Figure S1. Difference in clinical stage distribution among molecular clusters in the retrospective chemotherapy cohort. (A) The distribution of clinical stage was compared among the four clusters (C1, C2, C3 and C4) using Fisher's exact test (P=0.415). (B) The distribution of clinical stage was compared between C1 and C2/3/4 using Fisher's exact test (P=0.293). C, cluster.

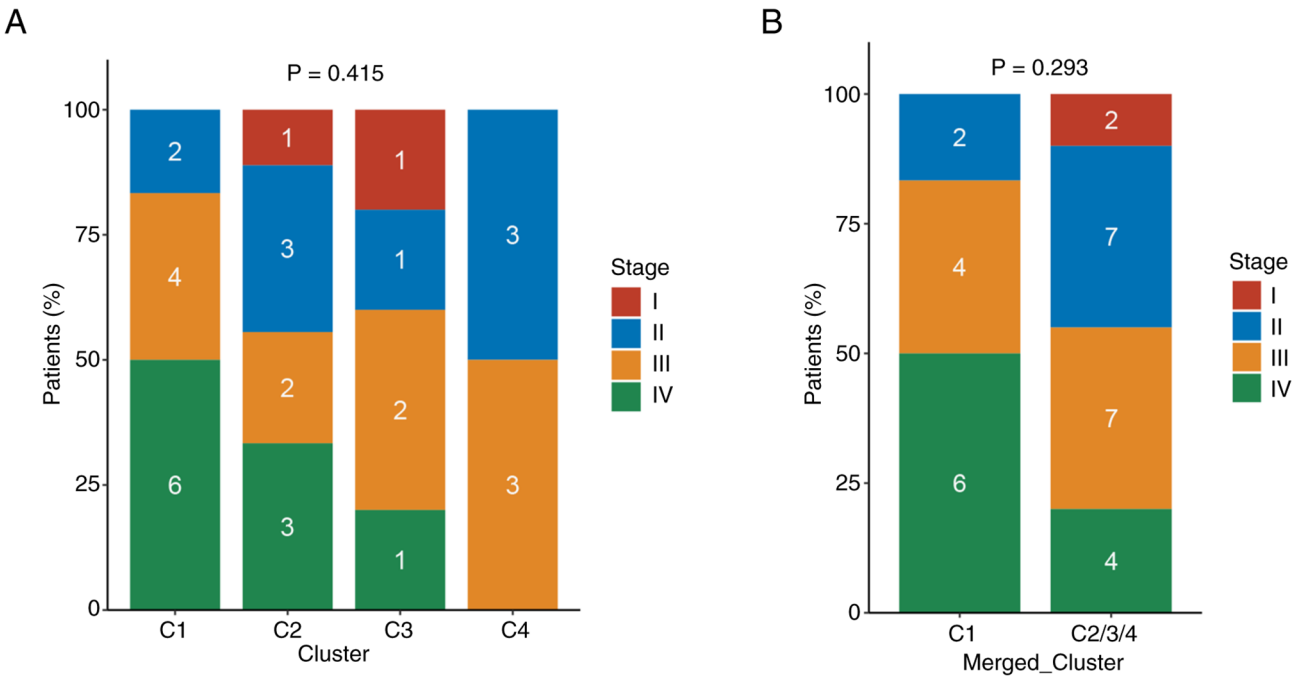

Figure S2. Difference in PFS between *TP53*-mutant and *TP53*-wild-type patients in the retrospective chemotherapy cohort. PFS, progression-free survival, Mut, mutation; WT, wild-type; HR, hazard ratio.

