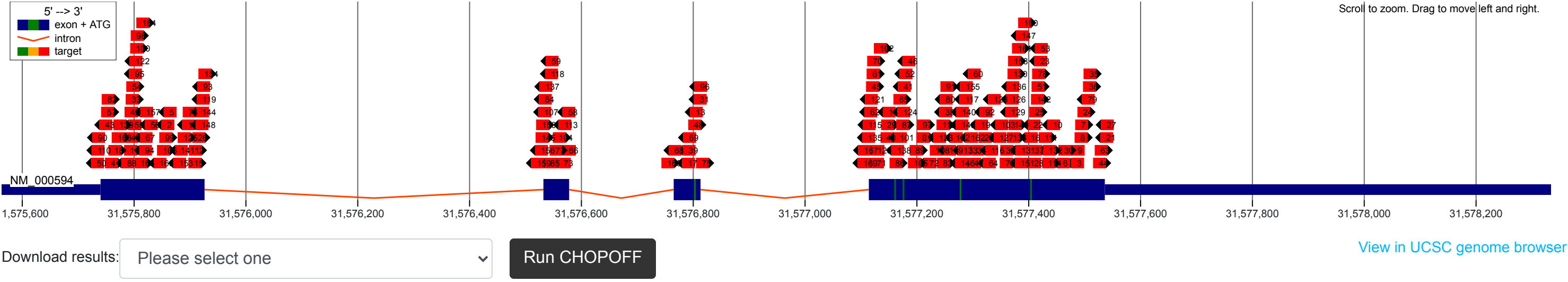


# TNF



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