

Figure S1. **The genomic map for *Bacillus velezensis* WRN014.** Circular representation of the genome of *Bacillus velezensis* WRN014. The innermost circle shows the scale. From the inside to outside circle, circle 1 shows the GC skew. Circle 2 represents the G + C content (%) of the *Bacillus velezensis* WRN014. Circle 3 shows the protein-coding gene sequences on the reverse chromosomal strand colored by COG categories. Circle 4 shows the CDS, tRNA and rRNA sequences on the reverse chromosomal strand. Circle 5 shows the genome sequences. Circle 6 shows the CDS, tRNA and rRNA sequences on the forward chromosomal strand. Circle 7 shows the protein-coding gene sequences on the forward chromosomal strand. Circle 8 shows the genomic island sequences on the genome of *Bacillus velezensis* WRN014. Circle 9 shows the gene cluster sequences on the genome of *Bacillus velezensis* WRN014. The capital letters represent different categories of COG (Clusters of Orthologous Groups of

proteins). **C**: Energy production and conversion **D**: Cell cycle control, cell division, chromosome partitioning **E**: Amino acid transport and metabolism **F**: Nucleotide transport and metabolism **G**: Carbohydrate transport and metabolism **H**: Coenzyme transport and metabolism **I**: Lipid transport and metabolism **J**: Translation, ribosomal structure and biogenesis **K**: Transcription **L**: Replication, recombination and repair **M**: Translation, ribosomal structure and biogenesis **N**: Cell motility **O**: Posttranslational modification, protein turnover, chaperones **P**: Inorganic ion transport and metabolism **Q**: Secondary metabolites biosynthesis, transport and catabolism **R**: General function prediction only **S**: Function unknown **T**: Signal transduction mechanisms

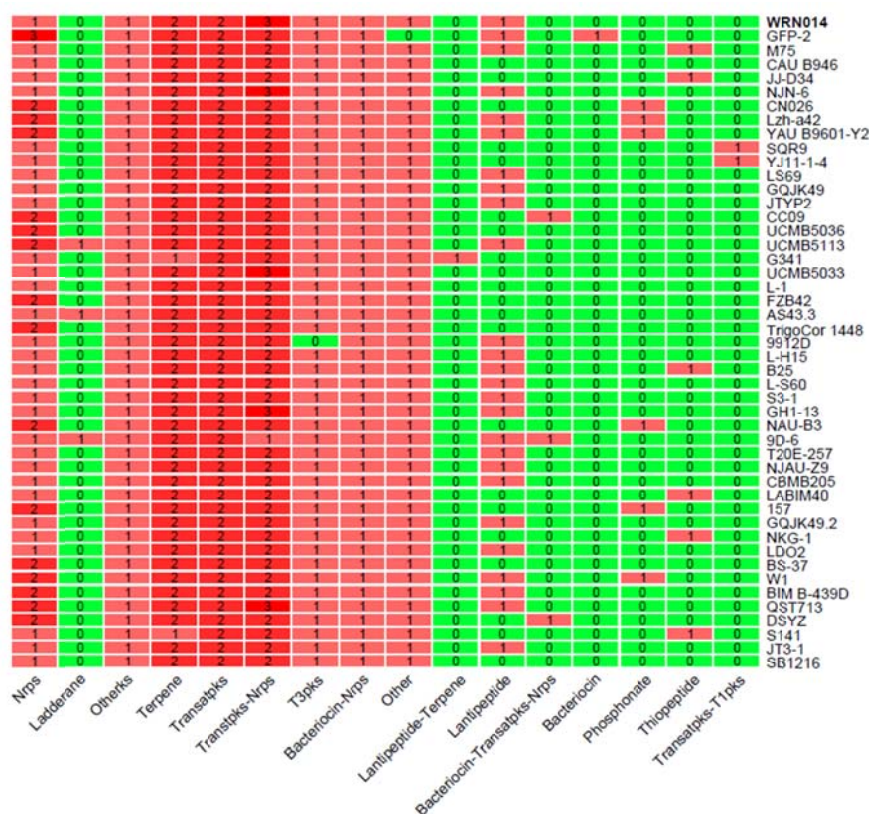


Figure S2. **The secondary metabolite gene clusters distribute in 46 *Bacillus velezensis* genomes.** The number in each square represents different types of gene cluster.

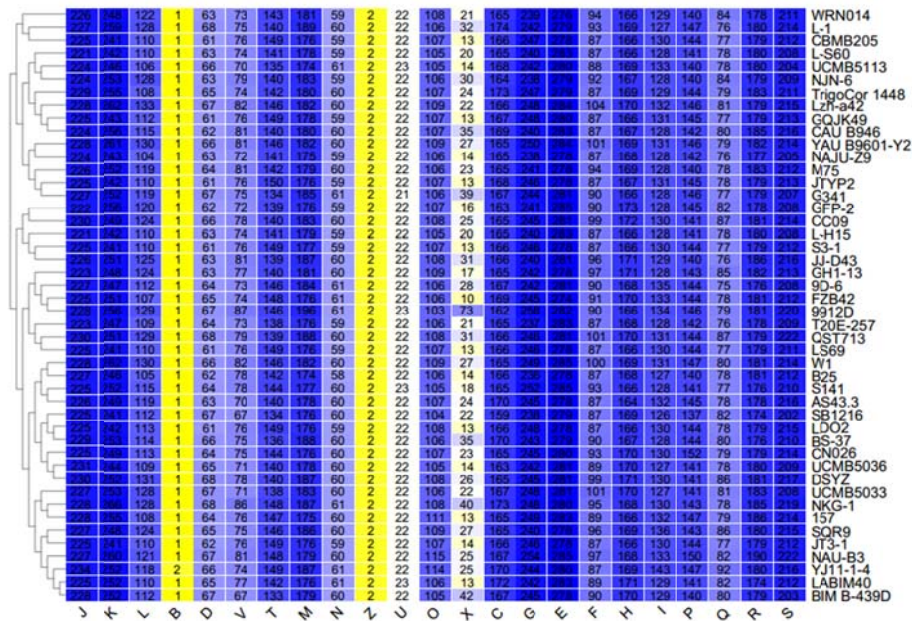


Figure S3. **Differential distribution of COG categories in protein coding genes of the 46 *Bacillus velezensis* strains.** The numbers in the box represent gene numbers of different COG categories. The results are clustered using Pearson Correlation Coefficient. The capital letters represent different categories of COG. **J**: Translation, ribosomal structure and biogenesis **K**: Transcription **L**: Replication, recombination and repair **B**: Chromatin structure and dynamics **D**: Cell cycle control, cell division, chromosome partitioning **V**: Defense mechanism **T**: Signal transduction mechanisms **M**: Translation, ribosomal structure and biogenesis **N**: Cell motility **Z**: Cytoskeleton **U**: Intracellular trafficking, secretion, and vesicular transport **O**: Posttranslational modification, protein turnover, chaperones **X**: Mobilome: prophages, transposons **C**: Energy production and conversion **G**: Carbohydrate transport and metabolism **E**: Amino acid transport and metabolism **F**: Nucleotide transport and metabolism **H**: Coenzyme transport and metabolism **I**: Lipid transport and metabolism **P**: Inorganic ion transport and metabolism **Q**: Secondary metabolites biosynthesis, transport and catabolism **R**: General function prediction only **S**: Function unknown

Table S1. The distance matrix of 47 *Bacillus* strains in this article.

Strains	1	2	3	4	5	6	7	8
<i>Bacillus v</i>0		0.0236	0.0234	0.024	0.0236	0.0059	0.0225	0.0233
<i>Bacillus ve</i> 0.0236	0		0.0174	0.0216	0.0099	0.023	0.0102	0.0104
<i>Bacillus ve</i> 0.0234	0.0174	0		0.0139	0.018	0.0234	0.0166	0.0173
<i>Bacillus ve</i> 0.024	0.0216	0.0139	0		0.0207	0.0231	0.0203	0.0213
<i>Bacillus ve</i> 0.0236	0.0099	0.018	0.0207	0		0.0233	0.0112	0.0119
<i>Bacillus ve</i> 0.0059	0.023	0.0234	0.0231	0.0233	0		0.0225	0.023
<i>Bacillus ve</i> 0.0225	0.0102	0.0166	0.0203	0.0112	0.0225	0		0.0069
<i>Bacillus ve</i> 0.0233	0.0104	0.0173	0.0213	0.0119	0.023	0.0069	0	
<i>Bacillus ve</i> 0.0065	0.0239	0.0232	0.0244	0.0236	0.006	0.0229	0.024	
<i>Bacillus ve</i> 0.0235	0.0179	0.0182	0.0205	0.0181	0.0235	0.0175	0.0182	
<i>Bacillus ve</i> 0.0243	0.0132	0.0184	0.0222	0.0134	0.0231	0.0126	0.0131	
<i>Bacillus ve</i> 0.0236	0.0176	0.0082	0.0142	0.0184	0.023	0.0167	0.0174	
<i>Bacillus ve</i> 0.0246	0.0135	0.0187	0.0227	0.0136	0.0232	0.0128	0.0131	
<i>Bacillus ve</i> 0.0229	0.0108	0.0167	0.0196	0.0106	0.0229	0.0116	0.0117	
<i>Bacillus ve</i> 0.023	0.0103	0.0167	0.0212	0.0117	0.0227	0.0067	0.0072	
<i>Bacillus ve</i> 0.0147	0.0226	0.0225	0.023	0.023	0.0144	0.0219	0.0221	
<i>Bacillus ve</i> 0.0146	0.023	0.0228	0.0227	0.0227	0.0138	0.0216	0.0221	
<i>Bacillus ve</i> 0.0235	0.0179	0.0182	0.0205	0.0181	0.0235	0.0175	0.0182	
<i>Bacillus ve</i> 0.0072	0.0242	0.0236	0.0239	0.0234	0.0061	0.0231	0.024	
<i>Bacillus ve</i> 0.0235	0.0179	0.0182	0.0205	0.0181	0.0235	0.0175	0.0182	
<i>Bacillus ve</i> 0.0235	0.0179	0.0182	0.0205	0.0182	0.0235	0.0175	0.0182	
<i>Bacillus ve</i> 0.0232	0.0098	0.018	0.0208	0.0105	0.0233	0.0101	0.0114	
<i>Bacillus ve</i> 0.024	0.0114	0.0176	0.0204	0.0119	0.0236	0.0116	0.0122	
<i>Bacillus ve</i> 0.0235	0.0179	0.0181	0.0205	0.0181	0.0235	0.0175	0.0182	
<i>Bacillus ve</i> 0.0065	0.024	0.0235	0.0239	0.0238	0.0063	0.0234	0.0243	
<i>Bacillus ve</i> 0.0064	0.024	0.0236	0.0238	0.0238	0.0062	0.0234	0.0242	
<i>Bacillus ve</i> 0.0235	0.0179	0.0182	0.0205	0.0181	0.0235	0.0176	0.0181	
<i>Bacillus ve</i> 0.0241	0.0178	0.0076	0.0159	0.0179	0.0226	0.0165	0.0171	
<i>Bacillus ve</i> 0.0064	0.0231	0.0231	0.0235	0.0227	0.0056	0.0226	0.0233	
<i>Bacillus ve</i> 0.0242	0.0179	0.0015	0.0143	0.018	0.0234	0.0169	0.0174	
<i>Bacillus ve</i> 0.006	0.023	0.0229	0.0233	0.0233	0.0063	0.0225	0.0228	
<i>Bacillus ve</i> 0.0061	0.023	0.023	0.0247	0.0236	0.0058	0.0225	0.0233	
<i>Bacillus ve</i> 0.0235	0.0102	0.0184	0.0213	0.0097	0.0232	0.0122	0.0135	
<i>Bacillus ve</i> 0.0247	0.0137	0.018	0.0217	0.0142	0.0238	0.0136	0.014	
<i>Bacillus ve</i> 0.0235	0.0179	0.0182	0.0205	0.0181	0.0235	0.0175	0.0182	
<i>Bacillus ve</i> 0.0234	0.0129	0.0177	0.0198	0.0134	0.0231	0.0127	0.0132	
<i>Bacillus ve</i> 0.0234	0.0109	0.0172	0.02	0.0119	0.0229	0.0072	0.0069	
<i>Bacillus ve</i> 0.0245	0.0168	0.0172	0.0215	0.017	0.0233	0.0159	0.0165	
<i>Bacillus ve</i> 0.007	0.0235	0.023	0.0237	0.0238	0.0065	0.0226	0.0233	
<i>Bacillus ve</i> 0.0238	0.0094	0.018	0.0205	0.0084	0.0235	0.0119	0.0123	
<i>Bacillus ve</i> 0.0235	0.0108	0.0165	0.0202	0.0113	0.0228	0.0072	0.0078	
<i>Bacillus ve</i> 0.0226	0.0129	0.0176	0.0209	0.0133	0.0223	0.0125	0.0126	
<i>Bacillus ve</i> 0.0224	0.0103	0.0166	0.0194	0.0112	0.0223	0.0069	0.0073	
<i>Bacillus ve</i> 0.0243	0.0182	0.0078	0.0154	0.018	0.0227	0.017	0.0175	
<i>Bacillus ve</i> 0.0241	0.0181	0.0076	0.0153	0.0179	0.0226	0.0169	0.0174	
<i>Bacillus ve</i> 0.0241	0.0163	0.0169	0.0211	0.0169	0.0236	0.015	0.0157	
<i>Bacillus an</i> 0.0601	0.0598	0.0586	0.0574	0.0592	0.06	0.0589	0.0594	

9	10	11	12	13	14	15	16	17
0.0065	0.0235	0.0243	0.0236	0.0246	0.0229	0.023	0.0147	0.0146
0.0239	0.0179	0.0132	0.0176	0.0135	0.0108	0.0103	0.0226	0.023
0.0232	0.0182	0.0184	0.0082	0.0187	0.0167	0.0167	0.0225	0.0228
0.0244	0.0205	0.0222	0.0142	0.0227	0.0196	0.0212	0.023	0.0227
0.0236	0.0181	0.0134	0.0184	0.0136	0.0106	0.0117	0.023	0.0227
0.006	0.0235	0.0231	0.023	0.0232	0.0229	0.0227	0.0144	0.0138
0.0229	0.0175	0.0126	0.0167	0.0128	0.0116	0.0067	0.0219	0.0216
0.024	0.0182	0.0131	0.0174	0.0131	0.0117	0.0072	0.0221	0.0221
0	0.0237	0.0236	0.0241	0.0239	0.0231	0.0239	0.0156	0.014
0.0237	0	0.0189	0.0179	0.0191	0.0172	0.0177	0.023	0.0237
0.0236	0.0189	0	0.0189	0.0006	0.0134	0.0129	0.0228	0.0245
0.0241	0.0179	0.0189	0	0.0191	0.0169	0.0171	0.0221	0.0225
0.0239	0.0191	0.0006	0.0191	0	0.0135	0.0133	0.0233	0.0248
0.0231	0.0172	0.0134	0.0169	0.0135	0	0.0117	0.0224	0.0224
0.0239	0.0177	0.0129	0.0171	0.0133	0.0117	0	0.0226	0.0218
0.0156	0.023	0.0228	0.0221	0.0233	0.0224	0.0226	0	0.0104
0.014	0.0237	0.0245	0.0225	0.0248	0.0224	0.0218	0.0104	0
0.0237	0	0.0189	0.0179	0.0191	0.0172	0.0177	0.023	0.0237
0.0066	0.0232	0.0246	0.0236	0.0252	0.023	0.0238	0.0151	0.0156
0.0237	0	0.0189	0.0179	0.0191	0.0172	0.0177	0.023	0.0237
0.0237	0	0.0189	0.0179	0.0191	0.0172	0.0177	0.023	0.0237
0.0234	0.0179	0.0139	0.0177	0.0144	0.011	0.0111	0.023	0.0228
0.0239	0.0184	0.0138	0.0177	0.014	0.011	0.0116	0.023	0.0231
0.0236	0.0022	0.0189	0.0178	0.0191	0.0172	0.0177	0.023	0.0237
0.0069	0.0234	0.0236	0.0236	0.0239	0.0231	0.0239	0.0152	0.0147
0.0066	0.0233	0.0235	0.0235	0.0238	0.023	0.0238	0.0151	0.0146
0.0237	0.0015	0.0189	0.0179	0.0191	0.0172	0.0178	0.023	0.0238
0.0237	0.0177	0.0194	0.0087	0.0201	0.0169	0.0171	0.0222	0.0233
0.0064	0.0233	0.0231	0.0235	0.0232	0.0227	0.0235	0.0144	0.0134
0.0234	0.0182	0.0196	0.0081	0.0202	0.0168	0.0168	0.0227	0.0238
0.006	0.0235	0.0229	0.0231	0.0229	0.0226	0.0225	0.0146	0.0143
0.0071	0.0231	0.0235	0.023	0.0236	0.0228	0.0229	0.0148	0.0138
0.0239	0.0179	0.0142	0.0187	0.0143	0.01	0.0133	0.0237	0.0231
0.0246	0.0194	0.0109	0.018	0.0113	0.014	0.0138	0.0235	0.024
0.0237	0	0.0189	0.0179	0.0191	0.0172	0.0177	0.023	0.0237
0.0234	0.0184	0.0147	0.017	0.0155	0.0124	0.0132	0.0218	0.0222
0.0233	0.0179	0.0128	0.0174	0.0131	0.0119	0.008	0.0226	0.0222
0.0244	0.0124	0.0194	0.0171	0.0198	0.0156	0.0161	0.0232	0.0237
0.0073	0.0236	0.023	0.0234	0.0231	0.0227	0.0228	0.0145	0.0139
0.0237	0.0182	0.0135	0.018	0.0137	0.0104	0.0119	0.0231	0.0229
0.0229	0.0175	0.0138	0.0172	0.014	0.0116	0.0073	0.0221	0.023
0.0226	0.0184	0.0077	0.0181	0.0078	0.0132	0.0126	0.0219	0.0224
0.0224	0.0173	0.0123	0.0167	0.0123	0.0115	0.0072	0.0215	0.0216
0.0239	0.0179	0.0197	0.009	0.0201	0.0171	0.0176	0.0226	0.0235
0.0237	0.0177	0.0195	0.0088	0.0199	0.0169	0.0175	0.0224	0.0232
0.0247	0.0127	0.0174	0.0171	0.0175	0.0156	0.0153	0.0231	0.0227
0.0602	0.06	0.0596	0.0596	0.0598	0.0587	0.059	0.059	0.0591

