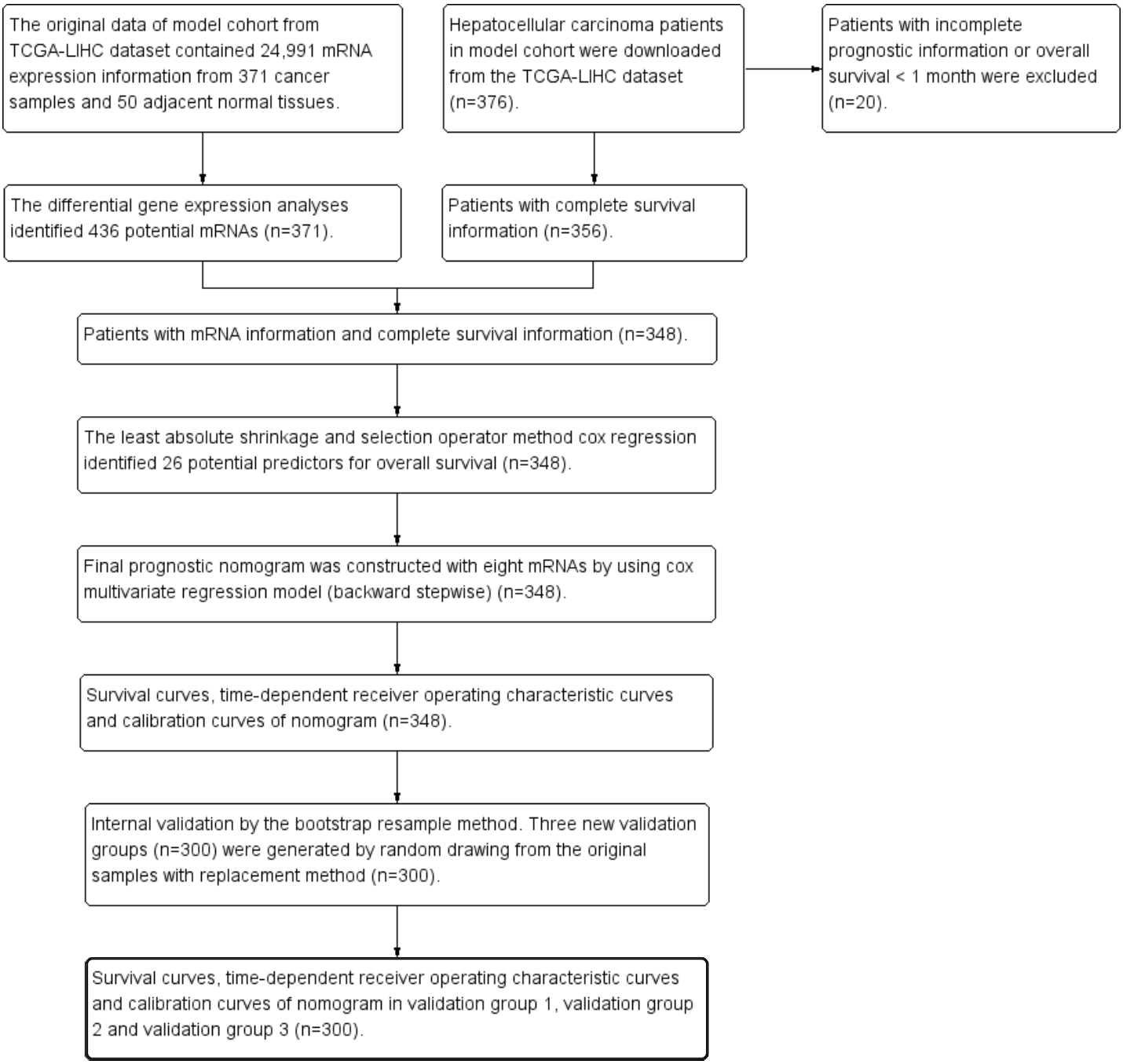
The original data of model cohort from TCGA-LIHC dataset contained 24,991 mRNA expression information from 371 cancer samples and 50 adjacent normal tissues.
Hepatocellular carcinoma patients in model cohort were downloaded from the TCGA-LIHC dataset (n=376).
Patients with incomplete prognostic information or overall survival < 1 month were excluded (n=20).
The differential gene expression analyses identified 436 potential mRNAs (n=371).
Patients with complete survival information (n=356).
Patients with mRNA information and complete survival information (n=348).
The least absolute shrinkage and selection operator method cox regression identified 26 potential predictors for overall survival (n=348).
Final prognostic nomogram was constructed with eight mRNAs by using cox multivariate regression model (backward stepwise) (n=348).
Survival curves, time-dependent receiver operating characteristic curves and calibration curves of nomogram (n=348).
Internal validation by the bootstrap resample method. Three new validation groups (n=300) were generated by random drawing from the original samples with replacement method (n=300).
Survival curves, time-dependent receiver operating characteristic curves and calibration curves of nomogram in validation group 1, validation group 2 and validation group 3 (n=300).