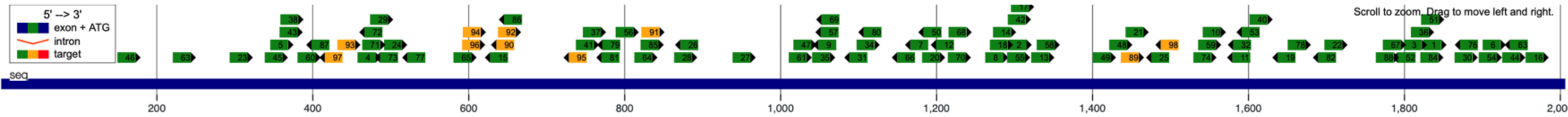


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Rank	Target sequence	Genomic location	Strand	GC content (%)	Self-complementarity	MM0	MM1	MM2	MM3	Efficiency
1	AAACTGGCAGACAAATTGGGTGG	seq:1826	+	45	0	1	0	0	0	68.23
2	TGGCAAAAAGATAAATCTTGGGG	seq:1294	+	30	0	1	0	0	0	67.83
3	GCAGAACTCAAAATGAAACAAGG	seq:1801	+	35	0	1	0	0	0	64.72
4	AATTTTAGACCGAAACAATGTGG	seq:459	+	30	0	1	0	0	0	64.43
5	TTGTTAAGAAGATGGTATGTGG	seq:347	+	30	0	1	0	0	0	63.86
6	AGATGTACAAGATAAAGGAATGG	seq:1902	+	30	0	1	0	0	0	59.93
7	ATCTGGAAC TTGTTGAGCAGAGG	seq:1168	-	45	0	1	0	0	0	59.84
8	AAAACAAGTTATAAAATCGATGG	seq:1264	+	20	0	1	0	0	0	59.34
9	ATAATTCACCTGTTTGAGGGTGG	seq:1050	-	40	0	1	0	0	0	58.91
10	GCTGATTCAGGTTACGGACAAGG	seq:1543	+	50	0	1	0	0	0	57.77