Supplemental Table 1: Anatomical Location of Tumors by Patient

Subject	Tumor Number	Location
A	1	Left Supraclavicular/cervical lymphadenopathy
B	1	Splenic metastases
	2	Liver metastases, posterior
	3	Peritoneal deposit (infra-hepatic)
	4	Pelvic mass Note: Tumor 4 was not within the field of view (FoV) in Week 4 scan due to patient being malpositioned thus excluding the anatomical region outside of the scanner FoV)
C	1	Suprasplenic metastases
	2	Liver metastases , mid liver (segment 7)
	3	Splenic metastases
	4	Liver metastases, inferior (segment 6)
	5	Pelvic mass
D	1	Pelvic mass (posterior) – just anterior to lower sacrum
	2	Pelvic mass (anterior)
	3	Upper abdominal mass (level of L3-L4)
	4	Pelvic mass (mid); right sided – anterior to upper sacrum
E	1	Para aortic lymphadenopathy (level of L1; left)
	2	Para caval lymphadenopathy (superior; level of L1-L2; right)
	3	Para caval lymphadenopathy (inferior; level of L3; right)
	4	Para aortic/Iliac lymphadenopathy (level of L2-L3)
F	1	Bowel/Descending colon(left side)
	2	Para aortic and iliac lymphadenopathy (left)
	3	Para caval and iliac lymphadenopathy (inferior, right)
	4	Para caval lymphadenopathy (right)
	5	Liver metastases
	6	Cardiophrenic angle lymph node
G	1	Para caval lymphadenopathy (right)
	2	Left Iliac lymphadenopathy
	3	Right Iliac lymphadenopathy
	4	Sacral metastases
	5	Right Iliac/Inguinal
	6	Lumbar metastases
H	1	Liver metastases, superior (segment 2)
	2	Liver metastases (segment 5)
	3	Liver metastases (segment 5; lateral to tumor 2)
	4	Right lung, posterior
	5	Right lung, lateral
	6	Liver metastases (segment 8)
	7	Diaphragmatic lymph node
	8	Liver metastases (segment 2)
I	1	Liver metastases, superior (segment 5)

Subject	Tumor Number	Location
	2	Liver metastases (segment 4)
	3	Omental metastases (perigastric)
	4	Perisplenic metastases (median)
	5	Porta hepatis lymphadenopathy
	6	Para aortic lymphadenopathy (left)
	7	Para caval lymphadenopathy (right)
	8	Peritoneal deposit (right abdomen)
J	1	Liver metastases (segment 2)
	2	Peritoneal deposit, abdomen
	3	Liver metastases (segment 4)
	4	Liver metastases (segment 5)
	5	Liver metastases (segment 8)
	6	Liver metastases (segment 4)
	7	Liver metastases (segment 6)
	8	Liver metastases (segment 6)
	9	Liver metastases (segment 6)
K	1	Liver, inferior (segment 6)
	2	Liver, post-superior (segment 7)
	3	Spleen, inferior
	4	Liver, superior most (segment 8)
	5	Spleen, superior
L	1	Para-aortic lymphadenopathy (superior; left sided)
	2	Para-caval lymphadenopathy (superior; right sided)
	3	Para-aortic (inferior) /left iliac lymphadenopathy NOTE: Tumor 3 was not within the field of view (FoV) in Week 4 scan as a different scanner with a smaller FoV was used due to technical problems.

Supplemental Table 2: List of Antibodies for IHC Staining of Tumor Biopsies

Biomarker tested	**Origin of monoclonal antibody**	**Catalog Name**	**Catalog Number**
AKT (pan)(clone 11E7)	Rabbit	Cell Signaling	4685
pAKT (Ser473 clone 14-5)	Mouse	DAKO	M362801
pPRAS40 (clone C77D7)	Rabbit	Cell Signaling	2997
Total PRAS40 (cloneD23C7)	Rabbit	Cell Signaling	2691
Total ERK (p44/42 MAPK (ERK 1/2), clone 3A7)	Mouse	Cell Signaling	9107
pERK (phopho-p44/42 MAPK (pERK), clone 20G11)	Rabbit	Cell Signaling	4376
ppERK (Anti-MAPK or diphosphorylated ERK 1/2, clone MAPK-YT)	Mouse	Sigma	M8159
Cleaved caspase 3 (ASP175 clone 5A1E)	Rabbit	Cell Signaling	9664
Ki67 (clone Mib-1)	Mouse	DAKO	M724001

Supplemental Table 3: Illumina Panel Gene List with Sequences

Gene	AA/Change Type	Sequence
ADAM12	D51G	GAACCAAGGAAGAGCTGATGAAGTTGTCAGTGCCTCTGTTGGGAGTGGGG[A/G]CCTCTGGATCCCAGTGAAGAGCTTCGACTCCAAGGTGAGTTCCTCTCCTT
ADAM12	A190T	AAAGCGTCCGGGGATCATGTGGATCACATCACAACACACCAAACCTCGCT[G/A]CAAAGAATGTGTTTCCACCACCCTCTCAGACATGGGCAAGAAGGGTAAGG
ADAM12	D301H	ATGAATTTCTGGACTGGAGGAAGATGAAGCTTCTACCTCGCAAATCCCAT[G/C]ACAATGCGCAGCTTGTCAGGTAGGGAGTTACGTCTTGTCTGCTTAAAAAA
ADAM12	G479E	CCGGGTGCATGTGTCATAAATGGCCCTCTCCTTCCAGCTGAAGCCTGCAG[G/A]AACAGCGTGCAGGGACTCCAGCAACTCCTGTGACCTCCCAGAGTTCTGCA
ADAM12	L792F	GCTATAGCATGGCTTTTTACTTTGACTGTACAGGACAATCCCAGGAGATT[G/T]CTGCAGTGTCAGAATGTTGACATCAGCAGACCCCTCAACGGCCTGAATGT
ADAMTS18	R382K	GAATAGTTTTTGTCAATGGCAGTCTGCCCTCATTGGAAAGAATGGCAAGA[G/A]ACATGATCATGCCATCTTACTAACAGGATTTGATATTTGTTCTTGGAAGA
ADAMTS18	A696fs*18	GAAGATCGATGCAAACTGTACTGCAAGGCTGAGAACTTTGAATTTTTTTT[/T]TGCAATGTCCGGCAAAGTGAAAGATGGAACTCCCTGCTCCCCAAACAAAAAT
ADAMTS18	K455T	CTGTTTCAGCTTTGGTATGATTCACGATGGAGAAGGGAATCCCTGCAGAA[A/C]GGCTGAAGGCAATATCATGTCTCCCACACTGACCGGAAACAATGGAGTGT
ADAMTS18	S156fs*19	GAGGTGCAGCAATGCTTCTATCAGGGATTTATCAGAAATGACAGCTCCTC[/CT]CTGTCGCTGTGTCTACGTGTGCTGGCTTGGTAAGTACACCCCAGTCTGAG
ADAMTSL3	A1315E	CAACCATCTGTCTGTTGTGGTTGGAGGCATCGTGGAGGCAGCCCTTGGAG[C/A]AAACGTGACAATCCGATGTCCTGTAAAAGGTAAGTGTGGTCATTTCAGTG
ADAMTSL3	D1482N	GTGATCACCTCCAGAAGCCACTGGCTGGGTTTGAGCCCTGTAACATCCGG[G/A]ACTGCCCAGCGAGGTAAGTGAAGTCACTCTTTGTATCTCATCAACACCAA
ADAMTSL3	I1645F	GGAGTTGCAAACCTGTGGCCAAGAGACACTGTGTACAGAAAAAGAAACCA[A/T]TTTCCTGGCGGCACTGTCTTGGGCCCTCCTGTGATAGTA

		CGTACACCTCC
ADAMTSL3	R587H	AGAACCCTGGTCAGCCTGCAGTACCACGTGTGGGCCGGGTGTGCAGGTCC[G/A]TGAGGTGAAGTGCCGTGTGCTCCTCACATTCACGCAGACTGAGACTGAGC
ADAMTSL3	R855C	GAATCCAGAGAAGAAAGCAGGTGTGTCAAAGGCTGGCAGCCAAAGGTCGG[C/T]GCATCCCCCTCAGTGAGATGATGTGCAGGGATCTACCAGGGCTCCCTCTT
ADAMTSL3	V330M	TTCTCACAGTTCTCTTTGTCCAGACCAGGTACACTGCAGCCAAAGACAGC[G/A]TGGTTCAGTTCTTCTTTTACCAGCCCATCAGTCATCAGTGGAGACAAACT
ADAMTSL3	W343C	AAAGACAGCGTGGTTCAGTTCTTCTTTTACCAGCCCATCAGTCATCAGTG[G/C]AGACAAACTGACTTCTTTCCCTGCACTGTGACGTGTGGAGGAGGTGAGGC
ADAMTSL3	W81*	TCAAGAAACACTCGTTCAGATGAAGACAAAGATGGCAACTGGGATGCTTG[G/A]GGCGACTGGAGTGACTGCTCCCGGACCTGTGGGGGAGGAGCATCATATTC
AIM1	A53S	ACGACGCGGTGTTCGACGACGAGGTGGCGCCAAACGCGGCCAGCGATAAC[G/T]CCTCGGCGGAAAAGAAAGTGAAATCTCCGCGGGCAGCCCTCGACGGGGGC
AIM1	E498G	TGTTCAATCACCCATAAGCAGTTTCCCATGCACTGATCTAAAAGTGTCAG[A/G]AAACCATAAAGGATGTGTTTTGCCTGTGTCTCGTCAGAACAATGAGAAAA
AIM1	I1639T	CTTACAGCTGGATACATATTTAAGATATCTGGTCTTTTCCACTGAGCAGA[T/C]AGCAGAAGACTGCTGCCTGACGATTGTGGGCAGCCTGGTAACATCTGGCT
AKT1	E17K	GTCTGACGGGTAGAGTGTGCGTGGCTCTCACCACCCGCACGTCTGTAGGG[A/G]AGTACATCAAGACCTGGCGGCCACGCTACTTCCTCCTCAAGAATGATGGC
AKT2	R371H	GCCTGCCCTTCTACAACCAGGACCACGAGCGCCTCTTCGAGCTCATCCTCATGGAAGAGATCCGCTTCCCGC[G/A]CACGCTCAGCCCCGAGGCCAAGTCCCTGCTTGCTGGGCTGCTTAAGAAGGACCCCAAGCAGAGGTGAGGGCTGGCGT
AKT2	S302G	GACTTTTCCAACAGCTGGAAAACCTCATGCTGGACAAAGATGGCCACATCAAGATCACTGACTTTGGCCTCTGCAAAGAGGGCATC[a/g]GTGACGGGGCCACCATGAAAACCTTCTGTGGGACCCCGGAGTACCTGGCGCCTGAGGTGTCTG
AKT3	E17K	GCTGCTGTTCATTTTTTTCAGCATTAACATGCGTGCTTTCCTCATGTAGGA[G/A]AATATATAAAAAACTGGAGGCCAAGATACTTCCTTTTGAA

		GACAGA
ALK	F1245I	ACGTGGCTCGGGACATTGCCTGTGGCTGTCAGTATTTGGAGGAAAACCAC[A/T]TCATCCACCGGTGAGTCAAAGTGACTGTGCTCTTCCTGTCATCCTGTCGC
ALK	F1174L	ACTCAGCTCAGTTAATTTTGGTTACATCCCTCTCTGCTCTGCAGCAAATT[A/C]AACCACCAGAACATTGTTCGCTGCATTGGGGTGAGCCTGCAATCCCTGCC
ALK	F1245C	CGTGGCTCGGGACATTGCCTGTGGCTGTCAGTATTTGGAGGAAAACCACT[T/G]CATCCACCGGTGAGTCAAAGTGACTGTGCTCTTCCTGTCATCCTGTCGCT
ALK	F1245L	GTGGCTCGGGACATTGCCTGTGGCTGTCAGTATTTGGAGGAAAACCACTT[C/G]ATCCACCGGTGAGTCAAAGTGACTGTGCTCTTCCTGTCATCCTGTCGCTG
ALK	F1245L	GTGGCTCGGGACATTGCCTGTGGCTGTCAGTATTTGGAGGAAAACCACTT[A/C]ATCCACCGGTGAGTCAAAGTGACTGTGCTCTTCCTGTCATCCTGTCGCTG
ALK	F1245V	ACGTGGCTCGGGACATTGCCTGTGGCTGTCAGTATTTGGAGGAAAACCAC[T/G]TCATCCACCGGTGAGTCAAAGTGACTGTGCTCTTCCTGTCATCCTGTCGC
ALK	L560F	TGCTCCTTCCCGGTTTTGTTCTCCACTAGCACCAAGGACACGTTTCCCCT[C/G]AAGACTCCACGAATGAGCCAGGACATTCGGAGCTGTGAGGGCGAGAAGAG
ALK	R1275Q	CTGTCCAGGCCCTGGAAGAGTGGCCAAGATTGGAGACTTCGGGATGGCCC[A/G]AGACATCTACAGGTGAGTAAAGACTGCCTCACCCCTCCGGGCCTGTCTCT
ARAF	G331C	AGAGGATCGGGACGGGCTCGTTTGGCACCGTGTTTCGAGGGCGGTGGCAT[T/G]GCGATGTGGCCGTGAAGGTGCTCAAGGTGTCCCAGCCCACAGCTGAGCAG
BRAF	G466V	TTGGGAGATTCCTGATGGGCAGATTACAGTGGGACAAAGAATTGGATCTG[T/G]ATCATTTGGAACAGTCTACAAGGGAAAGTGGCATGGTAAGTATGTAATGT
BRAF	G469A	TCCTGATGGGCAGATTACAGTGGGACAAAGAATTGGATCTGGATCATTTG[C/G]AACAGTCTACAAGGGAAAGTGGCATGGTAAGTATGTAATGTGGTGACATT
BRAF	L597V	CAGATATATTTCTTCATGAAGACCTCACAGTAAAAATAGGTGATTTTGGT[C/G]TAGCTACAGTGAAATCTCGATGGAGTGGGTCCCATCAGTTTGAACAGTTG

BRAF	V600E	TCTTCATGAAGACCTCACAGTAAAAATAGGTGATTTTGGTCTAGCTACAG[A/T]GAAATCTCGATGGAGTGGGTCCCATCAGTTTGAACAGTTGTCTGGATCCA
BRAF	V600E	TCTTCATGAAGACCTCACAGTAAAAATAGGTGATTTTGGTCTAGCTACAG[A/T]GAAATCTCGATGGAGTGGGTCCCATCAGTTTGAACAGTTGTCTGGATCCA
BRAF	V600E	TCTTCATGAAGACCTCACAGTAAAAATAGGTGATTTTGGTCTAGCTACAG[A/T]GAAATCTCGATGGAGTGGGTCCCATCAGTTTGAACAGTTGTCTGGATCCA
BRAF	D594G	CTACACCTCAGATATATTTCTTCATGAAGACCTCACAGTAAAAATAGGTG[A/G]TTTTGGTCTAGCTACAGTGAAATCTCGATGGAGTGGGTCCCATCAGTTTG
BRAF	K601E	TTCATGAAGACCTCACAGTAAAAATAGGTGATTTTGGTCTAGCTACAGTG[A/G]AATCTCGATGGAGTGGGTCCCATCAGTTTGAACAGTTGTCTGGATCCATT
BRAF	T529I	TATCCTACTCTTCATGGGCTATTCCACAAAGCCACAACTGGCTATTGTTA[T/C]CCAGTGGTGTGAGGGCTCCAGCTTGTATCACCATCTCCATATCATTGAGA
BRAF	T529N	TATCCTACTCTTCATGGGCTATTCCACAAAGCCACAACTGGCTATTGTTA[A/C]CCAGTGGTGTGAGGGCTCCAGCTTGTATCACCATCTCCATATCATTGAGA
BRAF	V471F	ATGGGCAGATTACAGTGGGACAAAGAATTGGATCTGGATCATTTGGAACA[T/G]TCTACAAGGGAAAGTGGCATGGTAAGTATGTAATGTGGTGACATTGTGAC
BRAF	V600A	TCTTCATGAAGACCTCACAGTAAAAATAGGTGATTTTGGTCTAGCTACAG[T/C]GAAATCTCGATGGAGTGGGTCCCATCAGTTTGAACAGTTGTCTGGATCCA
BRAF	V600G	TCTTCATGAAGACCTCACAGTAAAAATAGGTGATTTTGGTCTAGCTACAG[T/G]GAAATCTCGATGGAGTGGGTCCCATCAGTTTGAACAGTTGTCTGGATCCA
BRAF	V600M	TTCTTCATGAAGACCTCACAGTAAAAATAGGTGATTTTGGTCTAGCTACA[A/G]TGAAATCTCGATGGAGTGGGTCCCATCAGTTTGAACAGTTGTCTGGATCC
CDK4	R24C	AGCCAGTGGCTGAAATTGGTGTCGGTGCCTATGGGACAGTGTACAAGGCC[T/C]GTGATCCCCACAGTGGCCACTTTGTGGCCCTCAAGAGTGTGAGAGTCCCC
CDK4	R24H	GCCAGTGGCTGAAATTGGTGTCGGTGCCTATGGGACAGTGTACAAGGCCC[A/G]TGATCCCCACAGTGGCCACTTTGTGGCCCTCAAGAGT

		GTGAGAGTCCCCA
CDKN2A	cytogenetics	TTTCTTATATTTCATAGTATGAAAAATCTAAAAAGTAACCCATATGTAAA[T/A]ATTTAAATCATGATAGAAATCCAAAGCAAAAAGAAAATGAATCAATTGA
CDKN2A	cytogenetics	TTTAAGACATATTTAAAGAATAACATCAGCACTTAGCAATGAACTGGAGA[T/G]GGAAGATGAGGGAAGGGAAGGTGTTAGGCAGGTTTTTACAATGAGAGAGG
CDKN2A	cytogenetics	GTTTGCAGAGTGAAAATAAGATGGTCGGTTAGGAAGTTTGAGAATCGTAA[A/T]GGTTTGGAATACCTCTTATGAGTAGAGAGGATGGGTTGAGTAAGACTCA
CDKN2A	E120K	GCCCCCCGCAGCCGCGCGCAGGTACCGTGCGACATCGCGATGGCCCAGCT[C/T]CTCAGCCAGGTCCACGGGCAGACGGCCCCAGGCATCGCGCACGTCCAGCC
CDKN2A	R58*	GTCGGCGCAGTTGGGCTCCGCGCCGTGGAGCAGCAGCAGCTCCGCCACTC[G/A]GGCGCTGCCCATCATCATGACCTGCCAGAGAGAACAGAATGGTCAGAGCC
CDKN2A	R80*	TGCTGCTCCACGGCGCGGAGCCCAACTGCGCCGACCCCGCCACTCTCACC[C/T]GACCCGTGCACGACGCTGCCCGGGAGGGCTTCCTGGACACGCTGGTGGTG
CDKN2A	Y44*	TCCCCTGCTCCCGCTGCAGACCCTCTACCCACCTGGATCGGCCTCCGACC[G/T]TAACTATTCGGTGCGTTGGGCAGCGCCCCCGCCTCCAGCAGCGCCCGCAC
chr18q_arm1_40Mb	cytogenetics	TATATCCATATCTATATTTAGGTCTCTAACCATATGCCTTTGCATTGAGG[G/T]CACTATTGTCTTCAACAGCTGGTGGTAATCTAATACTCCCCTATTTGGGT
chr18q_arm2	cytogenetics	CACTCCAGCCTGGGCAACAAAAGTGAAACTCTGTCTCAAAAAGTGAAAAA[A/G]TAAAATGAATCCGTCTGGCACAGTGGCTCACCCCTGTAATCCTAGCGCTT
chr18q_arm3	cytogenetics	AAGACTGAAAAATTAGAAGGCGGGAAGTGGAGCGCGATGCCCAACAGAGA[G/C]CGGTCGTTCCCTGCGGGCTCAGCGTCTTTACGCTCTTCAGATGAAGGGTT
chr8_p_arm	cytogenetics	AACAGTAACTAAGAACAGAGAAGAGTGCAAAGGGATTCTGACCAAATTAT[A/G]GAAAAATCGAAGCGTGTCATAGGATGTTCCGCATCTCAATGCCATTAGC
chr8_p_arm	cytogenetics	CAATTCAAAGTAACTTCATTTTCCCCTGTGGAGTACTGAAAATTACTGTA[A/T]CTTATAATTTTATGGTAATTATAGTGAGAACTCCCATAATTAGTGTAGC

