

	<i>ERBB2</i> copy number	1 <sup>st</sup> breakage fusion junction	2 <sup>nd</sup> breakage fusion junction	3 <sup>rd</sup> breakage fusion junction	4 <sup>th</sup> breakage fusion junction	5 <sup>th</sup> breakage fusion junction	6 <sup>th</sup> breakage fusion junction	7 <sup>th</sup> breakage fusion junction
Diploid genome	1+1	0	0	0	0	0	0	0
1 <sup>st</sup> round BFB cycle	2+1	1	0	0	0	0	0	0
2 <sup>nd</sup> round BFB cycle	4+1	2	1	0	0	0	0	0
3 <sup>rd</sup> round BFB cycle	8+1	4	2	1	0	0	0	0
4 <sup>th</sup> round BFB cycle	16+1	8	4	2	1	0	0	0
5 <sup>th</sup> round BFB cycle	32+1	16	8	4	2	1	0	0
6 <sup>th</sup> round BFB cycle	64+1	32	16	8	4	2	1	0
7 <sup>th</sup> round BFB cycle	128+1	64	32	16	8	4	2	1
Expected representation	13.7	6.7	3.3	1.7	0.8	0.4	0.2	0.1
Actual representation	14.36	7	1	1	0	0	0	0

Supplementary Table 4. Estimated and actual copy number of *ERBB2* and breakage-fusion junctions through seven rounds of the break-fusion-bridge cycle. The expected copy numbers of *ERBB2* and each breakage-fusion junction are estimated from the total genome coverage of the BAC end-sequence library (0.105-fold coverage) and the amplification level of *ERBB2*, estimated at 65.6 fold over a diploid genome (the average from the estimates using qPCR and the clone distribution from the BAC end-sequence data). The actual representation of *ERBB2* in the BAC library is calculated from the total coverage of the genomic footprint of *ERBB2* in the BAC end-sequence library (data not shown). 12 clones contained a complete copy of the *ERBB2* gene with a further five clones containing partial sequence accounting for 2.36 copies of the genomic footprint of *ERBB2*, giving a total of 14.36 copies.