SupFig 1A: PDX show high conservation of histological and phenotypic characteristics of the tumor of origin. Scale bars 1mm
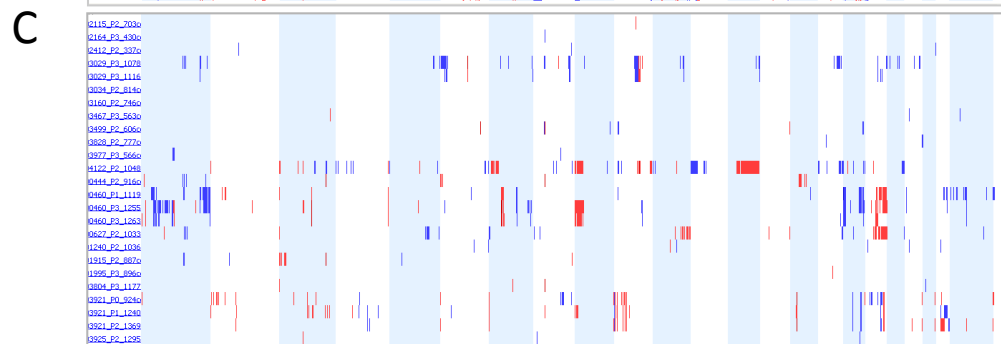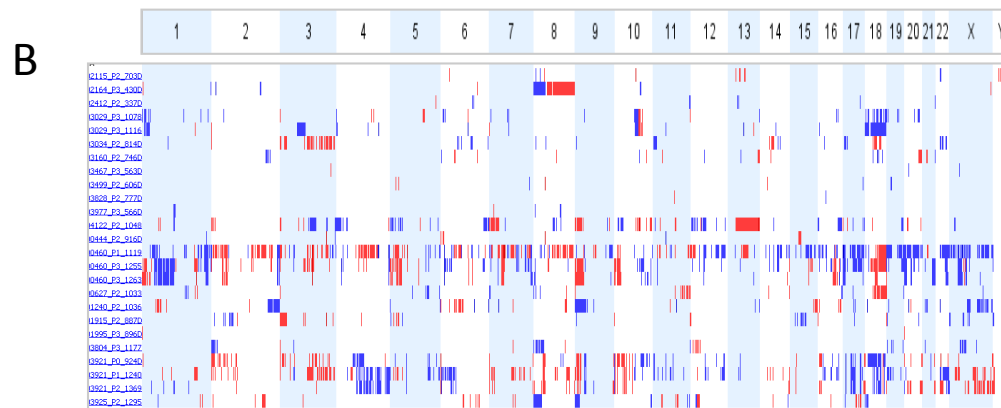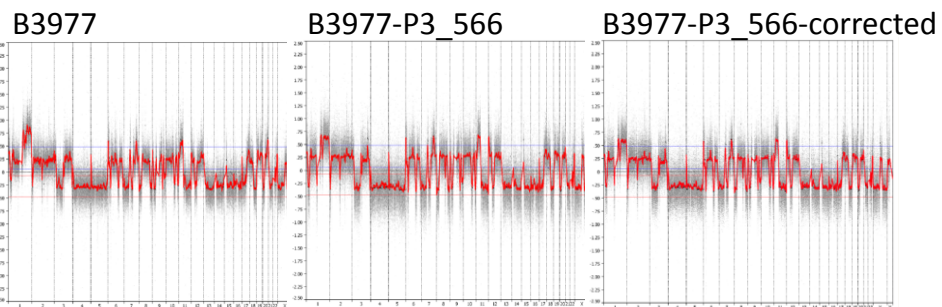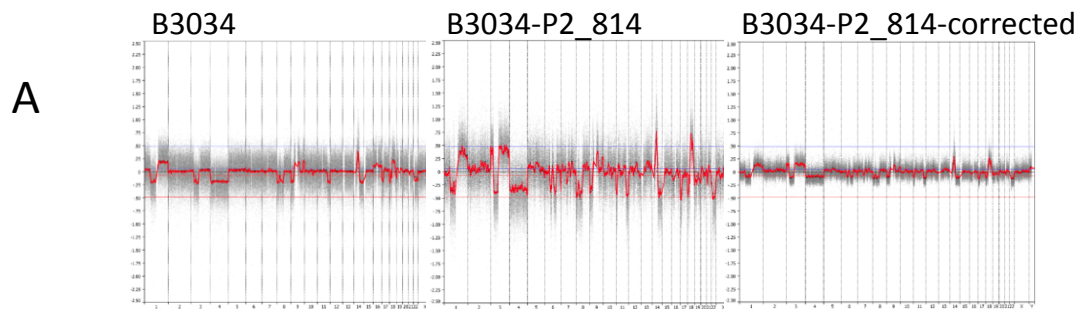
