

Table W1. Primer Sequences and siRNA/shRNA Clone Details.

Gene Symbol	Clone ID
<i>EGFR</i>	LU-003114-00-0002
<i>ERBB2</i>	SHCLNV-NM_004448
<i>RPS6KB1</i>	SHCLNV-NM_003161

Primer	Sequence
EGFR-f1	GGGCCAGGTCTTGAAGGCTGT
EGFR-r1	ATCCCAGGGCCACCACCAG
EGFR-f2	ACACCCTGGTCTGGAAGTACGCA
EGFR-r2	AGTGGGAGACTAAAGTCAGACAGTGAA
EGFR-f3	CCGAGGCAGGGAATGCGTGG
EGFR-r3	TGGCCTGAGGCAGGCACTCT
ERBB2-f1	TGCGCAGGCAGTGATGAGAGT
ERBB2-r1	TCTCGGGACTGGCAGGGAGC
ERBB2-f2	TCCTCCTCGCCCTCTTGCCC
ERBB2-r2	TCTCGGGACTGGCAGGGAGC
RPS6KB1-f1	TGCTGACTGGAGCACCCCCA
RPS6KB1-r1	GCTTCTTGTGTGAGGTAGGGAGGC
GAPDH-f1	GGCTGAGAACGGGAAGCTTGTCA
GAPDH-r1	TCTCCATGGTGGTGAAGACGCCA
MAST2_f1	GAAGTGAGTGAGGATGGCTGCCTT
MAST2_r1	GAGCCGCTCCATGCTGCTGTAC
MAST2_f2	ATTGAGGGCCATGGGGCATCT
MAST2_r2	CCCCATAGGCGCCATTGCTGATG

Table W2. List of Gene Fusions Identified in 14 Breast Cancer Cell Lines, along with Their Copy Number Status.

