

<b>Supplementary Table 19</b>		
<b>All binding sites at &lt; 33% knockdown</b>		
<b>Length</b>	<b>Not significantly downregulated</b>	<b>Significantly downregulated</b>
<b>Short</b>	1505	352
<b>Long</b>	1693	982
$\chi^2(1, N=4532) = 165.5, p < 2.2\text{e-}16$		
<b>Single binding site at &lt; 33% knockdown</b>		
<b>Length</b>	<b>Not significantly downregulated</b>	<b>Significantly downregulated</b>
<b>Short</b>	1390	310
<b>Long</b>	1375	723
$\chi^2(1, N=3798) = 124.05, p < 2.2\text{e-}16$		
<b>Multiple binding sites &lt; 33% knockdown</b>		
<b>Length</b>	<b>Not significantly downregulated</b>	<b>Significantly downregulated</b>
<b>Short</b>	115	42
<b>Long</b>	318	259
$\chi^2(1, N=734) = 16.04, p = 6.21\text{e-}05$		

Supplementary Table 10 investigation of short and long genes showing a degree of knockdown smaller than 33%. 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. In all cases the long genes are more likely significantly downregulated than the short genes