

## COAD - LINC00470 (p-value=3.79e-10)

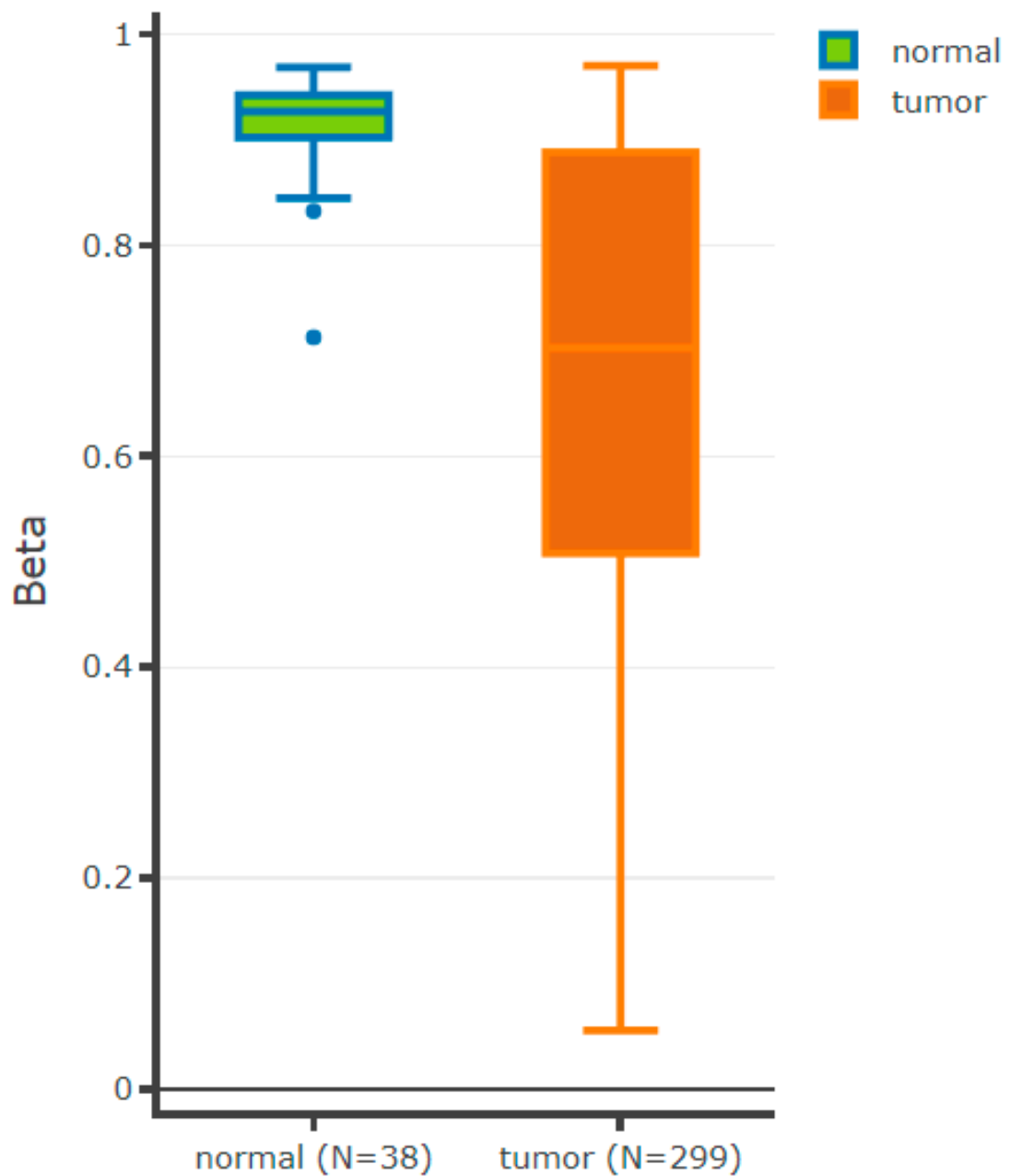


Figure S1-A. Differentially (tumor/normal tissues) methylated promoter region of *LINC00470* found in COAD cohort:  $|\text{beta-value difference}| > 0.2$  and independent Student's t-test adjusted p-value  $\leq 0.05$ ; hypermethylation and hypomethylation, beta-values  $> 0.2$  and  $< -0.2$  at adj. p-value  $\leq 0.05$ , respectively). Differentially methylated genes were explored using DNMIIVD: DNA Methylation Interactive Visualization Database [S1].

