

**S5 Table Result of GO term enrichment analysis of 285 genes that were upregulated in male and/or female embryos of parental species (primitive streak formation- and chromosome segregation-related GO-BP terms).**

| GO biological process   | Reference<br>( <i>Gallus gallus</i> ) | Input | Expected | Fold Enrichment | +/- | Raw P value | FDR      | Genes   |
|---|---------------------------------------|-------|----------|-----------------|-----|-------------|----------|---|
| <u>Primitive streak formation-related</u>                             |                                       |       |          |                 |     |             |          |   |
| anterior/posterior pattern specification (GO:0009952)                 | 190                                   | 7     | 2.44     | 2.87            | +   | 1.29E-02    | 7.85E-01 | <i>CDX1, DLL1, WNT3A, MSX2, CRB2, T, WNT5A</i>  |
| axis specification (GO:0009798)                                       | 62                                    | 4     | 0.8      | 5.03            | +   | 9.80E-03    | 7.03E-01 | <i>CDX1, DLL1, PITX2, WNT5A</i>   |
| gastrulation (GO:0007369)   | 118                                   | 6     | 1.51     | 3.96            | +   | 5.00E-03    | 5.89E-01 | <i>RPS6, WNT3A, CRB2, T, WNT5A, MMP9</i>  |
| anatomical structure formation involved in morphogenesis (GO:0048646) | 617                                   | 16    | 7.92     | 2.02            | +   | 9.49E-03    | 7.26E-01 | <i>PMP22, RECK, SLC40A1, DLL1, BMPER, PITX2, WNT3A, MSX2, CRB2, T, WNT5A, MMP9, ITGAV, S1PR1, RPS7, STRA6</i> |
| anterior/posterior axis specification (GO:0009948)                    | 37                                    | 2     | 0.47     | 4.21            | +   | 8.73E-02    | 1.00E+00 | <i>CDX1, WNT5A</i>  |
| gastrulation with mouth forming second (GO:0001702)                   | 20                                    | 2     | 0.26     | 7.79            | +   | 3.12E-02    | 9.34E-01 | <i>CRB2, WNT5A</i>  |
| primitive streak formation (GO:0090009)                               | 5                                     | 1     | 0.06     | 15.59           | +   | 7.37E-02    | 1.00E+00 | <i>WNT5A</i>  |
| <u>Chromosome segregation-related</u>                                 |                                       |       |          |                 |     |             |          |   |
| chromosome segregation (GO:0007059)                                   | 227                                   | 2     | 2.91     | 0.69            | -   | 1.00E+00    | 1.00E+00 | <i>HORMAD2, PHB2</i>  |
| nuclear chromosome segregation (GO:0098813)                           | 188                                   | 2     | 2.41     | 0.83            | -   | 1.00E+00    | 1.00E+00 | <i>HORMAD2, PHB2</i>  |