

Figure S1. Mutational landscape of HRR genes in UC patients. (A) Comparison of HRR mutations between UTUC and UCB groups in the Chinese cohort. (B) The proportion of molecular subtypes according to HRR mutation status. (C) The proportion of HRR mutations in different molecular subtypes. (D) Landscape of frequently mutated HRR genes in different molecular subtypes.

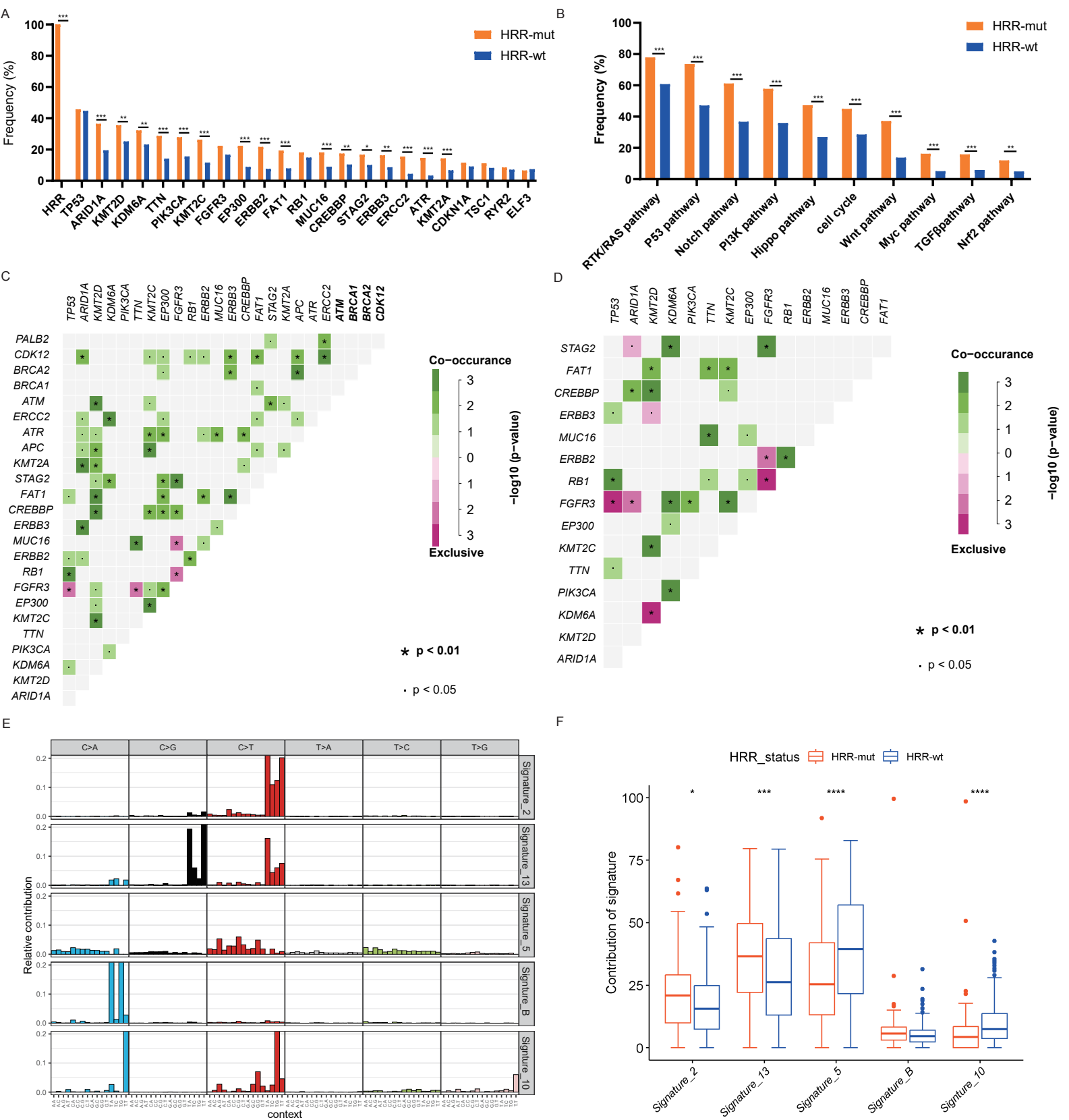
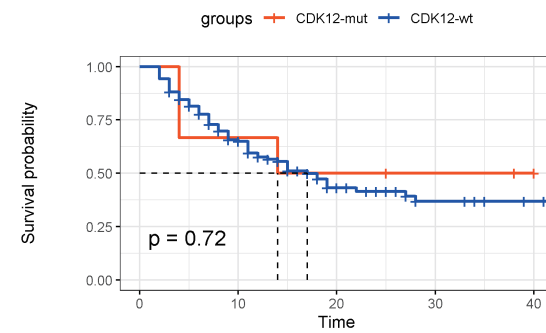
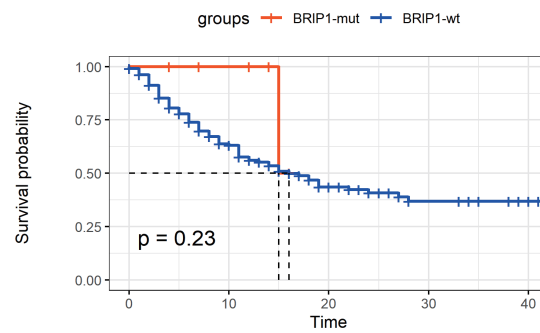
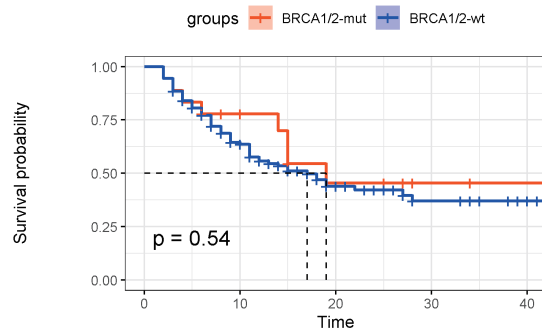
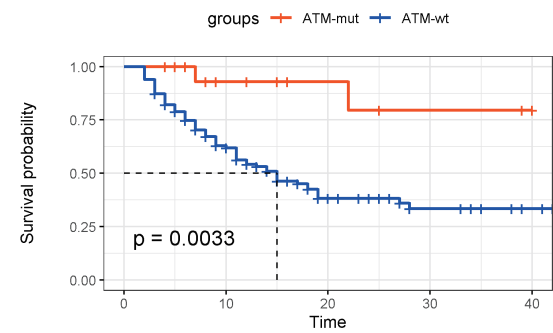


