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Gene	Gene Name	Cytoband	Entrez Gene ID	CCDS Accession ID	Ensembl Gene ID	Ensembl Transcript ID	Exons*	Forward Primer	Reverse Primer	Sequencing Primer
ABCA1	ATP-binding cassette, sub-family A (ABC1), member 1	9q31.1	19	CCDS6762.1	ENSG00000165029.	ENST00000374736	7	CTGATGCATTGGACTGTTGC	CCTCACATTCCGAAAGCATTA	GACCCAGCTTCCAATCTTCA
							19	CCCAAATAGGCCCTAAATAAAC	GATCAGCATGGTTTCCTAAGGT	GGACATGGAGAGAAGGCACT
							30	TGCTCTACGTCACCCTGATG	AATCAAACCAGGCAACAAGC	TGAGATCCTTCTGGGTGGTT
							48	CAGCATCATCCCTATATCCACAT	CCCAAGAGTCACAGAACCAGT	GCTGGAATGCTGGAAGTCAT
ADAMTSL3	ADAMTS-like 3	15q25.2	57188	CCDS10326.1	ENSG00000156218	ENST00000286744	10	GACTCTTGCCCCATAGTTTTTCT	GACATCTCTAATCACCACACCAA	AAGGTGTGGAAAGCACTAGCTC
							16	TTGAATGTGTCATCCTCCTTTT	AACTGTCCCTTAAGCAAAGGTTC	TGGCCTATATTAATGACCCTCA
							20	AGGAGGAAGAAACTCTCCATGAC	GAATCAGCATATCTTGGTGAAGC	CCTAGGAAATGGCTTTCTTCTTG
							23	GGGATACAGAGAGAACCAGGACT	CTGAGGTCTCGAATACCAAAATG	CAAAGGGCTCAACAAAGCTTAC
ATP8B1	ATPase, Class I, type 8B, member 1	18q21.31	5205	CCDS11965.1	ENSG00000081923	ENST00000283684	21	TCAGTGACATAATCCAAAAATTATCC	ATCCACCCCCTACACATTCC	GAATGGTACTCCTGGGGTAAAAC
							27	GACAGAACTGCCTGCATCAA	GATGAATGCAATTCACACACAC	GGAGTTCATCAGTGTTCATTTCTG
CUBN	Cubilin (intrinsic factor-cobalamin receptor)	10p12.31	8029	CCDS7113.1	ENSG00000107611	ENST00000377833	18	CAGCATTTCATGTTATTGCATTG	TGCCTGAGGAGATAACCGAAT	CTCCAAGTAACGCCACCATT
							44	CTCGATAGCAAATTGAGAATTTGT	GTGTTTTCAGGCCTGAGCC	TGATTTGTGGCCATTGACTG
							55	CACCCAGCTATGCAAAAAGG	CTGCCTGCCTGTGACAAC	CGTGTGAGTGCCATTATTTTG
							60	GAAAAGAGGGAGGGAGGAAAG	CACCTGTACTCAAAATTAGCAGGA	TCTCAGAGTGTGACAGAAAATGG
DIP2C	DIP2 disco-interacting protein 2 homolog C (Drosophila)	10p15.3	22982	CCDS7054.1	ENSG00000151240	ENST00000280886	10	CCGGGTGTGTGATGCTTATT	CATCCCTTATCGAGGCAACC	TGCCCTCTCACCTAGAACCA
							15	CTGAGAGCTGCTCCTCCACTA	CACCTGCTTTGGCCTCCT	CTGTGTGCATGGTGTCTGC
							16	GCTGGGTGACCAGTGATTCT	CGAGTGAGTGATTACTGTTTGGTG	TTGCAATAGGGGACGATCTG
							22	GGTAACATTATTCAGCTTTGGTGAG	AAGCATCAGCTTCCTGCAA	ACAGACTTCTGTGTATTGTGGATCA
							31	TTCACCAACTCCTGGTTTGTT	AGCCAGTCTGTGCTGTACCC	GTTTACGTGGGGATCTGTGG
EGFL6	EGF-like-domain, multiple 6	Xp22	25975	CCDS14155.1	ENSG00000198759	ENST00000380602	11	AAAAATTCCTCGGTTTTCTCTGAC	TAATCACCTTGCCTATTCAGCTC	GAAAAGGACTTCAGCTTTCCCTA
