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**Figure S3: Cohesin variant mESCs exhibit altered expression of cellular identity genes, Related to Figure 4.**

1. RT-qPCR analysis of pluripotency factors. Levels of *Pou5f1* *(*OCT4*)*, *Sox2,* and *Nanog* transcripts were measured in *Smc1aR586W* and matched wildtype mESC clones. n=3 biological replicates. Significance was determined by Dunnet’s multiple comparisons test; \*p<0.05.
2. RT-qPCR analysis of ectodermal regulators. Levels of *Pax6* and *Nestin* transcripts were measured in *Smc1aR586W* and matched wildtype mESC clones. n=3 biological replicates. Significance was determined by Dunnet’s multiple comparisons test; \*p<0.05.
3. RT-qPCR analysis of mesodermal regulators. Levels of *Foxa2* and *T* (Brachyury*)* transcripts were measured in *Smc1aR586W*and matched wildtype mESC clones. n=3 biological replicates. Significance was determined by Dunnet’s multiple comparisons test; \*p<0.05.
4. RT-qPCR analysis of endodermal regulators. Levels of *Gata6 and Sox17* transcripts were measured in *Smc1aR586W* and matched wildtype mESC clones. n=3 biological replicates. Significance was determined by Dunnet’s multiple comparisons test; \*p<0.05.