Figure 1: Gene expression for genes utilized by Prolaris, Oncotype and Decipher. *** denotes $p < 0.001$, ** $p < 0.01$, * $p < 0.05$. Log2 median FC is shown for those with a statistically significant difference in gene expression between EAM and AAM.
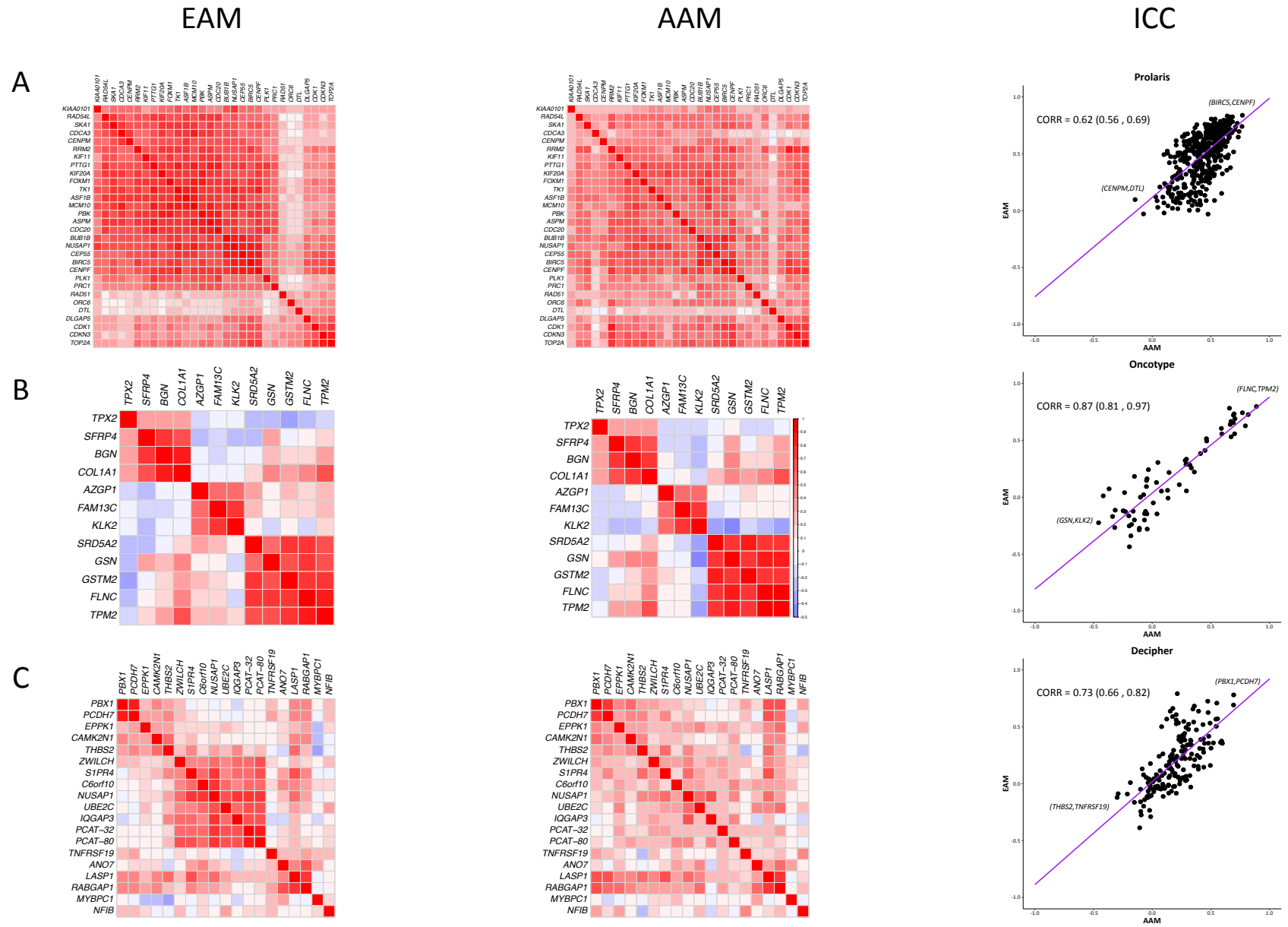
1

