Appendix I

List of Tables and Figures

Mortality patterns in 4106A (SUS-1) aphid clone

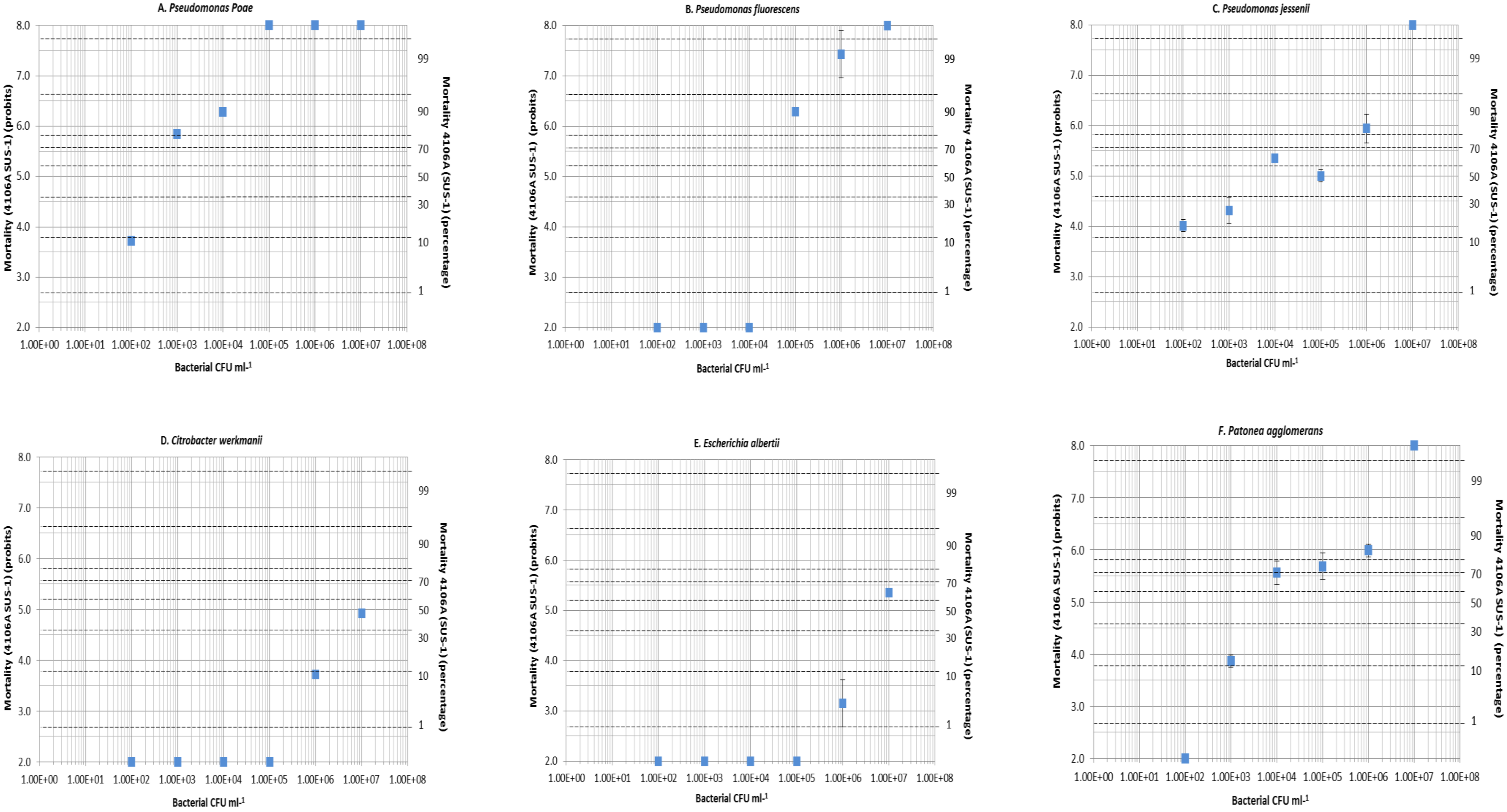

Figure 1: Estimation of 4106A aphid clone (SUS-1) mortality probits at various bacterial concentrations 4106A aphid clone (SUS-1) mortality calculated in terms of probits and percentage on log scale at different bacterial cell concentrations with three replicates after 72 hours.

Mortality patterns in 4225B (SUS-2) aphid clone

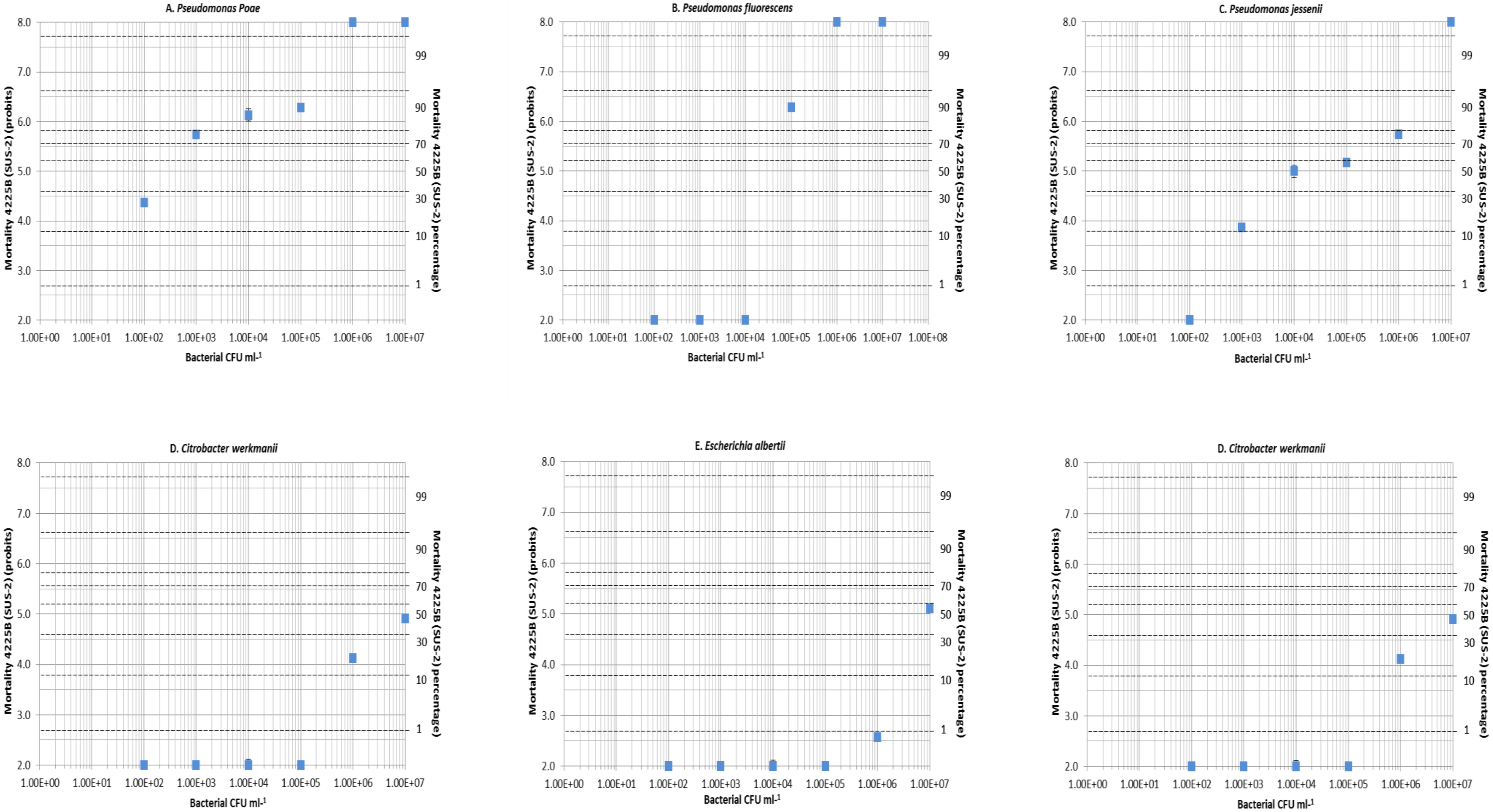

Figure 2: Estimation of 4225B aphid clone (SUS-2) mortality probits at various bacterial concentrations. 4225B aphid clone (SUS-2) mortality calculated in terms of probits and percentage on log scale at different bacterial cell concentrations with three replicates after 72 hours.

Mortality patterns in Clone-NS (SUS-3) aphid clone

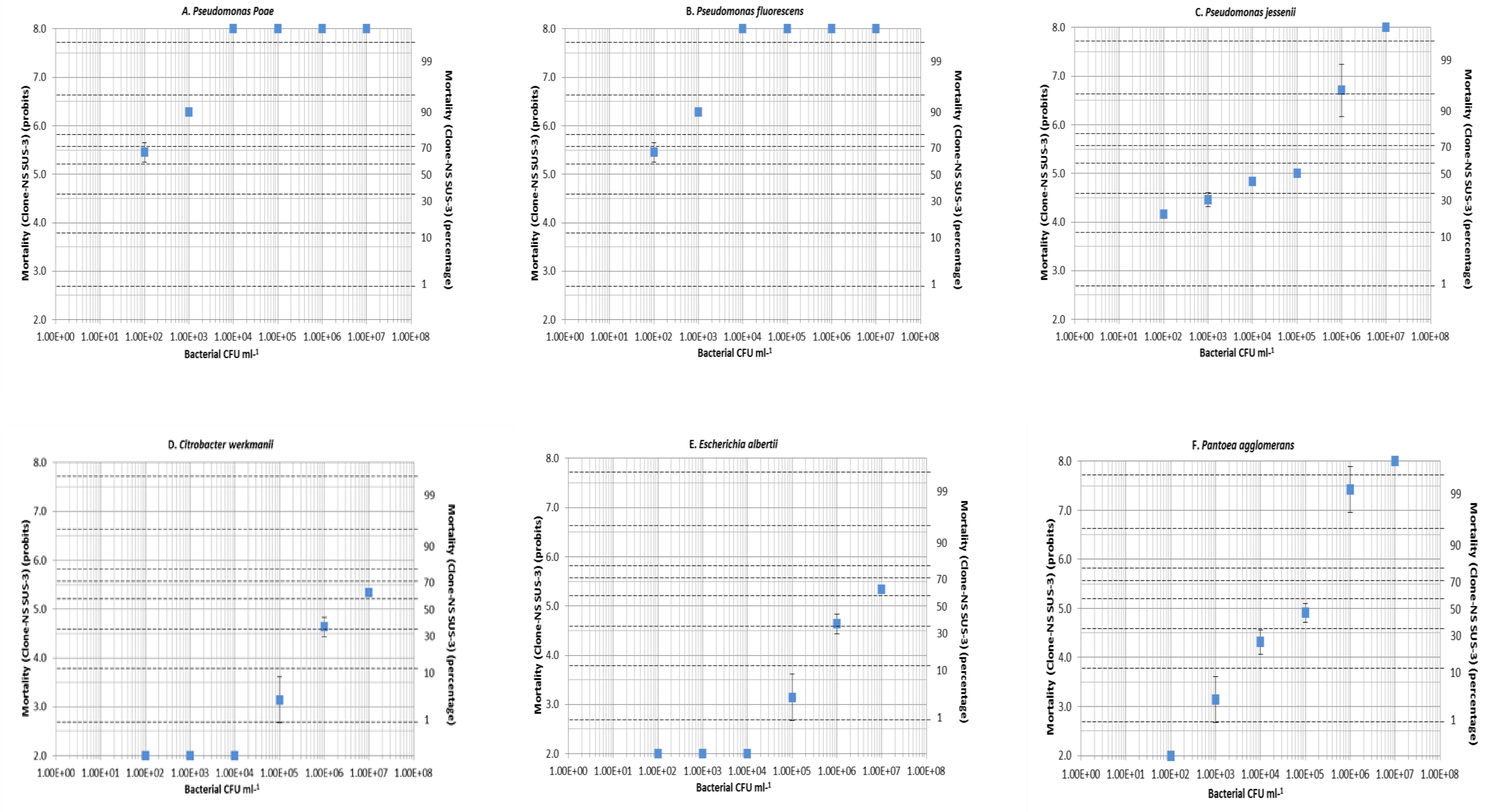

Figure 3: Estimation of Clone-NS aphid clone (SUS-3) mortality probits at various bacterial concentrations. Clone-NS aphid clone (SUS-3) mortality calculated in terms of probits and percentage on log scale at different bacterial cell concentrations with three replicates after 72 hours.

Mortality patterns in New green (RES-1) aphid clone

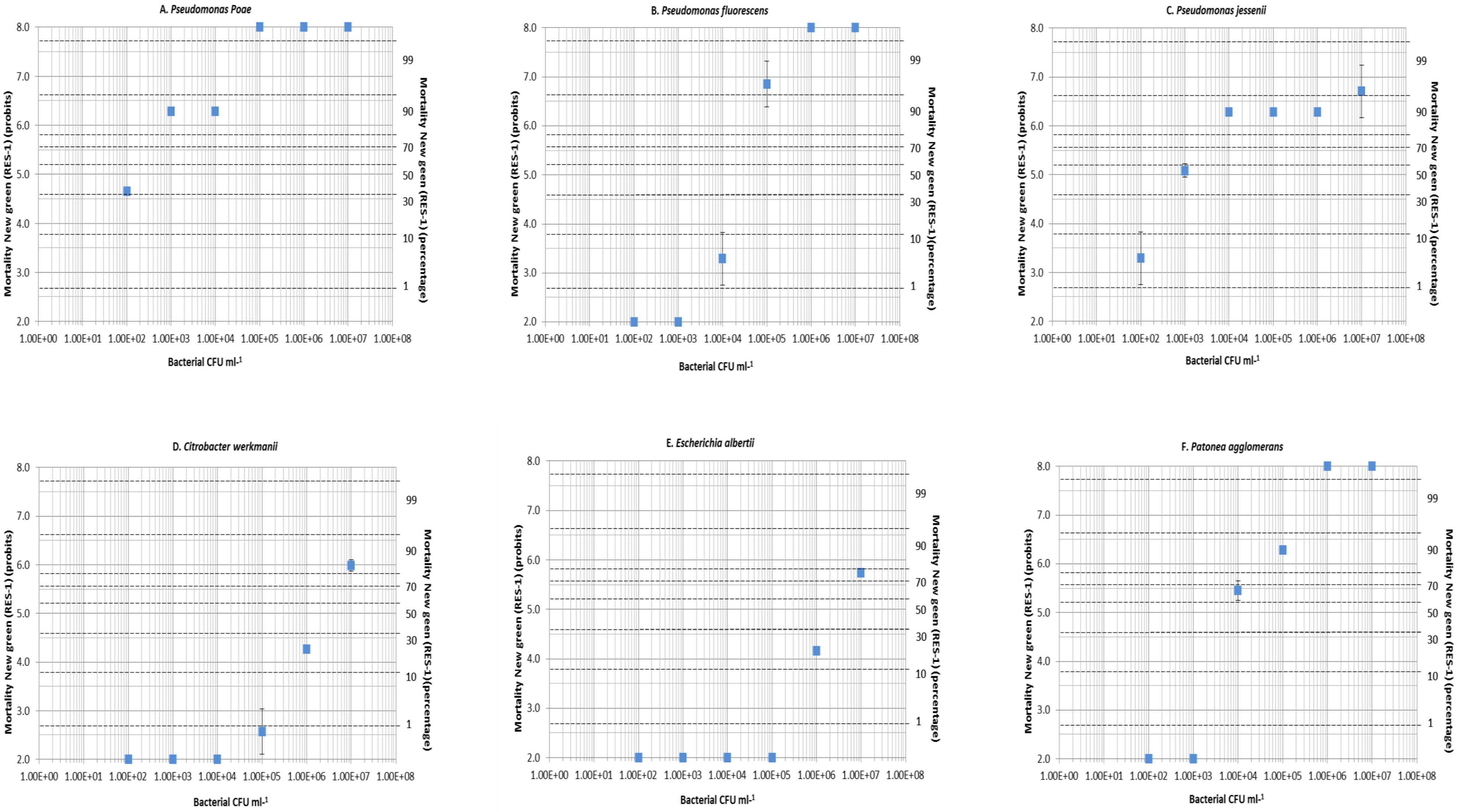

Figure 4: Estimation of New green aphid clone (RES-1) mortality probits at various bacterial concentrations New green aphid clone (RES-1) mortality calculated in terms of probits and percentage on log scale at different bacterial cell concentrations with three replicates after 72 hours.

Mortality patterns in 794J2 (RES-2) aphid clone

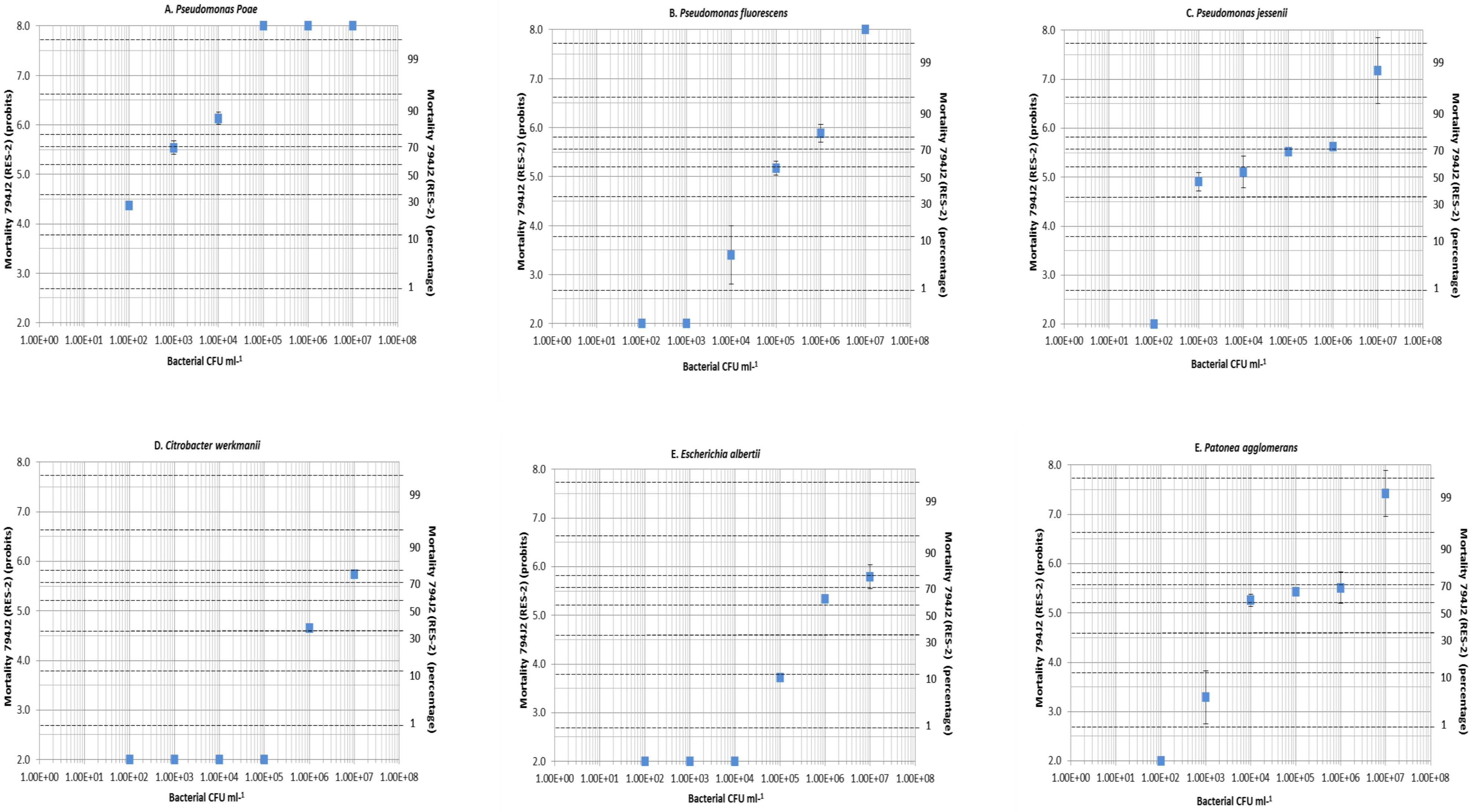

Figure 5: Estimation of 794J2 aphid clone (RES-2) mortality probits at various bacterial concentrations 794J2 aphid clone (RES-2) mortality calculated in terms of probits and percentage on log scale at different bacterial cell concentrations with three replicates after 72 hours.

Mortality patterns in 5191A (RES-3) aphid clone

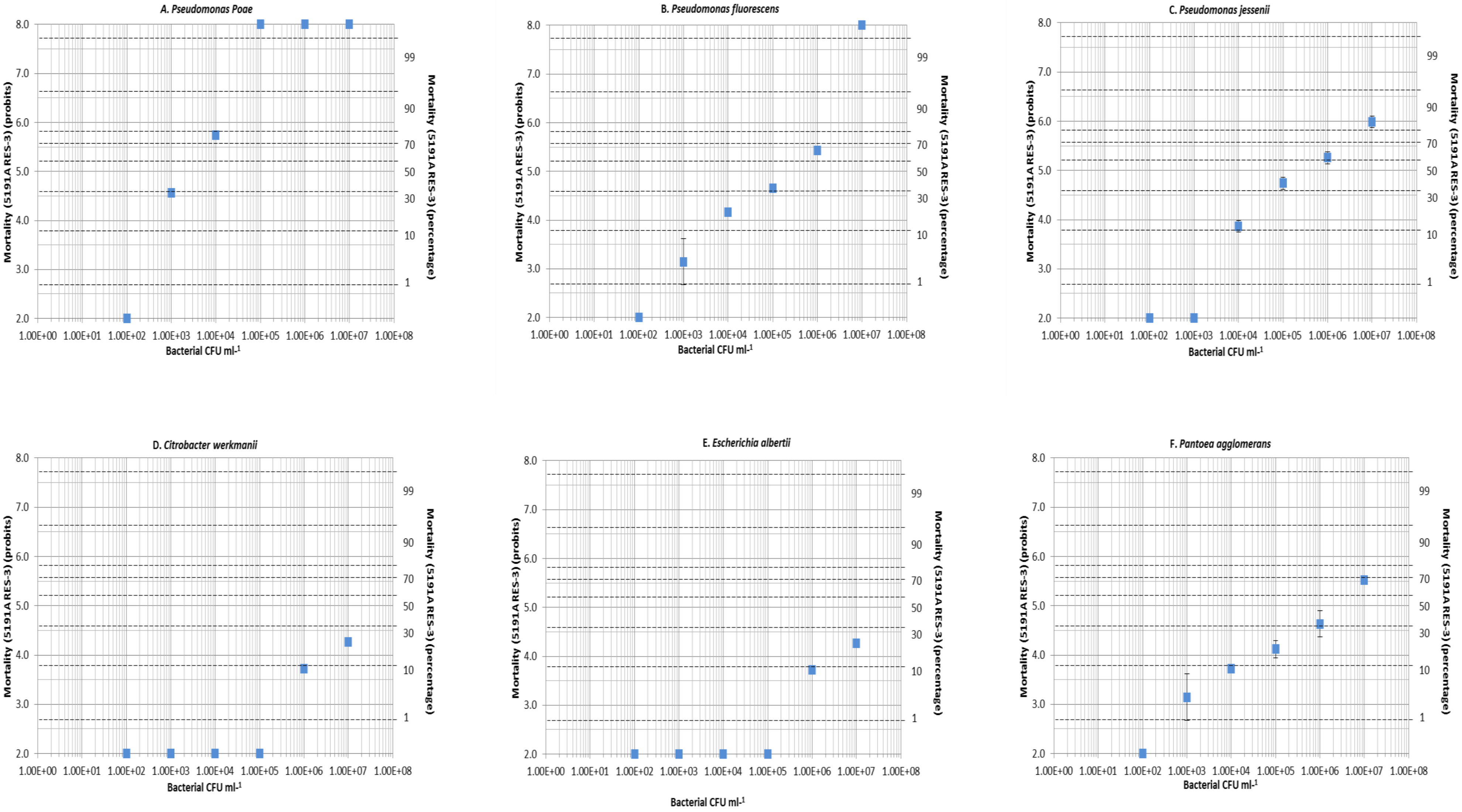

Figure 6: Estimation of 5191A aphid clone (RES-3) mortality probits at various bacterial concentrations 5191A aphid clone (RES-3) mortality calculated in terms of probits and percentage on log scale at different bacterial cell concentrations with three replicates after 72 hours.

