Supplementary Table 1

Transcriptome profiles of *Rhodopseudomonas palustris* strains

Cells grown in N-fixing mudium (N-fixing conditions) were compared with cells grown in the same medium supplemented with ammonium sulfate (non-N-fixing conditio

Remark 1 Profile was determined by 3 comparative experiments and 2 calibration experiments, and two slides were used in each experiment (10 slides per profile)
Remark 2 Empty cells indicate that data were not obtained due to the low signal intensities
Remark 3 Definition of gene expression change
Higher in N-fixing conditions: expression ratio (N-fixing conditions/non-N-fixing conditions) is greater than or equal to 2 AND score is less than 0.025 (at least 95% confident that the expresssion ratio of N-fixing conditions/non-N-fixing conditions is positive, i.e., higher in N-fixing conditions)
Lower in N-fixing conditions: expression ratio (N-fixing conditions/non-N-fixing conditions) is less than or equal to 0.5 AND scores is greater than 0.975 (at least 95% confident that the expresssion ratio of N-fixing conditions/non-N-fixing conditions is negative, i.e., lower in N-fixing conditions)
Remark 4 Mo strain (CGA753), V strain (CGA766), and Fe strain (CGA755) refer to Mo nitrogenase only strain, V nitrogenase only strain, and Fe nitrogenase only strain, respectively
Remark 5 Plus V indicates that 10 µM V was added to the growth medium

Col# 1 RPA#
Col# 2 The average expression ratio (N-fixing conditions/non-N-fixing conditions) based on (maximum) 12 comparative experimental data points
Red: average expression ratio is greater than or equal to 2 (greater than or equal to 2-fold higher in N-fixing conditio and Blue: average expression ratio is less than or equal to 0.5 (greater than or equal to 2-fold lower in N-fixing conditio
Col# 3 Score [the probability of logarithmic ratio (N-fixing conditions/non-N-fixing conditions) of expression level below 0] determined by a Markov chain Monte Carlo simulation
Red: score is less than 0.025 (the expression ratio is positive, i.e., high in N-fixing conditio and Blue: score is greater than 0.975 (the expression ratio is negative, i.e., low in N-fixing conditions
Col# 4 Annotation

Col# 1	Col# 2	Col# 3	Col# 2	Col# 3	Col# 2	Col# 3	Col# 2	Col# 3	Col# 2	Col# 3	Col# 4
	Wild-type strain (CGA009)		**Wild-type strain (plus V) (CGA009)**		**Mo strain (CGA753)**		**V strain (plus V) (CGA766)**		**Fe strain (CGA755)**		
RPA#	**W AvRt**	**W Sco**	**WV AvRt**	**WV Sco**	**Mo AvRt**	**Mo Sco**	**V AvRt**	**V Sco**	**Fe AvRt**	**Fe Sco**	**Annotation**
RPA0001	0.665963	0.995	0.66581	0.9995	0.535337	0.9995	0.582471	0.997	0.648473	0.9685	dnaA chromosomal replication initiator protein DnaA 679:2097 forward MW:52624
RPA0002	0.832078	0.945	0.713654	0.999	0.750162	0.991	0.632156	0.999	0.700926	0.9985	dnaN DNA polymerase III beta subunit 2332:3450 forward MW:40401
RPA0003											recF putative RecF protein 3667:4833 forward MW:41676
RPA0004	0.589961	1	0.627573	1	0.876581	0.9285	0.546938	0.998	0.704026	0.991	gyrB DNA gyrase subunit B 5050:7491 forward MW:89311
RPA0005	0.948484	0.736	1.012589	0.448	0.905783	0.853	1.185123	0.0515	2.079792	0.002	hpd 4-hydroxyphenylpyruvate dioxygenase 7673:8791 reverse MW:40713
RPA0006	0.660193	0.987	0.620895	0.9975	0.767535	0.9625	0.990005	0.5265	0.873999	0.9175	CDS transcriptional regulator, AsnC family 8917:9396 forward MW:17592
RPA0007	1.004884	0.467	1.013173	0.462	1.086041	0.19	0.788753	0.9625	0.801843	0.965	CDS putative signal transduction histidine kinase with PAS/PAC domains 9442:10893 reverse MW:51220
RPA0008	0.972158	0.6615	1.094975	0.147	1.083926	0.193	1.013045	0.457	0.969496	0.6055	kaiB circadian clock protein 10890:11174 reverse MW:10217
RPA0009	1.157415	0.1305	1.104502	0.1365	0.883592	0.8835	0.886024	0.8	1.021125	0.4	kaiC circadian clock protein 11184:12875 reverse MW:61906
RPA0010	0.756573	0.93	0.542423	0.9885	0.642433	0.978	0.770893	0.7905	0.640031	0.98	CDS possible glutamate uptake transcriptional regulator, AsnC family 13269:13778 reverse MW:18704
RPA0011	1.538605	0.004	1.250146	0.0475	1.37407	0.011	1.331754	0.071	1.078848	0.3385	CDS conserved hypothetical protein 14266:14514 reverse MW:9325
RPA0012	1.435202	0.048	1.511813	0.0035	1.494955	0.012	1.798991	0.004	1.418852	0.0105	rdxS, fixS possible fixS 14516:14701 reverse MW:6468
RPA0013	1.215864	0.027	1.183082	0.0665	1.195945	0.101	1.239875	0.0345	0.788519	0.9025	rdxI, fixI putative cation (heavy metal) transporting ATPase 14692:16890 reverse MW:77870
RPA0014	1.229704	0.027	1.58493	0.005	1.21545	0.125	1.525197	0.0385	1.034979	0.385	rdxH, fixH conserved hypothetical protein 16925:17428 reverse MW:18109
RPA0015	1.476543	0.003	1.763539	0.001	1.377831	0.022	1.835532	0.0125	1.543146	0.027	fixG, rdxB 4Fe-4S ferredoxin, iron-sulfur binding domain 17445:18902 reverse MW:54555
RPA0016	1.995855	0.0005	1.991599	0	1.948835	0.001	2.142437	0.003	1.549919	0.0035	ccoP, fixP cytochrome-c oxidase fixP chain 19019:19900 reverse MW:31591
RPA0017	1.474059	0.014	1.710393	0.0015	1.54257	0.006	1.414015	0.04	1.094925	0.197	ccoQ, fixQ cytochrome oxidase subunit, small membrane protein 19908:20072 reverse MW:6267
RPA0018	2.109964	0	2.205291	0.0015	2.23222	0.0015	2.169297	0.0045	1.441704	0.0325	ccoO, fixO cytochrome-c oxidase fixO chain 20082:20816 reverse MW:27263
RPA0019	1.818109	0.002	1.738453	0.001	1.941932	0.006	1.832428	0.005	1.333838	0.005	ccoN, fixN cytochrome-c oxidase fixN chain, heme and copper binding subunit 20829:22475 reverse MW:61588
RPA0020	0.729271	0.9785	0.799716	0.968	0.92995	0.7345	0.764698	0.9105	0.708331	0.9925	panE1 Ketopantoate reductase ApbA/PanE 22786:23706 reverse MW:32340
RPA0021	0.823356	0.896	0.753434	0.9755	0.905621	0.7475	0.799699	0.886	0.802977	0.912	CDS possible short chain dehydrogenase 23779:24516 reverse MW:26621
RPA0022											CDS DSBA oxidoreductase 24637:25239 reverse MW:22293
RPA0023	1.016277	0.413	0.891777	0.8805	0.956305	0.701	0.832687	0.9565	0.926943	0.6955	gstA3 possible glutathione transferase 25362:26123 forward MW:28571
RPA0024	0.938735	0.7555	1.132245	0.062	0.912631	0.7995	1.017442	0.4495	1.023153	0.4225	CDS Short-chain dehydrogenase/reductase SDR 26235:27110 reverse MW:30727
RPA0025	1.071125	0.313	0.804989	0.9825	0.978916	0.614	0.794189	0.9775	0.837225	0.959	ggt1 gamma-glutamyltranspeptidase 27385:29118 reverse MW:60414
RPA0026	0.780263	0.993	0.72297	0.997	0.836173	0.9415	0.494706	0.9985	0.682774	0.9815	CDS Major Facilitator Superfamily (MFS) transporter 29224:30621 forward MW:49109
RPA0027	0.626608	0.974	0.539779	0.9995	0.565933	1	0.457924	0.9975	0.51349	0.999	aroG1 2-dehydro-3-deoxyphosphoheptonate aldolase 30837:31931 forward MW:38504
RPA0028	0.825066	0.9675	0.875109	0.914	0.58885	1	0.836575	0.9275	1.121169	0.266	purH bifunctional purine biosynthesis protein 31989:33581 reverse MW:55969
RPA0029	0.845467	0.9365	0.768642	0.996	0.811002	0.983	0.641503	0.999	0.83785	0.962	CDS conserved hypothetical protein 33767:35653 reverse MW:69043
RPA0030	0.574225	0.996	0.608447	0.9805	0.83391	0.9625	0.429529	0.999	0.575819	0.9985	CDS Bacterial Sun/eukaryotic nucleolar Nop1/Nop2 35820:37172 reverse MW:48051
RPA0031	0.720167	0.92			0.825327	0.7185	0.831532	0.8675	0.618629	0.9795	CDS conserved hypothetical protein 37325:37543 forward MW:7774
RPA0032	0.894084	0.841	1.033433	0.437	0.903145	0.8715	0.809264	0.8275	0.846422	0.946	CDS possible Staphylococcal nuclease homologues 37629:38204 forward MW:21361
RPA0033	1.241882	0.1865	0.77885	0.931	1.215192	0.037	0.945283	0.627	0.831397	0.878	CDS conserved hypothetical protein 38208:39092 reverse MW:32310
RPA0034	0.507185	1	0.39952	0.9995	0.542011	0.9995	0.338681	0.9995	0.306156	1	CDS possible flavin containing amine oxidase 39440:40897 forward MW:50840
RPA0035	0.606665	0.996	0.59874	0.9975	0.613304	1	0.657503	0.975	0.617981	0.908	pheT putative phenylalanine-tRNA ligase beta chain 40904:43315 reverse MW:85210
RPA0036	0.702134	0.981	0.813587	0.92	0.727408	0.9975	0.589327	0.9975	0.626656	0.942	CDS conserved unknown protein 43460:43939 reverse MW:17908
RPA0037	0.595524	0.9885	0.873054	0.9605	0.576278	0.9995	0.702	0.995	0.962009	0.6255	pheS phenylalanyl-tRNA synthetase, alpha-subunit 44200:45282 reverse MW:40115
RPA0038	1.078039	0.3495	1.017722	0.388	0.745839	0.987	0.846019	0.961	0.941254	0.694	rplT ribosomal protein L20 45426:45785 reverse MW:13300
RPA0039	0.917195	0.8105	1.179395	0.047	0.775479	0.985	1.0775	0.234	1.182074	0.0665	rpmI 50S ribosomal protein L35 45869:46069 reverse MW:7547
RPA0040	0.933369	0.6405	1.48114	0.016	1.220435	0.069	1.313212	0.0755	1.062968	0.299	infC translation initiation factor IF-3 46403:46981 reverse MW:21922
RPA0041	0.80406	0.96	0.681026	0.9775	0.678227	0.988	0.612673	0.9825	0.760538	0.991	CDS conserved unknown protein 47263:48048 forward MW:28350
RPA0042	1.023413	0.425	0.870792	0.841	0.919883	0.764	1.367083	0.06	1.290854	0.0575	CDS possible iron-sulfur cluster binding protein 48211:49323 reverse MW:40319
RPA0043	0.862491	0.925	1.049005	0.3565	0.81973	0.9355	0.978042	0.5835	0.979389	0.6025	CDS possible glutathione S-transferase 49368:50060 reverse MW:26063
RPA0044	0.768773	0.9845	1.020344	0.407	0.656237	0.9985	0.644429	0.9945	0.803942	0.905	bacA bacitracin resistance protein 50260:51066 forward MW:29341
RPA0045	0.707499	1	0.699705	0.9935	0.823524	0.9745	0.839708	0.9435	0.813824	0.9885	CDS putative NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 51116:52081 reverse MW:33871
RPA0046	0.601368	0.9915	0.724339	0.9965	0.682884	0.998	0.620636	0.9995	0.707856	0.9875	CDS 3'-5' exonuclease 52495:53109 forward MW:22696
RPA0047	0.673268	0.991	0.777338	0.995	0.743545	0.9745	0.598133	0.9945	0.72011	0.997	CDS conserved hypothetical protein 53339:54079 forward MW:26825
RPA0048	0.659016	0.985	0.777336	0.984	0.72573	0.9865	0.57984	0.9985	0.748245	0.986	CDS conserved hypothetical protein 54088:54753 forward MW:23117
RPA0049	0.775013	0.9825	0.840694	0.9755	0.81778	0.9355	0.600636	0.9945	0.793467	0.9825	CDS possible ABC transporter ATP-binding protein (in rpoN upstream) 54870:55835 forward MW:35070
RPA0050	0.840839	0.9515	0.824187	0.9705	0.757602	0.986	0.780755	0.9915	0.945601	0.7615	rpoN RNA polymerase sigma 54 subunit, RpoN 56042:57688 forward MW:59457

RPA0051	0.695703	0.985	0.703335	0.9925	0.781716	0.99	0.760058	0.979	0.642336	0.997	CDS putative sigma-54 modulation protein 57746:58351 forward MW:21946
RPA0052	0.711207	0.998	0.937173	0.8255	0.818963	0.972	0.857854	0.926	0.998565	0.511	ptsN1 putative nitrogen regulatory IIA protein 58627:59088 forward MW:16523
RPA0053	0.943142	0.726	0.881585	0.916	1.079249	0.213	0.938146	0.7175	0.996001	0.5235	CDS conserved hypothetical protein 59691:59957 reverse MW:9239
RPA0054	0.805474	0.95	0.981281	0.6015	1.098177	0.1915	0.986465	0.5395	1.40631	0.002	CDS putative small heat shock protein 60008:60433 reverse MW:15984
RPA0055	0.964558	0.676	0.675063	0.9945	1.000931	0.4955	0.808933	0.915	0.887818	0.9265	ugpC ATP-binding component of sn-glycerol 3-phosphate transport system 60587:61678 reverse MW:38712
RPA0056	0.813583	0.8915	0.67905	0.995	0.936991	0.743	0.594837	0.9895	0.772343	0.986	ugpE sn-glycerol 3-phosphate transport system, integral membrane protein 61681:62529 reverse MW:31620
RPA0057	1.019074	0.4225	0.807082	0.9815	1.052135	0.264	0.680885	0.9885	0.768638	0.9765	ugpA sn-glycerol-3-phosphate transport system permease protein 62529:63410 reverse MW:32728
RPA0058	1.166168	0.2215	0.844232	0.9765	1.235861	0.063	0.773172	0.9795	0.888524	0.9515	ugpB1 putative sn-glycerol 3-phosphate transport system; periplasmic binding protein 63575:64903 reverse MW:48101
RPA0059	0.715825	0.997	0.86528	0.91	0.92929	0.801	0.648413	0.9955	0.547153	1	CDS L-carnitine dehydratase/bile acid-inducible protein F 65126:66331 reverse MW:43272
RPA0060	0.813401	0.939	1.223099	0.106	0.890878	0.9055	0.74058	0.9875	0.857759	0.8065	CDS conserved unknown protein 66656:67057 reverse MW:14461
RPA0061	0.594465	0.999	0.689509	0.9985	0.602112	0.992	0.543884	0.999	0.727604	0.9865	aroA 3-phosphoshikimate 1-carboxyvinyltransferase 67198:68535 forward MW:46372
RPA0062	0.788677	0.935	1.051133	0.268	0.804653	0.9365	0.899276	0.8455	1.003006	0.496	CDS conserved unknown protein 68539:69213 reverse MW:24437
RPA0063	0.977265	0.614	0.805061	0.9805	1.236049	0.012	1.377073	0.064	1.278557	0.092	cmk cytidylate monophosphate kinase 69377:70015 forward MW:22546
RPA0064	1.285695	0.008	1.606353	0.0185	0.794133	0.934	1.259204	0.259	1.408708	0.0595	rpsA ribosomal protein S1 70316:72013 forward MW:62801
RPA0065	0.878238	0.9325	0.713548	0.986	0.913385	0.8465	0.85344	0.8835	1.041888	0.3255	sppA putative protease IV 72242:73222 forward MW:34644
RPA0066	0.780741	0.9685	0.83665	0.965	0.90247	0.818	0.834844	0.8825	0.823109	0.965	ihfB integration host factor beta chain 73388:73702 forward MW:11674
RPA0067	0.917181	0.7825	1.000821	0.5105	0.792582	0.9675	0.908311	0.7545	1.020377	0.4115	CDS conserved unknown protein 73740:74126 forward MW:13968
RPA0068	0.623321	0.986	0.885886	0.953	0.665229	0.999	0.682047	0.992	0.814027	0.9785	trpF putative N-(5'-phosphoribosyl)anthranilate isomerase 74185:74826 forward MW:22677
RPA0069	0.662482	0.9845	0.859251	0.9625	0.601008	0.997	0.608185	0.995	0.747369	0.9585	trpB tryptophan synthase beta chain 74840:76054 forward MW:43570
RPA0070	0.732771	0.982	0.831198	0.9855	0.716709	0.9975	0.643555	0.997	0.809613	0.968	tCDSptophan synthase alpha subunit 76054:76890 forward MW:28607
RPA0071	0.69353	0.9795	0.843765	0.9095	0.696641	0.9805	0.729098	0.99	0.907066	0.798	accD acetyl-CoA carboxylase carboxyltransferase beta subunit 77000:77983 forward MW:35824
RPA0072	0.816009	0.9685	0.791701	0.9865	0.900198	0.79	0.778368	0.964	0.759626	0.9835	folC putative folylpolyglutamate synthase / dihydrofolate synthase 77980:79308 forward MW:47349
RPA0073	0.523955	0.9915	0.563543	0.9865	1.002795	0.494	0.415364	1	0.492246	0.994	trxA thioredoxin 79484:79804 reverse MW:11253
RPA0074	0.539969	0.996			0.871425	0.832			0.58401	0.9735	CDS Possible exonuclease V and helicase activity based on COG assignment 79901:83386 reverse MW:126615
RPA0075	0.880662	0.7405	0.560548	0.9995	0.934266	0.666	0.751031	0.927	0.642426	0.957	CDS conserved hypothetical protein 83383:86532 reverse MW:114172
RPA0076	0.621109	0.9805	0.545529	0.995	0.836445	0.7785	0.929086	0.77	1.004421	0.493	CDS Nucleotidyl transferase 86608:87330 reverse MW:25988
RPA0077	0.879487	0.9085	0.954613	0.6575	1.040922	0.345	1.431918	0.003	1.43003	0.0055	CDS conserved hypothetical protein 87488:87796 reverse MW:11543
RPA0078	0.578091	0.944	0.656262	1	0.575044	0.999	0.524089	0.999	0.537981	0.9995	CDS Protein of unknown function UPF0079 87900:89420 reverse MW:55111
RPA0079	0.450342	0.995	0.414412	1	0.393295	0.998	0.355926	0.999	0.370378	0.9995	CDS sensor histidine kinase with multiple PAS domains 89417:91963 reverse MW:92692
RPA0080	0.754204	0.992	0.65371	0.995	0.651201	0.9995	0.645139	0.9415	0.595056	0.9955	dut putative deoxyuridine 5'triphosphate nucleotidohydrolase 92150:92608 reverse MW:16001
RPA0081	0.863279	0.944	0.882526	0.7825	0.769453	0.986	0.851228	0.917	0.815461	0.9775	coaBC pantothenate metabolism flavoprotein 92605:93951 reverse MW:46828
RPA0082	0.755959	0.9505	0.985448	0.568	0.587526	0.9985	0.645812	0.988	0.809986	0.9315	ubiB ubiquinone biosynthesis protein AarF, a gene required for the first monooxygenase step in CoQ biosynthesis, recently renamed ubiB 94104:95681 reverse MW:58157
RPA0083	0.936542	0.772	0.950032	0.7925	0.707201	0.988	0.777284	0.9775	0.956439	0.6775	ubiE ubiquinone/menaquinone biosynthesis methlytransferase ubiE 95678:96439 reverse MW:28394
RPA0084	1.009762	0.444	0.980623	0.63	0.811229	0.9495	0.993844	0.518	1.111077	0.101	mutM formamidopyrimidine-DNA glycosylase 96685:97560 forward MW:32319
RPA0085	1.197225	0.0205	0.957694	0.689	1.071704	0.352	1.205768	0.113	1.279296	0.026	CDS unknown protein 97588:98931 reverse MW:45915
RPA0086	0.85795	0.9655	0.901487	0.862	0.94274	0.774	0.74729	0.9565	0.723266	0.998	moeB putative molybdenum cofactor biosynthesis protein 99139:99939 forward MW:28060
RPA0087	0.943719	0.7995	0.871587	0.9375	1.00309	0.476	0.79083	0.929	0.75145	0.995	CDS putative Major Facilitator Superfamily (MFS) transporter 100064:101752 forward MW:59387
RPA0088	0.847977	0.8125	0.800778	0.971	0.780795	0.925	0.807648	0.9325	0.841371	0.9375	CDS unknown protein 101883:102101 reverse MW:7666
RPA0089	1.050113	0.226	0.894506	0.935	1.180564	0.2155	1.038185	0.3425	1.18983	0.0435	CDS conserved unknown protein 102225:102566 reverse MW:12691
RPA0090	1.244142	0.061	1.391057	0.0055	1.594766	0.002	1.189888	0.08	1.240503	0.022	CDS hypothetical protein 102804:103208 reverse MW:15280
RPA0091	1.290164	0.031	1.308573	0.02	1.942683	0.0025	1.27426	0.027	1.547412	0.0035	CDS hypothetical protein 103287:103628 reverse MW:11250
RPA0092	1.025595	0.4355	1.35484	0.004	0.889226	0.9085	1.551469	0.0095	1.442594	0.0045	CDS conserved hypothetical protein 104169:104444 reverse MW:10122
RPA0093			0.60337	0.991	0.724161	0.9045	0.741068	0.7955	0.732496	0.976	CDS transcriptional regulator, TetR family 104575:105222 forward MW:23840
RPA0094	0.702875	0.995	0.710102	0.9985	0.860399	0.9695	0.633215	0.998	0.651172	0.9995	CDS hypothetical protein 105219:106136 forward MW:33165
RPA0095	0.889569	0.9225	0.906576	0.8305	1.072964	0.1855	0.676865	0.9925	0.688738	0.9985	CDS putative multidrug efflux membrane fusion protein 106266:107411 forward MW:40543
RPA0096	0.944656	0.6645	1.149897	0.2315	0.956856	0.5885	1.155244	0.1305	1.110019	0.1985	CDS putative multidrug-efflux transport protein 107415:110564 forward MW:111692
RPA0097	1.737049	0.0015	2.143379	0.0015	1.676641	0.067	3.281746	0.0005	2.028285	0.0035	CDS putative flagellar basal-body rod protein flgC 110707:111117 forward MW:13802
RPA0098	1.321877	0.0045	1.278604	0.008	1.395889	0.005	1.828959	0.0005	1.407376	0.011	oppF oligopeptide ABC transporter (ATP-binding protein) 111260:112318 reverse MW:38824
RPA0099	1.301604	0.0235	0.924459	0.7505	1.179076	0.0745	1.336719	0.062	0.945171	0.675	oppD putative oligopeptide ABC transporter (ATP-binding protein) 112315:113313 reverse MW:35721
RPA0100									0.689647	0.902	oppC putative ABC transporter permease protein 113316:114197 reverse MW:30513
RPA0101							1.195312	0.2825			oppB putative dipeptide transport system permease protein 1 114221:115201 reverse MW:35049
RPA0102	1.730123	0.0185	1.282824	0.0725	1.560641	0.005	1.907015	0.0015	1.54289	0.007	oppA putative ABC transporter oligopeptide-binding protein 115230:116831 reverse MW:58400
RPA0103	1.308549	0.0265	0.841656	0.9015	1.691064	0.031			1.457401	0.0805	CDS Cobalamin synthesis protein/P47K 116921:117877 reverse MW:33282
RPA0104	1.093837	0.3115	0.738421	0.947	1.294014	0.009	1.199714	0.156	1.18698	0.111	CDS Amidohydrolase 117874:119517 reverse MW:59058
RPA0105	0.755845	0.9935	0.773537	0.9845	0.788737	0.9915	1.306093	0.0285	0.924579	0.7145	CDS transcriptional regulator, GntR family with aminotransferase domain 119756:121297 forward MW:56281
RPA0106	0.736521	0.996	0.82892	0.978	0.880426	0.944	0.741606	0.9805	0.711331	0.9975	CDS possible branched-chain amino acid transport system substrate-binding protein 121313:122521 reverse MW:43899
RPA0107	0.570715	0.9955	0.397062	0.998	0.703741	0.995	0.318916	0.9995	0.372346	0.9985	CDS putative Zn-binding dehydrogenase 122541:123581 reverse MW:36015
RPA0108	0.828532	0.9345	0.69854	0.9815	0.897917	0.8265	0.776437	0.8775	1.084048	0.2125	CDS Possible benzaldehyde lyase 123611:125359 reverse MW:61974
RPA0109	0.371709	1	0.251156	1	0.469745	0.9995	0.26656	1	0.49222	1	CDS putative 3-oxoacyl-(acyl carrier ptn) reductase 125400:126188 reverse MW:27310
RPA0111			1.147166	0.2935	0.824186	0.79	1.142424	0.1385	1.456029	0.0415	CDS DUF81 127104:127892 reverse MW:27058
RPA0112	0.963985	0.6545	0.914295	0.745	0.902331	0.9175	0.757504	0.8845	0.756342	0.9875	betB putative betaine aldehyde dehydrogenase 127901:129412 reverse MW:52979
RPA0113											tauY taurine dehydrogenase large subunit 130028:131422 forward MW:51148
RPA0114	1.316882	0.0975	1.490153	0.0035	1.525229	0.005	1.852098	0.027	1.784153	0.002	CDS hypothetical protein 131546:131899 reverse MW:12709
RPA0116	1.02658	0.3985	1.000017	0.4885	0.960566	0.6885	1.10386	0.186	1.175053	0.0535	rmlB pseudogene possible dTDP-D-glucose-4,6-dehydratase 132389:132900 reverse MW:18942
RPA0117	1.050203	0.347	1.311674	0.1815	1.024185	0.4335	1.341822	0.3855	1.189618	0.287	rmlB pseudogene dTDP-D-glucose 4,6-dehydratase 132902:133303 forward MW:15210
RPA0118	0.654835	0.9465	0.851725	0.8385	0.705006	0.9575	0.681897	0.9795	0.632071	0.995	rmlC dTDP-6-deoxy-D-glucose-3,5-epimerase 133329:133886 forward MW:20424
RPA0119	0.941681	0.7555	1.098165	0.1805	0.840431	0.9505	1.054401	0.4165	1.131455	0.0995	rmlD putative dTDP-6-deoxy-L-mannose-dehydrogenase 133891:134784 forward MW:31624
RPA0120	1.239836	0.067	1.255836	0.03	0.921208	0.7105	1.099883	0.1365	1.253774	0.055	rmlA glucose-1-phosphate thymidylyltransferase 134786:135661 forward MW:32129
RPA0121	0.946758	0.63	0.969023	0.619	0.827393	0.85	0.759551	0.9235	1.061733	0.2525	CDS hypothetical protein 136107:136643 forward MW:20138
RPA0122	0.77932	0.803	1.709228	0.1235	1.290334	0.141			0.810104	0.812	phyB3 Bacteriophytochrome (light-regulated signal transduction histidine kinase), PhyB3 136734:139013 forward MW:83028
RPA0123											CDS possible KTN NAD-binding domain involved with K+ transport 139006:140646 forward MW:58875
RPA0124					0.902845	0.6435	0.723261	0.91			CDS possible 3',5'-cyclic-nucleotide phosphodiesterase, cpdA 140653:141477 reverse MW:30646
RPA0125											CDS possible 3',5'-cyclic-nucleotide phosphodiesterase, cpdA 141474:142298 reverse MW:30892
RPA0126											CDS possible sugar binding protein of ABC transporter 142363:143643 reverse MW:46517
RPA0127			1.082407	0.3345			0.887679	0.8195			CDS putative permease protein of sugar ABC transporter 143666:144502 reverse MW:30504
RPA0128	1.157224	0.0425	1.25666	0.0105	1.235278	0.017	1.718518	0	1.038024	0.3355	CDS possible permease protein of sugar ABC transporter 144499:145458 reverse MW:34753
RPA0129											CDS putative sugar binding protein of ABC transporter 145451:146605 reverse MW:41517

RPA0130											CDS transcriptional regulator, LysR family 146733:147611 forward MW:31851
RPA0131											CDS ABC sulfate transport system, ATP-binding protein 147617:148312 reverse MW:24706
RPA0132			0.888545	0.763			0.842928	0.84			CDS ABC sulfonate transport system, permease protein 148309:149082 reverse MW:27062
RPA0133	1.220335	0.12	1.410773	0.018	1.306739	0.0185	1.137318	0.2275	0.931791	0.7275	CDS ABC sulfate transport system, periplasmic binding protein 149072:150064 reverse MW:35234
RPA0134	1.484503	0.0015	1.62489	0.0075	1.194033	0.042	1.239486	0.0815	1.178606	0.098	hydC hydrogenase gamma-fused hydrogenase large and small subunit 150080:151939 reverse MW:68194
RPA0135	1.011716	0.458	1.00011	0.487	1.259207	0.0515	1.040645	0.375	0.829044	0.9565	CDS possible oxidoreductase 151939:153960 reverse MW:73333
RPA0136	0.624085	0.9995	0.63665	1	0.515142	0.9995	0.499823	0.999	0.777172	0.9825	CDS methyl-accepting chemotaxis receptor/sensory transducer 154100:155809 reverse MW:60855
RPA0137	0.735113	0.9965	0.709509	0.991	0.549727	0.998	0.596163	0.9985	0.928899	0.785	cheB1 chemotaxis methylesterase, CheB1 155814:156905 reverse MW:39080
RPA0138	0.583708	1	0.624904	0.998	0.5699	1	0.368729	1	0.691739	0.9895	cheR1 chemotaxis methyltransferase, CheR1 156926:157768 reverse MW:32305
RPA0139	0.577225	0.999	0.61478	0.9995	0.553989	0.999	0.283171	1	0.625749	0.9985	CDS methyl-accepting chemotaxis receptor/sensory transducer 157930:160131 reverse MW:77029
RPA0140	0.451051	0.9995	0.555527	1	0.414783	0.9995	0.215518	0.999	0.402375	0.998	cheW1-3 chemotaxis signal transduction/oligomerization protein CheW1-2 160198:160686 reverse MW:17416
RPA0141	0.52143	0.997	0.565469	1	0.474672	0.999	0.23119	0.999	0.3499	1	cheW1-1 chemotaxis signal transduction/oligomerization protein CheW1-1 160747:161217 reverse MW:17318
RPA0142	0.888645	0.8755	0.576611	0.999	0.544005	0.9995	0.319591	0.9975	0.505382	0.9975	cheA1 multidomain chemotaxis histidine kinase CheA1 (Hpt, CheA, & CheW domains) 161217:163283 reverse MW:74391
RPA0143	0.478001	1	0.476834	0.9995	0.443137	0.9985	0.254511	0.999	0.375456	0.997	cheY1 response regulator receiver, CheY1 163280:163645 reverse MW:12910
RPA0144	0.455214	0.997	0.409821	1	0.618512	0.9725	0.351441	0.997	0.251398	0.995	CDS Sulfate transporter/antisigma-factor antagonist domain 163645:163968 reverse MW:11491
RPA0145	0.425927	1	0.367451	1	0.364661	0.9995	0.235618	1	0.461493	0.999	CDS Metal dependent phosphohydrolase with a response regulator receiver domain 164246:165412 forward MW:42854
RPA0146	0.756112	0.9935	0.857285	0.8445	0.781633	0.9665	0.835734	0.9605	0.501777	0.9995	CDS hypothetical protein 165452:165883 forward MW:15493
RPA0147	0.8992	0.878	0.759747	0.992	0.947251	0.75	0.932318	0.684	0.929418	0.8	CDS transcriptional regulator, ModE family 165961:166752 reverse MW:28515
RPA0148	0.867154	0.64							1.617756	0.125	CDS conserved hypothetical protein 166873:167409 reverse MW:18860
RPA0149	1.033396	0.4245	1.508502	0.081	1.46597	0.017	1.120894	0.442	0.647014	0.997	CDS possible ABC-type iron-siderophore transport system ATP-binding protein 167433:168227 reverse MW:28098
RPA0150					0.514552	0.925			0.660064	0.9795	CDS putative ABC transporter, iron, hemin permease homolog 168224:169246 reverse MW:35269
RPA0151	0.646962	1	0.554521	0.9905	0.791972	0.95	0.590565	0.992	0.695084	0.975	CDS possible iron ABC transporter periplasmic binding protein 169248:170297 reverse MW:38157
RPA0152	0.735863	0.98			0.751325	0.9615			0.611219	0.887	CDS Protein of unknown function, UPF0066 170294:170797 reverse MW:18611
RPA0153	1.061957	0.1875			1.058784	0.301	1.219847	0.178	0.920756	0.845	CDS possible outer membrane receptor for Fe transport 171435:173618 forward MW:81136
RPA0154											CDS possible MotA/TolQ/ExbB proton channel family 173675:174313 forward MW:21964
RPA0155											CDS putative tolR/exbD protein 174326:174793 forward MW:16572
RPA0156	1.105484	0.0965			0.984631	0.552			1.053529	0.4315	CDS tonB like protein 174790:175608 forward MW:28869
RPA0157	1.847239	0.015	4.519621	0.0005	2.212045	0.0015	1.451273	0.133	3.026495	0.001	CDS conserved unknown protein 175963:177126 reverse MW:42540
RPA0158	0.939579	0.843	1.278045	0.0165	0.664298	0.995	0.994566	0.5025	1.374289	0.04	rplU, L21 putative ribosomal protein L21 177448:177828 forward MW:13490
RPA0159	0.791896	0.9755	0.833593	0.9765	0.961124	0.644	1.006904	0.4815	1.104118	0.1405	rpmA, L27 ribosomal protein L27 177918:178190 forward MW:9581
RPA0160	0.471292	1	0.374755	0.999	0.618768	0.9875	0.486937	0.958	0.569839	0.9945	CDS possible acetyltransferases. 178325:178924 forward MW:22367
RPA0161	1.201864	0.1285	1.519721	0.012	1.060442	0.2295	1.201615	0.068	1.012594	0.462	CDS Permeases of the drug/metabolite transporter (DMT) superfamily 179631:180536 reverse MW:31850
RPA0162	0.92947	0.859	0.942008	0.8045	0.905844	0.8845	0.921137	0.8255	0.994222	0.514	CDS possible GTP-binding proteins 180688:181749 forward MW:37743
RPA0163	0.707499	0.9935	0.740595	0.9915	0.633816	1	0.66227	0.9945	0.757516	0.984	proB glutamate 5-kinase 181888:183018 forward MW:39511
RPA0164	1.008779	0.4605	0.75208	0.9885	0.725164	0.954	0.816286	0.879	0.953562	0.718	proA gamma-glutamyl phosphate reductase 183222:184514 forward MW:45120
RPA0165	1.002952	0.4895			0.987875	0.535	1.020788	0.451	1.059169	0.3815	CDS possible nicotinate-nucleotide adneylyltransferase 184539:185168 forward MW:23301
RPA0166	0.920732	0.7965	0.802523	0.97	1.289226	0.006	1.132993	0.115	0.93087	0.7495	CDS Iojap-related protein 185539:185835 forward MW:10815
RPA0167	0.932672	0.6575	1.201679	0.1435	1.280206	0.071	1.795982	0.009	1.437663	0.002	CDS DUF163 185925:186407 forward MW:17640
RPA0168	0.948761	0.71	0.944664	0.7285	1.05168	0.3505	1.299637	0.03	1.646213	0.0005	CDS putative filament-A precursor 186427:187818 forward MW:48939
RPA0169	0.806983	0.9915	0.78704	0.9945	0.903761	0.9085	0.838047	0.942	1.003815	0.475	ctpA putative periplasmic carboxyl-terminal processing protease 187815:189191 forward MW:48865
RPA0170	0.830926	0.9675	0.640762	0.998	0.858938	0.9015	0.670715	0.991	0.869616	0.899	CDS conserved hypothetical protein 189342:190580 forward MW:43466
RPA0171	0.789109	0.996	0.682862	0.992	0.96746	0.673	0.846876	0.914	0.964397	0.649	invA1 putative dinucleoside polyphosphate hydrolase (AP4A pyrophosphatase) (invasion protein A, NUDIX family, NUDH subfamily. 190619:191125 forward MW:19281
RPA0173	0.864868	0.9495	1.057975	0.2035	0.692279	0.997	0.951467	0.7155	0.965718	0.642	CDS putative sugar nucleotide dehydratase 192604:193551 forward MW:35524
RPA0174			0.707656	0.919			0.746645	0.936			invA2 putative dinucleoside polyphosphate hydrolase (AP4A pyrophosphatase) (invasion protein A, NUDIX family hydrolase, NUDH subfamily. 193548:194069 forward MW:20010
RPA0175	0.760694	0.9875	0.855834	0.9295	0.928046	0.811	0.939604	0.7835	0.883238	0.7685	atpC putative H+-transporting ATP synthase epsilon chain. 194253:194660 reverse MW:14258
RPA0176	0.956985	0.7175	0.843388	0.9415	0.855458	0.9535	0.756415	0.9755	0.81531	0.88	atpD putative H+-transporting ATP synthase beta chain. 194774:196204 reverse MW:50717
RPA0177	0.826796	0.826	0.988751	0.537	0.821416	0.975	0.687436	0.9825	0.689309	0.962	atpG putative H+-transporting ATP synthase gamma chain. 196276:197151 reverse MW:31934
RPA0178	0.95127	0.6495	0.935191	0.714	0.85436	0.88	0.799776	0.956	0.829301	0.954	atpA putative H+-transporting ATP synthase alpha chain. 197295:198827 reverse MW:55178
RPA0179	0.848094	0.8915	1.295722	0.0425	0.735958	0.8895	0.862147	0.6745	1.007653	0.4595	atpH putative H+-transporting ATP synthase delta chain. 198827:199387 reverse MW:19513
RPA0180	1.331932	0.0065	1.850823	0.005	1.472628	0.0165	1.024448	0.447	0.919313	0.8085	rlpA1 Rare lipoprotein A 200091:200561 forward MW:16327
RPA0181	0.850829	0.9755	0.852403	0.9705	0.898761	0.9225	0.669838	0.999	0.746378	0.996	priA putative priA family helicase (primosomal protein N', replication factor Y) 200717:202927 reverse MW:80828
RPA0182	0.947008	0.7465	0.815366	0.861	0.91533	0.806	0.702639	0.951	0.84738	0.939	xerC putative site-specific recombinase, INTEGRASE/RECOMBINASE RIPX (xerC) 202981:204096 forward MW:40167
RPA0183	0.821032	0.9575	0.881299	0.8805	0.775627	0.985	0.57078	0.999	0.749371	0.9895	CDS unknown protein 204237:204827 forward MW:21072
RPA0184	0.840462	0.8705	0.913921	0.7645	1.078257	0.223	0.954231	0.5995	1.050772	0.345	CDS hypothetical protein 204891:205433 reverse MW:20379
RPA0185	1.009289	0.456	0.962652	0.716	1.114385	0.1255	0.997994	0.5185	0.872639	0.9485	dldH dihydrolipoamide dehydrogenase, E3 component of 2-oxoglutarate and pyruvate dehydrogenase complexes 205473:206876 reverse MW:48585
RPA0186	0.872306	0.8655	0.933237	0.8435	0.861342	0.9735	0.726723	0.9955	0.767821	0.9895	CDS putative short-chain dehydrogenase/reductase 206908:207654 reverse MW:25283
RPA0187	0.693697	0.9865	0.83952	0.903	0.981935	0.583	0.861272	0.8065	0.836207	0.96	CDS conserved hypothetical protein 207662:208111 reverse MW:15999
RPA0188	0.957854	0.6085	1.004052	0.459	0.896896	0.8795	0.940152	0.677	0.871997	0.9165	sucB dihydrolipoamide succinyl transferase 208123:209376 reverse MW:43864
RPA0189	1.10153	0.1755	1.018933	0.38	1.355267	0.0055	1.028258	0.3795	1.047778	0.3195	sucA putative alpha-ketoglutarate dehydrogenase (E1 subunit) 209481:212438 reverse MW:111339
RPA0190	1.004648	0.475	0.859614	0.955	0.875345	0.887	0.804194	0.9815	0.744286	0.917	sucD succinyl-CoA synthetase alpha-subunit 212566:213450 reverse MW:30063
RPA0191	0.977623	0.5645	0.97742	0.5885	0.872315	0.894	0.829399	0.9405	0.874235	0.8415	sucC succinyl-coA synthetase beta chain 213515:214711 reverse MW:42318
RPA0192	1.071643	0.233	1.057577	0.3045	0.879345	0.9025	1.058486	0.3545	0.99068	0.55	mdh malate dehydrogenase 214807:215775 reverse MW:33996
RPA0193	1.036385	0.313	1.107868	0.1795	0.903909	0.8205	0.962589	0.596	0.926543	0.7165	CDS AFG1-like ATPase 215921:217105 reverse MW:43902
RPA0194	0.799001	0.9415	0.621382	0.998	1.148528	0.206	0.852448	0.851	1.190923	0.0245	CDS 2'_5' RNA ligase 217188:217727 reverse MW:19693
RPA0195	0.69299	0.9825	0.729632	0.957	0.999524	0.4995	0.65646	0.9965	0.827902	0.971	tesA putative acyl-CoA thioesterase precursor 217933:218601 reverse MW:23301
RPA0196	0.659493	0.9975	0.760901	0.9945	0.893503	0.866	0.644831	0.998	0.683946	0.999	CDS putative ABC transporter, ATP-binding protein 218627:219370 forward MW:25712
RPA0197	0.815634	0.979	0.69322	0.981	0.923976	0.8475	0.636925	0.9955	0.772599	0.9875	CDS possible ABC transporter permeases 219374:221944 forward MW:90195
RPA0198	1.164311	0.0355	1.149637	0.1935	1.181547	0.1	1.093002	0.2665	1.119564	0.1015	CDS possible acetate transporter, stationary-phase anti-death (SAD) family 222285:223076 forward MW:28252
RPA0199	1.119672	0.147	1.247695	0.0285	1.082542	0.3305	1.296367	0.055	1.325696	0.025	CDS putative phosphinothricin acetyltransferase 223231:223761 forward MW:18852
RPA0200	0.981852	0.5785	0.645565	0.9925	1.35042	0.0635	1.175272	0.125	1.223294	0.0445	CDS conserved hypothetical protein 223821:224189 reverse MW:13710
RPA0201	1.039265	0.287	0.811426	0.9915	1.285195	0.0425	0.898577	0.866	0.752438	0.9305	CDS conserved hypothetical protein 224593:225468 reverse MW:30891
RPA0202	0.982204	0.5985	0.79214	0.9815	0.793478	0.912	0.806487	0.904	0.750053	0.9705	acnA aconitate hydratase 225515:228232 reverse MW:98545
RPA0203	0.898183	0.751			0.992138	0.5125	0.830639	0.8065	0.811792	0.8985	cycV, ccmA heme exporter protein A (heme ABC transporter ATP-binding protein), cytochrome c biogenesis 228448:229050 forward MW:21079
RPA0204	0.957709	0.6475	0.855194	0.9315	0.794475	0.983	0.664202	0.9775	0.795755	0.985	cycW, ccmB putative heme exporter protein B (heme ABC transporter membrane protein), cytochrome c biogenesis 229047:229715 forward MW:22546
RPA0205	0.856985	0.945	0.843632	0.9695	0.848662	0.9635	0.719505	0.9915	0.860133	0.9455	cycZ, ccmC heme exporter protein C (ABC transporter permease component) 229808:230542 forward MW:26684
RPA0206	0.943899	0.711	1.121305	0.11	0.896734	0.8165	0.799849	0.877	0.824621	0.982	cycY, ccmG putative cytochrome c biogenesis protein, thiol:disulfide interchange protein 230732:231328 forward MW:21366
RPA0207	0.595666	0.994	0.677559	0.999	1.064485	0.3375	0.532418	0.9985	0.926925	0.704	CDS unknown protein 231468:231866 forward MW:13746

