Table S1.

Gene	Forward primer	Reverse Primer	PCR product	Size
MYCL1	TCTCTAAGCGCCAACCCTCAC	GCACGTGGGTGTGTTGGTAAA	chr1:40138923-40139038	115
DNAH7	GCAGAGCACTGTCTCCTCCTTGT	GCCGGGAAATTCACCTCTAGAAA	chr2:196094670-196094785	115
PPARGC1A	CATGTTACCTGCGCAAGCTTCT	TGACCCTGCTTCCACCAAGA	chr4:23406539-23406627	88
TERT	TTGCTGGGTTTCCACGATAGA	AGAAGGAGTGTGAGCATTTGTGTTA	chr5:1310845-1310947	102
NPVF	AAATTGCCGTTGATGATCCATAG	TCCCTAAAGCTGTGGCCTGTA	chr7:25231147-25231250	103
ZNRF2	GGCTGCCCAGTAGAGAAAGTCTATT	TCTCCTCCTGACTTCCTGGTACTAA	chr7:30292207-30292327	120
LSM5	CCAAAGGACGGCGATTACCT	TCAAAGTCGTCCCACCATCA	chr7:32496439-32496550	111
HERPUD2	GGTGAGGAATGGGTGTTGCTATG	TTGTCTCTCAGCTCCTGGGTATCA	chr7:35208767-35208881	114
GRB10	TGGAAACGCAAGGCTGAAGTA	GCTGAATGGCCTCGCCTCTA	chr7:50627212-50627332	120
BNC2	CCAACAAATTGGCCTGTGGTTAT	GGGCACAAATGCCAAACAAA	chr9:16407925-16408039	114
ADAMTSL1	CTTGCCCGTACCGCCTTTAAT	TCTGGGTTGGCTGCAAAGAG	chr9:18464694-18464793	99
PTPLAD2	AGCAACCGTACTAAAGCAATTGTGA	TCTGCAGAAGGCTTGGCATAA	chr9:21005577-21005668	91
PTPRE	AGCAGTGGAGGAGGCCAAGT	GGCTGTGTCACCTCCCTTGA	chr10:129601126-129601239	113
RRAS2	TCCTGGCCGTTGGTAGCTAAA	TCCTCCTTCACCAGAACCAACA	chr11:14257426-14257525	99
NAV3	TTGGGTCAAAGCCTGTGCATAC	AGCATGGAGCTCTCTGTTTCAGTAA	chr12:76749416-76749527	111
TTC28	TGCAGGGACAGCTCCTTCAG	GGCTCCTGGCACGATGACTT	chr22:26708399-26708515	116

*Conditions for q-PCR reaction were as follows, one cycle of 94°C for 2 min, 40 cycles of 94°C for 15 s, 55°C for 10 s and 60°C for 50 s.

Table S2.

Tumor ID	Sex	Age	Group	Localization	Blood analyzed
G10	m	58	Primary	temporal left	
G1143	m	14	Primary	temporo-occipital left	
G153	m	49	Primary	no data	
G1596	f	65	Primary	temporal left	
G174	f	58	Primary	frontal right	
G1963	m	67	Primary	parietal left	Yes
G20844	m	43	Primary	temporal right	Yes
G20854	f	42	Primary	occipital right	Yes
G20856	m	45	Primary	no data	
G20890	m	56	Primary	no data	Yes
G20940	f	63	Primary	no data	
G20944	m	59	Primary	no data	Yes
G20972	m	44	Primary	no data	
G20990	m	67	Primary	frontal lobe left	Yes
G21576	f	47	Primary	no data	Yes
G21602	m	58	Primary	no data	
G21612	m	43	Primary	no data	
G21628	m	61	Primary	no data	Yes
G21694	f	46	Secondary	no data	Yes
G21800	m	51	Primary	no data	Yes
G21804	m	75	Primary	no data	Yes
G21820	f	55	Primary	no data	Yes
G21828	f	62	Primary	no data	Yes
G21830	f	63	Primary	no data	Yes
G21836	m	46	Primary	no data	Yes
G21864	f	41	Primary	no data	Yes
G22118	m	34	Secondary	no data	Yes
G22334	m	76	Primary	no data	Yes
G22368	m	49	Primary	no data	Yes
G22370	f	65	Primary	no data	Yes
G22520	m	74	Primary	occipital left	Yes
G22576	f	67	Primary	temporal right	Yes
G22616	m	70	Primary	occipital right	Yes
G22686	m	72	Primary	no data	Yes
G22872	m	49	Primary	parieto-occipital	Yes
G23120	m	53	Primary	left temporal	
G23218	f	71	Primary	no data	Yes
G23264	m	63	Primary	right cerebellum	
G23282	m	78	Primary	right fronto-temporal	

G23304	m	59	Primary	no data	Yes
G23316	f	43	Primary	no data	Yes
G23480	m	40	Primary	no data	Yes
G23786	m	66	Primary	temporo-parietal right	
G23906	f	76	Secondary	parietal left	
G24014	m	56	Primary	temporal right	
G24028	m	55	Primary	temporal right	
G24064	m	44	Primary	temporal left	Yes
G24158	m	18	Primary	parieto-occipital right	Yes
G24178	m	40	Primary	no data	Yes
G24454	f	64	Primary	no data	Yes
G24460	m	35	Primary	parietal right	Yes
G24528	f	47	Primary	no data	Yes
G24596	m	42	Primary	frontal right	
G24702	m	59	Primary	frontal left	Yes
G24930	m	45	Primary	no data	Yes
G25036	m	41	Primary	pontine left parasagital	Yes
G251	f	52	Primary	parietal right	
G25108	m	70	Primary	parietal	Yes
G25488	f	59	Primary	temporal right	Yes
G25496	f	58	Primary	frontal right	Yes
G27006	m	69	Primary	no data	
G27030	f	35	Primary	frontotemporal right	Yes
G27040	m	66	Primary	no data	Yes
G27614	f	73	Primary	no data	Yes
G27622	f	72	Primary	temporal left	
G28882	f	22	Secondary	no data	Yes
G29178	m	63	Primary	temporal right	
G29264	m	61	Primary	fronto-temporal right	
G29994	m	48	Primary	no data	
G30196	f	64	Primary	fronto-temporal	
G30276	m	63	Primary	no data	
G30296	f	41	Primary	no data	
G30726	f	67	Primary	frontal right	
G30758	m	53	Primary	frontal left	
G40	f	67	Primary	frontal parietal left	
G48	f	60	Primary	frontal temporal left	
G50	m	51	Primary	temporal right	
G8	m	64	Primary	temporal frontal left	Yes

Table S3.

