

CLUSTAL O(1.2.4) multiple sequence alignment

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Seq6	-----GCCAAATAGTATGTATTCTAAACTCACT	28
XM_001349494.1	AAATTTTCTTTCTCACTCTTCATTACATTATGCCAAATAGTATGTATTCTAAGCTCACT	900
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Seq3	-----GCCAAATAGTATGTATTCTAAGCTCACT	28

Seq34	ATTAGTCTCATTATTCAATAACACAAGTTTCTTATTTATTTTCGAGATCTAAATCATTTAT	88
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Seq46	ATTAGTCTCATTATTCAATAACACAAGTTCTTATTTATTTCAAGATCTAAATCATTGT	88
Seq43	ATTAGTCTCATTATTCAATAACACAAGTTCTTATTTATTTCAAGATCTAAATCATTGT	88
Seq42	ATTAGTCTCATTATTCAATAACACAAGTTCTTATTTATTTCAAGATCTAAATCATTGT	88
Seq40	ATTAGTCTCATTATTAAATAACACAAGTTCTTATTTATTTCAAGATCTAAATCATTGT	88
Seq37	ATTAGTCTCATTATTCAATAACACAAGTTCTTATTTATTTCAAGATCTAAATCATTGT	88
Seq36	ATTAGTCTCATTATTCAATAACACAAGTTCTTATTTATTTCAAGATCTAAATCATTGT	88
Seq6	ATTAGTCTCATTATTCAATAACACAAGTTCTTATTTATTTCAAGATCTAAATCATTGT	88
XM_001349494.1	ATTAGTCTCATTATTCAATAACACAAGTTCTTATTTATTTCAAGATCTAAATCATTGT	960
LN999943.1	ATTAGTCTCATTATTCAATAACACAAGTTCTTATTTATTTCAAGATCTAAATCATTGT	87
Seq3	ATTAGTCTCATTATTCAATAACACAAGTTCTTATTTATTTCAAGATCTAAATCATTGT	88
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Seq34	ATATTCACCTGTATCTGATAGCCTATGATGATGATTTGAAATCGTTCCCATAAATCATC	148
Seq41	ATATTCACCTGTATCTGATAGCCTATGATAATGTATTTGAAATCGTTCCCATAAATCATC	148
Seq31	ATATTCACCTGTATCTGATAGCCTATGATAATGTATTTGAAATCGTTCCCATAAATCATC	148
Seq29	ATATTCACCTGTATCTGATAGCCTATGATAATGTATTTGAAATCGTTCCCATAAATCATC	148
Seq27	ATATTCACCTGTATCTGATAGCCTATGATAATGTATTTGAAATCGTTCCCATAAATCATC	148
Seq12	ATATTCACCTGTATCTGATAGCCTATGATAATGTATTTGAAATCGTTCCCATAAATCATC	148
Seq10	ATATTCACCTGTATCTGATAGCCTATGATAATGTATTTGAAATCGTTCCCATAAATCATC	148
Seq9	ATATTCACCTGTATCTGATAGCCTATGATAATGTATTTGAAATCGTTCCCATAAATCATC	148
Seq8	ATATTCACCTGTATCTGATAGCCTATGATAATGTATTTGAAATCGTTCCCATAAATCATC	148
Seq7	ATATTCACCTGTATCTGATAGCCTATGATAATGTATTTGAAATCGTTCCCATAAATCATC	148
Seq1	ATATTCACCTGTATCTGATAGCCTATGATAATGTATTTGAAATCGTTCCCATAAATCATC	148
Seq4	ATATTCACCTGTATCTGATAGCCTATGATAATGTATTTGAAATCGTTCCCATAAATCATC	148
Seq16	ATATTCACCTGTATCTGATAGCCTATGATGATGATTTGAAATCGTTCCCATAAATCATC	148
Seq23	ATATTCACCTGTATCTGATAGCCTATGATGATGATTTGAAATCGTTCCCATAAATCATC	148
Seq13	ATATTCACCTGTATCTGATAGCCTATGATAATGTATTTGAAATCGTTCCCATAAATCATC	148
Seq21	ATATTCACCTGTATCTGATAGCCTATGATAATGTATTTGAAATCGTTCCCATAAATCATC	148
Seq45	ATATTCACCTGTATCTGATAGCCTATTATAATGTATTTGAAATCGTTCCCATAAATCATC	148
Seq44	ATATTCACCTGTATCTGATAGCCTATTATAATGTATTTGAAATCGTTCCCATAAATCATC	148
Seq39	ATATTCACCTGTATCTGATAGCCTATTATAATGTATTTGAAATCGTTCCCATAAATCATC	148
Seq32	ATATTCACCTGTATCTGATAGCCTATTATAATGTATTTGAAATCGTTCCCATAAATCATC	148
Seq30	ATATTCACCTGAACTCTGATAGCCTATTATAATGTATTTGAAATCGTTCCCATAAATCATC	148
Seq28	ATATTCACCTGTATCTGATAGCCTATTATAATGTATTTGAAATCGTTCCCATAAATCATC	148
Seq26	ATATTCACCTGAACTCTGATAGCCTATTATAATGTATTTGAAATCGTTCCCATAAATCATC	148
Seq15	ATATTCACCTGTATCTGATAGCCTATTATAATGTATTTGAAATCGTTCCCATAAATCATC	148
Seq2	ATATTCACCTGTATCTGATAGCCTATTATAATGTATTTGAAATCGTTCCCATAAATCATC	148
Seq5	ATATTCACCTGTATCTGATAGCCTATTATAATGTATTTGAAATCGTTCCCATAAATCATC	148
Seq18	ATATTCACCTATTTCTGATAACATATAATAACTTATTTCAAATCGTTCCCATAAATCATA	148
Seq25	ATATTCACCTATTTCTGATAACATATAATAACTTATTTCAAATCGTTCCCATAAATCATA	148
Seq38	ATATTCACCTATTTCTGATAACATATAATAACTTATTTCAAATCGTTCCCATAAATCATA	148
Seq11	ATATTCACCTATTTCTGATAACATATAATAACTTATTTCAAATCGTTCCCATAAATCATA	148
Seq19	ATATTCACCTATTTCTGATAACATATAATAACTTATTTCAAATCGTTCCCATAAATCATA	148
Seq17	ATATTCACCTATTTCTGATAACATATAATAACTTATTTCAAATCGTTCCCATAAATCATA	147
Seq24	ATATTCACCTATTTCTGATAACATATAATAACTTATTTCAAATCGTTCCCATAAATCATA	147
Seq33	ATATTCACCTATTTCTGATAACATATAATAACTTATTTCAAATCGTTCCCATAAATCATA	148
Seq35	ATATTCACCTATTTCTGATAACATATAATAACTTATTTCAAATCGTTCCCATAAATCATA	148
Seq22	ATATTCACCTATTTCTGATAACATATAATAACTTATTTCAAATCGTTCCCATAAATCATA	148
Seq14	ATATTCACCTATTTCTGATAACATATAATAACTTATTTCAAATCGTTCCCATAAATCATA	148
Seq20	ATATTCACCTATTTCTGATAACATATAATAACTTATTTCAAATCGTTCCCATAAATCATA	148
Seq46	ATATTCACCTATTTCTGATAACATATAATAACTTATTTCAAATCGTTCCCATAAATCATA	148
Seq43	ATATTCACCTATTTCTGATAACATATAATAACTTATTTCAAATCGTTCCCATAAATCATA	148
Seq42	ATATTCACCTATTTCTGATAACATATAATAACTTATTTCAAATCGTTCCCATAAATCATA	148

