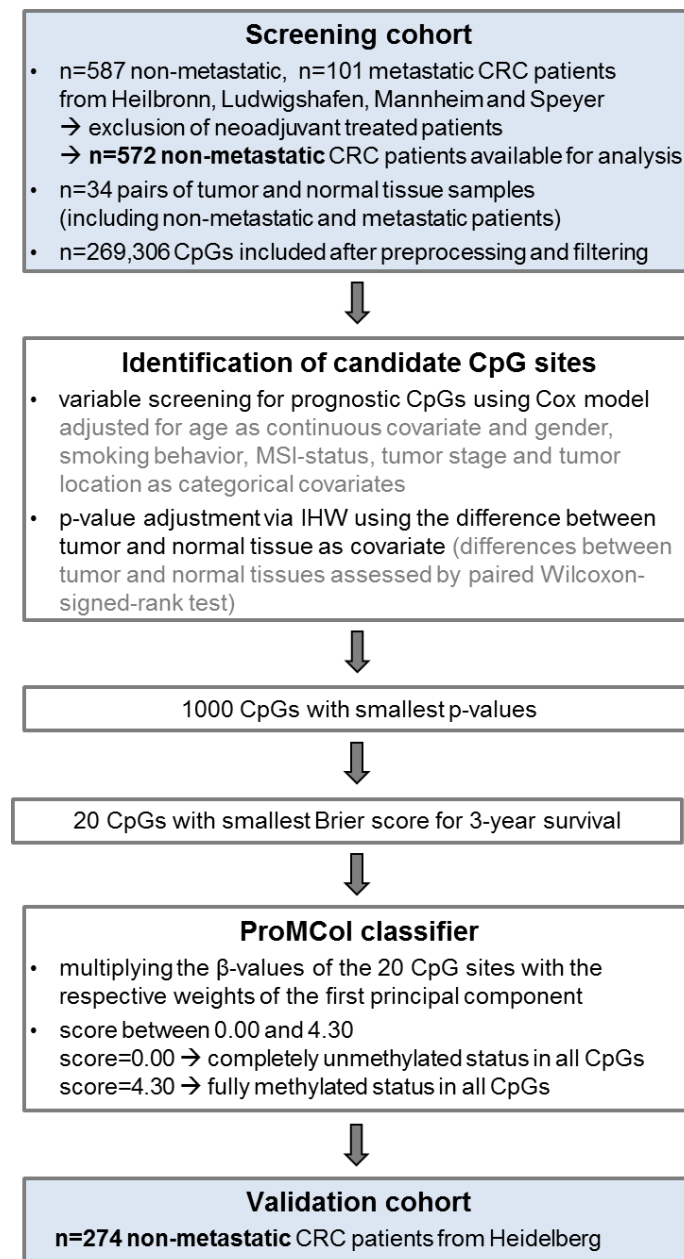
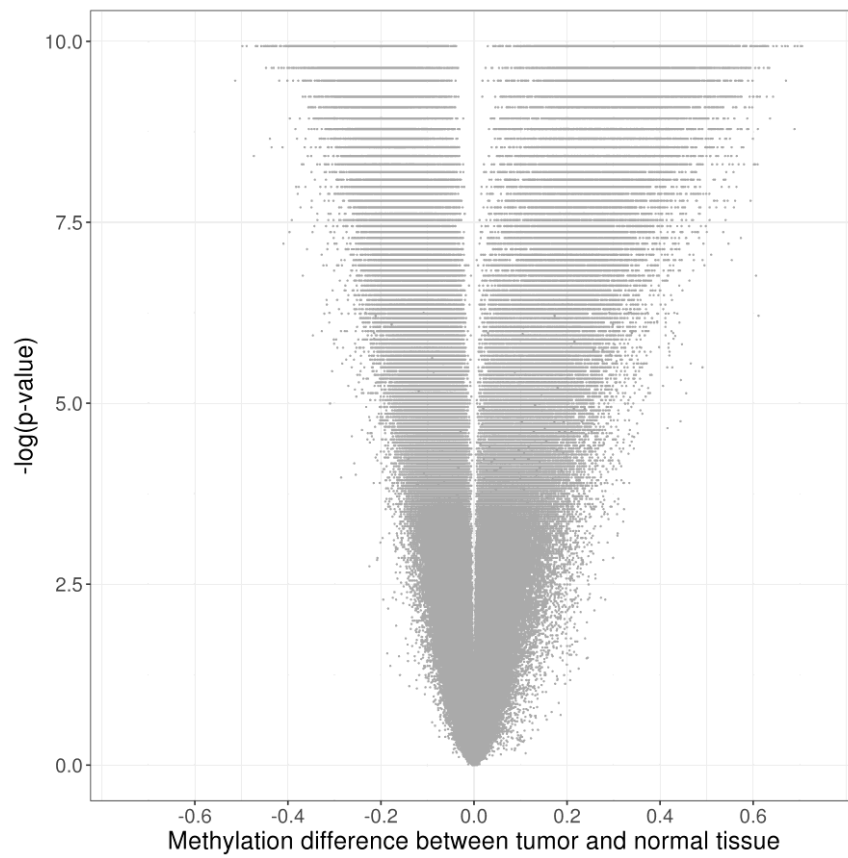


Supplementary Figure 1:



