

Supplementary Table 1 All predicted homozygous deletions^a

Chromosome ^b	Start (Mb) ^b	Stop (Mb) ^b	Sample
1	184.74	185.02	H524
1	193.03	193.96	H1819
2	18.36	22.20	H2882
2	51.02	51.59	S0177T
2	141.71	142.45	H2122
2	141.79	141.88	HCC95
2	141.94	142.20	H2126
2	142.00	142.20	H157
2	142.21	142.57	HCC95
2	142.70	142.78	HCC95
3	0.05	2.37	S0196T
3	49.85	50.82	S0189T
3	60.29	60.78	HCC95
3	60.32	60.40	H2887
3	62.24	62.57	S0170T
3	76.73	77.22	HCC95
3	85.27	85.79	H1963
3	152.82	152.95	H2882
3	152.82	152.95	S0177T
4	38.18	38.31	S0194T
4	92.20	92.57	H2126
4	131.18	131.30	H524
4	169.50	169.72	S0188T
4	182.98	183.52	S0169T
5	55.22	55.44	H1607
5	102.93	103.03	H2126
5	114.65	115.10	S0189T
5	136.38	136.49	H1963
6	53.54	54.11	H1993
6	162.84	163.19	HCC515
7	29.17	29.30	H1607
8	0.18	2.57	H2009
8	9.45	10.15	HCC1771
8	14.17	14.28	S0187T
8	16.42	16.54	H2887
8	137.65	137.86	H2122
9	5.42	5.84	H1993
9	8.61	9.12	S0177T
9	8.79	8.92	H358
9	9.41	9.55	H358
9	9.41	9.61	HCC1771
9	9.50	9.75	H2347
9	10.03	10.07	S0458T
9	20.90	22.94	H2126
9	21.20	22.19	HCC1359
9	21.58	25.10	HCC1771
9	21.70	22.94	H2882
9	21.84	26.83	HCC95
9	21.95	22.09	H2122
9	23.15	23.39	H2882
9	24.34	24.70	H157
10	11.23	11.80	H2126
10	34.63	34.79	H157
10	52.11	53.33	H1993
10	55.79	56.19	S0169T
10	68.10	68.59	H1963
10	75.49	76.13	H1963
10	89.03	89.40	H1607
10	89.18	89.88	S0187T
10	89.35	91.16	S0189T
10	116.49	117.43	S0189T
12	3.46	3.89	H1993
13	46.72	47.51	H2009
13	51.45	54.41	H2009
13	54.57	55.11	S0177T
17	12.16	12.40	S0187T
17	13.55	13.66	H2347
17	20.80	22.27	S0187T
18	19.83	24.48	H2887
18	26.34	26.72	NCI.H226
18	69.09	69.88	HCC461
21	9.93	24.51	HCC366
23	6.43	7.24	H157
23	25.29	26.27	S0187T
23	31.11	31.53	S0412T
23	126.71	127.03	H1607

^a Predicted regions of at least 5 kb in size containing at least 4 consecutive SNPs with inferred copy number = 0^b Based on hg16 genome assembly

Supplementary Table 2 All predicted high-level amplifications^a

Chromosome ^b	Start (Mb) ^b	Stop (Mb) ^b	Sample	Mean dCHIP copy number
1	30.81	31.36	H526	5.3
1	34.87	35.29	H2122	5.3
1	39.51	40.55	H1963	10.6
1	39.55	40.91	S0173T	10.7
1	56.91	65.68	S0198T	9.2
1	110.98	117.67	S0173T	7.6
1	242.77	243.19	S0377T	5.3
2	14.20	16.38	S0172T	14.2
2	15.25	17.06	H526	7.0
3	169.50	170.89	S0465T	6.9
3	174.86	175.18	S0465T	8.6
3	177.17	184.52	S0465T	7.0
3	182.50	184.47	S0515T	13.2
4	44.57	45.85	S0380T	7.9
5	8.88	14.31	S0376T	7.1
5	38.45	41.72	S0188T	7.0
5	90.09	90.65	MGH1622T	6.7
5	98.13	100.62	MGH1622T	4.8
5	104.61	104.81	MGH1622T	5.9
5	157.83	157.95	MGH1622T	6.8
6	11.60	11.96	HCC827	15.6
6	84.24	85.58	S0480T	7.9
6	135.41	135.58	H526	10.3
7	53.16	61.49	HCC827	11.3
7	54.24	69.62	AD347T	9.7
7	54.37	55.63	S0480T	13.7
7	115.70	116.09	H1993	9.1
7	118.07	123.35	H1993	7.1
8	32.16	32.30	HCC95	7.8
8	36.33	36.48	S0449T	7.3
8	38.05	39.97	MGH1622T	10.4
8	38.73	39.84	S0449T	6.4
8	40.30	42.23	S0458T	9.2
8	61.86	62.62	S0177T	13.6
8	74.22	76.27	HCC827	6.9
8	80.79	82.81	HCC827	6.9
8	100.57	100.75	AD309T	6.7
8	103.18	104.22	HCC827	6.9
8	124.15	124.52	HCC827	6.3
8	126.60	128.89	H524	6.6
8	127.46	128.89	HCC827	6.9
8	127.59	130.83	NCI.H23	8.0
8	127.90	129.62	H2122	3.6
8	128.44	129.60	H2087	7.9
8	133.08	133.65	HCC827	6.8
9	13.09	13.46	H1607	6.6
9	27.15	27.32	S0515T	6.7
9	39.01	62.64	S0465T	6.4
9	98.96	99.02	S0465T	6.3
10	86.63	87.16	HCC1359	6.8
11	34.05	39.37	HCC95	9.8
11	48.21	51.30	HCC95	6.8
11	65.15	69.34	HCC515	6.7
11	103.48	104.36	H1993	7.9
12	32.17	33.02	S0515T	8.8
12	32.69	36.59	H2087	7.8
12	56.26	57.37	H2087	8.8
12	59.44	59.78	H2087	7.1
12	62.95	63.61	HCC827	9.5
12	66.50	68.51	S0372T	7.0
14	27.57	27.87	S0480T	7.4
14	32.90	35.11	H1819	7.0
15	43.79	44.74	AD334T	6.4
15	48.27	51.62	AD334T	7.4
17	22.27	25.81	H2887	6.0
17	35.25	37.30	HCC515	10.5
17	37.93	39.11	H1819	8.0
17	51.10	52.51	H1819	7.9
19	34.02	35.55	S0524T	6.7
19	34.79	37.09	S0188T	7.9
19	43.01	45.00	S0515T	6.0
20	49.02	49.81	AD334T	6.8
20	52.72	53.40	AD334T	6.5
21	17.51	18.48	HCC827	6.9
22	16.99	20.31	H1819	6.8
22	17.51	21.44	HCC515	7.4
22	18.47	20.61	S0380T	6.4
22	19.45	20.75	HCC1359	6.5
22	27.84	30.18	S0480T	6.6

