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4860

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Donor Template SNV -> REV

Donor Template SNV -> REV  
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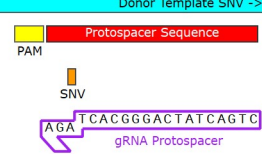
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Donor Template SNV -> REV



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GRN-201

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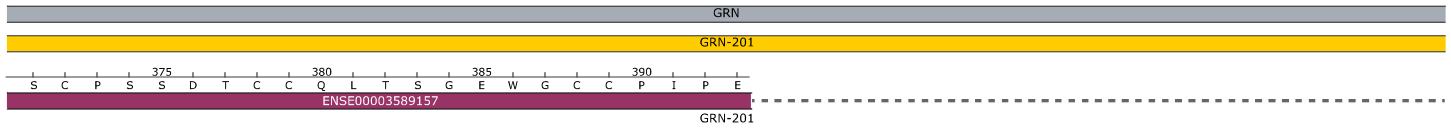
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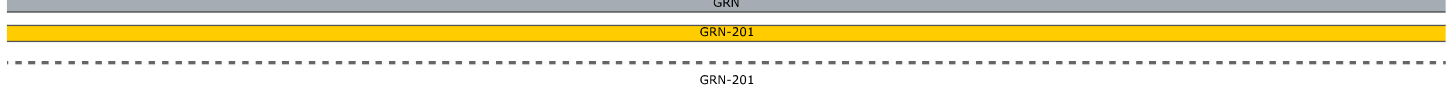
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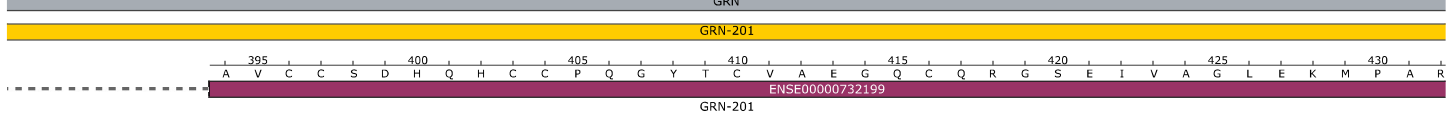
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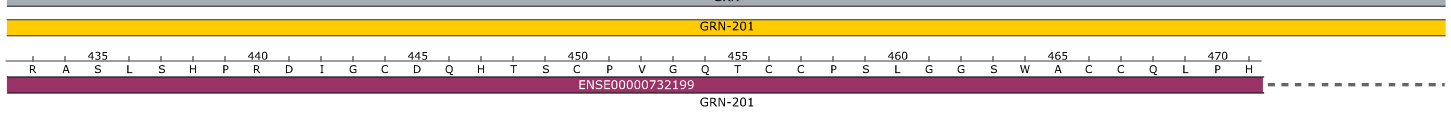
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6885



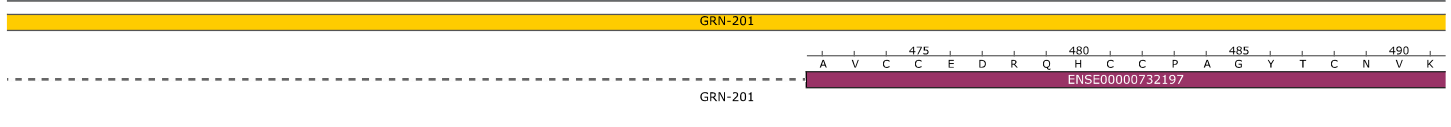
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7020