18	19	20	21	22	23	24	25	26
0.0235	0.0072	0.0235	0.0235	0.0232	0.024	0.0235	0.0065	0.0064
0.0179	0.0242	0.0179	0.0179	0.0098	0.0114	0.0179	0.024	0.024
0.0182	0.0236	0.0182	0.0182	0.018	0.0176	0.0181	0.0235	0.0236
0.0205	0.0239	0.0205	0.0205	0.0208	0.0204	0.0205	0.0239	0.0238
0.0181	0.0234	0.0181	0.0182	0.0105	0.0119	0.0181	0.0238	0.0238
0.0235	0.0061	0.0235	0.0235	0.0233	0.0236	0.0235	0.0063	0.0062
0.0175	0.0231	0.0175	0.0175	0.0101	0.0116	0.0175	0.0234	0.0234
0.0182	0.024	0.0182	0.0182	0.0114	0.0122	0.0182	0.0243	0.0242
0.0237	0.0066	0.0237	0.0237	0.0234	0.0239	0.0236	0.0069	0.0066
0	0.0232	0	0	0.0179	0.0184	0.0022	0.0234	0.0233
0.0189	0.0246	0.0189	0.0189	0.0139	0.0138	0.0189	0.0236	0.0235
0.0179	0.0236	0.0179	0.0179	0.0177	0.0177	0.0178	0.0236	0.0235
0.0191	0.0252	0.0191	0.0191	0.0144	0.014	0.0191	0.0239	0.0238
0.0172	0.023	0.0172	0.0172	0.011	0.011	0.0172	0.0231	0.023
0.0177	0.0238	0.0177	0.0177	0.0111	0.0116	0.0177	0.0239	0.0238
0.023	0.0151	0.023	0.023	0.023	0.023	0.023	0.0152	0.0151
0.0237	0.0156	0.0237	0.0237	0.0228	0.0231	0.0237	0.0147	0.0146
0	0.0232	0	0	0.0179	0.0184	0.0022	0.0234	0.0233
0.0232	0	0.0232	0.0232	0.0241	0.0241	0.0232	0.0063	0.0062
0	0.0232	0	0	0.0179	0.0184	0.0022	0.0234	0.0233
0	0.0232	0	0	0.0179	0.0184	0.0022	0.0234	0.0234
0.0179	0.0241	0.0179	0.0179	0	0.0119	0.0179	0.0239	0.0241
0.0184	0.0241	0.0184	0.0184	0.0119	0	0.0184	0.0239	0.0238
0.0022	0.0232	0.0022	0.0022	0.0179	0.0184	0	0.0234	0.0233
0.0234	0.0063	0.0234	0.0234	0.0239	0.0239	0.0234	0	0.0003
0.0233	0.0062	0.0233	0.0234	0.0241	0.0238	0.0233	0.0003	0
0.0015	0.0232	0.0015	0.0015	0.0179	0.0184	0.0037	0.0234	0.0234
0.0177	0.0249	0.0177	0.0177	0.0181	0.0175	0.0177	0.0237	0.0236
0.0233	0.007	0.0233	0.0233	0.0239	0.0232	0.0232	0.0069	0.0067
0.0183	0.0247	0.0182	0.0183	0.0182	0.0177	0.0182	0.0235	0.0236
0.0235	0.0064	0.0235	0.0235	0.0232	0.0234	0.0235	0.0062	0.0061
0.0231	0.0074	0.0231	0.0232	0.0243	0.0238	0.0231	0.0071	0.007
0.0179	0.0243	0.0179	0.0179	0.0121	0.0109	0.0179	0.0243	0.0242
0.0194	0.0256	0.0194	0.0194	0.0144	0.0141	0.0194	0.0243	0.0242
0	0.0232	0	0	0.0179	0.0184	0.0022	0.0234	0.0233
0.0184	0.023	0.0184	0.0184	0.0137	0.0096	0.0184	0.0231	0.0231
0.0179	0.0232	0.0179	0.0179	0.0108	0.012	0.0179	0.0234	0.0233
0.0124	0.0251	0.0124	0.0124	0.0166	0.0165	0.0124	0.0246	0.0245
0.0236	0.007	0.0236	0.0236	0.0233	0.0236	0.0236	0.0071	0.007
0.0182	0.0238	0.0182	0.0182	0.01	0.0113	0.0182	0.0241	0.0243
0.0175	0.024	0.0175	0.0175	0.0107	0.0117	0.0175	0.0228	0.0228
0.0184	0.0227	0.0184	0.0184	0.0126	0.0132	0.0183	0.0226	0.0226
0.0174	0.0224	0.0173	0.0174	0.0102	0.0115	0.0173	0.0227	0.0226
0.0179	0.025	0.0179	0.0179	0.0178	0.0176	0.0179	0.0238	0.0237
0.0177	0.0248	0.0177	0.0177	0.0177	0.0175	0.0177	0.0236	0.0236
0.0127	0.0245	0.0127	0.0127	0.016	0.0163	0.0126	0.0248	0.0247
0.06	0.0603	0.06	0.0601	0.0598	0.0597	0.06	0.0602	0.0602

27	28	29	30	31	32	33	34	35
0.0235	0.0241	0.0064	0.0242	0.006	0.0061	0.0235	0.0247	0.0235
0.0179	0.0178	0.0231	0.0179	0.023	0.023	0.0102	0.0137	0.0179
0.0182	0.0076	0.0231	0.0015	0.0229	0.023	0.0184	0.018	0.0182
0.0205	0.0159	0.0235	0.0143	0.0233	0.0247	0.0213	0.0217	0.0205
0.0181	0.0179	0.0227	0.018	0.0233	0.0236	0.0097	0.0142	0.0181
0.0235	0.0226	0.0056	0.0234	0.0063	0.0058	0.0232	0.0238	0.0235
0.0176	0.0165	0.0226	0.0169	0.0225	0.0225	0.0122	0.0136	0.0175
0.0181	0.0171	0.0233	0.0174	0.0228	0.0233	0.0135	0.014	0.0182
0.0237	0.0237	0.0064	0.0234	0.006	0.0071	0.0239	0.0246	0.0237
0.0015	0.0177	0.0233	0.0182	0.0235	0.0231	0.0179	0.0194	0
0.0189	0.0194	0.0231	0.0196	0.0229	0.0235	0.0142	0.0109	0.0189
0.0179	0.0087	0.0235	0.0081	0.0231	0.023	0.0187	0.018	0.0179
0.0191	0.0201	0.0232	0.0202	0.0229	0.0236	0.0143	0.0113	0.0191
0.0172	0.0169	0.0227	0.0168	0.0226	0.0228	0.01	0.014	0.0172
0.0178	0.0171	0.0235	0.0168	0.0225	0.0229	0.0133	0.0138	0.0177
0.023	0.0222	0.0144	0.0227	0.0146	0.0148	0.0237	0.0235	0.023
0.0238	0.0233	0.0134	0.0238	0.0143	0.0138	0.0231	0.024	0.0237
0.0015	0.0177	0.0233	0.0183	0.0235	0.0231	0.0179	0.0194	0
0.0232	0.0249	0.007	0.0247	0.0064	0.0074	0.0243	0.0256	0.0232
0.0015	0.0177	0.0233	0.0182	0.0235	0.0231	0.0179	0.0194	0
0.0015	0.0177	0.0233	0.0183	0.0235	0.0232	0.0179	0.0194	0
0.0179	0.0181	0.0239	0.0182	0.0232	0.0243	0.0121	0.0144	0.0179
0.0184	0.0175	0.0232	0.0177	0.0234	0.0238	0.0109	0.0141	0.0184
0.0037	0.0177	0.0232	0.0182	0.0235	0.0231	0.0179	0.0194	0.0022
0.0234	0.0237	0.0069	0.0235	0.0062	0.0071	0.0243	0.0243	0.0234
0.0234	0.0236	0.0067	0.0236	0.0061	0.007	0.0242	0.0242	0.0233
0	0.0177	0.0233	0.0183	0.0235	0.0232	0.0179	0.0194	0.0015
0.0177	0	0.0238	0.0099	0.0224	0.0231	0.019	0.0189	0.0177
0.0233	0.0238	0	0.0232	0.006	0.0077	0.0242	0.0238	0.0233
0.0183	0.0099	0.0232	0	0.0229	0.0231	0.0184	0.0192	0.0183
0.0235	0.0224	0.006	0.0229	0	0.0059	0.0232	0.0232	0.0235
0.0232	0.0231	0.0077	0.0231	0.0059	0	0.025	0.0242	0.0231
0.0179	0.019	0.0242	0.0184	0.0232	0.025	0	0.0149	0.0179
0.0194	0.0189	0.0238	0.0192	0.0232	0.0242	0.0149	0	0.0194
0.0015	0.0177	0.0233	0.0183	0.0235	0.0231	0.0179	0.0194	0
0.0184	0.0173	0.0228	0.0177	0.0229	0.0232	0.0124	0.0151	0.0184
0.0179	0.0174	0.0228	0.0172	0.0229	0.0232	0.0121	0.0141	0.0179
0.0124	0.0186	0.0238	0.0185	0.0232	0.0237	0.0178	0.02	0.0124
0.0236	0.0228	0.0067	0.023	0.0017	0.0069	0.0235	0.0237	0.0236
0.0182	0.0176	0.0232	0.018	0.0235	0.0236	0.0092	0.0139	0.0182
0.0175	0.0184	0.0225	0.0179	0.0224	0.023	0.0119	0.0145	0.0175
0.0184	0.018	0.0222	0.0178	0.0221	0.0225	0.0131	0.0092	0.0184
0.0174	0.0166	0.022	0.0166	0.0223	0.0223	0.0117	0.0133	0.0174
0.0179	0.0013	0.0233	0.0101	0.0225	0.0232	0.0183	0.0193	0.0179
0.0177	0.0011	0.0231	0.0099	0.0223	0.023	0.0181	0.0192	0.0177
0.0127	0.0171	0.024	0.0169	0.0234	0.0236	0.0175	0.0182	0.0127
0.0601	0.0594	0.0602	0.0587	0.0596	0.0604	0.0608	0.0595	0.06

36	37	38	39	40	41	42	43	44
0.0234	0.0234	0.0245	0.007	0.0238	0.0235	0.0226	0.0224	0.0243
0.0129	0.0109	0.0168	0.0235	0.0094	0.0108	0.0129	0.0103	0.0182
0.0177	0.0172	0.0172	0.023	0.018	0.0165	0.0176	0.0166	0.0078
0.0198	0.02	0.0215	0.0237	0.0205	0.0202	0.0209	0.0194	0.0154
0.0134	0.0119	0.017	0.0238	0.0084	0.0113	0.0133	0.0112	0.018
0.0231	0.0229	0.0233	0.0065	0.0235	0.0228	0.0223	0.0223	0.0227
0.0127	0.0072	0.0159	0.0226	0.0119	0.0072	0.0125	0.0069	0.017
0.0132	0.0069	0.0165	0.0233	0.0123	0.0078	0.0126	0.0073	0.0175
0.0234	0.0233	0.0244	0.0073	0.0237	0.0229	0.0226	0.0224	0.0239
0.0184	0.0179	0.0124	0.0236	0.0182	0.0175	0.0184	0.0173	0.0179
0.0147	0.0128	0.0194	0.023	0.0135	0.0138	0.0077	0.0123	0.0197
0.017	0.0174	0.0171	0.0234	0.018	0.0172	0.0181	0.0167	0.009
0.0155	0.0131	0.0198	0.0231	0.0137	0.014	0.0078	0.0123	0.0201
0.0124	0.0119	0.0156	0.0227	0.0104	0.0116	0.0132	0.0115	0.0171
0.0132	0.008	0.0161	0.0228	0.0119	0.0073	0.0126	0.0072	0.0176
0.0218	0.0226	0.0232	0.0145	0.0231	0.0221	0.0219	0.0215	0.0226
0.0222	0.0222	0.0237	0.0139	0.0229	0.023	0.0224	0.0216	0.0235
0.0184	0.0179	0.0124	0.0236	0.0182	0.0175	0.0184	0.0174	0.0179
0.023	0.0232	0.0251	0.007	0.0238	0.024	0.0227	0.0224	0.025
0.0184	0.0179	0.0124	0.0236	0.0182	0.0175	0.0184	0.0173	0.0179
0.0184	0.0179	0.0124	0.0236	0.0182	0.0175	0.0184	0.0174	0.0179
0.0137	0.0108	0.0166	0.0233	0.01	0.0107	0.0126	0.0102	0.0178
0.0096	0.012	0.0165	0.0236	0.0113	0.0117	0.0132	0.0115	0.0176
0.0184	0.0179	0.0124	0.0236	0.0182	0.0175	0.0183	0.0173	0.0179
0.0231	0.0234	0.0246	0.0071	0.0241	0.0228	0.0226	0.0227	0.0238
0.0231	0.0233	0.0245	0.007	0.0243	0.0228	0.0226	0.0226	0.0237
0.0184	0.0179	0.0124	0.0236	0.0182	0.0175	0.0184	0.0174	0.0179
0.0173	0.0174	0.0186	0.0228	0.0176	0.0184	0.018	0.0166	0.0013
0.0228	0.0228	0.0238	0.0067	0.0232	0.0225	0.0222	0.022	0.0233
0.0177	0.0172	0.0185	0.023	0.018	0.0179	0.0178	0.0166	0.0101
0.0229	0.0229	0.0232	0.0017	0.0235	0.0224	0.0221	0.0223	0.0225
0.0232	0.0232	0.0237	0.0069	0.0236	0.023	0.0225	0.0223	0.0232
0.0124	0.0121	0.0178	0.0235	0.0092	0.0119	0.0131	0.0117	0.0183
0.0151	0.0141	0.02	0.0237	0.0139	0.0145	0.0092	0.0133	0.0193
0.0184	0.0179	0.0124	0.0236	0.0182	0.0175	0.0184	0.0174	0.0179
0	0.0134	0.017	0.023	0.013	0.0127	0.014	0.0124	0.0175
0.0134	0	0.0162	0.0234	0.0123	0.0077	0.013	0.0074	0.0174
0.017	0.0162	0	0.0236	0.0165	0.0176	0.0176	0.0158	0.0194
0.023	0.0234	0.0236	0	0.0237	0.0228	0.0222	0.0224	0.0229
0.013	0.0123	0.0165	0.0237	0	0.0123	0.0135	0.012	0.0178
0.0127	0.0077	0.0176	0.0228	0.0123	0	0.0126	0.0071	0.0186
0.014	0.013	0.0176	0.0222	0.0135	0.0126	0	0.0125	0.0182
0.0124	0.0074	0.0158	0.0224	0.012	0.0071	0.0125	0	0.0167
0.0175	0.0174	0.0194	0.0229	0.0178	0.0186	0.0182	0.0167	0
0.0173	0.0173	0.0192	0.0227	0.0176	0.0185	0.018	0.0166	0.0006
0.0169	0.0157	0.0036	0.0239	0.0165	0.0156	0.017	0.015	0.0175
0.0598	0.0593	0.0598	0.0597	0.0595	0.0583	0.0588	0.0582	0.0594

45	46	47
0.0241	0.0241	0.0601
0.0181	0.0163	0.0598
0.0076	0.0169	0.0586
0.0153	0.0211	0.0574
0.0179	0.0169	0.0592
0.0226	0.0236	0.06
0.0169	0.015	0.0589
0.0174	0.0157	0.0594
0.0237	0.0247	0.0602
0.0177	0.0127	0.06
0.0195	0.0174	0.0596
0.0088	0.0171	0.0596
0.0199	0.0175	0.0598
0.0169	0.0156	0.0587
0.0175	0.0153	0.059
0.0224	0.0231	0.059
0.0232	0.0227	0.0591
0.0177	0.0127	0.06
0.0248	0.0245	0.0603
0.0177	0.0127	0.06
0.0177	0.0127	0.0601
0.0177	0.016	0.0598
0.0175	0.0163	0.0597
0.0177	0.0126	0.06
0.0236	0.0248	0.0602
0.0236	0.0247	0.0602
0.0177	0.0127	0.0601
0.0011	0.0171	0.0594
0.0231	0.024	0.0602
0.0099	0.0169	0.0587
0.0223	0.0234	0.0596
0.023	0.0236	0.0604
0.0181	0.0175	0.0608
0.0192	0.0182	0.0595
0.0177	0.0127	0.06
0.0173	0.0169	0.0598
0.0173	0.0157	0.0593
0.0192	0.0036	0.0598
0.0227	0.0239	0.0597
0.0176	0.0165	0.0595
0.0185	0.0156	0.0583
0.018	0.017	0.0588
0.0166	0.015	0.0582
0.0006	0.0175	0.0594
0	0.0173	0.0592
0.0173	0	0.0599
0.0592	0.0599	0

Table S2. The recombination rates of all internal and external nodes.

