

Gene	Locus	Reference	Alternate	type	Consequence
ALK	VUS chr2:29416667	T	C	snp	missense_variant
ALK	VUS chr2:29416794	G	A	snp	splice_region_variant&intron_variant
ALK	VUS chr2:29430136	G	A	snp	missense_variant&splice_region_variant
ALK	VUS chr2:29446209	G	T	snp	splice_region_variant&synonymous_variant
ALK	VUS chr2:29446307	G	A	snp	missense_variant
ALK	VUS chr2:29451831	T	G	snp	missense_variant
ALK	VUS chr2:29519746	G	C	snp	splice_region_variant&intron_variant
ALK	VUS chr2:29541192	G	C	snp	missense_variant
ALK	VUS chr2:30143270	C	T	snp	missense_variant
BRAF	chr7:140453155	C	G	snp	missense_variant
BRAF	VUS chr7:140434398	C	T	snp	stop_retained_variant
BRAF	VUS chr7:140453128	G	A	snp	stop_gained
BRAF	VUS chr7:140476756	C	A	snp	missense_variant
BRAF	VUS chr7:140481451	G	A	snp	missense_variant
EGFR	chr7:55241707	G	T	snp	missense_variant
EGFR	chr7:55241708	G	C	snp	missense_variant
EGFR	chr7:55242464	AGGAATTA	A	indel	inframe_deletion
EGFR	chr7:55242465	GGAATTA	G	indel	inframe_deletion
EGFR	chr7:55242467	AATTAAGA	A	indel	inframe_deletion
EGFR	chr7:55242469	TTAAGAGA	T	indel	inframe_deletion
EGFR	chr7:55248998	A	ATGGCCAGC	indel	inframe_insertion
EGFR	chr7:55249005	G	T	snp	missense_variant
EGFR	chr7:55249010	G	GACAACCCG	indel	inframe_insertion
EGFR	chr7:55249011	A	ACAACCCCG	indel	inframe_insertion
EGFR	chr7:55249071	C	T	snp	missense_variant
EGFR	chr7:55259439	T	G	snp	missense_variant
EGFR	chr7:55259446	A	T	snp	missense_variant
EGFR	chr7:55259515	T	G	snp	missense_variant
EGFR	chr7:55259524	T	A	snp	missense_variant
EGFR	VUS chr7:55221747	GC	G	indel	frameshift_variant
EGFR	VUS chr7:55221800	G	A	snp	missense_variant
EGFR	VUS chr7:55240692	A	G	snp	missense_variant
EGFR	VUS chr7:55240693	T	G	snp	missense_variant
EGFR	VUS chr7:55242466	GAATTAAG	GTTGCT	indel	frameshift_variant
EGFR	VUS chr7:55242468	ATT	ACC	indel	missense_variant
EGFR	VUS chr7:55242470	T	C	snp	missense_variant
EGFR	VUS chr7:55249131	G	T	snp	missense_variant
ERBB2	chr17:37880981	A	AGCATACGT	indel	inframe_insertion
ERBB2	VUS chr17:37866453	T	C	snp	missense_variant&splice_region_variant
ERBB2	VUS chr17:37880218	GTTGAGGC	GCCTC	indel	protein_altering_variant
ERBB2	VUS chr17:37881060	G	T	snp	missense_variant
ERBB2	VUS chr17:37884153	CCCT	C	indel	inframe_deletion
ERBB2	VUS chr17:37884181	G	A	snp	missense_variant
FGFR1	VUS chr8:38275514	C	CG	indel	splice_region_variant&intron_variant
FGFR1	VUS chr8:38275810	T	C	snp	missense_variant
