Database: ISfinder_Nucl
5,559 sequences; 8,208,285 total letters

*Query= MT-1_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_1*
*Length=308325*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | 131 | 7E-28 |
| IS*Aba1* | IS*4* | IS*10* | *Acinetobacter baumannii* | 131 | 7E-28 |
| IS*Aba33* | IS*4* | IS*10* | *Acinetobacter baumannii* | 69.9 | 0,000000002 |

*Query= MT-1_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_2*
*Length=289160*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Aba13* | IS*5* | IS*903* | *Acinetobacter baumannii* | 119 | 3E-24 |
| IS*Ppu12* | IS*L3* | | *Pseudomonas putida* | 119 | 3E-24 |
| IS*1396* | IS*L3* | | *Serratia marcescens* | 119 | 3E-24 |
| IS*Pst2* | IS*L3* | | *Pseudomonas stutzeri* | 85.7 | 4E-14 |
| IS*Pst9* | IS*L3* | | *Pseudomonas stutzeri* | 63.9 | 0,0000001 |

*Query= MT-1_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_3*
*Length=237801*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Aba1* | IS*4* | IS*10* | *Acinetobacter baumannii* | 180 | 7E-43 |
| IS*Aba33* | IS*4* | IS*10* | *Acinetobacter baumannii* | 111 | 5E-22 |

*Query= MT-1_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_4*
*Length=202703*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Aba1* | IS*4* | IS*10* | *Acinetobacter baumannii* | 180 | 6E-43 |
| IS*Aba13* | IS*5* | IS*903* | *Acinetobacter baumannii* | 119 | 2E-24 |
| IS*Aba33* | IS*4* | IS*10* | *Acinetobacter baumannii* | 111 | 4E-22 |
| IS*Aha1* | IS*5* | IS*903* | *Acinetobacter haemolyticus* | 111 | 4E-22 |
| IS*Aba53* | IS*5* | IS*903* | *Acinetobacter baumannii* | 103 | 1E-19 |
| IS*17* | IS*5* | IS*903* | *Acinetobacter haemolyticus* | 77.8 | 6E-12 |
| IS*Aba12* | IS*5* | IS*903* | *Acinetobacter baumannii* | 69.9 | 0,000000002 |
| IS*Aba40* | IS*5* | IS*903* | *Acinetobacter baumannii* | 56.0 | 0,00002 |
| IS*Ajo1* | IS*5* | IS*903* | *Acinetobacter johnsonii* | 54.0 | 0,00009 |
| IS*Aba5* | IS*5* | IS*903* | *Acinetobacter baumannii* | 54.0 | 0,00009 |

*Query= MT-1_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_6*
*Length=170838*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Aba1* | IS*4* | IS*10* | *Acinetobacter baumannii* | 131 | 4E-28 |
| IS*Aba33* | IS*4* | IS*10* | *Acinetobacter baumannii* | 69.9 | 0,000000001 |

*Query= MT-1_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_7*
*Length=155325*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Aba1* | IS*4* | IS*10* | *Acinetobacter baumannii* | 180 | 4E-43 |
| IS*Aba33* | IS*4* | IS*10* | *Acinetobacter baumannii* | 111 | 3E-22 |

*Query= MT-1_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_8*
*Length=153568*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | 131 | 4E-28 |
| IS*Aba13* | IS*5* | IS*903* | *Acinetobacter baumannii* | 119 | 1E-24 |
| IS*Alw34* | IS*66* | | *Acinetobacter lwoffii* | 58.0 | 0,000004 |
| IS*Alw16* | IS*66* | | *Acinetobacter lwoffii* | 58.0 | 0,000004 |
| IS*Aba16* | IS*66* | | *Acinetobacter baumannii* | 58.0 | 0,000004 |
| IS*Aba17* | IS*66* | | *Acinetobacter baumannii* | 58.0 | 0,000004 |

*Query= MT-1_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_9*
*Length=148232*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Aba1* | IS*4* | IS*10* | *Acinetobacter baumannii* | 180 | 4E-43 |
| IS*Aba13* | IS*5* | IS*903* | *Acinetobacter baumannii* | 119 | 1E-24 |
| IS*Aba33* | IS*4* | IS*10* | *Acinetobacter baumannii* | 111 | 3E-22 |
| IS*Aha1* | IS*5* | IS*903* | *Acinetobacter haemolyticus* | 111 | 3E-22 |
| IS*Aba53* | IS*5* | IS*903* | *Acinetobacter baumannii* | 103 | 8E-20 |
| IS*17* | IS*5* | IS*903* | *Acinetobacter haemolyticus* | 77.8 | 5E-12 |
| IS*Aba12* | IS*5* | IS*903* | *Acinetobacter baumannii* | 69.9 | 0,000000001 |
| IS*Aba40* | IS*5* | IS*903* | *Acinetobacter baumannii* | 56.0 | 0,00002 |
| IS*Ajo1* | IS*5* | IS*903* | *Acinetobacter johnsonii* | 54.0 | 0,00007 |

| | | | | | | |
|---|---|---|---|---|---|---|
| IS*Aba5* | IS*5* | IS*903* | *Acinetobacter baumannii* | 54.0 | | 0,00007 |

*Query= MT-1_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_10*
*Length=148131*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value | |
|---|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | | 131 | 4E-28 |

*Query= MT-1_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_11*
*Length=140828*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value | |
|---|---|---|---|---|---|---|
| IS*Aba1* | IS*4* | IS*10* | *Acinetobacter baumannii* | | 180 | 4E-43 |
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | | 131 | 3E-28 |
| IS*Aba33* | IS*4* | IS*10* | *Acinetobacter baumannii* | | 111 | 3E-22 |

*Query= MT-1_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_12*
*Length=138277*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value | |
|---|---|---|---|---|---|---|
| IS*Aba1* | IS*4* | IS*10* | *Acinetobacter baumannii* | | 180 | 4E-43 |
| IS*Aba33* | IS*4* | IS*10* | *Acinetobacter baumannii* | | 111 | 3E-22 |

*Query= MT-1_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_13*
*Length=125408*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value | |
|---|---|---|---|---|---|---|
| IS*Aba1* | IS*4* | IS*10* | *Acinetobacter baumannii* | | 180 | 4E-43 |
| IS*Aba33* | IS*4* | IS*10* | *Acinetobacter baumannii* | | 111 | 3E-22 |

*Query= MT-1_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_14*
*Length=120407*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value | |
|---|---|---|---|---|---|---|
| IS*Aba13* | IS*5* | IS*903* | *Acinetobacter baumannii* | | 2060 | 0.0 |
| IS*Aba12* | IS*5* | IS*903* | *Acinetobacter baumannii* | | 848 | 0.0 |
| IS*17* | IS*5* | IS*903* | *Acinetobacter haemolyticus* | | 835 | 0.0 |
| IS*Aba40* | IS*5* | IS*903* | *Acinetobacter baumannii* | | 803 | 0.0 |
| IS*Aha1* | IS*5* | IS*903* | *Acinetobacter haemolyticus* | | 801 | 0.0 |
| IS*Alw1* | IS*5* | IS*903* | *Acinetobacter lwoffii* | | 704 | 0.0 |
| IS*Ajo1* | IS*5* | IS*903* | *Acinetobacter johnsonii* | | 636 | 2E-180 |
| IS*Aba53* | IS*5* | IS*903* | *Acinetobacter baumannii* | | 617 | 2E-174 |
| IS*Aha3* | IS*5* | IS*903* | *Acinetobacter haemolyticus* | | 517 | 1E-144 |
| IS*Aha2* | IS*5* | IS*903* | *Acinetobacter haemolyticus* | | 428 | 9E-118 |
| IS*Aba7* | IS*5* | IS*903* | *Acinetobacter baumannii* | | 420 | 2E-115 |
| IS*Aba5* | IS*5* | IS*903* | *Acinetobacter baumannii* | | 387 | 3E-105 |

*Query= MT-1_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_15*
*Length=120157*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value | |
|---|---|---|---|---|---|---|
| IS*Aba1* | IS*4* | IS*10* | *Acinetobacter baumannii* | | 131 | 3E-28 |
| IS*Aba33* | IS*4* | IS*10* | *Acinetobacter baumannii* | 69.9 | | 9E-10 |

*Query= MT-1_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_16*
*Length=117829*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value | |
|---|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | | 119 | 1E-24 |

*Query= MT-1_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_17*
*Length=105540*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value | |
|---|---|---|---|---|---|---|
| IS*Aba1* | IS*4* | IS*10* | *Acinetobacter baumannii* | | 180 | 3E-43 |
| IS*Aba33* | IS*4* | IS*10* | *Acinetobacter baumannii* | | 111 | 2E-22 |

*Query= MT-1_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_18*
*Length=87980*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value | |
|---|---|---|---|---|---|---|
| IS*Aba26* | IS*256* | | *Acinetobacter baumannii* | | 2605 | 0.0 |
| IS*Aba13* | IS*5* | IS*903* | *Acinetobacter baumannii* | | 119 | 8E-25 |
| IS*Abe10* | IS*256* | | *Acinetobacter bereziniae* | | 111 | 2E-22 |
| IS*Aba42* | IS*256* | | *Acinetobacter baumannii* | 83.8 | | 4E-14 |
| IS*Aba50* | IS*256* | | *Acinetobacter baumannii* | 56.0 | | 0,00001 |

*Query= MT-1_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_19*
*Length=75938*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Aba13* | IS*5* | IS*903* | *Acinetobacter baumannii* | 119 | 7E-25 |
| IS*Aha1* | IS*5* | IS*903* | *Acinetobacter haemolyticus* | 111 | 2E-22 |
| IS*Aba53* | IS*5* | IS*903* | *Acinetobacter baumannii* | 103 | 4E-20 |
| IS*17* | IS*5* | IS*903* | *Acinetobacter haemolyticus* | 77.8 | 2E-12 |
| IS*Aba12* | IS*5* | IS*903* | *Acinetobacter baumannii* | 69.9 | 6E-10 |
| IS*Aba40* | IS*5* | IS*903* | *Acinetobacter baumannii* | 56.0 | 0,000009 |
| IS*Ajo1* | IS*5* | IS*903* | *Acinetobacter johnsonii* | 54.0 | 0,00003 |
| IS*Aba5* | IS*5* | IS*903* | *Acinetobacter baumannii* | 54.0 | 0,00003 |

*Query= MT-1_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_20*
*Length=73065*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Aba1* | IS*4* | IS*10* | *Acinetobacter baumannii* | 131 | 2E-28 |
| IS*Aba33* | IS*4* | IS*10* | *Acinetobacter baumannii* | 69.9 | 5E-10 |

*Query= MT-1_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_21*
*Length=67943*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Aba13* | IS*5* | IS*903* | *Acinetobacter baumannii* | 119 | 6E-25 |
| IS*Aha1* | IS*5* | IS*903* | *Acinetobacter haemolyticus* | 111 | 1E-22 |
| IS*Aba53* | IS*5* | IS*903* | *Acinetobacter baumannii* | 103 | 4E-20 |
| IS*17* | IS*5* | IS*903* | *Acinetobacter haemolyticus* | 77.8 | 2E-12 |
| IS*Aba12* | IS*5* | IS*903* | *Acinetobacter baumannii* | 69.9 | 5E-10 |
| IS*Aba40* | IS*5* | IS*903* | *Acinetobacter baumannii* | 56.0 | 0,000008 |
| IS*Ajo1* | IS*5* | IS*903* | *Acinetobacter johnsonii* | 54.0 | 0,00003 |
| IS*Aba5* | IS*5* | IS*903* | *Acinetobacter baumannii* | 54.0 | 0,00003 |

*Query= MT-1_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_22*
*Length=66290*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Aba1* | IS*4* | IS*10* | *Acinetobacter baumannii* | 131 | 2E-28 |
| IS*Aba33* | IS*4* | IS*10* | *Acinetobacter baumannii* | 69.9 | 5E-10 |

*Query= MT-1_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_23*
*Length=61070*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Ppu12* | IS*L3* | | *Pseudomonas putida* | 119 | 6E-25 |
| IS*1396* | IS*L3* | | *Serratia marcescens* | 119 | 6E-25 |
| IS*Pst2* | IS*L3* | | *Pseudomonas stutzeri* | 85.7 | 8E-15 |
| IS*Pst9* | IS*L3* | | *Pseudomonas stutzeri* | 63.9 | 0,00000003 |

*Query= MT-1_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_24*
*Length=55919*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Aba1* | IS*4* | IS*10* | *Acinetobacter baumannii* | 131 | 1E-28 |
| IS*Aba33* | IS*4* | IS*10* | *Acinetobacter baumannii* | 69.9 | 4E-10 |

*Query= MT-1_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_25*
*Length=53672*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Aba1* | IS*4* | IS*10* | *Acinetobacter baumannii* | 131 | 1E-28 |
| IS*Aba33* | IS*4* | IS*10* | *Acinetobacter baumannii* | 69.9 | 4E-10 |

*Query= MT-1_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_26*
*Length=50216*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Aba125* | IS*30* | | *Acinetobacter baumannii* | 119 | 5E-25 |
| IS*C1041* | IS*30* | | *Sulfolobus solfataricus* | 61.9 | 0,00000009 |

*Query= MT-1_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_27*
*Length=50075*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Aba1* | IS*4* | IS*10* | *Acinetobacter baumannii* | 131 | 1E-28 |
| IS*Aba33* | IS*4* | IS*10* | *Acinetobacter baumannii* | 69.9 | 4E-10 |

*Query= MT-1_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_29*
*Length=40833*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Aba1* | IS*4* | IS*10* | *Acinetobacter baumannii* | 180 | 1E-43 |
| IS*Aba13* | IS*5* | IS*903* | *Acinetobacter baumannii* | 119 | 4E-25 |

| | | | | | | |
|---|---|---|---|---|---|---|
| IS*Aba33* | IS*4* | IS*10* | *Acinetobacter baumannii* | | 111 | 9E-23 |
| IS*Ajo1* | IS*5* | IS*903* | *Acinetobacter johnsonii* | 52.0 | | 0,00007 |
| IS*Aha2* | IS*5* | IS*903* | *Acinetobacter haemolyticus* | 52.0 | | 0,00007 |

*Query= MT-1_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_31*
*Length=36859*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Aba1* | IS*4* | IS*10* | *Acinetobacter baumannii* | | 131 9E-29 |
| IS*Aba13* | IS*5* | IS*903* | *Acinetobacter baumannii* | | 119 3E-25 |
| IS*Aha1* | IS*5* | IS*903* | *Acinetobacter haemolyticus* | | 111 8E-23 |
| IS*Aba53* | IS*5* | IS*903* | *Acinetobacter baumannii* | | 103 2E-20 |
| IS*17* | IS*5* | IS*903* | *Acinetobacter haemolyticus* | 77.8 | 1E-12 |
| IS*Aba33* | IS*4* | IS*10* | *Acinetobacter baumannii* | 69.9 | 3E-10 |
| IS*Aba12* | IS*5* | IS*903* | *Acinetobacter baumannii* | 69.9 | 3E-10 |
| IS*Aba40* | IS*5* | IS*903* | *Acinetobacter baumannii* | 56.0 | 0,000004 |
| IS*Ajo1* | IS*5* | IS*903* | *Acinetobacter johnsonii* | 54.0 | 0,00002 |
| IS*Aba5* | IS*5* | IS*903* | *Acinetobacter baumannii* | 54.0 | 0,00002 |

*Query= MT-1_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_32*
*Length=34444*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | 119 | 3E-25 |