^a Predicted regions containing at least 4 SNPs, at least 5 kb in size and with an inferred copy number of > or = 7;^b Based on hg16 genome assembly

Supplementary Table 3 Genes within selected regions of amplification^a

Cytoband ^b	Minimally overlapped region ^{b,c}	Candidate genes ^d	Samples with copy number >= 7	Samples with copy number >= 4 and < 7
1p34.2	39.51 - 40.55	HEYL, NT5C1A, HPCAL4, PPIE, OXCT2, BMP8B, TRIT1, MYCL1 , FLJ14490, CAP1, PPT1, LOC441883, RLF, LOC127391, ZMPSTE24, COL9A2, LOC388621, LOC64744, LOC65243, FLJ16030, FLJ21144, MGC27466, RIMS3	H1963, S0173T	H1184, S0187T, S0193T, S0480T
		MYCNOS, MYCN , LOC391353		S0172T, H526 H1437, S0190T
2p24.3	16.00 - 16.38			
3q26.31	179.21 - 180.44	KCNMB2, WIG1, PIK3CA , KCNMB3, ZNF639, MFN1, GNB4	S0465T	S0446T, H1819, HCC95, S0168T, S0169T, S0187T, MGH1622T, H2882, S0515T
3q26.31	183.75 - 184.35	ATP11B, RP42, MCCC1, LAMP3, RNU3P4, KIAA0861, B3GNT5	S0465T, S0515T	S0446T, H1819, HCC95, S0168T, S0169T, S0173T, S0187T, MGH1622T
7p12.1-p11.2	54.36 - 54.84	MTERF, AKAP9, CYP51A1, LOC401387, CCM1, ANKIB1, LOC402286, ODAG, ERVWE1, PEX1, DKFZP564O00523, LOC442333, MGC40405, CDK6 , LOC441267, RN7SLP4	S0480T	S0405T, H1819, H1993
7q21.2	90.81 - 92.22			S0464T, H1993, H2122, AD311T
7q31.2	115.7 - 117.42	CAV2, CAV1, MET , CAPZA2, ST7, WNT2, ASZ1, CFTR, CTTNBP2, LSM8, ANKRD7	H1993	H2009, HOP-92
8p11.23	38.05 - 39.21	LSM1, BAG4, DDHD2, HTPAP, WHSC1L1, LOC441345, LETM2, FGFR1 , FLJ43582, LOC286140, TACC1, PLEKHA2, FLJ0724, BLP1, ADAM9, ADAM32, ADAM5	S0449T, MGH1622T	S0480T, H2882, HCC1359, HCC95
8q12.2-q12.3	61.86 - 62.22	LOC442389, NASPP1, LOC157813, LOC441350, (MGC34646, ASPH)	S0177T	S0170T, H1993, H2882, HCC827
8q24.21	128.66 - 128.89	MYC , PVT1	H2122, H524, NCI-H23, H2087, HCC827	S0535T, H2882, H2887, HCC827, S0170T, S0194T, AD330T, H358
11q13.3	68.58 - 69.34	TPCN2, MYEOV, LOC390218, LOC399919, LOC44049, ORAOV1, FGF19, FGF4, FGF3, CCND1	HCC515	HCC366, HOP-62, NCI-H23, HCC78
12p11.21	32.69 - 33.21	DNM1L, CGI-04, PKP2, LOC283343	S0515T, H2087	S0372T, S0376T, H157, H1993, H2009, HCC461, HOP-62
12q13.3	56.26 - 56.75	KIF5A, PIP5K2C, DTX3, GEFT, SLC26A10, GALGT, LOC441641, OS-9, CENTG1, SAS, CDK4 , LOC92979, CYP27B1, METTL1, DKFZP586D0919, TSFM, AVIL, CTDSP2	H2087, HCC827	H1993, S0372T, S0514T, S0539T
19q12	34.79 - 35.55	POP4, PLEKHF1, C19orf12, LOC126170, C19orf2, TAF2GL, CCNE1	S0188T, S0524T	H2887
22q11.21	19.45 - 20.31	KIF4CA, SERPIND1, SNAP29, CRKL , LOC400890, LOC400890, FLJ30473, FLJ30473, LZTR1, THAP7, LOC439931, MGC16703, P2RXL1, SLC7A4, LOC440799, LOC400891, LOC402037, FLJ42953, LOC440800, LOC376818, LOC284861, LOC440801, LOC440802, LOC400888, LOC388846, LOC440803, LOC440803, LOC391303, LOC391298, LOC388853, LOC440804, HIC2, LOC150221, UBE2L3, LOC150223	HCC515, H1819, HCC1359, S0380T	S0464T, S0446T, H524