Mortality patterns in 5444B (RES-4) aphid clone

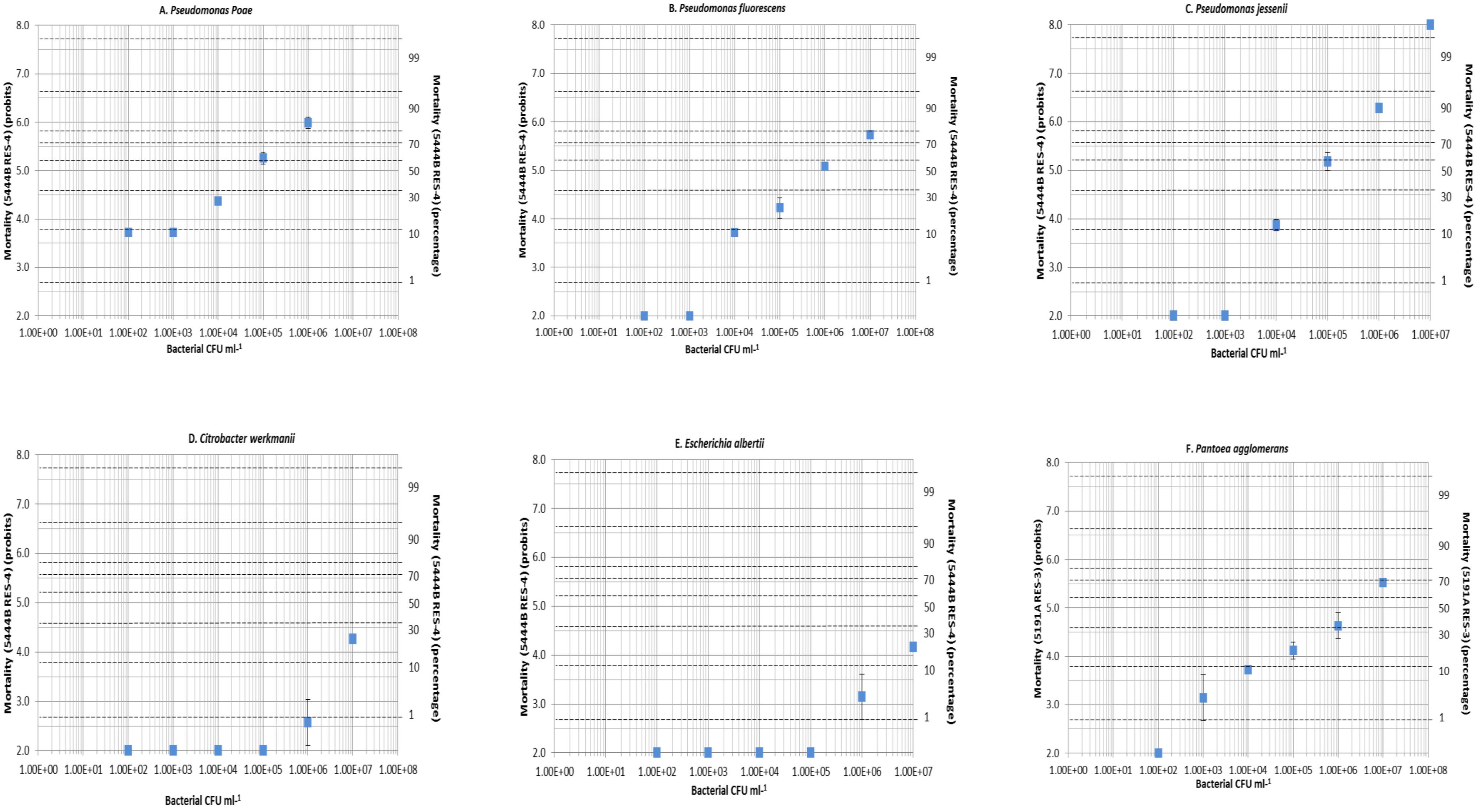

Figure 7: Estimation of 5444B aphid clone (RES-4) mortality probits at various bacterial concentrations 5444B aphid clone (RES-4) mortality calculated in terms of probits and percentage on log scale at different bacterial cell concentrations with three replicates after 72 hours.

Table 1: Differential expressed genes of *Myzus persicae* after *P. poae* bacterial infection: The table details fold change of all differential expressed genes with their log10FPKM values of *Myzus persicae* control and treated conditions and *P - value < 0.1 under different gene categories**.**

Gene name	Mp control FPKM	Mp treated FPKM	Fold change	Corrected P value
Cuticle precursor	50.85	26.48	0.52	0.0590
Phospholipase b-like 2	2.39	0.90	0.38	0.0590
Adhesive plaque matrix	138.42	70.11	0.51	0.0590
Hypothetical protein	48.97	19.22	0.39	0.0590
Hypothetical protein	131.76	53.65	0.41	0.0590
Myosin light chain smooth muscle-like	37.56	17.05	0.45	0.0590
Barwin-like endoglucanase	3.15	0.46	0.15	0.0590
Predicted: uncharacterized protein loc100570877	7.40	1.88	0.25	0.0590
Predicted: uncharacterized protein loc100570877	62.79	24.84	0.40	0.0590
Hypothetical protein kgm_03810	159.48	75.61	0.47	0.0590
Cuticular protein 23 precursor	20.10	7.39	0.37	0.0590
Adhesive plaque matrix	283.97	129.98	0.46	0.0590
Adhesive plaque matrix	197.10	100.38	0.51	0.0590
Hypothetical protein	72.15	42.30	0.59	0.0590
Cytochrome p450 4c1-like	31.31	12.70	0.41	0.0590
Cytochrome p450 4c1-like	31.31	12.70	0.41	0.0590
Cytochrome p450 4c1-like	31.31	12.70	0.41	0.0590
Predicted: uncharacterized protein loc100573101	2.10	9.30	4.42	0.0590
Uncharacterized protein loc100162290 precursor	2.56	1.08	0.42	0.0590
Hypothetical protein lotgidraft_120098, partial	1306.83	491.35	0.38	0.0590
Heat shock protein 70	4.84	19.31	3.99	0.0590
Heat shock protein 70	4.42	8.46	1.91	0.1077

Table 2: Differential expressed genes list of altered *P. poae* gene response during pathogenesis: The table depicts fold change of all differential expressed genes with their $\log_{10}$FPKM values of *P. poae* control and treated conditions and *P - value < 0.05 under different gene categories.

Gene_Name	***P. poae* control FPKM**	***P. poae* treated FPKM**	Fold change	Corrected P value
Alkyl hydroperoxide reductase protein C (EC 1.6.4.-)	7898.76	331.67	0.04	0.0200
Glutamate Aspartate periplasmic binding protein precursor GltI (TC 3.A.1.3.4)	43.19	946.61	21.92	0.0322
Arginine/ornithine antiporter ArcD	12392.20	677.63	0.05	0.0003
Arginine deiminase (EC 3.5.3.6)	29391.60	4768.21	0.16	0.0033
Ornithine carbamoyltransferase (EC 2.1.3.3)	27547.20	3474.22	0.13	0.0009
Carbamate kinase (EC 2.7.2.2)	7768.69	901.35	0.12	0.0031
hypothetical protein	16460.20	3609.33	0.22	0.0269
NAD-dependent glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12)	4444.42	924.01	0.21	0.0261
Probable two-component response regulator	2174.30	193.81	0.09	0.0029
Bacterioferritin	4793.93	698.46	0.15	0.0321
RTX toxin, putative	2225.18	346.68	0.16	0.0031
NfuA Fe-S protein maturation	6122.40	156.56	0.03	0.0490
Ferrous iron transport peroxidase EfeB	37.13	580.47	15.63	0.0132

Secreted alkaline metalloproteinase (EC 3.4.24.-), PrtA/B/C/G homolog	3254.53	547.64	0.17	0.0260
Hydrogenase assembly protein HoxX	1044.04	77.41	0.07	0.0430
protein of unknown function DUF955	2530.32	440.37	0.17	0.0358
ATP-dependent Clp protease ATP-binding subunit ClpA	1630.11	263.12	0.16	0.0091
Aerobic glycerol-3-phosphate dehydrogenase (EC 1.1.5.3)	1964.19	168.85	0.09	0.0082
Bacterioferritin	18380.50	3608.48	0.20	0.0133
Acyl-CoA dehydrogenases	4741.99	501.53	0.11	0.0205
Phage tail fiber protein	1478.88	218.54	0.15	0.0078
Ferredoxin--NADP(+) reductase (EC 1.18.1.2)	3515.70	557.39	0.16	0.0259
LysR family transcriptional regulator PA3398	3443.28	197.41	0.06	0.0056
Outer membrane lipoprotein omp16 precursor	13389.80	1414.03	0.11	0.0024
Probable transmembrane protein	66.43	542.50	8.17	0.0257
Coproporphyrinogen III oxidase, oxygen-independent (EC 1.3.99.22)	2735.68	120.69	0.04	0.0034
Putative analog of CcoH, COG3198	4198.34	784.42	0.19	0.0390
Type cbb3 cytochrome oxidase biogenesis protein CcoG, involved in Cu oxidation	2806.79	542.28	0.19	0.0189
LSU ribosomal protein L32p	799.66	8608.66	10.77	0.0423
Alcohol dehydrogenase (EC 1.1.1.1)	4374.19	150.76	0.03	0.0021
hypothetical protein	3362.02	405.12	0.12	0.0323
hypothetical protein	25221.30	1877.78	0.07	0.0009
hypothetical protein	8435.03	1146.16	0.14	0.0009
FIG027785: Fimbriae usher protein StfC	954.29	108.99	0.11	0.0380
Levansucrase (EC 2.4.1.10)	4222.74	872.62	0.21	0.0378
Inhibitor of vertebrate lysozyme precursor	7371.87	1644.34	0.22	0.0393
COG1683: Uncharacterized conserved protein / FIG143828: Hypothetical protein YbgA	3696.68	110.41	0.03	0.0269
ClpB protein	10932.20	690.82	0.06	0.0003
Chaperone protein DnaK	12649.60	3131.26	0.25	0.0209
Universal stress protein family 7	10266.80	939.26	0.09	0.0038
Translation elongation factor Tu	39406.70	18176.90	0.46	0.0160
Outer membrane protein W precursor	7625.28	1567.00	0.21	0.0179
hypothetical protein	3588.09	666.15	0.19	0.0110
ribosomal subunit interface protein, putative	61411.00	5041.57	0.08	0.0005
L-ornithine 5-monooxygenase (EC 1.13.12.-), PvdA of pyoverdin biosynthesis	3937.67	634.27	0.16	0.0064
N6-hydroxylysine O-acetyltransferase (EC 2.3.1.102), aerobactin biosynthesis protein IucB @ Siderophore synthetase small component, acetyltransferase	1855.13	305.11	0.16	0.0258
Dodecin (COG3360) Flavin-binding	59821.10	12565.60	0.21	0.0324
Alkyl hydroperoxide reductase subunit C-like protein	3898.83	329.82	0.08	0.0121
Betaine aldehyde dehydrogenase (EC 1.2.1.8)	2711.60	93.03	0.03	0.0164
HTH-type transcriptional regulator BetI	6993.76	431.09	0.06	0.0197
Acyl-CoA dehydrogenase (EC 1.3.99.3)	2190.21	266.13	0.12	0.0046
Uncharacterized hydroxylase PA0655	8339.28	780.16	0.09	0.0027
Putative formate dehydrogenase oxidoreductase protein	639.38	77.50	0.12	0.0293
hypothetical protein	27.80	244.57	8.80	0.0171
hypothetical protein	4030.04	392.85	0.10	0.0003
Chitinase (EC 3.2.1.14)	7440.88	262.42	0.04	0.0012
TonB-dependent receptor	12.15	151.21	12.45	0.0306
DNA helicase related protein	353.32	71.57	0.20	0.0316

L-asparaginase (EC 3.5.1.1)	2838.96	428.36	0.15	0.0236

Table 3: Differential expressed genes of *Myzus persicae* after *P. poae* bacterial infection: The table details fold change of all differential expressed genes with their log10FPKM values of *Myzus persicae* control and treated conditions and *P - value < 0.05 under different gene categories**.**

Table 3 A Transcription of Immune defence and other stress related genes				
Immune defence related genes				
Gene name	**Mp control FPKM**	**Mp treated FPKM**	**Fold change**	**Corrected P value**
Takeout isoform X1	0.49	1.10	2.26	0.0012
Takeout-like	34.06	90.14	2.65	0.0003
Cuticle 7-like	0.39	0.94	2.44	0.0240
Larval cuticle A2B-like	88.27	187.43	2.12	0.0003
Sterile alpha and TIR motif-containing 1 isoform X1	2.83	6.34	2.24	0.0003
Sterile alpha and TIR motif-containing 1-like	3.93	10.33	2.63	0.0003
Leucine-rich repeat soc-2 isoform X1	42.09	86.89	2.06	0.0003
Pv-fam-d protein	8.90	18.94	2.13	0.0003
Leucine-rich repeat-containing 58	71.14	145.88	2.05	0.0003
Uncharacterized family 31 glucosidase KIAA1161-like	12.58	25.32	2.01	0.0003
Cuticle , isoform B-like	28.04	13.22	-2.12	0.0003
Cuticle , isoform B-like	25.50	11.32	-2.25	0.0003
Cuticle , isoform A-like	865.73	429.57	-2.02	0.0003
Scavenger/ Detoxification Genes				
Gene name	**Mp control FPKM**	**Mp treated FPKM**	**Fold change**	**Corrected P value**
Nose resistant to fluoxetine 6-like	0.69	2.27	3.27	0.00035
Facilitated trehalose transporter Tret1-like	4.26	10.53	2.47	0.00035
Takeout-like	271.07	553.22	2.04	0.00035
Nose resistant to fluoxetine 6-like	1.60	4.19	2.61	0.00035
Gamma-glutamyltranspeptidase 1-like	37.76	7.83	-4.83	0.00035
Gamma-glutamyltranspeptidase 1-like	8.00	0.53	-15.17	0.00035
Drug metabolism genes				
Gene name	**Mp control FPKM**	**Mp treated FPKM**	**Fold change**	**Corrected P value**
Esterase E4-like	13.93	6.05	-2.30	0.00035
Esterase E4-like	14.15	6.77	-2.09	0.00035
Esterase E4-like	29.35	13.94	-2.11	0.00035
Esterase E4-like	33.87	16.75	-2.02	0.00035
Lysosomal Pro-X carboxypeptidase	45.88	21.35	-2.15	0.00035
UDP-glucuronosyltransferase 2C1-like	15.90	6.49	-2.45	0.00035
UDP-glucuronosyltransferase 2C1-like isoform X1	12.46	3.53	-3.53	0.00035

UDP-glucuronosyltransferase 2C1-like isoform X1	44.66	15.56	-2.87	0.00035
UDP-glucuronosyltransferase 2C1-like	0.73	1.98	2.71	0.00035
Cytochrome b561-like	14.03	6.28	-2.24	0.00035
Dehydrogenase reductase SDR family member 11-like	74.39	35.59	-2.09	0.00035
Heat shock 83	920.61	434.20	-2.12	0.00035
Peroxidase-like isoform X1	40.11	19.92	-2.01	0.00035
Dehydrogenase reductase SDR family member 11-like	12.21	35.20	2.88	0.00035
Apoptosis genes				
Gene name	**Mp control FPKM**	**Mp treated FPKM**	**Fold change**	**Corrected P value**
Centromere-associated E	12.02	29.61	2.46	0.00035
Comm3, isoform D	5.53	12.54	2.27	0.00035
Legumain isoform X1	10.72	3.77	-2.85	0.00035

Table 3 B Transcription of Proteases and other digestive enzymes

Gene name	**Mp control FPKM**	**Mp treated FPKM**	**Fold change**	**Corrected P value**
Cathepsin B-N	5.02	17.12	3.41	
Cathepsin B-N	6.26	22.24	3.55	0.00035
Cathepsin B-N	5.91	13.85	2.34	0.00035
TPA_inf: cathepsin B	1.29	4.26	3.31	0.00035
Venom protease-like	8.71	22.83	2.62	0.00035
Matrix metallo ase-14 isoform X2	21.53	44.90	2.09	0.00035
Regucalcin-like isoform X2 (protease inhibitor)	13.55	36.33	2.68	0.00035
PREDICTED: mucin-17-like	0.20	0.72	3.54	0.00035
Leucyl-cystinyl aminopeptidase	1.05	2.12	2.02	0.00035
Pancreatic lipase-related 2-like	5.16	21.55	4.17	0.00035
Cathepsin B	76.46	27.50	-2.78	0.00035
Aminopeptidase N-like	20.36	5.82	-3.50	0.00035
Cathepsin B	7.37	3.62	-2.04	0.00035
Cathepsin B-like	8.88	3.63	-2.44	0.00035
Cathepsin B	1.95	0.92	-2.13	0.00064

Table 3 C Transcription of Cell signalling and others pathway

Gene name	**Mp control FPKM**	**Mp treated FPKM**	**Fold change**	**Corrected P value**
Noggin-like (Cell growth regulator)	3.24	6.85	2.11	0.00035
N-acetyl-D-glucosamine kinase (phosphatidylinositol signalling)	78.11	182.73	2.34	0.00035
PREDICTED: uncharacterized protein LOC100165382 (Rho protein signal transduction)	0.17	0.76	4.49	0.00064
Probable phosphatase CG10417 (Tcell signalling pathway)	0.33	0.77	2.35	0.00545
Uncharacterized protein LOC100570671 precursor	89.51	236.47	2.64	0.00035

(mTOR signalling)				
Zinc finger MYM-type 1-like (Transcription regulator)	0.39	0.78	2.01	0.00567
Zinc finger MYM-type 1-like (Transcription regulator)	0.53	1.15	2.16	0.00035
Zinc finger 521 (Protein trafficing regulator)	0.82	1.70	2.09	0.00035
Zinc finger 36, (Transcription regulator)	85.90	172.17	2.00	0.00035
Zinc finger 271-like (Transcription regulator)	0.53	1.46	2.74	0.00731
Yippee-like 1 (Transcription regulator)	19.28	50.61	2.63	0.00035
Suppressor SRP40-like (Transcription regulator)	28.52	58.51	2.05	0.00035
Homeobox engrailed-2-B (Transcription regulator)	2.25	4.92	2.18	0.00035
KRAB-A domain-containing 2-like (Transcription regulator)	4.06	16.81	4.14	0.00035
Androgen-dependent TFPI-regulating -like (Transcription regulator)	66.60	134.36	2.02	0.00035
Dual specificity phosphatase 14-like	6.87	21.46	3.12	0.00035
Membrane-bound alkaline phosphatase-like isoform X2	150.45	55.57	-2.70	0.00035
Histone H3, partial (nucleosome assembly)	2.31	4.97	2.15	0.00326
PREDICTED: Somatostatin receptor (Somatostatin signalling)	19.50	7.04	-2.77	0.00035
Olfactory receptor-2 (Olfactory sensation)	6.01	1.67	-3.60	0.00035
Craniofacial development 2-like, partial (Neruogenesis)	1.39	0.47	-2.93	0.00567
Defense Hdd11 (Neruogenesis)	15.09	5.86	-2.58	0.00117
Cell Locomotion and cytoskeletal genes				
Gene name	**Mp control FPKM**	**Mp treated FPKM**	**Fold change**	**Corrected P value**
PREDICTED: protein kintoun-like	212.70	103.53	-2.05	0.00035
PDZ and LIM domain Zasp isoform X1	22.74	49.33	2.17	0.00035
Titin isoform X1	1.11	2.54	2.29	0.00035
Tubulin-specific chaperone cofactor E	25.41	62.23	2.45	0.00035
Nesprin-1 isoform X7	0.55	1.30	2.37	0.00035
Protein Ubiquitination and trafficking Genes				
Gene name	**Mp control FPKM**	**Mp treated FPKM**	**Fold change**	**Corrected P value**
Cysteine and histidine-rich 1 homolog	78.91	172.06	2.18	0.00035
Probable GPI-anchored adhesin PGA55	2.72	8.19	3.01	0.00035
Ring canal kelch homolog	7.96	3.51	-2.26	0.00035
Arrestin domain-containing 3-like	4.16	1.65	-2.52	0.00035

Table 3 D Transcription of membrane Transporters				
Gene name	**Mp control FPKM**	**Mp treated FPKM**	**Fold change**	**Corrected P value**
Cationic amino acid transporter 2	16.67	38.36	2.30	0.00035
Sodium channel 60E-like	0.59	1.28	2.15	0.02491
Sodium channel 60E-like	0.80	1.61	2.01	0.00035
Solute carrier organic anion transporter family member 2A1-like	1.88	4.06	2.16	0.00035
Clavesin-1 (sugar transporter)	57.61	179.24	3.11	0.00035
Alpha-tocopherol transfer -like	29.86	63.06	2.11	0.00035
Solute carrier family 46 member 3-like	15.09	6.56	-2.30	0.00035

Major facilitator superfamily domain-containing 6-like	4.11	1.39	-2.97	0.00035
Facilitated trehalose transporter Tret1-like	3.75	1.87	-2.00	0.00035
Proton-coupled amino acid transporter 1 isoform X2	9.54	4.60	-2.07	0.00035
Acetylcholine receptor subunit alpha-type acr-16-like	66.18	19.30	-3.43	0.00035
Facilitated trehalose transporter Tret1-like	59.70	14.71	-4.06	0.00035
Facilitated trehalose transporter Tret1-like	9.66	3.32	-2.91	0.00035
Peptide transporter family 1-like	1.13	0.52	-2.18	0.00035
Facilitated trehalose transporter Tret1-like	23.26	6.69	-3.48	0.00035
Major facilitator superfamily domain-containing 6-like	21.33	10.12	-2.11	0.00035
Major facilitator superfamily domain-containing 6-like	34.64	14.86	-2.33	0.00035
Peptidyl-trna hydrolase PTRHD1	11.41	5.28	-2.16	0.00035
Peptide transporter family 1-like	3.08	1.34	-2.29	0.00035
Zinc transporter ZIP1 (Iron transporter	35.73	16.31	-2.19	0.00035
Major facilitator superfamily domain-containing 6-like	38.85	16.35	-2.38	0.00035
Acetyl-coenzyme A transporter 1-like	0.87	0.36	-2.44	0.01524

