CLUSTAL W (1.83) multiple sequence alignment

HAP1\_t72 CCAGGACCACATTTTGAGAGCCACTGCTGTTGAATCCCCAGTTCCTTTCA

HepG2\_t15 CCAGGACCACATTTTGAGAGCCACTGCTGTTGAATCCCCAGTTCCTTTCA

reference CCAGGACCACATTTTGAGAGCCACTGCTGTTGAATCCCCAGTTCCTTTCA

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

HAP1\_t72 GTCCCTCACTGCTCCTCGTCTGCCAGTAGGAGTAAAAGCAAACAGCTTAG

HepG2\_t15 GTCCCTCACTGCTCCTCGTCTGCCAGTAGGAGTAAAAGCAAACAGCTTAG

reference GTCCCTCACTGCTCCTCGTCTGCCAGTAGGAGTAAAAGCAAACAGCTTAG

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

HAP1\_t72 GAAAAATCGAC---------------------------------------

HepG2\_t15 GAAAAATCGACA--------------------------------------

reference GAAAAATCGACACCCAGGACAAAAACAGTATCTCGAAAAGGCCAAAGAGG

\*\*\*\*\*\*\*\*\*\*

HAP1\_t72 --------------------------------------------------

HepG2\_t15 --------------------------------------------------

reference GGGCACCCGGATTTGAACCGGGGACCTCTTGATCTGCAGTCAAATGCTCT

HAP1\_t72 --------------------------------------------------

HepG2\_t15 --------------------------------------------------

reference ACCACTGAGCTATACCCCCTCTGCCGGCAAACCGACCGCACGTAGTCGTT

HAP1\_t72 --------------------------------------------------

HepG2\_t15 --------------------------------------------------

reference TAGTGGTATTGCTGCGCAGGCGCTGTGTGGCGTTCCCGAAGGGAAGTGGA

HAP1\_t72 --------------------------------------------------

HepG2\_t15 --------------------------------------------------

reference AGTGGGGTAAGACGTTTACAAGAGATGGAAAAAATACAACTCCCAGAAGA

HAP1\_t72 --------------------------------------------------

HepG2\_t15 --------------------------------------------------

reference ATTACTCACTTGGAAGCAGGGGTTGTTCCCTGAAGCTCTGAGCTGAAGAT

HAP1\_t72 --------------------------------------------------

HepG2\_t15 --------------------------------------------------

reference CCCCACTGGCAGTATAAGAAAATATATTCCTGGGGTGTGGAAGGAGAAGT

HAP1\_t72 --------------------------------------------------

HepG2\_t15 --------------------------------------------------

reference CTCTCGAAATATTTCACTTCGGGGGCGTCCCACTCTCCTGCCCTGCAGAA

HAP1\_t72 --------------------------------------------------

HepG2\_t15 --------------------------------------------------

reference GACCCCTTGCCACGTCTCGGAGCTTCTTTCTCCCTCCCACATGCTCACGC

HAP1\_t72 --------------------------------------------------

HepG2\_t15 --------------------------------------------------

reference GGCTTCTCCCGACCTGTCTTCCCCAGCCCAGCCCTTAGAAACTCAGCCTC

HAP1\_t72 --------------------------------------------------

HepG2\_t15 --------------------------------------------------

reference CTTCCCGCCAAGAAAGAGCCAGGCTGACCTGGGGGTGCGCTCGCCTCCGC

HAP1\_t72 --------------------------------------------------

HepG2\_t15 --------------------------------------------------

reference CCTGCCATTGCGAGGTTGAGCCACCCGTACCGTGTTCCAAGGGTCAGCCC

HAP1\_t72 --------------------------------------------------

HepG2\_t15 --------------------------------------------------

reference GGAGCTCCTCGCCCTCACTCGCATTGCATTCTACCCTGGGTACACACACA

HAP1\_t72 --------------------------------------------------

HepG2\_t15 --------------------------------------------------

reference GGCTGAGCCACTGGCAGGGGCCAGGACTCCATCCTCACTCGCCTGCGAAA

HAP1\_t72 --------------------------------------------------

HepG2\_t15 --------------------------------------------------

reference GCAAAAAGGGTGGCAGGGCTCGAGACTCCCTCCCATTCCATCTGTGCGGG

HAP1\_t72 --------------------------------------------------

HepG2\_t15 --------------------------------------------------

reference AACTCTTTAGAGGACCTCCGGAGACCAACAAAACGAGGTAACTCCGGAGC

HAP1\_t72 --------------------------------------------------

HepG2\_t15 --------------------------------------------------

reference ACAGAGGGGGCACCCGGATTTGAACCGGGGACCTCTTGATCTGCAGTCAA

HAP1\_t72 ----------------------------------ACTACGTTGTCATTAG

HepG2\_t15 ---------------------------------CACTACGTTGTCATTAG

reference ATGCTCTACCACTGAGCTATACCCCCGCCACGCCACTACGTTGTCATTAG

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

HAP1\_t72 AGTTAATTTCTATGGAATAGGGGTGTGGTCTTCATTTTCCCTTAAAGTTT

HepG2\_t15 AGTTAATTTCTATGGAATAGGGGTGTGGTCTTCATTTTCCCTTAAAGTTT

reference AGTTAATTTCTATGGAATAGGGGTGTGGTCTTCATTTTCCCTTAAAGTTT

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

HAP1\_t72 TAATCTGAGGGTTGCGTCGGGATACCTACTGAAAAAAACACAAAATACAA

HepG2\_t15 TAATCTGAGGGTTGCGTCGGGATACCTACTGAAAAAAACACAAAATACAA

reference TAATCTGAGGGTTGCGTCGGGATACCTACTGAAAAAAACACAAAATACAA

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

HAP1\_t72 TGGGAATGGCTAGAACTCCTGAGTTCTTCCTTCA

HepG2\_t15 TGGGAATGGCTAGAACTCCTGAGTTCTTCCTTCA

reference TGGGAATGGCTAGAACTCCTGAGTTCTTCCTTCA

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

NOTE:

Targeted tRNA genes highlighted in red

gRNA-Δt-1 highlighted in yellow

gRNA-Δt-2 highlighted in green