

Supplemental Material

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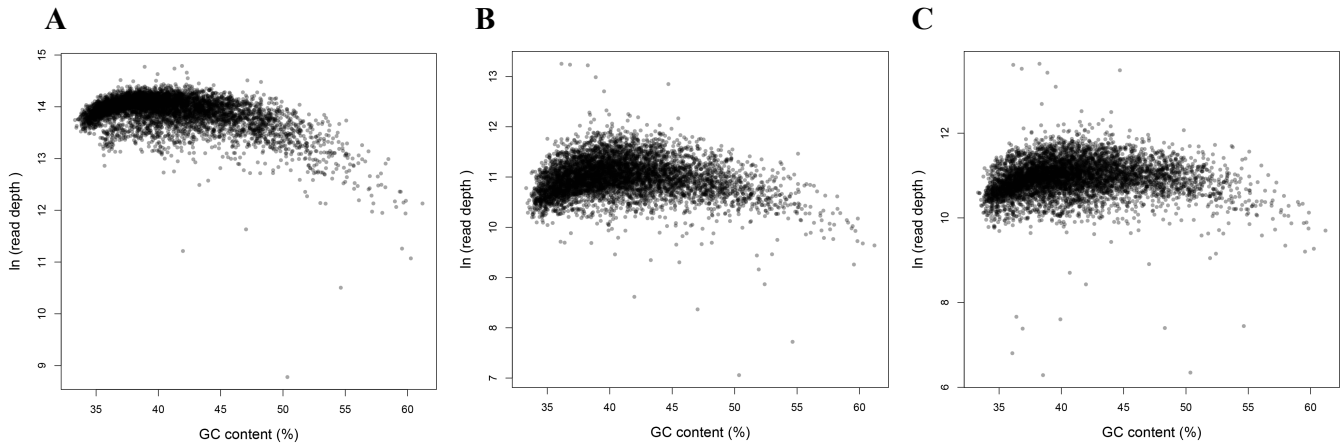


Figure S1. Distribution of mapped read depth across GC contents.

- (A) Sequence read depth versus GC percentage based on sequence data from a control leukocyte (CO1L1D). The bin size is 500 kb.
- (B) Sequence read depth versus GC percentage based on sequence data from a primary tumour cell (CO1PC28L). The bin size is 500 kb.
- (C) Sequence read depth versus GC percentage based on sequence data from a CTC (CO1C1L). The bin size is 500 kb.

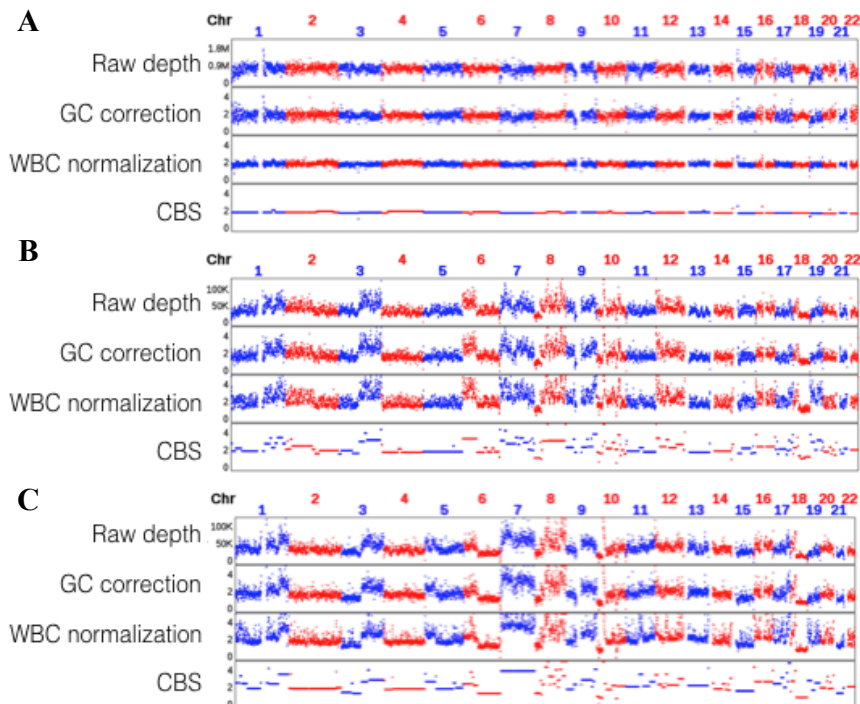


Figure S2. Normalization of read depth throughout the genome. Raw depth, Sequence read depth after GC correction, read depth normalized using white blood cells (WBCs) as the control, read depth segmented using the circular segmentation (CBS) algorithm after WBC normalization are plotted from sequence data from a control leukocyte (CO1L1D) (A), a primary tumour cell (CO1PC28L) (B), and a CTC (CO1C1L) (C).

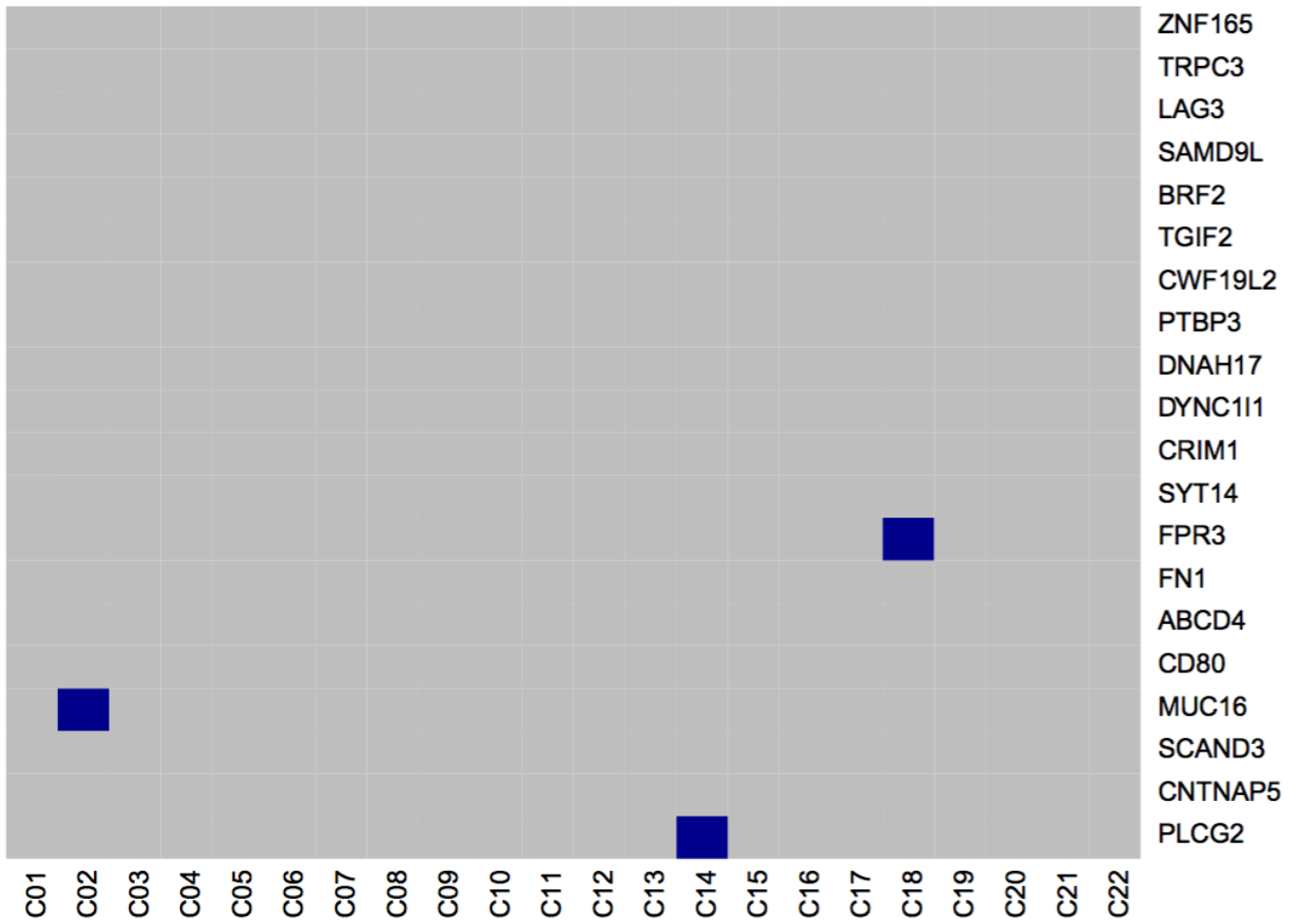


Figure S3. SNVs in normal leukocytes. The distribution of 20 non-synonymous mutations in Fig. 1B was assessed in 22 normal cells (DAPI+, anti-CD45+, and anti-cytokeratin-).

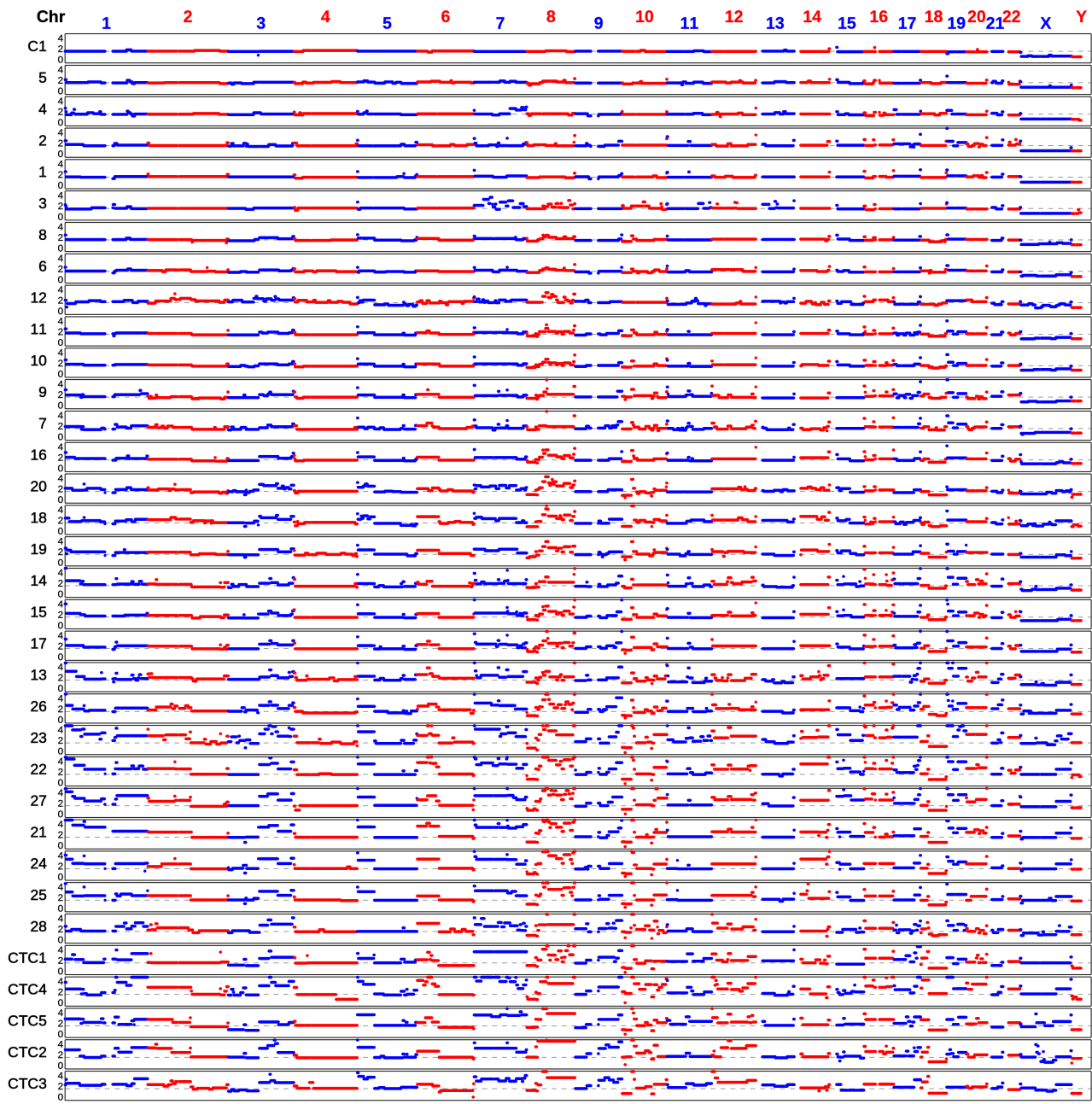


Figure S4. CBS segmentation of binned (500 kb) read depths of single cells from patient CO1.

