| **Supplementary Table 18** | | |
|---|---|---|
| **Any knockdown** | | |
| **Length** | **Not significantly downregulated** | **Significantly downregulated** |
| **Short** | 1627 | 475 |
| **Long** | 1923 | 1591 |
| $X^2$ (1, $N$=5632) = 286.17, p < 2.2e-16 | | |
| **< 33% knockdown** | | |
| **Length** | **Not significantly downregulated** | **Significantly downregulated** |
| **Short** | 1505 | 352 |
| **Long** | 1693 | 982 |
| $X^2$ (1, $N$=4532) = 165.5, p < 2.2e-16 | | |
| **33% - 66% knockdown** | | |
| **Length** | **Not significantly downregulated** | **Significantly downregulated** |
| **Short** | 94 | 105 |
| **Long** | 169 | 529 |
| $X^2$ (1, $N$= 897) = 38.51, p = 5.45e-10 | | |
| **> 66% knockdown** | | |
| **Length** | **Not significantly downregulated** | **Significantly downregulated** |
| **Short** | 28 | 18 |
| **Long** | 74 | 80 |
| $X^2$ (1, $N$=200) = 1.84, p = .17 | | |

Supplementary Table 9 number of genes that have one or more (all binding sites) in a short or long gene and are either not significantly downregulated or significantly downregulated. For the first part ("any knockdown") the complete set is used which was then splitted into three groups depending on the degree of knockdown.
Only in the group of > 66% knockdown the observation that long genes are more likely downregulated than the short genes, is not significant. Probably due to the small numbers.