

Figure S2

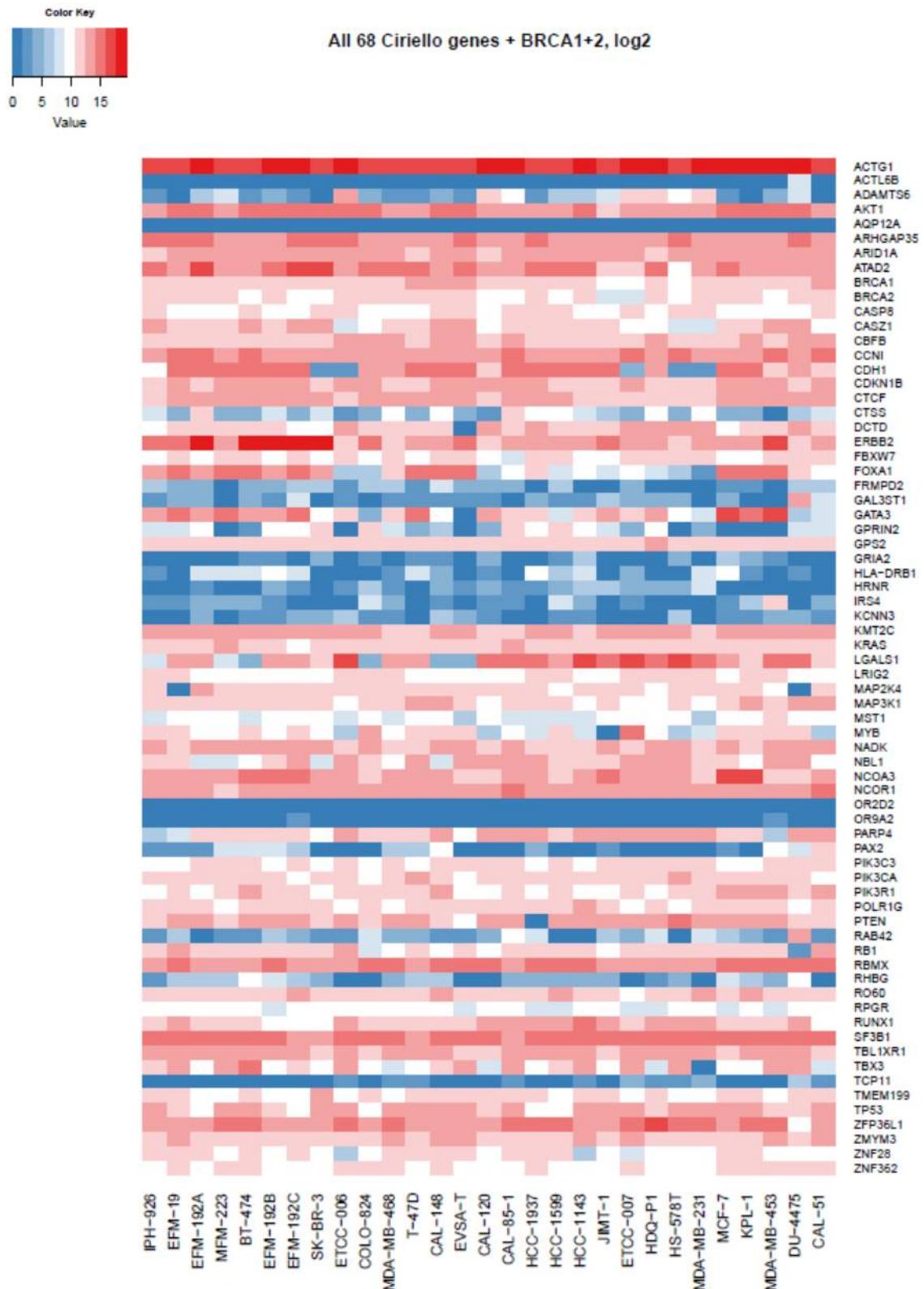


Figure S2. Expression heat map for the gene set analyzed for mutations. Normalized RNA-seq data were log2 transformed after adding 1 for avoiding non-defined values. Genes are ordered alphabetically and cell lines are ordered analogously as in Figure 3.