SupFig 1B: PDXs from ER+ primary breast cancer express ER. Scale bars 300μm
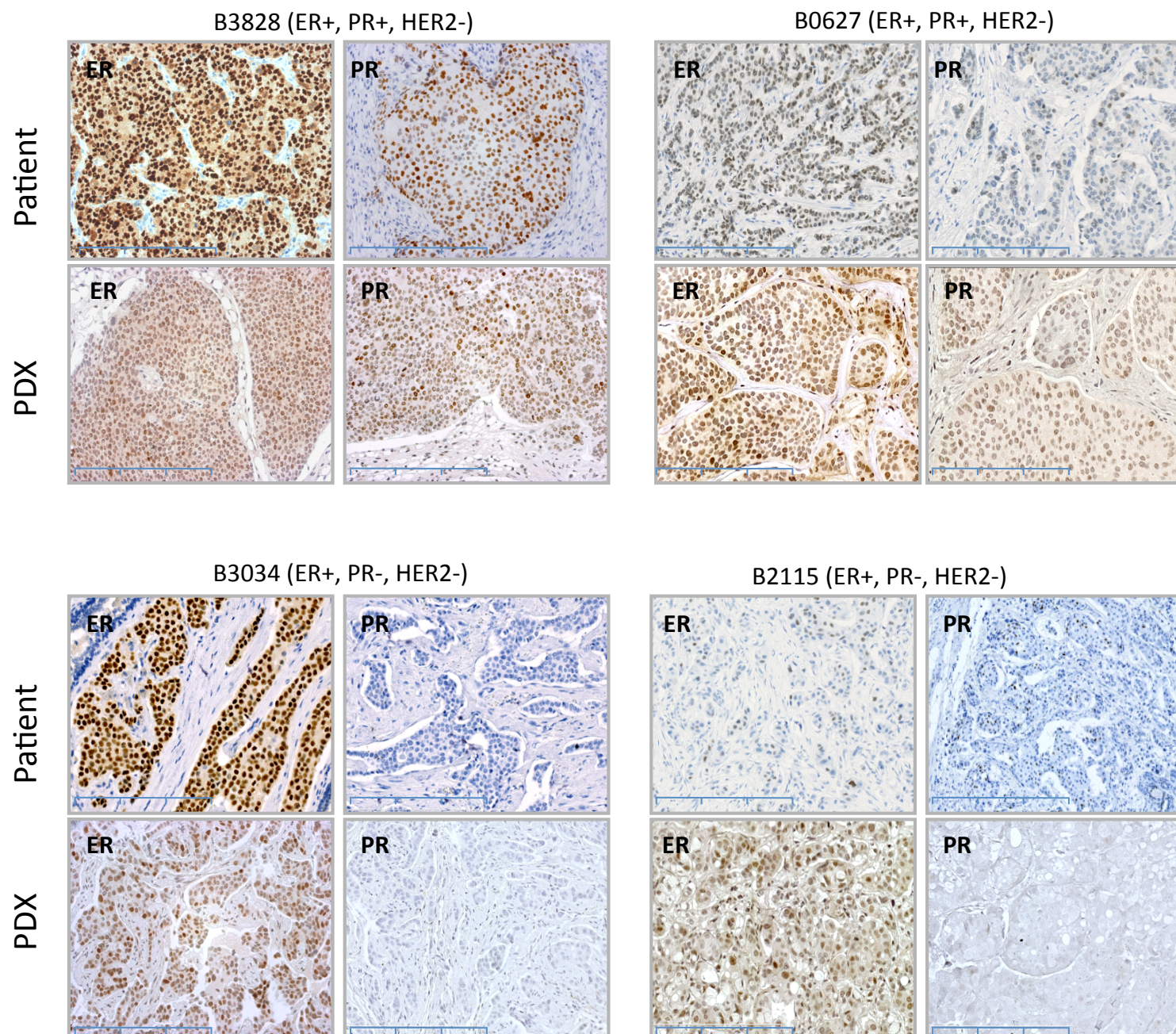
SupFig 1C: PDXs from HER2+ primary breast cancer express HER2 protein. Scale bars 20µm anti-HER2 (#A085, 1:800, Dako, Glostrup, Denmark) rabbit polyclonal antibody


