

# Genome analysis of two *Pseudonocardia* phylotypes associated with *Acromyrmex* leafcutter ants reveals their biosynthetic potential

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## Supplementary Information

**Supplementary Table 1. Summary of draft genome sequences.**

Sequencing Project	No. Unitigs	Largest Unitigs (bps)	Smallest Unitigs (bps)	No. of Preliminary Clusters (Antismash)
Ae150A_Ps1 Illumina	8	6135547	2072	15
Ae168_Ps1 Illumina	14	5473146	2073	15
Ae263_Ps1 Illumina	14	6157670	2073	15
Ae356_Ps1 Illumina	14	6162815	2206	15
Ae707_Ps1 PacBio	4	6361983	2594	14
Ae331_Ps2 Illumina	23	6075932	2005	11
Ae406_Ps2 Illumina	27	6080519	2001	11
Ae505_Ps2 Illumina	13	6031156	2260	13
Ae706_Ps2 Illumina	21	6111893	2111	11
Ae717_Ps2 PacBio	26	6288042	5131	15

Assembled genomes were submitted to antismash for secondary metabolite cluster prediction, outputs displayed below (Weber *et al.*, (2015).

Overview 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15

**Identified secondary metabolite clusters**

Cluster	Type	From	To	Most similar known cluster
The following clusters are from record c00001_MH_Ae15:				
Cluster 1	T1pks	25302	96128	Nystatin-like_Pseudonocardia_polyene_biosynthetic_gene_cluster (73% of genes show similarity)
Cluster 2	Bacteriocin	279830	310643	Endophenazines_biosynthetic_gene_cluster (13% of genes show similarity)
Cluster 3	T1pks	691938	784056	Pimaricin_biosynthetic_gene_cluster (47% of genes show similarity)
Cluster 4	Terpene	949311	970576	SF2575_biosynthetic_gene_cluster (4% of genes show similarity)
Cluster 5	Nrps	1174990	1247881	Erythrochelin_biosynthetic_gene_cluster (71% of genes show similarity)
Cluster 6	Bacteriocin	2487311	2498171	-
Cluster 7	Other	2867409	2914879	Stenothricin_biosynthetic_gene_cluster (13% of genes show similarity)
Cluster 8	Nrps	2953650	3007679	Mirubactin_biosynthetic_gene_cluster (42% of genes show similarity)
Cluster 9	Ectoine	3090854	3101249	Ectoine_biosynthetic_gene_cluster (75% of genes show similarity)
Cluster 10	Oligosaccharide	3667360	3688043	-
Cluster 11	Other	3836118	3876684	Thiocoraline_biosynthetic_gene_cluster (5% of genes show similarity)
Cluster 12	Lantipeptide	4073882	4094031	-
Cluster 13	Other	5013321	5057700	Kinamycin_biosynthetic_gene_cluster (8% of genes show similarity)
Cluster 14	Nrps	5353829	5407642	Gobichelin_biosynthetic_gene_cluster (16% of genes show similarity)
Cluster 15	Terpene	5720239	5741237	Sioxanthin_biosynthetic_gene_cluster (60% of genes show similarity)

**Supplementary Figure 1. Screen shot of the antismash output for *Pseudonocardia* Ae150A\_Ps1.**

Select Gene Cluster:  
Overview 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15

**Identified secondary metabolite clusters**

Cluster	Type	From	To	Most similar known cluster
The following clusters are from record c00001_MH_Ae16:				
Cluster 1	T1pks	29495	100321	Nystatin-like_Pseudonocardia_polyene_biosynthetic_gene_cluster (73% of genes show similarity)
Cluster 2	Bacteriocin	279174	309885	Endophenazines_biosynthetic_gene_cluster (13% of genes show similarity)
Cluster 3	T1pks	691404	783522	Pimaricin_biosynthetic_gene_cluster (47% of genes show similarity)
Cluster 4	Terpene	948624	969889	SF2575_biosynthetic_gene_cluster (4% of genes show similarity)
Cluster 5	Nrps	1174392	1247283	Erythrochelin_biosynthetic_gene_cluster (71% of genes show similarity)
Cluster 6	Bacteriocin	2485921	2496781	-
Cluster 7	Other	2866434	2913904	Stenothricin_biosynthetic_gene_cluster (13% of genes show similarity)
Cluster 8	Nrps	2952675	3006704	Mirubactin_biosynthetic_gene_cluster (42% of genes show similarity)
Cluster 9	Ectoine	3089879	3100274	Ectoine_biosynthetic_gene_cluster (75% of genes show similarity)
Cluster 10	Oligosaccharide	3670406	3691089	-
Cluster 11	Other	3839161	3879727	Thiocoraline_biosynthetic_gene_cluster (5% of genes show similarity)
Cluster 12	Lantipeptide	4076947	4097096	Kanamycin_biosynthetic_gene_cluster (1% of genes show similarity)
Cluster 13	Other	5026769	5071148	Kinamycin_biosynthetic_gene_cluster (8% of genes show similarity)
Cluster 14	Nrps	5367141	5420954	Gobichelin_biosynthetic_gene_cluster (16% of genes show similarity)
The following clusters are from record c00002_MH_Ae16:				
Cluster 15	Terpene	394356	415354	Sioxanthin_biosynthetic_gene_cluster (60% of genes show similarity)

**Supplementary Figure 2. Screen shot of the antismash output for *Pseudonocardia* Ae168\_Ps1.**

Overview **1** 2 3 4 5 6 7 8 9 10 11 12 13 14 15

**Identified secondary metabolite clusters**

Cluster	Type	From	To	Most similar known cluster
The following clusters are from record c00001_MH_Ae26:				
Cluster 1	Nrps	50728	104541	Gobichelin_biosynthetic_gene_cluster (22% of genes show similarity)
Cluster 2	Other	400667	445046	Kinamycin_biosynthetic_gene_cluster (8% of genes show similarity)
Cluster 3	Lantipeptide	1374731	1394880	-
Cluster 4	Other	1592018	1632584	Thiocoraline_biosynthetic_gene_cluster (5% of genes show similarity)
Cluster 5	Oligosaccharide	1780683	1801366	-
Cluster 6	Ectoine	2367786	2378181	Ectoine_biosynthetic_gene_cluster (75% of genes show similarity)
Cluster 7	Nrps	2465085	2519122	Mirubactin_biosynthetic_gene_cluster (42% of genes show similarity)
Cluster 8	Other	2557893	2605363	Stenothricin_biosynthetic_gene_cluster (13% of genes show similarity)
Cluster 9	Bacteriocin	2974454	2985314	-
Cluster 10	Nrps	4231090	4284904	Erythrochelin_biosynthetic_gene_cluster (71% of genes show similarity)
Cluster 11	Terpene	4508474	4529739	SF2575_biosynthetic_gene_cluster (6% of genes show similarity)
Cluster 12	T1pks	4694995	4783183	Nystatin-like_Pseudonocardia_polyene_biosynthetic_gene_cluster (43% of genes show similarity)
Cluster 13	Bacteriocin	5155393	5201206	Endophenazines_biosynthetic_gene_cluster (13% of genes show similarity)
Cluster 14	T1pks	5380061	5450887	Nystatin-like_Pseudonocardia_polyene_biosynthetic_gene_cluster (73% of genes show similarity)
Cluster 15	Terpene	5882622	5903620	Sioxanthin_biosynthetic_gene_cluster (60% of genes show similarity)

**Supplementary Figure 3. Screen shot of the antismash output for *Pseudonocardia* Ae263\_Ps1.**

Select Gene Cluster:  
Overview **1** 2 3 4 5 6 7 8 9 10 11 12 13 14 15

**Identified secondary metabolite clusters**

Cluster	Type	From	To	Most similar known cluster
The following clusters are from record c00001_MH_Ae16:				
Cluster 1	T1pks	29495	100321	Nystatin-like_Pseudonocardia_polyene_biosynthetic_gene_cluster (73% of genes show similarity)
Cluster 2	Bacteriocin	279174	309885	Endophenazines_biosynthetic_gene_cluster (13% of genes show similarity)
Cluster 3	T1pks	691404	783522	Pimaricin_biosynthetic_gene_cluster (47% of genes show similarity)
Cluster 4	Terpene	948624	969889	SF2575_biosynthetic_gene_cluster (4% of genes show similarity)
Cluster 5	Nrps	1174392	1247283	Erythrochelin_biosynthetic_gene_cluster (71% of genes show similarity)
Cluster 6	Bacteriocin	2485921	2496781	-
Cluster 7	Other	2866434	2913904	Stenothricin_biosynthetic_gene_cluster (13% of genes show similarity)
Cluster 8	Nrps	2952675	3006704	Mirubactin_biosynthetic_gene_cluster (42% of genes show similarity)
Cluster 9	Ectoine	3089879	3100274	Ectoine_biosynthetic_gene_cluster (75% of genes show similarity)
Cluster 10	Oligosaccharide	3670406	3691089	-
Cluster 11	Other	3839161	3879727	Thiocoraline_biosynthetic_gene_cluster (5% of genes show similarity)
Cluster 12	Lantipeptide	4076947	4097096	Kanamycin_biosynthetic_gene_cluster (1% of genes show similarity)
Cluster 13	Other	5026769	5071148	Kinamycin_biosynthetic_gene_cluster (8% of genes show similarity)
Cluster 14	Nrps	5367141	5420954	Gobichelin_biosynthetic_gene_cluster (16% of genes show similarity)
The following clusters are from record c00002_MH_Ae16:				
Cluster 15	Terpene	394356	415354	Sioxanthin_biosynthetic_gene_cluster (60% of genes show similarity)

**Supplementary Figure 4. Screen shot of the antismash output for *Pseudonocardia* Ae356\_Ps1.**

Select Gene Cluster:  
Overview 1 2 3 4 5 6 7 8 9 10 11 12 13 14

**Identified secondary metabolite clusters**

Cluster	Type	From	To	Most similar known cluster
The following clusters are from record unitig_0quiver:				
Cluster 1	Oligosaccharide	56032	85438	-
Cluster 2	Oligosaccharide	188517	240149	Tomaymycin_biosynthetic_gene_cluster (11% of genes show similarity)
Cluster 3	Other	414511	455164	Thiocoraline_biosynthetic_gene_cluster (5% of genes show similarity)
Cluster 4	Nrps	1719125	1776380	Gobichelin_biosynthetic_gene_cluster (16% of genes show similarity)
Cluster 5	Terpene	2177040	2198059	Sioxanthin_biosynthetic_gene_cluster (60% of genes show similarity)
Cluster 6	Bacteriocin	2911608	2942494	Endophenazines_biosynthetic_gene_cluster (13% of genes show similarity)
Cluster 7	T1pks	3345783	3488407	Nystatin-like_Pseudonocardia_polyene_biosynthetic_gene_cluster (95% of genes show similarity)
Cluster 8	Terpene	3638728	3659975	SF2575_biosynthetic_gene_cluster (4% of genes show similarity)
Cluster 9	Nrps	3866837	3939727	Erythrochelin_biosynthetic_gene_cluster (71% of genes show similarity)
Cluster 10	Other	4710606	4754841	-
Cluster 11	Bacteriocin	5327392	5338333	-
Cluster 12	Other	5676793	5724917	Stenothricin_biosynthetic_gene_cluster (13% of genes show similarity)
Cluster 13	Nrps	5753305	5806262	Mirubactin_biosynthetic_gene_cluster (50% of genes show similarity)
Cluster 14	Ectoine	5865458	5875904	Ectoine_biosynthetic_gene_cluster (75% of genes show similarity)

**Supplementary Figure 5. Screen shot of the antismash output for *Pseudonocardia* Ae707\_Ps1.**

Select Gene Cluster:  
Overview 1 2 3 4 5 6 7 8 9 10 11

**Identified secondary metabolite clusters**

Cluster	Type	From	To	Most similar known cluster
The following clusters are from record c00001_MH_Ae33:				
Cluster 1	Terpene	781011	802687	Brasilicardin_A_biosynthetic_gene_cluster (45% of genes show similarity)
Cluster 2	Bacteriocin	1174490	1185383	-
Cluster 3	Ectoine	1666066	1676461	Ectoine_biosynthetic_gene_cluster (75% of genes show similarity)
Cluster 4	Oligosaccharide	2231888	2252565	-
Cluster 5	Bacteriocin	3612149	3622970	-
Cluster 6	Terpene	4081263	4102255	Carotenoid_biosynthetic_gene_cluster (27% of genes show similarity)
Cluster 7	T1pks	4380747	4519777	Nystatin-like_Pseudonocardia_polyene_biosynthetic_gene_cluster (73% of genes show similarity)
Cluster 8	Nrps-T1pks	4721587	4863642	Amychelin_biosynthetic_gene_cluster (31% of genes show similarity)
Cluster 9	Terpene	5326209	5347564	SF2575_biosynthetic_gene_cluster (4% of genes show similarity)
Cluster 10	Other	6006054	6070086	UK-68,597_biosynthetic_gene_cluster (4% of genes show similarity)
The following clusters are from record c00002_MH_Ae33:				
Cluster 11	Lasso peptide	89260	111169	-

**Supplementary Figure 6. Screen shot of the antismash output for *Pseudonocardia* Ae331\_Ps2.**

Select Gene Cluster:  
Overview 1 2 3 4 5 6 7 8 9 10 11

**Identified secondary metabolite clusters**

Cluster	Type	From	To	Most similar known cluster
The following clusters are from record c00001_MH_Ae40:				
Cluster 1	Other	5853	69885	UK-68,597_biosynthetic_gene_cluster (4% of genes show similarity)
Cluster 2	Terpene	730605	751954	SF2575_biosynthetic_gene_cluster (6% of genes show similarity)
Cluster 3	Nrps-T1pks	1213868	1354303	Amychelin_biosynthetic_gene_cluster (31% of genes show similarity)
Cluster 4	T1pks	1554210	1688401	Nystatin-like_Pseudonocardia_polyene_biosynthetic_gene_cluster (73% of genes show similarity)
Cluster 5	Terpene	1982209	2003201	Carotenoid_biosynthetic_gene_cluster (27% of genes show similarity)
Cluster 6	Bacteriocin	2457460	2468281	-
Cluster 7	Oligosaccharide	3825163	3845840	-
Cluster 8	Ectoine	4409093	4419488	Ectoine_biosynthetic_gene_cluster (100% of genes show similarity)
Cluster 9	Bacteriocin	4897074	4907967	-
Cluster 10	Terpene	5281504	5303180	Brasilicardin_A_biosynthetic_gene_cluster (54% of genes show similarity)
The following clusters are from record c00002_MH_Ae40:				
Cluster 11	Lassoptide	92023	113932	-

**Supplementary Figure 7. Screen shot of the antismash output for *Pseudonocardia* Ae406\_Ps2.**

Select Gene Cluster:  
Overview 1 2 3 4 5 6 7 8 9 10 11 12 13

**Identified secondary metabolite clusters**

Cluster	Type	From	To	Most similar known cluster
The following clusters are from record c00001_MH_Ae50:				
Cluster 1	Terpene	153971	175647	Brasilicardin_A_biosynthetic_gene_cluster (45% of genes show similarity)
Cluster 2	Bacteriocin	545698	556591	-
Cluster 3	Ectoine	1027041	1037436	Ectoine_biosynthetic_gene_cluster (75% of genes show similarity)
Cluster 4	Oligosaccharide	1605297	1625992	-
Cluster 5	Bacteriocin	3018924	3029745	-
Cluster 6	Terpene	3264901	3285893	Isorenieratene_biosynthetic_gene_cluster (28% of genes show similarity)
Cluster 7	Other	3697921	3761893	UK-68,597_biosynthetic_gene_cluster (4% of genes show similarity)
Cluster 8	T1pks	4197361	4258545	Macbecin_biosynthetic_gene_cluster (39% of genes show similarity)
Cluster 9	Nrps	4302433	4362588	Kiamycin_biosynthetic_gene_cluster (10% of genes show similarity)
Cluster 10	T1pks-Nrps	4356144	4461507	Amychelin_biosynthetic_gene_cluster (31% of genes show similarity)
Cluster 11	Terpene	4926042	4947361	SF2575_biosynthetic_gene_cluster (4% of genes show similarity)
Cluster 12	T1pks	5232700	5300963	Nystatin-like_Pseudonocardia_polyene_biosynthetic_gene_cluster (47% of genes show similarity)
The following clusters are from record c00002_MH_Ae50:				
Cluster 13	Lassoptide	101953	123862	-

**Supplementary Figure 8. Screen shot of the antismash output for *Pseudonocardia* Ae505\_Ps2.**

Select Gene Cluster:  
Overview 1 2 3 4 5 6 7 8 9 10 11

**Identified secondary metabolite clusters**

Cluster	Type	From	To	Most similar known cluster
The following clusters are from record c00001_MH_Ae70:				
Cluster 1	Other	5853	69885	UK-68,597_biosynthetic_gene_cluster (4% of genes show similarity)
Cluster 2	Terpene	740562	761911	SF2575_biosynthetic_gene_cluster (6% of genes show similarity)
Cluster 3	Nrps-T1pks	1224015	1363220	Amychelin_biosynthetic_gene_cluster (31% of genes show similarity)
Cluster 4	T1pks	1563134	1702164	Nystatin-like_Pseudonocardia_polyene_biosynthetic_gene_cluster (73% of genes show similarity)
Cluster 5	Terpene	1992113	2013105	Carotenoid_biosynthetic_gene_cluster (27% of genes show similarity)
Cluster 6	Bacteriocin	2468953	2479774	-
Cluster 7	Oligosaccharide	3835997	3856674	-
Cluster 8	Ectoine	4424378	4434773	Ectoine_biosynthetic_gene_cluster (100% of genes show similarity)
Cluster 9	Bacteriocin	4915836	4926729	-
Cluster 10	Terpene	5302849	5324525	Brasilicardin_A_biosynthetic_gene_cluster (54% of genes show similarity)
The following clusters are from record c00002_MH_Ae70:				
Cluster 11	Lasso peptide	111865	133774	-

**Supplementary Figure 9. Screen shot of the antimash output for *Pseudonocardia* Ae706\_Ps2.**

Select Gene Cluster:  
Overview 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15

**Identified secondary metabolite clusters**

Cluster	Type	From	To	Most similar known cluster
The following clusters are from record unitig_4quiver:				
Cluster 1	Otherks	766234	807433	Galbonolides_biosynthetic_gene_cluster (16% of genes show similarity)
Cluster 2	Bacteriocin	1131133	1142233	-
Cluster 3	Other	1654291	1718271	UK-68,597_biosynthetic_gene_cluster (4% of genes show similarity)
Cluster 4	T1pks	2222655	2283874	Macbecin_biosynthetic_gene_cluster (47% of genes show similarity)
Cluster 5	Nrps	2326835	2386990	Kiamycin_biosynthetic_gene_cluster (10% of genes show similarity)
Cluster 6	T1pks-Nrps	2387695	2494012	Amychelin_biosynthetic_gene_cluster (31% of genes show similarity)
Cluster 7	Terpene	2956317	2977720	SF2575_biosynthetic_gene_cluster (4% of genes show similarity)
Cluster 8	T1pks	3259748	3397832	Nystatin-like_Pseudonocardia_polyene_biosynthetic_gene_cluster (73% of genes show similarity)
Cluster 9	Terpene	3688660	3709652	Isoreneratene_biosynthetic_gene_cluster (28% of genes show similarity)
Cluster 10	Terpene	4500688	4522868	Brasilicardin_A_biosynthetic_gene_cluster (45% of genes show similarity)
Cluster 11	Bacteriocin	4901917	4912810	-
Cluster 12	Ectoine	5387849	5398496	Ectoine_biosynthetic_gene_cluster (75% of genes show similarity)
Cluster 13	Oligosaccharide	5947675	5977172	-
The following clusters are from record unitig_6quiver:				
Cluster 14	Lasso peptide	60885	83439	-
The following clusters are from record unitig_17quiver:				
Cluster 15	T2pks	32985	76304	Arimetamycin_biosynthetic_gene_cluster (21% of genes show similarity)

**Supplementary Figure 10. Screen shot of the antimash output for *Pseudonocardia* Ae717\_Ps2.**

Clustal 2.1 (Larkin *et al.*, 2007) was used to align the 16S rRNA gene, the *rpsL* gene and the *rpoB* gene from different *Pseudonocardia* strains.