Over represented GO terms in 3000 top ranked gained clones

Biological Process Results, GO id term	Nr genes	p-values
GO:0006355 regulation of transcription, DNA-dependent	471	4.44E-29
GO:0032774 RNA biosynthetic process	476	1.18E-27
GO:0006351 transcription, DNA-dependent	475	1.51E-27
GO:0045449 regulation of transcription	486	7.09E-27
GO:0019219 regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	493	6.2E-26
GO:0006350 transcription	497	8.42E-26
GO:0031323 regulation of cellular metabolic process	515	2.23E-23
GO:0016070 RNA metabolic process	540	7.49E-23
GO:0019222 regulation of metabolic process	527	1.46E-22
GO:0006139 nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	622	2E-13
GO:0050794 regulation of cellular process	679	4.24E-12
GO:0050789 regulation of biological process	740	2.1E-11
GO:0065007 biological regulation	771	1.84E-10
GO:0043283 biopolymer metabolic process	767	5.92E-09
GO:0043170 macromolecule metabolic process	955	0.0000191
GO:0009988 cell-cell recognition	7	0.00156
GO:0044237 cellular metabolic process	1084	0.00194
GO:0044238 primary metabolic process	1053	0.00367
GO:0007224 smoothened signaling pathway	7	0.0044
GO:0007339 binding of sperm to zona pellucida	5	0.00655
GO:0030509 BMP signaling pathway	8	0.00732
GO:0000375 RNA splicing, via transesterification reactions	18	0.00868
GO:0000377 RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	18	0.00868
GO:0000398 nuclear mRNA splicing, via spliceosome	18	0.00868
GO:0040017 positive regulation of locomotion	6	0.00894
GO:0051272 positive regulation of cell motility	6	0.00894
GO:0035036 sperm-egg recognition	5	0.0114
GO:0051101 regulation of DNA binding	5	0.0114
GO:0042742 defense response to bacterium	19	0.0122
GO:0030099 myeloid cell differentiation	20	0.0123
GO:0008588 release of cytoplasmic sequestered NF-kappaB	3	0.0132
GO:0043388 positive regulation of DNA binding	3	0.0132
GO:0007202 phospholipase C activation	6	0.0136
GO:0008152 metabolic process	1137	0.0141
GO:0051704 multi-organism process	27	0.0147
GO:0008272 sulfate transport	5	0.0183
GO:0030516 regulation of axon extension	5	0.0183
GO:0051047 positive regulation of secretion	7	0.0195
GO:0048675 axon extension	6	0.0198
GO:0009617 response to bacterium	20	0.0213
GO:0045785 positive regulation of cell adhesion	4	0.024
GO:0006598 polyamine catabolic process	2	0.0241
GO:0006900 membrane budding	2	0.0241
GO:0006901 vesicle coating	2	0.0241

GO:0007402 ganglion mother cell fate determination	2	0.0241
GO:0008612 hypusine biosynthetic process from peptidyl-lysine	2	0.0241
GO:0015810 aspartate transport	2	0.0241
GO:0015979 photosynthesis	2	0.0241
GO:0046515 hypusine biosynthetic process	2	0.0241
GO:0046516 hypusine metabolic process	2	0.0241
GO:0046685 response to arsenic	2	0.0241
GO:0046794 virion transport	2	0.0241
GO:0046795 intracellular virion transport	2	0.0241
GO:0046800 enhancement of virulence	2	0.0241
GO:0046968 peptide antigen transport	2	0.0241
GO:0048012 hepatocyte growth factor receptor signaling pathway	2	0.0241
GO:0048268 clathrin cage assembly	2	0.0241
GO:0051403 stress-activated MAPK cascade	2	0.0241
GO:0051450 myoblast proliferation	2	0.0241
GO:0048609 reproductive process in a multicellular organism	24	0.0248

Cellular Component Results, GO id term	Nr genes	p-values
GO:0005634 nucleus	697	2.23E-10
GO:0043231 intracellular membrane-bound organelle	941	0.0000224
GO:0043227 membrane-bound organelle	941	0.0000249
GO:0043229 intracellular organelle	1036	0.000906
GO:0043226 organelle	1036	0.000924
GO:0030122 AP-2 adaptor complex	3	0.0132
GO:0030128 clathrin coat of endocytic vesicle	3	0.0132
GO:0030669 clathrin-coated endocytic vesicle membrane	3	0.0132
GO:0043189 H4/H2A histone acetyltransferase complex	4	0.0136
GO:0005622 intracellular	1230	0.0208
GO:0009579 thylakoid	2	0.0241
GO:0009842 cyanelle	2	0.0241
GO:0009843 cyanelle thylakoid	2	0.0241
GO:0030075 plasma membrane thylakoid	2	0.0241
GO:0030076 light-harvesting complex	2	0.0241
GO:0030089 phycobilisome	2	0.0241
GO:0042716 chromatophore	2	0.0241
GO:0044436 thylakoid part	2	0.0241

Molecular Function Results, GO id term	Nr genes	p-values
GO:0008270 zinc ion binding	449	7.14E-22
GO:0003676 nucleic acid binding	601	7.63E-20
GO:0003677 DNA binding	420	7.79E-18
GO:0046914 transition metal ion binding	496	9.9E-17
GO:0043169 cation binding	610	5.8E-10
GO:0046872 metal ion binding	636	2.11E-08
GO:0043167 ion binding	642	8.64E-08
GO:0016712 oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, reduced flavin or flavoprotein as one donor, and incorporation of one atom of oxygen	14	0.000033
GO:0050381 unspecific monooxygenase activity	12	0.0000785
GO:0005529 sugar binding	40	0.00144
GO:0030528 transcription regulator activity	222	0.00213

GO:0046790 virion binding	4	0.00248
GO:0004497 monooxygenase activity	25	0.00271
GO:0004064 arylesterase activity	3	0.00367
GO:0004293 tissue kallikrein activity	3	0.00367
GO:0017060 3-galactosyl-N-acetylglucosaminide 4-alpha-L-fucosyltransferase activity	3	0.00367
GO:0042607 exogenous peptide antigen binding	3	0.00367
GO:0003700 transcription factor activity	154	0.00379
GO:0008271 sulfate porter activity	5	0.00637
GO:0015116 sulfate transporter activity	5	0.00637
GO:0004982 N-formyl peptide receptor activity	4	0.00653
GO:0003823 antigen binding	12	0.00765
GO:0042605 peptide antigen binding	6	0.00866
GO:0008017 microtubule binding	12	0.012
GO:0008417 fucosyltransferase activity	6	0.0132
GO:0020037 heme binding	25	0.0142
GO:0046906 tetrapyrrole binding	25	0.0142
GO:0030246 carbohydrate binding	53	0.0156
GO:0000149 SNARE binding	7	0.0189
GO:0008236 serine-type peptidase activity	34	0.0217
GO:0005488 binding	1547	0.0221
GO:0015103 inorganic anion transporter activity	10	0.0233
GO:0003958 NADPH-hemoprotein reductase activity	2	0.0238
GO:0004063 aryldialkylphosphatase activity	2	0.0238
GO:0004074 biliverdin reductase activity	2	0.0238
GO:0005046 KDEL sequence binding	2	0.0238
GO:0005185 neurohypophyseal hormone activity	2	0.0238
GO:0015111 iodide transporter activity	2	0.0238
GO:0032396 inhibitory MHC class I receptor activity	2	0.0238
GO:0043237 laminin-1 binding	2	0.0238
GO:0050051 leukotriene-B4 20-monooxygenase activity	2	0.0238
GO:0050321 tau-protein kinase activity	2	0.0238

Over represented GO terms in 3000 top ranked deleted clones

Biological Process Results, GO id term	Nr genes	p-values
GO:0009615 response to virus	21	0.000042
GO:0009056 catabolic process	89	0.0000515
GO:0006629 lipid metabolic process	89	0.000648
GO:0044255 cellular lipid metabolic process	74	0.00105
GO:0016042 lipid catabolic process	19	0.00117
GO:0043450 alkene biosynthetic process	7	0.00137
GO:0009241 polyisoprenoid biosynthetic process	3	0.004
GO:0016109 tetraterpenoid biosynthetic process	3	0.004
GO:0016114 terpenoid biosynthetic process	3	0.004
GO:0016117 carotenoid biosynthetic process	3	0.004
GO:0046246 terpene biosynthetic process	3	0.004
GO:0007049 cell cycle	100	0.00423
GO:0006996 organelle organization and biogenesis	120	0.00442
GO:0008632 apoptotic program	14	0.00484
GO:0022402 cell cycle process	87	0.00644

