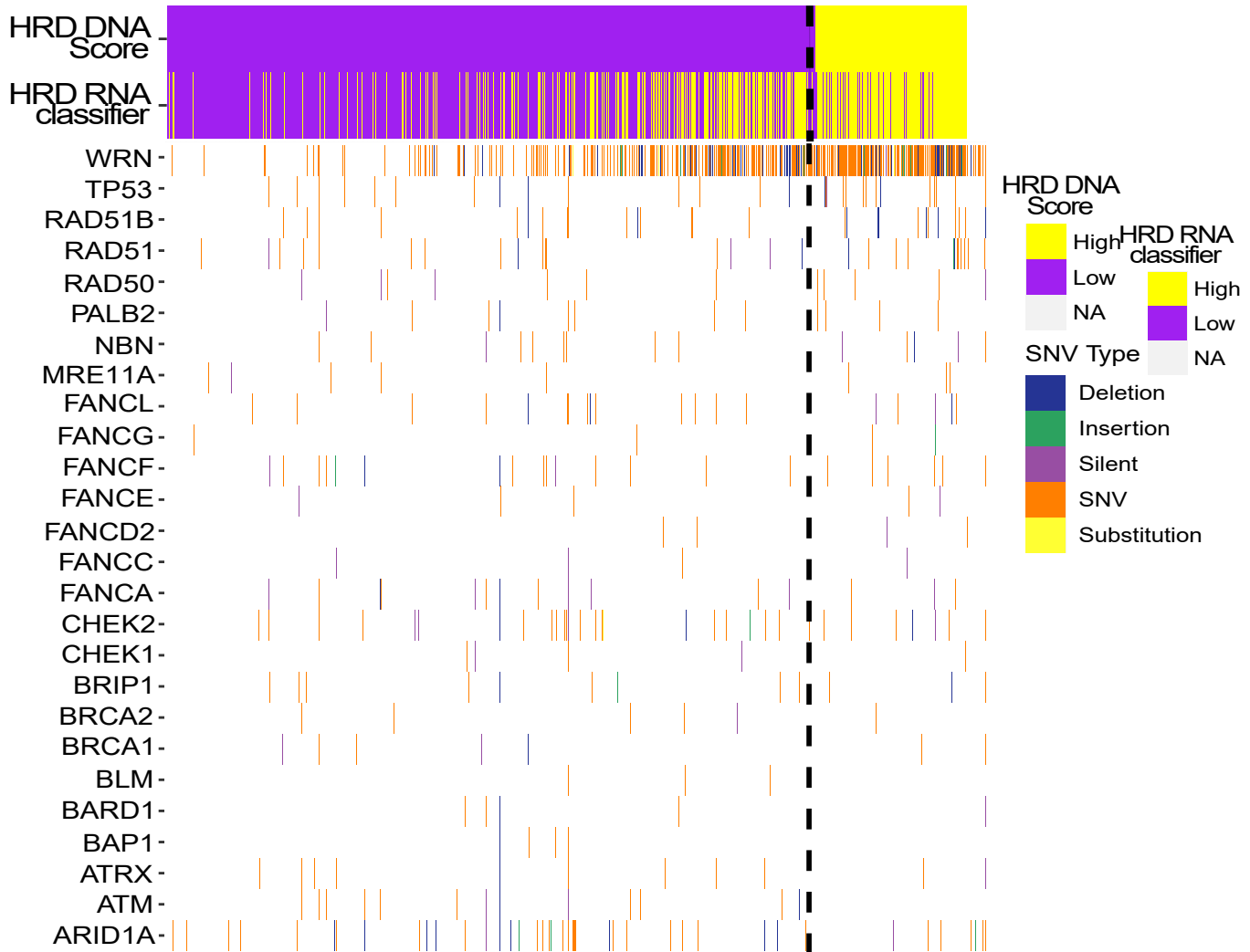


Supplemental Figure 1

A

Somatic Alteration	Areas Under the Curve			
	DNA Sorted		RNA Sorted	
	All Samples	HRD High Only	All Samples	HRD High Only
RAD51 Any	0.573	0.122	0.579	0.244
BRCA2 Any	0.591	0.134	0.591	0.247
BRCA1 Any	0.57	0.114	0.564	0.212
TP53 Any	0.59	0.13	0.593	0.258
RAD51 CNV	0.572	0.119	0.572	0.233
BRCA2 CNV	0.588	0.127	0.588	0.24
BRCA1 CNV	0.565	0.105	0.565	0.212
TP53 CNV	0.537	0.099	0.537	0.191
RAD51 Somatic	0.609	0.293	0.609	0.346
BRCA2 Somatic	0.671	0.275	0.671	0.367
BRCA1 Somatic	0.636	0.285	0.636	0.391
TP53 Somatic	0.732	0.215	0.732	0.396
RAD51 Germline	NA	NA	NA	NA
BRCA2 Germline	0.849	0.429	0.786	0.429
BRCA1 Germline	0.93	0.656	0.912	0.771
TP53 Germline	NA	NA	NA	NA

B



A) Table of AUC values of cumulative sum plots for all alterations, somatic and germline alterations for HRD DNA Score and HRD RNA Classifier. AUCs for both all samples and HRD-high samples only are shown.

B) Heatmap of somatic mutations in 26 HR associated genes, including TP53, RAD51, BRCA1, and BRCA2. Deletions, insertions, silent, SNV, and substitution mutations are shown with their corresponding colors.

Samples are sorted by HRD DNA score (above), and dashed line indicates cut-off for HRD high status. HRD RNA classifier calls are also labeled below.