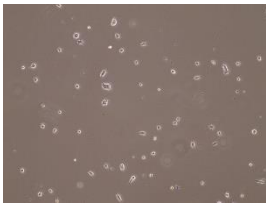
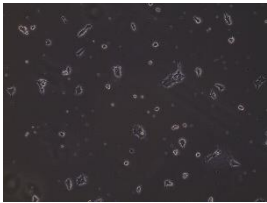


Product Information		
Cell Line	HEK293T PARK2 Knockout	
Parental	HEK293T	
Product ID	HEK293T-PARK2 KO B2	
Product Batch	HEK-PARK-KO-B2-210521	
Genotype	CRISPR/cas9-edited	
Passage	P6	
Date of Production	2017-01	
Properties		
Volume	1 ml/vial	
Storage Conditions	Liquid Nitrogen	
Cell Number/ Vial	1.x10 <sup>6</sup> cells/ml	
Viability	97%	
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      24h post-thaw	48h post-thaw
		
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	PARK2
Guide RNA Sequence	1. CUCCAGCCAUGGUUCCAG 2. CUGCGAAAAUCACACGCAAC
Genomic Location	Chromosome 6: 161,347,417-162,727,775 reverse strand
Gene	PARK2 ENSG00000185345
Target Protein	Parkin
Mutation	77 bp deletion in exon 2
<b>Forward Primer</b>	<b>Reverse Primer</b>
AAGGGCTTCGAGTGATGCTC	CCTTGCTGCTCCTGTAGTCA
Sequencing Data	
TAATACTCAAGCTATGCATCAAGCTTGGTACCGAGCTCGGATCCACTAGTAAACGGCCGCCAGTGTGCTGGAATTCGC CCTTCCTTGCTGCTCCTGTAGTCAGTAGACATTTATCACTAAGCCTAGCTCGTGTGTTCTTTCTCTCTCTTTCTCACT CGCAGTTGTTCTTCCAATCTTTCTGCTTGGCTGTTTTAATGCATAATTAAGAAGGTCAGAATTAATGAAGCAGTGTGGA GTAAAGTTCAAGGAATCCCCAGGCACTATTTATTCTATTAGATCTCAGGCATGAATGTCAGATTGGCAGCGCAGGCCG GCATGAGCAATGGAGCTGGCGGCATCCCAAGAACGGCCGCAAGGGAGACTCACCTGCACAGTCCAGTCATTCCCTC AGCTCCTTCCCTGCGAAAATCACACGCCACTGGGAAACCATGGCTGGAGTTGAACCTGACAAACACTGACCAAGGAA ATTGGAAGGGAGAAGAGAAAAGTGAGCATCACTCGAAGCCCTTAAGGGCGAATTCTGCAGATATCCATCACACTGGC GGCCGCTCGAGCATGCATCTAGAGGGCCCAATTGCCTATAGTGAGTCGTATTACATTCACTGGCCGTCGTTTACAA CGTCGTGACTGGGAAACCCTGCGTACCAACTAATCGCTGCAGCAMATCTGTTTCGCAGCTGCGTATAGC	
Sequence Alignment	
<pre> WT 1  GCCAAGGGGAGACTCACCTGCACAGTCCAGTCATTTCCTCAGCTCCTTCCCT 50           KO 353 GCCAAGGGGAGACTCACCTGCACAGTCCAGTCATTTCCTCAGCTCCTTCCCT 402        51  GCGAAAAATCACACGCAACTGGTCAAGCCGAAACCCCTGTCGCTTAGCAAC 100                 403 GCGAAAAATCACACG----- 416        101 CACCTCCTTGAGCTGGAAGATGCTGGTGTCAAGAATCGACCTCCACTGGGA 150                 416 -----CCACTGGGA 425        151 AACCATGGCTGGAGTTGAACCTGACAAACACTGACCAAGGAAATTGGAAG 200                 426 AACCATGGCTGGAGTTGAACCTGACAAACACTGACCAAGGAAATTGGAAG 475        201 GGAGAAGAGAAAAGTGAGCATCACTCGAAGCCCTTAA 236                 476 GGAGAAGAGAAAAGTGAGCATCACTCGAAGCCCTTAA 511 </pre>	