*Pseudonocardia* 16S rRNA gene alignment;

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Ae706Ps2_16S      AGAGTTTGATCCTGGCTCAGGACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAGC
Ae717Ps2_16S      AGAGTTTGATCCTGGCTCAGGACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAGC
Ae505Ps2_16S      AGAGTTTGATCCTGGCTCAGGACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAGC
Ae406Ps2_16S      AGAGTTTGATCCTGGCTCAGGACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAGC
Ae331Ps2_16S      AGAGTTTGATCCTGGCTCAGGACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAGC
Ae150APs1_16S     AGAGTTTGATCCTGGCTCAGGACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAGC
Ae707Ps1_16S      AGAGTTTGATCCTGGCTCAGGACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAGC
Ae168Ps1_16S      AGAGTTTGATCCTGGCTCAGGACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAGC

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Ae263Ps1\_16S AGAGTTTGATCCTGGCTCAGGACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAGC  
Ae356Ps1\_16S AGAGTTTGATCCTGGCTCAGGACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAGC  
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Ae706Ps2\_16S GGTAAGGCCCTTTCGGGGGTACACGAGCGGCGAACGGGTGAGTAACACGTGGGTGACCTG  
Ae717Ps2\_16S GGTAAGGCCCTTTCGGGGGTACACGAGCGGCGAACGGGTGAGTAACACGTGGGTGACCTG  
Ae505Ps2\_16S GGTAAGGCCCTTTCGGGGGTACACGAGCGGCGAACGGGTGAGTAACACGTGGGTGACCTG  
Ae406Ps2\_16S GGTAAGGCCCTTTCGGGGGTACACGAGCGGCGAACGGGTGAGTAACACGTGGGTGACCTG  
Ae331Ps2\_16S GGTAAGGCCCTTTCGGGGGTACACGAGCGGCGAACGGGTGAGTAACACGTGGGTGACCTG  
Ae150APs1\_16S GGTAAGGCCCTTTCGGGGGTACACGAGCGGCGAACGGGTGAGTAACACGTGGGTGACCTG  
Ae707Ps1\_16S GGTAAGGCCCTTTCGGGGGTACACGAGCGGCGAACGGGTGAGTAACACGTGGGTGACCTG  
Ae168Ps1\_16S GGTAAGGCCCTTTCGGGGGTACACGAGCGGCGAACGGGTGAGTAACACGTGGGTGACCTG  
Ae263Ps1\_16S GGTAAGGCCCTTTCGGGGGTACACGAGCGGCGAACGGGTGAGTAACACGTGGGTGACCTG  
Ae356Ps1\_16S GGTAAGGCCCTTTCGGGGGTACACGAGCGGCGAACGGGTGAGTAACACGTGGGTGACCTG  
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Ae706Ps2\_16S CCCTCCACTCTGGGATAAGCCTGGGAACTGGGTCTAATACCGGATAGGACCACTGGCTG  
Ae717Ps2\_16S CCCTCCACTCTGGGATAAGCCTGGGAACTGGGTCTAATACCGGATAGGACCACTGGCTG  
Ae505Ps2\_16S CCCTCCACTCTGGGATAAGCCTGGGAACTGGGTCTAATACCGGATAGGACCACTGGCTG  
Ae406Ps2\_16S CCCTCCACTCTGGGATAAGCCTGGGAACTGGGTCTAATACCGGATAGGACCACTGGCTG  
Ae331Ps2\_16S CCCTCCACTCTGGGATAAGCCTGGGAACTGGGTCTAATACCGGATAGGACCACTGGCTG  
Ae150APs1\_16S CCCTCCACTCTGGGATAAGCCCGGAACTGGGTCTAATACCGGATAGGACCTCTCAACG  
Ae707Ps1\_16S CCCTCCACTCTGGGATAAGCCCGGAACTGGGTCTAATACCGGATAGGACCTCTCAACG  
Ae168Ps1\_16S CCCTCCACTCTGGGATAAGCCCGGAACTGGGTCTAATACCGGATAGGACCTCTCAACG  
Ae263Ps1\_16S CCCTCCACTCTGGGATAAGCCCGGAACTGGGTCTAATACCGGATAGGACCTCTCAACG  
Ae356Ps1\_16S CCCTCCACTCTGGGATAAGCCCGGAACTGGGTCTAATACCGGATAGGACCTCTCAACG  
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Ae706Ps2\_16S CATGTTGGTGGTGGAAAGTTTTTT-CGGTGGGGGATGGGCCCGCGCCTATCAGCTTGT  
Ae717Ps2\_16S CATGTTGGTGGTGGAAAGTTTTTTTCGGTGGGGGATGGGCCCGCGCCTATCAGCTTGT  
Ae505Ps2\_16S CATGTTGGTGGTGGAAAGTTTTTT-CGGTGGGGGATGGGCCCGCGCCTATCAGCTTGT  
Ae406Ps2\_16S CATGTTGGTGGTGGAAAGTTTTTT-CGGTGGGGGATGGGCCCGCGCCTATCAGCTTGT  
Ae331Ps2\_16S CATGTTGGTGGTGGAAAGTTTTTT-CGGTGGGGGATGGGCCCGCGCCTATCAGCTTGT  
Ae150APs1\_16S CATGTTGGTGGTGGAAAGTTTTTT-CGGTGGGGGATGGGCCCGCGCCTATCAGCTTGT  
Ae707Ps1\_16S CATGTTGGTGGTGGAAAGTTTTTT-CGGTGGGGGATGGGCCCGCGCCTATCAGCTTGT  
Ae168Ps1\_16S CATGTTGGTGGTGGAAAGTTTTTT-CGGTGGGGGATGGGCCCGCGCCTATCAGCTTGT  
Ae263Ps1\_16S CATGTTGGTGGTGGAAAGTTTTTT-CGGTGGGGGATGGGCCCGCGCCTATCAGCTTGT  
Ae356Ps1\_16S CATGTTGGTGGTGGAAAGTTTTTT-CGGTGGGGGATGGGCCCGCGCCTATCAGCTTGT  
\*\*\*\* \* \*\*\*\*\*

Ae706Ps2\_16S TGGTGGGGTATGGCTACCAAGGCGGTGACGGGTAGCCGGCTGAGAGGGCGACCGGCC  
Ae717Ps2\_16S TGGTGGGGTATGGCTACCAAGGCGGTGACGGGTAGCCGGCTGAGAGGGCGACCGGCC  
Ae505Ps2\_16S TGGTGGGGTATGGCTACCAAGGCGGTGACGGGTAGCCGGCTGAGAGGGCGACCGGCC  
Ae406Ps2\_16S TGGTGGGGTATGGCTACCAAGGCGGTGACGGGTAGCCGGCTGAGAGGGCGACCGGCC  
Ae331Ps2\_16S TGGTGGGGTATGGCTACCAAGGCGGTGACGGGTAGCCGGCTGAGAGGGCGACCGGCC  
Ae150APs1\_16S TGGTGGGGTATGGCTACCAAGGCGGTGACGGGTAGCCGGCTGAGAGGGCGACCGGCC  
Ae707Ps1\_16S TGGTGGGGTATGGCTACCAAGGCGGTGACGGGTAGCCGGCTGAGAGGGCGACCGGCC  
Ae168Ps1\_16S TGGTGGGGTATGGCTACCAAGGCGGTGACGGGTAGCCGGCTGAGAGGGCGACCGGCC  
Ae263Ps1\_16S TGGTGGGGTATGGCTACCAAGGCGGTGACGGGTAGCCGGCTGAGAGGGCGACCGGCC  
Ae356Ps1\_16S TGGTGGGGTATGGCTACCAAGGCGGTGACGGGTAGCCGGCTGAGAGGGCGACCGGCC  
\*\*\*\*\*

Ae706Ps2\_16S ACACTGGGACTGAGACACGGCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCGC  
Ae717Ps2\_16S ACACTGGGACTGAGACACGGCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCGC  
Ae505Ps2\_16S ACACTGGGACTGAGACACGGCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCGC  
Ae406Ps2\_16S ACACTGGGACTGAGACACGGCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCGC  
Ae331Ps2\_16S ACACTGGGACTGAGACACGGCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCGC  
Ae150APs1\_16S ACACTGGGACTGAGACACGGCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCGC  
Ae707Ps1\_16S ACACTGGGACTGAGACACGGCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCGC  
Ae168Ps1\_16S ACACTGGGACTGAGACACGGCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCGC  
Ae263Ps1\_16S ACACTGGGACTGAGACACGGCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCGC  
Ae356Ps1\_16S ACACTGGGACTGAGACACGGCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCGC  
\*\*\*\*\*

Ae706Ps2\_16S AATGGGCGGAAGCCTGACGCAGCAGCAGCCGCGTGGGGGATGACGGCCTTCGGGTTGTAAA  
Ae717Ps2\_16S AATGGGCGGAAGCCTGACGCAGCAGCAGCCGCGTGGGGGATGACGGCCTTCGGGTTGTAAA  
Ae505Ps2\_16S AATGGGCGGAAGCCTGACGCAGCAGCAGCCGCGTGGGGGATGACGGCCTTCGGGTTGTAAA  
Ae406Ps2\_16S AATGGGCGGAAGCCTGACGCAGCAGCAGCCGCGTGGGGGATGACGGCCTTCGGGTTGTAAA  
Ae331Ps2\_16S AATGGGCGGAAGCCTGACGCAGCAGCAGCCGCGTGGGGGATGACGGCCTTCGGGTTGTAAA  
Ae150APs1\_16S AATGGGCGGAAGCCTGACGCAGCAGCAGCCGCGTGGGGGATGACGGCCTTCGGGTTGTAAA  
Ae707Ps1\_16S AATGGGCGGAAGCCTGACGCAGCAGCAGCCGCGTGGGGGATGACGGCCTTCGGGTTGTAAA  
Ae168Ps1\_16S AATGGGCGGAAGCCTGACGCAGCAGCAGCCGCGTGGGGGATGACGGCCTTCGGGTTGTAAA  
Ae263Ps1\_16S AATGGGCGGAAGCCTGACGCAGCAGCAGCCGCGTGGGGGATGACGGCCTTCGGGTTGTAAA  
Ae356Ps1\_16S AATGGGCGGAAGCCTGACGCAGCAGCAGCCGCGTGGGGGATGACGGCCTTCGGGTTGTAAA  
\*\*\*\*\*

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Ae717Ps2\_16S CCTCTTTCGCCAGGGACGAAGAGTGATTGACGGTACCTGGAGAAGAAGCACCGGCCAACT  
Ae505Ps2\_16S CCTCTTTCGCCAGGGACGAAGAGTGATTGACGGTACCTGGAGAAGAAGCACCGGCCAACT  
Ae406Ps2\_16S CCTCTTTCGCCAGGGACGAAGAGTGATTGACGGTACCTGGAGAAGAAGCACCGGCCAACT  
Ae331Ps2\_16S CCTCTTTCGCCAGGGACGAAGAGTGATTGACGGTACCTGGAGAAGAAGCACCGGCCAACT  
Ae150APs1\_16S CCTCTTTCGCCAGGGACGAAGCTTTTGTGACGGTACCTGGAGAAGAAGCACCGGCCAACT  
Ae707Ps1\_16S CCTCTTTCGCCAGGGACGAAGCTTTTGTGACGGTACCTGGAGAAGAAGCACCGGCCAACT  
Ae168Ps1\_16S CCTCTTTCGCCAGGGACGAAGCTTTTGTGACGGTACCTGGAGAAGAAGCACCGGCCAACT  
Ae263Ps1\_16S CCTCTTTCGCCAGGGACGAAGCTTTTGTGACGGTACCTGGAGAAGAAGCACCGGCCAACT  
Ae356Ps1\_16S CCTCTTTCGCCAGGGACGAAGCTTTTGTGACGGTACCTGGAGAAGAAGCACCGGCCAACT  
\*\*\*\*\* \* \*\*\*\*\*

Ae706Ps2\_16S ACGTGCCAGCAGCCGCGGTAACACGTAGGGTGCGAGCGTTGTCCGGAATTATTGGGCGTA  
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Ae505Ps2\_16S ACGTGCCAGCAGCCGCGGTAACACGTAGGGTGCGAGCGTTGTCCGGAATTATTGGGCGTA  
Ae406Ps2\_16S ACGTGCCAGCAGCCGCGGTAACACGTAGGGTGCGAGCGTTGTCCGGAATTATTGGGCGTA  
Ae331Ps2\_16S ACGTGCCAGCAGCCGCGGTAACACGTAGGGTGCGAGCGTTGTCCGGAATTATTGGGCGTA  
Ae150APs1\_16S ACGTGCCAGCAGCCGCGGTAACACGTAGGGTGCGAGCGTTGTCCGGAATTATTGGGCGTA  
Ae707Ps1\_16S ACGTGCCAGCAGCCGCGGTAACACGTAGGGTGCGAGCGTTGTCCGGAATTATTGGGCGTA  
Ae168Ps1\_16S ACGTGCCAGCAGCCGCGGTAACACGTAGGGTGCGAGCGTTGTCCGGAATTATTGGGCGTA  
Ae263Ps1\_16S ACGTGCCAGCAGCCGCGGTAACACGTAGGGTGCGAGCGTTGTCCGGAATTATTGGGCGTA  
Ae356Ps1\_16S ACGTGCCAGCAGCCGCGGTAACACGTAGGGTGCGAGCGTTGTCCGGAATTATTGGGCGTA  
\*\*\*\*\*

Ae706Ps2\_16S AAGAGCTCGTAGGCCGTTGTGTCGCGTCGGCCGTGAAAACCTGGGGCTTAACCTGAGCGT  
Ae717Ps2\_16S AAGAGCTCGTAGGCCGTTGTGTCGCGTCGGCCGTGAAAACCTGGGGCTTAACCTGAGCGT  
Ae505Ps2\_16S AAGAGCTCGTAGGCCGTTGTGTCGCGTCGGCCGTGAAAACCTGGGGCTTAACCTGAGCGT  
Ae406Ps2\_16S AAGAGCTCGTAGGCCGTTGTGTCGCGTCGGCCGTGAAAACCTGGGGCTTAACCTGAGCGT  
Ae331Ps2\_16S AAGAGCTCGTAGGCCGTTGTGTCGCGTCGGCCGTGAAAACCTGGGGCTTAACCTGAGCGT  
Ae150APs1\_16S AAGAGCTCGTAGGCCGTTGTGTCGCGTCGGCCGTGAAAACCTGGGGCTTAACCTGAGCGT  
Ae707Ps1\_16S AAGAGCTCGTAGGCCGTTGTGTCGCGTCGGCCGTGAAAACCTGGGGCTTAACCTGAGCGT  
Ae168Ps1\_16S AAGAGCTCGTAGGCCGTTGTGTCGCGTCGGCCGTGAAAACCTGGGGCTTAACCTGAGCGT  
Ae263Ps1\_16S AAGAGCTCGTAGGCCGTTGTGTCGCGTCGGCCGTGAAAACCTGGGGCTTAACCTGAGCGT  
Ae356Ps1\_16S AAGAGCTCGTAGGCCGTTGTGTCGCGTCGGCCGTGAAAACCTGGGGCTTAACCTGAGCGT  
\*\*\*\*\*

Ae706Ps2\_16S GCGGTCGATACGGGCATCACTTGAGTTCGGCAGGGGAGACTGGAATTCCTGGTGTAGCGG  
Ae717Ps2\_16S GCGGTCGATACGGGCATCACTTGAGTTCGGCAGGGGAGACTGGAATTCCTGGTGTAGCGG  
Ae505Ps2\_16S GCGGTCGATACGGGCATCACTTGAGTTCGGCAGGGGAGACTGGAATTCCTGGTGTAGCGG  
Ae406Ps2\_16S GCGGTCGATACGGGCATCACTTGAGTTCGGCAGGGGAGACTGGAATTCCTGGTGTAGCGG  
Ae331Ps2\_16S GCGGTCGATACGGGCATCACTTGAGTTCGGCAGGGGAGACTGGAATTCCTGGTGTAGCGG  
Ae150APs1\_16S GCGGTCGATACGGGCATCACTTGAGTTCGGCAGGGGAGACTGGAATTCCTGGTGTAGCGG  
Ae707Ps1\_16S GCGGTCGATACGGGCATCACTTGAGTTCGGCAGGGGAGACTGGAATTCCTGGTGTAGCGG  
Ae168Ps1\_16S GCGGTCGATACGGGCATCACTTGAGTTCGGCAGGGGAGACTGGAATTCCTGGTGTAGCGG  
Ae263Ps1\_16S GCGGTCGATACGGGCATCACTTGAGTTCGGCAGGGGAGACTGGAATTCCTGGTGTAGCGG  
Ae356Ps1\_16S GCGGTCGATACGGGCATCACTTGAGTTCGGCAGGGGAGACTGGAATTCCTGGTGTAGCGG  
\*\*\*\*\*

Ae706Ps2\_16S TGAAATGCCGAGATATCAGGAGGAACACCGGTGGCGAAGGCGGGTCTCTGGGCCGATACT  
Ae717Ps2\_16S TGAAATGCCGAGATATCAGGAGGAACACCGGTGGCGAAGGCGGGTCTCTGGGCCGATACT  
Ae505Ps2\_16S TGAAATGCCGAGATATCAGGAGGAACACCGGTGGCGAAGGCGGGTCTCTGGGCCGATACT  
Ae406Ps2\_16S TGAAATGCCGAGATATCAGGAGGAACACCGGTGGCGAAGGCGGGTCTCTGGGCCGATACT  
Ae331Ps2\_16S TGAAATGCCGAGATATCAGGAGGAACACCGGTGGCGAAGGCGGGTCTCTGGGCCGATACT  
Ae150APs1\_16S TGAAATGCCGAGATATCAGGAGGAACACCGGTGGCGAAGGCGGGTCTCTGGGCCGATACT  
Ae707Ps1\_16S TGAAATGCCGAGATATCAGGAGGAACACCGGTGGCGAAGGCGGGTCTCTGGGCCGATACT  
Ae168Ps1\_16S TGAAATGCCGAGATATCAGGAGGAACACCGGTGGCGAAGGCGGGTCTCTGGGCCGATACT  
Ae263Ps1\_16S TGAAATGCCGAGATATCAGGAGGAACACCGGTGGCGAAGGCGGGTCTCTGGGCCGATACT  
Ae356Ps1\_16S TGAAATGCCGAGATATCAGGAGGAACACCGGTGGCGAAGGCGGGTCTCTGGGCCGATACT  
\*\*\*\*\*