Table 3 E Transcription of Metabolic genes				
Caternoid biosynthesis				
Gene name	**Mp control FPKM**	**Mp treated FPKM**	**Fold change**	**Corrected P value**
Carotenoid desaturase, partial	3.45	0.09	-39.17	0.04031
Bifunctional lycopene cyclase phytoene synthase-like	0.74	0.34	-2.18	0.00448
Bifunctional lycopene cyclase phytoene synthase-like	7.35	3.00	-2.45	0.00035
Nucleic acid metabolism				
Gene name	**Mp control FPKM**	**Mp treated FPKM**	**Fold change**	**Corrected P value**
Multifunctional ADE2 (Purine metabolism)	139.67	59.85	-2.33	0.00034
Myb P (Purine metabolism regulator)	1.29	0.28	-4.66	0.03345
Alkaline nuclease (Nucleic acid metabolism)	131.14	61.41	-2.13	0.00035
ATP-dependent RNA helicase p62-like isoform X2	672.43	1363.43	2.03	0.00035
Amino acid metabolism				
Gene name	**Mp control FPKM**	**Mp treated FPKM**	**Fold change**	**Corrected P value**
Homocysteine S-methyltransferase 1-like (Cysteine and methionine metabolism)	22.33	9.00	-2.48	0.00035

Gamma-glutamyl hydrolase A-like (Glutamine Metabolism)	29.28	9.26	-3.16	0.00035
Omega-amidase NIT2 (Glutamine Metabolism)	350.29	99.02	-3.54	0.00035
Omega-amidase NIT2 (Glutamine Metabolism)	66.15	24.14	-2.74	0.00035
Enolase-phosphatase E1 (Methionine biosynthesis)	23.28	10.97	-2.12	0.00035
Threo-3-hydroxyaspartate ammonia-lyase isoform X1	37.75	81.47	2.16	0.00035
Kynurenine formamidase-like (Tyrosine Catabolism)	1.98	5.21	2.63	0.00035
Histone-lysine N-methyltransferase MLL5 (Lysine degradation)	480.29	1009.12	2.10	0.00035
Pyrroline-5-carboxylate reductase (Proline Catabolism)	19.58	45.24	2.31	0.00035
Other Metabolism				
Gene name	**Mp control FPKM**	**Mp treated FPKM**	**Fold change**	**Corrected P value**
Phosphoenolpyruvate carboxykinase [GTP]-like	47.08	145.17	3.08	0.00035
Hexokinase type 2 isoform X3 (Amino sugar and nucleotide sugar metabolism)	296.20	645.77	2.18	0.00035
Inositol oxygenase (Inositol catabolism)	69.25	218.60	3.16	0.00035
Prostatic acid phosphatase (Aminobenzoate metabolism)	4.06	11.19	2.75	0.00035
NAD(P) transhydrogenase (Nicotinate and Nicotinamide metabolism)	11.12	30.39	2.73	0.00035
Acyl- thioesterase 2 (Lipd metabolism)	182.33	73.41	-2.48	0.00035

Table 3 F Transcription of Hypothetical and other genes

Gene name	**Mp control FPKM**	**Mp treated FPKM**	**Fold change**	**Corrected P value**
A-agglutinin anchorage subunit-like isoform X1	13.18	61.28	4.65	0.00035
AP2 ERF domain-containing PFD0985w-like	1.22	3.34	2.74	0.00035
Atpase, histidine kinase-, DNA gyrase B	0.41	0.93	2.24	0.01822
Probable serine threonine- kinase clka	0.26	0.73	2.87	0.00761
Hypothetical protein	16.20	35.84	2.21	0.04360
PREDICTED: uncharacterized protein LOC103310813	1.67	5.09	3.04	0.00064
Phospholipase DDHD2-like isoform X1	20.73	45.99	2.22	0.00035
PREDICTED: uncharacterized protein LOC103309738	0.15	0.58	3.79	0.00667
PREDICTED: uncharacterized protein LOC100165045 isoform X1	7.04	18.55	2.63	0.00035
Nuclease HARBI1	0.50	1.26	2.51	0.00587
PREDICTED: uncharacterized protein LOC100570877	119.48	1838.71	15.39	0.00035
PREDICTED: uncharacterized protein LOC100570877	8.26	25.76	3.12	0.00035
Hypothetical protein	0.54	4.52	8.38	0.00851
Hypothetical protein	1.24	2.52	2.04	0.00211

PREDICTED: uncharacterized protein LOC100569497 isoform X1	0.47	1.06	2.28	0.00035
Hypothetical protein	0.49	3.60	7.32	0.01276
PREDICTED: uncharacterized protein LOC100570877	44.99	109.03	2.42	0.00035
PREDICTED: uncharacterized protein LOC100570877	57.59	334.29	5.80	0.00035
PREDICTED: uncharacterized protein LOC103308903	0.26	0.63	2.40	0.03150
PREDICTED: uncharacterized protein LOC100570877	131.38	280.63	2.14	0.00035
Poly [ADP-ribose] polymerase 12-like	3.13	8.00	2.56	0.00035
PREDICTED: uncharacterized protein LOC100574855	2.86	6.28	2.20	0.00035
Hypothetical protein	6.48	26.95	4.16	0.00035
Msta, isoform B-like	0.29	0.70	2.40	0.01075
PREDICTED: uncharacterized protein LOC100568592	4.85	10.46	2.16	0.00035
RNA-binding 33-like isoform X1	3.04	7.62	2.50	0.00035
Hypothetical protein	5.34	14.78	2.77	0.00990
PREDICTED: uncharacterized protein LOC103310381	84.33	184.52	2.19	0.00035
PREDICTED: uncharacterized protein LOC100163615, partial	91.34	212.06	2.32	0.00035
PREDICTED: uncharacterized protein LOC100159429 isoform X1	22.79	58.80	2.58	0.00035
Hypothetical protein	2.32	4.84	2.08	0.00035
Hypothetical protein	202.85	417.85	2.06	0.00035
PREDICTED: uncharacterized protein LOC105397400 isoform X2	0.47	1.25	2.66	0.00257
PREDICTED: uncharacterized protein LOC100569748	2.03	8.63	4.26	0.00035
PREDICTED: uncharacterized protein LOC100574342	0.81	1.80	2.22	0.00035
PREDICTED: putative uncharacterized protein DDB_G0286901	2.16	5.06	2.34	0.00035
PREDICTED: uncharacterized protein LOC100570877	13.91	69.58	5.00	0.00035
PREDICTED: uncharacterized protein LOC100570877	85.42	187.34	2.19	0.00035
THAP domain-containing 1-like	0.81	1.64	2.04	0.04375
THAP domain-containing 1-like	0.41	1.09	2.69	0.04043
Hypothetical protein RFI_02035	12.18	28.95	2.38	0.00035
PREDICTED: uncharacterized protein LOC100574885	9.15	21.91	2.39	0.00035
Hypothetical protein	15.70	7.16	-2.19	0.00922
Uncharacterized protein LOC100159913 precursor	1.65	0.66	-2.50	0.00035
Low-density lipo receptor-related 2	26.82	8.84	-3.04	0.00035
Low-density lipo receptor-related 2	27.76	10.34	-2.69	0.00035

CGG triplet repeat-binding 1	5.02	1.78	-2.83	0.00035
CD63 antigen-like	0.89	0.43	-2.07	0.02605
52 kda repressor of the inhibitor of the kinase-like	1.21	0.58	-2.08	0.02913
Dynamin-1 isoform X1	3.16	1.53	-2.07	0.00035
Hypothetical protein	18.76	9.19	-2.04	0.00035
PREDICTED: uncharacterized protein LOC103310537, partial	1.20	0.53	-2.25	0.00035
plexin A3-like	52.95	18.87	-2.81	0.00035
valacyclovir hydrolase	10.01	4.55	-2.20	0.00035
zinc finger 160-like	2.70	1.26	-2.14	0.01636
PREDICTED: uncharacterized protein LOC100163338	319.51	119.74	-2.67	0.00035
-26, partial	76.44	30.17	-2.53	0.00035
ACYPI001427	22.36	9.52	-2.35	0.00035
Hypothetical protein	169.75	61.22	-2.77	0.00035
Hypothetical protein	1080.45	360.65	-3.00	0.00035
proline-rich 4-like	950.30	377.75	-2.52	0.00035
Dynamin-1	27.63	13.69	-2.02	0.00035
UDP-glucuronosyltransferase 2C1-like	2.55	0.79	-3.25	0.00035
PREDICTED: uncharacterized protein LOC100574541 isoform X1	65.00	29.86	-2.18	0.00035

Table 4: Genes list of Immune defence genes:

A. The table is depicting fold change less than 2(both up and down regulation) of all differential expressed genes with their $\log_{10}$FPKM values of *Myzus persicae* control and treated conditions and *P - value < 0.05 under Immune defence gene category.
B. The table is depicting $\log_{10}$FPKM values of *Myzus persicae* control and treated conditions which were not differentially expressed under Immune defence category.

<table>
<tr><th colspan="5">Table 4   Transcription of Immune defence genes (Significant/Non Significant Differential expressed)</th></tr>
<tr><th colspan="5">A.   Significant</th></tr>
<tr><th>Gene name</th><th>Mp control FPKM</th><th>Mp treated FPKM</th><th>Fold change</th><th>Corrected P value</th></tr>
<tr><td>Chorion peroxidase</td><td>1.53</td><td>1.97</td><td>1.29</td><td>0.04005</td></tr>
<tr><td>Carboxyl-terminal PDZ ligand of neuronal nitric oxide synthase isoform X1</td><td>17.74</td><td>23.13</td><td>1.30</td><td>0.00142</td></tr>
<tr><td>Down syndrome cell adhesion molecule Dscam2</td><td>22.31</td><td>26.88</td><td>1.21</td><td>0.01409</td></tr>
<tr><td>Down syndrome cell adhesion molecule Dscam2</td><td>22.31</td><td>26.88</td><td>1.21</td><td>0.01409</td></tr>
<tr><td>Probable peroxisomal acyl-coenzyme A oxidase 1</td><td>32.23</td><td>38.26</td><td>1.19</td><td>0.02252</td></tr>
<tr><td>Heat shock 70 kda 14</td><td>60.71</td><td>47.99</td><td>0.79</td><td>0.02697</td></tr>
<tr><td>10 kda heat shock , mitochondrial</td><td>305.84</td><td>216.54</td><td>0.71</td><td>0.00035</td></tr>
<tr><td>Lysozyme 3-like</td><td>47.70</td><td>32.46</td><td>0.68</td><td>0.00035</td></tr>
<tr><td>Toll</td><td>19.12</td><td>23.49</td><td>1.23</td><td>0.00587</td></tr>
<tr><td>97 kda heat shock isoform X2</td><td>156.61</td><td>97.27</td><td>0.62</td><td>0.00035</td></tr>
<tr><td>FAD-linked sulfhydryl oxidase ALR</td><td>9.45</td><td>7.63</td><td>0.81</td><td>0.04150</td></tr>
<tr><td>Heat shock 83</td><td>920.61</td><td>434.20</td><td>0.47</td><td>0.00035</td></tr>
<tr><td>NADPH oxidase 5</td><td>18.79</td><td>22.94</td><td>1.22</td><td>0.00850</td></tr>
<tr><td>60 kda heat shock , mitochondrial-like</td><td>123.24</td><td>97.09</td><td>0.79</td><td>0.00117</td></tr>
<tr><td>Myeloperoxidase-like isoform X1</td><td>352.58</td><td>215.97</td><td>0.61</td><td>0.00035</td></tr>
<tr><td>Myeloperoxidase-like isoform X1</td><td>16.60</td><td>22.75</td><td>1.37</td><td>0.00035</td></tr>
</table>

B.Non-Significant				
Gene name	**Mp control FPKM**	**Mp treated FPKM**	**Fold change**	**Corrected P value**
Caspase-1	28.73	29.27	1.02	0.89
Chorion peroxidase-like	0.00	0.00	1.00	1
Heat shock 70	63.34	56.13	0.89	0.14
Cytochrome c oxidase 20 homolog	46.28	39.51	0.85	0.24
Cytochrome c oxidase assembly factor 6 homolog	54.85	40.61	0.74	0.10
Tol2 transposase	0.05	0.03	0.58	1
Cytochrome P450 6BQ10	7.03	6.84	0.97	0.93
Evolutionarily conserved signaling intermediate in Toll pathway, mitochondrial	20.36	17.34	0.85	0.16
Evolutionarily conserved signaling intermediate in Toll pathway, mitochondrial	20.36	17.34	0.85	0.16
Peroxisomal acyl-coenzyme A oxidase 3	18.65	17.50	0.94	0.59
Glutathione S-transferase-like	53.32	47.59	0.89	0.20
Cytochrome P450 4C1-like	0.00	0.05	#VALUE!	1
Cytochrome P450	0.02	0.01	0.71	1
Hemocyte -glutamine gamma-glutamyltransferase-like	35.93	33.43	0.93	0.42
Heat shock factor	18.32	21.42	1.17	0.06
WD repeat-containing 81	12.40	13.98	1.13	0.14
Heat shock 70 kda 12A isoform X3	2.35	2.08	0.88	0.37
PheNSloxidase 2-like	33.19	31.31	0.94	0.51
Sulfhydryl oxidase 1-like	75.01	71.83	0.96	0.65
Chitinase-3 2	27.26	26.94	0.99	0.95
Cytochrome c oxidase subunit iv	379.79	400.18	1.05	0.63
Cytochrome c oxidase assembly COX16 homolog, mitochondrial	14.90	15.02	1.01	0.95
Peroxidase-like isoform X1	11.47	11.36	0.99	0.94
Chorion peroxidase	13.88	15.62	1.13	0.17
Nitric oxide synthase, salivary gland	6.14	6.55	1.07	0.53
Pyridoxine-5 -phosphate oxidase	43.25	37.45	0.87	0.10
Heat shock 70	6.97	6.08	0.87	0.53
Heat shock 68-like	1.60	1.24	0.78	0.051
I-type lysozyme	342.08	372.95	1.09	0.38
Lysozyme 2-like	12.28	11.94	0.97	0.87
Heat shock beta-1 isoform X2	298.04	271.44	0.91	0.30
Cytochrome c oxidase assembly factor 7 homolog	25.44	23.00	0.90	0.34
Cytochrome c oxidase assembly COX11, mitochondrial	37.07	41.10	1.11	0.24
Serine proteases 1 2-like	0.00	0.00	1.00	1
Mitochondrial isoprenyl diphosphate synthase precursor	20.47	23.63	1.15	0.09
Cytochrome c oxidase subunit NDUFA4	311.64	337.52	1.08	0.38
N-acetylmuramoyl-L-alanine amidase	0.25	0.23	0.90	1
Serine threonine- kinase pelle-like	11.73	12.82	1.09	0.39
Apoptosis 1 inhibitor-like	0.00	0.00	1.00	1
Heat shock 68-like	3.52	2.86	0.81	0.05

Table 5: Differential expressed genes list of altered *P. poae* gene response during pathogenesis: The table depicts fold change of all differential expressed genes with their $\log_{10}$FPKM values of *P. poae* control and treated conditions and *P - value < 0.05 under different gene categories.

Table 5 A Transcriptional regulation by iron of genes for siderophore biosynthesis and transport

Pyoverdine biosynthesis gene cluster

Gene_Name	*P. poae control* FPKM	*P. poae treated* FPKM	Fold change	Corrected P value
Putative dipeptidase2C pyoverdine biosynthesis PvdM	15.65	209.93	13.41	0.00022
Pyoverdin biosynthesis protein PvdN2C putative aminotransferase2C class V	9.95	133.28	13.40	0.00022
PvdO2C pyoverdine responsive serine/threonine kinase (predicted by OlgaV)	20.95	257.74	12.31	0.00022
PvdE2C pyoverdine ABC export system2C fused ATPase and permease components	41.50	264.68	6.38	0.00022
Outer membrane ferripyoverdine receptor FpvA2C TonB-dependent	38.60	418.94	10.85	0.00022
Pyoverdine biosynthesis related protein PvdP	8.20	106.99	13.05	0.00022
Pyoverdine synthetase PvdF2C N5-hydroxyornithine formyltransferase	55.78	649.35	11.64	0.00022
Pyoverdine sidechain non-ribosomal peptide synthetase PvdD	32.68	232.35	7.11	0.00022
Sigma factor PvdS2C controling pyoverdin biosynthesis	34.61	1643.71	47.50	0.00022
Pyoverdin biosynthesis protein PvdH2C L-22C4-diaminobutyrate:2-oxoglutarate aminotransferase	45.87	428.27	9.34	0.00022
Sensor histidine kinase	82.78	221.04	2.67	0.00022
Pyoverdine chromophore precursor synthetase PvdL	32.47	292.90	9.02	0.00022
Thioesterase PvdG involved in non-ribosomal peptide biosynthesis	34.38	349.56	10.17	0.00022
L-ornithine 5-monooxygenase2C PvdA of pyoverdin biosynthesis	126.89	1255.15	9.89	0.00022
Sigma-70 factor FpvI (ECF subfamily)2C controling pyoverdin biosynthesis	45.54	212.17	4.66	0.00022

Siderophore uptake & Receptor

Gene_Name	*P. poae control* FPKM	*P. poae treated* FPKM	Fold change	Corrected P value
Outer membrane receptor for ferric coprogen and ferric-rhodotorulic acid	23.92	114.00	4.77	0.00022
Ferrichrome-iron receptor	31.79	97.61	3.07	0.00022
Outer membrane ferripyoverdine receptor	17.15	70.87	4.13	0.00022
TonB-dependent hemin 2C ferrichrome receptor	13.34	754.60	56.58	0.00022
Iron siderophore sensor protein	13.85	149.85	10.82	0.00022
Iron(III) dicitrate transport protein FecA @ Iron siderophore receptor protein	16.95	39.36	2.32	0.00022
FIG016502: iron uptake protein	12.18	134.72	11.06	0.01269
FIG138928: iron-regulated membrane protein	32.80	483.63	14.75	0.00022
Ferric siderophore transport system2C periplasmic binding protein TonB	397.16	1464.78	3.69	0.00022

Siderophore independent iron receptor

Gene_Name	*P. poae control*	*P. poae treated*	Fold change	Corrected P value

	FPKM	**FPKM**		
Ferric iron ABC transporter2C iron-binding protein	163.92	528.15	3.22	0.00022
putative iron ABC transporter ATP-binding protein	7.61	40.24	5.29	0.00712
ABC-type hemin transport system2C ATPase component	105.52	603.54	5.72	0.00022
Haem acquisition systems				
Gene_Name	***P. poae* *control* FPKM**	***P. poae* *treated* FPKM**	**Fold change**	**Corrected P value**
FIG006045: Sigma factor2C ECF subfamily	138.86	352.24	2.54	0.00040
Heme oxygenase HemO2C associated with heme uptake	18.35	1072.47	58.44	0.00022
FIG039061: hypothetical protein related to heme utilization	9.95	120.97	12.16	0.00912
RNA polymerase sigma-70 factor2C ECF subfamily	38.55	415.80	10.79	0.00022
ABC exporter for hemopore HasA2C outer membrane component HasF	37.67	191.50	5.08	0.00022
Hemophore HasA	117.41	1761.68	15.00	0.00022
Iron siderophore sensor protein	13.85	149.85	10.82	0.00022
FIG006045: Sigma factor2C ECF subfamily	10.28	262.82	25.56	0.00022
Iron transport across membrane				
Gene_Name	***P. poae* *control* FPKM**	***P. poae* *treated* FPKM**	**Fold change**	**Corrected P value**
Mg/Co/Ni transporter MgtE / CBS domain	96.00	245.69	2.56	0.00022
Zinc-regulated outer membrane receptor	33.37	137.96	4.13	0.00022
Zinc ABC transporter2C ATP-binding protein ZnuC	25.78	101.55	3.94	0.00022
Ferrous iron transport periplasmic protein EfeO2C contains peptidase-M75 domain and (frequently) cupredoxin-like domain	78.20	1958.95	25.05	0.00022
Ferrous iron transport peroxidase EfeB	51.26	1271.71	24.81	0.00022
Ferrous iron transport periplasmic protein EfeO2C contains peptidase-M75 domain and (frequently) cupredoxin-like domain	50.76	810.70	15.97	0.00022
Ferrous iron transport permease EfeU	53.06	1405.71	26.50	0.00022

Table 5 B Transcription of Metabolic genes				
Inositol Metabolism				
Gene_Name	***P. poae* *control* FPKM**	***P. poae* *treated* FPKM**	**Fold change**	**Corrected P value**
Inosose dehydratase	16.28	68.21	4.19	0.00022
5-deoxy-glucuronate isomerase	19.26	101.51	5.27	0.00022
Inosose isomerase	13.81	69.22	5.01	0.00022
Epi-inositol hydrolase	21.96	92.21	4.20	0.00022
Myo-inositol 2-dehydrogenase	26.92	148.52	5.52	0.00022
Myo-inositol 2-dehydrogenase	11.89	49.41	4.16	0.00022
Methylmalonate-semialdehyde dehydrogenase [inositol]	9.04	70.53	7.80	0.00022
Myo-inositol 2-dehydrogenase	31.01	80.45	2.59	0.00022

Polysaccharide synthesis

Gene_Name	***P. poae control* FPKM**	***P. poae treated* FPKM**	**Fold change**	**Corrected P value**
Alginate biosynthesis protein Alg8	25.74	3.12	-8.30	0.00158
GDP-mannose 6-dehydrogenase	29.69	12.41	-2.39	0.01187
polysaccharide deacetylase family protein	211.10	77.34	-2.73	0.00022

Lipid metabolism

Gene_Name	***P. poae control* FPKM**	***P. poae treated* FPKM**	**Fold change**	**Corrected P value**
Glycerophosphoryl diester phosphodiesterase	65.81	165.32	2.51	0.00022
1-acyl-sn-glycerol-3-phosphate acyltransferase	56.13	181.26	3.23	0.00022
UDP-4-amino-4-deoxy-L-arabinose--oxoglutarate aminotransferase	189.32	571.30	3.02	0.00022
CDP-diacylglycerol--serine O-phosphatidyltransferase	112.64	275.46	2.45	0.00022
UDP-4-amino-4-deoxy-L-arabinose--oxoglutarate aminotransferase	246.98	504.41	2.04	0.00022
lipopolysaccharide biosynthesis protein	96.92	240.50	2.48	0.00022
CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase	128.46	63.66	-2.02	0.00501
Phosphatidylserine/phosphatidylglycerophosphate/cardiolipi n synthases and related enzymes	6.99	20.00	2.86	0.01585
Cyclopropane-fatty-acyl-phospholipid synthase	823.79	366.02	-2.25	0.00022
Lipid A biosynthesis lauroyl acyltransferase	30.91	62.99	2.04	0.00630
UDP-glucose 4-epimerase	116.86	20.43	-5.72	0.00022