B3921 (HER2 + + +)
HER2

B3925 (HER2+ + +)
HER2

B2115 (HER2+ + +)
HER2

B0627 (HER2+ +)
HER2

B0460 (HER2+)
HER2

B1915 (HER2+)
HER2

B0444 (HER2+)
HER2

B3499 (HER2+)
HER2

Negative control
HER2

PDX
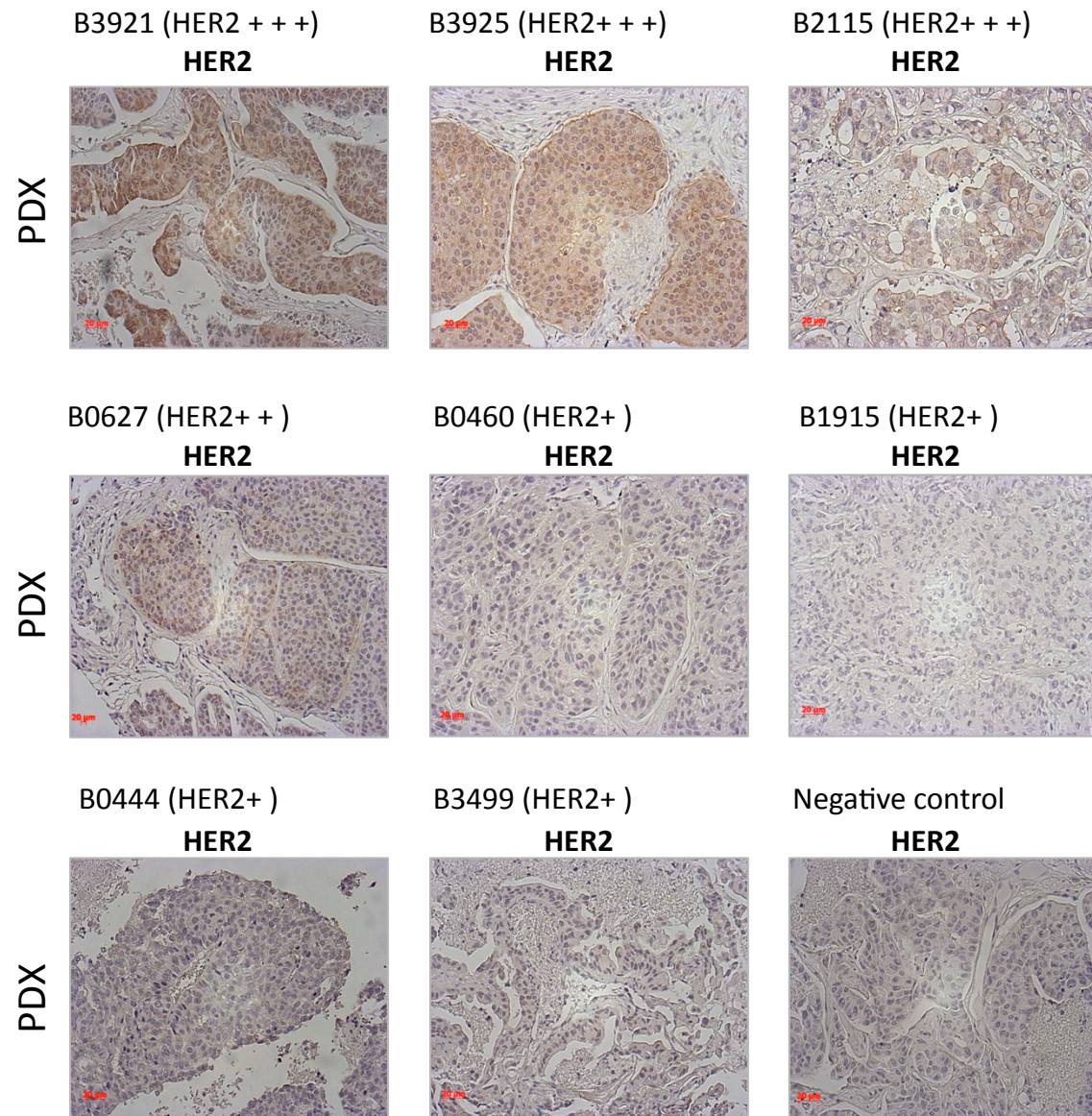
SupFig 2: Contamination by stromal tissue reduces the variation of the CNC profiles in primary tumors, artefactually leading to the conclusion that PDXs are more rearranged than tumors of origin.

