

Table S1. Comparison of SOLiD sequencing, Illumina SNP arrays, and Digital Karyotyping for analysis of copy number alterations

	Tumor Sample	Chr	Digital Karyotyping				Illumina SNP Arrays				SOLiD sequencing			
			Left Boundary	Right Boundary	Size (bp)	Tag Density Ratio*	Left Boundary	Right Boundary	Size (bp)	Log R Ratio*	Left Boundary	Right Boundary	Size (bp)	Tag Density Ratio*
Amplification	Co84C	6	41,273,307	43,008,812	1,735,506	9.1	41,419,345	42,485,546	1,066,202	1.9	41,418,000	42,537,000	1,119,001	16.4
Amplification	Co84C	8	127,618,526	128,009,287	390,762	19.2	127,621,008	127,995,012	374,005	2.7	127,617,000	128,010,000	393,001	150.0
Amplification	Co84C	8	128,750,189	128,857,861	107,673	8.3	128,750,181	128,848,183	98,003	2.0	128,748,000	128,859,000	111,001	43.1
Amplification	Co84C	8	129,473,672	129,667,129	193,458	13.8	129,472,209	129,677,099	204,891	3.4	129,471,000	129,678,000	207,001	116.6
Amplification	Co84C	11	34,337,207	35,266,401	929,195	33.0	34,359,268	35,265,359	906,092	3.0	34,338,000	35,268,000	930,001	91.2
Amplification	Co84C	13	109,096,557	109,553,930	457,374	9.2	109,108,212	109,557,712	449,501	2.3	109,107,000	109,557,000	450,001	33.6
Amplification	Co84C	15	88,545,070	89,258,106	713,037	26.2	88,561,995	89,253,599	691,605	3.6	88,542,000	88,953,000	411,001	93.2
											88,983,000	89,118,000	135,001	32.8
											89,133,000	89,166,000	33,001	84.8
											89,208,000	89,256,000	48,001	50.3
Amplification	Co84C	19	34,570,450	34,641,949	71,500	7.9	34,561,976	34,641,548	79,573	2.2	34,548,000	34,641,000	93,001	33.9
Amplification	Co84C	19	34,956,853	35,344,522	387,670	14.3	34,966,463	35,321,409	354,947	2.6	34,956,000	35,346,000	390,001	36.8
Amplification	Co84C	19	36,274,262	36,388,331	114,070	6.2	36,281,540	36,385,232	103,693	2.5	36,273,000	36,396,000	123,001	21.2
Amplification	Co84C	19	54,500,237	54,643,655	143,419	8.4	54,520,709	54,622,533	101,825	2.1	54,498,000	54,636,000	138,001	41.8

*Values for Tag Density Ratios and Log R Ratios represent observed maximum values for amplifications.

Table S2. Putative copy number alterations identified by SOLiD sequencing in Co84 that were not identified by Illumina SNP arrays or Digital Karyotyping

Alteration Type	Chromosome	Left Boundary	Right Boundary	Size (bp)	Tag Density
					Ratio *
Homozygous deletion	1	83,388,000	83,532,000	144,001	0.0
Amplification	1	151,188,000	151,194,000	6,001	11.2
Amplification	1	159,393,000	159,414,000	21,001	9.7
Amplification	1	172,101,000	172,107,000	6,001	18.1
Amplification	1	179,910,000	179,916,000	6,001	17.4
Amplification	1	200,238,000	200,256,000	18,001	9.6
Amplification	1	204,168,000	204,186,000	18,001	13.2
Homozygous deletion	4	9,804,000	9,813,000	9,001	0.0
Homozygous deletion	4	69,066,000	69,171,000	105,001	0.0
Homozygous deletion	4	147,138,000	147,147,000	9,001	0.0
Amplification	5	31,749,000	31,755,000	6,001	12.3
Homozygous deletion	5	114,279,000	114,288,000	9,001	0.0
Homozygous deletion	7	38,358,000	38,364,000	6,001	0.0
Amplification	8	145,698,000	145,725,000	27,001	11.5
Homozygous deletion	10	66,978,000	66,984,000	6,001	0.0
Homozygous deletion	13	108,681,000	108,687,000	6,001	0.0
Amplification	13	110,139,000	110,157,000	18,001	22.5
Homozygous deletion	16	54,357,000	54,378,000	21,001	0.0
Homozygous deletion	16	59,112,000	59,130,000	18,001	0.0
Amplification	17	76,467,000	76,482,000	15,001	17.8
Homozygous deletion	18	14,268,000	14,289,000	21,001	0.0
Amplification	19	50,271,000	50,277,000	6,001	9.3
Amplification	20	25,404,000	25,428,000	24,001	13.1
Homozygous deletion	X	49,050,000	49,059,000	9,001	0.0
Homozygous deletion	X	121,650,000	121,734,000	84,001	0.0