## HNSC - LINC00305 (p-value=7.99e-27)

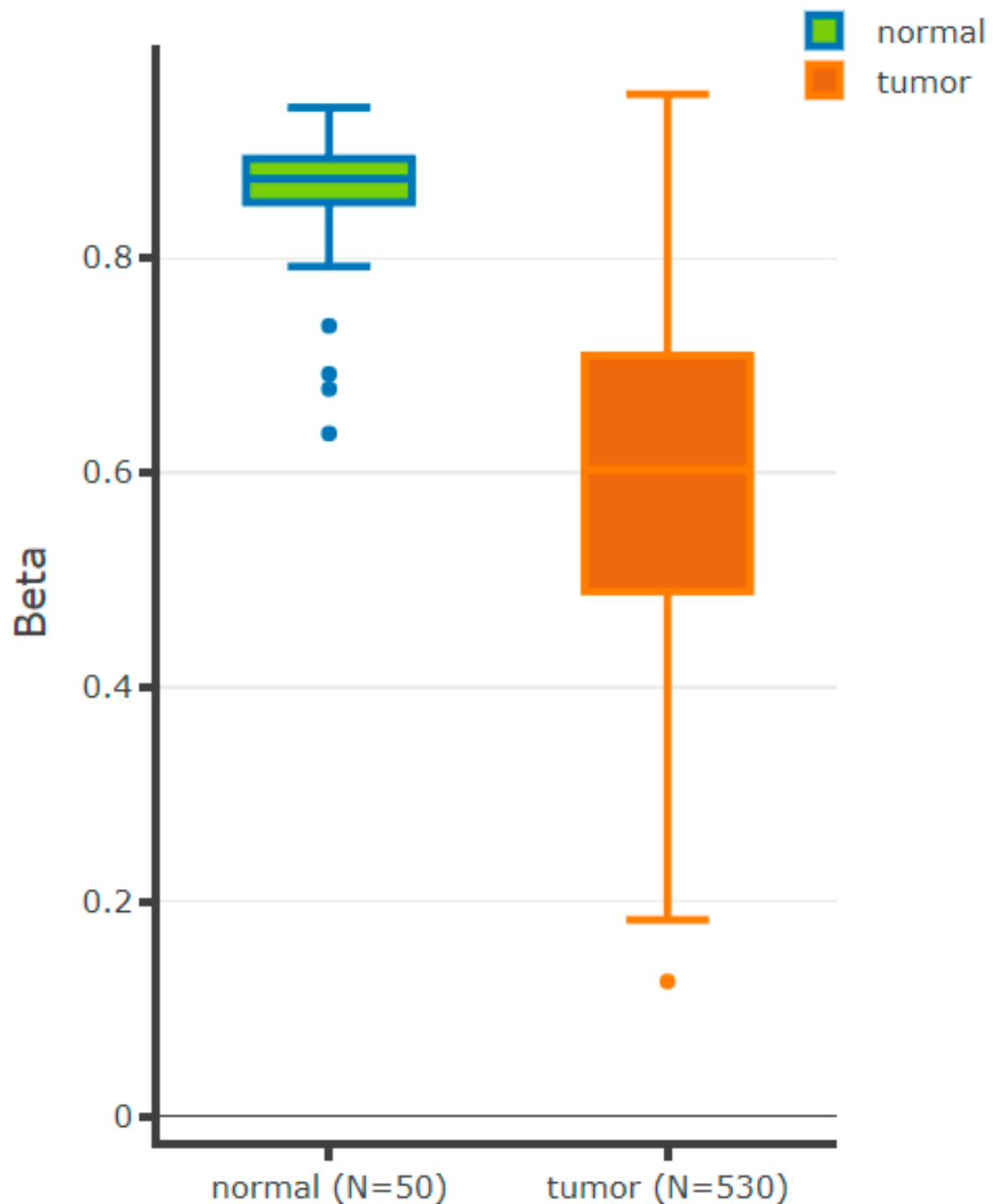


Figure S1-B. Differentially (tumor/normal tissues) methylated promoter region of *LINC00305* found in HNSC cohort:  $|\text{beta-value difference}| > 0.2$  and independent Student's t-test adjusted p-value  $\leq 0.05$ ; hypermethylation and hypomethylation, beta-values  $> 0.2$  and  $< -0.2$  at adj. p-value  $\leq 0.05$ , respectively). Differentially methylated genes were explored using DNMIIVD: DNA Methylation Interactive Visualization Database [S1].

