248Gln; p.Arg250Gln; p.Arg281Gln	1	FALSE	chr8:38282214:C:T	113:chr8:38282214:C:T	0.000184
86_c3-1	86	TSC2	MODIFIER; MODERATE	c.2837+1108G>A; c.2933G>A	; p.Arg978His	0	FALSE	chr16:2127694:G:A	113:chr16:2127694:G:A	0.000378
86_c3-1	86	CDH1	MODERATE	c.856G>A	p.Ala286Thr	0	FALSE	chr16:68845610:G:A	113:chr16:68845610:G:A	0.000442
86_c3-1	86	HGF	MODERATE	c.767G>A; c.782G>A	p.Arg256His; p.Arg261His	0	FALSE	chr7:81372752:C:T	113:chr7:81372752:C:T	0.000736
86_c3-1	86	PTEN	MODERATE	c.133G>A	p.Val45Ile	1	FALSE	chr10:89653835:G:A	113:chr10:89653835:G:A	0.00078

86_c3-1	86	TP53	MODIFIER; MODERATE	c.*137A>G; c.*225A>G; c.1001A>G; c.1118A>G; c.641A>G; c.722A>G	; p.Lys334Arg; p.Lys373Arg; p.Lys214Arg; p.Lys241Arg	1	FALSE	chr17:7572991:T:C	113:chr17:7572991:T:C	0.001469
86_c3-1	86	ALK	MODERATE	c.4409C>T	p.Ala1470Val	1	FALSE	chr2:29416544:G:A	113:chr2:29416544:G:A	0.00029
86_c3-1	86	CDH1	HIGH	c.1913G>A	p.Trp638*	0	FALSE	chr16:68856105:G:A	113:chr16:68856105:G:A	0.000311
86_c3-1	86	NTRK3	MODERATE	c.581G>A	p.Gly194Asp	0	FALSE	chr15:88680676:C:T	113:chr15:88680676:C:T	0.000343
86_c3-1	86	FLT3	MODERATE	c.1879G>A	p.Ala627Thr	0	FALSE	chr13:28608087:C:T	113:chr13:28608087:C:T	0.000407
86_c3-1	86	ATM	MODERATE	c.3925G>A	p.Ala1309Thr	0	FALSE	chr11:108155132:G:A	113:chr11:108155132:G:A	0.000395
86_c3-1	86	NTRK2	MODERATE	c.1628A>G; c.1676A>G	p.Glu543Gly; p.Glu559Gly	0	FALSE	chr9:87549119:A:G	113:chr9:87549119:A:G	0.000584
86_c3-1	86	TP53	MODIFIER; HIGH	c.-48C>T; c.313C>T; c.34C>T; c.430C>T	; p.Gln105*; p.Gln12*; p.Gln144*	42	FALSE	chr17:7578500:G:A	113:chr17:7578500:G:A	0.000722
86_c3-1	86	C9orf53; CDKN2A	MODIFIER; MODERATE; LOW	n.*616G>A; c.*180C>T; c.257C>T; c.300C>T	; p.Ala86Val; p.Cys100Cys	1	FALSE	chr9:21971101:G:A	113:chr9:21971101:G:A	0.000449
86_c3-1	86	CDH1	MODERATE	c.1207G>A	p.Ala403Thr	0	FALSE	chr16:68847285:G:A	113:chr16:68847285:G:A	0.0004
86_c3-1	86	ERBB2; MIR4728	MODERATE; LOW; MODIFIER	c.2215G>C; c.2260G>C; c.2305G>C; n.2629G>C; n.-1G>C	p.Asp739His; p.Asp754His; p.Asp769His;	5	FALSE	chr17:37880261:G:C	113:chr17:37880261:G:C	0.249795
86_c3-1	86	PIK3CA	MODERATE	c.3154A>G	p.Thr1052Ala	3	FALSE	chr3:178952099:A:G	113:chr3:178952099:A:G	0.000347
86_c3-1	86	RET	MODERATE	c.1867G>A	p.Glu623Lys	1	FALSE	chr10:43609111:G:A	113:chr10:43609111:G:A	0.000779

86_c3-1	86	NTRK2	MODERATE	c.2216T>C; c.2264T>C	p.Leu739Pro; p.Leu755Pro	0	FALSE	chr9:87635212:T:C	113:chr9:87635212:T:C	0.000562
86_c3-1	86	TP53	MODERATE	c.170C>T; c.449C>T; c.566C>T; c.89C>T	p.Ala57Val; p.Ala150Val; p.Ala189Val; p.Ala30Val	4	FALSE	chr17:7578283:G:A	113:chr17:7578283:G:A	0.000485
86_c3-1	86	CDH1	MODERATE	c.1423G>A	p.Val475Met	0	FALSE	chr16:68849520:G:A	113:chr16:68849520:G:A	0.000329
86_c3-1	86	ALK	MODERATE	c.562C>T	p.Arg188Cys	2	FALSE	chr2:30142964:G:A	113:chr2:30142964:G:A	0.00037
86_c3-1	86	PIK3R1	MODERATE	c.1715A>G; c.626A>G; c.815A>G; c.905A>G	p.Gln572Arg; p.Gln209Arg; p.Gln272Arg; p.Gln302Arg	1	FALSE	chr5:67591122:A:G	113:chr5:67591122:A:G	0.000366
86_c3-1	86	KIT	MODERATE	c.2197G>A; c.2209G>A	p.Asp733Asn; p.Asp737Asn	2	FALSE	chr4:55597561:G:A	113:chr4:55597561:G:A	0.000362
86_c3-1	86	NTRK3	MODERATE	c.1463C>T; c.1487C>T	p.Ala488Val; p.Ala496Val	0	FALSE	chr15:88576186:G:A	113:chr15:88576186:G:A	0.000423
86_c3-1	86	PIK3CA	MODERATE	c.3077T>C	p.Leu1026Pro	1	FALSE	chr3:178952022:T:C	113:chr3:178952022:T:C	0.000331
86_c3-1	86	TSC2	MODERATE	c.1136A>G	p.Glu379Gly	0	FALSE	chr16:2111888:A:G	113:chr16:2111888:A:G	0.001447
86_c3-1	86	DDR2	MODERATE	c.2516G>A	p.Arg839His	3	FALSE	chr1:162749984:G:A	113:chr1:162749984:G:A	0.000333
86_c3-1	86	TSC1	MODERATE	c.1547C>T; c.1697C>T; c.1700C>T	p.Ala516Val; p.Ala566Val; p.Ala567Val	0	FALSE	chr9:135781265:G:A	113:chr9:135781265:G:A	0.001084
86_c3-1	86	RET	MODERATE	c.2221G>A	p.Ala741Thr	1	FALSE	chr10:43612116:G:A	113:chr10:43612116:G:A	0.000562
86_c3-1	86	TSC2	MODERATE	c.3410C>T; c.3542C>T	p.Thr1137Met; p.Thr1181Met	0	FALSE	chr16:2130310:C:T	113:chr16:2130310:C:T	0.000499
86_c3-1	86	PIK3CA	MODERATE	c.1616C>G	p.Pro539Arg	19	FALSE	chr3:178936074:C:G	113:chr3:178936074:C:G	0.000627

86_c3-1	86	GAPDH; IFFO1; NCAPD2	MODERATE; MODIFIER	c.16G>A; c.-349G>A; c.*1743C>T; c.*1746C>T; c.*1770C>T; n.*2798C>T; c.*4252G>A	p.Val6Ile;	0	FALSE	chr12:6644014:G:A	113:chr12:6644014:G:A	0.000641
86_c3-1	86	KIT	MODERATE	c.365G>A	p.Arg122His	1	FALSE	chr4:55564477:G:A	113:chr4:55564477:G:A	0.000391
86_c3-1	86	KIT	MODERATE	c.287C>T	p.Thr96Met	1	FALSE	chr4:55561897:C:T	113:chr4:55561897:C:T	0.0005
86_c3-1	86	NOTCH1	MODERATE	c.2734C>T	p.Arg912Trp	0	FALSE	chr9:139405111:G:A	113:chr9:139405111:G:A	0.000598
86_c3-1	86	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2330T>C; n.1232A>G	p.Leu777Pro;	2	FALSE	chr7:55249032:T:C	113:chr7:55249032:T:C	0.000672
86_c3-1	86	C9orf53; CDKN2A	MODIFIER; MODERATE; LOW	n.*616C>T; c.*278G>A; c.355G>A; c.398G>A	; p.Glu119Lys; p.Ter133Ter	4	FALSE	chr9:21971003:C:T	113:chr9:21971003:C:T	0.000442
86_c3-1	86	EGFR	MODIFIER; MODERATE	c.*2364G>A; c.2092G>A	; p.Ala698Thr	2	FALSE	chr7:55241644:G:A	113:chr7:55241644:G:A	0.000372
86_c3-1	86	NTRK3	HIGH	c.1348C>T; c.1372C>T	p.Arg450*; p.Arg458*	0	FALSE	chr15:88669526:G:A	113:chr15:88669526:G:A	0.000347
86_c3-1	86	TP53	MODERATE	c.182A>G; c.263A>G; c.542A>G; c.659A>G	p.Tyr61Cys; p.Tyr88Cys; p.Tyr181Cys; p.Tyr220Cys	277	FALSE	chr17:7578190:T:C	113:chr17:7578190:T:C	0.000498
86_c3-1	86	TSC2	MODERATE	c.2702G>A	p.Arg901His	0	FALSE	chr16:2126131:G:A	113:chr16:2126131:G:A	0.000354
86_c3-1	86	PIK3R1	MODERATE	c.1082G>A; c.1271G>A; c.1361G>A; c.2171G>A	p.Arg361Gln; p.Arg424Gln; p.Arg454Gln; p.Arg724Gln	1	FALSE	chr5:67593425:G:A	113:chr5:67593425:G:A	0.000534

86_c3-1	86	ATM	MODERATE	c.2075G>A	p.Arg692His	0	FALSE	chr11:108124717:G:A	113:chr11:108124717:G:A	0.00074
86_c3-1	86	CDH1	MODERATE	c.760G>A	p.Asp254Asn	0	FALSE	chr16:68844172:G:A	113:chr16:68844172:G:A	0.00036
86_c3-1	86	NTRK1	MODERATE	c.1322C>A; c.1412C>A; c.1430C>A	p.Ser441Tyr; p.Ser471Tyr; p.Ser477Tyr	1	FALSE	chr1:156845387:C:A	113:chr1:156845387:C:A	0.000405
86_c3-1	86	TP53	MODIFIER; MODERATE	c.-13G>T; c.105G>T; c.-279G>T; c.-360G>T	; p.Leu35Phe	2	FALSE	chr17:7579582:C:A	113:chr17:7579582:C:A	0.000445
86_c3-1	86	NF1	HIGH	c.3826C>T	p.Arg1276*	4	FALSE	chr17:29562746:C:T	113:chr17:29562746:C:T	0.000371
86_c3-1	86	TP53	LOW; MODIFIER; MODERATE	c.-6C>T; c.355C>T; c.472C>T; c.76C>T	; p.Arg119Cys; p.Arg158Cys; p.Arg26Cys	17	FALSE	chr17:7578458:G:A	113:chr17:7578458:G:A	0.00036
86_c3-1	86	ERBB2; MIR4728	MODERATE; MODIFIER	c.1880C>T; c.1925C>T; c.1970C>T; n.2294C>T; n.-1C>T	p.Ala627Val; p.Ala642Val; p.Ala657Val;	1	FALSE	chr17:37879595:C:T	113:chr17:37879595:C:T	0.000658
86_c3-1	86	TP53	MODERATE; MODIFIER	c.128C>T; c.245C>T; c.-279C>T; c.-360C>T	p.Pro43Leu; p.Pro82Leu;	6	FALSE	chr17:7579442:G:A	113:chr17:7579442:G:A	0.000685

86_c3-1	86	FGFR2	MODERATE; MODIFIER	c.1858A>G; c.1861A>G; c.1864A>G; c.1873A>G; c.1942A>G; c.1945A>G; c.2209A>G; c.2212A>G; n.2659A>G	p.Arg620Gly; p.Arg621Gly; p.Arg622Gly; p.Arg625Gly; p.Arg648Gly; p.Arg649Gly; p.Arg737Gly; p.Arg738Gly;	1	FALSE	chr10:123243304:T:C	113:chr10:123243304:T:C	0.000452
86_c3-1	86	TP53	MODERATE	c.322C>T; c.403C>T; c.682C>T; c.799C>T	p.Arg108Trp; p.Arg135Trp; p.Arg228Trp; p.Arg267Trp	31	FALSE	chr17:7577139:G:A	113:chr17:7577139:G:A	0.000403
86_c3-1	86	TSC2	MODERATE	c.1654G>A	p.Ala552Thr	0	FALSE	chr16:2115574:G:A	113:chr16:2115574:G:A	0.000906
86_c3-1	86	GAPDH; IFFO1	MODERATE; MODIFIER	c.217G>A; c.343G>A; c.*1743C>T; c.*1746C>T; c.*1770C>T; n.*2798C>T	p.Gly73Arg; p.Gly115Arg;	0	FALSE	chr12:6646282:G:A	113:chr12:6646282:G:A	0.000639
86_c3-1	86	NF1	MODERATE	c.3407G>A	p.Arg1136Gln	2	FALSE	chr17:29559810:G:A	113:chr17:29559810:G:A	0.00034
86_c3-1	86	FGFR3	MODERATE	c.599G>A	p.Arg200His	1	FALSE	chr4:1803247:G:A	113:chr4:1803247:G:A	0.0006
86_c3-1	86	NTRK1	MODERATE	c.804C>G; c.894C>G	p.His268Gln; p.His298Gln	1	FALSE	chr1:156843468:C:G	113:chr1:156843468:C:G	0.00082
86_c3-1	86	ATM	MODERATE	c.5225C>T	p.Ala1742Val	0	FALSE	chr11:108172422:C:T	113:chr11:108172422:C:T	0.000854
86_c3-1	86	TSC2	MODERATE	c.1610G>A	p.Arg537His	0	FALSE	chr16:2115530:G:A	113:chr16:2115530:G:A	0.000686
86_c3-1	86	FLT3	MODERATE	c.2822C>T	p.Ser941Leu	0	FALSE	chr13:28588626:G:A	113:chr13:28588626:G:A	0.000261

86_c3-1	86	PIK3R1	MODERATE	c.1709T>C; c.620T>C; c.809T>C; c.899T>C	p.Leu570Pro; p.Leu207Pro; p.Leu270Pro; p.Leu300Pro	2	FALSE	chr5:67591116:T:C	113:chr5:67591116:T:C	0.000542
86_c3-1	86	PIK3CA	MODERATE	c.241G>A	p.Glu81Lys	38	FALSE	chr3:178916854:G:A	113:chr3:178916854:G:A	0.000685
86_c3-1	86	PDGFRA	MODERATE	c.421G>A	p.Glu141Lys	1	FALSE	chr4:55129887:G:A	113:chr4:55129887:G:A	0.000397
86_c3-1	86	AR	MODERATE	c.2086G>A; c.490G>A	p.Asp696Asn; p.Asp164Asn	0	FALSE	chrX:66931444:G:A	113:chrX:66931444:G:A	0.00033
86_c3-1	86	KIT	MODERATE	c.2454T>A; c.2466T>A	p.Asn818Lys; p.Asn822Lys	20	FALSE	chr4:55599340:T:A	113:chr4:55599340:T:A	0.000473
86_c3-1	86	TP53	MODERATE	c.364G>A; c.481G>A; c.4G>A; c.85G>A	p.Ala122Thr; p.Ala161Thr; p.Ala2Thr; p.Ala29Thr	53	FALSE	chr17:7578449:C:T	113:chr17:7578449:C:T	0.000533
86_c3-1	86	ATM	HIGH	c.3663G>A	p.Trp1221*	0	FALSE	chr11:108153523:G:A	113:chr11:108153523:G:A	0.000451
86_c3-1	86	ATM	MODERATE	c.3070G>A	p.Ala1024Thr	0	FALSE	chr11:108142126:G:A	113:chr11:108142126:G:A	0.00053
86_c3-1	86	TP53	MODERATE	c.167T>C; c.446T>C; c.563T>C; c.86T>C	p.Leu56Pro; p.Leu149Pro; p.Leu188Pro; p.Leu29Pro	1	FALSE	chr17:7578286:A:G	113:chr17:7578286:A:G	0.000491
86_c3-1	86	ATM	MODERATE	c.6179G>A	p.Arg2060His	0	FALSE	chr11:108186821:G:A	113:chr11:108186821:G:A	0.001056
86_c3-1	86	PDGFRA	MODERATE	c.571G>A	p.Ala191Thr	1	FALSE	chr4:55130037:G:A	113:chr4:55130037:G:A	0.000629
86_c3-1	86	IGF1R	MODERATE	c.4007G>A; c.4010G>A	p.Arg1336His; p.Arg1337His	0	FALSE	chr15:99500577:G:A	113:chr15:99500577:G:A	0.000519
86_c3-1	86	FGFR3	MODERATE	c.539G>A	p.Gly180Asp	1	FALSE	chr4:1803187:G:A	113:chr4:1803187:G:A	0.000351

86_c3-1	86	MITF	MODIFIER; MODERATE	c.-45G>A; c.109G>A; c.112G>A; c.64G>A	; p.Ala37Thr; p.Ala38Thr; p.Ala22Thr	0	FALSE	chr3:69928292:G:A	113:chr3:69928292:G:A	0.000443
86_c3-1	86	PTEN	MODERATE	c.397G>A	p.Val133Ile	2	FALSE	chr10:89692913:G:A	113:chr10:89692913:G:A	0.000395
86_c3-1	86	NTRK1	MODERATE	c.1009G>A; c.919G>A	p.Ala337Thr; p.Ala307Thr	2	FALSE	chr1:156843583:G:A	113:chr1:156843583:G:A	0.000318
86_c3-1	86	IGF1R	MODERATE	c.1732G>A	p.Ala578Thr	0	FALSE	chr15:99456415:G:A	113:chr15:99456415:G:A	0.000587
86_c3-1	86	MAP2K1	MODERATE	c.371C>A	p.Pro124Gln	1	FALSE	chr15:66729163:C:A	113:chr15:66729163:C:A	0.000461
86_c3-1	86	FBXW7	MODERATE	c.1039C>T; c.1153C>T; c.1393C>T	p.Arg347Cys; p.Arg385Cys; p.Arg465Cys	0	FALSE	chr4:153249385:G:A	113:chr4:153249385:G:A	0.001293
86_c3-1	86	CSDE1; NRAS	MODIFIER; MODERATE	c.*2430C>T; c.*2523C>T; c.*2817C>T; c.*2910C>T; c.*2964C>T; c.*3057C>T; c.173C>T	; p.Thr58Ile	1	FALSE	chr1:115256538:G:A	113:chr1:115256538:G:A	0.000666
86_c3-1	86	CDH1	MODERATE	c.893C>T	p.Ala298Val	0	FALSE	chr16:68845647:C:T	113:chr16:68845647:C:T	0.000637
86_c3-1	86	IGF1R	MODERATE	c.3005G>A; c.3008G>A	p.Arg1002Gln; p.Arg1003Gln	0	FALSE	chr15:99478104:G:A	113:chr15:99478104:G:A	0.000307
86_c3-1	86	SMO	MODERATE	c.1045A>C	p.Thr349Pro	0	FALSE	chr7:128846115:A:C	113:chr7:128846115:A:C	0.008646
86_c3-1	86	PDGFRA	MODERATE	c.827C>T	p.Thr276Met	1	FALSE	chr4:55133523:C:T	113:chr4:55133523:C:T	0.000394
86_c3-1	86	TP53	MODERATE	c.128G>A; c.407G>A; c.47G>A; c.524G>A	p.Arg43His; p.Arg136His; p.Arg16His; p.Arg175His	979	FALSE	chr17:7578406:C:T	113:chr17:7578406:C:T	0.000327

86_c3-1	86	MIR4673; NOTCH1	MODIFIER; MODERATE	n.*59A>C; c.1195A>C	; p.Thr399Pro	0	FALSE	chr9:139412649:T:G	113:chr9:139412649:T:G	0.005145
86_c3-1	86	KDR	MODERATE	c.1028C>T	p.Thr343Met	3	FALSE	chr4:55976884:G:A	113:chr4:55976884:G:A	0.000322
86_c3-1	86	PTEN	MODERATE	c.389G>A	p.Arg130Gln	89	FALSE	chr10:89692905:G:A	113:chr10:89692905:G:A	0.000593
86_c3-1	86	TSC2	MODERATE	c.1819G>A	p.Ala607Thr	0	FALSE	chr16:2120559:G:A	113:chr16:2120559:G:A	0.00032
86_c3-1	86	NOTCH1	MODERATE	c.4966G>A	p.Gly1656Ser	0	FALSE	chr9:139399177:C:T	113:chr9:139399177:C:T	0.001195
86_c3-1	86	MET	MODERATE	c.1640G>A	p.Arg547Gln	1	FALSE	chr7:116381018:G:A	113:chr7:116381018:G:A	0.000314
86_c3-1	86	ALK	MODERATE	c.1184G>A	p.Arg395His	1	FALSE	chr2:29606696:C:T	113:chr2:29606696:C:T	0.000391
86_c3-1	86	PKD1; TSC2	MODIFIER; MODERATE	c.*13118G>A; c.*13121G>A; c.4091C>T; c.4223C>T; c.4292C>T	; p.Ser1364Leu; p.Ser1408Leu; p.Ser1431Leu	0	FALSE	chr16:2134515:C:T	113:chr16:2134515:C:T	0.000606
86_c3-1	86	EPHA3	MODERATE	c.2800G>A	p.Gly934Ser	0	FALSE	chr3:89521723:G:A	113:chr3:89521723:G:A	0.000458
86_c3-1	86	NOTCH1	MODERATE	c.5852G>A	p.Ser1951Asn	0	FALSE	chr9:139395086:C:T	113:chr9:139395086:C:T	0.000491
86_c3-1	86	FGFR4	MODERATE	c.1978G>A; c.2062G>A; c.2182G>A	p.Ala660Thr; p.Ala688Thr; p.Ala728Thr	1	FALSE	chr5:176524321:G:A	113:chr5:176524321:G:A	0.000574
86_c3-1	86	CWH43	MODERATE	c.1393G>A; c.1474G>A	p.Asp465Asn; p.Asp492Asn	0	FALSE	chr4:49032943:G:A	113:chr4:49032943:G:A	0.000772
86_c3-1	86	PIK3CA	MODERATE	c.1624G>A	p.Glu542Lys	777	FALSE	chr3:178936082:G:A	113:chr3:178936082:G:A	0.004583
86_c3-1	86	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2300C>T; n.1262G>A	p.Ala767Val;	5	FALSE	chr7:55249002:C:T	113:chr7:55249002:C:T	0.000284
86_c3-1	86	CDKN2A	MODIFIER; HIGH	c.194-3575G>A; c.45G>A	; p.Trp15*	3	FALSE	chr9:21974782:C:T	113:chr9:21974782:C:T	0.000549
86_c3-1	86	CDKN2A	MODIFIER; MODERATE	c.194-3568A>C; c.52A>C	; p.Thr18Pro	1	FALSE	chr9:21974775:T:G	113:chr9:21974775:T:G	0.010839

86_c3-1	86	SMO	MODERATE	c.1685G>A	p.Arg562Gln	0	FALSE	chr7:128850838:G:A	113:chr7:128850838:G:A	0.000311
86_c3-1	86	KIT	MODERATE	c.2375G>A; c.2387G>A	p.Arg792Lys; p.Arg796Lys	18	FALSE	chr4:55599261:G:A	113:chr4:55599261:G:A	0.000473
86_c3-1	86	PDGFRA	MODERATE	c.401C>T	p.Thr134Met	3	FALSE	chr4:55129867:C:T	113:chr4:55129867:C:T	0.000359
86_c3-1	86	ERBB2; MIEN1; MIR4728	MODERATE; MODIFIER	c.2236G>A; c.2281G>A; c.2326G>A; n.2650G>A; c.*388C>T; n.-1G>A	p.Gly746Ser; p.Gly761Ser; p.Gly776Ser;	5	FALSE	chr17:37880997:G:A	113:chr17:37880997:G:A	0.000563
86_c3-1	86	TP53	MODIFIER; MODERATE	c.-11G>A; c.350G>A; c.467G>A; c.71G>A	; p.Arg117His; p.Arg156His; p.Arg24His	26	FALSE	chr17:7578463:C:T	113:chr17:7578463:C:T	0.000536
86_c3-1	86	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2393T>C; n.1169A>G	p.Leu798Pro;	3	FALSE	chr7:55249095:T:C	113:chr7:55249095:T:C	0.001772
86_c3-1	86	FGFR3	MODERATE	c.395G>A	p.Gly132Glu	1	FALSE	chr4:1801489:G:A	113:chr4:1801489:G:A	0.000448
86_c3-1	86	ERBB2; MIEN1; MIR4728	MODERATE; MODIFIER	c.2542C>T; c.2587C>T; c.2632C>T; n.2956C>T; c.*388G>A; n.-1C>T	p.His848Tyr; p.His863Tyr; p.His878Tyr;	2	FALSE	chr17:37881440:C:T	113:chr17:37881440:C:T	0.017694
86_c3-1	86	NOTCH1	MODERATE	c.4549G>A	p.Asp1517Asn	0	FALSE	chr9:139399799:C:T	113:chr9:139399799:C:T	0.000431
86_c3-1	86	IDH1	MODERATE	c.1013G>C	p.Arg338Thr	1	FALSE	chr2:209103936:C:G	113:chr2:209103936:C:G	0.000346
86_c3-1	86	HRAS; LRRC56	MODERATE; MODIFIER	c.175G>A; c.-506C>T	p.Ala59Thr;	2	FALSE	chr11:533881:C:T	113:chr11:533881:C:T	0.000542
86_c3-1	86	EGFR	MODERATE	c.3352G>A	p.Ala1118Thr	3	FALSE	chr7:55273029:G:A	113:chr7:55273029:G:A	0.000306
86_c3-1	86	CTNNB1	MODERATE	c.113G>A	p.Gly38Asp	0	FALSE	chr3:41266116:G:A	113:chr3:41266116:G:A	0.000574

86_c3-1	86	RET	MODERATE	c.1907C>T	p.Thr636Met	1	FALSE	chr10:43609955:C:T	113:chr10:43609955:C:T	0.000565
86_c3-1	86	NF1	MODERATE	c.5426G>A; c.5489G>A	p.Arg1809His; p.Arg1830His	1	FALSE	chr17:29654737:G:A	113:chr17:29654737:G:A	0.000298
86_c3-1	86	TP53	MODERATE	c.141T>A; c.420T>A; c.537T>A; c.60T>A	p.His47Gln; p.His140Gln; p.His179Gln; p.His20Gln	17	FALSE	chr17:7578393:A:T	113:chr17:7578393:A:T	0.000306
26_c11-1	26	MITF	MODERATE	c.127A>C; c.235A>C; c.280A>C; c.283A>C	p.Thr43Pro; p.Thr79Pro; p.Thr94Pro; p.Thr95Pro	0	FALSE	chr3:69928463:A:C	114:chr3:69928463:A:C	0.163651
26_c11-1	26	NF1	HIGH	c.3028C>T	p.Gln1010*	2	FALSE	chr17:29557315:C:T	114:chr17:29557315:C:T	0.001192
26_c11-1	26	TP53	MODIFIER; MODERATE	c.-18T>C; c.-99T>C; c.262T>C; c.379T>C	; p.Ser88Pro; p.Ser127Pro	12	FALSE	chr17:7578551:A:G	114:chr17:7578551:A:G	0.002851
26_c11-1	26	MIR4673; NOTCH1	MODIFIER; MODERATE	n.*59A>C; c.1195A>C	; p.Thr399Pro	0	FALSE	chr9:139412649:T:G	114:chr9:139412649:T:G	0.005341
26_c11-1	26	PIK3CA	MODERATE	c.1093G>A	p.Glu365Lys	6	FALSE	chr3:178922324:G:A	114:chr3:178922324:G:A	0.001198
26_c11-1	26	NRAS	MODERATE	c.553C>T	p.Pro185Ser	2	FALSE	chr1:115251173:G:A	114:chr1:115251173:G:A	0.001156
26_c11-1	26	ERBB2	MODERATE; MODIFIER	c.275C>T; c.320C>T; c.365C>T; n.689C>T	p.Pro92Leu; p.Pro107Leu; p.Pro122Leu;	1	FALSE	chr17:37864713:C:T	114:chr17:37864713:C:T	0.000951
26_c11-1	26	PDGFRA	MODERATE	c.577G>A	p.Val193Ile	2	FALSE	chr4:55130043:G:A	114:chr4:55130043:G:A	0.000916
26_c11-1	26	TP53	MODIFIER; MODERATE	c.-57T>C; c.25T>C; c.304T>C; c.421T>C	; p.Cys9Arg; p.Cys102Arg; p.Cys141Arg	23	FALSE	chr17:7578509:A:G	114:chr17:7578509:A:G	0.001142
26_c11-1	26	NOTCH1	MODERATE	c.5939T>C	p.Leu1980Pro	0	FALSE	chr9:139393707:A:G	114:chr9:139393707:A:G	0.001462

26_c11-1	26	CDKN2A	MODIFIER; MODERATE	c.194-3531C>T; c.89C>T	; p.Ala30Val	3	FALSE	chr9:21974738:G:A	114:chr9:21974738:G:A	0.001435
26_c11-1	26	FGFR2	MODIFIER; MODERATE	c.939+4813C>T; c.1238C>T; c.1241C>T; c.893C>T; c.902C>T; c.971C>T; c.974C>T; n.1688C>T	; p.Pro413Leu; p.Pro414Leu; p.Pro298Leu; p.Pro301Leu; p.Pro324Leu; p.Pro325Leu	1	FALSE	chr10:123274680:G:A	114:chr10:123274680:G:A	0.001526
26_c11-1	26	GNA11	MODERATE	c.1030G>A	p.Val344Met	1	FALSE	chr19:3121127:G:A	114:chr19:3121127:G:A	0.001585
26_c11-1	26	FBXW7	MODERATE	c.1160G>A; c.1274G>A; c.1514G>A	p.Arg387His; p.Arg425His; p.Arg505His	0	FALSE	chr4:153247288:C:T	114:chr4:153247288:C:T	0.001001
26_c11-1	26	BRAF	MODERATE	c.1799T>A	p.Val600Glu	23024	FALSE	chr7:140453136:A:T	114:chr7:140453136:A:T	0.004023
26_c11-1	26	NTRK2	MODERATE	c.2024G>A; c.2072G>A	p.Arg675His; p.Arg691His	0	FALSE	chr9:87570332:G:A	114:chr9:87570332:G:A	0.001117
26_c11-1	26	CDH1	MODERATE	c.1528G>A	p.Ala510Thr	0	FALSE	chr16:68849625:G:A	114:chr16:68849625:G:A	0.000986
26_c11-1	26	TP53	MODERATE	c.341G>A; c.422G>A; c.701G>A; c.818G>A	p.Arg114His; p.Arg141His; p.Arg234His; p.Arg273His	647	TRUE	chr17:7577120:C:T	114:chr17:7577120:C:T	0.001696
26_c11-1	26	STK11	MODERATE	c.613G>A	p.Ala205Thr	1	FALSE	chr19:1220595:G:A	114:chr19:1220595:G:A	0.001382
26_c11-1	26	MAP2K1	MODERATE	c.140G>A	p.Arg47Gln	4	FALSE	chr15:66727424:G:A	114:chr15:66727424:G:A	0.000994
26_c11-1	26	TP53	MODERATE	c.130T>C; c.409T>C; c.49T>C; c.526T>C	p.Cys44Arg; p.Cys137Arg; p.Cys17Arg; p.Cys176Arg	15	FALSE	chr17:7578404:A:G	114:chr17:7578404:A:G	0.001083

26_c11-1	26	NOTCH1	MODERATE	c.4252G>A	p.Ala1418Thr	0	FALSE	chr9:139400096:C:T	114:chr9:139400096:C:T	0.001271
26_c11-1	26	KDR	MODERATE	c.2323G>T	p.Ala775Ser	1	FALSE	chr4:55964914:C:A	114:chr4:55964914:C:A	0.013181
26_c11-1	26	IDH1	MODERATE	c.355C>T	p.Arg119Trp	1	FALSE	chr2:209113152:G:A	114:chr2:209113152:G:A	0.001255
26_c11-1	26	NTRK1	MODERATE	c.1937G>A; c.2027G>A; c.2045G>A	p.Arg646His; p.Arg676His; p.Arg682His	1	FALSE	chr1:156849153:G:A	114:chr1:156849153:G:A	0.001049
26_c11-1	26	RET	MODERATE	c.1690A>C	p.Thr564Pro	1	FALSE	chr10:43608342:A:C	114:chr10:43608342:A:C	0.052882
26_c11-1	26	ROS1	HIGH	c.5728C>T	p.Arg1910*	1	FALSE	chr6:117642471:G:A	114:chr6:117642471:G:A	0.001037
26_c11-1	26	SMO	MODERATE	c.1045A>C	p.Thr349Pro	0	FALSE	chr7:128846115:A:C	114:chr7:128846115:A:C	0.029444
26_c11-1	26	NF1	MODERATE	c.2695T>G	p.Leu899Val	3	FALSE	chr17:29556328:T:G	114:chr17:29556328:T:G	0.045861
26_c11-1	26	TP53	MODERATE	c.203C>T; c.284C>T; c.563C>T; c.680C>T	p.Ser68Phe; p.Ser95Phe; p.Ser188Phe; p.Ser227Phe	8	FALSE	chr17:7577601:G:A	114:chr17:7577601:G:A	0.001145
26_c11-1	26	ATM	MODERATE	c.2077T>C	p.Cys693Arg	0	FALSE	chr11:108124719:T:C	114:chr11:108124719:T:C	0.001077
26_c11-1	26	TP53	MODIFIER; MODERATE	c.*145T>C; c.*233T>C; c.1009T>C; c.1126T>C; c.649T>C; c.730T>C	; p.Ser337Pro; p.Ser376Pro; p.Ser217Pro; p.Ser244Pro	2	FALSE	chr17:7572983:A:G	114:chr17:7572983:A:G	0.004288
26_c11-1	26	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2518G>A; n.-1C>T	p.Ala840Thr;	2	FALSE	chr7:55259460:G:A	114:chr7:55259460:G:A	0.001102
26_c11-1	26	NTRK1	MODERATE	c.1940T>G; c.2030T>G; c.2048T>G	p.Val647Gly; p.Val677Gly; p.Val683Gly	2	FALSE	chr1:156849792:T:G	114:chr1:156849792:T:G	0.022727
26_c11-1	26	NF1	MODERATE	c.8070G>T; c.8133G>T	p.Leu2690Phe; p.Leu2711Phe	1	FALSE	chr17:29686006:G:T	114:chr17:29686006:G:T	0.006098

26_c11-1	26	ERBB2; MIEN1; MIR4728	MODERATE; MODIFIER	c.2720A>G; c.2765A>G; c.2810A>G; n.3134A>G; c.*388T>C; n.-1A>G	p.Lys907Arg; p.Lys922Arg; p.Lys937Arg;	1	FALSE	chr17:37882044:A:G	114:chr17:37882044:A:G	0.001619
26_c11-1	26	CTNNB1	MODERATE	c.1286G>A	p.Cys429Tyr	0	FALSE	chr3:41275120:G:A	114:chr3:41275120:G:A	0.000991
26_c11-1	26	MAP2K1	MODERATE	c.159T>A	p.Phe53Leu	1	FALSE	chr15:66727443:T:A	114:chr15:66727443:T:A	0.001063
26_c11-1	26	TP53	MODIFIER; LOW	c.-100C>T; c.-19C>T; c.261C>T; c.378C>T	; p.Tyr87Tyr; p.Tyr126Tyr	5	FALSE	chr17:7578552:G:A	114:chr17:7578552:G:A	0.001135
26_c11-1	26	EPHA3	MODERATE	c.947A>C	p.Asp316Ala	0	FALSE	chr3:89390198:A:C	114:chr3:89390198:A:C	0.001879
26_c11-1	26	C9orf53; CDKN2A	MODIFIER; MODERATE	n.*616C>G; c.*140G>C; c.217G>C; c.260G>C	; p.Ala73Pro; p.Arg87Pro	1	FALSE	chr9:21971141:C:G	114:chr9:21971141:C:G	0.011142
26_c11-1	26	EGFR	MODIFIER; MODERATE	c.*2133G>A; c.*2364G>A; c.2030G>A	; p.Arg677His	5	FALSE	chr7:55240786:G:A	114:chr7:55240786:G:A	0.001541
26_c11-1	26	FGFR2	MODERATE; MODIFIER	c.1591G>A; c.1594G>A; c.1597G>A; c.1606G>A; c.1675G>A; c.1678G>A; c.1942G>A; c.1945G>A; n.2392G>A	p.Ala531Thr; p.Ala532Thr; p.Ala533Thr; p.Ala536Thr; p.Ala559Thr; p.Ala560Thr; p.Ala648Thr; p.Ala649Thr;	3	FALSE	chr10:123247549:C:T	114:chr10:123247549:C:T	0.001257
26_c11-1	26	KDR	MODERATE	c.3152G>A	p.Arg1051Gln	1	FALSE	chr4:55956163:C:T	114:chr4:55956163:C:T	0.0011

26_c11-1	26	FGFR1; LETM2	MODERATE; MODIFIER	c.1927C>T; c.1933C>T; c.2170C>T; c.2194C>T; c.2200C>T; c.2293C>T; c.*1406G>A; c.*1423G>A; c.*1553G>A; c.*1567G>A; c.*1638G>A	p.Arg643Trp; p.Arg645Trp; p.Arg724Trp; p.Arg732Trp; p.Arg734Trp; p.Arg765Trp;	1	FALSE	chr8:38271528:G:A	114:chr8:38271528:G:A	0.001428
26_c11-1	26	NOTCH1	MODERATE	c.5281C>T	p.Arg1761Trp	0	FALSE	chr9:139396827:G:A	114:chr9:139396827:G:A	0.001332
26_c11-1	26	TP53	MODERATE	c.367C>T; c.448C>T; c.727C>T; c.844C>T	p.Arg123Trp; p.Arg150Trp; p.Arg243Trp; p.Arg282Trp	479	FALSE	chr17:7577094:G:A	114:chr17:7577094:G:A	0.001093
26_c11-1	26	EGFR	MODERATE	c.2872C>T	p.Arg958Cys	1	FALSE	chr7:55268032:C:T	114:chr7:55268032:C:T	0.001018
26_c11-1	26	NTRK1	MODERATE	c.821C>T; c.911C>T	p.Ser274Phe; p.Ser304Phe	1	FALSE	chr1:156843485:C:T	114:chr1:156843485:C:T	0.001188
26_c11-1	26	CTNNB1	MODERATE	c.643G>A	p.Ala215Thr	0	FALSE	chr3:41266972:G:A	114:chr3:41266972:G:A	0.001002
26_c11-1	26	NOTCH1	MODERATE	c.4571C>T	p.Ala1524Val	0	FALSE	chr9:139399777:G:A	114:chr9:139399777:G:A	0.001704
26_c11-1	26	IGF1R	MODERATE	c.3905T>C; c.3908T>C	p.Val1302Ala; p.Val1303Ala	0	FALSE	chr15:99500475:T:C	114:chr15:99500475:T:C	0.008706
26_c11-1	26	CDKN2A	MODIFIER; MODERATE	c.194-3537T>G; c.83T>G	; p.Val28Gly	1	FALSE	chr9:21974744:A:C	114:chr9:21974744:A:C	0.05456
26_c11-1	26	CTNNB1	MODERATE	c.122C>A	p.Thr41Asn	0	FALSE	chr3:41266125:C:A	114:chr3:41266125:C:A	0.001053

26_c11-1	26	TP53	MODERATE	c.374C>T; c.455C>T; c.734C>T; c.851C>T	p.Thr125Ile; p.Thr152Ile; p.Thr245Ile; p.Thr284Ile	1	FALSE	chr17:7577087:G:A	114:chr17:7577087:G:A	0.001082
26_c11-1	26	C9orf53; CDKN2A	MODIFIER; MODERATE	n.*616G>A; c.*314C>T; c.*35C>T; c.391C>T	; p.Arg131Cys	2	FALSE	chr9:21970967:G:A	114:chr9:21970967:G:A	0.001096
26_c11-1	26	C9orf53; CDKN2A	MODIFIER; MODERATE; HIGH	n.*616G>A; c.*161C>T; c.281C>T; c.238C>T	; ; p.Pro94Leu; p.Arg80*	124	FALSE	chr9:21971120:G:A	114:chr9:21971120:G:A	0.001932
26_c11-1	26	TP53	MODERATE	c.110G>A; c.191G>A; c.470G>A; c.587G>A	p.Arg37Gln; p.Arg64Gln; p.Arg157Gln; p.Arg196Gln	19	FALSE	chr17:7578262:C:T	114:chr17:7578262:C:T	0.001546
70_c8-1	70	DDR2	MODERATE	c.1418G>A	p.Arg473His	2	FALSE	chr1:162740216:G:A	115:chr1:162740216:G:A	0.001377
70_c8-1	70	CDKN2A	MODIFIER; MODERATE	c.194-3537T>G; c.83T>G	; p.Val28Gly	1	FALSE	chr9:21974744:A:C	115:chr9:21974744:A:C	0.069945
70_c8-1	70	NTRK1	MODERATE	c.1937G>A; c.2027G>A; c.2045G>A	p.Arg646His; p.Arg676His; p.Arg682His	1	FALSE	chr1:156849153:G:A	115:chr1:156849153:G:A	0.000962
70_c8-1	70	TP53	MODIFIER; HIGH	c.-48C>T; c.313C>T; c.34C>T; c.430C>T	; p.Gln105*; p.Gln12*; p.Gln144*	42	FALSE	chr17:7578500:G:A	115:chr17:7578500:G:A	0.000908
70_c8-1	70	CDH1	MODERATE	c.1198G>A	p.Asp400Asn	0	FALSE	chr16:68847276:G:A	115:chr16:68847276:G:A	0.001008
70_c8-1	70	C9orf53; CDKN2A	MODIFIER; MODERATE	n.*616A>C; c.*137T>G; c.214T>G; c.257T>G	; p.Cys72Gly; p.Leu86Arg	1	FALSE	chr9:21971144:A:C	115:chr9:21971144:A:C	0.002463
70_c8-1	70	EGFR	MODERATE	c.3289G>A	p.Val1097Ile	1	FALSE	chr7:55272966:G:A	115:chr7:55272966:G:A	0.001079

70_c8-1	70	FGFR3	MODIFIER; MODERATE	c.931-375C>T; c.1195C>T; c.1201C>T	; p.Arg399Cys; p.Arg401Cys	1	FALSE	chr4:1806176:C:T	115:chr4:1806176:C:T	0.001089
70_c8-1	70	TP53	MODERATE	c.365C>T; c.482C>T; c.5C>T; c.86C>T	p.Ala122Val; p.Ala161Val; p.Ala2Val; p.Ala29Val	9	FALSE	chr17:7578448:G:A	115:chr17:7578448:G:A	0.000956
70_c8-1	70	NTRK1	MODERATE	c.1940T>G; c.2030T>G; c.2048T>G	p.Val647Gly; p.Val677Gly; p.Val683Gly	2	FALSE	chr1:156849792:T:G	115:chr1:156849792:T:G	0.035489
70_c8-1	70	TSC1	MODERATE	c.1091C>T; c.1241C>T; c.1244C>T	p.Thr364Ile; p.Thr414Ile; p.Thr415Ile	0	FALSE	chr9:135785977:G:A	115:chr9:135785977:G:A	0.001271
70_c8-1	70	SMO	MODERATE	c.961G>A	p.Val321Met	0	FALSE	chr7:128846031:G:A	115:chr7:128846031:G:A	0.001854
70_c8-1	70	ALK	MODERATE	c.4319C>T	p.Ala1440Val	1	FALSE	chr2:29416634:G:A	115:chr2:29416634:G:A	0.000837
70_c8-1	70	RET	MODERATE	c.1907C>T	p.Thr636Met	1	FALSE	chr10:43609955:C:T	115:chr10:43609955:C:T	0.001174
70_c8-1	70	CDKN2A	MODIFIER; MODERATE	c.194-3568A>C; c.52A>C	; p.Thr18Pro	1	FALSE	chr9:21974775:T:G	115:chr9:21974775:T:G	0.048005
70_c8-1	70	INSRR; NTRK1	MODIFIER; MODERATE	c.3397+28C>T; c.13G>A	; p.Ala5Thr	3	FALSE	chr1:156811876:G:A	115:chr1:156811876:G:A	0.000851
70_c8-1	70	FOXL2; FOXL2NB; LINC01391	MODERATE; MODIFIER	c.205G>A; c.-132C>T; n.-1G>A	p.Glu69Lys;	0	FALSE	chr3:138665360:C:T	115:chr3:138665360:C:T	0.001032
70_c8-1	70	ESR1	MODERATE	c.571T>C	p.Tyr191His	0	FALSE	chr6:152163850:T:C	115:chr6:152163850:T:C	0.00106
70_c8-1	70	CTNNB1	MODERATE	c.1972G>T	p.Val658Phe	0	FALSE	chr3:41278096:G:T	115:chr3:41278096:G:T	0.003517
70_c8-1	70	FGFR3	MODERATE	c.905G>A	p.Gly302Asp	1	FALSE	chr4:1803727:G:A	115:chr4:1803727:G:A	0.001514
70_c8-1	70	BRAF	MODERATE	c.1061G>A	p.Arg354Gln	3	FALSE	chr7:140494187:C:T	115:chr7:140494187:C:T	0.001029

70_c8-1	70	C9orf53; CDKN2A	MODIFIER; MODERATE	n.*616C>G; c.*140G>C; c.217G>C; c.260G>C	; p.Ala73Pro; p.Arg87Pro	1	FALSE	chr9:21971141:C:G	115:chr9:21971141:C:G	0.010539
70_c8-1	70	ALK	MODERATE	c.3455T>C	p.Leu1152Pro	1	FALSE	chr2:29445270:A:G	115:chr2:29445270:A:G	0.004285
70_c8-1	70	IGF1R	MODERATE	c.3934T>C; c.3937T>C	p.Ser1312Pro; p.Ser1313Pro	0	FALSE	chr15:99500504:T:C	115:chr15:99500504:T:C	0.041176
70_c8-1	70	KIT	MODERATE	c.1366C>T	p.Pro456Ser	2	FALSE	chr4:55592042:C:T	115:chr4:55592042:C:T	0.000964
70_c8-1	70	BRAF	MODERATE	c.2044C>T	p.Arg682Trp	1	FALSE	chr7:140439695:G:A	115:chr7:140439695:G:A	0.001129
70_c8-1	70	MIR4673; NOTCH1	MODIFIER; MODERATE	n.*59A>C; c.1195A>C	; p.Thr399Pro	0	FALSE	chr9:139412649:T:G	115:chr9:139412649:T:G	0.010582
70_c8-1	70	MIR1225; PKD1; TSC2	MODIFIER; MODERATE	n.*90C>T; c.*13118C>T; c.*13121C>T; c.4954G>A; c.5086G>A; c.5155G>A	; p.Ala1652Thr; p.Ala1696Thr; p.Ala1719Thr	0	FALSE	chr16:2138135:G:A	115:chr16:2138135:G:A	0.000883
70_c8-1	70	EPHA3	MODERATE	c.1535G>A	p.Arg512Gln	0	FALSE	chr3:89448571:G:A	115:chr3:89448571:G:A	0.001683
70_c8-1	70	FLT3	MODERATE	c.2678C>T	p.Pro893Leu	0	FALSE	chr13:28589369:G:A	115:chr13:28589369:G:A	0.001169
70_c8-1	70	STK11	MODERATE	c.488G>A	p.Gly163Asp	1	FALSE	chr19:1220395:G:A	115:chr19:1220395:G:A	0.001948
70_c8-1	70	VHL	MODIFIER; MODERATE	c.341-3270A>C; c.344A>C	; p.His115Pro	0	FALSE	chr3:10188201:A:C	115:chr3:10188201:A:C	0.003565
70_c8-1	70	MET	MODERATE	c.3815T>C; c.3869T>C	p.Leu1272Pro; p.Leu1290Pro	2	FALSE	chr7:116435725:T:C	115:chr7:116435725:T:C	0.001465
70_c8-1	70	NOTCH1	HIGH	c.3225G>A	p.Trp1075*	0	FALSE	chr9:139402784:C:T	115:chr9:139402784:C:T	0.001024

70_c8-1	70	MITF	MODERATE	c.127A>C; c.235A>C; c.280A>C; c.283A>C	p.Thr43Pro; p.Thr79Pro; p.Thr94Pro; p.Thr95Pro	0	FALSE	chr3:69928463:A:C	115:chr3:69928463:A:C	0.184305
70_c8-1	70	SMO	MODERATE	c.1045A>C	p.Thr349Pro	0	FALSE	chr7:128846115:A:C	115:chr7:128846115:A:C	0.037727
70_c8-1	70	STK11	MODERATE	c.628T>C	p.Cys210Arg	1	FALSE	chr19:1220610:T:C	115:chr19:1220610:T:C	0.008479
70_c8-1	70	C9orf53; CDKN2A	MODIFIER; MODERATE; LOW	n.*616C>A; c.*183G>T; c.260G>T; c.303G>T	; p.Arg87Leu; p.Pro101Pro	2	FALSE	chr9:21971098:C:A	115:chr9:21971098:C:A	0.000918
70_c8-1	70	KIT	MODERATE	c.1835C>T; c.1847C>T	p.Ala612Val; p.Ala616Val	1	FALSE	chr4:55594061:C:T	115:chr4:55594061:C:T	0.001898
70_c8-1	70	ATM	MODERATE	c.5639C>G	p.Thr1880Arg	0	FALSE	chr11:108175544:C:G	115:chr11:108175544:C:G	0.011688
70_c8-1	70	FGFR1; LETM2	MODERATE; MODIFIER	c.1927C>T; c.1933C>T; c.2170C>T; c.2194C>T; c.2200C>T; c.2293C>T; c.*1406G>A; c.*1423G>A; c.*1553G>A; c.*1567G>A; c.*1638G>A	p.Arg643Trp; p.Arg645Trp; p.Arg724Trp; p.Arg732Trp; p.Arg734Trp; p.Arg765Trp;	1	FALSE	chr8:38271528:G:A	115:chr8:38271528:G:A	0.001258
70_c8-1	70	FOXL2; FOXL2NB; LINC01391	MODERATE; MODIFIER	c.282T>A; c.-132A>T; n.-1T>A	p.Asn94Lys;	0	FALSE	chr3:138665283:A:T	115:chr3:138665283:A:T	0.008677
70_c8-1	70	HGF	MODERATE	c.580G>A; c.595G>A	p.Glu194Lys; p.Glu199Lys	0	FALSE	chr7:81381466:C:T	115:chr7:81381466:C:T	0.001014

70_c8-1	70	FGFR3	MODERATE	c.682T>C	p.Cys228Arg	2	FALSE	chr4:1803413:T:C	115:chr4:1803413:T:C	0.001038
70_c8-1	70	TP53	MODIFIER; MODERATE	c.-3G>A; c.358G>A; c.475G>A; c.79G>A	; p.Ala120Thr; p.Ala159Thr; p.Ala27Thr	23	FALSE	chr17:7578455:C:T	115:chr17:7578455:C:T	0.000928
70_c8-1	70	TP53	MODERATE; MODIFIER	c.208G>A; c.91G>A; c.-279G>A; c.-360G>A	p.Ala70Thr; p.Ala31Thr;	1	FALSE	chr17:7579479:C:T	115:chr17:7579479:C:T	0.001828
70_c8-1	70	TP53	MODIFIER; MODERATE	c.-204G>A; c.-87G>A; c.31G>A; c.-279G>A; c.-360G>A	; p.Glu11Lys	11	FALSE	chr17:7579882:C:T	115:chr17:7579882:C:T	0.000944
70_c8-1	70	ERBB2; MIEN1; MIR4728	MODIFIER; MODERATE	c.3160-213A>G; c.3251A>G; c.3296A>G; c.3341A>G; n.3665A>G; c.*388T>C; n.*67A>G	; p.Glu1084Gly; p.Glu1099Gly; p.Glu1114Gly	1	FALSE	chr17:37883729:A:G	115:chr17:37883729:A:G	0.003467
70_c8-1	70	NF1	MODERATE	c.5426G>A; c.5489G>A	p.Arg1809His; p.Arg1830His	1	FALSE	chr17:29654737:G:A	115:chr17:29654737:G:A	0.000821
70_c8-1	70	NTRK2	MODIFIER; MODERATE	c.854-37G>A; c.856G>A	; p.Ala286Thr	0	FALSE	chr9:87342571:G:A	115:chr9:87342571:G:A	0.0012
70_c8-1	70	CTNNB1	MODERATE	c.62C>T	p.Ala21Val	0	FALSE	chr3:41266065:C:T	115:chr3:41266065:C:T	0.001134
70_c8-1	70	TP53	MODERATE	c.367C>T; c.448C>T; c.727C>T; c.844C>T	p.Arg123Trp; p.Arg150Trp; p.Arg243Trp; p.Arg282Trp	479	FALSE	chr17:7577094:G:A	115:chr17:7577094:G:A	0.00105

70_c8-1	70	TP53	MODIFIER; MODERATE	c.*145T>C; c.*233T>C; c.1009T>C; c.1126T>C; c.649T>C; c.730T>C	; p.Ser337Pro; p.Ser376Pro; p.Ser217Pro; p.Ser244Pro	2	FALSE	chr17:7572983:A:G	115:chr17:7572983:A:G	0.00727
70_c8-1	70	FGFR3	MODERATE	c.1162G>A; c.1498G>A; c.1504G>A	p.Ala388Thr; p.Ala500Thr; p.Ala502Thr	1	FALSE	chr4:1807167:G:A	115:chr4:1807167:G:A	0.001149
70_c8-1	70	RPL19	MODERATE	c.452G>A	p.Arg151His	0	FALSE	chr17:37360425:G:A	115:chr17:37360425:G:A	0.00108
70_c8-1	70	MET	MODERATE	c.487T>C	p.Ser163Pro	1	FALSE	chr7:116339625:T:C	115:chr7:116339625:T:C	0.000901
70_c8-1	70	NF1	MODERATE	c.2695T>G	p.Leu899Val	3	FALSE	chr17:29556328:T:G	115:chr17:29556328:T:G	0.039058
70_c8-1	70	FGFR1	MODERATE	c.475C>T; c.481C>T; c.724C>T; c.742C>T; c.748C>T; c.841C>T	p.Arg159Trp; p.Arg161Trp; p.Arg242Trp; p.Arg248Trp; p.Arg250Trp; p.Arg281Trp	2	FALSE	chr8:38282215:G:A	115:chr8:38282215:G:A	0.001432
70_c8-1	70	AKT3	MODERATE	c.899C>T	p.Ala300Val	0	FALSE	chr1:243727071:G:A	115:chr1:243727071:G:A	0.001172
70_c8-1	70	RPL19	MODERATE	c.406C>T	p.Arg136Trp	0	FALSE	chr17:37360379:C:T	115:chr17:37360379:C:T	0.000968
70_c8-1	70	NTRK3	LOW	c.1560G>A; c.1584G>A	p.Thr520Thr; p.Thr528Thr	0	FALSE	chr15:88576089:C:T	115:chr15:88576089:C:T	0.001026
70_c8-1	70	TP53	MODERATE	c.242G>C; c.323G>C; c.602G>C; c.719G>C	p.Ser81Thr; p.Ser108Thr; p.Ser201Thr; p.Ser240Thr	6	FALSE	chr17:7577562:C:G	115:chr17:7577562:C:G	0.001009

70_c8-1	70	TP53	MODIFIER; MODERATE	c.*117G>T; c.*29G>T; c.1010G>T; c.533G>T; c.614G>T; c.893G>T	; p.Arg337Leu; p.Arg178Leu; p.Arg205Leu; p.Arg298Leu	21	FALSE	chr17:7574017:C:A	115:chr17:7574017:C:A	0.029653
70_c8-1	70	EPHA3	MODERATE	c.1543G>A	p.Ala515Thr	0	FALSE	chr3:89448579:G:A	115:chr3:89448579:G:A	0.001103
70_c8-1	70	IGF1R	MODERATE	c.3905T>C; c.3908T>C	p.Val1302Ala; p.Val1303Ala	0	FALSE	chr15:99500475:T:C	115:chr15:99500475:T:C	0.010864
70_c8-1	70	IGF1R	MODERATE	c.3733C>T; c.3736C>T	p.Arg1245Cys; p.Arg1246Cys	0	FALSE	chr15:99500303:C:T	115:chr15:99500303:C:T	0.001224
70_c8-1	70	ERBB2; MIEN1; MIR4728	MODERATE; MODIFIER	c.2596C>T; c.2641C>T; c.2686C>T; n.3010C>T; c.*388G>A; n.-1C>T	p.Arg866Cys; p.Arg881Cys; p.Arg896Cys;	3	FALSE	chr17:37881616:C:T	115:chr17:37881616:C:T	0.001233
70_c8-1	70	ESR1	MODERATE	c.739G>A; c.745G>A	p.Glu247Lys; p.Glu249Lys	0	FALSE	chr6:152201885:G:A	115:chr6:152201885:G:A	0.001414
70_c8-1	70	CDH1	HIGH	c.172G>T	p.Glu58*	0	FALSE	chr16:68835581:G:T	115:chr16:68835581:G:T	0.001053
70_c8-1	70	DDR2	MODERATE	c.13C>T	p.Pro5Ser	1	FALSE	chr1:162688866:C:T	115:chr1:162688866:C:T	0.000976
70_c8-1	70	STK11	HIGH	c.409C>T	p.Gln137*	1	FALSE	chr19:1219357:C:T	115:chr19:1219357:C:T	0.001024
70_c8-1	70	CDH1	MODERATE	c.1901C>T	p.Ala634Val	0	FALSE	chr16:68856093:C:T	115:chr16:68856093:C:T	0.000962
70_c8-1	70	RET	MODERATE	c.1690A>C	p.Thr564Pro	1	FALSE	chr10:43608342:A:C	115:chr10:43608342:A:C	0.049311
70_c8-1	70	FGFR3	MODERATE	c.599G>A	p.Arg200His	1	FALSE	chr4:1803247:G:A	115:chr4:1803247:G:A	0.001108
75_c9-1	75	CDKN2A	MODIFIER; MODERATE	c.194-3537T>G; c.83T>G	; p.Val28Gly	1	FALSE	chr9:21974744:A:C	116:chr9:21974744:A:C	0.092486

75_c9-1	75	GAPDH; IFFO1	MODERATE; MODIFIER	c.683T>C; c.809T>C; c.*1743A>G; c.*1746A>G; c.*1770A>G; n.*2798A>G	p.Leu228Pro; p.Leu270Pro;	0	FALSE	chr12:6647033:T:C	116:chr12:6647033:T:C	0.003922
75_c9-1	75	CDKN2A	MODIFIER; MODERATE	c.194-3570C>G; c.50C>G	; p.Ala17Gly	1	FALSE	chr9:21974777:G:C	116:chr9:21974777:G:C	0.022222
75_c9-1	75	NTRK2	MODERATE	c.1225G>A; c.1264G>A	p.Val409Ile; p.Val422Ile	0	FALSE	chr9:87359956:G:A	116:chr9:87359956:G:A	0.00198
75_c9-1	75	TP53	MODERATE; MODIFIER	c.208G>A; c.91G>A; c.-279G>A; c.-360G>A	p.Ala70Thr; p.Ala31Thr;	1	FALSE	chr17:7579479:C:T	116:chr17:7579479:C:T	0.002717
75_c9-1	75	ERBB2; MIEN1; MIR4728	MODIFIER; MODERATE	c.3160-213A>G; c.3251A>G; c.3296A>G; c.3341A>G; n.3665A>G; c.*388T>C; n.*67A>G	; p.Glu1084Gly; p.Glu1099Gly; p.Glu1114Gly	1	FALSE	chr17:37883729:A:G	116:chr17:37883729:A:G	0.002323
75_c9-1	75	HGF	MODERATE	c.767G>A; c.782G>A	p.Arg256His; p.Arg261His	0	FALSE	chr7:81372752:C:T	116:chr7:81372752:C:T	0.002326
75_c9-1	75	FGFR4	MODERATE	c.976G>A	p.Glu326Lys	1	FALSE	chr5:176519704:G:A	116:chr5:176519704:G:A	0.002146
75_c9-1	75	EGFR	MODERATE	c.1159C>G	p.Leu387Val	1	FALSE	chr7:55224477:C:G	116:chr7:55224477:C:G	0.001899
75_c9-1	75	NF1	MODIFIER; HIGH	c.*2165C>T; c.2266C>T	; p.Gln756*	2	FALSE	chr17:29554250:C:T	116:chr17:29554250:C:T	0.002222

75_c9-1	75	C9orf53; CDKN2A	MODIFIER; MODERATE	n.*616C>G; c.*140G>C; c.217G>C; c.260G>C	; p.Ala73Pro; p.Arg87Pro	1	FALSE	chr9:21971141:C:G	116:chr9:21971141:C:G	0.011662
75_c9-1	75	TP53	MODERATE	c.340C>T; c.421C>T; c.700C>T; c.817C>T	p.Arg114Cys; p.Arg141Cys; p.Arg234Cys; p.Arg273Cys	601	FALSE	chr17:7577121:G:A	116:chr17:7577121:G:A	0.002309
75_c9-1	75	DDR2	HIGH	c.2125C>T	p.Arg709*	4	FALSE	chr1:162746002:C:T	116:chr1:162746002:C:T	0.001883
75_c9-1	75	EPHA3	MODERATE	c.1280C>T	p.Ala427Val	0	FALSE	chr3:89391214:C:T	116:chr3:89391214:C:T	0.002169
75_c9-1	75	EPHA3	MODERATE	c.1916G>A	p.Arg639His	0	FALSE	chr3:89468382:G:A	116:chr3:89468382:G:A	0.002639
75_c9-1	75	ALK	MODERATE	c.3599C>T	p.Ala1200Val	2	FALSE	chr2:29443618:G:A	116:chr2:29443618:G:A	0.003745
75_c9-1	75	NOTCH1	MODERATE	c.4906G>A	p.Glu1636Lys	0	FALSE	chr9:139399237:C:T	116:chr9:139399237:C:T	0.0025
75_c9-1	75	TP53	MODERATE	c.389T>C; c.470T>C; c.749T>C; c.866T>C	p.Leu130Pro; p.Leu157Pro; p.Leu250Pro; p.Leu289Pro	2	FALSE	chr17:7577072:A:G	116:chr17:7577072:A:G	0.002139
75_c9-1	75	MITF	MODERATE	c.127A>C; c.235A>C; c.280A>C; c.283A>C	p.Thr43Pro; p.Thr79Pro; p.Thr94Pro; p.Thr95Pro	0	FALSE	chr3:69928463:A:C	116:chr3:69928463:A:C	0.201653
75_c9-1	75	NF1	MODERATE	c.2695T>G	p.Leu899Val	3	FALSE	chr17:29556328:T:G	116:chr17:29556328:T:G	0.042117
75_c9-1	75	IGF1R	MODERATE	c.3934T>C; c.3937T>C	p.Ser1312Pro; p.Ser1313Pro	0	FALSE	chr15:99500504:T:C	116:chr15:99500504:T:C	0.064242
75_c9-1	75	ALK	MODERATE	c.3182G>A	p.Arg1061Gln	3	FALSE	chr2:29446385:C:T	116:chr2:29446385:C:T	0.001727

75_c9-1	75	C9orf53; CDKN2A	MODIFIER; MODERATE; LOW	n.*616G>A; c.*180C>T; c.257C>T; c.300C>T	; p.Ala86Val; p.Cys100Cys	1	FALSE	chr9:21971101:G:A	116:chr9:21971101:G:A	0.002404
75_c9-1	75	FGFR3	MODERATE	c.1133A>G; c.1469A>G; c.1475A>G	p.Glu378Gly; p.Glu490Gly; p.Glu492Gly	1	FALSE	chr4:1807138:A:G	116:chr4:1807138:A:G	0.002793
75_c9-1	75	CDKN2A	MODIFIER; MODERATE	c.194-3568A>C; c.52A>C	; p.Thr18Pro	1	FALSE	chr9:21974775:T:G	116:chr9:21974775:T:G	0.07069
75_c9-1	75	SMO	MODERATE	c.1045A>C	p.Thr349Pro	0	FALSE	chr7:128846115:A:C	116:chr7:128846115:A:C	0.039583
75_c9-1	75	IGF1R	MODERATE	c.3905T>C; c.3908T>C	p.Val1302Ala; p.Val1303Ala	0	FALSE	chr15:99500475:T:C	116:chr15:99500475:T:C	0.012081
75_c9-1	75	FGFR3	MODERATE	c.539G>A	p.Gly180Asp	1	FALSE	chr4:1803187:G:A	116:chr4:1803187:G:A	0.002242
75_c9-1	75	PTEN	MODERATE	c.355G>A	p.Val119Ile	3	FALSE	chr10:89692871:G:A	116:chr10:89692871:G:A	0.001927
75_c9-1	75	C9orf53; CDKN2A	MODIFIER; MODERATE; LOW	n.*616T>G; c.*120A>C; c.197A>C; c.240A>C	; p.His66Pro; p.Pro80Pro	1	FALSE	chr9:21971161:T:G	116:chr9:21971161:T:G	0.106267
75_c9-1	75	FGFR4	MODERATE	c.461G>A	p.Arg154His	3	FALSE	chr5:176517963:G:A	116:chr5:176517963:G:A	0.001944
75_c9-1	75	ATM	MODERATE	c.1009C>T	p.Arg337Cys	0	FALSE	chr11:108117798:C:T	116:chr11:108117798:C:T	0.001994
75_c9-1	75	RET	MODERATE	c.1690A>C	p.Thr564Pro	1	FALSE	chr10:43608342:A:C	116:chr10:43608342:A:C	0.068256
75_c9-1	75	TP53	MODIFIER; MODERATE	c.*145T>C; c.*233T>C; c.1009T>C; c.1126T>C; c.649T>C; c.730T>C	; p.Ser337Pro; p.Ser376Pro; p.Ser217Pro; p.Ser244Pro	2	FALSE	chr17:7572983:A:G	116:chr17:7572983:A:G	0.011686
75_c9-1	75	FLT3	HIGH	c.2500C>T	p.Arg834*	0	FALSE	chr13:28592645:G:A	116:chr13:28592645:G:A	0.002148

75_c9-1	75	NTRK1	MODERATE	c.1940T>G; c.2030T>G; c.2048T>G	p.Val647Gly; p.Val677Gly; p.Val683Gly	2	FALSE	chr1:156849792:T:G	116:chr1:156849792:T:G	0.030132
80_c5-1	80	IGF1R	MODERATE	c.3934T>C; c.3937T>C	p.Ser1312Pro; p.Ser1313Pro	0	FALSE	chr15:99500504:T:C	117:chr15:99500504:T:C	0.041743
80_c5-1	80	ERBB2	MODERATE; MODIFIER	c.379C>T; c.424C>T; c.469C>T; n.793C>T	p.Arg127Trp; p.Arg142Trp; p.Arg157Trp;	1	FALSE	chr17:37865600:C:T	117:chr17:37865600:C:T	0.00114
80_c5-1	80	CDKN2A	MODIFIER; MODERATE	c.194-3570C>G; c.50C>G	; p.Ala17Gly	1	FALSE	chr9:21974777:G:C	117:chr9:21974777:G:C	0.01223
80_c5-1	80	CDH1	MODERATE	c.221G>A	p.Arg74Gln	0	FALSE	chr16:68835630:G:A	117:chr16:68835630:G:A	0.001112
80_c5-1	80	HGF	MODERATE	c.767G>A; c.782G>A	p.Arg256His; p.Arg261His	0	FALSE	chr7:81372752:C:T	117:chr7:81372752:C:T	0.001352
80_c5-1	80	EGFR	MODERATE	c.967G>A	p.Val323Ile	2	FALSE	chr7:55223600:G:A	117:chr7:55223600:G:A	0.001898
80_c5-1	80	PDGFRA	MODERATE	c.1777C>A	p.Leu593Ile	1	FALSE	chr4:55141131:C:A	117:chr4:55141131:C:A	0.001965
80_c5-1	80	SMO	MODERATE	c.1045A>C	p.Thr349Pro	0	FALSE	chr7:128846115:A:C	117:chr7:128846115:A:C	0.041211
80_c5-1	80	BRAF	MODERATE	c.946T>C	p.Ser316Pro	1	FALSE	chr7:140500196:A:G	117:chr7:140500196:A:G	0.002994
80_c5-1	80	FGFR2	MODERATE; MODIFIER	c.1281C>A; c.1284C>A; c.1287C>A; c.1296C>A; c.1365C>A; c.1368C>A; c.1632C>A; c.1635C>A; n.2082C>A	p.His427Gln; p.His428Gln; p.His429Gln; p.His432Gln; p.His455Gln; p.His456Gln; p.His544Gln; p.His545Gln;	1	FALSE	chr10:123258049:G:T	117:chr10:123258049:G:T	0.001571
80_c5-1	80	CTNNB1	MODERATE	c.1972G>T	p.Val658Phe	0	FALSE	chr3:41278096:G:T	117:chr3:41278096:G:T	0.004528

80_c5-1	80	APC	MODERATE	c.1864C>T; c.1918C>T	p.Arg622Trp; p.Arg640Trp	0	FALSE	chr5:112170822:C:T	117:chr5:112170822:C:T	0.001701
80_c5-1	80	ALK	MODERATE	c.2575G>C	p.Glu859Gln	1	FALSE	chr2:29455227:C:G	117:chr2:29455227:C:G	0.001227
80_c5-1	80	IGF1R	MODERATE	c.3905T>C; c.3908T>C	p.Val1302Ala; p.Val1303Ala	0	FALSE	chr15:99500475:T:C	117:chr15:99500475:T:C	0.020861
80_c5-1	80	ERBB2; MIEN1; MIR4728	MODERATE; MODIFIER	c.3025G>A; c.3070G>A; c.3115G>A; n.3439G>A; c.*388C>T; n.*67G>A	p.Ala1009Thr; p.Ala1024Thr; p.Ala1039Thr;	2	FALSE	chr17:37883212:G:A	117:chr17:37883212:G:A	0.001626
80_c5-1	80	KDR	MODERATE	c.583G>T	p.Ala195Ser	1	FALSE	chr4:55981116:C:A	117:chr4:55981116:C:A	0.001048
80_c5-1	80	NTRK2	MODERATE	c.220G>A	p.Ala74Thr	0	FALSE	chr9:87317081:G:A	117:chr9:87317081:G:A	0.001477
80_c5-1	80	TP53	MODERATE; MODIFIER	c.199C>T; c.82C>T; c.-279C>T; c.-360C>T	p.Pro67Ser; p.Pro28Ser;	3	FALSE	chr17:7579488:G:A	117:chr17:7579488:G:A	0.002425
80_c5-1	80	FGFR1	MODERATE	c.1060C>T; c.1066C>T; c.1303C>T; c.1327C>T; c.1333C>T; c.1426C>T	p.Arg354Trp; p.Arg356Trp; p.Arg435Trp; p.Arg443Trp; p.Arg445Trp; p.Arg476Trp	2	FALSE	chr8:38275843:G:A	117:chr8:38275843:G:A	0.000996
80_c5-1	80	NTRK1	MODERATE	c.728G>A; c.818G>A	p.Arg243Gln; p.Arg273Gln	1	FALSE	chr1:156841515:G:A	117:chr1:156841515:G:A	0.00122
80_c5-1	80	PIK3R1	MODERATE	c.1694G>A; c.605G>A; c.794G>A; c.884G>A	p.Ser565Asn; p.Ser202Asn; p.Ser265Asn; p.Ser295Asn	1	FALSE	chr5:67591101:G:A	117:chr5:67591101:G:A	0.001145

80_c5-1	80	NF1	MODERATE	c.2659G>A	p.Ala887Thr	1	FALSE	chr17:29556292:G:A	117:chr17:29556292:G:A	0.001077
80_c5-1	80	NTRK1	MODERATE	c.1940T>G; c.2030T>G; c.2048T>G	p.Val647Gly; p.Val677Gly; p.Val683Gly	2	FALSE	chr1:156849792:T:G	117:chr1:156849792:T:G	0.031293
80_c5-1	80	CWH43	MODERATE	c.737C>T; c.818C>T	p.Ala246Val; p.Ala273Val	0	FALSE	chr4:49005767:C:T	117:chr4:49005767:C:T	0.001276
80_c5-1	80	BRAF	MODERATE	c.1061G>A	p.Arg354Gln	3	FALSE	chr7:140494187:C:T	117:chr7:140494187:C:T	0.001164
80_c5-1	80	CDH1	MODERATE	c.1528G>A	p.Ala510Thr	0	FALSE	chr16:68849625:G:A	117:chr16:68849625:G:A	0.001119
80_c5-1	80	PTEN	MODERATE	c.235G>A	p.Ala79Thr	3	FALSE	chr10:89690828:G:A	117:chr10:89690828:G:A	0.001376
80_c5-1	80	KDR	MODERATE	c.2323G>T	p.Ala775Ser	1	FALSE	chr4:55964914:C:A	117:chr4:55964914:C:A	0.008537
80_c5-1	80	ERBB2; MIEN1; MIR4728	MODERATE; MODIFIER	c.2607C>A; c.2652C>A; c.2697C>A; n.3021C>A; c.*388G>T; n.-1C>A	p.Phe869Leu; p.Phe884Leu; p.Phe899Leu;	1	FALSE	chr17:37881627:C:A	117:chr17:37881627:C:A	0.002041
80_c5-1	80	CDKN2A; CDKN2B-AS1	MODERATE; MODIFIER	c.22A>G; n.-1T>C	p.Thr8Ala;	1	FALSE	chr9:21994309:T:C	117:chr9:21994309:T:C	0.008322
80_c5-1	80	RET	MODERATE	c.1690A>C	p.Thr564Pro	1	FALSE	chr10:43608342:A:C	117:chr10:43608342:A:C	0.052878
80_c5-1	80	EGFR; EGFR-AS1	MODIFIER; MODERATE	c.*2364G>A; c.2224G>A; n.*2821C>T	; p.Val742Ile	2	FALSE	chr7:55242454:G:A	117:chr7:55242454:G:A	0.001813
80_c5-1	80	MITF	MODERATE	c.127A>C; c.235A>C; c.280A>C; c.283A>C	p.Thr43Pro; p.Thr79Pro; p.Thr94Pro; p.Thr95Pro	0	FALSE	chr3:69928463:A:C	117:chr3:69928463:A:C	0.140162
80_c5-1	80	AKT1	MODERATE	c.361C>T	p.Arg121Trp	2	FALSE	chr14:105242063:G:A	117:chr14:105242063:G:A	0.001187

80_c5-1	80	EPHA3	MODERATE	c.2222G>A	p.Gly741Asp	0	FALSE	chr3:89480385:G:A	117:chr3:89480385:G:A	0.001385
80_c5-1	80	NF1	MODERATE	c.6943G>A; c.7006G>A	p.Ala2315Thr; p.Ala2336Thr	2	FALSE	chr17:29667607:G:A	117:chr17:29667607:G:A	0.001206
80_c5-1	80	NOTCH1	MODERATE	c.4906G>A	p.Glu1636Lys	0	FALSE	chr9:139399237:C:T	117:chr9:139399237:C:T	0.00136
80_c5-1	80	CTNNB1	MODERATE	c.1346G>A	p.Arg449His	0	FALSE	chr3:41275180:G:A	117:chr3:41275180:G:A	0.001519
80_c5-1	80	FGFR1	MODERATE	c.1013C>T; c.1019C>T; c.1112C>T; c.746C>T; c.752C>T; c.995C>T	p.Thr338Met; p.Thr340Met; p.Thr371Met; p.Thr249Met; p.Thr251Met; p.Thr332Met	2	FALSE	chr8:38279377:G:A	117:chr8:38279377:G:A	0.002154
80_c5-1	80	STK11	MODERATE	c.628T>C	p.Cys210Arg	1	FALSE	chr19:1220610:T:C	117:chr19:1220610:T:C	0.007951
80_c5-1	80	C9orf53; CDKN2A	MODIFIER; MODERATE; LOW	n.*616C>T; c.*258G>A; c.335G>A; c.378G>A	; p.Arg112His; p.Pro126Pro	1	FALSE	chr9:21971023:C:T	117:chr9:21971023:C:T	0.001348
80_c5-1	80	ERBB2; MIEN1; MIR4728	MODERATE; MODIFIER	c.2516T>G; c.2561T>G; c.2606T>G; n.2930T>G; c.*388A>C; n.-1T>G	p.Leu839Arg; p.Leu854Arg; p.Leu869Arg;	1	FALSE	chr17:37881414:T:G	117:chr17:37881414:T:G	0.001249
80_c5-1	80	IGF1R	MODERATE	c.3121C>T; c.3124C>T	p.Arg1041Cys; p.Arg1042Cys	0	FALSE	chr15:99478220:C:T	117:chr15:99478220:C:T	0.001688
80_c5-1	80	ALG10	MODERATE	c.272G>A	p.Cys91Tyr	0	FALSE	chr12:34176997:G:A	117:chr12:34176997:G:A	0.001755

80_c5-1	80	FGFR1	MODERATE	c.487C>T; c.493C>T; c.736C>T; c.754C>T; c.760C>T; c.853C>T	p.Arg163Trp; p.Arg165Trp; p.Arg246Trp; p.Arg252Trp; p.Arg254Trp; p.Arg285Trp	1	FALSE	chr8:38282203:G:A	117:chr8:38282203:G:A	0.0012
80_c5-1	80	NTRK1	MODERATE	c.804C>G; c.894C>G	p.His268Gln; p.His298Gln	1	FALSE	chr1:156843468:C:G	117:chr1:156843468:C:G	0.001516
80_c5-1	80	CTNNB1	MODERATE	c.445G>A	p.Ala149Thr	0	FALSE	chr3:41266648:G:A	117:chr3:41266648:G:A	0.001239
80_c5-1	80	FGFR3	MODERATE	c.1526G>A; c.1862G>A; c.1868G>A	p.Arg509His; p.Arg621His; p.Arg623His	2	FALSE	chr4:1807803:G:A	117:chr4:1807803:G:A	0.001622
80_c5-1	80	CDH1	MODERATE	c.760G>A	p.Asp254Asn	0	FALSE	chr16:68844172:G:A	117:chr16:68844172:G:A	0.001183
80_c5-1	80	NF1	MODERATE	c.2695T>G	p.Leu899Val	3	FALSE	chr17:29556328:T:G	117:chr17:29556328:T:G	0.046036
80_c5-1	80	CDH1	MODERATE	c.2074G>A	p.Ala692Thr	0	FALSE	chr16:68857439:G:A	117:chr16:68857439:G:A	0.001788
80_c5-1	80	MET	MODERATE	c.3217C>T; c.3271C>T	p.Pro1073Ser; p.Pro1091Ser	1	FALSE	chr7:116415123:C:T	117:chr7:116415123:C:T	0.001252
80_c5-1	80	NOTCH1	MODERATE	c.3749G>A	p.Gly1250Asp	0	FALSE	chr9:139401320:C:T	117:chr9:139401320:C:T	0.001558
80_c5-1	80	FLT3	MODERATE	c.2678C>T	p.Pro893Leu	0	FALSE	chr13:28589369:G:A	117:chr13:28589369:G:A	0.001244
80_c5-1	80	TP53	MODERATE; MODIFIER	c.208G>A; c.91G>A; c.-279G>A; c.-360G>A	p.Ala70Thr; p.Ala31Thr;	1	FALSE	chr17:7579479:C:T	117:chr17:7579479:C:T	0.001664
80_c5-1	80	CDKN2A	MODIFIER; MODERATE	c.194-3568A>C; c.52A>C	; p.Thr18Pro	1	FALSE	chr9:21974775:T:G	117:chr9:21974775:T:G	0.061127
80_c5-1	80	MIR4673; NOTCH1	MODIFIER; MODERATE	n.*59A>C; c.1195A>C	; p.Thr399Pro	0	FALSE	chr9:139412649:T:G	117:chr9:139412649:T:G	0.011811
80_c5-1	80	CWH43	MODERATE	c.692G>A; c.773G>A	p.Arg231His; p.Arg258His	0	FALSE	chr4:49000536:G:A	117:chr4:49000536:G:A	0.001142

80_c5-1	80	TSC2	MODERATE	c.2035G>A	p.Val679Met	0	FALSE	chr16:2121873:G:A	117:chr16:2121873:G:A	0.001807
80_c5-1	80	ALK	MODERATE	c.4192C>T	p.Pro1398Ser	1	FALSE	chr2:29416761:G:A	117:chr2:29416761:G:A	0.001366
80_c5-1	80	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2336G>A; n.1226C>T	p.Gly779Asp;	2	FALSE	chr7:55249038:G:A	117:chr7:55249038:G:A	0.001162
80_c5-1	80	CDKN2A	MODIFIER; MODERATE	c.194-3537T>G; c.83T>G	; p.Val28Gly	1	FALSE	chr9:21974744:A:C	117:chr9:21974744:A:C	0.066259
80_c5-1	80	TSC1	MODERATE	c.457C>T; c.610C>T	p.Arg153Cys; p.Arg204Cys	0	FALSE	chr9:135797259:G:A	117:chr9:135797259:G:A	0.002028
80_c5-1	80	KDR	HIGH	c.2455C>T	p.Arg819*	2	FALSE	chr4:55964358:G:A	117:chr4:55964358:G:A	0.001155
80_c5-1	80	HOXD-AS2; HOXD8	MODIFIER; MODERATE	n.*692C>T; c.-123-177G>A; c.253G>A	; p.Gly85Ser	0	FALSE	chr2:176995347:G:A	117:chr2:176995347:G:A	0.005464
80_c5-1	80	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2507G>A; n.-1C>T	p.Arg836His;	2	FALSE	chr7:55259449:G:A	117:chr7:55259449:G:A	0.00136
80_c5-1	80	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2568T>G; n.-1A>C	p.Phe856Leu;	1	FALSE	chr7:55259510:T:G	117:chr7:55259510:T:G	0.001913
80_c5-1	80	EPHA3	MODERATE	c.1543G>A	p.Ala515Thr	0	FALSE	chr3:89448579:G:A	117:chr3:89448579:G:A	0.001279
80_c5-1	80	TP53	MODIFIER; HIGH	c.-48C>T; c.313C>T; c.34C>T; c.430C>T	; p.Gln105*; p.Gln12*; p.Gln144*	42	FALSE	chr17:7578500:G:A	117:chr17:7578500:G:A	0.001279
80_c5-1	80	TSC2	MODERATE	c.2702G>A	p.Arg901His	0	FALSE	chr16:2126131:G:A	117:chr16:2126131:G:A	0.001196
80_c5-1	80	FGFR4	HIGH	c.1041G>A	p.Trp347*	1	FALSE	chr5:176519769:G:A	117:chr5:176519769:G:A	0.001574
80_c5-1	80	TP53	LOW; MODIFIER; MODERATE	c.-6C>T; c.355C>T; c.472C>T; c.76C>T	; p.Arg119Cys; p.Arg158Cys; p.Arg26Cys	17	FALSE	chr17:7578458:G:A	117:chr17:7578458:G:A	0.001966
80_c5-1	80	IDH2	MODERATE	c.172C>T; c.406C>T; c.562C>T	p.Arg58Trp; p.Arg136Trp; p.Arg188Trp	1	FALSE	chr15:90631707:G:A	117:chr15:90631707:G:A	0.001958

80_c5-1	80	MIR1225; PKD1; TSC2	MODIFIER; MODERATE	n.*90C>T; c.*13118C>T; c.*13121C>T; c.4906G>A; c.5038G>A; c.5107G>A	; p.Val1636Met; p.Val1680Met; p.Val1703Met	0	FALSE	chr16:2138087:G:A	117:chr16:2138087:G:A	0.001295
86_bl-1	86	PIK3CA	MODERATE	c.1624G>A	p.Glu542Lys	777	FALSE	chr3:178936082:G:A	118:chr3:178936082:G:A	0.002543
86_bl-1	86	FGFR1	LOW; MODIFIER; MODERATE	c.-19C>T; c.173C>T; c.74C>T	; p.Pro58Leu; p.Pro25Leu	1	FALSE	chr8:38314891:G:A	118:chr8:38314891:G:A	0.000379
86_bl-1	86	CSDE1; NRAS	MODIFIER; MODERATE	c.*2430A>C; c.*2523A>C; c.*2817A>C; c.*2910A>C; c.*2964A>C; c.*3057A>C; c.48A>C	; p.Lys16Asn	1	FALSE	chr1:115258734:T:G	118:chr1:115258734:T:G	0.000946
86_bl-1	86	FGFR1	MODERATE	c.1048G>A; c.1066G>A; c.1072G>A; c.1165G>A; c.799G>A; c.805G>A	p.Val350Ile; p.Val356Ile; p.Val358Ile; p.Val389Ile; p.Val267Ile; p.Val269Ile	1	FALSE	chr8:38279324:C:T	118:chr8:38279324:C:T	0.000816
86_bl-1	86	TSC2	MODERATE	c.3410C>T; c.3542C>T	p.Thr1137Met; p.Thr1181Met	0	FALSE	chr16:2130310:C:T	118:chr16:2130310:C:T	0.002254
86_bl-1	86	CDKN2A	MODIFIER; HIGH	c.194-3575G>A; c.45G>A	; p.Trp15*	3	FALSE	chr9:21974782:C:T	118:chr9:21974782:C:T	0.001986

86_bl-1	86	ERBB2; MIEN1; MIR4728	MODERATE; MODIFIER	c.2239G>C; c.2284G>C; c.2329G>C; n.2653G>C; c.*388C>G; n.-1G>C	p.Val747Leu; p.Val762Leu; p.Val777Leu;	9	FALSE	chr17:37881000:G:C	118:chr17:37881000:G:C	0.028913
86_bl-1	86	GAPDH; IFFO1	MODERATE; MODIFIER	c.773G>A; c.899G>A; c.*1743C>T; c.*1746C>T; c.*1770C>T; n.*2798C>T	p.Gly258Asp; p.Gly300Asp;	0	FALSE	chr12:6647123:G:A	118:chr12:6647123:G:A	0.000643
86_bl-1	86	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2575G>A; n.-1C>T	p.Ala859Thr;	4	FALSE	chr7:55259517:G:A	118:chr7:55259517:G:A	0.001058
86_bl-1	86	PIK3R1	MODERATE	c.1709T>C; c.620T>C; c.809T>C; c.899T>C	p.Leu570Pro; p.Leu207Pro; p.Leu270Pro; p.Leu300Pro	2	FALSE	chr5:67591116:T:C	118:chr5:67591116:T:C	0.000907
86_bl-1	86	NTRK3	MODERATE	c.995C>T	p.Thr332Met	0	FALSE	chr15:88678541:G:A	118:chr15:88678541:G:A	0.000998
86_bl-1	86	CTNNB1	HIGH	c.283C>T	p.Arg95*	0	FALSE	chr3:41266486:C:T	118:chr3:41266486:C:T	0.001448
86_bl-1	86	CTNNB1	MODERATE	c.131C>A	p.Pro44His	0	FALSE	chr3:41266134:C:A	118:chr3:41266134:C:A	0.001035
86_bl-1	86	ERBB2; MIEN1; MIR4728	MODERATE; MODIFIER	c.2720A>G; c.2765A>G; c.2810A>G; n.3134A>G; c.*388T>C; n.-1A>G	p.Lys907Arg; p.Lys922Arg; p.Lys937Arg;	1	FALSE	chr17:37882044:A:G	118:chr17:37882044:A:G	0.002044
86_bl-1	86	TP53	MODERATE; MODIFIER	c.199C>T; c.82C>T; c.-279C>T; c.-360C>T	p.Pro67Ser; p.Pro28Ser;	3	FALSE	chr17:7579488:G:A	118:chr17:7579488:G:A	0.00134

86_bl-1	86	CTNNB1	MODERATE	c.1972G>T	p.Val658Phe	0	FALSE	chr3:41278096:G:T	118:chr3:41278096:G:T	0.002498
86_bl-1	86	NF1	HIGH	c.3721C>T	p.Arg1241*	5	FALSE	chr17:29562641:C:T	118:chr17:29562641:C:T	0.000988
86_bl-1	86	PIK3CA	MODERATE	c.3012G>A	p.Met1004Ile	8	FALSE	chr3:178951957:G:A	118:chr3:178951957:G:A	0.001668
86_bl-1	86	MET	HIGH	c.1639C>T	p.Arg547*	2	FALSE	chr7:116381017:C:T	118:chr7:116381017:C:T	0.000877
86_bl-1	86	TP53	MODERATE	c.110G>A; c.191G>A; c.470G>A; c.587G>A	p.Arg37Gln; p.Arg64Gln; p.Arg157Gln; p.Arg196Gln	19	FALSE	chr17:7578262:C:T	118:chr17:7578262:C:T	0.000872
86_bl-1	86	NTRK2	MODERATE	c.1240G>A; c.1279G>A	p.Gly414Ser; p.Gly427Ser	0	FALSE	chr9:87359971:G:A	118:chr9:87359971:G:A	0.001413
86_bl-1	86	DDR2	MODERATE	c.397C>T	p.Arg133Trp	1	FALSE	chr1:162724625:C:T	118:chr1:162724625:C:T	0.0011
86_bl-1	86	CDKN2A	MODIFIER; MODERATE	c.194-3567C>T; c.53C>T	; p.Thr18Met	1	FALSE	chr9:21974774:G:A	118:chr9:21974774:G:A	0.001821
86_bl-1	86	NOTCH1	MODERATE	c.4984C>T	p.Arg1662Trp	0	FALSE	chr9:139399159:G:A	118:chr9:139399159:G:A	0.001663
86_bl-1	86	FGFR3	MODERATE	c.1162G>A; c.1498G>A; c.1504G>A	p.Ala388Thr; p.Ala500Thr; p.Ala502Thr	1	FALSE	chr4:1807167:G:A	118:chr4:1807167:G:A	0.001958
86_bl-1	86	CTNNB1	MODERATE	c.1564G>A	p.Ala522Thr	0	FALSE	chr3:41275669:G:A	118:chr3:41275669:G:A	0.002081
86_bl-1	86	FGFR3	MODERATE	c.1070G>A; c.1406G>A; c.1412G>A	p.Arg357Gln; p.Arg469Gln; p.Arg471Gln	1	FALSE	chr4:1806690:G:A	118:chr4:1806690:G:A	0.002506
86_bl-1	86	NTRK1	MODERATE	c.804C>G; c.894C>G	p.His268Gln; p.His298Gln	1	FALSE	chr1:156843468:C:G	118:chr1:156843468:C:G	0.001211
86_bl-1	86	KDR	MODERATE	c.1028C>T	p.Thr343Met	3	FALSE	chr4:55976884:G:A	118:chr4:55976884:G:A	0.000857
86_bl-1	86	NTRK1	MODERATE	c.835C>T; c.925C>T	p.Pro279Ser; p.Pro309Ser	1	FALSE	chr1:156843499:C:T	118:chr1:156843499:C:T	0.001112
86_bl-1	86	PTEN	MODERATE	c.442G>A	p.Ala148Thr	2	FALSE	chr10:89692958:G:A	118:chr10:89692958:G:A	0.001098