RPA0208	0.956919	0.6725	0.856404	0.9295	0.811433	0.977	0.78163	0.977	0.879592	0.909	ispZ possible intracellular septation protein (ispZ family) 231999:232616 reverse MW:22661
RPA0209	0.808045	0.9635	0.836219	0.9095	0.741216	0.9945	0.804527	0.9545	0.782353	0.983	ftsY putative cell division protein FtsY 232613:233560 reverse MW:33143
RPA0210	0.903454	0.882	0.998355	0.507	0.950381	0.696	0.836795	0.8475	0.747729	0.9625	CDS Pseudouridine synthase:Pseudouridine synthase, Rlu 233589:234563 forward MW:34738
RPA0211	1.191732	0.1005	1.147607	0.0875	1.077228	0.207	0.81052	0.9735	1.004433	0.4775	CDS acetyl-CoA synthetase 234927:236879 forward MW:72459
RPA0212	1.388961	0.0155	1.11646	0.186	1.68561	0.0005	1.109152	0.261	1.113624	0.2665	CDS ErfK/YbiS/YcfS/YnhG 237262:237789 forward MW:18589
RPA0213	0.503426	1	0.612307	0.9915	0.669969	0.9865	0.328756	0.995	0.488957	0.996	CDS possible OmpA family member 237864:239933 reverse MW:70746
RPA0214	1.883419	0.0225	4.743479	0.01	2.092108	0.0065	1.930332	0.032	2.444933	0	CDS hypothetical protein 240179:240436 reverse MW:8651
RPA0215	2.148013	0.0185	5.469505	0	2.60475	0.0025	1.266103	0.1615	3.184176	0.011	CDS possible general stress protein 26 240436:240924 reverse MW:17991
RPA0216	0.98993	0.543	1.062356	0.2545	0.859886	0.9625	0.909427	0.831	0.986655	0.5585	sdhB succinate dehydrogenase iron-sulfur protein subunit 241162:241944 reverse MW:29531
RPA0217	1.042859	0.2625	1.083512	0.1515	0.930988	0.8575	1.032915	0.354	1.01965	0.3945	sdhA succinate dehydrogenase flavoprotein subunit 242052:243875 reverse MW:65896
RPA0218	0.870623	0.901	0.913792	0.863	1.018666	0.4105	0.842835	0.9	1.002918	0.4855	sdhD succinate dehydrogenase cytochrome b small subunit 243879:244292 reverse MW:14720
RPA0219	0.845893	0.908	0.91335	0.8955	0.960563	0.713	0.724216	0.976	0.820689	0.979	sdhC succinate dehydrogenase membrane anchor/cytochrome b subunit 244289:244687 reverse MW:14848
RPA0220	0.976947	0.5625	1.046994	0.248	1.419479	0.002	0.764538	0.9625	0.870243	0.9585	czcD putative cation efflux system protein 245070:246014 forward MW:32799
RPA0221	1.120713	0.127	1.103245	0.31	0.952484	0.596	1.526768	0.058	1.558874	0.0255	matB malonyl CoA synthetase 246248:247759 reverse MW:54453
RPA0222	1.111607	0.098	1.450234	0.023	1.150491	0.0605	1.095176	0.2555	1.48545	0.0415	CDS Beta-Ig-H3/Fasciclin domain 248034:248609 forward MW:19764
RPA0223	1.047416	0.3305	0.899391	0.817	1.066258	0.2745	0.926065	0.7555	1.181401	0.03	CDS conserved hypothetical protein 248831:249469 forward MW:23062
RPA0224	1.127465	0.1545	1.027299	0.353	1.143902	0.0685	0.990372	0.538	1.090518	0.1505	CDS similar to eukaryotic molybdopterin oxidoreductase:Tat pathway signal 249585:250364 forward MW:28795
RPA0225	1.411942	0.021	1.136382	0.063	1.708142	0.0035	1.227338	0.0275	1.285559	0.0205	sodC putative superoxide dismutase (Cu/Zn) 250637:251155 forward MW:17363
RPA0226	1.30776	0.1205	1.259384	0.0535	1.527953	0.008	1.45955	0.0105	1.593434	0.002	CDS Major Facilitator Family (MFS) transporter 251299:252486 reverse MW:40002
RPA0227	0.981151	0.5485	1.03088	0.332	0.855196	0.957	0.762074	0.989	0.89035	0.895	leuB beta-isopropylmalate dehydrogenase 252707:253819 forward MW:39643
RPA0228	0.988697	0.5305	0.730101	0.967	1.180926	0.1995	0.919782	0.7005	1.022311	0.415	CDS unknown protein 253976:254377 reverse MW:14481
RPA0229	1.30058	0.006	1.072793	0.177	1.138843	0.099	1.258288	0.043	1.137255	0.046	CDS hypothetical protein 254521:255330 reverse MW:28109
RPA0230	1.022728	0.3645	1.004648	0.483	0.781784	0.966	0.965116	0.6515	1.07949	0.2	asdB aspartate-semialdehyde dehydrogenase 255445:256479 forward MW:37476
RPA0231	1.0729	0.272	0.789925	0.941	0.961527	0.66	0.879396	0.873	0.989494	0.5355	CDS Uncharacterized protein family UPF0114 256615:257169 forward MW:20602
RPA0232	0.85853	0.922	0.946072	0.772	0.757087	0.995	0.734145	0.9885	0.784701	0.99	CDS putative carbonic anhydrase 257321:257965 reverse MW:23827
RPA0233	0.669656	0.9865	0.737193	0.9965	0.632042	0.998	0.490292	0.9985	0.499502	0.999	CDS putative Citrate lyase beta chain (acyl lyase subunit) (citE) 258147:259025 forward MW:31312
RPA0234	0.868434	0.829					0.687068	0.7805	0.584347	0.9785	CDS methyl-accepting chemotaxis receptor/sensory transducer 259203:260894 reverse MW:58781
RPA0235	0.686531	0.9585	0.65355	0.98	0.796965	0.851	0.565727	0.9845	0.628717	0.999	leuD 3-isopropylmalate dehydratase small subunit 261643:262248 reverse MW:22323
RPA0236	0.828195	0.917	1.029304	0.415	0.839055	0.976	0.870199	0.775	0.733057	0.9935	CDS conserved unknown protein 262334:262747 reverse MW:15578
RPA0237	1.167385	0.167	1.268449	0.0855	1.375387	0.0055	1.003398	0.499	1.288125	0.034	CDS conserved hypothetical protein 263432:263716 forward MW:11182
RPA0238	1.174829	0.141	0.875877	0.9485	1.163915	0.093	1.036284	0.385	1.273008	0.0145	CDS hypothetical protein 263816:264139 forward MW:11643
RPA0239	1.073234	0.2305	1.003525	0.476	1.094507	0.1575	1.136033	0.1595	1.886392	0	CDS hypothetical protein 264260:264946 forward MW:26134
RPA0240	0.619913	0.996	0.637864	0.989	0.569523	0.9955	0.499896	1	0.687624	0.9965	leuC 3-isopropylmalate dehydratase 265013:266422 reverse MW:50478
RPA0241	0.882116	0.8385	1.006701	0.452	0.81387	0.9835	1.04161	0.3265	1.008002	0.4515	rplS, L19 50s ribosomal protein L19 266732:267121 reverse MW:14297
RPA0242	0.700026	0.988	0.804088	0.868	0.670044	0.9935	0.657497	0.993	0.668129	0.938	trmD putative tRNA (guanine-N1)-methyltransferase 267235:267981 reverse MW:26361
RPA0243	0.780128	0.9815	0.858753	0.953	0.727381	0.9945	0.96941	0.632	0.677387	0.9985	rimM putative 16S rRNA processing protein. 268124:268654 reverse MW:18554
RPA0244	0.661095	0.9855	0.883825	0.822	0.737384	0.9885	0.589477	0.9985	0.502772	0.974	rpsP, S16 ribosomal protein S16 268667:268987 reverse MW:12149
RPA0245	0.699309	0.995	0.85045	0.9555	0.598359	0.993	0.664573	0.996	0.876179	0.8435	ffh/ftsY signal recognition particle protein 269157:270707 reverse MW:54743
RPA0246											CDS PilT protein, N-terminal 271220:271591 forward MW:13472
RPA0247	0.96951	0.59			0.942543	0.6985	0.838127	0.7745	0.801247	0.913	romA putative outer membrane protein 271596:272657 forward MW:39255
RPA0248	0.795021	0.975	0.764939	0.9905	0.830167	0.9745	0.595248	0.999	0.691697	0.9915	bp26 DUF541 272667:273365 reverse MW:23918
RPA0249	0.776469	0.9915	0.700834	0.996	0.829206	0.979	0.560362	0.9975	0.666862	0.999	CDS hypothetical protein 273362:274144 reverse MW:27161
RPA0250	0.6868	0.995	0.667965	0.9975	0.850777	0.908	0.607178	0.9935	0.803088	0.9895	dapF diaminopimelate epimerase 274381:275262 forward MW:31885
RPA0251	0.510067	0.997	0.769345	0.892	1.000824	0.4935	0.757338	0.906	0.52597	0.998	CDS MiaB-like tRNA modifying enzyme 275262:276533 forward MW:45950
RPA0252											CDS conserved hypothetical protein 276543:277205 reverse MW:23527
RPA0253	0.767779	0.9625	0.800237	0.9815	0.767568	0.9935	0.699892	0.987	0.735719	0.9935	CDS DUF589 277390:277803 reverse MW:15223
RPA0254	0.718343	0.992	0.724718	0.997	0.677523	0.9965	0.61726	0.991	0.645636	0.9975	gpdA putative glycerol-3-phosphate dehydrogenase 277806:278795 reverse MW:33867
RPA0255	0.954765	0.706	0.99447	0.5295	1.06164	0.211	0.911528	0.845	0.990993	0.5555	gcp putative o-sialoglycoprotein endopeptidase (gcp) 278831:280000 reverse MW:40429
RPA0256	0.852211	0.869	1.168555	0.059	0.881066	0.88	0.854874	0.8115	0.936183	0.752	CDS putative UROPORPHYRINOGEN-III synthase 280147:280893 forward MW:26604
RPA0257	0.771401	0.962	0.88534	0.917	0.892062	0.8945	0.664612	0.9945	0.911962	0.8545	CDS conserved unknown protein 280945:282354 forward MW:47487
RPA0258	0.86615	0.8575	0.989507	0.5465	0.807609	0.9465	0.744204	0.9915	0.849141	0.9745	CDS unknown protein 282363:284060 forward MW:60386
RPA0259	0.743019	0.942	0.665474	0.9975	1.330408	0.014	0.75939	0.99	0.710166	0.9905	CDS HTransmembrane sensor and HAMP domains 284749:285531 reverse MW:27423
RPA0260	1.173722	0.2825	2.0318	0.0005	1.614195	0.0175	1.258738	0.022	1.221023	0.157	CDS possible photosynthesis gene regulator, AppA/PpaA family 286170:287165 forward MW:36033
RPA0261	0.854387	0.7825	1.2775	0.0265	0.897315	0.913	0.76089	0.965	0.941422	0.6975	CDS unknown protein 287243:288424 forward MW:42275
RPA0262	0.825447	0.8925	1.418767	0.032	0.84654	0.916	1.124217	0.321	1.202819	0.1135	rlp2 ribulose bisphosphate carboxylase-like protein; rubisco-like protein 288452:289750 reverse MW:46464
RPA0263	0.746707	0.9955	0.742913	0.997	0.640879	0.9975	0.645234	0.9985	0.618546	1	CDS Protein of unknown function UPF0047 289865:290287 reverse MW:15967
RPA0264	0.835553	0.9595			1.172665	0.154	0.932698	0.5895	1.203074	0.1585	CDS possible O-antigen acetylase 290514:292451 forward MW:69718
RPA0265	0.678653	0.998	0.668007	0.9955	0.719287	0.9935	0.471212	0.9985	0.634544	0.998	algJ possible AlgJ protein, required for O-acetylation of alginate in Pseudomonas aeruginosa. 292504:293670 reverse MW:42621
RPA0266	0.805921	0.9925	0.960442	0.6425	0.798606	0.977	0.762098	0.9825	0.960925	0.68	CDS putative alginate o-acetyltransferase AlgI 293673:295085 reverse MW:52177
RPA0267	0.588322	0.9995	0.548879	1	0.810052	0.964	0.586443	0.9945	0.68501	0.998	trx possible thioredoxin 295679:296599 forward MW:32811
RPA0268	0.745475	0.9875	0.740976	0.995	0.922424	0.7645	0.615931	0.991	0.745425	0.992	CDS putative Lon family ATP-dependent protease 296626:297303 forward MW:24793
RPA0269	0.867737	0.7715	1.115738	0.219	0.893404	0.7685	1.104966	0.3285	0.969427	0.6025	CDS DUF343 297393:297590 forward MW:7214
RPA0270	0.992268	0.5355	0.892383	0.8975	0.855308	0.948	1.028392	0.3985	1.032337	0.385	ubiH putative UbiH protein, 2-octaprenyl-6-methoxyphenol 4-monoxygenase 297726:299087 reverse MW:48794
RPA0271	1.031378	0.376	0.903799	0.8845	0.862773	0.909	0.789671	0.9675	0.87673	0.92	tesB acyl-CoA thioesterase II 299186:300061 forward MW:33221
RPA0272	0.834681	0.926	0.757546	0.9725	0.663353	0.9935	0.419021	0.9945	0.520418	0.9965	glnK1 GlnK, nitrogen regulatory protein P-II 300253:300591 forward MW:12361
RPA0273	0.956231	0.578	0.864512	0.925	0.660289	0.9905	0.495899	1	0.564256	0.996	amtB1 ammonium transporter AmtB 300666:301997 forward MW:46247
RPA0274	29.17561	0.0005	21.10863	0	30.75035	0	67.46368	0	31.41015	0.0005	glnK2 GlnK, nitrogen regulatory protein P-II 302307:302645 forward MW:12061
RPA0275	24.54652	0	13.57813	0	20.37887	0	33.05445	0	27.52707	0	amtB2 putative ammonium transporter AmtB 302683:304125 forward MW:49789
RPA0277			1.233799	0.0915			1.873678	0.0075	1.312677	0.0525	CDS conserved hypothetical protein 304743:304937 forward MW:7355
RPA0278	0.778051	0.997	0.681323	0.9985	0.691745	0.9945	0.63142	0.9905	0.76146	0.9855	CDS putative N-succinyldiaminopimelate aminotransferase 304991:306286 forward MW:46379
RPA0279	0.908246	0.8675	0.848477	0.9545	0.888964	0.9175	0.924478	0.805	1.171538	0.063	CDS possible FtsK/SpoIIIE family 306300:308768 forward MW:88844
RPA0280	0.883063	0.8745	0.877832	0.945	1.00478	0.485	0.998042	0.4945	1.081862	0.242	CDS unknown protein 308786:309727 forward MW:33970
RPA0281	0.803593	0.966	0.951543	0.664	0.798775	0.958	0.963532	0.641	1.01181	0.4485	xthA1 possible exodeoxyribonuclease III 310015:310827 forward MW:31030
RPA0282	0.705294	0.9975	0.718108	0.979	0.950668	0.7545	0.921044	0.788	0.950201	0.7205	CDS Cyclic nucleotide binding protein 310879:311328 reverse MW:16149
RPA0283	0.786238	0.9595	0.542193	1	0.955879	0.6355	0.654871	0.976	0.64715	0.996	CDS two-component transcriptional regulator, winged helix family 311368:312054 reverse MW:25115
RPA0284	0.937938	0.851	0.75442	0.9925	1.096825	0.155	0.846436	0.9525	0.954616	0.733	CDS conserved hypothetical protein 312219:312782 forward MW:20800
RPA0285	0.857421	0.5925	1.501886	0.002	0.439606	0.9565	1.072407	0.3245	0.544379	0.9445	CDS Protein of unknown function UPF0001 312863:313522 reverse MW:23414

RPA0286	2.397044	0	1.687773	0	1.953372	0.001	3.453544	0	2.798968	0	CDS putative diguanylate cyclase (GGDEF) with HAMP domain 313693:315366 forward MW:59675
RPA0287	0.810387	0.9765	0.810064	0.9875	1.004537	0.4675	0.745801	0.9905	0.678169	0.9865	leuS leucyl-tRNA synthetase 315572:318202 forward MW:97725
RPA0288	0.703301	0.9875	0.6909	0.9905	0.868607	0.815	0.666434	0.9635	0.680682	0.993	CDS conserved unknown protein 318189:318752 forward MW:20275
RPA0289	0.619979	0.9955	0.773751	0.9485	0.723911	0.982	0.6584	0.995	0.694504	0.996	CDS conserved hypothetical protein 318809:319840 forward MW:36300
RPA0290	0.874449	0.92	0.914386	0.8795	0.926663	0.818	0.869083	0.9145	0.974002	0.589	CDS hypothetical protein 320082:320321 reverse MW:8492
RPA0291	0.916102	0.846	1.01086	0.4225	0.921295	0.843	0.98895	0.529	0.826302	0.9035	parB1 chromosome partitioning protein, ParB 320345:321235 reverse MW:32294
RPA0292	1.246452	0.0425	0.99622	0.5205	1.273084	0.005	0.981447	0.5605	1.160738	0.061	parA chromosome partitioning protein, ParA 321408:322262 reverse MW:30891
RPA0293	1.251656	0.0265	1.033745	0.374	1.083808	0.253	1.598774	0.0025	1.882582	0.0005	gidB putative glucose inhibited division protein B (GidB) 322290:322961 reverse MW:24100
RPA0294	1.305374	0.0045	1.309897	0.006	0.984375	0.5955	1.583077	0.002	1.645932	0.0015	gidA putative glucose inhibited division protein A (GidA) 323133:325073 reverse MW:70019
RPA0295	0.890732	0.874	0.872089	0.922	0.77945	0.9925	0.754656	0.957	0.898417	0.884	trmE, mnmE putative GTPase involved in synthesis of 5-methylaminomethyl-2-thiouridine, found in the wobble position of some tRNA's. 325167:326492 reverse MW:47076
RPA0296	0.869276	0.9075	0.942325	0.6975	0.849926	0.901	0.9494	0.6515	0.908079	0.7135	rho transcription termination factor rho 326580:327845 reverse MW:47129
RPA0297	0.748478	0.9875	1.123314	0.144	0.778445	0.9885	0.835176	0.858	0.806684	0.973	CDS conserved hypothetical protein 328106:328558 reverse MW:17479
RPA0298	0.773763	0.9905	0.860837	0.953	0.770943	0.984	0.836646	0.7825	0.820955	0.977	CDS DUF299 329001:329840 forward MW:30864
RPA0299	0.730032	0.9825	0.829375	0.983	0.737877	0.953	0.79494	0.9045	0.70395	0.9975	maf1 putative maf protein 329837:330445 forward MW:21328
RPA0300	0.779493	0.984	0.756843	0.989	0.758008	0.976	0.640721	0.9935	0.51902	0.9975	coaE putative dephospho-CoA kinase CoaE 330542:331141 forward MW:21554
RPA0302	0.734565	0.958	1.083213	0.161	0.733415	0.996	0.73512	0.9875	0.658478	0.996	secB putative protein-export protein SecB 331954:332427 reverse MW:17076
RPA0303	0.700303	0.9965	0.665845	0.9955	0.84287	0.954	0.696485	0.9935	0.701165	0.998	CDS conserved unknown protein 332729:333598 forward MW:31577
RPA0304	1.040994	0.361	1.122022	0.0495	1.364486	0.0375	1.259108	0.0475	1.14934	0.106	CDS possible outer membrane lipoprotein GNA33, membrane-bound lytic murein transglycosylase 333507:335069 forward MW:56538
RPA0305	0.85542	0.9105	0.820702	0.927	0.811396	0.9455	0.846213	0.9245	0.763672	0.9905	CDS possible DNA mismatch repair protein (MutS) 335075:335659 forward MW:21609
RPA0306	0.636464	0.997	0.661366	0.9985	0.703025	0.9945	0.561821	0.9995	0.622964	0.9945	hslU heat shock protein HslU, proteasome-related ATPase subunit 335995:337296 reverse MW:47489
RPA0307	0.821226	0.976	1.037659	0.4005	0.768991	0.8245	0.536373	0.9415	0.627064	0.9945	CDS conserved hypothetical protein 337338:337949 reverse MW:22475
RPA0308	0.72891	0.9955	0.8175	0.9875	0.857148	0.9525	0.626123	0.9955	0.729085	0.9965	hslV heat shock protein HslV, proteasome-related peptidase subunit 337946:338515 reverse MW:19797
RPA0309	0.919014	0.786	0.824462	0.973	0.874507	0.8905	0.726718	0.9865	0.759595	0.9535	hisB imidazoleglycerol-phosphate dehydratase 338703:339296 forward MW:21349
RPA0310			0.86222	0.707			0.867405	0.688			CDS conserved hypothetical protein 339324:339845 forward MW:19103
RPA0311	0.870155	0.913	0.963229	0.67	0.762681	0.9875	0.745521	0.9755	0.827479	0.9445	hisH imidazoleglycerol-phosphate synthase, amidotransferase component 339842:340492 forward MW:23630
RPA0312	0.859893	0.822	0.980887	0.5935	0.725255	0.996	0.858058	0.9055	0.767761	0.929	hisA phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase 340489:341226 forward MW:25514
RPA0313	0.833251	0.873	0.781754	0.962	0.776208	0.9735	0.48463	0.9985	0.625651	0.9775	hisF imidazoleglycerol-phosphate synthase, cyclase subunit 341237:342004 forward MW:27229
RPA0314	0.997145	0.5115	0.947503	0.6415	0.945309	0.649	0.813568	0.8515	0.856028	0.928	hisE1 putative phosphoribosyl-ATP pyrophosphatase 342058:342381 forward MW:11670
RPA0315	1.032968	0.374	0.845907	0.9545	1.027532	0.3865	0.831086	0.967	0.802703	0.934	coaA pantothenate kinase (RTS protein) 342456:343412 forward MW:36077
RPA0316	0.629706	0.986	0.625013	0.9985	0.828252	0.937	0.562569	0.992	0.494911	0.993	CDS conserved hypothetical protein 343601:344551 reverse MW:35143
RPA0317	1.592568	0.0015	1.910372	0.004	1.418469	0.0055	1.675348	0.0005	1.662245	0.001	CDS sensor histidine kinase with a response regulator receiver domain 344712:346622 reverse MW:67564
RPA0318	0.692848	0.944			1.390519	0.016	0.532091	0.959	0.728008	0.9825	CDS putative Mg(2+) chelatase family protein 346749:348287 reverse MW:53708
RPA0319	0.803197	0.866			1.06253	0.4475			1.079948	0.4215	CDS hypothetical protein 348387:348611 reverse MW:7956
RPA0320									0.926404	0.6265	CDS autoinducer (acylhomoserine lactone) synthase 348608:349264 reverse MW:24646
RPA0321	1.106553	0.152	0.771633	0.9785	1.051654	0.334	0.819545	0.9455	1.132967	0.1045	CDS two-component transcriptional regulator, LuxR family 349350:350081 reverse MW:26938
RPA0322	0.676027	0.997	0.561262	0.998	0.605726	0.998	0.542813	0.9715	0.448668	1	gshB putative glutathione synthetase 350318:351259 reverse MW:34553
RPA0323	0.663442	0.975	0.464423	0.966	0.706749	0.868	0.747532	0.897	0.607852	0.985	CDS Protein of unknown function UPF0102 351332:351724 reverse MW:14260
RPA0324	0.897193	0.814	0.833389	0.757	0.878004	0.885	1.191783	0.3915	0.955457	0.6355	CDS Uroporphyrin-III C/tetrapyrrole (Corrin/Porphyrin) methyltransferase 351711:352673 reverse MW:34579
RPA0325	0.972201	0.6145	0.671256	0.9765	0.921957	0.8465	1.035788	0.4145	0.817478	0.929	CDS conserved unknown protein 352886:354085 forward MW:40668
RPA0326	0.830223	0.856	0.826742	0.935	0.846663	0.936	1.273917	0.0955	1.036258	0.3735	CDS DUF24, predicted transcriptional regulator, related to MarR family 354103:354465 reverse MW:13495
RPA0327	0.858091	0.9455	0.733312	0.9985	1.017246	0.4245	0.810286	0.9495	0.81349	0.98	hemN2 possible oxygen-independent coproporphyrinogen III oxidase (hemN) 354870:356027 reverse MW:42048
RPA0328	0.657796	0.999	0.526529	0.9975	0.927318	0.754	0.544453	0.996	0.666472	0.9885	CDS Ham1-like protein 356017:356649 reverse MW:22219
RPA0329	0.705597	0.992	0.897636	0.931	0.518158	0.994	0.578149	0.999	0.72131	0.959	rph ribonuclease PH 356701:357414 reverse MW:25980
RPA0330	0.729528	0.994	0.562374	0.997	0.848646	0.923	0.607974	0.996	0.673408	0.988	hrcA transcriptional repressor of class I heat shock genes 357569:358657 forward MW:39044
RPA0331	0.635482	0.9995	0.681332	0.985	0.80991	0.98	0.662104	0.9905	0.754239	0.976	CDS possible heat shock protein (HSP-70 COFACTOR), grpE 358745:359371 forward MW:22207
RPA0332	0.701065	0.9935	0.751564	0.9685	0.883016	0.8875	0.532573	1	0.707788	0.992	CDS conserved unknown protein 359478:360419 reverse MW:33481
RPA0333	0.900468	0.77	0.594654	0.9995	0.863757	0.854	0.561186	0.991	0.625697	0.9955	dnaK heat shock protein DnaK (70) 360754:362649 forward MW:67947
RPA0334	0.668004	0.9895	0.707796	0.99	0.861404	0.934	0.683446	0.996	0.752704	0.9875	dnaJ heat shock protein DnaJ (40) 362864:364003 forward MW:40992
RPA0335	0.864961	0.865	1.188144	0.062	0.832075	0.9285	1.024837	0.4325	1.140619	0.0825	CDS putative phospholipid N-methyltransferase 364097:364702 forward MW:22385
RPA0336	0.912481	0.878	0.912747	0.8805	0.876412	0.95	0.817733	0.927	0.81426	0.976	CDS NADPH-dependent FMN reductase 364804:365385 forward MW:20919
RPA0337	0.80256	0.934	0.870682	0.726	0.776472	0.8995	0.716785	0.9395	0.640439	0.992	pyrF orotidine 5`-phosphate decarboxylase 365393:366106 forward MW:24690
RPA0338	0.930627	0.785	0.846781	0.913	0.855355	0.9205	0.706763	0.99	0.539182	0.995	CDS conserved unknown protein 366132:366440 forward MW:11500
RPA0339	0.836801	0.9465	0.85523	0.968	0.880879	0.9435	0.701163	0.994	0.678705	0.998	dapB dihydrodipicolinate reductase 366537:367352 forward MW:27784
RPA0340	0.734669	0.9915	0.628879	0.9975	0.808708	0.9765	0.53147	1	0.725554	0.995	pgm1 phosphoglycerate mutase 367433:368947 reverse MW:53352
RPA0341	0.759051	0.996	0.678193	0.9985	1.00939	0.442	0.762716	0.979	0.790546	0.981	ogt possible Ada polyprotein (O6-methylguanine-DNA methyltransferase) 369039:369971 reverse MW:33257
RPA0342	0.741326	0.96	1.032179	0.3515	0.984705	0.562	0.818429	0.925	0.761123	0.986	CDS conserved hypothetical protein 369987:370502 reverse MW:18695
RPA0343	0.782049	0.842	1.178308	0.062	0.930069	0.698	0.910782	0.7375	0.732077	0.949	nth endonuclease III DNA-(apurinic or apyrimidinic site) lyase 370525:371310 forward MW:28500
RPA0344	0.970467	0.5645	0.854099	0.824	1.069879	0.285	0.458392	0.9975	0.671214	0.997	CDS conserved hypothetical protein 371426:372997 reverse MW:56171
RPA0345	0.892124	0.9485	0.900992	0.788	1.022994	0.438	0.830861	0.944	0.817973	0.951	CDS putative protoporphyrin IX magnesium chelatase bchO 373120:374088 reverse MW:34345
RPA0346	0.680965	0.993	0.829475	0.9475	0.967566	0.672	0.644865	0.998	0.67188	0.998	CDS conserved hypothetical protein 374662:375405 reverse MW:26436
RPA0347	0.852211	0.691	1.307016	0.053	1.74534	0.042	0.824389	0.9485	0.455924	0.9845	aceK putative isocitrate dehydrogenase kinase/phosphatase 375493:377325 reverse MW:67975
RPA0348	1.044808	0.2485	1.073766	0.1525	1.187407	0.0355	1.074878	0.285	1.141769	0.0785	CDS possible hydrolase 377649:378572 reverse MW:32422
RPA0349	0.916721	0.8975	0.678266	0.994	1.121113	0.0665	0.815929	0.9485	0.786008	0.983	dcm possible site-specific DNA-methyltransferase 378721:379893 forward MW:42778
RPA0350	0.970866	0.6105	1.123246	0.0765	1.106601	0.162	1.088946	0.2695	0.994063	0.526	vsr putative patch repair protein 379890:380306 forward MW:16050
RPA0351	0.824598	0.9525	1.016596	0.4115	0.910714	0.8055	0.966511	0.599	0.867741	0.9555	CDS hypothetical protein 380311:381132 forward MW:30187
RPA0352	1.021794	0.397	1.080023	0.1685	0.801162	0.9685	0.966814	0.658	1.172647	0.0695	lepA possible GTP-binding protein LepA 381139:382950 reverse MW:66746
RPA0353	0.790624	0.992	0.746854	0.9965	0.673425	0.9955	0.504709	0.9995	0.680641	0.9985	CDS conserved hypothetical protein 383056:384633 forward MW:57388
RPA0354	0.916246	0.812	1.077892	0.176	0.923378	0.6865	0.875421	0.765	0.864941	0.84	CDS PTS system phosphocarrier protein HPr, nitrogen regulation 384654:384986 reverse MW:11408
RPA0355	0.867093	0.85	1.10968	0.1125	0.97957	0.5855	0.999193	0.5015	0.949044	0.738	CDS PTS system permease (IIAMan), nitrogen regulatory IIA protein 384983:385384 reverse MW:14152
RPA0356	1.239465	0.1415	1.375321	0.068	1.261395	0.14	0.847278	0.718	0.703063	0.9645	CDS PTS system Hpr Kinase 385572:386039 reverse MW:15882
RPA0357	0.804639	0.9875	0.871719	0.955	1.08715	0.1305	0.799042	0.9665	0.821579	0.959	exoS, chvG two component sensor histidine kinase 386036:387781 reverse MW:64625
RPA0358	0.726056	0.9685	0.990594	0.5445	0.992398	0.5245	0.606492	0.994	0.822786	0.9505	chvI two-component transcriptional regulator ChvI, winged helix family 387944:388645 reverse MW:26523
RPA0359	0.904403	0.8185	0.984435	0.5735	1.162495	0.1575	1.079889	0.2515	1.095433	0.205	CDS conserved unknown protein 388879:389613 forward MW:26825
RPA0360	0.834745	0.968	0.991848	0.5455	1.097471	0.216	0.639	0.999	0.577532	1	pckA phosphoenolpyruvate carboxykinase 389802:391415 forward MW:58772
RPA0361	0.891718	0.7885	0.935621	0.682	0.887839	0.9255	0.63167	0.9395	0.534038	0.983	CDS unknown protein 391503:392378 reverse MW:31170
RPA0362			0.619367	0.9955							penP, penA putative class A beta-lactamase precursor (penicillinase) 392647:393522 forward MW:30328
RPA0363	1.420614	0.015	0.941653	0.646	1.204706	0.0615	1.488994	0.037	1.414161	0.0195	CDS Endonuclease/Exonuclease/phosphatase family 393537:394664 reverse MW:42223

RPA0364	0.989653	0.545	0.85722	0.9665	1.085565	0.1425	0.897848	0.81	0.853129	0.9535	CDS possible permease 394743:395546 reverse MW:26800
RPA0365	1.345557	0.017	1.063845	0.2815	1.036804	0.335	1.236331	0.1815	1.508492	0	CDS Beta-lactamase-like 395640:396536 forward MW:32631
RPA0366	0.938123	0.7325	0.791216	0.9645	1.01253	0.4705	1.197018	0.1805	1.120377	0.1015	CDS unknown protein 396635:396997 forward MW:12830
RPA0367	1.005303	0.4645	1.04559	0.316	1.473388	0.002	1.26896	0.0265	1.675981	0.001	rpoH RNA polymerase sigma 32 subunit, RpoH, stress response sigma factor 397207:398106 reverse MW:33874
RPA0368	0.967829	0.6275	1.247966	0.0175	0.88584	0.783	1.701798	0.0035	1.947615	0.0005	rluD possible pseudouridine synthases 398328:399551 reverse MW:43239
RPA0369	1.164885	0.0475	1.716398	0.001	1.119898	0.1475	1.685264	0.0185	2.232559	0.001	CDS Aminoacyl-tRNA synthetase, class I:ATP-binding region, ATPase-like 400116:402719 reverse MW:96971
RPA0370	1.238817	0.0285	1.309694	0.0065	1.117002	0.17	1.535016	0.0125	1.262365	0.058	CDS putative diguanylate cyclase (GGDEF)/phosphodiesterase (EAL) with PAS domains 403032:405548 reverse MW:91868
RPA0371	1.084457	0.152	0.874777	0.962	1.045512	0.327	0.863606	0.898	1.223366	0.0215	metB putative cystathionine gamma-lyase 405749:406933 reverse MW:42189
RPA0372	1.127885	0.254	1.137315	0.1035	1.14768	0.3355	1.186875	0.12	1.40432	0.0165	CDS transcriptional regulators, AsnC family 407065:407526 forward MW:16525
RPA0373	0.784701	0.897	0.669687	0.9855	1.055689	0.3845	0.928483	0.6705	1.105014	0.249	trxC thioredoxin 407527:407964 reverse MW:15919
RPA0374	0.971704	0.647	0.878244	0.9105	1.159254	0.068	0.950746	0.6655	1.088878	0.1345	CDS putative Zn-containing alcohol dehydrogenase 408104:409087 reverse MW:34514
RPA0376	0.94296	0.6855	0.826707	0.969	0.931949	0.792	0.812314	0.8815	0.77453	0.9905	pimt1 putative L-isoaspartyl protein carboxyl methyltransferase 409612:410334 forward MW:25455
RPA0377	0.73077	0.9995	0.708846	0.997	1.097363	0.2405	0.674668	0.9725	0.558534	0.9995	CDS conserved unknown protein 410486:411310 forward MW:30156
RPA0378	0.857118	0.8465	1.150018	0.062	0.864803	0.8705	1.033541	0.4	0.795459	0.979	melA putative alpha-D-galactoside galactohydrolase 411507:412787 reverse MW:47421
RPA0379	0.661199	0.9145	1.044409	0.328	0.723984	0.943	0.64154	0.9915	0.439353	0.986	pfkB putative 6-phosphofructokinase 413011:413949 forward MW:32563
RPA0380	1.149844	0.1755	1.682868	0.0215	1.211326	0.094	1.040409	0.42	1.087409	0.243	CDS possible oxidoreductase similar to formate dehydrogenase and cbbBc of R. eutropha. 414065:416377 forward MW:85393
RPA0381	0.890953	0.721	1.352608	0.016	1.236666	0.064	0.897126	0.8115	0.787367	0.933	glgC glucose-1-phosphate adenylyltransferase 416649:417911 forward MW:47026
RPA0382	1.009883	0.4785	1.023598	0.392	0.982249	0.589	0.875697	0.792	0.709753	0.9955	glgA1 putative glycogen synthase 417908:419359 forward MW:51088
RPA0383	0.805818	0.979	0.797492	0.9585	0.892055	0.8125	0.628362	0.9905	0.566621	0.999	CDS probable enoyl CoA-hydratase/isomerase 419505:420305 forward MW:28279
RPA0384	0.766832	0.99	0.926976	0.846	0.853704	0.953	0.768437	0.9865	0.651051	1	CDS conserved unknown protein 420302:420874 forward MW:20328
RPA0385	1.291062	0.036	1.035118	0.397	1.202649	0.086	1.290788	0.063	1.348298	0.0225	radC possible DNA repair protein RadC 420890:421615 reverse MW:26634
RPA0386	1.350193	0.05	2.624545	0.004	1.396118	0.0405	1.759365	0.0025	2.252496	0.001	CDS Ku domain 421950:423050 forward MW:40157
RPA0387	0.904912	0.862	0.634347	0.9975	1.005408	0.479	0.865467	0.809	0.986393	0.574	map putative methionine aminopeptidase 423309:424133 reverse MW:29792
RPA0388	1.096227	0.189	0.857245	0.969	0.923488	0.8195	0.97489	0.621	1.026339	0.343	CDS possible Na+/H+ antiporter 424329:426122 forward MW:63208
RPA0389	0.905646	0.92	0.818284	0.947	1.134931	0.066	0.804129	0.973	0.943189	0.7495	mepA putative penicillin-insensitive murein endopeptidase A 426147:427109 reverse MW:35344
RPA0390	1.188487	0.123	0.861454	0.847	0.882336	0.729	1.160597	0.1505	1.376851	0.009	CDS putative diguanylate cyclase (GGDEF)/phosphodiesterase (EAL) with PAS domains 427489:429726 forward MW:82460
RPA0391	1.231487	0.05	1.25778	0.126	1.009524	0.497	1.924363	0.002	1.987788	0.0015	CDS possible alkaline phosphatase 429741:431498 reverse MW:62019
RPA0392	0.941651	0.701	0.913855	0.7205	0.683455	0.976	0.894108	0.8355	0.95793	0.6135	argG argininosuccinate synthase 431740:433077 reverse MW:48969
RPA0393	0.839339	0.962	0.902718	0.836	0.795054	0.988	0.678767	0.9195	0.719061	0.972	CDS PA-phosphatase related phosphoesterase 433170:433949 reverse MW:28714
RPA0394	1.0272	0.378	0.893483	0.8165	1.035662	0.354	0.701366	0.9925	0.711562	0.9735	CDS conserved hypothetical protein 433946:434446 reverse MW:17458
RPA0395	0.779127	0.954	0.992623	0.533	0.610756	0.9975	0.713932	0.959	1.184595	0.1105	CDS Metal dependent phosphohydrolase 434446:435039 reverse MW:21615
RPA0396	0.747878	0.9975	0.848358	0.9465	0.6666	0.997	0.88139	0.858	1.209492	0.0565	CDS Cfr family protein 435044:436318 reverse MW:47033
RPA0397	0.582367	0.999	0.792222	0.9475	0.771132	0.9855	0.383055	0.9995	0.470651	0.9985	CDS conserved unknown protein 436430:437005 reverse MW:19608
RPA0398							0.747097	0.8265			CDS putative 2, 4-dienoyl-CoA reductase (NADPH) precursor 437159:437995 reverse MW:29244
RPA0399											CDS possible transposase 438123:439292 reverse MW:44303
RPA0400	0.979288	0.589	0.855083	0.8935	0.740701	0.977	0.761711	0.9895	0.6977	0.998	CDS possible alcohol dehydrogenases and quinone oxidoreductases. 439493:440467 forward MW:34165
RPA0401	1.080659	0.133	0.937732	0.798	1.199371	0.0205	0.952357	0.6495	0.994569	0.5235	CDS NAD binding site:Amine oxidase 440595:442730 reverse MW:75940
RPA0402	0.856998	0.9525	0.806927	0.9475	1.199559	0.0875	0.951774	0.6125	1.206635	0.0375	CDS possible transcriptional regulator, TetR family 442869:443489 forward MW:22663
RPA0403	0.886907	0.9055	0.768651	0.995	1.206056	0.072	0.878929	0.854	1.132471	0.1515	CDS conserved hypothetical protein 443508:443882 reverse MW:14008
RPA0404	0.627661	0.9875	0.714187	0.9945	0.812965	0.878	0.637655	0.996	0.879764	0.8595	phhB 6-pyruvoyl-tetrahydropterin synthase/dimerization cofactor of hepatocyte nuclear factor 1 alpha (TCF1) 443965:444267 reverse MW:11321
RPA0405	1.161021	0.0695	0.987414	0.554	1.468409	0.012	0.914904	0.7025	1.151647	0.2895	CDS conserved hypothetical protein 444410:445855 forward MW:50957
RPA0406	0.456171	0.9985	0.360724	1	0.438514	0.9995	0.149253	1	0.353192	0.994	CDS conserved unknown protein 445859:447304 reverse MW:54585
RPA0407	0.532572	0.983	0.431	0.999	0.442057	0.9975	0.220259	0.9995	0.739559	0.9765	CDS possible TonB-dependent receptor (outer membrane siderophore receptor) 447309:449585 reverse MW:82182
RPA0408	0.974609	0.537	1.843457	0	0.67547	0.983	1.07116	0.2745	2.415327	0.007	bipA conserved GTPase 450314:452137 forward MW:67109
RPA0409	1.178859	0.0825	1.108479	0.1035	1.240109	0.021	1.705902	0.002	1.988296	0.001	CDS NAD binding site:Amine oxidase 452247:453515 forward MW:45063
RPA0410	0.951022	0.654	0.687711	0.994	1.210356	0.051	1.011568	0.455	1.028281	0.4135	CDS GCN5-related N-acetyltransferase 453691:454200 forward MW:18853
RPA0411	0.756531	0.993	0.863648	0.8835	0.851708	0.923	0.738365	0.994	0.788221	0.986	ppa inorganic pyrophosphatase 454277:454813 forward MW:19751
RPA0412	1.356279	0.002	1.13864	0.0335	1.277009	0.006	1.110249	0.116	1.108293	0.073	CPS1, CPS putative Gly-X carboxypeptidase YSCS precursor 454849:456330 forward MW:53821
RPA0413	0.724214	0.971	0.926751	0.7285	0.851467	0.941	0.895883	0.8175	0.933038	0.7275	CDS putative methylenetetrahydrofolate dehydrogenase 456520:457407 reverse MW:30536
RPA0414	0.72939	0.953	0.557645	0.9985	0.748044	0.8025	0.81471	0.954	0.687387	0.961	CDS DUF167 457514:457852 reverse MW:11799
RPA0415	0.737952	0.988	0.914064	0.7845	0.766191	0.9855	0.725798	0.991	0.647453	0.9985	CDS Family of unknown function YGGT 457866:458363 reverse MW:18327
RPA0416	1.065219	0.2495	1.072312	0.226	1.108161	0.157	2.608027	0	3.027401	0	CDS putative enoyl-CoA hydratase 458632:459444 reverse MW:29940
RPA0417	1.151901	0.2785	0.685613	0.9955	1.205257	0.016	0.898277	0.838	0.767996	0.9695	CDS conserved hypothetical protein 459526:460026 reverse MW:18935
RPA0418	1.049713	0.276	1.412512	0.0265	1.072365	0.227	2.201745	0.001	1.507301	0.002	CDS Glutamine amidotransferase class-I 460130:460927 reverse MW:29588
RPA0419	0.99547	0.5055	1.246667	0.0465	0.995885	0.529	1.274151	0.0245	1.276051	0.0015	CDS possible short chain dehydrogenase/reductase family member 461048:461827 reverse MW:27621
RPA0420	0.962411	0.643	1.447228	0.01	1.154428	0.1505	1.084618	0.302	1.071903	0.2205	CDS conserved hypothetical protein 462010:462630 reverse MW:22364
RPA0421	1.027241	0.417	0.913179	0.7855	1.025805	0.4015	0.928354	0.696	0.887248	0.844	CDS possible cytochrome P450 hydroxylase superfamily proteins 462674:464059 reverse MW:51065
RPA0422	0.976282	0.629	0.967052	0.678	0.773515	0.989	0.8579	0.9465	1.168094	0.0345	CDS possible dehydrogenase 464180:465181 reverse MW:36575
RPA0423	0.841693	0.9325	1.089781	0.1345	0.896839	0.8345	0.99896	0.51	1.100851	0.0825	CDS conserved hypothetical protein 465416:465940 forward MW:18999
RPA0424	2.295377	0	1.802914	0.0075	3.036484	0.005	2.794808	0.018	2.548678	0.001	CDS transcriptional regulator, FUR family; probable iron response regulator IRR 466048:466539 reverse MW:18455
RPA0425	0.805746	0.956	1.454317	0.0085	1.039033	0.4385	0.832355	0.8775	0.649017	0.9875	fabA 3-hydroxydecanoyl-acyl carrier protein dehydrase 466798:467325 forward MW:19385
RPA0426	0.855809	0.936	1.072158	0.156	0.898221	0.874	0.7913	0.982	0.773726	0.982	fabB beta-ketoacyl-ACP synthase I 467387:468613 forward MW:42904
RPA0427	0.438658	0.9915	0.951455	0.6385	0.441674	0.9985	0.466288	0.9925	0.381028	0.9885	CDS enoyl-acyl carrier protein reductase 468789:469598 forward MW:28524
RPA0428	0.920915	0.798	1.197558	0.0155	0.945456	0.7005	1.548325	0.001	1.300334	0.0245	CDS conserved hypothetical protein 469771:470289 reverse MW:17802
RPA0429	1.611046	0.077	2.434019	0.0005	1.962384	0.0025	5.690128	0	3.524593	0	katG catalase/peroxidase 470517:472727 reverse MW:80870
RPA0430	0.617038	0.9985	0.549735	0.9995	0.735177	0.9905	0.494724	0.997	0.847081	0.898	oxyR hydrogen peroxide-inducible transcriptional regulator OxyR, LysR family 472997:473935 forward MW:33796
RPA0431	0.532568	1	0.49671	1	0.64883	0.9985	0.319286	1	0.386452	1	CDS methyl-accepting chemotaxis receptor/sensory transducer with PAS domain 473947:475629 reverse MW:60547
RPA0432	0.92403	0.8625	0.853989	0.955	1.113201	0.174	0.809177	0.967	0.759798	0.895	pnp polyribonucleotide nucleotidyltransferase 475919:478087 reverse MW:78285
RPA0433	0.882915	0.88	1.00852	0.4495	1.009542	0.4555	0.984062	0.574	1.024303	0.42	rpsO ribosomal protein S15 478426:478695 reverse MW:10142
RPA0434	0.950866	0.7185	1.125408	0.0515	1.076122	0.1875	1.136393	0.1165	1.347808	0.0095	truB putative tRNA pseudouridine 55 synthase 478698:479798 reverse MW:39249
RPA0435	0.717475	0.9905	1.092982	0.2015	0.598333	0.9965	0.986429	0.5365	1.094634	0.349	rbfA putative ribosome-binding factor A 479798:480211 reverse MW:15482
RPA0436	0.869157	0.9585	0.917328	0.8705	0.794706	0.9695	0.844258	0.9315	0.979251	0.562	infB putative translation initiation factor if-2 480385:483036 reverse MW:95506
RPA0437	0.736175	0.8415			0.649437	0.9005			0.531129	0.8515	CDS DUF448 483029:483808 reverse MW:27266
RPA0438	0.94941	0.742	0.912805	0.807	1.120856	0.088	0.891373	0.7995	0.896769	0.8855	nusA putative NusA protein, transcriptional termination factor 483870:485483 reverse MW:59394
RPA0439	0.765731	0.998	0.956379	0.709	0.613073	0.992	0.746497	0.9855	0.825249	0.933	CDS DUF150 485486:486265 reverse MW:28333
RPA0440	1.239076	0.009	1.325898	0.001	1.359096	0.0095	1.366614	0.016	1.535023	0.0015	CDS conserved hypothetical protein 486599:487684 forward MW:39721
RPA0441	1.119525	0.266	0.860698	0.916	1.175874	0.0295	1.03976	0.3745	1.123582	0.123	CDS conserved hypothetical protein 487808:488656 forward MW:31381

