

**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.	TGGCCACCGGTTGATGTGA	TGG	13.15	AGGCCACAGTGGCTGCTCTG	GGG	27.29
EMX1	101	3'	-135	23	1	N.D.	ACTCTGCOCTGTTGGGTTTG	TGG	24.7	GAGTCGAGCAGAAGAAGAA	GGG	21.9
EMX1	48	3'	-82	23	17	N.D.	ACTCTGCOCTGTTGGGTTTG	TGG	24.7	CACGAAGCAGGCCAATGGGG	AGG	13.57
EMX1	25	3'	-59	10	13	N.D.	CAAACGGCAGAAGCTGGAGG	AGG	26.15	GGGCCCTTCTTCTCTCTCT	CGG	33.17
EMX1	15	3'	-49	4	5	N.D.	AGGCCACAGTGGCTGCTCTG	GGG	27.29	GGGCCACAGATGAGAAACTC	AGG	26.56
EMX1	8	3'	-42	7	9	N.D.	TGAAGTGTGTTTCCAGAAC	CGG	36.02	GCCGTTTGTACTTTGTCTCT	CGG	30.49
EMX1	26	5'	-8	9	19	13.7 ± 1.27	GCCGTTTGTACTTTGTCTCT	CGG	9.82	GGCAGAGTGTCTTGTCTGC	TGG	26.15
EMX1	30	5'	-4	9	10	19.72 ± 0.32	GCCGTTTGTACTTTGTCTCT	CGG	30.49	CAAACGGCAGAAGCTGGAGG	AGG	22.06
EMX1	31	5'	-3	6	7	21.35 ± 2.23	TCACTGGGCCAGGGAGGGA	GGG	10.75	TGAAGTGTGTTTCCAGAAC	CGG	36.02
EMX1	34	5'	0	15	16	26.89 ± 1.54	TGGCCACCGGTTGATGTGA	TGG	13.15	TTGCCACGAAAGCAGGCCAAT	GGG	13.77
EMX1	38	5'	4	15	17	36.31 ± 2.97	TGGCCACCGGTTGATGTGA	TGG	14.49	CACGAAGCAGGCCAATGGGG	AGG	13.57
EMX1	51	5'	17	5	7	31.12 ± 0.25	GGGCCACAGATGAGAAACTC	AGG	26.56	TGAAGTGTGTTTCCAGAAC	CGG	36.02
EMX1	54	5'	20	5	8	32.41 ± 3.68	GGGCCACAGATGAGAAACTC	AGG	26.56	AGGTGTGTTTCCAGAAGCCG	AGG	35.53
EMX1	65	5'	31	6	10	13.45 ± 1.99	TCACTGGGCCAGGGAGGGA	GGG	10.75	CAAACGGCAGAAGCTGGAGG	AGG	26.15
EMX1	69	5'	35	6	11	12.39 ± 1.29	TCACTGGGCCAGGGAGGGA	GGG	10.75	GGCAGAACCTGGAGGAGGA	AGG	22.06
EMX1	76	5'	42	9	14	21.71 ± 1.66	GCCGTTTGTACTTTGTCTCT	CGG	30.49	AGGGCTCCCATCAGATCAAC	CGG	41.27
EMX1	85	5'	51	5	10	21.89 ± 1.88	GGGCCACAGATGAGAAACTC	AGG	26.56	CAAACGGCAGAAGCTGGAGG	AGG	26.15
EMX1	95	5'	61	6	12	5.88 ± 1.81	TCACTGGGCCAGGGAGGGA	GGG	10.75	TGAGTCGAGCAGAAGAAGA	AGG	29.06
EMX1	135	5'	101	5	14	15.78 ± 2.19	GGGCCACAGATGAGAAACTC	AGG	26.56	AGGGCTCCCATCAGATCAAC	CGG	41.27
EMX1	145	5'	111	6	16	N.D.	TCACTGGGCCAGGGAGGGA	GGG	10.75	TTGCCACGAAAGCAGGCCAAT	GGG	13.77
EMX1	181	5'	147	6	18	N.D.	TCACTGGGCCAGGGAGGGA	GGG	10.75	TCACTCCAATGACTAGGGT	GGG	25.14
EMX1	201	5'	167	5	18	N.D.	GGGCCACAGATGAGAAACTC	AGG	26.56	TCACTCCAATGACTAGGGT	GGG	25.14
