Table S1. CRISPR/CAS elements present in *P. putida* PCL1760 using CRISPR Finder

Element	**CRISPR Id / Cas Type**	**Start**	**End**	**Spacer / Gene**	**Repeat consensus / cas genes**	**Direction**	**Evidence Level**
CRISPR	*P. putida* PCL1760 (1)	603294	603450	1	TTTTTGCTGTGCCGGCCTCTTCGCGGGTAAACCCGCTCCTACAGGGGGGCGC	ND	1
Cas cluster	CAS	1086887	5682683	10	cas3_TypeI, cas3_TypeI, cas3_TypeI, cas3_TypeI, cas3_TypeI, cas3_TypeI, cas3_TypeI, cas3_TypeI, cas3_TypeI, cas3_TypeI		
CRISPR	P. *putida* PCL1760 (2)	1309549	1309657	1	GTAGGAGCGGGTTCACCCGCGAAGGGCTGCAAAGCAGCCCC	ND	1
CRISPR	*P. putida* PCL1760 (3)	2302037	2302145	1	TGTAGGAGCGGGTTCACCCGCGAAAGGGCCGCAGAAACCAA	ND	1
CRISPR	*P. putida* PCL1760 (4)	2320088	2320185	1	CCAACACAGATTTCAGCCAGTAATCGGTGC	+	1
CRISPR	*P. putida* PCL1760 (5)	3000585	3000682	1	AAGGCAGCCGAAGAGGCCAAGAA	+	1

Table S2. CRISPR/CAS elements present in *P. putida* S12 using CRISPR Finder

Element	**CRISPR Id / Cas Type**	**Start**	**End**	**Spacer / Gene**	**Repeat consensus / cas genes**	**Direction**	**Evidence Level**
Cas cluster	CAS	599529	4070424	12	cas3_TypeI, cas3_TypeI, cas3_TypeI, cas3_TypeI, cas3_TypeI, cas3_TypeI, cas3_TypeI, cas3_TypeI, cas3_TypeI, cas3_TypeI, cas3_TypeI, cas3_TypeI		
CRISPR	*P. putida* S12 (1)	1383660	1383756	1	TTCTGCGGCCCTTTCGCGGGTGAACCCGC	ND	1
CRISPR	*P. putida* S12 (2)	2420905	2421013	1	GGGGCTGCTCTGCAGCCCTTCGCGGGTGAACCCGCTCCTAC	ND	1

Element	CRISPR Id / Cas Type	Start	End	Spacer / Gene	Repeat consensus / cas genes	Direction	Evidence Level
CRISPR	*P. putida* S12 (3)	3143834	3143990	1	GCGCCCCCCTGTAGGAGCGGGTTCACCCGCGAAGA GGCCGGCACAGCAAAAA	ND	1

Table S3. CRISPR/CAS elements present in *P. fluorescens* Pt14 using CRISPR Finder

Element	CRISPR Id / Cas Type	Start	End	Spacer / Gene	Repeat consensus / cas genes	Direction	Evidence Level
Cas cluster	CAS	508266	4726464	16	cas3_TypeI, cas3_TypeI, cas3_TypeI, cas3_TypeI, cas3_TypeI, cas3_TypeI, cas3_TypeI, cas3_TypeI, cas3_TypeI, cas3_TypeI, cas3_TypeI, cas3_TypeI, cas3_TypeI, cas3_TypeI, cas3_TypeI, cas3_TypeI, cas3_TypeI		
CRISPR	*P. fluorescens* Pt14 (1)	673054	673158	1	GCTGGCTTGCCTGCGATGACGGCCTGAAAGCC	ND	1
CRISPR	*P. fluorescens* Pt14 (2)	730220	730318	1	AGCTGGCTTGCCTGCGATGACGGCCTG	ND	1
CRISPR	*P. fluorescens* Pt14 (3)	1153261	1153364	1	CGATCCAACTGTGGGAGCTGGCTCGCCTGCGA	-	1
CRISPR	*P. fluorescens* Pt14 (4)	1311982	1312082	1	TCCAACTGTGGGAGCTGGCTTGCCTGCGA	-	1
CRISPR	*P. fluorescens* Pt14 (5)	1375038	1375142	1	TGTGGGAGCTGGCTTGCCTGCGATGGCGGCCTG	ND	1
CRISPR	*P. fluorescens* Pt14 (6)	2192777	2192885	1	CTGTGAGGCCGCCTTCGCAGGCAAGCCAGCTCCCA CA	ND	1
CRISPR	*P. fluorescens* Pt14 (7)	2250643	2250739	1	TCGCAGGCAAGCCAGCTCCCACAG	ND	1
CRISPR	*P. fluorescens* Pt14 (8)	2459140	2459208	1	CTGCACTACCCCCTGGTGCAGGAG	ND	1
CRISPR	*P. fluorescens* Pt14 (9)	2683820	2683926	1	GGGTGTCAGGTAGATTGGCGTCGGCTGTCAGGCCG	ND	1

Element	CRISPR Id / Cas Type	Start	End	Spacer / Gene	Repeat consensus / cas genes	Direction	Evidence Level
CRISPR	*P. fluorescens* Pt14 (10)	3659651	3659749	1	GCCGTCATCGCAGGCAAGCCAGCTCCC	ND	1
CRISPR	*P. fluorescens* Pt14 (11)	5194851	5194978	1	GCTCCCACAGGGGAATGCATTCCAAAGGTGGGAGC	ND	1

Table S4. CRISPR/CAS elements present in *P. fluorescens* W-6 using CRISPR Finder

Elements	CRISPR Id / Cas Type	Start	End	Spacer / Gene	Repeat consensus / cas genes	Direction	Evidence Level
CRISPR	*P. fluorescens* W-6 (1)	1155385	1155486	1	TGAGCTTATTTTCTGAGCAAACCTGCTCACCACAGG GG	ND	1
Cas cluster	CAS	2553823	6080320	16	cas3_TypeI, cas3_TypeI, cas3_TypeI, cas3_TypeI, cas3_TypeI, cas3_TypeI, cas3_TypeI, cas3_TypeI, cas3_TypeI, cas3_TypeI, cas3_TypeI, cas3_TypeI, cas3_TypeI, cas3_TypeI, cas3_TypeI, cas3_TypeI		

Table S5. CRISPR/CAS elements present in *P. simiae* PCL1751 using CRISPR Finder

Element	**CRISPR Id / Cas Type**	**Start**	**End**	**Spacer / Gene**	**Repeat consensus / cas genes**	**Direction**	**Evidence Level**
Cas cluster	CAS	1419190	5983525	14	cas3_TypeI, cas3_TypeI, cas3_TypeI, cas3_TypeI, cas3_TypeI, cas3_TypeI, cas3_TypeI, cas3_TypeI, cas3_TypeI, cas3_TypeI, cas3_TypeI, cas3_TypeI, cas3_TypeI, cas3_TypeI		
CRISPR	*P. simiae* PCL1751 (1)	2149705	2149803	1	GGCTTGCCTGCGAAGGCGGCCTGACAG	ND	**1**
CRISPR	*P. simiae* PCL1751 (2)	4125021	4125241	1	GCGACCTTGTGCTCGACCTTCACATCCGGCACGTTCTTGGCATCGGTGCCAGG	ND	**1**

