

1 **Supplemental Figure 1. Maternal licking/grooming behavior during the postnatal period**

2 Mean \pm SEM LG frequency (% of observations) for Low and High LG dams (A) averaged across the first

3 6 days postpartum, (B) on each of the first 6 days postpartum. Mean \pm SEM LG bouts (C) and average

4 LG bout duration (D) on postpartum day 10 by Low and High LG dams. * $p<0.05$, *** $p<0.001$

5

6 **Supplemental Figure 2 Post-translational histone modifications associated with offspring *Esr1***

7 Chromatin immunoprecipitation of the *Esr1* B/1b regulatory region by antibodies against (A) tri-

8 methylated histone H3 lysine 4 (H3K4me3) or (B) tri-methylated histone H3 lysine 9 (H3K9me3). Three

9 regions of the *Esr1* gene were examined for association with each antibody: the B promoter (-219 to -

10 103), the B/1b regulatory region including 6 of the 14 CpG sites analyzed for methylation (+22 to +151),

11 and within the first translated exon (exon 2, +2246 to +2479). Mean \pm SEM % of input among Low and

12 High LG female offspring at PN6, PN21, and PN66. * $p<0.05$, bar indicates main effect of maternal care

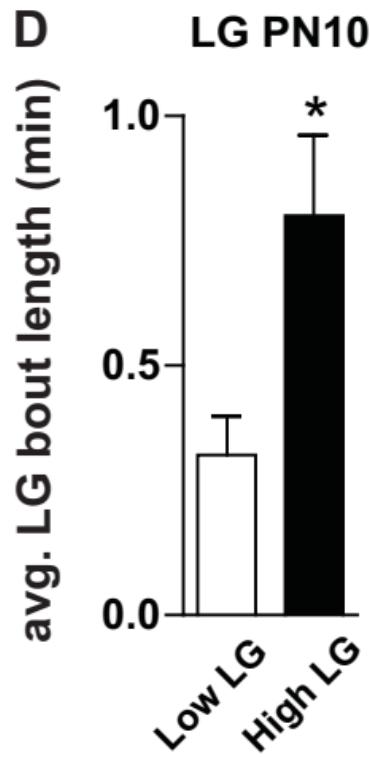
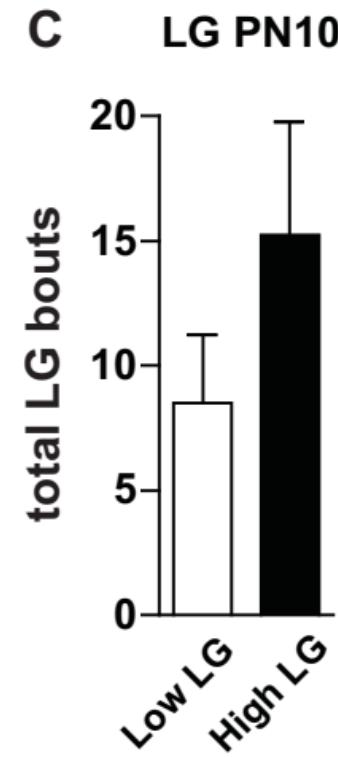
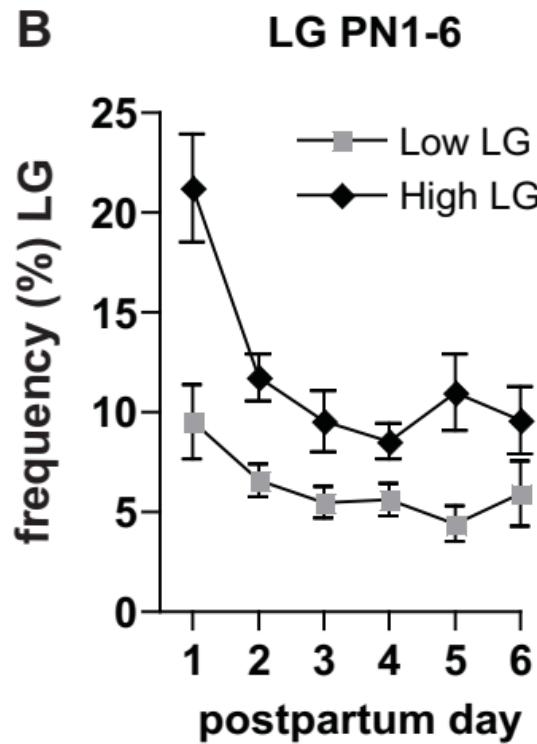
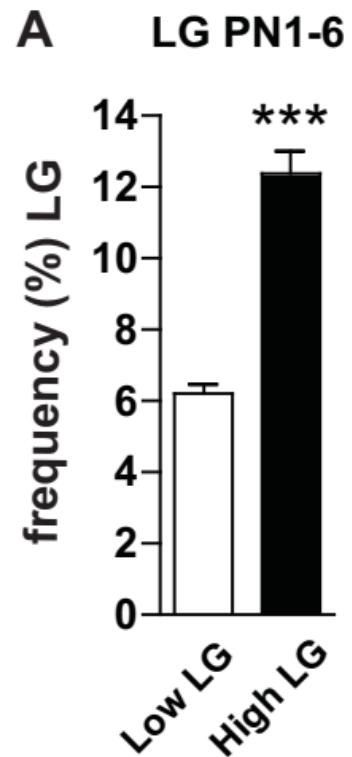
13 across ages