Seq40	ATATTCACTATTTCCCTGATAACATATAATAACTTATTTCAAATCGTTCCCATAAATCATA	148
Seq37	ATATTCACTATTTCCCTGATAACATATAATAACTTATTTCAAATAGTTCCCATAAATCATA	148
Seq36	ATATTCACTATTTCCCGATAACATATAATAACTTATTTCAAATCGTTCCCATAAATCATA	148
Seq6	ATATTCACTATTTCCCTGATAACATATAATAACTTATTTCAAATCGTTCCCATAAATCATA	148
XM_001349494.1	ATATTCACTATTTCCCTGATAACATATAATAACTTATTTCAAATCGTTCCCATAAATCATA	1020
LN999943.1	ATATTCACTATTTCCCTGATAACATATAATAACTTATTTCAAATCGTTCCCATAAATCATA	147
Seq3	ATATTCACTATTTCCCTGATAACATATAATAACTTATTTCAAATCGTTCCCATAAATCATA	148
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Seq34	CCTTAATAAATTCACGAATAAAAAATGAATACTTATTAAATACACTTTTTTCTGTTTTAAA	208
Seq41	CTTTAATAAATTCACGAATAAAAAATGAATACTTATTAAATACACTTTTTTCTGTTTTAAA	208
Seq31	CTTTAATAAATTCACGAATAAAAAATGAATACTTATTAAATACACTTTTTTCTGTTTTAAA	208
Seq29	CTTTAATAAATTCACGAATAAAAAATGAATACTTATTAAATACACTTTTTTCTGTTTTAAA	208
Seq27	CTTTAATAAATTCACGAATAAAAAATGAATACTTATTAAATACACTTTTTTCTGTTTTAAA	208
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Seq9	CTTTAATAAATTCACGAATAAAAAATGAATACTTATTAAATACACTTTTTTCTGTTTTAAA	208
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Seq4	CTTTAATAAATTCACGAATAAAAAATGAATACTTATTAAATACACTTTTTTCTGTTTTAAA	208
Seq16	CCTTAATAAATTCACGAATAAAAAATGAATACTTATTAAATACACTTTTTTCTGTTTTAAA	208
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Seq18	GTTGAATAAACTAGTGAATAAAATGTGAATACTTATTAAATAAACTTTTTTCAATTTTCAT	208
Seq25	GTTGAATAAACTAGTGAATAAAATGTGAATACTTATTAAATAAACTTTTTTCAATTTTCAT	208
Seq38	GTTGAATAAACTAGTGAATAAAATGTGAATACTTATTAAATGCACTTTTTCAATTTTCAT	208
Seq11	GTTGAATAAACTAGTGAATAAAATGTGAATACTTATTAAATGCACTTTTTCAATTTTCAT	208
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Seq35	GTTGAATAAACTAGTGAATAAAATGTGAATACTTATTAAATAAACTTTTTTCAATTTTCAT	208
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Seq43	GTTGAATAAACTAGTGAATAAAATGTGAATACTTATTAAATGCACTTTTTCAATTTTCAT	208
Seq42	GTTGAATAAACTAGTGAATAAAATGTGAATACTTATTAAATGCACTTTTTCAATTTTCAT	208
Seq40	GTTGAATAAACTAGTGAATAAAATGTGAATACTTATTAAATGCACTTTTTCAATTTTCAT	208
Seq37	GTTGAATAAACTAGTGAATAAAATGTGAATACTTATTAAATGCACTTTTTCAATTTTCAT	208
Seq36	GTTGAATAAACTAGTGAATAAAATGTGAATACTTATTAAATGCACTTTTTCAATTTTCAT	208
Seq6	GTTGAATAAACTAGTGAATAAAATGTGAATACTTATTAAATGCACTTTTTCAATTTTCAT	208
XM_001349494.1	GTTGAATAAACTAGTGAATAAAATGTGAATACTTATTAAATGCACTTTTTCAATTTTCAT	1080
LN999943.1	GTTGAATAAACTAGTGAATAAAATGTGAATACTTATTAAATGCACTTTTTCAATTTTCAT	207
Seq3	GTTGAATAAACTAGTGAATAAAATGTGAATACTTATTAAATGCACTTTTTCAATTTTCAT	208
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Seq34	TTTTTTTTTTTAACAAACGTTTTGTTGTTCCATATAAAGTCTCACCTAAATGCATTAACGT	268
Seq41	TTTTTTTTTTTAACAAACGTTTTGTTATTCCTATATAAAGTCTCACCTAAATCCATTAACGT	268
Seq31	TTTTTTTTTTTAACAAACGTTTTGTTGTTCCATATAAAGTCTCACCTAAATCCATTAACGT	268
Seq29	TTTTTTTTTTTAACAAACGTTTTGTTGTTCCATATAAAGTCTCACATAAATCCATTAACGT	268
Seq27	TTTTTTTTTTTAACAAACGTTTTGTTGTTCCATATAAAGTCTCACCTAAATCCATTAACGT	268
Seq12	TTTTTTTTTTTAACAAACGTTTTGTTGTTCCATATAAAGTCTCACCTAAATCCATTAACGT	268

