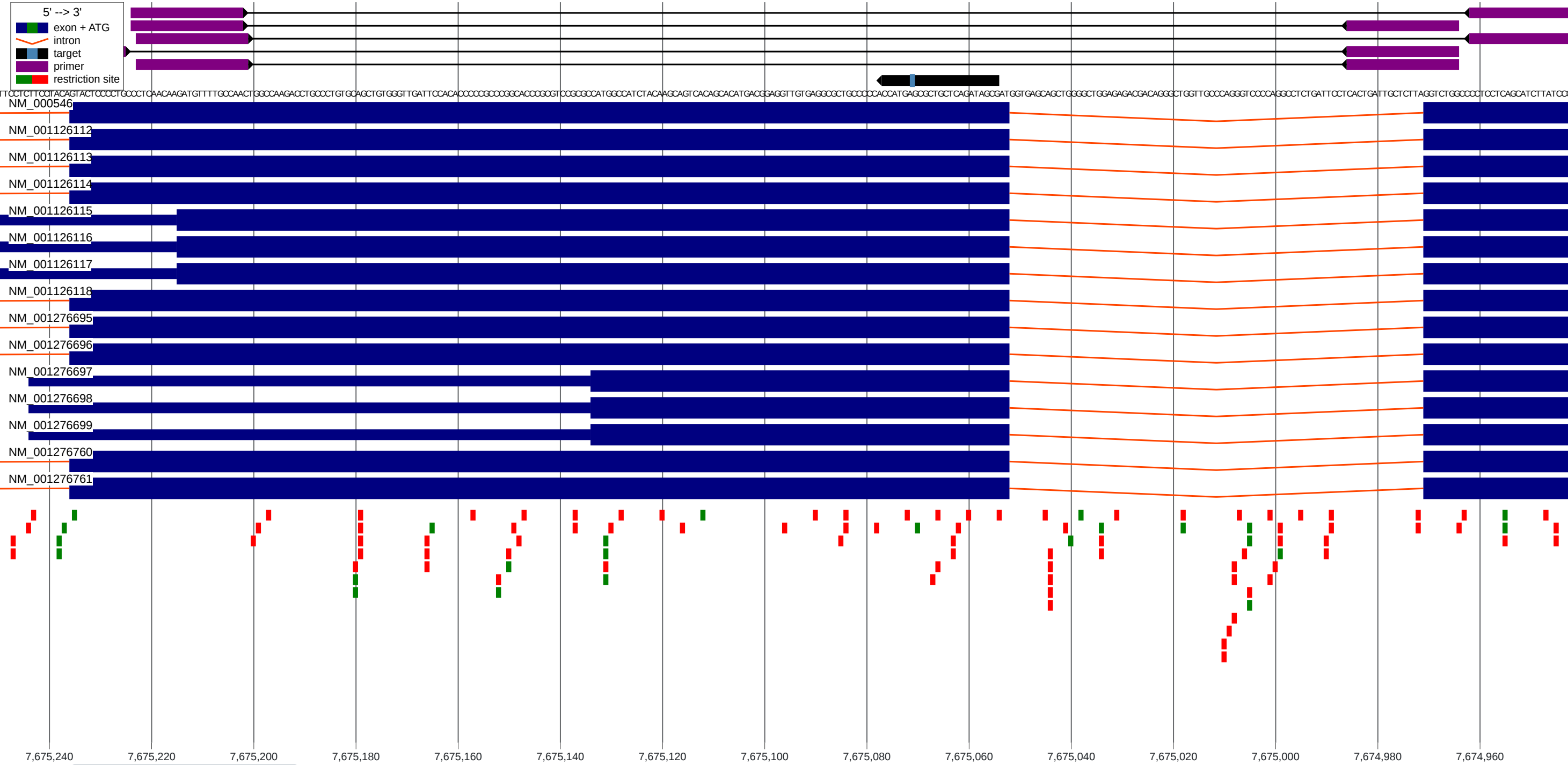


Target: **TP53**
Rank: **1**
Target sequence: **CGCTATCTGAGCAGCGCTCATGG**



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1	chr17:7675202-7675224	TCAACAAGATGTTTTGCCAACT	59.7	0	chr17:7674965-7674987	GCCAGACCTAAGAGCAATCAGT	59.9	0	0	259
2	chr17:7675226-7675248	TCTTCCTACAGTACTCCCCTGC	59.8	0	chr17:7674965-7674987	GCCAGACCTAAGAGCAATCAGT	59.9	0	0	283
3	chr17:7675202-7675224	TCAACAAGATGTTTTGCCAACT	59.7	0	chr17:7674941-7674963	ACTCGGATAAGATGCTGAGGAG	59.9	0	0	283
4	chr17:7675203-7675225	CTCAACAAGATGTTTTGCCAAC	59.7	0	chr17:7674965-7674987	GCCAGACCTAAGAGCAATCAGT	59.9	0	0	260
5	chr17:7675203-7675225	CTCAACAAGATGTTTTGCCAAC	59.7	0	chr17:7674941-7674963	ACTCGGATAAGATGCTGAGGAG	59.9	0	0	284

There are no off-targets.

Reference sequence	GGCAACCAGCCCTGTCGTCTCTCCAGCCCCAGCTGCTCACCATCGCTATCTGAGCAGCGC<>TCATGGTGGGGGCAGCGCCTCACAAACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGCC
Frameshift frequency	42.76
Precision score	0.56
Frame +0 frequency	57.24
Frame +1 frequency	20.49
Frame +2 frequency	22.27
1-bp ins frequency	8.14
Highest del frequency	44.83
Highest ins frequency	3.51
Highest outcome frequency	44.83
Microhomology deletion frequency	76.56
Microhomology-less deletion frequency	15.30