86_bl-1	86	CTNNB1	HIGH	c.75G>A	p.Trp25*	0	FALSE	chr3:41266078:G:A	118:chr3:41266078:G:A	0.001068
86_bl-1	86	IGF1R	MODERATE	c.1940G>A	p.Arg647His	0	FALSE	chr15:99459304:G:A	118:chr15:99459304:G:A	0.000702
86_bl-1	86	PIK3CA	MODERATE	c.1357G>C	p.Glu453Gln	20	FALSE	chr3:178928079:G:C	118:chr3:178928079:G:C	0.001029
86_bl-1	86	PIK3CA	MODERATE	c.2176G>A	p.Glu726Lys	26	FALSE	chr3:178938934:G:A	118:chr3:178938934:G:A	0.001129
86_bl-1	86	EGFR	MODERATE	c.445C>T	p.Arg149Trp	1	FALSE	chr7:55214319:C:T	118:chr7:55214319:C:T	0.001131
86_bl-1	86	TP53	MODERATE	c.229T>C; c.310T>C; c.589T>C; c.706T>C	p.Tyr77His; p.Tyr104His; p.Tyr197His; p.Tyr236His	18	FALSE	chr17:7577575:A:G	118:chr17:7577575:A:G	0.000983
86_bl-1	86	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2568T>G; n.-1A>C	p.Phe856Leu;	1	FALSE	chr7:55259510:T:G	118:chr7:55259510:T:G	0.001029
86_bl-1	86	ERBB2; MIR4728	MODERATE; MODIFIER	c.2211C>G; c.2256C>G; c.2301C>G; n.2625C>G; n.-1C>G	p.Ile737Met; p.Ile752Met; p.Ile767Met;	6	FALSE	chr17:37880257:C:G	118:chr17:37880257:C:G	0.00539
86_bl-1	86	CDH1	MODERATE	c.2071G>A	p.Ala691Thr	0	FALSE	chr16:68857436:G:A	118:chr16:68857436:G:A	0.000966
86_bl-1	86	STK11	MODERATE	c.628T>C	p.Cys210Arg	1	FALSE	chr19:1220610:T:C	118:chr19:1220610:T:C	0.01105
86_bl-1	86	ERBB2; MIEN1; MIR4728	MODERATE; MODIFIER	c.3025G>A; c.3070G>A; c.3115G>A; n.3439G>A; c.*388C>T; n.*67G>A	p.Ala1009Thr; p.Ala1024Thr; p.Ala1039Thr;	2	FALSE	chr17:37883212:G:A	118:chr17:37883212:G:A	0.001252
86_bl-1	86	RPL19	MODERATE	c.406C>T	p.Arg136Trp	0	FALSE	chr17:37360379:C:T	118:chr17:37360379:C:T	0.000903
86_bl-1	86	KIT	MODERATE	c.1493G>A	p.Gly498Asp	1	FALSE	chr4:55592169:G:A	118:chr4:55592169:G:A	0.001177
86_bl-1	86	FGFR3	MODERATE	c.599G>A	p.Arg200His	1	FALSE	chr4:1803247:G:A	118:chr4:1803247:G:A	0.001921

86_bl-1	86	PIK3CA	MODERATE	c.323G>A	p.Arg108His	33	FALSE	chr3:178916936:G:A	118:chr3:178916936:G:A	0.000942
86_bl-1	86	TP53	MODERATE	c.361A>G; c.442A>G; c.721A>G; c.838A>G	p.Arg121Gly; p.Arg148Gly; p.Arg241Gly; p.Arg280Gly	24	FALSE	chr17:7577100:T:C	118:chr17:7577100:T:C	0.001029
86_bl-1	86	ERBB2; MIR4728	MODERATE; LOW; MODIFIER	c.2215G>C; c.2260G>C; c.2305G>C; n.2629G>C; n.-1G>C	p.Asp739His; p.Asp754His; p.Asp769His;	5	FALSE	chr17:37880261:G:C	118:chr17:37880261:G:C	0.315158
86_bl-1	86	CTNNB1	MODERATE	c.37G>A	p.Ala13Thr	0	FALSE	chr3:41266040:G:A	118:chr3:41266040:G:A	0.001113
86_bl-1	86	CDH1	MODERATE	c.893C>T	p.Ala298Val	0	FALSE	chr16:68845647:C:T	118:chr16:68845647:C:T	0.001694
86_bl-1	86	FGFR1	MODERATE	c.487C>T; c.493C>T; c.736C>T; c.754C>T; c.760C>T; c.853C>T	p.Arg163Trp; p.Arg165Trp; p.Arg246Trp; p.Arg252Trp; p.Arg254Trp; p.Arg285Trp	1	FALSE	chr8:38282203:G:A	118:chr8:38282203:G:A	0.0004
86_bl-1	86	KIT	MODERATE	c.154G>A	p.Asp52Asn	7	FALSE	chr4:55561764:G:A	118:chr4:55561764:G:A	0.001267
86_bl-1	86	CDKN2A	MODIFIER; MODERATE	c.194-3570C>G; c.50C>G	; p.Ala17Gly	1	FALSE	chr9:21974777:G:C	118:chr9:21974777:G:C	0.015474
86_bl-1	86	HGF	MODERATE	c.686G>A; c.701G>A	p.Arg229His; p.Arg234His	0	FALSE	chr7:81374361:C:T	118:chr7:81374361:C:T	0.001228
86_bl-1	86	FOXL2; FOXL2NB; LINC01391	MODERATE; MODIFIER	c.282T>A; c.-132A>T; n.-1T>A	p.Asn94Lys;	0	FALSE	chr3:138665283:A:T	118:chr3:138665283:A:T	0.010458

86_bl-1	86	CSDE1; NRAS	MODIFIER; MODERATE	c.*2430C>T; c.*2523C>T; c.*2817C>T; c.*2910C>T; c.*2964C>T; c.*3057C>T; c.173C>T	; p.Thr58Ile	1	FALSE	chr1:115256538:G:A	118:chr1:115256538:G:A	0.001164
86_bl-1	86	KIT	MODERATE	c.155A>G	p.Asp52Gly	4	FALSE	chr4:55561765:A:G	118:chr4:55561765:A:G	0.000844
86_bl-1	86	IGF1R	MODERATE	c.1732G>A	p.Ala578Thr	0	FALSE	chr15:99456415:G:A	118:chr15:99456415:G:A	0.000748
86_bl-1	86	FGFR1; LETM2	MODERATE; MODIFIER	c.1777T>G; c.1783T>G; c.2020T>G; c.2044T>G; c.2050T>G; c.2143T>G; c.*1406A>C; c.*1423A>C; c.*1553A>C; c.*1567A>C; c.*1638A>C	p.Trp593Gly; p.Trp595Gly; p.Trp674Gly; p.Trp682Gly; p.Trp684Gly; p.Trp715Gly;	1	FALSE	chr8:38271806:A:C	118:chr8:38271806:A:C	0.002493
86_bl-1	86	IGF1R	MODERATE	c.1784G>A	p.Arg595His	0	FALSE	chr15:99456467:G:A	118:chr15:99456467:G:A	0.000767
86_bl-1	86	ATM	MODERATE	c.8158G>A	p.Asp2720Asn	0	FALSE	chr11:108206578:G:A	118:chr11:108206578:G:A	0.001031

86_bl-1	86	FGFR1; LETM2	MODERATE; MODIFIER	c.1927C>T; c.1933C>T; c.2170C>T; c.2194C>T; c.2200C>T; c.2293C>T; c.*1406G>A; c.*1423G>A; c.*1553G>A; c.*1567G>A; c.*1638G>A	p.Arg643Trp; p.Arg645Trp; p.Arg724Trp; p.Arg732Trp; p.Arg734Trp; p.Arg765Trp;	1	FALSE	chr8:38271528:G:A	118:chr8:38271528:G:A	0.00058
86_bl-1	86	FGFR4	MODIFIER; MODERATE	c.1098-65G>A; c.1251+10G>A; c.1067G>A	; p.Arg356His	1	FALSE	chr5:176520342:G:A	118:chr5:176520342:G:A	0.002418
86_bl-1	86	TP53	MODERATE	c.149G>A; c.428G>A; c.545G>A; c.68G>A	p.Cys50Tyr; p.Cys143Tyr; p.Cys182Tyr; p.Cys23Tyr	2	FALSE	chr17:7578385:C:T	118:chr17:7578385:C:T	0.000823
86_bl-1	86	BRAF	MODERATE	c.2153C>T	p.Ala718Val	1	FALSE	chr7:140434545:G:A	118:chr7:140434545:G:A	0.002671
86_bl-1	86	NF1	MODERATE	c.5381A>G; c.5444A>G	p.Gln1794Arg; p.Gln1815Arg	1	FALSE	chr17:29654692:A:G	118:chr17:29654692:A:G	0.000876
86_bl-1	86	CDKN2A	MODIFIER; MODERATE	c.194-3537T>G; c.83T>G	; p.Val28Gly	1	FALSE	chr9:21974744:A:C	118:chr9:21974744:A:C	0.085353
86_bl-1	86	HGF	MODERATE	c.167C>T	p.Ala56Val	0	FALSE	chr7:81392110:G:A	118:chr7:81392110:G:A	0.0011
86_bl-1	86	KDR	MODERATE	c.1699G>A	p.Val567Met	1	FALSE	chr4:55971098:C:T	118:chr4:55971098:C:T	0.000811
86_bl-1	86	VHL	MODIFIER; MODERATE	c.341-3270A>C; c.344A>C	; p.His115Pro	0	FALSE	chr3:10188201:A:C	118:chr3:10188201:A:C	0.001655
86_bl-1	86	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2320G>A; n.1242C>T	p.Val774Met;	6	FALSE	chr7:55249022:G:A	118:chr7:55249022:G:A	0.000927

86_bl-1	86	FGFR1	MODIFIER; MODERATE	c.-32G>A; c.160G>A; c.61G>A	; p.Ala54Thr; p.Ala21Thr	2	FALSE	chr8:38314904:C:T	118:chr8:38314904:C:T	0.000527
86_bl-1	86	TP53	MODIFIER; MODERATE	c.*116C>T; c.*28C>T; c.1009C>T; c.532C>T; c.613C>T; c.892C>T	; p.Arg337Cys; p.Arg178Cys; p.Arg205Cys; p.Arg298Cys	31	FALSE	chr17:7574018:G:A	118:chr17:7574018:G:A	0.000862
86_bl-1	86	IGF1R	MODERATE	c.3905T>C; c.3908T>C	p.Val1302Ala; p.Val1303Ala	0	FALSE	chr15:99500475:T:C	118:chr15:99500475:T:C	0.020372
86_bl-1	86	ATM	HIGH	c.6311G>A	p.Trp2104*	0	FALSE	chr11:108188212:G:A	118:chr11:108188212:G:A	0.001447
86_bl-1	86	GNA11	MODERATE	c.1030G>A	p.Val344Met	1	FALSE	chr19:3121127:G:A	118:chr19:3121127:G:A	0.001284
86_bl-1	86	NTRK1	MODERATE	c.1940T>G; c.2030T>G; c.2048T>G	p.Val647Gly; p.Val677Gly; p.Val683Gly	2	FALSE	chr1:156849792:T:G	118:chr1:156849792:T:G	0.037428
86_bl-1	86	TP53	MODIFIER; MODERATE	c.*145T>C; c.*233T>C; c.1009T>C; c.1126T>C; c.649T>C; c.730T>C	; p.Ser337Pro; p.Ser376Pro; p.Ser217Pro; p.Ser244Pro	2	FALSE	chr17:7572983:A:G	118:chr17:7572983:A:G	0.006628
86_bl-1	86	C9orf53; CDKN2A	MODIFIER; MODERATE	n.*616C>G; c.*167G>C; c.244G>C; c.287G>C	; p.Val82Leu; p.Arg96Pro	3	FALSE	chr9:21971114:C:G	118:chr9:21971114:C:G	0.001704

86_bl-1	86	ERBB2; MIEN1; MIR4728	MODERATE; MODIFIER	c.2542C>T; c.2587C>T; c.2632C>T; n.2956C>T; c.*388G>A; n.-1C>T	p.His848Tyr; p.His863Tyr; p.His878Tyr;	2	FALSE	chr17:37881440:C:T	118:chr17:37881440:C:T	0.001674
86_bl-1	86	SMO	MODERATE	c.703G>A	p.Ala235Thr	0	FALSE	chr7:128845209:G:A	118:chr7:128845209:G:A	0.001794
86_bl-1	86	PIK3CA	MODERATE	c.1022C>T	p.Ala341Val	2	FALSE	chr3:178921540:C:T	118:chr3:178921540:C:T	0.001637
86_bl-1	86	ATM	MODERATE	c.2075G>A	p.Arg692His	0	FALSE	chr11:108124717:G:A	118:chr11:108124717:G:A	0.000854
86_bl-1	86	IGF1R	MODERATE	c.1538G>A	p.Arg513Gln	0	FALSE	chr15:99454619:G:A	118:chr15:99454619:G:A	0.000669
86_bl-1	86	MAP2K1	MODERATE	c.199G>A	p.Asp67Asn	4	FALSE	chr15:66727483:G:A	118:chr15:66727483:G:A	0.0018
86_bl-1	86	FGFR1	MODERATE	c.359C>T; c.365C>T; c.608C>T; c.626C>T; c.632C>T; c.725C>T	p.Ala120Val; p.Ala122Val; p.Ala203Val; p.Ala209Val; p.Ala211Val; p.Ala242Val	1	FALSE	chr8:38283753:G:A	118:chr8:38283753:G:A	0.000654
86_bl-1	86	MIR4673; NOTCH1	MODIFIER; MODERATE	n.*59A>C; c.1195A>C	; p.Thr399Pro	0	FALSE	chr9:139412649:T:G	118:chr9:139412649:T:G	0.012048
86_bl-1	86	FGFR3	MODERATE	c.1543G>A; c.1879G>A; c.1885G>A	p.Glu515Lys; p.Glu627Lys; p.Glu629Lys	1	FALSE	chr4:1807820:G:A	118:chr4:1807820:G:A	0.001889
86_bl-1	86	NTRK3	MODERATE	c.2005C>T; c.2029C>T	p.His669Tyr; p.His677Tyr	0	FALSE	chr15:88472526:G:A	118:chr15:88472526:G:A	0.000953
86_bl-1	86	CDH1	MODERATE	c.1489G>A	p.Glu497Lys	0	FALSE	chr16:68849586:G:A	118:chr16:68849586:G:A	0.000865
86_bl-1	86	KLLN; PTEN	MODIFIER; MODERATE	c.-951A>G; c.79T>C	; p.Tyr27His	4	FALSE	chr10:89624305:T:C	118:chr10:89624305:T:C	0.001224
86_bl-1	86	NF1	MODERATE	c.2695T>G	p.Leu899Val	3	FALSE	chr17:29556328:T:G	118:chr17:29556328:T:G	0.063785

86_bl-1	86	C9orf53; CDKN2A	MODIFIER; MODERATE	n.*616C>G; c.*140G>C; c.217G>C; c.260G>C	; p.Ala73Pro; p.Arg87Pro	1	FALSE	chr9:21971141:C:G	118:chr9:21971141:C:G	0.005386
86_bl-1	86	DDR2	MODERATE	c.185G>A	p.Arg62Lys	1	FALSE	chr1:162722987:G:A	118:chr1:162722987:G:A	0.001057
86_bl-1	86	PKD1; TSC2	MODIFIER; MODERATE	c.*13118G>A; c.*13121G>A; c.4091C>T; c.4223C>T; c.4292C>T	; p.Ser1364Leu; p.Ser1408Leu; p.Ser1431Leu	0	FALSE	chr16:2134515:C:T	118:chr16:2134515:C:T	0.000814
86_bl-1	86	TSC2	MODERATE	c.2702G>A	p.Arg901His	0	FALSE	chr16:2126131:G:A	118:chr16:2126131:G:A	0.000984
86_bl-1	86	IGF1R	MODERATE	c.3934T>C; c.3937T>C	p.Ser1312Pro; p.Ser1313Pro	0	FALSE	chr15:99500504:T:C	118:chr15:99500504:T:C	0.043846
86_bl-1	86	RET	MODERATE	c.1867G>A	p.Glu623Lys	1	FALSE	chr10:43609111:G:A	118:chr10:43609111:G:A	0.001337
86_bl-1	86	AR	MODERATE	c.1933G>A; c.337G>A	p.Glu645Lys; p.Glu113Lys	0	FALSE	chrX:66931291:G:A	118:chrX:66931291:G:A	0.001017
86_bl-1	86	NF1	MODERATE	c.4463G>A; c.4526G>A	p.Arg1488His; p.Arg1509His	1	FALSE	chr17:29587482:G:A	118:chr17:29587482:G:A	0.00095
86_bl-1	86	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2591C>T; n.-1G>A	p.Ala864Val;	2	FALSE	chr7:55259533:C:T	118:chr7:55259533:C:T	0.001641
86_bl-1	86	DDR2	LOW	c.1503A>G	p.Ser501Ser	1	FALSE	chr1:162740301:A:G	118:chr1:162740301:A:G	0.001076
86_bl-1	86	GNAS	MODIFIER; MODERATE	c.*1002G>A; c.*957G>A; c.1051G>A; c.1054G>A; c.1096G>A; c.1099G>A; c.3025G>A; n.1186G>A	; p.Ala351Thr; p.Ala352Thr; p.Ala366Thr; p.Ala367Thr; p.Ala1009Thr	0	FALSE	chr20:57485795:G:A	118:chr20:57485795:G:A	0.001181

86_bl-1	86	IGF1R	MODERATE	c.1172G>A	p.Arg391His	0	FALSE	chr15:99442775:G:A	118:chr15:99442775:G:A	0.000807
86_bl-1	86	ERBB2	MODERATE; MODIFIER	c.322C>T; c.367C>T; c.412C>T; n.736C>T	p.Arg108Trp; p.Arg123Trp; p.Arg138Trp;	1	FALSE	chr17:37864760:C:T	118:chr17:37864760:C:T	0.000832
86_bl-1	86	C9orf53; CDKN2A	MODIFIER; MODERATE; LOW	n.*616G>A; c.*147C>T; c.224C>T; c.267C>T	; p.Pro75Leu; p.Pro89Pro	2	FALSE	chr9:21971134:G:A	118:chr9:21971134:G:A	0.002225
86_bl-1	86	CTNNB1	MODERATE	c.1345C>T	p.Arg449Cys	0	FALSE	chr3:41275179:C:T	118:chr3:41275179:C:T	0.000812
86_bl-1	86	CDKN2A	MODIFIER; MODERATE	c.194-3568A>C; c.52A>C	; p.Thr18Pro	1	FALSE	chr9:21974775:T:G	118:chr9:21974775:T:G	0.050962
86_bl-1	86	MET	HIGH	c.3064C>T; c.3118C>T	p.Arg1022*; p.Arg1040*	1	FALSE	chr7:116414970:C:T	118:chr7:116414970:C:T	0.000957
86_bl-1	86	FGFR1	LOW; MODIFIER; MODERATE	c.-25C>T; c.167C>T; c.68C>T	; p.Pro56Leu; p.Pro23Leu	1	FALSE	chr8:38314897:G:A	118:chr8:38314897:G:A	0.00037
86_bl-1	86	NOTCH1	MODERATE	c.5810G>A	p.Arg1937His	0	FALSE	chr9:139395128:C:T	118:chr9:139395128:C:T	0.001815
86_bl-1	86	DDR2	MODERATE	c.1418G>A	p.Arg473His	2	FALSE	chr1:162740216:G:A	118:chr1:162740216:G:A	0.001339
86_bl-1	86	KDR	MODERATE	c.2323G>T	p.Ala775Ser	1	FALSE	chr4:55964914:C:A	118:chr4:55964914:C:A	0.011189
86_bl-1	86	FGFR1	MODERATE	c.1060C>T; c.1066C>T; c.1303C>T; c.1327C>T; c.1333C>T; c.1426C>T	p.Arg354Trp; p.Arg356Trp; p.Arg435Trp; p.Arg443Trp; p.Arg445Trp; p.Arg476Trp	2	FALSE	chr8:38275843:G:A	118:chr8:38275843:G:A	0.000338
86_bl-1	86	PIK3CA	MODERATE	c.3149G>A	p.Gly1050Asp	3	FALSE	chr3:178952094:G:A	118:chr3:178952094:G:A	0.000923
86_bl-1	86	PDGFRA	MODERATE	c.577G>A	p.Val193Ile	2	FALSE	chr4:55130043:G:A	118:chr4:55130043:G:A	0.000779

86_bl-1	86	FGFR1	MODERATE	c.1666G>A; c.1672G>A; c.1909G>A; c.1933G>A; c.1939G>A; c.2032G>A	p.Asp556Asn; p.Asp558Asn; p.Asp637Asn; p.Asp645Asn; p.Asp647Asn; p.Asp678Asn	1	FALSE	chr8:38272335:C:T	118:chr8:38272335:C:T	0.000624
86_bl-1	86	TP53	MODERATE	c.421C>T; c.502C>T; c.781C>T; c.898C>T	p.Pro141Ser; p.Pro168Ser; p.Pro261Ser; p.Pro300Ser	3	FALSE	chr17:7577040:G:A	118:chr17:7577040:G:A	0.000924
86_bl-1	86	PIK3CA	MODERATE	c.1633G>A	p.Glu545Lys	1189	FALSE	chr3:178936091:G:A	118:chr3:178936091:G:A	0.004985
86_bl-1	86	NTRK1	MODERATE	c.1669C>T; c.1759C>T; c.1777C>T	p.Arg557Trp; p.Arg587Trp; p.Arg593Trp	1	FALSE	chr1:156846336:C:T	118:chr1:156846336:C:T	0.000983
86_bl-1	86	FGFR3	MODERATE	c.682T>C	p.Cys228Arg	2	FALSE	chr4:1803413:T:C	118:chr4:1803413:T:C	0.003121
86_bl-1	86	C9orf53; CDKN2A	MODIFIER; MODERATE	n.*616G>A; c.*318C>T; c.*39C>T; c.395C>T	; p.Ala132Val	1	FALSE	chr9:21970963:G:A	118:chr9:21970963:G:A	0.001552
86_bl-1	86	EPHA3	MODERATE	c.1532C>T	p.Ala511Val	0	FALSE	chr3:89448568:C:T	118:chr3:89448568:C:T	0.001445
86_bl-1	86	TP53	MODERATE	c.143A>G; c.422A>G; c.539A>G; c.62A>G	p.Glu48Gly; p.Glu141Gly; p.Glu180Gly; p.Glu21Gly	1	FALSE	chr17:7578391:T:C	118:chr17:7578391:T:C	0.001258
86_bl-1	86	EGFR	MODERATE	c.442G>A	p.Val148Met	1	FALSE	chr7:55214316:G:A	118:chr7:55214316:G:A	0.001716
86_bl-1	86	PDGFRA	MODERATE	c.571G>A	p.Ala191Thr	1	FALSE	chr4:55130037:G:A	118:chr4:55130037:G:A	0.00078
86_bl-1	86	FBXW7	MODERATE	c.589G>A; c.703G>A; c.943G>A	p.Ala197Thr; p.Ala235Thr; p.Ala315Thr	0	FALSE	chr4:153253790:C:T	118:chr4:153253790:C:T	0.000966

86_bl-1	86	PIK3CA	MODERATE	c.333G>C	p.Lys111Asn	9	FALSE	chr3:178916946:G:C	118:chr3:178916946:G:C	0.000994
86_bl-1	86	FGFR1; LETM2	MODERATE; MODIFIER	c.1834G>A; c.1840G>A; c.2077G>A; c.2101G>A; c.2107G>A; c.2200G>A; c.*1406C>T; c.*1423C>T; c.*1553C>T; c.*1567C>T; c.*1638C>T	p.Gly612Ser; p.Gly614Ser; p.Gly693Ser; p.Gly701Ser; p.Gly703Ser; p.Gly734Ser;	2	FALSE	chr8:38271749:C:T	118:chr8:38271749:C:T	0.000853
86_bl-1	86	MITF	MODERATE	c.127A>C; c.235A>C; c.280A>C; c.283A>C	p.Thr43Pro; p.Thr79Pro; p.Thr94Pro; p.Thr95Pro	0	FALSE	chr3:69928463:A:C	118:chr3:69928463:A:C	0.135701
86_bl-1	86	SMO	MODERATE	c.1045A>C	p.Thr349Pro	0	FALSE	chr7:128846115:A:C	118:chr7:128846115:A:C	0.043412
86_bl-1	86	KDR	MODERATE	c.2315C>T	p.Ala772Val	1	FALSE	chr4:55964922:G:A	118:chr4:55964922:G:A	0.001376
86_bl-1	86	FGFR2	MODIFIER; MODERATE	c.110-1053G>A; c.110-14173G>A; n.757-14173G>A; c.182G>A	; p.Arg61His	1	FALSE	chr10:123325146:C:T	118:chr10:123325146:C:T	0.001791
86_bl-1	86	CWH43	MODERATE	c.209C>T; c.290C>T	p.Ala70Val; p.Ala97Val	0	FALSE	chr4:48993525:C:T	118:chr4:48993525:C:T	0.001595
131_c1w2-1	131	CDKN2B; CDKN2B-AS1	MODERATE; MODIFIER	c.118C>T; n.371+13675G>A	p.Pro40Ser;	0	FALSE	chr9:22008835:G:A	119:chr9:22008835:G:A	0.001704

131_c1w2-1	131	TP53	MODERATE	c.362G>A; c.443G>A; c.722G>A; c.839G>A	p.Arg121Lys; p.Arg148Lys; p.Arg241Lys; p.Arg280Lys	64	FALSE	chr17:7577099:C:T	119:chr17:7577099:C:T	0.00112
131_c1w2-1	131	CDH1	MODERATE	c.2320A>G	p.Arg774Gly	0	FALSE	chr16:68863581:A:G	119:chr16:68863581:A:G	0.000998
131_c1w2-1	131	NTRK1	MODERATE	c.804C>G; c.894C>G	p.His268Gln; p.His298Gln	1	FALSE	chr1:156843468:C:G	119:chr1:156843468:C:G	0.001275
131_c1w2-1	131	EPHA3	MODERATE	c.2051G>A	p.Arg684Gln	0	FALSE	chr3:89468517:G:A	119:chr3:89468517:G:A	0.00095
131_c1w2-1	131	ERBB2	MODERATE; MODIFIER	c.632C>T; c.677C>T; c.722C>T; n.1046C>T	p.Ala211Val; p.Ala226Val; p.Ala241Val;	2	FALSE	chr17:37866417:C:T	119:chr17:37866417:C:T	0.001018
131_c1w2-1	131	DDR2	MODERATE	c.1022G>A	p.Arg341Gln	1	FALSE	chr1:162731167:G:A	119:chr1:162731167:G:A	0.000827
131_c1w2-1	131	MET	MODERATE	c.3280C>T; c.3334C>T	p.His1094Tyr; p.His1112Tyr	4	FALSE	chr7:116417463:C:T	119:chr7:116417463:C:T	0.00104
131_c1w2-1	131	EGFR	MODERATE	c.406C>A	p.Pro136Thr	1	FALSE	chr7:55211163:C:A	119:chr7:55211163:C:A	0.001344
131_c1w2-1	131	DDR2	MODERATE	c.2516G>A	p.Arg839His	3	FALSE	chr1:162749984:G:A	119:chr1:162749984:G:A	0.000973
131_c1w2-1	131	NTRK1	MODERATE	c.1975C>T; c.2065C>T; c.2083C>T	p.Pro659Ser; p.Pro689Ser; p.Pro695Ser	2	FALSE	chr1:156849827:C:T	119:chr1:156849827:C:T	0.001441
131_c1w2-1	131	TP53	HIGH	c.439C>T; c.520C>T; c.799C>T; c.916C>T	p.Arg147*; p.Arg174*; p.Arg267*; p.Arg306*	167	FALSE	chr17:7577022:G:A	119:chr17:7577022:G:A	0.001076
131_c1w2-1	131	IGF1R	MODERATE	c.3905T>C; c.3908T>C	p.Val1302Ala; p.Val1303Ala	0	FALSE	chr15:99500475:T:C	119:chr15:99500475:T:C	0.012165
131_c1w2-1	131	PTEN	HIGH	c.822G>A	p.Trp274*	3	FALSE	chr10:89720671:G:A	119:chr10:89720671:G:A	0.002317

131_c1w2-1	131	GAPDH; IFFO1; NCAPD2	MODERATE; MODIFIER	c.148G>A; c.274G>A; c.*1743C>T; c.*1746C>T; c.*1770C>T; n.*2798C>T; c.*4252G>A	p.Ala50Thr; p.Ala92Thr;	0	FALSE	chr12:6646123:G:A	119:chr12:6646123:G:A	0.001801
131_c1w2-1	131	FGFR4	MODIFIER; MODERATE	c.1193+43C>T; c.1270C>T; c.1390C>T	; p.Arg424Trp; p.Arg464Trp	1	FALSE	chr5:176520545:C:T	119:chr5:176520545:C:T	0.001068
131_c1w2-1	131	PIK3CA	MODERATE	c.1235G>A	p.Arg412Gln	1	FALSE	chr3:178927472:G:A	119:chr3:178927472:G:A	0.001627
131_c1w2-1	131	PTEN	MODERATE	c.235G>A	p.Ala79Thr	3	FALSE	chr10:89690828:G:A	119:chr10:89690828:G:A	0.00114
131_c1w2-1	131	TP53	MODERATE	c.257G>A; c.338G>A; c.617G>A; c.734G>A	p.Gly86Asp; p.Gly113Asp; p.Gly206Asp; p.Gly245Asp	126	FALSE	chr17:7577547:C:T	119:chr17:7577547:C:T	0.001644
131_c1w2-1	131	DDR2	MODERATE	c.1418G>A	p.Arg473His	2	FALSE	chr1:162740216:G:A	119:chr1:162740216:G:A	0.000934
131_c1w2-1	131	PTEN	MODERATE	c.133G>A	p.Val45Ile	1	FALSE	chr10:89653835:G:A	119:chr10:89653835:G:A	0.000984
131_c1w2-1	131	MAP2K1	MODERATE	c.379G>A	p.Val127Met	1	FALSE	chr15:66729171:G:A	119:chr15:66729171:G:A	0.001352
131_c1w2-1	131	APC	MODIFIER; MODERATE	c.676-8791C>T; c.688C>T	; p.Arg230Cys	0	FALSE	chr5:112128185:C:T	119:chr5:112128185:C:T	0.001063
131_c1w2-1	131	FGFR3	MODERATE	c.905G>A	p.Gly302Asp	1	FALSE	chr4:1803727:G:A	119:chr4:1803727:G:A	0.001229
131_c1w2-1	131	RET	MODERATE	c.1690A>C	p.Thr564Pro	1	FALSE	chr10:43608342:A:C	119:chr10:43608342:A:C	0.069824
131_c1w2-1	131	C9orf53; CDKN2A	MODIFIER; MODERATE; LOW	n.*616T>G; c.*216A>C; c.293A>C; c.336A>C	; p.His98Pro; p.Ala112Ala	2	FALSE	chr9:21971065:T:G	119:chr9:21971065:T:G	0.002831

131_c1w2-1	131	C9orf53; CDKN2A	MODIFIER; MODERATE; LOW	n.*616G>A; c.*222C>T; c.299C>T; c.342C>T	; p.Ala100Val; p.Gly114Gly	2	FALSE	chr9:21971059:G:A	119:chr9:21971059:G:A	0.001123
131_c1w2-1	131	PIK3CA	HIGH	c.3152G>A	p.Trp1051*	3	FALSE	chr3:178952097:G:A	119:chr3:178952097:G:A	0.000881
131_c1w2-1	131	PIK3CA	MODERATE	c.3154A>G	p.Thr1052Ala	3	FALSE	chr3:178952099:A:G	119:chr3:178952099:A:G	0.000889
131_c1w2-1	131	CTNNB1	MODERATE	c.1972G>T	p.Val658Phe	0	FALSE	chr3:41278096:G:T	119:chr3:41278096:G:T	0.004569
131_c1w2-1	131	NTRK1	MODERATE	c.1940T>G; c.2030T>G; c.2048T>G	p.Val647Gly; p.Val677Gly; p.Val683Gly	2	FALSE	chr1:156849792:T:G	119:chr1:156849792:T:G	0.02069
131_c1w2-1	131	DEAR; FBXW7	MODIFIER; HIGH	n.108G>A; c.475C>T; c.589C>T; c.829C>T	; p.Gln159*; p.Gln197*; p.Gln277*	0	FALSE	chr4:153258986:G:A	119:chr4:153258986:G:A	0.001194
131_c1w2-1	131	HRAS; LRRC56	MODERATE; MODIFIER	c.368G>A; c.-506C>T	p.Arg123His;	2	FALSE	chr11:533535:C:T	119:chr11:533535:C:T	0.00116
131_c1w2-1	131	FGFR2	MODERATE; MODIFIER	c.1591G>A; c.1594G>A; c.1597G>A; c.1606G>A; c.1675G>A; c.1678G>A; c.1942G>A; c.1945G>A; n.2392G>A	p.Ala531Thr; p.Ala532Thr; p.Ala533Thr; p.Ala536Thr; p.Ala559Thr; p.Ala560Thr; p.Ala648Thr; p.Ala649Thr;	3	FALSE	chr10:123247549:C:T	119:chr10:123247549:C:T	0.001784
131_c1w2-1	131	BRAF	MODERATE	c.914C>T	p.Ala305Val	2	FALSE	chr7:140500228:G:A	119:chr7:140500228:G:A	0.00225
131_c1w2-1	131	CDKN2A	MODIFIER; MODERATE	c.194-3537T>G; c.83T>G	; p.Val28Gly	1	FALSE	chr9:21974744:A:C	119:chr9:21974744:A:C	0.075614
131_c1w2-1	131	BRAF	MODERATE	c.2083G>A	p.Glu695Lys	2	FALSE	chr7:140439656:C:T	119:chr7:140439656:C:T	0.001065
131_c1w2-1	131	SMO	MODERATE	c.1045A>C	p.Thr349Pro	0	FALSE	chr7:128846115:A:C	119:chr7:128846115:A:C	0.030697

131_c1w2-1	131	EPHA3	MODERATE	c.1516G>A	p.Val506Ile	0	FALSE	chr3:89448552:G:A	119:chr3:89448552:G:A	0.001123
131_c1w2-1	131	CDKN2A	MODIFIER; MODERATE	c.194-3568A>C; c.52A>C	; p.Thr18Pro	1	FALSE	chr9:21974775:T:G	119:chr9:21974775:T:G	0.04665
131_c1w2-1	131	NOTCH1	MODERATE	c.5033T>C	p.Leu1678Pro	0	FALSE	chr9:139397768:A:G	119:chr9:139397768:A:G	0.001414
131_c1w2-1	131	IGF1R	MODERATE	c.3934T>C; c.3937T>C	p.Ser1312Pro; p.Ser1313Pro	0	FALSE	chr15:99500504:T:C	119:chr15:99500504:T:C	0.030199
131_c1w2-1	131	CTNNB1	MODERATE	c.1166C>T	p.Ser389Leu	0	FALSE	chr3:41274916:C:T	119:chr3:41274916:C:T	0.000869
131_c1w2-1	131	EGFR	MODIFIER; MODERATE	c.*1464C>T; c.1279C>T	; p.Arg427Cys	2	FALSE	chr7:55225427:C:T	119:chr7:55225427:C:T	0.00099
131_c1w2-1	131	TP53	MODERATE	c.254G>T; c.335G>T; c.614G>T; c.731G>T	p.Gly85Val; p.Gly112Val; p.Gly205Val; p.Gly244Val	44	FALSE	chr17:7577550:C:A	119:chr17:7577550:C:A	0.001065
131_c1w2-1	131	EGFR	MODIFIER; MODERATE	c.*2364T>C; c.2195T>C	; p.Ile732Thr	1	FALSE	chr7:55242425:T:C	119:chr7:55242425:T:C	0.001012
131_c1w2-1	131	NOTCH1	MODERATE	c.4984C>T	p.Arg1662Trp	0	FALSE	chr9:139399159:G:A	119:chr9:139399159:G:A	0.001319
131_c1w2-1	131	FGFR4	MODERATE	c.1978G>A; c.2062G>A; c.2182G>A	p.Ala660Thr; p.Ala688Thr; p.Ala728Thr	1	FALSE	chr5:176524321:G:A	119:chr5:176524321:G:A	0.001351
131_c1w2-1	131	TSC2	MODERATE	c.3032G>A; c.3164G>A	p.Gly1011Asp; p.Gly1055Asp	0	FALSE	chr16:2129309:G:A	119:chr16:2129309:G:A	0.001197
131_c1w2-1	131	CSDE1; NRAS	MODIFIER; MODERATE	c.*2430C>T; c.*2523C>T; c.*2817C>T; c.*2910C>T; c.*2964C>T; c.*3057C>T; c.173C>T	; p.Thr58Ile	1	FALSE	chr1:115256538:G:A	119:chr1:115256538:G:A	0.001208
131_c1w2-1	131	SMO	MODERATE	c.799C>T	p.Leu267Phe	0	FALSE	chr7:128845502:C:T	119:chr7:128845502:C:T	0.001103

131_c1w2-1	131	NTRK3	MODERATE	c.1420C>T; c.1444C>T	p.His474Tyr; p.His482Tyr	0	FALSE	chr15:88576229:G:A	119:chr15:88576229:G:A	0.001274
131_c1w2-1	131	STK11	MODERATE	c.455A>G	p.Gln152Arg	3	FALSE	chr19:1219403:A:G	119:chr19:1219403:A:G	0.002349
131_c1w2-1	131	EPHA3	MODERATE	c.1142G>A	p.Arg381His	0	FALSE	chr3:89391076:G:A	119:chr3:89391076:G:A	0.000891
131_c1w2-1	131	NOTCH1	MODERATE	c.5777G>A	p.Arg1926His	0	FALSE	chr9:139395161:C:T	119:chr9:139395161:C:T	0.001236
131_c1w2-1	131	CWH43	MODERATE	c.1535G>A; c.1616G>A	p.Gly512Asp; p.Gly539Asp	0	FALSE	chr4:49034690:G:A	119:chr4:49034690:G:A	0.000965
131_c1w2-1	131	NOTCH1	MODERATE	c.3859C>T	p.Arg1287Cys	0	FALSE	chr9:139401210:G:A	119:chr9:139401210:G:A	0.001151
131_c1w2-1	131	NF1	HIGH	c.3916C>T	p.Arg1306*	8	FALSE	chr17:29562981:C:T	119:chr17:29562981:C:T	0.000823
131_c1w2-1	131	MITF	MODERATE	c.127A>C; c.235A>C; c.280A>C; c.283A>C	p.Thr43Pro; p.Thr79Pro; p.Thr94Pro; p.Thr95Pro	0	FALSE	chr3:69928463:A:C	119:chr3:69928463:A:C	0.165873
131_c1w2-1	131	NOTCH1	MODERATE	c.4918G>A	p.Ala1640Thr	0	FALSE	chr9:139399225:C:T	119:chr9:139399225:C:T	0.001862
131_c1w2-1	131	IDH1	MODERATE	c.394C>T	p.Arg132Cys	626	FALSE	chr2:209113113:G:A	119:chr2:209113113:G:A	0.003279
131_c1w2-1	131	IDH2; ZNF710	LOW; MODIFIER	c.1023G>A; c.1179G>A; c.789G>A; c.*2147C>T	p.Arg341Arg; p.Arg393Arg; p.Arg263Arg;	1	FALSE	chr15:90628140:C:T	119:chr15:90628140:C:T	0.001185
131_c1w2-1	131	KIT	MODERATE	c.365G>A	p.Arg122His	1	FALSE	chr4:55564477:G:A	119:chr4:55564477:G:A	0.001507
131_c1w2-1	131	NOTCH1	MODERATE	c.5347C>T	p.Arg1783Trp	0	FALSE	chr9:139396761:G:A	119:chr9:139396761:G:A	0.001601
131_c1w2-1	131	EPHA3	MODERATE	c.1672G>A	p.Val558Ile	0	FALSE	chr3:89456496:G:A	119:chr3:89456496:G:A	0.000946
131_c1w2-1	131	NF1	MODERATE	c.2695T>G	p.Leu899Val	3	FALSE	chr17:29556328:T:G	119:chr17:29556328:T:G	0.045144
131_c1w2-1	131	CDKN2A	MODIFIER; MODERATE	c.194-3546T>G; c.74T>G	; p.Val25Gly	2	FALSE	chr9:21974753:A:C	119:chr9:21974753:A:C	0.198413

131_c1w2-1	131	SMO	MODERATE	c.869G>A	p.Arg290His	0	FALSE	chr7:128845572:G:A	119:chr7:128845572:G:A	0.001149
111_c3-1	111	CDKN2A	MODIFIER; MODERATE	c.194-3568A>C; c.52A>C	; p.Thr18Pro	1	FALSE	chr9:21974775:T:G	120:chr9:21974775:T:G	0.030075
111_c3-1	111	PIK3R1	MODERATE	c.1715A>G; c.626A>G; c.815A>G; c.905A>G	p.Gln572Arg; p.Gln209Arg; p.Gln272Arg; p.Gln302Arg	1	FALSE	chr5:67591122:A:G	120:chr5:67591122:A:G	0.001565
111_c3-1	111	PIK3CA	MODERATE	c.3034G>A	p.Glu1012Lys	2	FALSE	chr3:178951979:G:A	120:chr3:178951979:G:A	0.001294
111_c3-1	111	ATM	MODERATE	c.2075G>A	p.Arg692His	0	FALSE	chr11:108124717:G:A	120:chr11:108124717:G:A	0.001354
111_c3-1	111	NF1	MODERATE	c.7583C>T; c.7646C>T	p.Ser2528Leu; p.Ser2549Leu	3	FALSE	chr17:29683508:C:T	120:chr17:29683508:C:T	0.001365
111_c3-1	111	CDKN2A	MODIFIER; MODERATE	c.194-3537T>G; c.83T>G	; p.Val28Gly	1	FALSE	chr9:21974744:A:C	120:chr9:21974744:A:C	0.06192
111_c3-1	111	EGFR	MODERATE	c.787A>C	p.Thr263Pro	6	FALSE	chr7:55221743:A:C	120:chr7:55221743:A:C	0.001591
111_c3-1	111	SMO	MODERATE	c.1045A>C	p.Thr349Pro	0	FALSE	chr7:128846115:A:C	120:chr7:128846115:A:C	0.034783
111_c3-1	111	PIK3R1	MODERATE	c.1768C>T; c.679C>T; c.868C>T; c.958C>T	p.Arg590Trp; p.Arg227Trp; p.Arg290Trp; p.Arg320Trp	1	FALSE	chr5:67591270:C:T	120:chr5:67591270:C:T	0.002532
111_c3-1	111	NTRK3	MODERATE	c.560T>C	p.Leu187Pro	0	FALSE	chr15:88680697:A:G	120:chr15:88680697:A:G	0.002534
111_c3-1	111	MET	HIGH	c.1619G>A	p.Trp540*	1	FALSE	chr7:116380997:G:A	120:chr7:116380997:G:A	0.001276
111_c3-1	111	GNA11	MODERATE	c.805G>A	p.Val269Ile	1	FALSE	chr19:3119273:G:A	120:chr19:3119273:G:A	0.001808
111_c3-1	111	SMO	MODERATE	c.508A>C	p.Thr170Pro	0	FALSE	chr7:128843401:A:C	120:chr7:128843401:A:C	0.001663
111_c3-1	111	TP53	MODERATE	c.280A>C; c.361A>C; c.640A>C; c.757A>C	p.Thr94Pro; p.Thr121Pro; p.Thr214Pro; p.Thr253Pro	9	FALSE	chr17:7577524:T:G	120:chr17:7577524:T:G	0.008737

111_c3-1	111	CDKN2A	MODIFIER; MODERATE	c.194-3570C>G; c.50C>G	; p.Ala17Gly	1	FALSE	chr9:21974777:G:C	120:chr9:21974777:G:C	0.002506
111_c3-1	111	TP53	MODERATE; MODIFIER	c.230C>T; c.347C>T; c.-279C>T; c.-360C>T	p.Ser77Phe; p.Ser116Phe;	1	FALSE	chr17:7579340:G:A	120:chr17:7579340:G:A	0.001672
111_c3-1	111	CDKN2A; CDKN2B-AS1	MODERATE; MODIFIER	c.22A>G; n.-1T>C	p.Thr8Ala;	1	FALSE	chr9:21994309:T:C	120:chr9:21994309:T:C	0.005348
111_c3-1	111	C9orf53; CDKN2A	MODIFIER; MODERATE; LOW	n.*616T>G; c.*120A>C; c.197A>C; c.240A>C	; p.His66Pro; p.Pro80Pro	1	FALSE	chr9:21971161:T:G	120:chr9:21971161:T:G	0.095137
111_c3-1	111	ESR1	MODERATE	c.739G>A; c.745G>A	p.Glu247Lys; p.Glu249Lys	0	FALSE	chr6:152201885:G:A	120:chr6:152201885:G:A	0.001514
111_c3-1	111	EPHA3	MODERATE	c.608C>T	p.Pro203Leu	0	FALSE	chr3:89259464:C:T	120:chr3:89259464:C:T	0.001423
111_c3-1	111	PDGFRA	LOW	c.2001A>G	p.Ser667Ser	2	FALSE	chr4:55144172:A:G	120:chr4:55144172:A:G	0.002532
111_c3-1	111	AR	MODERATE	c.2086G>A; c.490G>A	p.Asp696Asn; p.Asp164Asn	0	FALSE	chrX:66931444:G:A	120:chrX:66931444:G:A	0.00141
111_c3-1	111	NTRK1	MODERATE	c.804C>G; c.894C>G	p.His268Gln; p.His298Gln	1	FALSE	chr1:156843468:C:G	120:chr1:156843468:C:G	0.004278
111_c3-1	111	KIT	MODERATE	c.2573T>C; c.2585T>C	p.Leu858Pro; p.Leu862Pro	1	FALSE	chr4:55602764:T:C	120:chr4:55602764:T:C	0.001364
111_c3-1	111	KIT	MODERATE	c.1156G>A	p.Glu386Lys	1	FALSE	chr4:55575630:G:A	120:chr4:55575630:G:A	0.001558
111_c3-1	111	NTRK1	MODERATE	c.1940T>G; c.2030T>G; c.2048T>G	p.Val647Gly; p.Val677Gly; p.Val683Gly	2	FALSE	chr1:156849792:T:G	120:chr1:156849792:T:G	0.029024
111_c3-1	111	EPHA3	MODERATE	c.1535G>A	p.Arg512Gln	0	FALSE	chr3:89448571:G:A	120:chr3:89448571:G:A	0.001519
111_c3-1	111	PIK3CA	MODERATE	c.193G>A	p.Glu65Lys	1	FALSE	chr3:178916806:G:A	120:chr3:178916806:G:A	0.001383

111_c3-1	111	TP53	MODERATE	c.268A>G; c.349A>G; c.628A>G; c.745A>G	p.Arg90Gly; p.Arg117Gly; p.Arg210Gly; p.Arg249Gly	36	FALSE	chr17:7577536:T:C	120:chr17:7577536:T:C	0.004026
111_c3-1	111	C9orf53; CDKN2A	MODIFIER; MODERATE; LOW	n.*616G>A; c.*222C>T; c.299C>T; c.342C>T	; p.Ala100Val; p.Gly114Gly	2	FALSE	chr9:21971059:G:A	120:chr9:21971059:G:A	0.001986
111_c3-1	111	FGFR3	MODERATE	c.1183G>A; c.1519G>A; c.1525G>A	p.Val395Met; p.Val507Met; p.Val509Met	1	FALSE	chr4:1807188:G:A	120:chr4:1807188:G:A	0.002193
111_c3-1	111	APC	HIGH	c.850C>T; c.904C>T	p.Arg284*; p.Arg302*	0	FALSE	chr5:112151261:C:T	120:chr5:112151261:C:T	0.001322
111_c3-1	111	TP53	MODIFIER; MODERATE	c.*145T>C; c.*233T>C; c.1009T>C; c.1126T>C; c.649T>C; c.730T>C	; p.Ser337Pro; p.Ser376Pro; p.Ser217Pro; p.Ser244Pro	2	FALSE	chr17:7572983:A:G	120:chr17:7572983:A:G	0.005405
111_c3-1	111	PTEN	MODERATE	c.1123G>A	p.Asp375Asn	3	FALSE	chr10:89725140:G:A	120:chr10:89725140:G:A	0.001885
111_c3-1	111	KDR	MODERATE	c.2323G>T	p.Ala775Ser	1	FALSE	chr4:55964914:C:A	120:chr4:55964914:C:A	0.01115
111_c3-1	111	NOTCH1	MODERATE	c.4733T>G	p.Val1578Gly	0	FALSE	chr9:139399410:A:C	120:chr9:139399410:A:C	0.004065
111_c3-1	111	KRAS	MODIFIER; MODERATE	c.451-5609G>A; c.491G>A	; p.Arg164Gln	1	FALSE	chr12:25368454:C:T	120:chr12:25368454:C:T	0.001225
111_c3-1	111	TP53	MODERATE	c.119T>G; c.38T>G; c.398T>G; c.515T>G	p.Val40Gly; p.Val13Gly; p.Val133Gly; p.Val172Gly	12	FALSE	chr17:7578415:A:C	120:chr17:7578415:A:C	0.001821
111_c3-1	111	VHL	MODIFIER; MODERATE	c.341-3270A>C; c.344A>C	; p.His115Pro	0	FALSE	chr3:10188201:A:C	120:chr3:10188201:A:C	0.001864

111_c3-1	111	NRAS	MODERATE	c.317C>T	p.Ser106Leu	1	FALSE	chr1:115252323:G:A	120:chr1:115252323:G:A	0.00189
80_c6-1	80	RET	MODERATE	c.1690A>C	p.Thr564Pro	1	FALSE	chr10:43608342:A:C	121:chr10:43608342:A:C	0.044542
80_c6-1	80	PTEN	MODERATE	c.133G>A	p.Val45Ile	1	FALSE	chr10:89653835:G:A	121:chr10:89653835:G:A	0.001232
80_c6-1	80	TP53	MODERATE	c.145C>T; c.424C>T; c.541C>T; c.64C>T	p.Arg49Cys; p.Arg142Cys; p.Arg181Cys; p.Arg22Cys	21	FALSE	chr17:7578389:G:A	121:chr17:7578389:G:A	0.001637
80_c6-1	80	ATM	MODERATE	c.3925G>A	p.Ala1309Thr	0	FALSE	chr11:108155132:G:A	121:chr11:108155132:G:A	0.001198
80_c6-1	80	CTNNB1	MODERATE	c.1345C>T	p.Arg449Cys	0	FALSE	chr3:41275179:C:T	121:chr3:41275179:C:T	0.001022
80_c6-1	80	MIR4673; NOTCH1	MODIFIER; MODERATE	n.*59A>C; c.1195A>C	; p.Thr399Pro	0	FALSE	chr9:139412649:T:G	121:chr9:139412649:T:G	0.005084
80_c6-1	80	TSC2	MODIFIER; MODERATE	c.2837+1108G>A; c.2933G>A	; p.Arg978His	0	FALSE	chr16:2127694:G:A	121:chr16:2127694:G:A	0.0012
80_c6-1	80	MITF	MODERATE	c.1091G>A; c.1136G>A; c.1139G>A; c.650G>A; c.818G>A; c.836G>A; c.983G>A	p.Arg364Gln; p.Arg379Gln; p.Arg380Gln; p.Arg217Gln; p.Arg273Gln; p.Arg279Gln; p.Arg328Gln	0	FALSE	chr3:70008549:G:A	121:chr3:70008549:G:A	0.001189
80_c6-1	80	FGFR1	MODERATE	c.359C>T; c.365C>T; c.608C>T; c.626C>T; c.632C>T; c.725C>T	p.Ala120Val; p.Ala122Val; p.Ala203Val; p.Ala209Val; p.Ala211Val; p.Ala242Val	1	FALSE	chr8:38283753:G:A	121:chr8:38283753:G:A	0.001127
80_c6-1	80	KDR	MODERATE	c.1028C>T	p.Thr343Met	3	FALSE	chr4:55976884:G:A	121:chr4:55976884:G:A	0.000867

80_c6-1	80	NF1	MODERATE	c.2695T>G	p.Leu899Val	3	FALSE	chr17:29556328:T:G	121:chr17:29556328:T:G	0.012696
80_c6-1	80	IGF1R	MODERATE	c.3934T>C; c.3937T>C	p.Ser1312Pro; p.Ser1313Pro	0	FALSE	chr15:99500504:T:C	121:chr15:99500504:T:C	0.032875
80_c6-1	80	C9orf53; CDKN2A	MODIFIER; MODERATE	n.*616C>G; c.*140G>C; c.217G>C; c.260G>C	; p.Ala73Pro; p.Arg87Pro	1	FALSE	chr9:21971141:C:G	121:chr9:21971141:C:G	0.005128
80_c6-1	80	NOTCH1	MODERATE	c.3859C>T	p.Arg1287Cys	0	FALSE	chr9:139401210:G:A	121:chr9:139401210:G:A	0.001979
80_c6-1	80	FBXW7	MODERATE	c.1090A>C; c.1204A>C; c.1444A>C	p.Thr364Pro; p.Thr402Pro; p.Thr482Pro	0	FALSE	chr4:153247358:T:G	121:chr4:153247358:T:G	0.001075
80_c6-1	80	CDH1	MODERATE	c.68A>G	p.Gln23Arg	0	FALSE	chr16:68772219:A:G	121:chr16:68772219:A:G	0.001153
80_c6-1	80	EGFR	MODERATE	c.719G>A	p.Cys240Tyr	1	FALSE	chr7:55220329:G:A	121:chr7:55220329:G:A	0.001736
80_c6-1	80	ALK	MODERATE	c.1307C>T	p.Ala436Val	1	FALSE	chr2:29551323:G:A	121:chr2:29551323:G:A	0.001397
80_c6-1	80	C9orf53; CDKN2A	MODIFIER; MODERATE; LOW	n.*616T>G; c.*120A>C; c.197A>C; c.240A>C	; p.His66Pro; p.Pro80Pro	1	FALSE	chr9:21971161:T:G	121:chr9:21971161:T:G	0.052345
80_c6-1	80	FGFR2	MODIFIER; MODERATE	c.110-14065C>T; c.110-945C>T; n.757-14065C>T; c.290C>T	; p.Ala97Val	1	FALSE	chr10:123325038:G:A	121:chr10:123325038:G:A	0.001201
80_c6-1	80	TP53	MODIFIER; MODERATE	c.*145T>C; c.*233T>C; c.1009T>C; c.1126T>C; c.649T>C; c.730T>C	; p.Ser337Pro; p.Ser376Pro; p.Ser217Pro; p.Ser244Pro	2	FALSE	chr17:7572983:A:G	121:chr17:7572983:A:G	0.00431

80_c6-1	80	ROS1	MODERATE	c.5827G>A	p.Glu1943Lys	1	FALSE	chr6:117641144:C:T	121:chr6:117641144:C:T	0.001074
80_c6-1	80	NTRK2	MODERATE	c.220G>A	p.Ala74Thr	0	FALSE	chr9:87317081:G:A	121:chr9:87317081:G:A	0.001323
80_c6-1	80	TP53	MODIFIER; MODERATE	c.*182C>T; c.*94C>T; c.1075C>T; c.598C>T; c.679C>T; c.958C>T	; p.Pro359Ser; p.Pro200Ser; p.Pro227Ser; p.Pro320Ser	1	FALSE	chr17:7573952:G:A	121:chr17:7573952:G:A	0.001013
80_c6-1	80	NOTCH1	MODERATE	c.4733T>G	p.Val1578Gly	0	FALSE	chr9:139399410:A:C	121:chr9:139399410:A:C	0.001559
80_c6-1	80	FBXW7	MODERATE	c.1391C>T; c.1505C>T; c.1745C>T	p.Ser464Leu; p.Ser502Leu; p.Ser582Leu	0	FALSE	chr4:153245446:G:A	121:chr4:153245446:G:A	0.001292
80_c6-1	80	TSC2	MODERATE	c.1654G>A	p.Ala552Thr	0	FALSE	chr16:2115574:G:A	121:chr16:2115574:G:A	0.001202
80_c6-1	80	C9orf53; CDKN2A	MODIFIER; MODERATE; LOW	n.*616C>T; c.*232G>A; c.352G>A; c.309G>A	; p.Ala118Thr; p.Arg103Arg	1	FALSE	chr9:21971049:C:T	121:chr9:21971049:C:T	0.001138
80_c6-1	80	EGFR	HIGH	c.3202C>T	p.Arg1068*	1	FALSE	chr7:55270249:C:T	121:chr7:55270249:C:T	0.001581
80_c6-1	80	PTEN	MODERATE	c.828T>A	p.Asn276Lys	1	FALSE	chr10:89720677:T:A	121:chr10:89720677:T:A	0.001689
80_c6-1	80	ERBB2; MIEN1; MIR4728	MODERATE; MODIFIER	c.2434G>A; c.2479G>A; c.2524G>A; n.2848G>A; c.*388C>T; n.-1G>A	p.Val812Ile; p.Val827Ile; p.Val842Ile;	17	FALSE	chr17:37881332:G:A	121:chr17:37881332:G:A	0.001135

80_c6-1	80	MIR1225; PKD1; TSC2	MODIFIER; MODERATE	n.*90C>T; c.*13118C>T; c.*13121C>T; c.4715G>A; c.4847G>A; c.4916G>A	; p.Arg1572His; p.Arg1616His; p.Arg1639His	0	FALSE	chr16:2136799:G:A	121:chr16:2136799:G:A	0.001097
80_c6-1	80	FGFR2	MODERATE; MODIFIER	c.1859G>T; c.1862G>T; c.1865G>T; c.1874G>T; c.1943G>T; c.1946G>T; c.2210G>T; c.2213G>T; n.2660G>T	p.Arg620Met; p.Arg621Met; p.Arg622Met; p.Arg625Met; p.Arg648Met; p.Arg649Met; p.Arg737Met; p.Arg738Met;	1	FALSE	chr10:123243303:C:A	121:chr10:123243303:C:A	0.001329
80_c6-1	80	MET	MODERATE	c.487T>C	p.Ser163Pro	1	FALSE	chr7:116339625:T:C	121:chr7:116339625:T:C	0.001479
80_c6-1	80	PIK3R1	MODERATE	c.1226G>A; c.137G>A; c.326G>A; c.416G>A	p.Arg409Gln; p.Arg46Gln; p.Arg109Gln; p.Arg139Gln	1	FALSE	chr5:67589238:G:A	121:chr5:67589238:G:A	0.001228
80_c6-1	80	PDGFRA	MODERATE	c.1499G>A	p.Arg500Gln	1	FALSE	chr4:55139838:G:A	121:chr4:55139838:G:A	0.001087
80_c6-1	80	IDH2; ZNF710	MODERATE; MODIFIER	c.1091C>T; c.1247C>T; c.857C>T; c.*2147G>A	p.Ala364Val; p.Ala416Val; p.Ala286Val;	1	FALSE	chr15:90628072:G:A	121:chr15:90628072:G:A	0.001158
80_c6-1	80	IGF1R	HIGH	c.2716C>T	p.Gln906*	0	FALSE	chr15:99467847:C:T	121:chr15:99467847:C:T	0.001068
80_c6-1	80	TSC2	MODERATE	c.1922G>A	p.Ser641Asn	0	FALSE	chr16:2121593:G:A	121:chr16:2121593:G:A	0.001088
80_c6-1	80	CTNNB1	MODERATE	c.1972G>T	p.Val658Phe	0	FALSE	chr3:41278096:G:T	121:chr3:41278096:G:T	0.003238

80_c6-1	80	CDKN2A	MODIFIER; MODERATE	c.194-3537T>G; c.83T>G	; p.Val28Gly	1	FALSE	chr9:21974744:A:C	121:chr9:21974744:A:C	0.03958
80_c6-1	80	CDKN2A	MODIFIER; MODERATE	c.194-3568A>C; c.52A>C	; p.Thr18Pro	1	FALSE	chr9:21974775:T:G	121:chr9:21974775:T:G	0.019697
80_c6-1	80	SMO	MODERATE	c.1045A>C	p.Thr349Pro	0	FALSE	chr7:128846115:A:C	121:chr7:128846115:A:C	0.025146
80_c6-1	80	PIK3CA	MODERATE	c.1849C>T	p.Arg617Trp	1	FALSE	chr3:178937461:C:T	121:chr3:178937461:C:T	0.001138
80_c6-1	80	MITF	MODIFIER; MODERATE	c.93+115G>A; c.208G>A; c.373G>A; c.481G>A; c.526G>A; c.529G>A	; p.Ala70Thr; p.Ala125Thr; p.Ala161Thr; p.Ala176Thr; p.Ala177Thr	0	FALSE	chr3:69987147:G:A	121:chr3:69987147:G:A	0.001724
80_c6-1	80	ROS1	MODERATE	c.5687T>G	p.Val1896Gly	1	FALSE	chr6:117642512:A:C	121:chr6:117642512:A:C	0.001912
80_c6-1	80	MIR1225; PKD1; TSC2	MODIFIER; MODERATE	n.*90C>T; c.*13118C>T; c.*13121C>T; c.5033G>A; c.5165G>A; c.5234G>A	; p.Arg1678His; p.Arg1722His; p.Arg1745His	0	FALSE	chr16:2138301:G:A	121:chr16:2138301:G:A	0.001397
80_c6-1	80	IGF1R	MODERATE	c.3905T>C; c.3908T>C	p.Val1302Ala; p.Val1303Ala	0	FALSE	chr15:99500475:T:C	121:chr15:99500475:T:C	0.008065
80_c6-1	80	PDGFRA	MODERATE	c.3080C>A	p.Pro1027His	1	FALSE	chr4:55156679:C:A	121:chr4:55156679:C:A	0.001029
80_c6-1	80	TP53	MODERATE	c.257G>A; c.338G>A; c.617G>A; c.734G>A	p.Gly86Asp; p.Gly113Asp; p.Gly206Asp; p.Gly245Asp	126	FALSE	chr17:7577547:C:T	121:chr17:7577547:C:T	0.00119
80_c6-1	80	DDR2	MODERATE	c.1418G>A	p.Arg473His	2	FALSE	chr1:162740216:G:A	121:chr1:162740216:G:A	0.000997
80_c6-1	80	IGF1R	MODERATE	c.3121C>T; c.3124C>T	p.Arg1041Cys; p.Arg1042Cys	0	FALSE	chr15:99478220:C:T	121:chr15:99478220:C:T	0.001093

80_c6-1	80	NTRK1	MODERATE	c.1940T>G; c.2030T>G; c.2048T>G	p.Val647Gly; p.Val677Gly; p.Val683Gly	2	FALSE	chr1:156849792:T:G	121:chr1:156849792:T:G	0.014563
80_c6-1	80	NTRK3	MODERATE	c.2137C>T; c.2161C>T; c.2203C>T	p.Arg713Cys; p.Arg721Cys; p.Arg735Cys	0	FALSE	chr15:88423632:G:A	121:chr15:88423632:G:A	0.001823
131_bl-1	131	ATM	MODERATE	c.7325A>G	p.Gln2442Arg	0	FALSE	chr11:108200958:A:G	122:chr11:108200958:A:G	0.00081
131_bl-1	131	MAP2K1	MODERATE	c.316G>A	p.Ala106Thr	1	FALSE	chr15:66729108:G:A	122:chr15:66729108:G:A	0.001598
131_bl-1	131	PIK3R1	MODERATE	c.1694G>A; c.605G>A; c.794G>A; c.884G>A	p.Ser565Asn; p.Ser202Asn; p.Ser265Asn; p.Ser295Asn	1	FALSE	chr5:67591101:G:A	122:chr5:67591101:G:A	0.00076
131_bl-1	131	ATM	MODERATE	c.8774G>A	p.Gly2925Asp	0	FALSE	chr11:108224595:G:A	122:chr11:108224595:G:A	0.000907
131_bl-1	131	TP53	LOW; MODIFIER; MODERATE	c.-6C>T; c.355C>T; c.472C>T; c.76C>T	; p.Arg119Cys; p.Arg158Cys; p.Arg26Cys	17	FALSE	chr17:7578458:G:A	122:chr17:7578458:G:A	0.00087
131_bl-1	131	GNA11	MODERATE	c.1030G>A	p.Val344Met	1	FALSE	chr19:3121127:G:A	122:chr19:3121127:G:A	0.000887
131_bl-1	131	KDR	MODERATE	c.2497C>T	p.Arg833Trp	1	FALSE	chr4:55964316:G:A	122:chr4:55964316:G:A	0.000815
131_bl-1	131	EGFR	MODERATE	c.445C>T	p.Arg149Trp	1	FALSE	chr7:55214319:C:T	122:chr7:55214319:C:T	0.000951
131_bl-1	131	NOTCH1	MODERATE	c.3635G>A	p.Gly1212Asp	0	FALSE	chr9:139401765:C:T	122:chr9:139401765:C:T	0.000939

131_bl-1	131	FGFR2	MODIFIER; MODERATE	c.939+4687C>T; c.1112C>T; c.1115C>T; c.767C>T; c.776C>T; c.845C>T; c.848C>T; n.1562C>T	; p.Ala371Val; p.Ala372Val; p.Ala256Val; p.Ala259Val; p.Ala282Val; p.Ala283Val	1	FALSE	chr10:123274806:G:A	122:chr10:123274806:G:A	0.000735
131_bl-1	131	IGF1R	MODERATE	c.3430G>A; c.3433G>A	p.Glu1144Lys; p.Glu1145Lys	0	FALSE	chr15:99482565:G:A	122:chr15:99482565:G:A	0.000938
131_bl-1	131	IGF1R	MODERATE	c.280G>A	p.Glu94Lys	0	FALSE	chr15:99250976:G:A	122:chr15:99250976:G:A	0.000762
131_bl-1	131	CDKN2A	MODIFIER; MODERATE	c.194-3568A>C; c.52A>C	; p.Thr18Pro	1	FALSE	chr9:21974775:T:G	122:chr9:21974775:T:G	0.039433
131_bl-1	131	PTEN	MODERATE	c.724G>A	p.Glu242Lys	2	FALSE	chr10:89717699:G:A	122:chr10:89717699:G:A	0.000879
131_bl-1	131	MET	MODERATE	c.3815T>C; c.3869T>C	p.Leu1272Pro; p.Leu1290Pro	2	FALSE	chr7:116435725:T:C	122:chr7:116435725:T:C	0.002208
131_bl-1	131	FGFR3	MODERATE	c.905G>A	p.Gly302Asp	1	FALSE	chr4:1803727:G:A	122:chr4:1803727:G:A	0.000912
131_bl-1	131	NOTCH1	MODERATE	c.5885G>A	p.Arg1962His	0	FALSE	chr9:139395053:C:T	122:chr9:139395053:C:T	0.000973
131_bl-1	131	CDH1	HIGH	c.1921C>T	p.Gln641*	0	FALSE	chr16:68856113:C:T	122:chr16:68856113:C:T	0.00075
131_bl-1	131	TP53	MODERATE	c.130T>C; c.409T>C; c.49T>C; c.526T>C	p.Cys44Arg; p.Cys137Arg; p.Cys17Arg; p.Cys176Arg	15	FALSE	chr17:7578404:A:G	122:chr17:7578404:A:G	0.000854
131_bl-1	131	EGFR	MODERATE	c.627A>C	p.Lys209Asn	1	FALSE	chr7:55219054:A:C	122:chr7:55219054:A:C	0.002288
131_bl-1	131	AKT1	MODERATE	c.361C>T	p.Arg121Trp	2	FALSE	chr14:105242063:G:A	122:chr14:105242063:G:A	0.001119
131_bl-1	131	IGF1R	MODERATE	c.3121C>T; c.3124C>T	p.Arg1041Cys; p.Arg1042Cys	0	FALSE	chr15:99478220:C:T	122:chr15:99478220:C:T	0.001124

131_bl-1	131	NF1	MODERATE	c.2695T>G	p.Leu899Val	3	FALSE	chr17:29556328:T:G	122:chr17:29556328:T:G	0.015926
131_bl-1	131	TP53	MODERATE; MODIFIER	c.140C>T; c.257C>T; c.-279C>T; c.-360C>T	p.Ala47Val; p.Ala86Val;	1	FALSE	chr17:7579430:G:A	122:chr17:7579430:G:A	0.001099
131_bl-1	131	TP53	MODIFIER; MODERATE	c.*145T>C; c.*233T>C; c.1009T>C; c.1126T>C; c.649T>C; c.730T>C	; p.Ser337Pro; p.Ser376Pro; p.Ser217Pro; p.Ser244Pro	2	FALSE	chr17:7572983:A:G	122:chr17:7572983:A:G	0.004345
131_bl-1	131	NOTCH1	MODERATE	c.4906G>A	p.Glu1636Lys	0	FALSE	chr9:139399237:C:T	122:chr9:139399237:C:T	0.000898
131_bl-1	131	TP53	MODIFIER; LOW	c.-100C>T; c.-19C>T; c.261C>T; c.378C>T	; p.Tyr87Tyr; p.Tyr126Tyr	5	FALSE	chr17:7578552:G:A	122:chr17:7578552:G:A	0.000801
131_bl-1	131	ERBB2; MIEN1; MIR4728	MODERATE; MODIFIER	c.2434G>A; c.2479G>A; c.2524G>A; n.2848G>A; c.*388C>T; n.-1G>A	p.Val812Ile; p.Val827Ile; p.Val842Ile;	17	FALSE	chr17:37881332:G:A	122:chr17:37881332:G:A	0.00127
131_bl-1	131	RET	MODERATE	c.1690A>C	p.Thr564Pro	1	FALSE	chr10:43608342:A:C	122:chr10:43608342:A:C	0.057449
131_bl-1	131	KIT	MODERATE	c.1897C>T; c.1909C>T	p.Leu633Phe; p.Leu637Phe	1	FALSE	chr4:55594206:C:T	122:chr4:55594206:C:T	0.000861
131_bl-1	131	C9orf53; CDKN2A	MODIFIER; MODERATE; LOW	n.*616T>G; c.*120A>C; c.197A>C; c.240A>C	; p.His66Pro; p.Pro80Pro	1	FALSE	chr9:21971161:T:G	122:chr9:21971161:T:G	0.065766
131_bl-1	131	CDKN2A	MODIFIER; MODERATE	c.194-3537T>G; c.83T>G	; p.Val28Gly	1	FALSE	chr9:21974744:A:C	122:chr9:21974744:A:C	0.070432
131_bl-1	131	PDGFRA	MODERATE	c.827C>T	p.Thr276Met	1	FALSE	chr4:55133523:C:T	122:chr4:55133523:C:T	0.001289

131_bl-1	131	TSC2	MODERATE	c.629C>T	p.Ala210Val	0	FALSE	chr16:2106226:C:T	122:chr16:2106226:C:T	0.001016
131_bl-1	131	EGFR	MODERATE	c.664C>T	p.Arg222Cys	8	FALSE	chr7:55220274:C:T	122:chr7:55220274:C:T	0.001461
131_bl-1	131	FGFR4	MODERATE	c.901T>C	p.Tyr301His	1	FALSE	chr5:176519495:T:C	122:chr5:176519495:T:C	0.000834
131_bl-1	131	FGFR1	MODERATE	c.292C>T; c.298C>T; c.541C>T; c.559C>T; c.565C>T; c.658C>T	p.Arg98Cys; p.Arg100Cys; p.Arg181Cys; p.Arg187Cys; p.Arg189Cys; p.Arg220Cys	1	FALSE	chr8:38285495:G:A	122:chr8:38285495:G:A	0.000861
131_bl-1	131	PTEN	MODERATE	c.923G>A	p.Arg308His	1	FALSE	chr10:89720772:G:A	122:chr10:89720772:G:A	0.001381
131_bl-1	131	ERBB2; MIEN1; MIR4728	MODERATE; MODIFIER	c.2261G>A; c.2306G>A; c.2351G>A; n.2675G>A; c.*388C>T; n.-1G>A	p.Arg754His; p.Arg769His; p.Arg784His;	1	FALSE	chr17:37881022:G:A	122:chr17:37881022:G:A	0.000753
131_bl-1	131	EGFR	MODIFIER; MODERATE	c.*1464C>T; c.1279C>T	; p.Arg427Cys	2	FALSE	chr7:55225427:C:T	122:chr7:55225427:C:T	0.000795
131_bl-1	131	CDKN2A; CDKN2B-AS1	MODERATE; MODIFIER	c.22A>G; n.-1T>C	p.Thr8Ala;	1	FALSE	chr9:21994309:T:C	122:chr9:21994309:T:C	0.003704
131_bl-1	131	ERBB2	MODERATE; MODIFIER	c.379C>T; c.424C>T; c.469C>T; n.793C>T	p.Arg127Trp; p.Arg142Trp; p.Arg157Trp;	1	FALSE	chr17:37865600:C:T	122:chr17:37865600:C:T	0.000748
131_bl-1	131	ALK	MODERATE	c.2825C>T	p.Ala942Val	1	FALSE	chr2:29450529:G:A	122:chr2:29450529:G:A	0.000985

131_bl-1	131	GNAS	MODIFIER; MODERATE	c.*927C>T; c.*972C>T; c.1021C>T; c.1024C>T; c.1066C>T; c.1069C>T; c.2995C>T; n.1156C>T	; p.Arg341Cys; p.Arg342Cys; p.Arg356Cys; p.Arg357Cys; p.Arg999Cys	0	FALSE	chr20:57485765:C:T	122:chr20:57485765:C:T	0.000926
131_bl-1	131	APC	MODERATE	c.721C>T; c.775C>T	p.Arg241Trp; p.Arg259Trp	0	FALSE	chr5:112137021:C:T	122:chr5:112137021:C:T	0.00115
131_bl-1	131	TSC1	MODERATE	c.1823C>T; c.1973C>T; c.1976C>T	p.Ala608Val; p.Ala658Val; p.Ala659Val	0	FALSE	chr9:135780989:G:A	122:chr9:135780989:G:A	0.000934
131_bl-1	131	C9orf53; CDKN2A	MODIFIER; MODERATE	n.*616C>T; c.*17G>A; c.*296G>A; c.373G>A	; p.Asp125Asn	2	FALSE	chr9:21970985:C:T	122:chr9:21970985:C:T	0.000946
131_bl-1	131	IGF1R	MODERATE	c.2824G>A; c.2827G>A	p.Ala942Thr; p.Ala943Thr	0	FALSE	chr15:99472831:G:A	122:chr15:99472831:G:A	0.000781
131_bl-1	131	FGFR1	MODERATE	c.359C>T; c.365C>T; c.608C>T; c.626C>T; c.632C>T; c.725C>T	p.Ala120Val; p.Ala122Val; p.Ala203Val; p.Ala209Val; p.Ala211Val; p.Ala242Val	1	FALSE	chr8:38283753:G:A	122:chr8:38283753:G:A	0.001371
131_bl-1	131	KDR	MODERATE	c.2323G>T	p.Ala775Ser	1	FALSE	chr4:55964914:C:A	122:chr4:55964914:C:A	0.002091
131_bl-1	131	SMO	MODERATE	c.1045A>C	p.Thr349Pro	0	FALSE	chr7:128846115:A:C	122:chr7:128846115:A:C	0.033017

131_bl-1	131	FGFR1	MODERATE	c.1211C>T; c.1217C>T; c.1454C>T; c.1478C>T; c.1484C>T; c.1577C>T	p.Ala404Val; p.Ala406Val; p.Ala485Val; p.Ala493Val; p.Ala495Val; p.Ala526Val	1	FALSE	chr8:38275456:G:A	122:chr8:38275456:G:A	0.000774
131_bl-1	131	CWH43	MODERATE	c.1972G>A; c.2053G>A	p.Glu658Lys; p.Glu685Lys	0	FALSE	chr4:49063860:G:A	122:chr4:49063860:G:A	0.000922
131_bl-1	131	INSRR; NTRK1	MODIFIER; MODERATE	c.3397+13C>T; c.28G>A	; p.Ala10Thr	1	FALSE	chr1:156811891:G:A	122:chr1:156811891:G:A	0.001041
131_bl-1	131	APC	MODERATE	c.1708G>A; c.1762G>A	p.Val570Ile; p.Val588Ile	0	FALSE	chr5:112170666:G:A	122:chr5:112170666:G:A	0.000835
131_bl-1	131	TP53	MODERATE	c.151T>C; c.430T>C; c.547T>C; c.70T>C	p.Ser51Pro; p.Ser144Pro; p.Ser183Pro; p.Ser24Pro	9	FALSE	chr17:7578383:A:G	122:chr17:7578383:A:G	0.001525
131_bl-1	131	ESR1	MODERATE	c.719G>A; c.725G>A	p.Cys240Tyr; p.Cys242Tyr	0	FALSE	chr6:152201865:G:A	122:chr6:152201865:G:A	8.00E-04
131_bl-1	131	STK11	MODERATE	c.644G>A	p.Gly215Asp	1	FALSE	chr19:1220626:G:A	122:chr19:1220626:G:A	0.001127
131_bl-1	131	NTRK1	MODERATE	c.1940T>G; c.2030T>G; c.2048T>G	p.Val647Gly; p.Val677Gly; p.Val683Gly	2	FALSE	chr1:156849792:T:G	122:chr1:156849792:T:G	0.030303
131_bl-1	131	MET	MODERATE	c.3509G>A; c.3563G>A	p.Arg1170Gln; p.Arg1188Gln	1	FALSE	chr7:116418998:G:A	122:chr7:116418998:G:A	0.000786
131_bl-1	131	ATM	MODERATE	c.1431G>T	p.Lys477Asn	0	FALSE	chr11:108121623:G:T	122:chr11:108121623:G:T	0.000849
131_bl-1	131	TP53	MODIFIER; MODERATE	c.*116C>T; c.*28C>T; c.1009C>T; c.532C>T; c.613C>T; c.892C>T	; p.Arg337Cys; p.Arg178Cys; p.Arg205Cys; p.Arg298Cys	31	FALSE	chr17:7574018:G:A	122:chr17:7574018:G:A	0.000769

131_bl-1	131	NTRK3	MODERATE	c.506G>A	p.Arg169His	0	FALSE	chr15:88680751:C:T	122:chr15:88680751:C:T	0.000789
131_bl-1	131	TP53	MODERATE	c.116A>G; c.35A>G; c.395A>G; c.512A>G	p.Glu39Gly; p.Glu12Gly; p.Glu132Gly; p.Glu171Gly	3	FALSE	chr17:7578418:T:C	122:chr17:7578418:T:C	0.004244
131_bl-1	131	ERBB2; MIEN1; MIR4728	MODIFIER; MODERATE	c.3160-213A>G; c.3251A>G; c.3296A>G; c.3341A>G; n.3665A>G; c.*388T>C; n.*67A>G	; p.Glu1084Gly; p.Glu1099Gly; p.Glu1114Gly	1	FALSE	chr17:37883729:A:G	122:chr17:37883729:A:G	0.002084
131_bl-1	131	EGFR	MODERATE	c.907G>A	p.Asp303Asn	1	FALSE	chr7:55223540:G:A	122:chr7:55223540:G:A	0.001317
131_bl-1	131	PTEN	MODERATE	c.455T>C	p.Leu152Pro	2	FALSE	chr10:89692971:T:C	122:chr10:89692971:T:C	0.00092
131_bl-1	131	NTRK2	MODERATE	c.2195C>T; c.2243C>T	p.Thr732Met; p.Thr748Met	0	FALSE	chr9:87635191:C:T	122:chr9:87635191:C:T	0.000916
131_bl-1	131	VHL	MODIFIER; MODERATE	c.341-3190G>A; c.424G>A	; p.Val142Ile	0	FALSE	chr3:10188281:G:A	122:chr3:10188281:G:A	0.000905
131_bl-1	131	PHLPP1	MODERATE	c.2452G>A	p.Val818Ile	0	FALSE	chr18:60570204:G:A	122:chr18:60570204:G:A	0.001133
131_bl-1	131	GNA11	MODERATE	c.997G>A	p.Asp333Asn	1	FALSE	chr19:3121094:G:A	122:chr19:3121094:G:A	0.00128
131_bl-1	131	MIR4673; NOTCH1	MODIFIER; MODERATE	n.*59A>C; c.1195A>C	; p.Thr399Pro	0	FALSE	chr9:139412649:T:G	122:chr9:139412649:T:G	0.012682
131_bl-1	131	PIK3CA	MODERATE	c.3101A>G	p.Glu1034Gly	2	FALSE	chr3:178952046:A:G	122:chr3:178952046:A:G	0.000738
131_bl-1	131	FBXW7	MODERATE	c.1274G>A; c.1388G>A; c.1628G>A	p.Arg425Lys; p.Arg463Lys; p.Arg543Lys	0	FALSE	chr4:153247174:C:T	122:chr4:153247174:C:T	0.001181
131_bl-1	131	GNA11	MODERATE	c.1052T>C	p.Leu351Pro	1	FALSE	chr19:3121149:T:C	122:chr19:3121149:T:C	0.003831

131_bl-1	131	BRAF	MODERATE	c.2285C>T	p.Ala762Val	2	FALSE	chr7:140434413:G:A	122:chr7:140434413:G:A	0.001201
131_bl-1	131	TP53	MODIFIER; MODERATE	c.*109G>A; c.*197G>A; c.1090G>A; c.613G>A; c.694G>A; c.973G>A	; p.Ala364Thr; p.Ala205Thr; p.Ala232Thr; p.Ala325Thr	1	FALSE	chr17:7573937:C:T	122:chr17:7573937:C:T	0.001121
131_bl-1	131	PTEN	MODERATE	c.295G>A	p.Glu99Lys	3	FALSE	chr10:89692811:G:A	122:chr10:89692811:G:A	0.000885
131_bl-1	131	IDH2; ZNF710	MODERATE; MODIFIER	c.1091C>T; c.1247C>T; c.857C>T; c.*2147G>A	p.Ala364Val; p.Ala416Val; p.Ala286Val;	1	FALSE	chr15:90628072:G:A	122:chr15:90628072:G:A	0.000824
131_bl-1	131	FGFR3	MODIFIER; MODERATE	c.931-374G>A; c.1196G>A; c.1202G>A	; p.Arg399His; p.Arg401His	1	FALSE	chr4:1806177:G:A	122:chr4:1806177:G:A	0.001406
131_bl-1	131	PIK3R1	MODERATE	c.1226G>A; c.137G>A; c.326G>A; c.416G>A	p.Arg409Gln; p.Arg46Gln; p.Arg109Gln; p.Arg139Gln	1	FALSE	chr5:67589238:G:A	122:chr5:67589238:G:A	0.000787
131_bl-1	131	NTRK1	MODERATE	c.1039C>T; c.949C>T	p.Arg347Cys; p.Arg317Cys	1	FALSE	chr1:156843613:C:T	122:chr1:156843613:C:T	0.000787
131_bl-1	131	C9orf53; CDKN2A	MODIFIER; MODERATE	n.*616C>T; c.*330G>A; c.*51G>A; c.407G>A	; p.Gly136Asp	2	FALSE	chr9:21970951:C:T	122:chr9:21970951:C:T	0.001013
131_bl-1	131	MET	MODERATE	c.2980G>A; c.3034G>A	p.Glu994Lys; p.Glu1012Lys	1	FALSE	chr7:116411995:G:A	122:chr7:116411995:G:A	0.000805
131_bl-1	131	DDR2	MODERATE	c.397C>T	p.Arg133Trp	1	FALSE	chr1:162724625:C:T	122:chr1:162724625:C:T	0.00092
131_bl-1	131	DDR2	MODERATE	c.1418G>A	p.Arg473His	2	FALSE	chr1:162740216:G:A	122:chr1:162740216:G:A	0.000763

131_bl-1	131	ROS1	HIGH	c.5728C>T	p.Arg1910*	1	FALSE	chr6:117642471:G:A	122:chr6:117642471:G:A	0.000805
131_bl-1	131	NTRK1	MODERATE	c.1150G>A; c.1240G>A; c.1258G>A	p.Val384Met; p.Val414Met; p.Val420Met	2	FALSE	chr1:156844704:G:A	122:chr1:156844704:G:A	0.000734
131_bl-1	131	NOTCH1	MODERATE	c.5033T>C	p.Leu1678Pro	0	FALSE	chr9:139397768:A:G	122:chr9:139397768:A:G	0.001086
131_bl-1	131	STK11	MODERATE	c.628T>C	p.Cys210Arg	1	FALSE	chr19:1220610:T:C	122:chr19:1220610:T:C	0.005982
131_bl-1	131	HGF	MODERATE	c.1951G>A; c.1966G>A	p.Glu651Lys; p.Glu656Lys	0	FALSE	chr7:81334750:C:T	122:chr7:81334750:C:T	0.000736
131_bl-1	131	ATM	MODERATE	c.2075G>A	p.Arg692His	0	FALSE	chr11:108124717:G:A	122:chr11:108124717:G:A	0.000797
131_bl-1	131	CWH43	MODERATE	c.691C>T; c.772C>T	p.Arg231Cys; p.Arg258Cys	0	FALSE	chr4:49000535:C:T	122:chr4:49000535:C:T	0.000791
131_bl-1	131	IGF1R	MODERATE	c.3934T>C; c.3937T>C	p.Ser1312Pro; p.Ser1313Pro	0	FALSE	chr15:99500504:T:C	122:chr15:99500504:T:C	0.036922
131_bl-1	131	IGF1R	MODERATE	c.3905T>C; c.3908T>C	p.Val1302Ala; p.Val1303Ala	0	FALSE	chr15:99500475:T:C	122:chr15:99500475:T:C	0.006211
131_bl-1	131	ERBB2	MODIFIER; HIGH	n.1375C>T; c.1006C>T; c.1051C>T; c.961C>T	; p.Arg336*; p.Arg351*; p.Arg321*	1	FALSE	chr17:37868604:C:T	122:chr17:37868604:C:T	0.000758
131_bl-1	131	IDH1	MODERATE	c.394C>T	p.Arg132Cys	626	FALSE	chr2:209113113:G:A	122:chr2:209113113:G:A	0.001279
131_bl-1	131	KIT	MODERATE	c.2671G>A; c.2683G>A	p.Ala891Thr; p.Ala895Thr	3	FALSE	chr4:55602973:G:A	122:chr4:55602973:G:A	0.000693
131_bl-1	131	EPHA3	MODERATE	c.947A>C	p.Asp316Ala	0	FALSE	chr3:89390198:A:C	122:chr3:89390198:A:C	0.000935

131_bl-1	131	ERBB2; MIEN1; MIR4728	MODERATE; MODIFIER	c.2600G>A; c.2645G>A; c.2690G>A; n.3014G>A; c.*388C>T; n.-1G>A	p.Arg867Gln; p.Arg882Gln; p.Arg897Gln;	2	FALSE	chr17:37881620:G:A	122:chr17:37881620:G:A	0.001112
131_bl-1	131	ATM	MODERATE	c.5833G>A	p.Ala1945Thr	0	FALSE	chr11:108180957:G:A	122:chr11:108180957:G:A	0.00079
131_bl-1	131	ERBB2	MODERATE; MODIFIER	c.560G>A; c.605G>A; c.650G>A; n.974G>A	p.Arg187His; p.Arg202His; p.Arg217His;	1	FALSE	chr17:37866345:G:A	122:chr17:37866345:G:A	0.000798
131_bl-1	131	NTRK3	MODERATE	c.560T>C	p.Leu187Pro	0	FALSE	chr15:88680697:A:G	122:chr15:88680697:A:G	0.000807
131_bl-1	131	TSC1	MODERATE	c.457C>T; c.610C>T	p.Arg153Cys; p.Arg204Cys	0	FALSE	chr9:135797259:G:A	122:chr9:135797259:G:A	0.000871
131_bl-1	131	VHL	MODIFIER; MODERATE	c.341-3270A>C; c.344A>C	; p.His115Pro	0	FALSE	chr3:10188201:A:C	122:chr3:10188201:A:C	0.001401
131_bl-1	131	C9orf53; CDKN2A	MODIFIER; MODERATE	n.*616C>G; c.*140G>C; c.217G>C; c.260G>C	; p.Ala73Pro; p.Arg87Pro	1	FALSE	chr9:21971141:C:G	122:chr9:21971141:C:G	0.007299
131_bl-1	131	NTRK3	MODERATE	c.1139C>T	p.Ala380Val	0	FALSE	chr15:88678397:G:A	122:chr15:88678397:G:A	0.000824
74_c7-1	74	MET	HIGH	c.1639C>T	p.Arg547*	2	FALSE	chr7:116381017:C:T	123:chr7:116381017:C:T	0.001086
74_c7-1	74	FBXW7	MODERATE	c.289G>A; c.403G>A; c.643G>A	p.Ala97Thr; p.Ala135Thr; p.Ala215Thr	0	FALSE	chr4:153268165:C:T	123:chr4:153268165:C:T	0.001147
74_c7-1	74	HRAS; LRRC56	MODERATE; MODIFIER	c.248C>T; c.-506G>A	p.Ala83Val;	1	FALSE	chr11:533808:G:A	123:chr11:533808:G:A	0.002333
74_c7-1	74	ATM	MODERATE	c.7330G>A	p.Glu2444Lys	0	FALSE	chr11:108200963:G:A	123:chr11:108200963:G:A	0.001364

74_c7-1	74	KIT	MODERATE	c.1486G>A	p.Asp496Asn	1	FALSE	chr4:55592162:G:A	123:chr4:55592162:G:A	0.001547
74_c7-1	74	PDGFRA	MODERATE	c.1711G>A	p.Glu571Lys	1	FALSE	chr4:55141065:G:A	123:chr4:55141065:G:A	0.002333
74_c7-1	74	AR	MODERATE	c.2360G>A; c.764G>A	p.Arg787Gln; p.Arg255Gln	0	FALSE	chrX:66941716:G:A	123:chrX:66941716:G:A	0.001414
74_c7-1	74	NTRK3	MODERATE	c.995C>T	p.Thr332Met	0	FALSE	chr15:88678541:G:A	123:chr15:88678541:G:A	0.00134
74_c7-1	74	FBXW7	MODERATE	c.182G>A; c.296G>A; c.536G>A	p.Arg61His; p.Arg99His; p.Arg179His	0	FALSE	chr4:153271242:C:T	123:chr4:153271242:C:T	0.002131
74_c7-1	74	EPHA3	MODERATE	c.2530C>T	p.Pro844Ser	0	FALSE	chr3:89499360:C:T	123:chr3:89499360:C:T	0.001444
74_c7-1	74	ALK	MODERATE	c.2527G>A	p.Gly843Arg	1	FALSE	chr2:29455275:C:T	123:chr2:29455275:C:T	0.001455
74_c7-1	74	FGFR2	MODIFIER; MODERATE	c.110-14009G>A; c.110-889G>A; n.757-14009G>A; c.346G>A	; p.Glu116Lys	1	FALSE	chr10:123324982:C:T	123:chr10:123324982:C:T	0.001282
74_c7-1	74	PTEN	MODERATE	c.725A>G	p.Glu242Gly	1	FALSE	chr10:89717700:A:G	123:chr10:89717700:A:G	0.001516
74_c7-1	74	CTNNB1	LOW	c.1956G>A	p.Ala652Ala	0	FALSE	chr3:41278080:G:A	123:chr3:41278080:G:A	0.00136
74_c7-1	74	KIT	MODERATE	c.1835C>T; c.1847C>T	p.Ala612Val; p.Ala616Val	1	FALSE	chr4:55594061:C:T	123:chr4:55594061:C:T	0.001182
74_c7-1	74	NTRK1	MODERATE	c.1967G>A; c.2057G>A; c.2075G>A	p.Arg656His; p.Arg686His; p.Arg692His	1	FALSE	chr1:156849819:G:A	123:chr1:156849819:G:A	0.003046
74_c7-1	74	KIT	LOW	c.1869G>A; c.1881G>A	p.Pro623Pro; p.Pro627Pro	1	FALSE	chr4:55594178:G:A	123:chr4:55594178:G:A	0.001483
74_c7-1	74	ALK	MODERATE	c.986C>T	p.Ser329Phe	1	FALSE	chr2:29754949:G:A	123:chr2:29754949:G:A	0.00147
74_c7-1	74	ATM	MODERATE	c.1009C>T	p.Arg337Cys	0	FALSE	chr11:108117798:C:T	123:chr11:108117798:C:T	0.003995