RPA0442	1.185936	0.0345	1.397832	0.0015	1.047465	0.312	1.097583	0.193	1.193228	0.029	CDS Putative methyltransferase 488669:489466 reverse MW:30230
RPA0443	1.412668	0.0045	1.693554	0	1.237506	0.0375	1.507016	0.012	1.361655	0.009	CDS possible transcriptional regulator, XRE family 489541:489960 reverse MW:15094
RPA0444	0.835577	0.9585	1.028776	0.348	0.860389	0.9115	0.878966	0.8795	0.872549	0.9455	lnt putative apolipoprotein n-acyltransferase 490161:491771 reverse MW:58083
RPA0445	1.050104	0.342	0.786863	0.9915	0.991372	0.545	0.929323	0.789	0.905542	0.873	CDS possible HlyC/CorC family of transporters with CBS domains 491768:492913 reverse MW:41272
RPA0446	0.772853	0.9465	0.747868	0.987	0.805351	0.9755	0.742788	0.92	0.737632	0.996	CDS Protein of unknown function UPF0054 492915:493487 reverse MW:20653
RPA0447	0.915645	0.81	1.014958	0.416	1.321016	0.1045	1.060738	0.299	0.981206	0.538	CDS possible phoH-like protein 493487:494368 reverse MW:31861
RPA0448	0.798298	0.9895	0.947101	0.7725	0.737537	0.983	0.654314	0.9955	1.094262	0.164	miaB tRNA-i(6)A37 modification enzyme MiaB 494549:495940 reverse MW:50589
RPA0449	0.608791	0.9845	0.934547	0.782	0.538425	0.996	0.826224	0.8935	0.872858	0.7875	CDS possible hydrolases/phosphatases 496060:496719 reverse MW:23133
RPA0450	0.913761	0.8465	1.043844	0.331	0.839025	0.96	0.828454	0.953	0.720435	0.995	CDS transcriptional regulator, FUR family; probable FUR protein 496807:497238 reverse MW:16719
RPA0451	0.66064	0.99	0.657275	0.988	0.50673	0.999	0.49871	0.991	0.540265	0.9985	rimI putative RimI protein, peptide N-acetyltransferase 497301:497786 reverse MW:18368
RPA0452	0.600269	0.9995	0.577604	0.9985	0.606886	0.9985	0.603159	0.999	0.678113	0.999	CDS Glycoprotease (M22) metalloprotease 497809:498504 reverse MW:23929
RPA0453	0.853956	0.965	0.784936	0.9745	1.002355	0.4915	0.845926	0.906	0.869146	0.9475	CDS possible NifU-like domain (residues 119-187) 498641:499207 reverse MW:20292
RPA0454	0.898318	0.8885	0.704138	0.9975	0.994082	0.5145	0.810375	0.921	0.82104	0.931	CDS conserved hypothetical protein 499353:499901 reverse MW:19550
RPA0455	1.020153	0.4175	1.179231	0.025	0.715369	0.9945	0.946299	0.738	1.044956	0.374	trpS trytophanyl-tRNA synthetase 500093:501145 reverse MW:38240
RPA0456											CDS possible mviN family virulence factors, possible efflux protein 501201:502757 reverse MW:52591
RPA0457	0.632683	0.9995	0.910715	0.9105	0.457552	1	0.577939	0.999	0.644297	0.9735	CDS possible cabohydrate kinases 503032:504099 forward MW:37478
RPA0458	0.948926	0.6055	0.594981	0.982	0.862988	0.784			0.577059	0.9925	CDS possible fatty acid-CoA ligases. 504322:505875 reverse MW:56768
RPA0459	1.277942	0.171	0.861369	0.953	1.454772	0.048	1.127054	0.1575	0.846967	0.852	CDS possible fatty acid-CoA ligases 505524:506015 reverse MW:17526
RPA0460	1.118564	0.2325	0.665765	0.998	1.341269	0.0245	0.896576	0.7335	0.590164	0.99	CDS putative esterase 506145:507332 reverse MW:42722
RPA0461	0.961696	0.651	0.903518	0.8725	1.103454	0.1655	1.131528	0.1465	0.899293	0.798	gabD1 succinate-semialdehyde dehydrogenase 508060:509553 forward MW:52773
RPA0462	0.98328	0.544	0.642347	0.9925	0.836309	0.9065	0.732302	0.927	0.703949	0.9785	CDS putative enoyl-CoA hydratase/isomerase superfamily 509765:510670 reverse MW:33430
RPA0463	0.807424	0.967	0.736078	0.995	0.83289	0.917	0.805954	0.9745	0.752315	0.989	CDS transcriptional regulator, TetR family 510757:511386 forward MW:23114
RPA0464	0.905996	0.7305	0.587414	0.9995	0.758213	0.9865	0.603229	0.994	0.555639	0.997	CDS putative long-chain fatty-acid-CoA ligase 511411:513036 forward MW:58390
RPA0465	0.775613	0.9895	0.696003	0.9505	1.322711	0.007	0.480318	0.9935	0.439285	0.9965	CDS possible transmembrane protein 513127:514560 reverse MW:52128
RPA0466	1.025973	0.369	0.943514	0.788	1.483727	0.0005	0.82253	0.9565	0.787463	0.9715	CDS conserved hypothetical protein 514700:515383 reverse MW:24869
RPA0467	0.93785	0.8265	0.707203	0.992	1.004557	0.475	0.708833	0.962	0.721312	0.9855	CDS putative glycerate dehydrogenase 515386:516372 reverse MW:35073
RPA0468	0.806983	0.9355	1.146274	0.0545	0.839286	0.912	0.902184	0.8165	0.983741	0.572	CDS putative ATP-binding protein of ABC transporter 516372:517196 reverse MW:29248
RPA0469	0.979453	0.56	0.794284	0.7465	1.071233	0.288	1.462942	0.2685	0.975518	0.5915	AtsC putative sulfate ester transporter; ATP-binding component. 517193:518023 reverse MW:29670
RPA0470	1.074918	0.226	0.819126	0.9835	1.115648	0.1645	0.922019	0.7935	1.087057	0.134	CDS perplasmic binding protein of ABC transporter 518032:519174 reverse MW:41705
RPA0471	1.085767	0.2265	0.821976	0.984	1.23717	0.008	0.940516	0.747	0.918699	0.7855	CDS putative creatine amidohydrolase 519304:520116 forward MW:29190
RPA0472	2.742382	0.047	6.580956	0	1.441412	0.0135	1.866479	0.0275	3.092324	0.0045	CDS OmpA-like transmembrane domain 520350:522560 forward MW:80065
RPA0473	0.959984	0.671	0.857452	0.942	0.901036	0.868	0.656237	0.9975	0.912187	0.8635	PA3602 possible glutamate synthase. 522591:524222 reverse MW:59584
RPA0474	0.882565	0.903	1.057226	0.369	0.685212	0.994	0.920163	0.6115	1.066504	0.259	CDS conserved unknown protein 524516:525466 forward MW:34156
RPA0475	0.934128	0.741	0.869151	0.8185	0.794998	0.956	0.851937	0.813	0.912106	0.7755	CDS putative oxidoreductase 525558:526559 forward MW:35474
RPA0476	1.463137	0.0025	1.059599	0.2265	1.05299	0.308	1.248498	0.0275	1.349628	0.0045	CDS conserved hypothetical protein 526913:528244 forward MW:46521
RPA0477	0.769384	0.9895	0.864204	0.932	0.879932	0.916	0.581613	0.995	0.738732	0.995	CDS conserved hypothetical protein 528378:528938 forward MW:19284
RPA0478	0.887061	0.823	0.869723	0.9595	0.908437	0.8885	0.828838	0.967	0.734118	0.9965	CDS conserved hypothetical protein 528996:529292 forward MW:10278
RPA0479	0.812102	0.975	1.079629	0.1585	1.004225	0.474	0.789169	0.976	0.985966	0.557	fabG1 possible 3-oxoacyl-acyl carrier protein reductase 529346:530128 reverse MW:26995
RPA0480	0.363777	0.998	0.462647	0.985	0.875082	0.638	0.492841	0.989	0.435157	0.996	CDS possible acyl-CoA dehydrogenase 530389:531453 forward MW:36801
RPA0481	0.867464	0.9055	0.828874	0.967	1.028556	0.3835	0.708316	0.9745	0.521554	0.9965	CDS putative acyl-CoA dehydrogenase 531480:532640 forward MW:43002
RPA0482	0.604415	0.9955	0.805207	0.983	0.617765	0.9965	0.62371	0.9995	0.447859	0.996	CDS probable short chain 3-hydroxyacyl-CoA dehydrogenase / enoyl-CoA hydratase 532674:533480 forward MW:28832
RPA0483	0.67202	0.996	0.588975	0.997	0.616315	0.9985	0.623699	0.966	0.468734	0.9995	CDS unknown protein 533625:534389 reverse MW:27274
RPA0484	0.66152	0.9705	0.612775	0.9995	0.734932	0.9975	0.582721	0.9995	0.336706	1	paaG1 putative enoyl-CoA hydratase 534392:535180 reverse MW:27542
RPA0485	0.932782	0.588	0.576151	0.998	0.816985	0.9635	0.584451	0.9935	0.869784	0.859	CDS possible urea/short-chain amide ABC transporter 535357:536562 reverse MW:43026
RPA0486	0.820793	0.9525	0.811379	0.9625	1.070951	0.3205	0.682237	0.989	0.600637	0.945	CDS Staphylococcus nuclease (SNase-like) 536979:537704 forward MW:25426
RPA0487	0.65411	0.998	0.722081	0.994	0.803135	0.963	0.526962	0.998	0.73778	0.9965	CDS conserved unknown protein 537716:539233 forward MW:55404
RPA0488	0.988778	0.5505	0.873185	0.925	0.981672	0.602	0.914647	0.796	1.095536	0.2295	CDS possible CarD-like transcriptional regulator 539338:540000 reverse MW:24183
RPA0489	0.797574	0.9875	1.01284	0.4435	0.918725	0.879	0.754778	0.9765	0.776809	0.9915	CDS ferredoxin II 540697:541035 reverse MW:12513
RPA0490	0.735888	0.9885	1.083006	0.14	0.956953	0.6865	1.130199	0.1305	1.105007	0.167	CDS conserved hypothetical protein 541110:541337 reverse MW:8073
RPA0491	0.855666	0.9765	0.749903	0.992	0.871092	0.9435	0.76427	0.9845	0.764813	0.9905	CDS possible MgpS, ATP-dependent helicase 541410:544691 reverse MW:118664
RPA0492	0.856658	0.7475			0.957192	0.5565			0.887029	0.644	CDS conserved hypothetical protein 544994:546031 reverse MW:36902
RPA0493	0.831338	0.804	1.349028	0.0255	0.74299	0.919	1.108246	0.1875	1.075187	0.3405	rpmB, L28 50S ribosomal protein L28 546167:546472 forward MW:10978
RPA0494	0.649459	0.999	0.510251	0.999	0.770435	0.99	0.537445	0.997	0.781469	0.9895	CDS sensor histidine kinase with PAS/PAC and Response regulator receiver domains 546761:550042 forward MW:118543
RPA0495	0.520808	0.9915	0.819828	0.9735	0.821153	0.7735	0.623376	0.972	0.632576	0.9985	CDS conserved hypothetical protein 550066:551214 reverse MW:41113
RPA0496	0.636346	0.992	0.656841	0.9975	0.645638	0.992	0.640184	0.9985	0.583718	0.999	cobT2 cobT protein 551239:553143 reverse MW:70170
RPA0497	0.719017	0.9945	0.844324	0.969	1.040741	0.3765	1.025558	0.425	0.794714	0.9575	CDS GCN5-related N-acetyltransferase 553140:553550 reverse MW:15725
RPA0498	0.673076	0.999	0.588974	0.9985	0.880441	0.9235	0.622451	0.9985	0.577994	0.9985	cobS2 cobS protein 553555:554550 reverse MW:36988
RPA0499	0.569267	0.983	0.616562	0.992	0.88849	0.7155	0.616359	0.9905	0.526166	0.9835	CDS DedA family 554830:555447 forward MW:21528
RPA0500	0.5353	0.9975	0.621654	0.9945	0.606588	0.9985	0.4499	0.999	0.498965	1	CDS Heat shock protein DnaJ, N-terminal 555512:556156 reverse MW:24385
RPA0501	0.94421	0.6445	1.021201	0.4265	1.202679	0.1375	1.456418	0.0265	2.045451	0.0005	CDS BolA-like protein 556277:556546 forward MW:9553
RPA0502	0.604235	0.9985	0.643187	0.9935	0.553526	0.998	0.49251	0.9995	0.637689	0.9955	CDS probable HlyC/CorC family of transporters with 2 CBS domains 556564:557925 reverse MW:50236
RPA0503	0.704601	0.872	0.56081	0.967	0.546832	0.97	0.566944	0.967	0.597294	0.991	aroB putative 3-dehydroquinate synthase 557973:559118 reverse MW:40366
RPA0504	0.772344	0.98	0.738278	0.9945	0.811468	0.9825	0.627214	0.996	1.152229	0.087	aroK putative shikimate kinase 559129:559740 reverse MW:22173
RPA0505	0.846784	0.918	1.108189	0.184	0.878991	0.8685	0.913972	0.7405	0.87014	0.7565	CDS conserved hypothetical protein 559870:560016 forward MW:5231
RPA0506	0.925257	0.8435	0.916405	0.6835	0.83935	0.956	0.786191	0.8715	0.84875	0.959	CDS site-specific integrase/recombinase XerD 560033:561049 forward MW:37024
RPA0507	0.62024	0.975	0.727207	0.8995	0.56655	0.931	0.597627	0.972	0.715997	0.966	CDS possible cytochrome b561 561056:561631 reverse MW:21247
RPA0508	0.688497	0.9975	0.830501	0.96	0.672308	0.9925	0.619976	0.999	0.784563	0.934	accA acetyl-CoA carboxylase carboxyltransferase alpha subunit 561895:562857 forward MW:34470
RPA0509	1.177156	0.044	1.177349	0.0315	1.379806	0.0135	1.519274	0.0055	1.490644	0.0385	CDS conserved hypothetical protein 563190:564665 forward MW:52653
RPA0510	0.813278	0.9885	0.782573	0.994	0.710001	0.991	0.692764	0.9965	0.698501	0.9975	secA preprotein translocase secA 564875:567715 reverse MW:106712
RPA0511	0.928911	0.763	1.040425	0.26	0.818525	0.9095	0.780434	0.9365	0.818834	0.9235	CDS PpiC-type peptidyl-prolyl cis-trans isomerase 568058:568993 forward MW:33354
RPA0512	0.895506	0.954	0.798633	0.9825	0.883103	0.9265	0.929001	0.788	0.902158	0.919	mutS DNA mismatch repair protein mutS 569086:571809 reverse MW:97473
RPA0513	1.010535	0.456	0.799239	0.987	0.903628	0.762	0.638672	0.98	0.652346	1	pcaF putative acetyl-CoA acetyltransferase 571985:573193 forward MW:41726
RPA0514	1.031375	0.308	0.977226	0.6155	0.994216	0.5385	0.930383	0.769	0.822965	0.9835	FarB putative efflux pump protein FarB 573372:574934 reverse MW:56050
RPA0515	1.251954	0.0775	1.034043	0.3235	2.299773	0.0005	1.070768	0.3335	1.057272	0.3725	CDS possible efflux pump protein FarA 574938:576107 reverse MW:41554
RPA0516	1.1787	0.151	0.783451	0.8955	1.405892	0.06	1.309049	0.1695	1.215922	0.0315	CDS transcriptional regulator, MarR family 576100:576585 reverse MW:18666
RPA0517	0.837837	0.974	0.695468	0.9815	0.971821	0.5755	0.862905	0.796	1.211131	0.043	CDS transcriptional regulator, Fur family; probable zinc uptake regulator ZUR 576775:577272 forward MW:17855
RPA0518	0.840773	0.8515	0.767227	0.9945	0.880898	0.806	0.854497	0.9215	0.754513	0.996	CDS Permeases of the drug/metabolite transporter (DMT) superfamily 577437:578360 forward MW:32409

RPA0519	1.020428	0.361	0.902262	0.925	1.009308	0.4595	0.88673	0.889	1.10544	0.0895	gcpE gcpE, Essential bacterial protein, involved in density-dependent regulation of peptidoglycan biosynthesis 578344:579669 forward MW:47189
RPA0520											nha possible sodium/hydrogen antiporter 579912:581564 reverse MW:59511
RPA0521			1.846443	0.0235			1.780156	0.067	1.446022	0.203	CDS putative diguanylate cyclase (GGDEF)/phosphodiesterase (EAL) 581747:583456 forward MW:61829
RPA0522	1.79146	0.01	1.650038	0.0125	0.87172	0.6575	1.466324	0.0255	1.486802	0.0075	CDS possible activator of photopigment and puc with BLUF domain 583474:583917 forward MW:16484
RPA0523	0.52706	0.9965	0.31083	1	1.314828	0.0635	0.332581	0.997	0.355214	1	CDS conserved hypothetical protein 583928:584614 reverse MW:25095
RPA0524	0.740116	0.975	0.903635	0.777	0.680066	0.9985	0.574735	0.999	0.576358	0.9975	CDS putative geranyltranstransferase (farnesyl-diphosphate synthase) 584622:585548 reverse MW:32901
RPA0525	0.775043	0.9685	0.854391	0.9515	0.925185	0.832	0.908309	0.8535	1.001757	0.482	CDS possible peptidoglycan transglycosylase 585650:586360 forward MW:25785
RPA0526	0.92582	0.7795	1.460158	0.005	0.729368	0.986	1.299598	0.112	1.206414	0.087	rpmF, L32 50S ribosomal protein L32 586522:586704 forward MW:6993
RPA0527	0.560329	0.9525	0.84476	0.9185	0.71314	0.9755	0.599432	1	0.929207	0.656	CDS conserved hypothetical protein 586947:587579 forward MW:21812
RPA0528	1.178157	0.0215	1.424043	0.0135	1.226381	0.0265	1.703696	0.0015	1.51863	0.006	CDS conserved hypothetical protein 587596:588057 reverse MW:16340
RPA0529	0.851947	0.9655	0.727453	0.996	1.090343	0.1495	0.74342	0.9905	0.914011	0.7845	CDS putative diguanylate cyclase (GGDEF)/phosphodiesterase (EAL) 588149:589891 forward MW:62800
RPA0530	1.076709	0.2785	0.812202	0.974	1.424125	0.01	0.998799	0.498	1.00656	0.486	CDS conserved unknown protein 590022:590690 reverse MW:25279
RPA0531	0.669565	0.9965	0.540733	0.997	0.907114	0.8975	0.553004	0.999	0.471625	1	CDS beta-ketothiolase, acetoacetyl-CoA thiolase 590894:592072 forward MW:40553
RPA0532	1.000751	0.502	0.442607	0.999	1.054358	0.3465	1.18097	0.22	0.720294	0.943	CDS beta-ketothiolase, acetoacetyl-CoA reductase 592255:592980 forward MW:25466
RPA0533	1.069862	0.3935	0.671723	0.9655	0.874372	0.815	1.851045	0.0075	1.116205	0.2045	CDS possible transmembrane protein 593057:593923 forward MW:29896
RPA0534	1.668784	0.001	1.36355	0.0245	1.747825	0.021	1.775767	0.0155	1.967411	0.0015	CDS conserved hypothetical protein 593943:594464 reverse MW:18440
RPA0535	0.871465	0.9265	0.886083	0.9065	0.69705	0.999	0.78018	0.983	0.84012	0.966	hrpB putative ATP-dependent helicase 594594:597071 reverse MW:89540
RPA0536	1.189314	0.0665	1.272882	0.027	0.942894	0.6855	1.827751	0.0045	1.666787	0.0015	CDS Acyltransferase 3 family 597245:598297 forward MW:38981
RPA0537	1.173436	0.0795	1.123444	0.157	1.028937	0.3375	1.77846	0.0075	1.30505	0.045	CDS coenzyme A transferase 598415:599974 reverse MW:56809
RPA0539	1.272653	0.0095	1.204767	0.0225	1.41111	0.009	1.961169	0.0005	2.41317	0	CDS transcriptional regulator, MarR family 602737:603270 forward MW:19512
RPA0540	1.34891	0.0865	0.910403	0.715	0.848658	0.835	1.28154	0.0995	1.239257	0.038	CDS hypothetical protein 603265:604290 reverse MW:36699
RPA0541	0.924284	0.7825	0.870643	0.705	0.934202	0.7365	0.672853	0.9555	0.719635	0.9905	CDS conserved hypothetical protein 604854:605402 forward MW:19377
RPA0542	1.157179	0.0475	1.405915	0.0025	1.58562	0.002	1.275364	0.014	1.165482	0.0695	CDS conserved hypothetical protein 605405:606457 reverse MW:36034
RPA0543	1.211984	0.0575	0.911348	0.7715	1.57662	0.002	1.203506	0.087	1.273688	0.1175	CDS unknown protein 606652:607179 forward MW:18483
RPA0544	1.065997	0.2505	1.247512	0.015	1.043626	0.2885	1.174932	0.0535	1.185432	0.037	CDS LrgA family holin protein 607333:607716 forward MW:13224
RPA0545	1.066699	0.2135	1.274559	0.006	1.125006	0.1405	1.049847	0.31	1.088285	0.167	CDS conserved hypothetical protein 607713:608435 forward MW:25071
RPA0546	0.873826	0.9125	0.482619	0.995	1.841064	0.0255	0.676429	0.942	0.786892	0.9625	CDS hypothetical protein 608530:608994 forward MW:15613
RPA0547	1.168559	0.052	0.980719	0.604	1.215845	0.015	0.969629	0.655	0.893018	0.931	CDS conserved hypothetical protein 608998:610074 reverse MW:39082
RPA0548	0.851692	0.9715	0.870194	0.9485	0.804425	0.9635	0.788564	0.9465	0.899564	0.8995	CDS Protein of unknown function UPF0118 610257:611417 forward MW:41290
RPA0549	0.576748	0.998	0.673321	0.977	1.12846	0.1545	0.54761	0.9935	0.437894	0.999	ChrR sensor protein ChrR, cytochrome cycA regulator 611414:612076 reverse MW:23799
RPA0550	0.686866	0.997	0.57562	0.9895	1.332539	0.0345	0.548782	0.9935	0.494429	1	CDS RNA polymerase ECF-type sigma factor 612073:612660 reverse MW:22082
RPA0551	0.9806	0.5655	0.957866	0.6295	1.484756	0.0415	1.074147	0.3765	0.937917	0.6835	CDS transcriptional regulator, LysR family 613289:614170 reverse MW:31669
RPA0552			0.793387	0.893			0.838765	0.902	1.027011	0.408	dctA1 dicarboxylate transport protein 614276:615583 forward MW:45228
RPA0553	1.076195	0.2345	1.025379	0.385	1.04952	0.324	0.97139	0.6035	1.084834	0.1445	CDS conserved hypothetical protein 615621:616460 forward MW:30288
RPA0554									1.369472	0.075	CDS putative ureidoglycolate hydrolase 616457:616969 forward MW:18211
RPA0555											CDS possible methyltransferase 617018:617614 reverse MW:21331
RPA0556	1.063104	0.1775	0.864141	0.895	1.206756	0.0445	1.437325	0.017	1.675286	0.0005	CDS HNH endonuclease:HNH nuclease 617758:618315 reverse MW:21316
RPA0557	0.884423	0.816	0.903472	0.7495	0.804417	0.9855	1.052826	0.3615	0.595986	0.9915	cysK cysteine synthase, cytosolic O-acetylserine(thiol)lyase 618596:619594 forward MW:34544
RPA0558	0.888222	0.9245	0.858597	0.9705	0.868017	0.956	0.950165	0.746	0.74643	0.997	purC1 putative phosphoribosylaminoimidazole-succinocarboxamide synthase 619666:620583 reverse MW:33568
RPA0559	0.866573	0.9085	1.04546	0.3005	0.963911	0.636	1.329998	0.089	0.946318	0.7485	CDS putative pirin 620654:621571 reverse MW:33510
RPA0560	1.115542	0.045	0.92253	0.849	1.174331	0.049	0.997394	0.503	0.980312	0.596	MLYCD, MCD malonyl-CoA decarboxylase 621701:623131 reverse MW:52130
RPA0561	0.642898	0.983			0.610773	0.9925	0.53026	0.9895	0.40307	1	CDS hypothetical protein 623297:623902 reverse MW:22207
RPA0562	0.559291	1	0.508725	1	0.902633	0.8225	0.459496	1	0.353425	0.9995	CDS MmgE/PrpD family 623978:625342 reverse MW:47872
RPA0563	0.580167	0.981	0.651523	0.9875	0.827826	0.833	0.654469	0.9575	0.518835	0.9955	CDS conserved hypothetical protein 625468:626625 forward MW:40706
RPA0564											CDS conserved hypothetical protein 626630:627091 reverse MW:16997
RPA0565	0.707431	0.905	1.01073	0.4495	1.023584	0.409	0.749154	0.907	0.916563	0.7475	CDS putative polyhydroxybutyrate depolymerase 627895:629082 forward MW:42395
RPA0566	1.761984	0.0095	4.015624	0.001	2.070794	0	1.472679	0.024	2.843911	0.0005	CDS conserved unknown protein 629211:629630 forward MW:14799
RPA0567	0.569984	1	0.531349	0.999	0.683369	0.9985	0.336958	1	0.374198	1	CDS probable transcriptional regulator, AraC family 629707:630684 reverse MW:35732
RPA0568	0.847734	0.959	0.800804	0.9855	0.847179	0.953	0.776235	0.9655	0.774599	0.993	CDS probable hydrolase 630945:631610 reverse MW:23481
RPA0569	1.174548	0.066	1.016447	0.4555	1.62864	0.0015	1.111226	0.182	1.364219	0.009	CDS conserved hypothetical protein 631700:632818 reverse MW:40641
RPA0570	0.864249	0.7365	0.894957	0.8	0.969665	0.633	1.136807	0.156	1.495795	0.0035	CDS conserved hypothetical protein 632974:633453 forward MW:17697
RPA0571	0.776821	0.871	0.737463	0.9825	0.984113	0.549	0.817896	0.939	0.815395	0.973	regR two-component transcriptional regulator RegR, Fis family 633579:634133 reverse MW:20139
RPA0572	1.093129	0.2705	0.882844	0.931	0.935987	0.7095	1.11721	0.169	1.009907	0.4665	regS two component sensor histidine kinase, RegS 634225:635547 reverse MW:48372
RPA0573	1.003534	0.5055	0.867953	0.948	0.868896	0.9355	0.839984	0.926	0.804183	0.9925	CDS putative ABC transporter (ATP-binding protein) 635655:636452 forward MW:28938
RPA0574	0.976846	0.6335	0.928028	0.784	0.786979	0.976	0.798502	0.949	0.851471	0.9545	CDS possible ABC transporter 636449:637279 forward MW:31058
RPA0575	1.855645	0.0005	1.776671	0.004	1.599864	0.004	1.948799	0.002	2.61147	0.0005	CDS putative intracellular PHB depolymerase 637418:638746 forward MW:49786
RPA0576	0.786627	0.9555	0.849647	0.9065	0.879204	0.9465	0.769612	0.9795	0.881309	0.919	CDS putative metal-dependent hydrolase 639003:639836 forward MW:31910
RPA0577	0.933291	0.8445	0.839297	0.9805	0.900095	0.8865	0.855919	0.9515	0.909216	0.8855	CDS possible penicillin-binding protein 640106:642052 reverse MW:69187
RPA0578	1.065716	0.3835	0.70265	0.9855	0.943815	0.6895	1.213286	0.1615	1.191947	0.0695	CDS unknown protein 642505:642759 forward MW:9410
RPA0579											CDS hypothetical protein 642855:643067 reverse MW:8091
RPA0580	1.375767	0.2315	0.467638	0.9935	2.016536	0.013	0.683553	0.954	0.441087	0.9785	CDS possible branched-chain amino acid binding protein, ABC transport system 643359:644579 reverse MW:44248
RPA0581	1.017525	0.427	0.846265	0.965	1.089379	0.1245	0.844778	0.893	0.769072	0.9915	CDS hypothetical protein 644730:645092 reverse MW:12685
RPA0582	0.94733	0.6455	0.579153	0.9985	0.978323	0.5605	0.683398	0.9355	0.636812	0.993	CDS conserved unknown protein 645175:645603 forward MW:16058
RPA0583	0.777655	0.9495	0.601273	0.999	0.85108	0.982	0.517023	0.998	0.659907	1	CDS sensor histidine kinase with PAS/PAC and Response regulator receiver domains 645698:648439 forward MW:97999
RPA0584	0.415836	0.9975	0.398865	1	0.469251	1	0.256998	1	0.399764	0.999	CDS transcriptional accessory protein 648631:650967 forward MW:84613
RPA0585	1.149428	0.125	1.111336	0.15	1.192933	0.1625	0.757881	0.9565	0.66769	0.991	CDS chromate transporter 650990:652144 reverse MW:39165
RPA0586	0.994474	0.52	0.904226	0.845	1.095206	0.1835	0.873386	0.877	0.892609	0.913	CDS putative PAN2 protein ; short shain alcohol dehydrogenase 652210:653103 reverse MW:32013
RPA0587	0.775077	0.742	1.239243	0.171	0.933893	0.664	0.651996	0.9845	0.569757	0.9715	CDS putative cationic amino acid transporter 653133:654614 reverse MW:51265
RPA0588	1.26338	0.0985	1.04281	0.3425	1.021004	0.416	0.968873	0.553	0.906388	0.795	CDS transcriptional regulator, TetR family 654655:655335 reverse MW:25318
RPA0589	0.972154	0.6165	0.73151	0.997	0.979766	0.5835	0.773507	0.938	0.848497	0.9525	CDS possible acyl-CoA dehydrogenase 655430:657097 forward MW:60557
RPA0590	0.840965	0.9795	0.978507	0.6285	0.864208	0.953	0.804223	0.942	0.867021	0.9515	prc putative carboxyl-terminal protease 657260:658600 reverse MW:46398
RPA0591	0.887953	0.912	0.73621	0.998	0.952523	0.7245	0.79354	0.9815	0.778105	0.9925	glnD Protein PII uridylyltransferase 658764:661613 reverse MW:106837
RPA0592	0.936625	0.782	0.800998	0.982	0.734671	0.978	0.703424	0.981	0.740597	0.985	argJ putative glutamate N-acetyltransferase/amino-acid acetyltransferase 661788:663029 forward MW:42582
RPA0593	1.148776	0.1745	1.186836	0.121	1.06259	0.318	1.229362	0.324	1.040885	0.3745	CDS hypothetical protein 663026:663523 forward MW:17619
RPA0594	0.863447	0.9205	1.032554	0.355	0.845138	0.9595	0.826747	0.9075	0.693943	0.995	mutT putative mutator protein mutT 663531:663932 forward MW:15001
RPA0595	0.790089	0.9925	0.899145	0.8695	0.823047	0.9705	0.694829	0.985	0.635591	0.9985	CDS conserved hypothetical protein 664109:664933 reverse MW:29974
RPA0596	0.830219	0.9185	1.018871	0.423	0.770641	0.9425	0.950506	0.6275	0.819114	0.9315	CDS conserved hypothetical protein 664960:665259 reverse MW:10484

