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Supplemental Information

Comprehensive landscape of epigenetic-dysregulated lncRNAs reveals a profound role of enhancers in carcinogenesis in BC subtypes

Hongying Zhao, Xiaoqin Liu, Lei Yu, Shihua Lin, Caiyu Zhang, Haotian Xu, Zhijun Leng, Waidong Huang, Junjie Lei, Tengyue Li, Jing Li, Fan Yang, and Li Wang

Table S1. The forward and reverse primers used for quantitative reverse transcription-polymerase chain reaction

Target genes		Primer sequences
RP1-140K8.5	Forward	5’-ACCTTGGCTGAGTCTTGACA-3’
	Reverse	5’-CAATTCCCACCAGCACGAAC-3’
KB-1836B5.1	Forward	5’-GAGGACCCCAGGTGTGTTTT-3’
	Reverse	5’-GGACCACAACAGTCTCGCTT-3’
CASC11	Forward	5’-GGCCTGTCAAGAGATGAGGT-3’
	Reverse	5’-TCGTTGGAACACATGCTTGG-3’
LINC00393	Forward	5’-CGTTGTTACGACAGCACAGA-3’
	Reverse	5’-TCACTGCAGTTGACCTCCAA-3’
AC005162.1	Forward	5’-CTTTCTCTTCTGACTGTCCAGTGAG-3’
	Reverse	5’-GTTCCCTTAAATTAGCTCCTCTGTC-3’
AC020916.2	Forward	5’-ATCCGTCCAGGCCGACTTCCTAACT-3’
	Reverse	5’-TGCACCTAGAAGCTCTCTTCTGTGG-3’
β-actin	Forward	5’-ATCGTCCACCGCAAATGCTTCTA-3’
	Reverse	5’-AGCCATGCCAATCTCATCTTGTT-3’