74_c7-1	74	ALK	MODERATE	c.3599C>T	p.Ala1200Val	2	FALSE	chr2:29443618:G:A	123:chr2:29443618:G:A	0.001623
74_c7-1	74	APC	MODERATE	c.1198G>A; c.1252G>A	p.Glu400Lys; p.Glu418Lys	0	FALSE	chr5:112154981:G:A	123:chr5:112154981:G:A	0.0013
74_c7-1	74	STK11	MODERATE	c.647C>T	p.Ser216Phe	3	FALSE	chr19:1220629:C:T	123:chr19:1220629:C:T	0.002635
74_c7-1	74	MET	MODERATE	c.1640G>A	p.Arg547Gln	1	FALSE	chr7:116381018:G:A	123:chr7:116381018:G:A	0.001076
74_c7-1	74	EGFR	MODIFIER; MODERATE	c.*2364G>A; c.2203G>A	; p.Gly735Ser	4	FALSE	chr7:55242433:G:A	123:chr7:55242433:G:A	0.001264
74_c7-1	74	MIR1225; PKD1; TSC2	MODIFIER; MODERATE	n.*90G>A; c.*13118G>A; c.*13121G>A; c.5032C>T; c.5164C>T; c.5233C>T	; p.Arg1678Cys; p.Arg1722Cys; p.Arg1745Cys	0	FALSE	chr16:2138300:C:T	123:chr16:2138300:C:T	0.00149
74_c7-1	74	KDR	MODERATE	c.1040G>A	p.Arg347His	4	FALSE	chr4:55976872:C:T	123:chr4:55976872:C:T	0.001057
74_c7-1	74	TSC2	MODERATE	c.1381G>A	p.Val461Met	0	FALSE	chr16:2112992:G:A	123:chr16:2112992:G:A	0.001918
74_c7-1	74	FOXL2; FOXL2NB; LINC01391	MODERATE; MODIFIER	c.205G>A; c.-132C>T; n.-1G>A	p.Glu69Lys;	0	FALSE	chr3:138665360:C:T	123:chr3:138665360:C:T	0.001627
74_c7-1	74	NOTCH1	MODERATE	c.3635G>A	p.Gly1212Asp	0	FALSE	chr9:139401765:C:T	123:chr9:139401765:C:T	0.001675
74_c7-1	74	C9orf53; CDKN2A	MODIFIER; MODERATE	n.*616G>A; c.*218C>T; c.295C>T; c.338C>T	; p.Arg99Trp; p.Pro113Leu	2	FALSE	chr9:21971063:G:A	123:chr9:21971063:G:A	0.002081

74_c7-1	74	CSDE1; NRAS	MODIFIER; MODERATE	c.*2430G>A; c.*2523G>A; c.*2817G>A; c.*2910G>A; c.*2964G>A; c.*3057G>A; c.145G>A	; p.Glu49Lys	1	FALSE	chr1:115256566:C:T	123:chr1:115256566:C:T	0.001779
74_c7-1	74	HGF	MODERATE	c.2068C>T; c.2083C>T	p.Arg690Cys; p.Arg695Cys	0	FALSE	chr7:81332001:G:A	123:chr7:81332001:G:A	0.001412
74_c7-1	74	AR	HIGH	c.2494C>T; c.898C>T	p.Arg832*; p.Arg300*	0	FALSE	chrX:66942713:C:T	123:chrX:66942713:C:T	0.001994
74_c7-1	74	TSC2	MODERATE	c.3530C>T; c.3662C>T	p.Ser1177Leu; p.Ser1221Leu	0	FALSE	chr16:2131647:C:T	123:chr16:2131647:C:T	0.00198
74_c7-1	74	ATM	MODERATE	c.8275C>T	p.Pro2759Ser	0	FALSE	chr11:108213955:C:T	123:chr11:108213955:C:T	0.003309
74_c7-1	74	PDGFRA	MODERATE	c.2692G>A	p.Gly898Ser	1	FALSE	chr4:55154983:G:A	123:chr4:55154983:G:A	0.001286
74_c7-1	74	ALK	MODERATE	c.1588G>A	p.Glu530Lys	1	FALSE	chr2:29541229:C:T	123:chr2:29541229:C:T	0.001312
74_c7-1	74	KIT	MODERATE	c.2338G>A; c.2350G>A	p.Ala780Thr; p.Ala784Thr	1	FALSE	chr4:55598153:G:A	123:chr4:55598153:G:A	0.001209
74_c7-1	74	GNA11	MODERATE	c.667G>A	p.Val223Met	1	FALSE	chr19:3118983:G:A	123:chr19:3118983:G:A	0.00165
74_c7-1	74	GNA11	MODERATE	c.1030G>A	p.Val344Met	1	FALSE	chr19:3121127:G:A	123:chr19:3121127:G:A	0.001402
74_c7-1	74	HOXD-AS2; HOXD8	MODIFIER; MODERATE	n.*692C>T; c.304G>A; c.853G>A; c.856G>A	; p.Glu102Lys; p.Glu285Lys; p.Glu286Lys	0	FALSE	chr2:176996323:G:A	123:chr2:176996323:G:A	0.00188
74_c7-1	74	TP53	MODERATE	c.145C>T; c.424C>T; c.541C>T; c.64C>T	p.Arg49Cys; p.Arg142Cys; p.Arg181Cys; p.Arg22Cys	21	FALSE	chr17:7578389:G:A	123:chr17:7578389:G:A	0.001312

74_c7-1	74	NOTCH1	MODERATE	c.4901C>T	p.Ala1634Val	0	FALSE	chr9:139399242:G:A	123:chr9:139399242:G:A	0.002901
74_c7-1	74	FBXW7	MODERATE	c.1274G>A; c.1388G>A; c.1628G>A	p.Arg425Lys; p.Arg463Lys; p.Arg543Lys	0	FALSE	chr4:153247174:C:T	123:chr4:153247174:C:T	0.00142
74_c7-1	74	BRAF	MODERATE	c.2173C>T	p.His725Tyr	1	FALSE	chr7:140434525:G:A	123:chr7:140434525:G:A	0.001609
74_c7-1	74	NF1	MODERATE	c.2659G>A	p.Ala887Thr	1	FALSE	chr17:29556292:G:A	123:chr17:29556292:G:A	0.00123
74_c7-1	74	IGF1R	MODERATE	c.322G>A	p.Gly108Ser	0	FALSE	chr15:99251018:G:A	123:chr15:99251018:G:A	0.001205
74_c7-1	74	TP53	MODERATE	c.236G>A; c.317G>A; c.596G>A; c.713G>A	p.Cys79Tyr; p.Cys106Tyr; p.Cys199Tyr; p.Cys238Tyr	74	FALSE	chr17:7577568:C:T	123:chr17:7577568:C:T	0.001248
74_c7-1	74	NOTCH1	MODERATE	c.4906G>A	p.Glu1636Lys	0	FALSE	chr9:139399237:C:T	123:chr9:139399237:C:T	0.001919
74_c7-1	74	DDR2	MODERATE	c.1418G>A	p.Arg473His	2	FALSE	chr1:162740216:G:A	123:chr1:162740216:G:A	0.001314
74_c7-1	74	NOTCH1	MODERATE	c.4252G>A	p.Ala1418Thr	0	FALSE	chr9:139400096:C:T	123:chr9:139400096:C:T	0.001845
74_c7-1	74	CDH1	MODERATE	c.871G>A	p.Asp291Asn	0	FALSE	chr16:68845625:G:A	123:chr16:68845625:G:A	0.001553
74_c7-1	74	TSC1	MODERATE	c.457C>T; c.610C>T	p.Arg153Cys; p.Arg204Cys	0	FALSE	chr9:135797259:G:A	123:chr9:135797259:G:A	0.001506
74_c7-1	74	TSC2	MODIFIER; MODERATE	c.2837+1108G>A; c.2933G>A	; p.Arg978His	0	FALSE	chr16:2127694:G:A	123:chr16:2127694:G:A	0.002366
74_c7-1	74	PTEN	MODERATE	c.766G>A	p.Glu256Lys	2	FALSE	chr10:89717741:G:A	123:chr10:89717741:G:A	0.001489
74_c7-1	74	TP53	MODERATE	c.224A>G; c.305A>G; c.584A>G; c.701A>G	p.Tyr75Cys; p.Tyr102Cys; p.Tyr195Cys; p.Tyr234Cys	94	FALSE	chr17:7577580:T:C	123:chr17:7577580:T:C	0.001187
74_c7-1	74	PTEN	MODERATE	c.476G>A	p.Arg159Lys	11	FALSE	chr10:89692992:G:A	123:chr10:89692992:G:A	0.001742

74_c7-1	74	NF1	MODERATE	c.5294C>T; c.5357C>T	p.Ser1765Leu; p.Ser1786Leu	1	FALSE	chr17:29654605:C:T	123:chr17:29654605:C:T	0.001325
74_c7-1	74	PHLPP1	MODERATE	c.3298G>A	p.Glu1100Lys	0	FALSE	chr18:60612478:G:A	123:chr18:60612478:G:A	0.001291
74_c7-1	74	RET	MODERATE	c.2116G>A	p.Val706Met	2	FALSE	chr10:43610164:G:A	123:chr10:43610164:G:A	0.001159
74_c7-1	74	HRAS; LRRC56	MODERATE; MODIFIER	c.404G>A; c.-506C>T	p.Arg135Gln;	1	FALSE	chr11:533499:C:T	123:chr11:533499:C:T	0.001488
74_c7-1	74	KDR	MODERATE	c.3065G>A	p.Arg1022Gln	1	FALSE	chr4:55958788:C:T	123:chr4:55958788:C:T	0.00202
74_c7-1	74	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2591C>T; n.-1G>A	p.Ala864Val;	2	FALSE	chr7:55259533:C:T	123:chr7:55259533:C:T	0.001509
74_c7-1	74	TP53	MODERATE; MODIFIER	c.100G>A; c.217G>A; c.-279G>A; c.-360G>A	p.Val34Met; p.Val73Met;	5	FALSE	chr17:7579470:C:T	123:chr17:7579470:C:T	0.001833
74_c7-1	74	FLT3	MODERATE	c.2845G>A	p.Asp949Asn	0	FALSE	chr13:28588603:C:T	123:chr13:28588603:C:T	0.00122
74_c7-1	74	IDH2; ZNF710	MODERATE; MODIFIER	c.1091C>T; c.1247C>T; c.857C>T; c.*2147G>A	p.Ala364Val; p.Ala416Val; p.Ala286Val;	1	FALSE	chr15:90628072:G:A	123:chr15:90628072:G:A	0.001509
74_c7-1	74	FGFR1	MODERATE	c.1211C>T; c.1217C>T; c.1454C>T; c.1478C>T; c.1484C>T; c.1577C>T	p.Ala404Val; p.Ala406Val; p.Ala485Val; p.Ala493Val; p.Ala495Val; p.Ala526Val	1	FALSE	chr8:38275456:G:A	123:chr8:38275456:G:A	0.001285
74_c7-1	74	NF1	MODERATE	c.2614G>A	p.Glu872Lys	1	FALSE	chr17:29556247:G:A	123:chr17:29556247:G:A	0.001238
74_c7-1	74	TSC2	MODERATE	c.2513G>A	p.Ser838Asn	0	FALSE	chr16:2124358:G:A	123:chr16:2124358:G:A	0.002137
74_c7-1	74	MIR4673; NOTCH1	MODIFIER; MODERATE	n.*59G>A; c.775G>A	; p.Asp259Asn	0	FALSE	chr9:139413985:C:T	123:chr9:139413985:C:T	0.001837
74_c7-1	74	KDR	MODERATE	c.2953G>A	p.Asp985Asn	1	FALSE	chr4:55960987:C:T	123:chr4:55960987:C:T	0.001596

74_c7-1	74	MET	MODERATE	c.467C>T	p.Ser156Leu	1	FALSE	chr7:116339605:C:T	123:chr7:116339605:C:T	0.001021
74_c7-1	74	ATM	MODERATE	c.7328G>A	p.Arg2443Gln	0	FALSE	chr11:108200961:G:A	123:chr11:108200961:G:A	0.002714
74_c7-1	74	PIK3CA	MODERATE	c.3101A>G	p.Glu1034Gly	2	FALSE	chr3:178952046:A:G	123:chr3:178952046:A:G	0.001174
74_c7-1	74	PIK3CA	MODERATE	c.3155C>A	p.Thr1052Lys	9	FALSE	chr3:178952100:C:A	123:chr3:178952100:C:A	0.00117
74_c7-1	74	FGFR1; LETM2	MODERATE; MODIFIER	c.1927C>T; c.1933C>T; c.2170C>T; c.2194C>T; c.2200C>T; c.2293C>T; c.*1406G>A; c.*1423G>A; c.*1553G>A; c.*1567G>A; c.*1638G>A	p.Arg643Trp; p.Arg645Trp; p.Arg724Trp; p.Arg732Trp; p.Arg734Trp; p.Arg765Trp;	1	FALSE	chr8:38271528:G:A	123:chr8:38271528:G:A	0.002092
74_c7-1	74	ERBB2	MODERATE; MODIFIER	c.379C>T; c.424C>T; c.469C>T; n.793C>T	p.Arg127Trp; p.Arg142Trp; p.Arg157Trp;	1	FALSE	chr17:37865600:C:T	123:chr17:37865600:C:T	0.001472
74_c7-1	74	NTRK1	MODERATE	c.804C>G; c.894C>G	p.His268Gln; p.His298Gln	1	FALSE	chr1:156843468:C:G	123:chr1:156843468:C:G	0.002538
130_bl-1	130	KIT	MODERATE	c.2338G>A; c.2350G>A	p.Ala780Thr; p.Ala784Thr	1	FALSE	chr4:55598153:G:A	124:chr4:55598153:G:A	0.00191
130_bl-1	130	TP53	MODERATE; MODIFIER	c.167C>T; c.284C>T; c.-279C>T; c.-360C>T	p.Ser56Phe; p.Ser95Phe;	3	FALSE	chr17:7579403:G:A	124:chr17:7579403:G:A	0.00266

130_bl-1	130	FGFR4	MODERATE	c.1274G>A; c.1358G>A; c.1478G>A	p.Arg425Gln; p.Arg453Gln; p.Arg493Gln	2	FALSE	chr5:176520735:G:A	124:chr5:176520735:G:A	0.001965
130_bl-1	130	IGF1R	MODERATE	c.3905T>C; c.3908T>C	p.Val1302Ala; p.Val1303Ala	0	FALSE	chr15:99500475:T:C	124:chr15:99500475:T:C	0.002232
130_bl-1	130	KLLN; PTEN	MODIFIER; MODERATE	c.-951G>A; c.8C>T	; p.Ala3Val	2	FALSE	chr10:89624234:C:T	124:chr10:89624234:C:T	0.002099
130_bl-1	130	RPL19	MODERATE	c.452G>A	p.Arg151His	0	FALSE	chr17:37360425:G:A	124:chr17:37360425:G:A	0.00348
130_bl-1	130	KDR	MODERATE	c.2497C>T	p.Arg833Trp	1	FALSE	chr4:55964316:G:A	124:chr4:55964316:G:A	0.002128
130_bl-1	130	APC	MODERATE	c.1771G>A; c.1825G>A	p.Val591Ile; p.Val609Ile	0	FALSE	chr5:112170729:G:A	124:chr5:112170729:G:A	0.002304
130_bl-1	130	STK11	MODERATE	c.536C>T	p.Pro179Leu	1	FALSE	chr19:1220443:C:T	124:chr19:1220443:C:T	0.003333
130_bl-1	130	RET	MODERATE	c.1538C>T	p.Ala513Val	1	FALSE	chr10:43607562:C:T	124:chr10:43607562:C:T	0.001951
130_bl-1	130	FGFR1	MODERATE	c.1060C>T; c.1066C>T; c.1303C>T; c.1327C>T; c.1333C>T; c.1426C>T	p.Arg354Trp; p.Arg356Trp; p.Arg435Trp; p.Arg443Trp; p.Arg445Trp; p.Arg476Trp	2	FALSE	chr8:38275843:G:A	124:chr8:38275843:G:A	0.001652
130_bl-1	130	ALK	MODERATE	c.886G>A	p.Glu296Lys	1	FALSE	chr2:29917782:C:T	124:chr2:29917782:C:T	0.001712
130_bl-1	130	NOTCH1	MODERATE	c.5819G>A	p.Arg1940His	0	FALSE	chr9:139395119:C:T	124:chr9:139395119:C:T	0.00314
130_bl-1	130	CDH1	MODERATE	c.856G>A	p.Ala286Thr	0	FALSE	chr16:68845610:G:A	124:chr16:68845610:G:A	0.002242
130_bl-1	130	NTHL1; TSC2	MODIFIER; MODERATE	c.-20C>T; c.170G>A	; p.Arg57His	0	FALSE	chr16:2100432:G:A	124:chr16:2100432:G:A	0.002257

130_bl-1	130	FGFR2	MODIFIER; MODERATE	c.749-4847G>A; c.407G>A; c.485G>A; c.752G>A; n.1054G>A	; p.Arg136Gln; p.Arg162Gln; p.Arg251Gln	2	FALSE	chr10:123279680:C:T	124:chr10:123279680:C:T	0.00222
130_bl-1	130	MIR4673; NOTCH1	MODIFIER; MODERATE	n.*59G>A; c.1024G>A	; p.Ala342Thr	0	FALSE	chr9:139413118:C:T	124:chr9:139413118:C:T	0.003476
130_bl-1	130	KIT	MODERATE	c.506G>A	p.Gly169Asp	1	FALSE	chr4:55564618:G:A	124:chr4:55564618:G:A	0.001857
130_bl-1	130	CDH1	MODERATE	c.760G>A	p.Asp254Asn	0	FALSE	chr16:68844172:G:A	124:chr16:68844172:G:A	0.001953
130_bl-1	130	PTEN	MODERATE	c.701G>A	p.Arg234Gln	1	FALSE	chr10:89717676:G:A	124:chr10:89717676:G:A	0.001953
130_bl-1	130	EGFR	MODERATE	c.755G>A	p.Arg252His	3	FALSE	chr7:55221711:G:A	124:chr7:55221711:G:A	0.002045
130_bl-1	130	IGF1R	MODERATE	c.3121C>T; c.3124C>T	p.Arg1041Cys; p.Arg1042Cys	0	FALSE	chr15:99478220:C:T	124:chr15:99478220:C:T	0.001826
130_bl-1	130	TP53	MODERATE; MODIFIER	c.254G>A; c.371G>A; c.-279G>A; c.-360G>A	p.Cys85Tyr; p.Cys124Tyr;	3	FALSE	chr17:7579316:C:T	124:chr17:7579316:C:T	0.002342
94_c6-1	94	ESR1	MODERATE	c.1171G>A; c.1174G>A; c.1180G>A	p.Val391Ile; p.Val392Ile; p.Val394Ile	0	FALSE	chr6:152332868:G:A	126:chr6:152332868:G:A	0.001357
94_c6-1	94	KDR	MODERATE	c.3110C>T	p.Ser1037Leu	2	FALSE	chr4:55956205:G:A	126:chr4:55956205:G:A	0.00158
94_c6-1	94	FLT3	MODERATE	c.2669C>T	p.Pro890Leu	0	FALSE	chr13:28589378:G:A	126:chr13:28589378:G:A	0.001597
94_c6-1	94	FGFR1	MODERATE	c.359C>T; c.365C>T; c.608C>T; c.626C>T; c.632C>T; c.725C>T	p.Ala120Val; p.Ala122Val; p.Ala203Val; p.Ala209Val; p.Ala211Val; p.Ala242Val	1	FALSE	chr8:38283753:G:A	126:chr8:38283753:G:A	0.001594

94_c6-1	94	HRAS; LRRC56	MODERATE; MODIFIER	c.248C>T; c.-506G>A	p.Ala83Val;	1	FALSE	chr11:533808:G:A	126:chr11:533808:G:A	0.001563
94_c6-1	94	NTRK1	MODERATE	c.1025G>A; c.935G>A	p.Arg342Gln; p.Arg312Gln	3	FALSE	chr1:156843599:G:A	126:chr1:156843599:G:A	0.001115
94_c6-1	94	MAP2K1	MODERATE	c.316G>A	p.Ala106Thr	1	FALSE	chr15:66729108:G:A	126:chr15:66729108:G:A	0.00201
94_c6-1	94	EGFR	MODIFIER; MODERATE	c.*2133G>A; c.*2364G>A; c.1883G>A	; p.Cys628Tyr	2	FALSE	chr7:55238870:G:A	126:chr7:55238870:G:A	0.001708
94_c6-1	94	C9orf53; CDKN2A	MODIFIER; MODERATE; LOW	n.*616C>T; c.*258G>A; c.335G>A; c.378G>A	; p.Arg112His; p.Pro126Pro	1	FALSE	chr9:21971023:C:T	126:chr9:21971023:C:T	0.001618
94_c6-1	94	TP53	MODIFIER; HIGH	c.-55C>A; c.27C>A; c.306C>A; c.423C>A	; p.Cys9*; p.Cys102*; p.Cys141*	13	FALSE	chr17:7578507:G:T	126:chr17:7578507:G:T	0.159091
94_c6-1	94	GNA11	MODERATE	c.547C>T	p.Arg183Cys	9	FALSE	chr19:3115012:C:T	126:chr19:3115012:C:T	0.001439
94_c6-1	94	PDGFRA	MODERATE	c.554G>A	p.Gly185Glu	1	FALSE	chr4:55130020:G:A	126:chr4:55130020:G:A	0.001311
94_c6-1	94	NTRK3	MODERATE	c.1744G>A; c.1768G>A	p.Glu582Lys; p.Glu590Lys	0	FALSE	chr15:88476364:C:T	126:chr15:88476364:C:T	0.001622
94_c6-1	94	FGFR3	MODIFIER; MODERATE	c.931-374G>A; c.1196G>A; c.1202G>A	; p.Arg399His; p.Arg401His	1	FALSE	chr4:1806177:G:A	126:chr4:1806177:G:A	0.001072
94_c6-1	94	PTEN	HIGH	c.822G>A	p.Trp274*	3	FALSE	chr10:89720671:G:A	126:chr10:89720671:G:A	0.011547
94_c6-1	94	VHL	MODIFIER; MODERATE	c.341-3202C>T; c.412C>T	; p.Pro138Ser	0	FALSE	chr3:10188269:C:T	126:chr3:10188269:C:T	0.001761
94_c6-1	94	ERBB2	MODERATE; MODIFIER	c.832G>A; c.877G>A; c.922G>A; n.1246G>A	p.Val278Met; p.Val293Met; p.Val308Met;	1	FALSE	chr17:37868201:G:A	126:chr17:37868201:G:A	0.000771

94_c6-1	94	HOXD-AS2; HOXD8	MODIFIER; MODERATE	n.*692C>T; c.-123-30G>A; c.400G>A	; p.Ala134Thr	0	FALSE	chr2:176995494:G:A	126:chr2:176995494:G:A	0.002817
94_c6-1	94	NOTCH1	MODERATE	c.5558T>C	p.Leu1853Pro	0	FALSE	chr9:139396280:A:G	126:chr9:139396280:A:G	0.001444
94_c6-1	94	ATM	HIGH	c.1262C>A	p.Ser421*	0	FALSE	chr11:108121454:C:A	126:chr11:108121454:C:A	0.001775
94_c6-1	94	PIK3R1	MODERATE	c.1003G>A; c.1093G>A; c.1903G>A; c.814G>A	p.Glu335Lys; p.Glu365Lys; p.Glu635Lys; p.Glu272Lys	1	FALSE	chr5:67592087:G:A	126:chr5:67592087:G:A	0.001579
94_c6-1	94	IGF1R	MODERATE	c.3905T>C; c.3908T>C	p.Val1302Ala; p.Val1303Ala	0	FALSE	chr15:99500475:T:C	126:chr15:99500475:T:C	0.00134
94_c6-1	94	ERBB2; MIEN1; MIR4728	MODIFIER; MODERATE	c.3160-213A>G; c.3251A>G; c.3296A>G; c.3341A>G; n.3665A>G; c.*388T>C; n.*67A>G	; p.Glu1084Gly; p.Glu1099Gly; p.Glu1114Gly	1	FALSE	chr17:37883729:A:G	126:chr17:37883729:A:G	0.001123
94_c6-1	94	FGFR3	MODERATE	c.1543G>A; c.1879G>A; c.1885G>A	p.Glu515Lys; p.Glu627Lys; p.Glu629Lys	1	FALSE	chr4:1807820:G:A	126:chr4:1807820:G:A	0.001102
94_c6-1	94	NOTCH1	MODERATE	c.4898G>T	p.Arg1633Leu	0	FALSE	chr9:139399245:C:A	126:chr9:139399245:C:A	0.001649
94_c6-1	94	CTNNB1	MODERATE	c.1544G>A	p.Arg515Gln	0	FALSE	chr3:41275649:G:A	126:chr3:41275649:G:A	0.001818
94_c6-1	94	HGF	MODERATE	c.775G>C; c.790G>C	p.Asp259His; p.Asp264His	0	FALSE	chr7:81372744:C:G	126:chr7:81372744:C:G	0.001512
94_c6-1	94	TSC2	MODERATE	c.2702G>A	p.Arg901His	0	FALSE	chr16:2126131:G:A	126:chr16:2126131:G:A	0.001349
94_c6-1	94	EGFR	MODERATE	c.1774G>A	p.Val592Ile	1	FALSE	chr7:55233024:G:A	126:chr7:55233024:G:A	0.001717

94_c6-1	94	RET	MODERATE	c.1538C>T	p.Ala513Val	1	FALSE	chr10:43607562:C:T	126:chr10:43607562:C:T	0.001391
94_c6-1	94	AR	MODERATE	c.2324G>A; c.728G>A	p.Arg775His; p.Arg243His	0	FALSE	chrX:66941680:G:A	126:chrX:66941680:G:A	0.001495
94_c6-1	94	NTRK2	MODERATE	c.220G>A	p.Ala74Thr	0	FALSE	chr9:87317081:G:A	126:chr9:87317081:G:A	0.001605
94_c6-1	94	ATM	MODERATE	c.6179G>A	p.Arg2060His	0	FALSE	chr11:108186821:G:A	126:chr11:108186821:G:A	0.001389
94_c6-1	94	C9orf53; CDKN2A	MODIFIER; LOW	n.*616G>A; c.*22C>T; c.*301C>T; c.378C>T	; p.Val126Val	3	FALSE	chr9:21970980:G:A	126:chr9:21970980:G:A	0.001605
94_c6-1	94	EPHA3	MODERATE	c.665C>T	p.Ser222Phe	0	FALSE	chr3:89259521:C:T	126:chr3:89259521:C:T	0.001476
94_c6-1	94	STK11	MODERATE	c.1100C>T	p.Thr367Met	1	FALSE	chr19:1223163:C:T	126:chr19:1223163:C:T	0.001684
94_c6-1	94	TP53	MODERATE	c.136T>G; c.217T>G; c.496T>G; c.613T>G	p.Tyr46Asp; p.Tyr73Asp; p.Tyr166Asp; p.Tyr205Asp	14	FALSE	chr17:7578236:A:C	126:chr17:7578236:A:C	0.001449
94_c6-1	94	MAP2K1	MODERATE	c.145C>T	p.Arg49Cys	1	FALSE	chr15:66727429:C:T	126:chr15:66727429:C:T	0.001387
94_c6-1	94	FGFR4	MODERATE	c.1978G>A; c.2062G>A; c.2182G>A	p.Ala660Thr; p.Ala688Thr; p.Ala728Thr	1	FALSE	chr5:176524321:G:A	126:chr5:176524321:G:A	0.001833
94_c6-1	94	TSC2	MODERATE	c.2513G>A	p.Ser838Asn	0	FALSE	chr16:2124358:G:A	126:chr16:2124358:G:A	0.001368
94_c6-1	94	FBXW7	MODERATE	c.232A>T; c.346A>T; c.586A>T	p.Thr78Ser; p.Thr116Ser; p.Thr196Ser	0	FALSE	chr4:153268222:T:A	126:chr4:153268222:T:A	0.0039
94_c6-1	94	IDH2; ZNF710	MODERATE; MODIFIER	c.1105G>A; c.1261G>A; c.871G>A; c.*2147C>T	p.Gly369Ser; p.Gly421Ser; p.Gly291Ser;	2	FALSE	chr15:90628058:C:T	126:chr15:90628058:C:T	0.001373

94_c6-1	94	ATM	MODERATE	c.2930G>A	p.Cys977Tyr	0	FALSE	chr11:108141986:G:A	126:chr11:108141986:G:A	0.001253
94_c6-1	94	MET	MODERATE	c.1336A>G	p.Ile446Val	1	FALSE	chr7:116371857:A:G	126:chr7:116371857:A:G	0.001952
112_bl-1	112	TSC1	MODERATE	c.2677G>A; c.2827G>A; c.2830G>A	p.Ala893Thr; p.Ala943Thr; p.Ala944Thr	0	FALSE	chr9:135772716:C:T	127:chr9:135772716:C:T	0.001137
112_bl-1	112	EGFR	MODIFIER; MODERATE	c.*2364C>T; c.2165C>T	; p.Ala722Val	2	FALSE	chr7:55241717:C:T	127:chr7:55241717:C:T	0.001197
112_bl-1	112	NTHL1; TSC2	MODIFIER; MODERATE	c.-20C>T; c.170G>A	; p.Arg57His	0	FALSE	chr16:2100432:G:A	127:chr16:2100432:G:A	0.001229
112_bl-1	112	MIR1225; PKD1; TSC2	MODIFIER; MODERATE	n.*90C>T; c.*13118C>T; c.*13121C>T; c.5033G>A; c.5165G>A; c.5234G>A	; p.Arg1678His; p.Arg1722His; p.Arg1745His	0	FALSE	chr16:2138301:G:A	127:chr16:2138301:G:A	0.00135
112_bl-1	112	FBXW7	MODERATE	c.232A>T; c.346A>T; c.586A>T	p.Thr78Ser; p.Thr116Ser; p.Thr196Ser	0	FALSE	chr4:153268222:T:A	127:chr4:153268222:T:A	0.003108
112_bl-1	112	FGFR4	MODERATE	c.175C>T	p.Arg59Trp	2	FALSE	chr5:176517474:C:T	127:chr5:176517474:C:T	0.00133
112_bl-1	112	TP53	MODERATE	c.460A>G; c.541A>G; c.820A>G; c.937A>G	p.Ser154Gly; p.Ser181Gly; p.Ser274Gly; p.Ser313Gly	2	FALSE	chr17:7576909:T:C	127:chr17:7576909:T:C	0.001294
112_bl-1	112	NF1	MODIFIER; MODERATE	c.*2165G>A; c.1976G>A	; p.Arg659Gln	1	FALSE	chr17:29552243:G:A	127:chr17:29552243:G:A	0.00125
112_bl-1	112	TP53	MODERATE	c.257G>A; c.338G>A; c.617G>A; c.734G>A	p.Gly86Asp; p.Gly113Asp; p.Gly206Asp; p.Gly245Asp	126	FALSE	chr17:7577547:C:T	127:chr17:7577547:C:T	0.001084

112_bl-1	112	KIT	MODERATE	c.2671G>A; c.2683G>A	p.Ala891Thr; p.Ala895Thr	3	FALSE	chr4:55602973:G:A	127:chr4:55602973:G:A	0.001003
112_bl-1	112	TSC2	MODERATE	c.1654G>A	p.Ala552Thr	0	FALSE	chr16:2115574:G:A	127:chr16:2115574:G:A	0.001867
112_bl-1	112	NTRK1	MODERATE	c.1751G>A; c.1841G>A; c.1859G>A	p.Gly584Asp; p.Gly614Asp; p.Gly620Asp	1	FALSE	chr1:156848967:G:A	127:chr1:156848967:G:A	0.001725
112_bl-1	112	HRAS; LRRC56	MODERATE; MODIFIER	c.248C>T; c.-506G>A	p.Ala83Val;	1	FALSE	chr11:533808:G:A	127:chr11:533808:G:A	0.001314
112_bl-1	112	IDH2	MODERATE	c.128A>C; c.362A>C; c.518A>C	p.His43Pro; p.His121Pro; p.His173Pro	1	FALSE	chr15:90631835:T:G	127:chr15:90631835:T:G	0.001181
112_bl-1	112	HRAS; LRRC56	MODERATE; MODIFIER	c.196G>A; c.-506C>T	p.Ala66Thr;	1	FALSE	chr11:533860:C:T	127:chr11:533860:C:T	0.001233
112_bl-1	112	AKT1	MODERATE	c.932G>A	p.Gly311Asp	1	FALSE	chr14:105239613:C:T	127:chr14:105239613:C:T	0.00144
112_bl-1	112	IDH2	MODERATE	c.124A>G; c.358A>G; c.514A>G	p.Arg42Gly; p.Arg120Gly; p.Arg172Gly	19	FALSE	chr15:90631839:T:C	127:chr15:90631839:T:C	0.001158
112_bl-1	112	TSC2	MODERATE	c.2035G>A	p.Val679Met	0	FALSE	chr16:2121873:G:A	127:chr16:2121873:G:A	0.001461
112_bl-1	112	ATM	MODERATE	c.7342G>A	p.Asp2448Asn	0	FALSE	chr11:108200975:G:A	127:chr11:108200975:G:A	0.001678
112_bl-1	112	FGFR1	MODERATE	c.475C>T; c.481C>T; c.724C>T; c.742C>T; c.748C>T; c.841C>T	p.Arg159Trp; p.Arg161Trp; p.Arg242Trp; p.Arg248Trp; p.Arg250Trp; p.Arg281Trp	2	FALSE	chr8:38282215:G:A	127:chr8:38282215:G:A	0.001119
112_bl-1	112	APC	MODERATE	c.1820A>G; c.1874A>G	p.Gln607Arg; p.Gln625Arg	0	FALSE	chr5:112170778:A:G	127:chr5:112170778:A:G	0.001145
112_bl-1	112	CDKN2A	MODIFIER; HIGH	c.194-3575G>A; c.45G>A	; p.Trp15*	3	FALSE	chr9:21974782:C:T	127:chr9:21974782:C:T	0.00207

112_bl-1	112	ATM	MODERATE	c.4682T>C	p.Leu1561Pro	0	FALSE	chr11:108164110:T:C	127:chr11:108164110:T:C	0.00114
112_bl-1	112	BRAF	MODERATE	c.1799T>A	p.Val600Glu	23024	FALSE	chr7:140453136:A:T	127:chr7:140453136:A:T	0.047331
112_bl-1	112	FGFR3	MODERATE	c.1177G>A; c.1513G>A; c.1519G>A	p.Val393Ile; p.Val505Ile; p.Val507Ile	1	FALSE	chr4:1807182:G:A	127:chr4:1807182:G:A	0.002017
112_bl-1	112	NF1	MODERATE	c.467G>A	p.Arg156His	1	FALSE	chr17:29490382:G:A	127:chr17:29490382:G:A	0.001814
112_bl-1	112	IDH2; ZNF710	MODERATE; MODIFIER	c.1105G>A; c.1261G>A; c.871G>A; c.*2147C>T	p.Gly369Ser; p.Gly421Ser; p.Gly291Ser;	2	FALSE	chr15:90628058:C:T	127:chr15:90628058:C:T	0.001124
112_bl-1	112	ERBB2; MIEN1; MIR4728	MODIFIER; MODERATE	c.3160-213A>G; c.3251A>G; c.3296A>G; c.3341A>G; n.3665A>G; c.*388T>C; n.*67A>G	; p.Glu1084Gly; p.Glu1099Gly; p.Glu1114Gly	1	FALSE	chr17:37883729:A:G	127:chr17:37883729:A:G	0.001801
112_bl-1	112	TP53	MODERATE	c.127C>T; c.208C>T; c.487C>T; c.604C>T	p.Arg43Cys; p.Arg70Cys; p.Arg163Cys; p.Arg202Cys	6	FALSE	chr17:7578245:G:A	127:chr17:7578245:G:A	0.001146
112_bl-1	112	C9orf53; CDKN2A	MODIFIER; MODERATE; LOW	n.*616G>A; c.*228C>T; c.305C>T; c.348C>T	; p.Ala102Val; p.Gly116Gly	5	FALSE	chr9:21971053:G:A	127:chr9:21971053:G:A	0.002232
112_bl-1	112	AKT1	MODERATE	c.1099C>T	p.Arg367Cys	1	FALSE	chr14:105239288:G:A	127:chr14:105239288:G:A	0.001283

112_bl-1	112	TP53	MODERATE; MODIFIER	c.125C>T; c.242C>T; c.-279C>T; c.-360C>T	p.Thr42Ile; p.Thr81Ile;	2	FALSE	chr17:7579445:G:A	127:chr17:7579445:G:A	0.001394
112_bl-1	112	TP53	MODERATE	c.149G>A; c.428G>A; c.545G>A; c.68G>A	p.Cys50Tyr; p.Cys143Tyr; p.Cys182Tyr; p.Cys23Tyr	2	FALSE	chr17:7578385:C:T	127:chr17:7578385:C:T	0.001063
112_bl-1	112	TP53	MODIFIER; MODERATE	c.-15C>T; c.-96C>T; c.265C>T; c.382C>T	; p.Pro89Ser; p.Pro128Ser	7	FALSE	chr17:7578548:G:A	127:chr17:7578548:G:A	0.001667
112_bl-1	112	PTEN	HIGH	c.822G>A	p.Trp274*	3	FALSE	chr10:89720671:G:A	127:chr10:89720671:G:A	0.008375
112_bl-1	112	NF1	MODIFIER; MODERATE	c.*2165C>T; c.1954C>T	; p.Arg652Cys	1	FALSE	chr17:29552221:C:T	127:chr17:29552221:C:T	0.001675
112_bl-1	112	EPHA3	MODERATE	c.1535G>A	p.Arg512Gln	0	FALSE	chr3:89448571:G:A	127:chr3:89448571:G:A	0.001235
112_bl-1	112	BRAF	MODERATE	c.2173C>T	p.His725Tyr	1	FALSE	chr7:140434525:G:A	127:chr7:140434525:G:A	0.003451
112_bl-1	112	FGFR1	MODERATE	c.1060C>T; c.1066C>T; c.1303C>T; c.1327C>T; c.1333C>T; c.1426C>T	p.Arg354Trp; p.Arg356Trp; p.Arg435Trp; p.Arg443Trp; p.Arg445Trp; p.Arg476Trp	2	FALSE	chr8:38275843:G:A	127:chr8:38275843:G:A	0.001468
112_bl-1	112	CDKN2A	MODIFIER; MODERATE	c.194-3519C>T; c.101C>T	; p.Ala34Val	2	FALSE	chr9:21974726:G:A	127:chr9:21974726:G:A	0.001468
112_bl-1	112	FGFR3	MODERATE	c.905G>A	p.Gly302Asp	1	FALSE	chr4:1803727:G:A	127:chr4:1803727:G:A	0.001307
112_bl-1	112	ATM	HIGH	c.103C>T	p.Arg35*	0	FALSE	chr11:108098533:C:T	127:chr11:108098533:C:T	0.001325
112_bl-1	112	KIT	MODERATE	c.2854C>T; c.2866C>T	p.Arg952Trp; p.Arg956Trp	3	FALSE	chr4:55604658:C:T	127:chr4:55604658:C:T	0.001172

112_bl-1	112	IGF1R	MODERATE	c.3862G>A; c.3865G>A	p.Glu1288Lys; p.Glu1289Lys	0	FALSE	chr15:99500432:G:A	127:chr15:99500432:G:A	0.001195
112_bl-1	112	CWH43	MODERATE	c.1535G>A; c.1616G>A	p.Gly512Asp; p.Gly539Asp	0	FALSE	chr4:49034690:G:A	127:chr4:49034690:G:A	0.001053
112_bl-1	112	FGFR3	MODIFIER; MODERATE	c.931-374G>A; c.1196G>A; c.1202G>A	; p.Arg399His; p.Arg401His	1	FALSE	chr4:1806177:G:A	127:chr4:1806177:G:A	0.001351
112_bl-1	112	IDH2	MODERATE	c.125G>T; c.359G>T; c.515G>T	p.Arg42Met; p.Arg120Met; p.Arg172Met	199	FALSE	chr15:90631838:C:A	127:chr15:90631838:C:A	0.001159
112_bl-1	112	DDR2	MODERATE	c.757G>A	p.Gly253Ser	1	FALSE	chr1:162729671:G:A	127:chr1:162729671:G:A	0.001172
112_bl-1	112	CDKN2A	MODIFIER; MODERATE	c.194-3531C>T; c.89C>T	; p.Ala30Val	3	FALSE	chr9:21974738:G:A	127:chr9:21974738:G:A	0.001498
112_bl-1	112	TP53	LOW; MODIFIER; MODERATE	c.-6C>T; c.355C>T; c.472C>T; c.76C>T	; p.Arg119Cys; p.Arg158Cys; p.Arg26Cys	17	FALSE	chr17:7578458:G:A	127:chr17:7578458:G:A	0.001165
112_bl-1	112	MIR1225; PKD1; TSC2	MODIFIER; MODERATE	n.*90C>T; c.*13118C>T; c.*13121C>T; c.4906G>A; c.5038G>A; c.5107G>A	; p.Val1636Met; p.Val1680Met; p.Val1703Met	0	FALSE	chr16:2138087:G:A	127:chr16:2138087:G:A	0.002377
112_bl-1	112	FGFR4	MODERATE	c.461G>A	p.Arg154His	3	FALSE	chr5:176517963:G:A	127:chr5:176517963:G:A	0.001181
5_t2c9-1	5	BRAF	MODERATE	c.1796C>T	p.Thr599Ile	4	FALSE	chr7:140453139:G:A	128:chr7:140453139:G:A	0.001857
5_t2c9-1	5	IGF1R	MODERATE	c.2453C>T	p.Ser818Phe	0	FALSE	chr15:99465628:C:T	128:chr15:99465628:C:T	0.001967
5_t2c9-1	5	RPL19	MODERATE	c.406C>T	p.Arg136Trp	0	FALSE	chr17:37360379:C:T	128:chr17:37360379:C:T	0.001874
5_t2c9-1	5	PDGFRA	MODERATE	c.1711G>A	p.Glu571Lys	1	FALSE	chr4:55141065:G:A	128:chr4:55141065:G:A	0.002014

5_t2c9-1	5	NTRK3	MODERATE	c.1351C>T; c.1375C>T	p.Arg451Trp; p.Arg459Trp	0	FALSE	chr15:88669523:G:A	128:chr15:88669523:G:A	0.001927
5_t2c9-1	5	PIK3CA	MODERATE	c.277C>T	p.Arg93Trp	24	FALSE	chr3:178916890:C:T	128:chr3:178916890:C:T	0.002433
5_t2c9-1	5	IGF1R	MODERATE	c.676G>A	p.Glu226Lys	0	FALSE	chr15:99434589:G:A	128:chr15:99434589:G:A	0.00224
5_t2c9-1	5	NTRK1	MODERATE	c.821C>T; c.911C>T	p.Ser274Phe; p.Ser304Phe	1	FALSE	chr1:156843485:C:T	128:chr1:156843485:C:T	0.002176
5_t2c9-1	5	KDR	MODERATE	c.1040G>A	p.Arg347His	4	FALSE	chr4:55976872:C:T	128:chr4:55976872:C:T	0.001478
5_t2c9-1	5	ALK	MODERATE	c.4517C>T	p.Thr1506Met	2	FALSE	chr2:29416436:G:A	128:chr2:29416436:G:A	0.001476
5_t2c9-1	5	FGFR2	MODERATE; MODIFIER	c.1639C>T; c.1642C>T; c.1645C>T; c.1654C>T; c.1723C>T; c.1726C>T; c.1990C>T; c.1993C>T; n.2440C>T	p.Arg547Trp; p.Arg548Trp; p.Arg549Trp; p.Arg552Trp; p.Arg575Trp; p.Arg576Trp; p.Arg664Trp; p.Arg665Trp;	2	FALSE	chr10:123246935:G:A	128:chr10:123246935:G:A	0.002911
5_t2c9-1	5	ATM	HIGH	c.5623C>T	p.Arg1875*	0	FALSE	chr11:108175528:C:T	128:chr11:108175528:C:T	0.001947
5_t2c9-1	5	FGFR2	MODIFIER; MODERATE	c.110-14065C>T; c.110-945C>T; n.757-14065C>T; c.290C>T	; p.Ala97Val	1	FALSE	chr10:123325038:G:A	128:chr10:123325038:G:A	0.001976
5_t2c9-1	5	MIR4673; NOTCH1	MODIFIER; MODERATE	n.*59A>G; c.890A>G	; p.Asp297Gly	0	FALSE	chr9:139413252:T:C	128:chr9:139413252:T:C	0.002064
5_t2c9-1	5	ATM	HIGH	c.2558C>A	p.Ser853*	0	FALSE	chr11:108137989:C:A	128:chr11:108137989:C:A	0.001661
5_t2c9-1	5	FGFR4	MODERATE	c.238C>T	p.Arg80Trp	3	FALSE	chr5:176517537:C:T	128:chr5:176517537:C:T	0.002123

5_t2c9-1	5	FGFR4	MODERATE	c.1978G>A; c.2062G>A; c.2182G>A	p.Ala660Thr; p.Ala688Thr; p.Ala728Thr	1	FALSE	chr5:176524321:G:A	128:chr5:176524321:G:A	0.003891
5_t2c9-1	5	C9orf53; CDKN2A	MODIFIER; MODERATE; LOW	n.*616G>A; c.*256C>T; c.376C>T; c.333C>T	; p.Pro126Ser; p.Gly111Gly	2	FALSE	chr9:21971025:G:A	128:chr9:21971025:G:A	0.0033
5_t2c9-1	5	IGF1R	MODERATE	c.2342G>A	p.Arg781Lys	0	FALSE	chr15:99465517:G:A	128:chr15:99465517:G:A	0.001762
5_t2c9-1	5	C9orf53; CDKN2A	MODIFIER; MODERATE	n.*616C>T; c.*245G>A; c.322G>A; c.365G>A	; p.Asp108Asn; p.Arg122Gln	14	FALSE	chr9:21971036:C:T	128:chr9:21971036:C:T	0.003413
5_t2c9-1	5	TP53	HIGH	c.439C>T; c.520C>T; c.799C>T; c.916C>T	p.Arg147*; p.Arg174*; p.Arg267*; p.Arg306*	167	FALSE	chr17:7577022:G:A	128:chr17:7577022:G:A	0.001974
5_t2c9-1	5	INSRR; NTRK1	MODIFIER; MODERATE	c.3397+13C>T; c.28G>A	; p.Ala10Thr	1	FALSE	chr1:156811891:G:A	128:chr1:156811891:G:A	0.001468
5_t2c9-1	5	RET	MODERATE	c.1907C>T	p.Thr636Met	1	FALSE	chr10:43609955:C:T	128:chr10:43609955:C:T	0.001575
5_t2c9-1	5	PTEN	MODERATE	c.424C>T	p.Arg142Trp	6	FALSE	chr10:89692940:C:T	128:chr10:89692940:C:T	0.001852
5_t2c9-1	5	HOXD-AS2; HOXD8	MODIFIER; MODERATE	n.*692C>T; c.304G>A; c.853G>A; c.856G>A	; p.Glu102Lys; p.Glu285Lys; p.Glu286Lys	0	FALSE	chr2:176996323:G:A	128:chr2:176996323:G:A	0.001646
5_t2c9-1	5	PDGFRA	MODERATE	c.401C>T	p.Thr134Met	3	FALSE	chr4:55129867:C:T	128:chr4:55129867:C:T	0.001925
5_t2c9-1	5	FLT3	MODERATE	c.2822C>T	p.Ser941Leu	0	FALSE	chr13:28588626:G:A	128:chr13:28588626:G:A	0.001559
5_t2c9-1	5	ALK	MODERATE	c.1753G>A	p.Ala585Thr	3	FALSE	chr2:29519818:C:T	128:chr2:29519818:C:T	0.001711

5_t2c9-1	5	TP53	MODERATE	c.200G>A; c.281G>A; c.560G>A; c.677G>A	p.Gly67Asp; p.Gly94Asp; p.Gly187Asp; p.Gly226Asp	5	FALSE	chr17:7577604:C:T	128:chr17:7577604:C:T	0.001778
5_t2c9-1	5	EPHA3	MODERATE	c.2306G>A	p.Arg769His	0	FALSE	chr3:89480469:G:A	128:chr3:89480469:G:A	0.001761
5_t2c9-1	5	NF1	HIGH	c.1105C>T	p.Gln369*	2	FALSE	chr17:29528097:C:T	128:chr17:29528097:C:T	0.003363
5_t2c9-1	5	FGFR4	MODERATE; LOW	c.1186G>A; c.1306G>A; c.1152G>A	p.Val396Met; p.Val436Met; p.Ala384Ala	1	FALSE	chr5:176520461:G:A	128:chr5:176520461:G:A	0.001934
5_t2c9-1	5	STK11	MODERATE	c.647C>T	p.Ser216Phe	3	FALSE	chr19:1220629:C:T	128:chr19:1220629:C:T	0.004032
5_t2c9-1	5	PIK3CA	MODERATE	c.2078G>A	p.Arg693His	1	FALSE	chr3:178938836:G:A	128:chr3:178938836:G:A	0.001932
5_t2c9-1	5	ATM	HIGH	c.5188C>T	p.Arg1730*	0	FALSE	chr11:108172385:C:T	128:chr11:108172385:C:T	0.002548
112_c2-1	112	PIK3R1	MODERATE	c.1508G>A; c.419G>A; c.608G>A; c.698G>A	p.Arg503Gln; p.Arg140Gln; p.Arg203Gln; p.Arg233Gln	2	FALSE	chr5:67590446:G:A	130:chr5:67590446:G:A	0.000772
112_c2-1	112	MET	HIGH	c.1639C>T	p.Arg547*	2	FALSE	chr7:116381017:C:T	130:chr7:116381017:C:T	0.000636
112_c2-1	112	EGFR	MODERATE	c.494G>A	p.Arg165Gln	3	FALSE	chr7:55214368:G:A	130:chr7:55214368:G:A	0.000834
112_c2-1	112	HGF	HIGH	c.1582C>T; c.1597C>T	p.Arg528*; p.Arg533*	0	FALSE	chr7:81336625:G:A	130:chr7:81336625:G:A	0.000959
112_c2-1	112	CWH43	MODERATE	c.1535G>A; c.1616G>A	p.Gly512Asp; p.Gly539Asp	0	FALSE	chr4:49034690:G:A	130:chr4:49034690:G:A	0.001142
112_c2-1	112	TP53	MODIFIER; MODERATE	c.-17G>A; c.344G>A; c.461G>A; c.65G>A	; p.Gly115Asp; p.Gly154Asp; p.Gly22Asp	39	FALSE	chr17:7578469:C:T	130:chr17:7578469:C:T	0.001555
112_c2-1	112	BRAF	MODERATE	c.550G>A	p.Ala184Thr	1	FALSE	chr7:140508750:C:T	130:chr7:140508750:C:T	0.000801

112_c2-1	112	FBXW7	MODERATE	c.232A>T; c.346A>T; c.586A>T	p.Thr78Ser; p.Thr116Ser; p.Thr196Ser	0	FALSE	chr4:153268222:T:A	130:chr4:153268222:T:A	0.000898
112_c2-1	112	TP53	MODERATE	c.110G>A; c.191G>A; c.470G>A; c.587G>A	p.Arg37Gln; p.Arg64Gln; p.Arg157Gln; p.Arg196Gln	19	FALSE	chr17:7578262:C:T	130:chr17:7578262:C:T	0.000734
112_c2-1	112	FGFR4	MODIFIER; MODERATE	c.1058-174G>A; c.1078G>A	; p.Ala360Thr	1	FALSE	chr5:176520159:G:A	130:chr5:176520159:G:A	0.000817
112_c2-1	112	TSC1	HIGH	c.1921C>T; c.2071C>T; c.2074C>T	p.Arg641*; p.Arg691*; p.Arg692*	0	FALSE	chr9:135779172:G:A	130:chr9:135779172:G:A	0.000719
112_c2-1	112	TP53	MODERATE	c.101C>T; c.20C>T; c.380C>T; c.497C>T	p.Ser34Leu; p.Ser7Leu; p.Ser127Leu; p.Ser166Leu	12	FALSE	chr17:7578433:G:A	130:chr17:7578433:G:A	0.00076
112_c2-1	112	BRAF	MODERATE	c.1799T>A	p.Val600Glu	23024	FALSE	chr7:140453136:A:T	130:chr7:140453136:A:T	0.008217
112_c2-1	112	ESR1	MODERATE	c.1468G>A; c.1471G>A; c.1477G>A	p.Ala490Thr; p.Ala491Thr; p.Ala493Thr	0	FALSE	chr6:152415621:G:A	130:chr6:152415621:G:A	0.000737
112_c2-1	112	NTRK1	MODERATE	c.804C>G; c.894C>G	p.His268Gln; p.His298Gln	1	FALSE	chr1:156843468:C:G	130:chr1:156843468:C:G	0.00225
112_c2-1	112	PIK3CA	MODERATE	c.3141T>A	p.His1047Gln	4	FALSE	chr3:178952086:T:A	130:chr3:178952086:T:A	0.000709
112_c2-1	112	FLT3	MODERATE	c.2822C>T	p.Ser941Leu	0	FALSE	chr13:28588626:G:A	130:chr13:28588626:G:A	0.000714
112_c2-1	112	PDGFRA	MODERATE	c.577G>A	p.Val193Ile	2	FALSE	chr4:55130043:G:A	130:chr4:55130043:G:A	0.00097
112_c2-1	112	IDH2; ZNF710	MODERATE; MODIFIER	c.1108G>A; c.718G>A; c.952G>A; c.*2147C>T	p.Ala370Thr; p.Ala240Thr; p.Ala318Thr;	1	FALSE	chr15:90628303:C:T	130:chr15:90628303:C:T	0.000975

112_c2-1	112	MIR4673; NOTCH1	MODIFIER; HIGH	n.*59C>T; c.1324C>T	; p.Gln442*	0	FALSE	chr9:139412321:G:A	130:chr9:139412321:G:A	0.000999
112_c2-1	112	NOTCH1	MODERATE	c.4984C>T	p.Arg1662Trp	0	FALSE	chr9:139399159:G:A	130:chr9:139399159:G:A	0.001129
112_c2-1	112	PIK3CA	MODERATE	c.2984C>A	p.Ala995Asp	1	FALSE	chr3:178951929:C:A	130:chr3:178951929:C:A	0.000788
112_c2-1	112	C9orf53; CDKN2A	MODIFIER; MODERATE	n.*616G>A; c.*324C>T; c.*45C>T; c.401C>T	; p.Ala134Val	1	FALSE	chr9:21970957:G:A	130:chr9:21970957:G:A	0.000892
112_c2-1	112	NTRK3	MODERATE	c.1585G>T; c.1609G>T	p.Asp529Tyr; p.Asp537Tyr	0	FALSE	chr15:88483961:C:A	130:chr15:88483961:C:A	0.000833
112_c2-1	112	TP53	HIGH	c.439C>T; c.520C>T; c.799C>T; c.916C>T	p.Arg147*; p.Arg174*; p.Arg267*; p.Arg306*	167	FALSE	chr17:7577022:G:A	130:chr17:7577022:G:A	0.000738
112_c2-1	112	TSC1	MODERATE	c.1547C>T; c.1697C>T; c.1700C>T	p.Ala516Val; p.Ala566Val; p.Ala567Val	0	FALSE	chr9:135781265:G:A	130:chr9:135781265:G:A	0.00101
112_c2-1	112	FBXW7	MODERATE	c.317G>A; c.431G>A; c.671G>A	p.Arg106Gln; p.Arg144Gln; p.Arg224Gln	0	FALSE	chr4:153268137:C:T	130:chr4:153268137:C:T	0.000721
112_c2-1	112	MAP2K1	MODERATE	c.146G>A	p.Arg49His	1	FALSE	chr15:66727430:G:A	130:chr15:66727430:G:A	0.000777
112_c2-1	112	ATM	MODERATE	c.1351C>T	p.Arg451Cys	0	FALSE	chr11:108121543:C:T	130:chr11:108121543:C:T	0.000721
112_c2-1	112	PDGFRA	MODERATE	c.533T>C	p.Phe178Ser	1	FALSE	chr4:55129999:T:C	130:chr4:55129999:T:C	0.000698
112_c2-1	112	HRAS; LRRC56	MODERATE; MODIFIER	c.368G>A; c.-506C>T	p.Arg123His;	2	FALSE	chr11:533535:C:T	130:chr11:533535:C:T	0.000794
112_c2-1	112	KIT	MODERATE	c.506G>A	p.Gly169Asp	1	FALSE	chr4:55564618:G:A	130:chr4:55564618:G:A	0.00071
112_c2-1	112	NF1	MODERATE	c.467G>A	p.Arg156His	1	FALSE	chr17:29490382:G:A	130:chr17:29490382:G:A	0.000869
112_c2-1	112	AKT3	MODERATE	c.899C>T	p.Ala300Val	0	FALSE	chr1:243727071:G:A	130:chr1:243727071:G:A	0.000818

112_c2-1	112	TP53	MODERATE	c.223T>C; c.304T>C; c.583T>C; c.700T>C	p.Tyr75His; p.Tyr102His; p.Tyr195His; p.Tyr234His	24	FALSE	chr17:7577581:A:G	130:chr17:7577581:A:G	0.001332
112_c2-1	112	MITF	MODIFIER; MODERATE	c.93+115G>A; c.208G>A; c.373G>A; c.481G>A; c.526G>A; c.529G>A	; p.Ala70Thr; p.Ala125Thr; p.Ala161Thr; p.Ala176Thr; p.Ala177Thr	0	FALSE	chr3:69987147:G:A	130:chr3:69987147:G:A	0.001219
112_c2-1	112	KIT	MODERATE	c.251C>T	p.Thr84Met	1	FALSE	chr4:55561861:C:T	130:chr4:55561861:C:T	0.00072
112_c2-1	112	BRAF	MODERATE	c.436C>T	p.Arg146Trp	1	FALSE	chr7:140534477:G:A	130:chr7:140534477:G:A	0.000727
112_c2-1	112	PDGFRA	MODERATE	c.187G>A	p.Glu63Lys	1	FALSE	chr4:55127399:G:A	130:chr4:55127399:G:A	0.00076
112_c2-1	112	CDH1	HIGH	c.1596G>A	p.Trp532*	0	FALSE	chr16:68853213:G:A	130:chr16:68853213:G:A	0.000848
112_c2-1	112	EGFR	MODERATE	c.445C>T	p.Arg149Trp	1	FALSE	chr7:55214319:C:T	130:chr7:55214319:C:T	0.000893
112_c2-1	112	FGFR2	MODERATE; MODIFIER	c.263G>A; c.341G>A; c.608G>A; n.910G>A	p.Arg88His; p.Arg114His; p.Arg203His;	2	FALSE	chr10:123310820:C:T	130:chr10:123310820:C:T	0.001592
112_c2-1	112	GNA11	MODERATE	c.766C>T	p.Arg256Trp	1	FALSE	chr19:3119234:C:T	130:chr19:3119234:C:T	0.000799
112_c2-1	112	PTEN	HIGH	c.822G>A	p.Trp274*	3	FALSE	chr10:89720671:G:A	130:chr10:89720671:G:A	0.004956
112_c2-1	112	TP53	MODIFIER; HIGH	c.-48C>T; c.313C>T; c.34C>T; c.430C>T	; p.Gln105*; p.Gln12*; p.Gln144*	42	FALSE	chr17:7578500:G:A	130:chr17:7578500:G:A	0.000753
112_c2-1	112	GNA11	MODERATE	c.440G>A	p.Arg147His	1	FALSE	chr19:3113446:G:A	130:chr19:3113446:G:A	0.000894
112_c2-1	112	PTEN	HIGH	c.821G>A	p.Trp274*	6	FALSE	chr10:89720670:G:A	130:chr10:89720670:G:A	0.001121

112_c2-1	112	CTNNB1	MODERATE	c.1406G>A	p.Arg469His	0	FALSE	chr3:41275240:G:A	130:chr3:41275240:G:A	0.000659
112_c2-1	112	MET	MODERATE	c.3443G>A; c.3497G>A	p.Arg1148Gln; p.Arg1166Gln	4	FALSE	chr7:116418932:G:A	130:chr7:116418932:G:A	0.000823
112_c2-1	112	MIR4673; NOTCH1	MODIFIER; MODERATE	n.*59G>A; c.1058G>A	; p.Arg353His	0	FALSE	chr9:139413084:C:T	130:chr9:139413084:C:T	0.001221
112_c2-1	112	APC	MODIFIER; MODERATE	c.676-8791C>T; c.688C>T	; p.Arg230Cys	0	FALSE	chr5:112128185:C:T	130:chr5:112128185:C:T	0.001332
112_c2-1	112	EGFR	MODERATE	c.755G>A	p.Arg252His	3	FALSE	chr7:55221711:G:A	130:chr7:55221711:G:A	0.001261
112_c2-1	112	ALK	MODERATE	c.617C>T	p.Ala206Val	2	FALSE	chr2:30142909:G:A	130:chr2:30142909:G:A	0.00096
112_c2-1	112	PTEN	MODERATE	c.133G>A	p.Val45Ile	1	FALSE	chr10:89653835:G:A	130:chr10:89653835:G:A	0.000801
112_c2-1	112	TP53	MODIFIER; MODERATE	c.-1G>C; c.-82G>C; c.279G>C; c.396G>C	; p.Lys93Asn; p.Lys132Asn	34	FALSE	chr17:7578534:C:G	130:chr17:7578534:C:G	0.00076
112_c2-1	112	IDH1	MODERATE	c.290G>A	p.Gly97Asp	4	FALSE	chr2:209113217:C:T	130:chr2:209113217:C:T	0.000819
112_c2-1	112	AKT1	MODERATE	c.1112C>T	p.Thr371Met	1	FALSE	chr14:105239275:G:A	130:chr14:105239275:G:A	0.000835
112_c2-1	112	ALK	MODERATE	c.4255G>A	p.Glu1419Lys	1	FALSE	chr2:29416698:C:T	130:chr2:29416698:C:T	0.000662
112_c2-1	112	EGFR	MODERATE	c.940G>A	p.Asp314Asn	1	FALSE	chr7:55223573:G:A	130:chr7:55223573:G:A	0.000722
112_c2-1	112	NRAS	MODERATE	c.553C>T	p.Pro185Ser	2	FALSE	chr1:115251173:G:A	130:chr1:115251173:G:A	0.000857
112_c2-1	112	PHLPP1	HIGH	c.1885C>T	p.Arg629*	0	FALSE	chr18:60506128:C:T	130:chr18:60506128:C:T	0.001018
112_c2-1	112	EVI2A; NF1	MODIFIER; MODERATE	c.-266G>A; c.-338G>A; c.5020C>T; c.5083C>T	; p.Arg1674Trp; p.Arg1695Trp	1	FALSE	chr17:29653085:C:T	130:chr17:29653085:C:T	0.000688

112_c2-1	112	EGFR	MODIFIER; MODERATE	c.*2133G>A; c.*2364G>A; c.2030G>A	; p.Arg677His	5	FALSE	chr7:55240786:G:A	130:chr7:55240786:G:A	0.001725
112_c2-1	112	TP53	MODERATE	c.341G>A; c.422G>A; c.701G>A; c.818G>A	p.Arg114His; p.Arg141His; p.Arg234His; p.Arg273His	647	TRUE	chr17:7577120:C:T	130:chr17:7577120:C:T	0.000817
112_c2-1	112	ALK	MODERATE	c.1753G>A	p.Ala585Thr	3	FALSE	chr2:29519818:C:T	130:chr2:29519818:C:T	0.000716
112_c2-1	112	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2596G>A; n.-1C>T	p.Glu866Lys;	3	FALSE	chr7:55259538:G:A	130:chr7:55259538:G:A	0.000881
112_c2-1	112	CTNNB1	HIGH	c.74G>A	p.Trp25*	0	FALSE	chr3:41266077:G:A	130:chr3:41266077:G:A	0.000784
112_c2-1	112	C9orf53; CDKN2A	MODIFIER; MODERATE; LOW	n.*616G>A; c.*165C>T; c.242C>T; c.285C>T	; p.Pro81Leu; p.Thr95Thr	9	FALSE	chr9:21971116:G:A	130:chr9:21971116:G:A	0.000942
112_c2-1	112	NTRK3	MODERATE	c.1801G>A; c.1825G>A	p.Asp601Asn; p.Asp609Asn	0	FALSE	chr15:88476307:C:T	130:chr15:88476307:C:T	0.000998
112_c2-1	112	HOXD-AS2; HOXD8	MODIFIER; MODERATE	n.*692C>T; c.304G>A; c.853G>A; c.856G>A	; p.Glu102Lys; p.Glu285Lys; p.Glu286Lys	0	FALSE	chr2:176996323:G:A	130:chr2:176996323:G:A	0.001049
112_c2-1	112	FGFR1	LOW; MODIFIER; MODERATE	c.-25C>T; c.167C>T; c.68C>T	; p.Pro56Leu; p.Pro23Leu	1	FALSE	chr8:38314897:G:A	130:chr8:38314897:G:A	0.000726
112_c2-1	112	EPHA3	MODERATE	c.1543G>A	p.Ala515Thr	0	FALSE	chr3:89448579:G:A	130:chr3:89448579:G:A	0.000834
112_c2-1	112	FGFR3	MODERATE	c.599G>A	p.Arg200His	1	FALSE	chr4:1803247:G:A	130:chr4:1803247:G:A	0.001573
112_c2-1	112	SMO	MODERATE	c.781C>T	p.Arg261Cys	0	FALSE	chr7:128845484:C:T	130:chr7:128845484:C:T	0.000779

112_c2-1	112	FGFR2	MODERATE; MODIFIER	c.1639C>T; c.1642C>T; c.1645C>T; c.1654C>T; c.1723C>T; c.1726C>T; c.1990C>T; c.1993C>T; n.2440C>T	p.Arg547Trp; p.Arg548Trp; p.Arg549Trp; p.Arg552Trp; p.Arg575Trp; p.Arg576Trp; p.Arg664Trp; p.Arg665Trp;	2	FALSE	chr10:123246935:G:A	130:chr10:123246935:G:A	0.00126
112_c2-1	112	IGF1R	MODERATE	c.3905T>C; c.3908T>C	p.Val1302Ala; p.Val1303Ala	0	FALSE	chr15:99500475:T:C	130:chr15:99500475:T:C	0.001201
112_c2-1	112	ERBB2; MIEN1; MIR4728	MODIFIER; MODERATE	c.3160-213A>G; c.3251A>G; c.3296A>G; c.3341A>G; n.3665A>G; c.*388T>C; n.*67A>G	; p.Glu1084Gly; p.Glu1099Gly; p.Glu1114Gly	1	FALSE	chr17:37883729:A:G	130:chr17:37883729:A:G	0.000767
112_c2-1	112	FOXL2; FOXL2NB; LINC01391	MODERATE; MODIFIER	c.112G>A; c.-132C>T; n.-1G>A	p.Gly38Ser;	0	FALSE	chr3:138665453:C:T	130:chr3:138665453:C:T	0.001004
112_c2-1	112	FGFR3	MODERATE	c.905G>A	p.Gly302Asp	1	FALSE	chr4:1803727:G:A	130:chr4:1803727:G:A	0.000884
112_c2-1	112	TP53	MODIFIER; MODERATE	c.-9G>A; c.352G>A; c.469G>A; c.73G>A	; p.Val118Ile; p.Val157Ile; p.Val25Ile	169	FALSE	chr17:7578461:C:T	130:chr17:7578461:C:T	0.001537
112_c2-1	112	FGFR2	MODIFIER; LOW; HIGH	c.749-4848C>T; n.1053C>T; c.406C>T; c.484C>T; c.751C>T	; p.Arg136*; p.Arg162*; p.Arg251*	2	FALSE	chr10:123279681:G:A	130:chr10:123279681:G:A	0.000883

112_c2-1	112	PTEN	MODERATE	c.361G>A	p.Ala121Thr	3	FALSE	chr10:89692877:G:A	130:chr10:89692877:G:A	0.00081
112_c2-1	112	TP53	MODERATE; MODIFIER	c.200C>T; c.83C>T; c.-279C>T; c.-360C>T	p.Pro67Leu; p.Pro28Leu;	1	FALSE	chr17:7579487:G:A	130:chr17:7579487:G:A	0.000933
112_c2-1	112	FGFR3	MODERATE	c.1526G>A; c.1862G>A; c.1868G>A	p.Arg509His; p.Arg621His; p.Arg623His	2	FALSE	chr4:1807803:G:A	130:chr4:1807803:G:A	0.00092
112_c2-1	112	RET	MODERATE	c.2116G>A	p.Val706Met	2	FALSE	chr10:43610164:G:A	130:chr10:43610164:G:A	0.000669
112_c2-1	112	IGF1R	MODERATE	c.3121C>T; c.3124C>T	p.Arg1041Cys; p.Arg1042Cys	0	FALSE	chr15:99478220:C:T	130:chr15:99478220:C:T	0.001101
112_c2-1	112	ATM	MODERATE	c.2075G>A	p.Arg692His	0	FALSE	chr11:108124717:G:A	130:chr11:108124717:G:A	0.002415
112_c2-1	112	AKT1	MODERATE	c.932G>A	p.Gly311Asp	1	FALSE	chr14:105239613:C:T	130:chr14:105239613:C:T	0.000898
112_c2-1	112	CACNB1; RPL19	MODIFIER; MODERATE	c.-209C>T; c.82G>A	; p.Glu28Lys	0	FALSE	chr17:37357542:G:A	130:chr17:37357542:G:A	0.000737
112_c2-1	112	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2507G>A; n.-1C>T	p.Arg836His;	2	FALSE	chr7:55259449:G:A	130:chr7:55259449:G:A	0.000849
112_c2-1	112	BRAF	MODERATE	c.305C>T	p.Ser102Phe	1	FALSE	chr7:140534608:G:A	130:chr7:140534608:G:A	0.000754
112_c2-1	112	KIT	MODERATE	c.530G>A	p.Arg177His	1	FALSE	chr4:55564642:G:A	130:chr4:55564642:G:A	0.000693
112_c2-1	112	PTEN	MODERATE	c.407G>A	p.Cys136Tyr	14	FALSE	chr10:89692923:G:A	130:chr10:89692923:G:A	0.000769
112_c2-1	112	TP53	MODERATE	c.103C>T; c.184C>T; c.463C>T; c.580C>T	p.Leu35Phe; p.Leu62Phe; p.Leu155Phe; p.Leu194Phe	22	FALSE	chr17:7578269:G:A	130:chr17:7578269:G:A	0.000747
112_c2-1	112	APC	MODERATE	c.1864C>T; c.1918C>T	p.Arg622Trp; p.Arg640Trp	0	FALSE	chr5:112170822:C:T	130:chr5:112170822:C:T	0.000811
130_c1w1-1	130	NOTCH1	MODERATE	c.4987C>T	p.Arg1663Trp	0	FALSE	chr9:139399156:G:A	131:chr9:139399156:G:A	0.003759

130_c1w1-1	130	TP53	MODIFIER; MODERATE	c.-11G>A; c.350G>A; c.467G>A; c.71G>A	; p.Arg117His; p.Arg156His; p.Arg24His	26	FALSE	chr17:7578463:C:T	131:chr17:7578463:C:T	0.002016
130_c1w1-1	130	EPHA3	MODERATE	c.2530C>T	p.Pro844Ser	0	FALSE	chr3:89499360:C:T	131:chr3:89499360:C:T	0.00199
130_c1w1-1	130	TP53	MODERATE; MODIFIER	c.239C>T; c.356C>T; c.-279C>T; c.-360C>T	p.Ala80Val; p.Ala119Val;	1	FALSE	chr17:7579331:G:A	131:chr17:7579331:G:A	0.002896
130_c1w1-1	130	PIK3CA	HIGH	c.1656G>A	p.Trp552*	1	FALSE	chr3:178936114:G:A	131:chr3:178936114:G:A	0.002176
130_c1w1-1	130	NOTCH1	MODERATE	c.6107C>T	p.Ala2036Val	0	FALSE	chr9:139393424:G:A	131:chr9:139393424:G:A	0.001998
130_c1w1-1	130	AKT1	MODERATE	c.932G>A	p.Gly311Asp	1	FALSE	chr14:105239613:C:T	131:chr14:105239613:C:T	0.002265
130_c1w1-1	130	ERBB2; MIEN1; MIR4728	MODERATE; MODIFIER	c.2720A>G; c.2765A>G; c.2810A>G; n.3134A>G; c.*388T>C; n.-1A>G	p.Lys907Arg; p.Lys922Arg; p.Lys937Arg;	1	FALSE	chr17:37882044:A:G	131:chr17:37882044:A:G	0.002051
130_c1w1-1	130	FGFR2	MODERATE; MODIFIER	c.1481C>T; c.1484C>T; c.1487C>T; c.1496C>T; c.1565C>T; c.1568C>T; c.1832C>T; c.1835C>T; n.2282C>T	p.Ala494Val; p.Ala495Val; p.Ala496Val; p.Ala499Val; p.Ala522Val; p.Ala523Val; p.Ala611Val; p.Ala612Val;	1	FALSE	chr10:123256077:G:A	131:chr10:123256077:G:A	0.001786

130_c1w1-1	130	TP53	MODERATE	c.248G>A; c.329G>A; c.608G>A; c.725G>A	p.Cys83Tyr; p.Cys110Tyr; p.Cys203Tyr; p.Cys242Tyr	72	FALSE	chr17:7577556:C:T	131:chr17:7577556:C:T	0.001815
130_c1w1-1	130	NTRK1	MODERATE	c.1751G>A; c.1841G>A; c.1859G>A	p.Gly584Asp; p.Gly614Asp; p.Gly620Asp	1	FALSE	chr1:156848967:G:A	131:chr1:156848967:G:A	0.001874
130_c1w1-1	130	NTRK1	MODERATE	c.804C>G; c.894C>G	p.His268Gln; p.His298Gln	1	FALSE	chr1:156843468:C:G	131:chr1:156843468:C:G	0.002174
130_c1w1-1	130	CSDE1; NRAS	MODIFIER; MODERATE	c.*2430T>A; c.*2523T>A; c.*2817T>A; c.*2910T>A; c.*2964T>A; c.*3057T>A; c.190T>A	; p.Tyr64Asn	2	FALSE	chr1:115256521:A:T	131:chr1:115256521:A:T	0.002181
130_c1w1-1	130	CDH1	MODERATE	c.1223C>T	p.Ala408Val	0	FALSE	chr16:68847301:C:T	131:chr16:68847301:C:T	0.001663
130_c1w1-1	130	C9orf53; CDKN2A	MODIFIER; MODERATE; LOW	n.*616A>G; c.*117T>C; c.194T>C; c.237T>C	; p.Leu65Pro; p.Ala79Ala	3	FALSE	chr9:21971164:A:G	131:chr9:21971164:A:G	0.002878
130_c1w1-1	130	PDGFRA	MODERATE	c.464C>T	p.Pro155Leu	1	FALSE	chr4:55129930:C:T	131:chr4:55129930:C:T	0.001914
130_c1w1-1	130	EGFR	MODERATE	c.719G>A	p.Cys240Tyr	1	FALSE	chr7:55220329:G:A	131:chr7:55220329:G:A	0.001931
130_c1w1-1	130	PIK3CA	MODERATE	c.1193G>A	p.Arg398His	1	FALSE	chr3:178927430:G:A	131:chr3:178927430:G:A	0.001965
130_c1w1-1	130	MIR4673; NOTCH1	MODIFIER; MODERATE	n.*59G>A; c.976G>A	; p.Gly326Ser	0	FALSE	chr9:139413166:C:T	131:chr9:139413166:C:T	0.002079
130_c1w1-1	130	TP53	MODERATE; MODIFIER	c.208G>A; c.91G>A; c.-279G>A; c.-360G>A	p.Ala70Thr; p.Ala31Thr;	1	FALSE	chr17:7579479:C:T	131:chr17:7579479:C:T	0.003676

130_c1w1-1	130	PIK3R1	MODERATE	c.637G>A	p.Val213Ile	2	FALSE	chr5:67576358:G:A	131:chr5:67576358:G:A	0.00213
130_c1w1-1	130	PDGFRA	MODERATE	c.1495G>A	p.Val499Met	2	FALSE	chr4:55139834:G:A	131:chr4:55139834:G:A	0.001833
130_c1w1-1	130	FBXW7	MODERATE	c.182G>A; c.296G>A; c.536G>A	p.Arg61His; p.Arg99His; p.Arg179His	0	FALSE	chr4:153271242:C:T	131:chr4:153271242:C:T	0.001946
73_c6-1	73	MET	MODERATE	c.3749T>C; c.3803T>C	p.Met1250Thr; p.Met1268Thr	11	FALSE	chr7:116423474:T:C	132:chr7:116423474:T:C	0.002597
73_c6-1	73	FGFR3	MODIFIER; MODERATE	c.931-425G>A; c.1145G>A; c.1151G>A	; p.Gly382Asp; p.Gly384Asp	1	FALSE	chr4:1806126:G:A	132:chr4:1806126:G:A	0.003106
73_c6-1	73	NTRK2	MODERATE	c.407G>A	p.Arg136His	0	FALSE	chr9:87322806:G:A	132:chr9:87322806:G:A	0.002985
73_c6-1	73	HOXD-AS2; HOXD8	MODIFIER; MODERATE	n.*692C>T; c.304G>A; c.853G>A; c.856G>A	; p.Glu102Lys; p.Glu285Lys; p.Glu286Lys	0	FALSE	chr2:176996323:G:A	132:chr2:176996323:G:A	0.003593
73_c6-1	73	KIT	MODERATE	c.365G>A	p.Arg122His	1	FALSE	chr4:55564477:G:A	132:chr4:55564477:G:A	0.002646
73_c6-1	73	TP53	HIGH; MODIFIER	c.156G>A; c.273G>A; c.-279G>A; c.-360G>A	p.Trp52*; p.Trp91*;	19	FALSE	chr17:7579414:C:T	132:chr17:7579414:C:T	0.003082
73_c6-1	73	RET	MODERATE	c.2116G>A	p.Val706Met	2	FALSE	chr10:43610164:G:A	132:chr10:43610164:G:A	0.002358
73_c6-1	73	FOXL2; FOXL2NB; LINC01391	MODERATE; MODIFIER	c.415G>A; c.-132C>T; n.-1G>A	p.Glu139Lys;	0	FALSE	chr3:138665150:C:T	132:chr3:138665150:C:T	0.005128
73_c6-1	73	TSC2	MODERATE	c.1654G>A	p.Ala552Thr	0	FALSE	chr16:2115574:G:A	132:chr16:2115574:G:A	0.002732
73_c6-1	73	NOTCH1	MODERATE	c.3374C>T	p.Ala1125Val	0	FALSE	chr9:139402543:G:A	132:chr9:139402543:G:A	0.00339

73_c6-1	73	TP53	MODERATE	c.421C>T; c.502C>T; c.781C>T; c.898C>T	p.Pro141Ser; p.Pro168Ser; p.Pro261Ser; p.Pro300Ser	3	FALSE	chr17:7577040:G:A	132:chr17:7577040:G:A	0.002457
73_c6-1	73	CDKN2B; CDKN2B-AS1	MODIFIER; MODERATE	c.*199C>T; c.313C>T; n.371+10930G>A	; p.Arg105Trp	0	FALSE	chr9:22006090:G:A	132:chr9:22006090:G:A	0.00363
73_c6-1	73	C9orf53; CDKN2A	MODIFIER; MODERATE	n.*616G>A; c.*318C>T; c.*39C>T; c.395C>T	; p.Ala132Val	1	FALSE	chr9:21970963:G:A	132:chr9:21970963:G:A	0.003401
73_c6-1	73	PDGFRA	MODERATE	c.2465G>A	p.Arg822His	3	FALSE	chr4:55152033:G:A	132:chr4:55152033:G:A	0.003793
73_c6-1	73	ATM	MODERATE	c.7357C>T	p.Arg2453Cys	0	FALSE	chr11:108200990:C:T	132:chr11:108200990:C:T	0.002345
73_c6-1	73	IGF1R	MODERATE	c.3905T>C; c.3908T>C	p.Val1302Ala; p.Val1303Ala	0	FALSE	chr15:99500475:T:C	132:chr15:99500475:T:C	0.002618
73_c6-1	73	CDH1	MODERATE	c.671G>A	p.Arg224His	0	FALSE	chr16:68842735:G:A	132:chr16:68842735:G:A	0.002782
73_c6-1	73	ATM	MODERATE	c.1009C>T	p.Arg337Cys	0	FALSE	chr11:108117798:C:T	132:chr11:108117798:C:T	0.00232
73_c6-1	73	EPHA3	HIGH	c.2757G>A	p.Trp919*	0	FALSE	chr3:89521680:G:A	132:chr3:89521680:G:A	0.002584
75_c8-1	75	PIK3R1	MODERATE	c.1226G>A; c.137G>A; c.326G>A; c.416G>A	p.Arg409Gln; p.Arg46Gln; p.Arg109Gln; p.Arg139Gln	1	FALSE	chr5:67589238:G:A	133:chr5:67589238:G:A	0.0033
75_c8-1	75	NTRK1	MODERATE	c.1025G>A; c.935G>A	p.Arg342Gln; p.Arg312Gln	3	FALSE	chr1:156843599:G:A	133:chr1:156843599:G:A	0.001778
75_c8-1	75	ALK	MODERATE	c.4280C>T	p.Ser1427Phe	2	FALSE	chr2:29416673:G:A	133:chr2:29416673:G:A	0.002379
75_c8-1	75	PIK3R1	MODERATE	c.637G>A	p.Val213Ile	2	FALSE	chr5:67576358:G:A	133:chr5:67576358:G:A	0.00199
75_c8-1	75	PIK3CA	MODERATE	c.1093G>A	p.Glu365Lys	6	FALSE	chr3:178922324:G:A	133:chr3:178922324:G:A	0.002183

75_c8-1	75	IGF1R	MODERATE	c.3905T>C; c.3908T>C	p.Val1302Ala; p.Val1303Ala	0	FALSE	chr15:99500475:T:C	133:chr15:99500475:T:C	0.003021
75_c8-1	75	FLT3	MODERATE	c.2672G>A	p.Gly891Asp	0	FALSE	chr13:28589375:C:T	133:chr13:28589375:C:T	0.002116
75_c8-1	75	PTEN	MODERATE	c.815A>C	p.His272Pro	2	FALSE	chr10:89720664:A:C	133:chr10:89720664:A:C	0.00277
75_c8-1	75	TP53	MODIFIER; MODERATE	c.-66G>A; c.16G>A; c.295G>A; c.412G>A	; p.Ala6Thr; p.Ala99Thr; p.Ala138Thr	17	FALSE	chr17:7578518:C:T	133:chr17:7578518:C:T	0.001786
75_c8-1	75	DDR2	MODERATE	c.1624G>A	p.Ala542Thr	1	FALSE	chr1:162741933:G:A	133:chr1:162741933:G:A	0.00188
75_c8-1	75	NTRK1	MODERATE	c.1129G>A; c.1219G>A; c.1237G>A	p.Glu377Lys; p.Glu407Lys; p.Glu413Lys	1	FALSE	chr1:156844404:G:A	133:chr1:156844404:G:A	0.001963
75_c8-1	75	TSC1	MODERATE	c.700T>G; c.853T>G	p.Phe234Val; p.Phe285Val	0	FALSE	chr9:135787729:A:C	133:chr9:135787729:A:C	0.001789
75_c8-1	75	FGFR4	MODIFIER; MODERATE	c.1098-65G>A; c.1251+10G>A; c.1067G>A	; p.Arg356His	1	FALSE	chr5:176520342:G:A	133:chr5:176520342:G:A	0.00363
75_c8-1	75	KDR	MODERATE	c.2003C>T	p.Thr668Met	1	FALSE	chr4:55968660:G:A	133:chr4:55968660:G:A	0.002491
75_c8-1	75	NF1	MODERATE	c.4463G>A; c.4526G>A	p.Arg1488His; p.Arg1509His	1	FALSE	chr17:29587482:G:A	133:chr17:29587482:G:A	0.001972
75_c8-1	75	FGFR3	MODIFIER; MODERATE	c.930+919G>A; c.931-748G>A; c.961G>A	; p.Val321Met	1	FALSE	chr4:1804671:G:A	133:chr4:1804671:G:A	0.002994
75_c8-1	75	FGFR3	MODERATE	c.1162G>A; c.1498G>A; c.1504G>A	p.Ala388Thr; p.Ala500Thr; p.Ala502Thr	1	FALSE	chr4:1807167:G:A	133:chr4:1807167:G:A	0.002181
75_c8-1	75	FGFR4	MODERATE	c.1274G>A; c.1358G>A; c.1478G>A	p.Arg425Gln; p.Arg453Gln; p.Arg493Gln	2	FALSE	chr5:176520735:G:A	133:chr5:176520735:G:A	0.001791

75_c8-1	75	ERBB2	MODERATE; MODIFIER	c.560G>A; c.605G>A; c.650G>A; n.974G>A	p.Arg187His; p.Arg202His; p.Arg217His;	1	FALSE	chr17:37866345:G:A	133:chr17:37866345:G:A	0.00283
75_c8-1	75	HOXD-AS2; HOXD8	MODIFIER; MODERATE	n.*692C>T; c.304G>A; c.853G>A; c.856G>A	; p.Glu102Lys; p.Glu285Lys; p.Glu286Lys	0	FALSE	chr2:176996323:G:A	133:chr2:176996323:G:A	0.001833
75_c8-1	75	KRAS	MODERATE	c.101C>T	p.Pro34Leu	2	FALSE	chr12:25398218:G:A	133:chr12:25398218:G:A	0.002217
75_c8-1	75	RET	MODERATE	c.2116G>A	p.Val706Met	2	FALSE	chr10:43610164:G:A	133:chr10:43610164:G:A	0.001575
75_c8-1	75	EGFR	MODERATE	c.866C>T	p.Ala289Val	34	FALSE	chr7:55221822:C:T	133:chr7:55221822:C:T	0.00194
75_c8-1	75	CDH1	HIGH	c.1596G>A	p.Trp532*	0	FALSE	chr16:68853213:G:A	133:chr16:68853213:G:A	0.002079
75_c8-1	75	FBXW7	MODERATE	c.1196G>A; c.1310G>A; c.1550G>A	p.Gly399Glu; p.Gly437Glu; p.Gly517Glu	0	FALSE	chr4:153247252:C:T	133:chr4:153247252:C:T	0.001795
75_c8-1	75	VHL	MODIFIER; MODERATE	c.341-3184G>A; c.430G>A	; p.Gly144Arg	0	FALSE	chr3:10188287:G:A	133:chr3:10188287:G:A	0.002413
75_c8-1	75	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2305G>A; n.1257C>T	p.Val769Met;	3	FALSE	chr7:55249007:G:A	133:chr7:55249007:G:A	0.001685
75_c8-1	75	NTRK1	MODERATE	c.804C>G; c.894C>G	p.His268Gln; p.His298Gln	1	FALSE	chr1:156843468:C:G	133:chr1:156843468:C:G	0.002296
75_c8-1	75	KIT	MODERATE	c.154G>A	p.Asp52Asn	7	FALSE	chr4:55561764:G:A	133:chr4:55561764:G:A	0.002742
75_c8-1	75	EPHA3	MODERATE	c.1280C>T	p.Ala427Val	0	FALSE	chr3:89391214:C:T	133:chr3:89391214:C:T	0.002077
75_c8-1	75	INSRR; NTRK1	MODIFIER; MODERATE	c.3397+13C>T; c.28G>A	; p.Ala10Thr	1	FALSE	chr1:156811891:G:A	133:chr1:156811891:G:A	0.0016
75_c8-1	75	NTRK3	MODIFIER; MODERATE	c.1205-1502C>T; c.1211C>T	; p.Thr404Met	0	FALSE	chr15:88671959:G:A	133:chr15:88671959:G:A	0.002081

75_c8-1	75	NF1	MODERATE	c.5420G>A; c.5483G>A	p.Arg1807Gln; p.Arg1828Gln	2	FALSE	chr17:29654731:G:A	133:chr17:29654731:G:A	0.001815
75_c8-1	75	NTHL1; TSC2	MODIFIER; MODERATE	c.-20C>T; c.170G>A	; p.Arg57His	0	FALSE	chr16:2100432:G:A	133:chr16:2100432:G:A	0.002099
75_c8-1	75	IDH2; ZNF710	MODERATE; MODIFIER	c.1108G>A; c.718G>A; c.952G>A; c.*2147C>T	p.Ala370Thr; p.Ala240Thr; p.Ala318Thr;	1	FALSE	chr15:90628303:C:T	133:chr15:90628303:C:T	0.002339
75_c8-1	75	TSC2	MODERATE	c.3032G>A; c.3164G>A	p.Gly1011Asp; p.Gly1055Asp	0	FALSE	chr16:2129309:G:A	133:chr16:2129309:G:A	0.002083
75_c8-1	75	NOTCH1	MODERATE	c.4901C>T	p.Ala1634Val	0	FALSE	chr9:139399242:G:A	133:chr9:139399242:G:A	0.002535
75_c8-1	75	NOTCH1	LOW	c.4587C>T	p.Asn1529Asn	0	FALSE	chr9:139399556:G:A	133:chr9:139399556:G:A	0.004016
75_c8-1	75	NOTCH1	MODERATE	c.2644G>A	p.Ala882Thr	0	FALSE	chr9:139405201:C:T	133:chr9:139405201:C:T	0.00271
75_c8-1	75	FBXW7	HIGH	c.1177C>T; c.823C>T; c.937C>T	p.Arg393*; p.Arg275*; p.Arg313*	0	FALSE	chr4:153250883:G:A	133:chr4:153250883:G:A	0.00216
75_c8-1	75	ALK	MODERATE	c.871C>T	p.Arg291Cys	3	FALSE	chr2:29917797:G:A	133:chr2:29917797:G:A	0.001604
75_c8-1	75	NTRK2	MODERATE	c.2023C>T; c.2071C>T	p.Arg675Cys; p.Arg691Cys	0	FALSE	chr9:87570331:C:T	133:chr9:87570331:C:T	0.002002
78_c11-1	78	IGF1R	MODERATE	c.3121C>T; c.3124C>T	p.Arg1041Cys; p.Arg1042Cys	0	FALSE	chr15:99478220:C:T	134:chr15:99478220:C:T	0.003231
78_c11-1	78	ERBB2; MIEN1; MIR4728	MODERATE; MODIFIER	c.2236G>A; c.2281G>A; c.2326G>A; n.2650G>A; c.*388C>T; n.-1G>A	p.Gly746Ser; p.Gly761Ser; p.Gly776Ser;	5	FALSE	chr17:37880997:G:A	134:chr17:37880997:G:A	0.003604
78_c11-1	78	BRAF	MODERATE	c.1799T>A	p.Val600Glu	23024	FALSE	chr7:140453136:A:T	134:chr7:140453136:A:T	0.014925
78_c11-1	78	PDGFRA	MODERATE	c.2942G>A	p.Arg981His	2	FALSE	chr4:55156541:G:A	134:chr4:55156541:G:A	0.00409