EMX1	222	5'	188	6	19	N.D.	TCACTGGGCCAGGGAGGGA	GGG	10.75	GGCAGAGTGTCTTGTCTGC	TGG	10.75
EMX1	242	5'	208	5	19	N.D.	GGGCCACAGATGAGAAACTC	AGG	26.56	GGCAGAGTGTCTTGTCTGC	TGG	17.22
DYRK1A	164	3'	-198	34	47	N.D.	ATCTGGTCAGAATATGATAA	AGG	10.65 ± 2.05	AAOCTCACTTATCTTCTTGT	AGG	19.02 ± 4.32
DYRK1A	105	3'	-139	35	47	N.D.	GTCACGTGACTGATGTGAAT	TGG	16.71 ± 2.47	AAOCTCACTTATCTTCTTGT	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.	GTCACGTGACTGATGTGAAT	TGG	17.83 ± 0.43	CCATGCTGCTGGCCTTCAGA	TGG	17.15 ± 3.29
DYRK1A	4	3'	-38	37	31	N.D.	TGATAAGGCAGAAOCTGTT	TGG	4.95 ± 0.66	GCCAAACATAAGTGAOCCAC	AGG	16.38 ± 3.39
DYRK1A	17	5'	-17	38	47	N.D.	GAAGATAAGTGAAGTTTAAA	AGG	5.30 ± 1.98	AAOCTCACTTATCTTCTTGT	AGG	24.18 ± 3.22
DYRK1A	21	5'	-13	39	33	10.54 ± 0.63	GTATCATTGACATATCTAA	TGG	26.90 ± 1.17	TGTCAAATGATACAAACATT	AGG	29.69 ± 0.86
DYRK1A	25	5'	-9	40	49	2.33 ± 0.11	CAGCATGGAATGAAATGAC	CGG	3.33 ± 0.56	CCATGCTGCTGGCCTTCAGA	TGG	20.43 ± 2.40
DYRK1A	29	5'	-5	41	50	27.76 ± 0.84	GCAGCATGGAATGAAATGA	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	TCAGCAACCTCAACTAACCC	AGG	24.14 ± 2.95
DYRK1A	35	5'	1	42	52	7.63 ± 0.51	GTGCAAGCCGACAGATGAA	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	GCCAAACATAAGTGAOCCAC	AGG	33.1 ± 0.4
DYRK1A	42	5'	8	43	31	38.36 ± 0.32	TCACTGTACTGATGTGAATG	GGG	24.68 ± 4.58	GCCAAACATAAGTGAOCCAC	AGG	29.46 ± 3.30
DYRK1A	43	5'	9	32	33	28.97 ± 0.32	GTCTTAAATAAGAAGTTT	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	CATGCAAAOCTTCATCTGTT	CGG	30.42 ± 1.14
DYRK1A	77	5'	43	36	31	6.63 ± 0.27	COCTGAAAGGCCAGCAGCAT	TGG	10.02 ± 1.17	GCCAAACATAAGTGAOCCAC	AGG	22.92 ± 5.16
DYRK1A	86	5'	52	38	52	N.D.	GAAGATAAGTGAAGTTTAAA	AGG	2.90 ± 0.82	TCATTTTCATTCCATGCTGC	TGG	17.30 ± 1.62
DYRK1A	97	5'	63	38	49	N.D.	GAAGATAAGTGAAGTTTAAA	AGG	2.16 ± 0.48	CCATGCTGCTGGCCTTCAGA	TGG	24.75 ± 2.50
DYRK1A	131	5'	97	45	52	N.D.	TATCATTGACATATCTAAT	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	GCCAAACATAAGTGAOCCAC	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.	CCAAACCAACCAAGACTTG	GGG	2.95 ± 0.21	CTGGTAGTGGAGTTGGGTT	TGG	17.25 ± 1.30
