
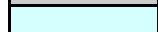


Table 2

Row	Gene	SRSF genome	SRSF secondary	HFA genome	Tertiary Screen (independent dsRNAs)
1	<i>dome</i>	-7.9	-7.1	-8.0	-6.7
2	<i>Stat92E</i>	-6.8	-11.4	-6.5	-6.8
3	<i>hop</i>	-5.7	-10.0	-2.6	-4.4
4	<i>mask</i>	-4.3	-6.6	-3.8	NS
5	<i>Mov34</i>	-3.2	-4.1	-3.0	0.1
6	<i>RpL24</i>	-2.6	-2.5	-6.8	0.1
7	<i>Ptp61F</i>	2.3	3.6	5.0	4.1
8	<i>CkIalpha</i>	4.1	2.6	4.8	2.5
9	<i>chinmo</i>	6.6	4.8	7.0	2.7
10	<i>TfIIA-L</i>	-3.8	-5.5	-1.8	NS
11	<i>Chd1</i>	-2.2	-1.7	-2.4	NS
12	<i>Saf-B</i>	2.5	1.8	4.6	NS
13	<i>Socs36E</i>	2.8	1.8	2.5	3.9
14	<i>shrb</i>	2.3	3.0	NA ¹	-0.4
15	<i>dom</i>	-3.4	-2.4	NA ²	0.9
16	<i>RpLP2</i>	-2.4	-2.2	NA ²	-0.5
17	<i>CG7185</i>	2.6	1.7	NA ³	1.6
18	<i>RpII215</i>	-2.2	-2.2	NA ³	-1.1
19	<i>Dp</i>	-2.2	-2.8	-2.8 *	-0.8
20	<i>CG32269</i>	-3.1	-1.7	-1.7 *	0.2
21	<i>E2f</i>	-3.1	-4.9	-1.0	-1.3
22	<i>CG11873</i>	2.2	2.2	0.0	2.5
23	<i>TSG101</i>	2.3	6.0	1.6	-1.1
24	<i>ftz-f1</i>	2.3	2.7	0.5	2.0
25	<i>kis</i>	2.3	2.5	0.9	0.0
26	<i>lola</i>	3.1	4.0	-0.8	-1.1
27	<i>srp</i>	8.6	8.5	-0.5	NS
28	<i>ctrip</i>	-2.6	-1.9	0.0	-1.1
29	<i>ham</i>	4.5	1.8	-0.5	1.7
30	<i>Tbp</i>	-4.5	0.5	-1.3	-2.0
31	<i>CG40121</i>	-3.6	-1.1	1.4	-3.3
32	<i>Dcp2</i>	-2.0	-0.6	-0.6	-0.4
33	<i>CG9723</i>	-2.0	1.3	-0.5	0.0
34	<i>pncr017:3R</i>	-2.0	-0.4	1.2	-0.4
35	<i>Cnot4</i>	2.1	0.7	0.5	0.4
36	<i>qkr54B</i>	2.2	0.4	0.3	0.7
37	<i>l(3)mbt</i>	2.6	0.5	-0.4	0.8
38	<i>Hsp60B</i>	2.7	0.1	0.0	0.0
39	<i>Sin</i>	2.7	1.2	1.5	-0.1
40	<i>CG11399</i>	2.8	1.4	0.3	0.2
41	<i>Surf4</i>	3.1	0.8	1.3	-0.7
42	<i>zfh1</i>	5.2	0.8	0.6	0.6

 = Zscore <-2 or >2

 = Zscore <-1.7 or >1.7

* = only one replicate significant

NA¹ = Excluded due to edge effects

NA² = Excluded due to liquid handling error

NA³ = One replicate excluded due to liquid handling error

NS = Not screened since previous clones are already independent designs