78_c11-1	78	PDGFRA	MODERATE	c.2692G>A	p.Gly898Ser	1	FALSE	chr4:55154983:G:A	134:chr4:55154983:G:A	0.003333
78_c11-1	78	FGFR3; LETM1	MODERATE; MODIFIER	c.1730C>T; c.2066C>T; c.2072C>T; c.*2517G>A	p.Thr577Met; p.Thr689Met; p.Thr691Met;	2	FALSE	chr4:1808308:C:T	134:chr4:1808308:C:T	0.004535
78_c11-1	78	ATM	MODERATE	c.743G>A	p.Arg248Gln	0	FALSE	chr11:108115595:G:A	134:chr11:108115595:G:A	0.003053
78_c11-1	78	CTNNB1	MODERATE	c.1702G>A	p.Glu568Lys	0	FALSE	chr3:41277233:G:A	134:chr3:41277233:G:A	0.004608
78_c11-1	78	MIR1225; PKD1; TSC2	MODIFIER; MODERATE	n.*90C>T; c.*13118C>T; c.*13121C>T; c.4906G>A; c.5038G>A; c.5107G>A	; p.Val1636Met; p.Val1680Met; p.Val1703Met	0	FALSE	chr16:2138087:G:A	134:chr16:2138087:G:A	0.004158
78_c11-1	78	ALK	HIGH	c.1651C>T	p.Arg551*	2	FALSE	chr2:29519920:G:A	134:chr2:29519920:G:A	0.004283
78_c11-1	78	TP53	MODIFIER; MODERATE	c.*168A>G; c.*80A>G; c.1061A>G; c.584A>G; c.665A>G; c.944A>G	; p.Gln354Arg; p.Gln195Arg; p.Gln222Arg; p.Gln315Arg	2	FALSE	chr17:7573966:T:C	134:chr17:7573966:T:C	0.003273
78_c11-1	78	CDH1	MODERATE	c.1901C>T	p.Ala634Val	0	FALSE	chr16:68856093:C:T	134:chr16:68856093:C:T	0.003252
78_c11-1	78	C9orf53; CDKN2A	MODIFIER; MODERATE; LOW	n.*616C>T; c.*96G>A; c.173G>A; c.216G>A	; p.Arg58Gln; p.Pro72Pro	6	FALSE	chr9:21971185:C:T	134:chr9:21971185:C:T	0.005464
78_c11-1	78	NF1	MODERATE	c.820C>T	p.Leu274Phe	1	FALSE	chr17:29509615:C:T	134:chr17:29509615:C:T	0.003356
78_c11-1	78	ATM	MODERATE	c.6200C>A	p.Ala2067Asp	0	FALSE	chr11:108188101:C:A	134:chr11:108188101:C:A	0.004264

78_c11-1	78	CTNNB1	HIGH	c.283C>T	p.Arg95*	0	FALSE	chr3:41266486:C:T	134:chr3:41266486:C:T	0.003509
78_c11-1	78	TP53	MODERATE	c.340C>T; c.421C>T; c.700C>T; c.817C>T	p.Arg114Cys; p.Arg141Cys; p.Arg234Cys; p.Arg273Cys	601	FALSE	chr17:7577121:G:A	134:chr17:7577121:G:A	0.022403
78_c11-1	78	ALK	MODERATE	c.4306C>T	p.Arg1436Cys	3	FALSE	chr2:29416647:G:A	134:chr2:29416647:G:A	0.003096
78_c11-1	78	RET	MODERATE	c.2161C>T	p.Arg721Trp	1	FALSE	chr10:43612056:C:T	134:chr10:43612056:C:T	0.003215
94_c5-1	94	CDKN2A	MODIFIER; MODERATE	c.194-3567C>T; c.53C>T	; p.Thr18Met	1	FALSE	chr9:21974774:G:A	135:chr9:21974774:G:A	0.001775
94_c5-1	94	NOTCH1	MODERATE	c.3635G>A	p.Gly1212Asp	0	FALSE	chr9:139401765:C:T	135:chr9:139401765:C:T	0.001656
94_c5-1	94	MET	MODERATE	c.1336A>G	p.Ile446Val	1	FALSE	chr7:116371857:A:G	135:chr7:116371857:A:G	0.002672
94_c5-1	94	BRAF	HIGH	c.1525C>T	p.Arg509*	1	FALSE	chr7:140476881:G:A	135:chr7:140476881:G:A	0.001723
94_c5-1	94	GNA11	MODERATE	c.1030G>A	p.Val344Met	1	FALSE	chr19:3121127:G:A	135:chr19:3121127:G:A	0.001472
94_c5-1	94	HGF	MODERATE	c.767G>A; c.782G>A	p.Arg256His; p.Arg261His	0	FALSE	chr7:81372752:C:T	135:chr7:81372752:C:T	0.00161
94_c5-1	94	TP53	MODIFIER; MODERATE	c.-66G>A; c.16G>A; c.295G>A; c.412G>A	; p.Ala6Thr; p.Ala99Thr; p.Ala138Thr	17	FALSE	chr17:7578518:C:T	135:chr17:7578518:C:T	0.002135
94_c5-1	94	KIT	MODERATE	c.365G>A	p.Arg122His	1	FALSE	chr4:55564477:G:A	135:chr4:55564477:G:A	0.001603
94_c5-1	94	ALK	MODERATE	c.2002G>A	p.Glu668Lys	1	FALSE	chr2:29498004:C:T	135:chr2:29498004:C:T	0.001727
94_c5-1	94	DEAR; FBXW7	MODIFIER; HIGH	n.105G>A; c.478C>T; c.592C>T; c.832C>T	; p.Arg160*; p.Arg198*; p.Arg278*	0	FALSE	chr4:153258983:G:A	135:chr4:153258983:G:A	0.00166
94_c5-1	94	PTEN	MODERATE	c.443C>A	p.Ala148Glu	1	FALSE	chr10:89692959:C:A	135:chr10:89692959:C:A	0.00173

94_c5-1	94	FGFR4	MODERATE	c.1745G>A; c.1829G>A; c.1949G>A	p.Arg582His; p.Arg610His; p.Arg650His	1	FALSE	chr5:176523292:G:A	135:chr5:176523292:G:A	0.002809
94_c5-1	94	FGFR3	MODERATE	c.1177G>A; c.1513G>A; c.1519G>A	p.Val393Ile; p.Val505Ile; p.Val507Ile	1	FALSE	chr4:1807182:G:A	135:chr4:1807182:G:A	0.00203
94_c5-1	94	FGFR4	MODIFIER; MODERATE	c.1098-65G>A; c.1251+10G>A; c.1067G>A	; p.Arg356His	1	FALSE	chr5:176520342:G:A	135:chr5:176520342:G:A	0.001306
94_c5-1	94	DDR2	MODERATE	c.404G>A	p.Arg135His	1	FALSE	chr1:162724632:G:A	135:chr1:162724632:G:A	0.00149
94_c5-1	94	FGFR3	MODIFIER; MODERATE	c.931-398C>T; c.1172C>T; c.1178C>T	; p.Ala391Val; p.Ala393Val	34	FALSE	chr4:1806153:C:T	135:chr4:1806153:C:T	0.001398
94_c5-1	94	NF1	HIGH	c.3826C>T	p.Arg1276*	4	FALSE	chr17:29562746:C:T	135:chr17:29562746:C:T	0.002433
94_c5-1	94	FGFR1; LETM2	MODERATE; MODIFIER	c.1927C>T; c.1933C>T; c.2170C>T; c.2194C>T; c.2200C>T; c.2293C>T; c.*1406G>A; c.*1423G>A; c.*1553G>A; c.*1567G>A; c.*1638G>A	p.Arg643Trp; p.Arg645Trp; p.Arg724Trp; p.Arg732Trp; p.Arg734Trp; p.Arg765Trp;	1	FALSE	chr8:38271528:G:A	135:chr8:38271528:G:A	0.004215
94_c5-1	94	MET	HIGH	c.1639C>T	p.Arg547*	2	FALSE	chr7:116381017:C:T	135:chr7:116381017:C:T	0.001154
94_c5-1	94	TSC2	MODERATE	c.1654G>A	p.Ala552Thr	0	FALSE	chr16:2115574:G:A	135:chr16:2115574:G:A	0.003925
94_c5-1	94	FGFR3	MODERATE	c.905G>A	p.Gly302Asp	1	FALSE	chr4:1803727:G:A	135:chr4:1803727:G:A	0.001242

94_c5-1	94	CDH1	MODERATE	c.1198G>A	p.Asp400Asn	0	FALSE	chr16:68847276:G:A	135:chr16:68847276:G:A	0.002169
94_c5-1	94	NTRK1	MODERATE	c.1975C>T; c.2065C>T; c.2083C>T	p.Pro659Ser; p.Pro689Ser; p.Pro695Ser	2	FALSE	chr1:156849827:C:T	135:chr1:156849827:C:T	0.001854
94_c5-1	94	FLT3	MODERATE	c.2039C>T	p.Ala680Val	0	FALSE	chr13:28602329:G:A	135:chr13:28602329:G:A	0.001479
94_c5-1	94	MET	HIGH	c.1619G>A	p.Trp540*	1	FALSE	chr7:116380997:G:A	135:chr7:116380997:G:A	0.001234
94_c5-1	94	NTRK3	MODERATE	c.581G>A	p.Gly194Asp	0	FALSE	chr15:88680676:C:T	135:chr15:88680676:C:T	0.001459
94_c5-1	94	CDH1	MODERATE	c.184G>A	p.Gly62Ser	0	FALSE	chr16:68835593:G:A	135:chr16:68835593:G:A	0.001408
94_c5-1	94	FBXW7	MODERATE	c.1160G>A; c.1274G>A; c.1514G>A	p.Arg387His; p.Arg425His; p.Arg505His	0	FALSE	chr4:153247288:C:T	135:chr4:153247288:C:T	0.001982
94_c5-1	94	PIK3CA	MODERATE	c.35G>A	p.Gly12Asp	5	FALSE	chr3:178916648:G:A	135:chr3:178916648:G:A	0.00133
94_c5-1	94	TP53	MODERATE; MODIFIER	c.254G>A; c.371G>A; c.-279G>A; c.-360G>A	p.Cys85Tyr; p.Cys124Tyr;	3	FALSE	chr17:7579316:C:T	135:chr17:7579316:C:T	0.001688
94_c5-1	94	ERBB2	MODERATE; MODIFIER	c.1042C>T; c.1087C>T; c.1132C>T; n.1456C>T	p.Pro348Ser; p.Pro363Ser; p.Pro378Ser;	1	FALSE	chr17:37868685:C:T	135:chr17:37868685:C:T	0.00105
94_c5-1	94	IGF1R	MODERATE	c.3121C>T; c.3124C>T	p.Arg1041Cys; p.Arg1042Cys	0	FALSE	chr15:99478220:C:T	135:chr15:99478220:C:T	0.001417
94_c5-1	94	TSC2	MODERATE	c.866C>T	p.Ala289Val	0	FALSE	chr16:2108765:C:T	135:chr16:2108765:C:T	0.001658
94_c5-1	94	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2495G>A; n.-1C>T	p.Arg832His;	2	FALSE	chr7:55259437:G:A	135:chr7:55259437:G:A	0.001761
94_c5-1	94	IGF1R	MODERATE	c.280G>A	p.Glu94Lys	0	FALSE	chr15:99250976:G:A	135:chr15:99250976:G:A	0.001288
94_c5-1	94	NOTCH1	MODERATE	c.4828G>A	p.Ala1610Thr	0	FALSE	chr9:139399315:C:T	135:chr9:139399315:C:T	0.001552

94_c5-1	94	C9orf53; CDKN2A	MODIFIER; MODERATE	n.*616C>T; c.*288G>A; c.*9G>A; c.365G>A	; p.Gly122Asp	4	FALSE	chr9:21970993:C:T	135:chr9:21970993:C:T	0.001591
94_c5-1	94	FBXW7	HIGH	c.357G>A; c.471G>A; c.711G>A	p.Trp119*; p.Trp157*; p.Trp237*	0	FALSE	chr4:153268097:C:T	135:chr4:153268097:C:T	0.003058
94_c5-1	94	NOTCH1	MODERATE	c.5347C>T	p.Arg1783Trp	0	FALSE	chr9:139396761:G:A	135:chr9:139396761:G:A	0.002634
94_c5-1	94	EGFR	MODERATE	c.610G>A	p.Glu204Lys	1	FALSE	chr7:55219037:G:A	135:chr7:55219037:G:A	0.001526
94_c5-1	94	TP53	MODERATE	c.145C>T; c.424C>T; c.541C>T; c.64C>T	p.Arg49Cys; p.Arg142Cys; p.Arg181Cys; p.Arg22Cys	21	FALSE	chr17:7578389:G:A	135:chr17:7578389:G:A	0.001327
94_c5-1	94	IGF1R	MODERATE	c.3905T>C; c.3908T>C	p.Val1302Ala; p.Val1303Ala	0	FALSE	chr15:99500475:T:C	135:chr15:99500475:T:C	0.001397
94_c5-1	94	FGFR1	MODERATE	c.487C>T; c.493C>T; c.736C>T; c.754C>T; c.760C>T; c.853C>T	p.Arg163Trp; p.Arg165Trp; p.Arg246Trp; p.Arg252Trp; p.Arg254Trp; p.Arg285Trp	1	FALSE	chr8:38282203:G:A	135:chr8:38282203:G:A	0.001464
94_c5-1	94	TSC1	MODERATE	c.365C>T; c.518C>T	p.Ala122Val; p.Ala173Val	0	FALSE	chr9:135797351:G:A	135:chr9:135797351:G:A	0.001794
94_c5-1	94	NTRK2	MODERATE	c.407G>A	p.Arg136His	0	FALSE	chr9:87322806:G:A	135:chr9:87322806:G:A	0.0018
94_c5-1	94	AKT3	HIGH	c.196C>T	p.Arg66*	0	FALSE	chr1:243828162:G:A	135:chr1:243828162:G:A	0.001595

94_c5-1	94	GAPDH; IFFO1; NCAPD2	MODERATE; MODIFIER	c.148G>A; c.274G>A; c.*1743C>T; c.*1746C>T; c.*1770C>T; n.*2798C>T; c.*4252G>A	p.Ala50Thr; p.Ala92Thr;	0	FALSE	chr12:6646123:G:A	135:chr12:6646123:G:A	0.002274
94_c5-1	94	NTRK2	MODERATE	c.2024G>A; c.2072G>A	p.Arg675His; p.Arg691His	0	FALSE	chr9:87570332:G:A	135:chr9:87570332:G:A	0.001453
94_c5-1	94	MIR4673; NOTCH1	MODIFIER; MODERATE	n.-1G>A; c.203G>A	; p.Cys68Tyr	0	FALSE	chr9:139418369:C:T	135:chr9:139418369:C:T	0.001883
94_c5-1	94	NOTCH1	MODERATE	c.2300C>T	p.Thr767Ile	0	FALSE	chr9:139407897:G:A	135:chr9:139407897:G:A	0.001688
94_c5-1	94	TP53	MODIFIER; HIGH	c.-55C>A; c.27C>A; c.306C>A; c.423C>A	; p.Cys9*; p.Cys102*; p.Cys141*	13	FALSE	chr17:7578507:G:T	135:chr17:7578507:G:T	0.104372
94_c5-1	94	AKT1	MODERATE	c.286C>T	p.Arg96Trp	1	FALSE	chr14:105242997:G:A	135:chr14:105242997:G:A	0.002591
94_c5-1	94	PTEN	HIGH	c.822G>A	p.Trp274*	3	FALSE	chr10:89720671:G:A	135:chr10:89720671:G:A	0.004344
94_c5-1	94	C9orf53; CDKN2A	MODIFIER; MODERATE; LOW	n.*616G>A; c.*180C>T; c.257C>T; c.300C>T	; p.Ala86Val; p.Cys100Cys	1	FALSE	chr9:21971101:G:A	135:chr9:21971101:G:A	0.001634
94_c5-1	94	ERBB2	MODIFIER; HIGH	n.1375C>T; c.1006C>T; c.1051C>T; c.961C>T	; p.Arg336*; p.Arg351*; p.Arg321*	1	FALSE	chr17:37868604:C:T	135:chr17:37868604:C:T	0.001433
94_c5-1	94	C9orf53; CDKN2A	MODIFIER; MODERATE	n.*616G>A; c.*242C>T; c.319C>T; c.362C>T	; p.Arg107Cys; p.Ala121Val	1	FALSE	chr9:21971039:G:A	135:chr9:21971039:G:A	0.001575
94_c5-1	94	DDR2	MODERATE	c.1418G>A	p.Arg473His	2	FALSE	chr1:162740216:G:A	135:chr1:162740216:G:A	0.002646

94_c5-1	94	ERBB2	MODERATE; MODIFIER	c.1180G>A; c.1225G>A; c.1270G>A; n.1594G>A	p.Val394Ile; p.Val409Ile; p.Val424Ile;	1	FALSE	chr17:37871746:G:A	135:chr17:37871746:G:A	0.000983
94_c5-1	94	NTRK2	MODERATE	c.1960C>A; c.2008C>A	p.Leu654Met; p.Leu670Met	0	FALSE	chr9:87570268:C:A	135:chr9:87570268:C:A	0.001609
94_c5-1	94	ERBB2; MIEN1; MIR4728	MODIFIER; MODERATE	c.3160-319G>A; c.3145G>A; c.3190G>A; c.3235G>A; n.3559G>A; c.*388C>T; n.*67G>A	; p.Glu1049Lys; p.Glu1064Lys; p.Glu1079Lys	1	FALSE	chr17:37883623:G:A	135:chr17:37883623:G:A	0.001361
94_c5-1	94	C9orf53; CDKN2A	MODIFIER; MODERATE	n.*616C>T; c.*350G>A; c.*71G>A; c.427G>A	; p.Ala143Thr	1	FALSE	chr9:21970931:C:T	135:chr9:21970931:C:T	0.001581
94_c5-1	94	FGFR4	MODIFIER; MODERATE	c.1058-174G>A; c.1078G>A	; p.Ala360Thr	1	FALSE	chr5:176520159:G:A	135:chr5:176520159:G:A	0.001505
94_c5-1	94	NTRK1	MODERATE	c.266G>A; c.356G>A	p.Arg89His; p.Arg119His	1	FALSE	chr1:156834588:G:A	135:chr1:156834588:G:A	0.0025
94_c5-1	94	PIK3R1	MODERATE	c.1694G>A; c.605G>A; c.794G>A; c.884G>A	p.Ser565Asn; p.Ser202Asn; p.Ser265Asn; p.Ser295Asn	1	FALSE	chr5:67591101:G:A	135:chr5:67591101:G:A	0.00161
94_c5-1	94	ERBB2; MIEN1; MIR4728	MODERATE; MODIFIER	c.2720A>G; c.2765A>G; c.2810A>G; n.3134A>G; c.*388T>C; n.-1A>G	p.Lys907Arg; p.Lys922Arg; p.Lys937Arg;	1	FALSE	chr17:37882044:A:G	135:chr17:37882044:A:G	0.002095

94_c5-1	94	NTRK1	MODERATE	c.415G>A; c.505G>A	p.Gly139Arg; p.Gly169Arg	1	FALSE	chr1:156837972:G:A	135:chr1:156837972:G:A	0.001405
94_c5-1	94	C9orf53; CDKN2A	MODIFIER; MODERATE	n.*616C>T; c.*167G>A; c.244G>A; c.287G>A	; p.Val82Met; p.Arg96His	3	FALSE	chr9:21971114:C:T	135:chr9:21971114:C:T	0.001652
95_c3-1	95	APC	HIGH	c.1606C>T; c.1660C>T	p.Arg536*; p.Arg554*	0	FALSE	chr5:112164586:C:T	136:chr5:112164586:C:T	0.002162
95_c3-1	95	TP53	MODIFIER; MODERATE	c.-26C>G; c.335C>G; c.452C>G; c.56C>G	; p.Pro112Arg; p.Pro151Arg; p.Pro19Arg	30	FALSE	chr17:7578478:G:C	136:chr17:7578478:G:C	0.002356
95_c3-1	95	MAP2K1	MODERATE	c.140G>A	p.Arg47Gln	4	FALSE	chr15:66727424:G:A	136:chr15:66727424:G:A	0.00211
95_c3-1	95	EGFR	MODERATE	c.442G>A	p.Val148Met	1	FALSE	chr7:55214316:G:A	136:chr7:55214316:G:A	0.002466
95_c3-1	95	PIK3CA	MODERATE	c.1483C>T	p.His495Tyr	1	FALSE	chr3:178928297:C:T	136:chr3:178928297:C:T	0.001921
95_c3-1	95	ERBB2	MODERATE; MODIFIER	c.1594C>T; c.1639C>T; c.1684C>T; n.2008C>T	p.Pro532Ser; p.Pro547Ser; p.Pro562Ser;	1	FALSE	chr17:37872805:C:T	136:chr17:37872805:C:T	0.001901
95_c3-1	95	AKT1	MODERATE	c.1108C>T	p.Arg370Cys	1	FALSE	chr14:105239279:G:A	136:chr14:105239279:G:A	0.002398
95_c3-1	95	MET	MODERATE	c.142G>A	p.Ala48Thr	1	FALSE	chr7:116339280:G:A	136:chr7:116339280:G:A	0.001584
95_c3-1	95	STK11	MODERATE	c.488G>A	p.Gly163Asp	1	FALSE	chr19:1220395:G:A	136:chr19:1220395:G:A	0.004283
95_c3-1	95	CTNNB1	MODERATE	c.1346G>A	p.Arg449His	0	FALSE	chr3:41275180:G:A	136:chr3:41275180:G:A	0.001554
95_c3-1	95	FGFR1	MODIFIER; MODERATE	c.-34C>T; c.158C>T; c.59C>T	; p.Thr53Ile; p.Thr20Ile	1	FALSE	chr8:38314906:G:A	136:chr8:38314906:G:A	0.001967
95_c3-1	95	EPHA3	MODERATE	c.1556C>T	p.Thr519Met	0	FALSE	chr3:89448592:C:T	136:chr3:89448592:C:T	0.002375

95_c3-1	95	AKT3	MODERATE	c.899C>T	p.Ala300Val	0	FALSE	chr1:243727071:G:A	136:chr1:243727071:G:A	0.001923
95_c3-1	95	TP53	HIGH	c.439C>T; c.520C>T; c.799C>T; c.916C>T	p.Arg147*; p.Arg174*; p.Arg267*; p.Arg306*	167	FALSE	chr17:7577022:G:A	136:chr17:7577022:G:A	0.002112
95_c3-1	95	NTRK2	MODERATE	c.2023C>T; c.2071C>T	p.Arg675Cys; p.Arg691Cys	0	FALSE	chr9:87570331:C:T	136:chr9:87570331:C:T	0.002304
95_c3-1	95	NTRK1	MODERATE	c.1837C>T; c.1927C>T; c.1945C>T	p.Arg613Trp; p.Arg643Trp; p.Arg649Trp	3	FALSE	chr1:156849053:C:T	136:chr1:156849053:C:T	0.002528
95_c3-1	95	PDGFRA	MODERATE	c.577G>A	p.Val193Ile	2	FALSE	chr4:55130043:G:A	136:chr4:55130043:G:A	0.001661
95_c3-1	95	AKT1	MODERATE	c.932G>A	p.Gly311Asp	1	FALSE	chr14:105239613:C:T	136:chr14:105239613:C:T	0.002915
95_c3-1	95	DDR2	MODERATE	c.1418G>A	p.Arg473His	2	FALSE	chr1:162740216:G:A	136:chr1:162740216:G:A	0.001761
95_c3-1	95	TP53	MODERATE; MODIFIER	c.134C>T; c.251C>T; c.-279C>T; c.-360C>T	p.Ala45Val; p.Ala84Val;	4	FALSE	chr17:7579436:G:A	136:chr17:7579436:G:A	0.002829
95_c3-1	95	EGFR	MODERATE	c.940G>A	p.Asp314Asn	1	FALSE	chr7:55223573:G:A	136:chr7:55223573:G:A	0.001946
95_c3-1	95	NF1	MODERATE	c.4321C>T; c.4384C>T	p.Arg1441Trp; p.Arg1462Trp	1	FALSE	chr17:29586101:C:T	136:chr17:29586101:C:T	0.001838
95_c3-1	95	ATM	HIGH	c.6100C>T	p.Arg2034*	0	FALSE	chr11:108186742:C:T	136:chr11:108186742:C:T	0.001637
95_c3-1	95	FGFR2	MODIFIER; MODERATE	c.939+4813C>T; c.1238C>T; c.1241C>T; c.893C>T; c.902C>T; c.971C>T; c.974C>T; n.1688C>T	; p.Pro413Leu; p.Pro414Leu; p.Pro298Leu; p.Pro301Leu; p.Pro324Leu; p.Pro325Leu	1	FALSE	chr10:123274680:G:A	136:chr10:123274680:G:A	0.003026

95_c3-1	95	TP53	MODERATE	c.421C>T; c.502C>T; c.781C>T; c.898C>T	p.Pro141Ser; p.Pro168Ser; p.Pro261Ser; p.Pro300Ser	3	FALSE	chr17:7577040:G:A	136:chr17:7577040:G:A	0.00209
95_c3-1	95	MET	HIGH	c.1639C>T	p.Arg547*	2	FALSE	chr7:116381017:C:T	136:chr7:116381017:C:T	0.001566
95_c3-1	95	TP53	HIGH	c.178C>T; c.457C>T; c.574C>T; c.97C>T	p.Gln60*; p.Gln153*; p.Gln192*; p.Gln33*	88	FALSE	chr17:7578275:G:A	136:chr17:7578275:G:A	0.001974
95_c3-1	95	PDGFRA	MODERATE	c.2942G>A	p.Arg981His	2	FALSE	chr4:55156541:G:A	136:chr4:55156541:G:A	0.002985
95_c3-1	95	KIT	MODERATE	c.1493G>A	p.Gly498Asp	1	FALSE	chr4:55592169:G:A	136:chr4:55592169:G:A	0.002212
95_c3-1	95	FBXW7	MODERATE	c.1088C>T; c.1202C>T; c.1442C>T	p.Ala363Val; p.Ala401Val; p.Ala481Val	0	FALSE	chr4:153247360:G:A	136:chr4:153247360:G:A	0.003247
95_c3-1	95	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2575G>A; n.-1C>T	p.Ala859Thr;	4	FALSE	chr7:55259517:G:A	136:chr7:55259517:G:A	0.0022
95_c3-1	95	BRAF	HIGH	c.532C>T	p.Arg178*	1	FALSE	chr7:140508768:G:A	136:chr7:140508768:G:A	0.001818
95_c3-1	95	ATM	MODERATE	c.2944C>T	p.Arg982Cys	0	FALSE	chr11:108142000:C:T	136:chr11:108142000:C:T	0.001431
95_c3-1	95	NTRK1	MODERATE	c.1669C>T; c.1759C>T; c.1777C>T	p.Arg557Trp; p.Arg587Trp; p.Arg593Trp	1	FALSE	chr1:156846336:C:T	136:chr1:156846336:C:T	0.002488
95_c3-1	95	TP53	MODERATE; MODIFIER	c.170C>T; c.287C>T; c.-279C>T; c.-360C>T	p.Ser57Phe; p.Ser96Phe;	3	FALSE	chr17:7579400:G:A	136:chr17:7579400:G:A	0.002937
95_c3-1	95	KRAS	MODERATE	c.35G>C	p.Gly12Ala	11213	FALSE	chr12:25398284:C:G	136:chr12:25398284:C:G	0.014359

94_c4-1	94	FGFR2	MODIFIER; MODERATE	c.110-14066G>A; c.110-946G>A; n.757-14066G>A; c.289G>A	; p.Ala97Thr	1	FALSE	chr10:123325039:C:T	137:chr10:123325039:C:T	0.002198
94_c4-1	94	NTRK1	MODERATE	c.1940T>G; c.2030T>G; c.2048T>G	p.Val647Gly; p.Val677Gly; p.Val683Gly	2	FALSE	chr1:156849792:T:G	137:chr1:156849792:T:G	0.019139
94_c4-1	94	TP53	MODIFIER; HIGH	c.-55C>A; c.27C>A; c.306C>A; c.423C>A	; p.Cys9*; p.Cys102*; p.Cys141*	13	FALSE	chr17:7578507:G:T	137:chr17:7578507:G:T	0.202358
94_c4-1	94	EGFR	MODERATE	c.1774G>A	p.Val592Ile	1	FALSE	chr7:55233024:G:A	137:chr7:55233024:G:A	0.002469
94_c4-1	94	MET	MODERATE	c.487T>C	p.Ser163Pro	1	FALSE	chr7:116339625:T:C	137:chr7:116339625:T:C	0.00273
94_c4-1	94	CDKN2A	MODIFIER; MODERATE	c.194-3568A>C; c.52A>C	; p.Thr18Pro	1	FALSE	chr9:21974775:T:G	137:chr9:21974775:T:G	0.005739
94_c4-1	94	TSC2	MODERATE	c.3032G>A; c.3164G>A	p.Gly1011Asp; p.Gly1055Asp	0	FALSE	chr16:2129309:G:A	137:chr16:2129309:G:A	0.003185
94_c4-1	94	CDH1	MODERATE	c.1901C>T	p.Ala634Val	0	FALSE	chr16:68856093:C:T	137:chr16:68856093:C:T	0.001835
94_c4-1	94	C9orf53; CDKN2A	MODIFIER; MODERATE	n.*616C>T; c.*167G>A; c.244G>A; c.287G>A	; p.Val82Met; p.Arg96His	3	FALSE	chr9:21971114:C:T	137:chr9:21971114:C:T	0.00319
94_c4-1	94	PIK3CA	MODERATE	c.277C>T	p.Arg93Trp	24	FALSE	chr3:178916890:C:T	137:chr3:178916890:C:T	0.002755
94_c4-1	94	ERBB2; MIEN1; MIR4728	MODERATE; MODIFIER	c.2720A>G; c.2765A>G; c.2810A>G; n.3134A>G; c.*388T>C; n.-1A>G	p.Lys907Arg; p.Lys922Arg; p.Lys937Arg;	1	FALSE	chr17:37882044:A:G	137:chr17:37882044:A:G	0.000983

94_c4-1	94	TP53	MODERATE	c.287T>C; c.368T>C; c.647T>C; c.764T>C	p.Ile96Thr; p.Ile123Thr; p.Ile216Thr; p.Ile255Thr	11	FALSE	chr17:7577517:A:G	137:chr17:7577517:A:G	0.001907
94_c4-1	94	EGFR	MODERATE	c.755G>A	p.Arg252His	3	FALSE	chr7:55221711:G:A	137:chr7:55221711:G:A	0.003191
94_c4-1	94	TP53	MODERATE; MODIFIER	c.100G>A; c.217G>A; c.-279G>A; c.-360G>A	p.Val34Met; p.Val73Met;	5	FALSE	chr17:7579470:C:T	137:chr17:7579470:C:T	0.002395
94_c4-1	94	NOTCH1	MODERATE	c.4903G>A	p.Ala1635Thr	0	FALSE	chr9:139399240:C:T	137:chr9:139399240:C:T	0.002743
94_c4-1	94	TP53	LOW; MODERATE	c.1A>C; c.361A>C; c.478A>C; c.82A>C	p.Met1?; p.Met121Leu; p.Met160Leu; p.Met28Leu	5	FALSE	chr17:7578452:T:G	137:chr17:7578452:T:G	0.003086
94_c4-1	94	FGFR3	MODERATE	c.905G>A	p.Gly302Asp	1	FALSE	chr4:1803727:G:A	137:chr4:1803727:G:A	0.001369
94_c4-1	94	FGFR3	MODERATE	c.742C>T	p.Arg248Cys	254	FALSE	chr4:1803564:C:T	137:chr4:1803564:C:T	0.002692
94_c4-1	94	STK11	MODERATE	c.628T>C	p.Cys210Arg	1	FALSE	chr19:1220610:T:C	137:chr19:1220610:T:C	0.005629
94_c4-1	94	TP53	MODIFIER; MODERATE	c.-66G>A; c.16G>A; c.295G>A; c.412G>A	; p.Ala6Thr; p.Ala99Thr; p.Ala138Thr	17	FALSE	chr17:7578518:C:T	137:chr17:7578518:C:T	0.001996
94_c4-1	94	C9orf53; CDKN2A	MODIFIER; MODERATE; LOW	n.*616G>A; c.*223C>T; c.343C>T; c.300C>T	; p.Arg115Trp; p.Ala100Ala	1	FALSE	chr9:21971058:G:A	137:chr9:21971058:G:A	0.002825
94_c4-1	94	EPHA3	MODERATE	c.1280C>T	p.Ala427Val	0	FALSE	chr3:89391214:C:T	137:chr3:89391214:C:T	0.002146
94_c4-1	94	C9orf53; CDKN2A	MODIFIER; MODERATE; LOW	n.*616T>G; c.*120A>C; c.197A>C; c.240A>C	; p.His66Pro; p.Pro80Pro	1	FALSE	chr9:21971161:T:G	137:chr9:21971161:T:G	0.04034

94_c4-1	94	CDH1	LOW	c.1137G>A	p.Thr379Thr	0	FALSE	chr16:68846166:G:A	137:chr16:68846166:G:A	0.00209
94_c4-1	94	DDR2	MODERATE	c.1418G>A	p.Arg473His	2	FALSE	chr1:162740216:G:A	137:chr1:162740216:G:A	0.001601
94_c4-1	94	IGF1R	MODERATE	c.3905T>C; c.3908T>C	p.Val1302Ala; p.Val1303Ala	0	FALSE	chr15:99500475:T:C	137:chr15:99500475:T:C	0.00444
94_c4-1	94	VHL	MODIFIER; MODERATE	c.341-3270A>C; c.344A>C	; p.His115Pro	0	FALSE	chr3:10188201:A:C	137:chr3:10188201:A:C	0.002584
94_c4-1	94	FGFR4	MODERATE; LOW	c.1186G>A; c.1306G>A; c.1152G>A	p.Val396Met; p.Val436Met; p.Ala384Ala	1	FALSE	chr5:176520461:G:A	137:chr5:176520461:G:A	0.003243
94_c4-1	94	ERBB2	MODERATE; MODIFIER	c.560G>A; c.605G>A; c.650G>A; n.974G>A	p.Arg187His; p.Arg202His; p.Arg217His;	1	FALSE	chr17:37866345:G:A	137:chr17:37866345:G:A	0.001589
94_c4-1	94	IGF1R	MODERATE	c.3005G>A; c.3008G>A	p.Arg1002Gln; p.Arg1003Gln	0	FALSE	chr15:99478104:G:A	137:chr15:99478104:G:A	0.002979
94_c4-1	94	C9orf53; CDKN2A	MODIFIER; MODERATE	n.*616G>A; c.*324C>T; c.*45C>T; c.401C>T	; p.Ala134Val	1	FALSE	chr9:21970957:G:A	137:chr9:21970957:G:A	0.002591
94_c4-1	94	CDH1	MODERATE	c.671G>A	p.Arg224His	0	FALSE	chr16:68842735:G:A	137:chr16:68842735:G:A	0.002237
94_c4-1	94	NOTCH1	MODERATE	c.3859C>T	p.Arg1287Cys	0	FALSE	chr9:139401210:G:A	137:chr9:139401210:G:A	0.002448
94_c4-1	94	FGFR2	MODIFIER; MODERATE	c.749-4847G>A; c.407G>A; c.485G>A; c.752G>A; n.1054G>A	; p.Arg136Gln; p.Arg162Gln; p.Arg251Gln	2	FALSE	chr10:123279680:C:T	137:chr10:123279680:C:T	0.00237

94_c4-1	94	PKD1; TSC2	MODIFIER; MODERATE	c.*13118C>T; c.*13121C>T; c.4192G>A; c.4324G>A; c.4393G>A	; p.Asp1398Asn; p.Asp1442Asn; p.Asp1465Asn	0	FALSE	chr16:2134616:G:A	137:chr16:2134616:G:A	0.001864
94_c4-1	94	RET	MODERATE	c.1690A>C	p.Thr564Pro	1	FALSE	chr10:43608342:A:C	137:chr10:43608342:A:C	0.007543
94_c4-1	94	TP53	MODERATE	c.196G>T; c.277G>T; c.556G>T; c.673G>T	p.Val66Phe; p.Val93Phe; p.Val186Phe; p.Val225Phe	2	FALSE	chr17:7577608:C:A	137:chr17:7577608:C:A	0.001783
94_c4-1	94	ERBB2; MIEN1; MIR4728	MODIFIER; MODERATE	c.3160-213A>G; c.3251A>G; c.3296A>G; c.3341A>G; n.3665A>G; c.*388T>C; n.*67A>G	; p.Glu1084Gly; p.Glu1099Gly; p.Glu1114Gly	1	FALSE	chr17:37883729:A:G	137:chr17:37883729:A:G	0.002443
94_c4-1	94	NTRK1	MODERATE	c.804C>G; c.894C>G	p.His268Gln; p.His298Gln	1	FALSE	chr1:156843468:C:G	137:chr1:156843468:C:G	0.003279
94_c4-1	94	NOTCH1	MODERATE	c.4984C>T	p.Arg1662Trp	0	FALSE	chr9:139399159:G:A	137:chr9:139399159:G:A	0.003454
94_c4-1	94	PIK3CA	MODERATE	c.3074C>A	p.Thr1025Asn	4	FALSE	chr3:178952019:C:A	137:chr3:178952019:C:A	0.001883
111_bl-1	111	ALK	MODERATE	c.3455T>C	p.Leu1152Pro	1	FALSE	chr2:29445270:A:G	141:chr2:29445270:A:G	0.006814
111_bl-1	111	BRAF	MODERATE	c.1943A>G	p.Glu648Gly	1	FALSE	chr7:140449136:T:C	141:chr7:140449136:T:C	0.003361
111_bl-1	111	MET	MODERATE	c.487T>C	p.Ser163Pro	1	FALSE	chr7:116339625:T:C	141:chr7:116339625:T:C	0.00274
111_bl-1	111	RET	MODERATE	c.1690A>C	p.Thr564Pro	1	FALSE	chr10:43608342:A:C	141:chr10:43608342:A:C	0.013783
111_bl-1	111	CDKN2A	MODIFIER; MODERATE	c.194-3568A>C; c.52A>C	; p.Thr18Pro	1	FALSE	chr9:21974775:T:G	141:chr9:21974775:T:G	0.011521

111_bl-1	111	STK11	MODERATE	c.488G>A	p.Gly163Asp	1	FALSE	chr19:1220395:G:A	141:chr19:1220395:G:A	0.005764
111_bl-1	111	VHL	MODIFIER; MODERATE	c.341-3270A>C; c.344A>C	; p.His115Pro	0	FALSE	chr3:10188201:A:C	141:chr3:10188201:A:C	0.007117
111_bl-1	111	AKT1	MODERATE	c.932G>A	p.Gly311Asp	1	FALSE	chr14:105239613:C:T	141:chr14:105239613:C:T	0.003697
111_bl-1	111	DDR2	MODERATE	c.1418G>A	p.Arg473His	2	FALSE	chr1:162740216:G:A	141:chr1:162740216:G:A	0.002525
111_bl-1	111	KDR	MODERATE	c.1028C>T	p.Thr343Met	3	FALSE	chr4:55976884:G:A	141:chr4:55976884:G:A	0.004084
71_c6-2	71	TP53	MODERATE	c.202T>C; c.283T>C; c.562T>C; c.679T>C	p.Ser68Pro; p.Ser95Pro; p.Ser188Pro; p.Ser227Pro	3	FALSE	chr17:7577602:A:G	143:chr17:7577602:A:G	0.005731
71_c6-2	71	FGFR4	MODIFIER; MODERATE	c.1098-65G>A; c.1251+10G>A; c.1067G>A	; p.Arg356His	1	FALSE	chr5:176520342:G:A	143:chr5:176520342:G:A	0.005831
71_c6-2	71	TP53	MODERATE	c.270G>T; c.351G>T; c.630G>T; c.747G>T	p.Arg90Ser; p.Arg117Ser; p.Arg210Ser; p.Arg249Ser	318	FALSE	chr17:7577534:C:A	143:chr17:7577534:C:A	0.086207
71_c6-2	71	IGF1R	MODERATE	c.755G>A	p.Arg252His	0	FALSE	chr15:99434668:G:A	143:chr15:99434668:G:A	0.00678
71_c6-2	71	FGFR4	MODERATE; LOW	c.1231A>G; c.1351A>G; c.1193+4A>G	p.Ser411Gly; p.Ser451Gly;	1	FALSE	chr5:176520506:A:G	143:chr5:176520506:A:G	0.005952
71_c6-2	71	IGF1R	MODERATE	c.3934T>C; c.3937T>C	p.Ser1312Pro; p.Ser1313Pro	0	FALSE	chr15:99500504:T:C	143:chr15:99500504:T:C	0.00885
71_c6-2	71	FBXW7	MODERATE	c.1088C>T; c.1202C>T; c.1442C>T	p.Ala363Val; p.Ala401Val; p.Ala481Val	0	FALSE	chr4:153247360:G:A	143:chr4:153247360:G:A	0.005479

71_c6-2	71	EGFR	MODIFIER; MODERATE	c.*2133G>A; c.*2364G>A; c.2030G>A	; p.Arg677His	5	FALSE	chr7:55240786:G:A	143:chr7:55240786:G:A	0.007576
26_c9-1	26	TP53	MODERATE; MODIFIER	c.199C>T; c.82C>T; c.-279C>T; c.-360C>T	p.Pro67Ser; p.Pro28Ser;	3	FALSE	chr17:7579488:G:A	144:chr17:7579488:G:A	0.003407
26_c9-1	26	TP53	MODERATE	c.212C>T; c.293C>T; c.572C>T; c.689C>T	p.Thr71Ile; p.Thr98Ile; p.Thr191Ile; p.Thr230Ile	9	FALSE	chr17:7577592:G:A	144:chr17:7577592:G:A	0.001931
26_c9-1	26	RET	MODERATE	c.1531G>A	p.Glu511Lys	1	FALSE	chr10:43607555:G:A	144:chr10:43607555:G:A	0.002427
26_c9-1	26	TP53	MODERATE	c.350C>T; c.431C>T; c.710C>T; c.827C>T	p.Ala117Val; p.Ala144Val; p.Ala237Val; p.Ala276Val	10	FALSE	chr17:7577111:G:A	144:chr17:7577111:G:A	0.002581
26_c9-1	26	EGFR	MODERATE	c.719G>A	p.Cys240Tyr	1	FALSE	chr7:55220329:G:A	144:chr7:55220329:G:A	0.002725
26_c9-1	26	FGFR3	MODERATE	c.1526G>A ; c.1862G>A ; c.1868G>A	p.Arg509His ; p.Arg621His ; p.Arg623His	2	FALSE	chr4:1807803:G:A	144:chr4:1807803:G:A	0.00311
26_c9-1	26	RET	MODERATE	c.1690A>C	p.Thr564Pro	1	FALSE	chr10:43608342:A:C	144:chr10:43608342:A:C	0.005525
26_c9-1	26	FGFR3	MODERATE	c.905G>A	p.Gly302Asp	1	FALSE	chr4:1803727:G:A	144:chr4:1803727:G:A	0.003012
26_c9-1	26	TP53	MODERATE	c.208T>A; c.289T>A; c.568T>A; c.685T>A	p.Cys70Ser; p.Cys97Ser; p.Cys190Ser ; p.Cys229Ser	2	FALSE	chr17:7577596:A:T	144:chr17:7577596:A:T	0.001992
26_c9-1	26	BRAF	MODERATE	c.1799T>A	p.Val600Glu	23024	FALSE	chr7:140453136:A:T	144:chr7:140453136:A:T	0.002793
26_c9-1	26	KDR	MODERATE	c.1028C>T	p.Thr343Met	3	FALSE	chr4:55976884:G:A	144:chr4:55976884:G:A	0.001529

26_c9-1	26	NTRK2	MODERATE	c.1984G>A; c.2032G>A	p.Ala662Thr; p.Ala678Thr	0	FALSE	chr9:87570292:G:A	144:chr9:87570292:G:A	0.002574
26_c9-1	26	TP53	MODERATE	c.371G>A; c.452G>A; c.731G>A; c.848G>A	p.Arg124His; p.Arg151His; p.Arg244His; p.Arg283His	24	FALSE	chr17:7577090:C:T	144:chr17:7577090:C:T	0.002736
26_c9-1	26	FGFR4	MODERATE	c.1745G>A; c.1829G>A; c.1949G>A	p.Arg582His; p.Arg610His; p.Arg650His	1	FALSE	chr5:176523292:G:A	144:chr5:176523292:G:A	0.005038
26_c9-1	26	INSRR; NTRK1	MODIFIER; MODERATE	c.3397+28C>T; c.13G>A	; p.Ala5Thr	3	FALSE	chr1:156811876:G:A	144:chr1:156811876:G:A	0.002401
26_c9-1	26	ALK	MODERATE	c.1262C>T	p.Ala421Val	1	FALSE	chr2:29606618:G:A	144:chr2:29606618:G:A	0.002491
26_c9-1	26	NTRK1	MODERATE	c.1359C>A; c.1449C>A; c.1467C>A	p.His453Gln; p.His483Gln; p.His489Gln	1	FALSE	chr1:156845424:C:A	144:chr1:156845424:C:A	0.002296
26_c9-1	26	MITF	MODIFIER; MODERATE	c.-45G>A; c.109G>A; c.112G>A; c.64G>A	; p.Ala37Thr; p.Ala38Thr; p.Ala22Thr	0	FALSE	chr3:69928292:G:A	144:chr3:69928292:G:A	0.002551
26_c9-1	26	C9orf53; CDKN2A	MODIFIER; MODERATE; LOW	n.*616G>A; c.*201C>T; c.278C>T; c.321C>T	; p.Thr93Met; p.His107His	2	FALSE	chr9:21971080:G:A	144:chr9:21971080:G:A	0.002597
26_c9-1	26	IGF1R	MODERATE	c.1940G>A	p.Arg647His	0	FALSE	chr15:99459304:G:A	144:chr15:99459304:G:A	0.002472
26_c9-1	26	TP53	MODERATE; MODIFIER	c.110C>T; c.227C>T; c.-279C>T; c.-360C>T	p.Ala37Val; p.Ala76Val;	1	FALSE	chr17:7579460:G:A	144:chr17:7579460:G:A	0.003311
26_c9-1	26	EPHA3	MODERATE	c.2306G>A	p.Arg769His	0	FALSE	chr3:89480469:G:A	144:chr3:89480469:G:A	0.002747
26_c9-1	26	NTRK2	HIGH	c.1972C>T; c.2020C>T	p.Gln658*; p.Gln674*	0	FALSE	chr9:87570280:C:T	144:chr9:87570280:C:T	0.002571

26_c9-1	26	NF1	MODERATE	c.2695T>G	p.Leu899Val	3	FALSE	chr17:29556328:T:G	144:chr17:29556328:T:G	0.003736
26_c9-1	26	DDR2	MODERATE	c.1418G>A	p.Arg473His	2	FALSE	chr1:162740216:G:A	144:chr1:162740216:G:A	0.002361
26_c9-1	26	TSC2	MODIFIER; MODERATE	c.2837+1108G>A; c.2933G>A	; p.Arg978His	0	FALSE	chr16:2127694:G:A	144:chr16:2127694:G:A	0.004076
26_c9-1	26	KIT	MODERATE	c.2671G>A; c.2683G>A	p.Ala891Thr; p.Ala895Thr	3	FALSE	chr4:55602973:G:A	144:chr4:55602973:G:A	0.002433
26_c9-1	26	TP53	MODIFIER; MODERATE	c.-17G>T; c.344G>T; c.461G>T; c.65G>T	; p.Gly115Val; p.Gly154Val; p.Gly22Val	39	FALSE	chr17:7578469:C:A	144:chr17:7578469:C:A	0.002976
26_c9-1	26	PIK3R1	MODERATE	c.386C>T	p.Pro129Leu	1	FALSE	chr5:67569269:C:T	144:chr5:67569269:C:T	0.005008
26_c9-1	26	PIK3CA	HIGH	c.3152G>A	p.Trp1051*	3	FALSE	chr3:178952097:G:A	144:chr3:178952097:G:A	0.002433
26_c9-1	26	CDKN2A	MODIFIER; MODERATE	c.194-3568A>C; c.52A>C	; p.Thr18Pro	1	FALSE	chr9:21974775:T:G	144:chr9:21974775:T:G	0.005085
26_c9-1	26	VHL	MODIFIER; MODERATE	c.341-3270A>C; c.344A>C	; p.His115Pro	0	FALSE	chr3:10188201:A:C	144:chr3:10188201:A:C	0.004601
26_c9-1	26	STK11	MODERATE	c.628T>C	p.Cys210Arg	1	FALSE	chr19:1220610:T:C	144:chr19:1220610:T:C	0.003454
26_c9-1	26	TP53	MODERATE	c.224A>G; c.305A>G; c.584A>G; c.701A>G	p.Tyr75Cys; p.Tyr102Cys; p.Tyr195Cys; p.Tyr234Cys	94	FALSE	chr17:7577580:T:C	144:chr17:7577580:T:C	0.001916
26_c9-1	26	EGFR	MODERATE	c.971G>A	p.Arg324His	3	FALSE	chr7:55223604:G:A	144:chr7:55223604:G:A	0.00311
26_c9-1	26	IGF1R	MODERATE	c.3905T>C; c.3908T>C	p.Val1302Ala; p.Val1303Ala	0	FALSE	chr15:99500475:T:C	144:chr15:99500475:T:C	0.002841
26_c9-1	26	BRAF	HIGH	c.1525C>T	p.Arg509*	1	FALSE	chr7:140476881:G:A	144:chr7:140476881:G:A	0.003077

11_t2c1-2	11	TP53	MODERATE	c.106C>T; c.25C>T; c.385C>T; c.502C>T	p.His36Tyr; p.His9Tyr; p.His129Tyr; p.His168Tyr	9	FALSE	chr17:7578428:G:A	145:chr17:7578428:G:A	0.002899
11_t2c1-2	11	EGFR	MODERATE	c.1159C>G	p.Leu387Val	1	FALSE	chr7:55224477:C:G	145:chr7:55224477:C:G	0.003053
11_t2c1-2	11	NOTCH1	MODERATE	c.4252G>A	p.Ala1418Thr	0	FALSE	chr9:139400096:C:T	145:chr9:139400096:C:T	0.00565
11_t2c1-2	11	EGFR	MODERATE	c.3352G>A	p.Ala1118Thr	3	FALSE	chr7:55273029:G:A	145:chr7:55273029:G:A	0.002551
11_t2c1-2	11	GNA11	MODERATE	c.88C>T	p.Arg30Trp	1	FALSE	chr19:3094737:C:T	145:chr19:3094737:C:T	0.00885
11_t2c1-2	11	C9orf53; CDKN2A	MODIFIER; MODERATE; LOW	n.*616G>A; c.*180C>T; c.257C>T; c.300C>T	; p.Ala86Val; p.Cys100Cys	1	FALSE	chr9:21971101:G:A	145:chr9:21971101:G:A	0.002837
11_t2c1-2	11	NTRK1	MODERATE	c.1940T>G; c.2030T>G; c.2048T>G	p.Val647Gly; p.Val677Gly; p.Val683Gly	2	FALSE	chr1:156849792:T:G	145:chr1:156849792:T:G	0.005155
11_t2c1-2	11	GNAQ	MODERATE	c.673T>C	p.Ser225Pro	1	FALSE	chr9:80409441:A:G	145:chr9:80409441:A:G	0.00315
11_t2c1-2	11	ATM	MODERATE	c.1010G>A	p.Arg337His	0	FALSE	chr11:108117799:G:A	145:chr11:108117799:G:A	0.003044
11_t2c1-2	11	FGFR1	MODERATE	c.1013C>T; c.1019C>T; c.1112C>T; c.746C>T; c.752C>T; c.995C>T	p.Thr338Met; p.Thr340Met; p.Thr371Met; p.Thr249Met; p.Thr251Met; p.Thr332Met	2	FALSE	chr8:38279377:G:A	145:chr8:38279377:G:A	0.0033
11_t2c1-2	11	PTEN	MODERATE	c.394G>A	p.Gly132Ser	3	FALSE	chr10:89692910:G:A	145:chr10:89692910:G:A	0.003021
11_t2c1-2	11	PTEN	MODERATE	c.821G>T	p.Trp274Leu	6	FALSE	chr10:89720670:G:T	145:chr10:89720670:G:T	0.004762
11_t2c1-2	11	NTRK3	MODERATE	c.1351C>T; c.1375C>T	p.Arg451Trp; p.Arg459Trp	0	FALSE	chr15:88669523:G:A	145:chr15:88669523:G:A	0.002721

11_t2c1-2	11	MITF	MODERATE	c.125A>C; c.233A>C; c.278A>C; c.281A>C	p.Gln42Pro; p.Gln78Pro; p.Gln93Pro; p.Gln94Pro	0	FALSE	chr3:69928461:A:C	145:chr3:69928461:A:C	0.002729
11_t2c1-2	11	TP53	MODIFIER; MODERATE	c.-11C>T; c.-92C>T; c.269C>T; c.386C>T	; p.Ala90Val; p.Ala129Val	2	FALSE	chr17:7578544:G:A	145:chr17:7578544:G:A	0.002959
11_t2c1-2	11	C9orf53; CDKN2A	MODIFIER; MODERATE	n.*616G>A; c.*218C>T; c.295C>T; c.338C>T	; p.Arg99Trp; p.Pro113Leu	2	FALSE	chr9:21971063:G:A	145:chr9:21971063:G:A	0.002621
11_t2c1-2	11	DDR2	MODERATE	c.1625C>T	p.Ala542Val	1	FALSE	chr1:162741934:C:T	145:chr1:162741934:C:T	0.002451
11_t2c1-2	11	VHL	MODIFIER; MODERATE	c.341-3270A>C; c.344A>C	; p.His115Pro	0	FALSE	chr3:10188201:A:C	145:chr3:10188201:A:C	0.003584
11_t2c1-2	11	MET	MODERATE	c.3965C>A; c.4019C>A	p.Pro1322His; p.Pro1340His	1	FALSE	chr7:116435970:C:A	145:chr7:116435970:C:A	0.002821
11_t2c1-2	11	NF1	MODERATE	c.5426G>A; c.5489G>A	p.Arg1809His; p.Arg1830His	1	FALSE	chr17:29654737:G:A	145:chr17:29654737:G:A	0.002384
11_t2c1-2	11	AR	MODERATE	c.2360G>A; c.764G>A	p.Arg787Gln; p.Arg255Gln	0	FALSE	chrX:66941716:G:A	145:chrX:66941716:G:A	0.002611
11_t2c1-2	11	FBXW7	MODERATE	c.1039C>T; c.1153C>T; c.1393C>T	p.Arg347Cys; p.Arg385Cys; p.Arg465Cys	0	FALSE	chr4:153249385:G:A	145:chr4:153249385:G:A	0.003252
11_t2c1-2	11	SMO	MODERATE	c.961G>A	p.Val321Met	0	FALSE	chr7:128846031:G:A	145:chr7:128846031:G:A	0.002717
11_t2c1-2	11	FGFR4	MODIFIER; MODERATE	c.1058-174G>A; c.1078G>A	; p.Ala360Thr	1	FALSE	chr5:176520159:G:A	145:chr5:176520159:G:A	0.002933
11_t2c1-2	11	NOTCH1	MODERATE	c.4901C>T	p.Ala1634Val	0	FALSE	chr9:139399242:G:A	145:chr9:139399242:G:A	0.002994
11_t2c1-2	11	KRAS	MODERATE	c.35G>T	p.Gly12Val	11213	FALSE	chr12:25398284:C:A	145:chr12:25398284:C:A	0.052727

11_t2c1-2	11	TP53	MODERATE	c.128G>A; c.407G>A; c.47G>A; c.524G>A	p.Arg43His; p.Arg136His; p.Arg16His; p.Arg175His	979	FALSE	chr17:7578406:C:T	145:chr17:7578406:C:T	0.035276
11_t2c1-2	11	IGF1R	MODERATE	c.1565G>A	p.Ser522Asn	0	FALSE	chr15:99454646:G:A	145:chr15:99454646:G:A	0.002597
11_t2c1-2	11	INSRR; NTRK1	MODIFIER; MODERATE	c.3397+24A>G; c.17T>C	; p.Leu6Pro	1	FALSE	chr1:156811880:T:C	145:chr1:156811880:T:C	0.002384
11_t2c1-2	11	KDR	MODERATE	c.2378A>G	p.Asn793Ser	1	FALSE	chr4:55964435:T:C	145:chr4:55964435:T:C	0.003745
11_t2c1-2	11	CTNNB1	MODERATE	c.643G>A	p.Ala215Thr	0	FALSE	chr3:41266972:G:A	145:chr3:41266972:G:A	0.002653
11_t2c1-2	11	STK11	MODERATE	c.628T>C	p.Cys210Arg	1	FALSE	chr19:1220610:T:C	145:chr19:1220610:T:C	0.010684
11_t2c1-2	11	KDR	MODERATE	c.2497C>T	p.Arg833Trp	1	FALSE	chr4:55964316:G:A	145:chr4:55964316:G:A	0.003086
132_c1w3-2	132	BRAF	MODERATE	c.1799T>A	p.Val600Glu	23024	FALSE	chr7:140453136:A:T	146:chr7:140453136:A:T	0.093443
132_c1w3-2	132	EGFR	MODERATE	c.1159C>G	p.Leu387Val	1	FALSE	chr7:55224477:C:G	146:chr7:55224477:C:G	0.004354
132_c1w3-2	132	RPL19	MODERATE	c.452G>A	p.Arg151His	0	FALSE	chr17:37360425:G:A	146:chr17:37360425:G:A	0.003284
132_c1w3-2	132	PDGFRA	MODERATE	c.2465G>A	p.Arg822His	3	FALSE	chr4:55152033:G:A	146:chr4:55152033:G:A	0.003322
132_c1w3-2	132	TP53	MODERATE	c.400G>T; c.481G>T; c.760G>T; c.877G>T	p.Gly134Trp; p.Gly161Trp; p.Gly254Trp; p.Gly293Trp	4	FALSE	chr17:7577061:C:A	146:chr17:7577061:C:A	0.00321
132_c1w3-2	132	ERBB2	MODERATE; MODIFIER	c.872A>G; c.917A>G; c.962A>G; n.1286A>G	p.Glu291Gly; p.Glu306Gly; p.Glu321Gly;	1	FALSE	chr17:37868241:A:G	146:chr17:37868241:A:G	0.003175
132_c1w3-2	132	EGFR	MODERATE	c.971G>A	p.Arg324His	3	FALSE	chr7:55223604:G:A	146:chr7:55223604:G:A	0.00565
132_c1w3-2	132	NF1	MODERATE	c.2695T>G	p.Leu899Val	3	FALSE	chr17:29556328:T:G	146:chr17:29556328:T:G	0.008584

132_c1w3-2	132	CDKN2B; CDKN2B-AS1	MODIFIER; MODERATE	c.*253C>T; c.367C>T; n.371+10876G>A	; p.Arg123Trp	0	FALSE	chr9:22006036:G:A	146:chr9:22006036:G:A	0.004184
132_c1w3-2	132	IDH2	MODERATE	c.320G>A; c.476G>A; c.86G>A	p.Arg107His; p.Arg159His; p.Arg29His	1	FALSE	chr15:90631877:C:T	146:chr15:90631877:C:T	0.004024
132_c1w3-2	132	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2515G>A; n.-1C>T	p.Ala839Thr;	4	FALSE	chr7:55259457:G:A	146:chr7:55259457:G:A	0.003101
132_c1w3-2	132	ATM	MODERATE	c.8369G>A	p.Arg2790Lys	0	FALSE	chr11:108214049:G:A	146:chr11:108214049:G:A	0.003155
132_c1w3-2	132	EGFR	MODERATE	c.977G>A	p.Cys326Tyr	1	FALSE	chr7:55223610:G:A	146:chr7:55223610:G:A	0.003839
132_c1w3-2	132	TP53	MODERATE	c.127C>T; c.208C>T; c.487C>T; c.604C>T	p.Arg43Cys; p.Arg70Cys; p.Arg163Cys; p.Arg202Cys	6	FALSE	chr17:7578245:G:A	146:chr17:7578245:G:A	0.002981
132_c1w3-2	132	CDKN2A	MODIFIER; MODERATE	c.194-3568A>C; c.52A>C	; p.Thr18Pro	1	FALSE	chr9:21974775:T:G	146:chr9:21974775:T:G	0.005464
132_c1w3-2	132	PIK3CA	MODERATE	c.3137C>A	p.Ala1046Glu	3	FALSE	chr3:178952082:C:A	146:chr3:178952082:C:A	0.002972
132_c1w3-2	132	MITF	MODIFIER; MODERATE	c.-45G>A; c.109G>A; c.112G>A; c.64G>A	; p.Ala37Thr; p.Ala38Thr; p.Ala22Thr	0	FALSE	chr3:69928292:G:A	146:chr3:69928292:G:A	0.003295
132_c1w3-2	132	GAPDH; IFFO1; NCAPD2	MODERATE; MODIFIER	c.148G>A; c.274G>A; c.*1743C>T; c.*1746C>T; c.*1770C>T; n.*2798C>T; c.*4252G>A	p.Ala50Thr; p.Ala92Thr;	0	FALSE	chr12:6646123:G:A	146:chr12:6646123:G:A	0.003861
132_c1w3-2	132	KIT	MODERATE	c.2854C>T; c.2866C>T	p.Arg952Trp; p.Arg956Trp	3	FALSE	chr4:55604658:C:T	146:chr4:55604658:C:T	0.00319

132_c1w3-2	132	TSC1	MODERATE	c.457C>T; c.610C>T	p.Arg153Cys; p.Arg204Cys	0	FALSE	chr9:135797259:G:A	146:chr9:135797259:G:A	0.003484
132_c1w3-2	132	NOTCH1	MODERATE	c.2644G>A	p.Ala882Thr	0	FALSE	chr9:139405201:C:T	146:chr9:139405201:C:T	0.005063
132_c1w3-2	132	IGF1R	MODERATE	c.3934T>C; c.3937T>C	p.Ser1312Pro; p.Ser1313Pro	0	FALSE	chr15:99500504:T:C	146:chr15:99500504:T:C	0.013008
132_c1w3-2	132	IDH2	MODERATE	c.122G>A; c.356G>A; c.512G>A	p.Gly41Asp; p.Gly119Asp; p.Gly171Asp	5	FALSE	chr15:90631841:C:T	146:chr15:90631841:C:T	0.003704
132_c1w3-2	132	FGFR1	MODERATE	c.1135C>T; c.1141C>T; c.1378C>T; c.1402C>T; c.1408C>T; c.1501C>T	p.Arg379Cys; p.Arg381Cys; p.Arg460Cys; p.Arg468Cys; p.Arg470Cys; p.Arg501Cys	1	FALSE	chr8:38275768:G:A	146:chr8:38275768:G:A	0.002899
132_c1w3-2	132	KDR	MODERATE	c.2323G>T	p.Ala775Ser	1	FALSE	chr4:55964914:C:A	146:chr4:55964914:C:A	0.00295
132_c1w3-2	132	CDH1	MODERATE	c.1676G>A	p.Ser559Asn	0	FALSE	chr16:68853293:G:A	146:chr16:68853293:G:A	0.003284
132_c1w3-2	132	PHLPP1	MODERATE	c.3499G>A	p.Ala1167Thr	0	FALSE	chr18:60630644:G:A	146:chr18:60630644:G:A	0.003361
132_c1w3-2	132	FGFR4	MODIFIER; MODERATE	c.1193+43C>T; c.1270C>T; c.1390C>T	; p.Arg424Trp; p.Arg464Trp	1	FALSE	chr5:176520545:C:T	146:chr5:176520545:C:T	0.003431
132_c1w3-2	132	KDR	HIGH	c.2830C>T	p.Arg944*	1	FALSE	chr4:55961110:G:A	146:chr4:55961110:G:A	0.003891
5_t2c9-2	5	CDKN2A; CDKN2B-AS1	MODERATE; MODIFIER	c.98A>G; n.-1T>C	p.Glu33Gly;	1	FALSE	chr9:21994233:T:C	148:chr9:21994233:T:C	0.021739
5_t2c9-2	5	ALK	MODERATE	c.3089A>C	p.His1030Pro	15	TRUE	chr2:29448410:T:G	148:chr2:29448410:T:G	0.106796
73_bl-2	73	NOTCH1	MODERATE	c.2528A>G	p.Glu843Gly	0	FALSE	chr9:139405663:T:C	150:chr9:139405663:T:C	0.214953

73_bl-2	73	FGFR1; LETM2	HIGH; MODIFIER	c.1972C>T; c.1978C>T; c.2215C>T; c.2239C>T; c.2245C>T; c.2338C>T; c.*1406G>A; c.*1423G>A; c.*1553G>A; c.*1567G>A; c.*1638G>A	p.Gln658*; p.Gln660*; p.Gln739*; p.Gln747*; p.Gln749*; p.Gln780*;	1	FALSE	chr8:38271483:G:A	150:chr8:38271483:G:A	0.011628
73_bl-2	73	KIT	MODERATE	c.13C>T	p.Arg5Cys	1	FALSE	chr4:55524194:C:T	150:chr4:55524194:C:T	0.013158
73_bl-2	73	NF1	MODERATE	c.6011C>T; c.6074C>T	p.Ser2004Leu; p.Ser2025Leu	1	FALSE	chr17:29663418:C:T	150:chr17:29663418:C:T	0.010363
73_c3-2	73	ESR1	MODERATE	c.739G>A; c.745G>A	p.Glu247Lys; p.Glu249Lys	0	FALSE	chr6:152201885:G:A	151:chr6:152201885:G:A	0.023256
73_c6-2	73	ALK	MODERATE	c.3089A>C	p.His1030Pro	15	TRUE	chr2:29448410:T:G	152:chr2:29448410:T:G	0.095745
73_c6-2	73	NOTCH1	MODERATE	c.2528A>G	p.Glu843Gly	0	FALSE	chr9:139405663:T:C	152:chr9:139405663:T:C	0.223881
69_bl-1	69	CDKN2A	MODIFIER; MODERATE	c.194-3537T>G; c.83T>G	; p.Val28Gly	1	FALSE	chr9:21974744:A:C	155:chr9:21974744:A:C	0.134921
69_bl-1	69	CDKN2A	MODIFIER; MODERATE	c.194-3546T>G; c.74T>G	; p.Val25Gly	2	FALSE	chr9:21974753:A:C	155:chr9:21974753:A:C	0.38125
69_bl-1	69	FOXL2; FOXL2NB; LINC01391	MODERATE; MODIFIER	c.282T>A; c.-132A>T; n.-1T>A	p.Asn94Lys;	0	FALSE	chr3:138665283:A:T	155:chr3:138665283:A:T	0.066225
69_bl-1	69	PIK3CA	MODERATE	c.35G>A	p.Gly12Asp	5	FALSE	chr3:178916648:G:A	155:chr3:178916648:G:A	0.006042
69_bl-1	69	RET	MODERATE	c.1690A>C	p.Thr564Pro	1	FALSE	chr10:43608342:A:C	155:chr10:43608342:A:C	0.033033
69_bl-1	69	PTEN	MODERATE	c.389G>A	p.Arg130Gln	89	FALSE	chr10:89692905:G:A	155:chr10:89692905:G:A	0.007634

69_bl-1	69	IGF1R	MODERATE	c.3934T>C; c.3937T>C	p.Ser1312Pro; p.Ser1313Pro	0	FALSE	chr15:99500504:T:C	155:chr15:99500504:T:C	0.041096
69_bl-1	69	GNA11	MODERATE	c.440G>A	p.Arg147His	1	FALSE	chr19:3113446:G:A	155:chr19:3113446:G:A	0.00885
73_c4-2	73	RET	MODERATE	c.1690A>C	p.Thr564Pro	1	FALSE	chr10:43608342:A:C	156:chr10:43608342:A:C	0.022346
73_c4-2	73	CDKN2A	MODIFIER; MODERATE	c.194-3546T>G; c.74T>G	; p.Val25Gly	2	FALSE	chr9:21974753:A:C	156:chr9:21974753:A:C	0.395349
73_c4-2	73	IGF1R	MODERATE	c.3934T>C; c.3937T>C	p.Ser1312Pro; p.Ser1313Pro	0	FALSE	chr15:99500504:T:C	156:chr15:99500504:T:C	0.012821
73_c4-2	73	C9orf53; CDKN2A	MODIFIER; MODERATE; LOW	n.*616T>G; c.*120A>C; c.197A>C; c.240A>C	; p.His66Pro; p.Pro80Pro	1	FALSE	chr9:21971161:T:G	156:chr9:21971161:T:G	0.2
106_c3-2	106	FOXL2; FOXL2NB; LINC01391	MODERATE; MODIFIER	c.282T>A; c.-132A>T; n.-1T>A	p.Asn94Lys;	0	FALSE	chr3:138665283:A:T	157:chr3:138665283:A:T	0.046948
106_c3-2	106	MITF	MODERATE	c.130C>T; c.175C>T; c.178C>T; c.22C>T	p.Arg44Cys; p.Arg59Cys; p.Arg60Cys; p.Arg8Cys	0	FALSE	chr3:69928358:C:T	157:chr3:69928358:C:T	0.005076
106_c3-2	106	ALK	MODERATE	c.619G>A	p.Ala207Thr	1	FALSE	chr2:30142907:C:T	157:chr2:30142907:C:T	0.00823
106_c3-2	106	SMO	MODERATE	c.1843T>C	p.Ser615Pro	0	FALSE	chr7:128851518:T:C	157:chr7:128851518:T:C	0.004878
106_c3-2	106	IGF1R	MODERATE	c.3934T>C; c.3937T>C	p.Ser1312Pro; p.Ser1313Pro	0	FALSE	chr15:99500504:T:C	157:chr15:99500504:T:C	0.036082
106_c3-2	106	CDKN2A	MODIFIER; MODERATE	c.194-3546T>G; c.74T>G	; p.Val25Gly	2	FALSE	chr9:21974753:A:C	157:chr9:21974753:A:C	0.325843
106_c3-2	106	KDR	MODERATE	c.1028C>T	p.Thr343Met	3	FALSE	chr4:55976884:G:A	157:chr4:55976884:G:A	0.00367
106_c3-2	106	PDGFRA	MODERATE	c.685G>A	p.Glu229Lys	3	FALSE	chr4:55131142:G:A	157:chr4:55131142:G:A	0.005556

106_c3-2	106	TP53	MODERATE	c.200G>A; c.281G>A; c.560G>A; c.677G>A	p.Gly67Asp; p.Gly94Asp; p.Gly187Asp; p.Gly226Asp	5	FALSE	chr17:7577604:C:T	157:chr17:7577604:C:T	0.00554
106_c3-2	106	KRAS	MODERATE	c.35G>A	p.Gly12Asp	11213	FALSE	chr12:25398284:C:T	157:chr12:25398284:C:T	0.034483
106_c3-2	106	TP53	MODIFIER; MODERATE	c.-17C>T; c.-98C>T; c.263C>T; c.380C>T	; p.Ser88Phe; p.Ser127Phe	38	FALSE	chr17:7578550:G:A	157:chr17:7578550:G:A	0.021407
106_c3-2	106	RET	MODERATE	c.1690A>C	p.Thr564Pro	1	FALSE	chr10:43608342:A:C	157:chr10:43608342:A:C	0.028902
106_c3-2	106	C9orf53; CDKN2A	MODIFIER; MODERATE; LOW	n.*616T>G; c.*120A>C; c.197A>C; c.240A>C	; p.His66Pro; p.Pro80Pro	1	FALSE	chr9:21971161:T:G	157:chr9:21971161:T:G	0.09322
106_c3-2	106	KIT	MODERATE	c.2671G>A; c.2683G>A	p.Ala891Thr; p.Ala895Thr	3	FALSE	chr4:55602973:G:A	157:chr4:55602973:G:A	0.005181
106_c3-2	106	CDKN2A	MODIFIER; MODERATE	c.194-3537T>G; c.83T>G	; p.Val28Gly	1	FALSE	chr9:21974744:A:C	157:chr9:21974744:A:C	0.116883
106_c3-2	106	SMO	MODERATE	c.1045A>C	p.Thr349Pro	0	FALSE	chr7:128846115:A:C	157:chr7:128846115:A:C	0.008696
106_bl-1	106	CDKN2A; CDKN2B-AS1	MODERATE; MODIFIER	c.98A>G; n.-1T>C	p.Glu33Gly;	1	FALSE	chr9:21994233:T:C	158:chr9:21994233:T:C	0.022523
106_bl-1	106	SMO	MODERATE	c.1045A>C	p.Thr349Pro	0	FALSE	chr7:128846115:A:C	158:chr7:128846115:A:C	0.005391
106_bl-1	106	NTRK3	MODERATE	c.1139C>T	p.Ala380Val	0	FALSE	chr15:88678397:G:A	158:chr15:88678397:G:A	0.005195
106_bl-1	106	CDKN2A	MODIFIER; MODERATE	c.194-3546T>G; c.74T>G	; p.Val25Gly	2	FALSE	chr9:21974753:A:C	158:chr9:21974753:A:C	0.1875
106_bl-1	106	NRAS	MODERATE	c.437C>T	p.Ala146Val	1	FALSE	chr1:115252203:G:A	158:chr1:115252203:G:A	0.007042
106_bl-1	106	TP53	MODIFIER; MODERATE	c.-17C>T; c.-98C>T; c.263C>T; c.380C>T	; p.Ser88Phe; p.Ser127Phe	38	FALSE	chr17:7578550:G:A	158:chr17:7578550:G:A	0.005747

106_bl-1	106	ERBB2; MIEN1; MIR4728	MODERATE; MODIFIER	c.2720A>G; c.2765A>G; c.2810A>G; n.3134A>G; c.*388T>C; n.-1A>G	p.Lys907Arg; p.Lys922Arg; p.Lys937Arg;	1	FALSE	chr17:37882044:A:G	158:chr17:37882044:A:G	0.00542
106_bl-1	106	SMO	MODERATE	c.628G>A	p.Val210Met	0	FALSE	chr7:128845134:G:A	158:chr7:128845134:G:A	0.005814
106_bl-1	106	CDKN2A	MODIFIER; MODERATE	c.194-3537T>G; c.83T>G	; p.Val28Gly	1	FALSE	chr9:21974744:A:C	158:chr9:21974744:A:C	0.079787
106_bl-1	106	KRAS	MODERATE	c.35G>A	p.Gly12Asp	11213	FALSE	chr12:25398284:C:T	158:chr12:25398284:C:T	0.017794
106_bl-1	106	IGF1R	MODERATE	c.3905T>C; c.3908T>C	p.Val1302Ala; p.Val1303Ala	0	FALSE	chr15:99500475:T:C	158:chr15:99500475:T:C	0.01497
80_c4-1	80	EPHA3	MODERATE	c.1234G>A	p.Val412Ile	0	FALSE	chr3:89391168:G:A	159:chr3:89391168:G:A	0.003831
80_c4-1	80	RET	MODERATE	c.1690A>C	p.Thr564Pro	1	FALSE	chr10:43608342:A:C	159:chr10:43608342:A:C	0.010471
80_c4-1	80	PIK3CA	MODERATE	c.365G>A	p.Gly122Asp	2	FALSE	chr3:178917490:G:A	159:chr3:178917490:G:A	0.003788
80_c4-1	80	SMO	MODERATE	c.961G>A	p.Val321Met	0	FALSE	chr7:128846031:G:A	159:chr7:128846031:G:A	0.00335
80_c4-1	80	ALK	MODERATE	c.4192C>T	p.Pro1398Ser	1	FALSE	chr2:29416761:G:A	159:chr2:29416761:G:A	0.004057
80_c4-1	80	IGF1R	MODERATE	c.3905T>C; c.3908T>C	p.Val1302Ala; p.Val1303Ala	0	FALSE	chr15:99500475:T:C	159:chr15:99500475:T:C	0.005445
80_c4-1	80	IGF1R	MODERATE	c.3934T>C; c.3937T>C	p.Ser1312Pro; p.Ser1313Pro	0	FALSE	chr15:99500504:T:C	159:chr15:99500504:T:C	0.010221
80_c4-1	80	ERBB2	MODERATE; MODIFIER	c.101T>C; c.146T>C; c.56T>C; n.407T>C	p.Leu34Pro; p.Leu49Pro; p.Leu19Pro;	1	FALSE	chr17:37863315:T:C	159:chr17:37863315:T:C	0.004098

80_c4-1	80	FGFR1	MODERATE	c.487C>T; c.493C>T; c.736C>T; c.754C>T; c.760C>T; c.853C>T	p.Arg163Trp; p.Arg165Trp; p.Arg246Trp; p.Arg252Trp; p.Arg254Trp; p.Arg285Trp	1	FALSE	chr8:38282203:G:A	159:chr8:38282203:G:A	0.003854
80_c4-1	80	EVI2A; NF1	MODIFIER; MODERATE	c.-266T>G; c.-338T>G; c.5125A>C; c.5188A>C	; p.Thr1709Pro; p.Thr1730Pro	1	FALSE	chr17:29653190:A:C	159:chr17:29653190:A:C	0.006525
80_c4-1	80	FBXW7	MODERATE	c.1028G>T; c.1268G>T; c.914G>T	p.Gly343Val; p.Gly423Val; p.Gly305Val	0	FALSE	chr4:153249510:C:A	159:chr4:153249510:C:A	0.004065
80_c4-1	80	NTRK1	MODERATE	c.1940T>G; c.2030T>G; c.2048T>G	p.Val647Gly; p.Val677Gly; p.Val683Gly	2	FALSE	chr1:156849792:T:G	159:chr1:156849792:T:G	0.008
80_c4-1	80	CDKN2A	MODIFIER; MODERATE	c.194-3537T>G; c.83T>G	; p.Val28Gly	1	FALSE	chr9:21974744:A:C	159:chr9:21974744:A:C	0.076087
80_c4-1	80	FGFR4	MODIFIER; MODERATE	c.1058-174G>A; c.1078G>A	; p.Ala360Thr	1	FALSE	chr5:176520159:G:A	159:chr5:176520159:G:A	0.004264
80_c4-1	80	HGF	MODERATE	c.767G>A; c.782G>A	p.Arg256His; p.Arg261His	0	FALSE	chr7:81372752:C:T	159:chr7:81372752:C:T	0.004149
80_c4-1	80	SMO	MODERATE	c.1045A>C	p.Thr349Pro	0	FALSE	chr7:128846115:A:C	159:chr7:128846115:A:C	0.013514
80_c4-1	80	STK11	MODERATE	c.455A>G	p.Gln152Arg	3	FALSE	chr19:1219403:A:G	159:chr19:1219403:A:G	0.005952
80_c4-1	80	CDH1	MODERATE	c.221G>A	p.Arg74Gln	0	FALSE	chr16:68835630:G:A	159:chr16:68835630:G:A	0.003752
80_c4-1	80	ERBB2	MODERATE; MODIFIER	c.560G>A; c.605G>A; c.650G>A; n.974G>A	p.Arg187His; p.Arg202His; p.Arg217His;	1	FALSE	chr17:37866345:G:A	159:chr17:37866345:G:A	0.004016

80_c4-1	80	CDKN2A	MODIFIER; MODERATE	c.194-3546T>G; c.74T>G	; p.Val25Gly	2	FALSE	chr9:21974753:A:C	159:chr9:21974753:A:C	0.177083
80_c4-1	80	EPHA3	MODERATE	c.2530C>T	p.Pro844Ser	0	FALSE	chr3:89499360:C:T	159:chr3:89499360:C:T	0.003937
80_c4-1	80	NOTCH1	MODERATE	c.4778T>C	p.Leu1593Pro	0	FALSE	chr9:139399365:A:G	159:chr9:139399365:A:G	0.005181
80_c4-1	80	C9orf53; CDKN2A	MODIFIER; MODERATE	n.*616C>G; c.*140G>C; c.217G>C; c.260G>C	; p.Ala73Pro; p.Arg87Pro	1	FALSE	chr9:21971141:C:G	159:chr9:21971141:C:G	0.015306
80_c4-1	80	CDKN2A; CDKN2B-AS1	MODERATE; MODIFIER	c.98A>G; n.-1T>C	p.Glu33Gly;	1	FALSE	chr9:21994233:T:C	159:chr9:21994233:T:C	0.019355
80_c4-1	80	NTRK3	MODERATE	c.2005C>T; c.2029C>T	p.His669Tyr; p.His677Tyr	0	FALSE	chr15:88472526:G:A	159:chr15:88472526:G:A	0.003656
80_c4-1	80	FOXL2; FOXL2NB; LINC01391	MODERATE; MODIFIER	c.282T>A; c.-132A>T; n.-1T>A	p.Asn94Lys;	0	FALSE	chr3:138665283:A:T	159:chr3:138665283:A:T	0.025707
74_bl-1	74	FGFR4	MODIFIER; MODERATE	c.1058-174G>A; c.1078G>A	; p.Ala360Thr	1	FALSE	chr5:176520159:G:A	161:chr5:176520159:G:A	0.005714
74_bl-1	74	NF1	MODERATE	c.1319G>A	p.Arg440Gln	1	FALSE	chr17:29533316:G:A	161:chr17:29533316:G:A	0.005405
74_bl-1	74	ROS1	MODERATE	c.5920G>A	p.Glu1974Lys	1	FALSE	chr6:117641051:C:T	161:chr6:117641051:C:T	0.005277
74_bl-1	74	BRAF	MODERATE	c.1799T>A	p.Val600Glu	23024	FALSE	chr7:140453136:A:T	161:chr7:140453136:A:T	0.00554
74_bl-1	74	STK11	MODERATE	c.889A>G	p.Arg297Gly	1	FALSE	chr19:1221974:A:G	161:chr19:1221974:A:G	0.010417
74_bl-1	74	MITF	MODIFIER; MODERATE	c.93+115G>A; c.208G>A; c.373G>A; c.481G>A; c.526G>A; c.529G>A	; p.Ala70Thr; p.Ala125Thr; p.Ala161Thr; p.Ala176Thr; p.Ala177Thr	0	FALSE	chr3:69987147:G:A	161:chr3:69987147:G:A	0.005391
74_bl-1	74	KDR	MODERATE	c.241G>A	p.Asp81Asn	2	FALSE	chr4:55984888:C:T	161:chr4:55984888:C:T	0.005128

74_bl-1	74	FOXL2; FOXL2NB; LINC01391	MODERATE; MODIFIER	c.282T>A; c.-132A>T; n.-1T>A	p.Asn94Lys;	0	FALSE	chr3:138665283:A:T	161:chr3:138665283:A:T	0.068627
74_bl-1	74	TP53	MODERATE	c.127C>T; c.208C>T; c.487C>T; c.604C>T	p.Arg43Cys; p.Arg70Cys; p.Arg163Cys; p.Arg202Cys	6	FALSE	chr17:7578245:G:A	161:chr17:7578245:G:A	0.005333
74_bl-1	74	NTRK1	MODERATE	c.1669C>T; c.1759C>T; c.1777C>T	p.Arg557Trp; p.Arg587Trp; p.Arg593Trp	1	FALSE	chr1:156846336:C:T	161:chr1:156846336:C:T	0.006309
74_bl-1	74	CDKN2A	MODIFIER; MODERATE	c.194-3546T>G; c.74T>G	; p.Val25Gly	2	FALSE	chr9:21974753:A:C	161:chr9:21974753:A:C	0.215
74_bl-1	74	IGF1R	MODERATE	c.3934T>C; c.3937T>C	p.Ser1312Pro; p.Ser1313Pro	0	FALSE	chr15:99500504:T:C	161:chr15:99500504:T:C	0.023599
74_bl-1	74	CDKN2A	MODIFIER; MODERATE	c.194-3537T>G; c.83T>G	; p.Val28Gly	1	FALSE	chr9:21974744:A:C	161:chr9:21974744:A:C	0.069364
76_bl-b	76	TSC1	MODERATE	c.1547C>T; c.1697C>T; c.1700C>T	p.Ala516Val; p.Ala566Val; p.Ala567Val	0	FALSE	chr9:135781265:G:A	166:chr9:135781265:G:A	0.005277
76_bl-b	76	BRAF	MODERATE	c.929C>T	p.Thr310Ile	1	FALSE	chr7:140500213:G:A	166:chr7:140500213:G:A	0.005038
76_bl-b	76	RET	MODERATE	c.1907C>T	p.Thr636Met	1	FALSE	chr10:43609955:C:T	166:chr10:43609955:C:T	0.004515
76_bl-b	76	BRAF	MODERATE	c.2044C>T	p.Arg682Trp	1	FALSE	chr7:140439695:G:A	166:chr7:140439695:G:A	0.005141
76_bl-b	76	FGFR1	MODERATE	c.1211C>T; c.1217C>T; c.1454C>T; c.1478C>T; c.1484C>T; c.1577C>T	p.Ala404Val; p.Ala406Val; p.Ala485Val; p.Ala493Val; p.Ala495Val; p.Ala526Val	1	FALSE	chr8:38275456:G:A	166:chr8:38275456:G:A	0.004854

76_bl-b	76	EVI2A; NF1	MODIFIER; MODERATE	c.-266G>A; c.-338G>A; c.5020C>T; c.5083C>T	; p.Arg1674Trp; p.Arg1695Trp	1	FALSE	chr17:29653085:C:T	166:chr17:29653085:C:T	0.004796
76_bl-b	76	FGFR4	MODIFIER; MODERATE	c.1193+43C>T; c.1270C>T; c.1390C>T	; p.Arg424Trp; p.Arg464Trp	1	FALSE	chr5:176520545:C:T	166:chr5:176520545:C:T	0.007273
16_pro-1	16	NTRK1	MODERATE	c.804C>G; c.894C>G	p.His268Gln; p.His298Gln	1	FALSE	chr1:156843468:C:G	167:chr1:156843468:C:G	0.002193
16_pro-1	16	IDH1	MODERATE	c.299G>T	p.Arg100Leu	5	FALSE	chr2:209113208:C:A	167:chr2:209113208:C:A	0.001649
16_pro-1	16	CWH43	MODERATE	c.1532C>T; c.1613C>T	p.Ser511Leu; p.Ser538Leu	0	FALSE	chr4:49034687:C:T	167:chr4:49034687:C:T	0.001493
16_pro-1	16	NF1	MODERATE	c.3748C>T	p.Arg1250Trp	1	FALSE	chr17:29562668:C:T	167:chr17:29562668:C:T	0.001486
16_pro-1	16	C9orf53; CDKN2A	MODIFIER; MODERATE; LOW	n.*616G>A; c.*102C>T; c.179C>T; c.222C>T	; p.Ala60Val; p.Gly74Gly	2	FALSE	chr9:21971179:G:A	167:chr9:21971179:G:A	0.003091
16_pro-1	16	HOXD-AS2; HOXD8	MODIFIER; MODERATE	n.*692G>T; c.22C>A; c.574C>A	; p.Gln8Lys; p.Gln192Lys	0	FALSE	chr2:176995668:C:A	167:chr2:176995668:C:A	0.002278
16_pro-1	16	HRAS; LRRC56	MODERATE; MODIFIER	c.175G>A; c.-506C>T	p.Ala59Thr;	2	FALSE	chr11:533881:C:T	167:chr11:533881:C:T	0.001934
16_pro-1	16	NTRK2	MODERATE	c.1318C>A; c.1357C>A	p.Leu440Met; p.Leu453Met	0	FALSE	chr9:87366961:C:A	167:chr9:87366961:C:A	0.001691
16_pro-1	16	C9orf53; CDKN2A	MODIFIER; MODERATE; LOW	n.*616T>G; c.*120A>C; c.197A>C; c.240A>C	; p.His66Pro; p.Pro80Pro	1	FALSE	chr9:21971161:T:G	167:chr9:21971161:T:G	0.02995
16_pro-1	16	NOTCH1	MODERATE	c.4733T>G	p.Val1578Gly	0	FALSE	chr9:139399410:A:C	167:chr9:139399410:A:C	0.004415
16_pro-1	16	NF1	MODERATE	c.2695T>G	p.Leu899Val	3	FALSE	chr17:29556328:T:G	167:chr17:29556328:T:G	0.002602

16_pro-1	16	NTRK2	MODERATE	c.1960C>A; c.2008C>A	p.Leu654Met; p.Leu670Met	0	FALSE	chr9:87570268:C:A	167:chr9:87570268:C:A	0.001833
16_pro-1	16	CTNNB1	HIGH	c.283C>T	p.Arg95*	0	FALSE	chr3:41266486:C:T	167:chr3:41266486:C:T	0.001475
16_pro-1	16	NOTCH1	MODERATE	c.3407G>T	p.Gly1136Val	0	FALSE	chr9:139402510:C:A	167:chr9:139402510:C:A	0.00202
16_pro-1	16	BRAF	HIGH	c.532C>T	p.Arg178*	1	FALSE	chr7:140508768:G:A	167:chr7:140508768:G:A	0.001584
16_pro-1	16	SMO	MODERATE	c.961G>A	p.Val321Met	0	FALSE	chr7:128846031:G:A	167:chr7:128846031:G:A	0.001616
16_pro-1	16	NOTCH1	MODERATE	c.4571C>T	p.Ala1524Val	0	FALSE	chr9:139399777:G:A	167:chr9:139399777:G:A	0.001859
16_pro-1	16	KRAS	MODERATE	c.35G>A	p.Gly12Asp	11213	FALSE	chr12:25398284:C:T	167:chr12:25398284:C:T	0.020134
16_pro-1	16	MITF	MODIFIER; MODERATE	c.93+61C>T; c.154C>T; c.319C>T; c.427C>T; c.472C>T; c.475C>T	; p.Pro52Ser; p.Pro107Ser; p.Pro143Ser; p.Pro158Ser; p.Pro159Ser	0	FALSE	chr3:69987093:C:T	167:chr3:69987093:C:T	0.001626
16_pro-1	16	FGFR1; LETM2	MODERATE; MODIFIER	c.1777T>G; c.1783T>G; c.2020T>G; c.2044T>G; c.2050T>G; c.2143T>G; c.*1406A>C; c.*1423A>C; c.*1553A>C; c.*1567A>C; c.*1638A>C	p.Trp593Gly; p.Trp595Gly; p.Trp674Gly; p.Trp682Gly; p.Trp684Gly; p.Trp715Gly;	1	FALSE	chr8:38271806:A:C	167:chr8:38271806:A:C	0.003241
16_pro-1	16	PTEN	MODERATE	c.392C>A	p.Thr131Asn	2	FALSE	chr10:89692908:C:A	167:chr10:89692908:C:A	0.002317
16_pro-1	16	RET	MODERATE	c.1690A>C	p.Thr564Pro	1	FALSE	chr10:43608342:A:C	167:chr10:43608342:A:C	0.00321

