Supplementary Material:

Analysis of the Tyrosine Kinome in Melanoma Reveals Recurrent Mutations in *ERBB4*

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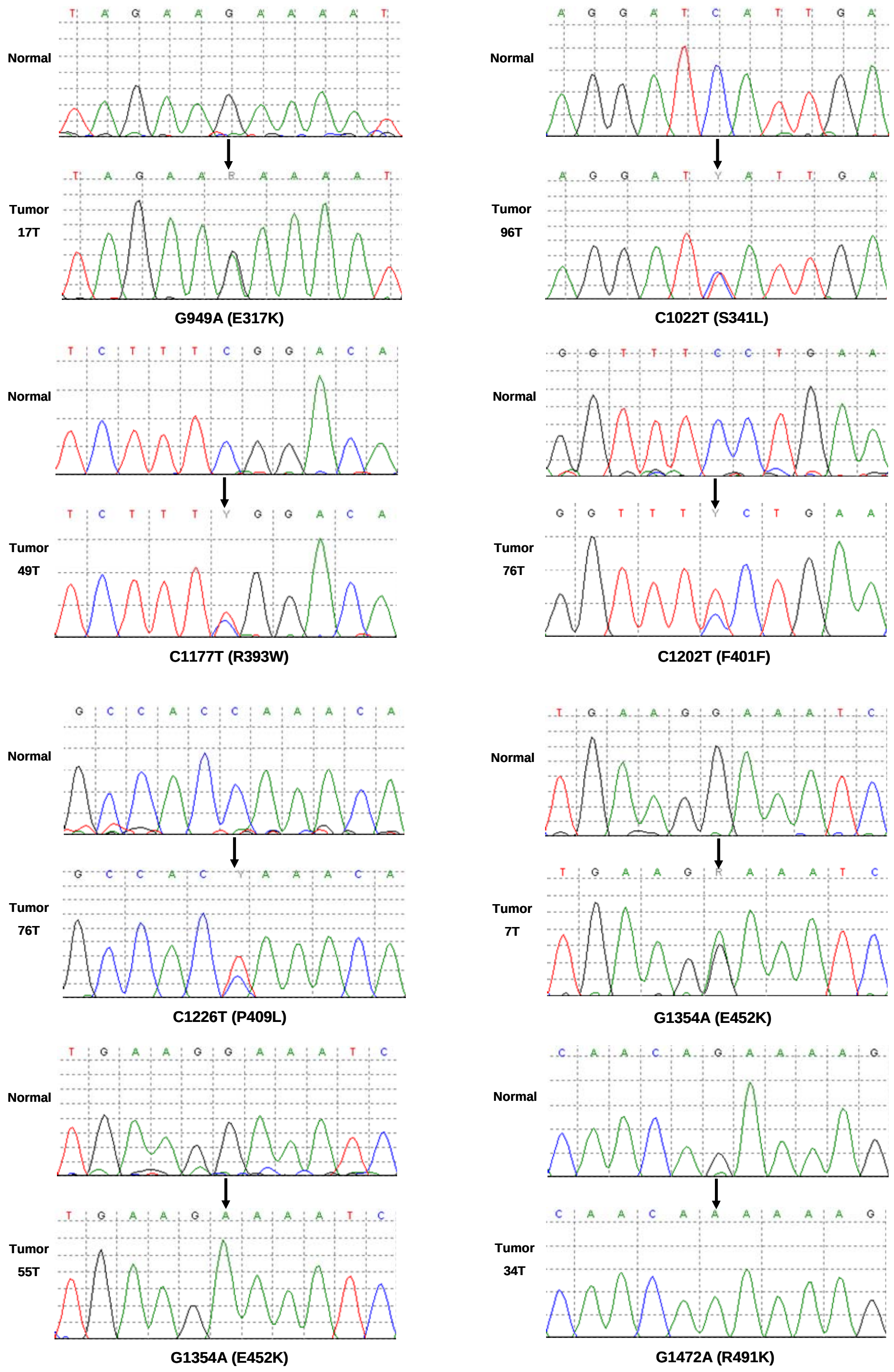
Supplementary Figures



G949A (E317K)

C1022T (S341L)

C1177T (R393W)

C1202T (F401F)

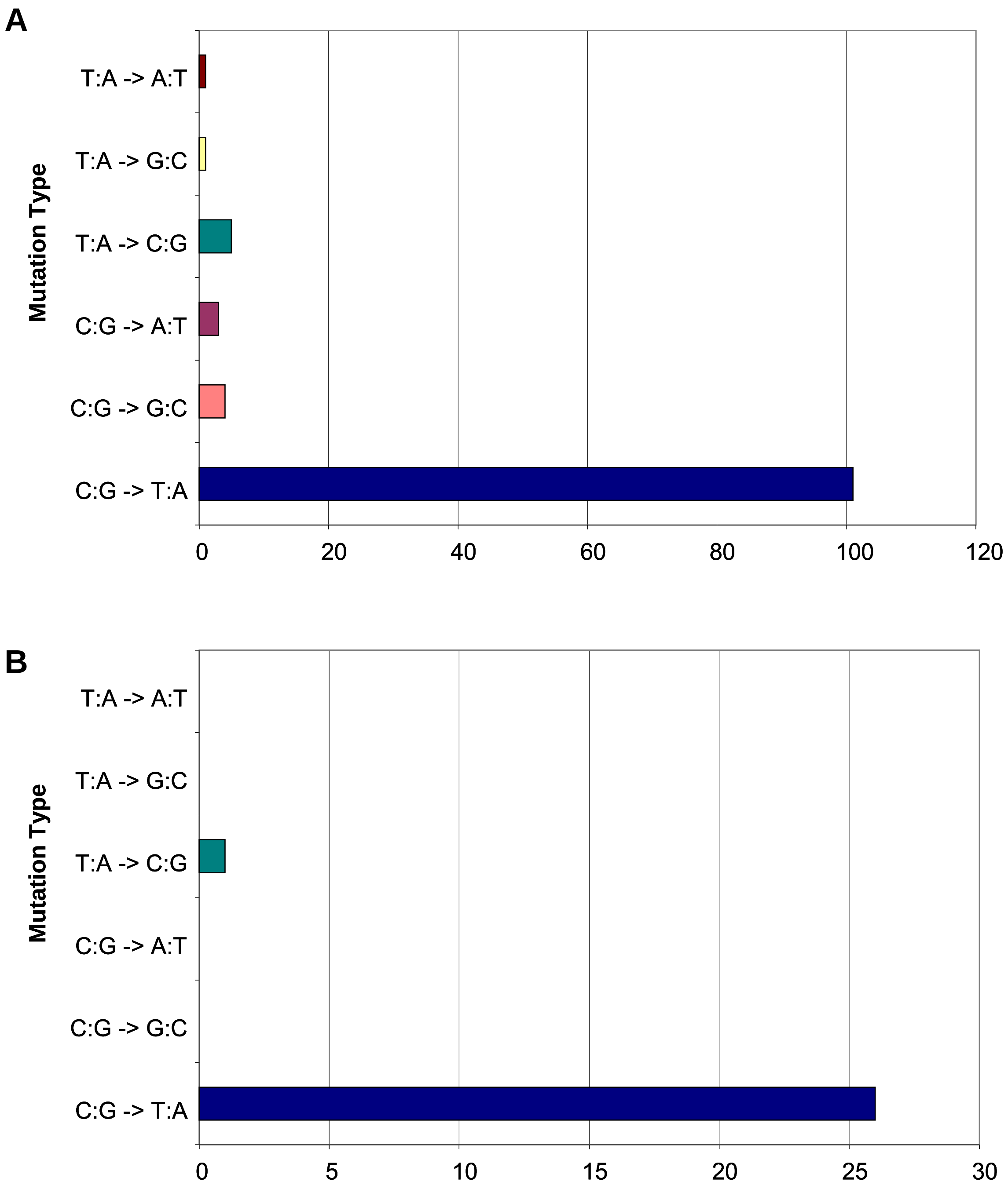
C1226T (P409L)

G1354A (E452K)

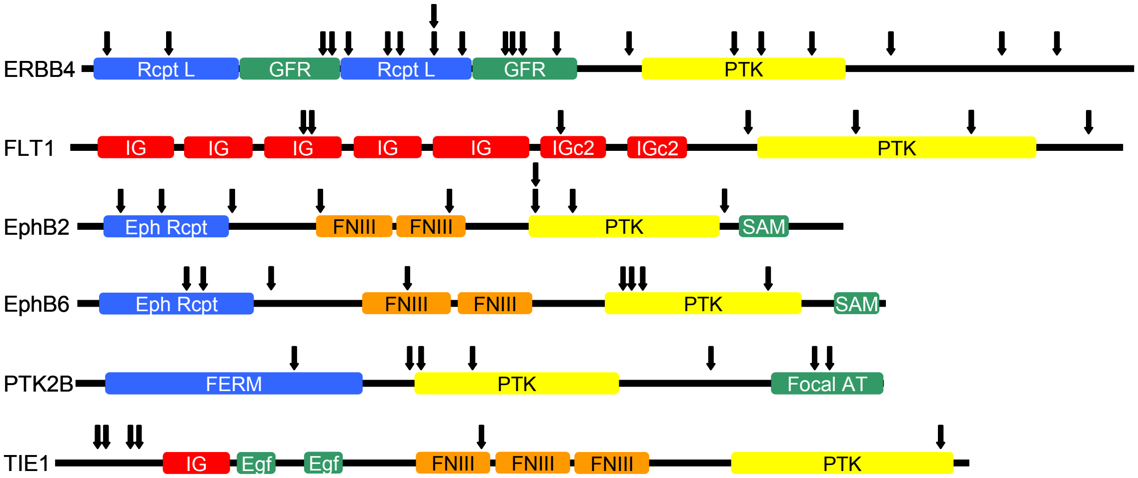
G1354A (E452K)

G1472A (R491K)

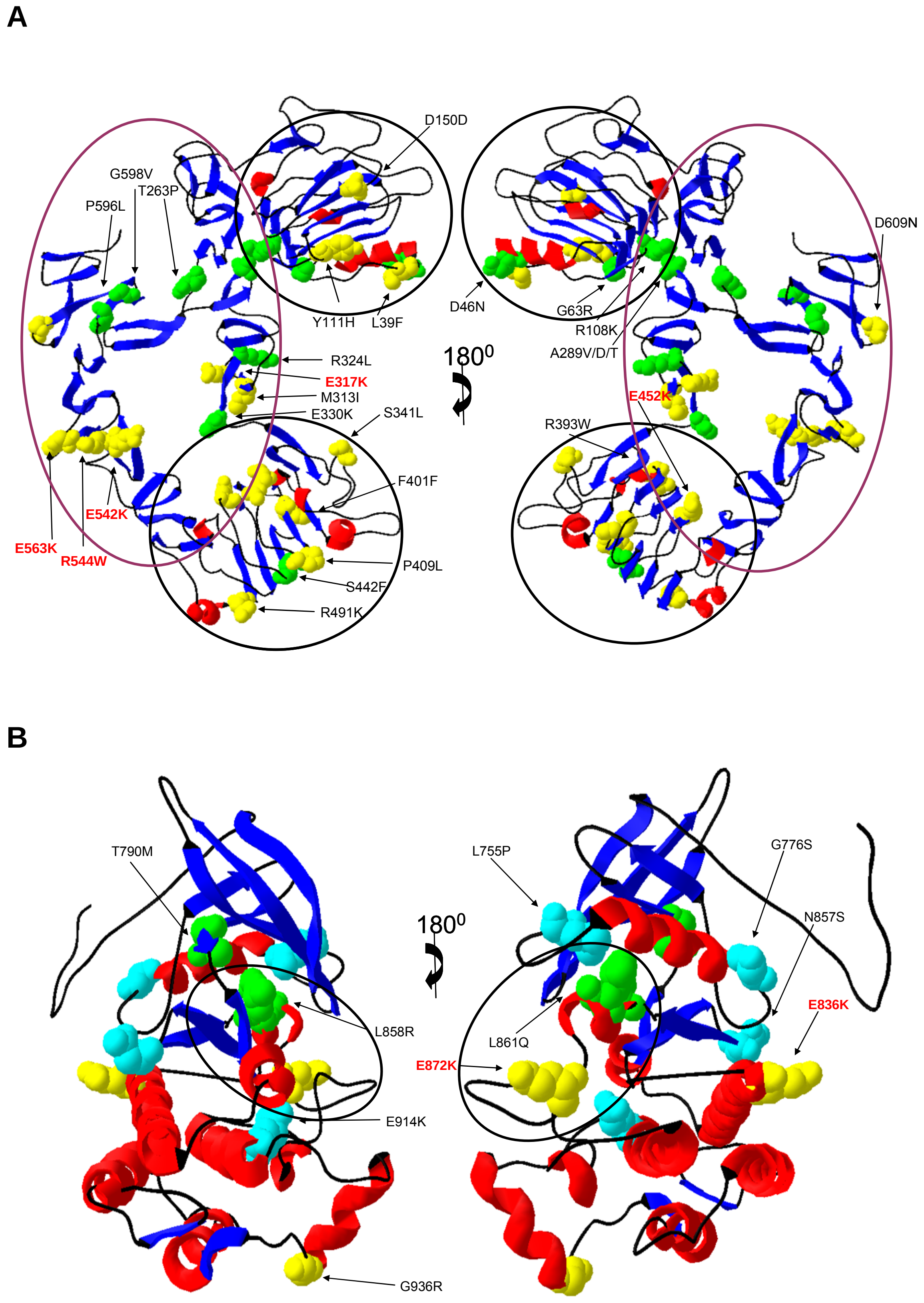
Supplementary Figure 1. Detection of mutations in ERBB4. Representative examples of mutations in ERBB4. In each case, the top sequence chromatogram was obtained from normal tissue and the lower sequence chromatogram from the indicated tumors. Arrows indicate the location of missense mutations. The nucleotide and amino acid alterations are indicated below the chromatograms.



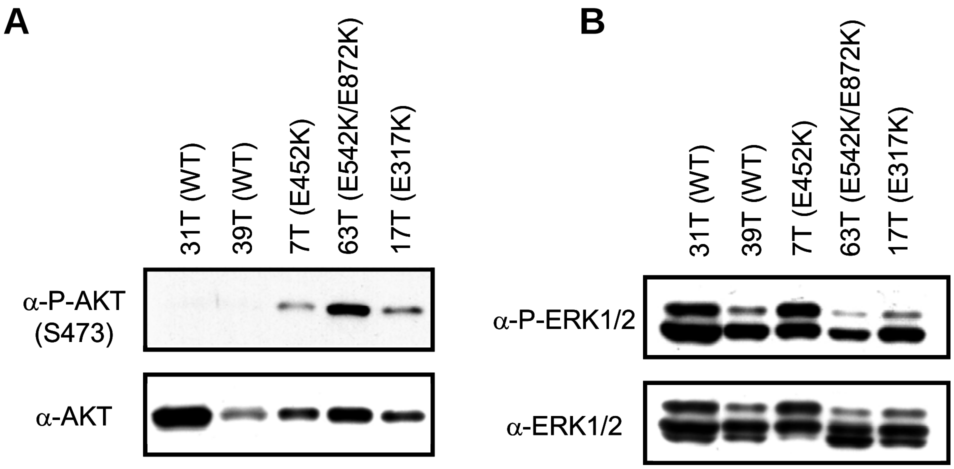
Supplementary Figure 2. Mutation spectra of single base pair substitutions. A. Kinome mutation spectrum. The number of each of the six classes of base substitutions resulting in nonsynonymous changes in the kinome screen is shown. B. Mutation spectra of single base pair substitutions in ERBB4. The number of each of the six classes of base substitutions resulting in nonsynonymous changes in ERBB4 is shown.



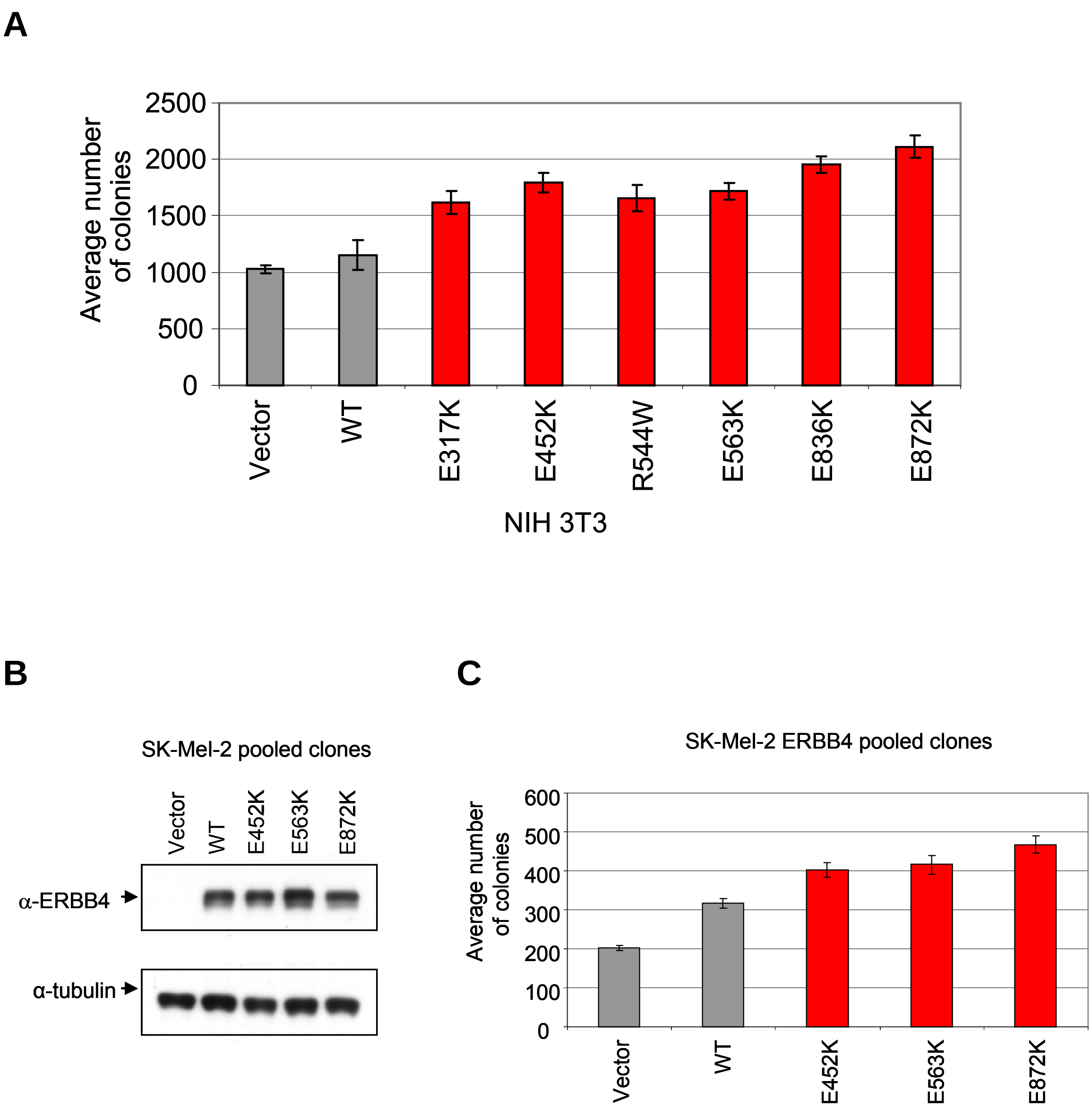
Supplementary Figure 3. Distribution of mutations in ERBB4, FLT1, EphB2, EphB6, PTK2B, and TIE1. Black arrows indicate positions of nonsynonymous mutations and boxes represent functional domains (Rcpt L, Receptor L; GFR, Growth Factor Receptor; PTK, Protein Tyrosine Kinase; IG, Immunoglobin; IGc2, Immunoglobin C-2 Type; Eph Rcpt, Ephrin Receptor; FNIII, Fibronectin Type III; SAM, Sterile Alpha Motif; FERM, Protein 4.1, Ezrin, Radixin, Moesin (FERM) Domain; Focal AT, Focal Adhesion Targeting Region)


A
D150D
G598V
T263P
P596L
D609N
D46N
Y111H
L39F
G63R
R108K
A289V/D/T
180⁰
R324L
E317K
M313I
E330K
S341L
E452K
R393W
F401F
E542K
E563K
R544W
P409L
S442F
R491K
B
T790M
L755P
G776S
N857S
180⁰
L858R
E836K
L861Q
E872K
E914K
G936R

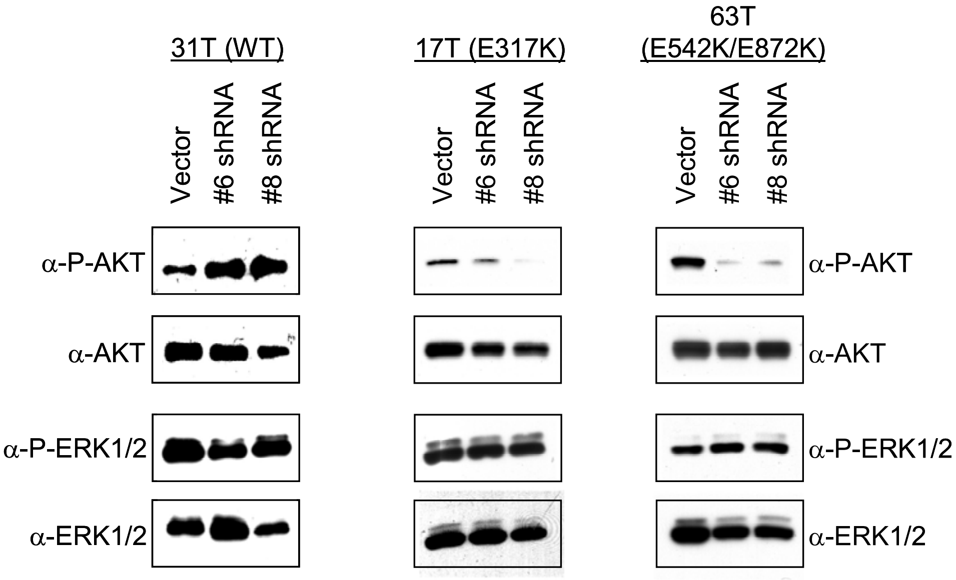
Supplementary Figure 4. Ribbon diagrams of ERBB4. A. Distribution of ERBB4 mutations in a ribbon diagram of its extracellular domain (PDB ID 2ahx). The two views are related to one another by a 180º rotation about a vertical axis. α-helices are shown in red, β-sheets are shown in blue, and loops are shown in black. All mutations are represented as space-filling molecules. ERBB4 mutations are shown in yellow, and the equivalent positions of known activating EGFR mutations are shown in green. The receptor L domain is denoted by black circles, the growth factor receptor domain is denoted by purple circles and cloned ERBB4 mutants are highlighted in red. B. Distribution of ERBB4 mutations in a ribbon of its kinase domain (PDB ID 2r4b). The two views are related to one another by a 180º rotation about a vertical axis. α-helices are shown in red, β-sheets are shown in blue, and loops are shown in black. All mutations are represented as space-filling molecules. ERBB4 mutations are shown in yellow, equivalent positions of known ERBB2 mutations are shown in cyan, and the equivalent positions of known activating EGFR mutations are shown in green. The activation loop is denoted by black circles. In A and B, Images were created by SWISS-MODEL. Determination of the location of previously reported EGFR and ERBB2 mutations is described in the experimental procedures and cloned ERBB4 mutants are highlighted in red.



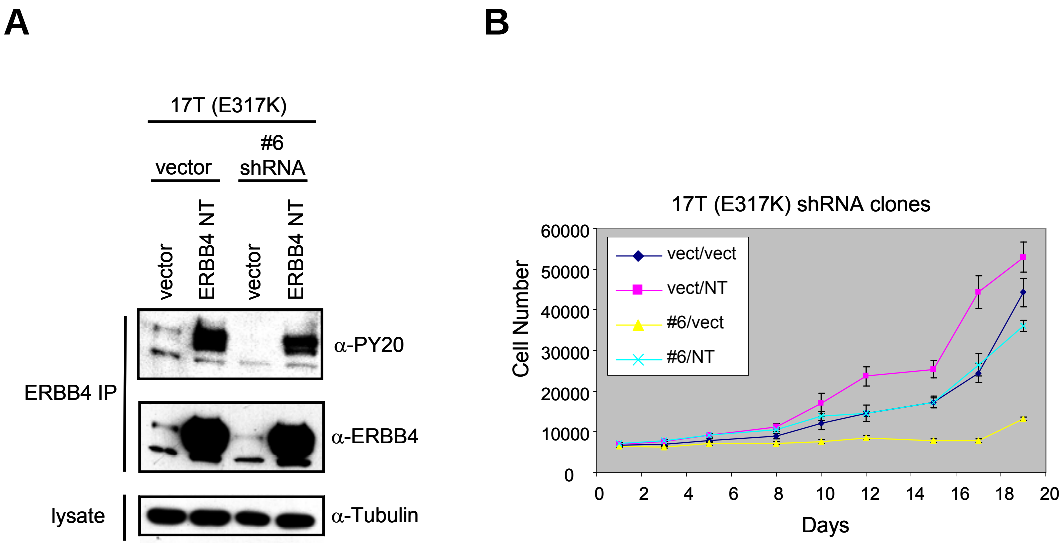
Supplementary Figure 5. Effects of ERBB4 mutation on AKT and ERK phosphorylation. Melanoma cell lines, containing either WT or mutant ERBB4, were harvested and analyzed by immunoblot. Shown are immunoblots of lysates probed with the indicated antibodies (α-P-ERK1/2 (recognizes phosphorylation of T202 and Y204 on ERK1 and T185 and Y187 on ERK2).



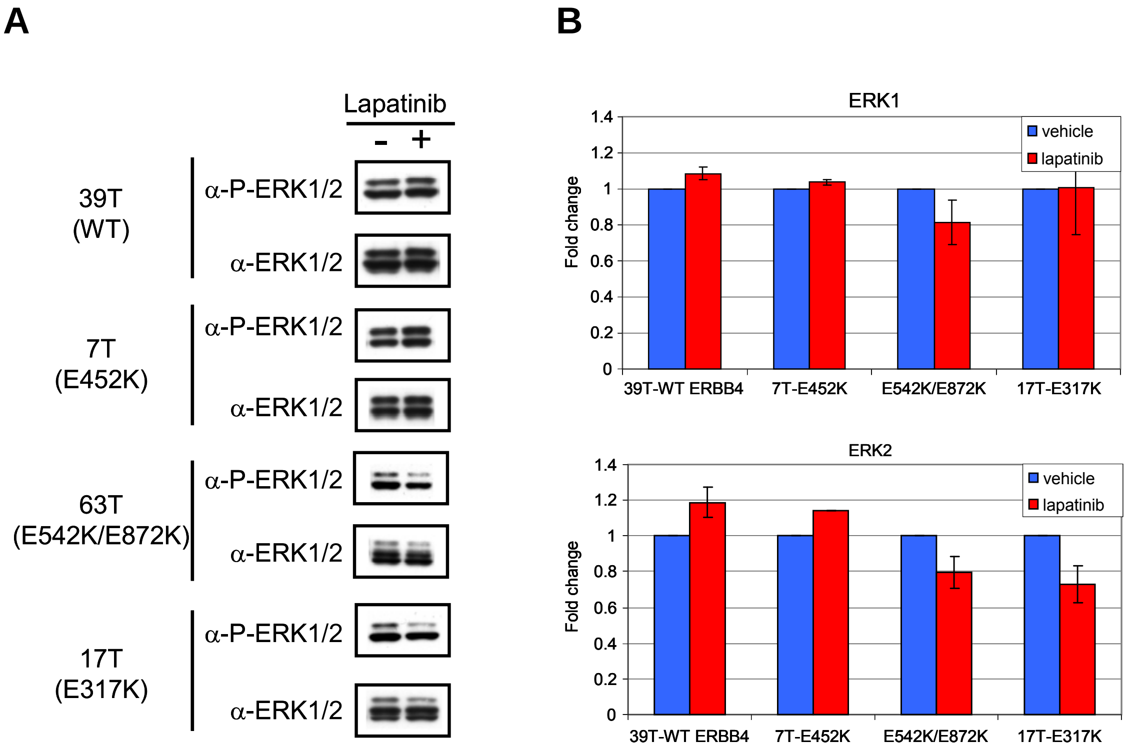
Supplementary Figure 6. Effect of ERBB4 mutations on cell growth in NIH 3T3 and SK-Mel-2 cells. A. Growth of NIH 3T3 cells expressing vector, WT ERBB4 or various ERBB4 missense mutants in soft agar. The graph indicates the number of colonies after 14 days. B. Detection of ERBB4 protein expression in stable transfectants of SK-Mel-2 melanoma cells by immunoblot analysis, lysates from the different clones stably transfected with an empty vector, human WT ERBB4 or the indicated ERBB4 mutants were immunoprecipitated and immunoblotted with ERBB4 antibody. C. Anchorage-independent proliferation of SK-Mel-2 cell clones expressing the indicated constructs was assessed by measuring colony formation in soft agar. Graph indicates number of colonies observed after 14 days of growth.



Supplementary Figure 7. Knockdown of ERBB4 protein causes reduced activation of the AKT pathway but not of the ERK pathway. Melanoma cell lines, containing either WT or mutant ERBB4, were harvested and analyzed by western blot. Shown are immunoblots of lysates probed with the indicated antibodies (α-P-ERK1/2 (recognizes phosphorylation of T202 and Y204 on ERK1 and T185 and Y187 on ERK2).



Supplementary Figure 8. Rescue of oncogene dependence by exogenous non-targetable ERBB4. A. Melanoma cells harboring mutant ERBB4 and stably expressing control or ERBB4 shRNA #6 transduced with either vector or non targetable (NT) ERBB4 were analyzed by immunoprecipitation of lysates with α-ERBB4. Samples were analyzed by immunoblotting with the indicated antibodies. As a loading control lysates were immunoblotted with α-Tubulin. B. Melanoma cells expressing vector or the ERBB4 shRNA #6 transduced with a vector or NT ERBB4 were evaluated for cell proliferation by measuring the average cell number at each time point by determining DNA content using SYBR Green I.



Supplementary Figure 9. Effect of lapatinib on ERK1/2 signaling pathways. A. Melanoma lines expressing mutant ERBB4 exhibit increased lapatinib sensitivity with respect to ERK1 and ERK2 phosphorylation. Cells were treated for 72 hrs with 5 μM lapatinib or vehicle as control. The activity of ERK1 and ERK2 was determined by immunoblotting with phospho-specific antibodies (α-P-ERK1/2 - recognizes phosphorylation of T202 and Y204 on ERK1 and T185 and Y187 on ERK2). Total ERK protein was also determined by immunoblotting. Shown are representative blots. B. Quantitative assessment of data from one melanoma cell line harboring WT ERBB4 and three melanoma cell lines harboring mutant ERBB4. The ratio of band intensities of P-ERK1/ERK1 or P-ERK2/ERK2 was analyzed for each melanoma cell line.

