Table S1 | List of sgRNA pairs used with Cas9 nickase (D10A) to identify the optimal target site spacing for double nicking across multiple genes, related to Figure 2. N.D.: Not detected. N.T.: Not tested

Table S2 | List of sgRNAs used in this study. Related to Figure 2.

Table S1. List of sgRNA pairs used with Cas9 nickase (D10A) to identify the optimal target site spacing for double nicking across multiple genes, related to Figure 2. N.D.: Not detected. N.T.: Not tested

Gene	Overhang Length (bp)	Overhang Type	Offset Length (bp)	Left sgRNA ID	Right sgRNA ID	Cas9n with left and right sgRNA indel (%)	left sgRNA target site		left sgRNA with wildtype Cas9 indel (%)	right sgRNA target site		right sgRNA with wildtype Cas9 indel (%)
							guide sequence (5' to 3')	PAM		guide sequence (5' to 3')	PAM	
EMX1	148	3'	-182	15	4	N.D.	TGCGCCACCGGTTGATGTGA	TGG	13.15	AGGCCCCAGTGGCTGCTCTG	GGG	27.29
EMX1	101	3'	-135	23	1	N.D.	ACTCTGCCCTCGTGGGTTTG	TGG	24.7	GAGTCCGAGCAGAAGAAGAA	GGG	21.9
EMX1	48	3'	-82	23	17	N.D.	ACTCTGCCCTCGTGGGTTTG	TGG	24.7	CACGAAGCAGGCCAATGGGG	AGG	13.57
EMX1	25	3'	-59	10	13	N.D.	CAAACGGCAGAAGCTGGAGG	AGG	26.15	GGAGCCCTTCTTCTTCTGCT	CGG	33.17
EMX1	15	3'	-49	4	5	N.D.	AGGCCCCAGTGGCTGCTCTG	GGG	27.29	GGGGCACAGATGAGAAACTC	AGG	26.56
EMX1	8	3'	-42	7	9	N.D.	TGAAGGTGTGGTTCCAGAAC	CGG	36.02	GCCGTTTGTACTTTGTCCTC	CGG	30.49
EMX1	26	5'	-8	9	19	13.7 ± 1.27	GCCGTTTGTACTTTGTCCTC	CGG	9.82	GGCAGAGTGCTGCTTGCTGC	TGG	26.15
EMX1	30	5'	-4	9	10	19.72 ± 0.32	GCCGTTTGTACTTTGTCCTC	CGG	30.49	CAAACGGCAGAAGCTGGAGG	AGG	22.06
EMX1	31	5'	-3	6	7	21.35 ± 2.23	TCACCTGGGCCAGGGAGGGA	GGG	10.75	TGAAGGTGTGGTTCCAGAAC	CGG	36.02
EMX1	34	5'	0	15	16	26.89 ± 1.54	TGCGCCACCGGTTGATGTGA	TGG	13.15	TTGCCACGAAGCAGGCCAAT	GGG	13.77
EMX1	38	5'	4	15	17	36.31 ± 2.97	TGCGCCACCGGTTGATGTGA	TGG	14.49	CACGAAGCAGGCCAATGGGG	AGG	13.57
EMX1	51	5'	17	5	7	31.12 ± 0.25	GGGGCACAGATGAGAAACTC	AGG	26.56	TGAAGGTGTGGTTCCAGAAC	CGG	36.02