FGFR1	VUS chr8:38277064	C	T	snp	missense_variant
FGFR1	VUS chr8:38285869	C	T	snp	splice_donor_variant
FGFR1	VUS chr8:38285870	G	A	snp	missense_variant&splice_region_variant
FGFR1	VUS chr8:38287254	C	T	snp	missense_variant
KRAS	chr12:25378562	C	G	snp	missense_variant
KRAS	chr12:25398284	C	G	snp	missense_variant
KRAS	chr12:25398284	C	T	snp	missense_variant
KRAS	chr12:25398285	C	A	snp	missense_variant
KRAS	chr12:25398285	C	T	snp	missense_variant
KRAS	VUS chr12:25368366	C	T	snp	splice_region_variant&intron_variant
KRAS	VUS chr12:25380262	C	T	snp	missense_variant

MET	VUS chr7:116339260	A	G	snp	missense variant
MET	VUS chr7:116339518	A	G	snp	missense variant
MET	VUS chr7:116371741	C	T	snp	missense variant
MET	VUS chr7:116397831	G	A	snp	splice region variant&intron variant
MET	VUS chr7:116398586	A	AT	indel	frameshift variant
MET	VUS chr7:116411964	T	TG	indel	frameshift variant
NRAS	VUS chr1:115252285	CACACT	CCCACA	indel	missense variant
PIK3CA	chr3:178927980	T	C	snp	missense variant
PIK3CA	chr3:178938934	G	A	snp	missense variant
PIK3CA	chr3:178952084	C	T	snp	missense variant
PIK3CA	chr3:178952085	A	G	snp	missense variant
PIK3CA	chr3:178952085	A	T	snp	missense variant
PIK3CA	VUS chr3:178916665	C	T	snp	missense variant
PIK3CA	VUS chr3:178916728	G	A	snp	missense variant
PIK3CA	VUS chr3:178916946	GATCCTCA	G	indel	inframe deletion
PIK3CA	VUS chr3:178927974	G	A	snp	missense variant&splice region variant
PIK3CA	VUS chr3:178928074	GATTAGAA	G	indel	inframe deletion
PIK3CA	VUS chr3:178947127	C	T	snp	missense variant
TP53	chr17:7574002	C	G	snp	missense variant
TP53	chr17:7577046	C	A	snp	stop gained
TP53	chr17:7577058	C	A	snp	stop gained
TP53	chr17:7577082	C	T	snp	missense variant
TP53	chr17:7577094	G	A	snp	missense variant
TP53	chr17:7577097	C	A	snp	missense variant
TP53	chr17:7577114	C	A	snp	missense variant
TP53	chr17:7577120	C	A	snp	missense variant
TP53	chr17:7577120	C	T	snp	missense variant
TP53	chr17:7577138	C	G	snp	missense variant
TP53	chr17:7577538	C	T	snp	missense variant
TP53	chr17:7577539	G	A	snp	missense variant
TP53	chr17:7577543	C	T	snp	missense variant
TP53	chr17:7577547	C	T	snp	missense variant
TP53	chr17:7577548	C	A	snp	missense variant
TP53	chr17:7577548	C	T	snp	missense variant
TP53	chr17:7577570	C	T	snp	missense variant
TP53	chr17:7578190	T	C	snp	missense variant
TP53	chr17:7578206	T	C	snp	missense variant
TP53	chr17:7578211	C	T	snp	missense variant
