Contig	**Gene function**	**Position in p34998-210.894kb**			**% protein sequence identity**		
		start	**stop**	**length (bp)**	**p34998**	**pENTd_4**	**pKOX105**
1	Hypotetical protein	36	245	210	-	-	-
1	Hypotetical protein	326	565	240	-	-	-
1	Hypotetical protein	665	784	120	-	-	-
1	Hypotetical protein	2865	1996	870	-	-	-
1	Putative replicase	3343	3080	264	-	-	-
1	Mobilization protein, MobC	3876	4220	345	-	-	-
2	Mobile element protein	102	281	180	-	-	-
2	Mobile element protein	102	281	180	98.31	-	-
2	Hypotetical protein	1362	970	393	100	-	-
2	Mobile element protein	2631	1708	924	99.67	-	-
2	Hypotetical protein	3121	2960	162	100	-	-
2	Hypotetical protein	3234	3425	192	100	-	-
2	Hypotetical protein	3475	3756	282	100	-	-
2	Hypotetical protein	4228	4097	132	100	-	-
2	Putative phage inhibition, colicin resistance and tellurite resistance protein	5560	4319	1242	100	-	-
2	Tellurium resistance protein, TerD	6564	5989	576	100	-	-
2	Tellurium resistance protein, TerD	7210	6632	579	100	-	-
2	Integral membrane protein, TerC	8299	7259	1041	100	-	-
2	Tellurite resistance protein, TerB	8777	8322	456	100	-	-
2	Tellurium resistance protein, TerA	9957	8800	1158	100	-	-
2	Tellurium resistance protein, TerD	10538	9957	582	100	-	-
2	Carbamoylphosphate synthase large subunit	10860	11918	1059	100	-	-

2	Adenine/guanine phosphoribosyltransferases and related PRPP-binding proteins	11928	13070	1143	100	-	-
2	Hypotetical protein	13063	13836	774	100	-	-
2	Putative ATP/GTP-binding protein protein	13838	14917	1080	100	-	-
2	Citrate lyase beta chain (EC 4.1.3.6)	14917	15873	957	100	-	-
2	Hypotetical protein	15884	17092	1209	100	-	-
2	TerW	17110	17577	468	100	-	-
2	Hypotetical protein	17878	17747	132	100	-	-
2	Hypotetical protein	18041	18679	639	100	-	-
2	Putative tellurium resistance protein	18702	19343	642	100	-	-
2	Hypotetical protein	19343	19981	639	100	-	-
2	Hypotetical protein	20067	21107	1041	99.71	-	-
2	Hypotetical protein	21107	22744	1638	100	-	-
2	Putative kinase protein	22761	24269	1509	100	-	-
2	Mobile element protein	25152	24280	873	100	-	-
2	Mobile element protein	25994	25212	783	100	-	-
2	Mobile element protein	27013	25991	1023	100	-	-
2	Mobile element protein	27419	27108	312	100	-	-
2	Hypotetical protein	29433	28273	1161	100	-	-
2	Integrase/recombinase	29657	30634	978	100	-	28.46
2	Hypotetical protein	31263	30847	417	100	-	-
2	Hypotetical protein	31781	31254	528	99.43	-	-
2	Outer membrane protein assembly factor YaeT precursor	32691	31906	786	100	-	-
2	IncF plasmid conjugative transfer DNA-nicking and unwinding protein, TraI	38142	32719	5424	100	25.14	34.84
2	IncF plasmid conjugative transfer protein, TraD	40694	38139	2556	100	26.18	27.8