EPHA3	EPH receptor A3	3p11.2	2042	CCDS2922.1	ENSG00000044524	ENST00000336596	1	CACAAAAGAGGGAGCATTTTTC	TGCTTTGAAGAGCGTGAGC	GCGGCCTCATCACATCTT
							2	TGCAAACAGTTTAAAAGGACACA	CAATAAATTCATCTGCTCCCTAAG	GCAACATCAACAACAGACAATG
							3_1	GTCCATTAACTCAGAGAACCTTGC	TCTTTGTAAACTGATGCTCTCG	GGCTCTGACACCCTTATGTTG
							3_2	CCAGGAACTCAGCTCAGAAGA	GAGTCCATGGGTACCGTGTC	TCCATTGGTTTTAGGAACTTGC
							3_3	TAGGTCCTGTCAACAAGAAGGG	TGCCAAGTGAGTTGAGACTGAG	GATGTTGGTGCTTGTGTTGC
							4	ACATTTGGTGCAAATTCAAGC	AAAGCTTTCAATTTGCACACG	TTGCTTCTGTAAATTCTTGGAGG
							5_1	CACAGCTGGGGGAAGACAGT	TGCCAGAAGGTCTGTCACTG	ATTTCCCTTGTAGTAGAAAACAGAAG
							5_2	CCGGAAAGATGTTACCTTCAAC	TTCCACCCAGAGTCAAAACC	CCAAATGTCCGCTTCCTC
							6	GGGGCCAGATTAATATTCAAGAG	GAAACAGCTTCTTGCCTACACAG	GATAGACTCCATTTGCATGTTCC
							7	GCCTAAGTTGCGTTCAGAGAATA	TCAGACATCTTTTGCAAGATCC	AGAATCAGGTTTGAGTGGTTCAC
							8	TATCAGACATTAAGCCATACTTCAGG	CACATTTTAACAGCAATCAGTGG	TGAATCAATCAACTGTTCCATGTAG
							9	CCAGAGAGAGGGGCTTTCTT	TCAATAACTGCTAAAGCTAAAACGG	TGCTTTGCACATTCTGAGC
							10	GTCCAATGTCACTGCCAGTTT	TTGCCTTTGATCATGAAATCAG	TGTGCACCTTATGGGGTAGG
							11	TGTACATCTTGCAGGTCAAAGG	TCTTAAATGGTTGGGGTTGG	GAAATAAAACAGTTGCTCTCTACTGATG
							12	CTGGAAACCAATCTTCTCCAA	TGGAGGGTGTCTCTAATGTTTTC	AAGACAGGCAAGTTCTTACATCTC
							13	TTCAGCCTTGTATCCATTTGC	CGTTTTGGGTCATGATTTCTACT	CATATCTTTGTCTTGAGTGCTTAGG
							14	GCTACTTCTGCTTGGTATTGAAA	ATGTTCCACTTCCTTGCACA	GAAATTCTGTCCGGTTTCAGA
							15	TCAGTTGTTATCCTTTTAGGCAACT	AAGGGGAAATACATCTCTCTAATATGG	CGCCCATGAAAACGTAAACT
							16	TCCTGCCGATGTTAGTGTCA	GTTACAAATCTTTCATGTCAAGCC	GACACACAGCAACTCTGCTGA
							17	TGAGGTTTGGGATTGACAGAG	GATGATGCTACGCCTTCCAC	GAACGGTCCGGACATAACAC
EPHB6	EPH receptor B6	7q33-q35	2051	CCDS5873.1	ENSG00000106123	ENST00000222847	5	GAGAGGGTGGGGTTCAGTCT	GTCACTCCAAATGCAAAGAGC	CTGCTGTGTGTTGGGAGC
							9	TGTTGTGTGTCCCTGTGCAT	AGGAGCACCAGTGTGAGGTT	CTGGGCACATGAACAAGC
							12	TCATTGGGACAGGTACAGCA	AGGACCTCGTCTCCTGGAA	CAGAGTCCCATCCAAACACA
							15	ACCTCATGCTCCACCAGATT	TCTTCATCTTAGCCCCTCTCC	ACCCAACAAAGTACTCCCCTCT
FBXW7	F-box and WD-40 domain protein 7 (archipelagohomolog, Drosophila)	4q31.3	55294	CCDS3777.1	ENSG00000109670	ENST00000281708	2_1	CTATGGTTTTTGTGCATGTCTTT	ACTCCAACAACTTCACCATTCC	GCCTTGGTGGCATCAATACT
							2_2	TGAGAGGTAACCCTTCCTCAAG	GAATGGGGAGGAGAGTTGGT	AGAGGAGGAACAGCAACAGC
