

shRNA ID	#hits in screen	Pos. cDNA	Sense		Ui- Tei	Amarz- guioui	Hsieh	Taka- saki	s- Biopredsi	i- Score	Rey- nolds	Katoh	DSIR	%KD
shp53-3	3462	520	CACATGTAGTTGTAGTGGATGGTGGT	glt	II	1	-1	0.3	0.676	53.2	4	60.5	75.6	>90
shp53-2	1959	369	GCGCTGCTCAGATAGCGATGGTCTGG	tlg	II	0	-1	6.1	0.36	41.2	0	48.4	66.2	>90
shp53-13	486	1365	CTGTTGAATTTCTCTAACTTCAAGG	tlg	<b>Ia</b>	3	<b>2</b>	9.4	<b>0.812</b>	<b>65.3</b>	<b>7</b>	<b>83.2</b>	84.1	>70
Axl2	-	762	GACATCCTCTTTCTCCTGCGAAGCCCAT	tlg	II	1	2	5	0.729	60	6	44.3	79	>95
Axl278	-	1587	ACGGGTCTCCTTCTTTCGCCG	glt	II	2	0	3	0.524	42	0	59.9	66.1	>80
Axl280	-	221	ATGCACGCCAGCCGCACAGCG	glt	II	1	1	2.7	0.3	32.6	-1	17.9	49.7	>95

**Supplementary figure 3. Functionally selected shRNA sequences fail in RNAi scoring algorithms.** Hairpin sequences from this study that gave good knockdown efficiency (actual efficiency) were scored with eight different RNAi scoring algorithms using the i-Score server ([http://www.med.nagoya-u.ac.jp/neurogenetics/i\\_Score/i\\_score.html](http://www.med.nagoya-u.ac.jp/neurogenetics/i_Score/i_score.html)). **Bold italic**: score within top 100 for gene. Glt: guide strand-loop-template strand orientation. Tlg: template strand-loop-guide strand orientation.