

Figure S1 Investigation of the expression of the 3-RNA prognostic risk model in GEO and another 22 TCGA cancer types. Expression data of miR-130a-3p were not available for SARC. *, P<0.05; **, P<0.01; ***, P<0.001, ****, P<0.0001; ns, not significant. HMGB3, high mobility group-box 3; HOTAIR, HOX antisense intergenic RNA; GEO, Gene Expression Omnibus; BLCA, bladder urothelial carcinoma; BRCA, breast invasive carcinoma; CESC, cervical squamous cell carcinoma and endocervical adenocarcinoma; CHOL, cholangiocarcinoma; COAD, colon adenocarcinoma; ESCA, esophageal carcinoma; HNSC, head and neck squamous cell carcinoma; KICH, kidney chromophobe; KIRC, kidney renal clear cell carcinoma; KIRP, kidney renal papillary cell carcinoma; LIHC, liver hepatocellular carcinoma; LUAD, lung adenocarcinoma; LUSC, lung squamous cell carcinoma; PAAD, pancreatic adenocarcinoma; PCPG, pheochromocytoma and paraganglioma; PRAD, prostate adenocarcinoma; READ, rectum adenocarcinoma; SARC, sarcoma; SKCM, skin cutaneous melanoma; STAD, stomach adenocarcinoma; THCA, thyroid carcinoma; THYM, thymoma; UCEC, uterine corpus endometrial carcinoma; TCGA, The Cancer Genome Atlas.

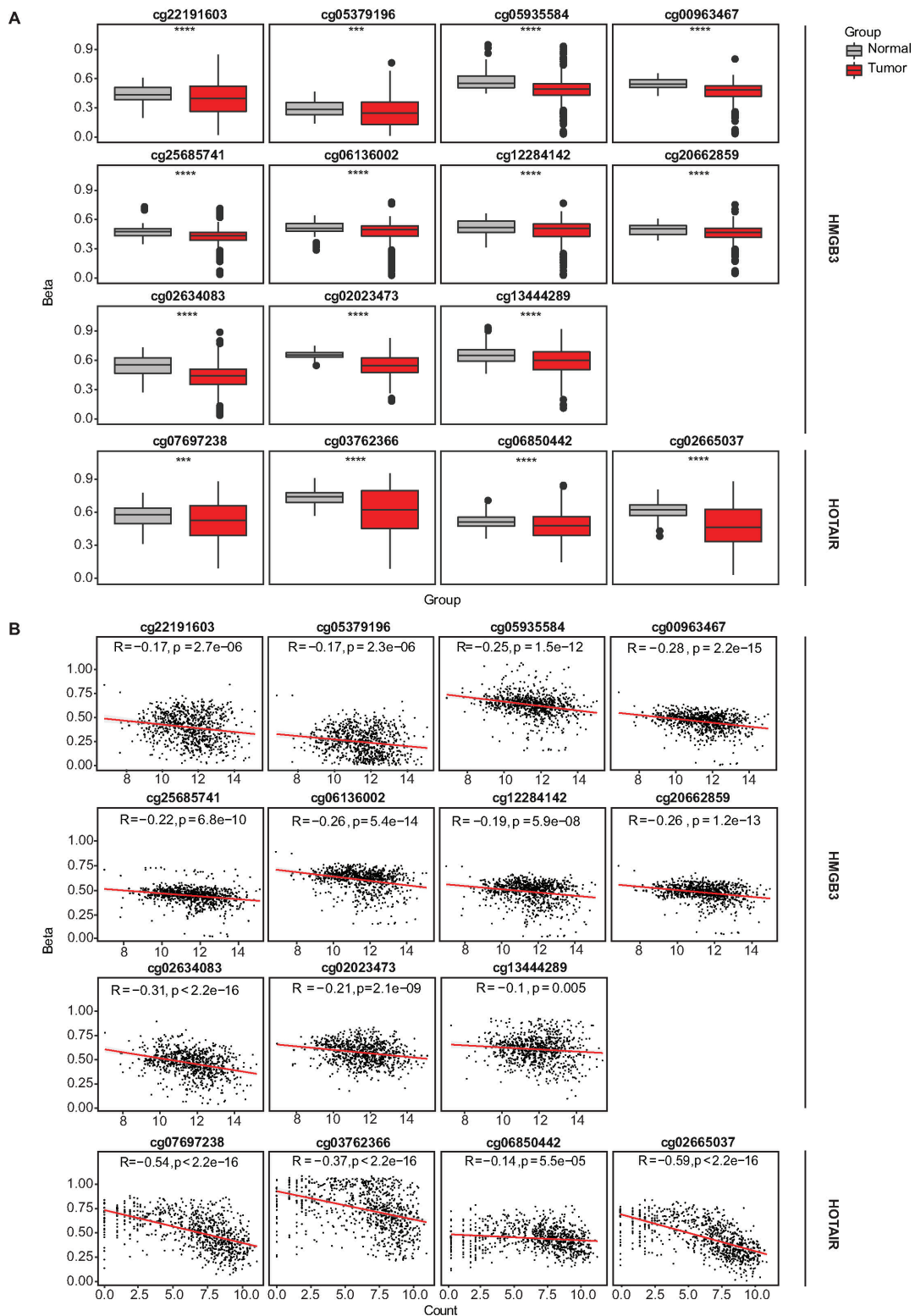


Figure S2 Investigation of the methylation level of mRNA and lncRNA in the prognostic risk model. (A) The difference of methylation level the between tumor and normal tissues. (B) The correlation of the methylation level and RNA expression. ***, $P < 0.001$; ****, $P < 0.0001$. HMGB3, high mobility group-box 3; HOTAIR, HOX antisense intergenic RNA; mRNA, messenger RNA; lncRNA, long non-coding RNA.