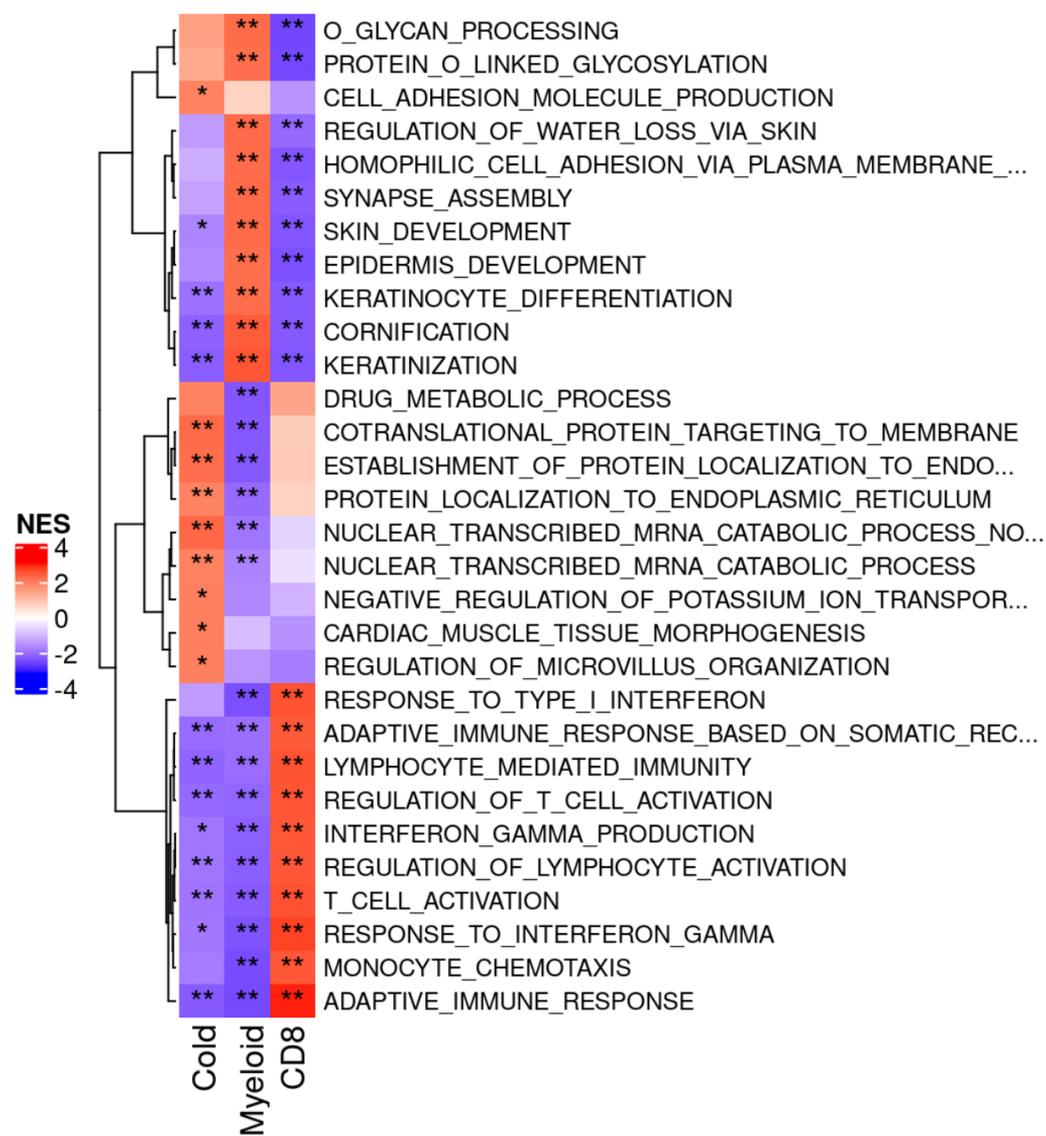