*Query= MT-1_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_34*
*Length=30872*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Alw4* | IS*3* | IS*51* | *Acinetobacter lwoffii* | 2044 | 0.0 |
| IS*Alw5* | IS*3* | IS*51* | *Acinetobacter lwoffii* | 1941 | 0.0 |
| IS*Alw23* | IS*3* | IS*51* | *Acinetobacter lwoffii* | 1885 | 0.0 |
| IS*Aba2* | IS*3* | IS*51* | *Acinetobacter baumannii* | 1721 | 0.0 |
| IS*Aba29* | IS*3* | IS*51* | *Acinetobacter baumannii* | 1552 | 0.0 |
| IS*Aba34* | IS*3* | IS*51* | *Acinetobacter baumannii* | 959 | 0.0 |
| IS*Aba19* | IS*3* | IS*51* | *Acinetobacter baumannii* | 910 | 0.0 |
| IS*Aba18* | IS*3* | IS*51* | *Acinetobacter baumannii* | 739 | 0.0 |
| IS*Aba27* | IS*5* | IS*L2* | *Acinetobacter baumannii* | 345 | 3E-93 |
| IS*Alw1* | IS*5* | IS*903* | *Acinetobacter lwoffii* | 161 | 8E-38 |
| IS*Aba13* | IS*5* | IS*903* | *Acinetobacter baumannii* | 153 | 2E-35 |
| IS*Aha1* | IS*5* | IS*903* | *Acinetobacter haemolyticus* | 153 | 2E-35 |
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | 131 | 7E-29 |
| IS*Ajo1* | IS*5* | IS*903* | *Acinetobacter johnsonii* | 127 | 1E-27 |
| IS*Alw35* | IS*481* | | *Acinetobacter lwoffii* | 107 | 1E-21 |
| IS*Aba40* | IS*5* | IS*903* | *Acinetobacter baumannii* | 107 | 1E-21 |
| IS*Alw24* | IS*481* | | *Acinetobacter lwoffii* | 99.6 | 3E-19 |
| IS*Aba53* | IS*5* | IS*903* | *Acinetobacter baumannii* | 95.6 | 4E-18 |
| IS*Sde2* | IS*481* | | *Shewanella denitrificans* | 83.8 | 2E-14 |
| IS*Aba7* | IS*5* | IS*903* | *Acinetobacter baumannii* | 83.8 | 2E-14 |
| IS*Aha3* | IS*5* | IS*903* | *Acinetobacter haemolyticus* | 69.9 | 2E-10 |
| IS*Aba12* | IS*5* | IS*903* | *Acinetobacter baumannii* | 69.9 | 2E-10 |
| IS*1006* | IS*6* | | *Acinetobacter junii* | 63.9 | 0,00000001 |
| IS*Rtr2* | IS*3* | IS*51* | *Rhizobium tropici* | 58.0 | 0,0000009 |
| IS*Aba52* | IS*6* | | *Acinetobacter baumannii* | 56.0 | 0,000003 |
| IS*Ppu33* | IS*3* | IS*51* | *Pseudomonas putida* | 56.0 | 0,000003 |
| IS*Stma17* | IS*3* | IS*51* | *Stenotrophomonas maltophilia* | 56.0 | 0,000003 |
| IS*Mca3* | IS*3* | IS*51* | *Methylococcus capsulatus* | 56.0 | 0,000003 |
| IS*Our1* | IS*6* | | *Oligella urethralis* | 56.0 | 0,000003 |
| IS*17* | IS*5* | IS*903* | *Acinetobacter haemolyticus* | 56.0 | 0,000003 |
| IS*1416* | IS*3* | IS*51* | *Burkholderia glumae* | 56.0 | 0,000003 |
| IS*Ali4* | IS*3* | IS*51* | *Azospirillum lipoferum* | 54.0 | 0,00001 |
| IS*Rme15* | IS*3* | IS*51* | *Ralstonia metallidurans* | 54.0 | 0,00001 |
| IS*Pmi1* | IS*3* | IS*51* | *Proteus mirabilis* | 52.0 | 0,00005 |

*Query= MT-1_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_35*
*Length=30125*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Aba13* | IS*5* | IS*903* | *Acinetobacter baumannii* | 119 | 3E-25 |
| IS*Ajo1* | IS*5* | IS*903* | *Acinetobacter johnsonii* | 52.0 | 0,00005 |
| IS*Aha2* | IS*5* | IS*903* | *Acinetobacter haemolyticus* | 52.0 | 0,00005 |
| IS*Alw1* | IS*5* | IS*903* | *Acinetobacter lwoffii* | 50.1 | 0,0002 |

*Query= MT-1_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_37*
*Length=18461*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| *Tn2* | *Tn3* | | *Escherichia coli* | 8851 | 0.0 |
| *Tn3* | *Tn3* | | *Salmonella enterica* | 8806 | 0.0 |
| *TnAs1* | *Tn3* | | *Aeromonas salmonicida* | 2962 | 0.0 |
| *TnAs2* | *Tn3* | | *Aeromonas salmonicida* | 1838 | 0.0 |
| IS*Pa40* | *Tn3* | | *Pseudomonas aeruginosa* | 1758 | 0.0 |
| IS*6100* | IS*6* | | *Mycobacterium fortuitum* | 1744 | 0.0 |
| IS*1R* | IS*1* | | *Escherichia coli* | 1451 | 0.0 |

| | | | | | | |
|---|---|---|---|---|---|---|
| IS*1B* | IS*1* | | *Escherichia coli* | | 1435 | 0.0 |
| IS*1D* | IS*1* | | *Escherichia coli* | | 1419 | 0.0 |
| IS*1G* | IS*1* | | *Escherichia coli* | | 1396 | 0.0 |
| IS*1A* | IS*1* | | *Escherichia coli* | | 1396 | 0.0 |
| IS*1SD* | IS*1* | | *Shigella dysenteriae* | | 1388 | 0.0 |
| IS*1S* | IS*1* | | *Shigella sonnei* | | 1372 | 0.0 |
| *TnAs3* | *Tn3* | | *Aeromonas salmonicida* | | 1338 | 0.0 |
| IS*Shes11* | *Tn3* | | *Shewanella sp.* | | 1322 | 0.0 |
| IS*Pa38* | *Tn3* | | *Pseudomonas aeruginosa* | | 1164 | 0.0 |
| IS*Sen9* | IS*1* | | *Salmonella enterica* | | 1150 | 0.0 |
| IS*1X2* | IS*1* | | *Escherichia vulneris* | | 1102 | 0.0 |
| IS*1X4* | IS*1* | | *Escherichia hermannii* | | 991 | 0.0 |
| IS*1X3* | IS*1* | | *Escherichia fergusonii* | | 912 | 0.0 |
| IS*1X1* | IS*1* | | *Shigella flexneri* | | 864 | 0.0 |
| IS*1F* | IS*1* | | *Escherichia coli* | | 864 | 0.0 |
| IS*Kpn14* | IS*1* | | *Klebsiella pneumoniae* | | 729 | 0.0 |
| *TnShfr1* | *Tn3* | | *Shewanella frigidimarina* | | 549 | 5E-155 |
| IS*Stma11* | IS*L3* | | *Stenotrophomonas maltophilia* | | 492 | 1E-137 |
| IS*Ec63* | *Tn3* | | *Escherichia coli* | | 486 | 7E-136 |
| IS*Sod9* | *Tn3* | | *Shewanella oneidensis* | | 371 | 3E-101 |
| IS*15* | IS*6* | | *Salmonella panama* | | 121 | 4E-26 |
| IS*15DI* | IS*6* | | *Salmonella panama* | | 119 | 2E-25 |
| IS*26* | IS*6* | | *Proteus vulgaris* | | 119 | 2E-25 |
| IS*Arsp6* | *Tn3* | | *Arthrobacter sp.* | | 117 | 7E-25 |
| IS*15DIV* | IS*6* | | *Salmonella typhimurium* | | 117 | 7E-25 |
| IS*15DII* | IS*6* | | *Salmonella panama* | | 111 | 4E-23 |
| IS*Acsp1* | *Tn3* | | *Acinetobacter species* | 75.8 | | 2E-12 |
| IS*Stag1* | IS*6* | | *Stappia aggregata* | 71.9 | | 3E-11 |
| *Tn5393* | *Tn3* | | *Erwinia amylovora* | 65.9 | | 0,000000002 |
| IS*Sf1* | IS*5* | IS*1031* | *Shigella flexneri* | 61.9 | | 0,00000003 |
| IS*Acr2* | IS*6* | | *Acidiphilium cryptum* | 54.0 | | 0,000008 |

*Query= MT-1_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_38*
*Length=17961*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Aba13* | IS*5* | IS*903* | *Acinetobacter baumannii* | 119 | 2E-25 |
| IS*Aha1* | IS*5* | IS*903* | *Acinetobacter haemolyticus* | 111 | 4E-23 |
| IS*Aba53* | IS*5* | IS*903* | *Acinetobacter baumannii* | 103 | 1E-20 |
| IS*17* | IS*5* | IS*903* | *Acinetobacter haemolyticus* | 77.8 | 6E-13 |
| IS*Aba12* | IS*5* | IS*903* | *Acinetobacter baumannii* | 69.9 | 1E-10 |
| IS*Aba40* | IS*5* | IS*903* | *Acinetobacter baumannii* | 56.0 | 0,000002 |
| IS*Ajo1* | IS*5* | IS*903* | *Acinetobacter johnsonii* | 54.0 | 0,000008 |
| IS*Aba5* | IS*5* | IS*903* | *Acinetobacter baumannii* | 54.0 | 0,000008 |
| IS*Aha2* | IS*5* | IS*903* | *Acinetobacter haemolyticus* | 52.0 | 0,00003 |
| IS*Alw1* | IS*5* | IS*903* | *Acinetobacter lwoffii* | 50.1 | 0,0001 |

*Query= MT-1_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_40*
*Length=16539*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | 119 | 1E-25 |
| IS*Aba13* | IS*5* | IS*903* | *Acinetobacter baumannii* | 119 | 1E-25 |
| IS*Aha1* | IS*5* | IS*903* | *Acinetobacter haemolyticus* | 111 | 4E-23 |
| IS*Aba53* | IS*5* | IS*903* | *Acinetobacter baumannii* | 103 | 9E-21 |
| IS*17* | IS*5* | IS*903* | *Acinetobacter haemolyticus* | 77.8 | 5E-13 |
| IS*Aba12* | IS*5* | IS*903* | *Acinetobacter baumannii* | 69.9 | 1E-10 |
| IS*Aba40* | IS*5* | IS*903* | *Acinetobacter baumannii* | 56.0 | 0,000002 |
| IS*Ajo1* | IS*5* | IS*903* | *Acinetobacter johnsonii* | 54.0 | 0,000007 |
| IS*Aba5* | IS*5* | IS*903* | *Acinetobacter baumannii* | 54.0 | 0,000007 |

*Query= MT-1_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_41*
*Length=16124*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Aba1* | IS*4* | IS*10* | *Acinetobacter baumannii* | 180 | 5E-44 |
| IS*Aba33* | IS*4* | IS*10* | *Acinetobacter baumannii* | 111 | 4E-23 |
| IS*Ppu12* | IS*L3* | | *Pseudomonas putida* | 103 | 9E-21 |

*Query= MT-1_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_43*
*Length=11589*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Aba125* | IS*30* | | *Acinetobacter baumannii* | 119 | 1E-25 |
| IS*C1041* | IS*30* | | *Sulfolobus solfataricus* | 103 | 6E-21 |

*Query= MT-1_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_44*
*Length=10415*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Aba13* | IS*5* | IS*903* | *Acinetobacter baumannii* | 119 | 9E-26 |
| IS*Ajo1* | IS*5* | IS*903* | *Acinetobacter johnsonii* | 52.0 | 0,00002 |
| IS*Aha2* | IS*5* | IS*903* | *Acinetobacter haemolyticus* | 52.0 | 0,00002 |
| IS*Alw1* | IS*5* | IS*903* | *Acinetobacter lwoffii* | 50.1 | 0,00007 |

*Query= MT-1_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_45*
*Length=10272*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Ppu12* | IS*L3* | | *Pseudomonas putida* | 103 | 6E-21 |

*Query= MT-1_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_47*
*Length=7773*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Aba1* | IS*4* | IS*10* | *Acinetobacter baumannii* | 131 | 2E-29 |
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | 119 | 7E-26 |
| IS*Aba33* | IS*4* | IS*10* | *Acinetobacter baumannii* | 69.9 | 6E-11 |

*Query= MT-1_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_48*
*Length=7724*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Aba1* | IS*4* | IS*10* | *Acinetobacter baumannii* | 111 | 2E-23 |
| IS*Aba33* | IS*4* | IS*10* | *Acinetobacter baumannii* | 63.9 | 0,000000004 |

*Query= MT-1_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_49*
*Length=7630*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Aba125* | IS*30* | | *Acinetobacter baumannii* | 1826 | 0.0 |
| *TnAs3* | *Tn3* | | *Aeromonas salmonicida* | 1364 | 0.0 |
| IS*C1041* | IS*30* | | *Sulfolobus solfataricus* | 668 | 0.0 |
| IS*Abe8* | IS*30* | | *Acinetobacter bereziniae* | 317 | 1E-85 |
| IS*15DI* | IS*6* | | *Salmonella panama* | 119 | 7E-26 |
| IS*15* | IS*6* | | *Salmonella panama* | 119 | 7E-26 |
| IS*26* | IS*6* | | *Proteus vulgaris* | 119 | 7E-26 |
| IS*15DIV* | IS*6* | | *Salmonella typhimurium* | 117 | 3E-25 |
| IS*15DII* | IS*6* | | *Salmonella panama* | 111 | 2E-23 |

*Query= MT-1_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_52*
*Length=5288*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Alw34* | IS*66* | | *Acinetobacter lwoffii* | 198 | 6E-50 |
| IS*Aba46* | IS*66* | | *Acinetobacter baumannii* | 198 | 6E-50 |
| IS*Aba16* | IS*66* | | *Acinetobacter baumannii* | 192 | 4E-48 |
| IS*Alw16* | IS*66* | | *Acinetobacter lwoffii* | 190 | 2E-47 |
| IS*Aba25* | IS*66* | | *Acinetobacter baumannii* | 167 | 2E-40 |
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | 131 | 1E-29 |
| IS*Aba49* | IS*66* | | *Acinetobacter baumannii* | 121 | 1E-26 |
| IS*Aba17* | IS*66* | | *Acinetobacter baumannii* | 58.0 | 0,0000002 |
| IS*Sod17* | IS*3* | IS*51* | *Shewanella oneidensis* | 52.0 | 0,000009 |

*Query= MT-1_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_53*
*Length=5191*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Alw22* | IS*NCY* | IS*1202* | *Acinetobacter lwoffii* | 1891 | 0.0 |
| IS*Aba32* | IS*NCY* | IS*1202* | *Acinetobacter baumannii* | 1891 | 0.0 |
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | 194 | 1E-48 |
| IS*Esa1* | IS*NCY* | IS*1202* | *Enterobacter sakazakii* | 60.0 | 0,00000004 |
| IS*V* IS*p7* | IS*NCY* | IS*1202* | *Vibrio splendidus* | 50.1 | 0,00004 |

*Query= MT-1_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_55*
*Length=4589*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| *TnAs3* | *Tn3* | | *Aeromonas salmonicida* | 2575 | 0.0 |
| *TnAs2* | *Tn3* | | *Aeromonas salmonicida* | 270 | 2E-71 |
| IS*Shes11* | *Tn3* | | *Shewanella sp.* | 182 | 3E-45 |
| IS*15DI* | IS*6* | | *Salmonella panama* | 119 | 4E-26 |
| IS*15* | IS*6* | | *Salmonella panama* | 119 | 4E-26 |
| IS*26* | IS*6* | | *Proteus vulgaris* | 119 | 4E-26 |
| IS*15DIV* | IS*6* | | *Salmonella typhimurium* | 117 | 2E-25 |
| IS*15DII* | IS*6* | | *Salmonella panama* | 111 | 1E-23 |

