Table S1: Source and histo-pathologic description of the 38 specimens studied

Sample ID	Sample source	ER	PR	Her2		Histology of primary site*	Notthingham grade	Histology				
				ISH ratio	IHC			In Situ	Invasive	Stroma	Immune Cell	Necrosis
AA0948	Lumpectomy	>80	<5	1.05	1+	IDC	I	0%	20%	70%	10%	0%
AA0930	Lumpectomy	90	50	NA	0	IDC + LF	I	0%	25%	75%	0%	0%
UCI2219330	Lumpectomy	100	0	NA		IDC	I	0%	35%	60%	5%	0%
UCI2076630	Mastectomy	95	20	2.8		IDC	I	5%	45%	30%	20%	0%
AA0960	Lumpectomy	80	<10		0	IDC	I	0%	60%	40%	0%	0%
UCI1804937	Mastectomy	100	50	1.2		IDC	I	0%	65%	30%	5%	0%
AA0957	Mastectomy	100	50		0	IDC +DCIS	I	10%	70%	20%	0%	0%
AA0926	Lumpectomy	90	50	1.47		IDC	I	0%	90%	5%	5%	0%
UCI1951813	Mastectomy	100	0	1		IDC	II	0%	10%	75%	5%	10%
UCI2649875	Lumpectomy	95	40	1.1		IDC	II	0%	25%	50%	5%	20%
AA1267	Lumpectomy	100	95	1.05	2+	IDC+LF	II	0%	30%	65%	5%	0%
UCI1546879	Mastectomy	70	0	1.5		IDC	II	10%	25%	50%	5%	10%
AA1090	Lumpectomy	100	<5		0	IDC	II	0%	40%	50%	10%	0%
UCI2564879	Mastectomy	90	90	1.2		IDC	II	20%	30%	40%	5%	5%
UCI8965412	Mastectomy	80	90	6.7		IDC	II	10%	45%	30%	5%	10%
UCI1908503	Lymphadenectomy	0	0	7.7		IDC	II	0%	60%	10%	10%	20%
UCI9135402	Mastectomy	90	90	1.4		IDC+LF	II	10%	50%	35%	5%	0%
AA1025	Mastectomy	100	30		0	IDC+LF+ DCIS	II	10%	50%	20%	10%	10%
AA1188	Mastectomy	85	25		0	ILC +LCIS	II	10%	50%	35%	5%	0%
UCI2224680	Mastectomy	90	80	1.2		IDC	II	0%	70%	25%	5%	0%
UCI1689380	Lumpectomy	100	70	1.3		IDC	II	0%	75%	20%	5%	0%
UCI3165498	Mastectomy	100	95	1.4		IDC	II	0%	75%	15%	10%	0%
UCI2231576	Mastectomy	100	100	1.4		IDC	II	0%	80%	15%	5%	0%
AA0952	Lumpectomy	95	30		0	IDC	II	0%	90%	5%	5%	0%
AA0943	Lumpectomy	>90	30	1.4		IDC+LF	III	0%	20%	75%	5%	0%
AA1204	Mastectomy	0	0		3+	DCIS	III	20%	0%	70%	10%	0%
UCI3564897	Mastectomy	0	0	2.3		IDC	III	20%	10%	0%	70%	0%
UCI1821517	Lumpectomy	0	0	1.1		IDC	III	0%	40%	40%	20%	0%
AA1307	Lumpectomy	0	0		0	IDC	III	0%	40%	0%	10%	50%
AA1367	Mastectomy	0	0	1.3	1+	IDC	III	0%	50%	40%	5%	5%
AA1077	Mastectomy	100	0		0	IDC	III	0%	70%	30%	0%	0%
AA1247	Mastectomy	0	0		3+	IDC	III	0%	70%	30%	0%	0%
AA1277	Mastectomy	0	0		0	IDC	III	0%	70%	30%	0%	0%
AA1222	Lumpectomy	90	60	3.5	2+	IDC+LF	III	0%	80%	10%	10%	0%
AA1106	Mastectomy	100	5		0	ILC +LCIS	III	10%	80%	5%	5%	0%
UCI2008866	Mastectomy	0	0	1.4		IDC	III	0%	97%	1%	1%	1%
UCI4216548	Brain metastasis	0	0	1.1		IDC	NA	0%	50%	35%	5%	10%
AA1515	Liver metastasis	100	30	1	1+	IDC+DCIS	NA	0%	50%	40%	10%	0%

* IDC: Invasise Ductal Carcinoma; DCIS: Ductal Carcinoma In Situ; LF: Lobular features; ILC: Invasive Lobular Carconima; LCIS, Lobular Carcinoma In Situ

Table S2: List of Primers used in the study

Primer ID	Amplicons coodrinates (hg19)	Primer sequence (without UDT-Seq tail)
RB1.11.14.RB1.1_F	chr13:48942526-48942776	GCAGCAGCTGGGTCATCTAT
RB1.11.14.RB1.1_R	chr13:48942526-48942776	TGAAACACTATAAAGCCATGAATAACA
RB1.7.14.RB1.1_F	chr13:48934101-48934338	TCTACCCTGCGATTTTCTCTCA
RB1.7.14.RB1.1_R	chr13:48934101-48934338	TCCTGTCAGCCTTAGAACCA
RB1.26.1.RB1.1_F	chr13:49051432-49051585	CGAAAGCATCATAGTTACTGGA
RB1.26.1.RB1.1_R	chr13:49051432-49051585	CGAAAAGACTTCTTGCAGTGT
RB1.2.14.RB1.1_F	chr13:48881426-48881667	TTTTCATTTGGTAGGCTTGAGTTT
RB1.2.14.RB1.1_R	chr13:48881426-48881667	AGCAGAGGTAAATTTCCTCTGGG
RB1.2.15.RB1.2_F	chr13:48881341-48881484	CACAGTAGTGTTATGTGCAAAC
RB1.2.15.RB1.2_R	chr13:48881341-48881484	ACCAAGCTCTCTCTCTGACA
RB1.17.5.RB1.1_F	chr13:48955446-48955604	CCCATGGATTCTGAATGTGC
RB1.17.5.RB1.1_R	chr13:48955446-48955604	AGCCATATGCACATGAATGAA
RB1.17.6.RB1.2_F	chr13:48955344-48955495	AAAAATACCTAGCTCAAGGGTT
RB1.17.6.RB1.2_R	chr13:48955344-48955495	CTTGTCAAGTTGCCTTCTGC
RB1.22.1.RB1.1_F	chr13:49039141-49039283	ACTGTTCTTCCTCAGACATTCA
RB1.22.1.RB1.1_R	chr13:49039141-49039283	GTTTTGGTGGACCCATTACA
RB1.22.11.RB1.2_F	chr13:49039023-49039149	TGTGCTTCTTACCAGTCAAAA
RB1.22.11.RB1.2_R	chr13:49039023-49039149	GAATCATACTCCTCTTCTTTGATCA
RB1.1.7.RB1.1_F	chr13:48878026-48878180	CTCCTCCACAGCTCGCT
RB1.1.7.RB1.1_R	chr13:48878026-48878180	CTGCTCGCTCACCTGAC
RB1.1.8.RB1.2_F	chr13:48878026-48878185	CTCCTCCACAGCTCGCT
RB1.1.8.RB1.2_R	chr13:48878026-48878185	GGCTCTGCTCGCTCAC
RB1.18.9.RB1.1_F	chr13:49027137-49027266	CATCATGTTTCATATAGGATTCACC
RB1.18.9.RB1.1_R	chr13:49027137-49027266	TGCAGTTTGAATGGTCAACA
RB1.18.10.RB1.2_F	chr13:49027026-49027173	ATTGCCACTGTCAATTGTGC
RB1.18.10.RB1.2_R	chr13:49027026-49027173	TCAAGGTGATCAGTTGGTCC
RB1.16.14.RB1.1_F	chr13:48954201-48954434	TCTGTTTCAGGAAGAAGAACGA
RB1.16.14.RB1.1_R	chr13:48954201-48954434	CTCCCCCGACCAAAGAAACA
RB1.23.1.RB1.1_F	chr13:49039349-49039504	TTTTTGCTCTAGCCCCCTAC
RB1.23.1.RB1.1_R	chr13:49039349-49039504	TCCCTAAAGAGAAAACACACAC
RB1.23.2.RB1.2_F	chr13:49039216-49039368	GGTCTTCATGCAGAGACTGA
RB1.23.2.RB1.2_R	chr13:49039216-49039368	CTTGTAAGGGCTTCGAGGAA
RB1.13.1.RB1.1_F	chr13:48951063-48951217	ACCTCCTAAAGAACTGCACA
RB1.13.1.RB1.1_R	chr13:48951063-48951217	ACTGGAAAGATGCTGCTTTT
RB1.13.4.RB1.2_F	chr13:48951028-48951153	TGATTACACAGTATCCTCGACA
RB1.13.4.RB1.2_R	chr13:48951028-48951153	GTTACCTGTGATCCAATTTCGA
RB1.25.1.RB1.1_F	chr13:49050856-49051014	AGACTTCTGAGAAGTTCCAGA
RB1.25.1.RB1.1_R	chr13:49050856-49051014	GGATTCCCCAGATGACCATC
RB1.25.2.RB1.2_F	chr13:49050759-49050897	TGCCTGATTTTTGACACACC
RB1.25.2.RB1.2_R	chr13:49050759-49050897	GTTGCTTCCTTCAGCACTTC
RB1.27.1.RB1.1_F	chr13:49054098-49054228	TTGCCAACTTACCCAGTACC
RB1.27.1.RB1.1_R	chr13:49054098-49054228	ATCCAGAGGTGTACACAGTG
RB1.6.12.RB1.1_F	chr13:48923063-48923208	TCTTTCAGTGATACATTTTTCCTGT
RB1.6.12.RB1.1_R	chr13:48923063-48923208	AGTCCAAAGGAATGCCAATT
RB1.3.1.RB1.1_F	chr13:48916742-48916872	TTTTTGTTCCCAGGGAGGTT
RB1.3.1.RB1.1_R	chr13:48916742-48916872	TCCTTTTATGGCAGAGGCTT
RB1.3.2.RB1.2_F	chr13:48916603-48916755	TGCCATCAGAAGGATGTGTT
RB1.3.2.RB1.2_R	chr13:48916603-48916755	CAGATTCCCCACAGTTCCTT
RB1.9.12.RB1.1_F	chr13:48938984-48939139	TGTTCAAGAGTCAAGAGATTAGAT
RB1.9.12.RB1.1_R	chr13:48938984-48939139	CCCTCCACAGTCTCAAAACA
RB1.12.12.RB1.1_F	chr13:48947517-48947662	CTCCCTTCATTGCTTAACACA
RB1.12.12.RB1.1_R	chr13:48947517-48947662	AATTTCAAGTTTCTTTGCCAAGA
RB1.20.1.RB1.1_F	chr13:49033833-49033987	TATTCCCACAGTGTATCGGC
RB1.20.1.RB1.1_R	chr13:49033833-49033987	GTAGGGAGGAGAGAAGGTGA
RB1.20.2.RB1.2_F	chr13:49033696-49033855	TGGGGGAAAGAAAAGAGTGG
RB1.20.2.RB1.2_R	chr13:49033696-49033855	GACAGAAGGCGTTCACAAAG
RB1.14.1.RB1.1_F	chr13:48953649-48953806	CTGGGCAAAACAGTGAGACT
RB1.14.1.RB1.1_R	chr13:48953649-48953806	CGCCCGGCTGAAATTTTT
RB1.15.5.RB1.1_F	chr13:48954147-48954298	TGCTGACACAAATAAGGTTTCA
RB1.15.5.RB1.1_R	chr13:48954147-48954298	TGTTGTCATTCAGAAGTTTGCT
RB1.8.9.RB1.1_F	chr13:48936977-48937128	CAGCTGTTATACCCATTAATGGT
RB1.8.9.RB1.1_R	chr13:48936977-48937128	GGGAGAACTTACATCTAAATCTACT
RB1.8.12.RB1.2_F	chr13:48936932-48937053	TGATGGATGTACAATTGTTCTTATC
RB1.8.12.RB1.2_R	chr13:48936932-48937053	TCATGTTCTTTACAGAGAACTTCA

RB1.4.12.RB1.1_F	chr13:48919225-48919376	TCTTTCCTTTGTAGTGTCCATAA
RB1.4.12.RB1.1_R	chr13:48919225-48919376	CAGAATCTAATTGTGAACAATGACA
RB1.4.13.RB1.2_F	chr13:48919122-48919272	AGTAGTGATTTGATGTAGAGCTGA
RB1.4.13.RB1.2_R	chr13:48919122-48919272	CTTCAACAGTCTTGACATAGCA
RB1.24.9.RB1.1_F	chr13:49047451-49047606	TGCTCATCTCTGCAAAATTGT
RB1.24.9.RB1.1_R	chr13:49047451-49047606	GGTGTTTGAATAACTGCATTTGG
RB1.19.1.RB1.1_F	chr13:49030369-49030524	TCTCCTGTAAGATCTCCAAAGA
RB1.19.1.RB1.1_R	chr13:49030369-49030524	TTTGAACCCAGTCAGCCTAG
RB1.19.2.RB1.2_F	chr13:49030277-49030434	TGGGTGTACAACCTTGAAGT
RB1.19.2.RB1.2_R	chr13:49030277-49030434	TTTCAATGGCTTCTGGGTCT
RB1.10.3.RB1.1_F	chr13:48941574-48941733	TGAAATCTGTGCCTCTGTGT
RB1.10.3.RB1.1_R	chr13:48941574-48941733	ACCATGTGCAATACCTGTCT
RB1.10.12.RB1.2_F	chr13:48941593-48941744	TGTGCTGAGAGATGTAATGACA
RB1.10.12.RB1.2_R	chr13:48941593-48941744	CAAATCAATCAAATATACCATGTGC
RB1.5.9.RB1.1_F	chr13:48921916-48922057	GCATGAGAAAACTACTATGACTTCT
RB1.5.9.RB1.1_R	chr13:48921916-48922057	ACCCTAACTATCAAGATGTTTGAG
CFTR.11.1.CFTR.1_F	chr7:117199584-117199739	GGGTAAAATTAAGCACAGTGGA
CFTR.11.1.CFTR.1_R	chr7:117199584-117199739	AGTGTGAAGGGTTCATATGCA
CFTR.11.2.CFTR.2_F	chr7:117199482-117199616	AGTGAATCCTGAGCGTGATT
CFTR.11.2.CFTR.2_R	chr7:117199482-117199616	TCTTTAATGGTGCCAGGCAT
CFTR.21.9.CFTR.1_F	chr7:117254659-117254805	GGTTCATTTACGTCTTTTGTGC
CFTR.21.9.CFTR.1_R	chr7:117254659-117254805	ACTCATACTTTGTTACTTGTCTGA
CFTR.7.10.CFTR.1_F	chr7:117176539-117176793	GACTTAAAACCTTGAGCAGTTCTT
CFTR.7.10.CFTR.1_R	chr7:117176539-117176793	TGAGGTGGAAGTCTACCATGA
CFTR.26.6.CFTR.1_F	chr7:117305495-117305636	CTGTTCTGTGATATTATGTGTGGT
CFTR.26.6.CFTR.1_R	chr7:117305495-117305636	CAAGGGCAATGAGATCTTAAGT
CFTR.2.7.CFTR.1_F	chr7:117144269-117144411	TCCAAATCTGTATGGAGACCA
CFTR.2.7.CFTR.1_R	chr7:117144269-117144411	CAATGTACATGAACATACCTTTCC
CFTR.2.8.CFTR.2_F	chr7:117144392-117144527	TCCCTTCTGTTGATTCTGCT
CFTR.2.8.CFTR.2_R	chr7:117144392-117144527	GCATTAGCCACCATACTTGG
CFTR.17.1.CFTR.1_F	chr7:117243693-117243847	GTGTTTTACATTTACGTGGGAG
CFTR.17.1.CFTR.1_R	chr7:117243693-117243847	CAGCAGTTTCATTTCTTAGACC
CFTR.17.2.CFTR.2_F	chr7:117243566-117243697	ACTTTGGCTGCCAAATAACG
CFTR.17.2.CFTR.2_R	chr7:117243566-117243697	CCCATAGCAAGCAAAGTGTC
CFTR.22.1.CFTR.1_F	chr7:117267594-117267755	TGCGATCTGTGAGCCGA
CFTR.22.1.CFTR.1_R	chr7:117267594-117267755	TCCACCTTCTGTGTATTTTGC
CFTR.22.2.CFTR.2_F	chr7:117267748-117267877	GGGCCAAATGACTGTCAAAG
CFTR.22.2.CFTR.2_R	chr7:117267748-117267877	ACACATTGCTTCAGGCTACT
CFTR.22.2.CFTR.3_F	chr7:117267468-117267612	GCCCGACAAATAACCAAGTG
CFTR.22.2.CFTR.3_R	chr7:117267468-117267612	AGGTTTACCTTCTGTTGGCA
CFTR.1.1.CFTR.1_F	chr7:117120105-117120257	GGTCTTTGGCATTAGGAGCT
CFTR.1.1.CFTR.1_R	chr7:117120105-117120257	CAAACCCAACCCATACACAC
CFTR.18.10.CFTR.1_F	chr7:117246643-117246899	TGGGTTCTGAATGCGTCTACT
CFTR.18.10.CFTR.1_R	chr7:117246643-117246899	AGACAGGACTTCAACCCTCA
CFTR.23.1.CFTR.1_F	chr7:117282505-117282648	CTTATAGGTGGGCCTCTTGG
CFTR.23.1.CFTR.1_R	chr7:117282505-117282648	TGGCTAAGTCCTTTTGCTCA
CFTR.23.2.CFTR.2_F	chr7:117282478-117282612	TCACAGAAGTGATCCCATCA
CFTR.23.2.CFTR.2_R	chr7:117282478-117282612	AAAGGCTTTCCTCCACTGTT
CFTR.16.1.CFTR.1_F	chr7:117242879-117243021	ACTGTGTCTTGTTCCATTCCA
CFTR.16.1.CFTR.1_R	chr7:117242879-117243021	CCACTACCATAATGCTTGGGA
CFTR.13.1.CFTR.1_F	chr7:117230382-117230538	CCAGGAAATAGAGAGGAAATGT
CFTR.13.1.CFTR.1_R	chr7:117230382-117230538	TGGGACAGTCTGTCTTTCTT
CFTR.6.1.CFTR.1_F	chr7:117175360-117175517	CAAGTGGCACTCCTCATGG
CFTR.6.1.CFTR.1_R	chr7:117175360-117175517	CCTGGTTTTACTAAAGTGGGC
CFTR.6.2.CFTR.2_F	chr7:117175288-117175434	TGACACCTGTTTTTGCTGTG
CFTR.6.2.CFTR.2_R	chr7:117175288-117175434	CATCATTCTCCCTAGCCCAG
CFTR.27.1.CFTR.1_F	chr7:117306992-117307152	GAACAAAGTGCGGCAGTAC
CFTR.27.1.CFTR.1_R	chr7:117306992-117307152	ATGCTGCTCTCTAAAGCCTT
CFTR.27.2.CFTR.2_F	chr7:117307024-117307182	AAACTGCTGAACGAGAGGAG
CFTR.27.2.CFTR.2_R	chr7:117307024-117307182	TCCATGAGCAAATGTCCCAT
CFTR.27.2.CFTR.3_F	chr7:117306853-117306997	TTCAAAATGCAAGGCTCTGG
CFTR.27.2.CFTR.3_R	chr7:117306853-117306997	TCGTTCAGCAGTTTCTGGAT
CFTR.25.1.CFTR.1_F	chr7:117304751-117304911	AACTGCAGGTTGGGCTC
CFTR.25.1.CFTR.1_R	chr7:117304751-117304911	CAGAACATCTGAAACTCACACT
CFTR.25.2.CFTR.2_F	chr7:117304805-117304963	ACTTTGTCCTTGTGGATGGG
CFTR.25.2.CFTR.2_R	chr7:117304805-117304963	TCACCATGAAGCAGGCATAA
CFTR.25.2.CFTR.3_F	chr7:117304621-117304779	TTCAAATGGTGGCAGGTAGT

CFTR.25.2.CFTR.3_R	chr7:117304621-117304779	CCACAAGGACAAAGTCAAGC
CFTR.3.9.CFTR.1_F	chr7:117149072-117149196	TGCAACTTATTGGTCCCACT
CFTR.3.9.CFTR.1_R	chr7:117149072-117149196	ATGAATGTACAAATGAGATCCTTAC
CFTR.9.10.CFTR.1_F	chr7:117182011-117182185	AGCACAATGAGAGTATAAAGTAGATGT
CFTR.9.10.CFTR.1_R	chr7:117182011-117182185	AGAAAACAGTTAGGTGTTTAGAGCA
CFTR.12.9.CFTR.1_F	chr7:117227738-117227894	GAAGGAAGATGTGCCTTTCA
CFTR.12.9.CFTR.1_R	chr7:117227738-117227894	TGCTTGCTAGACCAATAATTAGT
CFTR.20.9.CFTR.1_F	chr7:117251714-117251868	TTCGGACGGCAGCCTTA
CFTR.20.9.CFTR.1_R	chr7:117251714-117251868	TGCTTAGCTAAAGTTAATGAGTTCA
CFTR.20.10.CFTR.2_F	chr7:117251504-117251752	CAAAGAATGGCACCAGTGTGA
CFTR.20.10.CFTR.2_R	chr7:117251504-117251752	AGGTACAAGAACCAGTTGGCA
CFTR.14.1.CFTR.1_F	chr7:117232228-117232387	ACTGAGACCTTACACCGTTT
CFTR.14.1.CFTR.1_R	chr7:117232228-117232387	TCAGAATCCTCTTCGATGCC
CFTR.14.2.CFTR.2_F	chr7:117232408-117232567	GGCATCGAAGAGGATTCTGA
CFTR.14.2.CFTR.2_R	chr7:117232408-117232567	GCTGTTGTCTTTCGGTGAAT
CFTR.14.2.CFTR.3_F	chr7:117232094-117232237	TTTTGCATGAAGGTAGCAGC
CFTR.14.2.CFTR.3_R	chr7:117232094-117232237	AGGAGACAGGAGCATCTCC
CFTR.14.3.CFTR.4_F	chr7:117232376-117232524	CCATTGTGCAAAAGACTCCC
CFTR.14.3.CFTR.4_R	chr7:117232376-117232524	GTGTCATCAGGTTCAGGACA
CFTR.14.3.CFTR.5_F	chr7:117232562-117232718	ACACACTCAGTTAACCAAGGT
CFTR.14.3.CFTR.5_R	chr7:117232562-117232718	AAATACCCCCAAGCGATGTA
CFTR.14.10.CFTR.6_F	chr7:117231942-117232154	TGCTAAAATACGAGACATATTGCAA
CFTR.14.10.CFTR.6_R	chr7:117231942-117232154	TGGTCGAAAGAATCACATCCCA
CFTR.15.4.CFTR.1_F	chr7:117234950-117235102	TGGTGGCATGAAACTGTACT
CFTR.15.4.CFTR.1_R	chr7:117234950-117235102	ACATTCTTACCTCTGCCAGA
CFTR.15.6.CFTR.2_F	chr7:117235034-117235167	CCAGCAGTGACTACATGGAA
CFTR.15.6.CFTR.2_R	chr7:117235034-117235167	GTGCATATATATGTATACATCCCCA
CFTR.8.1.CFTR.1_F	chr7:117180174-117180333	AGAACAGAACTGAAACTGACTC
CFTR.8.1.CFTR.1_R	chr7:117180174-117180333	CAGGGAAATTGCCGAGTG
CFTR.8.2.CFTR.2_F	chr7:117180325-117180466	TCATTCTGCATTGTTCTGCG
CFTR.8.2.CFTR.2_R	chr7:117180325-117180466	CGCACATTTTTGCAAAGTTC
CFTR.8.2.CFTR.3_F	chr7:117180087-117180220	GACCATGCTCAGATCTTCCA
CFTR.8.2.CFTR.3_R	chr7:117180087-117180220	AACACCACAAAGAACCCTGA
CFTR.4.1.CFTR.1_F	chr7:117171013-117171170	TCATAGCTTCCTATGACCCG
CFTR.4.1.CFTR.1_R	chr7:117171013-117171170	GGCCTGTGCAAGGAAGTATT
CFTR.4.2.CFTR.2_F	chr7:117170901-117171036	CTTGTGTTGAAATTCTCAGGGT
CFTR.4.2.CFTR.2_R	chr7:117170901-117171036	GCCTATGCCTAGATAAATCGC
CFTR.24.10.CFTR.1_F	chr7:117292784-117293014	ACTTGATGGTAAGTACATGGGTGT
CFTR.24.10.CFTR.1_R	chr7:117292784-117293014	TGTGTTGGTATGAGTTACCCCT
CFTR.19.1.CFTR.1_F	chr7:117250605-117250730	TTGTGATTGGAGCTATAGCAGT
CFTR.19.1.CFTR.1_R	chr7:117250605-117250730	AGATGAGTATCGCACATTCACT
CFTR.19.2.CFTR.2_F	chr7:117250528-117250686	CACACTTTGTCCACTTTGCA
CFTR.19.2.CFTR.2_R	chr7:117250528-117250686	TTGAGTTGCTGTGAGGTTTG
CFTR.10.4.CFTR.1_F	chr7:117188688-117188848	GTGTGTGTGTGTGTGTTTTT
CFTR.10.4.CFTR.1_R	chr7:117188688-117188848	AGTGGATCCAGCAACCG
CFTR.10.5.CFTR.2_F	chr7:117188810-117188939	TCTTGGTACTCCTGTCCTGA
CFTR.10.5.CFTR.2_R	chr7:117188810-117188939	ACCTTCCAGCACTACAAACT
CFTR.5.10.CFTR.1_F	chr7:117174195-117174425	TGAACCTGAGAAGATAGTAAGCTAGA
CFTR.5.10.CFTR.1_R	chr7:117174195-117174425	AGTGCCTAAAAGATTAAATCAATAGGT
FGFR1OP.6.7.FGFR1OP.1_F	chr6:167424258-167424400	TGGAGTGTAATTGGTATATTTGTGT
FGFR1OP.6.7.FGFR1OP.1_R	chr6:167424258-167424400	AAGTCCAGACATGACTTCCG
FGFR1OP.11.1.FGFR1OP.1_F	chr6:167446056-167446184	GGTAGGTAAATTGTGACGCAC
FGFR1OP.11.1.FGFR1OP.1_R	chr6:167446056-167446184	TTGTCTTGTCTGTGTTCGGA
FGFR1OP.3.5.FGFR1OP.1_F	chr6:167416662-167416789	AGGGTAAACACATGACACTTAA
FGFR1OP.3.5.FGFR1OP.1_R	chr6:167416662-167416789	TCCTGATTTCTCCCAAATGGT
FGFR1OP.7.1.FGFR1OP.1_F	chr6:167426903-167427056	AGATGTTCCACTTCTGAGACA
FGFR1OP.7.1.FGFR1OP.1_R	chr6:167426903-167427056	CTCTGCCCTCATGCATGTTA
FGFR1OP.9.1.FGFR1OP.1_F	chr6:167438257-167438398	GAGCACCGATTAACTGTCCT
FGFR1OP.9.1.FGFR1OP.1_R	chr6:167438257-167438398	TCCCGAGTATTGAAGTCCAC
FGFR1OP.12.8.FGFR1OP.1_F	chr6:167447203-167447461	GCTGCTGCCCTTGCTACATT
FGFR1OP.12.8.FGFR1OP.1_R	chr6:167447203-167447461	TGGGAAATGCAGAACACCAT
FGFR1OP.2.5.FGFR1OP.1_F	chr6:167413479-167413611	TTGCTCGTGTTTGTTGCTG
FGFR1OP.2.5.FGFR1OP.1_R	chr6:167413479-167413611	ACAGCCATGTTAAAATCTGGA
FGFR1OP.14.1.FGFR1OP.1_F	chr6:167453512-167453647	AACAAGGACAGAGGACTGAC
FGFR1OP.14.1.FGFR1OP.1_R	chr6:167453512-167453647	AAATCTTCCACACATGGGCT
FGFR1OP.8.1.FGFR1OP.1_F	chr6:167435927-167436086	ATGAGGCCAATCAGAGTGAT
FGFR1OP.8.1.FGFR1OP.1_R	chr6:167435927-167436086	TGGCTTAGGAATGGGATCAT

FGFR1OP.8.2.FGFR1OP.2_F	chr6:167435984-167436138	GCCTTCACTTACTGTCCCAT
FGFR1OP.8.2.FGFR1OP.2_R	chr6:167435984-167436138	CCCCTAGTCTCATAGCTCAA
FGFR1OP.8.2.FGFR1OP.3_F	chr6:167435811-167435963	GCACACACACAGGTTTGATT
FGFR1OP.8.2.FGFR1OP.3_R	chr6:167435811-167435963	ATGGGACAGTAAGTGAAGGC
FGFR1OP.4.8.FGFR1OP.1_F	chr6:167417206-167417458	TGCTTACTTACCTTTTTCTTGATCTT
FGFR1OP.4.8.FGFR1OP.1_R	chr6:167417206-167417458	ACACTGGTGCCAGCTATCTG
FGFR1OP.1.5.FGFR1OP.1_F	chr6:167412901-167413040	GGTTGTCTTGGAGAAGCAAG
FGFR1OP.1.5.FGFR1OP.1_R	chr6:167412901-167413040	TGTCCACGCAAGCCCT
FGFR1OP.10.6.FGFR1OP.1_F	chr6:167439963-167440114	AGCCCCATATTGAACAACGA
FGFR1OP.10.6.FGFR1OP.1_R	chr6:167439963-167440114	ACGATCAGCACAAAAACTAGA
FGFR1OP.13.1.FGFR1OP.1_F	chr6:167453362-167453491	AGACTACTCACATTCTGACACT
FGFR1OP.13.1.FGFR1OP.1_R	chr6:167453362-167453491	GTCAGTCCTCTGTCCTTGTT
FGFR1OP.5.3.FGFR1OP.1_F	chr6:167417715-167417874	CTCCTTGAGAATAACTTCTGCT
FGFR1OP.5.3.FGFR1OP.1_R	chr6:167417715-167417874	TACTTCCCCAGTGGTTGG
FGFR1OP.5.4.FGFR1OP.2_F	chr6:167417788-167417942	GTCGAGAGAATTTAGCCCGA
FGFR1OP.5.4.FGFR1OP.2_R	chr6:167417788-167417942	TGCACTAATCTGCATGGCTA
BRCA1.11.18.BRCA1.1_F	chr17:41228514-41228663	TGATGTTTCTTACCTTTCCACT
BRCA1.11.18.BRCA1.1_R	chr17:41228514-41228663	ATCACTATCAGAACAAAGCAGT
BRCA1.11.20.BRCA1.2_F	chr17:41228407-41228543	AGTGTATAAATGCCTGTATGCA
BRCA1.11.20.BRCA1.2_R	chr17:41228407-41228543	AAGTTTGAGGTGTCTGCAGA
BRCA1.21.22.BRCA1.1_F	chr17:41258445-41258595	TTCCTACTGTGGTTGCTTCC
BRCA1.21.22.BRCA1.1_R	chr17:41258445-41258595	TGCCTTTTGAGTATTCTTTCTACA
BRCA1.7.1.BRCA1.1_F	chr17:41215879-41216031	AGGGAGGAGGGGAGAAATAG
BRCA1.7.1.BRCA1.1_R	chr17:41215879-41216031	ACTGAGGCTCTTTAGCTTCT
BRCA1.2.1.BRCA1.1_F	chr17:41199580-41199723	ATGTGCCAAGAACTGTGCTA
BRCA1.2.1.BRCA1.1_R	chr17:41199580-41199723	CTCTTTCCTTCCTGGGGATC
BRCA1.17.1.BRCA1.1_F	chr17:41249252-41249408	GCTTCATAGACAAAGGTTCTCT
BRCA1.17.1.BRCA1.1_R	chr17:41249252-41249408	GCCACAGTAGATGCTCAGTA
BRCA1.22.1.BRCA1.1_F	chr17:41267736-41267886	TGGAGCCACATAACACATTCA
BRCA1.22.1.BRCA1.1_R	chr17:41267736-41267886	TGACTCAGTCATAACAGCTCA
BRCA1.1.1.BRCA1.1_F	chr17:41197684-41197820	CTGTGGCTCTGTACCTGTG
BRCA1.1.1.BRCA1.1_R	chr17:41197684-41197820	GCTTGTGTTCTCTGTCTCCA
BRCA1.18.21.BRCA1.1_F	chr17:41251751-41251901	GGCAAAACTATAAGATAAGGAATCC
BRCA1.18.21.BRCA1.1_R	chr17:41251751-41251901	CTTGACTGTTCTTTACCATACTGT
BRCA1.23.23.BRCA1.1_F	chr17:41276029-41276253	CCCAAATTAATACACTCTTGTGCTGA
BRCA1.23.23.BRCA1.1_R	chr17:41276029-41276253	GGACGTTGTCATTAGTTCTTTGGT
BRCA1.13.1.BRCA1.1_F	chr17:41234447-41234599	CTGATGTGCTTTGTTCTGGA
BRCA1.13.1.BRCA1.1_R	chr17:41234447-41234599	TCTTGGTGCCATTTATCGTT
BRCA1.13.2.BRCA1.2_F	chr17:41234327-41234486	TGTGCTGAGCAAGGATCATA
BRCA1.13.2.BRCA1.2_R	chr17:41234327-41234486	GCCTTCTAACAGCTACCCTT
BRCA1.16.1.BRCA1.1_F	chr17:41247852-41247986	TGCCTGTTAAGTTGGCAAAC
BRCA1.16.1.BRCA1.1_R	chr17:41247852-41247986	GGTCATTTGACAGTTCTGCA
BRCA1.6.1.BRCA1.1_F	chr17:41215277-41215418	GGAAAGTGGTGCATTGATGG
BRCA1.6.1.BRCA1.1_R	chr17:41215277-41215418	GCACGTTCTTCTGCTGTATG
BRCA1.3.1.BRCA1.1_F	chr17:41201098-41201248	GTCTTGCTCACAGGAGAGAA
BRCA1.3.1.BRCA1.1_R	chr17:41201098-41201248	GCCTGGGTTAAGTATGCAGA
BRCA1.9.1.BRCA1.1_F	chr17:41222965-41223125	TTCTTCTGGGGTCAGGC
BRCA1.9.1.BRCA1.1_R	chr17:41222965-41223125	CTTCAACCTCTGCATTGAAAGT
BRCA1.9.16.BRCA1.2_F	chr17:41223089-41223248	TCAGTAGTATGAGCAGCAGC
BRCA1.9.16.BRCA1.2_R	chr17:41223089-41223248	CCATTCCTTTCAGAGGGAAC
BRCA1.9.17.BRCA1.3_F	chr17:41223244-41223377	GCTGATTCCAGATTCCAGGT
BRCA1.9.17.BRCA1.3_R	chr17:41223244-41223377	TGGATTTCCACCAACACTGT
BRCA1.9.21.BRCA1.4_F	chr17:41222917-41223068	CCAGAATGTTGTTAAGTCTTAGTCA
BRCA1.9.21.BRCA1.4_R	chr17:41222917-41223068	GCTGCTGCTCATACTACTGA
BRCA1.12.1.BRCA1.1_F	chr17:41231293-41231434	ATTCCTCCTTTTGGCCAGAA
BRCA1.12.1.BRCA1.1_R	chr17:41231293-41231434	CCGTTCCCTTGATGTCTACA
BRCA1.15.1.BRCA1.1_F	chr17:41243387-41243547	TGTAAAATGTGCTCCCCAAA
BRCA1.15.1.BRCA1.1_R	chr17:41243387-41243547	TCTGAAAGCCAGGGAGTTG
BRCA1.15.2.BRCA1.2_F	chr17:41243282-41243415	AAGATGACGTCCTAGCTGTG
BRCA1.15.2.BRCA1.2_R	chr17:41243282-41243415	TTTGTGTTTGCCCCAGTCTA
BRCA1.15.2.BRCA1.3_F	chr17:41243558-41243717	ACTCAGACCAACTCCCTG
BRCA1.15.2.BRCA1.3_R	chr17:41243558-41243717	GCAGTAACCAGGTAATATTGGC
BRCA1.15.3.BRCA1.4_F	chr17:41243438-41243596	GACTGGGGCAAACACAAAAA
BRCA1.15.3.BRCA1.4_R	chr17:41243438-41243596	ACACCCAGGATCCTTTCTTG
BRCA1.15.3.BRCA1.5_F	chr17:41243808-41243967	TAGACAGACACTCGGTAGCA
BRCA1.15.3.BRCA1.5_R	chr17:41243808-41243967	CAGGAGTCCTAGCCCTTTCA
BRCA1.15.4.BRCA1.6_F	chr17:41243657-41243808	TCCAATTCACTGCACTGTGA

BRCA1.15.4.BRCA1.6_R	chr17:41243657-41243808	GTCTACTAGGCATAGCACCG
BRCA1.15.4.BRCA1.7_F	chr17:41244108-41244267	ACAGGTCATCAGGTGTCTCA
BRCA1.15.4.BRCA1.7_R	chr17:41244108-41244267	GGTTTTGCAACCTGAGGTCT
BRCA1.15.5.BRCA1.8_F	chr17:41243946-41244107	TGGCCCCTCTTCGGTAA
BRCA1.15.5.BRCA1.8_R	chr17:41243946-41244107	TCATGCATCTCAGGTTTGTTC
BRCA1.15.5.BRCA1.9_F	chr17:41244708-41244867	GACAAAACCTAGAGCCTCCT
BRCA1.15.5.BRCA1.9_R	chr17:41244708-41244867	CCACTCTGGGTCCTTAAAGA
BRCA1.15.6.BRCA1.10_F	chr17:41244957-41245117	GCAAATGACTGGCGCTTT
BRCA1.15.6.BRCA1.10_R	chr17:41244957-41245117	CAGTGTGCAGCATTTGAAAAC
BRCA1.15.6.BRCA1.11_F	chr17:41244608-41244740	TTGATGGGAAAAAGTGGTGG
BRCA1.15.6.BRCA1.11_R	chr17:41244608-41244740	CCTGTGGTTGGTCAGAAAGA
BRCA1.15.7.BRCA1.12_F	chr17:41245148-41245307	TGCACACTGACTCACACA
BRCA1.15.7.BRCA1.12_R	chr17:41245148-41245307	TGTCTAATAATGCTGAAGACCC
BRCA1.15.7.BRCA1.13_F	chr17:41244487-41244644	GGCTAATTGTGCTCACTGTAC
BRCA1.15.7.BRCA1.13_R	chr17:41244487-41244644	CGAAACTGGACTCATTACTCC
BRCA1.15.8.BRCA1.14_F	chr17:41245033-41245166	TATGCTTGTTTCCCGACTGT
BRCA1.15.8.BRCA1.14_R	chr17:41245033-41245166	GTTAGCACTCTAGGGAAGGC
BRCA1.15.8.BRCA1.15_F	chr17:41244348-41244502	TCTACCTAGTTCTGCTTGAATG
BRCA1.15.8.BRCA1.15_R	chr17:41244348-41244502	TCACCTGAAAGAGAAATGGGA
BRCA1.15.8.BRCA1.16_F	chr17:41245387-41245547	TGGAAGGCTAGGATTGACAA
BRCA1.15.8.BRCA1.16_R	chr17:41245387-41245547	GGCACAGCAGAAACCTACA
BRCA1.15.9.BRCA1.17_F	chr17:41245292-41245442	TGCAAAACCCTTTCTCCACT
BRCA1.15.9.BRCA1.17_R	chr17:41245292-41245442	ACTTTCCCAGAGCTGAAGTT
BRCA1.15.9.BRCA1.18_F	chr17:41245568-41245729	TAGGTTTCTGCTGTGCCT
BRCA1.15.9.BRCA1.18_R	chr17:41245568-41245729	TCCACAATTCAAAAGCACCT
BRCA1.15.10.BRCA1.19_F	chr17:41245538-41245692	CCAGTTGCAGGTTCTTTACC
BRCA1.15.10.BRCA1.19_R	chr17:41245538-41245692	GAGGAAGTCTTCTACCAGGC
BRCA1.15.10.BRCA1.20_F	chr17:41245750-41245909	AGGTGCTTTTGAATTGTGGA
BRCA1.15.10.BRCA1.20_R	chr17:41245750-41245909	AGCAGAATGGTCAAGTGATG
BRCA1.15.11.BRCA1.21_F	chr17:41245655-41245789	TCAGTACAATTAGGTGGGCT
BRCA1.15.11.BRCA1.21_R	chr17:41245655-41245789	TCAAAACGAAAGCTGAACCT
BRCA1.15.11.BRCA1.22_F	chr17:41245980-41246139	CAGGAGTCTTTTGAACTGCC
BRCA1.15.11.BRCA1.22_R	chr17:41245980-41246139	AACCTATCGGAAGAAGGCAA
BRCA1.15.12.BRCA1.23_F	chr17:41246139-41246300	TGGCTTAAGTTGGGGAGG
BRCA1.15.12.BRCA1.23_R	chr17:41246139-41246300	GCTGATGTATTGGACGTTCT
BRCA1.15.12.BRCA1.24_F	chr17:41245847-41245997	CGAGTGATTCTATTGGGTTAGG
BRCA1.15.12.BRCA1.24_R	chr17:41245847-41245997	GGCCTTCATCCTGAGGATTT
BRCA1.15.13.BRCA1.25_F	chr17:41246341-41246501	GCTACTTTGGCATTTGATTCAG
BRCA1.15.13.BRCA1.25_R	chr17:41246341-41246501	GCTGATCCCCTGTGTGA
BRCA1.15.14.BRCA1.26_F	chr17:41246208-41246343	ACTCTCTACTGATTTGGAGTGA
BRCA1.15.14.BRCA1.26_R	chr17:41246208-41246343	TGATGACTCACATGATGGGG
BRCA1.15.14.BRCA1.27_F	chr17:41246522-41246681	CACACAGGGGATCAGCATT
BRCA1.15.14.BRCA1.27_R	chr17:41246522-41246681	TTACAGCATGAGAACAGCAG
BRCA1.15.15.BRCA1.28_F	chr17:41246479-41246611	ATTCTCTGAGCATGGCAGTT
BRCA1.15.15.BRCA1.28_R	chr17:41246479-41246611	ATAAAAGCAAACAGCCTGGC
BRCA1.15.16.BRCA1.29_F	chr17:41246632-41246791	GCCAGGCTGTTTGCTTTTAT
BRCA1.15.16.BRCA1.29_R	chr17:41246632-41246791	GAACACCACTGAGAAGCGT
BRCA1.15.17.BRCA1.30_F	chr17:41246789-41246949	TTTCTGGATGCCTCTCAGC
BRCA1.15.17.BRCA1.30_R	chr17:41246789-41246949	TGGTTGATTTCCACCTCCAA
BRCA1.15.18.BRCA1.31_F	chr17:41244256-41244382	TGCTTACAATTACTTCCAGGAA
BRCA1.15.18.BRCA1.31_R	chr17:41244256-41244382	TCCAGTACTAATGAAGTGGGC
BRCA1.15.21.BRCA1.32_F	chr17:41244862-41245012	CACATTCAAAAGTGACTTTTGGAC
BRCA1.15.21.BRCA1.32_R	chr17:41244862-41245012	ACAGTCGGGAAACAAGCATA
BRCA1.14.1.BRCA1.1_F	chr17:41242926-41243082	CTGAATGCAAAGGACACCAC
BRCA1.14.1.BRCA1.1_R	chr17:41242926-41243082	TGCAGCGTTTATAGTCTGCT
BRCA1.20.1.BRCA1.1_F	chr17:41256858-41256991	TTCATGGACAGCACTTGAGT
BRCA1.20.1.BRCA1.1_R	chr17:41256858-41256991	CACTTGCTGAGTGTGTTTCT
BRCA1.8.1.BRCA1.1_F	chr17:41219588-41219743	GCCTCATGTGGTTTTATGCA
BRCA1.8.1.BRCA1.1_R	chr17:41219588-41219743	GCTGTGTGCTAGAGGTAACT
BRCA1.4.1.BRCA1.1_F	chr17:41202997-41203143	TTCAGCAATCTGAGGAACCC
BRCA1.4.1.BRCA1.1_R	chr17:41202997-41203143	TGTCCCTCTCTCTTCCTCTC
BRCA1.24.1.BRCA1.1_F	chr17:41277065-41277207	TCCAGTTCCTATCACGAGGA
BRCA1.24.1.BRCA1.1_R	chr17:41277065-41277207	GAGAGTGGATTTCCGAAGCT
BRCA1.19.18.BRCA1.1_F	chr17:41256158-41256291	CCAAGGAAGGATTTTCGGGT
BRCA1.19.18.BRCA1.1_R	chr17:41256158-41256291	ACTGCAAACATAATGTTTTCCC
BRCA1.19.19.BRCA1.2_F	chr17:41256028-41256167	CAGCTACTAAGGGGGCTAAG
BRCA1.19.19.BRCA1.2_R	chr17:41256028-41256167	AAACCGTGCCAAAAGACTTC

BRCA1.10.1.BRCA1.1_F	chr17:41226393-41226551	TGTTTCCGTCAAATCGTGTG
BRCA1.10.1.BRCA1.1_R	chr17:41226393-41226551	GCGATGGTTTTCTCCTTCCA
BRCA1.10.2.BRCA1.2_F	chr17:41226337-41226479	GTGTTTGTTCCAATACAGCAGA
BRCA1.10.2.BRCA1.2_R	chr17:41226337-41226479	GTACATGCACAGTTGCTCTG
BRCA1.5.1.BRCA1.1_F	chr17:41209069-41209212	CTTGAGGGAGGGAGCTTTAC
BRCA1.5.1.BRCA1.1_R	chr17:41209069-41209212	ATATGACGTGTCTGCTCCAC
ERBB4.11.11.ERBB4.1_F	chr2:212488516-212488770	TCATTTGTGCAGCAACTTCTCA
ERBB4.11.11.ERBB4.1_R	chr2:212488516-212488770	CCTTCTTCTTTCCGCTTTGCA
ERBB4.21.1.ERBB4.1_F	chr2:212576791-212576918	CTGACCCATGAATACCAGTGA
ERBB4.21.1.ERBB4.1_R	chr2:212576791-212576918	AGTTTCTCAATCCCCTAACTCT
ERBB4.21.2.ERBB4.2_F	chr2:212576694-212576850	AACTCTTCAGCTTCCAGAGG
ERBB4.21.2.ERBB4.2_R	chr2:212576694-212576850	GTCAGCTCAGACTGTGGATT
ERBB4.7.8.ERBB4.1_F	chr2:212293122-212293275	ACAAGCTTTAATTCGCAAAGAA
ERBB4.7.8.ERBB4.1_R	chr2:212293122-212293275	CCAGCCCAAAGACTCACATT
ERBB4.26.4.ERBB4.1_F	chr2:212652718-212652865	CGCCACATAGGGTAGAACAT
ERBB4.26.4.ERBB4.1_R	chr2:212652718-212652865	CAGAAATCCTAAATGGTGGAGT
ERBB4.26.5.ERBB4.2_F	chr2:212652837-212652986	CCAATGAATGGTGTCTGCAT
ERBB4.26.5.ERBB4.2_R	chr2:212652837-212652986	TGGCTATTAGCAACATGACTCT
ERBB4.17.1.ERBB4.1_F	chr2:212543775-212543925	GCAACCCTAGAAGAAGCCTT
ERBB4.17.1.ERBB4.1_R	chr2:212543775-212543925	CCTCTGTTTTATTTCCCCTTGA
ERBB4.2.1.ERBB4.1_F	chr2:212251597-212251757	CCTTGTTTGGGTTTGTCTCG
ERBB4.2.1.ERBB4.1_R	chr2:212251597-212251757	AGGGTGCTACTGCTGAGA
ERBB4.2.2.ERBB4.2_F	chr2:212251752-212251897	GCCATTACAGCAGGAGTCAT
ERBB4.2.2.ERBB4.2_R	chr2:212251752-212251897	CTAACAACGCCTTCTCTCCA
ERBB4.2.2.ERBB4.3_F	chr2:212251469-212251607	TAGCCTAGGCCTTTACTGGA
ERBB4.2.2.ERBB4.3_R	chr2:212251469-212251607	GCTGGATGAGGAAGGTTACA
ERBB4.22.1.ERBB4.1_F	chr2:212578260-212578415	AATAATCTGAGCTACCACTCAC
ERBB4.22.1.ERBB4.1_R	chr2:212578260-212578415	TGAGCTTGTTTGCTGAATGT
ERBB4.1.1.ERBB4.1_F	chr2:212248370-212248529	GTATTCCGGTGTCTGTAAGG
ERBB4.1.1.ERBB4.1_R	chr2:212248370-212248529	CCTGACTACTGGAACCACAG
ERBB4.1.2.ERBB4.2_F	chr2:212248324-212248479	AGGTGTGTCTCTCCACCTAA
ERBB4.1.2.ERBB4.2_R	chr2:212248324-212248479	AGACTACCTGCAGGAGTACA
ERBB4.1.2.ERBB4.3_F	chr2:212248580-212248740	CTTTCTTGGCCTTCTCTGG
ERBB4.1.2.ERBB4.3_R	chr2:212248580-212248740	CCCTTTTGTTTCTCGGAGAA
ERBB4.1.3.ERBB4.4_F	chr2:212248661-212248804	AGGTACAGTGGCTCATTCAC
ERBB4.1.3.ERBB4.4_R	chr2:212248661-212248804	CCAGAAACTAGAGGTTAGCTGA
ERBB4.1.3.ERBB4.5_F	chr2:212248500-212248636	TGTACTCCTGCAGGTAGTCT
ERBB4.1.3.ERBB4.5_R	chr2:212248500-212248636	ATGAGCCACTGTACCTCAAC
ERBB4.18.1.ERBB4.1_F	chr2:212566737-212566892	CCCGGATTACTATTCTCTGGT
ERBB4.18.1.ERBB4.1_R	chr2:212566737-212566892	TTCTCACTTCCCCCTCCTTA
ERBB4.18.2.ERBB4.2_F	chr2:212566593-212566743	AAGGGTTGGGATAACAGAGC
ERBB4.18.2.ERBB4.2_R	chr2:212566593-212566743	ACTGGACAACACTCTTCAGC
ERBB4.13.6.ERBB4.1_F	chr2:212522455-212522584	AGGAAAGGATTTGAGCGACA
ERBB4.13.6.ERBB4.1_R	chr2:212522455-212522584	CATGTCACTGTGGATGGAGA
ERBB4.23.6.ERBB4.1_F	chr2:212587147-212587306	TCTTGACACAGAATGCTCCA
ERBB4.23.6.ERBB4.1_R	chr2:212587147-212587306	GGCAGCGTTTCATTAACAAG
ERBB4.23.7.ERBB4.2_F	chr2:212587007-212587157	GGGGGCAATAGTATCTATACCC
ERBB4.23.7.ERBB4.2_R	chr2:212587007-212587157	TGGAGCACAATTTCAATGCA
ERBB4.16.1.ERBB4.1_F	chr2:212537875-212538009	TAAGCCAACACACCACAGAT
ERBB4.16.1.ERBB4.1_R	chr2:212537875-212538009	TGACGCTTGTTTGCTTACAC
ERBB4.29.6.ERBB4.1_F	chr2:213403104-213403256	GATGGGTGAAGAGGGCA
ERBB4.29.6.ERBB4.1_R	chr2:213403104-213403256	CGGGATCTGAGACTTCCAAA
ERBB4.25.1.ERBB4.1_F	chr2:212615308-212615446	AGAGGCATGAAATGGACCAA
ERBB4.25.1.ERBB4.1_R	chr2:212615308-212615446	AACGTGCATGTCCTTTTTCC
ERBB4.27.1.ERBB4.1_F	chr2:212812194-212812343	CCAAGTTCTTGAAGTCCAAAGT
ERBB4.27.1.ERBB4.1_R	chr2:212812194-212812343	GGCAACTGTTTGTGTCTTTTC
ERBB4.27.6.ERBB4.2_F	chr2:212812068-212812223	TGCCTTAGAGTGTTCCTCAA
ERBB4.27.6.ERBB4.2_R	chr2:212812068-212812223	TGAGGATCGATATGCCTTGG
ERBB4.6.1.ERBB4.1_F	chr2:212288920-212289069	ACGTCAATAGTGCAGATGGG
ERBB4.6.1.ERBB4.1_R	chr2:212288920-212289069	AGTGCTGGTTTGTTCAACAT
ERBB4.6.2.ERBB4.2_F	chr2:212288763-212288922	GGCGTTCATATGTTCCTTTCA
ERBB4.6.2.ERBB4.2_R	chr2:212288763-212288922	AGGAGAACGTTTGCCTCAG
ERBB4.28.1.ERBB4.1_F	chr2:212989472-212989629	AAGAGAAAGAAAGCCACAGC
ERBB4.28.1.ERBB4.1_R	chr2:212989472-212989629	CGTGTATCTTCTTGTCTTTGCA
ERBB4.3.6.ERBB4.1_F	chr2:212252632-212252791	ACATGGTAAGCAAAGACCGA
ERBB4.3.6.ERBB4.1_R	chr2:212252632-212252791	ACCCATGTGGCTTTTCTTTT
ERBB4.9.4.ERBB4.1_F	chr2:212426580-212426738	TGAAAACTGTTCCAGGTTAGGA

ERBB4.9.4.ERBB4.1_R	chr2:212426580-212426738	GTGTCTGAGCCCAACCATC
ERBB4.9.5.ERBB4.2_F	chr2:212426730-212426874	CCATGGGGCATAAGTTGAGT
ERBB4.9.5.ERBB4.2_R	chr2:212426730-212426874	TCAGCACCATTAGTACAATCCA
ERBB4.12.1.ERBB4.1_F	chr2:212495200-212495356	ACCTCACCTCTGTTTCCAAG
ERBB4.12.1.ERBB4.1_R	chr2:212495200-212495356	TCCTCTGTCTTCTCTCTCTTCA
ERBB4.12.2.ERBB4.2_F	chr2:212495171-212495305	CCCCAAACACATGAAGAGGA
ERBB4.12.2.ERBB4.2_R	chr2:212495171-212495305	TGTCAGAACTCCCCTGATTG
ERBB4.20.9.ERBB4.1_F	chr2:212569963-212570118	CTGGGATTACTGGTGTGAGC
ERBB4.20.9.ERBB4.1_R	chr2:212569963-212570118	GGCTACATCTCTTCTTGATTTTCT
ERBB4.14.1.ERBB4.1_F	chr2:212522675-212522833	GAAGCAAGCACACCAAGTAC
ERBB4.14.1.ERBB4.1_R	chr2:212522675-212522833	CCTGGCTTGAAATTCATTGTG
ERBB4.15.1.ERBB4.1_F	chr2:212530078-212530239	TTTGGATGGCATGGGTGG
ERBB4.15.1.ERBB4.1_R	chr2:212530078-212530239	TCCAGAGGAAATGACACCAC
ERBB4.15.2.ERBB4.2_F	chr2:212530026-212530183	TAACACATACCAGGTGAGCC
ERBB4.15.2.ERBB4.2_R	chr2:212530026-212530183	GGGTCCTGACAACTGTACAA
ERBB4.8.1.ERBB4.1_F	chr2:212295694-212295848	TCCTCCATCAGCATTGTACTC
ERBB4.8.1.ERBB4.1_R	chr2:212295694-212295848	CCTGGGCATTAACTGAATATCA
ERBB4.8.2.ERBB4.2_F	chr2:212295549-212295703	CAGGAGAAGAGGCAAATGGT
ERBB4.8.2.ERBB4.2_R	chr2:212295549-212295703	CTAGCCAGACTCTTGGAAGG
ERBB4.4.1.ERBB4.1_F	chr2:212285186-212285342	ACCCTATTCGAGTCAATTCTTG
ERBB4.4.1.ERBB4.1_R	chr2:212285186-212285342	GTGTCTGATGGGCAATCTTTC
ERBB4.4.2.ERBB4.2_F	chr2:212285039-212285195	CACATCTTTTGTGGGTATGGT
ERBB4.4.2.ERBB4.2_R	chr2:212285039-212285195	ACATCCCACCTCCCATCTAT
ERBB4.24.1.ERBB4.1_F	chr2:212589770-212589921	TAGGGAAGGAAAGGAGAGCA
ERBB4.24.1.ERBB4.1_R	chr2:212589770-212589921	GGTCCTATCTCTGTCTTCTGC
ERBB4.19.10.ERBB4.1_F	chr2:212568820-212568972	GCCCTGCAGCTTTAAACATA
ERBB4.19.10.ERBB4.1_R	chr2:212568820-212568972	CACCATATTTCAAGAAAAATCAGCA
ERBB4.10.10.ERBB4.1_F	chr2:212483891-212484028	AAAATGTGATTGCCTGGGTG
ERBB4.10.10.ERBB4.1_R	chr2:212483891-212484028	AGAACTTAATAGGTTGAGATGTCA
ERBB4.5.10.ERBB4.1_F	chr2:212286707-212286861	TTTGCCATTGGCCTAGTCTT
ERBB4.5.10.ERBB4.1_R	chr2:212286707-212286861	TTCAACTCCTTTCTAGTTACGAA
RARA.6.1.RARA.1_F	chr17:38508633-38508792	GACATTGACCTCTGGGACAA
RARA.6.1.RARA.1_R	chr17:38508633-38508792	ATCTACCCAGGACACAGGG
RARA.6.2.RARA.2_F	chr17:38508504-38508643	GAAGTGAAGGCTGGGTAGAG
RARA.6.2.RARA.2_R	chr17:38508504-38508643	AATGATGCACTTGGTGGAGA
RARA.3.1.RARA.1_F	chr17:38504567-38504721	CCTCCCCTCTTCTCTCTCTA
RARA.3.1.RARA.1_R	chr17:38504567-38504721	CTTCCCAATGACCCCTTCAA
RARA.7.1.RARA.1_F	chr17:38510571-38510735	ATCCTGCGGATCTGCAC
RARA.7.1.RARA.1_R	chr17:38510571-38510735	AGATGAGGCAGATGGCG
RARA.7.2.RARA.2_F	chr17:38510724-38510870	GAGATGGATGATGCGGAGAC
RARA.7.2.RARA.2_R	chr17:38510724-38510870	CTGTGTAGTTGCAGACCAGA
RARA.7.2.RARA.3_F	chr17:38510447-38510586	TATCAGACAGCATTGCTCCG
RARA.7.2.RARA.3_R	chr17:38510447-38510586	GAGAAGGTCATGGTGTCCTG
RARA.9.1.RARA.1_F	chr17:38512319-38512484	TCCATGCCGCCTCTCAT
RARA.9.1.RARA.1_R	chr17:38512319-38512484	CTGTGTCCATGTGGCGT
RARA.9.2.RARA.2_F	chr17:38512190-38512325	ATTGATCTTCCCACCTCGAG
RARA.9.2.RARA.2_R	chr17:38512190-38512325	CCCTCTGAGTTCTCCAACAT
RARA.2.1.RARA.1_F	chr17:38498964-38499124	TTCGAGGGGAAAGATGTACG
RARA.2.1.RARA.1_R	chr17:38498964-38499124	AGACTGAGAGGCCGGTA
RARA.2.2.RARA.2_F	chr17:38498957-38499106	CTTGCCTTCGAGGGGAAAG
RARA.2.2.RARA.2_R	chr17:38498957-38499106	TACGTACAGTGGTTTGAGCC
RARA.8.1.RARA.1_F	chr17:38511515-38511676	GGTGGTTCTGCTTCCTCAG
RARA.8.1.RARA.1_R	chr17:38511515-38511676	TCCAGGTCTGTGAGCCT
RARA.1.3.RARA.1_F	chr17:38487468-38487628	TTCTGACTGTGGCCGCTT
RARA.1.3.RARA.1_R	chr17:38487468-38487628	CTGGGGATGGTGTGCTA
RARA.1.4.RARA.2_F	chr17:38487624-38487757	GCACCAGCTTCCAGTTAGT
RARA.1.4.RARA.2_R	chr17:38487624-38487757	AACTGGAGAAGACCTTGTCG
RARA.4.1.RARA.1_F	chr17:38506046-38506208	ATACCCAGGGCTTCTTCC
RARA.4.1.RARA.1_R	chr17:38506046-38506208	TCTGAGACCCCAACTGAGG
RARA.4.2.RARA.2_F	chr17:38505894-38506048	GTGAATCATTCTCCCCAGCT
RARA.4.2.RARA.2_R	chr17:38505894-38506048	CATGTTCTTCTGGATGCTGC
RARA.10.1.RARA.1_F	chr17:38566870-38567012	ATGGTGAGAAGCTACTGCAG
RARA.10.1.RARA.1_R	chr17:38566870-38567012	GATTTGCCCATACAAGCAGC
RARA.5.1.RARA.1_F	chr17:38508182-38508341	CTGTGAGAAACGACCGAAAC
RARA.5.1.RARA.1_R	chr17:38508182-38508341	GCAAATCCCACCCTGCA
RARA.5.2.RARA.2_F	chr17:38508144-38508300	TGCAGCTGCCCTCTTAAC
RARA.5.2.RARA.2_R	chr17:38508144-38508300	TAGTGTATTTGCCCAGCTGG

CTNNA1.11.1.CTNNA1.1_F	chr5:138260248-138260404	TGTGTCATTGCTCTCCAAGA
CTNNA1.11.1.CTNNA1.1_R	chr5:138260248-138260404	CACTGGAAAGGGAGAGTTCC
CTNNA1.11.2.CTNNA1.2_F	chr5:138260181-138260310	AGCCTCCTTCCTCATTCAAC
CTNNA1.11.2.CTNNA1.2_R	chr5:138260181-138260310	TCTCTGAGGTGACTACGTGA
CTNNA1.7.3.CTNNA1.1_F	chr5:138221837-138221986	TTGACATGAGCACAAATGGC
CTNNA1.7.3.CTNNA1.1_R	chr5:138221837-138221986	ACAATCAGCACTTTCATCCAG
CTNNA1.17.1.CTNNA1.1_F	chr5:138268565-138268698	ACCAAGGTCTGTCCATCATC
CTNNA1.17.1.CTNNA1.1_R	chr5:138268565-138268698	CCCAAGTAGCTGGGACTTAC
CTNNA1.2.1.CTNNA1.1_F	chr5:138118919-138119073	GGCCCTCTAATAAGAAGAGAGG
CTNNA1.2.1.CTNNA1.1_R	chr5:138118919-138119073	GCCTCTCTTTACCTAAAAAGCA
CTNNA1.2.2.CTNNA1.2_F	chr5:138118772-138118918	TGTTCAGTGGAATCTCATGTGA
CTNNA1.2.2.CTNNA1.2_R	chr5:138118772-138118918	CATGGGCCTTCTTAGAACGA
CTNNA1.1.1.CTNNA1.1_F	chr5:138117595-138117750	TGATGTTTGCCTGACTGACT
CTNNA1.1.1.CTNNA1.1_R	chr5:138117595-138117750	GGCCTGTGCTATAGAACCAT
CTNNA1.18.1.CTNNA1.1_F	chr5:138269521-138269681	ATGTCCCTGATCCAGGCA
CTNNA1.18.1.CTNNA1.1_R	chr5:138269521-138269681	TCTTGGTCTGTGTCTCATCC
CTNNA1.18.2.CTNNA1.2_F	chr5:138269660-138269808	GAAGGCACCAGAGAAAAAGC
CTNNA1.18.2.CTNNA1.2_R	chr5:138269660-138269808	GACTGATATTCAGGAGCCCC
CTNNA1.18.2.CTNNA1.3_F	chr5:138269405-138269564	CTGGTCTTGCAGAGGAGTAG
CTNNA1.18.2.CTNNA1.3_R	chr5:138269405-138269564	ATTTGGTAGAGGCGACGTAG
CTNNA1.16.1.CTNNA1.1_F	chr5:138268263-138268414	GTGTTAAGCCTGCTCTCTCT
CTNNA1.16.1.CTNNA1.1_R	chr5:138268263-138268414	CACTGGCCCTCTTTTTGTTC
CTNNA1.13.1.CTNNA1.1_F	chr5:138264930-138265088	CCTGTGATCTTTGTCTGGGT
CTNNA1.13.1.CTNNA1.1_R	chr5:138264930-138265088	CAAGAAAGGGGACAGGGAAA
CTNNA1.6.1.CTNNA1.1_F	chr5:138163224-138163383	GAAACAAATCATTGTGGACCC
CTNNA1.6.1.CTNNA1.1_R	chr5:138163224-138163383	CCATGTACTCCGAAAGCAG
CTNNA1.6.2.CTNNA1.2_F	chr5:138163363-138163515	TTGTGGCAGAGTGTAATGCT
CTNNA1.6.2.CTNNA1.2_R	chr5:138163363-138163515	ACCTACTCCCAAAAATCAAGGA
CTNNA1.6.2.CTNNA1.3_F	chr5:138163078-138163223	GCCCCTTACCTGCTAAGAAG
CTNNA1.6.2.CTNNA1.3_R	chr5:138163078-138163223	CTCCTCGCTGAAGCTCAAG
CTNNA1.3.1.CTNNA1.1_F	chr5:138145746-138145896	GGTGATTTGATGAAGGCTGC
CTNNA1.3.1.CTNNA1.1_R	chr5:138145746-138145896	ACAGACATAGGCCTGTATACT
CTNNA1.3.2.CTNNA1.2_F	chr5:138145597-138145747	AGGAACAGCAAACAACAACA
CTNNA1.3.2.CTNNA1.2_R	chr5:138145597-138145747	ATCATCTGCGAACTCTCCTG
CTNNA1.9.1.CTNNA1.1_F	chr5:138239983-138240141	TAGGGCCAGGTGTGTGTTT
CTNNA1.9.1.CTNNA1.1_R	chr5:138239983-138240141	TATGCTGTCACCAGTGTCAG
CTNNA1.12.1.CTNNA1.1_F	chr5:138260943-138261102	TACTGTGCCTCTTTCTCCAC
CTNNA1.12.1.CTNNA1.1_R	chr5:138260943-138261102	AAGACGTCTGAAATGCAGTT
CTNNA1.15.1.CTNNA1.1_F	chr5:138266491-138266625	GTGAGGGGCTTCACATACAA
CTNNA1.15.1.CTNNA1.1_R	chr5:138266491-138266625	CCTGGCAAGTCTGTCACTTA
CTNNA1.14.1.CTNNA1.1_F	chr5:138266171-138266331	TCTGATCACAGGCGATCATG
CTNNA1.14.1.CTNNA1.1_R	chr5:138266171-138266331	TGCTCACCGGGTAAAGTCT
CTNNA1.14.2.CTNNA1.2_F	chr5:138266299-138266434	AATGACATCATTGTGCTGGC
CTNNA1.14.2.CTNNA1.2_R	chr5:138266299-138266434	GAAGATTGTCCACAAAGCCC
CTNNA1.14.2.CTNNA1.3_F	chr5:138266045-138266189	CCTTCAGGCGAAATGAAACC
CTNNA1.14.2.CTNNA1.3_R	chr5:138266045-138266189	TTCCGCAATCTTCGCTTTTT
CTNNA1.8.1.CTNNA1.1_F	chr5:138223193-138223353	ATTAGCTCCGCAAAGCTGT
CTNNA1.8.1.CTNNA1.1_R	chr5:138223193-138223353	ACCAAGTTGCCTACAAGTCA
CTNNA1.8.2.CTNNA1.2_F	chr5:138223072-138223215	TCCTCATGTAAGTGCAGCAA
CTNNA1.8.2.CTNNA1.2_R	chr5:138223072-138223215	TGGAACATTGGTTTCCAGGA
CTNNA1.4.1.CTNNA1.1_F	chr5:138147863-138147991	TGGGTTTTGGGGTCTTTCTT
CTNNA1.4.1.CTNNA1.1_R	chr5:138147863-138147991	ATCCCCAAATCATGACTGTAC
CTNNA1.10.1.CTNNA1.1_F	chr5:138253446-138253598	TGCAGGTTATTAATGCTGCA
CTNNA1.10.1.CTNNA1.1_R	chr5:138253446-138253598	TCACATACTTCTCTGGGGAAC
CTNNA1.10.2.CTNNA1.2_F	chr5:138253360-138253518	CATGTGGTGTGATGTCTCCT
CTNNA1.10.2.CTNNA1.2_R	chr5:138253360-138253518	TGTGAGAACACGGACTTGTT
CTNNA1.5.1.CTNNA1.1_F	chr5:138160248-138160411	ATGTTGGCCATCGTGATCA
CTNNA1.5.1.CTNNA1.1_R	chr5:138160248-138160411	ATCGTCTGAGGCAGTGG
CTNNA1.5.2.CTNNA1.2_F	chr5:138160346-138160497	TGATGTCGCAGCCTATAAGG
CTNNA1.5.2.CTNNA1.2_R	chr5:138160346-138160497	CTGGAAATTTCCACCCAAGC
CTNNA1.5.2.CTNNA1.3_F	chr5:138160192-138160323	AGCCCATATAAAGAGTGCTCC
CTNNA1.5.2.CTNNA1.3_R	chr5:138160192-138160323	TTATAGGCTGCGACATCAGG
CDH1.6.1.CDH1.1_F	chr16:68844120-68844278	TCTTCTCTCACGCTGTGTC
CDH1.6.1.CDH1.1_R	chr16:68844120-68844278	GGTCCAAAGAACCTAAGAGTCT
CDH1.6.2.CDH1.2_F	chr16:68844059-68844197	CCCCTTCTCCCATGTTTTCT
CDH1.6.2.CDH1.2_R	chr16:68844059-68844197	CCTTAAAGACCTCCTGGGTG
CDH1.11.1.CDH1.1_F	chr16:68853182-68853337	AGAGCTTGTCCCCGTTCA