Chr8_p_arm2	cytogenetics	TTAGTGAGATTGAACATCTTTTAATATTGGTAATTTAGATTTCCTTTTCT[G/A]TGCATTCTGTATTCATATGCTTTGCACAGTATTCTTTTGAGTTGTTTTAT
Chr8_p_arm3	cytogenetics	GCAAAGGGGTCAGGGAAATATTCTCCTCTGGTAGGTTTTTCTGTTTTCAT[C/G]AACTTATCTGCTTTCTTCCTCTCCTCTCCTCTGCAGCTTAGGTTCCATGG
CPAMD8	K845M	CATGAGCCAATGCCACCCTCTGCAGGTGTACATGAAGCTCTCGGTTCCCA[A/T]GGGCATCCAGTTTGTTGGGCATCCTGGCAAACGCCATGTGACCAAGAAGA
CPAMD8	R558H	TGTGACCTCTCTTCATCTGGCCGTGACCCCCAGCATGGTCCCCCTTGGTC[G/A]CCTGCTGGTCTTCTACGTCAGGGAGAATGGAGAAGGGGTCGCCGACAGCC
CPAMD8	V1001I	GTGTGGCCTTGTCTTCTGGGCCCCAGGACACAGCAGGCATGATCGAGATC[G/A]TCCTGGGGGGGCATCAGAACACCAGGTCATGGATCTCCACCAGCAAGATG
CPAMD8	V1228L	TCACAGCCTTTGTCCTGAAGTCCTTCGCACAGGCTCGCAGCTTTATCTTC[G/C]TGGACCCCCGGGAGCTGGCTGCCGCCAAGAGCTGGATCATCCAGCAGCAG
CSMD3	L3444I	TTCCATCTCATGGGTATACACTGATTTATACCTGTCAGCCTGGCTTCTTC[T/A]TAGCAGGTGGAACAGAACATAGAGTGTGTAGATCCGATAACACCTGGACT
CSMD3	L3444I	TTCCATCTCATGGGTATACACTGATTTATACCTGTCAGCCTGGCTTCTTC[T/A]TAGCAGGTGGAACAGAACATAGAGTGTGTAGATCCGATAACACCTGGACT
CSMD3	R3079H	CGGCCATGGCTCTAGACAGGAAAGCAATTTCAGAACTAAAAGTACTGTAC[G/A]TTATGCTTGTGATACTGGTTACATCCTTCATGGCTCAGAAGAAAGAACAT
CSMD3	Splice Site	ATATCTATTGTAAATTTTAAAGGACTAATATCTTTTTAATCTTCATTTTA[G/C]AGCCTACCCAAACCTCTTGTGAAAACCCAGGTGTGCCTCGGCATGGATCT
CSMD3	D1548fs*19	CAGGGGTCCCCATGAATGGGACTCGAAATGGGGATGGAAGAGAACCTGGG[/G]ACACTGTTGTTTTTCAATGTGACCCAGGATATGAACTTCAAGGAGAGGAA
CSMD3	D3058N	GTTAACTTGAACTGTACTGCATTGCAGGTGATGCTACTGGGACATGTGGC[G/A]ATCCAGGTACTCCCGGCCATGGCTCTAGACAGGAAAGCAATTTCAGAACT
CSMD3	D607H	ATTTTGAAGAATTTGATCTGGAGATTGGCTATGATACCTTGACAATTGGC[G/C]ATGGGGGCGAAGTTGGAGATCCTAGGACAGTGCTCCAAG

		TGTAAGTTCCC
CSMD3	G1543R	CTGCGTGTCGTGACCCAGGGGTCCCCATGAATGGGACTCGAAATGGGGAT[G/A]GAAGAGAACCTGGGGACACTGTTGTTTTTCAATGTGACCCAGGATATGAA
CSMD3	N1961S	TAAGCGCAAAGGGACTATTTTGTCACCTGGATACCCTGAGCCTTATGACA[A/G]CAATCTGAATTGTGTGTGGAAGATCACAGTGCCAGAGGGAGCTGGCATTC
CSMD3	N409D	AGGAACAGCGAGTGCAAGTTACGAGTCTCAGAAATTCAGGTCTGGACCCC[A/G]ACACGTCCAAGGACGGGCTCTCTCCTCATCCAGCAGATACACAAAGTACC
CSMD3	R2231Q	CCTCTTTCCAGCCTATCAGTTGCAAAGCTGTCCTGATCCACGCCCGTTTC[G/A]AAATGGTTTTGTAATTGGTAATGATTTTACTGTGGGTCAAACCATTTCAT
CSMD3	R3359Q	CTTCATTTTAGAGCCTACCCAAACCTCTTGTGAAAACCCAGGTGTGCCTC[G/A]GCATGGATCTCAGAACAATACATTCGGATTTCAAGTGGGTACTTTAGCTA
CSMD3	S162N	AAGTACCAAATCTGTGTTCTCACTACGTTTGACCAGTGATTTTGCAGTTA[G/A]TGCTCATGGATTTAAGGTATATTACGAAGGTAAGTGATGGTAGTGGCAAA
CSMD3	V3561L	TATATAAAAGCCAGGAAGCTCGCCTAATGTTACGCATATATCTTATTAAA[G/T]TACCTGCTCATGCTTCTGTGAAGAAAATGAAGGAAGAAAATTGGGCAATG
CSMD3	V396M	TATCCAGTGTTACAGCTGTCACCATCCATAGACTTTCCGAGGAACAGCGA[G/A]TGCAAGTTACGAGTCTCAGAAATTCAGGTCTGGACCCCAACACGTCCAAG
CSMD3	V575F	CCTTTACATCTCCCAACTTTCCGTTCCAGTATGACAGCAATGCACAATGT[G/T]TCTGGGTCATCACAGCAGTGAATACAAATAAGGTAAGAGAACACCATCTG
CSMD3	W2745C	TATCATGGACTAGGTCCTGCCTCCATCGAATGTCTTCCTAATGGTACTTG[G/C]AGTTGGAGAAATGAAAGACCATATTGCCAAAGTAAGTATACACTCTGCTA
CTNNB1	S33C	AGACAGAAAAGCGGCTGTTAGTCACTGGCAGCAACAGTCTTACCTGGACT[C/G]TGGAATCCATTCTGGTGCCACTACCACAGCTCCTTCTCTGAGTGGTAAAG
CTNNB1	S37C	GGCTGTTAGTCACTGGCAGCAACAGTCTTACCTGGACTCTGGAATCCATT[C/G]TGGTGCCACTACCACAGCTCCTTCTCTGAGTGGTAAAGGCAATCCTGAGG

CTNNB1	S45F	GTCTTACCTGGACTCTGGAATCCATTCTGGTGCCACTACCACAGCTCCTT[C/T]TCTGAGTGGTAAAGGCAATCCTGAGGAAGAGGATGTGGATACCTCCCAAG
CTNNB1	S45P	AGTCTTACCTGGACTCTGGAATCCATTCTGGTGCCACTACCACAGCTCCT[T/C]CTCTGAGTGGTAAAGGCAATCCTGAGGAAGAGGATGTGGATACCTCCCAA
CTNNB1	T41A	ACTGGCAGCAACAGTCTTACCTGGACTCTGGAATCCATTCTGGTGCCACT[A/G]CCACAGCTCCTTCTCTGAGTGGTAAAGGCAATCCTGAGGAAGAGGATGTG
CTNNB1	G34E	CAGAAAAGCGGCTGTTAGTCACTGGCAGCAACAGTCTTACCTGGACTCTG[A/G]AATCCATTCTGGTGCCACTACCACAGCTCCTTCTCTGAGTGGTAAAGGCA
CTNNB1	D32Y	AACCAGACAGAAAAGCGGCTGTTAGTCACTGGCAGCAACAGTCTTACCTG[G/T]ACTCTGGAATCCATTCTGGTGCCACTACCACAGCTCCTTCTCTGAGTGGT
CTNNB1	S33Y	AGACAGAAAAGCGGCTGTTAGTCACTGGCAGCAACAGTCTTACCTGGACT[A/C]TGGAATCCATTCTGGTGCCACTACCACAGCTCCTTCTCTGAGTGGTAAAG
CTNNB1	S37F	GGCTGTTAGTCACTGGCAGCAACAGTCTTACCTGGACTCTGGAATCCATT[C/T]TGGTGCCACTACCACAGCTCCTTCTCTGAGTGGTAAAGGCAATCCTGAGG
CTNNB1	T41I	CTGGCAGCAACAGTCTTACCTGGACTCTGGAATCCATTCTGGTGCCACTA[T/C]CACAGCTCCTTCTCTGAGTGGTAAAGGCAATCCTGAGGAAGAGGATGTGG
CYLD1	cytogenetics	TGTGTGTATATATGTATGTGGCGGAGAGGGAGAGAGTGGGGAAGGAGAGC[A/T]GTGTTATCATACATAGAGAGGCTAAATGTGTCCCATCCCTCACTGTCAGC
CYLD1	cytogenetics	CAATTAAATAATTTAAAGATGATTACATAATAATTTGCACACAAGCAAGA[T/G]CTTAACATACTTCAGGAAAGTGGATTTAGAGTTCTCTACAAAATGAAGTG
CYLD1	cytogenetics	GGTATATCATAGCCTTCAGGTTTTTTGATTATCATCTGTTTGTATTTGTT[G/A]TGGGTCTCCAGAATCTCCTGTTTTGTTATCAATTAAATTTTGTTTATTTG
CYLD1	cytogenetics	CCATCATGTCTGATTATTCAGATGCCTCGATTTGGAAAAGACTTTAAACT[A/G]TTTAAAAAAATTTTTCCTTCTCTGGAATTAAATATAACAGATTTACTTGA
DBN1	E278K	GCTATCTCAGCTTGCCTGGCCCAGCCCCAACCTTTTCCTCGTGCCCTCAG[G/A]AGGCAGCAGCTATTATTGCCCAGCGGCCTGACAACCCA

		AGGGAGTTCTTC
DBN1	E640Q	CTAACGCCACAGAGATCGACATCACATGCTGGGATGCAGACCCAGTTCCA[G/C]AAGAGGAGGAGGGCTTCGAGGGTGGTGATTAGCGGTGGCGCCAGCCCTAG
DBN1	Splice Site	GCTATCTCAGCTTGCCTGGCCCAGCCCCAACCTTTTCCTCGTGCCCTCAG[G/T]AGGCAGCAGCTATTATTGCCCAGCGGCCTGACAACCCAAGGGAGTTCTTC
EGFR	S768I	GCCACACTGACGTGCCTCTCCCTCCCTCCAGGAAGCCTACGTGATGGCCA[T/G]CGTGGACAACCCCCACGTGTGCCGCCTGCTGGGCATCTGCCTCACCTCCA
EGFR	A289V	CACCACGTACCAGATGGATGTGAACCCCGAGGGCAAATACAGCTTTGGTG[T/C]CACCTGCGTGAAGAAGTGTCCCCGTGAGTCCTCCTCTGTGGGCCCTCTAA
EGFR	C311S	CTTCCCCAGGTAATTATGTGGTGACAGATCACGGCTCGTGCGTCCGAGCC[A/T]GTGGGGCCGACAGCTATGAGATGGAGGAAGACGGCGTCCGCAAGTGTAAG
EGFR	E709A	TACACCCAGTGGAGAAGCTCCCAACCAAGCTCTCTTGAGGATCTTGAAGG[A/C]AACTGAATTCAAAAAGATCAAAGTGCTGGGCTCCGGTGCGTTCGGCACGG
EGFR	E709K	TTACACCCAGTGGAGAAGCTCCCAACCAAGCTCTCTTGAGGATCTTGAAG[A/G]AAACTGAATTCAAAAAGATCAAAGTGCTGGGCTCCGGTGCGTTCGGCACG
EGFR	G598V	GTGTGCCCACTACATTGACGGCCCCCACTGCGTCAAGACCTGCCCGGCAG[T/G]AGTCATGGGAGAAAACAACACCCTGGTCTGGAAGTACGCAGACGCCGGCC
EGFR	G719A	TCTCTTGAGGATCTTGAAGGAAACTGAATTCAAAAAGATCAAAGTGCTGG[C/G]CTCCGGTGCGTTCGGCACGGTGTATAAGGTAAGGTCCCTGGCACAGGCCT
EGFR	G719C	CTCTCTTGAGGATCTTGAAGGAAACTGAATTCAAAAAGATCAAAGTGCTG[T/G]GCTCCGGTGCGTTCGGCACGGTGTATAAGGTAAGGTCCCTGGCACAGGCC
EGFR	G719D	TCTCTTGAGGATCTTGAAGGAAACTGAATTCAAAAAGATCAAAGTGCTGG[A/G]CTCCGGTGCGTTCGGCACGGTGTATAAGGTAAGGTCCCTGGCACAGGCCT
EGFR	G719S	CTCTCTTGAGGATCTTGAAGGAAACTGAATTCAAAAAGATCAAAGTGCTG[A/G]GCTCCGGTGCGTTCGGCACGGTGTATAAGGTAAGGTCCCTGGCACAGGCC

EGFR	H773R	CTCTCCCTCCCTCCAGGAAGCCTACGTGATGGCCAGCGTGGACAACCCCC[A/G]CGTGTGCCGCCTGCTGGGCATCTGCCTCACCTCCACCGTGCAGCTCATCA
EGFR	L858R	GAACGTACTGGTGAAAACACCGCAGCATGTCAAGATCACAGATTTTGGGC[T/G]GCCAAACTGCTGGGTGCGGAAGAGAAAGAATACCATGCAGAAGGAGGCAA
EGFR	L858R	GGAACGTACTGGTGAAAACACCGCAGCATGTCAAGATCACAGATTTTGGGC[T/G]GGCCAAACTGCTGGGTGCGGAAGAGAAAGAATACCATGCAGAAGGAGGC
EGFR	L861Q	GGTGAAAACACCGCAGCATGTCAAGATCACAGATTTTGGGCTGGCCAAAC[A/T]GCTGGGTGCGGAAGAGAAAGAATACCATGCAGAAGGAGGCAAAGTAAGGA
EGFR	E746_A750 del	TGTCATAGGGACTCTGGATCCCAGAAGGTGAGAAAGTTAAAATTCCCGTCGCTATCAAGG[/AATTAAGAGAAGCAA]CATCTCCGAAAGCCAACAAGGAAATCCTCGATGTGAGTTTCTGCTTTGCTGTGTGGGGGTCCATG
EGFR	E746_A750 del	GACTCTGGATCCCAGAAGGTGAGAAAGTTAAAATTCCCGTCGCTATCAAG[/GAATTAAGAGAAGCA]ACATCTCCGAAAGCCAACAAGGAAATCCTCGATGTGAGTTTCTGCTTTGCTGTGTGGGGGTCCATGGCTC
EGFR	L747_A750 >P	TCTGGATCCCAGAAGGTGAGAAAGTTAAAATTCCCGTCGCTATCAAGGAA[T/C]CAACATCTCCGAAAGCCAACAAGGAAATCCTCGATGTGAGTTTCTGCTTTGCTGTGTGGGGGTCCATGGC
EGFR	L747_P753 >S	TCTGTCATAGGGACTCTGGATCCCAGAAGGTGAGAAAGTTAAAATTCCCGTCGCTATCAA[-/GGAATTAAGAGAAGCAAC]ATCTCCGAAAGCCAACAAGGAAATCCTCGATGTGAGTTTCTGCTTTGCTGTGTGGGGGTCCA
EGFR	R222C	TTTGCTCTTTTTCAGTGACCAAAATCATCTGTGCCCAGCAGTGCTCCGGG[T/C]GCTGCCGTGGCAAGTCCCCCAGTGACTGCTGCCACAACCAGTGTGCTGCA
EGFR	R324L	CGTCCGAGCCTGTGGGGCCGACAGCTATGAGATGGAGGAAGACGGCGTCC[T/G]CAAGTGTAAGAAGTGCGAAGGGCCTTGCCGCAAAGGTAGGAAGCCCGCCG
EGFR	T790M	CGTGTGCCGCCTGCTGGGCATCTGCCTCACCTCCACCGTGCAGCTCATCA[T/C]GCAGCTCATGCCCTTCGGCTGCCTCCTGGACTATGTCCGGGAACACAAAG
EPHB6	R704Q	GGCCCTGTGGGCCGGGGGCGCCGAAAGCCTGCAGATGACCTTCCTGGGCC[G/A]GGCCGCAGTGCTGGGTCAGTTCCAGCACCCCAACATCCTGCGGCTGGAGG

EPHB6	A588P	CTTCCCAGCTTCCGGAAAGACTCTCCTTGGTGATCGGCTCCATCCTGGGG[G/C]CTTTGGCCTTCCTCCTGCTGGCAGCCATCACCGTGCTGGCGGTCGTCTTC
EPHB6	D345N	CAGCAGCCCCCGTTTGCCCCTGCCTGGAGGGCTTCTACCGGGCCAGTTCC[G/A]ACCCACCAGAGGCCCCCTGCACTGGTGAGTTCCTCACCCAGCCCTGCAAT
EPHB6	D915G	TGCATTTGACAAGATGATCCGCAAGCCAGATACCCTGCAGGCTGGCGGGG[A/G]CCCAGGGGAAAGGTCTGGAGCTTGGGGCTAGAGCCTGGGAAAGCCAGGGA
EPHB6	E860K	ACTTCCCATCATCATAGTCTTCCTCTGACCCCCAGGTACTAAATGCAATA[G/A]AGCAGGAGTTCCGGCTGCCCCCGCCTCCAGGCTGTCCTCCTGGATTACAT
EPHB6	P728S	TCCAGCACCCCAACATCCTGCGGCTGGAGGGCGTGGTCACCAAGAGCCGA[C/T]CCCTCATGGTGCTGACGGAGTTCATGGAGCTTGGCCCCCTGGACAGCTTC
ERBB2	A775_G776insYVMA	CTCCCATACCCTCTCAGCGTACCCTTGTCCCCAGGAAGCATACGTGATGGcTN[a/g]GGTGTGGGCTCCCCATATGTCTCCCGCCTTCTGGGCATCTGCCTGACAT
ERBB2	G776>VC	CCCATACCCTCTCAGCGTACCCTTGTCCCCAGGAAGCATACGTGATGGCTN[t/g]GTGTGGGCTCCCCATATGTCTCCCGCCTTCTGGGCATCTGCCTGACATCC
ERBB2	M774_A775insAYVM	GTCTCCCATACCCTCTCAGCGTACCCTTGTCCCCAGGAAGCATACGTGATgGCN[A/T]GGTGTGGGCTCCCCATATGTCTCCCGCCTTCTGGGCATCTGCCTGAC
ERBB2	P780_Y781insGSP	AGCGTACCCTTGTCCCCAGGAAGCATACGTGATGGCTGGTGTGGGCTCCCc[A/G]NTATGTCTCCCGCCTTCTGGGCATCTGCCTGACATCCACGGTGCAGCTGG
ERBB2	cytogenetics	CTCCCACCCCAAACTAGCCCTCAATCCCTGACCCTGGCTTCCGCCCCCAG[C/T]CCTCTGACGTCCATCATCTCTGCGGTGGTTGGCATTCTGCTGGTCGTGGT
ERBB2	cytogenetics	CCTCCCAGGTGCCCATCAAGTGGATGGCGCTGGAGTCCATTCTCCGCCGG[C/A]GGTTCACCCACCAGAGTGATGTGTGGAGTTATGGTGTGTGATGGGGGGTG
ERBB2	cytogenetics	CCACGGTGACTGTGTCATACCCCAAAGGTGACCTCTGTTTTTCTCCTGTG[A/G]CCCTGTCACCTTCCATGGAGTCCCCATCCCAGATCCGTGAGTGACCCCCA
ERBB4	S303Y	TCCCATTTTCTTCTACTTCCATCTTGGAACTAGGGCAGGCACGCACACAA[T/G]AACTGGAATCTACCACAAAGTTATCTGATTAAAAAAAAAA