EMX1	54	5'	20	5	8	32.41 ± 3.68	GGGGCACAGATGAGAAACTC	AGG	26.56	AGGTGTGGTTCCAGAACCGG	AGG	35.53
EMX1	65	5'	31	6	10	13.45 ± 1.99	TCACCTGGGCCAGGGAGGGA	GGG	10.75	CAAACGGCAGAAGCTGGAGG	AGG	26.15
EMX1	69	5'	35	6	11	12.39 ± 1.29	TCACCTGGGCCAGGGAGGGA	GGG	10.75	CGGCAGAAGCTGGAGGAGGA	AGG	22.06
EMX1	76	5'	42	9	14	21.71 ± 1.66	GCCGTTTGTACTTTGTCCTC	CGG	30.49	AGGGCTCCCATCACATCAAC	CGG	41.27
EMX1	85	5'	51	5	10	21.89 ± 1.88	GGGGCACAGATGAGAAACTC	AGG	26.56	CAAACGGCAGAAGCTGGAGG	AGG	26.15
EMX1	95	5'	61	6	12	5.88 ± 1.81	TCACCTGGGCCAGGGAGGGA	GGG	10.75	TGAGTCCGAGCAGAAGAAGA	AGG	29.06
EMX1	135	5'	101	5	14	15.78 ± 2.19	GGGGCACAGATGAGAAACTC	AGG	26.56	AGGGCTCCCATCACATCAAC	CGG	41.27
EMX1	145	5'	111	6	16	N.D.	TCACCTGGGCCAGGGAGGGA	GGG	10.75	TTGCCACGAAGCAGGCCAAT	GGG	13.77
EMX1	181	5'	147	6	18	N.D.	TCACCTGGGCCAGGGAGGGA	GGG	10.75	TCACCTCCAATGACTAGGGT	GGG	25.14
EMX1	201	5'	167	5	18	N.D.	GGGGCACAGATGAGAAACTC	AGG	26.56	TCACCTCCAATGACTAGGGT	GGG	25.14
EMX1	222	5'	188	6	19	N.D.	TCACCTGGGCCAGGGAGGGA	GGG	10.75	GGCAGAGTGCTGCTTGCTGC	TGG	10.75
EMX1	242	5'	208	5	19	N.D.	GGGGCACAGATGAGAAACTC	AGG	26.56	GGCAGAGTGCTGCTTGCTGC	TGG	17.22
DYRK1A	164	3'	-198	34	47	N.D.	ATCTGGTCAGAATATGATAA	AGG	10.65 ± 2.05	AACCTCACTTATCTTCTTGT	AGG	19.02 ± 4.32
DYRK1A	105	3'	-139	35	47	N.D.	GTCACTGTACTGATGTGAAT	TGG	16.71 ± 2.47	AACCTCACTTATCTTCTTGT	AGG	17.04 ± 1.30
DYRK1A	66	3'	-100	36	48	N.D.	CATCTGAAGGCCAGCAGCAT	TGG	8.82 ± 1.01	CTCACTTATCTTCTTGTAGG	AGG	18.79 ± 2.71
DYRK1A	25	3'	-59	35	49	N.D.	GTCACTGTACTGATGTGAAT	TGG	17.83 ± 0.43	CCATGCTGCTGGCCTTCAGA	TGG	17.15 ± 3.29
DYRK1A	4	3'	-38	37	31	N.D.	TGATAAGGCAGAAACCTGTT	TGG	4.95 ± 0.66	GCCAAACATAAGTGACCAAC	AGG	16.38 ± 3.39
DYRK1A	17	5'	-17	38	47	N.D.	GAAGATAAGTGAGGTTTAAA	AGG	5.30 ± 1.98	AACCTCACTTATCTTCTTGT	AGG	24.18 ± 3.22
DYRK1A	21	5'	-13	39	33	10.54 ± 0.63	GTATCATTTGACATATCTAA	TGG	26.90 ± 1.17	TGTCAAATGATACAAACATT	AGG	29.69 ± 0.86
DYRK1A	25	5'	-9	40	49	2.33 ± 0.11	CAGCATGGAATGAAAATGAC	CGG	3.33 ± 0.56	CCATGCTGCTGGCCTTCAGA	TGG	20.43 ± 2.40