Table S6. CRISPR/CAS elements present in *P. simiae* WCS417 using CRISPR Finder

Element	**CRISPR Id / Cas Type**	**Start**	**End**	**Spacer / Gene**	**Repeat consensus / cas genes**	**Direction**	**Evidence Level**
Cas cluster	CAS	1415550	6008943	14	cas3_TypeI, cas3_TypeI, cas3_TypeI, cas3_TypeI, cas3_TypeI, cas3_TypeI, cas3_TypeI, cas3_TypeI, cas3_TypeI, cas3_TypeI, cas3_TypeI, cas3_TypeI, cas3_TypeI, cas3_TypeI		
CRISPR	*P. simiae* WCS417 (1)	3658337	3658444	1	CCACTCTCCTACTGTTGCCCCGCGATCCAAATGTGG	ND	1

Figure S1. Analysis of secondary metabolites biosynthesis of *P. putida* PCL1760 (**A**), *P. putida* S12 (**B**), *P. Simiae* PCL1751 (**C**), *P. fluorescens* Pt14 **(D)**, *P. simiae* WCS417(**E**), and *P. fluorescens* W-6 (**F**) using antiSMASH.

Table S7. Prophages predicted in *P. putida* PCL1760 using PHASTER

Region	Region Length	Completeness	Score	Total Proteins	Region Position	Most Common Phage	GC %	Details
1	37.3Kb	incomplete	50	15	735221-772596	PHAGE Escher 500465 1 NC 049342(4)	60.32%	Show info outline
2	81.1Kb	intact	150	86	3796726-3877901	PHAGE Pseudo YMC11/02/R656 NC 028657(15)	58.87%	Show info outline
3	29Kb	questionable	90	24	5159654-5188739	PHAGE Pseudo JBD44 NC 030929(3)	58.22%	Show info outline

Table S8. Prophages predicted in *P. putida* S12 using PHASTER

Region	Region Length	Completeness	Score	Total Proteins	Region Position	Most Common Phage	GC %	Details
1	24.5Kb	incomplete	40	14	2976086-3000672	PHAGE Escher 500465 1 NC 049342(4)	59.98%	Show info outline
2	18.5Kb	incomplete	60	21	4393908-4412429	PHAGE Pseudo JBD44 NC 030929(3)	58.74%	Show info outline
3	10.1Kb	incomplete	40	9	5153763-5163931	PHAGE Bacill vB BtS BMBtp14 NC 048640(2)	64.13%	Show info outline

Table S9. Prophages predicted in *P. fluorescens* Pt14 using PHASTER

Region	Region Length	Completeness	Score	Total Proteins	Region Position	Most Common Phage	GC %	Details
1	18.1Kb	intact	150	27	383359-401474	PHAGE Vibrio VP882 NC 009016(14)	59.35%	Show info outline
2	58.4Kb	intact	150	80	2422039-2480508	PHAGE Pseudo YMC11/02/R656 NC 028657(17)	57.10%	Show info outline

Region	Region Length	Completeness	Score	Total Proteins	Region Position	Most Common Phage	GC %	Details
3	33.4Kb	incomplete	40	12	3971143-4004631	PHAGE Escher 500465 1NC 049342(6)	57.95%	Show info_outline
4	15.5Kb	incomplete	40	12	5122025-5137589	PHAGE Pseudo F10 NC 007805(2)	57.06%	Show info_outline

Table S10. Prophages predicted in *P. simiae* WCS417 using PHASTER

Region	Region Length	Completeness	Score	Total Proteins	Region Position	Most Common Phage	GC %	Details
1	20.4Kb	intact	130	29	1276815-1297309	PHAGE Vibrio VP882 NC 009016(13)	59.48%	Show info_outline
2	53.5Kb	intact	130	54	2138720-2192316	PHAGE Pseudo YMC11/02/R656 NC 028657(17)	57.11%	Show info_outline

Table S11. Prophages predicted in *P. simiae* PCL1751 using PHASTER

Region	Region Length	Completeness	Score	Total Proteins	Region Position	Most Common Phage	GC %	Details
1	20.4Kb	intact	140	28	1280518-1300948	PHAGE Vibrio VP882 NC 009016(13)	59.61%	Show info_outline
2	27.3Kb	questionable	70	30	1606761-1634112	PHAGE Vibrio vB VpaM MAR NC 019722(6)	58.08%	Show info_outline
3	32.2Kb	intact	130	40	4008459-4040669	PHAGE Pseudo YMC11/02/R656 NC 028657(13)	58.22%	Show info_outline
4	23.8Kb	incomplete	30	10	4055309-4079195	PHAGE Salmon SJ46 NC 031129(2)	56.91%	Show info_outline

Table S12. Prophages predicted in *P. fluorescens* W-6 using PHASTER

Region	Region Length	Completeness	Score	Total Proteins	Region Position	Most Common Phage	GC %	Details
1	46.3Kb	intact	150	51	1574172-1620495	PHAGE Pseudo YMC11/02/R656 NC 028657(14)	56.67%	Show info outline
2	23.7Kb	incomplete	30	13	5263333-5287124	PHAGE Escher 5004651 NC 049342(5)	54.20%	Show info outline

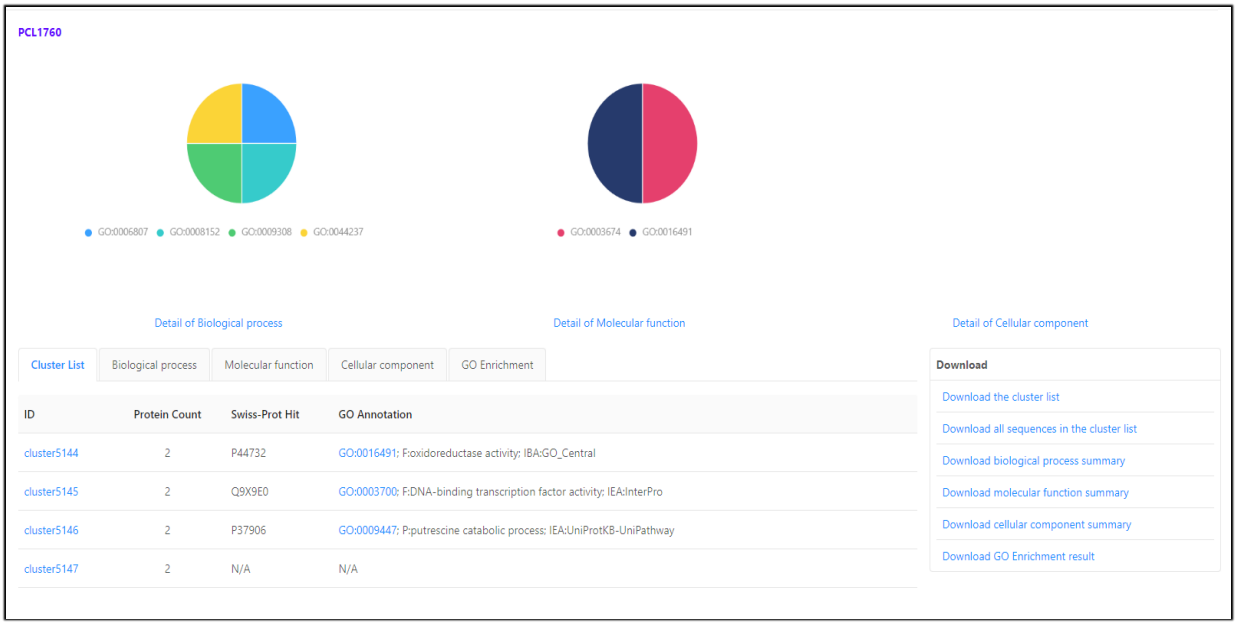


Figure S2. Clusters present in the strain of *P. putida* PCL1760 which are not included in any orthologous clusters with others strains.