*Query= MT-1_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_57*
*Length=4540*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| *TnAs3* | *Tn3* | | *Aeromonas salmonicida* | 119 | 4E-26 |
| IS*Ppu12* | IS*L3* | | *Pseudomonas putida* | 119 | 4E-26 |
| IS*1396* | IS*L3* | | *Serratia marcescens* | 119 | 4E-26 |
| IS*Pst2* | IS*L3* | | *Pseudomonas stutzeri* | 85.7 | 6E-16 |

| | | | | | |
|---|---|---|---|---|---|
| IS*Pst9* | IS*L3* | | *Pseudomonas stutzeri* | 63.9 | 0,000000002 |

*Query= MT-1_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_58*
*Length=4354*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Aba14* | IS*3* | IS*150* | *Acinetobacter baumannii* | 605 | 2E-172 |
| IS*Cfr1* | IS*1182* | | *Citrobacter freundii* | 577 | 6E-164 |
| IS*Psp5* | IS*1182* | | *Pseudomonas sp.* | 454 | 6E-127 |
| IS*Alw27* | IS*3* | IS*150* | *Acinetobacter lwoffii* | 383 | 2E-105 |
| IS*Pa94* | IS*1182* | | *Pseudomonas aeruginosa* | 309 | 2E-83 |
| IS*15DI* | IS*6* | | *Salmonella panama* | 119 | 4E-26 |
| IS*15* | IS*6* | | *Salmonella panama* | 119 | 4E-26 |
| IS*26* | IS*6* | | *Proteus vulgaris* | 119 | 4E-26 |
| IS*Aba52* | IS*6* | | *Acinetobacter baumannii* | 117 | 2E-25 |
| IS*1008* | IS*6* | | *Acinetobacter calcoaceticus* | 117 | 2E-25 |
| IS*Our1* | IS*6* | | *Oligella urethralis* | 117 | 2E-25 |
| IS*15DIV* | IS*6* | | *Salmonella typhimurium* | 117 | 2E-25 |
| IS*1007* | IS*6* | | *Acinetobacter sp.* | 117 | 2E-25 |
| IS*15DII* | IS*6* | | *Salmonella panama* | 111 | 1E-23 |
| IS*Acsp5* | IS*3* | IS*150* | *Acinetobacter sp.* | 58.0 | 0,0000001 |

*Query= MT-1_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_59*
*Length=3953*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Alw4* | IS*3* | IS*51* | *Acinetobacter lwoffii* | 1875 | 0.0 |
| IS*Aba2* | IS*3* | IS*51* | *Acinetobacter baumannii* | 1574 | 0.0 |
| IS*Alw23* | IS*3* | IS*51* | *Acinetobacter lwoffii* | 1538 | 0.0 |
| IS*Aba19* | IS*3* | IS*51* | *Acinetobacter baumannii* | 1463 | 0.0 |
| IS*Alw5* | IS*3* | IS*51* | *Acinetobacter lwoffii* | 1439 | 0.0 |
| IS*Aba29* | IS*3* | IS*51* | *Acinetobacter baumannii* | 1352 | 0.0 |
| IS*Aba34* | IS*3* | IS*51* | *Acinetobacter baumannii* | 1308 | 0.0 |
| IS*Aba18* | IS*3* | IS*51* | *Acinetobacter baumannii* | 1304 | 0.0 |
| IS*1008* | IS*6* | | *Acinetobacter calcoaceticus* | 504 | 6E-142 |
| IS*Our1* | IS*6* | | *Oligella urethralis* | 448 | 3E-125 |
| IS*Aba52* | IS*6* | | *Acinetobacter baumannii* | 432 | 2E-120 |
| IS*1006* | IS*6* | | *Acinetobacter junii* | 424 | 4E-118 |
| IS*1007* | IS*6* | | *Acinetobacter sp.* | 129 | 4E-29 |
| IS*15DIV* | IS*6* | | *Salmonella typhimurium* | 95.6 | 5E-19 |
| IS*15DII* | IS*6* | | *Salmonella panama* | 95.6 | 5E-19 |
| IS*15DI* | IS*6* | | *Salmonella panama* | 95.6 | 5E-19 |
| IS*15* | IS*6* | | *Salmonella panama* | 95.6 | 5E-19 |
| IS*26* | IS*6* | | *Proteus vulgaris* | 95.6 | 5E-19 |
| IS*1489v1* | IS*L3* | | *Pseudomonas putida* | 83.8 | 2E-15 |
| IS*Ppu33* | IS*3* | IS*51* | *Pseudomonas putida* | 56.0 | 0,0000004 |
| IS*Stma17* | IS*3* | IS*51* | *Stenotrophomonas maltophilia* | 56.0 | 0,0000004 |
| IS*Mca3* | IS*3* | IS*51* | *Methylococcus capsulatus* | 56.0 | 0,0000004 |
| IS*1416* | IS*3* | IS*51* | *Burkholderia glumae* | 56.0 | 0,0000004 |
| IS*Ali4* | IS*3* | IS*51* | *Azospirillum lipoferum* | 54.0 | 0,000002 |
| IS*Rme15* | IS*3* | IS*51* | *Ralstonia metallidurans* | 54.0 | 0,000002 |
| IS*Pmi1* | IS*3* | IS*51* | *Proteus mirabilis* | 52.0 | 0,000007 |
| IS*Rtr2* | IS*3* | IS*51* | *Rhizobium tropici* | 52.0 | 0,000007 |

*Query= MT-1_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_60*
*Length=3945*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Aba1* | IS*4* | IS*10* | *Acinetobacter baumannii* | 180 | 1E-44 |
| IS*Aba125* | IS*30* | | *Acinetobacter baumannii* | 119 | 4E-26 |
| IS*Aba33* | IS*4* | IS*10* | *Acinetobacter baumannii* | 111 | 9E-24 |
| IS*C1041* | IS*30* | | *Sulfolobus solfataricus* | 103 | 2E-21 |

*Query= MT-1_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_61*
*Length=3688*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| *Tn5393* | *Tn3* | | *Erwinia amylovora* | 1358 | 0.0 |
| IS*Ec63* | *Tn3* | | *Escherichia coli* | 307 | 7E-83 |
| *Tn3* | *Tn3* | | *Salmonella enterica* | 121 | 8E-27 |
| IS*15DIV* | IS*6* | | *Salmonella typhimurium* | 119 | 3E-26 |
| IS*15DII* | IS*6* | | *Salmonella panama* | 119 | 3E-26 |
| IS*15DI* | IS*6* | | *Salmonella panama* | 119 | 3E-26 |
| IS*15* | IS*6* | | *Salmonella panama* | 119 | 3E-26 |
| IS*26* | IS*6* | | *Proteus vulgaris* | 119 | 3E-26 |
| *Tn2* | *Tn3* | | *Escherichia coli* | 105 | 5E-22 |
| IS*Mex22* | *Tn3* | | *Methylobacterium extorquens* | 54.0 | 0,000002 |

*Query= MT-1_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_62*
*Length=3425*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | 119 | 3E-26 |

*Query= MT-1_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_63*
*Length=3231*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Ppu12* | IS*L3* | | *Pseudomonas putida* | 5525 | 0.0 |
| IS*1396* | IS*L3* | | *Serratia marcescens* | 2603 | 0.0 |
| IS*Pst2* | IS*L3* | | *Pseudomonas stutzeri* | 2325 | 0.0 |
| IS*Pst9* | IS*L3* | | *Pseudomonas stutzeri* | 1626 | 0.0 |
| IS*1489v1* | IS*L3* | | *Pseudomonas putida* | 46.1 | 0,0003 |

*Query= MT-1_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_64*
*Length=3053*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | 119 | 3E-26 |
| IS*15DIV* | IS*6* | | *Salmonella typhimurium* | 119 | 3E-26 |
| IS*15DII* | IS*6* | | *Salmonella panama* | 119 | 3E-26 |
| IS*15DI* | IS*6* | | *Salmonella panama* | 119 | 3E-26 |
| IS*15* | IS*6* | | *Salmonella panama* | 119 | 3E-26 |
| IS*26* | IS*6* | | *Proteus vulgaris* | 119 | 3E-26 |

*Query= MT-1_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_66*
*Length=2786*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*1008* | IS*6* | | *Acinetobacter calcoaceticus* | 519 | 7E-147 |
| IS*Our1* | IS*6* | | *Oligella urethralis* | 464 | 4E-130 |
| IS*Aba52* | IS*6* | | *Acinetobacter baumannii* | 448 | 2E-125 |
| IS*1006* | IS*6* | | *Acinetobacter junii* | 440 | 5E-123 |
| IS*1007* | IS*6* | | *Acinetobacter sp.* | 145 | 4E-34 |
| IS*15DIV* | IS*6* | | *Salmonella typhimurium* | 87.7 | 9E-17 |
| IS*15DII* | IS*6* | | *Salmonella panama* | 87.7 | 9E-17 |
| IS*15DI* | IS*6* | | *Salmonella panama* | 87.7 | 9E-17 |
| IS*15* | IS*6* | | *Salmonella panama* | 87.7 | 9E-17 |
| IS*26* | IS*6* | | *Proteus vulgaris* | 87.7 | 9E-17 |
| IS*1489v1* | IS*L3* | | *Pseudomonas putida* | 83.8 | 1E-15 |

*Query= MT-1_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_68*
*Length=2286*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Ppu12* | IS*L3* | | *Pseudomonas putida* | 361 | 3E-99 |
| *TnAs3* | *Tn3* | | *Aeromonas salmonicida* | 119 | 2E-26 |
| IS*Xc4* | *Tn3* | | *Xanthomonas campestris* | 73.8 | 1E-12 |
| IS*Psy42* | *Tn3* | | *Pseudomonas syringae* | 63.9 | 0,000000001 |
| IS*Thsp9* | *Tn3* | | *Thiomonas sp.* | 54.0 | 0,000001 |
| IS*Mex22* | *Tn3* | | *Methylobacterium extorquens* | 52.0 | 0,000004 |

*Query= MT-1_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_71*
*Length=1597*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| *TnAs3* | *Tn3* | | *Aeromonas salmonicida* | 3166 | 0.0 |

*Query= MT-1_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_72*
*Length=1570*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| *TnAs3* | *Tn3* | | *Aeromonas salmonicida* | 860 | 0.0 |
| IS*Aba125* | IS*30* | | *Acinetobacter baumannii* | 432 | 7E-121 |
| IS*C1041* | IS*30* | | *Sulfolobus solfataricus* | 335 | 1E-91 |
| IS*15DIV* | IS*6* | | *Salmonella typhimurium* | 119 | 1E-26 |
| IS*15DII* | IS*6* | | *Salmonella panama* | 119 | 1E-26 |
| IS*15DI* | IS*6* | | *Salmonella panama* | 119 | 1E-26 |
| IS*15* | IS*6* | | *Salmonella panama* | 119 | 1E-26 |
| IS*26* | IS*6* | | *Proteus vulgaris* | 119 | 1E-26 |
| IS*Abe8* | IS*30* | | *Acinetobacter bereziniae* | 58.0 | 0,00000004 |

*Query= MT-1_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_73*
*Length=1549*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*15* | IS*6* | | *Salmonella panama* | 466 | 5E-131 |
| IS*15DII* | IS*6* | | *Salmonella panama* | 347 | 3E-95 |
| IS*15DI* | IS*6* | | *Salmonella panama* | 339 | 8E-93 |
| IS*26* | IS*6* | | *Proteus vulgaris* | 339 | 8E-93 |
| IS*15DIV* | IS*6* | | *Salmonella typhimurium* | 337 | 3E-92 |
| IS*Aba52* | IS*6* | | *Acinetobacter baumannii* | 61.9 | 0,000000003 |
| IS*1008* | IS*6* | | *Acinetobacter calcoaceticus* | 61.9 | 0,000000003 |
| IS*Our1* | IS*6* | | *Oligella urethralis* | 61.9 | 0,000000003 |

| | | | | | | |
|---|---|---|---|---|---|---|
| IS*1006* | IS*6* | | *Acinetobacter junii* | 61.9 | | 0,000000003 |
| IS*1007* | IS*6* | | *Acinetobacter sp.* | 52.0 | | 0,000003 |

*Query= MT-1_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_74*
*Length=1476*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | 2268 | 0.0 |
| IS*Alw22* | IS*NCY* | IS*1202* | *Acinetobacter lwoffii* | 170 | 4E-42 |
| IS*Aba32* | IS*NCY* | IS*1202* | *Acinetobacter baumannii* | 159 | 2E-38 |
| IS*Esa1* | IS*NCY* | IS*1202* | *Enterobacter sakazakii* | 65.9 | 2E-10 |
| IS*Lad2* | IS*NCY* | IS*1202* | *Leclercia adecarboxylata* | 65.9 | 2E-10 |
| IS*CARN112* | IS*NCY* | IS*1202* | *Metagenomic data* | 48.1 | 0,00004 |

*Query= MT-1_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_76*
*Length=1139*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Aba1* | IS*4* | IS*10* | *Acinetobacter baumannii* | 2250 | 0.0 |
| IS*Aba33* | IS*4* | IS*10* | *Acinetobacter baumannii* | 1219 | 0.0 |

*Query= MT-1_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_78*
*Length=1039*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Aba13* | IS*5* | IS*903* | *Acinetobacter baumannii* | 2060 | 0.0 |
| IS*Aba12* | IS*5* | IS*903* | *Acinetobacter baumannii* | 848 | 0.0 |
| IS*17* | IS*5* | IS*903* | *Acinetobacter haemolyticus* | 835 | 0.0 |
| IS*Aba40* | IS*5* | IS*903* | *Acinetobacter baumannii* | 803 | 0.0 |
| IS*Aha1* | IS*5* | IS*903* | *Acinetobacter haemolyticus* | 801 | 0.0 |
| IS*Alw1* | IS*5* | IS*903* | *Acinetobacter lwoffii* | 704 | 0.0 |
| IS*Ajo1* | IS*5* | IS*903* | *Acinetobacter johnsonii* | 636 | 0.0 |
| IS*Aba53* | IS*5* | IS*903* | *Acinetobacter baumannii* | 617 | 2E-176 |
| IS*Aha3* | IS*5* | IS*903* | *Acinetobacter haemolyticus* | 517 | 1E-146 |
| IS*Aha2* | IS*5* | IS*903* | *Acinetobacter haemolyticus* | 428 | 7E-120 |
| IS*Aba7* | IS*5* | IS*903* | *Acinetobacter baumannii* | 420 | 2E-117 |
| IS*Aba5* | IS*5* | IS*903* | *Acinetobacter baumannii* | 387 | 3E-107 |

*Query= MT-1_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_79*
*Length=905*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Aba125* | IS*30* | | *Acinetobacter baumannii* | 119 | 8E-27 |
| IS*C1041* | IS*30* | | *Sulfolobus solfataricus* | 103 | 5E-22 |
| IS*Abe8* | IS*30* | | *Acinetobacter bereziniae* | 44.1 | 0,0004 |

*Query= MT-1_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_81*
*Length=820*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*15DI* | IS*6* | | *Salmonella panama* | 1626 | 0.0 |
| IS*15* | IS*6* | | *Salmonella panama* | 1626 | 0.0 |
| IS*15DIV* | IS*6* | | *Salmonella typhimurium* | 1608 | 0.0 |
| IS*26* | IS*6* | | *Proteus vulgaris* | 1602 | 0.0 |
| IS*15DII* | IS*6* | | *Salmonella panama* | 1594 | 0.0 |
| IS*1006* | IS*6* | | *Acinetobacter junii* | 180 | 2E-45 |
| IS*Aba52* | IS*6* | | *Acinetobacter baumannii* | 137 | 3E-32 |
| IS*1007* | IS*6* | | *Acinetobacter sp.* | 137 | 3E-32 |
| IS*Our1* | IS*6* | | *Oligella urethralis* | 121 | 2E-27 |
| IS*1008* | IS*6* | | *Acinetobacter calcoaceticus* | 113 | 4E-25 |
| IS*Stag1* | IS*6* | | *Stappia aggregata* | 65.9 | 9E-11 |
| IS*Acr2* | IS*6* | | *Acidiphilium cryptum* | 58.0 | 0,00000002 |