Figure 2: The panels are Prolaris (A), Oncotype Dx (B) and Decipher (C). Heatmap of inter-gene Spearman's correlations, EAM (left) and AAM (right), are shown in the first two columns. Correlation of CAPRA-S weighted correlations and 95% confidence intervals for genes in each panel are shown in the far right column. Gene pairs with the highest and lowest correlation in each panel are annotated.
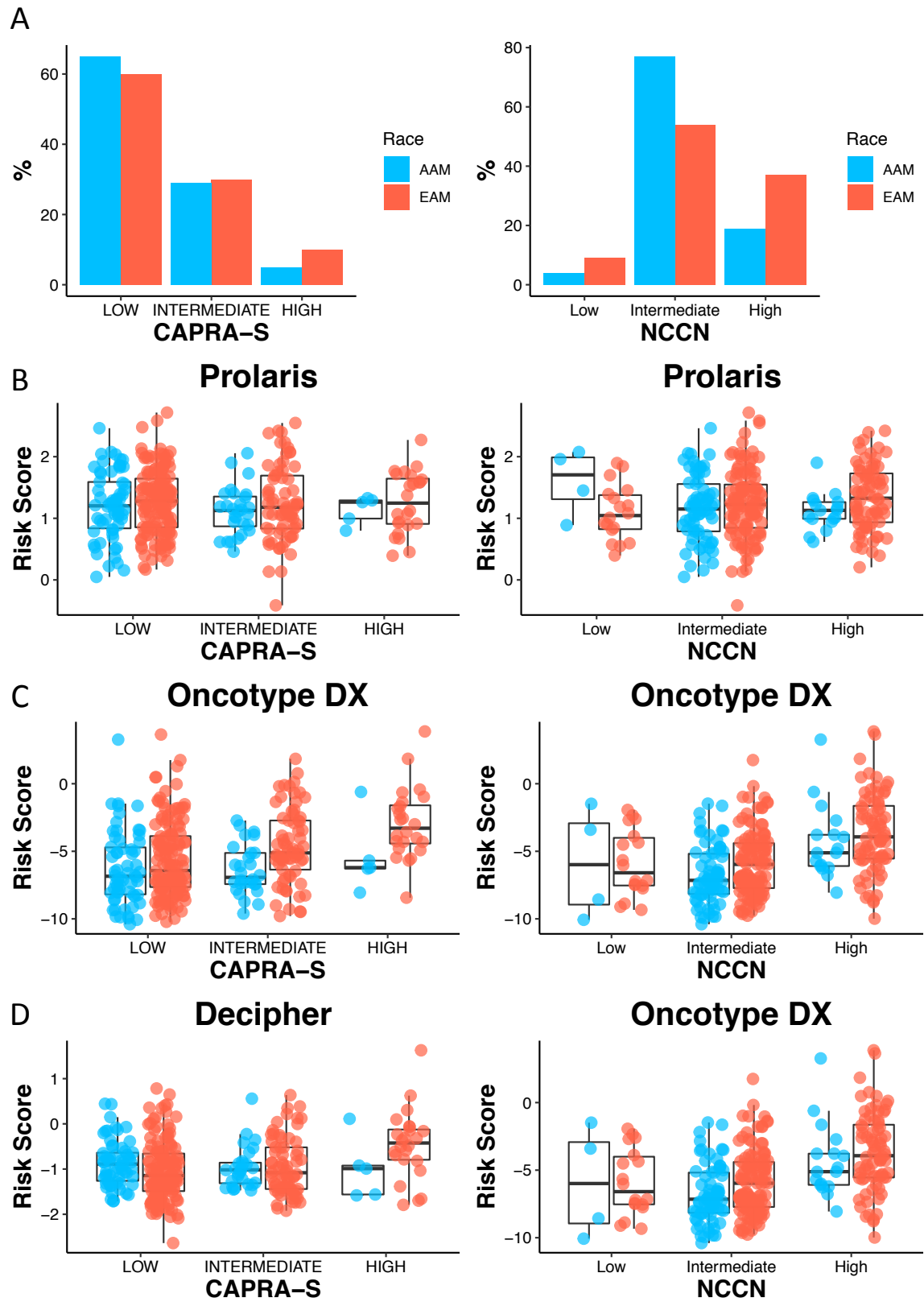
Figure 3: Percentage of EAM and AAM patients with low (0-2), intermediate (3-5), and high (6-12) CAPRA-S and with low, intermediate and high NCCN risk classification. Overall risk scores for Prolaris (B), Oncotype Dx (C) and Decipher (D) within CAPRA-S and NCCN groups.