Figure S3

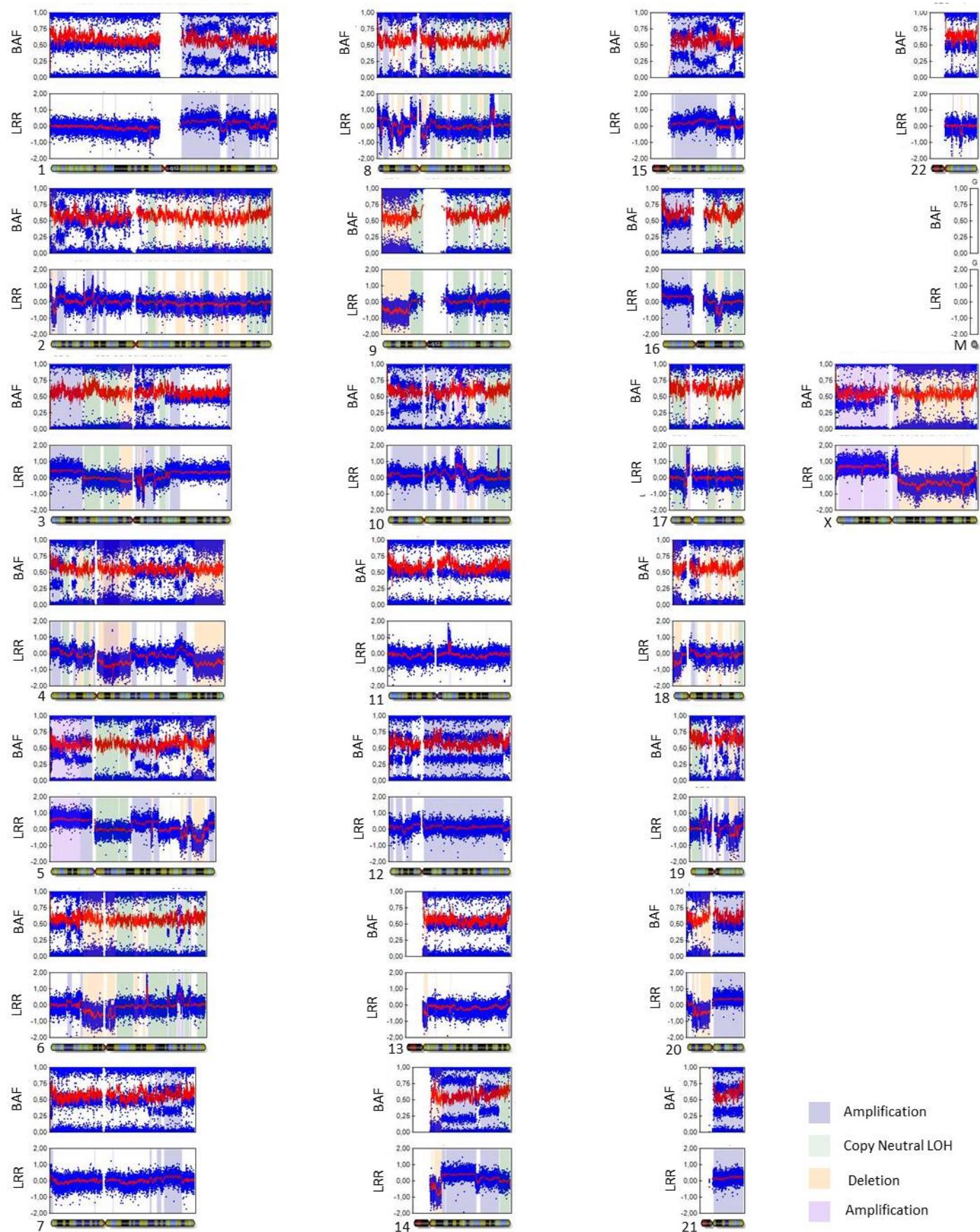


Figure S3. SNP array data for MFM-223. Overview of CNV analysis depicting B allele frequency (BAF) and LogR ratio (LRR) for each chromosome. Shaded regions in different colors indicate: blue: Amplification (CNV value of 3), green: Copy Neutral LOH (CNV value of 2), yellow: Deletion (CNV value of 1), purple: Amplification with higher intensity compared to the mean value (CNV value of 4). The results include copy number events, even when they are smaller than 350.000 bp.