*Query= MT-1_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_82*
*Length=662*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Aba1* | IS*4* | IS*10* | *Acinetobacter baumannii* | 180 | 2E-45 |
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | 131 | 2E-30 |
| IS*Aba33* | IS*4* | IS*10* | *Acinetobacter baumannii* | 111 | 1E-24 |
| IS*CARN112* | IS*NCY* | IS*1202* | *Metagenomic data* | 48.1 | 0,00002 |

*Query= MT-1_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_83*
*Length=619*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*1008* | IS*6* | | *Acinetobacter calcoaceticus* | 1209 | 0.0 |
| IS*Our1* | IS*6* | | *Oligella urethralis* | 1162 | 0.0 |
| IS*Aba52* | IS*6* | | *Acinetobacter baumannii* | 662 | 0.0 |
| IS*1007* | IS*6* | | *Acinetobacter sp.* | 525 | 3E-149 |
| IS*1006* | IS*6* | | *Acinetobacter junii* | 502 | 4E-142 |

| | | | | | |
|---|---|---|---|---|---|
| IS*15DIV* | IS*6* | | *Salmonella typhimurium* | 113 | 3E-25 |
| IS*15DII* | IS*6* | | *Salmonella panama* | 113 | 3E-25 |
| IS*15DI* | IS*6* | | *Salmonella panama* | 113 | 3E-25 |
| IS*15* | IS*6* | | *Salmonella panama* | 113 | 3E-25 |
| IS*26* | IS*6* | | *Proteus vulgaris* | 113 | 3E-25 |

*Query= MT-1_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_86*
*Length=550*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Aba125* | IS*30* | | *Acinetobacter baumannii* | 119 | 5E-27 |
| IS*C1041* | IS*30* | | *Sulfolobus solfataricus* | 103 | 3E-22 |
| IS*Abe8* | IS*30* | | *Acinetobacter bereziniae* | 46.1 | 0,00006 |

*Query= MT-1_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_88*
*Length=450*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Aba125* | IS*30* | | *Acinetobacter baumannii* | 876 | 0.0 |
| IS*C1041* | IS*30* | | *Sulfolobus solfataricus* | 581 | 4E-166 |
| IS*Abe8* | IS*30* | | *Acinetobacter bereziniae* | 196 | 2E-50 |

*Query= MT-1_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_92*
*Length=326*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Aba1* | IS*4* | IS*10* | *Acinetobacter baumannii* | 638 | 0.0 |
| IS*Aba33* | IS*4* | IS*10* | *Acinetobacter baumannii* | 416 | 9E-117 |

*Query= MT-1_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_98*
*Length=267*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | 355 | 2E-98 |
| IS*Alw22* | IS*NCY* | IS*1202* | *Acinetobacter lwoffii* | 54.0 | 0,0000001 |
| IS*Aba32* | IS*NCY* | IS*1202* | *Acinetobacter baumannii* | 54.0 | 0,0000001 |

*Query= MT-1_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_110*
*Length=222*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Aba125* | IS*30* | | *Acinetobacter baumannii* | 440 | 4E-124 |
| IS*C1041* | IS*30* | | *Sulfolobus solfataricus* | 327 | 4E-90 |
| IS*Abe8* | IS*30* | | *Acinetobacter bereziniae* | 58.0 | 0,000000006 |

*Query= MT-1_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_111*
*Length=220*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Aba1* | IS*4* | IS*10* | *Acinetobacter baumannii* | 180 | 6E-46 |
| IS*Aba33* | IS*4* | IS*10* | *Acinetobacter baumannii* | 111 | 5E-25 |

*Query= MT-1_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_116*
*Length=204*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| *TnAs1* | *Tn3* | | *Aeromonas salmonicida* | 250 | 7E-67 |
| IS*Pa40* | *Tn3* | | *Pseudomonas aeruginosa* | 170 | 5E-43 |

*Query= MT-1_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_117*
*Length=203*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | 228 | 3E-60 |
| IS*Alw22* | IS*NCY* | IS*1202* | *Acinetobacter lwoffii* | 54.0 | 0,00000008 |
| IS*Aba32* | IS*NCY* | IS*1202* | *Acinetobacter baumannii* | 54.0 | 0,00000008 |

*Query= MT-1_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_121*
*Length=268*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | 131 | 6E-31 |
| IS*CARN112* | IS*NCY* | IS*1202* | *Metagenomic data* | 48.1 | 0,000007 |

Database: ISfinder_Nucl
5,559 sequences; 8,208,285 total letters

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_1*
*Length=308335*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | 151 | 8E-34 |
| IS*Aba1* | IS*4* | IS*10* | *Acinetobacter baumannii* | 129 | 3E-27 |
| IS*Aba33* | IS*4* | IS*10* | *Acinetobacter baumannii* | 69.9 | 0,000000002 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_3*
*Length=202737*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Aba1* | IS*4* | IS*10* | *Acinetobacter baumannii* | 248 | 3E-63 |
| IS*Aba33* | IS*4* | IS*10* | *Acinetobacter baumannii* | 163 | 1E-37 |
| IS*Aba13* | IS*5* | IS*903* | *Acinetobacter baumannii* | 119 | 2E-24 |
| IS*Aha1* | IS*5* | IS*903* | *Acinetobacter haemolyticus* | 111 | 4E-22 |
| IS*Aba53* | IS*5* | IS*903* | *Acinetobacter baumannii* | 103 | 1E-19 |
| IS*17* | IS*5* | IS*903* | *Acinetobacter haemolyticus* | 77.8 | 6E-12 |
| IS*Aba12* | IS*5* | IS*903* | *Acinetobacter baumannii* | 69.9 | 0,000000002 |
| IS*Aba40* | IS*5* | IS*903* | *Acinetobacter baumannii* | 56.0 | 0,00002 |
| IS*Ajo1* | IS*5* | IS*903* | *Acinetobacter johnsonii* | 54.0 | 0,00009 |
| IS*Aba5* | IS*5* | IS*903* | *Acinetobacter baumannii* | 54.0 | 0,00009 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_4*
*Length=200470*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Aba1* | IS*4* | IS*10* | *Acinetobacter baumannii* | 248 | 3E-63 |
| IS*Aba33* | IS*4* | IS*10* | *Acinetobacter baumannii* | 163 | 1E-37 |
| IS*Ppu12* | IS*L3* | | *Pseudomonas putida* | 131 | 5E-28 |
| IS*1396* | IS*L3* | | *Serratia marcescens* | 131 | 5E-28 |
| IS*Pst2* | IS*L3* | | *Pseudomonas stutzeri* | 85.7 | 3E-14 |
| IS*Pst9* | IS*L3* | | *Pseudomonas stutzeri* | 75.8 | 2E-11 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_6*
*Length=184508*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Aba1* | IS*4* | IS*10* | *Acinetobacter baumannii* | 129 | 2E-27 |
| IS*Aba13* | IS*5* | IS*903* | *Acinetobacter baumannii* | 119 | 2E-24 |
| IS*Aha1* | IS*5* | IS*903* | *Acinetobacter haemolyticus* | 111 | 4E-22 |
| IS*Aba53* | IS*5* | IS*903* | *Acinetobacter baumannii* | 103 | 1E-19 |
| IS*17* | IS*5* | IS*903* | *Acinetobacter haemolyticus* | 77.8 | 6E-12 |
| IS*Aba33* | IS*4* | IS*10* | *Acinetobacter baumannii* | 69.9 | 0,000000001 |
| IS*Aba12* | IS*5* | IS*903* | *Acinetobacter baumannii* | 69.9 | 0,000000001 |
| IS*Aba40* | IS*5* | IS*903* | *Acinetobacter baumannii* | 56.0 | 0,00002 |
| IS*Ajo1* | IS*5* | IS*903* | *Acinetobacter johnsonii* | 54.0 | 0,00008 |
| IS*Aba5* | IS*5* | IS*903* | *Acinetobacter baumannii* | 54.0 | 0,00008 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_7*
*Length=170837*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Aba1* | IS*4* | IS*10* | *Acinetobacter baumannii* | 129 | 2E-27 |
| IS*Aba33* | IS*4* | IS*10* | *Acinetobacter baumannii* | 69.9 | 0,000000001 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_8*
*Length=163458*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Aba1* | IS*4* | IS*10* | *Acinetobacter baumannii* | 248 | 2E-63 |
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | 186 | 8E-45 |
| IS*Aba33* | IS*4* | IS*10* | *Acinetobacter baumannii* | 163 | 1E-37 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_9*
*Length=153580*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | 151 | 4E-34 |
| IS*Aba13* | IS*5* | IS*903* | *Acinetobacter baumannii* | 121 | 4E-25 |
| IS*Alw34* | IS*66* | | *Acinetobacter lwoffii* | 58.0 | 0,000004 |
| IS*Alw16* | IS*66* | | *Acinetobacter lwoffii* | 58.0 | 0,000004 |
| IS*Aba16* | IS*66* | | *Acinetobacter baumannii* | 58.0 | 0,000004 |
| IS*Aba17* | IS*66* | | *Acinetobacter baumannii* | 58.0 | 0,000004 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_10*
*Length=148266*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Aba1* | IS*4* | IS*10* | *Acinetobacter baumannii* | 248 | 2E-63 |
| IS*Aba33* | IS*4* | IS*10* | *Acinetobacter baumannii* | 163 | 1E-37 |
| IS*Aba13* | IS*5* | IS*903* | *Acinetobacter baumannii* | 119 | 1E-24 |
| IS*Aha1* | IS*5* | IS*903* | *Acinetobacter haemolyticus* | 111 | 3E-22 |
| IS*Aba53* | IS*5* | IS*903* | *Acinetobacter baumannii* | 103 | 8E-20 |
| IS*17* | IS*5* | IS*903* | *Acinetobacter haemolyticus* | 77.8 | 5E-12 |
| IS*Aba12* | IS*5* | IS*903* | *Acinetobacter baumannii* | 69.9 | 0,000000001 |
| IS*Aba40* | IS*5* | IS*903* | *Acinetobacter baumannii* | 56.0 | 0,00002 |
| IS*Ajo1* | IS*5* | IS*903* | *Acinetobacter johnsonii* | 54.0 | 0,00007 |
| IS*Aba5* | IS*5* | IS*903* | *Acinetobacter baumannii* | 54.0 | 0,00007 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_11*
*Length=140873*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Aba1* | IS*4* | IS*10* | *Acinetobacter baumannii* | 248 | 2E-63 |
| IS*Aba33* | IS*4* | IS*10* | *Acinetobacter baumannii* | 163 | 9E-38 |
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | 151 | 4E-34 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_12*
*Length=137934*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Aba1* | IS*4* | IS*10* | *Acinetobacter baumannii* | 248 | 2E-63 |
| IS*Aba33* | IS*4* | IS*10* | *Acinetobacter baumannii* | 163 | 9E-38 |
| IS*Aba13* | IS*5* | IS*903* | *Acinetobacter baumannii* | 119 | 1E-24 |
| IS*Aha1* | IS*5* | IS*903* | *Acinetobacter haemolyticus* | 111 | 3E-22 |
| IS*Aba53* | IS*5* | IS*903* | *Acinetobacter baumannii* | 103 | 7E-20 |
| IS*17* | IS*5* | IS*903* | *Acinetobacter haemolyticus* | 77.8 | 4E-12 |
| IS*Aba12* | IS*5* | IS*903* | *Acinetobacter baumannii* | 69.9 | 0,000000001 |
| IS*Aba40* | IS*5* | IS*903* | *Acinetobacter baumannii* | 56.0 | 0,00002 |
| IS*Ajo1* | IS*5* | IS*903* | *Acinetobacter johnsonii* | 54.0 | 0,00006 |
| IS*Aba5* | IS*5* | IS*903* | *Acinetobacter baumannii* | 54.0 | 0,00006 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_13*
*Length=125442*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Aba1* | IS*4* | IS*10* | *Acinetobacter baumannii* | 248 | 2E-63 |
| IS*Aba33* | IS*4* | IS*10* | *Acinetobacter baumannii* | 163 | 8E-38 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_14*
*Length=120407*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Aba13* | IS*5* | IS*903* | *Acinetobacter baumannii* | 2060 | 0.0 |
| IS*Aba12* | IS*5* | IS*903* | *Acinetobacter baumannii* | 848 | 0.0 |
| IS*17* | IS*5* | IS*903* | *Acinetobacter haemolyticus* | 835 | 0.0 |
| IS*Aba40* | IS*5* | IS*903* | *Acinetobacter baumannii* | 803 | 0.0 |
| IS*Aha1* | IS*5* | IS*903* | *Acinetobacter haemolyticus* | 801 | 0.0 |
| IS*Alw1* | IS*5* | IS*903* | *Acinetobacter lwoffii* | 704 | 0.0 |
| IS*Ajo1* | IS*5* | IS*903* | *Acinetobacter johnsonii* | 636 | 2E-180 |
| IS*Aba53* | IS*5* | IS*903* | *Acinetobacter baumannii* | 617 | 2E-174 |
| IS*Aha3* | IS*5* | IS*903* | *Acinetobacter haemolyticus* | 517 | 1E-144 |
| IS*Aha2* | IS*5* | IS*903* | *Acinetobacter haemolyticus* | 428 | 9E-118 |
| IS*Aba7* | IS*5* | IS*903* | *Acinetobacter baumannii* | 420 | 2E-115 |
| IS*Aba5* | IS*5* | IS*903* | *Acinetobacter baumannii* | 387 | 3E-105 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_15*
*Length=120155*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Aba1* | IS*4* | IS*10* | *Acinetobacter baumannii* | 129 | 1E-27 |
| IS*Aba33* | IS*4* | IS*10* | *Acinetobacter baumannii* | 69.9 | 9E-10 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_16*
*Length=117863*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | 186 | 5E-45 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_17*
*Length=87981*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Aba26* | IS*256* | | *Acinetobacter baumannii* | 2605 | 0.0 |
| IS*Aba13* | IS*5* | IS*903* | *Acinetobacter baumannii* | 121 | 2E-25 |
| IS*Abe10* | IS*256* | | *Acinetobacter bereziniae* | 111 | 2E-22 |
| IS*Aba42* | IS*256* | | *Acinetobacter baumannii* | 83.8 | 4E-14 |
| IS*Aba50* | IS*256* | | *Acinetobacter baumannii* | 56.0 | 0,00001 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_18*
*Length=75932*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Aba13* | IS*5* | IS*903* | *Acinetobacter baumannii* | 119 | 7E-25 |
| IS*Aha1* | IS*5* | IS*903* | *Acinetobacter haemolyticus* | 111 | 2E-22 |
| IS*Aba53* | IS*5* | IS*903* | *Acinetobacter baumannii* | 103 | 4E-20 |
| IS*17* | IS*5* | IS*903* | *Acinetobacter haemolyticus* | 77.8 | 2E-12 |
| IS*Aba12* | IS*5* | IS*903* | *Acinetobacter baumannii* | 69.9 | 6E-10 |
| IS*Aba40* | IS*5* | IS*903* | *Acinetobacter baumannii* | 56.0 | 0,000009 |
| IS*Ajo1* | IS*5* | IS*903* | *Acinetobacter johnsonii* | 54.0 | 0,00003 |
| IS*Aba5* | IS*5* | IS*903* | *Acinetobacter baumannii* | 54.0 | 0,00003 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_19*
*Length=74553*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | 151 | 2E-34 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_20*
*Length=73064*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Aba1* | IS*4* | IS*10* | *Acinetobacter baumannii* | 129 | 7E-28 |
| IS*Aba33* | IS*4* | IS*10* | *Acinetobacter baumannii* | 69.9 | 5E-10 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_21*
*Length=68579*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | 151 | 2E-34 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_22*
*Length=66289*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Aba1* | IS*4* | IS*10* | *Acinetobacter baumannii* | 129 | 6E-28 |
| IS*Aba33* | IS*4* | IS*10* | *Acinetobacter baumannii* | 69.9 | 5E-10 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_23*
*Length=53671*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Aba1* | IS*4* | IS*10* | *Acinetobacter baumannii* | 129 | 5E-28 |
| IS*Aba33* | IS*4* | IS*10* | *Acinetobacter baumannii* | 69.9 | 4E-10 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_24*
*Length=50233*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Aba125* | IS*30* | | *Acinetobacter baumannii* | 119 | 5E-25 |
| IS*C1041* | IS*30* | | *Sulfolobus solfataricus* | 61.9 | 0,00000009 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_25*
*Length=50074*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Aba1* | IS*4* | IS*10* | *Acinetobacter baumannii* | 129 | 5E-28 |
| IS*Aba33* | IS*4* | IS*10* | *Acinetobacter baumannii* | 69.9 | 4E-10 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_26*
*Length=49801*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Aba1* | IS*4* | IS*10* | *Acinetobacter baumannii* | 129 | 5E-28 |
| IS*Aba125* | IS*30* | | *Acinetobacter baumannii* | 119 | 4E-25 |
| IS*Aba33* | IS*4* | IS*10* | *Acinetobacter baumannii* | 69.9 | 4E-10 |
| IS*C1041* | IS*30* | | *Sulfolobus solfataricus* | 61.9 | 0,00000009 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_27*
*Length=44919*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | 186 | 2E-45 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_28*
*Length=42689*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | 151 | 1E-34 |
| IS*Aba13* | IS*5* | IS*903* | *Acinetobacter baumannii* | 121 | 1E-25 |
| IS*Ajo1* | IS*5* | IS*903* | *Acinetobacter johnsonii* | 52.0 | 0,00007 |
| IS*Aha2* | IS*5* | IS*903* | *Acinetobacter haemolyticus* | 52.0 | 0,00007 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_29*
*Length=40868*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Aba1* | IS*4* | IS*10* | *Acinetobacter baumannii* | 248 | 6E-64 |
| IS*Aba33* | IS*4* | IS*10* | *Acinetobacter baumannii* | 163 | 3E-38 |
| IS*Aba13* | IS*5* | IS*903* | *Acinetobacter baumannii* | 121 | 9E-26 |
| IS*Ajo1* | IS*5* | IS*903* | *Acinetobacter johnsonii* | 52.0 | 0,00007 |
| IS*Aha2* | IS*5* | IS*903* | *Acinetobacter haemolyticus* | 52.0 | 0,00007 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_31*
*Length=37160*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Aba1* | IS*4* | IS*10* | *Acinetobacter baumannii* | 248 | 5E-64 |
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | 186 | 2E-45 |
| IS*Aba33* | IS*4* | IS*10* | *Acinetobacter baumannii* | 163 | 2E-38 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_32*
*Length=36858*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Aba1* | IS*4* | IS*10* | *Acinetobacter baumannii* | 129 | 3E-28 |
| IS*Aba13* | IS*5* | IS*903* | *Acinetobacter baumannii* | 119 | 3E-25 |
| IS*Aha1* | IS*5* | IS*903* | *Acinetobacter haemolyticus* | 111 | 8E-23 |
| IS*Aba53* | IS*5* | IS*903* | *Acinetobacter baumannii* | 103 | 2E-20 |
| IS*17* | IS*5* | IS*903* | *Acinetobacter haemolyticus* | 77.8 | 1E-12 |
| IS*Aba33* | IS*4* | IS*10* | *Acinetobacter baumannii* | 69.9 | 3E-10 |
| IS*Aba12* | IS*5* | IS*903* | *Acinetobacter baumannii* | 69.9 | 3E-10 |
| IS*Aba40* | IS*5* | IS*903* | *Acinetobacter baumannii* | 56.0 | 0,000004 |
| IS*Ajo1* | IS*5* | IS*903* | *Acinetobacter johnsonii* | 54.0 | 0,00002 |
| IS*Aba5* | IS*5* | IS*903* | *Acinetobacter baumannii* | 54.0 | 0,00002 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_33*
*Length=34472*