Ae706Ps2\_16S GACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCCTGGTAGTCCACGCC  
Ae717Ps2\_16S GACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCCTGGTAGTCCACGCC  
Ae505Ps2\_16S GACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCCTGGTAGTCCACGCC  
Ae406Ps2\_16S GACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCCTGGTAGTCCACGCC  
Ae331Ps2\_16S GACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCCTGGTAGTCCACGCC  
Ae150APs1\_16S GACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCCTGGTAGTCCACGCC  
Ae707Ps1\_16S GACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCCTGGTAGTCCACGCC  
Ae168Ps1\_16S GACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCCTGGTAGTCCACGCC  
Ae263Ps1\_16S GACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCCTGGTAGTCCACGCC  
Ae356Ps1\_16S GACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCCTGGTAGTCCACGCC  
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Ae706Ps2\_16S GTAAACGTTGGGCGTAGGTGTGGGGACCATTCACCGTTTCTGTGCCGAGCTAACGCA  
Ae717Ps2\_16S GTAAACGTTGGGCGTAGGTGTGGGGACCATTCACCGTTTCTGTGCCGAGCTAACGCA  
Ae505Ps2\_16S GTAAACGTTGGGCGTAGGTGTGGGGACCATTCACCGTTTCTGTGCCGAGCTAACGCA  
Ae406Ps2\_16S GTAAACGTTGGGCGTAGGTGTGGGGACCATTCACCGTTTCTGTGCCGAGCTAACGCA  
Ae331Ps2\_16S GTAAACGTTGGGCGTAGGTGTGGGGACCATTCACCGTTTCTGTGCCGAGCTAACGCA  
Ae150APs1\_16S GTAAACGTTGGGCGTAGGTGTGGGGACCATTCACCGTTTCTGTGCCGAGCTAACGCA



Ae707Ps1\_16S GTAAACGTTGGGCGCTAGGTGTGGGGACCATTCACGGTTTCTGCGCCGCAGCTAACGCA  
Ae168Ps1\_16S GTAAACGTTGGGCGCTAGGTGTGGGGACCATTCACGGTTTCTGCGCCGCAGCTAACGCA  
Ae263Ps1\_16S GTAAACGTTGGGCGCTAGGTGTGGGGACCATTCACGGTTTCTGCGCCGCAGCTAACGCA  
Ae356Ps1\_16S GTAAACGTTGGGCGCTAGGTGTGGGGACCATTCACGGTTTCTGCGCCGCAGCTAACGCA  
\*\*\*\*\*

Ae706Ps2\_16S TTAAGCGCCCCGCCTGGGGAGTACGGCCGCAAGGCTAAAACCTCAAAGGAATTGACGGGGG  
Ae717Ps2\_16S TTAAGCGCCCCGCCTGGGGAGTACGGCCGCAAGGCTAAAACCTCAAAGGAATTGACGGGGG  
Ae505Ps2\_16S TTAAGCGCCCCGCCTGGGGAGTACGGCCGCAAGGCTAAAACCTCAAAGGAATTGACGGGGG  
Ae406Ps2\_16S TTAAGCGCCCCGCCTGGGGAGTACGGCCGCAAGGCTAAAACCTCAAAGGAATTGACGGGGG  
Ae331Ps2\_16S TTAAGCGCCCCGCCTGGGGAGTACGGCCGCAAGGCTAAAACCTCAAAGGAATTGACGGGGG  
Ae150APs1\_16S TTAAGCGCCCCGCCTGGGGAGTACGGCCGCAAGGCTAAAACCTCAAAGGAATTGACGGGGG  
Ae707Ps1\_16S TTAAGCGCCCCGCCTGGGGAGTACGGCCGCAAGGCTAAAACCTCAAAGGAATTGACGGGGG  
Ae168Ps1\_16S TTAAGCGCCCCGCCTGGGGAGTACGGCCGCAAGGCTAAAACCTCAAAGGAATTGACGGGGG  
Ae263Ps1\_16S TTAAGCGCCCCGCCTGGGGAGTACGGCCGCAAGGCTAAAACCTCAAAGGAATTGACGGGGG  
Ae356Ps1\_16S TTAAGCGCCCCGCCTGGGGAGTACGGCCGCAAGGCTAAAACCTCAAAGGAATTGACGGGGG  
\*\*\*\*\*

Ae706Ps2\_16S CCCGCACAAGCGGCGGAGCATGTGGATTAATTCGATGCAACGCGAAGAACCTTACCTGGG  
Ae717Ps2\_16S CCCGCACAAGCGGCGGAGCATGTGGATTAATTCGATGCAACGCGAAGAACCTTACCTGGG  
Ae505Ps2\_16S CCCGCACAAGCGGCGGAGCATGTGGATTAATTCGATGCAACGCGAAGAACCTTACCTGGG  
Ae406Ps2\_16S CCCGCACAAGCGGCGGAGCATGTGGATTAATTCGATGCAACGCGAAGAACCTTACCTGGG  
Ae331Ps2\_16S CCCGCACAAGCGGCGGAGCATGTGGATTAATTCGATGCAACGCGAAGAACCTTACCTGGG  
Ae150APs1\_16S CCCGCACAAGCGGCGGAGCATGTGGATTAATTCGATGCAACGCGAAGAACCTTACCTGGG  
Ae707Ps1\_16S CCCGCACAAGCGGCGGAGCATGTGGATTAATTCGATGCAACGCGAAGAACCTTACCTGGG  
Ae168Ps1\_16S CCCGCACAAGCGGCGGAGCATGTGGATTAATTCGATGCAACGCGAAGAACCTTACCTGGG  
Ae263Ps1\_16S CCCGCACAAGCGGCGGAGCATGTGGATTAATTCGATGCAACGCGAAGAACCTTACCTGGG  
Ae356Ps1\_16S CCCGCACAAGCGGCGGAGCATGTGGATTAATTCGATGCAACGCGAAGAACCTTACCTGGG  
\*\*\*\*\*

Ae706Ps2\_16S TTTGACATGCACCAGACATCCCTAGAGATAGGGCTTCCCTTGTGGTTGGTGTGCAGGTGG  
Ae717Ps2\_16S TTTGACATGCACCAGACATCCCTAGAGATAGGGCTTCCCTTGTGGTTGGTGTGCAGGTGG  
Ae505Ps2\_16S TTTGACATGCACCAGACATCCCTAGAGATAGGGCTTCCCTTGTGGTTGGTGTGCAGGTGG  
Ae406Ps2\_16S TTTGACATGCACCAGACATCCCTAGAGATAGGGCTTCCCTTGTGGTTGGTGTGCAGGTGG  
Ae331Ps2\_16S TTTGACATGCACCAGACATCCCTAGAGATAGGGCTTCCCTTGTGGTTGGTGTGCAGGTGG  
Ae150APs1\_16S TTTGACATGCACCAGATCGCGGCAGAGATGTCGTTCCCTTGTGGCCTGTGTGCAGGTGG  
Ae707Ps1\_16S TTTGACATGCACAGGATCGCGGCAGAGATGTCGTTCCCTTGTGGCCTGTGTGCAGGTGG  
Ae168Ps1\_16S TTTGACATGCACAGGATCGCGGCAGAGATGTCGTTCCCTTGTGGCCTGTGTGCAGGTGG  
Ae263Ps1\_16S TTTGACATGCACAGGATCGCGGCAGAGATGTCGTTCCCTTGTGGCCTGTGTGCAGGTGG  
Ae356Ps1\_16S TTTGACATGCACAGGATCGCGGCAGAGATGTCGTTCCCTTGTGGCCTGTGTGCAGGTGG  
\*\*\*\*\*

Ae706Ps2\_16S TGCATGGCTGTCGTGAGTGTGGGTTAAGTCCCGCAACGAGCGCAA  
Ae717Ps2\_16S TGCATGGCTGTCGTGAGTGTGGGTTAAGTCCCGCAACGAGCGCAA  
Ae505Ps2\_16S TGCATGGCTGTCGTGAGTGTGGGTTAAGTCCCGCAACGAGCGCAA  
Ae406Ps2\_16S TGCATGGCTGTCGTGAGTGTGGGTTAAGTCCCGCAACGAGCGCAA  
Ae331Ps2\_16S TGCATGGCTGTCGTGAGTGTGGGTTAAGTCCCGCAACGAGCGCAA  
Ae150APs1\_16S TGCATGGCTGTCGTGAGTGTGGGTTAAGTCCCGCAACGAGCGCAA  
Ae707Ps1\_16S TGCATGGCTGTCGTGAGTGTGGGTTAAGTCCCGCAACGAGCGCAA  
Ae168Ps1\_16S TGCATGGCTGTCGTGAGTGTGGGTTAAGTCCCGCAACGAGCGCAA  
Ae263Ps1\_16S TGCATGGCTGTCGTGAGTGTGGGTTAAGTCCCGCAACGAGCGCAA  
Ae356Ps1\_16S TGCATGGCTGTCGTGAGTGTGGGTTAAGTCCCGCAACGAGCGCAA  
\*\*\*\*\*

Ae706Ps2\_16S CCCTTGTTCCATGTTGCCAGCACGTTATGGTGGGGACTCATGGGAGACTGCCGGGGTCAA  
Ae717Ps2\_16S CCCTTGTTCCATGTTGCCAGCACGTTATGGTGGGGACTCATGGGAGACTGCCGGGGTCAA  
Ae505Ps2\_16S CCCTTGTTCCATGTTGCCAGCACGTTATGGTGGGGACTCATGGGAGACTGCCGGGGTCAA  
Ae406Ps2\_16S CCCTTGTTCCATGTTGCCAGCACGTTATGGTGGGGACTCATGGGAGACTGCCGGGGTCAA  
Ae331Ps2\_16S CCCTTGTTCCATGTTGCCAGCACGTTATGGTGGGGACTCATGGGAGACTGCCGGGGTCAA  
Ae150APs1\_16S CCCTTATTCATGTTGCCAGCACGTTAGTGGTGGGGACTCATGGGAGACTGCCGGGGTCAA  
Ae707Ps1\_16S CCCTTATTCATGTTGCCAGCACGTTAGTGGTGGGGACTCATGGGAGACTGCCGGGGTCAA  
Ae168Ps1\_16S CCCTTATTCATGTTGCCAGCACGTTAGTGGTGGGGACTCATGGGAGACTGCCGGGGTCAA  
Ae263Ps1\_16S CCCTTATTCATGTTGCCAGCACGTTAGTGGTGGGGACTCATGGGAGACTGCCGGGGTCAA  
Ae356Ps1\_16S CCCTTATTCATGTTGCCAGCACGTTAGTGGTGGGGACTCATGGGAGACTGCCGGGGTCAA  
\*\*\*\*\*

Ae706Ps2\_16S CTCGGAGGAAGGTGGGGATGACGTCAGTCAAGTCATCATGCCCTTATGTCCAGGGCTTCACAC  
Ae717Ps2\_16S CTCGGAGGAAGGTGGGGATGACGTCAGTCAAGTCATCATGCCCTTATGTCCAGGGCTTCACAC  
Ae505Ps2\_16S CTCGGAGGAAGGTGGGGATGACGTCAGTCAAGTCATCATGCCCTTATGTCCAGGGCTTCACAC  
Ae406Ps2\_16S CTCGGAGGAAGGTGGGGATGACGTCAGTCAAGTCATCATGCCCTTATGTCCAGGGCTTCACAC  
Ae331Ps2\_16S CTCGGAGGAAGGTGGGGATGACGTCAGTCAAGTCATCATGCCCTTATGTCCAGGGCTTCACAC  
Ae150APs1\_16S CTCGGAGGAAGGTGGGGATGACGTCAGTCAAGTCATCATGCCCTTATGTCCAGGGCTTCACAC  
Ae707Ps1\_16S CTCGGAGGAAGGTGGGGATGACGTCAGTCAAGTCATCATGCCCTTATGTCCAGGGCTTCACAC  
Ae168Ps1\_16S CTCGGAGGAAGGTGGGGATGACGTCAGTCAAGTCATCATGCCCTTATGTCCAGGGCTTCACAC  
Ae263Ps1\_16S CTCGGAGGAAGGTGGGGATGACGTCAGTCAAGTCATCATGCCCTTATGTCCAGGGCTTCACAC  
Ae356Ps1\_16S CTCGGAGGAAGGTGGGGATGACGTCAGTCAAGTCATCATGCCCTTATGTCCAGGGCTTCACAC  
\*\*\*\*\*

Ae706Ps2\_16S ATGCTACAATGGCTCATAACAGAGGGGCTGCGAGACCGTGAGGTGGAGCGAATCCCTTAAAG  
Ae717Ps2\_16S ATGCTACAATGGCTCATAACAGAGGGGCTGCGAGACCGTGAGGTGGAGCGAATCCCTTAAAG  
Ae505Ps2\_16S ATGCTACAATGGCTCATAACAGAGGGGCTGCGAGACCGTGAGGTGGAGCGAATCCCTTAAAG  
Ae406Ps2\_16S ATGCTACAATGGCTCATAACAGAGGGGCTGCGAGACCGTGAGGTGGAGCGAATCCCTTAAAG  
Ae331Ps2\_16S ATGCTACAATGGCTCATAACAGAGGGGCTGCGAGACCGTGAGGTGGAGCGAATCCCTTAAAG  
Ae150APs1\_16S ATGCTACAATGGCTCATAACAGAGGGGCTGCGAGACCGTGAGGTGGAGCGAATCCCTTAAAG  
Ae707Ps1\_16S ATGCTACAATGGCTCATAACAGAGGGGCTGCGAGACTGTGAGGTGGAGCGAATCCCTTAAAG  
Ae168Ps1\_16S ATGCTACAATGGCTCATAACAGAGGGGCTGCGAGACCGTGAGGTGGAGCGAATCCCTTAAAG  
Ae263Ps1\_16S ATGCTACAATGGCTCATAACAGAGGGGCTGCGAGACCGTGAGGTGGAGCGAATCCCTTAAAG  
Ae356Ps1\_16S ATGCTACAATGGCTCATAACAGAGGGGCTGCGAGACCGTGAGGTGGAGCGAATCCCTTAAAG  
\*\*\*\*\*

Ae706Ps2\_16S TGAGTCTCAGTTCGGATCGGGGTCTGCAACTCGACCCCGTGAAGTTGGAGTCGCTAGTAA  
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Ae505Ps2\_16S TGAGTCTCAGTTCGGATCGGGGTCTGCAACTCGACCCCGTGAAGTTGGAGTCGCTAGTAA  
Ae406Ps2\_16S TGAGTCTCAGTTCGGATCGGGGTCTGCAACTCGACCCCGTGAAGTTGGAGTCGCTAGTAA  
Ae331Ps2\_16S TGAGTCTCAGTTCGGATCGGGGTCTGCAACTCGACCCCGTGAAGTTGGAGTCGCTAGTAA  
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Ae707Ps1\_16S TGAGTCTCAGTTCGGATCGGGGTCTGCAACTCGACCCCGTGAAGTTGGAGTCGCTAGTAA  
Ae168Ps1\_16S TGAGTCTCAGTTCGGATCGGGGTCTGCAACTCGACCCCGTGAAGTTGGAGTCGCTAGTAA  
Ae263Ps1\_16S TGAGTCTCAGTTCGGATCGGGGTCTGCAACTCGACCCCGTGAAGTTGGAGTCGCTAGTAA  
Ae356Ps1\_16S TGAGTCTCAGTTCGGATCGGGGTCTGCAACTCGACCCCGTGAAGTTGGAGTCGCTAGTAA  
\*\*\*\*\*

Ae706Ps2\_16S TCGCAGATCAGCAACGCTGCGGTGAATACGTTCCCGGGCCTTGTACACACCCGCCGTCAC  
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Ae505Ps2\_16S TCGCAGATCAGCAACGCTGCGGTGAATACGTTCCCGGGCCTTGTACACACCCGCCGTCAC  
Ae406Ps2\_16S TCGCAGATCAGCAACGCTGCGGTGAATACGTTCCCGGGCCTTGTACACACCCGCCGTCAC  
Ae331Ps2\_16S TCGCAGATCAGCAACGCTGCGGTGAATACGTTCCCGGGCCTTGTACACACCCGCCGTCAC  
Ae150APs1\_16S TCGCAGATCAGCAACGCTGCGGTGAATACGTTCCCGGGCCTTGTACACACCCGCCGTCAC  
Ae707Ps1\_16S TCGCAGATCAGCAACGCTGCGGTGAATACGTTCCCGGGCCTTGTACACACCCGCCGTCAC  
Ae168Ps1\_16S TCGCAGATCAGCAACGCTGCGGTGAATACGTTCCCGGGCCTTGTACACACCCGCCGTCAC  
Ae263Ps1\_16S TCGCAGATCAGCAACGCTGCGGTGAATACGTTCCCGGGCCTTGTACACACCCGCCGTCAC  
Ae356Ps1\_16S TCGCAGATCAGCAACGCTGCGGTGAATACGTTCCCGGGCCTTGTACACACCCGCCGTCAC  
\*\*\*\*\*

Ae706Ps2\_16S GTCACGAAAGTTGGTAAACACCCGAAGCCGGCGGCCAACCCCTTGTGGAGGGAGCTGTCGA  
Ae717Ps2\_16S GTCACGAAAGTTGGTAAACACCCGAAGCTGGCGGCCAACCCCTTGTGGAGGGAGCTGTCGA  
Ae505Ps2\_16S GTCACGAAAGTTGGTAAACACCCGAAGCCGGCGGCCAACCCCTTGTGGAGGGAGCTGTCGA  
Ae406Ps2\_16S GTCACGAAAGTTGGTAAACACCCGAAGCCGGCGGCCAACCCCTTGTGGAGGGAGCTGTCGA  
Ae331Ps2\_16S GTCACGAAAGTTGGTAAACACCCGAAGCCGGCGGCCAACCCCTTGTGGAGGGAGCTGTCGA  
Ae150APs1\_16S GTCACGAAAGTTGGTAAACACCCGAAGCCGGCGGCCAACCCCTTGTGGAGGGAGCTGTCGA  
Ae707Ps1\_16S GTCACGAAAGTTGGTAAACACCCGAAGCCGGCGGCCAACCCCTTGTGGAGGGAGCTGTCGA  
Ae168Ps1\_16S GTCACGAAAGTTGGTAAACACCCGAAGCCGGCGGCCAACCCCTTGTGGAGGGAGCTGTCGA  
Ae263Ps1\_16S GTCACGAAAGTTGGTAAACACCCGAAGCCGGCGGCCAACCCCTTGTGGAGGGAGCTGTCGA  
Ae356Ps1\_16S GTCACGAAAGTTGGTAAACACCCGAAGCCGGCGGCCAACCCCTTGTGGAGGGAGCTGTCGA  
\*\*\*\*\*

Ae706Ps2\_16S AGGTGGGACTGGCGATTGGGACGAAGTCGTAACAAGGTAGCCGTACCGGAAGGTGCGGCT  
Ae717Ps2\_16S AGGTGGGACTGGCGATTGGGACGAAGTCGTAACAAGGTAGCCGTACCGGAAGGTGCGGCT  
Ae505Ps2\_16S AGGTGGGACTGGCGATTGGGACGAAGTCGTAACAAGGTAGCCGTACCGGAAGGTGCGGCT  
Ae406Ps2\_16S AGGTGGGACTGGCGATTGGGACGAAGTCGTAACAAGGTAGCCGTACCGGAAGGTGCGGCT  
Ae331Ps2\_16S AGGTGGGACTGGCGATTGGGACGAAGTCGTAACAAGGTAGCCGTACCGGAAGGTGCGGCT  
Ae150APs1\_16S AGGTGGGACTGGCGATTGGGACGAAGTCGTAACAAGGTAGCCGTACCGGAAGGTGCGGCT  
Ae707Ps1\_16S AGGTGGGACTGGCGATTGGGACGAAGTCGTAACAAGGTAGCCGTACCGGAAGGTGCGGCT  
Ae168Ps1\_16S AGGTGGGACTGGCGATTGGGACGAAGTCGTAACAAGGTAGCCGTACCGGAAGGTGCGGCT  
Ae263Ps1\_16S AGGTGGGACTGGCGATTGGGACGAAGTCGTAACAAGGTAGCCGTACCGGAAGGTGCGGCT  
Ae356Ps1\_16S AGGTGGGACTGGCGATTGGGACGAAGTCGTAACAAGGTAGCCGTACCGGAAGGTGCGGCT  
\*\*\*\*\*