CDH1.11.1.CDH1.1_R	chr16:68853182-68853337	AGCAAAGGCTCAGATGAGG
CDH1.3.1.CDH1.1_F	chr16:68835583-68835742	TGCCCTGCAGTGAATTTTGA
CDH1.3.1.CDH1.1_R	chr16:68835583-68835742	GTATTCAGCGTGACTTTGGT
CDH1.3.2.CDH1.2_F	chr16:68835685-68835824	AAAAGGCCTCTACGGTTTCA
CDH1.3.2.CDH1.2_R	chr16:68835685-68835824	ACAGCGCACTAAAACAACAG
CDH1.3.2.CDH1.3_F	chr16:68835513-68835662	ACAAGTTCGCTCTTTGGAGA
CDH1.3.2.CDH1.3_R	chr16:68835513-68835662	AAACCGTAGAGGCCTTTTGA
CDH1.7.1.CDH1.1_F	chr16:68845604-68845763	CAGGAACCTCTGTGATGGAG
CDH1.7.1.CDH1.1_R	chr16:68845604-68845763	ATCCTCCTGACCCCTGA
CDH1.7.2.CDH1.2_F	chr16:68845505-68845655	ATGTCCCCTCCTTTATCCCT
CDH1.7.2.CDH1.2_R	chr16:68845505-68845655	TTGGCTGAGGATGGTGTAAG
CDH1.9.1.CDH1.1_F	chr16:68847236-68847396	AAGGGTCAGGTGCCTGA
CDH1.9.1.CDH1.1_R	chr16:68847236-68847396	GCCAGGTACCATACAAACCT
CDH1.9.2.CDH1.2_F	chr16:68847266-68847408	AACGTCGTAATCACCACACT
CDH1.9.2.CDH1.2_R	chr16:68847266-68847408	TTTCTGCATCTTGCCAGGTA
CDH1.9.2.CDH1.3_F	chr16:68847097-68847245	TCAAATACACTCCAGCCTGG
CDH1.9.2.CDH1.3_R	chr16:68847097-68847245	AGTGTGGTGATTACGACGTT
CDH1.12.1.CDH1.1_F	chr16:68855944-68856103	ACAGGGACACTTCTGCTGAT
CDH1.12.1.CDH1.1_R	chr16:68855944-68856103	TCGTTGTACTGAATGGTCCA
CDH1.12.2.CDH1.2_F	chr16:68856080-68856223	CATCTCCCTTCACAGCAGAA
CDH1.12.2.CDH1.2_R	chr16:68856080-68856223	TCAATGGAAGGGGTGACATC
CDH1.12.2.CDH1.3_F	chr16:68855844-68855999	TCTAGACTTGGTCTGGTGGA
CDH1.12.2.CDH1.3_R	chr16:68855844-68855999	AGGCTTTGGATTCCTCTCAC
CDH1.2.1.CDH1.1_F	chr16:68772193-68772345	GTTCCATCTACCTTTCCCCC
CDH1.2.1.CDH1.1_R	chr16:68772193-68772345	TTTCCAACCCCTCCCTACT
CDH1.15.1.CDH1.1_F	chr16:68863574-68863730	AAGGACTTTGACTTGAGCCA
CDH1.15.1.CDH1.1_R	chr16:68863574-68863730	CCTGAGCTTAGAGATGAGCC
CDH1.15.2.CDH1.2_F	chr16:68863505-68863664	CTGAACATAGCCCTGTGTGT
CDH1.15.2.CDH1.2_R	chr16:68863505-68863664	CCAATTTCATCGGGATTGGC
CDH1.14.1.CDH1.1_F	chr16:68862064-68862218	TCAACACTTGCTCTGTCTCC
CDH1.14.1.CDH1.1_R	chr16:68862064-68862218	CCACTGAGCTACCAAGGTTT
CDH1.8.1.CDH1.1_F	chr16:68846038-68846184	TTGTGTCGATCTCTCTGCAG
CDH1.8.1.CDH1.1_R	chr16:68846038-68846184	ACCTTTCTTTGGAAACCCTCT
CDH1.4.1.CDH1.1_F	chr16:68842334-68842486	TCTTTCCTTTTAGGCCTCCG
CDH1.4.1.CDH1.1_R	chr16:68842334-68842486	ATCCCTCCCAGAGAAACAGA
CDH1.4.2.CDH1.2_F	chr16:68842229-68842380	TTCAAACTGTACACTGCCCA
CDH1.4.2.CDH1.2_R	chr16:68842229-68842380	CTCTTCTGTCTTCTGAGGCC
CDH1.1.1.CDH1.1_F	chr16:68771230-68771374	CAAAGCACCTGTGAGCTTG
CDH1.1.1.CDH1.1_R	chr16:68771230-68771374	TCGCAAGTCAGGGGATC
CDH1.10.1.CDH1.1_F	chr16:68849438-68849598	GGCTTGGATTTTGAGGCCAA
CDH1.10.1.CDH1.1_R	chr16:68849438-68849598	GATGTGATTTCCTGGCCCA
CDH1.10.2.CDH1.2_F	chr16:68849541-68849678	TGGATGTGCTGGATGTGAAT
CDH1.10.2.CDH1.2_R	chr16:68849541-68849678	GTTGCTGCAAGTCAGTTGAA
CDH1.10.2.CDH1.3_F	chr16:68849308-68849460	TGGCAGAAACCACAGTTACT
CDH1.10.2.CDH1.3_R	chr16:68849308-68849460	AGGTACCACATTCGTCACTG
CDH1.13.1.CDH1.1_F	chr16:68857386-68857544	TCAAGCTCATGGATAACCAGA
CDH1.13.1.CDH1.1_R	chr16:68857386-68857544	AGTCAAAGGCTGAGTCACTT
CDH1.13.2.CDH1.2_F	chr16:68857228-68857387	GCGGGTGTCTTTAGTTCACT
CDH1.13.2.CDH1.2_R	chr16:68857228-68857387	AAGGTGGTCACTTGGTCTTT
CDH1.16.1.CDH1.1_F	chr16:68867272-68867431	TGACTATGAAGGAAGCGGTT
CDH1.16.1.CDH1.1_R	chr16:68867272-68867431	TTCTGCATTTCCCAGCACAT
CDH1.16.2.CDH1.2_F	chr16:68867136-68867281	ATTGCTAGACTTCTTGCCCC
CDH1.16.2.CDH1.2_R	chr16:68867136-68867281	AGTTCAGGGAGCTCAGACTA
CDH1.5.1.CDH1.1_F	chr16:68842624-68842763	CCAACAAAGACAAAGAAGGCA
CDH1.5.1.CDH1.1_R	chr16:68842624-68842763	CCGGTGTCAACAAGCTTCTA
CDH1.5.2.CDH1.2_F	chr16:68842564-68842715	CCAGTGTTGGGATCCTTCTT
CDH1.5.2.CDH1.2_R	chr16:68842564-68842715	CGTTCTCTATCCAGAGGCTC
CDKN2A.1.1.CDKN2A.1_F	chr9:21968220-21968350	GAGGTTTCTCAGAGCCTCTC
CDKN2A.1.1.CDKN2A.1_R	chr9:21968220-21968350	GAAGCCATTGCGAGAACTTT
CDKN2A.4.1.CDKN2A.1_F	chr9:21974496-21974658	TCATTCCTCTTCCTTGGCTT
CDKN2A.4.1.CDKN2A.1_R	chr9:21974496-21974658	TGGGTAGAGGGTCTGCA
CDKN2A.4.2.CDKN2A.2_F	chr9:21974467-21974615	ATTCGAGAGATCTGTACGCG
CDKN2A.4.2.CDKN2A.2_R	chr9:21974467-21974615	ACTCTGGAGGACGAAGTTTG
CDKN2A.4.3.CDKN2A.3_F	chr9:21974636-21974791	CAAACTTCGTCCTCCAGAGT
CDKN2A.4.3.CDKN2A.3_R	chr9:21974636-21974791	AGCAGCATGGAGCCTTC
CDKN2A.4.4.CDKN2A.4_F	chr9:21974759-21974911	GCACCTCCTCTACCCGA
CDKN2A.4.4.CDKN2A.4_R	chr9:21974759-21974911	GAAGAAAGAGGAGGGGCTG

CDKN2A.3.1.CDKN2A.1_F	chr9:21971091-21971250	ACCAGCGTGTCCAGGAA
CDKN2A.3.1.CDKN2A.1_R	chr9:21971091-21971250	CAAGCTTCCTTTCCGTCATG
CDKN2A.3.4.CDKN2A.2_F	chr9:21970906-21971070	TCATCAGTCCTCACCTGAG
CDKN2A.3.4.CDKN2A.2_R	chr9:21970906-21971070	TGGACACGCTGGTGGT
CDKN2A.3.5.CDKN2A.3_F	chr9:21970763-21970919	AGGGCGATAGGGAGACTCA
CDKN2A.3.5.CDKN2A.3_R	chr9:21970763-21970919	GTAACCATGCCCGCATAGAT
CDKN2A.3.6.CDKN2A.4_F	chr9:21971015-21971160	CTCCTCAGCCAGGTCCA
CDKN2A.3.6.CDKN2A.4_R	chr9:21971015-21971160	AGCTGCTGCTGCTCCA
CDKN2A.2.1.CDKN2A.1_F	chr9:21968680-21968819	CAGCTTGCGATAACCAAAGG
CDKN2A.2.1.CDKN2A.1_R	chr9:21968680-21968819	ACGCAACGAGATTAGAGAGG
CDKN2A.5.1.CDKN2A.1_F	chr9:21994137-21994297	CTTTTCGAGGGCCTTTCCTA
CDKN2A.5.1.CDKN2A.1_R	chr9:21994137-21994297	TTGGTGACCCTCCGGATT
CDKN2A.5.2.CDKN2A.2_F	chr9:21994270-21994411	GATGTGAACCACGAAAACCC
CDKN2A.5.2.CDKN2A.2_R	chr9:21994270-21994411	GTCCCAGTCTGCAGTTAAGG
CYP2D6.6.1.CYP2D6.1_F	chr22:42524813-42524957	AAGCCCGACTCCTCCTT
CYP2D6.6.1.CYP2D6.1_R	chr22:42524813-42524957	ACCCCTTACCCGCATCT
CYP2D6.6.2.CYP2D6.2_F	chr22:42524692-42524851	AATGTCCTTTCCCAAACCCA
CYP2D6.6.2.CYP2D6.2_R	chr22:42524692-42524851	TTCGAGTACGACGACCCT
CYP2D6.3.1.CYP2D6.1_F	chr22:42523458-42523618	CCAGGCCTACCTTAGGGAT
CYP2D6.3.1.CYP2D6.1_R	chr22:42523458-42523618	CCGTGTCCAACAGGAGA
CYP2D6.3.2.CYP2D6.2_F	chr22:42523561-42523717	AATCACGGCAGTGGTGTAG
CYP2D6.3.2.CYP2D6.2_R	chr22:42523561-42523717	GATCCTGTAAGCCTGACCTC
CYP2D6.3.2.CYP2D6.3_F	chr22:42523352-42523482	GTGGCATTGAGGACTAGGTG
CYP2D6.3.2.CYP2D6.3_R	chr22:42523352-42523482	GTGACCCATATGACATCCCG
CYP2D6.7.3.CYP2D6.1_F	chr22:42525026-42525167	TTTGTGCCCTTCTGCCC
CYP2D6.7.3.CYP2D6.1_R	chr22:42525026-42525167	TGTTCCTGGCGCGCTAT
CYP2D6.7.4.CYP2D6.2_F	chr22:42525106-42525247	TGCTCCAGCGACTTCTTG
CYP2D6.7.4.CYP2D6.2_R	chr22:42525106-42525247	GAGCATAGGGTTGGAGTGG
CYP2D6.9.1.CYP2D6.1_F	chr22:42526623-42526784	TCCCTCACCTGGTCGAA
CYP2D6.9.1.CYP2D6.1_R	chr22:42526623-42526784	AGGCAGGTATGGGGCTA
CYP2D6.9.2.CYP2D6.2_F	chr22:42526638-42526793	TCGAAGCAGTATGGTGTGTT
CYP2D6.9.2.CYP2D6.2_R	chr22:42526638-42526793	CATTTGGTAGTGAGGCAGGT
CYP2D6.9.2.CYP2D6.3_F	chr22:42526486-42526627	AAATGCCCTTCTCCAGGAAG
CYP2D6.9.2.CYP2D6.3_R	chr22:42526486-42526627	GGACTTCCAGAACACACCAT
CYP2D6.2.1.CYP2D6.1_F	chr22:42522863-42523023	ACAGGCACCTGCTGAGAA
CYP2D6.2.1.CYP2D6.1_R	chr22:42522863-42523023	CAGCATCCTAGAGTCCAGTC
CYP2D6.2.2.CYP2D6.2_F	chr22:42522815-42522968	GTGATACCCCTGCAAGACTC
CYP2D6.2.2.CYP2D6.2_R	chr22:42522815-42522968	ACACTCATCACCAACCTGTC
CYP2D6.8.1.CYP2D6.1_F	chr22:42525748-42525909	GCTGCTTGCCTTGGGAA
CYP2D6.8.1.CYP2D6.1_R	chr22:42525748-42525909	ACCCTCCCTCTGCAGTT
CYP2D6.8.2.CYP2D6.2_F	chr22:42525863-42526002	ATTGAGCACGACCACCG
CYP2D6.8.2.CYP2D6.2_R	chr22:42525863-42526002	ACCTGCTCACTCCTGGTAG
CYP2D6.8.2.CYP2D6.3_F	chr22:42525724-42525875	CCACGGAAATCTGTCTCTGT
CYP2D6.8.2.CYP2D6.3_R	chr22:42525724-42525875	ACGTGTTCAGCCTGCAG
CYP2D6.4.1.CYP2D6.1_F	chr22:42523838-42523998	TGCACTGTTTCCCAGATGG
CYP2D6.4.1.CYP2D6.1_R	chr22:42523838-42523998	TTCTGTCCCGAGTATGCTCT
CYP2D6.1.5.CYP2D6.1_F	chr22:42522635-42522794	CACCAGGAAAGCAAAGACAC
CYP2D6.1.5.CYP2D6.1_R	chr22:42522635-42522794	GAGTCTTGCAGGGGTATCAC
CYP2D6.1.6.CYP2D6.2_F	chr22:42522516-42522670	CCGAGTTGGAACTACCACAT
CYP2D6.1.6.CYP2D6.2_R	chr22:42522516-42522670	CTGCAGCACTTCAGCTTCT
CYP2D6.5.1.CYP2D6.1_F	chr22:42524186-42524346	CCACTCTCACCTTCTCCATC
CYP2D6.5.1.CYP2D6.1_R	chr22:42524186-42524346	CTGTCTGGTGTAGGTGCTG
CYP2D6.5.2.CYP2D6.2_F	chr22:42524256-42524395	GGTCATCCTGTGCTCAGTTA
CYP2D6.5.2.CYP2D6.2_R	chr22:42524256-42524395	TGAGACTTGTCCAGGTGAAC
CYP2D6.5.2.CYP2D6.3_F	chr22:42524102-42524247	ATGCACTGGTCCAACCTTTT
CYP2D6.5.2.CYP2D6.3_R	chr22:42524102-42524247	TGGATGAGCTGCTAACTGAG
KRAS.1.6.KRAS.1_F	chr12:25362706-25362835	ACCACTTGTACTAGTATGCCT
KRAS.1.6.KRAS.1_R	chr12:25362706-25362835	TTTATGTATTTCAGGGTGTTGATG
KRAS.1.7.KRAS.2_F	chr12:25362761-25362887	ACACACTTTGTCTTTGACTTCT
KRAS.1.7.KRAS.2_R	chr12:25362761-25362887	TGTTACCTGTACACATGAAGC
KRAS.4.1.KRAS.1_F	chr12:25380235-25380366	TACACAAAGAAAGCCCTCCC
KRAS.4.1.KRAS.1_R	chr12:25380235-25380366	AGGTGCACTGTAATAATCCAGA
KRAS.4.4.KRAS.2_F	chr12:25380106-25380250	TGCATGGCATTAGCAAAGAC
KRAS.4.4.KRAS.2_R	chr12:25380106-25380250	AGTACAGTGCAATGAGGGAC
KRAS.3.1.KRAS.1_F	chr12:25378606-25378763	TCCATAACTTCTTGCTAAGTCC
KRAS.3.1.KRAS.1_R	chr12:25378606-25378763	GACAAAAGTTGTGGACAGGT
KRAS.3.5.KRAS.2_F	chr12:25378526-25378660	TGATTTTGCAGAAAACAGATCTG

KRAS.3.5.KRAS.2_R	chr12:25378526-25378660	TCTGAAGATGTACCTATGGTCC
KRAS.2.1.KRAS.1_F	chr12:25368374-25368522	GTGCTGAACTTAAACTTACCAG
KRAS.2.1.KRAS.1_R	chr12:25368374-25368522	ACTCTTACCAATGCAACAGAC
KRAS.5.2.KRAS.1_F	chr12:25398179-25398312	TCAAAGAATGGTCCTGCACC
KRAS.5.2.KRAS.1_R	chr12:25398179-25398312	AAGGCCTGCTGAAAATGACT
KRAS.5.3.KRAS.2_F	chr12:25398269-25398395	ATTAGCTGTATCGTCAAGGCA
KRAS.5.3.KRAS.2_R	chr12:25398269-25398395	AAAGGTACTGGTGGAGTATTTG
CTNNB1.6.1.CTNNB1.1_F	chr3:41268718-41268865	AGCTCATCATACTGGCTAGTG
CTNNB1.6.1.CTNNB1.1_R	chr3:41268718-41268865	TGCAGATGCTATACACAAGACT
CTNNB1.6.2.CTNNB1.2_F	chr3:41268654-41268809	TGGCTCTTCTCAGACATGTG
CTNNB1.6.2.CTNNB1.2_R	chr3:41268654-41268809	GCCGGCTTATTACTAGAGCA
CTNNB1.11.1.CTNNB1.1_F	chr3:41277844-41278000	TGTGTTTTCTCCTTAGCTGC
CTNNB1.11.1.CTNNB1.1_R	chr3:41277844-41278000	TGCTAAAGGCTTTGGTTCCT
CTNNB1.11.2.CTNNB1.2_F	chr3:41277760-41277890	GCCTCTTGCACTCTGAATTG
CTNNB1.11.2.CTNNB1.2_R	chr3:41277760-41277890	TTGTCCTGAGCAAGTTCACA
CTNNB1.3.1.CTNNB1.1_F	chr3:41266483-41266644	CAATGACTCGAGCTCAGAGG
CTNNB1.3.1.CTNNB1.1_R	chr3:41266483-41266644	GATTGCACGTGTGGCAAG
CTNNB1.3.2.CTNNB1.2_F	chr3:41266609-41266742	CACAGATGCTGAAACATGCA
CTNNB1.3.2.CTNNB1.2_R	chr3:41266609-41266742	GAAACTACTCCCCTTGAGCA
CTNNB1.3.2.CTNNB1.3_F	chr3:41266423-41266558	TGCTGAACTGTGGATAGTGA
CTNNB1.3.2.CTNNB1.3_R	chr3:41266423-41266558	CAAACGCTGGACATTAGTGG
CTNNB1.7.1.CTNNB1.1_F	chr3:41274810-41274947	TCTAGCTAATGACTAGGGCCT
CTNNB1.7.1.CTNNB1.1_R	chr3:41274810-41274947	ATTCCCATGGCACCAGTTTA
CTNNB1.9.1.CTNNB1.1_F	chr3:41275640-41275798	CTGTTTTTCAGGCTACTGTTG
CTNNB1.9.1.CTNNB1.1_R	chr3:41275640-41275798	AGCCAGGTATCACTGTAAGA
CTNNB1.9.2.CTNNB1.2_F	chr3:41275495-41275647	GTAGGAAGTATGGCTGCGAT
CTNNB1.9.2.CTNNB1.2_R	chr3:41275495-41275647	GGACAAAGGGCAAGATTTCG
CTNNB1.12.1.CTNNB1.1_F	chr3:41278074-41278233	GGGCCTTTTTCTCCTTGTCT
CTNNB1.12.1.CTNNB1.1_R	chr3:41278074-41278233	GCCATACCTGCTCTAGGAAA
CTNNB1.2.1.CTNNB1.1_F	chr3:41266047-41266206	AGTTGGACATGGCCATGG
CTNNB1.2.1.CTNNB1.1_R	chr3:41266047-41266206	GTGAAGGACTGAGAAAATCCC
CTNNB1.2.2.CTNNB1.2_F	chr3:41266126-41266265	ATCCATTCTGGTGCCACTAC
CTNNB1.2.2.CTNNB1.2_R	chr3:41266126-41266265	GCATTCTGACTTTCAGTAAGGC
CTNNB1.2.2.CTNNB1.3_F	chr3:41265901-41266051	TCTGCTTTTCTTGGCTGTCT
CTNNB1.2.2.CTNNB1.3_R	chr3:41265901-41266051	CTAACAGCCGCTTTTCTGTC
CTNNB1.14.1.CTNNB1.1_F	chr3:41280625-41280785	TGACACCCTGACTCTTCTAG
CTNNB1.14.1.CTNNB1.1_R	chr3:41280625-41280785	GATTGCTGTCACCTGGAGG
CTNNB1.14.2.CTNNB1.2_F	chr3:41280747-41280906	ACTATCCAGTTGATGGGCTG
CTNNB1.14.2.CTNNB1.2_R	chr3:41280747-41280906	ACCCTACCAACCAAGTCTTT
CTNNB1.8.1.CTNNB1.1_F	chr3:41275040-41275199	GAAGGGATGGAAGGTCTCCT
CTNNB1.8.1.CTNNB1.1_R	chr3:41275040-41275199	TCAGTGATGTCTTCCCTGTC
CTNNB1.8.2.CTNNB1.2_F	chr3:41274975-41275133	GTGCCATGGGAATAGAGTCA
CTNNB1.8.2.CTNNB1.2_R	chr3:41274975-41275133	TGGCAGACCATCATCTTGTT
CTNNB1.8.2.CTNNB1.3_F	chr3:41275240-41275397	CCTGCCATCTGTGCTCTTC
CTNNB1.8.2.CTNNB1.3_R	chr3:41275240-41275397	CAGCTAGAGATGCTTCATTTTC
CTNNB1.8.3.CTNNB1.4_F	chr3:41275176-41275319	TGGGTGGTATAGAGGCTCTT
CTNNB1.8.3.CTNNB1.4_R	chr3:41275176-41275319	GATGGTGGGTGTAAGAGCTT
CTNNB1.1.1.CTNNB1.1_F	chr3:41265557-41265709	GTTTTGAAAATCCAGCGTGG
CTNNB1.1.1.CTNNB1.1_R	chr3:41265557-41265709	TTCACCAAGCCATTAGGAGG
CTNNB1.4.1.CTNNB1.1_F	chr3:41266913-41267071	CATGCGTTCTCCTCAGATGG
CTNNB1.4.1.CTNNB1.1_R	chr3:41266913-41267071	GCTTCAAGCATTCTGACATGT
CTNNB1.4.2.CTNNB1.2_F	chr3:41266764-41266916	GCTCAAGGGGAGTAGTTTCA
CTNNB1.4.2.CTNNB1.2_R	chr3:41266764-41266916	TGCATGGTACGTACAATAGCA
CTNNB1.10.4.CTNNB1.1_F	chr3:41277190-41277319	TACAGAGGAGAATGCCCTGT
CTNNB1.10.4.CTNNB1.1_R	chr3:41277190-41277319	ACATACCTGCACAAACAATGG
CTNNB1.10.5.CTNNB1.2_F	chr3:41277258-41277415	AGTTGAAGGTTGTACCGGAG
CTNNB1.10.5.CTNNB1.2_R	chr3:41277258-41277415	TGGTAACCCTATTATGGTCCC
CTNNB1.13.1.CTNNB1.1_F	chr3:41279495-41279638	TCTATTCTTCCTTGCTTTGTGC
CTNNB1.13.1.CTNNB1.1_R	chr3:41279495-41279638	TGGTTTCCCAGATGAGCAAA
CTNNB1.5.1.CTNNB1.1_F	chr3:41267171-41267330	TTCACCAGTGGATTCTGTGT
CTNNB1.5.1.CTNNB1.1_R	chr3:41267171-41267330	TGCTTTCTTGGTTGCCATAA
CTNNB1.5.2.CTNNB1.2_F	chr3:41267276-41267426	GAAAATGGTTGCCTTGCTCA
CTNNB1.5.2.CTNNB1.2_R	chr3:41267276-41267426	TGGTGCCAAAAAGGTTAGGA
CTNNB1.5.2.CTNNB1.3_F	chr3:41267045-41267177	TAAGTCTGGAGGCATTCCTG
CTNNB1.5.2.CTNNB1.3_R	chr3:41267045-41267177	TGTGGAGAGTTGTAATGGCA
ABL2.6.1.ABL2.1_F	chr1:179086469-179086629	AGTCCCTTTCAACCTTACCC
ABL2.6.1.ABL2.1_R	chr1:179086469-179086629	TCTTGCAGCTCGTAACTGC

ABL2.6.2.ABL2.2_F	chr1:179086530-179086688	CTCTGGTGCTGTCCACTTAA
ABL2.6.2.ABL2.2_R	chr1:179086530-179086688	TCATGACCATTTTCCTCACCA
ABL2.6.2.ABL2.3_F	chr1:179086376-179086509	TGGCAGGTAAAGGTAGAGGA
ABL2.6.2.ABL2.3_R	chr1:179086376-179086509	TTAAGTGGACAGCACCAGAG
ABL2.11.1.ABL2.1_F	chr1:179100465-179100620	ACCTTTAGTGATGCTGAGTGT
ABL2.11.1.ABL2.1_R	chr1:179100465-179100620	TCCCTTCCCTTCTTATGTCTT
ABL2.11.2.ABL2.2_F	chr1:179100445-179100592	GGATGCTACATAGAAGCCTCA
ABL2.11.2.ABL2.2_R	chr1:179100445-179100592	TTTGCATCGTCCCTATGGTT
ABL2.3.1.ABL2.1_F	chr1:179079837-179079982	GCATGCCAACGTGTGAATAT
ABL2.3.1.ABL2.1_R	chr1:179079837-179079982	CGTATACCCTGTGATCCACC
ABL2.7.1.ABL2.1_F	chr1:179087780-179087939	AGAAGAAATCTGAGTGGCCA
ABL2.7.1.ABL2.1_R	chr1:179087780-179087939	AGTGGTTTGGAGTGTTTGAA
ABL2.7.2.ABL2.2_F	chr1:179087689-179087821	CTGCATGTCAAGCAAGATGG
ABL2.7.2.ABL2.2_R	chr1:179087689-179087821	TTTGCTGGATTACCTCCGAG
ABL2.9.1.ABL2.1_F	chr1:179090730-179090889	TGTAATTCTCAGCAACCCAC
ABL2.9.1.ABL2.1_R	chr1:179090730-179090889	TACCCAGCACCCAAGTGTAA
ABL2.9.2.ABL2.2_F	chr1:179090860-179091002	CCATTTCCCATTTGTCGTGG
ABL2.9.2.ABL2.2_R	chr1:179090860-179091002	GCTTTTCTCCTTTTCTTACCAG
ABL2.12.1.ABL2.1_F	chr1:179102420-179102577	ACTGCCAATGCCTTAGTTCA
ABL2.12.1.ABL2.1_R	chr1:179102420-179102577	TGAATGCCATGAAAAGGAGAC
ABL2.2.1.ABL2.1_F	chr1:179079416-179079576	ACCTGCTAAGGGACCCATA
ABL2.2.1.ABL2.1_R	chr1:179079416-179079576	TCACAGAGGTAGCTGAGGAG
ABL2.2.2.ABL2.2_F	chr1:179079506-179079660	CCTGTTTCTTCAGTGTCCGA
ABL2.2.2.ABL2.2_R	chr1:179079506-179079660	TCTTTCTCAGTTGTGTGCCT
ABL2.14.1.ABL2.1_F	chr1:179198403-179198564	GGTGAAGATATTGAAGCCGG
ABL2.14.1.ABL2.1_R	chr1:179198403-179198564	AGGAATGTGACCAGGGGT
ABL2.14.12.ABL2.2_F	chr1:179198376-179198517	GCTCCCAGACACACTCAC
ABL2.14.12.ABL2.2_R	chr1:179198376-179198517	GATGGGGCAGCAGGTG
ABL2.8.1.ABL2.1_F	chr1:179089298-179089436	GGCAAGCATTTTTGGAGGAA
ABL2.8.1.ABL2.1_R	chr1:179089298-179089436	GGTTTGTCCCTCTCGTTTTC
ABL2.4.1.ABL2.1_F	chr1:179081412-179081568	CACCACCACTACCCAGAATT
ABL2.4.1.ABL2.1_R	chr1:179081412-179081568	CCACTGGATATTGAATTTCTGC
ABL2.1.1.ABL2.1_F	chr1:179076851-179077012	TTCCCACCAGGCTAACAGT
ABL2.1.1.ABL2.1_R	chr1:179076851-179077012	TGGACTGCATCCCTCAAAC
ABL2.1.2.ABL2.2_F	chr1:179077010-179077172	CTCGGAAGGCAAATTTGTTG
ABL2.1.2.ABL2.2_R	chr1:179077010-179077172	AACCAAACAGGCCGCTG
ABL2.1.3.ABL2.3_F	chr1:179077182-179077342	GAGATTTTCTCAGCGGCCT
ABL2.1.3.ABL2.3_R	chr1:179077182-179077342	TCCACATCAGAAACACAGGA
ABL2.1.4.ABL2.4_F	chr1:179077343-179077502	AGCTGCCTTCTTTCCTCCT
ABL2.1.4.ABL2.4_R	chr1:179077343-179077502	TCTTATCTGAGCATCAGGTCA
ABL2.1.4.ABL2.5_F	chr1:179077049-179077197	CCACATAGCCTGAGCAGTAG
ABL2.1.4.ABL2.5_R	chr1:179077049-179077197	CAGCAGGTACTAAAGTGGCT
ABL2.1.5.ABL2.6_F	chr1:179077553-179077712	ATTCCCCTGAGAGTCTGTG
ABL2.1.5.ABL2.6_R	chr1:179077553-179077712	GTAAAGAGAAGAATGGTGGGG
ABL2.1.6.ABL2.7_F	chr1:179077713-179077875	AGCCATCCCAAGTCGTG
ABL2.1.6.ABL2.7_R	chr1:179077713-179077875	AATCAGAGGAAAGTGCTGCT
ABL2.1.6.ABL2.8_F	chr1:179077477-179077608	CACTTTGGTTTTACCCGTCG
ABL2.1.6.ABL2.8_R	chr1:179077477-179077608	CCACTCACAACCACAAAGTG
ABL2.1.7.ABL2.9_F	chr1:179077886-179078046	TGCTTGGAGCAGCACTT
ABL2.1.7.ABL2.9_R	chr1:179077886-179078046	TCCAAGGTCAAACTCTACATCT
ABL2.1.8.ABL2.10_F	chr1:179078047-179078206	AAGCCCTGAGGACATGGA
ABL2.1.8.ABL2.10_R	chr1:179078047-179078206	AACCTCTGTAATGACGACGG
ABL2.1.8.ABL2.11_F	chr1:179077854-179078005	TCCTCTGGGCAATAACTTGG
ABL2.1.8.ABL2.11_R	chr1:179077854-179078005	GAGCAGGATAGGATGGCAAT
ABL2.1.9.ABL2.12_F	chr1:179078227-179078386	CCGTCGTCATTACAGAGGTT
ABL2.1.9.ABL2.12_R	chr1:179078227-179078386	AAACGCAGCAGCTCCTT
ABL2.1.10.ABL2.13_F	chr1:179078387-179078549	GCTGATTCTCCATTTCTCGG
ABL2.1.10.ABL2.13_R	chr1:179078387-179078549	AGGTGCACAGGCCTCTA
ABL2.1.10.ABL2.14_F	chr1:179078165-179078307	TAAAGAAGCCTGTGATGCCA
ABL2.1.10.ABL2.14_R	chr1:179078165-179078307	TTGCTTCTCTACAGCATGCT
ABL2.1.11.ABL2.15_F	chr1:179078492-179078637	AGCATGTCTCTTTGGCATCT
ABL2.1.11.ABL2.15_R	chr1:179078492-179078637	CTCATAATGCAGCCTCGGTA
ABL2.10.1.ABL2.1_F	chr1:179095512-179095671	TGGTGACCAGGGAGTCTTAC
ABL2.10.1.ABL2.1_R	chr1:179095512-179095671	AAACACTCCTGGTACCATGG
ABL2.10.2.ABL2.2_F	chr1:179095661-179095810	AGATACTCAGCTGCACTGC
ABL2.10.2.ABL2.2_R	chr1:179095661-179095810	TCCTGTGATGACCTTATGGC
ABL2.13.1.ABL2.1_F	chr1:179112043-179112185	ATGTGGTTATCAAGCCTCCC

ABL2.13.1.ABL2.1_R	chr1:179112043-179112185	TAACTTTTGTGCTTCTGGGC
ABL2.5.1.ABL2.1_F	chr1:179084030-179084186	CTCACATGCTCTCATAAGTTCA
ABL2.5.1.ABL2.1_R	chr1:179084030-179084186	CGGAGAAGAAACACTAAGTGC
ABL2.5.2.ABL2.2_F	chr1:179083917-179084049	TGTCATGAGGCTGGATTCAA
ABL2.5.2.ABL2.2_R	chr1:179083917-179084049	ATCGAATGGAACAGCCTGAG
BRAF.11.3.BRAF.1_F	chr7:140494105-140494258	AGTTCTAGCAATGCTGGATACT
BRAF.11.3.BRAF.1_R	chr7:140494105-140494258	CATTTTTCCAGGCCCCAAAT
BRAF.11.11.BRAF.2_F	chr7:140494231-140494381	AAGGGCTGTGGAATTGGAAT
BRAF.11.11.BRAF.2_R	chr7:140494231-140494381	GTCATTACTGCTAGGTTTTTAATGC
BRAF.7.5.BRAF.1_F	chr7:140477734-140477881	TAGTTGCTACCACTGGGAAC
BRAF.7.5.BRAF.1_R	chr7:140477734-140477881	ACACTTGGAGTAACAATTGCC
BRAF.17.13.BRAF.1_F	chr7:140549836-140550087	TCCCACCTCCTAAAATAATCAAGA
BRAF.17.13.BRAF.1_R	chr7:140549836-140550087	ACACTGGCAGTTACTGTGATGT
BRAF.2.3.BRAF.1_F	chr7:140439570-140439722	GTGCTCAGAAATCTGTCTATGA
BRAF.2.3.BRAF.1_R	chr7:140439570-140439722	TTTTTATGGTGGGACGAGGA
BRAF.2.6.BRAF.2_F	chr7:140439671-140439803	GCACTCTGCCATTAATCTCT
BRAF.2.6.BRAF.2_R	chr7:140439671-140439803	TGTGTTTTCAATGAGTGTGAAG
BRAF.1.3.BRAF.1_F	chr7:140434391-140434550	CTCCTGAACTCTCTCACTCA
BRAF.1.3.BRAF.1_R	chr7:140434391-140434550	ATTCTCGCCTCTATTGAGCT
BRAF.1.4.BRAF.2_F	chr7:140434533-140434683	ATGCACTGCGGTGAATTTTT
BRAF.1.4.BRAF.2_R	chr7:140434533-140434683	TGTAAAGTGTGATGGGACTCT
BRAF.18.9.BRAF.1_F	chr7:140624386-140624552	TCCGGAATGGCAGGGT
BRAF.18.9.BRAF.1_R	chr7:140624386-140624552	TCTCCGCCTCCCTTCC
BRAF.18.10.BRAF.2_F	chr7:140624307-140624444	GCCGCCTCTTTCCAAAATAA
BRAF.18.10.BRAF.2_R	chr7:140624307-140624444	GGCCAGGCTCTGTTCAA
BRAF.13.11.BRAF.1_F	chr7:140501251-140501404	ACACACATCAGTGGAACTTCT
BRAF.13.11.BRAF.1_R	chr7:140501251-140501404	GTAGATACGTCAGTTTCTAGAAAGT
BRAF.13.12.BRAF.2_F	chr7:140501131-140501279	TGGAAGAAAAACCCTCACAGA
BRAF.13.12.BRAF.2_R	chr7:140501131-140501279	GTTTCCGCTGTCAAACATGT
BRAF.16.1.BRAF.1_F	chr7:140534429-140534588	CACTGTCCTCTGTTTGTTGG
BRAF.16.1.BRAF.1_R	chr7:140534429-140534588	TCTGGGGAACGGAACTGAT
BRAF.16.2.BRAF.2_F	chr7:140534535-140534694	GAAGGTAGCACTGAAAGGCT
BRAF.16.2.BRAF.2_R	chr7:140534535-140534694	GGACAAAGTCCGGATTGAAT
BRAF.16.2.BRAF.3_F	chr7:140534299-140534448	TCCTGTATGACATGGATGCC
BRAF.16.2.BRAF.3_R	chr7:140534299-140534448	CCCAAGTCACCACAAAAACC
BRAF.6.7.BRAF.1_F	chr7:140476678-140476830	ACATCCTCAATGGTCTTCAAAA
BRAF.6.7.BRAF.1_R	chr7:140476678-140476830	ATTCCACAAAGCCACAACTG
BRAF.6.8.BRAF.2_F	chr7:140476806-140476953	ATGGTGATACAAGCTGGAGC
BRAF.6.8.BRAF.2_R	chr7:140476806-140476953	ACCGACAGACTACTTTGGTT
BRAF.3.3.BRAF.1_F	chr7:140449054-140449209	TGGAGCCTTGTATATAGACGG
BRAF.3.3.BRAF.1_R	chr7:140449054-140449209	TGTTCTAACAGGCACCAGAA
BRAF.3.4.BRAF.2_F	chr7:140449136-140449289	GGTAACTGTCCAGTCATCAAT
BRAF.3.4.BRAF.2_R	chr7:140449136-140449289	TGGTAAAAGCATTGCTCTAGGA
BRAF.9.1.BRAF.1_F	chr7:140482840-140482983	ACCATTCGATTCCTGTCTTCT
BRAF.9.1.BRAF.1_R	chr7:140482840-140482983	CATACTTGCTCCTCCTTAATGT
BRAF.9.2.BRAF.2_F	chr7:140482784-140482933	TGGCTGTGACTTCTAAGAAGA
BRAF.9.2.BRAF.2_R	chr7:140482784-140482933	AACCACAGGTTTGTCTGCTA
BRAF.12.1.BRAF.1_F	chr7:140500158-140500313	CCAAGAGCAGAAGTCAAACC
BRAF.12.1.BRAF.1_R	chr7:140500158-140500313	ATGAAGCTTCTGGGTTTTGC
BRAF.14.13.BRAF.1_F	chr7:140507692-140507947	ACTCATCCATATTTCACATTCCCT
BRAF.14.13.BRAF.1_R	chr7:140507692-140507947	CACTGTTACTAGCCCCTCGA
BRAF.15.1.BRAF.1_F	chr7:140508689-140508821	TTCACGTCACATACAAACCA
BRAF.15.1.BRAF.1_R	chr7:140508689-140508821	TGTAATTTGCTCCCTTTACCTC
BRAF.8.1.BRAF.1_F	chr7:140481364-140481514	CTTGTCACAATGTCACCACA
BRAF.8.1.BRAF.1_R	chr7:140481364-140481514	TCTGTTTGGCTTGACTTGAC
BRAF.4.1.BRAF.1_F	chr7:140453081-140453228	AGCCTCAATTCTTACCATCCA
BRAF.4.1.BRAF.1_R	chr7:140453081-140453228	TGCTTGCTCTGATAGGAAAATG
BRAF.4.2.BRAF.2_F	chr7:140453034-140453165	TAACTCAGCAGCATCTCAGG
BRAF.4.2.BRAF.2_R	chr7:140453034-140453165	TCTTCATGAAGACCTCACAGT
BRAF.10.1.BRAF.1_F	chr7:140487301-140487429	AGGAAATAAGCAGCAAAGCA
BRAF.10.1.BRAF.1_R	chr7:140487301-140487429	CAGTGTTATCGCTACTCTCTGA
BRAF.5.1.BRAF.1_F	chr7:140453965-140454093	CAGGATGTTTTCAAACTTCGC
BRAF.5.1.BRAF.1_R	chr7:140453965-140454093	CACCCCCAAGTATGTTCTGT
EGFR.11.1.EGFR.1_F	chr7:55225328-55225466	AGAAACTCCTACGTGGTGTG
EGFR.11.1.EGFR.1_R	chr7:55225328-55225466	GGCAAATGTAATCTACCAGGC
EGFR.21.1.EGFR.1_F	chr7:55242382-55242516	GTGGCACCATCTCACAATTG
EGFR.21.1.EGFR.1_R	chr7:55242382-55242516	CACACAGCAAAGCAGAAACT

EGFR.7.1.EGFR.1_F	chr7:55221703-55221855	CGTGTCCTCTCTCCTCCATA
EGFR.7.1.EGFR.1_R	chr7:55221703-55221855	AGTTAGAGGGCCCACAGAG
EGFR.26.1.EGFR.1_F	chr7:55267952-55268110	GCCTTCTTTAAGCAATGCCA
EGFR.26.1.EGFR.1_R	chr7:55267952-55268110	GGAAGCACAGACTGCAATTT
EGFR.17.1.EGFR.1_F	chr7:55238010-55238172	CTTTCTCCAGGCCAGGAAAT
EGFR.17.1.EGFR.1_R	chr7:55238010-55238172	ATGGAGGTGGCTGCATC
EGFR.17.2.EGFR.2_F	chr7:55238168-55238323	TCAGAGTTTCAGCTGGGTTG
EGFR.17.2.EGFR.2_R	chr7:55238168-55238323	AGTGGAAGGAAGGAAATGGG
EGFR.17.2.EGFR.3_F	chr7:55237975-55238104	CCAGGCCTCTCACATATTGA
EGFR.17.2.EGFR.3_R	chr7:55237975-55238104	CTAAGCATGACTCCTGAGCA
EGFR.2.1.EGFR.1_F	chr7:55209989-55210133	TTTCTTCCAGTTTGCCAAGG
EGFR.2.1.EGFR.1_R	chr7:55209989-55210133	GTGTAGGAAAATCAAAGTCACC
EGFR.2.2.EGFR.2_F	chr7:55209879-55210038	TCTCTGTGTGGAGAGAGTGA
EGFR.2.2.EGFR.2_R	chr7:55209879-55210038	ATTGAACATCCTCTGGAGGC
EGFR.22.1.EGFR.1_F	chr7:55249005-55249165	AAGCCTACGTGATGGCCA
EGFR.22.1.EGFR.1_R	chr7:55249005-55249165	CCTTCCCTGATTACCTTTGC
EGFR.22.2.EGFR.2_F	chr7:55249120-55249254	GACTATGTCCGGGAACACAA
EGFR.22.2.EGFR.2_R	chr7:55249120-55249254	ACACATATCCCCATGGCAAA
EGFR.22.2.EGFR.3_F	chr7:55248915-55249064	CATTCATGCGTCTTCACCTG
EGFR.22.2.EGFR.3_R	chr7:55248915-55249064	GCATGAGCTGCGTGATGA
EGFR.1.4.EGFR.1_F	chr7:55086948-55087164	GTATTGATCGGGAGAGCCGG
EGFR.1.4.EGFR.1_R	chr7:55086948-55087164	AGGAAACAGGAAAGGACGGG
EGFR.18.1.EGFR.1_F	chr7:55238748-55238906	CCAACATCCAGACACATAGTG
EGFR.18.1.EGFR.1_R	chr7:55238748-55238906	ACAGAGCTGTGAACACTTAC
EGFR.30.1.EGFR.1_F	chr7:55272999-55273160	GCTGGCTCTGTGCAGAAT
EGFR.30.1.EGFR.1_R	chr7:55272999-55273160	CCAGGCTAATTTGGTGGCT
EGFR.30.2.EGFR.2_F	chr7:55272855-55273006	GCTCCCTGTCATAAGTCTCC
EGFR.30.2.EGFR.2_R	chr7:55272855-55273006	GGTTCAGAGGCTGATTGTGA
EGFR.30.2.EGFR.3_F	chr7:55273171-55273310	AGAAAGGCAGCCACCAAA
EGFR.30.2.EGFR.3_R	chr7:55273171-55273310	GCTCATACTATCCTCCGTGG
EGFR.30.3.EGFR.4_F	chr7:55273102-55273243	CCCCGAGTATCTCAACACTG
EGFR.30.3.EGFR.4_R	chr7:55273102-55273243	CTGCATTTTCAGCTGTGGAG
EGFR.23.1.EGFR.1_F	chr7:55259410-55259567	AGCAGGGTCTTCTCTGTTTC
EGFR.23.1.EGFR.1_R	chr7:55259410-55259567	ACCTAAAGCCACCTCCTTAC
EGFR.13.1.EGFR.1_F	chr7:55229187-55229345	CTGTGACCCACTCTGTCTC
EGFR.13.1.EGFR.1_R	chr7:55229187-55229345	TTTTTGATCAACGCAAGGGG
EGFR.16.1.EGFR.1_F	chr7:55236086-55236244	AGGTCCAGAAAGTGATTGGG
EGFR.16.1.EGFR.1_R	chr7:55236086-55236244	TGCAGTTTTAGTGGGAGACT
EGFR.29.1.EGFR.1_F	chr7:55270210-55270373	CCCTCATTTCCTCCTGCAG
EGFR.29.1.EGFR.1_R	chr7:55270210-55270373	ACTGGAGACTGGCTGCT
EGFR.29.2.EGFR.2_F	chr7:55270310-55270459	CATAGACGACACCTTCCTCC
EGFR.29.2.EGFR.2_R	chr7:55270310-55270459	TTTATCTGCTCCTTACGCCC
EGFR.27.1.EGFR.1_F	chr7:55268891-55269051	GCACCAGGGGGATGAAA
EGFR.27.1.EGFR.1_R	chr7:55268891-55269051	AGAGAGAGAGACAGAGATTTCA
EGFR.27.2.EGFR.2_F	chr7:55268790-55268930	AAATTGGCAAACACACAGGC
EGFR.27.2.EGFR.2_R	chr7:55268790-55268930	CTTCTTCATCCATCAGGGCA
EGFR.6.1.EGFR.1_F	chr7:55220200-55220358	CCTGGGAAATGATCCTACCC
EGFR.6.1.EGFR.1_R	chr7:55220200-55220358	TGCTGGAGGGGCATCTTA
EGFR.25.1.EGFR.1_F	chr7:55266396-55266557	CCCACTGCCTTCTTTTCTTG
EGFR.25.1.EGFR.1_R	chr7:55266396-55266557	AGACCCACCAGTCACTCA
EGFR.28.1.EGFR.1_F	chr7:55269421-55269579	TGGGCAACTTCTCTGTTTCT
EGFR.28.1.EGFR.1_R	chr7:55269421-55269579	ACCCACACAGGAAGAAAACT
EGFR.3.1.EGFR.1_F	chr7:55211038-55211198	TTATGTCCTCATTGCCCTCA
EGFR.3.1.EGFR.1_R	chr7:55211038-55211198	TTATGAACCCCCAGCCTTG
EGFR.3.2.EGFR.2_F	chr7:55210906-55211053	CGTGTGCATTAGGGTTCAAC
EGFR.3.2.EGFR.2_R	chr7:55210906-55211053	TCTGCAGGTTTTCCAAAGGA
EGFR.9.1.EGFR.1_F	chr7:55224211-55224356	TGTGAACGGAATACACGTCT
EGFR.9.1.EGFR.1_R	chr7:55224211-55224356	CAAGCAACTGAACCTGTGAC
EGFR.12.1.EGFR.1_F	chr7:55227872-55228031	TCGTCAGCCTGAACATAACA
EGFR.12.1.EGFR.1_R	chr7:55227872-55228031	AACAGAAAGCGGTGACTTAC
EGFR.12.2.EGFR.2_F	chr7:55227723-55227877	CACAGCATGACCTACCATCA
EGFR.12.2.EGFR.2_R	chr7:55227723-55227877	CCTTGAGGGAGCGTAATCC
EGFR.15.1.EGFR.1_F	chr7:55232972-55233130	TTTTTCTCCACCTTGGTGCA
EGFR.15.1.EGFR.1_R	chr7:55232972-55233130	TCTCCTTCACTTTCCACTCAC
EGFR.20.1.EGFR.1_F	chr7:55241601-55241736	TGACCCTTGTCTCTGTGTTC
EGFR.20.1.EGFR.1_R	chr7:55241601-55241736	TGTGCCAGGGACCTTAC
EGFR.14.1.EGFR.1_F	chr7:55231378-55231531	GAGGTGATTTGTGTTCCTGC

EGFR.14.1.EGFR.1_R	chr7:55231378-55231531	TGAAATGGACGTGGATAGCA
EGFR.8.1.EGFR.1_F	chr7:55223523-55223668	TTTCATGCTCTCTTCCCCAG
EGFR.8.1.EGFR.1_R	chr7:55223523-55223668	TCAGCAGCCGAGAACAAG
EGFR.4.1.EGFR.1_F	chr7:55214292-55214447	CTCACCGCAGTTCCATTCT
EGFR.4.1.EGFR.1_R	chr7:55214292-55214447	CTGGAGGCAGAGATAGTGTG
EGFR.24.1.EGFR.1_F	chr7:55260420-55260557	ACTTTTTCCAACAGAGGGAAAC
EGFR.24.1.EGFR.1_R	chr7:55260420-55260557	TTGGCCTCAGTACAAACTCA
EGFR.10.1.EGFR.1_F	chr7:55224452-55224586	TCACCCTGTTGTTTGTTTCAG
EGFR.10.1.EGFR.1_R	chr7:55224452-55224586	AGGGAACAGGAAATATGTCGA
EGFR.19.1.EGFR.1_F	chr7:55240695-55240853	GCCTAAGATCCCGTCCATC
EGFR.19.1.EGFR.1_R	chr7:55240695-55240853	TTGTTCCTGTCGGGGTG
EGFR.19.2.EGFR.2_F	chr7:55240594-55240747	ACAAGATGTCAGTGCACTGA
EGFR.19.2.EGFR.2_R	chr7:55240594-55240747	TTCGCATGAAGAGGCCG
EGFR.5.1.EGFR.1_F	chr7:55218943-55219092	GAAAGGGCGTCATCAGTTTC
EGFR.5.1.EGFR.1_R	chr7:55218943-55219092	CAAGTGAAGGAAGAGAGGGG
AKT1.6.3.AKT1.1_F	chr14:105239742-105239901	AAAGGTGGCCTCAGGTCA
AKT1.6.3.AKT1.1_R	chr14:105239742-105239901	CAGCTGTTCTTCCACCTGT
AKT1.6.4.AKT1.2_F	chr14:105239834-105239985	TTCTTCTCCGAGTGCAGGTA
AKT1.6.4.AKT1.2_R	chr14:105239834-105239985	GAGACCCGGTCTGAGAAAC
AKT1.11.5.AKT1.1_F	chr14:105242953-105243117	TGTCCCTCCTAAGCGCT
AKT1.11.5.AKT1.1_R	chr14:105242953-105243117	GCAGACAGAGGCTCTGC
AKT1.3.1.AKT1.1_F	chr14:105238666-105238799	GAGTGTGGATATGTGGGGAG
AKT1.3.1.AKT1.1_R	chr14:105238666-105238799	GACACTGTGGCCTTGTTTC
AKT1.7.1.AKT1.1_F	chr14:105240168-105240321	TCTGGTGCCATGGAGAGTA
AKT1.7.1.AKT1.1_R	chr14:105240168-105240321	TTCCAGCTCCCCTTCCTT
AKT1.9.3.AKT1.1_F	chr14:105241362-105241516	TAAAGCAGGGCTGGGTGA
AKT1.9.3.AKT1.1_R	chr14:105241362-105241516	CGAGTTTGAGTACCTGAAGC
AKT1.9.4.AKT1.2_F	chr14:105241495-105241655	CCTTCACCAGGATCACCTTG
AKT1.9.4.AKT1.2_R	chr14:105241495-105241655	CACCAGGTGTGAAGTGGAC
AKT1.2.1.AKT1.1_F	chr14:105237046-105237197	CCTCTCTGAGTGTGGAGAGA
AKT1.2.1.AKT1.1_R	chr14:105237046-105237197	CTCATGACTGTCCCGTCTG
AKT1.12.1.AKT1.1_F	chr14:105246435-105246582	GATACTTACGCGCCACAGA
AKT1.12.1.AKT1.1_R	chr14:105246435-105246582	GTCTGACGGGTAGAGTGTG
AKT1.12.2.AKT1.2_F	chr14:105246407-105246543	CCCAAATCTGAATCCCGAGA
AKT1.12.2.AKT1.2_R	chr14:105246407-105246543	ACGTCTGTAGGGGAGTACAT
AKT1.8.1.AKT1.1_F	chr14:105241206-105241343	CCAAGAAGACAGGACATCGT
AKT1.8.1.AKT1.1_R	chr14:105241206-105241343	TCACCCAGCCCTGCTTTA
AKT1.4.1.AKT1.1_F	chr14:105239235-105239399	CTGCTTGGGGTCCTTCTT
AKT1.4.1.AKT1.1_R	chr14:105239235-105239399	ATGACTACGGCCGTGCA
AKT1.4.2.AKT1.2_F	chr14:105239380-105239509	TCATCTCGTACATGACCACG
AKT1.4.2.AKT1.2_R	chr14:105239380-105239509	AATGCTGTGTCCTCTCTGTG
AKT1.4.2.AKT1.3_F	chr14:105239188-105239318	ATGAGGGGATGGAGGTGTAG
AKT1.4.2.AKT1.3_R	chr14:105239188-105239318	ACAACCAGGACCATGAGAAG
AKT1.1.1.AKT1.1_F	chr14:105236629-105236760	ATACAGATCATGGCACGAGG
AKT1.1.1.AKT1.1_R	chr14:105236629-105236760	TCTGAGCTGTCTACACCCA
AKT1.10.1.AKT1.1_F	chr14:105242029-105242165	CAGGGACACCTCCATCTCT
AKT1.10.1.AKT1.1_R	chr14:105242029-105242165	GGAGCTCCTGATCTGGTACA
AKT1.10.2.AKT1.2_F	chr14:105241904-105242063	GAGTGCTGAGTGTCTCCTG
AKT1.10.2.AKT1.2_R	chr14:105241904-105242063	AGGAGGAGGAGATGGACTTC
AKT1.13.1.AKT1.1_F	chr14:105258935-105259068	TGGCAGCGGGTACTAAC
AKT1.13.1.AKT1.1_R	chr14:105258935-105259068	TCACATTCAGCTTCCTTTGC
AKT1.5.1.AKT1.1_F	chr14:105239571-105239723	CAGCAACGCGTATGCAC
AKT1.5.1.AKT1.1_R	chr14:105239571-105239723	TGACCTGAGGCCACCTTT
MSH2.11.5.MSH2.1_F	chr2:47698066-47698223	ACACATTGCTTCTAGTACACAT
MSH2.11.5.MSH2.1_R	chr2:47698066-47698223	GCCAGGTGACATTCAGAACA
MSH2.7.1.MSH2.1_F	chr2:47656971-47657131	TCGATTCCCAGATCTTAACCG
MSH2.7.1.MSH2.1_R	chr2:47656971-47657131	AGGACAGCACATTGCCAA
MSH2.7.2.MSH2.2_F	chr2:47656825-47656981	TGAGACTTACGTGCTTAGTTGA
MSH2.7.2.MSH2.2_R	chr2:47656825-47656981	TGCTGCTTGTCTTTGAAACT
MSH2.2.3.MSH2.1_F	chr2:47635498-47635655	CAGCTAATACAGTGCTTGAACA
MSH2.2.3.MSH2.1_R	chr2:47635498-47635655	TCATTCTCCTTGGATGCCTT
MSH2.2.10.MSH2.2_F	chr2:47635633-47635784	GGTTCGTCAGTATAGAGTTGAAG
MSH2.2.10.MSH2.2_R	chr2:47635633-47635784	CTCAAACCATTCTACTATCACAATC
MSH2.17.1.MSH2.1_F	chr2:47739417-47739566	CCCGTGGAACTCCTACATTT
MSH2.17.1.MSH2.1_R	chr2:47739417-47739566	AACAGACACCAGGTCATGAG
MSH2.1.1.MSH2.1_F	chr2:47630331-47630491	GAGGTGAGGAGGTTTCGAC
MSH2.1.1.MSH2.1_R	chr2:47630331-47630491	TCTTGAACACCTCCCGG

MSH2.1.2.MSH2.2_F	chr2:47630461-47630598	GACCGGGGCGACTTCTATA
MSH2.1.2.MSH2.2_R	chr2:47630461-47630598	ACTCTCTGAGGCGGGAAA
MSH2.18.5.MSH2.1_F	chr2:47888122-47888263	TTTTGAGACAAGGTGTCATTCT
MSH2.18.5.MSH2.1_R	chr2:47888122-47888263	TCATTTGACAATTTCCTCCCA
MSH2.18.6.MSH2.2_F	chr2:47887997-47888134	GTTAGGCCCCTGGAAATCTT
MSH2.18.6.MSH2.2_R	chr2:47887997-47888134	AGATCGTGGCATTGCACTC
MSH2.13.1.MSH2.1_F	chr2:47703555-47703714	ATTCGACAAACTGGGGTGAT
MSH2.13.1.MSH2.1_R	chr2:47703555-47703714	CAAGGGACTAGGAGATGCAC
MSH2.13.2.MSH2.2_F	chr2:47703412-47703570	GTCAGTGTAAACCTACGCGA
MSH2.13.2.MSH2.2_R	chr2:47703412-47703570	CATGGCACAAAACACCCAAT
MSH2.16.1.MSH2.1_F	chr2:47709957-47710092	GGAGTTCCTGTCCAAGGTG
MSH2.16.1.MSH2.1_R	chr2:47709957-47710092	ACCTTCATTCCATTACTGGGA
MSH2.16.10.MSH2.2_F	chr2:47709871-47710012	TGTCACTGTCTAACATGACTTT
MSH2.16.10.MSH2.2_R	chr2:47709871-47710012	CTTTGCTATTACTTCAGCTTTTAGC
MSH2.6.1.MSH2.1_F	chr2:47643454-47643606	AGGGTTCTGTTGAAGATACCA
MSH2.6.1.MSH2.1_R	chr2:47643454-47643606	ATCATGTGGGTAACTGCAGG
MSH2.6.2.MSH2.2_F	chr2:47643378-47643521	TCCTCTGTTTTTCATGGCGT
MSH2.6.2.MSH2.2_R	chr2:47643378-47643521	AGAGGCTGCTTAATCCACTG
MSH2.3.1.MSH2.1_F	chr2:47637312-47637473	GCTTCCATTGGTGTTGTGG
MSH2.3.1.MSH2.1_R	chr2:47637312-47637473	TCTCCAGCAGTCTCTCCTC
MSH2.3.2.MSH2.2_F	chr2:47637406-47637540	GGACTGTGTGAATTCCCTGA
MSH2.3.2.MSH2.2_R	chr2:47637406-47637540	CCTTTCCTAGGCCTGGAATC
MSH2.3.11.MSH2.3_F	chr2:47637164-47637316	GGTTCATAGAGTTTGGATTTTTCC
MSH2.3.11.MSH2.3_R	chr2:47637164-47637316	CCATCAACTGCGGACATTTT
MSH2.9.1.MSH2.1_F	chr2:47690170-47690301	GTCACTTTGTTCTGTTTGCAG
MSH2.9.1.MSH2.1_R	chr2:47690170-47690301	ATTCCAACCTCCAATGACCC
MSH2.12.1.MSH2.1_F	chr2:47702254-47702412	GTGTCAAATGGAGCACCTG
MSH2.12.1.MSH2.1_R	chr2:47702254-47702412	AGCCCAAAAACCAGGTTTTT
MSH2.12.9.MSH2.2_F	chr2:47702105-47702255	GGGGGATTAAATGTATTTTTACGGC
MSH2.12.9.MSH2.2_R	chr2:47702105-47702255	ATGGCTGGTCGTACATATGG
MSH2.15.3.MSH2.1_F	chr2:47707832-47707990	ACGCTTCCCCAAATTTCTTA
MSH2.15.3.MSH2.1_R	chr2:47707832-47707990	CCTCTCTTTCCAGATAGCACT
MSH2.15.4.MSH2.2_F	chr2:47707930-47708061	AACAGAAAGCCCTGGAACTT
MSH2.15.4.MSH2.2_R	chr2:47707930-47708061	ACCTTCATCTTAGTGTCCTGT
MSH2.14.5.MSH2.1_F	chr2:47705535-47705684	ACAAAGATTGGTGCTTTTTGC
MSH2.14.5.MSH2.1_R	chr2:47705535-47705684	GTTTCCCATTACCAAGTTCTGA
MSH2.14.6.MSH2.2_F	chr2:47705419-47705565	TATGTGCTTCAGGTCTGCAA
MSH2.14.6.MSH2.2_R	chr2:47705419-47705565	TGGTATCTGATTGGCCAAGG
MSH2.14.7.MSH2.3_F	chr2:47705329-47705469	TTGTGGCATATCCTTCCCAA
MSH2.14.7.MSH2.3_R	chr2:47705329-47705469	TGCTAACCCAAATCCATCGT
MSH2.8.12.MSH2.1_F	chr2:47672697-47672839	ACTACTTTCTTTTAGGAAAACACCA
MSH2.8.12.MSH2.1_R	chr2:47672697-47672839	TCTTAAAGTGGCCTTTGCTT
MSH2.8.13.MSH2.2_F	chr2:47672576-47672708	ACTTTGGAGACCTGCTGTAC
MSH2.8.13.MSH2.2_R	chr2:47672576-47672708	GAGGAGTCACAAAAACTGCC
MSH2.4.14.MSH2.1_F	chr2:47639583-47639812	TCAAAGAGGAGGAATTCTGATCACA
MSH2.4.14.MSH2.1_R	chr2:47639583-47639812	TCATTGATACACAGTTTAGGTTTTGA
MSH2.4.15.MSH2.2_F	chr2:47639437-47639593	ATCAGTGTCTTGCACATTGT
MSH2.4.15.MSH2.2_R	chr2:47639437-47639593	GTCTTTTGTGGAAAAGTCAGCT
MSH2.19.1.MSH2.1_F	chr2:47905291-47905440	TGTCAGTTTGAAGGAGGCAA
MSH2.19.1.MSH2.1_R	chr2:47905291-47905440	TTGTGAGCTTGGCTATGTGA
MSH2.10.5.MSH2.1_F	chr2:47693846-47693994	GATTCCAGTGCACAGTTTGG
MSH2.10.5.MSH2.1_R	chr2:47693846-47693994	ACATTCACATCATGTTAGAGCA
MSH2.5.8.MSH2.1_F	chr2:47641383-47641537	CTGGATCCAGTGGTATAGAAATCT
MSH2.5.8.MSH2.1_R	chr2:47641383-47641537	CCTGAAAAAGGTTAAGGGCTC
MSH2.5.10.MSH2.2_F	chr2:47641487-47641631	TCCAACTTTGGACAGTTTGAAC
MSH2.5.10.MSH2.2_R	chr2:47641487-47641631	GCTCCTTTATAAGCTTCTTCAGT
JAK2.11.1.JAK2.1_F	chr9:5072508-5072660	GAAGAATGAAAGCCTTGGCC
JAK2.11.1.JAK2.1_R	chr9:5072508-5072660	GAGAGCACATCTTTAAACAGCA
JAK2.11.2.JAK2.2_F	chr9:5072453-5072605	TGTTCCTACTTCGTTCTCCA
JAK2.11.2.JAK2.2_R	chr9:5072453-5072605	CCTCTGAATAGTTTCTGTGTGC
JAK2.21.3.JAK2.1_F	chr9:5122961-5123118	GCAGGTAAAATCAAGAGTCCAC
JAK2.21.3.JAK2.1_R	chr9:5122961-5123118	ATAAAAAGCACACTGACCGC
JAK2.21.4.JAK2.2_F	chr9:5123074-5123222	TTTGGAGCTTTGGAGTGGTT
JAK2.21.4.JAK2.2_R	chr9:5123074-5123222	AAAGCTCTGACTTCACCACT
JAK2.7.3.JAK2.1_F	chr9:5064857-5065012	GAGTTGACTTTCTAAAAGGTGC
JAK2.7.3.JAK2.1_R	chr9:5064857-5065012	GCCATGACAGTTGCTTTGTA
JAK2.7.5.JAK2.2_F	chr9:5065000-5065159	GAAGTAGCACCTCCAGCC

JAK2.7.5.JAK2.2_R	chr9:5065000-5065159	CTGATTGCAAATAGCCTTTTGT
JAK2.17.7.JAK2.1_F	chr9:5081692-5081844	AGTCCAGAGAATGTTATTTGCT
JAK2.17.7.JAK2.1_R	chr9:5081692-5081844	TACCTTGCCAAGTTGCTGTA
JAK2.17.8.JAK2.2_F	chr9:5081825-5081980	CGGGATCCTACACAGTTTGA
JAK2.17.8.JAK2.2_R	chr9:5081825-5081980	TCTCCAACATCTGACAACCA
JAK2.2.5.JAK2.1_F	chr9:5029781-5029936	TTCCTTTCTCTGCTTCTTTTCT
JAK2.2.5.JAK2.1_R	chr9:5029781-5029936	CTCCCATTTTGCCTTTTAGCA
JAK2.22.5.JAK2.1_F	chr9:5126335-5126464	TGAAAGTGGGTTTGTTTTAGGA
JAK2.22.5.JAK2.1_R	chr9:5126335-5126464	AAATGCATGACTACCCTGGA
JAK2.22.6.JAK2.2_F	chr9:5126271-5126417	TTCCCATTGACTGGAGGAAA
JAK2.22.6.JAK2.2_R	chr9:5126271-5126417	GCATCCATCTGGTCTTGGTA
JAK2.1.1.JAK2.1_F	chr9:5021998-5022157	AAGACTCTGCATGGGAATGG
JAK2.1.1.JAK2.1_R	chr9:5021998-5022157	CAACATACTCCCCAGATGGA
JAK2.1.2.JAK2.2_F	chr9:5022155-5022311	AATCTGAGGCAGATTATCTGAC
JAK2.1.2.JAK2.2_R	chr9:5022155-5022311	GCCAGCCATACAAGCATTAA
JAK2.1.2.JAK2.3_F	chr9:5021861-5022020	GAGGCTTGTCTCCAACTTCT
JAK2.1.2.JAK2.3_R	chr9:5021861-5022020	GAAGAGGTGGATGTTCCCTC
JAK2.18.1.JAK2.1_F	chr9:5089711-5089866	GAGATGTGCCGGTATGACC
JAK2.18.1.JAK2.1_R	chr9:5089711-5089866	ATAGGTTTCAATGGGCAGCT
JAK2.18.2.JAK2.2_F	chr9:5089587-5089729	ACAGTCTGCTAATTCCAGCT
JAK2.18.2.JAK2.2_R	chr9:5089587-5089729	TTTTTACAGCGACCACCTCC
JAK2.13.16.JAK2.1_F	chr9:5077471-5077680	TGCAGATATTCTGGTTCAGGAGT
JAK2.13.16.JAK2.1_R	chr9:5077471-5077680	ACACAGACTATTTTACATGAATTGGCA
JAK2.13.17.JAK2.2_F	chr9:5077380-5077532	ACCTATAATGGTCACATGTAAGTAT
JAK2.13.17.JAK2.2_R	chr9:5077380-5077532	GTTTAGCAACTTCAAGTTTCCA
JAK2.16.3.JAK2.1_F	chr9:5080496-5080643	AGAAGGTTGGTGTGGCATTA
JAK2.16.3.JAK2.1_R	chr9:5080496-5080643	AGATCTCGTATGATGGCTCT
JAK2.16.4.JAK2.2_F	chr9:5080639-5080782	TGAACCAGATTTCAGGCCTT
JAK2.16.4.JAK2.2_R	chr9:5080639-5080782	TTAAGAGGGCCCAAATGACA
JAK2.23.1.JAK2.1_F	chr9:5126654-5126797	AAGATGGCCCTTAGTGTTCA
JAK2.23.1.JAK2.1_R	chr9:5126654-5126797	TGGTCTCAGAATGAAGGTCA
JAK2.6.7.JAK2.1_F	chr9:5055641-5055768	GGCTCTGTAAATTCTACCCGT
JAK2.6.7.JAK2.1_R	chr9:5055641-5055768	ACCAGATTTTTACCATCTTGCT
JAK2.6.11.JAK2.2_F	chr9:5055754-5055907	GGGTTCAAATGAAAGCCGAG
JAK2.6.11.JAK2.2_R	chr9:5055754-5055907	AGTTTACTGAACTGATGTTTAGAGT
JAK2.3.16.JAK2.1_F	chr9:5044382-5044633	TGAACTATTTGGAAGCTGACCA
JAK2.3.16.JAK2.1_R	chr9:5044382-5044633	ACTTCTCTGCACCTGCTGTG
JAK2.9.1.JAK2.1_F	chr9:5069092-5069246	AATGAAGAGTACAACCTCAGTG
JAK2.9.1.JAK2.1_R	chr9:5069092-5069246	CACGCCACATAAACAATCCA
JAK2.9.2.JAK2.2_F	chr9:5068997-5069139	CCATTGTGACTATCCCTCCC
JAK2.9.2.JAK2.2_R	chr9:5068997-5069139	TGAGCGAACAGTTTCCATCT
JAK2.12.1.JAK2.1_F	chr9:5073671-5073811	TGGACAACAGTCAAACAACA
JAK2.12.1.JAK2.1_R	chr9:5073671-5073811	ACAGATGCTCTGAGAAAGGC
JAK2.14.1.JAK2.1_F	chr9:5078335-5078492	ACACCCTTATTCATGGGAATGT
JAK2.14.1.JAK2.1_R	chr9:5078335-5078492	AACATGCCCTTTACACCACT
JAK2.14.2.JAK2.2_F	chr9:5078271-5078425	ATGCTCCAGTACTTGTGGAC
JAK2.14.2.JAK2.2_R	chr9:5078271-5078425	CTGTCCTTTGGCAAAACTGT
JAK2.15.3.JAK2.1_F	chr9:5080221-5080361	AACCCTACTCTGTTCGTATCA
JAK2.15.3.JAK2.1_R	chr9:5080221-5080361	ACTCTTTGAGAATCCAGAGCA
JAK2.15.4.JAK2.2_F	chr9:5080339-5080475	CCACTTTGTGGGAAATCTGC
JAK2.15.4.JAK2.2_R	chr9:5080339-5080475	TAATGCCACACCAACCTTCT
JAK2.20.5.JAK2.1_F	chr9:5090787-5090944	ATATCCACAGGGATCTGGCA
JAK2.20.5.JAK2.1_R	chr9:5090787-5090944	AAAGTTTGAAGTCTGTGCTCT
JAK2.20.10.JAK2.2_F	chr9:5090685-5090837	AGGGAATATATAGGGTTAAGACCA
JAK2.20.10.JAK2.2_R	chr9:5090685-5090837	GGCAAGACTTTGGTTAACCC
JAK2.8.10.JAK2.1_F	chr9:5066641-5066789	CACTTGGTCATAATATTATGGTGCT
JAK2.8.10.JAK2.1_R	chr9:5066641-5066789	CCACTAATAAGTGTGACATACTAAC
JAK2.4.11.JAK2.1_F	chr9:5050693-5050836	TTTTTGGTTTTAGTGGCGGC
JAK2.4.11.JAK2.1_R	chr9:5050693-5050836	TGTGTAAGGATTTGCAAAAGAAA
JAK2.4.12.JAK2.2_F	chr9:5050582-5050723	AGCCTGGCCAATTTGTATCT
JAK2.4.12.JAK2.2_R	chr9:5050582-5050723	TCCTGTGTTTCATGAGTCACA
JAK2.10.16.JAK2.1_F	chr9:5069889-5070112	TGGAGCAATTCATACTTTCAGTGT
JAK2.10.16.JAK2.1_R	chr9:5069889-5070112	TCCAATGTCACATGAATGTAAATCA
JAK2.19.1.JAK2.1_F	chr9:5090456-5090594	ATGTTAAAAGGTCGGCGTAA
JAK2.19.1.JAK2.1_R	chr9:5090456-5090594	ACACGGTTGCTTCATCTACA
JAK2.19.9.JAK2.2_F	chr9:5090433-5090581	GGCAGAGTAAAACATTATTTCCACC
JAK2.19.9.JAK2.2_R	chr9:5090433-5090581	GCTTCATCTACAGCAAATAATCAGG

