

Figure S1 Construction and verification of immune grouping in the ArrayExpress-NSCLC dataset. (A) The immune cells are highly expressed in the Immunity_H group and showed low expression in the Immunity_L group. Using ESTIMATE's algorithm, the tumor purity, ESTIMATE score, stromal score, and immune score are displayed together with the grouping information. (B) The box-plot shows there is a significant difference in tumor purity, ESTIMATE score, stromal score, and immune score between the two groups. The expression of HLA family genes (C) and CDL1 (D) in the Immunity_H group (red) are significantly higher than that in the Immunity_L group (green). **, $P < 0.01$; ***, $P < 0.001$.

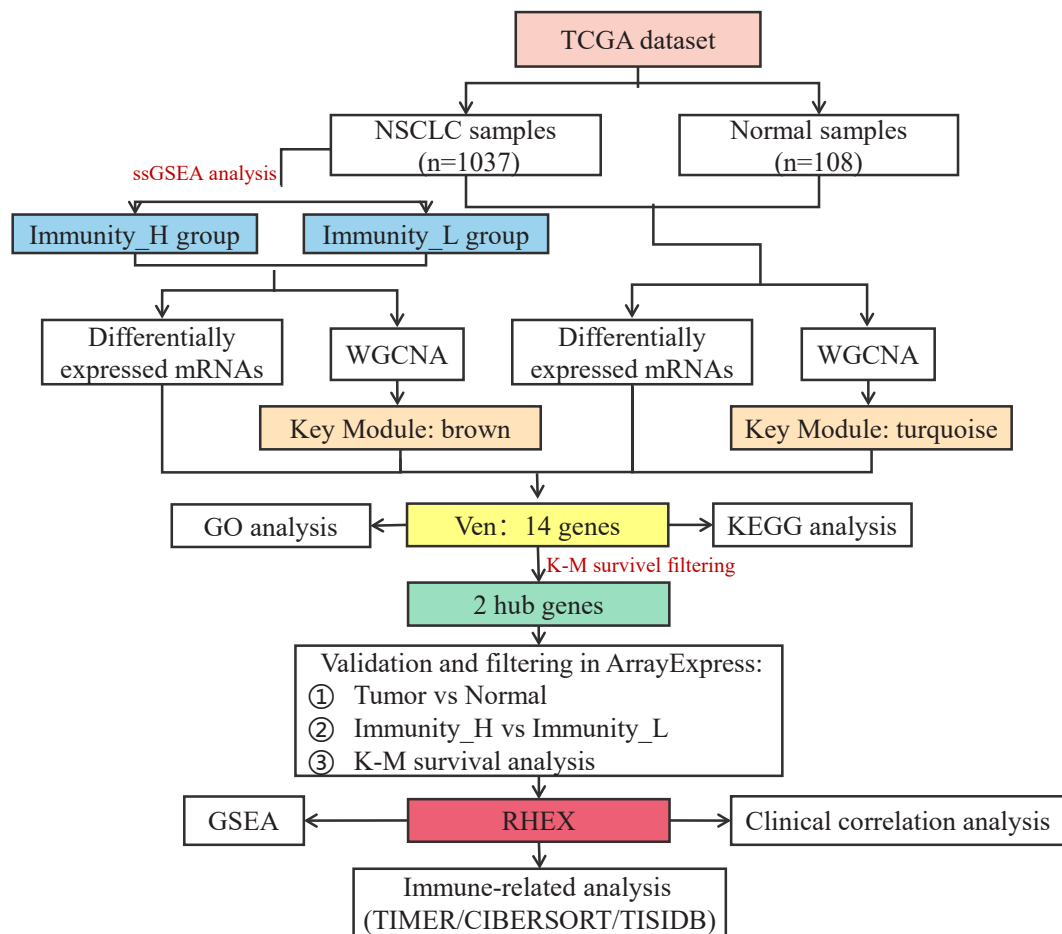


Figure S2 Flowchart for this study.