							2_3	GACTCCTCAGGAAACCAAGAAG	CTTTCCATTACCTTCTGTAAGACAAA	GAAGATGAAGAACATGCTGGTG
							9	CTACATACACAATTGCTTGTGCTTA	AAAGGGCCCAAATTCACC	ACGGATGTAATATTTTCTGAAGAGC
							10	TTGAAAATGGTTGTTGCTGTG	CTGGATCAGCAATTTGACAGTG	TGACTAAATCTACCATGTTTTCTCA
							11	TCCTGGCATTACCTGTTTCC	GAGGTTGACTCTTTTTGTGATGC	GGATTAAGGTCAGTAATTGATAGGAAG
FLNB	Filamin B, beta (actin binding protein 278)	3p14.3	2317	CCDS2885.1	ENSG00000136068	ENST00000295956	11	GAAAGGATCAGGCAAGTGGA	CGGAAGCCCTGTAATCCTC	ACTGCAGCTTATGGCTATAGTGAC
							13	AACCAACCTCTTATGTGGATACTGT	CGTGGTCAGATCTTGTTACCTG	CCCCTGGTTACCTGTCTTTGTAT
							14	TGCATGTCATATTTTGTCACTGG	TCCTTCCATATGTCTGCCTTG	AGTGGTGACTTGGCTGTCTTG
							16	CTTCCCAATTGCTTTTTGAGG	ATGAGACATGCACACAAGTGG	TGCACAGGACATGCTGTTTC
							27	GGCACCTTGACTAACTCACTGTC	TCGGTTATTGAAACCCTTGTTC	CCATCCCACTCTTATGTGTAAGAAA
GNAS	GNAS complex locus	20q13.3	2778	CCDS13472.1	ENSG00000087460	ENST00000265620	8	AGCGATCAGGTGTGCAAAA	GGTGAATGTCAAGAAACCATGA	CTGAGCCCTCTTTCCAAACTACT
MACF1	Microtubule-actin crosslinking factor 1	1p32-p31	23499	CCDS435.1	ENSG00000127603	ENST00000289894	8	TAAACCTCCTGCTTTTTCTCTAACT	GGAAAATGTTCTTTTACCGTAGCA	CAGCTCTGGGAACTTTCAGG
							76	TTACAAATAAAGCATGTTTGGACG	TAAAGGGGCATTTCTTTCAATTAG	TGAGCCTATAATTCCTGAAATTGG
							88	GTGACAGGCGCTTGTATTCC	AAGGCTAATATGATCACTGAACCC	GAACCAGGGAGACGGAAG

MLL3	Myeloid/lymphoid or mixed-lineage leukemia 3	7q36.1	58508	CCDS5931.1	ENSG00000055609	ENST00000262189	8	TGGTACCTCTTTCTGATTAGATGAC	TTACACAAACCTTTAGCACCTAGTAA	CTGAAAGGTTCATGATGCAAA
							9	TGGCAGGGTTACCTCTGTTAC	ATCCGATTTGTCTGGTCTCC	TGCAGTTCCCAGGACTGATTA
							10	GCTTAATGTATAATCCACAAATGATTC	GCTGTAAGATGGTAGAGCAAATGA	TTACATCAGAACTACAATTACAAATGC
							36_1	AATATGGGAGCAATCTGGTAGC	TCTGAGCCTGAGAAAGACTATCC	CCCCATGATGGTAGTTTCTTC
							36_2	TCTCCTGCACAGTCATTCCA	CCAAGGATTTGGGAAATTGA	TAAAGCCACAAGCTCCACCT
							36_3	CAACAGCAAATAGGCCATCC	GCTGACTATATGGATCATTTGACTG	TCTTCCACGACAAATAATGACC
							36_4	CAGTGTCACAGGCATCAAGG	CAGAAATTCCAGGTCTTGGTG	ATGAAAGGCCTGCTTTGACA
							36_5	GGCCTACTACTGTTGACCCATA	AGCAACATCATGGGCAGTTT	CACAAACTGACTTGTTTGTTACACC
							36_6	TGGACCTGGTCTTTCAGACA	GTTTGATGAAATGAACAGCTTCC	CCGTGATCCCTATGATCAGTC
							43_1	TTGCAGTTACCCAAGCAAAA	CTGGGGCTGGTGTACAAGTT	CATCAGCCAGTGTTTTACTTCAG
							43_2	GAATGCCCAGTTTACCTGGAT	CCTTGTTGTATATTCTGCTGCTG	ACCTGCCCCTCAATCCTC