JAK2.5.13.JAK2.1_F	chr9:5054550-5054685	TGTTTTGTTTTTCTGTATGTGCT
JAK2.5.13.JAK2.1_R	chr9:5054550-5054685	ACTTAAGTTTCAAGTTTCTGGCA
JAK2.5.14.JAK2.2_F	chr9:5054681-5054835	AGCAATTCAGCCAATGCAAA
JAK2.5.14.JAK2.2_R	chr9:5054681-5054835	GTTTCCCTCTTGACCACTGA
JAK2.5.15.JAK2.3_F	chr9:5054811-5054967	GTGAGGAGATTTTTGCAACCA
JAK2.5.15.JAK2.3_R	chr9:5054811-5054967	TGGGAGAAGTGCAATACCAT
PIK3R1.11.6.PIK3R1.1_F	chr5:67589187-67589340	TCGAGATGGGAAATATGGCT
PIK3R1.11.6.PIK3R1.1_R	chr5:67589187-67589340	AAGGATCTTGTCTAAACATCGT
PIK3R1.11.7.PIK3R1.2_F	chr5:67589041-67589200	CACTAAGGTAAGCCAGGGAA
PIK3R1.11.7.PIK3R1.2_R	chr5:67589041-67589200	TCAACCACAGAACTGAAGGT
PIK3R1.7.1.PIK3R1.1_F	chr5:67584507-67584642	ACTTGGTGGAAGAACAGCTT
PIK3R1.7.1.PIK3R1.1_R	chr5:67584507-67584642	ACACACACGTACTCCAAGAC
PIK3R1.2.1.PIK3R1.1_F	chr5:67569163-67569310	TGTACGTCCTTCATTGTGGT
PIK3R1.2.1.PIK3R1.1_R	chr5:67569163-67569310	CCCTCTAGCAGTCTGGTTAC
PIK3R1.17.1.PIK3R1.1_F	chr5:67593247-67593409	CTCTCCTCTCTAGGGTGGAC
PIK3R1.17.1.PIK3R1.1_R	chr5:67593247-67593409	TCGCCTCTGCTGTGCAT
PIK3R1.17.2.PIK3R1.2_F	chr5:67593363-67593509	CATTACCAACACACCTCCCT
PIK3R1.17.2.PIK3R1.2_R	chr5:67593363-67593509	TCTGCAGCTCAATTCACAGA
PIK3R1.17.2.PIK3R1.3_F	chr5:67593194-67593342	TGCCCTGAAGAGTTGTGAAT
PIK3R1.17.2.PIK3R1.3_R	chr5:67593194-67593342	AGGGAGGTGTGTTGGTAATG
PIK3R1.1.1.PIK3R1.1_F	chr5:67522522-67522683	CATGAGTGCTGAGGGGTAC
PIK3R1.1.1.PIK3R1.1_R	chr5:67522522-67522683	CCCTTTCCCCTGTGGTTTC
PIK3R1.1.2.PIK3R1.2_F	chr5:67522496-67522626	ACTGTTGCATGGTAGCAGAT
PIK3R1.1.2.PIK3R1.2_R	chr5:67522496-67522626	GCTTCCTGTCCATCACTGAA
PIK3R1.1.2.PIK3R1.3_F	chr5:67522702-67522852	ATGAAACCACAGGGGAAAGG
PIK3R1.1.2.PIK3R1.3_R	chr5:67522702-67522852	AGGGAGTCATTAAGCAACCA
PIK3R1.1.3.PIK3R1.4_F	chr5:67522643-67522794	TGGATTCAGTGATGGACAGG
PIK3R1.1.3.PIK3R1.4_R	chr5:67522643-67522794	GTTTTCGAAGAACCTGGTGC
PIK3R1.13.1.PIK3R1.1_F	chr5:67590382-67590511	GCAGGAAATCCAAATGAAAAGG
PIK3R1.13.1.PIK3R1.1_R	chr5:67590382-67590511	GCACAAGAACAAGGGAAACA
PIK3R1.13.2.PIK3R1.2_F	chr5:67590308-67590440	ATGTCCTGGTAGTGTCTTGC
PIK3R1.13.2.PIK3R1.2_R	chr5:67590308-67590440	ATTCTTTGCTGTACCGCTCT
PIK3R1.16.1.PIK3R1.1_F	chr5:67592069-67592227	AGACATGGAATGTTGGAAGC
PIK3R1.16.1.PIK3R1.1_R	chr5:67592069-67592227	CCCCCAAAACTCAATGAATGA
PIK3R1.16.2.PIK3R1.2_F	chr5:67591940-67592080	GTATGCCTAGGGAAGACAGC
PIK3R1.16.2.PIK3R1.2_R	chr5:67591940-67592080	CGCAACAGGTTTTCAGCTTT
PIK3R1.6.9.PIK3R1.1_F	chr5:67576745-67576893	GGGAAAAGGTTTCTAATAAACTCTC
PIK3R1.6.9.PIK3R1.1_R	chr5:67576745-67576893	TCAAAGGAGGTTTATAGCCATCA
PIK3R1.3.1.PIK3R1.1_F	chr5:67569731-67569877	GTTCTCCAGAGAGCTGTGTT
PIK3R1.3.1.PIK3R1.1_R	chr5:67569731-67569877	AACAGAAAGCCAAGACCTGT
PIK3R1.9.1.PIK3R1.1_F	chr5:67588073-67588231	GGGATTGCGAACAACTTTTTC
PIK3R1.9.1.PIK3R1.1_R	chr5:67588073-67588231	AGCTGGTGCTTTTCTTTCTT
PIK3R1.12.10.PIK3R1.1_F	chr5:67589491-67589740	TGTCAGCTATTTTGTTAAACAATTGTT
PIK3R1.12.10.PIK3R1.1_R	chr5:67589491-67589740	CCTCATTCGTAAAAACTCAACCT
PIK3R1.14.4.PIK3R1.1_F	chr5:67590976-67591132	TACGTTTCTTTTGCCTGCAG
PIK3R1.14.4.PIK3R1.1_R	chr5:67590976-67591132	ACATCAAGTATTGGTCTCTCGT
PIK3R1.14.5.PIK3R1.2_F	chr5:67591129-67591268	CCAGACCTTATCCAGCTGAG
PIK3R1.14.5.PIK3R1.2_R	chr5:67591129-67591268	CGTTCAACTTCTTTTGCCGA
PIK3R1.15.8.PIK3R1.1_F	chr5:67591210-67591334	TGGTGATTGCTACAATTCAGG
PIK3R1.15.8.PIK3R1.1_R	chr5:67591210-67591334	GAGAAAAATCTTCTGCTATCACCA
PIK3R1.8.1.PIK3R1.1_F	chr5:67586543-67586684	ATAACTGAGCTCAGCCAAGG
PIK3R1.8.1.PIK3R1.1_R	chr5:67586543-67586684	GCCACGAAATTAACTAACTCTC
PIK3R1.4.1.PIK3R1.1_F	chr5:67575443-67575597	TTCCTAGATACACCCTCCGT
PIK3R1.4.1.PIK3R1.1_R	chr5:67575443-67575597	GCACCTCTACATCTCCATGT
PIK3R1.4.2.PIK3R1.2_F	chr5:67575380-67575524	GTTCAGAAAATTAGCCCAACTG
PIK3R1.4.2.PIK3R1.2_R	chr5:67575380-67575524	ATTTCACTGTAAACGGCTGC
PIK3R1.10.1.PIK3R1.1_F	chr5:67588900-67589029	TCTGTGGTCACTAAACCTTAAG
PIK3R1.10.1.PIK3R1.1_R	chr5:67588900-67589029	TCAGCTATATTCCCTGGCTT
PIK3R1.5.1.PIK3R1.1_F	chr5:67576386-67576545	AGCTCCGAAGAATATATTCAGC
PIK3R1.5.1.PIK3R1.1_R	chr5:67576386-67576545	ACTTACCTGGCTGCTGAG
PIK3R1.5.2.PIK3R1.2_F	chr5:67576489-67576642	CTCTCTCAAACCTCCAGCAA
PIK3R1.5.2.PIK3R1.2_R	chr5:67576489-67576642	GCACATGCATCTCTGGAGTA
PIK3R1.5.2.PIK3R1.3_F	chr5:67576236-67576395	TACTGTGTGCTTCTCCCAAC
PIK3R1.5.2.PIK3R1.3_R	chr5:67576236-67576395	TGCTAGGCGACCTAATAAGC
NOTCH1.33.1.NOTCH1.1_F	chr9:139438406-139438565	AATGGCCTAGTGTTCTGTCC
NOTCH1.33.1.NOTCH1.1_R	chr9:139438406-139438565	GACTGACCTCTCTTCTCCTG
NOTCH1.32.1.NOTCH1.1_F	chr9:139418278-139418440	TTGTCCAGGGGTGTCAG

NOTCH1.32.1.NOTCH1.1_R	chr9:139418278-139418440	CTAACTGCCCTGGCACATC
NOTCH1.32.10.NOTCH1.2_F	chr9:139418162-139418305	CTCAGGCTGTGGGTCCT
NOTCH1.32.10.NOTCH1.2_R	chr9:139418162-139418305	CAGACTATGCCTGCAGCTG
NOTCH1.21.1.NOTCH1.1_F	chr9:139407835-139408000	CACTGAGAAACGCGCAG
NOTCH1.21.1.NOTCH1.1_R	chr9:139407835-139408000	TCGACCTGCAGTGTGGT
NOTCH1.7.10.NOTCH1.1_F	chr9:139396730-139396893	CGTCCGCTCACTTGAGG
NOTCH1.7.10.NOTCH1.1_R	chr9:139396730-139396893	GCAGCTGCACTTCATGTAC
NOTCH1.7.11.NOTCH1.2_F	chr9:139396883-139397044	GAACAGAAGCACAAAGGCG
NOTCH1.7.11.NOTCH1.2_R	chr9:139396883-139397044	ATGGAGGAGAGTGGGTGAG
NOTCH1.7.11.NOTCH1.3_F	chr9:139396600-139396761	TAGGAAGCCCCCAGAGA
NOTCH1.7.11.NOTCH1.3_R	chr9:139396600-139396761	TGAGGCCAGCAAGAAGAAG
NOTCH1.26.13.NOTCH1.1_F	chr9:139411686-139411843	TCAGGAGGCCAGGGTG
NOTCH1.26.13.NOTCH1.1_R	chr9:139411686-139411843	CTCACTGTTGCCCCACC
NOTCH1.2.1.NOTCH1.1_F	chr9:139393304-139393448	TTTGGCCCTCACTTCTCTG
NOTCH1.2.1.NOTCH1.1_R	chr9:139393304-139393448	CATCTGCTTCTTTCACGCAG
NOTCH1.17.1.NOTCH1.1_F	chr9:139404201-139404364	CACCTCTCTGTGCAGTCAG
NOTCH1.17.1.NOTCH1.1_R	chr9:139404201-139404364	GGCATCAACACGGCCTT
NOTCH1.17.2.NOTCH1.2_F	chr9:139404339-139404499	GTCCTCCTCACAGAAAGTGC
NOTCH1.17.2.NOTCH1.2_R	chr9:139404339-139404499	AACGAAAGGCTGGGCTG
NOTCH1.17.2.NOTCH1.3_F	chr9:139404047-139404205	ACAGGTCGGTACAATGAACA
NOTCH1.17.2.NOTCH1.3_R	chr9:139404047-139404205	GGGATCCACTGTGAGAACAA
NOTCH1.1.1.NOTCH1.1_F	chr9:139390541-139390703	TTTACTTGAAGGCCTCCGG
NOTCH1.1.1.NOTCH1.1_R	chr9:139390541-139390703	TCCTCGCCTGTGGACAA
NOTCH1.1.2.NOTCH1.2_F	chr9:139390447-139390595	TAAAAAGGCTCCTCTGGTCG
NOTCH1.1.2.NOTCH1.2_R	chr9:139390447-139390595	ATTCCAACGTCTCCGACTG
NOTCH1.1.2.NOTCH1.3_F	chr9:139390984-139391148	CAGGCTTTGCTGCTGCT
NOTCH1.1.2.NOTCH1.3_R	chr9:139390984-139391148	TGCAGCATGGCATGGTAG
NOTCH1.1.3.NOTCH1.4_F	chr9:139390829-139390983	CTCTCCTGGGGCAGAATAGT
NOTCH1.1.3.NOTCH1.4_R	chr9:139390829-139390983	GCAGCCAGCAAACATCC
NOTCH1.1.3.NOTCH1.5_F	chr9:139391317-139391480	ACAGTGAAATTCAGGGCCC
NOTCH1.1.3.NOTCH1.5_R	chr9:139391317-139391480	AACCACCTGCCTGGGAT
NOTCH1.1.4.NOTCH1.6_F	chr9:139390718-139390879	GTGTTGTCCACAGGCGA
NOTCH1.1.4.NOTCH1.6_R	chr9:139390718-139390879	GAGCTTCCTGAGTGGAGAG
NOTCH1.1.4.NOTCH1.7_F	chr9:139391498-139391663	ATCCCAGGCAGGTGGTT
NOTCH1.1.4.NOTCH1.7_R	chr9:139391498-139391663	AAGGAGGCCAAGGACCT
NOTCH1.1.5.NOTCH1.8_F	chr9:139390677-139390812	TGAGGAAGGGGTGCTCA
NOTCH1.1.5.NOTCH1.8_R	chr9:139390677-139390812	CACACTATTCTGCCCCAGG
NOTCH1.1.5.NOTCH1.9_F	chr9:139391664-139391828	TTCTTCCTCCGTGCCTTG
NOTCH1.1.5.NOTCH1.9_R	chr9:139391664-139391828	TACAACCTGGTGCGCAG
NOTCH1.1.5.NOTCH1.10_F	chr9:139391396-139391554	AGGTGGGCCAGTCTCAAA
NOTCH1.1.5.NOTCH1.10_R	chr9:139391396-139391554	CCATGGCTACCTGTCAGAC
NOTCH1.1.6.NOTCH1.11_F	chr9:139391144-139391297	AGCAAGGCTACTGTGCAG
NOTCH1.1.6.NOTCH1.11_R	chr9:139391144-139391297	GGGCCCTGAATTTCACTGT
NOTCH1.1.7.NOTCH1.12_F	chr9:139391234-139391377	AGAGGGTTGTATTGGTTCGG
NOTCH1.1.7.NOTCH1.12_R	chr9:139391234-139391377	TTTGAGACTGGCCCACCT
NOTCH1.1.10.NOTCH1.13_F	chr9:139391898-139392058	GCTCCTGTGCGATGTCG
NOTCH1.1.10.NOTCH1.13_R	chr9:139391898-139392058	AACCTTGGGGAGGGTCC
NOTCH1.1.11.NOTCH1.14_F	chr9:139391759-139391906	TTGAGGCTGCCCAGGTA
NOTCH1.1.11.NOTCH1.14_R	chr9:139391759-139391906	ATCACGGATCATATGGACCG
NOTCH1.18.6.NOTCH1.1_F	chr9:139405082-139405229	TGAGAGCTTCCTGGAGGAG
NOTCH1.18.6.NOTCH1.1_R	chr9:139405082-139405229	GTGAGGTCGACATCAACGA
NOTCH1.18.8.NOTCH1.2_F	chr9:139405200-139405354	TGGGTGTTCTGGCAGGAT
NOTCH1.18.8.NOTCH1.2_R	chr9:139405200-139405354	GTCACGGAAGCCTACTCCT
NOTCH1.30.1.NOTCH1.1_F	chr9:139413904-139414042	TATACGCGCCTGTCCACT
NOTCH1.30.1.NOTCH1.1_R	chr9:139413904-139414042	ACTGGACCTCAGGGAAGAG
NOTCH1.30.2.NOTCH1.2_F	chr9:139413837-139413968	ATGCCTGTGAGTGCAGTTTA
NOTCH1.30.2.NOTCH1.2_R	chr9:139413837-139413968	ATCGACGATTGTCCAGGAAA
NOTCH1.16.10.NOTCH1.1_F	chr9:139403342-139403505	CAGTTGGGGCCAGTGT
NOTCH1.16.10.NOTCH1.1_R	chr9:139403342-139403505	CTCCTGCTTCAACGGTGG
NOTCH1.16.11.NOTCH1.2_F	chr9:139403440-139403601	ACTCATTGACATCGTGCTGG
NOTCH1.16.11.NOTCH1.2_R	chr9:139403440-139403601	TTGAGCAGAAGGGGAGGT
NOTCH1.16.12.NOTCH1.3_F	chr9:139403261-139403418	GTGACCGTTCCCACCTC
NOTCH1.16.12.NOTCH1.3_R	chr9:139403261-139403418	CAGCACGATGTCAATGAGTG
NOTCH1.25.13.NOTCH1.1_F	chr9:139410404-139410568	TGTCCCGTCCCCAGTC
NOTCH1.25.13.NOTCH1.1_R	chr9:139410404-139410568	CTGTTGCACATGACTCCCT
NOTCH1.27.1.NOTCH1.1_F	chr9:139412274-139412435	TTCTGGCACGGGTTCGA
NOTCH1.27.1.NOTCH1.1_R	chr9:139412274-139412435	TGCAGTGAGGTGTTGCAG

NOTCH1.27.2.NOTCH1.2_F	chr9:139412137-139412277	GAAGCAACCCACAGATGTTC
NOTCH1.27.2.NOTCH1.2_R	chr9:139412137-139412277	AGATCGACGTCAACGAGTG
NOTCH1.28.6.NOTCH1.1_F	chr9:139412541-139412696	GACTTCTCATCGGTTCTGGG
NOTCH1.28.6.NOTCH1.1_R	chr9:139412541-139412696	ATCAGCAACCCCTGTAACG
NOTCH1.28.8.NOTCH1.2_F	chr9:139412678-139412812	CTTGCCATTGACAGGGTTG
NOTCH1.28.8.NOTCH1.2_R	chr9:139412678-139412812	TGTCAGTGGGGTTGGAC
NOTCH1.20.10.NOTCH1.1_F	chr9:139407480-139407620	CCACCCCTCACCTGTGTA
NOTCH1.20.10.NOTCH1.1_R	chr9:139407480-139407620	CAAGGTGCCTGGGAGTG
NOTCH1.20.11.NOTCH1.2_F	chr9:139407348-139407508	CTTTACCCTCCAGTCACGG
NOTCH1.20.11.NOTCH1.2_R	chr9:139407348-139407508	CACGTGTATTGACGACGTTG
NOTCH1.14.1.NOTCH1.1_F	chr9:139402443-139402599	AGGTAGTCCGTGCAGGT
NOTCH1.14.1.NOTCH1.1_R	chr9:139402443-139402599	ACCTGTCTACCACCCCATC
NOTCH1.14.2.NOTCH1.2_F	chr9:139402321-139402481	GGGCCTATCAGGTTCAGTTT
NOTCH1.14.2.NOTCH1.2_R	chr9:139402321-139402481	CAGCTACTGTGAGGACCTG
NOTCH1.24.1.NOTCH1.1_F	chr9:139409964-139410126	CTTCAGGCAGAAGCAGAGG
NOTCH1.24.1.NOTCH1.1_R	chr9:139409964-139410126	TGGACATCGATGAGTGCG
NOTCH1.24.2.NOTCH1.2_F	chr9:139410039-139410191	ACTCGTTGATGTTGGTCTCG
NOTCH1.24.2.NOTCH1.2_R	chr9:139410039-139410191	GCCAGTCCTAAGTCTTCCTG
NOTCH1.24.2.NOTCH1.3_F	chr9:139409853-139410011	TTGATCTCGCAGTTGGGTC
NOTCH1.24.2.NOTCH1.3_R	chr9:139409853-139410011	AACATCAACGAGTGCTCCAG
NOTCH1.10.1.NOTCH1.1_F	chr9:139399772-139399935	AGCCTTACTTGCACTGGC
NOTCH1.10.1.NOTCH1.1_R	chr9:139399772-139399935	CAGTGCAACAACCACGC
NOTCH1.10.2.NOTCH1.2_F	chr9:139399732-139399880	CACATCCAAGTTCAGGTCCT
NOTCH1.10.2.NOTCH1.2_R	chr9:139399732-139399880	TCAATGACCCCTGGAAGAAC
NOTCH1.10.2.NOTCH1.3_F	chr9:139399956-139400115	GTGGTTGTTGCACTGCAG
NOTCH1.10.2.NOTCH1.3_R	chr9:139399956-139400115	ACATCCGAGAGCCCCTT
NOTCH1.10.3.NOTCH1.4_F	chr9:139399911-139400052	GGGTCATTGAAGTTGAGGGA
NOTCH1.10.3.NOTCH1.4_R	chr9:139399911-139400052	CACATCCTGGACTACAGCTT
NOTCH1.10.3.NOTCH1.5_F	chr9:139400126-139400291	ACGGTAGAAGGGGCTCT
NOTCH1.10.3.NOTCH1.5_R	chr9:139400126-139400291	ATGACGCTCGTACCTGC
NOTCH1.10.4.NOTCH1.6_F	chr9:139400276-139400425	ATGTGCCGCCGTTGA
NOTCH1.10.4.NOTCH1.6_R	chr9:139400276-139400425	CCTCCCAGGTTAGAGGAGAG
NOTCH1.10.4.NOTCH1.7_F	chr9:139399972-139400127	AGGCTGCAGACCTTGTTG
NOTCH1.10.4.NOTCH1.7_R	chr9:139399972-139400127	ACCTGTGAGCCCACATC
NOTCH1.31.1.NOTCH1.1_F	chr9:139417507-139417640	CTTCTGGCCACACTCGTT
NOTCH1.31.1.NOTCH1.1_R	chr9:139417507-139417640	CTTGTCCCCTTGTCTCCAG
NOTCH1.31.8.NOTCH1.2_F	chr9:139417332-139417495	ACACTCGTGGGTGACGT
NOTCH1.31.8.NOTCH1.2_R	chr9:139417332-139417495	AGGATGTCAACGAGTGTGG
NOTCH1.31.9.NOTCH1.3_F	chr9:139417465-139417629	ACCTCGTTGTGGCAGGT
NOTCH1.31.9.NOTCH1.3_R	chr9:139417465-139417629	TCTCCAGGGAAATCGTGC
NOTCH1.31.13.NOTCH1.4_F	chr9:139417190-139417356	CATCCCGCCTTCCCAAC
NOTCH1.31.13.NOTCH1.4_R	chr9:139417190-139417356	CTCGCCCTGCCAGAAC
NOTCH1.11.10.NOTCH1.1_F	chr9:139400934-139401097	ACGTGGACCTCTCCAGG
NOTCH1.11.10.NOTCH1.1_R	chr9:139400934-139401097	CTCACTGCCCTGCTCTTAC
NOTCH1.22.6.NOTCH1.1_F	chr9:139408949-139409114	TGTGTCCCCATGATCGG
NOTCH1.22.6.NOTCH1.1_R	chr9:139408949-139409114	GATGAGTGTGCGGGCAA
NOTCH1.22.7.NOTCH1.2_F	chr9:139409083-139409214	CAGGTGAAGCCATTGATGC
NOTCH1.22.7.NOTCH1.2_R	chr9:139409083-139409214	AACAGACAGGGAAATCGAGG
NOTCH1.13.1.NOTCH1.1_F	chr9:139401735-139401889	ATGGATGGCCAACACCAG
NOTCH1.13.1.NOTCH1.1_R	chr9:139401735-139401889	TTCTGTCGCCTGCACAG
NOTCH1.23.1.NOTCH1.1_F	chr9:139409712-139409865	CTTGACCTCTGAGCACAGTG
NOTCH1.23.1.NOTCH1.1_R	chr9:139409712-139409865	AGGACTGACCGACACGT
NOTCH1.29.1.NOTCH1.1_F	chr9:139413071-139413235	ATGGGGACACTCGCAGTA
NOTCH1.29.1.NOTCH1.1_R	chr9:139413071-139413235	ACGAGTGCCAGCTGATG
NOTCH1.29.2.NOTCH1.2_F	chr9:139413188-139413322	TTGACACACACGCAGTTGTA
NOTCH1.29.2.NOTCH1.2_R	chr9:139413188-139413322	TCTTAGGGGACAGGGAGCT
NOTCH1.29.2.NOTCH1.3_F	chr9:139412994-139413129	TGAGGTCACACAGCTCAGG
NOTCH1.29.2.NOTCH1.3_R	chr9:139412994-139413129	CTGCAGCGAGAACATTGATG
NOTCH1.6.1.NOTCH1.1_F	chr9:139396388-139396548	ACATAGAGGGAGTGAGCAGA
NOTCH1.6.1.NOTCH1.1_R	chr9:139396388-139396548	CTCACTTCTCGACCCCTCA
NOTCH1.3.1.NOTCH1.1_F	chr9:139393577-139393739	GCTCACCCAGGTCATCTAC
NOTCH1.3.1.NOTCH1.1_R	chr9:139393577-139393739	TGTACGTCTGCCCAGCA
NOTCH1.3.2.NOTCH1.2_F	chr9:139393463-139393593	CTTGCCTGCGTGAAAGAAG
NOTCH1.3.2.NOTCH1.2_R	chr9:139393463-139393593	GGAGGACCTCATCAACTCAC
NOTCH1.9.6.NOTCH1.1_F	chr9:139399102-139399247	GAGAGTTGCGGGGATTGAC
NOTCH1.9.6.NOTCH1.1_R	chr9:139399102-139399247	CGCAAGCACCCCATCAA
NOTCH1.9.10.NOTCH1.2_F	chr9:139399348-139399514	ACGTTGGTGTGCAGCA

NOTCH1.9.10.NOTCH1.2_R	chr9:139399348-139399514	GACCACTTCAGCGACGG
NOTCH1.9.12.NOTCH1.3_F	chr9:139399508-139399663	CTGTTGCAGCCCTGGTC
NOTCH1.9.12.NOTCH1.3_R	chr9:139399508-139399663	CAGTTCTAAGGCTCTGCTCA
NOTCH1.9.12.NOTCH1.4_F	chr9:139399204-139399363	AGCGAGGCCTTCACCT
NOTCH1.9.12.NOTCH1.4_R	chr9:139399204-139399363	CAGCTCCTTCCACTTCCTG
NOTCH1.12.1.NOTCH1.1_F	chr9:139401267-139401431	TGGACAGGCACTCGTTGA
NOTCH1.12.1.NOTCH1.1_R	chr9:139401267-139401431	ACTGACGAAACCTGGCC
NOTCH1.12.10.NOTCH1.2_F	chr9:139401117-139401274	GTAAGAGCAGGGCAGTGAG
NOTCH1.12.10.NOTCH1.2_R	chr9:139401117-139401274	TGGGTGAGCGCTGTGA
NOTCH1.15.1.NOTCH1.1_F	chr9:139402684-139402842	TGGGCACAGCAGGTTAC
NOTCH1.15.1.NOTCH1.1_R	chr9:139402684-139402842	CAGCTGACCCCAATCTGTC
NOTCH1.8.1.NOTCH1.1_F	chr9:139397491-139397650	GCGGAGTGCCATTCAGAAAA
NOTCH1.8.1.NOTCH1.1_R	chr9:139397491-139397650	AGCCTCAACATCCCCTACAA
NOTCH1.8.2.NOTCH1.2_F	chr9:139397636-139397789	GATGGGGCCACACTTACTC
NOTCH1.8.2.NOTCH1.2_R	chr9:139397636-139397789	CAGCCCCTCTCTGATTGTC
NOTCH1.8.2.NOTCH1.3_F	chr9:139397379-139397537	CCAACAAAGAAAATTCAGGAGG
NOTCH1.8.2.NOTCH1.3_R	chr9:139397379-139397537	TTTGTGCCAGTTGCTACCC
NOTCH1.8.3.NOTCH1.4_F	chr9:139397219-139397378	CAACTTCAAATCGCTGCACT
NOTCH1.8.3.NOTCH1.4_R	chr9:139397219-139397378	GCTTCTCTCCCCACCCTTT
NOTCH1.4.1.NOTCH1.1_F	chr9:139395024-139395185	GGAAGACACCTTGTGCGT
NOTCH1.4.1.NOTCH1.1_R	chr9:139395024-139395185	GACTTCATCTACCAGGGCG
NOTCH1.4.2.NOTCH1.2_F	chr9:139395176-139395311	TGCGGTCTGTCTGGTTG
NOTCH1.4.2.NOTCH1.2_R	chr9:139395176-139395311	AGACTGAGCACCCGTCT
NOTCH1.4.2.NOTCH1.3_F	chr9:139394895-139395056	ACCAGTTGTCCCGGACT
NOTCH1.4.2.NOTCH1.3_R	chr9:139394895-139395056	CAACATCCAGGACAACATGG
NOTCH1.34.14.NOTCH1.1_F	chr9:139440140-139440342	CCGCCAAAGTTTCCAAAGGG
NOTCH1.34.14.NOTCH1.1_R	chr9:139440140-139440342	GGAAGAGAGGGCGGGACC
NOTCH1.19.1.NOTCH1.1_F	chr9:139405573-139405724	AGACATCCTGACCTCCCATC
NOTCH1.19.1.NOTCH1.1_R	chr9:139405573-139405724	TGTGTCTCCTTCCCGCA
NOTCH1.5.1.NOTCH1.1_F	chr9:139396230-139396367	ACATTGACGTCCATGCAGT
NOTCH1.5.1.NOTCH1.1_R	chr9:139396230-139396367	TCTGCTCACTCCCTCTATGT
NOTCH1.5.2.NOTCH1.2_F	chr9:139396103-139396264	GCTCTCACCCCCAATTCTAA
NOTCH1.5.2.NOTCH1.2_R	chr9:139396103-139396264	CTGCGCATGTCTGCCAT
FGFR1.11.1.FGFR1.1_F	chr8:38279174-38279335	GGATTCAGCCCTCAAAGCT
FGFR1.11.1.FGFR1.1_R	chr8:38279174-38279335	GGACTCTCCCATCACTCTG
FGFR1.11.2.FGFR1.2_F	chr8:38279326-38279469	AGTGTGTACCTTCCAGAACG
FGFR1.11.2.FGFR1.2_R	chr8:38279326-38279469	TGTCCATTTTGCTTCCGTTG
FGFR1.11.2.FGFR1.3_F	chr8:38279158-38279305	TCTTCTCTGAGCTGAGAGGA
FGFR1.11.2.FGFR1.3_R	chr8:38279158-38279305	CGTTCTGGAAGGTACACACT
FGFR1.7.1.FGFR1.1_F	chr8:38274789-38274946	CAGCTCAGATCTTCTCCCC
FGFR1.7.1.FGFR1.1_R	chr8:38274789-38274946	CCCAAGTAAATGAGTCTCAACG
FGFR1.2.4.FGFR1.1_F	chr8:38271423-38271566	AGCTCTGGCTCTGGCA
FGFR1.2.4.FGFR1.1_R	chr8:38271423-38271566	TATCCATCTCCAGGAGACGT
FGFR1.17.1.FGFR1.1_F	chr8:38297747-38297905	TAAAAGGAGCACAGAACAGC
FGFR1.17.1.FGFR1.1_R	chr8:38297747-38297905	ATTTTTGGGGCTCTCTCCAC
FGFR1.1.1.FGFR1.1_F	chr8:38271161-38271323	AGTCAGCGGCGTTTGAG
FGFR1.1.1.FGFR1.1_R	chr8:38271161-38271323	TTCCTCTCGCCCATCACA
FGFR1.1.2.FGFR1.2_F	chr8:38271114-38271273	GGTGAGGGTTACAGCTGAC
FGFR1.1.2.FGFR1.2_R	chr8:38271114-38271273	CAGTACTCCCCCAGCTTTC
FGFR1.18.1.FGFR1.1_F	chr8:38314924-38315068	TGCAGAGTGTGGCTGTG
FGFR1.18.1.FGFR1.1_R	chr8:38314924-38315068	CCCTCCTAACTTTTGGGGTT
FGFR1.18.2.FGFR1.2_F	chr8:38314812-38314970	ACCTGCAACCATATCACCTC
FGFR1.18.2.FGFR1.2_R	chr8:38314812-38314970	CACCAACCTCTAACTGCAGA
FGFR1.16.1.FGFR1.1_F	chr8:38287199-38287360	CAGGGCTTGGCTACCAA
FGFR1.16.1.FGFR1.1_R	chr8:38287199-38287360	GATGTGCAGAGCATCAACTG
FGFR1.16.2.FGFR1.2_F	chr8:38287344-38287505	GTTGCTTTCCGCCAGCT
FGFR1.16.2.FGFR1.2_R	chr8:38287344-38287505	TCTCCCTGTCTTCCTCTCTC
FGFR1.13.1.FGFR1.1_F	chr8:38283613-38283767	GGCTCTTCCCACTAAACTCA
FGFR1.13.1.FGFR1.1_R	chr8:38283613-38283767	TATCCCTTTGGCATTTCCCC
FGFR1.6.1.FGFR1.1_F	chr8:38273388-38273547	GAGCCTTCAGGTTCCACAC
FGFR1.6.1.FGFR1.1_R	chr8:38273388-38273547	GTCATCGTGGAGTATGCCTC
FGFR1.6.2.FGFR1.2_F	chr8:38273501-38273630	GGGGTTGTAGCAGTATTCCA
FGFR1.6.2.FGFR1.2_R	chr8:38273501-38273630	GGGTTTCTTTGAGGTGAAGC
FGFR1.3.1.FGFR1.1_F	chr8:38271670-38271828	GACATCTCCTCGGGCTTAC
FGFR1.3.1.FGFR1.1_R	chr8:38271670-38271828	GGAGAAGCTCTAACACCCTG
FGFR1.9.1.FGFR1.1_F	chr8:38275731-38275892	TGCCTTCAAAAAGTTGGGAG
FGFR1.9.1.FGFR1.1_R	chr8:38275731-38275892	ACCCCACTCTTCCTTGCA

FGFR1.12.1.FGFR1.1_F	chr8:38281837-38282002	CTGTTCCCAGCTCACCT
FGFR1.12.1.FGFR1.1_R	chr8:38281837-38282002	TGGCACCAGTCTTCGTG
FGFR1.12.2.FGFR1.2_F	chr8:38282000-38282162	GTCTCCTTCCCAGTAGACTG
FGFR1.12.2.FGFR1.2_R	chr8:38282000-38282162	CCCGCCAACAAAACAGT
FGFR1.12.2.FGFR1.3_F	chr8:38281745-38281885	GTCCAAATGCCTTCCTTGTG
FGFR1.12.2.FGFR1.3_R	chr8:38281745-38281885	CACACACACTCCATCTCAGT
FGFR1.12.3.FGFR1.4_F	chr8:38282105-38282253	ATGTGCTTTAGCCACTGGAT
FGFR1.12.3.FGFR1.4_R	chr8:38282105-38282253	CTCTTTAGCCATGGCAAGGT
FGFR1.14.1.FGFR1.1_F	chr8:38285435-38285598	CTTTCGCATGCACACACAC
FGFR1.14.1.FGFR1.1_R	chr8:38285435-38285598	GCAGCCGTAGCTCCATA
FGFR1.14.2.FGFR1.2_F	chr8:38285462-38285618	GTAGCCTCCAATTCTGTGGT
FGFR1.14.2.FGFR1.2_R	chr8:38285462-38285618	CTGTCTCTCTTGGCTTTCCC
FGFR1.15.1.FGFR1.1_F	chr8:38285847-38286000	GACCCAAAGGGCAGTAAGAT
FGFR1.15.1.FGFR1.1_R	chr8:38285847-38286000	TGCACTAGCCTTGGTGAAAT
FGFR1.8.1.FGFR1.1_F	chr8:38275358-38275516	TGCTTGGAATGGGACAAGAT
FGFR1.8.1.FGFR1.1_R	chr8:38275358-38275516	TATGCCACTCTCTGTTTCCC
FGFR1.4.1.FGFR1.1_F	chr8:38271986-38272148	TTTCTCTCTGGGGCAGAAAG
FGFR1.4.1.FGFR1.1_R	chr8:38271986-38272148	CCCCTGTGCTGCTTTCA
FGFR1.10.1.FGFR1.1_F	chr8:38277081-38277240	CGCAGAGGGATGCTCTT
FGFR1.10.1.FGFR1.1_R	chr8:38277081-38277240	ACTCAGCCCTGGAAGAGAG
FGFR1.10.2.FGFR1.2_F	chr8:38277204-38277345	GCCCCTGTGCAATAGATGAT
FGFR1.10.2.FGFR1.2_R	chr8:38277204-38277345	CTCCCTAAAAGTTCCCAGGG
FGFR1.10.2.FGFR1.3_F	chr8:38277048-38277183	GTGCAAATCCCCCATCTACT
FGFR1.10.2.FGFR1.3_R	chr8:38277048-38277183	ATCATCTATTGCACAGGGGC
FGFR1.19.1.FGFR1.1_F	chr8:38318531-38318669	CTAGGCTCCTGGGATTCATG
FGFR1.19.1.FGFR1.1_R	chr8:38318531-38318669	CTCCAGTGAGAAGACAGCAG
FGFR1.5.1.FGFR1.1_F	chr8:38272272-38272421	TCTCAGATGAAACCACCAGC
FGFR1.5.1.FGFR1.1_R	chr8:38272272-38272421	CTCTCCCTTCCTCCTTCCTC
CYP2C9.8.1.CYP2C9.1_F	chr10:96745800-96745946	TTGTTTCTAGGGCACAACCA
CYP2C9.8.1.CYP2C9.1_R	chr10:96745800-96745946	ACCCTGAAACACAAATGGAA
CYP2C9.8.2.CYP2C9.2_F	chr10:96745675-96745808	GGAAATGGTACTGCCCTTCT
CYP2C9.8.2.CYP2C9.2_R	chr10:96745675-96745808	ATGTAGCACAGAAGTCAGGG
CYP2C9.6.1.CYP2C9.1_F	chr10:96731881-96732040	GAAAAGCACAACCAACCATC
CYP2C9.6.1.CYP2C9.1_R	chr10:96731881-96732040	GCAACACCTTCCCAAAATCT
CYP2C9.6.4.CYP2C9.2_F	chr10:96731770-96731914	ACTTTCCAGTTTCTATGTTGGT
CYP2C9.6.4.CYP2C9.2_R	chr10:96731770-96731914	CCAGCTCCAAACAAGTCAAC
CYP2C9.1.1.CYP2C9.1_F	chr10:96698450-96698607	AGAAGGCTTCAATGGATTCTC
CYP2C9.1.1.CYP2C9.1_R	chr10:96698450-96698607	CCACTGAAGGAGCATACTTAC
CYP2C9.1.2.CYP2C9.2_F	chr10:96698380-96698537	ACACACCGAATTAGCATGGA
CYP2C9.1.2.CYP2C9.2_R	chr10:96698380-96698537	CAATCACTGGGAGAGGAGTG
CYP2C9.4.1.CYP2C9.1_F	chr10:96707551-96707699	TTTAGCCTCACCCTGTGATC
CYP2C9.4.1.CYP2C9.1_R	chr10:96707551-96707699	GGAAGCAAAAATCTTGGCCT
CYP2C9.4.2.CYP2C9.2_F	chr10:96707421-96707576	ATGCATGCCGAACTCTTTTT
CYP2C9.4.2.CYP2C9.2_R	chr10:96707421-96707576	ATGGAGCAGATCACATTGCA
CYP2C9.3.1.CYP2C9.1_F	chr10:96701963-96702106	CCTGTTAGGAATTGTTTTCAGC
CYP2C9.3.1.CYP2C9.1_R	chr10:96701963-96702106	GGTCAGTGATATGGAGTAGGG
CYP2C9.3.2.CYP2C9.2_F	chr10:96701836-96701969	GATGGGGAGGATGGAAAACA
CYP2C9.3.2.CYP2C9.2_R	chr10:96701836-96701969	CCGGATCTCCTTCCATTTCT
CYP2C9.7.1.CYP2C9.1_F	chr10:96740980-96741139	GAACGTGTGATTGGCAGAAA
CYP2C9.7.1.CYP2C9.1_R	chr10:96740980-96741139	ATGGAGTTGCAGTGTAGGAG
CYP2C9.7.2.CYP2C9.2_F	chr10:96740890-96741033	ACCCCTGAATTGCTACAACA
CYP2C9.7.2.CYP2C9.2_R	chr10:96740890-96741033	GTATCTCTGGACCTCGTGC
CYP2C9.9.1.CYP2C9.1_F	chr10:96748623-96748783	GGAAAACGGATTTGTGTGGG
CYP2C9.9.1.CYP2C9.1_R	chr10:96748623-96748783	AGGCCATCTGCTCTTCTTC
CYP2C9.9.2.CYP2C9.2_F	chr10:96748775-96748923	CTTCTACCAGCTGTGCTTCA
CYP2C9.9.2.CYP2C9.2_R	chr10:96748775-96748923	TCCGTAATGGAGGTCGAATG
CYP2C9.9.2.CYP2C9.3_F	chr10:96748571-96748704	ACTGTCACAGTTACGCATGA
CYP2C9.9.2.CYP2C9.3_R	chr10:96748571-96748704	GGAGTGGTGTCAAGGTTCTT
CYP2C9.2.1.CYP2C9.1_F	chr10:96701625-96701783	CTACTTTCCTAGCTCTCAAAGG
CYP2C9.2.1.CYP2C9.1_R	chr10:96701625-96701783	CTGAAACAGGCACATGCAC
CYP2C9.2.2.CYP2C9.2_F	chr10:96701572-96701720	TCAGGCTTAGCAAATGGACA
CYP2C9.2.2.CYP2C9.2_R	chr10:96701572-96701720	GCCTCTTCCAGAAAACTCCT
CYP2C9.5.1.CYP2C9.1_F	chr10:96708905-96709058	CCTATCATTGATTACTTCCCGG
CYP2C9.5.1.CYP2C9.1_R	chr10:96708905-96709058	ACAAGCAGTCACATAACTAAGC
CYP2C9.5.3.CYP2C9.2_F	chr10:96708815-96708969	CCAGAGCTTGGTATATGGTATG
CYP2C9.5.3.CYP2C9.2_R	chr10:96708815-96708969	TGTCCATTGATTCTTGGTGTTC
MET.11.1.MET.1_F	chr7:116399461-116399620	CAGTGGTGGGAGCACAATA

MET.11.1.MET.1_R	chr7:116399461-116399620	AAAGGCGAAACTGAGATGTC
MET.11.2.MET.2_F	chr7:116399583-116399715	GGTTCTACTCAGAGCTCTGC
MET.11.2.MET.2_R	chr7:116399583-116399715	TTTCCACATGGTTAGCCCAA
MET.11.2.MET.3_F	chr7:116399345-116399487	TTGATGTTGACTGTGCCTCT
MET.11.2.MET.3_R	chr7:116399345-116399487	ACCATTCTCGGGACACTAAC
MET.21.1.MET.1_F	chr7:116435694-116435851	TCTCACCTCATCTGTCCTGT
MET.21.1.MET.1_R	chr7:116435694-116435851	ACGTAAGAGGTACAGAAAGACT
MET.7.1.MET.1_F	chr7:116395418-116395576	TGTCCTTGTAGGTTTTCCCA
MET.7.1.MET.1_R	chr7:116395418-116395576	CCCCAGCAAAGCATTTTAAGA
MET.7.10.MET.2_F	chr7:116395266-116395417	TGTGACCCTTTTCCCTTTAGT
MET.7.10.MET.2_R	chr7:116395266-116395417	CCTTCAAGGGGTGCACTATT
MET.17.1.MET.1_F	chr7:116417443-116417594	CCAAGTTCTTTCTTTTGCACAG
MET.17.1.MET.1_R	chr7:116417443-116417594	GGGGAAAGTGTAAATCAACGT
MET.2.1.MET.1_F	chr7:116339125-116339284	CCTTGAACCTGTTTTGGCAG
MET.2.1.MET.1_R	chr7:116339125-116339284	TGACATTCTGGATGGGTGTT
MET.2.2.MET.2_F	chr7:116339395-116339555	AGAAGGTTGCTGAGTACAAGA
MET.2.2.MET.2_R	chr7:116339395-116339555	ACATGTCGCTGGCAGGT
MET.2.3.MET.3_F	chr7:116339280-116339409	ATCAGCTTCCCAACTTCACC
MET.2.3.MET.3_R	chr7:116339280-116339409	TGGGAAACAATCTGGGTGTT
MET.2.3.MET.4_F	chr7:116339596-116339755	TCCCCACAATCATACTGCTG
MET.2.3.MET.4_R	chr7:116339596-116339755	AATGCAATGGATGATCTGGG
MET.2.4.MET.5_F	chr7:116339542-116339701	TCAACTCATTAGCTGTGGCA
MET.2.4.MET.5_R	chr7:116339542-116339701	AGTTGATGAACCGGTCCTTT
MET.2.4.MET.6_F	chr7:116339846-116340005	ACGGACCAGTCCTACATTGA
MET.2.4.MET.6_R	chr7:116339846-116340005	AGAGGCATTTCCATGTAGGA
MET.2.5.MET.7_F	chr7:116340005-116340165	GTTCCATAAACTCTGGATTGCA
MET.2.5.MET.7_R	chr7:116340005-116340165	TTGTGCGAACACCCCGA
MET.2.5.MET.8_F	chr7:116339725-116339883	GGACCGGTTCATCAACTTCT
MET.2.5.MET.8_R	chr7:116339725-116339883	GCTTTCAAAGGCATGGACAT
MET.2.6.MET.9_F	chr7:116340179-116340340	TCTTTTCGGGGTGTTCGC
MET.2.6.MET.9_R	chr7:116340179-116340340	GTGGGGAACTGATGTGACTT
MET.2.7.MET.10_F	chr7:116340034-116340189	GGAAATGCCTCTGGAGTGTA
MET.2.7.MET.10_R	chr7:116340034-116340189	CATTGGTTCGGCAGAATCTG
MET.22.1.MET.1_F	chr7:116435970-116436131	ATGCTAAAATGCTGGCACC
MET.22.1.MET.1_R	chr7:116435970-116436131	CGTGTGTCCACCTCATCAT
MET.22.2.MET.2_F	chr7:116436072-116436203	TGTCCATGTGAACGCTACTT
MET.22.2.MET.2_R	chr7:116436072-116436203	ACCATTGGACAAAGTGTGGA
MET.22.2.MET.3_F	chr7:116435904-116436051	TACAGAAATGCCTGCCTTCA
MET.22.2.MET.3_R	chr7:116435904-116436051	AAGTAGCGTTCACATGGACA
MET.1.1.MET.1_F	chr7:116335808-116335965	ACTTCCTTCTTCACAGGGTG
MET.1.1.MET.1_R	chr7:116335808-116335965	CACTGGGGGTACAGGTTATG
MET.18.1.MET.1_F	chr7:116418858-116419014	CTGACATAGGAGAAGTTTCCCA
MET.18.1.MET.1_R	chr7:116418858-116419014	AGTAAGCTTGGCAGTCAACT
MET.18.2.MET.2_F	chr7:116418725-116418862	GTCAAACCCTCAGGACAAGA
MET.18.2.MET.2_R	chr7:116418725-116418862	CATGATGATTCCCTCGGTCA
MET.13.1.MET.1_F	chr7:116409799-116409954	TTCTGAAGCCGTTTTATGCA
MET.13.1.MET.1_R	chr7:116409799-116409954	GAATGCAGGCTGAGTTGATG
MET.13.2.MET.2_F	chr7:116409666-116409815	TTCCTGCAGAACTGTGAAGT
MET.13.2.MET.2_R	chr7:116409666-116409815	AGCTCGCTGTTCAATTTCAG
MET.16.1.MET.1_F	chr7:116415061-116415218	CCATTACTGCAAAATACTGTCC
MET.16.1.MET.1_R	chr7:116415061-116415218	AATCTGCAAAGGCCAAAGAT
MET.16.8.MET.2_F	chr7:116414896-116415053	TCAGTCCCCATTAAATGAGGT
MET.16.8.MET.2_R	chr7:116414896-116415053	CTGAGGTCAATGTGGACAGT
MET.16.9.MET.3_F	chr7:116414970-116415101	CATCTCAGAACGGTTCATGC
MET.16.9.MET.3_R	chr7:116414970-116415101	CCAATCACTACATGCTGCAC
MET.6.1.MET.1_F	chr7:116381056-116381215	CGGGACATGGACTCAACAG
MET.6.1.MET.1_R	chr7:116381056-116381215	AGCTGATGACTCACAGCTAA
MET.6.2.MET.2_F	chr7:116380904-116381058	TTTCCACCCCTTCTCTTCAC
MET.6.2.MET.2_R	chr7:116380904-116381058	TTGTAGATTGCAGGCAGACA
MET.3.1.MET.1_F	chr7:116364766-116364903	GCAAGGGAAGCTTTTGGAAG
MET.3.1.MET.1_R	chr7:116364766-116364903	AGGCACTGAGTGTTCACATT
MET.9.1.MET.1_F	chr7:116397740-116397899	AATACGGTCCTATGGCTGGT
MET.9.1.MET.1_R	chr7:116397740-116397899	CCACACACACACACAAAACA
MET.9.2.MET.2_F	chr7:116397604-116397759	TTCTCCTATGTGGTAAGGAAGA
MET.9.2.MET.2_R	chr7:116397604-116397759	CCCACTGTTTAGGTAATTTCCA
MET.12.8.MET.1_F	chr7:116403070-116403203	TGGATGTTGCCAAGCTGTAT
MET.12.8.MET.1_R	chr7:116403070-116403203	TGGAAAGGATCCCATCTAACA

MET.12.11.MET.2_F	chr7:116403233-116403388	TGGGATCCTTTCCAAATACTTT
MET.12.11.MET.2_R	chr7:116403233-116403388	GGCCAAGTACAACAATTGTATT
MET.12.12.MET.3_F	chr7:116403120-116403279	CTAGGCATGTCAACATCGCT
MET.12.12.MET.3_R	chr7:116403120-116403279	TGCCCATTGAGATCATCACT
MET.14.8.MET.1_F	chr7:116411534-116411678	CATGGCTAAATGCTGACTTTTC
MET.14.8.MET.1_R	chr7:116411534-116411678	GCTTTCTCTTTTTCAGCCACA
MET.14.9.MET.2_F	chr7:116411633-116411778	TCACAGGATTGATTGCTGGT
MET.14.9.MET.2_R	chr7:116411633-116411778	AGACAGCACACAAGAATCGA
MET.20.1.MET.1_F	chr7:116423378-116423532	AGGCTGGATGAAAAATTCACAG
MET.20.1.MET.1_R	chr7:116423378-116423532	AGGAGAAACTCAGAGATAACCA
MET.20.2.MET.2_F	chr7:116423245-116423383	AGGCCAGATGAAATACTTCCT
MET.20.2.MET.2_R	chr7:116423245-116423383	GGCAAGACCAAAATCAGCAA
MET.15.1.MET.1_F	chr7:116411922-116412078	AGATCTGGGCAGTGAATTAGT
MET.15.1.MET.1_R	chr7:116411922-116412078	ACAACCCACTGAGGTATATGT
MET.15.2.MET.2_F	chr7:116411799-116411953	TCGATTCTTGTGTGCTGTCT
MET.15.2.MET.2_R	chr7:116411799-116411953	GGCACTTACAAGCCTATCCA
MET.8.1.MET.1_F	chr7:116397511-116397667	GATTGAAATGCACAGTTGGTC
MET.8.1.MET.1_R	chr7:116397511-116397667	GGAGGGGAGATAAAAACAAAAC
MET.8.2.MET.2_F	chr7:116397408-116397544	GCAGTCAGCTCACCATTTAG
MET.8.2.MET.2_R	chr7:116397408-116397544	TCCCGTGGCCATTTGAAATA
MET.4.1.MET.1_F	chr7:116371772-116371932	GCGCCGTGATGAATATCG
MET.4.1.MET.1_R	chr7:116371772-116371932	CCAGATAGAACAGACACAGCT
MET.4.2.MET.2_F	chr7:116371643-116371796	CCATTATCCTCCAGGCTCTG
MET.4.2.MET.2_R	chr7:116371643-116371796	CCCATGAATAAGTCAACGCG
MET.19.1.MET.1_F	chr7:116422042-116422187	TTCTAACTCTCTTTGACTGCAG
MET.19.1.MET.1_R	chr7:116422042-116422187	ACAGATTCCTCCTTGTCACT
MET.10.1.MET.1_F	chr7:116398526-116398677	TGTTCAGTGTGTCAAACAGT
MET.10.1.MET.1_R	chr7:116398526-116398677	ACCCATCAGAAGCTTCTACT
MET.10.2.MET.2_F	chr7:116398402-116398531	AGAAAAGGCTTCCACTCAGG
MET.10.2.MET.2_R	chr7:116398402-116398531	TGGGCTGGGGTATAACATTC
MET.5.1.MET.1_F	chr7:116380014-116380168	TGCTGTTTAGGTTGTGGTTT
MET.5.1.MET.1_R	chr7:116380014-116380168	GCATTTGGGAAAAACCACGT
MET.5.2.MET.2_F	chr7:116379921-116380059	ACAAGCCCTGCTAATCTGTT
MET.5.2.MET.2_R	chr7:116379921-116380059	CTTCTGGAGACACTGGATGG
CHEK2.6.1.CHEK2.1_F	chr22:29092881-29093039	AGCCACATACAGAATGCCAA
CHEK2.6.1.CHEK2.1_R	chr22:29092881-29093039	TGTGAGATGTGTGTGTTGGT
CHEK2.11.8.CHEK2.1_F	chr22:29115337-29115477	TGAGAAACCACCAATCACAAA
CHEK2.11.8.CHEK2.1_R	chr22:29115337-29115477	ACCCATTTCTACTCTTTTCTTCC
CHEK2.3.9.CHEK2.1_F	chr22:29089989-29090214	CAGCAGGGCTTCCCATGTAT
CHEK2.3.9.CHEK2.1_R	chr22:29089989-29090214	TGTCTGCTGACTCCGTGATG
CHEK2.7.1.CHEK2.1_F	chr22:29095808-29095964	GAAAGGCAGCTGTCAAAAGA
CHEK2.7.1.CHEK2.1_R	chr22:29095808-29095964	TTCTGTCCAAGTGCGTTTTC
CHEK2.9.9.CHEK2.1_F	chr22:29105909-29106125	CCACCACACCTGGCCAATAT
CHEK2.9.9.CHEK2.1_R	chr22:29105909-29106125	CTCAGGCAGCCTTGAGTCAA
CHEK2.12.6.CHEK2.1_F	chr22:29120929-29121083	CCTCCTATGAGAGAGTGGAAA
CHEK2.12.6.CHEK2.1_R	chr22:29120929-29121083	GGGTCCTAAAAACTCTTACATTGC
CHEK2.12.7.CHEK2.2_F	chr22:29121076-29121224	TCCATTGCCACTGTGATCTT
CHEK2.12.7.CHEK2.2_R	chr22:29121076-29121224	TTCGGATTTTCAGGGTAGGT
CHEK2.2.1.CHEK2.1_F	chr22:29085095-29085254	GCTCCTTAAGCCCAGACTAC
CHEK2.2.1.CHEK2.1_R	chr22:29085095-29085254	TGCTAGCCCTGTCATTCTAG
CHEK2.14.1.CHEK2.1_F	chr22:29126402-29126554	GGAAAGACCCACAGCTAACA
CHEK2.14.1.CHEK2.1_R	chr22:29126402-29126554	CGTGGCTGGCCTAACTTTTT
CHEK2.15.1.CHEK2.1_F	chr22:29130411-29130570	CCAAGATTGGCAAATCCATCC
CHEK2.15.1.CHEK2.1_R	chr22:29130411-29130570	TCCTCTACCAGCACGATGC
CHEK2.15.2.CHEK2.2_F	chr22:29130571-29130727	GAGGACTGGCTGGAGTTTG
CHEK2.15.2.CHEK2.2_R	chr22:29130571-29130727	TCACCTTTGTTGTTGGACAC
CHEK2.15.2.CHEK2.3_F	chr22:29130324-29130466	TCCAATCAGAACCTTCCACC
CHEK2.15.2.CHEK2.3_R	chr22:29130324-29130466	CTGAGGACCAAGAACCTGAG
CHEK2.8.1.CHEK2.1_F	chr22:29099425-29099584	TGAGAAAGGCAAGCCTACAT
CHEK2.8.1.CHEK2.1_R	chr22:29099425-29099584	CCTCTTGGGAGTTTCTCACT
CHEK2.1.5.CHEK2.1_F	chr22:29083881-29084039	TCTTTCGTGTTCAAACCACG
CHEK2.1.5.CHEK2.1_R	chr22:29083881-29084039	ACTGGAAGCATATTGAGGAAC
CHEK2.4.3.CHEK2.1_F	chr22:29091076-29091220	CACCACAGCACATACACATT
CHEK2.4.3.CHEK2.1_R	chr22:29091076-29091220	ACCAATATTAAGCCTTAGTGGG
CHEK2.4.4.CHEK2.2_F	chr22:29091220-29091379	ATGCTCAGAGAAAGGTGGAT
CHEK2.4.4.CHEK2.2_R	chr22:29091220-29091379	GTGCTGGGATTACAAGCCTA
CHEK2.10.1.CHEK2.1_F	chr22:29107891-29108048	GGTGATCAGCCTTTTATTGGT

CHEK2.10.1.CHEK2.1_R	chr22:29107891-29108048	CAGGAGTGGTAGGTCTCATAA
CHEK2.13.1.CHEK2.1_F	chr22:29121218-29121372	AGCTCTCCTAGATACATGGGT
CHEK2.13.1.CHEK2.1_R	chr22:29121218-29121372	ATTCAACAGCCCTCTGATGC
CHEK2.5.1.CHEK2.1_F	chr22:29091738-29091879	TAAACTCCAGCAGTCCACAG
CHEK2.5.1.CHEK2.1_R	chr22:29091738-29091879	TGGCAAGTTCAACATTATTCCC
CHEK2.5.2.CHEK2.2_F	chr22:29091612-29091751	CAAGATCAAGCCACTGCATG
CHEK2.5.2.CHEK2.2_R	chr22:29091612-29091751	CTTGTTTCTGTTGGGACTGC
VKORC1.1.1.VKORC1.1_F	chr16:31102451-31102614	AGCCTGGCTTGGGTTGA
VKORC1.1.1.VKORC1.1_R	chr16:31102451-31102614	ATGCTGCTGAGCTCCCT
VKORC1.1.2.VKORC1.2_F	chr16:31102582-31102732	AGAGCACGAAGAACAGGATC
VKORC1.1.2.VKORC1.2_R	chr16:31102582-31102732	CTGGCATCTAGGTAGTGCAG
VKORC1.4.1.VKORC1.1_F	chr16:31105888-31106047	TGCACACCTGGAGGAGA
VKORC1.4.1.VKORC1.1_R	chr16:31105888-31106047	GGCGGAACCTGGAGATAATG
VKORC1.4.2.VKORC1.2_F	chr16:31106014-31106176	CGTCAGGCAAAGAGCGA
VKORC1.4.2.VKORC1.2_R	chr16:31106014-31106176	TGGAACAGCCATTTGGGTC
VKORC1.4.2.VKORC1.3_F	chr16:31105836-31105974	TAATCATCTGGCATCCTGGC
VKORC1.4.2.VKORC1.3_R	chr16:31105836-31105974	CTTAGTGCTCTCGCTCTACG
VKORC1.3.1.VKORC1.1_F	chr16:31104641-31104770	GGAGCCACTCACCTAACAAT
VKORC1.3.1.VKORC1.1_R	chr16:31104641-31104770	GGGTTGACAGTCCTAACCTG
VKORC1.3.2.VKORC1.2_F	chr16:31104488-31104647	CCTGTTAGTTACCTCCCCAC
VKORC1.3.2.VKORC1.2_R	chr16:31104488-31104647	CGGTTGCATCTTCTACACAC
VKORC1.2.1.VKORC1.1_F	chr16:31104082-31104212	TTTTCCACAAAACTGGGGTG
VKORC1.2.1.VKORC1.1_R	chr16:31104082-31104212	CACCACTATGCCCAGCTAAT
MLH1.11.1.MLH1.1_F	chr3:37061819-37061961	ACAGTTTAGAAATCAGTCCCCA
MLH1.11.1.MLH1.1_R	chr3:37061819-37061961	AAGTAGCTGGATGAGAAGCG
MLH1.11.2.MLH1.2_F	chr3:37061702-37061839	AGGTTTTGACCACTGTGTCA
MLH1.11.2.MLH1.2_R	chr3:37061702-37061839	GAACTTCATGCTTTGTGGGG
MLH1.7.1.MLH1.1_F	chr3:37053266-37053417	GGGCTCTGACATCTAGTGTG
MLH1.7.1.MLH1.1_R	chr3:37053266-37053417	ACCTTATCTCCACCAGCAAA
MLH1.17.1.MLH1.1_F	chr3:37090006-37090163	TTGTCCTTTTTCCTGCAAGC
MLH1.17.1.MLH1.1_R	chr3:37090006-37090163	CCAGATCAAAGGGTGGTCAT
MLH1.2.1.MLH1.1_F	chr3:37038082-37038238	ACATTAGAGTAGTTGCAGACTG
MLH1.2.1.MLH1.1_R	chr3:37038082-37038238	AGGTCCTGACTCTTCCATGA
MLH1.1.1.MLH1.1_F	chr3:37035026-37035182	TCTAGACGTTTCCTTGGCTC
MLH1.1.1.MLH1.1_R	chr3:37035026-37035182	CCGTTAAGTCGTAGCCCTTA
MLH1.18.1.MLH1.1_F	chr3:37090404-37090537	CTTTGGACCAGGTGAATTGG
MLH1.18.1.MLH1.1_R	chr3:37090404-37090537	ATGAGGTCCTGTCCTAGTCC
MLH1.18.2.MLH1.2_F	chr3:37090270-37090426	AGCAATATTCAGCAGTCCCA
MLH1.18.2.MLH1.2_R	chr3:37090270-37090426	CGCATTCTTTACTGAGGCTT
MLH1.13.1.MLH1.1_F	chr3:37070291-37070450	GCAGAAAGAGACATCGGGAA
MLH1.13.1.MLH1.1_R	chr3:37070291-37070450	CAGTTGAGGCCCTATGCAT
MLH1.13.2.MLH1.2_F	chr3:37070191-37070322	CAGCACAGAGAAGTTGCTTG
MLH1.13.2.MLH1.2_R	chr3:37070191-37070322	CTGCAGTCATTTCCTTTCGG
MLH1.16.1.MLH1.1_F	chr3:37089010-37089169	TCATGTTCTTGCTTCTTCCTAG
MLH1.16.1.MLH1.1_R	chr3:37089010-37089169	ATGGCTGTCACACCTCAT
MLH1.16.2.MLH1.2_F	chr3:37089153-37089312	GCTGAGATGCTTGCAGACTA
MLH1.16.2.MLH1.2_R	chr3:37089153-37089312	GGTTTCATCATGTTGGCCAG
MLH1.6.1.MLH1.1_F	chr3:37050250-37050404	CTTTTGCCAGGACATCTTGG
MLH1.6.1.MLH1.1_R	chr3:37050250-37050404	AGACCCACTCCCAGATTTTG
MLH1.3.6.MLH1.1_F	chr3:37042415-37042565	GAGATTTGGAAAAATGAGTAACATG
MLH1.3.6.MLH1.1_R	chr3:37042415-37042565	CATCACAGGAGGATATTTTACACA
MLH1.9.6.MLH1.1_F	chr3:37055918-37056054	TCAAAAGCTTCAGAATCTCTTTTCT
MLH1.9.6.MLH1.1_R	chr3:37055918-37056054	CCTGTGAGTGGATTTCCCAT
MLH1.12.1.MLH1.1_F	chr3:37067148-37067311	CTTTGCTACCAGGACTTGC
MLH1.12.1.MLH1.1_R	chr3:37067148-37067311	TGTGACAATGGCCTGGG
MLH1.12.2.MLH1.2_F	chr3:37067311-37067471	CAAACCCCTGTCCAGTCAG
MLH1.12.2.MLH1.2_R	chr3:37067311-37067471	TGCTGGAAGTAGGTCCTCTC
MLH1.12.2.MLH1.3_F	chr3:37067038-37067176	TAGTACTGCTCCATTTGGGG
MLH1.12.2.MLH1.3_R	chr3:37067038-37067176	AGACGAGGTCAGACTTGTTG
MLH1.12.3.MLH1.4_F	chr3:37067424-37067580	GAAGTGGCTGCCAAAAATCA
MLH1.12.3.MLH1.4_R	chr3:37067424-37067580	AGGCAGAGAGAAGATGCAAG
MLH1.14.1.MLH1.1_F	chr3:37081632-37081790	AATGAAGTGGGGTTGGTAGG
MLH1.14.1.MLH1.1_R	chr3:37081632-37081790	TTGTTCACACACTCAGCTGA
MLH1.20.1.MLH1.1_F	chr3:37107060-37107191	AAACCGATGTGTATAGGCCC
MLH1.20.1.MLH1.1_R	chr3:37107060-37107191	GCATAAGGGCTGAGACTCAA
MLH1.15.4.MLH1.1_F	chr3:37083712-37083862	GTCCCAACTGGTTGTATCTCA
MLH1.15.4.MLH1.1_R	chr3:37083712-37083862	GGAGAGCTACTATTTTCAGAAACG

MLH1.8.5.MLH1.1_F	chr3:37053492-37053643	TCCTTGTGTCTTCTGCTGTT
MLH1.8.5.MLH1.1_R	chr3:37053492-37053643	GGTTCCAAAATAATGTGATGGAATG
MLH1.4.1.MLH1.1_F	chr3:37045865-37046014	ACCCAGCAGTGAGTTTTTCT
MLH1.4.1.MLH1.1_R	chr3:37045865-37046014	ACTCTGAGACCTAGGCAAAA
MLH1.10.1.MLH1.1_F	chr3:37058971-37059106	CCCCTCAGGACAGTTTTGAA
MLH1.10.1.MLH1.1_R	chr3:37058971-37059106	TGTGAGTCTTGGTTGAGGAG
MLH1.19.1.MLH1.1_F	chr3:37091997-37092156	TGAAGTGCCTGGCTCCAT
MLH1.19.1.MLH1.1_R	chr3:37091997-37092156	AACACATCCCACAGTGCAT
MLH1.19.2.MLH1.2_F	chr3:37092105-37092241	GGAAATATCCTGCAGCTTGC
MLH1.19.2.MLH1.2_R	chr3:37092105-37092241	AGTCTTAAGTGCTACCAACACT
MLH1.19.2.MLH1.3_F	chr3:37091937-37092084	GACACCAGTGTATGTTGGGA
MLH1.19.2.MLH1.3_R	chr3:37091937-37092084	GCAAGCTGCAGGATATTTCC
MLH1.5.1.MLH1.1_F	chr3:37048431-37048568	TTTTCTCTTTTCCCCTTGGG
MLH1.5.1.MLH1.1_R	chr3:37048431-37048568	GCTTCAACAATTTACTCTCCCA
GATA3.1.6.GATA3.1_F	chr10:8097629-8097795	CGAGGCCATGGAGGTGA
GATA3.1.6.GATA3.1_R	chr10:8097629-8097795	CGTAGTAGGGCGGGAC
GATA3.1.7.GATA3.2_F	chr10:8097786-8097941	GCTTTTTAACATCGACGGTCA
GATA3.1.7.GATA3.2_R	chr10:8097786-8097941	CTTTCGCTTGACCTCTCCC
GATA3.1.8.GATA3.3_F	chr10:8097510-8097670	CCGAAAGCAAATCATTCAACG
GATA3.1.8.GATA3.3_R	chr10:8097510-8097670	TGCTGCCCGTTGAGCA
GATA3.4.1.GATA3.1_F	chr10:8111433-8111569	TCTCCTCTCTCCCCACTCT
GATA3.4.1.GATA3.1_R	chr10:8111433-8111569	CTGTTCTTGCTGATCCCAGT
GATA3.3.1.GATA3.1_F	chr10:8105950-8106102	GTGGCTTATCTGTGCTTTTGT
GATA3.3.1.GATA3.1_R	chr10:8105950-8106102	CATCCCTTCCCGAGAACTTA
GATA3.2.1.GATA3.1_F	chr10:8100307-8100467	CCTCTGCTTCATGGATCCC
GATA3.2.1.GATA3.1_R	chr10:8100307-8100467	AAGGTGAAGAGGTGCGG
GATA3.2.2.GATA3.2_F	chr10:8100243-8100372	ACTCACCCTCCTTCTCTCTC
GATA3.2.2.GATA3.2_R	chr10:8100243-8100372	GATGGACGTCTTGGAGAAGG
GATA3.2.3.GATA3.3_F	chr10:8100596-8100760	AAGTACCAGGTGCCCCT
GATA3.2.3.GATA3.3_R	chr10:8100596-8100760	ACTTGCATCCGAAGCCG
GATA3.2.4.GATA3.4_F	chr10:8100715-8100847	CTACGTGCCCGAGTACA
GATA3.2.4.GATA3.4_R	chr10:8100715-8100847	CCCTGGATTGAGGAAAAGGG
GATA3.2.5.GATA3.5_F	chr10:8100451-8100604	CCTCGTCCTCCTCCTTGT
GATA3.2.5.GATA3.5_R	chr10:8100451-8100604	GGACGACTCCAGCTTCATG
GATA3.5.1.GATA3.1_F	chr10:8115722-8115881	AGATTAACAGACCCCTGACTAT
GATA3.5.1.GATA3.1_R	chr10:8115722-8115881	ATGTGGCTGGAGTGGCT
GATA3.5.2.GATA3.2_F	chr10:8115865-8116025	AGACACATGTCCTCCCTGA
GATA3.5.2.GATA3.2_R	chr10:8115865-8116025	AAGTCGAAAGGGACTGCAG
GATA3.5.2.GATA3.3_F	chr10:8115593-8115722	GCCAGCTGAAATGGAAACAG
GATA3.5.2.GATA3.3_R	chr10:8115593-8115722	GTCTGGATGCCTTCCTTCTT
PIK3CA.11.9.PIK3CA.1_F	chr3:178937326-178937481	CATTCACAACTATCTTTCCCCT
PIK3CA.11.9.PIK3CA.1_R	chr3:178937326-178937481	ACTGAGAAAGTTTGTCATCTGT
PIK3CA.11.10.PIK3CA.2_F	chr3:178937476-178937603	CTGTTCGGTGCTTGGAAAAA
PIK3CA.11.10.PIK3CA.2_R	chr3:178937476-178937603	GCATAAAACTAGTTAGTGCAGTAGG
PIK3CA.7.1.PIK3CA.1_F	chr3:178928002-178928161	TCCATTGGCATGGGGAAATA
PIK3CA.7.1.PIK3CA.1_R	chr3:178928002-178928161	AGAGAAGGTTTGACTGCCAT
PIK3CA.7.2.PIK3CA.2_F	chr3:178927920-178928053	CCTTTTGGGGAAGAAAAGTGT
PIK3CA.7.2.PIK3CA.2_R	chr3:178927920-178928053	CATGAGGTACTGGCCAAAGA
PIK3CA.17.1.PIK3CA.1_F	chr3:178947130-178947289	GGTGGTGCGAAATTCTCAC
PIK3CA.17.1.PIK3CA.1_R	chr3:178947130-178947289	TCAGAGGAATACACAAACACC
PIK3CA.17.2.PIK3CA.2_F	chr3:178947060-178947194	AACGTGTTACTCCTCTTTCAG
PIK3CA.17.2.PIK3CA.2_R	chr3:178947060-178947194	TGTCTTTGAGCCACTGATGT
PIK3CA.2.1.PIK3CA.1_F	chr3:178917577-178917724	CTGAACGTTTGTAAAGAAGCTG
PIK3CA.2.1.PIK3CA.1_R	chr3:178917577-178917724	ACACAGGTAGAAGACTGCAC
PIK3CA.2.8.PIK3CA.2_F	chr3:178917441-178917585	ACATGTTCATGCTGTGTATGT
PIK3CA.2.8.PIK3CA.2_R	chr3:178917441-178917585	ATGAGGTGAATTGAGGTCCC
PIK3CA.1.1.PIK3CA.1_F	chr3:178916674-178916833	ACTTGATGCCCCCAAGAATC
PIK3CA.1.1.PIK3CA.1_R	chr3:178916674-178916833	TTCCCTTTCTGCTTCTTGAG
PIK3CA.1.2.PIK3CA.2_F	chr3:178916555-178916711	TAGGTTTCTGCTTTGGGACA
PIK3CA.1.2.PIK3CA.2_R	chr3:178916555-178916711	CCTCACGGAGGCATTCTAAA
PIK3CA.1.2.PIK3CA.3_F	chr3:178916853-178917006	ACTCAAGAAGCAGAAAGGGA
PIK3CA.1.2.PIK3CA.3_R	chr3:178916853-178917006	GAAAGGGACAACAGTTAAGCT
PIK3CA.1.3.PIK3CA.4_F	chr3:178916789-178916924	AGCAAGAAAATACCCCCTCC
PIK3CA.1.3.PIK3CA.4_R	chr3:178916789-178916924	TTTCTTCACGGTTGCCTACT
PIK3CA.18.4.PIK3CA.1_F	chr3:178947753-178947899	TCAAGTTGGCCTGAATCACT
PIK3CA.18.4.PIK3CA.1_R	chr3:178947753-178947899	GAAAACCATTACTTGTCCATCG
PIK3CA.18.5.PIK3CA.2_F	chr3:178947878-178948029	GGGAATTGGAGATCGTCACA