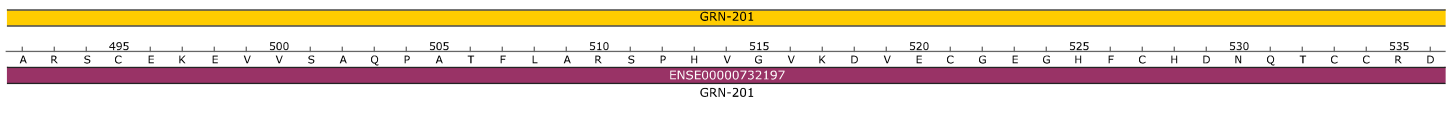
TGCCCTGGATAGGGAGCTAAGCCAGTGAAGGGACAGGAACATAATGCCATTCTGTGCTCCCTTCCCGCCAGGCTGTGTGCTGCGAGGATCGCCAGCACTGCTGCCCGGCTGGCTACACCTGCAACGTGAAG  
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7155



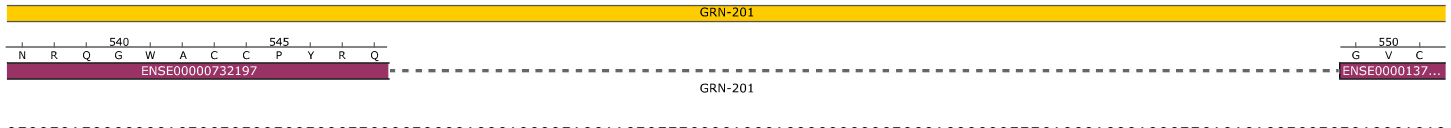
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7290



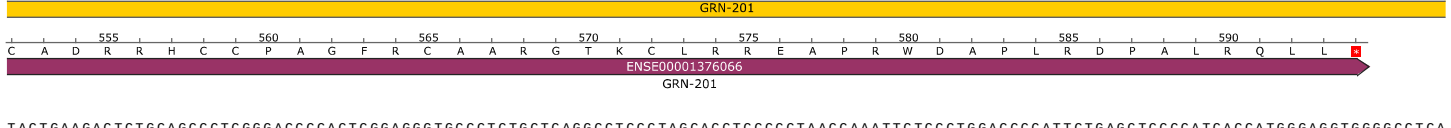
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7425



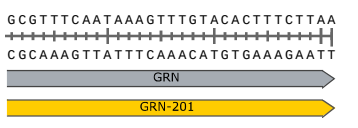
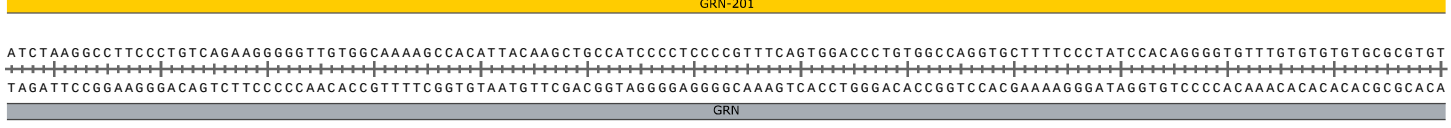
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7560



TACTGAAGACTCTGACGCCCTCGGGACCCACTCGGAGGGTGCCTCTGCTCAGGCTCCCTAGCCTCCCTAACCAATTCTCCCTGGACCCCAATCTGAGCTCCCATACCATGGGAGGTGGGGCTCA  
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7695



