Table S1 Summary of current and published editing frequencies using 3’ GG and non-GG guides

Our Guide Efficiencies

GG Guides

Target Gene	Guide RNA	Protospacer Sequence (PAM)	sgRNA Bases 19,20	Mutagenesis Rate (%)	Publication
lir-2	3' GG	GGCTGATTTTCGCAGTTCGG (GGG)	GG	72	This study
Y62E10A.17	3' GG	CGCACCGATGCTCTCCGAGG (AGG)	GG	57	This study
sex-1	3' GG (1)	GGATGAGAATCTGACAAAGG (TGG)	GG	54	This study
cpsf-2	3' GG	CACTTTCAATTTGATAATGG (AGG)	GG	52	This study
sex-1	3' GG (2)	AACATTTCCACAACGAGAGG (AGG)	GG	51	This study
fox-1	3' GG (1)	ATATGAGGGGAGTGAGGCGG (TGG)	GG	29	This study
fox-1	3' GG (3)	ATTACAGTGAAGTACAGCGG (AGG)	GG	21	This study
fox-1	3' GG (2)	AATATCGTTTACCAAAACGG (GGG)	GG	13	This study
xol-1	3' GG	AGCGATTTCTGGCGATTGGG (GGG)	GG	10	This study
			median:	**51**	

Non-GG Guides

sex-1	3' GG-shift (1)	AACGGATGAGAATCTGACAA (AGG)	AA	21	This study
fox-1	3' GG-shift (1)	CATTTGATATGAGGGGAGTG (AGG)	TG	20	This study
Y62E10A.17	3' GG-shift	ATACGCACCGATGCTCTCCG (AGG)	CG	14	This study
sex-1	3' GG-shift (2)	TGGAACATTTCCACAACGAG (AGG)	AG	8	This study
lir-2	3' GG-shift	CTCGGCTGATTTTCGCAGTT (CGG)	TT	1	This study
cpsf-2	3' GG-shift	AAACACTTTCAATTTGATAA (TGG)	AA	0	This study
fox-1	3' GG-shift (2)	TTGAATATCGTTTACCAAAA (CGG)	AA	0	This study
fox-1	3' GG-shift (3)	ACAATTACAGTGAAGTACAG (CGG)	AG	0	This study
xol-1	3' GG-shift	TCTAGCGATTTCTGGCGATT (GGG)	TT	0	This study
cpsf-2	3' non-GG (1)	GTGGTTGGGATGAGCGATTC (GGG)	TC	0	This study
lir-2	3' non-GG (1)	AATCAGCCGAGATGTAAGTT (TGG)	TT	0	This study
lir-2	3' non-GG (2)	TTGACTCGTTCCATTTCAGC (TGG)	GC	0	This study
sex-1	3' non-GG (1)	AAACCTGCCTCCTCTCGTTG (TGG)	TG	0	This study
			median:	**0**	

Published Guide Efficiencies

GG Guides

Target Gene	Guide RNA	Protospacer Sequence (PAM)	sgRNA Bases 19,20	Mutagenesis Rate (%)	Publication
klp-12		GATCCACAAGTTACAATTGG (TGG)	GG	80.3	Friedland *et al.* 2013
vet-2		GTTGGATCATAGGATACCGG (TGG)	GG	38	Kim *et al.* 2014
			median:	**59**	

Non-GG Guides

C35E7.6		GGGCACCATACCGAGTGATG (GGG)	TG	100	Kim *et al.* 2014
lon-2		GGGAAACTATACCCTCACTG (TGG)	TG	30	Kim *et al.* 2014
pie-1	a	GGCTCAGATTGACGAGGCGC (CGG)	GC	24	Kim *et al.* 2014
lin-5		GGAGCTTACTGAGACTCTTC (GGG)	TC	20.8	Waaijers *et al.* 2013
avr-14	(2)	GATTGGAGAGTTAGACCACG (TGG)	CG	20	Kim *et al.* 2014
Y61A9LA.1		GGATGGATGTGTAGTCAATT (CGG)	TT	18.1	Friedland *et al.* 2013
pie-1	b	GCTGAGAGAAGAATCCATCG (GGG)	CG	15	Kim *et al.* 2014
avr-14	(1)	GAATATTGAAAGACTATGAT (TGG)	AT	10	Kim *et al.* 2014
unc-4	(1)	GTTATCGTCATCCGGTGACG (TGG)	CG	10	Kim *et al.* 2014
dpy-11		GCAAGGATCTTCAAAAAGCA (TGG)	CA	10	Waaijers *et al.* 2013
pie-1	c	GGACAAAGAGAGGGGGTGAG (TGG)	AG	7.5	Kim *et al.* 2014
unc-22	(2)	GAACCCGTTGCCGAATACAC (AGG)	AC	5	Kim *et al.* 2014
pie-1	d	GTTGAGTGCAGCCATTTGCT (CGG)	CT	5	Kim *et al.* 2014
unc-119		GTTATAGCCTGTTCGGTTAC (CGG)	AC	4.9	Waaijers *et al.* 2013
unc-119		GAATTTTCTGAAATTAAAGA (CGG)	GA	3.7	Friedland *et al.* 2013
rol-1		GGAGGTTGACTCCAATACTA (AGG)	TA	1.4	Waaijers *et al.* 2013
dpy-13		GGACATTGACACTAAAATCA (AGG)	CA	0.5	Friedland *et al.* 2013
dpy-11	(2)	GCAAGGATCTTCAAAAAGCA (CGG)	CA	0.4	Kim *et al.* 2014
ben-1	(5)	GGGAGAAAGTGATTTGCAGT (TGG)	GT	0	Kim *et al.* 2014
ben-1	(3)	GGATATCACTTCCCAGAACT (TGG)	CT	0	Kim *et al.* 2014
bli-2	(2)	GATGGACGGGATGGTAGAGA (TGG)	GA	0	Kim *et al.* 2014
bli-2	(1)	GGATTTGCTGCTACTGAATC (CGG)	TC	0	Kim *et al.* 2014
dpy-5	(2)	GTCGGATTCGGCGCTGCATG (CGG)	TG	0	Kim *et al.* 2014
dpy-5	(3)	GGTTTCCTGGAGCTCCGGCT (GGG)	CT	0	Kim *et al.* 2014
dpy-11	(4)	GATGCTTGTAGTCTGGAACT (GGG)	CT	0	Kim *et al.* 2014
unc-22	(9)	GCCTTTGCTTCGATTTTCTT (TGG)	TT	0	Kim *et al.* 2014
unc-32	(1)	GATAGGAAGCATCAGATTGA (AGG)	GA	0	Kim *et al.* 2014
unc-32	(2)	GTTGCTGAACTGGGAGAGCT (CGG)	CT	0	Kim *et al.* 2014
			median:	**4.3**	