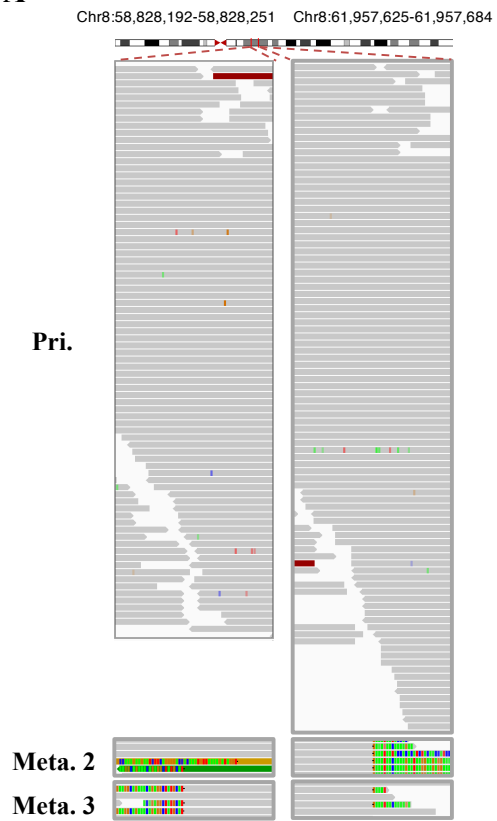
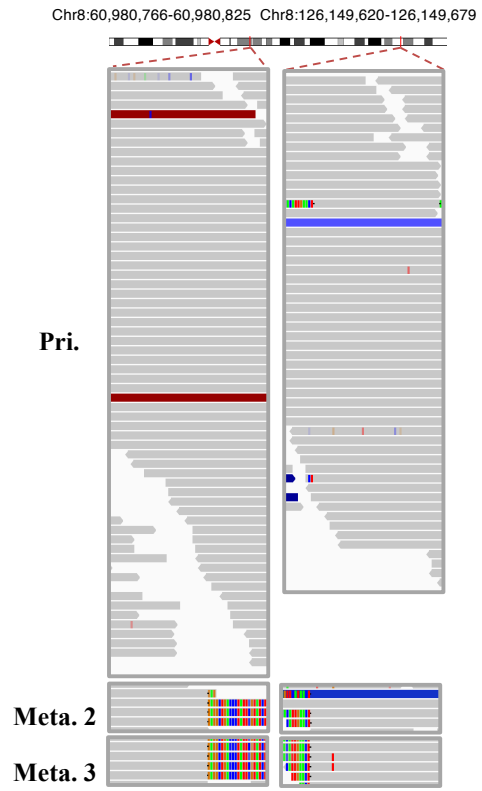
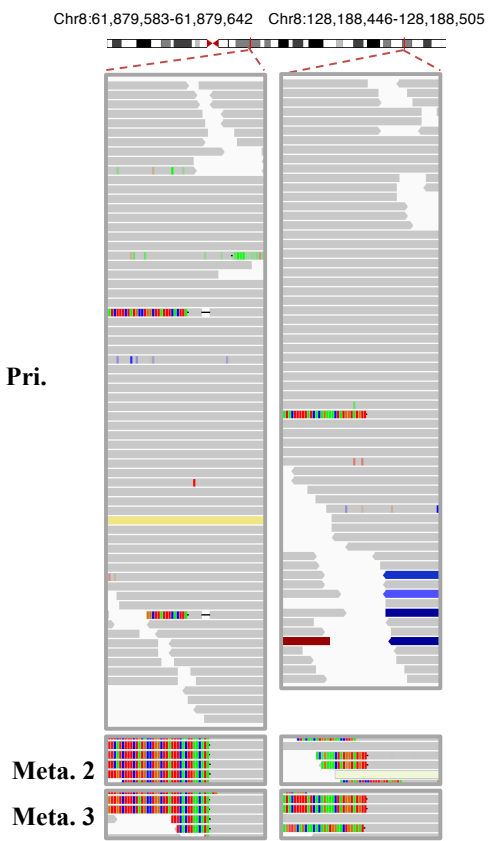
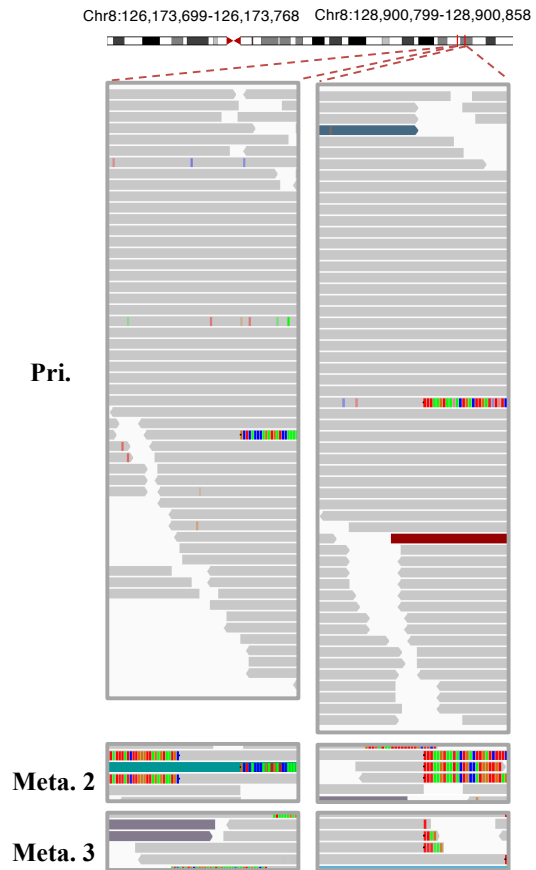
A**B****C****D**

Figure S5. Identification of junctions among DNA breakpoints at the CNA boundaries in primary tumour, and metastases 2 and 3.

- (A) Aligned reads around breakpoints **a** and **d** are visualized using IGV.
- (B) Aligned reads around breakpoints **b** and **e** are visualized using IGV.
- (C) Aligned reads around breakpoints **c** and **g** are visualized using IGV.
- (D) Aligned reads around breakpoints **f** and **h** are visualized using IGV.



Figure S6. Identification of the junction between DNA breakpoints b and e at the CNA boundaries.

(A) Visualization of aligned reads around breakpoints b and e using IGV. Alignments are represented as gray with base mismatches color-coded (“A”, green; “T”, red; “G”, yellow; “C”, blue). Soft-clipped (colorful) bases around one breakpoint can be mapped to the reference genome around another joined breakpoint. Read pairs mapped to chromosome regions separated much larger than the estimated insert size are indicated by red color. This junction has limited sequencing read supports in CTCs, probably due to the single cell amplification bias in this region. Further PCR amplification followed by deep sequencing confirms its unambiguous existence in all CTCs and metastases (Supplementary Figs. 8, 9).

(B) Sequences at the junction of breakpoints b and e. A representative sequence read (middle) is mapped to two regions (above and below) in the reference genome with appropriate orientation (“+”, forward strand).

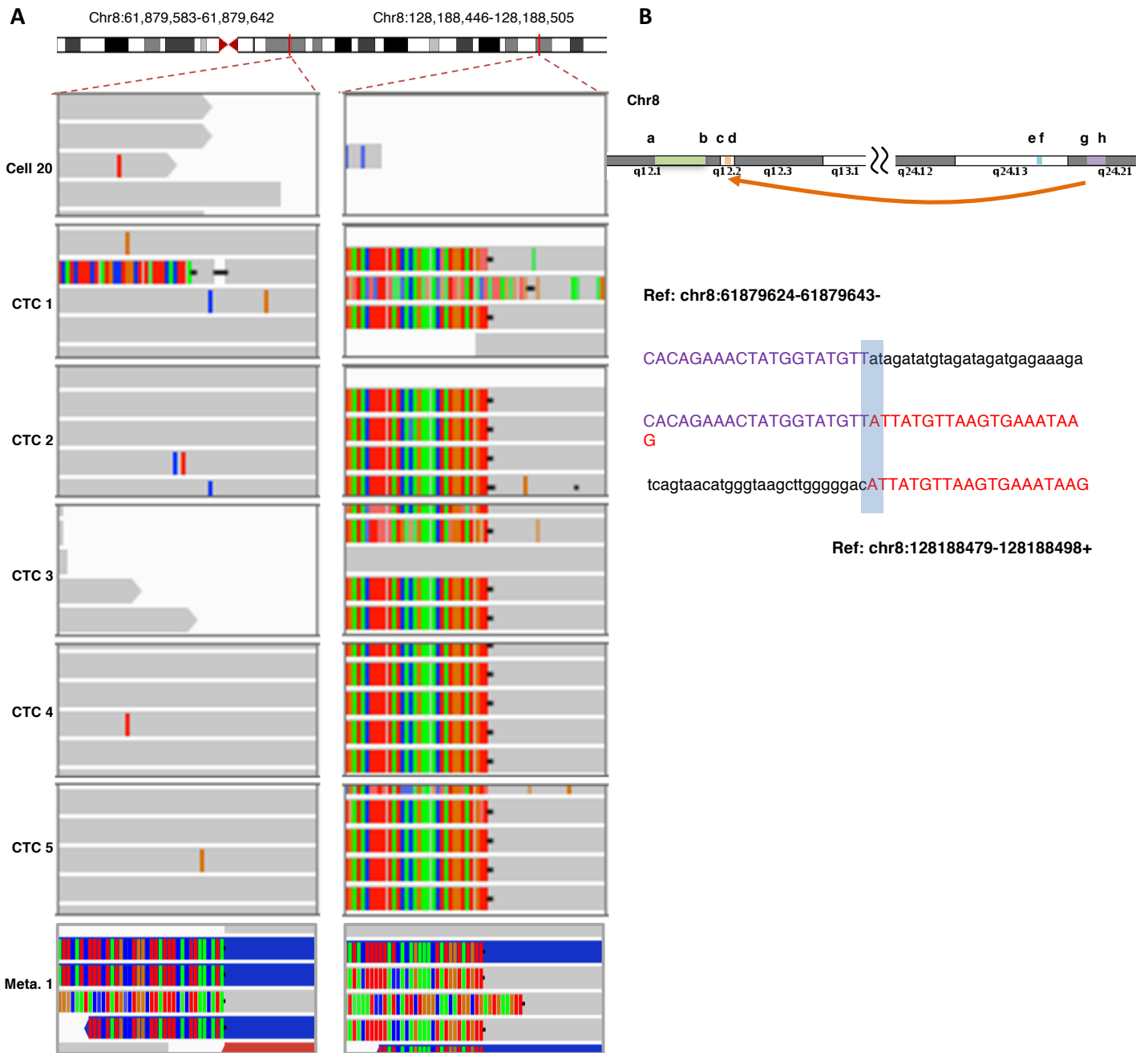


Figure S7. Identification of the junction between DNA breakpoints c and g at the CNA boundaries. (A) Visualization of aligned reads around breakpoints c and g using IGV. Alignments are represented as gray with base mismatches color-coded (“A”, green; “T”, red; “G”, yellow; “C”, blue). Soft-clipped (colorful) bases around one breakpoint can be mapped to the reference genome around another joined breakpoint. Read pairs mapped to chromosome regions separated much larger than the estimated insert size are indicated by red color. (B) Sequences at the junction of breakpoints c and g. A representative sequence read (middle) is mapped to two regions (above and below) in the reference genome with appropriate orientation (‘+’, forward strand; ‘-’, reverse strand).