* Values for Tag Density Ratios represent observed maximum values for amplifications.

Table S3. Confirmed somatic rearrangements in breast and colorectal cancer samples*

Sample	Forward tag		Reverse tag		Type	Primer 1	Primer 2
	Chromosome	Position	Chromosome	Position			
B5C	3	52,638,626	3	52,573,088	AAC	AAGTTTTTCAAGCTTTACCTGAAGT	TATATTGGAAGAATAGAAATGAATGG
B5C	4	93,109,700	4	-93,105,085	BAC	AGCCAAGTGCAATTCTCCAG	GCACACTGTTTGCAGGAATG
B5C	11	57,713,780	8	-48,889,516	C**	GCCACCTTTCTTTCTTTCTGA	AAGCTTTGTTGGTTGTTCTCA
B5C	18	19,141,985	20	-29,591,944	C**	TGGCTTTCAAACCCCACTG	TCCTTTCTGCCCATTAGGG
B5C	22	48,743,603	2	-104,047,142	C**	TCATGGTTTATCCACGGTGT	CACACCGCAATTCACACAAAC
B7C	1	-96,237,189	7	65,542,257	C**	TCAAAACAGAAAGCATTAGGC	CGCATCCAAAGTATTAATAGCAA
B7C	2	197,428,606	2	113,761,988	AAC	AACCTCTCCCACTCAAATC	CCAAATTGCCTGCTTAAGAGAT
B7C	2	-32,084,286	3	185,241,029	C**	TGCTACCAATACTTCCCACTTG	TACCGTCTCCAGGCATGT
B7C	2	114,604,628	18	53,562,784	C**	GGAGAAAACCCCTGGTTATTTTA	TCCCTCATCAGAGCAAATCA
B7C	3	-115,579,348	3	-115,651,310	AAC	AAATTGGGAAGGATCATACTGAC	TCTGAACATGCCTGATCTCATC
B7C	4	785,983	4	733,804	AAC	CTGAACCTCTGGGCTGAA	TTGCTAAGTGATGCTACCTGTG
B7C	5	107,405,959	5	107,231,803	AAC	CCTGGCCCTTAGGTAAGAT	TGAAGAATCCTCTAGTGATGGAA
B7C	5	38,284,430	10	-44,715,202	C**	TGCAGCTTTTCTGTCTTCA	CTGCCAGTCCAACTGGTG
B7C	6	106,401,376	6	90,853,847	AAC	TGCTGTTTCAAATTCCTACAGTC	TGAAATTAGGACCTGGAGCAC
B7C	6	101,933,981	6	102,444,426	ABC	GCCAGGTAACATGCTCACTTT	GATGCAGGAAGTTGACAGCA
B7C	9	22,003,033	9	21,761,298	AAC	GGGCTAAGCTTAAGAGTCTGG	GCCATGTGCAAGTCAAGAAG
B7C	11	-6,436,033	11	-6,519,897	AAC	TCTGCCCGCATACTGGAC	TAAGGGCGATGTGAACAAGG
B7C	12	65,950,588	12	65,923,399	AAC	GCCTATTTTTCAGAGAAAGTGTA	AACATCTCTTCTTTTGAAGATCC
B7C	13	60,438,525	13	52,159,979	AAC	AATTTGCTCTCATCGTATTGTGT	AGCTGAATCAAAATTTCCAATG
B7C	X	31,583,118	X	31,179,704	AAC	CTGAATCTCTTCCAGCAAAAT	AATGGGTAAAGCAGTTTAGGG
Co108C	2	191,184,628	5	-104,930,827	C**	TAGCATGCACCACTTTAGGC	AAAGGTAAAGGACTGTTTTAAGTTG
Co108C	2	78,849,963	6	-13,299,323	C**	GGTTCTGGAGGGTTGGAGA	GTTAAGATCAACATTTTTGTTTCAAG