GO:0044248 cellular catabolic process	67	0.00727
GO:0006643 membrane lipid metabolic process	27	0.00744
GO:0009057 macromolecule catabolic process	50	0.00833
GO:0005996 monosaccharide metabolic process	24	0.00853
GO:0007051 spindle organization and biogenesis	7	0.0086
GO:0043449 alkene metabolic process	7	0.0086
GO:0016108 tetraterpenoid metabolic process	3	0.00923
GO:0016116 carotenoid metabolic process	3	0.00923
GO:0050828 regulation of liquid surface tension	3	0.00923
GO:0008285 negative regulation of cell proliferation	31	0.00954
GO:0046365 monosaccharide catabolic process	14	0.00963
GO:0007052 mitotic spindle organization and biogenesis	5	0.0103
GO:0009065 glutamine family amino acid catabolic process	5	0.0103
GO:0006780 uroporphyrinogen III biosynthetic process	2	0.0105
GO:0009439 cyanate metabolic process	2	0.0105
GO:0009440 cyanate catabolic process	2	0.0105
GO:0019754 one-carbon compound catabolic process	2	0.0105
GO:0019858 cytosine metabolic process	2	0.0105
GO:0046502 uroporphyrinogen III metabolic process	2	0.0105
GO:0019748 secondary metabolic process	9	0.0109
GO:0007010 cytoskeleton organization and biogenesis	59	0.011
GO:0051260 protein homooligomerization	8	0.0112
GO:0007017 microtubule-based process	28	0.0113
GO:0019318 hexose metabolic process	23	0.0116
GO:0016568 chromatin modification	25	0.0123
GO:0046164 alcohol catabolic process	14	0.0124
GO:0006839 mitochondrial transport	9	0.013
GO:0042440 pigment metabolic process	8	0.0136
GO:0006007 glucose catabolic process	12	0.0136
GO:0006066 alcohol metabolic process	38	0.0152
GO:0051726 regulation of cell cycle	64	0.0168
GO:0006020 myo-inositol metabolic process	3	0.017
GO:0006266 DNA ligation	3	0.017
GO:0043094 metabolic compound salvage	3	0.017
GO:0008203 cholesterol metabolic process	13	0.0177
GO:0009066 aspartate family amino acid metabolic process	5	0.0189
GO:0006338 chromatin remodeling	10	0.0193
GO:0019320 hexose catabolic process	13	0.0199
GO:0046148 pigment biosynthetic process	7	0.0205
GO:0051301 cell division	30	0.0212
GO:0000074 regulation of progression through cell cycle	63	0.0218
GO:0045786 negative regulation of progression through cell cycle	27	0.0241
GO:0006304 DNA modification	5	0.0246
GO:0008584 male gonad development	5	0.0246
GO:0016358 dendrite development	5	0.0246

Cellular Component Results, GO id term	Nr genes	p-values
GO:0031966 mitochondrial membrane	32	0.00368
GO:0005739 mitochondrion	94	0.00491
GO:0005740 mitochondrial envelope	33	0.00689
GO:0005602 complement component C1q complex	2	0.0102
GO:0005916 fascia adherens	2	0.0102
GO:0005730 nucleolus	21	0.0141

GO:0005874 microtubule	28	0.0156
GO:0005615 extracellular space	60	0.0171
GO:0005737 cytoplasm	405	0.0195
GO:0044429 mitochondrial part	39	0.0199
GO:0005743 mitochondrial inner membrane	25	0.0219
GO:0005913 cell-cell adherens junction	5	0.0232

Molecular Function Results, GO id term	Nr genes	p-values
GO:0005132 interferon-alpha/beta receptor binding	10	1.24E-10
GO:0005126 hematopoietin/interferon-class (D200-domain) cytokine receptor binding	17	0.000000194
GO:0004033 aldo-keto reductase activity	7	0.0000579
GO:0004668 protein-arginine deiminase activity	4	0.000109
GO:0016810 hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds	22	0.000166
GO:0008132 pancreatic elastase activity	4	0.000501
GO:0042708 elastase activity	4	0.000501
GO:0003840 gamma-glutamyltransferase activity	4	0.00138
GO:0016813 hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amidines	5	0.00181
GO:0016814 hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in cyclic amidines	9	0.00181
GO:0004623 phospholipase A2 activity	8	0.00194
GO:0003824 catalytic activity	511	0.0022
GO:0004430 1-phosphatidylinositol 4-kinase activity	3	0.00395
GO:0047115 trans-1,2-dihydrobenzene-1,2-diol dehydrogenase activity	3	0.00395
GO:0004437 inositol or phosphatidylinositol phosphatase activity	8	0.00566
GO:0016789 carboxylic ester hydrolase activity	20	0.00633
GO:0016298 lipase activity	15	0.0073
GO:0016491 oxidoreductase activity	86	0.00829
GO:0004806 triacylglycerol lipase activity	4	0.00901
GO:0008013 beta-catenin binding	3	0.00911
GO:0047498 calcium-dependent phospholipase A2 activity	3	0.00911
GO:0016746 transferase activity, transferring acyl groups	26	0.00943
GO:0004098 cerebroside-sulfatase activity	2	0.0105
GO:0004281 pancreatic elastase II activity	2	0.0105
GO:0004452 isopentenyl-diphosphate delta-isomerase activity	2	0.0105
GO:0004537 caspase-activated deoxyribonuclease activity	2	0.0105
GO:0004911 interleukin-2 receptor activity	2	0.0105
GO:0005147 oncostatin-M receptor binding	2	0.0105
GO:0005161 platelet-derived growth factor receptor binding	2	0.0105
GO:0005353 fructose transporter activity	2	0.0105
GO:0008451 X-Pro aminopeptidase activity	2	0.0105
GO:0016314 phosphatidylinositol-3,4,5-trisphosphate 3-phosphatase activity	2	0.0105
GO:0018675 (S)-limonene 6-monooxygenase activity	2	0.0105
GO:0018676 (S)-limonene 7-monooxygenase activity	2	0.0105
GO:0019113 limonene monooxygenase activity	2	0.0105
GO:0019976 interleukin-2 binding	2	0.0105
GO:0032052 bile acid binding	2	0.0105
GO:0051219 phosphoprotein binding	4	0.0138
GO:0008415 acyltransferase activity	24	0.0156
GO:0016791 phosphoric monoester hydrolase activity	32	0.0165
GO:0001948 glycoprotein binding	3	0.0168

GO:0008171 O-methyltransferase activity	3	0.0168
GO:0016747 transferase activity, transferring groups other than amino-acyl groups	24	0.0169
GO:0016755 transferase activity, transferring amino-acyl groups	5	0.0186
GO:0016918 retinal binding	4	0.02
GO:0016787 hydrolase activity	218	0.0217
GO:0031072 heat shock protein binding	11	0.0219
GO:0004721 phosphoprotein phosphatase activity	23	0.0224
GO:0004722 protein serine/threonine phosphatase activity	8	0.0225

Table S4.