## LIHC - LINC00305 (p-value=2.11e-17)

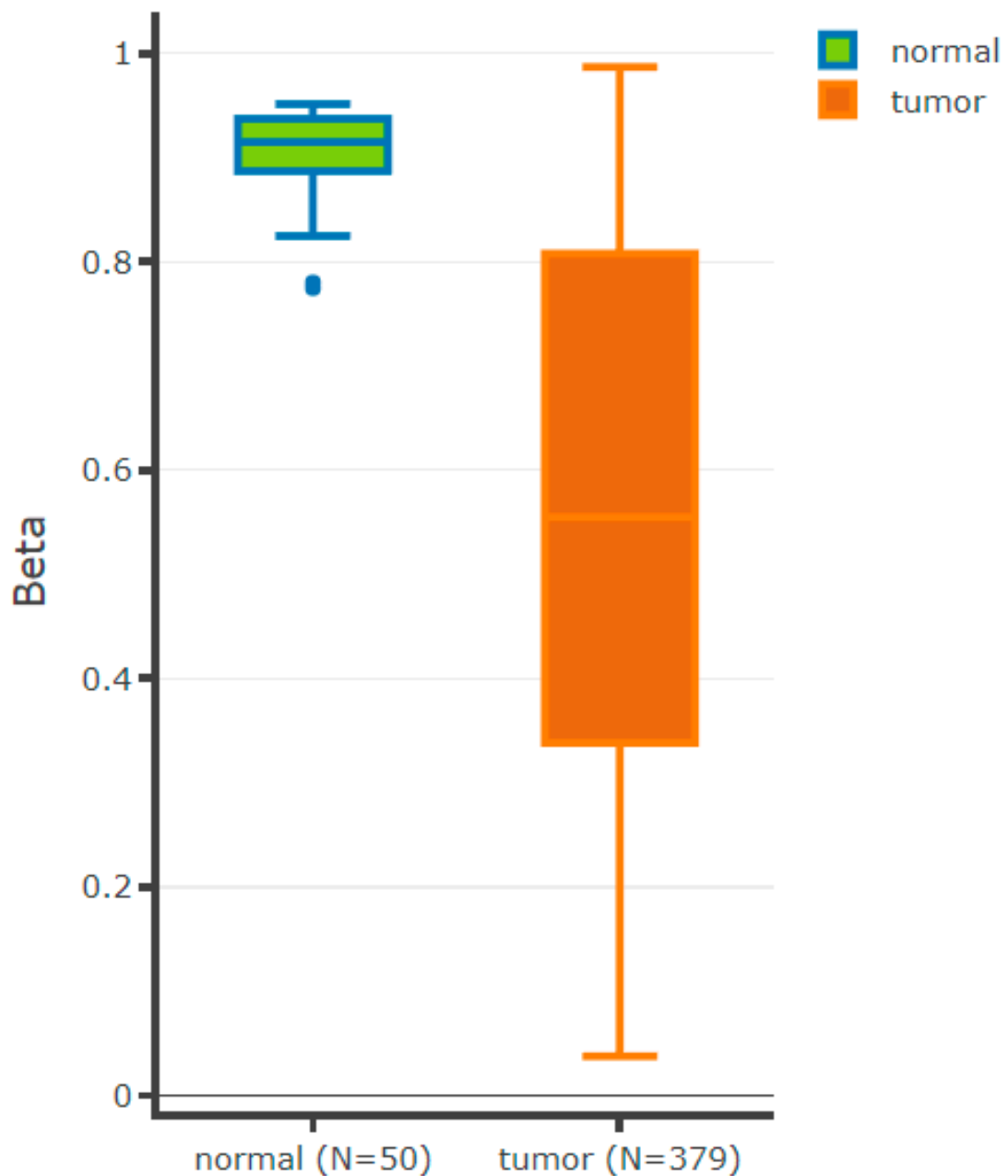


Figure S1-C. Differentially (tumor/normal tissues) methylated promoter region of *LINC00305* found in LIHC cohort:  $|\text{beta-value difference}| > 0.2$  and independent Student's t-test adjusted p-value  $\leq 0.05$ ; hypermethylation and hypomethylation, beta-values  $> 0.2$  and  $< -0.2$  at adj. p-value  $\leq 0.05$ , respectively). Differentially methylated genes were explored using DNMIIVD: DNA Methylation Interactive Visualization Database [S1].