TP53	chr17:7578212	G	A	snp	stop gained
TP53	chr17:7578268	A	C	snp	missense variant
TP53	chr17:7578395	G	A	snp	missense variant
TP53	chr17:7578403	C	A	snp	missense variant
TP53	chr17:7578406	C	A	snp	missense variant
TP53	chr17:7578406	C	T	snp	missense variant
TP53	chr17:7578442	T	C	snp	missense variant
TP53	chr17:7578457	C	A	snp	missense variant
TP53	chr17:7578529	A	C	snp	missense variant
TP53	chr17:7578534	C	A	snp	missense variant
TP53	chr17:7578550	G	A	snp	missense variant
TP53	chr17:7578556	T	C	snp	splice acceptor variant
TP53	chr17:7579415	C	T	snp	stop gained
TP53	VUS chr17:7572990	CT	C	indel	frameshift variant
TP53	VUS chr17:7573948	C	T	snp	missense variant
TP53	VUS chr17:7574029	CG	C	indel	frameshift variant
TP53	VUS chr17:7576851	A	T	snp	splice donor variant
TP53	VUS chr17:7576855	G	A	snp	stop gained&splice region variant
TP53	VUS chr17:7576888	T	TA	indel	frameshift variant
TP53	VUS chr17:7576902	GAGGAGC	G	indel	splice acceptor variant&coding sequenc
TP53	VUS chr17:7577018	C	T	snp	splice donor variant
TP53	VUS chr17:7577079	C	A	snp	stop gained
TP53	VUS chr17:7577090	C	G	snp	missense variant

TP53	VUS chr17:7577121	GCAC	GAAA	indel	missense variant
TP53	VUS chr17:7577157	T	A	snp	splice acceptor variant
TP53	VUS chr17:7577548	CGCCCATG	C	indel	inframe deletion
TP53	VUS chr17:7577559	G	T	snp	missense variant
TP53	VUS chr17:7577574	T	G	snp	missense variant
TP53	VUS chr17:7577610	T	A	snp	splice acceptor variant
TP53	VUS chr17:7578259	A	C	snp	missense variant
TP53	VUS chr17:7578265	A	T	snp	missense variant
TP53	VUS chr17:7578288	AC	A	indel	frameshift variant&splice region variant
TP53	VUS chr17:7578370	C	A	snp	splice donor variant
TP53	VUS chr17:7578395	GGTGGGG	G	indel	inframe deletion
TP53	VUS chr17:7578448	GCC	GAA	indel	missense variant
TP53	VUS chr17:7578455	CGC	CA	indel	frameshift variant
TP53	VUS chr17:7578457	CG	C	indel	frameshift variant
TP53	VUS chr17:7578463	C	A	snp	missense variant
TP53	VUS chr17:7578468	GC	G	indel	frameshift variant
TP53	VUS chr17:7578513	C	G	snp	missense variant
TP53	VUS chr17:7579311	C	G	snp	splice donor variant
TP53	VUS chr17:7579312	C	A	snp	splice region variant&synonymous varia
TP53	VUS chr17:7579370	CTGCCCTG	C	indel	frameshift variant
FUSION matrix					
chr10	32314222	+	KIF5B	chr10	43610580
chr10	32314228	-	KIF5B	chr10	43610582
chr10	32317265	-	KIF5B	chr10	43610258
chr2	29446616	+	ALK	chr2	42525761
chr2	29446745	+	ALK	chr2	42503597