45_bl-2	45	CDH1	HIGH	c.1792C>T	p.Arg598*	0	FALSE	chr16:68855984:C:T	169:chr16:68855984:C:T	0.001318
45_bl-2	45	NTRK2	MODERATE	c.770C>T	p.Ser257Phe	0	FALSE	chr9:87339188:C:T	169:chr9:87339188:C:T	0.001503
45_bl-2	45	PDGFRA	MODERATE	c.2465G>A	p.Arg822His	3	FALSE	chr4:55152033:G:A	169:chr4:55152033:G:A	0.001642
45_bl-2	45	FLT3	MODERATE	c.1160G>A	p.Arg387Gln	0	FALSE	chr13:28622457:C:T	169:chr13:28622457:C:T	0.002915
45_bl-2	45	NTRK1	MODERATE	c.821C>T; c.911C>T	p.Ser274Phe; p.Ser304Phe	1	FALSE	chr1:156843485:C:T	169:chr1:156843485:C:T	0.001762
45_bl-2	45	MET	MODERATE	c.2980G>A; c.3034G>A	p.Glu994Lys; p.Glu1012Lys	1	FALSE	chr7:116411995:G:A	169:chr7:116411995:G:A	0.001449
45_bl-2	45	PDGFRA	MODERATE	c.685G>A	p.Glu229Lys	3	FALSE	chr4:55131142:G:A	169:chr4:55131142:G:A	0.001335
45_bl-2	45	NF1	HIGH	c.5817C>A; c.5880C>A	p.Cys1939*; p.Cys1960*	1	FALSE	chr17:29661923:C:A	169:chr17:29661923:C:A	0.001787
45_bl-2	45	NF1	MODERATE	c.7381G>A; c.7444G>A	p.Asp2461Asn; p.Asp2482Asn	1	FALSE	chr17:29677323:G:A	169:chr17:29677323:G:A	0.001729
45_bl-2	45	NTRK2	MODERATE	c.2023C>T; c.2071C>T	p.Arg675Cys; p.Arg691Cys	0	FALSE	chr9:87570331:C:T	169:chr9:87570331:C:T	0.001699
45_bl-2	45	TSC1	MODERATE	c.2272G>A; c.2422G>A; c.2425G>A	p.Glu758Lys; p.Glu808Lys; p.Glu809Lys	0	FALSE	chr9:135777053:C:T	169:chr9:135777053:C:T	0.002055
45_bl-2	45	NTRK3	MODERATE	c.1368G>A; c.1392G>A	p.Met456Ile; p.Met464Ile	0	FALSE	chr15:88669506:C:T	169:chr15:88669506:C:T	0.001661
45_bl-2	45	ROS1	MODERATE	c.5920G>A	p.Glu1974Lys	1	FALSE	chr6:117641051:C:T	169:chr6:117641051:C:T	0.001695
45_bl-2	45	PIK3CA	MODERATE	c.3142C>T	p.His1048Tyr	2	FALSE	chr3:178952087:C:T	169:chr3:178952087:C:T	0.002216
45_bl-2	45	RET	MODERATE	c.1894G>A	p.Glu632Lys	1	FALSE	chr10:43609942:G:A	169:chr10:43609942:G:A	0.001279
45_bl-2	45	HOXD-AS2; HOXD8	MODIFIER; MODERATE	n.*692C>T; c.304G>A; c.853G>A; c.856G>A	; p.Glu102Lys; p.Glu285Lys; p.Glu286Lys	0	FALSE	chr2:176996323:G:A	169:chr2:176996323:G:A	0.00132

45_bl-2	45	ERBB2; MIEN1; MIR4728	MODIFIER; MODERATE	c.3160-319G>A; c.3145G>A; c.3190G>A; c.3235G>A; n.3559G>A; c.*388C>T; n.*67G>A	; p.Glu1049Lys; p.Glu1064Lys; p.Glu1079Lys	1	FALSE	chr17:37883623:G:A	169:chr17:37883623:G:A	0.001759
45_bl-2	45	ATM	HIGH	c.3382C>T	p.Gln1128*	0	FALSE	chr11:108150315:C:T	169:chr11:108150315:C:T	0.001366
45_bl-2	45	KDR	MODERATE	c.3065G>A	p.Arg1022Gln	1	FALSE	chr4:55958788:C:T	169:chr4:55958788:C:T	0.001509
45_bl-2	45	APC	MODERATE	c.851G>A; c.905G>A	p.Arg284Gln; p.Arg302Gln	0	FALSE	chr5:112151262:G:A	169:chr5:112151262:G:A	0.0015
45_bl-2	45	ATM	HIGH	c.5188C>T	p.Arg1730*	0	FALSE	chr11:108172385:C:T	169:chr11:108172385:C:T	0.001847
45_bl-2	45	KDR	MODERATE	c.1168G>A	p.Glu390Lys	2	FALSE	chr4:55976657:C:T	169:chr4:55976657:C:T	0.002096
45_bl-2	45	ALK	MODERATE	c.3599C>T	p.Ala1200Val	2	FALSE	chr2:29443618:G:A	169:chr2:29443618:G:A	0.002667
45_bl-2	45	KIT	MODERATE	c.682G>A	p.Glu228Lys	1	FALSE	chr4:55565858:G:A	169:chr4:55565858:G:A	0.001684
45_bl-2	45	TP53	MODERATE	c.107A>G; c.26A>G; c.386A>G; c.503A>G	p.His36Arg; p.His9Arg; p.His129Arg; p.His168Arg	15	FALSE	chr17:7578427:T:C	169:chr17:7578427:T:C	0.001771
45_bl-2	45	NF1	MODIFIER; HIGH	c.*2165G>A; c.2088G>A	; p.Trp696*	1	FALSE	chr17:29553539:G:A	169:chr17:29553539:G:A	0.00239
45_bl-2	45	ATM	MODERATE	c.7328G>A	p.Arg2443Gln	0	FALSE	chr11:108200961:G:A	169:chr11:108200961:G:A	0.002974
45_bl-2	45	PIK3CA	MODERATE	c.3133G>A	p.Asp1045Asn	6	FALSE	chr3:178952078:G:A	169:chr3:178952078:G:A	0.00142
45_bl-2	45	TP53	MODIFIER; MODERATE	c.-5G>T; c.356G>T; c.473G>T; c.77G>T	; p.Arg119Leu; p.Arg158Leu; ; p.Arg26Leu	80	FALSE	chr17:7578457:C:A	169:chr17:7578457:C:A	0.001808

45_bl-2	45	TP53	MODERATE	c.298G>A; c.379G>A; c.658G>A; c.775G>A	p.Asp100Asn; p.Asp127Asn; p.Asp220Asn; p.Asp259Asn	23	FALSE	chr17:7577506:C:T	169:chr17:7577506:C:T	0.001597
45_bl-2	45	ATM	MODERATE	c.743G>A	p.Arg248Gln	0	FALSE	chr11:108115595:G:A	169:chr11:108115595:G:A	0.001343
45_bl-2	45	NF1	MODERATE	c.1319G>A	p.Arg440Gln	1	FALSE	chr17:29533316:G:A	169:chr17:29533316:G:A	0.002412
45_bl-2	45	EGFR	MODERATE	c.844G>A	p.Glu282Lys	1	FALSE	chr7:55221800:G:A	169:chr7:55221800:G:A	0.001552
45_bl-2	45	NTRK1	MODERATE	c.1129G>A; c.1219G>A; c.1237G>A	p.Glu377Lys; p.Glu407Lys; p.Glu413Lys	1	FALSE	chr1:156844404:G:A	169:chr1:156844404:G:A	0.002063
45_bl-2	45	CTNNB1	MODERATE	c.121A>T	p.Thr41Ser	0	FALSE	chr3:41266124:A:T	169:chr3:41266124:A:T	0.0015
45_bl-2	45	EGFR	MODERATE	c.988G>A	p.Glu330Lys	1	FALSE	chr7:55223621:G:A	169:chr7:55223621:G:A	0.002469
45_bl-2	45	NF1	HIGH	c.1318C>T	p.Arg440*	10	FALSE	chr17:29533315:C:T	169:chr17:29533315:C:T	0.003215
45_bl-2	45	ATM	HIGH	c.5623C>T	p.Arg1875*	0	FALSE	chr11:108175528:C:T	169:chr11:108175528:C:T	0.002593
45_bl-2	45	VHL	MODIFIER; MODERATE	c.341-3271C>T; c.343C>T	; p.His115Tyr	0	FALSE	chr3:10188200:C:T	169:chr3:10188200:C:T	0.001753
45_bl-2	45	EPHA3	MODERATE	c.2408C>T	p.Ser803Leu	0	FALSE	chr3:89498436:C:T	169:chr3:89498436:C:T	0.001546
45_bl-2	45	CTNNB1	MODERATE	c.1604G>A	p.Arg535Gln	0	FALSE	chr3:41275709:G:A	169:chr3:41275709:G:A	0.001641
45_bl-2	45	IGF1R	MODERATE	c.2380C>T	p.Arg794Trp	0	FALSE	chr15:99465555:C:T	169:chr15:99465555:C:T	0.001461
45_bl-2	45	ALK	MODERATE	c.1588G>A	p.Glu530Lys	1	FALSE	chr2:29541229:C:T	169:chr2:29541229:C:T	0.002708
45_bl-2	45	PDGFRA	MODERATE	c.421G>A	p.Glu141Lys	1	FALSE	chr4:55129887:G:A	169:chr4:55129887:G:A	0.001521
45_bl-2	45	MAP2K1	MODERATE	c.140G>A	p.Arg47Gln	4	FALSE	chr15:66727424:G:A	169:chr15:66727424:G:A	0.001457

45_bl-2	45	TP53	MODERATE	c.367C>T; c.448C>T; c.727C>T; c.844C>T	p.Arg123Trp; p.Arg150Trp; p.Arg243Trp; p.Arg282Trp	479	FALSE	chr17:7577094:G:A	169:chr17:7577094:G:A	0.005824
45_bl-2	45	NF1	MODERATE	c.1247G>A	p.Arg416Gln	1	FALSE	chr17:29528490:G:A	169:chr17:29528490:G:A	0.002051
45_bl-2	45	FGFR2	MODIFIER; MODERATE	c.110-13073G>A; n.757-13073G>A; c.157G>A; c.424G>A	; p.Asp53Asn; p.Asp142Asn	1	FALSE	chr10:123324046:C:T	169:chr10:123324046:C:T	0.001676
45_bl-2	45	NTRK3	MODERATE	c.1351C>T; c.1375C>T	p.Arg451Trp; p.Arg459Trp	0	FALSE	chr15:88669523:G:A	169:chr15:88669523:G:A	0.001574
45_bl-2	45	FBXW7	MODERATE	c.1204G>A; c.1318G>A; c.1558G>A	p.Asp402Asn; p.Asp440Asn; p.Asp520Asn	0	FALSE	chr4:153247244:C:T	169:chr4:153247244:C:T	0.001409
45_bl-2	45	TP53	MODIFIER; MODERATE	c.-9G>T; c.352G>T; c.469G>T; c.73G>T	; p.Val118Phe; p.Val157Phe; p.Val25Phe	169	FALSE	chr17:7578461:C:A	169:chr17:7578461:C:A	0.001781
45_bl-2	45	SMO	MODERATE	c.1045A>C	p.Thr349Pro	0	FALSE	chr7:128846115:A:C	169:chr7:128846115:A:C	0.001419
45_bl-2	45	CWH43	MODERATE	c.1907G>A; c.1988G>A	p.Arg636Lys; p.Arg663Lys	0	FALSE	chr4:49052833:G:A	169:chr4:49052833:G:A	0.001935
45_bl-2	45	DDR2	HIGH	c.2258G>A	p.Trp753*	1	FALSE	chr1:162746135:G:A	169:chr1:162746135:G:A	0.001939
45_bl-2	45	TP53	MODERATE	c.128G>T; c.209G>T; c.488G>T; c.605G>T	p.Arg43Leu; p.Arg70Leu; p.Arg163Leu; p.Arg202Leu	4	FALSE	chr17:7578244:C:A	169:chr17:7578244:C:A	0.001718
45_bl-2	45	CWH43	MODERATE	c.1972G>A; c.2053G>A	p.Glu658Lys; p.Glu685Lys	0	FALSE	chr4:49063860:G:A	169:chr4:49063860:G:A	0.001629
45_bl-2	45	EPHA3	MODERATE	c.2288C>T	p.Ser763Phe	0	FALSE	chr3:89480451:C:T	169:chr3:89480451:C:T	0.001466

45_bl-2	45	BRAF	MODERATE	c.1394C>T	p.Ser465Phe	1	FALSE	chr7:140481414:G:A	169:chr7:140481414:G:A	0.001496
45_bl-2	45	CWH43	MODERATE	c.1273C>T; c.1354C>T	p.His425Tyr; p.His452Tyr	0	FALSE	chr4:49030733:C:T	169:chr4:49030733:C:T	0.001504
45_bl-2	45	NF1	MODERATE	c.5692G>A; c.5755G>A	p.Glu1898Lys; p.Glu1919Lys	1	FALSE	chr17:29657459:G:A	169:chr17:29657459:G:A	0.001577
45_bl-2	45	MITF	MODERATE	c.130C>T; c.175C>T; c.178C>T; c.22C>T	p.Arg44Cys; p.Arg59Cys; p.Arg60Cys; p.Arg8Cys	0	FALSE	chr3:69928358:C:T	169:chr3:69928358:C:T	0.001471
45_bl-2	45	KDR	MODERATE	c.3311C>T	p.Ser1104Phe	1	FALSE	chr4:55955634:G:A	169:chr4:55955634:G:A	0.001516
45_bl-2	45	NRAS	MODERATE	c.317C>T	p.Ser106Leu	1	FALSE	chr1:115252323:G:A	169:chr1:115252323:G:A	0.002555
45_bl-2	45	IGF1R	MODERATE	c.3821G>A; c.3824G>A	p.Arg1274Gln; p.Arg1275Gln	0	FALSE	chr15:99500391:G:A	169:chr15:99500391:G:A	0.001536
45_bl-2	45	NF1	MODERATE	c.859G>A	p.Asp287Asn	1	FALSE	chr17:29509654:G:A	169:chr17:29509654:G:A	0.001682
45_bl-2	45	KIT	MODERATE	c.1156G>A	p.Glu386Lys	1	FALSE	chr4:55575630:G:A	169:chr4:55575630:G:A	0.002264
45_bl-2	45	ALK	MODERATE	c.1801C>T	p.Leu601Phe	1	FALSE	chr2:29519770:G:A	169:chr2:29519770:G:A	0.00137
45_bl-2	45	ROS1	MODERATE	c.5782C>T	p.Leu1928Phe	1	FALSE	chr6:117641189:G:A	169:chr6:117641189:G:A	0.002408
45_bl-2	45	FGFR3	MODIFIER; MODERATE	c.931-432G>A; c.1138G>A; c.1144G>A	; p.Gly380Arg; p.Gly382Arg	13	FALSE	chr4:1806119:G:A	169:chr4:1806119:G:A	0.001947
45_bl-2	45	PTEN	MODERATE	c.1123G>A	p.Asp375Asn	3	FALSE	chr10:89725140:G:A	169:chr10:89725140:G:A	0.002516
45_bl-2	45	KDR	MODERATE	c.3062C>T	p.Ser1021Leu	1	FALSE	chr4:55958791:G:A	169:chr4:55958791:G:A	0.001497
45_bl-2	45	KIT	MODERATE	c.1726C>T; c.1738C>T	p.His576Tyr; p.His580Tyr	2	FALSE	chr4:55593672:C:T	169:chr4:55593672:C:T	0.002147
45_bl-2	45	NF1	MODERATE	c.1339C>T	p.Leu447Phe	1	FALSE	chr17:29533336:C:T	169:chr17:29533336:C:T	0.001781
45_bl-2	45	RET	MODERATE	c.1690A>C	p.Thr564Pro	1	FALSE	chr10:43608342:A:C	169:chr10:43608342:A:C	0.00148

45_bl-2	45	ATM	MODERATE	c.1010G>A	p.Arg337His	0	FALSE	chr11:108117799:G:A	169:chr11:108117799:G:A	0.001345
45_bl-2	45	KIT	MODERATE	c.1669G>A; c.1681G>A	p.Glu557Lys; p.Glu561Lys	6	FALSE	chr4:55593615:G:A	169:chr4:55593615:G:A	0.001635
45_bl-2	45	PIK3CA	MODERATE	c.772G>A	p.Asp258Asn	1	FALSE	chr3:178919287:G:A	169:chr3:178919287:G:A	0.001451
45_bl-2	45	PTEN	MODERATE	c.295G>A	p.Glu99Lys	3	FALSE	chr10:89692811:G:A	169:chr10:89692811:G:A	0.001667
45_bl-2	45	FBXW7	HIGH	c.1081C>T; c.1195C>T; c.1435C>T	p.Arg361*; p.Arg399*; p.Arg479*	0	FALSE	chr4:153247367:G:A	169:chr4:153247367:G:A	0.001262
45_bl-2	45	PIK3CA	MODERATE	c.277C>T	p.Arg93Trp	24	FALSE	chr3:178916890:C:T	169:chr3:178916890:C:T	0.002608
45_bl-2	45	PTEN	MODERATE	c.850G>A	p.Glu284Lys	2	FALSE	chr10:89720699:G:A	169:chr10:89720699:G:A	0.002827
45_bl-2	45	PIK3CA	MODERATE	c.2209G>A	p.Glu737Lys	1	FALSE	chr3:178941890:G:A	169:chr3:178941890:G:A	0.001439
45_bl-2	45	NF1	MODIFIER; HIGH	c.*2165G>A; c.2087G>A	; p.Trp696*	2	FALSE	chr17:29553538:G:A	169:chr17:29553538:G:A	0.003115
45_bl-2	45	IGF1R	MODERATE	c.3934T>C; c.3937T>C	p.Ser1312Pro; p.Ser1313Pro	0	FALSE	chr15:99500504:T:C	169:chr15:99500504:T:C	0.006359
47_bl-1	47	MITF	MODIFIER; MODERATE	c.93+115G>A; c.208G>A; c.373G>A; c.481G>A; c.526G>A; c.529G>A	; p.Ala70Thr; p.Ala125Thr; p.Ala161Thr; p.Ala176Thr; p.Ala177Thr	0	FALSE	chr3:69987147:G:A	170:chr3:69987147:G:A	0.001154
47_bl-1	47	ATM	HIGH	c.1262C>A	p.Ser421*	0	FALSE	chr11:108121454:C:A	170:chr11:108121454:C:A	0.001142
47_bl-1	47	KIT	MODERATE	c.1949T>C; c.1961T>C	p.Val650Ala; p.Val654Ala	23	FALSE	chr4:55594258:T:C	170:chr4:55594258:T:C	0.001225
47_bl-1	47	KDR	MODERATE	c.583G>T	p.Ala195Ser	1	FALSE	chr4:55981116:C:A	170:chr4:55981116:C:A	0.000976
47_bl-1	47	SMO	MODERATE	c.1045A>C	p.Thr349Pro	0	FALSE	chr7:128846115:A:C	170:chr7:128846115:A:C	0.006407

47_bl-1	47	ALK	MODERATE	c.2629G>T	p.Ala877Ser	1	FALSE	chr2:29455173:C:A	170:chr2:29455173:C:A	0.001343
47_bl-1	47	FGFR1	MODERATE	c.475C>T; c.481C>T; c.724C>T; c.742C>T; c.748C>T; c.841C>T	p.Arg159Trp; p.Arg161Trp; p.Arg242Trp; p.Arg248Trp; p.Arg250Trp; p.Arg281Trp	2	FALSE	chr8:38282215:G:A	170:chr8:38282215:G:A	0.001383
47_bl-1	47	TP53	HIGH	c.376G>T; c.457G>T; c.736G>T; c.853G>T	p.Glu126*; p.Glu153*; p.Glu246*; p.Glu285*	118	FALSE	chr17:7577085:C:A	170:chr17:7577085:C:A	0.152016
47_bl-1	47	PDGFRA	MODERATE	c.1516C>A	p.Leu506Ile	2	FALSE	chr4:55139855:C:A	170:chr4:55139855:C:A	0.001198
47_bl-1	47	SMO	MODERATE	c.628G>A	p.Val210Met	0	FALSE	chr7:128845134:G:A	170:chr7:128845134:G:A	0.001445
47_bl-1	47	AKT3	MODERATE	c.44G>T	p.Arg15Met	0	FALSE	chr1:244006429:C:A	170:chr1:244006429:C:A	0.00114
47_bl-1	47	TP53	MODIFIER; MODERATE	c.-5G>T; c.356G>T; c.473G>T; c.77G>T	; p.Arg119Leu; p.Arg158Leu; p.Arg26Leu	80	FALSE	chr17:7578457:C:A	170:chr17:7578457:C:A	0.001516
47_bl-1	47	CTNNB1	MODERATE	c.125C>A	p.Thr42Lys	0	FALSE	chr3:41266128:C:A	170:chr3:41266128:C:A	0.00109
47_bl-1	47	PIK3CA	MODERATE	c.892C>A	p.Pro298Thr	1	FALSE	chr3:178921410:C:A	170:chr3:178921410:C:A	0.000924
47_bl-1	47	DEAR; FBXW7	MODIFIER; HIGH	n.108G>A; c.475C>T; c.589C>T; c.829C>T	; p.Gln159*; p.Gln197*; p.Gln277*	0	FALSE	chr4:153258986:G:A	170:chr4:153258986:G:A	0.001161
47_bl-1	47	FGFR3	MODERATE	c.742C>T	p.Arg248Cys	254	FALSE	chr4:1803564:C:T	170:chr4:1803564:C:T	0.006831
47_bl-1	47	CTNNB1	MODERATE	c.98C>A	p.Ser33Tyr	0	FALSE	chr3:41266101:C:A	170:chr3:41266101:C:A	0.001623

47_bl-1	47	FGFR2	MODERATE; MODIFIER	c.1002G>T; c.1071G>T; c.1074G>T; c.1338G>T; c.1341G>T; c.987G>T; c.990G>T; c.993G>T; n.1788G>T	p.Arg334Ser; p.Arg357Ser; p.Arg358Ser; p.Arg446Ser; p.Arg447Ser; p.Arg329Ser; p.Arg330Ser; p.Arg331Ser;	1	FALSE	chr10:123263405:C:A	170:chr10:123263405:C:A	0.001878
47_bl-1	47	PIK3CA	MODERATE	c.1645G>A	p.Asp549Asn	4	FALSE	chr3:178936103:G:A	170:chr3:178936103:G:A	0.001019
47_bl-1	47	NTRK3	MODERATE	c.1459G>T; c.1483G>T	p.Asp487Tyr; p.Asp495Tyr	0	FALSE	chr15:88576190:C:A	170:chr15:88576190:C:A	0.001403
47_bl-1	47	FGFR2	MODERATE; MODIFIER	c.1073A>G; c.1076A>G; c.1079A>G; c.1088A>G; c.1157A>G; c.1160A>G; c.1424A>G; c.1427A>G; n.1874A>G	p.Glu358Gly; p.Glu359Gly; p.Glu360Gly; p.Glu363Gly; p.Glu386Gly; p.Glu387Gly; p.Glu475Gly; p.Glu476Gly;	2	FALSE	chr10:123263319:T:C	170:chr10:123263319:T:C	0.00207
47_bl-1	47	ALK	MODERATE	c.446C>T	p.Ala149Val	1	FALSE	chr2:30143080:G:A	170:chr2:30143080:G:A	0.001479
47_bl-1	47	NF1	HIGH	c.4006C>T	p.Gln1336*	1	FALSE	chr17:29576033:C:T	170:chr17:29576033:C:T	0.000999
47_bl-1	47	NTRK1	MODERATE	c.1246C>T; c.1336C>T; c.1354C>T	p.Arg416Cys; p.Arg446Cys; p.Arg452Cys	1	FALSE	chr1:156844800:C:T	170:chr1:156844800:C:T	0.001379

47_bl-1	47	FGFR2	MODERATE; MODIFIER	c.1486G>A; c.1489G>A; c.1492G>A; c.1501G>A; c.1570G>A; c.1573G>A; c.1837G>A; c.1840G>A; n.2287G>A	p.Gly496Ser; p.Gly497Ser; p.Gly498Ser; p.Gly501Ser; p.Gly524Ser; p.Gly525Ser; p.Gly613Ser; p.Gly614Ser;	2	FALSE	chr10:123256072:C:T	170:chr10:123256072:C:T	0.001168
47_bl-1	47	SMO	MODERATE	c.1640G>A	p.Arg547His	0	FALSE	chr7:128850377:G:A	170:chr7:128850377:G:A	0.001267
47_bl-1	47	IGF1R	MODERATE	c.3934T>C; c.3937T>C	p.Ser1312Pro; p.Ser1313Pro	0	FALSE	chr15:99500504:T:C	170:chr15:99500504:T:C	0.014393
47_bl-1	47	STK11	MODERATE	c.628T>C	p.Cys210Arg	1	FALSE	chr19:1220610:T:C	170:chr19:1220610:T:C	0.002188
47_bl-1	47	IGF1R	MODERATE	c.3905T>C; c.3908T>C	p.Val1302Ala; p.Val1303Ala	0	FALSE	chr15:99500475:T:C	170:chr15:99500475:T:C	0.003894
47_bl-1	47	PKD1; TSC2	MODIFIER; MODERATE	c.*13118G>A; c.*13121G>A; c.3935C>T; c.4067C>T; c.4136C>T	; p.Ser1312Leu; p.Ser1356Leu; p.Ser1379Leu	0	FALSE	chr16:2134359:C:T	170:chr16:2134359:C:T	0.001181
47_bl-1	47	DDR2	MODERATE	c.1963G>A	p.Glu655Lys	1	FALSE	chr1:162745548:G:A	170:chr1:162745548:G:A	0.001636
47_bl-1	47	PTEN	MODERATE	c.860C>T	p.Ser287Leu	3	FALSE	chr10:89720709:C:T	170:chr10:89720709:C:T	0.001145
47_bl-1	47	PIK3CA	MODERATE	c.478C>A	p.His160Asn	1	FALSE	chr3:178917603:C:A	170:chr3:178917603:C:A	0.000913
47_bl-1	47	TP53	MODIFIER; MODERATE	c.*145T>C; c.*233T>C; c.1009T>C; c.1126T>C; c.649T>C; c.730T>C	; p.Ser337Pro; p.Ser376Pro; p.Ser217Pro; p.Ser244Pro	2	FALSE	chr17:7572983:A:G	170:chr17:7572983:A:G	0.001947

47_bl-1	47	TP53	MODERATE; MODIFIER	c.115G>T; c.232G>T; c.-279G>T; c.-360G>T	p.Ala39Ser; p.Ala78Ser;	1	FALSE	chr17:7579455:C:A	170:chr17:7579455:C:A	0.001504
47_bl-1	47	C9orf53; CDKN2A	MODIFIER; MODERATE; LOW	n.*616T>G; c.*120A>C; c.197A>C; c.240A>C	; p.His66Pro; p.Pro80Pro	1	FALSE	chr9:21971161:T:G	170:chr9:21971161:T:G	0.040062
47_bl-1	47	HGF	HIGH	c.1993G>T; c.2008G>T	p.Glu665*; p.Glu670*	0	FALSE	chr7:81334708:C:A	170:chr7:81334708:C:A	0.00106
47_bl-1	47	TP53	MODIFIER; MODERATE	c.*137A>G; c.*225A>G; c.1001A>G; c.1118A>G; c.641A>G; c.722A>G	; p.Lys334Arg; p.Lys373Arg; p.Lys214Arg; p.Lys241Arg	1	FALSE	chr17:7572991:T:C	170:chr17:7572991:T:C	0.001857
47_bl-1	47	TSC2	MODIFIER; MODERATE	c.2837+1108G>A; c.2933G>A	; p.Arg978His	0	FALSE	chr16:2127694:G:A	170:chr16:2127694:G:A	0.001843
47_bl-1	47	RET	MODERATE	c.1690A>C	p.Thr564Pro	1	FALSE	chr10:43608342:A:C	170:chr10:43608342:A:C	0.005088
47_bl-1	47	ESR1	MODERATE	c.1019C>T; c.1022C>T; c.1028C>T	p.Ser340Leu; p.Ser341Leu; p.Ser343Leu	0	FALSE	chr6:152265569:C:T	170:chr6:152265569:C:T	0.001188
47_bl-1	47	FGFR2	MODIFIER; MODERATE	c.939+4699A>G; c.1124A>G; c.1127A>G; c.779A>G; c.788A>G; c.857A>G; c.860A>G; n.1574A>G	; p.Tyr375Cys; p.Tyr376Cys; p.Tyr260Cys; p.Tyr263Cys; p.Tyr286Cys; p.Tyr287Cys	9	FALSE	chr10:123274794:T:C	170:chr10:123274794:T:C	0.001024

47_bl-1	47	PIK3CA	MODERATE	c.1255C>A	p.His419Asn	1	FALSE	chr3:178927977:C:A	170:chr3:178927977:C:A	0.001465
33_bl-2	33	MIR4673; NOTCH1	MODIFIER; MODERATE	n.*59G>T; c.1343G>T	; p.Arg448Leu	0	FALSE	chr9:139412302:C:A	171:chr9:139412302:C:A	0.001855
33_bl-2	33	HOXD-AS2; HOXD8	MODIFIER; MODERATE	n.*692C>T; c.304G>A; c.853G>A; c.856G>A	; p.Glu102Lys; p.Glu285Lys; p.Glu286Lys	0	FALSE	chr2:176996323:G:A	171:chr2:176996323:G:A	0.001155
33_bl-2	33	HGF	MODERATE	c.251G>T	p.Cys84Phe	0	FALSE	chr7:81392026:C:A	171:chr7:81392026:C:A	0.001527
33_bl-2	33	FGFR1	MODERATE	c.1424A>G; c.1430A>G; c.1667A>G; c.1691A>G; c.1697A>G; c.1790A>G	p.Lys475Arg; p.Lys477Arg; p.Lys556Arg; p.Lys564Arg; p.Lys566Arg; p.Lys597Arg	1	FALSE	chr8:38273545:T:C	171:chr8:38273545:T:C	0.002757
33_bl-2	33	NTRK1	MODERATE	c.1940T>G; c.2030T>G; c.2048T>G	p.Val647Gly; p.Val677Gly; p.Val683Gly	2	FALSE	chr1:156849792:T:G	171:chr1:156849792:T:G	0.017505
33_bl-2	33	EGFR	MODIFIER; MODERATE	c.*2133C>A; c.*2364C>A; c.1922C>A	; p.Pro641His	1	FALSE	chr7:55240678:C:A	171:chr7:55240678:C:A	0.002064
33_bl-2	33	TP53	MODERATE	c.337G>T; c.418G>T; c.697G>T; c.814G>T	p.Val113Leu; p.Val140Leu; p.Val233Leu; p.Val272Leu	85	FALSE	chr17:7577124:C:A	171:chr17:7577124:C:A	0.001332
33_bl-2	33	FGFR3	MODERATE	c.1177G>A; c.1513G>A; c.1519G>A	p.Val393Ile; p.Val505Ile; p.Val507Ile	1	FALSE	chr4:1807182:G:A	171:chr4:1807182:G:A	0.001556
33_bl-2	33	RET	MODERATE	c.2161C>T	p.Arg721Trp	1	FALSE	chr10:43612056:C:T	171:chr10:43612056:C:T	0.00125

33_bl-2	33	TP53	LOW; MODIFIER; MODERATE	c.-2A>T; c.-83A>T; c.278A>T; c.395A>T	; p.Lys93Met; p.Lys132Met	42	FALSE	chr17:7578535:T:A	171:chr17:7578535:T:A	0.044816
33_bl-2	33	TSC1	MODERATE	c.457C>T; c.610C>T	p.Arg153Cys; p.Arg204Cys	0	FALSE	chr9:135797259:G:A	171:chr9:135797259:G:A	0.001263
33_bl-2	33	KRAS	HIGH	c.292G>T	p.Glu98*	1	FALSE	chr12:25378706:C:A	171:chr12:25378706:C:A	0.002013
33_bl-2	33	INSRR; NTRK1	MODIFIER; MODERATE	c.3397+13C>T; c.28G>A	; p.Ala10Thr	1	FALSE	chr1:156811891:G:A	171:chr1:156811891:G:A	0.001721
33_bl-2	33	PHLPP1	MODERATE	c.1753C>A	p.Leu585Met	0	FALSE	chr18:60497444:C:A	171:chr18:60497444:C:A	0.001165
33_bl-2	33	C9orf53; CDKN2A	MODIFIER; MODERATE; LOW	n.*616T>G; c.*120A>C; c.197A>C; c.240A>C	; p.His66Pro; p.Pro80Pro	1	FALSE	chr9:21971161:T:G	171:chr9:21971161:T:G	0.03753
33_bl-2	33	NTRK3	MODERATE	c.1744G>A; c.1768G>A	p.Glu582Lys; p.Glu590Lys	0	FALSE	chr15:88476364:C:T	171:chr15:88476364:C:T	0.0016
33_bl-2	33	CTNNB1	MODERATE	c.1000G>A	p.Glu334Lys	0	FALSE	chr3:41268762:G:A	171:chr3:41268762:G:A	0.001035
33_bl-2	33	FGFR3	MODIFIER; MODERATE	c.931-398C>A; c.1172C>A; c.1178C>A	; p.Ala391Glu; p.Ala393Glu	34	FALSE	chr4:1806153:C:A	171:chr4:1806153:C:A	0.001712
33_bl-2	33	TP53	MODERATE	c.141T>A; c.420T>A; c.537T>A; c.60T>A	p.His47Gln; p.His140Gln; p.His179Gln; p.His20Gln	17	FALSE	chr17:7578393:A:T	171:chr17:7578393:A:T	0.005952
33_bl-2	33	GAPDH; IFFO1	MODERATE; MODIFIER	c.217G>A; c.343G>A; c.*1743C>T; c.*1746C>T; c.*1770C>T; n.*2798C>T	p.Gly73Arg; p.Gly115Arg;	0	FALSE	chr12:6646282:G:A	171:chr12:6646282:G:A	0.001594
33_bl-2	33	MET	HIGH	c.1639C>T	p.Arg547*	2	FALSE	chr7:116381017:C:T	171:chr7:116381017:C:T	0.001536

33_bl-2	33	TP53	MODERATE	c.128G>T; c.209G>T; c.488G>T; c.605G>T	p.Arg43Leu; p.Arg70Leu; p.Arg163Leu; p.Arg202Leu	4	FALSE	chr17:7578244:C:A	171:chr17:7578244:C:A	0.001314
33_bl-2	33	PDGFRA	MODERATE	c.1499G>A	p.Arg500Gln	1	FALSE	chr4:55139838:G:A	171:chr4:55139838:G:A	0.001325
33_bl-2	33	NTRK3	MODERATE	c.1463C>T; c.1487C>T	p.Ala488Val; p.Ala496Val	0	FALSE	chr15:88576186:G:A	171:chr15:88576186:G:A	0.001619
33_bl-2	33	SMO	MODERATE	c.1045A>C	p.Thr349Pro	0	FALSE	chr7:128846115:A:C	171:chr7:128846115:A:C	0.007792
33_bl-2	33	BRAF	MODERATE	c.1799T>A	p.Val600Glu	23024	FALSE	chr7:140453136:A:T	171:chr7:140453136:A:T	0.024465
33_bl-2	33	RET	MODERATE	c.1690A>C	p.Thr564Pro	1	FALSE	chr10:43608342:A:C	171:chr10:43608342:A:C	0.007727
33_bl-2	33	EGFR	MODERATE	c.844G>A	p.Glu282Lys	1	FALSE	chr7:55221800:G:A	171:chr7:55221800:G:A	0.001241
33_bl-2	33	MIR4673; NOTCH1	MODIFIER; MODERATE	n.-1G>A; c.475G>A	; p.Glu159Lys	0	FALSE	chr9:139417569:C:T	171:chr9:139417569:C:T	0.00173
33_bl-2	33	NOTCH1	MODERATE	c.5257G>T	p.Gly1753Trp	0	FALSE	chr9:139396851:C:A	171:chr9:139396851:C:A	0.003546
33_bl-2	33	FBXW7	MODERATE	c.1078G>T; c.1318G>T; c.964G>T	p.Asp360Tyr; p.Asp440Tyr; p.Asp322Tyr	0	FALSE	chr4:153249460:C:A	171:chr4:153249460:C:A	0.001194
33_bl-2	33	ALK	MODERATE	c.2629G>T	p.Ala877Ser	1	FALSE	chr2:29455173:C:A	171:chr2:29455173:C:A	0.001494
33_bl-2	33	PIK3CA	MODERATE	c.518C>A	p.Ser173Tyr	1	FALSE	chr3:178917643:C:A	171:chr3:178917643:C:A	0.00104
33_bl-2	33	BRAF	MODERATE	c.1781A>G	p.Asp594Gly	59	FALSE	chr7:140453154:T:C	171:chr7:140453154:T:C	0.001264
33_bl-2	33	EPHA3	MODERATE	c.497C>A	p.Thr166Asn	0	FALSE	chr3:89259353:C:A	171:chr3:89259353:C:A	0.00114
33_bl-2	33	TP53	MODERATE	c.211A>G; c.292A>G; c.571A>G; c.688A>G	p.Thr71Ala; p.Thr98Ala; p.Thr191Ala; p.Thr230Ala	10	FALSE	chr17:7577593:T:C	171:chr17:7577593:T:C	0.001123

33_bl-2	33	TP53	MODIFIER; MODERATE	c.-9G>T; c.352G>T; c.469G>T; c.73G>T	; p.Val118Phe ; p.Val157Phe ; p.Val25Phe	169	FALSE	chr17:7578461:C:A	171:chr17:7578461:C:A	0.001444
33_bl-2	33	KIT	MODERATE	c.1156G>A	p.Glu386Lys	1	FALSE	chr4:55575630:G:A	171:chr4:55575630:G:A	0.001245
33_bl-2	33	FLT3	MODERATE	c.2678C>T	p.Pro893Leu	0	FALSE	chr13:28589369:G:A	171:chr13:28589369:G:A	0.001267
33_bl-2	33	CDKN2A; CDKN2B-AS1	MODERATE; MODIFIER	c.22A>G; n.-1T>C	p.Thr8Ala;	1	FALSE	chr9:21994309:T:C	171:chr9:21994309:T:C	0.003713
33_bl-2	33	KIT	MODERATE	c.1485C>A	p.Asn495Lys	1	FALSE	chr4:55592161:C:A	171:chr4:55592161:C:A	0.001305
33_bl-2	33	IGF1R	MODERATE	c.1511G>A	p.Arg504His	0	FALSE	chr15:99454592:G:A	171:chr15:99454592:G:A	0.00119
33_bl-2	33	CTNNB1	MODERATE	c.884C>A	p.Ala295Asp	0	FALSE	chr3:41267300:C:A	171:chr3:41267300:C:A	0.001215
33_bl-2	33	IGF1R	MODERATE	c.3905T>C; c.3908T>C	p.Val1302Ala; p.Val1303Ala	0	FALSE	chr15:99500475:T:C	171:chr15:99500475:T:C	0.007133
33_bl-2	33	PHLPP1	HIGH	c.3139C>T	p.Arg1047*	0	FALSE	chr18:60609129:C:T	171:chr18:60609129:C:T	0.001307
33_bl-2	33	C9orf53; CDKN2A	MODIFIER; MODERATE; LOW	n.*616A>G ; c.*114T>C; c.191T>C; c.234T>C	; p.Leu64Pro; p.Ala78Ala	1	FALSE	chr9:21971167:A:G	171:chr9:21971167:A:G	0.002372
33_bl-2	33	TP53	MODIFIER; MODERATE	c.*137A>G ; c.*225A>G ; c.1001A>G ; c.1118A>G ; c.641A>G; c.722A>G	; p.Lys334Arg ; p.Lys373Arg ; p.Lys214Arg ; p.Lys241Arg	1	FALSE	chr17:7572991:T:C	171:chr17:7572991:T:C	0.00282
46_bl-1	46	GNA11	MODERATE	c.440G>A	p.Arg147His	1	FALSE	chr19:3113446:G:A	172:chr19:3113446:G:A	0.001947
46_bl-1	46	FGFR4	MODERATE	c.1862C>T; c.1946C>T; c.2066C>T	p.Pro621Leu ; p.Pro649Leu ; p.Pro689Leu	1	FALSE	chr5:176523655:C:T	172:chr5:176523655:C:T	0.002203

46_bl-1	46	PTEN	HIGH	c.822G>A	p.Trp274*	3	FALSE	chr10:89720671:G:A	172:chr10:89720671:G:A	0.001541
46_bl-1	46	CDKN2A	MODIFIER; MODERATE	c.194-3567C>T; c.53C>T	; p.Thr18Met	1	FALSE	chr9:21974774:G:A	172:chr9:21974774:G:A	0.003378
46_bl-1	46	FBXW7	MODERATE	c.1081C>T; c.1321C>T; c.967C>T	p.Arg361Trp; p.Arg441Trp; p.Arg323Trp	0	FALSE	chr4:153249457:G:A	172:chr4:153249457:G:A	0.001773
46_bl-1	46	KRAS	MODERATE	c.35G>T	p.Gly12Val	11213	FALSE	chr12:25398284:C:A	172:chr12:25398284:C:A	0.00181
46_bl-1	46	TSC2	MODERATE	c.1654G>A	p.Ala552Thr	0	FALSE	chr16:2115574:G:A	172:chr16:2115574:G:A	0.00177
46_bl-1	46	TP53	MODIFIER; MODERATE	c.*137A>G; c.*225A>G; c.1001A>G; c.1118A>G; c.641A>G; c.722A>G	; p.Lys334Arg; p.Lys373Arg; p.Lys214Arg; p.Lys241Arg	1	FALSE	chr17:7572991:T:C	172:chr17:7572991:T:C	0.005181
46_bl-1	46	ATM	MODERATE	c.2075G>A	p.Arg692His	0	FALSE	chr11:108124717:G:A	172:chr11:108124717:G:A	0.001631
46_bl-1	46	RET	MODERATE	c.2116G>A	p.Val706Met	2	FALSE	chr10:43610164:G:A	172:chr10:43610164:G:A	0.001517
46_bl-1	46	KIT	MODERATE	c.2671G>A; c.2683G>A	p.Ala891Thr; p.Ala895Thr	3	FALSE	chr4:55602973:G:A	172:chr4:55602973:G:A	0.00153
46_bl-1	46	EGFR	MODERATE	c.755G>A	p.Arg252His	3	FALSE	chr7:55221711:G:A	172:chr7:55221711:G:A	0.001776
46_bl-1	46	EPHA3	MODERATE	c.686C>A	p.Ser229Tyr	0	FALSE	chr3:89259542:C:A	172:chr3:89259542:C:A	0.001736
46_bl-1	46	AKT3	MODERATE	c.797A>G	p.Lys266Arg	0	FALSE	chr1:243736250:T:C	172:chr1:243736250:T:C	0.002465
46_bl-1	46	PTEN	MODERATE	c.302T>C	p.Ile101Thr	8	FALSE	chr10:89692818:T:C	172:chr10:89692818:T:C	0.001947
46_bl-1	46	FGFR3	MODIFIER; MODERATE	c.931-374G>A; c.1196G>A; c.1202G>A	; p.Arg399His; p.Arg401His	1	FALSE	chr4:1806177:G:A	172:chr4:1806177:G:A	0.001934
46_bl-1	46	PDGFRA	MODERATE	c.2465G>A	p.Arg822His	3	FALSE	chr4:55152033:G:A	172:chr4:55152033:G:A	0.001732

48_bl-1	48	C9orf53; CDKN2A	MODIFIER; MODERATE; LOW	n.*616T>G; c.*120A>C; c.197A>C; c.240A>C	; p.His66Pro; p.Pro80Pro	1	FALSE	chr9:21971161:T:G	173:chr9:21971161:T:G	0.023438
48_bl-1	48	NF1	MODERATE	c.5302G>A; c.5365G>A	p.Glu1768Lys; p.Glu1789Lys	1	FALSE	chr17:29654613:G:A	173:chr17:29654613:G:A	0.001248
48_bl-1	48	ATM	MODERATE	c.2803A>G	p.Thr935Ala	0	FALSE	chr11:108139301:A:G	173:chr11:108139301:A:G	0.001259
48_bl-1	48	NF1	MODERATE	c.4321C>T; c.4384C>T	p.Arg1441Trp; p.Arg1462Trp	1	FALSE	chr17:29586101:C:T	173:chr17:29586101:C:T	0.001262
48_bl-1	48	APC	MODERATE	c.1171C>A; c.1225C>A	p.Leu391Ile; p.Leu409Ile	0	FALSE	chr5:112154954:C:A	173:chr5:112154954:C:A	0.001221
48_bl-1	48	EPHA3	MODERATE	c.2306G>A	p.Arg769His	0	FALSE	chr3:89480469:G:A	173:chr3:89480469:G:A	0.001288
48_bl-1	48	KDR	MODERATE	c.1040G>A	p.Arg347His	4	FALSE	chr4:55976872:C:T	173:chr4:55976872:C:T	0.001022
48_bl-1	48	PDGFRA	MODERATE	c.100G>A	p.Glu34Lys	1	FALSE	chr4:55127312:G:A	173:chr4:55127312:G:A	0.001271
48_bl-1	48	KDR	MODERATE	c.3760G>A	p.Asp1254Asn	1	FALSE	chr4:55948705:C:T	173:chr4:55948705:C:T	0.001385
48_bl-1	48	ERBB2; MIEN1; MIR4728	MODERATE; MODIFIER	c.2597G>A; c.2642G>A; c.2687G>A; n.3011G>A; c.*388C>T; n.-1G>A	p.Arg866His; p.Arg881His; p.Arg896His;	2	FALSE	chr17:37881617:G:A	173:chr17:37881617:G:A	0.001779
48_bl-1	48	CTNNB1	MODERATE	c.98C>A	p.Ser33Tyr	0	FALSE	chr3:41266101:C:A	173:chr3:41266101:C:A	0.001206
48_bl-1	48	PIK3CA	MODERATE	c.1612G>A	p.Asp538Asn	3	FALSE	chr3:178936070:G:A	173:chr3:178936070:G:A	0.001285
48_bl-1	48	FBXW7	MODERATE	c.1444G>T; c.1558G>T; c.1798G>T	p.Asp482Tyr; p.Asp520Tyr; p.Asp600Tyr	0	FALSE	chr4:153245393:C:A	173:chr4:153245393:C:A	0.001358
48_bl-1	48	NTRK3	MODERATE	c.446C>T	p.Thr149Met	0	FALSE	chr15:88690584:G:A	173:chr15:88690584:G:A	0.001639

48_bl-1	48	TSC2	MODERATE	c.1610G>A	p.Arg537His	0	FALSE	chr16:2115530:G:A	173:chr16:2115530:G:A	0.001281
48_bl-1	48	NF1	MODERATE	c.2695T>G	p.Leu899Val	3	FALSE	chr17:29556328:T:G	173:chr17:29556328:T:G	0.002651
48_bl-1	48	RET	MODERATE	c.1690A>C	p.Thr564Pro	1	FALSE	chr10:43608342:A:C	173:chr10:43608342:A:C	0.001352
48_bl-1	48	MAP2K2	MODERATE	c.169T>G	p.Phe57Val	0	FALSE	chr19:4117551:A:C	173:chr19:4117551:A:C	0.001446
48_bl-1	48	ALK	MODERATE	c.641G>A	p.Arg214His	1	FALSE	chr2:30142885:C:T	173:chr2:30142885:C:T	0.001942
48_bl-1	48	ROS1	MODERATE	c.5782C>T	p.Leu1928Phe	1	FALSE	chr6:117641189:G:A	173:chr6:117641189:G:A	0.001282
48_bl-1	48	TP53	MODIFIER; MODERATE	c.*137A>G; c.*225A>G; c.1001A>G; c.1118A>G; c.641A>G; c.722A>G	; p.Lys334Arg; p.Lys373Arg; p.Lys214Arg; p.Lys241Arg	1	FALSE	chr17:7572991:T:C	173:chr17:7572991:T:C	0.005703
48_bl-1	48	ERBB2	MODERATE; MODIFIER	c.1191C>A; c.1236C>A; c.1281C>A; n.1605C>A	p.Asn397Lys; p.Asn412Lys; p.Asn427Lys;	1	FALSE	chr17:37871757:C:A	173:chr17:37871757:C:A	0.001339
48_bl-1	48	EGFR	MODIFIER; MODERATE	c.*1464C>A; c.1476C>A	; p.Ser492Arg	4	FALSE	chr7:55228009:C:A	173:chr7:55228009:C:A	0.001254
48_bl-1	48	FBXW7	MODERATE	c.1159C>T; c.1273C>T; c.1513C>T	p.Arg387Cys; p.Arg425Cys; p.Arg505Cys	0	FALSE	chr4:153247289:G:A	173:chr4:153247289:G:A	0.001212
48_bl-1	48	FGFR3	MODIFIER; MODERATE	c.931-398C>A; c.1172C>A; c.1178C>A	; p.Ala391Glu; p.Ala393Glu	34	FALSE	chr4:1806153:C:A	173:chr4:1806153:C:A	0.002506
48_bl-1	48	ALK	MODERATE	c.886G>A	p.Glu296Lys	1	FALSE	chr2:29917782:C:T	173:chr2:29917782:C:T	0.001198

48_bl-1	48	FBXW7	HIGH	c.1027G>T; c.1267G>T; c.913G>T	p.Gly343*; p.Gly423*; p.Gly305*	0	FALSE	chr4:153249511:C:A	173:chr4:153249511:C:A	0.001321
48_bl-1	48	MAP2K1	MODERATE	c.145C>T	p.Arg49Cys	1	FALSE	chr15:66727429:C:T	173:chr15:66727429:C:T	0.001286
48_bl-1	48	ATM	MODERATE	c.743G>A	p.Arg248Gln	0	FALSE	chr11:108115595:G:A	173:chr11:108115595:G:A	0.00119
48_bl-1	48	NRAS	MODERATE	c.394G>A	p.Glu132Lys	2	FALSE	chr1:115252246:C:T	173:chr1:115252246:C:T	0.001783
49_bl-2	49	C9orf53; CDKN2A	MODIFIER; MODERATE; LOW	n.*616T>G; c.*120A>C; c.197A>C; c.240A>C	; p.His66Pro; p.Pro80Pro	1	FALSE	chr9:21971161:T:G	174:chr9:21971161:T:G	0.008114
49_bl-2	49	NF1	MODERATE	c.6405C>A; c.6468C>A	p.Phe2135Leu; p.Phe2156Leu	1	FALSE	chr17:29664426:C:A	174:chr17:29664426:C:A	0.0025
49_bl-2	49	IDH1	MODERATE	c.299G>T	p.Arg100Leu	5	FALSE	chr2:209113208:C:A	174:chr2:209113208:C:A	0.002509
49_bl-2	49	ATM	MODERATE	c.2803A>G	p.Thr935Ala	0	FALSE	chr11:108139301:A:G	174:chr11:108139301:A:G	0.002472
49_bl-2	49	SMO	MODERATE	c.1045A>C	p.Thr349Pro	0	FALSE	chr7:128846115:A:C	174:chr7:128846115:A:C	0.002323
49_bl-2	49	EGFR	MODERATE	c.406C>A	p.Pro136Thr	1	FALSE	chr7:55211163:C:A	174:chr7:55211163:C:A	0.002981
49_bl-2	49	KRAS	MODERATE	c.35G>A	p.Gly12Asp	11213	FALSE	chr12:25398284:C:T	174:chr12:25398284:C:T	0.010057
49_c2-b	49	C9orf53; CDKN2A	MODIFIER; MODERATE	n.*616C>G; c.*140G>C; c.217G>C; c.260G>C	; p.Ala73Pro; p.Arg87Pro	1	FALSE	chr9:21971141:C:G	175:chr9:21971141:C:G	0.056569

49_c2-b	49	CSDE1; NRAS	MODIFIER; MODERATE	c.*2430G>A; c.*2523G>A; c.*2817G>A; c.*2910G>A; c.*2964G>A; c.*3057G>A; c.52G>A	; p.Ala18Thr	13	TRUE	chr1:115258730:C:T	175:chr1:115258730:C:T	0.002401
49_c2-b	49	TP53	MODIFIER; MODERATE	c.*137A>G; c.*225A>G; c.1001A>G; c.1118A>G; c.641A>G; c.722A>G	; p.Lys334Arg; p.Lys373Arg; p.Lys214Arg; p.Lys241Arg	1	FALSE	chr17:7572991:T:C	175:chr17:7572991:T:C	0.003241
49_c2-b	49	FGFR1	LOW; MODIFIER; MODERATE	c.-25C>T; c.167C>T; c.68C>T	; p.Pro56Leu; p.Pro23Leu	1	FALSE	chr8:38314897:G:A	175:chr8:38314897:G:A	0.001852
49_c2-b	49	C9orf53; CDKN2A	MODIFIER; MODERATE; LOW	n.*616T>G; c.*120A>C; c.197A>C; c.240A>C	; p.His66Pro; p.Pro80Pro	1	FALSE	chr9:21971161:T:G	175:chr9:21971161:T:G	0.021944
49_c2-b	49	EGFR; EGFR-AS1	MODIFIER; MODERATE	c.*2364G>A; c.2281G>A; n.*2821C>T	; p.Asp761Asn	4	FALSE	chr7:55242511:G:A	175:chr7:55242511:G:A	0.002174
49_c2-b	49	EPHA3	MODERATE	c.2306G>A	p.Arg769His	0	FALSE	chr3:89480469:G:A	175:chr3:89480469:G:A	0.004592
49_c2-b	49	NOTCH1	MODERATE	c.4252G>A	p.Ala1418Thr	0	FALSE	chr9:139400096:C:T	175:chr9:139400096:C:T	0.003836
49_c2-b	49	PIK3CA	MODERATE	c.3154A>G	p.Thr1052Ala	3	FALSE	chr3:178952099:A:G	175:chr3:178952099:A:G	0.002101
49_c2-b	49	MIR4673; NOTCH1	MODIFIER; MODERATE	n.*59A>G; c.890A>G	; p.Asp297Gly	0	FALSE	chr9:139413252:T:C	175:chr9:139413252:T:C	0.004412

49_c2-b	49	C9orf53; CDKN2A	MODIFIER; MODERATE	n.*616A>C; c.*137T>G; c.214T>G; c.257T>G	; p.Cys72Gly; p.Leu86Arg	1	FALSE	chr9:21971144:A:C	175:chr9:21971144:A:C	0.003945
49_c2-b	49	NTRK1	MODERATE	c.2017G>A; c.2107G>A; c.2125G>A	p.Asp673Asn; p.Asp703Asn; p.Asp709Asn	1	FALSE	chr1:156849869:G:A	175:chr1:156849869:G:A	0.002381
49_c2-b	49	FBXW7	MODERATE	c.181C>T; c.295C>T; c.535C>T	p.Arg61Cys; p.Arg99Cys; p.Arg179Cys	0	FALSE	chr4:153271243:G:A	175:chr4:153271243:G:A	0.002361
56_bl-2	56	PIK3R1	MODERATE	c.1045C>T; c.1135C>T; c.1945C>T; c.856C>T	p.Arg349Trp; p.Arg379Trp; p.Arg649Trp; p.Arg286Trp	1	FALSE	chr5:67592129:C:T	176:chr5:67592129:C:T	0.001609
56_bl-2	56	NTRK1	MODERATE	c.804C>G; c.894C>G	p.His268Gln; p.His298Gln	1	FALSE	chr1:156843468:C:G	176:chr1:156843468:C:G	0.004798
56_bl-2	56	TP53	MODIFIER; MODERATE	c.*137A>G; c.*225A>G; c.1001A>G; c.1118A>G; c.641A>G; c.722A>G	; p.Lys334Arg; p.Lys373Arg; p.Lys214Arg; p.Lys241Arg	1	FALSE	chr17:7572991:T:C	176:chr17:7572991:T:C	0.007595
56_bl-2	56	MET	HIGH	c.1639C>T	p.Arg547*	2	FALSE	chr7:116381017:C:T	176:chr7:116381017:C:T	0.001314
56_bl-2	56	KDR	MODERATE	c.3434G>A	p.Gly1145Glu	1	FALSE	chr4:55955111:C:T	176:chr4:55955111:C:T	0.001163
56_bl-2	56	ATM	MODERATE	c.2150G>A	p.Arg717Gln	0	FALSE	chr11:108126967:G:A	176:chr11:108126967:G:A	0.001533
56_bl-2	56	KIT	MODERATE	c.365G>A	p.Arg122His	1	FALSE	chr4:55564477:G:A	176:chr4:55564477:G:A	0.001969
56_bl-2	56	NOTCH1	MODERATE	c.4966G>A	p.Gly1656Ser	0	FALSE	chr9:139399177:C:T	176:chr9:139399177:C:T	0.002997

56_bl-2	56	C9orf53; CDKN2A	MODIFIER; MODERATE; LOW	n.*616T>G; c.*120A>C; c.197A>C; c.240A>C	; p.His66Pro; p.Pro80Pro	1	FALSE	chr9:21971161:T:G	176:chr9:21971161:T:G	0.020408
56_bl-2	56	ALK	HIGH	c.3895G>T	p.Glu1299*	1	FALSE	chr2:29430080:C:A	176:chr2:29430080:C:A	0.001966
56_bl-2	56	FGFR3	MODIFIER; MODERATE	c.931-374G>A; c.1196G>A; c.1202G>A	; p.Arg399His; p.Arg401His	1	FALSE	chr4:1806177:G:A	176:chr4:1806177:G:A	0.002334
56_bl-2	56	AKT1	MODERATE	c.1108C>T	p.Arg370Cys	1	FALSE	chr14:105239279:G:A	176:chr14:105239279:G:A	0.001748
56_bl-2	56	TP53	MODERATE	c.10T>A; c.370T>A; c.487T>A; c.91T>A	p.Tyr4Asn; p.Tyr124Asn; p.Tyr163Asn; p.Tyr31Asn	23	FALSE	chr17:7578443:A:T	176:chr17:7578443:A:T	0.001702
56_bl-2	56	KRAS	MODERATE	c.38G>A	p.Gly13Asp	4010	FALSE	chr12:25398281:C:T	176:chr12:25398281:C:T	0.005158
56_bl-2	56	EGFR	MODERATE	c.494G>A	p.Arg165Gln	3	FALSE	chr7:55214368:G:A	176:chr7:55214368:G:A	0.001874
56_bl-2	56	SMO	MODERATE	c.1045A>C	p.Thr349Pro	0	FALSE	chr7:128846115:A:C	176:chr7:128846115:A:C	0.004605
56_bl-2	56	TP53	MODERATE; MODIFIER	c.115G>T; c.232G>T; c.-279G>T; c.-360G>T	p.Ala39Ser; p.Ala78Ser;	1	FALSE	chr17:7579455:C:A	176:chr17:7579455:C:A	0.002722
56_bl-2	56	NF1	MODERATE	c.2695T>G	p.Leu899Val	3	FALSE	chr17:29556328:T:G	176:chr17:29556328:T:G	0.001587
56_bl-2	56	TP53	MODERATE	c.167G>T; c.248G>T; c.527G>T; c.644G>T	p.Ser56Ile; p.Ser83Ile; p.Ser176Ile; p.Ser215Ile	20	FALSE	chr17:7578205:C:A	176:chr17:7578205:C:A	0.00183
24_c2-1	24	CDH1	MODERATE	c.856G>A	p.Ala286Thr	0	FALSE	chr16:68845610:G:A	177:chr16:68845610:G:A	0.002491
24_c2-1	24	RET	MODERATE	c.2116G>A	p.Val706Met	2	FALSE	chr10:43610164:G:A	177:chr10:43610164:G:A	0.002655

24_c2-1	24	PDGFRA	MODERATE	c.1711G>A	p.Glu571Lys	1	FALSE	chr4:55141065:G:A	177:chr4:55141065:G:A	0.002165
24_c2-1	24	PTEN	MODERATE	c.389G>A	p.Arg130Gln	89	FALSE	chr10:89692905:G:A	177:chr10:89692905:G:A	0.002062
24_c2-1	24	TP53	MODIFIER; MODERATE	c.*137A>G; c.*225A>G; c.1001A>G; c.1118A>G; c.641A>G; c.722A>G	; p.Lys334Arg; p.Lys373Arg; p.Lys214Arg; p.Lys241Arg	1	FALSE	chr17:7572991:T:C	177:chr17:7572991:T:C	0.017945
24_c2-1	24	KRAS	MODERATE	c.34G>T	p.Gly12Cys	3755	FALSE	chr12:25398285:C:A	177:chr12:25398285:C:A	0.025404
24_c2-1	24	MIR4674; MIR4674HG; NOTCH1	MODIFIER; MODERATE	n.*87G>T; n.-1C>A; c.62G>T	; p.Gly21Val	0	FALSE	chr9:139438554:C:A	177:chr9:139438554:C:A	0.003861
24_c2-1	24	SMO	MODERATE	c.469G>A	p.Val157Met	0	FALSE	chr7:128843362:G:A	177:chr7:128843362:G:A	0.002039
24_c2-1	24	NOTCH1	MODERATE	c.4987C>T	p.Arg1663Trp	0	FALSE	chr9:139399156:G:A	177:chr9:139399156:G:A	0.002649
24_c2-1	24	ROS1	HIGH	c.5209G>T	p.Glu1737*	2	FALSE	chr6:117658374:C:A	177:chr6:117658374:C:A	0.002151
24_c2-1	24	RET	MODERATE	c.1907C>T	p.Thr636Met	1	FALSE	chr10:43609955:C:T	177:chr10:43609955:C:T	0.001974
24_c2-1	24	ATM	MODERATE	c.1237C>A	p.Leu413Ile	0	FALSE	chr11:108121429:C:A	177:chr11:108121429:C:A	0.001912
24_c2-1	24	FBXW7	HIGH	c.1027G>T; c.1267G>T; c.913G>T	p.Gly343*; p.Gly423*; p.Gly305*	0	FALSE	chr4:153249511:C:A	177:chr4:153249511:C:A	0.002356
24_c2-1	24	TP53	MODIFIER; MODERATE	c.-75T>A; c.286T>A; c.403T>A; c.7T>A	; p.Cys96Ser; p.Cys135Ser; p.Cys3Ser	12	FALSE	chr17:7578527:A:T	177:chr17:7578527:A:T	0.004459
24_c2-1	24	EGFR	MODERATE	c.493C>T	p.Arg165Trp	1	FALSE	chr7:55214367:C:T	177:chr7:55214367:C:T	0.002105
24_c2-1	24	ATM	MODERATE	c.1477C>T	p.Arg493Cys	0	FALSE	chr11:108121669:C:T	177:chr11:108121669:C:T	0.002283
24_c2-1	24	PHLPP1	MODERATE	c.2303C>A	p.Ser768Tyr	0	FALSE	chr18:60563103:C:A	177:chr18:60563103:C:A	0.002451

24_c2-1	24	CTNNB1	MODERATE	c.884C>A	p.Ala295Asp	0	FALSE	chr3:41267300:C:A	177:chr3:41267300:C:A	0.002307
24_c2-1	24	APC	MODIFIER; MODERATE	c.676-8791C>T; c.688C>T	; p.Arg230Cys	0	FALSE	chr5:112128185:C:T	177:chr5:112128185:C:T	0.002265
24_c2-1	24	NOTCH1	MODERATE	c.4918G>A	p.Ala1640Thr	0	FALSE	chr9:139399225:C:T	177:chr9:139399225:C:T	0.002558
40_bl-2	40	ATM	MODERATE	c.1009C>T	p.Arg337Cys	0	FALSE	chr11:108117798:C:T	178:chr11:108117798:C:T	0.00625
40_bl-2	40	TP53	MODIFIER; MODERATE	c.*137A>G; c.*225A>G; c.1001A>G; c.1118A>G; c.641A>G; c.722A>G	; p.Lys334Arg; p.Lys373Arg; p.Lys214Arg; p.Lys241Arg	1	FALSE	chr17:7572991:T:C	178:chr17:7572991:T:C	0.013699
40_bl-2	40	KRAS	MODERATE	c.40G>A	p.Val14Ile	22	FALSE	chr12:25398279:C:T	178:chr12:25398279:C:T	0.00939
40_bl-2	40	TP53	MODERATE	c.270G>T; c.351G>T; c.630G>T; c.747G>T	p.Arg90Ser; p.Arg117Ser; p.Arg210Ser; p.Arg249Ser	318	FALSE	chr17:7577534:C:A	178:chr17:7577534:C:A	0.027211
40_bl-2	40	EGFR	MODERATE	c.493C>T	p.Arg165Trp	1	FALSE	chr7:55214367:C:T	178:chr7:55214367:C:T	0.52193
40_bl-2	40	ALK	MODERATE	c.3089A>C	p.His1030Pro	15	TRUE	chr2:29448410:T:G	178:chr2:29448410:T:G	0.14094
40_bl-2	40	MET	MODERATE	c.3583C>T; c.3637C>T	p.Leu1195Phe; p.Leu1213Phe	1	FALSE	chr7:116422102:C:T	178:chr7:116422102:C:T	0.010363
40_bl-2	40	KRAS	MODERATE	c.35G>T	p.Gly12Val	11213	FALSE	chr12:25398284:C:A	178:chr12:25398284:C:A	0.060185
49_c5-b	49	TP53	MODERATE	c.364G>A; c.481G>A; c.4G>A; c.85G>A	p.Ala122Thr; p.Ala161Thr; p.Ala2Thr; p.Ala29Thr	53	FALSE	chr17:7578449:C:T	179:chr17:7578449:C:T	0.001536
49_c5-b	49	CTNNB1	MODERATE	c.98C>A	p.Ser33Tyr	0	FALSE	chr3:41266101:C:A	179:chr3:41266101:C:A	0.001953
49_c5-b	49	PTEN	MODERATE	c.731C>A	p.Pro244His	2	FALSE	chr10:89717706:C:A	179:chr10:89717706:C:A	0.002158

49_c5-b	49	EVI2A; NF1	MODIFIER; MODERATE	c.-266C>T; c.-338C>T; c.4895G>A; c.4958G>A	; p.Arg1632His; p.Arg1653His	1	FALSE	chr17:29652960:G:A	179:chr17:29652960:G:A	0.00113
49_c5-b	49	TP53	MODIFIER; MODERATE	c.-9G>T; c.352G>T; c.469G>T; c.73G>T	; p.Val118Phe; p.Val157Phe; p.Val25Phe	169	FALSE	chr17:7578461:C:A	179:chr17:7578461:C:A	0.001533
49_c5-b	49	KDR	MODERATE	c.887G>T	p.Gly296Val	2	FALSE	chr4:55979560:C:A	179:chr4:55979560:C:A	0.002309
49_c5-b	49	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2441T>C; n.1121A>G	p.Leu814Pro;	4	FALSE	chr7:55249143:T:C	179:chr7:55249143:T:C	0.001906
49_c5-b	49	NTRK1	MODERATE	c.804C>G; c.894C>G	p.His268Gln; p.His298Gln	1	FALSE	chr1:156843468:C:G	179:chr1:156843468:C:G	0.001691
49_c5-b	49	PIK3CA	MODERATE	c.518C>A	p.Ser173Tyr	1	FALSE	chr3:178917643:C:A	179:chr3:178917643:C:A	0.001145
49_c5-b	49	TSC2	MODERATE	c.1654G>A	p.Ala552Thr	0	FALSE	chr16:2115574:G:A	179:chr16:2115574:G:A	0.001498
49_c5-b	49	ATM	MODERATE	c.4466G>A	p.Arg1489His	0	FALSE	chr11:108163375:G:A	179:chr11:108163375:G:A	0.001225
49_c5-b	49	FGFR4	MODERATE	c.1444G>A; c.1528G>A; c.1648G>A	p.Val482Met; p.Val510Met; p.Val550Met	2	FALSE	chr5:176522551:G:A	179:chr5:176522551:G:A	0.001672
49_c5-b	49	FGFR2	MODIFIER; MODERATE	c.110-14054G>T; c.110-934G>T; n.757-14054G>T; c.301G>T	; p.Asp101Tyr	3	FALSE	chr10:123325027:C:A	179:chr10:123325027:C:A	0.0013
49_c5-b	49	MIR4673; NOTCH1	MODIFIER; MODERATE	n.*59G>T; c.1286G>T	; p.Cys429Phe	0	FALSE	chr9:139412359:C:A	179:chr9:139412359:C:A	0.002255
49_c5-b	49	FBXW7	HIGH	c.1069G>T; c.1309G>T; c.955G>T	p.Gly357*; p.Gly437*; p.Gly319*	0	FALSE	chr4:153249469:C:A	179:chr4:153249469:C:A	0.00135

49_c5-b	49	NOTCH1	MODERATE	c.5347C>T	p.Arg1783Trp	0	FALSE	chr9:139396761:G:A	179:chr9:139396761:G:A	0.001881
49_c5-b	49	MET	MODERATE	c.3973G>A; c.4027G>A	p.Glu1325Lys; p.Glu1343Lys	1	FALSE	chr7:116435978:G:A	179:chr7:116435978:G:A	0.001291
49_c5-b	49	KDR	MODERATE	c.2075G>T	p.Gly692Val	1	FALSE	chr4:55968588:C:A	179:chr4:55968588:C:A	0.001726
49_c5-b	49	RAC1	MODERATE	c.203G>A	p.Arg68His	0	FALSE	chr7:6431650:G:A	179:chr7:6431650:G:A	0.001563
49_c5-b	49	KIT	MODERATE	c.235C>A	p.Gln79Lys	2	FALSE	chr4:55561845:C:A	179:chr4:55561845:C:A	0.001705
49_c5-b	49	IGF1R	MODERATE	c.3905T>C; c.3908T>C	p.Val1302Ala; p.Val1303Ala	0	FALSE	chr15:99500475:T:C	179:chr15:99500475:T:C	0.003751
49_c5-b	49	FBXW7	MODERATE	c.1084G>T; c.1198G>T; c.1438G>T	p.Asp362Tyr; p.Asp400Tyr; p.Asp480Tyr	0	FALSE	chr4:153247364:C:A	179:chr4:153247364:C:A	0.00116
49_c5-b	49	TP53	HIGH; MODIFIER	c.184G>T; c.67G>T; c.-279G>T; c.-360G>T	p.Glu62*; p.Glu23*;	8	FALSE	chr17:7579503:C:A	179:chr17:7579503:C:A	0.001857
49_c5-b	49	PIK3R1	MODERATE	c.1508G>A; c.419G>A; c.608G>A; c.698G>A	p.Arg503Gln; p.Arg140Gln; p.Arg203Gln; p.Arg233Gln	2	FALSE	chr5:67590446:G:A	179:chr5:67590446:G:A	0.001343
49_c5-b	49	KIT	HIGH	c.1698C>A; c.1710C>A	p.Tyr566*; p.Tyr570*	2	FALSE	chr4:55593644:C:A	179:chr4:55593644:C:A	0.00147
49_c5-b	49	NTRK2	MODERATE	c.2017G>A; c.2065G>A	p.Val673Met; p.Val689Met	0	FALSE	chr9:87570325:G:A	179:chr9:87570325:G:A	0.001465
49_c5-b	49	KIT	MODERATE	c.365G>A	p.Arg122His	1	FALSE	chr4:55564477:G:A	179:chr4:55564477:G:A	0.001347
49_c5-b	49	PTEN	MODERATE	c.379G>A	p.Gly127Arg	6	FALSE	chr10:89692895:G:A	179:chr10:89692895:G:A	0.001256
49_c5-b	49	PDGFRA	MODERATE	c.1526C>A	p.Ala509Asp	1	FALSE	chr4:55139865:C:A	179:chr4:55139865:C:A	0.002247

49_c5-b	49	FBXW7	MODERATE	c.1444G>T; c.1558G>T; c.1798G>T	p.Asp482Tyr; p.Asp520Tyr; p.Asp600Tyr	0	FALSE	chr4:153245393:C:A	179:chr4:153245393:C:A	0.001298
49_c5-b	49	PTEN	HIGH	c.720C>A	p.Tyr240*	3	FALSE	chr10:89717695:C:A	179:chr10:89717695:C:A	0.002147
49_c5-b	49	FGFR2	MODIFIER; MODERATE	c.1087+1222G>A; c.749-2141G>A; c.820+1222G>A; c.939+2519G>A; c.598G>A; c.676G>A; c.943G>A; n.1393G>A	; p.Ala200Thr; p.Ala226Thr; p.Ala315Thr	1	FALSE	chr10:123276974:C:T	179:chr10:123276974:C:T	0.001775
49_c5-b	49	IGF1R	MODERATE	c.1784G>A	p.Arg595His	0	FALSE	chr15:99456467:G:A	179:chr15:99456467:G:A	0.00128
49_c5-b	49	TP53	MODIFIER; MODERATE	c.-5G>T; c.356G>T; c.473G>T; c.77G>T	; p.Arg119Leu; p.Arg158Leu; p.Arg26Leu	80	FALSE	chr17:7578457:C:A	179:chr17:7578457:C:A	0.001541
49_c5-b	49	SMO	MODERATE	c.1684C>T	p.Arg562Trp	0	FALSE	chr7:128850837:C:T	179:chr7:128850837:C:T	0.001331
49_c5-b	49	APC	HIGH	c.350C>A; c.380C>A	p.Ser117*; p.Ser127*	0	FALSE	chr5:112103015:C:A	179:chr5:112103015:C:A	0.002292
49_c5-b	49	MIR4673; NOTCH1	MODIFIER; MODERATE	n.-1G>T; c.221G>T	; p.Cys74Phe	0	FALSE	chr9:139418351:C:A	179:chr9:139418351:C:A	0.003359
49_c5-b	49	PTEN	MODERATE	c.443C>A	p.Ala148Glu	1	FALSE	chr10:89692959:C:A	179:chr10:89692959:C:A	0.001459
49_c5-b	49	ALK	MODERATE	c.2629G>T	p.Ala877Ser	1	FALSE	chr2:29455173:C:A	179:chr2:29455173:C:A	0.002412
49_c5-b	49	NTRK3	MODERATE	c.1393G>T; c.1417G>T	p.Gly465Cys; p.Gly473Cys	0	FALSE	chr15:88576256:C:A	179:chr15:88576256:C:A	0.001901

49_c5-b	49	ERBB2; MIEN1; MIR4728	MODIFIER; MODERATE	c.3160-319G>A; c.3145G>A; c.3190G>A; c.3235G>A; n.3559G>A; c.*388C>T; n.*67G>A	; p.Glu1049Lys; p.Glu1064Lys; p.Glu1079Lys	1	FALSE	chr17:37883623:G:A	179:chr17:37883623:G:A	0.00177
49_c5-b	49	CDH1	MODERATE	c.1223C>A	p.Ala408Glu	0	FALSE	chr16:68847301:C:A	179:chr16:68847301:C:A	0.00128
49_c5-b	49	HGF	MODERATE	c.251G>T	p.Cys84Phe	0	FALSE	chr7:81392026:C:A	179:chr7:81392026:C:A	0.001661
49_c5-b	49	EGFR	MODIFIER; MODERATE	c.*2133C>T; c.*2364C>T; c.2011C>T	; p.Arg671Cys	2	FALSE	chr7:55240767:C:T	179:chr7:55240767:C:T	0.002339
49_c5-b	49	ATM	MODERATE	c.6751C>A	p.Leu2251Ile	0	FALSE	chr11:108196215:C:A	179:chr11:108196215:C:A	0.001465
49_c5-b	49	PIK3CA	MODERATE	c.2727C>A	p.Phe909Leu	1	FALSE	chr3:178947852:C:A	179:chr3:178947852:C:A	0.001341
49_c5-b	49	HGF	MODERATE	c.5G>T	p.Trp2Leu	0	FALSE	chr7:81399283:C:A	179:chr7:81399283:C:A	0.001337
49_c5-b	49	HGF	HIGH	c.1993G>T; c.2008G>T	p.Glu665*; p.Glu670*	0	FALSE	chr7:81334708:C:A	179:chr7:81334708:C:A	0.001305
49_c5-b	49	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2568T>G; n.-1A>C	p.Phe856Leu;	1	FALSE	chr7:55259510:T:G	179:chr7:55259510:T:G	0.00158
49_c5-b	49	FBXW7	MODERATE	c.1078G>T; c.1318G>T; c.964G>T	p.Asp360Tyr; p.Asp440Tyr; p.Asp322Tyr	0	FALSE	chr4:153249460:C:A	179:chr4:153249460:C:A	0.001387
49_c5-b	49	C9orf53; CDKN2A	MODIFIER; MODERATE	n.*616A>C; c.*137T>G; c.214T>G; c.257T>G	; p.Cys72Gly; p.Leu86Arg	1	FALSE	chr9:21971144:A:C	179:chr9:21971144:A:C	0.018104

49_c5-b	49	TP53	MODERATE	c.119G>T; c.200G>T; c.479G>T; c.596G>T	p.Gly40Val; p.Gly67Val; p.Gly160Val; p.Gly199Val	11	FALSE	chr17:7578253:C:A	179:chr17:7578253:C:A	0.001409
49_c5-b	49	HGF	MODERATE	c.6G>T	p.Trp2Cys	0	FALSE	chr7:81399282:C:A	179:chr7:81399282:C:A	0.001332
49_c5-b	49	CTNNB1	MODERATE	c.134C>A	p.Ser45Tyr	0	FALSE	chr3:41266137:C:A	179:chr3:41266137:C:A	0.001252
49_c5-b	49	TP53	MODIFIER; MODERATE	c.-3G>T; c.358G>T; c.475G>T; c.79G>T	; p.Ala120Ser; p.Ala159Ser; p.Ala27Ser	23	FALSE	chr17:7578455:C:A	179:chr17:7578455:C:A	0.001527
49_c5-b	49	ATM	MODERATE	c.6503C>T	p.Ser2168Leu	0	FALSE	chr11:108192078:C:T	179:chr11:108192078:C:T	0.00144
49_c5-b	49	ATM	MODERATE	c.2075G>A	p.Arg692His	0	FALSE	chr11:108124717:G:A	179:chr11:108124717:G:A	0.001279
69_c2-1	69	TP53	MODIFIER; MODERATE	c.-9G>T; c.352G>T; c.469G>T; c.73G>T	; p.Val118Phe; p.Val157Phe; p.Val25Phe	169	FALSE	chr17:7578461:C:A	180:chr17:7578461:C:A	0.001876
69_c2-1	69	IGF1R	MODERATE	c.2824G>A; c.2827G>A	p.Ala942Thr; p.Ala943Thr	0	FALSE	chr15:99472831:G:A	180:chr15:99472831:G:A	0.001647
69_c2-1	69	FGFR2	MODERATE; MODIFIER	c.262C>A; c.340C>A; c.607C>A; n.909C>A	p.Arg88Ser; p.Arg114Ser; p.Arg203Ser;	2	FALSE	chr10:123310821:G:T	180:chr10:123310821:G:T	0.0022
69_c2-1	69	NTRK1	MODERATE	c.804C>G; c.894C>G	p.His268Gln; p.His298Gln	1	FALSE	chr1:156843468:C:G	180:chr1:156843468:C:G	0.004008
69_c2-1	69	EPHA3	MODERATE	c.1543G>A	p.Ala515Thr	0	FALSE	chr3:89448579:G:A	180:chr3:89448579:G:A	0.003633
69_c2-1	69	EPHA3	MODERATE	c.2734A>G	p.Thr912Ala	0	FALSE	chr3:89521657:A:G	180:chr3:89521657:A:G	0.001805
69_c2-1	69	CTNNB1	MODERATE	c.98C>A	p.Ser33Tyr	0	FALSE	chr3:41266101:C:A	180:chr3:41266101:C:A	0.002383

69_c2-1	69	FBXW7	MODERATE	c.1241C>A; c.1355C>A; c.1595C>A	p.Thr414Asn; p.Thr452Asn; p.Thr532Asn	0	FALSE	chr4:153247207:G:T	180:chr4:153247207:G:T	0.002586
69_c2-1	69	TP53	MODERATE; MODIFIER	c.100G>T; c.217G>T; c.-279G>T; c.-360G>T	p.Val34Leu; p.Val73Leu;	5	FALSE	chr17:7579470:C:A	180:chr17:7579470:C:A	0.002039
69_c2-1	69	TP53	MODIFIER; HIGH	c.-104A>G; c.-23A>G; c.259-2A>G; c.376-2A>G		19	FALSE	chr17:7578556:T:C	180:chr17:7578556:T:C	0.003968
69_c2-1	69	NTRK1	MODERATE	c.1768C>A; c.1858C>A; c.1876C>A	p.Gln590Lys; p.Gln620Lys; p.Gln626Lys	1	FALSE	chr1:156848984:C:A	180:chr1:156848984:C:A	0.001671
69_c2-1	69	FGFR4	MODERATE	c.1699C>A; c.1783C>A; c.1903C>A	p.Arg567Ser; p.Arg595Ser; p.Arg635Ser	2	FALSE	chr5:176523139:C:A	180:chr5:176523139:C:A	0.002181
69_c2-1	69	TP53	MODERATE	c.349G>T; c.430G>T; c.709G>T; c.826G>T	p.Ala117Ser; p.Ala144Ser; p.Ala237Ser; p.Ala276Ser	16	FALSE	chr17:7577112:C:A	180:chr17:7577112:C:A	0.001855
69_c2-1	69	AKT1	MODERATE	c.361C>T	p.Arg121Trp	2	FALSE	chr14:105242063:G:A	180:chr14:105242063:G:A	0.001538
69_c2-1	69	EGFR	MODIFIER; MODERATE	c.*1464G>A; c.1321G>A	; p.Val441Ile	1	FALSE	chr7:55227854:G:A	180:chr7:55227854:G:A	0.001843
69_c2-1	69	CDH1	MODERATE	c.1489G>A	p.Glu497Lys	0	FALSE	chr16:68849586:G:A	180:chr16:68849586:G:A	0.001577
69_c2-1	69	TP53	MODIFIER; MODERATE	c.-11G>T; c.350G>T; c.467G>T; c.71G>T	; p.Arg117Leu; p.Arg156Leu; p.Arg24Leu	26	FALSE	chr17:7578463:C:A	180:chr17:7578463:C:A	0.001859
69_c2-1	69	ALK	MODERATE	c.2306A>G	p.Asp769Gly	1	FALSE	chr2:29462595:T:C	180:chr2:29462595:T:C	0.001612

69_c2-1	69	HGF	MODERATE	c.1435G>A; c.1450G>A	p.Val479Ile; p.Val484Ile	0	FALSE	chr7:81339554:C:T	180:chr7:81339554:C:T	0.001898
69_c2-1	69	C9orf53; CDKN2A	MODIFIER; MODERATE	n.*616A>C; c.*137T>G; c.214T>G; c.257T>G	; p.Cys72Gly; p.Leu86Arg	1	FALSE	chr9:21971144:A:C	180:chr9:21971144:A:C	0.010681
69_c2-1	69	TP53	MODIFIER; MODERATE	c.*137A>G; c.*225A>G; c.1001A>G; c.1118A>G; c.641A>G; c.722A>G	; p.Lys334Arg; p.Lys373Arg; p.Lys214Arg; p.Lys241Arg	1	FALSE	chr17:7572991:T:C	180:chr17:7572991:T:C	0.018846
69_c2-1	69	ATM	HIGH	c.5623C>T	p.Arg1875*	0	FALSE	chr11:108175528:C:T	180:chr11:108175528:C:T	0.002708
83_c1bl-1	83	CDH1	MODERATE	c.2074G>A	p.Ala692Thr	0	FALSE	chr16:68857439:G:A	183:chr16:68857439:G:A	0.00093
83_c1bl-1	83	NOTCH1	MODERATE	c.5011G>A	p.Val1671Ile	0	FALSE	chr9:139399132:C:T	183:chr9:139399132:C:T	0.475225
83_c1bl-1	83	IGF1R	MODERATE	c.3934T>C; c.3937T>C	p.Ser1312Pro; p.Ser1313Pro	0	FALSE	chr15:99500504:T:C	183:chr15:99500504:T:C	0.009824
83_c1bl-1	83	TP53	MODIFIER; MODERATE	c.-17G>T; c.344G>T; c.461G>T; c.65G>T	; p.Gly115Val; p.Gly154Val; p.Gly22Val	39	FALSE	chr17:7578469:C:A	183:chr17:7578469:C:A	0.000984
83_c1bl-1	83	ATM	MODERATE	c.1477C>T	p.Arg493Cys	0	FALSE	chr11:108121669:C:T	183:chr11:108121669:C:T	0.001034
83_c1bl-1	83	PIK3CA	MODERATE	c.49C>T	p.Pro17Ser	1	FALSE	chr3:178916662:C:T	183:chr3:178916662:C:T	0.000868
83_c1bl-1	83	NF1	HIGH	c.3942G>A	p.Trp1314*	1	FALSE	chr17:29563007:G:A	183:chr17:29563007:G:A	0.001349

83_c1bl-1	83	CSDE1; NRAS	MODIFIER; MODERATE	c.*2430G>A; c.*2523G>A; c.*2817G>A; c.*2910G>A; c.*2964G>A; c.*3057G>A; c.52G>A	; p.Ala18Thr	13	TRUE	chr1:115258730:C:T	183:chr1:115258730:C:T	0.001048
83_c1bl-1	83	IDH1	MODERATE	c.941G>A	p.Arg314His	1	FALSE	chr2:209104637:C:T	183:chr2:209104637:C:T	0.000945
83_c1bl-1	83	IDH2	MODIFIER; MODERATE	c.-17C>T; c.-17-2873C>T; c.140C>T	; p.Ala47Val	1	FALSE	chr15:90634852:G:A	183:chr15:90634852:G:A	0.001123
83_c1bl-1	83	FLT3	MODERATE	c.393G>C	p.Leu131Phe	0	FALSE	chr13:28631575:C:G	183:chr13:28631575:C:G	0.001491
83_c1bl-1	83	EPHA3	MODERATE	c.2530C>T	p.Pro844Ser	0	FALSE	chr3:89499360:C:T	183:chr3:89499360:C:T	0.000995
83_c1bl-1	83	APC	MODERATE	c.1771G>A; c.1825G>A	p.Val591Ile; p.Val609Ile	0	FALSE	chr5:112170729:G:A	183:chr5:112170729:G:A	0.497076
83_c1bl-1	83	C9orf53; CDKN2A	MODIFIER; MODERATE	n.*616C>G; c.*140G>C; c.217G>C; c.260G>C	; p.Ala73Pro; p.Arg87Pro	1	FALSE	chr9:21971141:C:G	183:chr9:21971141:C:G	0.008021
83_c1bl-1	83	NF1	MODERATE	c.4321C>T; c.4384C>T	p.Arg1441Trp; p.Arg1462Trp	1	FALSE	chr17:29586101:C:T	183:chr17:29586101:C:T	0.00098
83_c1bl-1	83	TP53	MODERATE	c.415G>A; c.496G>A; c.775G>A; c.892G>A	p.Glu139Lys; p.Glu166Lys; p.Glu259Lys; p.Glu298Lys	50	FALSE	chr17:7577046:C:T	183:chr17:7577046:C:T	0.00092
83_c1bl-1	83	TP53	MODIFIER; MODERATE	c.*145T>C; c.*233T>C; c.1009T>C; c.1126T>C; c.649T>C; c.730T>C	; p.Ser337Pro; p.Ser376Pro; p.Ser217Pro; p.Ser244Pro	2	FALSE	chr17:7572983:A:G	183:chr17:7572983:A:G	0.004866

83_c1bl-1	83	PDGFRA	MODERATE	c.389C>T	p.Pro130Leu	2	FALSE	chr4:55129855:C:T	183:chr4:55129855:C:T	0.00095
83_c1bl-1	83	KDR	MODERATE	c.1040G>A	p.Arg347His	4	FALSE	chr4:55976872:C:T	183:chr4:55976872:C:T	0.001255
83_c1bl-1	83	KIT	MODERATE	c.365G>A	p.Arg122His	1	FALSE	chr4:55564477:G:A	183:chr4:55564477:G:A	0.000968
83_c1bl-1	83	CDH1	MODERATE	c.2053G>A	p.Val685Met	0	FALSE	chr16:68857418:G:A	183:chr16:68857418:G:A	0.000933
83_c1bl-1	83	NTRK2	MODERATE	c.1981G>A; c.2029G>A	p.Ala661Thr; p.Ala677Thr	0	FALSE	chr9:87570289:G:A	183:chr9:87570289:G:A	0.001021
83_c1bl-1	83	NF1	MODERATE	c.2695T>G	p.Leu899Val	3	FALSE	chr17:29556328:T:G	183:chr17:29556328:T:G	0.003423
83_c1bl-1	83	BRAF	MODERATE	c.2153C>T	p.Ala718Val	1	FALSE	chr7:140434545:G:A	183:chr7:140434545:G:A	0.001045
83_c1bl-1	83	MIR1225; PKD1; TSC2	MODIFIER; MODERATE	n.*90C>T; c.*13118C>T; c.*13121C>T; c.4954G>A; c.5086G>A; c.5155G>A	; p.Ala1652Thr; p.Ala1696Thr; p.Ala1719Thr	0	FALSE	chr16:2138135:G:A	183:chr16:2138135:G:A	0.000937
83_c1bl-1	83	ALK	MODERATE	c.1274G>A	p.Cys425Tyr	1	FALSE	chr2:29606606:C:T	183:chr2:29606606:C:T	0.001181
83_c1bl-1	83	ALK	MODERATE	c.3455T>C	p.Leu1152Pro	1	FALSE	chr2:29445270:A:G	183:chr2:29445270:A:G	0.001784
83_c1bl-1	83	TP53	MODERATE	c.421C>T; c.502C>T; c.781C>T; c.898C>T	p.Pro141Ser; p.Pro168Ser; p.Pro261Ser; p.Pro300Ser	3	FALSE	chr17:7577040:G:A	183:chr17:7577040:G:A	0.000915
83_c1bl-1	83	PIK3CA	MODERATE	c.3058G>A	p.Ala1020Thr	1	FALSE	chr3:178952003:G:A	183:chr3:178952003:G:A	0.000833
83_c1bl-1	83	KRAS	MODERATE	c.35G>A	p.Gly12Asp	11213	FALSE	chr12:25398284:C:T	183:chr12:25398284:C:T	0.016623
83_c1bl-1	83	STK11	MODERATE	c.628T>C	p.Cys210Arg	1	FALSE	chr19:1220610:T:C	183:chr19:1220610:T:C	0.004509
83_c1bl-1	83	VHL	MODIFIER; MODERATE	c.341-3270A>C; c.344A>C	; p.His115Pro	0	FALSE	chr3:10188201:A:C	183:chr3:10188201:A:C	0.002323