2	Hypotetical protein	41123	40809	315	100	-	-
2	IncF plasmid conjugative transfer surface exclusion protein, TraT	41913	41482	432	100	-	-
2	IncF plasmid conjugative transfer protein, TraG	46149	42751	3399	100	-	-
2	IncF plasmid conjugative transfer pilus assembly protein, TraH	47513	46149	1365	100	-	-
2	Hypotetical protein	47910	47506	405	100	-	-
2	Hypotetical protein	48131	47907	225	98.65	-	-
2	IncF plasmid conjugative transfer protein, TrbB	48796	48188	609	100	-	-
2	Hypotetical protein	49004	48786	219	100	-	-
2	Hypotetical protein	49492	49001	492	100	-	-
2	IncF plasmid conjugative transfer pilus assembly protein, TraF	50284	49502	783	100	-	-
2	IncF plasmid conjugative transfer protein, TraN	52116	50281	1836	100	-	-
2	IncF plasmid conjugative transfer protein, TrbC	52739	52113	627	100	-	-
2	IncF plasmid conjugative transfer pilus assembly protein, TraU	53748	52750	999	100	-	-
2	Hypotetical protein	54068	53745	324	100	-	-
2	Hypotetical protein	54339	54124	216	100	-	-
2	Hypotetical protein	55457	54444	1014	100	-	-
2	Hypotetical protein	55684	55448	237	100	-	-
2	Hypotetical protein	56067	55675	393	100	-	-
2	IncF plasmid conjugative transfer pilus assembly protein, TraW	56699	56064	636	100	-	-
2	IncF plasmid conjugative transfer protein, TrbI	57109	56696	414	100	-	-
2	IncF plasmid conjugative transfer pilus assembly protein, TraC	59715	57106	2610	100	-	-
2	Hypotetical protein	59966	59712	255	100	-	-
2	IncF plasmid conjugative transfer pilus assembly protein, TraV	60505	59963	543	100	-	-
2	Hypotetical protein	60801	60571	231	98.68	-	-

2	Hypotetical protein	61344	60856	489	100	-	-
2	Hypotetical protein	61798	61358	441	100	-	-
2	Hypotetical protein	62079	61795	285	100	-	-
2	Hypotetical protein	62315	62076	240	100	-	-
2	IncF plasmid conjugative transfer pilus assembly protein, TraB	63731	62328	1404	100	-	-
2	IncF plasmid conjugative transfer pilus assembly protein, TraK	64468	63728	741	100	-	-
2	IncF plasmid conjugative transfer pilus assembly protein, TraE	65061	64480	582	100	-	-
2	Hypotetical protein	65369	65067	303	100	-	-
2	Hypotetical protein	65726	65373	354	100	-	-
2	Hypotetical protein	65923	66564	642	100	-	-
2	Hypotetical protein	66992	66597	396	100	-	-
2	Hpa2 protein	67632	68105	474	100	44.8	-
2	Unnamed protein product	68955	68134	822	100	-	-
2	Hypotetical protein	69265	68972	294	100	-	-
2	Hypotetical protein	69935	69669	267	100	-	-
2	Hypotetical protein	70289	69954	336	100	-	-
2	possible type I restriction enzyme M subunit	71122	70331	792	100	-	-
2	Succinate dehydrogenase flavoprotein subunit (EC 1.3.99.1)	71363	71163	201	100	-	-
2	Hypotetical protein	71912	71451	462	100	-	-
2	Hypotetical protein	72413	71973	441	100	-	-
2	Hypotetical protein	73321	73163	159	100	-	-
2	Mobile element protein	73393	74610	1218	100	-	-
2	RelB/StbD replicon stabilization protein (antitoxin to RelE/StbE)	74954	74781	174	100	45.71	-
2	Mobile element protein	75339	75602	264	100	-	-

2	Mobile element protein	75629	76459	831	100	-	-
2	Hypotetical protein	76495	76860	366	100	-	-
2	Putative ORF1 [Plasmid pTOM9]	76904	77641	738	100	-	-
2	Putative (L31491) ORF2; putative [Plasmid pTOM9]	77655	78344	690	100	-	-
2	Chromate transport protein, ChrA	79751	78375	1377	100	-	-
2	Chromate resistance protein, ChrB	80685	79708	978	100	-	-
2	Hypotetical protein	80763	80903	141	100	-	-
2	Hypotetical protein	81032	81403	372	100	-	-
2	Hypotetical protein	81466	82386	921	100	-	-
2	Hypotetical protein	82440	83198	759	100	-	-
2	Hypotetical protein	83415	83299	117	100	-	-
2	Probable NreB protein	83432	84730	1299	100	-	-
2	NreA-like protein	84836	85105	270	100	-	-
2	Nickel/cobalt efflux transporter, RcnA	85118	86248	1131	100	-	-
2	Protein ygiW precursor	86422	86832	411	100	-	-
2	Mobile element protein	88407	87088	1320	100	-	-
2	Acetyltransferase	89332	88847	486	100	-	-
2	Hypotetical protein	89586	89320	267	100	-	-
2	Transcriptional regulator, ArsR family	89959	90210	252	100	-	74.29
2	Arsenic resistance protein ArsH	90212	90925	714	100	-	-
2	Hypotetical protein	90934	91479	546	100	-	-
2	Arsenic resistance operon trans-acting repressor, ArsD	91555	91917	363	100	-	-
2	Arsenic pump-driving ATPase (EC 3.6.3.16)	91938	93695	1758	100	-	-
2	Phage tail assembly protein	94158	93763	396	100	-	-