A: Examples of CNC profiles of tumors showing different levels of contaminating human normal stroma. CNC profile of the tumor is compared to that of the PDX; B3034 presented 30% normal cells, B3977 10%. CNC profiles of the B3034 PDX is more accentuated than CNC profiles of the primary, while this is not the case for PDX B3977. After correction taking the dilution factor into account the profile of PDX B3034 is very similar to primary B3034.
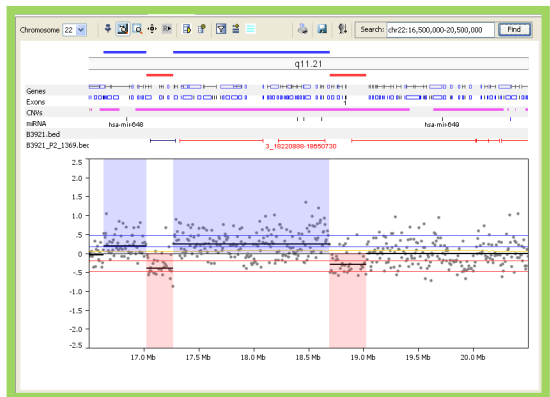
B: heatmaps showing differences between the profile of the primary and that of the cognate PDX before correction (blue : gain, red : loss) .

C: profiles as in B after correction

