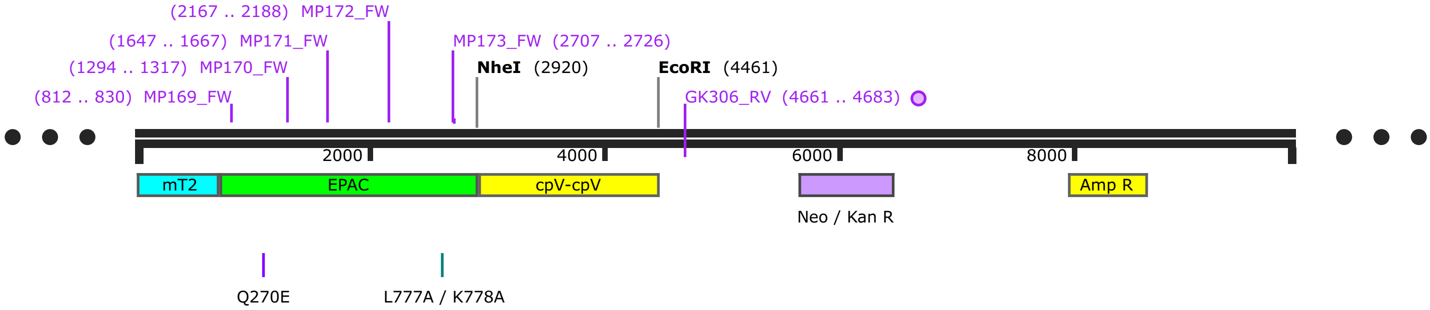
Sequence: H322_mTurq2del_EPACdDEPCD_Q270E_L777A_K778A_tdcp173V(ST).dna (Circular / 9846 bp)
Enzymes: Unique 6+ Cutters (34 of 678 total)
Features: 7 total
Primers: 6 total

Unique Cutters **Bold**



H322_mTurq2del_EPACdDEPCD_Q270E_L777A_K778A_tdcp173V(ST)
9846 bp

	Feature	Location	Size			Type
✓	**mT2**	16 .. 712	697 bp	🟦	↔	misc_feature
	/label = mT2					
✓	**EPAC**	719 .. 2919	2201 bp	🟩	↔	misc_feature
✓	**Q270E**	1084 .. 1086	3 bp	🟪	↔	misc_feature
	/label = Q270E					
✓	**L777A / K778A**	2605 .. 2610	6 bp	■	↔	misc_feature
✓	**cpV-cpV**	2926 .. 4460	1535 bp	🟨	↔	misc_feature
	/label = cpV-cpV					
✓	**Neo / Kan R**	5666 .. 6457	792 bp	🟪	↔	misc_feature
✓	**Amp R**	7965 .. 8624	660 bp	🟨	↔	misc_feature

	Primer	Length	●	Binding Sites	⇄	Tm	Date Added
✓	**MP169_FW**	19-mer		812 .. 830	→	59°C	22 Dec 2023
	/sequence = TTCGAAAGCCCCCAGGTCA 58% GC / 5757,8 Da						
✓	**MP170_FW**	24-mer		1294 .. 1317	→	61°C	18 Dec 2023
	/sequence = GGCAGGAACCGGTATACAGTGATG 54% GC / 7466,9 Da						
✓	**MP171_FW**	21-mer		1647 .. 1667	→	63°C	18 Dec 2023
	/sequence = GGACACCCGACTCAGCAACCT 62% GC / 6345,2 Da						
✓	**MP172_FW**	22-mer		2167 .. 2188	→	59°C	18 Dec 2023
	/sequence = CACGACTGGAGCCTCTTCAACA 55% GC / 6664,4 Da						
✓	**MP173_FW**	20-mer		2707 .. 2726	→	60°C	20 Dec 2023
	/sequence = CACCACTGCCGAAGCCACAA 60% GC / 6025,0 Da						
✓	**GK306_RV**	23-mer	●	4661 .. 4683	←	59°C	18 Dec 2023
	/sequence = CACCTACTCAGACAATGCGATGC 52% GC / 6977,6 Da						