## LUAD - LINC00305 (p-value=9.14e-12)

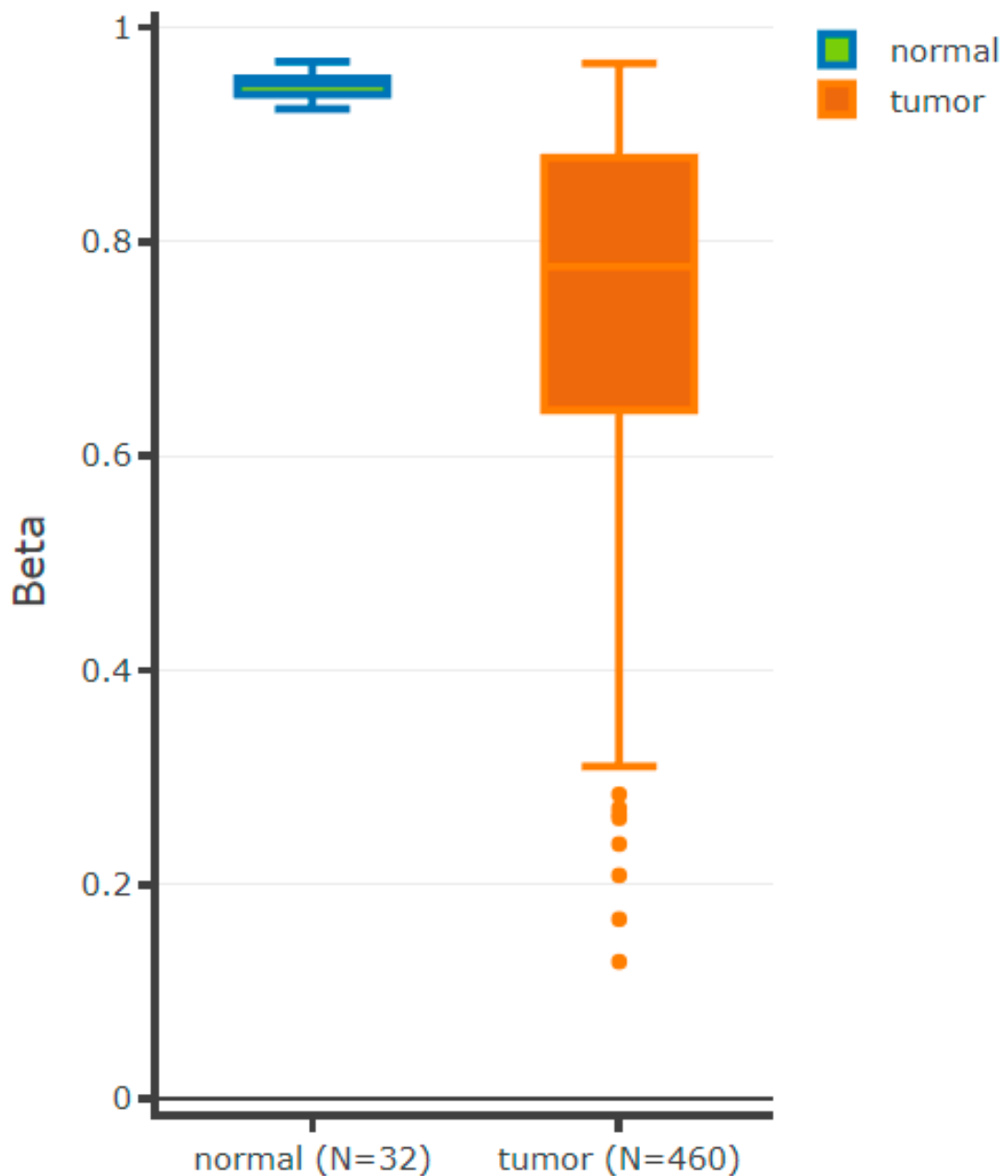


Figure S1-D. Differentially (tumor/normal tissues) methylated promoter region of *LINC00305* found in LUAD cohort:  $|\text{beta-value difference}| > 0.2$  and independent Student's t-test adjusted p-value  $\leq 0.05$ ; hypermethylation and hypomethylation, beta-values  $> 0.2$  and  $< -0.2$  at adj. p-value  $\leq 0.05$ , respectively). Differentially methylated genes were explored using DNMIIVD: DNA Methylation Interactive Visualization Database [S1].