Figure S2. Mutational patterns of HRR genes in the TCGA cohort. (A) The frequency of the top 20 mutations in the HRR-mut and HRR-wt groups. (B) Comparison of oncogenic signaling pathways between the HRR-mut and HRR-wt groups. (C) Co-occurring and exclusive mutations in the HRR-mut group. (D) Co-occurring and exclusive mutations in the HRR-wt group. (E) Mutational signatures in the TCGA cohort. (F) Dominant mutational signatures between the HRR-mut and HRR-wt groups in the TCGA cohort.



Number at risk

ATM-mut	18	11	7	4	1
ATM-wt	164	70	26	11	4

Number at risk

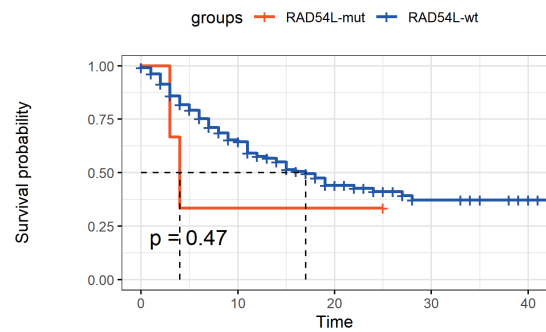
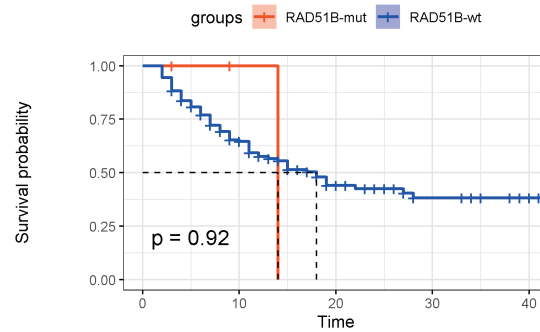
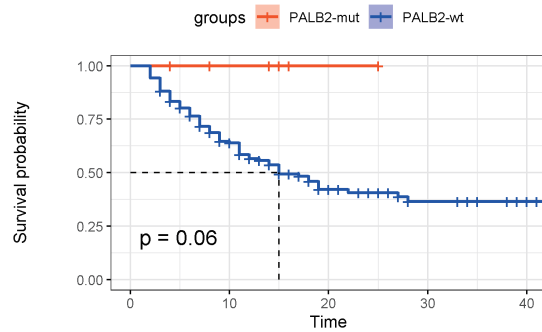
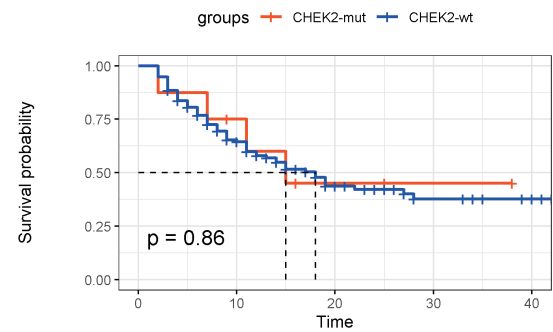
BRCA1/2-mut	18	11	5	2	1
BRCA1/2-wt	164	70	28	13	4

