Figure S1. Per-sample non-synonymous mutation rate for (A) HIM and (B) LIM samples. The horizontal red broken line indicate the median non-synonym mutation burden of HIM or LIM samples. HIM, high immune score; LIM, low immune score; Ins, insertion; Del, deletion.

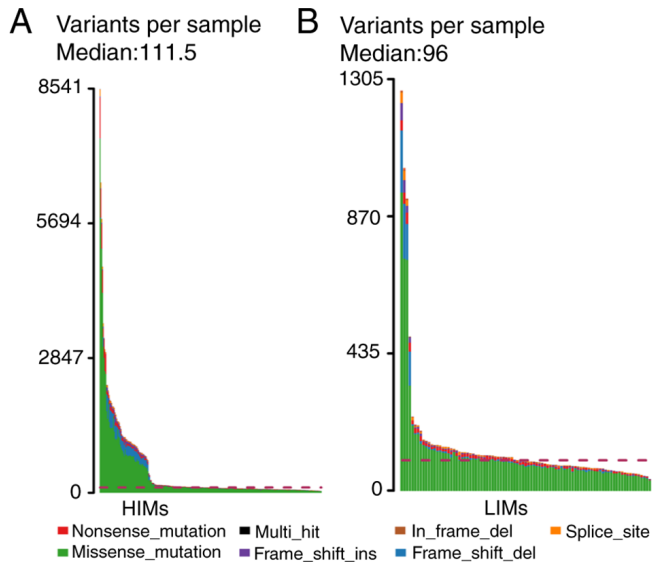

Figure S2. Gene Ontology term analysis for 283 differentially expressed genes.