Sample Name	5' Gene	3' Gene	Type	Sequencing Platform	No. Reads	Validation	Chromosomal Location	3' Gene	aCGH Data (5' and 3')			Amplicon Status	
									No. Probe	Average Log Ratio	No. Probe		Average Log Ratio
									Fusion QPCR				
BT-474	<i>RPS6KB1</i>	<i>SNF8</i>	Intra	GA II	92	Y	chr17:44362457-44377153	chr17:44362457-44377153	5	2.890	2	3.557	Yes
BT-474	<i>STX16</i>	<i>RAE1</i>	Intra	GA II	79	Y	chr20:55360024-55386926	chr20:55360024-55386926	4	2.910	4	2.910	Yes
BT-474	<i>ZMYND8</i>	<i>CEP250</i>	Intra	GA II	77	Y	chr20:45271787-45418881	chr20:33060636-33563217	15	3.650	5	1.876	Yes
BT-474	<i>TRPC4AP</i>	<i>MXRPL45</i>	Intra	GA II	30	Y	chr20:33053867-33144279	chr17:33053867-33144279	11	3.290	4	3.452	Yes
BT-474	<i>MEDI1</i>	<i>STXBP4</i>	Intra	GA II	28	Y	chr17:50401124-50596448	chr17:50401124-50596448	4	4.029	21	2.507	Yes
BT-474	<i>TOBI</i>	<i>ATX1BP1</i>	Intra	GA II	16	Y	chr17:32949013-33043559	chr17:32949013-33043559	1	2.787	10	2.556	Yes
BT-474	<i>ACACA</i>	<i>STAC2</i>	Intra	GA II	15	Y	chr17:346200314-34635566	chr17:346200314-34635566	35	2.556	3	4.029	Yes
BT-474	<i>MEDI13</i>	<i>BCAS3</i>	Intra	GA II	13	Y	chr17:57374747-57497425	chr17:56109953-56824981	13	1.012	73	1.934	Yes
BT-474	<i>VAPB</i>	<i>KZF3</i>	Intra	GA II	13	Y	chr20:56397580-56459562	chr19:1754724-35273967	7	3.404	10	3.701	Yes
BT-474	<i>RAB22A</i>	<i>MYO9B</i>	Intra	GA II	9	Y	chr20:56318176-56379605	chr19:17047590-17185104	6	3.404	13	2.122	Yes
BT-474	<i>GLI1</i>	<i>CMTM7</i>	Intra	GA II	7	Y	chr3:33013103-33113698	chr3:32408166-32471337	11	-0.425	6	0.428	Yes
BT-474	<i>NCOA2</i>	<i>ZNF704</i>	Intra	GA II	7	Y	chr8:11186820-71478574	chr8:81703240-81949571	35	0.916	26	0.640	Yes
BT-474	<i>BCAS3</i>	<i>MEDI13</i>	Intra	GA II	6	Y	chr17:56109953-56824981	chr17:57374747-57497425	73	1.934	13	1.012	Yes
BT-474	<i>PIP4K2B</i>	<i>RAD51C</i>	Intra	GA II	6	Y	chr17:34175469-34209684	chr17:54124961-54166691	6	4.813	5	1.700	Yes
BT-474	<i>PPP1R12A</i>	<i>MGAT4C</i>	Intra	GA II	6	Y	chr12:78691473-78853366	chr12:84897167-85756812	19	1.218	90	-0.397	Yes
BT-474	<i>STAR3</i>	<i>DOCK5</i>	Intra	GA II	6	Y	chr17:35046858-35073980	chr17:31925711-31965418	5	4.821	27	0.076	Yes
BT-474	<i>TRIM37</i>	<i>MYO19</i>	Intra	GA II	6	Y	chr17:54414781-54539048	chr17:31925711-31965418	14	2.244	6	2.344	Yes
BT-483	<i>SMARCB1</i>	<i>MARK3</i>	Intra	GA II	7	Y	chr22:22459149-22506705	chr14:102921453-103039919	8	1.170	17	0.381	Yes
BT-549	<i>CLTC</i>	<i>TMEM49</i>	Intra	GA II	18	Y	chr17:55051831-55129099	chr17:55139644-55272734	9	-0.283	18	-1.185	Yes
HCC1143	<i>C18orf45</i>	<i>HM13</i>	Intra	GA II	25	Y	chr18:19129977-19271923	chr20:29565901-29591257	18	1.280	2	1.403	Yes
HCC1143	<i>C2ORF48</i>	<i>RRM2</i>	Intra	GA II	23	Y	chr2:10198959-10269307	chr2:10180145-10188997	8	0.134	2	0.134	Yes
HCC1187	<i>PUM1</i>	<i>TREX1</i>	Intra	GA II	38	Y	chr1:31176939-31311151	chr6:42300646-42527761	14	1.648	27	0.336	Yes
HCC1187	<i>SEC22B</i>	<i>NOTCH2</i>	Intra	GA II	30	Y	chr1:14380763-143828279	chr1:120255698-120413799	2	1.557	11	0.253	Yes
HCC1187	<i>CTAGE5</i>	<i>SIP1</i>	Intra	GA II	15	Y	chr14:38806079-38890148	chr14:38806079-388675928	29	0.940	4	0.235	Yes
HCC1187	<i>MCPHI</i>	<i>AGPAT5</i>	Intra	GA II	11	Y	chr8:6251520-6488548	chr8:6553285-6606429	9	0.495	5	0.738	Yes
