

Figure S1. Optimal soft threshold selection for high-dimensional weighted gene co-expression network analysis.

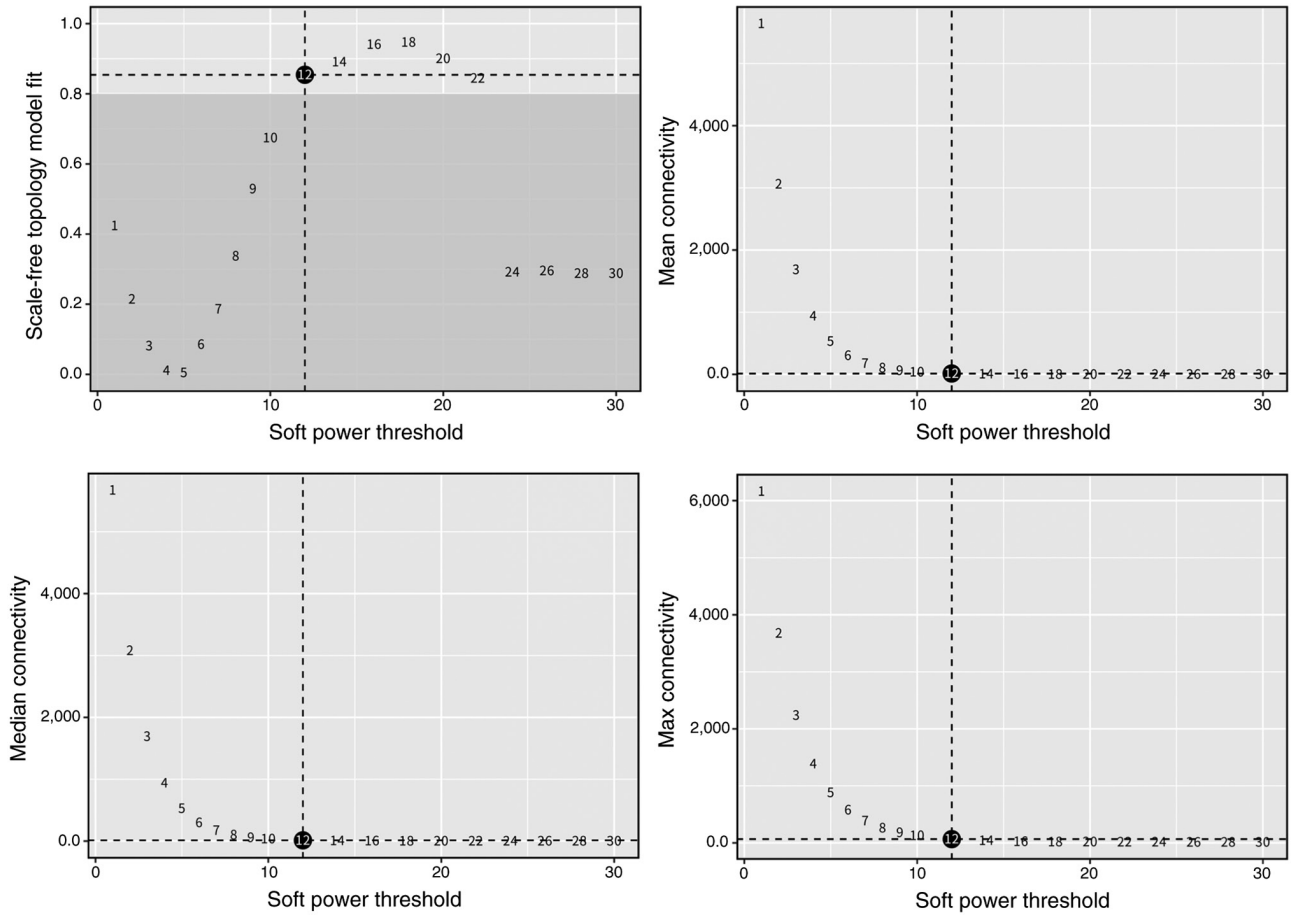


Figure S2. Heatmap displaying the 117 combined models ranked by descending concordance index in the validation cohort. Training cohort: The Cancer Genome Atlas-oral squamous cell carcinoma cohort (n=310); validation cohort: The GSE65858 dataset (n=131). StepCox, stepwise Cox; Enet, elastic network; RSF, random survival forests; XgBoost, extreme gradient boosting; SVM-REF, support vector machine recursive feature elimination; Lasso, least absolute shrinkage and selection operator; GBM, generalized boosted regression models; plsRcox, partial least squares regression for Cox; superPC, supervised principal components; survival-SVM, survival support vector machine.