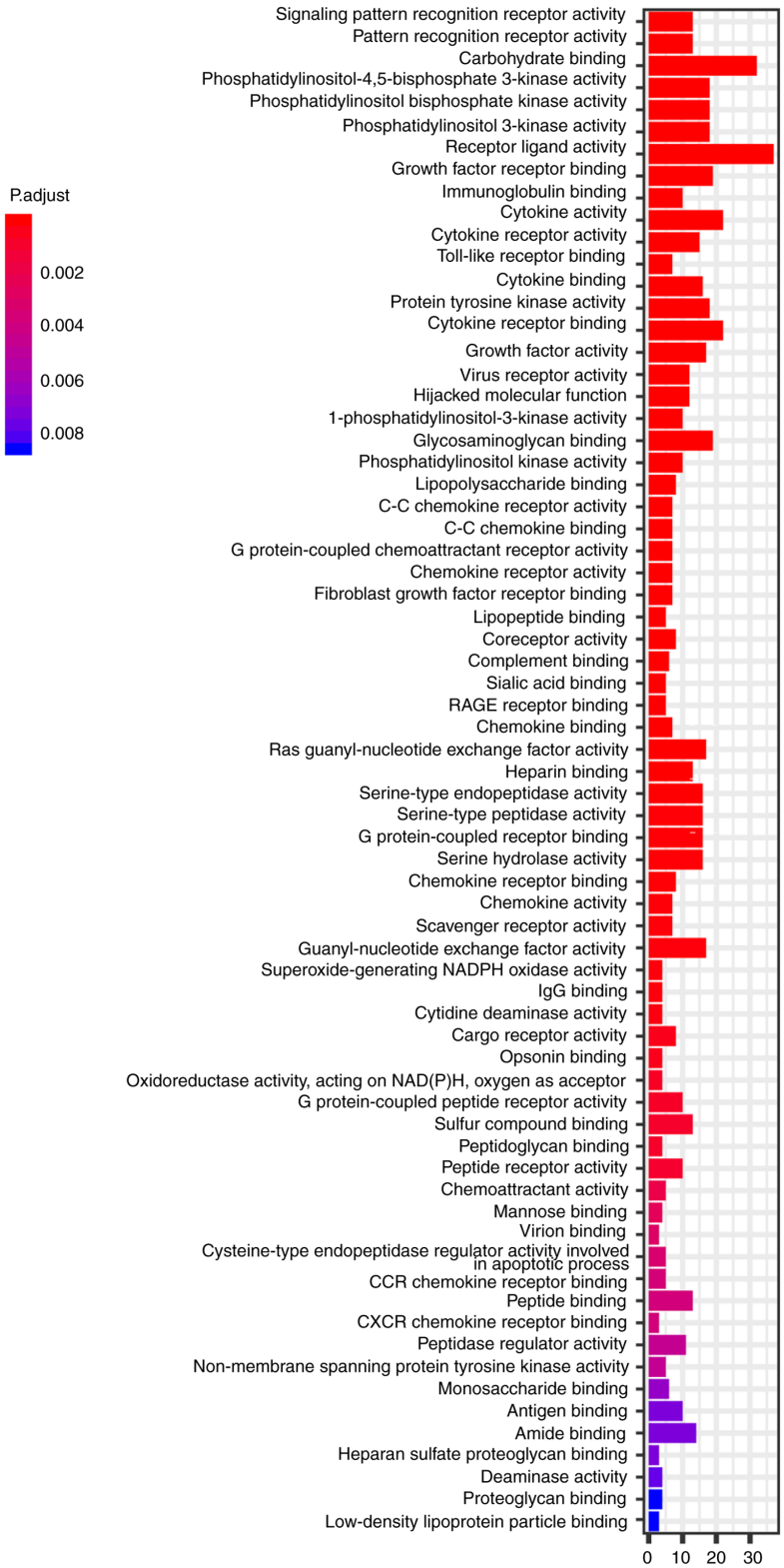

Figure S3. Kaplan-Meier plots with log-rank tests indicated that the 11 differentially expressed genes were significantly associated with survival. C5AR1, complement C5a receptor 1; FCGR1A, Fc fragment of IgG receptor Ia; LEP, leptin; LGALS2, galectin 2; NCF2, neutrophil cytosolic factor 2; NFATC1, nuclear factor of activated T cells 1; NLRP1, NLR family pyrin domain containing 1; PLCG2, phospholipase C gamma 2; SELE, selectin E; SLAMF9, SLAM family member 9; SPHK1, sphingosine kinase 1.

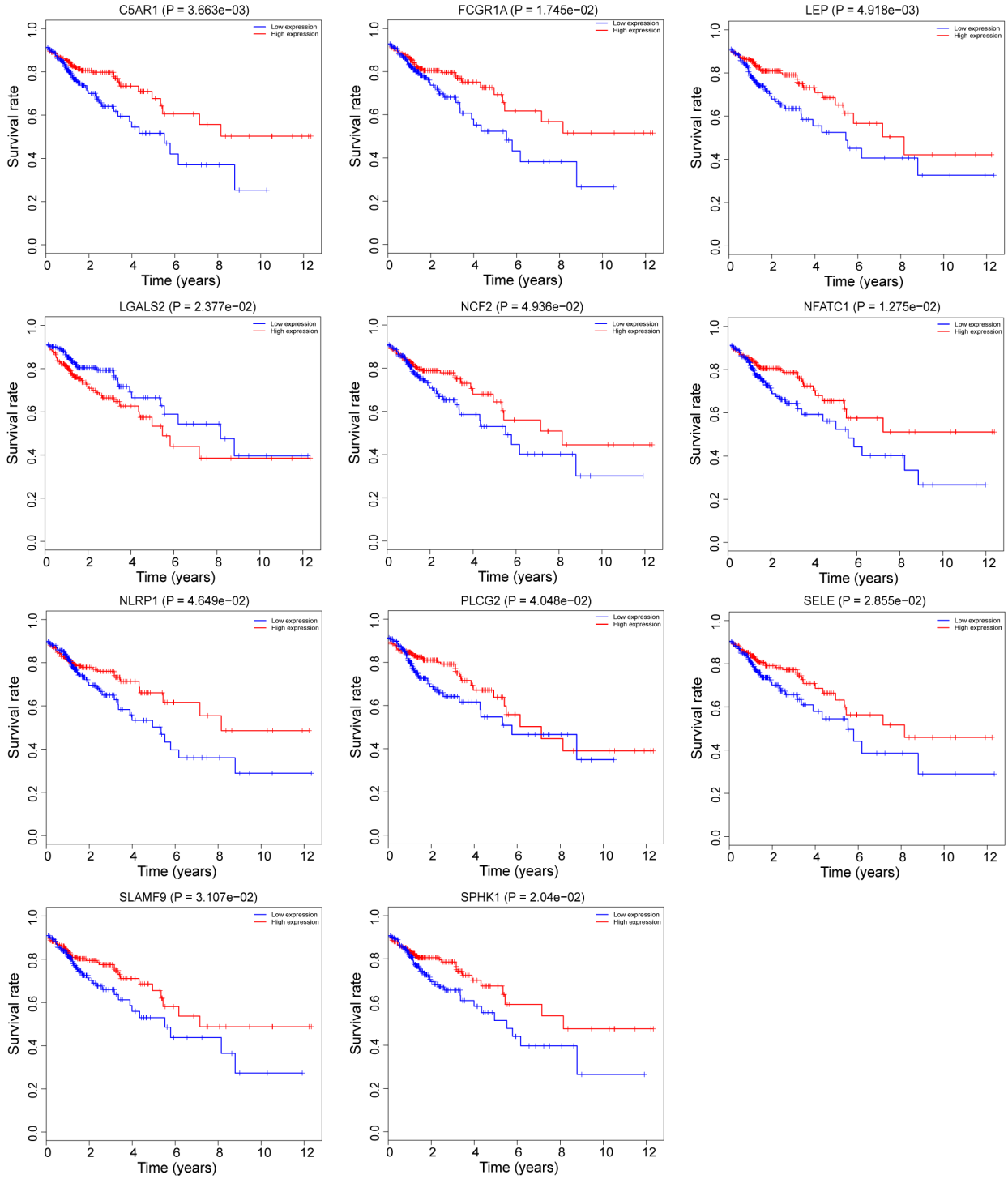

Figure S4. Copy number variation of (A) SERPINE1 and (B) UCHL1 was significantly associated with changes in the proportion of multiple tumor-infiltrating immune cells. The statistical difference between copy number abnormality and the proportion of infiltration of immune cell was compared through the two-sided Wilcoxon rank-sum test (*P<0.05, **P<0.01, ***P<0.001). SERPINE1, serpin family E member 1; UCHL1, ubiquitin C-terminal hydrolase L1.