HCC1187	<i>KLK5</i>	<i>CDH23</i>	Intra	GA II	5	Y	chr19:56138370-56148156	chr10:73225333-73245710	3	0.888	1	0.953	Yes
HCC1187	<i>BCO4L478</i>	<i>EXOSC10</i>	Intra	GA II	3	Y	chr19:42434668-42446354	chr1:11049262-11082525	1	0.816	4	0.156	Yes
HCC1395	<i>E1F3K</i>	<i>CYP39A1</i>	Intra	GA II	13	Y	chr19:43801561-43819435	chr6:46625403-46728482	2	0.852	11	0.611	Yes
HCC1395	<i>HNRNPUL2</i>	<i>AHNAK</i>	Intra	GA II	13	Y	chr11:62238795-62251397	chr11:62039949-62070908	2	0.629	5	1.172	Yes
HCC1395	<i>RAB7A</i>	<i>LRCH3</i>	Intra	GA II	6	Y	chr3:129927668-130016331	chr3:199002541-199082853	10	0.755	11	-0.615	Yes
HCC1395	<i>EROL1</i>	<i>FERMT2</i>	Intra	GA II	5	Y	chr14:52178354-52232169	chr14:52395955-52487565	7	0.934	14	0.934	Yes
HCC1395	<i>FOSL2</i>	<i>BRE</i>	Intra	GA II	5	Y	chr2:284669282-28491020	chr2:27966985-28415271	3	0.480	51	0.849	Yes
HCC1395	<i>BCAR3</i>	<i>ABCA4</i>	Intra	GA II	4	Y	chr1:93799936-93919973	chr1:94230981-94359293	13	0.849	13	0.849	Yes
HCC1954	<i>C6orf106</i>	<i>SPDEF</i>	Intra	GA II	24	Y	chr6:34663048-34772603	chr6:34613557-34632069	13	0.036	3	0.374	Yes
HCC1954	<i>INTS1</i>	<i>PRKAR1B</i>	Intra	GA II	22	Y	chr7:1476438-1510544	chr7:555359-718687	4	1.034	4	0.374	Yes
HCC1954	<i>GALNT7</i>	<i>ORC4L</i>	Intra	GA II	9	Y	chr4:174326478-174481693	chr2:148408201-148494933	15	0.409	7	0.504	Yes
HCC2218	<i>SEC16A</i>	<i>NOTCH1</i>	Intra	GA II	14	Y	chr9:138454368-138497328	chr9:138508716-138560059	6	0.000	7	-0.967	Yes
HCC2218	<i>POLDIP2</i>	<i>BRP1</i>	Intra	GA II	8	Y	chr17:23697785-23708730	chr17:57111328-57295702	3	1.113	19	3.925	Yes
HCC2218	<i>INTS2</i>	<i>ZNF652</i>	Intra	GA II	7	Y	chr17:57297509-57360159	chr17:44721566-44794834	9	3.925	6	2.649	Yes
HCC2218	<i>INTS2</i>	<i>TMEM49</i>	Intra	GA II	5	Y	chr17:57297509-57360159	chr17:55139644-55272734	9	3.925	18	3.202	Yes
HCC2218	<i>LRRCS9</i>	<i>NEUROD2</i>	Intra	GA II	5	Y	chr17:45813592-45829913	chr17:35015546-35017701	3	2.649	1	3.451	Yes
HCC2218	<i>PERLD1</i>	<i>PPM1D</i>	Intra	GA II	4	Y	chr17:35082579-35097833	chr17:56032335-56096818	2	3.451	7	3.340	Yes
MC7	<i>BCAS4</i>	<i>BCA3</i>	Intra	GA II	2788	Y	chr20:48844873-48927121	chr17:56109953-56824981	7	2.107	73	2.653	Yes
MC7	<i>ARFGAP2</i>	<i>SLEF2</i>	Intra	GA II	305	Y	chr20:46971681-47086637	chr20:45179556-45848215	11	0.823	13	3.398	Yes
MC7	<i>RPS6KB1</i>	<i>TMEM49</i>	Intra	GA II	78	Y	chr17:5532524-55382568	chr20:45179556-45848215	5	3.412	18	2.197	Yes
MC7	<i>STK11</i>	<i>MIDN</i>	Intra	GA II	25	Y	chr19:1156797-1179434	chr19:1199551-1210142	4	-1.367	2	-0.279	Yes
MC7	<i>PAPOLA</i>	<i>AK7</i>	Intra	GA II	16	Y	chr14:96038472-96103201	chr14:9528200-96024865	7	0.343	13	0.343	Yes
MC7	<i>AHCYL1</i>	<i>RAD51C</i>	Intra	GA II	11	Y	chr1:110328830-110367887	chr17:54124961-54166691	4	-0.063	5	2.788	Yes
MC7	<i>E1F3H</i>	<i>FAM65C</i>	Intra	GA II	12	Y	chr8:117726235-117837243	chr20:48636052-48686833	12	0.456	5	1.554	Yes
MC7	<i>BCO17255</i>	<i>TMEM49</i>	Intra	GA II	10	Y	chr17:54538741-54550409	chr17:55139644-55272734	1	3.515	18	2.197	Yes
MC7	<i>ADAMTS19</i>	<i>SLC27A6</i>	Intra	GA II	9	Y	chr5:128824001-129102275	chr5:128329108-128397234	30	0.051	8	0.051	Yes
MC7	<i>ARHGAP19</i>	<i>DRG1</i>	Intra	GA II	8	Y	chr10:98971919-99042403	chr22:30125538-30160172	8	0.387	5	-0.420	Yes