Node	Recombination	r/m	ρ/θ
157	0	0	0
9912D	159	0.692641	0.009575
9D-6	37	0.111712	0.002944
AS43.3	40	0.134269	0.003189
B25	16	0.137322	0.002743
BIM B-439D	22	0.104547	0.003087
BS-37	35	0.140092	0.003916
CAU B946	12	0.07926	0.00185
CBMB205	0	0	0
CC09	2	0.130631	0.009009
CN026	53	0.221981	0.00547
DSYZ	0	0	0
G341	32	0.134174	0.003418
GFP-2	25	0.068183	0.001598
GH1-13	17	0.058443	0.001468
GQJK49	1	1.4	0.2
JJ-D43	17	0.103872	0.002582
JT3-1	1	1.66667	0.166667
JTYP2	0	0	0
L-1	1	0.352941	0.058824
L-H15	1	0.352941	0.058824
L-S60	1	0.380952	0.047619
LABIM40	26	0.088107	0.002698
LDO2	1	3.5	0.5
LS69	0	0	0
Lzh-a42	0	0	0
M75	38	0.230727	0.005167
NAU-B3	58	45.24691	0.716049
NJAU-Z9	0	0	0
NJN-6	16	0.094591	0.002242
NKG-1	19	0.051403	0.001524
QST713	94	0.59074	0.010615
FZB42	46	0.098627	0.002664
S141	56	0.018103	0.003931
S3-1	1	3	0.5
SB1216	27	0.145256	0.004047
SQR9	67	55.50685	0.917808
T20E-257	69	28.69643	0.410714
TrigoCor 1448	11	0.040025	0.001156
UCMB5033	44	0.15632	0.003953
UCMB5036	49	0.246915	0.004616

UCMB5113	35	0.139276	0.003814
W1	0	0	0
WRN014	32	0.158671	0.003838
YAU B9601-Y2	6	1.538462	0.230769
YJ11-1-4	72	52.09524	0.685714
1	29	0.189734	0.003478
2	44	0.210573	0.004291
3	34	0.080129	0.001707
4	30	0.045308	0.001362
5	28	0.130364	0.003049
6	23	0.125414	0.002724
7	19	0.133727	0.003736
8	18	0.130577	0.002953
9	23	0.138436	0.003507
10	34	0.141924	0.0037
11	29	0.146757	0.003129
12	9	0.025948	0.000719
13	17	0.096897	0.002235
14	28	0.105647	0.002917
15	13	0.09578	0.002427
16	11	0.070286	0.001832
17	21	0.052782	0.001427
18	81	0.82327	0.013218
19	0	0	0
20	0	0	0
21	0	0	0
22	0	0	0
23	0	0	0
24	41	0.063587	0.001682
25	26	0.032036	0.000917
26	16	0.042405	0.001271
27	1	0.08	0.02
28	26	0.11361	0.002531
29	20	0.095056	0.002316
30	17	0.072748	0.001525
31	20	0.098681	0.002963
32	33	0.082911	0.002089
33	35	0.083722	0.002235
34	30	0.07799	0.001793
35	11	0.059784	0.001562
36	16	0.102659	0.002275
37	24	0.162504	0.003368
38	11	0.065761	0.002199

39	14	0.079207	0.001839
40	28	0.164555	0.003814
41	16	0.122511	0.003219
42	7	0.068711	0.002064
43	43	0.077473	0.001947
44	61	0.058777	0.001449

Table S3. The gene clusters of 46 *Bacillus velezensis* strains.

	Type	From	To	Lengths(bp)	Gene Num	Most similar known clusters	
<i>Bacillus velezensis</i> WRN014	Transatpks-Nrps	195568	273296	77729	48	Locillomycin biosynthetic gene cluster (35% of genes show similarity)	
	Nrps	342883	408290	65408	44	Surfactin biosynthetic gene cluster (82% of genes show similarity)	
	Otherks	977523	1018767	41245	43	Butirosin biosynthetic gene cluster (7% of genes show similarity)	
	Terpene	1100790	1121530	20741	24	-	
	Lantipeptide	1240233	1269122	28890	34	-	
	Transatpks	1435403	1521287	85885	44	Macrolactin biosynthetic gene cluster (100% of genes show similarity)	
	Transatpks-Nrps	1747406	1850098	102693	46	Bacillaene biosynthetic gene cluster (100% of genes show similarity)	
	Transatpks-Nrps	1905551	2043380	137830	64	Fengycin biosynthetic gene cluster (100% of genes show similarity)	
	Terpene	2065949	2087832	21884	24	-	
	T3pks	2156476	2197576	41101	61	-	
	Transatpks	2447625	2548063	100439	53	Difficidin biosynthetic gene cluster (100% of genes show similarity)	
	Bacteriocin-Nrps	3164646	3231439	66794	64	Bacillibactin biosynthetic gene cluster (100% of genes show similarity)	
	Other	3729239	3770657	41419	43	Bacilysin biosynthetic gene cluster (100% of genes show similarity)	
<i>Bacillus velezensis</i> AS43.3	Nrps	314462	379869	65408	43	Surfactin biosynthetic gene cluster(91% of genes show similarity)	
	Ladderane	668442	709563	41122	45	-	
	Otherks	949307	990551	41245	43	Butirosin biosynthetic gene cluster (7% of genes show similarity)	
	Terpene	1073379	1094119	20741	24	-	
	Transatpks	1436569	1522465	85897	44	Macrolactin biosynthetic gene cluster (100% of genes show similarity)	
	Transatpks-Nrps	1748582	1851260	102679	47	Bacillaene biosynthetic genecluster (100% of genes show similarity)	
	Transatpks-Nrps	1912742	2051827	139086	67	Fengycin biosynthetic gene cluster (100% of genes show similarity)	
	Terpene	2076553	2098436	21884	24	-	
	T3pks	2160610	2201710	41101	51	-	
	Transatpks	2317252	2417701	100450	52	Difficidin biosynthetic gene cluster (100% of genes show similarity)	
	Bacteriocin-Nrps	3033972	3100762	66791	64	Bacillibactin biosynthetic gene cluster (100% of genes show similarity)	
	Otherks	3611422	3652840	41419	43	Bacilysin biosynthetic gene cluster (100% of genes show similarity)	
	<i>Bacillus velezensis</i> CAU B946	Nrps	309519	374926	65408	43	Surfactin biosynthetic gene cluster (78% of genes show similarity)
Otherks		985055	1026299	41245	44	Butirosin biosynthetic gene cluster (7% of genes show similarity)	
Terpene		1108333	1129073	20741	24	-	
Transatpks		1428911	1514795	85885	44	Macrolactin biosynthetic gene cluster (100% of genes show similarity)	
Transatpks-Nrps		1740952	1843644	102693	46	Bacillaene biosynthetic gene cluster (100% of genes show similarity)	
Transatpks-Nrps		1900208	2038037	137830	70	Fengycin biosynthetic gene cluster (100% of genes show similarity)	
Terpene		2102542	2124425	21884	24	-	
T3pks		2195247	2236347	41101	53	-	
Transatpks		2351850	2447294	95445	49	Difficidin biosynthetic gene cluster (100% of genes show similarity)	
Bacteriocin-Nrps		3116937	3183730	66794	64	Bacillibactin biosynthetic gene cluster (100% of genes show similarity)	
Other		3693616	3735034	41419	44	Bacilysin biosynthetic gene cluster (100% of genes show similarity)	
<i>Bacillus velezensis</i> G341		Nrps	323383	388790	65408	42	Surfactin biosynthetic gene cluster (91% of genes show similarity)
		Otherks	961935	1003179	41245	43	Butirosin biosynthetic gene cluster (7% of genes show similarity)
	Lantipeptide-Terpi	1086531	1132426	45896	56	-	
	Transatpks	1405779	1491672	85894	44	Macrolactin biosynthetic gene cluster (100% of genes show similarity)	
	Transatpks-Nrps	1721337	1824035	102699	48	Bacillaene biosynthetic gene cluster (100% of genes show similarity)	
	Transatpks-Nrps	1884367	2023498	139132	64	Fengycin_biosynthetic_gene_cluster (100% of genes show similarity)	
	Terpene	2048791	2070674	21884	24	-	
	T3pks	2133040	2174140	41101	47	-	
	Transatpks	2332225	2432675	100451	52	Difficidin_biosynthetic_gene_cluster (100% of genes show similarity)	
	Bacteriocin-Nrps	3056128	3122922	66795	64	Bacillibactin_biosynthetic_gene_cluster (100% of genes show similarity)	
	Other	3665643	3707061	41419	43	Bacilysin_biosynthetic_gene_cluster (100% of genes show similarity)	
	<i>Bacillus velezensis</i> FZB42	Nrps	322618	388025	65408	42	Surfactin_biosynthetic_gene_cluster (91% of genes show similarity)
		Otherks	940737	981981	41245	43	Butirosin_biosynthetic_gene_cluster (7% of genes show similarity)
Terpene		1064781	1085521	20741	24	-	
Transatpks		1374169	1460068	85900	43	Macrolactin_biosynthetic_gene_cluster (100% of genes show similarity)	
Transatpks-Nrps		1688756	1791439	102684	47	Bacillaene_biosynthetic_gene_cluster (100% of genes show similarity)	
Transatpks-Nrps		1851172	1988997	137826	64	Fengycin_biosynthetic_gene_cluster (100% of genes show similarity)	
Terpene		2014214	2036097	21884	23	-	
T3pks		2102584	2143684	41101	49	-	
Transatpks		2260090	2360537	100448	52	Difficidin_biosynthetic_gene_cluster (100% of genes show similarity)	
Nrps		2848410	2904220	55811	45	-	
Bacteriocin-Nrps		3001250	3068041	66792	64	Bacillibactin_biosynthetic_gene_cluster (100% of genes show similarity)	
Other		3576267	3617685	41419	44	Bacilysin_biosynthetic_gene_cluster (100% of genes show similarity)	
<i>Bacillus velezensis</i> JTYP2		Nrps	322611	388018	65408	42	Surfactin_biosynthetic_gene_cluster (82% of genes show similarity)
	Otherks	924466	965710	41245	43	Butirosin_biosynthetic_gene_cluster (7% of genes show similarity)	
	Terpene	1047754	1068494	20741	26	-	
	Lantipeptide	1188985	1217873	28889	36	-	
	Transatpks	1386763	1472667	85905	46	Macrolactin_biosynthetic_gene_cluster (100% of genes show similarity)	
	Transatpks-Nrps	1698777	1801451	102675	47	Bacillaene_biosynthetic_gene_cluster (100% of genes show similarity)	
	Transatpks-Nrps	1866081	2003882	137802	64	Fengycin_biosynthetic_gene_cluster (100% of genes show similarity)	
	Terpene	2029109	2050992	21884	24	-	
	T3pks	2114311	2155411	41101	51	-	
	Transatpks	2270398	2370851	100454	52	Difficidin_biosynthetic_gene_cluster (100% of genes show similarity)	
	Bacteriocin-Nrps	3001284	3068076	66793	65	Bacillibactin_biosynthetic_gene_cluster (100% of genes show similarity)	
	Other	3589387	3630805	41419	43	Bacilysin_biosynthetic_gene_cluster (100% of genes show similarity)	
	<i>Bacillus velezensis</i> CC09	Bacteriocin-Trans:	1	128284	128284	65	Fengycin_biosynthetic_gene_cluster (93% of genes show similarity)

	Transatpks-Nrps	184844	287527	102684	47 Bacillaene_biosynthetic_gene_cluster (100% of genes show similarity)
	Transatpks	519293	605180	85888	42 Macrolactin_biosynthetic_gene_cluster (100% of genes show similarity)
	Terpene	922122	942862	20741	24 -
	Otherks	1025640	1066884	41245	43 Butirosin_biosynthetic_gene_cluster (7% of genes show similarity)
	Nrps	1606358	1671765	65408	41 Surfactin_biosynthetic_gene_cluster (91% of genes show similarity)
	Transatpks-Nrps	1749447	1827177	77731	49 Rhizoctcin_biosynthetic_gene_cluster (22% of genes show similarity)
	Other	2316452	2357870	41419	44 Bacilysin_biosynthetic_gene_cluster (100% of genes show similarity)
	Nrps	2563105	2623110	60006	39 -
	Bacteriocin-Nrps	2901026	2967820	66795	64 Bacillibactin_biosynthetic_gene_cluster (100% of genes show similarity)
	Transatpks	3598055	3698505	100451	54 Difficidin_biosynthetic_gene_cluster (100% of genes show similarity)
	T3pks	3952892	3993992	41101	66 -
	Terpene	4059090	4080973	21884	24 -
<i>Bacillus velezensis</i> LS69	Nrps	299263	364670	65408	42 Surfactin_biosynthetic_gene_cluster (82% of genes show similarity)
	Otherks	900856	942100	41245	43 Butirosin_biosynthetic_gene_cluster (7% of genes show similarity)
	Terpene	1024144	1044884	20741	25 -
	Lantipeptide	1165377	1194265	28889	36 -
	Transatpks	1363156	1449061	85906	44 Macrolactin_biosynthetic_gene_cluster (100% of genes show similarity)
	Transatpks-Nrps	1675171	1777845	102675	47 Bacillaene_biosynthetic_gene_cluster (100% of genes show similarity)
	Transatpks-Nrps	1842476	1980277	137802	64 Fengycin_biosynthetic_gene_cluster (100% of genes show similarity)
	Terpene	2005504	2027387	21884	24 -
	T3pks	2090705	2131805	41101	51 -
	Transatpks	2246791	2347244	100454	52 Difficidin_biosynthetic_gene_cluster (100% of genes show similarity)
	Bacteriocin-Nrps	2977677	3044468	66792	64 Bacillibactin_biosynthetic_gene_cluster (100% of genes show similarity)
	Other	3565778	3607196	41419	43 Bacilysin_biosynthetic_gene_cluster (100% of genes show similarity)
<i>Bacillus velezensis</i> GFP-2	T3pks	46817	87917	41101	46 -
	Transatpks	245325	345775	100451	52 Difficidin_biosynthetic_gene_cluster (100% of genes show similarity)
	Nrps	491094	543158	52065	52 -
	Bacteriocin-Nrps	998363	1065156	66794	71 Bacillibactin_biosynthetic_gene_cluster (100% of genes show similarity)
	Lantipeptide	1216587	1243248	26662	29 -
	Nrps	1567487	1651666	84180	70 Bacilysin_biosynthetic_gene_cluster (100% of genes show similarity)
	Nrps	2240948	2306355	65408	44 Surfactin_biosynthetic_gene_cluster (91% of genes show similarity)
	Bacteriocin	2321884	2332735	10852	10 -
	Otherks	2868521	2909765	41245	43 Butirosin_biosynthetic_gene_cluster (7% of genes show similarity)
	Terpene	2993982	3014722	20741	24 -
	Transatpks	3299302	3385177	85876	42 Macrolactin_biosynthetic_gene_cluster (100% of genes show similarity)
	Transatpks-Nrps	3615570	3718271	102702	47 Bacillaene_biosynthetic_gene_cluster (100% of genes show similarity)
	Transatpks-Nrps	3773675	3911526	137852	63 Fengycin_biosynthetic_gene_cluster (100% of genes show similarity)
	Terpene	3935979	3957862	21884	23 -
<i>Bacillus velezensis</i> GQJK49	Nrps	322336	387743	65408	42 Surfactin_biosynthetic_gene_cluster (82% of genes show similarity)
	Otherks	924186	965430	41245	43 Butirosin_biosynthetic_gene_cluster (7% of genes show similarity)
	Terpene	1047472	1068212	20741	25 -
	Lantipeptide	1188705	1217593	28889	37 -
	Transatpks	1386480	1472385	85906	44 Macrolactin_biosynthetic_gene_cluster (100% of genes show similarity)
	Transatpks-Nrps	1698494	1801168	102675	47 Bacillaene_biosynthetic_gene_cluster (100% of genes show similarity)
	Transatpks-Nrps	1865799	2003599	137801	65 Fengycin_biosynthetic_gene_cluster (100% of genes show similarity)
	Terpene	2028826	2050709	21884	24 -
	T3pks	2114027	2155127	41101	51 -
	Transatpks	2270111	2370563	100453	53 Difficidin_biosynthetic_gene_cluster (100% of genes show similarity)
	Bacteriocin-Nrps	3000986	3067777	66792	64 Bacillibactin_biosynthetic_gene_cluster (100% of genes show similarity)
	Other	3589086	3630504	41419	43 Bacilysin_biosynthetic_gene_cluster (100% of genes show similarity)
<i>Bacillus velezensis</i> CN026	Nrps	285731	351138	65408	42 Surfactin_biosynthetic_gene_cluster (82% of genes show similarity)
	Phosphonate	596266	637150	40885	38 -
	Otherks	915659	956903	41245	43 Butirosin_biosynthetic_gene_cluster (7% of genes show similarity)
	Terpene	1039597	1060337	20741	24 -
	Transatpks	1366572	1452474	85903	44 Macrolactin_biosynthetic_gene_cluster (100% of genes show similarity)
	Transatpks-Nrps	1680102	1782785	102684	49 Bacillaene_biosynthetic_gene_cluster (100% of genes show similarity)
	Transatpks-Nrps	1842381	1980212	137832	66 Fengycin_biosynthetic_gene_cluster (100% of genes show similarity)
	Terpene	2003750	2025633	21884	24 -
	T3pks	2090245	2131345	41101	45 -
	Transatpks	2288919	2389363	100445	52 Difficidin_biosynthetic_gene_cluster (100% of genes show similarity)
	Bacteriocin-Nrps	3032172	3098966	66795	64 Bacillibactin_biosynthetic_gene_cluster (100% of genes show similarity)
	Nrps	3364167	3429509	65343	40 -
	Other	3630234	3671652	41419	43 Bacilysin_biosynthetic_gene_cluster (100% of genes show similarity)
<i>Bacillus velezensis</i> JJ-D43	Nrps	304367	369774	65408	43 Surfactin_biosynthetic_gene_cluster (78% of genes show similarity)
	Thiopeptide	585268	613524	28257	24 Kjanimicin_biosynthetic_gene_cluster (4% of genes show similarity)
	Otherks	932347	973591	41245	43 Butirosin_biosynthetic_gene_cluster (7% of genes show similarity)
	Terpene	1055618	1076358	20741	24 -
	Transatpks	1376789	1462676	85888	44 Macrolactin_biosynthetic_gene_cluster (100% of genes show similarity)
	Transatpks-Nrps	1688836	1791528	102693	46 Bacillaene_biosynthetic_gene_cluster (100% of genes show similarity)
	Transatpks-Nrps	1848173	1986005	137833	67 Fengycin_biosynthetic_gene_cluster (100% of genes show similarity)
	Terpene	2048975	2070858	21884	24 -
	T3pks	2143670	2184770	41101	64 -
	Transatpks	2435109	2535559	100451	52 Difficidin_biosynthetic_gene_cluster (100% of genes show similarity)
	Bacteriocin-Nrps	3212836	3279628	66793	63 Bacillibactin_biosynthetic_gene_cluster (100% of genes show similarity)