		AAAGGTAAA
FASN	ss3172972	GCGGAACCGTCCGGTGTGTGCTGCTCTCCAACCTCAGCAGCACCTCCCAC[A/G]TCCCGGAGGTGGACCCGGGCTCCGCAGAACTGCAGAAGGTGTTGCA
FBXW7	278*	AACCAACACAAGTAAAACATATGATGCAAGTGATAGAACCCCAGTTTCAA[C/T]GAGACTTCATTTCATTGCTCCCTAAAGAGGTAAAGATTATCAATTACATT
FBXW7	R465H	AGAGACTGGAGAATGTATACACACCTTATATGGGCATACTTCCACTGTGC[G/A]TTGTATGCATCTTCATGAAAAAAGGTAAGGGAAAATCTTGTCATGGTTGG
FBXW7	S582L	TTGGGATGTGGAGACAGGGAATTGCATTCACACGTTAACAGGGCACCAGT[C/T]GTTAACAAGTGGAATGGAACTCAAAGACAATATTCTTGTCTCTGGGAATG
FBXW7	R465C	CAGAGACTGGAGAATGTATACACACCTTATATGGGCATACTTCCACTGTG[C/T]GTTGTATGCATCTTCATGAAAAAAGGTAAGGGAAAATCTTGTCATGGTTG
FBXW7	R479Q	TTTTGTTTTGTTTTTCTGTTTCTCCCTCTGCAGAGTTGTTAGCGGTTCTC[G/A]AGATGCCACTCTTAGGGTTTGGGATATTGAGACAGGCCAGTGTTTACATG
FBXW7	R505C	TTGAGACAGGCCAGTGTTTACATGTTTTGATGGGTCATGTTGCAGCAGTC[C/T]GCTGTGTTCAATATGATGGCAGGAGGGTTGTTAGTGGAGCATATGATTTT
FGFR3	G697C	TTGGGGTCCTGCTCTGGGAGATCTTCACGCTGGGGGGCTCCCCGTACCCC[T/G]GCATCCCTGTGGAGGAGCTCTTCAAGCTGCTGAAGGAGGGCCACCGCATG
FGFR3	S371C	CCCATGTCTTTGCAGCCGAGGAGGAGCTGGTGGAGGCTGACGAGGCGGGC[A/T]GTGTGTATGCAGGCATCCTCAGCTACGGGGTGGGCTTCTTCCTGTTCATC
FGFR3	Y373C	CTTTGCAGCCGAGGAGGAGCTGGTGGAGGCTGACGAGGCGGGCAGTGTGT[A/G]TGCAGGCATCCTCAGCTACGGGGTGGGCTTCTTCCTGTTCATCCTGGTGG
FGFR4	P672T	TGGAGGAGCTGTTCTCGCTGCTGCGGGAGGGACATCGGATGGACCGACCC[A/C]CACACTGCCCCCCAGAGCTGTGAGGCCTCACCCTGCCCTCGACCCCACTT
FHIT	cytogenetics	AAGGACAAATGAGCCAAGTGTCATGCCCCAAGTCACTAGGTTAATAAATG[C/G]TGGAGACACCAAATAACTGCCCTCTAACTCCAGGGAACATGCTCATAAC

FHIT	cytogenetics	GATCCTCCCAGTGTTTGAATTTTAAAAAATAAAGGTCAGTTTATCACTAG[A/C]GCGTTCAATTGGCTCCAGGGTTCATAGGGTATTGTTAGACTAGAGCTCC
FLT1	L422I	CTACCAGAACCAGAAGAAAGTATGAACAGCAAACTTACCATTGACAATTA[T/G]AGTGGCAGTGAGGTTTTTAAACACATTTGACTGTTTTATGCTCAGCAAGA
FLT3	D835E	GTCACCCACGGGAAAGTGGTGAAGATATGTGACTTTGGATTGGCTCGAGA[A/T]ATCATGAGTGATTCCAACTATGTTGTCAGGGGCAATGTGAGGCTGCTATT
FLT3	D835E	GTCACCCACGGGAAAGTGGTGAAGATATGTGACTTTGGATTGGCTCGAGA[T/G]ATCATGAGTGATTCCAACTATGTTGTCAGGGGCAATGTGAGGCTGCTATT
FLT3	D835H	TTGTCACCCACGGGAAAGTGGTGAAGATATGTGACTTTGGATTGGCTCGA[C/G]ATATCATGAGTGATTCCAACTATGTTGTCAGGGGCAATGTGAGGCTGCTA
FLT3	D835N	TTGTCACCCACGGGAAAGTGGTGAAGATATGTGACTTTGGATTGGCTCGA[A/G]ATATCATGAGTGATTCCAACTATGTTGTCAGGGGCAATGTGAGGCTGCTA
FLT3	D835V	TGTCACCCACGGGAAAGTGGTGAAGATATGTGACTTTGGATTGGCTCGAG[A/T]TATCATGAGTGATTCCAACTATGTTGTCAGGGGCAATGTGAGGCTGCTAT
FLT3	D835Y	TTGTCACCCACGGGAAAGTGGTGAAGATATGTGACTTTGGATTGGCTCGA[T/G]ATATCATGAGTGATTCCAACTATGTTGTCAGGGGCAATGTGAGGCTGCTA
FLT3	I836M	ACCCACGGGAAAGTGGTGAAGATATGTGACTTTGGATTGGCTCGAGATAT[C/G]ATGAGTGATTCCAACTATGTTGTCAGGGGCAATGTGAGGCTGCTATTTCC
FOXL2	C134W	GAGGGCGGCGGCGAGCGCAAGGGCAACTACTGGACGCTGGACCCGGCCTG[C/G]GAAGACATGTTCGAGAAGGGCAACTACCGGCGCCGCCGCCGCATGAAGAG
GAB1	R498M	TTTTTCCTCATTTGGAATGCAAGTTCCTCCTCCTGCTCATATGGGCTTCA[G/T]GTCCAGCCCAAAAACCCCTCCCAGAAGGCCAGTTCCTGTTGCAGACTGTG
GAB1	T387N	CAGTAGTTACTGTATCCCTACAGCAGGGATGTCGCCTTCACGTAGTAATA[C/A]CATTTCCACTGTGGATTTAAACAAATTGCGAAAAGGTCAGCTCTAGTTGA
GAB1	Y83C	ACAAGTAGATGCTGGATTGACATTTAACAAAAAAGAGTTTGAAAACAGCT[A/G]CATTTTTGATATCAACACTATTGACCGGATTTTCTACTTGG

		TAGCAGACA
GNA11	Q209L	TGGCTGAGTCCTGGCGCTGTGTCCTTTCAGGATGGTGGATGTGGGGGGCC[A/T]GCGGTCGGAGCGGAGGAAGTGGATCCACTGCTTTGAGAACGTGACATCCA
GNA11	R183C	GCATCGCCACCTTGGGCTACCTGCCCACCCAGCAGGACGTGCTGCGGGTC[T/C]GCGTGCCCACCACCGGCATCATCGAGTACCCTTTCGACCTGGAGAACATC
GNA11	Q209P	TGGCTGAGTCCTGGCGCTGTGTCCTTTCAGGATGGTGGATGTGGGGGGCC[A/C]GCGGTCGGAGCGGAGGAAGTGGATCCACTGCTTTGAGAACGTGACATCCA
GNA11	Q209R	TGGCTGAGTCCTGGCGCTGTGTCCTTTCAGGATGGTGGATGTGGGGGGCC[A/G]GCGGTCGGAGCGGAGGAAGTGGATCCACTGCTTTGAGAACGTGACATCCA
GNA11	R256W	TCTGCCTTCGCTCCCGCCAGAACCGGATGGAGGAGAGCAAAGCCCTGTTC[T/C]GGACCATCATCACCTACCCCTGGTTCCAGAACTCCTCCGTCATCCTCTTC
GNAQ	Q209R	TTATTAATATGAGTATTGTTAACCTTGCAGAATGGTCGATGTAGGGGGCC[A/G]AAGGTCAGAGAGAAGAAAATGGATACACTGCTTTGAAAATGTCACCTCTA
GNAQ	Q209L	TTATTAATATGAGTATTGTTAACCTTGCAGAATGGTCGATGTAGGGGGCC[A/T]AAGGTCAGAGAGAAGAAAATGGATACACTGCTTTGAAAATGTCACCTCTA
GNAQ	Q209P	TTATTAATATGAGTATTGTTAACCTTGCAGAATGGTCGATGTAGGGGGCC[A/C]AAGGTCAGAGAGAAGAAAATGGATACACTGCTTTGAAAATGTCACCTCTA
GNAS	Q227R	GGAATAACCAGCTGTCCTCCTCCCCACCAGCATGTTTGACGTGGGTGGCC[A/G]GCGCGATGAACGCCGCAAGTGGATCCAGTGCTTCAACGGTAGGATGCTGT
GNAS	R201C	TTTGGTGAGATCCATTGACCTCAATTTTGTTTCAGGACCTGCTTCGCTGC[C/T]GTGTCCTGACTTCTGGAATCTTTGAGACCAAGTTCCAGGTGGACAAAGTC
GNAS	R201H	TTGGTGAGATCCATTGACCTCAATTTTGTTTCAGGACCTGCTTCGCTGCC[G/A]TGTCCTGACTTCTGGAATCTTTGAGACCAAGTTCCAGGTGGACAAAGTCA
HIF1AN	Germline	GAAAGAAGCTACTGAGAAACCACTTT[G/T]TGATGTGTGCATTCAGCTCGCAGGG
HRAS	G12S	CAGGCCCCTGAGGAGCGATGACGGAATATAAGCTGGTGGTGGTGGGCGCC[A/G]GCGGTGTGGGCAAGAGTGCGCTGACCATCCAGCTGA

		TCCAGAACCATTTT
HRAS	G12V	AGGCCCCTGAGGAGCGATGACGGAATATAAGCTGGTGGTGGTGGGCGCCG[T/G]CGGTGTGGGCAAGAGTGCGCTGACCATCCAGCTGATCCAGAACCATTTTG
HRAS	Q61H	GTCATTGATGGGGAGACGTGCCTGTTGGACATCCTGGATACCGCCGGCCA[T/G]GAGGAGTACAGCGCCATGCGGGACCAGTACATGCGCACCGGGGAGGGCTT
HRAS	Q61K	TGGTCATTGATGGGGAGACGTGCCTGTTGGACATCCTGGATACCGCCGGC[A/C]AGGAGGAGTACAGCGCCATGCGGGACCAGTACATGCGCACCGGGGAGGGC
HRAS	Q61L	GGTCATTGATGGGGAGACGTGCCTGTTGGACATCCTGGATACCGCCGGCC[A/T]GGAGGAGTACAGCGCCATGCGGGACCAGTACATGCGCACCGGGGAGGGCT
HRAS	Q61R	GGTCATTGATGGGGAGACGTGCCTGTTGGACATCCTGGATACCGCCGGCC[A/G]GGAGGAGTACAGCGCCATGCGGGACCAGTACATGCGCACCGGGGAGGGCT
IDH1	R132H	AAATATCCCCCGGCTTGTGAGTGGATGGGTAAAACCTATCATCATAGGTC[G/A]TCATGCTTATGGGGATCAAGTAAGTCATGTTGGCAATAATGTGATTTTGC
IDH2	R172G	AAAACATCCCACGCCTAGTCCCTGGCTGGACCAAGCCCATCACCATTGGC[A/T]GGCACGCCCATGGCGACCAGGTAGGCCAGGGTGGAGAGGGGATCCACTGA
IDH2	R172K	AAACATCCCACGCCTAGTCCCTGGCTGGACCAAGCCCATCACCATTGGCA[G/A]GCACGCCCATGGCGACCAGGTAGGCCAGGGTGGAGAGGGGATCCACTGAC
IKBKB	A360S	ACACGGGCATCCCAGAGGAGGACCAGGAGCTGCTGCAGGAAGCGGGCCTG[G/T]CGTTGATCCCCGATAAGCCTGCCACTCAGTGTATTTCAGACGGCAAGGTG
IKBKB	Q611*	TGCTTCAGGCAATTCAGAGCTTCGAGAAGAAAGTGCGAGTGATCTATACG[C/T]AGCTCAGGTATGAGCCCCGACCTTCCTGCTCTGGAGGAAGGACTGGGAGA
IRS2	G607D	CTCCTCTGCCTCGCTGGATGAATACACCCTGATGCGGGCCACCTTCTCGG[G/A]CAGCGCGGGCCGCCTCTGCCCGTCCTGCCCCGCGTCCTCTCCCAAGGTGG
IRS4	A20V	TTGCTCCTTCACTCGCGACCAAGCGACAAGAAGACTAAGAGGTGCAGCAG[C/T]GGCGGCAGCGGCAGCTCTAGCAGCAGTGGTGACCACCCCGCTTCTTTCCT
IRS4	A972V	CTTTTCTAATTATGTGAATGTTGAGTTTGGAGTGCCATTTCCAAATCCAG[C/T]AAACGACCTCTCAGATCTTTTAAGAGCTATACCACGTGCCAACCCCTTATC
IRS4	G557R	CAGGAGGAAACCAGTGCTCTAGAGATGGCCAGGGCACCGCAGGTGGGCAC[G/C]GTTCAGGTGGTGGCCAGAGACCTGGAGGTGGGCATG

		GCTCAGGTGGTGGC
JAK2	V617F	TGATGAGCAAGCTTTCTCACAAGCATTTGGTTTTAAATTATGGAGTATGT[T/G]TCTGTGGAGACGAGAGTAAGTAAAACTACAGGCTTTCTAATGCCTTTCTC
KIT	N567K	CCCATGTATGAAGTACAGTGGAAGGTTGTTGAGGAGATAAATGGAAACAA[A/T]TATGTTTACATAGACCCAACACAACTTCCTTATGATCACAAATGGGAGTT
KIT	V559A	ATTTTTCCCTTTCTCCCCACAGAAACCCATGTATGAAGTACAGTGGAAGG[T/C]TGTTGAGGAGATAAATGGAAACAATTATGTTTACATAGACCCAACACAAC
KIT	V559G	ATTTTTCCCTTTCTCCCCACAGAAACCCATGTATGAAGTACAGTGGAAGG[T/G]TGTTGAGGAGATAAATGGAAACAATTATGTTTACATAGACCCAACACAAC
KIT	V559I	TATTTTTCCCTTTCTCCCCACAGAAACCCATGTATGAAGTACAGTGGAAG[A/G]TTGTTGAGGAGATAAATGGAAACAATTATGTTTACATAGACCCAACACAA
KIT	W557G	GTGATCTATTTTTCCCTTTCTCCCCACAGAAACCCATGTATGAAGTACAG[T/G]GGAAGGTTGTTGAGGAGATAAATGGAAACAATTATGTTTACATAGACCCA
KIT	W557R	GTGATCTATTTTTCCCTTTCTCCCCACAGAAACCCATGTATGAAGTACAG[A/T]GGAAGGTTGTTGAGGAGATAAATGGAAACAATTATGTTTACATAGACCCA
KIT	D816H	TCCTTACTCATGGTCGGATCACAAAGATTTGTGATTTTGGTCTAGCCAGA[C/G]ACATCAAGAATGATTCTAATTATGTGGTTAAAGGAAACGTGAGTACCCAT
KIT	D816V	CCTTACTCATGGTCGGATCACAAAGATTTGTGATTTTGGTCTAGCCAGAG[A/T]CATCAAGAATGATTCTAATTATGTGGTTAAAGGAAACGTGAGTACCCATT
KIT	D8I6Y	TCCTTACTCATGGTCGGATCACAAAGATTTGTGATTTTGGTCTAGCCAGA[T/G]ACATCAAGAATGATTCTAATTATGTGGTTAAAGGAAACGTGAGTACCCAT
KIT	L576P	TGTTGAGGAGATAAATGGAAACAATTATGTTTACATAGACCCAACACAAC[T/C]TCCTTATGATCACAAATGGGAGTTTCCCAGAAACAGGCTGAGTTTTGGTC
KIT	N822K	ACAAAGATTTGTGATTTTGGTCTAGCCAGAGACATCAAGAATGATTCTAA[T/G]TATGTGGTTAAAGGAAACGTGAGTACCCATTCTCTGCTTGACAGTCCTGC
KIT	N822K	ACAAAGATTTGTGATTTTGGTCTAGCCAGAGACATCAAGAATGATTCTAA[A/T]TATGTGGTTAAAGGAAACGTGAGTACCCATTCTCTGCTTGACAGTCCTGC
KIT	N822Y	TCACAAAGATTTGTGATTTTGGTCTAGCCAGAGACATCAAGAATGATTCT[A/T]ATTATGTGGTTAAAGGAAACGTGAGTACCCATTCTCTGCTT

		GACAGTCCT
KIT	Y503_F504insAY	GGCACGGTTGAATGTAAGGCTTACAACGATGTGGGCAAGACTTCTGCCTA[/T]TTTAACTTTGCATTTAAAGGTAACAACAAAGGTATATTTCTTTTTAATCCA
KIT	V559D	ATTTTTCCCTTTCTCCCCACAGAAACCCATGTATGAAGTACAGTGGAAGG[A/T]TGTTGAGGAGATAAATGGAAACAATTATGTTTACATAGACCCAACACAAC
KIT	V560D	TTTCCCTTTCTCCCCACAGAAACCCATGTATGAAGTACAGTGGAAGGTTG[A/T]TGAGGAGATAAATGGAAACAATTATGTTTACATAGACCCAACACAACTTC
KIT	V560G	TTTCCCTTTCTCCCCACAGAAACCCATGTATGAAGTACAGTGGAAGGTTG[T/G]TGAGGAGATAAATGGAAACAATTATGTTTACATAGACCCAACACAACTTC
KRAS	G12V	ATAAGGCCTGCTGAAAATGACTGAATATAAACTTGTGGTAGTTGGAGCTG[T/G]TGGCGTAGGCAAGAGTGCCTTGACGATACAGCTAATTCAGAATCATTTTG
KRAS	A146T	AGGCTCAGGACTTAGCAAGAAGTTATGGAATTCCTTTTATTGAAACATCA[A/G]CAAAGACAAGACAGGTAAGTAACACTGAAATAAATACAGATCTGTTTTCT
KRAS	G12A	ATAAGGCCTGCTGAAAATGACTGAATATAAACTTGTGGTAGTTGGAGCTG[C/G]TGGCGTAGGCAAGAGTGCCTTGACGATACAGCTAATTCAGAATCATTTTG
KRAS	G12C	TATAAGGCCTGCTGAAAATGACTGAATATAAACTTGTGGTAGTTGGAGCT[T/G]GTGGCGTAGGCAAGAGTGCCTTGACGATACAGCTAATTCAGAATCATTTT
KRAS	G12D	ATAAGGCCTGCTGAAAATGACTGAATATAAACTTGTGGTAGTTGGAGCTG[A/G]TGGCGTAGGCAAGAGTGCCTTGACGATACAGCTAATTCAGAATCATTTTG
KRAS	G13D	AGGCCTGCTGAAAATGACTGAATATAAACTTGTGGTAGTTGGAGCTGGTG[A/G]CGTAGGCAAGAGTGCCTTGACGATACAGCTAATTCAGAATCATTTTGTGG
KRAS	Germline	GTCTCGAACTCCTGACCTCAAGTGAT[G/T]CACCCACCTTGGCCTCATAAACCTG
KRAS	KRAS	TATAAGGCCTGCTGAAAATGACTGAATATAAACTTGTGGTAGTTGGAGCT[C/G]GTGGCGTAGGCAAGAGTGCCTTGACGATACAGCTAATTCAGAATCATTTT
KRAS	Q61H	GTAATTGATGGAGAAACCTGTCTCTTGGATATTCTCGACACAGCAGGTCA[A/C]GAGGAGTACAGTGCAATGAGGGACCAGTACATGAGGACTGGGGAGGGCTT
MAP2K1	L215P	CAACTCCCGTGGGGAGATCAAGCTCTGTGACTTTGGGGTCAGCGGGCAGC[T/C]CATCGACTCCATGGCCAACTCCTTCGTGGGCACAAGGTCCTACATGTCGG