Sugar Metabolism

Gene_Name	***P. poae control* FPKM**	***P. poae treated* FPKM**	**Fold change**	**Corrected P value**
Fructokinase	44.71	137.10	3.07	0.00022
Xylulose kinase	30.94	122.10	3.95	0.00022
Beta N-acetyl-glucosaminidase	455.10	171.30	-2.66	0.00022
Sorbitol dehydrogenase	13.43	32.89	2.45	0.00579
Aldose 1-epimerase	25.82	8.48	-3.04	0.02411
Glycerol kinase	95.76	201.52	2.10	0.00022
Glycerol-3-phosphate acyltransferase	376.47	78.76	-4.78	0.00022
Xylose activator XylR (AraC family)	49.24	21.80	-2.26	0.02097
Xylose isomerase	8.05	23.14	2.87	0.00630
L-arabinose-binding periplasmic protein precursor AraF (TC 3.A.1.2.2)	625.91	65.93	-9.49	0.00022
Glucosamine--fructose-6-phosphate aminotransferase [isomerizing]	138.36	286.82	2.07	0.00022
Aerobic glycerol-3-phosphate dehydrogenase	1020.52	296.89	-3.44	0.00022

Nucleic acid Metabolism

Gene_Name	***P. poae control* FPKM**	***P. poae treated* FPKM**	**Fold change**	**Corrected P value**
CTP synthase	55.91	22.01	-2.54	0.00474
Phosphoribosylglycinamide formyltransferase 2	110.20	225.23	2.04	0.00022
GMP synthase [glutamine-hydrolyzing]2C amidotransferase subunit / GMP synthase [glutamine-hydrolyzing]2C ATP pyrophosphatase subunit	198.69	426.18	2.14	0.00022

Queuosine Biosynthesis QueE Radical SAM	98.52	40.21	-2.45	0.00127
Phosphoribosylamine--glycine ligase	161.16	358.42	2.22	0.00022
Adenylosuccinate lyase	278.60	18.74	-14.87	0.00022
Thymidylate kinase	196.69	55.69	-3.53	0.00022
Adenylate kinase	368.08	876.12	2.38	0.00022
Deoxycytidine triphosphate deaminase	175.17	392.28	2.24	0.00022
Phosphoribosylaminoimidazole-succinocarboxamide synthase	361.32	748.53	2.07	0.00022
Deoxyguanosinetriphosphate triphosphohydrolase	321.46	151.16	-2.13	0.00022
Molybdopterin-guanine dinucleotide biosynthesis protein MobA	83.17	40.25	-2.07	0.01509
Orotidine 5'-phosphate decarboxylase	63.33	167.82	2.65	0.00022
Hydroxymethylpyrimidine phosphate synthase ThiC	242.59	50.81	-4.77	0.00022
Uracil phosphoribosyltransferase	91.56	253.67	2.77	0.00022
ATP synthase A chain	460.77	1052.71	2.28	0.00022
ATP synthase delta chain	1774.87	3658.13	2.06	0.00022
Ureidoglycolate hydrolase	36.54	92.44	2.53	0.00826
Queuosine biosynthesis QueD2C PTPS-I	44.57	122.92	2.76	0.01828
Adenylosuccinate lyase	151.25	329.17	2.18	0.00022
Phosphopantetheine				
Gene_Name	***P. poae* control FPKM**	***P. poae* treated FPKM**	**Fold change**	**Corrected P value**
Phosphopantetheine adenylyltransferase	274.98	562.78	2.05	0.00022
Aldehyde dehydrogenase%3B Probable coniferyl aldehyde dehydrogenase	193.49	36.91	-5.24	0.00022
Others metabolism				
Gene_Name	***P. poae* control FPKM**	***P. poae* treated FPKM**	**Fold change**	**Corrected P value**
Alkanesulfonate monooxygenase	33.86	9.32	-3.63	0.00357593
Carbonic anhydrase2C gamma class	42.47	182.96	4.31	0.00022
Prolipoprotein diacylglyceryl transferase (Lipo protein biogenesis)	118.61	288.39	2.43	0.00022
protein activator of alkane oxidation PraB (Alkane oxidation)	337.17	1146.05	3.40	0.00022
protein activator of alkane oxidation PraA (Alkane oxidation)	195.51	89.58	-2.18	0.00127
Alkane-1 monooxygenase	586.10	168.29	-3.48	0.00022
CobW GTPase involved in cobalt insertion for B12 biosynthesis	226.42	483.00	2.13	0.00022
N-carbamoyl-L-amino acid hydrolase	23.34	78.86	3.38	0.00022
Aldoxime dehydratase	47.65	9.42	-5.06	0.00076
Hydrogenase assembly protein HoxX	1074.42	476.86	-2.25	0.00022
Cyclohexanone monooxygenase	404.56	152.31	-2.66	0.00022
Arginine-tRNA-protein transferase	256.15	86.21	-2.97	0.00022
Epoxide hydrolase	16.52	5.78	-2.86	0.03448
4-amino-4-deoxy-L-arabinose transferase and related glycosyltransferases of PMT family	71.66	233.54	3.26	0.00022
Alpha-methylacyl-CoA racemase	179.49	51.62	-3.48	0.00022
Methylglutaconyl-CoA hydratase	96.82	337.36	3.48	0.01729

2-aminoethylphosphonate:pyruvate aminotransferase	590.52	13.63	-43.31	0.00022
Phosphonoacetaldehyde hydrolase	1461.82	49.71	-29.41	0.00022
2-hydroxy-3-keto-5-methylthiopentenyl-1-phosphate phosphatase related protein	497.66	1007.81	2.03	0.00022
Nucleoside-diphosphate-sugar epimerases	46.85	15.15	-3.09	0.00668
2-methylcitrate synthase	81.35	221.07	2.72	0.00022
2-methylaconitate isomerase	67.77	158.24	2.33	0.00022
Uroporphyrinogen-III methyltransferase	24.59	51.51	2.10	0.02914
FIG138056: a glutathione-dependent thiol reductase	183.55	378.93	2.06	0.00143
N-carbamoyl-L-amino acid hydrolase	45.68	16.83	-2.71	0.00076
P-hydroxybenzoate hydroxylase	38.82	7.58	-5.12	0.00040
Lactam utilization protein LamB	635.99	259.24	-2.45	0.00022
Metal-dependent hydrolase involved in phosphonate metabolism	332.00	73.18	-4.54	0.00022
Citrate synthase (si)	681.49	1473.79	2.16	0.00022
Muconate cycloisomerase	43.75	18.69	-2.34	0.00357
Catechol 12C2-dioxygenase	65.00	28.67	-2.27	0.00260
L-carnitine dehydratase/bile acid-inducible protein F	181.92	72.30	-2.52	0.00022
Glutaryl-CoA dehydrogenase	296.96	97.92	-3.03	0.00022
Carbonic anhydrase	254.62	112.94	-2.25	0.00093
glutamine synthetase family protein	74.34	24.13	-3.08	0.00022
Phenazine biosynthesis protein PhzF	82.78	183.74	2.22	0.00022
Ribose-phosphate pyrophosphokinase	1014.67	2222.66	2.19	0.00022
4-diphosphocytidyl-2-C-methyl-D-erythritol kinase	786.31	2088.53	2.66	0.00022
Ketol-acid reductoisomerase	749.45	1984.56	2.65	0.00022
Acetolactate synthase small subunit	334.59	749.35	2.24	0.00022
Predicted D-lactate dehydrogenase2C Fe-S protein2C FAD/FMN-containing	53.92	16.91	-3.19	0.00022
Serine hydroxymethyltransferase	673.87	1534.39	2.28	0.00022
Triosephosphate isomerase	433.01	990.37	2.29	0.00022
Multiple polyol-specific dehydrogenase	27.22	161.41	5.93	0.00022
Biotin carboxylase	84.93	38.91	-2.18	0.00127
dTDP-4-dehydrorhamnose reductase	927.85	220.28	-4.21	0.00022
Homogentisate 12C2-dioxygenase	795.47	331.66	-2.40	0.00022
N6-hydroxylysine O-acetyltransferase2C aerobactin biosynthesis protein IucB @ Siderophore synthetase small component2C acetyltransferase	659.90	223.61	-2.95	0.00022
predicted L-arabinose 1-dehydrogenase	232.84	53.40	-4.36	0.00022
Undecaprenyl-diphosphatase	45.11	227.81	5.05	0.00022
Monofunctional biosynthetic peptidoglycan transglycosylase	59.67	126.92	2.13	0.00022
Glycogen phosphorylase	122.17	290.95	2.38	0.00022
Mannose-6-phosphate isomerase	45.31	281.77	6.22	0.00040
UDP-galactose-lipid carrier transferase	595.67	203.04	-2.93	0.00022
2-dehydro-3-deoxyphosphogalactonate aldolase	18.46	42.80	2.32	0.04737
8-amino-7-oxononanoate synthase (Biotin metabolism)	169.87	70.08	-2.42	0.00022
2-nitropropane dioxygenase	105.15	232.74	2.21	0.00022
Cardiolipin synthetase	80.95	25.07	-3.23	0.00022
cytosolic long-chain acyl-CoA thioester hydrolase family protein	133.65	59.34	-2.25	0.00316

Acetyltransferase	146.24	57.39	-2.55	0.00488
putative 4-hydroxybenzoyl-CoA thioesterase	152.23	67.35	-2.26	0.00553
Imidazoleglycerol-phosphate dehydratase	391.83	948.13	2.42	0.00022
Allantoicase	66.28	182.14	2.75	0.00022
Demethylmenaquinone methyltransferase (menaquinone biosynthesis)	417.01	162.49	-2.57	0.00022
Glutamine synthetase type I	720.38	2250.21	3.12	0.00022
NADP-dependent malic enzyme	744.11	1614.89	2.17	0.00022
Dihydroflavonol-4-reductase (flavonoid biosynthesis)	46.71	16.90	-2.76	0.00143
22C4-dihydroxyhept-2-ene-12C7-dioic acid aldolase (ascorbate and aldarate metabolism.	33.53	14.17	-2.37	0.02311
Glucarate dehydratase(ascorbate and aldarate metabolism.	11.47	3.50	-3.28	0.04132
Transcriptional regulator PhaD	70.07	17.12	-4.09	0.00188
Polyhydroxyalkanoic acid synthase	133.97	46.00	-2.91	0.00022
Polyhydroxyalkanoate granule-associated protein PhaF	913.58	1885.83	2.06	0.00022
3-hydroxy-3isohexenylglutaryl-CoA:acetate lyase	266.57	76.24	-3.50	0.00022
Citronellol and citronellal dehydrogenase	247.31	70.80	-3.49	0.00022
Geranyl-CoA carboxylase carboxyl transferase subunit	201.75	53.43	-3.78	0.00022
Citronellyl-CoA dehydrogenase	292.57	91.71	-3.19	0.00022
Geranyl-CoA carboxylase biotin-containing subunit	60.60	16.12	-3.76	0.00022
Beta-glucosidase	28.90	10.24	-2.82	0.00022
5-keto-2-deoxygluconokinase / uncharacterized domain	31.10	91.14	2.93	0.00022
Molybdenum cofactor biosynthesis protein MoaC	215.70	435.26	2.02	0.01021
Fatty acid metabolism				
Gene_Name	***P. poae* control FPKM**	***P. poae* treated FPKM**	**Fold change**	**Corrected P value**
Acetyl-coenzyme A synthetase	162.17	396.50	2.44	0.00022
Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases	22.71	76.96	3.39	0.00022
Acetyl-CoA C-acyltransferase	47.59	148.65	3.12	0.00022
Acyl carrier protein	5157.84	13682.80	2.65	0.00022
Short-chain type dehydrogenase/reductase	37.25	86.65	2.33	0.00202
Medium-chain-fatty-acid--CoA ligase	31.01	68.53	2.21	0.00022
Long-chain-fatty-acid--CoA ligase	107.47	236.54	2.20	0.00022
Acyl-CoA dehydrogenase	81.41	167.06	2.05	0.00022
3-hydroxydecanoyl-[acyl-carrier-protein] dehydratase	371.92	746.95	2.01	0.00022
Long-chain-fatty-acid--CoA ligase	68.94	33.71	-2.05	0.00022
Long-chain-fatty-acid--CoA ligase	189.96	90.04	-2.11	0.00022
Butyryl-CoA dehydrogenase	247.34	115.33	-2.14	0.00022
22C4-dienoyl-CoA reductase [NADPH]	53.35	22.41	-2.38	0.00022
Acyl-CoA dehydrogenase	1258.60	508.62	-2.47	0.00022
Acetoacetyl-CoA synthetase / Long-chain-fatty-acid--CoA ligase	60.63	24.41	-2.48	0.00022
Long-chain-fatty-acid--CoA ligase	34.16	13.27	-2.57	0.00174
22C4-dienoyl-CoA reductase [NADPH]	22.50	8.52	-2.64	0.0213087
(3R)-hydroxymyristoyl-[acyl carrier protein] dehydratase	1851.15	642.50	-2.88	0.00022
Long-chain-fatty-acid--CoA ligase	809.32	258.23	-3.13	0.00022
3-oxoacyl-[acyl-carrier protein] reductase	37.94	11.35	-3.34	0.0182839
Long-chain-fatty-acid--CoA ligase	617.31	179.28	-3.44	0.00022
3-ketoacyl-CoA thiolase	288.16	76.54	-3.76	0.00022

Fatty acid desaturase	47.79	12.20	-3.92	0.00040
Enoyl-CoA hydratase	470.69	113.21	-4.16	0.00022
Sterol desaturase	539.49	85.71	-6.29	0.00022
3-ketoacyl-CoA thiolase @ Acetyl-CoA acetyltransferase	249.29	37.79	-6.60	0.00022
Oxidoreductases				
Gene_Name	***P. poae control*** **FPKM**	***P. poae treated*** **FPKM**	**Fold change**	**Corrected P value**
Alcohol dehydrogenase	347.98	41.43	-8.40	0.00022
2-polyprenylphenol hydroxylase and related flavodoxin oxidoreductases	248.21	43.11	-5.76	0.00022
Alcohol dehydrogenase	5591.07	1391.76	-4.02	0.00022
Bifunctional protein: zinc-containing alcohol dehydrogenase%3B quinone oxidoreductase (NADPH:quinone reductase)%3B Similar to arginate lyase	263.11	69.00	-3.81	0.00022
Glyoxalase/bleomycin resistance protein/dioxygenase	57.04	16.10	-3.54	0.00022
Formate dehydrogenase-O2C major subunit	78.56	24.42	-3.22	0.00022
N-ethylmaleimide reductase	90.60	28.65	-3.16	0.00022
Isoquinoline 1-oxidoreductase alpha subunit	329.39	110.04	-2.99	0.00022
Alcohol dehydrogenase	116.46	40.74	-2.86	0.00022
Alcohol dehydrogenase	275.93	102.38	-2.70	0.00022
DgcA Dimethylglycine demethylase subunit A	124.89	55.60	-2.25	0.00022
Fe(2+)/alpha-ketoglutarate-dependent dioxygenase LpxO	87.35	193.29	2.21	0.00022
Glucose dehydrogenase2C PQQ-dependent	194.92	465.85	2.39	0.00022
FMN reductase2C NADPH-dependent	149.80	361.61	2.41	0.00022
monooxygenase2C putative	8.54	23.70	2.78	0.01105
D-beta-hydroxybutyrate dehydrogenase	14.81	43.79	2.96	0.00604
Probable acyl-CoA dehydrogenase	36.54	113.95	3.12	0.00022
Ketoglutarate semialdehyde dehydrogenase	13.70	47.90	3.50	0.00022
Lactoylglutathione lyase	145.86	791.55	5.43	0.00022
Amino acid Degradation and metabolism				
Gene_Name	***P. poae control*** **FPKM**	***P. poae treated*** **FPKM**	**Fold change**	**Corrected P value**
Fumarylacetoacetate hydrolase family protein	144.25	5.01	-28.78	0.00275
Homocysteine S-methyltransferase	645.36	54.29	-11.89	0.00022
Enoyl-CoA hydratase [isoleucine degradation] / 3-hydroxyacyl-CoA dehydrogenase / 3-hydroxybutyryl-CoA epimerase	204.62	22.11	-9.26	0.00022
Cysteine dioxygenase	237.21	26.56	-8.93	0.00022
5-carboxymethyl-2-oxo-hex-3- ene-12C7-dioate decarboxylase	182.00	21.69	-8.39	0.00189
Formiminoglutamic iminohydrolase	913.57	109.52	-8.34	0.00022
Homoserine kinase	1523.74	226.09	-6.74	0.00022
Choline dehydrogenase	785.74	120.12	-6.54	0.00022
Arginine/ornithine antiporter ArcD	7835.32	1228.28	-6.38	0.00022
Betaine aldehyde dehydrogenase	1316.89	209.82	-6.28	0.00022
Arginine deiminase	12564.10	2397.17	-5.24	0.00022
Succinate-semialdehyde dehydrogenase [NAD]%3B Succinate-semialdehyde dehydrogenase [NADP+]	136.29	32.94	-4.14	0.00022
Ornithine carbamoyltransferase	11485.80	2779.67	-4.13	0.00022

Acetyl-CoA carboxylase alpha subunit	4812.78	1470.65	-3.27	0.00022
Phenylalanine-4-hydroxylase	725.91	221.90	-3.27	0.00022
Carbamate kinase	4063.97	1250.34	-3.25	0.00022
Glutaminase	71.10	22.23	-3.20	0.00022
Omega-amino acid--pyruvate aminotransferase	806.97	271.04	-2.98	0.00022
Leucine dehydrogenase	175.10	67.67	-2.59	0.00022
D-amino acid dehydrogenase small subunit	80.81	31.41	-2.57	0.00022
Ornithine cyclodeaminase	610.91	249.17	-2.45	0.00022
L-serine dehydratase	40.22	16.58	-2.43	0.00232
2-ketoglutaric semialdehyde dehydrogenase	16.71	6.93	-2.41	0.03071
Glycerate kinase	70.11	30.58	-2.29	0.00158
Sigma-54 dependent transcriptional regulator/sensory box protein	232.41	101.79	-2.28	0.00022
Phosphoserine phosphatase	183.89	81.61	-2.25	0.00040
Dihydrodipicolinate reductase	584.20	260.07	-2.25	0.00022
2-dehydropantoate 2-reductase	109.86	49.55	-2.22	0.00076
Catalyzes the cleavage of p-aminobenzoyl-glutamate to p-aminobenzoate and glutamate2C subunit A	456.40	216.09	-2.11	0.00022
Sarcosine oxidase gamma subunit	134.80	66.31	-2.03	0.00448
Aspartate-semialdehyde dehydrogenase	56.41	113.84	2.02	0.00093
NAD-specific glutamate dehydrogenase2C large form	252.66	517.12	2.05	0.00022
Carboxynorspermidine decarboxylase2C putative	112.94	235.25	2.08	0.00022
Succinylornithine transaminase	205.11	442.94	2.16	0.00022
Carboxynorspermidine dehydrogenase	231.70	524.77	2.26	0.00022
Methylmalonate-semialdehyde dehydrogenase	121.30	276.33	2.28	0.00022
Ornithine decarboxylase / Arginine decarboxylase	109.23	261.65	2.40	0.00022
3-isopropylmalate dehydrogenase	133.78	321.34	2.40	0.00022
Enoyl-CoA hydratase [valine degradation]	77.73	191.50	2.46	0.00022
3-hydroxyisobutyrate dehydrogenase	83.73	214.34	2.56	0.00022
D-amino acid dehydrogenase family protein in hydroxy-L-proline catabolic cluster	9.68	25.49	2.63	0.01328
Acetylornithine aminotransferase%3B Ornithine aminotransferase	35.41	97.88	2.76	0.00022
Omega-amino acid--pyruvate aminotransferase	119.50	334.15	2.80	0.00022
3-dehydroquinate dehydratase II	96.97	301.50	3.11	0.00022
Choline dehydrogenase	18.15	58.86	3.24	0.00022
Butyryl-CoA dehydrogenase	30.04	101.26	3.37	0.00022
L-pipecolate oxidase (1.5.3.7)	9.49	56.72	5.98	0.00022
4-hydroxyproline epimerase	3.06	21.99	7.19	0.02483
L-pipecolate dehydrogenase	20.20	151.06	7.48	0.00022
1-pyrroline-4-hydroxy-2-carboxylate deaminase	8.10	80.21	9.90	0.00022
Amino acid synthesis				
Gene_Name	***P. poae* *control* FPKM**	***P. poae* *treated* FPKM**	**Fold change**	**Corrected P value**
ATP phosphoribosyltransferase	148.53	303.36	2.04	0.00058
L-serine dehydratase	49.07	11.99	-4.09	0.00022
5-oxo-L-prolinase2C putative	43.61	13.74	-3.17	0.00128
Shikimate kinase I	304.58	98.07	-3.11	0.00022
Acetylornithine aminotransferase	34.31	11.06	-3.10	0.00410
Shikimate 5-dehydrogenase I alpha	1184.32	487.14	-2.43	0.00022

Isochorismatase	122.68	50.60	-2.42	0.00174
Acetolactate synthase2C large subunit	14.01	6.19	-2.26	0.04441
Tryptophan synthase beta chain like	588.49	292.45	-2.01	0.00143
22C32C42C5-tetrahydropyridine-22C6-dicarboxylate N-succinyltransferase	258.07	533.16	2.07	0.00022
Dihydrodipicolinate synthase	267.84	577.01	2.15	0.00022
2-Oxobutyrate oxidase2C putative	113.68	249.40	2.19	0.00022
Cysteine synthase	59.47	137.46	2.31	0.00022
Cysteine synthase	26.95	88.90	3.30	0.00022
Carbohydrate Metabolism				
Glyoxalate cycle				
Gene_Name	***P. poae* control FPKM**	***P. poae* treated FPKM**	**Fold change**	**Corrected P value**
Isocitrate lyase	71.18	340.90	4.79	0.00022
Malate synthase G	127.03	356.11	2.80	0.00022
Pentose Phosphate pathway				
Gene_Name	***P. poae* control FPKM**	***P. poae* treated FPKM**	**Fold change**	**Corrected P value**
Gluconolactonase	77.70	15.29	-5.08	0.00022
Ribulose-5-phosphate 4-epimerase and related epimerases and aldolases	67.96	20.40	-3.33	0.00022
Xylulose kinase	13.78	48.41	3.51	0.00022
Xylitol dehydrogenase	14.35	52.18	3.64	0.00040
Glycolysis				
Gene_Name	***P. poae* control FPKM**	***P. poae* treated FPKM**	**Fold change**	**Corrected P value**
Phosphoenolpyruvate carboxykinase [ATP]	347.39	748.95	2.16	0.00022
Enolase	519.07	1480.68	2.85	0.00022
D-3-phosphoglycerate dehydrogenase	31.27	136.07	4.35	0.00022
Kreb cycle (TCA cycle)				
Gene_Name	***P. poae* control FPKM**	***P. poae* treated FPKM**	**Fold change**	**Corrected P value**
Aconitate hydratase	869.65	226.56	-3.84	0.00022
Branched-chain alpha-keto acid dehydrogenase2C E1 component2C alpha subunit	413.01	121.80	-3.39	0.00022
Branched-chain alpha-keto acid dehydrogenase2C E1 component2C beta subunit	355.44	152.64	-2.33	0.00022
Dihydrolipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex	263.39	127.98	-2.06	0.00022
Pyruvate oxidase [ubiquinone2C cytochrome]	101.77	242.84	2.39	0.00022

Table 5 C Transcription of Transport genes across membrane				
Gene_Name	***P. poae* control FPKM**	***P. poae* treated FPKM**	**Fold change**	**Corrected P value**