	Other	3781918	3823336	41419	44 Bacilysin_biosynthetic_gene_cluster (100% of genes show similarity)
<i>Bacillus velezensis</i> L-1	Bacteriocin-Nrps	74354	141147	66794	64 Bacillibactin_biosynthetic_gene_cluster (100% of genes show similarity)
	Other	652052	693470	41419	43 Bacilysin_biosynthetic_gene_cluster (100% of genes show similarity)
	Nrps	1330801	1396208	65408	42 Surfactin_biosynthetic_gene_cluster (91% of genes show similarity)
	Otherks	1962395	2003639	41245	43 Butirosin_biosynthetic_gene_cluster (7% of genes show similarity)
	Terpene	2087709	2108449	20741	24 -
	Transatpks	2415108	2501013	85906	44 Macrolactin_biosynthetic_gene_cluster (100% of genes show similarity)
	Transatpks-Nrps	2728311	2831000	102690	47 Bacillaene_biosynthetic_gene_cluster (100% of genes show similarity)
	Transatpks-Nrps	2893705	3031528	137824	65 Fengycin_biosynthetic_gene_cluster (100% of genes show similarity)
	Terpene	3095309	3117192	21884	24 -
	T3pks	3180177	3221277	41101	51 -
	Transatpks	3338138	3438587	100450	51 Difficidin_biosynthetic_gene_cluster (100% of genes show similarity)
	<i>Bacillus velezensis</i> M75	Nrps	304602	370009	65408
Thiopeptide		590029	618291	28263	24 Kijanamicin_biosynthetic_gene_cluster (4% of genes show similarity)
Otherks		922799	964043	41245	43 Butirosin_biosynthetic_gene_cluster (7% of genes show similarity)
Terpene		1046077	1066817	20741	24 -
Lantipeptide		1251572	1280461	28890	36 -
Transatpks		1450432	1536316	85885	42 Macrolactin_biosynthetic_gene_cluster (100% of genes show similarity)
Transatpks-Nrps		1765155	1867856	102702	46 Bacillaene_biosynthetic_gene_cluster (100% of genes show similarity)
Transatpks-Nrps		1925320	2063149	137830	67 Fengycin_biosynthetic_gene_cluster (100% of genes show similarity)
Terpene		2127509	2149392	21884	24 -
T3pks		2218023	2259123	41101	52 -
Transatpks		2374615	2475062	100448	52 Difficidin_biosynthetic_gene_cluster (100% of genes show similarity)
Bacteriocin-Nrps		3104275	3171066	66792	64 Bacillibactin_biosynthetic_gene_cluster (100% of genes show similarity)
Other	3676454	3717872	41419	44 Bacilysin_biosynthetic_gene_cluster (100% of genes show similarity)	
<i>Bacillus velezensis</i> Lzh-a42	Nrps	315164	380575	65412	43 Surfactin_biosynthetic_gene_cluster (82% of genes show similarity)
	Phosphonate	626400	667284	40885	38 -
	Otherks	943006	984250	41245	43 Butirosin_biosynthetic_gene_cluster (7% of genes show similarity)
	Terpene	1066566	1087306	20741	24 -
	Transatpks	1376401	1462303	85903	44 Macrolactin_biosynthetic_gene_cluster (100% of genes show similarity)
	Transatpks-Nrps	1733668	1836348	102681	50 Bacillaene_biosynthetic_gene_cluster (100% of genes show similarity)
	Transatpks-Nrps	2040534	2178364	137831	65 Fengycin_biosynthetic_gene_cluster (100% of genes show similarity)
	Terpene	2204038	2225921	21884	26 -
	T3pks	2276225	2317325	41101	46 -
	Transatpks	2475681	2576125	100445	52 Difficidin_biosynthetic_gene_cluster (100% of genes show similarity)
	Bacteriocin-Nrps	3286321	3353117	66797	64 Bacillibactin_biosynthetic_gene_cluster (100% of genes show similarity)
	Nrps	3619229	3687649	68421	39 -
Other	3889874	3931292	41419	43 Bacilysin_biosynthetic_gene_cluster (100% of genes show similarity)	
Lantipeptide	4085555	4109539	23985	21 Mersacidin_biosynthetic_gene_cluster (100% of genes show similarity)	
<i>Bacillus velezensis</i> SQR9	Nrps	305671	371078	65408	41 Surfactin_biosynthetic_gene_cluster (78% of genes show similarity)
	Transatpks-T1pks	642183	752892	110710	55 Phormidolide_biosynthetic_gene_cluster (26% of genes show similarity)
	Otherks	974878	1016122	41245	43 Butirosin_biosynthetic_gene_cluster (7% of genes show similarity)
	Terpene	1098901	1119641	20741	25 -
	Transatpks	1400903	1486793	85891	44 Macrolactin_biosynthetic_gene_cluster (100% of genes show similarity)
	Transatpks-Nrps	1712866	1815537	102672	47 Bacillaene_biosynthetic_gene_cluster (100% of genes show similarity)
	Transatpks-Nrps	1878029	2015842	137814	66 Fengycin_biosynthetic_gene_cluster (100% of genes show similarity)
	Terpene	2081350	2103233	21884	24 -
	T3pks	2289682	2330782	41101	46 -
	Transatpks	2489289	2589742	100454	53 Difficidin_biosynthetic_gene_cluster (100% of genes show similarity)
	Bacteriocin-Nrps	3207313	3274104	66792	64 Bacillibactin_biosynthetic_gene_cluster (100% of genes show similarity)
	Other	3778450	3819868	41419	43 Bacilysin_biosynthetic_gene_cluster (100% of genes show similarity)
<i>Bacillus velezensis</i> NJN-6	Transatpks-Nrps	192212	269935	77724	49 Rhizoctin_biosynthetic_gene_cluster (22% of genes show similarity)
	Nrps	339237	404643	65407	44 Surfactin_biosynthetic_gene_cluster (78% of genes show similarity)
	Otherks	1001702	1042946	41245	43 Butirosin_biosynthetic_gene_cluster (7% of genes show similarity)
	Terpene	1124967	1145707	20741	24 -
	Lantipeptide	1280569	1309458	28890	35 -
	Transatpks	1475517	1561404	85888	42 Macrolactin_biosynthetic_gene_cluster (100% of genes show similarity)
	Transatpks-Nrps	1792248	1894952	102705	47 Bacillaene_biosynthetic_gene_cluster (100% of genes show similarity)
	Transatpks-Nrps	1949547	2087375	137829	67 Fengycin_biosynthetic_gene_cluster (100% of genes show similarity)
	Terpene	2150757	2172640	21884	24 -
	T3pks	2241267	2282367	41101	47 -
	Transatpks	2441302	2541740	100439	53 Difficidin_biosynthetic_gene_cluster (100% of genes show similarity)
	Bacteriocin-Nrps	3157056	3223848	66793	64 Bacillibactin_biosynthetic_gene_cluster (100% of genes show similarity)
Other	3730009	3771427	41419	44 Bacilysin_biosynthetic_gene_cluster (100% of genes show similarity)	
<i>Bacillus velezensis</i> UCMB5113	Lantipeptide	198217	220832	22616	21 Locillomycin_biosynthetic_gene_cluster (35% of genes show similarity)
	Nrps	320804	386211	65408	41 Surfactin_biosynthetic_gene_cluster (91% of genes show similarity)
	Ladderane	677016	718137	41122	47 -
	Otherks	927210	968454	41245	43 Butirosin_biosynthetic_gene_cluster (7% of genes show similarity)
	Terpene	1051782	1072522	20741	24 -
	Transatpks	1378143	1464042	85900	44 Macrolactin_biosynthetic_gene_cluster (100% of genes show similarity)
	Transatpks-Nrps	1692431	1795129	102699	47 Bacillaene_biosynthetic_gene_cluster (100% of genes show similarity)
	Transatpks-Nrps	1854083	1991931	137849	63 Fengycin_biosynthetic_gene_cluster (100% of genes show similarity)
	Terpene	2014953	2036836	21884	24 -
	T3pks	2087237	2128337	41101	49 -

	Transatpks	2244146	2344599	100454	52 Difficidin biosynthetic gene cluster (100% of genes show similarity)
	Nrps	2489905	2541971	52067	47 -
	Bacteriocin-Nrps	2994397	3061190	66794	64 Bacillibactin biosynthetic gene cluster (100% of genes show similarity)
	Other	3561785	3603203	41419	43 Bacilysin biosynthetic gene cluster (100% of genes show similarity)
<i>Bacillus velezensis</i> UCMB5033	Transatpks-Nrps	189466	258694	69229	39 Locillomycin biosynthetic gene cluster (100% of genes show similarity)
	Nrps	353462	418869	65408	41 Surfactin biosynthetic gene cluster (91% of genes show similarity)
	Otherks	969144	1010388	41245	43 Butirosin biosynthetic gene cluster (7% of genes show similarity)
	Terpene	1093740	1114480	20741	24 -
	Transatpks	1416133	1502029	85897	44 Macrolactin biosynthetic gene cluster (100% of genes show similarity)
	Transatpks-Nrps	1730420	1833115	102696	47 Bacillaene biosynthetic gene cluster (100% of genes show similarity)
	Transatpks-Nrps	1893475	2015911	122437	60 Fengycin biosynthetic gene cluster (93% of genes show similarity)
	Terpene	2041207	2063090	21884	24 -
	T3pks	2124324	2165424	41101	60 -
	Transatpks	2419654	2520104	100451	53 Difficidin biosynthetic gene cluster (100% of genes show similarity)
	Bacteriocin-Nrps	3151235	3218027	66793	64 Bacillibactin biosynthetic gene cluster (100% of genes show similarity)
	Other	3730537	3771955	41419	43 Bacilysin biosynthetic gene cluster (100% of genes show similarity)
<i>Bacillus velezensis</i> TrigoCor14	Nrps	327534	392941	65408	43 Surfactin biosynthetic gene cluster (91% of genes show similarity)
	Otherks	962102	1003346	41245	43 Butirosin biosynthetic gene cluster (7% of genes show similarity)
	Terpene	1086147	1106887	20741	24 -
	Transatpks	1415172	1501077	85906	44 Macrolactin biosynthetic gene cluster (100% of genes show similarity)
	Transatpks-Nrps	1728481	1831173	102693	47 Bacillaene biosynthetic gene cluster (100% of genes show similarity)
	Transatpks-Nrps	1892688	2030501	137814	64 Fengycin biosynthetic gene cluster (100% of genes show similarity)
	Terpene	2056888	2078771	21884	23 -
	T3pks	2142227	2183327	41101	50 -
	Transatpks	2298957	2399412	100456	53 Difficidin biosynthetic gene cluster (100% of genes show similarity)
	Nrps	2884999	2937665	52667	46 Micrococcin P1 biosynthetic gene cluster (8% of genes show similarity)
	Bacteriocin-Nrps	3033651	3100442	66792	64 Bacillibactin biosynthetic gene cluster (100% of genes show similarity)
	Other	3610188	3651606	41419	44 Bacilysin biosynthetic gene cluster (100% of genes show similarity)
<i>Bacillus velezensis</i> UCMB5036	Nrps	324993	390400	65408	41 Surfactin biosynthetic gene cluster (91% of genes show similarity)
	Otherks	906104	947348	41245	43 Butirosin biosynthetic gene cluster (7% of genes show similarity)
	Terpene	1030076	1050816	20741	24 -
	Transatpks	1367105	1452986	85882	42 Macrolactin biosynthetic gene cluster (100% of genes show similarity)
	Transatpks-Nrps	1684757	1787149	102393	47 Bacillaene biosynthetic gene cluster (100% of genes show similarity)
	Transatpks-Nrps	1849514	1987329	137816	63 Fengycin biosynthetic gene cluster (100% of genes show similarity)
	Terpene	2010491	2032374	21884	24 -
	T3pks	2095392	2136492	41101	50 -
	Transatpks	2252481	2352928	100448	54 Difficidin biosynthetic gene cluster (100% of genes show similarity)
	Bacteriocin-Nrps	2981142	3047933	66792	64 Bacillibactin biosynthetic gene cluster (100% of genes show similarity)
	Nrps	3319659	3363774	44116	39 -
	Other	3570299	3611717	41419	44 Bacilysin biosynthetic gene cluster (100% of genes show similarity)
<i>Bacillus velezensis</i> YJ11-1-4	Other	299737	341155	41419	43 Bacilysin biosynthetic gene cluster (100% of genes show similarity)
	Bacteriocin-Nrps	847974	914763	66790	66 Bacillibactin biosynthetic gene cluster (100% of genes show similarity)
	Transatpks	1536998	1637449	100452	55 Difficidin biosynthetic gene cluster (100% of genes show similarity)
	T3pks	1838829	1879929	41101	46 -
	Terpene	1930336	1952219	21884	25 -
	Transatpks-Nrps	1975160	2112970	137811	69 Fengycin biosynthetic gene cluster (100% of genes show similarity)
	Transatpks-Nrps	2175396	2278066	102671	49 Bacillaene biosynthetic gene cluster (100% of genes show similarity)
	Transatpks	2504129	2590018	85890	47 Macrolactin biosynthetic gene cluster (100% of genes show similarity)
	Terpene	2870418	2891158	20741	26 -
	Otherks	2973931	3015175	41245	44 Butirosin biosynthetic gene cluster (7% of genes show similarity)
	Transatpks-T1pks	3239473	3346060	106588	53 Bacillaene biosynthetic gene cluster (64% of genes show similarity)
	Nrps	3625106	3690512	65407	42 Surfactin biosynthetic gene cluster (78% of genes show similarity)
<i>Bacillus velezensis</i> YAU B9601	Nrps	320740	375380	54641	40 Surfactin biosynthetic gene cluster (82% of genes show similarity)
	Phosphonate	613750	654634	40885	38 -
	Otherks	930354	971598	41245	43 Butirosin biosynthetic gene cluster (7% of genes show similarity)
	Terpene	1053917	1074657	20741	24 -
	Transatpks	1399715	1485617	85903	45 Macrolactin biosynthetic gene cluster (100% of genes show similarity)
	Transatpks-Nrps	1758004	1860684	102681	49 Bacillaene biosynthetic gene cluster (100% of genes show similarity)
	Transatpks-Nrps	2064898	2202729	137832	66 Fengycin biosynthetic gene cluster (100% of genes show similarity)
	Terpene	2228296	2250179	21884	25 -
	T3pks	2300557	2341657	41101	46 -
	Transatpks	2499613	2600057	100445	51 Difficidin biosynthetic gene cluster (100% of genes show similarity)
	Bacteriocin-Nrps	3282811	3349607	66797	64 Bacillibactin biosynthetic gene cluster (100% of genes show similarity)
	Nrps	3615715	3684135	68421	39 -
	Other	3886357	3927775	41419	43 Bacilysin biosynthetic gene cluster (100% of genes show similarity)
	Lantipeptide	4082037	4106021	23985	21 Mersacidin biosynthetic gene cluster (100% of genes show similarity)
9912D	Nrps	317234	382641	65408	42 Surfactin_biosynthetic_gene_cluster (86% of genes show similarity)
	Otherks	1033490	1074734	41245	42 Butirosin_biosynthetic_gene_cluster (7% of genes show similarity)
	Terpene	1157495	1178235	20741	24 -
	Lantipeptide	1347052	1375941	28890	27 -
	Transatpks	1547816	1633718	85903	45 Macrolactin_biosynthetic_gene_cluster (100% of genes show similarity)
	Transatpks-Nrps	1863572	1947108	83537	51 Bacillaene_biosynthetic_gene_cluster (100% of genes show similarity)
	Transatpks-Nrps	2049917	2167296	117380	68 Fengycin_biosynthetic_gene_cluster (93% of genes show similarity)
	Terpene	2213335	2235218	21884	23 -

