

Supplemental Figure Legends

Supplemental Figure 1. Cycled GAPF. (A) A model depicting the fate of a palindrome after consecutive cycles of GAPF, or “cycled GAPF”, without formamide. One cycle of GAPF (GAPFx1) will enrich for palindromes over non-palindromic regions, but an additional cycle of GAPF (GAPFx2) will eliminate palindromes due to digestion of the non-palindromic spacer by S1 nuclease in the previous cycle. Notably, methylated regions are not eliminated after cycled GAPF performed without formamide (Diede et al. 2010b). (B-C) PCR-based enrichment analyses of GAPF-positive regions in breast cancer cell lines after cycled GAPF without formamide. Primers used in these analyses were targeted to a normally occurring inverted repeat (IR), a methylated region in the *MYOD1* promoter (MYOD), and the GAPF-positive regions in 8q24.21 in MCF7 (B) or the shared GAPF-positive regions in 11q22.1 in UACC893 and BT474 (C). These PCRs have been multiplexed with primers to a non-palindromic control (ARNT) to determine if the interrogated regions were enriched over non-palindromic regions following GAPF. (B) Note the enrichment of the IR and GAPF-positive region in 8q24.21 in MCF7 GAPFx1 samples and elimination of those regions in MCF7 GAPFx2 samples. In contrast, the MYOD region is enriched over the ARNT region in both MCF7 GAPFx1 and GAPFx2 samples. (C) Note enrichment of the IR (top gel panel) and GAPF-positive region in 11q22.1 (bottom gel panel) after one round of GAPF (GAPFx1), but elimination of this region following a second round of GAPF (GAPFx2). The MYOD region was not eliminated following cycled GAPF in either UACC983 or BT474 (middle gel panel). (D) Bisulfite sequencing of a region in the *MYOD1* promoter revealed heavy CpG methylation in the MCF7, UACC893, and BT474 cell lines as compared to normal PBLs.

Supplemental Figure 2. Sequencing of the palindromic junction of the GAPF-positive region in 8q24.21 in MCF7 cell line. (A) Multiplex PCR was performed with the primers shown in the schematic on left and the ARNT region, which is not palindromic. Primer X was multiplexed with primers A through D in separate reactions. These primers are all on the same strand (red) in the normal genomic sequence and, accordingly, do not produce a product in the normal, HFs (N), shown on the right.

However, products are observed in MCF7 (M), ranging from approximately 1400 bp when primers C and X were multiplexed, to 2000 bp with primers A and X, suggesting that this rearranged region in the MCF7 cell line contains an inversion, shown in the model. (B) DNA sequence in the center of the novel palindrome. The PCR product amplified by primers C and X was cloned and sequenced. Sequencing was performed using the Applied Biosystems BigDye Terminator kit and capillary DNA analyzer. The blue sequence maps to the negative strand of normal genome sequence and the red sequence maps to the normal positive strand (shown in (A)). In the rearranged locus, the sequence from the negative strand is inverted. Uppercase letters represent unique sequence and lowercase letters represent repeat sequences (Alus and LINEs). (C) Dot plot showing the sequence alignment of the novel rearrangement at the center of the palindrome. The novel sequence at the center of the palindrome obtained from sequencing and shown in (B) was input into the Pipmaker program (<http://pipmaker.bx.psu.edu/pipmaker/>). The resulting dot plot reveals the presence of significant inverted repeat sequence in this rearranged locus, as demonstrated by the lines running from the upper left corner to the lower right corner of the plot. The inverted-repeat nature of this rearranged sequence might have created a region susceptible to breakage and subsequent large palindrome formation.

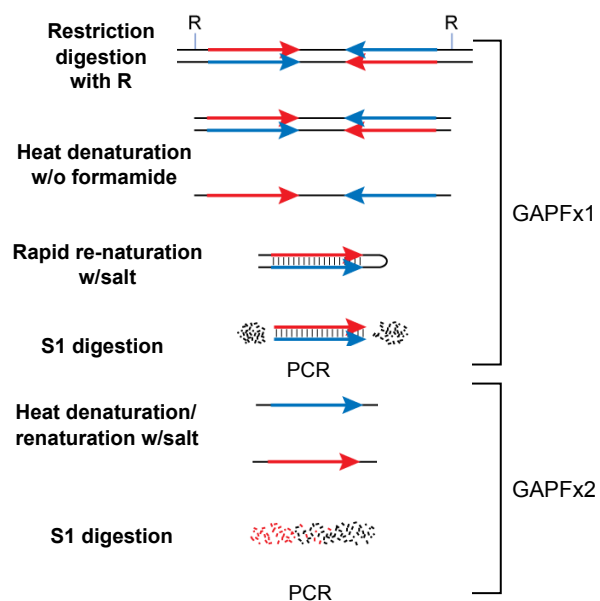
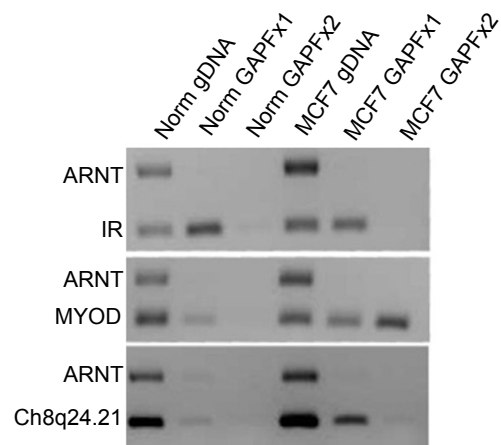
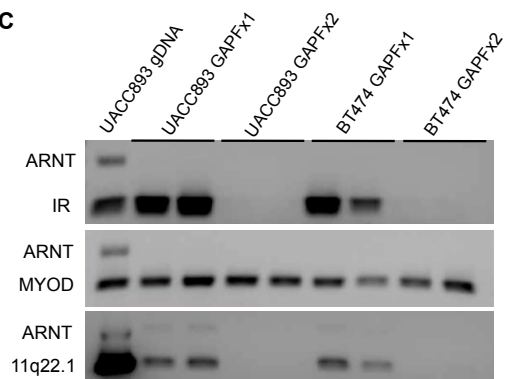
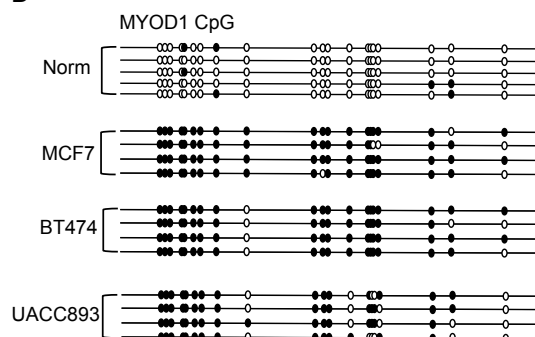
Supplemental Figure 3. Palindromes located at breakpoints of high-level amplicon ($\log_2$ signal ratio > 1.5) in 8p12 in ER-positive primary breast tumor, ERP1. (A-E) Blue graphs display GAPF p-values ($-10\log_{10}$) generated from tiling-array analysis comparing ERP1 with a pooled PBL reference. The solid bars under the graphs mark GAPF-positive regions ($p\text{-value } (-10\log_{10}) > 30$, run > 50 bp, gap < 100 bp). Graphs above display copy-number segments ($\log_2$ signal ratio) generated from SNP arrays coupled with wavelet-based statistical analysis, where red boxes mark different amplicons ($\log_2$ signal ratio > 0.3). The dashed line marks $\log_2$ signal ratio = 1.5. Three GAPF-positive regions located at amplicon breakpoints shown in (A) were further analyzed by PCR. (B-E) PCR-based enrichment analyses of three GAPF-positive regions. Digestion in the non-palindromic spacer of a palindrome will eliminate enrichment following GAPF. This assay both validates the palindromic nature of the GAPF-positive regions and locates the palindromic center. Genomic DNA from ERP1 was digested with SbfI, SmaI,

NcoI, or SpeI then processed through GAPF. Enrichment of the GAPF-positive regions over a non-palindromic region (ARNT) was then assessed using PCR primers, shown on each map. Enrichment of a normally occurring IR was assessed in all samples to confirm efficient GAPF preparations. (B) For the most telomeric GAPF-positive region, enrichment was observed in samples digested first with SpeI and SwaI, but not SbfI, EcoRV, or NcoI. Based on the map, the location of the non-palindromic spacer and the center of the palindrome was located telomeric to the GAPF-positive region, co-locating with the copy-number breakpoint. (C) The second GAPF-positive region was enriched over the ARNT region when the sample was first digested with SbfI and NcoI, but none of the other restriction enzymes, which places the palindromic center between the NcoI and SwaI recognition sites also at the copy-number breakpoint. (D) The most centromeric GAPF-positive region was enriched when ERP1 DNA was first digested with EcoRV and SwaI, but not with SbfI, NcoI, or SpeI. These results suggest that the palindromic center is centromeric to the positive region at the copy-number breakpoint.