Molybdenum transport system permease protein ModB (TC 3.A.1.8.1)	51.21	178.87	3.49	0.00022
Molybdenum ABC transporter2C periplasmic molybdenum-binding protein ModA (TC 3.A.1.8.1)	122.16	366.11	3.00	0.00022
Inositol transport system sugar-binding protein	24.25	214.07	8.83	0.00022
Inositol transport system ATP-binding protein	16.24	128.60	7.92	0.00022
Inositol transport system permease protein	30.08	107.89	3.59	0.00022
Phosphate ABC transporter2C periplasmic phosphate-binding protein PstS (TC 3.A.1.7.1)	30.47	414.42	13.60	0.00022
Phosphate transport system permease protein PstC (TC 3.A.1.7.1)	41.78	390.07	9.34	0.00022
Phosphate transport ATP-binding protein PstB (TC 3.A.1.7.1)	23.58	281.16	11.92	0.00022
FIG00957944: hypothetical protein	95.97	343.94	3.58	0.00022
Glucose-selective porin OprB	236.92	1395.92	5.89	0.00022
Glucose ABC transporter2C ATP-binding subunit	143.44	671.32	4.68	0.00022
Glucose ABC transport system2C inner membrane component 2	160.98	817.67	5.08	0.00022
Glucose ABC transport system2C periplasmic sugar-binding protein	137.97	1067.37	7.74	0.00022
PTS system2C glucose-specific IIA component / Phosphotransferase system2C phosphocarrier protein HPr / Phosphoenolpyruvate-protein phosphotransferase of PTS system	15.17	77.79	5.13	0.00022
Maltoporin (maltose/maltodextrin high-affinity receptor2C phage lambda receptor protein)	6.58	50.05	7.61	0.00022
PTS system2C trehalose-specific IIB component / PTS system2C trehalose-specific IIC component	12.52	90.33	7.21	0.00022
Urease accessory protein UreD	20.96	46.89	2.24	0.00977
Urea ABC transporter2C ATPase protein UrtE	8.01	114.05	14.23	0.00040
Urea ABC transporter2C ATPase protein UrtD	9.77	108.84	11.14	0.00022
Urea ABC transporter2C permease protein UrtC	15.82	141.35	8.94	0.00022
Urea ABC transporter2C substrate binding protein UrtA	8.91	243.92	27.38	0.00022
Inositol transport system sugar-binding protein	14.58	62.26	4.27	0.00022
Glycerol-3-phosphate ABC transporter2C permease protein UgpA (TC 3.A.1.1.3)	62.50	157.90	2.53	0.00058
probable MFS transporter	22.23	64.20	2.89	0.00202
Benzoate transport protein	17.56	57.79	3.29	0.00022
Long-chain fatty acid transport protein	304.78	1039.66	3.41	0.00022
Aerobic C4-dicarboxylate transporter for fumarate2C L-malate2C D-malate2C succunate2C aspartate	102.74	372.84	3.63	0.00022
Tricarboxylate transport transcriptional regulator TctD	67.37	135.54	2.01	0.00112
Tricarboxylate transport protein TctB	8.29	52.52	6.34	0.02943
Tricarboxylate transport protein TctC	12.63	46.90	3.71	0.00022
Tricarboxylate porin OpdH	11.04	41.30	3.74	0.00022
Hypothetical ABC transport system2C periplasmic component	70.00	386.49	5.52	0.00022
Potassium voltage-gated channel subfamily KQT%3B possible potassium channel2C VIC family	22.25	49.81	2.24	0.01338
MotA/TolQ/ExbB proton channel family protein	5.85	67.11	11.47	0.01338
Nucleoside-specific channel-forming protein Tsx precursor	15.58	131.31	8.43	0.00022

Purine nucleoside permease	24.70	141.95	5.75	0.00022
Thiosulfate sulfurtransferase2C rhodanese	89.76	184.58	2.06	0.00022
High-affinity leucine-specific transport system2C periplasmic binding protein LivK (TC 3.A.1.4.1)	530.99	1126.39	2.12	0.00022
Gluconate transporter family protein	23.25	61.03	2.62	0.00022
TonB-dependent receptor%3B Outer membrane receptor for ferrienterochelin and colicins	11.96	107.88	9.02	0.00022
Dipeptide transport ATP-binding protein DppF (TC 3.A.1.5.2)	97.44	228.36	2.34	0.00022
Dipeptide transport system permease protein DppB (TC 3.A.1.5.2)	28.46	105.00	3.69	0.00022
Dipeptide-binding ABC transporter2C periplasmic substrate-binding component (TC 3.A.1.5.2)	24.84	159.57	6.42	0.00022
Outer membrane porin2C OprD family	69.99	415.29	5.93	0.00022
Dipeptide-binding ABC transporter2C periplasmic substrate-binding component (TC 3.A.1.5.2)	45.90	158.25	3.45	0.00022
Dipeptide-binding ABC transporter2C periplasmic substrate-binding component (TC 3.A.1.5.2)	80.78	577.41	7.15	0.00022
Mg(2+) transport ATPase2C P-type	14.97	597.06	39.88	0.00022
Mg(2+) transport ATPase protein C	14.28	381.25	26.70	0.00022
Glutathione-regulated potassium-efflux system ATP-binding protein	249.29	510.97	2.05	0.00022
Various polyols ABC transporter2C ATP-binding component	49.31	175.66	3.56	0.00022
ABC-type antimicrobial peptide transport system2C permease component	36.29	109.16	3.01	0.00022
Ribose ABC transport system2C permease protein RbsC (TC 3.A.1.2.1)	20.70	42.64	2.06	0.00826
Xylose ABC transporter2C periplasmic xylose-binding protein XylF	14.19	51.18	3.61	0.00041
D-serine/D-alanine/glycine transporter	52.81	115.82	2.19	0.00022
Permeases of the major facilitator superfamily	11.09	37.13	3.35	0.00022
MotA/TolQ/ExbB proton channel family protein	141.33	842.95	5.96	0.00022
Ammonium transporter	243.07	659.94	2.71	0.00022
Sulfur carrier protein ThiS	202.63	856.51	4.23	0.00022
Phosphate ABC transporter2C periplasmic phosphate-binding protein PstS (TC 3.A.1.7.1)	120.04	1292.28	10.77	0.00022
Phosphate transport system permease protein PstC (TC 3.A.1.7.1)	25.69	64.17	2.50	0.00022
Oxalate/formate antiporter	63.37	143.16	2.26	0.00022
Amino acid Transporters				
Gene_Name	***P. poae* control FPKM**	***P. poae* treated FPKM**	**Fold change**	**Corrected P value**
Amino acid ABC transporter2C periplasmic amino acid-binding protein	89.91	244.49	2.72	0.00022
Aromatic amino acid transport protein AroP	31.88	102.33	3.21	0.00022
Glutamate Aspartate transport ATP-binding protein GltL (TC 3.A.1.3.4)	412.68	1090.03	2.64	0.00022
Glutamate Aspartate periplasmic binding protein precursor GltI (TC 3.A.1.3.4)	455.43	1437.61	3.16	0.00022

Proline/sodium symporter PutP (TC 2.A.21.2.1) @ Propionate/sodium symporter	142.83	738.02	5.17	0.00022
Methionine ABC transporter ATP-binding protein	55.45	203.48	3.67	0.00022
Glutamate transport ATP-binding protein	55.18	145.48	2.64	0.00022
L-Proline/Glycine betaine transporter ProP	48.44	97.00	2.00	0.00094
L-Proline/Glycine betaine transporter ProP	143.37	302.32	2.11	0.00022
Amino acid permease in 4-hydroxyproline catabolic gene cluster	4.02	22.40	5.57	0.00144
Glutamate Aspartate periplasmic binding protein precursor GltI (TC 3.A.1.3.4)	51.76	371.17	7.17	0.00022
Glutamate Aspartate transport system permease protein GltJ (TC 3.A.1.3.4)	17.79	58.90	3.31	0.00022
ABC-type polar amino acid transport system2C ATPase component	34.55	78.11	2.26	0.00216747
Glutamate Aspartate periplasmic binding protein precursor GltI (TC 3.A.1.3.4)	51.76	371.17	7.17	0.00022
Glutamate Aspartate transport system permease protein GltJ (TC 3.A.1.3.4)	17.79	58.90	3.31	0.00022
Aromatic amino acid transport protein AroP	31.88	102.33	3.21	0.00022
Branched-chain amino acid ABC transporter2C amino acid-binding protein (TC 3.A.1.4.1)	41.94	211.61	5.05	0.00022
Branched-chain amino acid transport ATP-binding protein LivG (TC 3.A.1.4.1)	31.79	136.66	4.30	0.00022
Leucine-2C isoleucine-2C valine-2C threonine-2C and alanine-binding protein	21.54	53.83	2.50	0.00144
Branched-chain amino acid transport system permease protein LivM (TC 3.A.1.4.1)	25.77	101.35	3.93	0.00022
Branched-chain amino acid ABC transporter2C amino acid-binding protein (TC 3.A.1.4.1)	41.94	211.61	5.05	0.00022
Branched-chain amino acid transport ATP-binding protein LivG (TC 3.A.1.4.1)	31.79	136.66	4.30	0.00022
Histidine ABC transporter2C permease protein HisQ (TC 3.A.1.3.1)	48.95	107.56	2.20	0.00202
Histidine ABC transporter2C ATP-binding protein HisP (TC 3.A.1.3.1)	26.11	90.67	3.47	0.00022
Branched-chain amino acid transport system permease protein LivM (TC 3.A.1.4.1)	25.77	101.35	3.93	0.00022
Arginine/ornithine ABC transporter2C ATP-binding protein AotP	131.61	274.09	2.08	0.00022
Arginine/ornithine ABC transporter2C periplasmic arginine/ornithine binding protein	276.68	1158.20	4.19	0.00022
Histidine ABC transporter2C ATP-binding protein HisP (TC 3.A.1.3.1)	12.87	33.87	2.63	0.02208
Histidine ABC transporter2C permease protein HisM (TC 3.A.1.3.1)	21.80	50.40	2.31	0.02499
Lysine-arginine-ornithine-binding periplasmic protein precursor (TC 3.A.1.3.1)	90.70	339.80	3.75	0.00022
L-lysine permease	103.24	24.15	-4.28	0.00022
Putative threonine efflux protein	38.71	12.73	-3.04	0.02153
Glutamate transport membrane-spanning protein	130.66	34.83	-3.75	0.00022
Methionine ABC transporter permease protein	145.55	54.00	-2.70	0.00040

Glutathione-regulated potassium-efflux system protein KefC	25.38	9.68	-2.62	0.00189
Prolyl oligopeptidase family protein	154.59	41.03	-3.77	0.00022
Oligopeptide transporter2C OPT family	40.72	19.28	-2.11	0.00316
Glutamate Aspartate periplasmic binding protein precursor GltI (TC 3.A.1.3.4)	68.30	31.17	-2.19	0.00383
L-proline glycine betaine ABC transport system permease protein ProW (TC 3.A.1.12.1)	140.87	49.56	-2.84	0.00022
Cationic amino acid transporter	13.30	3.90	-3.41	0.04393
Amino acid ABC transporter2C periplasmic amino acid-binding protein	52.47	18.68	-2.81	0.00370
Arginine/ornithine ABC transporter2C periplasmic arginine/ornithine binding protein	137.77	31.17	-4.42	0.00022
Glutathione-regulated potassium-efflux system protein KefB	497.65	57.92	-8.59	0.00022
Threonine and homoserine efflux system	69.97	20.36	-3.44	0.00022
Serine transporter	96.60	20.62	-4.68	0.00022
RND/Drug Efflux				
Gene_Name	***P. poae* control FPKM**	***P. poae* treated FPKM**	**Fold change**	**Corrected P value**
RND efflux system2C membrane fusion protein CmeA	409.87	27.36	-14.98	0.00022
RND efflux membrane fusion protein	224.55	34.82	-6.45	0.00022
RND efflux transporter	71.12	12.82	-5.55	0.00022
RND efflux system2C inner membrane transporter CmeB	395.22	135.19	-2.92	0.00022
RND efflux system2C membrane fusion protein CmeA	444.50	196.12	-2.27	0.00022
Permeases of the drug/metabolite transporter (DMT) superfamily	280.01	95.50	-2.93	0.00022
Permease of the drug/metabolite transporter (DMT) superfamily	35.38	11.97	-2.96	0.01214
Permease of the drug/metabolite transporter (DMT) superfamily	44.01	13.95	-3.15	0.00303
Permease of the drug/metabolite transporter (DMT) superfamily	44.23	16.83	-2.63	0.01199
Permease of the drug/metabolite transporter (DMT) superfamily	47.77	23.50	-2.03	0.02626
Multidrug efflux membrane fusion protein MexE	19.91	6.24	-3.19	0.01851
Inner membrane component of tripartite multidrug resistance system	33.62	15.60	-2.15	0.01472
Multidrug resistance transporter2C Bcr/CflA family	304.33	37.41	-8.14	0.00022
Others Transporters				
Gene_Name	***P. poae* control FPKM**	***P. poae* treated FPKM**	**Fold change**	**Corrected P value**
Xanthine transporter2Cputative	51.54	25.71	-2.00	0.04385
Xanthine and CO dehydrogenases maturation factor2C XdhC/CoxF family	390.01	145.08	-2.69	0.00022
Xanthine permease	27.67	8.72	-3.17	0.00127
Major facilitator family transporter	31.34	9.42	-3.33	0.00617
Permeases of the major facilitator superfamily	79.66	8.82	-9.03	0.00022
Permeases of the major facilitator superfamily	235.12	7.45	-31.57	0.00022
Major facilitator family transporter	99.28	29.95	-3.31	0.00022

Permeases of the major facilitator superfamily	683.24	68.10	-10.03	0.00022
Membrane fusion component of tripartite multidrug resistance system	37.27	7.70	-4.84	0.00275
MFS transporter	23.23	10.09	-2.30	0.01938
MFS transporter	36.45	14.62	-2.49	0.00410
ABC-type nitrate/sulfonate/bicarbonate transport systems2C periplasmic components	78.25	21.52	-3.64	0.00022
ABC-type nitrate/sulfonate/bicarbonate transport systems2C periplasmic components	24.95	3.46	-7.21	0.02301
Nitrate/nitrite transporter	14.64	4.44	-3.30	0.04800
Alkanesulfonates-binding protein	30.78	10.47	-2.94	0.01235
Alkanesulfonates transport system permease protein	59.53	15.59	-3.82	0.00076
Taurine-binding periplasmic protein TauA	150.26	55.94	-2.69	0.00022
Alpha-ketoglutarate-dependent taurine dioxygenase	36.89	9.41	-3.92	0.00694
Taurine transport system permease protein TauC	54.80	20.60	-2.66	0.00343
Alkanesulfonates ABC transporter ATP-binding protein / Sulfonate ABC transporter2C ATP-binding subunit SsuB	32.00	7.98	-4.01	0.01775
Niacin transporter NiaP	57.53	19.67	-2.92	0.00022
Potassium efflux system KefA protein / Small-conductance mechanosensitive channel	77.22	30.32	-2.55	0.00022
Macrolide-specific efflux protein MacA	135.21	45.33	-2.98	0.00022
Macrolide export ATP-binding/permease protein MacB	137.14	38.03	-3.61	0.00022
Zinc uptake regulation protein ZUR	1432.10	503.53	-2.84	0.00022
Sulfate permease	49.50	17.81	-2.78	0.00022
Ferric iron ABC transporter2C iron-binding protein	136.65	63.80	-2.14	0.00022
Ferric iron ABC transporter2C permease protein	72.58	25.45	-2.85	0.00022
Lead2C cadmium2C zinc and mercury transporting ATPase%3B Copper-translocating P-type ATPase	135.70	23.61	-5.75	0.00022
High-affinity choline uptake protein BetT	101.94	47.28	-2.16	0.00022
POTASSIUM/PROTON ANTIPORTER ROSB	76.69	16.32	-4.70	0.00022
Sulfate and thiosulfate import ATP-binding protein CysA	68.10	20.66	-3.30	0.00022
Potassium efflux system KefA protein / Small-conductance mechanosensitive channel	194.34	42.77	-4.54	0.00022
Putative sulfate permease	49.89	15.03	-3.32	0.00232
LysR family transcriptional regulator clustered with dicarboxylate transport	43.01	16.83	-2.55	0.00925
Outer membrane receptor proteins2C mostly Fe transport	14.09	5.32	-2.65	0.00592
TRAP-type C4-dicarboxylate transport system2C periplasmic component	27.61	10.00	-2.76	0.02033
Ethanolamine permease	55.30	10.48	-5.28	0.00022
Mg(2+) transport ATPase2C P-type	16.69	485.30	29.07	0.00022
Nitrate ABC transporter2C nitrate-binding protein	12.73	54.31	4.27	0.00022
pyoverdine-specific efflux macA-like protein	66.85	247.82	3.71	0.00022
D-xylose transport ATP-binding protein XylG	7.02	22.01	3.14	0.0016
Xylose ABC transporter2C periplasmic xylose-binding protein XylF	13.47	46.60	3.46	0.00022
Metal transporter2C ZIP family	101.63	712.16	7.01	0.00022
ABC transporter ATP-binding protein	203.77	56.96	-3.58	0.00022

Table 5 D Transcription of Toxin and other defence protein

Toxin/Proteases

Gene_Name	*P. poae control* FPKM	*P. poae treated* FPKM	Fold change	Corrected P value
Actin-ADP-ribosyltransferase2C toxin SpvB (TcaC toxin)	39.04	17.08	-2.29	0.00022
RTX toxin2C putative	1308.92	437.24	-2.99	0.00022
Rhs family protein	89.31	20.73	-4.31	0.00022
Rhs-family protein	22.14	8.11	-2.73	0.00022
D-alanyl-D-alanine carboxypeptidase	54.80	138.45	2.53	0.00022
HtrA protease/chaperone protein	308.61	734.16	2.38	0.00022
Secreted alkaline metalloproteinase2C PrtA/B/C/G homolog	3104.20	8015.24	2.58	0.00022
ABC-type protease exporter2C ATP-binding component PrtD/AprD	157.38	655.53	4.17	0.00022
ABC-type protease exporter2C outer membrane component PrtF/AprF	81.09	293.60	3.62	0.00022
Transglutaminase-like enzymes2C putative cysteine proteases	30.94	62.69	2.03	0.0324935
Aminopeptidase N	197.89	416.15	2.10	0.00579
Proline iminopeptidase	183.58	75.55	-2.64	0.00022
Proline iminopeptidase	824.61	408.26	-2.02	0.00040
Metalloprotease	36.31	9.55	-3.80	0.00022
Secreted alkaline metalloproteinase2C PrtA/B/C/G homolog	51.20	19.49	-2.63	0.00076
D-AMINOPEPTIDASE	90.37	32.77	-2.76	0.00022
Cytosol aminopeptidase PepA	312.11	804.67	2.58	0.00022
Leucyl aminopeptidase (aminopeptidase T)	332.29	1060.96	3.19	0.00022

Oxidative Stress

Gene_Name	*P. poae control* FPKM	*P. poae treated* FPKM	Fold change	Corrected P value
Alkyl hydroperoxide reductase protein F	286.78	42.01	-6.83	0.00022
Superoxide dismutase [Fe]	2067.53	884.23	-2.34	0.00022
Catalase	203.70	22.97	-8.87	0.00022
Catalase	375.94	172.12	-2.18	0.00022
Catalase	977.17	288.09	-3.39	0.00022
Superoxide dismutase [Mn]	179.06	1813.26	10.13	0.00022

Iron storage Protein

Gene_Name	*P. poae control* FPKM	*P. poae treated* FPKM	Fold change	Corrected P value
Bacterioferritin	1316.98	291.14	-4.52	0.00022
Bacterioferritin	2199.33	336.65	-6.53	0.00022
Bacterioferritin-associated ferredoxin	144.48	2230.86	15.44	0.00022

Other Stress and Defence related proteins

Gene_Name	*P. poae control* FPKM	*P. poae treated* FPKM	Fold change	Corrected P value
Hemolysin	66.49	381.59	5.74	0.00022
Urease accessory protein UreG	21.69	244.56	11.27	0.00022
Urease accessory protein UreF	41.63	429.97	10.33	0.00022

Glutathione S-transferase	64.05	151.34	2.36	0.00022
Gamma-glutamyltranspeptidase	23.31	49.34	2.12	0.00076
Putative multicopper oxidases	33.63	140.14	4.17	0.00792
Cytochrome B561	110.09	422.98	3.84	0.00022
Thiol peroxidase2C Tpx-type	521.31	1167.00	2.24	0.00022
Glutathione S-transferase2C omega	78.33	35.23	0.45	0.00059
Malate:quinone oxidoreductase	214.86	545.54	2.54	0.00022
Rubredoxin	177.31	1496.21	8.44	0.00127
Thioredoxin	797.34	1998.80	2.51	0.00022
Oxidoreductase2C aldo/keto reductase family	184.42	399.88	2.17	0.00022
Glutaredoxin	62.55	199.37	3.19	0.00059
putative cytochrome B561	39.15	150.05	3.83	0.00022
Universal stress protein family 7	4126.34	744.83	-5.54	0.00022
Heat shock protein GrpE	1956.15	935.85	-2.09	0.00022
cytochrome b(561)	2381.78	357.39	-6.66	0.00022
Multicopper oxidase	33.36	4.32	-7.72	0.00022
Oxidoreductase2C short chain dehydrogenase/reductase family	101.61	35.41	-2.87	0.00040
Periplasmic thiol:disulfide oxidoreductase DsbB2C required for DsbA reoxidation	75.47	37.22	-2.03	0.04204
FMN oxidoreductase	239.47	74.65	-3.21	0.00022
Putative oxidoreductase	848.08	136.83	-6.20	0.00022
Oxidoreductase2C short chain dehydrogenase/reductase family	358.65	161.75	-2.22	0.00022
Probable esterase	66.81	25.80	-2.59	0.00717
Cold shock protein CspA	1019.89	374.57	-2.72	0.00330
Putative diheme cytochrome c-553	116.00	21.65	-5.36	0.00022
Oxidoreductase	314.93	73.48	-4.29	0.00022
Oxidoreductase	699.52	254.91	-2.74	0.00022
Putative oxidoreductase	29.58	12.12	-2.44	0.00260
Putative formate dehydrogenase oxidoreductase protein	248.16	54.97	-4.51	0.00022
Coenzyme F420-dependent N52CN10-methylene tetrahydromethanopterin reductase and related flavin-dependent oxidoreductases	812.49	145.42	-5.59	0.00022
Oxidoreductase2C 2-nitropropane dioxygenase family	112.45	52.74	-2.13	0.00059
Putative oxidoreductase	77.20	20.97	-3.68	0.00022

