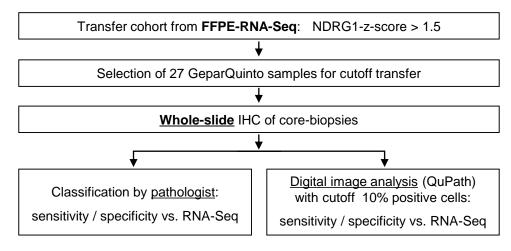
Part A: Marker selection

Gene cluster characterization in different cohorts (TNBC, ER negative, all subtypes) and platforms (Affymetrix, Agilent, Illumina, RNA-Seg, FFPE-RNA-Seg) Core sonsensus of six genes (VEGFA, NDRG1, ANGPTL4, ADM, DDIT4, CSTB) linked to hypoxia, angiogenesis, stress response Not in filtered GeparQuinto FFPE-RNA-Sea: ANGPTL4. ADM. DDIT4 Independent cohort of TNBC samples VEGFA, NDRG1, CSTB with Affymetrix microarray data Blinded IHC-scoring (26 samples) Correlation of IHC score and Affymetrix microarray data •Intra class correlation (ICC) of two observers Selection of **NDRG1**, R²=0.526, ICC=0.98 (95%CI 0.96-0.99)

Part B: IHC of core biopsy samples



Part C: Transfer to TMA format and validation of predictive value