Table S1. Tyrosine Kinase genes analyzed

CCDS accession and amplimer number	Ref Seq accession and amplimer number	Gene Name	Gene Description
CCDS35165.1	NM_007313.2	ABL1/ABL	v-abl Abelson murine leukemia viral oncogene homolog 1
CCDS30947.1	NM_007314.2	ABL2/ARG	v-abl Abelson murine leukemia viral oncogene homolog 2 (arg, Abelson-related gene)
CCDS33928.1	NM_005781.4	ACK1/TNK2	tyrosine kinase, non-receptor, 2
CCDS33172.1	NM_004304.3	ALK	anaplastic lymphoma kinase (Ki-1)
CCDS12575.1	NM_021913.3	AXL	AXL receptor tyrosine kinase
CCDS5982.1	NM_001715.2	BLK	B lymphoid tyrosine kinase
CCDS14168.1	NM_203281.2	BMX	BMX non-receptor tyrosine kinase
CCDS13524.1	NM_005975.2	BRK/PTK6	PTK6 protein tyrosine kinase 6
CCDS14482.1	NM_000061.1	BTK	Bruton agammaglobulinemia tyrosine kinase
CCDS4302.1	NM_005211.2	CSF1R	colony stimulating factor 1 receptor, formerly McDonough feline sarcoma viral (v-fms) oncogene homolog
CCDS10269.1	NM_004383.1	CSK	c-src tyrosine kinase
CCDS4690.1	NM_001954.4	DDR1	discoidin domain receptor family, member 1
CCDS1241.1	NM_006182.2	DDR2	discoidin domain receptor family, member 2
CCDS5514.1	NM_005228.3	EGFR	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian)
CCDS5884.1	NM_005232.3	EPHA1	ephrin receptor EphA1
CCDS169.1	NM_004431.2	EPHA2	ephrin receptor EphA2
CCDS2922.1	NM_005233.5	EPHA3	ephrin receptor EphA3 isoform a precursor
CCDS2447.1	NM_004438.3	EPHA4	ephrin receptor EphA4
CCDS3514.1	NM_182472.1	EPHA5	ephrin receptor EphA5 isoform b
N/A	NM_001080448.2	EPHA6	EPH receptor A6 isoform a
CCDS5031.1	NM_004440.2	EPHA7	ephrin receptor EphA7
CCDS30626.1	NM_001006943.1	EPHA8	EPH receptor A8 isoform 2 precursor
CCDS425.1	NM_173641.2	EPHA10	EPH receptor A10 isoform 2
N/A	NM_004441.3	EPHB1	ephrin receptor EphB1 precursor
CCDS230.1	NM_004442.6	EPHB2	ephrin receptor EphB2 isoform 2 precursor
CCDS3268.1	NM_004443.3	EPHB3	ephrin receptor EphB3 precursor
CCDS5706.1	NM_004444.4	EPHB4	ephrin receptor EphB4 precursor
CCDS5873.1	NM_004445.2	EPHB6	ephrin receptor EphB6 precursor
CCDS32642.1	NM_004448.2	ERBB2	v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene homolog (avian)
CCDS31833.1	NM_001982.2	ERBB3	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian)
CCDS2394.1	NM_005235.2	ERBB4	v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)
CCDS6381.1	NM_153831.2	FAK/PTK2	PTK2 protein tyrosine kinase 2
CCDS4098.1	NM_005246.2	FER	fer (fps/fes related) tyrosine kinase (phosphoprotein NCP94)
CCDS10365.1	NM_002005.2	FES	V-FES feline sarcoma viral/V-FPS fujinami avian
CCDS6107.1	NM_023110.2	FGFR1	fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndrome)
CCDS31298.1	NM_000141.3	FGFR2	fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor)
CCDS3353.1	NM_000142.2	FGFR3	fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism)
CCDS4410.1	NM_002011.3	FGFR4	fibroblast growth factor receptor 4 isoform 1
CCDS305.1	NM_005248.2	FGR	Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homolog
CCDS9330.1	NM_002019.3	FLT1/VEGFR1	fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular permeability factor receptor)
CCDS31953.1	NM_004119.2	FLT3	fms-related tyrosine kinase 3
CCDS4457.1	NM_182925.3	FLT4/VEGFR3	fms-related tyrosine kinase 4
CCDS5103.1	NM_002031.2	FRK	fyn-related kinase
CCDS5094.1	NM_002037.3	FYN	FYN oncogene related to SRC, FGR, YES
CCDS33460.1	NM_002110.2	HCK	hemopoietic cell kinase
CCDS10378.1	NM_000875.3	IGF1R	insulin-like growth factor 1 receptor
CCDS12176.1	NM_000208.2	INSR	insulin receptor
CCDS1160.1	NM_014215.1	INSRR	insulin receptor-related receptor
CCDS4336.1	NM_005546.3	ITK	IL2-inducible T-cell kinase
N/A	NM_002227.2	JAK1	Janus kinase 1
CCDS6457.1	NM_004972.2	JAK2	Janus kinase 2
CCDS12366.1	NM_000215.2	JAK3	Janus kinase 3
CCDS3497.1	NM_002253.1	KDR/VEGFR2	kinase insert domain receptor (a type III receptor tyrosine kinase)
CCDS3496.1	NM_000222.2	KIT	v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog
CCDS359.1	NM_005356.3	LCK	lymphocyte-specific protein tyrosine kinase
CCDS10078.1	NM_206961.1	LTK	leukocyte tyrosine kinase
CCDS6162.1	NM_002350.2	LYN	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog
CCDS12113.1	NM_002378.3	MATK	megakaryocyte-associated tyrosine kinase
CCDS2094.1	NM_006343.2	MERTK/MER	c-mer proto-oncogene tyrosine kinase
N/A	NM_000245.2	MET	met proto-oncogene (hepatocyte growth factor receptor)
CCDS2807.1	NM_002447.2	MST1R/RON	macrophage stimulating 1 receptor (c-met-related tyrosine kinase)
N/A	NM_005592.1	MUSK	muscle, skeletal, receptor tyrosine kinase
CCDS1161.1	NM_002529.3	NTRK1	neurotrophic tyrosine kinase, receptor, type 1
CCDS35053.1	NM_001007097.1	NTRK2	neurotrophic tyrosine kinase receptor type 2
CCDS32322.1	NM_001012338.1	NTRK3	neurotrophic tyrosine kinase receptor type 3
CCDS3495.1	NM_006206.3	PDGFRA	platelet-derived growth factor receptor alpha
CCDS4303.1	NM_002609.3	PDGFRB	platelet-derived growth factor receptor beta
CCDS4884.1	NM_002821.3	PTK7	PTK7 protein tyrosine kinase 7
CCDS6057.1	NM_004103.3	PYK2/PTK2B	PTK2B protein tyrosine kinase 2 beta
CCDS7200.1	NM_020975.4	RET	ret proto-oncogene
CCDS626.1	NM_005012.2	ROR1	receptor tyrosine kinase-like orphan receptor 1
CCDS6691.1	NM_004560.2	ROR2	receptor tyrosine kinase-like orphan receptor 2
CCDS5116.1	NM_002944.2	ROS1	v-ros UR2 sarcoma virus oncogene homolog 1 (avian)
N/A	NM_001005861.2	RYK	RYK receptor-like tyrosine kinase
CCDS13294.1	NM_005417.3	SRC	v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (avian)
CCDS13525.1	NM_080823.2	SRMS	src-related kinase lacking C-terminal regulatory tyrosine and N-terminal myristylation sites
CCDS6688.1	NM_003177.3	SYK	spleen tyrosine kinase
CCDS3481.1	NM_003215.2	TEC	tec protein tyrosine kinase
CCDS6519.1	NM_000459.2	TEK	TEK tyrosine kinase, endothelial (venous malformations, multiple cutaneous and mucosal)
CCDS482.1	NM_005424.2	TIE	tyrosine kinase with immunoglobulin-like and EGF-like domains 1
N/A	NM_003985.3	TNK1	tyrosine kinase, non-receptor, 1
CCDS3480.1	NM_003328.2	TXK	TXK tyrosine kinase
CCDS12236.1	NM_003331.3	TYK2	tyrosine kinase 2
CCDS10080.1	NM_006293.2	TYRO3	TYRO3 protein tyrosine kinase
CCDS11824.1	NM_005433.3	YES1	v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1
CCDS33254.1	NM_001079.3	ZAP70	zeta-chain (TCR) associated protein kinase 70kDa

Table S2. Primers used for PCR amplification and sequencing of kinase domains

Gene and Exon Name	CCDS accession	Ref Seq accession	Forward Primer	Reverse Primer	Sequencing Primer (Forward)	Sequencing Primer (Reverse)
ABL1_Exon-4	CCDS35165.1	NM_007313.2	CTCTGTCCTGTGTGGAGAGC	GGAATGATATAAGACGGAAAAGTCA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
ABL1_Exon-5	CCDS35165.1	NM_007313.2	AGCTGTCATGGAACCTGTCTG	ACTTGAATTTACGCAGGGAGAG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
ABL1_Exon-6	CCDS35165.1	NM_007313.2	AGTCTCAGGATGCAGGTGCT	CCCCGGAGGAACAATGAGTA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
ABL1_Exon-7	CCDS35165.1	NM_007313.2	ATGTTGGGATCTCAGGGTGT	GAAGAGCAAGAAAGAGGCAGA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
ABL1_Exon-8	CCDS35165.1	NM_007313.2	GACCTCAAATAATCCTCCCACTT	AGGGCCCAGGAATCTGTATTTA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
ABL2_Exon-5	CCDS30947.1	NM_007314.2	AGGGAGAGAAAGGACAGAACA	TTCTTAATCTCTTTTCAAGTTGTTTAG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
ABL2_Exon-6	CCDS30947.1	NM_007314.2	AAAAAGCATTTGGAGATAACAAG	GGACACGATTGCTGAATTTTG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
ABL2_Exon-7	CCDS30947.1	NM_007314.2	AGAATAGCAAAGGCCCCTTATT	GCCATGTGCAAAACTCTAGACA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
ABL2_Exon-8	CCDS30947.1	NM_007314.2	CTTTCAACCTTACCCCAGACG	AAATAACTTAGTCTTGTAGAAAAGCATC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
ABL2_Exon-9	CCDS30947.1	NM_007314.2	TTCAATCTAACAACACTGAGAGG	TGGTCATAGTTTATTTTCCCTCATTAC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
ACK1_Exon-3	CCDS33928.1	NM_005781.4	ACTCTGGGATGAGCCACACT	CATGCCTGTCGGTCTCTTTCT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
ACK1_Exon-4	CCDS33928.1	NM_005781.4	ACTGAGCACCAGCAAAATCC	AATATTCTCTCATCATACTGGTTATCTC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
ACK1_Exon-5	CCDS33928.1	NM_005781.4	GTGATTTCCAGCACCCAGAC	ACTCCTAGAGGTCCCCAGACAG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
ACK1_Exon-6	CCDS33928.1	NM_005781.4	CTCCCTGAGGCCATACAGATAC	CAGGCCCTACCCGAATTT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
ACK1_Exon-7	CCDS33928.1	NM_005781.4	CCCTACCTTCCCTCGATGAC	GGAGAGCCCAGCAAAGAGAC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
ALK_Exon-20	CCDS33172.1	NM_004304.3	CCCTGGTTCTCCTCTCATTGTA	TCTGATTTTTAGCTTTGCATTTACTT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
ALK_Exon-21;ALK_Exon-22	CCDS33172.1	NM_004304.3	GGGATTATTAGGCCACACAGAC	TCCTTCTTACCAGTTTTCAGGTG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
ALK_Exon-23	CCDS33172.1	NM_004304.3	CCCCTGTCCAAGCCTAAAGT	GCAAGTCTCACCCAGTCTCTCT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
ALK_Exon-24	CCDS33172.1	NM_004304.3	ATCCTACATCCAAATGGCTCTG	CTATTCCCCTGTGGTTTCCTC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
ALK_Exon-25	CCDS33172.1	NM_004304.3	AAGGTTTCCCATAGCCTGAAA	AAGGCCAGATAGCATTCCTTA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
ALK_Exon-26	CCDS33172.1	NM_004304.3	TTGTCGGGTGTATTGATTCTTC	TGCCTATACTGAACTAAATGCTGTG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
ALK_Exon-27	CCDS33172.1	NM_004304.3	CACTGAAGTCGCAGTCACATT	GGAAATGATAAGGCAAACCAACT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
ALK_Exon-28	CCDS33172.1	NM_004304.3	TTGTACTCTGACTGGCTTGACC	CTCCTGCTGGGAATGTGTGT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
AXL_Exon-13;AXL_Exon-14	CCDS12575.1	NM_021913.3	GGTGGAAGTAGAGGGGTGCT	CTCCATTGCCTATCTGGAAACA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
AXL_Exon-16	CCDS12575.1	NM_021913.3	CTGGGAACTCTGCTGGAAAC	CCTATGTTCTTGCCCTTGACTG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
AXL_Exon-17	CCDS12575.1	NM_021913.3	CTGCTCAGACCCTGGGAAGA	GGTCCCTGAAAGGCACTCAC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
AXL_Exon-17	CCDS12575.1	NM_021913.3	CAGTCTACAAATATTAACTGAGCATCT	GGTCCCTGAAAGGCACTCAC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
AXL_Exon-18	CCDS12575.1	NM_021913.3	GAAGCCCTTTGTCCCATCCT	TGGCTGTCCACATTCTATGAGT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
AXL_Exon-19	CCDS12575.1	NM_021913.3	CTCCCAGAGGATGGTTGTGA	CTCAGGTGTTGAGGAGCATGT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
AXL_Exon-20	CCDS12575.1	NM_021913.3	CCAGGACCCAACTCAGAAAT	GGTGGGATAGGTAGGAAGACAG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
BLK_Exon-10	CCDS5982.1	NM_001715.2	ACAGGTAGCCCCTGTGTCTC	AACTGTTTCTTTGCTGCAGGACT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
BLK_Exon-11	CCDS5982.1	NM_001715.2	CTGGTCATGTGTCCTGGTGT	GAATCCACTATGGGTGCAAAG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
BLK_Exon-12	CCDS5982.1	NM_001715.2	GAAAATCTACAGCCTCATTTCTAGG	GCTTACCAGTCCTGAACACCTT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
BLK_Exon-7	CCDS5982.1	NM_001715.2	GCGCAAACGAAGAGAAAGAG	GCACTCAGGCTCTGGAACAT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
BLK_Exon-8	CCDS5982.1	NM_001715.2	GGACCTGGAACGCAAGGTA	CAGTTGTAAATGGTTGCATGA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
BLK_Exon-9	CCDS5982.1	NM_001715.2	TGCTGAGACTGGCATTTTGTAA	CTGGGATGGGAAGTCCTACAG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
BMX_Exon-13	CCDS14168.1	NM_203281.2	GAAGAAATCACTTGGGAAGC	GTAAAGCACACTACCCCTAGCC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
BMX_Exon-14	CCDS14168.1	NM_203281.2	TGCCTCCAAAGATAATTGTGC	GCTGCTTTAGCACTAAGCCCTTC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
BMX_Exon-15	CCDS14168.1	NM_203281.2	TTTAGAGCACTTGGGGGTTGT	TGACAGACAAAAAGAGCTAGCAG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
BMX_Exon-16	CCDS14168.1	NM_203281.2	ACAAACCATAAGCAGCCTCCAG	AACTTTCATCCCCTTTGATG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
BMX_Exon-18	CCDS14168.1	NM_203281.2	TGTCTGTTGTGTTTCCACATTT	TGTCCACATTTCTGTACTTGGTAG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
BRK_Exon-4	CCDS13524.1	NM_005975.2	AATTGAAAGGGAACCACTCTCG	AGGCTGGCATTTCCTACTGG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
BRK_Exon-5	CCDS13524.1	NM_005975.2	GTGTGCACTTTATTTCCTCACG	AATGGAAAGCCATTAAAATAGATCACT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
BRK_Exon-6	CCDS13524.1	NM_005975.2	CTGCTGTGCGTGCCATTC	TGCTCCTTGGTTCGTGATAAA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
BRK_Exon-7	CCDS13524.1	NM_005975.2	CAGAGAATGGTGCAGGTGTG	GAAGTTGGGCTCCTGAAGGT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
BRK_Exon-7;BRK_Exon-8	CCDS13524.1	NM_005975.2	AGACACTCCACATTTGTGAACC	AGGTGCCCTACCCAGGTACT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
BTK_Exon-13	CCDS14482.1	NM_000061.1	CTGAGATGGTACACACCCATGA	ATAAAGGGATTTGGGGAGGTT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
BTK_Exon-14	CCDS14482.1	NM_000061.1	GGCACGCCTAACTTATAGTACTTTCT	CCTTTAACTGGCGGTAGTCCT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
BTK_Exon-15	CCDS14482.1	NM_000061.1	AGAAAGATCGGCAGAAAACG	CTCCCTTAATTCTTTCAGCATATCA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
BTK_Exon-16	CCDS14482.1	NM_000061.1	AGCAAGAACAATATCTCTGTGG	CCACCTCTTTCATCCTTTTGT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
BTK_Exon-16;BTK_Exon-17	CCDS14482.1	NM_000061.1	GGCTGAATGGCCAGCTAAAT	TTGGTAAGTGGATAAGATTACACAGA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
CSF1R_Exon-11	CCDS4302.1	NM_005211.2	TGTGATAGGAAGCTGTGGAGTG	GGAAACTGGTTGCACAAGGTAG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
CSF1R_Exon-13	CCDS4302.1	NM_005211.2	CCCTGACACTTGGAGCAGTAG	GTGAGGACTTGGGTTTTCTTGT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
CSF1R_Exon-14	CCDS4302.1	NM_005211.2	AACCTGTGGTGGCTACTTCC	CGCCAAAGCCATCTGTTTTA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
CSF1R_Exon-15;CSF1R_Exon-16	CCDS4302.1	NM_005211.2	CTGCCCAAATGACTCTCTCATA	CTGAGCAGTGCAGTGATGATGA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
CSF1R_Exon-15;CSF1R_Exon-16	CCDS4302.1	NM_005211.2	GCTGGAGAAGTGAAGCAGGT	TGACTGTTTTGTCCCTAGAGTTTC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
CSF1R_Exon-17;CSF1R_Exon-18	CCDS4302.1	NM_005211.2	AGGGAAGAGCCAGAAAGGAG	GGCCCTGGTAGAAGGTATAGACA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
CSF1R_Exon-19	CCDS4302.1	NM_005211.2	TTGTGTCCACTATGGGAGAGAT	TGCTGTTACCTGTTACCCTCCT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
CSF1R_Exon-20	CCDS4302.1	NM_005211.2	CTCGGCAGATTGGTATAGTCCT	GTCTGGAACTCCTGGCCTTAT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
CSK_Exon-11;CSK_Exon-12	CCDS10269.1	NM_004383.1	CTACAGAGGTGGGCAGGAGT	AGGTGCCAGCAGTTCTTCAT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
CSK_Exon-12	CCDS10269.1	NM_004383.1	GTCTGCGGCAAAGCTGAT	CGAGGGGTCCCTAGAGAGG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
CSK_Exon-6;CSK_Exon-7;CSK_Exon-8	CCDS10269.1	NM_004383.1	GATGAGTTCTACCGCAGTGAGT	GTTTCGGGGCAGTTGGAAG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
CSK_Exon-9;CSK_Exon-10;CSK_Exon-11	CCDS10269.1	NM_004383.1	CTCCTTCCCTGTCTCACACCT	GATCCCAGTACCCATACTCACAA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
DDR1_Exon-12;DDR1_Exon-13	CCDS4690.1	NM_001954.4	CGCATGGAATACTGGGAAGATA	GTCCTCACCTGGCATTCTTG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
DDR1_Exon-12;DDR1_Exon-13;DDR1_Exon-14	CCDS4690.1	NM_001954.4	CCAGTTTGGGGAGGTAAGGAG	CTGGTGGGCACTGAGGAACT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
DDR1_Exon-14	CCDS4690.1	NM_001954.4	ATCTCTGGGAGGGGATTTACA	CCCATGTGGAGGTGGAAT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
DDR2_Exon-11	CCDS1241.1	NM_006182.2	ATGAAGCAGGTTAGGCTTTCAC	CAGGAACTCCACAGCTATTTGA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
DDR2_Exon-12	CCDS1241.1	NM_006182.2	TGTTACACATATCTTCTTATTGGTCTTT	CTTTGTCAAGAGGAGGTAATGACA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
DDR2_Exon-13;DDR2_Exon-14	CCDS1241.1	NM_006182.2	CAAAAGTTATCCAAAGGGAAACA	AGTCAGCTATCTTGATTGTGTAGTTCTT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
DDR2_Exon-14	CCDS1241.1	NM_006182.2	CATGAGAGTAACCTGGGATCTG	ACAGTCTATTGAGTTTGCCTCCT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
DDR2_Exon-15	CCDS1241.1	NM_006182.2	TGTTTCTAAATACTCCATGCACATC	AGGACTTTGTTTCCTGCTACCTT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
DDR2_Exon-16	CCDS1241.1	NM_006182.2	AGTGGGCCAAAGAAAAATGT	TATATGAGTCAGGGGTAGGGAGT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
EGFR_Exon-18	CCDS5514.1	NM_005228.3	GGGTGCATCGCTGGTAAC	TTTATAGACTGCACGCCATCAT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
EGFR_Exon-19	CCDS5514.1	NM_005228.3	CAGCTTTTCCTCCATGAGTACG	CCTGGCTTGCTTACCTTGTTAT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
EGFR_Exon-20	CCDS5514.1	NM_005228.3	AGCAGCGGGTTACATCTTCTT	GCGCTATTGAAGGGGACTTAT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
EGFR_Exon-21	CCDS5514.1	NM_005228.3	GGTGCTCAGAAACCTACCAGAG	CACTTCAAATTCATGGCAACAT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
EGFR_Exon-22	CCDS5514.1	NM_005228.3	TTCTAAACATCAAGAAACAGTAACCAG	TGCAGAGACTTCACATAAATCCAC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
EGFR_Exon-23	CCDS5514.1	NM_005228.3	AAATGTACAGTGCTGGCATGG	AGACCATGCTTCTCTCTTAGACC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
EGFR_Exon-24	CCDS5514.1	NM_005228.3	TGAGGGGAGGCAGCTATAA	GCTTGTACCACATCTCATCCAC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
EGFR_Exon-25	CCDS5514.1	NM_005228.3	CCTTCACAATATACCCTCCATGA	TGGCTACTGGACACTTCACAT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
EPHA1_Exon-11	CCDS5884.1	NM_005232.3	GAGTGAGTACCTCTGGAAACTCTTG	AGCTTCTTGCTTGTCACCTCAT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
EPHA1_Exon-12;EPHA1_Exon-13	CCDS5884.1	NM_005232.3	GGGCTCCATTCTCCATAAATTC	CCGCACTAGCTTGCTCTTCAT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
EPHA1_Exon-12;EPHA1_Exon-13;EPHA1_Exon-14	CCDS5884.1	NM_005232.3	ATGTTACGGGGCAATGTGAAT	CAGGAGAGTTTGGGGAAGTGTA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
EPHA1_Exon-12;EPHA1_Exon-13;EPHA1_Exon-14	CCDS5884.1	NM_005232.3	CTGAGGTAGTTCATGCCAGATG	GCACTCCACGCTTCTGATTCT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
EPHA1_Exon-15	CCDS5884.1	NM_005232.3	GCCAGGAGTACAGAAAAACTGAA	ACATGCCATTCATACAGTCACA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
EPHA1_Exon-15;EPHA1_Exon-16	CCDS5884.1	NM_005232.3	GCCCAGCCATAACTGATTTT	CAGGAGGTGAGCCCAGAATA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
EPHA2_Exon-10;EPHA2_Exon-11	CCDS169.1	NM_004431.2	AGAGCCCCTGCTAAGTGG	TTCTCCAAGTCAGGTGAGACG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
EPHA2_Exon-10;EPHA2_Exon-11	CCDS169.1	NM_004431.2	CACTCGCTGCTTCTCTGTGTA	GACCAAAGTAGGGCCAGGAG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
EPHA2_Exon-12;EPHA2_Exon-13	CCDS169.1	NM_004431.2	GTTGGCCAGGTACTTCATGC	CCATACCTCTGCCCACTCCT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
EPHA2_Exon-12;EPHA2_Exon-13;EPHA2_Exon-14	CCDS169.1	NM_004431.2	CAGCGGATGGGGATCTTG	CCTACAGACAAGCCCATGATGA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
EPHA2_Exon-13;EPHA2_Exon-14	CCDS169.1	NM_004431.2	AGCAAGCCTAAGAAGGTTCATC	GCAACATCCTCGTCAACAGC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
EPHA2_Exon-15	CCDS169.1	NM_004431.2	TCTTCTTCTACAAAATGAGGATCA	AAAAAGTCCCTTCCAGTGAA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
EPHA3_Exon-10	CCDS2922.1	NM_005233.5	AAACTGAAGGTTGTGCACCTTAT	GTCAAGCAAGCATTAAAATGGA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
EPHA3_Exon-11	CCDS2922.1	NM_005233.5	TCACAAGGTTCATTTTCCAACA	CCCCACAATTCTTCTCTTAACTG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
EPHA3_Exon-12	CCDS2922.1	NM_005233.5	ATTGGTCATGGGCCTTTGTT	GTTTGGAAAGTAGATGGGCTGT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
EPHA3_Exon-13	CCDS2922.1	NM_005233.5	CCACATATCTTTGTCTTGAGTGC	GTCCTTAGAATTTATCCAATCTGCTA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
EPHA3_Exon-14	CCDS2922.1	NM_005233.5	GCATATTCCATTTCAGAACAGA	GCAGTTCAAATGGTGCCTTC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
EPHA3_Exon-15	CCDS2922.1	NM_005233.5	CAGTTGTTATCCTTTTAGGCAAC	AAGCCTGAATGTAGAGTCAAGATAG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
EPHA4_Exon-10	CCDS2447.1	NM_004438.3	TGATTTCAGATTGCATTAAGTTTC	AGGCAAGGGAGCTATGAGCA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
EPHA4_Exon-11	CCDS2447.1	NM_004438.3	ACACAAGCTGCCTTGGAGATAG	TTATTCTTAGAGAGAAACTTAATGCAA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
EPHA4_Exon-12	CCDS2447.1	NM_004438.3	CTCCAACAGCTCCACATTACAG	ATTGCCTATTGACCTCCTTAGC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
EPHA4_Exon-13	CCDS2447.1	NM_004438.3	TTTGCTTCTAGTTTGTGGCTGT	CTGTTGGAGCCGTAGATTCATT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
EPHA4_Exon-14	CCDS2447.1	NM_004438.3	GGTTGTAATGTTGAACTAGCTTGC	TAAGCATTGCCTTCCTTTGTG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
EPHA4_Exon-15	CCDS2447.1	NM_004438.3	TGACAGGTATTAGTTATTCAAAATGC	AGGGCCGTCACCAAAACT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
EPHA5_Exon-11	CCDS3514.1	NM_182472.1	TTTGCTGGTTTAAGCTTGAGTT	ACTAGTATTGCATTGTCCAGTTCG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
EPHA5_Exon-12	CCDS3514.1	NM_182472.1	AATTCATAGCAAATGGGTTAAAA	AAAGGTTTTTGTAAGTGAGATAGAGGA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
EPHA5_Exon-14	CCDS3514.1	NM_182472.1	CTTTGTTGCAGGAATGCTCTT	TGACCCAAGGCAGATACTAGGT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
EPHA5_Exon-15	CCDS3514.1	NM_182472.1	AACTCATTTTGAGCTCCTGCTT	ACCCAGGGAATTTGAGTCTTTT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
EPHA6_Exon-10	N/A	NM_001080448.2	TGGGACAGGAAGAAAAGAGAGA	TGACCTAAAACTACATTGAACCAAAT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
EPHA6_Exon-11	N/A	NM_001080448.2	TGCATTCCATTATTCATTAGAAGTG	ATGTTAGGAATGATTTGCAGGT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
EPHA6_Exon-12	N/A	NM_001080448.2	TGCTTCTAACCCTCTTTAATTGTAACT	ATTCCAAGTGGCAAAGTGTCTG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
EPHA6_Exon-13	N/A	NM_001080448.2	TTGTAATTCATGTCCCTTTTATGA	CAGATCAGTTAAGGAGTTCAGCA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
EPHA6_Exon-14	N/A	NM_001080448.2	GTCCTTTGTTTAGTTGTCCTTCACT	TGACATGGACGTTAAGCATGA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
EPHA6_Exon-15	N/A	NM_001080448.2	TGTGACTTATTTCCCATTAAAGCTA	AGGTCAAGGCTATTGCACAAAC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
EPHA6_Exon-16	N/A	NM_001080448.2	TGCAATTTTTGTTCACAGCTT	ACTTCTAAAGGTAAGGAAGGATCA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
EPHA7_Exon-11	CCDS5031.1	NM_004440.2	CATAAACAAGTACAGCCTCACTGC	TTTCCAAGTCCATTACAAACCTT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
EPHA7_Exon-12	CCDS5031.1	NM_004440.2	TCAGAGTTATTCTTCAACTCTAATCTTG	AGGAAAGCGTAACTTCTATGAAAGAG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
EPHA7_Exon-12	CCDS5031.1	NM_004440.2	AAAAAGTTTCAGGAGTCGTAACC	AATGTTGTCCATTTGGAAGG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
EPHA7_Exon-12	CCDS5031.1	NM_004440.2	TTCTGCTTTCTTTTCCCTTGAG	CACAGGGCTTTACCAAGTATTTTT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
EPHA7_Exon-14	CCDS5031.1	NM_004440.2	GCAGTCATGTTATCAACACTTTCC	TGGACTTGTGCAAACTCAAACT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
EPHA7_Exon-15	CCDS5031.1	NM_004440.2	TGGTAATTAGTGTGGTAGTAATTGTGG	TCATTGTTTGTTCAATATACTCTTGC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
EPHA7_Exon-16	CCDS5031.1	NM_004440.2	GAGTTTATACGTCAACACAAAAGTCAA	TGCTGTTCCCTATTGCTGAA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC

EPHA8_Exon-10;EPHA8_Exon-11	CCDS30626.1	NM_001006943.1	AGACTCCACAGCCCCATAGAA	CAGCCTCCCGTAGCAGACTT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
EPHA8_Exon-11;EPHA8_Exon-12	CCDS30626.1	NM_001006943.1	CAGAGGGAGCGTGTGACC	CAGGAAGGTGTCCAGAGAGC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
EPHA8_Exon-12	CCDS30626.1	NM_001006943.1	CATCCCCTCATCCATCCTG	CAATGACTGCTTACCCATTTTG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
EPHA8_Exon-13	CCDS30626.1	NM_001006943.1	CCTTAACTGCAAAGTGCTTCAG	CTGGGTACAATTCGGGGAGAT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
EPHA8_Exon-14;EPHA8_Exon-15	CCDS30626.1	NM_001006943.1	GTCCCTCTGGACTGGAAAACA	TAGTGTCAGGGCCAAACTGTC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
EPHA10_Exon10	CCDS41305.1	NM_001099439	CTTCCAGACACGAGCAGAGAC	TGGTCTAGGGCTACGGTTGTAT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
EPHA10_Exon13	CCDS41305.1	NM_001099439	GTGGAGGGAGAAGACTGAGG	GGCCAGGATGACCTTTCTGA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
EPHA10_Exon13;EPHA10_Exon14	CCDS41305.1	NM_001099439	CCCAACTCCAGCTTCACATCT	GATGATTGTCACCGAGTACATGA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
EPHA10_Exon15	CCDS41305.1	NM_001099439	CAGAACCAGAAGCAAGCAGAC	CTGCCCTGGAGCCCTTAACT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
EPHB1_Exon-10	N/A	NM_004441.3	AGCCTGGTGTGTAGGAGAGC	TCATGGTCTGTCTTCAAATTCAT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
EPHB1_Exon-11	N/A	NM_004441.3	GCCACTTTAATCACAATTCCAC	GCAACAAATCTCTGCTAACATCTC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
EPHB1_Exon-12	N/A	NM_004441.3	AGTGGGAAGAGAGGAGGACAC	CTCACAGTCCAAGCCCAAAT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
EPHB1_Exon-13	N/A	NM_004441.3	GTCACCTTGAGCTTCTCTAACTAGG	TACTGCTTAATTTGGGGCTGAT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
EPHB1_Exon-14	N/A	NM_004441.3	TGCACAGAAAATCCATTACAGC	CCAGGTATCCAAACCAGAAATC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
EPHB2_Exon-10	CCDS230.1	NM_004442.6	CAGGGAGTTGCCCAGTTCTTAT	GTCCAGAAAAGTTCCAGTCACC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
EPHB2_Exon-11	CCDS230.1	NM_004442.6	GAACTTTTCTGGACCCCTGAC	AGATTTCAGATGTGTGCCAACT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
EPHB2_Exon-12	CCDS230.1	NM_004442.6	GTCCCAAAGCATCTGAGTCCT	GTCACAGGACTTTGCCATGAG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
EPHB2_Exon-13	CCDS230.1	NM_004442.6	TTGAGGATGAGAAGGAGGTTTC	AATAATCGTCTTGTCCCCCAGT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
EPHB2_Exon-14	CCDS230.1	NM_004442.6	CTAGATGGTGGAAACCCAGGTC	TTAAAAGATGCCTCCTCTGCAC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
EPHB3_Exon-10;EPHB3_Exon-11	CCDS3268.1	NM_004443.3	GATTAGGGCAGCAACACAGAG	TATGGACTTGAATAGGGGCTGT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
EPHB3_Exon-12;EPHB3_Exon-13	CCDS3268.1	NM_004443.3	GTTGCAGGAGAGACGAGGTAGA	TACCCAACCACTCTGGCGTAG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
EPHB3_Exon-12;EPHB3_Exon-13;EPHB3_Exon-14	CCDS3268.1	NM_004443.3	TTCCCTGGTACAGGAAGC	TCGTGAAGGTTGTGTAATCTGG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
EPHB4_Exon-11;EPHB4_Exon-12	CCDS5706.1	NM_004444.4	GCTTAGCCCAAGAGGAAAAG	AACCACGGAGACAGGGGTTT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
EPHB4_Exon-14	CCDS5706.1	NM_004444.4	CAAGAACCCAGCAGTGATGA	CTATGAATGTGCCACTGTACTGC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
EPHB4_Exon-15	CCDS5706.1	NM_004444.4	ACACCAATGAACGGACACTTCT	ATAATCGCTTGAACCCAGGAAC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
EPHB4_Exon-15;EPHB4_Exon-16	CCDS5706.1	NM_004444.4	AGTGCAAGAAGACAGCATTGG	CTTCCCCTCTTTCCAGGTGAT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
EPHB6_Exon-10;EPHB6_Exon-11	CCDS5873.1	NM_004445.2	TGGGGATGAGGAGAGGAAAT	GATGTTGGGGTGCTGGAACT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
EPHB6_Exon-11;EPHB6_Exon-12	CCDS5873.1	NM_004445.2	CAGAGTCCCATCCAAACACAG	CTTGCACACCAAGTGGCTATT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
EPHB6_Exon-12	CCDS5873.1	NM_004445.2	GGTCCTGTATCTTTGCTTCTTACC	CTTTGTCTCGGTCCCTGAAAT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
EPHB6_Exon-13;EPHB6_Exon-14	CCDS5873.1	NM_004445.2	GTTGCTCCATAAACGTGACTATTG	CTTCTGCCAAGTGTCCAACATA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
EPHB6_Exon-14	CCDS5873.1	NM_004445.2	CCAGGTTGGAACATTCTAGGAC	ACTGAAGGTACAGAGGCCAAAC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
ERBB2_Exon-18;ERBB2_Exon-19	CCDS32642.1	NM_004448.2	ATTCTGCTGGTCGTGGTCTT	CCAAACCCCAATGAAGAGAG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
ERBB2_Exon-18;ERBB2_Exon-19	CCDS32642.1	NM_004448.2	AGATGCGGATCCTGAAAGAG	AAAAATTAGCGGGCGCTTGTA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
ERBB2_Exon-20;ERBB2_Exon-21	CCDS32642.1	NM_004448.2	GCTGGTACTTTGAGCCTTCAC	ACTGTGTGTTGTGGGGAGGT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
ERBB2_Exon-21;ERBB2_Exon-22;ERBB2_Exon-23	CCDS32642.1	NM_004448.2	GGGCAAGGTTAGGTGAAGGAC	ATACATCCTGGTCCCCTTTCAT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
ERBB2_Exon-23	CCDS32642.1	NM_004448.2	CCCAGGATTAGGGAAAGACC	ACAAGAGTGTTCCTCAAGAGTGG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
ERBB2_Exon-24	CCDS32642.1	NM_004448.2	CTGGCTGAAGACCCCAGAGT	GAGGTGACAGTTGAGGGAACAT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
ERBB3_Exon-18;ERBB3_Exon-19	CCDS31833.1	NM_001982.2	GAAAACCCAACCCCTTTGAT	CTTGAAAACTCTGCCGTCCA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
ERBB3_Exon-19;ERBB3_Exon-20	CCDS31833.1	NM_001982.2	TGACCTTATGCCAACTCCTG	CTGCCGCTCACATGCTCT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
ERBB3_Exon-21	CCDS31833.1	NM_001982.2	TTGTGCACTCCTTATGAGAATCTAAC	GGCCAGTCCCAAGTTCTTGAT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
ERBB3_Exon-22;ERBB3_Exon-23	CCDS31833.1	NM_001982.2	TCCTAAGAAAATTTGTGGAAATAA	AAAGAGAAAATGGTTGGGCTCAG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
ERBB3_Exon-22;ERBB3_Exon-23	CCDS31833.1	NM_001982.2	TCCTAAGAAAATTTGTGGAAATAA	AAAGAGAAAATGGTTGGGCTCAG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
ERBB3_Exon-24	CCDS31833.1	NM_001982.2	TGTCTCTACCTCCTACATCTTATCTCC	CTGATCCTAAAACCCAGCCTCT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
ERBB4_Exon-18	CCDS2394.1	NM_005235.2	TCATTTGTGCAGCAACTTCTC	CTGTCCTAGGGTTTTGGCATT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
ERBB4_Exon-19	CCDS2394.1	NM_005235.2	GCAGACAGTTGTGAAGCAAAAG	TGCTATCCTATTTCCATGCTGT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
ERBB4_Exon-22	CCDS2394.1	NM_005235.2	CAAGCTTTAATTCGCAAAGAAGA	TCCCCACTTAATTATTTTTACCTTT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
ERBB4_Exon-22	CCDS2394.1	NM_005235.2	TGCTTTAGGAAATTAGGCTTATC	GGCTACTCAGAGGCTAAGGTG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
ERBB4_Exon-23	CCDS2394.1	NM_005235.2	TTTTTCCTTCATGTTTAGATCATTT	TTTTTAATTGATTGGTGTTTGG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
ERBB4_Exon-23	CCDS2394.1	NM_005235.2	ACCTTGTCCTGCTAATTTGCTC	TGACCTGTAAGGAGTATTCTTTTACTAC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
ERBB4_Exon-24	CCDS2394.1	NM_005235.2	CAGTAGCAGAGCCACTTGAA	TGTCCACCAGGACAAATGTA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
FAK_Exon-15	CCDS6381.1	NM_153831.2	TGCACATCAATCTACCTTTACACA	GACTGCTGCCTCTGCTGTTC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
FAK_Exon-16	CCDS6381.1	NM_153831.2	TGCTACAAAGTGAATTCCCAAA	TTTCCTAGTAACAATGCGTCAGTT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
FAK_Exon-17	CCDS6381.1	NM_153831.2	AATTCTAATATGATACTTGGCAAACA	TGCAAGTAAGGAAATACAGTTTGG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
FAK_Exon-18	CCDS6381.1	NM_153831.2	TGAAATGGAATTCAGAGGTTT	AAAAATAAGCTGCATCAGCAA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
FAK_Exon-20	CCDS6381.1	NM_153831.2	GACTCTAGCAAGGTACAAAGAAATG	ACTGCATTAAGCCACGAAGTA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
FER_Exon-12	CCDS4098.1	NM_005246.2	CTGATAGAATTTGGCTGTAATGTAGA	AATCCCAAGAGGCAGTATTTCA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
FER_Exon-13	CCDS4098.1	NM_005246.2	AATGAGGCATTTTATACCACAA	GCAGTACTATCTAAGGAGGGTAGGA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
FER_Exon-14	CCDS4098.1	NM_005246.2	TCATAATTTGGGGTCATACTGAAA	CATTTAGAAGAGAGGTTGTGTGGA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
FER_Exon-15	CCDS4098.1	NM_005246.2	AAACGGTATCTAGAAGAGATTATGG	GTACATTCCATGTCACCGTTGT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
FER_Exon-17	CCDS4098.1	NM_005246.2	GGCTACCACATCACTAGGCAATA	AACACCACCCTATTTCTCTTAACG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
FER_Exon-18	CCDS4098.1	NM_005246.2	CTGTAATATTGAATTCTGCATCACCT	GAGTAGGGTCTGTGGCATAGGA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
FES_Exon-12	CCDS10365.1	NM_002005.2	GTCCCACCCCTGGTCACATA	CAGTCCCGCAGTTCTCTTCT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
FES_Exon-13	CCDS10365.1	NM_002005.2	CCCCATGTGCTCTCTAGGTTC	CACTGCTGCTCAGGATCTACG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
FES_Exon-13;FES_Exon-14;FES_Exon-15	CCDS10365.1	NM_002005.2	AAGCGAGGTGGGTGATAAAC	TCTGGAGCTGATGCCTGATG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
FES_Exon-15;FES_Exon-16;FES_Exon-17	CCDS10365.1	NM_002005.2	GCGACTTCCTGACCTTCCTC	AAGATGCCAAAGCTCCACAC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
FES_Exon-16;FES_Exon-17	CCDS10365.1	NM_002005.2	ATCAGCTCCAGAGGGGGAGT	GAAGGTTGGCATTAAGGGAGTT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
FES_Exon-18	CCDS10365.1	NM_002005.2	GAACAGTGCATCCTTCAGAACA	CACTTGTGCCTTCTGAGACCT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
FGFR1_Exon-10	CCDS6107.1	NM_023110.2	GACGCCAAGGAACAGAGTGA	CTGACTCCAGTGCATCCATGA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
FGFR1_Exon-10;FGFR1_Exon-11	CCDS6107.1	NM_023110.2	TTCCTGAATGAACACCAATGAG	AAGTGTAAGTGATGCTTCTGTCCT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
FGFR1_Exon-12	CCDS6107.1	NM_023110.2	ACAGATCGGACCCTGCATC	TCTCAAAATAAACAGACAAACTGG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
FGFR1_Exon-13;FGFR1_Exon-14	CCDS6107.1	NM_023110.2	TGCTATTACAAACTCACACATCACTC	AGACGCAGCAGAGGCATAAG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
FGFR1_Exon-13;FGFR1_Exon-14;FGFR1_Exon-15	CCDS6107.1	NM_023110.2	GACATCTCCTCGGGCTTACAG	GGACATTCACCACATCGACTAC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
FGFR1_Exon-15;FGFR1_Exon-16	CCDS6107.1	NM_023110.2	TACTCCTGTGATGGGCGAGAG	CTCCAGATGTTGAAAGGCTGAT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
FGFR2_Exon-10	CCDS31298.1	NM_000141.3	CACAGCTCAAGATAAATAGTCTGTCC	GGCAAGGAATGTGACCATAAAA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
FGFR2_Exon-11	CCDS31298.1	NM_000141.3	AAAGTCACCTGCACCCTCCT	GGTCTCCTCGCTGGTTTCAG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
FGFR2_Exon-11	CCDS31298.1	NM_000141.3	CCAGGTACGGGCACAGAC	ACCATGAAGTTTGGTGTGGTTT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
FGFR2_Exon-12	CCDS31298.1	NM_000141.3	AAGGGGGCCTTTAAAACCAT	AGCATGGGTTGTAATAACTAAAAA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
FGFR2_Exon-14	CCDS31298.1	NM_000141.3	CCAGCTCCTGCACCTTCTAC	CGATTCCCGTTCTTTTGACTTA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
FGFR2_Exon-15	CCDS31298.1	NM_000141.3	TAATGGTTGTCGGTGTCGCTAT	TATTCTGTCAACTGCCCATCCT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
FGFR2_Exon-16	CCDS31298.1	NM_000141.3	ATGTCCCTCTGTCTTTGGTTTC	GTGTGACGCCATTGTGAGAT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
FGFR3_Exon-10;FGFR3_Exon-11;FGFR3_Exon-12	CCDS3353.1	NM_000142.2	CCTCTCAAGGTGCCCTGTCT	CGTACTCCACCAGCACGTACA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
FGFR3_Exon-11;FGFR3_Exon-12;FGFR3_Exon-13	CCDS3353.1	NM_000142.2	GCACAGACGATGCCACTGA	GTGTGGGAAGGCGGTGTT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
FGFR3_Exon-13;FGFR3_Exon-14;FGFR3_Exon-15	CCDS3353.1	NM_000142.2	GAGAGGTGGAGAGGCTTCAG	CAGGTCGTGTGTGCAGTTG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
FGFR3_Exon-15;FGFR3_Exon-16	CCDS3353.1	NM_000142.2	CTGGGTGTGGTTTCTACCC	GCCGACAGGTCCAGGTACTC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
FGFR3_Exon-15;FGFR3_Exon-16	CCDS3353.1	NM_000142.2	CCAACTGCACACACGACCT	GTAGCTGTCTCTCCATCTGCAC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
FGFR4_Exon-11;FGFR4_Exon-12	CCDS4410.1	NM_002011.3	CTAGCAAGGATTCAGCCCTAGA	GAGTGGGGAATGCAGGAAAG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
FGFR4_Exon-11;FGFR4_Exon-12;FGFR4_Exon-13	CCDS4410.1	NM_002011.3	GTGTCTGCACCCAGGAAGGT	TTTTCTTATAGTAGTCAATGTGGTGGA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
FGFR4_Exon-13;FGFR4_Exon-14;FGFR4_Exon-15	CCDS4410.1	NM_002011.3	CCACTCGTTCCTCACCCTTC	ATCCCAAAAGACCACCTGGA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
FGFR4_Exon-13;FGFR4_Exon-14;FGFR4_Exon-15	CCDS4410.1	NM_002011.3	CAATGTGATGAAGATTGCTGAC	AGCGAGAACAGCTCCTCCAC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
FGFR4_Exon-16	CCDS4410.1	NM_002011.3	GTCCTGGCCTGGCTTCTACT	GACACGGCACAGCAACTCT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
FGR_Exon-10;FGR_Exon-11	CCDS305.1	NM_005248.2	CCAGAGCGGATGAGAGATCAG	CTTCTCCAGGTTCCAAGTTCC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
FGR_Exon-10;FGR_Exon-11	CCDS305.1	NM_005248.2	GTCCAGACGCCAGGTCTGTT	GTGCGATCTCAGGTTATTGA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
FGR_Exon-6	CCDS305.1	NM_005248.2	CTCCGTACCCAGCCACAC	GTGGAGGCCAGACTAAATCG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
FGR_Exon-6;FGR_Exon-7	CCDS305.1	NM_005248.2	TAGTGGGACTCTGCCCATTGT	AGGCTGGGATAGGATAAGGAGT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
FGR_Exon-8;FGR_Exon-9	CCDS305.1	NM_005248.2	TACATCAGGATGGGGCGACT	GCTGACTTTCTGGCTTCTTCC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
FLT1_Exon-17	CCDS9330.1	NM_002019.3	CAAACAGGTGCTGCGTGTC	CAAGTACAACACATAAGGTCACTGG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
FLT1_Exon-19	CCDS9330.1	NM_002019.3	TCTGTAGATGCACAAGCTGTTTC	GTGCTCCTTCTCTGTGACTCC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
FLT1_Exon-20	CCDS9330.1	NM_002019.3	CATCATTGGTCTACTGCTGATTG	TAGGTTAAACTGAAAAAGTCACCGTA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
FLT1_Exon-21	CCDS9330.1	NM_002019.3	TTGAGTTTCAACATGAACACCAG	CTGTCTAGAAGCCCAGGCAAG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
FLT1_Exon-22	CCDS9330.1	NM_002019.3	CTGGTATCCATGACTCCTCATTC	CTCTAATAAACATCCGTGGGAGA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
FLT1_Exon-23	CCDS9330.1	NM_002019.3	GATGGTTTTCAGGGACTACAGC	AACTCACAGGTTTCAGACTAGACAAA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
FLT1_Exon-24	CCDS9330.1	NM_002019.3	AGTAGAGGGCAGACATGCGTA	TTTGGAAACCACCACCAGTT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
FLT1_Exon-25	CCDS9330.1	NM_002019.3	CCCCACTGCAAGAAAACACT	GCTCACTAACCCAAAGGATGA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
FLT3_Exon-16;FLT3_Exon-17	CCDS31953.1	NM_004119.2	GTTGACACCCCAATCCACTC	CCAAGACAACATCTCATTCTATGC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
FLT3_Exon-18	CCDS31953.1	NM_004119.2	TTGGGTTTGAGAGTTCACACTG	ACACAGGATATTGTTTGTTTGTTT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
FLT3_Exon-19	CCDS31953.1	NM_004119.2	TGTACTGAAGGAAAGGGACAGG	AAGCAAACAGCAAATCAGCATA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
FLT3_Exon-20	CCDS31953.1	NM_004119.2	AGTTGAATGTTGACATAAAATCTACAG	GTGAAACGCTTACGGGACTCT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
FLT3_Exon-21	CCDS31953.1	NM_004119.2	GCTAGGTGACTCCAACAGTGAA	GGTCATCAAAGCAGTTCCAAAG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
FLT3_Exon-22	CCDS31953.1	NM_004119.2	TGAAGCTGCAGAAAAACCT	AAAAAGAAAAGAGATGCTATTTCTCAC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
FLT3_Exon-22	CCDS31953.1	NM_004119.2	AGCTAGCCCAAGGACAGATG	CCCACAATAAGAGTACTGGAGGA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
FLT3_Exon-23	CCDS31953.1	NM_004119.2	CATGGGCTGCAATACAAGT	GCTCCCCTCCCGACATTA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
FLT3_Exon-23;FLT3_Exon-24	CCDS31953.1	NM_004119.2	CTATACGCTTTGCACTAAGGAG	TCCTCTGGGTTTTCCACA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
FLT3_Exon-25	CCDS31953.1	NM_004119.2	CTTACCCCACACAACTTTGA	AAGGTCATTCGATTCTATCCAC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
FLT4_Exon-17	CCDS4457.1	NM_182925.3	ACCCTGGCTGAGGTTCTAGGTA	GATAAGGGCAGCATGGAGAT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
FLT4_Exon-18	CCDS4457.1	NM_182925.3	TACTAAGGGCCCCCAGGAC	GGCGTGGGTACCTAGAACCT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
FLT4_Exon-23	CCDS4457.1	NM_182925.3	TTGCCCCAAGATGCCTAA	CACCAGTCGCCAAGAAGTG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
FLT4_Exon-24	CCDS4457.1	NM_182925.3	ACGTTGGAGGCAAAGTCCTCT	CTTGTCAGGGGAGATGGTGAG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
FLT4_Exon-25	CCDS4457.1	NM_182925.3	GTGATGCTTTCCCTGAACACTC	AGAGAGGCTTTGTTGAAACTGC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
FLT4_Exon-26	CCDS4457.1	NM_182925.3	CAACAGAAAGATGCAAGGGTGT	GGTTGTGTCCATGAGAAGGTG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
FRK_Exon-4	CCDS5103.1	NM_002031.2	TTTTACTTGCCATCACAGGAA	ACAATTGCTCTTATTATTCTATGAAACA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
FRK_Exon-5	CCDS5103.1	NM_002031.2	GACATTCATTCTCACAGACATACACA	AAGGACAGGGCAGGTATCAGT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
FRK_Exon-6	CCDS5103.1	NM_002031.2	TGCAGGTAGTTTGTAAGGCTTTG	GCCAGACTCTCAGATAATTGCAG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
FRK_Exon-7;FRK_Exon-8	CCDS5103.1	NM_002031.2	TTCCAACGCAGTGTCTCAAA	TTGCTTTAACTCGGCCTGAT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
FRK_Exon-8	CCDS5103.1	NM_002031.2	TTACCAGGCAGTGAGGAAATTA	GCAGAGTTATGAGGCTGACCA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC

FYN_Exon-10	CCDS5094.1	NM_002037.3	AAAGCTGAGGATGGGGCTTA	AGCAGAACACATGGGCAGTAT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
FYN_Exon-11	CCDS5094.1	NM_002037.3	TCTGATCCTGGGCGGTTC	CCCACTTGGAGTTCCCTCT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
FYN_Exon-6	CCDS5094.1	NM_002037.3	CCAGAATGTTAAAACCAAAACTGA	GTGAGTACAGAAACCAAAGCAGTC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
FYN_Exon-7	CCDS5094.1	NM_002037.3	ACGAGCACATAACTGGTGGTTC	AACCCCTGGACTTTCATCACT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
FYN_Exon-8;FYN_Exon-9	CCDS5094.1	NM_002037.3	TGCAGAGCTGTCAAATTCCTG	TGTTACTTCTCCATGCCTATACTTTTT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
HCK_Exon-10	CCDS33460.1	NM_002110.2	TCACAGAATCCATCTAGCAATCA	CCAACATCTGCACCTCACTTTA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
HCK_Exon-11	CCDS33460.1	NM_002110.2	GATCCCCCTAACCTGAATGG	TATTTGCCCACTCCCTCTAAAA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
HCK_Exon-12	CCDS33460.1	NM_002110.2	ACTCAAGGCCCCCTGAAGTC	AAAAAGTCATAGGAGTGAGAGAGAA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
HCK_Exon-13	CCDS33460.1	NM_002110.2	AAGGTGAGGTGGGGAGTGAT	AGGAATTGGAAGGACAGGAAAA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
HCK_Exon-8	CCDS33460.1	NM_002110.2	CAGGTGGAACACTGGAGAGAT	CTTGGGGAAAATCAGCAGGT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
HCK_Exon-9	CCDS33460.1	NM_002110.2	CTGAGAGTTGAGATGAGCAGGA	ACTGTGAACCATAAGCCCCTTC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
IGF1R_Exon-16;IGF1R_Exon-17	CCDS10378.1	NM_000875.3	CATCGCCTCCTGGTATTCTCT	CCGTGTCATCAGTTCCATGA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
IGF1R_Exon-17	CCDS10378.1	NM_000875.3	ACAAGCCTCCCAGTATGTTCTT	CGCATCGAGAAGTTAGCAGAG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
IGF1R_Exon-18	CCDS10378.1	NM_000875.3	GAGCAAGTCCTGGTTTCTTAGC	GATGAATGCAAGGTTGGACAG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
IGF1R_Exon-19	CCDS10378.1	NM_000875.3	TCATCCCTTACTGTCTCCACCT	TGGGTCTAAATAAAGCACTGTCTG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
IGF1R_Exon-20	CCDS10378.1	NM_000875.3	TGAATTTAGTTTACGGGGAACA	CACATGGAGAGGATGAGTAAGG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
IGF1R_Exon-21	CCDS10378.1	NM_000875.3	AGAAAGCCAGGGATGGAGAG	AAGGATCAGCAGGTCGAAGA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
IGF1R_Exon-21	CCDS10378.1	NM_000875.3	CTACTACAGCGAGGAGAACAAGC	GTGTCAGGCGGGTGTGTA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
INSR_Exon-17	CCDS12176.1	NM_000208.2	GAGTGAGGGGTGGGTAGGAG	TGCAGAAACAGTAGTCTCAGGTG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
INSR_Exon-18;INSR_Exon-19	CCDS12176.1	NM_000208.2	TCAGAAAAGACTTAACGGCTCA	AAAAATACAAAGGCCTATCTGTCTGC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
INSR_Exon-20	CCDS12176.1	NM_000208.2	GGGGTTCACAATGCCTACAG	AAAAATGTAGCTTCTTTGTGATTTGGTA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
INSR_Exon-22	CCDS12176.1	NM_000208.2	TGGTAGAGTCGTGAGAATCCTG	CATGTGGTCCGTGGGTGT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
INSRR_Exon-19	CCDS1160.1	NM_014215.1	CACCAAGAACCCTGGAAAGTAG	ACTGTGGTCATAGCAGATCAGAA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
INSRR_Exon-19;INSRR_Exon-20;INSRR_Exon-21	CCDS1160.1	NM_014215.1	AGGGTCACAATCTCCCAGAGTA	GAAATGATCCAAATGGCTGGT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
INSRR_Exon-20;INSRR_Exon-21	CCDS1160.1	NM_014215.1	TGAGGGTCAGTGGATGTCAA	GAGCTAGTGCGTGGCTCTTATG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
INSRR_Exon-21;INSRR_Exon-22	CCDS1160.1	NM_014215.1	CCAGCCAGGGAATGAGGT	GTGGTACTCTGGGAGATTGTGA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
INSRR_Exon-22	CCDS1160.1	NM_014215.1	CTGAGCAGGAGATAATAGCAAG	AGGTAGGGCCAGCGACAT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
INSRR_Exon-22	CCDS1160.1	NM_014215.1	GGTGACTGTACTCCAAGGGATG	GCCTACCACCGATGCAGAG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
INSRR_Exon-22	CCDS1160.1	NM_014215.1	CTTCCCTGCTCCTGTTCTCTG	ATGATTCTGGCTCACCTCCTCT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
ITK_Exon-12	CCDS4336.1	NM_005546.3	CCATCTTTGAATTATATTAACAATAGGC	AAGGGGTGAGATGGCCTAAA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
ITK_Exon-13	CCDS4336.1	NM_005546.3	TTCAGGTCTCAGCTCCAATGA	ATGAAGCCCTTTCCACTAGGAC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
ITK_Exon-14;ITK_Exon-15	CCDS4336.1	NM_005546.3	TTAACTTCCAGCGGCATTTGT	CCAGAACTCTTGTTTCCACTTTT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
ITK_Exon-16	CCDS4336.1	NM_005546.3	ACATGAATCCTAATGCAAGGAGT	GTTGGGGTAAATGAGCCACCT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
ITK_Exon-17	CCDS4336.1	NM_005546.3	TGGAATACAGTCAACATGGAAG	ACTTAACTCACCAGTTTTCTTGGA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
JAK1_Exon-11	N/A	NM_002227.2	AGGCTGAGTGTGAGGAGCTGT	GTAGAAAGCAAGGAGCCGTTTA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
JAK1_Exon-12	N/A	NM_002227.2	TGACAAGAAAACATTACACAAATGAA	CCAGAGCTGAAAGGAAGAGAGA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
JAK1_Exon-13	N/A	NM_002227.2	AAACGACCATCTTCAGTAAGCAC	AGGGAAGTTTTGCCGTGTGA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
JAK1_Exon-14	N/A	NM_002227.2	AAAAATGACTCTCTAAAAGGAGACCA	GTGCCTGGTGCTTACTGAAGAT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
JAK1_Exon-15	N/A	NM_002227.2	AAACCCATGCCCATCTCTTC	GGGATGTTTTGCTGATCCTAA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
JAK1_Exon-16;JAK1_Exon-17	N/A	NM_002227.2	CAGTAAGGTGCTTTCGCTCAT	CCAGTCTCCTTGAATTTGGACT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
JAK1_Exon-18	N/A	NM_002227.2	AGCCTTGAGAGTGTGTGGGAAC	GGCCTGTCCTGTAACGTGAG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
JAK1_Exon-19	N/A	NM_002227.2	AGAAGCTAACTTTTCATCTAAATAATGC	CAGTCATTTGCCTGTGGTTT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
JAK1_Exon-20	N/A	NM_002227.2	AGGCTGAAAGGTGTGTTTCTTG	TAAGACATCAGGCACTCTGTCC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
JAK1_Exon-21	N/A	NM_002227.2	GCAAACCAAGTTAATGGGAAAG	GTGGGTGTCATTCAGCAAAGTA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
JAK1_Exon-22	N/A	NM_002227.2	GACTTCACTGCATCATTTCCTC	CACTTTCCCATTAACTTGGTTTG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
JAK1_Exon-23	N/A	NM_002227.2	GGTACCAAATTTAAAGAGGAAGTC	TTTTTGTGTGTAAGTTTATCCCACTT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
JAK2_Exon-11	CCDS6457.1	NM_004972.2	CAATGAGTTGACCCCTAAAATAA	TGGGAGTTGCGATATAGGTCTT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
JAK2_Exon-12	CCDS6457.1	NM_004972.2	TTAATTTGGAGTCTTAAATCTGGA	CTGGATGATGCCCAGAGG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
JAK2_Exon-13	CCDS6457.1	NM_004972.2	GGCAGTTGCAGGTCCATATAA	AAAAGGCCAGTTATTCCAATGT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
JAK2_Exon-14	CCDS6457.1	NM_004972.2	AGACTCCTACTCTTGCTGTTGTAAGT	TCCCCCTGGTATTCTTCTCTGT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
JAK2_Exon-15	CCDS6457.1	NM_004972.2	AATGCATGCCTCCAAATTATTA	TTGTGGCTCAAGGAATATTACAAA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
JAK2_Exon-16;JAK2_Exon-17	CCDS6457.1	NM_004972.2	ATCCAACCCCTCCAAAATAAAG	GCTGGAAAATCAATAAGATCATTC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
JAK2_Exon-18	CCDS6457.1	NM_004972.2	GCCTGTCAGATTATGGGTAATGA	CCTCTTGCTGAGATAGTGAAAACA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
JAK2_Exon-19	CCDS6457.1	NM_004972.2	GACAGTCTGCTAATTCCAGCTA	AAGCTTTGAAACTATTTGCGTTT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
JAK2_Exon-20;JAK2_Exon-21	CCDS6457.1	NM_004972.2	AATCAGTATAATATGGCAGAGTAAAACA	AGACTTAAAAGACTTAAATGTTCACTG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
JAK2_Exon-22	CCDS6457.1	NM_004972.2	TCCACATATCAAGTAACTGTCTTTT	CGATCCAGCATTCCCACTAT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
JAK2_Exon-24	CCDS6457.1	NM_004972.2	TCAAGGACTTCAGTTCACTTCC	ACCAGCCCTCATGTGTGTAAA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
JAK3_Exon-10;JAK3_Exon-11	CCDS12366.1	NM_000215.2	CCGACTCCAAAAGTCTGGTC	ATAGAAAAGTCCAACCTGATCGT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
JAK3_Exon-10;JAK3_Exon-11	CCDS12366.1	NM_000215.2	CCTTCAGCAGCACCTCTGTC	TTCTAGAGGGTACCTCAAACTAAGG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
JAK3_Exon-12	CCDS12366.1	NM_000215.2	CTTTCCAAGGAGTGATGATGG	AAAAACCATAGATGATAGTGGGAAC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
JAK3_Exon-13	CCDS12366.1	NM_000215.2	CCTGACATCCAAGAATGACTTGT	ACAGATACAGACAGGGCTCAAC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
JAK3_Exon-14;JAK3_Exon-15	CCDS12366.1	NM_000215.2	TGAGGGGCTCTGACCTTAGC	GAGACCAGGGTGCAAGTGTG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
JAK3_Exon-14;JAK3_Exon-15;JAK3_Exon-16	CCDS12366.1	NM_000215.2	TAGCTGTTGAAGCTCACACTGAC	GCTGTGTTAAGCCTGGAGAGT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
JAK3_Exon-17;JAK3_Exon-18	CCDS12366.1	NM_000215.2	CCCATGTGAATCTGGATCAATAA	TGCACAGAGAGGGTCAATATG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
JAK3_Exon-19	CCDS12366.1	NM_000215.2	GTGTGAGCGTGCAGAGAGGAT	ATGTGTCATTGTTGCGGTTC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
JAK3_Exon-19;JAK3_Exon-20	CCDS12366.1	NM_000215.2	CACCAGAAAATGGGGCTCTG	TGTATGTTGTAGAAAGTACTCAAGAGAT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
JAK3_Exon-21	CCDS12366.1	NM_000215.2	GCGCAGACAGGTTGGAGA	AACAGCACTGGCTCCTCTGT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
JAK3_Exon-21;JAK3_Exon-22	CCDS12366.1	NM_000215.2	AAGTGCTCTGACTTGCCACAC	AATCCCTCTCGGACAACATCT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
JAK3_Exon-23	CCDS12366.1	NM_000215.2	AACAGAGACCTAATCCAGAGGT	ATAGGGAGCCATGGGAGTTTT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
KDR_Exon-17	CCDS3497.1	NM_002253.1	CCTCTAAGTGGCTATATGAATGATTA	CCATGCACATTGGTTTTCAT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
KDR_Exon-17;KDR_Exon-18	CCDS3497.1	NM_002253.1	AGGCCCACATAAGCACAAAG	GGGGAACTGAAGACAGGCTACT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
KDR_Exon-19	CCDS3497.1	NM_002253.1	GAATCCGCAAAGTATTCTAAGCTA	CCTTAATTCGCCTGCACAGAT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
KDR_Exon-20	CCDS3497.1	NM_002253.1	AAGATTCCTCACAAGTTCTTCACA	ACTCCTCTGGCCTTGATTTTCT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
KDR_Exon-21	CCDS3497.1	NM_002253.1	CTAGGGCTTCCACACTTCACTT	AGGGTAGGACATCTCTGGGTTA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
KDR_Exon-22	CCDS3497.1	NM_002253.1	TGAACTCCTTAACCACTCTTACTCA	AGTTTGACTTTTGGCCTTTGTC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
KDR_Exon-25;KDR_Exon-26	CCDS3497.1	NM_002253.1	CAATGGCTGAGAGGATGG	CCTGGGGTAAAGATTGATGAAG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
KIT_Exon-11;KIT_Exon-12	CCDS3496.1	NM_000222.2	GAGCAAATCCATCCCCACAC	ATGGCCGCATCTGACTTAAT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
KIT_Exon-12;KIT_Exon-13	CCDS3496.1	NM_000222.2	AAATTGCGCCCCTTTTGATAG	ACTAGGGTATGTCCTGGGCTGT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
KIT_Exon-14	CCDS3496.1	NM_000222.2	CAGGTTAAAAGAGGCTTGCTTG	ATGCATGTAGTACCAAGCTCAA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
KIT_Exon-14	CCDS3496.1	NM_000222.2	TCCACTGAAGCTGAATATTAATGG	CAGGAATAATCCAGAGGTCGAT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
KIT_Exon-15	CCDS3496.1	NM_000222.2	CAAAAAGGACACCTAGTTTCTGG	TAGGCTGGGTTACAAAATCCAT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
KIT_Exon-15;KIT_Exon-16	CCDS3496.1	NM_000222.2	TCTATTATGTAGCAAAGGGGATGA	ATGGCGGGAGTCACATCTCT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
KIT_Exon-15;KIT_Exon-16	CCDS3496.1	NM_000222.2	CTCTCCCAGCAGCGATAGTA	CTTACATTCTTGGAGGCGAGGA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
KIT_Exon-17	CCDS3496.1	NM_000222.2	TGTGAACATCATTCAAGGCGTA	AATTTCTCCTGCTGTGACCTT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
KIT_Exon-18;KIT_Exon-19	CCDS3496.1	NM_000222.2	TGTGAGCCATGTATTTCAGAGG	CAGTGTGTCATAAAGAATCCAAGTG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
KIT_Exon-18;KIT_Exon-19;KIT_Exon-20	CCDS3496.1	NM_000222.2	AGGCTCGACTACCTGTGAAGTG	TTTGCTTGAATGTTGGTCTTTTT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
KIT_Exon-20	CCDS3496.1	NM_000222.2	CAGTTGCATAGCCCTGGAATTA	ATTTGAGATGAGGGAGGAAACA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
LCK_Exon-10;LCK_Exon-11;LCK_Exon-12	CCDS359.1	NM_005356.3	AACACACACTCCTCCATTCTCA	TTCCTGCCCTTGGCTCTAAC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
LCK_Exon-11;LCK_Exon-12	CCDS359.1	NM_005356.3	GGCAAGGGAACAGACCAGT	AAAAAGAGAAAAAGAAAAGAGCTG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
LCK_Exon-13	CCDS359.1	NM_005356.3	CTCCAAGTGGTGTGACTGATATTC	GAAATGGGAGAGCCAGAAAG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
LCK_Exon-8;LCK_Exon-9	CCDS359.1	NM_005356.3	CAGTGGGTGAGGTGTGGAAC	GGCAGGAAAGCTCAAGAAAC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
LCK_Exon-9	CCDS359.1	NM_005356.3	CGCTGAGGTGATGAGAGTCC	GATCTCAGCTCACTGCAACTGT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
LTK_Exon-11	CCDS10078.1	NM_206961.1	CTAAGAACTGGGACGGAGAG	AGCCTCCTTATGGTGTGTGG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
LTK_Exon-12;LTK_Exon-13	CCDS10078.1	NM_206961.1	GAGGGAGACGGAAACCATGT	GACCAGGGAAGTCCTCATCA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
LTK_Exon-13;LTK_Exon-14;LTK_Exon-15;LTK_Exon-16	CCDS10078.1	NM_206961.1	GCGGCAATATCCCTACAGAGT	CAGGATGAGCTGGATTTCCTC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
LTK_Exon-14;LTK_Exon-15;LTK_Exon-16;LTK_Exon-17	CCDS10078.1	NM_206961.1	CTGCGGTAATAACTGGCCCTAC	ATGGTTTCCGTCTCCCTCCT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
LTK_Exon-17;LTK_Exon-18;LTK_Exon-19	CCDS10078.1	NM_206961.1	GGGTCCTGTAATGGAAGAGTCA	ACCTTGGTGGTGAACAACTCAT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
LYN_Exon-10	CCDS6162.1	NM_002350.2	GAGATTTGGCAGAGGGTGGT	TTATATTCATTGTTTGAGTGAAAACTT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
LYN_Exon-11	CCDS6162.1	NM_002350.2	AAATACCCAAGTAAGAACCACATATC	CATGCCCGGAACATTCTAGT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
LYN_Exon-12	CCDS6162.1	NM_002350.2	CTGCAGTGCTTGACCCTCT	TTTTTAAACAAGTAAGCCAAAGC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
LYN_Exon-7	CCDS6162.1	NM_002350.2	CACAATTATGTCAAGGATGCATTT	AATGGGTTCCAGCCCTAAGATA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
LYN_Exon-8	CCDS6162.1	NM_002350.2	TATAAAGCATGCCCGCCTTC	ACTCTTCACATTTTAAGCATATGTATTT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
LYN_Exon-9	CCDS6162.1	NM_002350.2	AGATTAGAGGGGACTGCGTTTG	GGAGCAGGAAAGTGACATAGTTC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
MATK_Exon-12;MATK_Exon-13	CCDS12113.1	NM_002378.3	GGCACCAGGAGGATGACTTG	GGGGAGGACTCAATTAGGAGAA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
MATK_Exon-7	CCDS12113.1	NM_002378.3	CGCCTGCTTGAGTTCACTTACT	AGAGGGTATTTGGAGGGACAAG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
MATK_Exon-8;MATK_Exon-9	CCDS12113.1	NM_002378.3	GTTCTCGTGTTGCATCTTCCT	TCACAGACCCCTGGCTTAGAT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
MATK_Exon-8;MATK_Exon-9;MATK_Exon-10	CCDS12113.1	NM_002378.3	CGCAGCACCCTGAGAGTC	CCGCAGCTGTGTGAATGTTAC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
MATK_Exon-9;MATK_Exon-10;MATK_Exon-11	CCDS12113.1	NM_002378.3	TATGGGCCAAGAGCTTCCT	ATTGTCATGGAGCACGTGAG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
MERTK_Exon-12	CCDS2094.1	NM_006343.2	AGTACATAGCTTGGGAGTCAGTG	CAGAGCTGCTGGTTTCATGT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
MERTK_Exon-13	CCDS2094.1	NM_006343.2	ATCACCCTGGTTTGCGATGT	TTGATGCTCTACTTTGGAGTTGTT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
MERTK_Exon-14	CCDS2094.1	NM_006343.2	CAAAAGTCCCCTGTGCTTTG	ACCTCTGTGTCTTGCCTTTGAG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
MERTK_Exon-15	CCDS2094.1	NM_006343.2	AGAGTGTGAGTTAGGCGCTCTT	CAGTTGTGCAGTCTTCTTGGTC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
MERTK_Exon-16	CCDS2094.1	NM_006343.2	AGATGGGGAAAAGAGAATATGATG	TTTAAGAGGAGCTGACGTACACA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
MERTK_Exon-17	CCDS2094.1	NM_006343.2	GCATGCTCACAGGCTGGT	CCTCGTCACACATCTGCTTAGT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
MERTK_Exon-18	CCDS2094.1	NM_006343.2	TTTGCCAGATTTCCCAGAAC	ATGCACTACAAGGCGAAGCTAT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
MERTK_Exon-19	CCDS2094.1	NM_006343.2	TCTTCCTAGAAACAGAATCACTTTT	CAGGACTTCTGAGCCTTCTGAG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
MET_Exon-15	N/A	NM_000245.2	ACATTGCTTATATCCTTGGGTGA	AATGCCTCTGGGTAAAATGAGT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
MET_Exon-16	N/A	NM_000245.2	CAAAAGTGGGCATAGGTGGT	AGAGGGAAGGTAGAGCAAGGTT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
MET_Exon-17	N/A	NM_000245.2	GCTTTTCTAACTCTCTTTGACTGC	AGTGACCAAAACCAAGGTAGGA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
MET_Exon-18	N/A	NM_000245.2	TGTTAGTCAATAGAGGCCAGATGA	CCTGGGGCTATGAGAATCAG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
MET_Exon-19;MET_Exon-20	N/A	NM_000245.2	CGTATTGAGTATGTAAAGCCAAGTTT	TGGCAAGAGCAAAGAATATCG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
MST1R_Exon-14	CCDS2807.1	NM_002447.2	CATCTTGAGACTCCATCTCTGC	ACAGAGCACGCTCCTTGGTAT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
MST1R_Exon-15;MST1R_Exon-16	CCDS2807.1	NM_002447.2	GGCACATATAGGGCAGCAG	TAGCTGTGTGTAGTGGCAGTTG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
MST1R_Exon-16;MST1R_Exon-17	CCDS2807.1	NM_002447.2	CAGTGTCCAGTCCAAGTCTGC	CTGAGCAGGAGACCTTCATTTC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
MST1R_Exon-18;MST1R_Exon-19	CCDS2807.1	NM_002447.2	ACAGCAGCACACCAAATGAC	AAAAATTCTGTAAGGGCCTAGA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC

MST1R_Exon-19	CCDS2807.1	NM_002447.2	GAGCTCAGAATGCTGTTACCAT	GGAGTCCCCAGGGTAGATGAC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
MST1R_Exon-20	CCDS2807.1	NM_002447.2	CTGAAAGTTAAAGGGCAGGAAC	TGGAACAGTAATCATAGGGATGAG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
MUSK_Exon-13	N/A	NM_005592.1	TGACATCAAGGAGTTTTAAGTATGTTG	AAATAGGAGGCAGCAAAGACAG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
MUSK_Exon-14	N/A	NM_005592.1	ACTTTAGCCAAGGGACAGAAAC	TGCAGGCCATAGGAGAAGAT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
MUSK_Exon-14	N/A	NM_005592.1	AGCTGGCATGGCTTACCTCT	TTCCTAGCCTGTGTTTCCAATC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
NTRK1_Exon-13;NTRK1_Exon-14	CCDS1161.1	NM_002529.3	CCTGCCCAGAGTCACAGCTA	GCCGCATATACTCAAAGACCAT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
NTRK1_Exon-14	CCDS1161.1	NM_002529.3	AGCTCCATCACATCAGGACAG	TCGTTATCTAAACTGCTACCCTTACA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
NTRK1_Exon-15	CCDS1161.1	NM_002529.3	AGCTGCCTCTACTGTTCTCTCAA	CGAAGGTGCTGTTTCCATCT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
NTRK1_Exon-16	CCDS1161.1	NM_002529.3	TAATGATGGGGCTGGGGTAG	CAGCTGCTCTGGGAGACAGA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
NTRK1_Exon-17	CCDS1161.1	NM_002529.3	GACTGTGTCCATTCGGGTTATT	GTCAAAGGTGAGAGTGACAGGT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
NTRK2_Exon-13	CCDS35053.1	NM_001007097.1	AGATGGACACCCAGCTTCTTC	TCCAAAATTCAGTTAGCATGGAC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
NTRK2_Exon-14	CCDS35053.1	NM_001007097.1	TGTGTCATAAGCTGGAAAGC	TGACACCTGGGTACCTTAGCTC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
NTRK2_Exon-15	CCDS35053.1	NM_001007097.1	GCTAAGTCAGGCAGCATCTTTT	CAATGTGAGGGCATAGTGAGAA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
NTRK2_Exon-16	CCDS35053.1	NM_001007097.1	TGCTTGAGACTGTGAAGAAGTCA	GCTGGACTGTATGGATTCTGGA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
NTRK2_Exon-17	CCDS35053.1	NM_001007097.1	TGAGAAAACAAAACCAAGAGTGG	AGTAATGCAGAAGCCAGATTGA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
NTRK3_Exon-13	CCDS32322.1	NM_001012338.1	TTGCTCCCCTGGCATAGC	AAACTGTGGAGACTGCTTTGTG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
NTRK3_Exon-14	CCDS32322.1	NM_001012338.1	CCTACAAACCGGGGACAAAG	CAGGCTTTCCTCCTCACAGC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
NTRK3_Exon-15	CCDS32322.1	NM_001012338.1	TGGGCAATTGAGAACATAATAAA	CTTACCCACACGTACATAATCTAATTT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
NTRK3_Exon-16	CCDS32322.1	NM_001012338.1	ATTGCATTTTGGCATAGGGTAG	TAACTCTTTCCTCACCCCTCTC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
NTRK3_Exon-18	CCDS32322.1	NM_001012338.1	TGTATGTGTAGCAGGCACTTGA	GTCAGAAGCCCATGTCCACTAT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
PDGFRA_Exon-11	CCDS3495.1	NM_006206.3	GCATAGCAACCTAGTTCAGTGCT	GTATCTTTGCCAGCCCTCTTC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
PDGFRA_Exon-12;PDGFRA_Exon-13	CCDS3495.1	NM_006206.3	TGATTACTCCAAACAGGAAAGACA	CAGTTCAGACATGAGAGCTTGTT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
PDGFRA_Exon-13	CCDS3495.1	NM_006206.3	TTTTTGAGCATGGGGATATT	CCATGAATGGCTATGACTGGA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
PDGFRA_Exon-15	CCDS3495.1	NM_006206.3	TGATGCATGTATTTGTGCGACT	TACTGCAGGAACACACCAAG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
PDGFRA_Exon-16;PDGFRA_Exon-17	CCDS3495.1	NM_006206.3	TTTGCATAGTGATATTCATCTGTGAG	AGCCAGATCACGGTGGAC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
PDGFRA_Exon-17	CCDS3495.1	NM_006206.3	GAGTGGGTGGAGTGAGAACCT	GGCAGAACAGTCAAGTATCTAGC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
PDGFRA_Exon-18	CCDS3495.1	NM_006206.3	GCACAAGTTATTAAGAGCCCAAG	GATGTCAGGGTTATGGCTCATC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
PDGFRA_Exon-19;PDGFRA_Exon-20	CCDS3495.1	NM_006206.3	AAGGTTTGAGCTGGTCTCTGAA	CATCTGGAGAATAGTGCTTACAGG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
PDGFRA_Exon-19;PDGFRA_Exon-20	CCDS3495.1	NM_006206.3	GACCACGCTACCAGTGAAGTG	TCTGAGTTTTCCTCTCAACACC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
PDGFRB_Exon-11	CCDS4303.1	NM_002609.3	TCACAGGGTCACAGGATCATAG	AAGGCTGGGAGAGAAGCTAGAG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
PDGFRB_Exon-12	CCDS4303.1	NM_002609.3	CCTCTAGTGCCTGCAAATCAG	GAGATTAAAGATGGGGCAGAAA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
PDGFRB_Exon-12;PDGFRB_Exon-13	CCDS4303.1	NM_002609.3	TGAAGGTGTTGTGATTTTGTGA	GATGAAAGTGGCCGTCAAGAT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
PDGFRB_Exon-14	CCDS4303.1	NM_002609.3	GGACCATCTTGTGGAACAGC	TCGTTGTAAACAGTGGCCTTTA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
PDGFRB_Exon-15	CCDS4303.1	NM_002609.3	GAGGGTTCTACGCATGTTTC	ATAGGTAGCGGGGTGAATCC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
PDGFRB_Exon-16;PDGFRB_Exon-17	CCDS4303.1	NM_002609.3	GCTATACTTGCTCCATGCACTC	GTGACCCTCTGCTTCTCCTCTA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
PDGFRB_Exon-16;PDGFRB_Exon-17	CCDS4303.1	NM_002609.3	CAGGTCTCTGTGGACGCACT	CTGGCCTTTTGTCGTGGTAG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
PDGFRB_Exon-18	CCDS4303.1	NM_002609.3	TGTCACTGTTCAAACCTGTCAA	ATCATCCTGCCTGTCTCTCATC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
PDGFRB_Exon-18;PDGFRB_Exon-19	CCDS4303.1	NM_002609.3	TCCAGTTACACCAAGGCTTTCT	GCATCTTCAACAGCCTCTACAC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
PDGFRB_Exon-20	CCDS4303.1	NM_002609.3	ACAAAGGGTGGTCCCCTAAAT	ATTGCCCAAATGGCTACCAG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
PTK7_Exon-15	CCDS4884.1	NM_002821.3	TGCCTGTTTAGGGCTTTGC	TGCACGAAGGGCAGTGAATA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
PTK7_Exon-16	CCDS4884.1	NM_002821.3	GAGGGGGTCACAGCAGAAC	TTATTCTCAAGTGGGGACAAGC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
PTK7_Exon-17	CCDS4884.1	NM_002821.3	TGCCAATTCTCCTCCTTTCTAA	ACTAGGACTGCTTGCTGCTTCT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
PTK7_Exon-18	CCDS4884.1	NM_002821.3	TGTGCTTCTGGGCTTCCTAC	ATGGGTGCTGAGGCATAAGTC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
PTK7_Exon-19	CCDS4884.1	NM_002821.3	GCATGTGACCAATTTCTTGATG	ATTAGCCAGGGAGTGGAGGT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
PTK7_Exon-19	CCDS4884.1	NM_002821.3	TTCCAGATGGGGAGATGAGG	AGGCTATTTACCAACCAATATAGAA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
PTK7_Exon-20	CCDS4884.1	NM_002821.3	GTCCTACCAGCCAGAGTGAGTG	CAAAGTTGGCAGATGAGTGG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
PYK2_Exon-14	CCDS6057.1	NM_004103.3	CTTCAGAGGGAGCAGGGTGAT	TGCTAGAAGCGTTACCACAGC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
PYK2_Exon-15;PYK2_Exon-16	CCDS6057.1	NM_004103.3	GCAGCAAAATCTGCAGGAG	GTGCTGGCAACCCCTGAC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
PYK2_Exon-17	CCDS6057.1	NM_004103.3	AGGACCCTGCGATGACAACT	GAGGGGCTAGAAGGTCTTGATA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
PYK2_Exon-18;PYK2_Exon-19	CCDS6057.1	NM_004103.3	AGGTGTGCTGTGGCAAGAC	AGCAAAATAGAACCCTGGGAAC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
PYK2_Exon-18;PYK2_Exon-19	CCDS6057.1	NM_004103.3	ACTTTGGTCTTTCCCGGTACAT	TAAGGGGCTGTCTCTCTACACC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
PYK2_Exon-20	CCDS6057.1	NM_004103.3	TGCTCCTGGTGGAGACTGA	AAAGATCACTCCCTTCCTTGCT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
PYK2_Exon-21	CCDS6057.1	NM_004103.3	CCCATATCCAAGCCTGTCTC	GCGGGGTATAGATGTAGGGACT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
PYK2_Exon-22	CCDS6057.1	NM_004103.3	AGTGAGGTGGCTTCTTTGTACC	GTTCTGGATGGGGCCTCTTT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
RET_Exon-12	CCDS7200.1	NM_020975.4	GTTGCCGCTGGCTCAGAT	CCTTACTGGTGGTCTCTTCACC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
RET_Exon-13	CCDS7200.1	NM_020975.4	GATCCGGCATGTGTGGTT	TACCCTAGTACCCAGGATGCAC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
RET_Exon-14	CCDS7200.1	NM_020975.4	GTGGTTCAAGAGAAAGCTGAGG	GTAGCGGCCTGGTGAGAC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
RET_Exon-15	CCDS7200.1	NM_020975.4	GTCACACCCTGACTCCACCA	CAAAGAATGACGATCCTGCTAA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
RET_Exon-16	CCDS7200.1	NM_020975.4	CATCTCAGCAATCCACAGGAG	GGCACACCAATCTATAAACTCACA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
RET_Exon-17	CCDS7200.1	NM_020975.4	TGACATCTGTGAGCATCTGTG	TAAGACCATCTCCCCTGAGAGT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
RET_Exon-18	CCDS7200.1	NM_020975.4	GTCAGCGATGCAGAAATAGCTT	TGGGCACTTGCTTTAACTC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
ROR1_Exon-9	CCDS626.1	NM_005012.2	CATTTTGTGGCTGGGTTGAG	CCTTGTGGACAAAGAAGTGACTA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
ROR1_Exon-9	CCDS626.1	NM_005012.2	CTAATGGCAGAACTGCACCAC	GAGCTTGTGTGACTTGAGAGTCC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
ROR1_Exon-9	CCDS626.1	NM_005012.2	TGTATGGCAAATTCTCTTCTGATT	CCATTCCACCAGGATGATTT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
ROR1_Exon-9	CCDS626.1	NM_005012.2	CACAGACAACCTCCCTCAGTG	TTTTTCTGGCCGAGTGTCTG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
ROR2_Exon-9	CCDS6691.1	NM_004560.2	GGGTAGAAGTTGGGCAGGTAG	ACCCGCAATGTGCTAGTGTA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
ROR2_Exon-9	CCDS6691.1	NM_004560.2	AGATGTCTGAGTCGATGGAGAA	CTGCGGTGACAGTGATGTTT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
ROR2_Exon-9	CCDS6691.1	NM_004560.2	CTGTGTCAGAGGACAGAGAGGA	AGACCAGCTCCCTGAGCAC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
ROR2_Exon-9	CCDS6691.1	NM_004560.2	GTAGCTGAAGACCTCCCACAG	CTGCGGTGACAGTGATGTTT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
ROR2_Exon-9	CCDS6691.1	NM_004560.2	CTTTGTCCTTCAGCGTTTTGAT	TGTAGGGTGTGTGTGTGTGTCC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
ROS1_Exon-36	CCDS5116.1	NM_002944.2	TAGAGGTAATGCAAACCCTGGA	GCTACAATAAAAGTGTTGAGGCAAT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
ROS1_Exon-37	CCDS5116.1	NM_002944.2	GGCTCAGAAGATTGGCCTCTAT	TTGCTTGGGACTGGGAAC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
ROS1_Exon-38	CCDS5116.1	NM_002944.2	CCAGGGTTCTGATTGTCAAAAG	TGTCTTGAGAAAACTGTGTAGCC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
ROS1_Exon-39	CCDS5116.1	NM_002944.2	TGCTAGTTTGAAGGAATTAAAATG	TTGACTACTTATGAGAGCAGCAAC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
ROS1_Exon-40	CCDS5116.1	NM_002944.2	GGGGCATCATTCAAATAATAAA	ACTAGGGCTACTTCTTTGATTTCT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
ROS1_Exon-41	CCDS5116.1	NM_002944.2	TTGACACAATGAATTGATATTTTATG	TGCTCTGAAATTCTTAGATAATGGA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
ROS1_Exon-42	CCDS5116.1	NM_002944.2	AGATTATAAATCCAGGGGCCATA	TTTTCCCACCATCTACTTATCC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
RYK_Exon-17	N/A	NM_001005861.2	TGCTTCCTATCCTTATCTTAGACACA	AGATCAAAGCTTGTTTCATTTGG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
RYK_Exon-18	N/A	NM_001005861.2	TTCCAAAACAATTAGGCTCATA	GGCCTTCCCTTGAAGCTACT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
RYK_Exon-19	N/A	NM_001005861.2	AAGCTTTCAATTCAGAAGTCATCA	TTGATGAACCTGTTTTCTCACA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
RYK_Exon-20	N/A	NM_001005861.2	AAGCCAACATTTTCCTTTAAGC	TTTTTCATGTGTGATAATGGAGT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
RYK_Exon-21	N/A	NM_001005861.2	TCACCACCCTTAAATACAACACA	TTGAAAATAATCCCAAAGAGAGAA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
RYK_Exon-21;RYK_Exon-22	N/A	NM_001005861.2	TTACAAACAGTGCTGGCCTATG	TTTTTGGATGGAGTAGGATTGTG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
RYK_Exon-23;RYK_Exon-24;RYK_Exon-25;RYK_Exon-26	N/A	NM_001005861.2	GCATGAAAGAGTGAACGAATCTC	ACGTAGCTTGTAATCAACAGTAAAC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
SRC_Exon-10;SRC_Exon-11	CCDS13294.1	NM_005417.3	CAGGGGCTGTGTGGTATGTC	CAGCACTGGCACATGAGGTC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
SRC_Exon-11	CCDS13294.1	NM_005417.3	GATGTTAGGCTCTCTCGATGGT	CCCTTCTCCTGGTTCCTCTT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
SRC_Exon-6	CCDS13294.1	NM_005417.3	GTGTCCCCTGAAATCTGTGTG	AGACCTAAGCTTCCCAGCACTC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
SRC_Exon-7	CCDS13294.1	NM_005417.3	GCTTTGACTGGGTTTGTCACAT	AAATTACTGTGGCTCACACCTG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
SRC_Exon-8	CCDS13294.1	NM_005417.3	TGCATCCTTGTTGCATCTCC	AAAAGGCTTGTTGACCACTG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
SRC_Exon-9;SRC_Exon-10	CCDS13294.1	NM_005417.3	CTCTGCTCTGTGCCCTGTG	TCCGACTTGATGGTGAAGC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
SRMS_Exon-4;SRMS_Exon-5	CCDS13525.1	NM_080823.2	GTAGAGAGGCCCGGTTCAC	ACTTAGGCCCCCAGAGCAAT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
SRMS_Exon-4;SRMS_Exon-5	CCDS13525.1	NM_080823.2	CCCTTCAGTGTCTGGATCTCCT	GGGCAGTAATGAGCATGTGTAG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
SRMS_Exon-6;SRMS_Exon-7	CCDS13525.1	NM_080823.2	CAAGAGCTGCCTCGATTCTG	CCATCCTCGCCACGTCTTA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
SRMS_Exon-6;SRMS_Exon-7	CCDS13525.1	NM_080823.2	GCTCGGGGAGTAGATGTCGT	CCAGCCTTGGTCTAATGTGA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
SRMS_Exon-7;SRMS_Exon-8	CCDS13525.1	NM_080823.2	GTCTGCACGTCTGCCTGGT	CTCCAAGATCCCGGTCAAGT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
SYK_Exon-10	CCDS6688.1	NM_003177.3	CAAAGTTATTTGTCACCACTCG	GCAGTGCAGTAAACCCTCTAC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
SYK_Exon-11	CCDS6688.1	NM_003177.3	ATAGAGATGGGGTTTCCTCTTG	GGCTGATTTCATGGGTATGTTT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
SYK_Exon-12	CCDS6688.1	NM_003177.3	ATGCATATCTTGCATGTTGTAGG	GACTGAGGCCACCACTTCA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
SYK_Exon-13	CCDS6688.1	NM_003177.3	GCCCTAGAGTTAGCCACCAG	GGCCCGATGAGTAACAAATG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
SYK_Exon-8	CCDS6688.1	NM_003177.3	CATGAGCAGTGATGGTGCTATT	TTGATGTTTTTATTTTCTTATGTTTCTG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
SYK_Exon-9	CCDS6688.1	NM_003177.3	AGGCCAGCCATCCATTACAG	CAGTGAGAAAGGAGATTCCATGT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
TEC_Exon-12;TEC_Exon-13	CCDS3481.1	NM_003215.2	AAAAATAATGGTGAAAGATTGTTAAG	TTTATGAGGGAATTGGGAAGTG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
TEC_Exon-12;TEC_Exon-13	CCDS3481.1	NM_003215.2	CACACACCATAAAGCTGCACTAA	TGGTAAAGAAGGAAGTATTTGTTTGA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
TEC_Exon-14	CCDS3481.1	NM_003215.2	AAGAGAAGAAAAACACTGCAGACA	AAAAAGACAATTGGTAAAGATTATGTA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
TEC_Exon-15;TEC_Exon-16	CCDS3481.1	NM_003215.2	GAGGAAGCAGCCTGAATGTATC	GGTGTAAACCCATGGTGTGTCT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
TEC_Exon-15;TEC_Exon-16	CCDS3481.1	NM_003215.2	CATTCTGCCTTCCGTGAATACT	CCTGAAAGCCTGTGTGTTTCTA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
TEC_Exon-17	CCDS3481.1	NM_003215.2	AATCACCATTTCTAAGGCAACA	GCACAACAGTGGAGACAGTGG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
TEK_Exon-15	CCDS6519.1	NM_000459.2	AGCTGGTTTATCAGGGCAGTC	CTCATCCCAATGAATCAAGACA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
TEK_Exon-16	CCDS6519.1	NM_000459.2	GTTGATGGTGACTGAGGGTAGC	GGCATTCATGGCTTTTAACATT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
TEK_Exon-17	CCDS6519.1	NM_000459.2	CTGGCCCCTTTTGAGTATTG	AGAGGCAAACCAGGCTAAGAG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
TEK_Exon-18	CCDS6519.1	NM_000459.2	TAAGGGAACTGGATTGTGACTG	TTAGATGAGCCTGTAGAAGTTATGAAT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
TEK_Exon-19	CCDS6519.1	NM_000459.2	CATTCATATAACGCTGCTGGAC	CTATTCTGGGTTGCTTCCTCTG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
TEK_Exon-20	CCDS6519.1	NM_000459.2	TAAAGTGATTTGGGGGCTCTG	ATATTGATAAAACTAGGATCAGGGTAT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
TEK_Exon-21	CCDS6519.1	NM_000459.2	CAGCTTTGATGTGCAGTGAGTT	TCCCCAAGGATAGTGTTGTATG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
TEK_Exon-22	CCDS6519.1	NM_000459.2	CATGCATTGGGTGGCTTC	TGAATTACCACTTGGGTTTTGA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
TIE_Exon-15;TIE_Exon-16	CCDS482.1	NM_005424.2	CCTACCTGTGGCTCTGTTACCT	GGCTCACCTCGGTTCTTACAG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
TIE_Exon-15;TIE_Exon-16	CCDS482.1	NM_005424.2	TTATGTCCTCTGTCTGCCTGTC	CTACTCATGTGGTGGAGGTGAT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
TIE_Exon-16;TIE_Exon-17	CCDS482.1	NM_005424.2	CCTGATGCTCTCCTTTGTCC	TGACTTCTTCCACTGACACCAG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
TIE_Exon-17	CCDS482.1	NM_005424.2	ACCTGTGCACCACCCTTGAT	AAAAAGATAAAATGCCTTCCCTCA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
TIE_Exon-18;TIE_Exon-19	CCDS482.1	NM_005424.2	AGATTGCAGCCAGGAGGGTAG	CCCCGTCACTTACACAAACATA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
TIE_Exon-19	CCDS482.1	NM_005424.2	TCTCATTCAACCCTCACCCTTA	GGCATGTAGTGGTCAGAGGAGT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
TIE_Exon-20;TIE_Exon-21	CCDS482.1	NM_005424.2	GCCAAGGCCAGATACTTACAGA	CATTGCTGAGATGAGGAGTCAG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
TIE_Exon-20;TIE_Exon-21;TIE_Exon-22	CCDS482.1	NM_005424.2	CACATCTTGGGCAGGTAGAAG	CTAAGCAGTGGCCTTGGAAGAG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
TIE_Exon-21;TIE_Exon-22	CCDS482.1	NM_005424.2	GGTACACCCTACTGTGGCATGA	ATGCACTCTGCTCTGGCTCT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
TNK1_Exon-3;TNK1_Exon-4	N/A	NM_003985.3	ACTGGGTCTACAAGGTGTGTGTT	GTGGGTGCTCCAAGTTCATC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
TNK1_Exon-3;TNK1_Exon-4;TNK1_Exon-5	N/A	NM_003985.3	CTCAAGTGTCTGATCCCAGAGG	CAGCAGTAGGTTGCGCGTAG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
TNK1_Exon-4;TNK1_Exon-5	N/A	NM_003985.3	CTGCGAGAGGTATCGGTCAT	CGAAGGAAGTGGAGCTGAAAG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
TNK1_Exon-5;TNK1_Exon-6	N/A	NM_003985.3	CCATCAAGGTGGCTGACTTC	CTCCAGGTGGGAAAAGCTAGG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC

TNK1_Exon-6	N/A	NM_003985.3	AAAGAGGACTTTTGTGAAAGATGG	TGTCAACACGACTGCAACTG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
TXK_Exon-10	CCDS3480.1	NM_003328.2	GACATTGAGGCTTGGAAAGGT	TCCCAGGTCTAGTTTTGGTAGG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
TXK_Exon-11	CCDS3480.1	NM_003328.2	TAAATTTGCACCATACTTACCAA	AGTCACTCTTTCCTCCCTCTTG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
TXK_Exon-13	CCDS3480.1	NM_003328.2	ACAGTCGGGATGTGGTTAGAA	GCAGGCTTCTTTGTAGAGTTAAGA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
TXK_Exon-14	CCDS3480.1	NM_003328.2	TGCAAGAACCAATCTCAAACA	AAAAAGAAAAGAAAATGCTACTGG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
TXK_Exon-15	CCDS3480.1	NM_003328.2	GTGCAAATCCCTCTCACACATA	TCACGCCTCACTCAACTG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
TYK2_Exon-10;TYK2_Exon-11	CCDS12236.1	NM_003331.3	GGTCCTCGTCATCCATCTTG	CTACCGCCTGATCCTCACAG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
TYK2_Exon-10;TYK2_Exon-11;TYK2_Exon-12	CCDS12236.1	NM_003331.3	CGGGATCAGAGTACAGGTGAG	GGGTTGACCAGAAGGAGATCA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
TYK2_Exon-10;TYK2_Exon-11;TYK2_Exon-12	CCDS12236.1	NM_003331.3	AGGCTGGCTGTCTCGTAGAA	GGGTTGACCAGAAGGAGATCA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
TYK2_Exon-14;TYK2_Exon-15	CCDS12236.1	NM_003331.3	TCAAGTCTCTTACTTGCCTTCTG	ATAGTCACAGTTGTCCTTTTCACA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
TYK2_Exon-14;TYK2_Exon-15	CCDS12236.1	NM_003331.3	CTGCTGGTAGCCCAGAGAGA	ATAGTCACAGTTGTCCTTTTCACA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
TYK2_Exon-16	CCDS12236.1	NM_003331.3	CTTATGAATGCCACTGCAAGAA	GCCCCAGAAGAGGTTTTATCTA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
TYK2_Exon-17;TYK2_Exon-18	CCDS12236.1	NM_003331.3	GTACTGCAGCCTGGGGTTG	CTGCTGGGGAAAGGATCG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
TYK2_Exon-17;TYK2_Exon-18	CCDS12236.1	NM_003331.3	CTGCCTTGAGGGCTTTCAC	CCTCCCAAACAGGTGTCAGT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
TYK2_Exon-18;TYK2_Exon-19	CCDS12236.1	NM_003331.3	GTTCGGAGGTCAGTGCAAG	CACGAGCACATCATCAAGTACA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
TYK2_Exon-19;TYK2_Exon-20	CCDS12236.1	NM_003331.3	CTTCACTGGGATCATGCCCTAT	GCTCTTCGCCCAGCAGAT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
TYK2_Exon-20;TYK2_Exon-21	CCDS12236.1	NM_003331.3	ACCCCGAAGGACCAGACAT	CGCCCCACTGAAACTCAC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
TYK2_Exon-22	CCDS12236.1	NM_003331.3	CCTCTCCACAGCAGGATAGT	CAAACACCTGACTCACGCTTA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
TYK2_Exon-22;TYK2_Exon-23	CCDS12236.1	NM_003331.3	AGACAGGAGTAAGGCACACG	CTGCCTTTCATTGCCTCTTG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
TYRO3_Exon-12;TYRO3_Exon-13	CCDS10080.1	NM_006293.2	ACAAATCTGCCTGTGTGGAGTT	AGGCTACAGCTATCCCCCACT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
TYRO3_Exon-13	CCDS10080.1	NM_006293.2	GGATGTTTGTGGGGAATGGT	AGGTCTTGTCCTTCAGATGTCC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
TYRO3_Exon-14	CCDS10080.1	NM_006293.2	TTCACAAGCATAAACCCAAACA	TCTTCATGTGCAGACCTTTG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
TYRO3_Exon-15;TYRO3_Exon-16	CCDS10080.1	NM_006293.2	GGTAGTCCCCAGACCAGTGT	CTGGAGGGGTAGGTTCTAGTGG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
TYRO3_Exon-16;TYRO3_Exon-17	CCDS10080.1	NM_006293.2	GTCTTCCAGGCTCCCTCTTA	CTGCTCACCACGTCACTCTG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
TYRO3_Exon-17;TYRO3_Exon-18	CCDS10080.1	NM_006293.2	GGTAGCTTGGGAGCAAAGATG	CCATCAGCCAAAACTCCAGAT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
TYRO3_Exon-18	CCDS10080.1	NM_006293.2	CAGGACACCTAGTGACAGCTTCT	CAGTTCCCTTCTTCCCAGGAT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
TYRO3_Exon-19	CCDS10080.1	NM_006293.2	AACTCCTGGGCTCAAATAATACC	GCACAGCTTGGGAGGACTAC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
YES1_Exon-10	CCDS11824.1	NM_005433.3	TATCTCATGTGCTCACCCTGTC	AGCTATTAGGTGCCAGACTGTACTT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
YES1_Exon-11	CCDS11824.1	NM_005433.3	TTGTTTGGACCCTGAAATACG	TAATCAAATGGGGTTGGCTTTT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
YES1_Exon-6	CCDS11824.1	NM_005433.3	TTTTAAAGGATTTTAGACCAAACTTCA	CCATCTGCCTCAGCTTCCTTA	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
YES1_Exon-6;YES1_Exon-7	CCDS11824.1	NM_005433.3	ACAAAGTGTCAGGTTTCTTCTATCC	AGAACATGCTGATGGTTTATGC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
YES1_Exon-8	CCDS11824.1	NM_005433.3	TCCCACCATTTCACTACACATAC	CCGTAATCAGACTTCTAGCCTTTT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
YES1_Exon-9	CCDS11824.1	NM_005433.3	AGCTAAAACAATTCTTATTCTGGAAA	AAATTAATGGGATTATAGGTGTGG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
ZAP70_Exon-12	CCDS33254.1	NM_001079.3	CTCTCACACCCCAGAGTCCT	CTACCCTCACCCCGGAAAAG	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
ZAP70_Exon-7	CCDS33254.1	NM_001079.3	GTGCAGGAACACGCATGG	ATCGCCAAAAAGAATCCAAAGT	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
ZAP70_Exon-8	CCDS33254.1	NM_001079.3	CCTGGGTGGCGACTACAGTT	AATGGTGGACTGAGGGTTAGC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
ZAP70_Exon-9;ZAP70_Exon-10	CCDS33254.1	NM_001079.3	GTGTGGGTGATCCCTAAAGC	GTGACCCCATAGCTCCAGAC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC
ZAP70_Exon-9;ZAP70_Exon-10;ZAP70_Exon-11	CCDS33254.1	NM_001079.3	CTACGCCAAGATCAGCGACTTT	ACTGGAGCAGGACAGCAAAC	TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGACC

Table S3. Primers used for PCR amplification and sequencing of the whole coding region

Gene and Exon Name	CCDS accession	Ref Seq accession	Forward Primer	Reverse Primer	Sequencing Primer
DDR1-1	CCDS4690.1	NM_001954.3	GTAAAACGACGGCCAGTTGATTAACTTACGCACCACCC	GTGTGCCAAGTACCTGCTGTG	GTAAAACGACGGCCAGT
DDR1-2	CCDS4690.1	NM_001954.3	TTACTGCTGCTGCTCTTGGTG	GTAAAACGACGGCCAGTCCAGGTCTGCCTCCATCTC	GTAAAACGACGGCCAGT
DDR1-3	CCDS4690.1	NM_001954.3	GTAAAACGACGGCCAGTGCACACCTGGCACACTTGTAG	GTCGTCAGCGTATAGGTGGTG	GTAAAACGACGGCCAGT
DDR1-4	CCDS4690.1	NM_001954.3	GACAGAGCCAGAGGTCTCAGC	GTAAAACGACGGCCAGTGATGCCCATTCTCCACACTC	GTAAAACGACGGCCAGT
DDR1-5	CCDS4690.1	NM_001954.3	GTAAAACGACGGCCAGTCAAGAAGGGACCTGAAACCTG	CAGCTCTTCCATCTCACTCCC	GTAAAACGACGGCCAGT
DDR1-6	CCDS4690.1	NM_001954.3	GTAAAACGACGGCCAGTGAGCAGAATGCCTGGATGTC	ACAGGGTCAAGGCTAGGAGTG	GTAAAACGACGGCCAGT
DDR1-7	CCDS4690.1	NM_001954.3	CAGGCTATGCAGGTGAGTGAG	GTAAAACGACGGCCAGTTAGGGACACTGCAGGGTTAGG	GTAAAACGACGGCCAGT
DDR1-8	CCDS4690.1	NM_001954.3	GTAAAACGACGGCCAGTTAGGGTTAACACCCACCACAG	AGGGTCAGCACCACAGGAG	GTAAAACGACGGCCAGT
DDR1-9	CCDS4690.1	NM_001954.3	GTAAAACGACGGCCAGTAACTTCAGCAGCTTGGGTGAG	TTTACTAAGCCCTCCTCTTGGG	GTAAAACGACGGCCAGT
DDR1-10	CCDS4690.1	NM_001954.3	GTAAAACGACGGCCAGTAACGCAGGGATGGACACAG	ACAGACAAGATAGCACCACGG	GTAAAACGACGGCCAGT
DDR1-11	CCDS4690.1	NM_001954.3	GTAAAACGACGGCCAGTAGTCTCTCACTCAACCGGGAG	GGTCAAACGGATTAACACGG	GTAAAACGACGGCCAGT
DDR1-12	CCDS4690.1	NM_001954.3	GTAAAACGACGGCCAGTAGCCAGGAACCTTAGTCATTTG	CCCAGCGTACATGTAAATCCC	GTAAAACGACGGCCAGT
DDR1-13	CCDS4690.1	NM_001954.3	GGGATTTACATGTACGCTGGG	GTAAAACGACGGCCAGTCCTGGAACCTCTCTCCCTTC	GTAAAACGACGGCCAGT
DDR1-14	CCDS4690.1	NM_001954.3	GTAAAACGACGGCCAGTGAGTGGGCTCTCTCTCCTCTC	GTGTGACTGATGGAGACCAGG	GTAAAACGACGGCCAGT
DDR1-15	CCDS4690.1	NM_001954.3	GTAAAACGACGGCCAGTGGAGGAGAGTGGAGAGCCTG	GTGGCAGTGTGGATGAGAGTC	GTAAAACGACGGCCAGT
DDR1-16	CCDS4690.1	NM_001954.3	GTAAAACGACGGCCAGTGGGCAGAGTTGTCATCTTGG	ATTAGAGGTGATGGGCTGTCG	GTAAAACGACGGCCAGT
EPHA6-1	N/A	NM_001080448.2	GTAAAACGACGGCCAGTAGCAGCCTCAGCTAAAATATGA	AAGGGTTGAAGCAAAGAACAGA	GTAAAACGACGGCCAGT
EPHA6-2	N/A	NM_001080448.2	GTAAAACGACGGCCAGTTTCCTCAAGACTCCTTCCCTAC	CAACAACCAGTGCATTACCTCT	GTAAAACGACGGCCAGT
EPHA6-3	N/A	NM_001080448.2	GTAAAACGACGGCCAGTTTTTTCCTGTGTTCCCTAAGAGT	AAAACCCACTTCAGGTTATAGTAATTC	GTAAAACGACGGCCAGT
EPHA6-4	N/A	NM_001080448.2	GTAAAACGACGGCCAGTACTTTTGGTATTCAGAGCATAATTTC	AACCTATAATGTGCATGTCAGTGG	GTAAAACGACGGCCAGT
EPHA6-5	N/A	NM_001080448.2	GTAAAACGACGGCCAGTTGGCATCCGTTATTGTATTTTC	GGACCAGTTAGTCAGGATTCAAA	GTAAAACGACGGCCAGT
EPHA6-6	N/A	NM_001080448.2	GTAAAACGACGGCCAGTTTTAAAAGATGTCAGTGGTACATAAA	GCTGAAGTAGTTTGCAATTTGG	GTAAAACGACGGCCAGT
EPHA6-7	N/A	NM_001080448.2	GTAAAACGACGGCCAGTGCTTTAATATGGGACAGGAAGAAA	TGACCTAAAACTACATTGAACCAAAT	GTAAAACGACGGCCAGT
EPHA6-8	N/A	NM_001080448.2	GTAAAACGACGGCCAGTTGCATTCCATTATTCATTAGAAGTG	ATGTTAGGAATGATTTGCAGGT	GTAAAACGACGGCCAGT
EPHA6-9	N/A	NM_001080448.2	GTAAAACGACGGCCAGTTGCTTCTAACCCTCTTTAATTGTAACT	ATTCCAAGTGGCAAAGTGTCTG	GTAAAACGACGGCCAGT
EPHA6-10	N/A	NM_001080448.2	GTAAAACGACGGCCAGTTTGTAATTCATGTCCCTTTTATGA	CAGATCAGTTAAGGAGTTCAGCA	GTAAAACGACGGCCAGT
EPHA6-11	N/A	NM_001080448.2	GTAAAACGACGGCCAGTTTTAGTTGTCCTTCACTACTTCCAGTT	TCAAAGATACTTCAGCCCATGTT	GTAAAACGACGGCCAGT
EPHA6-12	N/A	NM_001080448.2	GTAAAACGACGGCCAGTTGTGACTTATTTCCCATTAAAGCTA	AGGTCAAGGCTATTGCACAAAC	GTAAAACGACGGCCAGT
EPHA6-13	N/A	NM_001080448.2	GTAAAACGACGGCCAGTCTCTCGTAGGGTGAGCAGATG	ACTTCTAAAGGTAAGGAAGGATCAA	GTAAAACGACGGCCAGT
EPHA6-14	N/A	NM_001080448.2	GTAAAACGACGGCCAGTAAAATCAGAGGCTTTCAAATGG	GCATGTAGGCAAAAGACAATCT	GTAAAACGACGGCCAGT
EPHA6-15	N/A	NM_001080448.2	GTAAAACGACGGCCAGTGTAAGCTACACTATTTTTGGTAACTGTG	ATCACTAAGGAAGCCCCACCT	GTAAAACGACGGCCAGT
EPHA10-1	CCDS41305.1	NM_001099439	GTAAAACGACGGCCAGTTCTCTCCAATGACTCCTTCCC	GATTGGTTCCCATGGATGATG	GTAAAACGACGGCCAGT
EPHA10-2	CCDS41305.1	NM_001099439	GTAAAACGACGGCCAGTGGAGACCACACACTCTGAGGAG	TCCTTCCCTACTGACTGTGGC	GTAAAACGACGGCCAGT
EPHA10-3	CCDS41305.1	NM_001099439	GTAAAACGACGGCCAGTCTGCTTGTAGTAGACGCGCAC	CTGCATCTTACAATTTCCGGG	GTAAAACGACGGCCAGT
EPHA10-3	CCDS41305.1	NM_001099439	CCTCTTTCCTCTAGGGCACAC	GTAAAACGACGGCCAGTACCTGCAAGGAGACCTTCAAC	GTAAAACGACGGCCAGT
EPHA10-3	CCDS41305.1	NM_001099439	GTAAAACGACGGCCAGTCTCCAGAGTCCAAGGCTTCTC	GTGCGCGTCTACTACAAGCAG	GTAAAACGACGGCCAGT
EPHA10-4	CCDS41305.1	NM_001099439	TGTAAAACGACGGCCAGTGAGTCCTGCCTTGGAAGAATG	GTTACCCTCCCCTTCTCCTGT	GTAAAACGACGGCCAGT
EPHA10-5	CCDS41305.1	NM_001099439	TGTAAAACGACGGCCAGTCACTCTCCCTCCGCTTCTCT	ACCTCACTGCACATCCTCCT	GTAAAACGACGGCCAGT
EPHA10-6	CCDS41305.1	NM_001099439	TGTAAAACGACGGCCAGTGTGACCAGGAGGATGTGCAGT	CTTCTCTGTCTGCTTGCTTCTG	GTAAAACGACGGCCAGT
EPHA10-7	CCDS41305.1	NM_001099439	TGTAAAACGACGGCCAGTCAGAACCAGAAGCAAGCAGAC	CTGCCCTGGAGCCCTTAACT	GTAAAACGACGGCCAGT
EPHA10-8	CCDS41305.1	NM_001099439	TGTAAAACGACGGCCAGTCCCAACTCCAGCTTCACATCT	GATGATTGTCACCGAGTACATGA	GTAAAACGACGGCCAGT
EPHA10-9	CCDS41305.1	NM_001099439	TGTAAAACGACGGCCAGTGTGGAGGGAGAAGACTGAGG	GGCCAGGATGACCTTTCTGA	GTAAAACGACGGCCAGT
EPHA10-10	CCDS41305.1	NM_001099439	TGTAAAACGACGGCCAGTGCTGAAGCTCCCTCCCATAG	AGGATTTAAGCTGGAAACAGTCC	GTAAAACGACGGCCAGT
EPHA10-11	CCDS41305.1	NM_001099439	TGTAAAACGACGGCCAGTCTTCCAGACACGAGCAGAGAC	TGGTCTAGGGCTACGGTTGTAT	GTAAAACGACGGCCAGT
EPHA10-12	CCDS41305.1	NM_001099439	TGTAAAACGACGGCCAGTAAATCTGCGTGTGTGCAAAGT#	ATGGTCTGGACTGGGGGTAG#	GTAAAACGACGGCCAGT
EPHA10-13	CCDS41305.1	NM_001099439	TGTAAAACGACGGCCAGTCCCTTCATTGCACAGATAACTC	CTTTCATGTGTCAGGGCTCATT	GTAAAACGACGGCCAGT
EPHA10-14	CCDS41305.1	NM_001099439	TGTAAAACGACGGCCAGTGACAATGGAGATGGTTGGTGTT	CAAGTATAGAAAGAGCCTGGAGGA	GTAAAACGACGGCCAGT
EPHA10-15	CCDS41305.1	NM_001099439	TGTAAAACGACGGCCAGTCGTGTACAGAGGATGGCTTCTC	CATGCCACTGTCTCTCCTGTC	GTAAAACGACGGCCAGT
EPHA10-16	CCDS41305.1	NM_001099439	TGTAAAACGACGGCCAGTACTCTCGCAGTTGTCCTGGT	CCCGGCTGAAAGTAAAATGT	GTAAAACGACGGCCAGT
EPHB1-1	N/A	NM_004441	CAGTTTCGGGCGCTAAGAG	GTAAAACGACGGCCAGTCGAAAGGATACCGAGAAGCC	GTAAAACGACGGCCAGT
EPHB1-2	N/A	NM_004441	GTAAAACGACGGCCAGTCCACAGGTACTGCTCTGGGTAG	TATCTGAGCCTTGGGCTTCAC	GTAAAACGACGGCCAGT
EPHB1-3	N/A	NM_004441	TTTACCTTCATCAGCCTTCCC	GTAAAACGACGGCCAGTTCAATCTGCTGGACTGGTGAG	
EPHB1-3	N/A	NM_004441	AGCAGAGGCTCCAAAGCTTAC	GTAAAACGACGGCCAGTCGCTTCACTGTGAGAGACTGC	
EPHB1-3	N/A	NM_004441	GCCTAGCACTAGGAATGGGAG	GTAAAACGACGGCCAGTTGTCATTGCCACCAAGAAGTC	GTAAAACGACGGCCAGT
EPHB1-4	N/A	NM_004441	GTAAAACGACGGCCAGTTGATGTCTTCTCTTCCTTGCC	TCCTCAACCTTAGATCTCCCTTG	GTAAAACGACGGCCAGT
EPHB1-5	N/A	NM_004441	CAGCTGTGTCCCTGCCTAGAG	GTAAAACGACGGCCAGTATGCACCAGAGGCAGACAAG	GTAAAACGACGGCCAGT
EPHB1-6	N/A	NM_004441	GTAAAACGACGGCCAGTCTCTGTCACCAGAATCCTCCC	GTACCTCTGGAAGATGGCCC	GTAAAACGACGGCCAGT
EPHB1-7	N/A	NM_004441	GGAATCCAGTTGGAGATCAGC	GTAAAACGACGGCCAGTATGCAGGACCAAGAAATGATG	GTAAAACGACGGCCAGT
EPHB1-8	N/A	NM_004441	GTAAAACGACGGCCAGTTCACACCCTATCTGATCCACG	AGTTCCCAGATTCTGTCACGG	GTAAAACGACGGCCAGT
EPHB1-9	N/A	NM_004441	GTAAAACGACGGCCAGTGAGAGAACTTGCCACTGGGAC	GTCCCTAATCCTGGGAGATGC	GTAAAACGACGGCCAGT
EPHB1-10	N/A	NM_004441	AGAGACCATCTAGGGTGGTGG	GTAAAACGACGGCCAGTAAGTTGCAGCCTGGTGTGTAG	GTAAAACGACGGCCAGT
EPHB1-11	N/A	NM_004441	TTCCTGATTGGTAGGTTGTGC	GTAAAACGACGGCCAGTGGCACCATTGTTCTCCATTAG	GTAAAACGACGGCCAGT
EPHB1-12	N/A	NM_004441	GTAAAACGACGGCCAGTTCACAGTTCCCAGCCATGTAG	ACAGAAGCTGACAAGCAGCAG	GTAAAACGACGGCCAGT
EPHB1-13	N/A	NM_004441	ACATCCATGCTAAGGGTGTCC	GTAAAACGACGGCCAGTGGAAGAATGTGCATGCCAAG	GTAAAACGACGGCCAGT
EPHB1-14	N/A	NM_004441	ATGATCATGGTCAGAGGCTGC	GTAAAACGACGGCCAGTAATCCATTACAGCGGAAGGTG	GTAAAACGACGGCCAGT
EPHB1-15	N/A	NM_004441	AGGCCAGAAATAGGACTCACAC	GTAAAACGACGGCCAGTTCCATGAAGTCAGCTGTCAGG	GTAAAACGACGGCCAGT
EPHB1-16	N/A	NM_004441	AGCTGAGAAGCCAGTCTCTCC	GTAAAACGACGGCCAGTGCTACTTCCCAAGAACATGGC	GTAAAACGACGGCCAGT
EPHB2-1	CCDS230.1	NM_017449.1	GTAAAACGACGGCCAGTCTCCTCCTGGCACAGTCAATC	CTGGATGGCTCATTCTGCTG	GTAAAACGACGGCCAGT
EPHB2-2	CCDS230.1	NM_017449.1	GTTGTCATGGTAACTGGCTCC	GTAAAACGACGGCCAGTAGGGCCCAACAGAAAGATTG	GTAAAACGACGGCCAGT
EPHB2-3	CCDS230.1	NM_017449.1	GTAAAACGACGGCCAGTGACAGGGTTTCCTGGAAGATG	GCAGAGTCTGTGTCTTCCACC	GTAAAACGACGGCCAGT
EPHB2-3	CCDS230.1	NM_017449.1	GTAAAACGACGGCCAGTCTAGAGTGCCTCATGGTCAGC	GAGAATCCATGGGTGAAGGTG	GTAAAACGACGGCCAGT
EPHB2-4	CCDS230.1	NM_017449.1	GTAAAACGACGGCCAGTAAAGACTGGCTGTAACCGGAC	CCTGGAGACTTCAAACCCTTC	GTAAAACGACGGCCAGT
EPHB2-5	CCDS230.1	NM_017449.1	GTAAAACGACGGCCAGTTCACTCCATAGATGTGAAGGAGTCTT	GGCACAGAGTGGTCACATGG	GTAAAACGACGGCCAGT
EPHB2-6	CCDS230.1	NM_017449.1	GTAAAACGACGGCCAGTAGGTCTCACAGTGGGAAGGAG	GAGTACCTCTGAGGGTGGGC	GTAAAACGACGGCCAGT
EPHB2-7	CCDS230.1	NM_017449.1	GAGGGCTGACATCTAGAAGGG	GTAAAACGACGGCCAGTTGTTTATCCAATGGCCAGACC	GTAAAACGACGGCCAGT
EPHB2-8	CCDS230.1	NM_017449.1	CTCGGTTCACCAGCACTGTAG	GTAAAACGACGGCCAGTATGGGCATGTAACAGGTGCTC	GTAAAACGACGGCCAGT
EPHB2-9	CCDS230.1	NM_004442.4	ATGGCTTAAGAGGTCACTGGG	GTAAAACGACGGCCAGTGAGAACCTGGACTTGAGGTGG	GTAAAACGACGGCCAGT
EPHB2-9	CCDS230.1	NM_017449.1	ATGGCTTAAGAGGTCACTGGG	GTAAAACGACGGCCAGTGAGAACCTGGACTTGAGGTGG	GTAAAACGACGGCCAGT
EPHB2-10	CCDS230.1	NM_017449.1	GTAAAACGACGGCCAGTGTCCCACATCCTACCTTCTGC	GGAGTTGCCCAGTTCTTATGG	GTAAAACGACGGCCAGT
EPHB2-11	CCDS230.1	NM_017449.1	GTAAAACGACGGCCAGTAAGGGAATGGAAAGTGACAGC	TGACAGGGAACAGGAAGGTG	GTAAAACGACGGCCAGT
EPHB2-12	CCDS230.1	NM_017449.1	GTGAAAGTGTCTTGCAGGGAG	GTAAAACGACGGCCAGTCAAAGCATCTGAGTCCTTCCC	GTAAAACGACGGCCAGT
EPHB2-13	CCDS230.1	NM_017449.1	CTCTGGGAGACTGGCACAAG	GTAAAACGACGGCCAGTAAGCTGCATGGTAAGTTTGGG	GTAAAACGACGGCCAGT
EPHB2-14	CCDS230.1	NM_017449.1	AGGAAGAGCATTTGCCTGAAG	GTAAAACGACGGCCAGTTCAGACGTGCAATGTACTGGG	GTAAAACGACGGCCAGT
EPHB2-15	CCDS230.1	NM_017449.1	ATTCCTCACCCTCCAGATCAC	GTAAAACGACGGCCAGTACGTGCACATTCACGCATAC	GTAAAACGACGGCCAGT
EPHB2-16	CCDS230.1	NM_004442.4	GTAAAACGACGGCCAGTCTGCAGTGGATAGAGCACCAG	TTCCACCTCACACCATAGTCG	GTAAAACGACGGCCAGT
EPHB2-16	CCDS230.1	NM_017449.1	GTAAAACGACGGCCAGTCTGCAGTGGATAGAGCACCAG	TTCCACCTCACACCATAGTCG	GTAAAACGACGGCCAGT
EPHB2-17	CCDS230.1	NM_017449.1	TCTGAAAGTGTTTCTTGGCTCTG	GTAAAACGACGGCCAGTTGGAGGTTTGACATTCACCTG	GTAAAACGACGGCCAGT
EPHB6-1	CCDS5873.1	NM_004445.1	GTAAAACGACGGCCAGTTCTTCATTATCCTCACCATGCC	GTGTCTCCTCAGGAAGCAAGC	GTAAAACGACGGCCAGT
EPHB6-2	CCDS5873.1	NM_004445.1	CATGAATTCCACTCTCCAGGG	GTAAAACGACGGCCAGTTCAATAAAGGGAAAGGCATGG	GTAAAACGACGGCCAGT
EPHB6-3	CCDS5873.1	NM_004445.1	GTAAAACGACGGCCAGTAGGAGGGAAAGCTCTCGTCTG	TTCTGAACCTGAATCCCTTGG	GTAAAACGACGGCCAGT
EPHB6-3	CCDS5873.1	NM_004445.1	GTAAAACGACGGCCAGTCCCTACTCCATCCTCCTCTGG	GGTTGCAGACACACTTTGTGG	GTAAAACGACGGCCAGT
EPHB6-3	CCDS5873.1	NM_004445.1	GTAAAACGACGGCCAGTTTCAGAGAGGAGCCCAAAGG	GCTTCTACGTGGCCTTCCAG	GTAAAACGACGGCCAGT
EPHB6-4	CCDS5873.1	NM_004445.1	GTCACTCCAAATGCAAAGAGC	GTAAAACGACGGCCAGTATACCTGCCTGCTGTGTGTTG	GTAAAACGACGGCCAGT
EPHB6-5	CCDS5873.1	NM_004445.1	AAGAGCTCACCTTCATGGCTG	GTAAAACGACGGCCAGTCCTTCTCTCCCTGACCCATC	GTAAAACGACGGCCAGT
EPHB6-5	CCDS5873.1	NM_004445.1	GTAAAACGACGGCCAGTGGCTGGAGATCAGGAGTAGGG	GACCTGCTCTTCAATGTCGTG	GTAAAACGACGGCCAGT
EPHB6-6	CCDS5873.1	NM_004445.1	ACTGTGAGCTCCTGCCAGC	GTAAAACGACGGCCAGTTCCCTACTCCTGATCTCCAGC	GTAAAACGACGGCCAGT
EPHB6-7	CCDS5873.1	NM_004445.1	GCACTCTCCTTTCCCACAGAAC	GTAAAACGACGGCCAGTCTGAGAGCCCTGTCAACCAG	GTAAAACGACGGCCAGT
EPHB6-8	CCDS5873.1	NM_004445.1	GTAAAACGACGGCCAGTAGCACCAGTGTGAGGTTTCTG	CATGTTGTGTGTGCCTGTGG	GTAAAACGACGGCCAGT
EPHB6-9	CCDS5873.1	NM_004445.1	TATGAGCGTGTTGTGAAAGGC	GTAAAACGACGGCCAGTAGCAGTCTGGAGGGTGACAAG	GTAAAACGACGGCCAGT
EPHB6-10	CCDS5873.1	NM_004445.1	CTGTGTTTGGATGGGACTCTG	GTAAAACGACGGCCAGTAGCTCCTTGGCACAACCTTC	GTAAAACGACGGCCAGT
EPHB6-11	CCDS5873.1	NM_004445.1	GAAGCAAAGATACAGGACCTCG	GTAAAACGACGGCCAGTCAGAGTCCCATCCAAACACAG	GTAAAACGACGGCCAGT
EPHB6-12	CCDS5873.1	NM_004445.1	TCCCTCCTTTCAGGGACTATG	GTAAAACGACGGCCAGTATGGTCTCCGTCCTTCCTTC	GTAAAACGACGGCCAGT
EPHB6-13	CCDS5873.1	NM_004445.1	CAAACGGAGTAGAGAATGGAGG	GTAAAACGACGGCCAGTTGCTCCATAAACGTGACTATTGC	GTAAAACGACGGCCAGT
EPHB6-14	CCDS5873.1	NM_004445.1	CAGGGTCAAGGTCTCCTCTTC	GTAAAACGACGGCCAGTCCACCCTCTTACCCAACAAAG	CAGGAAACAGCTATGACC
EPHB6-15	CCDS5873.1	NM_004445.1	GAGGGAAGGGATCAAATCTGG	GTAAAACGACGGCCAGTGAAAGCCAGGGAGGGTAGATG	GTAAAACGACGGCCAGT
EPHB6-16	CCDS5873.1	NM_004445.1	GGCATCTCTCACAGAGGCTG	GTAAAACGACGGCCAGTAGAGTAAGCAGGGAGTGGTGG	GTAAAACGACGGCCAGT
ERBB4-1	CCDS2394.1	NM_005235.1	GGAAATAGCTGCACAGTCCG	GTAAAACGACGGCCAGTATGGGTGAAGAGGGCAGG	GTAAAACGACGGCCAGT
ERBB4-2	CCDS2394.1	NM_005235.1	AGAACTGGGATAGGCTTGTGG	GTAAAACGACGGCCAGTTTCCAGGTATCAGCACACAGG	GTAAAACGACGGCCAGT
ERBB4-3	CCDS2394.1	NM_005235.1	GTAAAACGACGGCCAGTAAGCCAATTCTTTAGAATATGATATGG	TGCCTTAGAGTGTTCCTCAATG	GTAAAACGACGGCCAGT
ERBB4-4	CCDS2394.1	NM_005235.1	TCTTGGCTATTAGCAACATGACTC	GTAAAACGACGGCCAGTCAATGAATGCAATCAAAGTTCAA	GTAAAACGACGGCCAGT
ERBB4-5	CCDS2394.1	NM_005235.1	GTAAAACGACGGCCAGTAAATCCTCATAAAGGAGCAGGAG	CCAAAGCAAATCAACCACAAG	GTAAAACGACGGCCAGT
ERBB4-6	CCDS2394.1	NM_005235.1	GTAAAACGACGGCCAGTTGAATTGAGTCAAAGACAGGGTG	GGAATGACTTTGAGGAGGGC	GTAAAACGACGGCCAGT
ERBB4-7	CCDS2394.1	NM_005235.1	TTTGGAAACACACATGACTCTTAAA	GTAAAACGACGGCCAGTTTTGCTATGAAACTTTACACAAATCA	GTAAAACGACGGCCAGT
ERBB4-8	CCDS2394.1	NM_005235.1	GTGGAGCAGTAACCAAGCAAG	GTAAAACGACGGCCAGTGTGTGGGTAGGTTTGGTTGTG	GTAAAACGACGGCCAGT
ERBB4-9	CCDS2394.1	NM_005235.1	AAAGCAGAACCAGTAGTGAATGTTG	GTAAAACGACGGCCAGTGGTGAAACTCTTCAGCTTCCAG	GTAAAACGACGGCCAGT
ERBB4-10	CCDS2394.1	NM_005235.1	GTAAAACGACGGCCAGTCCTCCTCCACATCTAGCACAG	TCTCCTGACCTCATGATCCAC	GTAAAACGACGGCCAGT
ERBB4-11	CCDS2394.1	NM_005235.1	GTAAAACGACGGCCAGTCCTTTCTCACTTCCCAACTTTC	TACCTCACACCATCATCGGAG	GTAAAACGACGGCCAGT
ERBB4-12	CCDS2394.1	NM_005235.1	GTAAAACGACGGCCAGTTTGATTCAGTTTCCATTTATACACCA	GAGCAACAATTCTGACCGGAT	GTAAAACGACGGCCAGT
ERBB4-13	CCDS2394.1	NM_005235.1	GTAAAACGACGGCCAGTTAGGCCACCAAAGTCATTTGC	GAATGGCGTGAACCCAGG	GTAAAACGACGGCCAGT
ERBB4-14	CCDS2394.1	NM_005235.1	GTAAAACGACGGCCAGTTGATGCTCCTGGCACATAGAG	CCCATGGCATCCTGTAAGTAG	GTAAAACGACGGCCAGT
ERBB4-15	CCDS2394.1	NM_005235.1	TCTTAGAGGAAGATTTGCCACC	GTAAAACGACGGCCAGTCATTTCAGAGATGGTACCAGGG	GTAAAACGACGGCCAGT
ERBB4-16	CCDS2394.1	NM_005235.1	GCTTCCCATGTTCTTCCTCC	GTAAAACGACGGCCAGTAAGTAAGAAAGTTGGCTTGAGAAGG	GTAAAACGACGGCCAGT
ERBB4-17	CCDS2394.1	NM_005235.1	TGTGGATAATGTCTTGTACAACTGC	GTAAAACGACGGCCAGTTTCACAAGCTTTGTTTAACGGAC	GTAAAACGACGGCCAGT
ERBB4-18	CCDS2394.1	NM_005235.1	GGTTGTCAAGGCAAACCAAG	GTAAAACGACGGCCAGTAGACTGTATCCGTCCCAGCTC	GTAAAACGACGGCCAGT
ERBB4-19	CCDS2394.1	NM_005235.1	AAGCAGACAACAAAGTTGCAGAG	GTAAAACGACGGCCAGTTCTAGGCAGACAGTTGTGAAGC	GTAAAACGACGGCCAGT
ERBB4-20	CCDS2394.1	NM_005235.1	GTAAAACGACGGCCAGTTCAGCACCATTAGTACAATCCAA	TTTGGCACCTAGTCAATTCAA	GTAAAACGACGGCCAGT
ERBB4-21	CCDS2394.1	NM_005235.1	GTAAAACGACGGCCAGTGCACTTCCAACTGAAGGCTAAG	AGGCAAATGGTAGAACCAAGG	GTAAAACGACGGCCAGT
ERBB4-22	CCDS2394.1	NM_005235.1	GTAAAACGACGGCCAGTAGGCCAGCCCAAAGACTC	TAACTGCTTTAGGAAATTAGGCTTATC	GTAAAACGACGGCCAGT
ERBB4-23	CCDS2394.1	NM_005235.1	TGATTGGTGTTTGGATTGACC	GTAAAACGACGGCCAGTCAAAGAGGCGTTCATATGTTCC	GTAAAACGACGGCCAGT
ERBB4-24	CCDS2394.1	NM_005235.1	GTAAAACGACGGCCAGTGAGTCGTTTCTTTCACTAGCTTGC	TGTTTGTGGTCCTTTCCACAG	GTAAAACGACGGCCAGT
ERBB4-25	CCDS2394.1	NM_005235.1	TAGGTTTCTTAATGGCCGGTG	GTAAAACGACGGCCAGTGGCATCACATTGATTTGAGCTA	GTAAAACGACGGCCAGT
ERBB4-26	CCDS2394.1	NM_005235.1	TGCTTAGGAAGCTTCACTGTTG	GTAAAACGACGGCCAGTTAACTCACTGTTGGCAAAGGC	GTAAAACGACGGCCAGT
ERBB4-27	CCDS2394.1	NM_005235.1	TGGCTTTGATATCCTTGTGGC	GTAAAACGACGGCCAGTCAGCTATCTGGCAATTTCTATTCTG	GTAAAACGACGGCCAGT
ERBB4-28	CCDS2394.1	NM_005235.1	CCATATGCAGAAGAGACAAATGC	GTAAAACGACGGCCAGTAGGTAGTCTGGGTGCTGAAGG	GTAAAACGACGGCCAGT
ERBB4-28	CCDS2394.1	NM_005235.1	TGAATCCAGTGGAGGAGAACC	GTAAAACGACGGCCAGTGACCACCAGAGAAAGAGAGGG	GTAAAACGACGGCCAGT