Chrom	Band	From (Mb)	To (Mb)	Size (Mb)	Aberration *	Number of tumors	Underexpressed/Overexpressed genes
1	p36.31	5.87	6.35	0.48	del	19	*ACOT7,NPHP4,KCNAB2,ICMT,CHD5,GPR153*
1	p36.23	7.86	8.84	0.98	del	19	*ENO1,TNFRSF9,DKFZp566H0824*
1	p36.13,p36.12	16.66	22.68	6.02	del	11	*PADI3,LOC391012,PADI4,LOC729604,RNF186,PAX7,PLA2G2E,ACTL8,ELA3A,PADI1*
1	p36.11,p35.3	25.18	28.90	3.72	del	14	*FAM76A,GPR3,NR0B2,AIM1L,EXTL1,MED18,PAFAH2,PPP1R8,NUDC,RHD*
1	p34.3	36.22	38.08	1.86	del	12	*TEKT2,C1orf113,GRIK3,THRAP3*
1	p33,p32.3	48.84	52.13	3.29	del	8	*C1orf34*
1	p31.1	73.45	76.02	2.57	del	6	*TNNI3K*
1	p31.1	77.79	84.06	6.26	del	7	*USP33,ARID3B*
1	p22.2,p22.1	90.93	94.00	3.07	del	7	*BRDT,hCG_1811337,EVI5,DR1,BTBD8,LOC388907,LOC642146,LOC647436,RPL5,GFI1*
1	q41	216.86	221.28	4.42	del	4	*KIAA1822L,BPNT1,MOSC1,C1orf115*
1	q41,q42.11,q42.12	221.39	223.15	1.76	del	4	*CAPN2*
1	q42.13,q42.2	227.30	229.16	1.86	del	3	*CAPN9,ACTA1*
2	p25.3,p25.2,p25.1	3.61	8.33	4.73	del	6	*ALLC,COLEC11*
2	p24.1,p23.3	21.04	25.57	4.54	del	7	*APOB,ITSN2,FLJ14126,FKBP1B,EFR3B,LOC100131510,DTNB,POMC*
2	p22.3,p22.2,p22.1	36.22	38.59	2.37	del	5	*ARL6IP2,STRN,FEZ2*
2	p22.1	39.48	40.31	0.83	del	5	*SLC8A1*
2	p16.1	55.84	60.56	4.72	del	5	*VRK2,BCL11A*
2	p15,p14,p13.3	63.80	71.04	7.25	del	6	*BMP10,TGFA,ADD2,ANTXR1,AAK1,PNO1,GKN1,CD207*
2	p13.1,p12	74.64	80.08	5.44	del	6	*REG1A,SEMA4F,TACR1,REG1B,REGL,REG3A*
2	q14.3	122.98	127.89	4.91	del	5	*MAP3K2,BIN1*
2	q36.3	227.87	229.09	1.22	del	7	*COL4A3,DKFZp547H025,COL4A3,SLC19A3,TM4SF20,HRB*
2	q37.3	238.25	239.26	1.02	del	10	*SCLY,PER2,ASB1*
3	p26.1	5.63	8.16	2.54	del	3	*GRM7*
3	p21.31,p21.2,p21.1,p14.3,p14.2,p14.1	51.39	70.55	19.16	del	4	*LRTM1,GRM2,2-PDE,SUCLG2,CACNA1D,HESX1,ABHD6,PHF7,FRMD4B,ITIH3*
3	q13.33,q21.1,q21.2,q21.3	122.60	130.18	7.58	del	3	*CCDC37,GATA2,ROPN1B,UMPS,ZNF148,CASR,FBXO40,C3orf28,KLF15,KALRN*
4	p16.3	1.47	1.69	0.22	del	4	
4	p16.2	4.69	5.03	0.35	del	4	
4	p16.1	8.94	9.57	0.63	del	4	*SLC2A9*
4	p15.2,p15.1,p14,p13,p12	26.08	47.56	21.48	del	4	*CCKAR,CORIN,TBC1D1,RHOH,PHOX2B,APBB2,PDS5A,PABPCP1,PCDH7*
4	q31.21,q31.22	144.41	147.44	3.02	del	4	*GYPB,GYPB,GYPE,GYPA,GYPE*
4	q32.3	166.72	168.17	1.45	del	7	*TLL1*

4	q33,q34.1,q34.2,q34.3,q35.1,q35.2	170.48	191.14	20.66	del	7	*ADAM29,MTNR1A,SAP30,NEK1,GLRA3,ING2,F11,GALNT7,NBLA00301*
5	q34,q35.1	159.93	169.91	9.98	del	3	*FOXI1,SLIT3,MIRN218-2,LOC728095,MIRN585,ODZ2,GABRA6,PANK3,GABRB2,ATP10B*
6	p24.1,p23,p22.3,p22.2,p22.1,p21.33,p21.32,p21.31,p21.2,p21.1,p12.3,p12.2,p12.1,p11.2,p11.1	11.85	58.85	47.00	del	4	*CLPS,GPX5,TAP2,OR10C1,OR2J2,GSTA1,TFAP2B,CDKAL1,POM121L2*
6	q14.1,q14.2,q14.3,q15,q16.1,q16.2,q16.3,q21	77.45	109.45	32.00	del	7	*RARS2,LOC100130683,GABRR2,PRDM1,HTR1B,GABRR1,KRT18P50,CGA,ME1*
6	q23.3,q24.1,q24.2,q24.3,q25.1,q25.2,q25.3	137.33	157.51	20.18	del	10	*PBOV1,OPRM1,ESR1,LOC442271,MYCT1,ADAT2,EPM2A*
6	q26,q27	162.33	165.59	3.26	del	10	*PARK2*
8	p21.2,p21.1,p12	24.79	30.26	5.48	del	4	*ADRA1A,DOCK5,EBF2,CHRNA2,PTK2B,NEFL*
8	p12	32.97	33.94	0.97	del	4	*RNF122*
8	p12	34.46	36.61	2.15	del	4	*UNC5D*
8	q11.21,q11.22	49.12	52.06	2.94	del	3	*SNTG1,EFCAB1*
8	q24.12	119.66	121.31	1.65	del	4	*COL14A1,DCC1,COLEC10*
8	q24.21,q24.22	130.91	134.86	3.95	del	4	*ST3GAL1,FAM49B,HHLA1,TG,KCNQ3,WISP1,TG,SLA*
9	p24.3,p24.2,p24.1	1.57	6.10	4.53	del	20	*RLN1,RLN2,KCNV2,INSL6,MLANA,C9orf68,INSL4,PDCD1LG2,RFX3*
9	p21.3	21.21	21.97	0.76	del	46	*IFNA@,MTAP,CDKN2A*
9	p13.1,p12,p11.2	40.18	46.28	6.11	del	9	*FAM75A1,FAM75A2,FAM75A3,FAM75A4,FAM75A5,FAM75A7,RP11-138L21.1*
9	q12	67.48	69.19	1.71	del	6	
9	q31.1,q31.2,q31.3	103.65	112.27	8.62	del	5	*ACTL7A,EPB41L4B,CYLC2,ABCA1,ACTL7B,SVEP1,PTPN3*
9	q33.3,q34.11	125.90	130.84	4.94	del	8	*NR6A1,SPTAN1,LOC51145,SH2D3C,ZNF79,FLJ10232,C9orf16,FAM125B*
10	p12.1,p11.23,p11.22	28.05	33.32	5.27	del	72	*LOC645954,LOC731954,ITGB1,C10orf68,EPC1,LOC283079,SVIL*
10	q21.2,q21.3	61.25	67.80	6.55	del	71	*ANK3,CTNNA3,ANXA2P3*
10	q23.2,q23.31	89.59	90.40	0.81	del	73	*PTEN,C10orf59*
10	q26.12,q26.13,q26.2,q26.3	122.85	135.35	12.51	del	73	*GLRX3,ADAM12,UTF1,VENTX,CUZD1,FLJ12616,FGFR2,DMBT1,CYP2E1*
11	p15.5,p15.4,p15.3,p15.2,p15.1	0.20	18.81	18.61	del	12	*MUC5B,EIF3F,NAP1L4,ART1,PNPLA2,KIAA0409,SWAP70,PPFIBP2,MMP26*
11	q12.1,q12.2,q12.3,q13.1	59.47	64.75	5.28	del	8	*MS4A2,SCGB1A1,MARK2,MS4A12,HRASLS2,SCGB1D1,SLC22A6,SLC22A8,SCGB2A2,EML3*
11	q14.1	78.60	80.65	2.05	del	5	
11	q22.1,q22.2,q22.3	99.64	104.35	4.71	del	6	*MMP27,MMP20,MMP8,TRPC6,PGR,PPIA,PPIAL3,PPIAP8*
11	q24.2,q24.3,q25	126.85	130.94	4.09	del	7	*ST14,KCNJ1,KCNJ5,EWSR1,FLI1,APLP2,BARX2,PRDM10*