14

Supplemental Table 1

Gene	NCBI #	Forward-sequence	Reverse-sequence
<i>Esr1</i>	NM_012689.1	GCCTTCTACAGGTCCAATTCTGAC	ACAGCACAGTAGCGAGTCTCC
<i>Esr2</i>	NM_012754.1	GCAGAACCTCAAAAGAGTCCTGG	ACGCCGTAATGATAACCCAGATG
<i>Otr</i>	NM_012871	TTCTTCGTGCAGATGTGGAG	GAGCATGTAGATCCACGGGT
<i>Dnmt1</i>	NM_053354.3	GTGGGATGGCTTCTTCAGTA	GGCTTGGTCACAAAACAAAC
<i>Dnmt3a</i>	NM_001003958.1	GGGGCCCCAGCTGAAGGAGA	GCCCCGGGAGCCCTCCATT
<i>CypA</i>	NM_017101	ATGGTCAACCCCACCCTGTTCTC	ATCCTTCTCCCCAGTGCTCAGAG
<i>Actb</i>	NM_031144	ATGGATGACGATATCGCTGCG	GGTGACAATGCCGTGTTCAAT
<i>Esr1</i> 1b upstream	X98236	AGATGGCGCTGGAACCGGAG	TCTGCTGTTGGCTATGTGGCTTGC
<i>Esr1</i> 1b 5'UTR	X98236	CACACACCGCGCCACTCGAT	ACACCGATCCTACCCCTGCTGGT
<i>Esr1</i> exon1	X98236	CCAGGTGGCTCATCCGCTGC	TTGAACACGGCGGGCTTGCT

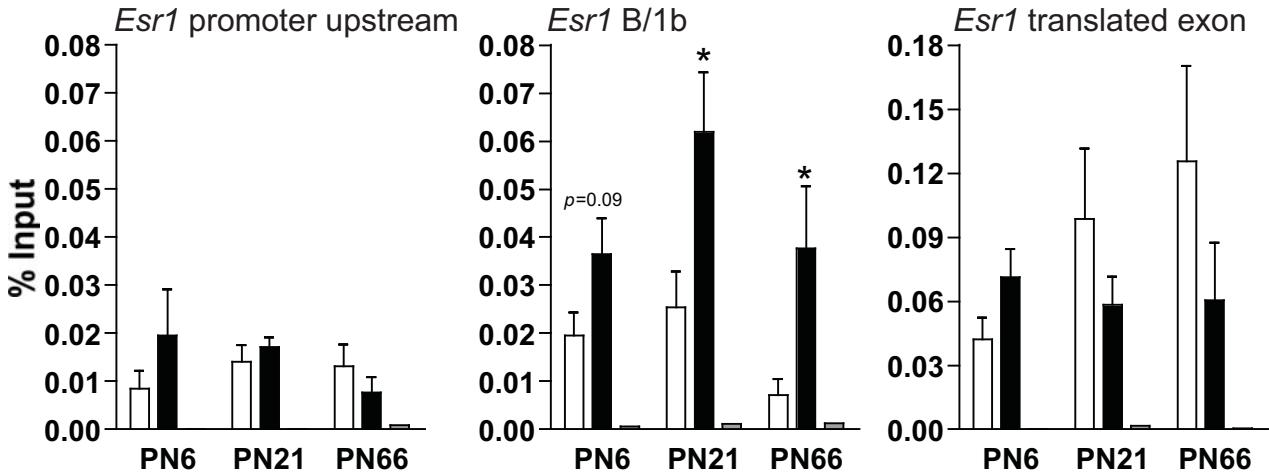
Supplemental Figure 1



Supplemental Figure 2

□ Low LG ■ High LG ▨ No-Ab Control

A H3K4me3



B H3K9me3

