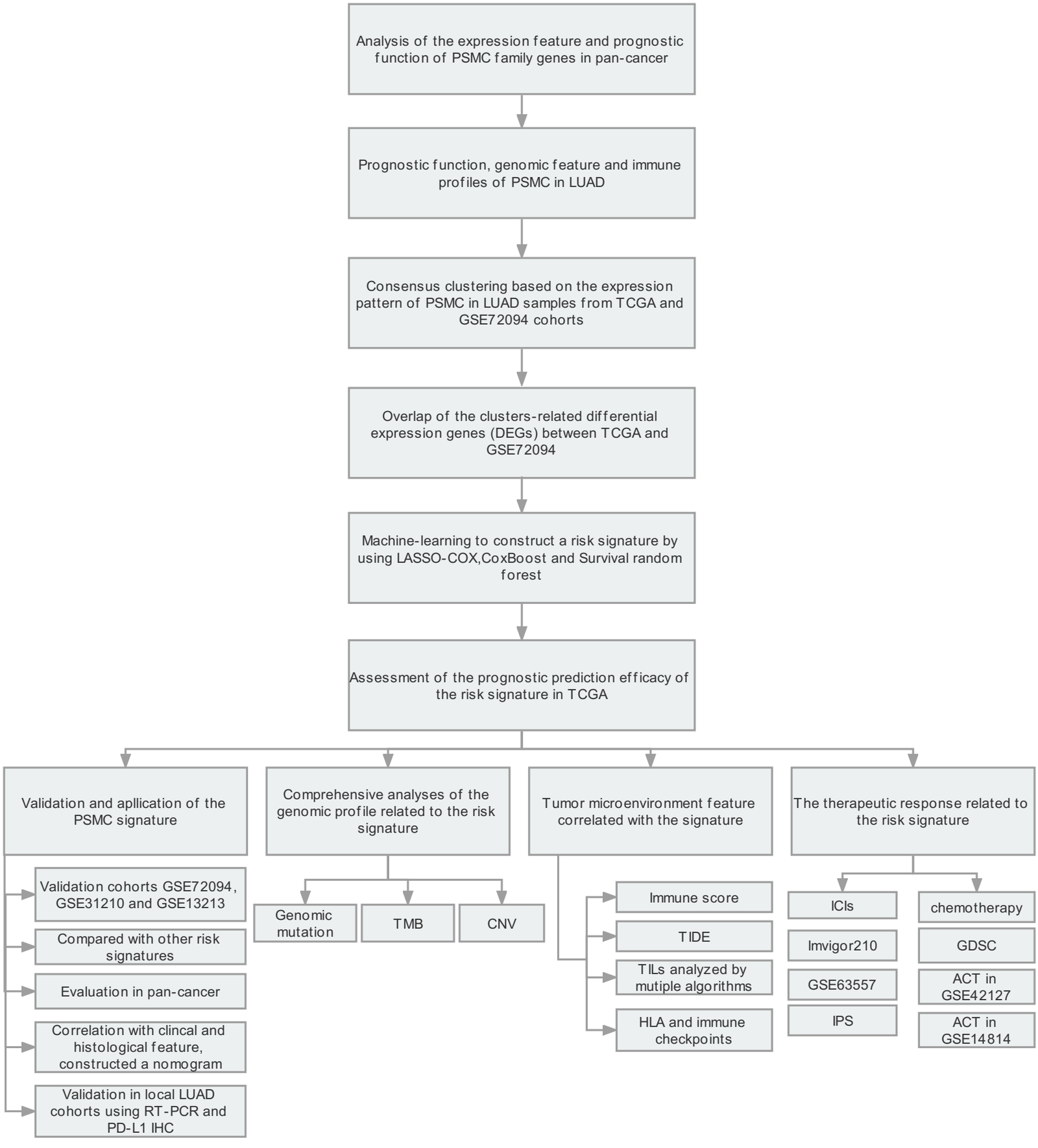
Analysis of the expression feature and prognostic function of PSMC family genes in pan-cancer
Prognostic function, genomic feature and immune profiles of PSMC in LUAD
Consensus clustering based on the expression pattern of PSMC in LUAD samples from TCGA and GSE72094 cohorts
Overlap of the clusters-related differential expression genes (DEGs) between TCGA and GSE72094
Machine-learning to construct a risk signature by using LASSO-COX,CoxBoost and Survival random forest
Assessment of the prognostic prediction efficacy of the risk signature in TCGA
Validation and apllication of the PSMC signature
Validation cohorts GSE72094, GSE31210 and GSE13213
Compared with other risk signatures
Evaluation in pan-cancer
Correlation with clincal and histological feature, constructed a nomogram
Validation in local LUAD cohorts using RT-PCR and PD-L1 IHC
Comprehensive analyses of the genomic profile related to the risk signature
Genomic mutation
TMB
CNV
Tumor microenvironment feature correlated with the signature
Immune score
TIDE
TILs analyzed by mutiple algorithms
HLA and immune checkpoints
The therapeutic response related to the risk signature
ICIs
Imvigor210
GSE63557
IPS
chemotherapy
GDSC
ACT in GSE42127
ACT in GSE14814