**S5 Table:** A set of 24 forward indexed primers containing (Illumina-specific region, 10 bp index tag [highlighted], and 18 bp common priming site U1). The common reverse primer contains (Illumina-specific region and a common priming site from the resistant KanMX gene region) [1].

|  |  |
| --- | --- |
| **Name of Primer** | **Sequence (5' - 3')** |
| Non\_Essentail\_1009\_1 | AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTCTTCCGATCTAATAGGCGCTGATGTCCACGAGGTCTCT |
| Non\_Essentail\_1009\_2 | AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTCTTCCGATCTTACAGTTGCGGATGTCCACGAGGTCTCT |
| Non\_Essentail\_1009\_3 | AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTCTTCCGATCTATCCTAGCAGGATGTCCACGAGGTCTCT |
| Non\_Essentail\_1009\_4 | AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTCTTCCGATCTGATTAGCCTCGATGTCCACGAGGTCTCT |
| Non\_Essentail\_MMS\_1 | AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTCTTCCGATCTAATGAGCCGTGATGTCCACGAGGTCTCT |
| Non\_Essentail\_MMS\_2 | AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTCTTCCGATCTACGCGGATTAGATGTCCACGAGGTCTCT |
| Non\_Essentail\_MMS\_3 | AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTCTTCCGATCTGCTTACGGAAGATGTCCACGAGGTCTCT |
| Non\_Essentail\_MMS\_4 | AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTCTTCCGATCTCGGTAGACTAGATGTCCACGAGGTCTCT |
| Non\_Essentail\_DMSO\_1 | AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTCTTCCGATCTATTGCCGGAAGATGTCCACGAGGTCTCT |
| Non\_Essentail\_DMSO\_2 | AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTCTTCCGATCTGACATGCTAGGATGTCCACGAGGTCTCT |
| Non\_Essentail\_DMSO\_3 | AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTCTTCCGATCTTACGCTGCATGATGTCCACGAGGTCTCT |
| Non\_Essentail\_DMSO\_4 | AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTCTTCCGATCTGTCAAGCACTGATGTCCACGAGGTCTCT |
| Essentail\_1009\_1 | AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTCTTCCGATCTAGCGTATGTCGATGTCCACGAGGTCTCT |
| Essentail\_1009\_2 | AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTCTTCCGATCTGCGGATTAACGATGTCCACGAGGTCTCT |
| Essentail\_1009\_3 | AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTCTTCCGATCTATACCTCGGAGATGTCCACGAGGTCTCT |
| Essentail\_1009\_4 | AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTCTTCCGATCTGGTAGACATCGATGTCCACGAGGTCTCT |
| Essentail\_MMS\_1 | AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTCTTCCGATCTAGGTACCTACGATGTCCACGAGGTCTCT |
| Essentail\_MMS\_2 | AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTCTTCCGATCTCGATAACGCTGATGTCCACGAGGTCTCT |
| Essentail\_MMS\_3 | AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTCTTCCGATCTTACCGGAATGGATGTCCACGAGGTCTCT |
| Essentail\_MMS\_4 | AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTCTTCCGATCTTAGGACCAGTGATGTCCACGAGGTCTCT |
| Essentail\_DMSO\_1 | AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTCTTCCGATCTCTGCAAGTTCGATGTCCACGAGGTCTCT |
| Essentail\_DMSO\_2 | AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTCTTCCGATCTTCGCGATTCAGATGTCCACGAGGTCTCT |
| Essentail\_DMSO\_3 | AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTCTTCCGATCTGGTAACGTACGATGTCCACGAGGTCTCT |
| Essentail\_DMSO\_4 | AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTCTTCCGATCTAAGACCTGTGGATGTCCACGAGGTCTCT |
| Common reverse primer | CAAGCAGAAGACGGCATACGAGCTCTTCCGATCTGCACGTCAAGACTGTCAAGG |

**A**

**B**

**References:**

1. Piotrowski, J.S., et al., *Chemical Genomic Profiling via Barcode Sequencing to Predict Compound Mode of Action.* Methods Mol. Biol. (N. Y., NY, U. S.), 2015. **1263**(Chemical Biology): p. 299-318.