

High *PTEN* gene expression is a negative prognostic marker in human primary breast cancers with preserved p53 function

Breast Cancer Research and Treatment

Authors:

Synnøve Yndestad^{1,2}, Eilin Austreid¹, Stian Knappskog^{1,2}, Ranjan Chrisanthar³, Peer Kåre Lilleng^{4,5}, Per Eystein Lønning^{1,2}, Hans Petter Eikesdal^{1,2*}

Author details:

¹Section of Oncology, Department of Clinical Science, University of Bergen, Bergen, Norway.

²Department of Oncology, Haukeland University Hospital, Bergen, Norway.

³Section of Molecular Pathology, Department of Pathology, Oslo University Hospital, Oslo, Norway.

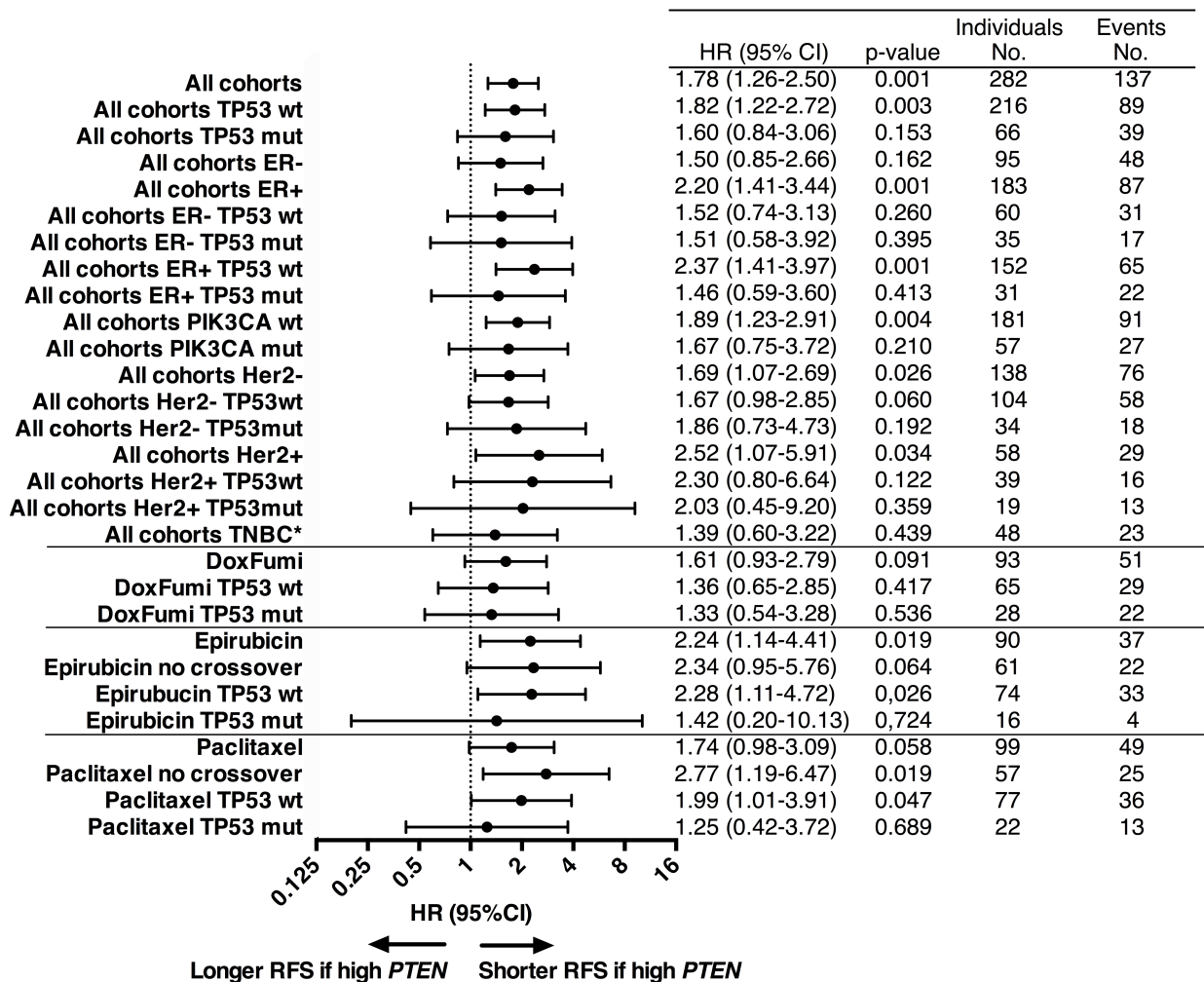
⁴Department of Pathology, Haukeland University Hospital, Bergen, Norway.

⁵Laboratory of Pathology, Department of Clinical Medicine, University of Bergen, Bergen, Norway.

***Correspondence:** hans.eikesdal@k2.uib.no

Online Resource 3

a-b Forest plot for the association between tumor *PTEN* gene expression level and recurrence-free (**a**) or disease-free survival (**b**) in patients with locally advanced breast cancer. Results are presented as individual hazard ratios (HRs) with corresponding 95% confidence intervals (CIs) for Study 1 (doxorubicin trial), Study 2 (FUMI trial) and Study 3 (epirubicin/paclitaxel trial) combined (i.e. all cohorts) or split by subgroups. $HR > 1$ indicates that the survival of patients with tumor *PTEN* gene expression above the median (*PTEN* high) is shorter than that of patients with *PTEN* low tumors, while $HR < 1$ indicates the opposite. RFS: recurrence-free survival, DSS: disease-specific survival, wt: wildtype, mut: mutated, ER: estrogen receptor, PGR: progesterone receptor, TNBC: triple negative breast cancer (ER/PGR/HER2 negative breast cancer), *for patients in Study 1 and 2 PGR status was not available, and TNBC was defined as ER/HER2 negative tumors

a**b**