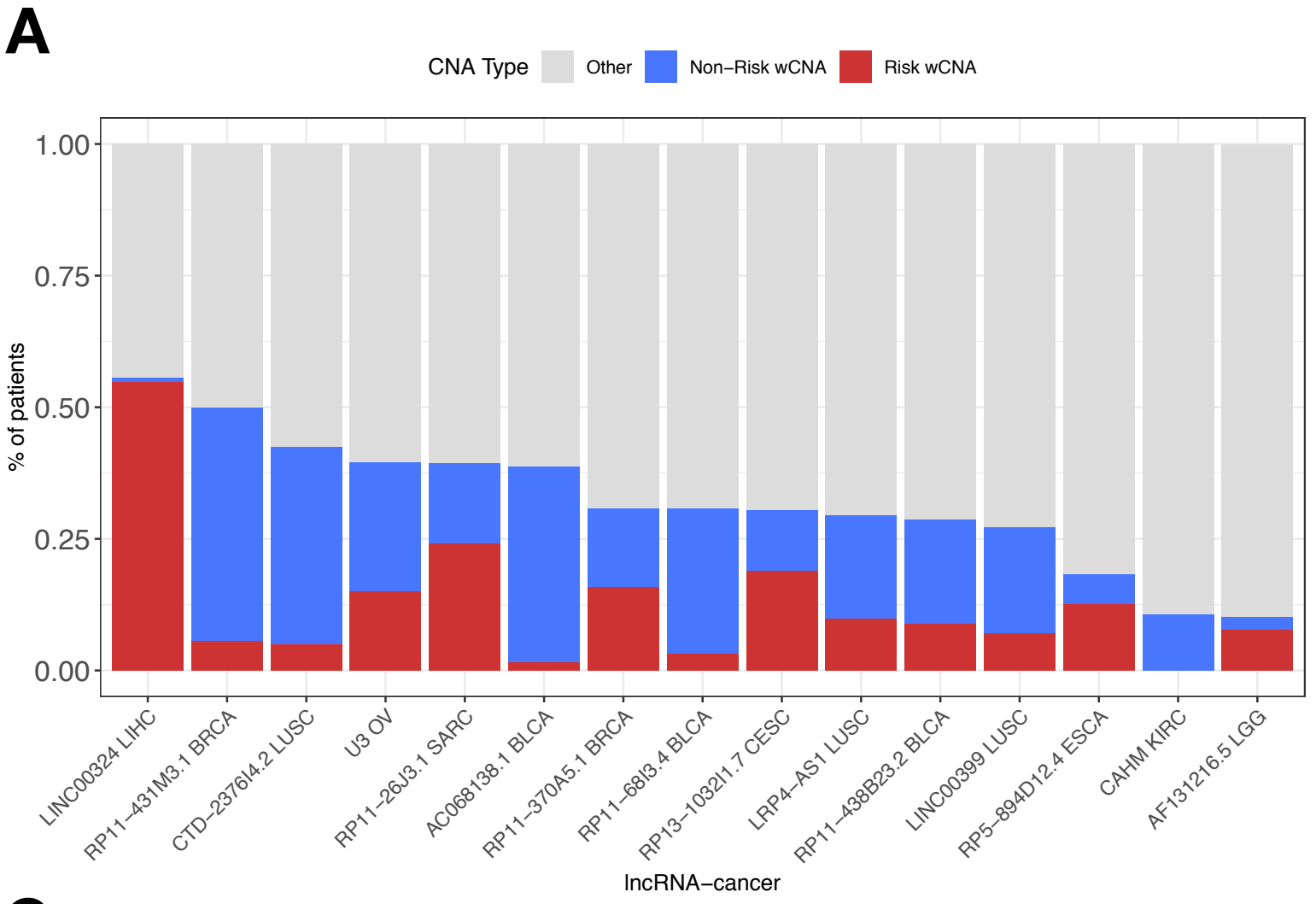

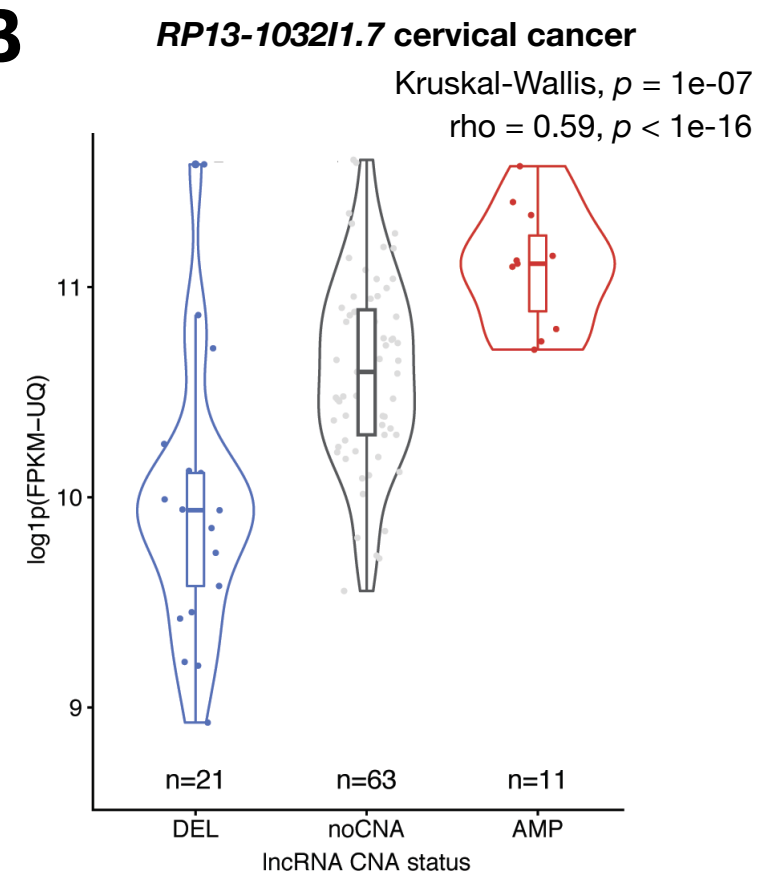

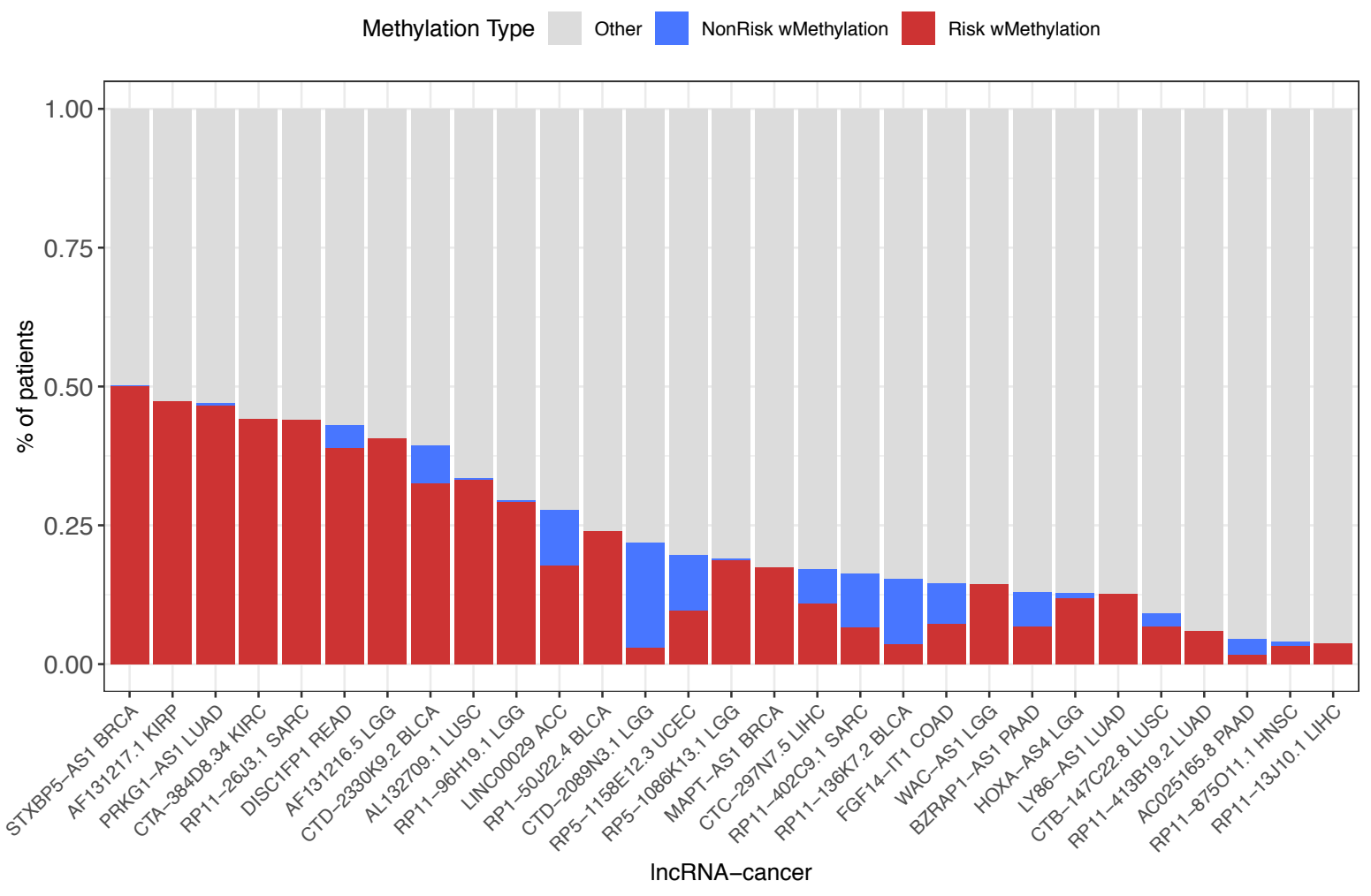

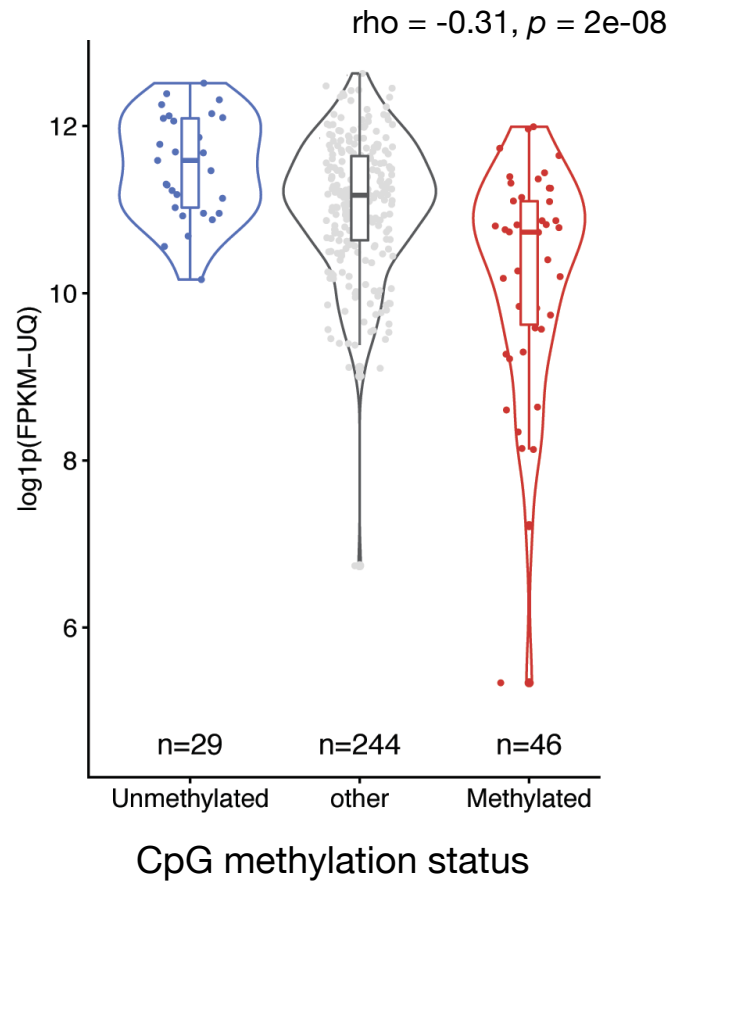

Fig 13. Copy number aberrations and epigenetic differences in lncRNA defined risk groups. (**A**) Summary of 15 lncRNA candidates whose expression was significantly associated with underlying SCNAs (adjusted p-value < 0.05). (**B**) *RP13-1032I1.7* lncRNA abundance between patients with varying levels of copy number aberrations in cervical cancer. DEL = detected detection (segment mean < 0.3), noCNA = neutral segment, AMP = detected amplification (segment mean > 0.3). (**C**) Summary of 29 lncRNA candidates significantly associated with probe methylation in promoters or gene bodies (adjusted p-value < 0.05). Risk wMethylation = risk patients with a significant correlation between probe methylation and lncRNA abundance, NonRisk wMethylation = non-risk patients with a significant correlation between probe methylation and lncRNA abundance. Other = all remaining patients with no significant association between probe methylation lncRNA abundance. (**D**) *CTC-297N7.5* lncRNA abundance between patients with varying levels of probe methylation in liver cancer. Unmethylated = probe with beta value less than 0.25, methylated = probe with beta value greater than 0.75 and other = patients with probe beta value between 0.25 and 0.75.

_RP13-1032I1.7_ cervical cancer