Figure S1. The comparison of LASSO, Ridge and Elastic net regressions in the prediction of prognosis for LGGs.
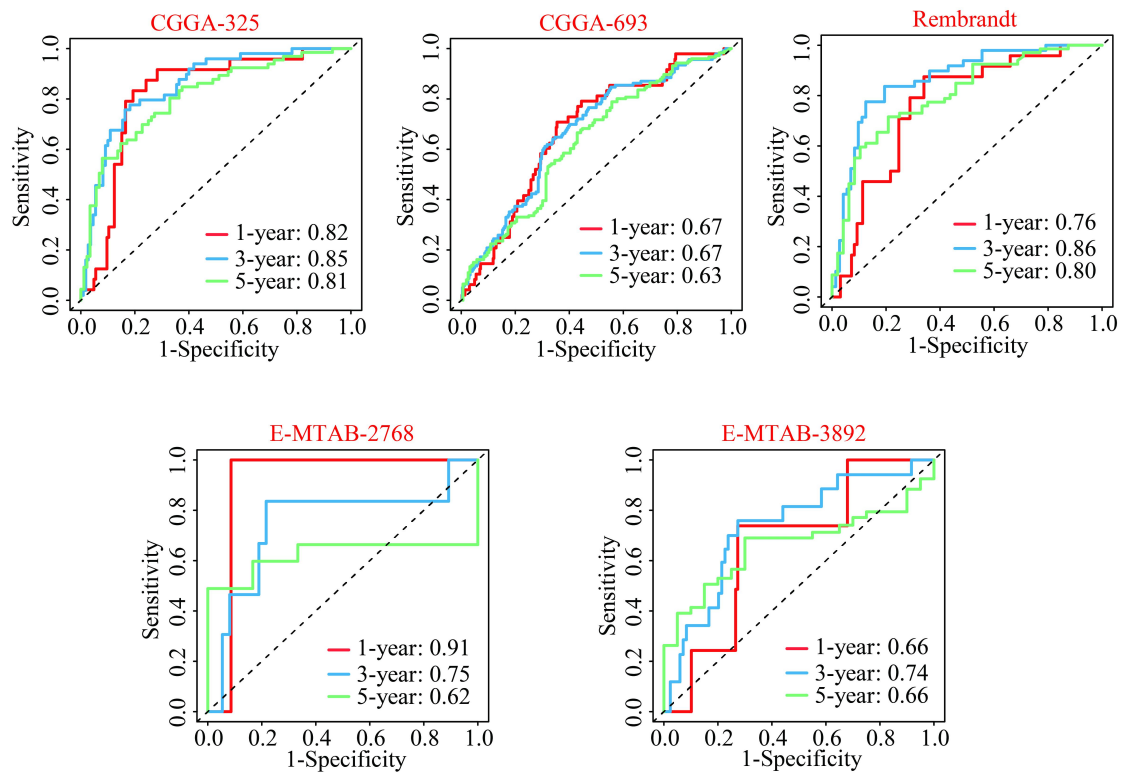

Figure S2. The AUC of 1-, 3-, and 5-year OS in CGGA-325, CGGA-693, Rembrandt,

E-MATB-2768 and E-MATB-3892 datasets, respectively.