Table W2. (continued)

Sample Name	5' Gene	3' Gene	Type	Sequencing Platform	No. Reads	Validation	Chromosomal Location		aCGH Data (5' and 3')				Amplicon Status		
							5' Gene	3' Gene	No. Probe	Average Log Ratio	No. Probe	Average Log Ratio		No. Probe	Average Log Ratio
MCF7	<i>MYO9B</i>	<i>FCHO1</i>	Intra	GA II	8	Y	chr19:17047590-17185104	chr19:17719526-17760377	13	-1.126	4	-0.529	Yes		
MCF7	<i>HSPE1</i>	<i>PREI3</i>	Intra	GA II	6	Y	chr2:198072965-198076432	chr2:198089016-198125760	1	-0.361	4	-0.361	Yes		
MCF7	<i>PARD6G</i>	<i>C18ORF1</i>	Intra	GA II	6	Y	chr18:76016105-76106388	chr18:13601664-13642753	10	-0.674	5	-0.407	Yes		
MCF7	<i>TRIM37</i>	<i>TMEM49</i>	Intra	GA II	6	Y	chr17:54414781-54539048	chr17:55139644-55272734	14	3.515	18	2.197	Yes		
MCF7	<i>SMARCA4</i>	<i>CARM1</i>	Intra	GA II	5	Y	chr19:10955827-11033958	chr19:10843252-10894448	8	0.041	6	0.041	Yes		
MCF7	<i>BCAS4</i>	<i>ZMYND8</i>	Intra	GA II	4	Y	chr20:48844873-48927121	chr20:45271787-45418881	7	2.107	15	3.860	Yes		
MCF7	<i>PVT1 (BC041065)</i>	<i>MYC</i>	Intra	GA II	4	Y	chr8:128875961-129182681	chr8:128817496-128822862	27	1.186	3	1.186	Yes		
MCF7	<i>TRIM37</i>	<i>RNFT1</i>	Intra	GA II	3	Y	chr17:54414781-54539048	chr17:55384504-55396899	14	3.515	2	3.412	Yes		
MDA-MB-361	<i>TMEM104</i>	<i>CRKRS</i>	Intra	GA II	18	Y	chr17:70284216-70347517	chr17:34871265-34944326	9	2.327	7	1.529	Yes		
MDA-MB-361	<i>TANC1</i>	<i>MTMR4</i>	Intra	GA II	12	Y	chr2:159533391-159797416	chr2:159533391-15950250	27	0.000	6	1.658	Yes		
MDA-MB-361	<i>TOX3</i>	<i>GNAO1</i>	Intra	GA II	7	Y	chr16:51029418-51139215	chr16:54782751-54939612	10	-0.157	19	0.281	Yes		
MDA-MB-453	<i>MECP2</i>	<i>TMLHE</i>	Intra	GA II	8	Y	chrX:152948879-153016382	chrX:154375389-154495816	8	1.611	11	1.602	Yes		
MDA-MB-453	<i>MYO15B</i>	<i>MAP3K3</i>	Intra	GA II	4	Y	chr17:71095733-71134522	chr17:59053532-59127402	3	0.543	10	0.494	Yes		
MDA-MB-468	<i>UBR5</i>	<i>SLC25A32</i>	Intra	GA II	8	Y	chr8:103334744-103493671	chr8:104480041-104496644	18	0.070	4	0.927	Yes		
MDA-MB-468	<i>ARD1A</i>	<i>MAST2</i>	Intra	GA II	5	Y	chr1:26895108-26981188	chr1:46041871-46274383	10	0.266	23	0.818	Yes		
MDA-MB-468	<i>EGFR</i>	<i>POLD1</i>	Intra	GA II	5	Y	chr7:55054218-55203822	chr19:55579404-55613083	17	4.944	4	0.732	Yes		
MDA-MB-468	<i>RDH13</i>	<i>FBXO3</i>	Intra	GA II	3	Y	chr19:60247503-60266397	chr11:33724866-33752647	2	0.853	3	1.507	Yes		
UACC-893	<i>FBXL20</i>	<i>CRKRS</i>	Intra	GA II	31	Y	chr17:34662422-34811435	chr17:34871265-34944326	17	2.069	7	4.175	Yes		
UACC-893	<i>CCDC6</i>	<i>ANK3</i>	Intra	GA II	27	Y	chr10:61218511-61336420	chr10:61458164-61570752	17	0.890	13	0.890	Yes		
UACC-893	<i>g67V</i>	<i>PPPIR1B</i>	Intra	GA II	23	Y	chr17:35152031-35157064	chr17:35038278-35046404	1	4.843	2	4.843	Yes		
UACC-893	<i>MEDI</i>	<i>IKZF3</i>	Intra	GA II	9	Y	chr17:34814063-34861053	chr17:35174724-35273967	4	3.908	10	4.843	Yes		
UACC-893	<i>EIF2AK3</i>	<i>PRKD3</i>	Intra	GA II	5	Y	chr2:88637373-88708209	chr2:37331149-37397726	8	1.213	8	1.278	Yes		
ZR-75-1	<i>FOXJ3</i>	<i>CAMTA1</i>	Intra	GA II	10	Y	chr1:42414796-42573490	chr1:6767970-6854694	17	-0.380	10	-0.089	Yes		
ZR-75-1	<i>GPATCH3</i>	<i>CAMTA1</i>	Intra	GA II	10	Y	chr1:27089565-27099549	chr1:6767970-6854694	3	-0.225	10	-0.089	Yes		
ZR-75-1	<i>C10RF151</i>	<i>RCC2</i>	Intra	GA II	9	Y	chr1:19796057-19828901	chr1:17605837-17637644	4	-0.013	4	-0.225	Yes		