Feature	Location	Size	Type
<b>GRN</b>	1 .. 7861	7861 bp	gene
/note	= gene <a href="#">ENSG00000030582</a> Protein coding		
<b>GRN-212</b>	1 .. 4649	4649 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000588170</a> Retained intron		
<b>GRN-215</b>	17 .. 4491	4475 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000589536</a>		
<b>GRN-209</b>	20 .. 5042	5023 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000587518</a>		
<b>GRN-207</b>	20 .. 4229	4210 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000587109</a>		
<b>GRN-211</b>	37 .. 5224	5188 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000588143</a>		
<b>GRN-221</b>	53 .. 5080	5028 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000593167</a>		
<b>GRN-201</b>	57 .. 7861	7805 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000053867</a>		
<b>GRN-213</b>	57 .. 5799	5743 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000588237</a>		
<b>GRN-208</b>	57 .. 5266	5210 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000587387</a>		
<b>GRN-220</b>	57 .. 5059	5003 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000592783</a>		
<b>GRN-218</b>	57 .. 5038	4982 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000591740</a>		
<b>GRN-219</b>	57 .. 4544	4488 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000592323</a> Retained intron		
<b>GRN-203</b>	57 .. 4030	3974 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000585512</a>		
<b>GRN-214</b>	60 .. 7837	7778 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000589265</a>		
<b>GRN-210</b>	61 .. 4566	4506 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000587958</a> Retained intron		
<b>GRN-206</b>	69 .. 5918	5850 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000586782</a> Nonsense mediated decay		
<b>GRN-201</b>	3920 .. 7553	3634 bp	CDS
▶ 12 segments = 1782 bp			
/note	= coding sequence <a href="#">ENSP00000053867</a>		
/translation	= MWTLVSWVALTAGLVA GTRCPDGGQFCPVACCLDPGGASYSCCRPLL,,DKWPTTLSRHLGGPCQVDAHCSAGHSCIFTVSGTSSCCPFPE,,AVACGDGHHCCPRGFHCSADGRSCFQRS,,GNNSV GAIQCPDSQFECPDFS TCCVMVDGSWGCCPMPQ,,ASCCEDRVHCCPHGAFCDLVHTRCITPTGTHPLAKKLPARTNRA,,VALSSSV MCDPARSRCPDGGSTCCCLPSGKYGCCPMPN,,ATCCSDHLHCCPQDVTVCDLIQSKLSKENATDDLTKL PAHT,,VGDVKCDMEVSCPDGYTCCRLQSGAWGCCPFTQ,,AVCCEDHIHCCPAGFTCDTQKGTCEQGPHQVPWMEKAPAHLSLPPDQALKRDVPCDNVSSCPSDTCCLQTSGEWGCCPIPE,,AVCCSDHQHCCPQGY TCVAEGQCQRGSEIVAGLEKMPARRASLSHPRDIGCDQHTSCPVGQTCPPSLGGSWACCQLPH,,AVCCEDRQHCCPAGYTCNVKARSCKEKVVSAQPATFLARSPHVGVKDVCEGEGHFCHDNQTCRRDRNQGWACC BBAARRGKCLREARWDPPLRDPALRQLL*		