Table 5 E Transcription of Motility genes

Gene_Name	***P. poae* control FPKM**	***P. poae* treated FPKM**	**Fold change**	**Corrected P value**
Segregation and condensation protein B	148.08	72.73	-2.04	0.00022
Segregation and condensation protein A	198.72	75.06	-2.65	0.00022
Sigma-fimbriae tip adhesin	102.84	33.09	-3.11	0.01316
Sigma-fimbriae usher protein	81.78	36.12	-2.26	0.00022
Sigma-fimbriae chaperone protein	222.44	85.30	-2.61	0.00022
Sigma-fimbriae uncharacterized paralogous subunit	432.98	182.35	-2.37	0.00022
FlhB domain protein	444.02	177.20	-2.51	0.00260

putative mannose-resistant/Proteus-like fimbrial protein	37.17	13.38	-2.78	0.03289
FIG027785: Fimbriae usher protein StfC	337.60	36.12	-9.35	0.00022
Fimbrial protein	121.34	19.44	-6.24	0.00501
Fimbrial protein	29.99	11.24	-2.67	0.00397
Sensory box histidine kinase	76.37	25.28	-3.02	0.00022
Flp pilus assembly protein TadG	187.59	58.32	-3.22	0.00022
Flp pilus assembly protein TadD2C contains TPR repeats	115.16	42.15	-2.73	0.00022
Type II/IV secretion system protein TadC2C associated with Flp pilus assembly	55.70	9.40	-5.92	0.00076
Flp pilus assembly protein TadB	57.60	25.24	-2.28	0.005922
Type II/IV secretion system ATP hydrolase TadA/VirB11/CpaF2C TadA subfamily	293.28	117.07	-2.51	0.00022
Flp pilus assembly protein RcpC/CpaB	126.83	53.22	-2.38	0.00022
Type IV pilin PilA	600.42	163.65	-3.67	0.00022
Type IV pilus biogenesis protein PilE	1077.36	173.34	-6.22	0.00022
Type IV pilus biogenesis protein PilM	432.92	176.52	-2.45	0.00022
Twitching motility protein PilT	99.96	34.67	-2.88	0.00022
Methyl-accepting chemotaxis protein	605.30	233.90	-2.59	0.001585
Methyl-accepting chemotaxis protein	796.33	192.99	-4.13	0.00022
gliding motility protein GldF	113.98	35.27	-3.23	0.00022
Beta-fimbriae probable major subunit	58.03	9.44	-6.15	0.005922
Beta-fimbriae chaperone protein	230.53	57.38	-4.02	0.00022
Beta-fimbriae usher protein	19.67	8.10	-2.43	0.001585
Methyl-accepting chemotaxis protein I (serine chemoreceptor protein)	17.49	5.01	-3.49	0.00144
Methyl-accepting chemotaxis protein	56.24	19.26	-2.92	0.00022
Methyl-accepting chemotaxis protein	29.34	69.15	2.36	0.00022
P pilus assembly/Cpx signaling pathway2C periplasmic inhibitor/zinc-resistance associated protein	18.74	97.11	5.18	0.00246
Methyl-accepting chemotaxis transducer	20.68	45.06	2.18	0.00022
Chemotactic transducer	196.44	486.22	2.48	0.00022
Methyl-accepting chemotaxis protein I (serine chemoreceptor protein)	92.11	198.54	2.16	0.00022
Flagellar hook protein FlgE	270.29	566.50	2.10	0.00022
Flagellar basal-body rod protein FlgC	186.68	467.60	2.50	0.00022
Flagellar basal-body rod protein FlgB	154.87	376.29	2.43	0.00022
Methyl-accepting chemotaxis protein	18.65	55.23	2.96	0.00022
Autotransporter adhesin	1059.98	2186.75	2.06	0.00022
Flagellin protein FlaB	4195.54	9194.66	2.19	0.00022

Table 5 F Transcription of various Transcriptional regulators

Gene_Name	***P. poae* *control* FPKM**	***P. poae* *treated* FPKM**	**Fold change**	**Corrected P value**

LysR-family transcriptional regulator	102.83	13.66	-7.53	0.00740
Transcriptional regulator2C GntR family	254.72	74.97	-3.40	0.00022
Transcriptional regulator2C TetR family	48.84	17.51	-2.79	0.01553
Transcriptional regulator2C AraC family	154.42	41.86	-3.69	0.00022
Predicted transcriptional regulator of N-Acetylglucosamine utilization2C GntR family	77.55	20.14	-3.85	0.00022
Transcriptional regulator2C AraC family	70.06	28.32	-2.47	0.01450
Transcriptional regulator2C AraC family	571.20	102.35	-5.58	0.00022
Transcriptional regulator2C AraC family	71.71	32.25	-2.22	0.00174
Transcriptional regulator BkdR of isoleucine and valine catabolism operon	319.57	83.53	-3.83	0.00022
Transcriptional regulatory protein	16.33	3.62	-4.51	0.01753
LysR family transcriptional regulator PA3398	1996.42	306.32	-6.52	0.00022
Transcriptional regulator2C AraC family	106.76	26.80	-3.98	0.00022
Transcriptional regulator2C TetR family	298.78	73.59	-4.06	0.00022
Transcriptional regulator2C AraC family	117.65	26.54	-4.43	0.00022
Translation initiation factor 2 (IF-2%3B GTPase)	1026.64	325.16	-3.16	0.00022
Transcriptional regulator2C LysR family	343.46	98.63	-3.48	0.00022
Transcriptional regulator2C HxlR family	228.69	43.98	-5.20	0.00202
Transcriptional regulator lysR family	215.31	74.29	-2.90	0.00022
Transcriptional regulators2C LysR family	143.09	69.24	-2.07	0.00094
RNA polymerase sigma factor RpoE	427.08	207.88	-2.05	0.00717
Transcriptional regulators2C LysR family	94.43	31.57	-2.99	0.00022
Transcriptional regulator SlyA	786.73	199.91	-3.94	0.00022
Transcriptional regulatory protein	36.66	16.92	-2.17	0.01428
Sigma factor RpoE negative regulatory protein RseB precursor	622.94	192.51	-3.24	0.00022
LysR-family transcriptional regulator clustered with PA0057	112.22	29.65	-3.78	0.00022
Transcription regulatory protein opdE	28.19	4.71	-5.99	0.00541
Transcriptional regulator PobR2C AraC family	460.61	221.20	-2.08	0.00022
Predicted transcriptional regulator for fatty acid degradation FadQ2C TetR family	2819.16	448.79	-6.28	0.00022
Transcription elongation factor	164.70	54.25	-3.04	0.00040
Transcriptional regulator2C LysR family	39.02	17.38	-2.24	0.01033
Transcriptional regulator2C LysR family	117.75	39.64	-2.97	0.00022
Similar to ribosomal large subunit pseudouridine synthase A	404.74	75.91	-5.33	0.00022
Transcriptional regulator2C GntR family domain / Aspartate aminotransferase	74.39	26.54	-2.80	0.00022
Transcriptional regulator2C Cro/CI family	1708.85	702.30	-2.43	0.00260
Transcriptional regulator2C TetR family	119.27	55.32	-2.16	0.00937
LysR family transcriptional regulator PA4989	81.29	25.88	-3.14	0.00022
Acetyltransferase2C GNAT family	77.32	30.39	-2.54	0.02578
benABC operon transcriptional activator BenR	36.88	18.32	-2.01	0.02861
Aromatic hydrocarbon utilization transcriptional regulator CatR (LysR family)	77.84	32.65	-2.38	0.00059
Transcriptional regulator2C MerR family2C associated with photolyase	826.83	259.81	-3.18	0.00022
Transcriptional regulator2C LysR family	124.66	40.33	-3.09	0.00022

Cu(I)-responsive transcriptional regulator	997.62	159.79	-6.24	0.00022
Transcriptional regulator2C LysR family	69.45	22.47	-3.09	0.00076
acetyltransferase2C GNAT family	176.35	80.69	-2.19	0.00289
Transcriptional regulator of various polyols utilization2C AraC family	160.69	72.44	-2.22	0.00040
Transcriptional regulator2C TetR family	197.19	59.10	-3.34	0.00059
Transcriptional regulator2C LysR family	61.43	28.16	-2.18	0.00541
Transcriptional regulator2C MerR family	141.34	23.35	-6.05	0.00022
type III transcriptional regulator HrpR	126.36	37.46	-3.37	0.00022
Transcriptional regulator2C MerR family2C associated with photolyase	2007.31	411.68	-4.88	0.00022
Transcriptional regulator2C GntR family domain / Aspartate aminotransferase	72.72	20.75	-3.50	0.00022
Transcriptional regulator2C LysR family	72.38	24.66	-2.93	0.00022
2-ketogluconate utilization repressor PtxS	332.47	111.79	-2.97	0.00022
Nitrogen regulation protein NR(I)	144.76	69.78	-2.07	0.00022
Transcriptional activator MetR	114.08	53.70	-2.12	0.00022
Transcriptional regulator2C PadR family	1325.34	290.11	-4.57	0.00022
acetyltransferase2C GNAT family	156.51	65.86	-2.38	0.00384
Glycine cleavage system transcriptional activator	92.09	23.25	-3.96	0.00022
transcriptional regulator2C LysR family	46.04	18.84	-2.44	0.00912
Transcriptional regulator2C LysR family	158.35	65.99	-2.40	0.00022
PAS domain containing response regulator2C LuxR family	186.34	54.43	-3.42	0.00022
Transcriptional regulator2C AsnC family	175.33	59.00	-2.97	0.00022
HTH-type transcriptional regulator BetI	2915.54	312.20	-9.34	0.00022
Vfr transcriptional regulator / Cyclic AMP receptor protein	324.71	161.79	-2.01	0.00987
Phosphogluconate repressor HexR2C RpiR family	200.78	90.36	-2.22	0.00022
Transcriptional regulator	189.38	65.35	-2.90	0.00022
Acetyltransferase2C GNAT family	222.06	64.62	-3.44	0.00022
Transcriptional regulator2C MarR family	892.60	227.91	-3.92	0.00022
putative transcriptional regulator	52.34	4.91	-10.66	0.01304
transcriptional regulator2C Crp/Fnr family	154.32	58.83	-2.62	0.00246
Transcriptional regulator2C LysR family	107.76	23.87	-4.51	0.00022
Functional role page for Anaerobic nitric oxide reductase transcription regulator NorR	113.72	21.45	-5.30	0.00022
Transcriptional regulator2C AraC family	48.34	22.57	-2.14	0.00717
Transcriptional regulator2C LuxR family	1649.36	670.49	-2.46	0.00022
RNA polymerase sigma factor for flagellar operon	4253.35	1428.81	-2.98	0.00022
Serine phosphatase RsbU2C regulator of sigma subunit / Serine-protein kinase RsbW	1221.65	585.55	-2.09	0.00717
Phenylalanine hydroxylase transcriptional activator PhhR	108.29	49.05	-2.21	0.00022
Cys regulon transcriptional activator CysB	46.21	18.93	-2.44	0.01142
LysR family transcriptional regulator YneJ	48.71	20.43	-2.38	0.00384
Transcriptional regulator2C ArsR family	732.63	42.17	-17.37	0.00022
Lactate-responsive regulator LldR in Enterobacteria2C GntR family	284.44	49.59	-3.28	0.00022

DNA-binding response regulator2C LuxR family	139.43	63.69	-2.25	0.00331
transcriptional regulator2C LysR family	469.36	141.71	-8.40	0.00022
Cyn operon transcriptional activator	120.13	26.56	-3.27	0.00022
Cys regulon transcriptional activator CysB	76.44	23.34	-2.28	0.00022
Transcriptional regulator2C AraC family	138.60	61.08	-2.27	0.00094
LysR family transcriptional regulator YnfL	27.41	12.38	-2.21	0.03166
Acetyltransferase2C GNAT family	199.42	50.79	-3.93	0.00022
Transcriptional regulator2C AraC family	135.77	56.65	-2.40	0.00022
RNA polymerase sigma-54 factor RpoN	130.65	49.42	-2.64	0.02433
probable transcriptional regulator	59.51	18.71	-3.18	0.00998
Phosphonate uptake and metabolism regulator2C LysR-family	106.25	30.02	-3.54	0.00022
Transcriptional regulator ahyR/asaR family	521.07	185.01	-2.82	0.00022
Transcription elongation factor GreB	285.29	127.46	-2.24	0.00040
Transcriptional regulators	1570.76	160.07	-9.81	0.00022
FIG032225: Transcriptional regulator2C LysR family	86.29	13.57	-6.36	0.00022
Transcriptional regulator2C AraC family	510.77	96.01	-5.32	0.00022
Regulator of competence-specific genes	205.98	92.96	-2.22	0.03660
transcriptional regulator TrpI	219.67	40.52	-5.42	0.00022
Transcriptional regulator2C AraC family	178.47	29.25	-6.10	0.00022
Transcriptional regulators2C LysR family	149.52	62.70	-2.38	0.00022
Transcriptional regulator2C MerR family	287.02	80.98	-3.54	0.00022
Mercuric resistance operon regulatory protein	848.94	104.83	-8.10	0.00022
Sugar diacid utilization regulator SdaR	14.61	41.89	2.87	0.00040
transcriptional regulator MvaT2C P16 subunit2C putative	993.96	2045.80	2.06	0.00022
Trehalose operon transcriptional repressor	61.08	133.32	2.18	0.00076
Response regulator/EAL domain protein	24.14	85.00	3.52	0.00022
Transcriptional regulator MexT	48.07	121.13	2.52	0.00022
Transcriptional regulator2C LysR family	33.89	73.65	2.17	0.00706
Transcriptional regulator2C LysR family	13.85	28.02	2.02	0.04332
Propionate catabolism operon transcriptional regulator of GntR family [predicted]	93.10	289.75	3.11	0.00022
Transcriptional regulator2C GntR family	135.24	295.73	2.19	0.00022
Acetyltransferase2C GNAT family	14.37	47.30	3.29	0.00159
Transcriptional regulator2C LuxR family	22.82	46.39	2.03	0.02985
Alginate regulatory protein AlgP	410.41	1123.28	2.74	0.00022
Transcriptional regulator2C ArsR family / Methyltransferase fusion	92.45	187.22	2.03	0.00022
Transcriptional regulator of glmS gene2C DeoR family	69.85	181.68	2.60	0.00022
Phosphate regulon transcriptional regulatory protein PhoB (SphR)	61.71	304.59	4.94	0.00022
L-rhamnose operon transcriptional activator RhaR	47.21	122.33	2.59	0.00022
RNA polymerase sigma-70 factor2C ECF subfamily	60.31	477.45	7.92	0.00022
Transcriptional regulator2C MarR family	85.84	221.06	2.58	0.00127

Table 5G Transcription of various Respiratory Chain and DNA repair Enzymes				
Gene_Name	***P. poae control* FPKM**	***P. poae treated* FPKM**	**Fold change**	**Corrected P value**
Coproporphyrinogen III oxidase2C oxygen-independent	1564.11	635.18	-2.46	0.00022
Heavy-metal-associated domain (N-terminus) and membrane-bounded cytochrome biogenesis cycZ-like domain2C possible membrane copper tolerance protein	926.00	233.17	-3.97	0.00022
FUPA27 P-type ATPase	209.78	60.85	-3.45	0.00022
Putative analog of CcoH2C COG3198	1295.72	232.47	-5.57	0.00022
Type cbb3 cytochrome oxidase biogenesis protein CcoG2C involved in Cu oxidation	979.46	234.37	-4.18	0.00022
ABC transporter involved in cytochrome c biogenesis2C ATPase component CcmA	1204.11	243.07	-4.95	0.00022
Cytochrome c-type biogenesis protein CcmC2C putative heme lyase for CcmE	746.50	218.50	-3.42	0.00022
Cytochrome c heme lyase subunit CcmF	1000.80	437.53	-2.29	0.00022
Cytochrome oxidase biogenesis protein Sco1/SenC/PrrC2C putative copper metallochaperone	449.98	172.34	-2.61	0.00022
Gluconate 2-dehydrogenase2C membrane-bound2C cytochrome c	183.22	71.54	-2.56	0.00022
Hydrolase2C alpha/beta fold family functionally coupled to Phosphoribulokinase	106.88	50.21	-2.13	0.00111
Radical SAM family enzyme2C similar to coproporphyrinogen III oxidase2C oxygen-independent2C clustered with nucleoside-triphosphatase RdgB	1043.62	487.97	-2.14	0.00022
Electron transfer flavoprotein2C beta subunit	64.65	25.18	-2.57	0.00384
Anaerobic nitric oxide reductase transcription regulator NorR	259.69	38.13	-6.81	0.00022
Flavohemoprotein (Hemoglobin-like protein) (Flavohemoglobin) (Nitric oxide dioxygenase)	47.75	5.76	-8.29	0.00022
NADH dehydrogenase	96.71	19.59	-4.94	0.00022
FAD/FMN-containing dehydrogenase	71.71	21.17	-3.39	0.00022
Heme O synthase2C protoheme IX farnesyltransferase COX10-CtaB	22.43	6.55	-3.43	0.03736
NADH:ubiquinone oxidoreductase subunit 2 (chain N)	57.70	-1.15	-2.23	0.00022
Coenzyme F420-dependent N52CN10-methylene tetrahydromethanopterin reductase and related flavin-dependent oxidoreductases	14.13	-2.78	-6.89	0.00022
Acyl-CoA dehydrogenase%3B probable dibenzothiophene desulfurization enzyme	13.91	-3.04	-8.20	0.00022
Cytochrome c2	89.45	-1.24	-2.36	0.00022
Heme O synthase2C protoheme IX farnesyltransferase COX10-CtaB	417.32	1277.38	3.06	0.00022
Cytochrome O ubiquinol oxidase subunit IV	1109.92	2762.49	2.49	0.00022
Cytochrome O ubiquinol oxidase subunit I	598.51	1686.04	2.82	0.00022

Cytochrome O ubiquinol oxidase subunit II	362.95	1369.73	3.77	0.00022
DNA repair				
Gene_Name	***P. poae* *control* FPKM**	***P. poae* *treated* FPKM**	**Fold change**	**Corrected P value**
DNA-3-methyladenine glycosylase II	537.04	117.07	-4.59	0.00022
RecA protein	2336.15	1060.50	-2.20	0.00022
SOS-response repressor and protease LexA	538.65	199.71	-2.70	0.00022
Chaperone protein DnaJ	690.36	316.09	-2.18	0.00022
Chaperone protein DnaK	4388.54	1767.22	-2.48	0.00022
DNA-3-methyladenine glycosylase	40.56	16.60	-2.44	0.03131
G:T/U mismatch-specific uracil/thymine DNA-glycosylase	1405.21	71.93	-19.54	0.00022
DnaJ-like protein DjlA	371.73	118.67	-3.13	0.00022
Alkylated DNA repair protein AlkB	166.00	71.05	-2.34	0.00022
DNA repair protein RecN	270.04	95.75	-2.82	0.00022

Table 5H Transcription of various other genes

Gene_Name	***P. poae* *control* FPKM**	***P. poae* *treated* FPKM**	**Fold change**	**Corrected P value**
putative DNA-binding protein	74.18	27.95	-2.65	0.00022
AFG1-like ATPase	59.65	19.01	-3.14	0.00094
Integral membrane protein TerC	58.19	24.43	-2.38	0.00706
ThiJ/PfpI family protein	574.91	237.96	-2.42	0.00022
Membrane protein2C putative	335.33	50.79	-6.60	0.00022
Putative transport protein	30.16	6.06	-4.98	0.00202
Phage-related integrase	37.42	10.85	-3.45	0.00232
Uncharacterized conserved protein	54.22	20.80	-2.61	0.00246
Poly(beta-D-mannuronate) C5 epimerase precursor	14.08	6.13	-2.30	0.04465
Response regulator protein	60.28	29.02	-2.08	0.00144
Outer membrane protein romA	1135.77	103.30	-11.00	0.00022
Lactam utilization protein LamB	69.54	26.75	-2.60	0.00202
FIG027190: Putative transmembrane protein	192.53	35.30	-5.45	0.01010
Putative two-component system sensor kinase	34.43	15.20	-2.26	0.00514
Zn-ribbon-containing2C possibly RNA-binding protein and truncated derivatives	429.21	88.60	-4.84	0.00022
COG06132C Predicted metal-dependent phosphoesterases (PHP family)	379.85	168.33	-2.26	0.00022
Non-specific DNA-binding protein Dps / Iron-binding ferritin-like antioxidant protein / Ferroxidase	5655.89	2563.53	-2.21	0.00022
glycosyl transferase2C group 1 family protein	509.05	166.62	-3.06	0.00022
INTEGRAL MEMBRANE PROTEIN (Rhomboid family)	48.49	20.27	-2.39	0.04155
FxsA protein	396.99	194.63	-2.04	0.00022
Signal transduction histidine kinase	30.42	14.22	-2.14	0.00022
Response regulator	172.49	37.95	-4.55	0.00410
bacteriophytochrome heme oxygenase BphO	438.70	198.31	-2.21	0.00040

