# Run summary for L270R MGA on 11-25-2024

Script version: PARERSv2\_multi\_cell\_line\_11-19-24.py

First read file: Z:/Stuart Lab/HPC/2023\_12\_29\_Carnes\_A3CNvMGA\_WTvL270R/Raw\_fastq\_files/input\_data\_for\_RSC/truncated\_MURF2\_A3\_L270R\_MGA\_S6\_R1\_001.fastq

Second read file: Z:/Stuart Lab/HPC/2023\_12\_29\_Carnes\_A3CNvMGA\_WTvL270R/Raw\_fastq\_files/input\_data\_for\_RSC/truncated\_MURF2\_A3\_L270R\_MGA\_S6\_R2\_001.fastq

Target gene: MURF2

Forward primer: ATAGAAAGGTATATAATCTATAATG

Reverse primer: GTCGTGTTTTTGATTTGTTATG

Portion of pre-edited sequence used for analysis: ATAGAAAGGTATATAATCTATAATGAAAGGGGATTTTAAGATTGGCTTTGATTGAGTCGTGTTTTTGATTTGTTATG

Portion of fully edited sequence used for analysis: ATAGAAAGGTATATAATCTATAATGATTTTAATGTTTGGTTGTTTTAATTTAGTTTTATTTTTGTGCTTTGATTGTAGTCGTGTTTTTGATTTGTTATG

Summary of quality control data:

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Step** | **Before Filter** | **After Filter** | **Sequences Removed** | **% Sequences Remaining** |
| Sequences Merged | 199 | 135 | 64 | 67.84% |
| Primer Binning | 135 | 115 | 20 | 57.79% |
| Deduplication | 115 | 115 | 0 | 57.79% |
| T-stripping | 115 | 96 | 19 | 48.24% |

Entire pre-edited sequence: TTTTATATAGAAAGGTATATAATCTATAATGAAAGGGGATTTTAAGATTGGCTTTGATTGAGTCGTGTTTTTGATTTGTTATGTATTAGAACATATGATTTTATATTGTGATGGTTTGATCTAGATTTTATATTATATGATTTTGTATTCGATTTTGTTGTATGTATTACATTTATATTTATATTTGTTTTAGGTTTTTTTATTAGAATTTTTTTTAGTTTTGTGTTTGTATTGTTATTTATAACATTTTTTGGAATTTGTTCATTAACAATGTTATTTACAGGGTATTATATATATTATATATATATATTATATAATTTTATATGTTTTTTTTTTGCATTTGGTATAAATTTTTTGATATATTATATCGAGTTTTTCATATTTATAACATTCCATATATTTTTCGATTTTATAAGTTTTTCTAATTATATATATAATTATTTTGGAATATTGTATATGTTTAATGTAATGTTTTGTGCATATTTATTTTGTTTATTTTATTTTGTGATATATTTTTTATTTTGTTTTATATTTTTTGTAATACGATGTTTATTTATAGTAATAATGGATTTTTTATTTTTTAATTTTGATATATTTGTATCTATATTATTATGTGATATAGTATATTTAGATTTTATAAGTTTATTATTATTATATTTTAATTTTATATTTAATTTTATTTATGGATTTTTTAGTTTTGTGATAATTTTAGGTTTATTATTTTTATTGTTATTTTTAGTAATAAATTTATTTTTTGGATTTACATTTTTAGTATATGGTATACAAATCATATTATTATATTATGTATATTGATTATATATGATATATAGTAGAAGTTGTTATATATTGATGCCAGCAATATTAATATTTTTTAAGTTTATATATTTTGATGTATTCTTTGTGTTTGTATTTATTTTAATTTTATTTATTATATCATTTTTTAGTTTTTTTTTAAAAGATTTTTTATTTTTATCATTATATTTTGATATATTCGGATCATTATATAATTACGATATATTATCATATAGTATATTTTATTATCAAAATAATCAGTTTTGTTTAACACAGTTATTATCAATTTATATATAAAA

Entire fully edited sequence: TTTTATATAGAAAGGTATATAATCTATAATGATTTTAATGTTTGGTTGTTTTAATTTAGTTTTATTTTTGTGCTTTGATTGTAGTCGTGTTTTTGATTTGTTATGTATTAGAACATATGATTTTATATTGTGATGGTTTGATCTAGATTTTATATTATATGATTTTGTATTCGATTTTGTTGTATGTATTACATTTATATTTATATTTGTTTTAGGTTTTTTTATTAGAATTTTTTTTAGTTTTGTGTTTGTATTGTTATTTATAACATTTTTTGGAATTTGTTCATTAACAATGTTATTTACAGGGTATTATATATATTATATATATATATTATATAATTTTATATGTTTTTTTTTTGCATTTGGTATAAATTTTTTGATATATTATATCGAGTTTTTCATATTTATAACATTCCATATATTTTTCGATTTTATAAGTTTTTCTAATTATATATATAATTATTTTGGAATATTGTATATGTTTAATGTAATGTTTTGTGCATATTTATTTTGTTTATTTTATTTTGTGATATATTTTTTATTTTGTTTTATATTTTTTGTAATACGATGTTTATTTATAGTAATAATGGATTTTTTATTTTTTAATTTTGATATATTTGTATCTATATTATTATGTGATATAGTATATTTAGATTTTATAAGTTTATTATTATTATATTTTAATTTTATATTTAATTTTATTTATGGATTTTTTAGTTTTGTGATAATTTTAGGTTTATTATTTTTATTGTTATTTTTAGTAATAAATTTATTTTTTGGATTTACATTTTTAGTATATGGTATACAAATCATATTATTATATTATGTATATTGATTATATATGATATATAGTAGAAGTTGTTATATATTGATGCCAGCAATATTAATATTTTTTAAGTTTATATATTTTGATGTATTCTTTGTGTTTGTATTTATTTTAATTTTATTTATTATATCATTTTTTAGTTTTTTTTTAAAAGATTTTTTATTTTTATCATTATATTTTGATATATTCGGATCATTATATAATTACGATATATTATCATATAGTATATTTTATTATCAAAATAATCAGTTTTGTTTAACACAGTTATTATCAATTTATATATAAAA