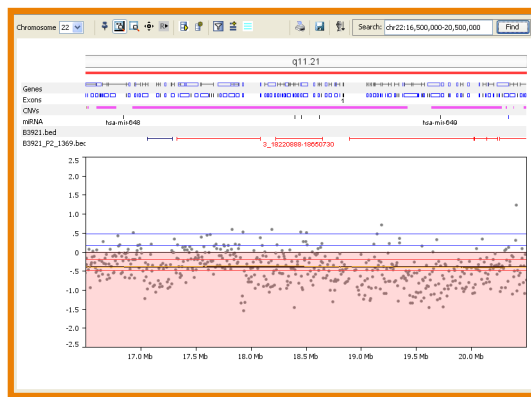NB: Stromal cells are of murine origin in PDX et do not hybridize on array due limited sequence homology.
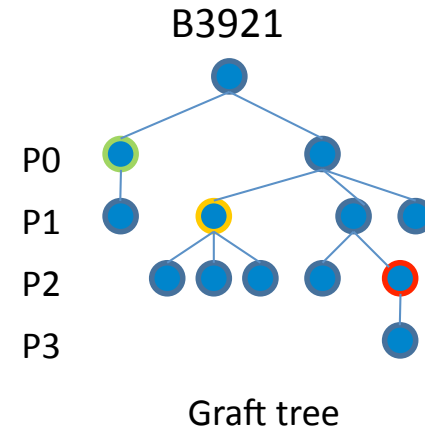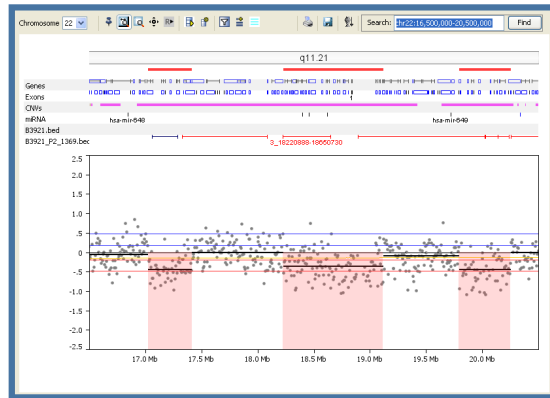
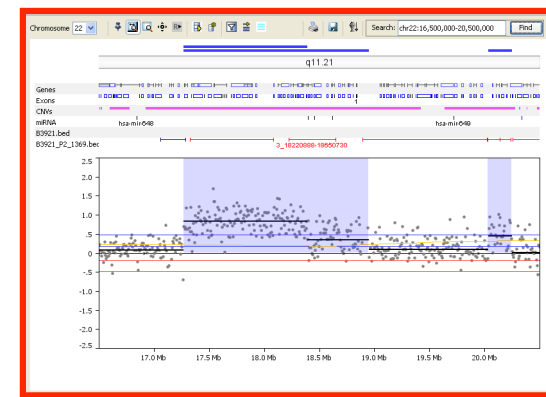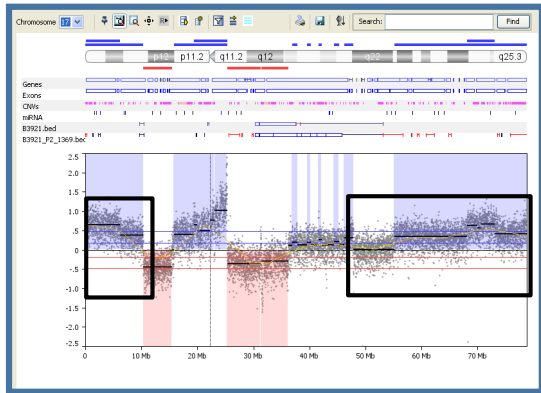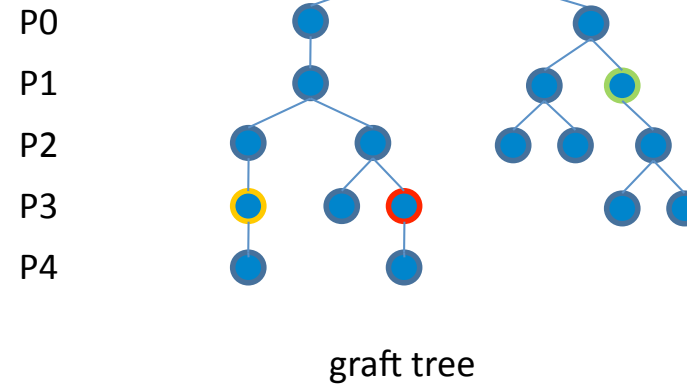SupFig 3A: fluctuating CNC profiles at specific loci in PDX from the same line at different passages. CNC profiles at 22q11 are presented in the patient sample and 3 PDXs from the same line corresponding to first graft (P0), passage 1 and 2 (P1, P2). The positions in the tree are presented by color circles. Highlighted sections indicate validated CNC (blue gain, red loss).
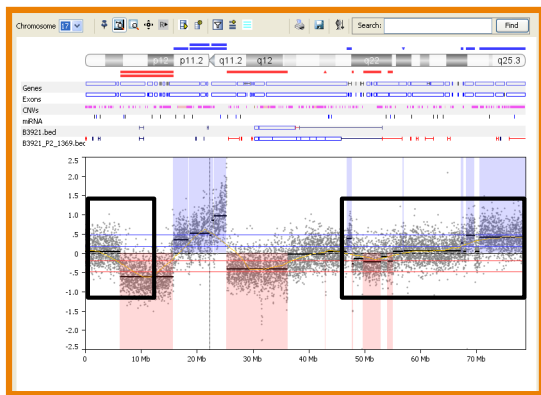