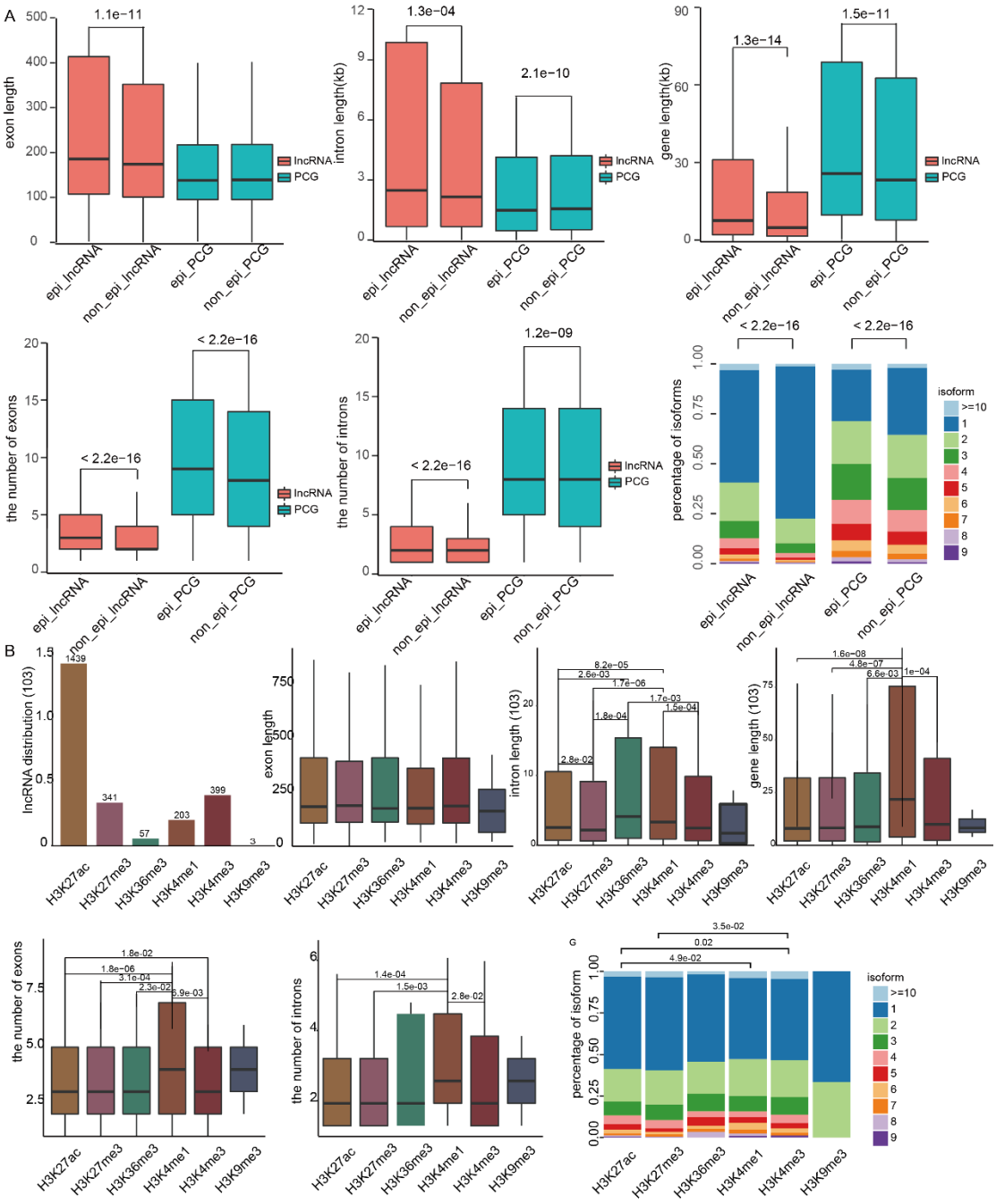

Figure S1. Genomic signatures of epigenetically dysregulated lncRNAs. (A)The comparison of epi-lncRNAs with non-epi-lncRNAs (epi-PCGs with non-epi-PCGs) and (B) comparison among lncRNAs with different aberrant epigenetic modifications in exon length, intron length, overall gene length, exon number, intron number and isoform number. *P* values were calculated by wilcoxon rank sum test.