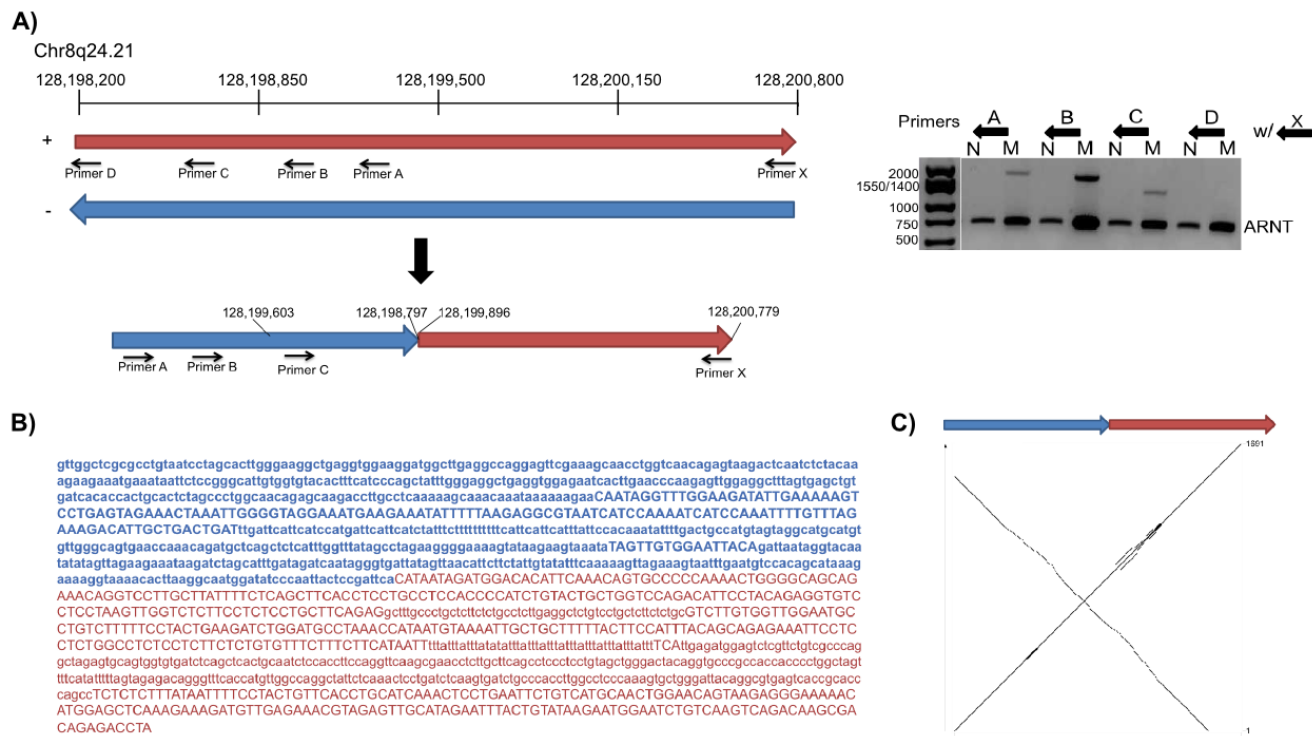
Supplemental Figure 4. GAPF-positive regions associated with commonly amplified regions in 8q and 11q13 in breast cancers. Graphical representation of GAPF-positive regions (p -value < 0.001, $\log_2$ signal ratio > 0.3; blue lines) and copy-number gains (average $\log_2$ signal ratio > 0.3; red boxes) in 8q (A) and 11q13-q21 (B). Wavelet-derived copy-number breakpoints are shown by the grey ticks at the bottom of the amplicon boxes. The height of the copy-number gain is not related to the level of amplification, and breakpoints that are located in the middle of amplicons mark regions of copy-number change within the larger amplified region. Only those samples with copy-number gains in these regions are shown. Three of the four cell lines (MCF7, BT474, UACC893) and two of the IDCs (ERP1, ERP3) have GAPF-positive regions associated with copy-number gains in 8q, and a subset of those GAPF-positive regions are located at the breakpoints. In 11q13-q21, we observed overlapping GAPF-positive regions and copy-number gains in three breast cancers (BT474, UACC893, ERP1). For example, the complex amplicons in UACC893 extending from 8q23.3 to 8qter contained nine GAPF-positive regions, one of which was located at a copy-number breakpoint.

Supplemental Figure 5. Majority of GAPF-positive regions located within 10 Mb of copy-number gains and associated breakpoints in cancer cell lines. Histograms depicting the distance between GAPF-positive regions, detected genome-wide in MCF7 (dark bars) and Colo320DM (light bars), and nearest copy-number gain (A) and copy-number gain breakpoint regions (B). The majority of GAPF-positive regions were overlapping with the copy-number gains and breakpoints (i.e., 0 Mb away) or within 10 Mb. GAPF-positive regions that are located on a chromosome containing no copy-number gains are called “NA”.

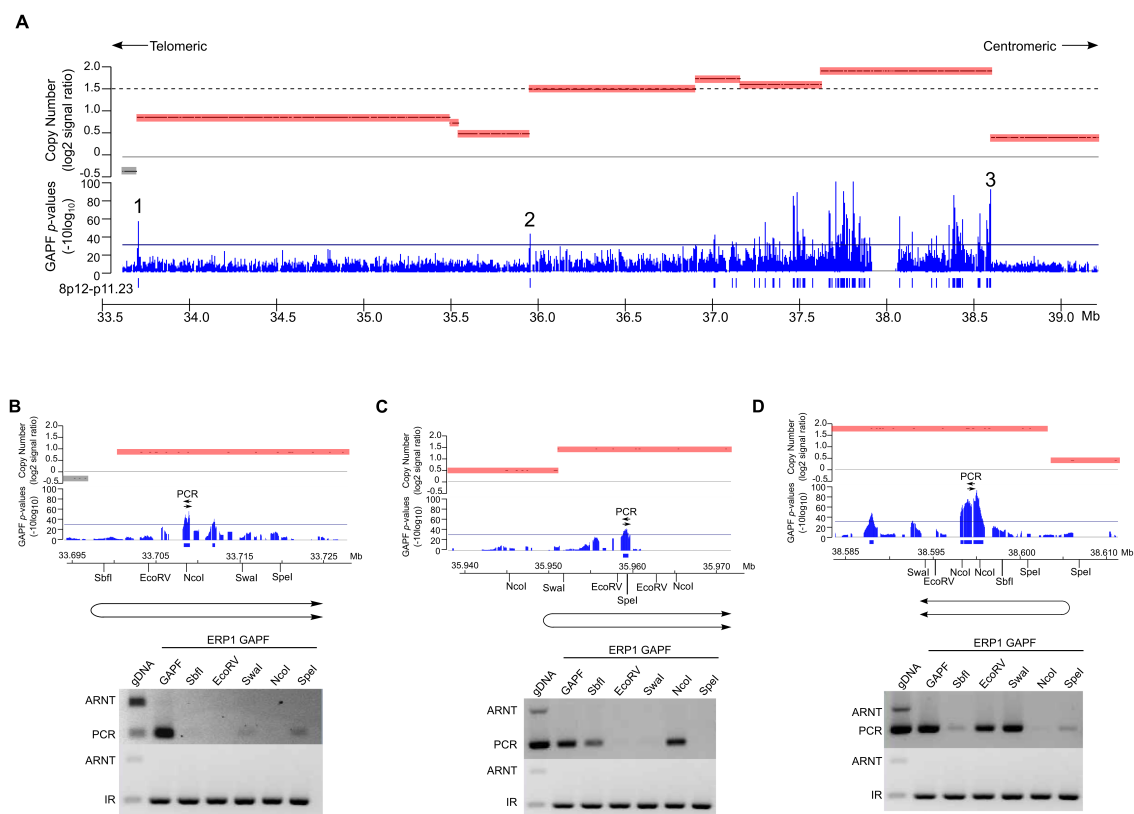
Supplemental Figure 1

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

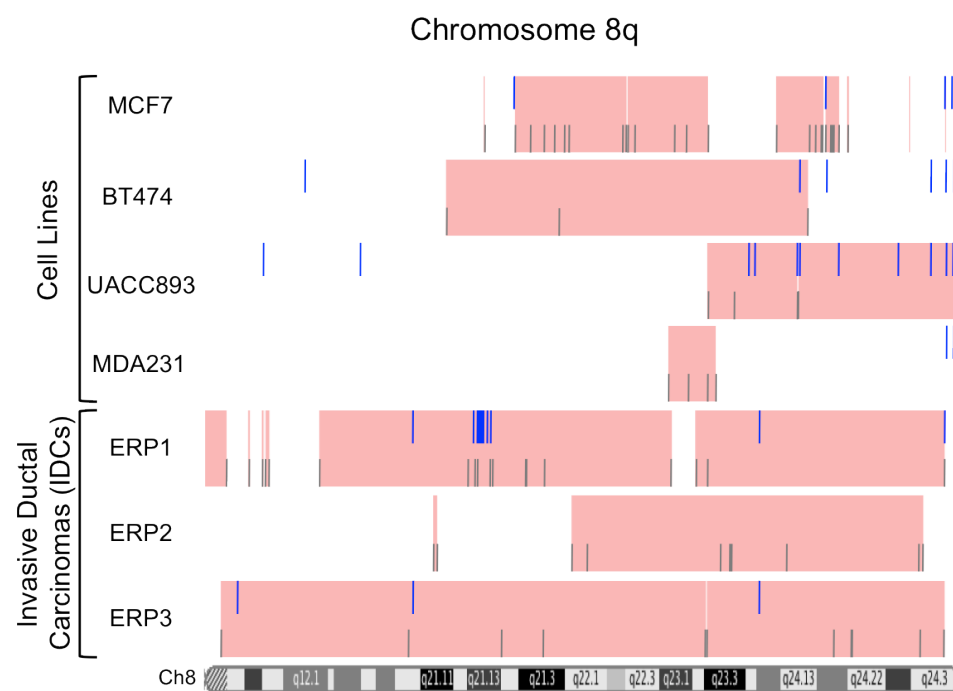
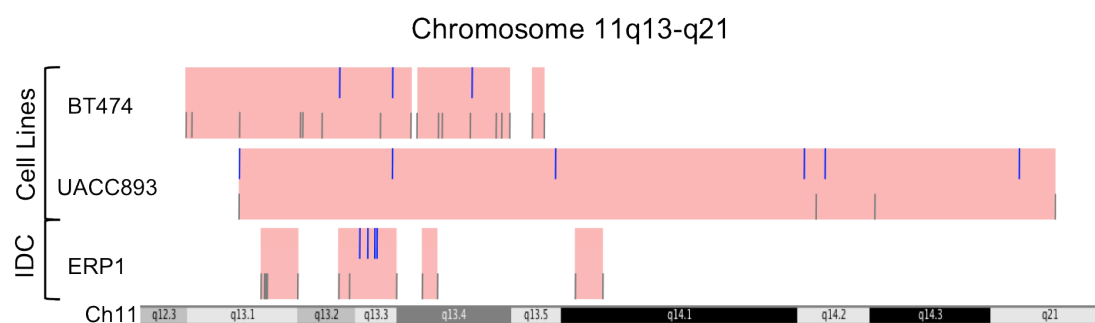
Supplemental Figure 2



