**Supplemental Table 4. Contingency table for enrichment of dysregulated miRNA targets.**

|  |  |  |  |
| --- | --- | --- | --- |
|  | Non-miRNA Targets | miRNA Targets | Total |
| Not dysregulated | 17083 | 2886 | 19967 |
| Dysregulated | 657 | 158 | 815 |
| **Total** | 17740 | 3044 | 20784 |
|  |  |  |  |
| Metric | X2 | z-score | *p*-value |
| Results | 14.86 | 3.86 | 0.0001 |

Chi-square analysis with Yates correction to determine if dysregulated genes are statistically enriched for miRNA targets. Total number of candidate miRNA targets was determined by miRNet ([38](#_ENREF_38)). Total number of genes was based on total genes detected by RNA-seq. Genes with low reads (sum across all samples less than 10 reads) were filtered out prior to analysis.