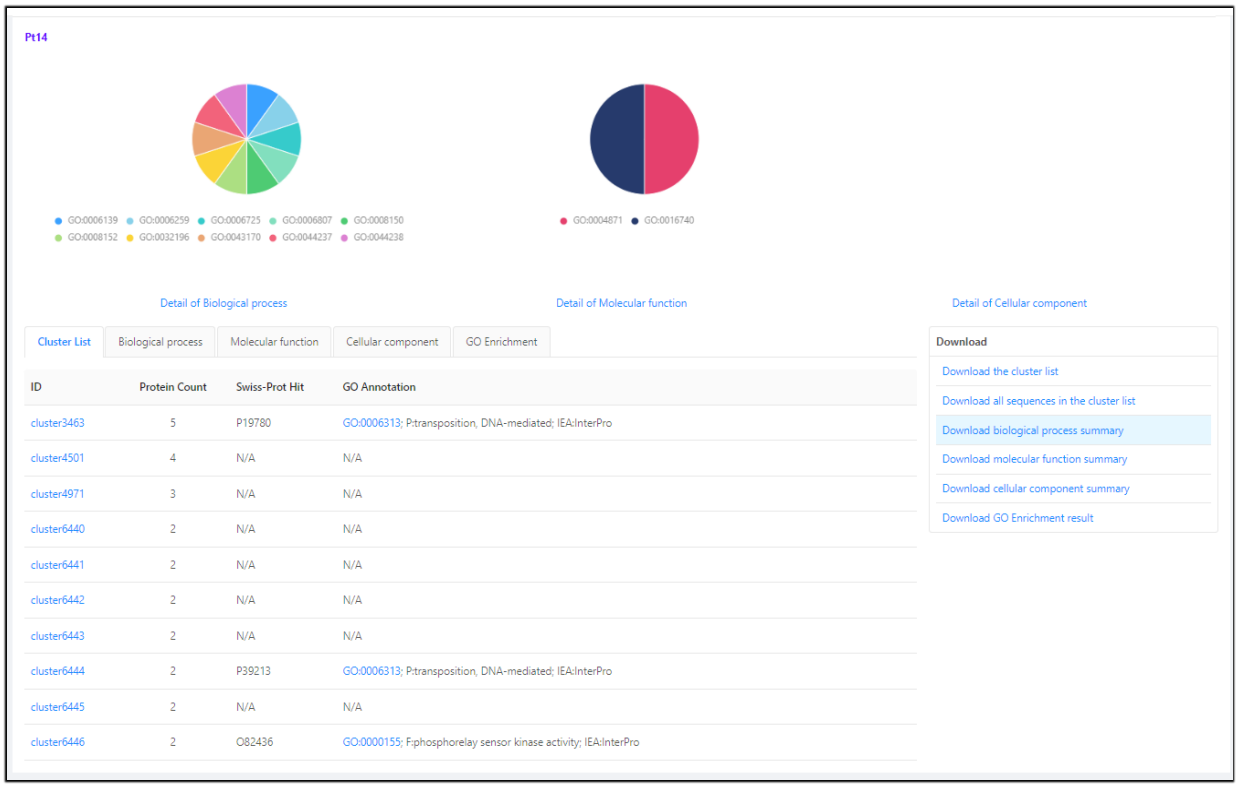


Figure S3. The unique clusters present in the strain of *P. fluorescens* Pt14 which are not included in any orthologous clusters with others strains.

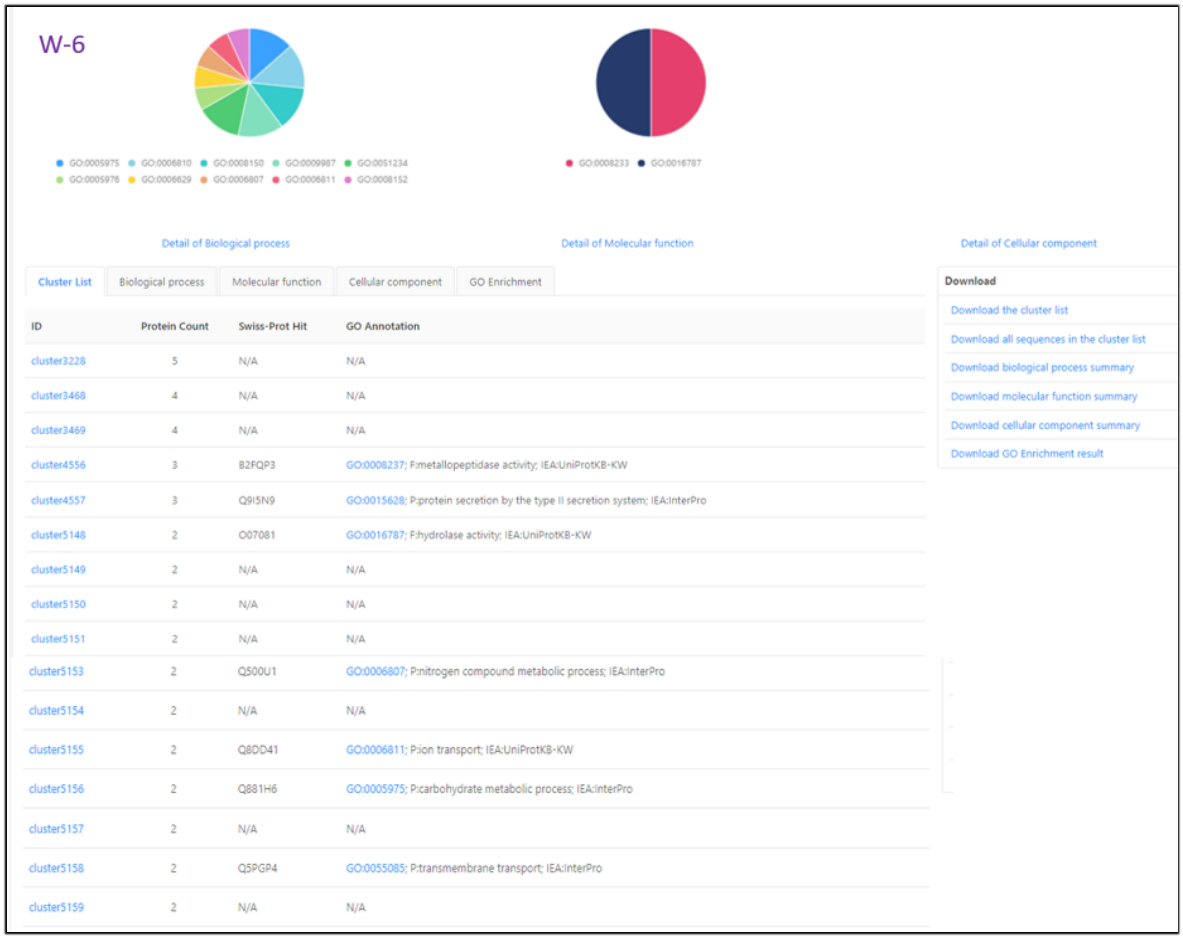


Figure S4. The unique clusters present in the strain of *P. fluorescens* W-6 which are not included in any orthologous clusters with others strains.