Fusions with a recurrent partner are highlighted in yellow.

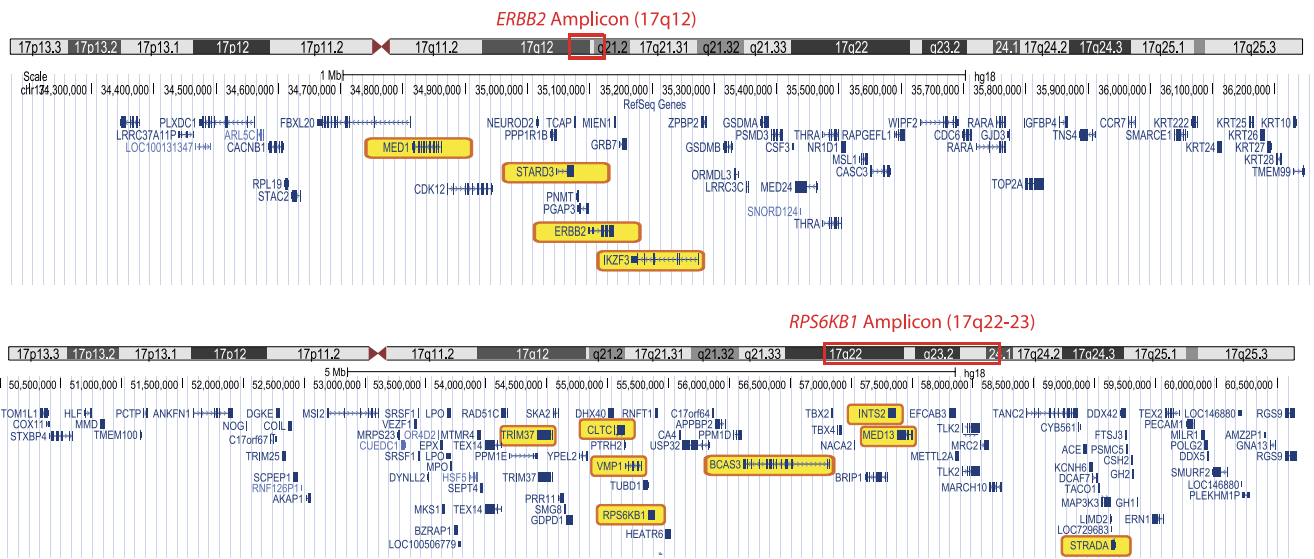


Figure W1. UCSC tracks displaying the *ERBB2* and *RPS6KB1* amplicons, with fusion genes highlighted in yellow.

