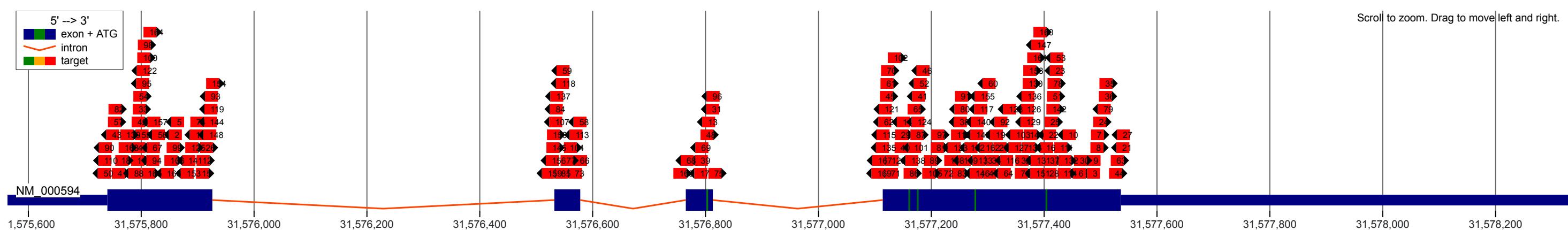


TNF



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Rank	Target sequence	Genomic location	Strand	GC content (%)	Self-complementarity	MM0	MM1	MM2	MM3	Efficiency
1	CGATCACTCCAAAGTGCAGC AGG	chr6:31575888	-	55	1	6	0	0	1	49.90
2	GGCGCCTGCCACGATCAGGA AGG	chr6:31575851	-	70	1	6	0	0	2	59.26
3	TCGGCAAAGTCGAGATAGTC GGG	chr6:31577478	-	50	2	7	0	0	0	43.25
4	TGAAAGCATGATCCGGGACG TGG	chr6:31575750	+	55	1	6	0	0	3	53.17
5	TGGTGGCGCTGCCACGATC AGG	chr6:31575855	-	70	2	6	0	0	3	46.31
6	GATTGATCTCAGCGCTGAGT CGG	chr6:31577453	-	50	3	7	0	0	1	57.52
7	ATCTCGACTTGGCGAGTCT GGG	chr6:31577485	+	50	2	7	0	0	1	49.77
8	TATCTCGACTTTGGCGAGTC TGG	chr6:31577484	+	50	2	7	0	0	1	30.61
9	CTCGGCAAAGTCGAGATAGT CGG	chr6:31577479	-	50	2	7	0	0	2	51.54
10	GTCGGTCACCCTCTCCACG TGG	chr6:31577435	-	65	0	7	0	0	2	48.20
11	GAGGCGCTCCCCAAGAACG AGG	chr6:31575784	+	65	0	6	0	1	3	45.60
12	TGGAGTGATGGCCCCCAGA GGG	chr6:31575900	+	65	0	6	0	0	5	62.00
13	TTACCTACAACATGGGTAC AGG	chr6:31576796	-	45	2	7	0	0	3	49.87
14	TGGCCCGGGGTTCAGCCAC TGG	chr6:31577141	-	75	0	7	0	0	3	39.48
15	TTGGAGTGATGGCCCCCAG AGG	chr6:31575899	+	65	0	6	0	1	5	68.09
16	GATGGGCTCATACCAGGGCT TGG	chr6:31577395	-	60	2	7	0	0	4	47.04
17	GGCTACAGGCTTGTCACTCG GGG	chr6:31576782	-	60	2	7	0	1	3	58.02
18	CATGATCCGGGACGTGGAGC TGG	chr6:31575756	+	65	1	6	0	0	7	40.64
19	TCTGGTAGGAGACGGCGATG CGG	chr6:31577306	-	60	0	7	0	0	5	73.59