

1 **Supplemental Figure 1:**

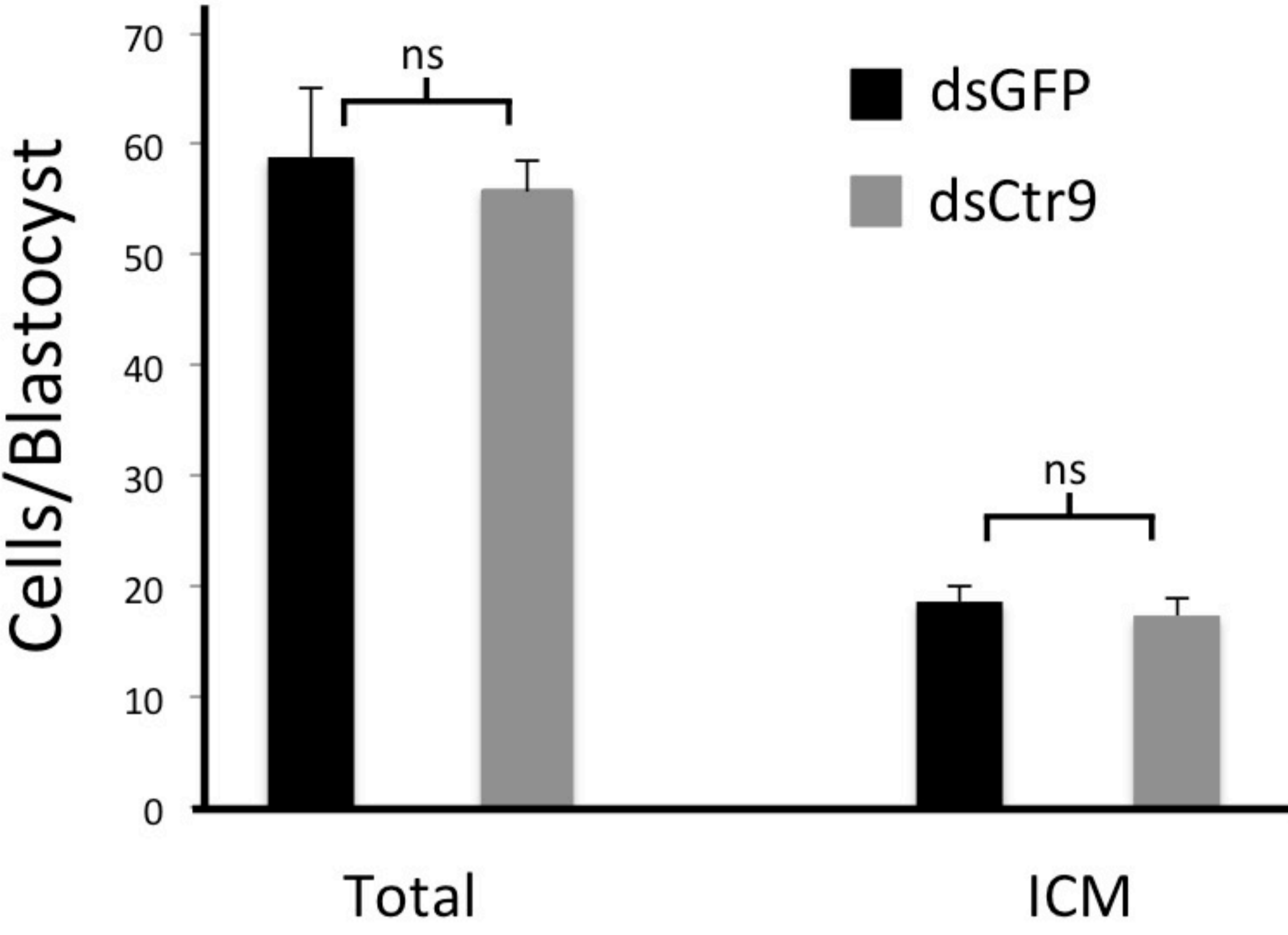
2 A) Analysis of cell number in dsGFP and dsCtr9 embryos. Total cells were counted by DAPI
3 stained nuclei (N=18 dsGFP and 18 dsCtr9) and ICM cells were identified as OCT4 positive
4 (and not on the periphery in dsCTR9, N=10 dsGFP and 10 dsCtr9 blastocysts). These analyses
5 revealed no difference in either total or ICM cell numbers as determined by student's T-test (p-
6 value =0.66 and 0.54, respectively. Error bars represent SEM. B) Bisulfite sequencing of the
7 *Oct4* promoter region using the precise assay in (Hattori et al., 2004) with primers, PRO F, 5'-
8 TGGGTTGAAATATTGGGTTTATTT-3'; PRO R, 5'-CTAAAACCAAATATCCAACCATA-3'
9 revealed no methylation in control dsGFP or dsCtr9 blastocysts. Open circle: unmethylated CpG;
10 Filled circle: methylated CpG.