Ae706Ps2\_16S GGATCACCT  
Ae717Ps2\_16S GGATCACCT  
Ae505Ps2\_16S GGATCACCT  
Ae406Ps2\_16S GGATCACCT  
Ae331Ps2\_16S GGATCACCT  
Ae150APs1\_16S GGATCACCT  
Ae707Ps1\_16S GGATCACCT  
Ae168Ps1\_16S GGATCACCT  
Ae263Ps1\_16S GGATCACCT  
Ae356Ps1\_16S GGATCACCT  
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**Supplementary Table 2. 16S rRNA gene percentage identity across *Pseudonocardia* strains.**

	<b>Ae150 A_Ps1 _16S</b>	<b>Ae168 _Ps1_ _16S</b>	<b>Ae263 _Ps1_ _16S</b>	<b>Ae356 _Ps1_ _16S</b>	<b>Ae707 _Ps1_ _16S</b>	<b>Ae331 _Ps2_ _16S</b>	<b>Ae406 _Ps2_ _16S</b>	<b>Ae505 _Ps2_ _16S</b>	<b>Ae706 _Ps2_ _16S</b>	<b>Ae717 _Ps2_ _16S</b>
<b>Ae150 A_Ps1 _16S</b>	100	100	100	100	99.93	97.74	97.74	97.74	97.74	97.68
<b>Ae168 _Ps1_ _16S</b>	100	100	100	100	99.93	97.74	97.74	97.74	97.74	97.68
<b>Ae263 _Ps1_ _16S</b>	100	100	100	100	99.93	97.74	97.74	97.74	97.74	97.68
<b>Ae356 _Ps1_ _16S</b>	100	100	100	100	99.93	97.74	97.74	97.74	97.74	97.68
<b>Ae707 _Ps1_ _16S</b>	99.93	99.93	99.93	99.93	100	97.68	97.68	97.68	97.68	97.61
<b>Ae331 _Ps2_ _16S</b>	97.74	97.74	97.74	97.74	97.68	100	100	100	100	99.93
<b>Ae406 _Ps2_ _16S</b>	97.74	97.74	97.74	97.74	97.68	100	100	100	100	99.93
<b>Ae505 _Ps2_ _16S</b>	97.74	97.74	97.74	97.74	97.68	100	100	100	100	99.93
<b>Ae706 _Ps2_ _16S</b>	97.74	97.74	97.74	97.74	97.68	100	100	100	100	99.93
<b>Ae717 _Ps2_ _16S</b>	97.68	97.68	97.68	97.68	97.61	99.93	99.93	99.93	99.93	100

***Pseudonocardia rpsL* gene alignment;**

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Ae706Ps2_rpsL      ATGCCACGATCCAGCAGCTGGTCCGCAAGGGCCGCGAGGACAAGGTCTCCAAGACCAAG
Ae717Ps2_rpsL      ATGCCACGATCCAGCAGCTGGTCCGCAAGGGCCGCGAGGACAAGGTCTCCAAGACCAAG
Ae505Ps2_rpsL      ATGCCACGATCCAGCAGCTGGTCCGCAAGGGCCGCGAGGACAAGGTCTCCAAGACCAAG
Ae406Ps2_rpsL      ATGCCACGATCCAGCAGCTGGTCCGCAAGGGCCGCGAGGACAAGGTCTCCAAGACCAAG
Ae331Ps2_rpsL      ATGCCACGATCCAGCAGCTGGTCCGCAAGGGCCGCGAGGACAAGGTCTCCAAGACCAAG
Ae150APs1_rpsL     ATGCCACGATCCAGCAGCTGGTCCGCAAGGGCCGCGAGGACAAGGTCTCCAAGACCAAG
Ae168APs1_rpsL     ATGCCACGATCCAGCAGCTGGTCCGCAAGGGCCGCGAGGACAAGGTCTCCAAGACCAAG
Ae263APs1_rpsL     ATGCCACGATCCAGCAGCTGGTCCGCAAGGGCCGCGAGGACAAGGTCTCCAAGACCAAG
Ae356Ps1_rpsL      ATGCCACGATCCAGCAGCTGGTCCGCAAGGGCCGCGAGGACAAGGTCTCCAAGACCAAG
Ae707Ps1_rpsL      ATGCCACGATCCAGCAGCTGGTCCGCAAGGGCCGCGAGGACAAGGTCTCCAAGACCAAG
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Ae706Ps2_rpsL      ACCGCCGCGCTGAAGGGAAGCCCCAGCGCCGCGGGGTCTGCACCCGCGTGTACACCACC
Ae717Ps2_rpsL      ACCGCCGCGCTGAAGGGAAGCCCCAGCGCCGCGGGGTCTGCACCCGCGTGTACACCACC
Ae505Ps2_rpsL      ACCGCCGCGCTGAAGGGAAGCCCCAGCGCCGCGGGGTCTGCACCCGCGTGTACACCACC
Ae406Ps2_rpsL      ACCGCCGCGCTGAAGGGAAGCCCCAGCGCCGCGGGGTCTGCACCCGCGTGTACACCACC
Ae331Ps2_rpsL      ACCGCCGCGCTGAAGGGAAGCCCCAGCGCCGCGGGGTCTGCACCCGCGTGTACACCACC
Ae150APs1_rpsL     ACCGCCGCGCTGAAGGGAAGCCCCAGCGCCGCGGGGTCTGCACCCGCGTGTACACCACC
Ae168APs1_rpsL     ACCGCCGCGCTGAAGGGAAGCCCCAGCGCCGCGGGGTCTGCACCCGCGTGTACACCACC
Ae263APs1_rpsL     ACCGCCGCGCTGAAGGGAAGCCCCAGCGCCGCGGGGTCTGCACCCGCGTGTACACCACC
Ae356Ps1_rpsL      ACCGCCGCGCTGAAGGGAAGCCCCAGCGCCGCGGGGTCTGCACCCGCGTGTACACCACC
Ae707Ps1_rpsL      ACCGCCGCGCTGAAGGGAAGCCCCAGCGCCGCGGGGTCTGCACCCGCGTGTACACCACC
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**Supplementary Table 3. *rpsL* gene percentage identity across *Pseudonocardia* strains.**

	<b>Ae150 A_Ps1 <i>rpsL</i></b>	<b>Ae168 A_Ps1 <i>rpsL</i></b>	<b>Ae263 A_Ps1 <i>rpsL</i></b>	<b>Ae35 6_Ps1 <i>rpsL</i></b>	<b>Ae70 7_Ps1 <i>rpsL</i></b>	<b>Ae33 1_Ps2 <i>rpsL</i></b>	<b>Ae40 6_Ps2 <i>rpsL</i></b>	<b>Ae50 5_Ps2 <i>rpsL</i></b>	<b>Ae70 6_Ps2 <i>rpsL</i></b>	<b>Ae71 7_Ps2 <i>rpsL</i></b>
<b>Ae150 A_Ps1 <i>rpsL</i></b>	100	100	100	100	100	92.8	92.8	92.8	92.8	92.8
<b>Ae168 A_Ps1 <i>rpsL</i></b>	100	100	100	100	100	92.8	92.8	92.8	92.8	92.8
<b>Ae263 A_Ps1 <i>rpsL</i></b>	100	100	100	100	100	92.8	92.8	92.8	92.8	92.8
<b>Ae356 Ps1_r <i>psL</i></b>	100	100	100	100	100	92.8	92.8	92.8	92.8	92.8
<b>Ae707 _Ps1_r <i>psL</i></b>	100	100	100	100	100	92.8	92.8	92.8	92.8	92.8
<b>Ae331 _Ps2_r <i>psL</i></b>	92.8	92.8	92.8	92.8	92.8	100	100	100	100	100
<b>Ae406 _Ps2_r <i>psL</i></b>	92.8	92.8	92.8	92.8	92.8	100	100	100	100	100
<b>Ae505 _Ps2_r <i>psL</i></b>	92.8	92.8	92.8	92.8	92.8	100	100	100	100	100
<b>Ae706 _Ps2_r <i>psL</i></b>	92.8	92.8	92.8	92.8	92.8	100	100	100	100	100
<b>Ae717 _Ps2_r <i>psL</i></b>	92.8	92.8	92.8	92.8	92.8	100	100	100	100	100

***Pseudonocardia rpoB* gene alignment;**

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Ae331Ps2_rpoB      TTGGCTGTCTCCCGCGCCGCGCGACACCTCGACCCTCTCCGCTTCGGCGAACCCGAAC
Ae505Ps2_rpoB      TTGGCTGTCTCCCGCGCCGCGCGACACCTCGACCCTCTCCGCTTCGGCGAACCCGAAC
Ae406Ps2_rpoB      TTGGCTGTCTCCCGCGCCGCGCGACACCTCGACCCTCTCCGCTTCGGCGAACCCGAAC
Ae717Ps2_rpoB      TTGGCTGTCTCCCGCGCCGCGCGACACCTCGACCCTCTCCGCTTCGGCGAACCCGAAC
Ae706Ps2_rpoB      TTGGCTGTCTCCCGCGCCGCGCGACACCTCGACCCTCTCCGCTTCGGCGAACCCGAAC
Ae150Aps1_rpoB     TTGGCTGTCTCCCGCGCCGCGCGACACCTCGACCCTCTCCGCTTCGGCGAACCCGAAC
Ae168Ps1_rpoB      TTGGCTGTCTCCCGCGCCGCGCGACACCTCGACCCTCTCCGCTTCGGCGAACCCGAAC
Ae263Ps1_rpoB      TTGGCTGTCTCCCGCGCCGCGCGACACCTCGACCCTCTCCGCTTCGGCGAACCCGAAC
Ae356Ps1_rpoB      TTGGCTGTCTCCCGCGCCGCGCGACACCTCGACCCTCTCCGCTTCGGCGAACCCGAAC
Ae707Ps1_rpoB      TTGGCTGTCTCCCGCGCCGCGCGACACCTCGACCCTCTCCGCTTCGGCGAACCCGAAC
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Ae331Ps2_rpoB      TACCCCGGCGCACCCACCCGGGTCACCTTCGCGAAGATCGCCAGCCGTTGGAGGTCCCC
Ae505Ps2_rpoB      TGCCCGGCGCACCCACCCGGGTCACCTTCGCGAAGATCGCCAGCCGTTGGAGGTCCCC
Ae406Ps2_rpoB      TACCCCGGCGCACCCACCCGGGTCACCTTCGCGAAGATCGCCAGCCGTTGGAGGTCCCC
Ae717Ps2_rpoB      TACCCCGGCGCACCCACCCGGGTCACCTTCGCGAAGATCGCCAGCCGTTGGAGGTCCCC
Ae706Ps2_rpoB      TACCCCGGCGCACCCACCCGGGTCACCTTCGCGAAGATCGCCAGCCGTTGGAGGTCCCC
Ae150Aps1_rpoB     TACCCCGGTGCACCCACTCGGGTCACCTTCGCGAAGATCTCCGAGCCGCTGGAGGTCCCG
Ae168Ps1_rpoB      TACCCCGGTGCACCCACTCGGGTCACCTTCGCGAAGATCTCCGAGCCGCTGGAGGTCCCG
Ae263Ps1_rpoB      TACCCCGGTGCACCCACTCGGGTCACCTTCGCGAAGATCTCCGAGCCGCTGGAGGTCCCG
Ae356Ps1_rpoB      TACCCCGGTGCACCCACTCGGGTCACCTTCGCGAAGATCTCCGAGCCGCTGGAGGTCCCG
Ae707Ps1_rpoB      TACCCCGGTGCACCCACTCGGGTCACCTTCGCGAAGATCTCCGAGCCGCTGGAGGTCCCG
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Ae331Ps2\_rpoB GACCTTCTCGACCTGCAGATCCAGTCCCTACGAGTGGCTGGTCGGCAGCGAGGCCCTGGTTC  
Ae505Ps2\_rpoB GACCTTCTCGACCTGCAGATCCAGTCCCTACGAGTGGCTGGTCGGCAGCGAGGCCCTGGTTC  
Ae406Ps2\_rpoB GACCTTCTCGACCTGCAGATCCAGTCCCTACGAGTGGCTGGTCGGCAGCGAGGCCCTGGTTC  
Ae717Ps2\_rpoB GACCTTCTCGACCTGCAGATCCAGTCCCTACGAGTGGCTGGTCGGCAGCGAGGCCCTGGTTC  
Ae706Ps2\_rpoB GACCTTCTCGACCTGCAGATCCAGTCCCTACGAGTGGCTGGTCGGCAGCGAGGCCCTGGTTC  
Ae150APs1\_rpoB GACCTCCTCGACCTGCAGATCCAGTCCCTACGAGTGGCTCGTCGGCAGCGAGGCCCTGGTTC  
Ae168Ps1\_rpoB GACCTCCTCGACCTGCAGATCCAGTCCCTACGAGTGGCTCGTCGGCAGCGAGGCCCTGGTTC  
Ae263Ps1\_rpoB GACCTCCTCGACCTGCAGATCCAGTCCCTACGAGTGGCTCGTCGGCAGCGAGGCCCTGGTTC  
Ae356Ps1\_rpoB GACCTCCTCGACCTGCAGATCCAGTCCCTACGAGTGGCTCGTCGGCAGCGAGGCCCTGGTTC  
Ae707Ps1\_rpoB GACCTCCTCGACCTGCAGATCCAGTCCCTACGAGTGGCTCGTCGGCAGCGAGGCCCTGGTTC  
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Ae331Ps2\_rpoB CAGCGCCGGATCGAGGCCGGTGACGAGCTTCCGGTGAGCGGTCTGGAGGAGATCCTCACC  
Ae505Ps2\_rpoB CAGCGCCGGATCGAGGCCGGTGACGAGCTTCCGGTGAGCGGTCTGGAGGAGATCCTCACC  
Ae406Ps2\_rpoB CAGCGCCGGATCGAGGCCGGTGACGAGCTTCCGGTGAGCGGTCTGGAGGAGATCCTCACC  
Ae717Ps2\_rpoB CAGCGCCGGATCGAGGCCGGTGACGAGCTTCCGGTGAGCGGTCTGGAGGAGATCCTCACC  
Ae706Ps2\_rpoB CAGCGCCGGATCGAGGCCGGTGACGAGCTTCCGGTGAGCGGTCTGGAGGAGATCCTCACC  
Ae150APs1\_rpoB CAGCGCCGGATCGAGGCCGGCGACGACCTCCCGTGAGCGGTCTCGAGGAGATCCTCACC  
Ae168Ps1\_rpoB CAGCGCCGGATCGAGGCCGGCGACGACCTCCCGTGAGCGGTCTCGAGGAGATCCTCACC  
Ae263Ps1\_rpoB CAGCGCCGGATCGAGGCCGGCGACGACCTCCCGTGAGCGGTCTCGAGGAGATCCTCACC  
Ae356Ps1\_rpoB CAGCGCCGGATCGAGGCCGGCGACGACCTCCCGTGAGCGGTCTCGAGGAGATCCTCACC  
Ae707Ps1\_rpoB CAGCGCCGGATCGAGGCCGGCGACGACCTCCCGTGAGCGGTCTCGAGGAGATCCTCACC  
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Ae331Ps2\_rpoB GAGATCTCGCCGATCGAGGACTTCTCCGGTTCGATGTCGTCGTCCTTCTCCGACCTCGC  
Ae505Ps2\_rpoB GAGATCTCGCCGATCGAGGACTTCTCCGGTTCGATGTCGTCGTCCTTCTCCGACCTCGC  
Ae406Ps2\_rpoB GAGATCTCGCCGATCGAGGACTTCTCCGGTTCGATGTCGTCGTCCTTCTCCGACCTCGC  
Ae717Ps2\_rpoB GAGATCTCGCCGATCGAGGACTTCTCCGGTTCGATGTCGTCGTCCTTCTCCGACCTCGC  
Ae706Ps2\_rpoB GAGATCTCGCCGATCGAGGACTTCTCCGGTTCGATGTCGTCGTCCTTCTCCGACCTCGC  
Ae150APs1\_rpoB GAGATCTCCCGATCGAGGACTTCTCCGGTTCGATGTCGTCGTCCTTCTCCGACCTCGC  
Ae168Ps1\_rpoB GAGATCTCCCGATCGAGGACTTCTCCGGTTCGATGTCGTCGTCCTTCTCCGACCTCGC  
Ae263Ps1\_rpoB GAGATCTCCCGATCGAGGACTTCTCCGGTTCGATGTCGTCGTCCTTCTCCGACCTCGC  
Ae356Ps1\_rpoB GAGATCTCCCGATCGAGGACTTCTCCGGTTCGATGTCGTCGTCCTTCTCCGACCTCGC  
Ae707Ps1\_rpoB GAGATCTCCCGATCGAGGACTTCTCCGGTTCGATGTCGTCGTCCTTCTCCGACCTCGC  
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Ae331Ps2\_rpoB TTCGACGAGGTCAAGGCCTCCGTCGAGGAGTCCCGGGACAAGGACATGACCTACGGTGCC  
Ae505Ps2\_rpoB TTCGACGAGGTCAAGGCCTCCGTCGAGGAGTCCCGGGACAAGGACATGACCTACGGTGCC  
Ae406Ps2\_rpoB TTCGACGAGGTCAAGGCCTCCGTCGAGGAGTCCCGGGACAAGGACATGACCTACGGTGCC  
Ae717Ps2\_rpoB TTCGACGAGGTCAAGGCCTCCGTCGAGGAGTCCCGGGACAAGGACATGACCTACGGTGCC  
Ae706Ps2\_rpoB TTCGACGAGGTCAAGGCCTCCGTCGAGGAGTCCCGGGACAAGGACATGACCTACGGTGCC  
Ae150APs1\_rpoB TTCGACGAGGTCAAGGCCTCCGTCGAGGAGTCCCGGGACAAGGACATGACCTACGGTGCC  
Ae168Ps1\_rpoB TTCGACGAGGTCAAGGCCTCCGTCGAGGAGTCCCGGGACAAGGACATGACCTACGGTGCC  
Ae263Ps1\_rpoB TTCGACGAGGTCAAGGCCTCCGTCGAGGAGTCCCGGGACAAGGACATGACCTACGGTGCC  
Ae356Ps1\_rpoB TTCGACGAGGTCAAGGCCTCCGTCGAGGAGTCCCGGGACAAGGACATGACCTACGGTGCC  
Ae707Ps1\_rpoB TTCGACGAGGTCAAGGCCTCCGTCGAGGAGTCCCGGGACAAGGACATGACCTACGGTGCC  
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Ae331Ps2\_rpoB CCGCTGTTTCGTCACGGCGGAGTTCACCAACAACACCACCGGTGAGATCAAGTCCCAGACC  
Ae505Ps2\_rpoB CCGCTGTTTCGTCACGGCGGAGTTCACCAACAACACCACCGGTGAGATCAAGTCCCAGACC  
Ae406Ps2\_rpoB CCGCTGTTTCGTCACGGCGGAGTTCACCAACAACACCACCGGTGAGATCAAGTCCCAGACC  
Ae717Ps2\_rpoB CCGCTGTTTCGTCACGGCGGAGTTCACCAACAACACCACCGGTGAGATCAAGTCCCAGACC  
Ae706Ps2\_rpoB CCGCTGTTTCGTCACGGCGGAGTTCACCAACAACACCACCGGTGAGATCAAGTCCCAGACC  
Ae150APs1\_rpoB CCGCTGTTTCGTCACGGCGGAGTTCACCAACAACACCACCGGTGAGATCAAGTCCCAGACC  
Ae168Ps1\_rpoB CCGCTGTTTCGTCACGGCGGAGTTCACCAACAACACCACCGGTGAGATCAAGTCCCAGACC  
Ae263Ps1\_rpoB CCGCTGTTTCGTCACGGCGGAGTTCACCAACAACACCACCGGTGAGATCAAGTCCCAGACC  
Ae356Ps1\_rpoB CCGCTGTTTCGTCACGGCGGAGTTCACCAACAACACCACCGGTGAGATCAAGTCCCAGACC  
Ae707Ps1\_rpoB CCGCTGTTTCGTCACGGCGGAGTTCACCAACAACACCACCGGTGAGATCAAGTCCCAGACC  
\*\*\*\*\*

