**Figure 5— source data 3: Cone *Txnip* mRNA raw reads in the RNA-seq data (from 1,000 FACS cones per retina).**

|  |  |  |
| --- | --- | --- |
| **Condition** | **Control** | **Txnip** |
| **P21 *rd1*** | 3.5 ± 2.2 (n=6) | 1834.3 ± 36.3 (n=3) |
| **P90 *Rho*-/-** | 2.3 ± 1.7 (n=4) | 2767.3 ± 232.2 (n=4) |
| **P21 BALB/c** | 1.0 ± 0.5 (n=6) |  3116.8 ± 859.6 (n=6) |
| **P35 C57BL/6J** | 0.7 ± 0.3 (n=3) | 5882.7 ± 1884.4 (n=3) |

*Data presented as: Mean ± SEM (n = sample size, i.e. number of retinas per condition.)*