| *Sequences producing* | IS *Family* | *Group* | Score |
|---|---|---|---|

| *significant alignments* | | | *Origin* | (bits) | E. value |
|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | 186 | 2E-45 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_35*
*Length=30907*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Alw4* | IS*3* | IS*51* | *Acinetobacter lwoffii* | 2044 | 0.0 |
| IS*Alw5* | IS*3* | IS*51* | *Acinetobacter lwoffii* | 1941 | 0.0 |
| IS*Alw23* | IS*3* | IS*51* | *Acinetobacter lwoffii* | 1885 | 0.0 |
| IS*Aba2* | IS*3* | IS*51* | *Acinetobacter baumannii* | 1721 | 0.0 |
| IS*Aba29* | IS*3* | IS*51* | *Acinetobacter baumannii* | 1552 | 0.0 |
| IS*Aba34* | IS*3* | IS*51* | *Acinetobacter baumannii* | 959 | 0.0 |
| IS*Aba19* | IS*3* | IS*51* | *Acinetobacter baumannii* | 910 | 0.0 |
| IS*Aba18* | IS*3* | IS*51* | *Acinetobacter baumannii* | 739 | 0.0 |
| IS*Aba27* | IS*5* | IS*L2* | *Acinetobacter baumannii* | 345 | 3E-93 |
| IS*Alw1* | IS*5* | IS*903* | *Acinetobacter lwoffii* | 161 | 8E-38 |
| IS*Aba13* | IS*5* | IS*903* | *Acinetobacter baumannii* | 153 | 2E-35 |
| IS*Aha1* | IS*5* | IS*903* | *Acinetobacter haemolyticus* | 153 | 2E-35 |
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | 151 | 8E-35 |
| IS*Ajo1* | IS*5* | IS*903* | *Acinetobacter johnsonii* | 127 | 1E-27 |
| IS*Alw35* | IS*481* | | *Acinetobacter lwoffii* | 107 | 1E-21 |
| IS*Aba40* | IS*5* | IS*903* | *Acinetobacter baumannii* | 107 | 1E-21 |
| IS*Alw24* | IS*481* | | *Acinetobacter lwoffii* | 99.6 | 3E-19 |
| IS*Aba53* | IS*5* | IS*903* | *Acinetobacter baumannii* | 95.6 | 4E-18 |
| IS*Sde2* | IS*481* | | *Shewanella denitrificans* | 83.8 | 2E-14 |
| IS*Aba7* | IS*5* | IS*903* | *Acinetobacter baumannii* | 83.8 | 2E-14 |
| IS*Aha3* | IS*5* | IS*903* | *Acinetobacter haemolyticus* | 69.9 | 2E-10 |
| IS*Aba12* | IS*5* | IS*903* | *Acinetobacter baumannii* | 69.9 | 2E-10 |
| IS*1006* | IS*6* | | *Acinetobacter junii* | 63.9 | 0,00000001 |
| IS*Rtr2* | IS*3* | IS*51* | *Rhizobium tropici* | 58.0 | 0,0000009 |
| IS*Aba52* | IS*6* | | *Acinetobacter baumannii* | 56.0 | 0,000003 |
| IS*Ppu33* | IS*3* | IS*51* | *Pseudomonas putida* | 56.0 | 0,000003 |
| IS*Stma17* | IS*3* | IS*51* | *Stenotrophomonas maltophilia* | 56.0 | 0,000003 |
| IS*Mca3* | IS*3* | IS*51* | *Methylococcus capsulatus* | 56.0 | 0,000003 |
| IS*Our1* | IS*6* | | *Oligella urethralis* | 56.0 | 0,000003 |
| IS*1416* | IS*3* | IS*51* | *Burkholderia glumae* | 56.0 | 0,000003 |
| IS*Ali4* | IS*3* | IS*51* | *Azospirillum lipoferum* | 54.0 | 0,00001 |
| IS*Rme15* | IS*3* | IS*51* | *Ralstonia metallidurans* | 54.0 | 0,00001 |
| IS*Pmi1* | IS*3* | IS*51* | *Proteus mirabilis* | 52.0 | 0,00005 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_36*
*Length=30126*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Aba13* | IS*5* | IS*903* | *Acinetobacter baumannii* | 121 | 7E-26 |
| IS*Ajo1* | IS*5* | IS*903* | *Acinetobacter johnsonii* | 52.0 | 0,00005 |
| IS*Aha2* | IS*5* | IS*903* | *Acinetobacter haemolyticus* | 52.0 | 0,00005 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_38*
*Length=23224*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | 151 | 6E-35 |
| IS*Aba13* | IS*5* | IS*903* | *Acinetobacter baumannii* | 119 | 2E-25 |
| IS*Aha1* | IS*5* | IS*903* | *Acinetobacter haemolyticus* | 111 | 5E-23 |
| IS*Aba53* | IS*5* | IS*903* | *Acinetobacter baumannii* | 103 | 1E-20 |
| IS*17* | IS*5* | IS*903* | *Acinetobacter haemolyticus* | 77.8 | 7E-13 |
| IS*Aba12* | IS*5* | IS*903* | *Acinetobacter baumannii* | 69.9 | 2E-10 |
| IS*Aba40* | IS*5* | IS*903* | *Acinetobacter baumannii* | 56.0 | 0,000003 |
| IS*Ajo1* | IS*5* | IS*903* | *Acinetobacter johnsonii* | 54.0 | 0,00001 |
| IS*Aba5* | IS*5* | IS*903* | *Acinetobacter baumannii* | 54.0 | 0,00001 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_40*
*Length=19221*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| *Tn2* | *Tn3* | | *Escherichia coli* | 8851 | 0.0 |
| *Tn3* | *Tn3* | | *Salmonella enterica* | 8806 | 0.0 |
| *TnAs1* | *Tn3* | | *Aeromonas salmonicida* | 2962 | 0.0 |
| *TnAs2* | *Tn3* | | *Aeromonas salmonicida* | 1838 | 0.0 |
| IS*Pa40* | *Tn3* | | *Pseudomonas aeruginosa* | 1758 | 0.0 |
| IS*6100* | IS*6* | | *Mycobacterium fortuitum* | 1744 | 0.0 |
| IS*26* | IS*6* | | *Proteus vulgaris* | 1626 | 0.0 |
| IS*15DII* | IS*6* | | *Salmonella panama* | 1618 | 0.0 |
| IS*15DIV* | IS*6* | | *Salmonella typhimurium* | 1616 | 0.0 |
| IS*15* | IS*6* | | *Salmonella panama* | 1604 | 0.0 |
| IS*15DI* | IS*6* | | *Salmonella panama* | 1602 | 0.0 |
| IS*1R* | IS*1* | | *Escherichia coli* | 1451 | 0.0 |
| IS*1B* | IS*1* | | *Escherichia coli* | 1435 | 0.0 |
| IS*1D* | IS*1* | | *Escherichia coli* | 1419 | 0.0 |
| IS*1G* | IS*1* | | *Escherichia coli* | 1396 | 0.0 |
| IS*1A* | IS*1* | | *Escherichia coli* | 1396 | 0.0 |
| IS*1SD* | IS*1* | | *Shigella dysenteriae* | 1388 | 0.0 |
| IS*1S* | IS*1* | | *Shigella sonnei* | 1372 | 0.0 |
| *TnAs3* | *Tn3* | | *Aeromonas salmonicida* | 1338 | 0.0 |
| IS*Shes11* | *Tn3* | | *Shewanella sp.* | 1322 | 0.0 |
| IS*Pa38* | *Tn3* | | *Pseudomonas aeruginosa* | 1164 | 0.0 |
| IS*Sen9* | IS*1* | | *Salmonella enterica* | 1150 | 0.0 |
| IS*1X2* | IS*1* | | *Escherichia vulneris* | 1102 | 0.0 |
| IS*1X4* | IS*1* | | *Escherichia hermannii* | 991 | 0.0 |
| IS*1X3* | IS*1* | | *Escherichia fergusonii* | 912 | 0.0 |
| IS*1X1* | IS*1* | | *Shigella flexneri* | 864 | 0.0 |
| IS*1F* | IS*1* | | *Escherichia coli* | 864 | 0.0 |
| IS*Kpn14* | IS*1* | | *Klebsiella pneumoniae* | 729 | 0.0 |
| *TnShfr1* | *Tn3* | | *Shewanella frigidimarina* | 549 | 6E-155 |
| IS*Stma11* | IS*L3* | | *Stenotrophomonas maltophilia* | 492 | 1E-137 |
| IS*Ec63* | *Tn3* | | *Escherichia coli* | 486 | 7E-136 |
| IS*Sod9* | *Tn3* | | *Shewanella oneidensis* | 371 | 3E-101 |
| IS*1006* | IS*6* | | *Acinetobacter junii* | 172 | 1E-41 |
| IS*Aba52* | IS*6* | | *Acinetobacter baumannii* | 137 | 7E-31 |