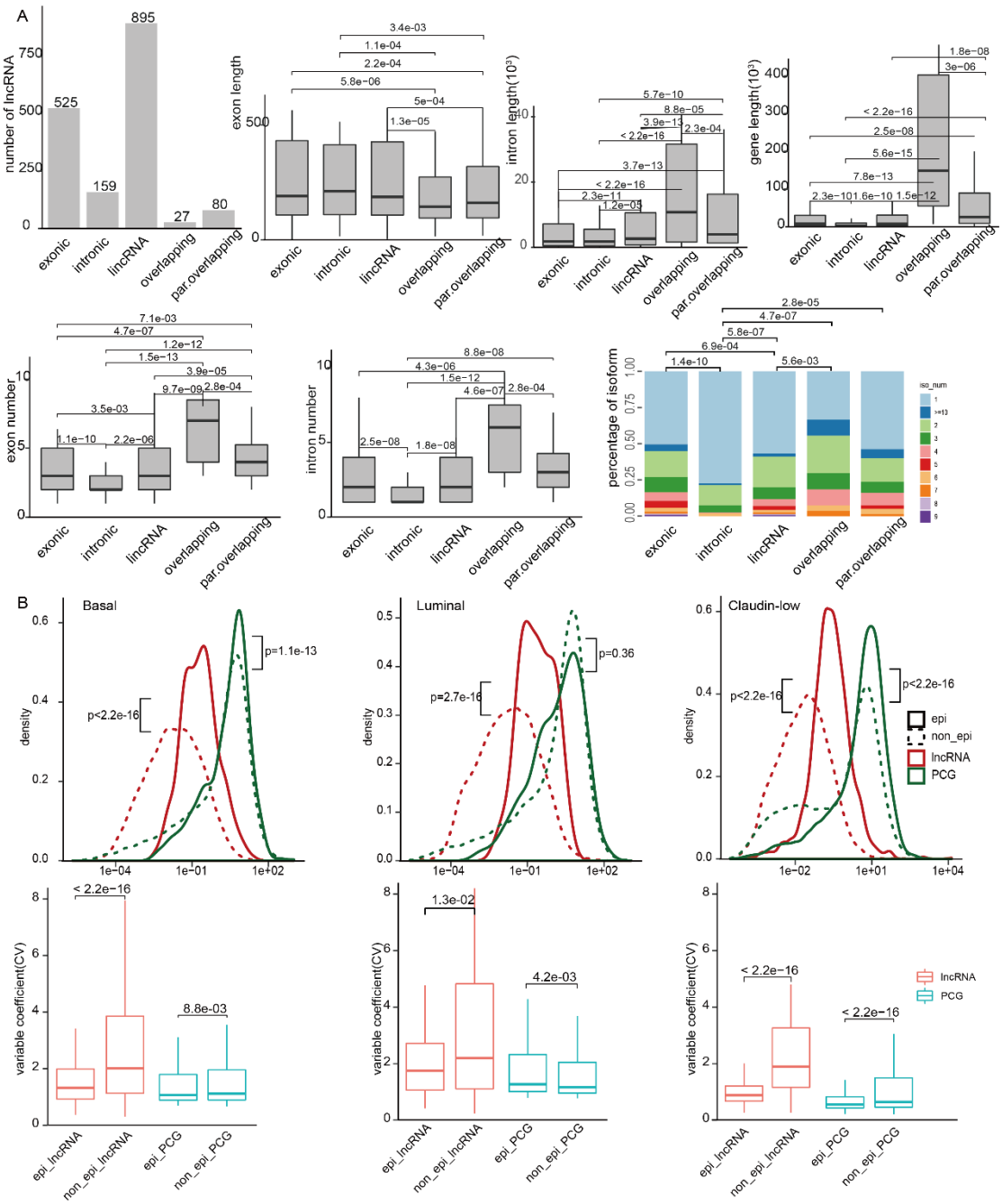

Figure S2. Genomic signatures of epigenetically dysregulated lncRNAs. (A) The comparison of epi-lncRNAs with non-epi-lncRNAs according to five categories in exon length, intron length, overall gene length, exon number, intron number and isoform number. (B) Expression characteristics of epi-lncRNAs. Comparison of average expression and coefficient of variation between epi-lncRNAs with non-epi-lncRNAs (epi-PCGs with non-epi-PCGs) in basal, luminal and claudin-low subtypes. *P* values were calculated by wilcoxon rank sum test.