ABI1

CAB008375

LGG tissue

Staining: Medium

Intensity: Moderate

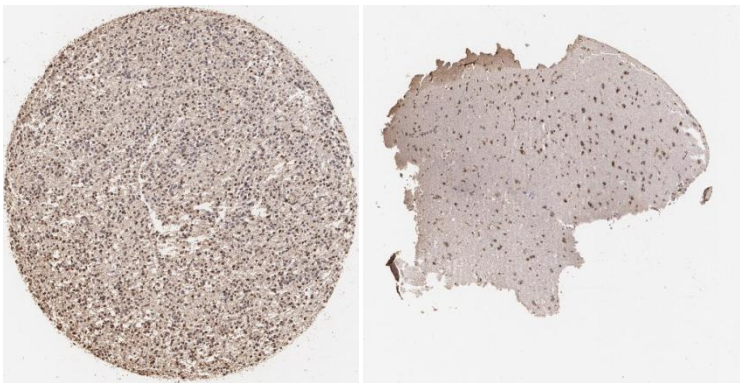Quality: > 75%

CAB008375

Normal tissue

Staining: Low

Intensity: Moderate

Quality: < 25%

BRCA1

CAB001946

LGG tissue

Staining: Medium
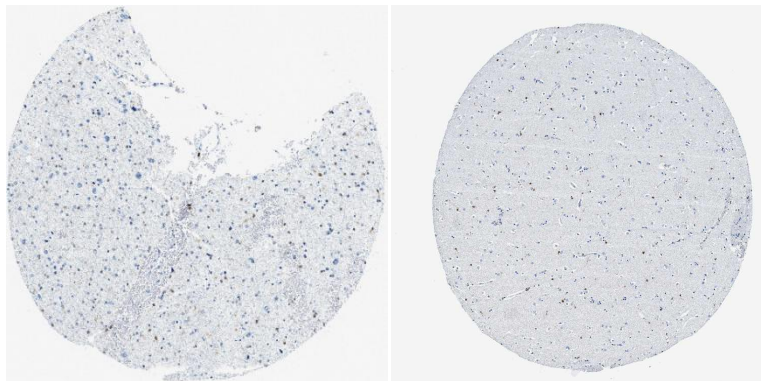
Intensity: Moderate

Quality: 75% ~ 25%

CAB001946

Normal tissue

Staining: Low

Intensity: Moderate

Quality: < 25%

CAPG

HPA019092

LGG tissue

Staining: Low
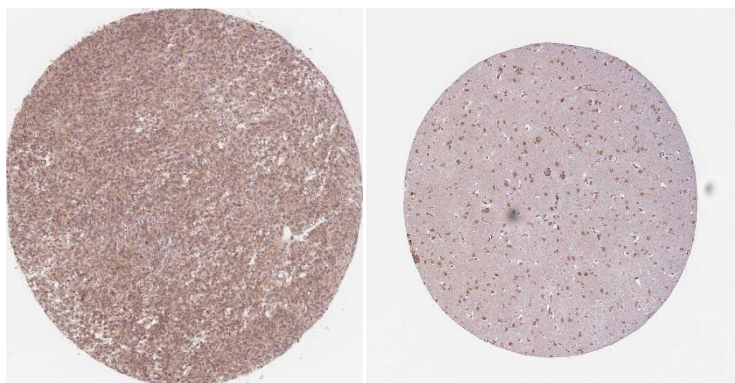
Intensity: Moderate

Quality: < 25%

HPA019092

Normal tissue

Staining: Not detected

Intensity: Week

Quality: < 25%

EIF3D

HPA066216

LGG tissue

Staining: Medium

Intensity: Moderate

Quality: > 75%
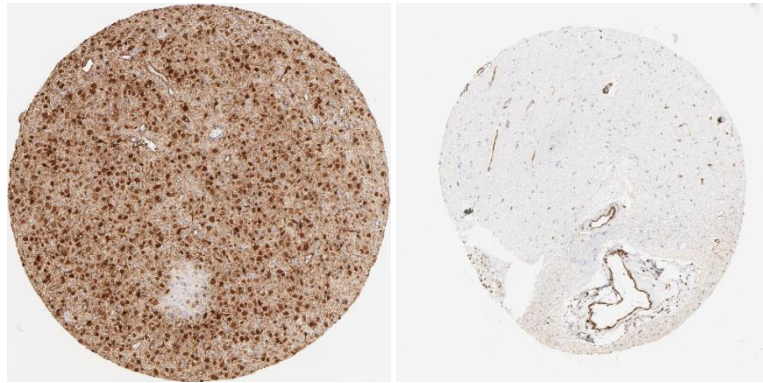
HPA066216

Normal tissue

Staining: Low

Intensity: Moderate

Quality: < 25%

FLNA

HPA002925	**HPA002925**
LGG tissue	Normal tissue
Staining: High	Staining: Low
Intensity: Strong	Intensity: Weak
Quality: > 75%	Quality: > 75%

Figure S3. The expression of five AR-related genes between LGG and corresponding normal tissues at the protein level.
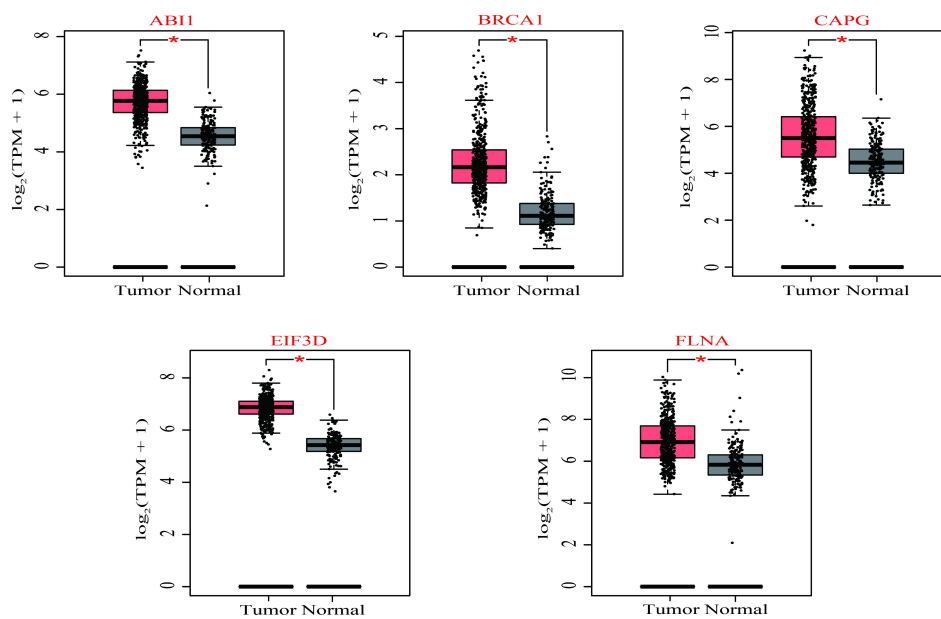