chr2	29447490	+	ALK	chr2	42526802
chr2	29447562	+	ALK	chr2	42507863
chr2	29448360	+	ALK	chr2	42526657
chr2	29448373	-	ALK	chr2	42534486
chr6	117646730	-	ROS1	chr6	159191713
chr6	117646791	+	ROS1	chr6	159191750
chr6	117647014	+	ROS1	chr6	159191152

				ADC
				Sample 1
ExonID	HGVSc	HGVSp		
29/29	c.4286A>G	p.Gln1429Arg		1
	c.4165-6C>T			1
26/29	c.3839C>T	p.Ala1280Val		1
20/29	c.3358C>A	c.3358C>A(p.=)		1
20/29	c.3260C>T	p.Thr1087Ile		1
16/29	c.2734A>C	p.Lys912Gln		1
	c.1817+8C>G			1
8/29	c.1625C>G	p.Pro542Arg		1
1/29	c.256G>A	p.Glu86Lys		1
15/18	c.1780G>C	p.Asp594His		1
18/18	c.2300G>A	c.2300G>A(p.=)		1
15/18	c.1807C>T	p.Arg603Ter		1
13/18	c.1650G>T	p.Met550Ile		1
11/18	c.1357C>T	p.Pro453Ser		1
18/28	c.2155G>T	p.Gly719Cys		2
18/28	c.2156G>C	p.Gly719Ala		3
19/28	c.2235_2249delGGAATTAAGAGAAGC	p.Glu746_Ala750del		9 0.1502 3521
19/28	c.2236_2250delGAATTAAGAGAAGCA	p.Glu746_Ala750del		5
19/28	c.2240_2254delTAAGAGAAGCAACAT	p.Leu747_Thr751del		1
19/28	c.2240_2257delTAAGAGAAGCAACATCTC	p.Leu747_Pro753delinsSer		1
20/28	c.2300_2308dupCCAGCGTGG	p.Ala767_Val769dup		1
20/28	c.2303G>T	p.Ser768Ile		4
20/28	c.2311_2319dupAACCCCCAC	p.Asn771_His773dup		1
20/28	c.2317_2318insCCAACCCCC	p.Pro772_His773insProAsnPro		1
20/28	c.2369C>T	p.Thr790Met		2
21/28	c.2497T>G	p.Leu833Val		1
21/28	c.2504A>T	p.His835Leu		1
21/28	c.2573T>G	p.Leu858Arg		25
21/28	c.2582T>A	p.Leu861Gln		3
7/28	c.797delC	p.Pro266HisfsTer14		1
7/28	c.844G>A	p.Glu282Lys		1
17/28	c.1936A>G	p.Ile646Val		1
17/28	c.1937T>G	p.Ile646Ser		1
19/28	c.2237_2253delAATTAAGAGAAGCAACAins	p.Glu746AaifsTer16		1
19/28	c.2238_2240delATTinsACC	p.Leu747Pro		1
19/28	c.2240T>C	p.Leu747Ser		1
20/28	c.2429G>T	p.Gly810Val		1
20/27	c.2223_2234dupATACGTGATGGC	p.Tyr742_Ala745dup		1
6/27	c.668T>C	p.Leu223Pro		1
19/27	c.2173_2179delTTGAGGGinsCCTC	p.Leu725_Glu727delinsProGln		1
20/27	c.2299G>T	p.Val767Leu		1
27/27	c.3541_3543delCCT	p.Pro1181del		1
27/27	c.3562G>A	p.Asp1188Asn		2
	c.1524-6dupC			1
11/19	c.1459A>G	p.Met487Val		1
10/19	c.1364G>A	p.Arg455His		1
	c.541+1G>A			1
5/19	c.541C>T	p.Pro181Ser		1
4/19	c.403G>A	p.Val135Ile		1
4/6	c.436G>C	p.Ala146Pro		1
2/6	c.35G>C	p.Gly12Ala		1
2/6	c.35G>A	p.Gly12Asp		1
2/6	c.34G>T	p.Gly12Cys		5
2/6	c.34G>A	p.Gly12Ser		1
	c.*4+5G>A			1
3/6	c.196G>A	p.Ala66Thr		1

2/21	c.122A>G	p.Tyr41Cys	1
2/21	c.380A>G	p.Asp127Gly	1
3/21	c.1220C>T	p.Ser407Leu	1
	c.2102+3G>A		1
9/21	c.2178dupT	p.Asp727Ter	1
14/21	c.2950dupG	p.Val984GlyfsTer16	1
