**Figure 2 - Figure Supplement 1 – source data 3.** Source data relating to Figure 2 – Figure Supplement 1F. qPCR analysis of gene expression in *Krt14CreERT2; Sox2fl/fl*and wild-type (WT) glands at E13.5. Data were normalized to *Rsp29* and WT. n = 3-4 SMG+SLG per genotype. s.d. = standard deviation.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Gene** | **WT** | s.d. | ***Krt14CreERT2;Sox2fl/fl*** | s.d. |
| *Trp53* | 1.00 | 0.13 | 1.93 | 0.52 |
| *Trp63* | 1.00 | 0.48 | 1.68 | 0.78 |
| *Ccnd1* | 1.00 | 0.19 | 1.67 | 0.35 |
| *Cdkn1a* | 1.00 | 0.07 | 1.49 | 0.37 |
| *Bax* | 1.00 | 0.16 | 1.92 | 0.47 |
| *Bbc3* | 1.00 | 0.46 | 3.09 | 0.89 |
| *Pmaip1* | 1.00 | 0.13 | 4.41 | 2.43 |