	Transatpks	2457899	2558346	100448	53 Difficidin_biosynthetic_gene_cluster (100% of genes show similarity)
	Bacteriocin-Nrps	3255108	3321896	66789	65 Bacillibactin_biosynthetic_gene_cluster (100% of genes show similarity)
	Other	3856315	3897733	41419	43 Bacilysin_biosynthetic_gene_cluster (100% of genes show similarity)
L-H15	Nrps	292431	357838	65408	46 Surfactin_biosynthetic_gene_cluster (82% of genes show similarity)
	Otherks	890715	931959	41245	42 Butirosin_biosynthetic_gene_cluster (7% of genes show similarity)
	Terpene	1013977	1034717	20741	26 -
	Lantipeptide	1155544	1184433	28890	32 -
	Transatpks	1357077	1442961	85885	46 Macrolactin_biosynthetic_gene_cluster (100% of genes show similarity)
	Transatpks-Nrps	1714316	1817020	102705	52 Bacillaene_biosynthetic_gene_cluster (100% of genes show similarity)
	Transatpks-Nrps	1872244	2010055	137812	67 Fengycin_biosynthetic_gene_cluster (100% of genes show similarity)
	Terpene	2032618	2054501	21884	23 -
	T3pks	2123169	2164269	41101	51 -
	Transatpks	2280636	2381095	100460	54 Difficidin_biosynthetic_gene_cluster (100% of genes show similarity)
	Bacteriocin-Nrps	3002014	3068803	66790	66 Bacillibactin_biosynthetic_gene_cluster (100% of genes show similarity)
	Other	3564391	3605809	41419	45 Bacilysin_biosynthetic_gene_cluster (100% of genes show similarity)
B25	Nrps	293003	358410	65408	44 Surfactin_biosynthetic_gene_cluster (82% of genes show similarity)
	Thiopeptide	572293	600603	28311	25 Kijanamicin_biosynthetic_gene_cluster (4% of genes show similarity)
	Otherks	909145	950389	41245	41 Butirosin_biosynthetic_gene_cluster (7% of genes show similarity)
	Terpene	1032409	1053149	20741	26 -
	Lantipeptide	1170756	1199432	28677	32 -
	Transatpks	1365993	1451862	85870	48 Macrolactin_biosynthetic_gene_cluster (100% of genes show similarity)
	Transatpks-Nrps	1678155	1780859	102705	48 Bacillaene_biosynthetic_gene_cluster (100% of genes show similarity)
	Transatpks-Nrps	1836930	1974757	137828	65 Fengycin_biosynthetic_gene_cluster (100% of genes show similarity)
	Terpene	1997283	2019166	21884	22 -
	T3pks	2069602	2110702	41101	49 -
	Transatpks	2226209	2326647	100439	53 Difficidin_biosynthetic_gene_cluster (100% of genes show similarity)
	Bacteriocin-Nrps	2951144	3017933	66790	64 Bacillibactin_biosynthetic_gene_cluster (100% of genes show similarity)
	Other	3522939	3564357	41419	45 Bacilysin_biosynthetic_gene_cluster (100% of genes show similarity)
L-S60	Nrps	293015	358422	65408	46 Surfactin_biosynthetic_gene_cluster (82% of genes show similarity)
	Otherks	891100	932344	41245	42 Butirosin_biosynthetic_gene_cluster (7% of genes show similarity)
	Terpene	1014362	1035102	20741	26 -
	Lantipeptide	1155957	1184846	28890	32 -
	Transatpks	1357490	1443374	85885	46 Macrolactin_biosynthetic_gene_cluster (100% of genes show similarity)
	Transatpks-Nrps	1711746	1814450	102705	48 Bacillaene_biosynthetic_gene_cluster (100% of genes show similarity)
	Transatpks-Nrps	1869674	2025100	155427	88 Fengycin_biosynthetic_gene_cluster (100% of genes show similarity)
	Terpene	2047663	2069546	21884	23 -
	T3pks	2119994	2161094	41101	51 -
	Transatpks	2277461	2377920	100460	53 Difficidin_biosynthetic_gene_cluster (100% of genes show similarity)
	Bacteriocin-Nrps	2998956	3065745	66790	66 Bacillibactin_biosynthetic_gene_cluster (100% of genes show similarity)
	Other	3561435	3602853	41419	45 Bacilysin_biosynthetic_gene_cluster (100% of genes show similarity)
S3-1	Nrps	322281	387688	65408	44 Surfactin_biosynthetic_gene_cluster (86% of genes show similarity)
	Otherks	924138	965382	41245	42 Butirosin_biosynthetic_gene_cluster (7% of genes show similarity)
	Terpene	1047426	1068166	20741	26 -
	Lantipeptide	1188659	1217547	28889	34 -
	Transatpks	1386438	1472343	85906	46 Macrolactin_biosynthetic_gene_cluster (100% of genes show similarity)
	Transatpks-Nrps	1698453	1801127	102675	50 Bacillaene_biosynthetic_gene_cluster (100% of genes show similarity)
	Transatpks-Nrps	1865758	2003559	137802	67 Fengycin_biosynthetic_gene_cluster (100% of genes show similarity)
	Terpene	2028786	2050669	21884	22 -
	T3pks	2113987	2155087	41101	48 -
	Transatpks	2270073	2370526	100454	55 Difficidin_biosynthetic_gene_cluster (100% of genes show similarity)
	Bacteriocin-Nrps	3000957	3067745	66789	65 Bacillibactin_biosynthetic_gene_cluster (100% of genes show similarity)
	Other	3589058	3630476	41419	44 Bacilysin_biosynthetic_gene_cluster (100% of genes show similarity)
GH1-13	Transatpks-Nrps	197846	275573	77728	48 Rhizoctacin_biosynthetic_gene_cluster (22% of genes show similarity)
	Nrps	347915	413325	65411	44 Surfactin_biosynthetic_gene_cluster (82% of genes show similarity)
	Otherks	947060	988304	41245	41 Butirosin_biosynthetic_gene_cluster (7% of genes show similarity)
	Terpene	1070358	1091098	20741	25 -
	Transatpks	1391133	1477017	85885	46 Macrolactin_biosynthetic_gene_cluster (100% of genes show similarity)
	Transatpks-Nrps	1706534	1809235	102702	53 Bacillaene_biosynthetic_gene_cluster (100% of genes show similarity)
	Transatpks-Nrps	2006356	2144209	137854	66 Fengycin_biosynthetic_gene_cluster (100% of genes show similarity)
	Terpene	2169133	2191016	21884	22 -
	T3pks	2255346	2296446	41101	49 -
	Transatpks	2411935	2512382	100448	57 Difficidin_biosynthetic_gene_cluster (100% of genes show similarity)
	Bacteriocin-Nrps	3140562	3207352	66791	63 Bacillibactin_biosynthetic_gene_cluster (100% of genes show similarity)
	Other	3724301	3765719	41419	44 Bacilysin_biosynthetic_gene_cluster (100% of genes show similarity)
	Lantipeptide	3906872	3930855	23984	21 Mersacidin_biosynthetic_gene_cluster (100% of genes show similarity)
NAU-B3	Nrps	320246	385654	65409	42 Surfactin_biosynthetic_gene_cluster (86% of genes show similarity)
	Phosphonate	628555	669445	40891	37 -
	Transatpks	1414107	1514551	100445	53 Difficidin_biosynthetic_gene_cluster (100% of genes show similarity)
	T3pks	1767323	1808423	41101	63 -
	Terpene	1888594	1910477	21884	22 -
	Transatpks-Nrps	1933731	2071562	137832	66 Fengycin_biosynthetic_gene_cluster (100% of genes show similarity)
	Transatpks-Nrps	2137267	2239950	102684	52 Bacillaene_biosynthetic_gene_cluster (100% of genes show similarity)
	Transatpks	2479390	2557908	78519	36 Macrolactin_biosynthetic_gene_cluster (100% of genes show similarity)
	Terpene	2865692	2886432	20741	24 -

	Otherks	2969142	3010386	41245	43 Butirosin_biosynthetic_gene_cluster (7% of genes show similarity)
	Bacteriocin-Nrps	3234248	3301040	66793	63 Bacillibactin_biosynthetic_gene_cluster (100% of genes show similarity)
	Nrps	3579861	3645203	65343	40 -
	Other	3847280	3888698	41419	42 Bacilysin_biosynthetic_gene_cluster (100% of genes show similarity)
9D-6	Other	174243	215661	41419	44 Bacilysin_biosynthetic_gene_cluster (100% of genes show similarity)
	Nrps	820469	885876	65408	42 Surfactin_biosynthetic_gene_cluster (95% of genes show similarity)
	Ladderane	1177384	1218583	41200	48 -
	Otherks	1451008	1492252	41245	41 Butirosin_biosynthetic_gene_cluster (7% of genes show similarity)
	Terpene	1575053	1595793	20741	25 -
	Lantipeptide	1714976	1743864	28889	34 -
	Transatpks	1893381	1979274	85894	48 Macrolactin_biosynthetic_gene_cluster (100% of genes show similarity)
	Transatpks-Nrps	2209276	2311962	102687	49 Bacillaene_biosynthetic_gene_cluster (100% of genes show similarity)
	Bacteriocin-Trans:	2364456	2489567	125112	74 Fengycin_biosynthetic_gene_cluster (93% of genes show similarity)
	Terpene	2517434	2539317	21884	22 -
	T3pks	2602290	2643390	41101	44 -
	Transatpks	2801002	2901455	100454	54 Difficidin_biosynthetic_gene_cluster (100% of genes show similarity)
	Bacteriocin-Nrps	3562018	3628825	66808	65 Bacillibactin_biosynthetic_gene_cluster (100% of genes show similarity)
T20E-257	Nrps	307387	372797	65411	44 Surfactin_biosynthetic_gene_cluster (82% of genes show similarity)
	Otherks	941428	982672	41245	43 Butirosin_biosynthetic_gene_cluster (7% of genes show similarity)
	Terpene	1064694	1085434	20741	26 -
	Lantipeptide	1202777	1231666	28890	35 -
	Transatpks	1399297	1485184	85888	49 Macrolactin_biosynthetic_gene_cluster (100% of genes show similarity)
	Transatpks-Nrps	1711486	1814193	102708	49 Bacillaene_biosynthetic_gene_cluster (100% of genes show similarity)
	Transatpks-Nrps	1868273	2006104	137832	67 Fengycin_biosynthetic_gene_cluster (100% of genes show similarity)
	Terpene	2028737	2050620	21884	22 -
	T3pks	2114557	2155657	41101	48 -
	Transatpks	2271979	2372429	100451	54 Difficidin_biosynthetic_gene_cluster (100% of genes show similarity)
	Bacteriocin-Nrps	2990196	3056986	66791	65 Bacillibactin_biosynthetic_gene_cluster (100% of genes show similarity)
	Other	3559815	3601233	41419	45 Bacilysin_biosynthetic_gene_cluster (100% of genes show similarity)
NJAU-Z9	Transatpks	598644	699094	100451	56 Difficidin_biosynthetic_gene_cluster (100% of genes show similarity)
	T3pks	815383	856483	41101	49 -
	Terpene	906935	928818	21884	23 -
	Transatpks-Nrps	951451	1089281	137831	67 Fengycin_biosynthetic_gene_cluster (100% of genes show similarity)
	Transatpks-Nrps	1143357	1246058	102702	47 Bacillaene_biosynthetic_gene_cluster (100% of genes show similarity)
	Transatpks	1472307	1558194	85888	51 Macrolactin_biosynthetic_gene_cluster (100% of genes show similarity)
	Lantipeptide	1725818	1754707	28890	35 -
	Terpene	1872015	1892755	20741	26 -
	Otherks	1974780	2016024	41245	43 Butirosin_biosynthetic_gene_cluster (7% of genes show similarity)
	Nrps	2552609	2618016	65408	45 Surfactin_biosynthetic_gene_cluster (82% of genes show similarity)
	Other	3217166	3258584	41419	44 Bacilysin_biosynthetic_gene_cluster (100% of genes show similarity)
	Bacteriocin-Nrps	3761415	3828205	66791	65 Bacillibactin_biosynthetic_gene_cluster (100% of genes show similarity)
CBMB205	Other	300737	342155	41419	44 Bacilysin_biosynthetic_gene_cluster (100% of genes show similarity)
	Bacteriocin-Nrps	863468	930256	66789	66 Bacillibactin_biosynthetic_gene_cluster (100% of genes show similarity)
	Transatpks	1560689	1661142	100454	55 Difficidin_biosynthetic_gene_cluster (100% of genes show similarity)
	T3pks	1776128	1817228	41101	53 -
	Terpene	1880546	1902429	21884	23 -
	Transatpks-Nrps	1927656	2065457	137802	68 Fengycin_biosynthetic_gene_cluster (100% of genes show similarity)
	Transatpks-Nrps	2130088	2232762	102675	48 Bacillaene_biosynthetic_gene_cluster (100% of genes show similarity)
	Transatpks	2458872	2544777	85906	49 Macrolactin_biosynthetic_gene_cluster (100% of genes show similarity)
	Lantipeptide	2713668	2742556	28889	34 -
	Terpene	2863049	2883789	20741	26 -
	Otherks	2965833	3007077	41245	43 Butirosin_biosynthetic_gene_cluster (7% of genes show similarity)
	Nrps	3543527	3608934	65408	44 Surfactin_biosynthetic_gene_cluster (86% of genes show similarity)
LABIM40	Thiopeptide	266213	295181	28969	27 -
	Nrps	306686	372093	65408	42 Surfactin_biosynthetic_gene_cluster (86% of genes show similarity)
	Otherks	903192	944436	41245	44 Butirosin_biosynthetic_gene_cluster (7% of genes show similarity)
	Terpene	1027237	1047977	20741	25 -
	Transatpks	1378274	1464182	85909	47 Macrolactin_biosynthetic_gene_cluster (100% of genes show similarity)
	Transatpks-Nrps	1695415	1798110	102696	49 Bacillaene_biosynthetic_gene_cluster (100% of genes show similarity)
	Transatpks-Nrps	1856920	1994574	137655	66 Fengycin_biosynthetic_gene_cluster (100% of genes show similarity)
	Terpene	2017590	2039473	21884	23 -
	T3pks	2123150	2164250	41101	48 -
	Transatpks	2283763	2384213	100451	55 Difficidin_biosynthetic_gene_cluster (100% of genes show similarity)
	Bacteriocin-Nrps	3022525	3089313	66789	66 Bacillibactin_biosynthetic_gene_cluster (100% of genes show similarity)
	Other	3602828	3644246	41419	46 Bacilysin_biosynthetic_gene_cluster (100% of genes show similarity)
157	Nrps	317617	383024	65408	42 Surfactin_biosynthetic_gene_cluster (86% of genes show similarity)
	Phosphonate	625787	666677	40891	37 -
	Otherks	944830	986074	41245	44 Butirosin_biosynthetic_gene_cluster (7% of genes show similarity)
	Terpene	1068391	1089131	20741	24 -
	Transatpks	1409197	1482839	73643	34 Macrolactin_biosynthetic_gene_cluster (100% of genes show similarity)
	Transatpks-Nrps	1714900	1817583	102684	52 Bacillaene_biosynthetic_gene_cluster (100% of genes show similarity)
	Transatpks-Nrps	1883269	2021102	137834	66 Fengycin_biosynthetic_gene_cluster (100% of genes show similarity)
	Terpene	2044355	2066238	21884	23 -
	T3pks	2146409	2187509	41101	52 -