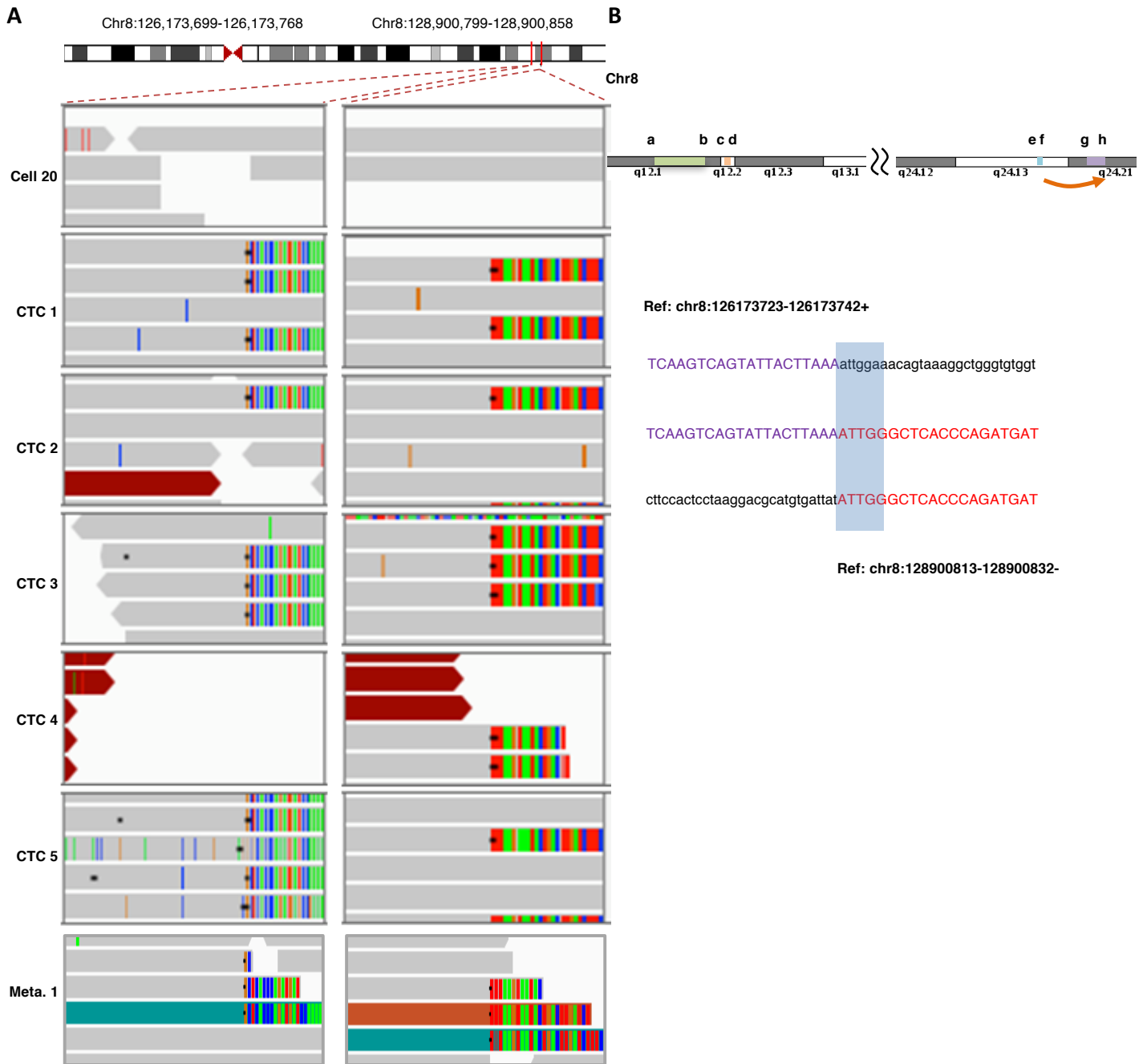


Figure S8. Identification of the junction between DNA breakpoints *f* and *h* at the CNA boundaries.
(A) Visualization of aligned reads around breakpoints *f* and *h* using IGV. Alignments are represented as gray with base mismatches color-coded (“A”, green; “T”, red; “G”, yellow; “C”, blue). Soft-clipped (colorful) bases around one breakpoint can be mapped to the reference genome around another joined breakpoint. Read pairs mapped to chromosome regions separated much larger than the estimated insert size are indicated by red color.
(B) Sequences at the junction of breakpoints *f* and *h*. A representative sequence read (middle) is mapped to two regions (above and below) in the reference genome with appropriate orientation (+, forward strand; -, reverse strand).

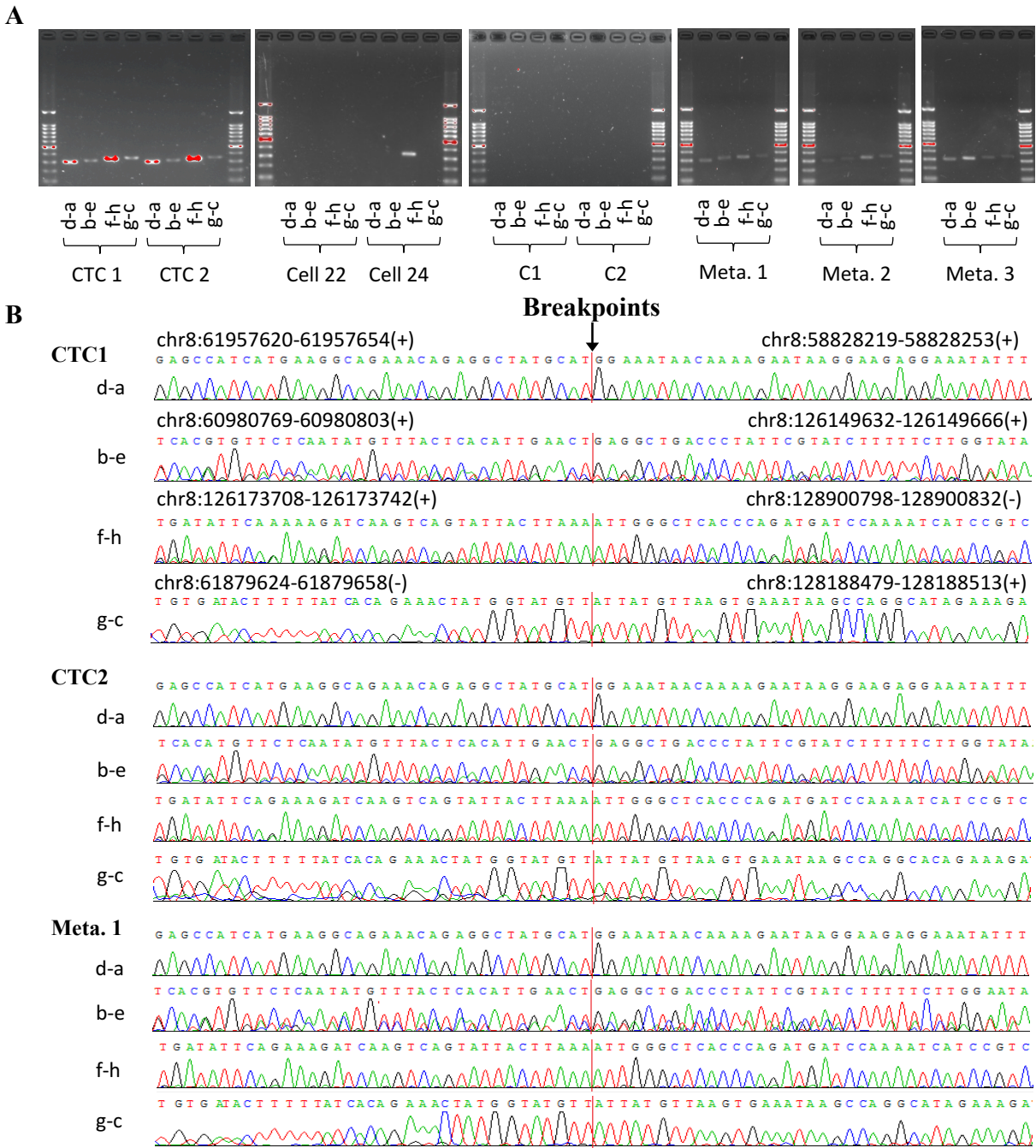


Figure S9. PCR validation of breakpoint junctions at Chromosome 8.

(A) Representative PCR products around breakpoint junctions are visualized in the agarose gel. Primers at each side of the breakpoint junction are designed in the appropriate orientation. The single bands observed in the gel from two CTCs (CTC 1 and CTC 2) represent PCR products of the four junctions (breakpoints **d-a**, **b-e**, **f-h**, **g-c**). Only one of the two primary tumour cells (Cell 24) shows a gel band corresponding to the junction of breakpoint **f-h**. The two control leukocytes (C1 and C2) have no band corresponding to the junctions. All three metastases (Meta. 1, 2 and 3) show gel bands corresponding to the four junctions (breakpoints **d-a**, **b-e**, **f-h**, **g-c**).

(B) Sanger sequencing of the PCR products in CTC 1, CTC 2, and a metastasis (Meta. 1). The genomic positions of the breakpoint junctions are marked by the red lines and the sequences at each side of the breakpoint junctions are identified.