MAP2K1	P124T	TCCGGAACCAGATCATAAGGGAGCTGCAGGTTCTGCATGAGTGCAACTCT[A/C]CGTACATCGTGGGCTTCTATGGTGCGTTCTACAGCGATGGCGAGATCAGT
MAP2K1	E120D	AAACCCGCAATCCGGAACCAGATCATAAGGGAGCTGCAGGTTCTGCATGA[T/G]TGCAACTCTCCGTACATCGTGGGCTTCTATGGTGCGTTCTACAGCGATGG
MAP2K1	E120D	AAACCCGCAATCCGGAACCAGATCATAAGGGAGCTGCAGGTTCTGCATGA[C/G]TGCAACTCTCCGTACATCGTGGGCTTCTATGGTGCGTTCTACAGCGATGG
MAP2K1	E368K	CGTTTCCTTACATGCAGGTTCATGCTTTTATCAAGAGATCTGATGCTGAG[A/G]AAGTGGATTTTGCAGGTTGGCTCTGCTCCACCATCGGCCTTAACCAGCCC
MAP2K1	F133L	AGGTTCTGCATGAGTGCAACTCTCCGTACATCGTGGGCTTCTATGGTGCG[T/C]TCTACAGCGATGGCGAGATCAGTATCTGCATGGAGCACATGGTATGTGAC
MAP2K1	F133L	GTTCTGCATGAGTGCAACTCTCCGTACATCGTGGGCTTCTATGGTGCGTT[A/C]TACAGCGATGGCGAGATCAGTATCTGCATGGAGCACATGGTATGTGACAC
MAP2K1	F133L	GTTCTGCATGAGTGCAACTCTCCGTACATCGTGGGCTTCTATGGTGCGTT[C/G]TACAGCGATGGCGAGATCAGTATCTGCATGGAGCACATGGTATGTGACAC
MAP2K1	G128D	CATAAGGGAGCTGCAGGTTCTGCATGAGTGCAACTCTCCGTACATCGTGG[A/G]CTTCTATGGTGCGTTCTACAGCGATGGCGAGATCAGTATCTGCATGGAGC
MAP2K1	H119P	GATCAAACCCGCAATCCGGAACCAGATCATAAGGGAGCTGCAGGTTCTGC[A/C]TGAGTGCAACTCTCCGTACATCGTGGGCTTCTATGGTGCGTTCTACAGCG
MAP2K1	I111N	CTTTCTCCAGCTAATTCATCTGGAGATCAAACCCGCAATCCGGAACCAGA[A/T]CATAAGGGAGCTGCAGGTTCTGCATGAGTGCAACTCTCCGTACATCGTGG
MAP2K1	I99T	TCCCTCTTTCTTTCATAAAACCTCTCTTTCTTCCACCTTTCTCCAGCTAA[T/C]TCATCTGGAGATCAAACCCGCAATCCGGAACCAGATCATAAGGGAGCTGC
MAP2K1	K104N	AAAACCTCTCTTTCTTCCACCTTTCTCCAGCTAATTCATCTGGAGATCAA[A/C]CCCGCAATCCGGAACCAGATCATAAGGGAGCTGCAGGTTCTGCATGAGTG
MAP2K1	K104N	AAAACCTCTCTTTCTTCCACCTTTCTCCAGCTAATTCATCTGGAGATCAA[A/T]CCCGCAATCCGGAACCAGATCATAAGGGAGCTGCAGGTTCTGCATGAGTG
MAP2K1	L115P	AATTCATCTGGAGATCAAACCCGCAATCCGGAACCAGATCATAAGGGAGC[T/C]GCAGGTTCTGCATGAGTGCAACTCTCCGTACATCGTGGGCTTCTATGGTG

MAP2K1	P326L	AATTTTTGAGTTGTTGGATTACATAGTCAACGAGCCTCCTCCAAAACTGC[T/C]CAGTGGAGTGTTCAGTCTGGAATTTCAAGATTTTGTGAATAAATGCCTAA
MAP2K1	Q56P	GCTAGAGCTTGATGAGCAGCAGCGAAAGCGCCTTGAGGCCTTTCTTACCC[A/C]GAAGCAGAAGGTGGGAGAACTGAAGGATGACGACTTTGAGAAGATCAGTG
MAP2K1	V211D	CAACATCCTAGTCAACTCCCGTGGGGAGATCAAGCTCTGTGACTTTGGGG[A/T]CAGCGGGCAGCTCATCGACTCCATGGCCAACTCCTTCGTGGGCACAAGGT
MAP2K2	E124D	AAGCCGGCCATCCGGAACCAGATCATCCGCGAGCTGCAGGTCCTGCACGA[A/T]TGCAACTCGCCGTACATCGTGGGCTTCTACGGGGCCTTCTACAGTGACGG
MAP2K2	E124D	AAGCCGGCCATCCGGAACCAGATCATCCGCGAGCTGCAGGTCCTGCACGA[A/C]TGCAACTCGCCGTACATCGTGGGCTTCTACGGGGCCTTCTACAGTGACGG
MAP2K2	E376K	CTCCCCTTTCCTTGCAGAACCACACCTTCATCAAGCGGTCCGAGGTGGAA[A/G]AAGTGGATTTTGCCGGCTGGTTGTGTAAAACCCTGCGGCTGAACCAGCCC
MAP2K2	F137L	GTCCTGCACGAATGCAACTCGCCGTACATCGTGGGCTTCTACGGGGCCTT[C/G]TACAGTGACGGGGAGATCAGCATTTGCATGGAACACATGGACGGCGGCTC
MAP2K2	F137L	GTCCTGCACGAATGCAACTCGCCGTACATCGTGGGCTTCTACGGGGCCTT[A/C]TACAGTGACGGGGAGATCAGCATTTGCATGGAACACATGGTGAGTGCGTC
MAP2K2	G132D	CATCCGCGAGCTGCAGGTCCTGCACGAATGCAACTCGCCGTACATCGTGG[A/G]CTTCTACGGGGCCTTCTACAGTGACGGGGAGATCAGCATTTGCATGGAAC
MAP2K2	G336R	CTGACCCCACCCTCTGTTCTCCTCCACAGCCACCTCCTAAGCTGCCCAAC[C/G]GTGTGTTCACCCCCGACTTCCAGGAGTTTGTCAATAAATGGTAGGTGGAG
MAP2K2	H123P	GATCAAGCCGGCCATCCGGAACCAGATCATCCGCGAGCTGCAGGTCCTGC[A/C]CGAATGCAACTCGCCGTACATCGTGGGCTTCTACGGGGCCTTCTACAGTG
MAP2K2	I103T	GTTTTCGGGCACCCCCCAAGCCAGTCTCGCCCCTCTCCCCTTGCAGCTGA[T/C]CCACCTTGAGATCAAGCCGGCCATCCGGAACCAGATCATCCGCGAGCTGC
MAP2K2	I115N	CCCCTTGCAGCTGATCCACCTTGAGATCAAGCCGGCCATCCGGAACCAGA[A/T]CATCCGCGAGCTGCAGGTCCTGCACGAATGCAACTCGCCGTACATCGTGG
MAP2K2	L119P	GATCCACCTTGAGATCAAGCCGGCCATCCGGAACCAGATCATCCGCGAGC[T/C]GCAGGTCCTGCACGAATGCAACTCGCCGTACATCGTGGGCTTCTACGGGG

MAP2K2	P128T	TCCGGAACCAGATCATCCGCGAGCTGCAGGTCCTGCACGAATGCAACTCG[A/C]CGTACATCGTGGGCTTCTACGGGGCCTTCTACAGTGACGGGGAGATCAGC
MAP2K2	Q60P	GCTGGAACTTGACGAGCAGCAGAAGAAGCGGCTGGAAGCCTTTCTCACCC[A/C]GAAAGCCAAGGTCGGCGAACTCAAAGACGATGACTTCGAAAGGATCTCAG
MAP2K7	R162H	CCTGCCTGTGCAGCAAATGCGGCGCTCCGGGAACAAGGAGGAGAACAAGC[G/A]CATCCTCATGGACCTGGATGTGGTGCTGAAGAGCCACGACTGCCCCTACA
MAP2K7	Splice Site	CTAGCCTTACTAAAGATCACAGGAAGAGACCAAAGTATAATAAGCTACTT[G/A]TGAGTACCTGAGCCCTCCCAGTCCCCGTCCTGTCCCTGCGGAGGCGCGAG
MAP2K7	Splice Site	TCGGAGGGAGGAGAACATAAACCTGTCCAGCCCTGCCCGTCTCCCTCCCA[G/A]GTGGAGCTGGCAACAGGACAGTTTCCCTACAAGAACTGCAAGACGGACTT
MAP2K7	R162C	CCCTGCCTGTGCAGCAAATGCGGCGCTCCGGGAACAAGGAGGAGAACAAG[C/T]GCATCCTCATGGACCTGGATGTGGTGCTGAAGAGCCACGACTGCCCCTAC
MET	R988C	AACAAGCTCTTTCTTTCTCTCTGTTTTAAGATCTGGGCAGTGAATTAGTT[T/C]GCTACGATGCAAGAGTACACACTCCTCATTTGGATAGGCTTGTAAGTGCC
MET	E168D	GCTGACATACAGTCGGAGGTTCACTGCATATTCTCCCCACAGATAGAAGA[T/G]CCCAGCCAGTGTCCTGACTGTGTGGTGAGCGCCCTGGGAGCCAAAGTCCT
MET	L229F	TCGATATCAGTGAGAAGGCTAAAGGAAACGAAAGATGGTTTTATGTTTTT[T/G]ACGGACCAGTCCTACATTGATGTTTTACCTGAGTTCAGAGATTCTTACCC
MET	M1268T	ATACTATAGTGTACACAACAAAACAGGTGCAAAGCTGCCAGTGAAGTGGA[T/C]GGCTTTGGAAAGTCTGCAAACTCAAAAGTTTACCACCAAGTCAGATGTGG
MET	T1010I	ACACACTCCTCATTTGGATAGGCTTGTAAGTGCCCGAAGTGTAAGCCCAA[T/C]TACAGAAATGGTTTCAAATGAATCTGTAGACTACCGAGCTACTTTTCCAG
MET	Y1248C	TGAAAAATTCACAGTCAAGGTTGCTGATTTTGGTCTTGCCAGAGACATGT[A/G]TGATAAAGAATACTATAGTGTACACAACAAAACAGGTGCAAAGCTGCCAG
MET	Y1253D	TCAAGGTTGCTGATTTTGGTCTTGCCAGAGACATGTATGATAAAGAATAC[T/G]ATAGTGTACACAACAAAACAGGTGCAAAGCTGCCAGTGAAGTGGATGGCT
MLL3	C347G	TCATTGTTTCACTGTTAATTATAGCGAAGGAAGATGCAAACTGTGCAGTG[T/G]GCGACAGCCCGGGAGACCTCTTAGATCAGTTCTTTTGTACTACTTGTGGT

MLL3	D400N	AAAGATAAGGCATCATTAATGCTATCTTATTTTTTAGACAATCGGGAGAA[G/A]ATAGCAAGATGCTAGTGTGTGATACGTGTGACAAAGGGTATCATACTTTT
MLL3	E3775*	GTCCTCCCCATTCTGCTGGGGCCCCTGCTGCCAAAGGAGACTCAGGGAAT[G/A]AACTTCTGAAACACTTGTTGAAAAATAAAAAGTCATCTTCTCTTTTGAAT
MLL3	G1517R	CTAGTCTTTTAATCTTGTTACTATTATTGTTTTATCTCCTAGAGCTTGGC[G/A]GAAAAGATGTTGAAGACTTATTTACAGCTGTACTTAGTCCTGCGAACACT
MLL3	G4445D	CCACTTGAACTGCGCTCTGTGGTCCACGGAGGTCTATGAGACTCAGGCTG[G/A]TGCCTTAATAAATGTGGAGCTAGCTCTGAGGAGAGGCCTACAAATGAAAT
MLL3	L478W	ACAGCAGGATAACTTATGTCCCTTCTGTGGGAAGTGTTATCATCCAGAAT[T/G]GCAGAAAGACATGCTTCATTGTAATATGTGCAAAAGGTAAGAAGATAGTT
MLL3	R1906*	CACGACCACCATCTCCAATGGATCCATATGCAAAAATGGTTGGTACCCCT[C/T]GACCACCTCCTGTGGGCCATAGTTTTTCCAGAAGAAATTCTGCTGCACCA
MLL3	T3698S	AGAACAAACTGCCCAATAGTGATTTCTCACAAGCAACTCCAAATCAACAG[A/T]CGTATGCAAATTCAGAAGTAGACAAGCTCTCCATGGAAACCCCTGCCAAA
MSH6	P1087fs*3	GATGGTCCTATGTGTCGCCCAGTAATTCTGTTGCCGGAAGATACCCCCCC[/C]TTCTTAGAGCTTAAAGGATCACGCCATCCTTGCATTACGAAGACTTTTTT
MSH6	P1087fs*5	GATGGTCCTATGTGTCGCCCAGTAATTCTGTTGCCGGAAGATACCCCCCC[/C]CTTCTTAGAGCTTAAAGGATCACGCCATCCTTGCATTACGAAGACTTTTTT
MYC	cytogenetics	TCCACGAAACTTTGCCCATAGCAGCGGGCGGGCACTTTGCACTGGAACTT[A/T]CAACACCCGAGCAAGGACGCGACTCTCCCGACGCGGGGAGGCTATTCTGC
MYC	cytogenetics	AAAGGGGGTGAAAGGGTGCTCCCTTTATTCCCCCACCAAGACCACCCAGC[C/A]GCTTTAGGGGATAGCTCTGCAAGGGGAGAGGTTCGGGACTGTGGCGCGCA
MYC	cytogenetics	ATTTTTCATTTCCAGTAAAATAGGGAGTTGCTAAAGTCATACCAAGCAAT[T/A]TGCAGCTATCATTTGCAACACCTGAAGTGTTCTTGGTAAAGTCCCTCAAA
MYC	cytogenetics	ACTGGTCCTCAAGAGGTGCCACGTCTCCACACATCAGCACAACTACGCAG[C/T]GCCTCCCTCCACTCGGAAGGACTATCCTGCTGCCAAGAGGGTCAAGTTGG
MYC	cytogenetics	GTTTCAAATGCATGATCAAATGCAACCTCACAACCTTGGCTGAGTCTTGA[G/T]ACTGAAAGATTTAGCCATAATGTAAACTGCCTCAAATTGGACTTTGGGCA

MYC	cytogenetics	ATGGGAGTTTATTCATAACGCGCTCTCCAAGTATACGTGGCAATGCGTTG[T/C]TGGGTTATTTTAATCATTCTAGGCATCGTTTTCCTCCTTATGCCTCTATC
MYC	cytogenetics	CTGGGTTATTTTAATCATTCTAGGCATCGTTTTCCTCCTTATGCCTCTAT[A/C]ATTCCTCCCTATCTACACTAACATCCCACGCTCTGAACGCGCGCCCATTA
NEK10	E379K	CTGCAGGCCGAATCCAGCAGCTTCATTTATCAGAAGACTTGAGCCCTAGG[G/A]AAATACAAGAAAATACTTTCTCACTTCAAGCAGGTATTTATGTTTTATTA
NEK10	A66V	CTTCGATAGTGCCCAAAATAGCATGACGAAGTCTGAGCCCGCCATCAGGG[C/T]GGGTGGACACAGAGCTCGGGGTCAGTGGCATGAATCCACAGAAGCTGTTG
NEK10	I783V	TCACTCCTGATGCGGAAGCTCGTCCAGATATTGTAGAAGTCAGTTCGATG[A/G]TATCAGATGTCATGATGAAATATTTAGACAACTTATCTACATCCCAGTTG
NEK10	P1115L	ACTATAGAGAATTCTTTCCACTTCTGAATCTTATAGGTATCATTCCTATC[C/T]ATGGGGGACCAAGAATCACCCAACCAAAAGATGAAAATGCTGCATTTTGA
NEK10	R878M	AGACCTGCCCCCTGAAGGCTTCCAGGCCTCCTATGGTAAAGACGAAGACA[G/T]GGCCTGTGACGAAATCCTGTCAGATGATAACTTCAACCTGGAAAATGCTG
NF1	D176E	AGGTTACAGGAATTAACTGTTTGTTCAGAAGACAATGTTGATGTTCATGA[A/T]ATAGAATTGTTACAGTATATCAATGTGGATTGTGCAAAATTAAAACGACT
NF1	A74D	CTAACTTTTATGTTCTGAATATCTTTTCTGTTAGAGAATATTTGGAGAAG[A/C]TGCTGAAAAAAATTTATATCTCTCTCAGTTGATTATATTGGATACACTGG
NF1	K1444E	TAGATAAAAAGCCACCACCTAGAATCGAAAGGGGCTTGAAGTTAATGTCA[A/G]AGGTGAATTATTTTGATAATCTAGCTATCTTAAATTCCCCTTCCAACTAA
NF1	P2477S	CACTTCTTCTTACTGATATTTCAATGGAAAATGTTCCTATGGATACATAT[T/C]CCATTCATCATGGTGACCCTTCCTATAGGTAAGTGGATTTACTCTCCTAT
NF1	P678fs*10	TTCCACCCTTGACTCTCAGGATAGTGCAGCAGGATGCAGCGGAACCCCCC[/C]GATTTGCCGACAAGCCCAGACCAAACTAGAAGTGGCCCCTGTACATGTTTC
NF1	R1276Q	CATGTTTTCTAAAGAAGTAGAATTGGCAGACTCCATGCAGACTCTCTTCC[A/G]AGGCAACAGCTTGGCCAGTAAAATAATGACATTCTGTTTCAAGGTTTGTA
NF1	Y1607fs*17	TTAAGTATTTTCTACCAAGCTGGGACTTCCAAAGCTGGGAATCCTATTTTT[/T]ATTATGTTGCACGGAGGTAAGAAATACTATGTTTTGGGTCTCTTAACAG

NFKB1	Splice Site	TATAATATAGGAAAAATAATGATTGAAACATTTAAATGTTCTTCTTTACA[G/A]ATGTTTCATTTGGATCCTTCTTTGACTCATACAATATTTAATCCAGAAGT
NFKBIA	R143fs*11	TTGCTGAGGCACTTCTGGGAGCTGGCTGTGATCCTGAGCTCCGAGACTTT[/C]CGAGGAAATACCCCCCTACACCTTGCCTGTGAGCAGGGCTGCCTGGCCAGCG
NFKBIE	D462E	GGCCGGGGTCTCATGGGCATCTCATCCACTCTGTGCAAGGCGGGTGCTGA[C/A]TCCCTGCTGCGGAATGTGGAGGATGAGACGCCCCAGGACCTGACTGAGGA
NFKBIE	Q380X	CTCACTCTCACCCCATCCCAGGTCTGGCTTGTCTCCACATTGCCACCCTT[C/T]AGAAGAACCAACCACTCATGGAATTGCTGCTTCGGAATGGAGCTGACATT
NRAS	G12D	TTCTTGCTGGTGTGAAATGACTGAGTACAAACTGGTGGTGGTTGGAGCAG[A/G]TGGTGTTGGGAAAAGCGCACTGACAATCCAGCTAATCCAGAACCACTTTG
NRAS	Q61H	GTTATAGATGGTGAAACCTGTTTGTTGGACATACTGGATACAGCTGGACA[A/T]GAAGAGTACAGTGCCATGAGAGACCAATACATGAGGACAGGCGAAGGCTT
NRAS	Q61K	TGGTTATAGATGGTGAAACCTGTTTGTTGGACATACTGGATACAGCTGGA[A/C]AAGAAGAGTACAGTGCCATGAGAGACCAATACATGAGGACAGGCGAAGGC
NRAS	Q61L	GGTTATAGATGGTGAAACCTGTTTGTTGGACATACTGGATACAGCTGGAC[A/T]AGAAGAGTACAGTGCCATGAGAGACCAATACATGAGGACAGGCGAAGGCT
NRAS	Q61R	GGTTATAGATGGTGAAACCTGTTTGTTGGACATACTGGATACAGCTGGAC[A/G]AGAAGAGTACAGTGCCATGAGAGACCAATACATGAGGACAGGCGAAGGCT
NRAS	G12S	GTTCTTGCTGGTGTGAAATGACTGAGTACAAACTGGTGGTGGTTGGAGCA[A/G]GTGGTGTTGGGAAAAGCGCACTGACAATCCAGCTAATCCAGAACCACTTG
NRAS	G13D	TTGCTGGTGTGAAATGACTGAGTACAAACTGGTGGTGGTTGGAGCAGGTG[A/G]TGTTGGGAAAAGCGCACTGACAATCCAGCTAATCCAGAACCACTTTGTAG
PDGFRA	D842V	CCTGGCACAAGGAAAAATTGTGAAGATCTGTGACTTTGGCCTGGCCAGAG[A/T]CATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTGTACGTCCTCACT
PDGFRA	V561D	TACCTGTCCTGGTCATTTATAGAAACCGAGGTATGAAATTCGCTGGAGGG[A/T]CATTGAATCAATCAGCCCAGATGGACATGAATATATTTATGTGGACCCGA
PIK3CA	P6539R	ATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACACGAGATC[C/G]TCTCTCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGGT

PIK3CA	C378R	ACCATGGAGGAGAACCCTTATGTGACAATGTGAACACTCAAAGAGTACCT[T/C]GTTCCAATCCCAGGTAAGGAAGTATATAGATTTATATTTCCAAAGGTTAT
PIK3CA	C420R	GTTTTATAATTTAGACTAGTGAATATTTTTCTTTGTTTTTAAGGAACAC[T/C]GTCCATTGGCATGGGGAAATATAAACTTGTTTGATTACACAGACACTCTA
PIK3CA	E542K	AAAATGACAAAGAACAGCTCAAAGCAATTTCTACACGAGATCCTCTCTCT[A/G]AAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGGTAAGTGCTA
PIK3CA	E545A	AGAACAGCTCAAAGCAATTTCTACACGAGATCCTCTCTCTGAAATCACTG[A/C]GCAGGAGAAAGATTTTCTATGGAGTCACAGGTAAGTGCTAAAATGGAGAT
PIK3CA	E545G	AGAACAGCTCAAAGCAATTTCTACACGAGATCCTCTCTCTGAAATCACTG[A/G]GCAGGAGAAAGATTTTCTATGGAGTCACAGGTAAGTGCTAAAATGGAGAT
PIK3CA	E545K	AAGAACAGCTCAAAGCAATTTCTACACGAGATCCTCTCTCTGAAATCACT[A/G]AGCAGGAGAAAGATTTTCTATGGAGTCACAGGTAAGTGCTAAAATGGAGA
PIK3CA	G118D	AATTGAACCAGTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAAATTG[A/G]TATGATACAATATCCTATTCTAAAATGCAAATAACCATAAAGCTTAACTG
PIK3CA	H1047L	AACTGAGCAAGAGGCTTTGGAGTATTTCATGAAACAAATGAATGATGCAC[A/T]TCATGGTGGCTGGACAACAAAAATGGATTGGATCTTCCACACAATTAAAC
PIK3CA	H1047R	AACTGAGCAAGAGGCTTTGGAGTATTTCATGAAACAAATGAATGATGCAC[A/G]TCATGGTGGCTGGACAACAAAAATGGATTGGATCTTCCACACAATTAAAC
PIK3CA	H1047Y	AAACTGAGCAAGAGGCTTTGGAGTATTTCATGAAACAAATGAATGATGCA[T/C]ATCATGGTGGCTGGACAACAAAAATGGATTGGATCTTCCACACAATTAAA
PIK3CA	M1043I	GCCTTAGATAAAACTGAGCAAGAGGCTTTGGAGTATTTCATGAAACAAAT[T/G]AATGATGCACATCATGGTGGCTGGACAACAAAAATGGATTGGATCTTCCA
PIK3CA	M1043I	GCCTTAGATAAAACTGAGCAAGAGGCTTTGGAGTATTTCATGAAACAAAT[G/T]AATGATGCACATCATGGTGGCTGGACAACAAAAATGGATTGGATCTTCCA
PIK3CA	M1043T	AGCCTTAGATAAAACTGAGCAAGAGGCTTTGGAGTATTTCATGAAACAAA[T/C]GAATGATGCACATCATGGTGGCTGGACAACAAAAATGGATTGGATCTTCC
PIK3CA	E545G	AGAACAGCTCAAAGCAATTTCTACACGAGATCCTCTCTCTGAAATCACTG[A/G]GCAGGAGAAAGATTTTCTATGGAGTCACAGGTAAGTGCTAAAATGGAGAT

PIK3CA	H1047R	AACTGAGCAAGAGGCTTTGGAGTATTTCATGAAACAAATGAATGATGCAC[A/G]TCATGGTGGCTGGACAACAAAAATGGATTGGATCTTCCACACAATTAAAC
PIK3CA	Q546K	AACAGCTCAAAGCAATTTCTACACGAGATCCTCTCTCTGAAATCACTGAG[A/C]AGGAGAAAGATTTTCTATGGAGTCACAGGTAAGTGCTAAAATGGAGATTC
PIK3CA	Q75E	TCCATCAACTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTTACT[C/G]AAGAAGCAGAAAGGGAAGAATTTTTTGATGAAACAAGACGACTTTGTGAC
PIK3CA	R108H	CCTTCGGCTTTTTCAACCCTTTTTAAAAGTAATTGAACCAGTAGGCAACC[A/G]TGAAGAAAAGATCCTCAATCGAGAAATTGGTATGATACAATATCCTATTC
PIK3CA	R38G	TAGTAGAATGTTTACTACCAAATGGAATGATAGTGACTTTAGAATGCCTC[C/G]GTGAGGCTACATTAATAACCATAAAGCATGAACTATTTAAAGAAGCAAGA
PIK3CA	T1025A	CTGGAATGCCAGAACTACAATCTTTTGATGACATTGCATACATTCGAAAG[A/G]CCCTAGCCTTAGATAAAACTGAGCAAGAGGCTTTGGAGTATTTCATGAAA
PIK3R1	449L>S	TAGGATCAAGTTGTCAAAGAAGATAATATTGAAGCTGTAGGGAAAAAAT[T/C]ACATGAATATAACACTCAGTTTCAAGAAAAAAGTCGAGAATATGATAGA
PIK3R1	527N>K	CGTTCCTGATGTACCCAGATAATAACAAATACGTTTCTTTTGCCTGCAGGATTATGCATAA[T/G]TATGATAAGTTGAAGTCTCGAATCAGTGAAATTATTGACAGTAGAAGAAGATTGGAAG
PIK3R1	666E>K	TGGACAAGCTCAAAAGACAGTTTTTCTTCTCTCCTCTCTAGGGTGGACGGC[G/A]AAGTAAAGCATTGTGTCATAAACAAAACAGCAACTGGCTATGGCT
PIK3R1	indel	GTTGTCAAAGAAGATAATATTGAAGCTGTAGGGAAAAAATTACATGAATATAA[/TAA]CACTCAGTTTCAAGAAAAAAGTCGAGAATATGATAGATTATATGAAGAAT
PIK3R1	162R>*	CTGGAATGTTCAACTCTATACAGAACACAGAGCTCCAGCAACCTGGCAGAATTA[C/T]GACAGCTTCTTGATTGTGGTGAGTGTCACAGAGCTAGAAATGCAAATGGGA
PIK3R1	285N>H	AAAAGGTTTCTAATAAACTCTCTTTCTTACAGCTCTGATAATACTGAA[A/C]ACCTCATAAAAGTTATAGAAATTTTAATCTCAACTGAATGGAATGAACGACAGCCTG
PIK3R1	348R>*	GATGAGCATTGTTTTGTGTTTTCATTTCAGGGAAGAAGTGAATGAAAAACTT[C/T]GAGATACAGCAGACGGGACCTTTTTGGTACGAGATGCGTCTACTAAAATGC
PIK3R1	543R>I	GCATAATTATGATAAGTTGAAGTCTCGAATCAGTGAAATTATTGACAGTAGAA[G/T]AAGATTGGAAGAAGACTTGAAGAAGCAGGCAGCTGA

		GTATCGAGAAATTGACAAAC
PIK3R1	564N>D	AGACTTGAAGAAGCAGGCAGCTGAGTATCGAGAAATTGACAAACGTATG[A/G]ACAGCATTAAACCAGACCTTATCCAGCTGAGAAAGACGAGAGACCAATACTTGATGTAAGTATTTG
PIK3R1	574R>I	GAGTATCGAGAAATTGACAAACGTATGAACAGCATTAAACCAGACCTTATCCAGCTGA[G/T]AAAGACGAGAGACCAATACTTGATGTAAGTATTTGAAATGGAATCCTA
PIK3R1	642R>*	GAATGTTGGAAGCAGCAACCGAAACAAAGCTGAAAACCTGTTGCGAGGGAAG[C/T]GAGATGGCACTTTTCTTGTCCGGGAGAGCAGTAAACAGGGCTGCT
PIK3R1	649R>Q	CAGCAACCGAAACAAAGCTGAAAACCTGTTGCGAGGGAAGCGAGATGGCACTTTTCTTGTCC[G/A]GGAGAGCAGTAAACAGGGCTGCTATGCCTGCTCTGTAGTGTATG
PIK3R1	682A>V	CGAAGTAAAGCATTGTGTCATAAACAAAACAGCAACTGGCTATGGCTTTG[C/T]CGAGCCCTATAACTTGTACAGCTCTCTGAAAGAACTGGTGCTACATTAC
PIK3R1	D464H	AAAAATTACATGAATATAACACTCAGTTTCAAGAAAAAAGTCGAGAATAT[G/C]ATAGATTATATGAAGAATATACCCGCACATCCCAGGTGAGTTTTCTATGA
PIK3R1	D560_S565 del	GACAGTAGAAGAAGATTGGAAGAAGACTTGAAGAAGCAGGCAGCTGAGTATCGAGAAAT[/TGACAAACGTATGAACAG]CATTAAACCAGACCTTATCCAGCTGAGAAAGACGAGAGACCAATACTTGATGTAA
PIK3R1	D560Y	GAAGATTGGAAGAAGACTTGAAGAAGCAGGCAGCTGAGTATCGAGAAATT[G/T]ACAAACGTATGAACAGCATTAAACCAGACCTTATCCAGCTGAGAAAGACG
PIK3R1	G376R	ATTCCAAAATGTTAATACCTTTATTTTTATATTGTTTTTACAGGAAAGGG[G/A]GAAATAACAAATTAATCAAAATATTTCATCGAGATGGGAAATATGGCTTC
PIK3R1	H450_E451 del	AGGATCAAGTTGTCAAAGAAGATAATATTGAAGCTGTAGGGAAAAAATTA[/CATGAA]TATAACACTCAGTTTCAAGAAAAAAGTCGAGAATATGATAGATTATATGA
PIK3R1	K459_S460 >N	GAAGCTGTAGGGAAAAAATTACATGAATATAACACTCAGTTTCAAGAAAA[/AAG]TCGAGAATATGATAGATTATATGAAGAATATACCCGCACATCCCAGGTGA
PIK3R1	K459E	TTGAAGCTGTAGGGAAAAAATTACATGAATATAACACTCAGTTTCAAGAA[A/G]AAAGTCGAGAATATGATAGATTATATGAAGAATATACCCGCACATCCCAG

PIK3R1	L570P	AGCTGAGTATCGAGAAATTGACAAACGTATGAACAGCATTAAACCAGACC[T/C]TATCCAGCTGAGAAAGACGAGAGACCAATACTTGATGTAAGTATTTGAAA
PIK3R1	N453_T454insN	TGTCAAAGAAGATAATATTGAAGCTGTAGGGAAAAAATTACATGAATATA[/TAA]ACACTCAGTTTCAAGAAAAAAGTCGAGAATATGATAGATTATATGAAGAATA
PIK3R1	N564K	GACTTGAAGAAGCAGGCAGCTGAGTATCGAGAAATTGACAAACGTATGAA[C/G]AGCATTAAACCAGACCTTATCCAGCTGAGAAAGACGAGAGACCAATACTT
PIK3R2	345R>Q	CCAAGGAGGTGTCACAGGGTGAGCGGGGTCTCCAGGTGGCTCGGCAGTCCCAATGTTGGATGTTCCCACAGGGAGGAGGTGAACGAGAAACTCC[G/A]GGACACTCCCGATGGCACCTTCCTAGTCCGAGATGCTTCTAGCAAGATCCAGGGC
PIK3R4	655E>K	TCTTTATGCCCTTACTTGTATGTGCCAGTTAGGACTGCTACAAAAACCCCATGTTTAC[G/A]AATTTGCCAGTGATATTGGTAAGTTTCTGTTTCTCAAAATTAGAATGAGATTGGAAGAACTTTATAAAATTTCTAGGTAATATAAAGAATT
PIK3R4	1047T>M	ACATTGGTTCATAAATGAATTTTATTTTTCTTTCATTCAGATCTATTCTTACATACAGCCGAATTGGAGGACGAGTCAAGA[C/T]GCTCACATTCTGCCAAGGCTCCCACTATTTAGCCATAGCATCTGATAATGGTGCTGTCCAGCTTCTTG
PIK3R4	R936Q	AAACACCTCCCCGGCTCCCTTGGACCGACCTGACCAGGAGGTGGAGCGGC[G/A]GCTGAGGCTGAGTCCATGCAGGCAGCGTTCCAGGGCATGCTGGATGCGGT
PIK3R5	12R>H	GCAGGCGATGACCCAGGATGCAGCCAGGGGCCACGACATGCACGGAGGACC[G/A]CATCCAGCATGCCCTGGAACGCTGCCTGCATGGACTCAGCCTCAGCCGCCGCTCCACCTCCTGGTCAGCTGGGCTGTGT
PIK3R5	R28C	ACCGCATCCAGCATGCCCTGGAACGCTGCCTGCATGGACTCAGCCTCAGC[C/T]GCCGCTCCACCTCCTGGTCAGGTCGGTCCAAGGGAGCCGGGGAGGTGTTT
PRKCZ	R519C	GCTGCCGGCCACAGACTGGATTTTCTGACATCAAGTCCCACGCGTTCTTC[C/T]GCAGCATAGACTGGGACTTGGTAAAGCATCACAAAGCCTATTTGCACCCC
PRKCZ	D230N	CTCCCGGGAACCCCCCTCTCACTTTCTGGGGTCTTGTTCTCCCTCCCTAG[G/A]ACCTTAAGCCAGTTATCGATGGGATGGATGGAATCAAAATCTCTCAGGGG
PRKCZ	E574K	CCCCTGCCACCTTTGCCCACAGGGATGCCATAAAGAGGATCGACCAGTCA[G/A]AGTTCGAAGGCTTTGAGTATATCAACCCATTATTGCTGTCCACCGAGGAG

PRKCZ	R260H	CTCTCAGGGGCTTGGGCTGCAGGACTTTGACCTAATCAGAGTCATCGGGC[G/A]CGGGAGCTACGCCAAGGTTCTCCTGGTGCGGTTGAAGAAGAATGACCAAA
PRKCZ	S514F	CAAAGAGAGGCTCGGCTGCCGGCCACAGACTGGATTTTCTGACATCAAGT[C/T]CCACGCGTTCTTCCGCAGCATAGACTGGGACTTGGTAAAGCATCACAAAG
PTEN	C105W	CCTTTTGAAGACCATAACCCACCACAGCTAGAACTTATCAAACCCTTTTG[T/G]GAAGATCTTGACCAATGGCTAAGTGAAGATGACAATCATGTTGCAGCAAT
PTEN	G129*	TAAGTGAAGATGACAATCATGTTGCAGCAATTCACTGTAAAGCTGGAAAG[T/G]GACGAACTGGTGTAATGATATGTGCATATTTATTACATCGGGGCAAATTT
PTEN	R130*	GTGAAGATGACAATCATGTTGCAGCAATTCACTGTAAAGCTGGAAAGGGA[T/C]GAACTGGTGTAATGATATGTGCATATTTATTACATCGGGGCAAATTTTA
PTEN	R335*	TTACTTTAACAAAAAATGATCTTGACAAAGCAAATAAAGACAAAGCCAAC[T/C]GATACTTTTCTCCAAATTTTAAGGTGAAGCTGTACTTCACAAAAACAGTA
PTEN	A86P	AATTCAAGAGTTTTTTTTTCTTATTCTGAGGTTATCTTTTTACCACAGTT[C/G]CACAATATCCTTTTGAAGACCATAACCCACCACAGCTAGAACTTATCAAA
PTEN	C105F	TCCTTTTGAAGACCATAACCCACCACAGCTAGAACTTATCAAACCCTTTT[T/G]TGAAGATCTTGACCAATGGCTAAGTGAAGATGACAATCATGTTGCAGCAA
PTEN	C105S	ATCCTTTTGAAGACCATAACCCACCACAGCTAGAACTTATCAAACCCTTT[A/T]GTGAAGATCTTGACCAATGGCTAAGTGAAGATGACAATCATGTTGCAGCA
PTEN	C105Y	TCCTTTTGAAGACCATAACCCACCACAGCTAGAACTTATCAAACCCTTTT[A/G]TGAAGATCTTGACCAATGGCTAAGTGAAGATGACAATCATGTTGCAGCAA
PTEN	K267fs*9	TGGTGATATCAAAGTAGAGTTCTTCCACAAACAGAACAAGATGCTAAAAA[/A]GGTTTGTACTTTACTTTCATTGGGAGAAATATCCAAAATAAGGACAGATTA
PTEN	K6I	CTCCTCCTTTTTCTTCAGCCACAGGCTCCCAGACATGACAGCCATCATCA[A/T]AGAGATCGTTAGCAGAAACAAAAGGAGATATCAAGAGGATGGATTCGACT
PTEN	L25F	GTTAGCAGAAACAAAAGGAGATATCAAGAGGATGGATTCGACTTAGACTT[C/G]ACCTGTATCCATTTCTGCGGCTGCTCCTCTTTACCTTTCT

		GTCACTCTCT
PTEN	Q171*	AATTTGGCTTCTCTTTTTTTTCTGTCCACCAGGGAGTAACTATTCCCAGT[T/C]AGAGGCGCTATGTGTATTATTATAGCTACCTGTTAAAGAATCATCTGGAT
PTEN	R130G	GTGAAGATGACAATCATGTTGCAGCAATTCACTGTAAAGCTGGAAAGGGA[C/G]GAACTGGTGTAATGATATGTGCATATTTATTACATCGGGGCAAATTTTTA
PTEN	R130L	TGAAGATGACAATCATGTTGCAGCAATTCACTGTAAAGCTGGAAAGGGAC[T/G]AACTGGTGTAATGATATGTGCATATTTATTACATCGGGGCAAATTTTTAA
PTEN	R130Q	TGAAGATGACAATCATGTTGCAGCAATTCACTGTAAAGCTGGAAAGGGAC[A/G]AACTGGTGTAATGATATGTGCATATTTATTACATCGGGGCAAATTTTTAA
PTEN	R173C	GCTTCTCTTTTTTTTCTGTCCACCAGGGAGTAACTATTCCCAGTCAGAGG[T/C]GCTATGTGTATTATTATAGCTACCTGTTAAAGAATCATCTGGATTATAGA
PTEN	R173H	CTTCTCTTTTTTTTCTGTCCACCAGGGAGTAACTATTCCCAGTCAGAGGC[A/G]CTATGTGTATTATTATAGCTACCTGTTAAAGAATCATCTGGATTATAGAC
PTEN	R233*	TGGTCTGCCAGCTAAAGGTGAAGATATATTCCTCCAATTCAGGACCCACA[T/C]GACGGGAAGACAAGTTCATGTACTTTGAGTTCCCTCAGCCGTTACCTGTG
PTEN	cytogenetics	GCTGCTCTTAGGGCAGGGATCAATTCCTTAATATCTTAGGAAGACTAGGT[A/T]TTGACAGTAATGGTGACAAAGCAATGAAAAGGAAAGGAAGAAGTGATAAG
PTEN	cytogenetics	TTTTGTGATGATGAAATAAATACTATAAATAGTATTATTCCTTTTGCATT[G/T]AGAGTCCTGACGAAATGTCCATGTGACAGTTCATTTTGGGTTTAGCTCTA
PTEN	cytogenetics	CAAGGGCTGGAAGAAACCTTAGTAGTAATCTCTTTGAGTCTAATTATCAT[G/A]TAGAATAGGAAATTGCGGTCTAGAAAGGTTAAGTGACTTGTCCAAATTACACAACTAGT
PTEN	cytogenetics	ATTTAGTTTAGAACAATTTATTTCTCAAGGCCCATGTAAATATTATTTTT[A/G]AAATATACAGTCTTAAGAATTCATGGCATATTTTATGAAAGGAGGAATTC
PTEN	cytogenetics	AAGAGCCTTGTTGCGGATACCATAGTGTTTCTTTGGAGGAAAATAAAAAC[T/C]ACAAAGCTTTGTATTTTTTGCACAACTGGATTCAGAATATAAGTAATAAA

RB1	R556*	AAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACAT[C/T]GAATCATGGAATCCCTTGCATGGCTCTCAGTAAGTAGCTAAATAATTGAA
RB1	Splice Site	TAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAAC[G/A]TAAGCCATATATGAAACATTATTTATTGTAATATCTTGGCAAAGAAACTT
RB1	L199*	TACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTT[T/A]ATTAGCTAAAGGTAAGTTCATTATATTTATTAAATGCTAATATTTCAAAT
RB1	R320*	AGGATAATTGTCAGTGACTTTTTTCTTTCAAGGTTGAAAATCTTTCTAAA[C/T]GATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTT
RB1	R455*	TTCTTTTTGTTTGTTTGTAGCGATACAAACTTGGAGTTCGCTTGTATTAC[C/T]GAGTAATGGAATCCATGCTTAAATCAGTAAGTTAAAAACAATATAAAAAA
RB1	R552*	TTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAA[C/T]GATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGTAAGTAGC
RB1	R579*	GTTTCATATAGGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGAC[C/T]GAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCT
RET	A664D	CGTCTCGGTGCTGCTGTCTGCCTTCTGCATCCACTGCTACCACAAGTTTG[A/C]CCACAAGCCACCCATCTCCTCAGCTGAGATGACCTTCCGGAGGCCCGCCC
RET	M918T	CAATGTCTTTATTCCATCTTCTCTTTAGGGTCGGATTCCAGTTAAATGGA[T/C]GGCAATTGAATCCCTTTTTGATCATATCTACACCACGCAAAGTGATGTGT
RET	R163Q	CTTCTCCTTCTTCAACACCTCCTTTCCAGCCTGCAGCTCCCTCAAGCCCC[A/G]GGAGCTCTGCTTCCCAGAGACAAGGCCCTCCTTCCGCATTCGGGAGAACC
RET	R360W	GCAGCTTGGTGGTCATTGTTGTGCCCCTACCTGCAGGGCTGGTTCTCAAC[T/C]GGAACCTCTCCATCTCGGAGAACCGCACCATGCAGCTGGCGGTGCTGGTC
RET	V145G	ACCCACATCCCTTCGTGAGGGCGAGTGCCAGTGGCCAGGCTGTGCCCGCG[T/G]ATACTTCTCCTTCTTCAACACCTCCTTTCCAGCCTGCAGCTCCCTCAAGC
RPS6KA2	Splice Site	ACGTCCTGTGCACCATCACCAAGACCATGGACTACCTCCATTCCCAGGGG[G/A]TAGGAGCCATGCCTGGGGCAGCCTTCGGGGAGGAGGG