	Transatpks	2302503	2402947	100445	55 Difficidin_biosynthetic_gene_cluster (100% of genes show similarity)
	Bacteriocin-Nrps	3053496	3120288	66793	65 Bacillibactin_biosynthetic_gene_cluster (100% of genes show similarity)
	Nrps	3398874	3464216	65343	39 -
	Other	3666299	3707717	41419	43 Bacilysin_biosynthetic_gene_cluster (100% of genes show similarity)
GQJK49	Nrps	322336	387743	65408	44 Surfactin_biosynthetic_gene_cluster (86% of genes show similarity)
	Otherks	924186	965430	41245	44 Butirosin_biosynthetic_gene_cluster (7% of genes show similarity)
	Terpene	1047472	1068212	20741	26 -
	Lantipeptide	1188705	1217593	28889	34 -
	Transatpks	1386480	1472385	85906	50 Macrolactin_biosynthetic_gene_cluster (100% of genes show similarity)
	Transatpks-Nrps	1698494	1801168	102675	48 Bacillaene_biosynthetic_gene_cluster (100% of genes show similarity)
	Transatpks-Nrps	1865799	2003599	137801	68 Fengycin_biosynthetic_gene_cluster (100% of genes show similarity)
	Terpene	2028826	2050709	21884	22 -
	T3pks	2114027	2155127	41101	50 -
	Transatpks	2276322	2370563	94242	45 Difficidin_biosynthetic_gene_cluster (100% of genes show similarity)
	Bacteriocin-Nrps	3000986	3067774	66789	65 Bacillibactin_biosynthetic_gene_cluster (100% of genes show similarity)
	Other	3589086	3630504	41419	44 Bacilysin_biosynthetic_gene_cluster (100% of genes show similarity)
NKG-1	Thiopeptide	291167	320132	28966	27 -
	Nrps	331637	397044	65408	42 Surfactin_biosynthetic_gene_cluster (95% of genes show similarity)
	Otherks	963112	1004356	41245	44 Butirosin_biosynthetic_gene_cluster (7% of genes show similarity)
	Terpene	1087154	1107894	20741	26 -
	Transatpks	1489560	1575462	85903	46 Macrolactin_biosynthetic_gene_cluster (100% of genes show similarity)
	Transatpks-Nrps	1804098	1906793	102696	48 Bacillaene_biosynthetic_gene_cluster (100% of genes show similarity)
	Transatpks-Nrps	1972713	2110524	137812	68 Fengycin_biosynthetic_gene_cluster (100% of genes show similarity)
	Terpene	2177203	2199086	21884	23 -
	T3pks	2282662	2323762	41101	50 -
	Transatpks	2439346	2527187	87842	43 Difficidin_biosynthetic_gene_cluster (100% of genes show similarity)
	Bacteriocin-Nrps	3263855	3330642	66788	65 Bacillibactin_biosynthetic_gene_cluster (100% of genes show similarity)
	Other	3849337	3890755	41419	45 Bacilysin_biosynthetic_gene_cluster (100% of genes show similarity)
LDO2	Bacteriocin-Nrps	302192	368980	66789	66 Bacillibactin_biosynthetic_gene_cluster (100% of genes show similarity)
	Transatpks	999412	1099865	100454	55 Difficidin_biosynthetic_gene_cluster (100% of genes show similarity)
	T3pks	1214851	1255951	41101	51 -
	Terpene	1319269	1341152	21884	23 -
	Transatpks-Nrps	1366379	1504180	137802	68 Fengycin_biosynthetic_gene_cluster (100% of genes show similarity)
	Transatpks-Nrps	1568812	1671486	102675	48 Bacillaene_biosynthetic_gene_cluster (100% of genes show similarity)
	Transatpks	1897595	1983500	85906	49 Macrolactin_biosynthetic_gene_cluster (100% of genes show similarity)
	Lantipeptide	2152391	2181279	28889	34 -
	Terpene	2301772	2322512	20741	26 -
	Otherks	2404556	2445800	41245	43 Butirosin_biosynthetic_gene_cluster (7% of genes show similarity)
	Nrps	2982249	3047656	65408	43 Surfactin_biosynthetic_gene_cluster (82% of genes show similarity)
	Other	3669251	3710669	41419	44 Bacilysin_biosynthetic_gene_cluster (100% of genes show similarity)
BS-37	Bacteriocin-Nrps	231733	298522	66790	66 Bacillibactin_biosynthetic_gene_cluster (100% of genes show similarity)
	Nrps	399137	454947	55811	44 -
	Transatpks	939457	1039907	100451	55 Difficidin_biosynthetic_gene_cluster (100% of genes show similarity)
	T3pks	1197833	1238933	41101	46 -
	Terpene	1339002	1360885	21884	23 -
	Transatpks-Nrps	1386183	1524027	137845	68 Fengycin_biosynthetic_gene_cluster (100% of genes show similarity)
	Transatpks-Nrps	1584039	1686737	102699	50 Bacillaene_biosynthetic_gene_cluster (100% of genes show similarity)
	Transatpks	1916423	2002334	85912	49 Macrolactin_biosynthetic_gene_cluster (100% of genes show similarity)
	Terpene	2307701	2328441	20741	26 -
	Otherks	2411768	2453012	41245	42 Butirosin_biosynthetic_gene_cluster (7% of genes show similarity)
	Nrps	3020714	3086121	65408	42 Surfactin_biosynthetic_gene_cluster (95% of genes show similarity)
	Other	3705853	3747271	41419	44 Bacilysin_biosynthetic_gene_cluster (100% of genes show similarity)
W1	Nrps	314559	369199	54641	41 Surfactin_biosynthetic_gene_cluster (86% of genes show similarity)
	Phosphonate	607538	648428	40891	37 -
	Otherks	924132	965376	41245	42 Butirosin_biosynthetic_gene_cluster (7% of genes show similarity)
	Terpene	1047692	1068432	20741	24 -
	Transatpks	1393506	1479408	85903	49 Macrolactin_biosynthetic_gene_cluster (100% of genes show similarity)
	Transatpks-Nrps	1751777	1854457	102681	52 Bacillaene_biosynthetic_gene_cluster (100% of genes show similarity)
	Transatpks-Nrps	2058681	2196557	137877	66 Fengycin_biosynthetic_gene_cluster (100% of genes show similarity)
	Terpene	2222387	2244270	21884	24 -
	T3pks	2294647	2335747	41101	47 -
	Transatpks	2493703	2594147	100445	54 Difficidin_biosynthetic_gene_cluster (100% of genes show similarity)
	Bacteriocin-Nrps	3277059	3343852	66794	68 Bacillibactin_biosynthetic_gene_cluster (100% of genes show similarity)
	Nrps	3610025	3678446	68422	40 -
	Other	3880681	3922099	41419	44 Bacilysin_biosynthetic_gene_cluster (100% of genes show similarity)
	Lantipeptide	4076362	4100346	23985	21 Mersacidin_biosynthetic_gene_cluster (100% of genes show similarity)
BIM B-439D	Lantipeptide	194078	216693	22616	20 Locillomycin_biosynthetic_gene_cluster (35% of genes show similarity)
	Nrps	315290	380697	65408	42 Surfactin_biosynthetic_gene_cluster (95% of genes show similarity)
	Otherks	914734	955978	41245	42 Butirosin_biosynthetic_gene_cluster (7% of genes show similarity)
	Terpene	1039329	1060069	20741	26 -
	Transatpks	1364859	1450770	85912	48 Macrolactin_biosynthetic_gene_cluster (100% of genes show similarity)
	Transatpks-Nrps	1680446	1783144	102699	51 Bacillaene_biosynthetic_gene_cluster (100% of genes show similarity)
	Transatpks-Nrps	1840152	1978016	137865	67 Fengycin_biosynthetic_gene_cluster (100% of genes show similarity)
	Terpene	2040862	2062745	21884	23 -

	T3pks	2123962	2165062	41101	50 -
	Transatpks	2280962	2381415	100454	55 Difficidin_biosynthetic_gene_cluster (100% of genes show similarity)
	Nrps	2907390	2963200	55811	44 -
	Bacteriocin-Nrps	3060149	3126940	66792	66 Bacillibactin_biosynthetic_gene_cluster (100% of genes show similarity)
	Other	3637022	3678440	41419	44 Bacilysin_biosynthetic_gene_cluster (100% of genes show similarity)
QST713	Transatpks-Nrps	191893	269628	77736	48 Rhizocticin_biosynthetic_gene_cluster (22% of genes show similarity)
	Nrps	347609	413022	65414	42 Surfactin_biosynthetic_gene_cluster (86% of genes show similarity)
	Otherks	986643	1027887	41245	43 Butirosin_biosynthetic_gene_cluster (7% of genes show similarity)
	Terpene	1110586	1131326	20741	24 -
	Transatpks	1440778	1526670	85893	49 Macrolactin_biosynthetic_gene_cluster (100% of genes show similarity)
	Transatpks-Nrps	1756070	1858741	102672	51 Bacillaene_biosynthetic_gene_cluster (100% of genes show similarity)
	Transatpks-Nrps	1919730	2057562	137833	67 Fengycin_biosynthetic_gene_cluster (100% of genes show similarity)
	Terpene	2080722	2102605	21884	23 -
	T3pks	2166999	2208099	41101	62 -
	Transatpks	2460543	2560999	100457	56 Difficidin_biosynthetic_gene_cluster (100% of genes show similarity)
	Bacteriocin-Nrps	3272524	3339310	66787	66 Bacillibactin_biosynthetic_gene_cluster (100% of genes show similarity)
	Lantipeptide	3482556	3509613	27058	32 Subtilin_biosynthetic_gene_cluster (100% of genes show similarity)
	Nrps	3625021	3693450	68430	39 -
	Other	3895380	3936798	41419	45 Bacilysin_biosynthetic_gene_cluster (100% of genes show similarity)
DSYZ	Transatpks-Nrps	197832	275562	77731	50 Rhizocticin_biosynthetic_gene_cluster (22% of genes show similarity)
	Nrps	372412	437815	65404	41 Surfactin_biosynthetic_gene_cluster (91% of genes show similarity)
	Otherks	977576	1018820	41245	43 Butirosin_biosynthetic_gene_cluster (7% of genes show similarity)
	Terpene	1101598	1122338	20741	25 -
	Transatpks	1439846	1525733	85888	46 Macrolactin_biosynthetic_gene_cluster (100% of genes show similarity)
	Transatpks-Nrps	1802122	1904640	102519	50 Bacillaene_biosynthetic_gene_cluster (100% of genes show similarity)
	Bacteriocin-Trans:	1961182	2112224	151043	81 Fengycin_biosynthetic_gene_cluster (100% of genes show similarity)
	Terpene	2175684	2197567	21884	23 -
	T3pks	2262665	2303765	41101	59 -
	Transatpks	2558152	2633933	75782	53 Difficidin_biosynthetic_gene_cluster (86% of genes show similarity)
	Bacteriocin-Nrps	3301515	3368306	66792	67 Bacillibactin_biosynthetic_gene_cluster (100% of genes show similarity)
	Nrps	3646225	3714669	68445	39 -
	Other	3919904	3961322	41419	45 Bacilysin_biosynthetic_gene_cluster (100% of genes show similarity)
S141	Thiopeptide	284789	313757	28969	26 -
	Nrps	325262	390672	65411	42 Surfactin_biosynthetic_gene_cluster (86% of genes show similarity)
	Otherks	958162	999406	41245	43 Butirosin_biosynthetic_gene_cluster (7% of genes show similarity)
	Terpene	1082208	1102948	20741	25 -
	Transatpks	1419151	1505058	85908	46 Macrolactin_biosynthetic_gene_cluster (100% of genes show similarity)
	Transatpks-Nrps	1733694	1836380	102687	49 Bacillaene_biosynthetic_gene_cluster (100% of genes show similarity)
	Transatpks-Nrps	1906232	2044099	137868	65 Fengycin_biosynthetic_gene_cluster (100% of genes show similarity)
	T3pks	2155745	2196845	41101	49 -
	Transatpks	2313645	2414101	100457	55 Difficidin_biosynthetic_gene_cluster (100% of genes show similarity)
	Bacteriocin-Nrps	3051153	3117944	66792	65 Bacillibactin_biosynthetic_gene_cluster (100% of genes show similarity)
	Other	3634072	3675490	41419	45 Bacilysin_biosynthetic_gene_cluster (100% of genes show similarity)
JT3-1	Otherks	491035	532279	41245	43 Butirosin_biosynthetic_gene_cluster (7% of genes show similarity)
	Terpene	614324	635064	20741	26 -
	Lantipeptide	755557	784445	28889	34 -
	Transatpks	953337	1039242	85906	49 Macrolactin_biosynthetic_gene_cluster (100% of genes show similarity)
	Transatpks-Nrps	1265354	1368028	102675	49 Bacillaene_biosynthetic_gene_cluster (100% of genes show similarity)
	Transatpks-Nrps	1432659	1570460	137802	68 Fengycin_biosynthetic_gene_cluster (100% of genes show similarity)
	Terpene	1595687	1617570	21884	23 -
	T3pks	1680888	1721988	41101	53 -
	Transatpks	1836974	1937427	100454	55 Difficidin_biosynthetic_gene_cluster (100% of genes show similarity)
	Bacteriocin-Nrps	2567860	2634648	66789	66 Bacillibactin_biosynthetic_gene_cluster (100% of genes show similarity)
	Other	3155962	3197380	41419	44 Bacilysin_biosynthetic_gene_cluster (100% of genes show similarity)
	Nrps	3818978	3884385	65408	44 Surfactin_biosynthetic_gene_cluster (86% of genes show similarity)
SB1216	Nrps	143716	209123	65408	41 Surfactin_biosynthetic_gene_cluster (91% of genes show similarity)
	Otherks	704239	745483	41245	43 Butirosin_biosynthetic_gene_cluster (7% of genes show similarity)
	Terpene	824762	845502	20741	25 -
	Transatpks	1194352	1267991	73640	33 Macrolactin_biosynthetic_gene_cluster (100% of genes show similarity)
	Transatpks-Nrps	1496083	1598775	102693	47 Bacillaene_biosynthetic_gene_cluster (100% of genes show similarity)
	Transatpks-Nrps	1654407	1791579	137173	64 Fengycin_biosynthetic_gene_cluster (100% of genes show similarity)
	Other	1821953	1863371	41419	44 Bacilysin_biosynthetic_gene_cluster (85% of genes show similarity)
	T3pks	1896143	1937243	41101	47 -
	Transatpks	2052692	2153148	100457	52 Difficidin_biosynthetic_gene_cluster (100% of genes show similarity)
	Bacteriocin-Nrps	2770132	2836921	66790	64 Bacillibactin_biosynthetic_gene_cluster (100% of genes show similarity)
	Terpene	2954123	2976006	21884	26 -

Table S4. The gene distribution of the secondary metabolite biosynthetic gene clusters of *Bacillus velezensis* WRN014.

Gene cluster	Gene	From	To	strand	Putative function	Identity values(%)
Transatpks-Nrps	1	195609	196431	+	Cyclic di-AMP synthase CdaA	
	2	196423	197863	+	CdaA regulatory protein CdaR	99 [AHI59103.1] [†]
	3	197880	199227	+	Phosphoglucosamine mutase	100 [AHI59104.1]
	4	199658	201461	+	Glutamine-fructose-6-phosphate aminotransferase [isomerizing]	100 [AHI59105.1]
	5	201879	202752	+	ABC transporter ATP-binding protein YtrB	97 [AHI59106.1]
	6	202729	203383	+	hypothetical protein	
	7	203514	204360	-	2,5-diketo-D-gluconic acid reductase B	99 [AHI59116.1]
	8	204470	205163	-	Holin-like protein CidB	
	9	205132	205630	-	Holin-like protein CidA	
	10	205731	206163	+	hypothetical protein	
	11	206588	207974	+	putative transport protein YifK	
	12	208066	208771	+	Putative HAD-hydrolase YfnB	
	13	208826	209984	+	Sensor histidine kinase LiaS	
	14	210007	210661	+	Transcriptional regulatory protein DegU	
	15	210878	211811	+	Daunorubicin/doxorubicin resistance ATP-binding protein DrrA	
	16	211826	213035	+	hypothetical protein	
	17	213037	214201	+	hypothetical protein	
	18	214256	214430	+	hypothetical protein	
	19	214501	215197	+	Linear gramicidin dehydrogenase LgrE	
	20	215567	223190	+	Tyrocidine synthase 2	
	21	223149	233904	+	Linear gramicidin synthase subunit D	
	22	233986	235240	+	Malonyl CoA-acyl carrier protein transacylase	
	23	235283	240056	+	Polyketide synthase PksN	
	24	240245	245036	+	Polyketide synthase PksN	
	25	245057	246581	+	Phytoene desaturase (neurosporene-forming)	
	26	246675	253296	+	Tyrocidine synthase 2	
	27	253316	254360	+	Mitomycin biosynthesis 6-O-methyltransferase	
	28	254515	254992	+	SPBc2 prophage-derived uncharacterized protein YoIA	
	29	255069	255321	+	hypothetical protein	
	30	255430	256129	+	hypothetical protein	
	31	256174	256435	-	hypothetical protein	
	32	256602	258240	+	Aspartate-proton symporter	
	33	258334	259222	-	Glycerophosphodiester phosphodiesterase	
	34	259317	260652	-	Glycerol-3-phosphate transporter	
	35	260986	261229	+	hypothetical protein	
	36	261284	262733	-	4-hydroxyphenylacetate 3-monooxygenase oxygenase component	
	37	262880	263306	-	hypothetical protein	
	38	263378	265553	-	putative protein FadG	
	39	265917	266361	+	hypothetical protein	
	40	266623	267094	+	hypothetical protein	
	41	267166	268237	+	Hydroxycarboxylate dehydrogenase A	
	42	268318	269473	+	Formate-dependent phosphoribosylglycinamide formyltransferase	
	43	269950	270484	+	CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase	
	44	270474	270963	+	Protein DedA	
	45	270955	271771	+	Phosphatidylserine decarboxylase proenzyme	
	46	271813	272089	+	hypothetical protein	
	47	272195	273164	+	hypothetical protein	
	48	273200	274451	-	Proton/glutamate-aspartate symporter	
Nrps	1	342237	343194	+	Cephalosporin-C deacetylase	
	2	343259	344045	+	hypothetical protein	
	3	344232	345144	+	Proline dehydrogenase 2	
	4	345161	346709	+	1-pyrroline-5-carboxylate dehydrogenase 2	
	5	346824	348255	+	High-affinity proline transporter PutP	
	6	348412	349648	+	Proline-responsive transcriptional activator PutR	
	7	349846	350857	+	Ferredoxin-NADP reductase 2	
	8	350911	352351	-	Uroporphyrinogen-III C-methyltransferase	
	9	352417	352738	-	Assimilatory nitrite reductase [NAD(P)H] small subunit	
	10	352758	355176	-	Nitrite reductase [NAD(P)H]	
	11	355572	356775	+	Putative metal chaperone YciC	99 [CAE02619.1]
	12	356839	357976	+	Glutathione-independent formaldehyde dehydrogenase	99 [CAE02620.1]
	13	357987	358425	+	hypothetical protein	97 [CAE02621.1]
	14	358496	358817	+	hypothetical protein	98 [CAE02622.1]
	15	358920	359037	+	Aryl-phospho-beta-D-glucosidase BglC	94 [CAE02623.1]
	16	359294	359693	-	DNA-entry nuclease inhibitor	96 [CAE02624.1]
	17	359714	360152	-	Sporulation-specific extracellular nuclease	99 [CAE02625.1]
	18	360510	361068	-	3-hexulose-6-phosphate isomerase	99 [CAE02626.1]
	19	361064	361700	-	3-hexulose-6-phosphate synthase	99 [CAE02627.1]
	20	361931	362294	+	HTH-type transcriptional activator HxIR	97 [CAE02628.1]
	21	362882	373637	+	Surfactin synthase subunit 1	98 [CAE02630.1]
	22	373658	384419	+	Surfactin synthase subunit 2	98 [CAE02631.1]
	23	384453	388290	+	Surfactin synthase subunit 3	98 [CAE02633.1]
	24	388309	389041	+	Surfactin synthase thioesterase subunit	100 [CAE02634.1]
	25	389162	390473	+	Aspartate aminotransferase	99 [CAE02635.1]
	26	390509	391184	-	4'-phosphopantetheinyl transferase Sfp	98 [CAE02638.1]
	27	391282	391912	-	hypothetical protein	98 [CAE02639.1]
	28	392010	392754	-	L-cystine import ATP-binding protein TcyC	99 [CAE02640.1]
	29	392766	393471	-	L-cystine transport system permease protein TcyB	99 [CAE02641.1]
	30	393457	394255	-	L-cystine-binding protein TcyA	
	31	394383	395256	-	HTH-type transcriptional regulator GlcC	