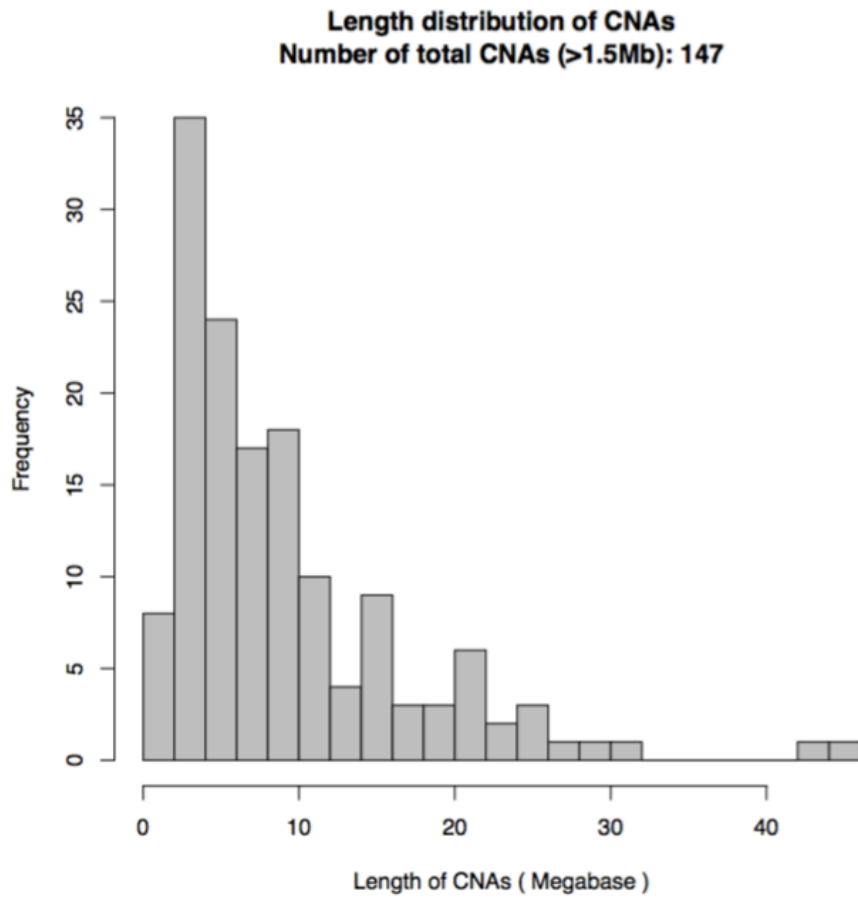


Figure S10. Length distribution of CNAs in a single cell (BR3).



Figure S11. CNAs of 97 CTCs from 23 patients of four cancer types. CNAs of individual CTCs from each patient are shown in a linear plot along the genome at a bin size of 500 kb (blue and red dots). Reproducible CNA patterns of CTCs from each patient are observed. (BR-, breast cancer; CO-, colon cancer; PR-, prostate cancer; GA-, gastric cancer)

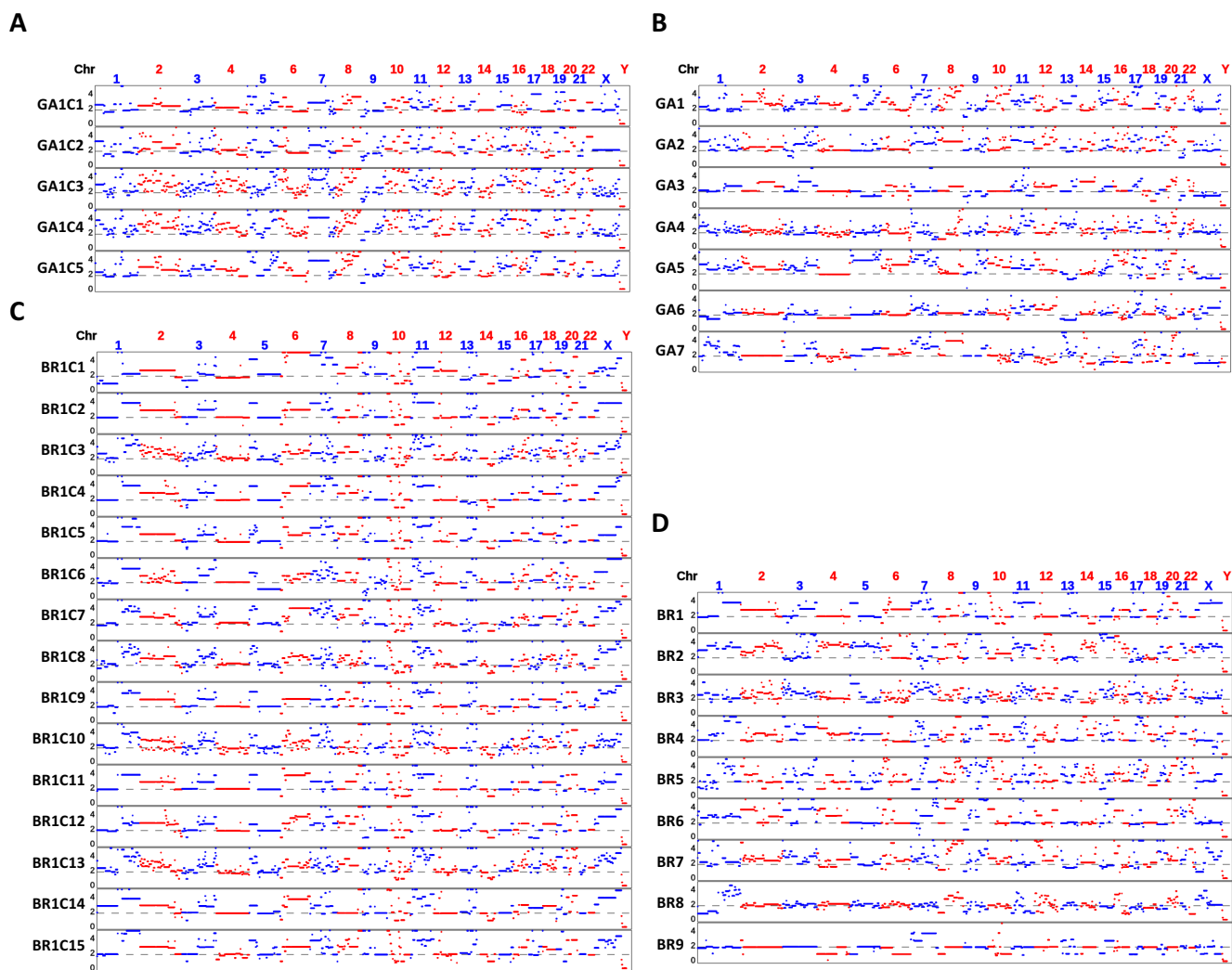


Figure S12. CBS segmentation of binned (500 kb) read depths of single cells from gastric and breast cancer patients.

(A) Segmented copy numbers in 5 CTCs from a gastric patient.

(B) Segmented copy numbers in CTCs from different gastric patients. One CTC was used for each patient.

(C) Segmented copy numbers in 15 CTCs from a breast cancer patient.

(D) Segmented copy numbers in CTCs from different breast cancer patients. One CTC was used for each patient.

Table S1. Patient information

Patient ID	Age	Sex	Primary Cancer	Stage	Number of CTCs isolated	Number of CTCs sequenced	Treatments before CTC isolation
*CO1	67	M	Colon cancer	IIIC	14	5	Surgery
CO2	61	F	Colon cancer	IV	12	7	Treatment naïve
BR1	46	F	Breast cancer	IIIA	50	15	Chemotherapy, surgery
BR2	47	F	Breast cancer	IV	9	3	Hormonal therapy, chemotherapy
BR3	44	F	Breast cancer	IIA	3	2	Surgery, chemotherapy
BR4	57	F	Breast cancer	IIIA	7	2	Surgery, chemotherapy, hormonal and targeted therapy
BR5	79	F	Breast cancer	IIA	20	4	Surgery, chemotherapy
BR6	34	F	Breast cancer	NA	10	4	Chemotherapy, surgery
BR7	61	F	Breast cancer	IV	6	3	Treatment naïve
BR8	55	F	Breast cancer	I	10	3	Surgery, hormonal therapy
BR9	56	F	Breast cancer	IIIA	29	4	Chemotherapy, surgery
GA1	52	M	Gastric cancer	IV	10	5	Treatment naïve
GA2	24	M	Gastric cancer	IV	5	2	Treatment naïve
GA3	61	M	Gastric cancer	IIIB	1	1	Surgery, chemotherapy
GA4	54	F	Gastric cancer	IIB	2	1	Surgery, chemotherapy
GA5	36	F	Gastric cancer	IV	5	3	Treatment naïve
GA6	31	F	Gastric cancer	IV	8	3	Treatment naïve
GA7	43	M	Gastric cancer	IV	9	4	Treatment naïve
PR1	73	M	Prostate cancer	IV	18	6	Hormonal therapy, surgery
PR2	58	M	Prostate cancer	IV	12	7	Surgery, hormonal therapy
PR3	72	M	Prostate cancer	IV	10	6	Hormonal therapy, radiotherapy
PR4	85	M	Prostate cancer	IV	6	4	Surgery, hormonal therapy, immunotherapy
PR5	76	M	Prostate cancer	NA	6	3	Surgery, radiotherapy, hormonal therapy, chemotherapy and immunotherapy

*For patient CO1, a total of 28 primary tumour cells were also sequenced.

Table S2. Summary of non-synonymous SNVs and INDELs identified in primary tumour tissue from Patient CO1.

