

## Formatted Alignments

MA 245625 MiSeq	1	ATGAGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCGTCCCGTCAGGCCCCCTC	60
MA 245626 Method A	1	ATGAGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCGTCCCGTCAGGCCCCCTC	60
MA 245626 Method S	1	ATGAGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCGTCCCGTCAGGCCCCCTC	60
MA 245626 Method K	1	ATGAGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCGTCCCGTCAGGCCCCCTC	60
MA 245626 Method N	1	ATGAGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCGTCCCGTCAGGCCCCCTC	60
MA 245625 MiSeq	61	AAAGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAG	120
MA 245626 Method A	61	AAAGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAG	120
MA 245626 Method S	61	AAAGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAG	120
MA 245626 Method K	61	AAAGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAG	120
MA 245626 Method N	61	AAAGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAG	120
MA 245625 MiSeq	121	GCTCTCATGGAATGGCTAAAGACAAGACCAATCCTGTACCTCTGACTAAGGGGATTTTG	180
MA 245626 Method A	121	GCTCTCATGGAATGGCTAAAGACAAGACCAATCCTGTACCTCTGACTAAGGGGATTTTG	180
MA 245626 Method S	121	GCTCTCATGGAATGGCTAAAGACAAGACCAATCCTGTACCTCTGACTAAGGGGATTTTG	180
MA 245626 Method K	121	GCTCTCATGGAATGGCTAAAGACAAGACCAATCCTGTACCTCTGACTAAGGGGATTTTG	180
MA 245626 Method N	121	GCTCTCATGGAATGGCTAAAGACAAGACCAATCCTGTACCTCTGACTAAGGGGATTTTG	180
MA 245625 MiSeq	181	GGATTTGTGTTTCACGCTCACCGTGCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTC	240
MA 245626 Method A	181	GGATTTGTGTTTCACGCTCACCGTGCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTC	240
MA 245626 Method S	181	GGATTTGTGTTTCACGCTCACCGTGCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTC	240
MA 245626 Method K	181	GGATTTGTGTTTCACGCTCACCGTGCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTC	240
MA 245626 Method N	181	GGATTTGTGTTTCACGCTCACCGTGCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTC	240
MA 245625 MiSeq	241	CAAAATGCTCTAAATGGAAATGGAGACCCAAACAACATGGACAGGGCAGTCAAGTTGTAC	300
MA 245626 Method A	241	CAAAATGCTCTAAATGGAAATGGAGACCCAAACAACATGGACAGGGCAGTCAAGTTGTAC	300
MA 245626 Method S	241	CAAAATGCTCTAAATGGAAATGGAGACCCAAACAACATGGACAGGGCAGTCAAGTTGTAC	300
MA 245626 Method K	241	CAAAATGCTCTAAATGGAAATGGAGACCCAAACAACATGGACAGGGCAGTCAAGTTGTAC	300
MA 245626 Method N	241	CAAAATGCTCTAAATGGAAATGGAGACCCAAACAACATGGACAGGGCAGTCAAGTTGTAC	300

MA 245625 MiSeq	301	AGGAAACTGAAGAGAGAGATAAACATTCCATGGGGCTAAAGAAGTTGCACTCAGTTACTCA	360
MA 245626 Method A	301	AGGAAACTGAAGAGAGAGATAAACATTCCATGGGGCTAAAGAAGTTGCACTCAGTTACTCA	360
MA 245626 Method S	301	AGGAAACTGAAGAGAGAGATAAACATTCCATGGGGCTAAAGAAGTTGCACTCAGTTACTCA	360
MA 245626 Method K	301	AGGAAACTGAAGAGAGAGATAAACATTCCATGGGGCTAAAGAAGTTGCACTCAGTTACTCA	360
MA 245626 Method N	301	AGGAAACTGAAGAGAGAGATAAACATTCCATGGGGCTAAAGAAGTTGCACTCAGTTACTCA	360

MA 245625 MiSeq	361	ACCGGTGCACTTGCCAGTTGTATGGGTCTCATATACAACAGGATGGGGACGGTGACCGCA	420
MA 245626 Method A	361	ACCGGTGCACTTGCCAGTTGTATGGGTCTCATATACAACAGGATGGGGACGGTGACCGCA	420
MA 245626 Method S	361	ACCGGTGCACTTGCCAGTTGTATGGGTCTCATATACAACAGGATGGGGACGGTGACCGCA	420
MA 245626 Method K	361	ACCGGTGCACTTGCCAGTTGTATGGGTCTCATATACAACAGGATGGGGACGGTGACCGCA	420
MA 245626 Method N	361	ACCGGTGCACTTGCCAGTTGTATGGGTCTCATATACAACAGGATGGGGACGGTGACCGCA	420