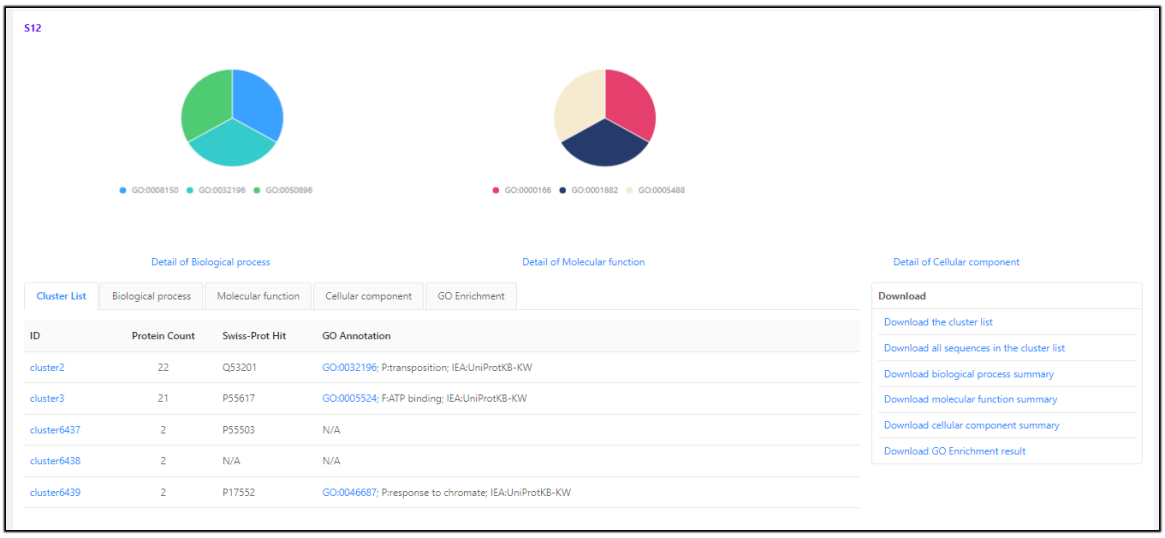


Figure S5. The unique clusters present in the strain of *P. putida* S12 which are not included in any orthologous clusters with others strains.

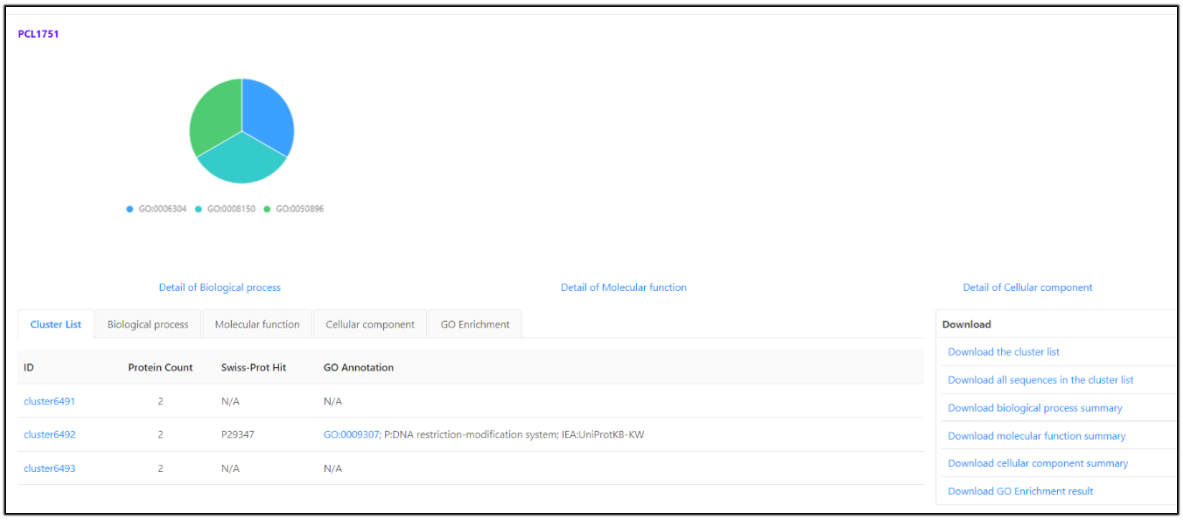


Figure S6. The unique clusters present in the strain of *P. simae* PCL1751 which are not included in any orthologous clusters with others strains.

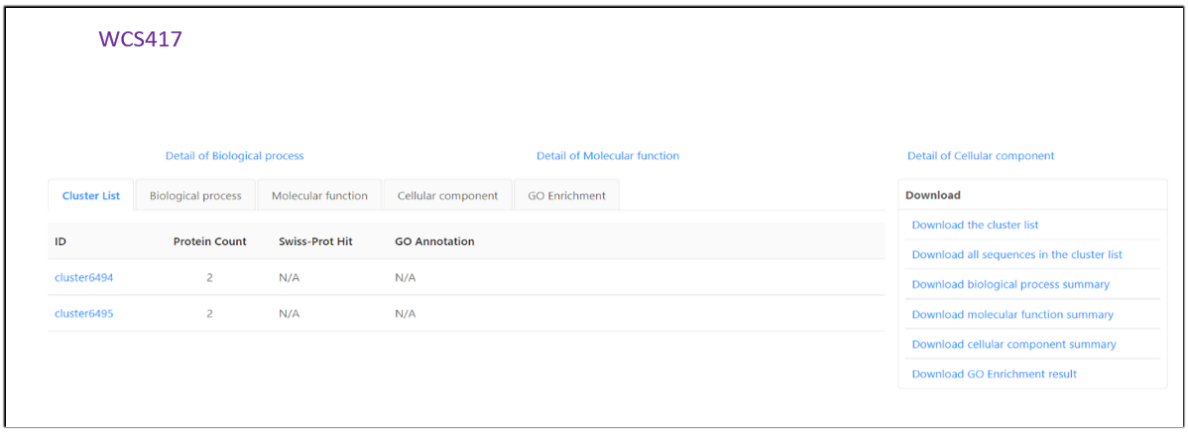


Figure S7. The unique clusters present in the strain of *P. simae* WCS417 which are not included in any orthologous clusters with others strains