Chr	Position	Wild type	Mutant	Change type	Gene name	Transcript_ID	Exon Rank	Effect	old_AA / new_AA	Old_codon / New_codon	Codon#	Wild type Coverage	Mutant Coverage
1	11854557	T	C	SNP	MTHFR	NM_005957	8	NON_SYNONYMOUS_CODING	D/G	gAc/gGc	402	65	16
1	37949192	T	A	SNP	ZC3H12A	NM_025079	6	NON_SYNONYMOUS_CODING	S/T	Tcc/Acc	594	9	8
1	117156600	T	C	SNP	IGSF3	NM_001542	4	NON_SYNONYMOUS_CODING	S/G	Agc/Ggc	207	41	24
1	197026149	A	C	SNP	F13B	NM_001994	7	NON_SYNONYMOUS_CODING	C/G	Tgt/Ggt	389	115	16
1	210334241	A	C	SNP	SYT14	NM_153262	8	NON_SYNONYMOUS_CODING	K/Q	Aaa/Caa	508	187	38
1	227268607	C	A	SNP	CDC42BPA	NM_003607	17	STOP_GAINED	E/*	Gaa/Taa	823	156	66
1	236734766	A	G	SNP	HEATR1	NM_018072	28	NON_SYNONYMOUS_CODING	L/S	tTa/tCa	1278	120	22
2	36706666	G	A	SNP	CRIM1	NM_016441	7	NON_SYNONYMOUS_CODING	A/T	Gct/Act	401	89	41
2	64147624	A	C	SNP	VPS54	NM_016516	14	NON_SYNONYMOUS_CODING	I/M	atT/atG	669	137	14
2	125521571	G	A	SNP	CNTNAP5	NM_130773	16	NON_SYNONYMOUS_CODING	V/I	Gtc/Atc	793	192	57
2	216272920	G	A	SNP	FN1	NM_002026	17	NON_SYNONYMOUS_CODING	A/V	gCg/gTg	810	71	40
2	241987743	G	C	SNP	SNED1	NM_001080437	9	NON_SYNONYMOUS_CODING	V/L	Gtg/Ctg	429	23	17
3	119276553	C	A	SNP	CD80	NM_005191	2	NON_SYNONYMOUS_CODING	G/V	gGa/gTa	8	53	20
3	173996677	A	C	SNP	NLGN1	NM_014932	6	NON_SYNONYMOUS_CODING	S/R	Agt/Cgt	296	129	21
3	184104439	C	T	SNP	CHRD	NM_003741	16	NON_SYNONYMOUS_CODING	R/W	Cgg/Tgg	698	25	20
4	366974	A	G	SNP	ZNF141	NM_003441	4	NON_SYNONYMOUS_CODING	T/A	Act/Gct	250	39	8
4	367001	G	A	SNP	ZNF141	NM_003441	4	NON_SYNONYMOUS_CODING	E/K	Gaa/Aaa	259	51	8
4	100052687	C	T	SNP	ADH4	NM_000670	6	NON_SYNONYMOUS_CODING	A/T	Gcc/Acc	271	14	4
4	122831528	C	G	SNP	TRPC3	NM_003305	5	NON_SYNONYMOUS_CODING	E/Q	Gaa/Caa	452	140	70
5	135561910	C	A	SNP	TRPC7	NM_020389	9	NON_SYNONYMOUS_CODING	A/S	Gca/Tca	692	79	21
5	138749926	C	T	SNP	DNAJC18	NM_152686	8	NON_SYNONYMOUS_CODING	D/N	Gat/Aat	330	102	25
5	158596061	C	G	SNP	RNF145	NM_144726	8	NON_SYNONYMOUS_CODING	G/A	gGc/gCc	342	42	11
5	178040560	*	+T	INS	CLK4	NM_020666	7	FRAME_SHIFT	-/?	-/A	247	34	12
6	28056791	A	C	SNP	ZNF165	NM_003447	4	NON_SYNONYMOUS_CODING	H/P	cAt/cCt	334	150	45
6	28543756	C	G	SNP	SCAND3	NM_052923	3	NON_SYNONYMOUS_CODING	K/N	aaG/aaC	242	126	31
6	30955051	A	G	SNP	MUC21	NM_001010909	2	NON_SYNONYMOUS_CODING	T/A	Acg/Gcg	367	58	8
7	92760652	T	A	SNP	SAMD9L	NM_152703	5	STOP_GAINED	K/*	Aaa/Taa	1545	158	18
7	95606859	G	T	SNP	DYNC111	NM_004411	7	NON_SYNONYMOUS_CODING	V/F	Gtt/Ttt	193	141	54
7	128413917	G	A	SNP	OPN1SW	NM_001708	4	NON_SYNONYMOUS_CODING	A/V	Gct/gTt	238	43	8
7	157931088	C	T	SNP	PTPRN2	NM_002847	7	NON_SYNONYMOUS_CODING	D/N	Gac/Aac	344	24	6
8	37702522	C	T	SNP	BRF2	NM_018310	4	NON_SYNONYMOUS_CODING	R/Q	cGa/cAa	249	69	18
8	131826347	G	A	SNP	ADCY8	NM_001115	14	NON_SYNONYMOUS_CODING	R/C	Cgc/Tgc	961	39	17
9	19573429	C	G	SNP	SLC24A2	NM_020344	6	NON_SYNONYMOUS_CODING	E/Q	Gaa/Caa	423	84	23
9	114989690	C	T	SNP	PTBP3	NM_005156		SPLICE_SITE_DONOR				61	35
9	136199031	G	A	SNP	SURF6	NM_006753	5	NON_SYNONYMOUS_CODING	R/C	Cgc/Tgc	254	67	21
9	139301992	C	T	SNP	SDCCAG3	NM_006643	4	NON_SYNONYMOUS_CODING	G/R	Gga/Aga	119	9	3
11	107197743	G	T	SNP	CWF19L2	NM_152434	18	NON_SYNONYMOUS_CODING	L/I	Ctt/Att	860	88	35
12	6883836	G	A	SNP	LAG3	NM_002286	4	NON_SYNONYMOUS_CODING	R/H	cGc/cAc	196	93	47
12	123875223	C	T	SNP	SETD8	NM_020382	3	NON_SYNONYMOUS_CODING	P/L	cCg/cTg	60	51	8
14	51707081	C	T	SNP	TMX1	NM_030755	1	NON_SYNONYMOUS_CODING	T/M	aCg/aTg	24	49	15
14	74753441	G	A	SNP	ABCD4	NM_005050	18	NON_SYNONYMOUS_CODING	T/M	aCg/aTg	572	46	19
14	92537353	C	T	SNP	ATXN3	NM_004993	10	NON_SYNONYMOUS_CODING	G/E	gGg/gAg	306	34	7
14	96707161	G	T	SNP	BDKRB2	NM_000623	3	NON_SYNONYMOUS_CODING	G/C	Ggc/Tgc	166	52	6
16	81942154	G	A	SNP	PLCG2	NM_002661	17	NON_SYNONYMOUS_CODING	R/Q	cGg/cAg	564	12	3
17	76422660	C	T	SNP	DNAH17	NM_173628	79	NON_SYNONYMOUS_CODING	D/N	Gac/Aac	4265	48	25
19	9028305	A	G	SNP	MUC16	NM_024690	11	NON_SYNONYMOUS_CODING	Y/H	Tac/Cac	12163	101	13
19	19757090	C	T	SNP	ATP13A1	NM_020410	23	NON_SYNONYMOUS_CODING	V/I	Gtc/Atc	1058	57	8
19	46443413	G	A	SNP	NOVA2	NM_002516	4	NON_SYNONYMOUS_CODING	T/M	aCg/aTg	396	37	5
19	50500776	C	T	SNP	VRK3	NM_016440	7	NON_SYNONYMOUS_CODING	A/T	Gcc/Acc	222	47	15
19	52327071	G	A	SNP	FPR3	NM_002030	2	NON_SYNONYMOUS_CODING	V/I	Gtt/Att	24	48	22
20	31812162	A	C	SNP	BPIFA3	NM_178466	3	NON_SYNONYMOUS_CODING	I/L	Atc/Ctc	94	52	10
20	35219641	G	A	SNP	TGIF2	NM_021809	3	NON_SYNONYMOUS_CODING	S/N	aGc/aAc	174	67	10
22	50716652	*	GGCCGCA CCAGGT	DEL	PLXNB2	NM_012401	31	FRAME_SHIFT	-/-	-/-	1590	26	27
X	106486523	T	C	SNP	CXorf41	NM_173494	7	NON_SYNONYMOUS_CODING	F/L	Ttc/Ctc	214	13	11

Table S3. Genomic sequencing information for all samples.

