

Figure S1 DFS of difference in different subgroups. (A) All patients with different HRD status; (B) Patients with different HRD status who received adjuvant therapy after surgery; (C) Patients with different HRD status who received adjuvant therapy with platinum after surgery; (D) Patients with different HRD status who not received adjuvant therapy after surgery. DFS, disease-free survival; HRD, homologous recombination defect.

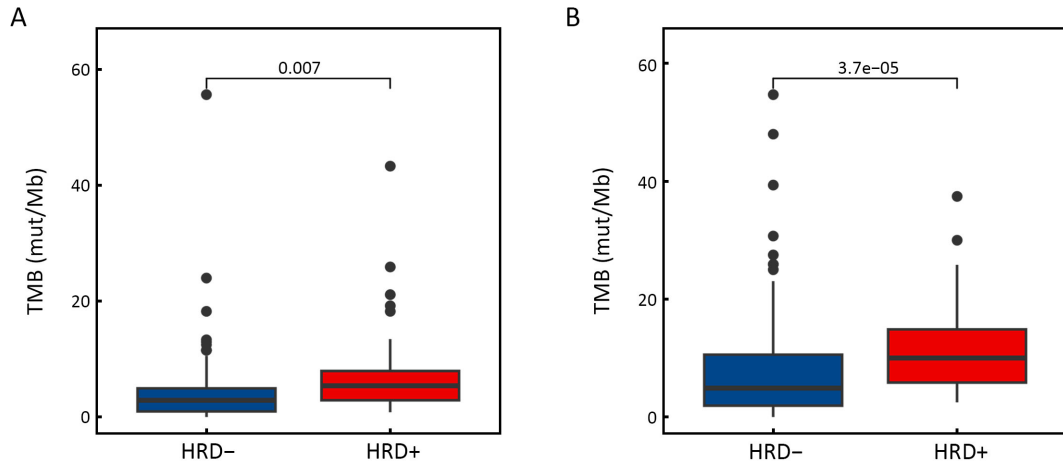


Figure S2 Difference of TMB values between HRD⁻ and HRD⁺ patients with mutant *EGFR* or *ALK* (A) or with wide-type *EGFR* or *ALK* (B). TMB, tumor mutation burden; HRD⁻, HRD-negative; HRD⁺, HRD-positive; HRD, homologous recombination defect; *EGFR*, epidermal growth factor receptor; *ALK*, anaplastic lymphoma kinase.