Seq10	TTTTTTTTTTTAAACAAACGTTTTGTTGTTCCCTATATAAGTCTCACCTAAATTCATTAACGT	268
Seq9	TTTTTTTTTTTAAACAAACGTTTTGTTGTTCCCTATATAAGTCTCACCTAAATGCATTAACGT	268
Seq8	TTTTTTTTTTTAAACAAACGTTTTGTTGTTCCCTATATAAGTCTCACCTAAATTCATTAACGT	268
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Seq1	TTTTTTTTTTTAAACAAACGTTTTGTTGTTCCCTATATAAGTCTCACCTAAATCCATTAACGT	268
Seq4	TTTTTTTTTTTAAACAAACGTTTTGTTGTTCCCTATATAAGTCTCACCTAAATCCATTAACGT	268
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Seq23	TTTTTTTTTTTAAACAAACGTTTTGTTGTTCCCTATATAAGTCTCACCTAAATCCATTAACGT	268
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Seq26	TTTTTTTTTTTAAACAAACGTTTTGTTGTTCCCTATATAAGTCTCACCTAAATGCATTAACGT	268
Seq15	TTTTTTTTTTTAAACAAACGTTTTGTTGTTCCCTATATAAGTCTCACCTAAATCCATTAACGT	268
Seq2	TTTTTTTTTTTAAACAAACGTTTTGTTGTTCCCTATATAAGTCTCACCTAAATCCATTAACGT	268
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Seq18	TTTCTTTGTTAACATATTTTTTT---GTGTCCATAAAACTCTCACTTAATTTGTATGAATT	265
Seq25	TTTCTTTGTTAACATATTTTTTT---GTGTCCATAAAACTCTCACTTAATTTGTATGAATT	265
Seq38	TTTCTTTGTTAACATATTTTTTT---GTGTCCATAAAACTCTCACTTAATTTGTATGAATT	265
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Seq14	TTTCTTTGTTAACATATTTTTTT---GTGTCCATAAAACTCTCACTTAATTTGTATGAATT	265
Seq20	TTTCTTTGTTAACATATTTTTTT---GTGTCCATAAAACTCTCACTTAATTTGTATGAATT	265
Seq46	TTTCTTTGTTAACATATTTTTTT---GTGTCCATAAAACCCTCACTTAATTTGTATGAATT	265
Seq43	TTTCTTTGTTAACATATTTTTTT---GTGTCCATAAAACTCTCACTTAATTTGTATGAATT	265
Seq42	TTTCTTTGTTAACATATTTTTTT---GTGTCCATAAAACTCTCACTTAATTTGTATGAATT	265
Seq40	TTTCTTTGTTAACATATTTTTTT---GTGTCCATAAAACTCTCACTTAATTTGTATGAATT	265
Seq37	TTTCTTTGTTAACATATTTTTTT---GTGTCCATAAAACTCTCACTTAATTTGTATGAATT	265
Seq36	TTTCTTTGTTAACATATTTTTTT---GTGTCCATAAAACTCTCACTTAATTTGTATGAATT	265
Seq6	TTTCTTTGTTAACATATTTTTTT---GTGTCCATAAAACTCTCACTTAATTTGTATGAATT	265
XM_001349494.1	TTTCTTTGTTAACATATTTTTTT---GTGTCCATAAAACTCTCACTTAATTTGTATGAATT	1137
LN999943.1	TTTCTTTGTTAACATATTTTTTT---GTGTCCATAAAACTCTCACTTAATTTGTATGAATT	264
Seq3	TTTCTTTGTTAACATATTTTTTT---GTGTCCATAAAACTCTCACTTAATTTGTATGAATT	265
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Seq34	CCTTTTCATAACTCTTACAAACTTCAGCAAGGGAAGGTTCTTTTCGAA-----	314
Seq41	CCTTTTCATAACTCTTACAAACTTCAGCAAGGGAAGGTTCTTTTCGAA-----	314
Seq31	CCTTTTCATAACTCTTACAAACTTCAGCAAGGGAAGGTTCTTTTCGAA-----	314
Seq29	CCTTTTCATAACTCTTACAAACTTCAGCAAGGGAAGGTTCTTTTCGAA-----	314
Seq27	CCTTTTCATAACTCTTACAAACTTCAGCAAGGGAAGGTTCTTTTCGAA-----	314
Seq12	CCTTTTATAACTCTTACAAACTTCAGCAAGGGAAGGTTCTTTTCGAA-----	314