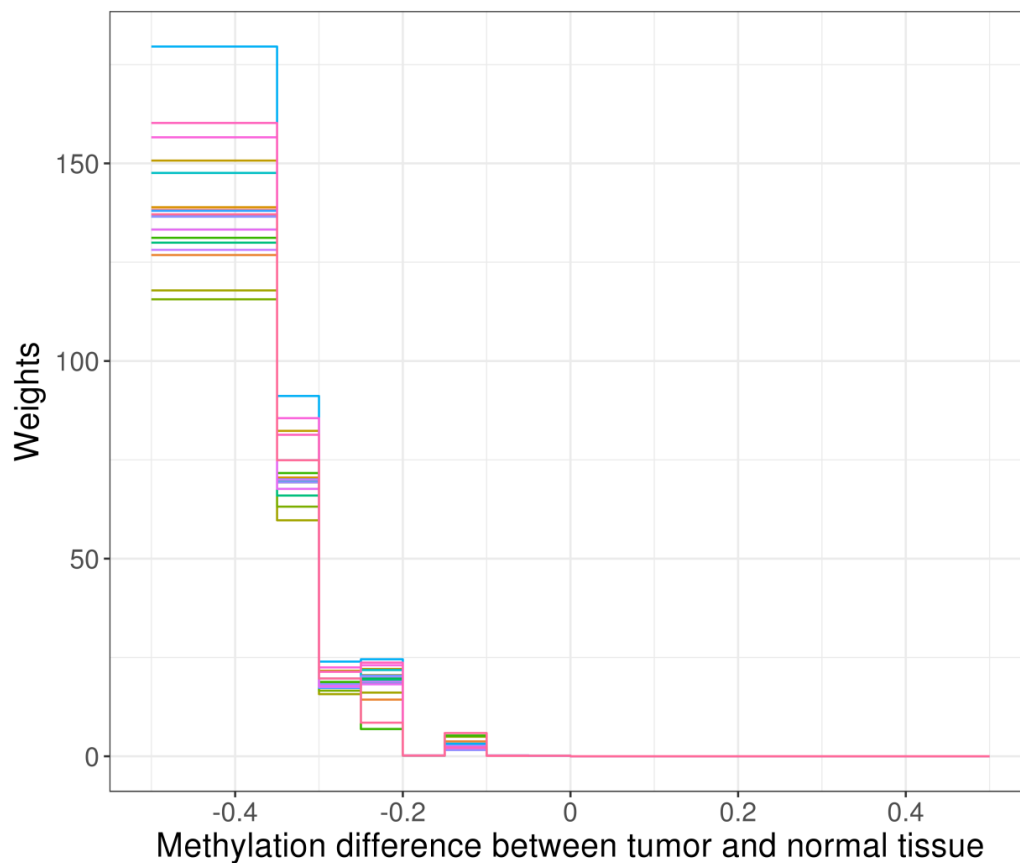
Supplementary Figure 1: Study design and analysis flowchart

Supplementary Figure 2:



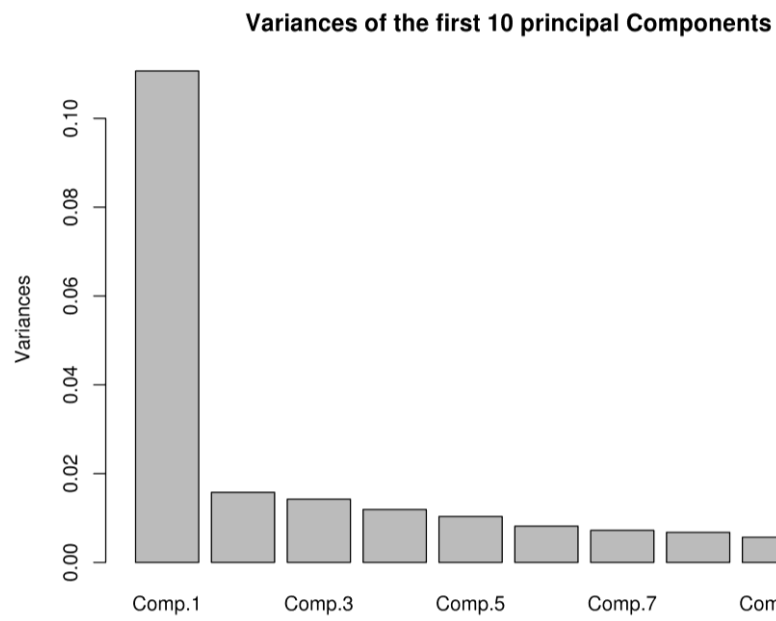
Supplementary Figure 2: Volcano plot showing differentially methylated CpG sites across the genome comparing 34 pairs of tumor and normal mucosa tissue. On the x-axis the β -value difference between tumor (TU) and normal tissue (NT) is shown and on the y-axis the corresponding $-\log(p\text{-value})$.

Supplementary Figure 3:



Supplementary Figure 3: Illustration of weighting in the IHW model. The left side of the plot, with β -value difference (x-axis) ranging between -0.5 and 0, represents the CpG sites with lower methylation in tumor than in normal mucosa tissue, the right side with β -value difference between 0 and 0.5, the CpG sites with higher methylation in tumor than in normal mucosa tissue. In all 20 folds, illustrated by the different colored lines, the highest weighting (y-axis) was given to CpG sites with clearly lower methylation levels in tumor than in normal mucosa tissue and no weight was given to CpG sites with higher methylation levels in tumor tissue.

Supplementary Figure 4:



Supplementary Figure 4: The depiction of the explained variance by the first 10 principal components of the 20 CpG sites included in our classifier shows that the usage of only the first component is sufficient for an appropriate presentation of their information value.