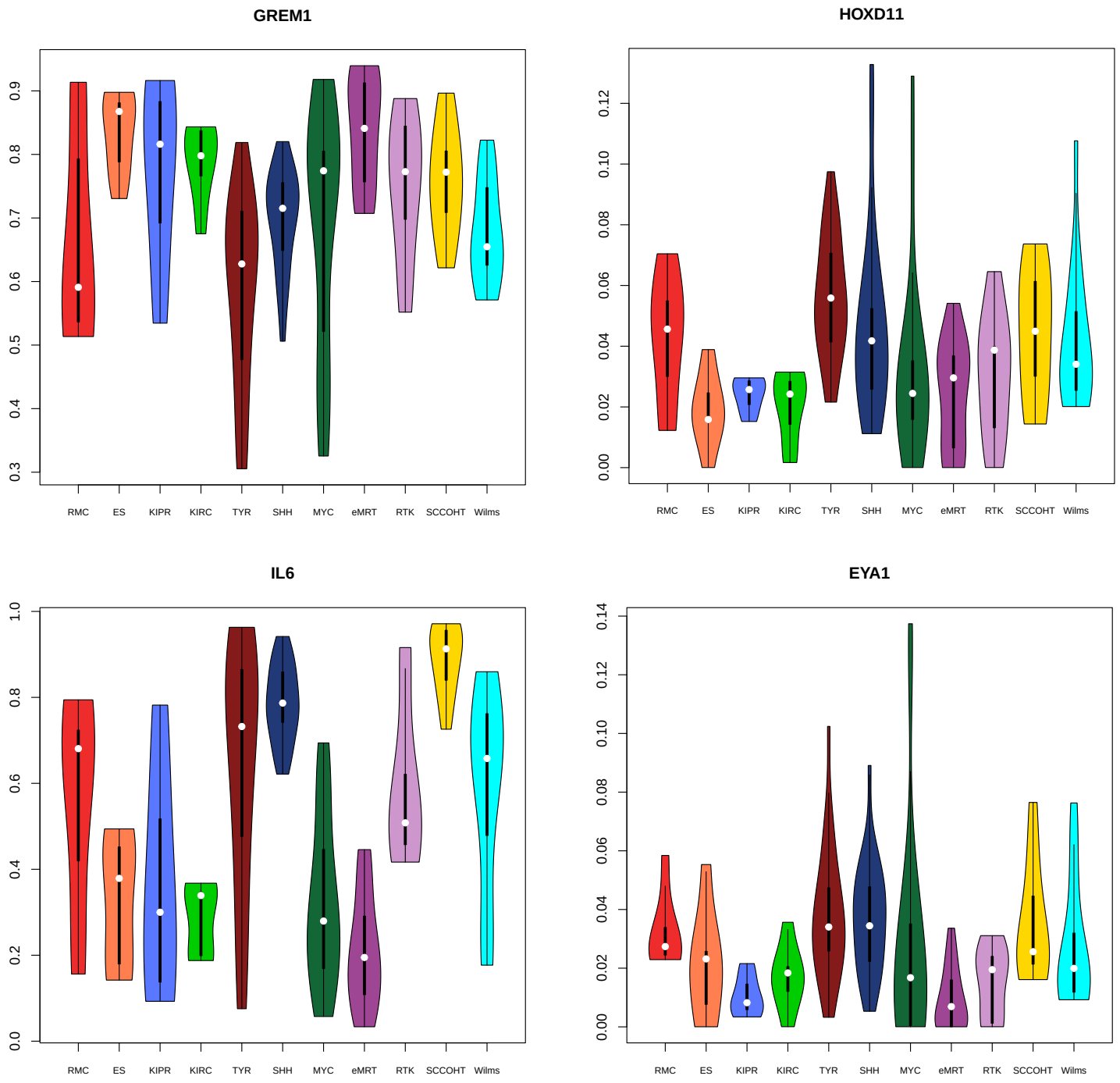

Supplementary Figure S5: Violin Plots displaying exemplary genes, that are significantly different methylated in RMCs compared to ES in the top row (GREM1 - ES mean = 0.833, RMC mean = 0.67, p = 0.0482; HOXD11 - ES mean = 0.0191, RMC mean = 0.0426, p = 0.029) and genes without significant differences in the bottom row (IL6 - ES mean = 0.325, RMC mean = 0.5597, p = 0.061; EYA1 - ES mean = 0.021, RMC mean = 0.0322, p = 0.21)