FER-1	CCDS4098.1	NM_005246.1	GTAAAACGACGGCCAGTGCTGACTTAAGTATGCTCATTCAATAGTTT	TTCATCTTGTTTCTGATCTTTGGA	GTAAAACGACGGCCAGT
FER-2	CCDS4098.1	NM_005246.1	GTAAAACGACGGCCAGTTTTCTTGTTGGGAAATGATGAA	TTGAACAGTTGCCAGAAACCT	GTAAAACGACGGCCAGT
FER-3	CCDS4098.1	NM_005246.1	TGACAATTAGCCAATGTGGGTT	GTAAAACGACGGCCAGTCCTGGCCTGATTTGCTATTCT	GTAAAACGACGGCCAGT
FER-4	CCDS4098.1	NM_005246.1	GTAAAACGACGGCCAGTGAAGAATCAAGGTCTGAAATACCC	TTTGCAAATCTAACAGTACCTTGC	GTAAAACGACGGCCAGT
FER-5	CCDS4098.1	NM_005246.1	GTAAAACGACGGCCAGTAAGCATGGATTAAATATGGATTAACAA	AGGTGGTACAGGAAACAACCA	GTAAAACGACGGCCAGT
FER-6	CCDS4098.1	NM_005246.1	GTAAAACGACGGCCAGTTCACACAGAACTTTGATATTCGG	TTTGAAACCCAGGATTTAGTTTG	GTAAAACGACGGCCAGT
FER-7	CCDS4098.1	NM_005246.1	GTAAAACGACGGCCAGTAGAAATGTTAGGTTCACACTGCC	CCACCATCCAGTAAGGTAGCC	GTAAAACGACGGCCAGT
FER-8	CCDS4098.1	NM_005246.1	GTAAAACGACGGCCAGTTGACCTGAGGTGACTGACAAG	TGGATTTGACTCCAAACACTTC	GTAAAACGACGGCCAGT
FER-9	CCDS4098.1	NM_005246.1	TTCTGTCTTCCCTATGTCAATGTTAC	GTAAAACGACGGCCAGTGATGGATAAGCTGTGGATAAGTACC	GTAAAACGACGGCCAGT
FER-10	CCDS4098.1	NM_005246.1	GTAAAACGACGGCCAGTCAGGCATTTATCACAAACCATTC	GGGAGGAACATTTGTAAGAAGC	GTAAAACGACGGCCAGT
FER-11	CCDS4098.1	NM_005246.1	GTAAAACGACGGCCAGTTCAAGGAAGTTTCATGTTTCAA	TGCATTTCAGGTCTGTTTGTT	GTAAAACGACGGCCAGT
FER-12	CCDS4098.1	NM_005246.1	AGACTTTCACACATCTATTTCAGTGAG	GTAAAACGACGGCCAGTCACTGGCTCAAATGCAACTTC	GTAAAACGACGGCCAGT
FER-13	CCDS4098.1	NM_005246.1	GTAAAACGACGGCCAGTCCTGGTTTGACTATGATTGCTG	TAAGCACCTCCTCCTCTTTGG	GTAAAACGACGGCCAGT
FER-14	CCDS4098.1	NM_005246.1	TCCTTGGAGACTTTACGAGGAG	GTAAAACGACGGCCAGTAGGGAAGGCTTTACTCGTTTG	GTAAAACGACGGCCAGT
FER-15	CCDS4098.1	NM_005246.1	CAACTAGCAGAGGACACTTTCACAC	GTAAAACGACGGCCAGTCCTCACGTCAAACAAATTGGG	GTAAAACGACGGCCAGT
FER-16	CCDS4098.1	NM_005246.1	TTTGTGTTGATCCTCAAATCATTC	GTAAAACGACGGCCAGTTGAGGACTGGTAAATCACAAGC	GTAAAACGACGGCCAGT
FER-17	CCDS4098.1	NM_005246.1	CCCTCCTCAAGCAGACACAC	GTAAAACGACGGCCAGTTGTGGTGCATGACTGACACAG	GTAAAACGACGGCCAGT
FER-18	CCDS4098.1	NM_005246.1	AAGAAAGCCCTTGGTAGGACTG	GTAAAACGACGGCCAGTAACTGCATAATGCCCTGTGTG	GTAAAACGACGGCCAGT
FLT1-1	CCDS9330.1	NM_002019.2	GTAAAACGACGGCCAGTGAAGTGGTTGTCTCCTGGCTG	ACTAGTGTCCCAGGTTCTCGC	GTAAAACGACGGCCAGT
FLT1-2	CCDS9330.2	NM_002019.2	TTTATGAGCAAGGGTAGAGCTAGAA	GTAAAACGACGGCCAGTGGTTTGCACTTTGCAGATCAC	GTAAAACGACGGCCAGT
FLT1-3	CCDS9330.3	NM_002019.2	GTAAAACGACGGCCAGTATGAATGCTGAGGAACTGGTG	AGGAAAGCAACCTTTCCAATG	GTAAAACGACGGCCAGT
FLT1-4	CCDS9330.4	NM_002019.2	CTGTGGCAATGCCTACCATAC	GTAAAACGACGGCCAGTACTGAGAAGCCCAGGTGTTTG	GTAAAACGACGGCCAGT
FLT1-5	CCDS9330.5	NM_002019.2	GTAAAACGACGGCCAGTCACAAACTGCTGGTGAAACAGT	GATTGTATTGGCTGCAAGCAT	GTAAAACGACGGCCAGT
FLT1-6	CCDS9330.6	NM_002019.2	GCATGAACATAAGCCGAAGTG	GTAAAACGACGGCCAGTACACTGCCACAGGAGTCAGG	GTAAAACGACGGCCAGT
FLT1-7	CCDS9330.7	NM_002019.2	CTCTAGGTGGATTTGACATGATTC	GTAAAACGACGGCCAGTACCATGGCCAAGCTGTATTC	GTAAAACGACGGCCAGT
FLT1-8	CCDS9330.8	NM_002019.2	GTAAAACGACGGCCAGTTTGATTACACCCTCCCTGAATG	TGTCTGAGGAACGTCTCTTGG	GTAAAACGACGGCCAGT
FLT1-9	CCDS9330.9	NM_002019.2	GTAAAACGACGGCCAGTTCAAAGGTTTGAAATTGGTCAAC	ATGCCGCCTATGGAATACAAC	GTAAAACGACGGCCAGT
FLT1-10	CCDS9330.10	NM_002019.2	GTAAAACGACGGCCAGTAAGCCAGTGAGAATGTGGTCC	ACATCCCACATGCAGATTCC	GTAAAACGACGGCCAGT
FLT1-11	CCDS9330.11	NM_002019.2	TTTGTTATCTGAGGACTTACACCAA	GTAAAACGACGGCCAGTGGACAGTGCCATCTCTACCAT	GTAAAACGACGGCCAGT
FLT1-12	CCDS9330.12	NM_002019.2	GTAAAACGACGGCCAGTTCAACCTCAGAAGTAGCTTGGG	AGAGCAAGGATGAAGGCACTC	GTAAAACGACGGCCAGT
FLT1-13	CCDS9330.13	NM_002019.2	GTAAAACGACGGCCAGTAATGTGGATACTGAGATAATTTGTGC	TTTGTGTGGTACAATCATTCCTTG	GTAAAACGACGGCCAGT
FLT1-14	CCDS9330.14	NM_002019.2	GTAAAACGACGGCCAGTGCAGCAGGTTAATGATTGAAGAG	ACGGGACTGTTAAGGGAAAGG	GTAAAACGACGGCCAGT
FLT1-15	CCDS9330.15	NM_002019.2	GAGCTCGGATTTCCTTGTCTG	GTAAAACGACGGCCAGTGGAGACTGGGAGGTGGAAAG	GTAAAACGACGGCCAGT
FLT1-16	CCDS9330.16	NM_002019.2	AACCATTTAGGGAAACTGAGCC	GTAAAACGACGGCCAGTGGGAAAGAAAGAGGGTCCAAC	GTAAAACGACGGCCAGT
FLT1-17	CCDS9330.17	NM_002019.2	GTAAAACGACGGCCAGTCTGGCCACACAGTTTCAACC	CTTTCGCATCTCTCAAAGCAC	GTAAAACGACGGCCAGT
FLT1-18	CCDS9330.18	NM_002019.2	ACTGGAGATTCCATGCCTCAC	GTAAAACGACGGCCAGTAGCTTGTGTCTGTTCCCAGG	GTAAAACGACGGCCAGT
FLT1-19	CCDS9330.19	NM_002019.2	GGGAAGTTAGTGAAGCAACCG	GTAAAACGACGGCCAGTGGAGAAGGAGCTGTAAGGCAG	GTAAAACGACGGCCAGT
FLT1-20	CCDS9330.20	NM_002019.2	GTAAAACGACGGCCAGTACAAAGGCTGGTTGGTTTGAG	GGGATCAAATGATTCTCTGTGC	GTAAAACGACGGCCAGT
FLT1-21	CCDS9330.21	NM_002019.2	TACCATTCGAGTCTCCCACG	GTAAAACGACGGCCAGTAGTTGAGGGACTGGTTTCCC	GTAAAACGACGGCCAGT
FLT1-22	CCDS9330.22	NM_002019.2	ATTAAGGCACTTGCAGTGGTG	GTAAAACGACGGCCAGTATGCTTGGATAAAGTGGGCTG	GTAAAACGACGGCCAGT
FLT1-23	CCDS9330.23	NM_002019.2	CGCTCATCTGGACTGTTTGTC	GTAAAACGACGGCCAGTTCACAGCATGTGAAATGGATTC	GTAAAACGACGGCCAGT
FLT1-24	CCDS9330.24	NM_002019.2	GCGTACGCCATTACTCATCTG	GTAAAACGACGGCCAGTAGGCCGTATGTTATCTGGGAG	GTAAAACGACGGCCAGT
FLT1-25	CCDS9330.25	NM_002019.2	GTAAAACGACGGCCAGTGGAAAGAAGAACCTTGGCATC	AGCAAGGATTTGCTGAGCTTC	GTAAAACGACGGCCAGT
FLT1-26	CCDS9330.26	NM_002019.2	GAGCTCTCGTTGCACCAATTC	GTAAAACGACGGCCAGTCAGCCCTCCCTTTGTAGTACG	GTAAAACGACGGCCAGT
FLT1-27	CCDS9330.1	NM_002019.2	ATGGGCATATGGGTGGTGAT	GTAAAACGACGGCCAGTCATAGTCAAAGTTGACATAATGGTTCA	GTAAAACGACGGCCAGT
FLT1-28	CCDS9330.2	NM_002019.2	ATTTCAGCCACTCCTGAATCC	GTAAAACGACGGCCAGTTCTTAGCTGGGATATGGTGCC	GTAAAACGACGGCCAGT
FLT1-29	CCDS9330.3	NM_002019.2	AACTCCCGGATACCACAGTTC	GTAAAACGACGGCCAGTTGTATCCCAGGATCATCCCTC	GTAAAACGACGGCCAGT
FLT1-30	CCDS9330.4	NM_002019.2	GTAAAACGACGGCCAGTGCTCCCATGGAAAGATAAAGG	GAAATCTGACAGCAATTGAGGG	GTAAAACGACGGCCAGT
MATK-1	CCDS12113.1	NM_002378.2	AACACCAGCTCCTTAAGTCCG	GTAAAACGACGGCCAGTAAACCACCATCACTTGCCTG	GTAAAACGACGGCCAGT
MATK-1	CCDS12113.1	NM_139355.1	GTAAAACGACGGCCAGTGGGAATGACCTTGACTCATCC	CAGTTCCTACCACTTCCAGCC	GTAAAACGACGGCCAGT
MATK-2	CCDS12113.1	NM_002378.2	GTAAAACGACGGCCAGTACCTGGGCTGGAAGTGGTAG	CTGGGACAGAAGGTCAGGAAG	GTAAAACGACGGCCAGT
MATK-3	CCDS12113.1	NM_002378.2	CATCTTGGCTTCCTGACCTTC	GTAAAACGACGGCCAGTCGGTACCAGCTCTTGTTCTGC	GTAAAACGACGGCCAGT
MATK-4	CCDS12113.1	NM_002378.2	GTAAAACGACGGCCAGTTATCACCAAATGCGAGCACAC	ACCAGGAACAGCCCATCC	GTAAAACGACGGCCAGT
MATK-5	CCDS12113.1	NM_002378.2	CAAGCTCAGCCTCATGCC	GTAAAACGACGGCCAGTACAGGAGGTAGGGATGGTGTC	GTAAAACGACGGCCAGT
MATK-6	CCDS12113.1	NM_002378.2	GTAAAACGACGGCCAGTAAACCAGCCTTTCTCCTCCTC	GAGACAGGCTTGGGTGATCTG	GTAAAACGACGGCCAGT
MATK-7	CCDS12113.1	NM_002378.2	TTCACACCACTATCCCTCCTG	GTAAAACGACGGCCAGTGCTCTGTGACTCCAAAGCCTC	GTAAAACGACGGCCAGT
MATK-8	CCDS12113.1	NM_002378.2	GTAAAACGACGGCCAGTTCCGTCTGTCTCTCTGTCCC	GCTCCATGACAATGTACAGCC	GTAAAACGACGGCCAGT
MATK-9	CCDS12113.1	NM_002378.2	GTGGCCGTGAAGAATATCAAG	GTAAAACGACGGCCAGTGTCCGCAGAAAGTTCACCAG	GTAAAACGACGGCCAGT
MATK-10	CCDS12113.1	NM_002378.2	AGGAAGATGCAACACGAGAAC	GTAAAACGACGGCCAGTGCTCTCCAGGTACTCCATGC	GTAAAACGACGGCCAGT
MATK-11	CCDS12113.1	NM_002378.2	GTAAAACGACGGCCAGTGAGGCTTTGTGAGCTTGTGG	CAGAGAGGCCAAGGGACATAC	GTAAAACGACGGCCAGT
MATK-12	CCDS12113.1	NM_002378.2	GAGCTAGACTCAACTGCGGG	GTAAAACGACGGCCAGTTCTTTCAGTGACTGCGGACAG	GTAAAACGACGGCCAGT
MATK-13	CCDS12113.1	NM_002378.2	GTAAAACGACGGCCAGTAGGTCTTCTCATATGGACGGG	ACCAGGAGGATGACTTGCC	GTAAAACGACGGCCAGT
MET-1	N/A	NM_000245	GTAAAACGACGGCCAGTTGACAACTGAACTGCTCTCGC	ACCACACAGTCAGGACACTGG	GTAAAACGACGGCCAGT
MET-1	N/A	NM_000245	TTGCTGAGTACAAGACTGGGC	GTAAAACGACGGCCAGTCTAGAGTTTCCCTTTGGACCG	GTAAAACGACGGCCAGT
MET-1	N/A	NM_000245	GTAAAACGACGGCCAGTAAGGACCGGTTCATCAACTTC	TGATAGGGAATGCACACATGG	GTAAAACGACGGCCAGT
MET-1	N/A	NM_000245	GTAAAACGACGGCCAGTTGACGGACCAGTCCTACATTG	AAGCAGTGCTCATGATTGGG	GTAAAACGACGGCCAGT
MET-2	N/A	NM_000245	ATCCTTGCCATTATCCTCCAG	GTAAAACGACGGCCAGTATTGTTTGGCTTTCAGTCTGTG	GTAAAACGACGGCCAGT
MET-3	N/A	NM_000245	CCACAAGCCCTGCTAATCTG	GTAAAACGACGGCCAGTGGCCAAGTGACACTGGTTG	GTAAAACGACGGCCAGT
MET-4	N/A	NM_000245	GTAAAACGACGGCCAGTCACCGTTATGACAGGATTTGC	AGCCAAGAGAGAGATGGTGC	GTAAAACGACGGCCAGT
MET-5	N/A	NM_000245	TGCTCTGAAATTTGTGACCCT	GTAAAACGACGGCCAGTGTGACAGGCCAAGACCCTTT	GTAAAACGACGGCCAGT
MET-6	N/A	NM_000245	TATGACTATGCCACTGCCCTC	GTAAAACGACGGCCAGTCCAGCCATAGGACCGTATTTC	GTAAAACGACGGCCAGT
MET-7	N/A	NM_000245	GTAAAACGACGGCCAGTACAGTACATTCTCCTATGTGGTAAGG	ACAATAAAGAGGGTGGATGGG	GTAAAACGACGGCCAGT
MET-8	N/A	NM_000245	TTCCCACTTAGGAACCATTGAG	GTAAAACGACGGCCAGTGCAACATAACAGCATCAAAGCC	GTAAAACGACGGCCAGT
MET-9	N/A	NM_000245	CCATTTGATGTTGACTGTGCC	GTAAAACGACGGCCAGTCTCAGGTACCATGAAAGCCAC	GTAAAACGACGGCCAGT
MET-10	N/A	NM_000245	TGCATGTATCGTGTTTCCAGA	GTAAAACGACGGCCAGTAAGATACAATGGCCAAGTACAACA	GTAAAACGACGGCCAGT
MET-11	N/A	NM_000245	TCATAGAATCGTGTGCCTTGG	GTAAAACGACGGCCAGTAATGCAGGCTGAGTTGATGAG	GTAAAACGACGGCCAGT
MET-12	N/A	NM_000245	GTAAAACGACGGCCAGTTGAAGGCAGTTATGCCATTTG	CACACAAGAATCGACGACAATC	TGTAAAACGACGGCCAGT
MET-13	N/A	NM_000245	CACTGGGTCAAAGTCTCCTGG	GTAAAACGACGGCCAGTGTGTCAAATACTTACTTGGCAGAGG	GTAAAACGACGGCCAGT
MET-14	N/A	NM_000245	AGCTCTTCCTGTTTCAGTCCC	GTAAAACGACGGCCAGTCCTAATCTGCAAAGGCCAAAG	GTAAAACGACGGCCAGT
MET-15	N/A	NM_000245	CACATTGCTTATATCCTTGGGTG	GTAAAACGACGGCCAGTGGCCCATAATTTCAGTGGTAGC	GTAAAACGACGGCCAGT
MET-16	N/A	NM_000245	TCAAACCCTCAGGACAAGATG	GTAAAACGACGGCCAGTTTTGAGGTGCATTTGAATGATG	GTAAAACGACGGCCAGT
MET-17	N/A	NM_000245	CAGGCTTGAGCCATTAAGACC	GTAAAACGACGGCCAGTGCATTGAACAGTGGGAAACAG	GTAAAACGACGGCCAGT
MET-18	N/A	NM_000245	GTAAAACGACGGCCAGTACTGAAGCCACTTGTTTAATCTGTAG	TAAGGAGCTGGTATGTTGCCC	GTAAAACGACGGCCAGT
MET-19	N/A	NM_000245	AAAGCCAAGTTTAGTTACCAAGACC	GTAAAACGACGGCCAGTATATCCGGGACACCAGTTCAG	GTAAAACGACGGCCAGT
MET-20	N/A	NM_000245	GTAAAACGACGGCCAGTTCCTACAACCCGAATACTGCC	TGGCAAGAGCAAAGAATATCG	GTAAAACGACGGCCAGT
NTRK1-1	CCDS1161.1	NM_002529.2	GTAAAACGACGGCCAGTGTAGGAAGCGGGTGGAGAAG	GCCTGACCAGCAAACAAGC	GTAAAACGACGGCCAGT
NTRK1-2	CCDS1161.1	NM_002529.2	GTAAAACGACGGCCAGTGGCATGTGCATGTGTATTGTG	TCCTGACTTCTCCCAGTCCC	GTAAAACGACGGCCAGT
NTRK1-3	CCDS1161.1	NM_002529.2	GTAAAACGACGGCCAGTCAGGAAGCTCAGGGCTTTG	AATGGTGAGGTGACTTCCCTG	GTAAAACGACGGCCAGT
NTRK1-4	CCDS1161.1	NM_002529.2	GTAAAACGACGGCCAGTCTACACACACTGCCTTCCAGG	GTCATCCAACAGACCCAAGTG	GTAAAACGACGGCCAGT
NTRK1-5	CCDS1161.1	NM_002529.2	CCTCCCTTTCACCTGTAGACG	GTAAAACGACGGCCAGTCTCAGTGCCCTCTCCCTCAG	GTAAAACGACGGCCAGT
NTRK1-6	CCDS1161.1	NM_002529.2	GTAAAACGACGGCCAGTCCCGCAGTAGAGTTCTGGG	TAAACCATCTCTGTCCGTCCC	GTAAAACGACGGCCAGT
NTRK1-7	CCDS1161.1	NM_002529.2	GTAAAACGACGGCCAGTCCTCTCCTTTCCATCTGGAGC	GAATCTGGAAACAGCTGGGAG	GTAAAACGACGGCCAGT
NTRK1-8	CCDS1161.1	NM_002529.2	GTAAAACGACGGCCAGTTGGACTTGTCGGGTGTGTG	GGTCAGGGCTATAGCAGGAAG	GTAAAACGACGGCCAGT
NTRK1-9	CCDS1161.1	NM_002529.2	GTAAAACGACGGCCAGTATGAGTCCCAGAGTAGGCAGG	GGGTCTCCAGATGTGCTGTTAG	GTAAAACGACGGCCAGT
NTRK1-10	CCDS1161.1	NM_002529.2	ATGAGTCCCAGAGTAGGCAGG	GTAAAACGACGGCCAGTGAAATGACATGCAGATGAGCC	GTAAAACGACGGCCAGT
NTRK1-11	CCDS1161.1	NM_002529.2	GTAAAACGACGGCCAGTGGGAGATCACTACCATCTGGC	GCCAGGCCTTCATTTATACCC	GTAAAACGACGGCCAGT
NTRK1-12	CCDS1161.1	NM_002529.2	GTAAAACGACGGCCAGTTCGCTCCCTAGCTTCTCAGTC	AGAAAGGGAGGGATCGTTCAG	GTAAAACGACGGCCAGT
NTRK1-13	CCDS1161.1	NM_002529.2	GTAAAACGACGGCCAGTGAGTCACAGCTAGCCCAAACC	ATGTCAGCCCTCTGCATCTC	GTAAAACGACGGCCAGT
NTRK1-14	CCDS1161.1	NM_002529.2	GTAAAACGACGGCCAGTATCACATCAGGACAGAGTGGG	CAGGGATGTCTATAGGGAAGGG	GTAAAACGACGGCCAGT
NTRK1-15	CCDS1161.1	NM_002529.2	GTAAAACGACGGCCAGTTGGACAGCTGCCTCTACTGTT	GAGCCAGTGAATCTCAGACCC	GTAAAACGACGGCCAGT
NTRK1-16	CCDS1161.1	NM_002529.2	GTAAAACGACGGCCAGTATCTCCTGACCTCGTGATTGC	AACAGGCTGTGGCAGAGG	GTAAAACGACGGCCAGT
NTRK1-17	CCDS1161.1	NM_002529.2	CGAGTAGTGTGAGCTGCCTTG	GTAAAACGACGGCCAGTGAACATCCTCTACTCCCAGCC	GTAAAACGACGGCCAGT