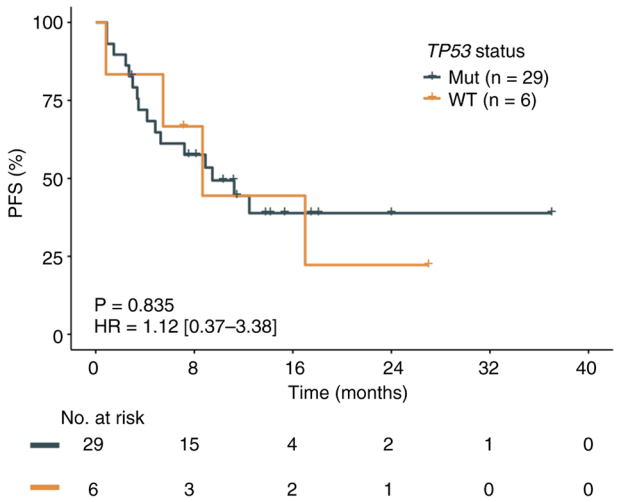

Figure S3. Difference in *TP53* LOF distribution among molecular clusters in the retrospective chemotherapy cohort. (A) The distribution of *TP53* LOF was compared among the four clusters (C1, C2, C3 and C4) using Fisher's exact test (P=0.389). (B) The distribution of *TP53* LOF was compared between C1 and C2/3/4 using Fisher's exact test (P=0.728). LOF, loss-of-function; C, cluster.

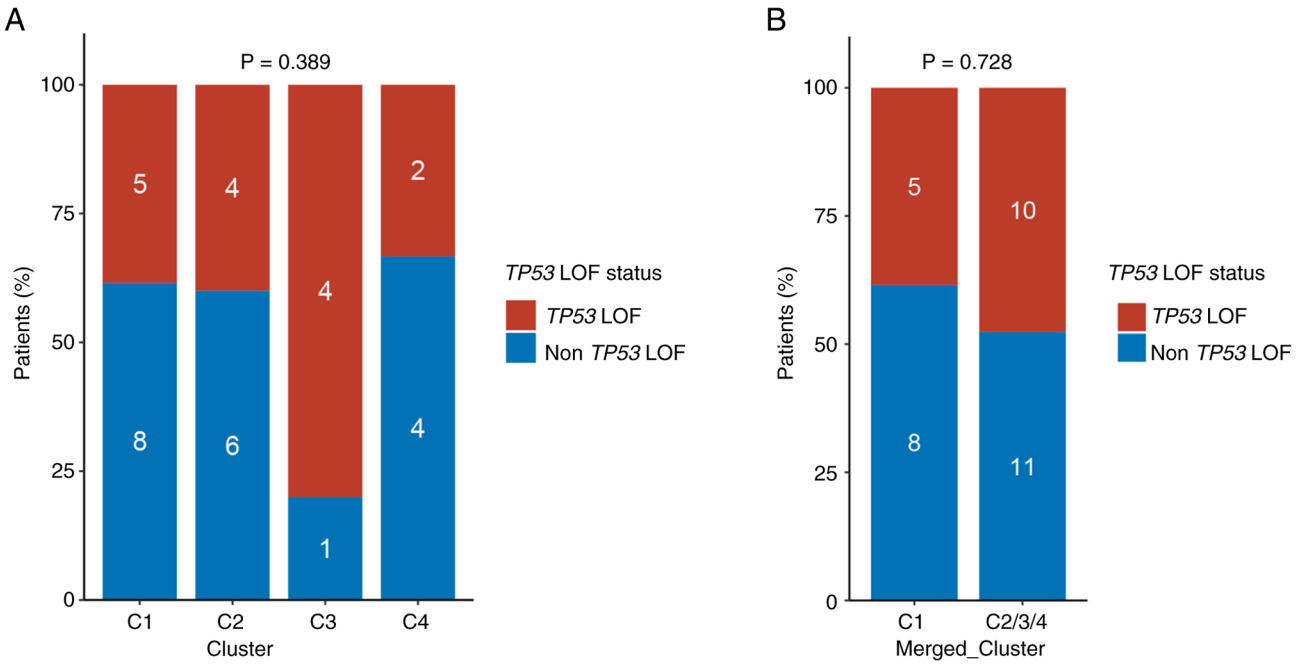

Figure S4. Multivariable Cox proportional hazards analysis in the retrospective chemotherapy cohort. (A) Multivariate Cox proportional hazards analysis was adjusted for tumor stage (I-IV) and the Amp(9G) and *TP53* LOF-based grouping. (B) Multivariate Cox proportional hazard analysis was adjusted for dichotomized tumor stage (stage I/II vs. stage III/IV) and the Amp(9G) and *TP53* LOF-based grouping. *P<0.05; **P<0.01. Amp(9G), amplification of at least one of nine genes; LOF, loss-of-function; AIC, Akaike Information Criterion.