12	q12,q13.11,q13.12	39.22	48.03	8.81	del	3	*LALBA,VDR,ADCY6,CACNB3,DDX23,RND1,P11,HSU79275,MLL2,PUS7L*
12	q13.2,q13.3	54.23	56.00	1.77	del	4	*MYO1A,CIP29,GPR182,MMP19,IL23A,CDK2,RDH16,MIP,NXPH4,APOF*
12	q14.1,q14.2	58.26	63.13	4.87	del	4	*LOC100133321,AVPR1A*
12	q14.3,q15	65.51	67.06	1.55	del	5	*IL22,IFNG,IL26,DYRK2*
12	q21.1,q21.2,q21.31	73.18	78.86	5.69	del	4	*CAPS2,PAWR,ZDHHC17,KCNC2,SYT1*
12	q24.31,q24.32,q24.33	124.06	129.97	5.91	del	4	*LOC400084,PIWIL1,FZD10,RIMBP2*
13	q12.13,q12.2,q12.3,q13.1,q13.2,q13.3,q14.11,q14.12,q14.13,q14.2,q14.3,q21.1	26.57	52.56	25.99	del	20	*GUCY1B2,TNFSF11,FLT3,SPG20,PDX1,CPB2,CYSLTR2,FAM48A,CG030*
13	q21.31,q21.32	63.45	65.01	1.56	del	20	
13	q31.1,q31.2,q31.3	85.72	91.33	5.61	del	17	*RP11-114G1.1,KRT18P27*
13	q32.1,q32.2,q32.3,q33.1	96.34	100.78	4.44	del	17	*RAP2A,DOCK9,SLC15A1,MBNL2,PCCA,GPR18,STK24*
13	q33.2,q33.3,q34	104.81	114.09	9.29	del	16	*ATP4B,F10,PROZ,SOX1,RASA3,GRTP1,MGC2780,F7,GRK1*
14	q11.2,q12	22.18	26.10	3.92	del	13	*NRL,SLC22A17,NFATC4,IL25,TGM1,GZMB,SLC7A8,DHRS2,LTB4R*
14	q22.1	50.66	51.96	1.31	del	13	*PTGDR,LOC100131689*
14	q22.2,q22.3,q23.1,q23.2,q23.3,q24.1	53.49	67.18	13.69	del	13	*C14orf135,AKAP5,GPR135,DHRS7,ESR2,GPX2,SAMD4A,PLEKHG3*
14	q24.3,q31.1,q31.2,q31.3,q32.11,q32.12,q32.13,q32.2,q32.31	75.41	101.73	26.32	del	12	*TCL1A,KCNK13,FOXN3,SERPINA6,DIO3,MYO5A,CATSPERB,TCL6,OTUB2*
15	q14,q15.1	33.28	38.86	5.59	del	13	*THBS1,CASC5,PLCB2,GPR176,RPUSD2,GCHFR,IVD*
15	q26.1,q26.2	91.13	95.88	4.75	del	7	*CHD2,MCTP2*
16	p12.2,p12.1	20.64	24.09	3.46	del	8	*DNAH3,SCNN1G,GGA2,ACSM3,CHP2,TMEM159,ERN2*
16	q21,q22.1	64.59	65.87	1.29	del	8	*CA7,TK2,E2F4,DYNC1LI2,HSF4,CDH16,TRADD,C16orf70*
16	q24.1,q24.2,q24.3	82.99	88.70	5.71	del	6	*CA5A,LOC642452,LOC651791,FOXL1,CDH15,KIAA1609,FLJ12547,DPEP1,ATP2C2*
17	p13.3,p13.2,p13.1	2.94	7.91	4.97	del	6	*PITPNM3,OR1D4,OR1D5,CTNS,DNAH2,ALOX12,ALOX12P2,OR1A2,YBX2,OR1A1*
17	p12	12.93	14.90	1.97	del	6	*HS3ST3B1,COX10*
17	q12,q21.1,q21.2,q21.31	33.82	38.40	4.58	del	6	*IKZF3,KRT34,CACNB1,KRT20,MED24,KCNH4,KRT37,KRT35,TNS4*
17	q23.2,q23.3,q24.1,q24.2,q24.3,q25.1	55.87	69.93	14.06	del	3	*APOH,CSHL1,KCNH6,CSH1,PRKCA,CSH1,CSH2,CSHL1,GH1,GH2*
17	q25.1,q25.2,q25.3	72.11	76.76	4.65	del	3	*CARD14,SEPT9,FLJ21865,CCDC40,CBX2,CARD14,CBX8,SOCS3*
18	p11.32,p11.31,p11.23,p11.22	0.02	9.79	9.77	del	13	*EMILIN2,ARHGAP28,PTPRM,YES1,CETN1,ADCYAP1,DLGAP1,TYMS*
18	q12.3	39.76	41.31	1.55	del	8	
18	q22.2,q22.3	66.09	68.40	2.31	del	11	