PDGFRA-1	CCDS3495.1	NM_006206.2	GTAAAACGACGGCCAGTCAAAGAGAACTAGGCTCCAGGG	GCAAAGGGAACTGAAGGTTTG	GTAAAACGACGGCCAGT
PDGFRA-2	CCDS3495.1	NM_006206.2	GTAAAACGACGGCCAGTGCTTCTCTCAGTTGTCGGGAT	TTTCAAACTTCCCGCAATAAA	GTAAAACGACGGCCAGT
PDGFRA-3	CCDS3495.1	NM_006206.2	GTAAAACGACGGCCAGTAATATCAATAATGCCAGTGGGATAG	CAAATCAGAATTTAGGATCACCAG	GTAAAACGACGGCCAGT
PDGFRA-4	CCDS3495.1	NM_006206.2	ACACCATCTCACAATCAAGCC	GTAAAACGACGGCCAGTGTGACAGACCGAGCTCAAATG	GTAAAACGACGGCCAGT
PDGFRA-5	CCDS3495.1	NM_006206.2	GTAAAACGACGGCCAGTTGAACCTCCATTGACACATCC	GCTGAAGGTGGGTTTGATTTC	GTAAAACGACGGCCAGT
PDGFRA-6	CCDS3495.1	NM_006206.2	GTAAAACGACGGCCAGTTTCTGTCCATGGTACATTCCG	ACTGACTTTGGGTCTGGGTTG	GTAAAACGACGGCCAGT
PDGFRA-7	CCDS3495.1	NM_006206.2	ATCCAGACCTTCAGTGTGTGC	GTAAAACGACGGCCAGTAAAGTGCCAGGCTTTCCTTG	GTAAAACGACGGCCAGT
PDGFRA-8	CCDS3495.1	NM_006206.2	GTAAAACGACGGCCAGTTTGTACAACTGGTTTCAGCCC	CACCCTGAAGCTATCACACCC	GTAAAACGACGGCCAGT
PDGFRA-9	CCDS3495.1	NM_006206.2	CTTAGAGTGTTCCCGTGGCTC	GTAAAACGACGGCCAGTATCTGGGATTCAAAGTTCCGC	GTAAAACGACGGCCAGT
PDGFRA-10	CCDS3495.1	NM_006206.2	GACACAGCCACACTACCTTGC	GTAAAACGACGGCCAGTGAGTCCAACAACGTTCACTCC	GTAAAACGACGGCCAGT
PDGFRA-11	CCDS3495.1	NM_006206.2	GTAAAACGACGGCCAGTGTCCAGTCACTGTGCTGCTTC	GCAAATTTCCATTGCCTAGTTC	GTAAAACGACGGCCAGT
PDGFRA-12	CCDS3495.1	NM_006206.2	GTAAAACGACGGCCAGTTCCAAACAGGAAAGACACTCG	CAACATACAGGCAGCAAGAGC	GTAAAACGACGGCCAGT
PDGFRA-13	CCDS3495.1	NM_006206.2	GCTCTTGCTGCCTGTATGTTG	GTAAAACGACGGCCAGTTTCTATTCCCTGCCATGTGTG	GTAAAACGACGGCCAGT
PDGFRA-14	CCDS3495.1	NM_006206.2	GTAAAACGACGGCCAGTTTTCTGTGCCATATGGTCTGC	AAGACTGGACAGGGTGGTTTG	GTAAAACGACGGCCAGT
PDGFRA-15	CCDS3495.1	NM_006206.2	GTAAAACGACGGCCAGTTCCCATGCCTACCTCAGTACC	TGGAAACATGTCACAGAACTGG	GTAAAACGACGGCCAGT
PDGFRA-16	CCDS3495.1	NM_006206.2	GTAAAACGACGGCCAGTTTTGGATGTGTTCTTTGGGC	GCCTGATGATTTCAGACTCCC	GTAAAACGACGGCCAGT
PDGFRA-17	CCDS3495.1	NM_006206.2	AGTGGGTGGAGTGAGAACCTG	GTAAAACGACGGCCAGTAGGCACCGAATCTCTAGAAGC	GTAAAACGACGGCCAGT
PDGFRA-18	CCDS3495.1	NM_006206.2	GTAAAACGACGGCCAGTTCAAATGGGACAAGATAATTAGCAC	AGGCACAACATGTGGTTTGAG	GTAAAACGACGGCCAGT
PDGFRA-19	CCDS3495.1	NM_006206.2	GGACTTGACCAACCTGGAGTC	GTAAAACGACGGCCAGTCAGCATTTCACCATGATCTCG	GTAAAACGACGGCCAGT
PDGFRA-20	CCDS3495.1	NM_006206.2	GTAAAACGACGGCCAGTCTGACCACGCTACCAGTGAAG	CCTCTAGAACTGCGGAACAGC	GTAAAACGACGGCCAGT
PDGFRA-21	CCDS3495.1	NM_006206.2	AACTAAGTCCCACATCTTCCAGG	GTAAAACGACGGCCAGTACCGGGAGTGCACCATTATC	GTAAAACGACGGCCAGT
PDGFRA-22	CCDS3495.1	NM_006206.2	AAGGCTTTCGTTTGTCTCTGG	GTAAAACGACGGCCAGTCTCCTCTCAACCTCTGCATTG	GTAAAACGACGGCCAGT
PTK2-1	CCDS6381.1	NM_153831.2	CCGCATATAACATATCAAGAGAGAGTAT	GTAAAACGACGGCCAGTTTAGAACGCTGGTCAGTCACATA	GTAAAACGACGGCCAGT
PTK2-2	CCDS6381.1	NM_153831.2	TCTCATACCAAAGATTTCTGATAATTG	GTAAAACGACGGCCAGTGACTAGAGGTCTAGAAGAGATCATTCG	GTAAAACGACGGCCAGT
PTK2-3	CCDS6381.1	NM_153831.2	TGTTTCCTTGAATCACTGAGCTG	GTAAAACGACGGCCAGTCCTCCAAACGTGAGCTTTAATC	GTAAAACGACGGCCAGT
PTK2-4	CCDS6381.1	NM_153831.2	GTAAAACGACGGCCAGTAAGCGTAATTACCGACATAATGTAAAC	GGGAGAGGCATCTGAATAATAAAC	GTAAAACGACGGCCAGT
PTK2-5	CCDS6381.1	NM_153831.2	GTTTATTATTCAGATGCCTCTCCC	GTAAAACGACGGCCAGTCACAATTAATGTCATCAAGGATTCTG	GTAAAACGACGGCCAGT
PTK2-6	CCDS6381.1	NM_153831.2	GTAAAACGACGGCCAGTCCCATCCTTCCTGTGAATATACTG	GCCTGTGAAGACCTAGATGACAG	GTAAAACGACGGCCAGT
PTK2-7	CCDS6381.1	NM_153831.2	GTAAAACGACGGCCAGTTGGCAGTAATTTGAATGTAGGTG	GAACAATTAACAAATCACAGGGA	GTAAAACGACGGCCAGT
PTK2-8	CCDS6381.1	NM_153831.2	TCCTTTAACATATCCACGGCTC	GTAAAACGACGGCCAGTAATTCCGAGGTATTTCAACAGC	GTAAAACGACGGCCAGT
PTK2-9	CCDS6381.1	NM_153831.2	GTAAAACGACGGCCAGTTCAGGACAACGAGGATTTCAC	TCTGTCTCCTGTCCTATTCTTGG	GTAAAACGACGGCCAGT
PTK2-10	CCDS6381.1	NM_153831.2	GTAAAACGACGGCCAGTTGTTTCATTCCCACTCTTCTCTG	GGCTTGTGGAAGGTGTGAAAC	GTAAAACGACGGCCAGT
PTK2-11	CCDS6381.1	NM_153831.2	GTAAAACGACGGCCAGTTCCCTGATTCTAGGCACCATC	AAGCAAATGTTTAACAACAGGCTC	GTAAAACGACGGCCAGT
PTK2-12	CCDS6381.1	NM_153831.2	GTAAAACGACGGCCAGTCAGTTCAACATTCCTTCAGTTGTG	AAATTTGGATAGCCAGAATGCTT	GTAAAACGACGGCCAGT
PTK2-13	CCDS6381.1	NM_153831.2	TGTTAGCCCTGTTTGCTCTCC	GTAAAACGACGGCCAGTGCTTCTGACCTTAGAGTGGGC	GTAAAACGACGGCCAGT
PTK2-14	CCDS6381.1	NM_153831.2	TTCATAGATTGATGTGCCACAGA	GTAAAACGACGGCCAGTTTGGTTTCTGAATACGCCAAG	GTAAAACGACGGCCAGT
PTK2-15	CCDS6381.1	NM_153831.2	TAATGTTTCACGTGCATGACC	GTAAAACGACGGCCAGTTTTCTTATTTCTTCAGAGACAGTTTGG	GTAAAACGACGGCCAGT
PTK2-16	CCDS6381.1	NM_153831.2	CAGCCTGGTGACAGAATGAG	GTAAAACGACGGCCAGTTGCTGCCAGTACTGCATAAGG	GTAAAACGACGGCCAGT
PTK2-17	CCDS6381.1	NM_153831.2	AATCTGAATCCAGAGTTTAAATGTTTC	GTAAAACGACGGCCAGTAAAGACGGTCCAAATGGGTC	GTAAAACGACGGCCAGT
PTK2-18	CCDS6381.1	NM_153831.2	TCTTTCAAAGTGCCTATTGGTATG	GTAAAACGACGGCCAGTGCTGTCGCTTCCTCCATTTAG	GTAAAACGACGGCCAGT
PTK2-19	CCDS6381.1	NM_153831.2	GTAAAACGACGGCCAGTTCTCCCAAATAAATGGAAGCC	TCAGGTTAGGGAAGGCAAATC	GTAAAACGACGGCCAGT
PTK2-20	CCDS6381.1	NM_153831.2	TTACCTCCCAGCTGGTACTCG	GTAAAACGACGGCCAGTAAATGCTATTACTGCAAGGAGGAG	GTAAAACGACGGCCAGT
PTK2-21	CCDS6381.1	NM_153831.2	CCATTTGGACCAAGGCTATTC	GTAAAACGACGGCCAGTGAGGGTAATACGAGAAGACGAGC	GTAAAACGACGGCCAGT
PTK2-22	CCDS6381.1	NM_153831.2	TAGCTATCCAGTTGCCACAGC	GTAAAACGACGGCCAGTTGCACAATGTACCGCTCTACC	GTAAAACGACGGCCAGT
PTK2-23	CCDS6381.1	NM_153831.2	GTAAAACGACGGCCAGTGTTTCCTTTGTGTGTGAAGCAG	CAGTCTGGTTTCAAACTCTGGG	GTAAAACGACGGCCAGT
PTK2-24	CCDS6381.1	NM_153831.2	TCTGTGAGCTAAAGGATTGCATAC	GTAAAACGACGGCCAGTCACCATGCCTGGCCTATTC	GTAAAACGACGGCCAGT
PTK2-25	CCDS6381.1	NM_153831.2	GTAAAACGACGGCCAGTAGCCAACCTTCATTTATCATCAC	CCTTGCAACATGCGATTTC	GTAAAACGACGGCCAGT
PTK2-26	CCDS6381.1	NM_153831.2	TGGCATCATTTGCTTATTTGC	GTAAAACGACGGCCAGTCTCACTGCAACCCTAAGGAGG	GTAAAACGACGGCCAGT
PTK2-27	CCDS6381.1	NM_153831.2	GTGATCTGCCCGCTTCAG	GTAAAACGACGGCCAGTCTCACTGCAGTTCCACTCTGC	GTAAAACGACGGCCAGT
PTK2-28	CCDS6381.1	NM_153831.2	TCTGAACTATATCCCGCACACAC	GTAAAACGACGGCCAGTCATCAGTTCTGACTTTGGTGGG	GTAAAACGACGGCCAGT
PTK2-29	CCDS6381.1	NM_153831.2	TGCCTTGAAACTTGTGGAAAG	GTAAAACGACGGCCAGTAGGGAAGGTCATCGCTTGTAG	GTAAAACGACGGCCAGT
PTK2-30	CCDS6381.1	NM_153831.2	GAGGCAAGCTTGGACAACAC	GTAAAACGACGGCCAGTGACACAGGGTTAATTCCTCGC	GTAAAACGACGGCCAGT
PTK2B-1	CCDS6057.1	NM_173176.1	GTAAAACGACGGCCAGTATGAGGTATGTGGGCCTGTG	GGTGGATATGGGAGAGCTGC	GTAAAACGACGGCCAGT
PTK2B-2	CCDS6057.1	NM_173176.1	CATGAAGACAGAATCCCACCC	GTAAAACGACGGCCAGTGCTCTAAGGGAGAAACTCCCAG	GTAAAACGACGGCCAGT
PTK2B-3	CCDS6057.1	NM_173176.1	GTAAAACGACGGCCAGTCACCTCCCTGTTGATGGTCTC	TCTGGGCTTTGTCTTTCCATC	GTAAAACGACGGCCAGT
PTK2B-4	CCDS6057.1	NM_173176.1	GTAAAACGACGGCCAGTAGGCCCTTAATCTTCTGAGGC	ATCCTGAAGACCCAACACCC	GTAAAACGACGGCCAGT
PTK2B-5	CCDS6057.1	NM_173176.1	GTAAAACGACGGCCAGTTCTTGGAATGACATTTGTGGG	CCTATGTGGCTCTGGTCTGG	GTAAAACGACGGCCAGT
PTK2B-6	CCDS6057.1	NM_173176.1	GTAAAACGACGGCCAGTTCTCACCTCTTCCTGATTGGC	GAGCTGATACGGCCTCGATAC	GTAAAACGACGGCCAGT
PTK2B-7	CCDS6057.1	NM_173176.1	GTAAAACGACGGCCAGTAGCAGTGGGCAGTCTCTCAG	CAACATTTCAGTGCCTGCTTC	GTAAAACGACGGCCAGT
PTK2B-8	CCDS6057.1	NM_173176.1	GTAAAACGACGGCCAGTCAGGAAACAGTGGCTTGTGTC	CATGCTGCCATCTCTAAATGC	GTAAAACGACGGCCAGT
PTK2B-9	CCDS6057.1	NM_173176.1	GTAAAACGACGGCCAGTAAACTCCCAGTTCCTCCTCAC	AAGCTCCTGGCTTCCTGTG	GTAAAACGACGGCCAGT
PTK2B-10	CCDS6057.1	NM_173176.1	GTAAAACGACGGCCAGTGTCCTGCCATCTCTTCTCCAG	GATTAGCAGGGCTGTGGGTAG	GTAAAACGACGGCCAGT
PTK2B-11	CCDS6057.1	NM_173176.1	GTAAAACGACGGCCAGTGGGAGGAGAGTCCCTTGTAGG	ATAACACCAGGTGGCATGAAG	GTAAAACGACGGCCAGT
PTK2B-12	CCDS6057.1	NM_173176.1	ATTCCTATGCCTTCATGCCAC	GTAAAACGACGGCCAGTTCTGTCACTTGGAGGAAACCC	GTAAAACGACGGCCAGT
PTK2B-13	CCDS6057.1	NM_173176.1	GTAAAACGACGGCCAGTAGCAGAGAGCAGGGAGTTCAG	ACGAAGGGAGGATAAAGGAGG	GTAAAACGACGGCCAGT
PTK2B-14	CCDS6057.1	NM_173176.1	GTAAAACGACGGCCAGTAGCCTGCAGACACTCAGGTTC	TAAATACCACCATGCCCAGTG	GTAAAACGACGGCCAGT
PTK2B-15	CCDS6057.1	NM_173176.1	GACCCTGATCAAGAAGAAGGG	GTAAAACGACGGCCAGTATGGGTCCCTGCACTGTTC	GTAAAACGACGGCCAGT
PTK2B-16	CCDS6057.1	NM_173176.1	GTAAAACGACGGCCAGTTCCCAGCTAGAAGAGCAAAGG	ACAGGGCCTCTGGCTTATTTC	GTAAAACGACGGCCAGT
PTK2B-17	CCDS6057.1	NM_173176.1	GTAAAACGACGGCCAGTCCACTGAAATAAGCCAGAGGC	ACACTGCTCTGTGTCACCCAC	GTAAAACGACGGCCAGT
PTK2B-18	CCDS6057.1	NM_173176.1	GAGGGAAGGAGATGGCAAAG	GTAAAACGACGGCCAGTTTCTGAAGACCCTTAGCCTGG	GTAAAACGACGGCCAGT
PTK2B-19	CCDS6057.1	NM_173176.1	GTAAAACGACGGCCAGTCCCAGGCTAAGGGTCTTCAG	AATAGAACCCTGGGAACGGAG	GTAAAACGACGGCCAGT
PTK2B-20	CCDS6057.1	NM_173176.1	GTAAAACGACGGCCAGTGACTGAGTGCTAATGGCGATG	CTCTGTGTGCTGGTCTTGCTC	GTAAAACGACGGCCAGT
PTK2B-21	CCDS6057.1	NM_173176.1	TCTGCAGTGAAGATCGAAACG	GTAAAACGACGGCCAGTGACTGAGAAAGGGCTGTAGGG	GTAAAACGACGGCCAGT
PTK2B-22	CCDS6057.1	NM_173176.1	TTTCCTTCCTTTGGAACAAGC	GTAAAACGACGGCCAGTTCAACCTAGGCCATCTCCATC	GTAAAACGACGGCCAGT
PTK2B-23	CCDS6057.1	NM_173176.1	TTGTGCTCGTGTTTGTAGCAG	GTAAAACGACGGCCAGTGTGTTTGCAAAGGGAAGGAAG	GTAAAACGACGGCCAGT
PTK2B-24	CCDS6057.1	NM_173176.1	GGACTGTCCCTCCCTGAGTC	GTAAAACGACGGCCAGTTCCTGCAGAGGAAGAAACAAG	GTAAAACGACGGCCAGT
PTK2B-25	CCDS6057.1	NM_173176.1	GTAAAACGACGGCCAGTCCATCTGTGTCCTCTTCCACC	TGACCCAATGTGACCTTTCTG	GTAAAACGACGGCCAGT
PTK2B-26	CCDS6057.1	NM_173176.1	CCAGAAAGGTCACATTGGGTC	GTAAAACGACGGCCAGTCAGGGAATGCAGACAGACTCC	GTAAAACGACGGCCAGT
PTK2B-27	CCDS6057.1	NM_173176.1	TGATGTCAGCAGGTACGAAGG	GTAAAACGACGGCCAGTGTGGGAGATTGGTTCTTCCTC	GTAAAACGACGGCCAGT
PTK2B-28	CCDS6057.1	NM_173176.1	GTAAAACGACGGCCAGTGAAGAGTCCTTTCCAATCGGG	CTCTAAGAGGATCTGCTGGGC	GTAAAACGACGGCCAGT
PTK2B-29	CCDS6057.1	NM_173176.1	CCTCTTAGAGCAAGCTGGGC	GTAAAACGACGGCCAGTAAGCCACATAGAACCCACCTG	GTAAAACGACGGCCAGT
PTK2B-30	CCDS6057.1	NM_173176.1	CACCTCTGTGGCTTCCCTATC	GTAAAACGACGGCCAGTAGTGGCAAGGGAAGGTGACTC	GTAAAACGACGGCCAGT
PTK6-1	CCDS13524.1	NM_005975.2	GCCTGTCATGAGGAAGTGGG	GTAAAACGACGGCCAGTTTCTTGGGCCTCCCTGAG	GTAAAACGACGGCCAGT
PTK6-2	CCDS13524.1	NM_005975.2	GTAAAACGACGGCCAGTGGAGCTTGAGGTGGCAGG	CTACCCTAGCAGCCAGTGACC	GTAAAACGACGGCCAGT
PTK6-3	CCDS13524.1	NM_005975.2	GTAAAACGACGGCCAGTGAAGCACCAACAGCAACTGTG	TCTCCCAGTAGGAAATGCCAG	GTAAAACGACGGCCAGT
PTK6-4	CCDS13524.1	NM_005975.2	GTAAAACGACGGCCAGTAAATCTGAGGCTAAATCCAGGC	GCAATTGAAAGGGAACCACTC	GTAAAACGACGGCCAGT
PTK6-5	CCDS13524.1	NM_005975.2	GTAAAACGACGGCCAGTACAGCTGCTGGGTGTGATG	TGTGTGTGTGTAGACGTGGG	GTAAAACGACGGCCAGT
PTK6-6	CCDS13524.1	NM_005975.2	GTAAAACGACGGCCAGTATGAGACATGGCCCAGCC	CCCAGCTCCACACACAGG	GTAAAACGACGGCCAGT
PTK6-7	CCDS13524.1	NM_005975.2	GTAAAACGACGGCCAGTATCACCGTCCCACTGCTG	ACTGCTAACACCTCCCTCTGG	GTAAAACGACGGCCAGT
PTK6-8	CCDS13524.1	NM_005975.2	TTAGCAGTGGACAGTGTGCTG	GTAAAACGACGGCCAGTACCCATCACCTCAGTAAACCC	GTAAAACGACGGCCAGT
PTK7-1	CCDS4884.1	NM_002821.3	GGGACTCGGAGGTACTGGG	GTAAAACGACGGCCAGTACTACTCCAGGGCCGTTCC	GTAAAACGACGGCCAGT
PTK7-2	CCDS4884.1	NM_002821.3	GTAAAACGACGGCCAGTCAAGGTGGCCTGTGTTAGGAC	AGAAGCTGAGGTAAGGGAGGG	GTAAAACGACGGCCAGT
PTK7-3	CCDS4884.1	NM_002821.3	GTAAAACGACGGCCAGTCTTCCTTGTGTCTGTTGGCAC	GAATGGAGCGAGGTAACATCC	GTAAAACGACGGCCAGT
PTK7-4	CCDS4884.1	NM_002821.3	AGCCCTGACCCTCTGATACTG	GTAAAACGACGGCCAGTTTCATCTGGAGAGGGAAAGATG	GTAAAACGACGGCCAGT
PTK7-5	CCDS4884.1	NM_002821.3	GTAAAACGACGGCCAGTCAGCCAGAACTTCACCTTGAG	TCTGTGATACAAATCGCACCC	GTAAAACGACGGCCAGT
PTK7-6	CCDS4884.1	NM_002821.3	GGTTCCCTTGCATTCCTTTC	GTAAAACGACGGCCAGTCCTCTTCCTACTCCCAGCATC	GTAAAACGACGGCCAGT
PTK7-7	CCDS4884.1	NM_002821.3	CTAGGCTTGCTGTGGGAGAAC	GTAAAACGACGGCCAGTGAAGCCTCTGTCCATCACACC	GTAAAACGACGGCCAGT
PTK7-8	CCDS4884.1	NM_002821.3	GTAAAACGACGGCCAGTTTCCGTAAAGGGAAACTCCTG	GTGCTATGGAGGTGAGCACAG	GTAAAACGACGGCCAGT
PTK7-9	CCDS4884.1	NM_002821.3	GTAAAACGACGGCCAGTACTCTTACCCTGGAGGCAGC	GTTTCAGCAGAGGGTGGGTAG	GTAAAACGACGGCCAGT
PTK7-10	CCDS4884.1	NM_002821.3	GTAAAACGACGGCCAGTTACCGTTGTATGAGCAGCACC	AATCTCCACATTTCCTGGCAC	GTAAAACGACGGCCAGT
PTK7-11	CCDS4884.1	NM_002821.3	CTCAGGAGTTTGGACTTTGCC	GTAAAACGACGGCCAGTCACAGTCGTACGCTCTGGTTC	GTAAAACGACGGCCAGT
PTK7-12	CCDS4884.1	NM_002821.3	GTAAAACGACGGCCAGTTACACTTGCATTGCCTCCAAC	GGGAGAAGCCATAGTGCTGG	GTAAAACGACGGCCAGT
PTK7-12	CCDS4884.1	NM_152882.2	GTAAAACGACGGCCAGTTACACTTGCATTGCCTCCAAC	GGGAGAAGCCATAGTGCTGG	GTAAAACGACGGCCAGT
PTK7-13	CCDS4884.1	NM_002821.3	CAGGTAGGGCCACCTCTCTC	GTAAAACGACGGCCAGTTGCCATGTTCTGTACACAGGG	GTAAAACGACGGCCAGT
PTK7-14	CCDS4884.1	NM_002821.3	TGTTAAAGCCAGTGAAGGTGG	GTAAAACGACGGCCAGTCTCCAGGACCCAGCAACAG	GTAAAACGACGGCCAGT
PTK7-15	CCDS4884.1	NM_002821.3	GTAAAACGACGGCCAGTAGTTGGCAAGAGTGGAAGACC	TCAGAACACTAGCCCGTACCC	GTAAAACGACGGCCAGT
PTK7-16	CCDS4884.1	NM_002821.3	GTAAAACGACGGCCAGTCCACTGTGGGAGAGGCTAGG	AACCACTGACTCCCACCTTTG	GTAAAACGACGGCCAGT
PTK7-16	CCDS4884.1	NM_152883.1	GTAAAACGACGGCCAGTCTGCACTCCCAGTGAACTTCC	TAAATGGTGCCTCTGTTGCTC	GTAAAACGACGGCCAGT
PTK7-17	CCDS4884.1	NM_002821.3	GTAAAACGACGGCCAGTCTGCACTCCCAGTGAACTTCC	TAAATGGTGCCTCTGTTGCTC	GTAAAACGACGGCCAGT
PTK7-18	CCDS4884.1	NM_002821.3	GTAAAACGACGGCCAGTGTGTTGAAACGCTACCAAGGG	AGCTTTGGACTAAGCAGGCAC	GTAAAACGACGGCCAGT
PTK7-19	CCDS4884.1	NM_002821.3	TCTGTATGTAGAAAGGCTGGGC	GTAAAACGACGGCCAGTTGAGAGGGAGGTAGGCTGAAC	GTAAAACGACGGCCAGT
PTK7-20	CCDS4884.1	NM_002821.3	GTAAAACGACGGCCAGTTGCAAGGTCCACAAAGTGTTG	AGACCTCAGCAATGCCTGTTG	GTAAAACGACGGCCAGT
ROR2-1	CCDS6691.1	NM_004560.2	GTAAAACGACGGCCAGTGGACGCATCGTAGAAAGGG	GCTTATTGTAACCAGCCCGAG	GTAAAACGACGGCCAGT
ROR2-2	CCDS6691.1	NM_004560.2	GTAAAACGACGGCCAGTCCCGCATTTGCTATTCTTGTG	AAACACAGGAATCAAGGTGGC	GTAAAACGACGGCCAGT
ROR2-3	CCDS6691.1	NM_004560.2	GTAAAACGACGGCCAGTTTCCCTTGGAAGAGTTCATAGC	TGCTGACTGGTGTGTGTTCAG	GTAAAACGACGGCCAGT
ROR2-4	CCDS6691.1	NM_004560.2	GTAAAACGACGGCCAGTCTTCCCTTGTGTGTGGTTTCC	CAAATTCGGCAAAGACATGAG	GTAAAACGACGGCCAGT
ROR2-5	CCDS6691.1	NM_004560.2	AATTGCTGGATCGCAAGATG	GTAAAACGACGGCCAGTCCCACTGACCATGCCATTAAC	GTAAAACGACGGCCAGT
ROR2-6	CCDS6691.1	NM_004560.2	GTAAAACGACGGCCAGTGTGGGCAGTCTGGGATGC	CCTGGGCTTCACCGACAC	GTAAAACGACGGCCAGT
ROR2-7	CCDS6691.1	NM_004560.2	GTAAAACGACGGCCAGTATTTGTGGGCTTGGGACTTC	GTCAGGACAGAACGCCCTC	GTAAAACGACGGCCAGT
ROR2-8	CCDS6691.1	NM_004560.2	GTAAAACGACGGCCAGTAGGTGGAGAGTGGGTTGGTAG	GCAGTGAATTCCCAACACG	GTAAAACGACGGCCAGT
ROR2-9	CCDS6691.1	NM_004560.2	GTAAAACGACGGCCAGTAGGAAGTCAGTGTGTCCCAGC	AGCTGAAGATCATGCTCAGGG	GTAAAACGACGGCCAGT
ROR2-9	CCDS6691.1	NM_004560.2	GACCGGTTTGGGAAAGTCTAC	GTAAAACGACGGCCAGTCACACCGTAGGACCAGATGTC	GTAAAACGACGGCCAGT
ROR2-9	CCDS6691.1	NM_004560.2	AGTACCTATCCAGCCACCACG	GTAAAACGACGGCCAGTGTTGCTCACATTGCTCACTGG	GTAAAACGACGGCCAGT