Co108C	2	-7,268,710	6	13,299,385	C**	TATGCCACCATCGCTTAGGT	TCCCAAGTCAATAAAACCAA
Co108C	2	-141,266,018	13	96,916,170	C**	GGTGTCTCTCTCCCATACCA	CGATCTATACACCACCCACA
Co108C	3	-60,400,269	3	-60,437,489	AAC	TGCTTTTAGTTTTGGGTACGG	GCTGATTTGTTTATACCCAGTGC
Co108C	3	-60,365,933	3	-60,498,861	AAC	ATCCTCGGACTGGACTGAGA	AACCCCATCTGAAGCTACC
Co108C	3	60,573,034	3	60,472,593	AAC	GGGTTATCTCAAAGGGCAGA	GCTCTCAATTTGTGTGATTTGG
Co108C	4	81,934,151	15	54,039,041	C**	TGTGTTCTCTCTCTTAAGCAT	GACTACAAATGGCCAGACTC
Co108C	6	-13,299,291	5	157,523,537	C**	ATCCCCACATTCCCAACC	CCCAGCCATATGTTGGTTTA
Co108C	6	13,299,271	2	-20,956,947	C**	GTATTTGTTCATGTTTGTAGGTGT	TCAATGGGGGAGAGAGAGC
Co108C	13	34,581,537	10	67,756,452	C**	ACGTGTGATTGGGGGTAGC	CCAGATGGCTGGGTAAATAAA
Co84C	8	128,442,121	19	49,144,200	C**	AGCTAGGTGGAGAATTTGTCG	GGCTCTGTAGAGTGCACATGA
Co84C	11	34,790,251	13	109,267,462	C**	AAGGAGATTGGTTATTGTGGAAA	CTGCAGGAATGTCTCATTTCTT
Co84C	11	-34,405,644	15	88,736,701	C**	TGCTGAATCATTCTCCCAACT	TGGTGATTCCACTGAGGTGA
Co84C	15	-89,096,347	8	127,747,412	C**	GCATTCTAAAGATGAAGTCCCAT	GGAAACCGTTAGTGGAAAAGTC
Hx402x	8	96,971,644	4	156,043,548	C**	CAGGTGATATACCAAGAAAATTAGG	TTTGGGTTCAATTCTATTGAAAG
Hx402x	5	-100,413,406	5	-137,521,052	AAC	AGTCAACGCCCTAGCATGG	TGGGCATGAGCAAGATATTC
Hx402x	8	-144,771,376	8	-144,787,051	AAC	AATCAGTTGGGTGACTGTG	GTGACAGGCTGGGTGTCC
Hx402x	14	-85,526,541	14	-85,560,400	AAC	TGAAGGTTGAGTTGCCAGTG	TGATGAAACATTGTAGAGGCTGT
Hx403x	1	119,547,240	1	-119,550,445	BBC	AGGAGGAAAGCAACACATAGAG	GGTGATTTTCAATGCATATTTCA
Hx403x	5	-27,160,637	5	27,150,736	BBC	AATTACCACAACCTCCAGCAG	CAAAAGATTTCCAAATGCAGGT
Hx403x	11	66,674,459	11	66,662,814	AAC	TGAATCAGAAAGCTGGCAGT	CACCTGAGAAATCAATGATATGAG
Hx403x	16	6,343,641	16	6,727,736	AAC	CCTAGCCCTTTGTTCCCTGT	TTTGTGTACCTAGACATTATCCAA
Hx403x	16	6,574,321	16	6,759,729	AAC	GCAGAGAACAGCAGAAAAGTTG	AGCCCAAGATCAAGCCACAGA
Hx403x	16	26,579,136	16	-26,582,595	BBC	TTCTCTTCTCTGCCTTCAGTG	TTGATGATTTAGAACTCTAGCCTGT
Hx403x	17	34,622,352	17	-34,624,284	BBA	GGCTCCCTCTCCATTCC	CTGCTGACGTGCTGGTCTT