PIK3CA.18.5.PIK3CA.2_R	chr3:178947878-178948029	CTTGTGATCCAAAAAGTGTCCA
PIK3CA.16.1.PIK3CA.1_F	chr3:178943710-178943843	CGTGATCCCCAAATTTGCAT
PIK3CA.16.1.PIK3CA.1_R	chr3:178943710-178943843	ACTTTCAACATACAGGTTGCC
PIK3CA.13.1.PIK3CA.1_F	chr3:178938813-178938970	ACAGTTAGCCAGAGGTTTGG
PIK3CA.13.1.PIK3CA.1_R	chr3:178938813-178938970	CCACTGCAGTGAAAAGAGTC
PIK3CA.13.14.PIK3CA.2_F	chr3:178938620-178938866	CCTGAAACTCATGGTGGTTTTGT
PIK3CA.13.14.PIK3CA.2_R	chr3:178938620-178938866	CCATTGCCTCGACTTGCCTA
PIK3CA.6.13.PIK3CA.1_F	chr3:178927355-178927498	CTTTGATGAAGACTTTTCTTGATGT
PIK3CA.6.13.PIK3CA.1_R	chr3:178927355-178927498	AGGTAAACATAATTGTTCCTTCTGA
PIK3CA.3.1.PIK3CA.1_F	chr3:178919222-178919374	ACTCGAAGTATGTTGCTATCCT
PIK3CA.3.1.PIK3CA.1_R	chr3:178919222-178919374	ACAGATACTCATCCTCAATGTG
PIK3CA.3.4.PIK3CA.2_F	chr3:178919060-178919209	AGAGAGATGGTGATTGCATCT
PIK3CA.3.4.PIK3CA.2_R	chr3:178919060-178919209	AGTTGTTCAGAGGATAGCAACA
PIK3CA.3.5.PIK3CA.3_F	chr3:178919167-178919309	TCAACCATGACTGTGTACCA
PIK3CA.3.5.PIK3CA.3_R	chr3:178919167-178919309	CACCTTATACTGACTCAGAGGA
PIK3CA.9.6.PIK3CA.1_F	chr3:178935963-178936112	TCCAGAGGGGAAAAATATGACA
PIK3CA.9.6.PIK3CA.1_R	chr3:178935963-178936112	TAGCACTTACCTGTGACTCC
PIK3CA.9.7.PIK3CA.2_F	chr3:178936050-178936176	AGGGAAAATGACAAAGAACAGC
PIK3CA.9.7.PIK3CA.2_R	chr3:178936050-178936176	CTGAGATCAGCCAAATTCAGT
PIK3CA.12.14.PIK3CA.1_F	chr3:178937712-178937936	GCCATGCAGAAACTGACCCT
PIK3CA.12.14.PIK3CA.1_R	chr3:178937712-178937936	GGAAAACTCTTCCAGCCAAACA
PIK3CA.15.11.PIK3CA.1_F	chr3:178942503-178942627	TTAAAGGCTTGAAGAGTGTCG
PIK3CA.15.11.PIK3CA.1_R	chr3:178942503-178942627	GCTAAATTCATGCATCATAAGCTC
PIK3CA.15.12.PIK3CA.2_F	chr3:178942473-178942601	AGCAAAGGTACCTAGTAAAGTTT
PIK3CA.15.12.PIK3CA.2_R	chr3:178942473-178942601	ACTCTTCCTTACCATCCCCA
PIK3CA.20.1.PIK3CA.1_F	chr3:178951922-178952081	CAAGGCTTATCTAGCTATTCGA
PIK3CA.20.1.PIK3CA.1_R	chr3:178951922-178952081	TCCAGCCACCATGATGTG
PIK3CA.20.2.PIK3CA.2_F	chr3:178952061-178952217	GCAAGAGGCTTTGGAGTATT
PIK3CA.20.2.PIK3CA.2_R	chr3:178952061-178952217	CTATGCAATCGGTCTTTGCC
PIK3CA.20.2.PIK3CA.3_F	chr3:178951796-178951954	AGCTTTGTCTACGAAAGCCT
PIK3CA.20.2.PIK3CA.3_R	chr3:178951796-178951954	ATTCCAGAGCCAAGCATCAT
PIK3CA.14.10.PIK3CA.1_F	chr3:178941854-178941978	GTCAGTTTCTTACTGTGACTATCC
PIK3CA.14.10.PIK3CA.1_R	chr3:178941854-178941978	TCAATGAAACCCCCAAGAAAG
PIK3CA.8.4.PIK3CA.1_F	chr3:178928184-178928344	GGCAGTCAAACCTTCTCTCT
PIK3CA.8.4.PIK3CA.1_R	chr3:178928184-178928344	TTTGCCTTACCAGTCCTGC
PIK3CA.8.5.PIK3CA.2_F	chr3:178928303-178928459	CAGTGATTGAAGAGCATGCC
PIK3CA.8.5.PIK3CA.2_R	chr3:178928303-178928459	GCAATATTGGTCCTAGAGTTCA
PIK3CA.4.4.PIK3CA.1_F	chr3:178921331-178921481	CGCCCCCTTAATCTCTTACA
PIK3CA.4.4.PIK3CA.1_R	chr3:178921331-178921481	CCCAAAGGGATTTTGTAGATGT
PIK3CA.4.8.PIK3CA.2_F	chr3:178921420-178921577	TTCTCAACTGCCAATGGACT
PIK3CA.4.8.PIK3CA.2_R	chr3:178921420-178921577	AAGCATCAGCATTTGACTTTAC
PIK3CA.19.1.PIK3CA.1_F	chr3:178948052-178948196	TGGACACTTTTTGGATCACAAG
PIK3CA.19.1.PIK3CA.1_R	chr3:178948052-178948196	TCTAATAGAGCAGCCAGAACTC
PIK3CA.19.2.PIK3CA.2_F	chr3:178947910-178948067	TGGTGAAAGACGATGGACAA
PIK3CA.19.2.PIK3CA.2_R	chr3:178947910-178948067	TGGCACACGTTCTCGTTTAT
PIK3CA.10.11.PIK3CA.1_F	chr3:178936950-178937094	ACCTTTTGAACAGCATGCAA
PIK3CA.10.11.PIK3CA.1_R	chr3:178936950-178937094	GTGACATACCAATTTGTACAACAG
PIK3CA.5.12.PIK3CA.1_F	chr3:178922248-178922402	CGAGTGTGTGCATATGTGTA
PIK3CA.5.12.PIK3CA.1_R	chr3:178922248-178922402	TGCTAAACACTAATATAACCTTTGG
TPMT.6.3.TPMT.1_F	chr6:18143792-18143929	CTGAGAAAAACTTTTGTGGGGA
TPMT.6.3.TPMT.1_R	chr6:18143792-18143929	GGGGACACAGTGTAGTTGG
TPMT.6.4.TPMT.2_F	chr6:18143928-18144078	TCCCAAGTTCACTGATTTCCA
TPMT.6.4.TPMT.2_R	chr6:18143928-18144078	CTGCATGTTCTTTGAAACCCT
TPMT.3.3.TPMT.1_F	chr6:18133939-18134094	TGCAGTATGCTTCCTATGAGA
TPMT.3.3.TPMT.1_R	chr6:18133939-18134094	GCAGATACAATGTTTTCCCTCC
TPMT.3.4.TPMT.2_F	chr6:18134040-18134197	ACCCAACAACTTTACCTGGA
TPMT.3.4.TPMT.2_R	chr6:18134040-18134197	AGCGAAAGTAACTTCTGGCT
TPMT.7.5.TPMT.1_F	chr6:18148021-18148172	CACCCAAAGAATTCATCATTAAGGC
TPMT.7.5.TPMT.1_R	chr6:18148021-18148172	TCACCTACCATACAATTGTCCT
TPMT.2.1.TPMT.1_F	chr6:18132292-18132441	TGCTGGAAATACAGGCATGA
TPMT.2.1.TPMT.1_R	chr6:18132292-18132441	AGTACACCTACGTCATTGGA
TPMT.8.1.TPMT.1_F	chr6:18149237-18149387	ACTGATGTCCTTGTTCCTGA
TPMT.8.1.TPMT.1_R	chr6:18149237-18149387	CGTAGGCACGGAAGACATAT
TPMT.8.2.TPMT.2_F	chr6:18149078-18149237	TACATCATGCCACAGATGCA
TPMT.8.2.TPMT.2_R	chr6:18149078-18149237	GAACGGCAAGACTGCTTTTC
TPMT.1.6.TPMT.1_F	chr6:18130877-18131010	CCTCAAAAACATGTCAGTGTGA
TPMT.1.6.TPMT.1_R	chr6:18130877-18131010	CATGTTACTCTTTCTTGTTTCAGG

TPMT.1.7.TPMT.2_F	chr6:18130996-18131153	TCAACCTTCTCAAGACAACGT
TPMT.1.7.TPMT.2_R	chr6:18130996-18131153	GGTCATGAACTCCTGACCTC
TPMT.4.8.TPMT.1_F	chr6:18139137-18139315	AGCTGATTTTCTAGAACCCAGAA
TPMT.4.8.TPMT.1_R	chr6:18139137-18139315	GGGACGCTGCTCATCTTCTT
TPMT.5.1.TPMT.1_F	chr6:18139865-18140019	GCCTGGCAAGCATTCAAATT
TPMT.5.1.TPMT.1_R	chr6:18139865-18140019	GAACTTTTGCTTTGCTTGGC
BRCA2.11.42.BRCA2.1_F	chr13:32918572-32918813	TCAAACATTAGGTCACTATTTGTTGT
BRCA2.11.42.BRCA2.1_R	chr13:32918572-32918813	ACCATACCTATAGAGGGAGAACAGA
BRCA2.21.37.BRCA2.1_F	chr13:32953454-32953602	ATTCCAATATCTTAAATGGTCACAG
BRCA2.21.37.BRCA2.1_R	chr13:32953454-32953602	CAATACGCAACTTCCACACG
BRCA2.21.38.BRCA2.2_F	chr13:32953601-32953755	AGGTTTATCAAGGGATGTCACA
BRCA2.21.38.BRCA2.2_R	chr13:32953601-32953755	GTAGTGGATTTTGCTTCTCTGA
BRCA2.7.21.BRCA2.1_F	chr13:32903520-32903664	TGTGCTTTTTGATGTCTGACA
BRCA2.7.21.BRCA2.1_R	chr13:32903520-32903664	AGGCATTCCAAAATTGTTAGCA
BRCA2.26.1.BRCA2.1_F	chr13:32972357-32972518	CCTTTATCACTTTGTATGGCCA
BRCA2.26.1.BRCA2.1_R	chr13:32972357-32972518	TGTGCAGCCGGAGAAA
BRCA2.26.2.BRCA2.2_F	chr13:32972201-32972357	GGAGGGAGACTGTGTGTAAT
BRCA2.26.2.BRCA2.2_R	chr13:32972201-32972357	GTGTGGAAACAGACTTCCTT
BRCA2.26.2.BRCA2.3_F	chr13:32972538-32972699	TCTCCGGCTGCACAGAA
BRCA2.26.2.BRCA2.3_R	chr13:32972538-32972699	GTTGAACCAGACAAAAGAGCT
BRCA2.26.3.BRCA2.4_F	chr13:32972402-32972540	CTCAGCCCAGATGACTTCAA
BRCA2.26.3.BRCA2.4_R	chr13:32972402-32972540	AACTCCTTGGTGGCTGAAAT
BRCA2.26.3.BRCA2.5_F	chr13:32972769-32972907	GAATCCACTAGGACTGCTCC
BRCA2.26.3.BRCA2.5_R	chr13:32972769-32972907	ATTGTCGCCTTTGCAAATGC
BRCA2.26.4.BRCA2.6_F	chr13:32972686-32972844	TAGCTGACGAAGAACTTGCA
BRCA2.26.4.BRCA2.6_R	chr13:32972686-32972844	TCACATTCTTCCGTACTGGC
BRCA2.17.1.BRCA2.1_F	chr13:32937355-32937515	AGAAGCAGAAGATCGGCTAT
BRCA2.17.1.BRCA2.1_R	chr13:32937355-32937515	AACTGGGCCTTAACAGCAT
BRCA2.17.2.BRCA2.2_F	chr13:32937281-32937410	ACAGTGGAATTCTAGAGTCACA
BRCA2.17.2.BRCA2.2_R	chr13:32937281-32937410	GCGCTCAATGAAATTATGTCAG
BRCA2.17.2.BRCA2.3_F	chr13:32937525-32937682	AGATGGGTGGTATGCTGTTA
BRCA2.17.2.BRCA2.3_R	chr13:32937525-32937682	GACTGATTTTTACCAAGAGTGC
BRCA2.17.3.BRCA2.4_F	chr13:32937393-32937528	GGATGACACAGCTGCAAAAA
BRCA2.17.3.BRCA2.4_R	chr13:32937393-32937528	AGAGGGGAGGATCTAACTGG
BRCA2.2.1.BRCA2.1_F	chr13:32893354-32893482	AAACTCCACAAAGGAAACCA
BRCA2.2.1.BRCA2.1_R	chr13:32893354-32893482	AGTTTGTAGTTCTCCCCAGTC
BRCA2.2.2.BRCA2.2_F	chr13:32893199-32893354	CTGGTTAAAACTAAGGTGGGAT
BRCA2.2.2.BRCA2.2_R	chr13:32893199-32893354	GTTGAAGCCAGCTGATTATAAG
BRCA2.22.14.BRCA2.1_F	chr13:32953882-32954038	GCATCTTTCTCATCTTTCTCCA
BRCA2.22.14.BRCA2.1_R	chr13:32953882-32954038	GGTTTGTACCGGTAGTTGTTG
BRCA2.22.15.BRCA2.2_F	chr13:32954024-32954162	ACATACAGTTAGCAGCGACA
BRCA2.22.15.BRCA2.2_R	chr13:32954024-32954162	CCGTGGCTGGTAAATCTGAA
BRCA2.1.16.BRCA2.1_F	chr13:32890590-32890741	CAAGCATTGGAGGAATATCGT
BRCA2.1.16.BRCA2.1_R	chr13:32890590-32890741	TCTAAGCAACACTGTGACGT
BRCA2.18.42.BRCA2.1_F	chr13:32944554-32944766	TGTCCAGATTTCTGCTAACAGT
BRCA2.18.42.BRCA2.1_R	chr13:32944554-32944766	GGCAAGAGACCGAAACTCCA
BRCA2.18.43.BRCA2.2_F	chr13:32944470-32944597	GGCAGTTCTAGAAGAATGAAAACTC
BRCA2.18.43.BRCA2.2_R	chr13:32944470-32944597	GCAGAGGAAAAGGTCTAGGG
BRCA2.23.29.BRCA2.1_F	chr13:32954113-32954252	TGCTTGTTAGTTTATGGAATCTCC
BRCA2.23.29.BRCA2.1_R	chr13:32954113-32954252	TTCACAACAGAAACGACAAATC
BRCA2.23.30.BRCA2.2_F	chr13:32954247-32954406	ATCTTGTTCTGAGGTGGACC
BRCA2.23.30.BRCA2.2_R	chr13:32954247-32954406	TCAGAGGTTCAAAGAGGCTT
BRCA2.16.23.BRCA2.1_F	chr13:32936698-32936852	AGGTGTGGATCCAAAGCTTA
BRCA2.16.23.BRCA2.1_R	chr13:32936698-32936852	CCATACTGCCGTATATGATTACG
BRCA2.16.26.BRCA2.2_F	chr13:32936626-32936750	TTGAATTCAGTATCATCCTATGTGG
BRCA2.16.26.BRCA2.2_R	chr13:32936626-32936750	GGAAAGGCACATTCCATAGC
BRCA2.13.1.BRCA2.1_F	chr13:32929027-32929187	AGGAACGTCAAGAGATACAGA
BRCA2.13.1.BRCA2.1_R	chr13:32929027-32929187	GACTTTGGTTGGTCTGCC
BRCA2.13.2.BRCA2.2_F	chr13:32928881-32929039	TGGCAACCATGGTGAATACA
BRCA2.13.2.BRCA2.2_R	chr13:32928881-32929039	GAAATTCTTGACCAGGTGCG
BRCA2.13.16.BRCA2.3_F	chr13:32929208-32929367	GGCAGACCAACCAAAGTCTT
BRCA2.13.16.BRCA2.3_R	chr13:32929208-32929367	ACTGCTTGATTGGAGTTGTT
BRCA2.13.17.BRCA2.4_F	chr13:32929135-32929272	AGCAGTTTCAGGACATCCAT
BRCA2.13.17.BRCA2.4_R	chr13:32929135-32929272	GCTTTTGTCTGTTTTCCTCCA
BRCA2.13.22.BRCA2.5_F	chr13:32929295-32929439	GGAGGAAAACAGACAAAAGCA
BRCA2.13.22.BRCA2.5_R	chr13:32929295-32929439	AGGCAAAAATTCATCACACAAA
BRCA2.25.1.BRCA2.1_F	chr13:32971063-32971215	GACATACTTTGCAATGAAGCAG

BRCA2.25.1.BRCA2.1_R	chr13:32971063-32971215	ACGATGGCCTCCATATATACT
BRCA2.25.2.BRCA2.2_F	chr13:32970957-32971107	GGTCCAAACTTTTCATTTCTGC
BRCA2.25.2.BRCA2.2_R	chr13:32970957-32971107	ACAGTCTTTAGTTGGGGTGG
BRCA2.6.1.BRCA2.1_F	chr13:32900640-32900773	TTTTCTTTCCTCCCAGGGTC
BRCA2.6.1.BRCA2.1_R	chr13:32900640-32900773	ACCTCATCTGCTCTTTCTTGT
BRCA2.6.2.BRCA2.2_F	chr13:32900534-32900673	AGCATTCTGCCTCATACAGG
BRCA2.6.2.BRCA2.2_R	chr13:32900534-32900673	TATCAGGATCCACCTCAGCT
BRCA2.3.42.BRCA2.1_F	chr13:32899166-32899418	AAACACTTCCAAAGAATGCAAATTT
BRCA2.3.42.BRCA2.1_R	chr13:32899166-32899418	GATCTTCTACCAGGCTCTTAGC
BRCA2.9.1.BRCA2.1_F	chr13:32906629-32906788	ATTTTCCATGAAGCAAACGC
BRCA2.9.1.BRCA2.1_R	chr13:32906629-32906788	AGTTGAGACCATTCACAGGC
BRCA2.9.2.BRCA2.2_F	chr13:32907089-32907248	AGCAGGCAATATCTGGAACT
BRCA2.9.2.BRCA2.2_R	chr13:32907089-32907248	GTCCTCCTTCTGTGAGCAAA
BRCA2.9.3.BRCA2.3_F	chr13:32906959-32907095	TCAGAGAATTCTTTGCCACG
BRCA2.9.3.BRCA2.3_R	chr13:32906959-32907095	ACCCTGAAATGAAGAAGCCA
BRCA2.9.4.BRCA2.4_F	chr13:32906835-32906985	TTCAGGTCTAAATGGAGCCC
BRCA2.9.4.BRCA2.4_R	chr13:32906835-32906985	CACTGTTTCCTCATTTAATGGC
BRCA2.9.5.BRCA2.5_F	chr13:32906785-32906939	TCCAAGGAAGTTGTACCGTC
BRCA2.9.5.BRCA2.5_R	chr13:32906785-32906939	ACGTGGCAAAGAATTCTCTG
BRCA2.9.18.BRCA2.6_F	chr13:32907269-32907429	TGCTCACAGAAGGAGGAC
BRCA2.9.18.BRCA2.6_R	chr13:32907269-32907429	TCTGATTTTTGGTCTTTCGGT
BRCA2.9.19.BRCA2.7_F	chr13:32907197-32907330	TCAGGTCATATGACTGATCCA
BRCA2.9.19.BRCA2.7_R	chr13:32907197-32907330	AACCTGCATTCTTCAAAGCT
BRCA2.9.23.BRCA2.8_F	chr13:32906529-32906670	GAAACAGTTGTAGATACCTCTGAAG
BRCA2.9.23.BRCA2.8_R	chr13:32906529-32906670	GGTTCCACTTCAGATACAAATGAG
BRCA2.9.26.BRCA2.9_F	chr13:32906429-32906580	AGGATTTGGAAAAACATCAGGG
BRCA2.9.26.BRCA2.9_R	chr13:32906429-32906580	TCCTAGTCTTGCTAGTTCTTACT
BRCA2.9.27.BRCA2.10_F	chr13:32906283-32906439	GCCAAGTACTCAGAATAACCC
BRCA2.9.27.BRCA2.10_R	chr13:32906283-32906439	GTGGTCTTTGCAGCTATTTACT
BRCA2.9.42.BRCA2.11_F	chr13:32907327-32907569	AGCCACCACCACACAGAATT
BRCA2.9.42.BRCA2.11_R	chr13:32907327-32907569	AACACAGAAGGAATCGTCATCT
BRCA2.12.42.BRCA2.1_F	chr13:32920859-32921066	TGAGCATCTGTTACATTCACTGA
BRCA2.12.42.BRCA2.1_R	chr13:32920859-32921066	AAAAACGAGACTTTTCTCATACTGT
BRCA2.20.29.BRCA2.1_F	chr13:32950760-32950908	GCTTGGTTCTTTAGTTTTAGTTGC
BRCA2.20.29.BRCA2.1_R	chr13:32950760-32950908	CTCAAGGTAAGCTGGGTCTG
BRCA2.20.30.BRCA2.2_F	chr13:32950850-32950988	CCATCACGTGCACTAACAAG
BRCA2.20.30.BRCA2.2_R	chr13:32950850-32950988	TGTGATGGCCAGAGAGTCTA
BRCA2.15.1.BRCA2.1_F	chr13:32931952-32932107	GCAGAGTCTTTTCAGTTTCACA
BRCA2.15.1.BRCA2.1_R	chr13:32931952-32932107	GAGAAGAAAGAGGGATGAGGG
BRCA2.15.42.BRCA2.2_F	chr13:32931805-32931999	TTTGGTAAATTCAGTTTTGGTTTGTT
BRCA2.15.42.BRCA2.2_R	chr13:32931805-32931999	CCATCCACCATCAGCCAACT
BRCA2.14.1.BRCA2.1_F	chr13:32930610-32930765	GCCAGAGATATACAGGATATGC
BRCA2.14.1.BRCA2.1_R	chr13:32930610-32930765	CTCTGTCATAAAAGCCATCAGT
BRCA2.14.2.BRCA2.2_F	chr13:32930525-32930678	CCAGGGGTTGTGCTTTTTAA
BRCA2.14.2.BRCA2.2_R	chr13:32930525-32930678	CAGAGAGATTCGAGGCAGAG
BRCA2.8.14.BRCA2.1_F	chr13:32905011-32905157	GGGGGACTACTACTATATGTGC
BRCA2.8.14.BRCA2.1_R	chr13:32905011-32905157	AGAGGACTTACCATGACTTGC
BRCA2.8.15.BRCA2.2_F	chr13:32905136-32905292	GCTTCTGTGACAGACAGTGA
BRCA2.8.15.BRCA2.2_R	chr13:32905136-32905292	TGAGGCAGGATCGCTTGA
BRCA2.4.18.BRCA2.1_F	chr13:32900229-32900374	ACCTAAGGGATTTGCTTTGTT
BRCA2.4.18.BRCA2.1_R	chr13:32900229-32900374	AAACTCCCACATACCACTGG
BRCA2.24.1.BRCA2.1_F	chr13:32968846-32969005	ACTTGCCCCTTTCGTCTAT
BRCA2.24.1.BRCA2.1_R	chr13:32968846-32969005	CCTCTTTTGGACTAGCAGAAA
BRCA2.24.2.BRCA2.2_F	chr13:32968935-32969086	AGCCTCATATGTTAATTGCTGC
BRCA2.24.2.BRCA2.2_R	chr13:32968935-32969086	ACCAAAATGTGTGGTGATGC
BRCA2.24.18.BRCA2.3_F	chr13:32968701-32968853	GCTTTCGCCAAATTCAGCTA
BRCA2.24.18.BRCA2.3_R	chr13:32968701-32968853	TGCCAGTAAATTGTAACATTCG
BRCA2.19.44.BRCA2.1_F	chr13:32945038-32945217	CTGTGCCTGGCCTGATACAA
BRCA2.19.44.BRCA2.1_R	chr13:32945038-32945217	ATTTTACCTTCATGTTCTTCAAATTCC
BRCA2.19.45.BRCA2.2_F	chr13:32945187-32945403	TGTGGAGGCCCAACAAAAGA
BRCA2.19.45.BRCA2.2_R	chr13:32945187-32945403	CCTGATATTTCTGTCCCTTGTTGC
BRCA2.10.1.BRCA2.1_F	chr13:32910710-32910872	TGGCTGCAGCATGTCAC
BRCA2.10.1.BRCA2.1_R	chr13:32910710-32910872	ACCTTTGAGCTTGTCTGACA
BRCA2.10.2.BRCA2.2_F	chr13:32911303-32911463	TGGAGACACAGGTGATAAACA
BRCA2.10.2.BRCA2.2_R	chr13:32911303-32911463	AGAGTCCTGCCCATTTGT
BRCA2.10.3.BRCA2.3_F	chr13:32911824-32911983	CCTAGCCAAAAGGCAGAAA
BRCA2.10.3.BRCA2.3_R	chr13:32911824-32911983	GGGGCATTCATTATGACATGA

BRCA2.10.4.BRCA2.4_F	chr13:32912014-32912175	GAATGCCCCATCGATTGG
BRCA2.10.4.BRCA2.4_R	chr13:32912014-32912175	GCAGAGCTTCAGTAGAAACA
BRCA2.10.5.BRCA2.5_F	chr13:32911938-32912068	TGAAGTGCCTGAAAACCAGA
BRCA2.10.5.BRCA2.5_R	chr13:32911938-32912068	TCATTTTTCAACAGGCCAGC
BRCA2.10.5.BRCA2.6_F	chr13:32912616-32912775	TTATCTGGCCAGTTTATGAAGG
BRCA2.10.5.BRCA2.6_R	chr13:32912616-32912775	TTCCCACTTGCAGTCTGA
BRCA2.10.6.BRCA2.7_F	chr13:32913036-32913195	CAACCCGAACGTGATGAAA
BRCA2.10.6.BRCA2.7_R	chr13:32913036-32913195	TCTTTACAGGCCTCTCTGTAC
BRCA2.10.7.BRCA2.8_F	chr13:32913266-32913428	CAGCTGCCCCAAAGTGT
BRCA2.10.7.BRCA2.8_R	chr13:32913266-32913428	TGCAGGACTTTTTGCTGTTT
BRCA2.10.8.BRCA2.9_F	chr13:32913189-32913321	TAGCCATCAATGGGCAAAGA
BRCA2.10.8.BRCA2.9_R	chr13:32913189-32913321	TTAAGAGCTTAGGTGGCACC
BRCA2.10.8.BRCA2.10_F	chr13:32914399-32914558	AGGGAAGCTTCATAAGTCAGT
BRCA2.10.8.BRCA2.10_R	chr13:32914399-32914558	CTTCTCTTGTGAGCTGGTC
BRCA2.10.9.BRCA2.11_F	chr13:32915218-32915345	TGGAAGATGATGAACTGACAGA
BRCA2.10.9.BRCA2.11_R	chr13:32915218-32915345	TGGCAACACGAAAGGTAAAA
BRCA2.10.9.BRCA2.12_F	chr13:32914276-32914426	TGCTGACATTCAGAGTGAAGA
BRCA2.10.9.BRCA2.12_R	chr13:32914276-32914426	GATTTTCCACTTGCTGTGCT
BRCA2.10.10.BRCA2.13_F	chr13:32915062-32915219	CAGGCTTCACCTAAAAACGT
BRCA2.10.10.BRCA2.13_R	chr13:32915062-32915219	GGCATGACTTGGCAGTTTAG
BRCA2.10.10.BRCA2.14_F	chr13:32914167-32914298	GCCAAACGAAAATTATGGCAG
BRCA2.10.10.BRCA2.14_R	chr13:32914167-32914298	GAAACTTTCTCCAATCCAGACA
BRCA2.10.11.BRCA2.15_F	chr13:32914018-32914172	AATTTTGAGGTAGGGCCACC
BRCA2.10.11.BRCA2.15_R	chr13:32914018-32914172	TGAATCATCCAATGCCTCGT
BRCA2.10.12.BRCA2.16_F	chr13:32913899-32914029	TGCAAATGCATACCCACAA
BRCA2.10.12.BRCA2.16_R	chr13:32913899-32914029	CAAACGATTTTACCACTGGCT
BRCA2.10.13.BRCA2.17_F	chr13:32913754-32913907	ACAGCTATTCCTACCATTCTGA
BRCA2.10.13.BRCA2.17_R	chr13:32913754-32913907	GTTCCTCAACGCAAATATCTTC
BRCA2.10.14.BRCA2.18_F	chr13:32910857-32911012	CCTAGTCATGATTTCTAGAGGC
BRCA2.10.14.BRCA2.18_R	chr13:32910857-32911012	TCTTGAAGGTGATGCTACTCT
BRCA2.10.14.BRCA2.19_F	chr13:32914531-32914671	ACCAAGCAAGTCTTTTCCAA
BRCA2.10.14.BRCA2.19_R	chr13:32914531-32914671	AAACTTGCTTTCCACTTGCT
BRCA2.10.18.BRCA2.20_F	chr13:32911691-32911847	AGCAAGCCTCAGTCAATTAAT
BRCA2.10.18.BRCA2.20_R	chr13:32911691-32911847	TCAAACTGACTTCCTGATTCTT
BRCA2.10.18.BRCA2.21_F	chr13:32912516-32912658	AGAATTTGATGGCAGTGATTCA
BRCA2.10.18.BRCA2.21_R	chr13:32912516-32912658	GAGCTTTCGCAACTTCCAAA
BRCA2.10.19.BRCA2.22_F	chr13:32911558-32911697	AGGAAATCAAGCTCTCTGAACA
BRCA2.10.19.BRCA2.22_R	chr13:32911558-32911697	ACACTACTCTGTAAATGTGCAG
BRCA2.10.19.BRCA2.23_F	chr13:32912412-32912542	TGACTACTGGCACTTTTGTTG
BRCA2.10.19.BRCA2.23_R	chr13:32912412-32912542	AGCAAGTCCGTTTCATCTTT
BRCA2.10.20.BRCA2.24_F	chr13:32914667-32914822	TTCATCTGCTTTCTCTGGATTT
BRCA2.10.20.BRCA2.24_R	chr13:32914667-32914822	CAGTGCTCTGGGTTTCTCTT
BRCA2.10.23.BRCA2.25_F	chr13:32911187-32911338	GTCTTCCAAGTAGCTAATGAAAGG
BRCA2.10.23.BRCA2.25_R	chr13:32911187-32911338	TGTTCTCCTCTGCAAGAACA
BRCA2.10.24.BRCA2.26_F	chr13:32911058-32911210	GGTACAATTCAACCAAAACACA
BRCA2.10.24.BRCA2.26_R	chr13:32911058-32911210	AGTCTGTTTCATGAAGTTCCTT
BRCA2.10.25.BRCA2.27_F	chr13:32910954-32911111	CCCATGGAAAAGAATCAAGATG
BRCA2.10.25.BRCA2.27_R	chr13:32910954-32911111	TCAGAGTCTGGATTGACAGT
BRCA2.10.26.BRCA2.28_F	chr13:32914927-32915081	TGAAGGTGGTTCTTCAGAAAA
BRCA2.10.26.BRCA2.28_R	chr13:32914927-32915081	CAGGAACATCAGAAAAAGTTTCAG
BRCA2.10.28.BRCA2.29_F	chr13:32914821-32914968	GTATCAAAAATACTTCCTCGTGTTG
BRCA2.10.28.BRCA2.29_R	chr13:32914821-32914968	ACCAACTGTTGTTTGTCTTGT
BRCA2.10.31.BRCA2.30_F	chr13:32910565-32910709	CTCAGGATCTTGATTATAAAGAAGC
BRCA2.10.31.BRCA2.30_R	chr13:32910565-32910709	TCCACTTTTGAATGTTGTACTGG
BRCA2.10.32.BRCA2.31_F	chr13:32910441-32910598	GTGAAAAGAAGCTGTTCACAGA
BRCA2.10.32.BRCA2.31_R	chr13:32910441-32910598	AGAGAATCAGCTTCTGGGGT
BRCA2.10.33.BRCA2.32_F	chr13:32910327-32910473	TGTGCCCAAACACTACCTTT
BRCA2.10.33.BRCA2.32_R	chr13:32910327-32910473	TCAGAATTGTCCCAAAAGAGC
BRCA2.10.34.BRCA2.33_F	chr13:32911426-32911566	AAAATCGGACATCTCCTTGAA
BRCA2.10.34.BRCA2.33_R	chr13:32911426-32911566	TCTTTGAAGAACATTTTGCTCTTC
BRCA2.10.34.BRCA2.34_F	chr13:32912299-32912449	CTTCAAGTAAATGTCATGATTCTGT
BRCA2.10.34.BRCA2.34_R	chr13:32912299-32912449	GGCAGCAGTATATTTGTTATCTTC
BRCA2.10.34.BRCA2.35_F	chr13:32912922-32913060	GACATAAGAAAGAACAAAATGGACA
BRCA2.10.34.BRCA2.35_R	chr13:32912922-32913060	TCCCGCTAGCTGTATGAAAA
BRCA2.10.35.BRCA2.36_F	chr13:32912811-32912966	GGGAAAAAATATTAGTGTCGCCA
BRCA2.10.35.BRCA2.36_R	chr13:32912811-32912966	ACCAACTGGGACACTTTCTT
BRCA2.10.36.BRCA2.37_F	chr13:32912696-32912842	CTCAAGAAGCATGTCATGGT

BRCA2.10.36.BRCA2.37_R	chr13:32912696-32912842	GCAATTCTTCTGGTTTCTGATC
BRCA2.10.37.BRCA2.38_F	chr13:32913382-32913533	GACAAACTGAAAATCTCAAAACATC
BRCA2.10.37.BRCA2.38_R	chr13:32913382-32913533	TTCAAGTAATGAAGTCTGACTCA
BRCA2.10.39.BRCA2.39_F	chr13:32913516-32913671	GCCTTAGCTTTTTACACAAGTT
BRCA2.10.39.BRCA2.39_R	chr13:32913516-32913671	TCGGAGAGATGATTTTTGTCAT
BRCA2.10.40.BRCA2.40_F	chr13:32912146-32912284	AATGAAGTGGGGTTTAGGGG
BRCA2.10.40.BRCA2.40_R	chr13:32912146-32912284	CATTGAAACAACAGAATCATGACA
BRCA2.10.41.BRCA2.41_F	chr13:32912256-32912395	TGAGGAAACTTCTGCAGAGG
BRCA2.10.41.BRCA2.41_R	chr13:32912256-32912395	TCTTCAACAAAAGTGCCAGT
BRCA2.10.42.BRCA2.42_F	chr13:32913548-32913792	AAACTTCTGTGAGTCAGACTTCA
BRCA2.10.42.BRCA2.42_R	chr13:32913548-32913792	ACTGGCTCAATACCAGAATCAAGT
BRCA2.5.34.BRCA2.1_F	chr13:32900308-32900455	GTCAGGTATGATTAAAAACAATGCT
BRCA2.5.34.BRCA2.1_R	chr13:32900308-32900455	ACGCTATTGTCAAATTCTCAATT
ALK.11.1.ALK.1_F	chr2:29448287-29448446	GACACTATTCAGTCCTGCCT
ALK.11.1.ALK.1_R	chr2:29448287-29448446	TGGTTGTCAATACCCCAGTG
ALK.21.1.ALK.1_F	chr2:29519754-29519913	GGGAGATGCATAGAGCCTAC
ALK.21.1.ALK.1_R	chr2:29519754-29519913	CCTCACAGCTCCGAATGT
ALK.21.2.ALK.2_F	chr2:29519908-29520062	CCTCAAGACTCCACGAATGA
ALK.21.2.ALK.2_R	chr2:29519908-29520062	AAAGCCTCTTGGTGAGACAG
ALK.7.1.ALK.1_F	chr2:29443560-29443706	AACAACTGCAGCAAAGACTG
ALK.7.1.ALK.1_R	chr2:29443560-29443706	GGTTACATCCCTCTCTGCTC
ALK.26.1.ALK.1_F	chr2:29754781-29754940	TTGGACATGGAGAAGTACTTAC
ALK.26.1.ALK.1_R	chr2:29754781-29754940	CAGCTGACTCCAAGCACA
ALK.26.2.ALK.2_F	chr2:29754865-29755016	GGGCAATGTACCTTCCAGAG
ALK.26.2.ALK.2_R	chr2:29754865-29755016	CTGCTGGTCTTACCTGAACA
ALK.2.1.ALK.1_F	chr2:29419630-29419780	TGTTGACCAAAGGGAGAAAATG
ALK.2.1.ALK.1_R	chr2:29419630-29419780	CCTGGGGCTGGAAGAAAATA
ALK.17.1.ALK.1_F	chr2:29462545-29462698	CCTGCTCTGGGCACTTA
ALK.17.1.ALK.1_R	chr2:29462545-29462698	AACGTTCTTTGTCCCATTGC
ALK.22.1.ALK.1_F	chr2:29541134-29541290	GAAGTGACAAGAGGTGGGAG
ALK.22.1.ALK.1_R	chr2:29541134-29541290	CTGATAATGGCGTGCTTGTG
ALK.1.1.ALK.1_F	chr2:29416088-29416250	AGTGAGTGTGCGACCGA
ALK.1.1.ALK.1_R	chr2:29416088-29416250	GCTGACTGCCAATATGAAGG
ALK.1.2.ALK.2_F	chr2:29416251-29416411	AGCCTGAACAGAGGTACCT
ALK.1.2.ALK.2_R	chr2:29416251-29416411	GGCTCCTGGTTTACAGAGAA
ALK.1.3.ALK.3_F	chr2:29416420-29416581	TTTTTGGTGGGTTTCTCTGT
ALK.1.3.ALK.3_R	chr2:29416420-29416581	GCTGCAAAGAAACCCACA
ALK.1.4.ALK.4_F	chr2:29416390-29416519	TGTGGCTCCTTCTTTGCTAT
ALK.1.4.ALK.4_R	chr2:29416390-29416519	GAAGGGGGACACGTGAATAT
ALK.1.4.ALK.5_F	chr2:29416591-29416751	CTCTGCAGCTGTGGGTTT
ALK.1.4.ALK.5_R	chr2:29416591-29416751	ACCGCTTTGCCGATAGAAT
ALK.1.5.ALK.6_F	chr2:29416735-29416877	ACAGGCACTTTCTCTTCCTC
ALK.1.5.ALK.6_R	chr2:29416735-29416877	CTGGTTTCCTCATCTGTAGAAT
ALK.1.5.ALK.7_F	chr2:29416539-29416668	CATATTCACGTGTCCCCCTT
ALK.1.5.ALK.7_R	chr2:29416539-29416668	CTCCTCTCCTGGTCTCTCAA
ALK.18.1.ALK.1_F	chr2:29473970-29474131	CCCCTCTTCCATACGCA
ALK.18.1.ALK.1_R	chr2:29473970-29474131	CTCCTCTTGTGCCACAGTT
ALK.18.2.ALK.2_F	chr2:29474065-29474202	CAGGTTGGAGTTCTGGTAGG
ALK.18.2.ALK.2_R	chr2:29474065-29474202	GAGCAGATATCTCAGAGGCC
ALK.13.1.ALK.1_F	chr2:29450411-29450541	GGAGGACTGACCTAAGCAAG
ALK.13.1.ALK.1_R	chr2:29450411-29450541	CTCTGCTCTGGTTTGCTACT
ALK.23.1.ALK.1_F	chr2:29543616-29543765	AAGGCAGGAGAGCAGTAGTA
ALK.23.1.ALK.1_R	chr2:29543616-29543765	TCCTGAAAATGATGGTGCCT
ALK.16.1.ALK.1_F	chr2:29456415-29456574	AGGAACCTGGTGGAAATCTG
ALK.16.1.ALK.1_R	chr2:29456415-29456574	CCACAAACCTAACGTGCTTT
ALK.29.1.ALK.1_F	chr2:30143118-30143283	ACCAACTGCTTGGCACG
ALK.29.1.ALK.1_R	chr2:30143118-30143283	TCCTCCTCGGAGCTGAA
ALK.29.2.ALK.2_F	chr2:30143374-30143532	AGTCAACTGCCAGACTCTTC
ALK.29.2.ALK.2_R	chr2:30143374-30143532	CAGTGTAAACGGCCTCCTC
ALK.29.2.ALK.3_F	chr2:30142983-30143141	ATCCTCAGTCGCCCTTC
ALK.29.2.ALK.3_R	chr2:30142983-30143141	TGTCCAGGGTGCTGAAG
ALK.29.3.ALK.4_F	chr2:30142839-30142991	AAACACTAAATCCCGGCACA
ALK.29.3.ALK.4_R	chr2:30142839-30142991	AGCTGTTCAGTTGGTGGATT
ALK.29.6.ALK.5_F	chr2:30143235-30143384	CCCAGCAACCTGAGCAG
ALK.29.6.ALK.5_R	chr2:30143235-30143384	GAGCCACTCAGCTACTCG
ALK.27.1.ALK.1_F	chr2:29917721-29917880	AGCCTCTCCCTTACCTCTG
ALK.27.1.ALK.1_R	chr2:29917721-29917880	GACCCTTGGCTATTATTGCAG

ALK.27.2.ALK.2_F	chr2:29917591-29917721	AAGCCATGGAAAGTCACAGA
ALK.27.2.ALK.2_R	chr2:29917591-29917721	AGAGCGTTCTAAGGAGATGC
ALK.25.1.ALK.1_F	chr2:29606575-29606725	ACAATAGGCTACCAAGGAGC
ALK.25.1.ALK.1_R	chr2:29606575-29606725	TCTGTTTTCCAATGCAACCAG
ALK.6.1.ALK.1_F	chr2:29436838-29436976	ATGACAGGAAGAGCACAGTC
ALK.6.1.ALK.1_R	chr2:29436838-29436976	CTCTCACTGACAAGCTCCTC
ALK.28.1.ALK.1_F	chr2:29940457-29940597	TACTTACCATATCGGCTGCG
ALK.28.1.ALK.1_R	chr2:29940457-29940597	TAAAAGACACACCCCAAGCA
ALK.28.2.ALK.2_F	chr2:29940317-29940460	GAGACAGAGGGCTCAGAAAG
ALK.28.2.ALK.2_R	chr2:29940317-29940460	GACTCCTTCCCTTTCCTGTC
ALK.3.1.ALK.1_F	chr2:29420395-29420551	AGTAACTAGCAGAAGTGTTCCT
ALK.3.1.ALK.1_R	chr2:29420395-29420551	CATCTCCATGTCCTCTGTCC
ALK.9.1.ALK.1_F	chr2:29445380-29445514	CTCAAGAGTGAGCCACTTCT
ALK.9.1.ALK.1_R	chr2:29445380-29445514	CAGCTGCCTCATTATTGTGG
ALK.12.1.ALK.1_F	chr2:29449798-29449941	CCCCCTTACCAATGCAGGA
ALK.12.1.ALK.1_R	chr2:29449798-29449941	CCCTCCCTCCTTGTCACTA
ALK.12.2.ALK.2_F	chr2:29449683-29449827	TAGGGGAGGGACAGAAAGTT
ALK.12.2.ALK.2_R	chr2:29449683-29449827	AGGTCATCTGCTTCTGTGAC
ALK.20.1.ALK.1_F	chr2:29498268-29498401	GGGGTCAGAGTGAACTCAC
ALK.20.1.ALK.1_R	chr2:29498268-29498401	AATCCTAAGACAAGACCCCC
ALK.15.1.ALK.1_F	chr2:29455173-29455333	CTTGCAGCGCTTTACCTG
ALK.15.1.ALK.1_R	chr2:29455173-29455333	AGCTCGGTTTCTCAATGTCT
ALK.15.2.ALK.2_F	chr2:29455047-29455188	TCCCTGGATATCGGTACCAA
ALK.15.2.ALK.2_R	chr2:29455047-29455188	CCTCGGTTCTAGGGCTAAAC
ALK.14.1.ALK.1_F	chr2:29451772-29451932	ATATATCCTCCGCCTCCTCC
ALK.14.1.ALK.1_R	chr2:29451772-29451932	TCCCTATCTCTTCCCGCAG
ALK.14.2.ALK.2_F	chr2:29451740-29451890	AGTGACACCTTGAACACGAA
ALK.14.2.ALK.2_R	chr2:29451740-29451890	TAACACTTCCTTGCTCTGGG
ALK.8.1.ALK.1_F	chr2:29445209-29445363	GGTGTCTCTCTGTGGCTTTA
ALK.8.1.ALK.1_R	chr2:29445209-29445363	GGTAAGAAGTGGCTCACTCT
ALK.4.1.ALK.1_F	chr2:29430029-29430163	GATACCTGGAGGATGATGGC
ALK.4.1.ALK.1_R	chr2:29430029-29430163	TGCCATCTCCAGATCCTAGT
ALK.24.1.ALK.1_F	chr2:29551215-29551355	GCAGCCCCATCTACTCA
ALK.24.1.ALK.1_R	chr2:29551215-29551355	CATGGTTGTGTGTCTGTGTG
ALK.19.1.ALK.1_F	chr2:29497961-29498096	CACATTTGTGAGCTGAACCC
ALK.19.1.ALK.1_R	chr2:29497961-29498096	CCGTGGGGTCTTCTCTATTG
ALK.10.1.ALK.1_F	chr2:29446227-29446389	CCGAATGAGGGTGATGTTTT
ALK.10.1.ALK.1_R	chr2:29446227-29446389	ACCCACCTGCAGTGTAC
ALK.10.2.ALK.2_F	chr2:29446293-29446447	AAAGCAGTAGTTGGGGTTGT
ALK.10.2.ALK.2_R	chr2:29446293-29446447	GTAGGAAGTGGCCTGTGTAG
ALK.10.2.ALK.3_F	chr2:29446080-29446235	GTCAAGGCTTGTCCTCCTAG
ALK.10.2.ALK.3_R	chr2:29446080-29446235	CATCAGTGACCTGAAGGAGG
ALK.5.1.ALK.1_F	chr2:29432651-29432793	GGTGAGGCAGTCTTTACTCA
ALK.5.1.ALK.1_R	chr2:29432651-29432793	CTAGTGATGGCCGTTGTACA
TP53.6.1.TP53.1_F	chr17:7576571-7576709	TCAGGAAGTAACACCATCGT
TP53.6.1.TP53.1_R	chr17:7576571-7576709	AAAGACAATGGCTCCTGGTT
TP53.11.1.TP53.1_F	chr17:7578380-7578540	GCTGCTCACCATCGCTAT
TP53.11.1.TP53.1_R	chr17:7578380-7578540	TACAGTACTCCCCTGCCCT
TP53.11.2.TP53.2_F	chr17:7578444-7578578	ATGTGCTGTGACTGCTTGTA
TP53.11.2.TP53.2_R	chr17:7578444-7578578	CTTGTGCCCTGACTTTCAAC
TP53.11.2.TP53.3_F	chr17:7578282-7578423	CGGATAAGATGCTGAGGAGG
TP53.11.2.TP53.3_R	chr17:7578282-7578423	TACAAGCAGTCACAGCACAT
TP53.3.1.TP53.1_F	chr17:7572854-7573011	CAAGCAAGGGTTCAAAGACC
TP53.3.1.TP53.1_R	chr17:7572854-7573011	CTCCCTGCTTCTGTCTCCTA
TP53.7.1.TP53.1_F	chr17:7576797-7576928	CAGTCAAGAAGAAAACGGCA
TP53.7.1.TP53.1_R	chr17:7576797-7576928	CCTTTCCTTGCCTCTTTCCT
TP53.9.1.TP53.1_F	chr17:7577451-7577609	GGTCAGAGGCAAGCAGA
TP53.9.1.TP53.1_R	chr17:7577451-7577609	TGGGCCTGTGTTATCTCCTA
TP53.12.1.TP53.1_F	chr17:7579322-7579484	CAACTGACCGTGCAAGTC
TP53.12.1.TP53.1_R	chr17:7579322-7579484	GAAGCTCCCAGAATGCCAG
TP53.12.2.TP53.2_F	chr17:7579463-7579596	TAGGAGCTGCTGGTGCA
TP53.12.2.TP53.2_R	chr17:7579463-7579596	TGACTGCTCTTTTCACCCAT
TP53.12.2.TP53.3_F	chr17:7579234-7579386	GGGTGAAGAGGAATCCCAAA
TP53.12.2.TP53.3_R	chr17:7579234-7579386	CATCTTCTGTCCCTTCCCAG
TP53.14.1.TP53.1_F	chr17:7579838-7579967	CCTTCCAATGGATCCACTCA
TP53.14.1.TP53.1_R	chr17:7579838-7579967	CAGGGTTGGAAGTGTCTCAT
TP53.15.1.TP53.1_F	chr17:7580598-7580738	AGTCATTCTCAGCCTGCAAT

TP53.15.1.TP53.1_R	chr17:7580598-7580738	GTTTGTAATGCAGGGCTGAG
TP53.8.1.TP53.1_F	chr17:7577019-7577174	CTTCTTGTCCTGCTTGCTTAC
TP53.8.1.TP53.1_R	chr17:7577019-7577174	CCTTACTGCCTCTTGCTTCT
TP53.1.1.TP53.1_F	chr17:7565193-7565338	GGTTAAGAGATCCTCCTGCC
TP53.1.1.TP53.1_R	chr17:7565193-7565338	GACTCCGTCTCTCTCTCTCT
TP53.4.1.TP53.1_F	chr17:7573892-7574043	TTTCCAACCTAGGAAGGCAG
TP53.4.1.TP53.1_R	chr17:7573892-7574043	CTTACTTCTCCCCCTCCTCT
TP53.10.1.TP53.1_F	chr17:7578135-7578292	AGGGCCACTGACAACCA
TP53.10.1.TP53.1_R	chr17:7578135-7578292	TGATTCCTCACTGATTGCTCT
TP53.13.1.TP53.1_F	chr17:7579617-7579753	ATGGGTGAAAAGAGCAGTCA
TP53.13.1.TP53.1_R	chr17:7579617-7579753	CCTGTGGGAAGCGAAAATTC
TP53.5.1.TP53.1_F	chr17:7576483-7576641	GCAGGCTAGGCTAAGCTATG
TP53.5.1.TP53.1_R	chr17:7576483-7576641	AAAGGACCAGACCAGCTTTC
DPYD.11.1.DPYD.1_F	chr1:97981312-97981471	GAGAAAGTTTTGGTGAGGGC
DPYD.11.1.DPYD.1_R	chr1:97981312-97981471	TATGGAGCTTCCGTTTCTGC
DPYD.11.2.DPYD.2_F	chr1:97981469-97981628	AAAAGAGGGGTAGTTCAGGC
DPYD.11.2.DPYD.2_R	chr1:97981469-97981628	CTCACTGACTTTTTGCCAGT
DPYD.11.9.DPYD.3_F	chr1:97981173-97981311	TGTGTAATGATAGGTCTTGTCAA
DPYD.11.9.DPYD.3_R	chr1:97981173-97981311	TTGAAGCTGGATGGGGTTTT
DPYD.21.10.DPYD.1_F	chr1:98205887-98206103	ACAAGCTGTATTCTGTACCCACA
DPYD.21.10.DPYD.1_R	chr1:98205887-98206103	ACTAGACACGGACTCTGAATGA
DPYD.7.1.DPYD.1_F	chr1:97771750-97771907	TACCTTCCTTTGCAGCTCTT
DPYD.7.1.DPYD.1_R	chr1:97771750-97771907	TGCTGTTGTTCCAGTACACA
DPYD.7.2.DPYD.2_F	chr1:97771606-97771764	TTGTGGGATCAAGTGCTCAA
DPYD.7.2.DPYD.2_R	chr1:97771606-97771764	CTGACCCCAAATGTCACTGA
DPYD.2.1.DPYD.1_F	chr1:97547879-97548035	AGCATTCTAATTCCAGCAGGA
DPYD.2.1.DPYD.1_R	chr1:97547879-97548035	GCTTGCTAAGTAATTCAGTGGC
DPYD.17.1.DPYD.1_F	chr1:98157235-98157365	AGTGTAGAGCTTACTCCTTTCT
DPYD.17.1.DPYD.1_R	chr1:98157235-98157365	TGATGCCTGTTTTTCTTTCTCC
DPYD.22.7.DPYD.1_F	chr1:98293661-98293790	TGACTGTTGCTATGGTGACC
DPYD.22.7.DPYD.1_R	chr1:98293661-98293790	CTGCATAGATACAATTTTTCTCAGG
DPYD.1.1.DPYD.1_F	chr1:97544570-97544727	AGATAAGGGTACGCCTCTCT
DPYD.1.1.DPYD.1_R	chr1:97544570-97544727	ACCTTTGTGGTCAGTGACAT
DPYD.1.2.DPYD.2_F	chr1:97544463-97544608	GGAAAGAGCTGAACACAAGG
DPYD.1.2.DPYD.2_R	chr1:97544463-97544608	TGTTTGCCCTATTGTCGACT
DPYD.18.1.DPYD.1_F	chr1:98164962-98165106	AGTGATGTCAGAGTACCCCA
DPYD.18.1.DPYD.1_R	chr1:98164962-98165106	CCATGACAATTGATTTCCCCG
DPYD.18.2.DPYD.2_F	chr1:98164822-98164964	ATCTGTGAGCCTGAAGTTCC
DPYD.18.2.DPYD.2_R	chr1:98164822-98164964	TTGTGCTTCCTTTTTGGCTC
DPYD.16.10.DPYD.1_F	chr1:98144579-98144805	CACGAAAATGTCTGAAGGCAGT
DPYD.16.10.DPYD.1_R	chr1:98144579-98144805	TGGCTGACTTTTCATTCTTTTTGA
DPYD.23.3.DPYD.1_F	chr1:98348778-98348920	TGCCTTACAATGTGTGGAGT
DPYD.23.3.DPYD.1_R	chr1:98348778-98348920	TGCTGTCTTTAGAGTATCCTGG
DPYD.23.4.DPYD.2_F	chr1:98348913-98349050	GCATGAGTTTGTGTTCGAGG
DPYD.23.4.DPYD.2_R	chr1:98348913-98349050	AGATTGTACCACTGCACTCC
DPYD.13.1.DPYD.1_F	chr1:98039315-98039477	TCAGCTCCCAGCACTGTA
DPYD.13.1.DPYD.1_R	chr1:98039315-98039477	TTTCTGCCATTCCTGTCCC
DPYD.13.6.DPYD.2_F	chr1:98039382-98039536	GGCTTTCAGATGGACCATCT
DPYD.13.6.DPYD.2_R	chr1:98039382-98039536	TCAAGTTTCTTCTCTGTTCTGT
DPYD.6.1.DPYD.1_F	chr1:97770804-97770960	AAGCACAATGCAAGAAGTGG
DPYD.6.1.DPYD.1_R	chr1:97770804-97770960	TCGTGTCTTATAAGAGCTGCA
DPYD.3.1.DPYD.1_F	chr1:97564064-97564210	ACCTTGATGGTAGGAATAGGC
DPYD.3.1.DPYD.1_R	chr1:97564064-97564210	TCTGAGCTAACATGCTTCCT
DPYD.3.5.DPYD.2_F	chr1:97563912-97564066	GCAGTTTTCACCATGGACAG
DPYD.3.5.DPYD.2_R	chr1:97563912-97564066	AGAGAAACTGTTTTATCCCCAA
DPYD.9.8.DPYD.1_F	chr1:97847895-97848044	CTCATGGCAGCTCTTTATTTAAAAC
DPYD.9.8.DPYD.1_R	chr1:97847895-97848044	GTACAACTGGATAACTACTTGAACT
DPYD.12.1.DPYD.1_F	chr1:98015166-98015324	TGCTTTCCATCATTCACCG
DPYD.12.1.DPYD.1_R	chr1:98015166-98015324	GTCTGTTGACTAGTGATTGTCT
DPYD.12.2.DPYD.2_F	chr1:98015112-98015242	GTGGAAATGATGGCAAATGC
DPYD.12.2.DPYD.2_R	chr1:98015112-98015242	GGTCTCCCAGAAGTAGATCC
DPYD.15.10.DPYD.1_F	chr1:98060526-98060748	GGTTGGGTGTGAGAGCTGAA
DPYD.15.10.DPYD.1_R	chr1:98060526-98060748	AAGCCCCTCCTCCTGCTAAT
DPYD.20.3.DPYD.1_F	chr1:98187036-98187178	TTGTGCATGGTGATGGTAGT
DPYD.20.3.DPYD.1_R	chr1:98187036-98187178	TTCTGACAACCCACTTGGTC
DPYD.20.5.DPYD.2_F	chr1:98187148-98187277	TGCATCCACCTACACAAAGA
DPYD.20.5.DPYD.2_R	chr1:98187148-98187277	TGTTTGTCGTAATTTGGCTGT

DPYD.14.1.DPYD.1_F	chr1:98058794-98058944	CTCCTCAGGGACAGCTCTTA
DPYD.14.1.DPYD.1_R	chr1:98058794-98058944	GGGGTTTTCCTTTCATCATTCA
DPYD.14.2.DPYD.2_F	chr1:98058658-98058810	GAAACAATTATGTGTAGCCCTG
DPYD.14.2.DPYD.2_R	chr1:98058658-98058810	CGTGTGTTCATCGTCTTCAG
DPYD.8.1.DPYD.1_F	chr1:97839109-97839250	ACTTAGTGGCAGCTGTCAAG
DPYD.8.1.DPYD.1_R	chr1:97839109-97839250	CAACGGTGAAAGCCTATTGG
DPYD.4.1.DPYD.1_F	chr1:97658653-97658809	TGAGTTCAGCTATACGTGGA
DPYD.4.1.DPYD.1_R	chr1:97658653-97658809	TGGTTGACTGCTCTGTCTTT
DPYD.4.2.DPYD.2_F	chr1:97658537-97658688	GAGGCACTGTGTTTCCTTTG
DPYD.4.2.DPYD.2_R	chr1:97658537-97658688	CAAGACTGGGATGGACAGAG
DPYD.24.1.DPYD.1_F	chr1:98386339-98386481	AAACTTTCCCGCGTCTCTC
DPYD.24.1.DPYD.1_R	chr1:98386339-98386481	ACTCGAGACTGTAGGCACT
DPYD.19.1.DPYD.1_F	chr1:98186399-98186539	ACCTGCTTGTTGACTCCAAA
DPYD.19.1.DPYD.1_R	chr1:98186399-98186539	TGGAAGCAGGTCTTTTATTTGG
DPYD.10.3.DPYD.1_F	chr1:97915588-97915745	TCACCAACTTATGCCAATTCTC
DPYD.10.3.DPYD.1_R	chr1:97915588-97915745	TGTTTCCCCCAGAATCATCC
DPYD.10.4.DPYD.2_F	chr1:97915717-97915869	AGAAAGGAGCTTTGTCCAGG
DPYD.10.4.DPYD.2_R	chr1:97915717-97915869	AAATGTGAGAAGGGACCTCA
DPYD.5.3.DPYD.1_F	chr1:97700405-97700542	GGGACAGACAAACACAATGAC
DPYD.5.3.DPYD.1_R	chr1:97700405-97700542	TGATTTTGTGTAGGGACAGCA
DPYD.5.4.DPYD.2_F	chr1:97700478-97700625	AGTCAATTCCACCAGTAGCC
DPYD.5.4.DPYD.2_R	chr1:97700478-97700625	TGACGCTGTCATCACATCAT
PMS2.6.9.PMS2.1_F	chr7:6029420-6029576	TTAGAAGCTGTTTGTACACTGT
PMS2.6.9.PMS2.1_R	chr7:6029420-6029576	TTTGCCTTAGAATGCGTTGA
PMS2.6.10.PMS2.2_F	chr7:6029524-6029652	GAGGTCTTTAAAACTGCCAACA
PMS2.6.10.PMS2.2_R	chr7:6029524-6029652	AGTGAGACGCTGTCTGAAAA
PMS2.11.1.PMS2.1_F	chr7:6042150-6042287	GAAAATAACTGCTGCACGCT
PMS2.11.1.PMS2.1_R	chr7:6042150-6042287	GTCTCTCACTGAACACACCA
PMS2.11.2.PMS2.2_F	chr7:6042052-6042211	TGCTCATGTGCATTAACCAA
PMS2.11.2.PMS2.2_R	chr7:6042052-6042211	GGTTGGAACTCGACTGATGT
PMS2.3.8.PMS2.1_F	chr7:6018214-6018357	ACCCAGCCGCTATAGTTCTA
PMS2.3.8.PMS2.1_R	chr7:6018214-6018357	AGCTAAATGTTTGACTTCAGGA
PMS2.7.1.PMS2.1_F	chr7:6031601-6031739	ACTGAAATGCCAATGGAACT
PMS2.7.1.PMS2.1_R	chr7:6031601-6031739	AATGTTGTTAGAATGCGGGG
PMS2.9.1.PMS2.1_F	chr7:6036951-6037095	AGTTCTCTTGCCAGCAATCT
PMS2.9.1.PMS2.1_R	chr7:6036951-6037095	ACAGATTAAGTCCACTCTGTCT
PMS2.12.11.PMS2.1_F	chr7:6043303-6043440	CTAAGGGGTCAAGTGAGTGG
PMS2.12.11.PMS2.1_R	chr7:6043303-6043440	GCACTTGAGATATCTTAGTCCTTAC
PMS2.2.1.PMS2.1_F	chr7:6017258-6017415	GAGGCAAACATCTGCTTGAC
PMS2.2.1.PMS2.1_R	chr7:6017258-6017415	ACGTGTTTGTCAAGTCATGG
PMS2.2.2.PMS2.2_F	chr7:6017214-6017366	TGACAGCCAGGCTTTCTTTA
PMS2.2.2.PMS2.2_R	chr7:6017214-6017366	CCAGTCACTGAAAGGGCTAA
PMS2.14.12.PMS2.1_F	chr7:6045516-6045652	TGTGGCTTAAAACTCTCCCA
PMS2.14.12.PMS2.1_R	chr7:6045516-6045652	ACTGATTTCTCTAGTACAGAACCT
PMS2.15.1.PMS2.1_F	chr7:6048583-6048716	AATGCCGTGGGTCTCAAAG
PMS2.15.1.PMS2.1_R	chr7:6048583-6048716	CCAATGGGAGTTCAGGAGG
PMS2.8.13.PMS2.1_F	chr7:6035143-6035282	AGTCAAAGGCATAAAGAACAAACT
PMS2.8.13.PMS2.1_R	chr7:6035143-6035282	CTCTGGAATCCTGCCCTTAC
PMS2.4.6.PMS2.1_F	chr7:6022451-6022605	TGGGAATGAACACTAAACACAC
PMS2.4.6.PMS2.1_R	chr7:6022451-6022605	GCAGTAAAACGATGTTTGCAG
PMS2.4.7.PMS2.2_F	chr7:6022594-6022736	TCCCAGGTTAAACTGACCAA
PMS2.4.7.PMS2.2_R	chr7:6022594-6022736	AAAAGAAAGCGGGATGGCTA
PMS2.1.1.PMS2.1_F	chr7:6013037-6013174	ACAGTGACTACGGTCAGTTC
PMS2.1.1.PMS2.1_R	chr7:6013037-6013174	ACCATTGTGTCTCACACTCA
PMS2.1.2.PMS2.2_F	chr7:6012879-6013038	GCAATGCTCCATCTGGTTTG
PMS2.1.2.PMS2.2_R	chr7:6012879-6013038	CCAACCTGGGTGTCATTTCT
PMS2.10.6.PMS2.1_F	chr7:6038720-6038878	AGAGCAATAAGAGGCGTTGA
PMS2.10.6.PMS2.1_R	chr7:6038720-6038878	CCAAAATGGTCCAGGTCTTAC
PMS2.10.7.PMS2.2_F	chr7:6038845-6038988	CAAGCTGATTGGTGCAACTT
PMS2.10.7.PMS2.2_R	chr7:6038845-6038988	TGCGATGATGTGAGAACCTT
PMS2.13.1.PMS2.1_F	chr7:6043568-6043721	TTCTGAGACATGTGACCCAA
PMS2.13.1.PMS2.1_R	chr7:6043568-6043721	TGATAGCATGGGTCCGTTTT
PMS2.5.1.PMS2.1_F	chr7:6026500-6026659	ACTTTGCTGTGCTTCATGATG
PMS2.5.1.PMS2.1_R	chr7:6026500-6026659	CCCCAAACACAAAGCGTTT
PMS2.5.2.PMS2.2_F	chr7:6026679-6026839	AAAACGCTTTGTGTTTGGGG
PMS2.5.2.PMS2.2_R	chr7:6026679-6026839	CACTGCAGCAGCGAGTA
PMS2.5.3.PMS2.3_F	chr7:6026551-6026682	ATAGAAAAGTCCAGGGGCAC

PMS2.5.3.PMS2.3_R	chr7:6026551-6026682	TGCCTCAGCCAACTAATCTC
PMS2.5.3.PMS2.4_F	chr7:6026860-6027021	TCGCTGCTGCAGTGACT
PMS2.5.3.PMS2.4_R	chr7:6026860-6027021	GGTATGCTGTCTTCTAGCACT
PMS2.5.4.PMS2.5_F	chr7:6026714-6026871	GCTGAGGCAAAACTCGAAAT
PMS2.5.4.PMS2.5_R	chr7:6026714-6026871	ATTCTGAGGGGTTCAGCATC
PMS2.5.4.PMS2.6_F	chr7:6027021-6027181	TTGTCAGAGATGGCACCTG
PMS2.5.4.PMS2.6_R	chr7:6027021-6027181	AAGCAGGATCAATCCCCTTC
PMS2.5.5.PMS2.7_F	chr7:6027115-6027268	GGCTTGTTCTCTGTTGTGTG
PMS2.5.5.PMS2.7_R	chr7:6027115-6027268	TAGTCCCTGACCCTCTTCTC
PTEN.6.1.PTEN.1_F	chr10:89711879-89712021	TTTTTCTGTCCACCAGGGAG
PTEN.6.1.PTEN.1_R	chr10:89711879-89712021	GGAAGGATGAGAATTTCAAGCA
PTEN.6.2.PTEN.2_F	chr10:89711800-89711952	AATGGCTACGACCCAGTTAC
PTEN.6.2.PTEN.2_R	chr10:89711800-89711952	TTGTGAAACAACAGTGCCAC
PTEN.3.1.PTEN.1_F	chr10:89685244-89685379	GCTCATTTTTGTTAATGGTGGC
PTEN.3.1.PTEN.1_R	chr10:89685244-89685379	ACCTCACTCTAACAAGCAGA
PTEN.7.3.PTEN.1_F	chr10:89717579-89717716	ACAGTTAAAGGCATTTCCTGTG
PTEN.7.3.PTEN.1_R	chr10:89717579-89717716	CTTTGATATCACCACACACAGG
PTEN.7.4.PTEN.2_F	chr10:89717717-89717877	TGAGTTCCCTCAGCCGTTA
PTEN.7.4.PTEN.2_R	chr10:89717717-89717877	GCAAAACACCTGCAGATCTA
PTEN.9.1.PTEN.1_F	chr10:89725084-89725240	AACAGTAGAGGAGCCGTCAA
PTEN.9.1.PTEN.1_R	chr10:89725084-89725240	CATGGTGTTTTATCCCTCTTGA
PTEN.9.5.PTEN.2_F	chr10:89724926-89725083	AGATCATGTTTGTTACAGTGCT
PTEN.9.5.PTEN.2_R	chr10:89724926-89725083	TGAACTGCTAGCCTCTGGAT
PTEN.2.6.PTEN.1_F	chr10:89653754-89654004	AGTTTGATTGCTGCATATTTCAGA
PTEN.2.6.PTEN.1_R	chr10:89653754-89654004	GTCCATTAGGTACGGTAAGCCA
PTEN.8.5.PTEN.1_F	chr10:89720757-89720884	TGTGATCAAGAAATCGATAGCA
PTEN.8.5.PTEN.1_R	chr10:89720757-89720884	CAACCCCCACAAAATGTTTAAT
PTEN.8.6.PTEN.2_F	chr10:89720570-89720758	TGCAAATGTTTAACATAGGTGACAGA
PTEN.8.6.PTEN.2_R	chr10:89720570-89720758	TCTGCACGCTCTATACTGCA
PTEN.1.1.PTEN.1_F	chr10:89624218-89624369	CCTTTTTCTTCAGCCACAGG
PTEN.1.1.PTEN.1_R	chr10:89624218-89624369	CTACGGACATTTTCGCATCC
PTEN.4.5.PTEN.1_F	chr10:89690736-89690884	GATTCAGGCAATGTTTGTTAGT
PTEN.4.5.PTEN.1_R	chr10:89690736-89690884	AGTAAGATACAGTCTATCGGGT
PTEN.5.1.PTEN.1_F	chr10:89692820-89692979	CCACCACAGCTAGAACTTATC
PTEN.5.1.PTEN.1_R	chr10:89692820-89692979	CTGGTCCTTACTTCCCCAT
PTEN.5.2.PTEN.2_F	chr10:89692906-89693035	TGTAAAGCTGGAAAGGGACG
PTEN.5.2.PTEN.2_R	chr10:89692906-89693035	TCTCAGATCCAGGAAGAGGA
PTEN.5.5.PTEN.3_F	chr10:89692693-89692829	CCTGTTAAGTTTGTATGCAACA
PTEN.5.5.PTEN.3_R	chr10:89692693-89692829	GCCATTGGTCAAGATCTTCAC
PDGFRB.11.1.PDGFRB.1_F	chr5:149504236-149504394	GAGAGGCTAAGTGTGTGGG
PDGFRB.11.1.PDGFRB.1_R	chr5:149504236-149504394	ATGGATCATCTCTGCACCAG
PDGFRB.21.1.PDGFRB.1_F	chr5:149515128-149515287	GCCCTTACCTGGCACAAA
PDGFRB.21.1.PDGFRB.1_R	chr5:149515128-149515287	GTGGTGTGGGAACGGAT
PDGFRB.21.2.PDGFRB.2_F	chr5:149515281-149515443	ATTTCCTGTGGGGGCTC
PDGFRB.21.2.PDGFRB.2_R	chr5:149515281-149515443	TCTGATACCTCCTCTCCCAA
PDGFRB.21.2.PDGFRB.3_F	chr5:149515031-149515187	TAGGATGGCTGCATTTCACA
PDGFRB.21.2.PDGFRB.3_R	chr5:149515031-149515187	GGCTAGACACGGGAGAATAC
PDGFRB.7.1.PDGFRB.1_F	chr5:149500766-149500898	CCACCAACACCACACGTA
PDGFRB.7.1.PDGFRB.1_R	chr5:149500766-149500898	AAGATAGCAGGTGACCCTCT
PDGFRB.2.1.PDGFRB.1_F	chr5:149497260-149497422	AGGCAGGGGGATGATATAGT
PDGFRB.2.1.PDGFRB.1_R	chr5:149497260-149497422	TTTGGTTCTCCCTGCCC
PDGFRB.2.2.PDGFRB.2_F	chr5:149497157-149497287	ACACACTGTGCACAATTTCC
PDGFRB.2.2.PDGFRB.2_R	chr5:149497157-149497287	CCAGCTCCGTCCTCTATACT
PDGFRB.17.1.PDGFRB.1_F	chr5:149512392-149512546	GTGCGGTTGTCTTTGAACC
PDGFRB.17.1.PDGFRB.1_R	chr5:149512392-149512546	CTTTGGGATTCAGTTGGTGC
PDGFRB.17.2.PDGFRB.2_F	chr5:149512302-149512445	CAAGAATGGGATGGGAGAGC
PDGFRB.17.2.PDGFRB.2_R	chr5:149512302-149512445	ACAATTTGCTGAGCTGCATC
PDGFRB.22.1.PDGFRB.1_F	chr5:149516460-149516610	AACTAAAGCTGAAGGGCAGG
PDGFRB.22.1.PDGFRB.1_R	chr5:149516460-149516610	GTTTAACTCTGCAGGACACC
PDGFRB.1.1.PDGFRB.1_F	chr5:149495351-149495509	GGAAGCTATCCTCTGCTTCC
PDGFRB.1.1.PDGFRB.1_R	chr5:149495351-149495509	CTCACTGCCTCTTTCCTCTAG
PDGFRB.1.2.PDGFRB.2_F	chr5:149495228-149495371	GAAGGGGACAGCTGATAAGG
PDGFRB.1.2.PDGFRB.2_R	chr5:149495228-149495371	TGGAACAGTTGCCGGATTC
PDGFRB.18.1.PDGFRB.1_F	chr5:149513156-149513319	AGGCACACACCAACCAC
PDGFRB.18.1.PDGFRB.1_R	chr5:149513156-149513319	AACCTGTTGCTGCAGAGTG
PDGFRB.18.2.PDGFRB.2_F	chr5:149513304-149513440	CCAAGAGGAAGTCAGTCACC
PDGFRB.18.2.PDGFRB.2_R	chr5:149513304-149513440	CATACCCCCGCAAAGAAGTA