Supplemental Figure 3

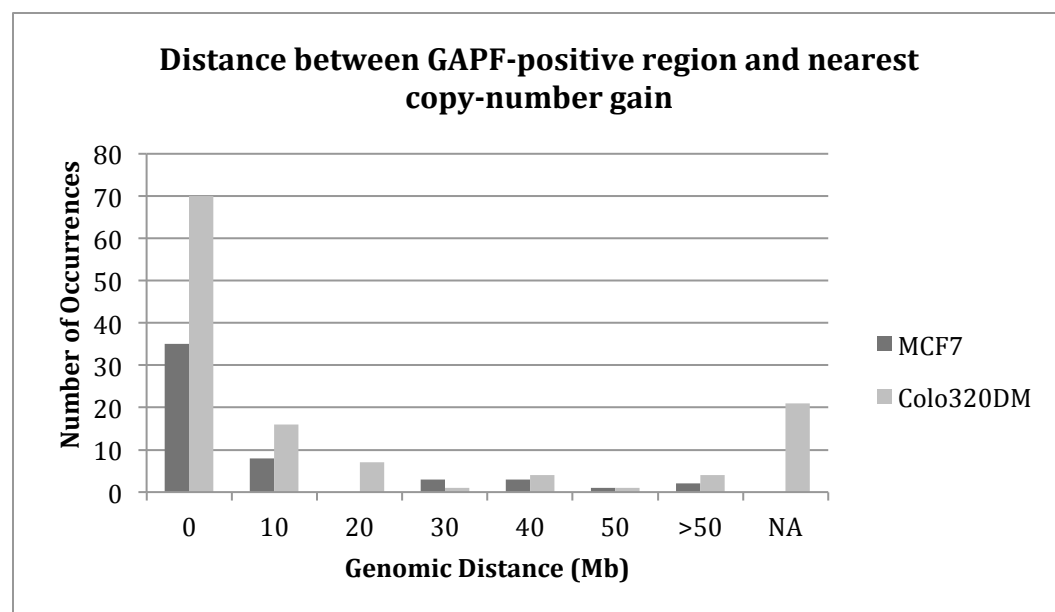


Supplemental Figure 4

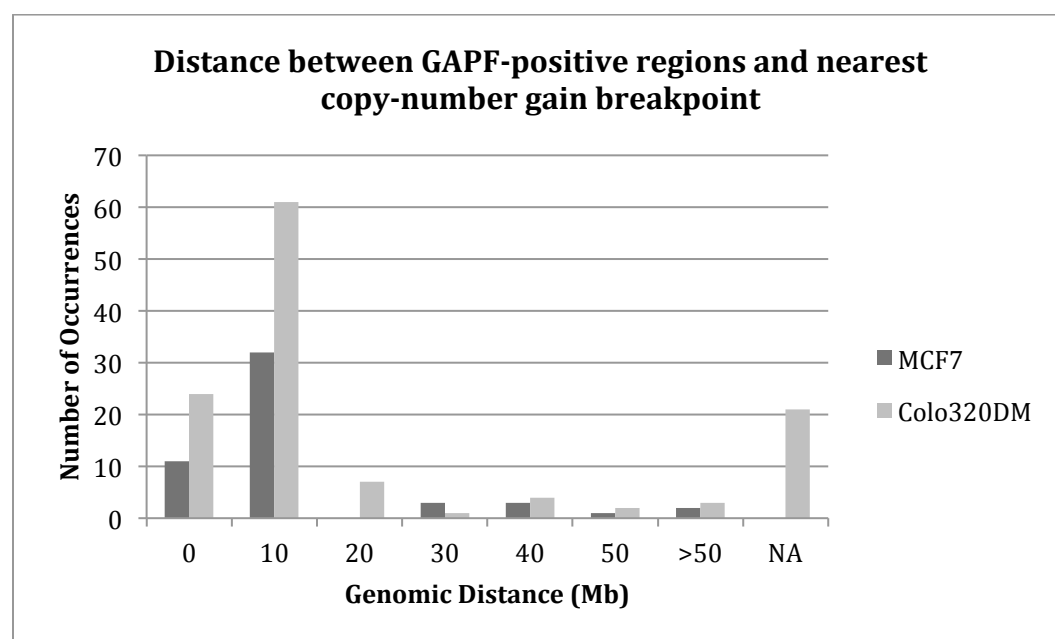
A**B**

Supplemental Figure 5

A)



B)



Supplemental Table 1

Chromosomal locations of GAPF-positive regions in cancer samples and association of each region with copy-number gain (x) or amplification (x)

MCF7 Whole Genome - Compared to HFs

Chromosome	Start	End	Size	Assoc'd with Gain	Assoc'd with Gain BP
chr1	29,951,024	29,951,587	563		
chr1	39,897,092	39,907,762	10,670		
chr1	107,712,242	107,712,506	264	x	x
chr1	112,332,326	112,332,468	142	x	x
chr1	114,316,238	114,316,757	519	x	
chr1	114,510,762	114,510,834	72	x	
chr1	200,911,842	200,912,484	642	x	
chr2	4,444,735	4,444,919	184		
chr2	15,730,991	15,734,791	3,800		
chr2	15,745,451	15,747,188	1,737		
chr5	168,080,245	168,080,769	524		
chr7	2,380,397	2,397,315	16,918		
chr7	69,177,700	69,180,814	3,114		
chr7	100,210,795	100,211,556	761	x	
chr7	113,934,518	113,934,664	146	x	x
chr8	86,479,238	86,479,314	76		x
chr8	128,201,619	128,208,246	6,627	x	x
chr9	34,208,316	34,208,505	189		
chr9	114,871,179	114,888,180	17,001		
chr9	137,522,101	137,522,843	742		
chr11	76,721,217	76,721,681	464		
chr12	128,748,287	128,748,897	610		
chr15	48,424,531	48,424,823	292	x	
chr15	75,119,338	75,119,511	173		
chr16	70,528,825	70,528,928	103	x	
chr16	84,233,709	84,249,709	16,000	x	
chr16	84,411,777	84,411,866	89	x	x
chr17	55,455,016	55,465,396	10,380	x	
chr17	55,545,532	55,546,042	510	x	
chr17	55,567,196	55,567,670	474	x	
chr17	55,989,670	55,989,769	99	x	
chr17	56,744,934	56,745,045	111	x	
chr17	56,784,566	56,784,638	72	x	
chr17	56,803,046	56,803,570	524	x	
chr17	56,817,272	56,850,388	33,116	x	
chr17	56,937,065	56,937,460	395	x	
chr17	57,035,416	57,035,600	184	x	
chr17	58,396,331	58,396,537	206	x	
chr17	63,992,683	63,992,822	139	x	
chr19	45,359,272	45,359,703	431		

chr20	45,249,865	45,250,021	156	x	x
chr20	45,389,094	45,389,265	171	x	
chr20	51,632,666	51,632,739	73	x	x
chr20	51,689,001	51,689,072	71	x	
chr20	51,854,764	51,864,321	9,557	x	
chr20	55,155,245	55,155,463	218	x	
chr20	55,183,089	55,183,200	111	x	
chr20	55,237,790	55,237,920	130	x	
chr20	55,249,666	55,249,946	280	x	x
chr20	55,268,186	55,269,880	1,694	x	x
chr20	55,284,551	55,284,733	182	x	x
chr20	62,328,909	62,339,401	10,492		

Colo320DM Whole Genome

Chromosome	Start	End	Size	Assoc'd with Gain	Assoc'd with Gain BP
chr1	103,999,837	104,000,822	985		
chr1	104,039,382	104,040,365	983		
chr1	104,094,046	104,094,961	915		
chr1	120,387,672	120,387,785	113		
chr1	142,481,364	142,481,908	544		
chr1	143,051,684	143,051,876	192	x	
chr1	143,231,932	143,232,158	226	x	
chr1	143,275,311	143,275,770	459	x	
chr1	143,540,907	143,541,057	150	x	x
chr1	144,744,815	144,744,888	73	x	
chr1	146,241,788	146,241,873	85	x	x
chr1	146,255,680	146,256,327	647	x	x
chr1	146,344,265	146,344,518	253		
chr1	146,398,077	146,398,298	221		
chr1	146,470,465	146,470,574	109		
chr1	146,790,246	146,790,709	463		
chr1	147,843,118	147,843,751	633		
chr1	147,985,841	147,986,067	226		
chr1	148,068,112	148,091,057	22,945	x	x
chr1	148,126,649	148,127,346	697	x	x
chr1	148,305,932	148,306,384	452	x	
chr1	148,473,525	148,473,590	65	x	
chr1	148,511,400	148,511,565	165	x	
chr1	148,603,971	148,604,432	461	x	
chr1	148,695,271	148,699,475	4,204	x	x
chr1	148,726,218	148,737,875	11,657	x	x
chr1	148,749,665	148,755,058	5,393	x	
chr1	148,807,158	148,818,012	10,854	x	
chr1	148,833,960	148,835,822	1,862	x	
chr1	148,855,766	148,856,418	652	x	
chr1	149,010,616	149,011,255	639	x	x
chr1	149,024,489	149,040,034	15,545	x	x

chr2	33,325,338	33,325,825	487	x	x
chr2	91,401,263	91,402,759	1,496		
chr2	91,527,536	91,527,610	74		
chr2	127,666,780	127,666,854	74	x	
chr2	128,707,756	128,712,620	4,864	x	x
chr2	132,197,571	132,197,633	62		
chr3	113,936,332	113,936,712	380		
chr4	83,243,282	83,243,510	228		
chr4	101,331,181	101,331,259	78		
chr4	109,916,696	109,917,244	548		
chr6	202,854	203,323	469	x	x
chr6	226,232	327,132	100,900	x	x
chr6	2,437,552	2,443,116	5,564		
chr6	3,405,151	3,405,565	414		
chr6	3,534,005	3,535,589	1,584	x	x
chr6	4,837,545	4,837,651	106	x	
chr6	26,824,871	26,831,454	6,583		
chr6	26,851,200	26,854,349	3,149		
chr6	26,879,468	26,893,229	13,761		
chr6	58,255,053	58,261,503	6,450		
chr7	23,715,940	23,716,068	128		
chr7	62,450,595	62,452,348	1,753		
chr7	62,491,375	62,492,166	791		
chr7	147,710,534	147,710,892	358		
chr8	127,507,951	127,508,553	602	x	x
chr8	127,519,092	127,519,255	163	x	x
chr8	127,531,813	127,545,400	13,587	x	x
chr8	127,557,862	127,572,875	15,013	x	
chr8	127,589,667	127,594,044	4,377	x	x
chr8	127,608,117	127,674,529	66,412	x	x
chr8	127,698,308	127,735,749	37,441	x	
chr8	127,760,054	127,779,084	19,030	x	
chr8	127,793,743	127,817,633	23,890	x	
chr8	127,835,300	127,864,805	29,505	x	
chr8	127,891,176	128,014,598	123,422	x	
chr8	128,025,992	128,050,469	24,477	x	
chr8	128,060,524	128,061,022	498	x	
chr8	128,072,141	128,143,131	70,990	x	
chr8	128,156,643	128,233,020	76,377	x	
chr8	128,243,484	128,261,681	18,197	x	
chr8	128,278,046	128,340,207	62,161	x	
chr8	128,356,912	128,388,956	32,044	x	
chr8	128,411,992	128,511,927	99,935	x	
chr8	128,523,408	128,564,423	41,015	x	
chr8	128,575,872	128,596,484	20,612	x	
chr8	128,606,677	128,615,376	8,699	x	
chr8	128,629,376	128,677,295	47,919	x	
chr8	128,697,498	128,772,054	74,556	x	