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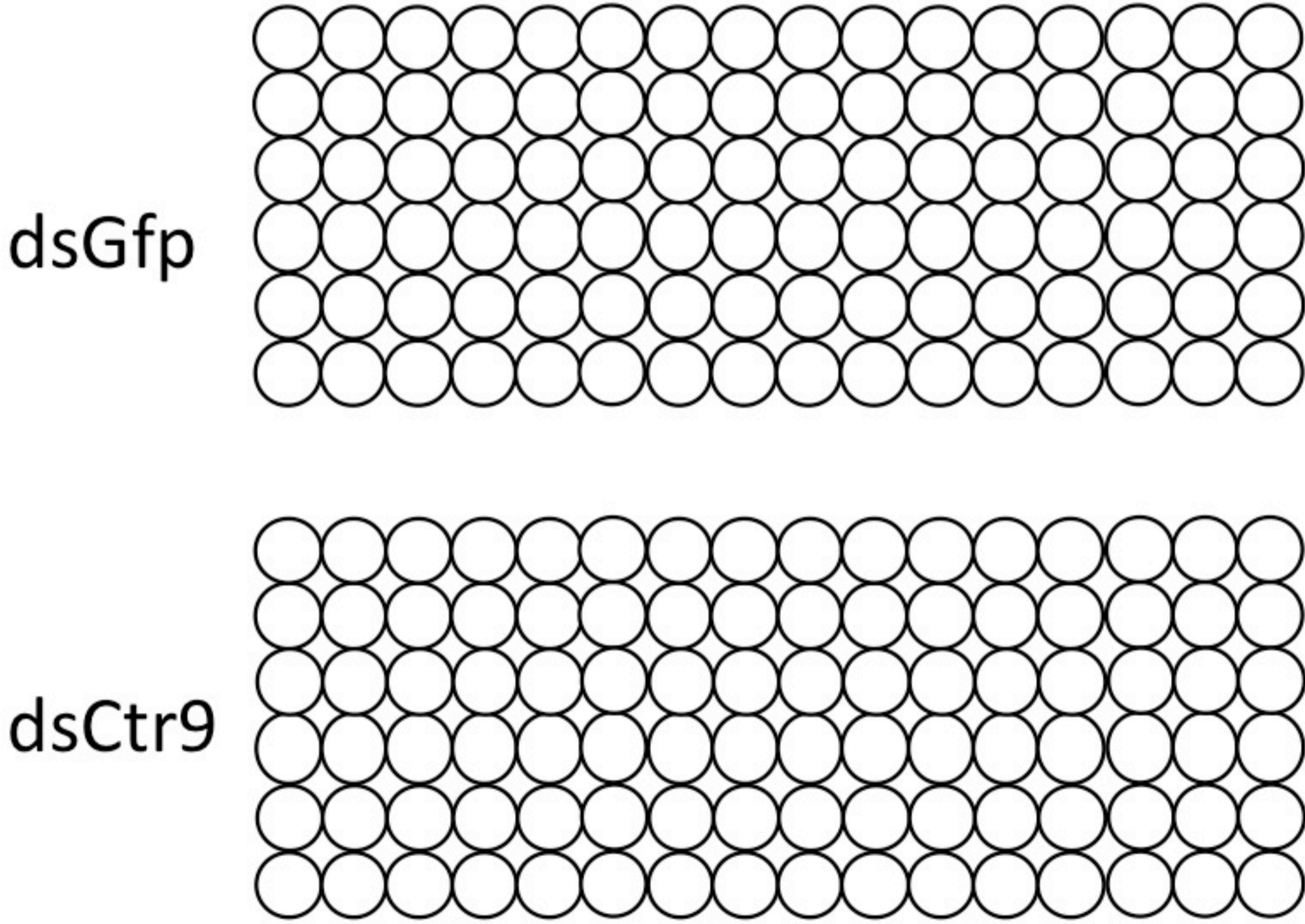
12 **Supplemental Figure 2: Additional qPCR expression assays.** A) *Setd2* and *Rtf9* are not altered
13 in dsCtr9 blastocysts. B) *Ctr9* is increased in dsRtf1 blastocysts, but *Setd2* is unchanged. C)
14 *Ctr9* and *Rtf1* are not altered in dsSetd2 blastocysts. D) *Eomes* and *Eilf5* are slightly (but not
15 significantly reduced) in dsSetd2 embryos. E) *Nanog* mRNA is increased in dsCtr9 embryos,
16 consistent with the observation of more NANOG positive blastomeres (Figure 4A). F) *Sox2*
17 mRNA remains unchanged in dsCtr9 embryos.

Supplemental Figure 1

A



B



Supplemental Figure 2