PDGFRB.18.2.PDGFRB.3_F	chr5:149513130-149513283	TGAAGGAATTGGGGATTGGG
PDGFRB.18.2.PDGFRB.3_R	chr5:149513130-149513283	GGTGACTGACTTCCTCTTGG
PDGFRB.13.1.PDGFRB.1_F	chr5:149506032-149506180	GGCAGAGGGGTGGAATTTAT
PDGFRB.13.1.PDGFRB.1_R	chr5:149506032-149506180	CTGCTCTCATCTCTGCCTC
PDGFRB.16.1.PDGFRB.1_F	chr5:149511523-149511685	AAGGAGCAGGGACATGG
PDGFRB.16.1.PDGFRB.1_R	chr5:149511523-149511685	ACTGTAAGAGTCCTTCCGAC
PDGFRB.6.1.PDGFRB.1_F	chr5:149500430-149500595	ACTGTGACTGCCCTGCA
PDGFRB.6.1.PDGFRB.1_R	chr5:149500430-149500595	TTGTCCCCAAGGCCTCA
PDGFRB.3.1.PDGFRB.1_F	chr5:149498261-149498418	CCTTGTACTCGGTGTCTGAC
PDGFRB.3.1.PDGFRB.1_R	chr5:149498261-149498418	CTGACCCTTCTCCCTATCCC
PDGFRB.9.1.PDGFRB.1_F	chr5:149502645-149502788	GGCAGAGCATTGCTGTAGA
PDGFRB.9.1.PDGFRB.1_R	chr5:149502645-149502788	TGAGGCCTCCATAGGGACT
PDGFRB.9.2.PDGFRB.2_F	chr5:149502577-149502733	GCTCCTCAGGTATCCCAAAG
PDGFRB.9.2.PDGFRB.2_R	chr5:149502577-149502733	ATCATCACTGAGTACTGCCG
PDGFRB.12.1.PDGFRB.1_F	chr5:149505004-149505145	ACATGAGGCCTCTCAGGAC
PDGFRB.12.1.PDGFRB.1_R	chr5:149505004-149505145	CTAATTCCTGGGGTTGGTCC
PDGFRB.14.1.PDGFRB.1_F	chr5:149509329-149509490	GGACTCACAGTGTGGCA
PDGFRB.14.1.PDGFRB.1_R	chr5:149509329-149509490	GCTGCTGGGGAACAGTT
PDGFRB.14.2.PDGFRB.2_F	chr5:149509467-149509623	CTCCCAGTACGTCACGTTAG
PDGFRB.14.2.PDGFRB.2_R	chr5:149509467-149509623	CAGTGGGACATAGGAACTGG
PDGFRB.14.2.PDGFRB.3_F	chr5:149509267-149509420	GGGCACATTACCAATTAGGC
PDGFRB.14.2.PDGFRB.3_R	chr5:149509267-149509420	CAGGAGTTTGAGGTGGTGAG
PDGFRB.15.1.PDGFRB.1_F	chr5:149510070-149510228	TTTTTCTAGCCAGCTGGGG
PDGFRB.15.1.PDGFRB.1_R	chr5:149510070-149510228	AACTCAGTGCTCTCTCCATG
PDGFRB.20.1.PDGFRB.1_F	chr5:149514279-149514438	TCTGTGGAGGGTTATACTTGC
PDGFRB.20.1.PDGFRB.1_R	chr5:149514279-149514438	AAGAAAGGGGACGTTGCAC
PDGFRB.20.2.PDGFRB.2_F	chr5:149514428-149514585	AAGCCACGTTGGTGATCATA
PDGFRB.20.2.PDGFRB.2_R	chr5:149514428-149514585	TTTATTCACGGCTCCACTCC
PDGFRB.8.1.PDGFRB.1_F	chr5:149501443-149501603	ATGTCACTATGTCCACCCAC
PDGFRB.8.1.PDGFRB.1_R	chr5:149501443-149501603	GATGCTCCTTTACCCCCAG
PDGFRB.4.1.PDGFRB.1_F	chr5:149499030-149499187	ATGCATGAGACTCCACTCAC
PDGFRB.4.1.PDGFRB.1_R	chr5:149499030-149499187	CCTTGTCCTGTAGAAGAGGG
PDGFRB.19.1.PDGFRB.1_F	chr5:149513443-149513581	TGCCTGGCCCCACATTA
PDGFRB.19.1.PDGFRB.1_R	chr5:149513443-149513581	CCCAGACCTAAGCCAATCTC
PDGFRB.10.1.PDGFRB.1_F	chr5:149503781-149503924	CTTGGTGGTGGGCACTTT
PDGFRB.10.1.PDGFRB.1_R	chr5:149503781-149503924	GGCCCCCATTTTCCTCA
PDGFRB.5.1.PDGFRB.1_F	chr5:149499532-149499686	CATGAGTGGTCGAGGTAGAC
PDGFRB.5.1.PDGFRB.1_R	chr5:149499532-149499686	TGTCCTGACCTCCCTACAG
MSH6.6.1.MSH6.1_F	chr2:48032046-48032181	GACCTTTTCCTCCCTCATTCA
MSH6.6.1.MSH6.1_R	chr2:48032046-48032181	ACTGAATGAGAACTTAAGTGGG
MSH6.3.1.MSH6.1_F	chr2:48023053-48023210	AGGTTCAAAATCAAAGGAAGCC
MSH6.3.1.MSH6.1_R	chr2:48023053-48023210	TAACAACTGAATGCTTGCCG
MSH6.3.2.MSH6.2_F	chr2:48023015-48023158	ACCCGGCCCTTATTGTTTAT
MSH6.3.2.MSH6.2_R	chr2:48023015-48023158	CTCTGAGGGCTCATCACAAA
MSH6.7.19.MSH6.1_F	chr2:48032629-48032849	GCCCGGCCAATAATTGCATA
MSH6.7.19.MSH6.1_R	chr2:48032629-48032849	AGTCTTCAAATGAGAAGTTTAATGTCT
MSH6.9.1.MSH6.1_F	chr2:48033681-48033840	GGGAGCTTGTCCTAAAAGC
MSH6.9.1.MSH6.1_R	chr2:48033681-48033840	CCTTCCCCTTTTACTGTTTCT
MSH6.9.2.MSH6.2_F	chr2:48033572-48033701	TTGCTAGCACATGTATCGCT
MSH6.9.2.MSH6.2_R	chr2:48033572-48033701	TCCTCTGGGAGATTAGCAAG
MSH6.2.1.MSH6.1_F	chr2:48018106-48018267	TTGGTTTGGGCCAAGATG
MSH6.2.1.MSH6.1_R	chr2:48018106-48018267	CACACATGGCAGTAGTGACT
MSH6.2.2.MSH6.2_F	chr2:48017991-48018120	TGCCAGAAGACTTGGAATTG
MSH6.2.2.MSH6.2_R	chr2:48017991-48018120	TTGTAAACCAGACAAGGCCA
MSH6.8.1.MSH6.1_F	chr2:48033392-48033551	GCAATAGCAAATGCAGTTGT
MSH6.8.1.MSH6.1_R	chr2:48033392-48033551	AGCGATACATGTGCTAGCAA
MSH6.8.16.MSH6.2_F	chr2:48033268-48033400	CCGATGTTGCTTTTCTGTCC
MSH6.8.16.MSH6.2_R	chr2:48033268-48033400	ACGACATTTTATAGTCTCAGCA
MSH6.4.1.MSH6.1_F	chr2:48025760-48025919	CTGGCAGGTAGGCACAA
MSH6.4.1.MSH6.1_R	chr2:48025760-48025919	CTTCCTCCTTAGTGTCTGGC
MSH6.4.2.MSH6.2_F	chr2:48025918-48026079	GTGGCTCTGATGTGGAATTT
MSH6.4.2.MSH6.2_R	chr2:48025918-48026079	TTGTTTGGTGGCTGAGGG
MSH6.4.2.MSH6.3_F	chr2:48025748-48025881	ATACTCTTTCCTTGCCTGGC
MSH6.4.2.MSH6.3_R	chr2:48025748-48025881	CCACCAATGTCACTCTCAGA
MSH6.4.3.MSH6.4_F	chr2:48026088-48026249	AAGGAAACGCCCTCAGC
MSH6.4.3.MSH6.4_R	chr2:48026088-48026249	CTGTGCTCATCTCTTCTCTTT
MSH6.4.4.MSH6.5_F	chr2:48026052-48026190	GTGACTGGAAATGGCTCTCT

MSH6.4.4.MSH6.5_R	chr2:48026052-48026190	GTAGGGCGACTACTGTCATC
MSH6.4.4.MSH6.6_F	chr2:48026286-48026450	AGGAGGAGGCCTGATCA
MSH6.4.4.MSH6.6_R	chr2:48026286-48026450	AGCCCCAGTTCACTGACT
MSH6.4.5.MSH6.7_F	chr2:48026211-48026351	GATGACAGTAGTCGCCCTAC
MSH6.4.5.MSH6.7_R	chr2:48026211-48026351	TAATCTGCCACCACTTCCTC
MSH6.4.5.MSH6.8_F	chr2:48026470-48026630	TCAGTGAACTGGGGCTG
MSH6.4.5.MSH6.8_R	chr2:48026470-48026630	CCTCACCACTCTATCATACTTG
MSH6.4.6.MSH6.9_F	chr2:48026441-48026592	TGAGCTGTACCACATGGATG
MSH6.4.6.MSH6.9_R	chr2:48026441-48026592	CTACATCGTGCCTCCATCAT
MSH6.4.6.MSH6.10_F	chr2:48026711-48026870	TACAGTGTGCTGGAAGGTG
MSH6.4.6.MSH6.10_R	chr2:48026711-48026870	GGATAGTGTGCCACTAGAGTC
MSH6.4.7.MSH6.11_F	chr2:48026613-48026765	ATGATGGAGGCACGATGTAG
MSH6.4.7.MSH6.11_R	chr2:48026613-48026765	CACGAGTATGGCCAGAAGAA
MSH6.4.7.MSH6.12_F	chr2:48026900-48027060	GCACACTATCCCCCAGTAC
MSH6.4.7.MSH6.12_R	chr2:48026900-48027060	ACCCCAATGCCATCACTTAG
MSH6.4.8.MSH6.13_F	chr2:48026863-48026997	CAGATGATCGCCATTGTTCG
MSH6.4.8.MSH6.13_R	chr2:48026863-48026997	TTGGATGCATCCCAAAACTG
MSH6.4.8.MSH6.14_F	chr2:48027090-48027250	GCATTGGGGTGATGTTACC
MSH6.4.8.MSH6.14_R	chr2:48027090-48027250	TGTGTCAGAATCCAAGGGAA
MSH6.4.9.MSH6.15_F	chr2:48027018-48027168	CAGTTTTGGGATGCATCCAA
MSH6.4.9.MSH6.15_R	chr2:48027018-48027168	AAGACACAACCACCTAGAGC
MSH6.4.9.MSH6.16_F	chr2:48027271-48027430	TTCCCTTGGATTCTGACACA
MSH6.4.9.MSH6.16_R	chr2:48027271-48027430	GCTTTAGGAGCCGCTTAC
MSH6.4.10.MSH6.17_F	chr2:48027183-48027312	CTCTCTGCTCTAGGTGGTTG
MSH6.4.10.MSH6.17_R	chr2:48027183-48027312	GCATCTAGCACCATTCGTTG
MSH6.4.10.MSH6.18_F	chr2:48027470-48027633	GCTTTGTGCCCCACTCT
MSH6.4.10.MSH6.18_R	chr2:48027470-48027633	TTATAGCCCTGCTGTCTGG
MSH6.4.11.MSH6.19_F	chr2:48027420-48027563	GAGAGGGTTGATACTTGCCA
MSH6.4.11.MSH6.19_R	chr2:48027420-48027563	GCCTCTCAAGATCTGGAAGC
MSH6.4.11.MSH6.20_F	chr2:48027654-48027813	CCAGACAGCAGGGCTATAAT
MSH6.4.11.MSH6.20_R	chr2:48027654-48027813	TCAGGAAAACGACCTTCAGG
MSH6.4.12.MSH6.21_F	chr2:48027536-48027694	CATGGTTGTGCCTGACAAAA
MSH6.4.12.MSH6.21_R	chr2:48027536-48027694	TCCTTCCAGAGCAGAAAGAA
MSH6.4.12.MSH6.22_F	chr2:48027834-48027993	CCTGAAGGTCGTTTTCCTGA
MSH6.4.12.MSH6.22_R	chr2:48027834-48027993	GCCAATTCTGTTGCGCTG
MSH6.4.13.MSH6.23_F	chr2:48027766-48027910	TGGAAGAAGTTGCTGATGGT
MSH6.4.13.MSH6.23_R	chr2:48027766-48027910	ATCAGAGTCAAAGCCTGCTT
MSH6.4.13.MSH6.24_F	chr2:48028014-48028173	GCGCAACAGAATTGGCTG
MSH6.4.13.MSH6.24_R	chr2:48028014-48028173	TCCGTTCTTCAGCATTTATGAG
MSH6.4.14.MSH6.25_F	chr2:48027921-48028052	ATTACTCCCAAAGCAGGCTT
MSH6.4.14.MSH6.25_R	chr2:48027921-48028052	TCTCAGGAATTTCCAGCTGG
MSH6.4.14.MSH6.26_F	chr2:48028199-48028329	AAATGCTGAAGAACGGAGGG
MSH6.4.14.MSH6.26_R	chr2:48028199-48028329	CTGGCAAACAGCACTACTTA
MSH6.4.15.MSH6.27_F	chr2:48028073-48028218	CCAGCTGGAAATTCCTGAGA
MSH6.4.15.MSH6.27_R	chr2:48028073-48028218	TTATAGAACAGTCGCCGCAT
MSH6.1.1.MSH6.1_F	chr2:48010412-48010572	TGTACAGCTTCTTCCCCAAG
MSH6.1.1.MSH6.1_R	chr2:48010412-48010572	GTTGAGGTTCTTCGCCTTG
MSH6.1.16.MSH6.2_F	chr2:48010250-48010413	TGTTGATTGGCCACTGGG
MSH6.1.16.MSH6.2_R	chr2:48010250-48010413	ATCACTCAGCGCCGGA
MSH6.1.17.MSH6.3_F	chr2:48010509-48010654	TCTCCTTCCCCAGGCG
MSH6.1.17.MSH6.3_R	chr2:48010509-48010654	CTATGCCCCCGCCTTC
MSH6.10.1.MSH6.1_F	chr2:48033875-48034024	GGGAAGGGATGATGCACTAT
MSH6.10.1.MSH6.1_R	chr2:48033875-48034024	ACCACCTTTGTCAGAAGTCA
MSH6.5.1.MSH6.1_F	chr2:48030579-48030738	ATGTTTTACTGTGCCTGGCT
MSH6.5.1.MSH6.1_R	chr2:48030579-48030738	ATTTTCCTGCTCCTCTTCCT
MSH6.5.2.MSH6.2_F	chr2:48030526-48030669	GCTGATAAAACCCCCAAACG
MSH6.5.2.MSH6.2_R	chr2:48030526-48030669	CTTCGTAATGCAAGGATGGC
MSH6.5.18.MSH6.3_F	chr2:48030739-48030887	CCTAATGACATTCTAATAGGCTGTG
MSH6.5.18.MSH6.3_R	chr2:48030739-48030887	CTGTGTTTGGAAAATGATCACC
JAK3.11.1.JAK3.1_F	chr19:17946732-17946891	AGGCAGAGGAGCACTCA
JAK3.11.1.JAK3.1_R	chr19:17946732-17946891	ACACAAGTGCAGTTCAGTCT
JAK3.21.1.JAK3.1_F	chr19:17953846-17953994	GGCTCTCACCTGACAGTCT
JAK3.21.1.JAK3.1_R	chr19:17953846-17953994	TCAGCTGATGCTCCCTGT
JAK3.21.2.JAK3.2_F	chr19:17953750-17953911	GAAAGCTTGCAGGAGAACTC
JAK3.21.2.JAK3.2_R	chr19:17953750-17953911	AGCAGGGTGAGTGTCTCA
JAK3.7.1.JAK3.1_F	chr19:17943604-17943750	TGCCCACCTTACCTTGC
JAK3.7.1.JAK3.1_R	chr19:17943604-17943750	TGCTTACCACTGCCCATG

JAK3.7.2.JAK3.2_F	chr19:17943478-17943623	GCACCTGTATTGTCGCCTA
JAK3.7.2.JAK3.2_R	chr19:17943478-17943623	ATCTTCGAGGAGAGACACCT
JAK3.17.1.JAK3.1_F	chr19:17951001-17951156	ATTCAAACGTCACCTCCTCC
JAK3.17.1.JAK3.1_R	chr19:17951001-17951156	CATTCCCTCTCACCTTCCC
JAK3.2.1.JAK3.1_F	chr19:17940839-17940998	CCTTTCTTCTCAGTACAGAGAC
JAK3.2.1.JAK3.1_R	chr19:17940839-17940998	GATGATGGGATGTGAGCG
JAK3.2.2.JAK3.2_F	chr19:17940902-17941034	GACTGGGAAACTGAGGCTAG
JAK3.2.2.JAK3.2_R	chr19:17940902-17941034	ACATGCGCTCCTCCTTG
JAK3.22.1.JAK3.1_F	chr19:17954184-17954315	TCAAACCCCAGGCAGAAC
JAK3.22.1.JAK3.1_R	chr19:17954184-17954315	CACTTTCATCCCAGGGTTCT
JAK3.1.1.JAK3.1_F	chr19:17937562-17937725	GGGCAGGAGCTATGAAAAG
JAK3.1.1.JAK3.1_R	chr19:17937562-17937725	ATTATCTGTCCCCCGCC
JAK3.1.2.JAK3.2_F	chr19:17937459-17937593	TCCTGAAGTAGAGGACCCTC
JAK3.1.2.JAK3.2_R	chr19:17937459-17937593	GTGAGACTCATGCCTTCACT
JAK3.18.1.JAK3.1_F	chr19:17952207-17952369	AGGTCCTTACGTGATGGGG
JAK3.18.1.JAK3.1_R	chr19:17952207-17952369	TTTCACTGGGCTCTGACG
JAK3.18.2.JAK3.2_F	chr19:17952095-17952250	GCAGGTGTGGTTTGAAAACT
JAK3.18.2.JAK3.2_R	chr19:17952095-17952250	ACTTCTTCTGCAAGGAGGTG
JAK3.23.1.JAK3.1_F	chr19:17954568-17954726	AATTGTACAATCCCTGGGGG
JAK3.23.1.JAK3.1_R	chr19:17954568-17954726	GACTCAGGAGGGAGCTGAT
JAK3.13.1.JAK3.1_F	chr19:17948729-17948872	GACTCCAAAAGTCTGGTCCA
JAK3.13.1.JAK3.1_R	chr19:17948729-17948872	CTGTCCCCTCACCATTCAG
JAK3.16.1.JAK3.1_F	chr19:17950292-17950455	AAGGGGCTCACCTTTGG
JAK3.16.1.JAK3.1_R	chr19:17950292-17950455	AACCCCCTTGGTCCTGA
JAK3.16.2.JAK3.2_F	chr19:17950422-17950561	CCAACCAGAAGGAAGGTTCC
JAK3.16.2.JAK3.2_R	chr19:17950422-17950561	CCAGACTCCGTCTCCAAAAA
JAK3.16.2.JAK3.3_F	chr19:17950268-17950401	CAGATCAGCCACTCATTCCA
JAK3.16.2.JAK3.3_R	chr19:17950268-17950401	GGAACCTTCCTTCTGGTTGG
JAK3.6.1.JAK3.1_F	chr19:17943348-17943508	GGCCATAGCTGACACCA
JAK3.6.1.JAK3.1_R	chr19:17943348-17943508	TATCCCCCAGGGCAACTTT
JAK3.6.2.JAK3.2_F	chr19:17943478-17943623	GCACCTGTATTGTCGCCTA
JAK3.6.2.JAK3.2_R	chr19:17943478-17943623	ATCTTCGAGGAGAGACACCT
JAK3.6.2.JAK3.3_F	chr19:17943243-17943387	TAATCACGTTCCCAGCCTAC
JAK3.6.2.JAK3.3_R	chr19:17943243-17943387	CTTTCAGCGGGAGATTCAGA
JAK3.3.1.JAK3.1_F	chr19:17941288-17941436	GTGGAGGGAGAAGAAGGCT
JAK3.3.1.JAK3.1_R	chr19:17941288-17941436	CATCTCAAGACCTTGTCCCC
JAK3.9.1.JAK3.1_F	chr19:17945666-17945822	TGAGGGGCTCTGACCTTAG
JAK3.9.1.JAK3.1_R	chr19:17945666-17945822	GGATCCCTGATCCCACTTTC
JAK3.9.2.JAK3.2_F	chr19:17945559-17945699	GAGAGGAGCAGTCGGTAATC
JAK3.9.2.JAK3.2_R	chr19:17945559-17945699	CGGTCTGGGAAGTGTTTAGT
JAK3.12.1.JAK3.1_F	chr19:17947883-17948031	CTCAGAACAGAGGTGGGAAG
JAK3.12.1.JAK3.1_R	chr19:17947883-17948031	CATCTTCTCTCCCTTCCCAC
JAK3.20.3.JAK3.1_F	chr19:17953235-17953400	CACGTGGAAGGTCTCGG
JAK3.20.3.JAK3.1_R	chr19:17953235-17953400	ACAAGGCCTGCCTACCC
JAK3.20.4.JAK3.2_F	chr19:17953383-17953536	AAGCTCAGGCCCTGGAT
JAK3.20.4.JAK3.2_R	chr19:17953383-17953536	AATGAGAGTCTGTGTGTGCC
JAK3.20.5.JAK3.3_F	chr19:17953135-17953267	GCCCTCACCTCCTGTTCT
JAK3.20.5.JAK3.3_R	chr19:17953135-17953267	GCTCATGGCCAAGTACATCA
JAK3.20.6.JAK3.4_F	chr19:17953065-17953216	ACATCCCCTACCACTCTCC
JAK3.20.6.JAK3.4_R	chr19:17953065-17953216	CGAGACCTTCCACGTGG
JAK3.14.1.JAK3.1_F	chr19:17949072-17949204	CATTTCCCAGGGCCTCTTAC
JAK3.14.1.JAK3.1_R	chr19:17949072-17949204	TTTCTCCCTCATCCTCTCCC
JAK3.15.1.JAK3.1_F	chr19:17949969-17950107	CGGTTCTACCAGGGATTCTG
JAK3.15.1.JAK3.1_R	chr19:17949969-17950107	AACCTTTAGGTCTGGCTTGA
JAK3.8.1.JAK3.1_F	chr19:17945394-17945538	GGCACCTGAAGAGATGAGG
JAK3.8.1.JAK3.1_R	chr19:17945394-17945538	GATTACCGACTGCTCCTCTC
JAK3.8.2.JAK3.2_F	chr19:17945346-17945505	CTGGGCCCAATATGACATCA
JAK3.8.2.JAK3.2_R	chr19:17945346-17945505	CCAATTTTATGAGGACCGGC
JAK3.4.1.JAK3.1_F	chr19:17942084-17942232	CGGACCACGTAGTAGTCTTT
JAK3.4.1.JAK3.1_R	chr19:17942084-17942232	TATCCTGGGATCCTCTCTGC
JAK3.4.2.JAK3.2_F	chr19:17941927-17942086	AAGCTGCAGCGGAGGAA
JAK3.4.2.JAK3.2_R	chr19:17941927-17942086	CTAAGCTGCTGCCGCTT
JAK3.24.1.JAK3.1_F	chr19:17955043-17955202	CCACTAGGGATGCACTCAC
JAK3.24.1.JAK3.1_R	chr19:17955043-17955202	CACCTCCAAGTGAAGAGACG
JAK3.24.2.JAK3.2_F	chr19:17955199-17955351	CATGAACGCTGAGGGATCA
JAK3.24.2.JAK3.2_R	chr19:17955199-17955351	CCTCCCAAAATGCTGTGATT
JAK3.10.1.JAK3.1_F	chr19:17945892-17946032	CTCCACCTCCAGGAACTTAC

JAK3.10.1.JAK3.1_R	chr19:17945892-17946032	GCATTTTCCTGTGTCTGGC
JAK3.19.1.JAK3.1_F	chr19:17952457-17952618	TCCTGCACCCACTAAAATCT
JAK3.19.1.JAK3.1_R	chr19:17952457-17952618	GTTCATGGGCGTGGTTTG
JAK3.19.2.JAK3.2_F	chr19:17952390-17952537	GTCAGAGCCCAGTGAAACC
JAK3.19.2.JAK3.2_R	chr19:17952390-17952537	CTGCGACTTTCCAGAAATCG
JAK3.5.1.JAK3.1_F	chr19:17942463-17942610	CAGCTGAATCCCCACAAGT
JAK3.5.1.JAK3.1_R	chr19:17942463-17942610	GTGACAGATCCTGCCTTCTC
TOP1.11.1.TOP1.1_F	chr20:39726838-39726995	CGTTGTTTTTCTTTCATCTCCC
TOP1.11.1.TOP1.1_R	chr20:39726838-39726995	TCCAGAATTCTCCAGAGGTT
TOP1.21.1.TOP1.1_F	chr20:39751806-39751943	CCATTGCTGAGTCACCCTAA
TOP1.21.1.TOP1.1_R	chr20:39751806-39751943	CACAGAACTCTGCCTCTTGA
TOP1.7.1.TOP1.1_F	chr20:39709736-39709889	GGAGGCATCCAAGAGTTTGT
TOP1.7.1.TOP1.1_R	chr20:39709736-39709889	CCCCAAAGGACCTAAGTCTC
TOP1.17.1.TOP1.1_F	chr20:39744916-39745071	TCTGTTGCTTTGTCTCCTCC
TOP1.17.1.TOP1.1_R	chr20:39744916-39745071	CAAGGTCACCGGATACCATT
TOP1.2.1.TOP1.1_F	chr20:39658081-39658244	TTTTTCCAGATCGAAGCGG
TOP1.2.1.TOP1.1_R	chr20:39658081-39658244	AAAGGGGGTCAAGAGGC
TOP1.2.2.TOP1.2_F	chr20:39658245-39658404	ATTGTTCCCATCGGGCC
TOP1.2.2.TOP1.2_R	chr20:39658245-39658404	AAAAGAAAATGGCGCAGAGA
TOP1.2.2.TOP1.3_F	chr20:39657932-39658086	AAGTTACAGTTCGAGGCAGG
TOP1.2.2.TOP1.3_R	chr20:39657932-39658086	GGCACACTCACCATTCAATC
TOP1.1.5.TOP1.1_F	chr20:39657668-39657832	TCTGCGTCTCCCCCAC
TOP1.1.5.TOP1.1_R	chr20:39657668-39657832	CTCCGGCCTGTCAAAGC
TOP1.18.1.TOP1.1_F	chr20:39746797-39746950	ACCCTCTTGCTACCATGTTC
TOP1.18.1.TOP1.1_R	chr20:39746797-39746950	GCAGACACAGTTCCCTTCAT
TOP1.16.1.TOP1.1_F	chr20:39743950-39744092	GCAAGTTTCTTTAAGTTTGGGG
TOP1.16.1.TOP1.1_R	chr20:39743950-39744092	CTCCCTTCAACATTGTGTGC
TOP1.13.1.TOP1.1_F	chr20:39729841-39729999	CACTATCCTCGTGCTCTGTT
TOP1.13.1.TOP1.1_R	chr20:39729841-39729999	AGTGCAGCTCTCAACTATCC
TOP1.6.6.TOP1.1_F	chr20:39708710-39708846	CTAGCACTCTGACCAGCAAT
TOP1.6.6.TOP1.1_R	chr20:39708710-39708846	AACTCCTCCTTTTTGTTTTCAAA
TOP1.3.1.TOP1.1_F	chr20:39689978-39690132	TGACCAGCTTGTCAAGGTAG
TOP1.3.1.TOP1.1_R	chr20:39689978-39690132	ACTTGCTTGATTCCACCCTT
TOP1.9.1.TOP1.1_F	chr20:39721104-39721255	AAATGAGGCTGTGCTTTGTC
TOP1.9.1.TOP1.1_R	chr20:39721104-39721255	GCAGATTTCTTTTCCTGGCC
TOP1.12.3.TOP1.1_F	chr20:39728696-39728853	ACTTTCTTGCTGTCTTCCAG
TOP1.12.3.TOP1.1_R	chr20:39728696-39728853	GTTGATGATTATATCCTCGGGC
TOP1.12.4.TOP1.2_F	chr20:39728852-39728996	GCATGCTGAAGAGACGAATC
TOP1.12.4.TOP1.2_R	chr20:39728852-39728996	CGCATGAAATACTGTCCTGC
TOP1.15.1.TOP1.1_F	chr20:39742620-39742779	TGGGCAGCTTGCTCTGA
TOP1.15.1.TOP1.1_R	chr20:39742620-39742779	CTTACTCGTTTCTCAACAGGG
TOP1.15.2.TOP1.2_F	chr20:39742753-39742899	GAGTTTGACTTCCTCGGGAA
TOP1.15.2.TOP1.2_R	chr20:39742753-39742899	ATGTTGCCTGTCTCAAGTCA
TOP1.15.2.TOP1.3_F	chr20:39742478-39742633	GCTTGCAGTGAGCCAAAATT
TOP1.15.2.TOP1.3_R	chr20:39742478-39742633	GCTGTTTCTCCTTCCTCCTT
TOP1.14.1.TOP1.1_F	chr20:39741418-39741575	ACATTTGGGTTTGGGTCTTT
TOP1.14.1.TOP1.1_R	chr20:39741418-39741575	TAGACAATGCCGATGGGAAG
TOP1.20.1.TOP1.1_F	chr20:39750636-39750795	TGGTTCTTGAGGACTTTGCT
TOP1.20.1.TOP1.1_R	chr20:39750636-39750795	AAGGAGGGCTCAACACTTAC
TOP1.8.1.TOP1.1_F	chr20:39713058-39713208	AAAACTGCCTCCAGAAGTGT
TOP1.8.1.TOP1.1_R	chr20:39713058-39713208	ACCCAGTGCTGAGATGTTAC
TOP1.4.1.TOP1.1_F	chr20:39704792-39704947	CTACTCTGGGCTAACGCTTT
TOP1.4.1.TOP1.1_R	chr20:39704792-39704947	CGTTCCTTCCTCCCCTACTA
TOP1.10.1.TOP1.1_F	chr20:39725848-39725981	ACCTCACTTTTTGGAACCAC
TOP1.10.1.TOP1.1_R	chr20:39725848-39725981	TTAACACATGGGCTACAGTAC
TOP1.19.1.TOP1.1_F	chr20:39750296-39750453	TCTCAGGTGGAGCCATTTTT
TOP1.19.1.TOP1.1_R	chr20:39750296-39750453	CTTTTCTCTACCAGCCCCAA
TOP1.5.1.TOP1.1_F	chr20:39706132-39706277	GCCAGCTTGTGATCATGATG
TOP1.5.1.TOP1.1_R	chr20:39706132-39706277	CGCAGCAGCAAAGTCTTAC
JAK1.11.1.JAK1.1_F	chr1:65311182-65311337	GGTGGGACCATTATGGACAT
JAK1.11.1.JAK1.1_R	chr1:65311182-65311337	CAGGTTCCAGACATGGCTAT
JAK1.21.1.JAK1.1_F	chr1:65339053-65339210	CTGGGCCCAAACTTCCTAC
JAK1.21.1.JAK1.1_R	chr1:65339053-65339210	GGCATTCATTTTCCTGCCTT
JAK1.7.1.JAK1.1_F	chr1:65306927-65307083	GCAGCACGGGTGTAACTTA
JAK1.7.1.JAK1.1_R	chr1:65306927-65307083	CTTGGGGAGAAACAGGAGC
JAK1.2.5.JAK1.1_F	chr1:65301084-65301242	GTGGCCCATAGATACCTCAT
JAK1.2.5.JAK1.1_R	chr1:65301084-65301242	TTCACCTTAATCTGTTTGGCA

JAK1.2.6.JAK1.2_F	chr1:65301018-65301160	CTCTACCCATTGCTGGACAA
JAK1.2.6.JAK1.2_R	chr1:65301018-65301160	AAAATGATAGGCCCAACCCA
JAK1.17.1.JAK1.1_F	chr1:65325792-65325946	AGGTTCTAGGACCAACCAGA
JAK1.17.1.JAK1.1_R	chr1:65325792-65325946	GGGAATTTCTTCTCTCTCAACA
JAK1.17.2.JAK1.2_F	chr1:65325733-65325880	AATGATGACATGCCCCATCA
JAK1.17.2.JAK1.2_R	chr1:65325733-65325880	CTGGTAGATGGCTACTTCCG
JAK1.22.1.JAK1.1_F	chr1:65344705-65344851	TACCAGGTCAGTACTTCCCA
JAK1.22.1.JAK1.1_R	chr1:65344705-65344851	CCGCCTTGATTTTCTGATGT
JAK1.1.7.JAK1.1_F	chr1:65300210-65300360	TTGTTGCAGGAGAAGGACTT
JAK1.1.7.JAK1.1_R	chr1:65300210-65300360	CCCAGATCTAACATTTTTACTGTTG
JAK1.18.1.JAK1.1_F	chr1:65330547-65330702	TGAGTGATTTCAGGGAAGTAAG
JAK1.18.1.JAK1.1_R	chr1:65330547-65330702	GCACTGACCTTTTACCAATAGA
JAK1.18.2.JAK1.2_F	chr1:65330426-65330557	GGAACTCAGCAATTCTCCCT
JAK1.18.2.JAK1.2_R	chr1:65330426-65330557	AACAAGATCCGGGAAGAGTG
JAK1.16.1.JAK1.1_F	chr1:65323311-65323465	GACACCTCATGGCTGTATGG
JAK1.16.1.JAK1.1_R	chr1:65323311-65323465	CCTTTGCCTACTTCTCCCTC
JAK1.13.1.JAK1.1_F	chr1:65313209-65313358	GGAGGAGTTCAGAGGAAGAC
JAK1.13.1.JAK1.1_R	chr1:65313209-65313358	CCTTCTGCTTCTTCCCTCAG
JAK1.23.1.JAK1.1_F	chr1:65348959-65349119	GCAGCTGCCAGTACTCA
JAK1.23.1.JAK1.1_R	chr1:65348959-65349119	CTGCAATGCCATGGCTTTC
JAK1.23.2.JAK1.2_F	chr1:65349065-65349212	GAAGATCACTTCCACCCCTG
JAK1.23.2.JAK1.2_R	chr1:65349065-65349212	AGAACACTCCCTTTTGCCAT
JAK1.6.1.JAK1.1_F	chr1:65305285-65305445	CCCCAGCCTTGCATAACATA
JAK1.6.1.JAK1.1_R	chr1:65305285-65305445	GGTTGAGCTCTGCAGGTAT
JAK1.6.2.JAK1.2_F	chr1:65305394-65305536	GTGGTTACCTCCACTCTCAG
JAK1.6.2.JAK1.2_R	chr1:65305394-65305536	TGAGGAGCAAGACTTCTGTG
JAK1.3.1.JAK1.1_F	chr1:65301764-65301920	TGGGTACTGGATTCAAATGAAG
JAK1.3.1.JAK1.1_R	chr1:65301764-65301920	GCCTCCCAGGAAATGAAGTT
JAK1.9.1.JAK1.1_F	chr1:65309746-65309905	CGGGAAACACCTGCTCA
JAK1.9.1.JAK1.1_R	chr1:65309746-65309905	TCCATCAGTGTGTCTGTTGT
JAK1.12.1.JAK1.1_F	chr1:65312274-65312426	GAAGAGCCTCCACCATCTC
JAK1.12.1.JAK1.1_R	chr1:65312274-65312426	ACATTCCTATGTCCTGCTCG
JAK1.14.1.JAK1.1_F	chr1:65316437-65316598	ATCCCCAAGCTGCTCCAT
JAK1.14.1.JAK1.1_R	chr1:65316437-65316598	CAGACTCCCCCAATCTCTTC
JAK1.20.1.JAK1.1_F	chr1:65334994-65335158	GCCAGTGGGAAGCTTTAC
JAK1.20.1.JAK1.1_R	chr1:65334994-65335158	TCTCCCCCTTGCTCCTA
JAK1.15.1.JAK1.1_F	chr1:65321191-65321351	TGGCACAGGGAGACGAA
JAK1.15.1.JAK1.1_R	chr1:65321191-65321351	TGCCCAGAAGCAGTTCAAG
JAK1.15.2.JAK1.2_F	chr1:65321277-65321420	TTCTTGAGGTGGCTCATGAG
JAK1.15.2.JAK1.2_R	chr1:65321277-65321420	TTACATACCCATGCCTGACC
JAK1.8.1.JAK1.1_F	chr1:65307127-65307285	GTTAAAGCAGCACATGGCAG
JAK1.8.1.JAK1.1_R	chr1:65307127-65307285	ATGTGCCCCTCTTGTTTACA
JAK1.4.4.JAK1.1_F	chr1:65303565-65303722	CCAGAAAGGGCCTATTAAAACA
JAK1.4.4.JAK1.1_R	chr1:65303565-65303722	GCAGCAAGAAATGTCCTTGT
JAK1.4.5.JAK1.2_F	chr1:65303654-65303799	GGTCATCCTTGACGGTGTAA
JAK1.4.5.JAK1.2_R	chr1:65303654-65303799	GCAATGTGCTTGACTTTTACT
JAK1.24.1.JAK1.1_F	chr1:65351873-65352007	CAATAGCCCTACAGCCTCAA
JAK1.24.1.JAK1.1_R	chr1:65351873-65352007	TAGCGCTTCTCTGAAGTAGC
JAK1.19.1.JAK1.1_F	chr1:65332549-65332709	ACTGCCAACAGCCACTTAC
JAK1.19.1.JAK1.1_R	chr1:65332549-65332709	CTTGGCTACCTTGGAAACTT
JAK1.19.2.JAK1.2_F	chr1:65332754-65332911	ACCTTCAGGTCATGCGTG
JAK1.19.2.JAK1.2_R	chr1:65332754-65332911	CCTGTACATGAAAAGGAGATGT
JAK1.19.3.JAK1.3_F	chr1:65332622-65332760	AGTAGAGAACGTTTCCACCG
JAK1.19.3.JAK1.3_R	chr1:65332622-65332760	CAAGACCATTTGTGACAGCA
JAK1.10.1.JAK1.1_F	chr1:65310436-65310589	GGAAGAGAGGGGAGACACA
JAK1.10.1.JAK1.1_R	chr1:65310436-65310589	GAGCAGCTTGGCTAAACTTG
JAK1.5.1.JAK1.1_F	chr1:65304125-65304282	GTGCCTGATGTCTTAATCTGT
JAK1.5.1.JAK1.1_R	chr1:65304125-65304282	CCTCAGACTGATGGATGTTTT
ATM.33.15.ATM.1_F	chr11:108170421-108170573	GATCTCTTACCTATGACTCTACTGA
ATM.33.15.ATM.1_R	chr11:108170421-108170573	GTTATTCAGGTAGGTCAGCATT
ATM.33.17.ATM.2_F	chr11:108170534-108170688	TGCATCTTATACCAAGGCCC
ATM.33.17.ATM.2_R	chr11:108170534-108170688	GGACAAAGCTTTAGTTACTGAGA
ATM.32.8.ATM.1_F	chr11:108167981-108168133	ACAAAAGTGTTGTCTTCATGCT
ATM.32.8.ATM.1_R	chr11:108167981-108168133	CCGCAGTTGACTGAAATGTC
ATM.21.1.ATM.1_F	chr11:108143447-108143604	AACCACAGTTCTTTTCCCGT
ATM.21.1.ATM.1_R	chr11:108143447-108143604	CCATCTGCAGCATTCCAAAT
ATM.7.8.ATM.1_F	chr11:108117701-108117856	TTTGGATTACAGGTGCTTATGA

ATM.7.8.ATM.1_R	chr11:108117701-108117856	TGTGACATGACCTACTTACTGT
ATM.7.9.ATM.2_F	chr11:108117648-108117791	GGGAGCTAGCAGTGTAAACA
ATM.7.9.ATM.2_R	chr11:108117648-108117791	TGACGGCAATATTACGAAATCC
ATM.26.8.ATM.1_F	chr11:108158337-108158493	GCCCTTGCAGATTGATCACT
ATM.26.8.ATM.1_R	chr11:108158337-108158493	AGGTGTCAACCAATAAACTTCT
ATM.26.9.ATM.2_F	chr11:108158278-108158423	GCCTTTTGAGCTGTCTTGAC
ATM.26.9.ATM.2_R	chr11:108158278-108158423	CCCTGAAAAGTCACAGAGGT
ATM.2.24.ATM.1_F	chr11:108098429-108098668	AGAGCTACAGAACGAAAGGTAGT
ATM.2.24.ATM.1_R	chr11:108098429-108098668	ACACACAAAAGTAATATCACAACAGA
ATM.17.1.ATM.1_F	chr11:108139157-108139316	GGTGCCATTAATCCTTTAGCT
ATM.17.1.ATM.1_R	chr11:108139157-108139316	ATATGCAGGTGGAGGGATT
ATM.17.2.ATM.2_F	chr11:108139316-108139457	CTAGCACGCTAGAACCTACC
ATM.17.2.ATM.2_R	chr11:108139316-108139457	TTCCAACTAGTCTCAGGTTCA
ATM.17.2.ATM.3_F	chr11:108139110-108139250	GCTGTTGTGCCCTTCTCTTA
ATM.17.2.ATM.3_R	chr11:108139110-108139250	CCGAATATCAGCTGCCCTAA
ATM.1.1.ATM.1_F	chr11:108098352-108098508	GTGTGTTCTGAAATTGTGAACC
ATM.1.1.ATM.1_R	chr11:108098352-108098508	CAGGCGCTTAAATTTCTCAAC
ATM.18.20.ATM.1_F	chr11:108141767-108141917	GTAAATGATTTGTGGATAAACCTGA
ATM.18.20.ATM.1_R	chr11:108141767-108141917	GCTTAACAGAACACATCAGTTATT
ATM.30.22.ATM.1_F	chr11:108163991-108164144	ACAGTAAGTTTTGTTGGCTTACT
ATM.30.22.ATM.1_R	chr11:108163991-108164144	TTTGCTGAGTAATACGCAAATC
ATM.30.23.ATM.2_F	chr11:108164135-108164258	TAGATCCTTTTCCTGACCATGT
ATM.30.23.ATM.2_R	chr11:108164135-108164258	TGCTAGAGCATTACAGATTTTTGA
ATM.16.3.ATM.1_F	chr11:108137871-108138023	CTCCTGCAAGAAGCCATCTT
ATM.16.3.ATM.1_R	chr11:108137871-108138023	TCGTTTGCATCACTAACACT
ATM.16.4.ATM.2_F	chr11:108137989-108138118	AATGGAGGTGGAGGATCAGT
ATM.16.4.ATM.2_R	chr11:108137989-108138118	GAGGCCTCTTATACTGCCAA
ATM.44.10.ATM.1_F	chr11:108191995-108192130	TTTCCCTGAAAACCTCTTCTTT
ATM.44.10.ATM.1_R	chr11:108191995-108192130	TACCTTGAGAAAAGCTCCCC
ATM.44.11.ATM.2_F	chr11:108192130-108192265	ATTGGAGAGCTGGAAAGCAT
ATM.44.11.ATM.2_R	chr11:108192130-108192265	CACCCACTTCAGCCTTCTAA
ATM.55.1.ATM.1_F	chr11:108206582-108206735	TATTCTGAAGGGCCGTGATG
ATM.55.1.ATM.1_R	chr11:108206582-108206735	CACTTCACCCAACCAAATGG
ATM.55.2.ATM.2_F	chr11:108206496-108206634	AGATTGGTTTGAGTGCCCTT
ATM.55.2.ATM.2_R	chr11:108206496-108206634	GTTTCCGTGTTTCTCTGCAG
ATM.25.17.ATM.1_F	chr11:108155079-108155230	ACAGACTGCTTTCCAAAGATTC
ATM.25.17.ATM.1_R	chr11:108155079-108155230	GGTTATATCTCATATCATTCAGGGA
ATM.25.24.ATM.2_F	chr11:108154868-108155109	AAAGTATGATACTTTAATGCTGATGGT
ATM.25.24.ATM.2_R	chr11:108154868-108155109	TCCCACTGTCTCTGGTACCC
ATM.27.3.ATM.1_F	chr11:108159655-108159812	TGGAAGTTCACTGGTCTATGA
ATM.27.3.ATM.1_R	chr11:108159655-108159812	ACAGGGCTTTTGGAAAGAAT
ATM.27.24.ATM.2_F	chr11:108159723-108159969	GGGATTTGGATCCTGCTCCT
ATM.27.24.ATM.2_R	chr11:108159723-108159969	TGCTGACAAGTAAAATACCATTTAAAC
ATM.28.19.ATM.1_F	chr11:108160302-108160452	GTAGCCGAGTATCTAATTAAACAAG
ATM.28.19.ATM.1_R	chr11:108160302-108160452	AGCTCCTCCTAAGCCACTTT
ATM.28.20.ATM.2_F	chr11:108160444-108160565	CACCTGTTTGTTAGTTTATTACTGA
ATM.28.20.ATM.2_R	chr11:108160444-108160565	AAAAACAGGAAGAACAGGATAGA
ATM.40.20.ATM.1_F	chr11:108186540-108186693	TCCTTCTTCAATTTTTGTTGTTTCC
ATM.40.20.ATM.1_R	chr11:108186540-108186693	AGCTTTGGGTTTTACACACAC
ATM.57.1.ATM.1_F	chr11:108216526-108216665	GTCTTCATGGATGTTTGCCA
ATM.57.1.ATM.1_R	chr11:108216526-108216665	ACCTGCCAAACAACAAAGTG
ATM.57.2.ATM.2_F	chr11:108216380-108216535	CCTGTTCATCTTTATTGCCCC
ATM.57.2.ATM.2_R	chr11:108216380-108216535	GCAGAAGTAACGGAAAACTGG
ATM.61.1.ATM.1_F	chr11:108235814-108235959	TGTTCTCTCTGTTTAGGTCCT
ATM.61.1.ATM.1_R	chr11:108235814-108235959	ACTGACAACAGGACCTTCTT
ATM.61.2.ATM.2_F	chr11:108235694-108235823	TGTGCATGATGTTTGTTCCC
ATM.61.2.ATM.2_R	chr11:108235694-108235823	ATGGTCCAGTCAAAGAGTGG
ATM.20.20.ATM.1_F	chr11:108143213-108143362	TCAGTGAGTTTTCTGAGTGCT
ATM.20.20.ATM.1_R	chr11:108143213-108143362	GACTGCTTTAAAATTTTCAATGGAG
ATM.14.14.ATM.1_F	chr11:108128194-108128319	AACTGGAATTTGCATTTTTCCT
ATM.14.14.ATM.1_R	chr11:108128194-108128319	AATCTTACCTTGGTACAGTTGC
ATM.14.24.ATM.2_F	chr11:108128316-108128444	TGCAGCTATGTACACGTTGC
ATM.14.24.ATM.2_R	chr11:108128316-108128444	TGAGGCAGGAGAATTGCTGG
ATM.59.16.ATM.1_F	chr11:108224472-108224607	AGCTGTCAAACCTCCTAACT
ATM.59.16.ATM.1_R	chr11:108224472-108224607	CCCTCCTTTACTTCATATCACTTAC
ATM.49.1.ATM.1_F	chr11:108200981-108201140	AGAGCTGGAGTTGGATGAA
ATM.49.1.ATM.1_R	chr11:108200981-108201140	GAGTAACACTTGCCTTCATCA

ATM.49.2.ATM.2_F	chr11:108201106-108201238	TTCCGACTTTGTTCCCTCTG
ATM.49.2.ATM.2_R	chr11:108201106-108201238	CTGGACCAAGTGCTAGGAAT
ATM.49.2.ATM.3_F	chr11:108200847-108200990	TTTTCCCTGGGATAAAAACCC
ATM.49.2.ATM.3_R	chr11:108200847-108200990	ACGATCCTCTTTCAGTGCAC
ATM.24.17.ATM.1_F	chr11:108153504-108153656	GAAGACTTTATGGCATCTCATTTAG
ATM.24.17.ATM.1_R	chr11:108153504-108153656	AGGGGACTTGCTAAGTATTGT
ATM.24.18.ATM.2_F	chr11:108153362-108153508	TGTTGTTTCTAGGTCCTACTCT
ATM.24.18.ATM.2_R	chr11:108153362-108153508	GATTTAGCCATTCCAAAACCAG
ATM.10.3.ATM.1_F	chr11:108122549-108122704	GCTTGCTTTTCACAATTGTCC
ATM.10.3.ATM.1_R	chr11:108122549-108122704	TTCTAAGTCACCCTCTAACTGA
ATM.10.8.ATM.2_F	chr11:108122630-108122762	CCAGGAACGGTAAAAATGGG
ATM.10.8.ATM.2_R	chr11:108122630-108122762	GCAGCATGCTAATGAACTTAAA
ATM.31.3.ATM.1_F	chr11:108165625-108165776	CACAGGCTTAACCAATACGTG
ATM.31.3.ATM.1_R	chr11:108165625-108165776	AAATTAGCACCCTGAGAAGC
ATM.31.4.ATM.2_F	chr11:108165709-108165853	TGCACTTCCATTGACAAGAC
ATM.31.4.ATM.2_R	chr11:108165709-108165853	GTGACAATGAAACCAAGAGCA
ATM.35.3.ATM.1_F	chr11:108173543-108173696	GGAAAGGTACAATGATTTCCAC
ATM.35.3.ATM.1_R	chr11:108173543-108173696	TGCCTCCACTGTCCAAAAA
ATM.35.4.ATM.2_F	chr11:108173696-108173850	GGATAAAGACACTGACTTGTGC
ATM.35.4.ATM.2_R	chr11:108173696-108173850	TACAACAGTTTGAGTGGGGG
ATM.11.24.ATM.1_F	chr11:108123525-108123758	GGCTTTTGGTCTTCTAAGTGAAGC
ATM.11.24.ATM.1_R	chr11:108123525-108123758	TCCCTGGCTAACAGTTGCAA
ATM.53.24.ATM.1_F	chr11:108204588-108204840	TGCTGTTCCTCAGTTTGTCACT
ATM.53.24.ATM.1_R	chr11:108204588-108204840	AGGGCTTGGGCAAAGGAAAT
ATM.48.1.ATM.1_F	chr11:108199768-108199927	GCAGTAGAAGTTGCTGGAAA
ATM.48.1.ATM.1_R	chr11:108199768-108199927	TGTTCCCTAAGGAGACCTAC
ATM.48.2.ATM.2_F	chr11:108199913-108200067	ACAAGCAAGCTCTCCTGAAA
ATM.48.2.ATM.2_R	chr11:108199913-108200067	TAAGCCGACCTTTAGAGCTC
ATM.48.2.ATM.3_F	chr11:108199618-108199773	GGGTTGGACAAGTTTGCAAT
ATM.48.2.ATM.3_R	chr11:108199618-108199773	AGCTCATCACTACTTTCTCCA
ATM.22.13.ATM.1_F	chr11:108150213-108150357	TGTTTGTTTGCTTGCTTGTT
ATM.22.13.ATM.1_R	chr11:108150213-108150357	AGCAAGCATATGATAACAGCA
ATM.42.1.ATM.1_F	chr11:108188117-108188276	TAGGCCTTGCAGAATTTGGG
ATM.42.1.ATM.1_R	chr11:108188117-108188276	AGAATGAGGAGAGAGGCAAA
ATM.42.2.ATM.2_F	chr11:108187972-108188116	CACCACACCCAGCTGATATT
ATM.42.2.ATM.2_R	chr11:108187972-108188116	ACGGAAAGAATATGGCAGAGT
ATM.46.1.ATM.1_F	chr11:108196843-108196968	AATTCAGTTAGCTGTGGAGTCT
ATM.46.1.ATM.1_R	chr11:108196843-108196968	ACAGTAAAACACTAATCCAGCC
ATM.46.2.ATM.2_F	chr11:108196709-108196860	TCAATGAATGGTAGTTGCTGC
ATM.46.2.ATM.2_R	chr11:108196709-108196860	TGCCCAGAATACTTGTGCTT
ATM.13.24.ATM.1_F	chr11:108126842-108127089	CACCTTTAACTCAGTTAACTGAACT
ATM.13.24.ATM.1_R	chr11:108126842-108127089	ACATTTCATTCAAATTTATCCGAAACT
ATM.23.20.ATM.1_F	chr11:108151762-108151916	CCCTGAAACTTTGGATGAAATTT
ATM.23.20.ATM.1_R	chr11:108151762-108151916	GTGACCTAAGGAAGCTTCTAAT
ATM.23.21.ATM.2_F	chr11:108151660-108151812	TCTGGAGTTCAGTTGGGATT
ATM.23.21.ATM.2_R	chr11:108151660-108151812	CTGTTTTTCGCAGATAGGGC
ATM.29.6.ATM.1_F	chr11:108163324-108163481	CAGAACTTACTGGTTGTTGTTG
ATM.29.6.ATM.1_R	chr11:108163324-108163481	TGCTCATACACAAGGGGTAT
ATM.29.8.ATM.2_F	chr11:108163397-108163527	AGCTTCTCCCTTTGTTGTGA
ATM.29.8.ATM.2_R	chr11:108163397-108163527	ACCATTTTGAAGATGAGTCAGA
ATM.6.3.ATM.1_F	chr11:108115494-108115647	CCCCCTGTTATACCCAGTTG
ATM.6.3.ATM.1_R	chr11:108115494-108115647	CATTAAGCCTATGTTGAGTCCA
ATM.6.17.ATM.2_F	chr11:108115641-108115784	TGAAATTCTTCCCACTTTGCT
ATM.6.17.ATM.2_R	chr11:108115641-108115784	GACTTCTATGTTTGAATGAAGAAGC
ATM.50.24.ATM.1_F	chr11:108202085-108202287	ACCACTTGTGCTAATAGAGGAGC
ATM.50.24.ATM.1_R	chr11:108202085-108202287	TGTGGTTTGATTTTCAGGTTTACT
ATM.39.1.ATM.1_F	chr11:108183137-108183291	GAGGTGTTCTTGTGACAAACA
ATM.39.1.ATM.1_R	chr11:108183137-108183291	ACATGGCATCTGTACAGTGT
ATM.3.10.ATM.1_F	chr11:108099888-108100039	TCAACGAGTTTCTGAAATTGC
ATM.3.10.ATM.1_R	chr11:108099888-108100039	ACATCACTTACTTCTGTTTGCA
ATM.3.12.ATM.2_F	chr11:108099960-108100087	ATGTCTGAGAATAGCAAAACCA
ATM.3.12.ATM.2_R	chr11:108099960-108100087	AACTCACGCGACAGTAATCT
ATM.36.3.ATM.1_F	chr11:108175388-108175540	CTCAAACTATTGGGTGGATTTG
ATM.36.3.ATM.1_R	chr11:108175388-108175540	GTTGTGGATCGGCTCGTTT
ATM.36.4.ATM.2_F	chr11:108175509-108175643	GCTTTCTACACATGTTCAGGG
ATM.36.4.ATM.2_R	chr11:108175509-108175643	AGTGCTTTTAGTGGGATTCCA
ATM.51.17.ATM.1_F	chr11:108202636-108202777	AGAATTTCAATGGATCACCCC

ATM.51.17.ATM.1_R	chr11:108202636-108202777	CACACTTCTAAAAGGTACGTATGT
ATM.51.18.ATM.2_F	chr11:108202510-108202656	GCTCTACCCACTGCAGTATC
ATM.51.18.ATM.2_R	chr11:108202510-108202656	TTTGCATTTGCTAAGGCCAG
ATM.9.1.ATM.1_F	chr11:108121538-108121698	ACCCCAACAGCGACATG
ATM.9.1.ATM.1_R	chr11:108121538-108121698	CTCCAAGTAAGCCAAAGTTTTC
ATM.9.2.ATM.2_F	chr11:108121689-108121844	TCGTGGTATAAGTTCTGAGCA
ATM.9.2.ATM.2_R	chr11:108121689-108121844	ATGTGAGTGTGTGTGTGTCT
ATM.9.20.ATM.3_F	chr11:108121393-108121537	CCTTTTAGTTTGTTAATGTGATGGA
ATM.9.20.ATM.3_R	chr11:108121393-108121537	CACATATGGTGTACGTTCCC
ATM.58.17.ATM.1_F	chr11:108217990-108218144	GGAATCAGTGATTTCAGATTGTTTG
ATM.58.17.ATM.1_R	chr11:108217990-108218144	GGTAGGCAAACAACATTCCA
ATM.12.1.ATM.1_F	chr11:108124551-108124710	ACTTTCTTGAAGTGAACACCAC
ATM.12.1.ATM.1_R	chr11:108124551-108124710	CCAGAAGACAGCGATCCA
ATM.12.2.ATM.2_F	chr11:108124683-108124825	ACCAGTCCAGTATTGGCTTC
ATM.12.2.ATM.2_R	chr11:108124683-108124825	CTGCCCCTATTTCTCCTTCC
ATM.12.2.ATM.3_F	chr11:108124510-108124662	GGCAAAGCATTAGGTACTTGG
ATM.12.2.ATM.3_R	chr11:108124510-108124662	GAAGCCAATACTGGACTGGT
ATM.41.1.ATM.1_F	chr11:108186715-108186850	GTGTGTGTAAAACCCAAAGCT
ATM.41.1.ATM.1_R	chr11:108186715-108186850	TGGCTTTACCAAATCTGGGA
ATM.15.1.ATM.1_F	chr11:108129657-108129809	GATAGAGAAAACACTGTCTGCC
ATM.15.1.ATM.1_R	chr11:108129657-108129809	TGATAGCAAAACAGGAAGCA
ATM.47.1.ATM.1_F	chr11:108198334-108198487	CAGTTGGGTACAGTCATGGT
ATM.47.1.ATM.1_R	chr11:108198334-108198487	AGGGTTGCTCCAAAAATCTT
ATM.8.6.ATM.1_F	chr11:108119621-108119760	GCGAAACTCTGGCTCAAAAA
ATM.8.6.ATM.1_R	chr11:108119621-108119760	ATTACTTCCCAGCCTAGTTCT
ATM.8.7.ATM.2_F	chr11:108119756-108119900	GTGTCCCTTGCAAAAGGAAG
ATM.8.7.ATM.2_R	chr11:108119756-108119900	TGGTTGAGATGAAAGGATTCCA
ATM.38.1.ATM.1_F	chr11:108180930-108181081	ATGATGCTTTCTGGCTGGAT
ATM.38.1.ATM.1_R	chr11:108180930-108181081	ACCCTTATTGAGACAATGCCA
ATM.38.2.ATM.2_F	chr11:108180807-108180940	TCTGTTAAGCAGTCACTACCA
ATM.38.2.ATM.2_R	chr11:108180807-108180940	GAGCTACCTTGGCAACTTCT
ATM.52.1.ATM.1_F	chr11:108203505-108203658	ATAGGATCGAACAGAGGCTG
ATM.52.1.ATM.1_R	chr11:108203505-108203658	ACAGAGAGTAACACAGCAAGA
ATM.52.8.ATM.2_F	chr11:108203398-108203548	TCCATTGTCTAGATTTGTGCA
ATM.52.8.ATM.2_R	chr11:108203398-108203548	AGTGCCTCAACACTTCTGAC
ATM.4.8.ATM.1_F	chr11:108106409-108106565	TGAAATAGGAGCACCTAGGC
ATM.4.8.ATM.1_R	chr11:108106409-108106565	CACAAACAACAACCTTCAAAAC
ATM.4.9.ATM.2_F	chr11:108106348-108106476	AGTTGCCATTCCAAGTGTCT
ATM.4.9.ATM.2_R	chr11:108106348-108106476	GTATGTTGCTACAATCAGCTCC
ATM.60.5.ATM.1_F	chr11:108225503-108225661	CGTTGACAACATTGGTGTGT
ATM.60.5.ATM.1_R	chr11:108225503-108225661	TCACATCAGTGACTTCCTGA
ATM.34.1.ATM.1_F	chr11:108172402-108172561	GTTCGATCAGCAGCTGTTAC
ATM.34.1.ATM.1_R	chr11:108172402-108172561	CCCACAGCAAACAGAACTGT
ATM.34.2.ATM.2_F	chr11:108172327-108172467	CAGTGGAGGTTAACATTCATCA
ATM.34.2.ATM.2_R	chr11:108172327-108172467	GATAGGCCAGCATTGGATCT
ATM.56.1.ATM.1_F	chr11:108213957-108214100	CTGTAACTCCAGGTGGTTCC
ATM.56.1.ATM.1_R	chr11:108213957-108214100	CCTTTAATTTTGGGTGTCACTC
ATM.56.2.ATM.2_F	chr11:108213822-108213975	CCTCCAAGGAGCTTTGTCTT
ATM.56.2.ATM.2_R	chr11:108213822-108213975	CCTGTGCACCATTCAAGAAC
ATM.37.1.ATM.1_F	chr11:108178584-108178720	AGGAAGAAGGTGTGTAAGCA
ATM.37.1.ATM.1_R	chr11:108178584-108178720	AACGTAAGAAGCAACACTCA
ATM.45.1.ATM.1_F	chr11:108196047-108196206	TGGCATTCAGATCAGTCACA
ATM.45.1.ATM.1_R	chr11:108196047-108196206	GTGTTTGGTGAGAATGTCCT
ATM.45.2.ATM.2_F	chr11:108196177-108196328	TGGAGATCCTGATGGAAAAGG
ATM.45.2.ATM.2_R	chr11:108196177-108196328	TCCCTCAGGCTTTCTGTTTT
ATM.45.2.ATM.3_F	chr11:108196033-108196162	TGAACTCTATGTCGTGGCAT
ATM.45.2.ATM.3_R	chr11:108196033-108196162	GTCCATTTCCTTTTCCATCAGG
ATM.43.24.ATM.1_F	chr11:108190616-108190825	AAATTTTGTCCTTTGGTGAAGCT
ATM.43.24.ATM.1_R	chr11:108190616-108190825	AGTTTTCAGAAAAGAAGCCATGACA
ATM.19.1.ATM.1_F	chr11:108141988-108142136	TTTACCACAGCAATGTGTGT
ATM.19.1.ATM.1_R	chr11:108141988-108142136	GGACCACAAAATAGACTGTACC
ATM.19.2.ATM.2_F	chr11:108141841-108141994	GAAGAGTACCCCTTGCCAAT
ATM.19.2.ATM.2_R	chr11:108141841-108141994	AACATCTTGGTCACGACGAT
ATM.62.1.ATM.1_F	chr11:108236091-108236246	CAACAAAGTAGCTGAACGTGT
ATM.62.1.ATM.1_R	chr11:108236091-108236246	GGCTGAATGAAAGGGTAATTCA
ATM.62.2.ATM.2_F	chr11:108235955-108236113	CGAAATCTCAGGTGAGCAGT
ATM.62.2.ATM.2_R	chr11:108235955-108236113	GCCTTCTTCCACTCCTTTCA

ATM.5.1.ATM.1_F	chr11:108114731-108114887	CTGAAACCTTCACAAGATGTTC
ATM.5.1.ATM.1_R	chr11:108114731-108114887	ACATGGTCTTGCAAGATCAA
ATM.5.17.ATM.2_F	chr11:108114601-108114741	CCTTTTTCTGTATGGGATTATGGA
ATM.5.17.ATM.2_R	chr11:108114601-108114741	ACAGCATGAATTATTCTAGCCAC
ATM.54.1.ATM.1_F	chr11:108205716-108205860	GTGGACCACACAGGAGAATA
ATM.54.1.ATM.1_R	chr11:108205716-108205860	TCATCACTAAAACTCTAAGGGC
ATM.54.2.ATM.2_F	chr11:108205597-108205750	CCACTATCACATCGTCATTTGT
ATM.54.2.ATM.2_R	chr11:108205597-108205750	ACCTCCTGCTAAGCGAAATT
ERBB3.11.1.ERBB3.1_F	chr12:56486713-56486867	AAGTTATAGGGGAGGAGCCA
ERBB3.11.1.ERBB3.1_R	chr12:56486713-56486867	GCCATTTCCTCCATACCCTT
ERBB3.21.1.ERBB3.1_F	chr12:56491599-56491756	CTACCTTGAGGAACATGGTATG
ERBB3.21.1.ERBB3.1_R	chr12:56491599-56491756	TATCCCCATGCTTCACTCCA
ERBB3.21.2.ERBB3.2_F	chr12:56491493-56491648	CACTGCTGAGAGGTACCTTC
ERBB3.21.2.ERBB3.2_R	chr12:56491493-56491648	CAAAATCTGCCACCTGAACC
ERBB3.7.1.ERBB3.1_F	chr12:56481795-56481947	ACATAAATCTGATGAGCCTCCT
ERBB3.7.1.ERBB3.1_R	chr12:56481795-56481947	TCCTTCCCCTCAGACACTTA
ERBB3.26.1.ERBB3.1_F	chr12:56493901-56494046	TTAACTACTCAAAGGCCCCC
ERBB3.26.1.ERBB3.1_R	chr12:56493901-56494046	TGATCCTAAAACCCAGCCTC
ERBB3.2.1.ERBB3.1_F	chr12:56477544-56477701	GCTTTGAACAGTGTGTCCTG
ERBB3.2.1.ERBB3.1_R	chr12:56477544-56477701	GAGCAGGTTGAGGAAGGAG
ERBB3.2.2.ERBB3.2_F	chr12:56477531-56477671	CACTCTTCCCTCTGCTTTGA
ERBB3.2.2.ERBB3.2_R	chr12:56477531-56477671	CTAACCTGCAGGAAGGAGAG
ERBB3.17.1.ERBB3.1_F	chr12:56489468-56489626	AGCAAAACCCATCTGACAATG
ERBB3.17.1.ERBB3.1_R	chr12:56489468-56489626	ACTTCCAGGACATGCAAAAA
ERBB3.17.2.ERBB3.2_F	chr12:56489375-56489518	CCAGGTCAGCATCATACCTT
ERBB3.17.2.ERBB3.2_R	chr12:56489375-56489518	CCACGCCAGTAGAGAAAAGT
ERBB3.22.1.ERBB3.1_F	chr12:56492238-56492372	TGGGACTTGGAAATCCTAAGA
ERBB3.22.1.ERBB3.1_R	chr12:56492238-56492372	GTGATGGTAGAGAGGGCATC
ERBB3.1.1.ERBB3.1_F	chr12:56474031-56474167	CTCTTGCCTCGATGTCCTAG
ERBB3.1.1.ERBB3.1_R	chr12:56474031-56474167	TGCTCTCGCGCCACTTA
ERBB3.18.1.ERBB3.1_F	chr12:56490275-56490422	TCCTGAGTAACTCCTTCCCA
ERBB3.18.1.ERBB3.1_R	chr12:56490275-56490422	TTCCCCACCTCTCCAGAATT
ERBB3.16.1.ERBB3.1_F	chr12:56488960-56489101	ATGCCACGGTAAGTTCTGAA
ERBB3.16.1.ERBB3.1_R	chr12:56488960-56489101	TTTCCAGAATCTCCAACCCC
ERBB3.13.1.ERBB3.1_F	chr12:56487556-56487719	TTCCTTTCCAGTGGCAGAG
ERBB3.13.1.ERBB3.1_R	chr12:56487556-56487719	AGTTCCATTGCAGGGCC
ERBB3.13.2.ERBB3.2_F	chr12:56487653-56487783	TTATAGCCGAGGAGGTGTCT
ERBB3.13.2.ERBB3.2_R	chr12:56487653-56487783	CTACCTCAATCCCACCAAGG
ERBB3.13.2.ERBB3.3_F	chr12:56487482-56487632	TGGAAGCAGTAACGAGGAAG
ERBB3.13.2.ERBB3.3_R	chr12:56487482-56487632	AGACACCTCCTCGGCTATAA
ERBB3.23.1.ERBB3.1_F	chr12:56492531-56492693	GCCAGTGACTAGTCCATGTC
ERBB3.23.1.ERBB3.1_R	chr12:56492531-56492693	TGGGCTCAGCAGGTAAC
ERBB3.23.2.ERBB3.2_F	chr12:56492393-56492536	GATGCCCTCTCTACCATCAC
ERBB3.23.2.ERBB3.2_R	chr12:56492393-56492536	CCAAACTGTCACACCTGTTG
ERBB3.27.1.ERBB3.1_F	chr12:56494865-56495024	GAGTCTGCAGTTTCTGGGAG
ERBB3.27.1.ERBB3.1_R	chr12:56494865-56495024	GAATGGTAGGCGCTATCTCC
ERBB3.27.2.ERBB3.2_F	chr12:56494768-56494927	AGGCAGTGAACAACCCAATA
ERBB3.27.2.ERBB3.2_R	chr12:56494768-56494927	TTACATGCCCCTCTGATGAC
ERBB3.27.2.ERBB3.3_F	chr12:56495045-56495178	GGAGATAGCGCCTACCATTC
ERBB3.27.2.ERBB3.3_R	chr12:56495045-56495178	CGGGGAAAGAATTCGAGGAA
ERBB3.27.3.ERBB3.4_F	chr12:56494950-56495108	CATCAGAGGGGCATGTAACA
ERBB3.27.3.ERBB3.4_R	chr12:56494950-56495108	GGCATGACATAACCGTTGAC
ERBB3.25.1.ERBB3.1_F	chr12:56493642-56493804	AGAGAGTGGGCCTGGAAT
ERBB3.25.1.ERBB3.1_R	chr12:56493642-56493804	TGTCTTACCCCACGTGG
ERBB3.25.2.ERBB3.2_F	chr12:56493740-56493880	CCTAGACTTGGAAGCAGAGG
ERBB3.25.2.ERBB3.2_R	chr12:56493740-56493880	GGGGGCCTTTGAGTAGTTAA
ERBB3.25.2.ERBB3.3_F	chr12:56493554-56493691	GTAGGGAGTAGGAGGTGCTA
ERBB3.25.2.ERBB3.3_R	chr12:56493554-56493691	TAGTTCTGGCTCCAGCTCTA
ERBB3.6.1.ERBB3.1_F	chr12:56481576-56481716	CCATGCTTTCTCTCCTTCCA
ERBB3.6.1.ERBB3.1_R	chr12:56481576-56481716	TCCCAATTTCAGAACCCAGG
ERBB3.28.1.ERBB3.1_F	chr12:56495351-56495514	AGGCACCCTTTCTTCAGTG
ERBB3.28.1.ERBB3.1_R	chr12:56495351-56495514	AACTCTGTGTGCTGCCC
ERBB3.28.2.ERBB3.2_F	chr12:56495199-56495355	TTCCTCGAATTCTTTCCCCG
ERBB3.28.2.ERBB3.2_R	chr12:56495199-56495355	CAGTACCCAGGACAGAACTG
ERBB3.28.2.ERBB3.3_F	chr12:56495555-56495715	ACTCCACCCTGTACCCATC
ERBB3.28.2.ERBB3.3_R	chr12:56495555-56495715	GGCATAATGGACATGGGGG
ERBB3.28.3.ERBB3.4_F	chr12:56495702-56495858	AGATGAGAGCTTTTCAGGGG