chr8	128,788,838	129,078,472	289,634	x	x
chr9	40,323,442	40,323,554	112		
chr10	38,943,520	38,944,266	746		
chr10	39,064,441	39,064,554	113		
chr10	42,056,614	42,057,182	568		
chr11	48,859,954	48,876,789	16,835		
chr11	48,942,060	48,945,040	2,980		
chr11	49,797,790	49,801,276	3,486		
chr11	49,835,167	49,835,549	382		
chr11	49,864,932	49,865,500	568		
chr11	54,803,813	54,807,453	3,640		
chr11	55,391,663	55,395,019	3,356		
chr12	27,542,171	27,542,248	77		
chr13	27,280,477	27,334,675	54,198	x	x
chr13	27,375,316	27,402,428	27,112	x	
chr13	27,413,732	27,452,010	38,278	x	x
chr13	38,510,572	38,510,799	227	x	
chr13	72,199,747	72,200,051	304	x	
chr13	72,517,134	72,517,761	627	x	
chr13	98,254,811	98,254,949	138	x	
chr13	105,044,695	105,044,800	105	x	
chr15	18,702,507	18,717,465	14,958		
chr15	18,745,515	18,745,757	242		
chr15	18,761,062	18,761,506	444		
chr15	18,793,138	18,793,212	74		
chr16	15,121,937	15,122,004	67		
chr16	32,205,512	32,209,024	3,512	x	
chr16	32,228,100	32,241,031	12,931	x	
chr16	32,266,502	32,271,739	5,237	x	
chr16	32,373,778	32,388,162	14,384	x	x
chr16	33,202,641	33,206,524	3,883	x	
chr16	33,225,495	33,239,154	13,659	x	
chr16	33,263,657	33,271,644	7,987	x	
chr16	33,281,747	33,284,163	2,416	x	
chr16	33,298,835	33,324,776	25,941	x	x
chr16	45,040,536	45,040,604	68		
chr16	65,340,192	65,345,547	5,355		
chr16	85,396,805	85,400,404	3,599		
chr19	38,184,893	38,185,529	636		
chr20	33,199,645	33,199,721	76		
chr22	14,503,179	14,503,716	537		
chr22	15,257,549	15,258,388	839		
chr22	15,382,264	15,382,516	252		
chr22	27,404,873	27,405,082	209		

MCF7 (Chr 8, 11, 12) - compared to PBLs

Chromosome	Start	End	Size	Assoc'd with Gain	Assoc'd with Gain BP
chr8	86,478,914	86,479,662	748		x
chr8	128,202,083	128,210,840	8,757	x	x
chr8	144,355,394	144,355,619	225		x
chr8	145,347,246	145,347,724	478		
chr11	65,053,114	65,053,694	580		
chr11	70,776,579	70,777,053	474		
chr11	116,949,083	116,952,841	3,758		
chr11	117,720,382	117,720,533	151		
chr11	118,734,574	118,734,945	371		
chr12	60,458,259	60,458,403	144		

BT474

Chromosome	Start	End	Size	Assoc'd with Gain	Assoc'd with Gain BP
chr8	6,522,431	6,523,430	999		
chr8	40,774,737	40,774,912	175		
chr8	58,281,760	58,282,299	539		
chr8	124,743,136	124,767,263	24,127	x	
chr8	128,386,648	128,386,793	145		
chr8	142,273,975	142,276,440	2,465		
chr8	142,286,811	142,289,578	2,767		
chr8	144,387,423	144,394,341	6,918		
chr8	145,475,807	145,476,037	230		
chr11	6,636,425	6,636,499	74		
chr11	8,787,324	8,787,395	71		
chr11	68,640,958	68,641,442	484	x	
chr11	70,535,835	70,554,582	18,747	x	
chr11	73,430,994	73,431,142	148	x	x
chr11	99,184,320	99,196,883	12,563	x	
chr12	132,824	132,979	155		
chr12	144,707	145,000	293		
chr12	49,265,061	49,265,722	661		
chr12	51,083,992	51,085,308	1,316		
chr12	80,929,210	80,929,700	490	x	x
chr12	112,805,384	112,805,603	219		
chr12	114,297,317	114,298,025	708		
chr12	114,610,690	114,628,494	17,804		
chr12	124,558,788	124,559,251	463		
chr12	128,024,780	128,025,090	310		
chr12	130,041,338	130,044,773	3,435		
chr12	131,150,704	131,150,973	269		

UACC893

Chromosome	Start	End	Size	Assoc'd with Gain	Assoc'd with Gain BP
chr8	4,002,438	4,002,789	351		
chr8	4,013,831	4,014,739	908		
chr8	52,604,683	52,606,788	2,105		
chr8	65,757,793	65,758,250	457		
chr8	117,767,777	117,768,255	478	x	
chr8	118,686,746	118,695,254	8,508	x	
chr8	124,409,779	124,410,192	413	x	x
chr8	124,743,656	124,752,589	8,933	x	
chr8	129,895,723	129,912,968	17,245	x	
chr8	138,035,308	138,035,739	431	x	
chr8	142,275,521	142,275,631	110	x	
chr8	142,288,883	142,288,957	74	x	
chr8	144,387,490	144,387,598	108	x	
chr8	145,340,977	145,351,897	10,920	x	
chr11	986,741	992,017	5,276		
chr11	37,280,429	37,280,895	466		
chr11	44,645,108	44,645,777	669		
chr11	45,723,307	45,723,560	253		
chr11	47,082,786	47,082,886	100		
chr11	64,966,518	64,979,641	13,123	x	x
chr11	70,535,799	70,541,974	6,175	x	
chr11	76,490,073	76,493,172	3,099	x	
chr11	85,506,823	85,512,257	5,434	x	
chr11	86,262,412	86,262,625	213	x	
chr11	86,276,961	86,277,034	73	x	
chr11	93,322,881	93,329,102	6,221	x	
chr11	99,184,281	99,197,945	13,664	x	x
chr11	118,723,620	118,734,945	11,325		
chr12	141,050	145,452	4,402		
chr12	1,627,862	1,649,083	21,221		
chr12	5,878,983	5,891,430	12,447		
chr12	8,678,187	8,679,229	1,042		
chr12	10,235,741	10,236,061	320		
chr12	10,249,055	10,249,301	246		
chr12	25,378,015	25,392,142	14,127		
chr12	31,297,854	31,298,543	689	x	
chr12	112,787,859	112,788,539	680		
chr12	114,613,987	114,623,821	9,834		
chr12	114,713,206	114,741,070	27,864		
chr12	128,752,342	128,752,451	109		
chr12	128,875,841	128,885,782	9,941		
chr12	131,150,704	131,150,894	190		
chr12	131,811,944	131,817,019	5,075		

MDA231

Chromosome	Start	End	Size	Assoc'd with Gain	Assoc'd with Gain BP
chr8	19,078,035	19,078,322	287		
chr8	22,516,642	22,517,269	627		
chr8	40,773,237	40,774,912	1,675		
chr8	144,387,391	144,387,888	497		
chr8	145,347,246	145,347,379	133		
chr11	247,307	247,417	110		
chr11	975,818	992,017	16,199		
chr11	4,578,169	4,578,356	187		
chr11	14,249,816	14,250,147	331		
chr11	44,630,727	44,630,801	74		
chr11	44,645,108	44,645,810	702		
chr11	68,637,169	68,641,401	4,232		
chr11	68,655,810	68,655,965	155		
chr11	70,530,419	70,542,022	11,603		
chr11	118,710,703	118,735,170	24,467		
chr12	5,883,245	5,883,622	377		
chr12	12,368,202	12,368,702	500		
chr12	49,261,016	49,275,971	14,955		
chr12	51,083,813	51,084,944	1,131		
chr12	94,808,230	94,808,405	175		
chr12	102,680,196	102,680,340	144		
chr12	104,010,730	104,011,076	346		
chr12	114,297,781	114,298,025	244		
chr12	114,610,559	114,623,678	13,119		
chr12	114,717,554	114,735,193	17,639		
chr12	115,397,256	115,397,364	108		
chr12	118,316,729	118,317,283	554		
chr12	118,327,339	118,327,411	72		
chr12	118,830,349	118,830,984	635		
chr12	128,737,496	128,738,053	557		
chr12	128,748,399	128,752,729	4,330		
chr12	128,885,177	128,885,677	500		
chr12	131,150,327	131,151,183	856		
chr12	131,799,876	131,800,316	440		
chr12	131,811,134	131,822,611	11,477		
chr12	132,036,267	132,036,911	644		

ERP1

Chromosome	Start	End	Size	Assoc'd with Gain	Assoc'd with Gain BP
chr8	33,708,337	33,712,039	3,702	x	x
chr8	35,958,813	35,959,305	492	x	x
chr8	37,017,860	37,018,356	496	x	
chr8	37,249,894	37,250,002	108	x	
chr8	37,306,426	37,307,091	665	x	

chr8	37,353,829	37,354,103	274	x	
chr8	37,471,411	37,474,070	2,659	x	
chr8	37,492,662	37,497,079	4,417	x	
chr8	37,524,240	37,530,210	5,970	x	
chr8	37,578,687	37,578,831	144	x	
chr8	37,676,102	37,680,037	3,935	x	x
chr8	37,690,430	37,690,558	128	x	
chr8	37,713,666	37,714,578	912	x	
chr8	37,725,098	37,761,708	36,610	x	
chr8	37,776,109	37,794,105	17,996	x	
chr8	37,805,765	37,827,161	21,396	x	
chr8	37,849,503	37,851,369	1,866	x	
chr8	37,863,073	37,863,454	381	x	
chr8	37,877,572	37,878,058	486	x	
chr8	37,907,052	37,907,609	557	x	
chr8	38,082,299	38,083,147	848	x	
chr8	38,152,119	38,152,671	552	x	
chr8	38,265,322	38,265,575	253	x	
chr8	38,363,099	38,363,530	431	x	
chr8	38,384,947	38,418,516	33,569	x	
chr8	38,432,384	38,443,875	11,491	x	x
chr8	38,530,930	38,543,853	12,923	x	
chr8	38,578,072	38,588,149	10,077	x	x
chr8	38,598,196	38,600,804	2,608	x	x
chr8	72,917,238	72,917,465	227	x	
chr8	80,967,298	80,967,437	139	x	x
chr8	81,505,106	81,505,869	763	x	x
chr8	81,640,710	81,641,141	431	x	
chr8	81,739,398	81,739,928	530	x	
chr8	81,866,183	81,866,368	185	x	
chr8	81,935,362	81,935,495	133	x	
chr8	82,006,844	82,007,249	405	x	
chr8	82,036,082	82,036,184	102	x	
chr8	82,051,190	82,051,988	798	x	
chr8	82,063,746	82,063,821	75	x	
chr8	82,221,401	82,221,911	510	x	
chr8	82,355,714	82,356,248	534	x	
chr8	82,385,784	82,386,042	258	x	
chr8	82,409,972	82,410,118	146	x	
chr8	82,763,514	82,764,371	857	x	
chr8	82,853,884	82,854,306	422	x	
chr8	83,164,526	83,164,937	411	x	x
chr8	119,385,749	119,385,894	145	x	
chr8	144,249,856	144,250,178	322	x	
chr11	69,391,918	69,391,992	74	x	
chr11	69,679,623	69,680,804	1,181	x	
chr11	69,943,958	69,944,030	72	x	
chr11	70,011,337	70,011,558	221	x	