Figure S4

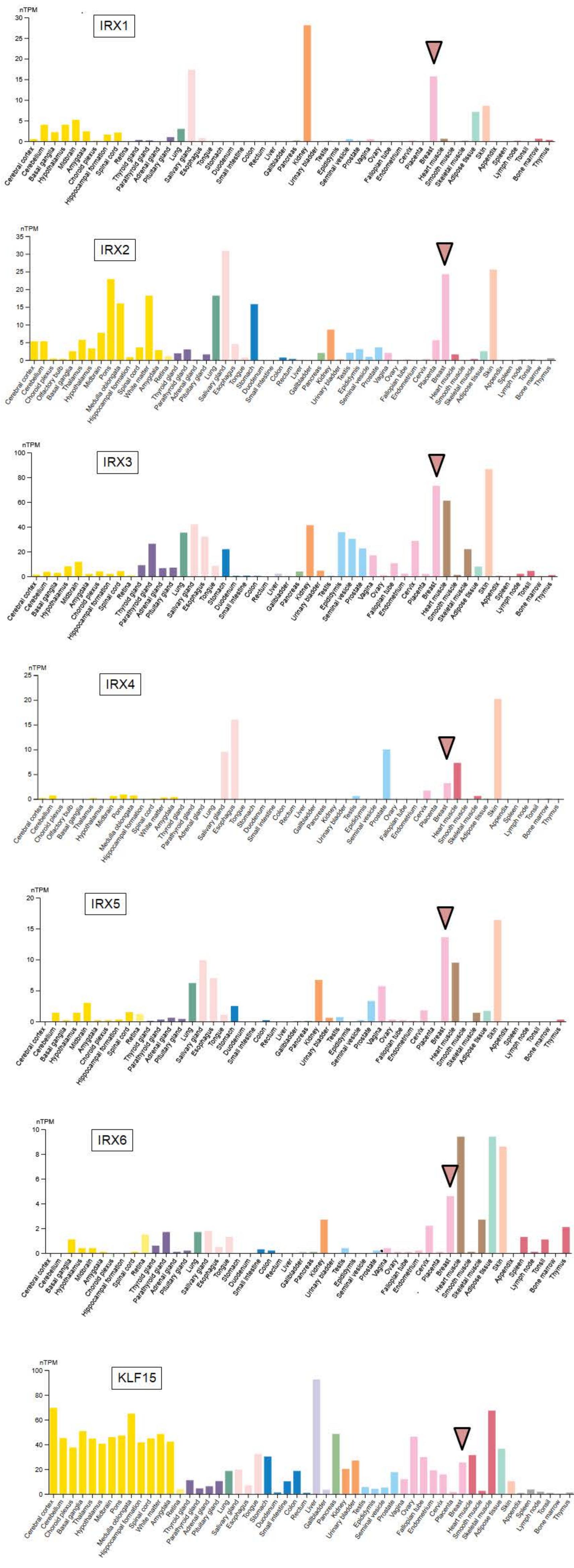


Figure S4: RNA-seq data for six IRX genes and KLF15 from different normal tissues. The data were obtained from the Human Protein Atlas. Breast tissue is indicated by arrow heads.