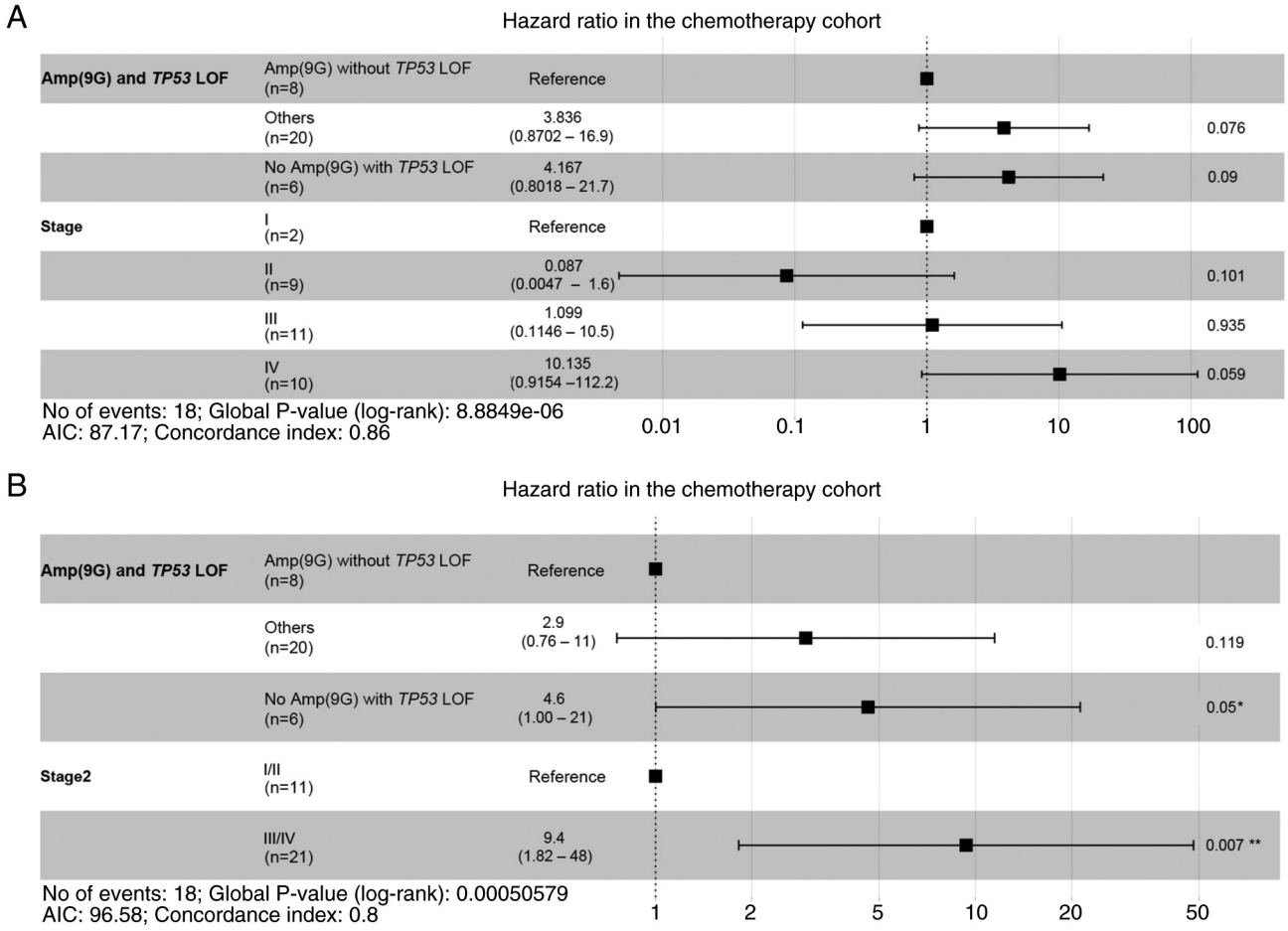

Figure S5. NMF-based molecular clustering of patients with LUSC treated with first-line chemotherapy from the TCGA database, classified into C1, C2, C3 and C4. NMF, non-negative matrix factorization; LUSC, lung squamous cell carcinoma; TCGA, The Cancer Genome Atlas; C, cluster; indel, insertions and deletions.