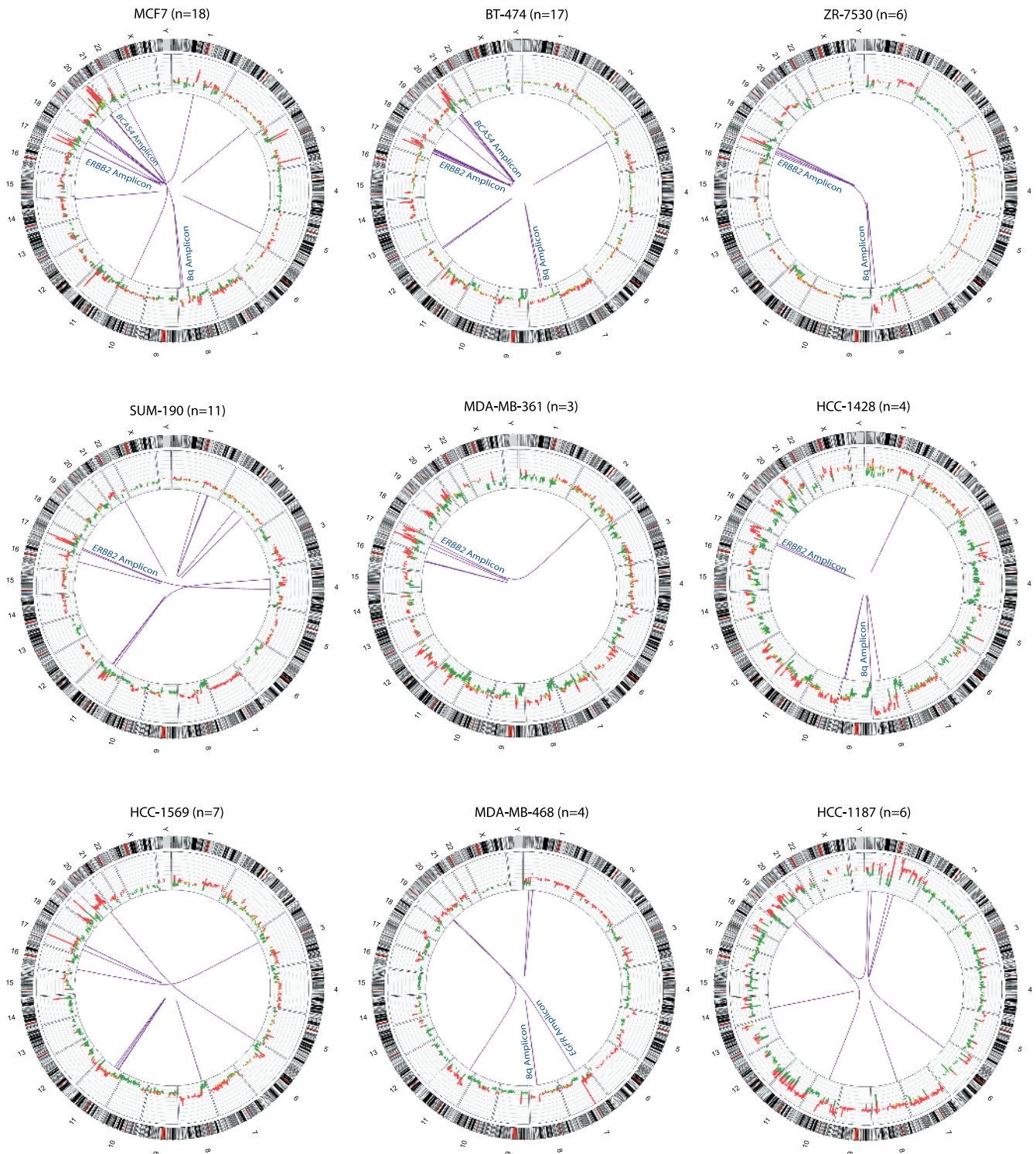


Figure W2. Graphical representation of integrative analysis of gene fusions with copy number analysis. Circos plots of the genome-wide distribution of gene fusions along with status of copy number alterations. Red and green peaks represent amplifications and deletions; purple line represents the fusions associated with amplicons and nonamplicons, respectively. “*n*” refers to the total number of fusions identified.