ERBB3.28.3.ERBB3.4_R	chr12:56495702-56495858	TGCCATTAAATGCTCCCTGA
ERBB3.28.3.ERBB3.5_F	chr12:56495499-56495657	GTACATGGATGTGGGGTCAG
ERBB3.28.3.ERBB3.5_R	chr12:56495499-56495657	ATACCCTTGCTCAGATGCTG
ERBB3.3.1.ERBB3.1_F	chr12:56478789-56478949	TCTGTCACAGTGGATTCGAG
ERBB3.3.1.ERBB3.1_R	chr12:56478789-56478949	ACCGGTGAGCTGAGTCAA
ERBB3.3.2.ERBB3.2_F	chr12:56478937-56479096	AACTCCAGCCACGCTCT
ERBB3.3.2.ERBB3.2_R	chr12:56478937-56479096	CTTAGGGAGCAATGGACCT
ERBB3.3.2.ERBB3.3_F	chr12:56478725-56478874	CCTGAAGGAGGAGAGGAGAT
ERBB3.3.2.ERBB3.3_R	chr12:56478725-56478874	ATGGCAAACTTCCCATCGTA
ERBB3.9.1.ERBB3.1_F	chr12:56482532-56482691	TGAACCTCTCTTACATTTGCAG
ERBB3.9.1.ERBB3.1_R	chr12:56482532-56482691	ATGAACTGTGAGGGGTGC
ERBB3.9.2.ERBB3.2_F	chr12:56482674-56482824	TTAGAGATCCTGCCTTCCCT
ERBB3.9.2.ERBB3.2_R	chr12:56482674-56482824	CAAAGATGTTCCTGAGGGGA
ERBB3.12.1.ERBB3.1_F	chr12:56487149-56487310	CGGGGCTTCTCATTGTTGA
ERBB3.12.1.ERBB3.1_R	chr12:56487149-56487310	TCTGCGCGGCCGATTAT
ERBB3.12.2.ERBB3.2_F	chr12:56487260-56487396	CTGCTACCACCACTCTTTGA
ERBB3.12.2.ERBB3.2_R	chr12:56487260-56487396	CCACGTCTAGGGCAGAATAG
ERBB3.12.2.ERBB3.3_F	chr12:56487034-56487163	TTCCCTCTCAGTGGATCTGA
ERBB3.12.2.ERBB3.3_R	chr12:56487034-56487163	GAAGCCCAGAGATGTGACAT
ERBB3.14.1.ERBB3.1_F	chr12:56487846-56487981	GAGCATGAAGGTCAGGACTT
ERBB3.14.1.ERBB3.1_R	chr12:56487846-56487981	CTTGGAGATCCTGGTGCTAC
ERBB3.15.1.ERBB3.1_F	chr12:56488196-56488354	TTCCACTCAGGGCTCTGATA
ERBB3.15.1.ERBB3.1_R	chr12:56488196-56488354	CCTGACCCCCTCTCCTTATT
ERBB3.15.2.ERBB3.2_F	chr12:56488140-56488296	CTTTGCTGGGAGGTATGGAA
ERBB3.15.2.ERBB3.2_R	chr12:56488140-56488296	GGCCGACATTCATTCTGAAC
ERBB3.20.1.ERBB3.1_F	chr12:56490846-56491009	GCATATGCTGGCCATTGG
ERBB3.20.1.ERBB3.1_R	chr12:56490846-56491009	AGGCTTCTCTCACCTTGG
ERBB3.20.2.ERBB3.2_F	chr12:56490873-56491020	GACCATGCCCACATTGTAAG
ERBB3.20.2.ERBB3.2_R	chr12:56490873-56491020	ACAGAATTCCTCCAGGCTTC
ERBB3.20.2.ERBB3.3_F	chr12:56490786-56490930	GTGCACATGCTGAGTGTATG
ERBB3.20.2.ERBB3.3_R	chr12:56490786-56490930	ACATGATCCAGCAGAGAACC
ERBB3.8.1.ERBB3.1_F	chr12:56482327-56482469	GTCCTCCTCCTCTTCCCTAG
ERBB3.8.1.ERBB3.1_R	chr12:56482327-56482469	CTCAGAGGAAAGGCTGTCTC
ERBB3.4.1.ERBB3.1_F	chr12:56480307-56480452	AACCCTGTCACTTCTTTCCC
ERBB3.4.1.ERBB3.1_R	chr12:56480307-56480452	ACTGGGGAGCAATCTTGATC
ERBB3.24.1.ERBB3.1_F	chr12:56493397-56493533	CCGGCCATGGAATGTATTCT
ERBB3.24.1.ERBB3.1_R	chr12:56493397-56493533	TAGCACCTCCTACTCCCTAC
ERBB3.19.1.ERBB3.1_F	chr12:56490503-56490638	TGACCTAGGGAGAATGACCT
ERBB3.19.1.ERBB3.1_R	chr12:56490503-56490638	AGCGGCATACAGAATTTCCT
ERBB3.10.1.ERBB3.1_F	chr12:56486490-56486634	GTGCTCATTGCCATTGAGTT
ERBB3.10.1.ERBB3.1_R	chr12:56486490-56486634	GCCAGTGGTTCACCTATTCT
ERBB3.5.1.ERBB3.1_F	chr12:56481331-56481466	AGCCTTTCTTAGCCCTGATG
ERBB3.5.1.ERBB3.1_R	chr12:56481331-56481466	TGGGGAGGAAGGGATATGAA
RET.11.1.RET.1_F	chr10:43609988-43610151	GCTGTCCTCTTCTCCTTCA
RET.11.1.RET.1_R	chr10:43609988-43610151	TCCACGGAGACCTGGTT
RET.11.2.RET.2_F	chr10:43610151-43610311	TCGCTGGACTCCATGGA
RET.11.2.RET.2_R	chr10:43610151-43610311	CTATGGAAATGGGGGCAGAA
RET.11.2.RET.3_F	chr10:43609864-43610017	CCATGAGGCAGAGCATACG
RET.11.2.RET.3_R	chr10:43609864-43610017	AAACTTGTGGTAGCAGTGGA
RET.7.1.RET.1_F	chr10:43606674-43606835	GATCGGGAAAGTCTGTGTGG
RET.7.1.RET.1_R	chr10:43606674-43606835	TGGCCACCACCATGTAGT
RET.7.2.RET.2_F	chr10:43606809-43606970	TGAATGACACCAAGGCCC
RET.7.2.RET.2_R	chr10:43606809-43606970	TTTTCTCAAAGGGCAGGAGG
RET.7.2.RET.3_F	chr10:43606579-43606708	CTGTTCCAGGACTTAGGCTG
RET.7.2.RET.3_R	chr10:43606579-43606708	CCAGAGGAATGCAGCTTGTA
RET.17.1.RET.1_F	chr10:43619119-43619278	GGTCCTTTCACTCTCTGCAG
RET.17.1.RET.1_R	chr10:43619119-43619278	TTCCCAAGTGAGGCTGG
RET.2.1.RET.1_F	chr10:43595907-43596066	CACTTCCCTACTTCCCACAG
RET.2.1.RET.1_R	chr10:43595907-43596066	TTGTTCTCATGCAGCCGT
RET.2.2.RET.2_F	chr10:43596057-43596218	CCAGCATCTCTACGGCA
RET.2.2.RET.2_R	chr10:43596057-43596218	GTGATAAGGGCGGCTTGAG
RET.1.5.RET.1_F	chr10:43572688-43572850	AGTCCCTCCAGCCGTG
RET.1.5.RET.1_R	chr10:43572688-43572850	AACAGAAAGGCGCTTCTGAA
RET.18.1.RET.1_F	chr10:43620313-43620443	TGCTTGGATCATATTGGCCT
RET.18.1.RET.1_R	chr10:43620313-43620443	TTCAGCTTGTGGGAATTGGA
RET.13.1.RET.1_F	chr10:43613821-43613979	GCTCTGTGCTGCATTTCAG
RET.13.1.RET.1_R	chr10:43613821-43613979	GAGAACAGGGCTGTATGGAG

RET.16.1.RET.1_F	chr10:43617356-43617488	CCCCTCCTTCCTAGAGAGTT
RET.16.1.RET.1_R	chr10:43617356-43617488	TGTTTCTGTAACCTCCACCC
RET.6.1.RET.1_F	chr10:43604508-43604668	CAACCGGAACCTCTCCATC
RET.6.1.RET.1_R	chr10:43604508-43604668	GGCTCACCTGGGCAAAT
RET.6.2.RET.2_F	chr10:43604557-43604710	GCTGGTCAATGACTCAGACT
RET.6.2.RET.2_R	chr10:43604557-43604710	ATGTCCCTTGGCCTTTCAAT
RET.6.2.RET.3_F	chr10:43604438-43604576	TGCTACACATGAGGAAGCAG
RET.6.2.RET.3_R	chr10:43604438-43604576	TTGAAGTGGAGCAAGAGGAC
RET.3.1.RET.1_F	chr10:43597790-43597950	GACCTGACTTCTCTCTGCAG
RET.3.1.RET.1_R	chr10:43597790-43597950	GGCCTTGTCTCTGGGAA
RET.3.2.RET.2_F	chr10:43597920-43598078	TTCAACACCTCCTTTCCAGC
RET.3.2.RET.2_R	chr10:43597920-43598078	CACAAGGTCGGCACTCA
RET.9.1.RET.1_F	chr10:43608286-43608423	ATGGGTGACAGCCTGCT
RET.9.1.RET.1_R	chr10:43608286-43608423	CTGTTCCCATGCCCTGATTA
RET.12.3.RET.1_F	chr10:43612029-43612169	CCCTTCCCTCATTTCCAACA
RET.12.3.RET.1_R	chr10:43612029-43612169	GGCAGGTACCTTTCAGCAT
RET.12.4.RET.2_F	chr10:43612121-43612272	GGAAAAGTGGTCAAGGCAAC
RET.12.4.RET.2_R	chr10:43612121-43612272	CTCTAGAACAGCATTGGGGG
RET.14.1.RET.1_F	chr10:43615016-43615179	TGGAGTACGCCAAATACGG
RET.14.1.RET.1_R	chr10:43615016-43615179	CACCTTCATCTCGGCCA
RET.14.2.RET.2_F	chr10:43615160-43615296	ATCTCATTTGCCTGGCAGAT
RET.14.2.RET.2_R	chr10:43615160-43615296	CATGGTGGGCTAGAGTGTG
RET.14.2.RET.3_F	chr10:43614884-43615046	CCCCTTACTCATTGGGTGG
RET.14.2.RET.3_R	chr10:43614884-43615046	TAGCCAGGCCCCACTTT
RET.20.1.RET.1_F	chr10:43623574-43623732	TTTTAGGCATGTCAGACCCG
RET.20.1.RET.1_R	chr10:43623574-43623732	CCCCTTGTGAGTCCATTACC
RET.20.2.RET.2_F	chr10:43623465-43623605	CACAGAAACCACGAGTTTGG
RET.20.2.RET.2_R	chr10:43623465-43623605	TGTTAGTGCCATCAGCTCTC
RET.15.1.RET.1_F	chr10:43615529-43615687	TCGTGCTATTTTTCCTCACAG
RET.15.1.RET.1_R	chr10:43615529-43615687	CATGGTGCACCTGGGAT
RET.8.1.RET.1_F	chr10:43607537-43607673	CTGTGACCCTGCTTGTCTG
RET.8.1.RET.1_R	chr10:43607537-43607673	GGCGTTTCCAGGGCTTA
RET.4.1.RET.1_F	chr10:43600496-43600656	GAGAAGTACGAGCTGGTGG
RET.4.1.RET.1_R	chr10:43600496-43600656	ACTGGGTAGACCACAGCA
RET.4.2.RET.2_F	chr10:43600399-43600558	TCTGCTTGGTGCGCA
RET.4.2.RET.2_R	chr10:43600399-43600558	AGTCGTCCTCGTCGTACA
RET.10.1.RET.1_F	chr10:43609019-43609167	AGGGGGCAGCATTGTTG
RET.10.1.RET.1_R	chr10:43609019-43609167	GATGTGCTGTTGAGACCTCT
RET.10.2.RET.2_F	chr10:43608947-43609081	GGACACTGCCCTGGAAATAT
RET.10.2.RET.2_R	chr10:43608947-43609081	GAAGCACTTCTCCTCCTCAG
RET.19.1.RET.1_F	chr10:43622033-43622192	TGTCTTCCAGGACTACTTGG
RET.19.1.RET.1_R	chr10:43622033-43622192	GACAGCGGTGCTAGAATCTA
RET.19.2.RET.2_F	chr10:43622067-43622225	ACTCCATCTGACTCCCTGAT
RET.19.2.RET.2_R	chr10:43622067-43622225	AAGCATCACAGAGAGGAAGG
RET.19.2.RET.3_F	chr10:43621962-43622097	CCTGAGGATGGCTTGTTGTA
RET.19.2.RET.3_R	chr10:43621962-43622097	TTATTACAGTCCACCAGCGG
RET.5.1.RET.1_F	chr10:43601891-43602053	ATCAGGGGAGCTGGTGA
RET.5.1.RET.1_R	chr10:43601891-43602053	GAGCACCTCATTTCCTGGG
RET.5.2.RET.2_F	chr10:43601729-43601892	CATCTGGTCCACCTATGGG
RET.5.2.RET.2_R	chr10:43601729-43601892	AGCGTGCTTGTGTACCG
FGFR2.11.1.FGFR2.1_F	chr10:123263324-123263481	ACTTATCTCTTGGAAACTCCCA
FGFR2.11.1.FGFR2.1_R	chr10:123263324-123263481	CAGATGGAGCCAGGATTACA
FGFR2.11.2.FGFR2.2_F	chr10:123263299-123263446	GGACATGGCCAAGAGAAGTA
FGFR2.11.2.FGFR2.2_R	chr10:123263299-123263446	TTTGTATCCAGGTTTCGGCT
FGFR2.7.1.FGFR2.1_F	chr10:123247512-123247671	GCCATCGACTTACATTGGTG
FGFR2.7.1.FGFR2.1_R	chr10:123247512-123247671	TTTCCTTTTTGTTCTGGCGG
FGFR2.7.2.FGFR2.2_F	chr10:123247466-123247602	CTGGAACATTCTGAGCCTCA
FGFR2.7.2.FGFR2.2_R	chr10:123247466-123247602	TCATCGAGATTTAGCAGCCA
FGFR2.2.1.FGFR2.1_F	chr10:123239377-123239535	GCAGACACAGTCATTCATGT
FGFR2.2.1.FGFR2.1_R	chr10:123239377-123239535	GTCTCTCTTCCCTTCTTTCAG
FGFR2.2.2.FGFR2.2_F	chr10:123239293-123239426	ACAAGTGGAGACAACAAGCT
FGFR2.2.2.FGFR2.2_R	chr10:123239293-123239426	TTTTTCTCCAGACCCCATGC
FGFR2.17.1.FGFR2.1_F	chr10:123310834-123310993	AATGCGATGCTCCTGCTT
FGFR2.17.1.FGFR2.1_R	chr10:123310834-123310993	GCTGTCCATCAGTATACATTCT
FGFR2.17.2.FGFR2.2_F	chr10:123310739-123310895	GCGAGACTCCATCGCAAAAA
FGFR2.17.2.FGFR2.2_R	chr10:123310739-123310895	GGCCAACACTGTCAAGTTTC
FGFR2.1.3.FGFR2.1_F	chr10:123239033-123239185	TCTGTAAGTGTGTGCTGACA

FGFR2.1.3.FGFR2.1_R	chr10:123239033-123239185	TGAAAACTTGTAATCTTCCCCA
FGFR2.18.1.FGFR2.1_F	chr10:123324016-123324161	GAGCCGGGCAGTTACTTAC
FGFR2.18.1.FGFR2.1_R	chr10:123324016-123324161	TGCTATGGAGAAGGTCTCAG
FGFR2.13.1.FGFR2.1_F	chr10:123276828-123276985	ACCCAGAGAGAAAGAACAGTA
FGFR2.13.1.FGFR2.1_R	chr10:123276828-123276985	CCTTTTCTTTTGCTTCCCTTG
FGFR2.13.2.FGFR2.2_F	chr10:123276682-123276837	GTGTGTGAATTTCCAAGGCA
FGFR2.13.2.FGFR2.2_R	chr10:123276682-123276837	TCTGCATGGTTGACAGTTCT
FGFR2.16.1.FGFR2.1_F	chr10:123298052-123298212	ACGTTCATGCTTTCAAACGA
FGFR2.16.1.FGFR2.1_R	chr10:123298052-123298212	GGTACGAAACCAGCACTG
FGFR2.16.2.FGFR2.2_F	chr10:123298075-123298233	AAGCAAGAATGGGCTGGTAT
FGFR2.16.2.FGFR2.2_R	chr10:123298075-123298233	CCGCCTTTGCTTTGATCTTT
FGFR2.6.1.FGFR2.1_F	chr10:123246836-123246991	TATTTTTGCAGCTCAAGCCC
FGFR2.6.1.FGFR2.1_R	chr10:123246836-123246991	TAGCCCTATTGAGCCTGCTA
FGFR2.3.1.FGFR2.1_F	chr10:123241664-123241821	CCTGACCAACTTTTCCCAGT
FGFR2.3.1.FGFR2.1_R	chr10:123241664-123241821	ACAGCTGACCTTCAGAAGTT
FGFR2.9.1.FGFR2.1_F	chr10:123257996-123258154	ATTTGGGCGAATGCAGTTTT
FGFR2.9.1.FGFR2.1_R	chr10:123257996-123258154	CTGCCCATGAGTTAGAGGAA
FGFR2.12.1.FGFR2.1_F	chr10:123274661-123274821	CGCAGGGGGATACGTTT
FGFR2.12.1.FGFR2.1_R	chr10:123274661-123274821	CAATCTAGCGCCTGGAAGAG
FGFR2.12.2.FGFR2.2_F	chr10:123274733-123274878	TTCTTCATTCGGCACAGGAT
FGFR2.12.2.FGFR2.2_R	chr10:123274733-123274878	GTCAGTCTGGTGTGCTAACT
FGFR2.12.2.FGFR2.3_F	chr10:123274556-123274712	ACAGAAGTCGATGGCATCAA
FGFR2.12.2.FGFR2.3_R	chr10:123274556-123274712	ATCCTGTGCCGAATGAAGAA
FGFR2.15.1.FGFR2.1_F	chr10:123279517-123279677	GAACCTTGAGGTAGGGCAG
FGFR2.15.1.FGFR2.1_R	chr10:123279517-123279677	CTCTCTCCACCAGAGCGAT
FGFR2.15.2.FGFR2.2_F	chr10:123279623-123279774	CAAACTCTACGTCTCCTCCG
FGFR2.15.2.FGFR2.2_R	chr10:123279623-123279774	CTTGAGGCTTTTCTGGCATG
FGFR2.15.2.FGFR2.3_F	chr10:123279418-123279577	CCTCTCTCAACTCCAACAGG
FGFR2.15.2.FGFR2.3_R	chr10:123279418-123279577	AAGGTTTACAGTGATGCCCA
FGFR2.14.1.FGFR2.1_F	chr10:123278205-123278364	AGCATTGTTACCTTGCTGTT
FGFR2.14.1.FGFR2.1_R	chr10:123278205-123278364	TCCTGGTTGGCCGTTATATT
FGFR2.14.2.FGFR2.2_F	chr10:123278117-123278266	ATCCTATAAGCTGCCTGCAG
FGFR2.14.2.FGFR2.2_R	chr10:123278117-123278266	GCGGATGCTGGGGAATATAT
FGFR2.20.1.FGFR2.1_F	chr10:123353233-123353388	AAATGACTTACCTTCTGGCTC
FGFR2.20.1.FGFR2.1_R	chr10:123353233-123353388	CCGTAGAGGAAGTGTGCAG
FGFR2.20.2.FGFR2.2_F	chr10:123353181-123353325	TTAACAATCTGCCCCCAGAC
FGFR2.20.2.FGFR2.2_R	chr10:123353181-123353325	TTGGTACCGTAACCATGGTC
FGFR2.8.1.FGFR2.1_F	chr10:123256066-123256225	CTTTTTGGGAAGCCAAGTACT
FGFR2.8.1.FGFR2.1_R	chr10:123256066-123256225	CTCAACAGGGCCTCTCTAT
FGFR2.8.2.FGFR2.2_F	chr10:123256207-123256348	TTCTCGGAGGTTGCCTTTAG
FGFR2.8.2.FGFR2.2_R	chr10:123256207-123256348	CCAGCCGCTGTATGTTAAAC
FGFR2.8.2.FGFR2.3_F	chr10:123256037-123256186	CCCAGCCAAGTAGAATGTGA
FGFR2.8.2.FGFR2.3_R	chr10:123256037-123256186	CTAAAGGCAACCTCCGAGAA
FGFR2.4.1.FGFR2.1_F	chr10:123243190-123243347	AAGACAACCAAGGACAAGGG
FGFR2.4.1.FGFR2.1_R	chr10:123243190-123243347	CACGTACCCAGTGCATATGA
FGFR2.10.1.FGFR2.1_F	chr10:123260309-123260466	GATAAGACTCTCCACCCAGC
FGFR2.10.1.FGFR2.1_R	chr10:123260309-123260466	GTGCTAATCCCCTATTTACACA
FGFR2.19.1.FGFR2.1_F	chr10:123324962-123325123	GCCAACTCACCTGTGACATT
FGFR2.19.1.FGFR2.1_R	chr10:123324962-123325123	CTGTTGAAAGATGCCGCC
FGFR2.19.2.FGFR2.2_F	chr10:123325119-123325272	CCCCATCCTTAGTCCAACTG
FGFR2.19.2.FGFR2.2_R	chr10:123325119-123325272	TGACCTTTGTTGGACGTTCT
FGFR2.19.2.FGFR2.3_F	chr10:123324865-123325012	ATGCCTGGCATCCAATTACA
FGFR2.19.2.FGFR2.3_R	chr10:123324865-123325012	CTAGAGACTCCGGCCTCTAT
FGFR2.5.1.FGFR2.1_F	chr10:123244907-123245055	CAGGAAAGACAACAGCCCTT
FGFR2.5.1.FGFR2.1_R	chr10:123244907-123245055	TAATGCCGTGCTTTCTCCTT
APC.11.36.APC.1_F	chr5:112157564-112157710	CATTGCTCTTCAAATAACAAAGCA
APC.11.36.APC.1_R	chr5:112157564-112157710	TCCACCAGTAATTGTCTATGTCA
APC.7.1.APC.1_F	chr5:112128079-112128235	GCTTTTAAGTGGTAGCCATAGT
APC.7.1.APC.1_R	chr5:112128079-112128235	CCCACAAACAAGAAAGGCAA
APC.2.1.APC.1_F	chr5:112090616-112090772	GCAGCTTCATATGATCAGTTGT
APC.2.1.APC.1_R	chr5:112090616-112090772	ACCTCAAGTTTACAAGAGGGA
APC.2.2.APC.2_F	chr5:112090585-112090717	TATAGGTCCAAGGGTAGCCA
APC.2.2.APC.2_R	chr5:112090585-112090717	AGTCACAGTCTTGATACCTTCA
APC.1.1.APC.1_F	chr5:112043465-112043614	CCTTTGCCCGCTTCTGT
APC.1.1.APC.1_R	chr5:112043465-112043614	AAGCCGAGGAAGCTTTGC
APC.1.2.APC.2_F	chr5:112043384-112043544	GGTGAGGAAGGTGAAGCAC
APC.1.2.APC.2_R	chr5:112043384-112043544	CAGTGGCCAGAAGTACGAG

APC.16.1.APC.1_F	chr5:112173359-112173519	ACTTTGTGGAATCTCTCAGCA
APC.16.1.APC.1_R	chr5:112173359-112173519	AAGCTTGAGCCAGGAGAC
APC.16.2.APC.2_F	chr5:112173219-112173371	ACTGCATACACATTGTGACC
APC.16.2.APC.2_R	chr5:112173219-112173371	GTCCCATAATGCTTCCTGGT
APC.16.2.APC.3_F	chr5:112173580-112173739	CAAAAAGCCCTAGAAGCAGA
APC.16.2.APC.3_R	chr5:112173580-112173739	GAAAGGACAGTCATGTTGCC
APC.16.3.APC.4_F	chr5:112173473-112173627	GAAGTGCTGCAGCTTTAAGG
APC.16.3.APC.4_R	chr5:112173473-112173627	GATGAGATGCCTTGGGACTT
APC.16.3.APC.5_F	chr5:112173760-112173919	GGCAACATGACTGTCCTTTC
APC.16.3.APC.5_R	chr5:112173760-112173919	TGGTGGAGATCTGCAAACC
APC.16.4.APC.6_F	chr5:112173648-112173782	AAGTCCCAAGGCATCTCATC
APC.16.4.APC.6_R	chr5:112173648-112173782	TGATGAAGAGGAGCTGGGTA
APC.16.4.APC.7_F	chr5:112174240-112174399	GGTCAAATGAAACCCTCGAT
APC.16.4.APC.7_R	chr5:112174240-112174399	GGACTTTGCCTTCCAGAGTT
APC.16.5.APC.8_F	chr5:112174410-112174569	TGAGCAGTTGAACTCTGGAA
APC.16.5.APC.8_R	chr5:112174410-112174569	AAACACATTCCTGCTGTCCA
APC.16.6.APC.9_F	chr5:112174299-112174437	TTATGGTCAATACCCAGCCG
APC.16.6.APC.9_R	chr5:112174299-112174437	TTATGTGTTTGGGTCTTGCC
APC.16.6.APC.10_F	chr5:112174640-112174799	CAGAAACAAATCGAGTGGGT
APC.16.6.APC.10_R	chr5:112174640-112174799	GGCTGATCCACATGACGTT
APC.16.7.APC.11_F	chr5:112174538-112174666	TCCTGTTTATACTGAGAGCACT
APC.16.7.APC.11_R	chr5:112174538-112174666	TCTTGACACAAAGACTGGCT
APC.16.7.APC.12_F	chr5:112174819-112174979	AAACGTCATGTGGATCAGCC
APC.16.7.APC.12_R	chr5:112174819-112174979	GCAGAACTTGGATGGAGCT
APC.16.8.APC.13_F	chr5:112174687-112174839	AGCCAGTCTTTGTGTCAAGA
APC.16.8.APC.13_R	chr5:112174687-112174839	TGATGAAGGAATATCTGTGGCA
APC.16.8.APC.14_F	chr5:112174999-112175159	AGCTCCATCCAAGTTCTGC
APC.16.8.APC.14_R	chr5:112174999-112175159	GCTTCCTGTGTCGTCTGAT
APC.16.9.APC.15_F	chr5:112174862-112174999	TGCCACAGATATTCCTTCATCA
APC.16.9.APC.15_R	chr5:112174862-112174999	GGCTGACCACTTCTACTCTG
APC.16.9.APC.16_F	chr5:112175260-112175420	GAAGATCCTGTGAGCGAAGT
APC.16.9.APC.16_R	chr5:112175260-112175420	ATGAGTGGGGTCTCCTGAA
APC.16.10.APC.17_F	chr5:112175149-112175277	CTTTGTCATCAGCTGAAGATGA
APC.16.10.APC.17_R	chr5:112175149-112175277	TGCTGGATTTGGTTCTAGGG
APC.16.10.APC.18_F	chr5:112175421-112175580	AAAGTCCACCTGAACACTATG
APC.16.10.APC.18_R	chr5:112175421-112175580	ACTTCTGCTTGGTGGCATG
APC.16.11.APC.19_F	chr5:112175631-112175791	CCACCTCCTCAAACAGCTC
APC.16.11.APC.19_R	chr5:112175631-112175791	CTCAGGCTGGATGAACAAGA
APC.16.12.APC.20_F	chr5:112175520-112175677	CTCCGTTCAGAGTGAACCAT
APC.16.12.APC.20_R	chr5:112175520-112175677	TGCTTAGGTCCACTCTCTCT
APC.16.12.APC.21_F	chr5:112175882-112176041	ATGCCTCCAGTTCAGGAA
APC.16.12.APC.21_R	chr5:112175882-112176041	GCTTTACGTGATGACTTTGTTG
APC.16.13.APC.22_F	chr5:112175749-112175897	CAGGTTCTTCCAGATGCTGA
APC.16.13.APC.22_R	chr5:112175749-112175897	AGGCTGCTCTGATTCTGTTT
APC.16.13.APC.23_F	chr5:112176052-112176211	CTGCCATGCCAACAAAGTC
APC.16.13.APC.23_R	chr5:112176052-112176211	TGTCCCTTCAACACAATACAC
APC.16.14.APC.24_F	chr5:112175918-112176073	AAACAGAATCAGAGCAGCCT
APC.16.14.APC.24_R	chr5:112175918-112176073	AATTTTGAAGCAGTCTGGGC
APC.16.14.APC.25_F	chr5:112176209-112176371	CGGGGGATGATATGCCA
APC.16.14.APC.25_R	chr5:112176209-112176371	AGCCTCATCTGTACTTCTGC
APC.16.15.APC.26_F	chr5:112176380-112176541	TTCCTACAGAAGGCAGAAGT
APC.16.15.APC.26_R	chr5:112176380-112176541	GACGCAGATGCTTGCTG
APC.16.16.APC.27_F	chr5:112176322-112176481	GCTGGAGAAGGAGTTAGAGG
APC.16.16.APC.27_R	chr5:112176322-112176481	CTTTTCCCTTTGGGCATAGC
APC.16.16.APC.28_F	chr5:112176922-112177081	GATGTTGACCTTTCCAGGGA
APC.16.16.APC.28_R	chr5:112176922-112177081	GATGACTGGGGAAAAGTGGA
APC.16.17.APC.29_F	chr5:112177111-112177271	CCCCAGTCATCCAAAGACAT
APC.16.17.APC.29_R	chr5:112177111-112177271	CTTGGTTCTCCCTGTGAGT
APC.16.17.APC.30_F	chr5:112176809-112176961	AGAGTCAGAGGAAGTTTTGCT
APC.16.17.APC.30_R	chr5:112176809-112176961	TGGCTGGTAACTTTAGCCTC
APC.16.18.APC.31_F	chr5:112176982-112177122	GAGGCTAAAGTTACCAGCCA
APC.16.18.APC.31_R	chr5:112176982-112177122	ACTTTTCATCAGTTGCTGCC
APC.16.18.APC.32_F	chr5:112177440-112177601	GCTCCGCAATGCCAAAAA
APC.16.18.APC.32_R	chr5:112177440-112177601	GGAATTTGCACCTTCCTGAA
APC.16.19.APC.33_F	chr5:112177622-112177781	TTCAGGAAGGTGCAAATTCC
APC.16.19.APC.33_R	chr5:112177622-112177781	TGGTTTTAGAATTCGTGGGC
APC.16.19.APC.34_F	chr5:112177291-112177444	GACTCACAGGGAGAACCAAG

APC.16.19.APC.34_R	chr5:112177291-112177444	CCCTTGAGTCTTGAAGGCTT
APC.16.20.APC.35_F	chr5:112177582-112177711	TGGTCTATCCCCTGATTCAGA
APC.16.20.APC.35_R	chr5:112177582-112177711	GGTGATCCCAGAGAGATTCC
APC.16.20.APC.36_F	chr5:112177269-112177398	TATCAAAGAGACTGAGCCCC
APC.16.20.APC.36_R	chr5:112177269-112177398	TACATTCCTGCAACAGGTCA
APC.16.20.APC.37_F	chr5:112177801-112177961	GGCCCACGAATTCTAAAACC
APC.16.20.APC.37_R	chr5:112177801-112177961	ATTGTCCTGCCTCGAGAGA
APC.16.21.APC.38_F	chr5:112177653-112177800	TTTACATCAAGCTGCTGCTG
APC.16.21.APC.38_R	chr5:112177653-112177800	TCCAATGTACTTTTCTCCCCT
APC.16.21.APC.39_F	chr5:112177972-112178131	ATGCCTTCAATCTCTCGAGG
APC.16.21.APC.39_R	chr5:112177972-112178131	TGGCAACAGGGCTTAATTC
APC.16.22.APC.40_F	chr5:112177959-112178110	CCTTCAAGCAAACATGCCTT
APC.16.22.APC.40_R	chr5:112177959-112178110	GATTTCACAGATGGCTTGGC
APC.16.22.APC.41_F	chr5:112178161-112178322	TGTTGCCAGGCAGACATC
APC.16.22.APC.41_R	chr5:112178161-112178322	GGGATGATGTCCTTGGAAGT
APC.16.23.APC.42_F	chr5:112178089-112178226	AGCCCTAGTGAAGGTCAAAC
APC.16.23.APC.42_R	chr5:112178089-112178226	TACTTAATGGTTGCTGGGCA
APC.16.23.APC.43_F	chr5:112178613-112178772	ACCTGTATTAGTACGCCAGT
APC.16.23.APC.43_R	chr5:112178613-112178772	CCTGAACAGACGAATGTGTG
APC.16.24.APC.44_F	chr5:112178793-112178952	CACACATTCGTCTGTTCAGG
APC.16.24.APC.44_R	chr5:112178793-112178952	CTCGAGGAAGGGATGATGAA
APC.16.24.APC.45_F	chr5:112178457-112178612	CAGGTTTATCCAAGAATGCCA
APC.16.24.APC.45_R	chr5:112178457-112178612	GGAGCTTCTTTGATGAAAGTTG
APC.16.25.APC.46_F	chr5:112178715-112178855	ATCTAGACCAGCTTCTCCCA
APC.16.25.APC.46_R	chr5:112178715-112178855	AATATCATGGCGCTTTGCTG
APC.16.25.APC.47_F	chr5:112178303-112178458	CCCTGGTAGAAATGGAATAAGT
APC.16.25.APC.47_R	chr5:112178303-112178458	CAGACTCACTTCTTGGAATACT
APC.16.25.APC.48_F	chr5:112179243-112179402	TTATCAAATGGCACCTGCTG
APC.16.25.APC.48_R	chr5:112179243-112179402	CACTGCCATTACCCACATTT
APC.16.26.APC.49_F	chr5:112179423-112179582	AAATGTGGGTAATGGCAGTG
APC.16.26.APC.49_R	chr5:112179423-112179582	TGTGTTTGCTTGAGCTGCTA
APC.16.26.APC.50_F	chr5:112179122-112179251	ACCAAGTATCCGCAAAAGGA
APC.16.26.APC.50_R	chr5:112179122-112179251	TCTCACCCAAACATCCTCTG
APC.16.27.APC.51_F	chr5:112179583-112179742	GAACGTACCCCATTCAGTTC
APC.16.27.APC.51_R	chr5:112179583-112179742	TCTGTGCTGTCAGTTTTGGA
APC.16.27.APC.52_F	chr5:112179324-112179463	TGGAAGATCTCCCACAGGTA
APC.16.27.APC.52_R	chr5:112179324-112179463	GGGGCATCCACCTGAATAAA
APC.16.28.APC.53_F	chr5:112178952-112179111	AAACGTGAGCACAGCAAAC
APC.16.28.APC.53_R	chr5:112178952-112179111	TTCTCCATGTTCCTTTTGCG
APC.16.28.APC.54_F	chr5:112176537-112176690	CGTGTGAAAAAGATAATGGACC
APC.16.28.APC.54_R	chr5:112176537-112176690	TCTGAGAAAACTCTCTCAGCA
APC.16.28.APC.55_F	chr5:112173920-112174069	CAGGAACTTCTTCAAAGCGA
APC.16.28.APC.55_R	chr5:112173920-112174069	TTTGAATGTGTATGGGCAGC
APC.16.29.APC.56_F	chr5:112179037-112179181	TGCTTCATCAGAATCCAGTGA
APC.16.29.APC.56_R	chr5:112179037-112179181	CCATTTGTAGCACCTGAGGA
APC.16.30.APC.57_F	chr5:112174069-112174219	GAAATGCACTTAGAAGAAGCTC
APC.16.30.APC.57_R	chr5:112174069-112174219	ATCGAGGGTTTCATTTGACC
APC.16.31.APC.58_F	chr5:112174148-112174278	GACATGTTCTATGCCTTATGCC
APC.16.31.APC.58_R	chr5:112174148-112174278	CGGCTGGGTATTGACCATAA
APC.16.33.APC.59_F	chr5:112176662-112176815	ACTGAATATAGGACACGTGTAAGA
APC.16.33.APC.59_R	chr5:112176662-112176815	AGGCGTGTAATGATGAGGTG
APC.16.36.APC.60_F	chr5:112179681-112179823	TAGGAAAAGCAGCGCAGATA
APC.16.36.APC.60_R	chr5:112179681-112179823	TCTTAGTTTCATTCTTCCTCTCTT
APC.13.1.APC.1_F	chr5:112163592-112163742	GCTTGGCTTCAAGTTGTCTT
APC.13.1.APC.1_R	chr5:112163592-112163742	GAGACCCTGCCTCAAAGAAA
APC.6.37.APC.1_F	chr5:112116384-112116618	TCATGCACCATGACTGACGT
APC.6.37.APC.1_R	chr5:112116384-112116618	AGCTCTTCGCTGTTTTATCACT
APC.3.37.APC.1_F	chr5:112101922-112102180	GGTGCGTGCTTTGAGAGTGA
APC.3.37.APC.1_R	chr5:112101922-112102180	ACCCAAATCGAGAGAAGCTGT
APC.9.33.APC.1_F	chr5:112151141-112151293	GGAGTACCTTAACATGATGTTATCT
APC.9.33.APC.1_R	chr5:112151141-112151293	ACCAGGGTTTGTAATCTTCTGT
APC.12.28.APC.1_F	chr5:112162794-112162926	TGTCTTTTTCCTCTTGCCCT
APC.12.28.APC.1_R	chr5:112162794-112162926	ACCTTGTTGGCTACATCTCC
APC.12.29.APC.2_F	chr5:112162917-112163064	GCTGGAATGGCTTTGACAAA
APC.12.29.APC.2_R	chr5:112162917-112163064	CGAATGTGAAGCACAGGTTT
APC.15.34.APC.1_F	chr5:112170646-112170797	GATGACCCATATTCTGTTTCTTACT
APC.15.34.APC.1_R	chr5:112170646-112170797	ATCCCACCTCCACTTTCAAT

APC.15.35.APC.2_F	chr5:112170774-112170906	TTGGCACTCTTACTTACCGG
APC.15.35.APC.2_R	chr5:112170774-112170906	GCTTACAATTAGGTCTTTTTGAGAG
APC.14.37.APC.1_F	chr5:112164563-112164722	TGATTAATTTGCAGGTTATTGCGA
APC.14.37.APC.1_R	chr5:112164563-112164722	TGGCTAAAAGAAGGCAGCAA
APC.14.38.APC.2_F	chr5:112164419-112164568	GCCTCCCAAAGTGATAGGAT
APC.14.38.APC.2_R	chr5:112164419-112164568	TCGCCAAGACAAATTCCTCA
APC.8.33.APC.1_F	chr5:112136976-112137123	ACTGATGTTAACTCCATCTTAACAG
APC.8.33.APC.1_R	chr5:112136976-112137123	CCATCTTGCTTCATACTTTTCTGA
APC.4.1.APC.1_F	chr5:112102956-112103109	ATGTCCCTCCGTTCTTATGG
APC.4.1.APC.1_R	chr5:112102956-112103109	TGGAGTACACAAGGCAATGT
APC.4.37.APC.2_F	chr5:112102730-112102986	TACCCTGACCCAAGTGGACT
APC.4.37.APC.2_R	chr5:112102730-112102986	GGAACAGGACTGCACTCTCC
APC.10.1.APC.1_F	chr5:112154742-112154902	GCGAACTTTGCTAGCTATGT
APC.10.1.APC.1_R	chr5:112154742-112154902	TGTCATCAGGCTGTGAGTG
APC.10.2.APC.2_F	chr5:112154903-112155054	CAGCACTCCACAACATCATT
APC.10.2.APC.2_R	chr5:112154903-112155054	ACATGCACTACGATGTACACT
APC.10.2.APC.3_F	chr5:112154663-112154796	CTAAACTCATTTGGCCCACAG
APC.10.2.APC.3_R	chr5:112154663-112154796	TGCCATGTAAAAGCTGGATG
APC.5.32.APC.1_F	chr5:112111281-112111436	ATTGCTCTTCTGCAGTCTTT
APC.5.32.APC.1_R	chr5:112111281-112111436	AAGTTGTACTGCCAAGTTACTT
ERBB2.11.1.ERBB2.1_F	chr17:37871458-37871617	GAGTGAAGGCATTCATGGTG
ERBB2.11.1.ERBB2.1_R	chr17:37871458-37871617	AACAGGATGCAGAGACAGAG
ERBB2.21.1.ERBB2.1_F	chr17:37880989-37881149	TGTCCCCAGGAAGCATACG
ERBB2.21.1.ERBB2.1_R	chr17:37880989-37881149	CATACCTTGGCAATCTGCAT
ERBB2.21.2.ERBB2.2_F	chr17:37881111-37881268	TAGACCATGTCCGGGAAAAC
ERBB2.21.2.ERBB2.2_R	chr17:37881111-37881268	CACCCATGTAGACCTTCTGG
ERBB2.21.2.ERBB2.3_F	chr17:37880915-37881059	CTGTGGTTTGTGATGGTTGG
ERBB2.21.2.ERBB2.3_R	chr17:37880915-37881059	TAGGGCATAAGCTGTGTCAC
ERBB2.7.1.ERBB2.1_F	chr17:37866294-37866454	GATGCTGATGAGGGTCTGG
ERBB2.7.1.ERBB2.1_R	chr17:37866294-37866454	CACAAAGCAGAGGCACATAC
ERBB2.26.1.ERBB2.1_F	chr17:37883075-37883237	CCTTCCTCCACAGAATGAGG
ERBB2.26.1.ERBB2.1_R	chr17:37883075-37883237	TGGTAGATGAGCTGCGG
ERBB2.26.2.ERBB2.2_F	chr17:37883204-37883350	CTTCTTCTGTCCAGACCCTG
ERBB2.26.2.ERBB2.2_R	chr17:37883204-37883350	AATGGGGTTTCCTTGAGAGG
ERBB2.26.2.ERBB2.3_F	chr17:37883002-37883147	GATGAGTCCAGTATGCCAGG
ERBB2.26.2.ERBB2.3_R	chr17:37883002-37883147	GATACTCCTCAGCATCCACC
ERBB2.2.8.ERBB2.1_F	chr17:37856491-37856657	GAGCCGCAGTGAGCAC
ERBB2.2.8.ERBB2.1_R	chr17:37856491-37856657	TAGGAGAGCTCGTCCGG
ERBB2.17.1.ERBB2.1_F	chr17:37875950-37876102	AATGGGGATAATGACCCAGC
ERBB2.17.1.ERBB2.1_R	chr17:37875950-37876102	GGCAATGAAGGGTACATCCT
ERBB2.22.1.ERBB2.1_F	chr17:37881310-37881457	TCCCATTCCAGGGGATGAG
ERBB2.22.1.ERBB2.1_R	chr17:37881310-37881457	TCCTTGGTCCTTCACCTAAC
ERBB2.22.2.ERBB2.2_F	chr17:37881293-37881430	AAGGTCTACATGGGTGCTTC
ERBB2.22.2.ERBB2.2_R	chr17:37881293-37881430	CCATCTGCATGGTACTCTGT
ERBB2.1.1.ERBB2.1_F	chr17:37855709-37855851	GGGCAACAAGAGCAAAAGTT
ERBB2.1.1.ERBB2.1_R	chr17:37855709-37855851	ATAGTCAAGGAGGGGGATGT
ERBB2.18.4.ERBB2.1_F	chr17:37879552-37879692	AAACTAGCCCTCAATCCCTG
ERBB2.18.4.ERBB2.1_R	chr17:37879552-37879692	TCCGTTTCCTGCAGCAG
ERBB2.18.5.ERBB2.2_F	chr17:37879682-37879837	GCAGAAGATCCGGAAGTACA
ERBB2.18.5.ERBB2.2_R	chr17:37879682-37879837	TCTCTTTCAGGATCCGCATC
ERBB2.23.1.ERBB2.1_F	chr17:37881563-37881717	ACACACAGTTGGAGGACTTC
ERBB2.23.1.ERBB2.1_R	chr17:37881563-37881717	CGTAATTCTCCCCATCCCAG
ERBB2.13.1.ERBB2.1_F	chr17:37871993-37872156	GCCCACCTTTCTCCCATAG
ERBB2.13.1.ERBB2.1_R	chr17:37871993-37872156	GTTGGCAGTGTGGAGCA
ERBB2.13.2.ERBB2.2_F	chr17:37872108-37872267	ATAACACCCACCTCTGCTTC
ERBB2.13.2.ERBB2.2_R	chr17:37872108-37872267	GTCTGCACAAGTCCAAGAAC
ERBB2.16.1.ERBB2.1_F	chr17:37873588-37873743	AGGAGGCTGACCAGTGT
ERBB2.16.1.ERBB2.1_R	chr17:37873588-37873743	CCTTTCTGCAGAAAAGACCG
ERBB2.16.2.ERBB2.2_F	chr17:37873442-37873598	GTGAAGAGCAAGGGTGTTTG
ERBB2.16.2.ERBB2.2_R	chr17:37873442-37873598	AGGGAGGGTCCTTATAGTGG
ERBB2.27.1.ERBB2.1_F	chr17:37883647-37883803	GGCTGGCTCCGATGTATTT
ERBB2.27.1.ERBB2.1_R	chr17:37883647-37883803	TCTGCTTAGACTGGACTCCA
ERBB2.27.2.ERBB2.2_F	chr17:37883495-37883646	CTGTCACCTTCCATGGAGTC
ERBB2.27.2.ERBB2.2_R	chr17:37883495-37883646	CCATTCCCAGGTCACCATC
ERBB2.25.1.ERBB2.1_F	chr17:37882805-37882965	TAGCATGCTGACCTCCCT
ERBB2.25.1.ERBB2.1_R	chr17:37882805-37882965	ATCTCTCCTTCCCACCCTC
ERBB2.6.1.ERBB2.1_F	chr17:37866066-37866222	GTCTCTGGTTCTGTCCTCAG

ERBB2.6.1.ERBB2.1_R	chr17:37866066-37866222	ACATCCCAAGCCTGTTATCC
ERBB2.28.1.ERBB2.1_F	chr17:37883942-37884101	CACCTTCTCTTGACCTTTCAG
ERBB2.28.1.ERBB2.1_R	chr17:37883942-37884101	CAAGTACTCGGGGTTCTCC
ERBB2.28.2.ERBB2.2_F	chr17:37884120-37884283	TGGAGAACCCCGAGTACTT
ERBB2.28.2.ERBB2.2_R	chr17:37884120-37884283	GGTTCACACTGGCACGT
ERBB2.28.3.ERBB2.3_F	chr17:37884277-37884419	CAGAGAACCCAGAGTACCTG
ERBB2.28.3.ERBB2.3_R	chr17:37884277-37884419	GGTTCCTTAGGACAGGTTCC
ERBB2.28.3.ERBB2.4_F	chr17:37884094-37884233	AAGACGTTTTTGCCTTTGGG
ERBB2.28.3.ERBB2.4_R	chr17:37884094-37884233	TAGGTGTCCCTTTGAAGGTG
ERBB2.3.4.ERBB2.1_F	chr17:37863235-37863380	CTCTGACCCATCTGCTCTCT
ERBB2.3.4.ERBB2.1_R	chr17:37863235-37863380	TCACCTGCAGGAAGGACA
ERBB2.3.5.ERBB2.2_F	chr17:37863364-37863502	AACCTGGAACTCACCTACCT
ERBB2.3.5.ERBB2.2_R	chr17:37863364-37863502	TCCTGGTTGAGAAACCACAA
ERBB2.9.1.ERBB2.1_F	chr17:37868210-37868370	TTCTACGGACGTGGGATCC
ERBB2.9.1.ERBB2.1_R	chr17:37868210-37868370	TGAGGAAGGATAGGACAGGG
ERBB2.9.2.ERBB2.2_F	chr17:37868078-37868237	ATGCGTGGTAGGGCATTTAA
ERBB2.9.2.ERBB2.2_R	chr17:37868078-37868237	ATCCTCTGCTGTCACCTCTT
ERBB2.9.2.ERBB2.3_F	chr17:37868401-37868562	CCTTCCTCAGACCCTCTTG
ERBB2.9.2.ERBB2.3_R	chr17:37868401-37868562	TAGCACACTGAGGAGGTGG
ERBB2.9.3.ERBB2.4_F	chr17:37868258-37868413	AAGAGGTGACAGCAGAGGAT
ERBB2.9.3.ERBB2.4_R	chr17:37868258-37868413	AGGGGTAGAGAGTAGAAGGC
ERBB2.12.1.ERBB2.1_F	chr17:37871641-37871789	TGTCTCTGCATCCTGTTCTG
ERBB2.12.1.ERBB2.1_R	chr17:37871641-37871789	CCCTCTTTCTCAGTGCTCAC
ERBB2.14.4.ERBB2.1_F	chr17:37872530-37872676	CCTCCCCTAAAAGTCCCCT
ERBB2.14.4.ERBB2.1_R	chr17:37872530-37872676	CCCTCATACCCCTGCAGTA
ERBB2.14.5.ERBB2.2_F	chr17:37872633-37872773	CCACCCAGTGTGTCAACTG
ERBB2.14.5.ERBB2.2_R	chr17:37872633-37872773	TGGCATTCACATACTCCCTG
ERBB2.20.1.ERBB2.1_F	chr17:37880164-37880323	TATCCTCCTCTTTCTGCCCA
ERBB2.20.1.ERBB2.1_R	chr17:37880164-37880323	AATGAAGAGAGACCAGAGCC
ERBB2.15.1.ERBB2.1_F	chr17:37872767-37872925	ACCACTGTCCCTTCTCTCA
ERBB2.15.1.ERBB2.1_R	chr17:37872767-37872925	CTACTGCATCTCGCCATCC
ERBB2.8.1.ERBB2.1_F	chr17:37866575-37866734	AAAACAGCACAGTGAAAGCC
ERBB2.8.1.ERBB2.1_R	chr17:37866575-37866734	GTTTCTCCCTGGCACTCAC
ERBB2.4.1.ERBB2.1_F	chr17:37864613-37864773	TACGTGCTCATCGCTCAC
ERBB2.4.1.ERBB2.1_R	chr17:37864613-37864773	CACCTGTGAGGCTTCGA
ERBB2.4.2.ERBB2.2_F	chr17:37864737-37864874	GAACAATACCACCCCTGTCA
ERBB2.4.2.ERBB2.2_R	chr17:37864737-37864874	CCAGAAGGGACACCATTTCT
ERBB2.4.2.ERBB2.3_F	chr17:37864557-37864715	GTTCCTATTTCAGCCCCACT
ERBB2.4.2.ERBB2.3_R	chr17:37864557-37864715	GACAGGGGTGGTATTGTTCA
ERBB2.24.4.ERBB2.1_F	chr17:37881959-37882101	TGACCCTGTCTCTGCCTTA
ERBB2.24.4.ERBB2.1_R	chr17:37881959-37882101	CTCAGCCACGCACATTTG
ERBB2.24.5.ERBB2.2_F	chr17:37882088-37882224	CCATCTGCACCATTGATGTC
ERBB2.24.5.ERBB2.2_R	chr17:37882088-37882224	AAGAAGGTTTTGAGGCTCCT
ERBB2.19.6.ERBB2.1_F	chr17:37879739-37879903	TGAAGTCCTCCCAGCCC
ERBB2.19.6.ERBB2.1_R	chr17:37879739-37879903	GCCCTGACCTTGTAGACT
ERBB2.19.7.ERBB2.2_F	chr17:37879889-37880030	AAGGTGAAGGTGCTTGGATC
ERBB2.19.7.ERBB2.2_R	chr17:37879889-37880030	CTCCCTTCTCCGCTGTAAC
ERBB2.10.1.ERBB2.1_F	chr17:37868584-37868739	CACCTCCTCAGTGTGCTATG
ERBB2.10.1.ERBB2.1_R	chr17:37868584-37868739	GGATCCTCAGGACTCTGTCT
ERBB2.10.2.ERBB2.2_F	chr17:37868464-37868623	AGCCCTACAAGTGTCCCTAT
ERBB2.10.2.ERBB2.2_R	chr17:37868464-37868623	ACTCCTGGATATTGGCACTG
ERBB2.5.1.ERBB2.1_F	chr17:37865565-37865722	TCCTCTGATCATTGCTCACC
ERBB2.5.1.ERBB2.1_R	chr17:37865565-37865722	CTGAGAGAAGAGGCAGCAG
PALB2.6.1.PALB2.1_F	chr16:23635293-23635429	CCAGCTGACAGAGACAAAGA
PALB2.6.1.PALB2.1_R	chr16:23635293-23635429	CCAAGCATAATTTTTGGCTGC
PALB2.11.1.PALB2.1_F	chr16:23649161-23649290	AGCAGGCATAAGTGAATGGT
PALB2.11.1.PALB2.1_R	chr16:23649161-23649290	GAAAACGTATTTCTGGGGCT
PALB2.3.1.PALB2.1_F	chr16:23625309-23625439	TAACACACAAAGTGGTCCCA
PALB2.3.1.PALB2.1_R	chr16:23625309-23625439	CTGGTTTGTTGGAAGAATGTGA
PALB2.7.1.PALB2.1_F	chr16:23637557-23637716	AGCTCGAGATTCCCACTTAC
PALB2.7.1.PALB2.1_R	chr16:23637557-23637716	CTGTTGCCATTGTGTCAGAA
PALB2.7.2.PALB2.2_F	chr16:23637580-23637739	TGCGAAGTGCCAGGTATAAA
PALB2.7.2.PALB2.2_R	chr16:23637580-23637739	ACTCGAGTGCCACTTTAACA
PALB2.9.1.PALB2.1_F	chr16:23640961-23641121	TCACAGAGGAAATGGATTGTAC
PALB2.9.1.PALB2.1_R	chr16:23640961-23641121	AGGCAGCCCAGCAAAAC
PALB2.9.2.PALB2.2_F	chr16:23641122-23641281	ACTTGCAGGGTGGTATGTG
PALB2.9.2.PALB2.2_R	chr16:23641122-23641281	CACCTGCTTTCCCCATCTTA

PALB2.9.3.PALB2.3_F	chr16:23641322-23641481	AACACATGTCTGTGGTAGGC
PALB2.9.3.PALB2.3_R	chr16:23641322-23641481	ACTGAGTCCTAAACGCATGG
PALB2.9.4.PALB2.4_F	chr16:23641237-23641376	CGTCCAGCAACTTCTGTAGA
PALB2.9.4.PALB2.4_R	chr16:23641237-23641376	TACAAAGACGGGCCTTTCTT
PALB2.9.4.PALB2.5_F	chr16:23641541-23641701	GCTTCCCTCTTTAAGATGTCTC
PALB2.9.4.PALB2.5_R	chr16:23641541-23641701	ATGCTTTCACGGCTCCA
PALB2.9.5.PALB2.6_F	chr16:23641696-23641826	AAACTCAGCATTCCATCCCT
PALB2.9.5.PALB2.6_R	chr16:23641696-23641826	CAGATTGTCTGTTTTGTTGGGT
PALB2.9.5.PALB2.7_F	chr16:23641429-23641567	GAGTTTGGCCTTTTGGGATG
PALB2.9.5.PALB2.7_R	chr16:23641429-23641567	TGCTCAGAAAAACCAGTGGA
PALB2.12.1.PALB2.1_F	chr16:23649309-23649466	ACAGCCCCAGAAATACGTTT
PALB2.12.1.PALB2.1_R	chr16:23649309-23649466	ACTTGCCCAGTATTGTTGGT
PALB2.2.1.PALB2.1_F	chr16:23619214-23619365	GCCCTGGAGGAAGACAGTA
PALB2.2.1.PALB2.1_R	chr16:23619214-23619365	TCCTGACATACTCTTGACAGTC
PALB2.2.2.PALB2.2_F	chr16:23619151-23619284	GCACAGTGCCTTTCAGAATG
PALB2.2.2.PALB2.2_R	chr16:23619151-23619284	CTGTGCCAAAGAGAGTGAGT
PALB2.8.1.PALB2.1_F	chr16:23640509-23640647	AAGACACGAGACACTGGAAG
PALB2.8.1.PALB2.1_R	chr16:23640509-23640647	TGATGAGTGGGTAATGCAGG
PALB2.1.8.PALB2.1_F	chr16:23614755-23614910	AGAGGCCCAATATATCCAGAA
PALB2.1.8.PALB2.1_R	chr16:23614755-23614910	TGCCATTTGGGACTTACTTC
PALB2.1.9.PALB2.2_F	chr16:23614907-23615055	GAGGAGGGCAGTACACTGA
PALB2.1.9.PALB2.2_R	chr16:23614907-23615055	TGGGAACATGGTTTTGACCT
PALB2.4.1.PALB2.1_F	chr16:23632681-23632838	AGGACCTAGAGGGAAAGCTT
PALB2.4.1.PALB2.1_R	chr16:23632681-23632838	GGCTACCTAGAGACTGCTTT
PALB2.13.1.PALB2.1_F	chr16:23652337-23652486	GGGGTGGTCAGATGATACTG
PALB2.13.1.PALB2.1_R	chr16:23652337-23652486	CTGCTCTTTTCGTTCTGTCG
PALB2.10.1.PALB2.1_F	chr16:23646283-23646442	GCTAGAAGTTGGCAAAAGTGG
PALB2.10.1.PALB2.1_R	chr16:23646283-23646442	GCACAGGACAACCAAGTTC
PALB2.10.2.PALB2.2_F	chr16:23646443-23646602	GAGAAGTTTCTGAGAGGTTCTT
PALB2.10.2.PALB2.2_R	chr16:23646443-23646602	TGTCCAATTGCCAGAGGA
PALB2.10.2.PALB2.3_F	chr16:23646128-23646285	AAGGAAGTGCCAGGCAAATA
PALB2.10.2.PALB2.3_R	chr16:23646128-23646285	CCCCAGCATCAGATCATTGT
PALB2.10.3.PALB2.4_F	chr16:23646613-23646772	GGCTACTTTCCTCTGGCA
PALB2.10.3.PALB2.4_R	chr16:23646613-23646772	AGTGACACTCTTGATGGCAG
PALB2.10.4.PALB2.5_F	chr16:23646464-23646612	AACTTGGTTGTCCTGTGCAT
PALB2.10.4.PALB2.5_R	chr16:23646464-23646612	CAACACGAAGCATGTCCAAT
PALB2.10.4.PALB2.6_F	chr16:23647003-23647165	TGCCTTGTGCCTCCAA
PALB2.10.4.PALB2.6_R	chr16:23647003-23647165	CCAACCAGAAAAAGGTGTTGA
PALB2.10.5.PALB2.7_F	chr16:23647196-23647358	CTGGTTGGGCAGTTGGT
PALB2.10.5.PALB2.7_R	chr16:23647196-23647358	CTTTGGCACTGATTCACTCA
PALB2.10.6.PALB2.8_F	chr16:23647153-23647291	GCCCTGGTGAAATTAGGTCT
PALB2.10.6.PALB2.8_R	chr16:23647153-23647291	AATCCTGCTAGATCACCAGT
PALB2.10.6.PALB2.9_F	chr16:23647369-23647528	CCCAGACAATCTGAGTGAATC
PALB2.10.6.PALB2.9_R	chr16:23647369-23647528	TTAACCCTGGAGATGGCCC
PALB2.10.7.PALB2.10_F	chr16:23647337-23647477	GCTACTGATTTCTTCCTGTTCC
PALB2.10.7.PALB2.10_R	chr16:23647337-23647477	ACCCAAGAACATTTTCCCCA
PALB2.10.10.PALB2.11_F	chr16:23646758-23646912	GGTTGACTTAGAATCTCACTTTCC
PALB2.10.10.PALB2.11_R	chr16:23646758-23646912	GCCAACTGCCCACAAGT
PALB2.10.11.PALB2.12_F	chr16:23646892-23647037	GGTGAGTTCATTTAGAGAACATGA
PALB2.10.11.PALB2.12_R	chr16:23646892-23647037	GCAGTGAACTTACTACTCACG
PALB2.10.12.PALB2.13_F	chr16:23647498-23647645	TGGGGAAAATGTTCTTGGGT
PALB2.10.12.PALB2.13_R	chr16:23647498-23647645	TTTTCCTCCTCAGAACCTAAAAA
PALB2.10.13.PALB2.14_F	chr16:23647612-23647768	CAGTTTCTTCATCAAGATGGGT
PALB2.10.13.PALB2.14_R	chr16:23647612-23647768	GCCTGAATGAAATGTCACTGA
PALB2.5.1.PALB2.1_F	chr16:23634319-23634470	TCTGCAAACGTCATGACTTC
PALB2.5.1.PALB2.1_R	chr16:23634319-23634470	CTCCTCACATCACCCCATTT
PALB2.5.2.PALB2.2_F	chr16:23634171-23634322	ACCTAGTGTTGATGCGGTAC
PALB2.5.2.PALB2.2_R	chr16:23634171-23634322	GGGACCCTTTCTGATCAACA

Table S3: Universal PCR primers

Illumjna IndexF	AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTCTTCCGATCTCTG
Illumina IndexR*	CAAGCAGAAGACGGCATACGAGATXXXXXXGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTGAC
Sequencing Primer read1	ACTCTTTCCCTACACGACGCTCTTCCGATCTCTG
Sequencing Primer read2	ACTGGAGTTCAGACGTGTGCTCTTCCGATCTGAC

* X represents the DNA barcode

Table S4: Significant copy number gains and losses

Gene	**Sample**	**Log2(T/N)**	**P-value**
ABL2	UCI8965412	1.62	0
BRAF	UCI1689380	1.05	3.77E-82
ERBB2	AA1204	1.37	6.81E-148
ERBB2	AA1222	1.98	0
ERBB2	AA1247	2.66	0
ERBB2	UCI1908503	1.78	0
ERBB2	UCI8965412	2.42	0
FGFR1	AA1090	1.41	1.55E-138
FGFR1	UCI2649875	1.54	4.06E-133
FGFR1OP	AA1277	-1.41	2.42E-08
FGFR2	AA1277	2.20	0
PIK3CA	UCI3564897	1.54	1.55E-169

Table S5: Read Alignment and Coverage Statistics

Patient ID	Sample ID[1]	Run ID	#Reads	#Aligned	Mean Read Coverage[2]	Coverage Uniformity[3]
AA1025	AA1025B	120719_M00436_0005	2,238,436	2,161,009	1,049	96%
AA1025	AA1025T	120719_M00436_0005	2,749,834	2,707,115	1,384	95%
AA1077	AA1077B	121025_M00436_0010	3,767,118	3,374,294	1,625	94%
AA1077	AA1077T	121025_M00436_0010	3,014,584	2,942,237	1,529	91%
AA1090	AA1090B	120823_M00436_0009	2,049,694	2,003,189	1,064	92%
AA1090	AA1090T	120823_M00436_0009	2,291,814	2,232,270	1,170	85%
AA943	AA943B	120831_M00436_0012	3,208,654	3,160,224	1,631	96%
AA943	AA943T	120831_M00436_0012	3,875,458	3,764,254	1,869	95%
AA1188	AA1188B	120814_M00436_0008	3,621,022	3,554,531	1,874	95%
AA1188	AA1188T	120814_M00436_0008	3,106,796	3,005,426	1,553	95%
AA1204	AA1204B	120719_M00436_0005	4,048,560	4,003,089	2,105	95%
AA1204	AA1204T	120719_M00436_0005	3,070,104	3,034,944	1,568	91%
AA1222	AA1222B	121025_M00436_0010	3,555,052	3,171,760	1,536	93%
AA1222	AA1222T	121025_M00436_0010	3,056,424	2,989,223	1,569	87%
AA1247	AA1247B	120814_M00436_0008	2,980,418	2,937,581	1,570	95%
AA1247	AA1247T	120814_M00436_0008	3,436,018	3,389,175	1,821	86%
AA1267	AA1267B	120827_M00436_0011	2,437,798	2,392,933	1,249	94%
AA1267	AA1267T	120827_M00436_0011	2,803,204	2,770,720	1,477	93%
AA1277	AA1277B	120825_M00436_0010	2,265,368	2,206,906	1,026	94%
AA1277	AA1277T	120825_M00436_0010	2,896,468	2,851,861	1,412	84%
AA1307	AA1307B	120827_M00436_0011	3,828,404	3,798,149	2,040	95%
AA1307	AA1307T	120827_M00436_0011	2,671,612	2,626,127	1,371	92%
AA957	AA957B	120831_M00436_0012	3,404,866	3,348,375	1,697	96%
AA957	AA957T	120831_M00436_0012	1,487,058	1,455,284	731	95%
AA926	AA926B	120712_M00436_0004	2,738,246	2,710,403	1,462	95%
AA926	AA926T	120712_M00436_0004	2,484,200	2,434,466	1,314	91%
AA930	AA930B	120727_M00436_0007	2,628,572	2,540,172	1,318	95%
AA930	AA930T	120727_M00436_0007	3,730,366	3,659,703	1,950	95%
AA1106	AA1106B	120918_M00436_0001	3,586,450	3,546,087	1,897	95%
AA1106	AA1106T	120918_M00436_0001	3,834,160	3,788,715	2,039	94%
AA948	AA948B	120723_M00436_0006	2,760,844	2,701,244	1,360	96%
AA948	AA948T	120723_M00436_0006	3,116,402	3,058,760	1,539	95%
AA952	AA952B	120723_M00436_0006	2,130,702	2,039,491	922	95%
AA952	AA952T	120723_M00436_0006	2,701,764	2,629,638	1,287	95%
AA1367	AA1367B	120918_M00436_0001	4,132,296	4,103,434	2,225	95%
AA1367	AA1367T	120918_M00436_0001	3,575,528	3,514,050	1,872	93%
AA960	AA960B	120825_M00436_0010	2,209,072	2,164,943	1,025	95%
AA960	AA960T	120825_M00436_0010	2,368,496	2,318,341	1,025	92%
AA1515	AA1515B	120702_M00436_0003	4,018,844	3,985,206	2,194	87%
AA1515	AA1515T	120702_M00436_0003	3,170,656	3,147,053	1,735	81%
UCI1546879	UCI1546879B	121017_M00436_0007	2,737,470	2,568,080	1,152	96%
UCI1546879	UCI1546879T	121017_M00436_0007	2,512,712	2,458,068	1,246	96%
UCI1689380	UCI1689380B	121025_M00436_0010	4,325,160	4,011,880	2,015	93%
UCI1689380	UCI1689380T	121025_M00436_0010	3,617,706	3,523,676	1,784	90%

Patient ID	Sample ID[1]	Run ID	#Reads	#Aligned	Mean Read Coverage[2]	Coverage Uniformity[3]
UCI1804937	UCI1804937B	120927_M00436_0002	2,782,872	2,645,891	1,166	92%
UCI1804937	UCI1804937T	120927_M00436_0002	3,666,490	3,525,204	1,609	87%
UCI1821517	UCI1821517B	121005_M00436_0003	2,200,514	1,995,831	731	94%
UCI1821517	UCI1821517T	121005_M00436_0003	2,543,556	2,458,056	1,085	94%
UCI1908503	UCI1908503B	121005_M00436_0003	3,047,486	2,839,649	1,386	94%
UCI1908503	UCI1908503T	121005_M00436_0003	3,497,798	3,443,995	1,773	89%
UCI1951813	UCI1951813B	120927_M00436_0002	2,631,032	2,356,453	956	92%
UCI1951813	UCI1951813T	120927_M00436_0002	3,049,180	2,891,836	1,253	90%
UCI2008866	UCI2008866B	120727_M00436_0007	2,716,066	2,515,828	1,277	95%
UCI2008866	UCI2008866T	120727_M00436_0007	2,711,774	2,640,608	1,370	94%
UCI2076630	UCI2076630B	121025_M00436_0010	2,222,134	2,051,676	889	95%
UCI2076630	UCI2076630T	121025_M00436_0010	3,020,010	2,930,941	1,453	89%
UCI2219330	UCI2219330B	121019_M00436_0008	3,396,468	3,245,237	1,501	96%
UCI2219330	UCI2219330T	121019_M00436_0008	3,518,830	3,471,425	1,816	95%
UCI2224680	UCI2224680B	121017_M00436_0007	4,821,386	4,319,722	2,026	93%
UCI2224680	UCI2224680T	121017_M00436_0007	3,174,400	3,067,894	1,573	90%
UCI2231576	UCI2231576B	121023_M00436_0009	2,284,128	1,655,820	834	95%
UCI2231576	UCI2231576T	121023_M00436_0009	1,841,322	1,697,647	871	94%
UCI2564879	UCI2564879B	121017_M00436_0007	3,805,480	3,368,913	1,660	88%
UCI2564879	UCI2564879T	121017_M00436_0007	3,494,980	3,397,756	1,776	87%
UCI2649875	UCI2649875B	121008_M00436_0004	2,531,122	2,300,017	720	95%
UCI2649875	UCI2649875T	121008_M00436_0004	2,931,292	2,857,110	1,228	91%
UCI3165498	UCI3165498B	121019_M00436_0008	5,049,092	4,901,483	2,499	96%
UCI3165498	UCI3165498T	121019_M00436_0008	3,348,012	3,308,405	1,741	91%
UCI3564897	UCI3564897B	121019_M00436_0008	3,816,162	3,622,730	1,751	96%
UCI3564897	UCI3564897T	121019_M00436_0008	3,390,376	3,333,686	1,747	88%
UCI4216548	UCI4216548B	121017_M00436_0007	2,781,236	2,535,992	1,181	96%
UCI4216548	UCI4216548T	121017_M00436_0007	2,543,478	2,485,579	1,238	90%
UCI8965412	UCI8965412B	121019_M00436_0008	4,590,764	4,421,800	2,258	95%
UCI8965412	UCI8965412T	121019_M00436_0008	3,166,474	3,125,612	1,658	84%
UCI9135402	UCI9135402B	121008_M00436_0004	2,536,108	2,371,253	839	95%
UCI9135402	UCI9135402T	121008_M00436_0004	3,244,088	3,168,386	1,375	93%

1: B suffix indicates blood germline DNA, T suffix indicates tumor DNA

2: Average number of reads per amplicon

3: Fraction of base pair within 2 fold of the mean coverage

Table S6: List of non-silent somatic mutations

									Allele Fraction (%)	
Sample	**Chr**	**Coord**	**Ref Allele**	**Alt Allele**	**Gene**	**AA Change***	**Type**	**Effect**	**Normal**	**Tumor**
UCI1804937	chr1	179078209	G	C	ABL2	D695E	MISSENSE	NON_SYNONY	3.87	5.92
UCI2649875	chr14	105246445	A	C	AKT1	L52R	MISSENSE	NON_SYNONY	0	63.21
AA952	chr5	112175825	G	A	APC	D1512N	MISSENSE	NON_SYNONY	0.22	13.84
AA952	chr11	108204663	G	C	ATM	E2660Q	MISSENSE	NON_SYNONY	0	13.54
UCI4216548	chr11	108124713	GATCGCTGTC	G	ATM	NA	NONE	FRAME_SHIFT	0	47.3
UCI1908503	chr7	140534596	C	T	BRAF	G106E	MISSENSE	NON_SYNONY	0.29	13.58
AA952	chr17	41245012	C	T	BRCA1	E550K	MISSENSE	NON_SYNONY	0.09	12.59
AA952	chr17	41246489	C	T	BRCA1	W306*	NONSENSE	STOP_GAINED	0.08	17.65
UCI2224680	chr13	32913979	G	C	BRCA2	L1829F	MISSENSE	NON_SYNONY	0	1.73
AA1106	chr13	32912745	T	C	BRCA2	I1418T	MISSENSE	NON_SYNONY	0.13	3.52
AA1106	chr16	68835732	G	A	CDH1	R108K	MISSENSE	NON_SYNONY	1.02	15.98
AA1106	chr16	68849442	C	T	CDH1	Q388*	NONSENSE	STOP_GAINED	0	16.01
AA1188	chr16	68842325	A	C	CDH1	NA	NONE	SPLICE_SITE_	0.16	22.18
AA930	chr16	68846167	G	A	CDH1	NA	NONE	SPLICE_SITE_	0.17	23.79
AA1090	chr9	21971104	G	T	CDKN2A	A85D	MISSENSE	NON_SYNONY	0.17	65.93
UCI1908503	chr10	96745907	A	G	CYP2C9	K423E	MISSENSE	NON_SYNONY	0.33	17.92
AA1247	chr17	37880261	G	C	ERBB2	D493H	MISSENSE	NON_SYNONY	0	4.85
AA952	chr17	37883585	C	G	ERBB2	S1036C	MISSENSE	NON_SYNONY	0	16.07
AA1106	chr17	37880220	T	C	ERBB2	L479S	MISSENSE	NON_SYNONY	0.41	16.6
AA952	chr17	37883167	C	G	ERBB2	L1009V	MISSENSE	NON_SYNONY	0.13	17.59
AA952	chr12	56495375	G	A	ERBB3	E1130K	MISSENSE	NON_SYNONY	0.15	16.86
UCI4216548	chr8	38271295	C	G	FGFR1	D683H	MISSENSE	NON_SYNONY	0.11	13.05
UCI1908503	chr10	123239488	G	C	FGFR2	Y666*	NONSENSE	STOP_GAINED	0.37	16.86
AA1367	chr10	123256219	C	G	FGFR2	V156L	MISSENSE	NON_SYNONY	0.47	21.53
AA952	chr10	8106058	T	A	GATA3	M293K	MISSENSE	NON_SYNONY	0	12.89
AA1025	chr10	8115874	C	CT	GATA3	NA	NONE	FRAME_SHIFT	0	17.49
AA948	chr10	8111478	A	AC	GATA3	NA	NONE	FRAME_SHIFT	0.34	29.84
AA960	chr10	8111506	A	ATGCC	GATA3	NA	NONE	FRAME_SHIFT	0	34.9
AA926	chr10	8111553	C	CT	GATA3	NA	NONE	FRAME_SHIFT	0	40.59
AA1090	chr10	8111513	T	TG	GATA3	NA	NONE	FRAME_SHIFT	0	43.46
AA952	chr9	5054787	C	T	JAK2	S131L	MISSENSE	NON_SYNONY	0	15.57
UCI1908503	chr9	5029872	G	A	JAK2	E106K	MISSENSE	NON_SYNONY	0.06	16.11
AA952	chr19	17951135	G	C	JAK3	I386M	MISSENSE	NON_SYNONY	0	12.77
AA952	chr2	47643468	C	G	MSH2	L112V	MISSENSE	NON_SYNONY	0	15.92
UCI2564879	chr9	139391413	C	A	NOTCH1	G2260W	MISSENSE	NON_SYNONY	0.03	35.05
UCI1689380	chr16	23637719	C	G	PALB2	NA	NONE	SPLICE_SITE_	0.09	45.22
AA1204	chr5	149515247	C	T	PDGFRB	G15S	MISSENSE	NON_SYNONY	0.15	11.36
UCI1951813	chr3	178936091	G	A	PIK3CA	E545K	MISSENSE	NON_SYNONY	0	6.5
AA952	chr3	178936091	G	A	PIK3CA	E545K	MISSENSE	NON_SYNONY	0.18	16.47
AA1204	chr3	178952085	A	G	PIK3CA	H1047R	MISSENSE	NON_SYNONY	0.21	26.31
AA957	chr3	178936082	G	A	PIK3CA	E542K	MISSENSE	NON_SYNONY	0.2	27.97
AA948	chr3	178936091	G	A	PIK3CA	E545K	MISSENSE	NON_SYNONY	0.2	34.12
UCI2564879	chr3	178927980	T	C	PIK3CA	C420R	MISSENSE	NON_SYNONY	0.63	35.9
AA1267	chr3	178952085	A	G	PIK3CA	H1047R	MISSENSE	NON_SYNONY	0	44.68
UCI1908503	chr3	178952085	A	G	PIK3CA	H1047R	MISSENSE	NON_SYNONY	0.13	49.04
AA1515	chr3	178936091	G	A	PIK3CA	E545K	MISSENSE	NON_SYNONY	0	69.74
UCI1546879	chr5	67591106	A	G	PIK3R1	K204E	MISSENSE	NON_SYNONY	1.68	30.26
AA1106	chr7	6038848	C	T	PMS2	R152H	MISSENSE	NON_SYNONY	0	6.32
UCI2076630	chr7	6029551	G	C	PMS2	Q236E	MISSENSE	NON_SYNONY	0.5	15.97
AA1106	chr10	89692856	GAAGAT	G	PTEN	NA	NONE	FRAME_SHIFT	0	5.24
UCI1689380	chr17	38512437	C	A	RARA	P337T	MISSENSE	NON_SYNONY	0.08	14.35
UCI2008866	chr13	49050847	AGT	A	RB1	NA	NONE	FRAME_SHIFT	0	78.52
AA1367	chr17	7578550	G	T	TP53	S116Y	MISSENSE	NON_SYNONY	0.16	36.33
AA1222	chr17	7578526	C	T	TP53	C124Y	MISSENSE	NON_SYNONY	0.15	40.37
AA1204	chr17	7577538	C	T	TP53	R116Q	MISSENSE	NON_SYNONY	0.23	41.52
UCI8965412	chr17	7576867	AT	A	TP53	NA	NONE	FRAME_SHIFT	0	42.22
UCI1821517	chr17	7579536	C	A	TP53	E51*	NONSENSE	STOP_GAINED	0	45.35
UCI1908503	chr17	7577538	C	T	TP53	R116Q	MISSENSE	NON_SYNONY	0.27	47.82
AA1077	chr17	7578505	G	A	TP53	P10L	MISSENSE	NON_SYNONY	0.23	48.35
AA1077	chr17	7578475	G	A	TP53	P141L	MISSENSE	NON_SYNONY	0.27	48.41
AA1077	chr17	7578458	G	A	TP53	R147C	MISSENSE	NON_SYNONY	0.11	48.53
AA1307	chr17	7577580	T	C	TP53	Y102C	MISSENSE	NON_SYNONY	0.48	56.96
UCI2008866	chr17	7577121	G	A	TP53	R141C	MISSENSE	NON_SYNONY	0	78.5
UCI3165498	chr17	7577094	G	A	TP53	R150W	MISSENSE	NON_SYNONY	0.2	79.04
UCI3564897	chr17	7574003	G	A	TP53	R331*	NONSENSE	STOP_GAINED	0	79.33
AA1090	chr17	7578441	G	T	TP53	Y152*	NONSENSE	STOP_GAINED	0	82.18
AA1277	chr17	7578382	G	C	TP53	S172*	NONSENSE	STOP_GAINED	0.12	85.52
UCI4216548	chr17	7579424	GC	G	TP53	NA	NONE	FRAME_SHIFT	0.12	85.55

* as reported y SNPEff

Table S7: List of mutations which segregate into two significantly different groups of alellelic fractions in the tumors of 3 patients.