RPA0597	0.991079	0.5535	0.7418	0.994	1.058598	0.231	0.922859	0.761	0.863041	0.9395	CDS possible competence protein F (COMF) 665365:666180 forward MW:29344
RPA0598	0.860683	0.953	0.711099	0.9915	1.007433	0.4515	0.748221	0.9895	0.847508	0.8745	CDS putative glutaredoxin 666223:666498 forward MW:9755
RPA0599	0.821719	0.986	0.667621	0.994	0.837791	0.949	0.585488	0.997	0.605097	0.999	CDS possible nitrilase 666495:667370 forward MW:31761
RPA0600	0.861998	0.9555	0.76542	0.995	0.867322	0.9425	0.919649	0.818	0.837925	0.942	CDS conserved hypothetical protein 667367:667861 forward MW:18132
RPA0601	0.823287	0.9225	1.02804	0.3925	0.743243	0.9875	1.284713	0.251	0.762209	0.947	CDS probable DMT superfamily transporter 668083:668520 forward MW:15062
RPA0602	0.842263	0.9595	0.639259	0.9945	0.987953	0.543	0.630917	0.9755	0.830327	0.9705	CDS Permeases of the drug/metabolite transporter (DMT) superfamily 668521:669420 reverse MW:31818
RPA0603	0.949935	0.729	1.02678	0.345	0.784469	0.9965	0.932975	0.773	0.901497	0.91	ubiG putative 3-demethylubiquinone-9 3-methyltransferase 669548:670330 reverse MW:28958
RPA0604	0.80241	0.92	0.89681	0.9195	0.621964	0.9945	0.725979	0.989	0.997668	0.5215	lysC putative aspartokinase, alpha and beta subunits 670503:671756 forward MW:44630
RPA0605	0.996072	0.516	0.94178	0.8185	0.865305	0.83	1.177244	0.063	1.239989	0.0105	ptsP nitrogen regulatory protein PTSI(NTR) 671957:674359 forward MW:87503
RPA0606	0.685095	0.9905	0.74627	0.986	0.673867	0.98	0.90719	0.703	0.862468	0.868	prfA peptide chain release factor 1 674416:675501 forward MW:39909
RPA0607	0.950641	0.639	0.914455	0.786	1.025343	0.393	1.081849	0.259	1.073623	0.243	hemK putative protoporphyrinogen oxidase, hemK protein 675498:676367 forward MW:30592
RPA0608	0.937594	0.6105	1.908798	0.0105	0.904064	0.73	2.730474	0.014	2.499459	0	CDS conserved unknown protein 676819:677514 forward MW:25756
RPA0609	0.930511	0.86	0.890126	0.928	1.011567	0.454	1.027288	0.4015	1.027134	0.3675	CDS conserved hypothetical protein 677617:678396 reverse MW:29091
RPA0610	0.719444	0.9985	0.628327	0.9985	0.880574	0.9055	0.685381	0.997	0.761029	0.992	CDS putative glyoxalase II 678565:679332 forward MW:27574
RPA0611	0.756917	0.9765	0.703652	0.965	0.840542	0.9695	0.711772	0.9745	0.648213	0.9925	CDS conserved unknown protein 679329:679766 forward MW:15653
RPA0612	0.700127	0.9955	0.788737	0.987	0.871303	0.9335	0.613669	0.9985	0.6603	0.998	CDS possible sugar kinase 679887:680825 reverse MW:32333
RPA0613	0.662633	0.9995	0.6955	0.9995	0.680589	0.994	0.561073	1	0.598755	0.9985	CDS NUDIX hydrolase 680822:681754 reverse MW:33692
RPA0614	0.682637	0.9875	0.880333	0.92	0.780462	0.984	0.71012	0.9965	0.719974	0.998	CDS conserved unknown protein 681759:682256 reverse MW:18522
RPA0615	0.791466	0.991	0.844078	0.9785	0.785795	0.9905	0.735775	0.989	0.872019	0.949	dnaX possible DNA polymerase III tau subunit 682649:684520 forward MW:66970
RPA0616	0.551414	0.9975	0.684367	0.9965	0.706921	0.998	0.604905	0.999	0.579383	0.998	CDS Uncharacterized BCR 684542:684862 forward MW:11188
RPA0617	0.556895	1	0.792501	0.72	1.127321	0.301	0.73844	0.9165	0.66323	0.962	recR putative recombination protein recR 684958:685560 forward MW:21161
RPA0618	0.562255	0.997	0.599932	0.997	0.709578	0.9985	0.52001	0.9995	0.55261	0.999	CDS unknown protein 685580:686008 forward MW:14739
RPA0619	0.695332	0.9985	0.781365	0.989	0.803505	0.9235	0.924038	0.72	1.160451	0.0985	ampG putative MFS transporter and signal transducer AmpG 686049:687347 reverse MW:45676
RPA0620	0.915645	0.8335	0.975132	0.6815	0.875168	0.923	1.32796	0.012	1.070407	0.176	CDS Uncharacterized BCR:Protein of unknown function DUF195 687496:688728 reverse MW:45108
RPA0621	0.811382	0.948	1.166984	0.135	0.969844	0.5495	0.716343	0.996	0.623631	0.9765	def putative N-formylmethionylaminoacyl-tRNA deformylase 688848:689375 forward MW:19838
RPA0622	0.780912	0.977	0.891954	0.921	0.671973	0.985	0.696651	0.9915	0.718085	0.9505	fmt putative methionyl-tRNA formyltransferase 689454:690386 forward MW:33035
RPA0623	1.042746	0.278	1.119747	0.086	1.217582	0.0195	1.708992	0.0025	2.570609	0	truA putative tRNA-pseudouridine synthase 690564:691310 forward MW:27214
RPA0624	0.857269	0.845	0.810834	0.9615	0.787439	0.967	0.637102	0.9935	0.696378	0.9945	dapE putative succinyl-diaminopimelate desuccinylase 691642:692805 reverse MW:41085
RPA0625	0.909297	0.7625	0.898467	0.921	0.647599	0.993	0.654151	0.9925	0.803281	0.9475	CDS conserved hypothetical protein 692805:693278 reverse MW:17212
RPA0626	0.69546	0.9875	0.77569	0.9815	0.578115	0.999	0.53119	0.997	0.60763	0.998	dapD 2,3,4,5-tetrahydropyridine-2-carboxylate N-succinyltransferase 693297:694142 reverse MW:29734
RPA0627	0.783726	0.995	0.817878	0.979	0.732615	0.996	0.754385	0.99	0.673229	0.9935	CDS putative haloacid dehalogenase superfamily hydrolase 694327:695028 reverse MW:26450
RPA0628	1.024117	0.3815	0.677102	0.957	0.869967	0.845	0.769426	0.9425	0.743678	0.951	CDS conserved unknown protein 695025:696146 reverse MW:39620
RPA0629	0.869578	0.9085	0.853163	0.9675	0.733439	0.993	0.61252	0.9985	0.707885	0.986	argB putative acetylglutamate kinase 696146:697042 reverse MW:31485
RPA0630			0.707087	0.9695	0.83028	0.7395	0.427711	0.9665	0.372865	0.974	CDS DUF423 697167:697535 reverse MW:12416
RPA0631	0.701573	0.945	1.158452	0.0565	0.722662	0.9585	1.05487	0.372	0.84651	0.8815	CDS possible GTPases 697535:698185 reverse MW:23374
RPA0632	0.805235	0.961	0.882648	0.934	0.568608	0.9985	0.668752	0.9965	0.953735	0.5835	CDS 60 kDa inner membrane protein 698337:700205 reverse MW:68719
RPA0633	0.884155	0.8955	1.366246	0.011	0.75137	0.986	0.996956	0.504	1.098798	0.2995	rnpA probable ribonuclease p protein component (protein c5) 700222:700563 reverse MW:12879
RPA0634	0.986777	0.5305	1.602445	0.007	0.87218	0.8435	1.352751	0.0735	1.380397	0.0215	rpmH, L34 possible ribosomal protein L34 700587:700721 reverse MW:5120
RPA0635	1.234852	0.065	0.982422	0.5635	1.331478	0.015	1.55915	0.006	2.131552	0	CDS sensor histidine kinase 701052:702530 forward MW:53569
RPA0636			1.008709	0.481			1.304581	0.1435	1.614028	0.002	CDS hypothetical protein 702970:703479 reverse MW:18687
RPA0637											CDS hypothetical protein 703506:704834 reverse MW:47705
RPA0638											CDS conserved hypothetical protein 704911:707313 reverse MW:87433
RPA0639											sigE RNA polymerase ECF-type sigma factor 707816:708514 forward MW:25993
RPA0640			0.912072	0.764	0.94253	0.611			0.854966	0.831	fliC putative flagellin 708657:709481 forward MW:27683
RPA0641	0.933573	0.718	1.121004	0.1285	1.129068	0.1635	1.254723	0.0395	1.593903	0.007	fliD possible flagellar hook-associated protein 2 (FliD, filament cap protein) 709543:711258 forward MW:57947
RPA0642	0.994879	0.5055			1.068292	0.4045			0.766646	0.7855	CDS conserved hypothetical protein 711258:711650 forward MW:14418
RPA0643	0.955298	0.5605			1.099343	0.4515					CDS conserved hypothetical protein 711650:712045 forward MW:14060
RPA0644									2.903548	0.0155	flgD possible basal-body rod modification protein flgD 712294:713091 forward MW:27363
RPA0645			1.161846	0.2685	1.353792	0.2275	1.47587	0.067	1.725842	0.0065	flgE possible flagellar hook protein FlgE 713111:714376 forward MW:42265
RPA0646	0.423179	0.9015							0.446532	0.7935	CDS conserved hypothetical protein 714382:714639 forward MW:9489
RPA0647			1.246334	0.1555	1.058976	0.428			1.100544	0.305	CDS hypothetical protein 714655:715116 forward MW:16787
RPA0648	0.951763	0.6995	0.88833	0.8495	0.957709	0.7085	1.178498	0.067	1.060329	0.2655	flgK1 possible flagellar hook-associated protein 1 (HAP1, FlgK protein) 715138:716901 forward MW:58188
RPA0649											flgL possible flagellin and hook associated protein. 716917:717828 forward MW:31313
RPA0650					0.774638	0.6815			0.405311	0.989	badK cyclohex-1-ene-1-carboxyl-CoA hydratase 717848:718624 reverse MW:27380
RPA0651	1.002453	0.5055	0.59143	0.997	0.889147	0.82	0.835095	0.899	0.607837	0.951	aliA cyclohexanecarboxylate-CoA ligase 718652:720295 reverse MW:59508
RPA0652	0.941964	0.736	0.678672	0.9855	0.897527	0.899	0.705801	0.8595	0.620409	0.9975	aliB cyclohexanecarboxyl-CoA dehydrogenase 720352:721503 reverse MW:41372
RPA0653	1.051987	0.4	0.624205	0.999	1.003961	0.4725	0.746279	0.9305	0.457405	0.9975	badI 2-ketocyclohexanecarboxyl-CoA hydrolase 721568:722350 reverse MW:28576
RPA0654	0.992607	0.523	0.521099	1	0.657781	0.966	0.563839	0.995	0.371876	1	badH 2-hydroxycyclohexanecarboxyl-CoA dehydrogenase 722381:723148 reverse MW:26129
RPA0655	0.908519	0.909	0.664064	0.991	0.530464	0.993	0.820138	0.9475	0.416049	1	badR Benzoate anaerobic degradation transcriptional regulator BadR, MarR family 723271:723798 forward MW:19519
RPA0657	1.08907	0.266	1.177306	0.0695	0.896527	0.742	0.929793	0.7085	0.587671	0.995	badD benzoyl-CoA reductase subunit 725062:726246 forward MW:44015
RPA0658	1.443109	0.1165	1.150014	0.169	0.927189	0.745	0.77301	0.982	0.563495	0.979	badE benzoyl-CoA reductase subunit 726243:727553 forward MW:49664
RPA0659	1.327816	0.082	0.799373	0.853	0.807925	0.8305	0.738191	0.936	0.498027	0.996	badF benzoyl-CoA reductase subunit 727565:728878 forward MW:47897
RPA0660	0.827095	0.7885	0.734509	0.9325	0.896961	0.646	0.793613	0.8895	0.521134	0.9965	badG benzoyl-CoA reductase subunit 728971:729804 forward MW:29471
RPA0661	1.475292	0.128	0.596989	0.9965	1.290479	0.138	0.796392	0.786	0.633352	0.956	badA benzoate-CoA ligase 729921:731495 forward MW:56701
RPA0662	1.076713	0.3135	0.950277	0.7745	1.060304	0.231	1.117706	0.112	0.991146	0.53	badB ferredoxin 731512:731757 forward MW:8946
RPA0663	1.040547	0.3485	0.982593	0.5855	0.99932	0.5025	0.995734	0.513	0.981547	0.581	badM putative transcriptional regulator, badM 731806:732276 reverse MW:17065
RPA0664	1.125609	0.138	1.066331	0.2065	0.97821	0.584	1.290435	0.0625	2.931285	0.0005	badL possible acetyltransferase 732331:732810 reverse MW:17561
RPA0665	1.195071	0.091	0.809224	0.9475	1.165495	0.065	0.936659	0.68	0.463051	0.985	hbaH putative ABC transporter subunit, ATP-binding component 732909:733631 reverse MW:26403
RPA0666	1.385055	0.103	0.706082	0.9765	1.140692	0.04	0.953747	0.633	0.555662	0.9915	hbaG putative ABC transporter subunit, membrane spanning domain + ATP-binding component 733628:735415 reverse MW:63467
RPA0667	1.559667	0.134	0.699541	0.9815	1.278371	0.0205	0.867494	0.7295	0.433248	0.9785	hbaF putative membrane spanning subunit of ABC transporter 735418:736278 reverse MW:30624
RPA0668	1.583139	0.083	0.599021	0.9925	1.060041	0.3935	0.815975	0.749	0.42022	0.9975	hbaE putative ABC transporter subunit, substrate-binding component 736364:737542 reverse MW:40675
RPA0669									0.198409	0.999	hbaA 4-hydroxybenzoate-CoA ligase 737719:739338 reverse MW:58930
RPA0670									0.130529	0.9975	hbaB 4-hydroxybenzoyl-CoA reductase, first of three subunits 739505:739996 forward MW:17642
RPA0671	1.064926	0.346	1.028456	0.4195	1.204841	0.0425	1.068503	0.3585	0.248747	0.992	hbaC 4-hydroxybenzoyl-CoA reductase,second of three subunits 739993:742326 forward MW:82594
RPA0672	0.766237	0.7885	0.506971	0.9895	1.027249	0.3825	0.884878	0.6515	0.303693	0.99	hbaD 4-hydroxybenzoyl-CoA reductase, third of three subunits 742323:743306 forward MW:34630
RPA0673	1.024407	0.461	0.750997	0.988	1.068157	0.231	1.133743	0.137	0.741471	0.9815	hbaR Hydroxybenzoate anaerobic degradation regulatory protein HbaR, Crp/Fnr family 743331:744056 reverse MW:25783
RPA0674	1.166259	0.16	0.689777	0.9915	1.195613	0.017	1.602098	0.004	1.168013	0.1875	CDS possible alcohol dehydrogenase class III family 744248:745360 forward MW:39262

RPA0675	0.896049	0.6685			0.990571	0.5215			0.975918	0.553	CDS possible hydrolases (alpha/beta hydrolase superfamily) 745396:746217 forward MW:29530
RPA0676	1.824059	0.0335	1.370705	0.021	1.298126	0.0115	1.513269	0.0325	2.301543	0	CDS possible enoyl-CoA hydratase/isomerase family member 746346:748040 forward MW:61660
RPA0677	1.306929	0.19	1.633601	0.0005	1.213798	0.0625	1.198718	0.089	1.826905	0.001	CDS hypothetical protein 748211:749662 forward MW:55184
RPA0678	0.623718	0.9585	1.054975	0.3325	0.693137	0.994	0.531855	0.9965	0.34721	1	gltA possible pyridine nucleotide-linked oxidoreductase, possible glutamate synthase 749866:752973 forward MW:113435
RPA0679	1.031839	0.2955	0.956682	0.719	0.926467	0.8645	1.108226	0.1475	1.212478	0.009	CDS Protein of unknown function UPF0004:Elongator protein 3/MiaB/NifB 752997:755030 reverse MW:75657
RPA0680	0.792403	0.9955	0.762255	0.9825	0.825908	0.955	0.936006	0.6485	1.236809	0.0255	CDS possible transcriptional regulator, TetR family 755097:755714 reverse MW:22133
RPA0681	0.777986	0.913	0.905065	0.8325	0.856336	0.738	0.922667	0.647	0.759354	0.953	CDS membrane permeases, predicted cation efflux pump 755856:756890 forward MW:37556
RPA0682	0.671976	0.927	0.99556	0.518	0.629283	0.9885	0.680124	0.994	0.580164	0.955	CDS possible ABC transporter ATP-binding component, membrane bound 756887:759601 forward MW:99211
RPA0683	0.619394	0.9355	1.111003	0.189	1.187631	0.128	0.722497	0.9915	0.715707	0.985	CDS possible ABC transporter permease component 759598:760731 forward MW:41064
RPA0684			2.971988	0.001			1.751475	0.13	2.151845	0.055	CDS hypothetical protein 760739:760918 reverse MW:6708
RPA0685	2.067302	0.0005	1.894153	0.0015	2.109255	0	1.680912	0.005	1.502924	0.03	CDS transcriptional regulator, IclR family 761061:761936 forward MW:31290
RPA0686	1.856047	0.0005	1.723209	0	1.927694	0	1.919862	0.0035	1.811065	0.0045	CDS Uncharacterized protein family UPF0065 762097:763071 forward MW:34483
RPA0687	0.876704	0.7655	0.922488	0.622	0.911134	0.6945	0.943734	0.5625	0.72259	0.963	CDS conserved hypothetical protein 763121:763768 reverse MW:23747
RPA0688	0.914298	0.89	0.796438	0.975	0.834565	0.951	0.690426	0.9935	0.564051	0.9995	phnN ATP-binding component, PhnN protein, possible kinase 763749:764333 reverse MW:20472
RPA0689	1.339708	0.0815	0.714345	0.984	0.946548	0.5675	0.795169	0.9135	0.847012	0.791	phnM1 possible phosphonate utilization (C-P lyase) component 764330:765466 reverse MW:41191
RPA0690	0.791774	0.833	0.841733	0.8685	0.911779	0.82	0.720039	0.976	0.676849	0.992	phnL phosphonate ABC transporter, ATP-binding component, PhnL protein 765505:766209 reverse MW:24816
RPA0691											phnK phosphonate ABC transporter, ATP-binding component,PhnK protein 766215:767033 reverse MW:29563
RPA0692	0.802145	0.7805	0.517747	0.991	1.107388	0.3565	0.847821	0.8245			phnJ PhnJ protein, phosphonate metabolism, function unknown. 767026:767904 reverse MW:32458
RPA0693	0.810942	0.968	0.553404	0.9995	0.999382	0.4955	0.605696	0.996	0.505814	0.9995	phnI PhnI protein, phosphonate metabolism, function unknown 767901:768998 reverse MW:40045
RPA0694											phnH putative PhnH protein, phosphonate metabolism, function unknown 769002:769604 reverse MW:21105
RPA0695	0.768952	0.997	0.630812	0.997	0.819586	0.9855	0.584459	0.988	0.497492	1	phnG PhnG protein, phosphonate metabolism, function unknown 769607:770080 reverse MW:16472
RPA0696			1.215438	0.2545	1.085198	0.4155			1.10299	0.281	CDS possible transcriptional regulator, GntR family 770192:770920 forward MW:25975
RPA0697			1.220734	0.2535	1.553771	0.1525			1.605628	0.149	phnE1 putative PhnE protein, phosphonate ABC transporter, permease component 771245:772111 reverse MW:31161
RPA0698											phnE2 possible PhnE protein, phosphonate ABC transporter, permease component 772108:772989 reverse MW:32194
RPA0699			0.829308	0.8975	0.941875	0.634	0.554144	0.986	0.612264	0.9985	phnD putative PhnD protein, phosphonate ABC transporter, periplasmic binding protein precursor 773058:773966 reverse MW:33304
RPA0700			0.887403	0.6605	1.078556	0.4095	1.657437	0.1115	1.239919	0.369	phnC PhnC protein, phosphonate ABC transporter, ATP-binding component 774076:774888 reverse MW:29235
RPA0701											CDS putative acetyltransferase (virginiamycin, streptogramin A, chloramphenicol) 775029:775748 forward MW:26159
RPA0702	0.93124	0.7115			0.984541	0.5235			0.558525	0.97	phnM2 possible phosphonate ABC transporter, permease component 775745:776938 forward MW:43039
RPA0703							1.096557	0.2765	0.945353	0.639	CDS conserved hypothetical protein 776961:777665 forward MW:25925
RPA0704	0.886489	0.7605	0.902805	0.682			1.788336	0.008	1.586094	0.0105	CDS conserved unknown protein 777662:778642 reverse MW:35810
RPA0705	1.095311	0.3045	0.724449	0.978	1.263377	0.125	1.270791	0.0205	0.880726	0.662	CDS hypothetical protein 778886:779080 forward MW:7086
RPA0706	0.749711	0.9655	0.722321	0.982	0.837958	0.921	0.768576	0.7155	0.740352	0.9975	CDS possible endonuclease III 779578:780054 forward MW:16624
RPA0707	0.906569	0.833	0.84193	0.722	0.81616	0.9585	0.911002	0.5575	0.821642	0.876	cutA putative periplasmic divalent cation resistance protein CutA 780032:780355 reverse MW:11861
RPA0708	0.753151	0.929	1.623035	0.0195	0.983504	0.5605	0.734201	0.9635	1.063698	0.355	CDS hypothetical protein 780767:781288 forward MW:18053
RPA0709											CDS conserved unknown protein 781403:781948 forward MW:18714
RPA0710	0.703612	0.9915	0.491565	1	0.841826	0.8625	0.340335	1	0.393062	1	CDS hypothetical protein 781991:782251 forward MW:9279
RPA0711	0.7787	0.8485	0.970441	0.658	0.698924	0.9945	0.609892	0.9945	0.682768	0.9945	CDS Nitroreductase family 782498:783169 reverse MW:25001
RPA0712	0.695332	0.9915	0.679119	0.9875	0.69211	0.972	0.599149	0.996	0.696372	0.9965	cobT, cobU putative nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase 783196:784251 reverse MW:36047
RPA0713	0.618563	0.9975	0.685547	0.994	0.737128	0.964	0.37444	1	0.624012	0.9985	CDS conserved unknown protein 784566:785087 forward MW:18119
RPA0714	0.57582	0.9995	0.63442	0.996	0.62203	0.999	0.276466	1	0.629764	0.999	cobU bifunctional cobinamide kinase, cobinamide phosphate guanylyltransferase protein 785084:785614 forward MW:18765
RPA0715	0.593723	0.9855	0.68877	0.982	0.587449	0.9995	0.364818	0.999	0.635763	0.9955	cobW putative cobalamin synthesis protein cobW 785618:786622 forward MW:35110
RPA0716	0.662468	0.9995	0.493798	0.997	0.844085	0.9565	0.360277	1	0.628895	0.9985	cobN putative cobaltochelatase subunit CobN. 786757:790506 forward MW:135081
RPA0717	0.592375	0.999	0.531642	0.9965	0.767895	0.993	0.326567	0.9995	0.521969	0.9965	cobO, cobA, btuR putative cob(I)alamin adenosyltransferase 790503:791129 forward MW:23315
RPA0718	0.686863	0.9945	0.61876	0.995	0.777906	0.969	0.462358	0.9985	0.658046	0.992	cobQ1, cbiP cobyric acid synthase 791277:792761 forward MW:51602
RPA0719	0.753345	0.991	0.559755	0.999	0.863894	0.9205	0.505386	0.9975	0.64986	0.9915	cobD, cbiB putative cobalamin biosynthetic protein cobD 792734:793705 reverse MW:34275
RPA0721	0.809394	0.9695	0.879436	0.8875	0.668353	0.9995	0.471576	0.999	0.551367	0.996	cobC putative cobalamin biosynthetic protein CobC 794583:795572 forward MW:35262
RPA0722	0.632712	0.968	0.625361	0.9855	0.554785	0.9975	0.308604	1	0.516984	0.9985	fecE putative iron(III) dicitrate ABC transporter, ATP-binding component FecE 795584:796363 reverse MW:27352
RPA0723	0.893261	0.9405	0.616168	0.992	0.903255	0.8925	0.68285	0.9935	0.783969	0.9665	CDS possible hemin ABC transporter, permease component 796360:797385 reverse MW:34418
RPA0724	0.593707	0.9995	0.834706	0.962	0.5894	0.999	0.382665	0.9995	0.566576	0.999	nxiA, nixA, hoxN, hupN putative high-affinity nickel-transport protein 797393:798451 reverse MW:37867
RPA0725											sugE possible chaperone 798784:799107 reverse MW:11061
RPA0726											btaB putative BtaB protein, S-adenosylmethionine:diacylgycerolhomoserine-N-methyltransf erase 799104:799841 reverse MW:27425
RPA0727	0.766048	0.963	0.856723	0.897	0.960115	0.5995	0.647819	0.9295	0.747004	0.946	CDS S-adenosylmethionine:diacylglycerol 3-amino-3-carboxypropyl transferase 799994:801217 forward MW:46094
RPA0728	1.736909	0.0015	1.448138	0.008	1.327825	0.021	1.777989	0.0025	1.930172	0.0005	CDS conserved unknown protein 801773:803179 forward MW:49267
RPA0729											CDS conserved hypothetical protein 803190:803768 forward MW:20599
RPA0730	1.286278	0.012	1.271742	0.0115	1.342239	0.0025	1.355754	0.035	1.260518	0.0095	CDS conserved hypothetical protein 803781:804470 forward MW:24071
RPA0731	0.892386	0.8665	0.970947	0.5475	0.927396	0.8405	0.917414	0.684	1.2051	0.0225	CDS transcriptional regulator, LysR family 805004:805897 forward MW:32586
RPA0732			0.767589	0.86			0.700379	0.8735	3.815953	0	fdsG putative NAD-dependent formate dehydrogenase gamma subunit 806161:806631 forward MW:16647
RPA0733	0.718861	0.89	0.738661	0.9965	1.11191	0.1045	0.723419	0.982	5.147496	0	fdsB NAD-dependent formate dehydrogenase beta subunit 806628:808184 forward MW:54958
RPA0734	0.94054	0.8225	0.943146	0.7615	1.104227	0.169	1.039652	0.344	4.508613	0	fdsA NAD-dependent formate dehydrogenase alpha subunit 808197:811043 forward MW:103442
RPA0735	0.895057	0.897	1.008471	0.4665	1.05869	0.3705	1.046701	0.322	4.864262	0	fdsC putative FdsC protein, formate dehydrogenase chain D 811043:811873 forward MW:29194
RPA0736	1.023543	0.4485	1.102003	0.2555	1.068698	0.3405	1.097664	0.3375	3.008985	0.0005	fdsD possible NAD-dependent formate dehydrogenase delta subunit 811863:812078 forward MW:7702
RPA0737	0.956075	0.6355	0.62833	0.995	1.193186	0.056	0.745466	0.9285	2.109667	0.004	CDS putative oxalate/formate Major Facilitator Superfamily (MFS) antiporter 812088:813791 forward MW:60876
RPA0738	1.722118	0.1645	0.496428	0.99	2.943629	0.0025	0.658503	0.9305	0.656233	0.994	CDS possible L-sorbosone dehydrogenase. 813898:815307 forward MW:51078
RPA0739	1.220658	0.3985	0.565361	0.9845	2.3352	0.0015	0.689368	0.888	0.420019	0.9905	cyc putative cytochrome c 815452:816042 forward MW:21151
RPA0740			0.6878	0.865	0.661592	0.8845			0.612107	0.9975	CDS possible Acyl-CoA dehydrogenase 816117:817226 forward MW:38885
RPA0741	0.796758	0.803	0.769586	0.896	0.536111	0.952	0.64686	0.932	0.556272	0.9995	CDS conserved unknown protein 817223:818170 forward MW:34736
RPA0742									0.421941	0.996	CDS conserved hypothetical protein 818170:819561 forward MW:51671
RPA0743	1.31959	0.074	0.702537	0.985	1.148005	0.1085	1.098804	0.3765	0.968805	0.5575	CDS putative acid-CoA ligase 819739:821265 forward MW:54643
RPA0744	3.952947	0.001	1.459315	0.0885	2.150161	0.0245					CDS putative high potential iron sulfur protein (HiPIP) 821440:821724 reverse MW:9858
RPA0745	4.321823	0.002	1.693304	0.015	2.627223	0.0015	1.884716	0.0195	1.743669	0.0295	CDS possible outer membrane protein precursor 821865:824297 reverse MW:90045
RPA0746	5.024143	0.0285	1.191211	0.2685	3.347904	0.001	1.461369	0.066	1.791872	0.001	CDS possible deca-heme c-type cytochrome. 824397:826001 reverse MW:57671
RPA0747	0.905661	0.781	1.139473	0.087	0.953277	0.684	1.065406	0.323	1.132177	0.1185	cysA putative sulfate ABC transporter, ATP-binding component 826776:827822 reverse MW:38521
RPA0748	0.687385	0.796	1.288015	0.069	0.580378	0.962	0.783684	0.872	0.517533	0.9995	cysW possible sulfate ABC transporter, permease component 827812:828726 reverse MW:32365
RPA0749	0.562692	0.8255	1.601688	0.0085	0.439248	0.984	0.741254	0.9215	0.393566	0.997	cysT putative sulfate ABC transporter, permease component 828731:829567 reverse MW:30072
RPA0750	0.518896	0.9425	1.209983	0.091	0.370995	0.9925	0.783966	0.8965	0.326745	1	sbp sulfate ABC transporter, periplasmic binding protein component 829860:830849 reverse MW:35743
RPA0751	0.96095	0.622	0.613804	0.985	0.61017	0.999	0.576668	0.963	0.774833	0.9845	cysH putative phosphoadenosine phosphosulfate reductase 830974:831714 reverse MW:26536
RPA0752	1.267019	0.005	1.308013	0.1315	0.526765	0.996	0.755014	0.9275	0.652011	0.9935	cysD putative ATP sulfurylase small subunit 832014:832883 forward MW:32572

RPA0753	0.884594	0.5985	1.788006	0.0145	0.596661	0.987	0.853683	0.8145	0.63244	0.99	cysN putative CysN/CysC bifunctional enzyme, ATP-sulfurylase large subunit and adenylyl sulfate kinase 832905:834815 forward MW:67736
RPA0754	0.899982	0.81	1.263883	0.045	0.820123	0.9475	1.293981	0.051	0.995914	0.514	CDS putative signal transduction histidine kinase with PAS/PAC domains 834822:836258 reverse MW:53830
RPA0755	0.914653	0.6605	0.924858	0.663	1.054606	0.415	1.503966	0.2195	0.987288	0.52	CDS putative oligopeptide ABC transporter, ATP-binding component 836321:837298 reverse MW:34976
RPA0756	1.388488	0.2065							1.512366	0.1655	CDS putative amidase 837299:838711 reverse MW:49453
RPA0757											CDS hypothetical protein 838708:838902 reverse MW:6614
RPA0758	2.183419	0	3.17904	0	1.830421	0	9.629107	0	5.9389	0	CDS putative oligopeptide ABC transporter, ATP-binding component 838916:839974 reverse MW:37946
RPA0759	4.987547	0	4.933658	0	4.411192	0	12.28287	0	11.45065	0	CDS putative oligopeptide ABC transporter, permease component 839979:840884 reverse MW:31756
RPA0760	4.621192	0.0005	6.594851	0	4.083156	0	20.19203	0	14.61942	0	CDS putative oligopeptide ABC transporter, permease component 840889:841842 reverse MW:33957
RPA0761	2.21978	0.0185	4.926801	0	1.715078	0.117	14.58478	0	3.923765	0.0005	CDS possible oligopeptide ABC transporter, periplasmic binding protein component 842040:843701 reverse MW:61462
RPA0762	2.78305	0	4.945839	0	2.319487	0.0015	24.34165	0	6.830366	0	CDS possible oligopeptide ABC transporter, periplasmic binding protein component 843889:845487 forward MW:58777
RPA0763	1.484339	0.149	2.234153	0	2.085398	0.0005	2.326548	0.0055	2.485633	0	CDS possible methyltransferases 845640:846434 forward MW:28445
RPA0764	0.84024	0.7185	1.460377	0.0035	0.950051	0.553	1.226521	0.2095	0.847662	0.775	CDS conserved hypothetical protein 846490:846924 reverse MW:15834
RPA0765	1.202733	0.0165	1.444907	0.006	1.307459	0.0075	1.068731	0.2305	0.992045	0.5365	CDS putative outer membrane receptor for iron transport 846945:849308 reverse MW:84739
RPA0766	1.057206	0.329	1.215558	0.1095	1.085286	0.3075	1.056147	0.336	1.15489	0.1525	CDS transcriptional regulator, Crp/Fnr family 849702:850409 forward MW:25479
RPA0767	1.212771	0.065	1.54343	0.001	1.244814	0.0275	1.540114	0.007	1.675143	0	CDS putative diguanylate cyclase (GGDEF) with PAS/PAC domain 850515:851456 forward MW:34957
RPA0768	1.260611	0.0165	1.267337	0.041	1.392557	0.013	1.68331	0.0035	1.7611	0.022	CDS possible transposase 851947:852750 forward MW:30623
RPA0769	1.317717	0.0135	1.848592	0.007	1.068346	0.328	1.533455	0.045	1.757317	0.0045	CDS hypothetical protein 853002:853823 forward MW:30392
RPA0772	1.506555	0.008	1.619344	0.0055	1.480482	0.026	1.571549	0.0485	1.935005	0.0015	CDS Pentapeptide repeat 855099:856412 forward MW:47476
RPA0773	1.331147	0.014	1.40508	0.004	1.215357	0.119	1.860142	0.0025	2.183378	0	CDS hypothetical protein 856721:857179 reverse MW:17741
RPA0774	0.999932	0.5095	0.953717	0.7185	1.192439	0.0255	0.775738	0.9805	0.999934	0.481	CDS conserved hyhpothetical protein 857784:858209 forward MW:14977
RPA0775	0.722316	0.9515	1.076414	0.2915	1.010428	0.4675	0.739343	0.9935	1.555726	0.0125	CDS hypothetical protein 858557:859069 forward MW:18975
RPA0776	0.786204	0.9795	0.996016	0.5245	1.766973	0.0075	0.738057	0.951	0.579014	0.9875	CDS possible gamma-glutamyltranspeptidase precursor 859102:860694 reverse MW:56468
RPA0777	1.289279	0.0145	1.843236	0.001	1.45914	0.002	1.272744	0.0595	1.245246	0.0115	CDS putative diguanylate cyclase (GGDEF)/phosphodiesterase (EAL) with PAS domain 860813:863527 reverse MW:99030
RPA0778	1.211212	0.1865	1.838222	0.0015	1.745694	0	1.184477	0.102	1.210843	0.0315	CDS conserved hypothetical protein 863776:864177 reverse MW:14337
RPA0779	1.023102	0.466	1.289811	0.0205	0.975255	0.587	0.921202	0.6845	0.958618	0.6045	CDS conserved hypothetical protein 864609:864803 forward MW:7028
RPA0780	0.991474	0.512	1.091685	0.3535	1.131174	0.228	0.694141	0.8755	0.306351	0.9995	CDS possible acyl-CoA dehydrogenase 864804:866069 reverse MW:47093
RPA0781	1.355992	0.177	1.740448	0.0035	1.749029	0.033	1.524414	0.0085	1.182525	0.3415	CDS putative cytochrome c552 precursor 866150:866500 reverse MW:12558
RPA0782	1.218022	0.2615	1.674152	0.002	1.687575	0.0355	1.350038	0.0645	0.974321	0.516	CDS conserved unknown protein 866503:866937 reverse MW:16292
RPA0783	1.406847	0.0055	1.28288	0.017	0.954832	0.7565	1.401506	0.01	1.310424	0.047	CDS putative diguanylate cyclase (GGDEF)/phosphodiesterase (EAL) 867126:868943 reverse MW:66563
RPA0784	1.20081	0.0975	0.927482	0.667	1.161272	0.154	0.924661	0.635	0.945405	0.6645	CDS putative short-chain alcohol dehydrogenase-like protein 869122:869964 forward MW:28785
RPA0785	1.450511	0.0885	0.802366	0.9785	1.462719	0.006	0.89104	0.719	0.947058	0.71	CDS possible cytochrome P450 family proteins 870091:871470 reverse MW:50741
RPA0786	0.791332	0.916	0.547743	0.999	1.275334	0.0815	0.496597	0.9995	0.446327	1	CDS putative Adenylate/Guanylate cyclase 871591:872985 reverse MW:49470
RPA0787	0.746191	0.9135	1.006607	0.4745	1.024175	0.4125	1.002161	0.4935	1.010152	0.4585	CDS putative heat shock protein (htpX) 873042:874016 forward MW:34187
RPA0788	0.991309	0.5365	0.734385	0.9735	1.021985	0.443	0.795428	0.8935	0.878683	0.791	CDS possible Major Facilitator Superfamily (MFS) efflux pump 874269:875684 forward MW:48740
RPA0789	0.574315	0.9975	0.615007	0.9985	0.73232	0.9985	0.561269	0.9815	0.565459	0.9955	CDS putative serine-glyoxylate aminotransferase 875681:876868 reverse MW:42653
RPA0790	0.60176	0.9955	0.648691	0.998	0.752161	0.8595	0.479981	0.9975	0.388493	1	CDS conserved hypothetical protein 876924:877778 reverse MW:31303
RPA0791	0.809225	0.9515	0.6357	0.9995	1.123044	0.085	0.568777	1	0.675977	0.994	exoI1 similar to Staphylococcus nuclease (SNase-like) 877812:878633 reverse MW:30057
RPA0792	0.798039	0.9705	0.762176	0.9905	0.734573	0.9865	0.737994	0.993	0.818785	0.963	CDS conserved unknown protein 878657:880396 reverse MW:63923
RPA0793	0.916913	0.596	1.976615	0.006	0.870282	0.7705	1.064704	0.3365	1.365099	0.005	CDS conserved hypothetical protein 880850:881716 forward MW:30303
RPA0794	0.970405	0.557	1.09312	0.198	1.031687	0.371	0.707452	0.988	0.738892	0.998	acaP a-type carbonic anhydrase 881807:882565 reverse MW:27007
RPA0795	0.927175	0.8765	0.720659	0.993	0.924526	0.7545	0.834567	0.895	1.212423	0.034	CDS Peptidase family S24 882652:883284 reverse MW:22842
RPA0796	0.876433	0.933	0.909581	0.828	1.08213	0.1295	1.235508	0.0245	1.203418	0.053	CDS conserved unknown protein 883368:883958 forward MW:20880
RPA0797	0.595406	1	0.644687	0.999	0.768934	0.874	0.573869	0.9945	0.615629	1	uraI dihydroorotate dehydrogenase 883955:885049 forward MW:39178
RPA0798	1.128088	0.187	1.289211	0.033	0.864337	0.917	1.429226	0.028	1.507613	0.007	CDS Beta-lactamase-like 885190:885924 reverse MW:26933
RPA0799									1.472384	0.069	CDS putative carbonic anhydrase 886068:886733 reverse MW:22930
RPA0800	0.894265	0.9305	0.905661	0.9065	0.85091	0.915	0.797859	0.9645	0.922296	0.854	matE1 putative cation efflux pump, DNA-damage-inducible protein 886913:888235 reverse MW:46856
RPA0801	0.992761	0.5355	1.067819	0.27	0.889117	0.889	1.108033	0.272	1.053076	0.363	CDS conserved hypothetical protein 888254:888589 reverse MW:12684
RPA0802	0.860572	0.897	0.696139	0.9845	0.75024	0.9735	0.726705	0.9605	0.649857	0.969	CDS possible DNA ligase 888628:890493 reverse MW:69255
RPA0803	0.85309	0.941	0.794368	0.986	0.918917	0.8275	0.839147	0.9665	0.806023	0.99	CDS hypothetical protein 890490:891536 reverse MW:37343
RPA0804	0.90074	0.769	0.77123	0.9235	0.680873	0.985	0.984477	0.5325	0.801659	0.9135	CDS conserved hypothetical protein 891595:892530 forward MW:33339
RPA0805	0.982076	0.5125	0.560347	0.998	1.112269	0.1645	0.914712	0.6525	1.012781	0.4675	CDS possible outer membrane protein 892683:894032 reverse MW:47385
RPA0806	0.857039	0.7545	0.519406	0.998	0.894612	0.8	0.560581	0.9855	0.474238	0.9985	CDS possible high-affinity branched-chain amino acid transport system substrate-binding protein 894376:895596 forward MW:44249
RPA0807	0.822411	0.845			0.871863	0.713			0.727508	0.9475	CDS possible ATP dependent DNA helicase 895772:898489 forward MW:99185
RPA0808	0.789265	0.9655	0.769719	0.909	0.903428	0.85	0.62804	0.993	0.751068	0.9685	CDS hypothetical protein 898734:899276 forward MW:19089
RPA0809	0.679233	0.9965	0.555267	0.999	0.656481	0.9795	0.788571	0.941	1.066343	0.2195	CDS transcriptional regulator, LysR family 899416:900279 reverse MW:31356
RPA0810	1.028067	0.37	0.9123	0.845	0.92848	0.823	0.969307	0.5705	0.797142	0.967	CDS Permeases of the drug/metabolite transporter (DMT) superfamily 900378:901298 forward MW:32012
RPA0811	1.160495	0.1065	0.917665	0.721	0.981638	0.548	0.966339	0.6145	0.892265	0.8545	CDS Putative manganese transp 901384:902730 forward MW:47808
RPA0812	1.204357	0.0525	1.012511	0.4615	0.850573	0.9395	1.215827	0.044	1.163472	0.0595	CDS putative transmembrane protein 902897:903697 reverse MW:29560
RPA0813	0.810073	0.951	0.830175	0.909	0.924801	0.752	0.903679	0.794	0.772787	0.9775	CDS possible permease 903694:904656 reverse MW:33900
RPA0814	1.064506	0.188	0.953691	0.7135	0.770357	0.979	1.155309	0.1245	1.140016	0.0625	CDS conserved unknown protein 904892:908287 reverse MW:119316
RPA0815	1.06758	0.1745	1.122763	0.075	1.145415	0.103	1.151072	0.161	1.079831	0.1915	CDS conserved hypothetical protein 909116:909763 forward MW:23746
RPA0816	0.928583	0.7005	0.85307	0.9695	0.972429	0.624	0.819135	0.9625	0.876364	0.947	CDS putative acyl-CoA dehydrogenase 909857:911647 forward MW:63864
RPA0817	1.078032	0.251	1.018735	0.4	1.223562	0.02	0.7428	0.9895	0.845375	0.907	CDS probable acyl-CoA thiolase 911818:913026 forward MW:42217
RPA0818	1.038997	0.3325	0.965316	0.6995	1.137206	0.0495	0.789	0.9695	0.865224	0.8645	CDS probable 3-hydroxyacyl-CoA dehydrogenase 913151:915367 forward MW:80102
RPA0819	1.051512	0.3445	1.852119	0.005	1.015184	0.4215	1.319803	0.126	1.694193	0.001	CDS conserved hypothetical protein 915791:917596 forward MW:67018
RPA0820	0.844366	0.8635	0.878665	0.911	0.823703	0.943	0.771232	0.9875	0.797235	0.977	gst2 putative glutathionine S-transferase 917708:918319 reverse MW:22159
RPA0821	0.946799	0.701	0.920699	0.8415	0.943477	0.751	0.993951	0.522	1.155756	0.073	CDS transcriptional regulator, MarR family 918366:918932 forward MW:20928
RPA0822	0.882798	0.9555	0.886242	0.9355	0.797468	0.9755	0.828529	0.966	0.918856	0.8235	gshA gamma-glutamylcysteine synthetase 918960:920396 forward MW:53247
RPA0823	0.856292	0.98	0.903084	0.828	0.826297	0.984	1.003654	0.468	1.286675	0.0175	CDS Apple domain:N/apple PAN 920542:921093 forward MW:20032
RPA0824	1.159204	0.099	1.097438	0.1465	1.104978	0.1805	0.997975	0.5005	1.203416	0.065	lepB1 signal peptidase I 921127:921897 reverse MW:27374
RPA0825	0.860239	0.8215	0.701691	0.996	0.960092	0.692	0.868305	0.875	0.881116	0.9145	CDS TldD protein, suppresses inhibitory activity of CsrA 921894:923321 reverse MW:50632
RPA0826	1.040049	0.387	1.046797	0.2745	0.898175	0.757	1.47516	0.002	1.379806	0.0195	CDS DUF433 923443:923664 forward MW:8211
RPA0827	1.186377	0.134	1.036333	0.35	0.978894	0.591	1.738333	0.0025	2.273034	0.001	CDS conserved hypothetical protein 923664:923993 forward MW:12220
RPA0828	0.91365	0.8755	1.523404	0.0765	0.513028	0.9865	1.915504	0.031	1.609344	0.0025	CDS transcriptional regulator, MarR family 924075:924545 forward MW:17842
RPA0829	0.433334	0.9995	0.520831	0.9985	0.530653	0.995	0.402751	0.998	0.499767	1	ohr organic hydroperoxide resistance protein 924660:925085 forward MW:14427
RPA0830	0.710572	0.9815	0.985968	0.595	0.812563	0.984	0.700563	0.9985	0.915147	0.8605	CDS conserved unknown protein 925367:926035 reverse MW:23371
RPA0831	3.249234	0.0025	2.522394	0	6.701777	0.001	5.378374	0.003	4.481486	0	coxB cytochrome c oxidase subunit II 926324:927181 forward MW:31837