2	Mobile element protein	94149	94553	405	100	-	-
2	Mobile element protein	94550	94897	348	100	-	-
2	Mobile element protein	94946	96484	1539	100	-	-
2	Hypotetical protein	96627	96818	192	100	-	-
2	Arsenate reductase (EC 1.20.4.1)	97278	96853	426	100	-	-
2	Arsenic efflux pump protein	98580	97291	1290	100	-	-
2	Arsenic pump-driving ATPase (EC 3.6.3.16)	100379	98628	1752	100	-	-
2	Arsenic resistance operon trans-acting repressor, ArsD	100759	100397	363	100	-	-
2	Arsenic resistance operon repressor	101157	100807	351	100	-	-
2	Mobile element protein	102178	101375	804	100	-	-
2	Mobile element protein	102744	102235	510	100	-	-
2	Hypotetical protein	103190	102966	225	100	-	-
2	Hypotetical protein	103417	103187	231	100	-	-
2	PsiA protein	104145	103414	732	100	-	-
2	PsiB protein	104576	104142	435	100	-	-
2	Hypotetical protein	106626	104614	2013	100	-	-
2	Hypotetical protein	107059	106694	366	100	-	-
2	Hypotetical protein	107375	107103	273	100	-	-
2	Hypotetical protein	107725	107591	135	100	-	-
2	Hypotetical protein	107866	108045	180	92.19	-	-
2	Hypotetical protein	108325	108095	231	98.46	-	-
2	Orf52 protein	108753	108343	411	100	-	-
2	Putative antirestriction protein	109224	108796	429	100	-	-
2	Hypotetical protein	109548	109417	132	100	-	-

2	Hypotetical protein	110003	109581	423	100	-	-
2	Putative cytoplasmic protein	110280	110059	222	100	-	-
2	Adenine-specific methyltransferase (EC 2.1.1.72)	110969	110277	693	100	-	-
2	Hypotetical protein	111959	111492	468	100	-	-
2	Hypotetical protein	111958	112074	117	100	-	-
2	Hypotetical protein	112537	112334	204	100	-	-
2	Hypotetical protein	112829	112566	264	100	-	-
2	Mediator of plasmid stability	113495	112833	663	100	-	-
2	Putative stability/partitioning protein encoded within prophage CP-933T	114472	113498	975	100	-	-
2	Error-prone repair protein UmuD	114701	115132	432	100	-	-
3	Hypotetical protein	148	1494	1347	100	-	-
3	Hypotetical protein	2190	2306	117	100	-	-
3	Hypotetical protein	2440	3270	831	100	-	-
3	Hypotetical protein	3848	3976	129	-	-	-
3	Putative Glyoxalase/bleomycin resistance protein/dioxygenase family protein	4019	4837	819	100	-	-
3	Acetyltransferase	5689	5204	486	100	-	-
3	Hypotetical protein	5943	5677	267	100	-	-
3	Hypotetical protein	6560	6303	258	100	-	-
3	Replication initiation protein	6596	7609	1014	100	-	-
3	Hypotetical protein	8331	8492	162	-	-	-
3	Putative membrane protein	8560	9366	807	100	-	-
3	Hypotetical protein	9670	9341	330	100	-	-
3	Hypotetical protein	10091	9753	339	100	-	-
3	IncF plasmid conjugative transfer pilin acetylase, TraX	10876	10106	771	100	-	-