4/7	c.350_355delAGTGTGinsTGTGGG	p.LysCys117MetTrp	1
8/21	c.1258T>C	p.Cys420Arg	1
14/21	c.2176G>A	p.Glu726Lys	1
21/21	c.3139C>T	p.His1047Tyr	1
21/21	c.3140A>G	p.His1047Arg	1
21/21	c.3140A>T	p.His1047Leu	1
2/21	c.52C>T	p.Pro18Ser	1
2/21	c.115G>A	p.Glu39Lys	1
2/21	c.334_342delATCCTCAAT	p.Ile112_Asn114del	1
8/21	c.1252G>A	p.Glu418Lys	1
8/21	c.1353_1361delATTAGAAGA	p.Glu453_Leu455del	1
18/21	c.2563C>T	p.His855Tyr	1
10/11	c.1025G>C	p.Arg342Pro	1
8/11	c.892G>T	p.Glu298Ter	1
8/11	c.880G>T	p.Glu294Ter	1
8/11	c.856G>A	p.Glu286Lys	1
8/11	c.844C>T	p.Arg282Trp	1
8/11	c.841G>T	p.Asp281Tyr	1
8/11	c.824G>T	p.Cys275Phe	1
8/11	c.818G>T	p.Arg273Leu	2
8/11	c.818G>A	p.Arg273His	1
8/11	c.800G>C	p.Arg267Pro	1
7/11	c.743G>A	p.Arg248Gln	1
7/11	c.742C>T	p.Arg248Trp	1
7/11	c.738G>A	p.Met246Ile	1
7/11	c.734G>A	p.Gly245Asp	1
7/11	c.733G>T	p.Gly245Cys	1
7/11	c.733G>A	p.Gly245Ser	1
7/11	c.711G>A	p.Met237Ile	1
6/11	c.659A>G	p.Tyr220Cys	1
6/11	c.643A>G	p.Ser215Gly	1
6/11	c.638G>A	p.Arg213Gln	1
6/11	c.637C>T	p.Arg213Ter	1
6/11	c.581T>G	p.Leu194Arg	2
5/11	c.535C>T	p.His179Tyr	1
5/11	c.527G>T	p.Cys176Phe	1
5/11	c.524G>T	p.Arg175Leu	1
5/11	c.524G>A	p.Arg175His	2
5/11	c.488A>G	p.Tyr163Cys	1
5/11	c.473G>T	p.Arg158Leu	3
5/11	c.401T>G	p.Phe134Cys	1
5/11	c.396G>T	p.Lys132Asn	1
5/11	c.380C>T	p.Ser127Phe	1
	c.376-2A>G		1
4/11	c.272G>A	p.Trp91Ter	1
11/11	c.1118delA	p.Lys373ArgfsTer49	1
10/11	c.1079G>A	p.Gly360Glu	1
10/11	c.997delC	p.Arg333ValfsTer12	2
	c.993+2T>A		1
9/11	c.991C>T	p.Gln331Ter	1
9/11	c.957_958insT	p.Lys320Ter	1
9/11	c.920-2_943delAGCACTGCCCAACAACACC		1
	c.919+1G>A		1
8/11	c.859G>T	p.Glu287Ter	1
8/11	c.848G>C	p.Arg283Pro	1

8/11	c.814 817delGTGCinsTTTC	p.Val272Phe	1	
	c.783-2A>T		1	
7/11	c.724 732delTGCATGGGC	p.Cys242_Gly244del	1	
7/11	c.722C>A	p.Ser241Tyr	1	
7/11	c.707A>C	p.Tyr236Ser	1	
	c.673-2A>T		1	
6/11	c.590T>G	p.Val197Gly	1	
6/11	c.584T>A	p.Ile195Asn	1	
6/11	c.560delG	p.Gly187ValfsTer60	1	
	c.559+1G>T		1	
5/11	c.505 534delATGACGGAGGTTGTGAGGCC	p.Met169_His178del	1	
5/11	c.480 482delGGCinsTTC	p.MetAla160IleSer	1	
5/11	c.473 474delGCinsT	p.Arg158LeufsTer12	1	
5/11	c.472delC	p.Arg158AlafsTer12	1	
5/11	c.467G>T	p.Arg156Leu	1	
5/11	c.461delG	p.Gly154AlafsTer16	1	
5/11	c.417G>C	p.Lys139Asn	1	
	c.375+1G>C		1	
4/11	c.375G>T	c.375G>T(p.=)	1	
4/11	c.307 316delTACCAGGGCA	p.Tyr103AlafsTer17	1	
-	RET			
+	RET			
+	RET			
-	EML4			
-	EML4			
-	EML4			
-	EML4			
-	EML4			
-	EML4			
-	EZR			
+	EZR			
+	EZR			