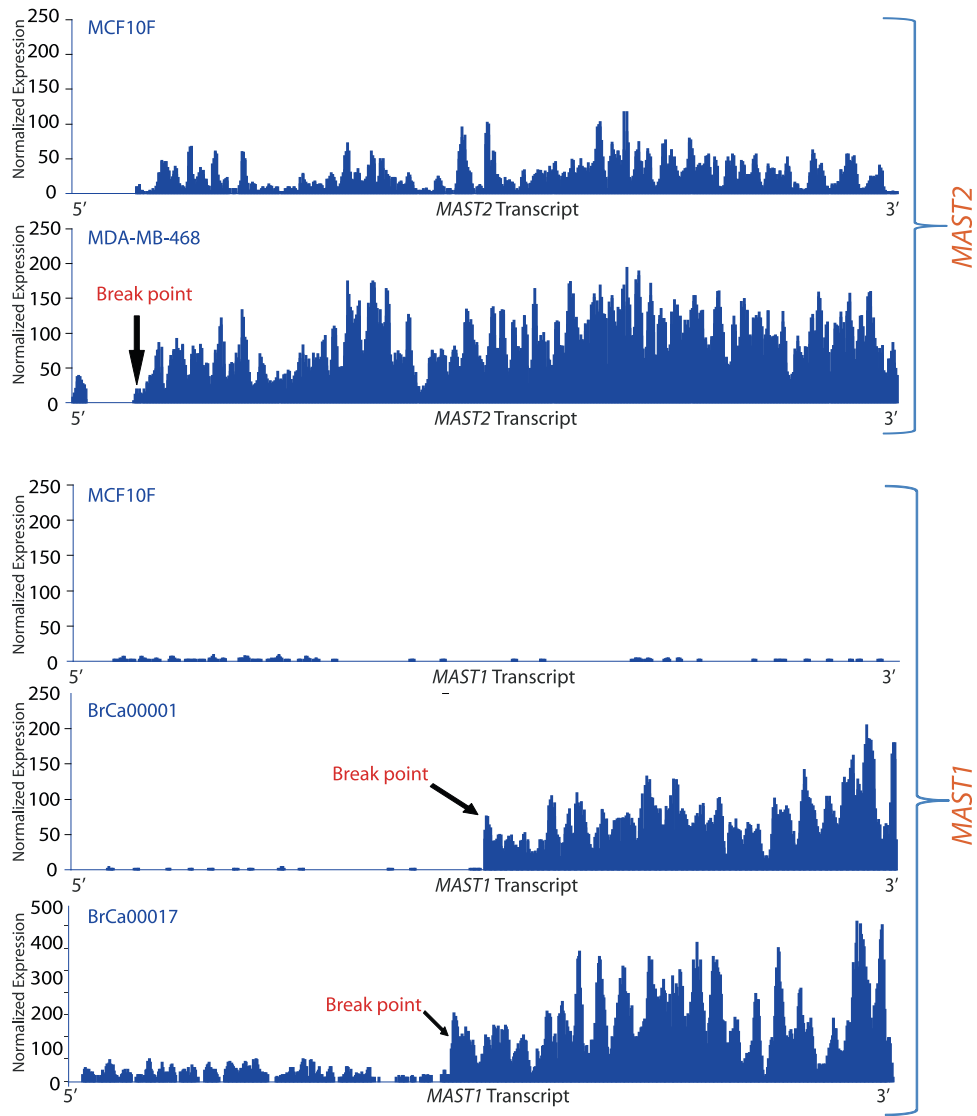


Figure W3. Plot of normalized coverage of *MAST1* and *MAST2* transcripts in *MAST* fusion-positive samples (breakpoint indicated by arrow).