83_c1bl-1	83	NTRK1	MODERATE	c.1768C>A; c.1858C>A; c.1876C>A	p.Gln590Lys; p.Gln620Lys; p.Gln626Lys	1	FALSE	chr1:156848984:C:A	183:chr1:156848984:C:A	0.000963
83_c1bl-1	83	FGFR2	MODIFIER; MODERATE	c.110-14065C>T; c.110-945C>T; n.757-14065C>T; c.290C>T	; p.Ala97Val	1	FALSE	chr10:123325038:G:A	183:chr10:123325038:G:A	0.000951
83_c1bl-1	83	KDR	MODERATE	c.2323G>T	p.Ala775Ser	1	FALSE	chr4:55964914:C:A	183:chr4:55964914:C:A	0.010496
83_c1bl-1	83	KDR	MODERATE	c.1028C>T	p.Thr343Met	3	FALSE	chr4:55976884:G:A	183:chr4:55976884:G:A	0.000772
83_c1bl-1	83	TP53	MODERATE	c.236G>A; c.317G>A; c.596G>A; c.713G>A	p.Cys79Tyr; p.Cys106Tyr; p.Cys199Tyr; p.Cys238Tyr	74	FALSE	chr17:7577568:C:T	183:chr17:7577568:C:T	0.006115
83_c1bl-1	83	NOTCH1	MODERATE	c.5777G>A	p.Arg1926His	0	FALSE	chr9:139395161:C:T	183:chr9:139395161:C:T	0.001365
83_c1bl-1	83	RPL19	MODERATE	c.452G>A	p.Arg151His	0	FALSE	chr17:37360425:G:A	183:chr17:37360425:G:A	0.001574
83_c1bl-1	83	HGF	MODERATE	c.1172G>A; c.1187G>A	p.Gly391Asp; p.Gly396Asp	0	FALSE	chr7:81350145:C:T	183:chr7:81350145:C:T	0.00095
83_c1bl-1	83	MIR4673; NOTCH1	MODIFIER; MODERATE	n.*59A>C; c.1195A>C	; p.Thr399Pro	0	FALSE	chr9:139412649:T:G	183:chr9:139412649:T:G	0.005013
83_c1bl-1	83	PTEN	MODERATE	c.698G>A	p.Arg233Gln	2	FALSE	chr10:89717673:G:A	183:chr10:89717673:G:A	0.000968
83_c1bl-1	83	PHLPP1	MODERATE	c.2197G>A	p.Val733Ile	0	FALSE	chr18:60562374:G:A	183:chr18:60562374:G:A	0.001067
83_c1bl-1	83	CDH1	MODERATE	c.2218C>T	p.Pro740Ser	0	FALSE	chr16:68862130:C:T	183:chr16:68862130:C:T	0.000925
83_c1bl-1	83	IGF1R	MODERATE	c.3905T>C; c.3908T>C	p.Val1302Ala; p.Val1303Ala	0	FALSE	chr15:99500475:T:C	183:chr15:99500475:T:C	0.006024
83_c1bl-1	83	CDH1	HIGH	c.1792C>T	p.Arg598*	0	FALSE	chr16:68855984:C:T	183:chr16:68855984:C:T	0.00084
83_c1bl-1	83	SMO	MODERATE	c.1045A>C	p.Thr349Pro	0	FALSE	chr7:128846115:A:C	183:chr7:128846115:A:C	0.009052

83_c1bl-1	83	ZNF716	HIGH	c.31C>T	p.Arg11*	0	FALSE	chr7:57510025:C:T	183:chr7:57510025:C:T	0.001291
83_c1bl-1	83	FGFR1	MODERATE	c.181G>A; c.187G>A; c.430G>A; c.448G>A; c.454G>A; c.547G>A	p.Ala61Thr; p.Ala63Thr; p.Ala144Thr; p.Ala150Thr; p.Ala152Thr; p.Ala183Thr	1	FALSE	chr8:38285606:C:T	183:chr8:38285606:C:T	0.00126
83_c1bl-1	83	TP53	MODERATE	c.134A>G; c.215A>G; c.494A>G; c.611A>G	p.Glu45Gly; p.Glu72Gly; p.Glu165Gly; p.Glu204Gly	3	FALSE	chr17:7578238:T:C	183:chr17:7578238:T:C	0.000994
83_c1bl-1	83	MAP2K1	MODERATE	c.316G>A	p.Ala106Thr	1	FALSE	chr15:66729108:G:A	183:chr15:66729108:G:A	0.001445
83_c1bl-1	83	C9orf53; CDKN2A	MODIFIER; MODERATE; LOW	n.*616T>G; c.*120A>C; c.197A>C; c.240A>C	; p.His66Pro; p.Pro80Pro	1	FALSE	chr9:21971161:T:G	183:chr9:21971161:T:G	0.035256
83_c1bl-1	83	MIR4673; NOTCH1	MODIFIER; MODERATE	n.*59G>A; c.1024G>A	; p.Ala342Thr	0	FALSE	chr9:139413118:C:T	183:chr9:139413118:C:T	0.002353
83_c1bl-1	83	ERBB2; MIEN1; MIR4728	MODIFIER; MODERATE	c.3160-213A>G; c.3251A>G; c.3296A>G; c.3341A>G; n.3665A>G; c.*388T>C; n.*67A>G	; p.Glu1084Gly; p.Glu1099Gly; p.Glu1114Gly	1	FALSE	chr17:37883729:A:G	183:chr17:37883729:A:G	0.003049
83_c1bl-1	83	RET	MODERATE	c.1690A>C	p.Thr564Pro	1	FALSE	chr10:43608342:A:C	183:chr10:43608342:A:C	0.007496
83_c1bl-1	83	BRAF	MODERATE	c.436C>T	p.Arg146Trp	1	FALSE	chr7:140534477:G:A	183:chr7:140534477:G:A	0.000898
83_c1bl-1	83	PIK3CA	MODERATE	c.518C>A	p.Ser173Tyr	1	FALSE	chr3:178917643:C:A	183:chr3:178917643:C:A	0.000884

94_c9-1	94	MET	MODERATE	c.487T>C	p.Ser163Pro	1	FALSE	chr7:116339625:T:C	184:chr7:116339625:T:C	0.001748
94_c9-1	94	C9orf53; CDKN2A	MODIFIER; MODERATE	n.*616C>G; c.*140G>C; c.217G>C; c.260G>C	; p.Ala73Pro; p.Arg87Pro	1	FALSE	chr9:21971141:C:G	184:chr9:21971141:C:G	0.009901
94_c9-1	94	AKT1	MODERATE	c.1112C>T	p.Thr371Met	1	FALSE	chr14:105239275:G:A	184:chr14:105239275:G:A	0.002092
94_c9-1	94	NOTCH1	MODERATE	c.4906G>A	p.Glu1636Lys	0	FALSE	chr9:139399237:C:T	184:chr9:139399237:C:T	0.002075
94_c9-1	94	TSC2	MODERATE	c.2702G>A	p.Arg901His	0	FALSE	chr16:2126131:G:A	184:chr16:2126131:G:A	0.001783
94_c9-1	94	TSC2	MODIFIER; MODERATE	c.2837+1092G>A; c.2917G>A	; p.Glu973Lys	0	FALSE	chr16:2127678:G:A	184:chr16:2127678:G:A	0.001978
94_c9-1	94	MAP2K2	MODERATE	c.281C>T	p.Ser94Leu	0	FALSE	chr19:4117439:G:A	184:chr19:4117439:G:A	0.002699
94_c9-1	94	ERBB2; MIEN1; MIR4728	MODERATE; MODIFIER	c.2306A>C; c.2351A>C; c.2396A>C; n.2720A>C; c.*388T>G; n.-1A>C	p.Gln769Pro; p.Gln784Pro; p.Gln799Pro;	1	FALSE	chr17:37881067:A:C	184:chr17:37881067:A:C	0.002107
94_c9-1	94	TP53	MODIFIER; MODERATE	c.*137A>G; c.*225A>G; c.1001A>G; c.1118A>G; c.641A>G; c.722A>G	; p.Lys334Arg; p.Lys373Arg; p.Lys214Arg; p.Lys241Arg	1	FALSE	chr17:7572991:T:C	184:chr17:7572991:T:C	0.003175
94_c9-1	94	MET	MODERATE	c.1336A>G	p.Ile446Val	1	FALSE	chr7:116371857:A:G	184:chr7:116371857:A:G	0.003215
94_c9-1	94	BRAF	MODERATE	c.1061G>A	p.Arg354Gln	3	FALSE	chr7:140494187:C:T	184:chr7:140494187:C:T	0.002002
94_c9-1	94	ALK	MODERATE	c.3455T>C	p.Leu1152Pro	1	FALSE	chr2:29445270:A:G	184:chr2:29445270:A:G	0.005269

94_c9-1	94	ERBB2; MIEN1; MIR4728	MODIFIER; MODERATE	c.3160-213A>G; c.3251A>G; c.3296A>G; c.3341A>G; n.3665A>G; c.*388T>C; n.*67A>G	; p.Glu1084Gly; p.Glu1099Gly; p.Glu1114Gly	1	FALSE	chr17:37883729:A:G	184:chr17:37883729:A:G	0.001777
94_c9-1	94	IGF1R	MODERATE	c.1940G>A	p.Arg647His	0	FALSE	chr15:99459304:G:A	184:chr15:99459304:G:A	0.003774
94_c9-1	94	CTNNB1	MODERATE	c.1972G>T	p.Val658Phe	0	FALSE	chr3:41278096:G:T	184:chr3:41278096:G:T	0.002045
94_c9-1	94	CDKN2A	MODIFIER; MODERATE	c.194-3568A>C; c.52A>C	; p.Thr18Pro	1	FALSE	chr9:21974775:T:G	184:chr9:21974775:T:G	0.006764
94_c9-1	94	TP53	MODERATE	c.274A>T; c.355A>T; c.634A>T; c.751A>T	p.Ile92Phe; p.Ile119Phe; p.Ile212Phe; p.Ile251Phe	8	FALSE	chr17:7577530:T:A	184:chr17:7577530:T:A	0.001781
94_c9-1	94	NTRK1	MODERATE	c.804C>G; c.894C>G	p.His268Gln; p.His298Gln	1	FALSE	chr1:156843468:C:G	184:chr1:156843468:C:G	0.001953
94_c9-1	94	ERBB2; MIEN1; MIR4728	MODIFIER; MODERATE	c.3160-319G>A; c.3145G>A; c.3190G>A; c.3235G>A; n.3559G>A; c.*388C>T; n.*67G>A	; p.Glu1049Lys; p.Glu1064Lys; p.Glu1079Lys	1	FALSE	chr17:37883623:G:A	184:chr17:37883623:G:A	0.001277
94_c9-1	94	NTRK3	MODERATE	c.1744G>A; c.1768G>A	p.Glu582Lys; p.Glu590Lys	0	FALSE	chr15:88476364:C:T	184:chr15:88476364:C:T	0.002262
94_c9-1	94	MITF	MODERATE	c.157A>C; c.265A>C; c.310A>C; c.313A>C	p.Thr53Pro; p.Thr89Pro; p.Thr104Pro; p.Thr105Pro	0	FALSE	chr3:69928493:A:C	184:chr3:69928493:A:C	0.002058

94_c9-1	94	IGF1R	MODERATE	c.3005G>A; c.3008G>A	p.Arg1002Gln; p.Arg1003Gln	0	FALSE	chr15:99478104:G:A	184:chr15:99478104:G:A	0.001919
94_c9-1	94	RET	MODERATE	c.1690A>C	p.Thr564Pro	1	FALSE	chr10:43608342:A:C	184:chr10:43608342:A:C	0.004032
94_c9-1	94	TP53	MODIFIER; HIGH	c.-55C>A; c.27C>A; c.306C>A; c.423C>A	; p.Cys9*; p.Cys102*; p.Cys141*	13	FALSE	chr17:7578507:G:T	184:chr17:7578507:G:T	0.239815
94_c9-1	94	TP53	MODIFIER; MODERATE	c.-11G>C; c.350G>C; c.467G>C; c.71G>C	; p.Arg117Pro; p.Arg156Pro; p.Arg24Pro	26	FALSE	chr17:7578463:C:G	184:chr17:7578463:C:G	0.001885
132_bl-1	132	IDH1	MODERATE	c.1077G>T	p.Leu359Phe	1	FALSE	chr2:209103872:C:A	185:chr2:209103872:C:A	0.000937
132_bl-1	132	C9orf53; CDKN2A	MODIFIER; MODERATE; LOW	n.*616T>G; c.*120A>C; c.197A>C; c.240A>C	; p.His66Pro; p.Pro80Pro	1	FALSE	chr9:21971161:T:G	185:chr9:21971161:T:G	0.037383
132_bl-1	132	MIR4673; NOTCH1	MODIFIER; HIGH	n.*59C>T; c.1828C>T	; p.Gln610*	0	FALSE	chr9:139410010:G:A	185:chr9:139410010:G:A	0.001385
132_bl-1	132	MIR1225; PKD1; TSC2	MODIFIER; MODERATE	n.*90G>A; c.*13118G>A; c.*13121G>A; c.5032C>T; c.5164C>T; c.5233C>T	; p.Arg1678Cys; p.Arg1722Cys; p.Arg1745Cys	0	FALSE	chr16:2138300:C:T	185:chr16:2138300:C:T	0.001287
132_bl-1	132	APC	HIGH	c.1606C>T; c.1660C>T	p.Arg536*; p.Arg554*	0	FALSE	chr5:112164586:C:T	185:chr5:112164586:C:T	0.001171
132_bl-1	132	CWH43	MODERATE	c.1535G>A; c.1616G>A	p.Gly512Asp; p.Gly539Asp	0	FALSE	chr4:49034690:G:A	185:chr4:49034690:G:A	0.00121

132_bl-1	132	FGFR1	MODERATE	c.359C>T; c.365C>T; c.608C>T; c.626C>T; c.632C>T; c.725C>T	p.Ala120Val; p.Ala122Val; p.Ala203Val; p.Ala209Val; p.Ala211Val; p.Ala242Val	1	FALSE	chr8:38283753:G:A	185:chr8:38283753:G:A	0.001452
132_bl-1	132	ATM	MODERATE	c.4466G>A	p.Arg1489His	0	FALSE	chr11:108163375:G:A	185:chr11:108163375:G:A	0.000903
132_bl-1	132	FGFR3	MODERATE	c.905G>A	p.Gly302Asp	1	FALSE	chr4:1803727:G:A	185:chr4:1803727:G:A	0.001621
132_bl-1	132	RET	MODERATE	c.1826G>A	p.Cys609Tyr	1	FALSE	chr10:43609070:G:A	185:chr10:43609070:G:A	0.001326
132_bl-1	132	NTRK1	MODERATE	c.1039C>T; c.949C>T	p.Arg347Cys; p.Arg317Cys	1	FALSE	chr1:156843613:C:T	185:chr1:156843613:C:T	0.001422
132_bl-1	132	EPHA3	MODERATE	c.2408C>T	p.Ser803Leu	0	FALSE	chr3:89498436:C:T	185:chr3:89498436:C:T	0.001065
132_bl-1	132	ALK	MODERATE	c.4411G>A	p.Val1471Met	1	FALSE	chr2:29416542:C:T	185:chr2:29416542:C:T	0.000907
132_bl-1	132	FGFR4	MODERATE; LOW	c.1186G>A; c.1306G>A; c.1152G>A	p.Val396Met; p.Val436Met; p.Ala384Ala	1	FALSE	chr5:176520461:G:A	185:chr5:176520461:G:A	0.001015
132_bl-1	132	MIR4673; NOTCH1	MODIFIER; MODERATE	n.*59G>A; c.1775G>A	; p.Arg592His	0	FALSE	chr9:139410063:C:T	185:chr9:139410063:C:T	0.001572
132_bl-1	132	ALK	MODERATE	c.1307C>T	p.Ala436Val	1	FALSE	chr2:29551323:G:A	185:chr2:29551323:G:A	0.000982
132_bl-1	132	TSC1	MODERATE	c.365C>T; c.518C>T	p.Ala122Val; p.Ala173Val	0	FALSE	chr9:135797351:G:A	185:chr9:135797351:G:A	0.00146
132_bl-1	132	NF1	MODIFIER; MODERATE	c.*2165G>A; c.1976G>A	; p.Arg659Gln	1	FALSE	chr17:29552243:G:A	185:chr17:29552243:G:A	0.00109

132_bl-1	132	FGFR2	MODERATE; MODIFIER	c.1639C>T; c.1642C>T; c.1645C>T; c.1654C>T; c.1723C>T; c.1726C>T; c.1990C>T; c.1993C>T; n.2440C>T	p.Arg547Trp; p.Arg548Trp; p.Arg549Trp; p.Arg552Trp; p.Arg575Trp; p.Arg576Trp; p.Arg664Trp; p.Arg665Trp;	2	FALSE	chr10:123246935:G:A	185:chr10:123246935:G:A	0.003141
132_bl-1	132	MITF	MODERATE	c.142G>A; c.250G>A; c.295G>A; c.298G>A	p.Val48Ile; p.Val84Ile; p.Val99Ile; p.Val100Ile	0	FALSE	chr3:69928478:G:A	185:chr3:69928478:G:A	0.00117
132_bl-1	132	AR	MODERATE	c.2324G>A; c.728G>A	p.Arg775His; p.Arg243His	0	FALSE	chrX:66941680:G:A	185:chrX:66941680:G:A	0.001485
132_bl-1	132	CDKN2A	MODIFIER; MODERATE	c.194-3568A>C; c.52A>C	; p.Thr18Pro	1	FALSE	chr9:21974775:T:G	185:chr9:21974775:T:G	0.008794
132_bl-1	132	NTRK2	MODERATE	c.1628A>G; c.1676A>G	p.Glu543Gly; p.Glu559Gly	0	FALSE	chr9:87549119:A:G	185:chr9:87549119:A:G	0.001488
132_bl-1	132	ATM	HIGH	c.3663G>A	p.Trp1221*	0	FALSE	chr11:108153523:G:A	185:chr11:108153523:G:A	0.001057
132_bl-1	132	NOTCH1	MODERATE	c.5161G>A	p.Val1721Met	0	FALSE	chr9:139397640:C:T	185:chr9:139397640:C:T	0.001754
132_bl-1	132	AKT1	MODERATE	c.1339A>G	p.Ile447Val	1	FALSE	chr14:105237106:T:C	185:chr14:105237106:T:C	0.001393

132_bl-1	132	FGFR2	MODIFIER; MODERATE	c.939+4720G>A; c.1145G>A; c.1148G>A; c.800G>A; c.809G>A; c.878G>A; c.881G>A; n.1595G>A	; p.Cys382Tyr; p.Cys383Tyr; p.Cys267Tyr; p.Cys270Tyr; p.Cys293Tyr; p.Cys294Tyr	2	FALSE	chr10:123274773:C:T	185:chr10:123274773:C:T	0.00099
132_bl-1	132	DDR2	MODERATE	c.313C>T	p.Arg105Cys	2	FALSE	chr1:162724541:C:T	185:chr1:162724541:C:T	0.000935
132_bl-1	132	HOXD-AS2; HOXD8	MODIFIER; MODERATE	n.*692C>T; c.-123-30G>A; c.400G>A	; p.Ala134Thr	0	FALSE	chr2:176995494:G:A	185:chr2:176995494:G:A	0.002636
132_bl-1	132	TP53	MODERATE	c.100C>T; c.181C>T; c.460C>T; c.577C>T	p.His34Tyr; p.His61Tyr; p.His154Tyr; p.His193Tyr	46	FALSE	chr17:7578272:G:A	185:chr17:7578272:G:A	0.001186
132_bl-1	132	FGFR3	MODERATE	c.1526G>A; c.1862G>A; c.1868G>A	p.Arg509His; p.Arg621His; p.Arg623His	2	FALSE	chr4:1807803:G:A	185:chr4:1807803:G:A	0.001657
132_bl-1	132	MIR4673; NOTCH1	MODIFIER; HIGH	n.-1G>T; c.574G>T	; p.Gly192*	0	FALSE	chr9:139417470:C:A	185:chr9:139417470:C:A	0.001767
132_bl-1	132	IGF1R	MODERATE	c.3934T>C; c.3937T>C	p.Ser1312Pro; p.Ser1313Pro	0	FALSE	chr15:99500504:T:C	185:chr15:99500504:T:C	0.005663
132_bl-1	132	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2387G>A; n.1175C>T	p.Gly796Asp;	3	FALSE	chr7:55249089:G:A	185:chr7:55249089:G:A	0.001494
132_bl-1	132	CDH1	MODERATE	c.2074G>A	p.Ala692Thr	0	FALSE	chr16:68857439:G:A	185:chr16:68857439:G:A	0.001115
132_bl-1	132	TP53	MODERATE	c.422C>T; c.503C>T; c.782C>T; c.899C>T	p.Pro141Leu; p.Pro168Leu; p.Pro261Leu; p.Pro300Leu	6	FALSE	chr17:7577039:G:A	185:chr17:7577039:G:A	0.001228

132_bl-1	132	ATM	HIGH	c.7324C>T	p.Gln2442*	0	FALSE	chr11:108200957:C:T	185:chr11:108200957:C:T	0.000998
132_bl-1	132	FGFR4	MODIFIER; MODERATE	c.1098-65G>A; c.1251+10G>A; c.1067G>A	; p.Arg356His	1	FALSE	chr5:176520342:G:A	185:chr5:176520342:G:A	0.002404
132_bl-1	132	PTEN	MODERATE	c.851A>G	p.Glu284Gly	7	FALSE	chr10:89720700:A:G	185:chr10:89720700:A:G	0.001306
132_bl-1	132	RET	MODERATE	c.1901G>A	p.Cys634Tyr	7	FALSE	chr10:43609949:G:A	185:chr10:43609949:G:A	0.000905
132_bl-1	132	KDR	MODERATE	c.3062C>T	p.Ser1021Leu	1	FALSE	chr4:55958791:G:A	185:chr4:55958791:G:A	0.001074
132_bl-1	132	KIT	MODERATE	c.1493G>A	p.Gly498Asp	1	FALSE	chr4:55592169:G:A	185:chr4:55592169:G:A	0.001349
132_bl-1	132	ERBB2; MIEN1; MIR4728	MODERATE; MODIFIER	c.2261G>A; c.2306G>A; c.2351G>A; n.2675G>A; c.*388C>T; n.-1G>A	p.Arg754His; p.Arg769His; p.Arg784His;	1	FALSE	chr17:37881022:G:A	185:chr17:37881022:G:A	0.000981
132_bl-1	132	ALK	MODERATE	c.3626G>A	p.Arg1209Gln	2	FALSE	chr2:29443591:C:T	185:chr2:29443591:C:T	0.002471
132_bl-1	132	BRAF	MODERATE	c.1799T>A	p.Val600Glu	23024	FALSE	chr7:140453136:A:T	185:chr7:140453136:A:T	0.268267
132_bl-1	132	ALK	MODERATE	c.2577G>T	p.Glu859Asp	1	FALSE	chr2:29455225:C:A	185:chr2:29455225:C:A	0.00106
132_bl-1	132	IGF1R	MODERATE	c.3613G>A; c.3616G>A	p.Ala1205Thr; p.Ala1206Thr	0	FALSE	chr15:99491831:G:A	185:chr15:99491831:G:A	0.001168
132_bl-1	132	NTRK1	MODERATE	c.804C>G; c.894C>G	p.His268Gln; p.His298Gln	1	FALSE	chr1:156843468:C:G	185:chr1:156843468:C:G	0.001883
132_bl-1	132	C9orf53; CDKN2A	MODIFIER; MODERATE	n.*616C>G; c.*140G>C; c.217G>C; c.260G>C	; p.Ala73Pro; p.Arg87Pro	1	FALSE	chr9:21971141:C:G	185:chr9:21971141:C:G	0.008639
132_bl-1	132	ALK	MODERATE	c.2623G>A	p.Gly875Arg	1	FALSE	chr2:29455179:C:T	185:chr2:29455179:C:T	0.001875

132_bl-1	132	ATM	MODERATE	c.8122G>A	p.Asp2708Asn	0	FALSE	chr11:108205807:G:A	185:chr11:108205807:G:A	0.000987
132_bl-1	132	NTRK2	MODERATE	c.220G>A	p.Ala74Thr	0	FALSE	chr9:87317081:G:A	185:chr9:87317081:G:A	0.00143
132_bl-1	132	MAP2K1	MODERATE	c.395C>T	p.Ala132Val	1	FALSE	chr15:66729187:C:T	185:chr15:66729187:C:T	0.001563
132_bl-1	132	TSC1	MODERATE	c.2272G>A; c.2422G>A; c.2425G>A	p.Glu758Lys; p.Glu808Lys; p.Glu809Lys	0	FALSE	chr9:135777053:C:T	185:chr9:135777053:C:T	0.001411
132_bl-1	132	MAP2K1	MODERATE	c.146G>A	p.Arg49His	1	FALSE	chr15:66727430:G:A	185:chr15:66727430:G:A	0.001232
132_bl-1	132	PIK3CA	MODERATE	c.56G>A	p.Arg19Lys	1	FALSE	chr3:178916669:G:A	185:chr3:178916669:G:A	0.000904
132_bl-1	132	MET	MODERATE	c.487T>C	p.Ser163Pro	1	FALSE	chr7:116339625:T:C	185:chr7:116339625:T:C	0.002065
132_bl-1	132	TSC2	MODERATE	c.1610G>A	p.Arg537His	0	FALSE	chr16:2115530:G:A	185:chr16:2115530:G:A	0.001059
132_bl-1	132	EPHA3	MODERATE	c.1142G>A	p.Arg381His	0	FALSE	chr3:89391076:G:A	185:chr3:89391076:G:A	0.000992
132_bl-1	132	IGF1R	MODERATE	c.3905T>C; c.3908T>C	p.Val1302Ala; p.Val1303Ala	0	FALSE	chr15:99500475:T:C	185:chr15:99500475:T:C	0.008526
132_bl-1	132	CTNNB1	MODERATE	c.559G>A	p.Ala187Thr	0	FALSE	chr3:41266888:G:A	185:chr3:41266888:G:A	0.001252
132_bl-1	132	MET	MODERATE	c.470A>G	p.Glu157Gly	1	FALSE	chr7:116339608:A:G	185:chr7:116339608:A:G	0.001232
132_bl-1	132	TP53	MODIFIER; MODERATE	c.*109G>A; c.*197G>A; c.1090G>A; c.613G>A; c.694G>A; c.973G>A	; p.Ala364Thr; p.Ala205Thr; p.Ala232Thr; p.Ala325Thr	1	FALSE	chr17:7573937:C:T	185:chr17:7573937:C:T	0.001178
132_bl-1	132	HGF	MODERATE	c.401G>A	p.Arg134His	0	FALSE	chr7:81386586:C:T	185:chr7:81386586:C:T	0.000966
132_bl-1	132	STK11	MODERATE	c.455A>G	p.Gln152Arg	3	FALSE	chr19:1219403:A:G	185:chr19:1219403:A:G	0.002611

132_bl-1	132	ERBB2; MIEN1; MIR4728	MODIFIER; MODERATE	c.3160-213A>G; c.3251A>G; c.3296A>G; c.3341A>G; n.3665A>G; c.*388T>C; n.*67A>G	; p.Glu1084Gly; p.Glu1099Gly; p.Glu1114Gly	1	FALSE	chr17:37883729:A:G	185:chr17:37883729:A:G	0.002448
132_bl-1	132	FGFR4	HIGH	c.1041G>A	p.Trp347*	1	FALSE	chr5:176519769:G:A	185:chr5:176519769:G:A	0.001262
132_bl-1	132	CDH1	MODERATE	c.263C>A	p.Pro88His	0	FALSE	chr16:68835672:C:A	185:chr16:68835672:C:A	0.00117
132_bl-1	132	TP53	MODERATE	c.284T>C; c.365T>C; c.644T>C; c.761T>C	p.Ile95Thr; p.Ile122Thr; p.Ile215Thr; p.Ile254Thr	9	FALSE	chr17:7577520:A:G	185:chr17:7577520:A:G	0.001923
132_bl-1	132	VHL	MODIFIER; MODERATE	c.341-3270A>C; c.344A>C	; p.His115Pro	0	FALSE	chr3:10188201:A:C	185:chr3:10188201:A:C	0.002076
132_bl-1	132	NTRK1	MODERATE	c.239C>T; c.329C>T	p.Ala80Val; p.Ala110Val	1	FALSE	chr1:156834561:C:T	185:chr1:156834561:C:T	0.001815
132_bl-1	132	TSC2	MODERATE	c.1654G>A	p.Ala552Thr	0	FALSE	chr16:2115574:G:A	185:chr16:2115574:G:A	0.003513
132_bl-1	132	TP53	MODIFIER; MODERATE	c.*111G>T; c.*23G>T; c.1004G>T; c.527G>T; c.608G>T; c.887G>T	; p.Arg335Leu; p.Arg176Leu; p.Arg203Leu; p.Arg296Leu	2	FALSE	chr17:7574023:C:A	185:chr17:7574023:C:A	0.001168
132_bl-1	132	EGFR	MODIFIER; MODERATE	c.*2133G>A; c.*2364G>A; c.2030G>A	; p.Arg677His	5	FALSE	chr7:55240786:G:A	185:chr7:55240786:G:A	0.002504

132_bl-1	132	NTRK1	MODERATE	c.1940T>G; c.2030T>G; c.2048T>G	p.Val647Gly; p.Val677Gly; p.Val683Gly	2	FALSE	chr1:156849792:T:G	185:chr1:156849792:T:G	0.006205
132_bl-1	132	ATM	HIGH	c.5623C>T	p.Arg1875*	0	FALSE	chr11:108175528:C:T	185:chr11:108175528:C:T	0.002701
132_bl-1	132	CDH1	MODERATE	c.2053G>A	p.Val685Met	0	FALSE	chr16:68857418:G:A	185:chr16:68857418:G:A	0.001124
132_bl-1	132	EPHA3	MODERATE	c.1543G>A	p.Ala515Thr	0	FALSE	chr3:89448579:G:A	185:chr3:89448579:G:A	0.001182
132_bl-1	132	NF1	MODERATE	c.2695T>G	p.Leu899Val	3	FALSE	chr17:29556328:T:G	185:chr17:29556328:T:G	0.000984
132_bl-1	132	NF1	MODERATE	c.7381G>A; c.7444G>A	p.Asp2461Asn; p.Asp2482Asn	1	FALSE	chr17:29677323:G:A	185:chr17:29677323:G:A	0.00196
132_bl-1	132	NTRK3	MODERATE	c.346C>T	p.Arg116Trp	0	FALSE	chr15:88726698:G:A	185:chr15:88726698:G:A	0.002797
132_bl-1	132	NF1	MODERATE	c.647T>C	p.Leu216Pro	1	FALSE	chr17:29508500:T:C	185:chr17:29508500:T:C	0.001361
132_bl-1	132	RET	MODERATE	c.1339G>A	p.Ala447Thr	1	FALSE	chr10:43606730:G:A	185:chr10:43606730:G:A	0.000932
132_bl-1	132	EGFR	MODERATE	c.866C>T	p.Ala289Val	34	FALSE	chr7:55221822:C:T	185:chr7:55221822:C:T	0.001205
132_bl-1	132	KIT	MODERATE	c.1835C>T; c.1847C>T	p.Ala612Val; p.Ala616Val	1	FALSE	chr4:55594061:C:T	185:chr4:55594061:C:T	0.001009
132_bl-1	132	FGFR1; LETM2	MODERATE; MODIFIER	c.1927C>T; c.1933C>T; c.2170C>T; c.2194C>T; c.2200C>T; c.2293C>T; c.*1406G>A; c.*1423G>A; c.*1553G>A; c.*1567G>A; c.*1638G>A	p.Arg643Trp; p.Arg645Trp; p.Arg724Trp; p.Arg732Trp; p.Arg734Trp; p.Arg765Trp;	1	FALSE	chr8:38271528:G:A	185:chr8:38271528:G:A	0.001938

132_bl-1	132	TSC2	MODERATE	c.1381G>A	p.Val461Met	0	FALSE	chr16:2112992:G:A	185:chr16:2112992:G:A	0.001536
132_bl-1	132	CSDE1; NRAS	MODIFIER; MODERATE	c.*2430A>G; c.*2523A>G; c.*2817A>G; c.*2910A>G; c.*2964A>G; c.*3057A>G; c.182A>G	; p.Gln61Arg	1103	FALSE	chr1:115256529:T:C	185:chr1:115256529:T:C	0.006901
132_bl-1	132	CDH1	MODERATE	c.1252G>A	p.Asp418Asn	0	FALSE	chr16:68847330:G:A	185:chr16:68847330:G:A	0.001143
132_bl-1	132	RET	MODERATE	c.1690A>C	p.Thr564Pro	1	FALSE	chr10:43608342:A:C	185:chr10:43608342:A:C	0.004828
132_bl-1	132	INSRR; NTRK1	MODIFIER; MODERATE	c.3397+28C>T; c.13G>A	; p.Ala5Thr	3	FALSE	chr1:156811876:G:A	185:chr1:156811876:G:A	0.000987
132_bl-1	132	TSC2	MODIFIER; MODERATE	c.2837+1108G>A; c.2933G>A	; p.Arg978His	0	FALSE	chr16:2127694:G:A	185:chr16:2127694:G:A	0.003023
132_bl-1	132	FBXW7	MODERATE	c.1160G>A; c.1274G>A; c.1514G>A	p.Arg387His; p.Arg425His; p.Arg505His	0	FALSE	chr4:153247288:C:T	185:chr4:153247288:C:T	0.00108
132_bl-1	132	ATM	MODERATE	c.5873C>T	p.Ala1958Val	0	FALSE	chr11:108180997:C:T	185:chr11:108180997:C:T	0.000991
132_bl-1	132	KDR	MODERATE	c.2068G>A	p.Ala690Thr	1	FALSE	chr4:55968595:C:T	185:chr4:55968595:C:T	0.00135
132_bl-1	132	APC	HIGH	c.1042C>T; c.988C>T	p.Arg348*; p.Arg330*	0	FALSE	chr5:112154771:C:T	185:chr5:112154771:C:T	0.000977
132_bl-1	132	PIK3CA	MODERATE	c.2078G>A	p.Arg693His	1	FALSE	chr3:178938836:G:A	185:chr3:178938836:G:A	0.001163
132_bl-1	132	SMO	MODERATE	c.1045A>C	p.Thr349Pro	0	FALSE	chr7:128846115:A:C	185:chr7:128846115:A:C	0.004995
132_bl-1	132	EGFR	MODERATE	c.445C>T	p.Arg149Trp	1	FALSE	chr7:55214319:C:T	185:chr7:55214319:C:T	0.001268
132_bl-1	132	KDR	MODERATE	c.1028C>T	p.Thr343Met	3	FALSE	chr4:55976884:G:A	185:chr4:55976884:G:A	0.000902

132_bl-1	132	C9orf53; CDKN2A	MODIFIER; MODERATE	n.*616A>G; c.*312T>C; c.*33T>C; c.389T>C	; p.Leu130Pro	5	FALSE	chr9:21970969:A:G	185:chr9:21970969:A:G	0.003382
132_bl-1	132	MITF	MODERATE	c.157A>C; c.265A>C; c.310A>C; c.313A>C	p.Thr53Pro; p.Thr89Pro; p.Thr104Pro; p.Thr105Pro	0	FALSE	chr3:69928493:A:C	185:chr3:69928493:A:C	0.001144
132_bl-1	132	AR	MODERATE	c.2360G>A; c.764G>A	p.Arg787Gln; p.Arg255Gln	0	FALSE	chrX:66941716:G:A	185:chrX:66941716:G:A	0.001217
111_c5-1	111	FGFR2	MODIFIER; MODERATE	c.749-4752G>A; c.502G>A; c.580G>A; c.847G>A; n.1149G>A	; p.Asp168Asn; p.Asp194Asn; p.Asp283Asn	1	FALSE	chr10:123279585:C:T	186:chr10:123279585:C:T	0.002841
111_c5-1	111	IGF1R	MODERATE	c.3905T>C; c.3908T>C	p.Val1302Ala; p.Val1303Ala	0	FALSE	chr15:99500475:T:C	186:chr15:99500475:T:C	0.002981
111_c5-1	111	NTRK1	MODERATE	c.1751G>A; c.1841G>A; c.1859G>A	p.Gly584Asp; p.Gly614Asp; p.Gly620Asp	1	FALSE	chr1:156848967:G:A	186:chr1:156848967:G:A	0.002907
111_c5-1	111	MITF	MODERATE	c.1004C>T; c.1049C>T; c.1052C>T; c.563C>T; c.731C>T; c.749C>T; c.896C>T	p.Ser335Phe; p.Ser350Phe; p.Ser351Phe; p.Ser188Phe; p.Ser244Phe; p.Ser250Phe; p.Ser299Phe	0	FALSE	chr3:70008462:C:T	186:chr3:70008462:C:T	0.003017
111_c5-1	111	CDKN2A; CDKN2B-AS1	MODERATE; MODIFIER	c.22A>G; n.-1T>C	p.Thr8Ala;	1	FALSE	chr9:21994309:T:C	186:chr9:21994309:T:C	0.005682

111_c5-1	111	TP53	MODERATE	c.266G>A; c.347G>A; c.626G>A; c.743G>A	p.Arg89Gln; p.Arg116Gln; p.Arg209Gln; p.Arg248Gln	673	FALSE	chr17:7577538:C:T	186:chr17:7577538:C:T	0.002736
111_c5-1	111	NTRK1	MODERATE	c.1940T>G; c.2030T>G; c.2048T>G	p.Val647Gly; p.Val677Gly; p.Val683Gly	2	FALSE	chr1:156849792:T:G	186:chr1:156849792:T:G	0.00431
111_c5-1	111	TSC2	MODIFIER; MODERATE	c.2837+1092G>A; c.2917G>A	; p.Glu973Lys	0	FALSE	chr16:2127678:G:A	186:chr16:2127678:G:A	0.0032
111_c5-1	111	VHL	MODIFIER; MODERATE	c.341-3270A>C; c.344A>C	; p.His115Pro	0	FALSE	chr3:10188201:A:C	186:chr3:10188201:A:C	0.003846
82_c5-1	82	NOTCH1	MODERATE	c.4733T>G	p.Val1578Gly	0	FALSE	chr9:139399410:A:C	188:chr9:139399410:A:C	0.001691
82_c5-1	82	NF1	MODERATE	c.3407G>A	p.Arg1136Gln	2	FALSE	chr17:29559810:G:A	188:chr17:29559810:G:A	0.001049
82_c5-1	82	ESR1	MODERATE	c.1297C>T; c.1300C>T; c.1306C>T	p.Arg433Trp; p.Arg434Trp; p.Arg436Trp	0	FALSE	chr6:152382190:C:T	188:chr6:152382190:C:T	0.001133
82_c5-1	82	NOTCH1	MODERATE	c.5885G>A	p.Arg1962His	0	FALSE	chr9:139395053:C:T	188:chr9:139395053:C:T	0.001452
82_c5-1	82	ERBB2; MIEN1; MIR4728	MODERATE; MODIFIER	c.3025G>A; c.3070G>A; c.3115G>A; n.3439G>A; c.*388C>T; n.*67G>A	p.Ala1009Thr; p.Ala1024Thr; p.Ala1039Thr;	2	FALSE	chr17:37883212:G:A	188:chr17:37883212:G:A	0.002172
82_c5-1	82	TSC1	MODERATE	c.1547C>T; c.1697C>T; c.1700C>T	p.Ala516Val; p.Ala566Val; p.Ala567Val	0	FALSE	chr9:135781265:G:A	188:chr9:135781265:G:A	0.000862
82_c5-1	82	CDH1	MODERATE	c.1423G>A	p.Val475Met	0	FALSE	chr16:68849520:G:A	188:chr16:68849520:G:A	0.000969

82_c5-1	82	FLT3	MODERATE	c.1192G>A	p.Asp398Asn	0	FALSE	chr13:28622425:C:T	188:chr13:28622425:C:T	0.001252
82_c5-1	82	CDH1	MODERATE	c.221G>A	p.Arg74Gln	0	FALSE	chr16:68835630:G:A	188:chr16:68835630:G:A	0.001041
82_c5-1	82	FGFR3	MODERATE	c.1526G>A; c.1862G>A; c.1868G>A	p.Arg509His; p.Arg621His; p.Arg623His	2	FALSE	chr4:1807803:G:A	188:chr4:1807803:G:A	0.001438
82_c5-1	82	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2305G>A; n.1257C>T	p.Val769Met;	3	FALSE	chr7:55249007:G:A	188:chr7:55249007:G:A	0.000997
82_c5-1	82	ALK	MODERATE	c.446C>T	p.Ala149Val	1	FALSE	chr2:30143080:G:A	188:chr2:30143080:G:A	0.001497
82_c5-1	82	SMO	MODERATE	c.1045A>C	p.Thr349Pro	0	FALSE	chr7:128846115:A:C	188:chr7:128846115:A:C	0.006229
82_c5-1	82	PDGFRA	MODERATE	c.2266G>A	p.Asp756Asn	1	FALSE	chr4:55146592:G:A	188:chr4:55146592:G:A	0.000982
82_c5-1	82	FLT3	MODERATE	c.2678C>T	p.Pro893Leu	0	FALSE	chr13:28589369:G:A	188:chr13:28589369:G:A	0.001198
82_c5-1	82	HGF	MODERATE	c.1255C>T; c.1270C>T	p.Arg419Cys; p.Arg424Cys	0	FALSE	chr7:81350062:G:A	188:chr7:81350062:G:A	0.001325
82_c5-1	82	TP53	HIGH	c.109C>T; c.190C>T; c.469C>T; c.586C>T	p.Arg37*; p.Arg64*; p.Arg157*; p.Arg196*	191	FALSE	chr17:7578263:G:A	188:chr17:7578263:G:A	0.135036
82_c5-1	82	TP53	MODERATE	c.337G>A; c.418G>A; c.697G>A; c.814G>A	p.Val113Met; p.Val140Met; p.Val233Met; p.Val272Met	85	FALSE	chr17:7577124:C:T	188:chr17:7577124:C:T	0.016622
82_c5-1	82	FLT3	MODERATE	c.393G>C	p.Leu131Phe	0	FALSE	chr13:28631575:C:G	188:chr13:28631575:C:G	0.001705
82_c5-1	82	APC	MODERATE	c.1708G>A; c.1762G>A	p.Val570Ile; p.Val588Ile	0	FALSE	chr5:112170666:G:A	188:chr5:112170666:G:A	0.001182
82_c5-1	82	APC	HIGH	c.1042C>T; c.988C>T	p.Arg348*; p.Arg330*	0	FALSE	chr5:112154771:C:T	188:chr5:112154771:C:T	0.001607
82_c5-1	82	EGFR	MODERATE	c.1061C>T	p.Thr354Met	1	FALSE	chr7:55224280:C:T	188:chr7:55224280:C:T	0.001259

82_c5-1	82	NTRK1	MODERATE	c.1940T>G; c.2030T>G; c.2048T>G	p.Val647Gly; p.Val677Gly; p.Val683Gly	2	FALSE	chr1:156849792:T:G	188:chr1:156849792:T:G	0.007098
82_c5-1	82	CDKN2A	MODIFIER; MODERATE	c.194-3568A>C; c.52A>C	; p.Thr18Pro	1	FALSE	chr9:21974775:T:G	188:chr9:21974775:T:G	0.007563
82_c5-1	82	IGF1R	MODERATE	c.755G>A	p.Arg252His	0	FALSE	chr15:99434668:G:A	188:chr15:99434668:G:A	0.001285
82_c5-1	82	SMO	MODERATE	c.1640G>A	p.Arg547His	0	FALSE	chr7:128850377:G:A	188:chr7:128850377:G:A	0.001298
82_c5-1	82	IGF1R	MODERATE	c.3905T>C; c.3908T>C	p.Val1302Ala; p.Val1303Ala	0	FALSE	chr15:99500475:T:C	188:chr15:99500475:T:C	0.004929
82_c5-1	82	MAP2K1	MODERATE	c.692C>T	p.Ser231Leu	1	FALSE	chr15:66774216:C:T	188:chr15:66774216:C:T	0.001487
82_c5-1	82	DDR2	MODERATE	c.1625C>T	p.Ala542Val	1	FALSE	chr1:162741934:C:T	188:chr1:162741934:C:T	0.000745
82_c5-1	82	IGF1R	MODERATE	c.1828G>A	p.Val610Ile	0	FALSE	chr15:99456511:G:A	188:chr15:99456511:G:A	0.001192
82_c5-1	82	PIK3CA	MODERATE	c.1633G>A	p.Glu545Lys	1189	FALSE	chr3:178936091:G:A	188:chr3:178936091:G:A	0.115237
82_c5-1	82	NF1	MODIFIER; HIGH	c.*2165G>A; c.2087G>A	; p.Trp696*	2	FALSE	chr17:29553538:G:A	188:chr17:29553538:G:A	0.001106
82_c5-1	82	AR	MODERATE	c.2086G>A; c.490G>A	p.Asp696Asn; p.Asp164Asn	0	FALSE	chrX:66931444:G:A	188:chrX:66931444:G:A	0.001062
82_c5-1	82	C9orf53; CDKN2A	MODIFIER; MODERATE	n.*616C>G; c.*140G>C; c.217G>C; c.260G>C	; p.Ala73Pro; p.Arg87Pro	1	FALSE	chr9:21971141:C:G	188:chr9:21971141:C:G	0.021651
82_c5-1	82	PTEN	MODERATE	c.574G>A	p.Ala192Thr	1	FALSE	chr10:89711956:G:A	188:chr10:89711956:G:A	0.001217
82_c5-1	82	MIR1225; PKD1; TSC2	MODIFIER; MODERATE	n.*90C>T; c.*13118C>T; c.*13121C>T; c.4954G>A; c.5086G>A; c.5155G>A	; p.Ala1652Thr; p.Ala1696Thr; p.Ala1719Thr	0	FALSE	chr16:2138135:G:A	188:chr16:2138135:G:A	0.0012

82_c5-1	82	GNA11	MODERATE	c.1030G>A	p.Val344Met	1	FALSE	chr19:3121127:G:A	188:chr19:3121127:G:A	0.001217
82_c5-1	82	TP53	HIGH	c.152C>G; c.431C>G; c.548C>G; c.71C>G	p.Ser51*; p.Ser144*; p.Ser183*; p.Ser24*	26	FALSE	chr17:7578382:G:C	188:chr17:7578382:G:C	0.001144
82_c5-1	82	TP53	MODERATE	c.406C>T; c.487C>T; c.766C>T; c.883C>T	p.Pro136Ser; p.Pro163Ser; p.Pro256Ser; p.Pro295Ser	2	FALSE	chr17:7577055:G:A	188:chr17:7577055:G:A	0.001173
82_c5-1	82	MET	MODERATE	c.1829G>A	p.Cys610Tyr	2	FALSE	chr7:116395536:G:A	188:chr7:116395536:G:A	0.000996
82_c5-1	82	EGFR	MODIFIER; MODERATE	c.*2364C>T; c.2165C>T	; p.Ala722Val	2	FALSE	chr7:55241717:C:T	188:chr7:55241717:C:T	0.001129
82_c5-1	82	ERBB2; MIEN1; MIR4728	MODIFIER; MODERATE	c.3160-213A>G; c.3251A>G; c.3296A>G; c.3341A>G; n.3665A>G; c.*388T>C; n.*67A>G	; p.Glu1084Gly; p.Glu1099Gly; p.Glu1114Gly	1	FALSE	chr17:37883729:A:G	188:chr17:37883729:A:G	0.004566
82_c5-1	82	NTRK2	MODERATE	c.250G>A	p.Glu84Lys	0	FALSE	chr9:87317111:G:A	188:chr9:87317111:G:A	0.001089
82_c5-1	82	FGFR1	MODERATE	c.1051G>A; c.685G>A; c.691G>A; c.934G>A; c.952G>A; c.958G>A	p.Asp351Asn; p.Asp229Asn; p.Asp231Asn; p.Asp312Asn; p.Asp318Asn; p.Asp320Asn	1	FALSE	chr8:38279438:C:T	188:chr8:38279438:C:T	0.001359
82_c5-1	82	FGFR3	MODERATE	c.1177G>A; c.1513G>A; c.1519G>A	p.Val393Ile; p.Val505Ile; p.Val507Ile	1	FALSE	chr4:1807182:G:A	188:chr4:1807182:G:A	0.001521

82_c5-1	82	KLLN; PTEN	MODIFIER; MODERATE	c.-951C>T; c.32G>A	; p.Arg11Lys	1	FALSE	chr10:89624258:G:A	188:chr10:89624258:G:A	0.001377
82_c5-1	82	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2387G>A; n.1175C>T	p.Gly796Asp;	3	FALSE	chr7:55249089:G:A	188:chr7:55249089:G:A	0.001634
82_c5-1	82	NF1	MODERATE	c.2695T>G	p.Leu899Val	3	FALSE	chr17:29556328:T:G	188:chr17:29556328:T:G	0.002036
82_c5-1	82	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2327G>A; n.1235C>T	p.Arg776His;	7	FALSE	chr7:55249029:G:A	188:chr7:55249029:G:A	0.001108
82_c5-1	82	NTRK3	MODERATE	c.265C>T	p.Arg89Cys	0	FALSE	chr15:88727514:G:A	188:chr15:88727514:G:A	0.001356
82_c5-1	82	DDR2	MODERATE	c.1963G>A	p.Glu655Lys	1	FALSE	chr1:162745548:G:A	188:chr1:162745548:G:A	0.000881
82_c5-1	82	INSRR; NTRK1	MODIFIER; MODERATE	c.3397+24A>G; c.17T>C	; p.Leu6Pro	1	FALSE	chr1:156811880:T:C	188:chr1:156811880:T:C	0.000907
82_c5-1	82	SMO	MODERATE	c.869G>A	p.Arg290His	0	FALSE	chr7:128845572:G:A	188:chr7:128845572:G:A	0.001093
82_c5-1	82	C9orf53; CDKN2A	MODIFIER; MODERATE; LOW	n.*616A>G; c.*117T>C; c.194T>C; c.237T>C	; p.Leu65Pro; p.Ala79Ala	3	FALSE	chr9:21971164:A:G	188:chr9:21971164:A:G	0.010727
82_c5-1	82	NTRK3	MODERATE	c.389G>A	p.Arg130His	0	FALSE	chr15:88726655:C:T	188:chr15:88726655:C:T	0.003876
82_c5-1	82	RET	MODERATE	c.1690A>C	p.Thr564Pro	1	FALSE	chr10:43608342:A:C	188:chr10:43608342:A:C	0.005053
82_c5-1	82	TSC1	MODERATE	c.1823C>T; c.1973C>T; c.1976C>T	p.Ala608Val; p.Ala658Val; p.Ala659Val	0	FALSE	chr9:135780989:G:A	188:chr9:135780989:G:A	0.001195
82_c5-1	82	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2548C>A; n.-1G>T	p.His850Asn;	1	FALSE	chr7:55259490:C:A	188:chr7:55259490:C:A	0.001206
82_c5-1	82	EPHA3	MODERATE	c.2530C>T	p.Pro844Ser	0	FALSE	chr3:89499360:C:T	188:chr3:89499360:C:T	0.001186
82_c5-1	82	KIT	MODERATE	c.2671G>A; c.2683G>A	p.Ala891Thr; p.Ala895Thr	3	FALSE	chr4:55602973:G:A	188:chr4:55602973:G:A	0.000923
82_c5-1	82	VHL	MODIFIER; MODERATE	c.341-3217A>T; c.397A>T	; p.Thr133Ser	0	FALSE	chr3:10188254:A:T	188:chr3:10188254:A:T	0.001311

82_c5-1	82	FGFR1	MODERATE	c.475C>T; c.481C>T; c.724C>T; c.742C>T; c.748C>T; c.841C>T	p.Arg159Trp; p.Arg161Trp; p.Arg242Trp; p.Arg248Trp; p.Arg250Trp; p.Arg281Trp	2	FALSE	chr8:38282215:G:A	188:chr8:38282215:G:A	0.001676
82_c5-1	82	ERBB2; MIEN1; MIR4728	MODERATE; MODIFIER	c.2818C>T; c.2863C>T; c.2908C>T; n.3232C>T; c.*388G>A; n.*67C>T	p.Arg940Trp; p.Arg955Trp; p.Arg970Trp;	2	FALSE	chr17:37882850:C:T	188:chr17:37882850:C:T	0.001004
11_t2c1-1	11	FGFR3	MODERATE	c.1409G>T; c.1745G>T; c.1751G>T	p.Cys470Phe; p.Cys582Phe; p.Cys584Phe	1	FALSE	chr4:1807576:G:T	189:chr4:1807576:G:T	0.004926
11_t2c1-1	11	KIT	MODERATE	c.1485C>A	p.Asn495Lys	1	FALSE	chr4:55592161:C:A	189:chr4:55592161:C:A	0.001285
11_t2c1-1	11	PIK3CA	MODERATE	c.1645G>A	p.Asp549Asn	4	FALSE	chr3:178936103:G:A	189:chr3:178936103:G:A	0.001177
11_t2c1-1	11	TP53	MODERATE	c.131G>T; c.410G>T; c.50G>T; c.527G>T	p.Cys44Phe; p.Cys137Phe; p.Cys17Phe; p.Cys176Phe	143	FALSE	chr17:7578403:C:A	189:chr17:7578403:C:A	0.002407
11_t2c1-1	11	NF1	MODERATE	c.6405C>A; c.6468C>A	p.Phe2135Leu; p.Phe2156Leu	1	FALSE	chr17:29664426:C:A	189:chr17:29664426:C:A	0.001812
11_t2c1-1	11	AKT3	MODERATE	c.44G>T	p.Arg15Met	0	FALSE	chr1:244006429:C:A	189:chr1:244006429:C:A	0.001232
11_t2c1-1	11	EGFR	MODERATE	c.1159C>G	p.Leu387Val	1	FALSE	chr7:55224477:C:G	189:chr7:55224477:C:G	0.001089
11_t2c1-1	11	ROS1	MODERATE	c.5890G>A	p.Ala1964Thr	1	FALSE	chr6:117641081:C:T	189:chr6:117641081:C:T	0.001085

11_t2c1-1	11	TP53	HIGH	c.379G>T; c.460G>T; c.739G>T; c.856G>T	p.Glu127*; p.Glu154*; p.Glu247*; p.Glu286*	82	FALSE	chr17:7577082:C:A	189:chr17:7577082:C:A	0.001211
11_t2c1-1	11	FGFR1	MODERATE	c.488G>T; c.494G>T; c.737G>T; c.755G>T; c.761G>T; c.854G>T	p.Arg163Leu; p.Arg165Leu; p.Arg246Leu; p.Arg252Leu; p.Arg254Leu; p.Arg285Leu	1	FALSE	chr8:38282202:C:A	189:chr8:38282202:C:A	0.00093
11_t2c1-1	11	TP53	MODERATE	c.400G>T; c.481G>T; c.760G>T; c.877G>T	p.Gly134Trp; p.Gly161Trp; p.Gly254Trp; p.Gly293Trp	4	FALSE	chr17:7577061:C:A	189:chr17:7577061:C:A	0.001074
11_t2c1-1	11	TP53	MODIFIER; MODERATE	c.-3G>T; c.358G>T; c.475G>T; c.79G>T	; p.Ala120Ser; p.Ala159Ser; p.Ala27Ser	23	FALSE	chr17:7578455:C:A	189:chr17:7578455:C:A	0.002177
11_t2c1-1	11	TP53	MODERATE	c.368G>T; c.449G>T; c.728G>T; c.845G>T	p.Arg123Leu; p.Arg150Leu; p.Arg243Leu; p.Arg282Leu	26	FALSE	chr17:7577093:C:A	189:chr17:7577093:C:A	0.001189
11_t2c1-1	11	EPHA3	HIGH	c.1643C>A	p.Ser548*	0	FALSE	chr3:89456467:C:A	189:chr3:89456467:C:A	0.001059
11_t2c1-1	11	HOXD-AS2; HOXD8	MODIFIER; MODERATE	n.*692G>T; c.22C>A; c.574C>A	; p.Gln8Lys; p.Gln192Lys	0	FALSE	chr2:176995668:C:A	189:chr2:176995668:C:A	0.002408
11_t2c1-1	11	ALK	MODERATE	c.1359G>T	p.Gln453His	1	FALSE	chr2:29551271:C:A	189:chr2:29551271:C:A	0.0013
11_t2c1-1	11	TP53	MODERATE	c.340C>T; c.421C>T; c.700C>T; c.817C>T	p.Arg114Cys; p.Arg141Cys; p.Arg234Cys; p.Arg273Cys	601	FALSE	chr17:7577121:G:A	189:chr17:7577121:G:A	0.001194

11_t2c1-1	11	CTNNB1	MODERATE	c.131C>A	p.Pro44His	0	FALSE	chr3:41266134:C:A	189:chr3:41266134:C:A	0.0011
11_t2c1-1	11	AKT1	MODERATE	c.1099C>T	p.Arg367Cys	1	FALSE	chr14:105239288:G:A	189:chr14:105239288:G:A	0.001259
11_t2c1-1	11	CTNNB1	MODERATE	c.884C>A	p.Ala295Asp	0	FALSE	chr3:41267300:C:A	189:chr3:41267300:C:A	0.004566
11_t2c1-1	11	ALK	MODERATE	c.4409C>T	p.Ala1470Val	1	FALSE	chr2:29416544:G:A	189:chr2:29416544:G:A	0.000927
11_t2c1-1	11	FGFR1	MODERATE	c.292C>T; c.298C>T; c.541C>T; c.559C>T; c.565C>T; c.658C>T	p.Arg98Cys; p.Arg100Cys; p.Arg181Cys; p.Arg187Cys; p.Arg189Cys; p.Arg220Cys	1	FALSE	chr8:38285495:G:A	189:chr8:38285495:G:A	0.001093
11_t2c1-1	11	NF1	MODERATE	c.7352C>A; c.7415C>A	p.Pro2451His; p.Pro2472His	6	FALSE	chr17:29677294:C:A	189:chr17:29677294:C:A	0.001122
11_t2c1-1	11	ERBB2	MODERATE; MODIFIER	c.560G>A; c.605G>A; c.650G>A; n.974G>A	p.Arg187His; p.Arg202His; p.Arg217His;	1	FALSE	chr17:37866345:G:A	189:chr17:37866345:G:A	0.001058
11_t2c1-1	11	DDR2	MODERATE	c.313C>A	p.Arg105Ser	2	FALSE	chr1:162724541:C:A	189:chr1:162724541:C:A	0.001453
11_t2c1-1	11	PTEN	HIGH	c.844G>T	p.Gly282*	1	FALSE	chr10:89720693:G:T	189:chr10:89720693:G:T	0.002119
11_t2c1-1	11	CTNNB1	MODERATE	c.134C>G	p.Ser45Cys	0	FALSE	chr3:41266137:C:G	189:chr3:41266137:C:G	0.001092
11_t2c1-1	11	HGF	MODERATE	c.251G>T	p.Cys84Phe	0	FALSE	chr7:81392026:C:A	189:chr7:81392026:C:A	0.001572
11_t2c1-1	11	CTNNB1	MODERATE	c.86C>A	p.Ser29Tyr	0	FALSE	chr3:41266089:C:A	189:chr3:41266089:C:A	0.001769
11_t2c1-1	11	PTEN	HIGH	c.633C>A	p.Cys211*	2	FALSE	chr10:89712015:C:A	189:chr10:89712015:C:A	0.002262
11_t2c1-1	11	NF1	HIGH	c.6792C>A; c.6855C>A	p.Tyr2264*; p.Tyr2285*	2	FALSE	chr17:29665757:C:A	189:chr17:29665757:C:A	0.001376

11_t2c1-1	11	TP53	MODERATE	c.248G>T; c.329G>T; c.608G>T; c.725G>T	p.Cys83Phe; p.Cys110Phe; p.Cys203Phe; p.Cys242Phe	72	FALSE	chr17:7577556:C:A	189:chr17:7577556:C:A	0.001091
11_t2c1-1	11	KRAS	MODERATE	c.35G>T	p.Gly12Val	11213	FALSE	chr12:25398284:C:A	189:chr12:25398284:C:A	0.052861
11_t2c1-1	11	CTNNB1	MODERATE	c.1972G>T	p.Val658Phe	0	FALSE	chr3:41278096:G:T	189:chr3:41278096:G:T	0.001104
11_t2c1-1	11	PTEN	MODERATE	c.829A>T	p.Thr277Ser	1	FALSE	chr10:89720678:A:T	189:chr10:89720678:A:T	0.002805
11_t2c1-1	11	TP53	MODIFIER; MODERATE	c.-5G>T; c.356G>T; c.473G>T; c.77G>T	; p.Arg119Leu; p.Arg158Leu; p.Arg26Leu	80	FALSE	chr17:7578457:C:A	189:chr17:7578457:C:A	0.001483
11_t2c1-1	11	TP53	MODERATE; MODIFIER	c.115G>T; c.232G>T; c.-279G>T; c.-360G>T	p.Ala39Ser; p.Ala78Ser;	1	FALSE	chr17:7579455:C:A	189:chr17:7579455:C:A	0.002201
11_t2c1-1	11	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2527G>A; n.-1C>T	p.Val843Ile;	6	FALSE	chr7:55259469:G:A	189:chr7:55259469:G:A	0.001263
11_t2c1-1	11	KIT	MODERATE	c.1640C>A; c.1652C>A	p.Pro547His; p.Pro551His	3	FALSE	chr4:55593586:C:A	189:chr4:55593586:C:A	0.001138
11_t2c1-1	11	TP53	MODERATE	c.128G>A; c.407G>A; c.47G>A; c.524G>A	p.Arg43His; p.Arg136His; p.Arg16His; p.Arg175His	979	FALSE	chr17:7578406:C:T	189:chr17:7578406:C:T	0.028834
11_t2c1-1	11	RET	MODERATE	c.1690A>C	p.Thr564Pro	1	FALSE	chr10:43608342:A:C	189:chr10:43608342:A:C	0.001532

11_t2c1-1	11	ERBB2; MIEN1; MIR4728	MODIFIER; MODERATE	c.*174C>A; c.3505C>A; c.3550C>A; c.3595C>A; n.3919C>A; c.*388G>T; n.*67C>A	; p.Pro1169Thr; p.Pro1184Thr; p.Pro1199Thr	2	FALSE	chr17:37884124:C:A	189:chr17:37884124:C:A	0.001134
11_t2c1-1	11	NF1	MODERATE	c.8070G>T; c.8133G>T	p.Leu2690Phe; p.Leu2711Phe	1	FALSE	chr17:29686006:G:T	189:chr17:29686006:G:T	0.011099
11_t2c1-1	11	ALK	MODERATE	c.2629G>T	p.Ala877Ser	1	FALSE	chr2:29455173:C:A	189:chr2:29455173:C:A	0.001181
11_t2c1-1	11	CTNNB1	MODERATE	c.110C>A	p.Ser37Tyr	0	FALSE	chr3:41266113:C:A	189:chr3:41266113:C:A	0.001128
11_t2c1-1	11	HOXD-AS2; HOXD8	MODIFIER; MODERATE	n.*692C>T; c.-123-30G>A; c.400G>A	; p.Ala134Thr	0	FALSE	chr2:176995494:G:A	189:chr2:176995494:G:A	0.001354
11_t2c1-1	11	CTNNB1	MODERATE	c.122C>A	p.Thr41Asn	0	FALSE	chr3:41266125:C:A	189:chr3:41266125:C:A	0.001117
11_t2c1-1	11	FGFR1	MODERATE	c.487C>T; c.493C>T; c.736C>T; c.754C>T; c.760C>T; c.853C>T	p.Arg163Trp; p.Arg165Trp; p.Arg246Trp; p.Arg252Trp; p.Arg254Trp; p.Arg285Trp	1	FALSE	chr8:38282203:G:A	189:chr8:38282203:G:A	0.00093
11_t2c1-1	11	ALK	HIGH	c.1651C>T	p.Arg551*	2	FALSE	chr2:29519920:G:A	189:chr2:29519920:G:A	0.00105
11_t2c1-1	11	EPHA3	MODERATE	c.2662C>A	p.Leu888Met	0	FALSE	chr3:89499492:C:A	189:chr3:89499492:C:A	0.001554
11_t2c1-1	11	ROS1	HIGH	c.5209G>T	p.Glu1737*	2	FALSE	chr6:117658374:C:A	189:chr6:117658374:C:A	0.001282
11_t2c1-1	11	TP53	MODIFIER; MODERATE	c.-9G>T; c.352G>T; c.469G>T; c.73G>T	; p.Val118Phe; p.Val157Phe; p.Val25Phe	169	FALSE	chr17:7578461:C:A	189:chr17:7578461:C:A	0.001487

11_t2c1-1	11	MAP2K1	MODERATE	c.395C>T	p.Ala132Val	1	FALSE	chr15:66729187:C:T	189:chr15:66729187:C:T	0.000891
11_t2c1-1	11	MITF	MODIFIER; MODERATE	c.-45G>A; c.109G>A; c.112G>A; c.64G>A	; p.Ala37Thr; p.Ala38Thr; p.Ala22Thr	0	FALSE	chr3:69928292:G:A	189:chr3:69928292:G:A	0.001181
11_t2c1-1	11	PIK3CA	MODERATE	c.518C>A	p.Ser173Tyr	1	FALSE	chr3:178917643:C:A	189:chr3:178917643:C:A	0.001793
11_t2c1-1	11	PTEN	MODERATE	c.443C>A	p.Ala148Glu	1	FALSE	chr10:89692959:C:A	189:chr10:89692959:C:A	0.001337
11_t2c1-1	11	TP53	MODERATE	c.151T>C; c.430T>C; c.547T>C; c.70T>C	p.Ser51Pro; p.Ser144Pro; p.Ser183Pro; p.Ser24Pro	9	FALSE	chr17:7578383:A:G	189:chr17:7578383:A:G	0.001059
11_t2c1-1	11	NF1	MODERATE	c.2533T>C	p.Cys845Arg	2	FALSE	chr17:29556166:T:C	189:chr17:29556166:T:C	0.001198
11_t2c1-1	11	AKT3	MODERATE	c.797A>G	p.Lys266Arg	0	FALSE	chr1:243736250:T:C	189:chr1:243736250:T:C	0.00253
11_t2c1-1	11	ERBB2; MIEN1; MIR4728	MODERATE; MODIFIER	c.2434G>A; c.2479G>A; c.2524G>A; n.2848G>A; c.*388C>T; n.-1G>A	p.Val812Ile; p.Val827Ile; p.Val842Ile;	17	FALSE	chr17:37881332:G:A	189:chr17:37881332:G:A	0.001052
11_t2c1-1	11	FGFR1	MODIFIER; MODERATE	c.-85G>T; c.107G>T; c.8G>T	; p.Ser36Ile; p.Ser3Ile	1	FALSE	chr8:38314957:C:A	189:chr8:38314957:C:A	0.002812
11_t2c1-1	11	TP53	MODERATE	c.349G>T; c.430G>T; c.709G>T; c.826G>T	p.Ala117Ser; p.Ala144Ser; p.Ala237Ser; p.Ala276Ser	16	FALSE	chr17:7577112:C:A	189:chr17:7577112:C:A	0.001198
11_t2c1-1	11	KIT	MODERATE	c.530G>A	p.Arg177His	1	FALSE	chr4:55564642:G:A	189:chr4:55564642:G:A	0.000909

11_t2c1-1	11	TP53	MODERATE; MODIFIER	c.100G>T; c.217G>T; c.-279G>T; c.-360G>T	p.Val34Leu; p.Val73Leu;	5	FALSE	chr17:7579470:C:A	189:chr17:7579470:C:A	0.001475
60_bl-2	60	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2568T>G; n.-1A>C	p.Phe856Leu;	1	FALSE	chr7:55259510:T:G	190:chr7:55259510:T:G	0.001733
60_bl-2	60	TP53	MODIFIER; MODERATE	c.*173G>T; c.*85G>T; c.1066G>T; c.589G>T; c.670G>T; c.949G>T	; p.Gly356Trp; p.Gly197Trp; p.Gly224Trp; p.Gly317Trp	2	FALSE	chr17:7573961:C:A	190:chr17:7573961:C:A	0.001332
60_bl-2	60	AKT3	HIGH	c.289G>T	p.Glu97*	0	FALSE	chr1:243809335:C:A	190:chr1:243809335:C:A	0.002358
60_bl-2	60	ALK	MODERATE	c.3512T>C	p.Ile1171Thr	5	FALSE	chr2:29445213:A:G	190:chr2:29445213:A:G	0.003096
60_bl-2	60	CTNNB1	MODERATE	c.134C>A	p.Ser45Tyr	0	FALSE	chr3:41266137:C:A	190:chr3:41266137:C:A	0.002439
60_bl-2	60	TP53	MODIFIER; MODERATE	c.-5G>T; c.356G>T; c.473G>T; c.77G>T	; p.Arg119Leu; p.Arg158Leu; p.Arg26Leu	80	FALSE	chr17:7578457:C:A	190:chr17:7578457:C:A	0.00283
60_bl-2	60	HGF	MODERATE	c.251G>T	p.Cys84Phe	0	FALSE	chr7:81392026:C:A	190:chr7:81392026:C:A	0.002911
60_bl-2	60	TP53	MODERATE	c.347G>T; c.428G>T; c.707G>T; c.824G>T	p.Cys116Phe; p.Cys143Phe; p.Cys236Phe; p.Cys275Phe	57	FALSE	chr17:7577114:C:A	190:chr17:7577114:C:A	0.001776
60_bl-2	60	EPHA3	MODERATE	c.1535G>A	p.Arg512Gln	0	FALSE	chr3:89448571:G:A	190:chr3:89448571:G:A	0.002037
60_bl-2	60	CTNNB1	MODERATE	c.110C>A	p.Ser37Tyr	0	FALSE	chr3:41266113:C:A	190:chr3:41266113:C:A	0.001724
60_bl-2	60	MAP2K1	MODERATE	c.371C>A	p.Pro124Gln	1	FALSE	chr15:66729163:C:A	190:chr15:66729163:C:A	0.001385
60_bl-2	60	KIT	MODERATE	c.1486G>A	p.Asp496Asn	1	FALSE	chr4:55592162:G:A	190:chr4:55592162:G:A	0.001996

60_bl-2	60	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2410G>A; n.1152C>T	p.Glu804Lys;	2	FALSE	chr7:55249112:G:A	190:chr7:55249112:G:A	0.001233
60_bl-2	60	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2507G>A; n.-1C>T	p.Arg836His;	2	FALSE	chr7:55259449:G:A	190:chr7:55259449:G:A	0.001946
60_bl-2	60	DDR2	MODERATE	c.313C>A	p.Arg105Ser	2	FALSE	chr1:162724541:C:A	190:chr1:162724541:C:A	0.002594
60_bl-2	60	MITF	MODIFIER; MODERATE	c.93+115G>A; c.208G>A; c.373G>A; c.481G>A; c.526G>A; c.529G>A	; p.Ala70Thr; p.Ala125Thr; p.Ala161Thr; p.Ala176Thr; p.Ala177Thr	0	FALSE	chr3:69987147:G:A	190:chr3:69987147:G:A	0.002394
60_bl-2	60	KIT	MODERATE	c.875C>T	p.Ala292Val	1	FALSE	chr4:55570008:C:T	190:chr4:55570008:C:T	0.001699
60_bl-2	60	HRAS; LRRC56	MODERATE; MODIFIER	c.183G>T; c.-506C>A	p.Gln61His;	15	FALSE	chr11:533873:C:A	190:chr11:533873:C:A	0.001464
60_bl-2	60	MET	HIGH	c.1639C>T	p.Arg547*	2	FALSE	chr7:116381017:C:T	190:chr7:116381017:C:T	0.001284
60_bl-2	60	RET	MODERATE	c.1991C>A	p.Ala664Asp	2	FALSE	chr10:43610039:C:A	190:chr10:43610039:C:A	0.003731
60_bl-2	60	TP53	MODERATE	c.359G>T; c.440G>T; c.719G>T; c.836G>T	p.Gly120Val; p.Gly147Val; p.Gly240Val; p.Gly279Val	37	FALSE	chr17:7577102:C:A	190:chr17:7577102:C:A	0.001701
60_bl-2	60	MET	MODERATE	c.3443G>A; c.3497G>A	p.Arg1148Gln; p.Arg1166Gln	4	FALSE	chr7:116418932:G:A	190:chr7:116418932:G:A	0.001484
60_bl-2	60	CTNNB1	MODERATE	c.1972G>T	p.Val658Phe	0	FALSE	chr3:41278096:G:T	190:chr3:41278096:G:T	0.002646
60_bl-2	60	EGFR	MODERATE	c.988G>A	p.Glu330Lys	1	FALSE	chr7:55223621:G:A	190:chr7:55223621:G:A	0.001702
60_bl-2	60	TP53	MODERATE	c.341G>A; c.422G>A; c.701G>A; c.818G>A	p.Arg114His; p.Arg141His; p.Arg234His; p.Arg273His	647	TRUE	chr17:7577120:C:T	190:chr17:7577120:C:T	0.116801

60_bl-2	60	PIK3CA	MODERATE	c.1636C>A	p.Gln546Lys	127	FALSE	chr3:178936094:C:A	190:chr3:178936094:C:A	0.076118
60_bl-2	60	TP53	MODERATE	c.112G>T; c.193G>T; c.472G>T; c.589G>T	p.Val38Leu; p.Val65Leu; p.Val158Leu; p.Val197Leu	12	FALSE	chr17:7578260:C:A	190:chr17:7578260:C:A	0.001456
60_bl-2	60	MET	MODERATE	c.1450C>A	p.His484Asn	1	FALSE	chr7:116380061:C:A	190:chr7:116380061:C:A	0.00156
60_bl-2	60	AKT3	MODERATE	c.44G>T	p.Arg15Met	0	FALSE	chr1:244006429:C:A	190:chr1:244006429:C:A	0.001759
60_bl-2	60	PIK3CA	MODERATE	c.263G>A	p.Arg88Gln	97	FALSE	chr3:178916876:G:A	190:chr3:178916876:G:A	0.086194
60_bl-2	60	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2591C>A; n.-1G>T	p.Ala864Glu;	2	FALSE	chr7:55259533:C:A	190:chr7:55259533:C:A	0.001779
60_bl-2	60	HGF	MODERATE	c.2157G>T; c.2172G>T	p.Lys719Asn; p.Lys724Asn	0	FALSE	chr7:81331912:C:A	190:chr7:81331912:C:A	0.00177
60_bl-2	60	CTNNB1	MODERATE	c.125C>A	p.Thr42Lys	0	FALSE	chr3:41266128:C:A	190:chr3:41266128:C:A	0.001658
60_bl-2	60	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2305G>A; n.1257C>T	p.Val769Met;	3	FALSE	chr7:55249007:G:A	190:chr7:55249007:G:A	0.00117
60_bl-2	60	NF1	HIGH	c.5817C>A; c.5880C>A	p.Cys1939*; p.Cys1960*	1	FALSE	chr17:29661923:C:A	190:chr17:29661923:C:A	0.004813
60_bl-2	60	FGFR1; LETM2	MODERATE; MODIFIER	c.1777T>G; c.1783T>G; c.2020T>G; c.2044T>G; c.2050T>G; c.2143T>G; c.*1406A>C; c.*1423A>C; c.*1553A>C; c.*1567A>C; c.*1638A>C	p.Trp593Gly; p.Trp595Gly; p.Trp674Gly; p.Trp682Gly; p.Trp684Gly; p.Trp715Gly;	1	FALSE	chr8:38271806:A:C	190:chr8:38271806:A:C	0.003537

60_bl-2	60	TP53	MODERATE	c.127C>T; c.208C>T; c.487C>T; c.604C>T	p.Arg43Cys; p.Arg70Cys; p.Arg163Cys; p.Arg202Cys	6	FALSE	chr17:7578245:G:A	190:chr17:7578245:G:A	0.001412
60_bl-2	60	KRAS	MODERATE	c.35G>A	p.Gly12Asp	11213	FALSE	chr12:25398284:C:T	190:chr12:25398284:C:T	0.102876
60_bl-2	60	TP53	HIGH; MODIFIER	c.184G>T; c.67G>T; c.-279G>T; c.-360G>T	p.Glu62*; p.Glu23*;	8	FALSE	chr17:7579503:C:A	190:chr17:7579503:C:A	0.002257
62_bl-2	62	EPHA3	MODERATE	c.1132C>A	p.Pro378Thr	0	FALSE	chr3:89391066:C:A	191:chr3:89391066:C:A	0.000709
62_bl-2	62	EPHA3	MODERATE	c.1280C>T	p.Ala427Val	0	FALSE	chr3:89391214:C:T	191:chr3:89391214:C:T	0.000859
62_bl-2	62	PIK3CA	MODERATE	c.478C>A	p.His160Asn	1	FALSE	chr3:178917603:C:A	191:chr3:178917603:C:A	0.002375
62_bl-2	62	TP53	MODERATE	c.343G>T; c.424G>T; c.703G>T; c.820G>T	p.Val115Phe; p.Val142Phe; p.Val235Phe; p.Val274Phe	25	FALSE	chr17:7577118:C:A	191:chr17:7577118:C:A	0.001517
62_bl-2	62	TP53	MODERATE	c.126G>T; c.207G>T; c.486G>T; c.603G>T	p.Leu42Phe; p.Leu69Phe; p.Leu162Phe; p.Leu201Phe	4	FALSE	chr17:7578246:C:A	191:chr17:7578246:C:A	0.001183
62_bl-2	62	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2591C>T; n.-1G>A	p.Ala864Val;	2	FALSE	chr7:55259533:C:T	191:chr7:55259533:C:T	0.002114
62_bl-2	62	CTNNB1	MODERATE	c.1345C>T	p.Arg449Cys	0	FALSE	chr3:41275179:C:T	191:chr3:41275179:C:T	0.001744
62_bl-2	62	FGFR1	MODERATE	c.475C>T; c.481C>T; c.724C>T; c.742C>T; c.748C>T; c.841C>T	p.Arg159Trp; p.Arg161Trp; p.Arg242Trp; p.Arg248Trp; p.Arg250Trp; p.Arg281Trp	2	FALSE	chr8:38282215:G:A	191:chr8:38282215:G:A	0.001352

62_bl-2	62	EGFR; EGFR-AS1	LOW; MODIFIER	c.2472C>A; n.-1G>T	p.Gly824Gly;	1	FALSE	chr7:55259414:C:A	191:chr7:55259414:C:A	0.003361
62_bl-2	62	PTEN	MODERATE	c.443C>A	p.Ala148Glu	1	FALSE	chr10:89692959:C:A	191:chr10:89692959:C:A	0.003663
62_bl-2	62	DDR2	MODERATE	c.691C>A	p.Gln231Lys	1	FALSE	chr1:162729605:C:A	191:chr1:162729605:C:A	0.001991
62_bl-2	62	RET	MODERATE	c.2242G>T	p.Gly748Cys	1	FALSE	chr10:43612137:G:T	191:chr10:43612137:G:T	0.001361
62_bl-2	62	TP53	MODERATE	c.421C>T; c.502C>T; c.781C>T; c.898C>T	p.Pro141Ser; p.Pro168Ser; p.Pro261Ser; p.Pro300Ser	3	FALSE	chr17:7577040:G:A	191:chr17:7577040:G:A	0.001556
62_bl-2	62	HRAS; LRRC56	MODERATE; MODIFIER	c.383G>T; c.-506C>A	p.Arg128Leu;	1	FALSE	chr11:533520:C:A	191:chr11:533520:C:A	0.001471
62_bl-2	62	MAP2K1	MODERATE	c.722C>A	p.Ser241Tyr	2	FALSE	chr15:66777356:C:A	191:chr15:66777356:C:A	0.002201
62_bl-2	62	PIK3CA	HIGH	c.816T>A	p.Tyr272*	1	FALSE	chr3:178921334:T:A	191:chr3:178921334:T:A	0.002317
62_bl-2	62	EGFR	MODIFIER; MODERATE	c.*2364C>T; c.2174C>T	; p.Thr725Met	2	FALSE	chr7:55241726:C:T	191:chr7:55241726:C:T	0.001919
62_bl-2	62	PIK3CA	MODERATE	c.1090G>A	p.Gly364Arg	3	FALSE	chr3:178922321:G:A	191:chr3:178922321:G:A	0.002257
62_bl-2	62	FGFR1	MODIFIER; MODERATE	c.-85G>T; c.107G>T; c.8G>T	; p.Ser36Ile; p.Ser3Ile	1	FALSE	chr8:38314957:C:A	191:chr8:38314957:C:A	0.003561
62_bl-2	62	PIK3CA	MODERATE	c.1255C>A	p.His419Asn	1	FALSE	chr3:178927977:C:A	191:chr3:178927977:C:A	0.006316
62_bl-2	62	TP53	MODERATE; MODIFIER	c.170C>T; c.287C>T; c.-279C>T; c.-360C>T	p.Ser57Phe; p.Ser96Phe;	3	FALSE	chr17:7579400:G:A	191:chr17:7579400:G:A	0.002112
62_bl-2	62	PIK3CA	MODERATE	c.1615C>A	p.Pro539Thr	3	FALSE	chr3:178936073:C:A	191:chr3:178936073:C:A	0.002296
62_bl-2	62	TP53	MODIFIER; MODERATE	c.-3G>T; c.358G>T; c.475G>T; c.79G>T	; p.Ala120Ser; p.Ala159Ser; p.Ala27Ser	23	FALSE	chr17:7578455:C:A	191:chr17:7578455:C:A	0.003735

62_bl-2	62	MAP2K1	MODERATE	c.316G>A	p.Ala106Thr	1	FALSE	chr15:66729108:G:A	191:chr15:66729108:G:A	0.001635
62_bl-2	62	MET	MODERATE	c.608C>A	p.Ser203Tyr	1	FALSE	chr7:116339746:C:A	191:chr7:116339746:C:A	0.002423
62_bl-2	62	PTEN	MODERATE	c.421C>A	p.His141Asn	2	FALSE	chr10:89692937:C:A	191:chr10:89692937:C:A	0.003297
62_bl-2	62	EPHA3	MODERATE	c.1379C>A	p.Pro460His	0	FALSE	chr3:89445059:C:A	191:chr3:89445059:C:A	0.001293
62_bl-2	62	MET	MODERATE	c.487T>C	p.Ser163Pro	1	FALSE	chr7:116339625:T:C	191:chr7:116339625:T:C	0.002527
62_bl-2	62	ERBB2; MIEN1; MIR4728	MODERATE; MODIFIER	c.2818C>T; c.2863C>T; c.2908C>T; n.3232C>T; c.*388G>A; n.*67C>T	p.Arg940Trp; p.Arg955Trp; p.Arg970Trp;	2	FALSE	chr17:37882850:C:T	191:chr17:37882850:C:T	0.001232
62_bl-2	62	ERBB2; MIEN1; MIR4728	MODERATE; MODIFIER	c.3025G>A; c.3070G>A; c.3115G>A; n.3439G>A; c.*388C>T; n.*67G>A	p.Ala1009Thr; p.Ala1024Thr; p.Ala1039Thr;	2	FALSE	chr17:37883212:G:A	191:chr17:37883212:G:A	0.002326
62_bl-2	62	MAP2K1	MODERATE	c.198C>A	p.Asp66Glu	4	FALSE	chr15:66727482:C:A	191:chr15:66727482:C:A	0.002972
62_bl-2	62	ALK	MODERATE	c.874C>T	p.Arg292Cys	1	FALSE	chr2:29917794:G:A	191:chr2:29917794:G:A	0.001356
62_bl-2	62	EPHA3	HIGH	c.1515C>A	p.Tyr505*	0	FALSE	chr3:89448551:C:A	191:chr3:89448551:C:A	0.001984
62_bl-2	62	KIT	MODERATE	c.1485C>A	p.Asn495Lys	1	FALSE	chr4:55592161:C:A	191:chr4:55592161:C:A	0.002743
62_bl-2	62	TP53	MODERATE	c.367C>T; c.448C>T; c.727C>T; c.844C>T	p.Arg123Trp; p.Arg150Trp; p.Arg243Trp; p.Arg282Trp	479	FALSE	chr17:7577094:G:A	191:chr17:7577094:G:A	0.001572

62_bl-2	62	TP53	MODERATE; HIGH	c.363G>T; c.480G>T; c.84G>T; c.3G>T	p.Met121Ile; p.Met160Ile; p.Met28Ile; p.Met1?	4	FALSE	chr17:7578450:C:A	191:chr17:7578450:C:A	0.00188
62_bl-2	62	PTEN	MODERATE	c.729C>A	p.Phe243Leu	1	FALSE	chr10:89717704:C:A	191:chr10:89717704:C:A	0.00216
62_bl-2	62	CSDE1; NRAS	MODIFIER; MODERATE	c.*2430A>G; c.*2523A>G; c.*2817A>G; c.*2910A>G; c.*2964A>G; c.*3057A>G; c.182A>G	; p.Gln61Arg	1103	FALSE	chr1:115256529:T:C	191:chr1:115256529:T:C	0.472279
62_bl-2	62	NF1	MODERATE	c.6405C>A; c.6468C>A	p.Phe2135Leu; p.Phe2156Leu	1	FALSE	chr17:29664426:C:A	191:chr17:29664426:C:A	0.002304
62_bl-2	62	DDR2	MODERATE	c.1598C>A	p.Thr533Lys	1	FALSE	chr1:162741907:C:A	191:chr1:162741907:C:A	0.001311
62_bl-2	62	PHLPP1	MODERATE	c.2303C>A	p.Ser768Tyr	0	FALSE	chr18:60563103:C:A	191:chr18:60563103:C:A	0.003049
62_bl-2	62	TP53	MODERATE	c.128G>T; c.209G>T; c.488G>T; c.605G>T	p.Arg43Leu; p.Arg70Leu; p.Arg163Leu; p.Arg202Leu	4	FALSE	chr17:7578244:C:A	191:chr17:7578244:C:A	0.0012
62_bl-2	62	TP53	MODERATE	c.110G>T; c.191G>T; c.470G>T; c.587G>T	p.Arg37Leu; p.Arg64Leu; p.Arg157Leu; p.Arg196Leu	19	FALSE	chr17:7578262:C:A	191:chr17:7578262:C:A	0.001195
62_bl-2	62	AKT1	MODERATE	c.286C>T	p.Arg96Trp	1	FALSE	chr14:105242997:G:A	191:chr14:105242997:G:A	0.001741
62_bl-2	62	BRAF	MODERATE	c.603G>T	p.Gln201His	1	FALSE	chr7:140508697:C:A	191:chr7:140508697:C:A	0.002421
62_bl-2	62	CTNNB1	MODERATE	c.125C>A	p.Thr42Lys	0	FALSE	chr3:41266128:C:A	191:chr3:41266128:C:A	0.002674

62_bl-2	62	ALK	MODERATE	c.3640C>T	p.Arg1214Cys	1	FALSE	chr2:29443577:G:A	191:chr2:29443577:G:A	0.002789
62_bl-2	62	AKT3	MODERATE	c.44G>T	p.Arg15Met	0	FALSE	chr1:244006429:C:A	191:chr1:244006429:C:A	0.001566
62_bl-2	62	PIK3CA	MODERATE	c.3180C>A	p.His1060Gln	2	FALSE	chr3:178952125:C:A	191:chr3:178952125:C:A	0.001453
62_bl-2	62	DDR2	MODERATE	c.313C>A	p.Arg105Ser	2	FALSE	chr1:162724541:C:A	191:chr1:162724541:C:A	0.0027
62_bl-2	62	TP53	MODIFIER; MODERATE	c.*135A>G; c.*47A>G; c.1028A>G; c.551A>G; c.632A>G; c.911A>G	; p.Glu343Gly; p.Glu184Gly; p.Glu211Gly; p.Glu304Gly	1	FALSE	chr17:7573999:T:C	191:chr17:7573999:T:C	0.001385
62_bl-2	62	BRAF	MODERATE	c.914C>T	p.Ala305Val	2	FALSE	chr7:140500228:G:A	191:chr7:140500228:G:A	0.001681
62_bl-2	62	EPHA3	HIGH	c.318C>A	p.Cys106*	0	FALSE	chr3:89259174:C:A	191:chr3:89259174:C:A	0.001412
62_bl-2	62	CTNNB1	MODERATE	c.1564G>A	p.Ala522Thr	0	FALSE	chr3:41275669:G:A	191:chr3:41275669:G:A	0.002457
62_bl-2	62	EPHA3	MODERATE	c.2306G>A	p.Arg769His	0	FALSE	chr3:89480469:G:A	191:chr3:89480469:G:A	0.000839
62_bl-2	62	PTEN	HIGH	c.720C>A	p.Tyr240*	3	FALSE	chr10:89717695:C:A	191:chr10:89717695:C:A	0.002024
62_bl-2	62	CTNNB1	MODERATE	c.98C>A	p.Ser33Tyr	0	FALSE	chr3:41266101:C:A	191:chr3:41266101:C:A	0.002793
62_bl-2	62	TP53	MODIFIER; HIGH	c.*143G>T; c.*55G>T; c.1036G>T; c.559G>T; c.640G>T; c.919G>T	; p.Glu346*; p.Glu187*; p.Glu214*; p.Glu307*	4	FALSE	chr17:7573991:C:A	191:chr17:7573991:C:A	0.001317
62_bl-2	62	HRAS; LRRC56	MODERATE; MODIFIER	c.248C>T; c.-506G>A	p.Ala83Val;	1	FALSE	chr11:533808:G:A	191:chr11:533808:G:A	0.001604
62_bl-2	62	MET	MODERATE	c.142G>A	p.Ala48Thr	1	FALSE	chr7:116339280:G:A	191:chr7:116339280:G:A	0.001453

62_bl-2	62	RET	MODERATE	c.1991C>A	p.Ala664Asp	2	FALSE	chr10:43610039:C:A	191:chr10:43610039:C:A	0.001168
62_bl-2	62	PTEN	MODERATE	c.392C>A	p.Thr131Asn	2	FALSE	chr10:89692908:C:A	191:chr10:89692908:C:A	0.002882
62_bl-2	62	ERBB2	MODERATE; MODIFIER	c.560G>A; c.605G>A; c.650G>A; n.974G>A	p.Arg187His; p.Arg202His; p.Arg217His;	1	FALSE	chr17:37866345:G:A	191:chr17:37866345:G:A	0.001523
62_bl-2	62	CTNNB1	MODERATE	c.110C>A	p.Ser37Tyr	0	FALSE	chr3:41266113:C:A	191:chr3:41266113:C:A	0.002774
62_bl-2	62	TP53	MODERATE; MODIFIER	c.158C>T; c.275C>T; c.-279C>T; c.-360C>T	p.Pro53Leu; p.Pro92Leu;	1	FALSE	chr17:7579412:G:A	191:chr17:7579412:G:A	0.002179
62_bl-2	62	EGFR	MODERATE	c.988G>A	p.Glu330Lys	1	FALSE	chr7:55223621:G:A	191:chr7:55223621:G:A	0.001559
62_bl-2	62	EGFR	MODIFIER; MODERATE	c.*2364G>A; c.2125G>A	; p.Glu709Lys	21	FALSE	chr7:55241677:G:A	191:chr7:55241677:G:A	0.001674
70_bl-2	70	ROS1	MODERATE	c.5412G>T	p.Lys1804Asn	1	FALSE	chr6:117647532:C:A	192:chr6:117647532:C:A	0.001404
70_bl-2	70	EPHA3	MODERATE	c.237C>A	p.Asn79Lys	0	FALSE	chr3:89259093:C:A	192:chr3:89259093:C:A	0.001021
70_bl-2	70	ERBB2; MIEN1; MIR4728	MODERATE; MODIFIER	c.2720A>G; c.2765A>G; c.2810A>G; n.3134A>G; c.*388T>C; n.-1A>G	p.Lys907Arg; p.Lys922Arg; p.Lys937Arg;	1	FALSE	chr17:37882044:A:G	192:chr17:37882044:A:G	0.000677
70_bl-2	70	KIT	MODERATE	c.148G>A	p.Val50Met	4	FALSE	chr4:55561758:G:A	192:chr4:55561758:G:A	0.000868
70_bl-2	70	TP53	MODERATE	c.169G>T; c.250G>T; c.529G>T; c.646G>T	p.Val57Leu; p.Val84Leu; p.Val177Leu; p.Val216Leu	72	FALSE	chr17:7578203:C:A	192:chr17:7578203:C:A	0.000868
70_bl-2	70	RET	MODERATE	c.2116G>A	p.Val706Met	2	FALSE	chr10:43610164:G:A	192:chr10:43610164:G:A	0.000519