Sample Name	Sample Type	Patient ID	Sequencing Type	Raw Reads (MB)	Raw Bases (MB)	Mapped Reads (MB)	Mapping Rate (reads)	Mapped Bases (MB)	Mapping Rate (bases)	Duplication Rate
CO1B1E	Blood gDNA	CO1	WES	71.39	6425.39	71.13	99.62%	6303.47	98.10%	13.95%
CO1P1E	Primary tumour gDNA	CO1	WES	71.95	7050.73	71.71	99.67%	6971.67	98.88%	8.20%
CO1B1D	Blood gDNA	CO1	WGS	602.86	84816.54	569.15	94.41%	79539.72	93.78%	8.93%
CO1P1D	Primary tumour gDNA	CO1	WGS	829.68	116654.65	789.71	95.18%	109986.23	94.28%	10.66%
CO1M1D	Lymph node metastasis 1 gDNA	CO1	WGS	151.20	15619.60	150.24	99.37%	13905.50	89.03%	7.83%
CO1M2D	Lymph node metastasis 2 gDNA	CO1	WGS	150.18	15243.32	149.50	99.55%	13475.18	88.40%	8.52%
CO1M3D	Lymph node metastasis 3 gDNA	CO1	WGS	220.15	21278.09	219.07	99.51%	18930.82	88.97%	7.54%
CO1L1D	Single leucocyte	CO1	WGS	65.79	8237.15	56.13	85.33%	6703.83	81.39%	10.45%
CO1C1D2	Circulating tumor cell 1	CO1	WGS	143.31	18717.89	133.45	93.12%	17172.31	91.74%	16.85%
CO1C2D	Circulating tumor cell 2	CO1	WGS	97.39	12654.45	88.68	91.06%	11032.66	87.18%	5.25%
CO1C3D	Circulating tumor cell 3	CO1	WGS	160.83	21017.34	149.53	92.97%	19274.13	91.71%	17.92%
CO1C4D	Circulating tumor cell 4	CO1	WGS	128.04	16610.59	118.07	92.21%	14764.70	88.89%	6.48%
CO1C5D	Circulating tumor cell 5	CO1	WGS	100.37	12979.40	91.92	91.58%	11424.41	88.02%	6.10%
CO1PC10D	Primary tumor cell 10	CO1	WGS	82.82	9569.83	73.11	88.27%	8109.09	84.74%	15.38%
CO1PC14D	Primary tumor cell 14	CO1	WGS	90.21	11413.73	79.26	87.86%	9569.57	83.84%	7.90%
CO1PC15D	Primary tumor cell 15	CO1	WGS	79.82	10145.82	69.03	86.48%	8321.17	82.02%	7.25%
CO1PC16D	Primary tumor cell 16	CO1	WGS	88.38	11112.28	76.81	86.90%	9200.72	82.80%	6.66%
CO1PC17D	Primary tumor cell 17	CO1	WGS	99.71	12610.62	89.35	89.62%	10745.96	85.21%	7.31%
CO1PC18D	Primary tumor cell 18	CO1	WGS	87.73	10514.17	60.35	68.79%	6599.34	62.77%	15.72%
CO1PC19D	Primary tumor cell 19	CO1	WGS	78.36	6268.74	66.61	85.01%	5158.08	82.28%	15.85%
CO1PC20D	Primary tumor cell 20	CO1	WGS	77.88	9092.40	67.54	86.73%	7546.42	83.00%	14.96%
CO1PC21D	Primary tumor cell 21	CO1	WGS	139.13	17774.02	125.43	90.15%	15722.74	88.46%	16.26%
CO1PC22D	Primary tumor cell 22	CO1	WGS	132.23	17009.11	121.86	92.16%	15429.73	90.71%	16.65%
CO1PC24D	Primary tumor cell 24	CO1	WGS	112.59	13999.26	100.81	89.53%	12235.69	87.40%	10.58%
CO1PC25D	Primary tumor cell 25	CO1	WGS	100.78	12507.13	92.17	91.46%	11213.05	89.65%	9.67%
CO1PC26D	Primary tumor cell 26	CO1	WGS	74.19	9450.65	62.46	84.19%	7508.15	79.45%	5.81%
CO1PC27D	Primary tumor cell 27	CO1	WGS	123.90	15893.08	110.64	89.30%	13927.17	87.63%	15.98%
CO1PC28D	Primary tumor cell 28	CO1	WGS	144.39	18704.56	131.98	91.40%	16826.09	89.96%	17.29%
CO1PC01L	Primary tumor cell 1	CO1	WGS	6.02	541.93	4.75	78.80%	379.62	70.05%	1.51%
CO1PC02L	Primary tumor cell 2	CO1	WGS	5.23	338.94	4.62	88.33%	288.45	85.10%	0.53%
CO1PC03L	Primary tumor cell 3	CO1	WGS	6.03	542.26	4.73	78.54%	378.52	69.80%	1.60%
CO1PC04L	Primary tumor cell 4	CO1	WGS	5.92	532.53	4.58	77.36%	365.79	68.69%	1.65%
CO1PC05L	Primary tumor cell 5	CO1	WGS	5.14	332.79	4.48	87.05%	279.08	83.86%	0.52%
CO1PC06L	Primary tumor cell 6	CO1	WGS	5.89	529.82	4.76	80.87%	382.84	72.26%	1.47%
CO1PC07L	Primary tumor cell 7	CO1	WGS	4.67	300.68	4.25	90.98%	264.33	87.91%	0.33%
CO1PC08L	Primary tumor cell 8	CO1	WGS	2.74	273.86	2.25	82.27%	210.17	76.74%	0.36%
CO1PC09L	Primary tumor cell 9	CO1	WGS	4.92	317.77	4.33	88.02%	269.50	84.81%	0.51%
CO1PC10L	Primary tumor cell 10	CO1	WGS	4.56	295.86	3.98	87.39%	248.64	84.04%	0.57%
CO1PC11L	Primary tumor cell 11	CO1	WGS	4.91	320.18	4.25	86.57%	266.15	83.12%	0.58%
CO1PC12L	Primary tumor cell 12	CO1	WGS	6.01	540.82	4.61	76.75%	368.54	68.15%	1.81%
CO1PC13L	Primary tumor cell 13	CO1	WGS	2.92	291.59	2.39	81.85%	221.25	75.88%	0.38%
CO1PC14L	Primary tumor cell 14	CO1	WGS	2.68	267.81	2.25	83.93%	209.13	78.09%	0.34%
CO1PC15L	Primary tumor cell 15	CO1	WGS	4.22	274.86	3.59	84.89%	224.16	81.55%	0.55%
CO1PC16L	Primary tumor cell 16	CO1	WGS	4.68	302.65	4.10	87.51%	255.64	84.47%	0.50%
CO1PC17L	Primary tumor cell 17	CO1	WGS	3.86	249.20	3.46	89.71%	215.70	86.56%	0.36%
CO1PC18L	Primary tumor cell 18	CO1	WGS	5.88	528.96	4.34	73.75%	346.50	65.51%	1.65%
CO1PC19L	Primary tumor cell 19	CO1	WGS	5.93	533.82	4.60	77.59%	367.18	68.78%	1.63%
CO1PC20L	Primary tumor cell 20	CO1	WGS	6.12	550.94	4.79	78.14%	381.71	69.28%	1.63%
CO1PC21L	Primary tumor cell 21	CO1	WGS	4.72	303.84	4.16	88.12%	257.96	84.90%	0.43%
CO1PC22L	Primary tumor cell 22	CO1	WGS	2.29	229.24	1.95	85.14%	182.52	79.62%	0.24%
CO1PC23L	Primary tumor cell 23	CO1	WGS	3.09	199.77	2.70	87.29%	168.20	84.20%	0.43%
CO1PC24L	Primary tumor cell 24	CO1	WGS	2.51	251.44	2.08	82.59%	193.83	77.09%	0.35%
CO1PC25L	Primary tumor cell 25	CO1	WGS	3.35	334.65	2.78	83.01%	257.78	77.03%	0.37%
CO1PC26L	Primary tumor cell 26	CO1	WGS	2.88	187.23	2.46	85.44%	153.43	81.95%	0.32%
CO1PC27L	Primary tumor cell 27	CO1	WGS	2.84	284.39	2.41	84.63%	223.91	78.73%	0.30%
CO1PC28L	Primary tumor cell 28	CO1	WGS	5.81	522.93	4.74	81.62%	379.65	72.60%	1.41%
CO1C1L	Circulating tumor cell 1	CO1	WGS	4.74	394.98	4.50	94.94%	362.82	91.86%	1.06%
CO1C2L	Circulating tumor cell 2	CO1	WGS	4.58	406.37	4.14	90.28%	339.60	83.57%	0.63%
CO1C3L	Circulating tumor cell 3	CO1	WGS	5.25	458.56	4.70	89.43%	393.39	85.79%	0.79%
CO1C4L	Circulating tumor cell 4	CO1	WGS	4.63	413.06	4.14	89.39%	355.57	86.08%	0.56%
CO1C5L	Circulating tumor cell 5	CO1	WGS	5.14	454.09	4.63	90.06%	379.23	83.52%	0.63%
BR1C1L	Circulating tumor cell 1	BR1	WGS	1.17	117.18	1.04	88.75%	100.17	85.49%	2.34%
BR1C2L	Circulating tumor cell 2	BR1	WGS	1.82	181.63	1.60	88.22%	154.39	85.00%	2.00%
BR1C3L	Circulating tumor cell 3	BR1	WGS	5.91	385.86	5.49	92.89%	347.59	90.08%	0.40%
BR1C4L	Circulating tumor cell 4	BR1	WGS	1.74	174.22	1.56	89.28%	150.18	86.20%	1.26%
BR1C5L	Circulating tumor cell 5	BR1	WGS	1.88	187.56	1.67	89.04%	160.94	85.80%	1.85%
BR1C6L	Circulating tumor cell 6	BR1	WGS	4.50	308.50	4.04	89.86%	271.91	88.14%	0.34%
BR1C7L	Circulating tumor cell 7	BR1	WGS	6.45	418.12	5.86	90.92%	370.07	88.51%	0.63%
BR1C8L	Circulating tumor cell 8	BR1	WGS	5.69	367.73	5.10	89.68%	320.94	87.27%	0.53%
BR1C9L	Circulating tumor cell 9	BR1	WGS	6.05	393.60	5.62	92.90%	355.04	90.20%	0.48%
BR1C10L	Circulating tumor cell 10	BR1	WGS	5.57	363.91	5.25	94.17%	332.62	91.40%	0.35%
BR1C11L	Circulating tumor cell 11	BR1	WGS	6.37	437.90	5.93	93.15%	401.63	91.72%	0.16%
BR1C12L	Circulating tumor cell 12	BR1	WGS	5.20	356.83	4.89	93.92%	329.98	92.48%	0.12%
BR1C13L	Circulating tumor cell 13	BR1	WGS	5.70	388.77	5.33	93.37%	357.10	91.85%	0.13%
BR1C14L	Circulating tumor cell 14	BR1	WGS	6.73	461.63	6.30	93.72%	426.85	92.47%	0.17%
BR1C15L	Circulating tumor cell 15	BR1	WGS	5.93	396.64	5.56	93.70%	363.87	91.74%	0.25%
BR2C1L	Circulating tumor cell 1	BR2	WGS	3.78	378.01	3.49	92.43%	334.70	88.54%	0.28%
BR2C2L	Circulating tumor cell 2	BR2	WGS	4.82	482.32	4.51	93.60%	435.43	90.28%	0.32%
BR2C3L	Circulating tumor cell 3	BR2	WGS	4.57	456.76	4.22	92.48%	405.38	88.75%	0.32%
BR3C1L	Circulating tumor cell 1	BR3	WGS	4.54	407.95	3.85	84.98%	310.09	76.01%	0.94%