							43_3	GATTCCCTTCTACAGTTCCGACT	CTGCATCATCATCTCTTTTCTTC	CAACCTCTAGGACCCCTTCA
							43_4	ATAACCCATGGACACAGTTATCC	CCTTACTACCATTCTGTTCCTCCA	CCAATCGCTCATTCAGTTGT
							43_5	GAAACCCCTGCCAAAACAG	CAGTTGCTGGTACTAATCTGCTG	CTGGAAAAGGCTGAGACAGAG
OBSCN	Obscurin, cytoskeletal calmodulin and Titin-interacting RhoGEF	1q42.13	84033	CCDS1570.1	ENSG00000154358	ENST00000284548	10	CTTTTTGTTGAGAAATCCAGGAA	CACCTCCACGCTAATGTCAC	TTGTGGCTGAACCATCAGAG
							11	GCTGTTTGCTGTTACTGAATCC	CCTTGGGTGAGACCTCCATA	GCCTGTGAAATGGGTTGG
							19	GGTAGTTGATGGTGCTCAGGA	AGACTTGAGCCCCAGCTTC	TGAAGAGCAATGGGTATCAGG
							21	ATGTAAGGGGTCGAGTGTCC	CACTCAGAACCAGCCCACA	CGTAAGGGCTCTGCCAGTC
							23	CTGTGCCCCAGGGTTCTAA	AGCTGGACGGAGTTATACGG	CAGAGAACCCACCGACCTT
							27	TAGTGGGGTCCAACTGAGG	GTGTAGGGCAAACCATGGAC	AGCCTGGAGCACCATCTCT
							46	CTGCCTCCTTCCTCGTAGC	ACTGCGGAGTATGCAGGAAG	TCTGCCATGCATTACACCTG
							53	CACCTGCAGCCAGTATCAGA	GTCCACGGACAGAGGACAG	CTTCCAGAGGGACTGTTGGT
							55	AGCCCAGCTGCATACTGATAA	GTCTCAGACCTCTCCTTGCAG	TACTGATAAGCAGCTGAGGTCTG
							56_1	ATGTGCTTGACACCTGTTGTG	TGGTCGATGTGATGGTGC	CTGTTCCTGGCCTCAGATTC
							56_2	GAAGGAGATGAAGCAGCAGG	GCTTCACTCTCTGACCCACTG	CCCATGTTCTCCCACACATT
							56_3	TGCTCTCTGCTGATCACTGG	CGACTAGCCTGGATCCTTCTC	CCTGTCAGGTGAGCAACAAG
							70	AGCCTCTCTCCACCTGCTCT	ATGCATGGACGTGTGTGTGT	ATCTAGCAGCTGAGGGAGTGG
PKHD1	Polycystic kidney and hepatic disease 1 (autosomal recessive)	6p12.2	5314	CCDS4935.1	ENSG00000170927.	ENST00000371117	29	GAGAAGAGAGAGACTTGGAAGTAGGA	GAGGACATTGATTGCCCTTTT	TGGAGTTCTCTTCCCTTAAGTCAG
							32_1	GTTTCACTAACACATGCCCTACC	GAGAGGTTACTTCCTCCCACAT	AGGACTTCCACAGGTGCTATG
							32_2	CGTGGTCCTTCACCCAAGC	GAGAGGTCAACCCGAACTGA	GGCAGCAACACCAGTAGTCA
							32_3	GCAGTGATGCCTCGGATAAT	CTGGGGCCAAGTCTCTTGT	CTTCCCATCGCAGGGTTC
							32_4	TGCTGATTAGGGGTCAGAGG	CTGGGGTAAAGGCCTTGTTAT	GATGAGCCGATGGTATTTGTG
							32_5	CTCATCCGGTGCATTGTTC	CCAGAAGTGAAAGGAGCTACCA	TGTTGCCCTGGAAATAGAGG
							34	CTGCTAACTTCATATTCCTATTGGTC	ACATCCACCCAGCCTACACT	CATTTGTGAAACCGACTAGAGG
SPTAN1	Spectrin, alpha, non-erythrocytic 1 (alpha-fodrin)	9q33-q34	6709	CCDS6905.1	ENSG00000197694	ENST00000372731	19	TTATGAAAGGGCACAGCTCAC	CTCCTAACTTCCTTCTCAGTACAAGC	GCCGTGAACACACAGAGAAA
							22	GGCCGTTTTGGACCTCTTA	CCCATGTGGAACAGAGTATGC	ACCTCCTTGGATTCTCCCTC
							41	AGATGGACAGAGGTTCTTGGTC	TCAGTGAAATAAGCGCAAGG	GTTGACCTGATGTCCCCACT