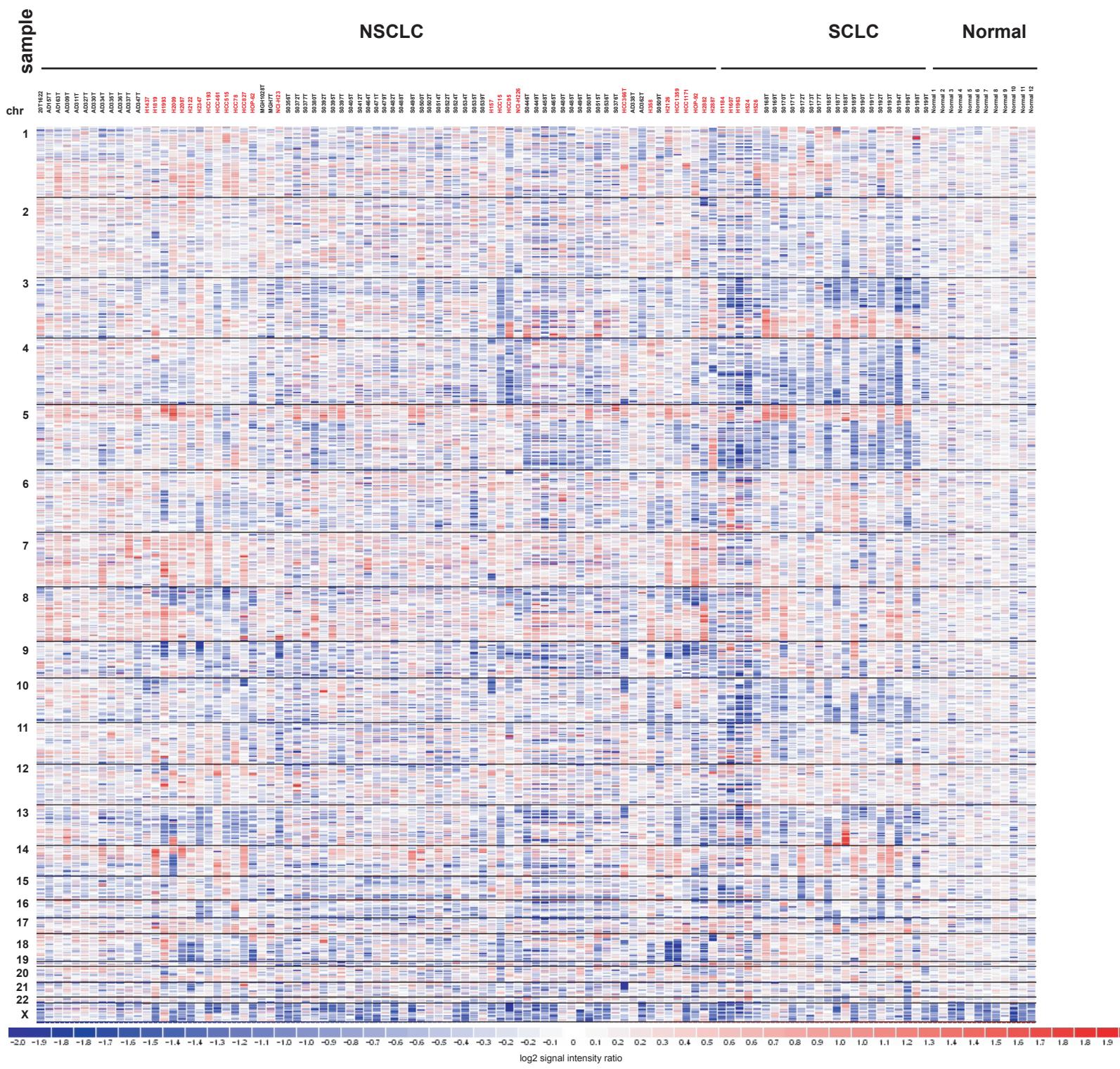
^a Regions with at least two amplifications >= 7 or regions surrounding other loci discussed in text^b Based on hg16 assembly^c Region of minimal overlap between samples, of copy number >= 4^d Bold indicates likely oncogene; genes in parentheses occur outside of minimal region, but within the high-level amplicon of at least one sample

SUPPLEMENTARY FIGURE LEGENDS

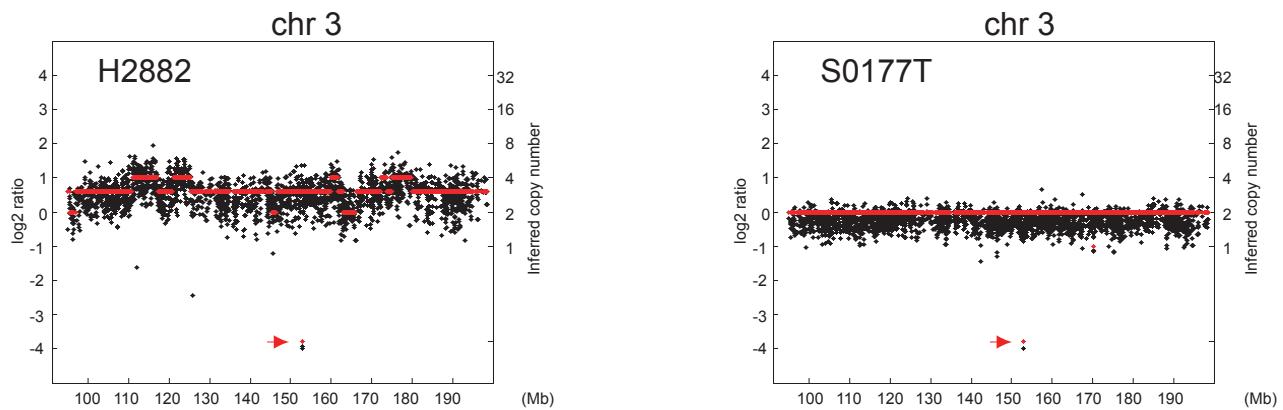
Supplementary Figure 1. The global view of copy number alterations across chromosomes 1-X in 101 tumor and cell line samples and 12 normal samples is shown using log₂ signal intensity ratio for each sample. Colors vary from dark blue to dark red representing the range of log₂ ratio. Each column represents a different cell line or tumor, and each row represents SNP markers, ordered by genomic position from p arm (top) to q arm (bottom).

Supplementary Figure 2. (A) Deletions of the 3q25 region are shown by scatter plots of log 2 copy number ratios (black dots, left axis) and inferred copy number (red dots, right axis) against chromosomal SNP position using the hg16 genome assembly in non-small cell carcinoma line H2882 and primary small cell carcinoma S0177T. (B) High-level amplifications of the 12p11 and *CDK4* locus are shown by scatter plots of log 2 copy number ratios (black dots, left axis) and inferred copy number (red dots, right axis) against chromosomal SNP position using the hg16 genome assembly. The adenocarcinoma cell line H2087 shows amplification of both the 12p11 and *CDK4* loci and the primary squamous cell carcinoma S0515T shows 12p11 amplification. (C) High-level amplification of the 22q11 locus. Amplifications within the 22q11 region are shown by scatter plots of log 2 copy number ratios (black dots, left axis) and inferred copy number (red dots, right axis) against chromosomal SNP position using the hg16 genome assembly in adenocarcinoma cell line HCC515 and primary adenocarcinoma S0380T.