RPA0832	6.913023	0.0005	14.69062	0.0015	8.810894	0			8.122505	0.001	coxA cytochrome c oxidase subunit I 927249:928874 forward MW:59662
RPA0833	2.059667	0	3.302623	0.0005	3.30111	0.0005	3.411473	0.0005	3.428894	0.0065	coxE heme O synthase 928920:929885 forward MW:34788
RPA0834	1.632992	0.0045			2.844572	0.001			2.291448	0.063	CoxF putative CoxF 929885:930064 forward MW:6360
RPA0835	1.36415	0.121			1.825833	0.026			1.382617	0.1515	coxG possible cytochrome-c oxidase assembly protein 930061:930705 forward MW:23318
RPA0836	3.160203	0.015	4.086683	0.001	4.12369	0.0035	3.668428	0	3.707994	0.0015	coxC cytochrome c oxidase subunit III 930777:931631 forward MW:31987
RPA0837	1.284337	0.0815			1.454488	0.0135			1.195731	0.152	CDS conserved hypothetical protein in cyt c oxidase gene clusters 931794:932189 forward MW:14400
RPA0838	1.031471	0.4085			1.105113	0.1825			1.20661	0.1455	CDS possible surfeit 1 932186:932989 forward MW:29000
RPA0839	0.692674	0.996	0.757155	0.9925	0.611221	0.9935	0.651228	0.999	0.757229	0.986	thrC threonine synthase 933049:934554 forward MW:54298
RPA0840	0.787164	0.9625	0.804065	0.9845	0.683749	0.997	0.718987	0.9885	0.717497	0.9875	mpp putative protease 934551:935840 forward MW:46352
RPA0841	0.819404	0.985	0.65078	0.99	1.128092	0.1145	0.879191	0.7655	0.988181	0.55	CDS putative ribosomal-protein-alanine N-acetyltransferase 935893:936489 forward MW:22471
RPA0842	0.731885	0.981	0.722673	0.9855	0.707483	0.9935	0.534163	0.9975	0.73944	0.9925	CDS conserved unknown protein 936587:937240 forward MW:22834
RPA0843	0.903954	0.718	1.082626	0.3035	0.935621	0.6515	0.867838	0.895	0.735911	0.948	atpF1 putative Fo ATP synthase B chain 937373:937864 reverse MW:17586
RPA0844	0.853234	0.837	1.099223	0.237	0.896654	0.7875	0.828542	0.9275	0.670843	0.976	atpF2 putative FoF1 ATP synthase, subunit B' 937870:938427 reverse MW:19190
RPA0845	0.809273	0.8115	0.870732	0.72	0.674783	0.8705	1.471679	0.0835	1.338813	0.083	atpE probable ATP synthase subunit C TRANSMEMBRANE protein 938485:938712 reverse MW:7444
RPA0846	0.749884	0.993	1.010243	0.4605	0.586938	0.997	0.816627	0.828	0.981952	0.5515	atpB Fo ATP synthase subunit A 938761:939507 reverse MW:26951
RPA0847	0.937861	0.7705	1.433692	0.0015	0.846756	0.962	1.268499	0.017	1.481668	0.012	atpI FoF1 ATP synthase, subunit I 939577:939963 reverse MW:13514
RPA0848	0.810618	0.9565	0.812693	0.93	1.119481	0.135	0.787278	0.966	0.850416	0.934	CDS conserved unknown protein 940266:940889 forward MW:23558
RPA0849	0.746291	0.955	0.635401	0.9995	0.93512	0.7245	0.616388	0.9955	0.857743	0.964	CDS conserved hypothetical protein 940935:941519 forward MW:20876
RPA0850	0.49895	0.9995	0.604944	0.9995	0.792857	0.944	0.512293	0.9985	0.52656	0.999	CDS Protein of unknown function UPF0047 941543:942016 forward MW:16804
RPA0851	3.310839	0.0055	4.101493	0.005	1.5383	0.072	2.434894	0.0085	3.699389	0.0005	CDS possible MFS transporter 942213:943877 reverse MW:59739
RPA0852	1.049305	0.3455	1.094747	0.1335	1.166872	0.146	1.086192	0.3105	1.036746	0.4055	CDS two-component transcriptional regulator, LuxR family 944214:944891 forward MW:24190
RPA0853	1.085197	0.332	1.685928	0.0025	1.198833	0.0845	1.544017	0.0715	1.101724	0.3385	CDS sensor histidine kinase, possible proline sensor PrlS 945053:948562 reverse MW:126916
RPA0854	1.137183	0.157	1.153816	0.032	1.156747	0.184	0.796764	0.9785	0.722885	0.9755	hemO 5-aminolevulinic acid synthase (ALAS) 948749:949978 reverse MW:44754
RPA0855	0.986095	0.5815	0.870997	0.9665	1.016549	0.3985	0.653604	0.995	0.607785	0.9995	CDS Beta-lactamase-like 950199:951263 reverse MW:39617
RPA0856	1.844107	0	1.530721	0.0015	1.022862	0.4145	1.551544	0.0015	1.293475	0.0185	CDS methyl-accepting chemotaxis receptor/sensory transducer 951429:953567 reverse MW:75246
RPA0857	1.197633	0.0405	1.035053	0.3755	1.195878	0.073	1.12068	0.232	1.065399	0.325	CDS possible outer membrane protein 953782:954516 reverse MW:25814
RPA0858	0.814149	0.9795	0.769855	0.9625	0.963051	0.6945	0.707493	0.9795	0.766087	0.9865	CDS ABC transporter, ATP-binding protein 955056:955805 forward MW:26789
RPA0859	0.684526	0.9525	0.826504	0.969	0.673088	0.9615	0.508237	0.9995	0.625289	0.986	CDS ABC transporter, permease protein 955810:956682 forward MW:30409
RPA0860	0.738611	0.929	0.842757	0.8535	0.833591	0.9705	0.64445	0.993	0.714324	0.957	CDS ABC transporter, periplasmic binding protein 956688:957605 forward MW:32245
RPA0861	0.752627	0.996	0.783717	0.996	0.89767	0.8885	0.818698	0.9655	0.85828	0.968	CDS possible CobW protein involved in cobalamin synthesis 957713:958801 forward MW:40347
RPA0862	0.739733	0.988	0.726534	0.991	0.689658	0.9935	0.613277	0.9975	0.612544	0.997	CDS G-protein beta WD-40 repeat 958798:959817 forward MW:35355
RPA0863	0.848483	0.9055	0.710896	0.9635	0.654362	0.987	0.888842	0.748	0.83424	0.962	CDS possible MgtC-magnesium transport 959852:960574 forward MW:25369
RPA0864	0.677315	0.965	0.840671	0.8445	0.588524	0.997	0.51819	0.998	0.708159	0.937	CDS hypothetical protein 960635:961033 forward MW:13836
RPA0865	0.365485	0.9995	0.423983	0.9995	0.206998	1	0.248305	1	0.398962	0.9905	CDS homospermidine synthase 961340:962770 reverse MW:53002
RPA0866	0.187926	1	0.334032	0.999	0.149816	1	0.229613	0.9985	0.268196	0.9965	rnk putative nucleoside diphosphate kinase regulator 962880:963284 reverse MW:14312
RPA0867	0.599634	0.953	0.848664	0.86	0.46956	0.9965	0.424804	0.994	0.737928	0.8965	CDS Endoribonuclease L-PSP 963579:963965 reverse MW:13914
RPA0868	0.375177	0.957	0.911441	0.761	0.375153	0.99	0.524123	0.946	0.978839	0.5315	CDS hypothetical protein 964063:964221 reverse MW:6073
RPA0869	0.453117	0.976	0.707486	0.9975	0.591293	0.998	0.648844	0.9765	0.771788	0.9275	CDS GCN5-related N-acetyltransferase 964232:964819 reverse MW:20256
RPA0870	0.638275	0.9115	1.132598	0.0915	0.579182	0.989	1.212439	0.1075	1.251213	0.092	CDS putative ornithine decarboxylase 964962:966104 reverse MW:41868
RPA0871	1.031442	0.399	1.339334	0.0445	0.994794	0.522	1.072022	0.2805	1.137195	0.0735	CDS conserved hypothetical protein 966769:967029 reverse MW:8982
RPA0872	1.100575	0.0815	0.994161	0.513	1.028019	0.3825	0.85307	0.9325	1.113178	0.1475	CDS putative peptidyl-dipeptidase 967238:969328 forward MW:77742
RPA0873	0.928672	0.7395	0.88271	0.7875	0.968078	0.61	0.545345	0.997	0.691363	0.981	CDS conserved hypothetical protein 969333:969986 forward MW:23900
RPA0874	0.882557	0.9175	0.882642	0.921	1.136868	0.074	0.742521	0.961	0.888755	0.846	CDS conserved hypothetical protein 969983:971296 forward MW:45092
RPA0875	0.890247	0.938	0.799954	0.986	0.95431	0.7195	0.96777	0.618	1.046943	0.2395	hemZ ferrochelatase 971472:972509 forward MW:38462
RPA0876	0.756129	0.9775	0.704266	0.966	0.834811	0.8465	0.930567	0.654	0.822289	0.9455	CDS conserved unknown protein 972666:973661 forward MW:36325
RPA0877	0.884717	0.874	0.971805	0.601	0.931838	0.8145	0.785136	0.9165	0.790764	0.9935	CDS conserved hypothetical protein 973678:974127 forward MW:15950
RPA0878	0.938884	0.816	1.154384	0.042	0.897073	0.8665	1.332754	0.029	1.203499	0.0355	CDS transcriptional regulator, AraC type; possible DNA gyrase inhibitor 974231:975136 reverse MW:33390
RPA0879	0.663271	0.9985	0.59338	1	0.78398	0.9885	0.537322	0.999	0.596655	0.9965	kpsF CBS domain:Sugar isomerase (SIS):KpsF/GutQ family protein 975442:976455 reverse MW:35178
RPA0880	0.854874	0.956	0.649826	0.998	0.582679	0.9965	0.691017	0.981	0.823652	0.973	CDS hypothetical protein 976660:978375 forward MW:61208
RPA0881	1.141956	0.109	0.984686	0.5805	0.991962	0.549	1.0805	0.2395	1.228317	0.04	CDS hypothetical protein 978487:979503 forward MW:35435
RPA0882	0.823419	0.99	0.810236	0.961	0.766205	0.993	0.583021	0.9945	0.610762	0.9925	CDS ABC transporter, permease 979493:980344 reverse MW:30237
RPA0883	0.85587	0.969	0.901924	0.9045	0.851553	0.9375	0.820572	0.944	0.729904	0.9975	CDS ABC transporter, ATP-binding protein 980454:981248 reverse MW:29124
RPA0884	0.782557	0.944	0.676237	0.995	0.726256	0.964	0.639247	0.9755	0.708952	0.989	CDS ABC transporter, substrate-binding protein 981450:982448 reverse MW:35236
RPA0885	1.256591	0.087	1.527545	0.011	1.076946	0.318	2.026138	0.003	1.306962	0.051	CDS conserved hypothetical protein 982576:982848 reverse MW:10328
RPA0886	0.841642	0.992	1.004655	0.4705	0.745279	0.9915	0.998204	0.5175	1.187458	0.031	CDS putative diguanylate cyclase (GGDEF) 983016:984524 forward MW:55574
RPA0887	0.597365	0.9855	0.819791	0.9895	0.564789	1	0.511505	0.9975	0.622011	0.9935	exoN UTP-glucose-1-phosphate uridylyltransferase 984555:985430 reverse MW:32230
RPA0888	0.800488	0.993	0.870186	0.958	0.709459	0.994	0.696077	0.9925	0.969089	0.6895	CDS putative lysophospholipase L2 985554:986600 reverse MW:38515
RPA0889	0.968019	0.596	0.883573	0.7925	1.116721	0.2385	1.118786	0.202	1.80655	0.002	hspD small heat shock protein 986719:987195 forward MW:17205
RPA0890	0.846972	0.782	0.941148	0.6095	1.664474	0.0065	0.319963	0.999	0.576925	1	CDS hypothetical protein 987337:988113 reverse MW:26899
RPA0891	1.045339	0.3375	0.828978	0.978	0.860701	0.9345	0.859308	0.8505	0.954454	0.5765	gltB glutamate synthase, large subunit 988573:993300 forward MW:171786
RPA0892	0.719118	0.9605	0.67524	0.9905	0.707201	0.998	0.902644	0.784	0.896957	0.8065	gltD glutamate synthase (NADPH) small chain 993473:994927 forward MW:51807
RPA0893			0.53685	0.984	1.570988	0.0665	1.054708	0.412			CDS conserved hypothetical protein 995274:995675 forward MW:14940
RPA0895	0.873487	0.7745	0.532483	0.999	0.944311	0.6725	0.570508	0.9835	0.403038	0.999	CDS putative 3-oxoacyl-[ACP] reductase 997027:997803 reverse MW:26686
RPA0896	0.972634	0.612	0.992936	0.5055	1.06887	0.249	1.30553	0.023	1.141253	0.1745	CDS putative 3-oxoacyl-acyl carrier protein reductase 997944:998678 forward MW:25577
RPA0898	0.985446	0.559	1.006496	0.4815	1.122792	0.084	1.237487	0.1545	0.979858	0.5665	dapA2 putative dihydrodipicolinate synthase 1000591:1001508 reverse MW:32848
RPA0899	0.929133	0.8245	0.787196	0.985	0.886553	0.8705	0.853303	0.905	1.004638	0.472	CDS putative transglycolase 1002043:1003440 reverse MW:50920
RPA0900	0.814929	0.951	0.714169	0.979	1.008161	0.4695	0.741286	0.949	0.67846	0.9965	CDS probable Rht family transporter, amino acid efflux 1003627:1004259 forward MW:21867
RPA0901	0.973229	0.655	0.862064	0.875	1.299607	0.0075	1.14485	0.1205	0.913413	0.7265	CDS DUF81 1004276:1005043 reverse MW:26716
RPA0902			0.659865	0.967	0.848591	0.7195	0.884485	0.762			CDS Glyoxalase/Bleomycin resistance protein/dioxygenase domain 1005076:1005507 reverse MW:15564
RPA0903											CDS possible transcriptional regulator, TetR family 1005555:1006154 forward MW:20575
RPA0904	0.764429	0.985	0.958028	0.748	0.779132	0.9835	0.84562	0.9045	0.871157	0.9315	CDS putative Mono-phosphatase 1006170:1007090 reverse MW:33227
RPA0906	0.909249	0.804	0.81192	0.9225	1.281224	0.0355	0.924852	0.8125	1.201375	0.0625	CDS putative N-formylglutamate amidohydrolase 1007978:1008865 reverse MW:33217
RPA0907	1.092808	0.101	1.335463	0.0075	1.071163	0.205	1.317541	0.007	1.286042	0.007	CDS response regulator receiver (CheY-like protein) 1009176:1009535 forward MW:13338
RPA0908	1.404637	0.017	1.558443	0.0005	1.195389	0.209	1.461393	0.005	2.18945	0.004	CDS hypothetical protein 1009925:1010050 forward MW:4169
RPA0909	0.659171	0.959	0.644082	0.989	1.038071	0.406	0.769368	0.851	0.741232	0.849	wrbA Trp repressor binding protein 1010498:1011097 reverse MW:20793
RPA0910	0.882171	0.867	0.835026	0.9205	0.829462	0.9355	0.703012	0.975	0.833805	0.9355	CDS DUF209:Cupin domain 1011260:1011958 reverse MW:25106
RPA0911			0.834666	0.766	0.93379	0.584	0.691173	0.9805	0.72758	0.893	CDS transcriptional regulator, LysR family 1012091:1013014 forward MW:32875

RPA0912	0.773688	0.9935	0.727532	0.993	0.945932	0.6435	0.524245	1	0.617281	0.997	CDS unknown protein 1013029:1013862 reverse MW:28951
RPA0913	1.023736	0.3755	1.089753	0.189	1.327856	0.045	0.981172	0.5725	1.236189	0.048	CDS DUF179 1013997:1014650 forward MW:23154
RPA0914	0.870342	0.976	0.753215	0.997	0.68783	0.997	0.665132	0.9975	0.782831	0.9785	CDS putative diguanylate cyclase (GGDEF)/phosphodiesterase (EAL) with PAS domain 1014871:1017750 reverse MW:105237
RPA0915	0.95076	0.719	0.801856	0.95	0.806905	0.959	0.742865	0.9195	0.887967	0.9185	CDS putative NADPH quinone oxidoreductase 1017873:1018871 reverse MW:34576
RPA0916	1.082685	0.253	0.982688	0.5515	1.13113	0.301	1.334747	0.1405	0.996079	0.512	CDS conserved unknown protein 1018985:1019176 forward MW:7041
RPA0917	0.811593	0.9155	0.620523	1	0.850194	0.893	0.849486	0.8665	1.062008	0.2215	CDS probable transcriptional regulator, AraC family 1019597:1020106 forward MW:18562
RPA0918	0.979013	0.593	1.372395	0.024	0.952353	0.7155	1.129216	0.127	1.083664	0.277	CDS possible 50S ribosomal protein L31 1020328:1020555 reverse MW:8567
RPA0919	0.780448	0.994	0.789829	0.994	0.758738	0.985	0.65205	0.992	0.614632	0.994	CDS ABC transporter, ATP-binding protein 1020753:1022657 forward MW:67428
RPA0920	0.841693	0.9185	0.80077	0.96	0.879129	0.914	0.822582	0.933	0.753932	0.9605	CDS GCN5-related N-acetyltransferase 1022801:1023247 reverse MW:17065
RPA0921	1.081625	0.2795	0.870426	0.9615	1.09074	0.1065	1.17961	0.088	0.967369	0.631	CDS possible flagellar motor protein MotB 1023394:1024419 reverse MW:37853
RPA0922	0.98986	0.575	0.726939	0.995	1.073018	0.158	0.938586	0.7075	0.849568	0.921	CDS conserved hypothetical protein 1024419:1025438 reverse MW:36523
RPA0923	0.963101	0.682	0.767706	0.9825	1.089234	0.1935	0.898988	0.749	0.963982	0.6785	CDS conserved hypothetical protein 1025618:1026445 forward MW:30524
RPA0924	1.027927	0.3405	1.191936	0.076	0.963753	0.6255	1.048613	0.3695	0.863841	0.9515	CDS possible cyclopropane-fatty-acyl-phospholipid synthase 1026442:1027467 forward MW:39189
RPA0925	1.175933	0.035	1.001905	0.504	1.233695	0.0735	1.199243	0.1615	0.844836	0.892	CDS hypothetical protein 1027750:1027944 forward MW:7086
RPA0926	0.987891	0.563	0.960363	0.63	1.36766	0.0605	1.108999	0.21	0.721426	0.9595	CDS hypothetical protein 1028028:1028222 forward MW:7078
RPA0928			1.00625	0.5005	1.061314	0.434	0.752288	0.901	0.564326	0.9985	CDS conserved hypothetical protein 1028533:1029108 reverse MW:19910
RPA0929	0.856681	0.811	0.773897	0.732	0.931268	0.615			0.679232	0.934	CDS hypothetical protein 1029178:1029765 forward MW:21187
RPA0930	0.931322	0.819	0.995812	0.507	1.113042	0.117	0.780421	0.9875	0.636886	0.998	CDS possible 3-octaprenyl-4-hydroxybenzoate carboxy-lyase 1029992:1030594 reverse MW:21477
RPA0931	0.711238	0.9825	0.874412	0.924	0.939029	0.8285	0.69891	0.9945	0.571242	0.995	ubiD Carboxylyase-related protein 1030591:1032129 reverse MW:56488
RPA0932	0.571928	0.986	0.824996	0.976	0.633135	0.9995	0.485945	0.9995	0.476692	0.9995	CDS conserved unknown protein 1032245:1032790 forward MW:19632
RPA0933	0.68352	0.992	0.897283	0.87	0.73702	0.988	0.905961	0.8435	0.569411	0.9965	CDS putative protease, putative 1032794:1033771 forward MW:35195
RPA0934	0.647987	0.9525	1.025606	0.4295	0.807068	0.9395	0.427931	0.999	0.386719	1	CDS conserved unknown protein 1033840:1034760 forward MW:33323
RPA0935	0.867387	0.972	0.890342	0.8795	0.852198	0.9425	1.008665	0.458	1.105719	0.088	CDS conserved hypothetical protein 1035248:1036549 reverse MW:47270
RPA0936											CDS possible transcriptional regulator, TetR family 1036631:1037203 forward MW:20614
RPA0937	0.69938	0.999	1.012129	0.4365	0.544322	0.9965	0.64595	0.9855	0.718798	0.979	CDS extragenic suppressor protein SuhB; Inositol monophosphatase family 1037232:1038020 reverse MW:28472
RPA0938	0.641486	0.987	0.875718	0.936	0.696033	0.9685	0.644108	0.9925	0.717819	0.9935	CDS conserved unknown protein 1038125:1039216 reverse MW:38355
RPA0939	0.801682	0.9445	0.943828	0.799	0.784939	0.978	0.779083	0.9785	0.792454	0.97	CDS possible thiamine-phosphate pyrophosphorylase 1039233:1039892 reverse MW:22550
RPA0940	0.81512	0.972	0.755541	0.996	0.692775	0.9895	0.654594	0.9905	0.714057	0.9985	CDS fructose-bisphosphate aldolase 1039898:1040932 reverse MW:37250
RPA0941	0.810715	0.988	1.096588	0.096	0.800342	0.9595	1.244917	0.0475	1.57469	0.0235	CDS conserved hypothetical protein 1040987:1041310 reverse MW:11459
RPA0942	0.786397	0.988	0.884777	0.8875	0.751945	0.992	0.829348	0.904	0.836057	0.9545	CDS conserved hypothetical protein 1041307:1041591 reverse MW:10680
RPA0943	0.611881	0.9615	0.796013	0.9515	0.417158	0.999	0.399179	1	0.441208	0.9995	cbbK phosphoglycerate kinase 1041690:1042886 reverse MW:41884
RPA0944	0.657676	0.981	0.841773	0.8565	0.482251	1	0.391215	1	0.477174	0.996	cbbG glyceraldehyde-3-phosphate dehydrogenase(GAPDH) 1043108:1044115 reverse MW:35956
RPA0945	0.576713	0.994	0.639651	0.998	0.774464	0.992	0.466008	1	0.495605	0.9995	cbbT2 transketolase 1044331:1046316 reverse MW:70382
RPA0946	0.843293	0.9635	0.680541	0.998	1.022847	0.4095	0.685046	0.9855	0.742826	0.997	CDS hypothetical protein 1046611:1046988 forward MW:13654
RPA0947	0.948431	0.7105	0.687209	0.999	1.016456	0.4225	0.630404	0.99	0.778175	0.969	CDS conserved hypothetical protein 1046985:1047395 forward MW:14446
RPA0948	0.861689	0.9355	1.065269	0.3335	0.846014	0.903	0.963014	0.6475	1.292582	0.072	CDS possible hypothetical RNA methyltransferase 1047902:1049140 reverse MW:44139
RPA0949	0.668282	0.993	0.709506	0.9825	0.621783	0.997	0.503158	0.995	0.69092	0.992	matE2 putative multidrug efflux protein (NorM) 1049187:1050611 reverse MW:49852
RPA0950	0.959721	0.6805	1.060894	0.2505	0.878924	0.9165	0.962844	0.6625	0.889903	0.8555	tly putative hemolysin 1050674:1051414 reverse MW:25976
RPA0951	0.937883	0.828	0.847293	0.9135	0.939941	0.7745	1.012915	0.4595	0.720359	0.9965	CDS Nucleoside 2-deoxyribosyltransferase 1051417:1051980 reverse MW:20275
RPA0952	1.069112	0.1575	1.066599	0.1775	0.93817	0.7705	1.169381	0.0495	1.122472	0.1115	dxs 1-D-deoxyxylulose 5-phosphate synthase 1052203:1054128 reverse MW:68804
RPA0953	0.921176	0.8705	0.936084	0.747	0.973493	0.5935	1.24836	0.0355	1.286009	0.019	xseB possible exodeoxyribonuclease small subunit 1054542:1054793 reverse MW:9273
RPA0954	1.314068	0.1605	0.822309	0.969	1.231241	0.056	1.061935	0.2985	1.072935	0.2325	CDS possible histone deacetylase or acetylpolyamine aminohydrolase or acetoin utilization protein 1054877:1055806 reverse MW:33254
RPA0955	0.866114	0.9825	0.716368	0.999	0.636461	0.993	0.680954	0.994	0.777129	0.9855	CDS putative 5`-nucleotidase family protein 1055912:1057630 reverse MW:59779
RPA0956	0.82796	0.96	0.829306	0.9495	0.785277	0.981	0.592613	0.9845	0.674836	0.9935	CDS hypothetical protein 1057814:1058290 forward MW:16967
RPA0957	0.842711	0.978	0.75338	0.996	0.798922	0.9615	0.781212	0.966	0.746999	0.997	CDS putative enoyl-CoA hydratase 1058329:1059123 reverse MW:28722
RPA0958	0.915127	0.6735	0.784614	0.974			0.902652	0.678	0.678821	0.997	CDS putative acyl-CoA dehydrogenase 1059297:1061078 reverse MW:62131
RPA0959	0.958583	0.6735	0.586246	0.9915	1.053857	0.3355	0.566598	0.9755	0.740556	0.958	hupU uptake hydrogenase accessory protein hupU 1061498:1062499 forward MW:34392
RPA0960	0.968712	0.599	0.915027	0.8415	0.976449	0.5685	1.064798	0.3115	0.833532	0.9405	hupV pseudogene uptake hydrogenase regulatory protein hupV pseudogene, frameshifted 1062496:1063937 forward MW:51857
RPA0962	0.970313	0.657	1.376354	0.02	1.22015	0.017	1.39668	0.0325	1.143973	0.2625	hupS hydrogenase small chain 1064173:1065285 forward MW:40275
RPA0963	1.806962	0.0055	1.288861	0.0195	2.338304	0.0025			0.542088	0.924	hupL hydrogenase large chain 1065304:1067097 forward MW:65672
RPA0964	1.976555	0.015	1.42723	0.004	3.292835	0	4.760001	0.0065	0.598636	0.811	hupC Ni/Fe-hydrogenase 1 B-type cytochrome subunit 1067114:1067842 forward MW:28030
RPA0965			1.214707	0.0335			1.164728	0.292	1.145661	0.29	hupD hydrogenase maturation protein hupD 1067904:1068557 forward MW:23320
RPA0966			1.339233	0.0395			37.22117	0	6.242463	0.0005	hupE putative membrane-bound hydrogenase component hupE 1068571:1069164 forward MW:19325
RPA0967	1.238951	0.207	1.58974	0.004	1.174407	0.098			1.208697	0.2645	hupF hydrogenase expression/formation protein hupF 1069185:1069487 forward MW:11020
RPA0968	1.390942	0.0015	1.309474	0.0265	0.966441	0.664	1.155927	0.208	1.028158	0.4385	hupG putative hydrogenase expression/formation protein hupG 1069708:1070109 forward MW:13973
RPA0969	0.981806	0.5845	1.097682	0.1465	0.910594	0.879	1.005164	0.4855	1.077482	0.169	hupH hydrogenase expression/formation protein hupH 1070106:1070972 forward MW:30709
RPA0970	0.685154	0.9755	0.721968	0.9085	0.733812	0.9085	0.920486	0.7215	0.600348	0.9965	hupI putative rubredoxin hupI 1070969:1071181 forward MW:7672
RPA0971	1.280947	0.1745	1.203704	0.153	0.877755	0.7305			1.033556	0.454	hupJ putative hydrogenase expression/formation protein hupJ 1071171:1071695 forward MW:18332
RPA0972	0.907022	0.6655	1.03778	0.3495	0.785728	0.974	0.602331	0.997	0.763616	0.832	hupK putative hydrogenase expression/formation protein hupK 1071692:1072801 forward MW:38373
RPA0973	1.104102	0.4125	1.139982	0.0995			1.74569	0.0155	1.215648	0.045	hypA hydrogenase formation/expression protein hypA 1072794:1073135 forward MW:12533
RPA0974	0.997539	0.505	0.886434	0.746	0.76154	0.9845	1.047875	0.3425	1.094624	0.2495	hypB hydrogenase expression/formation protein hypB 1073135:1074091 forward MW:33885
RPA0975	1.225976	0.06	1.067132	0.3135	0.99231	0.5245	1.338699	0.0575	1.324607	0.1135	hypF hydrogenase maturation protein hypF 1074096:1076369 forward MW:80313
RPA0976	1.379806	0.0205	1.199695	0.031	1.149785	0.046	1.382853	0.0115	1.580258	0.0185	hypC putative hypC 1076369:1076602 forward MW:8106
RPA0977	1.345104	0.0135	1.04102	0.2815	0.962436	0.667	1.139906	0.3	1.245539	0.165	hypD hydrogenase expression/formation protein hypD 1076599:1077741 forward MW:41154
RPA0978	1.170004	0.0605	1.179602	0.0735	1.016625	0.446	1.457817	0.017	1.367134	0.0925	hypE hydrogenase expression/formation protein hypE 1077738:1078784 forward MW:36366
RPA0979	1.428374	0.005	1.254161	0.054	1.170671	0.126	1.990531	0.0005	2.003886	0.0025	hoxA two component sigma-54-dependent hydrogenase transcriptional regulator hoxA, Fis family 1078825:1080273 forward MW:53729
RPA0980			1.008532	0.4575							CDS sensor histidine kinase with a PAS domain 1080263:1081615 forward MW:48939
RPA0981	1.539668	0.0085	1.030399	0.351	1.868164	0.0025	2.045003	0.0015	2.185204	0	CDS sensor histidine kinase with multiple PAS and a response regulator receiver domain 1081721:1084108 forward MW:87807
RPA0982	1.539427	0.004	1.513443	0.0015	1.415986	0.009	2.553254	0.004	2.356004	0.0005	pcaR putativetranscriptional regulator PcaR, IclR family 1084132:1084923 reverse MW:28407
RPA0983	4.884825	0	3.280998	0.0005	5.960243	0	13.84331	0	12.7075	0	CDS possible phthalate dioxygenase 1085284:1086642 forward MW:50794
RPA0984	2.197496	0	3.103745	0	2.149003	0	12.06091	0.0005	7.635931	0	glnA4 putative glutamine synthetase-like protein 1086639:1088099 forward MW:54483
RPA0985	2.866903	0	2.250951	0.0005	3.191001	0.001	7.085149	0	5.624125	0	CDS putative branched-chain amino acid transport system substrate-binding protein 1088146:1089318 forward MW:41577
RPA0986	1.393054	0.0065	1.838404	0.0005	1.674114	0.0015	3.424948	0	3.037484	0	CDS possible urea/short-chain amide transport system permease protein 1089530:1090396 forward MW:30828
RPA0987	2.056965	0.007	1.532622	0.0145	1.709598	0.0345	3.523879	0.0035	3.226272	0.001	CDS possible branched-chain amino acid ABC transporter, permease protein 1090399:1091397 forward MW:34656
RPA0988	1.625698	0.019	1.877941	0.0145	1.624916	0.002	5.974602	0.004	1.959418	0.008	CDS putative branched-chain amino acid ABC transporter, ATP-binding protein 1091394:1092158 forward MW:27286
RPA0989	1.761931	0.0025	1.125234	0.125	1.487733	0.0065	2.610544	0	1.732766	0.004	CDS putative ATP-binding component of ABC transporter 1092139:1092852 forward MW:25589
RPA0990	1.623503	0.025			1.1369	0.3385			0.755327	0.9435	phyB5 Bacteriophytochrome (light-regulated signal transduction histidine kinase), PhyB5 1092866:1095403 reverse MW:91829

RPA0991	2.495543	0.0195	2.452212	0.003			1.649636	0.0325	3.022011	0.001	CDS possible transcriptional regulator, Crp/Fnr family 1095619:1096404 forward MW:28614
RPA0992	2.209902	0.0025	3.909336	0	2.294648	0.004	2.216205	0.0075	4.568157	0.0015	CDS probable transcriptional regulator, Crp/Fnr family 1096426:1097157 reverse MW:27428
RPA0993	0.777344	0.8985			1.323899	0.024			0.727974	0.9925	CDS possible alpha-ribazole-5`-phosphate phosphatase CobC (vit B12 synthesis) 1097324:1097899 forward MW:20616
RPA0994	0.8368	0.9605	0.897366	0.916	0.722808	0.998	0.837699	0.9525	0.999264	0.4915	CDS unknown protein 1098342:1098677 forward MW:13040
RPA0995	0.68883	0.998	0.699154	0.999	0.645396	0.9985	0.582587	0.998	0.752501	0.995	CDS probable acyl-CoA dehydrogenase 1098742:1099887 reverse MW:42307
RPA0996	1.025994	0.439	0.958543	0.643	0.764751	0.962	0.809618	0.843	0.854957	0.912	CDS Alpha/beta hydrolase fold 1100262:1101284 reverse MW:38230
RPA0997											CDS possible transcriptional regulator, ArsR family 1101329:1101757 forward MW:15847
RPA0998											CDS conserved hypothetical protein 1101771:1102151 reverse MW:13683
RPA0999											PA5115 conserved hypothetical protein 1102360:1102974 forward MW:22369
RPA1000											CDS Nitrogenase-associated protein:Arsenate reductase and related 1102982:1103377 reverse MW:14439
RPA1001	2.063398	0.0425					5.265189	0.004	2.696143	0.0055	CDS conserved hypothetical protein 1103391:1103981 reverse MW:20379
RPA1002	0.625184	0.992	0.707916	0.931	0.748252	0.929	0.848625	0.818	0.542684	0.9925	modD putative molybdenum transport system protein 1104195:1105070 forward MW:30051
RPA1003	1.12243	0.351	0.73184	0.986	1.200994	0.035	0.679473	0.9755	0.483739	1	CDS putative acyl-CoA synthase 1105201:1106835 reverse MW:59264
RPA1005	1.085415	0.306	0.826325	0.8125	1.048597	0.4125	0.95185	0.5825	0.940339	0.654	CDS NUDIX hydrolase 1107364:1108014 forward MW:23972
RPA1006	1.154335	0.312	1.503263	0.005	1.354332	0.165	1.022549	0.4245	0.646117	0.841	CDS possible protocatechuate 4,5-dioxygenase small subunit (AB035121) 1108128:1108529 forward MW:14155
RPA1007	1.295833	0.185	1.971714	0.0015	1.777322	0.0505	1.020515	0.4595	0.733794	0.827	mhpB possible 2,3-dihydroxyphenylpropionate 1,2-dioxygenase 1108545:1109402 forward MW:31141
RPA1008	0.964867	0.6535	1.213867	0.065	1.191323	0.0525	1.099345	0.237	1.020376	0.4115	CDS probable transcriptional regulator, AraC family 1109469:1110359 reverse MW:33337
RPA1009	0.748095	0.989	0.315089	1	0.63669	0.9745	1.50335	0.12	2.260008	0	CDS possible cytochrome P450 1110510:1111697 forward MW:44011
RPA1010	1.249122	0.1065	0.838528	0.875	1.015456	0.4235	1.146326	0.1345	1.027693	0.406	CDS Beta-lactamase-like:ATP/GTP-binding site motif A (P-loop) 1111734:1113680 reverse MW:71553
RPA1011	1.079884	0.3025	0.89576	0.7375	0.958603	0.5965			0.832972	0.929	CDS DSBA oxidoreductase 1113940:1114593 forward MW:24768
RPA1012	1.006365	0.491	1.19209	0.055	1.163446	0.182	1.823522	0.031	1.425427	0.0185	CDS possible integral membrane protein 1114724:1115488 forward MW:27008
RPA1013	0.788947	0.8375	1.013122	0.483	1.160473	0.2675	1.21297	0.366	0.766625	0.9565	fixG nitrogen fixation protein fixG, homologous to rdxB of R. sphaeroides 1115514:1116956 reverse MW:54231
RPA1014	0.907707	0.775	1.126176	0.1425	1.065538	0.3445	1.308142	0.0755	1.022275	0.4415	CDS conserved hypothetical protein 1117075:1117368 reverse MW:10399
RPA1015	1.406222	0.01	0.799766	0.9065	1.134326	0.154	2.118839	0.0025	3.382385	0	CDS transcriptional regulator, PadR family 1117580:1118170 forward MW:21264
RPA1016	1.561935	0.0075	1.583824	0.002	1.723201	0.001	3.324337	0.0005	3.727512	0	petA ubiquinol-cytochrome-c reductase, Rieske iron-sulfur protein 1118259:1118792 forward MW:19307
RPA1017	0.90524	0.621	1.144871	0.244	0.781826	0.98	2.722024	0.003	1.810431	0.001	CDS Nitrogen fixation-related protein 1119042:1119434 forward MW:13768
RPA1018	0.914961	0.907	0.992401	0.535	0.749047	0.9715	0.680351	0.87	0.734228	0.9845	CDS conserved hypothetical protein 1119616:1119816 reverse MW:6990
RPA1019											CDS possible NolR/HlyU transcriptional regulator, ArsR family 1119897:1120238 forward MW:12320
RPA1020											CDS possible membrane fusion protein precursor; predicted cation efflux pumps 1120240:1121235 forward MW:35964
RPA1021	0.871373	0.83	0.672029	0.9985	0.807437	0.9355	0.644444	0.9895	0.730574	0.9955	CDS putative transporter, AcrB/D/F family; Cation efflux system protein 1121232:1124456 forward MW:115658
RPA1022	1.100197	0.229	0.792496	0.991	0.923016	0.8085	0.850487	0.8665	0.894737	0.9235	CDS possible outer membrane protein 1124518:1125171 forward MW:23335
RPA1023			1.011712	0.4575	0.982751	0.533	1.109111	0.326	0.909672	0.613	CDS hypothetical protein 1125380:1125691 forward MW:11434
RPA1024	1.41958	0.011	1.342165	0.0025	1.730318	0.0005	1.425398	0.005	1.097532	0.206	CDS putative oxidoreductase 1125696:1126958 forward MW:44848
RPA1025			1.610642	0.0005			1.56669	0.0225			CDS possible Ectothiorhodospira Vacuolata Cytochrome 1126955:1127320 forward MW:13331
RPA1026	1.021148	0.367	0.87911	0.9215	0.886692	0.8185	0.886226	0.833	0.93048	0.796	CDS possible adenine DNA methyltransferase 1127420:1128550 reverse MW:42039
RPA1027	0.834581	0.964	0.830929	0.9745	0.904676	0.907	0.810187	0.976	0.942237	0.789	CDS conserved hypothetical protein 1128929:1129846 forward MW:32884
RPA1028	0.635468	0.979	0.75149	0.915	0.687238	0.969	0.585781	0.991	0.511935	0.9965	moaB molybdopterin biosynthesis, protein B 1129985:1130533 forward MW:19836
RPA1029	0.878623	0.7175	0.469797	1	0.971273	0.601	0.586599	0.9825	0.556663	0.9945	CDS possible CoA transferase, subunit A 1130697:1131464 forward MW:26643
RPA1030	0.934704	0.5865	0.636526	0.9835	0.978269	0.567	0.633552	0.7875	0.572813	0.9915	CDS possible CoA transferase, subunit B 1131461:1132213 forward MW:26938
RPA1031	0.770064	0.896	0.778309	0.8865	0.856006	0.8315	0.981951	0.5275	0.725002	0.9975	CDS transcriptional regulator, MarR family; N-acetyltransferase 1132371:1133378 reverse MW:36897
RPA1032	1.181153	0.0565	1.006807	0.476	1.079323	0.232	0.885732	0.8165	1.143558	0.109	CDS Glycosyl transferase, family 2 1133477:1134043 reverse MW:19653
RPA1033	0.799754	0.831	0.761544	0.7765	1.072609	0.235	0.707362	0.9585	1.068283	0.2485	CDS DUF85:Elongator protein 3/MiaB/NifB 1134224:1135384 forward MW:43077
RPA1034	0.774082	0.9955	0.683814	0.989	0.961277	0.6685	0.785183	0.945	0.863606	0.909	rnh2 possible ribonuclease HII 1135479:1136393 forward MW:32176
RPA1035	0.501914	0.9975	0.522691	0.9915	0.582802	0.9885	0.415615	0.992	0.358506	0.9995	CDS conserved hypothetical protein 1136390:1137973 forward MW:56573
RPA1036	0.819423	0.903	1.054496	0.3155	1.024687	0.4515	1.00559	0.481	1.037856	0.4035	polN possible phage DNA polymerases 1138032:1138862 reverse MW:29857
RPA1037	1.050111	0.3405	0.970118	0.6845	0.900613	0.7875	0.785688	0.984	1.015584	0.415	CDS possible electron transfer flavoprotein dehydrogenases 1139064:1140722 forward MW:59954
RPA1038	0.899937	0.939	0.838252	0.9695	0.923269	0.7775	0.789258	0.984	0.856806	0.9535	CDS TPR repeat 1140980:1142764 forward MW:65540
RPA1039	0.631856	0.9925	0.63948	0.995	0.834872	0.967	0.448394	0.982	0.489443	0.9955	ispE possible isopentenyl monophosphate kinase 1142869:1143768 forward MW:30418
RPA1040	0.89859	0.9065	0.898455	0.92	0.778264	0.9825	0.785865	0.967	0.993702	0.5325	CDS octaprenyl-diphosphate synthase 1143914:1144924 reverse MW:36218
RPA1041	0.515815	0.9585			0.883947	0.748	0.86348	0.678	0.900395	0.6425	CDS conserved hypothetical protein 1145132:1145359 forward MW:8054
RPA1042	0.951021	0.7245	1.040058	0.3615	1.183378	0.095	1.183068	0.102	1.239747	0.023	CDS conserved unknown protein 1145352:1146131 forward MW:26725
RPA1043	0.86888	0.8505	0.740723	0.9355	0.978641	0.5915	0.664485	0.984	0.831718	0.98	CDS possible protease SohB 1146377:1147279 forward MW:31916
RPA1044	1.063192	0.3295			0.968407	0.529			1.066799	0.4205	CDS hypothetical protein 1147380:1147691 reverse MW:11273
RPA1045	0.883195	0.8735	1.072559	0.152	0.639834	0.995	0.843935	0.9635	1.042794	0.3495	sygA glycyl-tRNA synthetase alpha chain 1147992:1148942 forward MW:35891
RPA1046	0.908102	0.753	1.112034	0.1325	0.649658	0.9935	0.892872	0.8325	1.220987	0.09	CDS conserved hypothetical protein 1149072:1149506 forward MW:16255
RPA1047	1.169451	0.0795	0.924779	0.779	0.781144	0.9685	0.59729	0.9975	0.904948	0.6275	sygB putative glycyl-tRNA synthetase, beta chain 1149506:1151836 forward MW:86021
RPA1048	0.789127	0.989	0.575629	0.995	0.715746	0.97	0.762746	0.93	0.63274	0.999	CDS conserved unknown protein 1152596:1153699 forward MW:38287
RPA1049	0.824041	0.9645	0.867273	0.9045	0.873887	0.8695	0.651745	0.9955	0.840586	0.972	CDS conserved hypothetical protein 1153713:1155209 reverse MW:52672
RPA1050	0.866803	0.9505	1.170513	0.1285	0.804501	0.9125	0.495129	0.9985	0.598267	0.9955	CDS hypothetical protein 1155473:1155628 forward MW:5481
RPA1051	0.926101	0.7425	0.932747	0.811	0.868084	0.8905	0.738974	0.9955	0.686879	0.9805	CDS pyruvate phosphate dikinase 1156005:1158746 forward MW:99423
RPA1052	1.115937	0.1345	1.265162	0.065	0.861132	0.7335	1.280551	0.0295	1.156448	0.19	CDS conserved hypothetical protein 1159062:1160492 forward MW:51521
RPA1053	0.58344	0.9985	0.680639	0.9975	0.5714	0.9995	0.538174	0.9975	0.521413	1	nadC nicotinate-mononucleotide pyrophosphorylase 1161049:1161924 reverse MW:30496
RPA1054	0.926642	0.8525	0.811421	0.936	1.213692	0.0355	0.898597	0.8665	1.06499	0.2975	nadB putative L-aspartate oxidase 1161941:1163557 reverse MW:55306
RPA1055	0.79531	0.99	0.647542	0.994	1.061612	0.2255	0.768865	0.872	1.001457	0.507	nadA quinolinate synthetase A 1163651:1164763 reverse MW:40946
RPA1056	0.89926	0.8075	1.025109	0.384	0.817807	0.9555	0.812685	0.946	0.906586	0.907	CDS putative dehydrogenase (zinc-binding alcohol dehydrogenase, NADPH quinone oxidoreductase, oxidoreductase) 1165116:1166102 forward MW:34420
RPA1057	1.093037	0.2675	0.953255	0.6525	1.114508	0.1845	0.869197	0.811	1.090454	0.221	CDS hypothetical protein 1166217:1166786 forward MW:20244
RPA1058	0.890074	0.806	0.768525	0.956	0.933155	0.7075	0.690109	0.959	0.742393	0.911	CDS probable transcriptional regulator, AraC family 1167398:1168333 forward MW:33880
RPA1059	0.914605	0.82	1.268046	0.044	0.742091	0.9925	0.843341	0.835	1.194933	0.042	CDS probable outer membrane protein, TonB-dependent receptor 1168419:1170635 forward MW:80229
RPA1060			1.462308	0.067					0.91407	0.605	CDS hypothetical protein 1170643:1171086 forward MW:16280
RPA1061					0.684192	0.8965			1.055253	0.4495	tcmP possible polyketide synthesis protein 1171079:1171933 forward MW:31256
RPA1062	0.725884	0.7935	0.856894	0.852	1.129096	0.3605	1.075046	0.391	0.712528	0.973	CDS conserved hypothetical protein 1171930:1174602 reverse MW:92580
RPA1063	1.009023	0.4435	1.222016	0.0425	1.029818	0.349	0.878551	0.829	0.892923	0.755	CDS conserved hypothetical protein 1174654:1175649 reverse MW:36937
RPA1064	0.700558	0.946	0.509773	0.9965	0.994119	0.5265	0.572014	0.99	0.662775	0.9985	CDS conserved hypothetical protein 1175646:1176152 reverse MW:18154
RPA1065	0.615782	0.9735	0.527911	1	0.607876	0.9925	0.427291	0.996	0.367304	0.9995	CDS Metal dependent phosphohydrolase 1176219:1176836 reverse MW:22753
RPA1066	1.213396	0.074	1.239582	0.062	2.492212	0.0065	0.994784	0.5085	1.224867	0.0185	CDS hypothetical protein 1176912:1177184 forward MW:10034
RPA1067	1.180001	0.065	1.452995	0.03	2.010106	0.009	0.950745	0.6785	1.935063	0.0055	tag possible 3-methyladenine DNA glycosylase I 1177191:1177847 reverse MW:24145
RPA1068	0.885697	0.9535	0.693183	0.997	1.034233	0.326	1.000691	0.497	0.935148	0.742	CDS Glycine cleavage T protein (aminomethyl transferase) 1177844:1178725 reverse MW:31062

