Supplementary Table 20		
All binding sites at 33% - 66% knockdown		
Length	Not significantly downregulated	Significantly downregulated
Short	94	105
Long	169	529
$X^{2}(1, N=897) = 38.51, p = 5.45e-10$		
Single binding site at 33% - 66% knockdown		
Length	Not significantly downregulated	Significantly downregulated
Short	84	78
Long	115	341
$X^{2}(1, N=618) = 37.63, p = 8.57e-10$		
Multiple binding sites at 33% - 66% knockdown		
Length	Not significantly downregulated	Significantly downregulated
Short	10	27
Long	54	188
$X^2(1, N=279) = 0.18$, p-value = .67		

Supplementary Table 11 investigation of genes showing a degree of knockdown between 33% and 66%. The number of genes that have one or more (all binding sites), one (single binding site), two or more (multiple binding sites) in a short or long gene and are either not significantly downregulated or significantly downregulated is shown. Only in the group of genes with multiple binding sites the observation that long genes are more likely downregulated than the short genes, is not significant. Probably due to the small numbers.