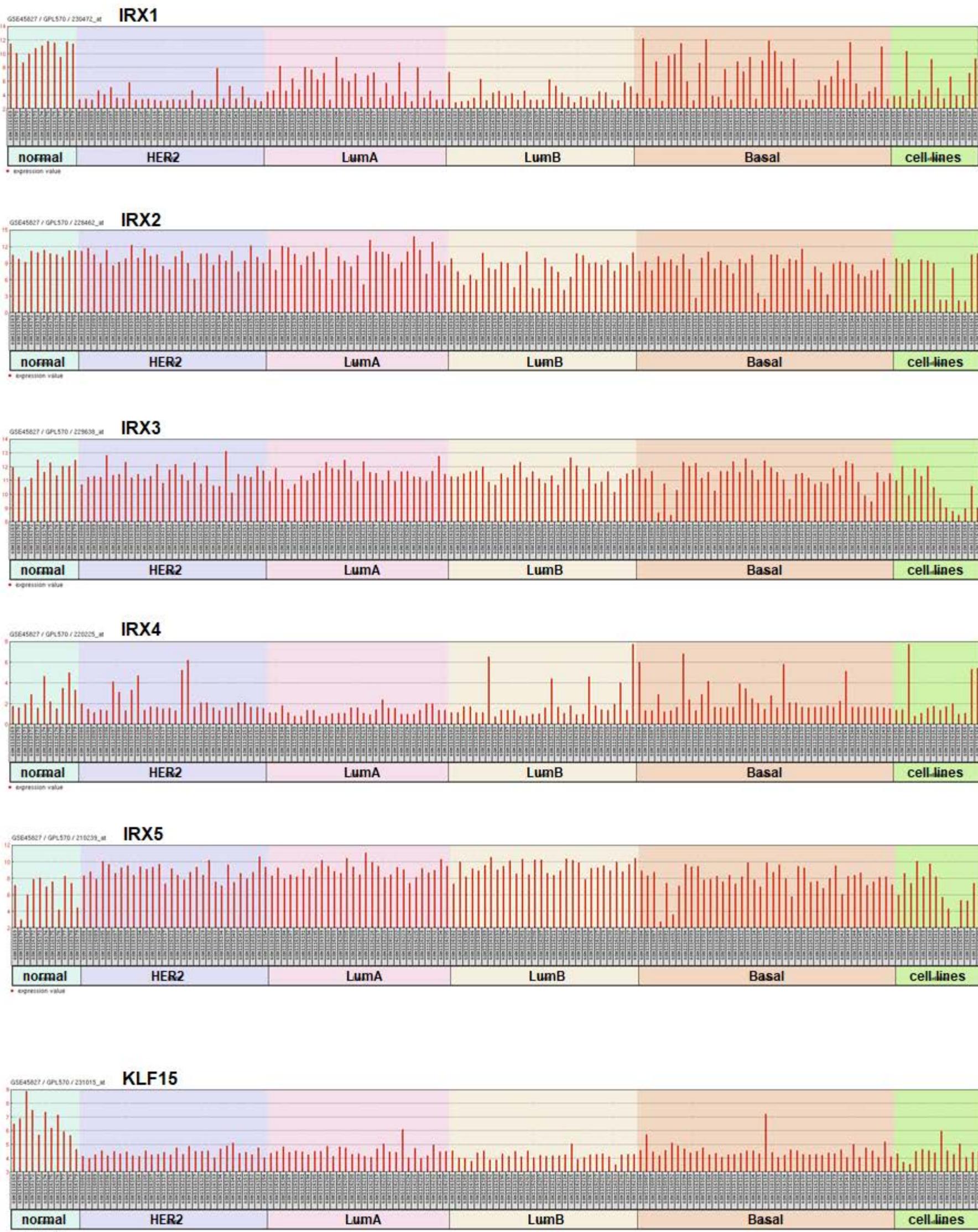


Figure S5: Gene expression profiling data (obtained from GEO data set GSE45827) for normal breast tissue and breast cancer samples, classified as HER2-positive (HER2), Luminal A (LumA), Luminal B (LumB), Triple negative (TNBC), and breast cancer cell lines (cell lines).