GRIN2B	67	3'	-101	71	83	N.D.	ACAGCAATGCAATGCTGGG	GGG	18.00 ± 2.31	AGTGTGTTCTCCAAAGTTC	TGG	28.64 ± 0.69
GRIN2B	42	3'	-76	72	84	N.D.	GTGAAATCATCTTTCTCGT	TGG	14.56 ± 7.84	GGCATTGCTGTCTOCTGTT	GGG	21.26 ± 2.68
GRIN2B	16	3'	-50	73	85	N.D.	TCTGCTGCTGACACGGCCA	AGG	4.24 ± 0.79	TOCCAAGTTCGTGGTGGTGT	TGG	19.64 ± 0.23
GRIN2B	2	3'	-36	74	86	N.D.	OGAGCTCTGCTGCTGACAC	CGG	2.99 ± 0.31	TTGGCCGCTGCTGGCCTGTC	AGG	4.74 ± 0.15
GRIN2B	9	5'	-25	75	87	1.04 ± 0.53	TCCTTGATGGCCACTGCTG	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	TGGCATTGCTGTCTOCTG	TGG	16.35 ± 1.25
GRIN2B	23	5'	-11	77	88	2.28 ± 0.34	AGCAATGCCAATGCTGGGG	GGG	3.19 ± 0.51	TGGCATTGCTGTCTOCTG	TGG	15.17 ± 2.02
GRIN2B	28	5'	-6	78	86	1.45 ± 0.12	GCCAAACCAACCAAGACTT	TGG	17.80 ± 2.30	TTGGCCGCTGCTGGCCTGTC	AGG	4.46 ± 1.35
GRIN2B	30	5'	-4	69	85	11.80 ± 0.29	GGAGAACGCACTCOGCTCT	TGG	21.80 ± 1.40	TOCCAAGTTCGTGGTGGTGT	TGG	21.33 ± 0.63
GRIN2B	33	5'	-1	76	65	24.24 ± 0.23	ATGACAGCAATGCCAATGCT	TGG	19.48 ± 1.88	OCTGCTGGCCTTCCGAGC	AGG	21.19 ± 3.42
GRIN2B	34	5'	0	79	65	20.83 ± 0.95	TGACAGCAATGCCAATGCTG	GGG	21.44 ± 3.02	OCTGCTGGCCTTCCGAGC	AGG	24.11 ± 0.14
GRIN2B	36	5'	2	58	59	31.76 ± 1.00	COGGCCAAAGAOCTTGAAGCC	AGG	32.50 ± 0.50	CTGGTTGTAGGATTTGAGTT	AGG	26.7 ± 2.9
GRIN2B	38	5'	4	54	55	34.45 ± 0.45	TATTACAGAAATGAGACTG	TGG	30.90 ± 1.40	TTATTTCTGAAGAATATTAA	AGG	27.6 ± 2.5
GRIN2B	38	5'	4	56	57	44.22 ± 0.55	AAAAGAOCTAAACAAAAGAA	TGG	23.20 ± 2.10	TGTGTGAGGATAAAGAGATT	GGG	29.4 ± 2.7
GRIN2B	38	5'	4	77	65	9.60 ± 0.25	AGCAATGCCAATGCTGGGG	GGG	4.19 ± 0.58	OCTGCTGGCCTTCCGAGC	AGG	21.78 ± 1.70
GRIN2B	40	5'	6	60	61	42.54 ± 1.39	TCAGAGCTTCTGACAOCCA	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	AGCAATGCCAATGCTGGGG	GGG	4.93 ± 2.06	TTCCGACGAGGTGGCCATCA	AGG	12.51 ± 1.21
GRIN2B	89	5'	55	80	89	7.31 ± 0.83	GAGAAGCACTCOGCTCTG	GGG	3.09 ± 0.54	CAGAAGAGGCCCCCAGCAT	TGG	25.02 ± 1.86
GRIN2B	105	5'	71	78	90	10.56 ± 1.21	GCCAAACCAACCAAGACTT	TGG	25.29 ± 1.65	CGTGGCCTTCCGAGCAGG	TGG	23.32 ± 0.78