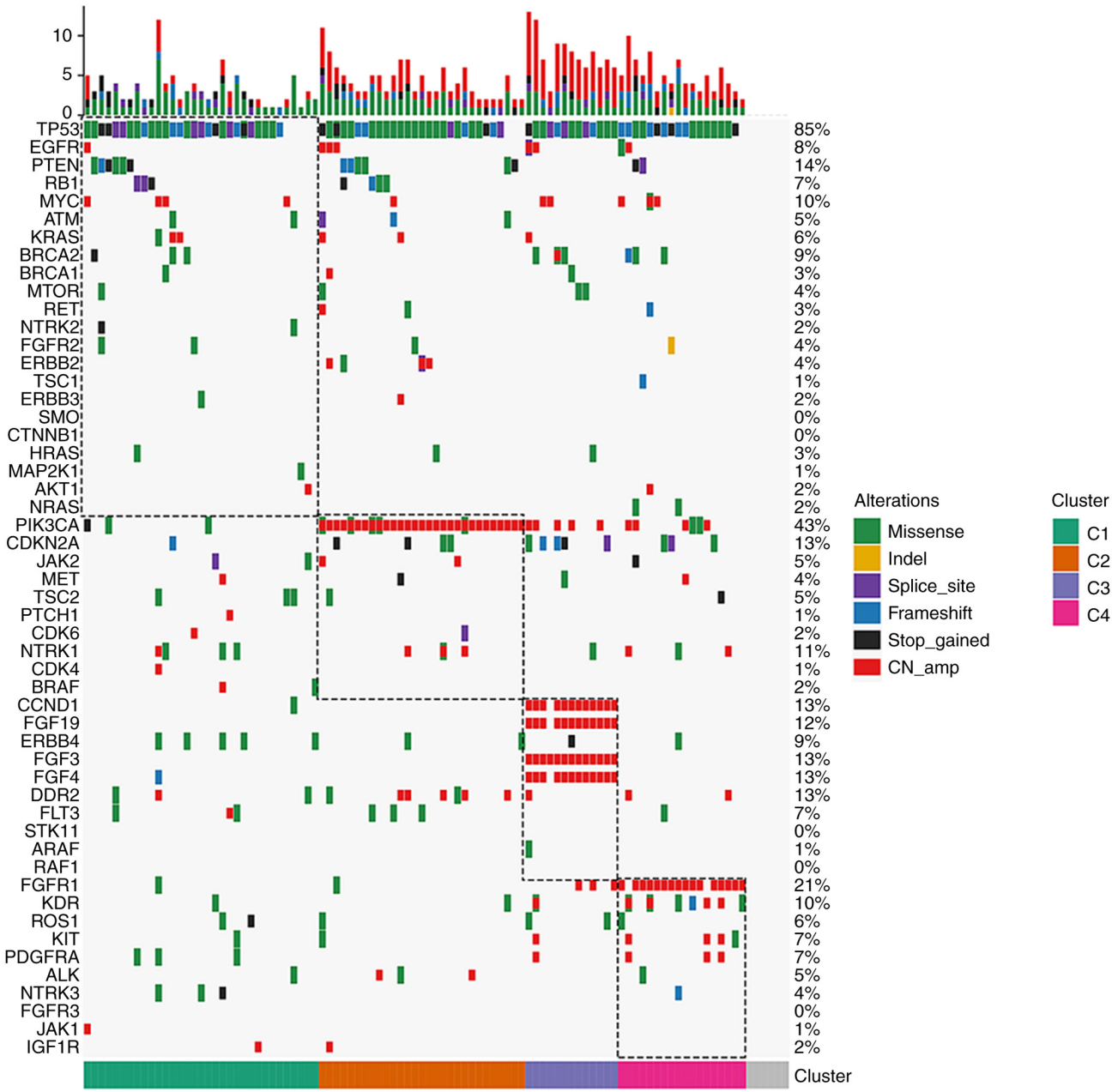

Figure S6. Multivariable Cox proportional hazards analysis in the TCGA cohort. (A) Multivariate Cox proportional hazards analysis was adjusted for tumor stage (I-IV) and the Amp(9G) and *TP53* LOF-based grouping. (B) Multivariate Cox proportional hazard analysis was adjusted for dichotomized tumor stage (stage I/II vs. stage III/IV) and Amp(9G) and *TP53* LOF-based grouping. *P<0.05. TCGA, The Cancer Genome Atlas; Amp(9G), amplification of at least one of nine genes; LOF, loss-of-function; AIC, Akaike Information Criterion.