<b>GRN-214</b>	3920 .. 7553	3634 bp	CDS
▶ 8 segments = 1311 bp			
/note	= coding sequence <a href="#">ENSP000000467616</a>		
/translation	= MWTLVSWVALTAGLVA GTRCPDGGQFCPVACCLDPGGASYSCCRPLL,,DKWPTTLSRHLGGPCQVDAHCSAGHSCIFTVSGTSSCCPFPE,,AVACGDGHHCCPRGFHCSADGRSCFQRS,,GNNSV GAIQCPDSQFECPDFS TCCVMVDGSWGCCPMPQ,,AVCCEDRVHCCPHGAFCDLVHTRCITPTGTHPLAKKLPARTNRA,,VALSSSV MCDPARSRCPDGGSTCCCLPSGKYGCCPMPN,,ATCCSDHLHCCPQDVTVCDLIQSKLSKENATDDLTKL MPARRASLSHPRDIGCDQHTSCPVGQTCPPSLGGSWACCQLPH,,AVCCEDRQHCCPAGYTCNVKARSCKEKVVSAQPATFLARSPHVGVKDVCEGEGHFCHDNQTCRRDRNQGWACC BBAARRGKCLREARWDPPLRDPALRQLL*		
<b>GRN-222</b>	3920 .. 7550	3631 bp	CDS
▶ 11 segments = 1314 bp			
/note	= coding sequence <a href="#">ENSP000000492014</a>		
/translation	= MWTLVSWVALTAGLVA GTRCPDGGQFCPVACCLDPGGASYSCCRPLL,,DKWPTTLSRHLGGPCQVDAHCSAGHSCIFTVSGTSSCCPFPE,,AVACGDGHHCCPRGFHCSADGRSCFQRS,,GNNSV GAIQCPDSQFECPDFS TCCVMVDGSWGCCPMPQ,,ASCCEDRVHCCPHGAFCDLVHTRCITPTGTHPLAKKLPARTNRA,,VALSSSV MCDPARSRCPDGGSTCCCLPSGKYGCCPMPN,,ATCCSDHLHCCPQDVTVCDLIQSKLSKENATDDLTKL PAHT,,VGDVKCDMEVSCPDGYTCCRLQSGAWGCCPFTQ,,AVCCEDHIHCCPAGFTCDTQKGTCEQGPHQVPWMEKAPAHLSLPPDQALKRDVPCDNVSSCPSDTCCLQTSGEWGCCPIPE,,AVCCSDHQHCCPQGYT CVAEGQCQRGSEIVAGLEKMPARRASLSHPRDIGCDQHTSCPVGQTCPPSLGGSWACCQLPH,,AVCCEDRQHCCPAGYTCNVKARSCKEKVVSAQPATFLARSPHVGVKDVCEGEGHFCHDNQTCRRDRNQGWACC BBAARRGKCLREARWDPPLRDPALRQLL*		
<b>GRN-222</b>	3920 .. 7550	3631 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000639447</a>		
<b>GRN-213</b>	3920 .. 5799	1880 bp	CDS
▶ 5 segments = 518 bp			
/note	= coding sequence <a href="#">ENSP000000466611</a>		
/translation	= MWTLVSWVALTAGLVA GTRCPDGGQFCPVACCLDPGGASYSCCRPLL,,DKWPTTLSRHLGGPCQVDAHCSAGHSCIFTVSGTSSCCPFPE,,ASCCEDRVHCCPHGAFCDLVHTRCITPTGTHPLAKKLPARTNRA,,VALSS SVMCDPARSRCPDGGSTCCCLPSGKYGCCPMPN,,AT 172 amino acids = 18.1 kDa		
<b>GRN-208</b>	3920 .. 5266	1347 bp	CDS
▶ 5 segments = 574 bp			
/note	= coding sequence <a href="#">ENSP000000467431</a>		
/translation	= MWTLVSWVALTAGLVA GTRCPDGGQFCPVACCLDPGGASYSCCRPLL,,DKWPTTLSRHLGGPCQVDAHCSAGHSCIFTVSGTSSCCPFPE,,IKGPCQCRFLCVPQAVACGDGHHCCPRGFHCSADGRSCFQRS,,GNNSV G AIQCPDSQFECPDFSTCCVMVDGSWGCCPMPQ,,ASCCEDRVHCCPHGAFCDLVHTR 191 amino acids = 20.3 kDa		