GRIN2B	132	5'	98	81	67	2.66 ± 0.89	CTGCTGACACGGCCAGGAC	CGG	4.34 ± 0.62	TGATTTCCACCATCTCTCG	TGG	20.95 ± 0.79
GRIN2B	175	5'	141	80	67	N.D.	GAGAAGCACTCOGCTCTG	GGG	2.96 ± 0.93	TGATTTCCACCATCTCTCG	TGG	19.77 ± 2.20
GRIN2B	231	5'	197	81	91	N.D.	CTGCTGACACGGCCAGGAC	CGG	6.17 ± 2.09	TGACCGAAGATCCAGGGGG	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	GCGCTGTTTGGGGAAAGCCG	AGG	N.T	GGCTCCATTATCCGTGACCG	GGG	N.T
VEGFA	50	5'	16	96	97	23.92 ± 0.54	GGGTGGGGGAGTTTCTCTC	TGG	14.15 ± 1.07	TCCTCTTTAGCCAGAGCCG	GGG	33.59 ± 0.88
VEGFA	54	5'	20	98	99	16.32 ± 1.01	GACCCCTCCACCCCGCCTC	CGG	24.52 ± 1.80	GAACTTTTTCGTCCAACTTC	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	+	<i>H. sapiens</i>
EMX1	2	GGAAAGGCOCTGAGTCCGAGCCAGAAGAAGA	GGG	+	<i>H. sapiens</i>
EMX1	3	GGCOCTCAAGGAGTCCGAGCAGAAGAAGA	GGG	+	<i>H. sapiens</i>
EMX1	4	AGGCOCCAGTGGCTGCTCTG	GGG	+	<i>H. sapiens</i>
EMX1	5	GGGGCACAGATGAGAACTC	AGG	-	<i>H. sapiens</i>
EMX1	6	TCACTGGGCCAGGAGGGA	GGG	-	<i>H. sapiens</i>
EMX1	7	TGAAGGTGTGTTCCAGAAC	CGG	+	<i>H. sapiens</i>
EMX1	8	AGGTGTGTTCCAGAACCGG	AGG	+	<i>H. sapiens</i>
EMX1	9	GCOGTTTGTACTTTGCTCTC	CGG	-	<i>H. sapiens</i>
EMX1	10	CAAAACGGCAGAAGCTGGAAGG	AGG	+	<i>H. sapiens</i>
EMX1	11	CGGCAGAAGCTGAGGAGGA	AGG	+	<i>H. sapiens</i>
EMX1	12	TGAGTCCGAGCAGAAGAAGA	AGG	+	<i>H. sapiens</i>
EMX1	13	GGAGCOCTTCTTCTCTGCT	CGG	-	<i>H. sapiens</i>
EMX1	14	AGGGCTOCCATCACATCAAC	CGG	+	<i>H. sapiens</i>
EMX1	15	TGGCCACCGGTTGATGTGA	TGG	-	<i>H. sapiens</i>
EMX1	16	TTGCCACGAGCAGCCCAAT	GGG	+	<i>H. sapiens</i>
EMX1	17	CACGAAACGAGCCCAATGGGG	AGG	+	<i>H. sapiens</i>
EMX1	18	TCACTCCAATGACTAGGGT	GGG	+	<i>H. sapiens</i>
EMX1	19	GGCAGAGTGTCTCTCTGCT	TGG	+	<i>H. sapiens</i>
EMX1	20	GACATCGATGCTCTCCCAT	TGG	-	<i>H. sapiens</i>
EMX1	21	GTCACCTCCAATGACTAGGG	TGG	+	<i>H. sapiens</i>
EMX1	22	GGGCAACCCACAACCCACGA	GGG	+	<i>H. sapiens</i>
EMX1	23	ACTCTGCOCTGTGGGTTTG	TGG	-	<i>H. sapiens</i>
EMX1	24	CAAGCAGCACTCTGCOCTCG	TGG	-	<i>H. sapiens</i>
EMX1	25	TTCTTCTTCTGCTGGACTC	AGG	-	<i>H. sapiens</i>
EMX1	26	CTCOCCATTGGCTGCTCG	AGG	-	<i>H. sapiens</i>