DYRK1A	29	5'	-5	41	50	27.76 ± 0.84	GCAGCATGGAATGAAAATGA	CGG	17.84 ± 5.46	GCTGCTGGCCTTCAGATGGC	TGG	21.92 ± 3.46
DYRK1A	33	5'	-1	34	51	10.42 ± 0.90	ATCTGGTCAGAATATGATAA	AGG	9.13 ± 2.32	TCAGCAACCTCTAACTAACC	AGG	24.14 ± 2.95
DYRK1A	35	5'	1	42	52	7.63 ± 0.51	GTGCAAGCCGAACAGATGAA	AGG	6.65 ± 2.19	TCATTTTCATTCCATGCTGC	TGG	20.61 ± 3.64
DYRK1A	36	5'	2	28	29	38.46 ± 0.74	GGAGTATCAGAAATGACTAT	TGG	20.88 ± 9.09	GGAGTATCAGAAATGACTAT	TGG	30.3 ± 0.7
DYRK1A	41	5'	7	30	31	34.41 ± 0.87	GGTCACTGTACTGATGTGAA	TGG	25.68 ± 5.95	GCCAAACATAAGTGACCAAC	AGG	33.1 ± 0.4
DYRK1A	42	5'	8	43	31	38.36 ± 0.32	TCACTGTACTGATGTGAATG	GGG	24.68 ± 4.58	GCCAAACATAAGTGACCAAC	AGG	29.46 ± 3.30
DYRK1A	43	5'	9	32	33	28.97 ± 0.32	GTTCCTTAAATAAGAACTTT	AGG	23.60 ± 2.56	TGTCAAATGATACAAACATT	AGG	22.4 ± 1.6
DYRK1A	46	5'	12	44	53	11.90 ± 1.65	TCCTACAAGAAGATAAGTGA	AGG	6.57 ± 1.36	CATGCAAACCTTCATCTGTT	CGG	30.42 ± 1.14
DYRK1A	77	5'	43	36	31	6.63 ± 0.27	CATCTGAAGGCCAGCAGCAT	TGG	10.02 ± 1.17	GCCAAACATAAGTGACCAAC	AGG	22.92 ± 5.16
DYRK1A	86	5'	52	38	52	N.D.	GAAGATAAGTGAGGTTTAAA	AGG	2.90 ± 0.82	TCATTTTCATTCCATGCTGC	TGG	17.30 ± 1.62
DYRK1A	97	5'	63	38	49	N.D.	GAAGATAAGTGAGGTTTAAA	AGG	2.16 ± 0.48	CCATGCTGCTGGCCTTCAGA	TGG	24.75 ± 2.50
DYRK1A	131	5'	97	45	52	N.D.	TATCATTTGACATATCTAAT	TGG	8.21 ± 2.83	TCATTTTCATTCCATGCTGC	TGG	14.61 ± 4.10
DYRK1A	155	5'	121	44	31	N.D.	TCCTACAAGAAGATAAGTGA	AGG	9.99 ± 4.12	GCCAAACATAAGTGACCAAC	AGG	19.74 ± 2.91
DYRK1A	191	5'	157	46	52	N.D.	AACTTTTCTAACTACAAACA	AGG	5.74 ± 2.24	TCATTTTCATTCCATGCTGC	TGG	21.37
GRIN2B	165	3'	-199	70	82	N.D.	CCAACACCAACCAGAACTTG	GGG	2.95 ± 0.21	CTGGTAGATGGAGTTGGGTT	TGG	17.25 ± 1.30
GRIN2B	67	3'	-101	71	83	N.D.	ACAGCAATGCCAATGCTGGG	GGG	18.00 ± 2.31	AGTGCTGTTCTCCCAAGTTC	TGG	28.64 ± 0.69
GRIN2B	42	3'	-76	72	84	N.D.	GTGGAAATCATCTTTCTCGT	TGG	14.56 ± 7.84	GGCATTGCTGTCATCCTCGT	GGG	21.26 ± 2.68
GRIN2B	16	3'	-50	73	85	N.D.	TCTGCTGCCTGACACGGCCA	AGG	4.24 ± 0.79	TCCCAAGTTCTGGTTGGTGT	TGG	19.64 ± 0.23
