

Table S6 PANTHER analysis of Yan datasets. PANTHER (Thomas et al., 2003) was used to perform pathway analysis of genes assigned to Yan-bound regions at stage 5-7 and stage 11 and of genes assigned to Yan-bound regions in the *D. virilis* datasets. Only Bonferroni-corrected p-values of <0.005 were considered significant.

| Pathway | Stage 5-7 | | | | Stage 11 | | | | D. virilis | | | |
|--|-----------|----------|------------|----------|----------|----------|------------|----------|------------|----------|------------|----------|
| | Counts | Expected | Over/Under | p-value | Counts | Expected | Over/Under | p-value | Counts | Expected | Over/Under | p-value |
| Notch signaling pathway | 13 | 2.53 | + | 2.56E-06 | 13 | 2.53 | + | 2.64E-06 | 11 | 2.18 | + | 1.79E-05 |
| Wnt signaling pathway | 27 | 13.43 | + | 6.83E-04 | 36 | 13.47 | + | 2.25E-07 | 20 | 11.26 | + | 1.14E-02 |
| Ras Pathway | 10 | 3.23 | + | 1.86E-03 | 7 | 3.24 | + | 4.70E-02 | 6 | 2.45 | + | 3.83E-02 |
| Insulin/IGF pathway-mitogen activated protein kinase kinase/MAP kinase cascade | 9 | 3.54 | + | 1.04E-02 | 8 | 3.55 | + | 2.84E-02 | 6 | 1.22 | + | 1.63E-03 |
| p53 pathway | 11 | 4.04 | + | 3.01E-03 | 7 | 4.05 | + | 1.16E-01 | 7 | 3.75 | + | 8.64E-02 |
| TGF-beta signaling pathway | 12 | 5.86 | + | 1.69E-02 | 16 | 5.88 | + | 3.94E-04 | 10 | 4.8 | + | 2.50E-02 |
| PDGF signaling pathway | 10 | 5.66 | + | 6.19E-02 | 11 | 5.67 | + | 3.03E-02 | 12 | 4.89 | + | 4.51E-03 |
| Interleukin signaling pathway | 8 | 3.84 | + | 4.19E-02 | 10 | 3.85 | + | 6.24E-03 | 8 | 2.97 | + | 1.11E-02 |
| Cadherin signaling pathway | 11 | 5.45 | + | 2.37E-02 | 15 | 5.47 | + | 5.50E-04 | 10 | 4.45 | + | 1.59E-02 |
| Angiogenesis | 11 | 6.26 | + | 5.40E-02 | 15 | 6.28 | + | 2.10E-03 | 9 | 5.06 | + | 7.20E-02 |
| Glutamine glutamate conversion | 2 | 0.4 | + | 6.26E-02 | 3 | 0.41 | + | 8.20E-03 | 0 | 0.35 | - | 7.05E-01 |
| Alzheimer disease-presenilin pathway | 7 | 3.94 | + | 1.04E-01 | 12 | 3.95 | + | 8.07E-04 | 3 | 2.71 | + | 5.08E-01 |