EMX1	27	GTCACCTCCAATGACTAGGG	TGG	+	<i>H. sapiens</i>
DYRK1A	28	GAACCTAOCCTGGTTAGTTAG	AGG	-	<i>H. sapiens</i>
DYRK1A	29	GGAGTATCAGAAATGACTAT	TGG	+	<i>H. sapiens</i>
DYRK1A	30	GGTCACTGTACTGATGTGAA	TGG	-	<i>H. sapiens</i>
DYRK1A	31	GCCAAACATAAGTGAACCAAC	AGG	+	<i>H. sapiens</i>
DYRK1A	32	GTTCTTAAATAAGAACTTT	AGG	-	<i>H. sapiens</i>
DYRK1A	33	TGTCAAATGATACAAACATT	AGG	+	<i>H. sapiens</i>
DYRK1A	34	ATCTGGTCAGAATATGATAA	AGG	-	<i>H. sapiens</i>
DYRK1A	35	GTCACCTGTACTGATGTGAAT	TGG	-	<i>H. sapiens</i>
DYRK1A	36	CATCTGAAGGCCAGCAGCAT	TGG	-	<i>H. sapiens</i>
DYRK1A	37	TGATAAGGCAGAAACCTGTT	TGG	-	<i>H. sapiens</i>
DYRK1A	38	GAAGATAAGTGAAGTTAAA	AGG	-	<i>H. sapiens</i>
DYRK1A	39	GTATCATTGACATATCTAA	TGG	-	<i>H. sapiens</i>
DYRK1A	40	CAGCATGGAATGAAAATGAC	CGG	-	<i>H. sapiens</i>
DYRK1A	41	GCAGCATGGAATGAAAATGA	CGG	-	<i>H. sapiens</i>
DYRK1A	42	GTGCAAGCCGACAGATGAA	AGG	-	<i>H. sapiens</i>
DYRK1A	43	TCACTGTACTGATGTGAATG	GGG	-	<i>H. sapiens</i>
DYRK1A	44	TOCTACAAGAAGATAAGTGA	AGG	-	<i>H. sapiens</i>
DYRK1A	45	TATCATTGACATATCTAAT	TGG	-	<i>H. sapiens</i>
DYRK1A	46	AACTTTTCTAACTACAAACA	AGG	-	<i>H. sapiens</i>
DYRK1A	47	AAOCTCACTTATCTTCTGT	AGG	+	<i>H. sapiens</i>
DYRK1A	48	CTCACTTATCTTCTGTAGG	AGG	+	<i>H. sapiens</i>
DYRK1A	49	CCATGCTGCTGGCTTCAGA	TGG	+	<i>H. sapiens</i>
DYRK1A	50	GCTGCTGGCTTCAGATGGC	TGG	+	<i>H. sapiens</i>
DYRK1A	51	TCAGCAOCTCTAACTAACC	AGG	+	<i>H. sapiens</i>
DYRK1A	52	TCATTTTCATTCCATGCTGC	TGG	+	<i>H. sapiens</i>
DYRK1A	53	CATGCAAOCTTCATCTGTT	CGG	+	<i>H. sapiens</i>
DYRK1A	54	TATTACAGAATGAGAGACTG	TGG	-	<i>H. sapiens</i>
DYRK1A	55	TTATTTCTGAAGAATATTAA	AGG	+	<i>H. sapiens</i>
DYRK1A	56	AAAAAGCOCTAAACAAAAGAA	TGG	-	<i>H. sapiens</i>
DYRK1A	57	TGTGTGAGGATAAAAGAGTT	GGG	+	<i>H. sapiens</i>
DYRK1A	58	COGGCCAAAGCOCTTGAAGCC	AGG	-	<i>H. sapiens</i>
DYRK1A	59	CTGGTGTAGGATTTGAGTT	AGG	+	<i>H. sapiens</i>
DYRK1A	60	TCAGAGCTTCTGACACCCA	TGG	-	<i>H. sapiens</i>
DYRK1A	61	AATACCTAGTTACAGGCATT	TGG	+	<i>H. sapiens</i>
GRIN2B	62	GGTGTGATGCTCTTTGGGT	CGG	-	<i>H. sapiens</i>