ERP3

Chromosome	Start	End	Size	Assoc'd with Gain	Assoc'd with Gain BP
chr8	7,101,124	7,140,581	39,457		
chr8	7,384,833	7,385,219	386	x	
chr8	7,396,704	7,428,843	32,139	x	
chr8	7,609,616	7,664,577	54,961	x	
chr8	7,675,638	7,678,938	3,300	x	x
chr8	7,847,566	7,856,948	9,382		x
chr8	7,909,858	7,926,500	16,642		
chr8	11,578,016	11,578,081	65	x	
chr8	11,588,715	11,621,098	32,383	x	x
chr8	11,635,372	11,705,306	69,934	x	x
chr8	11,716,887	11,754,346	37,459	x	
chr8	11,765,653	11,801,638	35,985	x	
chr8	11,816,736	11,817,166	430	x	x
chr8	11,837,083	11,837,747	664	x	x
chr8	11,850,041	11,888,093	38,052	x	x
chr8	12,008,000	12,017,410	9,410	x	
chr8	12,070,226	12,071,615	1,389	x	
chr8	12,261,233	12,285,020	23,787	x	x
chr8	12,320,159	12,320,861	702	x	x
chr8	49,352,369	49,352,477	108	x	
chr8	72,917,332	72,917,465	133	x	
chr8	119,385,172	119,385,894	722	x	
chr11	71,195,904	71,196,434	530		
chr12	8,232,672	8,232,742	70		
chr12	8,268,271	8,269,067	796		
chr12	47,563,559	47,569,831	6,272	x	x
chr12	64,503,365	64,503,703	338	x	x
chr12	64,516,850	64,516,968	118	x	x
chr12	64,641,628	64,641,993	365	x	x
chr12	64,914,121	64,914,627	506	x	
chr12	65,035,642	65,036,077	435	x	
chr12	65,248,013	65,248,624	611	x	
chr12	65,266,187	65,266,701	514	x	
chr12	65,369,239	65,369,424	185	x	x
chr12	65,404,316	65,404,707	391	x	
chr12	65,421,984	65,430,242	8,258	x	
chr12	65,443,505	65,444,015	510	x	
chr12	65,479,920	65,480,067	147	x	x
chr12	65,946,553	65,946,627	74	x	
chr12	66,163,353	66,164,026	673	x	
chr12	66,190,771	66,206,051	15,280	x	
chr12	66,252,435	66,253,106	671	x	
chr12	66,327,374	66,327,625	251	x	
chr12	66,338,183	66,338,435	252	x	

chr12	66,390,290	66,390,608	318	x	
chr12	66,667,000	66,667,262	262	x	x
chr12	66,684,278	66,709,178	24,900	x	x
chr12	66,721,329	66,721,465	136	x	x
chr12	66,772,935	66,773,114	179	x	
chr12	66,786,690	66,794,887	8,197	x	
chr12	66,817,319	66,823,375	6,056	x	x
chr12	66,844,000	66,844,568	568	x	x
chr12	66,877,884	66,880,927	3,043	x	x
chr12	66,914,025	66,914,510	485	x	x
chr12	66,971,513	66,971,769	256	x	x
chr12	66,991,273	66,992,874	1,601	x	x
chr12	67,009,029	67,009,894	865	x	x
chr12	67,030,244	67,031,006	762	x	
chr12	67,050,214	67,056,515	6,301	x	
chr12	67,112,322	67,113,684	1,362	x	
chr12	67,154,958	67,159,913	4,955	x	
chr12	67,195,468	67,195,607	139	x	
chr12	67,256,961	67,257,240	279	x	
chr12	67,271,664	67,276,266	4,602	x	
chr12	67,292,648	67,293,075	427	x	
chr12	67,312,606	67,313,114	508	x	
chr12	67,344,874	67,348,120	3,246	x	
chr12	67,358,834	67,372,254	13,420	x	
chr12	67,385,845	67,386,450	605	x	
chr12	67,426,955	67,427,153	198	x	
chr12	67,450,480	67,464,208	13,728	x	
chr12	67,487,861	67,488,004	143	x	
chr12	67,519,419	67,519,780	361	x	
chr12	67,536,107	67,551,996	15,889	x	
chr12	67,593,691	67,593,764	73	x	
chr12	67,612,743	67,614,293	1,550	x	
chr12	67,631,572	67,631,840	268	x	
chr12	67,653,595	67,661,816	8,221	x	
chr12	67,726,868	67,729,845	2,977	x	
chr12	67,748,981	67,749,165	184	x	
chr12	67,770,342	67,785,557	15,215	x	
chr12	67,799,488	67,806,440	6,952	x	
chr12	67,840,988	67,841,170	182	x	
chr12	67,884,615	67,884,725	110	x	
chr12	67,957,800	67,958,157	357	x	
chr12	68,004,740	68,004,979	239	x	
chr12	68,095,797	68,124,546	28,749	x	
chr12	68,139,646	68,140,323	677	x	
chr12	68,247,208	68,247,998	790	x	
chr12	68,277,228	68,277,301	73	x	
chr12	68,300,184	68,304,235	4,051	x	
chr12	68,321,695	68,333,440	11,745	x	x

chr12	68,346,499	68,347,220	721	x	x
chr12	68,358,563	68,359,055	492	x	x
chr12	68,657,754	68,657,828	74	x	
chr12	68,750,368	68,750,932	564	x	
chr12	69,115,240	69,115,424	184	x	
chr12	69,332,781	69,332,854	73	x	
chr12	69,486,021	69,486,914	893	x	x
chr12	69,506,621	69,507,100	479	x	x

ERN1

Chromosome	Start	End	Size	Assoc'd with Gain	Assoc'd with Gain BP
chr8	58,281,723	58,286,606	4,883		
chr11	32,992,674	32,996,145	3,471	x	x
chr11	35,595,287	35,596,315	1,028	x	
chr11	36,301,289	36,301,728	439	x	x
chr11	56,314,232	56,314,930	698	x	x
chr11	56,384,409	56,385,707	1,298	x	
chr11	56,398,455	56,399,344	889	x	
chr11	56,480,537	56,480,911	374	x	
chr11	56,602,860	56,603,860	1,000	x	
chr11	56,614,910	56,622,638	7,728	x	
chr11	56,675,871	56,676,766	895	x	
chr11	56,705,703	56,713,505	7,802	x	
chr11	56,729,119	56,748,138	19,019	x	
chr11	56,759,971	56,766,146	6,175	x	
chr11	56,825,355	56,844,564	19,209	x	
chr11	56,856,202	56,888,746	32,544	x	
chr11	56,916,873	56,920,242	3,369	x	
chr11	56,938,756	56,939,515	759	x	
chr11	56,955,401	56,958,077	2,676	x	
chr11	56,981,231	56,989,421	8,190	x	
chr11	57,007,199	57,012,366	5,167	x	
chr11	57,024,486	57,024,559	73	x	
chr11	57,046,274	57,055,164	8,890	x	
chr11	57,082,734	57,093,820	11,086	x	
chr11	57,130,034	57,131,238	1,204	x	
chr11	57,151,389	57,185,422	34,033	x	
chr11	57,196,962	57,236,610	39,648	x	
chr11	57,266,109	57,266,586	477	x	
chr11	57,276,777	57,285,393	8,616	x	
chr11	57,301,933	57,311,426	9,493	x	
chr11	57,327,644	57,330,747	3,103	x	
chr11	57,349,641	57,354,162	4,521	x	
chr11	57,389,772	57,398,351	8,579	x	
chr11	57,426,340	57,426,929	589	x	
chr11	57,457,425	57,464,978	7,553	x	
chr11	57,496,400	57,503,354	6,954	x	

chr11	57,517,247	57,517,891	644	x	
chr11	57,527,976	57,528,181	205	x	
chr11	57,545,702	57,547,463	1,761	x	
chr11	57,582,220	57,595,217	12,997	x	
chr11	57,642,937	57,650,288	7,351	x	
chr11	57,669,026	57,669,244	218	x	
chr11	57,714,563	57,714,989	426	x	
chr11	57,729,938	57,737,772	7,834	x	
chr11	57,752,306	57,752,556	250	x	
chr11	57,792,866	57,796,394	3,528	x	
chr11	57,868,079	57,868,337	258	x	
chr11	58,101,912	58,102,483	571	x	
chr11	58,389,738	58,390,050	312	x	
chr11	58,420,718	58,430,924	10,206	x	x
chr11	58,479,280	58,488,139	8,859	x	x
chr11	58,516,865	58,517,401	536	x	x
chr11	58,573,426	58,594,506	21,080	x	x
chr11	58,617,067	58,622,722	5,655	x	x

ERN2

Chromosome	Start	End	Size	Assoc'd with Gain	Assoc'd with Gain BP
chr8	28,319,293	28,319,589	296		

ERN3

Chromosome	Start	End	Size	Assoc'd with Gain	Assoc'd with Gain BP
chr11	118,363	118,535	172	x	
chr12	123,467,329	123,467,593	264		
chr12	131,701,890	131,702,535	645		

Supplemental Table 2

Chromosomal locations of copy-number gains and amplifications in cancer samples with log2 signal ratio

Colo320DM

Chromosome	Start	End	Log2 signal ratio
Chr1	72,541,492	72,589,343	0.7465
Chr1	142,778,395	143,552,507	0.4405
Chr1	143,560,901	144,503,409	0.3084
Chr1	144,643,813	146,274,242	0.5802
Chr1	146,274,340	146,292,286	0.4362
Chr1	147,509,337	147,516,059	0.4207
Chr1	148,038,514	148,083,384	0.5485
Chr1	148,083,418	148,100,108	0.6299
Chr1	148,100,390	148,101,153	0.5002
Chr1	148,101,390	148,695,300	0.8183
Chr1	148,695,443	149,042,061	1.4054
Chr2	4,213,259	33,295,068	0.3326
Chr2	33,296,932	34,552,819	0.548
Chr2	34,590,549	34,605,088	0.534
Chr2	34,605,270	52,645,616	0.4683
Chr2	52,646,320	57,505,674	0.4015
Chr2	57,522,808	59,646,999	0.4429
Chr2	59,647,304	59,664,128	0.3186
Chr2	88,914,227	89,189,757	0.8565
Chr2	89,200,032	89,254,935	0.5413
Chr2	125,058,275	125,094,984	0.3836
Chr2	125,095,816	126,868,706	0.5836
Chr2	126,874,564	126,957,270	0.8743
Chr2	126,959,413	130,924,227	0.772
Chr3	157,579,200	163,972,465	0.3726
Chr3	163,973,176	163,989,212	0.421
Chr3	163,990,860	175,627,874	0.354
Chr3	175,628,822	175,673,239	0.3101
Chr3	175,673,269	179,706,865	0.327
Chr3	179,707,948	194,357,441	0.3303
Chr3	194,369,185	199,380,402	0.3354
Chr4	69,057,931	69,203,992	0.6463
Chr4	115,391,058	115,406,002	0.3449
Chr5	57,357,343	57,376,771	1.4268
Chr6	199,255	327,897	1.4651
Chr6	3,532,744	8,211,857	0.3123
Chr7	141,680,871	141,721,998	0.4247
Chr8	127,507,820	127,641,341	2.0836
Chr8	127,642,943	129,079,104	2.1475
Chr13	17,943,628	27,278,682	0.3418