Ae331Ps2\_rpoB GTCTTCATGGGCGAGTTCGCCGTGATGACCGACAAGGGCACGTTTCATCATCAACGGCACC  
Ae505Ps2\_rpoB GTCTTCATGGGCGAGTTCGCCGTGATGACCGACAAGGGCACGTTTCATCATCAACGGCACC  
Ae406Ps2\_rpoB GTCTTCATGGGCGAGTTCGCCGTGATGACCGACAAGGGCACGTTTCATCATCAACGGCACC  
Ae717Ps2\_rpoB GTCTTCATGGGCGAGTTCGCCGTGATGACCGACAAGGGCACGTTTCATCATCAACGGCACC  
Ae706Ps2\_rpoB GTCTTCATGGGCGAGTTCGCCGTGATGACCGACAAGGGCACGTTTCATCATCAACGGCACC  
Ae150APs1\_rpoB GTGTTTCATGGGTGAGTTCGCCGTGATGACCGACAAGGGCACCTTCATCATCAACGGCACC  
Ae168Ps1\_rpoB GTGTTTCATGGGTGAGTTCGCCGTGATGACCGACAAGGGCACCTTCATCATCAACGGCACC  
Ae263Ps1\_rpoB GTGTTTCATGGGTGAGTTCGCCGTGATGACCGACAAGGGCACCTTCATCATCAACGGCACC  
Ae356Ps1\_rpoB GTGTTTCATGGGTGAGTTCGCCGTGATGACCGACAAGGGCACCTTCATCATCAACGGCACC  
Ae707Ps1\_rpoB GTGTTTCATGGGTGAGTTCGCCGTGATGACCGACAAGGGCACCTTCATCATCAACGGCACC  
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Ae331Ps2\_rpoB GAGCGCGTCGTCGTCGTCGAGTCCGTTCCGCGGGTGTCTACTTCGACCACGCGATC  
Ae505Ps2\_rpoB GAGCGCGTCGTCGTCGTCGAGTCCGTTCCGCGGGTGTCTACTTCGACCACGCGATC  
Ae406Ps2\_rpoB GAGCGCGTCGTCGTCGTCGAGTCCGTTCCGCGGGTGTCTACTTCGACCACGCGATC  
Ae717Ps2\_rpoB GAGCGCGTCGTCGTCGTCGAGTCCGTTCCGCGGGTGTCTACTTCGACCACGCGATC  
Ae706Ps2\_rpoB GAGCGCGTCGTCGTCGTCGAGTCCGTTCCGCGGGTGTCTACTTCGACCACGCGATC

Ae150Aps1\_rpoB GAGCGCGTTCGTCGTGTCGCAGCTCGTCCGGTCGCCGGGTGTGTACTTCGACCACTCGATC  
Ae168Ps1\_rpoB GAGCGCGTTCGTCGTGTCGCAGCTCGTCCGGTCGCCGGGTGTGTACTTCGACCACTCGATC  
Ae263Ps1\_rpoB GAGCGCGTTCGTCGTGTCGCAGCTCGTCCGGTCGCCGGGTGTGTACTTCGACCACTCGATC  
Ae356Ps1\_rpoB GAGCGCGTTCGTCGTGTCGCAGCTCGTCCGGTCGCCGGGTGTGTACTTCGACCACTCGATC  
Ae707Ps1\_rpoB GAGCGCGTTCGTCGTGTCGCAGCTCGTCCGGTCGCCGGGTGTGTACTTCGACCACTCGATC  
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Ae331Ps2\_rpoB GACAAGACGACCCGAGAAGGACGCTACTCGGTCAAGATCATCCCAGCCGGGGCGCGTGG  
Ae505Ps2\_rpoB GACAAGACGACCCGAGAAGGACGCTACTCGGTCAAGATCATCCCAGCCGGGGCGCGTGG  
Ae406Ps2\_rpoB GACAAGACGACCCGAGAAGGACGCTACTCGGTCAAGATCATCCCAGCCGGGGCGCGTGG  
Ae717Ps2\_rpoB GACAAGACGACCCGAGAAGGACGCTACTCGGTCAAGATCATCCCAGCCGGGGCGCGTGG  
Ae706Ps2\_rpoB GACAAGACGACCCGAGAAGGACGCTACTCGGTCAAGATCATCCCAGCCGGGGCGCGTGG  
Ae150Aps1\_rpoB GACAAGACGACCCGAGAAGGACGCTACTCGGTCAAGATCATCCCAGCCGGGGTGCCTGG  
Ae168Ps1\_rpoB GACAAGACGACCCGAGAAGGACGCTACTCGGTCAAGATCATCCCAGCCGGGGTGCCTGG  
Ae263Ps1\_rpoB GACAAGACGACCCGAGAAGGACGCTACTCGGTCAAGATCATCCCAGCCGGGGTGCCTGG  
Ae356Ps1\_rpoB GACAAGACGACCCGAGAAGGACGCTACTCGGTCAAGATCATCCCAGCCGGGGTGCCTGG  
Ae707Ps1\_rpoB GACAAGACGACCCGAGAAGGACGCTACTCGGTCAAGATCATCCCAGCCGGGGTGCATGG  
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Ae331Ps2\_rpoB CTGGAGTTCGACGTCGACAAGCGCGACACCGTCCGGTGTCCGCATCGACCCGCAAGCGCCG  
Ae505Ps2\_rpoB CTGGAGTTCGACGTCGACAAGCGCGACACCGTCCGGTGTCCGCATCGACCCGCAAGCGCCG  
Ae406Ps2\_rpoB CTGGAGTTCGACGTCGACAAGCGCGACACCGTCCGGTGTCCGCATCGACCCGCAAGCGCCG  
Ae717Ps2\_rpoB CTGGAGTTCGACGTCGACAAGCGCGACACCGTCCGGTGTCCGCATCGACCCGCAAGCGCCG  
Ae706Ps2\_rpoB CTGGAGTTCGACGTCGACAAGCGCGACACCGTCCGGTGTCCGCATCGACCCGCAAGCGCCG  
Ae150Aps1\_rpoB CTGGAGTTCGACGTCGACAAGCGCGACACCGTCCGGTGTCCGCATCGACCCGCAAGCGCCG  
Ae168Ps1\_rpoB CTGGAGTTCGACGTCGACAAGCGCGACACCGTCCGGTGTCCGCATCGACCCGCAAGCGCCG  
Ae263Ps1\_rpoB CTGGAGTTCGACGTCGACAAGCGCGACACCGTCCGGTGTCCGCATCGACCCGCAAGCGCCG  
Ae356Ps1\_rpoB CTGGAGTTCGACGTCGACAAGCGCGACACCGTCCGGTGTCCGCATCGACCCGCAAGCGCCG  
Ae707Ps1\_rpoB CTGGAGTTCGACGTCGACAAGCGCGACACCGTCCGGTGTCCGCATCGACCCGCAAGCGCCG  
\*\*\*\*\*

Ae331Ps2\_rpoB CAGCCGGTACCCTGCTGCTGAAGGCCCTGGGCTGGACCCGCGAGCAGATCGGTGAGCGT  
Ae505Ps2\_rpoB CAGCCGGTACCCTGCTGCTGAAGGCCCTGGGCTGGACCCGCGAGCAGATCGGTGAGCGT  
Ae406Ps2\_rpoB CAGCCGGTACCCTGCTGCTGAAGGCCCTGGGCTGGACCCGCGAGCAGATCGGTGAGCGT  
Ae717Ps2\_rpoB CAGCCGGTACCCTGCTGCTGAAGGCCCTGGGCTGGACCCGCGAGCAGATCGGTGAGCGT  
Ae706Ps2\_rpoB CAGCCGGTACCCTGCTGCTGAAGGCCCTGGGCTGGACCCGCGAGCAGATCGGTGAGCGT  
Ae150Aps1\_rpoB CAGCCGGTACCCTGCTGCTGAAGGCCCTGGGCTGGACCCGCGAGCAGATCGGTGAGCGT  
Ae168Ps1\_rpoB CAGCCGGTACCCTGCTGCTGAAGGCCCTGGGCTGGACCCGCGAGCAGATCGGTGAGCGT  
Ae263Ps1\_rpoB CAGCCGGTACCCTGCTGCTGAAGGCCCTGGGCTGGACCCGCGAGCAGATCGGTGAGCGT  
Ae356Ps1\_rpoB CAGCCGGTACCCTGCTGCTGAAGGCCCTGGGCTGGACCCGCGAGCAGATCGGTGAGCGT  
Ae707Ps1\_rpoB CAGCCGGTACCCTGCTGCTGAAGGCCCTGGGCTGGACCCGCGAGCAGATCGGTGAGCGT  
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Ae331Ps2\_rpoB TTCGGGTTTCCGAGACGATCATGACGACGCTCGAGAAGGACAACACCCGCGGGCCAGGAC  
Ae505Ps2\_rpoB TTCGGGTTTCCGAGACGATCATGACGACGCTCGAGAAGGACAACACCCGCGGGCCAGGAC  
Ae406Ps2\_rpoB TTCGGGTTTCCGAGACGATCATGACGACGCTCGAGAAGGACAACACCCGCGGGCCAGGAC  
Ae717Ps2\_rpoB TTCGGGTTTCCGAGACGATCATGACGACGCTCGAGAAGGACAACACCCGCGGGCCAGGAC  
Ae706Ps2\_rpoB TTCGGGTTTCCGAGACGATCATGACGACGCTCGAGAAGGACAACACCCGCGGGCCAGGAC  
Ae150Aps1\_rpoB TTCGGGTTTCCGAGACGATCATGACGACGCTCGAGAAGGACAACACCCGCGGGTCAAGGAC  
Ae168Ps1\_rpoB TTCGGGTTTCCGAGACGATCATGACGACGCTCGAGAAGGACAACACCCGCGGGTCAAGGAC  
Ae263Ps1\_rpoB TTCGGGTTTCCGAGACGATCATGACGACGCTCGAGAAGGACAACACCCGCGGGTCAAGGAC  
Ae356Ps1\_rpoB TTCGGGTTTCCGAGACGATCATGACGACGCTCGAGAAGGACAACACCCGCGGGTCAAGGAC  
Ae707Ps1\_rpoB TTCGGGTTTCCGAGACGATCATGACGACGCTCGAGAAGGACAACACCCGCGGGTCAAGGAC  
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Ae331Ps2\_rpoB GAGGCGTGTCTCGACATCTACCGCAAGCTGCGCCCCGGCGAGCCCGGACGCGGAGTCCG  
Ae505Ps2\_rpoB GAGGCGTGTCTCGACATCTACCGCAAGCTGCGCCCCGGCGAGCCCGGACGCGGAGTCCG  
Ae406Ps2\_rpoB GAGGCGTGTCTCGACATCTACCGCAAGCTGCGCCCCGGCGAGCCCGGACGCGGAGTCCG  
Ae717Ps2\_rpoB GAGGCGTGTCTCGACATCTACCGCAAGCTGCGCCCCGGCGAGCCCGGACGCGGAGTCCG  
Ae706Ps2\_rpoB GAGGCGTGTCTCGACATCTACCGCAAGCTGCGCCCCGGCGAGCCCGGACGCGGAGTCCG  
Ae150Aps1\_rpoB GAGGCGTGTCTCGACATCTACCGCAAGCTGCGCCCCGGTGTAGCCCGGACGCGGAGAGC  
Ae168Ps1\_rpoB GAGGCGTGTCTCGACATCTACCGCAAGCTGCGCCCCGGTGTAGCCCGGACGCGGAGAGC  
Ae263Ps1\_rpoB GAGGCGTGTCTCGACATCTACCGCAAGCTGCGCCCCGGTGTAGCCCGGACGCGGAGAGC  
Ae356Ps1\_rpoB GAGGCGTGTCTCGACATCTACCGCAAGCTGCGCCCCGGTGTAGCCCGGACGCGGAGAGC  
Ae707Ps1\_rpoB GAGGCGTGTCTCGACATCTACCGCAAGCTGCGCCCCGGTGTAGCCCGGACGCGGAGAGC  
\*\*\*\*\*

Ae331Ps2\_rpoB GCCCAGGCGCTCCTGGAGAACCTGTTCTTCAAGGACAAGCGCTACGACATGGCCAAGGTC  
Ae505Ps2\_rpoB GCCCAGGCGCTCCTGGAGAACCTGTTCTTCAAGGACAAGCGCTACGACATGGCCAAGGTC  
Ae406Ps2\_rpoB GCCCAGGCGCTCCTGGAGAACCTGTTCTTCAAGGACAAGCGCTACGACATGGCCAAGGTC  
Ae717Ps2\_rpoB GCCCAGGCGCTCCTGGAGAACCTGTTCTTCAAGGACAAGCGCTACGACATGGCCAAGGTC  
Ae706Ps2\_rpoB GCCCAGGCGCTCCTGGAGAACCTGTTCTTCAAGGACAAGCGCTACGACATGGCCAAGGTC  
Ae150Aps1\_rpoB GCCCAGGCGCTCCTGGAGAACCTGTTCTTCAAGGACAAGCGCTACGACATGGCCAAGGTC  
Ae168Ps1\_rpoB GCCCAGGCGCTCCTGGAGAACCTGTTCTTCAAGGACAAGCGCTACGACATGGCCAAGGTC  
Ae263Ps1\_rpoB GCCCAGGCGCTCCTGGAGAACCTGTTCTTCAAGGACAAGCGCTACGACATGGCCAAGGTC  
Ae356Ps1\_rpoB GCCCAGGCGCTCCTGGAGAACCTGTTCTTCAAGGACAAGCGCTACGACATGGCCAAGGTC  
Ae707Ps1\_rpoB GCCCAGGCGCTCCTGGAGAACCTGTTCTTCAAGGACAAGCGCTACGACATGGCCAAGGTC

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Ae331Ps2\_rpoB GGTGCTACAAGGCCAACAGAAGCTCGGTCTCGACATCGACAACTCGGTCGGCAGCCTG  
Ae505Ps2\_rpoB GGTGCTACAAGGCCAACAGAAGCTCGGTCTCGACATCGACAACTCGGTCGGCAGCCTG  
Ae406Ps2\_rpoB GGTGCTACAAGGCCAACAGAAGCTCGGTCTCGACATCGACAACTCGGTCGGCAGCCTG  
Ae717Ps2\_rpoB GGTGCTACAAGGCCAACAGAAGCTCGGTCTCGACATCGACAACTCGGTCGGCAGCCTG  
Ae706Ps2\_rpoB GGTGCTACAAGGCCAACAGAAGCTCGGTCTCGACATCGACAACTCGGTCGGCAGCCTG  
Ae150APs1\_rpoB GGGCGCTACAAGGCCAACAGAAGCTCGGTCTGGACATCGAGAACTCGGTCGGCAGCCTG  
Ae168Ps1\_rpoB GGGCGCTACAAGGCCAACAGAAGCTCGGTCTGGACATCGAGAACTCGGTCGGCAGCCTG  
Ae263Ps1\_rpoB GGGCGCTACAAGGCCAACAGAAGCTCGGTCTGGACATCGAGAACTCGGTCGGCAGCCTG  
Ae356Ps1\_rpoB GGGCGCTACAAGGCCAACAGAAGCTCGGTCTGGACATCGAGAACTCGGTCGGCAGCCTG  
Ae707Ps1\_rpoB GGGCGCTACAAGGCCAACAGAAGCTCGGTCTGGACATCGAGAACTCGGTCGGCAGCCTG  
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Ae331Ps2\_rpoB ACCGAGGAGGATGTCCGCCACCACATCGAGTACCTCGTCCGGCTGCACGCCGCGGAGACC  
Ae505Ps2\_rpoB ACCGAGGAGGATGTCCGCCACCACATCGAGTACCTCGTCCGGCTGCACGCCGCGGAGACC  
Ae406Ps2\_rpoB ACCGAGGAGGATGTCCGCCACCACATCGAGTACCTCGTCCGGCTGCACGCCGCGGAGACC  
Ae717Ps2\_rpoB ACCGAGGAGGATGTCCGCCACCACATCGAGTACCTCGTCCGGCTGCACGCCGCGGAGACC  
Ae706Ps2\_rpoB ACCGAGGAGGATGTCCGCCACCACATCGAGTACCTCGTCCGGCTGCACGCCGCGGAGACC  
Ae150APs1\_rpoB ACCGAGGAGGACGTCCGCCACGACATCGAGTACCTCGTCCGGCTGCACGCCGCGGAGACC  
Ae168Ps1\_rpoB ACCGAGGAGGACGTCCGCCACGACATCGAGTACCTCGTCCGGCTGCACGCCGCGGAGACC  
Ae263Ps1\_rpoB ACCGAGGAGGACGTCCGCCACGACATCGAGTACCTCGTCCGGCTGCACGCCGCGGAGACC  
Ae356Ps1\_rpoB ACCGAGGAGGACGTCCGCCACGACATCGAGTACCTCGTCCGGCTGCACGCCGCGGAGACC  
Ae707Ps1\_rpoB ACCGAGGAGGACGTCCGCCACGACATCGAGTACCTCGTCCGGCTGCACGCCGCGGAGACC  
\*\*\*\*\*

Ae331Ps2\_rpoB ACGATGACCGTGGGTTCGGGTGACTCCGCGGGGAGATCCCGGTGAGACCGACGACATC  
Ae505Ps2\_rpoB ACGATGACCGTGGGTTCGGGTGACTCCGCGGGGAGATCCCGGTGAGACCGACGACATC  
Ae406Ps2\_rpoB ACGATGACCGTGGGTTCGGGTGACTCCGCGGGGAGATCCCGGTGAGACCGACGACATC  
Ae717Ps2\_rpoB ACGATGACCGTGGGTTCGGGTGACTCCGCGGGGAGATCCCGGTGAGACCGACGACATC  
Ae706Ps2\_rpoB ACGATGACCGTGGGTTCGGGTGACTCCGCGGGGAGATCCCGGTGAGACCGACGACATC  
Ae150APs1\_rpoB ACGATGTCGGTGGGCTCCGCGGACTCCGCCGGGAGATCCCGGTGAGACCGACGACATC  
Ae168Ps1\_rpoB ACGATGTCGGTGGGCTCCGCGGACTCCGCCGGGAGATCCCGGTGAGACCGACGACATC  
Ae263Ps1\_rpoB ACGATGTCGGTGGGCTCCGCGGACTCCGCCGGGAGATCCCGGTGAGACCGACGACATC  
Ae356Ps1\_rpoB ACGATGTCGGTGGGCTCCGCGGACTCCGCCGGGAGATCCCGGTGAGACCGACGACATC  
Ae707Ps1\_rpoB ACGATGTCGGTGGGCTCCGCGGACTCCGCCGGGAGATCCCGGTGAGACCGACGACATC  
\*\*\*\*\*