RPA1069	0.934646	0.7	0.800603	0.9645	0.780977	0.966	0.748509	0.9305	0.818945	0.957	pyrC possible dihydroorotase 1178873:1180207 forward MW:48616
RPA1070	1.560142	0.0105	1.430283	0.027	0.955002	0.643	2.479425	0.0015	2.393641	0	CDS hypothetical protein 1180716:1180871 forward MW:5746
RPA1071	0.97363	0.6395	0.792018	0.99	0.908652	0.819	0.916222	0.814	1.020034	0.402	CDS conserved hypothetical protein 1180892:1181155 reverse MW:9396
RPA1072	0.953485	0.6675	1.176973	0.1035	0.91384	0.8795	1.058293	0.3305	1.04183	0.282	CDS conserved hypothetical protein 1181286:1181726 reverse MW:15988
RPA1073	1.006833	0.476	1.060575	0.35	0.862404	0.85	0.924803	0.7035	0.829358	0.9085	CDS possible ADP-RIBOSE PHOSPHOHYDROLASE 1181726:1182160 reverse MW:15465
RPA1074	2.218671	0.0005	1.928764	0.0005	2.127953	0	1.205157	0.0695	1.681295	0.0015	CDS conserved hypothetical protein 1182166:1182522 reverse MW:12906
RPA1075	1.059976	0.219	1.108066	0.1775	1.186553	0.0435	1.088284	0.222	1.236594	0.029	CDS DUF159 1182725:1183498 forward MW:28153
RPA1076	0.948157	0.756	0.987565	0.557	0.653678	0.9985	0.962106	0.625	0.818777	0.952	CDS putative oxidoreductase 1183607:1185034 reverse MW:50788
RPA1077	1.124573	0.0765	1.095143	0.253	1.092864	0.1375	1.251243	0.025	1.383522	0.005	CDS Sua5/YciO/YrdC/YwlC protein family:SUA5 domain 1185153:1186199 reverse MW:36137
RPA1078	1.094201	0.151	0.830868	0.8925	1.196258	0.1425	1.05152	0.3965	1.04243	0.3365	CDS probable transcriptional regulator, AraC family 1186379:1187281 forward MW:32774
RPA1079	0.941732	0.808	1.005654	0.488	0.814663	0.9795	0.763322	0.9755	0.92866	0.799	CDS probable 4-methylmuconolactone Major Facilitator Family (MFS) transporter 1187407:1188693 forward MW:46020
RPA1080	0.847214	0.81	1.095311	0.2495	0.947903	0.704	0.853176	0.8265	0.886256	0.7135	CDS possible 2-pyrone-4,6-dicarboxylate hydrolase 1188686:1189588 forward MW:32571
RPA1081	1.217802	0.0495	1.012487	0.446	1.499036	0.009	0.808517	0.8905	1.806521	0.003	CDS hypothetical protein 1189896:1190549 reverse MW:22917
RPA1082	1.327862	0.03	0.94471	0.73	1.745923	0.007	0.718593	0.9365	1.542951	0.0045	CDS conserved hypothetical protein 1190900:1192234 forward MW:45449
RPA1083											CDS conserved hypothetical protein 1192349:1192669 forward MW:10911
RPA1084	0.9161	0.756	0.886343	0.8635	1.044614	0.327	0.551168	0.999	0.873665	0.925	csgB, agfB possible minor curlin subunit precursor (fimbrin sef17 minor subunit). 1192666:1193157 forward MW:16526
RPA1085	0.886642	0.9005	0.88154	0.896	1.02636	0.3895	0.789591	0.8995	0.59688	0.989	CDS hypothetical protein 1193154:1193570 forward MW:14241
RPA1086	0.985324	0.571	0.957677	0.7675	1.115285	0.1145	0.988913	0.5395	1.307919	0.005	csgG possible curli production assembly/transport component csgg precursor 1193607:1194563 forward MW:35139
RPA1087	1.394107	0.008	1.207544	0.16	1.107121	0.2025	2.697354	0.041	1.64666	0.0035	CDS possible transglycosylase SLT domain 1194566:1195360 forward MW:26639
RPA1088	1.248602	0.023	1.012853	0.476	1.359697	0.0085	1.22566	0.109	1.1694	0.0705	CDS hypothetical protein 1195392:1195730 reverse MW:12609
RPA1089	1.039294	0.2775	1.703229	0.024	1.176617	0.063	1.208336	0.133	1.064986	0.254	CDS hypothetical protein 1195939:1196199 forward MW:9416
RPA1090	0.703246	0.9665	0.802297	0.989	0.847186	0.855	0.74848	0.943	0.54779	0.984	CDS transcriptional regulatorn, Crp/Fnr family 1196347:1197024 forward MW:23909
RPA1091									0.451009	0.9565	CDS hypothetical protein 1197140:1197328 forward MW:6578
RPA1092	0.855965	0.912	1.16113	0.0565	0.793612	0.984	0.91361	0.8375	0.933928	0.8255	CDS Carboxymuconolactone decarboxylase 1197405:1197776 forward MW:12945
RPA1093	0.96234	0.684	0.926556	0.7635	0.690119	0.9785	0.742935	0.9905	1.087024	0.2605	ribB possible GTP cyclohydrolase II, riboflavin biosynthesis 1197881:1198990 forward MW:39822
RPA1094	1.027479	0.4155	0.951498	0.79	0.859885	0.8795	0.762637	0.9905	0.928144	0.733	CDS glutaryl-CoA dehydrogenase 1199051:1200265 forward MW:44561
RPA1095	0.820834	0.9775	0.857465	0.928	0.671049	0.994	0.663763	0.9895	0.728843	0.923	CDS Beta-lactamase-like 1200414:1201391 forward MW:35310
RPA1096	1.164053	0.019	1.001276	0.4855	1.070418	0.1545	1.047242	0.2855	1.148181	0.056	CDS methyl-accepting chemotaxis sensory transducer 1201404:1203155 reverse MW:62734
RPA1097	0.783082	0.9055	1.201952	0.098	0.590601	0.997	0.737237	0.9755	0.989774	0.515	CDS DUF28 1203352:1204098 forward MW:26941
RPA1098	0.847211	0.974	0.865935	0.9095	1.005474	0.476	0.989808	0.529	0.903429	0.7885	CDS hypothetical protein 1204145:1204450 reverse MW:10845
RPA1099	0.663474	0.998	0.813625	0.985	0.975147	0.6445	0.846278	0.9575	0.94034	0.839	ruvC RuvC; Holliday junction nuclease 1204649:1205173 forward MW:18219
RPA1100	0.541278	0.9975	0.604148	0.9925	0.782755	0.988	0.521021	0.999	0.535585	0.9995	ruvA RuvA; Holliday branch migration protein 1205358:1205975 forward MW:21627
RPA1101	0.610813	0.998	0.638446	0.9725	0.765338	0.9835	0.430252	0.996	0.624589	0.9965	CDS putative cytidine deaminase 1205972:1206397 forward MW:15484
RPA1102	0.966202	0.646	0.911716	0.8195	0.965699	0.674	0.82672	0.8485	0.814753	0.9895	ruvB RuvB; Holliday branch migration protein 1206575:1207624 forward MW:37779
RPA1103	0.797699	0.988	0.621401	0.9985	0.880808	0.91	0.600435	0.9985	0.637726	0.9985	CDS Thioesterase superfamily:4-hydroxybenzoyl-CoA thioesterase 1207632:1208096 forward MW:17246
RPA1104	1.453952	0	1.490421	0.0005	1.076041	0.2	1.559172	0.0025	1.757321	0	ndh putative NADH dehydrogenase 1208196:1209506 forward MW:47544
RPA1105	0.811524	0.9625	0.5805	0.9985	0.751735	0.911	0.461099	0.9975	0.619333	0.9935	CDS possible OpgC protein, require for succinylation of osmoregulated periplasmic glucans 1209652:1210866 forward MW:45438
RPA1106	0.761398	0.993	0.649953	0.9995	0.825251	0.961	0.592445	0.9605	0.77466	0.9335	CDS conserved hypothetical protein 1210924:1211391 forward MW:18392
RPA1107	0.494914	0.9955	0.695527	0.983	0.745952	0.981	0.614898	0.9825	0.519755	0.9995	CDS possible transcriptional regulator, TetR family 1211408:1211956 forward MW:19568
RPA1108	0.874711	0.921	0.803398	0.8765	0.817391	0.9705	1.047526	0.462	0.869339	0.8685	CDS DGPF domain 1212076:1212480 forward MW:14492
RPA1109	0.992732	0.5245	0.752919	0.998	1.106647	0.117	0.856104	0.9285	0.797533	0.975	CDS RNA polymerase ECF-type sigma factor 1212477:1213745 forward MW:46307
RPA1110	0.546739	1	0.788717	0.924	0.581178	0.996	0.418883	0.962	0.545863	0.98	CDS putative 3-oxoacyl-acyl carrier protein reductase 1213766:1214554 reverse MW:27567
RPA1111	0.677336	0.998	0.72243	0.9525	1.01852	0.433	0.351525	0.999	0.714562	0.995	CDS hypothetical protein 1215047:1215313 reverse MW:9330
RPA1112											CDS DGPF domain 1215473:1215892 forward MW:15140
RPA1113	0.722425	0.998	0.685821	0.9955	0.614969	0.997	0.850555	0.917	0.911992	0.767	CDS probable transcriptional regulator, TetR family 1216030:1216734 forward MW:25456
RPA1114	0.334186	1	0.355162	0.9985	0.651558	0.984	0.735057	0.936	0.512353	0.998	CDS conserved unknown protein 1216877:1217344 forward MW:18273
RPA1115											CDS conserved hypothetical protein 1217494:1217961 forward MW:17014
RPA1116	0.666623	0.923	0.637964	0.9875	1.132883	0.169	0.8118	0.912	0.673349	0.9965	CDS RNA polymerase ECF-type sigma factor 1217945:1218850 forward MW:32659
RPA1117	0.871488	0.9745	0.921235	0.8495	0.763725	0.9935	0.755249	0.9875	0.975739	0.5935	TolQ TolQ protein, inner membrane protein, tolerance to group A colicins 1219157:1219867 forward MW:26123
RPA1118	0.961114	0.6995	0.983325	0.583	0.860296	0.8815	0.777259	0.983	1.100567	0.2705	TolR putative tolR protein, uptake of enterochelin; tonB-dependent uptake of B colicins 1219902:1220372 forward MW:16666
RPA1119	1.034233	0.328	1.09603	0.0895	1.224304	0.0385	0.968974	0.626	1.10065	0.2015	TolA putative TolA 1220421:1221404 forward MW:36247
RPA1120	0.874006	0.863	0.783325	0.9755	0.816707	0.9465	0.646411	0.998	0.731885	0.9655	TolB putative tolB protein precursor, periplasmic protein involved in the tonb-independent uptake of group A colicins 1221477:1222811 forward MW:48348
RPA1121	1.127922	0.0485	1.196973	0.028	0.905359	0.7875	1.315616	0.032	1.294714	0.0345	CDS putative diguanylate cyclase (GGDEF)/phosphodiesterase (EAL) 1222982:1225312 forward MW:85854
RPA1122	1.620522	0.0265	1.37091	0.007	1.555493	0.002	1.313908	0.067	1.639283	0.0005	CDS conserved hypothetical protein 1225507:1226256 forward MW:28233
RPA1123	0.837165	0.772	0.841923	0.7145	0.941999	0.598	0.670064	0.91	0.667237	0.9445	CDS omp16 protein 1226585:1227082 forward MW:17810
RPA1124	0.9169	0.8835	0.96442	0.6965	0.936082	0.8595	0.884009	0.9195	0.963884	0.707	CDS conserved hypothetical protein 1227238:1228275 forward MW:36566
RPA1125	0.849948	0.8425	0.877638	0.857	1.001062	0.498	0.661956	0.9895	1.030975	0.3945	CDS YaeN protein 1228330:1229370 forward MW:36825
RPA1126	0.923913	0.6995	0.764191	0.9845	1.07618	0.2135	0.806613	0.9705	0.77033	0.986	ftsH metalloprotease (cell division protein) FtsH 1229602:1231518 forward MW:69829
RPA1127	0.737067	0.987	0.720683	0.9935	0.686036	0.989	0.566318	0.9935	0.595701	0.9995	CDS probable branched-chain amino acid transport protein AzlC 1231651:1232400 forward MW:26759
RPA1128	1.06206	0.305	1.05058	0.3795	1.065022	0.3335	1.044534	0.397	0.677877	0.923	CDS conserved hypothetical protein 1232397:1232714 forward MW:10931
RPA1129	0.997386	0.5075	0.83998	0.8475	0.971148	0.5775	0.990898	0.5105	1.37912	0.015	CDS possible transcriptional regulator, TetR family 1232997:1233575 forward MW:19734
RPA1130	1.190614	0.0355	1.015977	0.3975	1.029603	0.3925	1.088925	0.225	1.322784	0.0025	glcD glycolate oxidase subunit GlcD 1233699:1235192 forward MW:53314
RPA1131	1.076004	0.213	0.905176	0.917	1.081424	0.217	0.773597	0.979	0.964994	0.6625	CDS putative glycolate oxidase subunit GlcE 1235355:1236596 forward MW:42945
RPA1132	1.842468	0.01	1.156268	0.0585	1.789357	0.001	1.683542	0.0005	1.830168	0.0005	glcF glycolate oxidase subunit, (Fe-S)protein, GlcF 1236593:1237906 forward MW:47601
RPA1133	1.998297	0.005	1.404064	0.006	2.400391	0	2.579853	0	2.383955	0.002	CDS unknown protein 1237981:1238919 forward MW:31489
RPA1134	1.341918	0.0155	1.032337	0.3835	1.116044	0.2475	1.220965	0.0825	1.245293	0.0195	CDS conserved hypothetical protein 1239338:1240309 forward MW:34400
RPA1135	0.646428	0.9965	0.709473	0.9975	0.798596	0.9795	0.4964	0.9985	0.618798	0.998	CDS probable ABC transporter with fused ATPase and permease domains for long chain FA substrate 1240568:1242328 reverse MW:64790
RPA1136	1.423807	0.0115	1.089496	0.216	1.190817	0.0625	1.348932	0.0335	1.239954	0.099	ictP putative L-lactate permease 1242599:1244263 forward MW:58775
RPA1137	0.996108	0.517	1.063022	0.265	0.891388	0.909	0.966434	0.602	0.971955	0.653	CDS unknown protein 1244408:1244824 forward MW:14699
RPA1138	0.708783	0.988	0.843568	0.88	0.664791	0.9965	0.581478	0.9205	0.668478	0.9985	CDS Amine oxidase 1244827:1246332 reverse MW:52432
RPA1139	0.757972	0.995	0.729501	0.9965	0.816795	0.969	0.689206	0.998	0.753637	0.9975	CDS conserved unknown protein 1246445:1247638 reverse MW:42006
RPA1140	1.451045	0.136	0.995395	0.523	1.011199	0.451	1.103893	0.247	0.993506	0.529	groEL1 chaperonin GroEL1, cpn60 1247853:1249496 reverse MW:57626
RPA1141	1.406132	0.1285	1.325827	0.173	0.87348	0.928	1.008702	0.4955	1.036679	0.3905	groES1 chaperonin GroES1, cpn10 1249536:1249832 reverse MW:10624
RPA1142	0.746643	0.994	0.884492	0.9415	0.896152	0.8575	0.766957	0.9915	0.71683	0.999	CDS unknown protein 1250132:1250647 forward MW:17872
RPA1143	0.574423	0.9815	0.813994	0.8345	0.644607	0.967	0.626532	0.9765	0.621567	0.9965	CDS possible Major Facilitator Family (MFS) transporter 1250691:1251899 forward MW:41617
RPA1144	1.433996	0.0045	1.410532	0.006	1.190426	0.1	1.629349	0.0005	1.379288	0.003	CDS unknown protein 1251915:1252706 reverse MW:28573
RPA1145	1.417875	0.007	1.346211	0.0255	1.06029	0.3265	0.875273	0.8735	0.893667	0.9235	CDS ErfK/YbiS/YcfS/YnhG 1252992:1253795 forward MW:29437

RPA1146	0.59862	0.9965	0.67065	0.9715	1.029447	0.4225	0.580385	0.9925	0.775934	0.971	CDS conserved unknown protein 1253883:1254737 reverse MW:29041
RPA1147	1.056329	0.2395	0.992493	0.51	1.211127	0.0425	1.028619	0.3785	0.915955	0.7875	CDS conserved hypothetical protein 1254853:1255746 reverse MW:32450
RPA1148	0.978403	0.591	0.823766	0.9725	0.96793	0.6355	0.874163	0.7625	0.959382	0.647	CDS putative sugar transferase 1255743:1256786 reverse MW:37436
RPA1149	0.842452	0.898	0.878133	0.951	0.651075	0.9985	0.698131	0.997	0.785344	0.9515	hisG ATP phosphoribosyltransferase 1256880:1257857 reverse MW:34744
RPA1150	0.940851	0.7435	0.824558	0.9425	0.761849	0.9905	0.68955	0.9295	0.767086	0.9925	CDS putative histidyl-tRNA synthetase 1257854:1259002 reverse MW:40285
RPA1151	0.808575	0.969	0.936944	0.7495	0.78607	0.9835	0.918753	0.7875	0.961262	0.6635	CDS conserved hypothetical protein 1259147:1259902 reverse MW:27123
RPA1152	0.881807	0.8785	0.96076	0.7	0.897046	0.9265	0.853092	0.9445	0.971877	0.66	CDS hypothetical protein 1260277:1260810 forward MW:18110
RPA1153	1.221609	0.0135	1.347007	0.0045	1.083623	0.169	2.030388	0.004	1.782765	0	ubiA putative 4-hydroxybenzoate-octaprenyl transferase 1260807:1261757 forward MW:34177
RPA1154	1.598542	0.003	2.117649	0.001	1.456244	0.004	2.002189	0.0035	1.35562	0	CDS conserved hypothetical protein 1261793:1262317 reverse MW:19973
RPA1155	0.909135	0.898	0.795721	0.993	0.906762	0.826	0.802645	0.9505	0.876294	0.8975	CDS putative pmbA protein, maturation of antibiotic MccB17 1262616:1264013 forward MW:48746
RPA1156	0.915187	0.8385	0.914326	0.8315	0.780008	0.982	0.768713	0.9495	0.731198	0.9835	CDS putative myo-inositol monophosphatase 2 family protein 1264072:1264815 forward MW:26649
RPA1157	0.881682	0.8275	0.997392	0.5125	0.870805	0.893	1.017659	0.422	0.885358	0.9135	CDS conserved unknown protein 1264853:1265101 forward MW:9441
RPA1158	0.565521	0.9985	0.788557	0.981	0.540809	0.999	0.592652	0.998	0.584639	0.9985	CDS putative 3-deoxy-D-manno-octulosonic-acid transferase 1265171:1266475 forward MW:46912
RPA1159	0.688231	0.9915	0.834033	0.9775	0.646184	0.9975	0.696269	0.992	0.707056	0.997	lpxK putative tetraacyldisaccharide 4'-kinase 1266468:1267490 forward MW:35595
RPA1160	0.695532	0.995	0.668652	0.995	0.874447	0.8775	0.74401	0.9505	0.924161	0.813	CDS conserved unknown protein 1267500:1267835 reverse MW:12629
RPA1161	0.812696	0.9585	0.773745	0.997	0.859822	0.959	0.709591	0.993	0.686133	0.997	xseA putative exonuclease VII, large subunit OB-fold nucleic acid binding domain 1267876:1269489 reverse MW:57995
RPA1162	0.749245	0.9875	0.753442	0.997	0.697585	0.9975	0.616325	0.9985	0.644328	0.9965	garS Phosphoribosylglycinamide synthetase (GARS) 1269727:1271010 forward MW:44942
RPA1163	0.760025	0.9585	0.993269	0.529	0.903207	0.878	0.721435	0.992	0.719437	0.996	CDS possible epoxide hydrolase 1271174:1272082 forward MW:33692
RPA1164	2.115325	0	1.638174	0	2.201375	0.0005	3.391665	0	1.104863	0.189	CDS possible cytidine and deoxycytidylate deaminase 1272066:1272512 reverse MW:15853
RPA1165	1.083219	0.2505	1.728646	0.0775	0.862408	0.8525			1.48519	0.0235	CDS Pseudouridine synthase, Rsu:RNA-binding S4:Pseudouridine synthase 1272678:1274873 forward MW:82135
RPA1166											CDS N-6 Adenine-specific DNA methylase:Conserved hypothetical protein 95 1275097:1275678 forward MW:20902
RPA1167	0.750286	0.9925	0.892707	0.843	0.723401	0.962	0.57482	0.994	0.614329	0.9815	yfcB possible adenine-specific methylase 1275882:1276904 reverse MW:36628
RPA1168	0.877143	0.833	0.773241	0.9075	0.702834	0.998	0.486471	0.844	0.687914	0.9915	moaE molybdopterin converting factor, subunit 2 1276904:1277371 reverse MW:17130
RPA1169	0.851947	0.878	0.835994	0.8135	0.811438	0.9625	0.870904	0.6265	0.782389	0.956	moaD molybdopterin converting factor, subunit 1 1277397:1277648 reverse MW:9119
RPA1170	0.836306	0.954	0.788644	0.9685	0.834914	0.974	0.684178	0.995	0.71757	0.993	pgsA possible CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase 1277645:1278271 reverse MW:22621
RPA1171	0.719232	0.998	0.659344	0.9995	0.875204	0.896	0.6127	0.9985	0.693927	0.997	uvrC putative excinuclease ABC subunit C 1278411:1280525 reverse MW:77232
RPA1172	0.871379	0.907	0.961749	0.677	1.144203	0.1045	0.93366	0.716	0.997882	0.523	CDS possible outer membrane protein 1280779:1281459 forward MW:24311
RPA1173	1.688647	0.0055	1.361185	0.0035	1.767348	0.006	2.018743	0.0005	2.580929	0	cspA1 cold shock DNA binding protein 1281878:1282138 reverse MW:9299
RPA1174	1.336306	0.002	1.245186	0.011	1.244619	0.011	1.811044	0.0005	1.741165	0.0015	CDS conserved hypothetical protein 1282367:1283224 reverse MW:31371
RPA1175	0.693761	0.969	0.82201	0.8665	0.740314	0.9365	0.882924	0.874	0.750262	0.9675	CDS response regulator receiver (CheY-like protein) 1283518:1283913 forward MW:14439
RPA1176	0.79115	0.952	0.617246	0.9895	0.887512	0.8225	0.430733	0.8825	0.492341	0.999	CDS conserved hypothetical protein 1283999:1284394 reverse MW:14215
RPA1177	0.941905	0.771	0.971802	0.6095	1.002919	0.4925	0.881106	0.8755	0.639912	0.9925	CDS 4-oxalocrotonate tautomerase 1284607:1284810 reverse MW:7211
RPA1178	0.888906	0.895	1.010233	0.457	0.764267	0.979	0.750832	0.9865	0.828002	0.937	CDS putative histidyl-tRNA synthetase 1284950:1286521 reverse MW:57222
RPA1179	0.794695	0.99	0.79942	0.9915	1.081457	0.23	0.684537	0.991	0.523574	1	CDS beta-alanine-pyruvate transaminase 1286629:1288083 forward MW:51752
RPA1180	1.012116	0.435	0.679573	0.9875	1.123922	0.204	0.774642	0.92	0.846323	0.9345	CDS putative cylclic diguanylate phosphodiesterase (EAL) 1288180:1289745 forward MW:54655
RPA1181	0.45492	0.998	0.719949	0.989	0.477877	0.998	0.396958	0.996	0.456396	0.9995	CDS Haloacid dehalogenase-like hydrolase 1289758:1290612 forward MW:31466
RPA1182	0.802614	0.9175									CDS conserved hypothetical protein 1290644:1292707 reverse MW:74545
RPA1183	0.952757	0.667	0.653564	0.9655	1.01658	0.469	0.57187	0.9865	0.427351	0.998	CDS conserved unknown protein 1292874:1295699 reverse MW:100014
RPA1184	0.885178	0.871	0.817702	0.7975	1.154085	0.312	0.510303	0.9975	0.471895	0.998	CDS DUF58 1295696:1296628 reverse MW:33750
RPA1185	0.838472	0.969	0.570189	0.998	1.084737	0.1235	0.586749	0.995	0.739513	0.9895	CDS putative methanol dehydrogenase regulator 1296628:1297731 reverse MW:39412
RPA1186	0.827193	0.98	0.766152	0.996	0.935394	0.767	0.782317	0.986	0.911508	0.891	CDS conserved hypothetical protein 1297866:1298477 forward MW:22341
RPA1187	0.86057	0.9455	0.708185	0.9875	0.822237	0.955	0.692582	0.936	0.639498	0.995	CDS NUDIX hydrolase 1298486:1299151 forward MW:24187
RPA1188	0.715962	0.9945	0.750679	0.9545	0.957532	0.72	0.724474	0.997	0.555265	0.997	CDS possible poly(A) polymerase 1299408:1300664 forward MW:45346
RPA1189	0.941762	0.648	1.072792	0.4505	0.997249	0.509	1.650893	0.3295	1.25883	0.2905	CDS conserved hypothetical protein 1300794:1301021 reverse MW:8106
RPA1190	0.963829	0.591	1.074229	0.1615	0.855611	0.8805	0.843729	0.9105	0.97065	0.6245	CDS conserved hypothetical protein 1301099:1301731 reverse MW:23242
RPA1191	1.176741	0.051	1.371213	0.0075	1.077412	0.237	1.178917	0.061	1.308811	0.0075	CDS putative RNA methyltransferase 1301742:1302197 reverse MW:16930
RPA1192	1.538098	0.0185	1.254397	0.026	0.994221	0.5195	1.376502	0.0145	1.418022	0.004	CDS cytochrome b6-F complex iron-sulfur subunit 1302375:1303001 forward MW:22433
RPA1193	1.453262	0.0255	1.438292	0.0115	1.002726	0.501	1.236447	0.031	1.087481	0.341	CDS cytochrome b/c1 precursor 1303042:1305108 forward MW:77000
RPA1194	1.900256	0.0005	1.732399	0.0005	1.935958	0	2.059439	0.003	1.661633	0	CDS putative carboxymethylenebutenolidase 1305267:1305941 forward MW:24086
RPA1195	0.946243	0.741	1.109903	0.111	1.047408	0.259	0.8036	0.9755	0.856328	0.915	fixR1 short-chain dehydrogenase 1306424:1307200 reverse MW:27613
RPA1196	0.924572	0.7995	0.842208	0.968	0.940941	0.7425	0.804351	0.8985	0.840427	0.935	pdxH pyridoxamine 5'-phosphate oxidase 1307197:1307835 reverse MW:24203
RPA1197	0.90199	0.8245	1.087984	0.259	0.947182	0.6745	0.929374	0.7765	0.872888	0.896	CDS conserved hypothetical protein 1307959:1308369 forward MW:14500
RPA1198	0.733377	0.998	0.787958	0.9915	0.72098	0.9975	0.711335	0.9905	0.953723	0.7385	CDS putative heat shock protein DnaJ 1308489:1309457 forward MW:34180
RPA1199	0.696662	0.9955	0.744751	0.996	0.611116	0.9985	0.590778	0.9995	0.699563	0.9815	CDS enoyl-acyl carrier protein reductase 1309856:1310677 forward MW:29288
RPA1200	0.679274	0.998	0.797652	0.9905	0.77298	0.989	0.674385	0.993	0.690718	0.9965	CDS possible phosphoglycerate mutase 1310785:1311378 forward MW:21465
RPA1201	0.850324	0.946	1.083121	0.2495	0.740227	0.99	0.73284	0.9315	0.871675	0.815	aroC chorismate synthase 1311494:1312582 forward MW:38512
RPA1202	0.876343	0.8885	0.807719	0.914	1.066718	0.2585	0.915563	0.7795	0.865195	0.91	CDS putative Adenylate/Guanylate cyclase 1312686:1313885 forward MW:43304
RPA1203	1.111382	0.1715	0.972253	0.652	1.199138	0.037	1.37648	0.0045	1.472513	0.0355	CDS conserved hypothetical protein 1314063:1314299 reverse MW:8681
RPA1204	1.630553	0.01	0.604295	0.988	2.200118	0.0035	1.59226	0.015	1.316543	0.1735	CDS conserved hypothetical protein 1314621:1315457 forward MW:30047
RPA1205	2.228835	0.0075	0.739358	0.8465	1.532361	0.005	14.86483	0.0005	5.239116	0.038	CDS putative alcohol dehydrogenase 1315582:1316733 reverse MW:39657
RPA1206	3.362745	0.0025	1.093252	0.355	2.295895	0.0075	23.40346	0.001	9.980263	0.007	CDS aldehyde dehydrogenase 1316922:1318442 reverse MW:55041
RPA1207	1.528893	0.0225	0.691769	0.9845	1.638174	0.026	0.91196	0.617	0.977211	0.5255	CDS PAS domain:sigma-54-dependent transcriptional regulator, Fis family 1318680:1320569 forward MW:67818
RPA1208	1.143941	0.057	1.271994	0.0165	1.306544	0.0075	0.992755	0.532	1.236105	0.017	CDS putative dioxygenase 1320610:1322013 reverse MW:51959
RPA1209	1.091806	0.289	1.224555	0.042	1.387142	0.012	1.342196	0.026	1.30553	0.06	CDS conserved hypothetical protein 1322055:1323434 reverse MW:50276
RPA1210	1.165195	0.038	1.095001	0.254	1.484322	0.005	1.046486	0.3895	0.944512	0.7735	CDS conserved hypothetical protein 1323427:1324536 reverse MW:40223
RPA1211	1.322431	0.049	1.001145	0.5015	2.130743	0.0005	1.082345	0.3555	1.637016	0.0145	CDS hypothetical protein 1324555:1325616 reverse MW:39077
RPA1212	1.108765	0.15	2.085029	0.0015	1.651023	0.0015	1.36162	0.0675	2.351738	0.002	CDS Alpha/beta hydrolase fold 1325781:1326776 reverse MW:36657
RPA1213	1.076659	0.3645	0.771253	0.8855	0.974328	0.5405	1.056654	0.3755	1.208635	0.1385	CDS conserved unknown protein 1326998:1328503 reverse MW:53049
RPA1214	1.400177	0.009	1.384481	0.038	1.481945	0.002	2.983191	0	1.240244	0.142	CDS putative ABC transporter ATP-binding protein 1328639:1330291 reverse MW:60470
RPA1215	1.498473	0.0825	1.094081	0.295	1.550565	0.0035	3.85363	0.008	1.257416	0.0865	CDS putative ABC transporter, permease protein 1330400:1331290 reverse MW:31572
RPA1216	1.393423	0.0535	1.116946	0.153	1.879836	0	2.500363	0.0005	1.233802	0.054	CDS putative ABC transporter, permease protein 1331304:1332245 reverse MW:34168
RPA1217	1.863237	0.0175	1.208064	0.146	1.986067	0.0005	2.166312	0.0005	1.176204	0.11	CDS putative carboxypeptidase G2 1332410:1333540 reverse MW:39882
RPA1218	2.299545	0.002	1.669076	0.0045	2.491409	0	3.531661	0	2.114828	0.0045	CDS putative ABC transporter periplasmic protein 1333792:1335405 forward MW:59038
RPA1219	0.952984	0.64	1.502855	0.021	0.950377	0.6625	0.800855	0.9215	0.756375	0.948	CDS conserved unknown protein 1335945:1336595 reverse MW:21592
RPA1220	0.554553	0.992	0.581211	0.997	1.084492	0.179	0.335745	1	0.385707	1	CDS CBS domain 1337065:1338081 forward MW:37008
RPA1221	1.046404	0.3225	0.988858	0.5405	1.013227	0.442	0.954211	0.645	0.916712	0.831	CDS hypothetical protein 1338132:1338923 reverse MW:29731
RPA1222	1.333982	0.02	1.141606	0.1135	1.508746	0.003	1.586167	0.0015	1.374333	0.022	CDS conserved hypothetical protein 1338952:1339974 reverse MW:38117

RPA1223	1.478826	0.003	1.591512	0.0015	1.637774	0.0015	1.184123	0.0465	0.891931	0.7945	CDS hypothetical protein 1339991:1340314 reverse MW:11398
RPA1224	1.65885	0.003	1.297998	0.0385	1.525095	0.002	0.897054	0.76	0.605586	0.993	iorA putative indolepyruvate ferredoxin oxidoreductase, alpha subunit 1340580:1342406 forward MW:65175
RPA1225	1.73398	0.0035	1.105422	0.1675	1.825652	0.0005	0.823744	0.9055	0.539213	0.998	CDS possible pyruvate ferredoxin/flavodoxin oxidoreductas 4Fe-4S binding domain 1342448:1343347 forward MW:32517
RPA1226	1.440134	0.0155	0.909249	0.873	1.196749	0.0435	0.882473	0.7975	0.704779	0.9825	CDS putative 2-oxoglutarate ferredoxin oxidoreductase, alpha subunit 1343344:1344507 forward MW:41346
RPA1227	1.569578	0.0275	1.058663	0.214	1.615742	0.0025	0.806829	0.9435	0.551964	0.997	oorB putative 2-oxoglutarate ferredoxin oxidoreductase, beta subunit 1344509:1345339 forward MW:29900
RPA1228	1.43754	0.0305	1.024512	0.3895	1.470513	0.0055	0.736621	0.9925	0.516766	0.998	CDS putative 2-oxoglutarate ferredoxin oxidoreductase, gamma subunit 1345354:1345914 forward MW:19757
RPA1229	1.726418	0.006	0.995527	0.5125	1.51623	0.006	0.709676	0.9805	0.61407	0.9925	CDS probable aerobic phenylacetate-CoA ligase 1345938:1347272 forward MW:48484
RPA1230	0.999866	0.5	0.522845	0.998	1.005092	0.4885	0.607033	0.9855	0.470816	0.998	CDS putative ABC transporter, permease protein 1347482:1348354 forward MW:30727
RPA1231	1.098672	0.3325	0.440564	0.9975	1.033918	0.3525	0.569018	0.985	0.583555	0.996	CDS possible ABC transporter, permease protein 1348357:1349502 forward MW:41048
RPA1232	0.841619	0.625	0.417256	0.996	0.829631	0.934	0.521142	0.9865	0.42469	0.9995	CDS putative branched-chain amino acid transport system ATP-binding protein 1349499:1350260 forward MW:28187
RPA1233	1.021188	0.4685	0.494558	0.9915	1.001826	0.491	0.611057	0.978	0.499657	0.996	CDS putative branched-chain amino acid transport system ATP-binding protein 1350264:1351013 forward MW:27465
RPA1234	1.005734	0.4895	0.504588	0.9845	0.897406	0.783	0.481397	0.997	0.356043	0.992	CDS possible long-chain-fatty-acid--CoA ligase 1350997:1352697 forward MW:60633
RPA1235	1.111326	0.1175	0.75952	0.974	1.072626	0.2685	1.065228	0.3495	0.921622	0.7225	CDS possible Leucine-Binding Protein (LBP) 1352737:1353942 forward MW:43375
RPA1236	0.684856	0.998	0.71502	0.987	0.748009	0.982	0.488793	0.9965	0.325603	0.9985	CDS putative acyl-CoA dehydrogenase 1354133:1355329 reverse MW:43550
RPA1237	0.605991	0.9945	0.602933	0.9955	0.924477	0.7245	0.38319	1	0.29938	1	CDS possible acyl-CoA dehydrogenase 1355348:1356484 reverse MW:40375
RPA1238	0.802393	0.926	0.84475	0.9655	1.044493	0.327	0.766782	0.9765	0.572884	1	CDS putative enoyl-CoA hydratase/isomerase superfamily 1356488:1357336 reverse MW:30824
RPA1239	0.674073	0.9885	1.021253	0.475	0.894131	0.8705	0.774264	0.957	0.528348	0.9965	exbB1 putative biopolymer transport protein ExbB 1357474:1358460 forward MW:34768
RPA1240	1.112871	0.2445	0.848199	0.95	1.40643	0.042	1.187616	0.082	0.893704	0.78	exbD1 biopolymer transport protein ExbD 1358465:1358902 forward MW:15217
RPA1241	0.830713	0.811	1.270141	0.0695	1.03991	0.318	0.776279	0.913	0.562358	0.996	CDS possible tonB transport protein 1358899:1359771 forward MW:31021
RPA1242	1.094742	0.177	0.733084	0.997	0.930208	0.7195	0.688784	0.982	0.729066	0.9975	fadD1 putative long-chain-fatty-acid CoA ligase 1359791:1361302 reverse MW:53403
RPA1243	1.072116	0.1335	1.131197	0.0805	1.156148	0.0465	0.892886	0.883	1.307995	0.012	CDS hypothetical protein 1361637:1362803 forward MW:40859
RPA1244	1.083784	0.146	1.281655	0.0505	1.354067	0.0045	0.905828	0.8	1.09828	0.1535	CDS conserved unknown protein 1362819:1363424 forward MW:21588
RPA1245	1.061075	0.176	1.225851	0.056	1.226108	0.0125	0.909413	0.858	1.145835	0.053	CDS conserved hypothetical protein 1363411:1363803 forward MW:13691
RPA1246	1.190389	0.08	1.281389	0.0495	1.252668	0.0415	0.958944	0.653	1.203899	0.0615	CDS conserved unknown protein 1363800:1364501 forward MW:24670
RPA1247	0.911804	0.754	1.110322	0.2495	0.951703	0.616	1.933107	0.0075	1.602035	0.0485	rbn2 Ribonuclease BN 1364565:1365647 forward MW:38432
RPA1248	0.973614	0.617	1.048991	0.2995	1.015418	0.428	1.485498	0.0075	1.459715	0.0135	CDS two-component transcriptional regulator, LuxR family 1365644:1366570 reverse MW:33700
RPA1249	1.210987	0.035	1.474328	0.0055	1.175562	0.0655	2.651911	0	1.943144	0.0005	CDS sensor histidine kinase with a response regulator receiver domain 1366560:1369928 reverse MW:123737
RPA1250	1.253211	0.066	1.097532	0.0965	1.22494	0.0365	1.031415	0.3875	1.160388	0.0505	CDS amide-urea binding protein 1370185:1371447 forward MW:46077
RPA1251	1.349311	0.042	1.091507	0.1515	1.155761	0.0855	1.339874	0.062	1.059203	0.377	CDS putative branched-chain amino acid transport system permease protein 1371614:1372540 forward MW:33323
RPA1252	0.985351	0.534	1.193467	0.105	1.02862	0.4045			0.938713	0.628	CDS putative high-affinity branched-chain amino acid transport system permease protein 1372555:1373706 forward MW:41645
RPA1253											CDS branched-chain amino acid transport system ATP-binding protein 1373717:1374472 forward MW:27846
RPA1254	0.684149	0.926	0.828176	0.9615	0.762658	0.85	0.649201	0.988	0.603912	0.9125	CDS putative ATP-binding component of ABC transporter 1374483:1375172 forward MW:24796
RPA1255	1.031655	0.379	1.018065	0.403	1.17357	0.0325	1.146247	0.097	1.059776	0.2505	fmdA formamide amidohydrolase 1375209:1376438 forward MW:44363
RPA1256									0.829912	0.6645	fmdB putative formamidase regulatory protein FmdB 1376627:1376971 forward MW:12440
RPA1257	0.604972	0.9975	0.634883	0.9855	0.62959	0.9845	0.436226	1	0.577827	0.9985	cobS possible cobalamin (5`-phosphate) synthase 1377086:1377883 reverse MW:26924
RPA1258	1.019714	0.4325	0.774415	0.676	1.144316	0.13			0.794888	0.8475	CDS hypothetical protein 1378063:1378485 forward MW:15368
RPA1259	0.370603	0.9995	0.482597	0.9995	0.498837	0.996	0.607384	0.999	0.279486	1	CDS putative cation-transporting P-type ATPase 1378745:1381489 forward MW:97684
RPA1260	0.392305	1	0.531037	0.9885	0.541575	0.9935	0.562156	0.9955	0.250391	0.9985	CDS Universal stress protein (Usp) 1381578:1382483 forward MW:32630
RPA1261	0.823415	0.7755	0.417895	0.9985	0.948123	0.6555	0.555353	0.975	0.384733	0.9995	CDS FAD linked oxidase, C-terminal:FAD linked oxidase, N-terminal 1382580:1384175 forward MW:57767
RPA1262	1.04835	0.331	1.105923	0.2475	0.838465	0.938	1.169516	0.0865	1.132782	0.116	CDS hypothetical protein 1384147:1384611 reverse MW:16324
RPA1263	1.628883	0	1.630512	0.0035	1.426895	0.0055	2.551632	0.0015	2.295694	0	CDS putative II.1 protein 1384843:1385118 forward MW:10285
RPA1264	0.880084	0.808	0.66061	0.999	0.547792	1	0.835229	0.9545	0.980062	0.617	fliF putative flagellar M-ring protein 1385366:1386934 forward MW:56429
RPA1265	0.958854	0.6095	0.703997	0.998	0.6767	0.998	0.804677	0.965	1.00745	0.4615	fliG putative flagellar motor switch protein 1386941:1388029 forward MW:40261
RPA1266	0.784164	0.974	0.677812	0.9985	0.764934	0.967	0.783522	0.977	0.739061	0.9925	CDS possible FlbE protein 1388029:1388655 forward MW:22102
RPA1267	0.935815	0.758	0.817466	0.9635	0.835295	0.9445	0.755602	0.992	0.817073	0.9795	fliY putative flagellar motor switch protein 1388673:1389020 forward MW:12241
RPA1268	0.777297	0.9845	0.678553	0.998	0.701182	0.9935	0.798551	0.961	0.791393	0.989	flbD two-component flagellar transcriptional activator FlbD, Fis-type 1389068:1390447 forward MW:49443
RPA1269	1.230603	0.0225	1.428226	0.0105	1.034942	0.3545	1.336011	0.0615	1.342774	0.003	CDS hypothetical protein 1390811:1390966 reverse MW:5709
RPA1270							1.570775	0.1155			CDS conserved hypothetical protein 1391021:1391299 reverse MW:10425
RPA1271	1.027748	0.412	0.880975	0.8215	0.782245	0.85	1.897047	0	2.564968	0.001	CDS conserved hypothetical protein 1391337:1391768 reverse MW:15914
RPA1273	0.628348	0.9975	0.623459	0.9955	0.684391	0.9855	0.478034	0.9905	0.710534	0.9935	CDS possible deoxyribonuclease 1392794:1393903 forward MW:41323
RPA1274	2.068288	0.0025	3.513719	0.003	2.201618	0.0015	2.20354	0.0055	3.048927	0	CDS possible Dps protein family starvation-inducible DNA-binding protein 1394619:1395500 forward MW:32711
RPA1275	1.294714	0.2475	2.903247	0.0005	1.286039	0.099	1.311288	0.1545	1.79542	0.0045	CDS conserved hypothetical protein 1395763:1396287 reverse MW:19248
RPA1276	0.942631	0.8615	1.171048	0.0565	0.850811	0.9645	0.892939	0.831	1.396082	0.009	carA carbamoyl-phosphate synthase small subunit 1396520:1397713 reverse MW:42616
RPA1277	0.963663	0.65	0.720105	0.9935	1.384867	0.0025	0.666368	0.9935	0.72642	0.998	CDS possible beta-ketoadipate enol-lactone hydrolase 1397862:1398566 forward MW:24967
RPA1278	0.715331	0.9795	0.740116	0.953	0.808133	0.8765	0.664214	0.983	0.571533	0.999	CDS GatB/Yqey 1398724:1399179 forward MW:16225
RPA1279	0.631108	0.914	0.762653	0.9835	0.709702	0.9815	0.890973	0.806	1.211899	0.1395	CDS hypothetical protein 1399267:1399575 reverse MW:10944
RPA1280	1.030555	0.4385	0.787465	0.97	1.49886	0.004	0.94986	0.6525	1.018877	0.4115	CDS conserved hypothetical protein 1399766:1400614 forward MW:29979
RPA1281											CDS conserved hypothetical protein 1400728:1401201 reverse MW:17904
RPA1282	1.212945	0.037	1.196835	0.0465	1.080215	0.239	2.695572	0.0005	1.201051	0.0465	CDS possible transcriptional regulator, ArsR family 1401194:1401508 reverse MW:11868
RPA1283	0.654975	0.9985	0.703422	0.9845	0.888155	0.8885	0.6264	0.982	0.603452	0.9965	CDS homoserine/homoserine lactone/threonine efflux protein 1401637:1402254 forward MW:22028
RPA1284	0.631114	0.9995	0.5927	0.996	0.759901	0.983	0.603369	0.996	0.622631	0.999	CDS conserved unknown protein 1402378:1403175 reverse MW:29264
RPA1285	0.849215	0.9615	0.815477	0.9815	1.111628	0.077	0.998733	0.5115	0.90322	0.863	CDS conserved hypothetical protein 1403337:1403744 forward MW:15338
RPA1286	0.719232	0.751	2.475489	0.0015	1.147229	0.2505	1.735861	0.0155	1.906654	0.0215	CDS hypothetical protein 1403761:1404003 reverse MW:8649
RPA1287	0.860136	0.9005	0.935423	0.7375	0.947769	0.7065	0.808229	0.956	0.895257	0.881	dnaG putative DNA primase 1404459:1406468 forward MW:73013
RPA1288	1.016069	0.46	0.972962	0.6075	0.917306	0.8345	0.947005	0.723	1.015165	0.4065	rpoD RNA polymerase sigma 70 subunit, RpoD 1406728:1408824 forward MW:78741
RPA1289	0.829613	0.9575	0.901531	0.8995	0.812695	0.9785	0.852545	0.929	0.959318	0.7105	CDS hypothetical protein 1408843:1409175 forward MW:12057
RPA1290	1.657826	0.003	1.437216	0.0045	1.551812	0.004	1.365378	0.014	1.490383	0.0085	CDS possible plasmid maintenance system antidote protein 1409572:1409895 reverse MW:11842
RPA1291	0.996326	0.5115	1.109517	0.2815	1.06611	0.408	1.975327	0.005	1.31265	0.0685	CDS putative proteic killer suppression protein 1409905:1410195 reverse MW:11320
RPA1292	1.369519	0.065	1.264681	0.056	1.281708	0.0575	1.606357	0.0035	1.218458	0.071	CDS hypothetical protein 1410470:1410664 reverse MW:7374
RPA1293									1.331659	0.1045	CDS putative IS5 transposase 1410628:1411431 reverse MW:29464
RPA1294	1.554057	0.041	1.287538	0.0465	1.320408	0.0235	1.629945	0.0025	1.666886	0.0025	CDS hypothetical protein 1411896:1413359 forward MW:54266
RPA1295	1.018841	0.4065	0.761076	0.847	0.96464	0.6085			1.202103	0.153	CDS putative signal transduction histidine kinase 1413532:1414743 forward MW:43347
RPA1296	0.902501	0.911	0.827884	0.974	0.862283	0.962	0.832494	0.9685	0.808573	0.986	CDS putative diguanylate cyclase (GGDEF) with HAMP domain 1414958:1416721 forward MW:64878
RPA1297	0.839901	0.8425	0.715336	0.9945	0.829588	0.9025	0.639206	0.9985	0.748645	0.981	CDS Short-chain dehydrogenase/reductase SDR:Glucose/ribitol dehydrogenase 1416913:1417764 reverse MW:30189
RPA1298	0.884802	0.9	0.901546	0.7835	0.795558	0.953	0.674073	0.9825	0.675559	0.993	CDS putative 3-oxoacyl-acyl carrier protein synthase III 1417955:1419070 reverse MW:40270
RPA1299	0.99306	0.533	2.914533	0.056	0.984496	0.5525	2.938583	0.0195	1.235834	0.117	CDS conserved hypothetical protein 1419368:1419715 forward MW:12697
RPA1300	1.19232	0.067	1.314631	0.018	1.196912	0.0665	2.05422	0.002	1.987541	0	CDS possible restriction system protein 1419941:1420894 forward MW:34646