70_bl-2	70	TP53	MODIFIER; HIGH	c.*143G>T; c.*55G>T; c.1036G>T; c.559G>T; c.640G>T; c.919G>T	; p.Glu346*; p.Glu187*; p.Glu214*; p.Glu307*	4	FALSE	chr17:7573991:C:A	192:chr17:7573991:C:A	0.000866
70_bl-2	70	RET	MODERATE	c.1991C>A	p.Ala664Asp	2	FALSE	chr10:43610039:C:A	192:chr10:43610039:C:A	0.001088
70_bl-2	70	TP53	MODERATE	c.337G>T; c.418G>T; c.697G>T; c.814G>T	p.Val113Leu; p.Val140Leu; p.Val233Leu; p.Val272Leu	85	FALSE	chr17:7577124:C:A	192:chr17:7577124:C:A	0.001016
70_bl-2	70	TP53	MODERATE	c.110G>T; c.191G>T; c.470G>T; c.587G>T	p.Arg37Leu; p.Arg64Leu; p.Arg157Leu; p.Arg196Leu	19	FALSE	chr17:7578262:C:A	192:chr17:7578262:C:A	0.000842
70_bl-2	70	EPHA3	HIGH	c.318C>A	p.Cys106*	0	FALSE	chr3:89259174:C:A	192:chr3:89259174:C:A	0.002535
70_bl-2	70	KRAS	MODERATE	c.34G>T	p.Gly12Cys	3755	FALSE	chr12:25398285:C:A	192:chr12:25398285:C:A	0.000881
70_bl-2	70	ERBB2; MIR4728	MODERATE; MODIFIER	c.2020G>A; c.2065G>A; c.2110G>A; n.2434G>A; n.-1G>A	p.Gly674Arg; p.Gly689Arg; p.Gly704Arg;	1	FALSE	chr17:37879815:G:A	192:chr17:37879815:G:A	0.000864
70_bl-2	70	CTNNB1	MODERATE	c.91C>A	p.Leu31Met	0	FALSE	chr3:41266094:C:A	192:chr3:41266094:C:A	0.001942
70_bl-2	70	HRAS; LRRC56	MODERATE; MODIFIER	c.175G>A; c.-506C>T	p.Ala59Thr;	2	FALSE	chr11:533881:C:T	192:chr11:533881:C:T	0.000923
70_bl-2	70	BRAF	MODERATE	c.929C>T	p.Thr310Ile	1	FALSE	chr7:140500213:G:A	192:chr7:140500213:G:A	0.000616
70_bl-2	70	HGF	HIGH	c.1969G>T; c.1984G>T	p.Glu657*; p.Glu662*	0	FALSE	chr7:81334732:C:A	192:chr7:81334732:C:A	0.000975
70_bl-2	70	CTNNB1	MODERATE	c.559G>A	p.Ala187Thr	0	FALSE	chr3:41266888:G:A	192:chr3:41266888:G:A	0.001448

70_bl-2	70	ERBB2	MODERATE; MODIFIER	c.1042C>T; c.1087C>T; c.1132C>T; n.1456C>T	p.Pro348Ser; p.Pro363Ser; p.Pro378Ser;	1	FALSE	chr17:37868685:C:T	192:chr17:37868685:C:T	0.000598
70_bl-2	70	NF1	MODERATE	c.6405C>A; c.6468C>A	p.Phe2135Leu; p.Phe2156Leu	1	FALSE	chr17:29664426:C:A	192:chr17:29664426:C:A	0.001718
70_bl-2	70	TP53	MODIFIER; MODERATE	c.-13G>T; c.105G>T; c.-279G>T; c.-360G>T	; p.Leu35Phe	2	FALSE	chr17:7579582:C:A	192:chr17:7579582:C:A	0.002113
70_bl-2	70	DDR2	MODERATE	c.1234C>A	p.Leu412Ile	1	FALSE	chr1:162737090:C:A	192:chr1:162737090:C:A	0.001336
70_bl-2	70	TP53	MODERATE	c.248G>T; c.329G>T; c.608G>T; c.725G>T	p.Cys83Phe; p.Cys110Phe; p.Cys203Phe; p.Cys242Phe	72	FALSE	chr17:7577556:C:A	192:chr17:7577556:C:A	0.001078
70_bl-2	70	DDR2	MODERATE	c.2255G>A	p.Arg752His	1	FALSE	chr1:162746132:G:A	192:chr1:162746132:G:A	0.000895
70_bl-2	70	NF1	HIGH	c.6792C>A; c.6855C>A	p.Tyr2264*; p.Tyr2285*	2	FALSE	chr17:29665757:C:A	192:chr17:29665757:C:A	0.000955
70_bl-2	70	EGFR	MODERATE	c.1159C>G	p.Leu387Val	1	FALSE	chr7:55224477:C:G	192:chr7:55224477:C:G	0.001103
70_bl-2	70	NF1	MODERATE	c.3559C>A	p.Leu1187Ile	1	FALSE	chr17:29560082:C:A	192:chr17:29560082:C:A	0.000842
70_bl-2	70	TP53	MODERATE; MODIFIER	c.100G>T; c.217G>T; c.-279G>T; c.-360G>T	p.Val34Leu; p.Val73Leu;	5	FALSE	chr17:7579470:C:A	192:chr17:7579470:C:A	0.00132
70_bl-2	70	RET	MODERATE	c.1867G>A	p.Glu623Lys	1	FALSE	chr10:43609111:G:A	192:chr10:43609111:G:A	0.000817

70_bl-2	70	GAPDH; IFFO1; NCAPD2	MODERATE; MODIFIER	c.148G>A; c.274G>A; c.*1743C>T; c.*1746C>T; c.*1770C>T; n.*2798C>T; c.*4252G>A	p.Ala50Thr; p.Ala92Thr;	0	FALSE	chr12:6646123:G:A	192:chr12:6646123:G:A	0.00079
70_bl-2	70	PIK3CA	MODERATE	c.35G>A	p.Gly12Asp	5	FALSE	chr3:178916648:G:A	192:chr3:178916648:G:A	0.000562
70_bl-2	70	DDR2	MODERATE	c.1598C>A	p.Thr533Lys	1	FALSE	chr1:162741907:C:A	192:chr1:162741907:C:A	0.001661
70_bl-2	70	PTEN	HIGH	c.633C>A	p.Cys211*	2	FALSE	chr10:89712015:C:A	192:chr10:89712015:C:A	0.002747
70_bl-2	70	GAPDH; IFFO1	MODERATE; MODIFIER	c.217G>A; c.343G>A; c.*1743C>T; c.*1746C>T; c.*1770C>T; n.*2798C>T	p.Gly73Arg; p.Gly115Arg;	0	FALSE	chr12:6646282:G:A	192:chr12:6646282:G:A	0.000805
70_bl-2	70	TP53	MODERATE	c.175G>T; c.256G>T; c.535G>T; c.652G>T	p.Val59Leu; p.Val86Leu; p.Val179Leu; p.Val218Leu	7	FALSE	chr17:7578197:C:A	192:chr17:7578197:C:A	0.000861
70_bl-2	70	ALK	HIGH	c.1120G>T	p.Glu374*	1	FALSE	chr2:29754815:C:A	192:chr2:29754815:C:A	0.001036
70_bl-2	70	TP53	MODERATE; MODIFIER	c.175G>T; c.58G>T; c.-279G>T; c.-360G>T	p.Gly59Cys; p.Gly20Cys;	3	FALSE	chr17:7579512:C:A	192:chr17:7579512:C:A	0.001416
70_bl-2	70	BRAF	MODERATE	c.914C>T	p.Ala305Val	2	FALSE	chr7:140500228:G:A	192:chr7:140500228:G:A	0.000799

70_bl-2	70	TP53	MODERATE	c.367C>T; c.448C>T; c.727C>T; c.844C>T	p.Arg123Trp; p.Arg150Trp; p.Arg243Trp; p.Arg282Trp	479	FALSE	chr17:7577094:G:A	192:chr17:7577094:G:A	0.000995
70_bl-2	70	PTEN	MODERATE	c.389G>A	p.Arg130Gln	89	FALSE	chr10:89692905:G:A	192:chr10:89692905:G:A	0.00157
70_bl-2	70	CTNNB1	MODERATE	c.125C>A	p.Thr42Lys	0	FALSE	chr3:41266128:C:A	192:chr3:41266128:C:A	0.00129
70_bl-2	70	CSDE1; NRAS	MODIFIER; HIGH	c.*2430G>T; c.*2523G>T; c.*2817G>T; c.*2910G>T; c.*2964G>T; c.*3057G>T; c.187G>T	; p.Glu63*	1	FALSE	chr1:115256524:C:A	192:chr1:115256524:C:A	0.001061
70_bl-2	70	BRAF	MODERATE	c.2285C>T	p.Ala762Val	2	FALSE	chr7:140434413:G:A	192:chr7:140434413:G:A	0.000507
70_bl-2	70	MET	MODERATE	c.4023C>A; c.4077C>A	p.Phe1341Leu; p.Phe1359Leu	1	FALSE	chr7:116436028:C:A	192:chr7:116436028:C:A	0.000516
70_bl-2	70	NF1	HIGH	c.5294C>A; c.5357C>A	p.Ser1765*; p.Ser1786*	1	FALSE	chr17:29654605:C:A	192:chr17:29654605:C:A	0.00105
70_bl-2	70	MAP2K1	MODERATE	c.146G>A	p.Arg49His	1	FALSE	chr15:66727430:G:A	192:chr15:66727430:G:A	0.000702
70_bl-2	70	FGFR3	MODERATE	c.1409G>T; c.1745G>T; c.1751G>T	p.Cys470Phe; p.Cys582Phe; p.Cys584Phe	1	FALSE	chr4:1807576:G:T	192:chr4:1807576:G:T	0.003215
70_bl-2	70	CTNNB1	MODERATE	c.1972G>T	p.Val658Phe	0	FALSE	chr3:41278096:G:T	192:chr3:41278096:G:T	0.001159
70_bl-2	70	HOXD-AS2; HOXD8	MODIFIER; MODERATE	n.*692C>T; c.-123-30G>A; c.400G>A	; p.Ala134Thr	0	FALSE	chr2:176995494:G:A	192:chr2:176995494:G:A	0.001009

70_bl-2	70	TP53	MODERATE	c.364G>T; c.481G>T; c.4G>T; c.85G>T	p.Ala122Ser; p.Ala161Ser; p.Ala2Ser; p.Ala29Ser	53	FALSE	chr17:7578449:C:A	192:chr17:7578449:C:A	0.001182
70_bl-2	70	MET	HIGH	c.1619G>A	p.Trp540*	1	FALSE	chr7:116380997:G:A	192:chr7:116380997:G:A	0.000537
70_bl-2	70	PTEN	MODERATE	c.295G>A	p.Glu99Lys	3	FALSE	chr10:89692811:G:A	192:chr10:89692811:G:A	0.001243
70_bl-2	70	MAP2K1	MODERATE	c.198C>A	p.Asp66Glu	4	FALSE	chr15:66727482:C:A	192:chr15:66727482:C:A	0.00176
70_bl-2	70	TP53	MODIFIER; MODERATE	c.-56G>T; c.26G>T; c.305G>T; c.422G>T	; p.Cys9Phe; p.Cys102Phe; p.Cys141Phe	81	FALSE	chr17:7578508:C:A	192:chr17:7578508:C:A	0.001861
70_bl-2	70	BRAF	MODERATE	c.2223G>T	p.Glu741Asp	1	FALSE	chr7:140434475:C:A	192:chr7:140434475:C:A	0.000645
70_bl-2	70	HOXD-AS2; HOXD8	MODIFIER; MODERATE	n.*692G>T; c.105C>A; c.654C>A; c.657C>A	; p.Asn35Lys; p.Asn218Lys; p.Asn219Lys	0	FALSE	chr2:176996124:C:A	192:chr2:176996124:C:A	0.001092
70_bl-2	70	MET	MODERATE	c.608C>A	p.Ser203Tyr	1	FALSE	chr7:116339746:C:A	192:chr7:116339746:C:A	0.001143
70_bl-2	70	PTEN	MODERATE	c.518G>A	p.Arg173His	27	FALSE	chr10:89711900:G:A	192:chr10:89711900:G:A	0.001302
70_bl-2	70	CTNNB1	MODERATE	c.131C>A	p.Pro44His	0	FALSE	chr3:41266134:C:A	192:chr3:41266134:C:A	0.001947
70_bl-2	70	EGFR	MODIFIER; MODERATE	c.*2133C>T; c.*2364C>T; c.2011C>T	; p.Arg671Cys	2	FALSE	chr7:55240767:C:T	192:chr7:55240767:C:T	0.001207
70_bl-2	70	KRAS	HIGH	c.292G>T	p.Glu98*	1	FALSE	chr12:25378706:C:A	192:chr12:25378706:C:A	0.001059
70_bl-2	70	HOXD-AS2; HOXD8	MODIFIER; MODERATE	n.*692G>T; c.22C>A; c.574C>A	; p.Gln8Lys; p.Gln192Lys	0	FALSE	chr2:176995668:C:A	192:chr2:176995668:C:A	0.001187

70_bl-2	70	MITF	MODIFIER; MODERATE	c.-53+197C>A; c.104+24188C>A; c.48C>A	; p.Phe16Leu	0	FALSE	chr3:69813040:C:A	192:chr3:69813040:C:A	0.001145
70_bl-2	70	TP53	HIGH	c.133G>T; c.214G>T; c.493G>T; c.610G>T	p.Glu45*; p.Glu72*; p.Glu165*; p.Glu204*	35	FALSE	chr17:7578239:C:A	192:chr17:7578239:C:A	0.000867
70_bl-2	70	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2576C>A; n.-1G>T	p.Ala859Asp;	1	FALSE	chr7:55259518:C:A	192:chr7:55259518:C:A	0.001285
70_bl-2	70	PIK3CA	MODERATE	c.3180C>A	p.His1060Gln	2	FALSE	chr3:178952125:C:A	192:chr3:178952125:C:A	0.001137
70_bl-2	70	DDR2	MODERATE	c.2021C>A	p.Ser674Tyr	1	FALSE	chr1:162745606:C:A	192:chr1:162745606:C:A	0.000602
70_bl-2	70	BRAF	HIGH	c.1378G>T	p.Gly460*	1	FALSE	chr7:140481430:C:A	192:chr7:140481430:C:A	0.00071
70_bl-2	70	PTEN	MODERATE	c.1007A>T	p.Tyr336Phe	1	FALSE	chr10:89720856:A:T	192:chr10:89720856:A:T	0.004243
70_bl-2	70	EGFR	MODIFIER; MODERATE	c.*2364T>A; c.2135T>A	; p.Phe712Tyr	2	FALSE	chr7:55241687:T:A	192:chr7:55241687:T:A	0.000804
70_bl-2	70	ERBB2; MIEN1; MIR4728	MODERATE; MODIFIER	c.2261G>A; c.2306G>A; c.2351G>A; n.2675G>A; c.*388C>T; n.-1G>A	p.Arg754His; p.Arg769His; p.Arg784His;	1	FALSE	chr17:37881022:G:A	192:chr17:37881022:G:A	0.000505
70_bl-2	70	TP53	MODERATE	c.364G>T; c.445G>T; c.724G>T; c.841G>T	p.Asp122Tyr; p.Asp149Tyr; p.Asp242Tyr; p.Asp281Tyr	28	FALSE	chr17:7577097:C:A	192:chr17:7577097:C:A	0.001007
70_bl-2	70	CTNNB1	MODERATE	c.884C>A	p.Ala295Asp	0	FALSE	chr3:41267300:C:A	192:chr3:41267300:C:A	0.001616
70_bl-2	70	ALK	MODERATE	c.2586G>T	p.Glu862Asp	1	FALSE	chr2:29455216:C:A	192:chr2:29455216:C:A	0.000875
70_bl-2	70	DDR2	MODERATE	c.313C>A	p.Arg105Ser	2	FALSE	chr1:162724541:C:A	192:chr1:162724541:C:A	0.00127

70_bl-2	70	KIT	MODERATE	c.1156G>A	p.Glu386Lys	1	FALSE	chr4:55575630:G:A	192:chr4:55575630:G:A	0.001063
70_bl-2	70	HGF	MODERATE	c.1678C>T; c.1693C>T	p.Leu560Phe; p.Leu565Phe	0	FALSE	chr7:81335667:G:A	192:chr7:81335667:G:A	0.000818
70_bl-2	70	ERBB2	MODERATE; MODIFIER	c.1191C>A; c.1236C>A; c.1281C>A; n.1605C>A	p.Asn397Lys; p.Asn412Lys; p.Asn427Lys;	1	FALSE	chr17:37871757:C:A	192:chr17:37871757:C:A	0.002293
70_bl-2	70	MET	HIGH	c.2387C>A; c.2441C>A	p.Ser796*; p.Ser814*	1	FALSE	chr7:116403126:C:A	192:chr7:116403126:C:A	0.001088
70_bl-2	70	TP53	MODIFIER; MODERATE	c.*117G>T; c.*29G>T; c.1010G>T; c.533G>T; c.614G>T; c.893G>T	; p.Arg337Leu; p.Arg178Leu; p.Arg205Leu; p.Arg298Leu	21	FALSE	chr17:7574017:C:A	192:chr17:7574017:C:A	0.815146
70_bl-2	70	TP53	MODIFIER; MODERATE	c.-61G>T; c.21G>T; c.300G>T; c.417G>T	; p.Lys7Asn; p.Lys100Asn; p.Lys139Asn	7	FALSE	chr17:7578513:C:A	192:chr17:7578513:C:A	0.001266
70_bl-2	70	MET	MODERATE	c.783C>A	p.Phe261Leu	2	FALSE	chr7:116339921:C:A	192:chr7:116339921:C:A	0.000778
70_bl-2	70	FGFR1	MODIFIER; MODERATE	c.-34C>T; c.158C>T; c.59C>T	; p.Thr53Ile; p.Thr20Ile	1	FALSE	chr8:38314906:G:A	192:chr8:38314906:G:A	0.001131
70_bl-2	70	TP53	LOW; MODIFIER; MODERATE	c.-6C>T; c.355C>T; c.472C>T; c.76C>T	; p.Arg119Cys; p.Arg158Cys; p.Arg26Cys	17	FALSE	chr17:7578458:G:A	192:chr17:7578458:G:A	0.001196
70_bl-2	70	PTEN	MODERATE	c.421C>A	p.His141Asn	2	FALSE	chr10:89692937:C:A	192:chr10:89692937:C:A	0.002394

70_bl-2	70	ERBB2; MIEN1; MIR4728	MODERATE; MODIFIER	c.3025G>A; c.3070G>A; c.3115G>A; n.3439G>A; c.*388C>T; n.*67G>A	p.Ala1009Thr; p.Ala1024Thr; p.Ala1039Thr;	2	FALSE	chr17:37883212:G:A	192:chr17:37883212:G:A	0.000839
70_bl-2	70	TP53	MODERATE	c.116A>G; c.35A>G; c.395A>G; c.512A>G	p.Glu39Gly; p.Glu12Gly; p.Glu132Gly; p.Glu171Gly	3	FALSE	chr17:7578418:T:C	192:chr17:7578418:T:C	0.00103
70_bl-2	70	DDR2	MODERATE	c.700G>A	p.Asp234Asn	1	FALSE	chr1:162729614:G:A	192:chr1:162729614:G:A	0.000794
70_bl-2	70	HGF	MODERATE	c.434G>T	p.Ser145Ile	0	FALSE	chr7:81386553:C:A	192:chr7:81386553:C:A	0.000775
70_bl-2	70	PIK3CA	MODERATE	c.1255C>A	p.His419Asn	1	FALSE	chr3:178927977:C:A	192:chr3:178927977:C:A	0.001917
70_bl-2	70	EGFR	MODERATE	c.2764G>A	p.Glu922Lys	1	FALSE	chr7:55266472:G:A	192:chr7:55266472:G:A	0.000539
70_bl-2	70	TP53	MODIFIER; MODERATE	c.-9G>T; c.352G>T; c.469G>T; c.73G>T	; p.Val118Phe; p.Val157Phe; p.Val25Phe	169	FALSE	chr17:7578461:C:A	192:chr17:7578461:C:A	0.001784
70_bl-2	70	ALK	MODERATE	c.4411G>A	p.Val1471Met	1	FALSE	chr2:29416542:C:T	192:chr2:29416542:C:T	0.000683
70_bl-2	70	TP53	MODIFIER; MODERATE	c.-3G>T; c.358G>T; c.475G>T; c.79G>T	; p.Ala120Ser; p.Ala159Ser; p.Ala27Ser	23	FALSE	chr17:7578455:C:A	192:chr17:7578455:C:A	0.001161
70_bl-2	70	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2527G>A; n.-1C>T	p.Val843Ile;	6	FALSE	chr7:55259469:G:A	192:chr7:55259469:G:A	0.000871
70_bl-2	70	EGFR	MODERATE	c.755G>A	p.Arg252His	3	FALSE	chr7:55221711:G:A	192:chr7:55221711:G:A	0.001704

70_bl-2	70	TP53	MODIFIER; MODERATE	c.*137A>G; c.*225A>G; c.1001A>G; c.1118A>G; c.641A>G; c.722A>G	; p.Lys334Arg; p.Lys373Arg; p.Lys214Arg; p.Lys241Arg	1	FALSE	chr17:7572991:T:C	192:chr17:7572991:T:C	0.004244
70_bl-2	70	CTNNB1	MODERATE	c.122C>A	p.Thr41Asn	0	FALSE	chr3:41266125:C:A	192:chr3:41266125:C:A	0.00262
70_bl-2	70	PIK3CA	MODERATE	c.1636C>A	p.Gln546Lys	127	FALSE	chr3:178936094:C:A	192:chr3:178936094:C:A	0.000687
70_bl-2	70	PTEN	MODERATE	c.443C>A	p.Ala148Glu	1	FALSE	chr10:89692959:C:A	192:chr10:89692959:C:A	0.002554
70_bl-2	70	BRAF	MODERATE	c.1827G>T	p.Gln609His	1	FALSE	chr7:140453108:C:A	192:chr7:140453108:C:A	0.000524
70_bl-2	70	ERBB2	MODERATE; MODIFIER	c.839C>A; c.884C>A; c.929C>A; n.1253C>A	p.Ser280Tyr; p.Ser295Tyr; p.Ser310Tyr;	28	FALSE	chr17:37868208:C:A	192:chr17:37868208:C:A	0.000599
70_bl-2	70	RET	MODERATE	c.1690A>C	p.Thr564Pro	1	FALSE	chr10:43608342:A:C	192:chr10:43608342:A:C	0.00399
70_bl-2	70	MET	MODERATE	c.487T>C	p.Ser163Pro	1	FALSE	chr7:116339625:T:C	192:chr7:116339625:T:C	0.000721
70_bl-2	70	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2507G>A; n.-1C>T	p.Arg836His;	2	FALSE	chr7:55259449:G:A	192:chr7:55259449:G:A	0.000935
70_bl-2	70	NF1	MODERATE	c.8070G>T; c.8133G>T	p.Leu2690Phe; p.Leu2711Phe	1	FALSE	chr17:29686006:G:T	192:chr17:29686006:G:T	0.021116
70_bl-2	70	ALK	MODERATE	c.1753G>A	p.Ala585Thr	3	FALSE	chr2:29519818:C:T	192:chr2:29519818:C:T	0.001178
70_bl-2	70	EPHA3	MODERATE	c.1169C>A	p.Thr390Asn	0	FALSE	chr3:89391103:C:A	192:chr3:89391103:C:A	0.001041
70_bl-2	70	RET	MODERATE	c.1783G>A	p.Glu595Lys	1	FALSE	chr10:43609027:G:A	192:chr10:43609027:G:A	0.000928
70_bl-2	70	DDR2	MODERATE	c.397C>T	p.Arg133Trp	1	FALSE	chr1:162724625:C:T	192:chr1:162724625:C:T	0.001328
70_bl-2	70	EGFR	MODERATE	c.2763C>A	p.Ser921Arg	3	FALSE	chr7:55266471:C:A	192:chr7:55266471:C:A	0.000539

70_bl-2	70	EGFR	MODIFIER; MODERATE	c.*2364C>T; c.2165C>T	; p.Ala722Val	2	FALSE	chr7:55241717:C:T	192:chr7:55241717:C:T	0.000808
70_bl-2	70	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2354C>A; n.1208G>T	p.Thr785Asn;	2	FALSE	chr7:55249056:C:A	192:chr7:55249056:C:A	0.000637
70_bl-2	70	HGF	MODERATE	c.251G>T	p.Cys84Phe	0	FALSE	chr7:81392026:C:A	192:chr7:81392026:C:A	0.001467
70_bl-2	70	NF1	HIGH	c.6932C>A; c.6995C>A	p.Ser2311*; p.Ser2332*	2	FALSE	chr17:29667596:C:A	192:chr17:29667596:C:A	0.001254
70_bl-2	70	NF1	MODERATE	c.2695T>G	p.Leu899Val	3	FALSE	chr17:29556328:T:G	192:chr17:29556328:T:G	0.002274
70_bl-2	70	EGFR	MODERATE	c.445C>T	p.Arg149Trp	1	FALSE	chr7:55214319:C:T	192:chr7:55214319:C:T	0.002119
70_bl-2	70	CTNNB1	MODERATE	c.86C>A	p.Ser29Tyr	0	FALSE	chr3:41266089:C:A	192:chr3:41266089:C:A	0.001314
70_bl-2	70	ALK	MODERATE	c.4192C>T	p.Pro1398Ser	1	FALSE	chr2:29416761:G:A	192:chr2:29416761:G:A	0.001071
70_bl-2	70	CTNNB1	MODERATE	c.861C>A	p.Asn287Lys	0	FALSE	chr3:41267277:C:A	192:chr3:41267277:C:A	0.002333
71_c5-1	71	MIR4673; NOTCH1	MODIFIER; MODERATE	n.*59A>C; c.931A>C	; p.Thr311Pro	0	FALSE	chr9:139413211:T:G	193:chr9:139413211:T:G	0.637681
71_c5-1	71	CWH43	MODERATE	c.1535G>A; c.1616G>A	p.Gly512Asp; p.Gly539Asp	0	FALSE	chr4:49034690:G:A	193:chr4:49034690:G:A	0.002805
71_c5-1	71	CDKN2A; CDKN2B-AS1	MODERATE; MODIFIER	c.22A>G; n.-1T>C	p.Thr8Ala;	1	FALSE	chr9:21994309:T:C	193:chr9:21994309:T:C	0.015267
71_c5-1	71	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2575G>A; n.-1C>T	p.Ala859Thr;	4	FALSE	chr7:55259517:G:A	193:chr7:55259517:G:A	0.002972
71_c5-1	71	NF1	HIGH	c.5380C>T; c.5443C>T	p.Gln1794*; p.Gln1815*	2	FALSE	chr17:29654691:C:T	193:chr17:29654691:C:T	0.002841
71_c5-1	71	IGF1R	MODERATE	c.1511G>A	p.Arg504His	0	FALSE	chr15:99454592:G:A	193:chr15:99454592:G:A	0.004354
71_c5-1	71	FBXW7	MODERATE	c.182G>A; c.296G>A; c.536G>A	p.Arg61His; p.Arg99His; p.Arg179His	0	FALSE	chr4:153271242:C:T	193:chr4:153271242:C:T	0.00321
71_c5-1	71	IGF1R	MODERATE	c.3934T>C; c.3937T>C	p.Ser1312Pro; p.Ser1313Pro	0	FALSE	chr15:99500504:T:C	193:chr15:99500504:T:C	0.024014

71_c5-1	71	TP53	MODERATE	c.270G>T; c.351G>T; c.630G>T; c.747G>T	p.Arg90Ser; p.Arg117Ser; p.Arg210Ser; p.Arg249Ser	318	FALSE	chr17:7577534:C:A	193:chr17:7577534:C:A	0.043974
71_c5-1	71	NF1	MODERATE	c.5420G>A; c.5483G>A	p.Arg1807Gln; p.Arg1828Gln	2	FALSE	chr17:29654731:G:A	193:chr17:29654731:G:A	0.00277
71_c5-1	71	MIR4673; NOTCH1	MODIFIER; MODERATE	n.*59A>C; c.1195A>C	; p.Thr399Pro	0	FALSE	chr9:139412649:T:G	193:chr9:139412649:T:G	0.007212
71_c5-1	71	NF1	MODERATE	c.2695T>G	p.Leu899Val	3	FALSE	chr17:29556328:T:G	193:chr17:29556328:T:G	0.004666
77_c4-2	77	KIT	MODERATE	c.2197G>A; c.2209G>A	p.Asp733Asn; p.Asp737Asn	2	FALSE	chr4:55597561:G:A	194:chr4:55597561:G:A	0.001389
77_c4-2	77	TP53	MODERATE	c.128G>A; c.407G>A; c.47G>A; c.524G>A	p.Arg43His; p.Arg136His; p.Arg16His; p.Arg175His	979	FALSE	chr17:7578406:C:T	194:chr17:7578406:C:T	0.001813
77_c4-2	77	HRAS; LRRC56	MODERATE; MODIFIER	c.182A>T; c.-506T>A	p.Gln61Leu;	188	FALSE	chr11:533874:T:A	194:chr11:533874:T:A	0.009488
77_c4-2	77	MIR4673; NOTCH1	MODIFIER; MODERATE	n.*59A>C; c.1195A>C	; p.Thr399Pro	0	FALSE	chr9:139412649:T:G	194:chr9:139412649:T:G	0.006205
77_c4-2	77	PTEN	MODERATE	c.829A>T	p.Thr277Ser	1	FALSE	chr10:89720678:A:T	194:chr10:89720678:A:T	0.003086
77_c4-2	77	IGF1R	MODERATE	c.3934T>C; c.3937T>C	p.Ser1312Pro; p.Ser1313Pro	0	FALSE	chr15:99500504:T:C	194:chr15:99500504:T:C	0.01435
77_c4-2	77	NTRK2	MODERATE	c.412C>A	p.Leu138Ile	0	FALSE	chr9:87322811:C:A	194:chr9:87322811:C:A	0.002123
77_c4-2	77	C9orf53; CDKN2A	MODIFIER; MODERATE; LOW	n.*616G>A; c.*180C>T; c.257C>T; c.300C>T	; p.Ala86Val; p.Cys100Cys	1	FALSE	chr9:21971101:G:A	194:chr9:21971101:G:A	0.002157
77_c4-2	77	APC	MODERATE	c.596C>T; c.626C>T	p.Ala199Val; p.Ala209Val	0	FALSE	chr5:112116551:C:T	194:chr5:112116551:C:T	0.001556

77_c4-2	77	NF1	MODERATE	c.8070G>T; c.8133G>T	p.Leu2690Phe; p.Leu2711Phe	1	FALSE	chr17:29686006:G:T	194:chr17:29686006:G:T	0.024963
77_c4-2	77	NF1	MODERATE	c.4030G>A	p.Glu1344Lys	2	FALSE	chr17:29576057:G:A	194:chr17:29576057:G:A	0.001579
77_c4-2	77	PIK3CA	MODERATE	c.1633G>A	p.Glu545Lys	1189	FALSE	chr3:178936091:G:A	194:chr3:178936091:G:A	0.010621
77_c4-2	77	FGFR2	MODIFIER; MODERATE	c.110-13073G>A; n.757-13073G>A; c.157G>A; c.424G>A	; p.Asp53Asn; p.Asp142Asn	1	FALSE	chr10:123324046:C:T	194:chr10:123324046:C:T	0.00183
77_c4-2	77	SMO	MODERATE	c.1045A>C	p.Thr349Pro	0	FALSE	chr7:128846115:A:C	194:chr7:128846115:A:C	0.022881
77_c4-2	77	NTRK3	MODERATE	c.389G>A	p.Arg130His	0	FALSE	chr15:88726655:C:T	194:chr15:88726655:C:T	0.004172
77_c4-2	77	KIT	MODERATE	c.287C>T	p.Thr96Met	1	FALSE	chr4:55561897:C:T	194:chr4:55561897:C:T	0.001502
77_c4-2	77	CDH1	MODERATE	c.2204C>T	p.Ala735Val	0	FALSE	chr16:68862116:C:T	194:chr16:68862116:C:T	0.001517
77_c4-2	77	IGF1R	MODERATE	c.3905T>C; c.3908T>C	p.Val1302Ala; p.Val1303Ala	0	FALSE	chr15:99500475:T:C	194:chr15:99500475:T:C	0.005725
77_c4-2	77	TP53	MODERATE	c.688A>C; c.292A>C; c.211A>C; c.571A>C	p.Thr230Pro; p.Thr98Pro; p.Thr71Pro; p.Thr191Pro	10	FALSE	chr17:7577593:T:G	194:chr17:7577593:T:G	0.001617
77_c4-2	77	ESR1	MODERATE	c.472C>T	p.Arg158Cys	0	FALSE	chr6:152163751:C:T	194:chr6:152163751:C:T	0.001625
77_c4-2	77	NOTCH1	MODERATE	c.4901C>T	p.Ala1634Val	0	FALSE	chr9:139399242:G:A	194:chr9:139399242:G:A	0.002227
77_c4-2	77	TSC1	MODERATE	c.2678C>T; c.2828C>T; c.2831C>T	p.Ala893Val; p.Ala943Val; p.Ala944Val	0	FALSE	chr9:135772715:G:A	194:chr9:135772715:G:A	0.00161
77_c4-2	77	FLT3	MODERATE	c.2440G>A	p.Ala814Thr	0	FALSE	chr13:28592705:C:T	194:chr13:28592705:C:T	0.001668
77_c4-2	77	IGF1R	MODERATE	c.1172G>A	p.Arg391His	0	FALSE	chr15:99442775:G:A	194:chr15:99442775:G:A	0.001789

77_c4-2	77	ERBB2; MIEN1; MIR4728	MODIFIER; MODERATE	c.3160-213A>G; c.3251A>G; c.3296A>G; c.3341A>G; n.3665A>G; c.*388T>C; n.*67A>G	; p.Glu1084Gly; p.Glu1099Gly; p.Glu1114Gly	1	FALSE	chr17:37883729:A:G	194:chr17:37883729:A:G	0.002566
77_c4-2	77	IGF1R	MODERATE	c.314T>C	p.Val105Ala	0	FALSE	chr15:99251010:T:C	194:chr15:99251010:T:C	0.003213
77_c4-2	77	NF1	MODERATE	c.2695T>G	p.Leu899Val	3	FALSE	chr17:29556328:T:G	194:chr17:29556328:T:G	0.004212
77_c4-2	77	FGFR3	MODERATE	c.1573G>T; c.1909G>T; c.1915G>T	p.Gly525Trp; p.Gly637Trp; p.Gly639Trp	1	FALSE	chr4:1807850:G:T	194:chr4:1807850:G:T	0.002167
77_c4-2	77	NTRK1	MODERATE	c.1940T>G; c.2030T>G; c.2048T>G	p.Val647Gly; p.Val677Gly; p.Val683Gly	2	FALSE	chr1:156849792:T:G	194:chr1:156849792:T:G	0.031596
82_c6-1	82	PIK3CA	MODERATE	c.1633G>A	p.Glu545Lys	1189	FALSE	chr3:178936091:G:A	195:chr3:178936091:G:A	0.130056
82_c6-1	82	VHL	MODIFIER; MODERATE	c.341-3238G>A; c.376G>A	; p.Asp126Asn	0	FALSE	chr3:10188233:G:A	195:chr3:10188233:G:A	0.001718
82_c6-1	82	TP53	MODERATE	c.337G>A; c.418G>A; c.697G>A; c.814G>A	p.Val113Met; p.Val140Met; p.Val233Met; p.Val272Met	85	FALSE	chr17:7577124:C:T	195:chr17:7577124:C:T	0.023992
82_c6-1	82	MIR4673; NOTCH1	MODIFIER; HIGH	n.*59C>T; c.1324C>T	; p.Gln442*	0	FALSE	chr9:139412321:G:A	195:chr9:139412321:G:A	0.002513
82_c6-1	82	ATM	MODERATE	c.2075G>A	p.Arg692His	0	FALSE	chr11:108124717:G:A	195:chr11:108124717:G:A	0.001446
82_c6-1	82	PHLPP1	LOW	c.2706A>G	p.Ser902Ser	0	FALSE	chr18:60572515:A:G	195:chr18:60572515:A:G	0.002162

82_c6-1	82	IGF1R	MODERATE	c.3934T>C; c.3937T>C	p.Ser1312Pro; p.Ser1313Pro	0	FALSE	chr15:99500504:T:C	195:chr15:99500504:T:C	0.016708
82_c6-1	82	TP53	MODIFIER; MODERATE	c.*145T>C; c.*233T>C; c.1009T>C; c.1126T>C; c.649T>C; c.730T>C	; p.Ser337Pro; p.Ser376Pro; p.Ser217Pro; p.Ser244Pro	2	FALSE	chr17:7572983:A:G	195:chr17:7572983:A:G	0.004213
82_c6-1	82	KDR	MODERATE	c.1399G>A	p.Ala467Thr	2	FALSE	chr4:55973917:C:T	195:chr4:55973917:C:T	0.00304
82_c6-1	82	KDR	MODERATE	c.2323G>T	p.Ala775Ser	1	FALSE	chr4:55964914:C:A	195:chr4:55964914:C:A	0.001663
82_c6-1	82	NOTCH1	MODERATE	c.4901C>T	p.Ala1634Val	0	FALSE	chr9:139399242:G:A	195:chr9:139399242:G:A	0.002105
82_c6-1	82	NF1	MODERATE	c.5426G>A; c.5489G>A	p.Arg1809His; p.Arg1830His	1	FALSE	chr17:29654737:G:A	195:chr17:29654737:G:A	0.001439
82_c6-1	82	TP53	HIGH	c.109C>T; c.190C>T; c.469C>T; c.586C>T	p.Arg37*; p.Arg64*; p.Arg157*; p.Arg196*	191	FALSE	chr17:7578263:G:A	195:chr17:7578263:G:A	0.14924
82_c6-1	82	FGFR3	MODERATE	c.1582C>T; c.1918C>T; c.1924C>T	p.Arg528Trp; p.Arg640Trp; p.Arg642Trp	1	FALSE	chr4:1807859:C:T	195:chr4:1807859:C:T	0.002026
82_c6-1	82	KIT	MODERATE	c.391G>A	p.Asp131Asn	1	FALSE	chr4:55564503:G:A	195:chr4:55564503:G:A	0.001559
82_c6-1	82	IGF1R	MODERATE	c.3905T>C; c.3908T>C	p.Val1302Ala; p.Val1303Ala	0	FALSE	chr15:99500475:T:C	195:chr15:99500475:T:C	0.002636
82_c6-1	82	TP53	MODERATE	c.119T>C; c.38T>C; c.398T>C; c.515T>C	p.Val40Ala; p.Val13Ala; p.Val133Ala; p.Val172Ala	12	FALSE	chr17:7578415:A:G	195:chr17:7578415:A:G	0.001892

82_c6-1	82	PIK3R1	MODIFIER; MODERATE	c.-17G>A; c.1073G>A; c.173G>A; c.263G>A	; p.Arg358Gln; p.Arg58Gln; p.Arg88Gln	1	FALSE	chr5:67588982:G:A	195:chr5:67588982:G:A	0.002398
82_c6-1	82	TP53	MODERATE	c.815T>G; c.419T>G; c.338T>G; c.698T>G	p.Val272Gly; p.Val140Gly; p.Val113Gly; p.Val233Gly	9	FALSE	chr17:7577123:A:C	195:chr17:7577123:A:C	0.001932
82_c6-1	82	TP53	MODIFIER; MODERATE	c.-9G>C; c.352G>C; c.469G>C; c.73G>C	; p.Val118Leu; p.Val157Leu; p.Val25Leu	169	FALSE	chr17:7578461:C:G	195:chr17:7578461:C:G	0.001988
82_c6-1	82	SMO	MODERATE	c.628G>A	p.Val210Met	0	FALSE	chr7:128845134:G:A	195:chr7:128845134:G:A	0.001876
82_c6-1	82	NOTCH1	MODERATE	c.5098G>A	p.Ala1700Thr	0	FALSE	chr9:139397703:C:T	195:chr9:139397703:C:T	0.001892
82_c6-1	82	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2432C>T; n.1130G>A	p.Ser811Phe;	1	FALSE	chr7:55249134:C:T	195:chr7:55249134:C:T	0.001478
82_c6-1	82	SMO	MODERATE	c.1045A>C	p.Thr349Pro	0	FALSE	chr7:128846115:A:C	195:chr7:128846115:A:C	0.017195
82_c6-1	82	C9orf53; CDKN2A	MODIFIER; MODERATE	n.*616C>G; c.*140G>C; c.217G>C; c.260G>C	; p.Ala73Pro; p.Arg87Pro	1	FALSE	chr9:21971141:C:G	195:chr9:21971141:C:G	0.006
82_c6-1	82	HGF	MODERATE	c.1856A>G; c.1841A>G	p.Tyr619Cys; p.Tyr614Cys	0	FALSE	chr7:81334971:T:C	195:chr7:81334971:T:C	0.001845
82_c6-1	82	C9orf53; CDKN2A	MODIFIER; MODERATE; LOW	n.*616C>T; c.*232G>A; c.352G>A; c.309G>A	; p.Ala118Thr; p.Arg103Arg	1	FALSE	chr9:21971049:C:T	195:chr9:21971049:C:T	0.002162
82_c6-1	82	NTRK1	MODERATE	c.1940T>G; c.2030T>G; c.2048T>G	p.Val647Gly; p.Val677Gly; p.Val683Gly	2	FALSE	chr1:156849792:T:G	195:chr1:156849792:T:G	0.025192

82_c6-1	82	CTNNB1	MODERATE	c.643G>A	p.Ala215Thr	0	FALSE	chr3:41266972:G:A	195:chr3:41266972:G:A	0.00158
105_c2-1	105	NOTCH1	MODERATE	c.4571C>T	p.Ala1524Val	0	FALSE	chr9:139399777:G:A	197:chr9:139399777:G:A	0.002621
105_c2-1	105	NTRK1	MODERATE	c.1940T>G; c.2030T>G; c.2048T>G	p.Val647Gly; p.Val677Gly; p.Val683Gly	2	FALSE	chr1:156849792:T:G	197:chr1:156849792:T:G	0.025896
105_c2-1	105	STK11	MODERATE	c.971C>T	p.Pro324Leu	2	FALSE	chr19:1223034:C:T	197:chr19:1223034:C:T	0.002688
105_c2-1	105	MIR4673; NOTCH1	MODIFIER; MODERATE	n.*59A>C; c.1195A>C	; p.Thr399Pro	0	FALSE	chr9:139412649:T:G	197:chr9:139412649:T:G	0.008523
105_c2-1	105	BRAF	MODERATE	c.1781A>G	p.Asp594Gly	59	FALSE	chr7:140453154:T:C	197:chr7:140453154:T:C	0.004878
105_c2-1	105	RET	MODERATE	c.1690A>C	p.Thr564Pro	1	FALSE	chr10:43608342:A:C	197:chr10:43608342:A:C	0.008979
105_c2-1	105	TP53	MODERATE	c.11A>G; c.371A>G; c.488A>G; c.92A>G	p.Tyr4Cys; p.Tyr124Cys; p.Tyr163Cys; p.Tyr31Cys	132	FALSE	chr17:7578442:T:C	197:chr17:7578442:T:C	0.002367
105_c2-1	105	C9orf53; CDKN2A	MODIFIER; MODERATE	n.*616C>G; c.*140G>C; c.217G>C; c.260G>C	; p.Ala73Pro; p.Arg87Pro	1	FALSE	chr9:21971141:C:G	197:chr9:21971141:C:G	0.023316
105_c2-1	105	NTRK1	MODERATE	c.2017G>A; c.2107G>A; c.2125G>A	p.Asp673Asn; p.Asp703Asn; p.Asp709Asn	1	FALSE	chr1:156849869:G:A	197:chr1:156849869:G:A	0.00246
105_c2-1	105	SMO	MODERATE	c.1225G>A	p.Gly409Ser	0	FALSE	chr7:128846389:G:A	197:chr7:128846389:G:A	0.002301
105_c2-1	105	NF1	MODERATE	c.7718G>A; c.7781G>A	p.Arg2573His; p.Arg2594His	3	FALSE	chr17:29684020:G:A	197:chr17:29684020:G:A	0.002215
105_c2-1	105	NTRK3	MODERATE	c.2119C>T; c.2143C>T; c.2185C>T	p.His707Tyr; p.His715Tyr; p.His729Tyr	0	FALSE	chr15:88423650:G:A	197:chr15:88423650:G:A	0.003356

105_c2-1	105	FOXL2; FOXL2NB; LINC01391	MODERATE; MODIFIER	c.415G>A; c.-132C>T; n.-1G>A	p.Glu139Lys;	0	FALSE	chr3:138665150:C:T	197:chr3:138665150:C:T	0.003781
105_c2-1	105	PIK3CA	MODERATE	c.2230T>A	p.Phe744Ile	1	FALSE	chr3:178941911:T:A	197:chr3:178941911:T:A	0.002334
105_c2-1	105	PIK3CA	MODERATE	c.2209G>A	p.Glu737Lys	1	FALSE	chr3:178941890:G:A	197:chr3:178941890:G:A	0.002307
105_c2-1	105	RET	MODERATE	c.1783G>A	p.Glu595Lys	1	FALSE	chr10:43609027:G:A	197:chr10:43609027:G:A	0.002384
105_c2-1	105	TP53	MODERATE; MODIFIER	c.377A>C; c.260A>C; c.-20A>C; c.-101A>C	p.Tyr126Ser; p.Tyr87Ser;	10	FALSE	chr17:7578553:T:G	197:chr17:7578553:T:G	0.002356
105_c2-1	105	NF1	MODERATE	c.2695T>G	p.Leu899Val	3	FALSE	chr17:29556328:T:G	197:chr17:29556328:T:G	0.003444
105_c2-1	105	NOTCH1	MODERATE	c.4984C>T	p.Arg1662Trp	0	FALSE	chr9:139399159:G:A	197:chr9:139399159:G:A	0.004038
105_c2-1	105	SMO	MODERATE	c.1045A>C	p.Thr349Pro	0	FALSE	chr7:128846115:A:C	197:chr7:128846115:A:C	0.024775
105_c2-1	105	NOTCH1	MODERATE	c.4828G>A	p.Ala1610Thr	0	FALSE	chr9:139399315:C:T	197:chr9:139399315:C:T	0.002778
105_c2-1	105	IGF1R	MODERATE	c.3934T>C; c.3937T>C	p.Ser1312Pro; p.Ser1313Pro	0	FALSE	chr15:99500504:T:C	197:chr15:99500504:T:C	0.010582
105_c2-1	105	TP53	MODERATE	c.341G>A; c.422G>A; c.701G>A; c.818G>A	p.Arg114His; p.Arg141His; p.Arg234His; p.Arg273His	647	TRUE	chr17:7577120:C:T	197:chr17:7577120:C:T	0.008393
105_c2-1	105	MAP2K1	MODERATE	c.140G>A	p.Arg47Gln	4	FALSE	chr15:66727424:G:A	197:chr15:66727424:G:A	0.002002
5_t3c2-1	5	CDKN2A	MODIFIER; MODERATE	c.194-3607G>A; c.13G>A	; p.Ala5Thr	2	FALSE	chr9:21974814:C:T	198:chr9:21974814:C:T	0.02381
5_t3c2-1	5	ATM	HIGH	c.5623C>T	p.Arg1875*	0	FALSE	chr11:108175528:C:T	198:chr11:108175528:C:T	0.018519
69_t2c3-2	69	TP53	MODERATE; MODIFIER	c.170C>T; c.287C>T; c.-279C>T; c.-360C>T	p.Ser57Phe; p.Ser96Phe;	3	FALSE	chr17:7579400:G:A	200:chr17:7579400:G:A	0.011905

69_t2c3-2	69	KDR	MODERATE	c.1028C>T	p.Thr343Met	3	FALSE	chr4:55976884:G:A	200:chr4:55976884:G:A	0.005474
69_t2c3-2	69	PHLPP1	HIGH	c.2179C>T	p.Arg727*	0	FALSE	chr18:60562356:C:T	200:chr18:60562356:C:T	0.00905
84_bl-2	84	PIK3CA	MODERATE	c.1624G>A	p.Glu542Lys	777	FALSE	chr3:178936082:G:A	201:chr3:178936082:G:A	0.021944
84_bl-2	84	IGF1R	MODERATE	c.3905T>C; c.3908T>C	p.Val1302Ala; p.Val1303Ala	0	FALSE	chr15:99500475:T:C	201:chr15:99500475:T:C	0.006689
84_bl-2	84	CWH43	MODERATE	c.1396G>A; c.1315G>A	p.Glu466Lys; p.Glu439Lys	0	FALSE	chr4:49032865:G:A	201:chr4:49032865:G:A	0.006135
87_c1-2	87	C9orf53; CDKN2A	MODIFIER; MODERATE; LOW	n.*616T>G; c.*120A>C; c.197A>C; c.240A>C	; p.His66Pro; p.Pro80Pro	1	FALSE	chr9:21971161:T:G	202:chr9:21971161:T:G	0.016529
87_c1-2	87	APC	MODIFIER; HIGH	c.676-8785C>T; c.694C>T	; p.Arg232*	0	FALSE	chr5:112128191:C:T	202:chr5:112128191:C:T	0.032258
87_c1-2	87	EGFR	MODERATE	c.844G>A	p.Glu282Lys	1	FALSE	chr7:55221800:G:A	202:chr7:55221800:G:A	0.008264
87_c1-2	87	KRAS	MODERATE	c.183A>C	p.Gln61His	149	FALSE	chr12:25380275:T:G	202:chr12:25380275:T:G	0.027778
5_bl-3	5	PTEN	MODERATE	c.850G>A	p.Glu284Lys	2	FALSE	chr10:89720699:G:A	203:chr10:89720699:G:A	0.003231
5_bl-3	5	RET	MODERATE	c.1690A>C	p.Thr564Pro	1	FALSE	chr10:43608342:A:C	203:chr10:43608342:A:C	0.004155
5_bl-3	5	CDKN2A	MODIFIER; MODERATE	c.194-3568A>C; c.52A>C	; p.Thr18Pro	1	FALSE	chr9:21974775:T:G	203:chr9:21974775:T:G	0.004264
5_bl-3	5	BRAF	MODERATE	c.2153C>T	p.Ala718Val	1	FALSE	chr7:140434545:G:A	203:chr7:140434545:G:A	0.005587
5_bl-3	5	IGF1R	MODERATE	c.3934T>C; c.3937T>C	p.Ser1312Pro; p.Ser1313Pro	0	FALSE	chr15:99500504:T:C	203:chr15:99500504:T:C	0.007837
5_bl-3	5	ATM	MODERATE	c.7183G>A	p.Asp2395Asn	0	FALSE	chr11:108199841:G:A	203:chr11:108199841:G:A	0.00303

5_bl-3	5	ERBB2; MIEN1; MIR4728	MODIFIER; MODERATE	c.3160-213A>G; c.3251A>G; c.3296A>G; c.3341A>G; n.3665A>G; c.*388T>C; n.*67A>G	; p.Glu1084Gly; p.Glu1099Gly; p.Glu1114Gly	1	FALSE	chr17:37883729:A:G	203:chr17:37883729:A:G	0.009245
5_bl-3	5	C9orf53; CDKN2A	MODIFIER; MODERATE	n.*616C>G; c.*140G>C; c.217G>C; c.260G>C	; p.Ala73Pro; p.Arg87Pro	1	FALSE	chr9:21971141:C:G	203:chr9:21971141:C:G	0.01634
70_c7-2	70	FOXL2; FOXL2NB; LINC01391	MODERATE; MODIFIER	c.282T>A; c.-132A>T; n.-1T>A	p.Asn94Lys;	0	FALSE	chr3:138665283:A:T	204:chr3:138665283:A:T	0.030151
70_c7-2	70	IGF1R	MODERATE	c.3934T>C; c.3937T>C	p.Ser1312Pro; p.Ser1313Pro	0	FALSE	chr15:99500504:T:C	204:chr15:99500504:T:C	0.012048
70_c7-2	70	IGF1R	MODERATE	c.3905T>C; c.3908T>C	p.Val1302Ala; p.Val1303Ala	0	FALSE	chr15:99500475:T:C	204:chr15:99500475:T:C	0.006154
70_c7-2	70	PIK3CA	MODERATE	c.400C>T	p.Pro134Ser	2	FALSE	chr3:178917525:C:T	204:chr3:178917525:C:T	0.005025
70_c7-2	70	TP53	MODIFIER; MODERATE	c.*117G>T; c.*29G>T; c.1010G>T; c.533G>T; c.614G>T; c.893G>T	; p.Arg337Leu; p.Arg178Leu; p.Arg205Leu; p.Arg298Leu	21	FALSE	chr17:7574017:C:A	204:chr17:7574017:C:A	0.019718
70_c7-2	70	SMO	MODERATE	c.1045A>C	p.Thr349Pro	0	FALSE	chr7:128846115:A:C	204:chr7:128846115:A:C	0.007042
80_c4-2	80	EGFR	MODIFIER; MODERATE	c.*2133G>A; c.*2364G>A; c.2030G>A	; p.Arg677His	5	FALSE	chr7:55240786:G:A	205:chr7:55240786:G:A	0.003683

80_c4-2	80	C9orf53; CDKN2A	MODIFIER; MODERATE; LOW	n.*616T>G; c.*120A>C; c.197A>C; c.240A>C	; p.His66Pro; p.Pro80Pro	1	FALSE	chr9:21971161:T:G	205:chr9:21971161:T:G	0.015152
80_c4-2	80	KDR	MODERATE	c.3154G>A	p.Asp1052Asn	2	FALSE	chr4:55956161:C:T	205:chr4:55956161:C:T	0.00267
80_c4-2	80	C9orf53; CDKN2A	MODIFIER; MODERATE	n.*616C>T; c.*245G>A; c.322G>A; c.365G>A	; p.Asp108Asn; p.Arg122Gln	14	FALSE	chr9:21971036:C:T	205:chr9:21971036:C:T	0.00315
80_c4-2	80	NF1	MODERATE	c.109G>A	p.Glu37Lys	1	FALSE	chr17:29483049:G:A	205:chr17:29483049:G:A	0.002869
80_c4-2	80	IGF1R	MODERATE	c.3934T>C; c.3937T>C	p.Ser1312Pro; p.Ser1313Pro	0	FALSE	chr15:99500504:T:C	205:chr15:99500504:T:C	0.002972
80_c4-2	80	STK11	MODERATE	c.455A>G	p.Gln152Arg	3	FALSE	chr19:1219403:A:G	205:chr19:1219403:A:G	0.004008
80_c4-2	80	TP53	MODERATE	c.389T>C; c.470T>C; c.749T>C; c.866T>C	p.Leu130Pro; p.Leu157Pro; p.Leu250Pro; p.Leu289Pro	2	FALSE	chr17:7577072:A:G	205:chr17:7577072:A:G	0.00303
80_c4-2	80	RET	MODERATE	c.1690A>C	p.Thr564Pro	1	FALSE	chr10:43608342:A:C	205:chr10:43608342:A:C	0.002801
80_c4-2	80	VHL	MODIFIER; MODERATE	c.341-3270A>C; c.344A>C	; p.His115Pro	0	FALSE	chr3:10188201:A:C	205:chr3:10188201:A:C	0.003396
80_c4-2	80	PIK3CA	MODERATE	c.328G>A	p.Glu110Lys	4	FALSE	chr3:178916941:G:A	205:chr3:178916941:G:A	0.003058
80_c4-2	80	CDKN2A	MODIFIER; MODERATE	c.194-3568A>C; c.52A>C	; p.Thr18Pro	1	FALSE	chr9:21974775:T:G	205:chr9:21974775:T:G	0.008696
88_bl-2	88	TP53	MODERATE	c.340C>T; c.421C>T; c.700C>T; c.817C>T	p.Arg114Cys; p.Arg141Cys; p.Arg234Cys; p.Arg273Cys	601	FALSE	chr17:7577121:G:A	206:chr17:7577121:G:A	0.127572
88_bl-2	88	PIK3CA	MODERATE	c.1624G>A	p.Glu542Lys	777	FALSE	chr3:178936082:G:A	206:chr3:178936082:G:A	0.055762

88_bl-2	88	NTRK2	MODERATE	c.1822G>A; c.1870G>A	p.Val608Met; p.Val624Met	0	FALSE	chr9:87563482:G:A	206:chr9:87563482:G:A	0.101754
88_bl-2	88	AR	MODERATE	c.2488G>A; c.892G>A	p.Glu830Lys; p.Glu298Lys	0	FALSE	chrX:66942707:G:A	206:chrX:66942707:G:A	0.014599
88_bl-2	88	KRAS	MODERATE	c.35G>A	p.Gly12Asp	11213	FALSE	chr12:25398284:C:T	206:chr12:25398284:C:T	0.119469
105_c3-1	105	ALK	MODERATE	c.4280C>T	p.Ser1427Phe	2	FALSE	chr2:29416673:G:A	207:chr2:29416673:G:A	0.002639
105_c3-1	105	IGF1R	MODERATE	c.3905T>C; c.3908T>C	p.Val1302Ala; p.Val1303Ala	0	FALSE	chr15:99500475:T:C	207:chr15:99500475:T:C	0.005964
105_c3-1	105	CTNNB1	MODERATE	c.134C>G	p.Ser45Cys	0	FALSE	chr3:41266137:C:G	207:chr3:41266137:C:G	0.003077
105_c3-1	105	TP53	MODERATE	c.11A>G; c.371A>G; c.488A>G; c.92A>G	p.Tyr4Cys; p.Tyr124Cys; p.Tyr163Cys; p.Tyr31Cys	132	FALSE	chr17:7578442:T:C	207:chr17:7578442:T:C	0.006012
105_c3-1	105	CDH1	MODERATE	c.221G>A	p.Arg74Gln	0	FALSE	chr16:68835630:G:A	207:chr16:68835630:G:A	0.002972
105_c3-1	105	BRAF	MODERATE	c.1385G>A	p.Arg462Lys	2	FALSE	chr7:140481423:C:T	207:chr7:140481423:C:T	0.00241
105_c3-1	105	ATM	HIGH	c.5623C>T	p.Arg1875*	0	FALSE	chr11:108175528:C:T	207:chr11:108175528:C:T	0.004566
105_c3-1	105	NF1	MODIFIER; MODERATE	c.*2165C>T; c.2117C>T	; p.Ala706Val	1	FALSE	chr17:29553568:C:T	207:chr17:29553568:C:T	0.002361
105_c3-1	105	FGFR1	MODERATE	c.107C>T; c.350C>T; c.374C>T; c.473C>T	p.Ser36Leu; p.Ser117Leu; p.Ser125Leu; p.Ser158Leu	2	FALSE	chr8:38285938:G:A	207:chr8:38285938:G:A	0.003053
105_c3-1	105	STK11	HIGH	c.667G>T	p.Glu223*	2	FALSE	chr19:1220649:G:T	207:chr19:1220649:G:T	0.013477
105_c3-1	105	NF1	HIGH	c.1318C>T	p.Arg440*	10	FALSE	chr17:29533315:C:T	207:chr17:29533315:C:T	0.003597
105_c3-1	105	ALK	MODERATE	c.3824G>A	p.Arg1275Gln	79	FALSE	chr2:29432664:C:T	207:chr2:29432664:C:T	0.003026
105_c3-1	105	TSC1	HIGH	c.982C>T; c.829C>T	p.Gln328*; p.Gln277*	0	FALSE	chr9:135786887:G:A	207:chr9:135786887:G:A	0.002907

105_c3-1	105	KDR	MODERATE	c.1699G>A	p.Val567Met	1	FALSE	chr4:55971098:C:T	207:chr4:55971098:C:T	0.002591
105_c3-1	105	ATM	MODERATE	c.2576A>T	p.Asn859Ile	0	FALSE	chr11:108138007:A:T	207:chr11:108138007:A:T	0.002688
105_c3-1	105	FBXW7	MODERATE	c.1225G>A; c.1339G>A; c.1579G>A	p.Asp409Asn; p.Asp447Asn; p.Asp527Asn	0	FALSE	chr4:153247223:C:T	207:chr4:153247223:C:T	0.003155
105_c3-1	105	ESR1	MODERATE	c.739G>A; c.745G>A	p.Glu247Lys; p.Glu249Lys	0	FALSE	chr6:152201885:G:A	207:chr6:152201885:G:A	0.004464
105_c3-1	105	PIK3CA	MODERATE	c.3109G>A	p.Glu1037Lys	2	FALSE	chr3:178952054:G:A	207:chr3:178952054:G:A	0.002564
105_c3-1	105	DDR2	HIGH	c.2258G>A	p.Trp753*	1	FALSE	chr1:162746135:G:A	207:chr1:162746135:G:A	0.00243
105_c3-1	105	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2561C>T; n.-1G>A	p.Thr854Ile;	1	FALSE	chr7:55259503:C:T	207:chr7:55259503:C:T	0.002874
105_c3-1	105	BRAF	HIGH	c.1349G>A	p.Trp450*	1	FALSE	chr7:140481459:C:T	207:chr7:140481459:C:T	0.002372
105_c3-1	105	ATM	HIGH	c.4852C>T	p.Arg1618*	0	FALSE	chr11:108165729:C:T	207:chr11:108165729:C:T	0.002699
105_c3-1	105	BRAF	MODERATE	c.2083G>A	p.Glu695Lys	2	FALSE	chr7:140439656:C:T	207:chr7:140439656:C:T	0.002825
105_c3-1	105	TSC1	MODERATE	c.2677G>A; c.2827G>A; c.2830G>A	p.Ala893Thr; p.Ala943Thr; p.Ala944Thr	0	FALSE	chr9:135772716:C:T	207:chr9:135772716:C:T	0.003077
105_c3-1	105	PDGFRA	MODERATE	c.685G>A	p.Glu229Lys	3	FALSE	chr4:55131142:G:A	207:chr4:55131142:G:A	0.002778
105_c3-1	105	KIT	MODERATE	c.1648G>A; c.1660G>A	p.Glu550Lys; p.Glu554Lys	3	FALSE	chr4:55593594:G:A	207:chr4:55593594:G:A	0.002829
105_c3-1	105	AKT3	HIGH	c.1324C>T	p.Gln442*	0	FALSE	chr1:243675656:G:A	207:chr1:243675656:G:A	0.00316
105_c3-1	105	MET	MODERATE	c.3583C>T; c.3637C>T	p.Leu1195Phe; p.Leu1213Phe	1	FALSE	chr7:116422102:C:T	207:chr7:116422102:C:T	0.002717
105_c3-1	105	PTEN	MODERATE	c.724G>A	p.Glu242Lys	2	FALSE	chr10:89717699:G:A	207:chr10:89717699:G:A	0.004071
105_c3-1	105	BRAF	MODERATE	c.1781A>G	p.Asp594Gly	59	FALSE	chr7:140453154:T:C	207:chr7:140453154:T:C	0.009563

61_c4-1	61	KIT	MODERATE	c.2329G>A; c.2341G>A	p.Ala777Thr; p.Ala781Thr	1	FALSE	chr4:55598144:G:A	209:chr4:55598144:G:A	0.004926
61_c4-1	61	ESR1	MODERATE; HIGH	c.643G>T	p.Gly215Cys; p.Gly215*	0	FALSE	chr6:152163922:G:T	209:chr6:152163922:G:T	0.004444
61_c4-1	61	IDH2; ZNF710	MODERATE; MODIFIER	c.1091C>T; c.1247C>T; c.857C>T; c.*2147G>A	p.Ala364Val; p.Ala416Val; p.Ala286Val;	1	FALSE	chr15:90628072:G:A	209:chr15:90628072:G:A	0.00551
61_c4-1	61	FGFR3	MODIFIER; MODERATE	c.931-374G>A; c.1196G>A; c.1202G>A	; p.Arg399His; p.Arg401His	1	FALSE	chr4:1806177:G:A	209:chr4:1806177:G:A	0.007067
61_c4-1	61	KIT	MODERATE	c.365G>A	p.Arg122His	1	FALSE	chr4:55564477:G:A	209:chr4:55564477:G:A	0.007335
61_c4-1	61	RET	MODERATE	c.2038G>A	p.Ala680Thr	1	FALSE	chr10:43610086:G:A	209:chr10:43610086:G:A	0.003676
61_c4-1	61	TP53	HIGH; MODIFIER	c.181C>T; c.298C>T; c.-279C>T; c.-360C>T	p.Gln61*; p.Gln100*;	16	FALSE	chr17:7579389:G:A	209:chr17:7579389:G:A	0.029508
61_c4-1	61	ESR1	MODERATE	c.719G>A; c.725G>A	p.Cys240Tyr; p.Cys242Tyr	0	FALSE	chr6:152201865:G:A	209:chr6:152201865:G:A	0.004008
61_c4-1	61	PTEN	HIGH	c.822G>A	p.Trp274*	3	FALSE	chr10:89720671:G:A	209:chr10:89720671:G:A	0.016461
61_c4-1	61	NTRK2	MODERATE	c.407G>A	p.Arg136His	0	FALSE	chr9:87322806:G:A	209:chr9:87322806:G:A	0.006494
61_c4-1	61	FBXW7	MODERATE	c.1160G>A; c.1274G>A; c.1514G>A	p.Arg387His; p.Arg425His; p.Arg505His	0	FALSE	chr4:153247288:C:T	209:chr4:153247288:C:T	0.004065
61_c4-1	61	MAP2K1	MODERATE	c.146G>A	p.Arg49His	1	FALSE	chr15:66727430:G:A	209:chr15:66727430:G:A	0.004141
61_c4-1	61	TP53	MODIFIER; MODERATE	c.-9G>A; c.352G>A; c.469G>A; c.73G>A	; p.Val118Ile; p.Val157Ile; p.Val25Ile	169	FALSE	chr17:7578461:C:T	209:chr17:7578461:C:T	0.004405

61_c4-1	61	PIK3R1	HIGH	c.1494C>A; c.405C>A; c.594C>A; c.684C>A	p.Cys498*; p.Cys135*; p.Cys198*; p.Cys228*	1	FALSE	chr5:67590432:C:A	209:chr5:67590432:C:A	0.004785
61_c4-1	61	MAP2K1	MODERATE	c.383G>A	p.Gly128Asp	3	FALSE	chr15:66729175:G:A	209:chr15:66729175:G:A	0.00597
61_c4-1	61	TSC2	MODERATE	c.721G>A	p.Val241Ile	0	FALSE	chr16:2106717:G:A	209:chr16:2106717:G:A	0.005405
61_c4-1	61	EPHA3	MODERATE	c.1916G>A	p.Arg639His	0	FALSE	chr3:89468382:G:A	209:chr3:89468382:G:A	0.007407
61_c4-1	61	HGF	MODERATE	c.294G>T	p.Trp98Cys	0	FALSE	chr7:81388081:C:A	209:chr7:81388081:C:A	0.004525
61_c4-1	61	BRAF	MODERATE	c.1799T>A	p.Val600Glu	23024	FALSE	chr7:140453136:A:T	209:chr7:140453136:A:T	0.346582
61_c4-1	61	PTEN	MODERATE	c.283C>T	p.Pro95Ser	3	FALSE	chr10:89692799:C:T	209:chr10:89692799:C:T	0.017722
105_bl-1	105	EPHA3	MODERATE	c.545C>T	p.Ala182Val	0	FALSE	chr3:89259401:C:T	210:chr3:89259401:C:T	0.003125
105_bl-1	105	IGF1R	MODERATE	c.3905T>C; c.3908T>C	p.Val1302Ala; p.Val1303Ala	0	FALSE	chr15:99500475:T:C	210:chr15:99500475:T:C	0.004695
105_bl-1	105	RPL19	MODERATE	c.452G>A	p.Arg151His	0	FALSE	chr17:37360425:G:A	210:chr17:37360425:G:A	0.003731
105_bl-1	105	FGFR3	MODERATE	c.796G>A	p.Val266Met	1	FALSE	chr4:1803618:G:A	210:chr4:1803618:G:A	0.011494
105_bl-1	105	TSC1	HIGH	c.1921C>T; c.2071C>T; c.2074C>T	p.Arg641*; p.Arg691*; p.Arg692*	0	FALSE	chr9:135779172:G:A	210:chr9:135779172:G:A	0.002837
105_bl-1	105	EGFR	MODERATE	c.739G>A	p.Asp247Asn	1	FALSE	chr7:55220349:G:A	210:chr7:55220349:G:A	0.003945
105_bl-1	105	ALK	MODERATE	c.4192C>T	p.Pro1398Ser	1	FALSE	chr2:29416761:G:A	210:chr2:29416761:G:A	0.005051
105_bl-1	105	CTNNB1	MODERATE	c.1346G>A	p.Arg449His	0	FALSE	chr3:41275180:G:A	210:chr3:41275180:G:A	0.002478
105_bl-1	105	TP53	MODERATE	c.170C>T; c.449C>T; c.566C>T; c.89C>T	p.Ala57Val; p.Ala150Val; p.Ala189Val; p.Ala30Val	4	FALSE	chr17:7578283:G:A	210:chr17:7578283:G:A	0.004511

105_bl-1	105	TSC1	MODERATE	c.1547C>T; c.1697C>T; c.1700C>T	p.Ala516Val; p.Ala566Val; p.Ala567Val	0	FALSE	chr9:135781265:G:A	210:chr9:135781265:G:A	0.002525
105_bl-1	105	FBXW7	MODERATE	c.1160G>A; c.1274G>A; c.1514G>A	p.Arg387His; p.Arg425His; p.Arg505His	0	FALSE	chr4:153247288:C:T	210:chr4:153247288:C:T	0.00274
105_bl-1	105	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2495G>A; n.-1C>T	p.Arg832His;	2	FALSE	chr7:55259437:G:A	210:chr7:55259437:G:A	0.003436
105_bl-1	105	CDKN2A	MODIFIER; MODERATE	c.194-3470G>T; c.150G>T	; p.Gln50His	1	FALSE	chr9:21974677:C:A	210:chr9:21974677:C:A	0.003431
105_bl-1	105	PDGFRA	MODERATE	c.1495G>A	p.Val499Met	2	FALSE	chr4:55139834:G:A	210:chr4:55139834:G:A	0.003322
105_bl-1	105	CDH1	MODERATE	c.781G>A	p.Glu261Lys	0	FALSE	chr16:68844193:G:A	210:chr16:68844193:G:A	0.003044
105_bl-1	105	PTEN	HIGH	c.822G>A	p.Trp274*	3	FALSE	chr10:89720671:G:A	210:chr10:89720671:G:A	0.005602
105_bl-1	105	FGFR4	MODERATE	c.1246G>A; c.1330G>A; c.1450G>A	p.Ala416Thr; p.Ala444Thr; p.Ala484Thr	1	FALSE	chr5:176520707:G:A	210:chr5:176520707:G:A	0.003017
105_bl-1	105	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2303G>A; n.1259C>T	p.Ser768Asn;	37	FALSE	chr7:55249005:G:A	210:chr7:55249005:G:A	0.002445
105_bl-1	105	HGF	HIGH	c.517C>T; c.532C>T	p.Arg173*; p.Arg178*	0	FALSE	chr7:81381529:G:A	210:chr7:81381529:G:A	0.003077
105_bl-1	105	TP53	MODERATE	c.341G>A; c.422G>A; c.701G>A; c.818G>A	p.Arg114His; p.Arg141His; p.Arg234His; p.Arg273His	647	TRUE	chr17:7577120:C:T	210:chr17:7577120:C:T	0.003328
105_bl-1	105	BRAF	MODERATE	c.1781A>G	p.Asp594Gly	59	FALSE	chr7:140453154:T:C	210:chr7:140453154:T:C	0.003442
105_bl-1	105	APC	MODIFIER; MODERATE	c.676-8791C>T; c.688C>T	; p.Arg230Cys	0	FALSE	chr5:112128185:C:T	210:chr5:112128185:C:T	0.003591

105_bl-1	105	TP53	MODERATE	c.322C>T; c.403C>T; c.682C>T; c.799C>T	p.Arg108Trp; p.Arg135Trp; p.Arg228Trp; p.Arg267Trp	31	FALSE	chr17:7577139:G:A	210:chr17:7577139:G:A	0.004348
105_bl-1	105	FGFR2	MODIFIER; LOW; HIGH	c.749-4848C>T; n.1053C>T; c.406C>T; c.484C>T; c.751C>T	; p.Arg136*; p.Arg162*; p.Arg251*	2	FALSE	chr10:123279681:G:A	210:chr10:123279681:G:A	0.003929
105_bl-1	105	MET	MODERATE	c.1640G>A	p.Arg547Gln	1	FALSE	chr7:116381018:G:A	210:chr7:116381018:G:A	0.002141
105_bl-1	105	PIK3R1	LOW; MODIFIER	c.1017G>A; c.117G>A; c.207G>A; c.-233G>A	p.Ser339Ser; p.Ser39Ser; p.Ser69Ser;	1	FALSE	chr5:67588187:G:A	210:chr5:67588187:G:A	0.00321
105_bl-1	105	NOTCH1	MODERATE	c.4549G>A	p.Asp1517Asn	0	FALSE	chr9:139399799:C:T	210:chr9:139399799:C:T	0.003527
105_bl-1	105	GAPDH; IFFO1; NCAPD2	MODERATE; MODIFIER	c.157G>A; c.283G>A; c.*1743C>T; c.*1746C>T; c.*1770C>T; n.*2798C>T; c.*4252G>A	p.Val53Ile; p.Val95Ile;	0	FALSE	chr12:6646132:G:A	210:chr12:6646132:G:A	0.004008
105_bl-1	105	AR	MODERATE	c.2360G>A; c.764G>A	p.Arg787Gln; p.Arg255Gln	0	FALSE	chrX:66941716:G:A	210:chrX:66941716:G:A	0.002797
105_bl-1	105	C9orf53; CDKN2A	MODIFIER; MODERATE; LOW	n.*616G>A; c.*165C>T; c.242C>T; c.285C>T	; p.Pro81Leu; p.Thr95Thr	9	FALSE	chr9:21971116:G:A	210:chr9:21971116:G:A	0.004963
105_bl-1	105	MAP2K1	MODERATE	c.140G>A	p.Arg47Gln	4	FALSE	chr15:66727424:G:A	210:chr15:66727424:G:A	0.003044

105_bl-1	105	IDH2; ZNF710	MODERATE; MODIFIER	c.1091C>T; c.1247C>T; c.857C>T; c.*2147G>A	p.Ala364Val; p.Ala416Val; p.Ala286Val;	1	FALSE	chr15:90628072:G:A	210:chr15:90628072:G:A	0.003509
105_bl-1	105	NOTCH1	MODERATE	c.4918G>A	p.Ala1640Thr	0	FALSE	chr9:139399225:C:T	210:chr9:139399225:C:T	0.004158
105_bl-1	105	RET	MODERATE	c.1438G>A	p.Glu480Lys	1	FALSE	chr10:43606829:G:A	210:chr10:43606829:G:A	0.002813
105_bl-1	105	IGF1R	MODERATE	c.3622G>A; c.3625G>A	p.Ala1208Thr; p.Ala1209Thr	0	FALSE	chr15:99491840:G:A	210:chr15:99491840:G:A	0.003284
105_bl-1	105	C9orf53; CDKN2A	MODIFIER; MODERATE	n.*616G>A; c.*318C>T; c.*39C>T; c.395C>T	; p.Ala132Val	1	FALSE	chr9:21970963:G:A	210:chr9:21970963:G:A	0.004484
105_bl-1	105	TP53	MODERATE	c.347G>T; c.428G>T; c.707G>T; c.824G>T	p.Cys116Phe; p.Cys143Phe; p.Cys236Phe; p.Cys275Phe	57	FALSE	chr17:7577114:C:A	210:chr17:7577114:C:A	0.003215
105_bl-1	105	ZNF716	MODERATE	c.241G>A	p.Glu81Lys	0	FALSE	chr7:57522853:G:A	210:chr7:57522853:G:A	0.00295
105_bl-1	105	PTEN	MODERATE	c.392C>A	p.Thr131Asn	2	FALSE	chr10:89692908:C:A	210:chr10:89692908:C:A	0.003106
106_bl-1	106	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2387G>A; n.1175C>T	p.Gly796Asp;	3	FALSE	chr7:55249089:G:A	211:chr7:55249089:G:A	0.002165
106_bl-1	106	MITF	MODIFIER; MODERATE	c.93+115G>A; c.208G>A; c.373G>A; c.481G>A; c.526G>A; c.529G>A	; p.Ala70Thr; p.Ala125Thr; p.Ala161Thr; p.Ala176Thr; p.Ala177Thr	0	FALSE	chr3:69987147:G:A	211:chr3:69987147:G:A	0.002782
106_bl-1	106	DDR2	MODERATE	c.1418G>A	p.Arg473His	2	FALSE	chr1:162740216:G:A	211:chr1:162740216:G:A	0.003521
106_bl-1	106	MAP2K1	MODERATE	c.145C>T	p.Arg49Cys	1	FALSE	chr15:66727429:C:T	211:chr15:66727429:C:T	0.002356

106_bl-1	106	TP53	MODERATE	c.236G>A; c.317G>A; c.596G>A; c.713G>A	p.Cys79Tyr; p.Cys106Tyr; p.Cys199Tyr; p.Cys238Tyr	74	FALSE	chr17:7577568:C:T	211:chr17:7577568:C:T	0.001866
106_bl-1	106	C9orf53; CDKN2A	MODIFIER; MODERATE	n.*616G>A; c.*318C>T; c.*39C>T; c.395C>T	; p.Ala132Val	1	FALSE	chr9:21970963:G:A	211:chr9:21970963:G:A	0.002841
106_bl-1	106	MITF	MODIFIER; MODERATE	c.93+61C>T; c.154C>T; c.319C>T; c.427C>T; c.472C>T; c.475C>T	; p.Pro52Ser; p.Pro107Ser; p.Pro143Ser; p.Pro158Ser; p.Pro159Ser	0	FALSE	chr3:69987093:C:T	211:chr3:69987093:C:T	0.002692
106_bl-1	106	FGFR3	MODERATE	c.599G>A	p.Arg200His	1	FALSE	chr4:1803247:G:A	211:chr4:1803247:G:A	0.003344
106_bl-1	106	C9orf53; CDKN2A	MODIFIER; MODERATE	n.*616C>T; c.*176G>A; c.253G>A; c.296G>A	; p.Ala85Thr; p.Arg99His	1	FALSE	chr9:21971105:C:T	211:chr9:21971105:C:T	0.003263
106_bl-1	106	EGFR	MODERATE	c.1789G>A	p.Ala597Thr	1	FALSE	chr7:55233039:G:A	211:chr7:55233039:G:A	0.003992
106_bl-1	106	MIR4673; NOTCH1	MODIFIER; MODERATE	n.*59G>A; c.1058G>A	; p.Arg353His	0	FALSE	chr9:139413084:C:T	211:chr9:139413084:C:T	0.002688
106_bl-1	106	PDGFRA	MODERATE	c.703T>C	p.Cys235Arg	1	FALSE	chr4:55131160:T:C	211:chr4:55131160:T:C	0.004367
106_bl-1	106	TSC2	MODIFIER; MODERATE	c.2837+1108G>A; c.2933G>A	; p.Arg978His	0	FALSE	chr16:2127694:G:A	211:chr16:2127694:G:A	0.002361
106_bl-1	106	AKT3	MODERATE	c.899C>T	p.Ala300Val	0	FALSE	chr1:243727071:G:A	211:chr1:243727071:G:A	0.002574

106_bl-1	106	TP53	MODERATE	c.134A>G; c.215A>G; c.494A>G; c.611A>G	p.Glu45Gly; p.Glu72Gly; p.Glu165Gly; p.Glu204Gly	3	FALSE	chr17:7578238:T:C	211:chr17:7578238:T:C	0.002181
106_bl-1	106	STK11	HIGH	c.409C>T	p.Gln137*	1	FALSE	chr19:1219357:C:T	211:chr19:1219357:C:T	0.002857
106_bl-1	106	KRAS	MODERATE	c.35G>A	p.Gly12Asp	11213	FALSE	chr12:25398284:C:T	211:chr12:25398284:C:T	0.010152
106_bl-1	106	NTRK2	MODERATE	c.1984G>A; c.2032G>A	p.Ala662Thr; p.Ala678Thr	0	FALSE	chr9:87570292:G:A	211:chr9:87570292:G:A	0.002404
106_bl-1	106	NTRK2	MODERATE	c.2024G>A; c.2072G>A	p.Arg675His; p.Arg691His	0	FALSE	chr9:87570332:G:A	211:chr9:87570332:G:A	0.002304
106_bl-1	106	NTRK1	MODERATE	c.1853G>A; c.1943G>A; c.1961G>A	p.Arg618His; p.Arg648His; p.Arg654His	3	FALSE	chr1:156849069:G:A	211:chr1:156849069:G:A	0.002915
106_bl-1	106	FGFR2	MODIFIER; MODERATE	c.110-1053G>A; c.110-14173G>A; n.757-14173G>A; c.182G>A	; p.Arg61His	1	FALSE	chr10:123325146:C:T	211:chr10:123325146:C:T	0.00226
106_bl-1	106	ATM	MODERATE	c.2075G>A	p.Arg692His	0	FALSE	chr11:108124717:G:A	211:chr11:108124717:G:A	0.002203
106_bl-1	106	PIK3CA	MODERATE	c.1235G>A	p.Arg412Gln	1	FALSE	chr3:178927472:G:A	211:chr3:178927472:G:A	0.002729
106_bl-1	106	C9orf53; CDKN2A	MODIFIER; MODERATE; LOW	n.*616G>A; c.*175C>T; c.295C>T; c.252C>T	; p.Arg99Cys; p.Asp84Asp	3	FALSE	chr9:21971106:G:A	211:chr9:21971106:G:A	0.003257
106_bl-1	106	TSC1	MODERATE	c.169G>A	p.Ala57Thr	0	FALSE	chr9:135802629:C:T	211:chr9:135802629:C:T	0.002132
106_bl-1	106	MIR4673; NOTCH1	MODIFIER; MODERATE	n.*59G>A; c.1024G>A	; p.Ala342Thr	0	FALSE	chr9:139413118:C:T	211:chr9:139413118:C:T	0.002646
106_bl-1	106	TSC2	MODERATE	c.3289G>A; c.3421G>A	p.Ala1097Thr; p.Ala1141Thr	0	FALSE	chr16:2130189:G:A	211:chr16:2130189:G:A	0.002817

106_bl-1	106	PTEN	HIGH	c.822G>A	p.Trp274*	3	FALSE	chr10:89720671:G:A	211:chr10:89720671:G:A	0.004854
106_bl-1	106	TP53	MODIFIER; MODERATE	c.-17C>T; c.-98C>T; c.263C>T; c.380C>T	; p.Ser88Phe; p.Ser127Phe	38	FALSE	chr17:7578550:G:A	211:chr17:7578550:G:A	0.003018
106_bl-1	106	NTRK1	MODERATE	c.1039C>T; c.949C>T	p.Arg347Cys; p.Arg317Cys	1	FALSE	chr1:156843613:C:T	211:chr1:156843613:C:T	0.002055
106_bl-1	106	TSC1	MODERATE	c.365C>T; c.518C>T	p.Ala122Val; p.Ala173Val	0	FALSE	chr9:135797351:G:A	211:chr9:135797351:G:A	0.004249
106_bl-1	106	TP53	MODERATE	c.371G>A; c.452G>A; c.731G>A; c.848G>A	p.Arg124His; p.Arg151His; p.Arg244His; p.Arg283His	24	FALSE	chr17:7577090:C:T	211:chr17:7577090:C:T	0.002535
106_bl-1	106	ESR1	MODERATE	c.719G>A; c.725G>A	p.Cys240Tyr; p.Cys242Tyr	0	FALSE	chr6:152201865:G:A	211:chr6:152201865:G:A	0.002088
106_bl-1	106	NF1	MODERATE	c.5426G>A; c.5489G>A	p.Arg1809His; p.Arg1830His	1	FALSE	chr17:29654737:G:A	211:chr17:29654737:G:A	0.001757
106_bl-1	106	NTRK3	MODERATE	c.1351C>T; c.1375C>T	p.Arg451Trp; p.Arg459Trp	0	FALSE	chr15:88669523:G:A	211:chr15:88669523:G:A	0.003708
106_bl-1	106	ERBB2	MODERATE; MODIFIER	c.560G>A; c.605G>A; c.650G>A; n.974G>A	p.Arg187His; p.Arg202His; p.Arg217His;	1	FALSE	chr17:37866345:G:A	211:chr17:37866345:G:A	0.002418
106_bl-1	106	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2516C>T; n.-1G>A	p.Ala839Val;	1	FALSE	chr7:55259458:C:T	211:chr7:55259458:C:T	0.002415
106_bl-1	106	EPHA3	MODERATE	c.2242G>A	p.Ala748Thr	0	FALSE	chr3:89480405:G:A	211:chr3:89480405:G:A	0.002759
106_bl-1	106	ALK	MODERATE	c.871C>T	p.Arg291Cys	3	FALSE	chr2:29917797:G:A	211:chr2:29917797:G:A	0.00206
106_bl-1	106	C9orf53; CDKN2A	MODIFIER; MODERATE; LOW	n.*616C>T; c.*258G>A; c.335G>A; c.378G>A	; p.Arg112His; p.Pro126Pro	1	FALSE	chr9:21971023:C:T	211:chr9:21971023:C:T	0.003058

106_bl-1	106	ALK	MODERATE	c.446C>T	p.Ala149Val	1	FALSE	chr2:30143080:G:A	211:chr2:30143080:G:A	0.003916
106_bl-1	106	MET	MODERATE	c.2067C>A	p.His689Gln	3	FALSE	chr7:116397793:C:A	211:chr7:116397793:C:A	0.003026
106_bl-1	106	FGFR3	MODERATE	c.743G>A	p.Arg248His	2	FALSE	chr4:1803565:G:A	211:chr4:1803565:G:A	0.004751
106_bl-1	106	IGF1R	MODERATE	c.719G>A	p.Ser240Asn	0	FALSE	chr15:99434632:G:A	211:chr15:99434632:G:A	0.002525
106_bl-1	106	NOTCH1	MODERATE	c.6107C>T	p.Ala2036Val	0	FALSE	chr9:139393424:G:A	211:chr9:139393424:G:A	0.002721
61_bl-1	61	TSC1	MODERATE	c.1547C>T; c.1697C>T; c.1700C>T	p.Ala516Val; p.Ala566Val; p.Ala567Val	0	FALSE	chr9:135781265:G:A	212:chr9:135781265:G:A	0.00321
61_bl-1	61	TSC2	MODIFIER; MODERATE	c.2837+1092G>A; c.2917G>A	; p.Glu973Lys	0	FALSE	chr16:2127678:G:A	212:chr16:2127678:G:A	0.005435
61_bl-1	61	EGFR	MODERATE	c.752G>A	p.Cys251Tyr	1	FALSE	chr7:55221708:G:A	212:chr7:55221708:G:A	0.005602
61_bl-1	61	NOTCH1	MODERATE	c.4906G>A	p.Glu1636Lys	0	FALSE	chr9:139399237:C:T	212:chr9:139399237:C:T	0.007653
61_bl-1	61	RET	MODERATE	c.1826G>A	p.Cys609Tyr	1	FALSE	chr10:43609070:G:A	212:chr10:43609070:G:A	0.006452
61_bl-1	61	PTEN	HIGH	c.822G>A	p.Trp274*	3	FALSE	chr10:89720671:G:A	212:chr10:89720671:G:A	0.020408
61_bl-1	61	DDR2	MODERATE	c.700G>A	p.Asp234Asn	1	FALSE	chr1:162729614:G:A	212:chr1:162729614:G:A	0.00565
61_bl-1	61	CTNNB1	MODERATE	c.1346G>A	p.Arg449His	0	FALSE	chr3:41275180:G:A	212:chr3:41275180:G:A	0.002911
61_bl-1	61	BRAF	MODERATE	c.1799T>A	p.Val600Glu	23024	FALSE	chr7:140453136:A:T	212:chr7:140453136:A:T	0.430124
61_bl-1	61	PIK3CA	MODERATE	c.1235G>A	p.Arg412Gln	1	FALSE	chr3:178927472:G:A	212:chr3:178927472:G:A	0.005348
61_bl-1	61	PIK3R1	LOW; MODIFIER; HIGH	c.-48C>T; c.1042C>T; c.142C>T; c.232C>T	; p.Arg348*; p.Arg48*; p.Arg78*	24	FALSE	chr5:67588951:C:T	212:chr5:67588951:C:T	0.005263
61_bl-1	61	CDH1	MODERATE	c.304G>A	p.Ala102Thr	0	FALSE	chr16:68835713:G:A	212:chr16:68835713:G:A	0.006135