| | | | | | | |
|---|---|---|---|---|---|---|
| IS*1007* | IS*6* | | *Acinetobacter sp.* | | 137 | 7E-31 |
| IS*Our1* | IS*6* | | *Oligella urethralis* | | 121 | 4E-26 |
| IS*Arsp6* | *Tn3* | | *Arthrobacter sp.* | | 117 | 7E-25 |
| IS*1008* | IS*6* | | *Acinetobacter calcoaceticus* | | 113 | 1E-23 |
| IS*Acsp1* | *Tn3* | | *Acinetobacter species* | 75.8 | | 2E-12 |
| IS*Stag1* | IS*6* | | *Stappia aggregata* | 71.9 | | 4E-11 |
| *Tn5393* | *Tn3* | | *Erwinia amylovora* | 65.9 | | 0,000000002 |
| IS*Sf1* | IS*5* | IS*1031* | *Shigella flexneri* | 61.9 | | 0,00000004 |
| IS*Acr2* | IS*6* | | *Acidiphilium cryptum* | 58.0 | | 0,0000005 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_41*
*Length=18940*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Aba13* | IS*5* | IS*903* | *Acinetobacter baumannii* | 2060 | 0.0 |
| IS*Aba12* | IS*5* | IS*903* | *Acinetobacter baumannii* | 848 | 0.0 |
| IS*17* | IS*5* | IS*903* | *Acinetobacter haemolyticus* | 835 | 0.0 |
| IS*Aba40* | IS*5* | IS*903* | *Acinetobacter baumannii* | 803 | 0.0 |
| IS*Aha1* | IS*5* | IS*903* | *Acinetobacter haemolyticus* | 801 | 0.0 |
| IS*Alw1* | IS*5* | IS*903* | *Acinetobacter lwoffii* | 704 | 0.0 |
| IS*Ajo1* | IS*5* | IS*903* | *Acinetobacter johnsonii* | 636 | 0.0 |
| IS*Aba53* | IS*5* | IS*903* | *Acinetobacter baumannii* | 617 | 3E-175 |
| IS*Aha3* | IS*5* | IS*903* | *Acinetobacter haemolyticus* | 517 | 2E-145 |
| IS*Aha2* | IS*5* | IS*903* | *Acinetobacter haemolyticus* | 428 | 1E-118 |
| IS*Aba7* | IS*5* | IS*903* | *Acinetobacter baumannii* | 420 | 3E-116 |
| IS*Aba5* | IS*5* | IS*903* | *Acinetobacter baumannii* | 387 | 5E-106 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_42*
*Length=17554*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Aba1* | IS*4* | IS*10* | *Acinetobacter baumannii* | 129 | 2E-28 |
| IS*Aba13* | IS*5* | IS*903* | *Acinetobacter baumannii* | 121 | 4E-26 |
| IS*Aba33* | IS*4* | IS*10* | *Acinetobacter baumannii* | 69.9 | 1E-10 |
| IS*Ajo1* | IS*5* | IS*903* | *Acinetobacter johnsonii* | 52.0 | 0,00003 |
| IS*Aha2* | IS*5* | IS*903* | *Acinetobacter haemolyticus* | 52.0 | 0,00003 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_43*
*Length=16573*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | 186 | 8E-46 |
| IS*Aba13* | IS*5* | IS*903* | *Acinetobacter baumannii* | 119 | 1E-25 |
| IS*Aha1* | IS*5* | IS*903* | *Acinetobacter haemolyticus* | 111 | 4E-23 |
| IS*Aba53* | IS*5* | IS*903* | *Acinetobacter baumannii* | 103 | 9E-21 |
| IS*17* | IS*5* | IS*903* | *Acinetobacter haemolyticus* | 77.8 | 5E-13 |
| IS*Aba12* | IS*5* | IS*903* | *Acinetobacter baumannii* | 69.9 | 1E-10 |
| IS*Aba40* | IS*5* | IS*903* | *Acinetobacter baumannii* | 56.0 | 0,000002 |
| IS*Ajo1* | IS*5* | IS*903* | *Acinetobacter johnsonii* | 54.0 | 0,000007 |
| IS*Aba5* | IS*5* | IS*903* | *Acinetobacter baumannii* | 54.0 | 0,000007 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_44*
*Length=16158*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Aba1* | IS*4* | IS*10* | *Acinetobacter baumannii* | 248 | 2E-64 |
| IS*Aba33* | IS*4* | IS*10* | *Acinetobacter baumannii* | 163 | 1E-38 |
| IS*Ppu12* | IS*L3* | | *Pseudomonas putida* | 103 | 9E-21 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_45*
*Length=11589*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Aba125* | IS*30* | | *Acinetobacter baumannii* | 119 | 1E-25 |
| IS*C1041* | IS*30* | | *Sulfolobus solfataricus* | 103 | 6E-21 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_46*
*Length=10398*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Aba13* | IS*5* | IS*903* | *Acinetobacter baumannii* | 121 | 2E-26 |
| IS*Ajo1* | IS*5* | IS*903* | *Acinetobacter johnsonii* | 52.0 | 0,00002 |
| IS*Aha2* | IS*5* | IS*903* | *Acinetobacter haemolyticus* | 52.0 | 0,00002 |
| IS*Alw1* | IS*5* | IS*903* | *Acinetobacter lwoffii* | 50.1 | 0,00007 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_47*
*Length=10272*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Ppu12* | IS*L3* | | *Pseudomonas putida* | 103 | 6E-21 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_48*
*Length=9499*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Aba1* | IS*4* | IS*10* | *Acinetobacter baumannii* | 2323 | 0.0 |
| IS*Aba33* | IS*4* | IS*10* | *Acinetobacter baumannii* | 1279 | 0.0 |
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | 186 | 4E-46 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_49*
*Length=7724*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Aba1* | IS*4* | IS*10* | *Acinetobacter baumannii* | 111 | 2E-23 |
| IS*Aba33* | IS*4* | IS*10* | *Acinetobacter baumannii* | 63.9 | 0,000000004 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_50*
*Length=6652*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| *TnAs3* | *Tn3* | | *Aeromonas salmonicida* | 1364 | 0.0 |
| IS*15DI* | IS*6* | | *Salmonella panama* | 119 | 6E-26 |
| IS*15* | IS*6* | | *Salmonella panama* | 119 | 6E-26 |
| IS*26* | IS*6* | | *Proteus vulgaris* | 119 | 6E-26 |
| IS*15DIV* | IS*6* | | *Salmonella typhimurium* | 117 | 2E-25 |
| IS*15DII* | IS*6* | | *Salmonella panama* | 111 | 1E-23 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_52*
*Length=5379*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Alw22* | IS*NCY* | IS*1202* | *Acinetobacter lwoffii* | 1891 | 0.0 |
| IS*Aba32* | IS*NCY* | IS*1202* | *Acinetobacter baumannii* | 1891 | 0.0 |
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | 325 | 4E-88 |
| IS*Esa1* | IS*NCY* | IS*1202* | *Enterobacter sakazakii* | 60.0 | 0,00000004 |
| IS*V* IS*p7* | IS*NCY* | IS*1202* | *Vibrio splendidus* | 50.1 | 0,00004 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_53*
*Length=5310*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Alw34* | IS*66* | | *Acinetobacter lwoffii* | 198 | 6E-50 |
| IS*Aba46* | IS*66* | | *Acinetobacter baumannii* | 198 | 6E-50 |
| IS*Aba16* | IS*66* | | *Acinetobacter baumannii* | 192 | 4E-48 |
| IS*Alw16* | IS*66* | | *Acinetobacter lwoffii* | 190 | 2E-47 |
| IS*Aba25* | IS*66* | | *Acinetobacter baumannii* | 167 | 2E-40 |
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | 151 | 1E-35 |
| IS*Aba49* | IS*66* | | *Acinetobacter baumannii* | 121 | 1E-26 |
| IS*Aba17* | IS*66* | | *Acinetobacter baumannii* | 58.0 | 0,0000002 |
| IS*Sod17* | IS*3* | IS*51* | *Shewanella oneidensis* | 52.0 | 0,000009 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_55*
*Length=4589*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| *TnAs3* | *Tn3* | | *Aeromonas salmonicida* | 2575 | 0.0 |
| *TnAs2* | *Tn3* | | *Aeromonas salmonicida* | 270 | 2E-71 |
| IS*Shes11* | *Tn3* | | *Shewanella sp.* | 182 | 3E-45 |
| IS*15DI* | IS*6* | | *Salmonella panama* | 119 | 4E-26 |
| IS*15* | IS*6* | | *Salmonella panama* | 119 | 4E-26 |
| IS*26* | IS*6* | | *Proteus vulgaris* | 119 | 4E-26 |
| IS*15DIV* | IS*6* | | *Salmonella typhimurium* | 117 | 2E-25 |
| IS*15DII* | IS*6* | | *Salmonella panama* | 111 | 1E-23 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_57*
*Length=4546*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Ppu12* | IS*L3* | | *Pseudomonas putida* | 131 | 1E-29 |
| IS*1396* | IS*L3* | | *Serratia marcescens* | 131 | 1E-29 |
| *TnAs3* | *Tn3* | | *Aeromonas salmonicida* | 119 | 4E-26 |
| IS*Pst2* | IS*L3* | | *Pseudomonas stutzeri* | 85.7 | 6E-16 |
| IS*Pst9* | IS*L3* | | *Pseudomonas stutzeri* | 75.8 | 5E-13 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_58*
*Length=4354*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Aba14* | IS*3* | IS*150* | *Acinetobacter baumannii* | 605 | 2E-172 |
| IS*Cfr1* | IS*1182* | | *Citrobacter freundii* | 577 | 6E-164 |
| IS*Psp5* | IS*1182* | | *Pseudomonas sp.* | 454 | 6E-127 |
| IS*Alw27* | IS*3* | IS*150* | *Acinetobacter lwoffii* | 383 | 2E-105 |
| IS*Pa94* | IS*1182* | | *Pseudomonas aeruginosa* | 309 | 2E-83 |
| IS*15DI* | IS*6* | | *Salmonella panama* | 119 | 4E-26 |
| IS*15* | IS*6* | | *Salmonella panama* | 119 | 4E-26 |
| IS*26* | IS*6* | | *Proteus vulgaris* | 119 | 4E-26 |
| IS*Aba52* | IS*6* | | *Acinetobacter baumannii* | 117 | 2E-25 |
| IS*1008* | IS*6* | | *Acinetobacter calcoaceticus* | 117 | 2E-25 |
| IS*Our1* | IS*6* | | *Oligella urethralis* | 117 | 2E-25 |
| IS*15DIV* | IS*6* | | *Salmonella typhimurium* | 117 | 2E-25 |
| IS*1007* | IS*6* | | *Acinetobacter sp.* | 117 | 2E-25 |
| IS*15DII* | IS*6* | | *Salmonella panama* | 111 | 1E-23 |
| IS*Acsp5* | IS*3* | IS*150* | *Acinetobacter sp.* | 58.0 | 0,0000001 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_59*
*Length=4029*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*15DI* | IS*6* | | *Salmonella panama* | 1626 | 0.0 |
| IS*15* | IS*6* | | *Salmonella panama* | 1626 | 0.0 |
| IS*15DIV* | IS*6* | | *Salmonella typhimurium* | 1608 | 0.0 |
| IS*26* | IS*6* | | *Proteus vulgaris* | 1602 | 0.0 |
| IS*15DII* | IS*6* | | *Salmonella panama* | 1594 | 0.0 |
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | 400 | 7E-111 |
| IS*1006* | IS*6* | | *Acinetobacter junii* | 180 | 1E-44 |
| IS*Aba52* | IS*6* | | *Acinetobacter baumannii* | 137 | 2E-31 |
| IS*1007* | IS*6* | | *Acinetobacter sp.* | 137 | 2E-31 |
| IS*Our1* | IS*6* | | *Oligella urethralis* | 121 | 9E-27 |
| IS*1008* | IS*6* | | *Acinetobacter calcoaceticus* | 113 | 2E-24 |
| IS*Stag1* | IS*6* | | *Stappia aggregata* | 65.9 | 5E-10 |
| IS*Acr2* | IS*6* | | *Acidiphilium cryptum* | 58.0 | 0,0000001 |
| IS*Aba32* | IS*NCY* | IS*1202* | *Acinetobacter baumannii* | 50.1 | 0,00003 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_60*
*Length=3979*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Aba1* | IS*4* | IS*10* | *Acinetobacter baumannii* | 248 | 6E-65 |
| IS*Aba33* | IS*4* | IS*10* | *Acinetobacter baumannii* | 163 | 3E-39 |
| IS*Aba125* | IS*30* | | *Acinetobacter baumannii* | 119 | 4E-26 |
| IS*C1041* | IS*30* | | *Sulfolobus solfataricus* | 103 | 2E-21 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_61*
*Length=3953*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Alw4* | IS*3* | IS*51* | *Acinetobacter lwoffii* | 1875 | 0.0 |
| IS*Aba2* | IS*3* | IS*51* | *Acinetobacter baumannii* | 1574 | 0.0 |
| IS*Alw23* | IS*3* | IS*51* | *Acinetobacter lwoffii* | 1538 | 0.0 |
| IS*Aba19* | IS*3* | IS*51* | *Acinetobacter baumannii* | 1463 | 0.0 |
| IS*Alw5* | IS*3* | IS*51* | *Acinetobacter lwoffii* | 1439 | 0.0 |
| IS*Aba29* | IS*3* | IS*51* | *Acinetobacter baumannii* | 1352 | 0.0 |
| IS*Aba34* | IS*3* | IS*51* | *Acinetobacter baumannii* | 1308 | 0.0 |
| IS*Aba18* | IS*3* | IS*51* | *Acinetobacter baumannii* | 1304 | 0.0 |
| IS*1008* | IS*6* | | *Acinetobacter calcoaceticus* | 504 | 6E-142 |
| IS*Our1* | IS*6* | | *Oligella urethralis* | 448 | 3E-125 |
| IS*Aba52* | IS*6* | | *Acinetobacter baumannii* | 432 | 2E-120 |
| IS*1006* | IS*6* | | *Acinetobacter junii* | 424 | 4E-118 |
| IS*1007* | IS*6* | | *Acinetobacter sp.* | 129 | 4E-29 |
| IS*15DIV* | IS*6* | | *Salmonella typhimurium* | 95.6 | 5E-19 |
| IS*15DII* | IS*6* | | *Salmonella panama* | 95.6 | 5E-19 |
| IS*15DI* | IS*6* | | *Salmonella panama* | 95.6 | 5E-19 |
| IS*15* | IS*6* | | *Salmonella panama* | 95.6 | 5E-19 |
| IS*26* | IS*6* | | *Proteus vulgaris* | 95.6 | 5E-19 |
| IS*1489v1* | IS*L3* | | *Pseudomonas putida* | 83.8 | 2E-15 |
| IS*Ppu33* | IS*3* | IS*51* | *Pseudomonas putida* | 56.0 | 0,0000004 |
| IS*Stma17* | IS*3* | IS*51* | *Stenotrophomonas maltophilia* | 56.0 | 0,0000004 |
| IS*Mca3* | IS*3* | IS*51* | *Methylococcus capsulatus* | 56.0 | 0,0000004 |
| IS*1416* | IS*3* | IS*51* | *Burkholderia glumae* | 56.0 | 0,0000004 |
| IS*Ali4* | IS*3* | IS*51* | *Azospirillum lipoferum* | 54.0 | 0,000002 |
| IS*Rme15* | IS*3* | IS*51* | *Ralstonia metallidurans* | 54.0 | 0,000002 |
| IS*Pmi1* | IS*3* | IS*51* | *Proteus mirabilis* | 52.0 | 0,000007 |
| IS*Rtr2* | IS*3* | IS*51* | *Rhizobium tropici* | 52.0 | 0,000007 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_62*
*Length=3688*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| *Tn5393* | *Tn3* | | *Erwinia amylovora* | 1358 | 0.0 |
| IS*Ec63* | *Tn3* | | *Escherichia coli* | 307 | 7E-83 |
| *Tn3* | *Tn3* | | *Salmonella enterica* | 121 | 8E-27 |
| IS*15DIV* | IS*6* | | *Salmonella typhimurium* | 119 | 3E-26 |
| IS*15DII* | IS*6* | | *Salmonella panama* | 119 | 3E-26 |
| IS*15DI* | IS*6* | | *Salmonella panama* | 119 | 3E-26 |
| IS*15* | IS*6* | | *Salmonella panama* | 119 | 3E-26 |
| IS*26* | IS*6* | | *Proteus vulgaris* | 119 | 3E-26 |
| *Tn2* | *Tn3* | | *Escherichia coli* | 105 | 5E-22 |
| IS*Mex22* | *Tn3* | | *Methylobacterium extorquens* | 54.0 | 0,000002 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_63*
*Length=3459*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | 186 | 2E-46 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_64*
*Length=3225*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Ppu12* | IS*L3* | | *Pseudomonas putida* | 5513 | 0.0 |
| IS*1396* | IS*L3* | | *Serratia marcescens* | 2591 | 0.0 |
| IS*Pst2* | IS*L3* | | *Pseudomonas stutzeri* | 2313 | 0.0 |
| IS*Pst9* | IS*L3* | | *Pseudomonas stutzeri* | 1620 | 0.0 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_65*
*Length=2804*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*1008* | IS*6* | | *Acinetobacter calcoaceticus* | 519 | 7E-147 |
| IS*Our1* | IS*6* | | *Oligella urethralis* | 464 | 4E-130 |
| IS*Aba52* | IS*6* | | *Acinetobacter baumannii* | 448 | 2E-125 |
| IS*1006* | IS*6* | | *Acinetobacter junii* | 440 | 5E-123 |
| IS*1007* | IS*6* | | *Acinetobacter sp.* | 145 | 4E-34 |
| IS*15DIV* | IS*6* | | *Salmonella typhimurium* | 87.7 | 9E-17 |
| IS*15DII* | IS*6* | | *Salmonella panama* | 87.7 | 9E-17 |
| IS*15DI* | IS*6* | | *Salmonella panama* | 87.7 | 9E-17 |
| IS*15* | IS*6* | | *Salmonella panama* | 87.7 | 9E-17 |
| IS*26* | IS*6* | | *Proteus vulgaris* | 87.7 | 9E-17 |
| IS*1489v1* | IS*L3* | | *Pseudomonas putida* | 83.8 | 1E-15 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_66*
*Length=2667*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Aba1* | IS*4* | IS*10* | *Acinetobacter baumannii* | 212 | 2E-54 |
| IS*Aba33* | IS*4* | IS*10* | *Acinetobacter baumannii* | 135 | 4E-31 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_68*

