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| --- | --- | --- | --- |
| **Table S3.** Top five enriched GO categories among genes associated with H3K4me3 or H3K27me3 in the fetal germ cells, using pooled data from female E13.5 replicates | | | |
|  |  |  |
| **H3K4me3** |  |  |
| **Description** | **p-value** | **enrichment** |
| metabolic process | 3.45E-294 | 1.34 |
| organic substance metabolic process | 1.22E-285 | 1.36 |
| primary metabolic process | 6.63E-285 | 1.37 |
| macromolecule metabolic process | 6.02E-265 | 1.41 |
| cellular nitrogen compound metabolic process | 3.51E-205 | 1.46 |
|  |  |  |
|  |  |  |
| **H3K27me3** |  |  |
| **Description** | **p-value** | **enrichment** |
| single-organism developmental process | 1.40E-28 | 2.97 |
| developmental process | 4.15E-27 | 2.49 |
| anatomical structure morphogenesis | 4.20E-27 | 4.16 |
| regulation of cellular macromolecule biosynthetic process | 6.45E-24 | 2.64 |
| regulation of macromolecule biosynthetic process | 1.51E-23 | 2.6 |