Ae331Ps2\_rpoB GACCACTTCGGCAACCGGCGCTGCGCACCGTCCGGCAGCTGATCCAGAACCAGGTCCGG  
Ae505Ps2\_rpoB GACCACTTCGGCAACCGGCGCTGCGCACCGTCCGGCAGCTGATCCAGAACCAGGTCCGG  
Ae406Ps2\_rpoB GACCACTTCGGCAACCGGCGCTGCGCACCGTCCGGCAGCTGATCCAGAACCAGGTCCGG  
Ae717Ps2\_rpoB GACCACTTCGGCAACCGGCGCTGCGCACCGTCCGGCAGCTGATCCAGAACCAGGTCCGG  
Ae706Ps2\_rpoB GACCACTTCGGCAACCGGCGCTGCGCACCGTCCGGCAGCTGATCCAGAACCAGGTCCGG  
Ae150APs1\_rpoB GACCACTTCGGCAACCGGCGCTGCGCACCGTCCGGCAGCTGATCCAGAACCAGGTCCGG  
Ae168Ps1\_rpoB GACCACTTCGGCAACCGGCGCTGCGCACCGTCCGGCAGCTGATCCAGAACCAGGTCCGG  
Ae263Ps1\_rpoB GACCACTTCGGCAACCGGCGCTGCGCACCGTCCGGCAGCTGATCCAGAACCAGGTCCGG  
Ae356Ps1\_rpoB GACCACTTCGGCAACCGGCGCTGCGCACCGTCCGGCAGCTGATCCAGAACCAGGTCCGG  
Ae707Ps1\_rpoB GACCACTTCGGCAACCGGCGCTGCGCACCGTCCGGCAGCTGATCCAGAACCAGGTCCGG  
\*\*\*\*\*

Ae331Ps2\_rpoB GTCGGTCTGTCCCGCACCAGCGGGTCTCGTCCGCGAGCGGATGACCACCCAGGACGTCGAG  
Ae505Ps2\_rpoB GTCGGTCTGTCCCGCACCAGCGGGTCTCGTCCGCGAGCGGATGACCACCCAGGACGTCGAG  
Ae406Ps2\_rpoB GTCGGTCTGTCCCGCACCAGCGGGTCTCGTCCGCGAGCGGATGACCACCCAGGACGTCGAG  
Ae717Ps2\_rpoB GTCGGTCTGTCCCGCACCAGCGGGTCTCGTCCGCGAGCGGATGACCACCCAGGACGTCGAG  
Ae706Ps2\_rpoB GTCGGTCTGTCCCGCACCAGCGGGTCTCGTCCGCGAGCGGATGACCACCCAGGACGTCGAG  
Ae150APs1\_rpoB GTCGGTCTGTCCCGCACCAGCGGGTCTCGTCCGCGAGCGGATGACCACCCAGGACGTCGAG  
Ae168Ps1\_rpoB GTCGGTCTGTCCCGCACCAGCGGGTCTCGTCCGCGAGCGGATGACCACCCAGGACGTCGAG  
Ae263Ps1\_rpoB GTCGGTCTGTCCCGCACCAGCGGGTCTCGTCCGCGAGCGGATGACCACCCAGGACGTCGAG  
Ae356Ps1\_rpoB GTCGGTCTGTCCCGCACCAGCGGGTCTCGTCCGCGAGCGGATGACCACCCAGGACGTCGAG  
Ae707Ps1\_rpoB GTCGGTCTGTCCCGCACCAGCGGGTCTCGTCCGCGAGCGGATGACCACCCAGGACGTCGAG  
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Ae331Ps2\_rpoB GCCATCACGCCGAGACCCCTGATCAACACCCGGCCGATCACGGCCGCGATCCGGGAGTTC  
Ae505Ps2\_rpoB GCCATCACGCCGAGACCCCTGATCAACACCCGGCCGATCACGGCCGCGATCCGGGAGTTC  
Ae406Ps2\_rpoB GCCATCACGCCGAGACCCCTGATCAACACCCGGCCGATCACGGCCGCGATCCGGGAGTTC  
Ae717Ps2\_rpoB GCCATCACGCCGAGACCCCTGATCAACACCCGGCCGATCACGGCCGCGATCCGGGAGTTC  
Ae706Ps2\_rpoB GCCATCACGCCGAGACCCCTGATCAACACCCGGCCGATCACGGCCGCGATCCGGGAGTTC  
Ae150APs1\_rpoB GCGATCACGCCGAGACCCCTGATCAACACCCGGCCGATCACGGCCGCGATCCGGGAGTTC  
Ae168Ps1\_rpoB GCGATCACGCCGAGACCCCTGATCAACACCCGGCCGATCACGGCCGCGATCCGGGAGTTC  
Ae263Ps1\_rpoB GCGATCACGCCGAGACCCCTGATCAACACCCGGCCGATCACGGCCGCGATCCGGGAGTTC  
Ae356Ps1\_rpoB GCGATCACGCCGAGACCCCTGATCAACACCCGGCCGATCACGGCCGCGATCCGGGAGTTC  
Ae707Ps1\_rpoB GCGATCACGCCGAGACCCCTGATCAACACCCGGCCGATCACGGCCGCGATCCGGGAGTTC  
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Ae331Ps2\_rpoB TTCGGCACCTCGCAGCTGTGCGAGTTCATGGACCAGCACAACCCGCTGGCCGGACTGACC  
Ae505Ps2\_rpoB TTCGGCACCTCGCAGCTGTGCGAGTTCATGGACCAGCACAACCCGCTGGCCGGACTGACC  
Ae406Ps2\_rpoB TTCGGCACCTCGCAGCTGTGCGAGTTCATGGACCAGCACAACCCGCTGGCCGGACTGACC





Ae356Ps1\_rpoB GACGGCTCGTTCCGCCGAGGACCGGGTCCTGGTCCGCCGCAAGGGCGGCGAGGTCGACCTG  
Ae707Ps1\_rpoB GACGGCTCGTTCCGCCGAGGACCGGGTCCTGGTCCGCCGCAAGGGCGGCGAGGTCGACCTG  
\*\*\*\*\* \*\* \*\*\*\*\* \* \* \* \* \* \*\*\*\*\*

Ae331Ps2\_rpoB ATCTCGCCCTCGGGCGTGGAGTACATCGACGTCTCGCCGCGCCAGATGGTGTCCGGTCGCG  
Ae505Ps2\_rpoB ATCTCGCCCTCGGGCGTGGAGTACATCGACGTCTCGCCGCGCCAGATGGTGTCCGGTCGCG  
Ae406Ps2\_rpoB ATCTCGCCCTCGGGCGTGGAGTACATCGACGTCTCGCCGCGCCAGATGGTGTCCGGTCGCG  
Ae717Ps2\_rpoB ATCTCGCCCTCGGGCGTGGAGTACATCGACGTCTCGCCGCGCCAGATGGTGTCCGGTCGCG  
Ae706Ps2\_rpoB ATCTCGCCCTCGGGCGTGGAGTACATCGACGTCTCGCCGCGCCAGATGGTGTCCGGTCGCG  
Ae150APs1\_rpoB ATCTCGCCACCGGGCGTGGAGTACATCGACGTCTCGCCGCGCCAGATGGTGTCCGGTCGCG  
Ae168Ps1\_rpoB ATCTCGCCACCGGGCGTGGAGTACATCGACGTCTCGCCGCGCCAGATGGTGTCCGGTCGCG  
Ae263Ps1\_rpoB ATCTCGCCACCGGGCGTGGAGTACATCGACGTCTCGCCGCGCCAGATGGTGTCCGGTCGCG  
Ae356Ps1\_rpoB ATCTCGCCACCGGGCGTGGAGTACATCGACGTCTCGCCGCGCCAGATGGTGTCCGGTCGCG  
Ae707Ps1\_rpoB ATCTCGCCACCGGGCGTGGAGTACATCGACGTCTCGCCGCGCCAGATGGTGTCCGGTCGCG  
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Ae331Ps2\_rpoB ACGGCGATGATCCCGTTCCTCGAGCACGACGACGCGAACC GCGCGCTGATGGGCGCGAAC  
Ae505Ps2\_rpoB ACGGCGATGATCCCGTTCCTCGAGCACGACGACGCGAACC GCGCGCTGATGGGCGCGAAC  
Ae406Ps2\_rpoB ACGGCGATGATCCCGTTCCTCGAGCACGACGACGCGAACC GCGCGCTGATGGGCGCGAAC  
Ae717Ps2\_rpoB ACGGCGATGATCCCGTTCCTCGAGCACGACGACGCGAACC GCGCGCTGATGGGCGCGAAC  
Ae706Ps2\_rpoB ACGGCGATGATCCCGTTCCTCGAGCACGACGACGCGAACC GCGCGCTGATGGGCGCGAAC  
Ae150APs1\_rpoB ACCGCGATGATCCCGTTCCTCGAGCACGACGACGCGAACC GCGGCCCTCATGGGTGCGAAC  
Ae168Ps1\_rpoB ACCGCGATGATCCCGTTCCTCGAGCACGACGACGCGAACC GCGGCCCTCATGGGTGCGAAC  
Ae263Ps1\_rpoB ACCGCGATGATCCCGTTCCTCGAGCACGACGACGCGAACC GCGGCCCTCATGGGTGCGAAC  
Ae356Ps1\_rpoB ACCGCGATGATCCCGTTCCTCGAGCACGACGACGCGAACC GCGGCCCTCATGGGTGCGAAC  
Ae707Ps1\_rpoB ACCGCGATGATCCCGTTCCTCGAGCACGACGACGCGAACC GCGGCCCTCATGGGTGCGAAC  
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Ae331Ps2\_rpoB ATGCAGCGCCAGTCCGTGCCGCTGCTGCGCTCGGAGTCGCGCTGGTCCGGTACCGGCATG  
Ae505Ps2\_rpoB ATGCAGCGCCAGTCCGTGCCGCTGCTGCGCTCGGAGTCGCGCTGGTCCGGTACCGGCATG  
Ae406Ps2\_rpoB ATGCAGCGCCAGTCCGTGCCGCTGCTGCGCTCGGAGTCGCGCTGGTCCGGTACCGGCATG  
Ae717Ps2\_rpoB ATGCAGCGCCAGTCCGTGCCGCTGCTGCGCTCGGAGTCGCGCTGGTCCGGTACCGGCATG  
Ae706Ps2\_rpoB ATGCAGCGCCAGTCCGTGCCGCTGCTGCGCTCGGAGTCGCGCTGGTCCGGTACCGGCATG  
Ae150APs1\_rpoB ATGCAGCGTCAGTCCGTGCCGCTGCTGCGTCCGAGTCGCGCTGGTCCGGCACCGGCATG  
Ae168Ps1\_rpoB ATGCAGCGTCAGTCCGTGCCGCTGCTGCGTCCGAGTCGCGCTGGTCCGGCACCGGCATG  
Ae263Ps1\_rpoB ATGCAGCGTCAGTCCGTGCCGCTGCTGCGTCCGAGTCGCGCTGGTCCGGCACCGGCATG  
Ae356Ps1\_rpoB ATGCAGCGTCAGTCCGTGCCGCTGCTGCGTCCGAGTCGCGCTGGTCCGGCACCGGCATG  
Ae707Ps1\_rpoB ATGCAGCGTCAGTCCGTGCCGCTGCTGCGTCCGAGTCGCGCTGGTCCGGCACCGGCATG  
\*\*\*\*\* \*\*\*\*\*

Ae331Ps2\_rpoB GAGCTGCGTGCCGCCGTCGACGCCGGTGACGTCTGACCCGCCGAGTCCGCCGGTGTGCTC  
Ae505Ps2\_rpoB GAGCTGCGTGCCGCCGTCGACGCCGGTGACGTCTGACCCGCCGAGTCCGCCGGTGTGCTC  
Ae406Ps2\_rpoB GAGCTGCGTGCCGCCGTCGACGCCGGTGACGTCTGACCCGCCGAGTCCGCCGGTGTGCTC  
Ae717Ps2\_rpoB GAGTGCCTGCGCCCGCTCGACGCCGGTGACGTCTGACCCGCCGAGTCCGCCGGTGTGCTC  
Ae706Ps2\_rpoB GAGCTGCGTGCCGCCGTCGACGCCGGTGACGTCTGACCCGCCGAGTCCGCCGGTGTGCTC  
Ae150APs1\_rpoB GAGCTGCGGGCCCGGGTTCGACGCCGGCGACGTCTGCTGGTGGCCGAGCAGGCCGGTGTGGTC  
Ae168Ps1\_rpoB GAGCTGCGGGCCCGGGTTCGACGCCGGCGACGTCTGCTGGTGGCCGAGCAGGCCGGTGTGGTC  
Ae263Ps1\_rpoB GAGCTGCGGGCCCGGGTTCGACGCCGGCGACGTCTGCTGGTGGCCGAGCAGGCCGGTGTGGTC  
Ae356Ps1\_rpoB GAGCTGCGGGCCCGGGTTCGACGCCGGCGACGTCTGCTGGTGGCCGAGCAGGCCGGTGTGGTC  
Ae707Ps1\_rpoB GAGCTGCGGGCCCGGGTTCGACGCCGGCGACGTCTGCTGGTGGCCGAGCAGGCCGGTGTGGTC  
\*\*\*\*\* \*\*\*\*\*

Ae331Ps2\_rpoB GAGGAGCTGTGCGCCGACTACATCACCGTTCATGGACGACGAGGGCCAGCGTCAGACCTAC  
Ae505Ps2\_rpoB GAGGAGCTGTGCGCCGACTACATCACCGTTCATGGACGACGAGGGCCAGCGTCAGACCTAC  
Ae406Ps2\_rpoB GAGGAGCTGTGCGCCGACTACATCACCGTTCATGGACGACGAGGGCCAGCGTCAGACCTAC  
Ae717Ps2\_rpoB GAGGAGCTGTGCGCCGACTACATCACCGTTCATGGACGACGAGGGCCAGCGTCAGACCTAC  
Ae706Ps2\_rpoB GAGGAGCTGTGCGCCGACTACATCACCGTTCATGGACGACGAGGGCCAGCGTCAGACCTAC  
Ae150APs1\_rpoB GAGGAGCTGTGCGCCGACTACATCACCGTTCATGGACGACGAGGGCCAGCGTCAGACCTAC  
Ae168Ps1\_rpoB GAGGAGCTGTGCGCCGACTACATCACCGTTCATGGACGACGAGGGCCAGCGTCAGACCTAC  
Ae263Ps1\_rpoB GAGGAGCTGTGCGCCGACTACATCACCGTTCATGGACGACGAGGGCCAGCGTCAGACCTAC  
Ae356Ps1\_rpoB GAGGAGCTGTGCGCCGACTACATCACCGTTCATGGACGACGAGGGCCAGCGTCAGACCTAC  
Ae707Ps1\_rpoB GAGGAGCTGTGCGCCGACTACATCACCGTTCATGGACGACGAGGGCCAGCGTCAGACCTAC  
\*\*\*\*\* \*\*\*\*\*

Ae331Ps2\_rpoB CGTCTGAACAAGTTCCGCCGCTCGAACCAGGGCACCTGCAACAACCAGAAGCCCATCGTC  
Ae505Ps2\_rpoB CGTCTGAACAAGTTCCGCCGCTCGAACCAGGGCACCTGCAACAACCAGAAGCCCATCGTC  
Ae406Ps2\_rpoB CGTCTGAACAAGTTCCGCCGCTCGAACCAGGGCACCTGCAACAACCAGAAGCCCATCGTC  
Ae717Ps2\_rpoB CGTCTGAACAAGTTCCGCCGCTCGAACCAGGGCACCTGCAACAACCAGAAGCCCATCGTC  
Ae706Ps2\_rpoB CGTCTGAACAAGTTCCGCCGCTCGAACCAGGGCACCTGCAACAACCAGAAGCCCATCGTC  
Ae150APs1\_rpoB CGTCTGAACAAGTTCCGCCGCTCGAACCAGGGCACCTGCAACAACCAGAAGCCCATCGTC  
Ae168Ps1\_rpoB CGTCTGAACAAGTTCCGCCGCTCGAACCAGGGCACCTGCAACAACCAGAAGCCCATCGTC  
Ae263Ps1\_rpoB CGTCTGAACAAGTTCCGCCGCTCGAACCAGGGCACCTGCAACAACCAGAAGCCCATCGTC  
Ae356Ps1\_rpoB CGTCTGAACAAGTTCCGCCGCTCGAACCAGGGCACCTGCAACAACCAGAAGCCCATCGTC  
Ae707Ps1\_rpoB CGTCTGAACAAGTTCCGCCGCTCGAACCAGGGCACCTGCAACAACCAGAAGCCCATCGTC  
\*\*\*\*\* \*\*\*\*\*