19	q13.33	54.51	56.31	1.80	del	10	*KLK8,KLK5,KLK10,KLK11,KLK13,TSKS,PRRG2,MED25*
19	q13.41	57.78	58.34	0.56	del	9	*LOC731901,ZNF816A*
21	q21.1	19.90	22.20	2.29	del	6	*NCAM2*
21	q22.11,q22.12,q22.13	33.58	38.08	4.50	del	5	*DYRK1A,RUNX1,DOPEY2,KCNE2,ITSN1*
22	q11.23,q12.1,q12.2,q12.3	22.51	33.32	10.81	del	30	*C22orf24,SLC5A1,LRP5L,RHBDD3,UPB1,CRYBA4,RFPL1,NF2*
22	q12.3,q13.1,q13.2,q13.31,q13.32,q13.33	35.61	49.57	13.96	del	29	*ACO2,POLR3H,BIK,SERHL,SERHL2,FBLN1,POLDIP3,ZC3H7B,XRCC6,ACR,CELSR1*
1	p36.21	13.56	13.84	0.28	gain	4	
1	p34.2	39.64	40.34	0.69	gain	4	*PPT1,PABPC4,CAP1,MACF1,TRIT1*
1	p34.2	42.56	43.01	0.46	gain	4	*YBX1,FOXJ3*
1	p13.2	114.88	115.56	0.68	gain	5	*BCAS2,CSDE1*
1	q21.1,q21.2,q21.3	143.05	151.54	8.49	gain	8	*CCT8,NBPF@,XXyac-YX155B6.1,ANP32E,VPS45,RBM8A,GPR89A,GPR89B,GPR89C,MCL1,CHD1L*
1	q25.3	179.41	179.62	0.20	gain	6	
1	q31.1	184.51	185.51	1.00	gain	6	*C1orf27,TPR*
1	q32.1	202.72	203.41	0.69	gain	9	
1	q43,q44	241.24	242.33	1.09	gain	8	*AKT3*
2	p24.3	14.72	16.15	1.44	gain	4	*DDX1,NAG*
2	p22.1	38.47	39.53	1.05	gain	3	*RPLP0,SFRS7,SOS1,MAP4K3*
2	p21	42.69	43.41	0.72	gain	3	*ZFP36L2*
3	q11.2,q12.1	95.08	101.19	6.11	gain	5	*HNRPK,PROS1*
3	q13.13,q13.2,q13.31,q13.32,q13.33	112.25	120.94	8.69	gain	5	*NAT13,ATG3,SLC35A5,ZBTB20,DULLARD*
3	q22.3,q23,q24	139.40	145.80	6.41	gain	5	*SR140,SLC25A36,ATR,ARMC8,ATP1B3,COPB2,MRPS22,FAIM*
3	q26.2,q26.31,q26.32,q26.33,q27.1	169.47	185.82	16.35	gain	9	*DVL3,FXR1,NLGN1,PIK3CA,TLOC1,FNDC3B,TNIK,RPL22,TBL1XR1,PRKCI*
3	q28,q29	191.30	196.50	5.20	gain	8	*CENTB2,ENAH,LSG1,NDUFB5,MFN1,PSMD2,ACTL6A,YEATS2,POLR2H*
4	p16.3,p16.2	1.54	4.57	3.03	gain	3	*C4orf8,MXD4,C4orf15,SLBP,WHSC1,LETM1*
4	p15.2	23.25	24.06	0.81	gain	3	
4	p15.2	24.95	26.24	1.29	gain	4	*RBPJ*
4	q11,q12	52.35	54.56	2.21	gain	9	*SGCB,DCUN1D4*
4	q12	54.66	55.08	0.41	gain	12	*PDGFRA*
5	p15.33	1.26	1.47	0.21	gain	5	
7	p22.3,p22.2	1.25	2.12	0.87	gain	61	
7	p15.3,p15.2	21.42	26.56	5.13	gain	64	*HNRNPA2B1,CBX3,LOC653972,CBX3,LOC653972,TRA2A,TRA2A,NUPL2,TOMM7,DFNA5*
7	p15.1	29.61	31.17	1.57	gain	64	*DKFZp586I1420,C7orf24*
7	p14.3	32.69	33.00	0.32	gain	63	*KBTBD2*
7	p14.3,p14.2	35.00	35.75	0.75	gain	63	
7	p12.3	47.61	49.60	2.00	gain	64	*CDC14B*

7	p12.3,p12.2	49.62	49.82	0.20	gain	64	
7	p11.2	54.79	55.49	0.70	gain	68	*SEC61G,EGFR*
7	q11.21	61.99	62.92	0.93	gain	62	
7	q11.22	68.58	69.10	0.53	gain	61	*AUTS2*
7	q11.23	73.58	74.75	1.17	gain	58	*GTF2I,GTF2IP1,LOC100093631,LOC732437,GTF2I,GTF2IP1,PMS2L5*
7	q11.23,q21.11	77.03	81.35	4.32	gain	62	*PHTF2,PTPN12*
7	q21.13	89.44	89.66	0.23	gain	62	
7	q21.13,q21.2,q21.3	90.70	95.07	4.38	gain	62	*AKAP9,PON2,KRIT1,SGCE,BET1,GATAD1,DKFZP564O0523*
7	q22.1,q22.2	102.83	105.60	2.78	gain	60	*SRPK2,PUS7,RINT1,ORC5L,SYPL1*
7	q32.2,q32.3,q33	129.53	137.17	7.64	gain	60	*EEF1G,LOC729998,KIAA0265,CALD1,PTN,NUP205,CNOT4,MEST*
9	p24.3,p24.2,p24.1	1.88	4.61	2.73	gain	6	
9	p23,p22.3	12.70	15.51	2.81	gain	7	*PSIP1,NFIB*
9	p22.3,p22.2,p22.1	16.08	18.74	2.66	gain	5	
9	p21.1,p13.3	32.70	33.78	1.08	gain	7	*DNAJA1,CHMP5*
9	p11.2	44.74	46.28	1.54	gain	5	
9	q21.33	88.26	89.49	1.23	gain	8	
9	q22.31	93.04	94.36	1.32	gain	8	*SPTLC1,IARS,NOL8,NFIL3*
9	q31.3	111.36	112.01	0.65	gain	9	
9	q32,q33.1,q33.2	114.00	123.03	9.03	gain	9	*RAB14,SLC31A1,TNC,PRPF4,HSDL2,ATP6V1G1,PSMD5,POLE3*
9	q33.3	126.77	127.41	0.64	gain	8	*GAPVD1,PPP6C,HSPA5,PRPS1*
10	q21.3	67.75	69.84	2.09	gain	3	*HNRPH3*
11	q13.5,q14.1	76.39	81.47	5.08	gain	3	*CLNS1A,NDUFC2,GAB2,C11orf67,ORC3L,RSF1,ALG8*
11	q23.3	117.19	118.19	1.00	gain	3	*UBE4A,ARCN1,ATP5L*
12	p13.32	3.14	3.76	0.63	gain	6	
12	p12.1,p11.23,p11.22,p11.21	22.10	32.04	9.94	gain	6	*H3F3B,C12orf11,MED21,KRAS,MRPS35,KIAA0528,CAPRIN2*
12	q11	36.14	36.24	0.10	gain	5	
12	q12	39.22	39.61	0.39	gain	5	
12	q13.13	52.49	53.07	0.58	gain	4	*HNRNPA@,COPZ1,CBX5*
12	q13.2	53.31	53.53	0.23	gain	4	
12	q13.2	54.12	54.30	0.18	gain	4	
12	q13.2	54.48	54.72	0.24	gain	4	
12	q13.3,q14.1	56.29	56.51	0.23	gain	19	*CDK4,OS9*
12	q14.1	56.96	58.51	1.55	gain	11	
12	q14.1	60.47	61.16	0.69	gain	6	
12	q14.2	62.55	62.66	0.11	gain	6	
12	q14.2	62.98	63.13	0.15	gain	6	*XPOT*
12	q14.3	63.99	64.64	0.64	gain	6	
12	q14.3	65.47	65.53	0.06	gain	9	
12	q15	67.30	67.74	0.44	gain	13	*hCG_1757335 , RAP1B,NUP107,ATP5H*