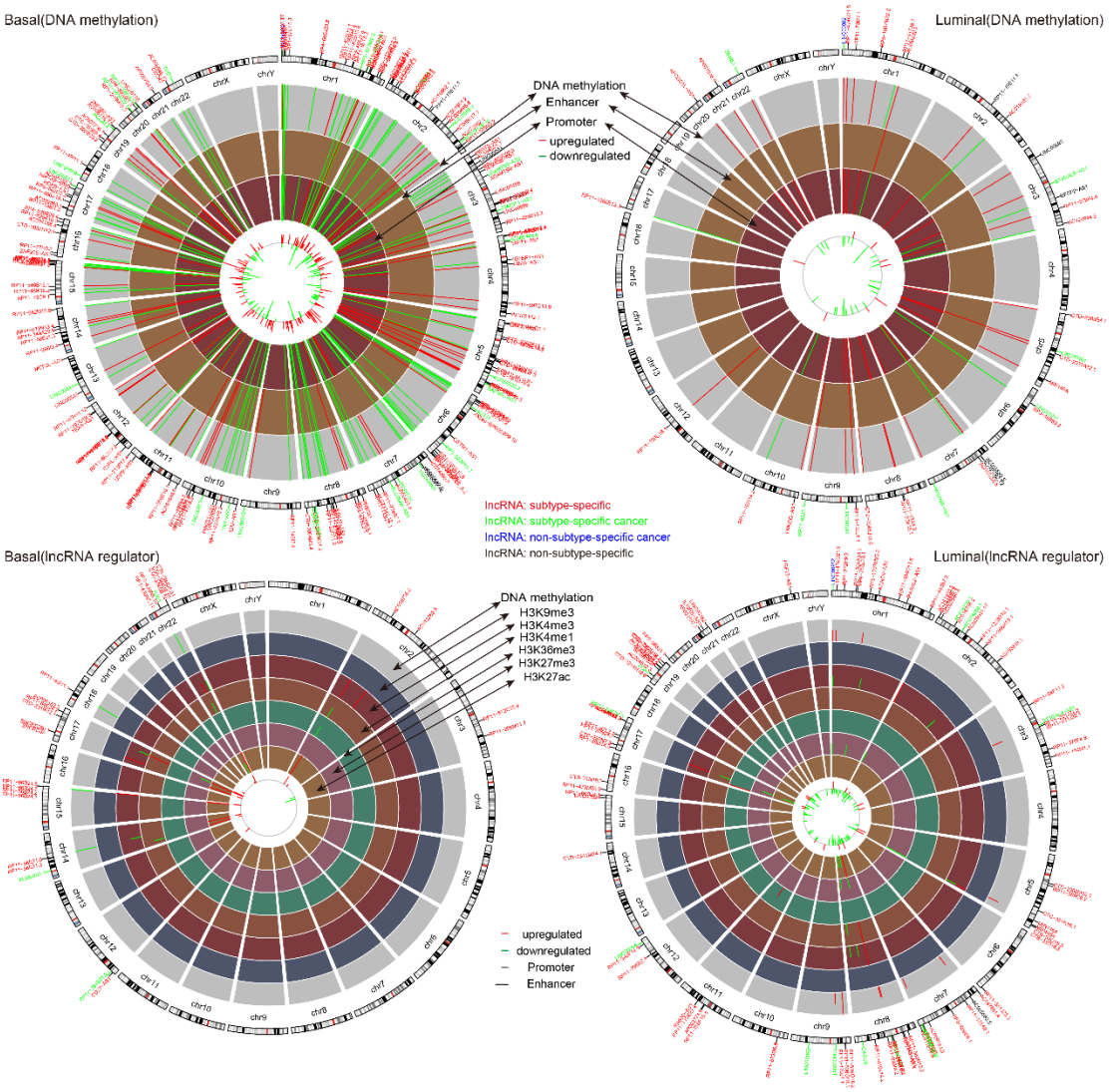

Figure S3. Landscape of DNA methylation-dysregulated lncRNAs and lncRNA regulators in basal subtype and luminal subtype.

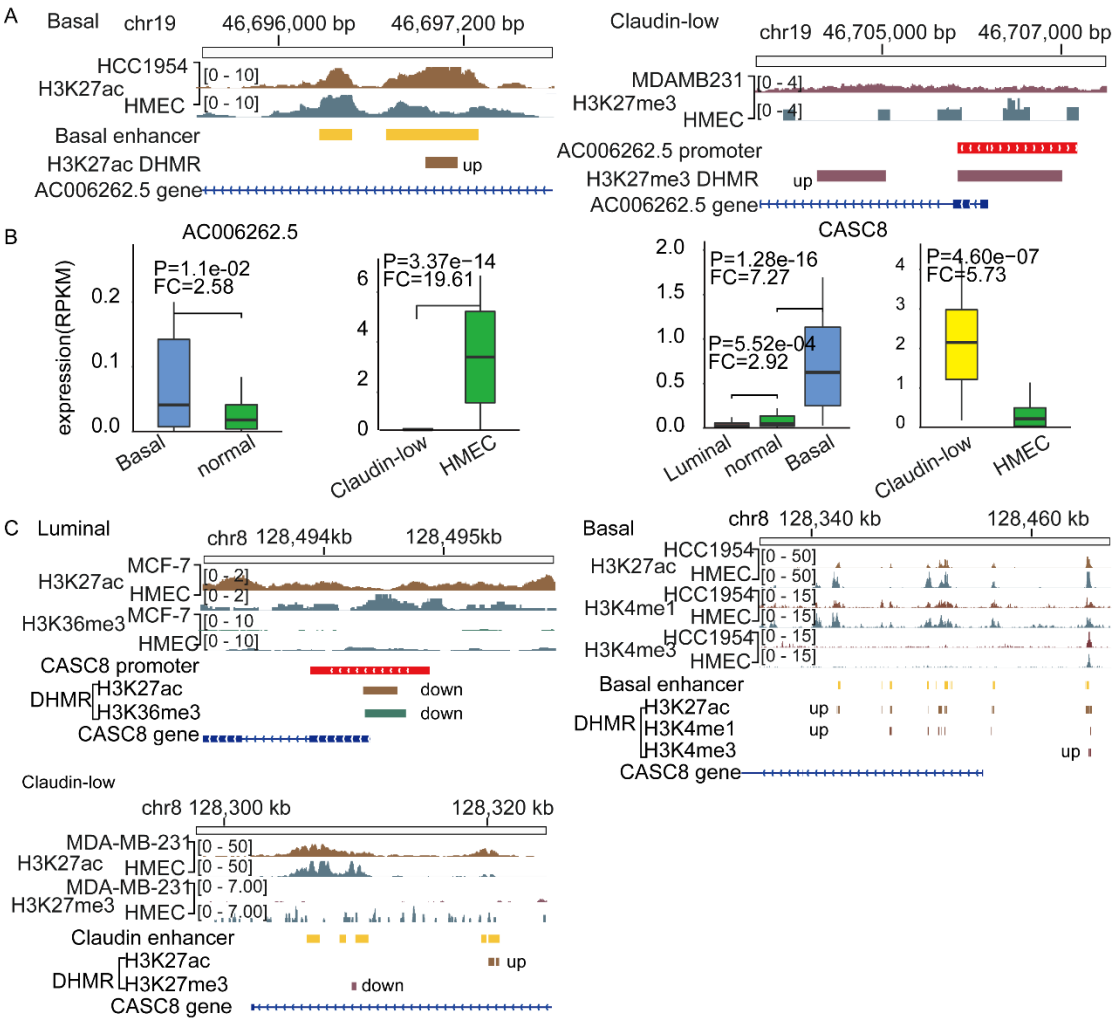

Figure S4. Examples of common epi-lncRNAs in different breast cancer subtypes. (A) Histone modification profile of AC006262.5 shared by basal and claudin-low subtypes. (B) Histone modification profile of CASC8 shared by luminal, basal and claudin-low subtypes. (C) Expression distribution of AC006262.5 and CASC8 in breast cancer and control samples.