		AGCTTCAGGGCAG
RPS6KA2	E311K	TGATGATCATTTCTGTGTTGTTGACAGGTGCTGGCATTGACGGAGTGGAG[G/A]AAATTAAGCGCCATCCCTTCTTTGTGACCATAGACTGGAACGTAAGTTGC
RPS6KA2	R732Q	GTCATCCAACCTGGCTCAGCGCAGAGGCATGAAGAGACTCACGTCCACGC[G/A]GCTGTAGCGGGTGGGACCCTGGCCCCAGCGTCCCCTGCCAGCATCCTCGT
RPS6KA2	S427*	CTTCACCGATGGCTACGAGATCAAGGAGGACATCGGGGTGGGCTCCTACT[C/G]AGTGTGCAAGCGATGTGTGCATAAAGCCACAGACACCGAGTATGCCGTGA
RPS6KA3	I416V	GGGACTCTTCACCAATTTATAATTTTTTGTAGCAGTTACACAGGAACAGT[A/G]TTCAGTTTACTGATGGATATGAAGTAAAAGAAGATATTGGAGTTGGCTCC
RPS6KA3	L381H	ACTCTTTTCAGATTCACCTGGCATTCCACCTAGTGCTAATGCACATCAGC[T/A]TTTTCGGGGGTTTAGTTTTGTTGCTATTACCTCAGATGATGAAAGCCAAG
RPS6KA3	L608F	AAAGACAAGGCTATGATGCTGCTTGTGATATATGGAGTCTTGGTGTCCTA[C/T]TCTATACAATGCTTACCGGGTGAGTGTATACCATATGTTCTAAGCACCTA
RPS6KA3	Y483C	CATATAGTTTCAAATAATATTTACATTTTGATGTTGAAATTTATAGGTAT[A/G]TGATGATGGAAAGTATGTGTATGTAGTAACAGAACTTATGAAAGGAGGTG
RPS6KB1	G289E	TGCTGTGGATTGGTGGAGTTTGGGAGCATTAATGTATGACATGCTGACTG[G/A]AGCAGTAGGTGCACAGTTAAAAGCTGCATGTATTATTGGTCTGTGCTGAG
SMAD4	D351N	AGGTAGGAGAGACATTTAAGGTTCCTTCAAGCTGCCCTATTGTTACTGTT[G/A]ATGGATACGTGGACCCTTCTGGAGGAGATCGCTTTTGTTTGGGTCAACTC
SMAD4	G386R	CAAGATAAAATGTAATTTCTTTTTTCTTCCTAAGGTTGCACATAGGCAAA[G/C]GTGTGCAGTTGGAATGTAAAGGTGAAGGTGATGTTTGGGTCAGGTGCCTT
SMAD4	H132L	TCAGTATGCGTTTGACTTAAAATGTGATAGTGTCTGTGTGAATCCATATC[A/T]CTACGAACGAGTTGTATCACCTGGAATTGGTAAGTAGACTTTGCTTTCAT
SMAD4	P130S	AATATTGTCAGTATGCGTTTGACTTAAAATGTGATAGTGTCTGTGTGAAT[C/T]CATATCACTACGAACGAGTTGTATCACCTGGAATTGGTAAGTAGACTTTG

SMAD4	R361C	GCTGCCCTATTGTTACTGTTGATGGATACGTGGACCCTTCTGGAGGAGAT[C/T]GCTTTTGTTTGGGTCAACTCTCCAATGTCCACAGGACAGAAGCCATTGAG
SMAD4	R445*	TAGTATGAAATGTTTTTTCTTAAAAGGTCTTTGATTTGCGTCAGTGTCAT[C/T]GACAGATGCAGCAGCAGGCGGCTACTGCACAAGCTGCAGCAGCTGCCCAG
SMAD4	W323fs*11	CTCATGGGAGGATGTTCTTTCCCATTTATTTCCTATAGCTCCTGAGTATT[/GGTGTTC]CATTGCTTACTTTGAAATGGATGTTCAGGTAGGAGAGACATTTAAGGTTC
SMAD4	Y353C	AGAGACATTTAAGGTTCCTTCAAGCTGCCCTATTGTTACTGTTGATGGAT[A/G]CGTGGACCCTTCTGGAGGAGATCGCTTTTGTTTGGGTCAACTCTCCAATG
SMG1	D2416V	AGCAGCAGCTTGCCTTCCAGGATTTTATACCAAGCTGGCCCCCTACCACC[A/T]CAAGATGTCAACATTCCTTTTTTTAATAGAAGATTTTCTTTTATTGTGGG
SMG1	I3235T	GGAAGGAAGATCTGGCAAAACACACCTGAACTGTTGCAATAGAAGTTTCA[A/G]TCTGGCTCAGGGTATGCAGCTTCTTTTTCATGCTGGTTAGGATAGCAGAC
SMG1	K3579Q	CCCAGTTTTAGGGTCTCTGACTGCCTTTTTAGGACTACAAGCAACACTCT[T/G]GCCAGTTCCTGGAACGGTGCTTGGTGGAGTATCAGCTGATGTAGCAAGAT
SMG1	Q1978*	GCGTAAGGTGTTGTTGTTCTGGACTCTCTTCACCTCATCTTCAAGCTGCT[G/A]AATTCGTCTCAGGACATACATGTGTTGTTGCAGCAAAACTCCCAGCCAGA
SMG1	S2167C	ACCGGGGTGTTTCTTGGCGATTAATTGTAGCAAACATGGTATTCACAATA[G/C]ATAGGAACTGCATTATTCTCTCATCCAGATGTAAATCCTCCAGTCCTATG
SMO	R199W	TGCAGAACATCAAGTTCAACAGTTCAGGCCAGTGCGAAGTGCCCTTGGTT[C/T]GGACAGACAACCCCAAGAGCTGGTACGAGGACGTGGAGGGCTGCGGCATC
SMO	V404M	GTGGGATTTGTTTTGTGGGCTACAAGAACTACCGATACCGTGCGGGCTTC[G/A]TGCTGGCCCCAATCGGCCTGGTGCTCATCGTGGGAGGCTACTTCCTCATC
SMO	A324T	GCTCCAATGAGACTCTGTCCTGCGTCATCATCTTTGTCATCGTGTACTAC[G/A]CCCTGATGGCTGGTGTGGTTTGGTTTGTGGTCCTCACCTATGCCTGGCAC
SMO	A652V	CCCCAGGCTCGTGTTGTCTCTCCTCCTGTCAGTGCCCCCAGAGGAACAAG[C/T]CAACCTGTGGCTGGTTGAGGCAGAGATCTCCCCAGAGCTGCAGAAGCGCC
SMO	C78_L79>C	AGCCACTGCGGCCGGGCTGCCCCCTGCGAGCCGCTGCGCTACAACGTGTG[C/T]NTGGGCTCGGTGCTGCCCTACGGGGCCACCTCCACA

	L	CTGCTGGCCGGAGAC
SMO	D473H	GCTTCCTGGCCTTTGGCTTTGTGCTCATTACCTTCAGCTGCCACTTCTAC[G/C]ACTTCTTCAACCAGGCTGAGTGGGAGCGCAGCTTCCGGGACTATGTGCTG
SMO	K575M	TGAGCCAAAGCGGATCAAGAAGAGCAAGATGATTGCCAAGGCCTTCTCTA[A/T]GCGGCACGAGCTCCTGCAGAACCCAGGCCAGGAGCTGTCCTTCAGCATGC
SMO	L514F	CTGCCCACCAAGCAGCCCATCCCTGACTGTGAGATCAAGAATCGCCCGAG[C/T]NTCTGGTGGAGAAGATCAACCTGTTTGCCATGTTTGGAACTGGCATCGCC
SMO	R484W	AGCTGCCACTTCTACGACTTCTTCAACCAGGCTGAGTGGGAGCGCAGCTT[C/T]NGGGACTATGTGCTGTGAGTGAGGGGCATGGAGGCGGCAGTGCTGGGAGCT
SMO	R562Q	TATCCCTTCTGCTCTCAGGTTGACTGGGCAGAGTGACGATGAGCCAAAGC[G/A]GATCAAGAAGAGCAAGATGATTGCCAAGGCCTTCTCTAAGCGGCACGAGC
SMO	S533N	GGTGGAGAAGATCAACCTGTTTGCCATGTTTGGAACTGGCATCGCCATGA[G/A]CACCTGGGTCTGGACCAAGGCCACGCTGCTCATCTGGAGGCGTACCTGGT
SMO	T349I	TGTGGTCCTCACCTATGCCTGGCACACTTCCTTCAAAGCCCTGGGCACCA[C/T]NTACCAGCCTCTCTCGGGCAAGACCTCCTACTTCCACCTGCTCACCTGGTC
SMO	T640A	CCAAGATGGTGGCTCGGAGAGGAGCCATACTGCCCCAGGATATTTCTGTC[A/G]CCCCTGTGGCAACTCCAGGTATGAGAGTTCAAGCTTCTGGAGGAAGGTGG
SMO	W535L	GAAGATCAACCTGTTTGCCATGTTTGGAACTGGCATCGCCATGAGCACCT[G/T]GGTCTGGACCAAGGCCACGCTGCTCATCTGGAGGCGTACCTGGTGCAGGT
STK11	D194Y	TCAAGCCGGGGAACCTGCTGCTCACCACCGGTGGCACCCTCAAAATCTCC[T/G]ACCTGGGCGTGGCCGAGGTAGGCACGTGCTAGGGGGGGCCCTGGGGCGCC
STK11	G171S	GCAGGTACTTCTGTCAGCTGATTGACGGCCTGGAGTACCTGCATAGCCAG[A/G]GCATTGTGCACAAGGACATCAAGCCGGGGAACCTGCTGCTCACCACCGGT
STK11	F354L	GTGCCGTACTTGGAGGACCTGCACGGCGCGGACGAGGACGAGGACCTCTT[C/G]GACATCGAGGATGACATCATCTACACTCAGGACTTCACGGTGCCCGGTGA
STK11	E57fs*7	GCAAGCGGGCCAAGCTCATCGGCAAGTACCTGATGGGGGACCTGCTGGGG[/G]AAGGCTCTTACGGCAAGGTGAAGGAGGTGCTGGACTCGGAGACGCTGTGC
STK11	F354L	GTGCCGTACTTGGAGGACCTGCACGGCGCGGACGAGGACGAGGACCTCTT[C/G]GACATCGAGGATGACATCATCTACACTCAGGACTTCA

		CGGTGCCCGGACA
STK11	P281fs	TTGTTTGAGAACATCGGGAAGGGGAGCTACGCCATCCCGGGCGACTGTGGCCCCC[/C]GCTCTCTGACCTGCTGAAAGGTGGGAGCCTCATCCCTCTGCCCGC
STK11	P281L	TGAGAACATCGGGAAGGGGAGCTACGCCATCCCGGGCGACTGTGGCCCCC[T/C]GCTCTCTGACCTGCTGAAAGGTGGGAGCCTCATCCCTCTGCCCGCAGCCC
STK11	P281L	TGAGAACATCGGGAAGGGGAGCTACGCCATCCCGGGCGACTGTGGCCCCC[T/C]GCTCTCTGACCTGCTGAAAGGTGGGAGCCTCATCCCTCTGCCCGCAGCCC
STK11	Q170*	CCCGCAGGTACTTCTGTCAGCTGATTGACGGCCTGGAGTACCTGCATAGC[T/C]AGGGCATTGTGCACAAGGACATCAAGCCGGGGAACCTGCTGCTCACCACC
STK11	Q37*	TGGGTATGGACACGTTCATCCACCGCATCGACTCCACCGAGGTCATCTAC[T/C]AGCCGCGCCGCAAGCGGGCCAAGCTCATCGGCAAGTACCTGATGGGGGAC
STK11	W332*	GCTGAAGCACCAGTGCCCATCCCACCGAGCCCAGACACCAAGGACCGGTG[A/G]CGCAGCATGACTGTGGTGCCGTACTTGGAGGACCTGCACGGCGCGGACGA
TBX22	A51T	AGCTGCGGGAGAAAAAGGGCGGAGAGGAAGAGGAGGAGAGAAGGAGCAGC[G/A]CTGCAGGGAAGAGCGAGCCGCTTGGTAAGTACTGCCATTGCCCTGAGCCC
TBX22	D307N	TATTGGATGGGCTTTTAGAGACCTACCCATGGAGGCCTTCTTTCACTCTC[G/A]ATTTTAAAACCTTTGGCGCAGACACACAAAGTAAGAAAACTTGGAACGTT
TBX22	P411T	TAGCAAGCAGCAACAGTTCTCAGTCTTTAGCCCCACTCATGATGGAAGTG[C/A]CTATGTTATCTTCCCTGGGGGTCACCAATTCAAAAAGCGGTTCATCTGAA
TBX22	V12M	CTTCACCCCCTCCAGGGATGGCTCTGAGCTCTCGGGCGCGTGCCTTCTCC[G/A]TGGAAGCCTTGGTGGGGAGACCCAGCAAAAGAAAACTCCAAGACCCAATA
TBX22	V16A	AGGGATGGCTCTGAGCTCTCGGGCGCGTGCCTTCTCCGTGGAAGCCTTGG[T/C]GGGGAGACCCAGCAAAAGAAAACTCCAAGACCCAATACAGGCGGAGCAGC
TP53	R213*	GAGTGGAAGGAAATTTGCGTGTGGAGTATTTGGATGACAGAAACACTTTT[T/C]GACATAGTGTGGTGGTGCCCTATGAGCCGCCTGAGGTCTGGTTTGCAACT
TP53	R248L	CATCCACTACAACTACATGTGTAACAGTTCCTGCATGGGCGGCATGAACC[T/G]GAGGCCCATCCTCACCATCATCACACTGGAAGACTCCAGGTCAGGAGCCA
TP53	R342*	CTCCTTCCCAGCCTGGGCATCCTTGAGTTCCAAGGCCTCATTCAGCTCTC[A/G]GAACATCTCGAAGCGCTCACGCCCACGGATCTGCAGCA

		ACAGAGGAGGGG
TP53	Y220C	GGAGTATTTGGATGACAGAAACACTTTTCGACATAGTGTGGTGGTGCCCT[A/G]TGAGCCGCCTGAGGTCTGGTTTGCAACTGGGGTCTCTGGGAGGAGGGGTT
TP53	cytogenetics	TTAAAGGACCAGACCAGCTTTCAAAAAGAAAATTGTTAAAGAGAGCATGA[A/T]AATGGTTCTATGACTTTGCCTGATACAGATGCTACTTGACTTACGATGGT
TP53	cytogenetics	CCATCTCAGCTCACTGCAGCCTTGACCTCCCTGGGCTCCGGTGATTTCAC[C/A]CTCCCAAGTAGCTAGGACTACAGGCACATGCCACGACACCCAGCTAATTT
TP53	cytogenetics	AGTGCTGGGATTACAGGCGTGAGCCACTGCACCTGCCTAGCCTATACTAA[G/A]TTCTCTAAAATCTGGCAAGGCAAATAGGACCCCCTCTCCATTCTGTTGCT
TP53	E204*	ATAGGGCACCACCACACTATGTCGAAAAGTGTTTCTGTCATCCAAATACT[A/C]CACACGCAAATTTCCTTCCACTCGGATAAGATGCTGAGGAGGGGCCAGAC
TP53	E224D	GACAGAAACACTTTTCGACATAGTGTGGTGGTGCCCTATGAGCCGCCTGA[T/G]GTCTGGTTTGCAACTGGGGTCTCTGGGAGGAGGGGTTAAGGGTGGTTGTC
TP53	E298*	CGCTTCTTGTCCTGCTTGCTTACCTCGCTTAGTGCTCCCTGGGGGCAGCT[A/C]GTGGTGAGGCTCCCCTTTCTTGCGGAGATTCTCTTCCTCTGTGCGCCGGT
TP53	G245S	ACTGTACCACCATCCACTACAACTACATGTGTAACAGTTCCTGCATGGGC[A/G]GCATGAACCGGAGGCCCATCCTCACCATCATCACACTGGAAGACTCCAGG
TP53	G245V	CTGTACCACCATCCACTACAACTACATGTGTAACAGTTCCTGCATGGGCG[T/G]CATGAACCGGAGGCCCATCCTCACCATCATCACACTGGAAGACTCCAGGT
TP53	P309S	TCCATCCAGTGGTTTCTTCTTTGGCTGGGGAGAGGAGCTGGTGTTGTTGG[A/G]CAGTGCTAGGAAAGAGGCAAGGAAAGGTGATAAAAGTGAATCTGAGGCAT
TP53	R158L	GCCTCACAACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGCCATGGCG[A/C]GGACGCGGGTGCCGGGCGGGGGTGTGGAATCAACCCACAGCTGCACAGGG
TP53	R175H	CGCCATGGCCATCTACAAGCAGTCACAGCACATGACGGAGGTTGTGAGGC[A/G]CTGCCCCCACCATGAGCGCTGCTCAGATAGCGATGGTGAGCAGCTGGGG
TP53	R196*	AAAAGTGTTTCTGTCATCCAAATACTCCACACGCAAATTTCCTTCCACTC[A/G]GATAAGATGCTGAGGAGGGGCCAGACCTAAGAGCAATCAGTGAGGAATCA
TP53	R213Q	AGTGGAAGGAAATTTGCGTGTGGAGTATTTGGATGACAGAAACACTTTTC[A/G]ACATAGTGTGGTGGTGCCCTATGAGCCGCCTGAGGTCT

		GGTTTGCAACTG
TP53	R248Q	TGGCTCCTGACCTGGAGTCTTCCAGTGTGATGATGGTGAGGATGGGCCTC[A/G]GGTTCATGCCGCCCATGCAGGAACTGTTACACATGTAGTTGTAGTGGATG
TP53	R248W	GGCTCCTGACCTGGAGTCTTCCAGTGTGATGATGGTGAGGATGGGCCTC[T/C]GGTTCATGCCGCCCATGCAGGAACTGTTACACATGTAGTTGTAGTGGATGG
TP53	R273C	TTCCTATCCTGAGTAGTGGTAATCTACTGGGACGGAACAGCTTTGAGGTG[T/C]GTGTTTGTGCCTGTCCTGGGAGAGACCGGCGCACAGAGGAAGAGAATCTC
TP53	R273H	TCCTATCCTGAGTAGTGGTAATCTACTGGGACGGAACAGCTTTGAGGTGC[A/G]TGTTTGTGCCTGTCCTGGGAGAGACCGGCGCACAGAGGAAGAGAATCTCC
TP53	R273L	TCCTATCCTGAGTAGTGGTAATCTACTGGGACGGAACAGCTTTGAGGTGC[T/G]TGTTTGTGCCTGTCCTGGGAGAGACCGGCGCACAGAGGAAGAGAATCTCC
TP53	R306*	AACTGCACCCTTGGTCTCCTCCACCGCTTCTTGTCCTGCTTGCTTACCTC[A/G]CTTAGTGCTCCCTGGGGGCAGCTCGTGGTGAGGCTCCCCTTTCTTGCGGA
TP53	S166*	AGCAGCGCTCATGGTGGGGGCAGCGCCTCACAACCTCCGTCATGTGCTGT[T/G]ACTGCTTGTAGATGGCCATGGCGCGGACGCGGGTGCCGGGCGGGGGTGTG
TP53	S241F	CCAGTGTGATGATGGTGAGGATGGGCCTCCGGTTCATGCCGCCCATGCAG[A/G]AACTGTTACACATGTAGTTGTAGTGGATGGTGGTACAGTCAGAGCCAACC
TP53	V157F	CACAACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGCCATGGCGCGGA[A/C]GCGGGTGCCGGGCGGGGGTGTGGAATCAACCCACAGCTGCACAGGGCAGG
TP53	V272M	ATTCTCTTCCTCTGTGCGCCGGTCTCTCCCAGGACAGGCACAAACACGCA[T/C]CTCAAAGCTGTTCCGTCCCAGTAGATTACCACTACTCAGGATAGGAAAAG
TP53	Y126*	ACAGGGCAGGTCTTGGCCAGTTGGCAAAACATCTTGTTGAGGGCAGGGGA[T/G]TACTGTAGGAAGAGGAAGGAGACAGAGTTGAAAGTCAGGGCACAAGTGAA
WNK2	A1253T	TGAAGGATGTCATGGACAAGGCAGAGGACATGCTCAGCGAGGACACAGAC[G/A]CCGACCGTGGCTCCGACCCAGGGACCAGCCCGCCACACCTCAGCACCTGC
WNK2	G1619E	TTTGTGTTTCTTTCTCCAGGTGGAGAAGTCAGAACTGGCCCCCACTCGAG[G/A]GGCCGTGATGGAGCAGGGCACGTCCTCGTCAATGACAGGTAACAGCTTCC
WNK2	S1373fs*5	CAGGCGGGCCCCAGCAACCCTCCTGGGGCACCCCCAGCCCCTTTGGCCCC[/C]TCCTCCCCTCCTGTGACTGCTCTGCCCCAAGATGGAGC