Probable transmembrane protein	180.48	36.42	-4.96	0.00022
Probable two-component response regulator	2135.60	229.83	-9.29	0.00022
PROBABLE REMNANT OF A TRANSPOSASE GENE PROTEIN	72.75	26.21	-2.78	0.00059
NfuA Fe-S protein maturation	2075.46	362.07	-5.73	0.00022
Domain often clustered or fused with uracil-DNA glycosylase	193.89	79.32	-2.44	0.00022
putative membrane protein	49.81	15.16	-3.29	0.00022
Uncharacterized protein ImpA	17.63	6.74	-2.61	0.02508
Uncharacterized protein ImpC	11.63	3.00	-3.88	0.02493
IcmF-related protein	28.86	13.84	-2.08	0.03796
Serine/threonine protein kinase	126.36	38.23	-3.31	0.00022
SAM-dependent methyltransferases	191.75	15.06	-12.73	0.00022
Secreted protein Hcp	53.96	21.33	-2.53	0.03003
Pirin	39.80	13.54	-2.94	0.02358
FIG006442: Integral membrane protein	129.27	30.67	-4.22	0.00022
protein of unknown function DUF955	881.47	314.28	-2.80	0.00022
site-specific recombinase2C phage integrase family	64.69	26.53	-2.44	0.00174
TonB-dependent receptor	104.81	29.69	-3.53	0.00022
Gifsy-2 prophage protein	114.36	45.60	-2.51	0.00410
phage replication protein O2C putative	54.96	22.78	-2.41	0.00424
Protein sprT	163.01	66.26	-2.46	0.00127
ATP-dependent Clp protease adaptor protein ClpS	3602.98	1417.87	-2.54	0.00022
Ferredoxin--NADP(+) reductase	2174.94	558.56	-3.89	0.00022
COG1720: Uncharacterized conserved protein	249.63	99.11	-2.52	0.00022
putative membrane protein	84.76	23.74	-3.57	0.00022
Hydrolase of the alpha/beta superfamily in cluster with COG2110	1546.76	394.19	-3.92	0.00022
VapC toxin protein	523.48	61.32	-8.54	0.00022
Copper resistance protein B	24.42	6.17	-3.96	0.02690
sodium-solute symporter2C putative	378.00	48.05	-7.87	0.00022
Ribosomal large subunit pseudouridine synthase C	737.76	322.47	-2.29	0.00022
Conserved domain protein	908.34	316.50	-2.87	0.00344
Copper tolerance protein	143.08	35.96	-3.98	0.00111
Cell division inhibitor-related protein	572.59	202.83	-2.82	0.00022
Chromosome segregation ATPases	4570.42	1160.94	-3.94	0.00022
Phage terminase2C small subunit	298.29	86.04	-3.47	0.00022
Membrane protein2C distant similarity to thiosulphate:quinone oxidoreductase DoxD	294.97	90.01	-3.28	0.00022
Conserved domain protein	1049.62	460.52	-2.28	0.00040
Putative cytoplasmic protein	143.41	43.94	-3.26	0.00022
Thiopurine S-methyltransferase	198.15	62.88	-3.15	0.00022
Hybrid sensory histidine kinase in two-component regulatory system with EvgA	20.97	10.11	-2.07	0.00174
Type IIA topoisomerase (DNA gyrase/topo II2C topoisomerase IV)2C A subunit	68.70	32.46	-2.12	0.00528
DUF1232 domain-containing protein	231.72	102.48	-2.26	0.00159

diguanylate cyclase/phosphodiesterase (GGDEF & EAL domains) with PAS/PAC sensor(s)	152.23	65.82	-2.31	0.00371
Ethidium bromide-methyl viologen resistance protein EmrE	337.45	48.53	-6.95	0.00022
Conidiation-specific protein 10	531.22	99.16	-5.36	0.04631
putative membrane protein	315.89	116.97	-2.70	0.00022
conserved domain protein	302.72	103.06	-2.94	0.00022
conserved hypothetical membrane-anchored protein	51.00	19.62	-2.60	0.04695
Probable two-component response regulator	19.42	6.11	-3.18	0.01862
Excinuclease ABC subunit C	310.10	133.39	-2.32	0.00022
BarA-associated response regulator UvrY (GacA SirA)	1456.47	397.79	-3.66	0.00022
Inner membrane protein YfiN	86.79	30.86	-2.81	0.00022
Integral membrane protein	51.08	23.76	-2.15	0.01730
porin2C putative	25.62	11.79	-2.17	0.02321
C4-dicarboxylate anaerobic carrier	38.49	13.61	-2.83	0.00076
Plasmid stabilization system protein	812.45	338.14	-2.40	0.00022
L-arabinose-binding periplasmic protein precursor AraF (TC 3.A.1.2.2)	98.06	31.87	-3.08	0.00022
Carbohydrate kinase2C PfkB family	118.73	50.90	-2.33	0.00022
ADP-ribosylglycohydrolase YegU	698.96	159.99	-4.37	0.00022
FIG003620: Proteophosphoglycan precursor (Fragment)	507.37	109.26	-4.64	0.00022
Holliday junction resolvasome2C helicase subunit	503.69	154.31	-3.26	0.00303
Metalloprotease2C insulinase family	93.43	45.91	-2.04	0.00040
membrane protein2C putative	100.90	41.59	-2.43	0.00022
Sensory box histidine kinase	109.82	49.71	-2.21	0.00022
Fused spore maturation proteins A and B	356.90	97.06	-3.68	0.00022
Response regulator	304.58	142.35	-2.14	0.00189
Copper chaperone	3606.62	121.03	-29.80	0.00022
regulatory protein2C ArsR	26.83	4.93	-5.44	0.04541
PE_PGRS family protein	36.80	13.48	-2.73	0.00987
Phosphotransferase system2C HPr-related proteins	1181.06	413.72	-2.85	0.00022
Outer membrane porin2C OprD family	22.87	7.16	-3.19	0.00643
Methyl-accepting chemotaxis protein I (serine chemoreceptor protein)	46.31	20.26	-2.29	0.00059
membrane protein2C putative	50.62	17.99	-2.81	0.00371
FIG003879: Predicted amidohydrolase / Omega amidase (Nit2 homolog)	533.75	222.64	-2.40	0.00022
Putative deoxyribonuclease YjjV	667.90	100.65	-6.64	0.00022
Fructose repressor FruR2C LacI family	2096.61	369.94	-5.67	0.00022
FIG000506: Predicted P-loop-containing kinase	633.31	243.36	-2.60	0.00022
PTS IIA-like nitrogen-regulatory protein PtsN	1659.70	375.38	-4.42	0.00022
Cell division protein MraZ	3514.68	1642.18	-2.14	0.00260
Multidrug resistance protein B	127.56	58.13	-2.19	0.00040
type III secretion protein HrpJ	82.69	33.66	-2.46	0.00040
type III secretion protein HrpQ	110.89	53.96	-2.05	0.00246

Type III secretion inner membrane protein (YscQ2Chomologous to flagellar export components)	172.63	29.42	-5.87	0.03433
Type III secretion inner membrane protein (YscT2CHrcT2CSpaR2CEscT2CEpaR12Chomologous to flagellar export components)	85.11	41.25	-2.06	0.00303
Cell division inhibitor	517.11	218.11	-2.37	0.00022
Ferrochelatase2C protoheme ferro-lyase	617.22	297.27	-2.08	0.00022
negative regulator of hrp expression HrpV	133.28	65.41	-2.04	0.02531
Type III secretion bridge between inner and outermembrane lipoprotein (YscJ2CHrcJ2CEscJ2C PscJ)	48.01	13.03	-3.68	0.00398
COG1683: Uncharacterized conserved protein / FIG143828: Hypothetical protein YbgA	4386.55	682.01	-6.43	0.00022
ClpB protein	3503.12	590.38	-5.93	0.00022
L-lactate permease	109.08	32.62	-3.34	0.00022
Phage integrase	230.28	78.17	-2.95	0.00022
putative integrase	23.90	6.05	-3.95	0.02011
Nicotinamidase/isochorismatase family protein	298.54	45.38	-6.58	0.00022
UPF0125 protein yfjF	943.57	406.66	-2.32	0.00022
FOG: Ankyrin repeat	54.48	7.44	-7.32	0.02216
Periplasmic aromatic aldehyde oxidoreductase2C molybdenum binding subunit YagR	244.46	110.04	-2.22	0.00449
Antiholin-like protein LrgA	152.74	65.62	-2.33	0.00217
Sensor histidine kinase	185.52	42.50	-4.37	0.00022
Ribosomal large subunit pseudouridine synthase E	154.43	72.36	-2.13	0.01044
Inner membrane protein YbhQ	456.81	156.41	-2.92	0.00022
non-ribosomal peptide synthase	4956.36	1617.08	-3.07	0.00022
sensor histidine kinase	783.55	111.48	-7.03	0.00022
Membrane carboxypeptidase (penicillin-binding protein)	38.99	14.77	-2.64	0.00022
LSU ribosomal protein L31p @ LSU ribosomal protein L31p2C zinc-independent	5959.63	2238.13	-2.66	0.00022
CFA/I fimbrial subunit C precursor	19.01	8.30	-2.29	0.00174
Integral membrane protein	293.16	40.99	-7.15	0.00022
diguanylate cyclase/phosphodiesterase (GGDEF & EAL domains) with PAS/PAC sensor(s)	98.44	36.20	-2.72	0.00111
Protein sirB1	144.60	70.52	-2.05	0.00059
ribosomal subunit interface protein2C putative	15285.30	3667.39	-4.17	0.00022
Glutathione S-transferase2C unnamed subgroup 2	476.45	98.03	-4.86	0.00022
ThiJ/PfpI family protein	320.80	119.51	-2.68	0.00022
YapH protein	166.39	49.20	-3.38	0.00022
Nudix hydrolase family protein YffH	193.42	74.66	-2.59	0.00022
GTP-binding protein EngB	576.80	158.91	-3.63	0.00022
Radical SAM domain protein	136.96	22.44	-6.10	0.00022
Gluconate 2-dehydrogenase2C membrane-bound2C flavoprotein	214.83	88.76	-2.42	0.00022
Dodecin (COG3360) Flavin-binding	2958.78	1062.68	-2.78	0.00022
Predicted signal transduction protein	459.26	140.20	-3.28	0.00022

Autolysis response regulater LytR	1630.83	625.72	-2.61	0.00022
Porphobilinogen deaminase	893.89	380.53	-2.35	0.00022
MG(2+) CHELATASE FAMILY PROTEIN / ComM-related protein	18.50	5.93	-3.12	0.01033
Protein of unknown function DUF55	206.51	45.11	-4.58	0.00022
Type II secretory pathway2C ATPase PulE/Tfp pilus assembly pathway2C ATPase PilB	42.24	18.08	-2.34	0.00094
FMN reductase	136.38	37.63	-3.62	0.00022
Alkanesulfonate monooxygenase	33.86	9.32	-3.63	0.00358
glutamine synthetase family protein	1140.05	209.89	-5.43	0.00022
glutamine synthetase family protein	1623.49	281.42	-5.77	0.00022
Penicillin acylase II	636.12	90.22	-7.05	0.00022
Thiol-disulfide isomerase and thioredoxins	1197.08	121.35	-9.86	0.00022
Purine nucleoside phosphorylase	126.28	56.18	-2.25	0.00475
TonB-dependent siderophore receptor	56.33	20.32	-2.77	0.00022
FIG022869: Oxidoreductase2C GMC family	19.68	7.69	-2.56	0.00682
probable TonB protein	150.36	42.47	-3.54	0.00022
periplasmic binding protein2C putative	313.03	65.46	-4.78	0.00022
Uncharacterized protein with LysM domain2C COG1652	28.32	9.33	-3.03	0.02343
Membrane protein2C putative	57.89	14.83	-3.90	0.00275
Inner membrane protein CreD	35.92	6.49	-5.54	0.00344
GGDEF domain protein	149.97	33.66	-4.46	0.00022
COG3178: Predicted phosphotransferase related to Ser/Thr protein kinases	1132.25	249.45	-4.54	0.00022
tRNA nucleotidyltransferase	188.00	92.49	-2.03	0.00022
Uncharacterized protein conserved in bacteria2C NMA0228-like	67.60	26.90	-2.51	0.00202
Signal transduction histidine kinase	70.14	33.46	-2.10	0.00022
Outer membrane autotransporter barrel	19.12	5.97	-3.21	0.02216
Ribosome-associated heat shock protein implicated in the recycling of the 50S subunit (S4 paralog)	215.69	63.97	-3.37	0.00022
bacterial luciferase family protein	805.17	78.87	-10.21	0.00022
Formate dehydrogenase chain D	190.40	64.39	-2.96	0.00022
Histone acetyltransferase HPA2 and related acetyltransferases	100.53	45.82	-2.19	0.02546
Cell division protein FtsN	570.98	213.55	-2.67	0.00022
Chromosome (plasmid) partitioning protein ParA	298.08	123.06	-2.42	0.00022
Inner membrane component of tripartite multidrug resistance system	53.06	10.56	-5.02	0.00022
Membrane fusion component of tripartite multidrug resistance system	56.55	26.32	-2.15	0.00410
outer membrane ferrichrome-iron receptor	110.45	37.56	-2.94	0.00022
Phage tail assembly protein I	65.85	12.90	-5.11	0.04376
PROBABLE HYDROLASE TRANSMEMBRANE PROTEIN(EC:3.-)	166.42	25.30	-6.58	0.00022
FIG028593: membrane protein	108.00	14.31	-7.55	0.00232
DNA/RNA non-specific endonuclease	40.37	15.70	-2.57	0.02493
ThiJ/PfpI family protein	38.38	3.51	-10.93	0.01010

GGDEF domain protein	43.63	7.68	-5.68	0.00094
Chitinase	1888.07	258.84	-7.29	0.00022
Chitin binding protein	1938.74	273.58	-7.09	0.00022
ThiJ/PfpI family protein	1954.98	390.24	-5.01	0.00022
Multiple antibiotic resistance protein MarC	67.90	31.21	-2.18	0.04249
GGDEF domain protein	289.39	59.16	-4.89	0.00022
Deblocking aminopeptidase @ Cyanophycinase 2	200.12	92.46	-2.16	0.00022
Endonuclease I precursor	181.64	32.20	-5.64	0.00022
Sensory box/GGDEF family protein	66.32	30.12	-2.20	0.00076
Histone acetyltransferase HPA2 and related acetyltransferases	60.24	191.25	3.17	0.00022
Outer membrane protein	157.40	327.30	2.08	0.00022
Copper metallochaperone2C bacterial analog of Cox17 protein	476.54	1169.61	2.45	0.00022
sensor histidine kinase	49.91	627.14	12.57	0.00022
putative membrane protein	115.56	253.39	2.19	0.00604
Oxidoreductase2C aldo/keto reductase family	141.82	303.42	2.14	0.00022
penicillin amidase family protein	30.98	173.47	5.60	0.00022
Outer membrane vitamin B12 receptor BtuB	63.99	285.67	4.46	0.00022
hydrolase2C alpha/beta fold family	28.88	224.58	7.78	0.00022
Nicotinamidase family protein YcaC	35.40	99.14	2.80	0.00059
Extracellular serine protease precursor	33.51	448.84	13.39	0.00022
Ferrichrome-iron receptor	12.28	91.80	7.48	0.00022
Sensor protein PhoQ	457.97	1206.32	2.63	0.00022
Iron-regulated protein A precursor	190.14	1021.73	5.37	0.00022
Cold-shock protein2C DNA-binding	2172.30	4395.34	2.02	0.00059
TPR repeat containing exported protein%3B Putative periplasmic protein contains a protein prenylyltransferase domain	257.58	768.35	2.98	0.00022
18K peptidoglycan-associated outer membrane lipoprotein%3B Peptidoglycan-associated lipoprotein precursor%3B Outer membrane protein P6%3B OmpA/MotB precursor	2214.71	7294.16	3.29	0.00022
Iron-regulated protein A precursor	197.06	494.58	2.51	0.00022
Nitroreductase family protein	100.02	267.96	2.68	0.00022
SAM-dependent methyltransferases	69.71	183.94	2.64	0.00022
Peptide chain release factor RF-3	86.77	177.12	2.04	0.00022
tRNA (Guanine37-N1) -methyltransferase	1001.66	3125.66	3.12	0.00022
16S rRNA processing protein RimM	1882.20	5145.25	2.73	0.00022
SSU ribosomal protein S16p	2082.67	5207.91	2.50	0.00022
Signal recognition particle2C subunit Ffh SRP54 (TC 3.A.5.1.1)	188.99	438.93	2.32	0.00022
Preprotein translocase subunit YajC (TC 3.A.5.1.1)	476.22	1105.79	2.32	0.00022
putative aminotransferase	18.45	38.04	2.06	0.01282
Translation initiation factor SUI1-related protein	176.11	402.89	2.29	0.00022
Uncharacterized iron-regulated membrane protein%3B Iron-uptake factor PiuB	67.39	196.44	2.92	0.00022
Outer membrane receptor proteins2C mostly Fe transport	162.29	513.50	3.16	0.00022

Copper metallochaperone2C bacterial analog of Cox17 protein	291.38	628.18	2.16	0.00022
FIG00955840: hypothetical protein	206.72	538.52	2.61	0.00022
DNA-binding protein Fis	144.57	364.78	2.52	0.00344
tRNA dihydrouridine synthase B	133.73	344.25	2.57	0.00022
Ribosomal protein L11 methyltransferase	63.33	150.31	2.37	0.00022
HupE-UreJ family metal transporter	35.45	353.00	9.96	0.00022
FIG00955561: hypothetical protein	377.97	1441.33	3.81	0.00059
DNA-binding protein HU-beta	2467.92	7634.36	3.09	0.00022
Cell division trigger factor	935.82	2707.25	2.89	0.00022
Possible pyrimidine permease in reductive pathway	15.91	39.61	2.49	0.00232
Cell division protein DivIC (FtsB)2C stabilizes FtsL against RasP cleavage	67.89	148.96	2.19	0.00022
FIG002984: FAD-dependent pyridine nucleotide-disulphide oxidoreductase	75.72	233.11	3.08	0.00022
CDP-diacylglycerol--serine O-phosphatidyltransferase	71.48	341.47	4.78	0.00022
Histone acetyltransferase HPA2 and related acetyltransferases	74.13	201.19	2.71	0.00260
Serine protease homologue	48.75	289.55	5.94	0.00022
Serine protease homologue	48.59	455.71	9.38	0.00022
Lipase	18.24	139.00	7.62	0.00022
Protein containing domains DUF403	17.38	78.31	4.51	0.02332
Protein containing domains DUF4042C DUF407	16.23	66.26	4.08	0.00022
Gentisate 12C2-dioxygenase	32.57	110.84	3.40	0.00022
Polymyxin resistance protein ArnC2C glycosyl transferase	617.37	2675.29	4.33	0.00022
Polymyxin resistance protein PmrM	190.83	779.12	4.08	0.00022
putative exported protein	37.57	77.62	2.07	0.00040
hypothetical protein	454.40	1078.70	2.37	0.00059
Two-component sensor histidine kinase PfeS2C enterobactin	85.32	186.39	2.18	0.00022
tRNA 5-methylaminomethyl-2-thiouridine synthase TusD	63.02	126.46	2.01	0.02861
Translation initiation factor 1	599.68	1600.34	2.67	0.00022
Peptidyl-prolyl cis-trans isomerase ppiB	820.30	2365.03	2.88	0.00022
Exodeoxyribonuclease III	76.26	199.66	2.62	0.00022
FIG033889: YebC paralog in Betaproteobacteria	193.40	431.43	2.23	0.00022
Aminotransferase2C class III	1078.77	2768.19	2.57	0.00022
Ferrichrome-iron receptor	34.73	155.86	4.49	0.00022
Ferrichrome-iron receptor	6.84	29.06	4.25	0.00022
Fe2+-dicitrate sensor2C membrane component	21.73	148.57	6.84	0.00022
Porin B precursor	9.12	23.94	2.62	0.04139
Quinate/shikimate dehydrogenase [Pyrroloquinoline-quinone]	19.91	62.12	3.12	0.00022
CrfX protein	218.99	505.67	2.31	0.00475
FIG002060: uncharacterized protein YggL	499.59	1498.88	3.00	0.00022
Assimilatory nitrate reductase large subunit (EC:1.7.99.4)	17.20	277.98	16.16	0.00022

Serine/threonine protein kinase	11.33	142.74	12.60	0.00022
CAAX amino terminal protease family protein	51.04	106.50	2.09	0.00127
Outer membrane receptor for ferric coprogen and ferric-rhodotorulic acid	35.05	381.91	10.90	0.00022
NLP/P60 family protein	249.23	884.13	3.55	0.00022
NLP/P60 family protein	54.47	158.75	2.91	0.00040
Outer membrane receptor proteins2C likely involved in siderophore uptake @ TonB-dependent siderophore receptor	100.26	963.20	9.61	0.00022
Translation elongation factor Ts	1548.51	3317.21	2.14	0.00022
Collagen pro alpha-chain precursor	133.55	286.58	2.15	0.00022
Outer membrane lipoprotein	585.80	1374.60	2.35	0.00022
COG1399 protein2C clustered with ribosomal protein L32p	1310.97	2839.45	2.17	0.00022
Non-ribosomal peptide synthetase modules2C pyoverdine	17.01	168.47	9.91	0.00022
probable transmembrane sensor	49.97	162.90	3.26	0.00022
Membrane protein	115.13	305.73	2.66	0.00022
Rrf2-linked NADH-flavin reductase	57.39	197.16	3.44	0.00022
Metallo-beta-lactamase superfamily protein PA0057	17.67	54.12	3.06	0.00189
Ribonuclease D	198.00	398.11	2.01	0.01794
Nitroreductase family protein	199.79	423.05	2.12	0.00022
VacJ-like lipoprotein precursor	238.91	760.50	3.18	0.00022
UDP-glucose 4-epimerase	294.25	627.01	2.13	0.00022
NOHBY730%3B no homolog in Saccharomyces cerevisiae	60.81	186.14	3.06	0.00022
UPF0028 protein YchK	64.26	129.80	2.02	0.00022
putative thioredoxin	504.34	1503.18	2.98	0.01700
Translation elongation factor P	883.79	2626.90	2.97	0.00022
putative ATP/GTP-binding protein	153.61	320.67	2.09	0.00111
Putative membrane protein2C clustering with ActP	272.81	738.86	2.71	0.00289
Sensor histidine kinase	47.50	107.29	2.26	0.00022
Putative NADP-dependent oxidoreductase PA1648	33.23	74.30	2.24	0.00094
FIG00956448: hypothetical protein	76.22	175.07	2.30	0.00022
Uncharacterized glutathione S-transferase-like protein	103.92	218.24	2.10	0.00022
FKBP-type peptidyl-prolyl cis-trans isomerase FklB	765.00	1569.05	2.05	0.00022
TonB-dependent receptor	19.98	55.62	2.78	0.00022
LSU ribosomal protein L27p	3211.22	7246.28	2.26	0.00022
putative membrane protein	46.51	176.05	3.79	0.00022
probable transmembrane protein	68.42	173.97	2.54	0.00022
Acid phosphatase	5.68	88.22	15.52	0.00022
Iron-uptake factor PiuC	31.81	138.67	4.36	0.00022
ATPase2C AFG1 family	113.28	256.78	2.27	0.00022
LSU ribosomal protein L13p (L13Ae)	2420.50	6067.39	2.51	0.00022
SSU ribosomal protein S9p (S16e)	2441.50	5679.25	2.33	0.00022

Ferrichrome-iron receptor	26.70	81.65	3.06	0.00022
FagA protein	58.12	1134.91	19.53	0.00022
YrbA protein	325.50	725.74	2.23	0.00189
Probable transmembrane protein	38.16	88.92	2.33	0.00371
DNA-binding response regulator2C LuxR family	97.28	262.93	2.70	0.00022
Transcriptional regulator2C AraC family	37.30	132.21	3.54	0.00022
Peptidyl-tRNA hydrolase	94.19	200.51	2.13	0.00040
Ferrichrome-iron receptor	43.11	108.66	2.52	0.00022
SSU ribosomal protein S20p	1289.94	5483.10	4.25	0.00022
C4-type zinc finger protein2C DksA/TraR family	423.79	1572.97	3.71	0.00022
Polymyxin resistance protein ArnT2C undecaprenyl phosphate-alpha-L-Ara4N transferase%3B Melittin resistance protein PqaB	34.24	132.37	3.87	0.00022
FIG000325: clustered with transcription termination protein NusA	307.39	652.18	2.12	0.00022
Putative inner membrane protein (Fragment)	91.38	198.77	2.18	0.00022
2-hydroxychromene-2-carboxylate isomerase/DsbA-like thioredoxin domain	82.59	184.60	2.24	0.00022
Preprotein translocase subunit SecE (TC 3.A.5.1.1)	1339.45	3174.60	2.37	0.00022
LSU ribosomal protein L10p (P0)	4736.63	9902.80	2.09	0.00022
LSU ribosomal protein L7/L12 (P1/P2)	5875.89	12363.00	2.10	0.00022
SSU ribosomal protein S12p (S23e)	3893.60	8215.18	2.11	0.00022
Single-stranded DNA-binding protein	527.61	1386.23	2.63	0.00022
Predicted zinc-binding protein	87.57	404.16	4.62	0.00022
Inorganic pyrophosphatase	376.84	1156.95	3.07	0.00022
DedA protein	63.23	131.61	2.08	0.00216
Ais protein2C putative	10.16	26.70	2.63	0.04355
Polymyxin resistance protein ArnT2C undecaprenyl phosphate-alpha-L-Ara4N transferase%3B Melittin resistance protein PqaB	15.50	55.83	3.60	0.00022
Polymyxin resistance protein ArnT2C undecaprenyl phosphate-alpha-L-Ara4N transferase%3B Melittin resistance protein PqaB	9.26	22.72	2.45	0.01129
Bll5876 protein	39.63	82.32	2.08	0.00289
Aromatic-L-amino-acid decarboxylase	62.87	128.38	2.04	0.03631
Hydrolase2C alpha/beta fold family	8.07	28.73	3.56	0.00289
Periplasmic thiol:disulfide interchange protein DsbA	530.17	1314.46	2.48	0.00022
Ribonuclease PH	167.36	351.67	2.10	0.00022
FIG004064: hypothetical protein	258.06	751.09	2.91	0.00022
FIG00953808: hypothetical protein	328.25	993.34	3.03	0.00022
Putative stomatin/prohibitin-family membrane protease subunit YbbK	113.75	258.32	2.27	0.00022
Outer membrane porin2C OprD family	660.98	2083.77	3.15	0.00022
YceI-like family protein	747.07	3253.09	4.35	0.00022
Transmembrane sensor	50.41	460.82	9.14	0.00022
Putative phosphatase	20.59	47.27	2.30	0.00022
SSU ribosomal protein S21p	2224.69	5493.47	2.47	0.00022
Ribonuclease P protein component	813.71	1707.76	2.10	0.00022
C4-type zinc finger protein2C DksA/TraR family	24.04	83.75	3.48	0.01394