							44	TGCATGGACAGGGACCATA	TCCCAGGAAGTGAACTTTGG	GCCTAGCCCACAACACATAG
							56_1	AAGTCCCGGATCTGCTTGTAG	GAAGCGGGTTAGTGAAGCAC	ACCTGGGAGGTCGGGTTT
							56_2	TTTCGTGAACTGAGCCACTC	GAAGCTGAGGACCTGGACTG	TCTGTGTGCTCTCACTTTCCA
SYNE1	Spectrin repeat containing, nuclear envelope 1	6q25	23345	CCDS5236.1	ENSG00000131018	ENST00000265368	68	CATCTTCTAAACCTACACTGAAACCA	CAGGGCCTTTGTTGATGAAT	AAGAAGATATACATTTGGCTTATTCG
							77	TTAAGGAACTTAGAGTGTTTAAAGGTC	GCACCTGGGCACATTTTA	TTTATTTGGGCATTTCTTAACAC
							86	AGGAAAATGTTAGCCTTCTCACTC	AGAGAAAAAGCAGAACATGGAAGT	CCAGCATTACAACATATCCTGC
						ENST00000367256	55	CACAGCCATTGTACCCATGT	GTAAGAGCAGCTCGAACTAGAGG	GCCAACCTATGTTTAAAGCATTTC
TECTA	Tectorin alpha	11q22-q24	7007	CCDS8434.1	ENSG00000109927	ENST00000264037	6_1	TCAAATGAGGGTGACCATACC	CTGGAAGTCTGCAAACACTGTC	TAATGGAAGTAAAGCATTTAGCCC
							6_2	CTGCAGCGCTGTGGAGA	TCTTCCCTAGGCTGAAGAATCT	GGGAGCCACACTACCACACT
							8_1	TCAATTCTGTCTTCCCCGAGT	ACAGTGCAGTTGGCCGTG	CAGGAGGAGCGTTAAGATTCTG
							8_2	AACCAGGGCTTCGTCCTC	AGGTCTTCAGGAGGGTGTAGG	GCGTCCCTCTGCACAAGT
							8_3	GGCTACCAGGGCTGCTTC	CACTCATAGGCAGAGGCAGAA	CTCAGCCAGAACCAGGTG
							9_1	AAGGCTAGCAATAGGGCAGA	CAGGTTGTCCGTGCACTTG	GAAATGGAAGTGCTCTGTGTG
							9_2	GGCTGTCCACCACATACTTC	CATACCGGGCCACAGAGT	GCTTGTGCGGCTTCTACAAT
							9_3	TCGGAGCTGCTCAAGTTTTATC	AGCATGGCACCTATTTCCC	CATCAACGACCCCTCCAA
ZNF668	Zinc finger protein 668	16p11.2	79759	CCDS10701.1	ENSG00000167394	ENST00000300849	2_1	ATGTCAGAGCCAGGAATGCT	TCTGCCTTAGCTTCTGTCTCTG	GAGATAGGGTTCTTCTCTGAGGC
							2_2	GTCCTGTACCAAGACATTTCCAA	CTGGTGGATCTTGAGCTTGG	GCAGACTGCTCTGAAGAGGT
							2_3	CTATGCCCCAAGGCCTAC	TGGCTCACTTTACCCTGAGACT	CTTCATGCAGCCCGTGT
							3_1	GCCTGAAGGCTTCTTCCTCT	AAGTCCTTGCCGCACTTCT	CCCTAAAGTACAGCCCAGACAG
							3_2	GTTCCTACCAGAGCCACGAG	GGATTTCCCACATGCGTTAC	CTCCGACCCCTCGAGCTT
							3_3	CCTTCCGCTGTGAGGAGT	CTCGTCAGCCTCCTCACC	CAGCCTCACGAAGCATAGC
							3_4	CGGAGTCAGGTGGTGTGAT	ATTCCTAGCAAAGCCACCAG	GAATGCCAAGATGCTGGTG
							3_5	CTACACCTGCCCCCATTGT	TTACCTGATGCCCAAACTCC	TCTTGAGTGCCAGCGACTT

Supplementary Table S1. Gene information, exons and primers used for mutational profiling in Chapter 4 Sequenced genes are listed alongside their full names, chromosomal locations, Entrez gene ID, CCDS accession number, Gene ID and Transcript ID according to Ensembl release 49, sequenced exons and primers.