## LUSC - LINC00305 (p-value=2.61e-14)

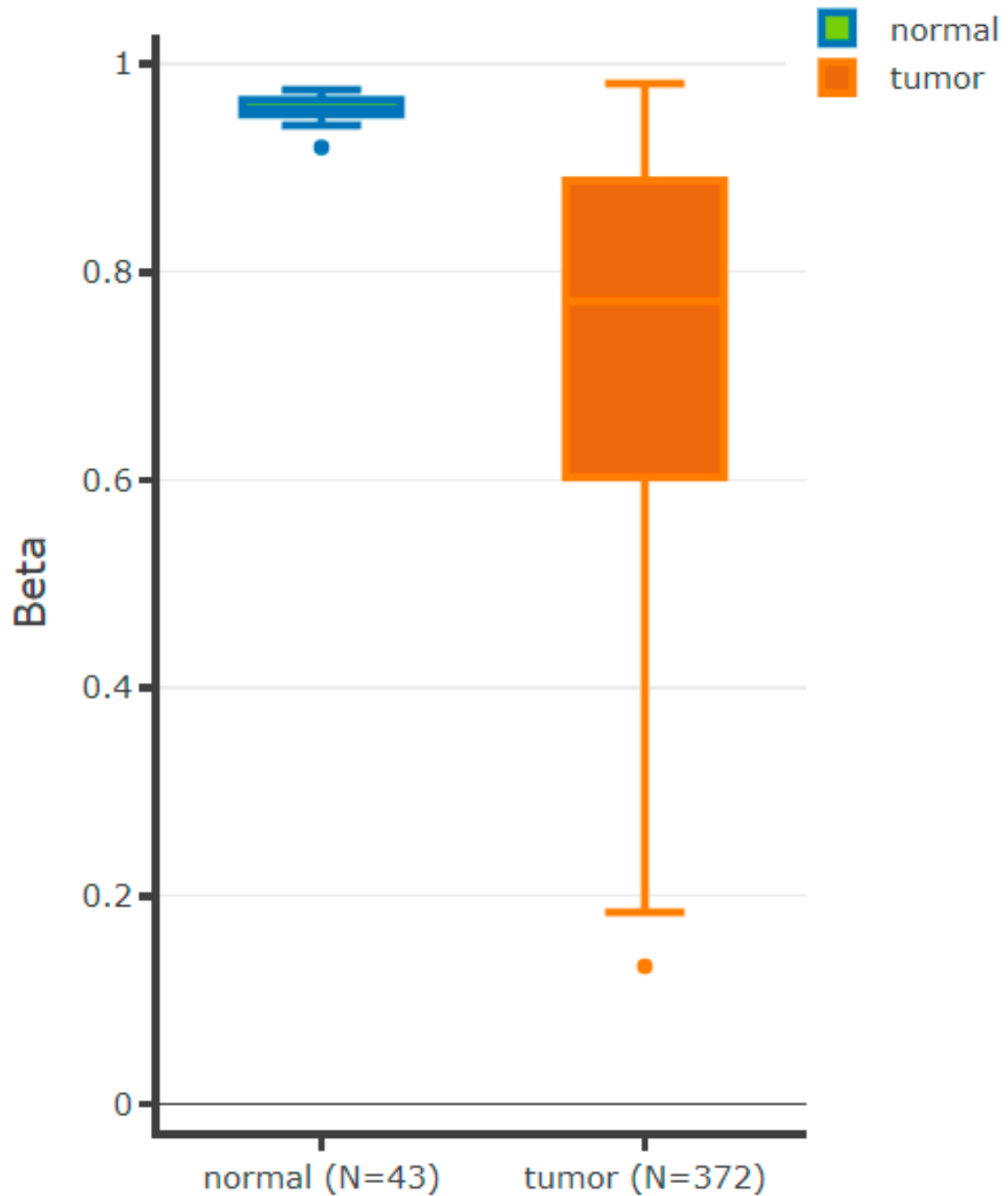


Figure S1-E. Differentially (tumor/normal tissues) methylated promoter region of *LINC00305* found in LUSC cohort:  $|\text{beta-value difference}| > 0.2$  and independent Student's t-test adjusted p-value  $\leq 0.05$ ; hypermethylation and hypomethylation, beta-values  $> 0.2$  and  $< -0.2$  at adj. p-value  $\leq 0.05$ , respectively). Differentially methylated genes were explored using DNMIIVD: DNA Methylation Interactive Visualization Database [S1].