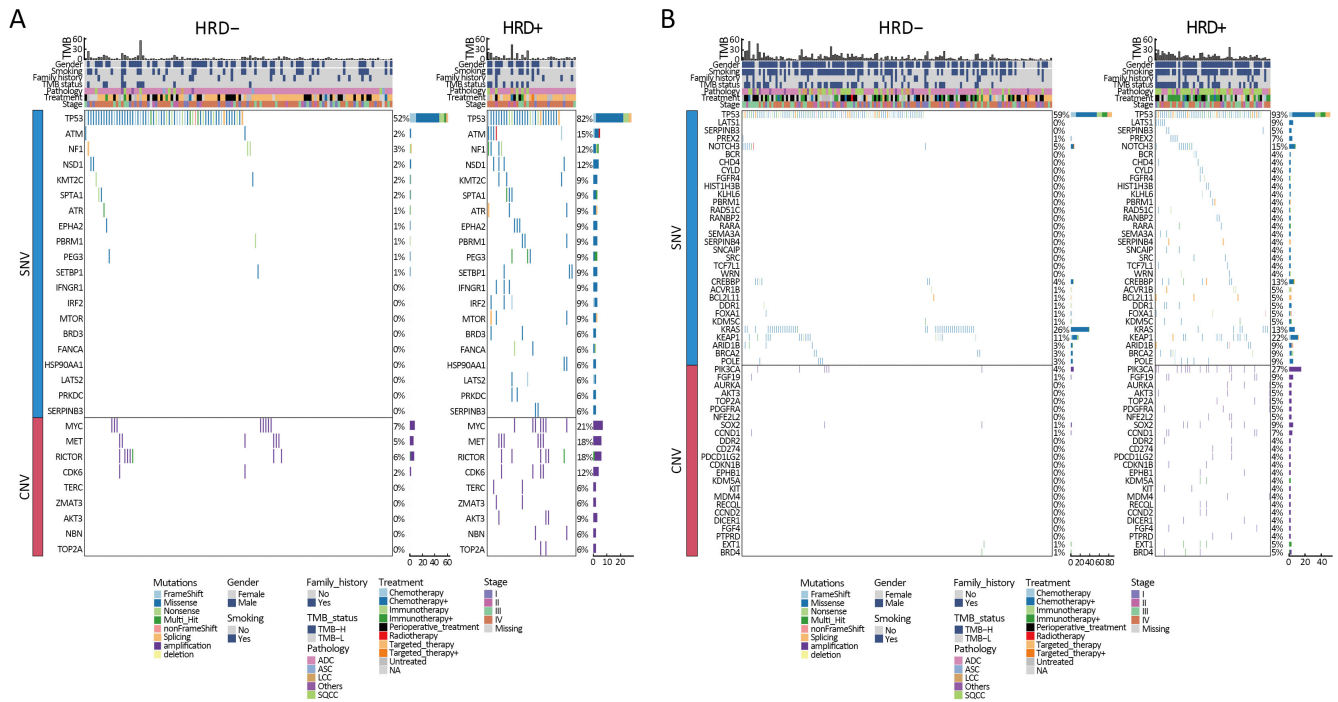


Figure S3 Genetic alterations with significant difference between HRD⁻ and HRD⁺ patients with mutant *EGFR* or *ALK* (A) or with wide-type *EGFR* or *ALK* (B). HRD⁻, HRD-negative; HRD⁺, HRD-positive; HRD, homologous recombination defect; SNV, single nucleotide variation; CNV, copy number variation; *EGFR*, epidermal growth factor receptor; *ALK*, anaplastic lymphoma kinase; TMB, tumor mutation burden.

