

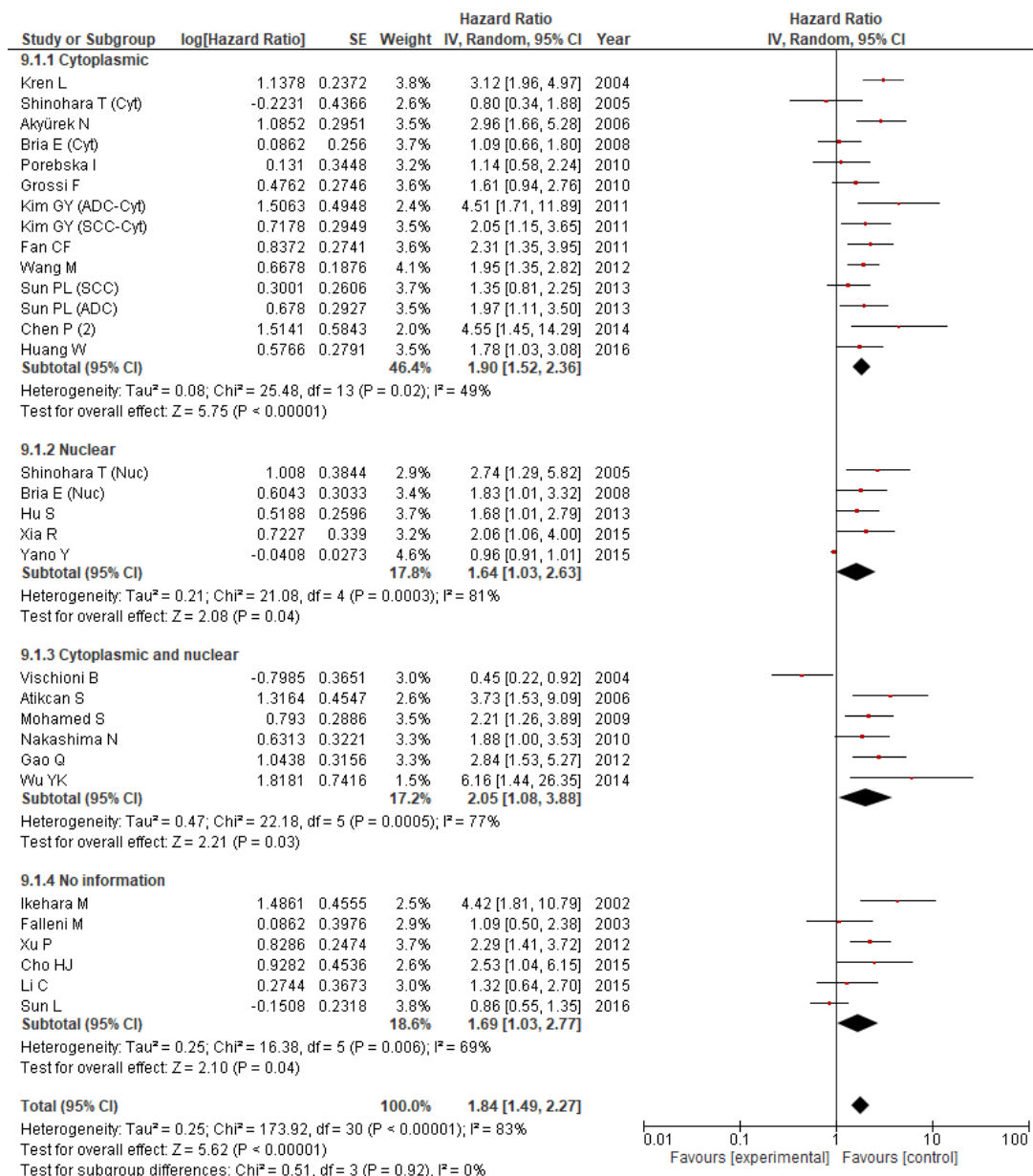


Figure S1. Meta-analysis comparing the subcellular expression of survivin with OS in patients with lung cancer. Forest plot reflects the individual and pooled HR with 95% CI. Heterogeneity was quantified by the Cochrane Q test (Chi-squared test; χ^2) and inconsistency (I^2).