* A single representative mate pair is shown for each rearrangement. Forward and reverse tags and their genomic coordinates correspond to F3 and R3 SOLiD mate pair tags. The type of rearrangement corresponds to the categories described in http://www3.appliedbiosystems.com/cms/groups/mcb_marketing/documents/generaldocuments/cms_058717.pdf. AAC corresponds to mate pairs spanning deletions; codes starting with B denote incorrect strand orientation; codes containing a B at the middle position denote incorrect ordering; and C** corresponds to interchromosomal translocations. Primers 1 and 2 correspond to primers used for confirming tumor-specific rearranged sequences.

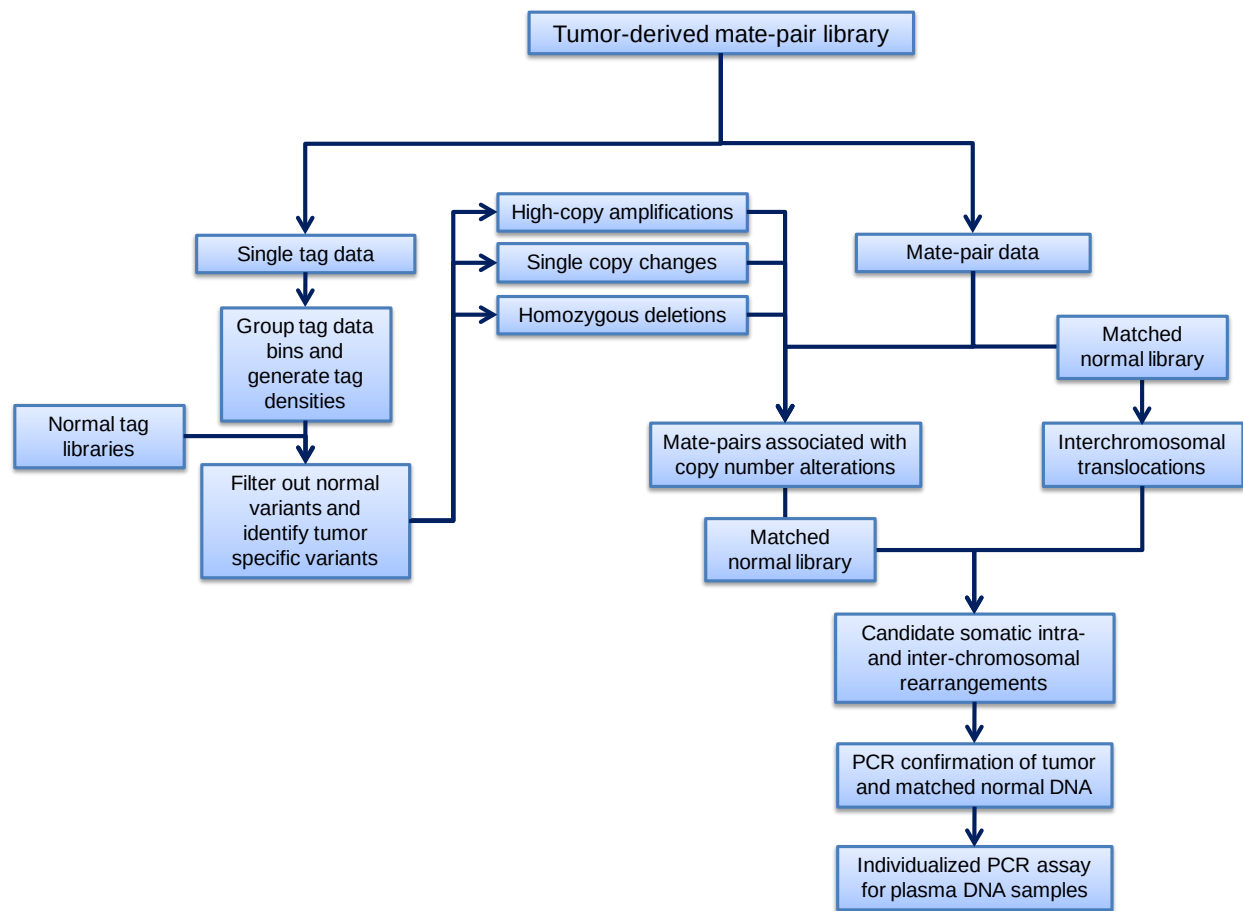


Fig. S1. Flow chart of approach used to identify rearranged sequences

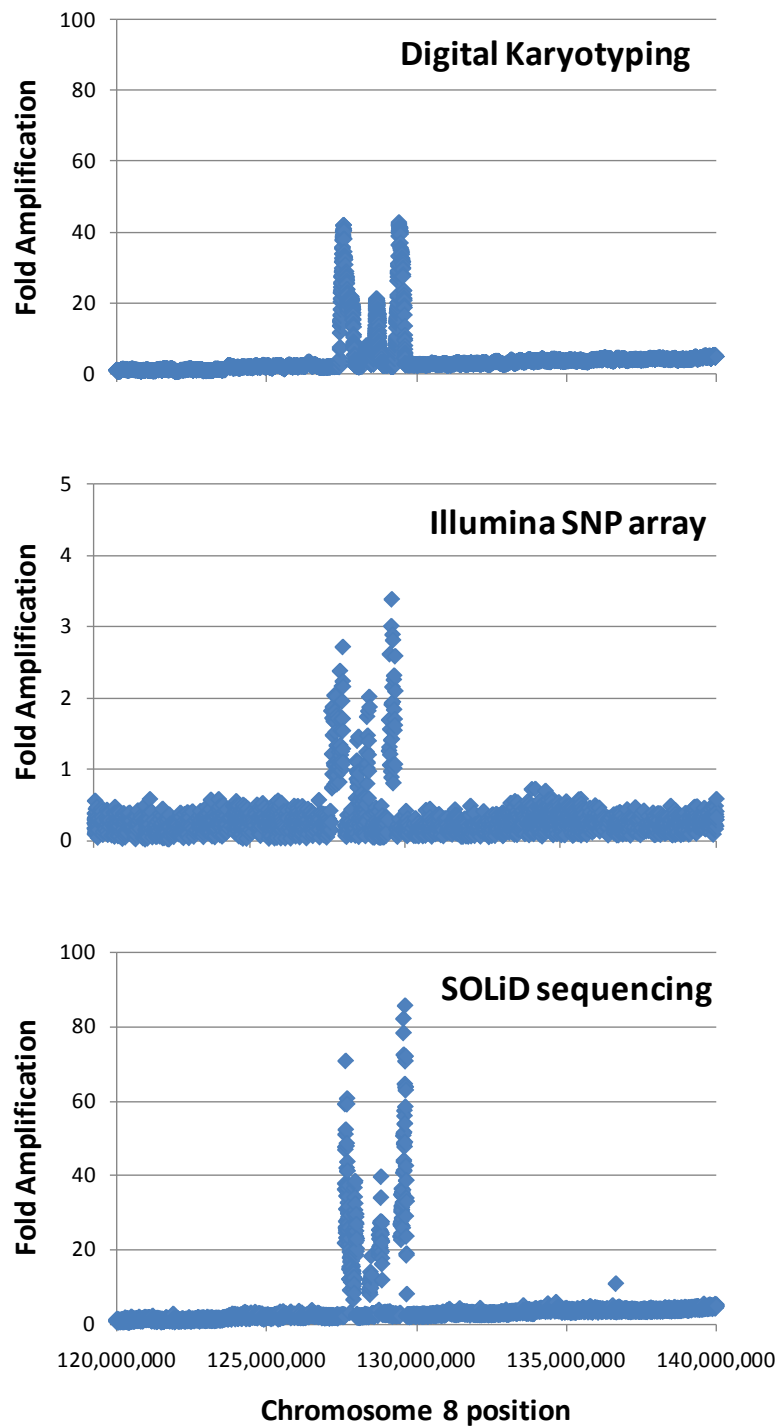


Fig. S2. Comparison of Digital Karyotyping, Illumina SNP array, and SOLiD sequencing results on chromosome 8.