3	Hypotetical protein	11734	11243	492	100	-	-
3	Putative transcriptional regulators containing the CopG/Arc/MetJ DNA-binding domain and a metal-binding domain	11909	12169	261	100	-	-
3	Hypotetical protein	12156	12452	297	100	-	-
3	Probable copper-binding protein	13106	12672	435	100	-	-
3	Hypotetical protein	13105	13242	138	100	-	-
3	Heavy metal sensor histidine kinase	14724	13324	1401	99.57	-	-
3	DNA-binding heavy metal response regulator	15401	14721	681	100	-	-
3	Copper resistance protein D	16385	15456	930	100	-	-
3	Copper resistance protein CopC	16728	16390	339	100	-	-
3	Copper resistance protein B	17706	16810	897	100	-	-
3	Multicopper oxidase	19523	17706	1818	100	-	-
3	Copper-binding protein PcoE	19758	20207	450	100	-	-
3	Cell wall endopeptidase, family M23/M37	20496	21233	738	100	-	-
3	Hypotetical protein	21464	21267	198	100	-	-
3	Lead, cadmium, zinc and mercury transporting ATPase (EC 3.6.3.3) (EC 3.6.3.5); Copper-translocating P-type ATPase (EC 3.6.3.4)	23493	21505	1989	100	-	-
3	Hypotetical protein	23599	23892	294	-	-	-
3	CopG protein	24514	24074	441	100	-	-
3	Cobalt-zinc-cadmium resistance protein CzcA; Cation efflux system protein CusA	27746	24600	3147	100	-	-
3	Cobalt/zinc/cadmium efflux RND transporter, membrane fusion protein, CzcB family	29049	27757	1293	100	-	-
3	Cation efflux system protein CusF precursor	29516	29163	354	100	-	-
3	Cation efflux system protein CusC precursor	30930	29545	1386	100	-	-
3	Copper-sensing two-component system response regulator CusR	31120	31800	681	100	-	-
3	Osmosensitive K+ channel histidine kinase KdpD (EC 2.7.3.-)	31793	33268	1476	100	-	-
3	Silver-binding protein	33402	33950	549	100	-	-

3	Putative exported protein	34096	34446	351	100	-	-
3	Hnh endonuclease	35540	34632	909	100	-	-
3	Hypotetical protein	35966	36085	120	100	-	-
3	Hypotetical protein	37109	36087	1023	100	-	-
3	Predicted ATP-dependent endonuclease of the OLD family	38656	37094	1563	100	-	-
3	VagD	39140	38730	411	100	-	-
3	Virulence-associated protein, VagC	39367	39137	231	100	-	-
3	Hypotetical protein	40330	40860	531	100	-	-
3	Resolvase	40879	41655	777	100	-	-
3	Hypotetical protein	41939	41823	117	100	-	-
3	Hypotetical protein	42007	42120	114	100	-	-
3	DNA replication protein	43368	42358	1011	100	-	-
3	Chromosome (plasmid) partitioning protein ParA	44109	45275	1167	100	23.98	-
3	Chromosome (plasmid) partitioning protein ParB	45275	46240	966	100	-	-
3	Error-prone, lesion bypass DNA polymerase V (UmuC)	47459	46890	570	100	-	-
4	Dihydropteroate synthase (EC 2.5.1.15)	432	1247	816	100	-	-
4	Aminoglycoside 3'-phosphotransferase (EC 2.7.1.95), Streptomycin 3'-kinase StrA (EC 2.7.1.87)	1308	2111	804	100	-	-
4	Aminoglycoside 3'-phosphotransferase 2 (EC 2.7.1.95), Streptomycin 3'-kinase StrB (EC 2.7.1.87)	2111	2947	837	100	-	-
4	Hypotetical protein	3105	3245	141	-	-	-
4	Beta-lactamase (EC 3.5.2.6)	4528	3668	861	100	-	-
4	Mobile element protein	5112	4711	402	100	-	-
4	Mobile element protein	5267	5115	153	97.92	-	-
4	Mobile element protein	5272	8436	3165	100	-	-
4	Hypotetical protein	8604	8461	144	100	-	-

