



Supplementary Figure S7: Poor detection of NDRG1 expression signal in TMA analysis

Scatterplot comparing NDRG1-RNA-Seq expression (x-axis) and IHC detection on TMA (y-axis) as percent positive cells from digital image analysis by QuPath. Horizontal and vertical lines represent 1.5 z-score cutoff values for RNA-Seq and TMA-IHC, respectively. In general, samples with high percentage of positive cell in the TMA analysis are associated with higher RNA-Seq values (Spearman rank correlation = 0.429). But for many samples with high RNA expression the signal was lost in TMA analysis. 23 of the samples, which were also analyzed by whole-slide IHC of core biopsies, are coloured in orange ($\geq 10\%$ positive cells) and green ($< 10\%$ positive cells) according to the whole-slide result. The majority of the positive samples from whole slide IHC (orange) did not reach the 10% value in the TMA analysis.