Ae331Ps2\_rpoB GACGAGGGGCGAGCGGGTTCGAGGTGGGCCAGGTGCTCGCCGACGGTCCCTGCACCGAGAAC

Ae505Ps2\_rpoB GACGAGGGGCAGCGGGTCGAGGTGGGCCAGGTGCTCGCCGACGGTCCCTGCACCCGAGAAC  
Ae406Ps2\_rpoB GACGAGGGGCAGCGGGTCGAGGTGGGCCAGGTGCTCGCCGACGGTCCCTGCACCCGAGAAC  
Ae717Ps2\_rpoB GACGAGGGGCAGCGGGTCGAGGTGGGCCAGGTGCTCGCCGACGGTCCCTGCACCCGAGAAC  
Ae706Ps2\_rpoB GACGAGGGGCAGCGGGTCGAGGTGGGCCAGGTGCTCGCCGACGGTCCCTGCACCCGAGAAC  
Ae150APs1\_rpoB GACGAGGGGCATGCGGGTCGAGGTGGGCCAGGTGCTCGCCGACGGACCGTGCACCCGAGAAC  
Ae168Ps1\_rpoB GACGAGGGGCATGCGGGTCGAGGTGGGCCAGGTGCTCGCCGACGGACCGTGCACCCGAGAAC  
Ae263Ps1\_rpoB GACGAGGGGCATGCGGGTCGAGGTGGGCCAGGTGCTCGCCGACGGACCGTGCACCCGAGAAC  
Ae356Ps1\_rpoB GACGAGGGGCATGCGGGTCGAGGTGGGCCAGGTGCTCGCCGACGGACCGTGCACCCGAGAAC  
Ae707Ps1\_rpoB GACGAGGGGCATGCGGGTCGAGGTGGGCCAGGTGCTCGCCGACGGACCGTGCACCCGAGAAC  
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Ae331Ps2\_rpoB GGTGAGATGGCGCTGGGCAAGAACCTGCTCGTGGCGATCATGCCGTGGGAGGGCCACAAC  
Ae505Ps2\_rpoB GGTGAGATGGCGCTGGGCAAGAACCTGCTCGTGGCGATCATGCCGTGGGAGGGCCACAAC  
Ae406Ps2\_rpoB GGTGAGATGGCGCTGGGCAAGAACCTGCTCGTGGCGATCATGCCGTGGGAGGGCCACAAC  
Ae717Ps2\_rpoB GGTGAGATGGCGCTGGGCAAGAACCTGCTCGTGGCGATCATGCCGTGGGAGGGCCACAAC  
Ae706Ps2\_rpoB GGTGAGATGGCGCTGGGCAAGAACCTGCTCGTGGCGATCATGCCGTGGGAGGGCCACAAC  
Ae150APs1\_rpoB GGCAGATGGCGCTGGGCAAGAACCTCCTCGTGGCGATCATGCCGTGGGAGGGCCACAAC  
Ae168Ps1\_rpoB GGCAGATGGCGCTGGGCAAGAACCTCCTCGTGGCGATCATGCCGTGGGAGGGCCACAAC  
Ae263Ps1\_rpoB GGCAGATGGCGCTGGGCAAGAACCTCCTCGTGGCGATCATGCCGTGGGAGGGCCACAAC  
Ae356Ps1\_rpoB GGCAGATGGCGCTGGGCAAGAACCTCCTCGTGGCGATCATGCCGTGGGAGGGCCACAAC  
Ae707Ps1\_rpoB GGCAGATGGCGCTGGGCAAGAACCTCCTCGTGGCGATCATGCCGTGGGAGGGCCACAAC  
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Ae331Ps2\_rpoB TACGAGGACGCGATCATCCTGTGCGAGCGCCTCGTGCAGGACGACGTGCTCACCTCGATC  
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Ae406Ps2\_rpoB TACGAGGACGCGATCATCCTGTGCGAGCGCCTCGTGCAGGACGACGTGCTCACCTCGATC  
Ae717Ps2\_rpoB TACGAGGACGCGATCATCCTGTGCGAGCGCCTCGTGCAGGACGACGTGCTCACCTCGATC  
Ae706Ps2\_rpoB TACGAGGACGCGATCATCCTGTGCGAGCGCCTCGTGCAGGACGACGTGCTCACCTCGATC  
Ae150APs1\_rpoB TACGAGGACGCGATCATCCTGTGCGAGCGCCTCGTCCAGGACGACGTGCTCACCTCGATC  
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Ae707Ps1\_rpoB TACGAGGACGCGATCATCCTGTGCGAGCGCCTCGTCCAGGACGACGTGCTCACCTCGATC  
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Ae331Ps2\_rpoB CACATCGAGGAGCAGAGATCGACGCGCGGACACGAAGCTGGGCGCCGAGGAGATCACC  
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Ae406Ps2\_rpoB CACATCGAGGAGCAGAGATCGACGCGCGGACACGAAGCTGGGCGCCGAGGAGATCACC  
Ae717Ps2\_rpoB CACATCGAGGAGCAGAGATCGACGCGCGGACACGAAGCTGGGCGCCGAGGAGATCACC  
Ae706Ps2\_rpoB CACATCGAGGAGCAGAGATCGACGCGCGGACACGAAGCTGGGCGCCGAGGAGATCACC  
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Ae331Ps2\_rpoB CGGGACATCCCGAACGTCTCCGAGGACGTGCTGGCCGACCTCGACGAGCGCGGCATCATC  
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Ae406Ps2\_rpoB CGGGACATCCCGAACGTCTCCGAGGACGTGCTGGCCGACCTCGACGAGCGCGGCATCATC  
Ae717Ps2\_rpoB CGGGACATCCCGAACGTCTCCGAGGACGTGCTGGCCGACCTCGACGAGCGCGGCATCATC  
Ae706Ps2\_rpoB CGGGACATCCCGAACGTCTCCGAGGACGTGCTGGCCGACCTCGACGAGCGCGGCATCATC  
Ae150APs1\_rpoB CGGGACATCCCGAACGTCTCCGAGGACGTGCTGGCCGACCTCGACGAGCGCGGCATCATC  
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Ae263Ps1\_rpoB CGGGACATCCCGAACGTCTCCGAGGACGTGCTGGCCGACCTCGACGAGCGCGGCATCATC  
Ae356Ps1\_rpoB CGGGACATCCCGAACGTCTCCGAGGACGTGCTGGCCGACCTCGACGAGCGCGGCATCATC  
Ae707Ps1\_rpoB CGGGACATCCCGAACGTCTCCGAGGACGTGCTGGCCGACCTCGACGAGCGCGGCATCATC  
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Ae331Ps2\_rpoB CGGATCGGCGCCGAGGTCCAGCCCGGCGACATCCTGGTCCGCAAGGTCACGCCAAGGGC  
Ae505Ps2\_rpoB CGGATCGGCGCCGAGGTCCAGCCCGGCGACATCCTGGTCCGCAAGGTCACGCCAAGGGC  
Ae406Ps2\_rpoB CGGATCGGCGCCGAGGTCCAGCCCGGCGACATCCTGGTCCGCAAGGTCACGCCAAGGGC  
Ae717Ps2\_rpoB CGGATCGGCGCCGAGGTCCAGCCCGGCGACATCCTGGTCCGCAAGGTCACGCCAAGGGC  
Ae706Ps2\_rpoB CGGATCGGCGCCGAGGTCCAGCCCGGCGACATCCTGGTCCGCAAGGTCACGCCAAGGGC  
Ae150APs1\_rpoB CGGATCGGTCGCCGAGGTCCAGCCCGGCGACATCCTGGTCCGCAAGGTCACGCCAAGGGC  
Ae168Ps1\_rpoB CGGATCGGTCGCCGAGGTCCAGCCCGGCGACATCCTGGTCCGCAAGGTCACGCCAAGGGC  
Ae263Ps1\_rpoB CGGATCGGTCGCCGAGGTCCAGCCCGGCGACATCCTGGTCCGCAAGGTCACGCCAAGGGC  
Ae356Ps1\_rpoB CGGATCGGTCGCCGAGGTCCAGCCCGGCGACATCCTGGTCCGCAAGGTCACGCCAAGGGC  
Ae707Ps1\_rpoB CGGATCGGTCGCCGAGGTCCAGCCCGGCGACATCCTGGTCCGCAAGGTCACGCCAAGGGC  
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Ae331Ps2\_rpoB GAGACCGAGCTGACCCGGAGGAGCGCCTGCTCCGCGCATCTTCGGTGAGAAGGCGCGC  
Ae505Ps2\_rpoB GAGACCGAGCTGACCCGGAGGAGCGCCTGCTCCGCGCATCTTCGGTGAGAAGGCGCGC  
Ae406Ps2\_rpoB GAGACCGAGCTGACCCGGAGGAGCGCCTGCTCCGCGCATCTTCGGTGAGAAGGCGCGC  
Ae717Ps2\_rpoB GAGACCGAGCTGACCCGGAGGAGCGCCTGCTCCGCGCATCTTCGGTGAGAAGGCGCGC  
Ae706Ps2\_rpoB GAGACCGAGCTGACCCGGAGGAGCGCCTGCTCCGCGCATCTTCGGTGAGAAGGCGCGC  
Ae150APs1\_rpoB GAGACCGAGCTGACCCGGAGGAGCGCCTGCTCCGCGCATCTTCGGTGAGAAGGCGCGC



Ae331Ps2\_rpoB GAGTGGGCGGCGCAGATGCCCGAGGAGCTCTACTCGGTGCCCGCCGACACGAACACCGCGG  
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Ae406Ps2\_rpoB GAGTGGGCGGCGCAGATGCCCGAGGAGCTCTACTCGGTGCCCGCCGACACGAACACCGCGG  
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Ae706Ps2\_rpoB GAGTGGGCGGCGCAGATGCCCGAGGAGCTCTACTCGGTGCCCGCCGACACGAACACCGCGG  
Ae150APs1\_rpoB GAATGGGCGTCCCGGATGCCCGAGGAGCTCTACTCGGTGCCCGCCGACACGAAGACCGCGG  
Ae168Ps1\_rpoB GAATGGGCGTCCCGGATGCCCGAGGAGCTCTACTCGGTGCCCGCCGACACGAAGACCGCGG  
Ae263Ps1\_rpoB GAATGGGCGTCCCGGATGCCCGAGGAGCTCTACTCGGTGCCCGCCGACACGAAGACCGCGG  
Ae356Ps1\_rpoB GAATGGGCGTCCCGGATGCCCGAGGAGCTCTACTCGGTGCCCGCCGACACGAAGACCGCGG  
Ae707Ps1\_rpoB GAATGGGCGTCCCGGATGCCCGAGGAGCTCTACTCGGTGCCCGCCGACACGAAGACCGCGG  
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Ae331Ps2\_rpoB ACGCCGGTGTTCGACGGTGC CGCGGAGCAGAGATCACGGGTCTGCTCGGCTCGACCCGC  
Ae505Ps2\_rpoB ACGCCGGTGTTCGACGGTGC CGCGGAGCAGAGATCACGGGTCTGCTCGGCTCGACCCGC  
Ae406Ps2\_rpoB ACGCCGGTGTTCGACGGTGC CGCGGAGCAGAGATCACGGGTCTGCTCGGCTCGACCCGC  
Ae717Ps2\_rpoB ACGCCGGTGTTCGACGGTGC CGCGGAGCAGAGATCACGGGTCTGCTCGGCTCGACCCGC  
Ae706Ps2\_rpoB ACGCCGGTGTTCGACGGTGC CGCGGAGCAGAGATCACGGGTCTGCTCGGCTCGACCCGC  
Ae150APs1\_rpoB ACGCCGGTGTTCGACGGTGC CGCGGAGCAGAGATCACGGGTCTGCTCGGCTCGACCCGC  
Ae168Ps1\_rpoB ACGCCGGTGTTCGACGGTGC CGCGGAGCAGAGATCACGGGTCTGCTCGGCTCGACCCGC  
Ae263Ps1\_rpoB ACGCCGGTGTTCGACGGTGC CGCGGAGCAGAGATCACGGGTCTGCTCGGCTCGACCCGC  
Ae356Ps1\_rpoB ACGCCGGTGTTCGACGGTGC CGCGGAGCAGAGATCACGGGTCTGCTCGGCTCGACCCGC  
Ae707Ps1\_rpoB ACGCCGGTGTTCGACGGTGC CGCGGAGCAGAGATCACGGGTCTGCTCGGCTCGACCCGC  
\* \* \* \* \*

Ae331Ps2\_rpoB CCCAACCGGGACGGCGAGCGGATGGTCCGGTCCGGACGGCAAGGGCGAGCTGCTCGACGGC  
Ae505Ps2\_rpoB CCCAACCGGGACGGCGAGCGGATGGTCCGGTCCGGACGGCAAGGGCGAGCTGCTCGACGGC  
Ae406Ps2\_rpoB CCCAACCGGGACGGCGAGCGGATGGTCCGGTCCGGACGGCAAGGGCGAGCTGCTCGACGGC  
Ae717Ps2\_rpoB CCCAACCGGGACGGCGAGCGGATGGTCCGGTCCGGACGGCAAGGGCGAGCTGCTCGACGGC  
Ae706Ps2\_rpoB CCCAACCGGGACGGCGAGCGGATGGTCCGGTCCGGACGGCAAGGGCGAGCTGCTCGACGGC  
Ae150APs1\_rpoB CCGAACCCGCGACGGTGAGCGGATGGTGCAGCCGGACGGCAAGGGCGAGCTGCTCGACGGG  
Ae168Ps1\_rpoB CCGAACCCGCGACGGTGAGCGGATGGTGCAGCCGGACGGCAAGGGCGAGCTGCTCGACGGG  
Ae263Ps1\_rpoB CCGAACCCGCGACGGTGAGCGGATGGTGCAGCCGGACGGCAAGGGCGAGCTGCTCGACGGG  
Ae356Ps1\_rpoB CCGAACCCGCGACGGTGAGCGGATGGTGCAGCCGGACGGCAAGGGCGAGCTGCTCGACGGG  
Ae707Ps1\_rpoB CCGAACCCGCGACGGTGAGCGGATGGTGCAGCCGGACGGCAAGGGCGAGCTGCTCGACGGG  
\* \* \* \* \*

Ae331Ps2\_rpoB CGCTCCGGTGGAGCCGTACCCGTTCCCGGTCGCGGTCGGGTACATGTACATCCTGAAGCTG  
Ae505Ps2\_rpoB CGCTCCGGTGGAGCCGTACCCGTTCCCGGTCGCGGTCGGGTACATGTACATCCTGAAGCTG  
Ae406Ps2\_rpoB CGCTCCGGTGGAGCCGTACCCGTTCCCGGTCGCGGTCGGGTACATGTACATCCTGAAGCTG  
Ae717Ps2\_rpoB CGCTCCGGTGGAGCCGTACCCGTTCCCGGTCGCGGTCGGGTACATGTACATCCTGAAGCTG  
Ae706Ps2\_rpoB CGCTCCGGTGGAGCCGTACCCGTTCCCGGTCGCGGTCGGGTACATGTACATCCTGAAGCTG  
Ae150APs1\_rpoB CGCTCCGGTGGAGCCGTACCCGTTCCCGGTCGCGGTCGGGTACATGTACATCCTGAAGCTG  
Ae168Ps1\_rpoB CGCTCCGGTGGAGCCGTACCCGTTCCCGGTCGCGGTCGGGTACATGTACATCCTGAAGCTG  
Ae263Ps1\_rpoB CGCTCCGGTGGAGCCGTACCCGTTCCCGGTCGCGGTCGGGTACATGTACATCCTGAAGCTG  
Ae356Ps1\_rpoB CGCTCCGGTGGAGCCGTACCCGTTCCCGGTCGCGGTCGGGTACATGTACATCCTGAAGCTG  
Ae707Ps1\_rpoB CGCTCCGGTGGAGCCGTACCCGTTCCCGGTCGCGGTCGGGTACATGTACATCCTGAAGCTG  
\* \* \* \* \*

Ae331Ps2\_rpoB GCCCACCTGGTGGACGACAAGATCCACGCCGGTTCGACCGGCCCTACTCGATGATCACC  
Ae505Ps2\_rpoB GCCCACCTGGTGGACGACAAGATCCACGCCGGTTCGACCGGCCCTACTCGATGATCACC  
Ae406Ps2\_rpoB GCCCACCTGGTGGACGACAAGATCCACGCCGGTTCGACCGGCCCTACTCGATGATCACC  
Ae717Ps2\_rpoB GCCCACCTGGTGGACGACAAGATCCACGCCGGTTCGACCGGCCCTACTCGATGATCACC  
Ae706Ps2\_rpoB GCCCACCTGGTGGACGACAAGATCCACGCCGGTTCGACCGGCCCTACTCGATGATCACC  
Ae150APs1\_rpoB GCGCACCTGGTGGACGACAAGATCCACGCCGGTTCGACCGGCCCTACTCGATGATCACC  
Ae168Ps1\_rpoB GCGCACCTGGTGGACGACAAGATCCACGCCGGTTCGACCGGCCCTACTCGATGATCACC  
Ae263Ps1\_rpoB GCGCACCTGGTGGACGACAAGATCCACGCCGGTTCGACCGGCCCTACTCGATGATCACC  
Ae356Ps1\_rpoB GCGCACCTGGTGGACGACAAGATCCACGCCGGTTCGACCGGCCCTACTCGATGATCACC  
Ae707Ps1\_rpoB GCGCACCTGGTGGACGACAAGATCCACGCCGGTTCGACCGGCCCTACTCGATGATCACC  
\* \* \* \* \*

Ae331Ps2\_rpoB CAGCAGCCGCTGGGCGGTAAGGCGCAGTTCGGTGGCCAGCGCTTCGGCGAGATGGAGTGC  
Ae505Ps2\_rpoB CAGCAGCCGCTGGGCGGTAAGGCGCAGTTCGGTGGCCAGCGCTTCGGCGAGATGGAGTGC  
Ae406Ps2\_rpoB CAGCAGCCGCTGGGCGGTAAGGCGCAGTTCGGTGGCCAGCGCTTCGGCGAGATGGAGTGC  
Ae717Ps2\_rpoB CAGCAGCCGCTGGGCGGTAAGGCGCAGTTCGGTGGCCAGCGCTTCGGCGAGATGGAGTGC  
Ae706Ps2\_rpoB CAGCAGCCGCTGGGCGGTAAGGCGCAGTTCGGTGGCCAGCGCTTCGGCGAGATGGAGTGC  
Ae150APs1\_rpoB CAGCAGCCGCTGGGCGGTAAGGCGCAGTTCGGTGGTTCAGCGCTTCGGTGGAGATGGAGTGC  
Ae168Ps1\_rpoB CAGCAGCCGCTGGGCGGTAAGGCGCAGTTCGGTGGTTCAGCGCTTCGGTGGAGATGGAGTGC  
Ae263Ps1\_rpoB CAGCAGCCGCTGGGCGGTAAGGCGCAGTTCGGTGGTTCAGCGCTTCGGTGGAGATGGAGTGC  
Ae356Ps1\_rpoB CAGCAGCCGCTGGGCGGTAAGGCGCAGTTCGGTGGTTCAGCGCTTCGGTGGAGATGGAGTGC  
Ae707Ps1\_rpoB CAGCAGCCGCTGGGCGGTAAGGCGCAGTTCGGTGGTTCAGCGCTTCGGTGGAGATGGAGTGC  
\* \* \* \* \*

Ae331Ps2\_rpoB TGGGCGATGCAGGCGTACGGCGCGGCTACACCCCTGCAGGAGCTGCTGACGATCAAGTCC  
Ae505Ps2\_rpoB TGGGCGATGCAGGCGTACGGCGCGGCTACACCCCTGCAGGAGCTGCTGACGATCAAGTCC  
Ae406Ps2\_rpoB TGGGCGATGCAGGCGTACGGCGCGGCTACACCCCTGCAGGAGCTGCTGACGATCAAGTCC  
Ae717Ps2\_rpoB TGGGCGATGCAGGCGTACGGCGCGGCTACACCCCTGCAGGAGCTGCTGACGATCAAGTCC

Ae706Ps2\_rpoB TGGGCGATGCAGGCGTACGGCGCGGCCACACCCCTGCAGGAGCTGCTGACGATCAAGTCC  
Ae150APs1\_rpoB TGGGCGATGCAGGCGTACGGCGCGGCCACACCCCTGCAGGAGCTGCTGACGATCAAGTCC  
Ae168Ps1\_rpoB TGGGCGATGCAGGCGTACGGCGCGGCCACACCCCTGCAGGAGCTGCTGACGATCAAGTCC  
Ae263Ps1\_rpoB TGGGCGATGCAGGCGTACGGCGCGGCCACACCCCTGCAGGAGCTGCTGACGATCAAGTCC  
Ae356Ps1\_rpoB TGGGCGATGCAGGCGTACGGCGCGGCCACACCCCTGCAGGAGCTGCTGACGATCAAGTCC  
Ae707Ps1\_rpoB TGGGCGATGCAGGCGTACGGCGCGGCCACACCCCTGCAGGAGCTGCTGACGATCAAGTCC  
\*\*\*\*\*