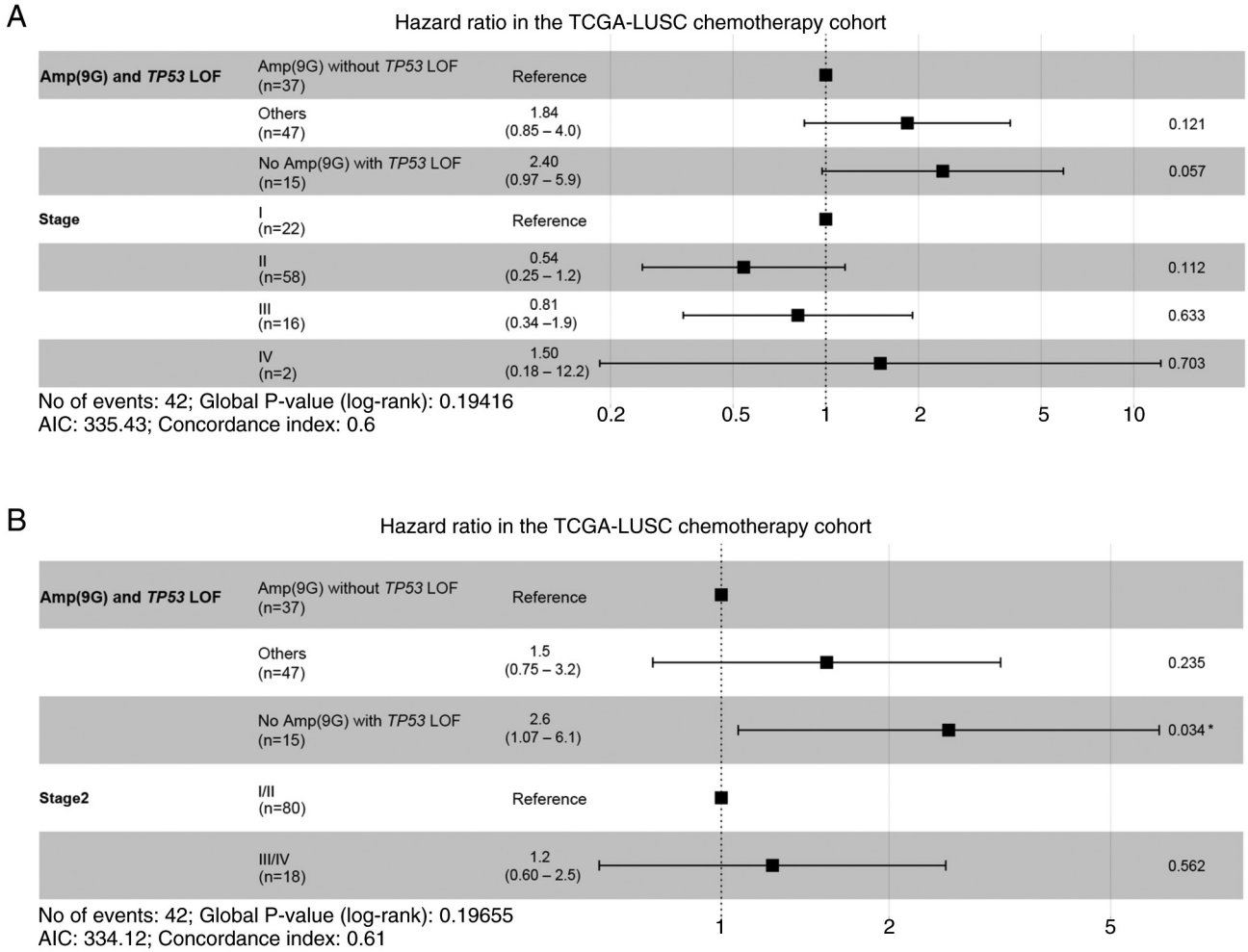

Figure S7. Difference in PFS among patients harboring *TP53* LOF without Amp(9G), Amp(9G) without *TP53* LOF and others [including those with Amp(9G) and *TP53* LOF, and those without Amp(9G) and *TP53* LOF] who received first-line radiochemotherapy. PFS, progression-free survival; Amp(9G), amplification of at least one of nine genes; LOF, loss-of-function.