## UCEC - LINC00526 (p-value=2.03e-21)

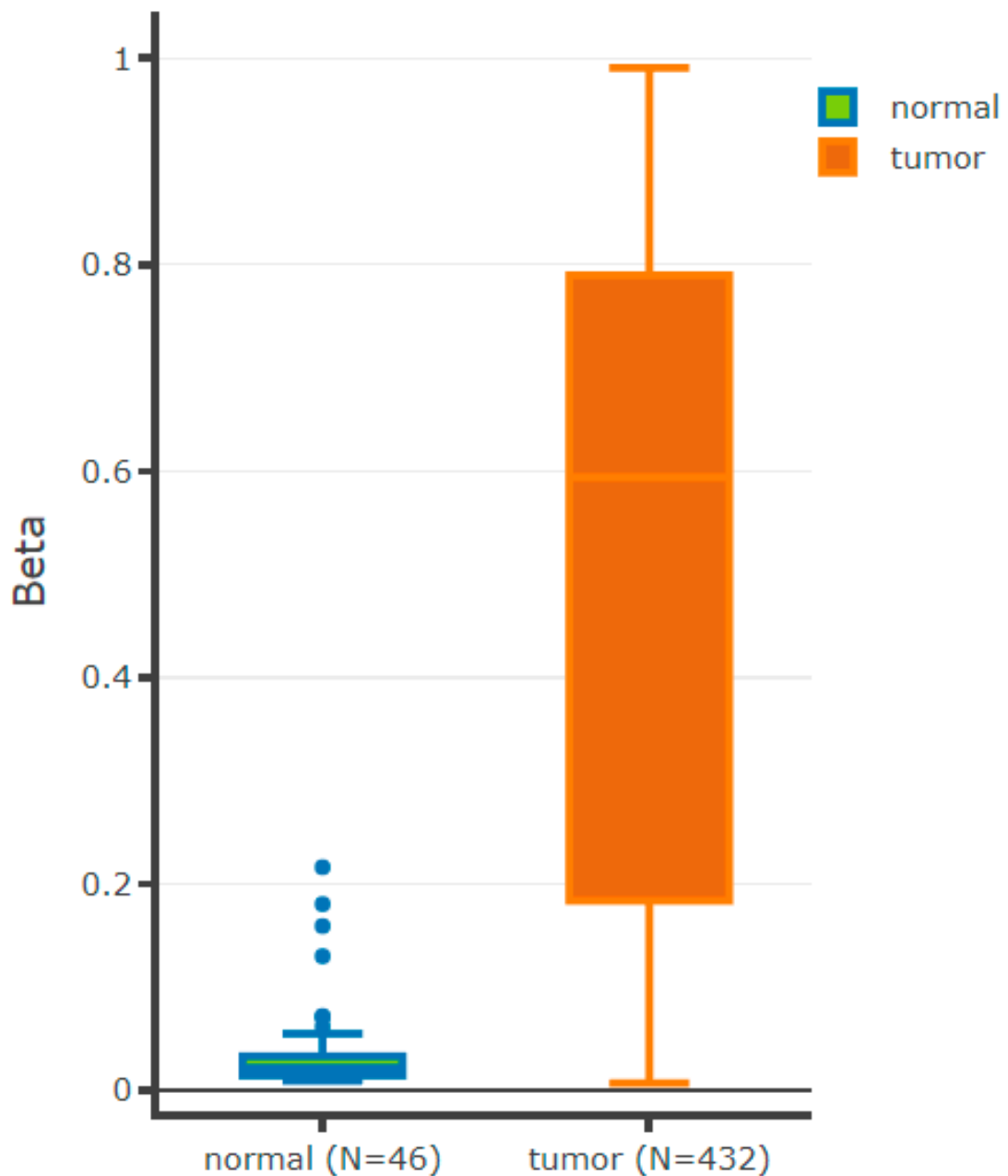


Figure S1-F. Differentially (tumor/normal tissues) methylated promoter region of *LINC00526* found in UCEC cohort: |beta-value difference| > 0.2 and independent Student's t-test adjusted p-value  $\leq 0.05$ ; hypermethylation and hypomethylation, beta-values > 0.2 and  $< -0.2$  at adj. p-value  $\leq 0.05$ , respectively). Differentially methylated genes were explored using DNMIIVD: DNA Methylation Interactive Visualization Database [S1].

### References

[S1] Ding, W.; Chen, J.; Feng, G.; Chen, G.; Wu, J.; Guo, Y.; Ni, X.; Shi, T. DNMIIVD: DNA Methylation Interactive Visualization Database. *Nucleic Acids Res* 2020, 48, D856–D862, doi:10.1093/nar/gkz830