SupFig 3**B**: : fluctuating CNC profiles at specific loci in PDX from the same line at different passages. CNC profiles on chromome 17 are presented in the patient sample and 3 PDXs from the same line corresponding to passages 1 and 2 of different PDXs at passage 3 (P1, P3). The positions in the tree are presented by color circles. Highlighted sections indicate validated CNC (blue gain, red loss) and regions of important fluctuation are boxed.
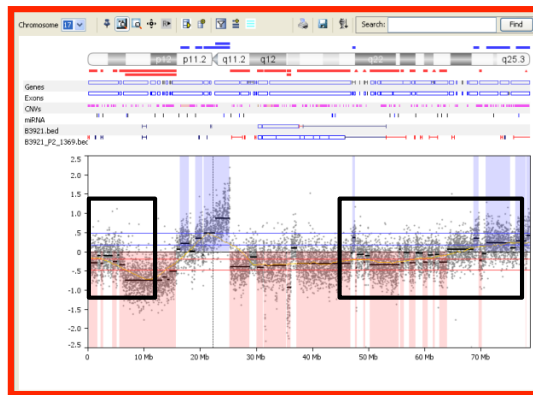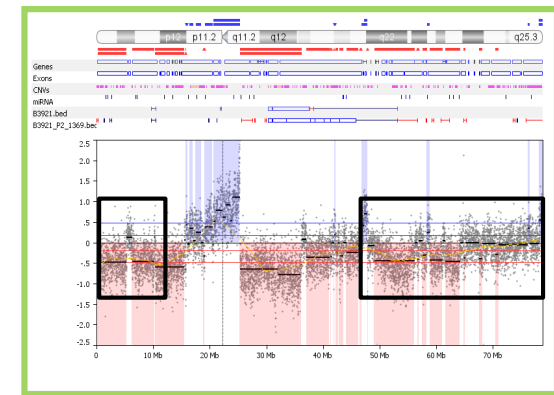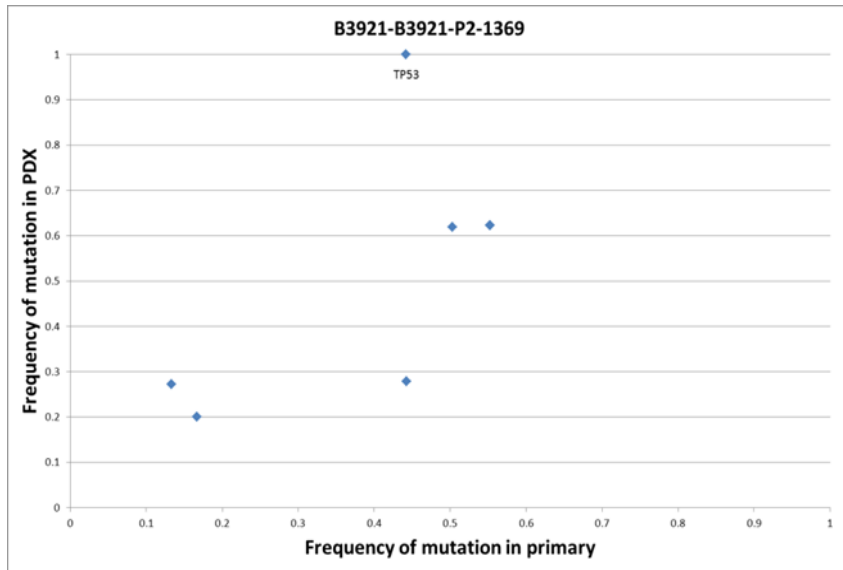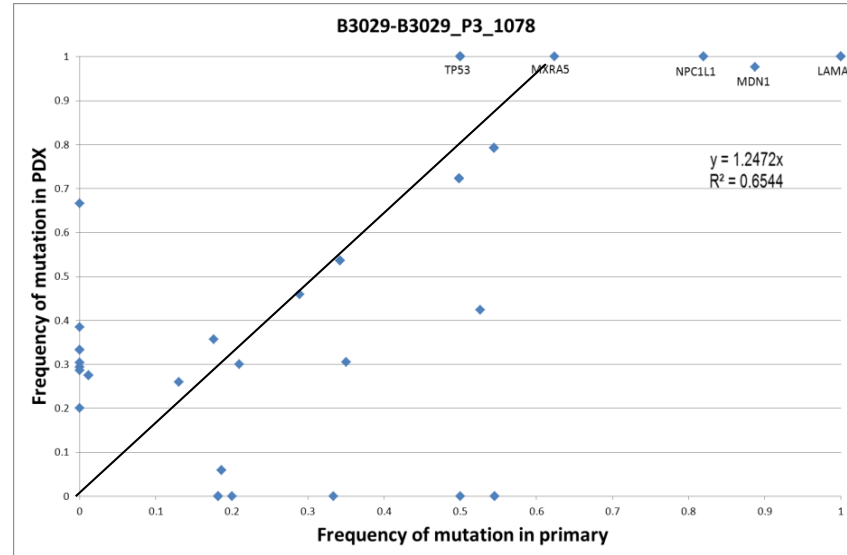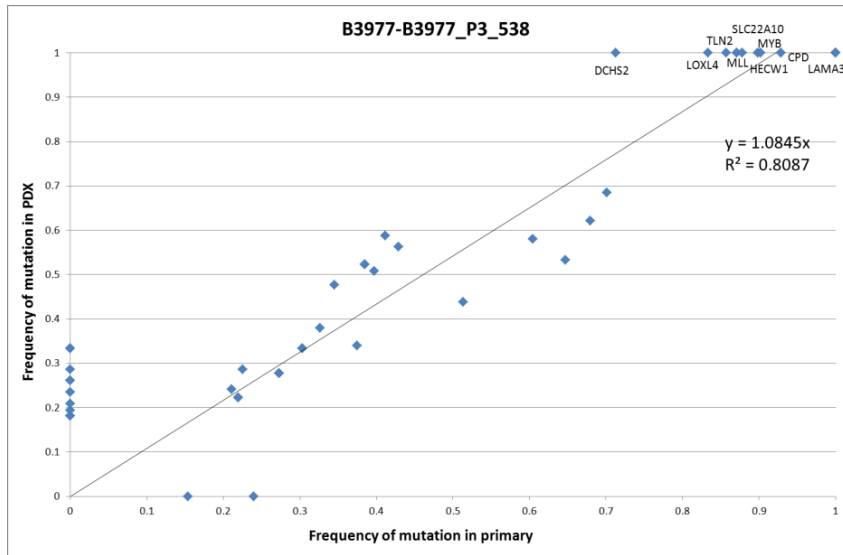
SupFig 4: Frequency of mutations in the primary tumor compared to that in the corresponding PDX