Gene	Gene Name	Cytoband	Entrez Gene ID	Ensembl Gene ID	Ensembl Transcript ID	Exons*	Forward Primer	Reverse Primer	Number of tumor samples
ADAM12	ADAM metallopeptidase domain 12	10q26.3	8038	ENSG00000148848	ENST00000368679	9	M13-TATTAACGTGATCCCAACTCCAA	AGCAGACAAGACGTAACTCCCTA	63
						14	M13-ACTTATGGCCTTGTCCACTCC	GTCAATCACTCCCGACTGAAC	62
						21	M13-ACCTTGGCCTTCAGCTATAACA	ATTTTACAGAGGCACCGAGAAGT	61
ADAMTS18	ADAM metallopeptidase with thrombospondin type 1 motif, 18	16q23	170692	ENSG00000140873	ENST00000282849	7	M13-TGTGTTTGCCTGTACAAATGG	ACATAAGGGCTATCCATCATCC	62
						9	GACCATTCTTTGATTCTGTGGTC	M13-TCCACTGAGTATTCGTTTGCAG	63
						14	TTACATGGGACTCATGCTTCG	M13-CTCTCACACCACTGTTCACGG	63
AIM1	Absent in melanoma 1	6q21	202	ENSG00000112297	ENST00000369066	1_1	M13-CCACCCTGCTAAGGTGCTAAC	GTGCCCTTGGTGACTGGG	63
						1_2	GAGCCCAGAGTCCAAGCC	M13-TCTTCCACAATGCAGATACCC	63
						2_1	GTACAAACAGATGCTGGCTGC	M13-GGATGGACATCACTTCCCAC	63
						2_2	CGGAAATCACTTAGCCACTCC	M13-TTAATGCCACCATTTTGTGACG	63
						19	M13-GGCTAAGAGCTGAACTGCCTC	CAGCAGCTGGCACACAGTAG	63
ALK	Anaplastic lymphoma receptor tyrosine kinase	2p23	238	ENSG00000171094	ENST00000389048	5	M13-AATGTGAGTCCTGAAGTCCCTG	ATAAGTGTGCACATTCCCAGC	63
						13	ATGTGCTTAGCCCACTGGAAG	M13-GAGGAGGGTGTTGAGTGTTGG	63
						22	M13-GGTGTATGAAGGCCAGGTGTC	ACAACACGATTTCCCTTGGAG	63
GAB1	GRB2-associated-binding protein 1	4q31.21	2549	ENSG00000109458	ENST00000262995	3	M13-TTTGATAAATGTGCATCTTCTTGA	CCAAACTAATTAAAGGATTCAGTGC	63
						5_1	M13-ATTCCAGTGCTTCAGGGATTG	CATGGGAATAACTCCTGGGC	62
						5_2	M13-AAATCCTGCTTCCTCCCAGAG	TACTACGTGAAGGCGACATCC	63
						5_3	CATTTCCAGAAGGAACCTTGG	M13-GCAGAGCATGAATGCAATATACC	63
GUCY1A2	Guanylate cyclase 1, soluble, alpha 2	11q21-q22	2977	ENSG00000152402	ENST00000347596	2	M13-GCCGAGTGCCTCATATTAGTTTC	AATCAGGTTGACCTGGGTAGC	63
						9	M13-TGATGAAGGCCACATCTATACAAAG	GAGACACAATCTCTTTCCACCC	63
KIAA0999	KIAA0999 protein	11q23.3	23387	ENSG00000160584	ENST00000292055	9	GAAGGAAAGAAGGTGCTTTGG	M13-TGGGAGGAGACAGAGGTAAGG	63
						20	TGCTACAAATCAGGGCACAAG	M13-CCAATACCCACTTCCTACATGC	63
IRS4	Insulin receptor substrate 4	Xq22.3	8471	ENSG00000133124	ENST00000372129	1_1	M13-ACGAGGGTAGACAGCCTCTTC	TCAGCAGTCTCGAGTTTGAGC	63
						1_2	M13-CCAGCTCGGCTGGAATACTAC	ACAGTGGACCTGCCTACTTCC	63
						1_3	M13-GAAGCGGAGGTGACTACATGC	ATCACCATCGGATCCTTTCC	63
MAP2K7	Mitogen-activated protein kinase kinase 7	19p13.3-p13.2	5609	ENSG00000076984	ENST00000397981	3	M13-AGGGTGGTTAAACCGGTGG	TCTCCAGGTCGTTGATTTCTG	63
						7	M13-GTGCACTGGGCAAGATGAC	GTTTATGTTCTCCTCCCTCCG	63
MMP2	Matrix metallopeptidase 2 (gelatinase A, 72kDa gelatinase, 72kDa type IV collagenase)	16q13-q21	4313	ENSG00000087245	ENST00000219070	1	M13-GGAGCAGGCTCCAACCAG	TCCAATAGCTTGCCAAAGACC	62