BR3C2L	Circulating tumor cell 2	BR3	WGS	4.74	426.22	4.04	85.39%	324.97	76.25%	1.14%
BR4C1L	Circulating tumor cell 1	BR4	WGS	5.05	454.29	4.32	85.54%	346.77	76.33%	1.07%
BR4C2L	Circulating tumor cell 2	BR4	WGS	4.46	401.34	3.89	87.18%	312.84	77.95%	0.98%
BR5C1L	Circulating tumor cell 1	BR5	WGS	4.08	350.25	3.90	95.56%	326.94	93.34%	0.26%
BR5C2L	Circulating tumor cell 2	BR5	WGS	4.31	369.37	4.08	94.70%	341.53	92.46%	0.26%
BR5C3L	Circulating tumor cell 3	BR5	WGS	4.41	377.60	4.19	95.08%	350.60	92.85%	0.23%
BR5C4L	Circulating tumor cell 4	BR5	WGS	4.79	410.32	4.50	94.06%	375.79	91.58%	0.34%
BR6C1L	Circulating tumor cell 1	BR6	WGS	4.37	392.84	3.77	86.23%	305.88	77.86%	0.96%
BR6C2L	Circulating tumor cell 2	BR6	WGS	4.44	399.29	3.85	86.55%	311.15	77.92%	0.91%
BR6C3L	Circulating tumor cell 3	BR6	WGS	4.58	411.75	3.99	86.97%	325.35	79.02%	0.81%
BR6C4L	Circulating tumor cell 4	BR6	WGS	4.29	385.56	3.68	85.81%	297.50	77.16%	0.94%
BR7C1L	Circulating tumor cell 1	BR7	WGS	3.84	345.22	3.34	87.20%	269.00	77.92%	0.88%
BR7C2L	Circulating tumor cell 2	BR7	WGS	4.09	368.00	3.53	86.33%	283.62	77.07%	0.95%
BR7C3L	Circulating tumor cell 3	BR7	WGS	4.23	380.78	3.69	87.29%	296.95	77.98%	0.97%
BR8C1L	Circulating tumor cell 1	BR8	WGS	2.30	230.48	1.55	67.39%	144.38	62.64%	0.43%
BR8C2L	Circulating tumor cell 2	BR8	WGS	2.14	214.41	1.47	68.70%	136.80	63.80%	0.36%
BR8C3L	Circulating tumor cell 3	BR8	WGS	2.21	221.24	1.55	70.07%	144.95	65.52%	0.47%
BR9C1L	Circulating tumor cell 1	BR9	WGS	6.14	524.25	5.88	95.75%	494.42	94.31%	0.51%
BR9C2L	Circulating tumor cell 2	BR9	WGS	6.25	533.73	5.94	95.04%	499.36	93.56%	0.52%
BR9C3L	Circulating tumor cell 3	BR9	WGS	6.53	552.67	6.25	95.63%	520.04	94.10%	0.54%
BR9C4L	Circulating tumor cell 4	BR9	WGS	7.15	607.90	6.83	95.50%	571.34	93.99%	0.42%
CO2C1L	Circulating tumor cell 1	CO2	WGS	7.94	517.00	7.41	93.38%	468.76	90.67%	0.47%
CO2C2L	Circulating tumor cell 2	CO2	WGS	6.85	618.27	6.13	89.43%	529.36	85.62%	0.84%
CO2C3L	Circulating tumor cell 3	CO2	WGS	5.27	342.09	4.92	93.45%	310.46	90.75%	0.32%
CO2C4L	Circulating tumor cell 4	CO2	WGS	4.43	392.13	3.98	89.86%	325.76	83.07%	0.56%
CO2C5L	Circulating tumor cell 5	CO2	WGS	4.43	391.57	3.99	90.08%	327.79	83.71%	0.59%
CO2C6L	Circulating tumor cell 6	CO2	WGS	7.11	463.38	6.66	93.67%	422.33	91.14%	0.50%
CO2C7L	Circulating tumor cell 7	CO2	WGS	6.14	554.52	5.54	90.27%	480.29	86.61%	0.85%
GA1C1L	Circulating tumor cell 1	GA1	WGS	5.08	443.36	4.65	91.44%	383.44	86.48%	0.38%
GA1C2L	Circulating tumor cell 2	GA1	WGS	5.22	452.94	4.81	92.22%	395.98	87.42%	0.40%
GA1C3L	Circulating tumor cell 3	GA1	WGS	7.78	503.26	7.13	91.62%	449.07	89.23%	0.52%
GA1C4L	Circulating tumor cell 4	GA1	WGS	6.83	443.11	6.26	91.68%	395.04	89.15%	0.48%
GA1C5L	Circulating tumor cell 5	GA1	WGS	4.52	293.64	4.21	93.00%	265.73	90.49%	0.32%
GA2C1L	Circulating tumor cell 1	GA2	WGS	4.14	355.72	3.93	94.79%	329.05	92.50%	0.26%
GA2C2L	Circulating tumor cell 2	GA2	WGS	5.31	464.71	4.82	90.79%	398.88	85.83%	0.45%
GA3C1L	Circulating tumor cell 1	GA3	WGS	4.82	420.23	4.41	91.55%	361.99	86.14%	0.47%
GA4C1L	Circulating tumor cell 1	GA4	WGS	3.81	332.04	3.42	89.72%	279.03	84.04%	0.34%
GA5C1L	Circulating tumor cell 1	GA5	WGS	3.83	382.98	3.38	88.13%	323.33	84.42%	0.04%
GA5C2L	Circulating tumor cell 2	GA5	WGS	3.88	333.51	3.69	95.22%	310.15	93.00%	0.27%
GA5C3L	Circulating tumor cell 3	GA5	WGS	4.27	426.55	3.73	87.42%	358.31	84.00%	0.05%
GA6C1L	Circulating tumor cell 1	GA6	WGS	3.46	300.51	3.15	91.04%	259.60	86.38%	0.43%
GA6C2L	Circulating tumor cell 2	GA6	WGS	4.69	389.38	4.38	93.47%	351.45	90.26%	0.99%
GA6C3L	Circulating tumor cell 3	GA6	WGS	4.30	356.94	4.07	94.63%	326.75	91.54%	0.95%
GA7C1L	Circulating tumor cell 1	GA7	WGS	4.27	426.65	3.75	87.91%	359.92	84.36%	0.04%
GA7C2L	Circulating tumor cell 2	GA7	WGS	3.56	356.07	3.11	87.32%	297.07	83.43%	0.06%
GA7C3L	Circulating tumor cell 3	GA7	WGS	3.62	362.17	3.20	88.39%	305.89	84.46%	0.04%
GA7C4L	Circulating tumor cell 4	GA7	WGS	4.21	421.16	3.70	87.96%	356.55	84.66%	0.06%
PR1C1L	Circulating tumor cell 1	PR1	WGS	3.64	329.51	3.26	89.56%	283.78	86.12%	0.70%
PR1C2L	Circulating tumor cell 2	PR1	WGS	4.47	381.86	4.24	94.90%	353.48	92.57%	0.28%
PR1C3L	Circulating tumor cell 3	PR1	WGS	3.83	346.65	3.46	90.19%	300.27	86.62%	0.66%
PR1C4L	Circulating tumor cell 4	PR1	WGS	4.90	422.11	4.64	94.77%	390.70	92.56%	0.26%
PR1C5L	Circulating tumor cell 5	PR1	WGS	4.98	428.87	4.70	94.51%	395.99	92.33%	0.28%
PR1C6L	Circulating tumor cell 6	PR1	WGS	4.49	385.58	4.25	94.58%	355.19	92.12%	0.30%
PR2C1L	Circulating tumor cell 1	PR2	WGS	2.71	271.49	2.43	89.65%	235.80	86.85%	0.13%
PR2C2L	Circulating tumor cell 2	PR2	WGS	2.40	240.09	2.07	86.26%	199.41	83.06%	0.28%
PR2C3L	Circulating tumor cell 3	PR2	WGS	4.68	427.49	4.26	90.98%	375.32	87.80%	0.70%
PR2C4L	Circulating tumor cell 4	PR2	WGS	2.01	200.71	1.74	86.54%	167.28	83.34%	0.34%
PR2C5L	Circulating tumor cell 5	PR2	WGS	4.12	375.63	3.73	90.47%	328.71	87.51%	0.69%
PR2C6L	Circulating tumor cell 6	PR2	WGS	2.55	255.40	2.26	88.50%	217.80	85.28%	0.11%
PR2C7L	Circulating tumor cell 7	PR2	WGS	2.38	238.33	2.07	86.81%	199.86	83.86%	0.12%
PR3C1L	Circulating tumor cell 1	PR3	WGS	5.18	441.42	4.91	94.76%	411.63	93.25%	0.30%
PR3C2L	Circulating tumor cell 2	PR3	WGS	4.82	410.49	4.57	94.68%	382.01	93.06%	0.30%
PR3C3L	Circulating tumor cell 3	PR3	WGS	6.21	530.71	5.88	94.69%	494.53	93.18%	0.31%
PR3C4L	Circulating tumor cell 4	PR3	WGS	6.28	572.35	5.70	90.73%	502.28	87.76%	0.77%
PR3C5L	Circulating tumor cell 5	PR3	WGS	3.99	363.87	3.60	90.35%	317.66	87.30%	0.65%
PR3C6L	Circulating tumor cell 6	PR3	WGS	4.32	389.25	3.90	90.35%	338.87	87.06%	0.74%
PR4C1L	Circulating tumor cell 1	PR4	WGS	2.55	254.57	2.19	86.14%	210.24	82.59%	0.18%
PR4C2L	Circulating tumor cell 2	PR4	WGS	4.61	418.17	4.07	88.38%	355.04	84.90%	0.71%
PR4C3L	Circulating tumor cell 3	PR4	WGS	2.35	235.48	2.05	86.88%	196.07	83.27%	0.13%
PR4C4L	Circulating tumor cell 4	PR4	WGS	2.09	208.70	1.82	87.21%	176.08	84.37%	0.29%
PR5C1L	Circulating tumor cell 1	PR5	WGS	3.58	358.48	3.41	95.00%	335.80	93.67%	0.20%
PR5C2L	Circulating tumor cell 2	PR5	WGS	5.07	507.21	4.77	94.08%	466.72	92.02%	0.80%
PR5C3L	Circulating tumor cell 3	PR5	WGS	5.08	507.92	4.80	94.44%	468.45	92.23%	0.52%
BR1C2D	circulating tumor cell 2	BR1	WGS	24.48	2018.89	22.58	92.27%	1805.15	89.41%	2.14%
BR2C1D	circulating tumor cell 1	BR2	WGS	26.84	2202.70	25.66	95.63%	2059.97	93.52%	2.11%
BR3C1D	circulating tumor cell 1	BR3	WGS	29.52	2439.03	28.06	95.06%	2266.08	92.91%	2.17%
BR4C2D	circulating tumor cell 2	BR4	WGS	28.49	2347.24	27.25	95.65%	2196.49	93.58%	1.93%
BR5C2D	circulating tumor cell 2	BR5	WGS	30.35	2584.11	29.07	95.80%	2441.44	94.48%	0.37%
BR6C1D	circulating tumor cell 1	BR6	WGS	26.96	2216.22	25.53	94.69%	2049.91	92.50%	2.50%
BR7C2D	circulating tumor cell 2	BR7	WGS	26.98	2216.83	25.77	95.52%	2071.24	93.43%	1.85%
BR8C1D	circulating tumor cell 1	BR8	WGS	27.78	2274.51	26.58	95.70%	2129.63	93.63%	2.93%
BR9C1D	circulating tumor cell 1	BR9	WGS	29.02	2297.94	27.21	93.75%	2123.98	92.43%	0.57%
CO1C1D1	circulating tumor cell 1	CO1	WGS	27.97	2303.44	26.97	96.43%	2170.95	94.25%	2.27%
CO2C7D	circulating tumor cell 7	CO2	WGS	25.88	2138.56	24.62	95.12%	1983.35	92.74%	1.82%

GA1C5D	circulating tumor cell 5	GA1	WGS	25.90	2123.79	24.72	95.45%	1979.00	93.18%	1.88%
GA2C1D	circulating tumor cell 1	GA2	WGS	27.41	2337.34	26.21	95.62%	2203.08	94.26%	0.31%
GA3C1D	circulating tumor cell 1	GA3	WGS	15.85	1071.65	14.74	93.04%	975.53	91.03%	0.36%
GA4C1D	circulating tumor cell 1	GA4	WGS	16.65	1120.23	15.16	91.05%	996.67	88.97%	0.31%
GA5C1D	circulating tumor cell 1	GA5	WGS	29.61	2527.66	28.53	96.36%	2400.90	94.99%	0.31%
GA6C2D	circulating tumor cell 2	GA6	WGS	23.35	1916.13	22.14	94.85%	1772.92	92.53%	1.74%
GA7C2D	circulating tumor cell 2	GA7	WGS	28.93	2466.74	27.83	96.20%	2339.31	94.83%	0.41%
PR1C1D	circulating tumor cell 1	PR1	WGS	29.83	1957.15	26.75	89.68%	1689.53	86.33%	2.00%
PR2C2D	circulating tumor cell 2	PR2	WGS	25.19	2071.86	22.86	90.76%	1818.48	87.77%	2.49%
PR3C1D	circulating tumor cell 1	PR3	WGS	30.75	2622.86	29.22	95.05%	2457.59	93.70%	0.40%
PR4C3D	circulating tumor cell 3	PR4	WGS	29.02	2386.95	26.72	92.08%	2127.68	89.14%	2.55%
PR5C2D	circulating tumor cell 2	PR5	WGS	24.25	1996.74	23.46	96.76%	1893.14	94.81%	3.08%

Table S4. Mutation information and PCR primers for the 20 SNVs in Patient CO1

Gene	Chromosome	Position	Wild Type	Mutant	Primers	sequence (5'-3')
ZNF165	Chr6	28056791	A	C	Forward Reverse	CCTGTGACCAGAGCTTCAA GTGAATTCGCCGATGTCTAGTA
TRPC3	Chr4	122831528	C	G	Forward Reverse	AGATGGACAGCATCCCAAAG TTAGCAGGAGCTTCTCCATTTA
LAG3	Chr12	6883836	G	A	Forward Reverse	TGATGTGGGAGAGGAGAAGA GAGGAAGCTTCCGCTAAGT
SAMD9L	Chr7	92760652	T	A	Forward Reverse	TGCCATGAGAATAGAGAGAGAGA ACCTCTGCGTCTCTAA
BRF2	Chr8	37702522	C	T	Forward Reverse	CGATGTGCTTCACCACAGA AGAAGATGCTGTCTCGAACAAAT
TGIF2	Chr20	35219641	G	A	Forward Reverse *Forward *Reverse	CAATGTGCTCTCCTGTCTG TGTGCAGTAATGGGAGTGATG TGTCTGTGTGCTCCATGC TGGTGCGTGTGAAGAG
CWF19L2	Chr11	107197743	G	T	Forward Reverse *Forward *Reverse	TGAGGGTCAGTTGCTTCATTAG TACATGCTTGTGTTTGTGCTTT AAGTCATATGGTTCCACCACT GGAAATCATAGGTGGGATGCT
PTBP3	Chr9	114989690	C	T	Forward Reverse	TTTAGAGTGTAGGATTGGAGATAACC GACCAAGGTCTGACTAAGGATTT
DNAH17	Chr17	76422660	C	T	Forward Reverse	CGAGTCTTAGGAAGCCTCTCA AGAGGCGCAGCACAAAG
DYNC111	Chr7	95606859	G	T	Forward Reverse	TGATTGGAACCTTACCCTTACC CAGTCAAGAAATAAATGACTCTTGC
CRIM1	Chr2	36706666	G	A	Forward Reverse	GAAGATGCTCAGTCTAACTGAA TTGACGCACTGGCAGAAT
SYT14	Chr1	210334241	A	C	Forward Reverse	ATGGGTCAAGAGATGTCCAAAT TGCTGCCTTTGATGGTAACT
FPR3	Chr19	52327071	G	A	Forward Reverse	GTTGTATTGTAAGATGGTGTACAG AGGATGGCACTGAAAGAGAAG
FN1	Chr2	216272920	G	A	Forward Reverse *Forward *Reverse	CAGGTCCGCACTCAGAATC AGCCACTTCTGTGAACATCC CGCTTAGCTGACCTGTGAT GCCTGTAGTAGCACTTCTG
ABCD4	Chr14	74753441	G	A	Forward Reverse	CTGAGCCTTTGGGTTCTTTCT GAAGCCAGAGCAGCTTTCA
CD80	Chr3	119276553	C	A	Forward Reverse	CCTGAAAGTTGCTTACCTGAAC TTTGGAGACCCAGGAACAC
MUC16	Chr19	9028305	A	G	Forward Reverse *Forward *Reverse	CATGTAGAGCACAGGACCAAA ATGGAGAGGTGGATGGACTAA ATCACAGCTGCTCACCATT AAGACCTCGGACTGGACA
SCAND3	Chr6	28543756	C	G	Forward Reverse *Forward *Reverse	TGTCCAATGCTGAGATGTGTATTA AGAAGCTTAGCAAGTTACTGG GCGACGGTAGTCAACTGATTC AGAAGCTTAGCAAGTTACTGG
CNTNAP5	Chr2	125521571	G	A	Forward Reverse *Forward *Reverse	CAGTGTGCCCTAGTCTTGAAA TACAAATGCCACTAGTGACTG TGTCCAGTGCTTCCCATAC AGGTAGGAAAGTGGAGGTAAGA
PLCG2	Chr16	81942154	G	A	Forward Reverse	GTTCCACAAGAAGGTGGAGAAG TTACCAAGAAGGACAGGGTGTAG

*A second primer pair was used for single cell samples that do not have PCR products with the first primer pair.