Putative metal chaperone2C involved in Zn homeostasis2C GTPase of COG0523 family	53.41	159.85	2.99	0.00022
Fe2+-dicitrate sensor2C membrane component	84.76	227.09	2.68	0.00022
Uncharacterized protein ImpC	584.00	1307.98	2.24	0.00022
Uncharacterized protein ImpB	498.65	1347.44	2.70	0.00022
lipoprotein2C putative	238.96	590.25	2.47	0.00159
nitrogen regulation protein NR(I)	95.11	216.72	2.28	0.00022
Probable lipoprotein signal peptide	26.99	54.49	2.02	0.00630
SAM-dependent methyltransferases	43.40	121.30	2.79	0.00040
GTP cyclohydrolase I type 1	117.67	348.33	2.96	0.00022
Protein-N(5)-glutamine methyltransferase PrmB2C methylates LSU ribosomal protein L3p	114.14	242.49	2.12	0.00022
Septum site-determining protein MinC	81.49	235.15	2.89	0.00022
Septum site-determining protein MinD	351.80	930.41	2.64	0.00022
Cell division topological specificity factor MinE	449.70	1149.21	2.56	0.00022
Cold shock protein CspG	8362.96	30572.20	3.66	0.00022
LSU ribosomal protein L20p	3401.37	10191.10	3.00	0.00022
LSU ribosomal protein L35p	2449.49	5129.50	2.09	0.00022
Translation initiation factor 3	2503.87	6259.28	2.50	0.00022
FIG001614: Membrane protein	28.42	93.43	3.29	0.00022
Zn-dependent protease with chaperone function	185.53	474.71	2.56	0.00022
lipoprotein2C putative	150.10	310.97	2.07	0.00022
lipoprotein2C putative	164.11	597.74	3.64	0.00022
Surface lipoprotein	66.62	198.06	2.97	0.00022
methylated-DNA--protein-cysteine methyltransferase-related protein	352.44	85.20	-4.14	0.00022
DNA polymerase IV	55.58	25.75	-2.16	0.00303

Table 5 I Transcription of Hypothetical Protein

Gene_Name	*P. poae control* FPKM	*P. poae treated* FPKM	Fold change	Corrected P value
FIG00960186: Hypothetical protein	2744.40	818.44	-3.35	0.00022
Hypothetical protein	37.55	13.21	-2.84	0.00022
Hypothetical protein	42.81	18.36	-2.33	0.00022
Hypothetical protein	48.67	22.74	-2.14	0.00331
Hypothetical protein	76.07	30.19	-2.52	0.00398
Hypothetical protein	380.99	45.86	-8.31	0.01862
Hypothetical protein	51.67	10.35	-4.99	0.00022
Hypothetical protein	31.46	2.00	-15.73	0.00643
Hypothetical protein	169.17	75.47	-2.24	0.00022
Hypothetical protein PA2244 (similar to DNA topoisomerase IB2C but possibly involved in glycosyl-transfer)	62.13	20.15	-3.08	0.00022
FIG00954920: Hypothetical protein	220.63	74.42	-2.96	0.00424
FIG00963002: Hypothetical protein	351.70	100.41	-3.50	0.00022
Hypothetical protein	83.71	17.62	-4.75	0.00987
Hypothetical protein	17.10	5.27	-3.25	0.01450
Hypothetical protein	78.07	22.82	-3.42	0.00022
Hypothetical protein	230.32	109.00	-2.11	0.00022
Hypothetical protein	221.67	107.84	-2.06	0.00022

Hypothetical protein	38.30	18.78	-2.04	0.00022
Hypothetical protein	123.03	19.82	-6.21	0.00022
Hypothetical protein	113.68	29.26	-3.89	0.00022
Hypothetical protein	17.04	2.33	-7.32	0.02208
Hypothetical protein	186.99	38.35	-4.88	0.00022
Hypothetical protein	457.94	47.12	-9.72	0.00022
Hypothetical YciO protein2C TsaC/YrdC paralog	438.45	216.82	-2.02	0.00022
FIG00955846: Hypothetical protein	1914.55	678.42	-2.82	0.00022
FIG00955324: Hypothetical protein	105.78	28.87	-3.66	0.00022
FIG00955483: Hypothetical protein	371.44	130.87	-2.84	0.00815
FIG00954888: Hypothetical protein	268.82	70.97	-3.79	0.00040
Hypothetical protein	47.28	5.90	-8.02	0.00022
FIG00953349: Hypothetical protein	563.37	276.55	-2.04	0.00316
FIG00963947: Hypothetical protein	1638.53	450.81	-3.63	0.00022
FIG00962374: Hypothetical protein	262.33	99.74	-2.63	0.00022
FIG00953564: Hypothetical protein	72.34	25.57	-2.83	0.00094
Hypothetical protein	93.71	16.37	-5.73	0.00022
Hypothetical protein	47.95	17.35	-2.76	0.00022
Hypothetical protein	56.17	20.97	-2.68	0.00022
Hypothetical protein	68.53	12.41	-5.52	0.04361
Hypothetical protein	305.63	89.70	-3.41	0.00384
Hypothetical protein	395.64	53.75	-7.36	0.00022
FIG00960493: Hypothetical protein	48.37	19.68	-2.46	0.00111
Hypothetical protein	23.04	8.33	-2.77	0.01928
FIG00954362: Hypothetical protein	218.32	13.08	-16.69	0.00022
FIG00953193: Hypothetical protein	164.41	14.41	-11.41	0.00022
Hypothetical protein2C restriction endonuclease-like VRR-NUC domain	135.06	47.46	-2.85	0.00040
Hypothetical protein	609.33	261.75	-2.33	0.01417
Hypothetical protein	237.87	80.00	-2.97	0.00174
Hypothetical protein	54.58	21.06	-2.59	0.00022
FIG00964870: Hypothetical protein	362.62	143.91	-2.52	0.00022
Hypothetical protein	490.64	172.06	-2.85	0.00022
Hypothetical protein	321.48	46.63	-6.89	0.00022
FIG002776: Hypothetical protein	595.80	258.67	-2.30	0.00022
FIG00958844: Hypothetical protein	774.23	198.52	-3.90	0.00022
FIG00961846: Hypothetical protein	459.71	191.64	-2.40	0.03269
FIG00953347: Hypothetical protein	741.68	103.79	-7.15	0.00022
Hypothetical protein	1261.32	544.80	-2.32	0.01117
FIG00958830: Hypothetical protein	544.14	219.65	-2.48	0.00022
FIG00954614: Hypothetical protein	207.06	73.79	-2.81	0.00289
Hypothetical protein Pfl_5213	23.23	8.07	-2.88	0.02952
FIG00957412: Hypothetical protein	1999.10	741.28	-2.70	0.00022
Hypothetical protein	346.95	113.57	-3.05	0.00076
Hypothetical protein	918.76	383.95	-2.39	0.00022
Hypothetical protein	955.57	113.55	-8.42	0.00022
Hypothetical protein	177.66	45.15	-3.94	0.00022
FIG00955308: Hypothetical protein	1996.51	712.07	-2.80	0.00022
FIG006285: Hypothetical protein	1018.17	220.25	-4.62	0.00022

Hypothetical protein	234.41	81.53	-2.88	0.00022
Hypothetical protein	235.83	31.82	-7.41	0.00780
Hypothetical protein	781.72	165.05	-4.74	0.00022
FIG00954094: Hypothetical protein	3393.06	802.57	-4.23	0.01608
FIG00954767: Hypothetical protein	2866.86	1167.13	-2.46	0.00022
Hypothetical protein	6664.68	1745.10	-3.82	0.00022
Hypothetical protein	140.58	28.21	-4.98	0.00189
FIG00957636: Hypothetical protein	355.61	150.87	-2.36	0.00232
Hypothetical protein	57.94	17.33	-3.34	0.00022
Hypothetical protein	23.91	10.16	-2.35	0.00127
FIG00953885: Hypothetical protein	91.42	19.98	-4.58	0.00022
Hypothetical protein	29.48	12.34	-2.39	0.00159
FIG00959545: Hypothetical protein	509.22	237.39	-2.15	0.00022
Hypothetical protein	55.60	20.58	-2.70	0.00076
Hypothetical protein	79.59	13.56	-5.87	0.04045
Hypothetical protein	60.74	20.73	-2.93	0.00144
FIG00956570: Hypothetical protein	302.10	61.36	-4.92	0.00998
Hypothetical protein	168.20	45.88	-3.67	0.00022
FIG00963086: Hypothetical protein	316.32	47.31	-6.69	0.00022
FIG002188: Hypothetical protein	85.63	5.08	-16.87	0.00022
Hypothetical protein	1582.76	706.99	-2.24	0.00022
FIG00965925: Hypothetical protein	2568.34	615.05	-4.18	0.00022
FIG00953482: Hypothetical protein	92.34	32.78	-2.82	0.00022
FIG00957090: Hypothetical protein	276.35	61.62	-4.48	0.00436
Hypothetical protein	1091.18	242.45	-4.50	0.00022
Hypothetical protein	217.52	64.86	-3.35	0.03974
Hypothetical protein	40.65	11.64	-3.49	0.00040
FIG00964012: Hypothetical protein	235.46	46.90	-5.02	0.00022
FIG00953333: Hypothetical protein	116.45	41.74	-2.79	0.00022
Hypothetical protein	51.47	14.55	-3.54	0.00022
Hypothetical protein	160.86	22.47	-7.16	0.00022
FIG00954698: Hypothetical protein	208.02	37.34	-5.57	0.04763
FIG00956396: Hypothetical protein	80.60	39.42	-2.04	0.01655
FIG00958504: Hypothetical protein	1650.08	337.51	-4.89	0.00022
Hypothetical protein	209.42	77.87	-2.69	0.03958
FIG00954216: Hypothetical protein	450.47	76.75	-5.87	0.00022
FIG00960839: Hypothetical protein	223.54	74.97	-2.98	0.00022
FIG00956889: Hypothetical protein	694.68	137.30	-5.06	0.00022
Hypothetical protein	282.80	49.84	-5.67	0.00022
FIG00955280: Hypothetical protein	891.02	103.26	-8.63	0.00022
Hypothetical protein	81.48	34.65	-2.35	0.00022
FIG00962118: Hypothetical protein	707.10	137.02	-5.16	0.00022
Hypothetical protein	53.90	16.94	-3.18	0.00022
FIG00954755: Hypothetical protein	331.17	145.27	-2.28	0.04680
Hypothetical protein	639.83	92.04	-6.95	0.00022
FIG00954871: Hypothetical protein	672.24	238.01	-2.82	0.00022
Hypothetical protein	37.22	17.11	-2.18	0.00022
Hypothetical protein	125.67	35.45	-3.54	0.00022
Hypothetical protein	47.59	11.96	-3.98	0.00022
Hypothetical protein	45.13	11.99	-3.77	0.00202

Hypothetical protein	34.64	3.32	-10.45	0.01553
Hypothetical protein	178.56	21.06	-8.48	0.00022
FIG00957554: Hypothetical protein	711.36	224.01	-3.18	0.00022
Hypothetical protein	1050.79	253.91	-4.14	0.00022
Hypothetical protein	249.42	69.15	-3.61	0.03401
Hypothetical protein	4076.26	1422.67	-2.87	0.00022
FIG00953549: Hypothetical protein	4236.86	1108.12	-3.82	0.00022
FIG00955509: Hypothetical protein	634.19	279.63	-2.27	0.00541
Hypothetical protein	2219.13	126.67	-17.52	0.00022
Hypothetical protein	437.03	166.68	-2.62	0.00022
FIG028932: Hypothetical protein	85.50	33.42	-2.56	0.00804
Hypothetical protein	114.90	46.88	-2.45	0.01794
Hypothetical protein	553.29	151.23	-3.66	0.00316
Hypothetical protein	306.60	30.95	-9.91	0.00022
FIG00953113: Hypothetical protein	104.13	48.47	-2.15	0.01021
Hypothetical protein	43.06	11.18	-3.85	0.02546
Hypothetical protein Pfl_5213	43.66	13.95	-3.13	0.00384
Hypothetical protein	903.10	223.63	-4.04	0.00022
Hypothetical protein	41.00	9.99	-4.10	0.00022
Hypothetical protein	245.40	18.64	-13.16	0.00022
Hypothetical protein	77.80	16.01	-4.86	0.00022
FIG00961586: Hypothetical protein	498.76	159.80	-3.12	0.00022
Hypothetical protein	151.14	54.10	-2.79	0.03051
Hypothetical protein	36.77	17.56	-2.09	0.00260
FIG00957146: Hypothetical protein	401.77	115.06	-3.49	0.00022
FIG00955714: Hypothetical protein	207.29	100.62	-2.06	0.01044
Hypothetical protein	2419.48	600.46	-4.03	0.00643
Hypothetical protein	2883.46	597.63	-4.82	0.00022
Hypothetical protein	228.19	30.25	-7.54	0.00022
Hypothetical protein	163.77	65.55	-2.50	0.00022
Hypothetical protein	344.52	127.12	-2.71	0.00753
Hypothetical protein	63.55	18.64	-3.41	0.03683
Hypothetical protein	139.54	16.59	-8.41	0.00022
FIG00953394: Hypothetical protein	270.40	54.48	-4.96	0.00022
FIG00956726: Hypothetical protein	135.99	61.67	-2.21	0.02089
FIG00956879: Hypothetical protein	227.16	30.22	-7.52	0.00022
Hypothetical protein	137.63	43.40	-3.17	0.00022
Hypothetical protein	55.55	13.84	-4.01	0.00059
Hypothetical protein	141.78	25.35	-5.59	0.00159
FIG00953060: Hypothetical protein	2313.04	273.49	-8.46	0.00246
Hypothetical protein	42.19	16.47	-2.56	0.00217
FIG00953562: Hypothetical protein	310.91	146.32	-2.12	0.00217
FIG00953167: Hypothetical protein	3218.33	861.73	-3.73	0.00022
Hypothetical protein	660.77	189.67	-3.48	0.00144
Hypothetical protein	960.19	439.12	-2.19	0.00022
FIG00953874: Hypothetical protein	384.19	70.09	-5.48	0.00111
Hypothetical protein	150.19	71.68	-2.10	0.04712
FIG00956858: Hypothetical protein	221.54	100.11	-2.21	0.00528
Hypothetical protein	557.10	266.41	-2.09	0.00159
FIG024285: Hypothetical protein	4213.80	2059.26	-2.05	0.00022

Hypothetical protein	44.77	356.52	7.96	0.02381
Hypothetical protein	16.88	82.55	4.89	0.00217
FIG00958773: Hypothetical protein	264.59	544.81	2.06	0.00040
FIG00953950: Hypothetical protein	30.92	76.55	2.48	0.00826
Hypothetical protein	17.25	353.79	20.51	0.00022
FIG00965772: Hypothetical protein	10.07	325.98	32.38	0.00436
Hypothetical protein	14.38	905.23	62.94	0.00475
Hypothetical protein	179.47	816.27	4.55	0.00189
FIG00963784: Hypothetical protein	234.04	732.48	3.13	0.00022
Hypothetical protein	374.68	1474.07	3.93	0.00022
FIG00961830: Hypothetical protein	29.99	107.36	3.58	0.00488
FIG00959125: Hypothetical protein	4639.71	17001.20	3.66	0.00022
FIG00953674: Hypothetical protein	252.59	820.96	3.25	0.00040
FIG00955097: Hypothetical protein	105.51	542.84	5.15	0.00232
FIG00958024: Hypothetical protein	48.05	104.07	2.17	0.02836
Hypothetical protein	174.60	1219.73	6.99	0.00022
Hypothetical protein	218.61	1202.24	5.50	0.00040
FIG00958640: Hypothetical protein	33.84	77.46	2.29	0.04979
FIG00966283: Hypothetical protein	107.93	270.51	2.51	0.00022
FIG00954480: Hypothetical protein	79.42	182.46	2.30	0.00022
FIG00953102: Hypothetical protein	207.50	8177.27	39.41	0.00022
Hypothetical protein	34.39	211.47	6.15	0.00022
Hypothetical protein	43.43	287.47	6.62	0.00022
Hypothetical protein	31.85	120.41	3.78	0.02658
Hypothetical protein	55.19	140.03	2.54	0.00022
Hypothetical protein	31.53	183.93	5.83	0.00022
Hypothetical protein	39.81	261.04	6.56	0.00022
Hypothetical protein	24.28	212.33	8.75	0.00022
Hypothetical protein	28.52	224.35	7.87	0.00022
Hypothetical protein	47.47	257.80	5.43	0.00022
Hypothetical protein	174.35	427.84	2.45	0.00059
Hypothetical protein	18.16	56.32	3.10	0.00331
Hypothetical protein	80.51	200.45	2.49	0.00022
FIG00953595: Hypothetical protein	491.56	2866.44	5.83	0.00022
FIG00955830: Hypothetical protein	119.14	248.51	2.09	0.01730
FIG00956005: Hypothetical protein	647.10	1567.51	2.42	0.00022
Hypothetical protein	51.29	843.73	16.45	0.00022
FIG00955916: Hypothetical protein	469.65	1325.33	2.82	0.00022
FIG002188: Hypothetical protein	108.13	245.22	2.27	0.00022
FIG003461: Hypothetical protein	68.16	212.55	3.12	0.00022
FIG01220986: Hypothetical protein	35.98	154.50	4.29	0.00022
FIG00954572: Hypothetical protein	51.33	137.04	2.67	0.00111
Uncharacterized protein conserved in bacteria	63.77	186.00	2.92	0.00022
Alpha/beta hydrolase fold	28.60	73.98	2.59	0.00076
Hypothetical protein	342.72	1371.01	4.00	0.00022
FIG00964523: Hypothetical protein	100.36	516.96	5.15	0.00022
FIG00953362: Hypothetical protein	57.06	168.81	2.96	0.00022
Hypothetical protein	94.96	264.44	2.78	0.00076
Hypothetical protein	34.23	80.08	2.34	0.00022

Hypothetical protein	26.64	70.26	2.64	0.04435
Hypothetical protein	31.49	88.04	2.80	0.00022
FIG00961517: Hypothetical protein	20.36	64.86	3.19	0.00022
Hypothetical protein	454.40	1078.70	2.37	0.00059
Hypothetical protein	16057.20	36250.80	2.26	0.00174
FIG00956224: Hypothetical protein	105.82	219.34	2.07	0.00022

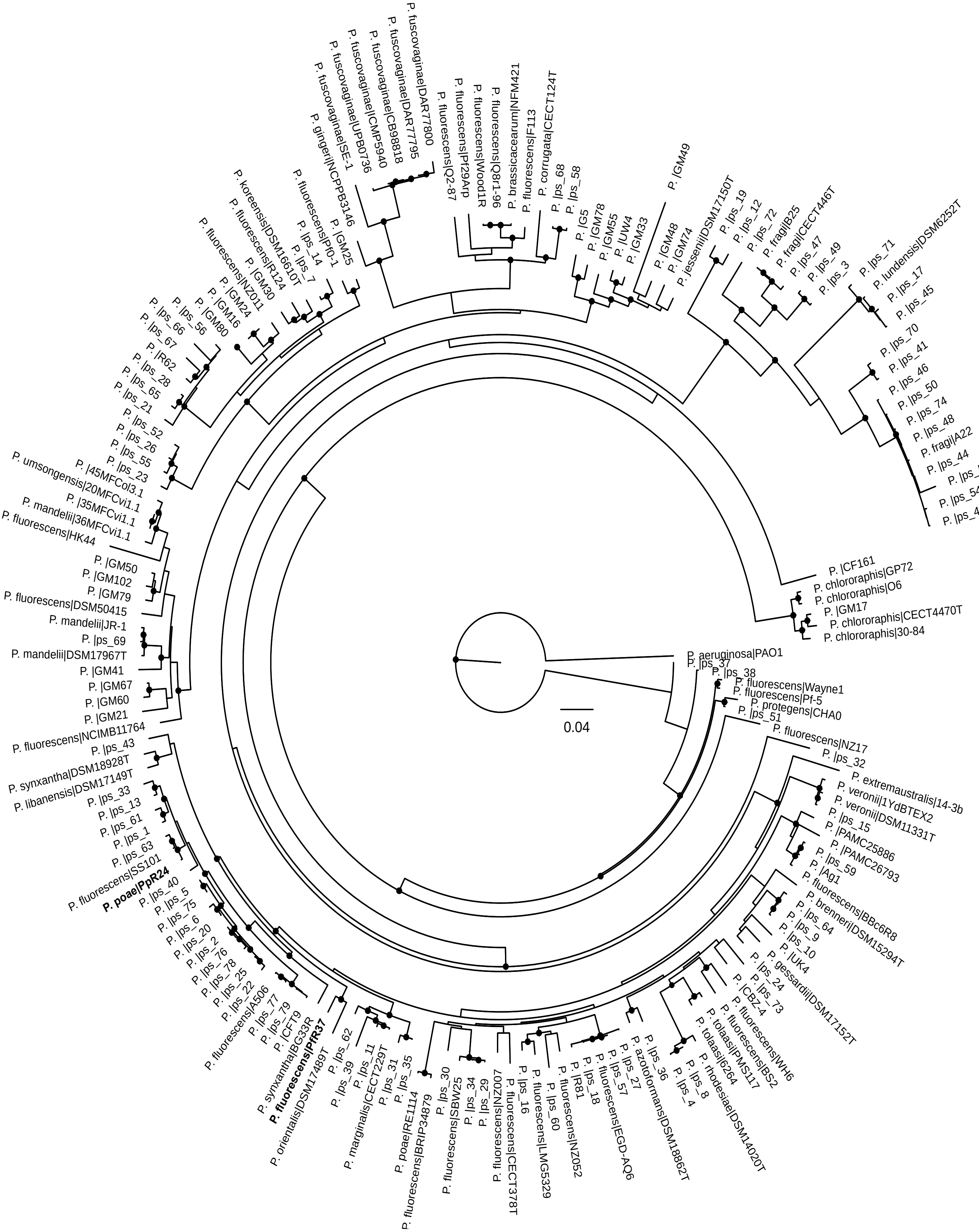

Figure 8: Maximum Likelihood (ML) tree of the 177 *Pseudomonas fluorescens* related strains based on the MLST scheme of Andreani *et al*. (2014) rooted with *Pseudomonas aeruginosa* strain PAO1. Trees were drawn to scale and branches length represents the number of base substitutions per site. Nodes annotated with a circle are supported by bootstraps values superior to 70%. The scale bar depicts branch length of tree.