						2	TGATTGCTACAGCCTGCTTTG	M13-CTGAGTGGAGAGAATGCATGG	62
						3	CTGTGCACACACACATACTTGC	M13-ACTGTCCTATCTAAGCCGCCC	63
						4	M13-AGCTCCTGTTGACAGTCCTGG	CTCTCTGGTCCAAGCAAATGG	63
						5	CATTTGCTTGGACCAGAGAGG	M13-AGTGTGGAGGGAAGAGCACAC	63
						6	M13-TGCATCAACTTCACTGGTGTG	TGGGCACTCGGAGTCTTATG	61
						7	M13-TGTGGTTCATTAAGGTCAGCG	ATGCTTGAAGTGGGTGAGGTC	61
						8	CCAGGGTTCTCAGCCTTACTG	M13-ATGAGATCTTGCTGGTCCCAC	60
						9	ACTCTTAGATGGTTGGGTGGG	M13-ATTCAGGTCATTCTGGGAAGC	61
						10	TCCAACCTTCCTTTGATCCTG	M13-AGGAACTGTGGTTTGAGAGGG	63
						11	M13-TGGACAGACAGATGATGGGAG	CACCAACCTCTGAACTCAGCC	63
						12	GAAGGGCTAGGTCCAGTTTCC	M13-GTGTATTTGCAAGGAGCTGGG	61
						13	CCTCAGCCTTTCAAAGCTCTC	M13-CTGTAGAGCTGAAGGCACGG	62
MYLK4	MYLK4 myosin light chain kinase family, member 4	6p25.2	340156	ENSG00000145949	ENST00000274643	2	M13-TTGCAGTCAAGAGAAAGAAGCAC	ATTGTACTCACAAGCGGCTCC	63
						4	M13-GATGCTGCTGTCCTGTAATGC	CTGCACAGGGCTTTATGAATG	61
						9	TCTGAAGTTTGCTGTATGGCTG	M13-TAGAAGGCAACTGAGGATGGG	63
MYO18B	Myosin XVIIIB	22q11.2-q12.1	84700	ENSG00000133454	ENST00000335473	7	M13-TTAGTGTGTGTTTGGTTGCGG	TGGTGACTGATCTTTCCCTCC	63
						15	TTGAAACCAGTTCTGCTGGAG	M13-TTCTCTGGTGAACCAAACAGG	63
						28	M13-AAGTGGAGGAGAGCCACTCAC	CTTCCTCCCTCTTCAGGCTC	63
						29	M13-GGTAGTCAAGACAGGGTCTCCC	ACAAGGGAGTTGAAGTGAGGG	63
NAV3	Neuron navigator 3	12q14.3	89795	ENSG00000067798	ENST00000378640	5	TTCAGGTTTGTTTGTGATTCAAC	M13-AATCCCATCACACTGATACAAGC	63
						8_1	CCTCAGGACAGAAATCCATGC	M13-GATAAGGACTGGGAAGGGCTC	63
						8_2	CCTCAGGACAGAAATCCATGC	AAAGCAAACCATTTCACCTGG	61
						8_3	AAAGCAAACCATTTCACCTGG	M13-CCAGACTAAGATTCCGCACTG	62
						15_1	M13-CATTGTTTCACGAAGTGTGGTG	TCTCTCAGTTTCGAGGTGGTG	63
						15_2	M13-AGGCCACAGATCCAGTACCAG	CATCCTTACCTTCGAAATGTGG	62
						34	CTGCAGGTGTTTGGTACTGGA	M13-GCATACAGGTACAAGAAGGCAAA	62
						39	M13-AGAAACAGCATAGGAGCCAGG	CCTCCTTGGAGACCACAACTC	63

NOTCH1	Notch homolog 1, translocation-associated (Drosophila)	9q34.3	4851	ENSG00000148400	ENST00000277541	11	M13-CAGGTCTGGTCATGGGTGTC	GTTGATCTCGCAGTTGGGTC	63
						18	M13-AGACACCTTTGTCACAGGGC	CAGGCTGCCAGCTACTGC	63
						23	CTCTCCCGAGTGTCCGTG	M13-GGTAAGAGCAGGGCAGTGAG	63
OR51E1	Olfactory Receptor, family 51, subfamily E, member 1	11p15.4	143503	ENSG00000180785	ENST00000326310	1	M13-TCCAGTTTGATGCTTGTCTGC	AGACAATTGGGTTGAGCACAG	61
PRKD1	Protein kinase D1	14q11	5587	ENSG00000184304	ENST00000389985	3	M13-GGGAGTTATATCCGTACTGGCA	TTTCTCAACCAAACGAGTGGA	63
						18	M13-TCAGCGCTGTTAGAGTGGAAG	TCTGCAAGGCAAATGTTAAACC	61
PRPF4B	PRP4 pre-mRNA processing factor 4 homolog B (yeast)	6p25.2	8899	ENSG00000112739	ENST00000283003	8	M13-GGTCTCATGTTTCAGCTATGTTGG	ATGCAGCTGTTGGATGTGC	63