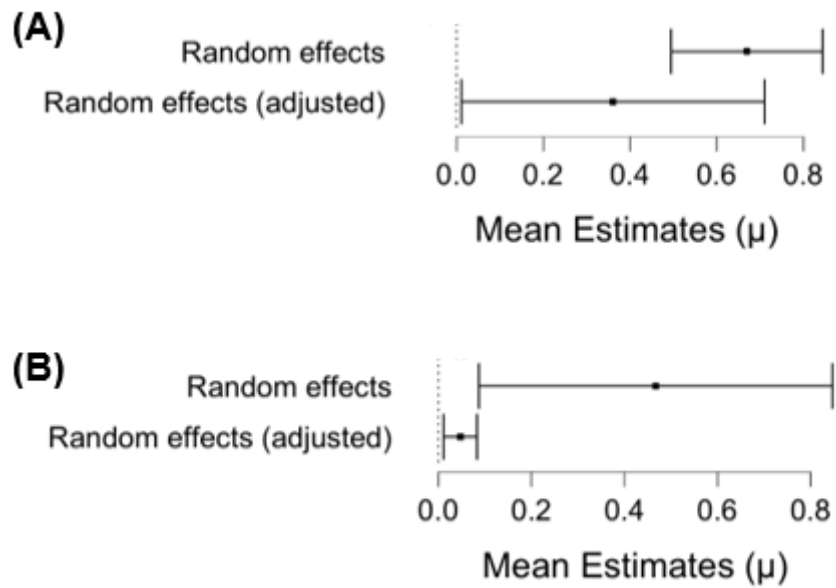


Figure S2. Comparison of effect size estimates of the adjusted/unadjusted random effects model for the association of survivin expression and (A) OS or (B) DFS. After adjusting for publication bias the estimated effect sizes are still statistically significant. Mean estimates (μ) corresponds to the log [Hazard Ratio].

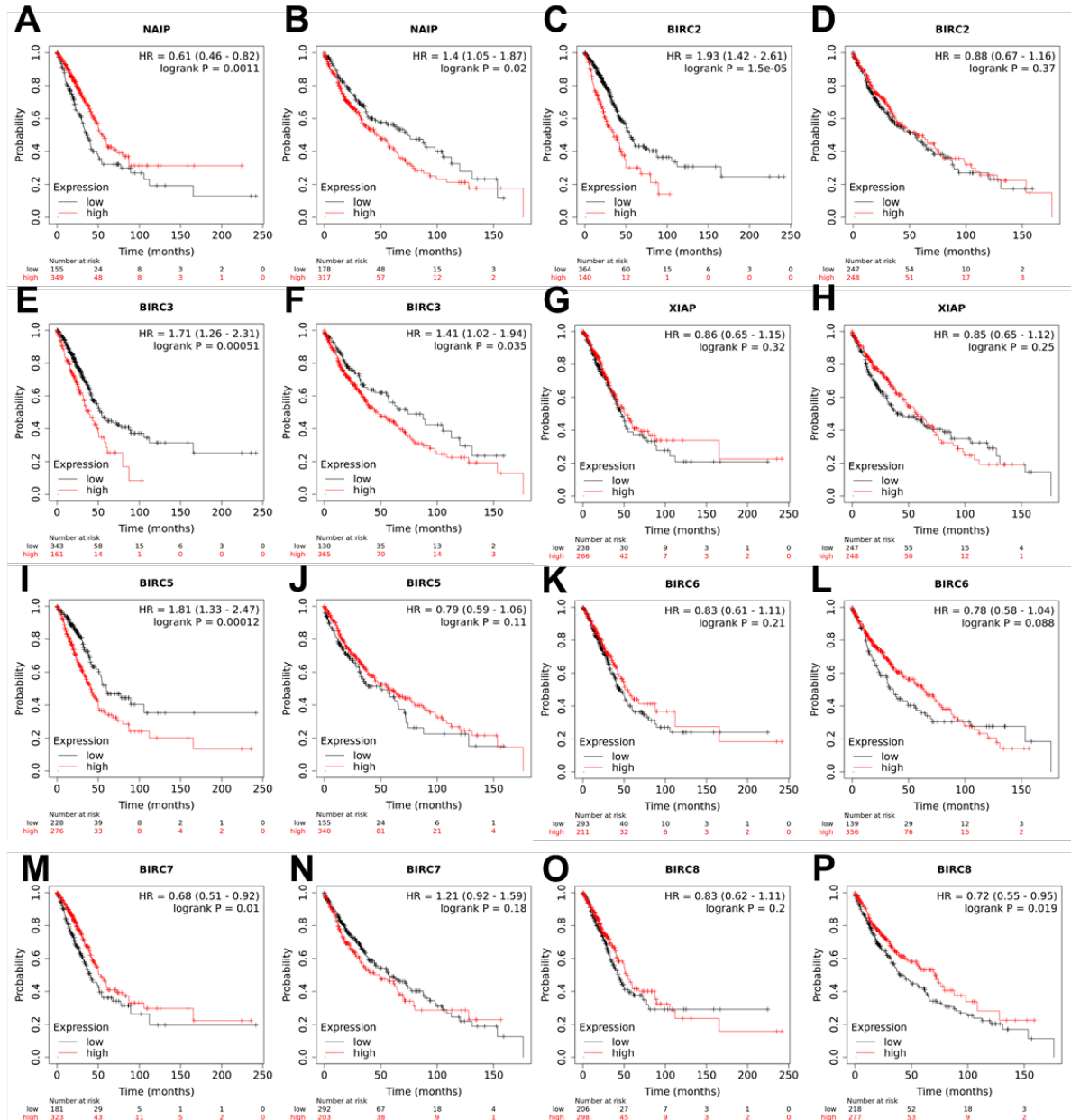


Figure S3. Kaplan-Meier curves for overall survival (OS) in lung cancer patients depending on the IAP/BIRC family member. The TCGA dataset was used to analyse the expression of (A, B) NAIP/BIRC1, (C, D) cIAP1/BIRC2, (E, F) cIAP2/BIRC3, (G, H) XIAP/BIRC4, (I, J) survivin/BIRC5, (K, L) BRUCE/BIRC6, (M, N) livin/BIRC7 and (O, P) Ts-IAP/BIRC8 in (A, C, E, G, I, K, M, O) lung adenocarcinoma (LUAD) or (B, D, F, H, J, L, N, P) lung squamous cell carcinoma (LUSC).