		AGCTCCAGCCAC
WNK2	S1978I	CTTGGCTGACTCCAGCAGAGGCCCTCCCGCTAAGGACCCTGCCCAAGCCA[G/T]TGTGGGGCTCACTGCAGACAGCACGGGCCTGAGCGGGAAGGCAGTGCAGA
WNK2	T2215fs*31	GGCGCCCTCGGAACCGCCCGGAGAAACCAGGTGTGGTTTGGCCTCCGAGT[/C]CCCCCCACCGCCTGCTGTGGGCACAGCACTCAGCCGCGAGGGGGACAGCG
WNK2	V496L	ATGGAGCCATAGAGTTCACCTTCGACCTGGAGAAGGAGACGCCGGATGAG[G/T]TGGCCCAAGAGATGGTAAGCAGGACTCAGATGGGGTGAGGTGGGTGCAGG
ZNF668	G286S	GCCACGAGCGCACGCACTCGGGGGAGAAGCCCTTCCTGTGCCCGCGCTGC[G/A]GCCGCATGTTCTCCGACCCCTCGAGCTTCCGTCGCCACCAGCGCGCCCAT
ZNF668	A66T	GCTCTGAAGAGGTGGCCGAGGTGAAGCCAAAGCCAGAGACAGAAGCTAAG[G/A]CAGAGGAAGCCAGTGGGGAGAAGGTGTCAGGCTCCGCGGCCAAGCCTAGG
ZNF668	R556Q	GGAGCTCCGGCCCTTCCCCTGCACCCAGTGCGGCAAGAGCTTCTCTGACC[G/A]GGCTGGGCTGCGCAAACACAGCCGCACTCACAGCTCAGTGCGCCCCTACA
ZNF668	T331R	CAAGGACTTCCGGCAGCCGGCGGACCTGGCCATGCACCGGCGTGTGCACA[C/G]AGGCGACCGGCCGTTCAAGTGCCTGCAATGTGACAAGACGTTCGTGGCGT

Supplemental Table 4: Sequenom Panel Gene List

Sequenom Assay	Forward PCR Primer	Reverse PCR prime	Extension Primer
AKT1_G173R_G517C	ACGTTGGATGTGATCCTGGTGAAGGAGAAG	ACGTTGGATGTCCTTGGCCACGATGACTTC	GGTGAAGGAGAAGGCCACA
AKT1_K179M_A536T	ACGTTGGATGTGATCCTGGTGAAGGAGAAG	ACGTTGGATGTCCTTGGCCACGATGACTTC	CGCTACTACGCCATGA
AKT2_E17K_G49A	ACGTTGGATGCTTCAGCAGGAAGTACCGTG	ACGTTGGATGCACTCAACCTTGTCCTAACC	CCTCCAGGTCTTGATGTATT
AKT2_G175R_G523C	ACGTTGGATGTTGGCAAAGTCATCCTGGTG	ACGTTGGATGATGATGACTTCCTTCCGCAG	TGGTGCGGGAGAAGGCCACT
AKT3_G171R_G511A	ACGTTGGATGTAGGTAAAGGCACTTTTGGG	ACGTTGGATGTCTTCAGAATCTTCATAGC	TCGAGAGAAGGCAAGT
ALK_F1174LIV_T3520CAG	ACGTTGGATGAAGATTTGCCCAGACTCAGC	ACGTTGGATGTGCAGCGAACAATGTTCTGG	GGATCTCTGCTCTGCAGCAAA
ALK_F1174L_C3522AG	ACGTTGGATGTTGGTTACATCCCTCTCTGC	ACGTTGGATGATTGCAGGCTCACCCCAATG	CATCCCTCTCTGCTCTGCAGCAAATT
ALK_F1245C_T3734G	ACGTTGGATGATGACAGGAAGAGCACAGTC	ACGTTGGATGCCTGTGGCTGTCAGTATTTG	TCACTTTGACTCACCGGTGGATG
ALK_F1245VI_T3733GA	ACGTTGGATGCCTGTGGCTGTCAGTATTTG	ACGTTGGATGATGACAGGAAGAGCACAGTC	TCAGTATTTGGAGGAAAACCAC
ALK_I1171N_T3512A	ACGTTGGATGACCTCTCCAGGTTCTTTGGG	ACGTTGGATGCTGGATTTCCTCATGGAAGC	GCTCTCTGTGGCTTTACCTG
ALK_R1275QL_G3824AT	ACGTTGGATGTGAGGCAGTCTTTACTCACC	ACGTTGGATGAAGAGTGGCCAAGATTGGAG	CTTTACTCACCTGTAGATGTCT
BRAF_D594GV_A1781GT	ACGTTGGATGTTCAAACTGATGGGACCCAC	ACGTTGGATGTCTTCATGAAGACCTCACAG	TTCACTGTAGCTAGACCAAAA
BRAF_E586K_G1756A	ACGTTGGATGCCACTCCATCGAGATTTCAC	ACGTTGGATGCCTTTACTTACTACACCTCAG	CCTATTTTTACTGTGAGGTCTT
BRAF_G464EVA_G1391ATC	ACGTTGGATGTACCATGCCACTTTCCCTTG	ACGTTGGATGTCCTGATGGGCAGATTACAG	AGATTACAGTGGGACAAAGAATTG
BRAF_G466EVA_G1397ATC	ACGTTGGATGTACCATGCCACTTTCCCTTG	ACGTTGGATGTCCTGATGGGCAGATTACAG	CCTTGTAGACTGTTCCAAATGAT
BRAF_G466R_G1396CA	ACGTTGGATGTACCATGCCACTTTCCCTTG	ACGTTGGATGTCCTGATGGGCAGATTACAG	ACCTTGTAGACTGTTCCAAATGATC
BRAF_G469EVA_G1406ATC	ACGTTGGATGTCCTGATGGGCAGATTACAG	ACGTTGGATGTACCATGCCACTTTCCCTTG	ACAGAATTGGATCTGGATCATTTG
BRAF_G469R_G1405CA	ACGTTGGATGTCCTGATGGGCAGATTACAG	ACGTTGGATGTACCATGCCACTTTCCCTTG	AGAATTGGATCTGGATCATTT
BRAF_K601E_A1801G	ACGTTGGATGTTCAAACTGATGGGACCCAC	ACGTTGGATGTCTTCATGAAGACCTCACAG	GACCCACTCCATCGAGATT
BRAF_L597R_T1790G	ACGTTGGATGTCTTCATGAAGACCTCACAG	ACGTTGGATGTTCAAACTGATGGGACCCAC	GTAAAAATAGGTGATTTTGGTC
BRAF_V600EAG_T1799ACG_F	ACGTTGGATGTCTTCATGAAGACCTCACAG	ACGTTGGATGTTCAAACTGATGGGACCCAC	AGGTGATTTTGGTCTAGCTACAG
BRAF_V600LM_G1798TA	ACGTTGGATGTCTTCATGAAGACCTCACAG	ACGTTGGATGTTCAAACTGATGGGACCCAC	TAGGTGATTTTGGTCTAGCTACA
BRAF_V600_G1800	ACGTTGGATGTTCAAACTGATGGGACCCAC	ACGTTGGATGTCTTCATGAAGACCTCACAG	ACCCACTCCATCGAGATTT
CDK4_R24H_G71A	ACGTTGGATGACTCTCACACTCTTGAGGGC	ACGTTGGATGAATTGGTGTCGGTGCCTATG	GGCCACTGTGGGGATCA
CTNNB1_D32HNY_G94CAT	ACGTTGGATGAAAGCGGCTGTTAGTCACTG	ACGTTGGATGTTACCACTCAGAGAAGGAGC	GAGCAACAGTCTTACCTG
CTNNB1_G34EV	ACGTTGGATGACTGGCA	ACGTTGGATGGCCTTTA	GTCTTACCTGGACTC

A_G101ATC	GCAACAGTCTTAC	CCACTCAGAGAAG	TG
CTNNB1_S33APT_T97GCA	ACGTTGGATGGCCTTTACCACTCAGAGAAG	ACGTTGGATGACTGGCAGCAACAGTCTTAC	GTCACCAGAATGGATTCCAG
CTNNB1_S37APT_T109GCA	ACGTTGGATGGCCTTTACCACTCAGAGAAG	ACGTTGGATGACTGGCAGCAACAGTCTTAC	GTGGTAGTGGCACCAG
CTNNB1_S37CFY_C110GTA	ACGTTGGATGACTGGCAGCAACAGTCTTAC	ACGTTGGATGGCCTTTACCACTCAGAGAAG	CTGGACTCTGGAATCCATT
CTNNB1_S45APT_T133GCA	ACGTTGGATGTCTGGAATCCATTCTGGTGC	ACGTTGGATGGTATCCACATCCTCTTCCTC	GCCACTACCACAGCTCCT
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EGFR_G719_G2155TA	ACGTTGGATGGAGGATCTTGAAGGAAACTG	ACGTTGGATGCCTTACCTTATACACCGTGC	TTCAAAAAGATCAAAGTGCTG
EGFR_K860I_A2579T	ACGTTGGATGATTCTTTCTCTTCCGCACCC	ACGTTGGATGACGTACTGGTGAAAACACCG	CTCTTCCGCACCCAGCAGT
EGFR_L858R_T2573G	ACGTTGGATGACGTACTGGTGAAAACACCG	ACGTTGGATGATTCTTTCTCTTCCGCACCC	GTCAAGATCACAGATTTTGGGC
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MET_R988C_C2962T	ACGTTGGATGCTCTGTTTTAAGATCTGGGC	ACGTTGGATGGCCTATCCAAATGAGGAGTG	ATCTGGGCAGTGAATTAGTT
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Supplemental Table 5: PK/PD Analysis of 1,5-AG

Values for 1,5-anhydroglucitol (1,5-AG) were obtained on Week 3 (W3) and Week 5 (W5) while serial samples for pharmacokinetics (PK) were obtained on W2 and W4. The 1,5-AG percent change from baseline from W3 and W5 was assessed with PK parameters from W2 and W4, respectively. The comparisons will be referred to by PK weeks.

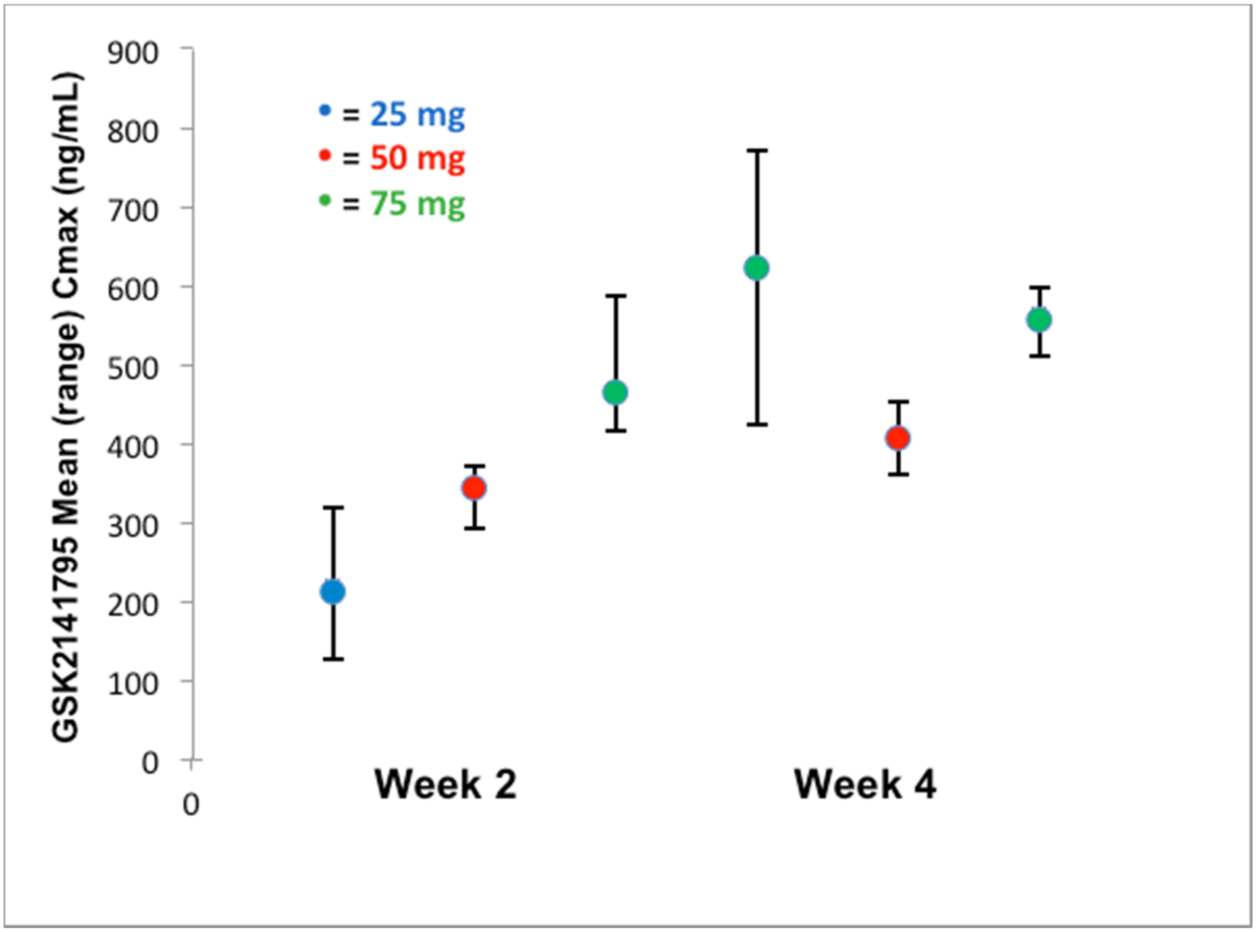
The relationship between 1,5-AG percent change from baseline and PK parameters were evaluated at W2 and W4 separately. 3 subjects did not have either a PK parameter and/or a 1,5-AG value on W4. Therefore, a third analyses was completed called Week 4/2 (W4/2). In the W4/2 analysis, W4 values were included for those subjects with W4 values and W2 values were included for the 3 subjects without W4 values.

Linear Regression Results

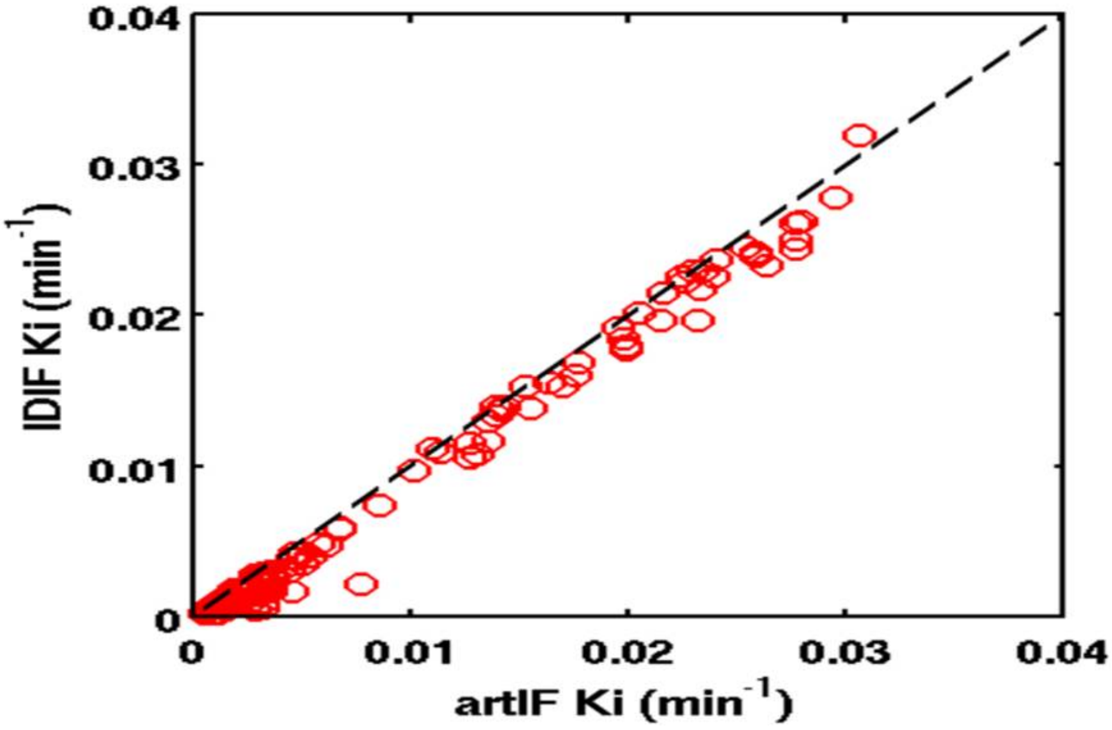
Pharmacokinetic Parameter	Slope (SE) [p-value]	Intercept (SE)	r^2
Week 3 1,5-AG Percent Change from Baseline/ Week 2 PK Parameter			
Ct(pre-dose) (ng/mL)	-0.0613 (0.0376) [0.1415]	12.457 (10.634)	0.2496
Cmax (ng/mL)	-0.0535 (0.0325) [0.1386]	14.710 (11.826)	0.2528
AUC(0-5) (ng*h/mL)	-0.0144 (0.0077) [0.0992]	16.586 (11.495)	0.303
Week 5 1,5-AG Percent Change from Baseline/ Week 4 PK Parameter			
Ct(pre-dose) (ng/mL)	-0.2762 (0.0536) [0.0021]	80.159 (22.062)	0.8156
Cmax (ng/mL)	-0.2446 (0.0629) [0.0081]	100.28 (34.117)	0.7161
AUC(0-5) (ng*h/mL)	-0.0594 (0.0155) [0.0086]	97.13 (33.752)	0.7108
Week 5/3 1,5-AG Percent Change from Baseline/ Week 4/2 PK Parameter			
Ct(pre-dose) (ng/mL)	-0.2583 (0.0434) [0.0002]	73.382 (16.436)	0.7975
Cmax (ng/mL)	-0.2124 (0.0420) [0.0007]	81.673 (20.880)	0.7393
AUC(0-5) (ng*h/mL)	-0.0559 (0.0106) [0.0005]	88.883 (21.368)	0.7549

Abbreviations: 1,5-AG, 1,5-anhydroglucitol; AUC, area under the concentration-time curve; Cmax, maximum observed concentration; pre-dose concentration; SE, standard error, W2, Week2, W4, Week 4, W4/2, Week 4/2

Supplemental Figure 1: Mean plasma maximal concentrations (Cmax) of GSK2141795 at various doses at Week 2 and Week 4. Plot represent GSK2141795 mean (min, max) plasma Cmax at Week 2 (3 circles on the left) and Week 4 (3 circles on the right). Each circle represents a cohort per week at a specific dose; blue = 25 mg, red = 50 mg, and green = 75 mg. This plot clearly shows the overlap of Cmax for the various doses and a lack of a relationship between dose-plasma Cmax.