Chr13	27,279,355	27,453,260	2.0342
Chr13	27,456,668	32,008,271	0.3536
Chr13	32,013,649	71,737,394	0.402
Chr13	71,745,610	71,855,991	0.9454
Chr13	71,856,734	73,698,575	0.8812
Chr13	73,699,273	73,737,621	0.6793
Chr13	73,738,713	100,987,476	0.4146
Chr13	101,432,636	114,126,487	0.3904
Chr14	18,508,599	19,492,423	0.5307
Chr14	105,322,139	105,366,801	0.4818
Chr14	105,400,192	105,764,511	0.7066
Chr14	105,777,135	105,817,991	0.607
Chr14	105,818,132	105,841,890	0.3946
Chr14	105,848,006	105,934,557	0.3391
Chr14	105,934,559	105,974,076	0.3516
Chr16	32,088,465	32,419,256	0.6646
Chr16	32,962,147	33,347,885	0.7713
Chr16	49,199,209	49,385,912	0.4371
Chr16	69,393,871	69,763,397	0.3867
Chr18	19,914,057	19,945,963	0.3941
Chr18	46,818,909	46,820,316	1.1484
Chr20	1,508,775	1,547,572	0.769

MCF7

Chromosome	Start	End	Log2 signal ratio
Chr1	72,535,252	72,589,343	1.0478
Chr1	106,537,258	106,856,913	1.1823
Chr1	106,857,234	107,731,728	1.2217
Chr1	107,935,633	108,442,428	0.4175
Chr1	108,443,342	108,787,284	0.6155
Chr1	110,023,238	110,051,747	0.7031
Chr1	112,167,345	112,375,147	0.7589
Chr1	113,838,302	114,018,594	0.4819
Chr1	114,019,050	114,105,331	0.6482
Chr1	114,106,625	114,133,168	0.7333
Chr1	114,133,353	114,563,630	0.9699
Chr1	114,563,805	115,418,929	1.0276
Chr1	115,419,088	115,446,066	0.631
Chr1	115,446,324	116,541,150	0.3217
Chr1	116,541,718	116,598,296	0.3651
Chr1	116,598,889	116,633,415	0.5388
Chr1	116,634,561	116,766,897	0.6854
Chr1	116,767,081	118,262,794	0.3788
Chr1	142,718,394	142,770,309	0.3898
Chr1	142,770,353	144,106,797	0.4346
Chr1	144,106,961	144,173,453	0.5355
Chr1	144,175,846	147,220,608	0.6334
Chr1	147,969,147	150,654,431	0.6383

Chr1	150,654,762	150,713,452	0.5857
Chr1	156,344,543	156,699,609	0.3735
Chr1	178,867,222	178,933,716	0.4567
Chr1	178,940,856	179,093,175	0.7326
Chr1	179,094,532	179,869,743	0.5374
Chr1	179,870,179	179,889,447	0.3451
Chr1	180,647,723	194,946,078	0.3896
Chr1	194,946,352	199,484,990	0.4502
Chr1	199,485,987	199,942,935	0.4597
Chr1	199,943,182	199,994,493	0.4834
Chr1	200,243,103	202,209,497	0.5083
Chr1	202,210,867	205,979,757	0.4579
Chr1	212,883,987	217,834,951	0.6369
Chr2	40,759,840	40,813,313	0.3515
Chr2	88,787,860	88,861,509	0.3284
Chr2	88,914,734	88,928,008	0.7623
Chr2	88,928,023	89,189,757	0.874
Chr2	89,200,032	89,254,935	0.4708
Chr3	18,311,704	20,931,807	0.3703
Chr3	61,581,183	63,903,254	1.0908
Chr3	63,904,813	63,953,397	0.3059
Chr3	63,953,899	64,923,121	1.5492
Chr3	162,233,128	162,899,162	0.5646
Chr3	162,899,341	163,990,874	0.4557
Chr3	163,990,950	164,111,325	0.9263
Chr3	164,111,361	176,879,329	0.3721
Chr3	192,472,857	194,360,644	0.3758
Chr3	194,360,877	194,369,205	1.2263
Chr3	194,369,261	194,371,924	0.524
Chr3	194,405,555	199,380,402	0.372
Chr4	9,823,258	9,848,047	0.3895
Chr4	65,484,526	65,584,859	0.3445
Chr4	107,048,791	107,294,248	0.4815
Chr5	168,993,144	173,599,925	0.3113
Chr5	173,601,406	174,930,871	0.3868
Chr5	174,932,437	174,961,979	0.3349
Chr5	174,962,076	176,266,354	0.3046
Chr5	176,266,375	176,421,265	0.5052
Chr5	176,481,162	177,415,113	0.4121
Chr5	177,415,724	177,565,722	0.7464
Chr5	177,567,981	177,598,337	0.336
Chr5	177,598,975	178,984,144	0.396
Chr5	178,984,255	178,998,612	0.4801
Chr5	179,248,400	179,251,865	0.3464
Chr5	179,260,119	179,281,096	0.3428
Chr5	179,282,746	179,385,742	0.7013
Chr5	179,386,172	180,223,966	0.3438
Chr5	180,230,213	180,652,396	0.3306

Chr6	32,538,145	32,638,264	0.7171
Chr6	32,665,279	32,786,951	0.3143
Chr7	31,660,901	35,249,507	0.3929
Chr7	76,558,518	78,683,769	0.3661
Chr7	78,685,537	78,694,007	0.5237
Chr7	78,694,573	92,805,671	0.5296
Chr7	92,806,196	97,210,032	0.4937
Chr7	97,210,064	97,244,985	0.4145
Chr7	97,255,531	97,949,371	0.4958
Chr7	97,950,910	97,976,729	0.5579
Chr7	97,977,135	109,221,022	0.6738
Chr7	109,245,981	109,249,459	0.5597
Chr7	109,249,923	113,899,658	0.7023
Chr7	113,901,264	113,938,848	0.6893
Chr7	122,544,339	122,670,673	0.4603
Chr7	124,751,019	127,358,389	0.3318
Chr7	152,777,563	153,889,932	0.3129
Chr7	154,034,680	157,255,238	0.3139
Chr7	157,255,339	157,920,023	0.3439
Chr7	157,920,073	158,322,658	0.7812
Chr7	158,663,920	158,812,469	0.4446
Chr8	82,319,137	82,407,494	0.359
Chr8	86,481,516	88,573,901	0.7141
Chr8	88,574,504	90,402,223	0.687
Chr8	90,402,795	91,777,868	0.599
Chr8	91,782,672	91,793,149	0.5337
Chr8	91,794,554	91,821,159	0.5132
Chr8	91,822,408	93,093,654	0.3078
Chr8	93,093,748	100,996,484	0.352
Chr8	100,998,212	101,407,119	0.5295
Chr8	101,584,266	102,516,898	0.4493
Chr8	102,518,557	109,510,556	0.5994
Chr8	109,511,382	112,439,117	0.6549
Chr8	121,600,339	125,972,676	0.6376
Chr8	125,974,567	126,819,588	0.6701
Chr8	126,824,618	126,835,907	0.6428
Chr8	126,837,082	127,654,555	0.7377
Chr8	127,656,310	127,890,765	0.7285
Chr8	128,194,686	128,771,264	0.6525
Chr8	128,774,343	128,898,587	0.7124
Chr8	128,898,740	129,019,540	0.869
Chr8	129,019,898	129,054,826	0.3659
Chr8	129,059,258	129,142,148	0.6679
Chr8	129,142,628	129,343,689	0.993
Chr8	129,344,034	129,972,871	0.6736
Chr8	131,045,970	131,296,298	0.4965
Chr8	139,482,948	139,543,509	0.4485
Chr8	144,257,163	144,355,026	0.6613

Chr9	641,006	1,010,933	0.3779
Chr9	1,014,022	1,047,528	0.3633
Chr10	13,569,795	13,703,100	0.3937
Chr10	24,415,257	24,418,902	0.8462
Chr11	75,213,170	75,519,001	0.3109
Chr12	3,642,833	3,647,492	0.4644
Chr12	32,937,776	33,991,506	0.4206
Chr12	33,992,241	34,621,608	0.3202
Chr12	38,440,975	38,572,160	0.3847
Chr12	62,156,710	65,582,221	0.4014
Chr12	65,582,311	68,198,181	0.3653
Chr12	68,424,130	91,437,099	0.3439
Chr12	96,404,189	96,535,644	0.356
Chr12	98,706,063	99,160,616	0.4378
Chr12	131,232,049	131,677,822	0.3265
Chr13	45,488,774	45,967,935	0.4291
Chr13	45,971,343	45,991,047	0.6362
Chr13	45,992,013	46,018,188	0.6489
Chr13	46,018,337	47,002,783	0.8352
Chr14	37,101,387	37,288,281	0.6527
Chr14	37,290,061	37,327,129	0.4312
Chr14	50,517,419	58,257,851	0.3009
Chr14	58,258,816	59,210,999	0.3585
Chr14	59,211,296	63,772,543	0.3364
Chr14	63,815,632	63,821,986	0.7357
Chr14	63,910,780	63,950,990	0.3501
Chr14	63,952,389	64,131,441	0.5784
Chr14	64,131,739	64,158,115	0.3432
Chr14	64,159,117	64,201,109	0.3659
Chr14	64,201,519	71,450,456	0.3098
Chr14	71,451,944	71,868,408	0.3255
Chr14	71,868,756	73,042,288	0.3473
Chr14	73,146,732	73,733,110	0.3981
Chr14	73,734,463	73,748,866	0.3844
Chr14	75,456,733	88,834,671	0.3392
Chr14	88,841,101	90,926,910	0.3187
Chr14	90,960,703	95,292,150	0.3366
Chr14	95,852,530	96,117,899	0.5549
Chr14	96,120,155	97,249,721	0.3212
Chr14	97,250,714	100,311,051	0.3426
Chr14	100,311,677	104,638,586	0.3601
Chr14	104,639,832	105,150,057	0.3883
Chr14	105,153,622	105,174,066	0.8284
Chr14	105,187,894	105,400,262	0.8443
Chr14	105,413,350	105,601,720	1.0453
Chr14	105,605,177	105,974,076	0.8494
Chr14	105,974,101	105,989,682	0.7881
Chr14	105,993,564	106,160,517	0.6291