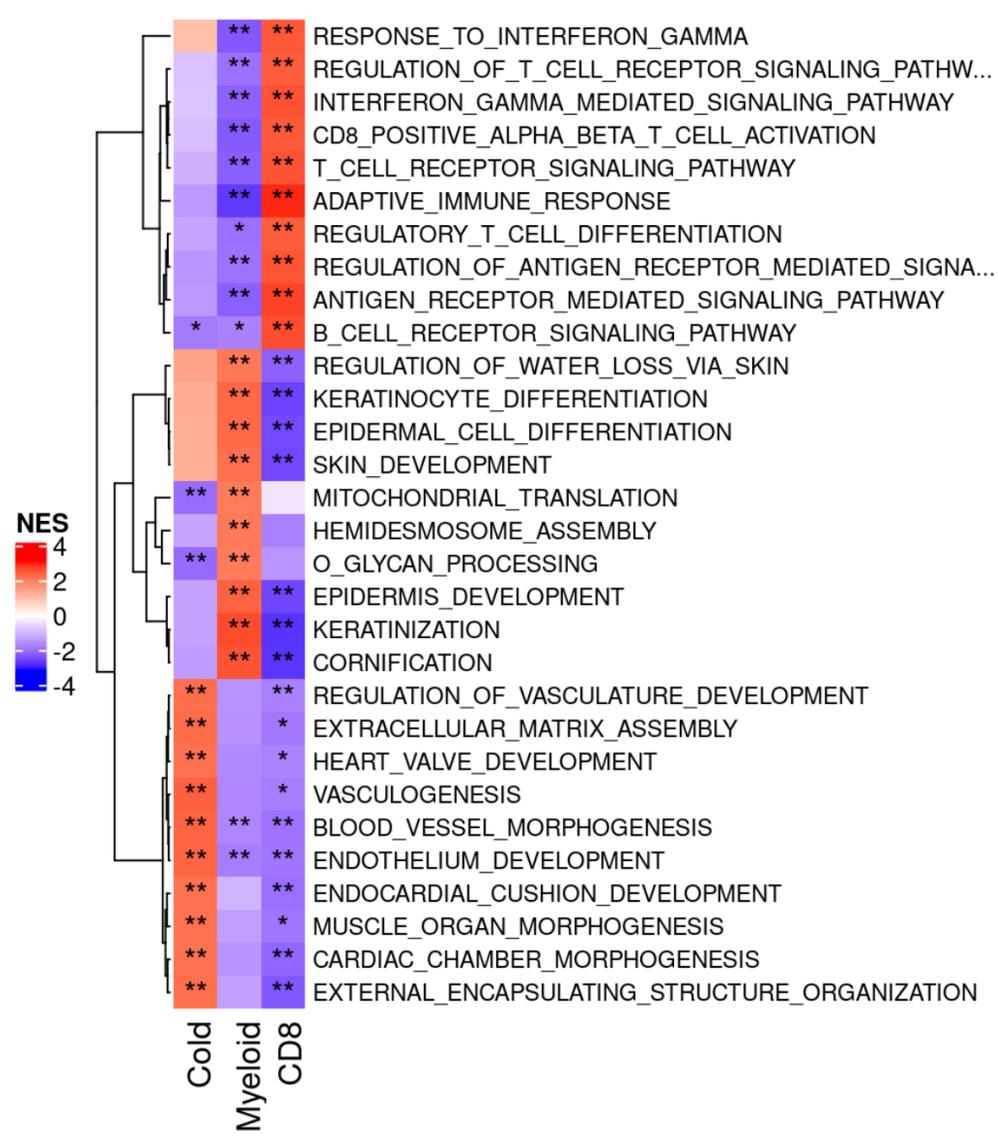