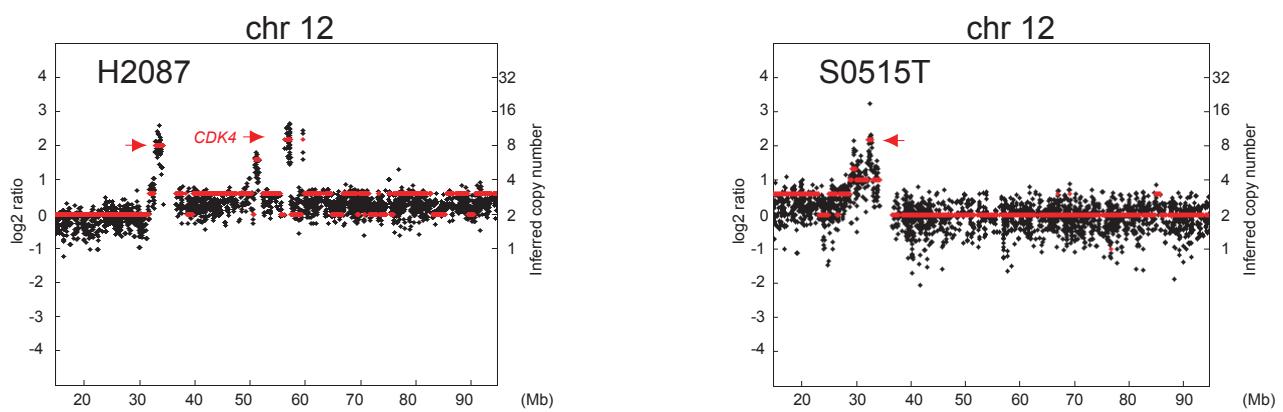
Supplementary Figure 3. Alignment of human PTPRD (NM_13091) with PTPRD-like transcripts in human (BC028038) and mouse (AK034145). Nucleotide sequences were aligned with AlignX, a component of the VectorNTI Suite 9.0.0 and exported in MSF format. The alignment file was processed with the GeneDoc program (<http://www.psc.edu/biomed/genedoc>). Shading levels represent 100% (darkest), > 80%, > 60% and < 60% conservation of amino acid residues among the sequences for a given position. Only the first 1849 bp of PTPRD are shown.