Table S5. Concurrent and mutually exclusive regions

Concurrent CNV regions						
Region 1			Region 2			P-value(-log10)
Cytoband	GISTIC	Oncogenes / TSGs	Cytoband	GISTIC	Oncogenes / TSGs	
7p12.2	gain	IKZF1	6p21.1	gain		7.00
9q34.2	gain		8q22.3	gain		6.48
9q34.12	gain	ABL1	6p21.1	gain		7.09
3q26.33	gain	SOX2	7p12.2	gain	IKZF1	6.55
3q24	gain		7q21.2	gain		6.88
3q27.3	gain		7p12.3	gain		6.67
3q24	gain		7q21.3	gain		6.90
9q34.12	gain	ABL1	8q22.3	gain		6.92
9q34.2	gain		6p21.1	gain		6.85
3q26.33	gain	SOX2	8q13.2	gain		6.86
9q34.12	gain	ABL1	8q24.11	gain		7.16
3q26.33	gain	SOX2	8q22.2	gain		7.17
3q26.33	gain	SOX2	8q22.3	gain		6.78
3q24	gain		8q13.1	gain		7.57
13q22.1	loss	DIS3	8p22	loss		6.80
3q26.33	gain	SOX2	8q23.1	gain		7.43
3q26.33	gain	SOX2	8q23.2	gain		7.78
3q26.33	gain	SOX2	8q23.3	gain		6.59
14q32.32	loss		8p11.21	gain		8.89
9q34.2	gain		11q13.3	gain	CCND1	7.03
3q26.32	gain	PIK3CA	8q22.2	gain		6.61
10q11.21	loss	RET	8p22	loss		7.10
3q26.32	gain	PIK3CA	8q23.1	gain		6.47
7q11.23	gain		5p15.33	gain	TERT	6.94
3q23	gain		8q13.1	gain		7.52
3q23	gain		8q22.1	gain		7.12
3q23	gain		8q22.2	gain		7.16
3q23	gain		8q13.3	gain		6.65
3q23	gain		8q22.3	gain		6.70
11q13.3	gain	CCND1	6p21.1	gain		8.23
3q26.32	gain	PIK3CA	7p12.2	gain	IKZF1	8.48
8q23.3	gain		17q23.2	gain		6.60
3q25.1	gain		8q13.1	gain		7.35
1q22	gain		17q25.1	gain	SRSF2	6.56
13q22.1	loss	DIS3	19p13.11	gain	JAK3	6.56
1q22	gain		17q25.3	gain		6.50
7q22.1	gain		5p15.33	gain	TERT	6.83
3q25.1	gain		7q21.2	gain		8.24
11q13.1	gain	MEN1	20q11.22	gain		6.84
9q34.3	gain	NOTCH1	6p21.1	gain		8.30
3q25.1	gain		7q21.3	gain		8.56
7q31.31	gain		18q21.2	loss	SMAD4	6.45
3q28	gain		8q23.3	gain		6.56
9q34.3	gain	NOTCH1	7p12.2	gain	IKZF1	6.99

Mutually Exclusive CNV regions						
Region 1			Region 2			P-value(-log10)
Cytoband	GISTIC	Oncogenes / TSGs	Cytoband	GISTIC	Oncogenes / TSGs	
3q27.2	gain		10q11.21	loss	RET	4.17
3q22.2	gain		10q11.21	loss	RET	4.80
9q34.3	gain	NOTCH1	13q21.1	loss		4.95
8q23.1	gain		7p22.2	gain	CARD11	3.94
9q34.3	gain	NOTCH1	13q21.2	loss		4.05
8q22.3	gain		13q22.2	loss		3.73
9q34.2	gain		13q21.1	loss		4.94
3q26.31	gain		13q21.33	loss		4.02

9q34.2	gain		13q21.2	loss		4.21
9q34.2	gain		13q21.31	loss		3.84
3q27.3	gain		10q11.21	loss	RET	4.48
3q26.31	gain		8p22	loss		3.85
8q23.2	gain		10q11.21	loss	RET	3.75
3q22.2	gain		8p21.2	loss	NKX3-1	3.78
3q26.31	gain		8p12	loss		4.79
3q26.1	gain		10q11.21	loss	RET	3.91
7q31.2	gain	MET	8p21.1	loss		3.80
3q26.32	gain	PIK3CA	8p22	loss		3.96
6q26	loss		8q22.3	gain		3.83
6p21.1	gain		8p23.1	loss		4.08
3q26.32	gain	PIK3CA	8p21.2	loss	NKX3-1	4.17
3q26.32	gain	PIK3CA	7p22.3	gain		3.89
6p21.1	gain		8p22	loss		3.92
3q26.33	gain	SOX2	13q21.2	loss		3.95
13q14.13	loss		6p21.1	gain		3.70
6p21.1	gain		8p21.3	loss		4.66
3q26.32	gain	PIK3CA	8p12	loss		4.42
6q26	loss		9p22.3	loss	PSIP1	4.19
6p21.1	gain		8p21.2	loss	NKX3-1	5.94
3q27.3	gain		8p22	loss		4.08
9q34.12	gain	ABL1	13q21.1	loss		4.71
8q23.2	gain		7p22.2	gain	CARD11	4.60
6p21.1	gain		8p21.1	loss		4.26
3q26.32	gain	PIK3CA	10q11.21	loss	RET	3.75
9q34.12	gain	ABL1	13q21.2	loss		3.82
8q23.3	gain		7p22.1	gain	RAC1	4.35
8q23.2	gain		7p22.1	gain	RAC1	4.68
6p21.1	gain		8p12	loss		4.06
3q27.3	gain		8p21.2	loss	NKX3-1	4.33
3q26.33	gain	SOX2	8p21.2	loss	NKX3-1	4.31
3q26.33	gain	SOX2	7p22.3	gain		3.76
20q13.13	gain		8p23.1	loss		4.19
9q34.12	gain	ABL1	13q21.31	loss		3.69
3q26.33	gain	SOX2	13q22.2	loss		3.72
3q28	gain		8p22	loss		3.87
3q27.3	gain		8p12	loss		3.91
3q26.33	gain	SOX2	8p12	loss		4.03
20q13.13	gain		8p21.3	loss		3.83
13q14.2	loss	RB1	6p21.1	gain		3.98
3q28	gain		7p22.3	gain		4.84
3q26.33	gain	SOX2	10q11.21	loss	RET	4.49
20q13.13	gain		8p21.2	loss	NKX3-1	4.14
8q23.2	gain		13q22.2	loss		4.56
3q28	gain		8p21.2	loss	NKX3-1	4.11
3q26.1	gain		7p22.3	gain		4.35
3q26.33	gain	SOX2	8p22	loss		4.76
8q24.21	gain	MYC	15q15.2	loss		4.49
20q13.12	gain	NCOA3	8p22	loss		3.85
3q22.3	gain	FOXL2	16q11.2	loss		4.01
3q22.3	gain	FOXL2	10q11.21	loss	RET	4.50
10q11.21	loss	RET	6p21.1	gain		4.48
3q27.1	gain		8p21.2	loss	NKX3-1	3.85
20q13.12	gain	NCOA3	8p21.2	loss	NKX3-1	3.92
10q23.31	loss	PTEN	9p22.3	loss	PSIP1	4.31
3q28	gain		10q11.21	loss	RET	4.30
10q23.31	loss	PTEN	9p22.2	loss		4.86
7p14.3	gain		8p21.2	loss	NKX3-1	3.91
20q13.11	gain		8p22	loss		4.78
3q23	gain		10q11.21	loss	RET	4.81
20q13.11	gain		8p21.3	loss		4.31
7p12.2	gain	IKZF1	8p21.2	loss	NKX3-1	3.84
3q26.1	gain		15q13.1	loss		3.98

20q13.11	gain		8p21.2	loss	NKX3-1	4.68
11q13.4	gain		13q21.2	loss		4.39
3q27.1	gain		8p22	loss		3.70
20q13.11	gain		8p21.1	loss		6.62
11q13.4	gain		13q21.32	loss		3.99
11q13.4	gain		13q14.12	loss		4.39
20q13.32	gain	GNAS	8p21.1	loss		4.50
11q13.4	gain		13q21.33	loss		4.15
11q13.4	gain		13q14.13	loss		5.37
11q13.4	gain		13q14.2	loss	RB1	5.80
8q22.1	gain		13q21.31	loss		3.86
11q13.4	gain		13q14.3	loss		4.84
20q13.31	gain		8p23.1	loss		4.07
7p12.3	gain		8p21.2	loss	NKX3-1	4.15
20q13.31	gain		8p21.3	loss		3.89
20q13.31	gain		8p21.2	loss	NKX3-1	4.05
20q13.31	gain		8p21.1	loss		5.43
3q27.1	gain		13q21.2	loss		4.85
13q22.1	loss	DIS3	11q13.4	gain		4.38
11q13.5	gain		13q14.3	loss		4.38
3q27.1	gain		13q21.31	loss		3.82
8q24.11	gain		7p22.2	gain	CARD11	4.16
3q26.2	gain		13q21.2	loss		3.77
11q13.5	gain		13q21.2	loss		4.37
8q24.11	gain		7p22.1	gain	RAC1	3.92
3q27.1	gain		13q14.13	loss		3.77
20q13.2	gain		8p21.1	loss		5.47
3q26.2	gain		8p22	loss		4.48
11q13.5	gain		13q14.12	loss		4.05
3q27.1	gain		13q22.2	loss		4.43
3q26.2	gain		13q21.33	loss		4.15
17q24.2	gain		8p21.2	loss	NKX3-1	4.87
11q13.5	gain		13q14.13	loss		4.88
3q27.1	gain		13q21.1	loss		4.43
3q26.2	gain		8p21.2	loss	NKX3-1	4.13
11q13.5	gain		13q22.1	loss	DIS3	3.86
11q13.5	gain		13q14.2	loss	RB1	4.85
3q26.2	gain		13q22.2	loss		3.71
3q26.2	gain		8p12	loss		5.08
8q22.2	gain		13q22.2	loss		4.38
7p12.1	gain		8p12	loss		3.96
20q13.33	gain		8p21.2	loss	NKX3-1	3.92
8q23.1	gain		7p22.1	gain	RAC1	4.94
3q26.31	gain		10q11.21	loss	RET	3.91
3q26.2	gain		10q11.21	loss	RET	4.63
20q13.33	gain		8p21.1	loss		4.89
17q24.2	gain		8p21.3	loss		4.14
8q24.12	gain		10q11.21	loss	RET	4.23