PTK7-20	CCDS4884.1	NM_002821.3	GTAAAACGACGGCCAGTTGCAAGGTCCACAAAGTGTTG	AGACCTCAGCAATGCCTGTTG	GTAAAACGACGGCCAGT
ROR2-1	CCDS6691.1	NM_004560.2	GTAAAACGACGGCCAGTGGACGCATCGTAGAAAGGG	GCTTATTGTAACCAGCCCGAG	GTAAAACGACGGCCAGT
ROR2-2	CCDS6691.1	NM_004560.2	GTAAAACGACGGCCAGTCCCGCATTTGCTATTCTTGTG	AAACACAGGAATCAAGGTGGC	GTAAAACGACGGCCAGT
ROR2-3	CCDS6691.1	NM_004560.2	GTAAAACGACGGCCAGTTTCCCTTGGAAGAGTTCATAGC	TGCTGACTGGTGTGTGTTCAG	GTAAAACGACGGCCAGT
ROR2-4	CCDS6691.1	NM_004560.2	GTAAAACGACGGCCAGTCTTCCCTTGTGTGTGGTTTCC	CAAATTCGGCAAAGACATGAG	GTAAAACGACGGCCAGT
ROR2-5	CCDS6691.1	NM_004560.2	AATTGCTGGATCGCAAGATG	GTAAAACGACGGCCAGTCCCACTGACCATGCCATTAAC	GTAAAACGACGGCCAGT
ROR2-6	CCDS6691.1	NM_004560.2	GTAAAACGACGGCCAGTGTGGGCAGTCTGGGATGC	CCTGGGCTTCACCGACAC	GTAAAACGACGGCCAGT
ROR2-7	CCDS6691.1	NM_004560.2	GTAAAACGACGGCCAGTATTTGTGGGCTTGGGACTTC	GTCAGGACAGAACGCCCTC	GTAAAACGACGGCCAGT
ROR2-8	CCDS6691.1	NM_004560.2	GTAAAACGACGGCCAGTAGGTGGAGAGTGGGTTGGTAG	GCAGTGAATTCCCAACACG	GTAAAACGACGGCCAGT
ROR2-9	CCDS6691.1	NM_004560.2	GTAAAACGACGGCCAGTAGGAAGTCAGTGTGTCCCAGC	AGCTGAAGATCATGCTCAGGG	GTAAAACGACGGCCAGT
ROR2-9	CCDS6691.1	NM_004560.2	GACCGGTTTGGGAAAGTCTAC	GTAAAACGACGGCCAGTCACACCGTAGGACCAGATGTC	GTAAAACGACGGCCAGT
ROR2-9	CCDS6691.1	NM_004560.2	AGTACCTATCCAGCCACCACG	GTAAAACGACGGCCAGTGTTGCTCACATTGCTCACTGG	GTAAAACGACGGCCAGT
ROR2-9	CCDS6691.1	NM_004560.2	GTAAAACGACGGCCAGTGCAAGTTCTCCATCGACTCAG	ATCTGCATTGGGATCTGCAC	GTAAAACGACGGCCAGT
ROR2-9	CCDS6691.1	NM_004560.2	CCAGTGAGCAATGTGAGCAAC	GTAAAACGACGGCCAGTCTCAAAGGTGACTGAGGTCCC	GTAAAACGACGGCCAGT
TIE1-1	CCDS482.1	NM_005424.2	GTAAAACGACGGCCAGTAGCCACCTCATTTCCTCTTCC	AATTGATCCTCCCATCTCAGC	GTAAAACGACGGCCAGT
TIE1-2	CCDS482.1	NM_005424.2	GTAAAACGACGGCCAGTAGTAAGACCAGAGGGCTGGG	GACCTTGTCTGGAAGCAGGTG	GTAAAACGACGGCCAGT
TIE1-3	CCDS482.1	NM_005424.2	ACAGCCCTGGAGGTGAGTTAG	GTAAAACGACGGCCAGTCTACAGAGGAGAGGCCCTGG	GTAAAACGACGGCCAGT
TIE1-4	CCDS482.1	NM_005424.2	AGCTGAGCAGAGGTGGACAG	GTAAAACGACGGCCAGTCTGGAGGAAGGTGTCTTCAGC	GTAAAACGACGGCCAGT
TIE1-5	CCDS482.1	NM_005424.2	GTAAAACGACGGCCAGTGCCCTATGGGTACTTCCTGTG	CACCCACATGGTTCTAGGGTC	GTAAAACGACGGCCAGT
TIE1-6	CCDS482.1	NM_005424.2	GACCCTAGAACCATGTGGGTG	GTAAAACGACGGCCAGTAAGTCAGAGGCAGAGTGGAGG	GTAAAACGACGGCCAGT
TIE1-7	CCDS482.1	NM_005424.2	GTAAAACGACGGCCAGTCCAGTCCTTCTATCCTCAGCC	AGAGCTCCCTGTCCATCAGAC	GTAAAACGACGGCCAGT
TIE1-8	CCDS482.1	NM_005424.2	GTAAAACGACGGCCAGTCTCCACTGAGAAACAGAACACG	CTGACCTCATGTGAGCAATGG	GTAAAACGACGGCCAGT
TIE1-9	CCDS482.1	NM_005424.2	GTAAAACGACGGCCAGTATCAGTCCAGACGGACACCTG	AGTATCTCCAGCCTGAGCAGC	GTAAAACGACGGCCAGT
TIE1-10	CCDS482.1	NM_005424.2	CCCAGCTTGAAACAAAGATGC	GTAAAACGACGGCCAGTCTAGAAGCTGCCATGCTCCC	GTAAAACGACGGCCAGT
TIE1-11	CCDS482.1	NM_005424.2	GTAAAACGACGGCCAGTGTGAGTAGGGAGAGAGCTGGG	CAAGGAAGAACAACCTCCAGTG	GTAAAACGACGGCCAGT
TIE1-12	CCDS482.1	NM_005424.2	GTAAAACGACGGCCAGTTGTTCTTCCTTGTTCACTGGG	CCTCCCGTGTCTCCTAGGTC	GTAAAACGACGGCCAGT
TIE1-13	CCDS482.1	NM_005424.2	GTAAAACGACGGCCAGTCTAGAGCAGATGTGTCCAGCC	TGTGGAAGGAGAGCGTGC	GTAAAACGACGGCCAGT
TIE1-14	CCDS482.1	NM_005424.2	GTAAAACGACGGCCAGTGGGATCTTTCACCTCTCCCTC	CACACACAAGGTGTACAAGGTATTG	GTAAAACGACGGCCAGT
TIE1-15	CCDS482.1	NM_005424.2	GTAAAACGACGGCCAGTTGACACTGAAACCTCCTCGTG	GTCAATTGCTGGAGGAAGCC	GTAAAACGACGGCCAGT
TIE1-16	CCDS482.1	NM_005424.2	GTAAAACGACGGCCAGTCTTTGTCCCACAAATCCCAG	GATGAAGGAGGATCAAGGGTG	GTAAAACGACGGCCAGT
TIE1-17	CCDS482.1	NM_005424.2	GTAAAACGACGGCCAGTATCCCTGTCTGTTACCATCGG	GGCTGACTTCTTCCACTGACAC	GTAAAACGACGGCCAGT
TIE1-18	CCDS482.1	NM_005424.2	CGAAGACTGACTCCTTACTGGC	GTAAAACGACGGCCAGTCCCTAGGAGAGAATGGGTTTG	GTAAAACGACGGCCAGT
TIE1-19	CCDS482.1	NM_005424.2	AGTCTCATTCAACCCTCACCC	GTAAAACGACGGCCAGTCACCTGTGTCACACCTGGAAC	GTAAAACGACGGCCAGT
TIE1-20	CCDS482.1	NM_005424.2	GTAAAACGACGGCCAGTTGGCCAAGGCCAGATACTTAC	ACACTTCATCGTCACAGTTTCG	GTAAAACGACGGCCAGT
TIE1-21	CCDS482.1	NM_005424.2	GTAAAACGACGGCCAGTGGGAGATAGTGAGCCTTGGTG	CTAGCTGTAGCGCAATCTGGG	GTAAAACGACGGCCAGT
TIE1-22	CCDS482.1	NM_005424.2	GTAAAACGACGGCCAGTCAGCTTTGATCCCTGTGACC	GCCTGGTGTCTAAACCAGTGAG	GTAAAACGACGGCCAGT
TIE1-23	CCDS482.1	NM_005424.2	GTAAAACGACGGCCAGTATGGAAGTCCAGGAGCTTGAG	CACCTACAAAGCATGGGAACC	GTAAAACGACGGCCAGT

#The primer pair did not meet our quality criteria that ≥90% of bases in the target region have a Phred quality score of at least 20 in three quarters of the tumor samples analyzed.

Table S4. Characteristics of melanoma patients with PTK mutations

Sample	Patient Age (years)*	Patient Gender	Tumor Source	Matched normal source
1T	29	F	Lung	Blood
2T	30	M	Pectoral muscle	Blood
3T	18	M	Forehead, subcutaneous	Blood
4T	33	F	Supraclavicular, soft tissue	Blood
4T	34	F	Lung	Blood
5T	47	M	External iliac soft tissue	Blood
6T	42	M	Neck, soft tissue	Blood
7T	53	M	Stomach	Blood
8T	61	M	Inguinal soft tissue	Blood
9T	62	M	Back, subcutaneous	Blood
10T	55	M	Axillary soft tissue	Blood
12T	53	M	Upper arm, subcutaneous	Blood
13T	49	M	Chest wall, subcutaneous	Blood
15T	39	M	Thigh, subcutaneous	Blood
16T	62	M	Lung	Blood
17T	33	M	Shoulder, subcutaneous	Blood
18T	55	M	Clavicle, soft tissue	Blood
19T	49	M	Scapula, subcutaneous	Blood
20T	58	F	Axillary soft tissue	Blood
21T	59	M	Omentum	Blood
22T	51	M	Chest wall, subcutaneous	Blood
23T	44	M	Lung	Blood
24T	49	M	Axillary soft tissue	Blood
26T	48	F	Lung	Blood
28T	28	F	Axillary soft tissue	Blood
29T	51	M	Inguinal soft tissue	Blood
30T	53	F	Lung	Blood
31T	49	F	Thigh, subcutaneous	Blood
32T	58	M	Omentum	Blood
33T	33	M	Chest wall subcutaneous, & pleura **	Blood
34T	31	M	Shoulder, subcutaneous	Blood
35T	23	F	Thigh, subcutaneous	Blood
36T	25	M	Thigh, subcutaneous	Blood
37T	38	F	Omentum	Blood
38T	27	M	Skull	Blood
39T	56	M	Mesentery	Blood
41T	45	M	Neck, soft tissue	Blood
43T	19	F	Popliteal soft tissue	Blood
44T	56	M	Lung	Blood
45T	48	M	Mediastinum	Blood
49T	43	M	Thigh, subcutaneous	Blood
50T	49	F	Inguinal soft tissue	Blood
51T	50	F	Adnexa	Blood
52T	39	F	Lung	Blood
54T	27	M	Subcutaneous	Blood
55T	60	M	Lung	Blood
56T	52	M	Lung	Blood
58T	46	F	Hip, subcutaneous	Blood
59T	64	F	Abdomen, subcutaneous	Blood
60T	46	M	Flank, subcutaneous	Blood
62T	58	F	Thigh, subcutaneous	Blood
63T	30	M	Jejunum	Blood
64T	32	F	Ovary	Blood
68T	49	M	Lung	Blood
69T	36	M	Axillary soft tissue	Blood
71T	67	M	Lung	Blood
72T	53	M	Liver	Blood
73T	45	F	Breast	Blood
74T	40	F	Lower extremity, subcutaneous	Blood
76T	40	M	Neck, soft tissue	Blood
77T	39	M	Lung	Blood
78T	27	F	Lung	Blood
79T	53	M	Supraclavicular, soft tissue	Blood
80T	36	F	Popliteal soft tissue	Blood
81T	60	F	Upper arm, subcutaneous	Blood
83T	33	F	Back, subcutaneous	Blood
84T	60	F	Thigh, subcutaneous	Blood
85T	44	M	Chest wall, subcutaneous	Blood
86T	42	F	Liver	Blood
87T	27	M	Small bowel & mesentary **	Blood
88T	37	F	Chest wall, subcutaneous	Blood
90T	19	M	Neck, soft tissue	Blood
91T	55	F	Subcostal soft tissue	Blood
92T	37	F	Femur	Blood
93T	42	F	Axillary soft tissue	Blood
94T	44	M	Adrenal gland	Blood
95T	58	F	Inguinal soft tissue	Blood
96T	49	M	Inguinal soft tissue	Blood
99T	57	M	Liver	Blood

* Patient's age when tumor was surgically removed. ** Cell line generated by cells mixed from 2 tumors resected during the patient's surgery. Abbreviations: F, female; M, male.

Table S5. Mutations Identified in RAF and RAS isoforms in melanoma samples containing ERBB4 mutations

Sample	ERBB4	BRAF	NRAS	ARAF	CRAF	HRAS	KRAS
7T	E452K	wt	Q61R	wt	wt	wt	wt
12T	E563K	wt	Q61Q/R	wt	wt	wt	wt
17T	E317K	wt	Q61Q/K	wt	wt	wt	wt
31T	wt	wt	wt	wt	wt	wt	wt
34T	R491K	V600V/E	wt	wt	T362T/A	wt	wt
39T	wt	wt	wt	wt	wt	wt	wt
49T	R393R/W	V600V/E	wt	wt	wt	wt	wt
55T	E452K	V600V/E	wt	P216S, P254L	wt	wt	wt
56T	R544R/W	V600V/E	wt	wt	wt	wt	wt
63T	E542K, E872K	wt	Q61Q/K	wt	wt	wt	wt
68T	Splice Site / LOH	V600V/E	wt	wt	wt	wt	wt
71T	L39L/F, S1246S/N	V600V/M, V600V/E	wt	wt	wt	wt	wt
86T	E836E/K	V600V/E	wt	wt	wt	wt	wt
93T	wt	wt	wt	A345A/G	wt	wt	wt

Table S6. Primers used for PCR amplification and sequencing of RAS and Raf isoforms

Gene and Exon Name	Forward Primer	Reverse Primer	Sequencing Primer
ARAF-1	TGAGCAGGATCTCTTGGACTG	GTAAAACGACGGCCAGTCAGCTGATGTTCCCATCCTTC	GTAAAACGACGGCCAGT
ARAF-2	GTCATGGAAGCGAAATGGC	GTAAAACGACGGCCAGTCAGAAGGAATCAAATGACTGAGG	GTAAAACGACGGCCAGT
ARAF-3	GTAAAACGACGGCCAGTTATCCCTCTGAGCCTGTTTCC	AGCAGGGAAGTTTGAGACCTG	GTAAAACGACGGCCAGT
ARAF-4	GTAAAACGACGGCCAGTTACCCAACCTCCCACTCATTC	CACGGGTCAGCTGTCTGTAAG	GTAAAACGACGGCCAGT
ARAF-5	AGTACCAACCGCCAACAGTG	GTAAAACGACGGCCAGTGAGAAATGAGGTGACTTGCCC	GTAAAACGACGGCCAGT
ARAF-6	CAAATGCATGTTTATGGCTGG	GTAAAACGACGGCCAGTCATCAGTGCTGAAACTCTGGC	GTAAAACGACGGCCAGT
ARAF-7	GTAAAACGACGGCCAGTCAACGTCCATATGGTCAGCAC	CTGGTGACTTGGAATGTGGG	GTAAAACGACGGCCAGT
ARAF-8	CCAGAGTTTCAGCACTGATGG	GTAAAACGACGGCCAGTCCAGATGGGTGGCATCTAAG	GTAAAACGACGGCCAGT
ARAF-9	GTAAAACGACGGCCAGTAGAAAGTGGTATGCTCGAGGG	ATGTCCAGGAAGCACTCCAAG	GTAAAACGACGGCCAGT
ARAF-10	GTAAAACGACGGCCAGTAGAACAGTGCCACTCCTGATG	TCTCGGTGGATGATGTTCTTG	GTAAAACGACGGCCAGT
ARAF-11	GGATTTGCCATCATCACACAG	GTAAAACGACGGCCAGTCCCTTGTAATTCCCAGAACCC	GTAAAACGACGGCCAGT
ARAF-12	GTAAAACGACGGCCAGTCAAGGTTGTGGATAGTTTGCG	GTGGGACATGAGGAGTCCAG	GTAAAACGACGGCCAGT
ARAF-13	GTGTGGGTGGCTCTGAGTTG	GTAAAACGACGGCCAGTTGGCATTTATCAGTGCAAAGG	GTAAAACGACGGCCAGT
ARAF-14	GTAAAACGACGGCCAGTAGCAGAGAATCCTCCCAAGTC	TCACATCTGCCTCCATCTCAG	GTAAAACGACGGCCAGT
ARAF15[#]	GTGTGTGTTTCACCATGAGGC	GTAAAACGACGGCCAGTGGCAGAGACGAACATTGATTG	GTAAAACGACGGCCAGT
BRAF-1	GTAAAACGACGGCCAGTAGCTCTCCGCCTCCCTTC	AAGGTGGCTGAGGGCATC	GTAAAACGACGGCCAGT
BRAF-2	GTAAAACGACGGCCAGTGAGGAACACTGGCAGTTACTGTG	TCTCTTCCCAAATCTATTCCTAATCC	GTAAAACGACGGCCAGT
BRAF-3	TGGTGTTGTATCTGACCTAGTAACCC	GTAAAACGACGGCCAGTCCTCATATGGCCTACAGTATTTCTTC	GTAAAACGACGGCCAGT
BRAF-4	GTAAAACGACGGCCAGTCCTCCCTCACTGTTACTAGCCC	TTACTCATCCATATTTCACATTCCC	GTAAAACGACGGCCAGT
BRAF-5	GTAAAACGACGGCCAGTGTGTAGTCCATCTATTATCTTGAACCC	GGGAGAGAAATACTGTCCATTCC	GTAAAACGACGGCCAGT
BRAF-6	GTTGTTTCTGAGAATGGAATTTGA	GTAAAACGACGGCCAGTTCTGAGTGGTATGATAAGTTATTTGGG	GTAAAACGACGGCCAGT
BRAF-7	GTAAAACGACGGCCAGTCAGCTTTGGCAGTATTGGATT	TCATCAGAGAGAAACCAGAAGC	GTAAAACGACGGCCAGT
BRAF-8	GTAAAACGACGGCCAGTGGTTTACATTGGCAAGTGCTTC	GTTACTTGAAAGAGGCAAGTATAAAGG	GTAAAACGACGGCCAGT
BRAF-9	GTAAAACGACGGCCAGTTTTGGCCCATCCTTTCCA	GCAGTGCCGTAGAAATATGCTT	GTAAAACGACGGCCAGT
BRAF-10	CTTCCTGTATCCCTCTCAGGC	GTAAAACGACGGCCAGTCGAACAGTGAATATTTCCTTTGATG	GTAAAACGACGGCCAGT
BRAF-11	GTAAAACGACGGCCAGTCCATGGAACAAACAAGGTTGG	AATAGTTGCTACCACTGGGAACC	GTAAAACGACGGCCAGT
BRAF-12	CAATTGCCAGTCTCTTCTAAATGTATC	GTAAAACGACGGCCAGTTTAGCATCCTTATGTTCCTGGAC	GTAAAACGACGGCCAGT
BRAF-13	GTAAAACGACGGCCAGTCATGGATAAATAGGCTTGACTGG	CCTATACATGCATGCACAATCC	GTAAAACGACGGCCAGT
BRAF-14	TCATCCTAACACATTTCAAGCC	GTAAAACGACGGCCAGTTTTGTGAATACTGGGAACTATGAAA	GTAAAACGACGGCCAGT
BRAF-15	GAATTCATCTGGCAATGATGGT	GTAAAACGACGGCCAGTTTCACGCTTACCCAGGAGTTA	GTAAAACGACGGCCAGT
BRAF-16	CCATCTATGATGTGGCATTGG	GTAAAACGACGGCCAGTCTCAACCCTCATGAAGCCATC	GTAAAACGACGGCCAGT
BRAF-17	GCTTTCTTGTAAAGTGTGATGGG	GTAAAACGACGGCCAGTCCACACAAGTGTTCTTTGGTTC	GTAAAACGACGGCCAGT
RAF1-1	GTAAAACGACGGCCAGTCTGGTCCCATTTTCCTCATC	ATAGGGGGTGTGGAAGGAAC	GTAAAACGACGGCCAGT
RAF1-2	GTAAAACGACGGCCAGTTATTTCTGTGCCCACCTTTCC	AGGTATTGGTCATCAGGCCC	GTAAAACGACGGCCAGT
RAF1-3	GTAAAACGACGGCCAGTGGCCTTGAGCAAATTACCTTC	TTGCCTTACTGTAAACAACAGCA	GTAAAACGACGGCCAGT
RAF1-4	GTAAAACGACGGCCAGTGGAGGCCAAGAAATGAAGTTG	ATGAATGCCACCAAACCTAGC	GTAAAACGACGGCCAGT
RAF1-5	GTAAAACGACGGCCAGTAAAGCAAGGCATGCTGATTG	CCACAGAAGCAGCAAGGG	GTAAAACGACGGCCAGT
RAF1-6	GTAAAACGACGGCCAGTGGTTGTACAGGTAGAGTTTGCCC	TCCTTGATCAGATTTGAAACCC	GTAAAACGACGGCCAGT
RAF1-7	GTAAAACGACGGCCAGTTGAAAAATCAGCCTTGGAGA	TTGGCAGGAGGTACTGTTGTC	GTAAAACGACGGCCAGT
RAF1-8	GGATGCAATTCGAAGTCACAG	GTAAAACGACGGCCAGTACTGTCTGATGCAAGTGTGCC	GTAAAACGACGGCCAGT
RAF1-9	AACAGATGACATGGGTTGATCC	GTAAAACGACGGCCAGTCTCAGTCCTCTCCTCCTCCTG	GTAAAACGACGGCCAGT
RAF1-10	GTAAAACGACGGCCAGTTGGAAATTTGCCGTATCTGTG	GCGGCACAGTCCACTAACTC	GTAAAACGACGGCCAGT
RAF1-11	GTAAAACGACGGCCAGTGACAGCACAGAACCCACTGTC	GGCTTGTGCAAAGATATCACAG	GTAAAACGACGGCCAGT
RAF1-12	GTAAAACGACGGCCAGTCCCTGTGTGTAACACTCCTTGG	TTCCTGTCCTCTGCCTCTTTC	GTAAAACGACGGCCAGT
RAF1-13	GCTGTGACAGAGGTAAGGTGG	GTAAAACGACGGCCAGTAATCTACAATTGCCCTGAGGC	GTAAAACGACGGCCAGT
RAF1-14	GTAAAACGACGGCCAGTCTAATGAAAGGGACAGCCTGG	AGCCTCTTCATTGCTTTGGG	GTAAAACGACGGCCAGT
RAF1-15	CAGGTAAGTCTGTGCTGGTGC	GTAAAACGACGGCCAGTCCATCTTGTAGAGGACCTGGG	GTAAAACGACGGCCAGT
RAF1-16	CCCAGGTCCTCTACAAGATGG	GTAAAACGACGGCCAGTAAACATGTGTTCTGCCTCTGG	GTAAAACGACGGCCAGT
HRAS-1	TGGGTCATTAAGAGCAAGTGG	GTAAAACGACGGCCAGTTAGAGGAAGCAGGAGACAGG	GTAAAACGACGGCCAGT
HRAS-2	GTAAAACGACGGCCAGTGAGAGGCTGGCTGTGTGAAC	GACATGCGCAGAGAGGACAG	GTAAAACGACGGCCAGT
HRAS-3	TTCCTGTGTGTGTTTGCCATC	GTAAAACGACGGCCAGTAGTGAGTGCTGCTCCCTGG	GTAAAACGACGGCCAGT
HRAS-4	GCCTCCTGTCCTCTCTGC	GTAAAACGACGGCCAGTAGCTCTCCCCAAGGACCTC	GTAAAACGACGGCCAGT
KRAS-1	GTAAAACGACGGCCAGTAAAGCCCACTGTAAGCTGGTG	AGAGAAGCAGGCCTAAGGTTG	GTAAAACGACGGCCAGT
KRAS-2	GTAAAACGACGGCCAGTCTGTTCCGGATGGAGATATGG	TTTCAATGCTCCTCTTCCCTC	GTAAAACGACGGCCAGT
KRAS-3	GTAAAACGACGGCCAGTAAGCTTGGCATAGTCCCTGAC	ACTCGAGTCACAGCACAGGC	GTAAAACGACGGCCAGT
KRAS-4	ATTTCCACATTCGAGGCTGAG	GTAAAACGACGGCCAGTGCAATGCTAACATGGGAAGG	GTAAAACGACGGCCAGT
NRAS-1	GTAAAACGACGGCCAGTCCAAATGGAAGGTCACACTAGG	GAACTCAACACTGAGTTTGCAATAG	GTAAAACGACGGCCAGT
NRAS-2	GTAAAACGACGGCCAGTAATAGCATTGCATTCCCTGTG	CTCTGGTTCCAAGTCATTCCC	GTAAAACGACGGCCAGT
NRAS-3	GTAAAACGACGGCCAGTAAGCAGTCTGCCCTCCTCAG	CAAGAGACAGAGGCTGCAGTG	GTAAAACGACGGCCAGT
NRAS-4	GCCTGTTCTTGTGATTCAATAGG	GTAAAACGACGGCCAGTTGTGCAGAAGAGGATAGGCAG	GTAAAACGACGGCCAGT

[#] The primer pair did not meet our quality criteria that ≥90% of bases in the target region have a Phred quality score of at least 20 in three quarters of the tumor samples analyzed.

Table S7. Primers used for ERBB4 plasmid construction

Gene Name	Forward Primer	Reverse Primer
ERBB4 into pCDF-MCS2-EF1-Puro™	CGGCTCTAGAGCCACCATGAAGCCGGCGAC	ATCGGCGGCCGCTTACACCACAGTATTCCGG
Knockdown resistant ERBB4 primers into pCDF1-MCS2-EF1-puro	CACCAAAATCAAGGGGACTT	GGAGCCAGTACACGACATCA
Knockdown resistant ERBB4 primer set #1 into pcDNA3.1	GATTCCTGTGGCCATTAAGATTCT	AGAATCTTAATGGCCACAGGAATC
Knockdown resistant ERBB4 primer set #2 into pcDNA3.1	CCTGTGGCCATCAAGATTCT	AGAATCTTGATGGCCACAGG
Knockdown resistant ERBB4 primer set #3 into pcDNA3.1	CCTGTGGCCATCAAAATTCTTAATGAGAC	GTCTCATTAAGAATTTTGATGGCCACAGG

Supplementary Note

Tumor Tissue Collection

A panel of 79 pathology-confirmed metastatic melanoma tumor resections was assembled from patients referred to the Surgery Branch of the National Cancer Institute for enrollment in IRB-approved Surgery Branch clinical trials of immunotherapy. All of the patients had progressive metastatic melanoma that had failed available conventional treatments, were 16 years or older and passed eligibility testing for the relevant protocol. None had received therapy for 1 month prior to entering the protocol. Before tissue was acquired all patients signed written informed consents. The melanoma tissue panel was selected on the basis of an available pathology-confirmed, melanoma tissue culture line, paired with freshly frozen tissue from the resected melanoma metastasis and apheresis-collected, peripheral blood mononuclear cells.