RASGRF2	Ras protein-specific guanine nucleotide-releasing factor 2	5q13	5924	ENSG00000113319	ENST00000265080	2	M13-AGAGTCATTGCCAACTGGACC	TGGAATGTAGCCATGGAAAGC	63
						11	M13-AGTGAGAGTGGGTTGAAAGGG	ACAAGGCTCATGGGCTAAATG	61
						14	ATCAAATGCAGTGAGAAGCCC	M13-CTCATCCTCATGGTGACTCCG	63
RET	Ret proto-oncogene	10q11.2	5979	ENSG00000165731	ENST00000355710	3	GGGACCAGGGTTTACACCAG	M13-ACTGATGGCATGAAGGTGAAG	63
						6	M13-CTGTGTCTGGGAAGAGGTGTG	GTCTACTCTGTGCTGGTTGGG	63
						10	M13-CTATGCTTGCGACACCAGTTG	AATTTCCTCCCTTGTTGGGAC	63
SIX4	SIX homeobox 4	14q23	51804	ENSG00000100625	ENST00000216513	1	M13-AAGAGTGCGAGGGAGTGAGG	TTCCGAGTGGAGTTGTACCTG	63
						2	AAGATGAATCCAGCAAGGGAC	M13-GGGATCTGGACAATGCCATAC	63
						3	ATCGTTTGGTTCTGCAATCG	M13-CATGCAGATCAATCTAAAGTCTCTTG	62
SMAD2	SMAD family member 2	18q21.1	4087	ENSG00000175387	ENST00000262160	8	GGCTGGCATAGAGCATGTAAAG	M13-ATGTGTCGGCACTTAAACCAC	61
						11	TTTGCGGAATAATCGTGTCC	M13-GGGACCACACACAATGCTATG	63
SMAD4	SMAD family member 4	18q21.1	4089	ENSG00000141646	ENST00000342988	4	ACTGAGTTGGTAGGATTGTGAGG	ACTGAGTTGGTAGGATTGTGAGG	63
						10	M13-TGGGTGCATTACATTTCCATC	TGGGTGCATTACATTTCCATC	63
SORL1	Sortilin-related receptor, L(DLR class) A repeats-containing	11q23.2-q24.2	6653	ENSG00000137642	ENST00000260197	2	TCTGCTTGACAAAGGAGGAAAG	M13-ACATTGCATGGATCTGTTTGC	63
						30	M13-GGAACTTGGGTCTGGAGGAG	ATCCTGCATAGCTGGTGGAAC	63
						34	M13-ATTGCCCAGGCCAGTCTC	GGCTGAGATGTCTGACTCCG	63
						44	M13-TCAAACTCTTGTTGCTGTGGG	CTGTCTCTGGAGGTCTAGCGG	63
TAF1	TAF1 RNA polymerase II, TATA box binding protein	Xq13.1	6872	ENSG00000147133	ENST00000276072	7	CATCCTCAGTTTCTCTAAGTTCCC	M13-CAAAGAAACCCTACCACCCAG	63
	(TBP)-associated factor, 250kDa					34	CCTGTTCCCTTGAATGAGGAG	M13-CACGAAAGGCATATGAAGAGG	61
TCF7L2	Transcription factor 7-like 2 (T-cell specific, HMG-box)	10q25.3	6934	ENSG00000148737	ENST00000340914	14	AGCTGAGATTTCACATCCAACTG	M13-TCATTAGTCATTGATGCCAGAGG	63
TGM3	Transglutaminase 3 (E polypeptide,	20q11.2	7053	ENSG00000125780	ENST00000381458	5	M13-AGTGCAGTTCCCTTCTTGAGC	ACCAGCTGTAATTGGTGAGGC	63
	protein-glutamine-gamma-glutamyltransferase)					6	GAATTCTGCATGTCAGTCTCCC	M13-GTGGTGGAGATGGTACCTTGG	63
UBR5	Ubiquitin protein ligase E3 component n-recognin 5	8q22	51366	ENSG00000104517	ENST00000220959	9	TTGCATCCTGAAGGGTCTTTAC	M13-AAATGGAAACCTTAGAGGGAGG	63
						42	GAAATTGGTTAGATACATTAGCGACC	M13-GAGAAATTCCCACCCAGACAG	63

Supplementary Table S2. Gene information, exons and primers used for mutational profiling in Chapter 5
Sequenced genes are listed alongside their full names, chromosomal locations, Entrez gene ID, Gene ID and Transcript ID according to Ensembl release 49, sequenced exons and primers. The number of tumor samples successfully amplified and analyzed is also indicated.