
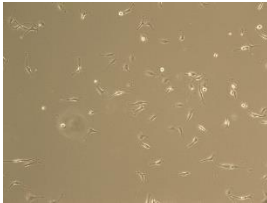
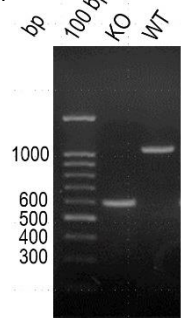


Product Information		
Cell Line	HELA NEK1 Knockout	
Parental	HELA	
Product ID	HELA-NEK1 KO 29	
Product Batch	HEL-NEK1-29-191114	
Genotype	CRISPR/cas9-edited	
Passage	P24	
Date of Production	2018-04-01	
Properties		
Volume	1 ml/vial	
Storage Conditions	Liquid Nitrogen	
Cell Number/ Vial	5.43x10 <sup>5</sup> cells/ml	
Viability	55%	
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	NEK1
Guide RNA Sequence	1. GAGACUAGUACAGGCCUGUU 2. AGAAACGCUGGUCCAAAUCC
Genomic Location	Chromosome 4: 169,392,857-169,612,629 reverse strand
Gene	NEK1 ENSG00000137601
Target Protein	NIMA related kinase 1
Mutation	Deletion of 447 bp including deletion of entire exon 17 and exon 18
<b>Forward Primer</b>	<b>Reverse Primer</b>
TTGGAAGCTTGTTTCAAAACCTGT	AAATGCACTGGGGTTCTGCAT
<b>PCR Products</b>	
Image description: PCR products of NEK1 KO clone along with WT were resolved on 2% agarose gel	 <p>bp 100 bp KO WT</p> <p>1000 600 500 400 300</p>
<p>agtattacttttaaaagtgagcattgaaattactttttcttttgagactagtagtac aggcattatcatcatgtgtgtaattttgtcgtttgtcacaatagcttagtaccta cacttttgatgttttctccattgtcacaatgatgtttttgcctctgggtaca ataattttctgaggtgcaaattggcccttgattactctgtgaaagcatgtagctt tccagttcagcctgattttgtgtctgtttgtgggttagactgaaatataactatta aaggaacatgtgataacattctgccaacataattataacattttatcaccactt ccttaataaataacaggatataaaactaaattgaatcacactttatgcagaacc ccagtgcat</p>	
Sequence Alignment	
<pre> 1 AGTAATTACTTTTTAAAAGTGAAGCATTGAAATTACTTTTTCTTTTGGAG 50 1 agta-ttactttttaaagtgagcattgaaattactttttcttttgag 49 51 ACTAGTACAGCCCTGTTAGGCCCTTATAGATAAACAATGTGAGAGCTCTTT 100 50 actagtagcagggcct----- 63 101 GTTTAAATCCCTAGGCTCCCTTTTCTGGGCAGTGGAGGACTATAGCTCCAT 150 63 ----- 63 151 CATCTTTTTCTTTCGAGGACAGTATGAACATTAACCATGCCATTTTTGAC 200 63 ----- 63 201 CAAATGCAGCAACAAGAGCAGAGATTAATGAAGCTAAATGAAAAGAGA 250 63 ----- 63 251 AATATATGGTCAGGCTCTCCAGAAAGGTATGGCTATGTTCTGCAGAAAT 300 63 ----- 63 301 TGCTTATGCTTTTGTCTGAGATAGTAAATGAAAGTCACTGTGCATATTTA 350 63 ----- 63 351 TCTACAGAGAAATCTGCTGGAGTTCGTCAGGATTTCTTATGGGGCT 400 63 ----- 0 401 GCAGGTCATCAACCAATTTCTGTGATGATATAGAAAACTTTGAA 450 63 ----- 63 451 AAGATGAAGGCGGTGTCTAAACAAGCCAATGCARACAGGTTGACTGTG 500 63 ----- 63 501 ATGATCCATGAATTCATCCATGTGTGTAATTTTGTGCTTTGTGATACATA 550 63 -----attccatccatgtgtgtaattttgtcgtttgtcacaata 102 551 GCTTAGTACCTACACTTTTGGGATGTTTTCTCCATTTGTCACATATGATG 600 103 gcttagtagcactacactttgtggatgtttctccatgttcacatagatg 152 601 TTTTTGCCCTCTGGGTACAAATAATTTCTGAGGTGCAAAATTTGGCCCTT 650 153 tttttgacctctgggtacataaattttctgaggtgcaaatttggccctt 202 651 GATTACTC--TGAAGCATGTAGCTTTCCAGTTCAGCCCTGATTTTTGTGT 698 203 gattactctgtgaaagcatgtagctttccagttcagcctgattttgtgt 252 </pre>	