GRIN2B	2	3'	-36	74	86	N.D.	CGAGCTCTGCTGCCTGACAC	CGG	2.99 ± 0.31	TTGGCCGTCCTGGCCGTGTC	AGG	4.74 ± 0.15
GRIN2B	9	5'	-25	75	87	1.04 ± 0.53	TCCTTGATGGCCACCTCGTC	CGG	2.25 ± 1.08	TTCCGACGAGGTGGCCATCA	AGG	17.13 ± 2.90
GRIN2B	18	5'	-16	76	88	5.93 ± 1.25	ATGACAGCAATGCCAATGCT	TGG	16.46 ± 2.28	TGGCATTGCTGTCATCCTCG	TGG	16.35 ± 1.25
GRIN2B	23	5'	-11	77	88	2.28 ± 0.34	AGCAATGCCAATGCTGGGGG	GGG	3.19 ± 0.51	TGGCATTGCTGTCATCCTCG	TGG	15.17 ± 2.02
GRIN2B	28	5'	-6	78	86	1.45 ± 0.12	GCCAACACCAACCAGAACTT	TGG	17.80 ± 2.30	TTGGCCGTCCTGGCCGTGTC	AGG	4.46 ± 1.35
GRIN2B	30	5'	-4	69	85	11.80 ± 0.29	GGAGAACAGCACTCCGCTCT	TGG	21.80 ± 1.40	TCCCAAGTTCTGGTTGGTGT	TGG	21.33 ± 0.63
GRIN2B	33	5'	-1	76	65	24.24 ± 0.23	ATGACAGCAATGCCAATGCT	TGG	19.48 ± 1.88	CCTCGTGGGCACTTCCGACG	AGG	21.19 ± 3.42
GRIN2B	34	5'	0	79	65	20.83 ± 0.95	TGACAGCAATGCCAATGCTG	GGG	21.44 ± 3.02	CCTCGTGGGCACTTCCGACG	AGG	24.11 ± 0.14
GRIN2B	36	5'	2	58	59	31.76 ± 1.00	CCGGCCAAGACCTTGAAGCC	AGG	32.50 ± 0.50	CTGGTTGTAGGATTTGAGTT	AGG	26.7 ± 2.9
GRIN2B	38	5'	4	54	55	34.45 ± 0.45	TATTACAGAATGAGAGACTG	TGG	30.90 ± 1.40	TTATTTCTGAAGAATATTAA	AGG	27.6 ± 2.5
GRIN2B	38	5'	4	56	57	44.22 ± 0.55	AAAAGACCTAAACAAAAGAA	TGG	23.20 ± 2.10	TGTGTGAGGATAAAAGAGTT	GGG	29.4 ± 2.7
GRIN2B	38	5'	4	77	65	9.60 ± 0.25	AGCAATGCCAATGCTGGGGG	GGG	4.19 ± 0.58	CCTCGTGGGCACTTCCGACG	AGG	21.78 ± 1.70
GRIN2B	40	5'	6	60	61	42.54 ± 1.39	TCAGAGCTTCCTGACACCCA	TGG	14.20 ± 1.50	AATACCTAGTTACAGGCATT	TGG	24.8 ± 1.0
GRIN2B	45	5'	11	76	87	18.96 ± 0.93	ATGACAGCAATGCCAATGCT	TGG	20.45 ± 0.98	TTCCGACGAGGTGGCCATCA	AGG	13.21 ± 0.74
GRIN2B	50	5'	16	77	87	5.33 ± 0.57	AGCAATGCCAATGCTGGGGG	GGG	4.93 ± 2.06	TTCCGACGAGGTGGCCATCA	AGG	12.51 ± 1.21
GRIN2B	89	5'	55	80	89	7.31 ± 0.83	GAGAACAGCACTCCGCTCTG	GGG	3.09 ± 0.54	CAGAAGAGCCCCCCCAGCAT	TGG	25.02 ± 1.86
GRIN2B	105	5'	71	78	90	10.56 ± 1.21	GCCAACACCAACCAGAACTT	TGG	25.29 ± 1.65	CGTGGGCACTTCCGACGAGG	TGG	23.32 ± 0.78