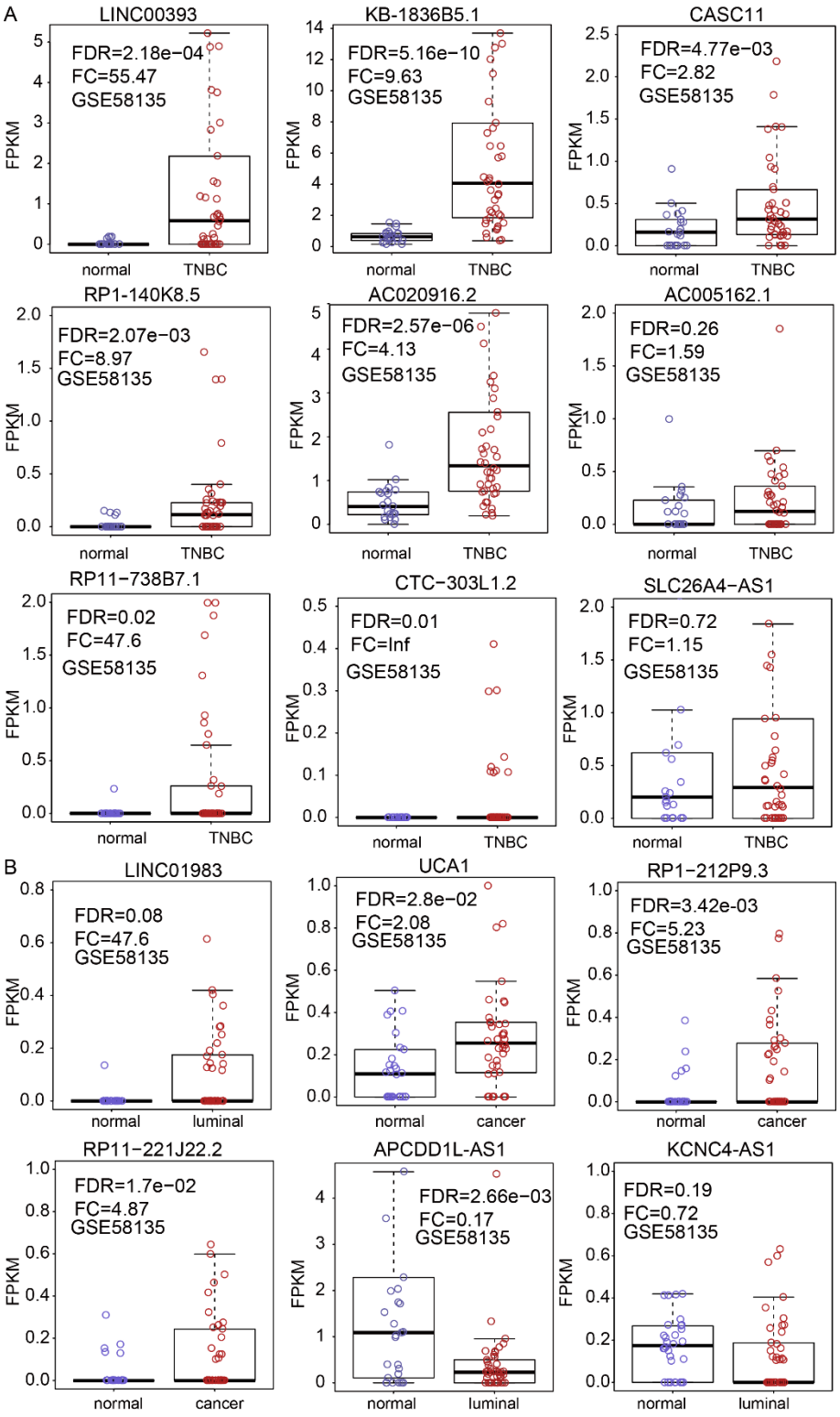

Figure S5. Confirmation of the differential expression of selected lncRNAs in the basal (A) and luminal (B) subtypes of breast cancer.