Ae331Ps2\_rpoB GACGACGTCGTGGGCGCGTGAAGGTCTACGAGGCGATCGTCAAGGGCGAGAACATCCCG  
Ae505Ps2\_rpoB GACGACGTCGTGGGCGCGTGAAGGTCTACGAGGCGATCGTCAAGGGCGAGAACATCCCG  
Ae406Ps2\_rpoB GACGACGTCGTGGGCGCGTGAAGGTCTACGAGGCGATCGTCAAGGGCGAGAACATCCCG  
Ae717Ps2\_rpoB GACGACGTCGTGGGCGCGTGAAGGTCTACGAGGCGATCGTCAAGGGCGAGAACATCCCG  
Ae706Ps2\_rpoB GACGACGTCGTGGGCGCGTGAAGGTCTACGAGGCGATCGTCAAGGGCGAGAACATCCCG  
Ae150APs1\_rpoB GACGACGTCGTGGGCGCGTGAAGGTCTACGAGGCGATCGTCAAGGGCGAGAACATCCCG  
Ae168Ps1\_rpoB GACGACGTCGTGGGCGCGTGAAGGTCTACGAGGCGATCGTCAAGGGCGAGAACATCCCG  
Ae263Ps1\_rpoB GACGACGTCGTGGGCGCGTGAAGGTCTACGAGGCGATCGTCAAGGGCGAGAACATCCCG  
Ae356Ps1\_rpoB GACGACGTCGTGGGCGCGTGAAGGTCTACGAGGCGATCGTCAAGGGCGAGAACATCCCG  
Ae707Ps1\_rpoB GACGACGTCGTGGGCGCGTGAAGGTCTACGAGGCGATCGTCAAGGGCGAGAACATCCCG  
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Ae331Ps2\_rpoB GAGCCGGGGATCCCCGAGTCGTTCAAGGTGCTCCTCAAGGAGCTGCAGTCGCTCTGCCTG  
Ae505Ps2\_rpoB GAGCCGGGGATCCCCGAGTCGTTCAAGGTGCTCCTCAAGGAGCTGCAGTCGCTCTGCCTG  
Ae406Ps2\_rpoB GAGCCGGGGATCCCCGAGTCGTTCAAGGTGCTCCTCAAGGAGCTGCAGTCGCTCTGCCTG  
Ae717Ps2\_rpoB GAGCCGGGGATCCCCGAGTCGTTCAAGGTGCTCCTCAAGGAGCTGCAGTCGCTCTGCCTG  
Ae706Ps2\_rpoB GAGCCGGGGATCCCCGAGTCGTTCAAGGTGCTCCTCAAGGAGCTGCAGTCGCTCTGCCTG  
Ae150APs1\_rpoB GAGCCGGGGATCCCCGAGTCGTTCAAGGTGCTCCTCAAGGAGCTGCAGTCGCTCTGCCTG  
Ae168Ps1\_rpoB GAGCCGGGGATCCCCGAGTCGTTCAAGGTGCTCCTCAAGGAGCTGCAGTCGCTCTGCCTG  
Ae263Ps1\_rpoB GAGCCGGGGATCCCCGAGTCGTTCAAGGTGCTCCTCAAGGAGCTGCAGTCGCTCTGCCTG  
Ae356Ps1\_rpoB GAGCCGGGGATCCCCGAGTCGTTCAAGGTGCTCCTCAAGGAGCTGCAGTCGCTCTGCCTG  
Ae707Ps1\_rpoB GAGCCGGGGATCCCCGAGTCGTTCAAGGTGCTCCTCAAGGAGCTGCAGTCGCTCTGCCTG  
\*\*\*\*\*

Ae331Ps2\_rpoB AACGTCGAGGTGCTCTCCAGCGACGGTGC GGCGATCGAGATGCGGGACGCCGACGACGAA  
Ae505Ps2\_rpoB AACGTCGAGGTGCTCTCCAGCGACGGTGC GGCGATCGAGATGCGGGACGCCGACGACGAA  
Ae406Ps2\_rpoB AACGTCGAGGTGCTCTCCAGCGACGGTGC GGCGATCGAGATGCGGGACGCCGACGACGAA  
Ae717Ps2\_rpoB AACGTCGAGGTGCTCTCCAGCGACGGTGC GGCGATCGAGATGCGGGACGCCGACGACGAA  
Ae706Ps2\_rpoB AACGTCGAGGTGCTCTCCAGCGACGGTGC GGCGATCGAGATGCGGGACGCCGACGACGAA  
Ae150APs1\_rpoB AACGTCGAGGTGCTCTCCAGCGACGGTGC GGCGATCGAGATGCGGGACGCCGACGACGAA  
Ae168Ps1\_rpoB AACGTCGAGGTGCTCTCCAGCGACGGTGC GGCGATCGAGATGCGGGACGCCGACGACGAA  
Ae263Ps1\_rpoB AACGTCGAGGTGCTCTCCAGCGACGGTGC GGCGATCGAGATGCGGGACGCCGACGACGAA  
Ae356Ps1\_rpoB AACGTCGAGGTGCTCTCCAGCGACGGTGC GGCGATCGAGATGCGGGACGCCGACGACGAA  
Ae707Ps1\_rpoB AACGTCGAGGTGCTCTCCAGCGACGGTGC GGCGATCGAGATGCGGGACGCCGACGACGAA  
\*\*\*\*\*

Ae331Ps2\_rpoB GACCTCGAGCGTGC CGCGCGAATCTGGGCATCAACCTGTCCAGCCGCCGGGCTCGGAG  
Ae505Ps2\_rpoB GACCTCGAGCGTGC CGCGCGAATCTGGGCATCAACCTGTCCAGCCGCCGGGCTCGGAG  
Ae406Ps2\_rpoB GACCTCGAGCGTGC CGCGCGAATCTGGGCATCAACCTGTCCAGCCGCCGGGCTCGGAG  
Ae717Ps2\_rpoB GACCTCGAGCGTGC CGCGCGAATCTGGGCATCAACCTGTCCAGCCGCCGGGCTCGGAG  
Ae706Ps2\_rpoB GACCTCGAGCGTGC CGCGCGAATCTGGGCATCAACCTGTCCAGCCGCCGGGCTCGGAG  
Ae150APs1\_rpoB GACCTCGAGCGTGC CGCGCGAATCTGGGCATCAACCTGTCCAGCCGCCGGGCTCGGAG  
Ae168Ps1\_rpoB GACCTCGAGCGTGC CGCGCGAATCTGGGCATCAACCTGTCCAGCCGCCGGGCTCGGAG  
Ae263Ps1\_rpoB GACCTCGAGCGTGC CGCGCGAATCTGGGCATCAACCTGTCCAGCCGCCGGGCTCGGAG  
Ae356Ps1\_rpoB GACCTCGAGCGTGC CGCGCGAATCTGGGCATCAACCTGTCCAGCCGCCGGGCTCGGAG  
Ae707Ps1\_rpoB GACCTCGAGCGTGC CGCGCGAATCTGGGCATCAACCTGTCCAGCCGCCGGGCTCGGAG  
\*\*\*\*\*

Ae331Ps2\_rpoB TCGATGACCGTTCGACGACGTCGTC AACTGA  
Ae505Ps2\_rpoB TCGATGACCGTTCGACGACGTCGTC AACTGA  
Ae406Ps2\_rpoB TCGATGACCGTTCGACGACGTCGTC AACTGA  
Ae717Ps2\_rpoB TCGATGACCGTTCGACGACGTCGTC AACTGA  
Ae706Ps2\_rpoB TCGATGACCGTTCGACGACGTCGTC AACTGA  
Ae150APs1\_rpoB TCGATGACCGTTCGACGACGTCGTC AACTGA  
Ae168Ps1\_rpoB TCGATGACCGTTCGACGACGTCGTC AACTGA  
Ae263Ps1\_rpoB TCGATGACCGTTCGACGACGTCGTC AACTGA  
Ae356Ps1\_rpoB TCGATGACCGTTCGACGACGTCGTC AACTGA  
Ae707Ps1\_rpoB TCGATGACCGTTCGACGACGTCGTC AACTGA  
\*\*\*\*\*

**Supplementary Table 4. *rpoB* gene percentage identity across *Pseudonocardia* strains.**

	<b>Ae150 A_Ps1 _rpoB</b>	<b>Ae168 _Ps1_ rpoB</b>	<b>Ae263 _Ps1_ rpoB</b>	<b>Ae356 _Ps1_ rpoB</b>	<b>Ae707 _Ps1_ rpoB</b>	<b>Ae331 _Ps2_ rpoB</b>	<b>Ae406 _Ps2_ rpoB</b>	<b>Ae505 _Ps2_ rpoB</b>	<b>Ae706 _Ps2_ rpoB</b>	<b>Ae717 _Ps2_ rpoB</b>
<b>Ae150 A_Ps1 _rpoB</b>	100	100	100	100	99.74	95.01	95.01	94.96	94.99	95.01
<b>Ae168 Ps1_rp oB</b>	100	100	100	100	99.74	95.01	95.01	94.96	94.99	95.01
<b>Ae263 _Ps1_r poB</b>	100	100	100	100	99.74	95.01	95.01	94.96	94.99	95.01
<b>Ae356 Ps1_rp oB</b>	100	100	100	100	99.74	95.01	95.01	94.96	94.99	95.01
<b>Ae707 _Ps1_r poB</b>	99.74	99.74	99.74	99.74	100	95.1	95.1	95.04	95.07	95.1
<b>Ae331 _Ps2_r poB</b>	95.01	95.01	95.01	95.01	95.1	100	100	99.94	99.97	100
<b>Ae406 _Ps2_r poB</b>	95.01	95.01	95.01	95.01	95.1	100	100	99.94	99.97	100
<b>Ae505 _Ps2_r poB</b>	94.96	94.96	94.96	94.96	95.04	99.94	99.94	100	99.91	99.94
<b>Ae706 _Ps2_r poB</b>	94.99	94.99	94.99	94.99	95.07	99.97	99.97	99.91	100	99.97
<b>Ae717 _Ps2_r poB</b>	95.01	95.01	95.01	95.01	95.1	100	100	99.94	99.97	100

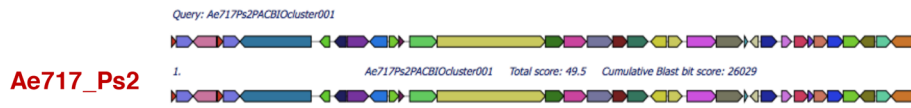
A

### Cluster S: Ae707\_Ps1 BGC 10



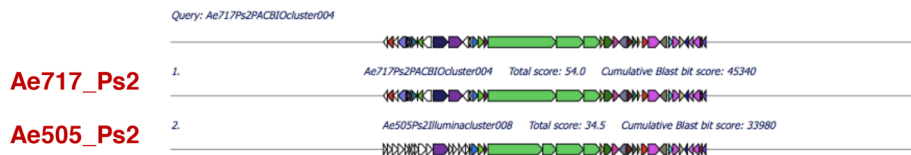
B

### Cluster T: Ae717\_Ps2 Iterative T1PKS



C

### Cluster U: Ps2 T1PKS



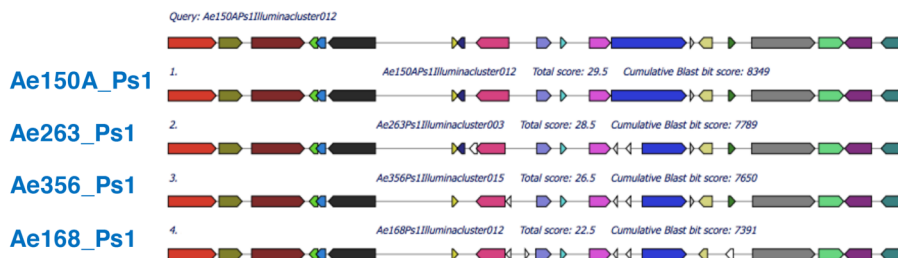
D

### Cluster V: Ae717\_Ps2 T2PKS



E

### Cluster W: Ps1 Lantipeptide





**Supplementary Figure 11. Multigene blast outputs of other biosynthetic gene clusters that are not shared amongst or between Ps phylotypes.** Unique clusters include; cluster S: Ae707\_Ps1 encodes a unique cluster forming an unknown product (A), cluster T: Ae717\_Ps2 encodes an iterative PKS cluster not found in other Ps strains (B), cluster U: Ae717\_Ps2 and Ae505\_Ps2 are the only strains to have an additional T1PKS cluster (C), cluster V: Ae717\_Ps2 encodes a T2PKS cluster not found in other Ps strains (D), cluster W: a subset of Ps1 strains encode a cluster for production of a lantipeptide (E).

**Supplementary Table 5: tBlastn of *Pseudonocardia autotrophica* polyene NPP BGC amino acid sequences against putative nystatin clusters of Ae707\_Ps1 (PacBio) and Ae717\_Ps2 (PacBio).** NppC against Ae707\_Ps1 nystatin cluster has two results as the blast algorithm separated the sequences into two. All PKS type I proteins against Ae706\_Ps2 were given the 3 top hits, as the conservation is low it is difficult to assign identity of the PKS proteins to the respective homologues present in the *P. autotrophica* cluster.

NPP BGC	Amino Acid Length	Protein Function	Ae707_Ps 1 Cluster % Identity	Ae707_Ps 1 Query % Coverage	Ae717_Ps 2 Cluster % Identity	Ae717_Ps 2 Query % Coverage
NppY	475	Glycosyltransferase	83	98	43	94
NppF	224	Phosphopantetheinyl transferase	90	99	70	0.045
NppG	592	ABC transporter	90	99	56	86
NppH	584	ABC transporter	89	100	52	97
NppDII I	344	GDP-mannose-4,6-dehydratase	97	100	79	100
NppI	9499	Type I PKS	90	100	59 49 62	26 32 15
NppJ	5425	Type I PKS	86	100	57 59 53	35 23 34
NppK	2031	Type I PKS	89	100	60 59 60	55 49 50
NppL	403	P450 mono oxygenase	85	97	47	90
NppN	413	P450 mono oxygenase	84	100	69	90
NppDII	352	Aminotransferase	96	100	74	99
NppDI	489	Glycosyltransferase	93	97	60	96
NppA	1097	Type I PKS	89	100	59 57 60	79 79 78
NppB	3175	Type I PKS	90	100	54 48	78 47

					48	46
NppC	10876	Type I PKS	87	56	54	43
			89	43	52	37
					53	32
NppE	274	Thioesterase	91	100	53	82
NppRI	946	Regulation	86	100	47	97
NppRII	765	Regulation	79	100	45	93
NppRII I	925	Regulation	77	97	43	62
NppO	526	Decarboxylase	97	100	87	98
NppRI V	213	Regulation	94	100	68	91
NppM	138	Ferredoxin	74	90	55	69
NppRV	963	Regulation	69	97	40	95
NppRV I	684	Regulation	70	97	38	97

**Supplementary Table 6. Blastx of the PKS amino acid sequences from either the Ae707\_Ps1 PacBio nystatin cluster against Ps1 strains nucleotide sequence or the PKS amino acid sequences from the Ae717\_Ps2 PacBio nystatin cluster against Ps2 strains nucleotide sequence. (\*) The PKS modules in PKS amino acid sequences for 3119 do not cover the full amino acid length in any of the other Ps1 strains and this corresponds to an amino acid sequence that encodes two modules.**

Amino Acid	Length (aa)	Ae150A_Ps1 Illumina Identity	Ae150A_Ps1 Illumina Locus	Ae168_Ps1 Illumina Identity	Ae168_Ps1 Illumina Locus	Ae263_Ps1 Illumina Identity	Ae263_Ps1 Illumina Locus	Ae356_Ps1 Illumina Identity	Ae356_Ps1 Illumina Locus	Ae707_Ps1 PacBio Identity	Ae707_Ps1 PacBio Locus
Ae707_Ps1_3121 NypA/NppA	1106	565/603 (94%) 391/431 (91%)	43301-45049 42105-43289	565/603 (94%) 391/431 (91%)	47494-49242 46298-47482	565/603 (94%) 391/431 (91%)	5432888-5431140 5434084-5432900	565/603 (94%) 391/431 (91%)	1678228-1679976 1677032-1678216	1106/1106 (100%)	3411435-3408118
Ae707_Ps1_3120 NypB/NppB	3188	1530/1555 (98%) 832/843 (99%) 750/767 (98%)	50138-54793 45302-47830 47842-50133	1530/1555 (98%) 832/843 (99%) 750/767 (98%)	54331-58986 49495-52023 52035-54326	1530/1555 (98%) 832/843 (99%) 750/767 (98%)	5426051-5421396 5430887-5428359 5428347-5426056	1530/1555 (98%) 832/843 (99%) 750/767 (98%)	1685065-1689720 1680409-1682757 1682769-1685060	3188/3188 (100%)	3408069-3398506
Ae707_Ps1_3119 NypC/NppC *	10899	3683/4065 (91%) 1826/1857 (98%) 1118/1139 (98%)	6846-76113 54817-60387 60389-63805	3685/4065 (91%) 1826/1857 (98%) 1118/1139 (98%)	68136-80306 59010-64580 64582-67998	3685/4065 (91%) 1825/1857 (98%) 1118/1139 (98%)	5412246-5400076 5421192-5415802 5415800-5412384	3685/4065 (91%) 1826/1857 (98%) 1118/1139 (98%)	1698870-1711040 1689744-1695314 1695316-1698732	10895/10895 (100%)	3398482-3365798
Ae707_Ps1_3128 NypI/NppI	9524	6924/7034 (98%) 1448/1470 (99%) 994/1007 (99%)	760991-739890 739869-735466 764056-761042	6924/7034 (98%) 1448/1470 (99%) 994/1007 (99%)	760457-739356 739335-734932 763522-760508	6925/7034 (98%) 1448/1470 (99%) 994/1007 (99%)	4718060-4739161 4739182-4743585 4714995-4718009	6925/7034 (98%) 1448/1470 (99%) 994/1007 (99%)	2393068-2371967 2371946-2367543 2396133-2393119	9524/9524 (100%)	3468317-3439746
Ae707_Ps1_3127 NypJ/NppJ	5420	3079/3163 (97%) 2178/2248 (97%)	735442-726068 726011-719274	3079/3163 (97%) 2178/2248 (97%)	734908-725534 725477-718740	3079/3163 (97%) 2178/2248 (97%)	4743609-4752983 4753040-4759777	3079/3163 (97%) 2178/2248 (97%)	2367519-2358145 2358088-2351351	5420/5420 (100%)	3439722-3423463
Ae707_Ps1_3126 NypK/NppK	2027	969/981 (99%) 1003/1007 (99%)	719233-716291 716166-713146	969/981 (99%) 1002/1007 (99%)	718699-715757 715632-712612	969/981 (99%) 1001/1006 (99%)	4759818-4762760 4762889-4765906	969/981 (99%) 1001/1006 (99%)	2351310-2348368 2348239-2345222	2025/2025 (100%)	3423422-3417348
Amino Acid	Length (aa)	Ae331_Ps2 Illumina Identity	Ae331_Ps2 Illumina Locus	Ae406_Ps2 Illumina Identity	Ae406_Ps2 Illumina Locus	Ae505_Ps2 Illumina Identity	Ae505_Ps2 Illumina Similarity	Ae706_Ps2 Illumina Identity	Ae706_Ps2 Illumina Similarity	Ae717_Ps2 PacBio Identity	Ae717_Ps2 PacBio Similarity
Ae717_Ps2_3010 PKS A	2554	2540/2540 (100%)	4471485-4479104	2540/2540 (100%)	1602520-1594901	2539/2540 (99%)	5280963-5273347	2540/2540 (100%)	1611426-1603807	2540/2540 (100%)	3308031-3300412
Ae717_Ps2_3009 PKS B	6856	6838/6859 (99%)	4479198-4499774	6838/6865 (99%)	1594807-1574213	6192/6239 (99%) 613/632 (97%)	5271344-5252703 5273253-5271358	6838/6859 (99%)	1603713-1583137	6856/6856 (100%)	3300318-3279751
Ae717_Ps2_3026 PKS C	3490	3344/3351 (99%)	4400747-4410799	3344/3351 (99%)	1668401-1658349	-	-	3344/3351 (99%)	1682164-1672112	3361/3361 (100%)	3377832-3367750
Ae717_Ps2_3025 PKS D	5917	5878/5917 (99%)	4411202-4428913	5879/5917 (99%)	1657946-1640235	-	-	5879/5917 (99%)	1671709-1653998	5917/5917 (100%)	3367381-3349631
Ae717_Ps2_3024 PKS E	3234	3074/3078 (99%) 155/155 (100%)	4428930-4438163 4438177-4438641	3074/3078 (99%) 155/155 (100%)	1640218-1630985 1630971-1630507	-	-	3074/3078 (99%) 155/155 (100%)	1653981-1644748 1644734-1644270	3234/3234 (100%)	3349614-3339913
Ae717_Ps2_3023 PKS F	3747	3740/3747 (99%)	4438641-4449881	3740/3747 (99%)	1630507-1619267	-	-	3739/3747 (99%)	1644270-1633030	3747/3747 (100%)	3339913-3328673
Ae717_Ps2_3022 PKS G	2048	2047/2048 (99%)	4449921-4456064	2047/2048 (99%)	1619227-1613084	-	-	2047/2048 (99%)	1632990-1626847	2048/2048 (100%)	3328633-3322490

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