	32	395385	395964	+	putative UbiX-like flavin prenyltransferase
	33	395966	397388	+	Phenolic acid decarboxylase subunit C
	34	397405	397633	+	Phenolic acid decarboxylase subunit D
	35	397632	398094	+	hypothetical protein
	36	398136	399615	-	Di-/tripeptide transporter
	37	399893	401639	+	hypothetical protein
	38	401731	401953	-	hypothetical protein
	39	402074	403715	+	Spore germination protein B1
	40	403701	404928	+	Spore germination protein B3
	41	404952	406071	+	Spore germination protein YndE
	42	406242	407565	+	Nitritotriacetate monooxygenase component A
	43	407578	408070	+	putative N-acetyltransferase Ytml
	44	408098	408890	+	putative amino-acid-binding protein YxeM
Otherks	1	977249	978704	-	Peptidoglycan endopeptidase LytF
	2	978882	979317	-	HTH-type transcriptional repressor NsrR
	3	979448	980963	-	hypothetical protein
	4	981132	982539	+	hypothetical protein
	5	982576	983956	-	Alkaline phosphatase 4
	6	984414	985239	+	putative peptidoglycan endopeptidase LytE
	7	985307	986183	+	HTH-type transcriptional regulator CysL
	8	986286	987396	+	Citrate synthase 1
	9	987475	988345	+	General stress protein 39
	10	988675	990079	+	putative amino acid permease YhdG
	11	990241	991549	+	hypothetical protein
	12	991585	991876	-	putative anti-sigma-M factor YhdK
	13	991863	992937	-	putative anti-sigma-M factor YhdL
	14	992929	993421	-	ECF RNA polymerase sigma factor SigM
	15	993659	994259	+	1-acyl-sn-glycerol-3-phosphate acyltransferase
	16	994304	995639	-	hypothetical protein
	17	995700	996126	-	Mercuric resistance operon regulatory protein
	18	996305	997490	+	Aspartate aminotransferase
	19	997522	998767	+	Polyketide biosynthesis malonyl-ACP decarboxylase PksF
	20	998996	1000385	+	hypothetical protein
	21	1000398	1000758	-	Putative fluoride ion transporter CrcB
	22	1000754	1001150	-	Putative fluoride ion transporter CrcB
	23	1001151	1001868	-	Glycerophosphodiester phosphodiesterase
	24	1002037	1002142	+	hypothetical protein
	25	1002305	1003421	+	Low conductance mechanosensitive channel Ynal
	26	1003472	1004216	+	NAD-dependent protein deacetylase
	27	1004249	1005098	-	Peptidoglycan-N-acetylglucosamine deacetylase
	28	1005354	1006206	+	D-alanine aminotransferase
	29	1006248	1006755	-	HTH-type transcriptional regulator BetI
	30	1006941	1007493	+	hypothetical protein
	31	1007531	1008032	-	Stress response protein NhaX
	32	1008324	1008429	+	hypothetical protein
	33	1008452	1010210	+	putative multidrug resistance ABC transporter ATP-binding/permease prc54 [BAE07080.1]
	34	1010206	1012228	+	putative multidrug resistance ABC transporter ATP-binding/permease prc46 [BAE07081.1]
	35	1012266	1012887	-	Aspartate-semialdehyde dehydrogenase
	36	1012915	1013041	-	hypothetical protein
	37	1013142	1013349	-	Small, acid-soluble spore protein 2
	38	1013573	1013780	-	hypothetical protein
	39	1013871	1015230	-	Endospore coat-associated protein YheD
	40	1015219	1016311	-	Endospore coat-associated protein YheD
	41	1016548	1017682	+	hypothetical protein
	42	1017767	1018118	+	hypothetical protein
	43	1018156	1019296	-	putative protein YhaZ
Terpene	1	1100236	1103629	+	Nuclease SbcCD subunit C
	2	1103644	1103938	+	hypothetical protein
	3	1103981	1104200	-	putative spore germination protein GerPF
	4	1104239	1104635	-	putative spore germination protein GerPE
	5	1104634	1104811	-	putative spore germination protein GerPD
	6	1104807	1105425	-	putative spore germination protein GerPC
	7	1105460	1105697	-	putative spore germination protein GerPB
	8	1105709	1105931	-	putative spore germination protein GerPA
	9	1106121	1106331	-	Aspartyl-phosphate phosphatase YisI
	10	1106546	1107452	+	putative protein YisK
	11	1107545	1107902	+	hypothetical protein
	12	1108144	1108687	-	hypothetical protein
	13	1108862	1110704	+	Asparagine synthetase [glutamine-hydrolyzing] 3
	14	1110789	1111530	+	Putative phytoene/squalene synthase YisP
	15	1111565	1112933	-	putative FMN/FAD exporter YeeO
	16	1113055	1113919	+	Arabinose operon regulatory protein
	17	1113954	1114980	+	HTH-type transcriptional regulator DegA
	18	1115205	1116237	+	scyllo-inositol 2-dehydrogenase (NAD(+))
	19	1116282	1116777	-	hypothetical protein
	20	1116949	1117576	-	hypothetical protein
	21	1117811	1118252	-	Acetyltransferase
	22	1118334	1120176	-	Bifunctional homocysteine S-methyltransferase/5,10-methylenetetrahydrofolate reductase
	23	1120488	1120980	-	hypothetical protein
	24	1121127	1121976	+	Conserved virulence factor B
Lantipeptide	1	1239586	1240585	+	putative HTH-type transcriptional repressor ExuR

2	1240658	1243595	+	Altronate dehydratase		
3	1243778	1244450	+	Alkaline phosphatase synthesis transcriptional regulatory protein SphR		
4	1244446	1245805	+	Sensor histidine kinase CssS		
5	1245924	1246860	+	putative ABC transporter ATP-binding protein YxIF		
6	1246840	1247572	+	hypothetical protein		
7	1247589	1247781	+	hypothetical protein		
8	1247846	1249097	+	Sensor histidine kinase ComP		
9	1249108	1249774	+	Transcriptional regulatory protein ComA		
10	1249965	1250148	+	hypothetical protein		
11	1250232	1253415	+	hypothetical protein		
12	1253404	1255552	+	Lactococcin-G-processing and transport ATP-binding protein LagD		
13	1255758	1255935	+	hypothetical protein		
14	1255971	1256148	+	hypothetical protein		
15	1256236	1259122	+	hypothetical protein		
16	1259168	1259933	-	hypothetical protein		
17	1260080	1260548	-	putative protein YjoA		
18	1260758	1261889	+	Response regulator aspartate phosphatase A		
19	1261878	1262013	+	hypothetical protein		
20	1262155	1263109	+	N-acetylmuramoyl-L-alanine amidase CwlA		
21	1263146	1263524	-	hypothetical protein		
22	1263633	1264239	+	hypothetical protein		
23	1264228	1264378	+	hypothetical protein		
24	1264393	1264984	-	hypothetical protein		
25	1265132	1265471	-	HTH-type transcriptional regulator Xre		
26	1265662	1265842	+	hypothetical protein		
27	1266558	1267359	+	Chromosomal replication initiator protein DnaA		
28	1267358	1267526	+	hypothetical protein		
29	1267623	1267965	+	hypothetical protein		
30	1267954	1268158	+	hypothetical protein		
31	1268270	1268783	+	hypothetical protein		
32	1268895	1269693	+	hypothetical protein		
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Transatpks	1	1434046	1435951	+	PTS system fructose-specific EIIABC component	
	2	1436081	1436663	+	Signal peptidase I T	
	3	1436699	1436969	-	hypothetical protein	
	4	1437131	1438751	+	putative ABC transporter ATP-binding protein YbiT	
	5	1438863	1439772	+	2-dehydropanoate 2-reductase	
	6	1439802	1441035	-	Aminopeptidase 2	
	7	1441135	1441270	-	hypothetical protein	
	8	1441341	1442361	-	Protein MreBH	
	9	1442617	1442902	+	Putative transition state regulator Abh	
	10	1443074	1444379	+	Sporulation kinase A	
	11	1444380	1445208	+	Putative gamma-glutamylcyclotransferase YkqA	
	12	1445248	1445914	+	Ktr system potassium uptake protein A	
	13	1446062	1447796	+	Adenine deaminase	
	14	1447827	1449495	-	Ribonuclease J1	
	15	1449500	1449710	-	hypothetical protein	
	16	1450064	1450838	+	Putative bifunctional phosphatase/peptidyl-prolyl cis-trans isomerase	
	17	1450871	1451426	-	Peptide deformylase 2	
	18	1451538	1451724	-	hypothetical protein	
	19	1451964	1452609	+	hypothetical protein	
	20	1453075	1455382	+	Polyketide biosynthesis protein BaeE	96 [CAG23963.1]
	21	1455402	1467654	+	Polyketide synthase PksJ	97 [CAG23964.1]
	22	1467653	1472426	+	Polyketide synthase PksL	97 [CAG23965.1]
	23	1472473	1481179	+	Polyketide synthase PksN	97 [CAG23966.1]
	24	1481171	1488170	+	Polyketide synthase PksJ	97 [CAG23967.1]
	25	1488193	1493905	+	Polyketide synthase PksL	97 [CAG23968.1]
	26	1493904	1501287	+	Polyketide synthase PksL	97 [CAG23969.1]
	27	1501337	1505192	+	Polyketide synthase PksJ	96 [CAG23970.1]
	28	1505224	1506316	+	Putative penicillin-binding protein PbpX	97 [CAJ57404.1]
	29	1506787	1507903	+	Pyruvate dehydrogenase E1 component subunit alpha	100 [CAJ57405.1]
	30	1507906	1508884	+	Pyruvate dehydrogenase E1 component subunit beta	
	31	1509008	1510337	+	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex	
	32	1510341	1511754	+	Dihydrolipoyl dehydrogenase	
	33	1511801	1512176	-	hypothetical protein	
	34	1512423	1513215	+	Bifunctional xylanase/deacetylase	
	35	1513496	1514969	-	Arginine decarboxylase	
	36	1515149	1515416	+	hypothetical protein	
	37	1515451	1516084	-	hypothetical protein	
	38	1516332	1516509	+	hypothetical protein	
	39	1516642	1517440	+	Inositol-1-monophosphatase	
	40	1517426	1517879	+	hypothetical protein	
	41	1517929	1519495	-	Bacillolysin	
	42	1519992	1520385	+	hypothetical protein	
	43	1520328	1520946	-	hypothetical protein	
	44	1521257	1521446	-	hypothetical protein	
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Transatpks-Nrps	1	1747167	1747428	+	Stage V sporulation protein S	
	2	1747686	1748733	+	L-threonine 3-dehydrogenase	
	3	1748748	1749924	+	8-amino-7-oxononanoate synthase/2-amino-3-ketobutyrate coenzyme A ligase	
	4	1750066	1751596	+	tRNA-2-methylthio-N(6)-dimethylallyladenosine synthase	
	5	1751595	1752030	+	putative protein YmcA	
	6	1752284	1752830	+	Spore coat protein E	

7	1752945	1755534	+	DNA mismatch repair protein MutS		
8	1755549	1757427	+	DNA mismatch repair protein MutL		
9	1757746	1757956	-	hypothetical protein		
10	1758979	1759672	+	putative polyketide biosynthesis zinc-dependent hydrolase BaeB	100 [CAG23949.2]	
11	1759986	1760856	+	Polyketide biosynthesis malonyl CoA-acyl carrier protein transacylase Ba	98 [CAG23950.2]	
12	1760992	1761967	+	Polyketide biosynthesis acyltransferase BaeD	99 [CAG23951.2]	
13	1761968	1764209	+	Polyketide biosynthesis protein BaeE	98 [CAG23952.2]	
14	1764274	1764523	+	Polyketide biosynthesis acyl-carrier-protein AcpK	96 [CAG23953.2]	
15	1764574	1765837	+	Polyketide biosynthesis 3-hydroxy-3-methylglutaryl-ACP synthase PksG	99 [CAG23954.2]	
16	1765833	1766607	+	putative polyketide biosynthesis enoyl-CoA hydratase PksH	98 [CAG23955.2]	
17	1766616	1767366	+	Putative polyketide biosynthesis enoyl-CoA isomerase PksI	100 [CAG23956.2]	
18	1767405	1782360	+	Polyketide synthase PksJ	97 [CAG23957.2]	
19	1782361	1795780	+	Polyketide synthase PksL	98 [CAG23958.2]	
20	1795797	1806339	+	Polyketide synthase PksM	97 [CAG23959.2]	
21	1806328	1822627	+	Polyketide synthase PksN	98 [CAG23960.2]	
22	1822640	1830098	+	Polyketide synthase PksR	97 [CAG23961.2]	
23	1830230	1831442	-	Polyketide biosynthesis cytochrome P450 PksS	99 [CAG23962.2]	
24	1831730	1832165	+	Sporulation-specific extracellular nuclease		
25	1832263	1832980	+	hypothetical protein		
26	1833012	1833375	-	hypothetical protein		
27	1833567	1834896	-	Serine protease AprX		
28	1835566	1836274	+	hypothetical protein		
29	1836334	1836787	+	hypothetical protein		
30	1836800	1837154	-	Multidrug resistance protein EbrB		
31	1837170	1837503	-	Multidrug resistance protein EbrA		
32	1837623	1837917	-	hypothetical protein		
33	1838018	1838423	+	hypothetical protein		
34	1838521	1839466	+	tRNA dimethylallyltransferase		
35	1839505	1839727	+	RNA-binding protein Hfq		
36	1839823	1840099	+	putative protein YmzC		
37	1840181	1840397	+	hypothetical protein		
38	1840656	1841049	+	Protein NrdI		
39	1841008	1843111	+	Ribonucleoside-diphosphate reductase subunit alpha 1		
40	1843128	1844118	+	Ribonucleoside-diphosphate reductase subunit beta		
41	1844166	1844787	+	hypothetical protein		
42	1844835	1845594	-	Sporulation-specific N-acetylmuramoyl-L-alanine amidase		
43	1845900	1846869	+	Stage V sporulation protein K		
44	1846998	1848261	+	GTPase HflX		
45	1848277	1849543	+	L-methionine gamma-lyase		
46	1849652	1850057	+	HTH-type transcriptional regulator GlnR		
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Transatpks-Nrps	1	1904671	1906090	+	Amino-acid carrier protein AlsT	
	2	1906293	1907250	+	2-dehydro-3-deoxygluconokinase	
	3	1907279	1908299	+	putative zinc-type alcohol dehydrogenase-like protein Yjmd	
	4	1908312	1908948	+	KHG/KDPG aldolase	
	5	1908949	1910026	+	Mannonate dehydratase	
	6	1910022	1910859	+	putative oxidoreductase UxB	
	7	1910942	1911944	+	HTH-type transcriptional regulator KdgR	
	8	1912010	1913282	+	Hexuronate transporter	
	9	1913400	1914216	+	hypothetical protein	
	10	1914212	1914821	+	hypothetical protein	
	11	1914814	1916443	+	hypothetical protein	
	12	1917127	1917589	-	hypothetical protein	
	13	1917780	1919280	-	Endoglucanase	
	14	1919748	1920060	+	hypothetical protein	
	15	1920111	1921512	-	Sensor histidine kinase ResE	
	16	1921514	1922222	-	Alkaline phosphatase synthesis transcriptional regulatory protein SphR	
	17	1922363	1923635	-	Glucuronoxylanase XynC	
	18	1923686	1925225	-	Arabinoxylan arabinofuranohydrolase	
	19	1925550	1933404	-	Linear gramicidin synthase subunit D	
	20	1933492	1949581	-	Linear gramicidin synthase subunit B	
	21	1949625	1961574	-	Tyrocidine synthase 3	
	22	1961593	1962796	-	Malonyl CoA-acyl carrier protein transacylase	
	23	1963351	1964137	-	D-beta-hydroxybutyrate dehydrogenase	
	24	1964149	1964812	-	putative succinyl-CoA:3-ketoacid coenzyme A transferase subunit B	
	25	1964829	1965513	-	putative succinyl-CoA:3-ketoacid coenzyme A transferase subunit A	
	26	1965555	1967001	-	hypothetical protein	
	27	1967304	1968501	-	Biotin biosynthesis cytochrome P450	
	28	1968502	1969522	-	Biotin synthase	
	29	1969524	1970226	-	ATP-dependent dethiobiotin synthetase BioD 1	
	30	1970222	1971383	-	8-amino-7-oxononanoate synthase 2	
	31	1971372	1972719	-	L-Lysine--8-amino-7-oxononanoate transaminase	
	32	1972715	1973486	-	6-carboxyhexanoate--CoA ligase	
	33	1973764	1974172	+	hypothetical protein	
	34	1974178	1975072	+	UTP--glucose-1-phosphate uridylyltransferase	
	35	1975146	1975737	+	putative membrane protein	
	36	1975790	1977320	-	Methylmalonyl-CoA carboxyltransferase 12S subunit	100 [RBAM_018330]
	37	1977337	1978117	-	Short-chain-enoyl-CoA hydratase	100 [RBAM_018340]
	38	1978130	1979030	-	Hydroxymethylglutaryl-CoA lyase YngG	98 [RBAM_018350]
	39	1979045	1979258	-	Biotin/lipoyl attachment protein	100 [RBAM_018360]
	40	1979254	1980604	-	2-oxoglutarate carboxylase small subunit	99 [RBAM_018370]
	41	1980625	1982266	-	3-[(3aS,4S,7aS)-7a-methyl-1, 5-dioxo-octahydro-1H-inden-4-yl]propanoyl	98 [RBAM_018380]