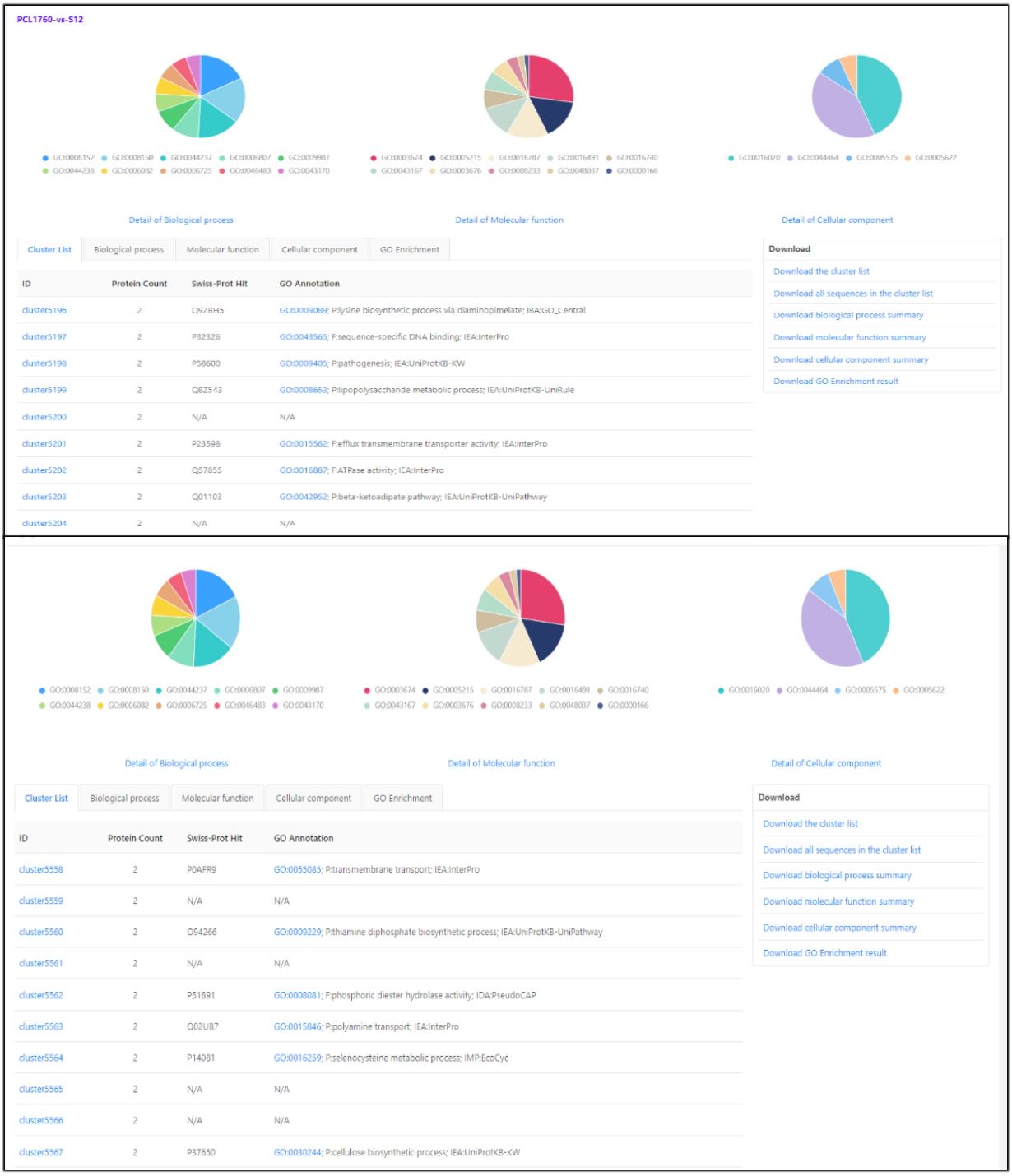
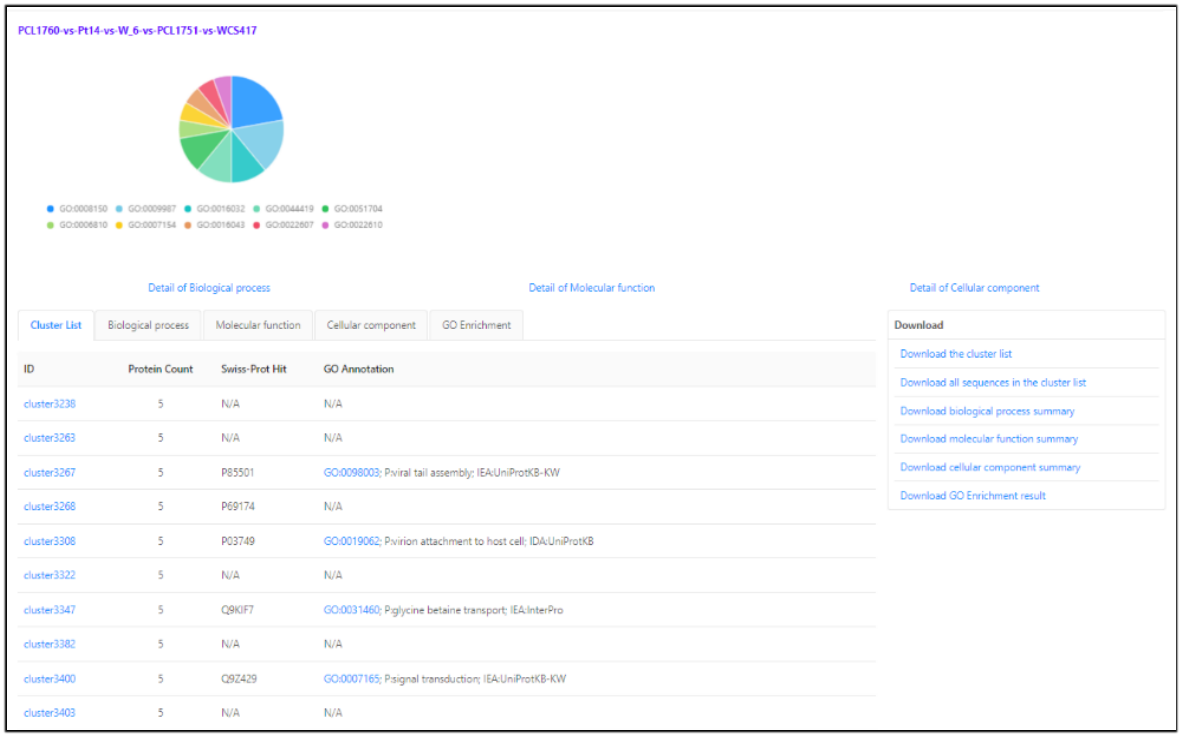