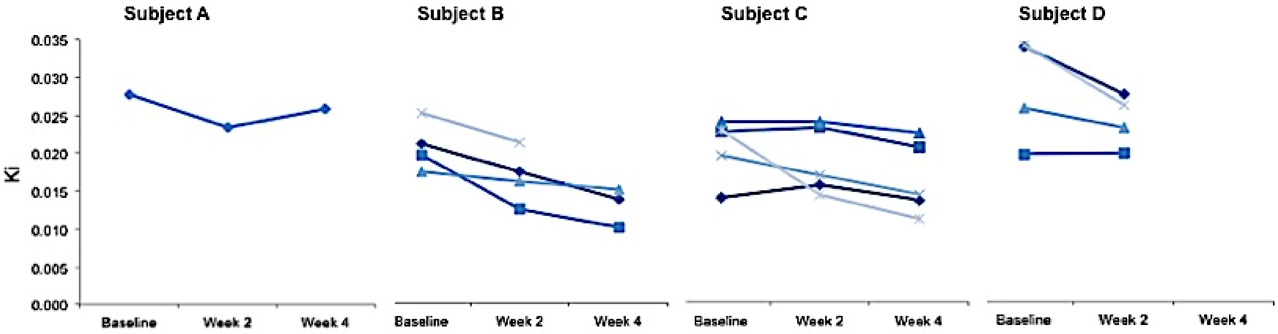
Supplemental Figure 2: AIF versus IDF. Scatter plot of Ki values for each tumor in each patient enrolled in Cohort 1. The solid line is a reference line with slope = 1.



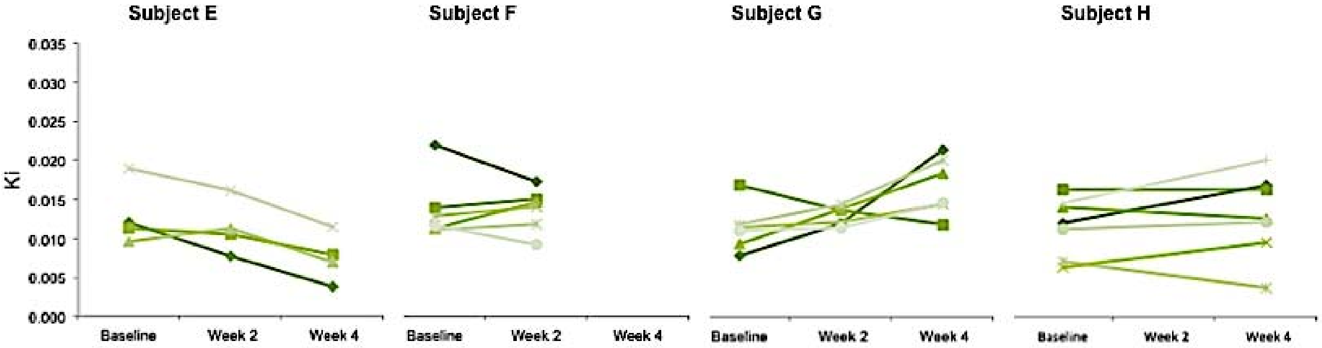
Supplemental Figure 3: FDG uptake parameter Ki Values over Time. Each patient is represented in an individual panel with individual tumors represented by separate lines. The X axis represents the time points (baseline, Week 2 and Week 4) at which the parameter Ki [(mL of plasma/mL of tissue)/min were determined. Subjects were treated with 50 mg for 4 weeks (A), 75 mg for 4 weeks (B) and 25 mg for 2 weeks and 75 mg thereafter (C).

Individual patient profiles over time – Ki from tumor tissue

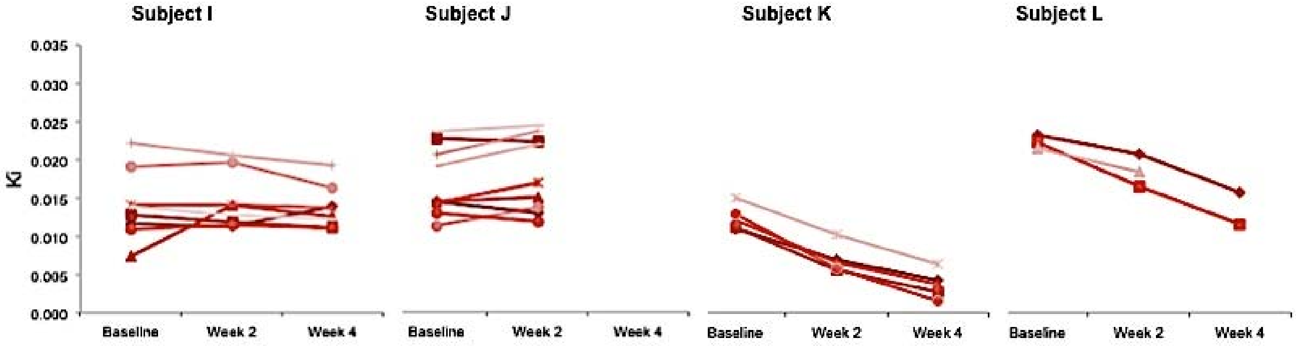
A. Cohort I (50 mg for 4 weeks followed by dose escalation to 75 mg)



B. Cohort 2 (75 mg continuously)



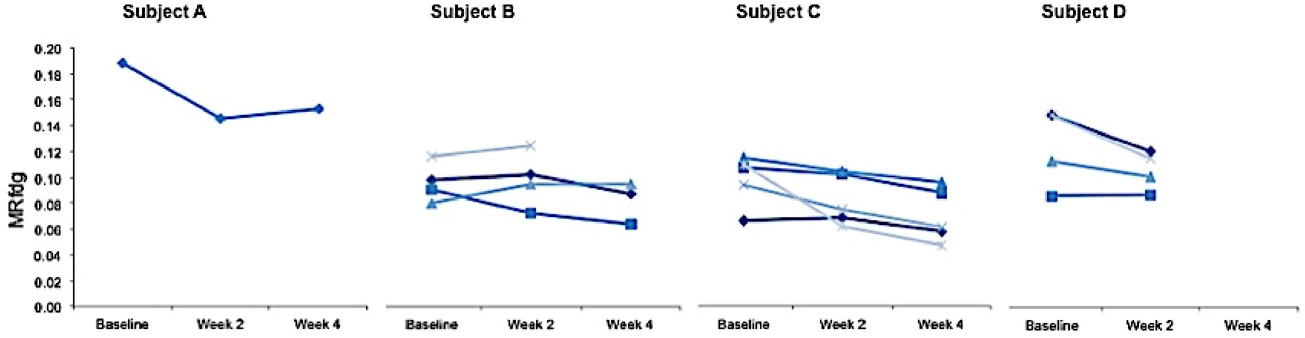
C. Cohort 3 (25 mg for 2 weeks followed by dose escalation to 75 mg thereafter)



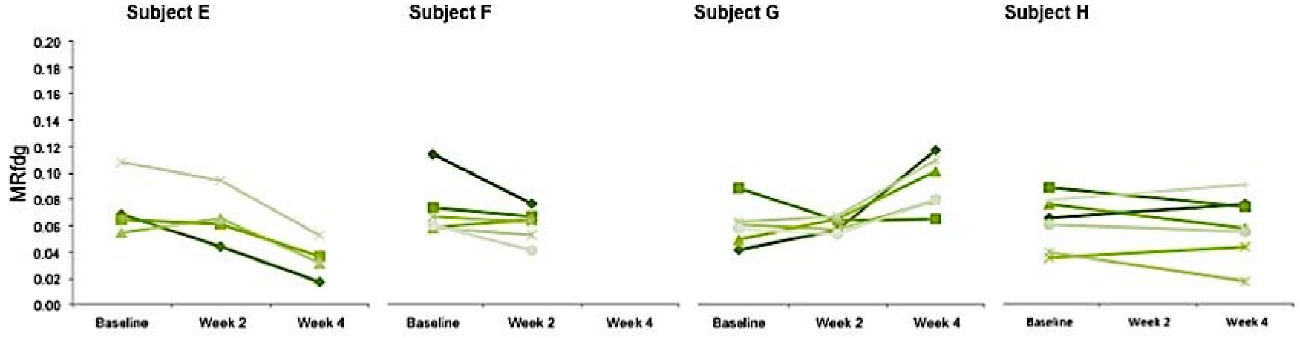
Supplemental Figure 4: FDG uptake parameter MRfdg Values over Time. Each patient is represented in an individual panel with individual tumors represented by separate lines. The X axis represents the time points (baseline, Week 2 and Week 4) at which the parameter MRfdg [(µmol/mL of tissue)/min were determined. Subjects were treated with 50 mg for 4 weeks (A), 75 mg for 4 weeks (B) and 25 mg for 2 weeks and 75 mg thereafter (C).

Individual patient profiles over time – MRfdg from tumor tissue

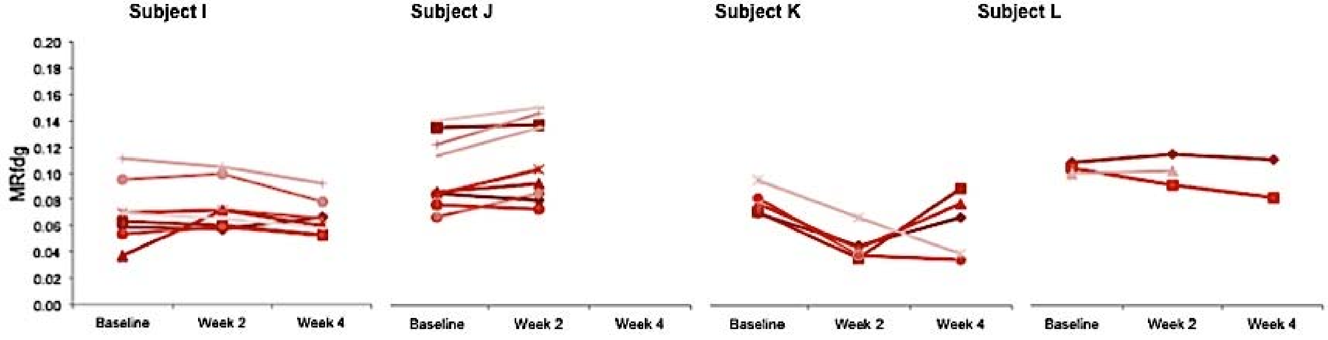
A. Cohort I (50 mg for 4 weeks followed by dose escalation to 75 mg)



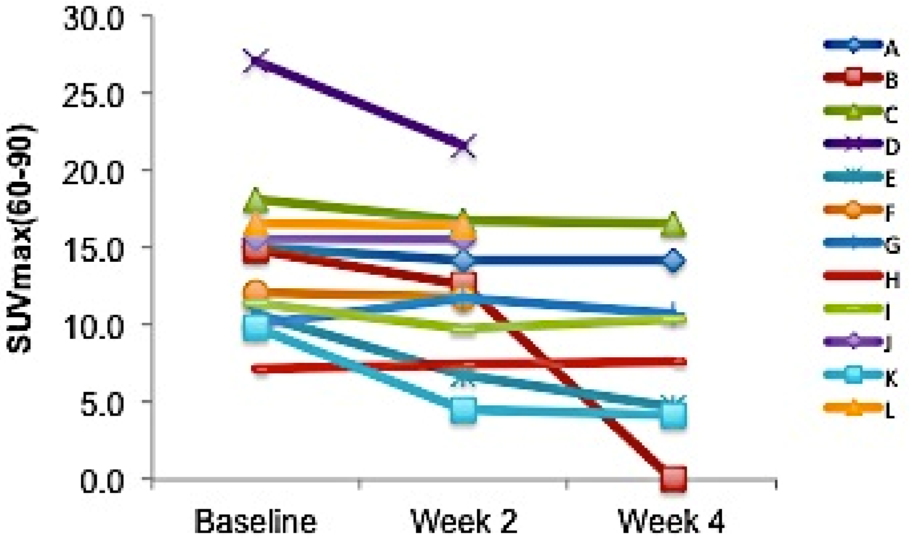
B. Cohort 2 (75 mg continuously)



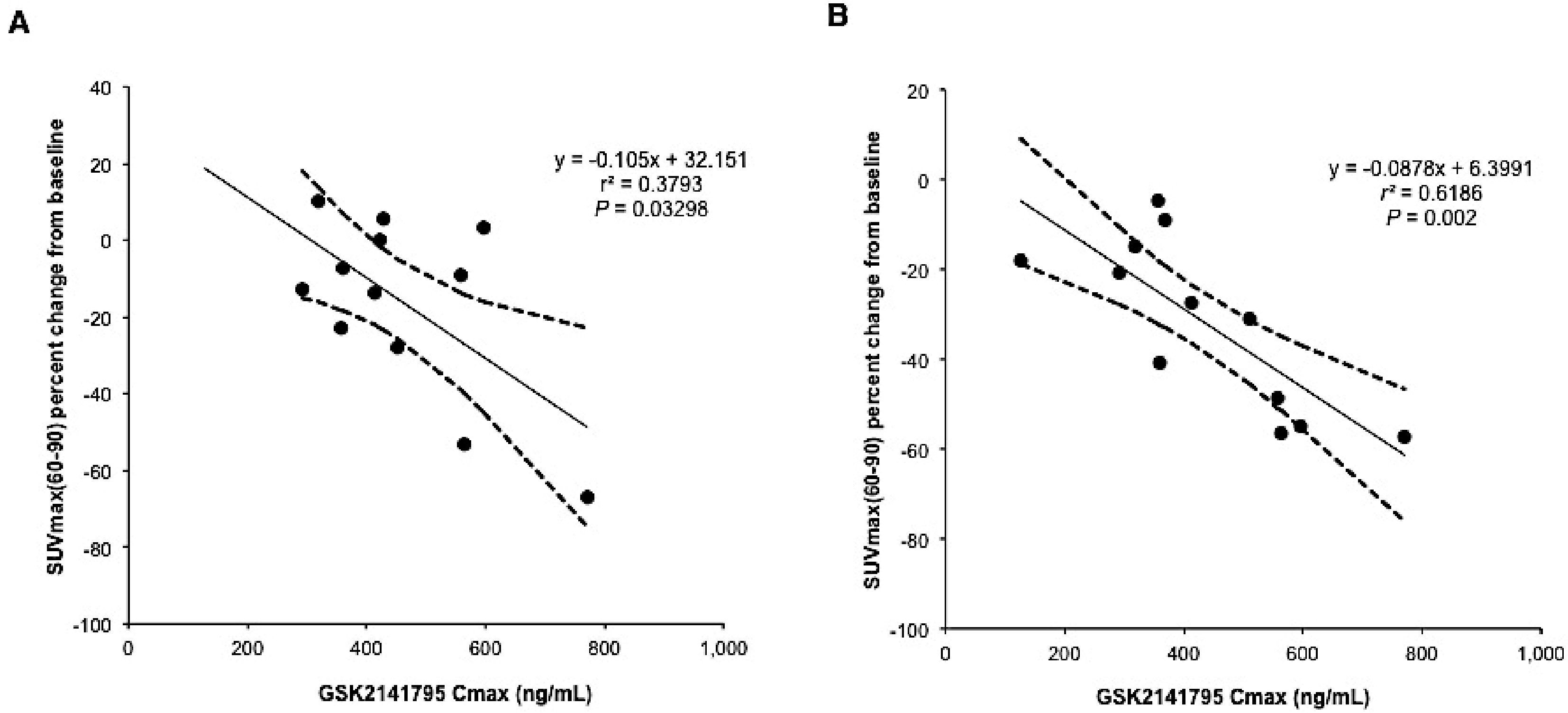
C. Cohort 3 (25 mg for 2 weeks followed by dose escalation to 75 mg thereafter)

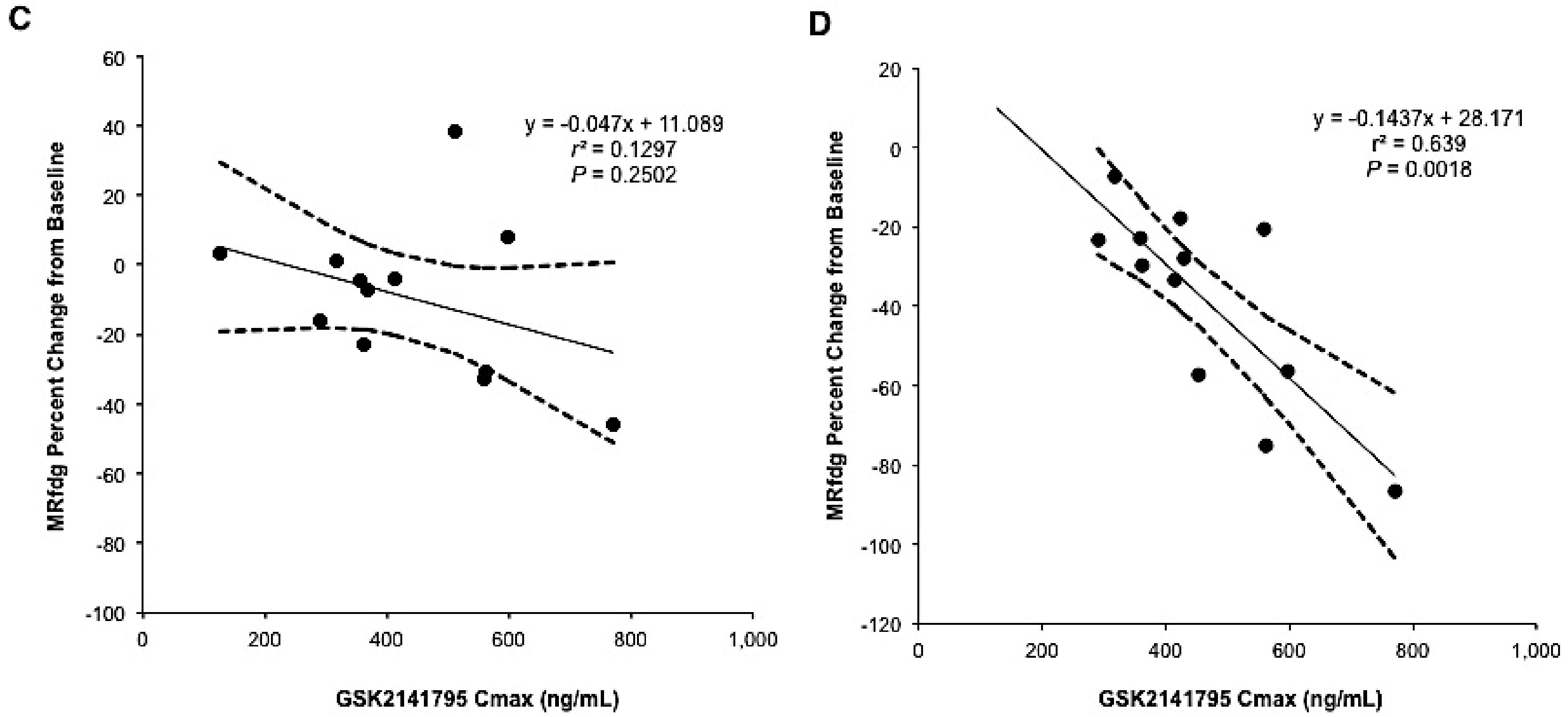


Supplemental Figure 5: SUVmax(60-90) of dominant tumor(lesion with the highest FDG uptake) for each patient over time. Each patient's dominant tumor is represented by separate lines at different time points (Baseline, Week 2 and Week 4) which SUVmax(60-90) were determined for that lesion. Decrease in SUVmax of dominant tumors was significant (p=0.04) at Week 2 but non-significant at Week 4 (p=0.128). For subject B dominant tumor has disappeared at Week 4, following 4 weeks daily 50 mg oral GSK2141795.



Supplemental Figure 6: **Linear Regression Analysis of PK/PD Relationships**. (A) The greatest percent change from baseline for SUVmax(60-90) averaged over tumors versus Cmax. (B) The greatest percent change from baseline irrespective of week for SUVmax(60-90) for an individual tumor versus Cmax . (C) The greatest percent change from baseline for MRfdg averaged over tumors versus Cmax. (D) The greatest percent change from baseline irrespective of week for MRfdg for an individual tumor versus Cmax. Each point represents the data from one patient. The solid line represents the linear regression line with the dotted lines representing 90% confidence intervals. Regression estimates, the r^2, and p-values associated with tests assessing the significance of the regression slope are provided.




C
60
40
20
0
-20
-40
-60
-80
-100
0
200
400
600
800
1,000
MRfdg Percent Change from Baseline
GSK2141795 Cmax (ng/mL)
y = -0.047x + 11.089
r^2 = 0.1297
P = 0.2502
D
20
0
-20
-40
-60
-80
-100
-120
0
200
400
600
800
1,000
MRfdg Percent Change from Baseline
GSK2141795 Cmax (ng/mL)
y = -0.1437x + 28.171
r^2 = 0.639
P = 0.0018