Number at risk

BRIP1-mut	6	4	0	0	0
BRIP1-wt	209	88	39	15	5

Number at risk

CDK12-mut	6	4	3	2	1
CDK12-wt	176	77	30	13	4



Number at risk

CHEK2-mut	8	5	2	1	0
CHEK2-wt	174	76	31	14	5

Number at risk

PALB2-mut	6	4	1	0	0
PALB2-wt	176	77	32	15	5

Number at risk

RAD51B-mut	3	1	0	0	0
RAD51B-wt	179	80	33	15	5

Number at risk

RAD54L-mut	3	1	1	0	0
RAD54L-wt	212	91	38	15	5

Figure S3. Survival outcomes of UC patients with and without specific HRR mutations after immunotherapy.

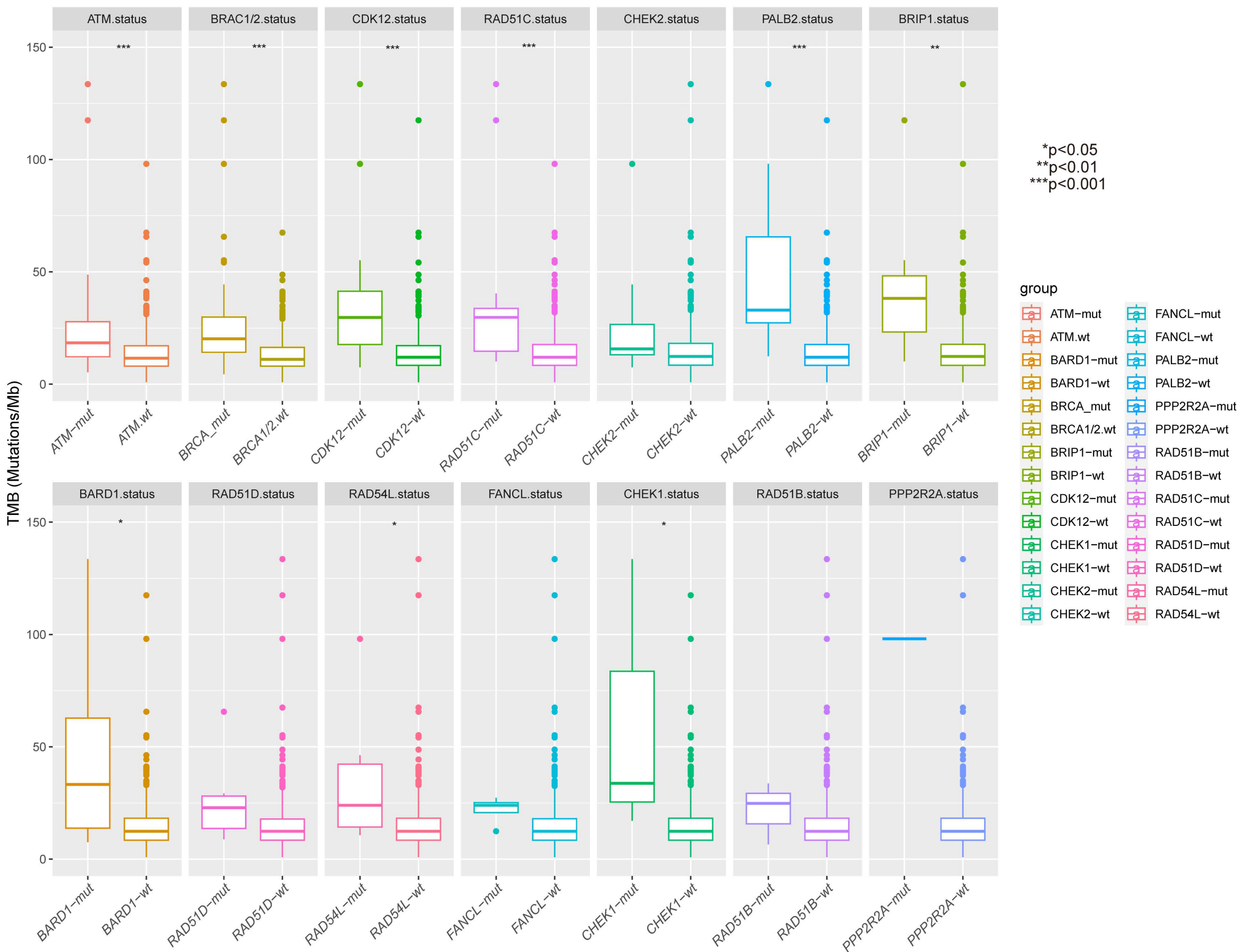


Figure S4. Relationship between specific HRR mutations and tumor mutational burden.

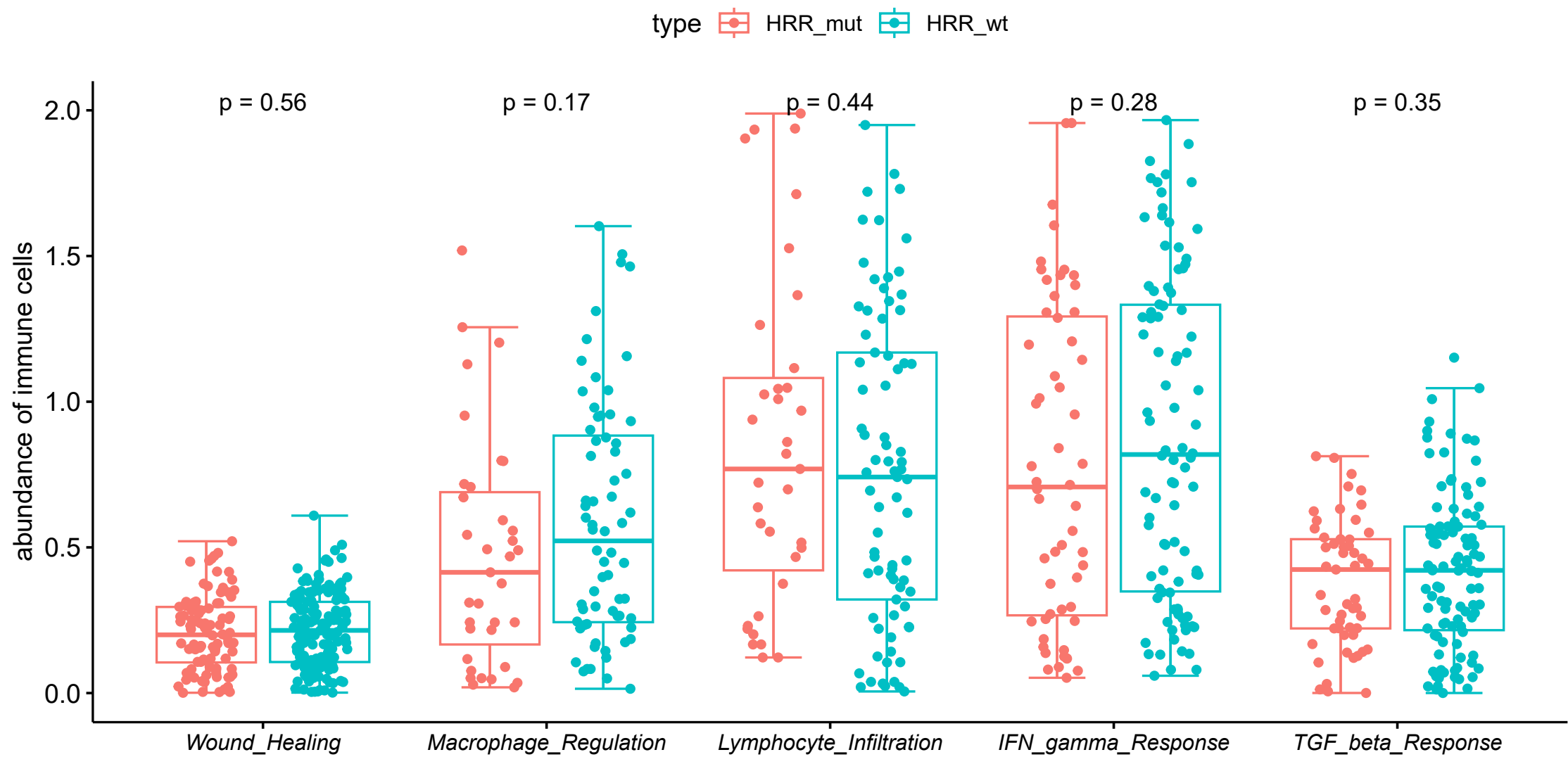


Figure S5. Comparison of expression levels of five intratumoral immune signatures between the HRR-mut and HRR-wt groups.