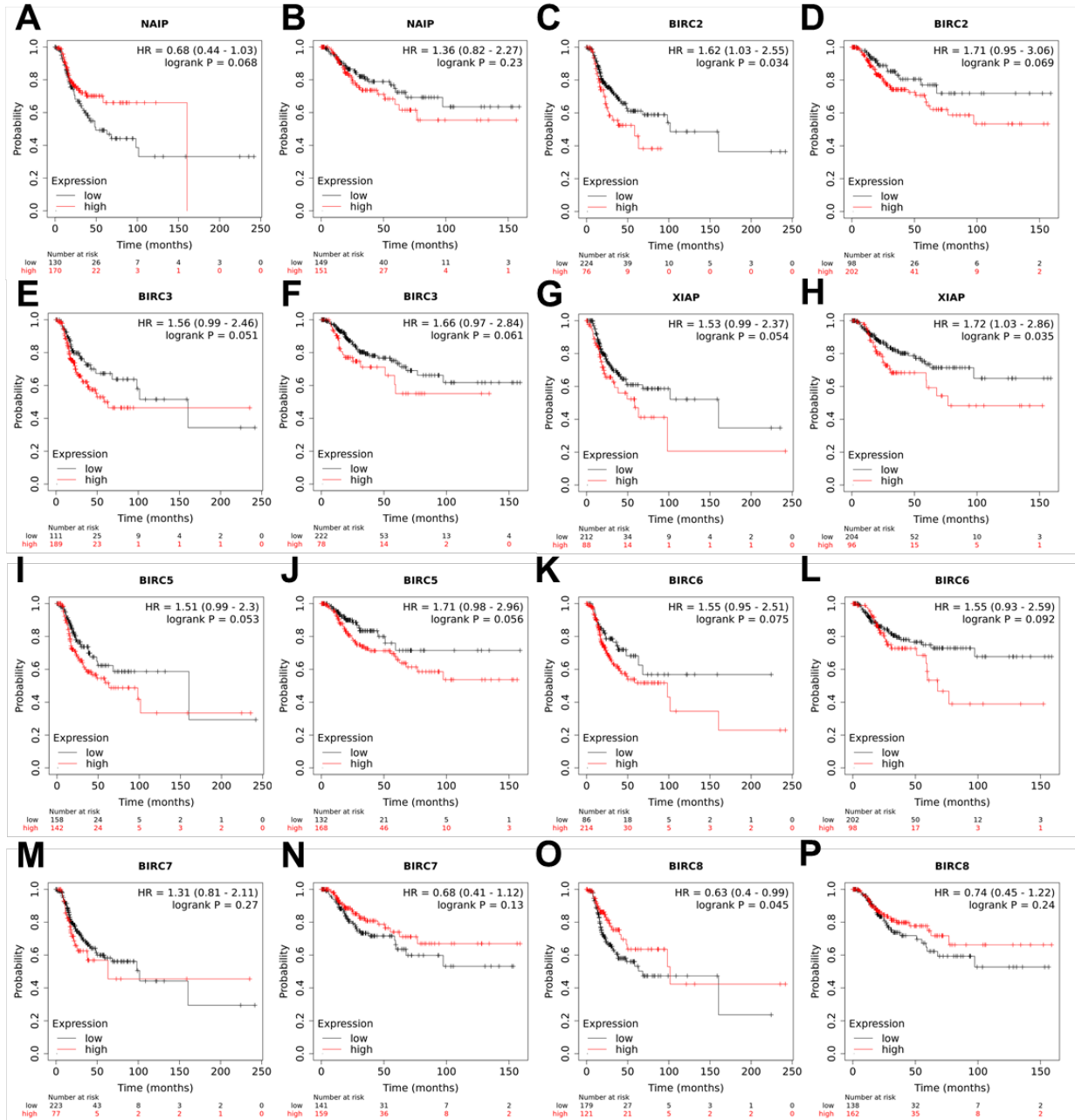


Figure S4. Kaplan-Meier curves for disease free survival (DFS) in lung cancer patients depending on the IAP/BIRC family member. The TCGA dataset was used to analyse the expression of (A, B) NAIP/BIRC1, (C, D) cIAP1/BIRC2, (E, F) cIAP2/BIRC3, (G, H) XIAP/BIRC4, (I, J) survivin/BIRC5, (K, L) BRUCE/BIRC6, (M, N) livin/BIRC7 and (O, P) Ts-IAP/BIRC8 in (A, C, E, G, I, K, M, O) lung adenocarcinoma (LUAD) or (B, D, F, H, J, L, N, P) lung squamous cell carcinoma (LUSC).