42	1982310	1983453	-	Acyl-CoA dehydrogenase, short-chain specific	100 [RBAM_018390]
43	1983595	1985134	-	hypothetical protein	97 [RBAM_018400]
44	1985255	1985636	-	Sporulation protein YjcA	99 [RBAM_018410]
45	1985710	1989514	-	Plipastatin synthase subunit E	97 [RBAM_018420]
46	1989532	2000308	-	Plipastatin synthase subunit D	97 [RBAM_018430]
47	2000333	2007983	-	Plipastatin synthase subunit C	97 [RBAM_018440]
48	2007998	2015696	-	Plipastatin synthase subunit B	97 [RBAM_018450]
49	2015721	2023380	-	Plipastatin synthase subunit A	97 [RBAM_018460]
50	2023859	2025335	-	D-alanyl-D-alanine carboxypeptidase DacC	97 [RBAM_018470]
51	2025353	2026328	-	Aldose 1-epimerase	
52	2026437	2027826	-	Multidrug export protein MepA	
53	2028054	2028597	+	putative protein YoeB	
54	2028857	2029403	-	Tyrosine recombinase XerH	
55	2029717	2029948	-	hypothetical protein	
56	2030191	2031967	+	Glutathione hydrolase proenzyme	
57	2032013	2033189	-	Purine efflux pump PbuE	
58	2033332	2033635	-	Transcriptional activator HlyU	
59	2033672	2033969	-	Threonine-tRNA ligase 1	
60	2033965	2034832	-	HTH-type transcriptional regulator YofA	
61	2034950	2035931	+	Crotonyl-CoA reductase	
62	2036306	2037788	-	Glutamate synthase [NADPH] small chain	
63	2037804	2042364	-	Glutamate synthase [NADPH] large chain	
64	2042500	2043412	+	HTH-type transcriptional regulator GltC	
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Terpene	1	2065036	2066014	+	putative murein peptide carboxypeptidase
	2	2066045	2066468	-	hypothetical protein
	3	2066596	2067475	-	Cell wall-binding protein YochI
	4	2067710	2069489	-	ATP-dependent DNA helicase RecQ
	5	2069996	2070623	-	FMN-dependent NADH-azoreductase 1
	6	2070646	2070748	-	hypothetical protein
	7	2070767	2071259	-	General stress protein 16O
	8	2071342	2071690	-	hypothetical protein
	9	2071815	2072049	+	hypothetical protein
	10	2072035	2072518	-	Spore coat protein P
	11	2072588	2072861	+	hypothetical protein
	12	2072857	2073091	+	hypothetical protein
	13	2073135	2073480	-	hypothetical protein
	14	2073772	2073913	-	hypothetical protein
	15	2073978	2074182	-	hypothetical protein
	16	2074364	2075852	+	Phenylacetaldehyde dehydrogenase
	17	2075948	2077832	+	Sporuleniol synthase
	18	2077828	2078674	+	Superoxide dismutase [Mn/Fe]
	19	2078714	2080052	-	hypothetical protein
	20	2080255	2081224	+	Pantothenate precursors transporter PanS
	21	2081251	2081998	-	putative metallo-hydrolase YfiN
	22	2082070	2083318	-	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex
	23	2083333	2086168	-	2-oxoglutarate dehydrogenase E1 component
	24	2086395	2088312	-	hypothetical protein
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T3pks	1	2156195	2156819	-	hypothetical protein
	2	2156834	2157320	-	Dihydrofolate reductase
	3	2157316	2158111	-	Thymidylate synthase 2
	4	2158210	2158819	-	hypothetical protein
	5	2159081	2159852	-	Ribosomal RNA small subunit methyltransferase J
	6	2159891	2160326	-	hypothetical protein
	7	2160408	2162085	-	Dihydroxy-acid dehydratase
	8	2162343	2163477	-	hypothetical protein
	9	2163545	2164154	-	putative protein YedJ
	10	2164165	2164648	-	Hydroperoxy fatty acid reductase gpx1
	11	2164929	2165838	+	Homoserine O-acetyltransferase
	12	2166062	2167205	+	Processive diacylglycerol beta-glucosyltransferase
	13	2167426	2167627	+	Cold shock protein CspD
	14	2167678	2167861	-	Regulatory protein DegR
	15	2168022	2168280	+	hypothetical protein
	16	2168306	2168489	-	hypothetical protein
	17	2168491	2169163	-	Ribonuclease H
	18	2169244	2169925	+	Queuosine precursor transporter
	19	2169928	2170324	+	14.7 kDa ribonuclease H-like protein
	20	2170375	2170504	+	Small, acid-soluble spore protein L
	21	2170509	2171397	-	5'-3' exonuclease
	22	2171492	2171636	-	hypothetical protein
	23	2171712	2171970	-	hypothetical protein
	24	2172037	2175664	-	Bacterial dynamin-like protein
	25	2175969	2176476	-	hypothetical protein
	26	2176475	2177576	-	Alpha-pyrone synthesis polyketide synthase-like Pks11
	27	2177741	2178350	+	Putative ribosomal N-acetyltransferase YdaF
	28	2178379	2178688	-	DNA base-flipping protein
	29	2178909	2179173	+	hypothetical protein
	30	2179518	2179719	+	hypothetical protein
	31	2179854	2180307	+	hypothetical protein
	32	2180290	2180857	-	Streptothricin hydrolase
	33	2181228	2181504	+	hypothetical protein
	34	2181916	2182810	-	Uric acid permease Puck

35	2182872	2183037	-	hypothetical protein		
36	2183033	2183588	-	hypothetical protein		
37	2183914	2184046	-	hypothetical protein		
38	2184166	2184331	-	hypothetical protein		
39	2184327	2184498	-	hypothetical protein		
40	2184498	2185047	-	hypothetical protein		
41	2185027	2185573	-	hypothetical protein		
42	2185562	2185718	-	hypothetical protein		
43	2185750	2185963	-	hypothetical protein		
44	2185996	2186827	-	hypothetical protein		
45	2186985	2187198	+	Small, acid-soluble spore protein C		
46	2187279	2187468	-	hypothetical protein		
47	2187625	2187961	-	hypothetical protein		
48	2187977	2188298	-	hypothetical protein		
49	2188444	2188975	+	hypothetical protein		
50	2189026	2189392	-	hypothetical protein		
51	2189521	2190028	-	Dihydrofolate reductase type 3		
52	2190027	2190867	-	Thymidylate synthase 1		
53	2191642	2191942	-	hypothetical protein		
54	2191934	2192243	-	hypothetical protein		
55	2192263	2192569	-	hypothetical protein		
56	2192586	2192751	-	hypothetical protein		
57	2192860	2193475	-	hypothetical protein		
58	2193716	2193956	-	Thioredoxin		
59	2193952	2194939	-	Ribonucleoside-diphosphate reductase subunit beta		
60	2194939	2195260	-	hypothetical protein		
61	2195279	2198534	-	Ribonucleoside-diphosphate reductase subunit alpha 1		
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Transatpks	1	2446747	2447737	-	L-asparaginase 1	
	2	2447913	2448267	+	HTH-type transcriptional regulator Xre	
	3	2448277	2449441	-	hypothetical protein	
	4	2449440	2449998	-	ADP-ribose pyrophosphatase	
	5	2450073	2450196	+	hypothetical protein	
	6	2450258	2451179	+	Aldo-keto reductase IolS	
	7	2451211	2451439	-	hypothetical protein	
	8	2451558	2452299	+	hypothetical protein	
	9	2452237	2452471	+	hypothetical protein	
	10	2452510	2452750	-	hypothetical protein	
	11	2452724	2453087	-	hypothetical protein	
	12	2453158	2454127	-	Dephospho-CoA kinase	
	13	2454123	2454468	-	putative protein YqjZ	
	14	2454480	2454951	-	putative protein YqjY	
	15	2455166	2456393	+	DNA polymerase IV	
	16	2456407	2456752	+	hypothetical protein	
	17	2456848	2457058	+	hypothetical protein	
	18	2457130	2458201	+	Putative transport protein	
	19	2458292	2458460	+	hypothetical protein	
	20	2458461	2458854	-	hypothetical protein	
	21	2458875	2459835	-	Pantothenate kinase	
	22	2459910	2461260	-	D-serine dehydratase	
	23	2461276	2462053	-	putative oxidoreductase	
	24	2462058	2463018	-	Hydroxyacylglutathione hydrolase	
	25	2463411	2464254	+	Pyrroline-5-carboxylate reductase	
	26	2464288	2465035	-	Putative polyketide biosynthesis enoyl-CoA isomerase PksI	99 [CAG23986.1]
	27	2465084	2466392	-	Polyketide biosynthesis 3-hydroxy-3-methylglutaryl-ACP synthase PksG	99 [CAG23985.1]
	28	2466388	2467543	-	Putative cytochrome P450 YjIB	100 [CAG23984.1]
	29	2467624	2473840	-	Polyketide synthase PksL	98 [CAG23983.1]
	30	2473836	2479992	-	Polyketide synthase PksN	97 [CAJ57411.1]
	31	2480014	2487733	-	Polyketide synthase PksJ	97 [CAJ57410.1]
	32	2487737	2503349	-	Polyketide synthase PksN	97 [CAJ57409.1]
	33	2503400	2509127	-	Polyketide synthase PksL	97 [CAJ57408.1]
	34	2509166	2515463	-	Polyketide synthase PksJ	97 [CAG23978.1]
	35	2515481	2528063	-	Polyketide synthase PksN	96 [CAG23977.1]
	36	2528102	2528840	-	3-oxoacyl-[acyl-carrier-protein] reductase FabG	98 [CAG23976.1]
	37	2528854	2530219	-	2-succinylbenzoate--CoA ligase	99 [CAJ57407.1]
	38	2530215	2530488	-	Acyl carrier protein	100 [CAJ57406.1]
	39	2530512	2531493	-	hypothetical protein	99 [CAG23975.2]
	40	2531532	2533791	-	Polyketide biosynthesis protein PksE	99 [CAG23974.1]
	41	2534524	2535055	+	Transcription termination/antitermination protein NusG	
	42	2535391	2536270	-	HTH-type transcriptional activator CmpR	
	43	2536408	2536732	+	hypothetical protein	
	44	2536871	2537888	+	NADPH dehydrogenase	
	45	2538002	2538776	+	Putative aminoacylate hydrolase RutD	
	46	2539054	2539981	-	Ribonuclease Z	
	47	2540189	2541659	+	Glucose-6-phosphate 1-dehydrogenase	
	48	2541749	2543159	-	6-phosphogluconate dehydrogenase, NADP(+)-dependent, decarboxylating	
	49	2543267	2544512	-	DNA polymerase IV	
	50	2544587	2544869	+	Membrane protein insertion and folding monitor	
	51	2544901	2545738	+	Membrane protein insertase MisCB	
	52	2545851	2546967	-	Peptidase T	
	53	2546983	2548507	-	Propionyl-CoA carboxylase beta chain	
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Bacteriocin-Nrps	1	3164443	3165910	-	Nicotinate phosphoribosyltransferase pncB2	

2	3165927	3166479	-	Isochorismatase family protein YecD		
3	3166575	3166974	-	putative protein Yuel		
4	3167039	3167288	-	hypothetical protein		
5	3167360	3167582	-	putative spore germination protein GerPF		
6	3167643	3168747	-	Putative transport protein		
7	3168885	3169122	-	hypothetical protein		
8	3169259	3169790	-	hypothetical protein		
9	3169954	3170686	-	Benzil reductase ((S)-benzoin forming)		
10	3170747	3171221	-	hypothetical protein		
11	3171228	3174354	-	ESX secretion system protein YueB		
12	3174350	3178826	-	ESX secretion system protein EccC		
13	3178883	3180170	-	ESAT-6 secretion machinery protein EssB		
14	3180184	3180430	-	ESX secretion system protein YukD		
15	3180499	3180793	-	Protein YukE		
16	3181108	3182338	+	Proline-responsive transcriptional activator PutR		
17	3182441	3183572	+	Alanine dehydrogenase	90 [BSU31930]	
18	3183689	3184367	+	hypothetical protein	81 [BSU31945]	
19	3184411	3184627	-	Protein MbtH	58 [BSU31959]	
20	3184645	3191773	-	Dimodular nonribosomal peptide synthase	70 [BSU31960]	
21	3191787	3192714	-	Isochorismatase	72 [BSU31970]	
22	3192731	3194357	-	2,3-dihydroxybenzoate-AMP ligase	82 [BSU31980]	
23	3194375	3195572	-	Isochorismate synthase DhbC	66 [BSU31990]	
24	3195595	3196381	-	2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase	70 [BSU32000]	
25	3196516	3197386	-	Ferri-bacillibactin esterase BesA	64 [BSU32010]	
26	3197561	3198158	-	Putative protein-methionine-sulfoxide reductase subunit YedZ1	85 [BSU32020]	
27	3198257	3198851	+	Biotin transporter BioY	77 [BSU32030]	
28	3198897	3200226	-	hypothetical protein	90 [BSU32040]	
29	3200358	3201849	-	putative cytosol aminopeptidase	83 [BSU32050]	
30	3201996	3202473	+	hypothetical protein		
31	3202501	3203143	-	putative protein YuiC		
32	3203243	3203564	-	hypothetical protein		
33	3203931	3205152	-	NADH dehydrogenase-like protein		
34	3205463	3206459	+	Ferredoxin--NADP reductase 2		
35	3206499	3206643	-	hypothetical protein		
36	3206860	3207841	+	GMP reductase		
37	3207903	3208125	-	hypothetical protein		
38	3208141	3208666	-	hypothetical protein		
39	3208665	3209370	-	putative ABC transporter ATP-binding protein YxIF		
40	3209362	3211018	-	hypothetical protein		
41	3211100	3211439	-	hypothetical protein		
42	3211503	3212076	-	hypothetical protein		
43	3212483	3212783	+	putative HTH-type transcriptional regulator		
44	3212822	3213584	+	NADP-dependent 3-hydroxy acid dehydrogenase YdfG		
45	3213726	3214089	-	Iron-sulfur cluster insertion protein ErpA		
46	3214166	3215021	-	Diaminopimelate epimerase		
47	3215144	3216362	-	Putative nucleoside permease NupX		
48	3216495	3216732	-	hypothetical protein		
49	3216998	3218066	+	NADH dehydrogenase		
50	3218103	3218430	-	hypothetical protein		
51	3218608	3218845	+	Fe/S biogenesis protein NfuA		
52	3218885	3220862	-	Dipeptidyl-peptidase 5		
53	3220964	3221894	-	Homoserine kinase		
54	3221890	3222958	-	Threonine synthase		
55	3222948	3224250	-	Homoserine dehydrogenase		
56	3224451	3225468	-	hypothetical protein		
57	3225586	3226123	+	putative protein YpjQ		
58	3226149	3226920	-	Acid sugar phosphatase		
59	3226953	3227388	-	hypothetical protein		
60	3227413	3227689	-	putative protein YutD		
61	3227907	3228804	-	Lipoyl synthase		
62	3229005	3229983	+	L-Ala--D-Glu endopeptidase		
63	3230020	3230779	-	Sporulation protein YunB		
64	3230905	3232300	-	Mannosylglucosyl-3-phosphoglycerate phosphatase		
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Other	1	3729327	3729516	+	2-hydroxyomuconate tautomerase	
	2	3729553	3729973	-	putative HTH-type transcriptional regulator YusO	
	3	3730360	3731743	+	putative amino acid permease YhdG	
	4	3731806	3732307	-	hypothetical protein	
	5	3732346	3733648	-	Deoxyguanosinetriphosphate triphosphohydrolase-like protein	99 [RBAM_034880]
	6	3733808	3734033	-	hypothetical protein	100 [RBAM_034890]
	7	3734237	3735011	+	Prespore-specific transcriptional regulator RsfA	99 [RBAM_034900]
	8	3735272	3735587	+	hypothetical protein	99 [RBAM_034910]
	9	3735587	3736142	+	hypothetical protein	100 [RBAM_034920]
	10	3736239	3737160	+	Fluoroquinolones export ATP-binding protein	100 [RBAM_034930]
	11	3737156	3738110	+	hypothetical protein	98 [RBAM_034940]
	12	3738099	3738936	-	hypothetical protein	
	13	3738926	3739691	-	hypothetical protein	
	14	3739692	3740616	-	hypothetical protein	
	15	3740664	3740844	-	hypothetical protein	
	16	3740995	3741859	-	Octanoyl-[GcvH]:protein N-octanoyltransferase	
	17	3741905	3742805	-	HTH-type transcriptional regulator CysL	
	18	3742926	3743898	+	hypothetical protein	

19	3743934	3744906	-	Phosphate acetyltransferase
20	3745168	3745933	+	Putative heme-dependent peroxidase
21	3746031	3746832	+	NADPH-dependent reductase BacG
22	3746848	3748048	-	Transaminase BacF
23	3748060	3749242	-	Putative bacilysin exporter BacE
24	3749238	3750657	-	Alanine--anticapsin ligase
25	3750674	3751436	-	Dihydroanticapsin 7-dehydrogenase
26	3751432	3752143	-	H2HPP isomerase
27	3752132	3752747	-	Prephenate decarboxylase
28	3752908	3754147	-	Inner membrane transport protein YdhP
29	3754370	3755573	+	Bicyclomycin resistance protein
30	3755605	3757024	-	Amino-acid permease RocC
31	3757048	3758731	-	Protein RocB
32	3758802	3760350	-	1-pyrroline-5-carboxylate dehydrogenase
33	3760557	3761844	-	Catabolic NAD-specific glutamate dehydrogenase RocG
34	3762029	3762494	-	putative protein YweA
35	3762706	3763162	-	dTDP-4-dehydrorhamnose 3,5-epimerase
36	3763158	3764007	-	dTDP-4-dehydrorhamnose reductase
37	3764027	3764975	-	dTDP-glucose 4,6-dehydratase
38	3764977	3765715	-	Glucose-1-phosphate thymidyltransferase
39	3765742	3766747	-	UDP-N-acetylglucosamine--N-acetylmuramyl- (pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase
40	3766748	3767492	-	3-deoxy-manno-octulosonate cytidyltransferase
41	3767481	3768603	-	Spore coat polysaccharide biosynthesis protein SpsE
42	3768602	3769466	-	dTDP-fucosamine acetyltransferase
43	3769466	3770636	-	UDP-4-amino-4-deoxy-L-arabinose--oxoglutarate aminotransferase

99 [AHI59103.1] The 99 is the identity value and the accession number of reference is in the bracket.