Patient	Gene	AA Change	TAF	Average TAF	P-value
AA 952	APC	D1512N	13.8	13.1	8.8E-06
	ATM	E1312Q	13.5		
	GATA3	M294K	12.9		
	JAK3	I386M	12.8		
	BRCA1	E550K	12.6		
	BRCA1	W57*	17.7	16.6	
	ERBB2	L1024V	17.6		
	ERBB3	E1189K	16.8		
	PIK3CA	E545K	16.5		
	ERBB2	S1066C	16.1		
	MSH2	L326V	15.9		
	JAK2	S280L	15.6		
AA1106	BRCA2	I1418T	3.52	5.0	1.8E-04
	PTEN	E114fs	5.24		
	PMS2	R199H	6.32		
	CDH1	R108K	15.98	16.2	
	CDH1	Q449*	16.01		
	ERBB2	L755S	16.6		
UCI1908503	BRAF	G106E	13.58	16.1	2.3E-05
	CYP2C9	K423E	17.92		
	FGFR2	Y783*	16.86		
	JAK2	E106K	16.11		
	PIK3CA	H1047R	49.04	48.4	
	TP53	R248Q	47.82		

Table S8: List of non-silent germline variants

Sample	Chr	Cord	rsID	Ref Allele	Alt Allele	Allelic Fraction		Gene	AA change	Type	Effect	Mutation Taster Prediction
						Normal	Tumor					
AA1025	chr1	179112145	rs1318056	C	G	46.49	65.25	ABL2	S12T	MISSENSE	NON_SYNON	P
AA1090	chr1	179112145	rs1318056	C	G	50.77	60.16	ABL2	S12T	MISSENSE	NON_SYNON	P
AA943	chr1	179112145	rs1318056	C	G	53.16	45.83	ABL2	S12T	MISSENSE	NON_SYNON	P
AA1188	chr1	179112145	rs1318056	C	G	52.28	40.18	ABL2	S12T	MISSENSE	NON_SYNON	P
AA1222	chr1	179112145	rs1318056	C	G	51.74	44.85	ABL2	S12T	MISSENSE	NON_SYNON	P
AA1267	chr1	179112145	rs1318056	C	G	49.79	36.8	ABL2	S12T	MISSENSE	NON_SYNON	P
AA1307	chr1	179112145	rs1318056	C	G	50	50.89	ABL2	S12T	MISSENSE	NON_SYNON	P
AA926	chr1	179112145	rs1318056	C	G	51.71	28.38	ABL2	S12T	MISSENSE	NON_SYNON	P
UCI1821517	chr1	179112145	rs1318056	C	G	45.1	81.14	ABL2	S12T	MISSENSE	NON_SYNON	P
UCI2008866	chr1	179112145	rs1318056	C	G	51.71	54.03	ABL2	S12T	MISSENSE	NON_SYNON	P
UCI2076630	chr1	179112145	rs1318056	C	G	43.15	69.14	ABL2	S12T	MISSENSE	NON_SYNON	P
UCI2649875	chr1	179112145	rs1318056	C	G	45.35	17.04	ABL2	S12T	MISSENSE	NON_SYNON	P
UCI3564897	chr1	179112145	rs1318056	C	G	53.56	10.37	ABL2	S12T	MISSENSE	NON_SYNON	P
UCI2231576	chr14	105238734	rs146483593	C	T	43.51	55.37	AKT1	G105S	MISSENSE	NON_SYNON	D
UCI3564897	chr7	117188715	rs3034796	GAAAGC	G	15.06	14.83	CFTR	NA	NONE	FRAME_SHIF	NA
AA1025	chr2	29416366	rs1881421	G	C	52.74	47.01	ALK	D1529E	MISSENSE	NON_SYNON	P
AA1025	chr2	29416481	rs1881420	T	C	47.17	48.57	ALK	K1491R	MISSENSE	NON_SYNON	P
AA1025	chr2	29416572	rs1670283	T	C	99.83	99.85	ALK	I1461V	MISSENSE	NON_SYNON	N
AA1077	chr2	29416366	rs1881421	G	C	43.57	54.35	ALK	D1529E	MISSENSE	NON_SYNON	P
AA1077	chr2	29416481	rs1881420	T	C	50.09	52.43	ALK	K1491R	MISSENSE	NON_SYNON	P
AA1090	chr2	29416572	rs1670283	T	C	100	99.93	ALK	I1461V	MISSENSE	NON_SYNON	N
AA943	chr2	29416572	rs1670283	T	C	99.93	99.94	ALK	I1461V	MISSENSE	NON_SYNON	N
AA1188	chr2	29416572	rs1670283	T	C	99.95	99.93	ALK	I1461V	MISSENSE	NON_SYNON	N
AA1204	chr2	29416572	rs1670283	T	C	99.96	99.73	ALK	I1461V	MISSENSE	NON_SYNON	N
AA1222	chr2	29416572	rs1670283	T	C	99.81	99.88	ALK	I1461V	MISSENSE	NON_SYNON	N
AA1247	chr2	29416572	rs1670283	T	C	100	99.9	ALK	I1461V	MISSENSE	NON_SYNON	N
AA1267	chr2	29416366	rs1881421	G	C	46.95	44.18	ALK	D1529E	MISSENSE	NON_SYNON	P
AA1267	chr2	29416481	rs1881420	T	C	46.23	52.19	ALK	K1491R	MISSENSE	NON_SYNON	P
AA1267	chr2	29416572	rs1670283	T	C	99.93	99.87	ALK	I1461V	MISSENSE	NON_SYNON	N
AA1277	chr2	29416366	rs1881421	G	C	100	99.79	ALK	D1529E	MISSENSE	NON_SYNON	P
AA1277	chr2	29416481	rs1881420	T	C	100	99.6	ALK	K1491R	MISSENSE	NON_SYNON	P
AA1277	chr2	29416572	rs1670283	T	C	99.83	99.78	ALK	I1461V	MISSENSE	NON_SYNON	N
AA1307	chr2	29416572	rs1670283	T	C	99.87	99.87	ALK	I1461V	MISSENSE	NON_SYNON	N
AA957	chr2	29416366	rs1881421	G	C	99.75	99.71	ALK	D1529E	MISSENSE	NON_SYNON	P
AA957	chr2	29416481	rs1881420	T	C	46.98	47.03	ALK	K1491R	MISSENSE	NON_SYNON	P
AA957	chr2	29416572	rs1670283	T	C	99.71	99.74	ALK	I1461V	MISSENSE	NON_SYNON	N
AA926	chr2	29416366	rs1881421	G	C	99.93	99.83	ALK	D1529E	MISSENSE	NON_SYNON	P
AA926	chr2	29416481	rs1881420	T	C	99.56	99.68	ALK	K1491R	MISSENSE	NON_SYNON	P
AA926	chr2	29416572	rs1670283	T	C	99.82	99.93	ALK	I1461V	MISSENSE	NON_SYNON	N
AA930	chr2	29416366	rs1881421	G	C	99.7	99.88	ALK	D1529E	MISSENSE	NON_SYNON	P
AA930	chr2	29416481	rs1881420	T	C	99.33	99.22	ALK	K1491R	MISSENSE	NON_SYNON	P
AA930	chr2	29416572	rs1670283	T	C	99.62	99.91	ALK	I1461V	MISSENSE	NON_SYNON	N
AA1106	chr2	29416366	rs1881421	G	C	53.4	42.74	ALK	D1529E	MISSENSE	NON_SYNON	P
AA1106	chr2	29416481	rs1881420	T	C	46.55	37.58	ALK	K1491R	MISSENSE	NON_SYNON	P
AA1106	chr2	29416572	rs1670283	T	C	99.89	99.95	ALK	I1461V	MISSENSE	NON_SYNON	N
AA948	chr2	29416366	rs1881421	G	C	50.86	52.3	ALK	D1529E	MISSENSE	NON_SYNON	P
AA948	chr2	29416481	rs1881420	T	C	58.7	48.91	ALK	K1491R	MISSENSE	NON_SYNON	P
AA948	chr2	29416572	rs1670283	T	C	100	100	ALK	I1461V	MISSENSE	NON_SYNON	N
UCI8965412	chr2	29474026	rs147858673	C	T	55.52	52.9	ALK	E717K	MISSENSE	NON_SYNON	D
AA952	chr2	29416366	rs1881421	G	C	51.83	49.14	ALK	D1529E	MISSENSE	NON_SYNON	P
AA952	chr2	29416572	rs1670283	T	C	100	99.91	ALK	I1461V	MISSENSE	NON_SYNON	N
AA1367	chr2	29416366	rs1881421	G	C	49.42	50.85	ALK	D1529E	MISSENSE	NON_SYNON	P
AA1367	chr2	29416481	rs1881420	T	C	51.07	49.16	ALK	K1491R	MISSENSE	NON_SYNON	P
AA1367	chr2	29416572	rs1670283	T	C	99.89	99.92	ALK	I1461V	MISSENSE	NON_SYNON	N
AA960	chr2	29416366	rs1881421	G	C	48.64	63.2	ALK	D1529E	MISSENSE	NON_SYNON	P
AA960	chr2	29416481	rs1881420	T	C	46.98	58.39	ALK	K1491R	MISSENSE	NON_SYNON	P
AA960	chr2	29416572	rs1670283	T	C	100	99.68	ALK	I1461V	MISSENSE	NON_SYNON	N
AA1515	chr2	29416366	rs1881421	G	C	51.74	49.39	ALK	D1529E	MISSENSE	NON_SYNON	P
AA1515	chr2	29416481	rs1881420	T	C	46.98	50.02	ALK	K1491R	MISSENSE	NON_SYNON	P
AA1515	chr2	29416572	rs1670283	T	C	99.86	99.96	ALK	I1461V	MISSENSE	NON_SYNON	N
UCI1546879	chr2	29416572	rs1670283	T	C	100	100	ALK	I1461V	MISSENSE	NON_SYNON	N
UCI1689380	chr2	29416366	rs1881421	G	C	55.72	58.02	ALK	D1529E	MISSENSE	NON_SYNON	P
UCI1689380	chr2	29416481	rs1881420	T	C	43.3	63.5	ALK	K1491R	MISSENSE	NON_SYNON	P
UCI1689380	chr2	29416572	rs1670283	T	C	99.53	100	ALK	I1461V	MISSENSE	NON_SYNON	N
UCI8965412	chr2	29446394	.	A	G	50.42	49.28	ALK	V1058A	MISSENSE	NON_SYNON	D
UCI1804937	chr2	29416572	rs1670283	T	C	99.38	99.55	ALK	I1461V	MISSENSE	NON_SYNON	N
UCI1821517	chr7	117188715	rs3034796	GAAAGC	G	15.18	11.65	CFTR	NA	NONE	FRAME_SHIF	NA
UCI1821517	chr2	29416572	rs1670283	T	C	99.34	99.55	ALK	I1461V	MISSENSE	NON_SYNON	N
AA1204	chr2	29497967	rs35228363	G	A	50.58	47.05	ALK	T680I	MISSENSE	NON_SYNON	D
AA930	chr22	42524820	rs3831704	T	TC	15.26	12.19	CYP2D6	NA	NONE	FRAME_SHIF	NA
UCI1908503	chr2	29416366	rs1881421	G	C	44.43	45.69	ALK	D1529E	MISSENSE	NON_SYNON	P
UCI1908503	chr2	29416481	rs1881420	T	C	40.82	49.39	ALK	K1491R	MISSENSE	NON_SYNON	P
UCI1908503	chr2	29416572	rs1670283	T	C	99.18	99.94	ALK	I1461V	MISSENSE	NON_SYNON	N
UCI2649875	chr2	29497967	rs35228363	G	A	56.91	46.5	ALK	T680I	MISSENSE	NON_SYNON	D
UCI1951813	chr2	29416366	rs1881421	G	C	48.01	49.55	ALK	D1529E	MISSENSE	NON_SYNON	P
UCI1951813	chr2	29416481	rs1881420	T	C	44.92	51.16	ALK	K1491R	MISSENSE	NON_SYNON	P
UCI1951813	chr2	29416572	rs1670283	T	C	99.32	99.28	ALK	I1461V	MISSENSE	NON_SYNON	N
UCI2008866	chr2	29416572	rs1670283	T	C	100	99.76	ALK	I1461V	MISSENSE	NON_SYNON	N
UCI2076630	chr2	29416572	rs1670283	T	C	100	99.47	ALK	I1461V	MISSENSE	NON_SYNON	N
UCI2076630	chr2	29543736	rs35093491	A	G	47.82	60.98	ALK	V476A	MISSENSE	NON_SYNON	N
UCI2219330	chr2	29416572	rs1670283	T	C	45.72	47.34	ALK	I1461V	MISSENSE	NON_SYNON	N
UCI8965412	chr7	117188715	rs3034796	GAAAGC	G	15.27	11.71	CFTR	NA	NONE	FRAME_SHIF	NA
UCI2224680	chr2	29416366	rs1881421	G	C	99.67	99.54	ALK	D1529E	MISSENSE	NON_SYNON	P
UCI2224680	chr2	29416481	rs1881420	T	C	99.89	99.66	ALK	K1491R	MISSENSE	NON_SYNON	P
UCI2224680	chr2	29416572	rs1670283	T	C	99.7	99.96	ALK	I1461V	MISSENSE	NON_SYNON	N
UCI1951813	chr8	38277052	.	GT	G	15.36	10.42	FGFR1	NA	NONE	FRAME_SHIF	NA
UCI2231576	chr2	29416366	rs1881421	G	C	99.37	99.85	ALK	D1529E	MISSENSE	NON_SYNON	P
UCI2231576	chr2	29416481	rs1881420	T	C	47.35	50.13	ALK	K1491R	MISSENSE	NON_SYNON	P
UCI2231576	chr2	29416572	rs1670283	T	C	100	99.57	ALK	I1461V	MISSENSE	NON_SYNON	N
UCI1546879	chr2	29497967	rs35228363	G	A	43.74	36.75	ALK	T680I	MISSENSE	NON_SYNON	D
UCI2564879	chr2	29416366	rs1881421	G	C	53.41	64.06	ALK	D1529E	MISSENSE	NON_SYNON	P
UCI2564879	chr2	29416481	rs1881420	T	C	48.33	60.73	ALK	K1491R	MISSENSE	NON_SYNON	P
UCI2564879	chr2	29416572	rs1670283	T	C	100	100	ALK	I1461V	MISSENSE	NON_SYNON	N
UCI2649875	chr2	29416366	rs1881421	G	C	99.15	98.8	ALK	D1529E	MISSENSE	NON_SYNON	P
UCI2649875	chr2	29416481	rs1881420	T	C	98.91	99.56	ALK	K1491R	MISSENSE	NON_SYNON	P
UCI2649875	chr2	29416572	rs1670283	T	C	99.79	99.24	ALK	I1461V	MISSENSE	NON_SYNON	N
UCI3165498	chr2	29416366	rs1881421	G	C	99.76	99.86	ALK	D1529E	MISSENSE	NON_SYNON	P
UCI3165498	chr2	29416481	rs1881420	T	C	99.81	99.55	ALK	K1491R	MISSENSE	NON_SYNON	P
UCI3165498	chr2	29416572	rs1670283	T	C	99.96	99.69	ALK	I1461V	MISSENSE	NON_SYNON	N
UCI3564897	chr2	29416572	rs1670283	T	C	99.88	99.95	ALK	I1461V	MISSENSE	NON_SYNON	N

Table S8: List of non-silent germline variants

Sample	Chr	Cord	rsID	Ref Allele	Alt Allele	Allelic Fraction		Gene	AA change	Type	Effect	Mutation Taster Prediction
						Normal	Tumor					
UCI4216548	chr2	29416572	rs1670283	T	C	99.82	99.21	ALK	I1461V	MISSENSE	NON_SYNON	N
UCI8965412	chr2	29416366	rs1881421	G	C	46.47	46.63	ALK	D1529E	MISSENSE	NON_SYNON	P
UCI8965412	chr2	29416481	rs1881420	T	C	52.43	50.36	ALK	K1491R	MISSENSE	NON_SYNON	P
UCI8965412	chr2	29416572	rs1670283	T	C	99.55	100	ALK	I1461V	MISSENSE	NON_SYNON	N
UCI9135402	chr9	139407486	.	CA	C	15.38	15	NOTCH1	NA	NONE	FRAME_SHIF	NA
UCI9135402	chr2	29416366	rs1881421	G	C	99.17	98.98	ALK	D1529E	MISSENSE	NON_SYNON	P
UCI9135402	chr2	29416572	rs1670283	T	C	99.63	99.44	ALK	I1461V	MISSENSE	NON_SYNON	N
AA1025	chr5	112176756	rs459552	T	A	52.65	70.77	APC	V1822D	MISSENSE	NON_SYNON	P
AA1077	chr5	112176756	rs459552	T	A	99.85	99.65	APC	V1822D	MISSENSE	NON_SYNON	P
AA1090	chr5	112176756	rs459552	T	A	54.3	39.75	APC	V1822D	MISSENSE	NON_SYNON	P
AA943	chr5	112176756	rs459552	T	A	99.31	99.61	APC	V1822D	MISSENSE	NON_SYNON	P
AA1188	chr5	112176756	rs459552	T	A	99.72	99.73	APC	V1822D	MISSENSE	NON_SYNON	P
AA1204	chr5	112176756	rs459552	T	A	99.48	99.48	APC	V1822D	MISSENSE	NON_SYNON	P
AA1222	chr5	112176756	rs459552	T	A	99.68	100	APC	V1822D	MISSENSE	NON_SYNON	P
AA1247	chr5	112176756	rs459552	T	A	99.78	99.78	APC	V1822D	MISSENSE	NON_SYNON	P
AA1247	chr5	112178795	rs2229995	G	A	48.9	37.51	APC	G2502S	MISSENSE	NON_SYNON	N
AA1267	chr5	112176756	rs459552	T	A	99.69	99.71	APC	V1822D	MISSENSE	NON_SYNON	P
AA1277	chr5	112176756	rs459552	T	A	58.49	9.98	APC	V1822D	MISSENSE	NON_SYNON	P
AA1307	chr5	112176756	rs459552	T	A	54.23	71.24	APC	V1822D	MISSENSE	NON_SYNON	P
AA957	chr5	112176756	rs459552	T	A	45.91	53.97	APC	V1822D	MISSENSE	NON_SYNON	P
AA926	chr5	112176756	rs459552	T	A	99.81	99.7	APC	V1822D	MISSENSE	NON_SYNON	P
AA930	chr5	112176756	rs459552	T	A	98.49	99.91	APC	V1822D	MISSENSE	NON_SYNON	P
AA1106	chr5	112176756	rs459552	T	A	99.35	99.19	APC	V1822D	MISSENSE	NON_SYNON	P
AA948	chr5	112176756	rs459552	T	A	98.73	99.51	APC	V1822D	MISSENSE	NON_SYNON	P
AA952	chr5	112176756	rs459552	T	A	99.85	100	APC	V1822D	MISSENSE	NON_SYNON	P
AA952	chr5	112178795	rs2229995	G	A	52.77	49.44	APC	G2502S	MISSENSE	NON_SYNON	N
AA1367	chr5	112176756	rs459552	T	A	52.33	27.44	APC	V1822D	MISSENSE	NON_SYNON	P
AA960	chr5	112176756	rs459552	T	A	100	99.76	APC	V1822D	MISSENSE	NON_SYNON	P
AA1515	chr5	112176756	rs459552	T	A	99.73	99.92	APC	V1822D	MISSENSE	NON_SYNON	P
UCI1546879	chr5	112176756	rs459552	T	A	99.88	99.75	APC	V1822D	MISSENSE	NON_SYNON	P
UCI1689380	chr5	112102960	rs139196838	C	T	49.52	92.48	APC	R109W	MISSENSE	NON_SYNON	N
UCI1689380	chr5	112176756	rs459552	T	A	52.28	10.79	APC	V1822D	MISSENSE	NON_SYNON	P
UCI1804937	chr5	112176756	rs459552	T	A	98.42	97.89	APC	V1822D	MISSENSE	NON_SYNON	P
UCI1821517	chr5	112176756	rs459552	T	A	98.9	99.62	APC	V1822D	MISSENSE	NON_SYNON	P
UCI1908503	chr5	112176756	rs459552	T	A	99.86	99.22	APC	V1822D	MISSENSE	NON_SYNON	P
UCI1951813	chr5	112176756	rs459552	T	A	96.98	97.64	APC	V1822D	MISSENSE	NON_SYNON	P
UCI2008866	chr5	112176756	rs459552	T	A	100	99.74	APC	V1822D	MISSENSE	NON_SYNON	P
UCI2076630	chr5	112176756	rs459552	T	A	52.85	46.38	APC	V1822D	MISSENSE	NON_SYNON	P
UCI2219330	chr5	112176756	rs459552	T	A	41.36	46.76	APC	V1822D	MISSENSE	NON_SYNON	P
UCI2224680	chr5	112176756	rs459552	T	A	99.51	99.65	APC	V1822D	MISSENSE	NON_SYNON	P
UCI2231576	chr5	112176756	rs459552	T	A	98.73	100	APC	V1822D	MISSENSE	NON_SYNON	P
UCI2564879	chr5	112176756	rs459552	T	A	99.24	100	APC	V1822D	MISSENSE	NON_SYNON	P
UCI2649875	chr5	112176756	rs459552	T	A	48.63	48.27	APC	V1822D	MISSENSE	NON_SYNON	P
UCI3165498	chr5	112176756	rs459552	T	A	99.7	98.89	APC	V1822D	MISSENSE	NON_SYNON	P
UCI3165498	chr5	112178795	rs2229995	G	A	45.24	19.29	APC	G2502S	MISSENSE	NON_SYNON	N
UCI3564897	chr5	112176756	rs459552	T	A	99.62	99.79	APC	V1822D	MISSENSE	NON_SYNON	P
UCI4216548	chr5	112176756	rs459552	T	A	100	99.71	APC	V1822D	MISSENSE	NON_SYNON	P
UCI8965412	chr5	112176756	rs459552	T	A	60.31	56.37	APC	V1822D	MISSENSE	NON_SYNON	P
UCI9135402	chr5	112176756	rs459552	T	A	98.97	98.9	APC	V1822D	MISSENSE	NON_SYNON	P
AA1025	chr11	108183167	rs659243	A	G	100	99.92	ATM	N1983S	MISSENSE	NON_SYNON	N
AA1077	chr11	108106443	rs2234997	T	A	48.8	17.8	ATM	D126E	MISSENSE	NON_SYNON	N
AA1077	chr11	108175462	rs1801516	G	A	55.74	81.53	ATM	D1853N	MISSENSE	NON_SYNON	P
AA1077	chr11	108183167	rs659243	A	G	99.89	99.76	ATM	N1983S	MISSENSE	NON_SYNON	N
AA1090	chr11	108175462	rs1801516	G	A	99.7	99.69	ATM	D1853N	MISSENSE	NON_SYNON	P
AA1090	chr11	108183167	rs659243	A	G	99.89	99.6	ATM	N1983S	MISSENSE	NON_SYNON	N
AA943	chr11	108183167	rs659243	A	G	99.74	99.79	ATM	N1983S	MISSENSE	NON_SYNON	N
AA1188	chr11	108183167	rs659243	A	G	100	100	ATM	N1983S	MISSENSE	NON_SYNON	N
AA1204	chr11	108183167	rs659243	A	G	99.88	99.89	ATM	N1983S	MISSENSE	NON_SYNON	N
AA1222	chr11	108183167	rs659243	A	G	99.92	99.93	ATM	N1983S	MISSENSE	NON_SYNON	N
AA1247	chr11	108183167	rs659243	A	G	99.89	100	ATM	N1983S	MISSENSE	NON_SYNON	N
AA1267	chr11	108183167	rs659243	A	G	99.61	100	ATM	N1983S	MISSENSE	NON_SYNON	N
AA1277	chr11	108183167	rs659243	A	G	99.64	99.63	ATM	N1983S	MISSENSE	NON_SYNON	N
AA1307	chr11	108183167	rs659243	A	G	100	99.83	ATM	N1983S	MISSENSE	NON_SYNON	N
AA957	chr11	108183167	rs659243	A	G	99.8	99.68	ATM	N1983S	MISSENSE	NON_SYNON	N
AA926	chr11	108175462	rs1801516	G	A	50.13	44.73	ATM	D1853N	MISSENSE	NON_SYNON	P
AA926	chr11	108183167	rs659243	A	G	99.81	99.76	ATM	N1983S	MISSENSE	NON_SYNON	N
AA930	chr11	108183167	rs659243	A	G	100	99.95	ATM	N1983S	MISSENSE	NON_SYNON	N
AA1106	chr11	108175462	rs1801516	G	A	40.38	22.21	ATM	D1853N	MISSENSE	NON_SYNON	P
AA1106	chr11	108183167	rs659243	A	G	99.72	99.74	ATM	N1983S	MISSENSE	NON_SYNON	N
AA948	chr11	108175462	rs1801516	G	A	52.64	47.82	ATM	D1853N	MISSENSE	NON_SYNON	P
AA948	chr11	108183167	rs659243	A	G	100	100	ATM	N1983S	MISSENSE	NON_SYNON	N
AA952	chr11	108183167	rs659243	A	G	99.81	99.93	ATM	N1983S	MISSENSE	NON_SYNON	N
AA1367	chr11	108168053	rs55870064	A	G	49.69	55.14	ATM	N1650S	MISSENSE	NON_SYNON	N
AA1367	chr11	108183167	rs659243	A	G	100	99.57	ATM	N1983S	MISSENSE	NON_SYNON	N
AA960	chr11	108183167	rs659243	A	G	99.6	99.74	ATM	N1983S	MISSENSE	NON_SYNON	N
AA1515	chr11	108175462	rs1801516	G	A	52.22	45.24	ATM	D1853N	MISSENSE	NON_SYNON	P
AA1515	chr11	108183167	rs659243	A	G	99.89	100	ATM	N1983S	MISSENSE	NON_SYNON	N
UCI1546879	chr11	108183167	rs659243	A	G	100	99.71	ATM	N1983S	MISSENSE	NON_SYNON	N
UCI1689380	chr11	108183167	rs659243	A	G	99.77	99.93	ATM	N1983S	MISSENSE	NON_SYNON	N
AA930	chr11	108098576	rs1800054	C	G	42.89	48.56	ATM	S49C	MISSENSE	NON_SYNON	D
UCI1804937	chr11	108183167	rs659243	A	G	96.07	93.39	ATM	N1983S	MISSENSE	NON_SYNON	N
UCI1821517	chr11	108183167	rs659243	A	G	98.41	98.02	ATM	N1983S	MISSENSE	NON_SYNON	N
UCI1908503	chr11	108183167	rs659243	A	G	98.69	98.03	ATM	N1983S	MISSENSE	NON_SYNON	N
UCI1951813	chr11	108183167	rs659243	A	G	95.41	93.59	ATM	N1983S	MISSENSE	NON_SYNON	N
UCI2008866	chr11	108175462	rs1801516	G	A	47.07	63.17	ATM	D1853N	MISSENSE	NON_SYNON	P
UCI2008866	chr11	108183167	rs659243	A	G	99.81	100	ATM	N1983S	MISSENSE	NON_SYNON	N
UCI2076630	chr11	108183167	rs659243	A	G	100	99.88	ATM	N1983S	MISSENSE	NON_SYNON	N
UCI2219330	chr11	108175462	rs1801516	G	A	48.28	47.62	ATM	D1853N	MISSENSE	NON_SYNON	P
UCI2219330	chr11	108183167	rs659243	A	G	99.71	99.8	ATM	N1983S	MISSENSE	NON_SYNON	N
UCI2219330	chr11	108196896	rs56009889	C	T	54.18	48.72	ATM	L2307F	MISSENSE	NON_SYNON	N
UCI2224680	chr11	108183167	rs659243	A	G	100	99.94	ATM	N1983S	MISSENSE	NON_SYNON	N
UCI2231576	chr11	108119823	rs56128736	T	C	56.88	45.68	ATM	V410A	MISSENSE	NON_SYNON	N
UCI2231576	chr11	108183167	rs659243	A	G	100	100	ATM	N1983S	MISSENSE	NON_SYNON	N
UCI2564879	chr11	108183167	rs659243	A	G	99.8	99.91	ATM	N1983S	MISSENSE	NON_SYNON	N
UCI2649875	chr11	108183167	rs659243	A	G	97.93	97.95	ATM	N1983S	MISSENSE	NON_SYNON	N
UCI3165498	chr11	108183167	rs659243	A	G	99.78	99.72	ATM	N1983S	MISSENSE	NON_SYNON	N
UCI3564897	chr11	108175462	rs1801516	G	A	54.1	12.9	ATM	D1853N	MISSENSE	NON_SYNON	P
UCI3564897	chr11	108183167	rs659243	A	G	99.82	99.83	ATM	N1983S	MISSENSE	NON_SYNON	N
UCI4216548	chr11	108183167	rs659243	A	G	99.82	99.92	ATM	N1983S	MISSENSE	NON_SYNON	N
UCI8965412	chr11	108183167	rs659243	A	G	99.92	100	ATM	N1983S	MISSENSE	NON_SYNON	N

Table S8: List of non-silent germline variants

Sample	Chr	Cord	rsID	Ref Allele	Alt Allele	Allelic Fraction		Gene	AA change	Type	Effect	Mutation Taster Prediction
						Normal	Tumor					
AA1277	chr11	108235879	rs139379666	C	T	49.94	11.35	ATM	P2974L	MISSENSE	NON_SYNON	D
UCI9135402	chr11	108175462	rs1801516	G	A	99.25	98.82	ATM	D1853N	MISSENSE	NON_SYNON	P
UCI9135402	chr11	108183167	rs659243	A	G	98.66	98.15	ATM	N1983S	MISSENSE	NON_SYNON	N
AA957	chr7	117188715	rs3034796	GAAAGC	G	15.61	12.61	CFTR	NA	NONE	FRAME_SHIF	NA
AA943	chr14	105243085	.	CT	C	16.04	16.27	AKT1	NA	NONE	FRAME_SHIF	NA
AA943	chr17	41223094	rs1799966	T	C	99.87	98.98	BRCA1	S1317G	MISSENSE	NON_SYNON	P
AA943	chr17	41244000	rs16942	T	C	100	98.73	BRCA1	K1136R	MISSENSE	NON_SYNON	P
AA943	chr17	41244435	rs16941	T	C	99.75	98.13	BRCA1	E1038G	MISSENSE	NON_SYNON	P
AA943	chr17	41244936	rs799917	G	A	99.85	98.81	BRCA1	P575L	MISSENSE	NON_SYNON	P
AA943	chr17	41245471	rs4986850	C	T	52.67	51.88	BRCA1	D397N	MISSENSE	NON_SYNON	P
AA1188	chr17	41243840	rs28897687	A	C	47.55	48.74	BRCA1	N1189K	MISSENSE	NON_SYNON	N
UCI1804937	chr2	29451760	.	TCC	T	16.25	13.62	ALK	NA	NONE	FRAME_SHIF	NA
AA1204	chr17	41223094	rs1799966	T	C	53.4	27.2	BRCA1	S1317G	MISSENSE	NON_SYNON	P
AA1204	chr17	41244000	rs16942	T	C	54.36	22.04	BRCA1	K1136R	MISSENSE	NON_SYNON	P
AA1204	chr17	41244435	rs16941	T	C	46.83	27.07	BRCA1	E1038G	MISSENSE	NON_SYNON	P
AA1204	chr17	41244936	rs799917	G	A	52.24	28.2	BRCA1	P575L	MISSENSE	NON_SYNON	P
AA1222	chr17	41223094	rs1799966	T	C	49.16	70.16	BRCA1	S1317G	MISSENSE	NON_SYNON	P
AA1222	chr17	41244000	rs16942	T	C	60.9	67.99	BRCA1	K1136R	MISSENSE	NON_SYNON	P
AA1222	chr17	41244435	rs16941	T	C	55.42	66.88	BRCA1	E1038G	MISSENSE	NON_SYNON	P
AA1222	chr17	41244936	rs799917	G	A	48.32	71.71	BRCA1	P575L	MISSENSE	NON_SYNON	P
AA1247	chr17	41223094	rs1799966	T	C	49.28	17.48	BRCA1	S1317G	MISSENSE	NON_SYNON	P
AA1247	chr17	41244000	rs16942	T	C	46.76	15.93	BRCA1	K1136R	MISSENSE	NON_SYNON	P
AA1247	chr17	41244435	rs16941	T	C	48.71	18.46	BRCA1	E1038G	MISSENSE	NON_SYNON	P
AA1247	chr17	41244936	rs799917	G	A	44.73	17.29	BRCA1	P575L	MISSENSE	NON_SYNON	P
AA1267	chr17	41223094	rs1799966	T	C	48.75	50.75	BRCA1	S1317G	MISSENSE	NON_SYNON	P
AA1267	chr17	41244000	rs16942	T	C	50.03	52.61	BRCA1	K1136R	MISSENSE	NON_SYNON	P
AA1267	chr17	41244435	rs16941	T	C	52.95	50.17	BRCA1	E1038G	MISSENSE	NON_SYNON	P
AA1267	chr17	41244936	rs799917	G	A	48.17	53.43	BRCA1	P575L	MISSENSE	NON_SYNON	P
AA957	chr17	41223094	rs1799966	T	C	51.21	51.27	BRCA1	S1317G	MISSENSE	NON_SYNON	P
AA957	chr17	41244000	rs16942	T	C	45.22	47.22	BRCA1	K1136R	MISSENSE	NON_SYNON	P
AA957	chr17	41244435	rs16941	T	C	43.58	44.31	BRCA1	E1038G	MISSENSE	NON_SYNON	P
AA957	chr17	41244936	rs799917	G	A	46.99	51.38	BRCA1	P575L	MISSENSE	NON_SYNON	P
AA926	chr17	41244936	rs799917	G	A	48.11	51.95	BRCA1	P575L	MISSENSE	NON_SYNON	P
AA930	chr17	41223094	rs1799966	T	C	54.35	51.38	BRCA1	S1317G	MISSENSE	NON_SYNON	P
AA930	chr17	41244000	rs16942	T	C	54.2	52.49	BRCA1	K1136R	MISSENSE	NON_SYNON	P
AA930	chr17	41244435	rs16941	T	C	46.78	51.74	BRCA1	E1038G	MISSENSE	NON_SYNON	P
AA930	chr17	41244936	rs799917	G	A	42.81	52.41	BRCA1	P575L	MISSENSE	NON_SYNON	P
AA1106	chr17	41243509	rs28897689	T	C	50.79	48.94	BRCA1	R1051G	MISSENSE	NON_SYNON	N
AA948	chr17	41244710	.	G	C	47.33	45.26	BRCA1	I650M	MISSENSE	NON_SYNON	N
AA952	chr17	41246481	rs1799950	T	C	46.18	49.73	BRCA1	Q309R	MISSENSE	NON_SYNON	N
AA1515	chr17	41219694	rs80357087	C	A	51.47	52	BRCA1	A1373S	MISSENSE	NON_SYNON	D
AA1367	chr17	41244982	rs80356892	A	G	45.23	70.69	BRCA1	Y560H	MISSENSE	NON_SYNON	N
UCI1546879	chr17	41222975	rs1799967	C	T	51.31	60.25	BRCA1	M1356I	MISSENSE	NON_SYNON	N
UCI1546879	chr17	41223094	rs1799966	T	C	99.62	99.47	BRCA1	S1317G	MISSENSE	NON_SYNON	P
UCI1546879	chr17	41244000	rs16942	T	C	99.78	99.69	BRCA1	K1136R	MISSENSE	NON_SYNON	P
UCI1546879	chr17	41244435	rs16941	T	C	99.56	99.35	BRCA1	E1038G	MISSENSE	NON_SYNON	P
UCI1546879	chr17	41244936	rs799917	G	A	99.71	99.61	BRCA1	P575L	MISSENSE	NON_SYNON	P
UCI1821517	chr17	41223094	rs1799966	T	C	98.58	98	BRCA1	S1317G	MISSENSE	NON_SYNON	P
UCI1821517	chr17	41244000	rs16942	T	C	98.58	98.77	BRCA1	K1136R	MISSENSE	NON_SYNON	P
UCI1821517	chr17	41244435	rs16941	T	C	99.24	98.88	BRCA1	E1038G	MISSENSE	NON_SYNON	P
UCI1821517	chr17	41244936	rs799917	G	A	99.24	98.7	BRCA1	P575L	MISSENSE	NON_SYNON	P
UCI1908503	chr17	41244429	rs4986852	C	T	50.63	46.93	BRCA1	S1040N	MISSENSE	NON_SYNON	N
UCI2076630	chr17	41223094	rs1799966	T	C	99.46	99.35	BRCA1	S1317G	MISSENSE	NON_SYNON	P
UCI2076630	chr17	41244000	rs16942	T	C	98.38	98.1	BRCA1	K1136R	MISSENSE	NON_SYNON	P
UCI2076630	chr17	41244435	rs16941	T	C	99.6	98.88	BRCA1	E1038G	MISSENSE	NON_SYNON	P
UCI2076630	chr17	41244936	rs799917	G	A	98.83	98.78	BRCA1	P575L	MISSENSE	NON_SYNON	P
UCI2219330	chr17	41246481	rs1799950	T	C	49.02	49.12	BRCA1	Q309R	MISSENSE	NON_SYNON	N
UCI2224680	chr17	41223094	rs1799966	T	C	46.06	74.04	BRCA1	S1317G	MISSENSE	NON_SYNON	P
UCI2224680	chr17	41244000	rs16942	T	C	49.49	79.81	BRCA1	K1136R	MISSENSE	NON_SYNON	P
UCI2224680	chr17	41244435	rs16941	T	C	47.7	72.07	BRCA1	E1038G	MISSENSE	NON_SYNON	P
UCI2224680	chr17	41244936	rs799917	G	A	50.19	71.74	BRCA1	P575L	MISSENSE	NON_SYNON	P
UCI2224680	chr17	41245471	rs4986850	C	T	42.86	73.57	BRCA1	D397N	MISSENSE	NON_SYNON	P
UCI2231576	chr17	41244252	rs80357201	G	A	50.83	51.41	BRCA1	P1052L	MISSENSE	NON_SYNON	N
UCI2564879	chr17	41223094	rs1799966	T	C	47.68	49.99	BRCA1	S1317G	MISSENSE	NON_SYNON	P
UCI2564879	chr17	41244000	rs16942	T	C	55.6	53.77	BRCA1	K1136R	MISSENSE	NON_SYNON	P
UCI2564879	chr17	41244435	rs16941	T	C	52.62	50.35	BRCA1	E1038G	MISSENSE	NON_SYNON	P
UCI2564879	chr17	41244936	rs799917	G	A	49.52	52.51	BRCA1	P575L	MISSENSE	NON_SYNON	P
UCI2649875	chr17	41244936	rs799917	G	A	49.09	53.03	BRCA1	P575L	MISSENSE	NON_SYNON	P
UCI2649875	chr17	41256956	rs80357209	G	C	43.87	48.01	BRCA1	T30R	MISSENSE	NON_SYNON	N
UCI9135402	chr17	41223094	rs1799966	T	C	47.08	50.99	BRCA1	S1317G	MISSENSE	NON_SYNON	P
UCI9135402	chr17	41244000	rs16942	T	C	45.14	54.11	BRCA1	K1136R	MISSENSE	NON_SYNON	P
UCI9135402	chr17	41244435	rs16941	T	C	53.65	49.5	BRCA1	E1038G	MISSENSE	NON_SYNON	P
UCI9135402	chr17	41244936	rs799917	G	A	53.7	44.4	BRCA1	P575L	MISSENSE	NON_SYNON	P
AA1025	chr13	32914236	rs4987117	C	T	56.52	33.93	BRCA2	T1915M	MISSENSE	NON_SYNON	N
AA1025	chr13	32929387	rs169547	T	C	99.92	99.94	BRCA2	V2466A	MISSENSE	NON_SYNON	N
AA1077	chr13	32929387	rs169547	T	C	99.86	100	BRCA2	V2466A	MISSENSE	NON_SYNON	N
AA1090	chr13	32912928	rs80358678	G	C	51.36	47.54	BRCA2	S1479T	MISSENSE	NON_SYNON	N
AA1090	chr13	32929387	rs169547	T	C	100	99.94	BRCA2	V2466A	MISSENSE	NON_SYNON	N
AA943	chr13	32929387	rs169547	T	C	99.81	100	BRCA2	V2466A	MISSENSE	NON_SYNON	N
AA1188	chr13	32929387	rs169547	T	C	99.74	99.66	BRCA2	V2466A	MISSENSE	NON_SYNON	N
AA1204	chr13	32929387	rs169547	T	C	99.92	99.88	BRCA2	V2466A	MISSENSE	NON_SYNON	N
AA1222	chr13	32906729	rs144848	A	C	57.57	80.48	BRCA2	N370H	MISSENSE	NON_SYNON	P
AA1222	chr13	32929387	rs169547	T	C	99.78	99.48	BRCA2	V2466A	MISSENSE	NON_SYNON	N
AA1247	chr13	32929387	rs169547	T	C	99.8	99.78	BRCA2	V2466A	MISSENSE	NON_SYNON	N
AA1267	chr13	32929387	rs169547	T	C	99.81	100	BRCA2	V2466A	MISSENSE	NON_SYNON	N
AA1277	chr13	32910842	rs11571653	A	G	45.82	67.44	BRCA2	M784V	MISSENSE	NON_SYNON	N
AA1277	chr13	32929387	rs169547	T	C	99.35	100	BRCA2	V2466A	MISSENSE	NON_SYNON	N
AA1307	chr13	32929387	rs169547	T	C	99.96	100	BRCA2	V2466A	MISSENSE	NON_SYNON	N
AA957	chr13	32929387	rs169547	T	C	99.96	100	BRCA2	V2466A	MISSENSE	NON_SYNON	N
AA926	chr13	32914236	rs4987117	C	T	50	62.88	BRCA2	T1915M	MISSENSE	NON_SYNON	N
AA926	chr13	32929387	rs169547	T	C	100	100	BRCA2	V2466A	MISSENSE	NON_SYNON	N
AA930	chr13	32906729	rs144848	A	C	48.09	52.48	BRCA2	N370H	MISSENSE	NON_SYNON	P
AA930	chr13	32929387	rs169547	T	C	99.74	99.88	BRCA2	V2466A	MISSENSE	NON_SYNON	N
AA1106	chr13	32914592	rs1799954	C	T	51.79	46.64	BRCA2	R2034C	MISSENSE	NON_SYNON	N
AA1106	chr13	32929387	rs169547	T	C	99.6	99.85	BRCA2	V2466A	MISSENSE	NON_SYNON	N
AA948	chr13	32906729	rs144848	A	C	46.76	50.25	BRCA2	N370H	MISSENSE	NON_SYNON	P
AA948	chr13	32914947	rs80358881	C	A	48.15	46.74	BRCA2	S2152Y	MISSENSE	NON_SYNON	N
AA948	chr13	32929387	rs169547	T	C	100	100	BRCA2	V2466A	MISSENSE	NON_SYNON	N
AA952	chr13	32906729	rs144848	A	C	99.85	99.41	BRCA2	N370H	MISSENSE	NON_SYNON	P
AA952	chr13	32929387	rs169547	T	C	99.83	99.87	BRCA2	V2466A	MISSENSE	NON_SYNON	N

Table S8: List of non-silent germline variants

Sample	Chr	Cord	rsID	Ref Allele	Alt Allele	Allelic Fraction		Gene	AA change	Type	Effect	Mutation Taster Prediction
						Normal	Tumor					
AA1367	chr13	32906729	rs144848	A	C	50.73	70.94	BRCA2	N370H	MISSENSE	NON_SYNON	P
AA1367	chr13	32929387	rs169547	T	C	99.93	99.9	BRCA2	V2466A	MISSENSE	NON_SYNON	N
AA960	chr13	32906729	rs144848	A	C	48.67	49.6	BRCA2	N370H	MISSENSE	NON_SYNON	P
AA960	chr13	32914236	rs4987117	C	T	46.43	45.87	BRCA2	T1915M	MISSENSE	NON_SYNON	N
AA960	chr13	32929387	rs169547	T	C	99.49	99.86	BRCA2	V2466A	MISSENSE	NON_SYNON	N
AA960	chr13	32930598	rs11571707	T	C	46.28	53.85	BRCA2	I2490T	MISSENSE	NON_SYNON	N
AA1515	chr13	32906480	rs766173	A	C	59.11	50.69	BRCA2	N287H	MISSENSE	NON_SYNON	N
AA1515	chr13	32911463	rs1799944	A	G	50.89	53.88	BRCA2	N991D	MISSENSE	NON_SYNON	P
AA1515	chr13	32929387	rs169547	T	C	99.91	99.85	BRCA2	V2466A	MISSENSE	NON_SYNON	N
UCI1546879	chr13	32906729	rs144848	A	C	44.8	31.14	BRCA2	N370H	MISSENSE	NON_SYNON	P
UCI1546879	chr13	32929387	rs169547	T	C	99.58	100	BRCA2	V2466A	MISSENSE	NON_SYNON	N
UCI1689380	chr13	32906729	rs144848	A	C	41.44	61.95	BRCA2	N370H	MISSENSE	NON_SYNON	P
UCI1689380	chr13	32929387	rs169547	T	C	99.42	99.72	BRCA2	V2466A	MISSENSE	NON_SYNON	N
UCI1804937	chr13	32929387	rs169547	T	C	99.68	99.78	BRCA2	V2466A	MISSENSE	NON_SYNON	N
UCI1821517	chr13	32929387	rs169547	T	C	99.62	99.63	BRCA2	V2466A	MISSENSE	NON_SYNON	N
UCI1908503	chr13	32929387	rs169547	T	C	99.49	99.55	BRCA2	V2466A	MISSENSE	NON_SYNON	N
UCI1951813	chr13	32906729	rs144848	A	C	99.59	99.75	BRCA2	N370H	MISSENSE	NON_SYNON	P
UCI1951813	chr13	32929387	rs169547	T	C	99.77	99.72	BRCA2	V2466A	MISSENSE	NON_SYNON	N
UCI2008866	chr13	32906729	rs144848	A	C	54.32	10.51	BRCA2	N370H	MISSENSE	NON_SYNON	P
UCI2008866	chr13	32929387	rs169547	T	C	99.93	99.82	BRCA2	V2466A	MISSENSE	NON_SYNON	N
UCI2076630	chr13	32929387	rs169547	T	C	100	99.69	BRCA2	V2466A	MISSENSE	NON_SYNON	N
UCI2219330	chr13	32906729	rs144848	A	C	99.56	99.62	BRCA2	N370H	MISSENSE	NON_SYNON	P
UCI2219330	chr13	32929387	rs169547	T	C	99.79	99.91	BRCA2	V2466A	MISSENSE	NON_SYNON	N
UCI2224680	chr13	32929387	rs169547	T	C	99.76	99.52	BRCA2	V2466A	MISSENSE	NON_SYNON	N
UCI2224680	chr13	32972884	rs1801426	A	G	53.2	34.16	BRCA2	I3412V	MISSENSE	NON_SYNON	P
UCI2231576	chr13	32906480	rs766173	A	C	55.74	47.48	BRCA2	N287H	MISSENSE	NON_SYNON	N
UCI2231576	chr13	32911463	rs1799944	A	G	52.76	54.43	BRCA2	N991D	MISSENSE	NON_SYNON	P
UCI2231576	chr13	32929387	rs169547	T	C	99.65	99.91	BRCA2	V2466A	MISSENSE	NON_SYNON	N
UCI2564879	chr13	32929387	rs169547	T	C	100	100	BRCA2	V2466A	MISSENSE	NON_SYNON	N
UCI2649875	chr13	32929387	rs169547	T	C	99.31	99.67	BRCA2	V2466A	MISSENSE	NON_SYNON	N
UCI3165498	chr13	32929387	rs169547	T	C	99.88	99.85	BRCA2	V2466A	MISSENSE	NON_SYNON	N
UCI3564897	chr13	32906480	rs766173	A	C	53.57	53.7	BRCA2	N287H	MISSENSE	NON_SYNON	N
UCI3564897	chr13	32906729	rs144848	A	C	52.27	49.3	BRCA2	N370H	MISSENSE	NON_SYNON	P
UCI3564897	chr13	32911463	rs1799944	A	G	51.3	48.31	BRCA2	N991D	MISSENSE	NON_SYNON	P
UCI3564897	chr13	32929387	rs169547	T	C	99.9	100	BRCA2	V2466A	MISSENSE	NON_SYNON	N
UCI4216548	chr13	32929387	rs169547	T	C	99.72	99.72	BRCA2	V2466A	MISSENSE	NON_SYNON	N
UCI8965412	chr13	32929387	rs169547	T	C	63	71.34	BRCA2	V2466A	MISSENSE	NON_SYNON	N
UCI2008866	chr13	32972626	rs11571833	A	T	45.99	12.16	BRCA2	K3326*	NONSENSE	STOP_GAINE	D
UCI9135402	chr13	32906729	rs144848	A	C	51.08	51.13	BRCA2	N370H	MISSENSE	NON_SYNON	P
UCI9135402	chr13	32929387	rs169547	T	C	99.24	99.58	BRCA2	V2466A	MISSENSE	NON_SYNON	N
AA1247	chr16	68855966	rs35187787	G	A	54.15	59.36	CDH1	A531T	MISSENSE	NON_SYNON	N
UCI3165498	chr16	68842734	.	C	T	45.15	37.66	CDH1	R224C	MISSENSE	NON_SYNON	N
UCI2224680	chr9	21970916	rs3731249	C	T	52.5	51.15	CDKN2A	A148T	MISSENSE	NON_SYNON	N
AA1025	chr7	117199533	rs213950	G	A	99.32	99.33	CFTR	V409M	MISSENSE	NON_SYNON	P
AA1025	chr7	117227832	rs113993959	G	T	50.84	55.83	CFTR	G481*	NONSENSE	STOP_GAINE	A
AA1077	chr7	117199533	rs213950	G	A	44.47	81.3	CFTR	V409M	MISSENSE	NON_SYNON	P
AA1090	chr7	117199533	rs213950	G	A	49.29	9.52	CFTR	V409M	MISSENSE	NON_SYNON	P
AA943	chr7	117199533	rs213950	G	A	53.95	45.71	CFTR	V409M	MISSENSE	NON_SYNON	P
AA1188	chr7	117199533	rs213950	G	A	49.63	45.96	CFTR	V409M	MISSENSE	NON_SYNON	P
AA1204	chr7	117199533	rs213950	G	A	50.51	59.27	CFTR	V409M	MISSENSE	NON_SYNON	P
AA1222	chr7	117199533	rs213950	G	A	53.5	50.22	CFTR	V409M	MISSENSE	NON_SYNON	P
AA1247	chr7	117199533	rs213950	G	A	99.94	99.1	CFTR	V409M	MISSENSE	NON_SYNON	P
UCI1821517	chr7	117182116	rs143860237	C	T	54.27	79.84	CFTR	T358M	MISSENSE	NON_SYNON	D
AA1204	chr7	117267812	rs34911792	T	G	47.92	60.22	CFTR	S1174R	MISSENSE	NON_SYNON	D
AA930	chr7	117199533	rs213950	G	A	55.13	48.58	CFTR	V409M	MISSENSE	NON_SYNON	P
UCI2224680	chr7	117267812	rs34911792	T	G	58.03	50.95	CFTR	S1174R	MISSENSE	NON_SYNON	D
AA1367	chr7	117199533	rs213950	G	A	52.05	47.22	CFTR	V409M	MISSENSE	NON_SYNON	P
AA960	chr7	117199533	rs213950	G	A	47.27	47.84	CFTR	V409M	MISSENSE	NON_SYNON	P
UCI1546879	chr7	117199533	rs213950	G	A	54.22	42.18	CFTR	V409M	MISSENSE	NON_SYNON	P
UCI9135402	chr7	117175323	rs138338446	G	A	50.05	49.49	CFTR	V171M	MISSENSE	NON_SYNON	D
UCI1689380	chr7	117199533	rs213950	G	A	57.08	34.56	CFTR	V409M	MISSENSE	NON_SYNON	P
UCI1804937	chr7	117199533	rs213950	G	A	46.94	46.81	CFTR	V409M	MISSENSE	NON_SYNON	P
UCI9135402	chr7	117282582	rs11971167	G	A	45.16	47.4	CFTR	D1209N	MISSENSE	NON_SYNON	D
UCI1821517	chr7	117199533	rs213950	G	A	44.39	76.49	CFTR	V409M	MISSENSE	NON_SYNON	P
UCI1908503	chr7	117199533	rs213950	G	A	99.59	99.73	CFTR	V409M	MISSENSE	NON_SYNON	P
UCI9135402	chr7	117149143	rs115545701	C	T	51.85	45.86	CFTR	R74W	MISSENSE	NON_SYNON	D
UCI1951813	chr7	117199533	rs213950	G	A	39.17	44.43	CFTR	V409M	MISSENSE	NON_SYNON	P
UCI2008866	chr7	117199533	rs213950	G	A	50.12	35.77	CFTR	V409M	MISSENSE	NON_SYNON	P
UCI3564897	chr7	117171122	rs35516286	T	C	45.19	43.52	CFTR	I148T	MISSENSE	NON_SYNON	D
UCI2076630	chr7	117199533	rs213950	G	A	55.72	21.12	CFTR	V409M	MISSENSE	NON_SYNON	P
UCI1546879	chr7	117267812	rs34911792	T	G	47.89	42.15	CFTR	S1174R	MISSENSE	NON_SYNON	D
UCI2219330	chr7	117199533	rs213950	G	A	48.79	54.26	CFTR	V409M	MISSENSE	NON_SYNON	P
UCI2224680	chr7	117199533	rs213950	G	A	41.5	55.67	CFTR	V409M	MISSENSE	NON_SYNON	P
AA926	chr7	117149147	rs1800076	G	A	44.33	37.99	CFTR	R75Q	MISSENSE	NON_SYNON	D
UCI2231576	chr7	117199533	rs213950	G	A	55.08	49.57	CFTR	V409M	MISSENSE	NON_SYNON	P
UCI2564879	chr7	117199533	rs213950	G	A	99.53	99.43	CFTR	V409M	MISSENSE	NON_SYNON	P
UCI2649875	chr7	117199533	rs213950	G	A	99.87	99.63	CFTR	V409M	MISSENSE	NON_SYNON	P
AA943	chr7	140481383	.	CT	C	16.89	16.78	BRAF	NA	NONE	FRAME_SHIF	NA
UCI1908503	chr7	6018228	.	AT	A	16.96	17.35	PMS2	NA	NONE	FRAME_SHIF	NA
UCI3165498	chr7	117199533	rs213950	G	A	55.95	49.08	CFTR	V409M	MISSENSE	NON_SYNON	P
UCI3564897	chr7	117199533	rs213950	G	A	45.85	45.91	CFTR	V409M	MISSENSE	NON_SYNON	P
UCI1951813	chr5	149500767	.	GT	G	17.33	18.31	PDGFRB	NA	NONE	FRAME_SHIF	NA
UCI1908503	chr9	139391529	.	GA	G	17.34	18.78	NOTCH1	NA	NONE	FRAME_SHIF	NA
UCI1821517	chr7	6018228	.	AT	A	17.47	17.88	PMS2	NA	NONE	FRAME_SHIF	NA
AA943	chr7	117188715	rs3034796	GAAAGC	G	18.03	19.82	CFTR	NA	NONE	FRAME_SHIF	NA
AA1277	chr7	117188715	rs3034796	GAAAGC	G	18.34	13.2	CFTR	NA	NONE	FRAME_SHIF	NA
AA1025	chr7	117188715	rs3034796	GAAAGC	G	18.54	15	CFTR	NA	NONE	FRAME_SHIF	NA
UCI2224680	chr7	117188715	rs3034796	GAAAGC	G	18.72	17.4	CFTR	NA	NONE	FRAME_SHIF	NA
UCI1951813	chr9	139390569	.	GT	G	19.17	17.98	NOTCH1	NA	NONE	FRAME_SHIF	NA
AA1367	chr9	139390569	.	GT	G	19.93	17.48	NOTCH1	NA	NONE	FRAME_SHIF	NA
UCI1804937	chr3	37090032	.	CT	C	20.3	19.94	MLH1	NA	NONE	FRAME_SHIF	NA
UCI9135402	chr7	117199533	rs213950	G	A	54.77	50.16	CFTR	V409M	MISSENSE	NON_SYNON	P
AA960	chr22	29121087	rs17879961	A	G	46.53	62.59	CHEK2	I157T	MISSENSE	NON_SYNON	NA
UCI2649875	chr22	29121087	rs17879961	A	G	57.08	49.87	CHEK2	I157T	MISSENSE	NON_SYNON	NA
UCI2076630	chr22	29126440	.	A	G	59.77	43.31	CHEK2	V139A	MISSENSE	NON_SYNON	NA
AA960	chr5	138160248	rs150893072	G	C	47.84	28.06	CTNAA1	Q103H	MISSENSE	NON_SYNON	D
AA1077	chr10	96702066	rs7900194	G	A	46.19	24.91	CYP2C9	R150H	MISSENSE	NON_SYNON	N
UCI3564897	chr10	96702047	rs1799853	C	T	53.16	81.91	CYP2C9	R144C	MISSENSE	NON_SYNON	D
UCI2649875	chr10	96702047	rs1799853	C	T	43.89	61.77	CYP2C9	R144C	MISSENSE	NON_SYNON	D
AA1307	chr10	96741053	rs1057910	A	C	45.58	51.45	CYP2C9	I359L	MISSENSE	NON_SYNON	D

Table S8: List of non-silent germline variants

Sample	Chr	Cord	rsID	Ref Allele	Alt Allele	Allelic Fraction		Gene	AA change	Type	Effect	Mutation Taster Prediction
						Normal	Tumor					
AA948	chr10	96748777	rs9332239	C	T	48.21	51.16	CYP2C9	P489S	MISSENSE	NON_SYNON	D
UCI2219330	chr10	96741053	rs1057910	A	C	46.05	50.95	CYP2C9	I359L	MISSENSE	NON_SYNON	D
AA948	chr10	96702047	rs1799853	C	T	55.15	50.79	CYP2C9	R144C	MISSENSE	NON_SYNON	D
AA1515	chr10	96702047	rs1799853	C	T	52.95	50.26	CYP2C9	R144C	MISSENSE	NON_SYNON	D
UCI1689380	chr10	96741053	rs1057910	A	C	49.72	49.81	CYP2C9	I359L	MISSENSE	NON_SYNON	D
AA926	chr10	96702047	rs1799853	C	T	47.71	49.78	CYP2C9	R144C	MISSENSE	NON_SYNON	D
UCI1689380	chr10	96702047	rs1799853	C	T	54.96	49.46	CYP2C9	R144C	MISSENSE	NON_SYNON	D
AA1267	chr10	96702047	rs1799853	C	T	51.72	47.7	CYP2C9	R144C	MISSENSE	NON_SYNON	D
AA952	chr10	96741053	rs1057910	A	C	52.58	47.03	CYP2C9	I359L	MISSENSE	NON_SYNON	D
AA1025	chr10	96702047	rs1799853	C	T	48.83	45.36	CYP2C9	R144C	MISSENSE	NON_SYNON	D
UCI8965412	chr10	96740981	rs28371685	C	T	49.46	72.69	CYP2C9	R335W	MISSENSE	NON_SYNON	P
AA1188	chr22	42522613	rs1135840	G	C	100	100	CYP2D6	T432S	MISSENSE	NON_SYNON	NA
UCI1821517	chr22	42523943	rs16947	A	G	99.89	100	CYP2D6	C242R	MISSENSE	NON_SYNON	NA
UCI2231576	chr22	42522613	rs1135840	G	C	97.63	100	CYP2D6	T432S	MISSENSE	NON_SYNON	NA
UCI9135402	chr22	42523943	rs16947	A	G	99.85	100	CYP2D6	C242R	MISSENSE	NON_SYNON	NA
UCI1951813	chr22	42523943	rs16947	A	G	99.36	99.94	CYP2D6	C242R	MISSENSE	NON_SYNON	NA
AA952	chr22	42523943	rs16947	A	G	99.51	99.93	CYP2D6	C242R	MISSENSE	NON_SYNON	NA
AA1188	chr22	42523943	rs16947	A	G	99.91	99.86	CYP2D6	C242R	MISSENSE	NON_SYNON	NA
AA1267	chr22	42522613	rs1135840	G	C	99.93	99.86	CYP2D6	T432S	MISSENSE	NON_SYNON	NA
UCI2231576	chr22	42523943	rs16947	A	G	99.02	99.81	CYP2D6	C242R	MISSENSE	NON_SYNON	NA
AA1090	chr22	42523943	rs16947	A	G	99.86	99.8	CYP2D6	C242R	MISSENSE	NON_SYNON	NA
UCI2564879	chr22	42523943	rs16947	A	G	99.66	99.79	CYP2D6	C242R	MISSENSE	NON_SYNON	NA
AA1106	chr22	42523943	rs16947	A	G	99.96	99.77	CYP2D6	C242R	MISSENSE	NON_SYNON	NA
AA1367	chr22	42523943	rs16947	A	G	99.84	99.77	CYP2D6	C242R	MISSENSE	NON_SYNON	NA
UCI1908503	chr22	42523943	rs16947	A	G	99.41	99.76	CYP2D6	C242R	MISSENSE	NON_SYNON	NA
AA1025	chr22	42523943	rs16947	A	G	99.71	99.72	CYP2D6	C242R	MISSENSE	NON_SYNON	NA
UCI2649875	chr22	42522613	rs1135840	G	C	99.2	99.68	CYP2D6	T432S	MISSENSE	NON_SYNON	NA
AA1267	chr22	42523943	rs16947	A	G	99.87	99.63	CYP2D6	C242R	MISSENSE	NON_SYNON	NA
UCI2008866	chr22	42523943	rs16947	A	G	99.89	99.57	CYP2D6	C242R	MISSENSE	NON_SYNON	NA
UCI3165498	chr22	42523943	rs16947	A	G	99.53	99.54	CYP2D6	C242R	MISSENSE	NON_SYNON	NA
AA960	chr22	42523943	rs16947	A	G	99.84	99.4	CYP2D6	C242R	MISSENSE	NON_SYNON	NA
UCI2649875	chr22	42523943	rs16947	A	G	99.21	99.39	CYP2D6	C242R	MISSENSE	NON_SYNON	NA
UCI2564879	chr22	42526694	rs1065852	G	A	99.55	99.36	CYP2D6	P34S	MISSENSE	NON_SYNON	NA
AA1247	chr22	42523943	rs16947	A	G	99.59	99.35	CYP2D6	C242R	MISSENSE	NON_SYNON	NA
AA1204	chr22	42523943	rs16947	A	G	99.59	99.28	CYP2D6	C242R	MISSENSE	NON_SYNON	NA
UCI3165498	chr22	42522613	rs1135840	G	C	99.59	99.27	CYP2D6	T432S	MISSENSE	NON_SYNON	NA
AA1106	chr22	42522613	rs1135840	G	C	99.73	98.95	CYP2D6	T432S	MISSENSE	NON_SYNON	NA
AA1515	chr22	42522613	rs1135840	G	C	91.42	94.89	CYP2D6	T432S	MISSENSE	NON_SYNON	NA
UCI9135402	chr22	42526694	rs1065852	G	A	95.62	94.83	CYP2D6	P34S	MISSENSE	NON_SYNON	NA
UCI2008866	chr22	42526694	rs1065852	G	A	68.22	93.02	CYP2D6	P34S	MISSENSE	NON_SYNON	NA
UCI1689380	chr22	42523943	rs16947	A	G	46.82	92.63	CYP2D6	C242R	MISSENSE	NON_SYNON	NA
UCI1689380	chr22	42522613	rs1135840	G	C	50.25	90.03	CYP2D6	T432S	MISSENSE	NON_SYNON	NA
UCI3165498	chr22	42526712	rs138100349	G	A	47.01	88.58	CYP2D6	R28C	MISSENSE	NON_SYNONYMOUS_CODING	
UCI1821517	chr22	42526694	rs1065852	G	A	60.65	85.04	CYP2D6	P34S	MISSENSE	NON_SYNON	NA
AA1090	chr22	42522613	rs1135840	G	C	53.3	84.61	CYP2D6	T432S	MISSENSE	NON_SYNON	NA
AA1367	chr22	42526694	rs1065852	G	A	64.72	75.39	CYP2D6	P34S	MISSENSE	NON_SYNON	NA
AA1247	chr22	42526694	rs1065852	G	A	64.51	73.07	CYP2D6	P34S	MISSENSE	NON_SYNON	NA
UCI1951813	chr22	42526694	rs1065852	G	A	63.7	67.61	CYP2D6	P34S	MISSENSE	NON_SYNON	NA
UCI2008866	chr22	42523528	rs1058172	C	T	50.33	64.96	CYP2D6	R311H	MISSENSE	NON_SYNON	NA
AA1025	chr22	42526694	rs1065852	G	A	48.1	63.65	CYP2D6	P34S	MISSENSE	NON_SYNON	NA
UCI1908503	chr22	42522613	rs1135840	G	C	51.17	61.43	CYP2D6	T432S	MISSENSE	NON_SYNON	NA
UCI9135402	chr22	42523528	rs1058172	C	T	64.95	60.28	CYP2D6	R311H	MISSENSE	NON_SYNON	NA
AA926	chr22	42523943	rs16947	A	G	52.72	59.91	CYP2D6	C242R	MISSENSE	NON_SYNON	NA
UCI1821517	chr22	42523528	rs1058172	C	T	56.49	59.07	CYP2D6	R311H	MISSENSE	NON_SYNON	NA
AA926	chr22	42526694	rs1065852	G	A	50.36	58.85	CYP2D6	P34S	MISSENSE	NON_SYNON	NA
UCI1804937	chr22	42522613	rs1135840	G	C	54.98	55.44	CYP2D6	T432S	MISSENSE	NON_SYNON	NA
AA960	chr22	42522613	rs1135840	G	C	44.94	55.2	CYP2D6	T432S	MISSENSE	NON_SYNON	NA
UCI1804937	chr22	42523943	rs16947	A	G	48.75	55.15	CYP2D6	C242R	MISSENSE	NON_SYNON	NA
UCI2219330	chr22	42523943	rs16947	A	G	47.83	54.82	CYP2D6	C242R	MISSENSE	NON_SYNON	NA
AA948	chr22	42522613	rs1135840	G	C	46.24	54.58	CYP2D6	T432S	MISSENSE	NON_SYNON	NA
AA1515	chr22	42523943	rs16947	A	G	49.61	54.12	CYP2D6	C242R	MISSENSE	NON_SYNON	NA
AA1204	chr22	42522613	rs1135840	G	C	49.38	53.99	CYP2D6	T432S	MISSENSE	NON_SYNON	NA
UCI1908503	chr22	42526694	rs1065852	G	A	64.81	52.97	CYP2D6	P34S	MISSENSE	NON_SYNON	NA
AA952	chr22	42522613	rs1135840	G	C	49.52	52.78	CYP2D6	T432S	MISSENSE	NON_SYNON	NA
AA1367	chr9	139391529	.	GA	G	20.96	21.41	NOTCH1	NA	NONE	FRAME_SHIF	NA
UCI2219330	chr22	42522613	rs1135840	G	C	51.69	50.76	CYP2D6	T432S	MISSENSE	NON_SYNON	NA
UCI1951813	chr22	42523528	rs1058172	C	T	48.49	50.34	CYP2D6	R311H	MISSENSE	NON_SYNON	NA
AA1307	chr22	42523943	rs16947	A	G	47.81	49.93	CYP2D6	C242R	MISSENSE	NON_SYNON	NA
AA1204	chr22	42526694	rs1065852	G	A	50.98	49.5	CYP2D6	P34S	MISSENSE	NON_SYNON	NA
AA957	chr22	42523943	rs16947	A	G	55.47	49.1	CYP2D6	C242R	MISSENSE	NON_SYNON	NA
AA943	chr22	42523943	rs16947	A	G	47.32	48.95	CYP2D6	C242R	MISSENSE	NON_SYNON	NA
AA952	chr22	42526694	rs1065852	G	A	48.47	48.9	CYP2D6	P34S	MISSENSE	NON_SYNON	NA
AA957	chr22	42526694	rs1065852	G	A	48.89	48.76	CYP2D6	P34S	MISSENSE	NON_SYNON	NA
UCI2649875	chr7	116371802	.	TG	T	21.12	21.01	MET	NA	NONE	FRAME_SHIF	NA
AA1307	chr22	42522613	rs1135840	G	C	44.56	48.16	CYP2D6	T432S	MISSENSE	NON_SYNON	NA
AA948	chr22	42523943	rs16947	A	G	49.13	48.08	CYP2D6	C242R	MISSENSE	NON_SYNON	NA
AA1077	chr22	42526694	rs1065852	G	A	51.19	47.85	CYP2D6	P34S	MISSENSE	NON_SYNON	NA
UCI1908503	chr22	42523528	rs1058172	C	T	47.83	47.85	CYP2D6	R311H	MISSENSE	NON_SYNON	NA
AA1247	chr22	42523528	rs1058172	C	T	50.24	47.84	CYP2D6	R311H	MISSENSE	NON_SYNON	NA
AA943	chr22	42522613	rs1135840	G	C	46.7	46.83	CYP2D6	T432S	MISSENSE	NON_SYNON	NA
AA1077	chr22	42523943	rs16947	A	G	50.18	46.7	CYP2D6	C242R	MISSENSE	NON_SYNON	NA
AA1222	chr22	42523943	rs16947	A	G	53.04	45.92	CYP2D6	C242R	MISSENSE	NON_SYNON	NA
UCI1951813	chr22	42522613	rs1135840	G	C	48.69	43.55	CYP2D6	T432S	MISSENSE	NON_SYNON	NA
UCI4216548	chr22	42522613	rs1135840	G	C	44.3	43.53	CYP2D6	T432S	MISSENSE	NON_SYNON	NA
AA1222	chr22	42522613	rs1135840	G	C	48.15	43.33	CYP2D6	T432S	MISSENSE	NON_SYNON	NA
UCI2076630	chr22	42523943	rs16947	A	G	46.39	43.05	CYP2D6	C242R	MISSENSE	NON_SYNON	NA
AA1025	chr22	42523528	rs1058172	C	T	32.27	42.14	CYP2D6	R311H	MISSENSE	NON_SYNON	NA
UCI2076630	chr22	42522613	rs1135840	G	C	58.98	41.69	CYP2D6	T432S	MISSENSE	NON_SYNON	NA
AA1247	chr22	42522613	rs1135840	G	C	49.4	41.33	CYP2D6	T432S	MISSENSE	NON_SYNON	NA
AA1367	chr22	42522613	rs1135840	G	C	50.73	40.72	CYP2D6	T432S	MISSENSE	NON_SYNON	NA
UCI4216548	chr22	42523943	rs16947	A	G	52.92	39.74	CYP2D6	C242R	MISSENSE	NON_SYNON	NA
AA948	chr7	117188715	rs3034796	GAAAGC	G	22.29	14.68	CFTR	NA	NONE	FRAME_SHIF	NA
AA960	chr22	42526694	rs1065852	G	A	50.98	35.29	CYP2D6	P34S	MISSENSE	NON_SYNON	NA
AA926	chr22	42523528	rs1058172	C	T	32.07	35.02	CYP2D6	R311H	MISSENSE	NON_SYNON	NA
AA957	chr22	42523528	rs1058172	C	T	31.75	34.62	CYP2D6	R311H	MISSENSE	NON_SYNON	NA
AA1025	chr22	42522613	rs1135840	G	C	42.71	34.35	CYP2D6	T432S	MISSENSE	NON_SYNON	NA
AA943	chr22	42524817	rs139779104	C	T	29.99	33.74	CYP2D6	G158E	MISSENSE	NON_SYNON	NA
AA1077	chr22	42523528	rs1058172	C	T	30.18	32.85	CYP2D6	R311H	MISSENSE	NON_SYNON	NA
UCI2224680	chr22	42522613	rs1135840	G	C	46.51	30.36	CYP2D6	T432S	MISSENSE	NON_SYNON	NA
UCI2224680	chr22	42523943	rs16947	A	G	50.52	29.59	CYP2D6	C242R	MISSENSE	NON_SYNON	NA