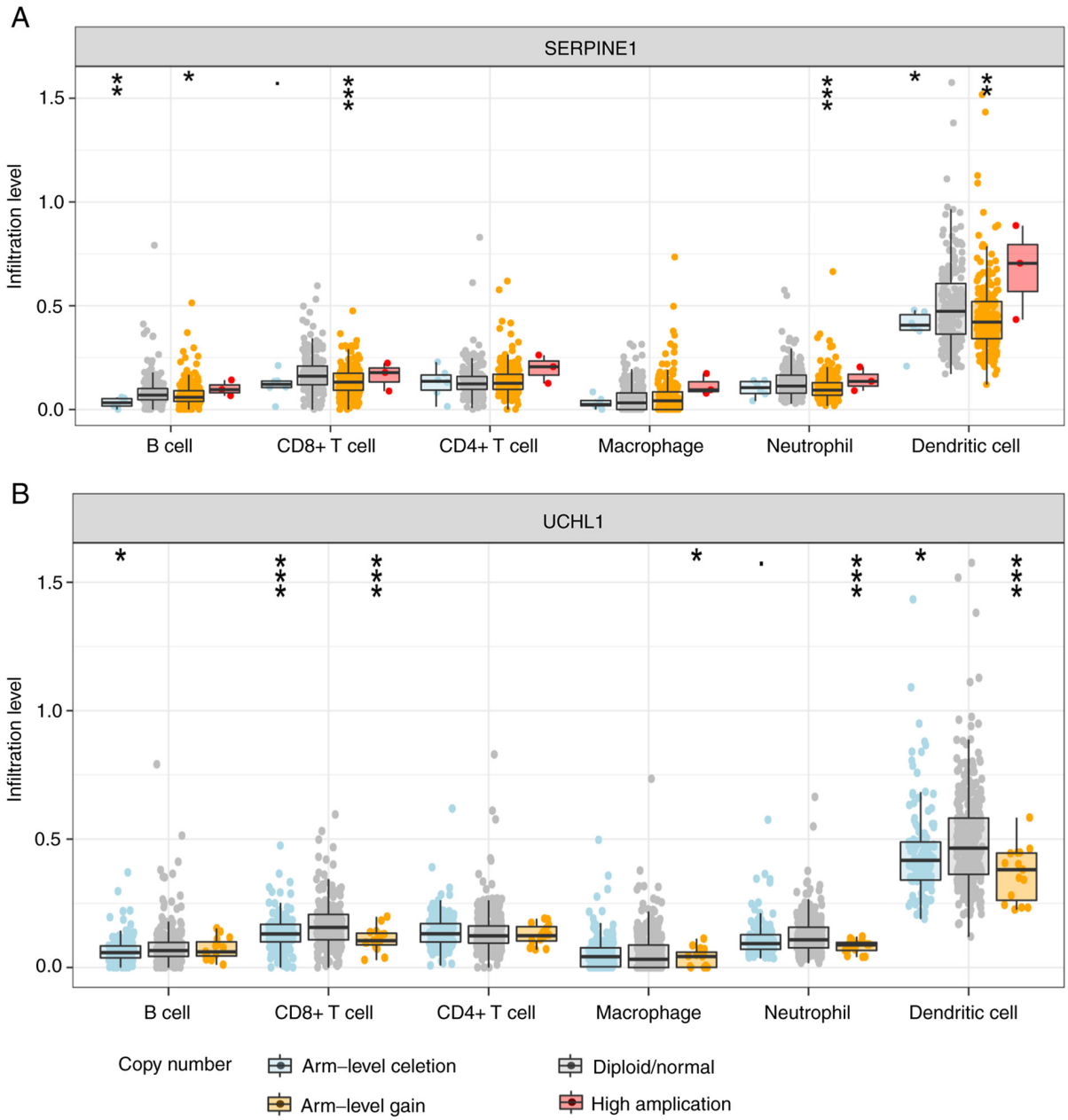

Figure S5. Comprehensive validation in Gene Expression Omnibus datasets. (A) The results of batch correction of GSE17536 and GSE21510 datasets. The broken vertical lines indicate the corrected distribution of the expression of the sample. (B) Bar graph summarizing the immune cell subset proportions in the samples with a high immune score. NK, natural killer.