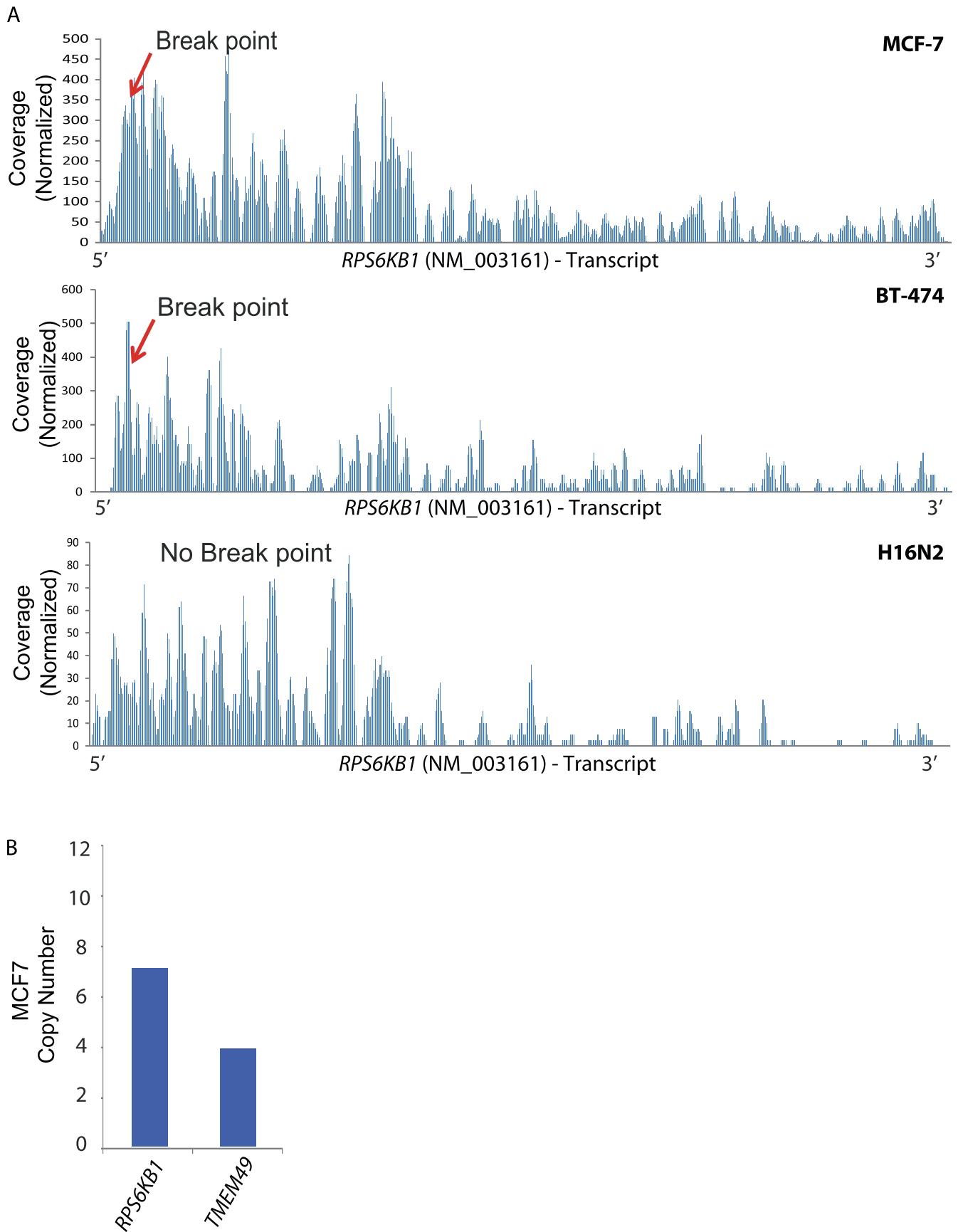


Figure W4. (A) Plot of normalized coverage of *RPS6KB1* transcript in BT-474, MCF7, and H16N2 cell lines. (B) Bar graph representing the copy number of *RPS6KB1* and *TMEM49* in MCF7.