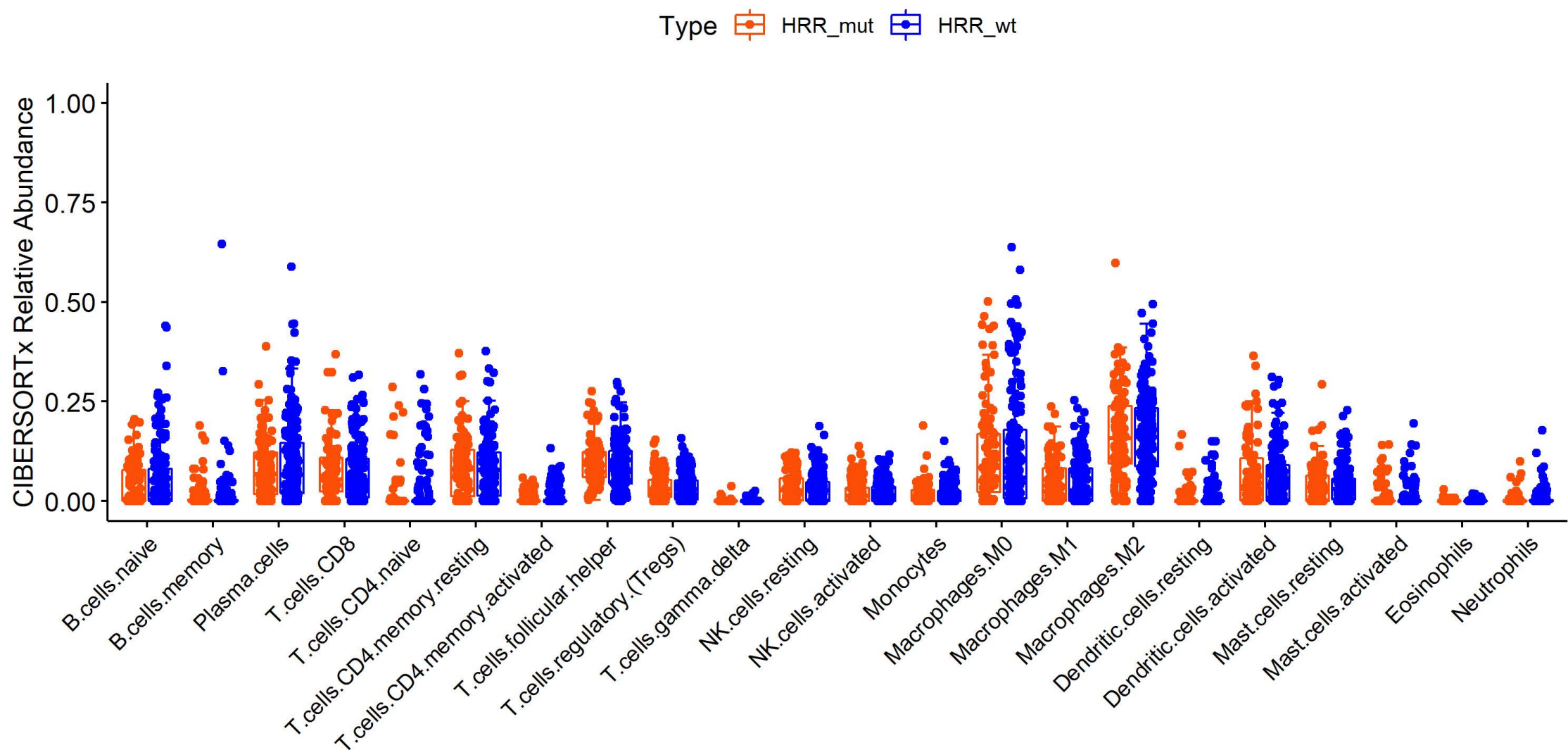


Figure S6. Association between immune cell abundance and HRR mutation status by CIBERSORT method.