

Table S2 Comparison of observed versus predicted guide RNA editing efficiency using the Doench *et al.* 2014 algorithm

GG Guides

Target Gene	Guide RNA	Protospacer Sequence (PAM)	sgRNA Bases 19,20	Mutagenesis Rate (%)	sgRNA Score (Doench <i>et al.</i> 2014)
<i>lir-2</i>	3' GG	GGCTGATTTTCGCAGTTCGG (GGG)	GG	72	no value
<i>Y62E10A.17</i>	3' GG	CGCACCGATGCTCTCCGAGG (AGG)	GG	57	0.041
<i>sex-1</i>	3' GG (1)	GGATGAGAATCTGACAAAGG (TGG)	GG	54	0.198
<i>cpsf-2</i>	3' GG	CACTTCAATTTGATAATGG (AGG)	GG	52	0.063
<i>sex-1</i>	3' GG (2)	AACATTTCCACAACGAGAGG (AGG)	GG	51	0.439
<i>fox-1</i>	3' GG (1)	ATATGAGGGGAGTGAGGCGG (TGG)	GG	29	0.178
<i>fox-1</i>	3' GG (3)	ATTACAGTGAAGTACAGCGG (AGG)	GG	21	0.749
<i>fox-1</i>	3' GG (2)	AATATCGTTTACCAAAACGG (GGG)	GG	13	0.422
<i>xol-1</i>	3' GG	AGCGATTTCTGGCGATTGGG (GGG)	GG	10	0.277

Non-GG Guides

<i>sex-1</i>	3' GG-shift (1)	AACGGATGAGAATCTGACAA (AGG)	AA	21	0.282
<i>fox-1</i>	3' GG-shift (1)	CATTTGATATGAGGGGAGTG (AGG)	TG	20	0.063
<i>Y62E10A.17</i>	3' GG-shift	ATACGCACCGATGCTCTCCG (AGG)	CG	14	0.887
<i>sex-1</i>	3' GG-shift (2)	TGGAACATTTCCACAACGAG (AGG)	AG	8	0.355
<i>lir-2</i>	3' GG-shift	CTCGGCTGATTTTCGCAGTT (CGG)	TT	1	no value
<i>cpsf-2</i>	3' GG-shift	AAACACTTTCAATTTGATAA (TGG)	AA	0	0.026
<i>fox-1</i>	3' GG-shift (2)	TTGAATATCGTTTACCAAAA (CGG)	AA	0	0.106
<i>fox-1</i>	3' GG-shift (3)	ACAATTACAGTGAAGTACAG (CGG)	AG	0	0.669
<i>xol-1</i>	3' GG-shift	TCTAGCGATTTCTGGCGATT (GGG)	TT	0	0.010
<i>cpsf-2</i>	3' non-GG (1)	GTGGTTGGGATGAGCGATTC (GGG)	TC	0	0.005
<i>lir-2</i>	3' non-GG (1)	AATCAGCCGAGATGTAAGTT (TGG)	TT	0	0.045
<i>lir-2</i>	3' non-GG (2)	TTGACTCGTTCATTTCAGC (TGG)	GC	0	0.108
<i>sex-1</i>	3' non-GG (1)	AAACCTGCCTCCTCTCGTTG (TGG)	TG	0	0.156

This table provides a comparison of our observed editing frequencies using 3' GG and non-GG guides compared to the scores we derived using the algorithm from Doench *et al.* (2014) that predicts guide editing frequencies based on experiments in mammalian cells. See website: <http://www.broadinstitute.org/rnai/public/analysis-tools/sgRNA-design>. The presence of the 3' GG motif in the protospacer is a better predictor of editing outcome than the algorithm. A score of 1 by this algorithm indicates a highly efficient guide.