Feature	Location	Size	Start	End	Type
<b>GRN-211</b>	3920 .. 5224	1305 bp	■	→	CDS
▶ 5 segments = 490 bp					
/note	= coding sequence <a href="#">ENSP00000465375</a>				
/translation	= MWTLVSWVALTAGLVA GTRCPDGGQFCPVACCLDPGGASYSCCRPLL,,DKWPTTLRHLGGPCQVDAHCSAGHSCIFTVSGTSSCCPFPE,,AVACGDGHHCCPRGFHCSADGRSCFQRS,,GNNSVGAIQCPDSQFECPDFS I6SVMMDGGSWGCSPMIDASCCEDRVH				
<b>GRN-221</b>	3920 .. 5080	1161 bp	■	→	CDS
▶ 4 segments = 447 bp					
/note	= coding sequence <a href="#">ENSP00000466405</a>				
/translation	= MWTLVSWVALTAGLVA GTRCPDGGQFCPVACCLDPGGASYSCCRPLL,,DKWPTTLRHLGGPCQVDAHCSAGHSCIFTVSGTSSCCPFPE,,AVACGDGHHCCPRGFHCSADGRSCFQRS,,GNNSVGAIQCPDSQFECPDFS I6SVMMDGGSWGCSPMIDASCCEDRVH 15.6 kDa				
<b>GRN-220</b>	3920 .. 5059	1140 bp	■	→	CDS
▶ 4 segments = 426 bp					
/note	= coding sequence <a href="#">ENSP00000467870</a>				
/translation	= MWTLVSWVALTAGLVA GTRCPDGGQFCPVACCLDPGGASYSCCRPLL,,DKWPTTLRHLGGPCQVDAHCSAGHSCIFTVSGTSSCCPFPE,,AVACGDGHHCCPRGFHCSADGRSCFQRS,,GNNSVGAIQCPDSQFECPDFS I6SVMMDGGSWGCSPMIDASCCEDRVH 14.9 kDa				
<b>GRN-209</b>	3920 .. 5042	1123 bp	■	→	CDS
▶ 4 segments = 409 bp					
/note	= coding sequence <a href="#">ENSP00000465518</a>				
/translation	= MWTLVSWVALTAGLVA GTRCPDGGQFCPVACCLDPGGASYSCCRPLL,,DKWPTTLRHLGGPCQVDAHCSAGHSCIFTVSGTSSCCPFPE,,AVACGDGHHCCPRGFHCSADGRSCFQRS,,GNNSVGAIQCPDSQFECPDF 136 amino acids = 14.3 kDa				
<b>GRN-218</b>	3920 .. 5038	1119 bp	■	→	CDS
▶ 4 segments = 405 bp					
/note	= coding sequence <a href="#">ENSP00000467022</a>				
/translation	= MWTLVSWVALTAGLVA GTRCPDGGQFCPVACCLDPGGASYSCCRPLL,,DKWPTTLRHLGGPCQVDAHCSAGHSCIFTVSGTSSCCPFPE,,AVACGDGHHCCPRGFHCSADGRSCFQRS,,GNNSVGAIQCPDSQFECPDF 135 amino acids = 14.1 kDa				
<b>GRN-215</b>	3920 .. 4491	572 bp	■	→	CDS
▶ 3 segments = 334 bp					
/note	= coding sequence <a href="#">ENSP00000466956</a>				
/translation	= MWTLVSWVALTAGLVA GTRCPDGGQFCPVACCLDPGGASYSCCRPLL,,DKWPTTLRHLGGPCQVDAHCSAGHSCIFTVSGTSSCCPFPE,,AVACGDGHHCCPRGFHCSADGRS 111 amino acids = 11.5 kDa				
<b>GRN-207</b>	3920 .. 4229	310 bp	■	→	CDS
▶ 2 segments = 187 bp					
/note	= coding sequence <a href="#">ENSP00000466271</a>				
/translation	= MWTLVSWVALTAGLVA GTRCPDGGQFCPVACCLDPGGASYSCCRPLL,,DKWPTTLRHLGGPCQ 62 amino acids = 6.6 kDa				
<b>GRN-203</b>	3920 .. 4030	111 bp	■	→	CDS
/note	= coding sequence <a href="#">ENSP00000467745</a>				
/translation	= MWTLVSWVALTAGLVA GTRCPDGGQFCPVACCLDPGGA 37 amino acids = 3.8 kDa				
<b>Donor Template SNV -&gt; REV</b>	4942 .. 5041	100 bp	■	↔	misc_feature
<b>PAM</b>	5001 .. 5003	3 bp	■	↔	misc_feature
<b>Protospacer Sequence</b>	5004 .. 5023	20 bp	■	↔	misc_feature
<b>SNV</b>	5006 .. 5006	1 bp	■	↔	misc_feature
/note	= WT = C SNV = T				
<b>GRN-217</b>	5044 .. 6055	1012 bp	■	→	prim_transcript
/note	= primary transcript <a href="#">ENST00000590984</a> Retained intron				
<b>GRN-205</b>	5294 .. 7798	2505 bp	■	→	prim_transcript
/note	= primary transcript <a href="#">ENST00000586443</a>				
<b>GRN-205</b>	5294 .. 7407	2114 bp	■	→	CDS
▶ 7 segments = 1166 bp					
/note	= coding sequence <a href="#">ENSP00000465673</a>				
/translation	= WQRSSLRGLTGQ,,WPCPARSCVTRTHGPGALMVLPAVSCPVGSMASAAQCPT,,PPAAPITCTAAPKTLCVT*SRVSA SPRRTLPRTSLSLCLRTQ,,WGM*NVTWR*AAQMAIPAAVYSRGPAAALLPR,,LC AVRTTYTAVP RGLRVTRRRV/PVNRGPTRCPGWRPQLTSACQTHKP*REMSPVIMSAVPPPIPAANSRLGSGAAVQSQR,,LSAARTTSTAAPRATRV*LRGSVSEEARSWLDWRRCPLAGLPYPTPETSATVSTPAARWGRPAARAWVGA GPAASCPM,,LCAARIASTAARLATPAT*RLDPARRKWSLPLPPSWPVALTWV*RTWSVGKDTSAMITRPAEETTDRA GPAVPTARSVPPTILGLGMARDQVPPRPTLSPSS 388 codons (7 internal stop codons)				
<b>GRN-216</b>	5527 .. 6550	1024 bp	■	→	prim_transcript
/note	= primary transcript <a href="#">ENST00000589923</a>				
<b>GRN-202</b>	5666 .. 6354	689 bp	■	→	prim_transcript
/note	= primary transcript <a href="#">ENST00000585348</a> Retained intron				
<b>GRN-204</b>	6957 .. 7857	901 bp	■	→	prim_transcript
/note	= primary transcript <a href="#">ENST00000586242</a>				
<b>GRN-204</b>	6957 .. 7524	568 bp	■	→	CDS
▶ 3 segments = 332 bp					
/note	= coding sequence <a href="#">ENSP00000467837</a>				
/translation	= AARAWVGAPAA SCPM,,LCAARIASTAARLATPAT*RLDPARRKWSLPLPPSWPVALTWV*RTWSVGKDTSAMITRPAEETTDRA GPAVPTAS,,QGYQVFAQGGPALGRPF 110 codons (2 internal stop codons)				