4	Universal stress protein UspA and related nucleotide-binding proteins	9428	8601	828	100	-	-
4	Sulfate permease	10925	9447	1479	100	-	-
4	Hypotetical protein	10959	11072	114	100	-	-
4	Hypotetical protein	11259	11059	201	100	-	-
4	Hypotetical protein	11393	11256	138	100	-	-
4	Arsenical resistance operon repressor	11408	11761	354	100	-	-
4	Arsenic efflux pump protein	11857	13140	1284	100	-	-
4	Arsenate reductase (EC 1.20.4.1)	13190	13618	429	100	-	-
4	Arsenic resistance protein, ArsH	14458	13676	783	99.58	-	-
5	DNA-invertase	571	14	558	100	-	-
5	Hypotetical protein	936	565	372	100	-	-
5	Hypotetical protein	1457	933	525	100	-	-
5	TniA putative transposase	1526	3205	1680	100	-	-
5	TniB NTP-binding protein	3208	4116	909	100	-	-
5	TniQ	4113	5330	1218	100	-	-
5	Resolvase/integrase	5391	6005	615	100	-	-
5	Mercuric transport protein, MerE	6294	6058	237	100	-	-
5	Mercuric resistance operon coregulator	6656	6291	366	100	-	-
5	Mercuric ion reductase (EC 1.16.1.1)	8319	6673	1647	100	-	-
5	MerF	8561	8316	246	100	-	-
5	Periplasmic Hg^{+2} binding protein	8839	8564	276	100	-	-
5	Mercuric transport protein, MerT	9205	8855	351	100	-	-
5	Mercuric resistance operon regulatory protein	9277	9711	435	100	-	-
6	Probable membrane protein STY4561	134	643	510	99.38	54.68	-

6	Hypotetical protein	648	854	207	-	-	-
6	Mobile element protein	1131	865	267	100	-	-
6	DNA-cytosine methyltransferase (EC 2.1.1.37)	1236	2669	1434	100	-	-
6	Hypotetical protein	3911	2703	1209	100	-	-
6	TniB NTP-binding protein	4046	3924	123	100	-	-
6	Mobile element protein	4972	4178	795	100	-	100
6	TniB NTP-binding protein	5052	5405	354	100	-	-
6	Dihydrofolate reductase (EC 1.5.1.3)	6045	5572	474	100	-	100
6	Integron integrase, IntI	6201	7214	1014	100	40	100
7	Hypotetical protein	283	399	117	-	-	-
7	Hypotetical protein	815	603	213	-	-	-
7	Helix-turn-helix motif	1063	818	246	-	-	-
7	Hypotetical protein	1179	1051	129	-	-	-
7	Putative membrane protein	1487	1185	303	-	-	-
7	LOS biosynthesis enzyme LBGB	2374	1763	612	-	-	-
7	Hypotetical protein	3249	3028	222		-	-
7	Hypotetical protein	3300	3446	147	-	-	-
7	Hypotetical protein	4127	3690	438	-	-	-
7	Hypotetical protein	4795	4247	549	-	75.27	-
7	Hypotetical protein	5211	5074	138	-	-	-
7	Hypotetical protein	6077	5472	606	-	84.02	-
7	Hypotetical protein	6661	6449	213	-	84.29	-
7	Hypotetical protein	7110	6787	324	-	96.26	-
7	Hypotetical protein	7367	7185	183	-	95	-