Figure S8. Orthologous gene clusters shared by PCL160 with the strain of S12



ID	Protein Count	Swiss-Prot Hit	GO Annotation
cluster3238	5	N/A	N/A
cluster3263	5	N/A	N/A
cluster3267	5	P85501	GO:0098003; P:viral tail assembly; IEA:UniProtKB-KW
cluster3268	5	P69174	N/A
cluster3308	5	P03749	GO:0019062; P:virion attachment to host cell; IDA:UniProtKB
cluster3322	5	N/A	N/A
cluster3347	5	Q9KIF7	GO:0031460; P:glycine betaine transport; IEA:InterPro
cluster3382	5	N/A	N/A
cluster3400	5	Q9Z429	GO:0007165; P:signal transduction; IEA:UniProtKB-KW
cluster3403	5	N/A	N/A

Figure S9. Clusters shared among strains of PCL1760, Pt14, W-6, PCL1751, and WCS417

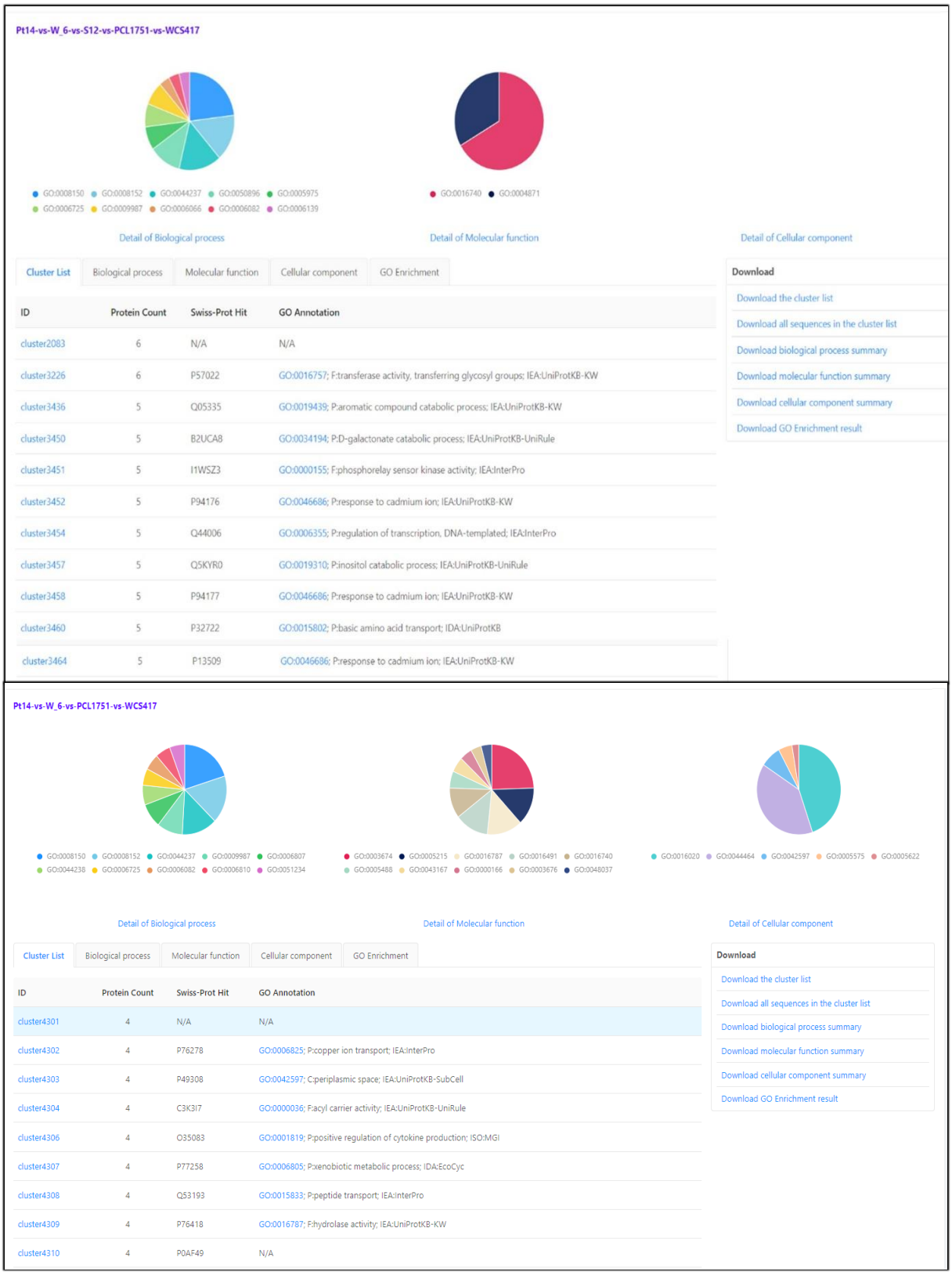


Figure S10. Clusters shared among strains of Pt14, W-6, S12, PCL1751, and WCS417

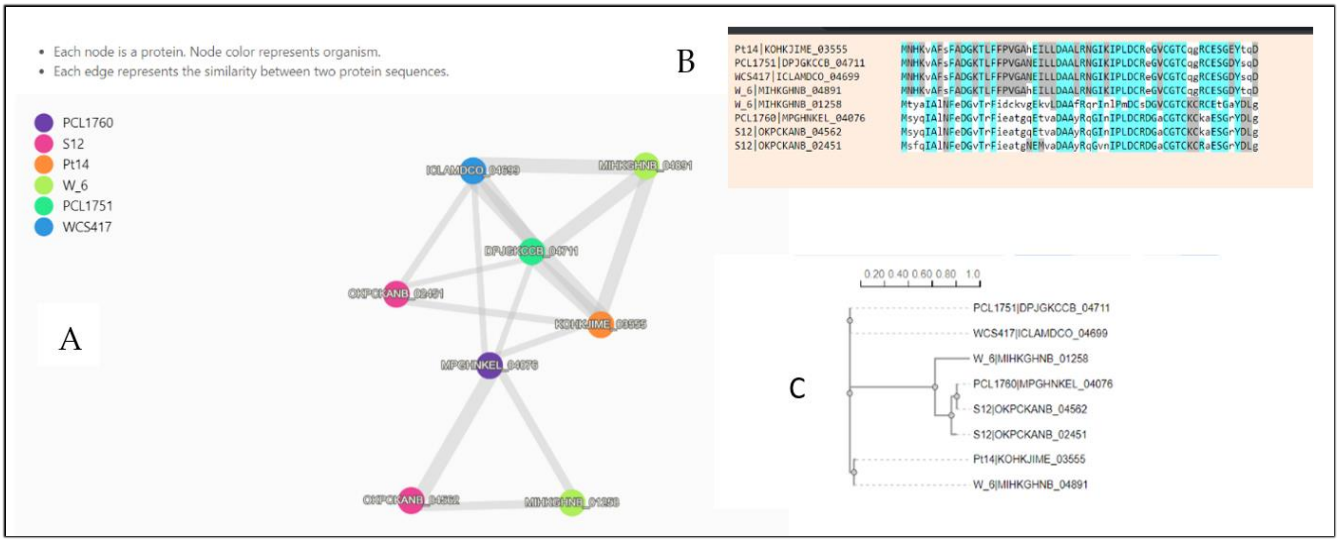


Figure S11. Cluster GO:0019439; P:aromatic compound catabolic process; IEA:UniProtKB-KW shared by the strain of PCL1760 with Pt14, W-6, S12, PCL1751, and WCS417. Layout of the cluster (A); multiple sequence alignment (B), phylogenetic Tree (C).