MA 245625 MiSeq	421	GAAGTGGCATTGGGCCTAGTGTGTGCCACCTGTGAGCAGATTGCTGATTACAGCATCGG	480
MA 245626 Method A	421	GAAGTGGCATTGGGCCTAGTGTGTGCCACCTGTGAGCAGATTGCTGATTACAGCATCGG	480
MA 245626 Method S	421	GAAGTGGCATTGGGCCTAGTGTGTGCCACCTGTGAGCAGATTGCTGATTACAGCATCGG	480
MA 245626 Method K	421	GAAGTGGCATTGGGCCTAGTGTGTGCCACCTGTGAGCAGATTGCTGATTACAGCATCGG	480
MA 245626 Method N	421	GAAGTGGCATTGGGCCTAGTGTGTGCCACCTGTGAGCAGATTGCTGATTACAGCATCGG	480

MA 245625 MiSeq	481	TCTCACAGACAGATAGCTACCACCACCAACCCACTAATCAGACATGAAAACAGAATGGTG	540
MA 245626 Method A	481	TCTCACAGACAGATAGCTACCACCACCAACCCACTAATCAGACATGAAAACAGAATGGTG	540
MA 245626 Method S	481	TCTCACAGACAGATAGCTACCACCACCAACCCACTAATCAGACATGAAAACAGAATGGTG	540
MA 245626 Method K	481	TCTCACAGACAGATAGCTACCACCACCAACCCACTAATCAGACATGAAAACAGAATGGTG	540
MA 245626 Method N	481	TCTCACAGACAGATAGCTACCACCACCAACCCACTAATCAGACATGAAAACAGAATGGTG	540

MA 245625 MiSeq	541	TTGGCCAGTACTACAGCTAAGGCTATGGAGCAGATGGCTGGATCGAGTGAGCAAGCAGTG	600
MA 245626 Method A	541	TTGGCCAGTACTACAGCTAAGGCTATGGAGCAGATGGCTGGATCGAGTGAGCAAGCAGTG	600
MA 245626 Method S	541	TTGGCCAGTACTACAGCTAAGGCTATGGAGCAGATGGCTGGATCGAGTGAGCAAGCAGTG	600
MA 245626 Method K	541	TTGGCCAGTACTACAGCTAAGGCTATGGAGCAGATGGCTGGATCGAGTGAGCAAGCAGTG	600
MA 245626 Method N	541	TTGGCCAGTACTACAGCTAAGGCTATGGAGCAGATGGCTGGATCGAGTGAGCAAGCAGTG	600

MA 245625 MiSeq	601	GAAGCCATGGAGGTTGCTAGTCAGGCTAGGCAGATGGTGCAGGCGATGAGGACCATTGGA	660
MA 245626 Method A	601	GAAGCCATGGAGGTTGCTAGTCAGGCTAGGCAGATGGTGCAGGCGATGAGGACCATTGGA	660
MA 245626 Method S	601	GAAGCCATGGAGGTTGCTAGTCAGGCTAGGCAGATGGTGCAGGCGATGAGGACCATTGGA	660
MA 245626 Method K	601	GAAGCCATGGAGGTTGCTAGTCAGGCTAGGCAGATGGTGCAGGCGATGAGGACCATTGGA	660
MA 245626 Method N	601	GAAGCCATGGAGGTTGCTAGTCAGGCTAGGCAGATGGTGCAGGCGATGAGGACCATTGGA	660

MA 245625 MiSeq	661	ACTCATCCTAGCTCCAGTGCCGGTCTGAGAGATGATCTCCTTGAAAATTTGCAGGCCTAC	720
MA 245626 Method A	661	ACTCATCCTAGCTCCAGTGCCGGTCTGAGAGATGATCTCCTTGAAAATTTGCAGGCCTAC	720
MA 245626 Method S	661	ACTCATCCTAGCTCCAGTGCCGGTCTGAGAGATGATCTCCTTGAAAATTTGCAGGCCTAC	720
MA 245626 Method K	661	ACTCATCCTAGCTCCAGTGCCGGTCTGAGAGATGATCTCCTTGAAAATTTGCAGGCCTAC	720
MA 245626 Method N	661	ACTCATCCTAGCTCCAGTGCCGGTCTGAGAGATGATCTCCTTGAAAATTTGCAGGCCTAC	720