GRIN2B	63	TCTGTGATCTCATGTCTGAC	CGG	+	<i>H. sapiens</i>
GRIN2B	64	CAGCAATGCCAATGCTGGGG	GGG	-	<i>H. sapiens</i>
GRIN2B	65	CCTCGTGGCCACTTCCGAGG	AGG	+	<i>H. sapiens</i>
GRIN2B	66	TTTCTCGTGGCATOCTTGA	TGG	-	<i>H. sapiens</i>
GRIN2B	67	TGATTTCCACCATCTCTCCG	TGG	+	<i>H. sapiens</i>
GRIN2B	68	GGAGAACAACCACTCCGCTCT	GGG	-	<i>H. sapiens</i>
GRIN2B	69	CTGGTGTGTTGGCCCTCC	TGG	+	<i>H. sapiens</i>
GRIN2B	70	CCAACAACAACCAAGACTTG	GGG	-	<i>H. sapiens</i>
GRIN2B	71	ACAGCAATGCCAATGCTGGG	GGG	-	<i>H. sapiens</i>
GRIN2B	72	GTGGAATCATCTTTCTGTT	TGG	-	<i>H. sapiens</i>
GRIN2B	73	TCTGCTGCTGACACGGCCA	AGG	-	<i>H. sapiens</i>
GRIN2B	74	CGAGCTCTGCTGCTGACAC	CGG	-	<i>H. sapiens</i>
GRIN2B	75	TOCTTGATGGCCACTCGTC	CGG	-	<i>H. sapiens</i>
GRIN2B	76	ATGACAGCAATGCCAATGCT	TGG	-	<i>H. sapiens</i>
GRIN2B	77	AGCAATGCCAATGCTGGGG	GGG	-	<i>H. sapiens</i>
GRIN2B	78	GCCAACAACAACCAAGACTT	TGG	-	<i>H. sapiens</i>
GRIN2B	79	TGACAGCAATGCCAATGCTG	GGG	-	<i>H. sapiens</i>
GRIN2B	80	GAGAACAACCACTCCGCTCTG	GGG	-	<i>H. sapiens</i>
GRIN2B	81	CTGCTGACACGGCCAGGAC	CGG	-	<i>H. sapiens</i>
GRIN2B	82	CTGGTAGATGAGTTGGGTT	TGG	+	<i>H. sapiens</i>
GRIN2B	83	AGTGTGTTCTCCAAAGTTT	TGG	+	<i>H. sapiens</i>
GRIN2B	84	GGCATTGCTGTATCCTCGT	GGG	+	<i>H. sapiens</i>
GRIN2B	85	TOCCAAGTTCTGGTTGGTGT	TGG	+	<i>H. sapiens</i>
GRIN2B	86	TTGGCCGCTGCTGGCCGTGT	AGG	+	<i>H. sapiens</i>
GRIN2B	87	TTGGCCGCTGCTGGCCGTGT	AGG	+	<i>H. sapiens</i>
GRIN2B	88	TGGCATTGCTGTATCCTCG	TGG	+	<i>H. sapiens</i>
GRIN2B	89	CAGAAGAGCCGCCAGCAT	TGG	+	<i>H. sapiens</i>
GRIN2B	90	CGTGGCCACTTCCGAGG	TGG	+	<i>H. sapiens</i>
GRIN2B	91	TGACCCGAAAGATCCAGGGG	TGG	+	<i>H. sapiens</i>
MeCP2	92	GTCCAACCTTCAAGCAAGGT	GGG	-	<i>M. musculus</i>
MeCP2	93	AAGCTTAAACAAGGAAGTG	TGG	+	<i>M. musculus</i>
MeCP2	94	GGCTGTTTGGGGGAGCCG	AGG	-	<i>M. musculus</i>
MeCP2	95	GGCTOATTATCOGTGACCG	GGG	+	<i>M. musculus</i>
VEGFA	96	GGTGGGGGAGTTTCTCC	TGG	-	<i>H. sapiens</i>
VEGFA	97	TOCTCTTTAGCCAGAGCCG	GGG	+	<i>H. sapiens</i>
VEGFA	98	GACCCCTCCACCCCGCTC	CGG	-	<i>H. sapiens</i>
VEGFA	99	GAAACTTTTCTGCTCAACTTC	TGG	+	<i>H. sapiens</i>