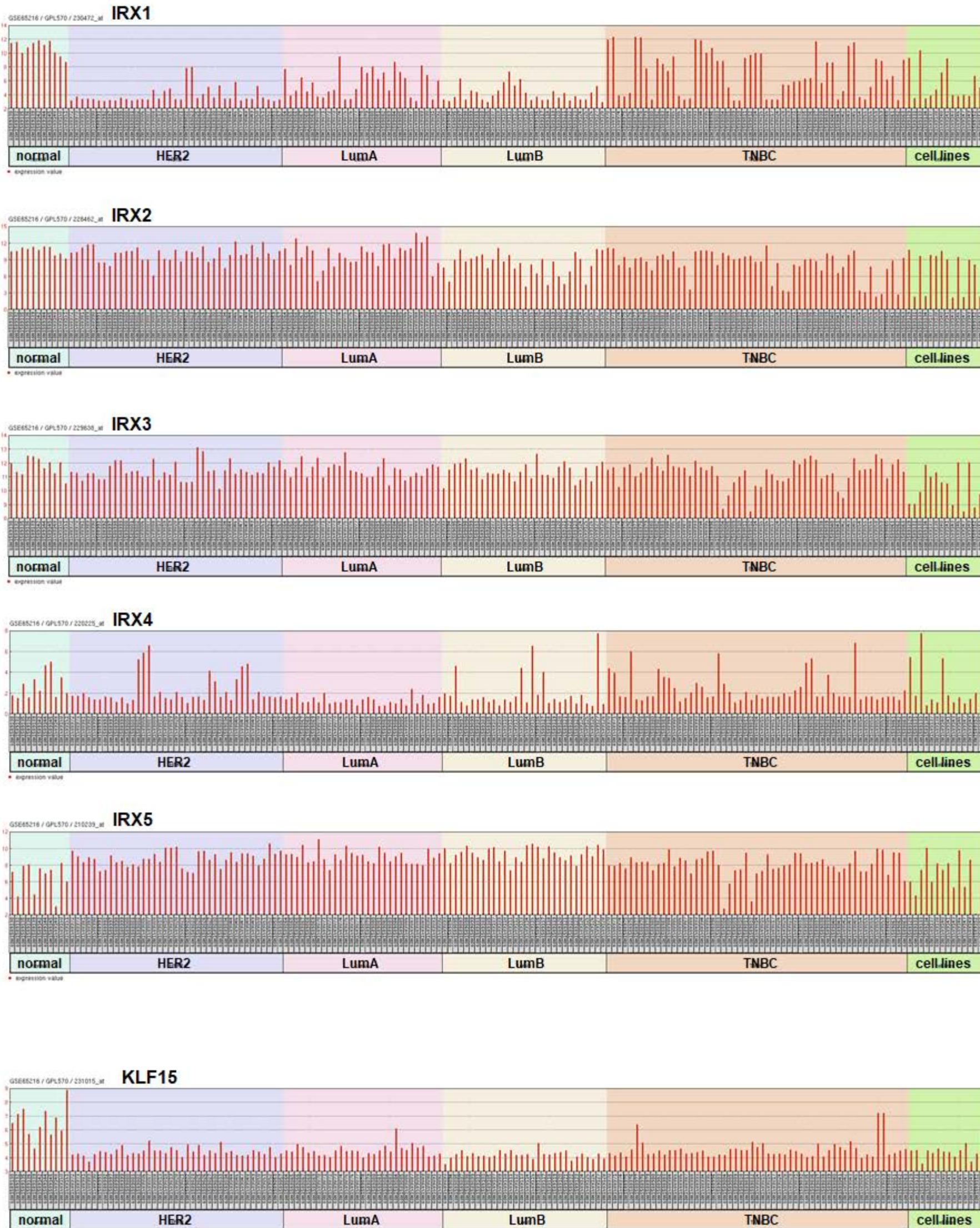


Figure S6: Gene expression profiling data (obtained from GEO data set GSE65216) for normal breast tissue and breast cancer samples, classified as HER2-positive (HER2), Luminal A (LumA), Luminal B (LumB), Triple negative (TNBC), and breast cancer cell lines (cell lines).