Chr14	106,162,126	106,288,690	0.4283
Chr14	106,288,923	106,356,482	0.4918
Chr15	47,524,783	50,123,014	1.0624
Chr15	50,124,710	51,556,867	1.0136
Chr15	51,557,013	52,338,559	0.9431
Chr15	82,976,754	83,386,161	0.4653
Chr15	85,185,181	85,197,526	0.369
Chr15	85,198,368	85,449,005	0.5475
Chr15	85,449,100	85,487,972	0.3034
Chr16	69,385,037	70,679,970	0.3614
Chr16	70,800,116	71,916,198	0.3737
Chr16	71,917,191	75,880,000	0.4059
Chr16	75,880,258	76,162,946	0.3722
Chr16	76,164,773	76,902,031	0.4857
Chr16	76,902,936	76,931,253	0.4443
Chr16	77,066,948	79,561,808	0.3668
Chr16	79,828,611	81,390,450	0.3139
Chr16	81,391,328	82,178,594	0.354
Chr16	82,184,563	82,256,212	0.603
Chr16	82,260,588	82,273,050	0.4685
Chr16	82,273,161	84,422,290	0.339
Chr16	85,079,938	85,226,067	0.4309
Chr16	85,226,953	85,642,092	0.3576
Chr16	85,651,622	86,566,595	0.3986
Chr16	86,567,146	86,630,075	0.3769
Chr16	86,674,060	88,815,024	0.3583
Chr17	24,619,031	24,825,196	0.3151
Chr17	52,638,331	53,994,793	0.3013
Chr17	53,998,108	54,554,192	1.4948
Chr17	54,554,871	54,737,950	0.5426
Chr17	54,745,076	55,252,629	0.4941
Chr17	55,268,305	56,230,342	1.5501
Chr17	56,230,992	56,644,840	0.5897
Chr17	56,645,694	57,342,051	1.766
Chr17	57,349,644	57,575,219	0.5651
Chr17	57,575,645	57,721,746	0.3773
Chr17	57,728,345	58,243,876	0.4299
Chr17	58,245,805	58,779,372	0.5666
Chr17	58,779,728	59,697,823	0.3415
Chr17	59,698,705	59,740,943	0.3473
Chr17	59,741,796	59,781,643	1.4099
Chr17	59,782,626	59,827,767	0.3488
Chr17	59,829,576	64,847,563	0.3704
Chr17	67,653,713	67,764,568	0.3526
Chr17	67,765,494	67,801,683	0.3237
Chr18	2,288,724	3,191,697	0.3184
Chr18	3,197,370	3,277,381	0.7765
Chr18	3,281,714	3,310,996	0.5569

Chr18	3,311,039	3,875,559	0.3519
Chr18	41,399,481	41,551,736	0.334
Chr18	41,551,841	41,651,756	0.7087
Chr18	41,652,904	42,120,550	0.4138
Chr18	42,619,716	42,774,375	0.4659
Chr18	42,778,120	42,792,205	0.3754
Chr18	58,507,571	58,945,596	0.3653
Chr18	59,010,221	59,780,300	0.3835
Chr18	70,106,729	70,224,584	0.3015
Chr19	12,578,847	12,976,480	0.4209
Chr19	51,910,439	52,138,192	0.3087
Chr20	15,235,009	15,327,898	0.3109
Chr20	38,951,840	39,050,812	0.5186
Chr20	39,052,109	39,689,593	0.6593
Chr20	39,690,270	40,249,913	0.5738
Chr20	40,250,180	40,310,488	0.8023
Chr20	40,311,632	40,433,987	0.3655
Chr20	40,435,946	40,515,646	0.5715
Chr20	40,518,286	40,540,022	0.7315
Chr20	40,541,070	40,659,716	0.9309
Chr20	40,661,006	40,674,266	0.6318
Chr20	40,674,622	40,686,495	0.6734
Chr20	40,686,912	40,702,735	0.6669
Chr20	40,702,819	40,741,296	0.4518
Chr20	45,227,374	45,816,354	1.6212
Chr20	45,816,487	45,946,920	1.2636
Chr20	45,949,963	46,007,508	1.163
Chr20	46,009,213	46,164,628	1.5192
Chr20	46,165,461	46,175,099	1.2708
Chr20	46,176,657	46,216,070	1.1244
Chr20	46,216,243	46,968,811	1.0782
Chr20	48,712,418	48,868,132	1.5859
Chr20	49,580,831	49,801,071	0.4233
Chr20	49,801,103	50,122,690	0.6797
Chr20	51,478,190	51,615,163	0.3793
Chr20	51,615,827	51,746,291	1.9733
Chr20	51,751,088	51,757,224	1.4974
Chr20	51,759,113	51,783,455	1.8429
Chr20	51,785,517	52,070,469	1.9099
Chr20	52,071,470	52,990,621	1.6717
Chr20	52,990,657	53,576,178	0.5524
Chr20	53,576,216	53,599,873	1.3092
Chr20	53,599,961	53,622,912	0.624
Chr20	53,624,124	55,098,368	0.3555
Chr20	55,110,266	55,285,876	1.8017
Chr20	55,291,318	57,841,277	0.3751
Chr20	57,843,338	58,995,933	0.351
Chr21	9,976,048	10,061,441	0.3756

Chr21	38,307,004	38,721,508	0.3221
Chr21	38,790,573	41,146,591	0.3475
Chr21	41,151,124	41,464,857	0.3507

BT474

Chromosome	Start	End	Log2 signal ratio
Chr8	77,200,190	125,824,931	0.3323
Chr11	4,923,940	4,933,575	0.6563
Chr11	50,056,280	51,193,822	0.3082
Chr11	63,032,139	63,270,497	0.4657
Chr11	63,270,994	67,228,721	0.4741
Chr11	67,228,897	67,286,775	0.4431
Chr11	67,287,662	68,017,791	0.6586
Chr11	68,022,337	71,267,813	0.3219
Chr11	71,467,853	72,240,032	0.4953
Chr11	72,241,849	72,362,546	0.5306
Chr11	72,364,401	73,391,208	0.8512
Chr11	73,391,239	73,431,975	0.7777
Chr11	73,434,107	74,342,627	0.5318
Chr11	74,345,111	74,553,149	0.8556
Chr11	74,554,148	74,828,304	0.5679
Chr11	74,830,679	74,837,144	0.3517
Chr11	75,633,045	76,093,437	0.6283
Chr11	98,795,897	101,686,040	0.8091
Chr11	101,686,684	102,406,212	0.4996
Chr12	1,437,061	1,916,752	0.3108
Chr12	8,564,544	8,586,577	0.5816
Chr12	34,279,302	34,727,104	0.461
Chr12	62,519,302	64,185,429	0.3253
Chr12	78,046,477	85,645,369	0.3408

UACC893

Chromosome	Start	End	Log2 signal ratio
Chr8	112,327,195	112,351,107	0.4509
Chr8	112,372,497	124,401,614	0.3735
Chr8	124,529,730	146,268,947	0.3701
Chr11	64,968,081	85,970,093	0.5818
Chr11	85,992,810	94,679,062	0.5942
Chr11	97,829,195	98,834,209	0.4024
Chr11	98,834,366	99,223,458	0.8954
Chr12	31,189,138	34,557,796	0.4051
Chr12	34,566,049	34,673,902	0.4529
Chr12	123,641,613	123,825,930	0.3511

MDA231

Chromosome	Start	End	Log2 signal ratio
Chr8	107,117,450	107,142,664	0.3696
Chr8	107,144,169	112,328,345	0.3118

Chr8	112,329,151	112,354,820	0.3039
Chr8	112,372,815	113,452,014	0.3171
Chr11	18,896,898	18,918,486	0.3903

ERP1

Chromosome	Start	End	Log2 signal ratio
Chr8	33,703,169	35,496,080	0.8431
Chr8	35,496,438	35,547,208	0.7202
Chr8	35,549,466	35,950,815	0.4929
Chr8	35,951,014	36,908,891	1.4362
Chr8	36,909,152	37,164,161	1.6622
Chr8	37,164,911	37,627,824	1.5341
Chr8	37,630,070	38,606,127	1.8378
Chr8	38,610,957	47,737,596	0.4052
Chr8	47,743,461	47,769,969	0.3355
Chr8	47,771,122	47,826,246	1.4462
Chr8	50,787,846	50,960,772	0.5999
Chr8	52,585,658	52,880,987	0.6559
Chr8	53,137,940	53,565,871	0.7164
Chr8	60,299,631	80,074,588	0.6685
Chr8	80,081,942	81,016,829	1.1601
Chr8	81,016,953	81,500,486	1.3965
Chr8	81,501,697	83,162,392	1.7527
Chr8	83,167,792	87,836,964	0.7234
Chr8	87,841,470	87,899,436	0.8909
Chr8	87,902,141	87,932,979	1.6557
Chr8	87,933,596	90,398,287	0.8094
Chr8	90,399,787	107,656,252	0.777
Chr8	110,851,399	112,372,347	0.7577
Chr8	112,372,497	144,381,980	0.7751
Chr8	144,385,752	146,268,947	0.7182
Chr11	65,823,240	66,006,496	0.7501
Chr11	66,007,933	66,028,813	0.8892
Chr11	66,029,400	67,180,468	0.8608
Chr11	68,617,281	69,004,819	0.7515
Chr11	69,013,682	70,739,436	1.1557
Chr11	71,636,829	72,211,503	0.6201
Chr11	77,138,262	78,178,911	0.7695

ERP2

Chromosome	Start	End	Log2 signal ratio
Chr8	18,137,713	18,309,434	0.3458
Chr8	34,173,801	34,191,844	0.5892
Chr8	34,198,937	34,230,680	0.4316
Chr8	34,235,453	34,404,750	0.5988
Chr8	35,234,781	35,615,391	0.7621
Chr8	35,620,392	35,646,856	0.6114
Chr8	36,374,690	39,838,665	0.5605

Chr8	39,841,095	39,904,478	0.5835
Chr8	41,918,759	41,951,191	0.3909
Chr8	41,951,441	42,979,158	0.526
Chr8	75,587,671	75,621,729	0.3343
Chr8	75,622,474	75,642,913	0.3462
Chr8	75,668,284	76,200,821	0.4555
Chr8	94,228,380	114,186,772	0.4531
Chr8	114,188,052	115,649,535	0.5406
Chr8	115,649,741	115,700,458	0.5185
Chr8	115,723,932	140,855,354	0.4978
Chr8	140,855,647	140,875,911	0.6048
Chr8	140,878,531	140,898,951	0.5803
Chr8	140,899,423	140,910,496	0.6613
Chr8	140,911,905	141,445,132	0.6583
Chr11	62,262,576	62,427,717	0.3065
Chr12	31,142,817	31,301,551	0.4011