A

EAM = 0.26 (0.14 , 0.38)
AAM = 0.17 (−0.02 , 0.37)

B

EAM = 0.66 (0.59 , 0.75)
AAM = 0.61 (0.50 , 0.76)

C
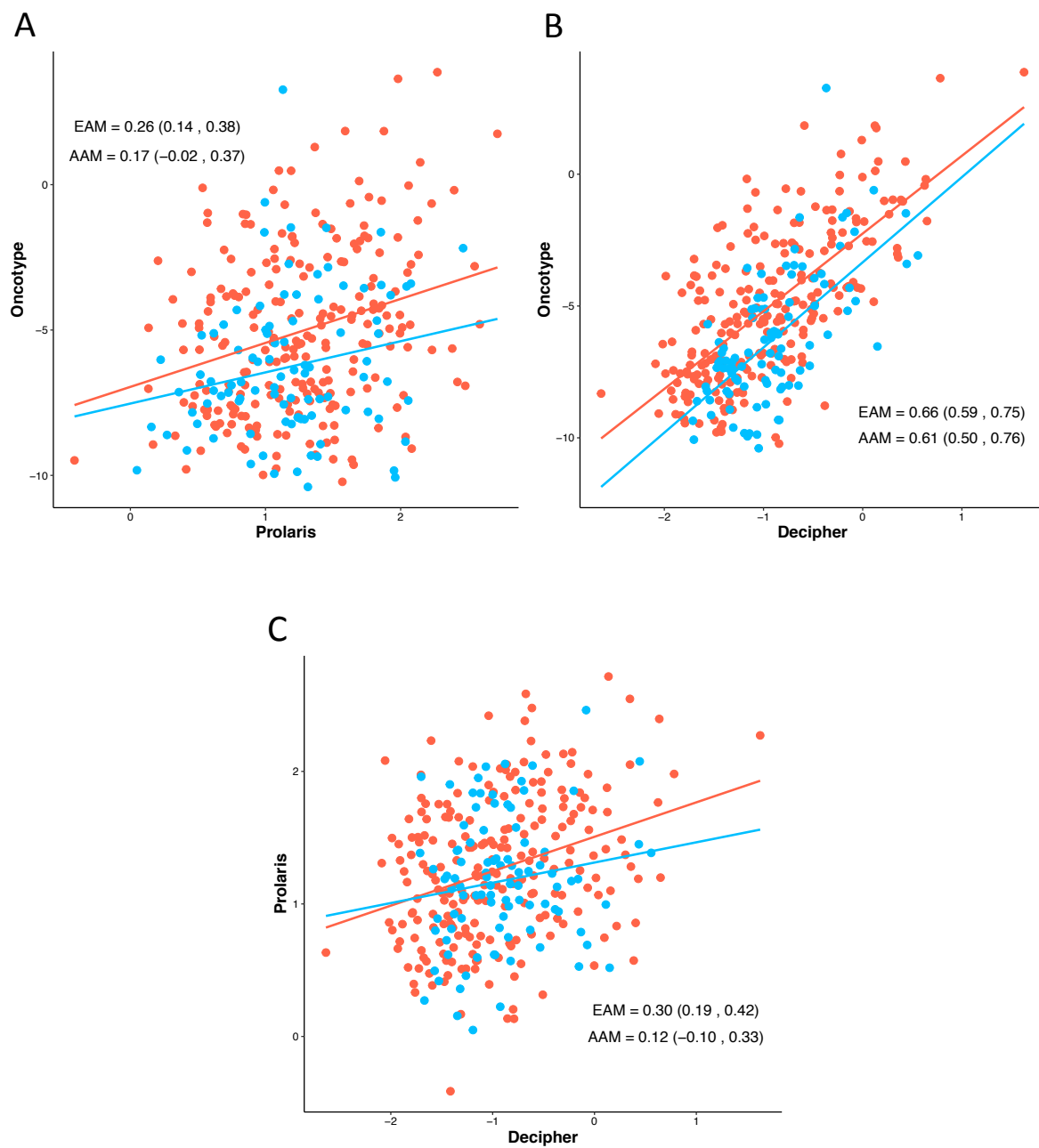
EAM = 0.30 (0.19 , 0.42)
AAM = 0.12 (−0.10 , 0.33)

Figure 4: Spearman's correlation and 95% confidence intervals of overall risk scores between each panel and within each race.