



Figure S2. Description and validation of BJ stepwise tumorigenesis system. **a**, The scheme illustrates expression pattern of co-regulated genes based on comparative transcriptomics of primary, immortalized and transformed cells. **b**, Statistics of changes of differentially expressed genes during cell transformation. **c**, RT-qPCR validation of exogenous (*cMYC*, *TERT*) and transformation-relevant (*CCND2*, *THBS1*) gene expression. **d**, Western blot analysis of whole cell extracts of BJ, BJEL and BJELM cells confirms overexpression of T antigen and MYC-ER at the immortalization and tumorigenic steps, respectively. **e**, Validation of acquisition of TRAIL sensitivity⁶⁶ during the transformation process. TRAIL-induced apoptosis was observed specifically in BJELM cells, while BJ and BJEL cells are showing resistance to TRAIL treatment. **f**, Reproducibility between replicates evaluated by calculation of Pearson correlation coefficient **g**, Reproducibility between replicates evaluated by calculation of skewness parameter between BJEL and BJELM replicates relative to BJ replicates.