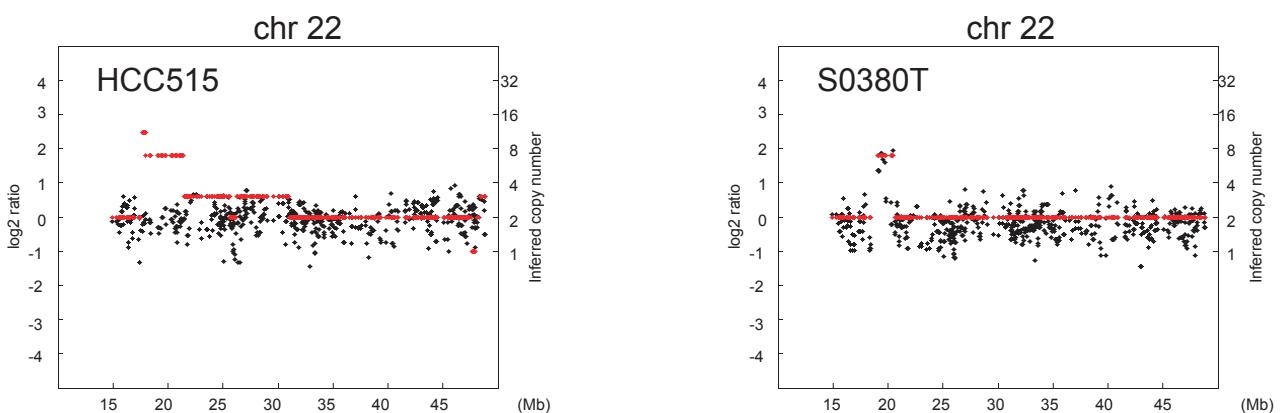
A



B



C



NM_130391:	*	20	*	40	*	60	*	80	*	100
bc028038 :	-	-	-	-	-	-	-	-	-	-	-
AK034145 :	GGCCCCGCCCGCCCCGCCGCACCGACGCACCTGCGGGCACTCGCCCCGGCTCTGCGGGACCCGCGGGCTCCGAGCGCGCCACCCCTCCCGT	:	100								
NM_130391:	*	120	*	140	*	160	*	180	*	200
bc028038 :	-	-	-	-	-	-	-	-	-	-	-
AK034145 :	GCCGACCTCGCACACGCAGATAACCACCTTTAAAGAAGCCGAAGCGCTGCAGCCCACCGACGCCAGCGACGCCGTGCCGCTAGGCCTCTCCTG	:	200								
NM_130391:	*	220	*	240	*	260	*	280	*	300
bc028038 :	AG TGCAGTTT T TCTGGC CTGTG TGG AATAGAAAAGACA ATTCT TTA TTGACTGTTAGAAGAAAGAGAAGACTCCTTAGGTTTCAGAGTTTG	:	129								
AK034145 :	TC TGCAGTTGAGCCGGACCTGGGAGACAGAGAAAGACA GTTCT CGG TTGACTGAAAGAAAGAGAAGACTCCTTAGGTTTGAGAGTTTG	:	292								
NM_130391:	*	320	*	340	*	360	*	380	*	400
bc028038 :	GGAGCGGCTGTTAGTGAAGAAATAGAAGAATCAAAGAAGTAAAGGAACTGTCATAAGAACCTAGGAAATTCTTGAGGGAGTTTGATACTTTTCAT	:	229								
AK034145 :	GGAGCGGCTGCCTAGTGAAGAAATAGAAGAATCAAAGAAGTAAAGGAACTATCTCATATCACA TAACTAGGAAACCTTGAGGGAGTTGCACACTTTCAT	:	392								
NM_130391:	*	420	*	440	*	460	*	480	*	500
bc028038 :	CCTCCAGCTATAAAATCATCTTGTAGGGGA A CTGTACATTGGTGGAAATTAAGGCAAGCAGTTCCTGGCC C GTGATAITCCAGITAGAGTCTCTG	:	329								
AK034145 :	CC.CCAGTCACTGC.TCCCCTTCG.GGGGGAG G TCTACTTCTCGAAA.TAGAAGGCAAGCAGTTCCTGGCC T GTGAAATCTGAGTG.GCAGTCCTG	:	487								
NM_130391:	*	520	*	540	*	560	*	580	*	600
bc028038 :	ACTGACACCATGTTGGCACC.....GAGGGAGAGCGAAGGGCTTCCGGCTCAGGGTCTCAGGGTGTGAACCTTCTGAGCTTACGAAAAGGGAGCATGCC	:	423								
AK034145 :	GCTGTCACTATGCTGGCCCOAATGTGATGGACATGAACTTGT	:	587								
NM_130391:	*	620	*	640	*	660	*	680	*	700
bc028038 :	GACTCTTGATCTCTGGTAACTTCAAAATCTGGTCTCAGGGTGTGAACCTTCTTCCATCTAACCTGTGAGCTTACGAAAAGGGAGCATGCC	:	523								
AK034145 :	GACTCTGGATCTCTGGTCACTTCAACGGTCTCAGGGTGTGAACCTTCTTCTATGCTAACCTGTGAG	:	662								
NM_130391:	*	720	*	740	*	760	*	780	*	800
bc028038 :	TG TCTTATTCTCAGTCCTCATGGAAATAAAAGATTGGAGATGATAGCTACCTGATGATGGTGCCTGTCCATTAAC TGAAACTGTGGTTTGAACT	:	623								
AK034145 :	TC.....G.....A.....	:	712								
NM_130391:	*	820	*	840	*	860	*	880	*	900
bc028038 :	TCTTGAGGCCAGGACTGTGCTGAAACACCCACGGTGGCTA.....CTGAGACCTGATAGATGGGAGAAGTCTGGTGAACCCCCAGGGATCTAAC	:	61								
AK034145 :	TCTTGAGGCCAGGACTGTGCTGAAACACCCACGGTGGCTA.....CTGAGACCTGATAGATGGGAGAAGTCTGGTGAACCCCCAGGGATCTAAC	:	723								
NM_130391:	*	920	*	940	*	960	*	980	*	1000
bc028038 :	GTTCCAGCTGAAATTTCAAGTCGGACAGTCGCTGGCTCGGCTCGGCTCGCTGAGACACCCAGGATTAGATGAAAGACACAGGGTC	:	161								
AK034145 :	GTTCCAGCTGAAATTTCAAGTCGGACAGTCGCTGGCTCGGCTCGCTGAGACACCCAGGATTAGATGAAAGACACAGGGTC	:	823								
NM_130391:	*	1020	*	1040	*	1060	*	1080	*	1100
bc028038 :	CGTAGGCCAGGCCTGCTGCTCCCTCACCTTCTCCCTCGGA.....GGATGCTGAGACACCCAGGATTAGATGAAAGACACAGGGTC	:	261								
AK034145 :	CGTAGGCCAGGCCTGCTGCTCCCTCACCTTCTCCCTCGGA.....GGATGCTGAGACACCCAGGATTAGATGAAAGACACAGGGTC	:	923								
NM_130391:	*	1120	*	1140	*	1160	*	1180	*	1200
bc028038 :	TCTGGGGAGGTTGCTCTTCATCTGCAAGCTACGGGAGACCCAAGACCTAAATTGTCGGAAACAAAAAAGGAAAGAAAGTCAGCAA	:	361								
AK034145 :	TCTGGGGAGGTTGCTCTTCATCTGCAAGCTACGGGAGACCCAAGACCTAAATTGTCGGAAACAAAAAAGGAAAGAAAGTCAGCAA	:	1023								
NM_130391:	*	1220	*	1240	*	1260	*	1280	*	1300
bc028038 :	AGGTAATAGAATTGACGATGGGTCTGGATCAGTCAGAATACACCCCTACGGGATCCCTGAGACGGGATGAGGCCATTATGAATGTGTCCTCAAAATAA	:	461								
AK034145 :	AGGTAATAGAATTGACGATGGGTCTGGATCAGTCAGAATACACCCCTACGGGATGAGGCCATTATGAATGTGTCCTCAAAATAA	:	1123								
NM_130391:	*	1320	*	1340	*	1360	*	1380	*	1400
bc028038 :	TGTGGGAGAATAAGTGTACACAGCTACAGTTGGCTCTGGATCAGTCAGAATACACCCCTACGGGATGAGGCCATTATGAATGTGTCCTCAAAATAA	:	561								
AK034145 :	TGTGGGAGAATAAGTGTACACAGCTACAGTTGGCTCTGGATCAGTCAGAATACACCCCTACGGGATGAGGCCATTATGAATGTGTCCTCAAAATAA	:	1223								

* 1420 * 1440 * 1460 * 1480 * 1500

NM_130391: GT₁ GAGC₂ G₃ AACTCGCAC₄ GGCCACCATGCT₅ TTGTGCAGCCAGT₆ GGTAAATCCGGATCCA₇ GAAATCACTTGTTAAAGATTCTTACCTGT₈ GGACACAAGCA₉ : 661
bc028038 : GT₁ GAGC₂ G₃ AACTCGCAC₄ GGCCACCATGCT₅ TTGTGCAGCCAGT₆ GGTAAATCCGGATCCA₇ GAAATCACTTGTTAAAGATTCTTACCTGT₈ GGACACAAGCA₉ : 1323
AK034145 : GT₁ GAAAC₂ G₃ ACCCGCAC₄ GGCCACCATGCT₅ TTGTGCAGCCAC₆ GGTAAATCCGGATCCA₇ GAAATCACTTGTTAAAGATTCTTACCTGT₈ TGACACAAGCA₉ : 1410