*Length=2286*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Ppu12* | IS*L3* | | *Pseudomonas putida* | 361 | 3E-99 |
| *TnAs3* | *Tn3* | | *Aeromonas salmonicida* | 119 | 2E-26 |
| IS*Xc4* | *Tn3* | | *Xanthomonas campestris* | 73.8 | 1E-12 |
| IS*Psy42* | *Tn3* | | *Pseudomonas syringae* | 63.9 | 0,000000001 |
| IS*Thsp9* | *Tn3* | | *Thiomonas sp.* | 54.0 | 0,000001 |
| IS*Mex22* | *Tn3* | | *Methylobacterium extorquens* | 52.0 | 0,000004 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_71*
*Length=1597*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| *TnAs3* | *Tn3* | | *Aeromonas salmonicida* | 3166 | 0.0 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_72*
*Length=1578*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| *TnAs3* | *Tn3* | | *Aeromonas salmonicida* | 860 | 0.0 |
| IS*Aba125* | IS*30* | | *Acinetobacter baumannii* | 448 | 1E-125 |
| IS*C1041* | IS*30* | | *Sulfolobus solfataricus* | 343 | 5E-94 |
| IS*15DIV* | IS*6* | | *Salmonella typhimurium* | 119 | 1E-26 |
| IS*15DII* | IS*6* | | *Salmonella panama* | 119 | 1E-26 |
| IS*15DI* | IS*6* | | *Salmonella panama* | 119 | 1E-26 |
| IS*15* | IS*6* | | *Salmonella panama* | 119 | 1E-26 |
| IS*26* | IS*6* | | *Proteus vulgaris* | 119 | 1E-26 |
| IS*Abe8* | IS*30* | | *Acinetobacter bereziniae* | 58.0 | 0,00000004 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_73*
*Length=1549*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*15* | IS*6* | | *Salmonella panama* | 466 | 5E-131 |
| IS*15DII* | IS*6* | | *Salmonella panama* | 347 | 3E-95 |
| IS*15DI* | IS*6* | | *Salmonella panama* | 339 | 8E-93 |
| IS*26* | IS*6* | | *Proteus vulgaris* | 339 | 8E-93 |
| IS*15DIV* | IS*6* | | *Salmonella typhimurium* | 337 | 3E-92 |
| IS*Aba52* | IS*6* | | *Acinetobacter baumannii* | 61.9 | 0,000000003 |
| IS*1008* | IS*6* | | *Acinetobacter calcoaceticus* | 61.9 | 0,000000003 |
| IS*Our1* | IS*6* | | *Oligella urethralis* | 61.9 | 0,000000003 |
| IS*1006* | IS*6* | | *Acinetobacter junii* | 61.9 | 0,000000003 |
| IS*1007* | IS*6* | | *Acinetobacter sp.* | 52.0 | 0,000003 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_75*
*Length=1038*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Aba13* | IS*5* | IS*903* | *Acinetobacter baumannii* | 2058 | 0.0 |
| IS*Aba12* | IS*5* | IS*903* | *Acinetobacter baumannii* | 848 | 0.0 |
| IS*17* | IS*5* | IS*903* | *Acinetobacter haemolyticus* | 835 | 0.0 |
| IS*Aba40* | IS*5* | IS*903* | *Acinetobacter baumannii* | 803 | 0.0 |
| IS*Aha1* | IS*5* | IS*903* | *Acinetobacter haemolyticus* | 801 | 0.0 |
| IS*Alw1* | IS*5* | IS*903* | *Acinetobacter lwoffii* | 702 | 0.0 |
| IS*Ajo1* | IS*5* | IS*903* | *Acinetobacter johnsonii* | 634 | 0.0 |
| IS*Aba53* | IS*5* | IS*903* | *Acinetobacter baumannii* | 617 | 2E-176 |
| IS*Aha3* | IS*5* | IS*903* | *Acinetobacter haemolyticus* | 517 | 1E-146 |
| IS*Aha2* | IS*5* | IS*903* | *Acinetobacter haemolyticus* | 428 | 7E-120 |
| IS*Aba7* | IS*5* | IS*903* | *Acinetobacter baumannii* | 420 | 2E-117 |
| IS*Aba5* | IS*5* | IS*903* | *Acinetobacter baumannii* | 387 | 3E-107 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_76*
*Length=1030*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Aba125* | IS*30* | | *Acinetobacter baumannii* | 1810 | 0.0 |
| IS*C1041* | IS*30* | | *Sulfolobus solfataricus* | 668 | 0.0 |
| IS*Abe8* | IS*30* | | *Acinetobacter bereziniae* | 317 | 2E-86 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_77*
*Length=905*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Aba125* | IS*30* | | *Acinetobacter baumannii* | 119 | 8E-27 |
| IS*C1041* | IS*30* | | *Sulfolobus solfataricus* | 103 | 5E-22 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_78*
*Length=705*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | 894 | 0.0 |
| IS*Aba32* | IS*NCY* | IS*1202* | *Acinetobacter baumannii* | 159 | 7E-39 |
| IS*Alw22* | IS*NCY* | IS*1202* | *Acinetobacter lwoffii* | 145 | 1E-34 |
| IS*Esa1* | IS*NCY* | IS*1202* | *Enterobacter sakazakii* | 65.9 | 8E-11 |
| IS*Lad2* | IS*NCY* | IS*1202* | *Leclercia adecarboxylata* | 65.9 | 8E-11 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_80*
*Length=619*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*1008* | IS*6* | | *Acinetobacter calcoaceticus* | 1209 | 0.0 |
| IS*Our1* | IS*6* | | *Oligella urethralis* | 1162 | 0.0 |
| IS*Aba52* | IS*6* | | *Acinetobacter baumannii* | 662 | 0.0 |
| IS*1007* | IS*6* | | *Acinetobacter sp.* | 525 | 3E-149 |
| IS*1006* | IS*6* | | *Acinetobacter junii* | 502 | 4E-142 |
| IS*15DIV* | IS*6* | | *Salmonella typhimurium* | 113 | 3E-25 |

| | | | | | |
|---|---|---|---|---|---|
| IS*15DII* | IS*6* | | *Salmonella panama* | 113 | 3E-25 |
| IS*15DI* | IS*6* | | *Salmonella panama* | 113 | 3E-25 |
| IS*15* | IS*6* | | *Salmonella panama* | 113 | 3E-25 |
| IS*26* | IS*6* | | *Proteus vulgaris* | 113 | 3E-25 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_84*
*Length=550*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Aba125* | IS*30* | | *Acinetobacter baumannii* | 119 | 5E-27 |
| IS*C1041* | IS*30* | | *Sulfolobus solfataricus* | 103 | 3E-22 |
| IS*Abe8* | IS*30* | | *Acinetobacter bereziniae* | 46.1 | 0,00006 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_86*
*Length=451*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Aba125* | IS*30* | | *Acinetobacter baumannii* | 878 | 0.0 |
| IS*C1041* | IS*30* | | *Sulfolobus solfataricus* | 581 | 4E-166 |
| IS*Abe8* | IS*30* | | *Acinetobacter bereziniae* | 196 | 2E-50 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_87*
*Length=441*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | 708 | 0.0 |
| IS*Alw22* | IS*NCY* | IS*1202* | *Acinetobacter lwoffii* | 117 | 2E-26 |
| IS*Aba32* | IS*NCY* | IS*1202* | *Acinetobacter baumannii* | 111 | 9E-25 |
| IS*Esa1* | IS*NCY* | IS*1202* | *Enterobacter sakazakii* | 65.9 | 5E-11 |
| IS*Lad2* | IS*NCY* | IS*1202* | *Leclercia adecarboxylata* | 65.9 | 5E-11 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_88*
*Length=405*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Aba1* | IS*4* | IS*10* | *Acinetobacter baumannii* | 248 | 6E-66 |
| IS*Aba33* | IS*4* | IS*10* | *Acinetobacter baumannii* | 163 | 3E-40 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_91*
*Length=392*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | 422 | 2E-118 |
| IS*Alw22* | IS*NCY* | IS*1202* | *Acinetobacter lwoffii* | 61.9 | 7E-10 |
| IS*Aba32* | IS*NCY* | IS*1202* | *Acinetobacter baumannii* | 61.9 | 7E-10 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_92*
*Length=315*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | 509 | 7E-145 |
| IS*Alw22* | IS*NCY* | IS*1202* | *Acinetobacter lwoffii* | 135 | 5E-32 |
| IS*Aba32* | IS*NCY* | IS*1202* | *Acinetobacter baumannii* | 105 | 4E-23 |
| IS*Lad2* | IS*NCY* | IS*1202* | *Leclercia adecarboxylata* | 50.1 | 0,000002 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_93*
*Length=309*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | 391 | 5E-109 |
| IS*Aba32* | IS*NCY* | IS*1202* | *Acinetobacter baumannii* | 63.9 | 1E-10 |
| IS*Alw22* | IS*NCY* | IS*1202* | *Acinetobacter lwoffii* | 61.9 | 5E-10 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_94*
*Length=309*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | 391 | 5E-109 |
| IS*Alw22* | IS*NCY* | IS*1202* | *Acinetobacter lwoffii* | 56.0 | 0,00000003 |
| IS*Aba32* | IS*NCY* | IS*1202* | *Acinetobacter baumannii* | 56.0 | 0,00000003 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_95*
*Length=309*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | 391 | 5E-109 |
| IS*Alw22* | IS*NCY* | IS*1202* | *Acinetobacter lwoffii* | 56.0 | 0,00000003 |
| IS*Aba32* | IS*NCY* | IS*1202* | *Acinetobacter baumannii* | 56.0 | 0,00000003 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_96*
*Length=309*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | 383 | 1E-106 |
| IS*Aba32* | IS*NCY* | IS*1202* | *Acinetobacter baumannii* | 56.0 | 0,00000003 |
| IS*Alw22* | IS*NCY* | IS*1202* | *Acinetobacter lwoffii* | 54.0 | 0,0000001 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_97*
*Length=309*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | 391 | 5E-109 |

| | | | | | | |
|---|---|---|---|---|---|---|
| IS*Alw22* | IS*NCY* | IS*1202* | *Acinetobacter lwoffii* | 61.9 | | 5E-10 |
| IS*Aba32* | IS*NCY* | IS*1202* | *Acinetobacter baumannii* | 61.9 | | 5E-10 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_98*
*Length=309*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value | |
|---|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | | 391 | 5E-109 |
| IS*Aba32* | IS*NCY* | IS*1202* | *Acinetobacter baumannii* | 56.0 | | 0,00000003 |
| IS*Alw22* | IS*NCY* | IS*1202* | *Acinetobacter lwoffii* | 54.0 | | 0,0000001 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_99*
*Length=309*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value | |
|---|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | | 391 | 5E-109 |
| IS*Aba32* | IS*NCY* | IS*1202* | *Acinetobacter baumannii* | 63.9 | | 1E-10 |
| IS*Alw22* | IS*NCY* | IS*1202* | *Acinetobacter lwoffii* | 61.9 | | 5E-10 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_100*
*Length=309*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value | |
|---|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | | 391 | 5E-109 |
| IS*Alw22* | IS*NCY* | IS*1202* | *Acinetobacter lwoffii* | 61.9 | | 5E-10 |
| IS*Aba32* | IS*NCY* | IS*1202* | *Acinetobacter baumannii* | 61.9 | | 5E-10 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_102*
*Length=306*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value | |
|---|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | | 367 | 7E-102 |
| IS*Alw22* | IS*NCY* | IS*1202* | *Acinetobacter lwoffii* | | 117 | 1E-26 |
| IS*Aba32* | IS*NCY* | IS*1202* | *Acinetobacter baumannii* | 99.6 | | 2E-21 |
| IS*Esa1* | IS*NCY* | IS*1202* | *Enterobacter sakazakii* | 65.9 | | 3E-11 |
| IS*Lad2* | IS*NCY* | IS*1202* | *Leclercia adecarboxylata* | 65.9 | | 3E-11 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_103*
*Length=298*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value | |
|---|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | | 361 | 4E-100 |
| IS*Alw22* | IS*NCY* | IS*1202* | *Acinetobacter lwoffii* | 54.0 | | 0,0000001 |
| IS*Aba32* | IS*NCY* | IS*1202* | *Acinetobacter baumannii* | 54.0 | | 0,0000001 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_105*
*Length=290*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value | |
|---|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | | 392 | 1E-109 |
| IS*Alw22* | IS*NCY* | IS*1202* | *Acinetobacter lwoffii* | | 117 | 1E-26 |
| IS*Aba32* | IS*NCY* | IS*1202* | *Acinetobacter baumannii* | 99.6 | | 2E-21 |
| IS*Esa1* | IS*NCY* | IS*1202* | *Enterobacter sakazakii* | 65.9 | | 3E-11 |
| IS*Lad2* | IS*NCY* | IS*1202* | *Leclercia adecarboxylata* | 65.9 | | 3E-11 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_106*
*Length=284*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value | |
|---|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | | 349 | 1E-96 |
| IS*Aba32* | IS*NCY* | IS*1202* | *Acinetobacter baumannii* | 71.9 | | 5E-13 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_107*
*Length=284*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value | |
|---|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | | 349 | 1E-96 |
| IS*Aba32* | IS*NCY* | IS*1202* | *Acinetobacter baumannii* | 71.9 | | 5E-13 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_108*
*Length=284*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value | |
|---|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | | 349 | 1E-96 |
| IS*Aba32* | IS*NCY* | IS*1202* | *Acinetobacter baumannii* | 71.9 | | 5E-13 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_109*
*Length=283*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value | |
|---|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | | 333 | 9E-92 |
| IS*Aba32* | IS*NCY* | IS*1202* | *Acinetobacter baumannii* | 71.9 | | 5E-13 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_110*
*Length=282*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value | |
|---|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | | 295 | 2E-80 |
| IS*Aba32* | IS*NCY* | IS*1202* | *Acinetobacter baumannii* | 63.9 | | 1E-10 |
| IS*Alw22* | IS*NCY* | IS*1202* | *Acinetobacter lwoffii* | 61.9 | | 5E-10 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_113*
*Length=270*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | 470 | 5E-133 |
| IS*Alw22* | IS*NCY* | IS*1202* | *Acinetobacter lwoffii* | 111 | 6E-25 |
| IS*Aba32* | IS*NCY* | IS*1202* | *Acinetobacter baumannii* | 111 | 6E-25 |
| IS*Lad2* | IS*NCY* | IS*1202* | *Leclercia adecarboxylata* | 56.0 | 0,00000003 |
| IS*Rel10* | IS*NCY* | IS*1202* | *Rhizobium etli* | 46.1 | 0,00003 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_114*
*Length=269*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | 329 | 1E-90 |
| IS*Aba32* | IS*NCY* | IS*1202* | *Acinetobacter baumannii* | 58.0 | 0,000000007 |
| IS*Alw22* | IS*NCY* | IS*1202* | *Acinetobacter lwoffii* | 56.0 | 0,00000003 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_115*
*Length=268*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | 278 | 4E-75 |
| IS*Aba32* | IS*NCY* | IS*1202* | *Acinetobacter baumannii* | 56.0 | 0,00000003 |
| IS*Alw22* | IS*NCY* | IS*1202* | *Acinetobacter lwoffii* | 54.0 | 0,0000001 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_116*
*Length=266*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | 311 | 3E-85 |
| IS*Alw22* | IS*NCY* | IS*1202* | *Acinetobacter lwoffii* | 117 | 9E-27 |
| IS*Aba32* | IS*NCY* | IS*1202* | *Acinetobacter baumannii* | 101 | 5E-22 |
| IS*Esa1* | IS*NCY* | IS*1202* | *Enterobacter sakazakii* | 65.9 | 3E-11 |
| IS*Lad2* | IS*NCY* | IS*1202* | *Leclercia adecarboxylata* | 65.9 | 3E-11 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_117*
*Length=265*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | 303 | 7E-83 |
| IS*Alw22* | IS*NCY* | IS*1202* | *Acinetobacter lwoffii* | 61.9 | 5E-10 |
| IS*Aba32* | IS*NCY* | IS*1202* | *Acinetobacter baumannii* | 61.9 | 5E-10 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_118*
*Length=258*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | 337 | 5E-93 |
| IS*Alw22* | IS*NCY* | IS*1202* | *Acinetobacter lwoffii* | 117 | 9E-27 |
| IS*Aba32* | IS*NCY* | IS*1202* | *Acinetobacter baumannii* | 101 | 5E-22 |
| IS*Esa1* | IS*NCY* | IS*1202* | *Enterobacter sakazakii* | 65.9 | 3E-11 |
| IS*Lad2* | IS*NCY* | IS*1202* | *Leclercia adecarboxylata* | 65.9 | 3E-11 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_119*
*Length=248*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | 317 | 4E-87 |
| IS*Alw22* | IS*NCY* | IS*1202* | *Acinetobacter lwoffii* | 117 | 8E-27 |
| IS*Aba32* | IS*NCY* | IS*1202* | *Acinetobacter baumannii* | 101 | 5E-22 |
| IS*Esa1* | IS*NCY* | IS*1202* | *Enterobacter sakazakii* | 65.9 | 3E-11 |
| IS*Lad2* | IS*NCY* | IS*1202* | *Leclercia adecarboxylata* | 65.9 | 3E-11 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_121*
*Length=246*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | 270 | 9E-73 |
| IS*Alw22* | IS*NCY* | IS*1202* | *Acinetobacter lwoffii* | 61.9 | 4E-10 |
| IS*Aba32* | IS*NCY* | IS*1202* | *Acinetobacter baumannii* | 61.9 | 4E-10 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_122*
*Length=242*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | 305 | 2E-83 |
| IS*Alw22* | IS*NCY* | IS*1202* | *Acinetobacter lwoffii* | 117 | 8E-27 |
| IS*Aba32* | IS*NCY* | IS*1202* | *Acinetobacter baumannii* | 99.6 | 2E-21 |
| IS*Esa1* | IS*NCY* | IS*1202* | *Enterobacter sakazakii* | 65.9 | 3E-11 |
| IS*Lad2* | IS*NCY* | IS*1202* | *Leclercia adecarboxylata* | 65.9 | 3E-11 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_126*
*Length=238*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | 297 | 4E-81 |
| IS*Aba32* | IS*NCY* | IS*1202* | *Acinetobacter baumannii* | 60.0 | 0,000000002 |
| IS*Alw22* | IS*NCY* | IS*1202* | *Acinetobacter lwoffii* | 58.0 | 0,000000006 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_127*
*Length=237*