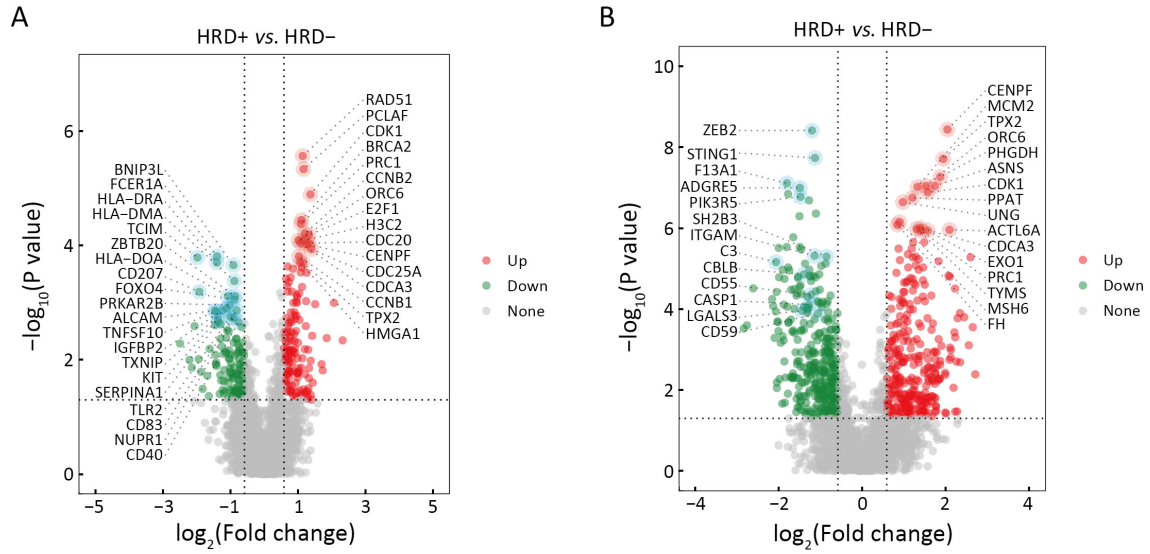


Figure S4 Differential genes volcano map between HRD+ and HRD- patients with mutant *EGFR* or *ALK* (A) or with wide-type *EGFR* or *ALK* (B). Red is HRD+ up-regulated gene, green is HRD+ down-regulated gene. HRD-, HRD-negative; HRD+, HRD-positive; HRD, homologous recombination defect; *EGFR*, epidermal growth factor receptor; *ALK*, anaplastic lymphoma kinase.