GRIN2B	132	5'	98	81	67	2.66 ± 0.89	CTGCCTGACACGGCCAGGAC	CGG	4.34 ± 0.62	TGATTTCCACCATCTCTCCG	TGG	20.95 ± 0.79
GRIN2B	175	5'	141	80	67	N.D.	GAGAACAGCACTCCGCTCTG	GGG	2.96 ± 0.93	TGATTTCCACCATCTCTCCG	TGG	19.77 ± 2.20
GRIN2B	231	5'	197	81	91	N.D.	CTGCCTGACACGGCCAGGAC	CGG	6.17 ± 2.09	TGACCGGAAGATCCAGGGGG	TGG	23.36 ± 2.34
MeCP2	38	5'	4	92	93	12.16 ± 2.58	GTCCAACCTTCAGGCAAGGT	GGG	24.11 ± 3.48	AAGCTTAAACAAAGGAAGTC	TGG	35.76 ± 2.65
MeCP2	34	5'	0	94	95	11.72 ± 2.40	GCGCTGTTTGGGGGAAGCCG	AGG	N.T	GGCTCCATTATCCGTGACCG	GGG	N.T
VEGFA	50	5'	16	96	97	23.92 ± 0.54	GGGTGGGGGGAGTTTGCTCC	TGG	14.15 ± 1.07	TCCCTCTTTAGCCAGAGCCG	GGG	33.59 ± 0.88
VEGFA	54	5'	20	98	99	16.32 ± 1.01	GACCCCCTCCACCCCGCCTC	CGG	24.52 ± 1.80	GAAACTTTTCGTCCAACTTC	TGG	10.45 ± 1.14

Table S2. List of sgRNAs used in this study. Related to Figure 2.

gene	sgRNA ID	guide sequence (5' to 3')	PAM	strand	species
EMX1	1	GAGTCCGAGCAGAAGAAGAA	GGG	+	*H. sapiens*
EMX1	2	GGAAGGGCCTGAGTCCGAGCAGAAGAAGA	GGG	+	*H. sapiens*
EMX1	3	GGCCTCCAAGGAGTCCGAGCAGAAGAAGAA	GGG	+	*H. sapiens*
EMX1	4	AGGCCCCAGTGGCTGCTCTG	GGG	+	*H. sapiens*
EMX1	5	GGGGCACAGATGAGAAACTC	AGG	—	*H. sapiens*
EMX1	6	TCACCTGGGCCAGGGAGGGA	GGG	—	*H. sapiens*
EMX1	7	TGAAGGTGTGGTTCCAGAAC	CGG	+	*H. sapiens*
EMX1	8	AGGTGTGGTTCCAGAACCGG	AGG	+	*H. sapiens*
EMX1	9	GCCGTTTGTACTTTGTCCTC	CGG	—	*H. sapiens*
EMX1	10	CAAACGGCAGAAGCTGGAGG	AGG	+	*H. sapiens*
EMX1	11	CGGCAGAAGCTGGAGGAGGA	AGG	+	*H. sapiens*
EMX1	12	TGAGTCCGAGCAGAAGAAGA	AGG	+	*H. sapiens*
EMX1	13	GGAGCCCTTCTTCTTCTGCT	CGG	—	*H. sapiens*
EMX1	14	AGGGCTCCCATCACATCAAC	CGG	+	*H. sapiens*
EMX1	15	TGCGCCACCGGTTGATGTGA	TGG	—	*H. sapiens*
EMX1	16	TTGCCACGAAGCAGGCCAAT	GGG	+	*H. sapiens*
EMX1	17	CACGAAGCAGGCCAATGGGG	AGG	+	*H. sapiens*
EMX1	18	TCACCTCCAATGACTAGGGT	GGG	+	*H. sapiens*
EMX1	19	GGCAGAGTGCTGCTTGCTGC	TGG	+	*H. sapiens*
EMX1	20	GACATCGATGTCCTCCCCAT	TGG	—	*H. sapiens*
EMX1	21	GTCACCTCCAATGACTAGGG	TGG	+	*H. sapiens*
EMX1	22	GGGCAACCACAAACCCACGA	GGG	+	*H. sapiens*