12	q21.1	71.41	71.74	0.33	gain	6	
12	q21.1	72.58	72.82	0.24	gain	6	
12	q21.2	74.25	74.63	0.38	gain	4	
12	q21.2	76.38	77.15	0.76	gain	4	
12	q21.2	77.77	78.08	0.32	gain	4	
12	q21.31	78.81	79.11	0.30	gain	4	*PPP1R12A*
13	q31.3,q32.1	92.75	95.31	2.56	gain	7	
14	q13.3,q21.1,q21.2,q21.3,q22.1	36.36	50.76	14.40	gain	3	*SDCCAG1,COIL,PNN,SOS2,ARF6,MGAT2,SEC23A,SAV1*
14	q23.3,q24.1	65.38	68.90	3.52	gain	3	*SF3B4,ZFP36L1,EIF2S1,ATP6V1D,MPP5,RDH11*
17	q21.32	43.75	44.19	0.43	gain	3	
17	q21.33	45.75	46.77	1.02	gain	5	*UTP18,CROP,LRRC59,SPAG9,NME1*
17	q21.33,q22	46.82	51.75	4.93	gain	5	*MMD,PCTP*
17	q24.1,q24.2	60.58	61.64	1.07	gain	6	
17	q25.3	76.73	78.62	1.88	gain	5	*ACTG1,CSNK1D,WDR45L*
18	q23	71.83	76.10	4.27	gain	4	*ADNP2*
19	p13.2	8.36	9.03	0.67	gain	28	*HNRPM*
19	q12,q13.11	32.42	37.60	5.18	gain	25	*C19orf2,POP4,C19orf2*
19	q13.42,q13.43	60.05	63.77	3.72	gain	23	*CHMP2A,RPL28,LOC392424,RPS5,U2AF2,TRIM28,ZNF587*
20	p13	2.82	4.89	2.08	gain	27	*PANK2,RASSF2,CDC25B,MGC3260,LOC390183,LOC442162*
20	p12.3	5.70	6.15	0.44	gain	27	*SYNCRIP*
20	q11.21,q11.22,q11.23,q12,q13.11,q13.12,q13.13,q13.2	29.95	51.57	21.61	gain	27	*MAPRE1,CSE1L,RPN2,TMEM189-UBE2V1,UBE2V1,STAU1,SFRS6,DPM1*
21	p11.2,p11.1	9.93	10.14	0.22	gain	9	
21	q21.1,q21.2	22.14	23.40	1.26	gain	13	
21	q22.13,q22.2	38.08	38.68	0.60	gain	11	
21	q22.3	42.13	46.30	4.17	gain	9	*PTTG1IP,RRP1B,CSTB,UBE2G2,POFUT2*

Table S5.

Pathway	Nr. of genes	p-value	Genes
hsa05214:Glioma	12.0	0.00002	*PIK3CA, PRKCA, PTEN, PDGFRA, SOS1, CDKN2A, TGFA, AKT3, EGFR, SOS2, KRAS, CDK4*
hsa05223:Non-small cell lung cancer	10.0	0.00022	*PIK3CA, PRKCA, SOS1, CDKN2A, TGFA, AKT3, EGFR, SOS2, KRAS, CDK4*
hsa04912:GnRH signaling pathway	12.0	0.00144	*PRKCA, SOS1, PTK2B, PLCB2, ADCY6, EGFR, CGA, MAP3K2, SOS2, PLA2G2E, KRAS, CACNA1D*
hsa05215:Prostate cancer	11.0	0.00270	*PIK3CA, FGFR2, CDK2, PTEN, PDGFRA, SOS1, TGFA, AKT3, EGFR, SOS2, KRAS*
hsa04080:Neuroactive ligand-receptor interaction	21.0	0.00335	*GH2, GABRR2, GLRA3, GABRB2, CGA, GABRA6, ADRA1A, GRM2, GRM7, LTB4R, OPRM1, MTNR1A, CCKAR, HTR1B, GRIK3, CSH1, GH1, CSH2, AVPR1A, CYSLTR2, PTGDR, TACR1, GABRR1*
hsa05213:Endometrial cancer	8.0	0.00390	*PIK3CA, PTEN, SOS1, AKT3, EGFR, SOS2, KRAS, CTNNA3*
hsa05220:Chronic myeloid leukemia	9.0	0.01022	*PIK3CA, GAB2, SOS1, CDKN2A, AKT3, RUNX1, SOS2, KRAS, CDK4*
hsa04664:Fc epsilon RI signaling pathway	9.0	0.01022	*PIK3CA, PRKCA, GAB2, SOS1, AKT3, SOS2, PLA2G2E, KRAS, MS4A2*
hsa04540:Gap junction	10.0	0.01516	*CSNK1D, PRKCA, PDGFRA, SOS1, PLCB2, ADCY6, EGFR, MAP3K2, SOS2, KRAS*
hsa04510:Focal adhesion	16.0	0.01563	*PIK3CA, PRKCA, PTEN, RAP1B, AKT3, ITGB1, KRAS, ACTG1, TNC, CAPN2, PPP1R12A, SOS1, PDGFRA, EGFR, SOS2, THBS1*
hsa00363:Bisphenol A degradation	4.0	0.01772	*RDH11, PON2, DHRS7, DHRS2*
hsa05218:Melanoma	8.0	0.02199	*PIK3CA, PTEN, PDGFRA, CDKN2A, AKT3, EGFR, KRAS, CDK4*
hsa05210:Colorectal cancer	9.0	0.02232	*PIK3CA, DVL3, PDGFRA, SOS1, AKT3, EGFR, FZD10, SOS2, KRAS*
hsa05221:Acute myeloid leukemia	7.0	0.02402	*PIK3CA, FLT3, SOS1, AKT3, RUNX1, SOS2, KRAS*
hsa05110:Cholera - Infection	6.0	0.02492	*ATP6V1D, PRKCA, SEC61G, ATP6V1G1, ACTG1, ARF6*
hsa04320:Dorso-ventral axis formation	5.0	0.02600	*SOS1, PIWIL1, EGFR, SOS2, KRAS*
hsa04530:Tight junction	11.0	0.04334	*SPTAN1, YES1, PRKCA, PTEN, PRKCI, MPP5, AKT3, KRAS, ACTG1, CTNNA3, CDK4*
hsa05211:Renal cell carcinoma	7.0	0.05545	*PIK3CA, SOS1, RAP1B, TGFA, AKT3, SOS2, KRAS*
hsa04012:ErbB signaling pathway	8.0	0.05855	*PIK3CA, PRKCA, SOS1, TGFA, AKT3, EGFR, SOS2, KRAS*
hsa04010:MAPK signaling pathway	17.0	0.06386	*PRKCA, RAP1B, AKT3, MAP3K2, KRAS, MAP4K3, FGFR2, SOS1, PDGFRA, NFATC4, CACNB3, EGFR, PLA2G2E, SOS2, CACNB1, CDC25B, CACNA1D*
hsa00240:Pyrimidine metabolism	8.0	0.06808	*UPB1, POLE3, UMPS, TYMS, POLR3H, TK2, NME1, POLR2H*
hsa05212:Pancreatic cancer	7.0	0.07761	*PIK3CA, CDKN2A, TGFA, AKT3, EGFR, KRAS, CDK4*
hsa05219:Bladder cancer	5.0	0.07968	*CDKN2A, EGFR, KRAS, THBS1, CDK4*
hsa04660:T cell receptor signaling pathway	8.0	0.08980	*PIK3CA, IFNG, SOS1, NFATC4, AKT3, SOS2, KRAS, CDK4*
hsa04630:Jak-STAT signaling pathway	11.0	0.09307	*PIK3CA, IFNG, GH2, SOCS3, SOS1, IL22, IL23A, AKT3, IL26, CSH1, GH1, CSH2, SOS2*
hsa04020:Calcium signaling pathway	12.0	0.09993	*PRKCA, PDGFRA, PTK2B, PLCB2, CCKAR, EGFR, AVPR1A, CYSLTR2, SLC8A1, TACR1, CACNA1D, ADRA1A*

Table S6.