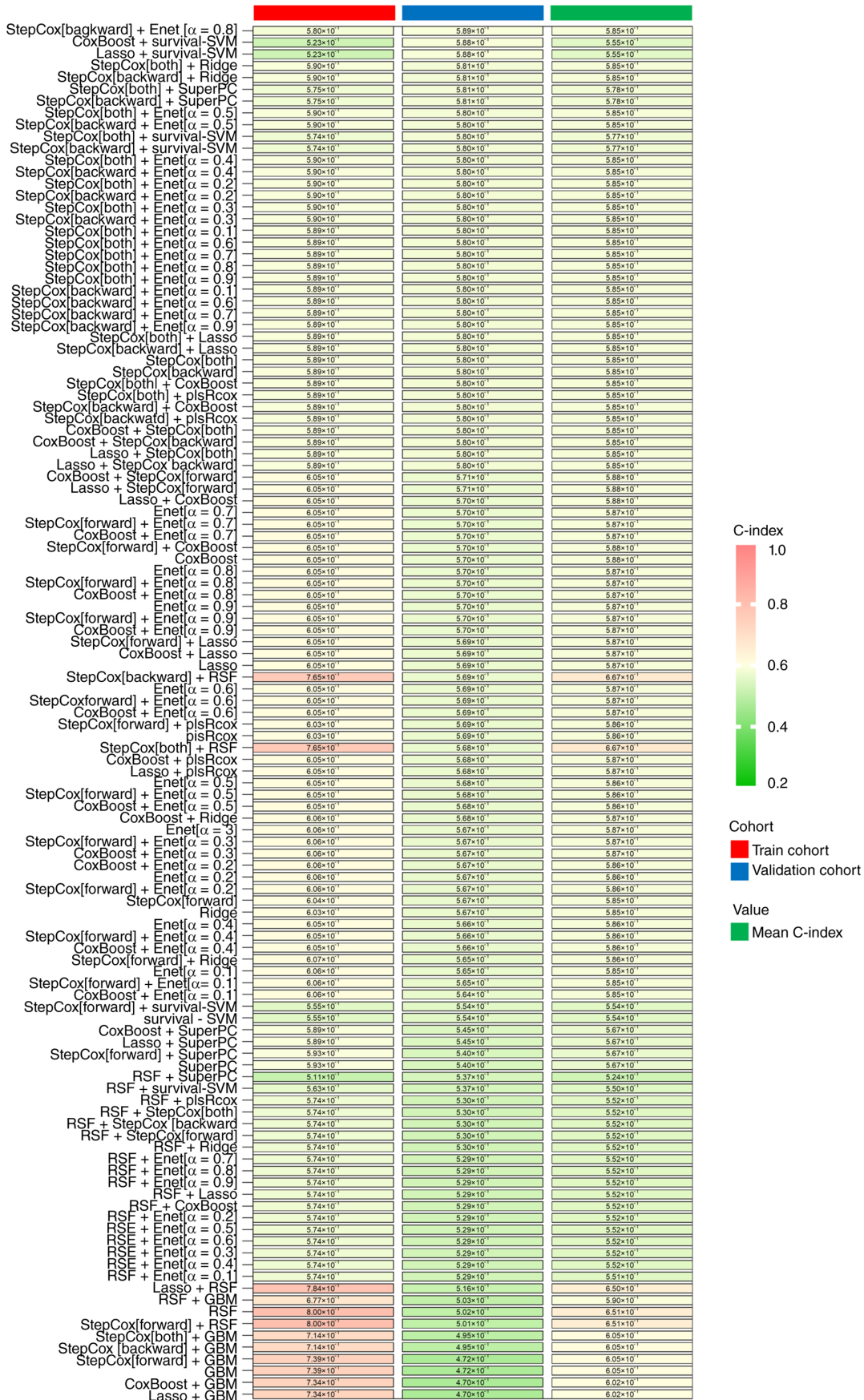


Figure S3. Knockdown and overexpression efficiencies of DYNC1H1 and FOSL2 were examined under hypoxic conditions. Knockdown efficiency of DYNC1H1 under hypoxic conditions was assessed by (A) RT-qPCR and (B) western blotting. ** $P < 0.01$ vs. KD-ctrl. Overexpression efficiency of DYNC1H1 under hypoxic conditions was assessed by (C) RT-qPCR and (D) western blotting. ** $P < 0.01$ vs. OE-ctrl. Knockdown efficiency of FOSL2 under hypoxic conditions was measured by (E) RT-qPCR and (F) western blotting. ** $P < 0.01$ vs. KD-ctrl. Overexpression efficiency of FOSL2 under hypoxic conditions was detected by (G) RT-qPCR and (H) western blotting. ** $P < 0.01$ vs. OE-ctrl. DYNC1H1, dynein cytoplasmic 1 heavy chain 1; RTqPCR, reverse transcription-quantitative PCR; KD, knockdown; OE, overexpression; ctrl, control; FOSL2, FOS-like 2.