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Seq9	CCTTTTCATAACTCTTACAAACTTCAGCAAGGGAAGGTTCTTTTCGAA-----	314
Seq8	CCTTTTCATAACTCTTACAAACTTCAGCAAGGGAAGGTTCTTTTCGAA-----	314
Seq7	CCTTTTCATAACTCTTACAAACTTCAGCAAGGGAAGGTTCTTTTCGAA-----	314
Seq1	CCTTTTCATAACTCTTACAAACTTCAGCAAGGGAAGGTTCTTTTCGAA-----	314
Seq4	CCTTTTCATAACTCTTACAAACTTCAGCAAGGGAAGGTTCTTTTCGAA-----	314
Seq16	CCTTTTATAACTCTTACAAACTTCAGCAAGGGAAGGTTCTTTTCGAA-----	314
Seq23	CCTTTTATAACTCTTACAAACTTCAGCAAGGGAAGGTTCTTTTCGAA-----	314
Seq13	CCTTTTATAACTCTTACAAACTTCAGCAAGGGAAGGTTCTTTTCGAA-----	314
Seq21	CCTTTTATAACTCTTACAAACTTCAGCAAGGGAAGGTTCTTTTCGAA-----	314
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Seq28	CCTTTTCATAACTCTTACAAACTTCAGCAAGGGAAGGTTCTTTTCGAA-----	314
Seq26	CCTTTTATAACTCTTACAAACTTCAGCAAGGGAAGGTTCTTTTCGAA-----	314
Seq15	CCTTTTCATAACTCTTACAAACTTCAGCAAGGGAAGGTTCTTTTCGAA-----	314
Seq2	CCTTTTATAACTCTTACAAACTTCAGCAAGGGAAGGTTCTTTTCGAA-----	314
Seq5	CCTTTTATAACTCTTACAAACTTCAGCAAGGGAAGGTTCTTTTCGAA-----	314
Seq18	CTTTTTATAAAATTTAAAAAAATCGTCAAGGGAAGGTTCTTTTCGAA-----	311
Seq25	CTTTTTATAAAATTTAAAAAAATCGTCAAGGGAAGGTTCTTTTCGAA-----	311
Seq38	CTTTTTATAAAATTTAAAAAAATCGTCAAGGGAAGGTTCTTTTCGAA-----	311
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Seq35	CTTTTTATAAAATTTAAAAAAATCGTCAAGGGAAGGTTCTTTTCGAA-----	311
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Seq40	CTTTTTATAAAATTTAAAAAAATCGTCAAGGGAAGGTTCTTTTCGAA-----	311
Seq37	CTTTTTATAAAATTTAAAAAAATCGTCAAGGGAAGGTTCTTTTCGAA-----	311
Seq36	CTTTTTATAAAATTTAAAAAAATCGTCAAGGGAAGGTTCTTTTCGAA-----	311
Seq6	CTTTTTATAAAATTTAAAAAAATCGTCAAGGGAAGGTTCTTTTCGAA-----	311
XM_001349494.1	CTTTTTATAAAATTTAAAAAAATCGTCAAGGGAAGGTTCTTTTCGAACCTTAAATTTCTTTT	1197
LN999943.1	CTTTTTATAAAATTTAAAAAAATCGTCAAGGGAAGGTTCTTTTCGAA-----	310
Seq3	CTTTTTATAAAATTTAAAAAAATCGTCAAGGGAAGGTTCTTTTCGAA-----	311
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Seq34	-----	314
Seq41	-----	314
Seq31	-----	314
Seq29	-----	314
Seq27	-----	314
Seq12	-----	314
Seq10	-----	314
Seq9	-----	314
Seq8	-----	314
Seq7	-----	314
Seq1	-----	314
Seq4	-----	314
Seq16	-----	314
Seq23	-----	314
Seq13	-----	314
Seq21	-----	314
Seq45	-----	314
Seq44	-----	314
Seq39	-----	314
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Seq28	-----	314
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Seq15	-----	314
Seq2	-----	314
Seq5	-----	314
Seq18	-----	311
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Seq38	-----	311
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Seq19	-----	311
Seq17	-----	310
Seq24	-----	310
Seq33	-----	311
Seq35	-----	311
Seq22	-----	311