Primer	Length	Binding Sites	Tm	Date Added
✓ <b>PCR Forward</b>	20-mer	4738 .. 4757 →	59°C	Jun 17, 2022
/sequence = GAGCTGGGCCGGTCTAATAC 60% GC / 6158.1 Da				
✓ <b>Sanger Sequencing Primer</b>	20-mer	4738 .. 4757 →	59°C	Jun 17, 2022
/sequence = GAGCTGGGCCGGTCTAATAC 60% GC / 6158.1 Da				
✓ <b>Donor Template SNV -&gt; REV</b>	100-mer	4942 .. 5041 →	79°C	Jun 17, 2022
/sequence = cctgagtgggctgtagtctcctgggtcatcttggccacagGTAACAACCTCCGTGGGTGCCATCCAGTGCCCTGATAGTCAGTTCGAATGCCCGGACTTC 56% GC / 30,799.9 Da				
✓ <b>gRNA Protospacer</b>	20-mer	5007 .. 5023 ←	52°C	Jun 17, 2022
/sequence = CTGACTATCAGGGCACTAGA 50% GC / 6126.1 Da				
✓ <b>PCR Reverse</b>	20-mer	5166 .. 5185 ←	57°C	Jun 17, 2022
/sequence = TGGTCCTGACTCCGTCTTCA 55% GC / 6035.0 Da				