RPA1301			2.076763	0.0165			1.103938	0.2915	2.05043	0.0015	pfpI putative intracellular protease, PfpI family 1421072:1421635 forward MW:20279
RPA1302	1.047564	0.2885	0.784258	0.937	1.373185	0.087	1.40794	0.125	1.475679	0.0025	CDS unknown protein 1421829:1422200 reverse MW:12694
RPA1303	0.833806	0.953	0.805989	0.889	0.945519	0.7025	0.630182	0.9865	0.725661	0.989	CDS putative transglycolase 1422427:1423245 forward MW:29442
RPA1304	0.944581	0.7705	0.932809	0.8285	1.006189	0.4705	0.973236	0.6315	0.848336	0.892	CDS possible flagellar basal-body rod modification protein FlgD 1423276:1423989 reverse MW:25112
RPA1305	1.010048	0.4485	0.792248	0.9875	0.808129	0.9655	0.836384	0.924	0.658972	0.999	CDS possible flagellar hook length determination protein 1424002:1425594 reverse MW:53250
RPA1306	0.975157	0.6585	0.795671	0.9705	0.924142	0.8785	0.893484	0.8455	1.012603	0.4395	trmU tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase 1425895:1427100 forward MW:43613
RPA1307	0.68301	0.9905	0.858791	0.786	0.825769	0.8625	0.649531	0.9685	0.620839	0.991	CDS putative phosphatidylethanolamine-N-methyltransferase 1427120:1427758 forward MW:23543
RPA1308	0.999583	0.493							0.879821	0.5935	CDS hypothetical protein 1428428:1428691 reverse MW:9872
RPA1309									1.132298	0.2125	CDS possible transposase 1429578:1429871 forward MW:10354
RPA1310											CDS putative NADH:flavin oxidoreductase 1430328:1431443 forward MW:40432
RPA1311											CDS possible 4-carboxymuconolactone decarboxylase 1431728:1432060 forward MW:11619
RPA1312	0.991308	0.518	0.953477	0.543	0.929521	0.703			0.789098	0.915	CDS hypothetical protein 1432289:1432831 forward MW:19890
RPA1313	0.967775	0.5895	1.031875	0.4045	0.920165	0.6645	1.051556	0.346	1.133858	0.3075	CDS sensor histidine kinase with multiple PAS/PAC domains 1433238:1435136 forward MW:68438
RPA1314	1.172745	0.077	0.828977	0.908	1.186042	0.0475	0.901613	0.8135	1.058653	0.232	CDS response regulator receiver (CheY-like protein) 1435192:1435623 forward MW:15442
RPA1315	1.232824	0.134	0.774981	0.8405	1.181361	0.1805			0.720508	0.9445	CDS two-component transcriptional regulator, LuxR family 1435620:1436306 forward MW:24873
RPA1316											CDS hypothetical protein 1436415:1436669 reverse MW:9443
RPA1318											cydA pseudogene possible cytochrome bd-I oxidase subunit I [EC:1.10.3.-] 1436683:1437559 forward MW:32024
RPA1319											cioB putative cytochrome bd-I oxidase subunit II 1437556:1438581 forward MW:36521
RPA1320											CDS conserved hypothetical protein 1438689:1438997 forward MW:11412
RPA1321											CDS probable transcriptional regulator, AraC family 1439181:1440020 forward MW:30624
RPA1322											CDS putative signal transduction histidine kinase 1440217:1440915 forward MW:24743
RPA1323	1.04333	0.3205	1.506326	0.0225	0.969057	0.5855	1.34368	0.096	1.133839	0.174	CDS hypothetical protein 1441280:1441510 reverse MW:7851
RPA1324	1.184892	0.1825	1.022952	0.4615	0.926586	0.7085	1.175516	0.294	1.566946	0.004	CDS possible FusB/FusC fusaric acid resistance pump 1441783:1443834 forward MW:72431
RPA1325	0.960453	0.688	1.011404	0.4745	0.969042	0.607	1.158631	0.112	1.144316	0.1335	CDS putative FusE-MFP/HlyD family membrane fusion protein 1444051:1444992 forward MW:32970
RPA1326											CDS probable transcriptional regulator, AraC family 1445131:1446114 reverse MW:36439
RPA1327	1.078625	0.3375	1.122902	0.228	1.080645	0.234	1.283093	0.0515	1.279084	0.0385	CDS Ser/Thr protein kinase 1446214:1447170 forward MW:34160
RPA1328	1.216334	0.083	1.073927	0.2845	1.240207	0.061	1.371624	0.017	1.739959	0.0025	CDS sensor histidine kinase with a GAF and an unknown domain 1447208:1451350 forward MW:150340
RPA1329	2.109837	0.021			2.377004	0.0055			2.935878	0.012	fumC1 fumarate hydratase 1451481:1452938 forward MW:51652
RPA1330	0.983307	0.6025	0.836248	0.9655	0.975824	0.58	0.849848	0.884	0.849807	0.964	CDS conserved hypothetical protein 1452940:1454220 forward MW:42709
RPA1331	0.938688	0.7705	0.933709	0.7185	0.913105	0.819	1.133837	0.2275	1.093157	0.1535	mqoB malate quinone oxidoreductase 1454615:1456108 forward MW:54007
RPA1332	1.669841	0	1.607352	0.0005	1.6121	0.0005	2.414449	0	2.644953	0	CDS possible phage integrase/recombinase 1456158:1457000 forward MW:31784
RPA1333	1.248787	0.1495	1.657116	0.052	1.32368	0.0435	2.127639	0.047	1.327129	0.127	CDS conserved hypothetical protein 1457225:1457881 forward MW:22590
RPA1334											CDS RNA polymerase ECF-type sigma factor, possible FecI 1457878:1458423 forward MW:20909
RPA1335			0.956343	0.61	0.941281	0.604	0.852863	0.7305	1.109592	0.251	CDS probable FecR, iron siderophore sensor protein 1458444:1459430 forward MW:34662
RPA1336	1.293692	0.0675	0.869355	0.914	1.132718	0.121	0.909297	0.7315	0.825075	0.9265	CDS conserved hypothetical protein 1459664:1469554 forward MW:333125
RPA1337	1.400187	0.002	1.287499	0.0165	1.130349	0.0865	1.819077	0.0005	2.170326	0.0015	CDS conserved hypothetical protein 1469449:1471704 forward MW:77712
RPA1338									1.17119	0.142	CDS conserved hypothetical protein 1472806:1473558 forward MW:26173
RPA1339											CDS RNA polymerase ECF-type sigma factor, possible FecI 1473555:1474103 forward MW:21222
RPA1340	0.934897	0.655	1.003478	0.4905	1.173586	0.33	1.019615	0.4615	1.044575	0.3915	CDS probable FecR, iron siderophore sensor protein 1474165:1475148 forward MW:35541
RPA1341	1.072554	0.329			1.122491	0.397					CDS conserved hypothetical protein 1475303:1488310 forward MW:434749
RPA1342							1.603168	0.011	1.793143	0.122	CDS hypothetical protein 1488669:1488935 reverse MW:10074
RPA1343	1.46399	0.0265	1.017386	0.456	1.134622	0.1255	1.186496	0.149	1.183007	0.183	CDS conserved hypothetical protein 1489054:1489806 forward MW:26220
RPA1344	1.595361	0.0015	1.324195	0.0015	1.517665	0.0005	2.272841	0	2.330473	0.0005	CDS hypothetical protein 1489856:1490317 forward MW:16944
RPA1345	1.044489	0.2525	1.01121	0.434	1.10353	0.137	0.991819	0.547	1.479347	0.0005	CDS conserved hypothetical protein 1490469:1491218 forward MW:26487
RPA1346	0.823049	0.838	0.913628	0.682	0.782083	0.956	0.754298	0.9455	0.918282	0.818	CDS possible TonB protein, possible colicin J receptor 1491235:1491948 forward MW:26091
RPA1347	0.859284	0.9615	0.720084	0.9905	1.131963	0.0555	1.002256	0.4875	1.32248	0.0075	CDS RNA polymerase ECF-type sigma factor, possible FecI 1492084:1492635 forward MW:20785
RPA1348	0.713684	0.9525	0.721986	0.9665	0.932501	0.803	0.76587	0.9245	0.843967	0.9	fecR3 probable FecR, iron siderophore sensor protein 1492975:1493943 forward MW:34536
RPA1349											CDS Hemolysin activation/secretion protein 1494203:1495957 forward MW:63230
RPA1350	0.981231	0.5615	1.008577	0.4685	1.055648	0.3215	0.877738	0.739	0.588146	0.9955	exbB2 putative transport protein ExbB2 1495957:1497984 forward MW:70499
RPA1351	0.903362	0.8455	0.707242	0.955	0.849628	0.827	0.70796	0.9685	0.697697	0.911	exbD2 transport protein ExbD 1497989:1498393 forward MW:14563
RPA1352			0.588758	0.9825					0.511427	0.9535	CDS hypothetical protein 1498390:1498887 forward MW:17736
RPA1353	0.854286	0.7575	0.961621	0.5665	1.032031	0.456	1.029906	0.45	1.063405	0.328	CDS conserved hypothetical protein 1498884:1499624 forward MW:26553
RPA1354	1.287167	0.004	1.595185	0	1.212937	0.015	1.552594	0.003	1.765936	0	CDS conserved hypothetical protein 1499664:1501541 forward MW:68579
RPA1355	1.221097	0.123			0.866508	0.6305			0.992979	0.518	CDS conserved hypothetical protein 1501544:1502137 forward MW:21955
RPA1356	1.112381	0.0935	1.140519	0.0825	1.013252	0.4235	0.986124	0.5655	1.026469	0.3775	CDS PpiC-type peptidyl-prolyl cis-trans isomerase 1502134:1503177 forward MW:37852
RPA1357											CDS conserved hypothetical protein 1503219:1503734 forward MW:18582
RPA1358	0.786117	0.729			0.833114	0.784			0.71458	0.7355	CDS hypothetical protein 1503755:1504246 forward MW:17255
RPA1359											CDS possible transglycosylase 1504243:1505148 forward MW:30645
RPA1360											CDS hypothetical protein 1505154:1505711 forward MW:19024
RPA1361	0.869188	0.658			0.712013	0.737					CDS hypothetical protein 1505812:1505994 reverse MW:7007
RPA1362	0.66793	0.9135	1.359894	0.1415	0.420705	0.996	1.609648	0.0125	0.412155	1	CDS putative sulfate ester transport system substrate-binding protein 1506856:1507920 forward MW:38441
RPA1363	1.060865	0.411	1.876338	0.0005	1.033571	0.4065	1.725143	0.007	0.825683	0.912	CDS sulfate ester transport system permease protein 1507917:1509533 forward MW:56839
RPA1364	0.760062	0.7745	1.952765	0.0095	0.597325	0.9735	2.025816	0.0475	0.745535	0.9945	CDS sulfate ester transport system ATP-binding protein 1509530:1510339 forward MW:29143
RPA1365	0.440794	0.998	1.175575	0.095	0.497029	0.991	1.110905	0.3945	0.615812	0.9035	CDS putative sulfatase 1510381:1512045 forward MW:62995
RPA1366					0.418021	0.9815	1.676069	0.1385	0.528129	0.9675	soxZ1 putative sulfur oxidation protein 1512100:1512435 reverse MW:12238
RPA1367	0.771925	0.983	0.63531	0.943	0.850228	0.909	1.535243	0.288	0.726713	0.9515	soxY1 putative sulfur oxidation protein 1512432:1512902 reverse MW:16423
RPA1368									0.859813	0.6605	CDS conserved hypothetical protein 1513015:1513605 forward MW:21268
RPA1369	1.099771	0.094	1.096588	0.078	1.048531	0.2745	1.35042	0.005	1.235619	0.0095	CDS conserved hypothetical protein 1513712:1514713 forward MW:35566
RPA1370	1.548439	0.0295			1.89223	0.001	197.7379	0	143.2419	0	CDS Nitrogen-fixing NifU, C-terminal 1515576:1516643 reverse MW:39283
RPA1371							283.6416	0.0005	148.4123	0	vnfX putative vanadium nitrogenase protein 1516647:1517132 reverse MW:17184
RPA1372							67.24965	0	13.62856	0	vnfN putative nitrogenase cofactor synthesis protein 1517129:1518511 reverse MW:48485
RPA1373	4.610096	0.001	2.610147	0.0005	4.621192	0	249.6606	0	198.5089	0	vnfE putative nitrogenase cofactor synthesis protein 1518523:1519905 reverse MW:50054
RPA1374	2.58832	0	2.493475	0	3.071744	0	78.31591	0	30.88873	0	vnfA Sigma-54 dependent, Vanadium nitrogenase transcriptional regulator, VnfA 1520222:1521856 forward MW:60647
RPA1375	1.190364	0.052	1.077447	0.1645	1.124151	0.1095	36.32286	0	6.283723	0	CDS hypothetical protein 1521861:1522259 forward MW:13791
RPA1376	1.183917	0.1035	1.553696	0.014	Mutated		53.66239	0	Mutated		vnfH nitrogenase iron protein, vnfH 1522488:1523378 reverse MW:31745
RPA1377					2.554565	0	206.7141	0	44.20689	0	CDS possible glyoxalase 1523442:1524245 reverse MW:29330
RPA1378							927.1927	0	135.1481	0	vnfD nitrogenase vanadium-iron protein alpha chain 1524697:1526115 forward MW:53424

RPA1379							493.9693	0	44.09405	0.0005	vnfG vanadium dinitrogenase delta subunit 1526112:1526453 forward MW:13409
RPA1380							711.0498	0	109.711	0	vnfK nitrogenase vanadium-iron protein, VnfK subunit 1526517:1527905 forward MW:51127
RPA1381	1.36607	0.05	1.318205	0.0435	1.079243	0.2775	50.16491	0	40.40359	0	CDS hypothetical protein 1527884:1528840 forward MW:35748
RPA1382	0.759284	0.8935	1.0074	0.473	0.860791	0.7985	168.5854	0	42.51087	0	CDS Nitrogen fixation-related protein 1528871:1529356 forward MW:17594
RPA1383	1.048881	0.2985	1.030428	0.363	1.065339	0.2695	5.506023	0	3.350025	0	CDS putative transcriptional regulator, ModE family 1529451:1529894 forward MW:15872
RPA1384	0.800925	0.862	0.922928	0.7315	0.857917	0.923	82.86288	0	97.77099	0	ptxC putative phosphate permease component of ATP-dependent phosphate uptake system 1529885:1530706 reverse MW:29139
RPA1385	0.874406	0.5875					459.7164	0	225.5226	0	ptxB putative phosphonate transport system substrate-binding protein 1530703:1531593 reverse MW:31613
RPA1386	1.151969	0.2425	0.656667	0.9935	0.81884	0.7785	162.3006	0	70.53749	0	ptxA putative ATP-binding component of ABC phosphonate transporter 1531578:1532432 reverse MW:30161
RPA1387							238.9186	0	31.96465	0	CDS conserved unknown protein 1532499:1533791 reverse MW:45991
RPA1388	0.787515	0.937	0.598807	0.991	0.696691	0.995	11.26704	0	1.466014	0.0075	CDS hypothetical protein 1534069:1535079 forward MW:36710
RPA1389							147.133	0	33.48343	0.0005	CDS conserved hypothetical protein 1535067:1536164 forward MW:40290
RPA1390							67.07335	0	24.80847	0	CDS conserved hypothetical protein 1536155:1536853 forward MW:24745
RPA1391	0.877724	0.911			0.928432	0.725	11.60433	0	1.489402	0.034	CDS possible ABC transporter ATP-binding protein 1536850:1537893 forward MW:37472
RPA1392							182.0958	0	49.08401	0.0005	CDS nitroreductase family proteins 1537893:1538441 forward MW:19761
RPA1393	1.942339	0.001	1.594906	0.0015	1.959932	0	28.39619	0	37.59759	0	CDS conserved hypothetical protein 1538532:1539338 forward MW:30728
RPA1394	1.290396	0.1575	1.565568	0.01	1.444315	0.2535	8.098545	0.0005	11.86506	0	CDS transcriptional regulator, GntR family with aminotransferase domain 1539494:1540996 reverse MW:55357
RPA1395							81.59058	0	119.0748	0.001	CDS possible trehalose/maltose binding protein 1541222:1542790 forward MW:58229
RPA1396	0.71397	0.8295	0.855947	0.865	0.930677	0.678	17.85213	0.002	36.47791	0	CDS possible multiple sugar transport system permease protein 1542824:1543879 forward MW:39278
RPA1397	1.028459	0.446	1.474983	0.012			29.75569	0.0005	42.76712	0	CDS putative sugar ABC transporter, permease protein 1543879:1544739 forward MW:30827
RPA1398							5.533386	0.0005	3.782596	0	CDS putative sugar ABC transporter, ATP-binding protein 1544736:1545839 forward MW:38839
RPA1399			1.135868	0.269	1.110338	0.4135	2.963507	0	2.167534	0.0015	CDS putative transport system ATP-binding protein 1545836:1546921 forward MW:39090
RPA1400							5.794994	0	15.23947	0	CDS possible Glutamine amidotransferase 1546928:1547713 forward MW:28231
RPA1401	1.280929	0.0225	1.291561	0.0465	0.98843	0.5395	11.07414	0.0005	12.81563	0	glnAIII putative glutamine synthetase III 1547728:1549113 forward MW:51320
RPA1402			0.870125	0.7655	0.987583	0.5235	1.801188	0.01	1.944599	0	CDS putative Glu-tRNA amidotransferase, subunit A 1549121:1550575 forward MW:50478
RPA1403	1.13984	0.0585	0.900386	0.8585	1.036785	0.3725	2.855229	0.0005	2.696864	0	CDS possible Glutamine amidotransferase 1550579:1551406 forward MW:29797
RPA1404	2.202855	0.001	1.813519	0.007	1.945329	0.001	1.683573	0.011	2.006735	0.0015	CDS glutamyl-tRNA(Gln) amidotransferase subunit A 1551670:1553496 reverse MW:62919
RPA1405	1.052949	0.257	1.002077	0.4885	1.125129	0.117	1.146376	0.424	0.987144	0.5445	CDS putative urea amidolyase 1553493:1557041 reverse MW:127624
RPA1406											CDS conserved hypothetical protein 1557044:1557679 reverse MW:23031
RPA1407	0.903256	0.662	0.929747	0.7115	0.762204	0.9675	1.043459	0.4275	0.963229	0.586	CDS conserved hypothetical protein 1557682:1558521 reverse MW:30453
RPA1408	1.551794	0.0185	1.601272	0.001	1.490651	0.0045	1.973249	0.0015	1.95857	0.001	CDS putative ABC transporter protein 1558560:1559351 reverse MW:29542
RPA1409					1.400097	0.0535					CDS possible taurine transport system permease protein 1559348:1560166 reverse MW:29700
RPA1410	1.658624	0.005	1.518113	0.003	1.343158	0.01	2.253876	0	1.99677	0.002	CDS possible taurine transport system protein 1560201:1561271 reverse MW:37829
RPA1411	1.223979	0.187	0.668641	0.952	1.397127	0.053	1.254136	0.1935	1.262441	0.0405	CDS possible enoyl-CoA hydratase/isomerase 1561646:1562437 reverse MW:27799
RPA1412	1.293266	0.1165	0.902932	0.774	1.198457	0.062	1.105085	0.284	1.113566	0.173	CDS putative fatty-acid--CoA ligase 1562558:1564117 forward MW:56328
RPA1413	0.780324	0.9095	0.830591	0.842	1.052296	0.3795	0.921197	0.6375	0.659133	0.906	CDS transcriptional regulator, IclR family 1564275:1565213 reverse MW:33514
RPA1414	0.730019	0.977	0.495632	1	0.83444	0.862	0.575743	0.992	0.608587	0.998	CDS MaoC-like dehydratase 1565333:1566193 forward MW:31159
RPA1415	0.738287	0.962	0.719615	0.982	0.832878	0.9645	0.691013	0.9725	0.728484	0.9965	CDS possible branched-chain amino acid transport system substrate-binding protein 1566319:1567563 forward MW:45001
RPA1416	0.909299	0.8265	0.771498	0.9865	0.788562	0.979	0.898083	0.8135	0.715588	0.9875	CDS putative branched-chain amino acid transport system ATP-binding protein 1567571:1568290 forward MW:25738
RPA1417	0.527152	0.997	0.46322	0.993	0.439855	0.9995	0.447012	0.9965	0.356632	1	CDS putative branched-chain amino acid transport system ATP-binding protein 1568283:1568987 forward MW:25615
RPA1418	0.593151	0.998	0.802454	0.803	0.637686	0.9955	2.29394	0.043	0.534912	0.9935	CDS possible transport system permease protein 1569001:1569864 forward MW:30547
RPA1419	0.855542	0.9745	0.715338	0.9965	0.839287	0.8685	0.613481	0.999	0.625861	0.9975	CDS possible transport system permease protein 1569861:1570871 forward MW:35578
RPA1420			0.524455	0.999	0.568613	0.9925	0.6239	0.952	0.66976	0.9855	ybdE putative inner membrane component for iron transport 1570899:1574057 reverse MW:113568
RPA1421	1.737477	0.072	0.77825	0.938	0.615504	0.913			0.501232	0.997	CDS possible efflux protein 1574054:1575457 reverse MW:50362
RPA1422	1.033287	0.465	1.745304	0.007	0.476034	0.9915	1.352842	0.045	0.311715	1	CDS unknown protein 1575534:1575932 reverse MW:13914
RPA1423	0.838245	0.6985	1.620675	0.003	0.496113	0.989	1.237848	0.048	0.571059	0.999	CDS putative membrane protein 1576971:1577915 forward MW:35127
RPA1424	0.775675	0.6455	3.049313	0.0015	0.394734	0.99	2.097341	0.0415	0.956585	0.5975	CDS possible selenocysteine lyase 1577902:1579875 forward MW:69072
RPA1425	1.110972	0.4045	2.761818	0.006	1.291984	0.036	1.859478	0.078	1.354899	0.145	cysE1 serine acetyltransferase 1580040:1580987 forward MW:34005
RPA1426	0.998783	0.502	1.142865	0.2985	0.447797	0.9955	0.705351	0.8925	0.46233	1	CDS ABC transporter, ATP-binding protein 1581162:1582283 forward MW:40036
RPA1427	0.970514	0.529	1.025882	0.473	0.797539	0.751	0.371056	0.8425	0.529712	0.957	CDS putative ABC transporter, permease protein 1582273:1582941 forward MW:23210
RPA1428	0.897787	0.56	2.382446	0.013	0.555753	0.9445	1.023173	0.4675	0.67771	0.8515	CDS possible lipoprotein 1582970:1583743 forward MW:27813
RPA1429	0.452559	0.872	1.596905	0.0455	0.334812	0.9915	0.848367	0.813	0.374806	0.993	CDS putative coenzyme F390 synthetase 1584105:1585541 reverse MW:53022
RPA1430	0.714593	0.893	1.106621	0.3075	0.344511	1	1.011407	0.4705	0.40912	0.998	CDS putative outer membrane protein 1585538:1586323 reverse MW:28190
RPA1431									65.17034	0	draT1 putative NAD+ ADP-ribosyltransferase 1587454:1588287 forward MW:31904
RPA1432									287.72	0	CDS putative nitroimidazole resistance protein 1588459:1588989 reverse MW:19566
RPA1433			0.980756	0.542	0.802506	0.8385	1.719369	0.009	179.0235	0	CDS conserved hypothetical protein 1589047:1589637 reverse MW:21605
RPA1434			0.818519	0.8015			5.013546	0.0005	225.8188	0	CDS conserved hypothetical protein 1589634:1590326 reverse MW:25936
RPA1435	1.07142	0.1945	0.870279	0.97	0.947645	0.7185	2.834836	0.002	93.68283	0	anfK alternative nitrogenase 3 beta chain 1590406:1591791 reverse MW:50971
RPA1436									1043.855	0	anfG dinitrogenase 3 delta subunit 1591804:1592244 reverse MW:16492
RPA1437	1.200534	0.275	0.755536	0.938	1.031385	0.413	9.469891	0	402.8469	0	anfD putative nitrogenase molybdenum-iron protein alpha chain (nitrogenase component I) (dinitrogenase) 1592257:1593825 reverse MW:58542
RPA1439	0.805719	0.976	0.98002	0.5915	0.867536	0.8105	Mutated		68.68944	0	anfA Sigma-54 dependent, Iron nitrogenase transcriptional regulator, AnfA 1595226:1596854 reverse MW:60171
RPA1440	1.081692	0.3805					8.398409	0.0005	4.579172	0	CDS conserved hypothetical protein 1597076:1597600 reverse MW:18359
RPA1441	1.209698	0.1495	1.626646	0.0035	1.030458	0.3775	1.416762	0.026	1.5556	0.0035	CDS possible uridylate kinase 1597783:1598604 reverse MW:28717
RPA1442	1.510946	0.023	2.25023	0.001	1.464816	0.0235	1.689931	0.044	2.051767	0.0005	CDS possible uridine monophosphate kinase 1598614:1599426 reverse MW:28801
RPA1443							0.935447	0.5895	1.275011	0.2755	CDS transcriptional regulator, GntR family 1599719:1600534 reverse MW:29910
RPA1444	0.684427	0.955			0.761951	0.9265					CDS putative oligopeptide binding protein precursor 1600910:1601911 forward MW:35641
RPA1445	0.924218	0.724	0.571117	0.999	0.600196	0.998	0.55992	0.998	0.539281	0.9995	CDS putative oligopeptide transport ATP-binding protein 1601908:1602957 forward MW:38228
RPA1446	0.809772	0.8855	0.561915	0.9935	0.780405	0.883	0.517351	0.948	0.461321	0.9975	CDS possible dipeptide ABC transporter (dipeptide-binding protein) 1602948:1604501 forward MW:56790
RPA1447	0.847005	0.8395	0.584595	0.9995	0.774367	0.9675	0.435668	0.9985	0.503256	0.9995	CDS putative oligopeptide ABC transporter (permease) 1604542:1605510 forward MW:34088
RPA1448	0.926474	0.691	0.690729	0.998	0.76499	0.9605	0.586838	0.992	0.597548	0.997	CDS putative oligopeptide ABC transporter (permease) 1605507:1606391 forward MW:31741
RPA1449	0.988559	0.572	0.871007	0.934	0.794868	0.9805	0.752438	0.9515	0.939003	0.8365	CDS putative long-chain fatty acid--CoA ligase 1606418:1608133 forward MW:62364
RPA1450	0.806387	0.994	0.644438	0.998	0.729778	0.9905	0.4738	0.9965	0.505116	0.9975	CDS putative pyruvate carboxylase 1608197:1611508 forward MW:118132
RPA1451	0.938877	0.7535	0.77489	0.9835	0.841662	0.8725	0.635224	0.9845	0.628547	0.996	CDS unknown protein 1611539:1612492 forward MW:34855
RPA1452											CDS conserved hypothetical protein 1612499:1612654 reverse MW:5338
RPA1453											norE putative denitrification protein NorE 1612792:1613400 forward MW:21316
RPA1454			1.718233	0.0245							CDS hypothetical protein 1613405:1613674 forward MW:9442
RPA1455											norC nitric-oxide reductase subunit C 1613786:1614238 forward MW:16742
RPA1457											norQ regulatory protein NorQ, probable ATPase 1615677:1616489 forward MW:29004

RPA1458											norD dinitrification protein NorD 1616615:1618525 forward MW:71136
RPA1460											CDS conserved hypothetical protein 1618537:1619230 reverse MW:25010
RPA1461	0.965961	0.6935	0.888216	0.8885	0.947069	0.721	0.857928	0.9285	0.97641	0.5995	CDS conserved hypothetical protein 1619349:1620434 reverse MW:39653
RPA1462											CDS conserved hypothetical protein 1620457:1621665 reverse MW:45220
RPA1463	0.868344	0.953	0.94835	0.7645	0.82385	0.9765	0.790948	0.9835	0.835078	0.9315	ilvD2 dihydroxy-acid dehydratase 1621994:1623850 forward MW:65722
RPA1464	0.97478	0.641	1.11388	0.0795	1.031261	0.321	1.028373	0.377	0.96838	0.6815	CDS possible glutamine amidotransferase 1623973:1624776 reverse MW:29166
RPA1465	1.17752	0.201	1.150214	0.1005	1.410214	0.038	1.232568	0.212	0.985453	0.5425	CDS possible chloride channel 1625022:1626836 forward MW:64081
RPA1466			0.717667	0.9025	1.194285	0.1995	0.940032	0.6005	0.852169	0.724	CDS putative glutamyl-tRNA(Gln) amidotransferase subunit A 1626850:1628655 reverse MW:62480
RPA1467	1.272673	0.0735	1.098776	0.164	1.260712	0.036	1.534988	0.0235	1.460956	0.0105	CDS transcriptional regulator, GntR family 1628652:1629317 reverse MW:25045
RPA1468											CDS conserved hypothetical protein 1629395:1629790 reverse MW:14567
RPA1469	0.928236	0.86	0.931118	0.834	0.921002	0.852	0.899673	0.884	0.829538	0.9665	gatA1 possible glutamyl-tRNA (Gln) amidotransferase subunit A 1629793:1631250 reverse MW:50959
RPA1470	2.05814	0.04							1.250514	0.1325	CDS putative dipeptide ABC transporter 1631482:1633305 reverse MW:65551
RPA1471	2.939003	0	2.62027	0	2.918374	0.0005	8.751329	0	6.194425	0	CDS putative dipeptide ABC transporter (permease) 1633461:1634375 reverse MW:32522
RPA1472	2.124139	0	1.826657	0	1.829393	0.003	3.287827	0	3.135169	0.0005	CDS putative dipeptide transport permease protein 1634380:1635393 reverse MW:36360
RPA1473	1.777665	0	3.517386	0	1.423872	0.0085	10.53707	0	2.057951	0	CDS possible peptide transport system substrate-binding protein 1635563:1637233 reverse MW:61807
RPA1474	1.223418	0.0575	1.136423	0.1495	1.590915	0.007	1.134403	0.2135	1.215531	0.014	CDS hypothetical protein 1637561:1638025 reverse MW:16822
RPA1475	2.52804	0.017	13.19866	0.0015	2.951733	0.0015	3.879806	0.025	4.245531	0.001	CDS hypothetical protein 1638270:1638509 reverse MW:8652
RPA1476	1.391438	0.0125	1.48101	0.0305	1.345417	0.0185	1.938287	0.002	1.931506	0.0025	CDS putative periplasmic solute-binding protein 1638835:1639842 forward MW:36578
RPA1477	1.009706	0.4755	0.975604	0.5885	1.094554	0.2315	1.107595	0.2375	1.151954	0.075	CDS putative permease protein 1639890:1640705 forward MW:28531
RPA1478									0.803346	0.7905	CDS putative permease protein 1640710:1641495 forward MW:28299
RPA1479	1.024489	0.4235	1.031432	0.479	1.009727	0.46			1.034314	0.4185	CDS putative transport system ATP-binding protein 1641492:1642553 forward MW:37305
RPA1480	0.944647	0.611	0.774456	0.976	0.999247	0.505	0.836463	0.7005	0.955986	0.6255	cpdA putative ICC protein 1642550:1643407 forward MW:30904
RPA1481	1.439518	0.0085	1.206891	0.046	1.048344	0.4125	1.68906	0.011	1.875249	0	CDS response regulator receiver (CheY-like protein) 1643544:1643906 forward MW:13068
RPA1482	0.943115	0.7295	0.748923	0.9955	0.86575	0.906	0.977596	0.6	1.181012	0.0265	CDS hypothetical protein 1644037:1644882 forward MW:31195
RPA1483	2.331895	0.005	4.6651	0.001	1.944205	0.1195	1.159824	0.296	2.900481	0.0035	CDS NAD binding site:FAD dependent oxidoreductase 1644893:1646128 reverse MW:44858
RPA1484	1.221294	0.0495	1.081237	0.2755	1.228498	0.072	1.489574	0.0305	1.343674	0.042	pgm2 phosphoglucomutase 1646478:1648130 forward MW:58363
RPA1485	0.925084	0.8775	0.922601	0.8265	1.325962	0.014	0.966652	0.598	0.772869	0.959	nnrU putative NnrU protein 1648233:1649000 forward MW:28265
RPA1486	0.956976	0.6035	1.581547	0.003	1.042954	0.408			0.597398	0.958	CDS conserved hypothetical protein 1649216:1650442 forward MW:43847
RPA1487	1.18524	0.101	1.377841	0.0855	1.355898	0.0135	1.846541	0.0945	1.105163	0.292	CDS conserved hypothetical protein 1650481:1650729 forward MW:9547
RPA1488	0.898002	0.8415	0.662822	0.992	0.970146	0.644	0.759838	0.9815	0.580591	0.988	CDS L-carnitine dehydratase/bile acid-inducible protein F 1650733:1651935 reverse MW:43722
RPA1489	1.001038	0.507	0.899466	0.923	0.755435	0.9875	1.048953	0.3085	0.988044	0.552	CDS two-component transcriptional regulator, LuxR family 1652068:1652739 reverse MW:23856
RPA1490	0.8788	0.941	0.800785	0.9845	0.990809	0.5525	1.019406	0.4125	0.828013	0.9485	phyB4 Bacteriophytochrome (light-regulated signal transduction histidine kinase), PhyB4 1652759:1655071 reverse MW:83535
RPA1493	0.966348	0.6335	1.129787	0.1865	1.180581	0.036	1.002648	0.4955	0.879772	0.874	pucC PucC, possible chlorophyll Major Facilitator Superfamily (MFS) exporter 1655951:1657387 forward MW:50213
RPA1494	1.394094	0.012	1.601364	0.0045	1.538321	0.018	1.500984	0.0085	1.611109	0	CDS unknown protein 1657406:1658056 forward MW:22587
RPA1496	1.394826	0.213	0.659983	0.9915	1.366036	0.006	0.844778	0.807	0.581575	0.996	CDS possible monooxygenase 1658506:1660047 forward MW:57262
RPA1497	0.746081	0.9085	1.221495	0.026	0.852806	0.814	1.097078	0.2145	1.382353	0.0125	mexC1 putative RND multidrug efflux membrane fusion protein MexC precursor 1660402:1661601 forward MW:42620
RPA1498	0.72836	0.836	1.528586	0.0085	0.792229	0.8935	1.194024	0.1975	1.342966	0.0795	mexD2 RND multidrug efflux transporter MexD 1661612:1664779 forward MW:113519
RPA1499	1.275029	0.024	2.822117	0.012	1.801196	0.0015	1.510998	0.047	2.781365	0.0065	CDS hypothetical protein 1664916:1665368 forward MW:15434
RPA1500	2.563604	0.001	3.324742	0.0075	2.756855	0	1.705258	0.009	3.437376	0	CDS unknown protein 1665626:1666225 reverse MW:21445
RPA1501	0.996869	0.492	1.064548	0.27	1.12824	0.228	0.876903	0.89	0.985719	0.559	CDS possible coenzyme F420 hydrogenase beta subunit 1666188:1667417 reverse MW:45760
RPA1502	1.129333	0.0555	1.101312	0.1215	0.968548	0.625	0.945853	0.6285	0.777677	0.992	CDS conserved hypothetical protein 1667478:1667966 reverse MW:18090
RPA1503	1.340732	0.0075	1.142354	0.0995	1.080681	0.131	1.082979	0.2585	0.894126	0.8885	CDS hypothetical protein 1667966:1669576 reverse MW:57625
RPA1504	1.037517	0.2825	0.916734	0.81	0.907942	0.8585	0.771843	0.983	0.740064	0.9965	CDS conserved unknown protein 1669576:1670889 reverse MW:47776
RPA1505	0.845772	0.82	1.14187	0.101	0.933601	0.7095	0.833613	0.9665	0.586912	0.9855	CDS putative porphobilinogen deaminase 1671137:1672120 forward MW:35601
RPA1506	0.9958	0.528	1.227546	0.048	1.084093	0.184	0.879478	0.843	0.804082	0.9545	bchI putative Mg chelatase subunit BchI 1672126:1673148 forward MW:37203
RPA1507	1.135836	0.281	1.471299	0.0605	1.19171	0.059	0.782094	0.627	0.6927	0.9605	bchD putative magnesium chelatase subunit BchD 1673145:1674917 forward MW:63187
RPA1508	1.098688	0.253	1.348988	0.009	1.223372	0.1225	1.112588	0.217	1.391314	0.039	CDS conserved hypothetical protein 1674960:1675691 reverse MW:26636
RPA1509	0.887371	0.733	1.297699	0.031	0.656953	0.9965	0.928974	0.688	0.824473	0.864	hemE uroporphyrinogen decarboxylase 1676073:1677050 reverse MW:35798
RPA1510	1.088902	0.287	1.02166	0.3845	1.201901	0.034	1.040813	0.3165	1.020851	0.407	CDS conserved unknown protein 1677230:1678183 forward MW:35283
RPA1511	1.123953	0.0665	1.122216	0.08	1.43233	0.0015	1.769816	0.0005	1.513547	0.014	CDS Alpha/beta hydrolase fold 1678194:1679081 forward MW:31718
RPA1512	0.968738	0.6935	1.111259	0.0945	0.947672	0.758	1.139455	0.0645	1.485556	0.0035	crtI phytoene dehydrogenase CrtI 1679157:1680692 forward MW:56701
RPA1513	1.236252	0.078	1.518441	0.005	1.63549	0.002	1.414526	0.008	1.093918	0.1775	crtB CrtB phytoene synthase 1680689:1681756 forward MW:39494
RPA1514	1.251843	0.033	1.120324	0.0875	1.389524	0.016	1.241017	0.085	1.207888	0.022	hemF putative coproporphyrinogen III oxidase precursor 1682058:1682969 forward MW:33661
RPA1515	0.850038	0.9895	0.885972	0.8755	1.12029	0.122	0.974322	0.59	0.681656	0.999	CDS conserved unknown protein 1683019:1683855 reverse MW:29194
RPA1516	0.792655	0.9515	0.849422	0.869	1.201733	0.1455	1.056211	0.4205	0.730412	0.957	CDS hypothetical protein 1684156:1684290 forward MW:5116
RPA1517	0.600045	0.999	0.713034	0.9975	0.584264	0.998	0.574163	0.997	0.668724	0.999	crtC hydroxyneurosporene dehydrogenase 1684504:1685457 reverse MW:36201
RPA1518	0.972366	0.683	0.906239	0.9105	0.823436	0.9795	0.934089	0.7525	0.914299	0.8755	crtD methoxyneurosporene dehydrogenase 1685462:1687021 reverse MW:55324
RPA1519	0.753092	0.978	0.670019	0.9865	0.897547	0.713	0.680382	0.931	0.686708	0.981	crtE geranylgeranyl pyrophosphate synthase 1687143:1688009 forward MW:30293
RPA1520	0.604564	0.9945	0.861923	0.9365	0.694511	0.993	0.697151	0.986	0.619495	0.9995	crtF hydroxyneurosporene methyltransferase CrtF 1688059:1689180 forward MW:40126
RPA1521	0.85473	0.968	0.617583	0.9925	0.978011	0.6265	0.977439	0.582	1.241369	0.0065	bchC 2-desacetyl-2-hydroxyethyl bacteriochlorophyllide a dehydrogenase 1689269:1690207 forward MW:33255
RPA1522	0.743505	0.952	0.977659	0.576	1.126339	0.1945	0.871065	0.901	0.777301	0.917	bchX bacteriochlorophyllide reductase subunit BchX 1690207:1691205 forward MW:34988
RPA1523	0.838499	0.978	0.919296	0.872	0.790156	0.982	0.776451	0.9885	0.734313	0.9905	bchY bacteriochlorophyllide reductase subunit BchY 1691229:1692815 forward MW:56607
RPA1524	0.765311	0.944	1.084899	0.178	0.826932	0.977	0.883762	0.8065	0.830853	0.9775	bchZ bacteriochlorophyllide reductase subunit 1692815:1694263 forward MW:53279
RPA1525	0.977546	0.565	0.960648	0.6895	1.031641	0.39	0.945351	0.7	0.825288	0.988	pufB light-harvesting complex 1 beta chain 1694719:1694916 forward MW:7278
RPA1526	1.151639	0.0585	1.037926	0.355	1.030974	0.3915	1.111186	0.258	1.156351	0.03	pufA light-harvesting complex 1 alpha chain 1694932:1695123 forward MW:7241
RPA1527	1.105352	0.207	1.03315	0.377	1.172914	0.122	1.123806	0.2345	1.162943	0.035	pufL photosynthetic reaction center L subunit 1695255:1696088 forward MW:30837
RPA1528	1.043268	0.385	1.094706	0.142	1.099813	0.193	0.949524	0.677	0.89416	0.922	pufM photosynthetic reaction center M protein 1696116:1697039 forward MW:34429
RPA1529	0.775838	0.8255	1.14443	0.0725	0.80087	0.898	0.739983	0.9845	0.723378	0.9145	ppsR1 transcriptional regulator PpsR1; Fis family 1697302:1698756 forward MW:52585
RPA1530	0.735933	0.8725	1.151046	0.18	1.03108	0.372	0.67099	0.9955	0.524955	0.9975	bchG geranylgeranyl bacteriochlorophyll synthase 1698749:1699642 forward MW:31542
RPA1531	0.922331	0.703	1.070639	0.3275	1.120556	0.0825	0.724308	0.974	0.626682	0.997	CDS possible Bch2, light harvesting pigment Major Facilitator Family (MFS) transporter 1699645:1700961 forward MW:45172
RPA1532	1.056139	0.364	0.990655	0.5305	1.192825	0.109	0.730004	0.976	0.844499	0.897	bchP geranylgeranyl reductase 1700963:1702168 forward MW:44012
RPA1533	0.73184	0.9835	1.008196	0.4985	0.902165	0.8465	0.715731	0.988	0.73011	0.9835	tspO tryptophan-rich sensory protein 1702188:1702652 forward MW:17458
RPA1534	0.654058	0.999	0.827859	0.892	0.791196	0.947	0.665552	0.8975	0.602719	0.998	CDS hypothetical protein 1702689:1702961 forward MW:9690
RPA1535	1.262194	0.0655	1.159606	0.1795	1.26048	0.115	0.999115	0.5105	0.946012	0.6955	cycA cytochrome c2 1703088:1703507 reverse MW:14633
RPA1536	1.202435	0.045	1.028348	0.391	1.205987	0.0305	1.006026	0.4705	1.34534	0.0185	ppsR2 transcriptional regulator PpsR2; Fis family 1703829:1705223 forward MW:50792
RPA1537	0.918286	0.768	1.174923	0.0405	1.039113	0.3245	1.30278	0.026	1.30167	0.026	CDS Bacteriophytochrome, apparent pseudogene, frameshifted 1705224:1707418 forward MW:80207
RPA1539	1.159826	0.0375	1.001354	0.493	0.958581	0.6685	1.24848	0.03	1.28627	0.0135	CDS putative heme oxygenase 1707550:1708212 reverse MW:23556