ERP3

Chromosome	Start	End	Log2 signal ratio
Chr8	7,237,778	7,670,521	0.7547
Chr8	7,673,036	7,847,304	0.9012
Chr8	8,000,046	8,132,173	0.7785
Chr8	8,357,439	8,440,552	0.4144
Chr8	11,519,090	11,634,746	1.9122
Chr8	11,634,812	11,862,504	2.1632
Chr8	11,865,672	11,934,586	2.1373
Chr8	11,972,069	12,242,613	1.2325
Chr8	12,276,640	12,286,335	1.758
Chr8	12,286,514	12,291,714	1.4324
Chr8	12,291,766	12,371,881	1.2991
Chr8	12,387,820	12,667,407	1.34
Chr8	14,625,722	14,756,902	0.58
Chr8	14,757,573	14,942,759	0.3558
Chr8	14,944,106	15,053,008	1.2002
Chr8	15,053,069	15,074,417	0.9528
Chr8	15,075,938	15,090,690	0.8272
Chr8	15,090,979	15,133,824	0.7738
Chr8	15,136,614	15,162,999	0.7844
Chr8	15,163,909	15,615,558	0.3693
Chr8	16,089,956	16,137,759	0.5849
Chr8	16,561,674	17,884,814	0.8856
Chr8	18,665,612	19,209,113	0.6896
Chr8	47,031,180	72,366,549	0.8884
Chr8	72,372,751	90,398,287	0.9605
Chr8	90,399,787	112,252,640	0.9437
Chr8	112,253,235	112,357,732	0.9937
Chr8	112,372,497	112,476,092	1.1244
Chr8	112,482,960	131,915,389	1.0376

Chr8	131,915,474	141,032,284	1.0033
Chr8	141,032,458	144,381,980	1.0907
Chr8	144,385,752	146,268,947	1.1274
Chr12	47,568,342	51,300,684	0.7714
Chr12	51,305,649	51,623,256	0.7269
Chr12	51,626,660	51,752,924	0.7993
Chr12	54,601,305	54,665,565	0.4499
Chr12	56,321,973	57,849,831	0.6684
Chr12	62,681,543	63,443,969	0.623
Chr12	64,242,724	64,443,669	0.9645
Chr12	64,498,585	65,116,278	1.4077
Chr12	65,116,332	65,142,934	1.8078
Chr12	65,143,185	65,339,384	1.8298
Chr12	65,340,149	65,501,982	1.9303
Chr12	65,503,175	65,531,545	1.6626
Chr12	65,533,269	66,463,922	1.7004
Chr12	66,464,029	66,660,071	1.5301
Chr12	66,662,394	66,679,073	1.7452
Chr12	66,679,417	66,859,987	2.074
Chr12	66,864,032	66,948,878	1.8723
Chr12	66,949,581	66,974,173	1.5634
Chr12	66,974,797	68,352,547	2.0342
Chr12	68,355,121	68,383,519	1.8067
Chr12	68,383,667	69,031,342	1.4
Chr12	69,037,542	69,517,287	1.6098
Chr12	78,395,121	78,473,926	0.323
Chr12	80,837,812	80,971,899	1.379

ERN1

Chromosome	Start	End	Log2 signal ratio
Chr8	7,903,262	8,046,602	0.3085
Chr11	32,991,061	36,271,785	0.8653
Chr11	36,272,744	36,298,319	0.6342
Chr11	36,298,868	38,950,503	0.3124
Chr11	38,951,759	39,382,675	0.5032
Chr11	55,186,537	55,423,089	0.4867
Chr11	55,423,129	55,465,391	0.7794
Chr11	55,465,668	55,493,035	0.8207
Chr11	55,496,733	55,709,235	1.0729
Chr11	55,709,827	56,303,161	0.9335
Chr11	56,309,577	58,468,640	1.7719
Chr11	58,475,626	58,635,746	1.5538
Chr12	8,414,189	8,493,621	0.512

ERN2

Chromosome	Start	End	Log2 signal ratio
Chr11	34,447,113	34,485,560	0.6043
Chr11	34,485,572	34,591,235	0.9648

Chr12	74,339,013	74,553,754	0.3654
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ERN3

Chromosome	Start	End	Log2 signal ratio
Chr8	39,222,608	39,255,708	0.8102
Chr8	39,256,976	40,269,078	0.7409
Chr8	40,269,752	41,100,276	0.4436
Chr11	188,510	966,019	0.3777
Chr11	4,926,841	4,934,958	0.4504
Chr11	13,030,285	13,052,692	0.5712
Chr11	13,053,050	13,059,266	0.5501
Chr11	13,059,466	13,243,853	0.6982
Chr11	13,244,792	13,403,441	0.405
Chr11	27,149,109	31,073,236	0.3279
Chr11	36,501,832	36,521,213	0.5749
Chr11	36,675,875	36,686,899	0.3628
Chr11	36,688,579	39,621,360	0.3226
Chr11	39,621,440	39,670,505	0.3214
Chr11	50,703,790	54,596,847	0.4158
Chr11	65,214,745	65,264,181	0.4016
Chr11	65,266,600	65,293,720	0.3508
Chr11	69,004,819	69,632,060	0.3739
Chr12	20,691	6,109,035	0.4403
Chr12	6,109,107	6,115,841	0.4609
Chr12	6,119,214	6,522,659	0.7649
Chr12	6,523,006	6,571,042	0.7026
Chr12	6,573,669	9,598,577	0.4077
Chr12	9,637,364	11,757,330	0.4098
Chr12	11,757,455	11,764,555	0.5223
Chr12	11,767,661	12,026,051	0.7591
Chr12	12,026,247	12,096,749	0.6211
Chr12	12,097,064	12,118,007	0.4272
Chr12	12,118,362	12,265,313	0.381
Chr12	98,889,955	99,267,763	0.3471
Chr8	38,206,469	39,222,172	0.9325

Supplemental Table 3

**Number of GAPF-positive regions per
autosomal chromosome in Colo320DM
and MCF7**

	Colo320DM	MCF7
Chr 1	32	7
Chr 2	6	3
Chr 3	1	0
Chr 4	3	0
Chr 5	0	1
Chr 6	10	0
Chr 7	4	4
Chr 8	25	2
Chr 9	1	3
Chr 10	3	0
Chr 11	7	1
Chr 12	1	1
Chr 13	8	0
Chr 14	0	0
Chr 15	4	2
Chr 16	13	3
Chr 17	0	12
Chr 18	0	0
Chr 19	1	1
Chr 20	1	12
Chr 21	0	0
Chr 22	4	0
Total	139	52

Supplemental Table 4

GAPF-positive cytogenetic bands in Colo320DM and MCF7 with shared cytogenetic bands shown in bold

Colo320DM		MCF7	
1p12	12q11.23	1p13.2	17q23.1
1p21.1	13q12.2	1p13.3	17q23.2
2p11.1	13q13.3	1p34.2	17q24.2
2p22.3	13q22.1	1p35.2	19q13.2
2q14.3	13q32.3	1q32.1	20q13.12
2q21.1	13q33.2	2p24.3	20q13.2
3q13.2	15q11.2	2p25.2	20q13.31
4q21.22	16p11.2	5q35.1	20q13.33
4q23	16p13.11	7p22.2	
4q25	16q11.2	7q11.22	
6p11.2	16q22.1	7q22.1	
6p22.1	16q24.1	7q31.1	
6p25.1	19q13.11	8q21.2	
6p25.2	20q11.22	8q24.21	
6p25.3	22q11.1	9p13.3	
7p15.3	22q12.1	9q32	
7q11.21	Xp11.22	9q34.3	
7q36.1	Xp22.12	11q14.1	
8q24.21	Xq13.1	12q24.33	
9p12	Xq22.1	15q21.2	
10p11.1	Xq26.3	15q24.3	
11p11.12	Xq27.2	16q22.3	
11q11	Xq28	16q24.1	

Supplemental Table 5

Locations of significant clusters (p -value < 0.05) of > 3 GAPF-positive regions in cancer genomes with p -values

Sample	Cytogenetic Band	p -value from 5 Mb bins	p -value from 10 Mb bins
Colo320DM WG*	1p21.1	0.0279	NS***
	1q21.1	5.37x10 ⁻¹²	1.11x10 ⁻¹⁶
	1q21.1-q21.2	1.11x10 ⁻¹⁶	
	2q14.3-q21.1	0.000285	0.00209
	6p25.3-p25.1	6.59x10 ⁻⁷	3.35x10 ⁻⁵
	6p22.1	0.00335	0.0217
	8q24.21	0	0
	10p11.1-q11.1	0.000208	0.00154
	11p11.12	7.90x10 ⁻⁶	1.23x10 ⁻⁸
	13q12.2	0.00876	NS***
	15q11.2	0.00012	0.00159
	16p11.2	7.98x10 ⁻⁸	2.23x10 ⁻⁵
	22q11.1	0.0201	NS
	Xp11.22	1.15x10 ⁻⁵	0.000499
	Xq26.3-q27.2	0.0132	NS***
MCF7 WG*	1p13.3-p13.2	NS***	0.000214
	17q23.2	6.19x10 ⁻¹⁰	8.07x10 ⁻⁸
	20q13.2-q13.31	8.03x10 ⁻⁷	5.71x10 ⁻⁶
ERP1**	8p12	1.11x10 ⁻¹⁶	0
	8q21.13	3.45x10 ⁻¹²	9.92x10 ⁻⁸
	11q13.3	1.81x10 ⁻⁵	0.000259
ERP2**	No GAPF-positive regions		
ERP3**	8p23.1	0	4.22x10 ⁻¹⁵
	12q14.3-q15	0	1.02x10 ⁻¹²
ERN1**	11q12.1	1.11x10 ⁻¹⁶	2.22x10 ⁻¹⁶
ERN2**	No clusters of GAPF-positive regions		
ERN3**	No clusters of GAPF-positive regions		
MCF7**	11q23.3	0.000936	0.00653
BT474**	8q24.3	0.000291	0.00367
	11q13.2-q13.4	0.00157	0.0107

	12q24.21	0.0111	NS***
	12q24.32-q24.33	NS***	0.0138
UACC893**	8q24.11-q24.13	NS***	0.0164
	8q24.23-q24.3	0.0128	0.00303
	11p11.2	0.016	NS***
	11q14.2	0.016	0.0217
	12p13.31-p13.2	0.00273	0.00112
	12q24.21	0.0199	NS***
	12q24.33	0.00273	0.0282
MDA231**	11p15.5-p15.4	0.00651	0.0398
	11q13.2-q13.3	0.00651	0.0398
	12q24.21-q24.23	1.95x10 ⁻⁵	0.00127
	12q24.33	1.95x10 ⁻⁵	0.00127

*Whole genome

**GAPF profiles of chromosomes 8, 11, 12

***Not significant at p-value<0.05