A: B3977 pair; B: B3029 pair; C: B3921 pair. In B3921 the limited number of mutations impairs the general trend of interpretation

For B3977 and B3029 the frequencies were commonly correlated for most of the mutations. Tumor specific or PDX specific events are present at low frequency. Analysis was restricted to genes found mutated in 2 previous Breast cancer TCGA studies. Only missense or non-sense mutations were considered. Regression was calculated excluding PDX or Tumor specific events. See materials et methods for details.
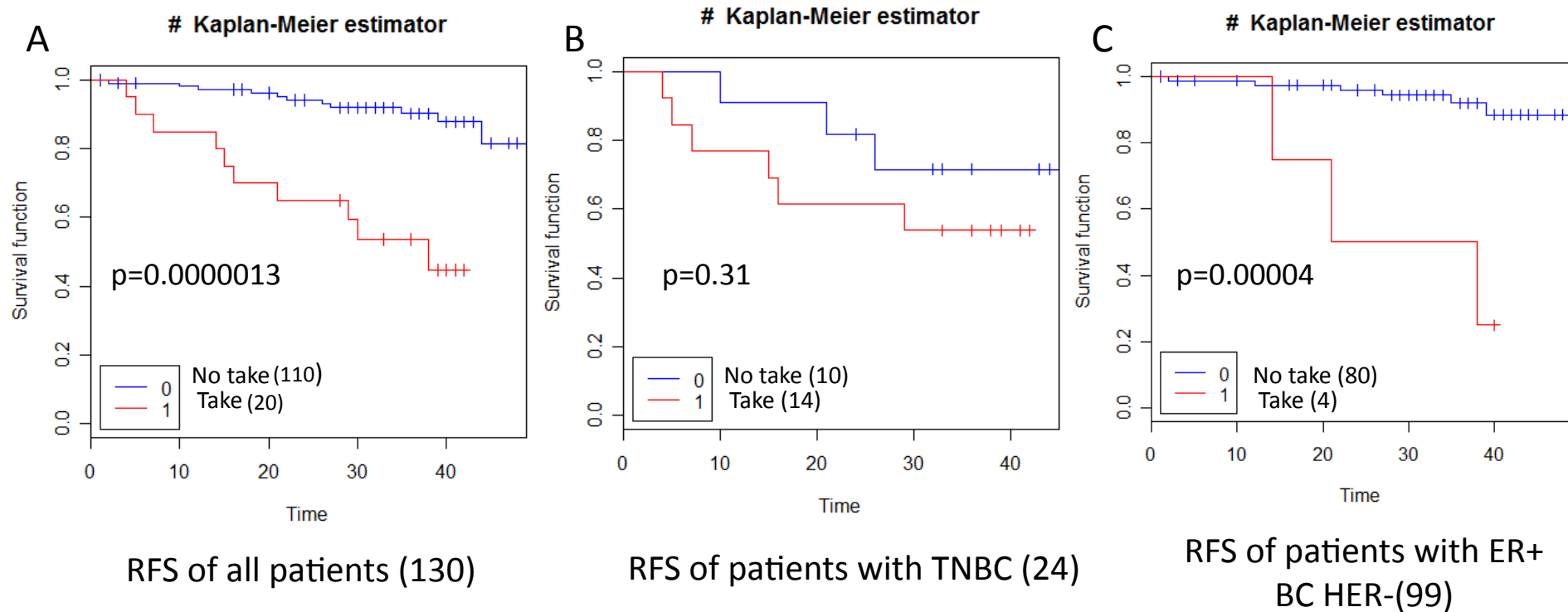
SupFig 5: Breast tumors that give rise to stable PDX are of adverse outcome. Recurrence Free Survival of patients whose breast tumor gave rise to a PDX (at least passage 3 : take) was compared to that of patients with tumors which did not graft successfully (no take). Patients in the take group presented shortened RFS in all settings (all patients, Triple Negative only, ER+ breast cancer), Median follow-up 33.5 to 35 months. Log-rank (cox-Mantel-Haenzel) test.