MA 245625 MiSeq	721	CAAAAACGGATGGGAGTGCAACTGCAGCGATTCAAGTGATCCTCTCGTTATTGCCGCAAG	780
MA 245626 Method A	721	CAAAAACGGATGGGAGTGCAACTGCAGCGATTCAAGTGATCCTCTCGTTATTGCCGCAAG	780
MA 245626 Method S	721	CAAAAACGGATGGGAGTGCAACTGCAGCGATTCAAGTGATCCTCTCGTTATTGCCGCAAG	780
MA 245626 Method K	721	CAAAAACGGATGGGAGTGCAACTGCAGCGATTCAAGTGATCCTCTCGTTATTGCCGCAAG	780
MA 245626 Method N	721	CAAAAACGGATGGGAGTGCAACTGCAGCGATTCAAGTGATCCTCTCGTTATTGCCGCAAG	780

MA 245625 MiSeq	781	TATCGTTGGGATCTTGCACTTGATATTGTGGATTCTTGATCGCCTTTTCTTCAAATGCGT	840
MA 245626 Method A	781	TATCGTTGGGATCTTGCACTTGATATTGTGGATTCTTGATCGCCTTTTCTTCAAATGCGT	840
MA 245626 Method S	781	TATCGTTGGGATCTTGCACTTGATATTGTGGATTCTTGATCGCCTTTTCTTCAAATGCGT	840
MA 245626 Method K	781	TATCGTTGGGATCTTGCACTTGATATTGTGGATTCTTGATCGCCTTTTCTTCAAATGCGT	840
MA 245626 Method N	781	TATCGTTGGGATCTTGCACTTGATATTGTGGATTCTTGATCGCCTTTTCTTCAAATGCGT	840

MA 245625 MiSeq	841	TTATCGTCGCCTTAAATACGGTTTGAAAGGAGGGCCTTCTACGGAAGGAGTACCTGAGTC	900
MA 245626 Method A	841	TTATCGTCGCCTTAAATACGGTTTGAAAGGAGGGCCTTCTACGGAAGGAGTACCTGAGTC	900
MA 245626 Method S	841	TTATCGTCGCCTTAAATACGGTTTGAAAGGAGGGCCTTCTACGGAAGGAGTACCTGAGTC	900
MA 245626 Method K	841	TTATCGTCGCCTTAAATACGGTTTGAAAGGAGGGCCTTCTACGGAAGGAGTACCTGAGTC	900
MA 245626 Method N	841	TTATCGTCGCCTTAAATACGGTTTGAAAGGAGGGCCTTCTACGGAAGGAGTACCTGAGTC	900

<b>MA 245625 MiSeq</b>	901	CATGAGGGAAGAGTACCGGCAGGAACAGCAGAGTGCTGTGGATGTTGACGATGGTCATTT	960
<b>MA 245626 Method A</b>	901	CATGAGGGAAGAGTACCGGCAGGAACAGCAGAGTGCTGTGGATGTTGACGATGGTCATTT	960
<b>MA 245626 Method S</b>	901	CATGAGGGAAGAGTACCGGCAGGAACAGCAGAGTGCTGTGGATGTTGACGATGGTCATTT	960
<b>MA 245626 Method K</b>	901	CATGAGGGAAGAGTACCGGCAGGAACAGCAGAGTGCTGTGGATGTTGACGATGGTCATTT	960
<b>MA 245626 Method N</b>	901	CATGAGGGAAGAGTACCGGCAGGAACAGCAGAGTGCTGTGGATGTTGACGATGGTCATTT	960

<b>MA 245625 MiSeq</b>	961	TGTCAACATAGAGCTGGAGTAA	982
<b>MA 245626 Method A</b>	961	TGTCAACATAGAGCTGGAGTAA	982
<b>MA 245626 Method S</b>	961	TGTCAACATAGAGCTGGAGTAA	982
<b>MA 245626 Method K</b>	961	TGTCAACATAGAGCTGGAGTAA	982
<b>MA 245626 Method N</b>	961	TGTCAACATAGAGCTGGAGTAA	982