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Data in Brief

The HER2 amplicon includes several genes required for the growth and survival of HER2 positive breast cancer cells — A data description

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ABSTRACT

A large number of breast cancers are characterized by amplification and overexpression of the chromosome segment surrounding the *HER2* (*ERBB2*) oncogene. As the HER2 amplicon at 17q12 contains multiple genes, we have systematically explored the role of the HER2 co-amplified genes in breast cancer cell growth and their relation to trastuzumab resistance. We integrated array comparative genomic hybridization (aCGH) data of the HER2 amplicon from 71 HER2 positive breast tumors and 10 cell lines with systematic functional RNA interference analysis of 23 core amplicon genes with several phenotypic endpoints in a panel of trastuzumab responding and non-responding HER2 positive breast cancer cells. In this Data in Brief we give a detailed description of the experimental procedures and the data analysis methods used in the study (1).

Specifications	
Organism/cell line/ tissue	Human/BT474, HCC202, SKBR3, UACC812, HCC1954, HCC1569, JIMT1, SUM190, SUM225, KPL4, MCF7/breast cancer tumor tissue
Sex	Female
Sequencer or array type	Agilent Human Genome CGH 244K microarrays, plate based siRNA screen, protein lysate microarrays
Data format	aCGH microarrays raw- and PCF segmented data from tumors and cell lines, siRNA raw- and normalized data from cell lines, protein lysate microarray raw- and normalized data from cell lines
Experimental factors	HER2 positive breast cancer patients, HER2 positive cell lines, siRNA screens, drug treatments
Experimental features	Determination of the HER2 amplicon size from patient samples; siRNA screens and protein lysate microarrays of breast cancer cell line panel to discover significant HER2 co-amplified genes; validation of their importance in cancer cell survival
Consent	Patients have given informed consent and/or the studies are approved by regional ethical review boards
Sample source location	Norway, Finland and France

Direct link to deposited data

Deposited data can be found here:

http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE34236
http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE17907
http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE32291
http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE20394

Material, methods and experimental design

Cell lines and primary tumors

11 breast cancer cell lines were grown and cultured following recommended conditions. Of these 10 were HER2 positive (HER2+); BT474, HCC202, SKBR3, UACC812, HCC1954 and HCC1569 were obtained from the American Type Culture Collection (ATCC, USA) and JIMT1 was obtained from the German Collection of Microorganisms and Cell Cultures (DSMZ, Germany). Both ATCC and the DSMZ authenticate all human cell lines by DNA-typing using short tandem repeats. SUM190 and SUM225 were kindly given by Stephen Ethier from Karmanos Cancer Institute in Michigan USA, whereas KPL4 was kindly provided by Junichi Kurebayashi from Kawasaki Medical School in Japan. The HER2 negative (HER2-) MCF7 cells were obtained from the Interlab Cell Line Collection (ICLC, Italy) and used as the control. Cells were cultured for a maximum of 30 passages prior to use.

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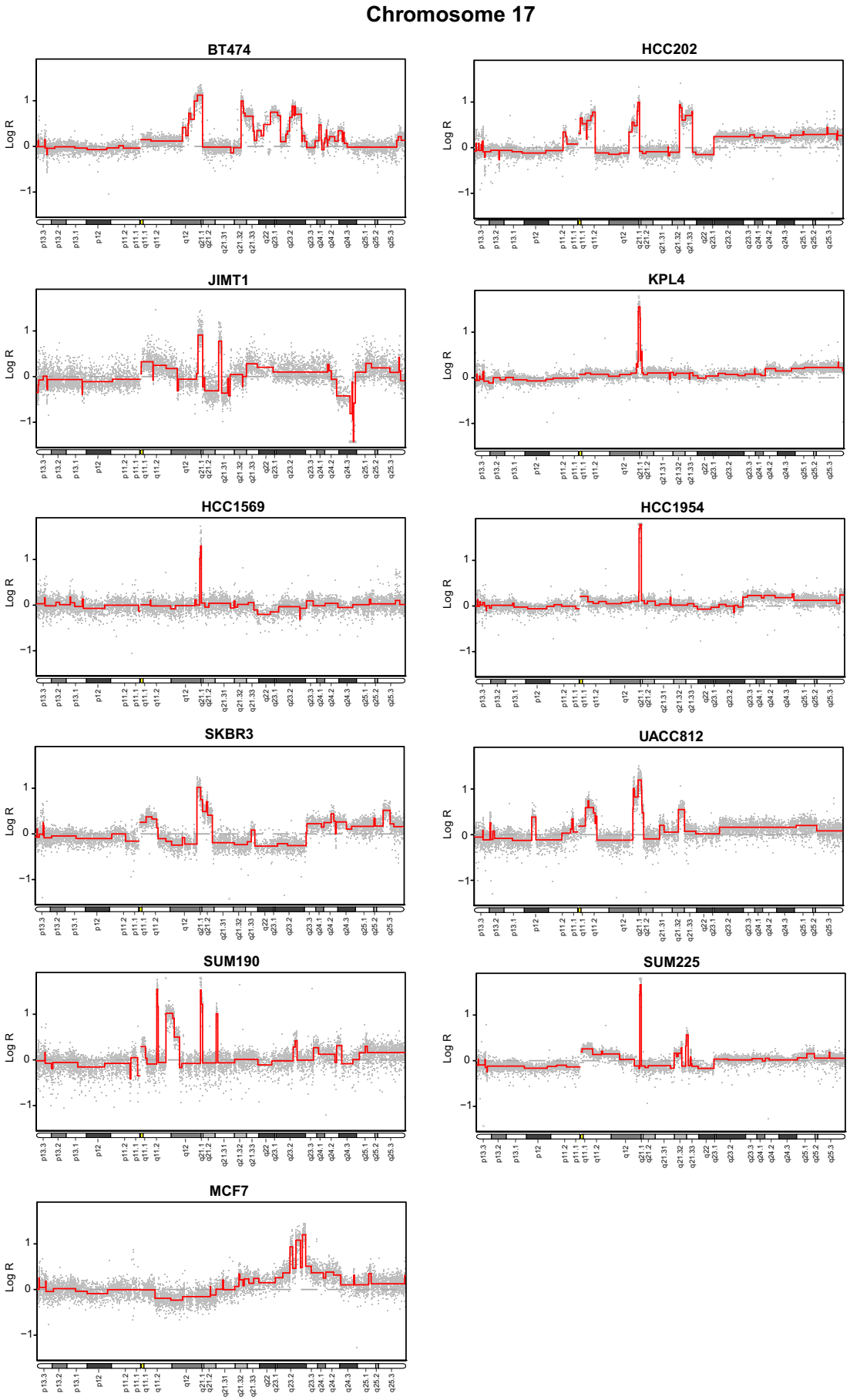
Chromosome 17
BT474
HCC202
JIMT1
KPL4
HCC1569
HCC1954
SKBR3
UACC812
SUM190
SUM225
MCF7
Log R