Fig. S14

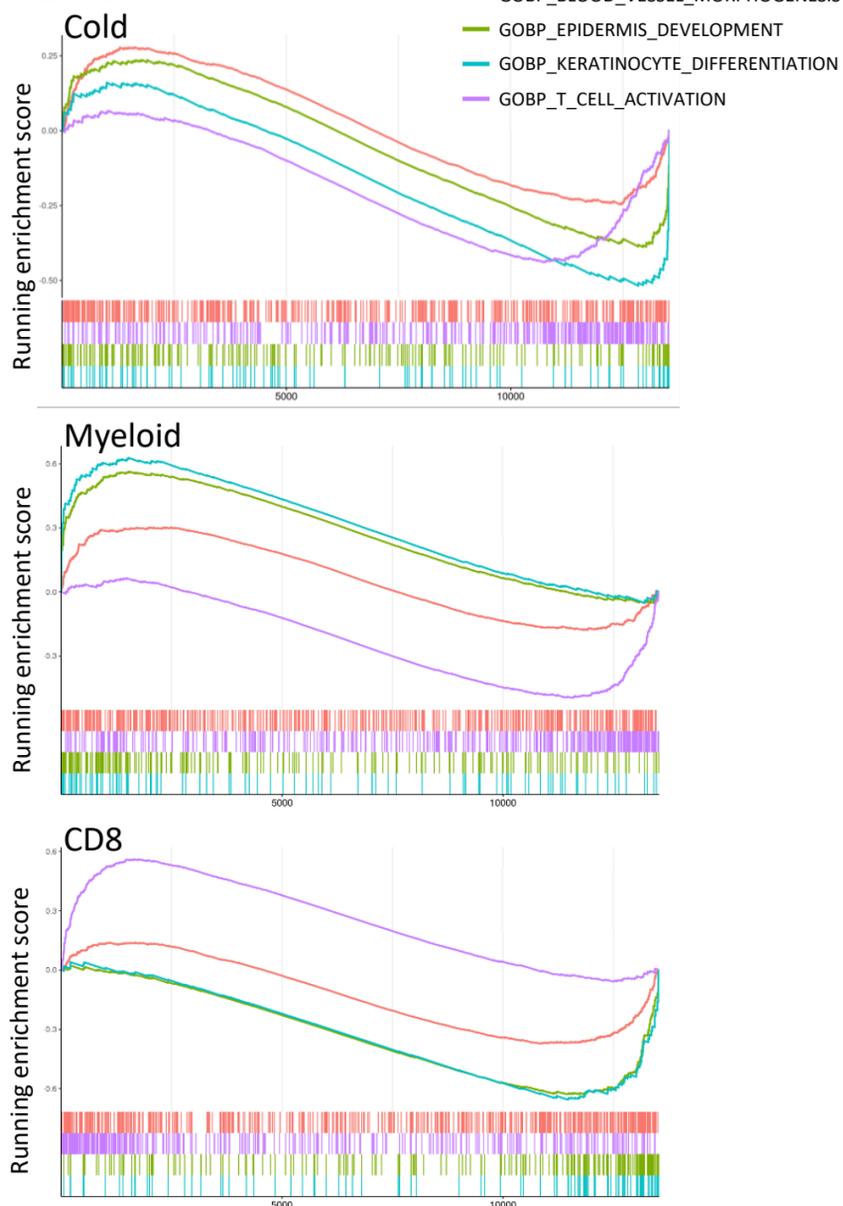
a LUAD



b LUSQ



c LUAD



d LUSQ

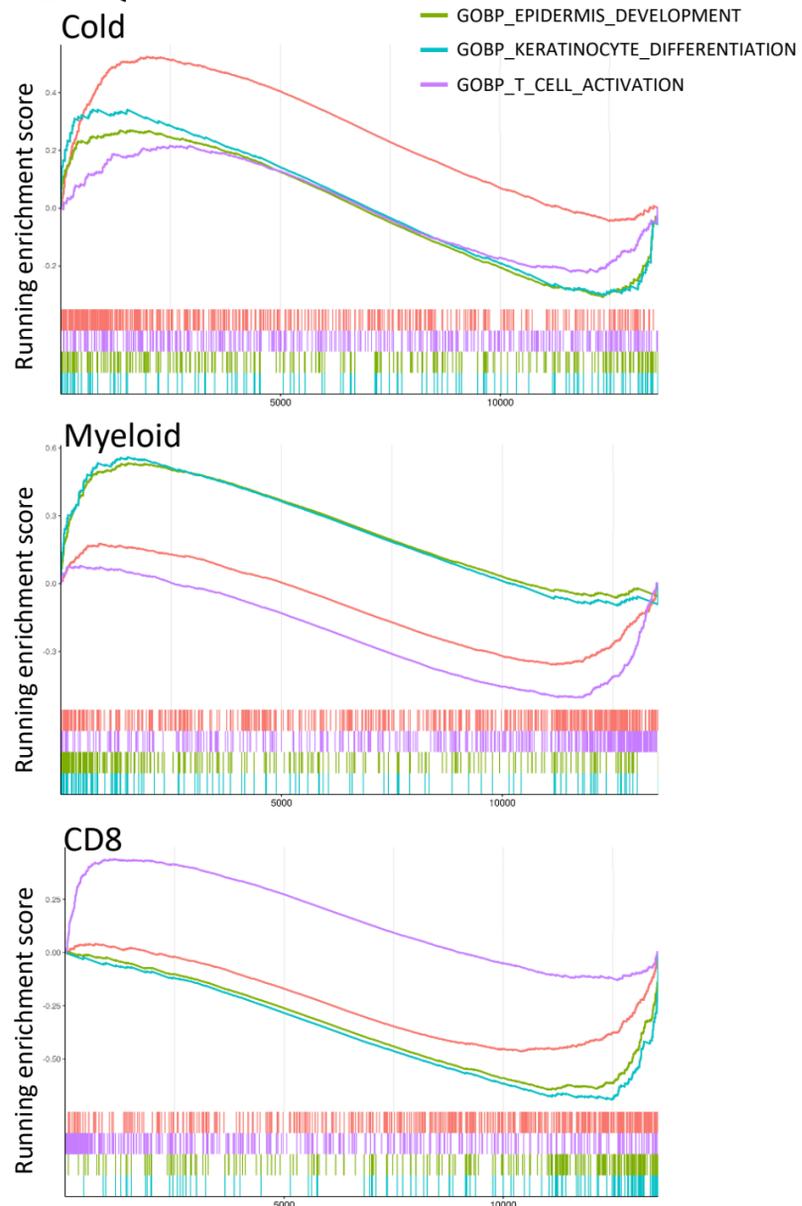


Figure S14. Activated and suppressed pathways identified by GSEA with GO gene set in respective immune subtypes. (a, b) Heatmap representing top scored pathways enriched in genes showing commonly increased and decreased expression in respective immune subtypes in LUAD (a) and LUSQ (b). Top signaling pathways for genes showing increased expression are presented in red and those for genes showing decreased expression are presented in blue. (c, d) Running enrichment score with GO gene set of blood vessel morphogenesis, epidermis development, keratinocyte differentiation, and T cell activation signatures as the activated pathways in respective immune subtypes of LUAD (c) and LUSQ (d).