Sample	Position (Mb)	Ratio by 32-K	Ratio by qPCR (stdev)	Gene validated	Reference gene
G20844	chr1: 39.84-40.34	10.6	21 (0.02)	*MYCL1*	*DNAH7*
G23316	chr4: 23.25-24.06	20.1	55.7 (0.00)	*PPARGC1A*	*DNAH7*
G21576	chr5: 1.02-1.50	3.3	1.1 (0.06)	*TERT*	*DNAH7*
G24528	chr5: 1.02-1.78	4.4	9.5 (0.05)	*TERT*	*DNAH7*
G20844	chr5: 1.26-1.90	10.2	10.2 (0.01)	*TERT*	*DNAH7*
G24064	chr7: 25.13-26.01	4.6	3.6 (0.14)	*NPVF*	*DNAH7*
G21804	chr7: 29.61-31.17	9.6	49.7 (0.08)	*ZNRF2*	*DNAH7*
G24064	chr7: 29.99-31.15	4.0	3.7 (0.05)	*ZNRF2*	*DNAH7*
G22118	chr7: 30.20-30.49	2.2	3.3 (0.05)	*ZNRF2*	*DNAH7*
G24064	chr7: 32.41-33.32	8.0	2.7 (0.12)	*LSM5*	*DNAH7*
G21804	chr7: 35.17-35.69	5.6	0.8 (0.02)	*HERPUD2*	*DNAH7*
G24064	chr7: 35.28-35.75	6.7	6.9 (0.02)	*HERPUD2*	*DNAH7*
G22118	chr7: 50.07-50.97	2.5	5.5 (0.04)	*GRB10*	*DNAH7*
G24064	chr7: 50.16-51.36	3.6	7.7 (0.02)	*GRB10*	*DNAH7*
G20940	chr7: 50.41-50.79	5.8	116 (0.00)	*GRB10*	*DNAH7*
G20890	chr7: 50.44-50.79	3.7	1.9 (0.09)	*GRB10*	*DNAH7*
G10	chr7: 50.64-51.97	2.3	2.7 (0.09)	*GRB10*	*DNAH7*
G23282	chr9: 15.87-16.44	0.4	0.5 (0.06)	*BNC2*	*DNAH7*
G20854	chr9: 17.98-18.88	0.5	0.5 (0.05)	*ADAMTSL1*	*DNAH7*
G20990	chr9: 19.43-23.05	0.5	0.3 (0.16)	*PTPLAD2*	*DNAH7*
G29994	chr9: 19.94-22.15	0.5	0.2 (0.01)	*PTPLAD2*	*DNAH7*
G22686	chr9: 20.13-23.18	0.6	0.3 (0.24)	*PTPLAD2*	*DNAH7*
G27030	chr9: 20.56-21.97	0.5	0.3 (0.05)	*PTPLAD2*	*DNAH7*
G20854	chr9: 20.56-23.56	0.6	0.5 (0.07)	*PTPLAD2*	*DNAH7*
G29178	chr9: 20.56-30.70	0.5	0.2 (0.05)	*PTPLAD2*	*DNAH7*
G22334	chr9: 21.00-22.47	0.4	0.2 (0.10)	*PTPLAD2*	*DNAH7*
G24528	chr9: 21.51-29.59	0.7	0.6 (0.05)	*PTPLAD2*	*DNAH7*
G22520	chr10: 129.37-131.18	0.4	0.5 (0.03)	*PTPRE*	*DNAH7*
G21800	chr11: 14.02-15.06	12.3	5.9 (0.05)	*RRAS2*	*DNAH7*
G27622	chr12: 76.38-77.15	9.4	17.7 (0.09)	*NAV3*	*DNAH7*
G21864	chr22: 26.69-26.86	10.4	6.2 (0.35)	*TTC28*	*DNAH7*

qPCR conditions and primers for all genes are available in Sup. Table 1

Table S7.

Region	Band	From (Mb)	To (Mb)	Size (Mb)	Genes
A	12q13.13	52.49	53.03	0.54	*HOXC13,HOXC12,HOTAIR,HOXC11,HOXC10,MIRN196A2,HOXC9,HOXC8,HOXC4,HOXC5,HOXC6,SMUG1,CBX5,HNRNPA1,NFE2,COPZ1,MIRN148B*
B	12q13.2	53.35	53.55	0.20	*VDAC5P,MUCL1*
C	12q13.2	54.48	54.74	0.25	*CIP29,ORMDL2,DNAJC14,MMP19,GSTPP,WIBG,DGKA,SILV,CDK2,RAB5B,SUOX,IKZF4,RPS26*
D	12q13.3, 12q14.1	56.29	56.70	0.42	*DTX3,GEFT,SLC26A10,B4GALNT1,OS9,CENTG1,TSPAN31,CDK4,MARCH9,CYP27B1,METTL1,FAM119B,TSFM,AVIL,CTDSP2,MIRN26A2,XRCC6BP1*
E	12q14.1	57.00	57.59	0.59	*LRIG3*
F	12q14.1	57.76	58.51	0.75	*SLC16A7*
G	12q14.1	60.08	61.06	0.98	*FAM19A2,KRT8P19,USP15*
H	12q14.2	62.23	62.43	0.20	*DPY19L2*
I	12q14.2	62.55	62.93	0.38	*SRGAP1,FLJ32549*
J	12q14.2, 12q14.3	63.30	63.68	0.39	*RASSF3,MIRN548C,GNS,KIAA0984,FLJ41278*
K	12q14.3	63.79	64.64	0.85	*WIF1,LEMD3,MSRB3,HMGA2*
L	12q14.3	65.32	65.69	0.37	*GRIP1*
M	12q15	67.30	68.00	0.70	*RAP1B,NUP107,SLC35E3,MDM2,CPM,CPSF6*
N	12q15	67.93	68.56	0.63	*CPSF6,LYZ,YEATS4,FRS2,CCT2,LRRC10,BEST3,RAB3IP,C12orf28*
O	12q15	68.59	69.36	0.76	*CNOT2,KCNMB4,PTPRB,C12orf28,PTPRR*
P	12q15,12q21.1	69.54	70.61	1.07	*PTPRR,TSPAN8,LGR5,CCDC131,THAP2,TMEM19,RAB21,TBC1D15*
Q	12q21.2	74.25	74.60	0.35	
R	12q21.2	76.38	77.15	0.76	*NAV3*
S	12q21.2	77.87	78.11	0.24	*SYT1*
T	12q21.31	78.81	79.11	0.30	*PPP1R12A*

Table S8.

Region	Band	From (Mb)	To (Mb)	Size (Mb)	Genes
A	9p23	9.19	9.87	0.69	*PTPRD*
B	9p22.3	15.87	16.44	0.57	*C9orf93,BNC2*
C	9p22.2,9p22.1	17.98	18.88	0.89	*ADAMTSL1*
D	9p21.3	20.13	21.34	1.20	*SMNP,MLLT3,KIAA1797,MIRN491,PTPLAD2,IFNB1,IFNW1,IFNA21,IFNA4,IFNA7,IFNA10,LEIF-M,IFNA16,IFNA17,IFNA14,IFNAP22,IFNA5,KLHL9*
E	9p21.3	21.75	22.29	0.54	*MTAP,C9orf53,CDKN2A,ANRIL,CDKN2B*
F	9p21.3	23.51	24.34	0.82	*ELAVL2*
G	9p21.1	29.03	30.28	1.25	-