Figure S4. The expression of five AR-related genes between tumor and normal tissues via GEPIA database.
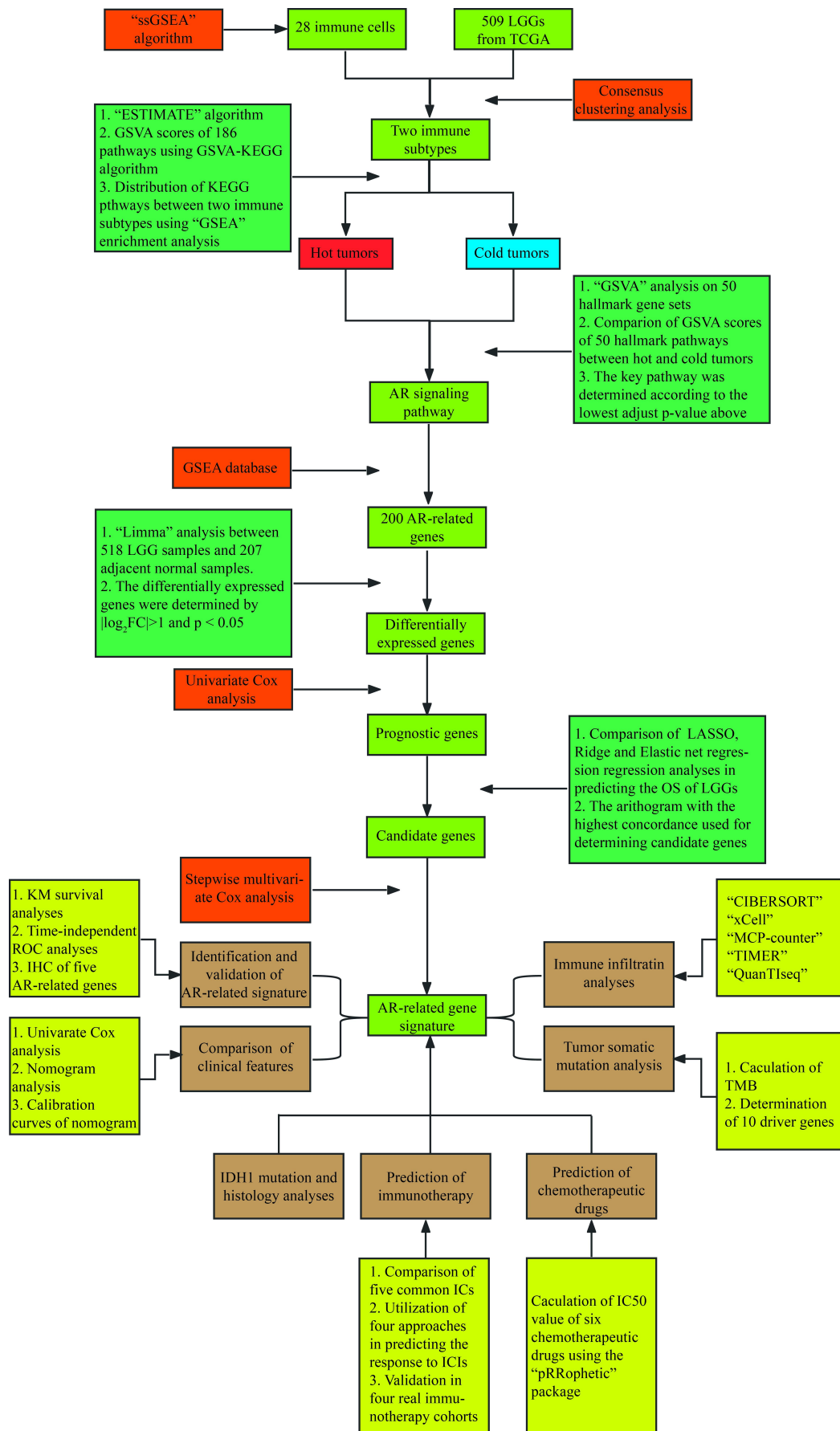
Figure S5. The flow chart in this study.