8	Hypotetical protein	468	283	186	-	100	-
8	Hypotetical protein	1054	1269	216	-	91.55	-
8	Stability protein, StdB	1426	2004	579	-	90.84	35.04
8	Hypotetical protein	1968	2123	156	-	98.04	-
8	zinc metalloproteinase Mpr protein	2622	3239	618	-	100	64.37
8	Hypotetical protein	3280	3414	135	-	-	-
8	Hypotetical protein	4146	3778	369	-	98.36	-
8	Hypotetical protein	4645	4187	459	-	100	-
8	Hypotetical protein	4978	4697	282	-	100	-
8	COG2214: DnaJ-class molecular chaperone	6012	5734	279	-	100	-
8	DnaJ-like protein	6248	5979	270	-	96.3	-
8	Hypotetical protein	6724	6446	279	-	100	-
8	Hypotetical protein	7683	7489	195	-	96.88	-
8	Hypotetical protein	8286	7936	351	-	97.41	-
8	DNA sulfur modification protein, DndB	9017	8397	621	-	99.47	-
9	Hypotetical protein	130	8	123	-	-	-
9	Hypotetical protein	582	193	390	-	87.39	-
9	IncI1 plasmid conjugative transfer lipoprotein, PilN	1094	807	288	-	100	-
9	Hypotetical protein	2970	2071	900	-	97.81	-
9	ATPase required for both assembly of type IV secretion complex and secretion of T-DNA complex, VirB11	4461	3859	603	-	93.57	-
9	Inner membrane protein of type IV secretion of T-DNA complex, TonB-like, VirB10	5632	4475	1158	-	95.84	25.29
9	Outer membrane and periplasm component of type IV secretion of T-DNA complex, VirB9	5801	5622	180	-	96.61	42.62
9	Outer membrane and periplasm component of type IV secretion of T-DNA complex, VirB9	6352	5921	432	-	92.42	43.08
9	Inner membrane protein forms channel for type IV secretion of T-DNA complex, VirB8	6874	6458	417	-	97.83	32.59

9	Hypotetical protein	7343	7188	156	-	-	-
9	Hypotetical protein	7937	7764	174	-	96.49	-
9	Hypotetical protein	8074	8238	165	-	-	-
9	Minor pilin of type IV secretion complex, VirB5	8536	8228	309	-	98.04	38.75
9	Minor pilin of type IV secretion complex, VirB5	8879	8670	210	-	96.77	-
9	ATPase required for assembly of type IV secretion complex and secretion of T-DNA complex, VirB4	9130	8876	255	-	97.6	-
9	ATPase required for assembly of type IV secretion complex and secretion of T-DNA complex, VirB4	9885	9172	714	-	94.2	30.81
9	ATPase required for assembly of type IV secretion complex and secretion of T-DNA complex, VirB4	11597	9864	1734	-	95.98	38.81
9	Hypotetical protein	130	8	123	-	94.62	-
9	Hypotetical protein	582	193	390	-	-	-
10	Hypotetical protein	1321	1127	195	-	93.75	-
10	Type II secretion inner membrane protein (PulF)	3518	2628	891	-	98.31	-
10	IncI1 plasmid conjugative transfer ATPase, PilQ	5157	4531	627	-	95.83	-
10	Hypotetical protein	5552	5232	321	-	99	-
11	Shufflon-specific DNA recombinase	36	1172	1137	-	85	-
11	Hypotetical protein	1217	1372	156	-	-	-
11	Hypotetical protein	2920	3045	126	-	92.68	-
11	IncQ plasmid conjugative transfer protein, TraQ (RP4 TrbM homolog)	3072	3620	549	-	92.31	-
11	Serine acetyltransferase (EC 2.3.1.30)	4687	5268	582	-	95.34	-
12	IncF plasmid conjugative transfer protein, TraD	562	1302	741	27.98	98.78	40.34
12	IncW plasmid conjugative relaxase protein, TrwC (TraI homolog)	1299	2282	984	37.14	94.85	47.53
12	Hypotetical protein	2362	2901	540	-	98.87	35.91
12	Hypotetical protein	3023	3199	177	-	-	-
12	IncW plasmid conjugative relaxase protein, TrwC (TraI homolog)	3193	4188	996	22.84	97.89	44.83

12	Hypotetical protein	4175	4363	189	-	90.32	-
12	Hypotetical protein	4550	4416	135	-	-	-
12	Hypotetical protein	4831	4998	168	-	98.18	-
12	Hypotetical protein	5224	5084	141	-	97.73	-
12	Resolvase	5933	5685	249	58.97	97.56	40.58
12	Resolvase	6607	5951	657	44.81	98.08	-
12	Hypotetical protein	7200	7006	195	-	-	-

Table 1S. Sequence-based comparison using BLASTP for each ORF of pHP19 versus the respective ORFs of p34998 (CP012169.1), pENT_d4 (CP08900.1) and pKOX105 (HM126016) plasmids.