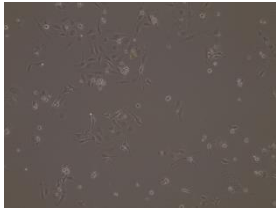
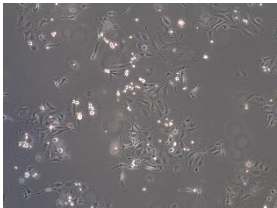


Product Information		
Cell Line	HELA SNCA Knockout	
Parental	HELA	
Product ID	HELA-SNCA KO #9	
Product Batch	HELA-SNCA-KO-9-210628	
Genotype	CRISPR/cas9-edited	
Passage	P10	
Date of Production	2017-08	
Properties		
Volume	1 ml/vial	
Storage Conditions	Liquid Nitrogen	
Cell Number/ Vial	1.x10 <sup>6</sup> cells/ml	
Viability	85%	
Quality Control		
Test	Test Method	Pass/Fail
Viability	Post thawing culture	Pass
Mycoplasma	MycoAlert™ Mycoplasma Detection Kit (Lonza)	Pass
Cell Line Characterization	Sanger Sequencing (DNA)	Pass
Morphology Images	10x objective	<div style="display: flex; justify-content: space-around;"> <div style="text-align: center;"> <p>24h Post-Thaw</p>  </div> <div style="text-align: center;"> <p>48h Post-Thaw</p>  </div> </div>
Growth Conditions		
Culture Media	Dulbecco's Modified Eagle's Medium (DMEM) supplemented with FBS 10%, L-glutamine 2mM, Penicillin-Streptomycin 100U/ml	
Passage Method	Trypsin	
Freezing Media	FBS with 10% DMSO	
Recommended Subculture	Cells are cultured as a monolayer at 37°C in a humidified atmosphere with 5% CO <sub>2</sub> . Cells should be passaged every 5-7 days. Split at 80-85% confluency, approximately 1:10-1:20.	
Cell Line Revival	Rapidly thaw cells in a 37°C water bath. Transfer contents into a tube containing 5 ml pre-warmed media. Centrifuge cells, remove supernatant wash cells with 10 ml PBS, centrifuge cells, remove PBS and seed into a 10 cm flask containing pre-warmed media.	

Cell Line Characterization (DNA)	
Target Gene	SNCA
Guide RNA Sequence	1. GCCAUGGAUGUAUUC AUGAA 2. AAGCACCAAACUGACAUUUG
Genomic Location	Chromosome 4: 89,700,345-89,838,315 reverse strand
Gene	SNCA ENSG00000145335
Target Protein	Alpha-synuclein
Mutation	122 bp deletion, which include part of exon 1 and part of intron
<b>Forward Primer</b>	<b>Reverse Primer</b>
TCCACATTTCCGGGGTTCTGG	GCGACCCGCTCCTAGCAAA
Sequencing Data	
<p>GTCCTGGTTAGGTGGCTAGACTTTTACTAGCCAAGATGGATGGGAGATGCTAAATTTTTAATGCCAGAGCTAAAAATGTCTGCT          TTGTCCAATGGTTAAATGAGTGTACACTTAAAAGAGTCTCACACTTTGGAGGGTTTCTCATGATTTTTCAGTGTTTTTGTATTTT          TCCCGAAAGTTCTCATTCAAAGTGTATTTATGTTTTCCAGTGTGGTGTAAGGAATTCATTAGCCATGGATGATTCATATGTCA          GTTTGGTGCTTGTTCATGAGTGATGGGTTAGGATAATCAATACTCTAAATGCTGGTAGTTCTCTCTCTTGATTCATTTTTGCATCAT          TGCTTGCAAAAAGGTGGACTGAGTCAGAGGTATGTGTAGGTAGGTGAATGTGAACGTGTGATTTGAGCTAATAGTAAAAAAT          GCGACTGTTTGTCTTCCAGATCATGGTTTTACCTCCTGAATTCGGATCCCTCGAGCGATACACACTTCTATAGTGCACCTAAAT          GCGTTTAAACCTTCTGCAGGTGACGATTACCTAACAAATCGGTCGATTGTTGATGTTATGTTTTGTTCTCGCTTTGGTTGGCAGG          TTACGGCCAAGTTCGGTAAGAGTGAGAGTTTTACAGTCAAGTAATGCGTGGCAAGCCAACGTTAAGCTGTTGAGTCGTTTTAAGT          GTAATTCGGGGCAGAATTGGTAAAGAGAGTCGTGTAATAATCGAGTTCGCACATCTTGTGCTGATTATTGATTTTTCCGGAAA          CCATTTAATCATATGACAAGATGTGTGCCACCTTAACCTAATGATTTTTACCAAAATCATTAGGGGATTCATCAGC</p>	
Sequence Alignment	
<pre> WT 1  GAGTGTACACTTAAAAGAGTCTCACACTTTGGAGGGTTTCTCATGATTTT 50         KO 103 GAGTGTACACTTAAAAGAGTCTCACACTTTGGAGGGTTTCTCATGATTTT 152  51  TCAGTGTTTTTTGTTTATTTTCCCGAAAGTTCTCATTCAAAGTGATTT 100         153 TCAGTGTTTTTTGTTTATTTTCCCGAAAGTTCTCATTCAAAGTGATTT 202  101 TTATGTTTTTCCAGTGTGGTGTAAGGAATTCATTAGCCATGGATGATTT 150         203 TTATGTTTTTCCAGTGTGGTGTAAGGAATTCATTAGCCATGGATGATTT 252  151 ATGAAAGGACTTTCAAAGGCCAAGGAGGGAGTTGTGGCTGCTGCTGAGAA 200        253 AT----- 254  201 AACCAAACAGGGTGTGGCAGAAAGCAGCAGGAAAGACAAAAGAGGGTGTT 250 254 ----- 254  251 TCTATGTAGGTAGGTAAACCCCAATGTCAGTTTTGGTGCTTGTTTCATGAG 300         254 -----ATGTCAGTTTTGGTGCTTGTTTCATGAG 280  301 TGATGGGTTAGGATAATCAATACTCTAAATGCTGGTAGTTCTCTCTCTTG 350         281 TGATGGGTTAGGATAATCAATACTCTAAATGCTGGTAGTTCTCTCTCTTG 330 </pre>	