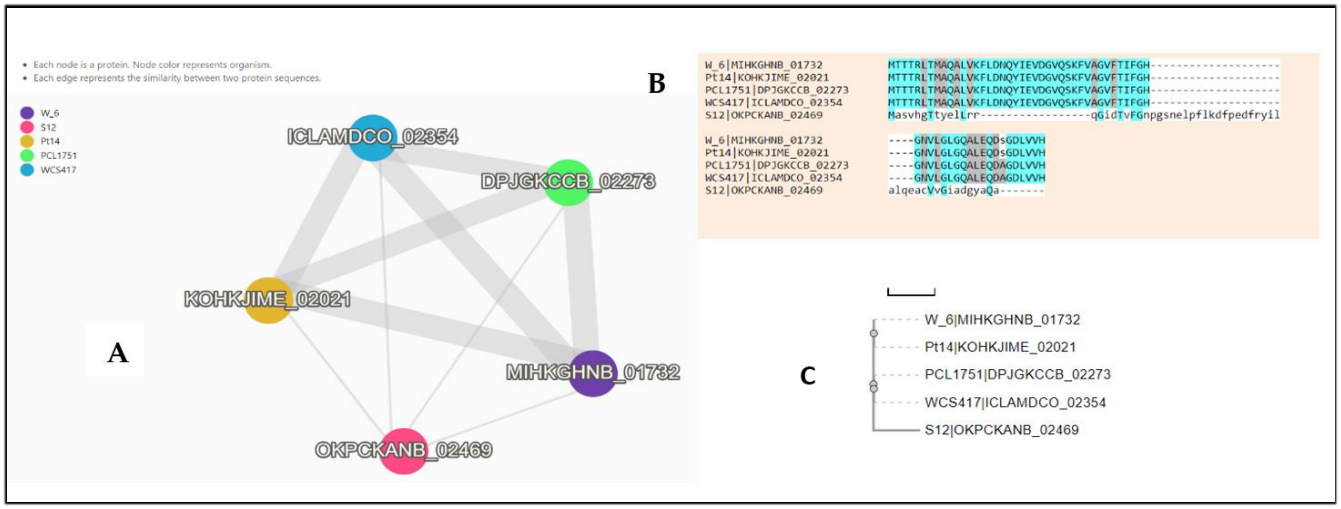
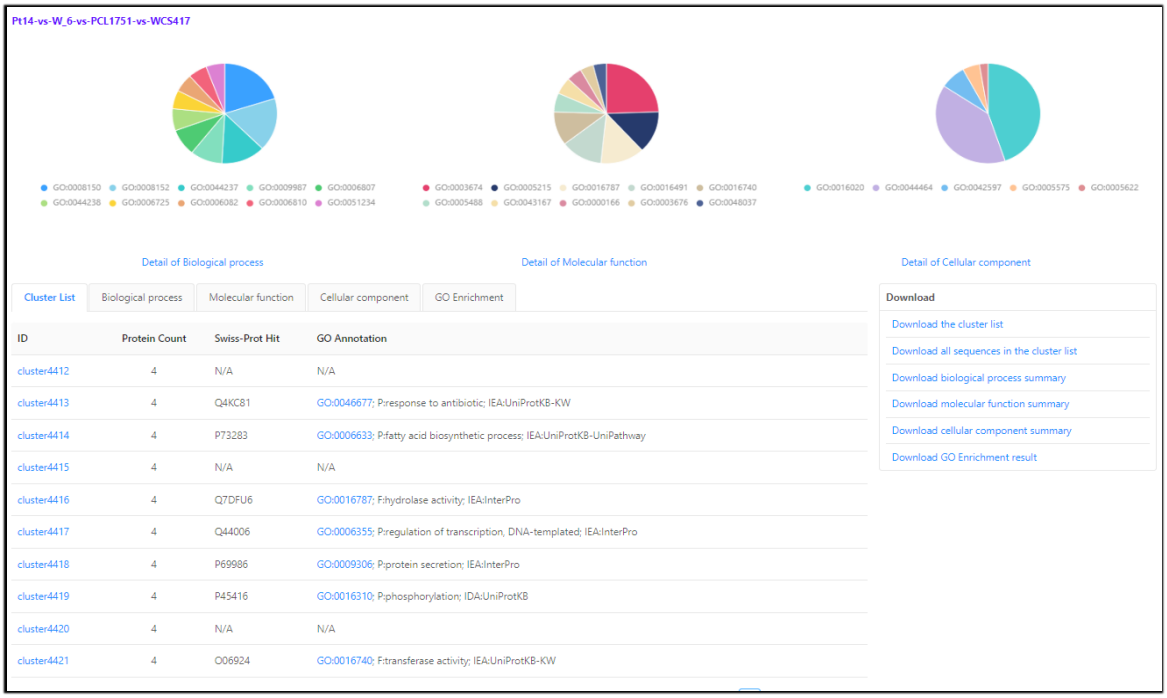


Figure S12. Cluster GO:0019310; P:inositol catabolic process; IEA:UniProtKB-UniRule shared by the strain of PCL1760 with Pt14, W-6, S12, PCL1751, and WCS417. Layout of the cluster (A); multiple sequence alignment (B); and phylogenetic Tree (C).



ID	Protein Count	Swiss-Prot Hit	GO Annotation
cluster4412	4	N/A	N/A
cluster4413	4	Q4KC81	GO:0046677; P:response to antibiotic; IEA:UniProtKB-KW
cluster4414	4	P73283	GO:0006633; P:fatty acid biosynthetic process; IEA:UniProtKB-UniPathway
cluster4415	4	N/A	N/A
cluster4416	4	Q7DFU6	GO:0016787; F:hydrolase activity; IEA:InterPro
cluster4417	4	Q44006	GO:0006355; P:regulation of transcription, DNA-templated; IEA:InterPro
cluster4418	4	P69986	GO:0009306; P:protein secretion; IEA:InterPro
cluster4419	4	P45416	GO:0016310; P:phosphorylation; IDA:UniProtKB
cluster4420	4	N/A	N/A
cluster4421	4	O06924	GO:0016740; F:transferase activity; IEA:UniProtKB-KW

Figure S13. Clusters shared among strains of Pt14, W-6, PCL1751, and WCS417 which are not included in any orthologous clusters with other strains.