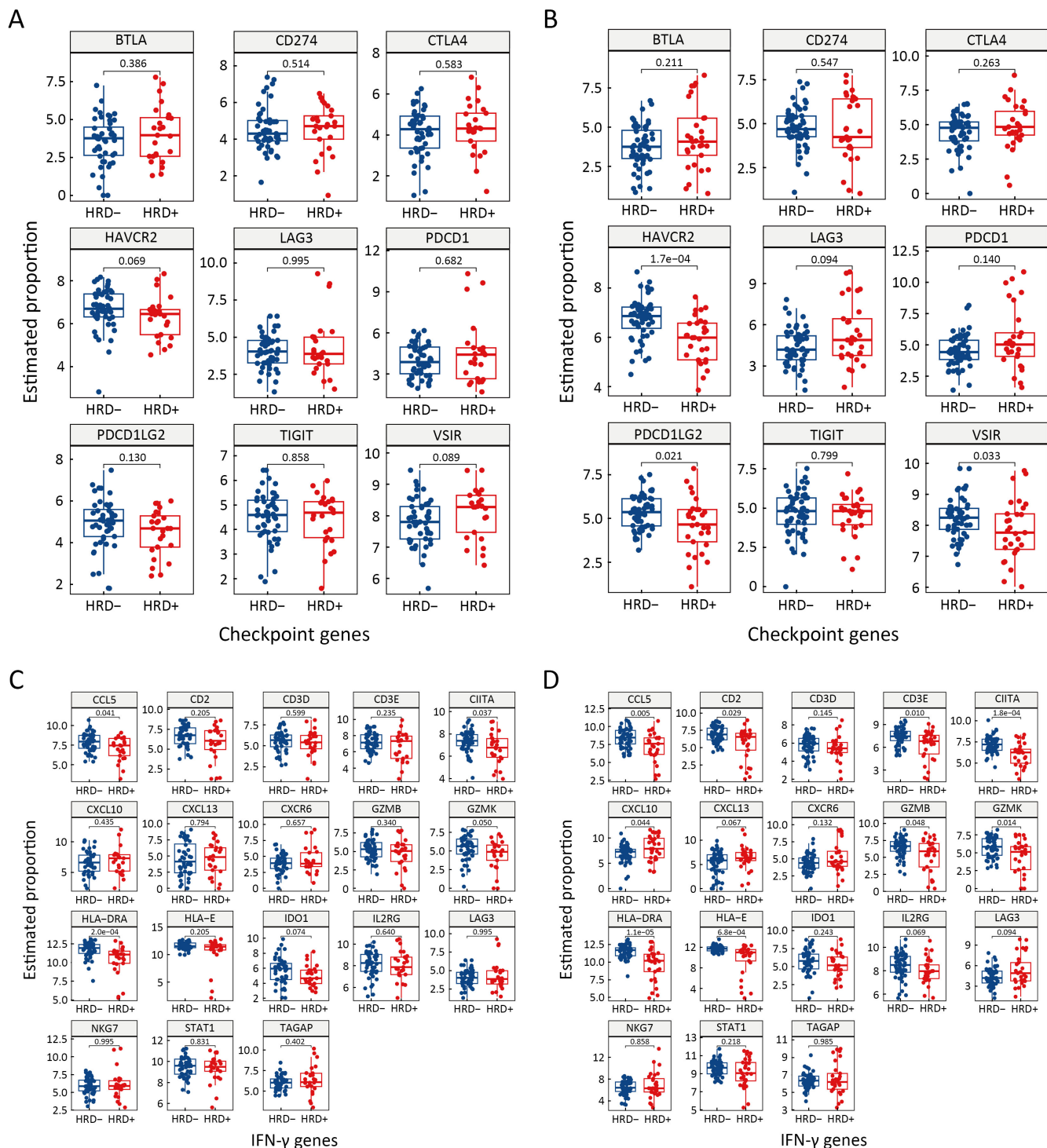


Figure S5 Expression difference of immune checkpoint and IFN- γ genes between HRD+ and HRD- patients with mutant *EGFR/ALK* or with wide-type *EGFR/ALK*. Immune checkpoint genes with mutant *EGFR/ALK* (A) or with wide-type *EGFR/ALK* (B); IFN- γ genes with mutant *EGFR/ALK* (C) or with wide-type *EGFR/ALK* (D). HRD-, HRD-negative; HRD+, HRD-positive; HRD, homologous recombination defect; IFN, interferon; *EGFR*, epidermal growth factor receptor; *ALK*, anaplastic lymphoma kinase.

Table S1 Statistics of HRR mutations loci

HRR	No.			
	Mutation	Somatic	Germline	Somatic+germline
<i>ATM</i>	22	16	4	2
<i>ATR</i>	19	16	3	0
<i>BARD1</i>	8	4	4	0
<i>BRCA1</i>	6	5	1	0
<i>BRCA2</i>	21	15	6	0
<i>BRIP1</i>	10	10	0	0
<i>CDK12</i>	10	4	6	0
<i>CHEK1</i>	8	7	1	0
<i>CHEK2</i>	9	7	2	0
<i>FANCA</i>	23	12	11	0
<i>FANCL</i>	5	3	2	0
<i>NBN</i>	9	5	4	0
<i>PALB2</i>	6	4	2	0
<i>MRE11A</i>	3	3	0	0
<i>RAD51B</i>	1	0	1	0
<i>RAD51C</i>	4	3	1	0
<i>RAD51D</i>	1	0	1	0
<i>RAD54L</i>	5	1	4	0
Total	170	115	53	2

HRR, homologous recombination repair.

Table S2 HRR mutation status between HRD-positive and -negative

Mutation type	n (%)		P
	HRD-positive (n=89)	HRD-negative (n=266)	
HR gene pathogenic mutation			0.007
Yes	14 (15.7)	17 (6.4)	
No	75 (84.3)	249 (93.6)	
Germline HR gene mutations			0.632
Yes	1 (1.1)	5 (1.9)	
No	88 (98.9)	261 (98.1)	
Somatic HR gene mutations			0.001
Yes	13 (14.6)	12 (4.5)	
No	76 (85.4)	254 (95.5)	

HRR, homologous recombination repair; HRD, homologous recombination deficiency.

Table S3 Patient statistics of HRR pathogenic mutations

HRR	No.		
	Pathogenic	Somatic	Germline
<i>ATM</i>	7	5	2
<i>ATR</i>	3	3	0
<i>BARD1</i>	2	1	1
<i>BRCA1</i>	2	2	0
<i>BRCA2</i>	7	6	1
<i>BRIP1</i>	1	1	0
<i>CDK12</i>	1	1	0
<i>CHEK1</i>	2	2	0
<i>CHEK2</i>	2	2	0
<i>FANCA</i>	4	3	1
<i>FANCL</i>	0	0	0
<i>NBN</i>	0	0	0
<i>PALB2</i>	0	0	0
<i>MRE11A</i>	0	0	0
<i>RAD51B</i>	0	0	0
<i>RAD51C</i>	1	1	0
<i>RAD51D</i>	1	0	1
<i>RAD54L</i>	1	1	0
Total	34-3=31 [†]	28	6

[†], There are three co-mutations between patients. HRR, homologous recombination repair.