**Supplementary Figures**

*Please see uploaded Supplementary Data.*

**Supplementary Figure S1.** ACC-TCGA patients with CIMP-low or CIMP-intermediate tumor status exhibit indistinguishable disease kinetics, while patients with CIMP-high tumor status have deadly disease course. See “Supplement\_Figs1-7-v2.pdf”.

**Supplementary Figure S2.** Schematic of the *G0S2* locus.See “Supplement\_Figs1-7-v2.pdf”.

**Supplementary Figure S3.** *G0S2* is highly expressed in the human adrenal gland.See “Supplement\_Figs1-7-v2.pdf”.

**Supplementary Figure S4.** Unsupervised hierarchical clustering of *G0S2* CpG island methylation enables identification of CIMP-high ACC.See “Supplement\_Figs1-7-v2.pdf”.

**Supplementary Figure S5.** *G0S2* hypermethylation is exclusive to malignant adrenocortical tumors and can be reliably measured by EpiTect.See “Supplement\_Figs1-7-v2.pdf”.

**Supplementary Figure S6.** *G0S2* expression/methylation ROC curve. See “Supplement\_Figs1-7-v2.pdf”.

**Supplementary Figure S7.** *BUB1B-PINK1* score can predict metastasis in *G0S2* Unmethylated ACC.See “Supplement\_Figs1-7-v2.pdf”.

**Supplementary Tables**

*Please see uploaded Supplementary Data.*

**Supplementary Table S1.** Results of differentially expressed genes analysis on ACC-TCGA CIMP-high v. non-CIMP-high and results of gene ontology analysis on ACC-TCGA CIMP-high v. non-CIMP-high. See “Supplement\_Table1.xlsx”.

**Supplementary Table S2.** Results of DMRcate analysis on ACC-TCGA non-CIMP-high v. CIMP-high. See “Supplement\_Table2.xlsx”.

**Supplementary Table S3.** *G0S2* hypermethylation predicts CIMP-high. See “Supplement\_Table34678.pdf”.

**Supplementary Table S4.** Clinical characteristics of FMUSP+UM ACC and ACA Cohorts. See “Supplement\_Table34678.pdf”.

**Supplementary Table S5.** Results of *G0S2* targeted bisulfite sequencing. See “Supplement\_Table5.xlsx”.

**Supplementary Table S6.** EpiTect accurately measures binary *G0S2* methylation status. See “Supplement\_Table34678.pdf”.

**Supplementary Table S7.** Hypermethylation and silencing of *G0S2* is heterogeneous in recurrent, metastatic, and non-treatment naive carcinomas. See “Supplement\_Table34678.pdf”.

**Supplementary Table S8.** *BUB1B-PINK1* can predict any history of metastasis in patients with *G0S2* Unmethylated ACC.See “Supplement\_Table34678.pdf”.

**Supplementary Table S9.** Complete clinical and molecular data of all samples used in this study. See “Supplement\_Table9.xlsx”.