



Figure 4: Analysis of prognostic genes and in pre-Tx biopsies and post-Tx residual tumors.
(A-D) Comparison of genes relevant for prognosis in pre-Tx biopsies and post-Tx tumor resections. All 335 differentially regulated genes are displayed in a scatter plot according to their impact on disease free survival in either pre-Tx biopsies (x-axis) or post-Tx resections (y-axis). The inverse hazard ratio (1/HR) is shown, so that the quadrants are identical to main Figure 4A, with genes that are linked to improved survival, in both pre-Tx and post-Tx tumors, located in the upper right quadrant. In panels A and D, the genes are color coded according to both the main gene clusters 1-4 and the subclusters (1A-1D) from the gene clustering shown in Figure 3 (with more details in Suppl. Figure 5, Suppl. Figure 6, and Suppl. Figure 9). In panel B, genes are color coded only according to main gene clusters 1-4, while in panel C information from functionals pathways has been applied for color coding (complete details are given in the Supplementary Material).