Table S8: List of non-silent germline variants

Sample	Chr	Cord	rsID	Ref Allele	Alt Allele	Allelic Fraction		Gene	AA change	Type	Effect	Mutation Taster Prediction
						Normal	Tumor					
AA1204	chr22	42523528	rs1058172	C	T	31.48	27.85	CYP2D6	R311H	MISSENSE	NON_SYNON	NA
UCI1821517	chr22	42522613	rs1135840	G	C	48.37	23.26	CYP2D6	T432S	MISSENSE	NON_SYNON	NA
AA1090	chr22	42526694	rs1065852	G	A	47.13	15.31	CYP2D6	P34S	MISSENSE	NON_SYNON	NA
UCI2564879	chr7	117188715	rs3034796	GAAAGC	G	22.39	17.15	CFTR	NA	NONE	FRAME_SHIF	NA
AA1090	chr22	42523528	rs1058172	C	T	33.49	10.91	CYP2D6	R311H	MISSENSE	NON_SYNON	NA
UCI2008866	chr22	42522613	rs1135840	G	C	51.51	7.63	CYP2D6	T432S	MISSENSE	NON_SYNON	NA
AA1367	chr1	97547962	.	A	G	50.98	49.64	DPYD	V944A	MISSENSE	NON_SYNON	D
UCI2008866	chr1	97770920	rs1801160	C	T	42.18	49.77	DPYD	V732I	MISSENSE	NON_SYNON	D
UCI1804937	chr1	97770920	rs1801160	C	T	48.73	48.91	DPYD	V732I	MISSENSE	NON_SYNON	D
AA952	chr1	97770920	rs1801160	C	T	48.21	47.18	DPYD	V732I	MISSENSE	NON_SYNON	D
UCI1546879	chr1	98144726	rs45589337	T	C	49.13	45.82	DPYD	K259E	MISSENSE	NON_SYNON	D
AA948	chr1	98144726	rs45589337	T	C	48.18	44.7	DPYD	K259E	MISSENSE	NON_SYNON	D
AA1025	chr1	98348885	rs1801265	G	A	53.3	53.25	DPYD	R29C	MISSENSE	NON_SYNON	None
AA1077	chr1	98348885	rs1801265	G	A	50.87	69.92	DPYD	R29C	MISSENSE	NON_SYNON	None
AA1090	chr1	98348885	rs1801265	G	A	44.09	51.46	DPYD	R29C	MISSENSE	NON_SYNON	None
AA943	chr1	98348885	rs1801265	G	A	99.67	99.85	DPYD	R29C	MISSENSE	NON_SYNON	None
AA1188	chr1	98348885	rs1801265	G	A	99.84	99.64	DPYD	R29C	MISSENSE	NON_SYNON	None
AA1204	chr1	98348885	rs1801265	G	A	99.73	99.32	DPYD	R29C	MISSENSE	NON_SYNON	None
AA1222	chr1	98348885	rs1801265	G	A	99.72	99.57	DPYD	R29C	MISSENSE	NON_SYNON	None
AA1247	chr1	98348885	rs1801265	G	A	99.82	99.9	DPYD	R29C	MISSENSE	NON_SYNON	None
AA1267	chr1	98348885	rs1801265	G	A	99.81	99.8	DPYD	R29C	MISSENSE	NON_SYNON	None
AA1277	chr1	98348885	rs1801265	G	A	99.59	98.89	DPYD	R29C	MISSENSE	NON_SYNON	None
AA1307	chr1	98348885	rs1801265	G	A	48.69	57.06	DPYD	R29C	MISSENSE	NON_SYNON	None
AA957	chr1	98348885	rs1801265	G	A	99.64	99.58	DPYD	R29C	MISSENSE	NON_SYNON	None
AA926	chr1	98348885	rs1801265	G	A	46.27	61.67	DPYD	R29C	MISSENSE	NON_SYNON	None
AA930	chr1	98348885	rs1801265	G	A	99.69	100	DPYD	R29C	MISSENSE	NON_SYNON	None
AA1106	chr1	98348885	rs1801265	G	A	46.9	41.07	DPYD	R29C	MISSENSE	NON_SYNON	None
AA952	chr1	98348885	rs1801265	G	A	99.05	98.43	DPYD	R29C	MISSENSE	NON_SYNON	None
AA1367	chr1	98348885	rs1801265	G	A	49.68	48.17	DPYD	R29C	MISSENSE	NON_SYNON	None
AA960	chr1	98348885	rs1801265	G	A	99.18	99.67	DPYD	R29C	MISSENSE	NON_SYNON	None
AA1515	chr1	98348885	rs1801265	G	A	99.68	100	DPYD	R29C	MISSENSE	NON_SYNON	None
UCI1546879	chr1	98348885	rs1801265	G	A	54.6	46.67	DPYD	R29C	MISSENSE	NON_SYNON	None
UCI1689380	chr1	98348885	rs1801265	G	A	49.26	7.82	DPYD	R29C	MISSENSE	NON_SYNON	None
UCI1804937	chr1	98348885	rs1801265	G	A	99.56	99.72	DPYD	R29C	MISSENSE	NON_SYNON	None
UCI1821517	chr1	98348885	rs1801265	G	A	99.85	99.74	DPYD	R29C	MISSENSE	NON_SYNON	None
UCI1908503	chr1	98348885	rs1801265	G	A	99.16	99.44	DPYD	R29C	MISSENSE	NON_SYNON	None
UCI1951813	chr1	98348885	rs1801265	G	A	99.36	99.46	DPYD	R29C	MISSENSE	NON_SYNON	None
UCI2008866	chr1	98348885	rs1801265	G	A	100	99.81	DPYD	R29C	MISSENSE	NON_SYNON	None
UCI2076630	chr1	98348885	rs1801265	G	A	99.74	99.63	DPYD	R29C	MISSENSE	NON_SYNON	None
UCI2219330	chr1	98348885	rs1801265	G	A	49.84	51.54	DPYD	R29C	MISSENSE	NON_SYNON	None
UCI2224680	chr1	98348885	rs1801265	G	A	99.76	99.62	DPYD	R29C	MISSENSE	NON_SYNON	None
UCI2231576	chr1	98348885	rs1801265	G	A	99.04	100	DPYD	R29C	MISSENSE	NON_SYNON	None
UCI2564879	chr1	98348885	rs1801265	G	A	99.52	99.52	DPYD	R29C	MISSENSE	NON_SYNON	None
UCI2649875	chr1	98348885	rs1801265	G	A	99.66	99.61	DPYD	R29C	MISSENSE	NON_SYNON	None
UCI3165498	chr1	98348885	rs1801265	G	A	99.54	99.55	DPYD	R29C	MISSENSE	NON_SYNON	None
UCI3564897	chr1	98348885	rs1801265	G	A	56.6	62.3	DPYD	R29C	MISSENSE	NON_SYNON	None
UCI4216548	chr1	98348885	rs1801265	G	A	42.97	34.24	DPYD	R29C	MISSENSE	NON_SYNON	None
UCI8965412	chr1	98348885	rs1801265	G	A	50	28.43	DPYD	R29C	MISSENSE	NON_SYNON	None
UCI9135402	chr1	98348885	rs1801265	G	A	99.32	99.29	DPYD	R29C	MISSENSE	NON_SYNON	None
AA1025	chr1	98165091	rs2297595	T	C	50.68	52.45	DPYD	M166V	MISSENSE	NON_SYNON	P
AA1277	chr1	97981395	rs1801159	T	C	50.7	51.41	DPYD	I543V	MISSENSE	NON_SYNON	P
AA1307	chr1	97981395	rs1801159	T	C	55.5	58	DPYD	I543V	MISSENSE	NON_SYNON	P
AA926	chr1	97981395	rs1801159	T	C	49.05	65.39	DPYD	I543V	MISSENSE	NON_SYNON	P
AA1106	chr1	98165091	rs2297595	T	C	51.31	56.62	DPYD	M166V	MISSENSE	NON_SYNON	P
AA1515	chr1	97981395	rs1801159	T	C	55.66	23.34	DPYD	I543V	MISSENSE	NON_SYNON	P
UCI1689380	chr1	97981395	rs1801159	T	C	50.67	8.63	DPYD	I543V	MISSENSE	NON_SYNON	P
UCI1821517	chr1	97981395	rs1801159	T	C	52.06	37.27	DPYD	I543V	MISSENSE	NON_SYNON	P
UCI1908503	chr1	97981395	rs1801159	T	C	53.61	51.82	DPYD	I543V	MISSENSE	NON_SYNON	P
UCI1951813	chr1	97981395	rs1801159	T	C	50.22	45.62	DPYD	I543V	MISSENSE	NON_SYNON	P
UCI2008866	chr1	97981395	rs1801159	T	C	50.47	48.61	DPYD	I543V	MISSENSE	NON_SYNON	P
UCI2076630	chr1	97981395	rs1801159	T	C	52.51	40.7	DPYD	I543V	MISSENSE	NON_SYNON	P
UCI2224680	chr1	97981395	rs1801159	T	C	49.21	51.76	DPYD	I543V	MISSENSE	NON_SYNON	P
UCI2231576	chr1	97981395	rs1801159	T	C	46.64	46.7	DPYD	I543V	MISSENSE	NON_SYNON	P
UCI2564879	chr1	97981395	rs1801159	T	C	56.11	58.89	DPYD	I543V	MISSENSE	NON_SYNON	P
UCI8965412	chr1	98165091	rs2297595	T	C	44.19	65.79	DPYD	M166V	MISSENSE	NON_SYNON	P
AA1222	chr7	55214348	rs2072454	C	T	99.76	99.94	EGFR	NA	NONE	SPLICE_SITE_ACCEPTOR	
AA1077	chr7	55229255	rs2227983	G	A	47.74	26.73	EGFR	R315K	MISSENSE	NON_SYNON	N
UCI2076630	chr7	55214348	rs2072454	C	T	99.43	99.8	EGFR	NA	NONE	SPLICE_SITE_ACCEPTOR	
UCI2564879	chr7	55214348	rs2072454	C	T	99.66	99.74	EGFR	NA	NONE	SPLICE_SITE_ACCEPTOR	
UCI2008866	chr7	55214348	rs2072454	C	T	99.83	99.63	EGFR	NA	NONE	SPLICE_SITE_ACCEPTOR	
UCI2231576	chr7	55214348	rs2072454	C	T	99.24	99.55	EGFR	NA	NONE	SPLICE_SITE_ACCEPTOR	
UCI3165498	chr7	55214348	rs2072454	C	T	99.62	99.43	EGFR	NA	NONE	SPLICE_SITE_ACCEPTOR	
AA1277	chr7	55214348	rs2072454	C	T	98.96	99.39	EGFR	NA	NONE	SPLICE_SITE_ACCEPTOR	
AA1367	chr7	55214348	rs2072454	C	T	98.96	98.71	EGFR	NA	NONE	SPLICE_SITE_ACCEPTOR	
UCI1951813	chr7	55214348	rs2072454	C	T	88.82	88.5	EGFR	NA	NONE	SPLICE_SITE_ACCEPTOR	
AA1277	chr7	55229255	rs2227983	G	A	51.62	49.69	EGFR	R315K	MISSENSE	NON_SYNON	N
UCI2649875	chr7	55214348	rs2072454	C	T	50.78	58.97	EGFR	NA	NONE	SPLICE_SITE_ACCEPTOR	
UCI1546879	chr7	55211102	.	T	A	51.88	58.71	EGFR	N115K	MISSENSE	NON_SYNON	D
UCI1546879	chr7	55214348	rs2072454	C	T	46.21	57.54	EGFR	NA	NONE	SPLICE_SITE_ACCEPTOR	
AA1204	chr7	55214348	rs2072454	C	T	50.15	56.03	EGFR	NA	NONE	SPLICE_SITE_ACCEPTOR	
UCI1908503	chr7	55214348	rs2072454	C	T	39.01	55.59	EGFR	NA	NONE	SPLICE_SITE_ACCEPTOR	
AA1106	chr7	55214348	rs2072454	C	T	48.9	53.49	EGFR	NA	NONE	SPLICE_SITE_ACCEPTOR	
AA1188	chr7	55214348	rs2072454	C	T	49.73	53.42	EGFR	NA	NONE	SPLICE_SITE_ACCEPTOR	
AA952	chr7	55229255	rs2227983	G	A	54.89	40.55	EGFR	R315K	MISSENSE	NON_SYNON	N
UCI8965412	chr7	55214348	rs2072454	C	T	51.71	52.08	EGFR	NA	NONE	SPLICE_SITE_ACCEPTOR	
AA1367	chr7	55229255	rs2227983	G	A	49.66	47.64	EGFR	R315K	MISSENSE	NON_SYNON	N
AA943	chr7	55214348	rs2072454	C	T	49.79	50.81	EGFR	NA	NONE	SPLICE_SITE_ACCEPTOR	
AA960	chr7	55229255	rs2227983	G	A	50.73	51.64	EGFR	R315K	MISSENSE	NON_SYNON	N
UCI1546879	chr7	55229255	rs2227983	G	A	38.63	55.89	EGFR	R315K	MISSENSE	NON_SYNON	N
AA1025	chr7	55214348	rs2072454	C	T	52.34	49.34	EGFR	NA	NONE	SPLICE_SITE_ACCEPTOR	
UCI2224680	chr7	55214348	rs2072454	C	T	49.53	49.17	EGFR	NA	NONE	SPLICE_SITE_ACCEPTOR	
AA948	chr7	55214348	rs2072454	C	T	45.64	48.17	EGFR	NA	NONE	SPLICE_SITE_ACCEPTOR	
UCI1804937	chr7	55229255	rs2227983	G	A	48.2	44.07	EGFR	R315K	MISSENSE	NON_SYNON	N
UCI1821517	chr7	55229255	rs2227983	G	A	97.35	96.5	EGFR	R315K	MISSENSE	NON_SYNON	N
UCI2219330	chr7	55214348	rs2072454	C	T	47.07	46.7	EGFR	NA	NONE	SPLICE_SITE_ACCEPTOR	
UCI1951813	chr7	55229255	rs2227983	G	A	48.27	47.56	EGFR	R315K	MISSENSE	NON_SYNON	N
AA930	chr7	55214348	rs2072454	C	T	49.59	45.55	EGFR	NA	NONE	SPLICE_SITE_ACCEPTOR	
UCI1804937	chr7	55223641	.	T	G	45.2	45.1	EGFR	NA	NONE	SPLICE_SITE_	NA
AA957	chr7	55214348	rs2072454	C	T	45.85	43.73	EGFR	NA	NONE	SPLICE_SITE_ACCEPTOR	
AA1247	chr7	55214348	rs2072454	C	T	51.16	43.64	EGFR	NA	NONE	SPLICE_SITE_ACCEPTOR	

Table S8: List of non-silent germline variants

Sample	Chr	Cord	rsID	Ref Allele	Alt Allele	Allelic Fraction		Gene	AA change	Type	Effect	Mutation Taster Prediction
						Normal	Tumor					
UCI2076630	chr7	55229255	rs2227983	G	A	57.79	58.63	EGFR	R315K	MISSENSE	NON_SYNON	N
UCI1804937	chr7	55214348	rs2072454	C	T	46.47	43.15	EGFR	NA	NONE	SPLICE_SITE_ACCEPTOR	
AA952	chr7	55214348	rs2072454	C	T	56.13	42.31	EGFR	NA	NONE	SPLICE_SITE_ACCEPTOR	
UCI2219330	chr7	55229255	rs2227983	G	A	53.58	53.89	EGFR	R315K	MISSENSE	NON_SYNON	N
UCI1804937	chr7	140481383	.	CT	C	23.36	25.83	BRAF	NA	NONE	FRAME_SHIF	NA
UCI1804937	chr7	55223636	.	A	C	25.69	29.4	EGFR	K129Q	MISSENSE	NON_SYNON	D
UCI1689380	chr7	55214348	rs2072454	C	T	47.24	29.24	EGFR	NA	NONE	SPLICE_SITE_ACCEPTOR	
UCI1821517	chr7	55214348	rs2072454	C	T	42.77	27.13	EGFR	NA	NONE	SPLICE_SITE_ACCEPTOR	
UCI2649875	chr7	55229255	rs2227983	G	A	47.93	63.59	EGFR	R315K	MISSENSE	NON_SYNON	N
UCI3564897	chr7	55229255	rs2227983	G	A	47.49	37.08	EGFR	R315K	MISSENSE	NON_SYNON	N
UCI4216548	chr7	55229255	rs2227983	G	A	48.25	92.38	EGFR	R315K	MISSENSE	NON_SYNON	N
UCI8965412	chr7	55229255	rs2227983	G	A	49.66	46.37	EGFR	R315K	MISSENSE	NON_SYNON	N
UCI9135402	chr7	55238227	rs10258568	C	T	48.74	69.88	EGFR	S703F	MISSENSE	NON_SYNON	N
AA1025	chr17	37884037	rs61552325	C	G	48.64	35.13	ERBB2	P1140A	MISSENSE	NON_SYNON	P
AA1077	chr17	37884037	rs61552325	C	G	58.22	22.31	ERBB2	P1140A	MISSENSE	NON_SYNON	P
AA1090	chr17	37884037	rs61552325	C	G	99.83	99.63	ERBB2	P1140A	MISSENSE	NON_SYNON	P
AA943	chr17	37884037	rs61552325	C	G	57.08	53.89	ERBB2	P1140A	MISSENSE	NON_SYNON	P
AA1188	chr17	37884037	rs61552325	C	G	99.85	99.94	ERBB2	P1140A	MISSENSE	NON_SYNON	P
UCI1821517	chr17	37879588	rs1136201	A	G	97.02	97.4	ERBB2	I379V	MISSENSE	NON_SYNON	D
UCI8965412	chr17	37879588	rs1136201	A	G	52.19	95.5	ERBB2	I379V	MISSENSE	NON_SYNON	D
AA1247	chr17	37855834	rs4252596	C	A	45.24	94.81	ERBB2	P8T	MISSENSE	NON_SYNON	NA
UCI2649875	chr17	37855834	rs4252596	C	A	95.49	94.34	ERBB2	P8T	MISSENSE	NON_SYNON	NA
AA1204	chr17	37884037	rs61552325	C	G	46.8	15.08	ERBB2	P1140A	MISSENSE	NON_SYNON	P
AA1222	chr17	37879588	rs1136201	A	G	51.36	92.33	ERBB2	I379V	MISSENSE	NON_SYNON	D
AA1222	chr17	37884037	rs61552325	C	G	99.67	99.83	ERBB2	P1140A	MISSENSE	NON_SYNON	P
UCI3165498	chr17	37855834	rs4252596	C	A	51.28	86.35	ERBB2	P8T	MISSENSE	NON_SYNON	NA
AA1247	chr17	37884037	rs61552325	C	G	51.93	96.2	ERBB2	P1140A	MISSENSE	NON_SYNON	P
AA960	chr17	37879588	rs1136201	A	G	52.54	78.4	ERBB2	I379V	MISSENSE	NON_SYNON	D
AA1267	chr17	37872589	.	C	T	23.75	2.45	ERBB2	R241*	NONSENSE	STOP_GAINE	A
AA1267	chr17	37884037	rs61552325	C	G	99.91	99.74	ERBB2	P1140A	MISSENSE	NON_SYNON	P
AA1277	chr17	37884037	rs61552325	C	G	52.24	95.93	ERBB2	P1140A	MISSENSE	NON_SYNON	P
AA1106	chr17	37879588	rs1136201	A	G	51.63	58.36	ERBB2	I379V	MISSENSE	NON_SYNON	D
UCI1546879	chr17	37879588	rs1136201	A	G	50.6	58.31	ERBB2	I379V	MISSENSE	NON_SYNON	D
AA926	chr17	37884037	rs61552325	C	G	99.94	99.52	ERBB2	P1140A	MISSENSE	NON_SYNON	P
AA1515	chr17	37855834	rs4252596	C	A	53.28	56.17	ERBB2	P8T	MISSENSE	NON_SYNON	NA
AA930	chr17	37884037	rs61552325	C	G	50.29	47.57	ERBB2	P1140A	MISSENSE	NON_SYNON	P
AA930	chr17	37884070	.	G	A	49.96	47.38	ERBB2	V1151I	MISSENSE	NON_SYNON	N
AA1106	chr17	37884037	rs61552325	C	G	47.33	61.23	ERBB2	P1140A	MISSENSE	NON_SYNON	P
AA948	chr17	37884037	rs61552325	C	G	50.62	51.51	ERBB2	P1140A	MISSENSE	NON_SYNON	P
UCI1804937	chr17	37855834	rs4252596	C	A	41.34	52.48	ERBB2	P8T	MISSENSE	NON_SYNON	NA
AA952	chr17	37884037	rs61552325	C	G	99.79	98.66	ERBB2	P1140A	MISSENSE	NON_SYNON	P
AA926	chr17	37855834	rs4252596	C	A	51.02	52.25	ERBB2	P8T	MISSENSE	NON_SYNON	NA
AA1267	chr17	37855834	rs4252596	C	A	46.64	51.83	ERBB2	P8T	MISSENSE	NON_SYNON	NA
AA1367	chr17	37884037	rs61552325	C	G	99.82	99.61	ERBB2	P1140A	MISSENSE	NON_SYNON	P
AA960	chr17	37884037	rs61552325	C	G	49.07	83.65	ERBB2	P1140A	MISSENSE	NON_SYNON	P
AA1188	chr17	37879588	rs1136201	A	G	48.97	50.3	ERBB2	I379V	MISSENSE	NON_SYNON	D
AA1515	chr17	37884037	rs61552325	C	G	99.68	99.64	ERBB2	P1140A	MISSENSE	NON_SYNON	P
AA1267	chr17	37879588	rs1136201	A	G	48.02	49.39	ERBB2	I379V	MISSENSE	NON_SYNON	D
UCI1546879	chr17	37884037	rs61552325	C	G	99.9	99.75	ERBB2	P1140A	MISSENSE	NON_SYNON	P
UCI1689380	chr17	37884037	rs61552325	C	G	50.64	44.94	ERBB2	P1140A	MISSENSE	NON_SYNON	P
UCI9135402	chr17	37884176	rs55943169	C	A	46.3	48.18	ERBB2	A1186D	MISSENSE	NON_SYNON	D
AA1188	chr17	37855834	rs4252596	C	A	50.81	48.08	ERBB2	P8T	MISSENSE	NON_SYNON	NA
UCI1804937	chr17	37884037	rs61552325	C	G	47.36	63.41	ERBB2	P1140A	MISSENSE	NON_SYNON	P
UCI1821517	chr17	37884037	rs61552325	C	G	54.64	27.07	ERBB2	P1140A	MISSENSE	NON_SYNON	P
AA930	chr17	37855834	rs4252596	C	A	46.46	46.74	ERBB2	P8T	MISSENSE	NON_SYNON	NA
UCI9135402	chr17	37879588	rs1136201	A	G	54.95	46.14	ERBB2	I379V	MISSENSE	NON_SYNON	D
AA957	chr17	37879588	rs1136201	A	G	54.25	46.1	ERBB2	I379V	MISSENSE	NON_SYNON	D
UCI1951813	chr17	37884037	rs61552325	C	G	53.69	53.72	ERBB2	P1140A	MISSENSE	NON_SYNON	P
UCI2231576	chr17	37855834	rs4252596	C	A	44.96	45.28	ERBB2	P8T	MISSENSE	NON_SYNON	NA
AA948	chr17	37855834	rs4252596	C	A	44.04	44.94	ERBB2	P8T	MISSENSE	NON_SYNON	NA
UCI2008866	chr17	37884037	rs61552325	C	G	99.87	99.71	ERBB2	P1140A	MISSENSE	NON_SYNON	P
UCI2076630	chr17	37855834	rs4252596	C	A	41.68	43.29	ERBB2	P8T	MISSENSE	NON_SYNON	NA
UCI2076630	chr17	37884037	rs61552325	C	G	99.79	99.71	ERBB2	P1140A	MISSENSE	NON_SYNON	P
AA943	chr17	37879588	rs1136201	A	G	48.67	41.78	ERBB2	I379V	MISSENSE	NON_SYNON	D
UCI2219330	chr17	37884037	rs61552325	C	G	52.16	51.99	ERBB2	P1140A	MISSENSE	NON_SYNON	P
UCI1689380	chr17	37879588	rs1136201	A	G	52.07	40.2	ERBB2	I379V	MISSENSE	NON_SYNON	D
UCI1546879	chr17	37855834	rs4252596	C	A	48.24	38.62	ERBB2	P8T	MISSENSE	NON_SYNON	NA
UCI2224680	chr17	37884037	rs61552325	C	G	99.64	99.5	ERBB2	P1140A	MISSENSE	NON_SYNON	P
AA1025	chr17	37855834	rs4252596	C	A	53.14	35.16	ERBB2	P8T	MISSENSE	NON_SYNON	NA
UCI2231576	chr17	37884037	rs61552325	C	G	57.2	49.22	ERBB2	P1140A	MISSENSE	NON_SYNON	P
UCI1821517	chr17	37884176	rs55943169	C	A	42.72	25.95	ERBB2	A1186D	MISSENSE	NON_SYNON	D
AA1077	chr17	37879588	rs1136201	A	G	55.01	23.24	ERBB2	I379V	MISSENSE	NON_SYNON	D
UCI2649875	chr17	37884037	rs61552325	C	G	98.01	99.02	ERBB2	P1140A	MISSENSE	NON_SYNON	P
AA1307	chr17	37879588	rs1136201	A	G	46.85	19.79	ERBB2	I379V	MISSENSE	NON_SYNON	D
UCI3165498	chr17	37884037	rs61552325	C	G	99.87	99.86	ERBB2	P1140A	MISSENSE	NON_SYNON	P
UCI3564897	chr17	37884037	rs61552325	C	G	99.14	100	ERBB2	P1140A	MISSENSE	NON_SYNON	P
AA1090	chr17	37879588	rs1136201	A	G	48.91	13.64	ERBB2	I379V	MISSENSE	NON_SYNON	D
UCI8965412	chr17	37884037	rs61552325	C	G	51.25	94.65	ERBB2	P1140A	MISSENSE	NON_SYNON	P
UCI9135402	chr17	37884037	rs61552325	C	G	49.81	47.18	ERBB2	P1140A	MISSENSE	NON_SYNON	P
AA1222	chr17	37855834	rs4252596	C	A	47.87	7.86	ERBB2	P8T	MISSENSE	NON_SYNON	NA
UCI1689380	chr12	56494998	rs773123	A	T	99.28	99.33	ERBB3	S1060C	MISSENSE	NON_SYNON	D
UCI2008866	chr12	56494998	rs773123	A	T	53.41	89.18	ERBB3	S1060C	MISSENSE	NON_SYNON	D
UCI3564897	chr12	56494998	rs773123	A	T	46.53	88.63	ERBB3	S1060C	MISSENSE	NON_SYNON	D
UCI3165498	chr12	56494998	rs773123	A	T	50.54	64.31	ERBB3	S1060C	MISSENSE	NON_SYNON	D
AA957	chr12	56495339	rs55699040	C	A	46.98	53.19	ERBB3	L1118I	MISSENSE	NON_SYNON	D
UCI2649875	chr12	56494998	rs773123	A	T	53.88	50.94	ERBB3	S1060C	MISSENSE	NON_SYNON	D
UCI2231576	chr12	56494998	rs773123	A	T	45.66	50.59	ERBB3	S1060C	MISSENSE	NON_SYNON	D
AA1267	chr12	56494998	rs773123	A	T	52.05	50.09	ERBB3	S1060C	MISSENSE	NON_SYNON	D
UCI2219330	chr12	56493677	rs56259600	A	G	50.79	47.27	ERBB3	K118R	MISSENSE	NON_SYNON	D
UCI1804937	chr12	56494998	rs773123	A	T	46.09	47.14	ERBB3	S1060C	MISSENSE	NON_SYNON	D
AA1025	chr12	56494998	rs773123	A	T	52.82	44.5	ERBB3	S1060C	MISSENSE	NON_SYNON	D
AA1106	chr12	56494998	rs773123	A	T	17.66	38.69	ERBB3	S1060C	MISSENSE	NON_SYNON	D
AA1204	chr12	56494998	rs773123	A	T	52.5	31.69	ERBB3	S1060C	MISSENSE	NON_SYNON	D
AA1247	chr8	38275808	.	C	A	46.39	82.95	FGFR1	M365I	MISSENSE	NON_SYNON	D
UCI2076630	chr8	38285913	rs138489552	G	GTCA	48.57	75.33	FGFR1	D125VN	NONE	CODON_CHA	NA
UCI2564879	chr8	38287238	rs140382957	G	A	54.75	55.7	FGFR1	S107L	MISSENSE	NON_SYNON	D
UCI2219330	chr7	117188715	rs3034796	GAAAGC	G	23.48	16.42	CFTR	NA	NONE	FRAME_SHIF	NA
UCI1546879	chr8	38282083	.	C	T	15.33	2.22	FGFR1	E134K	MISSENSE	NON_SYNON	D
AA957	chr10	123260337	.	CA	C	43.25	43.76	FGFR2	NA	NONE	SPLICE_SITE_	NA
UCI2224680	chr10	123310871	rs755793	A	G	45.05	31.04	FGFR2	M186T	MISSENSE	NON_SYNON	P

Table S8: List of non-silent germline variants

Sample	Chr	Cord	rsID	Ref Allele	Alt Allele	Allelic Fraction		Gene	AA change	Type	Effect	Mutation Taster Prediction
						Normal	Tumor					
UCI2564879	chr10	123310871	rs755793	A	G	48.26	57.51	FGFR2	M186T	MISSENSE	NON_SYNON	P
AA1267	chr10	8100506	rs143627754	C	G	55.42	45.93	GATA3	D160E	MISSENSE	NON_SYNON	D
AA1025	chr9	5126715	rs142269166	A	G	45.85	63.61	JAK2	N1108S	MISSENSE	NON_SYNON	D
AA943	chr9	5126343	rs41316003	G	A	50.45	50.54	JAK2	R1063H	MISSENSE	NON_SYNON	D
UCI1821517	chr9	5072561	rs139504737	G	A	50.59	26.71	JAK2	G422S	MISSENSE	NON_SYNON	D
AA943	chr19	17945696	rs3213409	C	T	48.03	48.45	JAK3	V722I	MISSENSE	NON_SYNON	None
AA1267	chr19	17943490	.	G	A	53.27	53.54	JAK3	R840C	MISSENSE	NON_SYNON	None
AA1277	chr19	17953321	.	C	T	50.84	31.16	JAK3	R222H	MISSENSE	NON_SYNON	None
AA1090	chr7	116364823	rs34822187	CA	C	99.82	100	MET	NA	NONE	SPLICE_SITE	NA
AA960	chr7	116364823	rs34822187	CA	C	99.7	100	MET	NA	NONE	SPLICE_SITE	NA
AA1277	chr7	116364823	rs34822187	CA	C	99.91	99.86	MET	NA	NONE	SPLICE_SITE	NA
AA1106	chr7	116364823	rs34822187	CA	C	99.84	99.81	MET	NA	NONE	SPLICE_SITE	NA
UCI3165498	chr7	116364823	rs34822187	CA	C	100	99.69	MET	NA	NONE	SPLICE_SITE	NA
UCI1689380	chr7	116364823	rs34822187	CA	C	99.67	99.68	MET	NA	NONE	SPLICE_SITE	NA
AA1077	chr7	116335811	rs80153920	A	T	45.71	82.03	MET	M1L	MISSENSE	NON_SYNON	NA
UCI1821517	chr7	116335811	rs80153920	A	T	53.76	76.42	MET	M1L	MISSENSE	NON_SYNON	NA
UCI8965412	chr7	116335811	rs80153920	A	T	50.93	68.94	MET	M1L	MISSENSE	NON_SYNON	NA
AA1307	chr7	116339642	rs55985569	G	T	43.12	63.01	MET	E168D	MISSENSE	NON_SYNON	N
AA926	chr7	116339600	.	A	G	49.98	63.77	MET	I154M	MISSENSE	NON_SYNON	D
AA1204	chr7	116364823	rs34822187	CA	C	47.2	60.56	MET	NA	NONE	SPLICE_SITE	NA
AA1515	chr7	116364823	rs34822187	CA	C	53.63	58.35	MET	NA	NONE	SPLICE_SITE	NA
UCI1546879	chr7	116364823	rs34822187	CA	C	47.17	56.82	MET	NA	NONE	SPLICE_SITE	NA
UCI1908503	chr7	116364823	rs34822187	CA	C	51.3	54.44	MET	NA	NONE	SPLICE_SITE	NA
AA957	chr7	116364823	rs34822187	CA	C	50.35	54.24	MET	NA	NONE	SPLICE_SITE	NA
UCI1951813	chr7	116364823	rs34822187	CA	C	48.31	52.53	MET	NA	NONE	SPLICE_SITE	NA
UCI2224680	chr7	116364823	rs34822187	CA	C	54.31	51.18	MET	NA	NONE	SPLICE_SITE	NA
AA1188	chr7	116364823	rs34822187	CA	C	44.72	50.76	MET	NA	NONE	SPLICE_SITE	NA
AA943	chr7	116364823	rs34822187	CA	C	48.73	50.49	MET	NA	NONE	SPLICE_SITE	NA
AA948	chr7	116364823	rs34822187	CA	C	52.62	50.22	MET	NA	NONE	SPLICE_SITE	NA
UCI2231576	chr7	116364823	rs34822187	CA	C	50.91	50.15	MET	NA	NONE	SPLICE_SITE	NA
UCI2219330	chr7	116411990	rs56391007	C	T	54.2	48.74	MET	T1010I	MISSENSE	NON_SYNON	D
AA1367	chr7	116436122	.	G	C	47.29	48.61	MET	D1373H	MISSENSE	NON_SYNON	D
AA930	chr7	116364823	rs34822187	CA	C	48.55	48.39	MET	NA	NONE	SPLICE_SITE	NA
AA1367	chr7	116364823	rs34822187	CA	C	54.35	46.87	MET	NA	NONE	SPLICE_SITE	NA
UCI2219330	chr7	116364823	rs34822187	CA	C	62.82	45.96	MET	NA	NONE	SPLICE_SITE	NA
UCI4216548	chr7	116364823	rs34822187	CA	C	47.51	45.77	MET	NA	NONE	SPLICE_SITE	NA
UCI1804937	chr7	116340262	rs33917957	A	G	48.64	44.95	MET	N375S	MISSENSE	NON_SYNON	D
UCI2224680	chr7	116335811	rs80153920	A	T	52.77	44.75	MET	M1L	MISSENSE	NON_SYNON	NA
AA1025	chr7	116364823	rs34822187	CA	C	50.61	41.75	MET	NA	NONE	SPLICE_SITE	NA
AA1307	chr7	116364823	rs34822187	CA	C	53.04	39.38	MET	NA	NONE	SPLICE_SITE	NA
UCI2649875	chr7	116335811	rs80153920	A	T	49.57	39.05	MET	M1L	MISSENSE	NON_SYNON	NA
UCI2564879	chr7	116364823	rs34822187	CA	C	49.12	38.22	MET	NA	NONE	SPLICE_SITE	NA
AA926	chr7	116364823	rs34822187	CA	C	54.9	36.06	MET	NA	NONE	SPLICE_SITE	NA
AA1247	chr7	116364823	rs34822187	CA	C	55.77	34.4	MET	NA	NONE	SPLICE_SITE	NA
UCI8965412	chr7	116364823	rs34822187	CA	C	47.46	30.65	MET	NA	NONE	SPLICE_SITE	NA
UCI1951813	chr7	117188715	rs3034796	GAAAGC	G	26.08	20.38	CFTR	NA	NONE	FRAME_SHIF	NA
UCI1821517	chr7	116364823	rs34822187	CA	C	45.87	18.78	MET	NA	NONE	SPLICE_SITE	NA
AA1077	chr7	116364823	rs34822187	CA	C	49.59	17.71	MET	NA	NONE	SPLICE_SITE	NA
AA1025	chr3	37053568	rs1799977	A	G	48.58	47.59	MLH1	I121V	MISSENSE	NON_SYNON	P
AA1090	chr3	37053568	rs1799977	A	G	47.8	49.69	MLH1	I121V	MISSENSE	NON_SYNON	P
AA1188	chr3	37053568	rs1799977	A	G	50.06	49.05	MLH1	I121V	MISSENSE	NON_SYNON	P
AA1204	chr3	37053568	rs1799977	A	G	54.18	53.05	MLH1	I121V	MISSENSE	NON_SYNON	P
AA1267	chr3	37053568	rs1799977	A	G	45.84	47.46	MLH1	I121V	MISSENSE	NON_SYNON	P
AA1307	chr3	37053568	rs1799977	A	G	54.39	40.77	MLH1	I121V	MISSENSE	NON_SYNON	P
AA926	chr3	37053568	rs1799977	A	G	51.54	42.17	MLH1	I121V	MISSENSE	NON_SYNON	P
AA1106	chr3	37053568	rs1799977	A	G	53.29	56.87	MLH1	I121V	MISSENSE	NON_SYNON	P
AA948	chr3	37053568	rs1799977	A	G	45.2	50.27	MLH1	I121V	MISSENSE	NON_SYNON	P
AA952	chr3	37053568	rs1799977	A	G	99.67	98.46	MLH1	I121V	MISSENSE	NON_SYNON	P
AA960	chr3	37053568	rs1799977	A	G	59.42	48.51	MLH1	I121V	MISSENSE	NON_SYNON	P
AA1515	chr3	37053568	rs1799977	A	G	38.87	41.96	MLH1	I121V	MISSENSE	NON_SYNON	P
UCI1689380	chr3	37053568	rs1799977	A	G	99.72	99.46	MLH1	I121V	MISSENSE	NON_SYNON	P
UCI1908503	chr3	37053568	rs1799977	A	G	99.78	99.32	MLH1	I121V	MISSENSE	NON_SYNON	P
UCI1951813	chr3	37053568	rs1799977	A	G	48.8	52.74	MLH1	I121V	MISSENSE	NON_SYNON	P
UCI2008866	chr3	37053568	rs1799977	A	G	51.78	62.92	MLH1	I121V	MISSENSE	NON_SYNON	P
UCI2076630	chr3	37053568	rs1799977	A	G	99.76	98.94	MLH1	I121V	MISSENSE	NON_SYNON	P
UCI2219330	chr3	37053568	rs1799977	A	G	52.72	45.46	MLH1	I121V	MISSENSE	NON_SYNON	P
UCI2224680	chr3	37053568	rs1799977	A	G	53.73	62.69	MLH1	I121V	MISSENSE	NON_SYNON	P
UCI2649875	chr3	37053568	rs1799977	A	G	41.73	46.78	MLH1	I121V	MISSENSE	NON_SYNON	P
AA930	chr7	55266424	.	GA	G	39.25	38.46	EGFR	NA	NONE	FRAME_SHIF	NA
UCI4216548	chr3	37053568	rs1799977	A	G	59.31	5.83	MLH1	I121V	MISSENSE	NON_SYNON	P
UCI8965412	chr3	37053568	rs1799977	A	G	48.51	43.51	MLH1	I121V	MISSENSE	NON_SYNON	P
UCI2008866	chr2	47739551	rs2303424	A	G	100	99.8	MSH2	Q915R	MISSENSE	NON_SYNON	NA
AA1367	chr2	47739551	rs2303424	A	G	99.78	99.77	MSH2	Q915R	MISSENSE	NON_SYNON	NA
AA957	chr2	47739551	rs2303424	A	G	99.79	99.76	MSH2	Q915R	MISSENSE	NON_SYNON	NA
AA1090	chr2	47739551	rs2303424	A	G	100	99.75	MSH2	Q915R	MISSENSE	NON_SYNON	NA
UCI2564879	chr2	47739551	rs2303424	A	G	99.7	99.6	MSH2	Q915R	MISSENSE	NON_SYNON	NA
UCI2008866	chr2	47643457	rs4987188	G	A	47.73	92.67	MSH2	G108D	MISSENSE	NON_SYNON	D
UCI4216548	chr2	47739551	rs2303424	A	G	39.23	89.66	MSH2	Q915R	MISSENSE	NON_SYNON	NA
AA960	chr2	47739551	rs2303424	A	G	48.48	68.14	MSH2	Q915R		NON_SYNON	NA
UCI1689380	chr2	47739551	rs2303424	A	G	53.65	65.47	MSH2	Q915R	MISSENSE	NON_SYNON	NA
UCI2224680	chr2	47739551	rs2303424	A	G	42.5	57.51	MSH2	Q915R	MISSENSE	NON_SYNON	NA
UCI1804937	chr2	47739551	rs2303424	A	G	45.67	56.44	MSH2	Q915R	MISSENSE	NON_SYNON	NA
AA1222	chr2	47739551	rs2303424	A	G	58	54.4	MSH2	Q915R	MISSENSE	NON_SYNON	NA
UCI9135402	chr2	47739533	rs116117580	G	A	52.52	52.37	MSH2	R909Q	MISSENSE	NON_SYNON	NA
AA943	chr2	47739551	rs2303424	A	G	52.21	50.81	MSH2	Q915R	MISSENSE	NON_SYNON	NA
AA1090	chr2	47643457	rs4987188	G	A	49.97	50.33	MSH2	G108D	MISSENSE	NON_SYNON	D
AA1204	chr2	47739551	rs2303424	A	G	48.19	50.18	MSH2	Q915R	MISSENSE	NON_SYNON	NA
UCI1821517	chr2	47739551	rs2303424	A	G	52.99	50.07	MSH2	Q915R	MISSENSE	NON_SYNON	NA
AA1367	chr2	47656972	rs17224367	C	T	48.51	48.42	MSH2	L176F	MISSENSE	NON_SYNON	D
AA926	chr2	47739551	rs2303424	A	G	49.53	47.98	MSH2	Q915R	MISSENSE	NON_SYNON	NA
UCI2231576	chr2	47635690	.	A	G	52.55	46.97	MSH2	I7V	MISSENSE	NON_SYNON	D
UCI2649875	chr2	47739551	rs2303424	A	G	55.36	46.31	MSH2	Q915R	MISSENSE	NON_SYNON	NA
UCI1951813	chr2	47739551	rs2303424	A	G	53.3	46.27	MSH2	Q915R	MISSENSE	NON_SYNON	NA
UCI1546879	chr2	47739533	rs116117580	G	A	46.58	42.3	MSH2	R909Q	MISSENSE	NON_SYNON	NA
UCI3564897	chr2	47637301	rs63750124	T	G	49.04	48.36	MSH2	I145M	MISSENSE	NON_SYNON	N
AA1025	chr2	48010488	rs1042821	G	A	47.32	40.53	MSH6	G39E	MISSENSE	NON_SYNON	N
AA1204	chr2	48010488	rs1042821	G	A	49.11	46.97	MSH6	G39E	MISSENSE	NON_SYNON	N
AA1267	chr2	48010488	rs1042821	G	A	50.47	53.06	MSH6	G39E	MISSENSE	NON_SYNON	N
AA1277	chr2	48010488	rs1042821	G	A	51.36	47.75	MSH6	G39E	MISSENSE	NON_SYNON	N
AA1307	chr2	48010488	rs1042821	G	A	98.83	98.76	MSH6	G39E	MISSENSE	NON_SYNON	N

Table S8: List of non-silent germline variants

Sample	Chr	Cord	rsID	Ref Allele	Alt Allele	Allelic Fraction		Gene	AA change	Type	Effect	Mutation Taster Prediction
						Normal	Tumor					
AA930	chr2	48010488	rs1042821	G	A	49.16	49.35	MSH6	G39E	MISSENSE	NON_SYNON	N
AA1106	chr2	48010488	rs1042821	G	A	48.88	49.94	MSH6	G39E	MISSENSE	NON_SYNON	N
UCI2219330	chr2	48026648	rs63751005	T	C	54.02	52.44	MSH6	V207A	MISSENSE	NON_SYNON	D
UCI9135402	chr2	48018236	rs3211299	G	T	49.44	49.25	MSH6	S142I	MISSENSE	NON_SYNON	D
AA1204	chr2	48018236	rs3211299	G	T	48.46	47.02	MSH6	S142I	MISSENSE	NON_SYNON	D
UCI1908503	chr2	48010488	rs1042821	G	A	47.68	45.73	MSH6	G39E	MISSENSE	NON_SYNON	N
UCI3564897	chr2	48027755	rs2020912	T	C	52.14	46.15	MSH6	V576A	MISSENSE	NON_SYNON	D
UCI1951813	chr2	48010488	rs1042821	G	A	50.88	45.49	MSH6	G39E	MISSENSE	NON_SYNON	N
AA1025	chr2	48025785	rs41557217	A	C	48.88	45.19	MSH6	E122D	MISSENSE	NON_SYNON	D
UCI2219330	chr2	48010488	rs1042821	G	A	49.94	50.04	MSH6	G39E	MISSENSE	NON_SYNON	N
UCI2564879	chr2	48010488	rs1042821	G	A	45.93	38.52	MSH6	G39E	MISSENSE	NON_SYNON	N
UCI3564897	chr2	48010488	rs1042821	G	A	98.75	98.85	MSH6	G39E	MISSENSE	NON_SYNON	N
UCI8965412	chr2	48010488	rs1042821	G	A	43.39	43.02	MSH6	G39E	MISSENSE	NON_SYNON	N
AA1090	chr9	139401233	rs61751543	C	T	99.61	99.8	NOTCH1	R1279H	MISSENSE	NON_SYNON	D
AA1267	chr9	139400219	rs61751542	G	A	47.25	50.16	NOTCH1	P1377S	MISSENSE	NON_SYNON	N
AA1307	chr9	139400219	rs61751542	G	A	45.34	51.8	NOTCH1	P1377S	MISSENSE	NON_SYNON	N
UCI1689380	chr9	139407858	.	C	T	49.8	61.97	NOTCH1	R780Q	MISSENSE	NON_SYNON	D
UCI1546879	chr9	139400219	rs61751542	G	A	50.26	39.83	NOTCH1	P1377S	MISSENSE	NON_SYNON	N
UCI2231576	chr9	139399320	rs76371972	C	T	46.27	48.66	NOTCH1	R1608H	MISSENSE	NON_SYNON	D
UCI2224680	chr9	139391338	rs61751489	C	T	47.32	55.38	NOTCH1	V2285I	MISSENSE	NON_SYNON	N
UCI2564879	chr9	139391219	.	G	T	52.4	59.37	NOTCH1	N2324K	MISSENSE	NON_SYNON	None
UCI1908503	chr2	29519780	.	CA	C	39.49	39.08	ALK	NA	NONE	FRAME_SHIF	NA
UCI1951813	chr22	42524175	rs5030656	CCTT	C	42.41	36.7	CYP2D6	K227-	NONE	CODON_DEL	NA
UCI1908503	chr2	29451759	.	CT	C	43.93	42.01	ALK	NA	NONE	FRAME_SHIF	NA
AA1204	chr2	29451759	.	CT	C	46	46.83	ALK	NA	NONE	FRAME_SHIF	NA
AA1025	chr2	29451759	.	CT	C	48.54	48.36	ALK	NA	NONE	FRAME_SHIF	NA
AA1077	chr16	23646191	rs152451	T	C	47.01	51.74	PALB2	Q559R	MISSENSE	NON_SYNON	N
AA1090	chr16	23646857	rs45494092	A	G	51.56	50.8	PALB2	L337S	MISSENSE	NON_SYNON	N
AA1188	chr16	23646857	rs45494092	A	G	50.23	45.98	PALB2	L337S	MISSENSE	NON_SYNON	N
AA1204	chr16	23646191	rs152451	T	C	46.88	48.56	PALB2	Q559R	MISSENSE	NON_SYNON	N
AA1277	chr16	23646191	rs152451	T	C	58.07	63.29	PALB2	Q559R	MISSENSE	NON_SYNON	N
AA1307	chr16	23646191	rs152451	T	C	48.98	35.78	PALB2	Q559R	MISSENSE	NON_SYNON	N
UCI2231576	chr16	23634293	rs45551636	C	T	50.11	54.81	PALB2	G998E	MISSENSE	NON_SYNON	D
AA1277	chr17	41243479	rs80357508	CTTGA	C	49.14	94.57	BRCA1	NA	NONE	FRAME_SHIF	NA
UCI1908503	chr16	23635370	rs45624036	C	T	33.05	59.23	PALB2	V932M	MISSENSE	NON_SYNON	N
UCI2008866	chr16	23646191	rs152451	T	C	99.66	99.88	PALB2	Q559R	MISSENSE	NON_SYNON	N
UCI2076630	chr16	23641461	rs45532440	C	G	59.13	44.88	PALB2	E672Q	MISSENSE	NON_SYNON	N
UCI2076630	chr16	23646191	rs152451	T	C	56.24	42.98	PALB2	Q559R	MISSENSE	NON_SYNON	N
UCI2076630	chr16	23634293	rs45551636	C	T	46.2	42.35	PALB2	G998E	MISSENSE	NON_SYNON	D
UCI2219330	chr16	23646191	rs152451	T	C	42.53	51.6	PALB2	Q559R	MISSENSE	NON_SYNON	N
UCI2231576	chr16	23641461	rs45532440	C	G	53.23	53.75	PALB2	E672Q	MISSENSE	NON_SYNON	N
UCI2231576	chr16	23646191	rs152451	T	C	51.75	47.52	PALB2	Q559R	MISSENSE	NON_SYNON	N
UCI3165498	chr16	23646191	rs152451	T	C	99.65	99.68	PALB2	Q559R	MISSENSE	NON_SYNON	N
AA1277	chr5	149515397	rs17110944	T	A	54.74	9.29	PDGFRB	I29F	MISSENSE	NON_SYNON	P
AA1307	chr5	149495354	rs151236133	C	T	52.15	58.89	PDGFRB	R1098Q	MISSENSE	NON_SYNON	N
AA926	chr5	149497358	rs35731372	C	T	51.38	50.47	PDGFRB	R657Q	MISSENSE	NON_SYNON	D
UCI1951813	chr5	149497347	rs140261309	G	A	59.93	48.65	PDGFRB	R661C	MISSENSE	NON_SYNON	D
UCI1804937	chr5	149515397	rs17110944	T	A	52.59	37.15	PDGFRB	I29F	MISSENSE	NON_SYNON	P
UCI2231576	chr5	149509446	rs41287110	C	T	49.4	50.22	PDGFRB	E155K	MISSENSE	NON_SYNON	N
UCI2231576	chr22	42524175	rs5030656	CCTT	C	51.5	52.49	CYP2D6	K227-	NONE	CODON_DEL	NA
AA1025	chr3	178927410	rs3729680	A	G	50.42	57.7	PIK3CA	I391M	MISSENSE	NON_SYNON	P
AA1090	chr3	178927410	rs3729680	A	G	46.7	54.49	PIK3CA	I391M	MISSENSE	NON_SYNON	P
AA952	chr3	178927410	rs3729680	A	G	45.64	53.97	PIK3CA	I391M	MISSENSE	NON_SYNON	P
UCI1951813	chr3	178927410	rs3729680	A	G	58.49	50.45	PIK3CA	I391M	MISSENSE	NON_SYNON	P
UCI3564897	chr3	178927410	rs3729680	A	G	52.49	7.11	PIK3CA	I391M	MISSENSE	NON_SYNON	P
AA1025	chr5	67588148	rs3730089	G	A	48.3	67.94	PIK3R1	M26I	MISSENSE	NON_SYNON	P
AA1090	chr5	67588148	rs3730089	G	A	48.31	57.8	PIK3R1	M26I	MISSENSE	NON_SYNON	P
AA943	chr5	67588148	rs3730089	G	A	49.17	43.67	PIK3R1	M26I	MISSENSE	NON_SYNON	P
AA1188	chr5	67588148	rs3730089	G	A	50.44	47.13	PIK3R1	M26I	MISSENSE	NON_SYNON	P
AA1247	chr5	67588148	rs3730089	G	A	50.39	59.94	PIK3R1	M26I	MISSENSE	NON_SYNON	P
AA1267	chr5	67588148	rs3730089	G	A	51.34	47.99	PIK3R1	M26I	MISSENSE	NON_SYNON	P
AA1277	chr5	67588148	rs3730089	G	A	49.56	88.46	PIK3R1	M26I	MISSENSE	NON_SYNON	P
AA926	chr5	67588148	rs3730089	G	A	51.03	47.79	PIK3R1	M26I	MISSENSE	NON_SYNON	P
AA930	chr5	67588148	rs3730089	G	A	42.32	49.51	PIK3R1	M26I	MISSENSE	NON_SYNON	P
UCI1951813	chr5	67588148	rs3730089	G	A	40.93	44.23	PIK3R1	M26I	MISSENSE	NON_SYNON	P
UCI2076630	chr5	67588148	rs3730089	G	A	50.6	34.71	PIK3R1	M26I	MISSENSE	NON_SYNON	P
UCI2219330	chr5	67588148	rs3730089	G	A	43.51	44.24	PIK3R1	M26I	MISSENSE	NON_SYNON	P
UCI2564879	chr5	67588148	rs3730089	G	A	52.3	52.28	PIK3R1	M26I	MISSENSE	NON_SYNON	P
UCI8965412	chr5	67588148	rs3730089	G	A	55.19	40.09	PIK3R1	M26I	MISSENSE	NON_SYNON	P
UCI1689380	chr5	67593246	rs114163757	C	G	51.24	6.55	PIK3R1	D301E	MISSENSE	NON_SYNON	D
AA1025	chr7	6026988	rs1805321	G	A	99.22	98.53	PMS2	P364S	MISSENSE	NON_SYNON	N
AA1090	chr7	6026988	rs1805321	G	A	49.21	83.05	PMS2	P364S	MISSENSE	NON_SYNON	N
AA943	chr7	6026988	rs1805321	G	A	51.2	51.53	PMS2	P364S	MISSENSE	NON_SYNON	N
AA943	chr7	6045627	rs10254120	C	T	47.29	50.4	PMS2	R20Q	MISSENSE	NON_SYNON	N
AA1188	chr7	6026988	rs1805321	G	A	52.02	49.46	PMS2	P364S	MISSENSE	NON_SYNON	N
AA1204	chr7	6026942	rs1805323	G	T	47.61	38.83	PMS2	T379K	MISSENSE	NON_SYNON	N
AA1204	chr7	6045627	rs10254120	C	T	51.38	57.01	PMS2	R20Q	MISSENSE	NON_SYNON	N
AA1222	chr7	6026942	rs1805323	G	T	53.97	51.62	PMS2	T379K	MISSENSE	NON_SYNON	N
AA1247	chr7	6026988	rs1805321	G	A	98.71	98.43	PMS2	P364S	MISSENSE	NON_SYNON	N
AA1267	chr7	6026708	rs63750668	C	A	42.49	46.15	PMS2	R457L	MISSENSE	NON_SYNON	N
AA1267	chr7	6026988	rs1805321	G	A	48.8	48.73	PMS2	P364S	MISSENSE	NON_SYNON	N
AA1277	chr7	6026942	rs1805323	G	T	45.49	83.37	PMS2	T379K	MISSENSE	NON_SYNON	N
AA1277	chr7	6045627	rs10254120	C	T	50.78	11.63	PMS2	R20Q	MISSENSE	NON_SYNON	N
AA1367	chr7	6029571	.	T	C	51.88	61.95	PMS2	N229S	MISSENSE	NON_SYNON	D
AA957	chr7	6026942	rs1805323	G	T	99.04	99.09	PMS2	T379K	MISSENSE	NON_SYNON	N
AA926	chr7	6026988	rs1805321	G	A	39.91	59.4	PMS2	P364S	MISSENSE	NON_SYNON	N
AA930	chr7	6026530	rs1805324	C	T	53.47	49.05	PMS2	M516I	MISSENSE	NON_SYNON	N
AA1106	chr7	6026942	rs1805323	G	T	42.28	18.4	PMS2	T379K	MISSENSE	NON_SYNON	N
AA1106	chr7	6026988	rs1805321	G	A	43.83	41.8	PMS2	P364S	MISSENSE	NON_SYNON	N
AA948	chr7	6026988	rs1805321	G	A	50.59	40.49	PMS2	P364S	MISSENSE	NON_SYNON	N
AA948	chr7	6045627	rs10254120	C	T	49.12	50.89	PMS2	R20Q	MISSENSE	NON_SYNON	N
AA1367	chr7	6026988	rs1805321	G	A	50.61	54.41	PMS2	P364S	MISSENSE	NON_SYNON	N
AA960	chr7	6026988	rs1805321	G	A	46.44	49.21	PMS2	P364S	MISSENSE	NON_SYNON	N
AA1515	chr7	6026988	rs1805321	G	A	43.76	32.54	PMS2	P364S	MISSENSE	NON_SYNON	N
UCI1546879	chr7	6026988	rs1805321	G	A	98.55	98.5	PMS2	P364S	MISSENSE	NON_SYNON	N
UCI1689380	chr7	6026942	rs1805323	G	T	50.64	23.56	PMS2	T379K	MISSENSE	NON_SYNON	N
UCI1804937	chr7	6026942	rs1805323	G	T	44.69	44.56	PMS2	T379K	MISSENSE	NON_SYNON	N
AA952	chr7	6045634	rs63750123	T	C	43.72	47.96	PMS2	I18V	MISSENSE	NON_SYNON	D
UCI1821517	chr7	6026988	rs1805321	G	A	45.3	19.44	PMS2	P364S	MISSENSE	NON_SYNON	N
UCI1908503	chr7	6026865	rs2228007	T	C	53.19	57.81	PMS2	T405A	MISSENSE	NON_SYNON	N

Table S8: List of non-silent germline variants

Sample	Chr	Cord	rsID	Ref Allele	Alt Allele	Allelic Fraction		Gene	AA change	Type	Effect	Mutation Taster Prediction
						Normal	Tumor					
UCI1951813	chr7	6026607	rs1805318	T	A	52.73	54.34	PMS2	T491S	MISSENSE	NON_SYNON	N
UCI1951813	chr7	6026988	rs1805321	G	A	39.28	40.8	PMS2	P364S	MISSENSE	NON_SYNON	N
UCI2076630	chr7	6026942	rs1805323	G	T	53.01	37.03	PMS2	T379K	MISSENSE	NON_SYNON	N
UCI2224680	chr7	6026988	rs1805321	G	A	48.62	44.58	PMS2	P364S	MISSENSE	NON_SYNON	N
UCI2231576	chr7	6026988	rs1805321	G	A	97.81	99.34	PMS2	P364S	MISSENSE	NON_SYNON	N
UCI2564879	chr7	6026942	rs1805323	G	T	50.11	59.79	PMS2	T379K	MISSENSE	NON_SYNON	N
UCI2564879	chr7	6045627	rs10254120	C	T	53.21	33.11	PMS2	R20Q	MISSENSE	NON_SYNON	N
UCI2649875	chr7	6026988	rs1805321	G	A	43.24	59.2	PMS2	P364S	MISSENSE	NON_SYNON	N
UCI3165498	chr7	6026988	rs1805321	G	A	48.1	48.54	PMS2	P364S	MISSENSE	NON_SYNON	N
AA1307	chr22	42524243	rs35742686	CT	C	52.02	48.38	CYP2D6	NA	NONE	FRAME_SHIF	NA
UCI3564897	chr7	6026988	rs1805321	G	A	99.12	99.14	PMS2	P364S	MISSENSE	NON_SYNON	N
UCI1689380	chr16	23619289	.	ACT	A	53.98	46.5	PALB2	E1082fs	NONE	FRAME_SHIF	NA
UCI8965412	chr7	6026988	rs1805321	G	A	98.2	99.21	PMS2	P364S	MISSENSE	NON_SYNON	N
UCI9135402	chr7	6026988	rs1805321	G	A	41.23	57.86	PMS2	P364S	MISSENSE	NON_SYNON	N
AA1077	chr17	38512480	rs2229773	C	T	43.75	67.7	RARA	R456C	MISSENSE	NON_SYNON	NA
AA1025	chr10	43595999	rs145633958	C	A	51.99	51.04	RET	L56M	MISSENSE	NON_SYNON	N
AA1090	chr10	43610119	rs1799939	G	A	50.94	52.84	RET	G691S	MISSENSE	NON_SYNON	P
AA1307	chr10	43610119	rs1799939	G	A	54.07	79.21	RET	G691S	MISSENSE	NON_SYNON	P
AA957	chr10	43610119	rs1799939	G	A	55.76	52.14	RET	G691S	MISSENSE	NON_SYNON	P
AA952	chr10	43610119	rs1799939	G	A	59.37	50.71	RET	G691S	MISSENSE	NON_SYNON	P
UCI1546879	chr10	43610119	rs1799939	G	A	47.28	57.23	RET	G691S	MISSENSE	NON_SYNON	P
UCI1821517	chr10	43610119	rs1799939	G	A	42.51	52	RET	G691S	MISSENSE	NON_SYNON	P
UCI1908503	chr10	43610119	rs1799939	G	A	94.98	96.12	RET	G691S	MISSENSE	NON_SYNON	P
UCI2224680	chr10	43610119	rs1799939	G	A	54.42	50.43	RET	G691S	MISSENSE	NON_SYNON	P
UCI2564879	chr10	43610119	rs1799939	G	A	49.82	44.45	RET	G691S	MISSENSE	NON_SYNON	P
UCI3564897	chr10	43610119	rs1799939	G	A	99.51	99.29	RET	G691S	MISSENSE	NON_SYNON	P
UCI3564897	chr10	43620335	rs17158558	C	T	50.79	32.14	RET	R982C	MISSENSE	NON_SYNON	P
UCI4216548	chr10	43610119	rs1799939	G	A	44.22	47.64	RET	G691S	MISSENSE	NON_SYNON	P
UCI4216548	chr10	43620335	rs17158558	C	T	48.88	46.29	RET	R982C	MISSENSE	NON_SYNON	P
UCI9135402	chr10	43610119	rs1799939	G	A	56.33	69.69	RET	G691S	MISSENSE	NON_SYNON	P
AA1025	chr17	7579472	rs1042522	G	C	47.54	35.9	TP53	P72R	MISSENSE	NON_SYNON	P
AA1077	chr17	7579472	rs1042522	G	C	99.62	99.73	TP53	P72R	MISSENSE	NON_SYNON	P
AA1090	chr17	7579472	rs1042522	G	C	99.68	99.32	TP53	P72R	MISSENSE	NON_SYNON	P
AA943	chr17	7579472	rs1042522	G	C	99.29	99.27	TP53	P72R	MISSENSE	NON_SYNON	P
AA1188	chr17	7579472	rs1042522	G	C	99.37	99.56	TP53	P72R	MISSENSE	NON_SYNON	P
AA1204	chr17	7579472	rs1042522	G	C	99.67	99.83	TP53	P72R	MISSENSE	NON_SYNON	P
AA1222	chr17	7579472	rs1042522	G	C	50.35	26.09	TP53	P72R	MISSENSE	NON_SYNON	P
AA1247	chr17	7579472	rs1042522	G	C	49.16	87.85	TP53	P72R	MISSENSE	NON_SYNON	P
AA1267	chr17	7579472	rs1042522	G	C	99.26	99.42	TP53	P72R	MISSENSE	NON_SYNON	P
AA960	chr17	7578146	rs34949160	T	C	50.2	71.17	TP53	R89G	MISSENSE	NON_SYNONYMOUS_CODING	
UCI2219330	chr17	7578146	rs34949160	T	C	42.59	70.49	TP53	R89G	MISSENSE	NON_SYNONYMOUS_CODING	
AA1277	chr17	7579472	rs1042522	G	C	51	7.27	TP53	P72R	MISSENSE	NON_SYNON	P
AA1307	chr17	7579472	rs1042522	G	C	99.4	99.48	TP53	P72R	MISSENSE	NON_SYNON	P
AA957	chr17	7579472	rs1042522	G	C	99.21	99	TP53	P72R	MISSENSE	NON_SYNON	P
AA926	chr17	7579472	rs1042522	G	C	52.15	55.16	TP53	P72R	MISSENSE	NON_SYNON	P
AA930	chr17	7579472	rs1042522	G	C	51.98	51.78	TP53	P72R	MISSENSE	NON_SYNON	P
AA948	chr17	7579472	rs1042522	G	C	99.8	99.81	TP53	P72R	MISSENSE	NON_SYNON	P
AA952	chr17	7579472	rs1042522	G	C	99.41	99.69	TP53	P72R	MISSENSE	NON_SYNON	P
AA1367	chr17	7579472	rs1042522	G	C	99.3	98.83	TP53	P72R	MISSENSE	NON_SYNON	P
AA960	chr17	7579472	rs1042522	G	C	47.12	16.84	TP53	P72R	MISSENSE	NON_SYNON	P
AA1515	chr17	7579472	rs1042522	G	C	52.78	50.98	TP53	P72R	MISSENSE	NON_SYNON	P
UCI1546879	chr17	7579472	rs1042522	G	C	47.12	41.31	TP53	P72R	MISSENSE	NON_SYNON	P
UCI1689380	chr17	7579472	rs1042522	G	C	99.55	99.45	TP53	P72R	MISSENSE	NON_SYNON	P
UCI1821517	chr17	7579472	rs1042522	G	C	44.83	25.58	TP53	P72R	MISSENSE	NON_SYNON	P
UCI2008866	chr17	7579472	rs1042522	G	C	99.35	99.39	TP53	P72R	MISSENSE	NON_SYNON	P
UCI2076630	chr17	7579472	rs1042522	G	C	51.26	14.78	TP53	P72R	MISSENSE	NON_SYNON	P
UCI2219330	chr17	7579472	rs1042522	G	C	47.78	30.92	TP53	P72R	MISSENSE	NON_SYNON	P
UCI2224680	chr17	7579472	rs1042522	G	C	99.55	99.04	TP53	P72R	MISSENSE	NON_SYNON	P
UCI2231576	chr17	7579472	rs1042522	G	C	96.6	99.33	TP53	P72R	MISSENSE	NON_SYNON	P
UCI2649875	chr17	7579472	rs1042522	G	C	97.34	97.23	TP53	P72R	MISSENSE	NON_SYNON	P
UCI3165498	chr17	7579472	rs1042522	G	C	49.92	87.05	TP53	P72R	MISSENSE	NON_SYNON	P
UCI3564897	chr17	7579472	rs1042522	G	C	99.68	99.67	TP53	P72R	MISSENSE	NON_SYNON	P
UCI8965412	chr17	7579472	rs1042522	G	C	99.59	99.56	TP53	P72R	MISSENSE	NON_SYNON	P
UCI9135402	chr17	7579472	rs1042522	G	C	97.15	96.46	TP53	P72R	MISSENSE	NON_SYNON	P
UCI9135402	chr6	18139228	rs1800460	C	T	52.39	50.13	TPMT	A154T	MISSENSE	NON_SYNON	D
UCI9135402	chr6	18130918	rs1142345	T	C	53.78	44.31	TPMT	Y240C	MISSENSE	NON_SYNON	D

Table S9: list of predicted deleterious inherited variants in BRCA1 or BRCA2

					Allelic Fraction	
Sample	**rsID**	**Gene**	**AA change**	**Type**	**Normal**	**Tumor**
AA1277	rs80357508	BRCA1	Q1355_E1356fs	FRAMESHIFT	49.14	94.57
AA1515	rs80357087	BRCA1	A1373S	MISSENSE	51.47	52
UCI2008866	rs11571833	BRCA2	K3326*	NONSENSE	45.99	12.16