* 1520 * 1540 * 1560 * 1580 * 1600

NM_130391: ACAACAAATG₁ TCGTATTAAAGCAGTTACGATCAGG₂ AGCCC₃ TT₄ CAGATT₅ GAGAGAG₆ GAAGAG₇ TC₈ TGA₉ CAA₁₀ GAAA₁₁ AT₁₂ TGA₁₃ G₁₄ G₁₅ G₁₆ G₁₇ G₁₈ G₁₉ G₂₀ G₂₁ G₂₂ G₂₃ G₂₄ G₂₅ G₂₆ G₂₇ G₂₈ G₂₉ G₃₀ G₃₁ G₃₂ G₃₃ G₃₄ G₃₅ G₃₆ G₃₇ G₃₈ G₃₉ G₄₀ G₄₁ G₄₂ G₄₃ G₄₄ G₄₅ G₄₆ G₄₇ G₄₈ G₄₉ G₅₀ G₅₁ G₅₂ G₅₃ G₅₄ G₅₅ G₅₆ G₅₇ G₅₈ G₅₉ G₆₀ G₆₁ G₆₂ G₆₃ G₆₄ G₆₅ G₆₆ G₆₇ G₆₈ G₆₉ G₇₀ G₇₁ G₇₂ G₇₃ G₇₄ G₇₅ G₇₆ G₇₇ G₇₈ G₇₉ G₈₀ G₈₁ G₈₂ G₈₃ G₈₄ G₈₅ G₈₆ G₈₇ G₈₈ G₈₉ G₉₀ G₉₁ G₉₂ G₉₃ G₉₄ G₉₅ G₉₆ G₉₇ G₉₈ G₉₉ G₁₀₀ G₁₀₁ G₁₀₂ G₁₀₃ G₁₀₄ G₁₀₅ G₁₀₆ G₁₀₇ G₁₀₈ G₁₀₉ G₁₁₀ G₁₁₁ G₁₁₂ G₁₁₃ G₁₁₄ G₁₁₅ G₁₁₆ G₁₁₇ G₁₁₈ G₁₁₉ G₁₂₀ G₁₂₁ G₁₂₂ G₁₂₃ G₁₂₄ G₁₂₅ G₁₂₆ G₁₂₇ G₁₂₈ G₁₂₉ G₁₃₀ G₁₃₁ G₁₃₂ G₁₃₃ G₁₃₄ G₁₃₅ G₁₃₆ G₁₃₇ G₁₃₈ G₁₃₉ G₁₄₀ G₁₄₁ G₁₄₂ G₁₄₃ G₁₄₄ G₁₄₅ G₁₄₆ G₁₄₇ G₁₄₈ G₁₄₉ G₁₅₀ G₁₅₁ G₁₅₂ G₁₅₃ G₁₅₄ G₁₅₅ G₁₅₆ G₁₅₇ G₁₅₈ G₁₅₉ G₁₆₀ G₁₆₁ G₁₆₂ G₁₆₃ G₁₆₄ G₁₆₅ G₁₆₆ G₁₆₇ G₁₆₈ G₁₆₉ G₁₇₀ G₁₇₁ G₁₇₂ G₁₇₃ G₁₇₄ G₁₇₅ G₁₇₆ G₁₇₇ G₁₇₈ G₁₇₉ G₁₈₀ G₁₈₁ G₁₈₂ G₁₈₃ G₁₈₄ G₁₈₅ G₁₈₆ G₁₈₇ G₁₈₈ G₁₈₉ G₁₉₀ G₁₉₁ G₁₉₂ G₁₉₃ G₁₉₄ G₁₉₅ G₁₉₆ G₁₉₇ G₁₉₈ G₁₉₉ G₂₀₀ G₂₀₁ G₂₀₂ G₂₀₃ G₂₀₄ G₂₀₅ G₂₀₆ G₂₀₇ G₂₀₈ G₂₀₉ G₂₁₀ G₂₁₁ G₂₁₂ G₂₁₃ G₂₁₄ G₂₁₅ G₂₁₆ G₂₁₇ G₂₁₈ G₂₁₉ G₂₂₀ G₂₂₁ G₂₂₂ G₂₂₃ G₂₂₄ G₂₂₅ G₂₂₆ G₂₂₇ G₂₂₈ G₂₂₉ G₂₃₀ G₂₃₁ G₂₃₂ G₂₃₃ G₂₃₄ G₂₃₅ G₂₃₆ G₂₃₇ G₂₃₈ G₂₃₉ G₂₄₀ G₂₄₁ G₂₄₂ G₂₄₃ G₂₄₄ G₂₄₅ G₂₄₆ G₂₄₇ G₂₄₈ G₂₄₉ G₂₅₀ G₂₅₁ G₂₅₂ G₂₅₃ G₂₅₄ G₂₅₅ G₂₅₆ G₂₅₇ G₂₅₈ G₂₅₉ G₂₆₀ G₂₆₁ G₂₆₂ G₂₆₃ G₂₆₄ G₂₆₅ G₂₆₆ G₂₆₇ G₂₆₈ G₂₆₉ G₂₇₀ G₂₇₁ G₂₇₂ G₂₇₃ G₂₇₄ G₂₇₅ G₂₇₆ G₂₇₇ G₂₇₈ G₂₇₉ G₂₈₀ G₂₈₁ G₂₈₂ G₂₈₃ G₂₈₄ G₂₈₅ G₂₈₆ G₂₈₇ G₂₈₈ G₂₈₉ G₂₉₀ G₂₉₁ G₂₉₂ G₂₉₃ G₂₉₄ G₂₉₅ G₂₉₆ G₂₉₇ G₂₉₈ G₂₉₉ G₃₀₀ G₃₀₁ G₃₀₂ G₃₀₃ G₃₀₄ G₃₀₅ G₃₀₆ G₃₀₇ G₃₀₈ G₃₀₉ G₃₁₀ G₃₁₁ G₃₁₂ G₃₁₃ G₃₁₄ G₃₁₅ G₃₁₆ G₃₁₇ G₃₁₈ G₃₁₉ G₃₂₀ G₃₂₁ G₃₂₂ G₃₂₃ G₃₂₄ G₃₂₅ G₃₂₆ G₃₂₇ G₃₂₈ G₃₂₉ G₃₃₀ G₃₃₁ G₃₃₂ G₃₃₃ G₃₃₄ G₃₃₅ G₃₃₆ G₃₃₇ G₃₃₈ G₃₃₉ G₃₄₀ G₃₄₁ G₃₄₂ G₃₄₃ G₃₄₄ G₃₄₅ G₃₄₆ G₃₄₇ G₃₄₈ G₃₄₉ G₃₅₀ G₃₅₁ G₃₅₂ G₃₅₃ G₃₅₄ G₃₅₅ G₃₅₆ G₃₅₇ G₃₅₈ G₃₅₉ G₃₆₀ G₃₆₁ G₃₆₂ G₃₆₃ G₃₆₄ G₃₆₅ G₃₆₆ G₃₆₇ G₃₆₈ G₃₆₉ G₃₇₀ G₃₇₁ G₃₇₂ G₃₇₃ G₃₇₄ G₃₇₅ G₃₇₆ G₃₇₇ G₃₇₈ G₃₇₉ G₃₈₀ G₃₈₁ G₃₈₂ G₃₈₃ G₃₈₄ G₃₈₅ G₃₈₆ G₃₈₇ G₃₈₈ G₃₈₉ G₃₉₀ G₃₉₁ G₃₉₂ G₃₉₃ G₃₉₄ G₃₉₅ G₃₉₆ G₃₉₇ G₃₉₈ G₃₉₉ G₄₀₀ G₄₀₁ G₄₀₂ G₄₀₃ G₄₀₄ G₄₀₅ G₄₀₆ G₄₀₇ G₄₀₈ G₄₀₉ G₄₁₀ G₄₁₁ G₄₁₂ G₄₁₃ G₄₁₄ G₄₁₅ G₄₁₆ G₄₁₇ G₄₁₈ G₄₁₉ G₄₂₀ G₄₂₁ G₄₂₂ G₄₂₃ G₄₂₄ G₄₂₅ G₄₂₆ G₄₂₇ G₄₂₈ G₄₂₉ G₄₃₀ G₄₃₁ G₄₃₂ G₄₃₃ G₄₃₄ G₄₃₅ G₄₃₆ G₄₃₇ G₄₃₈ G₄₃₉ G₄₄₀ G₄₄₁ G₄₄₂ G₄₄₃ G₄₄₄ G₄₄₅ G₄₄₆ G₄₄₇ G₄₄₈ G₄₄₉ G₄₅₀ G₄₅₁ G₄₅₂ G₄₅₃ G₄₅₄ G₄₅₅ G₄₅₆ G₄₅₇ G₄₅₈ G₄₅₉ G₄₆₀ G₄₆₁ G₄₆₂ G₄₆₃ G₄₆₄ G₄₆₅ G₄₆₆ G₄₆₇ G₄₆₈ G₄₆₉ G₄₇₀ G₄₇₁ G₄₇₂ G₄₇₃ G₄₇₄ G₄₇₅ G₄₇₆ G₄₇₇ G₄₇₈ G₄₇₉ G₄₈₀ G₄₈₁ G₄₈₂ G₄₈₃ G₄₈₄ G₄₈₅ G₄₈₆ G₄₈₇ G₄₈₈ G₄₈₉ G₄₉₀ G₄₉₁ G₄₉₂ G₄₉₃ G₄₉₄ G₄₉₅ G₄₉₆ G₄₉₇ G₄₉₈ G₄₉₉ G₅₀₀ G₅₀₁ G₅₀₂ G₅₀₃ G₅₀₄ G₅₀₅ G₅₀₆ G₅₀₇ G₅₀₈ G₅₀₉ G₅₁₀ G₅₁₁ G₅₁₂ G₅₁₃ G₅₁₄ G₅₁₅ G₅₁₆ G₅₁₇ G₅₁₈ G₅₁₉ G₅₂₀ G₅₂₁ G₅₂₂ G₅₂₃ G₅₂₄ G₅₂₅ G₅₂₆ G₅₂₇ G₅₂₈ G₅₂₉ G₅₃₀ G₅₃₁ G₅₃₂ G₅₃₃ G₅₃₄ G₅₃₅ G₅₃₆ G₅₃₇ G₅₃₈ G₅₃₉ G₅₄₀ G₅₄₁ G₅₄₂ G₅₄₃ G₅₄₄ G₅₄₅ G₅₄₆ G₅₄₇ G₅₄₈ G₅₄₉ G₅₅₀ G₅₅₁ G₅₅₂ G₅₅₃ G₅₅₄ G₅₅₅ G₅₅₆ G₅₅₇ G₅₅₈ G₅₅₉ G₅₆₀ G₅₆₁ G₅₆₂ G₅₆₃ G₅₆₄ G₅₆₅ G₅₆₆ G₅₆₇ G₅₆₈ G₅₆₉ G₅₇₀ G₅₇₁ G₅₇₂ G₅₇₃ G₅₇₄ G₅₇₅ G₅₇₆ G₅₇₇ G₅₇₈ G₅₇₉ G₅₈₀ G₅₈₁ G₅₈₂ G₅₈₃ G₅₈₄ G₅₈₅ G₅₈₆ G₅₈₇ G₅₈₈ G₅₈₉ G₅₉₀ G₅₉₁ G₅₉₂ G₅₉₃ G₅₉₄ G₅₉₅ G₅₉₆ G₅₉₇ G₅₉₈ G₅₉₉ G₆₀₀ G₆₀₁ G₆₀₂ G₆₀₃ G₆₀₄ G₆₀₅ G₆₀₆ G₆₀₇ G₆₀₈ G₆₀₉ G₆₁₀ G₆₁₁ G₆₁₂ G₆₁₃ G₆₁₄ G₆₁₅ G₆₁₆ G₆₁₇ G₆₁₈ G₆₁₉ G₆₂₀ G₆₂₁ G₆₂₂ G₆₂₃ G₆₂₄ G₆₂₅ G₆₂₆ G₆₂₇ G₆₂₈ G₆₂₉ G₆₃₀ G₆₃₁ G₆₃₂ G₆₃₃ G₆₃₄ G₆₃₅ G₆₃₆ G₆₃₇ G₆₃₈ G₆₃₉ G₆₄₀ G₆₄₁ G₆₄₂ G₆₄₃ G₆₄₄ G₆₄₅ G₆₄₆ G₆₄₇ G₆₄₈ G₆₄₉ G₆₅₀ G₆₅₁ G₆₅₂ G₆₅₃ G₆₅₄ G₆₅₅ G₆₅₆ G₆₅₇ G₆₅₈ G₆₅₉ G₆₆₀ G₆₆₁ G₆₆₂ G₆₆₃ G₆₆₄ G₆₆₅ G₆₆₆ G₆₆₇ G₆₆₈ G₆₆₉ G₆₇₀ G₆₇₁ G₆₇₂ G₆₇₃ G₆₇₄ G₆₇₅ G₆₇₆ G₆₇₇ G₆₇₈ G₆₇₉ G₆₈₀ G₆₈₁ G₆₈₂ G₆₈₃ G₆₈₄ G₆₈₅ G₆₈₆ G₆₈₇ G₆₈₈ G₆₈₉ G₆₉₀ G₆₉₁ G₆₉₂ G₆₉₃ G₆₉₄ G₆₉₅ G₆₉₆ G₆₉₇ G₆₉₈ G₆₉₉ G₇₀₀ G₇₀₁ G₇₀₂ G₇₀₃ G₇₀₄ G₇₀₅ G₇₀₆ G₇₀₇ G₇₀₈ G₇₀₉ G₇₁₀ G₇₁₁ G₇₁₂ G₇₁₃ G₇₁₄ G₇₁₅ G₇₁₆ G₇₁₇ G₇₁₈ G₇₁₉ G₇₂₀ G₇₂₁ G₇₂₂ G₇₂₃ G₇₂₄ G₇₂₅ G₇₂₆ G₇₂₇ G₇₂₈ G₇₂₉ G₇₃₀ G₇₃₁ G₇₃₂ G₇₃₃ G₇₃₄ G₇₃₅ G₇₃₆ G₇₃₇ G₇₃₈ G₇₃₉ G₇₄₀ G₇₄₁ G₇₄₂ G₇₄₃ G₇₄₄ G₇₄₅ G₇₄₆ G₇₄₇ G₇₄₈ G₇₄₉ G₇₅₀ G₇₅₁ G₇₅₂ G₇₅₃ G₇₅₄ G₇₅₅ G₇₅₆ G₇₅₇ G₇₅₈ G₇₅₉ G₇₆₀ G₇₆₁ G₇₆₂ G₇₆₃ G₇₆₄ G₇₆₅ G₇₆₆ G₇₆₇ G₇₆₈ G₇₆₉ G₇₇₀ G₇₇₁ G₇₇₂ G₇₇₃ G₇₇₄ G₇₇₅ G₇₇₆ G₇₇₇ G₇₇₈ G₇₇₉ G₇₈₀ G₇₈₁ G₇₈₂ G₇₈₃ G₇₈₄ G₇₈₅ G₇₈₆ G₇₈₇ G₇₈₈ G₇₈₉ G₇₉₀ G₇₉₁ G₇₉₂ G₇₉₃ G₇₉₄ G₇₉₅ G₇₉₆ G₇₉₇ G₇₉₈ G₇₉₉ G₈₀₀ G₈₀₁ G₈₀₂ G₈₀₃ G₈₀₄ G₈₀₅ G₈₀₆ G₈₀₇ G₈₀₈ G₈₀₉ G₈₁₀ G₈₁₁ G₈₁₂ G₈₁₃ G₈₁₄ G₈₁₅ G₈₁₆ G₈₁₇ G₈₁₈ G₈₁₉ G₈₂₀ G₈₂₁ G₈₂₂ G₈₂₃ G₈₂₄ G₈₂₅ G₈₂₆ G₈₂₇ G₈₂₈ G₈₂₉ G₈₃₀ G₈₃₁ G₈₃₂ G₈₃₃ G₈₃₄ G₈₃₅ G₈₃₆ G₈₃₇ G₈₃₈ G₈₃₉ G₈₄₀ G₈₄₁ G₈₄₂ G₈₄₃ G₈₄₄ G₈₄₅ G₈₄₆ G₈₄₇ G₈₄₈ G₈₄₉ G₈₅₀ G₈₅₁ G₈₅₂ G₈₅₃ G₈₅₄ G₈₅₅ G₈₅₆ G₈₅₇ G₈₅₈ G₈₅₉ G₈₆₀ G₈₆₁ G₈₆₂ G₈₆₃ G₈₆₄ G₈₆₅ G₈₆₆ G₈₆₇ G₈₆₈ G₈₆₉ G₈₇₀ G₈₇₁ G₈₇₂ G₈₇₃ G₈₇₄ G₈₇₅ G₈₇₆ G₈₇₇ G₈₇₈ G₈₇₉ G₈₈₀ G₈₈₁ G₈₈₂ G₈₈₃ G₈₈₄ G₈₈₅ G₈₈₆ G₈₈₇ G₈₈₈ G₈₈₉ G₈₉₀ G₈₉₁ G₈₉₂ G₈₉₃ G₈₉₄ G₈₉₅ G₈₉₆ G₈₉₇ G₈₉₈ G₈₉₉ G₉₀₀ G₉₀₁ G₉₀₂ G₉₀₃ G₉₀₄ G₉₀₅ G₉₀₆ G₉₀₇ G₉₀₈ G₉₀₉ G₉₁₀ G₉₁₁ G₉₁₂ G₉₁₃ G₉₁₄ G₉₁₅ G₉₁₆ G₉₁₇ G₉₁₈ G₉₁₉ G₉₂₀ G₉₂₁ G₉₂₂ G₉₂₃ G₉₂₄ G₉₂₅ G₉₂₆ G₉₂₇ G₉₂₈ G₉₂₉ G₉₃₀ G₉₃₁ G₉₃₂ G₉₃₃ G₉₃₄ G₉₃₅ G₉₃₆ G₉₃₇ G₉₃₈ G₉₃₉ G₉₄₀ G₉₄₁ G₉₄₂ G₉₄₃ G₉₄₄ G₉₄₅ G₉₄₆ G₉₄₇ G₉₄₈ G₉₄₉ G₉₅₀ G₉₅₁ G₉₅₂ G₉₅₃ G₉₅₄ G₉₅₅ G₉₅₆ G₉₅₇ G₉₅₈ G₉₅₉ G₉₆₀ G₉₆₁ G₉₆₂ G₉₆₃ G₉₆₄ G₉₆₅ G₉₆₆ G₉₆₇ G₉₆₈ G₉₆₉ G₉₇₀ G₉₇₁ G₉₇₂ G₉₇₃ G₉₇₄ G₉₇₅ G₉₇₆ G₉₇₇ G₉₇₈ G₉₇₉ G₉₈₀ G₉₈₁ G₉₈₂ G₉₈₃ G₉₈₄ G₉₈₅ G₉₈₆ G₉₈₇ G₉₈₈ G₉₈₉ G₉₉₀ G₉₉₁ G₉₉₂ G₉₉₃ G₉₉₄ G₉₉₅ G₉₉₆ G₉₉₇ G₉₉₈ G₉₉₉ G₁₀₀₀