Supplementary material has been published as submitted. It has not been copyedited or typeset by Acta Oncologica.

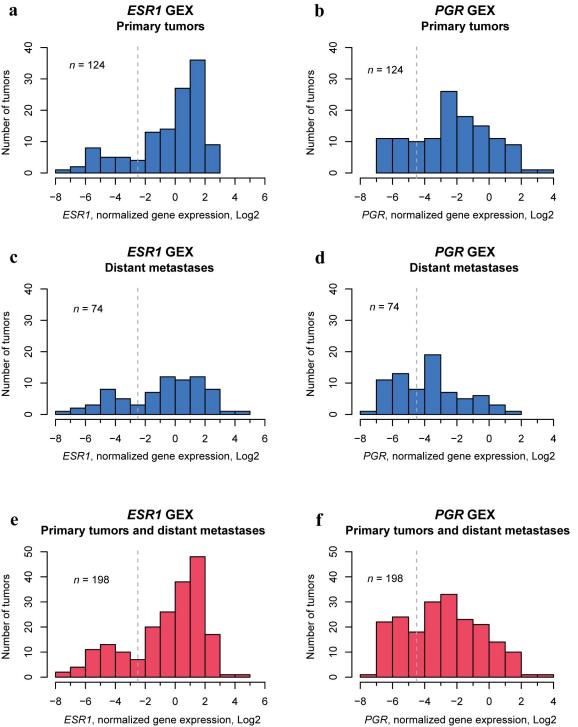


Figure S1

Distribution of mRNA expression levels of ESR1 (a, c, e) and PGR (b, d, f) in an independent cohort of patients with metastatic breast cancer containing GEX data from paired primary tumor and distant metastasis samples previously described in detail (14, 15). The data distribution is shown separately for primary tumors (a-b), distant metastasis (c-d), and both primary tumors and distant metastases pooled together (e-f). The vertical grey dotted lines mark a suggested cutoff for positive/negative ESR1 and PGR status respectively, selected as described in the manuscript.

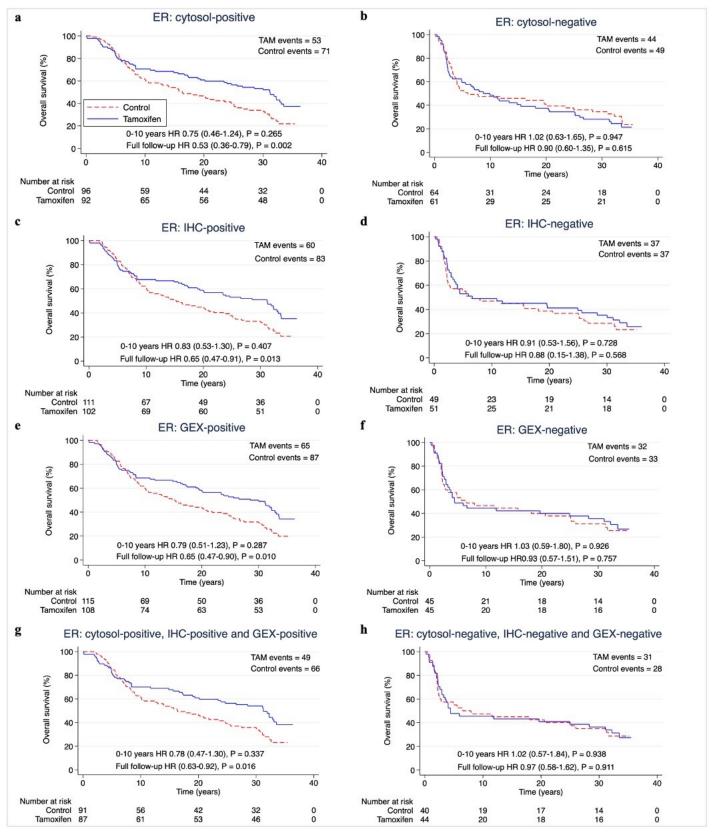


Figure S2

Overall survival according to positive or negative ER status by different methods. Patients with available data for all methods for ER and PR were included (n=313). P-value by log-rank test, 5% significance level. a-b) cytosol-based method. c-d) IHC, e-f) gene expression, g-h) same result for all methods.

ER, Estrogen receptor; cytosol, cytosol-based method; IHC, immunohistochemistry; GEX, gene expression; PR, Progesterone receptor; TAM, Tamoxifen.

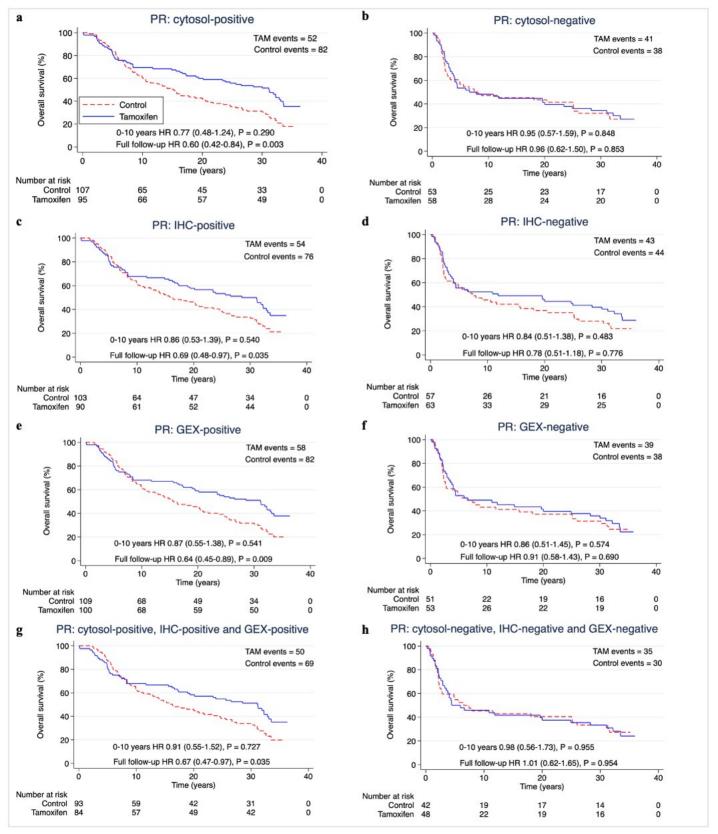


Figure S3

Overall survival according to positive or negative PR status by different methods. Patients with available data for all methods for ER and PR were included (n=313). P-value by log-rank test, 5% significance level. a-b) cytosol-based method. c-d) IHC, e-f) gene expression, g-h) same result for all methods.

ER, Estrogen receptor; cytosol, cytosol-based method; IHC, immunohistochemistry; GEX, gene expression; PR, Progesterone receptor; TAM, Tamoxifen.