Table S1 Gene set enrichment analysis (GSEA) pathways up-regulated and down-regulated due to the expression level of regulator of hemoglobinization and erythroid cell expansion (RHEX)

Gene sets	SIZE	NES	NOM P-val	FDR q-val
Enriched gene sets in high RHEX expression group				
HALLMARK_KRAS_SIGNALING_UP	198	1.906	0.002	0.030
HALLMARK_INFLAMMATORY_RESPONSE	199	1.988	0.008	0.033
HALLMARK_INTERFERON_GAMMA_RESPONSE	198	1.847	0.024	0.033
HALLMARK_COMPLEMENT	198	1.823	0.021	0.033
HALLMARK_ALLOGRAFT_REJECTION	191	1.924	0.010	0.038
HALLMARK_IL6_JAK_STAT3_SIGNALING	86	1.851	0.020	0.039
HALLMARK_IL2_STAT5_SIGNALING	198	1.723	0.014	0.062
HALLMARK_COAGULATION	134	1.704	0.021	0.062
Enriched gene sets in low RHEX expression group				
HALLMARK_G2M_CHECKPOINT	195	-2.090	0.000	0.007
HALLMARK_MYC_TARGETS_V1	196	-2.074	0.000	0.004
HALLMARK_MYC_TARGETS_V2	58	-2.044	0.000	0.004
HALLMARK_E2F_TARGETS	198	-2.040	0.000	0.003
HALLMARK_DNA_REPAIR	149	-1.923	0.004	0.010
HALLMARK_MTORC1_SIGNALING	196	-1.79	0.021	0.034
HALLMARK_GLYCOLYSIS	197	-1.69	0.020	0.060

Table S2 Detailed correlation coefficient and P value of correlation between regulator of hemoglobinization and erythroid cell expansion (RHEX) and the immunomodulators (immunoinhibitors and immunostimulators) in The Cancer Genome Atlas (TCGA)

Gene_1	Gene_2	Correlation	P_value	Gene_1	Gene_2	Correlation	P_value
RHEX	CD28	0.62	2.62E-111	RHEX	CD160	0.42	1.78E-46
RHEX	CD40LG	0.61	6.33E-108	RHEX	TNFRSF9	0.42	3.32E-46
RHEX	BTLA	0.60	6.36E-103	RHEX	HHLA2	0.41	4.01E-44
RHEX	TMEM173	0.57	3.25E-89	RHEX	ADORA2A	0.41	7.24E-43
RHEX	CSF1R	0.56	8.15E-88	RHEX	TMIGD2	0.39	1.58E-39
RHEX	CD80	0.56	8.24E-86	RHEX	PDCD1	0.38	1.75E-36
RHEX	TNFSF13B	0.54	1.73E-80	RHEX	TNFSF15	0.38	2.95E-36
RHEX	CD48	0.54	3.96E-80	RHEX	TNFRSF8	0.37	1.89E-34
RHEX	ENTPD1	0.54	1.24E-78	RHEX	PDCD1LG2	0.36	1.28E-33
RHEX	ICOS	0.53	1.13E-77	RHEX	NT5E	0.35	1.35E-31
RHEX	TNFRSF13B	0.53	4.56E-77	RHEX	CD40	0.35	2.55E-31
RHEX	CD96	0.53	1.04E-74	RHEX	MICB	0.30	3.05E-23
RHEX	HAVCR2	0.52	6.51E-74	RHEX	CD70	0.30	1.16E-22
RHEX	CD86	0.52	4.15E-72	RHEX	KLRK1	0.29	8.48E-22
RHEX	CXCR4	0.50	8.22E-68	RHEX	TNFSF4	0.29	1.51E-21
RHEX	CD27	0.50	1.05E-66	RHEX	IDO1	0.26	3.16E-17
RHEX	TNFSF13	0.50	1.42E-66	RHEX	CD274	0.25	1.36E-16
RHEX	TNFSF14	0.49	7.65E-64	RHEX	TGFB1	0.24	2.31E-15
RHEX	KDR	0.49	2.30E-62	RHEX	LAG3	0.24	7.82E-15
RHEX	LTA	0.48	2.16E-61	RHEX	TNFRSF13C	0.23	1.97E-13
RHEX	IL10	0.48	1.53E-60	RHEX	TNFSF18	0.20	1.75E-10
RHEX	CTLA4	0.48	6.64E-60	RHEX	TGFBR1	0.19	6.09E-10
RHEX	CD244	0.46	9.70E-57	RHEX	KIR2DL3	0.19	1.74E-09
RHEX	TIGIT	0.46	9.71E-57	RHEX	KIR2DL1	0.18	1.21E-08
RHEX	CXCL12	0.45	5.53E-53	RHEX	RAET1E	0.15	7.88E-07
RHEX	IL6R	0.45	1.69E-52	RHEX	ICOSLG	0.13	3.24E-05
RHEX	IL2RA	0.45	1.88E-52	RHEX	TNFSF9	0.11	0.00
RHEX	TNFRSF14	0.45	1.29E-51	RHEX	IL6	0.08	0.02
RHEX	TNFRSF17	0.44	5.01E-51	RHEX	ULBP1	-0.08	0.01
RHEX	LGALS9	0.44	2.28E-50				