Seq14	-----	311
Seq20	-----	311
Seq46	-----	311
Seq43	-----	311
Seq42	-----	311
Seq40	-----	311
Seq37	-----	311
Seq36	-----	311
Seq6	-----	311
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LN9999943.1	-----	310
Seq3	-----	311

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Seq41	-----	314
Seq31	-----	314
Seq29	-----	314
Seq27	-----	314
Seq12	-----	314
Seq10	-----	314
Seq9	-----	314
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Seq7	-----	314
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Seq22	-----	311
Seq14	-----	311
Seq20	-----	311
Seq46	-----	311
Seq43	-----	311
Seq42	-----	311
Seq40	-----	311
Seq37	-----	311
Seq36	-----	311
Seq6	-----	311
XM_001349494.1	TAGGATTATATATAATATCCCAACAATAGGCAATAGAAAAATATCTACATTTTGATATATT	1317
LN9999943.1	-----	310
Seq3	-----	311

Seq34	-----	314
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Seq41	-----	314
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Seq29	-----	314
Seq27	-----	314
Seq12	-----	314
Seq10	-----	314
Seq9	-----	314
Seq8	-----	314
Seq7	-----	314
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Seq14	-----	311
Seq20	-----	311
Seq46	-----	311
Seq43	-----	311
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Seq40	-----	311
Seq37	-----	311
Seq36	-----	311
Seq6	-----	311
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Seq3	-----	311

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Seq41	-----	314
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