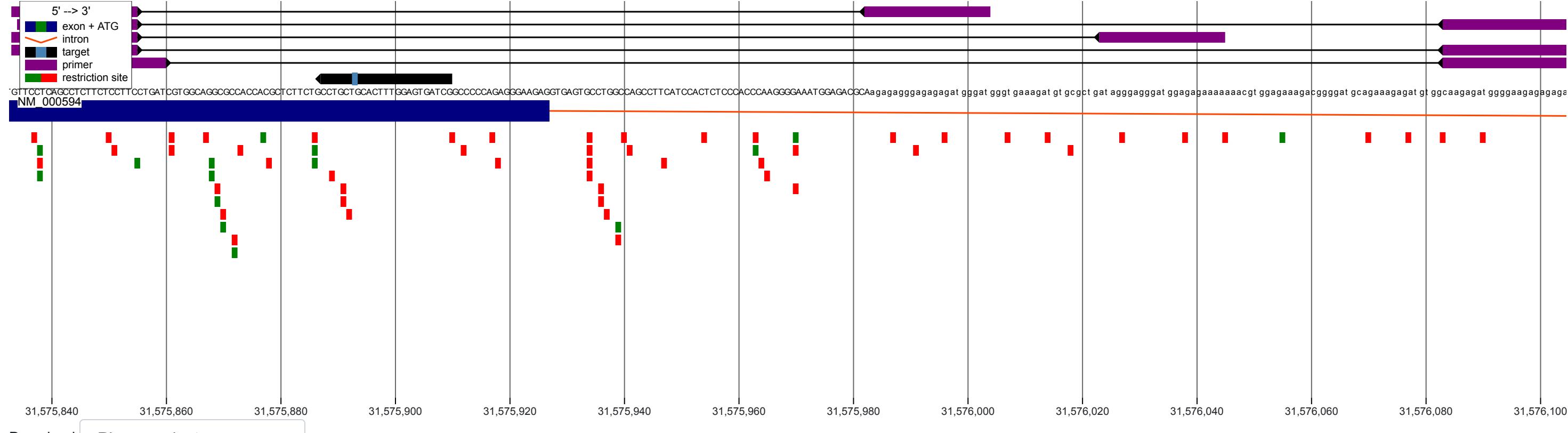


Target: TNF

Rank: 1

Target sequence: CGATCACTCCAAAGTGCAGC**AGG**

Download: Please select one ▾

Pair	Left primer coordinates	Left primer	Left primer Tm	Left primer off-targets	Right primer coordinates	Right primer	Right primer Tm	Right primer off-targets	Pair off-targets	Product size
1	chr6:31575840-31575861	CAGCCTCTCCTCCTGAT	60.0	6	chr6:31576084-31576106	tctctcttccatcttttg	60.0	7	0	266
2	chr6:31575834-31575856	GTTCCCTAGCCTCTTCCTTC	60.9	6	chr6:31576084-31576106	tctctcttccatcttttg	60.0	7	0	272
3	chr6:31575834-31575856	GTTCCCTAGCCTCTTCCTTC	60.9	6	chr6:31576024-31576046	ttttctccatccctccat	60.3	7	0	212
4	chr6:31575835-31575856	TTCCTCAGCCTCTTCCTTC	60.1	6	chr6:31576084-31576106	tctctcttccatcttttg	60.0	7	0	271
5	chr6:31575834-31575856	GTTCCCTAGCCTCTTCCTTC	60.9	6	chr6:31575983-31576005	atccccatctctccctctt	59.7	7	0	171

Off-targets		
Location	Number of mismatches	Sequence (including mismatches)
chr17:69047480	3	<b>gac</b> TCACTCCAAAGTGCAGCTGG
chr6_GL000251v2_alt:3053175	0	CCTGCTGCACTTGGAGTGATCG
chr6_GL000252v2_alt:2823621	0	CCTGCTGCACTTGGAGTGATCG
chr6_GL000253v2_alt:2880929	0	CCTGCTGCACTTGGAGTGATCG
chr6_GL000254v2_alt:2917786	0	CCTGCTGCACTTGGAGTGATCG
chr6_GL000255v2_alt:2831707	0	CCTGCTGCACTTGGAGTGATCG
chr6_GL000256v2_alt:2875168	0	CCTGCTGCACTTGGAGTGATCG

Shen et al. 2018 predictions of repair profile - statistics	
Reference sequence	TGGATGAAGGCTGGCCAGGCACTCACCTCTCCCTGGGGGCCGATCACTCAAAGTGC>>AGCAGGCAGAAGAGCGTGGTGGCGCTGCCACGATCAGGAAGGAGAAGAGGCTGAGGAAC
Frameshift frequency	59.29
Precision score	0.49
Frame +0 frequency	40.71
Frame +1 frequency	33.78
Frame +2 frequency	25.51
1-bp ins frequency	8.62
Highest del frequency	24.25
Highest ins frequency	6.19
Highest outcome frequency	24.25
Microhomology deletion frequency	73.73
Microhomology-less deletion frequency	17.65