VEGF in human primary tumors (428 cases CIT cohort)
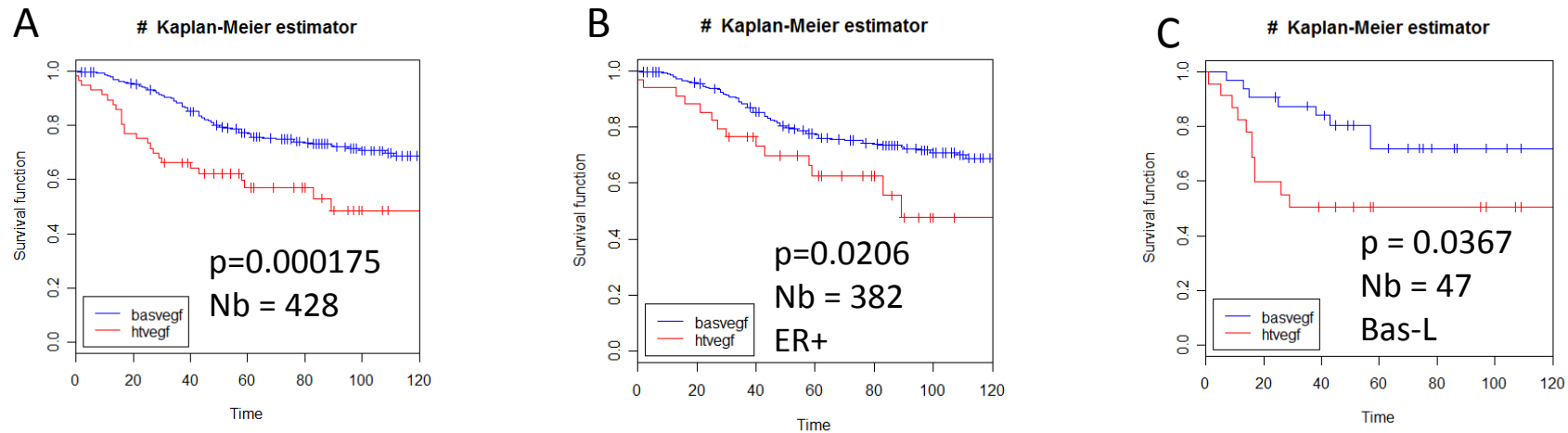
SupFig 6: increased VEGF RNA expression is of prognostic significance in an independent breast cancer set (CIT cohort). Kaplan-Meier curves comparing the metastatic free survival in patients with high (red) and low (blue) expressing primary breast tumors. A: whole dataset. B: ER+ tumors. C: Bas-L tumors. Log-rank (cox-Mantel-Haenzel) test.