EMX1	23	ACTCTGCCCTCGTGGGTTTG	TGG	—	*H. sapiens*
EMX1	24	CAAGCAGCACTCTGCCCTCG	TGG	—	*H. sapiens*
EMX1	25	TTCTTCTTCTGCTCGGACTC	AGG	—	*H. sapiens*
EMX1	26	CTCCCCATTGGCCTGCTTCG	AGG	—	*H. sapiens*
EMX1	27	GTCACCTCCAATGACTAGGG	TGG	+	*H. sapiens*
DYRK1A	28	GAACTTACCTGGTTAGTTAG	AGG	—	*H. sapiens*
DYRK1A	29	GGAGTATCAGAAATGACTAT	TGG	+	*H. sapiens*
DYRK1A	30	GGTCACTGTACTGATGTGAA	TGG	—	*H. sapiens*
DYRK1A	31	GCCAAACATAAGTGACCAAC	AGG	+	*H. sapiens*
DYRK1A	32	GTTCCTTAAATAAGAACTTT	AGG	—	*H. sapiens*
DYRK1A	33	TGTCAAATGATACAAACATT	AGG	+	*H. sapiens*
DYRK1A	34	ATCTGGTCAGAATATGATAA	AGG	—	*H. sapiens*
DYRK1A	35	GTCACTGTACTGATGTGAAT	TGG	—	*H. sapiens*
DYRK1A	36	CATCTGAAGGCCAGCAGCAT	TGG	—	*H. sapiens*
DYRK1A	37	TGATAAGGCAGAAACCTGTT	TGG	—	*H. sapiens*
DYRK1A	38	GAAGATAAGTGAGGTTTAAA	AGG	—	*H. sapiens*
DYRK1A	39	GTATCATTTGACATATCTAA	TGG	—	*H. sapiens*
DYRK1A	40	CAGCATGGAATGAAAATGAC	CGG	—	*H. sapiens*
DYRK1A	41	GCAGCATGGAATGAAAATGA	CGG	—	*H. sapiens*
DYRK1A	42	GTGCAAGCCGAACAGATGAA	AGG	—	*H. sapiens*
DYRK1A	43	TCACTGTACTGATGTGAATG	GGG	—	*H. sapiens*
DYRK1A	44	TCCTACAAGAAGATAAGTGA	AGG	—	*H. sapiens*
DYRK1A	45	TATCATTTGACATATCTAAT	TGG	—	*H. sapiens*
DYRK1A	46	AACTTTTCTAACTACAAACA	AGG	—	*H. sapiens*
DYRK1A	47	AACCTCACTTATCTTCTTGT	AGG	+	*H. sapiens*
DYRK1A	48	CTCACTTATCTTCTTGTAGG	AGG	+	*H. sapiens*
DYRK1A	49	CCATGCTGCTGGCCTTCAGA	TGG	+	*H. sapiens*
DYRK1A	50	GCTGCTGGCCTTCAGATGGC	TGG	+	*H. sapiens*
DYRK1A	51	TCAGCAACCTCTAACTAACC	AGG	+	*H. sapiens*
DYRK1A	52	TCATTTTCATTCCATGCTGC	TGG	+	*H. sapiens*
DYRK1A	53	CATGCAAACCTTCATCTGTT	CGG	+	*H. sapiens*
DYRK1A	54	TATTACAGAATGAGAGACTG	TGG	—	*H. sapiens*
DYRK1A	55	TTATTTCTGAAGAATATTAA	AGG	+	*H. sapiens*
DYRK1A	56	AAAAGACCTAAACAAAAGAA	TGG	—	*H. sapiens*
DYRK1A	57	TGTGTGAGGATAAAAGAGTT	GGG	+	*H. sapiens*
DYRK1A	58	CCGGCCAAGACCTTGAAGCC	AGG	—	*H. sapiens*
DYRK1A	59	CTGGTTGTAGGATTTGAGTT	AGG	+	*H. sapiens*
DYRK1A	60	TCAGAGCTTCCTGACACCCA	TGG	—	*H. sapiens*
DYRK1A	61	AATACCTAGTTACAGGCATT	TGG	+	*H. sapiens*