| Sequences producing significant alignments | IS Family | Group | Origin | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | 287 | 4E-78 |
| IS*Alw22* | IS*NCY* | IS*1202* | *Acinetobacter lwoffii* | 61.9 | 4E-10 |
| IS*Aba32* | IS*NCY* | IS*1202* | *Acinetobacter baumannii* | 61.9 | 4E-10 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_128*
*Length=236*

| Sequences producing significant alignments | IS Family | Group | Origin | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | 428 | 2E-120 |
| IS*Alw22* | IS*NCY* | IS*1202* | *Acinetobacter lwoffii* | 111 | 5E-25 |
| IS*Aba32* | IS*NCY* | IS*1202* | *Acinetobacter baumannii* | 111 | 5E-25 |
| IS*Lad2* | IS*NCY* | IS*1202* | *Leclercia adecarboxylata* | 56.0 | 0,00000002 |
| IS*Rel10* | IS*NCY* | IS*1202* | *Rhizobium etli* | 46.1 | 0,00002 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_129*
*Length=234*

| Sequences producing significant alignments | IS Family | Group | Origin | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | 289 | 9E-79 |
| IS*Aba32* | IS*NCY* | IS*1202* | *Acinetobacter baumannii* | 63.9 | 1E-10 |
| IS*Alw22* | IS*NCY* | IS*1202* | *Acinetobacter lwoffii* | 61.9 | 4E-10 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_130*
*Length=233*

| Sequences producing significant alignments | IS Family | Group | Origin | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | 276 | 1E-74 |
| IS*Alw22* | IS*NCY* | IS*1202* | *Acinetobacter lwoffii* | 61.9 | 4E-10 |
| IS*Aba32* | IS*NCY* | IS*1202* | *Acinetobacter baumannii* | 61.9 | 4E-10 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_131*
*Length=231*

| Sequences producing significant alignments | IS Family | Group | Origin | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | 276 | 1E-74 |
| IS*Aba32* | IS*NCY* | IS*1202* | *Acinetobacter baumannii* | 115 | 3E-26 |
| IS*Alw22* | IS*NCY* | IS*1202* | *Acinetobacter lwoffii* | 91.7 | 4E-19 |
| IS*Esa1* | IS*NCY* | IS*1202* | *Enterobacter sakazakii* | 50.1 | 0,000001 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_132*
*Length=231*

| Sequences producing significant alignments | IS Family | Group | Origin | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | 283 | 6E-77 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_133*
*Length=231*

| Sequences producing significant alignments | IS Family | Group | Origin | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | 339 | 1E-93 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_135*
*Length=230*

| Sequences producing significant alignments | IS Family | Group | Origin | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Aba125* | IS*30* | | *Acinetobacter baumannii* | 456 | 7E-129 |
| IS*C1041* | IS*30* | | *Sulfolobus solfataricus* | 335 | 2E-92 |
| IS*Abe8* | IS*30* | | *Acinetobacter bereziniae* | 58.0 | 0,000000006 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_136*
*Length=228*

| Sequences producing significant alignments | IS Family | Group | Origin | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | 335 | 2E-92 |
| IS*Alw22* | IS*NCY* | IS*1202* | *Acinetobacter lwoffii* | 111 | 5E-25 |
| IS*Aba32* | IS*NCY* | IS*1202* | *Acinetobacter baumannii* | 111 | 5E-25 |
| IS*Lad2* | IS*NCY* | IS*1202* | *Leclercia adecarboxylata* | 56.0 | 0,00000002 |
| IS*Rel10* | IS*NCY* | IS*1202* | *Rhizobium etli* | 46.1 | 0,00002 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_137*
*Length=227*

| Sequences producing significant alignments | IS Family | Group | Origin | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Alw22* | IS*NCY* | IS*1202* | *Acinetobacter lwoffii* | 194 | 4E-50 |
| IS*Aba32* | IS*NCY* | IS*1202* | *Acinetobacter baumannii* | 178 | 2E-45 |
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | 75.8 | 3E-14 |
| IS*Esa1* | IS*NCY* | IS*1202* | *Enterobacter sakazakii* | 60.0 | 0,000000002 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_139*
*Length=225*

| Sequences producing significant alignments | IS Family | Group | Origin | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Aba1* | IS*4* | IS*10* | *Acinetobacter baumannii* | 414 | 2E-116 |
| IS*Aba33* | IS*4* | IS*10* | *Acinetobacter baumannii* | 216 | 1E-56 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_140*
*Length=223*

| Sequences producing significant alignments | IS Family | Group | Origin | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | 414 | 2E-116 |
| IS*Alw22* | IS*NCY* | IS*1202* | *Acinetobacter lwoffii* | 111 | 5E-25 |
| IS*Aba32* | IS*NCY* | IS*1202* | *Acinetobacter baumannii* | 111 | 5E-25 |
| IS*Lad2* | IS*NCY* | IS*1202* | *Leclercia adecarboxylata* | 56.0 | 0,00000002 |

| | | | | | | |
|---|---|---|---|---|---|---|
| IS*Rel10* | IS*NCY* | IS*1202* | *Rhizobium etli* | 46.1 | | 0,00002 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_141*
*Length=222*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value | |
|---|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | | 206 | 1E-53 |
| IS*Alw22* | IS*NCY* | IS*1202* | *Acinetobacter lwoffii* | | 117 | 7E-27 |
| IS*Aba32* | IS*NCY* | IS*1202* | *Acinetobacter baumannii* | 99.6 | | 2E-21 |
| IS*Esa1* | IS*NCY* | IS*1202* | *Enterobacter sakazakii* | 65.9 | | 2E-11 |
| IS*Lad2* | IS*NCY* | IS*1202* | *Leclercia adecarboxylata* | 65.9 | | 2E-11 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_142*
*Length=222*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value | |
|---|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | | 147 | 8E-36 |
| IS*Aba32* | IS*NCY* | IS*1202* | *Acinetobacter baumannii* | 85.7 | | 3E-17 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_144*
*Length=221*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value | |
|---|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | | 327 | 4E-90 |
| IS*Aba32* | IS*NCY* | IS*1202* | *Acinetobacter baumannii* | 50.1 | | 0,000001 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_147*
*Length=218*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value | |
|---|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | | 276 | 1E-74 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_149*
*Length=217*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value | |
|---|---|---|---|---|---|---|
| IS*Aba1* | IS*4* | IS*10* | *Acinetobacter baumannii* | | 414 | 2E-11 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_150*
*Length=215*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value | |
|---|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | | 295 | 1E-80 |
| IS*CARN112* | IS*NCY* | IS*1202* | *Metagenomic data* | 48.1 | | 0,000006 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_151*
*Length=215*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value | |
|---|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | | 295 | 1E-80 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_152*
*Length=214*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value | |
|---|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | | 281 | 2E-76 |
| IS*Alw22* | IS*NCY* | IS*1202* | *Acinetobacter lwoffii* | | 109 | 2E-24 |
| IS*Aba32* | IS*NCY* | IS*1202* | *Acinetobacter baumannii* | 93.7 | | 1E-19 |
| IS*Esa1* | IS*NCY* | IS*1202* | *Enterobacter sakazakii* | 58.0 | | 0,000000006 |
| IS*Lad2* | IS*NCY* | IS*1202* | *Leclercia adecarboxylata* | 58.0 | | 0,000000006 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_153*
*Length=213*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value | |
|---|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | | 335 | 2E-92 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_155*
*Length=213*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value | |
|---|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | | 335 | 2E-92 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_156*
*Length=213*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value | |
|---|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | | 335 | 2E-92 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_157*
*Length=213*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value | |
|---|---|---|---|---|---|---|
| IS*Aba1* | IS*4* | IS*10* | *Acinetobacter baumannii* | | 406 | 5E-114 |
| IS*Aba33* | IS*4* | IS*10* | *Acinetobacter baumannii* | | 226 | 1E-59 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_158*
*Length=213*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value | |
|---|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | | 151 | 5E-37 |
| IS*CARN112* | IS*NCY* | IS*1202* | *Metagenomic data* | 48.1 | | 0,000005 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_159*
*Length=213*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | 343 | 7E-95 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_160*
*Length=213*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Aba1* | IS*4* | IS*10* | *Acinetobacter baumannii* | 414 | 2E-116 |
| IS*Aba33* | IS*4* | IS*10* | *Acinetobacter baumannii* | 218 | 3E-57 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_162*
*Length=212*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | 319 | 1E-87 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_164*
*Length=208*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | 262 | 2E-70 |
| IS*Alw22* | IS*NCY* | IS*1202* | *Acinetobacter lwoffii* | 117 | 7E-27 |
| IS*Aba32* | IS*NCY* | IS*1202* | *Acinetobacter baumannii* | 99.6 | 2E-21 |
| IS*Esa1* | IS*NCY* | IS*1202* | *Enterobacter sakazakii* | 65.9 | 2E-11 |
| IS*Lad2* | IS*NCY* | IS*1202* | *Leclercia adecarboxylata* | 65.9 | 2E-11 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_168*
*Length=206*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | 258 | 3E-69 |
| IS*Aba32* | IS*NCY* | IS*1202* | *Acinetobacter baumannii* | 50.1 | 0,000001 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_169*
*Length=206*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | 254 | 5E-68 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_171*
*Length=205*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | 192 | 1E-49 |
| IS*Alw22* | IS*NCY* | IS*1202* | *Acinetobacter lwoffii* | 61.9 | 3E-10 |
| IS*Aba32* | IS*NCY* | IS*1202* | *Acinetobacter baumannii* | 61.9 | 3E-10 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_172*
*Length=204*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | 254 | 5E-68 |
| IS*Aba32* | IS*NCY* | IS*1202* | *Acinetobacter baumannii* | 85.7 | 2E-17 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_173*
*Length=204*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | 270 | 8E-73 |
| IS*Aba32* | IS*NCY* | IS*1202* | *Acinetobacter baumannii* | 77.8 | 6E-15 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_174*
*Length=204*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | 246 | 1E-65 |
| IS*Aba32* | IS*NCY* | IS*1202* | *Acinetobacter baumannii* | 81.8 | 4E-16 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_175*
*Length=204*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | 161 | 5E-40 |
| IS*Alw22* | IS*NCY* | IS*1202* | *Acinetobacter lwoffii* | 52.0 | 0,0000003 |
| IS*Aba32* | IS*NCY* | IS*1202* | *Acinetobacter baumannii* | 52.0 | 0,0000003 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_177*
*Length=204*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | 262 | 2E-70 |
| IS*Aba32* | IS*NCY* | IS*1202* | *Acinetobacter baumannii* | 77.8 | 6E-15 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_179*
*Length=203*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|

| | | | | | | |
|---|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | | 394 | 2E-110 |
| IS*Alw22* | IS*NCY* | IS*1202* | *Acinetobacter lwoffii* | | 111 | 4E-25 |
| IS*Aba32* | IS*NCY* | IS*1202* | *Acinetobacter baumannii* | | 111 | 4E-25 |
| IS*Lad2* | IS*NCY* | IS*1202* | *Leclercia adecarboxylata* | 56.0 | | 0,00000002 |
| IS*Rel10* | IS*NCY* | IS*1202* | *Rhizobium etli* | 46.1 | | 0,00002 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_180*
*Length=203*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Aba1* | IS*4* | IS*10* | *Acinetobacter baumannii* | 379 | 1E-105 |
| IS*Aba33* | IS*4* | IS*10* | *Acinetobacter baumannii* | 192 | 1E-49 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_181*
*Length=203*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | 313 | 6E-86 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_182*
*Length=202*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Ppu12* | IS*L3* | | *Pseudomonas putida* | 283 | 5E-77 |

*Query= MT-2_S8_L001_R1_001_(paired)_trimmed_(paired)_contig_185*
*Length=200*

| *Sequences producing significant alignments* | IS *Family* | *Group* | *Origin* | Score (bits) | E. value |
|---|---|---|---|---|---|
| IS*Ajo2* | IS*NCY* | IS*1202* | *Acinetobacter johnsonii* | 262 | 2E-70 |
| IS*Aba32* | IS*NCY* | IS*1202* | *Acinetobacter baumannii* | 52.0 | 0,0000003 |
| IS*Alw22* | IS*NCY* | IS*1202* | *Acinetobacter lwoffii* | 44.1 | 0,00008 |