61_bl-1	61	TP53	HIGH; MODIFIER	c.181C>T; c.298C>T; c.-279C>T; c.-360C>T	p.Gln61*; p.Gln100*;	16	FALSE	chr17:7579389:G:A	212:chr17:7579389:G:A	0.297872
61_bl-1	61	NF1	MODERATE	c.4462C>T; c.4525C>T	p.Arg1488Cys; p.Arg1509Cys	1	FALSE	chr17:29587481:C:T	212:chr17:29587481:C:T	0.004762
61_bl-1	61	EPHA3	MODERATE	c.2530C>T	p.Pro844Ser	0	FALSE	chr3:89499360:C:T	212:chr3:89499360:C:T	0.004484
61_bl-1	61	EGFR	MODERATE	c.755G>A	p.Arg252His	3	FALSE	chr7:55221711:G:A	212:chr7:55221711:G:A	0.007109
61_bl-1	61	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2516C>T; n.-1G>A	p.Ala839Val;	1	FALSE	chr7:55259458:C:T	212:chr7:55259458:C:T	0.004283
61_bl-1	61	MET	HIGH	c.1619G>A	p.Trp540*	1	FALSE	chr7:116380997:G:A	212:chr7:116380997:G:A	0.004082
61_bl-1	61	FLT3	MODERATE	c.2845G>A	p.Asp949Asn	0	FALSE	chr13:28588603:C:T	212:chr13:28588603:C:T	0.00304
61_bl-1	61	NOTCH1	MODERATE	c.4901C>T	p.Ala1634Val	0	FALSE	chr9:139399242:G:A	212:chr9:139399242:G:A	0.005076
61_bl-1	61	PDGFRA	MODERATE	c.1499G>A	p.Arg500Gln	1	FALSE	chr4:55139838:G:A	212:chr4:55139838:G:A	0.004202
61_bl-1	61	NTRK2	MODERATE	c.1408G>A; c.1456G>A	p.Val470Ile; p.Val486Ile	0	FALSE	chr9:87482169:G:A	212:chr9:87482169:G:A	0.005181
61_bl-1	61	TSC1	MODERATE	c.169G>A	p.Ala57Thr	0	FALSE	chr9:135802629:C:T	212:chr9:135802629:C:T	0.003584
61_bl-1	61	EGFR	MODERATE	c.988G>A	p.Glu330Lys	1	FALSE	chr7:55223621:G:A	212:chr7:55223621:G:A	0.003571
61_bl-1	61	PTEN	MODERATE	c.283C>T	p.Pro95Ser	3	FALSE	chr10:89692799:C:T	212:chr10:89692799:C:T	0.308157
61_bl-1	61	STK11	MODERATE	c.488G>A	p.Gly163Asp	1	FALSE	chr19:1220395:G:A	212:chr19:1220395:G:A	0.010363
61_bl-1	61	ESR1	MODERATE	c.739G>A; c.745G>A	p.Glu247Lys; p.Glu249Lys	0	FALSE	chr6:152201885:G:A	212:chr6:152201885:G:A	0.005141
80_c3-2	80	ESR1	HIGH	c.469C>T	p.Arg157*	0	FALSE	chr6:152163748:C:T	213:chr6:152163748:C:T	0.002237

80_c3-2	80	ERBB2; MIEN1; MIR4728	MODERATE; MODIFIER	c.2720A>G; c.2765A>G; c.2810A>G; n.3134A>G; c.*388T>C; n.-1A>G	p.Lys907Arg; p.Lys922Arg; p.Lys937Arg;	1	FALSE	chr17:37882044:A:G	213:chr17:37882044:A:G	0.002618
80_c3-2	80	ATM	HIGH	c.6100C>T	p.Arg2034*	0	FALSE	chr11:108186742:C:T	213:chr11:108186742:C:T	0.002128
80_c3-2	80	RET	MODERATE	c.1538C>T	p.Ala513Val	1	FALSE	chr10:43607562:C:T	213:chr10:43607562:C:T	0.002077
80_c3-2	80	MIR4673; NOTCH1	MODIFIER; MODERATE	n.*59G>A; c.1058G>A	; p.Arg353His	0	FALSE	chr9:139413084:C:T	213:chr9:139413084:C:T	0.002591
80_c3-2	80	ALK	MODERATE	c.886G>A	p.Glu296Lys	1	FALSE	chr2:29917782:C:T	213:chr2:29917782:C:T	0.001951
80_c3-2	80	PIK3CA	MODERATE	c.1531G>A	p.Ala511Thr	1	FALSE	chr3:178928345:G:A	213:chr3:178928345:G:A	0.002789
80_c3-2	80	KDR	MODERATE	c.887G>T	p.Gly296Val	2	FALSE	chr4:55979560:C:A	213:chr4:55979560:C:A	0.001894
80_c3-2	80	NTRK3	MODERATE	c.1463C>T; c.1487C>T	p.Ala488Val; p.Ala496Val	0	FALSE	chr15:88576186:G:A	213:chr15:88576186:G:A	0.002667
80_c3-2	80	TP53	MODERATE	c.106C>T; c.25C>T; c.385C>T; c.502C>T	p.His36Tyr; p.His9Tyr; p.His129Tyr; p.His168Tyr	9	FALSE	chr17:7578428:G:A	213:chr17:7578428:G:A	0.002384
80_c3-2	80	NOTCH1	MODERATE	c.3635G>A	p.Gly1212Asp	0	FALSE	chr9:139401765:C:T	213:chr9:139401765:C:T	0.00303
80_c3-2	80	INSRR; NTRK1	MODIFIER; MODERATE	c.3397+28C>T; c.13G>A	; p.Ala5Thr	3	FALSE	chr1:156811876:G:A	213:chr1:156811876:G:A	0.002153
80_c3-2	80	TP53	MODIFIER; MODERATE	c.*122G>A; c.*34G>A; c.1015G>A; c.538G>A; c.619G>A; c.898G>A	; p.Glu339Lys; p.Glu180Lys; p.Glu207Lys; p.Glu300Lys	18	FALSE	chr17:7574012:C:T	213:chr17:7574012:C:T	0.002073
80_c3-2	80	KDR	MODERATE	c.2831G>A	p.Arg944Gln	2	FALSE	chr4:55961109:C:T	213:chr4:55961109:C:T	0.002774

80_c3-2	80	DDR2	MODERATE	c.2255G>A	p.Arg752His	1	FALSE	chr1:162746132:G:A	213:chr1:162746132:G:A	0.001744
80_c3-2	80	FGFR2	MODERATE; MODIFIER	c.148C>T; c.226C>T; c.493C>T; n.795C>T	p.Arg50Trp; p.Arg76Trp; p.Arg165Trp;	1	FALSE	chr10:123310935:G:A	213:chr10:123310935:G:A	0.00246
80_c3-2	80	GNA11	MODERATE	c.1030G>A	p.Val344Met	1	FALSE	chr19:3121127:G:A	213:chr19:3121127:G:A	0.00225
80_c3-2	80	APC	HIGH	c.1209G>A; c.1263G>A	p.Trp403*; p.Trp421*	0	FALSE	chr5:112154992:G:A	213:chr5:112154992:G:A	0.002186
80_c3-2	80	C9orf53; CDKN2A	MODIFIER; MODERATE; LOW	n.*616G>A; c.*222C>T; c.299C>T; c.342C>T	; p.Ala100Val; p.Gly114Gly	2	FALSE	chr9:21971059:G:A	213:chr9:21971059:G:A	0.005348
80_c3-2	80	HGF	MODERATE	c.1172G>A; c.1187G>A	p.Gly391Asp; p.Gly396Asp	0	FALSE	chr7:81350145:C:T	213:chr7:81350145:C:T	0.002469
80_c3-2	80	MET	HIGH	c.1619G>A	p.Trp540*	1	FALSE	chr7:116380997:G:A	213:chr7:116380997:G:A	0.002715
80_c3-2	80	NTRK2	MODERATE	c.1285G>A; c.1324G>A	p.Val429Met; p.Val442Met	0	FALSE	chr9:87366928:G:A	213:chr9:87366928:G:A	0.002387
80_c3-2	80	ATM	MODERATE	c.6115G>A	p.Glu2039Lys	0	FALSE	chr11:108186757:G:A	213:chr11:108186757:G:A	0.002055
80_c3-2	80	TSC2	MODIFIER; MODERATE	c.2837+1108G>A; c.2933G>A	; p.Arg978His	0	FALSE	chr16:2127694:G:A	213:chr16:2127694:G:A	0.002628
80_c3-2	80	FGFR1	MODERATE	c.487C>T; c.493C>T; c.736C>T; c.754C>T; c.760C>T; c.853C>T	p.Arg163Trp; p.Arg165Trp; p.Arg246Trp; p.Arg252Trp; p.Arg254Trp; p.Arg285Trp	1	FALSE	chr8:38282203:G:A	213:chr8:38282203:G:A	0.002191
80_c3-2	80	CTNNB1	MODERATE	c.1345C>T	p.Arg449Cys	0	FALSE	chr3:41275179:C:T	213:chr3:41275179:C:T	0.001744

80_c3-2	80	NOTCH1	MODERATE	c.4918G>A	p.Ala1640Thr	0	FALSE	chr9:139399225:C:T	213:chr9:139399225:C:T	0.003781
80_c3-2	80	GNA11	MODERATE	c.805G>A	p.Val269Ile	1	FALSE	chr19:3119273:G:A	213:chr19:3119273:G:A	0.002608
80_c3-2	80	MET	MODERATE	c.2684C>T; c.2738C>T	p.Thr895Met; p.Thr913Met	1	FALSE	chr7:116409799:C:T	213:chr7:116409799:C:T	0.002188
80_c3-2	80	ALK	MODERATE	c.536G>A	p.Arg179His	1	FALSE	chr2:30142990:C:T	213:chr2:30142990:C:T	0.002247
80_c3-2	80	IGF1R	MODERATE	c.1511G>A	p.Arg504His	0	FALSE	chr15:99454592:G:A	213:chr15:99454592:G:A	0.001934
80_c3-2	80	CTNNB1	MODERATE	c.149G>A	p.Gly50Asp	0	FALSE	chr3:41266152:G:A	213:chr3:41266152:G:A	0.002415
80_c3-2	80	NF1	MODERATE	c.2740C>T	p.Arg914Trp	1	FALSE	chr17:29556373:C:T	213:chr17:29556373:C:T	0.003198
80_c3-2	80	CTNNB1	MODERATE	c.1564G>A	p.Ala522Thr	0	FALSE	chr3:41275669:G:A	213:chr3:41275669:G:A	0.002395
55_bl-1	55	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2410G>A; n.1152C>T	p.Glu804Lys;	2	FALSE	chr7:55249112:G:A	214:chr7:55249112:G:A	0.007018
55_bl-1	55	ERBB2; MIR4728; MIEN1	MODERATE; MODIFIER	c.3518T>C; c.3428T>C; c.3473T>C; c.*97T>C; n.*67T>C; c.*388A>G; n.3842T>C	p.Leu1173Pro; p.Leu1143Pro; p.Leu1158Pro;	1	FALSE	chr17:37884047:T:C	214:chr17:37884047:T:C	0.00813
38_c2-2	38	KRAS	MODERATE	c.35G>A	p.Gly12Asp	11213	FALSE	chr12:25398284:C:T	215:chr12:25398284:C:T	0.078864
38_c2-2	38	PIK3CA	MODERATE	c.1634A>C	p.Glu545Ala	132	FALSE	chr3:178936092:A:C	215:chr3:178936092:A:C	0.006579
38_c2-2	38	TP53	MODERATE	c.265C>T; c.346C>T; c.625C>T; c.742C>T	p.Arg89Trp; p.Arg116Trp; p.Arg209Trp; p.Arg248Trp	559	FALSE	chr17:7577539:G:A	215:chr17:7577539:G:A	0.058741
38_c2-2	38	MAP2K1	MODERATE	c.145C>T	p.Arg49Cys	1	FALSE	chr15:66727429:C:T	215:chr15:66727429:C:T	0.002026

54_bl-b	54	ROS1	MODERATE	c.5687T>G	p.Val1896Gly	1	FALSE	chr6:117642512:A:C	216:chr6:117642512:A:C	0.004348
54_bl-b	54	TP53	MODERATE; MODIFIER	c.215C>G; c.98C>G; c.-279C>G; c.-360C>G	p.Pro72Arg; p.Pro33Arg;	9	TRUE	chr17:7579472:G:C	216:chr17:7579472:G:C	0.08046
54_bl-b	54	MAP2K1	MODERATE	c.145C>T	p.Arg49Cys	1	FALSE	chr15:66727429:C:T	216:chr15:66727429:C:T	0.003315
54_bl-b	54	TP53	LOW; MODIFIER; MODERATE	c.-23C>T; c.338C>T; c.455C>T; c.59C>T	; p.Pro113Leu; p.Pro152Leu; p.Pro20Leu	72	FALSE	chr17:7578475:G:A	216:chr17:7578475:G:A	0.004673
54_bl-b	54	TP53	MODERATE	c.261G>T; c.342G>T; c.621G>T; c.738G>T	p.Met87Ile; p.Met114Ile; p.Met207Ile; p.Met246Ile	21	FALSE	chr17:7577543:C:A	216:chr17:7577543:C:A	0.002833
54_bl-b	54	RET	MODERATE	c.1438G>A	p.Glu480Lys	1	FALSE	chr10:43606829:G:A	216:chr10:43606829:G:A	0.004054
54_bl-b	54	ALK	MODERATE	c.3455T>C	p.Leu1152Pro	1	FALSE	chr2:29445270:A:G	216:chr2:29445270:A:G	0.009736
54_bl-b	54	FGFR1	MODERATE	c.1060C>T; c.1066C>T; c.1303C>T; c.1327C>T; c.1333C>T; c.1426C>T	p.Arg354Trp; p.Arg356Trp; p.Arg435Trp; p.Arg443Trp; p.Arg445Trp; p.Arg476Trp	2	FALSE	chr8:38275843:G:A	216:chr8:38275843:G:A	0.004435
54_bl-b	54	TP53	MODIFIER; HIGH	c.*143G>T; c.*55G>T; c.1036G>T; c.559G>T; c.640G>T; c.919G>T	; p.Glu346*; p.Glu187*; p.Glu214*; p.Glu307*	4	FALSE	chr17:7573991:C:A	216:chr17:7573991:C:A	0.003807
54_bl-b	54	RET	MODERATE	c.1690A>C	p.Thr564Pro	1	FALSE	chr10:43608342:A:C	216:chr10:43608342:A:C	0.002433

54_bl-b	54	DDR2	MODERATE	c.1418G>A	p.Arg473His	2	FALSE	chr1:162740216:G:A	216:chr1:162740216:G:A	0.002577
38_c3-2	38	EPHA3	MODERATE	c.2734A>T	p.Thr912Ser	0	FALSE	chr3:89521657:A:T	217:chr3:89521657:A:T	0.004843
38_c3-2	38	TP53	MODERATE	c.265C>T; c.346C>T; c.625C>T; c.742C>T	p.Arg89Trp; p.Arg116Trp; p.Arg209Trp; p.Arg248Trp	559	FALSE	chr17:7577539:G:A	217:chr17:7577539:G:A	0.080831
38_c3-2	38	PIK3CA	MODERATE	c.1634A>C	p.Glu545Ala	132	FALSE	chr3:178936092:A:C	217:chr3:178936092:A:C	0.006024
38_c3-2	38	KRAS	MODERATE	c.35G>A	p.Gly12Asp	11213	FALSE	chr12:25398284:C:T	217:chr12:25398284:C:T	0.086093
70_c3-1	70	GNA11	MODERATE	c.340C>T	p.Arg114Trp	1	FALSE	chr19:3113346:C:T	218:chr19:3113346:C:T	0.001228
70_c3-1	70	TP53	MODIFIER; MODERATE	c.-24C>T; c.337C>T; c.454C>T; c.58C>T	; p.Pro113Ser; p.Pro152Ser; p.Pro20Ser	24	FALSE	chr17:7578476:G:A	218:chr17:7578476:G:A	0.001745
70_c3-1	70	NF1	MODERATE	c.6943G>A; c.7006G>A	p.Ala2315Thr; p.Ala2336Thr	2	FALSE	chr17:29667607:G:A	218:chr17:29667607:G:A	0.001078
70_c3-1	70	TP53	MODERATE; MODIFIER	c.115G>T; c.232G>T; c.-279G>T; c.-360G>T	p.Ala39Ser; p.Ala78Ser;	1	FALSE	chr17:7579455:C:A	218:chr17:7579455:C:A	0.001934
70_c3-1	70	TP53	MODERATE	c.266G>A; c.347G>A; c.626G>A; c.743G>A	p.Arg89Gln; p.Arg116Gln; p.Arg209Gln; p.Arg248Gln	673	FALSE	chr17:7577538:C:T	218:chr17:7577538:C:T	0.001558
70_c3-1	70	TP53	MODIFIER; MODERATE	c.*182C>T; c.*94C>T; c.1075C>T; c.598C>T; c.679C>T; c.958C>T	; p.Pro359Ser; p.Pro200Ser; p.Pro227Ser; p.Pro320Ser	1	FALSE	chr17:7573952:G:A	218:chr17:7573952:G:A	0.000978

70_c3-1	70	PTEN	MODERATE	c.729C>A	p.Phe243Leu	1	FALSE	chr10:89717704:C:A	218:chr10:89717704:C:A	0.001223
70_c3-1	70	CTNNB1	MODERATE	c.98C>A	p.Ser33Tyr	0	FALSE	chr3:41266101:C:A	218:chr3:41266101:C:A	0.001651
70_c3-1	70	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2527G>A; n.-1C>T	p.Val843Ile;	6	FALSE	chr7:55259469:G:A	218:chr7:55259469:G:A	0.001818
70_c3-1	70	PIK3CA	MODERATE	c.518C>A	p.Ser173Tyr	1	FALSE	chr3:178917643:C:A	218:chr3:178917643:C:A	0.000986
70_c3-1	70	NF1	MODERATE	c.7583C>T; c.7646C>T	p.Ser2528Leu; p.Ser2549Leu	3	FALSE	chr17:29683508:C:T	218:chr17:29683508:C:T	0.0011
70_c3-1	70	CTNNB1	HIGH	c.283C>T	p.Arg95*	0	FALSE	chr3:41266486:C:T	218:chr3:41266486:C:T	0.001124
70_c3-1	70	HOXD-AS2; HOXD8	MODIFIER; MODERATE	n.*692G>T; c.22C>A; c.574C>A	; p.Gln8Lys; p.Gln192Lys	0	FALSE	chr2:176995668:C:A	218:chr2:176995668:C:A	0.002114
70_c3-1	70	NRAS	MODERATE	c.394G>A	p.Glu132Lys	2	FALSE	chr1:115252246:C:T	218:chr1:115252246:C:T	0.001082
70_c3-1	70	CTNNB1	MODERATE	c.861C>A	p.Asn287Lys	0	FALSE	chr3:41267277:C:A	218:chr3:41267277:C:A	0.001135
70_c3-1	70	EGFR	MODERATE	c.445C>T	p.Arg149Trp	1	FALSE	chr7:55214319:C:T	218:chr7:55214319:C:T	0.001263
70_c3-1	70	AKT3	MODERATE	c.793G>A	p.Gly265Arg	0	FALSE	chr1:243736254:C:T	218:chr1:243736254:C:T	0.00108
70_c3-1	70	MET	MODERATE	c.1450C>A	p.His484Asn	1	FALSE	chr7:116380061:C:A	218:chr7:116380061:C:A	0.001048
70_c3-1	70	KIT	MODERATE	c.1156G>A	p.Glu386Lys	1	FALSE	chr4:55575630:G:A	218:chr4:55575630:G:A	0.001139
70_c3-1	70	NF1	MODERATE	c.5482G>A; c.5545G>A	p.Asp1828Asn; p.Asp1849Asn	1	FALSE	chr17:29654793:G:A	218:chr17:29654793:G:A	0.001116
70_c3-1	70	HGF	HIGH	c.1993G>T; c.2008G>T	p.Glu665*; p.Glu670*	0	FALSE	chr7:81334708:C:A	218:chr7:81334708:C:A	0.001265
70_c3-1	70	TP53	MODIFIER; MODERATE	c.*117G>T; c.*29G>T; c.1010G>T; c.533G>T; c.614G>T; c.893G>T	; p.Arg337Leu; p.Arg178Leu; p.Arg205Leu; p.Arg298Leu	21	FALSE	chr17:7574017:C:A	218:chr17:7574017:C:A	0.01206

61_c2-2	61	PIK3CA	MODERATE	c.49C>T	p.Pro17Ser	1	FALSE	chr3:178916662:C:T	219:chr3:178916662:C:T	0.00216
61_c2-2	61	PTEN	HIGH	c.822G>A	p.Trp274*	3	FALSE	chr10:89720671:G:A	219:chr10:89720671:G:A	0.00464
61_c2-2	61	EPHA3	MODERATE	c.1123C>T	p.Pro375Ser	0	FALSE	chr3:89391057:C:T	219:chr3:89391057:C:T	0.001978
61_c2-2	61	TP53	MODERATE; MODIFIER	c.254G>A; c.371G>A; c.-279G>A; c.-360G>A	p.Cys85Tyr; p.Cys124Tyr;	3	FALSE	chr17:7579316:C:T	219:chr17:7579316:C:T	0.003086
61_c2-2	61	CDH1	MODERATE	c.2204C>T	p.Ala735Val	0	FALSE	chr16:68862116:C:T	219:chr16:68862116:C:T	0.002413
61_c2-2	61	ALK	MODERATE	c.4435G>A	p.Ala1479Thr	1	FALSE	chr2:29416518:C:T	219:chr2:29416518:C:T	0.002804
61_c2-2	61	NTRK1	MODERATE	c.1927G>A; c.2017G>A; c.2035G>A	p.Asp643Asn; p.Asp673Asn; p.Asp679Asn	1	FALSE	chr1:156849143:G:A	219:chr1:156849143:G:A	0.002778
61_c2-2	61	EPHA3	MODERATE	c.2248C>T	p.Arg750Trp	0	FALSE	chr3:89480411:C:T	219:chr3:89480411:C:T	0.002786
61_c2-2	61	MITF	MODIFIER; MODERATE	c.-45G>A; c.109G>A; c.112G>A; c.64G>A	; p.Ala37Thr; p.Ala38Thr; p.Ala22Thr	0	FALSE	chr3:69928292:G:A	219:chr3:69928292:G:A	0.00226
61_c2-2	61	PDGFRA	MODERATE	c.862T>C	p.Tyr288His	1	FALSE	chr4:55133558:T:C	219:chr4:55133558:T:C	0.002364
61_c2-2	61	IGF1R	MODERATE	c.3637C>A; c.3640C>A	p.Gln1213Lys; p.Gln1214Lys	0	FALSE	chr15:99491855:C:A	219:chr15:99491855:C:A	0.002252
61_c2-2	61	ALK	MODERATE	c.4306C>T	p.Arg1436Cys	3	FALSE	chr2:29416647:G:A	219:chr2:29416647:G:A	0.001949
61_c2-2	61	FLT3	MODERATE	c.2858C>T	p.Ala953Val	0	FALSE	chr13:28588590:G:A	219:chr13:28588590:G:A	0.002415
61_c2-2	61	AKT1	MODERATE	c.340G>C	p.Glu114Gln	1	FALSE	chr14:105242084:C:G	219:chr14:105242084:C:G	0.002509
61_c2-2	61	MET	MODERATE	c.1627G>A	p.Asp543Asn	1	FALSE	chr7:116381005:G:A	219:chr7:116381005:G:A	0.002755
61_c2-2	61	CDH1	MODERATE	c.2074G>A	p.Ala692Thr	0	FALSE	chr16:68857439:G:A	219:chr16:68857439:G:A	0.002301

61_c2-2	61	MET	MODERATE	c.1234C>T	p.Arg412Cys	1	FALSE	chr7:116371755:C:T	219:chr7:116371755:C:T	0.002296
61_c2-2	61	EGFR	MODIFIER; MODERATE	c.*2364G>A; c.2161G>A	; p.Gly721Ser	5	FALSE	chr7:55241713:G:A	219:chr7:55241713:G:A	0.002481
61_c2-2	61	NOTCH1	MODERATE	c.3374C>T	p.Ala1125Val	0	FALSE	chr9:139402543:G:A	219:chr9:139402543:G:A	0.00346
61_c2-2	61	IGF1R	MODERATE	c.1565G>A	p.Ser522Asn	0	FALSE	chr15:99454646:G:A	219:chr15:99454646:G:A	0.003513
61_c2-2	61	GNA11	MODERATE	c.1030G>A	p.Val344Met	1	FALSE	chr19:3121127:G:A	219:chr19:3121127:G:A	0.005195
61_c2-2	61	TSC2	MODERATE	c.1654G>A	p.Ala552Thr	0	FALSE	chr16:2115574:G:A	219:chr16:2115574:G:A	0.003968
61_c2-2	61	TP53	LOW; MODIFIER; MODERATE	c.-6C>T; c.355C>T; c.472C>T; c.76C>T	; p.Arg119Cys; p.Arg158Cys; p.Arg26Cys	17	FALSE	chr17:7578458:G:A	219:chr17:7578458:G:A	0.002663
61_c2-2	61	ERBB2	MODIFIER; HIGH	n.2202C>A; c.1788C>A; c.1833C>A; c.1878C>A	; p.Cys596*; p.Cys611*; p.Cys626*	2	FALSE	chr17:37873713:C:A	219:chr17:37873713:C:A	0.00274
61_c2-2	61	ERBB2	MODERATE; MODIFIER	c.560G>A; c.605G>A; c.650G>A; n.974G>A	p.Arg187His; p.Arg202His; p.Arg217His;	1	FALSE	chr17:37866345:G:A	219:chr17:37866345:G:A	0.002484
61_c2-2	61	MET	HIGH	c.1619G>A	p.Trp540*	1	FALSE	chr7:116380997:G:A	219:chr7:116380997:G:A	0.001931
61_c2-2	61	PTEN	MODERATE	c.283C>T	p.Pro95Ser	3	FALSE	chr10:89692799:C:T	219:chr10:89692799:C:T	0.004559
61_c2-2	61	MIR4673; NOTCH1	MODIFIER; MODERATE	n.*59G>A; c.1058G>A	; p.Arg353His	0	FALSE	chr9:139413084:C:T	219:chr9:139413084:C:T	0.002762
61_c2-2	61	KIT	MODERATE	c.1486G>A	p.Asp496Asn	1	FALSE	chr4:55592162:G:A	219:chr4:55592162:G:A	0.00292
61_c2-2	61	C9orf53; CDKN2A	MODIFIER; MODERATE; LOW	n.*616G>A; c.*222C>T; c.299C>T; c.342C>T	; p.Ala100Val; p.Gly114Gly	2	FALSE	chr9:21971059:G:A	219:chr9:21971059:G:A	0.003953

61_c2-2	61	EGFR	MODIFIER; MODERATE	c.*2364G>A; c.2125G>A	; p.Glu709Lys	21	FALSE	chr7:55241677:G:A	219:chr7:55241677:G:A	0.002252
61_c2-2	61	PTEN	HIGH	c.821G>A	p.Trp274*	6	FALSE	chr10:89720670:G:A	219:chr10:89720670:G:A	0.004706
61_c2-2	61	FBXW7	MODERATE	c.314G>T; c.428G>T; c.668G>T	p.Arg105Leu; p.Arg143Leu; p.Arg223Leu	0	FALSE	chr4:153268140:C:A	219:chr4:153268140:C:A	0.003222
61_c2-2	61	FGFR1; LETM2	MODERATE; MODIFIER	c.1927C>T; c.1933C>T; c.2170C>T; c.2194C>T; c.2200C>T; c.2293C>T; c.*1406G>A; c.*1423G>A; c.*1553G>A; c.*1567G>A; c.*1638G>A	p.Arg643Trp; p.Arg645Trp; p.Arg724Trp; p.Arg732Trp; p.Arg734Trp; p.Arg765Trp;	1	FALSE	chr8:38271528:G:A	219:chr8:38271528:G:A	0.00409
61_c2-2	61	NF1	MODERATE	c.6943G>A; c.7006G>A	p.Ala2315Thr; p.Ala2336Thr	2	FALSE	chr17:29667607:G:A	219:chr17:29667607:G:A	0.002488
61_c2-2	61	KIT	MODERATE	c.2671G>A; c.2683G>A	p.Ala891Thr; p.Ala895Thr	3	FALSE	chr4:55602973:G:A	219:chr4:55602973:G:A	0.00388
61_c2-2	61	NOTCH1	MODERATE	c.4984C>T	p.Arg1662Trp	0	FALSE	chr9:139399159:G:A	219:chr9:139399159:G:A	0.003861
61_c2-2	61	FGFR3	MODERATE	c.905G>A	p.Gly302Asp	1	FALSE	chr4:1803727:G:A	219:chr4:1803727:G:A	0.003035
61_c2-2	61	ERBB2; MIEN1; MIR4728	MODERATE; MODIFIER	c.2720A>G; c.2765A>G; c.2810A>G; n.3134A>G; c.*388T>C; n.-1A>G	p.Lys907Arg; p.Lys922Arg; p.Lys937Arg;	1	FALSE	chr17:37882044:A:G	219:chr17:37882044:A:G	0.002882

61_c2-2	61	NF1	MODERATE	c.5426G>A; c.5489G>A	p.Arg1809His; p.Arg1830His	1	FALSE	chr17:29654737:G:A	219:chr17:29654737:G:A	0.002868
61_c2-2	61	TP53	HIGH; MODIFIER	c.181C>T; c.298C>T; c.-279C>T; c.-360C>T	p.Gln61*; p.Gln100*;	16	FALSE	chr17:7579389:G:A	219:chr17:7579389:G:A	0.042781
61_c2-2	61	ALK	MODERATE	c.872G>A	p.Arg291His	1	FALSE	chr2:29917796:C:T	219:chr2:29917796:C:T	0.00224
61_c2-2	61	BRAF	MODERATE	c.1799T>A	p.Val600Glu	23024	FALSE	chr7:140453136:A:T	219:chr7:140453136:A:T	0.034351
61_c2-2	61	TP53	MODERATE	c.127C>T; c.208C>T; c.487C>T; c.604C>T	p.Arg43Cys; p.Arg70Cys; p.Arg163Cys; p.Arg202Cys	6	FALSE	chr17:7578245:G:A	219:chr17:7578245:G:A	0.002424
26_t2c2d1-1	26	TP53	MODERATE	c.256G>A; c.337G>A; c.616G>A; c.733G>A	p.Gly86Ser; p.Gly113Ser; p.Gly206Ser; p.Gly245Ser	361	FALSE	chr17:7577548:C:T	220:chr17:7577548:C:T	0.00468
26_t2c2d1-1	26	TSC2	MODERATE	c.3032G>A; c.3164G>A	p.Gly1011Asp; p.Gly1055Asp	0	FALSE	chr16:2129309:G:A	220:chr16:2129309:G:A	0.003534
26_t2c2d1-1	26	IDH2; ZNF710	MODERATE; MODIFIER	c.602C>T; c.836C>T; c.992C>T; c.*2147G>A	p.Thr201Met; p.Thr279Met; p.Thr331Met;	1	FALSE	chr15:90628595:G:A	220:chr15:90628595:G:A	0.003333
26_t2c2d1-1	26	FGFR2	MODERATE; MODIFIER	c.148C>T; c.226C>T; c.493C>T; n.795C>T	p.Arg50Trp; p.Arg76Trp; p.Arg165Trp;	1	FALSE	chr10:123310935:G:A	220:chr10:123310935:G:A	0.003284
26_t2c2d1-1	26	BRAF	MODERATE	c.1799T>A	p.Val600Glu	23024	FALSE	chr7:140453136:A:T	220:chr7:140453136:A:T	0.004792
26_t2c2d1-1	26	ALK	MODERATE	c.1307C>T	p.Ala436Val	1	FALSE	chr2:29551323:G:A	220:chr2:29551323:G:A	0.003995
26_t2c2d1-1	26	CDH1	MODERATE	c.2204C>T	p.Ala735Val	0	FALSE	chr16:68862116:C:T	220:chr16:68862116:C:T	0.00312

26_t2c2d1-1	26	PKD1; TSC2	MODIFIER; MODERATE	c.*13118C>T; c.*13121C>T; c.4192G>A; c.4324G>A; c.4393G>A	; p.Asp1398Asn; p.Asp1442Asn; p.Asp1465Asn	0	FALSE	chr16:2134616:G:A	220:chr16:2134616:G:A	0.002743
26_t2c2d1-1	26	EPHA3	MODERATE	c.2306G>A	p.Arg769His	0	FALSE	chr3:89480469:G:A	220:chr3:89480469:G:A	0.003185
26_t2c2d1-1	26	FGFR1	MODERATE	c.292C>T; c.298C>T; c.541C>T; c.559C>T; c.565C>T; c.658C>T	p.Arg98Cys; p.Arg100Cys; p.Arg181Cys; p.Arg187Cys; p.Arg189Cys; p.Arg220Cys	1	FALSE	chr8:38285495:G:A	220:chr8:38285495:G:A	0.003215
26_t2c2d1-1	26	APC	HIGH	c.1042C>T; c.988C>T	p.Arg348*; p.Arg330*	0	FALSE	chr5:112154771:C:T	220:chr5:112154771:C:T	0.002911
26_t2c2d1-1	26	HRAS; LRRC56	MODERATE; MODIFIER	c.175G>A; c.-506C>T	p.Ala59Thr;	2	FALSE	chr11:533881:C:T	220:chr11:533881:C:T	0.003384
26_t2c2d1-1	26	FGFR4	MODERATE	c.1444G>A; c.1528G>A; c.1648G>A	p.Val482Met; p.Val510Met; p.Val550Met	2	FALSE	chr5:176522551:G:A	220:chr5:176522551:G:A	0.008032
26_t2c2d1-1	26	MET	MODERATE	c.959C>T	p.Ala320Val	1	FALSE	chr7:116340097:C:T	220:chr7:116340097:C:T	0.002642
26_t2c2d1-1	26	MET	HIGH	c.1619G>A	p.Trp540*	1	FALSE	chr7:116380997:G:A	220:chr7:116380997:G:A	0.002635
26_t2c2d1-1	26	NTRK1	MODERATE	c.1927G>A; c.2017G>A; c.2035G>A	p.Asp643Asn; p.Asp673Asn; p.Asp679Asn	1	FALSE	chr1:156849143:G:A	220:chr1:156849143:G:A	0.003717
26_t2c2d1-1	26	PDGFRA	MODERATE	c.2152C>T	p.Arg718Trp	1	FALSE	chr4:55144678:C:T	220:chr4:55144678:C:T	0.003378
26_t2c2d1-1	26	TP53	MODERATE	c.406C>T; c.487C>T; c.766C>T; c.883C>T	p.Pro136Ser; p.Pro163Ser; p.Pro256Ser; p.Pro295Ser	2	FALSE	chr17:7577055:G:A	220:chr17:7577055:G:A	0.003284

26_t2c2d1-1	26	FGFR2	MODERATE; MODIFIER	c.1591G>A; c.1594G>A; c.1597G>A; c.1606G>A; c.1675G>A; c.1678G>A; c.1942G>A; c.1945G>A; n.2392G>A	p.Ala531Thr; p.Ala532Thr; p.Ala533Thr; p.Ala536Thr; p.Ala559Thr; p.Ala560Thr; p.Ala648Thr; p.Ala649Thr;	3	FALSE	chr10:123247549:C:T	220:chr10:123247549:C:T	0.003704
26_t2c2d1-1	26	NTRK3	MODERATE	c.1351C>T; c.1375C>T	p.Arg451Trp; p.Arg459Trp	0	FALSE	chr15:88669523:G:A	220:chr15:88669523:G:A	0.003322
26_t2c2d1-1	26	CTNNB1	MODERATE	c.1346G>A	p.Arg449His	0	FALSE	chr3:41275180:G:A	220:chr3:41275180:G:A	0.002681
26_t2c2d1-1	26	EPHA3	MODERATE	c.1142G>A	p.Arg381His	0	FALSE	chr3:89391076:G:A	220:chr3:89391076:G:A	0.002821
26_t2c2d1-1	26	CDH1	MODERATE	c.2074G>A	p.Ala692Thr	0	FALSE	chr16:68857439:G:A	220:chr16:68857439:G:A	0.002817
26_t2c2d1-1	26	NF1	HIGH	c.3942G>A	p.Trp1314*	1	FALSE	chr17:29563007:G:A	220:chr17:29563007:G:A	0.002475
26_t2c1d1-12	26	FGFR3	MODERATE	c.599G>A	p.Arg200His	1	FALSE	chr4:1803247:G:A	221:chr4:1803247:G:A	0.004608
26_t2c1d1-12	26	APC	MODERATE	c.1708G>A; c.1762G>A	p.Val570Ile; p.Val588Ile	0	FALSE	chr5:112170666:G:A	221:chr5:112170666:G:A	0.003515
26_t2c1d1-12	26	AKT1	MODERATE	c.458T>C	p.Leu153Pro	1	FALSE	chr14:105241522:A:G	221:chr14:105241522:A:G	0.003247
26_t2c1d1-12	26	NTRK2	MODERATE	c.1984G>A; c.2032G>A	p.Ala662Thr; p.Ala678Thr	0	FALSE	chr9:87570292:G:A	221:chr9:87570292:G:A	0.003373
26_t2c1d1-12	26	KDR	HIGH	c.3352C>T	p.Arg1118*	2	FALSE	chr4:55955593:G:A	221:chr4:55955593:G:A	0.002959
26_t2c1d1-12	26	PTEN	MODERATE	c.389G>A	p.Arg130Gln	89	FALSE	chr10:89692905:G:A	221:chr10:89692905:G:A	0.003185
26_t2c1d1-12	26	SMO	MODERATE	c.1640G>A	p.Arg547His	0	FALSE	chr7:128850377:G:A	221:chr7:128850377:G:A	0.003236
26_t2c1d1-12	26	BRAF	MODERATE	c.1799T>A	p.Val600Glu	23024	FALSE	chr7:140453136:A:T	221:chr7:140453136:A:T	0.009317

26_t2c1d1-12	26	CWH43	MODERATE	c.782G>A; c.863G>A	p.Cys261Tyr; p.Cys288Tyr	0	FALSE	chr4:49005812:G:A	221:chr4:49005812:G:A	0.003058
26_t2c1d1-12	26	FOXL2; FOXL2NB; LINC01391	MODERATE; MODIFIER	c.205G>A; c.-132C>T; n.-1G>A	p.Glu69Lys;	0	FALSE	chr3:138665360:C:T	221:chr3:138665360:C:T	0.003759
26_t2c1d1-12	26	EGFR	MODERATE	c.3025G>A	p.Asp1009Asn	1	FALSE	chr7:55268959:G:A	221:chr7:55268959:G:A	0.003322
26_t2c1d1-12	26	TP53	MODERATE	c.229T>C; c.310T>C; c.589T>C; c.706T>C	p.Tyr77His; p.Tyr104His; p.Tyr197His; p.Tyr236His	18	FALSE	chr17:7577575:A:G	221:chr17:7577575:A:G	0.003155
26_t2c1d1-12	26	APC	MODIFIER; MODERATE	c.676-8784G>A; c.695G>A	; p.Arg232Gln	0	FALSE	chr5:112128192:G:A	221:chr5:112128192:G:A	0.003591
26_t2c1d1-12	26	FGFR2	MODIFIER; MODERATE	c.110-14065C>T; c.110-945C>T; n.757-14065C>T; c.290C>T	; p.Ala97Val	1	FALSE	chr10:123325038:G:A	221:chr10:123325038:G:A	0.003317
26_t2c1d1-12	26	HOXD-AS2; HOXD8	MODIFIER; MODERATE	n.*692G>T; c.22C>A; c.574C>A	; p.Gln8Lys; p.Gln192Lys	0	FALSE	chr2:176995668:C:A	221:chr2:176995668:C:A	0.005263
26_t2c1d1-12	26	C9orf53; CDKN2A	MODIFIER; MODERATE; HIGH	n.*616G>A; c.*161C>T; c.281C>T; c.238C>T	; p.Pro94Leu; p.Arg80*	124	FALSE	chr9:21971120:G:A	221:chr9:21971120:G:A	0.014409
26_t2c1d1-12	26	NOTCH1	MODERATE	c.5585C>T	p.Pro1862Leu	0	FALSE	chr9:139396253:G:A	221:chr9:139396253:G:A	0.003891
26_t2c1d1-12	26	TSC2	MODERATE	c.781C>T	p.Arg261Trp	0	FALSE	chr16:2107112:C:T	221:chr16:2107112:C:T	0.005464
26_t2c1d1-12	26	MIR4673; NOTCH1	MODIFIER; MODERATE	n.*59G>A; c.1058G>A	; p.Arg353His	0	FALSE	chr9:139413084:C:T	221:chr9:139413084:C:T	0.003759
26_t2c1d1-12	26	C9orf53; CDKN2A	MODIFIER; MODERATE; LOW	n.*616G>A; c.*276C>T; c.353C>T; c.396C>T	; p.Ala118Val; p.Gly132Gly	1	FALSE	chr9:21971005:G:A	221:chr9:21971005:G:A	0.004866

26_t2c1d1-12	26	FGFR4	MODERATE	c.784G>A	p.Val262Met	1	FALSE	chr5:176519378:G:A	221:chr5:176519378:G:A	0.004338
26_t2c1d15	26	TP53	MODERATE; MODIFIER	c.100G>A; c.217G>A; c.-279G>A; c.-360G>A	p.Val34Met; p.Val73Met;	5	FALSE	chr17:7579470:C:T	222:chr17:7579470:C:T	0.00463
26_t2c1d15	26	CDH1	MODERATE	c.1093G>A	p.Val365Ile	0	FALSE	chr16:68846122:G:A	222:chr16:68846122:G:A	0.002472
26_t2c1d15	26	PDGFRA	MODERATE	c.1738C>A	p.Leu580Met	1	FALSE	chr4:55141092:C:A	222:chr4:55141092:C:A	0.004274
26_t2c1d15	26	KDR	MODERATE	c.3065G>A	p.Arg1022Gln	1	FALSE	chr4:55958788:C:T	222:chr4:55958788:C:T	0.003236
26_t2c1d15	26	TSC2	MODIFIER; MODERATE	c.2837+1108G>A; c.2933G>A	; p.Arg978His	0	FALSE	chr16:2127694:G:A	222:chr16:2127694:G:A	0.003597
26_t2c1d15	26	IDH2; ZNF710	MODERATE; MODIFIER	c.1091C>T; c.1247C>T; c.857C>T; c.*2147G>A	p.Ala364Val; p.Ala416Val; p.Ala286Val;	1	FALSE	chr15:90628072:G:A	222:chr15:90628072:G:A	0.003623
26_t2c1d15	26	AR	MODERATE	c.1789G>A; c.193G>A	p.Ala597Thr; p.Ala65Thr	0	FALSE	chrX:66905872:G:A	222:chrX:66905872:G:A	0.005814
26_t2c1d15	26	MET	MODERATE	c.1640G>A	p.Arg547Gln	1	FALSE	chr7:116381018:G:A	222:chr7:116381018:G:A	0.002372
26_t2c1d15	26	BRAF	MODERATE	c.1799T>A	p.Val600Glu	23024	FALSE	chr7:140453136:A:T	222:chr7:140453136:A:T	0.003049
26_t2c1d15	26	PIK3R1	MODERATE	c.1082G>A; c.1271G>A; c.1361G>A; c.2171G>A	p.Arg361Gln; p.Arg424Gln; p.Arg454Gln; p.Arg724Gln	1	FALSE	chr5:67593425:G:A	222:chr5:67593425:G:A	0.002326
26_t2c1d15	26	DDR2	MODERATE	c.2038C>T	p.Arg680Cys	1	FALSE	chr1:162745623:C:T	222:chr1:162745623:C:T	0.002378
26_t2c1d15	26	KIT	LOW	c.1869G>A; c.1881G>A	p.Pro623Pro; p.Pro627Pro	1	FALSE	chr4:55594178:G:A	222:chr4:55594178:G:A	0.003236
26_t2c1d15	26	KDR	MODERATE	c.1028C>T	p.Thr343Met	3	FALSE	chr4:55976884:G:A	222:chr4:55976884:G:A	0.001934

26_t2c1d15	26	PDGFRA	MODERATE	c.2692G>A	p.Gly898Ser	1	FALSE	chr4:55154983:G:A	222:chr4:55154983:G:A	0.002732
26_t2c1d15	26	TP53	MODERATE	c.224A>G; c.305A>G; c.584A>G; c.701A>G	p.Tyr75Cys; p.Tyr102Cys; p.Tyr195Cys; p.Tyr234Cys	94	FALSE	chr17:7577580:T:C	222:chr17:7577580:T:C	0.003968
26_t2c1d15	26	RET	MODERATE	c.1385C>T	p.Ser462Leu	1	FALSE	chr10:43606776:C:T	222:chr10:43606776:C:T	0.002577
26_t2c1d15	26	MET	HIGH	c.1619G>A	p.Trp540*	1	FALSE	chr7:116380997:G:A	222:chr7:116380997:G:A	0.002577
26_t2c1d15	26	NOTCH1	MODERATE	c.4252G>A	p.Ala1418Thr	0	FALSE	chr9:139400096:C:T	222:chr9:139400096:C:T	0.004008
26_t2c1d15	26	MIR1225; PKD1; TSC2	MODIFIER; MODERATE	n.*90C>T; c.*13118C>T; c.*13121C>T; c.4954G>A; c.5086G>A; c.5155G>A	; p.Ala1652Thr; p.Ala1696Thr; p.Ala1719Thr	0	FALSE	chr16:2138135:G:A	222:chr16:2138135:G:A	0.002937
26_t2c1d15	26	ATM	MODERATE	c.8275C>T	p.Pro2759Ser	0	FALSE	chr11:108213955:C:T	222:chr11:108213955:C:T	0.00365
26_t2c1d15	26	ATM	MODERATE	c.2075G>A	p.Arg692His	0	FALSE	chr11:108124717:G:A	222:chr11:108124717:G:A	0.00271
26_t2c1d15	26	MET	MODERATE	c.788C>T	p.Thr263Met	1	FALSE	chr7:116339926:C:T	222:chr7:116339926:C:T	0.002667
26_t2c1d15	26	ALK	MODERATE	c.617C>T	p.Ala206Val	2	FALSE	chr2:30142909:G:A	222:chr2:30142909:G:A	0.004545
26_t2c1d15	26	GNA11	MODERATE	c.440G>A	p.Arg147His	1	FALSE	chr19:3113446:G:A	222:chr19:3113446:G:A	0.003413
26_t2c1d15	26	PTEN	MODERATE	c.389G>A	p.Arg130Gln	89	FALSE	chr10:89692905:G:A	222:chr10:89692905:G:A	0.002941
26_t2c1d15	26	ALK	MODERATE	c.446C>T	p.Ala149Val	1	FALSE	chr2:30143080:G:A	222:chr2:30143080:G:A	0.003636
26_t2c1d15	26	HRAS; LRRC56	MODERATE; MODIFIER	c.404G>A; c.-506C>T	p.Arg135Gln;	1	FALSE	chr11:533499:C:T	222:chr11:533499:C:T	0.002981
26_t2c1d15	26	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2356G>A; n.1206C>T	p.Val786Met;	6	FALSE	chr7:55249058:G:A	222:chr7:55249058:G:A	0.00271

26_t2c1d15	26	TP53	MODERATE	c.128G>A; c.407G>A; c.47G>A; c.524G>A	p.Arg43His; p.Arg136His; p.Arg16His; p.Arg175His	979	FALSE	chr17:7578406:C:T	222:chr17:7578406:C:T	0.002946
26_t2c1d15	26	NF1	MODERATE	c.4463G>A; c.4526G>A	p.Arg1488His; p.Arg1509His	1	FALSE	chr17:29587482:G:A	222:chr17:29587482:G:A	0.003072
26_t2c1d15	26	TP53	MODIFIER; MODERATE	c.-2C>T; c.359C>T; c.476C>T; c.80C>T	; p.Ala120Val; p.Ala159Val; p.Ala27Val	41	FALSE	chr17:7578454:G:A	222:chr17:7578454:G:A	0.00313
26_t2c1d15	26	NTRK2	MODERATE	c.220G>A	p.Ala74Thr	0	FALSE	chr9:87317081:G:A	222:chr9:87317081:G:A	0.004049
26_t2c1d15	26	NTRK2	MODERATE	c.1981G>A; c.2029G>A	p.Ala661Thr; p.Ala677Thr	0	FALSE	chr9:87570289:G:A	222:chr9:87570289:G:A	0.003101
26_t2c1d15	26	TP53	MODIFIER; MODERATE	c.*137A>G; c.*225A>G; c.1001A>G; c.1118A>G; c.641A>G; c.722A>G	; p.Lys334Arg; p.Lys373Arg; p.Lys214Arg; p.Lys241Arg	1	FALSE	chr17:7572991:T:C	222:chr17:7572991:T:C	0.004975
26_t2c1d15	26	TSC1	MODERATE	c.1547C>T; c.1697C>T; c.1700C>T	p.Ala516Val; p.Ala566Val; p.Ala567Val	0	FALSE	chr9:135781265:G:A	222:chr9:135781265:G:A	0.002389
26_t2c1d15	26	FGFR3	MODERATE	c.1183G>A; c.1519G>A; c.1525G>A	p.Val395Met; p.Val507Met; p.Val509Met	1	FALSE	chr4:1807188:G:A	222:chr4:1807188:G:A	0.00404
131_c1w3-2	131	BRAF	MODERATE	c.1202C>T	p.Thr401Ile	1	FALSE	chr7:140482933:G:A	228:chr7:140482933:G:A	0.005988
131_c1w3-2	131	EGFR	MODERATE	c.755G>A	p.Arg252His	3	FALSE	chr7:55221711:G:A	228:chr7:55221711:G:A	0.005848
131_c1w3-2	131	KIT	MODERATE	c.1460G>A	p.Gly487Asp	1	FALSE	chr4:55592136:G:A	228:chr4:55592136:G:A	0.003861
131_c1w3-2	131	PIK3CA	MODERATE	c.2594G>A	p.Gly865Asp	1	FALSE	chr3:178947158:G:A	228:chr3:178947158:G:A	0.003578

131_c1w3-2	131	ESR1	MODERATE	c.719G>A; c.725G>A	p.Cys240Tyr; p.Cys242Tyr	0	FALSE	chr6:152201865:G:A	228:chr6:152201865:G:A	0.003578
131_c1w3-2	131	EGFR	MODIFIER; MODERATE	c.*1464G>A; c.1321G>A	; p.Val441Ile	1	FALSE	chr7:55227854:G:A	228:chr7:55227854:G:A	0.003817
131_c1w3-2	131	ALK	MODERATE	c.956C>T	p.Ser319Phe	2	FALSE	chr2:29754979:G:A	228:chr2:29754979:G:A	0.00381
131_c1w3-2	131	PIK3CA	MODERATE	c.35G>A	p.Gly12Asp	5	FALSE	chr3:178916648:G:A	228:chr3:178916648:G:A	0.003086
131_c1w3-2	131	APC	MODERATE	c.1708G>A; c.1762G>A	p.Val570Ile; p.Val588Ile	0	FALSE	chr5:112170666:G:A	228:chr5:112170666:G:A	0.003922
131_c1w3-2	131	FBXW7	MODERATE	c.1039C>T; c.1153C>T; c.1393C>T	p.Arg347Cys; p.Arg385Cys; p.Arg465Cys	0	FALSE	chr4:153249385:G:A	228:chr4:153249385:G:A	0.003711
131_c1w3-2	131	NTHL1; TSC2	MODIFIER; MODERATE	c.-20C>T; c.170G>A	; p.Arg57His	0	FALSE	chr16:2100432:G:A	228:chr16:2100432:G:A	0.004211
131_c1w3-2	131	EPHA3	MODERATE	c.1646C>T	p.Ala549Val	0	FALSE	chr3:89456470:C:T	228:chr3:89456470:C:T	0.004115
131_c1w3-2	131	EPHA3	MODERATE	c.1543G>A	p.Ala515Thr	0	FALSE	chr3:89448579:G:A	228:chr3:89448579:G:A	0.004049
131_c1w3-2	131	AKT3	MODERATE	c.899C>T	p.Ala300Val	0	FALSE	chr1:243727071:G:A	228:chr1:243727071:G:A	0.003401
131_c1w3-2	131	TSC2	MODERATE	c.2702G>A	p.Arg901His	0	FALSE	chr16:2126131:G:A	228:chr16:2126131:G:A	0.005859
131_c1w3-2	131	ATM	MODERATE	c.7330G>A	p.Glu2444Lys	0	FALSE	chr11:108200963:G:A	228:chr11:108200963:G:A	0.003466
131_c1w3-2	131	ESR1	MODERATE	c.1171G>A; c.1174G>A; c.1180G>A	p.Val391Ile; p.Val392Ile; p.Val394Ile	0	FALSE	chr6:152332868:G:A	228:chr6:152332868:G:A	0.003515
131_c1w3-2	131	NTRK3	MODERATE	c.1463C>T; c.1487C>T	p.Ala488Val; p.Ala496Val	0	FALSE	chr15:88576186:G:A	228:chr15:88576186:G:A	0.005376
130_c1w2-1	130	CDKN2A	MODIFIER; HIGH	c.194-3575G>A; c.45G>A	; p.Trp15*	3	FALSE	chr9:21974782:C:T	238:chr9:21974782:C:T	0.004367

130_c1w2-1	130	FBXW7	MODERATE	c.232A>T; c.346A>T; c.586A>T	p.Thr78Ser; p.Thr116Ser; p.Thr196Ser	0	FALSE	chr4:153268222:T:A	238:chr4:153268222:T:A	0.021807
130_c1w2-1	130	ATM	HIGH	c.5623C>T	p.Arg1875*	0	FALSE	chr11:108175528:C:T	238:chr11:108175528:C:T	0.003509
130_c1w2-1	130	FGFR1	MODERATE	c.475C>T; c.481C>T; c.724C>T; c.742C>T; c.748C>T; c.841C>T	p.Arg159Trp; p.Arg161Trp; p.Arg242Trp; p.Arg248Trp; p.Arg250Trp; p.Arg281Trp	2	FALSE	chr8:38282215:G:A	238:chr8:38282215:G:A	0.002454
130_c1w2-1	130	C9orf53; CDKN2A	MODIFIER; MODERATE; LOW	n.*616T>G; c.*120A>C; c.197A>C; c.240A>C	; p.His66Pro; p.Pro80Pro	1	FALSE	chr9:21971161:T:G	238:chr9:21971161:T:G	0.035422
130_c1w2-1	130	ERBB2; MIEN1; MIR4728	MODIFIER; MODERATE	c.3160-213A>G; c.3251A>G; c.3296A>G; c.3341A>G; n.3665A>G; c.*388T>C; n.*67A>G	; p.Glu1084Gly; p.Glu1099Gly; p.Glu1114Gly	1	FALSE	chr17:37883729:A:G	238:chr17:37883729:A:G	0.00314
130_c1w2-1	130	SMO	MODERATE	c.1045A>C	p.Thr349Pro	0	FALSE	chr7:128846115:A:C	238:chr7:128846115:A:C	0.00753
130_c1w2-1	130	TP53	MODIFIER; MODERATE	c.-15A>C; c.346A>C; c.463A>C; c.67A>C	; p.Thr116Pro; p.Thr155Pro; p.Thr23Pro	17	FALSE	chr17:7578467:T:G	238:chr17:7578467:T:G	0.004438
130_c1w2-1	130	IGF1R	MODERATE	c.3934T>C; c.3937T>C	p.Ser1312Pro; p.Ser1313Pro	0	FALSE	chr15:99500504:T:C	238:chr15:99500504:T:C	0.004754
130_c1w2-1	130	PIK3CA	MODERATE	c.1022C>T	p.Ala341Val	2	FALSE	chr3:178921540:C:T	238:chr3:178921540:C:T	0.003221

132_c2-1	132	IGF1R	MODERATE	c.3934T>C; c.3937T>C	p.Ser1312Pro; p.Ser1313Pro	0	FALSE	chr15:99500504:T:C	239:chr15:99500504:T:C	0.005295
132_c2-1	132	FGFR4	MODERATE	c.1745G>A; c.1829G>A; c.1949G>A	p.Arg582His; p.Arg610His; p.Arg650His	1	FALSE	chr5:176523292:G:A	239:chr5:176523292:G:A	0.00227
132_c2-1	132	CSDE1; NRAS	MODIFIER; MODERATE	c.*2430A>G; c.*2523A>G; c.*2817A>G; c.*2910A>G; c.*2964A>G; c.*3057A>G; c.182A>G	; p.Gln61Arg	1103	FALSE	chr1:115256529:T:C	239:chr1:115256529:T:C	0.00388
132_c2-1	132	BRAF	MODERATE	c.1799T>A	p.Val600Glu	23024	FALSE	chr7:140453136:A:T	239:chr7:140453136:A:T	0.05667
132_c2-1	132	GNA11	MODERATE	c.548G>A	p.Arg183His	1	FALSE	chr19:3115013:G:A	239:chr19:3115013:G:A	0.001709
132_c2-1	132	KIT	MODERATE	c.2855G>A; c.2867G>A	p.Arg952Gln; p.Arg956Gln	3	FALSE	chr4:55604659:G:A	239:chr4:55604659:G:A	0.001736
132_c2-1	132	NOTCH1	MODERATE	c.5777G>A	p.Arg1926His	0	FALSE	chr9:139395161:C:T	239:chr9:139395161:C:T	0.001908
132_c2-1	132	ERBB2; MIEN1; MIR4728	MODERATE; MODIFIER	c.2512C>T; c.2557C>T; c.2602C>T; n.2926C>T; c.*388G>A; n.-1C>T	p.Arg838Trp; p.Arg853Trp; p.Arg868Trp;	1	FALSE	chr17:37881410:C:T	239:chr17:37881410:C:T	0.001546
132_c2-1	132	C9orf53; CDKN2A	MODIFIER; MODERATE	n.*616C>G; c.*140G>C; c.217G>C; c.260G>C	; p.Ala73Pro; p.Arg87Pro	1	FALSE	chr9:21971141:C:G	239:chr9:21971141:C:G	0.003899
132_c2-1	132	KDR	MODERATE	c.2323G>T	p.Ala775Ser	1	FALSE	chr4:55964914:C:A	239:chr4:55964914:C:A	0.001524
132_c2-1	132	RET	MODERATE	c.2116G>A	p.Val706Met	2	FALSE	chr10:43610164:G:A	239:chr10:43610164:G:A	0.001999

132_c2-1	132	BRAF	MODERATE	c.2173C>T	p.His725Tyr	1	FALSE	chr7:140434525:G:A	239:chr7:140434525:G:A	0.002246
132_c2-1	132	PIK3CA	MODERATE	c.3059C>T	p.Ala1020Val	4	FALSE	chr3:178952004:C:T	239:chr3:178952004:C:T	0.001437
132_c2-1	132	FBXW7	MODERATE	c.232A>T; c.346A>T; c.586A>T	p.Thr78Ser; p.Thr116Ser; p.Thr196Ser	0	FALSE	chr4:153268222:T:A	239:chr4:153268222:T:A	0.00652
132_c2-1	132	FLT3	MODERATE	c.2146G>A	p.Glu716Lys	0	FALSE	chr13:28601286:C:T	239:chr13:28601286:C:T	0.002725
132_c2-1	132	TP53	MODERATE; MODIFIER	c.128C>T; c.245C>T; c.-279C>T; c.-360C>T	p.Pro43Leu; p.Pro82Leu;	6	FALSE	chr17:7579442:G:A	239:chr17:7579442:G:A	0.002081
132_c2-1	132	PTEN	MODERATE	c.518G>A	p.Arg173His	27	FALSE	chr10:89711900:G:A	239:chr10:89711900:G:A	0.001953
132_c2-1	132	NTRK1	MODERATE	c.804C>G; c.894C>G	p.His268Gln; p.His298Gln	1	FALSE	chr1:156843468:C:G	239:chr1:156843468:C:G	0.00186
132_c2-1	132	ATM	HIGH	c.5623C>T	p.Arg1875*	0	FALSE	chr11:108175528:C:T	239:chr11:108175528:C:T	0.002193
132_c2-1	132	VHL	MODIFIER; MODERATE	c.341-3270A>C; c.344A>C	; p.His115Pro	0	FALSE	chr3:10188201:A:C	239:chr3:10188201:A:C	0.00183
132_c2-1	132	NTRK1	MODERATE	c.1940T>G; c.2030T>G; c.2048T>G	p.Val647Gly; p.Val677Gly; p.Val683Gly	2	FALSE	chr1:156849792:T:G	239:chr1:156849792:T:G	0.021277
132_c2-1	132	PIK3R1	MODERATE	c.386C>T	p.Pro129Leu	1	FALSE	chr5:67569269:C:T	239:chr5:67569269:C:T	0.001899
132_c2-1	132	SMO	MODERATE	c.508A>C	p.Thr170Pro	0	FALSE	chr7:128843401:A:C	239:chr7:128843401:A:C	0.002322
132_c2-1	132	PIK3R1	HIGH	c.1630A>T; c.541A>T; c.730A>T; c.820A>T	p.Arg544*; p.Arg181*; p.Arg244*; p.Arg274*	1	FALSE	chr5:67591037:A:T	239:chr5:67591037:A:T	0.001668
73_c2-1	73	KDR	MODERATE	c.1028C>T	p.Thr343Met	3	FALSE	chr4:55976884:G:A	240:chr4:55976884:G:A	0.00346

73_c2-1	73	NTRK1	MODERATE	c.1940T>G; c.2030T>G; c.2048T>G	p.Val647Gly; p.Val677Gly; p.Val683Gly	2	FALSE	chr1:156849792:T:G	240:chr1:156849792:T:G	0.025381
73_c2-1	73	C9orf53; CDKN2A	MODIFIER; MODERATE	n.*616C>T; c.*245G>A; c.322G>A; c.365G>A	; p.Asp108Asn; p.Arg122Gln	14	FALSE	chr9:21971036:C:T	240:chr9:21971036:C:T	0.015038
73_c2-1	73	KDR	MODERATE	c.1588T>A	p.Cys530Ser	1	FALSE	chr4:55972056:A:T	240:chr4:55972056:A:T	0.010169
73_c2-1	73	ATM	MODERATE	c.7328G>A	p.Arg2443Gln	0	FALSE	chr11:108200961:G:A	240:chr11:108200961:G:A	0.006873
73_c2-1	73	TP53	MODERATE	c.107A>C; c.26A>C; c.386A>C; c.503A>C	p.His36Pro; p.His9Pro; p.His129Pro; p.His168Pro	15	FALSE	chr17:7578427:T:G	240:chr17:7578427:T:G	0.008
69_c5-1	69	PDGFRA	MODERATE	c.1955G>T	p.Gly652Val	1	FALSE	chr4:55144126:G:T	241:chr4:55144126:G:T	0.001512
69_c5-1	69	NOTCH1	MODERATE	c.4571C>T	p.Ala1524Val	0	FALSE	chr9:139399777:G:A	241:chr9:139399777:G:A	0.001817
69_c5-1	69	C9orf53; CDKN2A	MODIFIER; MODERATE	n.*616C>G; c.*140G>C; c.217G>C; c.260G>C	; p.Ala73Pro; p.Arg87Pro	1	FALSE	chr9:21971141:C:G	241:chr9:21971141:C:G	0.007273
69_c5-1	69	C9orf53; CDKN2A	MODIFIER; MODERATE; LOW	n.*616T>G; c.*120A>C; c.197A>C; c.240A>C	; p.His66Pro; p.Pro80Pro	1	FALSE	chr9:21971161:T:G	241:chr9:21971161:T:G	0.035511
69_c5-1	69	KIT	MODERATE	c.13C>T	p.Arg5Cys	1	FALSE	chr4:55524194:C:T	241:chr4:55524194:C:T	0.001907
69_c5-1	69	ATM	MODERATE	c.2803A>G	p.Thr935Ala	0	FALSE	chr11:108139301:A:G	241:chr11:108139301:A:G	0.001618

69_c5-1	69	TP53	MODIFIER; MODERATE	c.-5G>A; c.356G>A; c.473G>A; c.77G>A	; p.Arg119His; p.Arg158His; p.Arg26His	80	FALSE	chr17:7578457:C:T	241:chr17:7578457:C:T	0.001533
69_c5-1	69	KRAS	MODERATE	c.35G>T	p.Gly12Val	11213	FALSE	chr12:25398284:C:A	241:chr12:25398284:C:A	0.002622
69_c5-1	69	C9orf53; CDKN2A	MODIFIER; MODERATE	n.*616A>C; c.*137T>G; c.214T>G; c.257T>G	; p.Cys72Gly; p.Leu86Arg	1	FALSE	chr9:21971144:A:C	241:chr9:21971144:A:C	0.003891
69_c5-1	69	EVI2A; NF1	MODIFIER; MODERATE	c.-266C>T; c.-338C>T; c.4895G>A; c.4958G>A	; p.Arg1632His; p.Arg1653His	1	FALSE	chr17:29652960:G:A	241:chr17:29652960:G:A	0.001522
69_c5-1	69	PTEN	MODERATE	c.1004G>A	p.Arg335Gln	1	FALSE	chr10:89720853:G:A	241:chr10:89720853:G:A	0.001974
69_c5-1	69	VHL	MODIFIER; MODERATE	c.341-3256A>G; c.358A>G	; p.Arg120Gly	0	FALSE	chr3:10188215:A:G	241:chr3:10188215:A:G	0.005892
69_c5-1	69	RET	MODERATE	c.1690A>C	p.Thr564Pro	1	FALSE	chr10:43608342:A:C	241:chr10:43608342:A:C	0.007536
69_c5-1	69	RET	MODERATE	c.1888T>G	p.Cys630Gly	4	FALSE	chr10:43609936:T:G	241:chr10:43609936:T:G	0.002226
69_c5-1	69	PIK3CA	MODERATE	c.1636C>A	p.Gln546Lys	127	FALSE	chr3:178936094:C:A	241:chr3:178936094:C:A	0.001706
69_c5-1	69	TP53	MODIFIER; MODERATE	c.-15A>C; c.346A>C; c.463A>C; c.67A>C	; p.Thr116Pro; p.Thr155Pro; p.Thr23Pro	17	FALSE	chr17:7578467:T:G	241:chr17:7578467:T:G	0.004666
69_c5-1	69	CDKN2A; CDKN2B-AS1	MODERATE; MODIFIER	c.22A>G; n.-1T>C	p.Thr8Ala;	1	FALSE	chr9:21994309:T:C	241:chr9:21994309:T:C	0.005427
69_c5-1	69	VHL	MODIFIER; MODERATE	c.341-3270A>C; c.344A>C	; p.His115Pro	0	FALSE	chr3:10188201:A:C	241:chr3:10188201:A:C	0.001838
69_c5-1	69	PTEN	MODERATE	c.370T>C	p.Cys124Arg	4	FALSE	chr10:89692886:T:C	241:chr10:89692886:T:C	0.001657

69_c5-1	69	APC	MODERATE	c.721C>T; c.775C>T	p.Arg241Trp; p.Arg259Trp	0	FALSE	chr5:112137021:C:T	241:chr5:112137021:C:T	0.001618
69_c5-1	69	CDKN2A	MODIFIER; MODERATE	c.194-3519C>T; c.101C>T	; p.Ala34Val	2	FALSE	chr9:21974726:G:A	241:chr9:21974726:G:A	0.002101
69_c5-1	69	MITF	MODERATE	c.157A>C; c.265A>C; c.310A>C; c.313A>C	p.Thr53Pro; p.Thr89Pro; p.Thr104Pro; p.Thr105Pro	0	FALSE	chr3:69928493:A:C	241:chr3:69928493:A:C	0.004065
69_c5-1	69	NTRK1	MODERATE	c.1940T>G; c.2030T>G; c.2048T>G	p.Val647Gly; p.Val677Gly; p.Val683Gly	2	FALSE	chr1:156849792:T:G	241:chr1:156849792:T:G	0.019231
69_c5-1	69	EGFR	MODERATE	c.655T>G	p.Cys219Gly	2	FALSE	chr7:55220265:T:G	241:chr7:55220265:T:G	0.001667
69_c5-1	69	MIR4673; NOTCH1	MODIFIER; MODERATE	n.*59A>C; c.1195A>C	; p.Thr399Pro	0	FALSE	chr9:139412649:T:G	241:chr9:139412649:T:G	0.010368
69_c5-1	69	KIT	MODERATE	c.2149T>C; c.2161T>C	p.Tyr717His; p.Tyr721His	1	FALSE	chr4:55597513:T:C	241:chr4:55597513:T:C	0.001645
130_c2-1	130	IGF1R	MODERATE	c.3934T>C; c.3937T>C	p.Ser1312Pro; p.Ser1313Pro	0	FALSE	chr15:99500504:T:C	244:chr15:99500504:T:C	0.04026
130_c2-1	130	TP53	LOW; MODIFIER; MODERATE	c.-51G>A; c.310G>A; c.31G>A; c.427G>A	; p.Val104Met; p.Val11Met; p.Val143Met	24	FALSE	chr17:7578503:C:T	244:chr17:7578503:C:T	0.00224
130_c2-1	130	FOXL2; FOXL2NB; LINC01391	MODERATE; MODIFIER	c.282T>A; c.-132A>T; n.-1T>A	p.Asn94Lys;	0	FALSE	chr3:138665283:A:T	244:chr3:138665283:A:T	0.006508
130_c2-1	130	MIR4673; NOTCH1	MODIFIER; MODERATE	n.*59A>C; c.1195A>C	; p.Thr399Pro	0	FALSE	chr9:139412649:T:G	244:chr9:139412649:T:G	0.005587

130_c2-1	130	ERBB2; MIEN1; MIR4728	MODIFIER; MODERATE	c.3160-213A>G; c.3251A>G; c.3296A>G; c.3341A>G; n.3665A>G; c.*388T>C; n.*67A>G	; p.Glu1084Gly; p.Glu1099Gly; p.Glu1114Gly	1	FALSE	chr17:37883729:A:G	244:chr17:37883729:A:G	0.002424
130_c2-1	130	MET	HIGH	c.1619G>A	p.Trp540*	1	FALSE	chr7:116380997:G:A	244:chr7:116380997:G:A	0.002247
130_c2-1	130	NTRK1	MODERATE	c.1940T>G; c.2030T>G; c.2048T>G	p.Val647Gly; p.Val677Gly; p.Val683Gly	2	FALSE	chr1:156849792:T:G	244:chr1:156849792:T:G	0.046512
130_c2-1	130	SMO	MODERATE	c.1045A>C	p.Thr349Pro	0	FALSE	chr7:128846115:A:C	244:chr7:128846115:A:C	0.028769
130_c2-1	130	IDH2	MODERATE	c.128A>C; c.362A>C; c.518A>C	p.His43Pro; p.His121Pro; p.His173Pro	1	FALSE	chr15:90631835:T:G	244:chr15:90631835:T:G	0.006046
130_c2-1	130	FLT3	HIGH	c.1096G>T	p.Glu366*	0	FALSE	chr13:28622521:C:A	244:chr13:28622521:C:A	0.002342
130_c2-1	130	EGFR	MODERATE	c.627A>C	p.Lys209Asn	1	FALSE	chr7:55219054:A:C	244:chr7:55219054:A:C	0.003175
130_c2-1	130	TP53	MODIFIER; HIGH	c.-48C>T; c.313C>T; c.34C>T; c.430C>T	; p.Gln105*; p.Gln12*; p.Gln144*	42	FALSE	chr17:7578500:G:A	244:chr17:7578500:G:A	0.00224
130_c2-1	130	NOTCH1	MODERATE	c.6088T>C	p.Ser2030Pro	0	FALSE	chr9:139393443:A:G	244:chr9:139393443:A:G	0.005442
74_c8-1	74	TP53	MODERATE	c.688A>C; c.292A>C; c.211A>C; c.571A>C	p.Thr230Pro; p.Thr98Pro; p.Thr71Pro; p.Thr191Pro	10	FALSE	chr17:7577593:T:G	246:chr17:7577593:T:G	0.008403
74_c8-1	74	VHL	MODIFIER; MODERATE	c.341-3270A>C; c.344A>C	; p.His115Pro	0	FALSE	chr3:10188201:A:C	246:chr3:10188201:A:C	0.004695
74_c8-1	74	HGF	HIGH	c.517C>T; c.532C>T	p.Arg173*; p.Arg178*	0	FALSE	chr7:81381529:G:A	246:chr7:81381529:G:A	0.004329

74_c8-1	74	SMO	MODERATE	c.1045A>C	p.Thr349Pro	0	FALSE	chr7:128846115:A:C	246:chr7:128846115:A:C	0.023576
74_c8-1	74	NTRK1	MODERATE	c.1940T>G; c.2030T>G; c.2048T>G	p.Val647Gly; p.Val677Gly; p.Val683Gly	2	FALSE	chr1:156849792:T:G	246:chr1:156849792:T:G	0.034591
9_bl-4	9	EGFR	MODERATE	c.1159C>G	p.Leu387Val	1	FALSE	chr7:55224477:C:G	247:chr7:55224477:C:G	0.004211
9_bl-4	9	KRAS	MODERATE	c.35G>A	p.Gly12Asp	11213	FALSE	chr12:25398284:C:T	247:chr12:25398284:C:T	0.041958
23_bl-3	23	NF1	HIGH	c.6652C>T; c.6715C>T	p.Gln2218*; p.Gln2239*	2	FALSE	chr17:29665053:C:T	248:chr17:29665053:C:T	0.013841
23_bl-3	23	TP53	MODERATE	c.845G>C; c.449G>C; c.368G>C; c.728G>C	p.Arg282Pro; p.Arg150Pro; p.Arg123Pro; p.Arg243Pro	26	FALSE	chr17:7577093:C:G	248:chr17:7577093:C:G	0.005013
23_bl-3	23	EGFR	MODERATE	c.445C>T	p.Arg149Trp	1	FALSE	chr7:55214319:C:T	248:chr7:55214319:C:T	0.004425
23_bl-3	23	CWH43	MODERATE	c.1990C>T; c.2071C>T	p.His664Tyr; p.His691Tyr	0	FALSE	chr4:49063878:C:T	248:chr4:49063878:C:T	0.00813
23_bl-3	23	TP53	MODERATE	c.139C>T; c.418C>T; c.535C>T; c.58C>T	p.His47Tyr; p.His140Tyr; p.His179Tyr; p.His20Tyr	92	FALSE	chr17:7578395:G:A	248:chr17:7578395:G:A	0.016204
23_bl-3	23	BRAF	MODERATE	c.1790T>A	p.Leu597Gln	18	FALSE	chr7:140453145:A:T	248:chr7:140453145:A:T	0.010695
23_bl-3	23	EPHA3	MODERATE	c.2416G>A	p.Asp806Asn	0	FALSE	chr3:89498444:G:A	248:chr3:89498444:G:A	0.004444
23_bl-3	23	TP53	MODERATE	c.361A>G; c.442A>G; c.721A>G; c.838A>G	p.Arg121Gly; p.Arg148Gly; p.Arg241Gly; p.Arg280Gly	24	FALSE	chr17:7577100:T:C	248:chr17:7577100:T:C	0.005076
26_c2-1	26	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2419G>A; n.1143C>T	p.Asp807Asn;	1	FALSE	chr7:55249121:G:A	249:chr7:55249121:G:A	0.000841

26_c2-1	26	AKT3	MODERATE	c.469G>T	p.Gly157Cys	0	FALSE	chr1:243801005:C:A	249:chr1:243801005:C:A	0.001096
26_c2-1	26	CTNNB1	MODERATE	c.166G>A	p.Asp56Asn	0	FALSE	chr3:41266169:G:A	249:chr3:41266169:G:A	0.000872
26_c2-1	26	FGFR1	MODERATE	c.1135C>T; c.1141C>T; c.1378C>T; c.1402C>T; c.1408C>T; c.1501C>T	p.Arg379Cys; p.Arg381Cys; p.Arg460Cys; p.Arg468Cys; p.Arg470Cys; p.Arg501Cys	1	FALSE	chr8:38275768:G:A	249:chr8:38275768:G:A	0.000867
26_c2-1	26	NF1	MODERATE	c.2695T>G	p.Leu899Val	3	FALSE	chr17:29556328:T:G	249:chr17:29556328:T:G	0.010118
26_c2-1	26	HGF	MODERATE	c.404G>T	p.Ser135Ile	0	FALSE	chr7:81386583:C:A	249:chr7:81386583:C:A	0.00137
26_c2-1	26	BRAF	MODERATE	c.1385G>T	p.Arg462Ile	2	FALSE	chr7:140481423:C:A	249:chr7:140481423:C:A	0.000903
26_c2-1	26	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2591C>A; n.-1G>T	p.Ala864Glu;	2	FALSE	chr7:55259533:C:A	249:chr7:55259533:C:A	0.00113
26_c2-1	26	EGFR; EGFR-AS1	MODERATE; MODIFIER	c.2546A>G; n.-1T>C	p.Gln849Arg;	2	FALSE	chr7:55259488:A:G	249:chr7:55259488:A:G	0.001172
26_c2-1	26	PTEN	MODERATE	c.443C>A	p.Ala148Glu	1	FALSE	chr10:89692959:C:A	249:chr10:89692959:C:A	0.001738
26_c2-1	26	MAP2K1	MODERATE	c.379G>A	p.Val127Met	1	FALSE	chr15:66729171:G:A	249:chr15:66729171:G:A	0.001152
26_c2-1	26	TP53	MODIFIER; MODERATE	c.-5G>T; c.356G>T; c.473G>T; c.77G>T	; p.Arg119Leu; p.Arg158Leu; p.Arg26Leu	80	FALSE	chr17:7578457:C:A	249:chr17:7578457:C:A	0.001284
26_c2-1	26	MAP2K1	MODERATE	c.371C>A	p.Pro124Gln	1	FALSE	chr15:66729163:C:A	249:chr15:66729163:C:A	0.000785
26_c2-1	26	EPHA3	MODERATE	c.1516G>A	p.Val506Ile	0	FALSE	chr3:89448552:G:A	249:chr3:89448552:G:A	0.001034
26_c2-1	26	NF1	HIGH	c.3721C>T	p.Arg1241*	5	FALSE	chr17:29562641:C:T	249:chr17:29562641:C:T	0.000958
26_c2-1	26	EGFR	MODIFIER; MODERATE	c.*1464C>T; c.1279C>T	; p.Arg427Cys	2	FALSE	chr7:55225427:C:T	249:chr7:55225427:C:T	0.000888

26_c2-1	26	KIT	MODERATE	c.1611G>A; c.1623G>A	p.Met537Ile; p.Met541Ile	1	FALSE	chr4:55593466:G:A	249:chr4:55593466:G:A	0.000955
26_c2-1	26	TP53	MODERATE	c.242G>T; c.323G>T; c.602G>T; c.719G>T	p.Ser81Ile; p.Ser108Ile; p.Ser201Ile; p.Ser240Ile	6	FALSE	chr17:7577562:C:A	249:chr17:7577562:C:A	0.001023
26_c2-1	26	PTEN	MODERATE	c.274G>A	p.Asp92Asn	3	FALSE	chr10:89692790:G:A	249:chr10:89692790:G:A	0.001076
26_c2-1	26	PIK3CA	MODERATE	c.3001C>A	p.Leu1001Ile	3	FALSE	chr3:178951946:C:A	249:chr3:178951946:C:A	0.000815
26_c2-1	26	CSDE1; NRAS	MODIFIER; MODERATE	c.*2430G>T; c.*2523G>T; c.*2817G>T; c.*2910G>T; c.*2964G>T; c.*3057G>T; c.34G>T	; p.Gly12Cys	154	FALSE	chr1:115258748:C:A	249:chr1:115258748:C:A	0.000963
26_c2-1	26	CTNNB1	MODERATE	c.1358G>A	p.Arg453Gln	0	FALSE	chr3:41275192:G:A	249:chr3:41275192:G:A	0.000727
26_c2-1	26	TP53	MODERATE	c.128G>A; c.407G>A; c.47G>A; c.524G>A	p.Arg43His; p.Arg136His; p.Arg16His; p.Arg175His	979	FALSE	chr17:7578406:C:T	249:chr17:7578406:C:T	0.001123
26_c2-1	26	TP53	MODIFIER; MODERATE	c.*182C>T; c.*94C>T; c.1075C>T; c.598C>T; c.679C>T; c.958C>T	; p.Pro359Ser; p.Pro200Ser; p.Pro227Ser; p.Pro320Ser	1	FALSE	chr17:7573952:G:A	249:chr17:7573952:G:A	0.000836
26_c2-1	26	NRAS	MODERATE	c.553C>T	p.Pro185Ser	2	FALSE	chr1:115251173:G:A	249:chr1:115251173:G:A	0.000971
26_c2-1	26	NF1	MODERATE	c.7381G>A; c.7444G>A	p.Asp2461Asn; p.Asp2482Asn	1	FALSE	chr17:29677323:G:A	249:chr17:29677323:G:A	0.00115

26_c2-1	26	TP53	MODERATE	c.371G>T; c.452G>T; c.731G>T; c.848G>T	p.Arg124Leu; p.Arg151Leu; p.Arg244Leu; p.Arg283Leu	24	FALSE	chr17:7577090:C:A	249:chr17:7577090:C:A	0.000972
26_c2-1	26	RET	MODERATE	c.1538C>T	p.Ala513Val	1	FALSE	chr10:43607562:C:T	249:chr10:43607562:C:T	0.000887
26_c2-1	26	TP53	MODERATE	c.405G>T; c.486G>T; c.765G>T; c.882G>T	p.Glu135Asp; p.Glu162Asp; p.Glu255Asp; p.Glu294Asp	4	FALSE	chr17:7577056:C:A	249:chr17:7577056:C:A	0.00092
26_c2-1	26	EGFR	MODERATE	c.866C>T	p.Ala289Val	34	FALSE	chr7:55221822:C:T	249:chr7:55221822:C:T	0.001135
26_c2-1	26	TP53	MODERATE; MODIFIER	c.218G>A; c.335G>A; c.-279G>A; c.-360G>A	p.Gly73Asp; p.Gly112Asp;	1	FALSE	chr17:7579352:C:T	249:chr17:7579352:C:T	0.001101
26_c2-1	26	TP53	MODIFIER; MODERATE	c.-9G>T; c.352G>T; c.469G>T; c.73G>T	; p.Val118Phe; p.Val157Phe; p.Val25Phe	169	FALSE	chr17:7578461:C:A	249:chr17:7578461:C:A	0.001276
26_c2-1	26	CTNNB1	MODERATE	c.125C>A	p.Thr42Lys	0	FALSE	chr3:41266128:C:A	249:chr3:41266128:C:A	0.001412
26_c2-1	26	PIK3CA	MODERATE	c.1070G>A	p.Arg357Gln	2	FALSE	chr3:178922301:G:A	249:chr3:178922301:G:A	0.000936
26_c2-1	26	TP53	MODERATE	c.127C>T; c.406C>T; c.46C>T; c.523C>T	p.Arg43Cys; p.Arg136Cys; p.Arg16Cys; p.Arg175Cys	20	FALSE	chr17:7578407:G:A	249:chr17:7578407:G:A	0.001129
26_c2-1	26	PTEN	MODERATE	c.421C>A	p.His141Asn	2	FALSE	chr10:89692937:C:A	249:chr10:89692937:C:A	0.001507
26_c2-1	26	HOXD-AS2; HOXD8	MODIFIER; MODERATE	n.*692C>T; c.304G>A; c.853G>A; c.856G>A	; p.Glu102Lys; p.Glu285Lys; p.Glu286Lys	0	FALSE	chr2:176996323:G:A	249:chr2:176996323:G:A	0.000834

26_c2-1	26	AKT1	MODERATE	c.286C>T	p.Arg96Trp	1	FALSE	chr14:105242997:G:A	249:chr14:105242997:G:A	0.001234
26_c2-1	26	PIK3CA	MODERATE	c.1633G>A	p.Glu545Lys	1189	FALSE	chr3:178936091:G:A	249:chr3:178936091:G:A	0.000871
26_c2-1	26	ALK	MODERATE	c.2677G>A	p.Gly893Arg	1	FALSE	chr2:29451888:C:T	249:chr2:29451888:C:T	0.001438
26_c2-1	26	RET	MODERATE	c.1690A>C	p.Thr564Pro	1	FALSE	chr10:43608342:A:C	249:chr10:43608342:A:C	0.008285
26_c2-1	26	TP53	MODERATE; HIGH	c.363G>T; c.480G>T; c.84G>T; c.3G>T	p.Met121Ile; p.Met160Ile; p.Met28Ile; p.Met1?	4	FALSE	chr17:7578450:C:A	249:chr17:7578450:C:A	0.001247
26_c2-1	26	TP53	MODERATE	c.499G>A; c.580G>A; c.859G>A; c.976G>A	p.Glu167Lys; p.Glu194Lys; p.Glu287Lys; p.Glu326Lys	4	FALSE	chr17:7576870:C:T	249:chr17:7576870:C:T	0.00115
26_c2-1	26	HOXD-AS2; HOXD8	MODIFIER; MODERATE	n.*692G>T; c.105C>A; c.654C>A; c.657C>A	; p.Asn35Lys; p.Asn218Lys; p.Asn219Lys	0	FALSE	chr2:176996124:C:A	249:chr2:176996124:C:A	0.001532
26_c2-1	26	PTEN	HIGH	c.720C>A	p.Tyr240*	3	FALSE	chr10:89717695:C:A	249:chr10:89717695:C:A	0.001468
26_c2-1	26	FGFR1	MODIFIER; MODERATE	c.-85G>T; c.107G>T; c.8G>T	; p.Ser36Ile; p.Ser3Ile	1	FALSE	chr8:38314957:C:A	249:chr8:38314957:C:A	0.002478
26_c2-1	26	TP53	MODIFIER; HIGH	c.*143G>T; c.*55G>T; c.1036G>T; c.559G>T; c.640G>T; c.919G>T	; p.Glu346*; p.Glu187*; p.Glu214*; p.Glu307*	4	FALSE	chr17:7573991:C:A	249:chr17:7573991:C:A	0.001208
26_c2-1	26	CTNNB1	MODERATE	c.110C>A	p.Ser37Tyr	0	FALSE	chr3:41266113:C:A	249:chr3:41266113:C:A	0.001931
26_c2-1	26	HGF	HIGH	c.1873C>T; c.1888C>T	p.Arg625*; p.Arg630*	0	FALSE	chr7:81334828:G:A	249:chr7:81334828:G:A	0.000972

26_c2-1	26	NF1	MODERATE	c.590C>A	p.Thr197Lys	1	FALSE	chr17:29508443:C:A	249:chr17:29508443:C:A	0.001685
26_c2-1	26	ERBB2; MIEN1; MIR4728	MODIFIER; MODERATE	c.*174C>A; c.3505C>A; c.3550C>A; c.3595C>A; n.3919C>A; c.*388G>T; n.*67C>A	; p.Pro1169Thr; p.Pro1184Thr; p.Pro1199Thr	2	FALSE	chr17:37884124:C:A	249:chr17:37884124:C:A	0.001121
26_c2-1	26	RET	MODERATE	c.2116G>A	p.Val706Met	2	FALSE	chr10:43610164:G:A	249:chr10:43610164:G:A	0.000739
26_c2-1	26	PIK3CA	MODERATE	c.1645G>A	p.Asp549Asn	4	FALSE	chr3:178936103:G:A	249:chr3:178936103:G:A	0.000935
26_c2-1	26	MAP2K1	MODERATE	c.140G>A	p.Arg47Gln	4	FALSE	chr15:66727424:G:A	249:chr15:66727424:G:A	0.00076
26_c2-1	26	EGFR	MODIFIER; MODERATE	c.*1464G>T; c.1507G>T	; p.Gly503Cys	1	FALSE	chr7:55229200:G:T	249:chr7:55229200:G:T	0.001202
26_c2-1	26	EGFR	MODIFIER; MODERATE	c.*1464C>A; c.1476C>A	; p.Ser492Arg	4	FALSE	chr7:55228009:C:A	249:chr7:55228009:C:A	0.000966
26_c2-1	26	TP53	MODERATE	c.234G>T; c.315G>T; c.594G>T; c.711G>T	p.Met78Ile; p.Met105Ile; p.Met198Ile; p.Met237Ile	81	FALSE	chr17:7577570:C:A	249:chr17:7577570:C:A	0.000997
26_c2-1	26	TP53	HIGH	c.772G>T; c.376G>T; c.295G>T; c.655G>T	p.Glu258*; p.Glu126*; p.Glu99*; p.Glu219*	46	FALSE	chr17:7577509:C:A	249:chr17:7577509:C:A	0.001088
26_c2-1	26	HGF	MODERATE	c.5G>T	p.Trp2Leu	0	FALSE	chr7:81399283:C:A	249:chr7:81399283:C:A	0.001369
26_c2-1	26	RET	MODERATE	c.1339G>A	p.Ala447Thr	1	FALSE	chr10:43606730:G:A	249:chr10:43606730:G:A	0.000777
26_c2-1	26	KIT	MODERATE	c.235C>A	p.Gln79Lys	2	FALSE	chr4:55561845:C:A	249:chr4:55561845:C:A	0.001098

26_c2-1	26	KIT	HIGH	c.1698C>A; c.1710C>A	p.Tyr566*; p.Tyr570*	2	FALSE	chr4:55593644:C:A	249:chr4:55593644:C:A	0.000969
26_c2-1	26	CACNB1; RPL19	MODIFIER; MODERATE	c.-209C>T; c.91G>A	; p.Glu31Lys	0	FALSE	chr17:37357551:G:A	249:chr17:37357551:G:A	0.001868
26_c2-1	26	PIK3CA	MODERATE	c.478C>A	p.His160Asn	1	FALSE	chr3:178917603:C:A	249:chr3:178917603:C:A	0.000934
26_c2-1	26	NF1	MODERATE	c.4526C>A; c.4589C>A	p.Ala1509Asp; p.Ala1530Asp	1	FALSE	chr17:29588740:C:A	249:chr17:29588740:C:A	0.001161
26_c2-1	26	RET	MODERATE	c.1891G>A	p.Asp631Asn	1	FALSE	chr10:43609939:G:A	249:chr10:43609939:G:A	0.000737
44_bl-2	44	TP53	LOW; MODIFIER; MODERATE	c.-6C>T; c.355C>T; c.472C>T; c.76C>T	; p.Arg119Cys; p.Arg158Cys; p.Arg26Cys	17	FALSE	chr17:7578458:G:A	251:chr17:7578458:G:A	0.00166
44_bl-2	44	TP53	MODERATE	c.341G>A; c.422G>A; c.701G>A; c.818G>A	p.Arg114His; p.Arg141His; p.Arg234His; p.Arg273His	647	TRUE	chr17:7577120:C:T	251:chr17:7577120:C:T	0.00788
44_bl-2	44	NF1	HIGH	c.3721C>T	p.Arg1241*	5	FALSE	chr17:29562641:C:T	251:chr17:29562641:C:T	0.001538
44_bl-2	44	TP53	MODIFIER; MODERATE	c.-44T>C; c.317T>C; c.38T>C; c.434T>C	; p.Leu106Pro; p.Leu13Pro; p.Leu145Pro	19	FALSE	chr17:7578496:A:G	251:chr17:7578496:A:G	0.00159
44_bl-2	44	TP53	MODIFIER; MODERATE	c.-3G>T; c.358G>T; c.475G>T; c.79G>T	; p.Ala120Ser; p.Ala159Ser; p.Ala27Ser	23	FALSE	chr17:7578455:C:A	251:chr17:7578455:C:A	0.003236
44_bl-2	44	ALK	MODERATE	c.2009C>T	p.Ser670Leu	1	FALSE	chr2:29497997:G:A	251:chr2:29497997:G:A	0.001617
44_bl-2	44	CTNNB1	MODERATE	c.125C>A	p.Thr42Lys	0	FALSE	chr3:41266128:C:A	251:chr3:41266128:C:A	0.001293
44_bl-2	44	NF1	MODERATE	c.2695T>G	p.Leu899Val	3	FALSE	chr17:29556328:T:G	251:chr17:29556328:T:G	0.007148
44_bl-2	44	MET	MODERATE	c.1076G>A	p.Arg359Gln	1	FALSE	chr7:116340214:G:A	251:chr7:116340214:G:A	0.00125

44_bl-2	44	NF1	MODIFIER; HIGH	c.*2165G>A; c.2088G>A	; p.Trp696*	1	FALSE	chr17:29553539:G:A	251:chr17:29553539:G:A	0.002214