GRIN2B	62	GGTGATGATGCTCTTTGGGT	CGG	—	*H. sapiens*
GRIN2B	63	TCTGTGATCTCATGTCTGAC	CGG	+	*H. sapiens*
GRIN2B	64	CAGCAATGCCAATGCTGGGG	GGG	—	*H. sapiens*
GRIN2B	65	CCTCGTGGGCACTTCCGACG	AGG	+	*H. sapiens*
GRIN2B	66	TTTCTCGTGGGCATCCTTGA	TGG	—	*H. sapiens*
GRIN2B	67	TGATTTCCACCATCTCTCCG	TGG	+	*H. sapiens*
GRIN2B	68	GGAGAACAGCACTCCGCTCT	GGG	—	*H. sapiens*
GRIN2B	69	CTGGTTGGTGTTGGCCGTCC	TGG	+	*H. sapiens*
GRIN2B	70	CCAACACCAACCAGAACTTG	GGG	—	*H. sapiens*
GRIN2B	71	ACAGCAATGCCAATGCTGGG	GGG	—	*H. sapiens*
GRIN2B	72	GTGGAAATCATCTTTCTCGT	TGG	—	*H. sapiens*
GRIN2B	73	TCTGCTGCCTGACACGGCCA	AGG	—	*H. sapiens*
GRIN2B	74	CGAGCTCTGCTGCCTGACAC	CGG	—	*H. sapiens*
GRIN2B	75	TCCTTGATGGCCACCTCGTC	CGG	—	*H. sapiens*
GRIN2B	76	ATGACAGCAATGCCAATGCT	TGG	—	*H. sapiens*
GRIN2B	77	AGCAATGCCAATGCTGGGGG	GGG	—	*H. sapiens*
GRIN2B	78	GCCAACACCAACCAGAACTT	TGG	—	*H. sapiens*
GRIN2B	79	TGACAGCAATGCCAATGCTG	GGG	—	*H. sapiens*
GRIN2B	80	GAGAACAGCACTCCGCTCTG	GGG	—	*H. sapiens*
GRIN2B	81	CTGCCTGACACGGCCAGGAC	CGG	—	*H. sapiens*
GRIN2B	82	CTGGTAGATGGAGTTGGGTT	TGG	+	*H. sapiens*
GRIN2B	83	AGTGCTGTTCTCCCAAGTTC	TGG	+	*H. sapiens*
GRIN2B	84	GGCATTGCTGTCATCCTCGT	GGG	+	*H. sapiens*
GRIN2B	85	TCCCAAGTTCTGGTTGGTGT	TGG	+	*H. sapiens*
GRIN2B	86	TTGGCCGTCCTGGCCGTGTC	AGG	+	*H. sapiens*
GRIN2B	87	TTCCGACGAGGTGGCCATCA	AGG	+	*H. sapiens*
GRIN2B	88	TGGCATTGCTGTCATCCTCG	TGG	+	*H. sapiens*
GRIN2B	89	CAGAAGAGCCCCCCCAGCAT	TGG	+	*H. sapiens*
GRIN2B	90	CGTGGGCACTTCCGACGAGG	TGG	+	*H. sapiens*
GRIN2B	91	TGACCGGAAGATCCAGGGGG	TGG	+	*H. sapiens*
MeCP2	92	GTCCAACCTTCAGGCAAGGT	GGG	—	*M. musculus*
MeCP2	93	AAGCTTAAACAAAGGAAGTC	TGG	+	*M. musculus*
MeCP2	94	GCGCTGTTTGGGGGAAGCCG	AGG	—	*M. musculus*
MeCP2	95	GGCTCCATTATCCGTGACCG	GGG	+	*M. musculus*
VEGFA	96	GGGTGGGGGGAGTTTGCTCC	TGG	—	*H. sapiens*
VEGFA	97	TCCCTCTTTAGCCAGAGCCG	GGG	+	*H. sapiens*
VEGFA	98	GACCCCCTCCACCCCGCCTC	CGG	—	*H. sapiens*
VEGFA	99	GAAACTTTTCGTCCAACTTC	TGG	+	*H. sapiens*