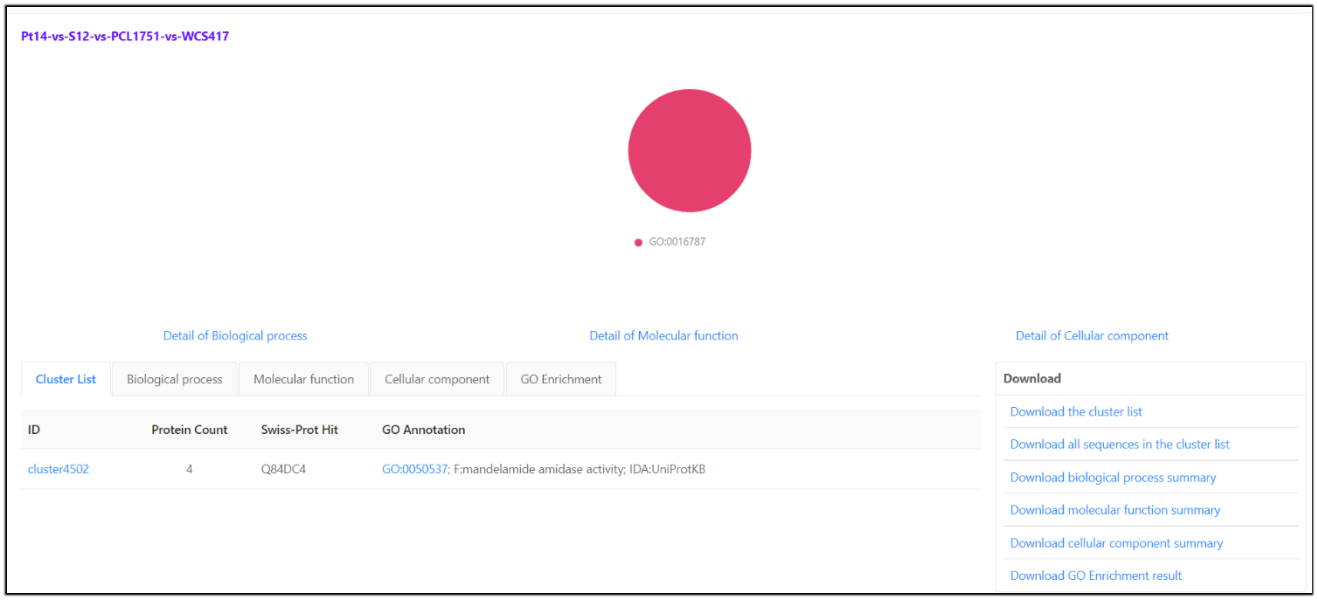


Figure S14. Cluster GO:0050537; F:mandelamide amidase activity; IDA:UniProtKB shared by the strain of Pt14, S12, PCL1751, and WCS417.

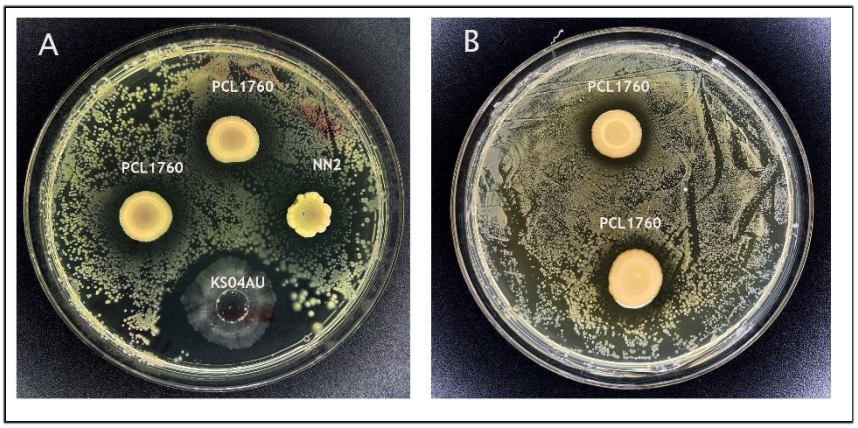


Figure S15. Antagonistic activity of *P. putida* PCL1760 against *P. syringae* on M9 Minimal (A) and King's B (B) agar plates. *Bacillus velezensis* KS04AU and *Bacillus aryabhattai* NN2 were used as positive controls, respectively.

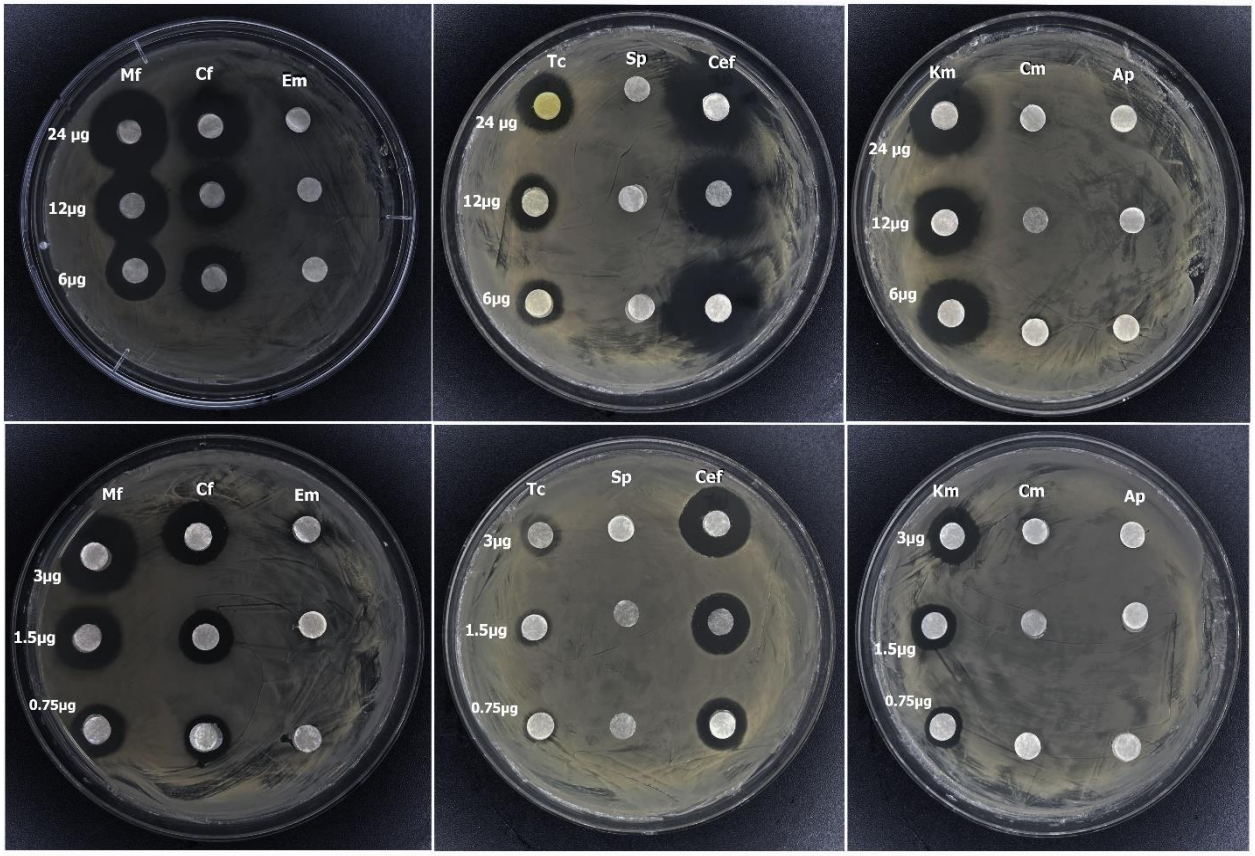


Figure S16: The antibiotic susceptibility test of *P. putida* PCL1760 using the disk diffusion method performed on Multer-Hinter agar.