RPA1540	0.777463	0.9015	1.477063	0.015	1.0263	0.4545	1.106187	0.144	0.648884	0.855	CDS Coenzyme B12-binding 1708273:1709154 reverse MW:32290
RPA1542	0.71617	0.9785	0.896583	0.862	1.14854	0.041	0.650236	0.996	0.571166	0.999	bchN protochlorophyllide reductase subunit BchN 1709968:1711257 forward MW:46835
RPA1543	0.80589	0.988	0.860512	0.9295	0.821017	0.974	0.665322	0.994	0.621759	0.9995	bchB protochlorophyllide reductase BchB subunit 1711260:1712882 forward MW:58462
RPA1544	0.913246	0.8315	1.038229	0.3585	0.911619	0.845	0.701544	0.986	0.849049	0.925	bchH magnesium-protoporphyrin O-methyltransferase BchH subunit 1712857:1716603 forward MW:135985
RPA1545	0.879695	0.8215	1.067423	0.342	1.004776	0.4875	0.77024	0.974	0.758784	0.987	bchL protochlorophyllide reductase iron-sulfur ATP-binding protein BchL 1716600:1717538 forward MW:33898
RPA1546	0.752875	0.938	1.016089	0.4505	0.992589	0.5355	0.73879	0.978	0.659851	0.998	bchM Mg-protoporphyrin IX methyl transferase 1717538:1718239 forward MW:25591
RPA1547	1.14545	0.0495	1.297514	0.0335	1.456052	0.0025	1.034429	0.4055	1.009593	0.438	lhaA photosynthetic complex (LH1) assembly protein LhaA, probable Major Facilitator Superfamily (MFS) transporter 1718236:1719669 forward MW:49574
RPA1548	1.056696	0.374	1.130769	0.1665	1.251986	0.0625	0.875334	0.8455	0.842907	0.963	puhA H subunit of photosynthetic reaction center complex 1719692:1720459 forward MW:27242
RPA1549	1.265147	0.0545	1.275546	0.044	1.486993	0.0035	0.937846	0.6565	0.924896	0.834	CDS possible photosynthetic complex assembly protein 1720456:1721118 forward MW:23975
RPA1550	1.506049	0.019	1.621384	0.008	1.751854	0.0005	1.145359	0.231	1.065856	0.1845	CDS possible photosynthetic complex assembly protein 1721134:1721640 forward MW:17686
RPA1551	1.461955	0.0065	1.682519	0.008	1.71468	0.001	1.204302	0.2165	1.177219	0.0655	CDS hypothetical protein 1721643:1721942 forward MW:11056
RPA1552	1.419999	0.005	1.557482	0.03	1.40735	0.019	1.099922	0.2525	1.059486	0.2385	CDS conserved unknown protein 1721939:1723036 forward MW:42483
RPA1553	1.241363	0.0265	1.070373	0.251	1.133973	0.1815	1.168732	0.12	1.075805	0.161	CDS conserved hypothetical protein 1723050:1724114 forward MW:37969
RPA1554	1.293305	0.056	1.076982	0.26	1.524713	0.029	0.937398	0.717	0.874039	0.943	hemA 5-aminolevulinic acid synthase (ALAS) 1724111:1725322 forward MW:43799
RPA1555	0.74268	0.996	0.646571	0.994	0.916766	0.776	0.669094	0.995	0.609813	1	cbbR cbb operon transcriptional regulator CbbR, LysR family 1725664:1726632 reverse MW:35087
RPA1556			0.654351	0.9845			1.30046	0.191			CDS phosphotransfer protein with response regulator receiver and Hpt domains 1727226:1727915 forward MW:24856
RPA1557											CDS response regulator receiver with duplicated domains 1727937:1728773 forward MW:30407
RPA1558	0.908012	0.7095	0.943374	0.679	0.970902	0.588	0.963765	0.5615	0.891667	0.757	CDS sensor histidine kinase with multiple PAS/PAC and a response regulator receiver domain 1728789:1731500 forward MW:98469
RPA1559	1.046608	0.4435	12.00052	0.0005	1.191327	0.122	0.801055	0.69	0.242124	0.997	cbbL ribulose-bisphosphate carboxylase large chain 1731700:1733157 forward MW:53914
RPA1560	1.276286	0.1855	12.42854	0.0005	0.745865	0.876	0.756591	0.6845	0.219015	0.999	cbbS ribulose-bisphosphate carboxylase small chain 1733171:1733593 forward MW:16301
RPA1561	1.033729	0.352	1.024312	0.418	1.004671	0.483	0.81817	0.881	0.785357	0.937	cbbX cbbX protein homolog 1733596:1734522 forward MW:34563
RPA1562	0.732717	0.748	9.641531	0.004	0.382068	0.996	2.071395	0.203	0.299012	0.9875	CDS transcriptional regulator, LysR family 1734580:1735554 reverse MW:35886
RPA1563	0.973814	0.64	1.171588	0.1285	0.890817	0.885	1.396905	0.019	0.83397	0.9175	CDS putative nitrilase 1735691:1736740 forward MW:37833
RPA1564					0.542402	0.941					CDS possible urea/short-chain amide transport system substrate-binding protein 1736816:1738132 forward MW:47336
RPA1565	0.96082	0.6245	1.502042	0.002	0.825027	0.935	1.21578	0.076	1.003745	0.4995	CDS putative urea/short-chain amide transport system permease protein 1738141:1739016 forward MW:30617
RPA1566	0.945204	0.832	1.001567	0.491	0.745247	0.9325	0.669689	0.874	0.609674	1	CDS possible branched-chain amino acid transport system ATP-binding protein 1739013:1740878 forward MW:66165
RPA1567	1.113384	0.1585	0.955604	0.7515	0.980338	0.5775	0.897496	0.8385	1.19422	0.063	CDS putative branched-chain amino acid transport system ATP-binding protein 1740865:1741569 forward MW:25098
RPA1568	0.85556	0.9435	0.808091	0.995	0.794667	0.989	0.653201	0.9995	0.529557	0.9985	CDS possible carboxylesterase 1741619:1742401 reverse MW:26916
RPA1569	0.763992	0.993	0.683827	0.9995	0.740771	0.997	0.51493	0.9955	0.510858	1	CDS O-acetylhomoserine sulfhydrylase 1742405:1743700 reverse MW:45789
RPA1570	0.904294	0.811	0.734703	0.993	0.841672	0.962	0.618727	0.998	0.607084	0.994	CDS putative aminopeptidase 1743857:1745974 reverse MW:77591
RPA1571	0.891134	0.805	0.795678	0.9875	0.811384	0.9555	0.876227	0.824	0.892836	0.834	dapA1 putative dihydrodipicolinate synthetase 1746102:1746980 forward MW:31462
RPA1572	0.934588	0.851	0.757769	0.992	0.81691	0.9695	0.783653	0.971	0.723867	0.996	CDS putative carbon-monoxide dehydrogenase large subunit 1747205:1749535 forward MW:81725
RPA1573	0.919452	0.784	0.840021	0.976	0.877312	0.895	0.868029	0.944	0.876076	0.9025	CDS LemA family 1749613:1750227 forward MW:22473
RPA1574	0.92691	0.8865	0.946849	0.742	0.923184	0.852	0.82297	0.968	0.792532	0.996	CDS DUF477 1750232:1751155 forward MW:31619
RPA1575	1.010326	0.4505	0.870382	0.916	0.941808	0.714	0.762732	0.964	0.72139	0.9965	CDS conserved hypothetical protein 1751169:1751666 forward MW:18548
RPA1576	0.777888	0.983	0.663714	0.994	1.09896	0.1005	0.703646	0.992	0.582394	0.9985	CDS putative glutathione S-transferase 1751748:1752359 reverse MW:22892
RPA1577	0.711399	0.995	0.670767	0.996	0.897407	0.852	0.683883	0.992	0.804071	0.9785	CDS hypothetical protein 1752568:1753539 forward MW:33332
RPA1578	0.650521	0.7985	1.273884	0.025	0.596049	0.9965	0.766547	0.9915	0.774456	0.9775	fpr ferredoxin--NADP+ reductase 1753696:1754469 reverse MW:28788
RPA1579	0.859902	0.913	0.60526	0.9835	0.965652	0.621	0.600665	0.9595	0.528585	0.9995	CDS L-carnitine dehydratase/bile acid-inducible protein F 1754786:1755994 reverse MW:44043
RPA1580			0.564903	0.99	0.621551	0.921	0.655067	0.9215	0.507404	0.996	putA proline dehydrogenase PutA 1756159:1759167 reverse MW:106920
RPA1581	0.986408	0.5505	0.861051	0.9375	0.983185	0.5635	0.91194	0.81	0.892252	0.865	CDS hypothetical protein 1759231:1759959 forward MW:26688
RPA1582	0.665661	0.998	0.642523	0.9925	0.587916	0.989	0.472007	0.996	0.642933	0.993	cyaA Ferredoxin:Adenylate/Guanylate cyclase 1759984:1761765 reverse MW:65029
RPA1583	0.879581	0.8575	0.758317	0.982	1.007475	0.476	0.612317	0.9905	0.714824	0.998	CDS conserved hypothetical protein 1761958:1763067 reverse MW:39403
RPA1584	0.86688	0.9475	0.867241	0.904	0.885773	0.9355	0.906706	0.815	0.823508	0.915	CDS conserved hypothetical protein 1763064:1764533 reverse MW:54484
RPA1585	1.176046	0.0355	1.060721	0.368	1.540686	0.0015	1.155115	0.076	1.466307	0.0065	CDS putative hemmolysin III, HlyIII family 1764777:1765472 forward MW:25130
RPA1586	0.97163	0.606	1.036004	0.3755	0.819909	0.9005	0.737116	0.9775	0.866031	0.9595	CDS putative short-chain dehydrogenase/reductase 1765532:1766332 forward MW:28088
RPA1587	0.856195	0.955	1.020491	0.414	0.960159	0.651	0.813884	0.869	0.773487	0.984	CDS hypothetical protein 1766530:1766814 forward MW:9885
RPA1588	0.689428	0.999	0.495887	0.999	0.802153	0.9905	0.505301	0.9985	0.600868	0.999	CDS putative L-allo-threonine aldolase 1766818:1767900 reverse MW:38224
RPA1589	0.663097	0.956	0.994206	0.527	0.619126	0.995	0.703257	0.9965	0.760151	0.9455	rpsD 30S ribosomal protein S4 1768213:1768830 reverse MW:23559
RPA1590	0.990096	0.5445	0.818359	0.9525	0.98234	0.592	0.739215	0.9615	0.720414	0.981	CDS conserved hypothetical protein 1769020:1769796 reverse MW:28473
RPA1591	1.105888	0.114	0.837191	0.9235	1.179581	0.0885	0.871066	0.838	0.831288	0.897	CDS conserved unknown protein 1769796:1770191 reverse MW:13654
RPA1592	0.901132	0.7345	0.958949	0.612	1.026276	0.442	0.980059	0.569	1.068622	0.257	murI putative glutamate racemase 1770245:1771039 reverse MW:27962
RPA1593	0.963632	0.6985	1.260222	0.019	0.879051	0.8715	1.110085	0.22	1.279862	0.0125	CDS Thioesterase superfamily 1771122:1771610 reverse MW:18040
RPA1594	0.813044	0.9825	0.825871	0.962	1.027473	0.3645	0.609555	0.9985	0.49224	1	trpB-1 putative tryptophan synthase beta chain 1771765:1773129 forward MW:49412
RPA1595	0.747569	0.9975	0.687689	0.998	1.072173	0.2675	0.765188	0.9585	0.95164	0.7425	CDS conserved unknown protein 1773467:1774417 forward MW:35500
RPA1596	0.732093	0.987	0.841578	0.945	1.001617	0.5025	0.925425	0.6305	0.804751	0.988	CDS possible tryptophan synthase beta chain 1774809:1775177 forward MW:13460
RPA1597	0.839383	0.91	0.78029	0.986	0.691887	0.993	0.62252	0.9935	0.685158	0.994	purQ phosphoribosylformylglycinamide synthetase 1775573:1777783 forward MW:78471
RPA1598	0.71238	0.98	0.700563	0.9965	0.831513	0.948	0.594095	0.998	0.707457	0.9905	CDS Peptidylprolyl isomerase, FKBP-type:Acyltransferase 3 family 1778029:1779210 reverse MW:44428
RPA1599	0.675467	0.9885	0.722542	0.9965	0.826935	0.971	0.714144	0.9915	0.822305	0.968	CDS conserved hypothetical protein 1779285:1779647 reverse MW:13269
RPA1600	0.766016	0.92	0.642257	0.996	0.808612	0.8405	0.878602	0.8005	0.819802	0.894	CDS BolA-like protein 1779811:1780047 forward MW:8390
RPA1601	0.629458	0.999	0.688751	0.9855	0.746574	0.989	0.928177	0.766	1.060445	0.2335	CDS possible transcriptional regulator, MarR family 1780122:1780646 reverse MW:19276
RPA1602	0.781281	0.988	1.069517	0.263	0.848368	0.788	1.558232	0.0075	1.331165	0.038	CDS hypothetical protein 1781319:1782041 forward MW:27474
RPA1603									1.665896	0.011	CDS putative fatty acid desaturase 1782103:1783170 reverse MW:40546
RPA1604	1.262182	0.1315	1.367889	0.0335	1.754486	0	0.823602	0.9205	1.214164	0.154	CDS conserved hypothetical protein 1783527:1784507 reverse MW:36246
RPA1605	0.984097	0.572	1.196849	0.081	1.110915	0.0875	0.590477	0.9975	0.760298	0.8755	CDS conserved hypothetical protein 1784553:1785812 reverse MW:47025
RPA1606	0.898571	0.807	0.848363	0.9075	1.025184	0.4125	0.996625	0.5045	0.774911	0.987	CDS conserved unknown protein 1786040:1786423 forward MW:14105
RPA1607	1.072312	0.3095	1.153114	0.13	1.034468	0.4385	1.180689	0.177	1.267217	0.0235	CDS Appr-1''-p processing enzyme family protein homolog 1786420:1786962 forward MW:18416
RPA1608	1.024692	0.4255	0.984763	0.5685	1.046548	0.3055	0.939322	0.7235	0.87407	0.837	CDS Beta-lactamase 1787022:1788302 forward MW:47784
RPA1609	1.061638	0.309	0.692633	0.9865	0.847567	0.945	0.634378	0.891	0.526485	0.995	mdlC benzoylformate decarboxylase 1788313:1789941 reverse MW:57398
RPA1610	0.619202	1	0.729822	0.9965	0.606109	0.999	0.529966	0.9995	0.57355	1	CDS conserved unknown protein 1790211:1791068 reverse MW:30858
RPA1611	0.547255	0.9995	0.795335	0.984	0.564021	0.9965	0.528903	0.998	0.56713	0.998	CDS putative dehydratase 1791081:1792175 reverse MW:39309
RPA1612	0.810223	0.9775	0.827055	0.917	0.766863	0.983	0.85316	0.9305	0.846044	0.9495	CDS putative acyl-CoA dehydrogenase 1792376:1793548 reverse MW:43105
RPA1613	1.123348	0.348	0.803713	0.9585	1.234266	0.045	0.730742	0.972	0.661065	0.9985	CDS putative cytochrome P-450 1793582:1794847 reverse MW:48554
RPA1614	0.980767	0.6145	0.773977	0.9955	0.839577	0.9365	0.720976	0.981	0.603272	1	ivd2 isovaleryl-CoA dehydrogenase 1795195:1796367 forward MW:42136
RPA1615	0.942143	0.8045	0.861815	0.8945	0.981964	0.5635	0.516009	0.9985	0.705287	0.994	CDS putative methyltransferase 1796463:1797257 forward MW:28942
RPA1616	0.885515	0.8965	0.880011	0.9295	1.382827	0.004	1.06085	0.31	0.87491	0.899	CDS conserved hypothetical protein 1797254:1798060 reverse MW:30111
RPA1617	0.800195	0.8575	0.761241	0.972	0.99092	0.5245	0.617278	0.991	0.573299	0.9875	CDS ErfK/YbiS/YcfS/YnhG 1798147:1798728 reverse MW:21203

RPA1618	0.790276	0.9775	0.800685	0.936	0.903491	0.767	0.667693	0.9475	0.406281	0.9995	ilvX putative acetolactate synthase large subunit 1798909:1800453 forward MW:53599
RPA1619	0.826044	0.8185			0.944658	0.626			0.645125	0.992	CDS hypothetical protein 1800509:1800997 forward MW:17183
RPA1620	1.292814	0.308	0.476257	0.9995	1.603109	0.0925	0.562486	0.949	0.398357	0.9945	CDS unknown protein 1801160:1801480 reverse MW:11535
RPA1621	1.39715	0.0085	2.3571	0.001	1.347932	0.0795	2.684275	0.0025	3.022943	0	CDS hypothetical protein 1801680:1802552 forward MW:31646
RPA1622	0.943483	0.835	0.945361	0.805	0.924093	0.803	1.049088	0.2755	1.259038	0.0075	CDS conserved unknown protein 1802706:1803986 reverse MW:46966
RPA1623	0.831566	0.889	0.905308	0.7775	1.009143	0.4375	0.777848	0.9775	0.73819	0.9865	CDS conserved unknown protein 1804226:1804879 reverse MW:22914
RPA1624	1.02609	0.3405	1.243544	0.0085	0.940355	0.779	1.177923	0.063	1.266447	0.013	CDS conserved hypothetical protein 1804927:1805433 forward MW:18745
RPA1625	0.863536	0.967	0.994039	0.533	0.756234	0.994	0.761814	0.9785	0.745889	0.995	cysQ putative CysQ protein 1805442:1806269 reverse MW:28317
RPA1626	0.750431	0.9945	0.851641	0.9505	0.736344	0.9905	0.759184	0.9925	0.729704	0.9875	CDS conserved unknown protein 1806403:1807059 forward MW:23104
RPA1629	1.186441	0.0875	1.080854	0.1865	1.092379	0.156	0.840675	0.933	0.875801	0.88	cheY2 chemotaxis response regulator, CheY2 1810628:1810993 forward MW:13503
RPA1630	1.064112	0.2035	0.951009	0.7085	0.978991	0.6	0.845849	0.954	0.910211	0.815	cheB2 chemotaxis methylesterase, CheB2 1811072:1812247 forward MW:40957
RPA1631	1.091589	0.123	0.898861	0.8845	0.829024	0.8835	1.020913	0.4365	1.02701	0.435	cheR2 chemotaxis methyltransferase, CheR2 1812244:1813122 forward MW:32647
RPA1632	1.059321	0.2645	0.860858	0.9375	0.848693	0.891	0.975047	0.617	1.331211	0.0065	ctrA two-component cell cycle transcriptional regulator ctrA, winged helix family 1813413:1814114 reverse MW:26064
RPA1633	0.983446	0.6035	0.911548	0.8975	0.922212	0.8185	0.972848	0.6125	1.503911	0.003	fliI flagellum-specific ATP synthase 1814482:1815807 forward MW:47566
RPA1634	1.178264	0.0195	1.111103	0.104	1.102595	0.163	1.223708	0.032	1.226452	0.0305	CDS conserved unknown protein 1815917:1816345 forward MW:16325
RPA1635	0.961243	0.6795	0.931973	0.7775	0.839778	0.973	0.806718	0.9075	1.007778	0.461	CDS RNA polymerase ECF-type sigma factor 1816522:1817070 forward MW:20498
RPA1636	1.05559	0.2335	1.169339	0.0685	0.950302	0.7495	1.0782	0.247	1.237022	0.0125	CDS conserved unknown protein 1817070:1818017 forward MW:33080
RPA1637	0.733743	0.9445	0.7894	0.923	0.75303	0.9405	1.023715	0.4625	0.844083	0.877	CDS hypothetical protein 1818215:1818415 reverse MW:6808
RPA1638	0.927797	0.803	0.605536	0.997	0.590288	0.9865	0.671853	0.9785	0.670679	0.9865	flhA putative flagellar export protein FlhA 1818747:1820879 reverse MW:75137
RPA1639	0.874412	0.9155	0.84328	0.884	1.094696	0.19	0.737262	0.9135	0.614816	0.9905	CDS possible oxalate/formate Major Facilitator Family (MFS) antiporter 1821142:1822386 forward MW:42860
RPA1641	0.853005	0.929	1.256937	0.007	0.847628	0.8165	1.083624	0.281	1.172576	0.077	CDS possible transcriptional regulator, AraC family 1825086:1826006 forward MW:33948
RPA1642	0.600684	0.997	0.619358	0.9915	0.883088	0.7885	0.578381	0.995	0.773521	0.996	CDS putative diguanylate cyclase (GGDEF) 1826387:1827901 forward MW:56512
RPA1643	1.189249	0.033	1.506999	0.003	1.39207	0.0405	1.698983	0.0075	1.682163	0.001	CDS possible high affinity iron permease FTR1 1828098:1828964 forward MW:30781
RPA1644	1.554684	0	1.538272	0	1.083663	0.199	1.155672	0.0855	1.069819	0.25	CDS conserved unknown protein 1828955:1829704 reverse MW:27108
RPA1645	0.919021	0.8765	1.00711	0.4705	1.055066	0.237	0.921085	0.743	0.940565	0.7085	CDS unknown protein 1829694:1829921 reverse MW:8009
RPA1646	1.132091	0.266	2.130649	0.0085	1.291273	0.1145	1.17868	0.298	0.950281	0.608	CDS hypothetical protein 1830020:1830289 reverse MW:9852
RPA1647	0.995046	0.505	0.954117	0.664	0.868111	0.8775	0.952223	0.625	0.877343	0.9225	CDS putative esterase 1830366:1831367 reverse MW:35838
RPA1648	0.730828	0.908	1.254799	0.0375	1.012892	0.454	0.941886	0.732	0.737838	0.903	CDS membrane permeases, predicted cation efflux pumps 1831520:1832782 forward MW:44747
RPA1649	1.012838	0.4675	1.288125	0.135	1.076788	0.309			0.543698	0.9945	CDS predicted ABC-type transport systems, involved in lipoprotein release, permease components 1832779:1834005 forward MW:43663
RPA1650	1.311641	0.0885	1.375504	0.0265	1.182483	0.069	0.812031	0.8665	0.71148	0.9935	CDS putative ABC transporter, ATP-binding protein 1833998:1834678 forward MW:24789
RPA1651	0.849925	0.661	0.464374	0.997	0.859967	0.9285	0.608048	0.985	0.288091	1	CDS possible leucine/isoleucine/valine-binding protein precursor 1834778:1835995 reverse MW:44250
RPA1652	0.866677	0.821	1.214534	0.0205	1.092954	0.2935	1.229739	0.0725	1.042398	0.3475	CDS possible flagellar basal-body rod protein FlgG 1836597:1837418 forward MW:28064
RPA1654	1.210705	0.1975	0.988776	0.55	1.34063	0.006	1.25549	0.047	0.923369	0.763	CDS putative oxido-reductase 1838052:1839065 reverse MW:37171
RPA1655	0.886059	0.7765	0.719615	0.9755	0.874903	0.9115	0.799625	0.9255	0.778709	0.991	CDS possible urea/short-chain binding protein of ABC transporter 1839226:1840434 reverse MW:43328
RPA1656	1.20276	0.065	1.012744	0.4375	1.283486	0.011	1.30383	0.027	0.957242	0.617	CDS possible urease accessory protein 1840537:1841232 forward MW:24426
RPA1657	0.819156	0.9825	1.006006	0.48	0.894998	0.879	0.968105	0.6525	0.914102	0.8535	CDS putative diguanylate cyclase (GGDEF) 1841261:1842475 reverse MW:44045
RPA1658	1.00399	0.4785	1.334799	0.0125	1.159478	0.056	1.273078	0.023	1.167189	0.045	ptpS putative 6-pyruvol tetrahydrobiopterin synthase 1843254:1843616 forward MW:13894
RPA1659	1.165273	0.2225	1.680316	0.006	1.399429	0.0555	1.526441	0.002	1.202406	0.2405	CDS conserved unknown protein 1843683:1844273 reverse MW:23016
RPA1660	1.360382	0.04	0.887334	0.797	0.95726	0.7005	0.801102	0.945	0.985916	0.5535	CDS putative cation transporting P-type ATPase 1844415:1847336 reverse MW:101253
RPA1661							2.007026	0.0065	1.580334	0.007	CDS DUF156 1847388:1847663 forward MW:10266
RPA1662	1.397449	0.009	1.34556	0.0115	1.660447	0	1.590999	0.001	1.364809	0.066	CDS hypothetical protein 1847694:1848374 reverse MW:24735
RPA1663	1.656094	0.0065	1.875271	0.003	2.741839	0.002	1.114799	0.2965	0.804836	0.8715	hpaD putative 3,4-dihydroxyphenylacetate 2,3-dioxygenase 1848482:1849333 reverse MW:31149
RPA1664	1.235288	0.0365	1.361329	0.0095	1.664125	0.0225	0.950523	0.721	0.676248	0.882	CDS Glyoxalase/Bleomycin resistance protein/dioxygenase domain 1849361:1849903 reverse MW:20106
RPA1665	0.915599	0.7785	1.132387	0.121	1.255991	0.1305	1.100805	0.3375	0.823527	0.82	CDS hypothetical protein 1850059:1850361 reverse MW:10502
RPA1666	1.05827	0.351	1.412076	0.0245	1.169269	0.2405	0.843147	0.8945	0.627307	0.984	hemN1 putative coproporphyrinogen oxidase III 1850616:1851965 reverse MW:49338
RPA1667	1.317428	0.1655	1.661212	0.0245	1.674596	0.016	1.029491	0.449	0.741534	0.9955	bchJ putative 4-vinyl protochlorophyllide reductase 1851994:1852656 reverse MW:23325
RPA1668	1.451654	0.034	1.029933	0.389	1.221958	0.141	1.113898	0.2395	1.037431	0.3345	bchE Mg-protoporphyrin IX monomethyl ester oxidative cyclase 66kD subunit 1852676:1854373 reverse MW:63685
RPA1669	0.940268	0.608	1.444066	0.0115	1.034734	0.428	0.890275	0.8625	0.822634	0.6925	CDS unknown protein 1854531:1854959 reverse MW:15286
RPA1670	0.944026	0.6935	0.953933	0.715	1.169552	0.104	0.884888	0.8035	0.836741	0.883	CDS Metallo-phosphoesterase 1855181:1855921 forward MW:26914
RPA1671	0.851781	0.8935	0.956537	0.7	0.901022	0.787	0.755155	0.929	0.642433	0.9955	CDS putative serine/threonine protein kinase 1855925:1857364 forward MW:53372
RPA1672	0.762025	0.8095	1.302738	0.0245	1.27778	0.146	0.925524	0.808	0.565474	0.913	CDS conserved hypothetical protein 1857410:1858060 reverse MW:23891
RPA1673	0.814661	0.9885	0.940231	0.8015	1.13872	0.1095	0.95648	0.6715	0.658819	0.9985	CDS D-xylulose 5-phosphate/D-fructose 6-phosphate phosphoketolase 1858439:1860790 forward MW:88477
RPA1674	1.233992	0.0955	1.516066	0.067	1.103779	0.1965	2.941738	0.0275	1.213621	0.108	cheY3 response regulator receiver, CheY3 1860968:1861471 forward MW:18048
RPA1675			0.582818	0.937	1.006864	0.489			0.69898	0.8715	CDS methyl-accepting chemotaxis receptor/sensory transducer with PAS domain 1862118:1864268 forward MW:77601
RPA1678	0.891437	0.7645	0.584987	0.9905	0.813512	0.9675	0.758033	0.9675	0.715876	0.902	cheR3 chemotaxis methyltransferase, CheR3 1867811:1868686 forward MW:32542
RPA1679	1.063134	0.416	0.624134	0.9945	0.902281	0.7165	1.125334	0.244	1.086749	0.3175	CDS unknown protein 1868698:1869012 forward MW:11603
RPA1680	1.013638	0.46	0.689577	0.919	1.001195	0.493	1.001247	0.4965	0.79338	0.803	CDS putative response regulator and cylclic diguanylate phosphodiesterase (EAL) 1869241:1870491 forward MW:45142
RPA1681	0.866864	0.9655	0.57044	0.9995	0.805106	0.98	0.699728	0.985	0.679068	0.9955	CDS sensor histidine kinase with a response regulator receiver domain 1870522:1873113 reverse MW:93242
RPA1682	1.142239	0.0385	1.046498	0.267	1.227546	0.0165	1.513781	0.001	1.408818	0.0025	CDS ptwo-component transcriptional regulator, LuxR family 1873536:1874162 forward MW:22536
RPA1683	0.931304	0.722	0.960899	0.676	1.103682	0.161	1.03819	0.3665	1.01391	0.438	CDS 3-oxoacyl-acyl carrier protein reductase 1874213:1874995 reverse MW:26966
RPA1684	0.833879	0.9875	0.819941	0.9755	0.751114	0.9875	0.820909	0.9685	0.644098	0.999	CDS putative 3-ketoacyl-acyl carrier protein reductase 1875104:1875865 forward MW:26455
RPA1685	0.940205	0.8015	1.000384	0.496	0.951084	0.7015	0.914308	0.7895	0.790639	0.9895	CDS possible serine protease/outer membrane autotransporter 1876349:1880449 forward MW:130747
RPA1686	0.993972	0.526	0.737816	0.96	1.074437	0.192	0.792206	0.865	0.799673	0.9855	CDS putative alcohol dehydrogenase 1880602:1882206 reverse MW:58389
RPA1687	0.932976	0.6785	0.550125	0.9975	1.001274	0.486	0.473823	0.996	0.487585	0.992	CDS putative aldehyde dehydrogenase 1882277:1883710 reverse MW:52265
RPA1688											CDS GCN5-related N-acetyltransferase 1884296:1884817 forward MW:19193
RPA1689	0.814735	0.9705	0.920712	0.787	0.838182	0.9165	0.906587	0.8535	0.802593	0.9565	CDS conserved hypothetical protein 1885144:1886307 forward MW:40985
RPA1690	0.609037	0.987	0.613775	0.9905	0.979393	0.586	0.486663	0.9995	0.69048	0.9955	CDS conserved unknown protein 1886304:1886744 reverse MW:15237
RPA1691	1.1349	0.2305	1.142001	0.335	0.984624	0.547	0.909766	0.7505	1.066441	0.303	matE3 probable cation efflux pump (multidrug resistance protein) 1886876:1888249 reverse MW:46500
RPA1692	1.320566	0.0295	1.052139	0.294	2.655853	0.001	0.747655	0.948	1.942741	0.0015	CDS putative transmembrane transport protein 1888524:1889759 forward MW:42973
RPA1693	1.196934	0.0395	1.04829	0.3355	1.077754	0.3165	1.131574	0.193	1.107175	0.092	sodB superoxide dismutase 1889961:1890557 forward MW:22515
RPA1694	0.880735	0.818	1.05906	0.3995	0.873845	0.9055	1.060136	0.4435	1.082079	0.3155	crcB Camphor resistance CrcB protein 1890635:1891084 forward MW:16107
RPA1695	1.20078	0.078	1.081943	0.247	1.034401	0.3605	1.754103	0.0015	1.367194	0.0045	CDS CUPIN domain:transcriptional regulator, AraC family 1891147:1892007 reverse MW:31927
RPA1696	0.792759	0.928	1.035638	0.386	0.912494	0.895	1.165995	0.2765	0.991621	0.5415	CDS conserved hypothetical protein 1892427:1893062 forward MW:23015
RPA1697	0.828857	0.9595	0.562546	0.9975	0.765473	0.9655	0.647032	0.9695	0.6331	0.995	CDS Competence-damaged protein 1893265:1893807 reverse MW:19101
RPA1698	0.653996	0.989	0.923598	0.634	0.812946	0.929	1.318873	0.147	1.036323	0.3925	CDS DUF81 1893871:1894614 reverse MW:26376
RPA1699	0.797228	0.9915	0.956946	0.6085	0.796073	0.8015	0.996998	0.512	0.748976	0.981	CDS putative acyl-CoA dehydrogenase 1894760:1896547 forward MW:64855
RPA1700	0.913953	0.921	0.792067	0.9715	0.816985	0.9595	0.689606	0.985	0.68716	0.999	CDS putative amidase 1896682:1898184 reverse MW:52919

RPA1701	1.178556	0.028	1.151844	0.0665	1.200382	0.031	1.394884	0.0095	1.282233	0.0215	CDS conserved hypothetical protein 1898566:1899336 reverse MW:26987
RPA1702	0.860652	0.763	0.554062	0.9985	0.99024	0.543	0.640488	0.975	0.637721	0.9915	CDS putative acyl-CoA ligase 1899531:1901087 reverse MW:57036
RPA1703	0.832632	0.8735	0.658243	0.992	0.934147	0.73	0.758602	0.928	0.79016	0.9585	CDS putative acetyl-CoA acyltransferase 1901366:1902541 reverse MW:40978
RPA1704	1.347817	0.032	1.5876	0.0365	0.700411	0.8725	1.869941	0.1005	2.2077	0.0005	CDS probable transcriptional regulator, TetR family 1902643:1903350 forward MW:25648
RPA1705	0.765831	0.9935	0.589105	0.999	0.827915	0.983	0.600907	0.9985	0.443812	1	CDS possible 3-hydroxyacyl-CoA dehydrogenase type II 1903489:1904565 forward MW:37664
RPA1706	0.969907	0.6155	0.626419	0.9965	1.106408	0.1545	0.526606	0.9915	0.640687	0.9915	CDS putative enoyl-CoA hydratase 1904789:1905595 forward MW:28809
RPA1707	0.933936	0.5835	0.639362	0.997	0.749656	0.9965	0.599106	0.9945	0.502211	1	fcs1 putative feruloyl-CoA synthetase 1905646:1907520 forward MW:68544
RPA1708	0.598773	0.997	0.740594	0.952	0.752813	0.991	0.51068	0.9975	0.368485	1	CDS putative acyl-CoA dehydrogenase 1907687:1908814 forward MW:40249
RPA1709	0.933878	0.7355	0.913154	0.845	0.940544	0.752	0.685903	0.994	0.619863	0.997	CDS putative acyl-CoA dehydrogenase 1908951:1910198 forward MW:45384
RPA1710	0.678178	0.999	0.701392	0.997	0.694316	0.998	0.441017	1	0.387778	1	CDS putative acyl-CoA dehydrogenase 1910349:1911593 forward MW:45110
RPA1711	0.638428	0.9975	0.737449	0.9905	0.649468	0.9985	0.467494	0.9985	0.365884	1	pnbA putative nitroreductase 1911756:1912454 forward MW:24880
RPA1712	0.685648	1	0.715761	0.9985	0.62171	0.9985	0.502822	1	0.584439	1	CDS putative enoyl-CoA hydratase 1912856:1913638 reverse MW:28187
RPA1713	0.714192	0.943	0.57057	0.989	0.863717	0.778	0.68691	0.91	0.684703	0.9985	CDS possible cyclic nucleotide-binding domain 1913941:1914615 forward MW:24995
RPA1714											CDS hypothetical protein 1914669:1915511 forward MW:31453
RPA1715	0.814963	0.9555	0.709058	0.9065	0.945489	0.6465	0.875764	0.557	0.685681	0.9975	CDS conserved hypothetical protein 1915666:1916166 forward MW:18491
RPA1716	1.521935	0.003	2.517636	0.002	1.554558	0.003	3.129443	0.0015	3.610381	0	CDS putative diguanylate cyclase (GGDEF) 1916440:1918650 forward MW:80790
RPA1717	1.901183	0.001	1.175974	0.089	2.03624	0.004	2.025401	0.002	3.633147	0	CDS hypothetical protein 1918857:1919243 reverse MW:14279
RPA1718	1.039312	0.301	0.878032	0.8925	1.258593	0.1385	0.896361	0.7605	1.044426	0.319	CDS hypothetical protein 1919490:1919897 forward MW:14770
RPA1719	0.90451	0.8685	0.686996	0.9875	0.985984	0.5695	0.897892	0.7	1.351936	0.024	CDS Protein of unknown function UPF0153 1919904:1920236 reverse MW:11829
RPA1720											CDS conserved hypothetical protein 1920300:1920920 reverse MW:22836
RPA1721	0.911813	0.8115	0.611526	0.989	0.999578	0.4965	0.709651	0.956	0.500322	0.9985	CDS transcriptional regulator, LysR family 1921022:1921939 forward MW:32690
RPA1722											alkB alkylated DNA repair protein 1921936:1922586 forward MW:23513
RPA1723	1.431881	0.073	0.920951	0.8	1.060116	0.2395	0.853178	0.9115	0.783011	0.898	paaK phenylacetyl-CoA ligase 1922593:1923924 reverse MW:49232
RPA1724	1.136338	0.2845	0.661692	0.995	1.094014	0.2525	0.780676	0.9155	0.62842	0.99	paaI putative phenylacetic acid degredation protein 1923939:1924412 reverse MW:16206
RPA1725	0.910774	0.7315	0.713137	0.9985	0.937199	0.717	0.7103	0.8725	0.694928	0.9895	CDS putative aldehyde dehydrogenase 1924637:1926676 forward MW:72858
RPA1726			0.406748	0.995			0.426416	0.948	0.621501	0.9235	CDS putative oxidoreductase 1926733:1927749 forward MW:35347
RPA1727	0.885754	0.7975	1.135971	0.2205	1.004518	0.496	1.030655	0.4215	1.291909	0.053	CDS hypothetical protein 1927991:1928728 forward MW:27388
RPA1728	1.056031	0.2125	1.229443	0.0315	1.019059	0.4355	1.17483	0.087	1.263907	0.0075	CDS conserved unknown protein 1929247:1933506 reverse MW:156857
RPA1729	0.843656	0.9725	0.83116	0.9795	1.145745	0.0985	0.573279	0.9985	1.16834	0.06	CDS Fatty acid desaturase family 1934248:1935210 reverse MW:35581
RPA1730	0.953783	0.645	0.775641	0.895	1.033684	0.3435			0.752428	0.9705	CDS possible hydrolase 1935263:1936486 reverse MW:43287
RPA1731	1.531969	0.0935	0.750212	0.982	1.396304	0.0055	0.951557	0.627	0.720844	0.974	CDS similar to eukaryotic molybdopterin oxidoreductase 1936665:1937330 reverse MW:25434
RPA1732	1.117358	0.337	0.697964	0.9865	1.069662	0.269	0.660151	0.9835	0.749677	0.992	CDS possible cytochrome P450 1937353:1938552 reverse MW:44789
RPA1733	1.724356	0.1165	0.75438	0.978	1.48329	0.012	1.01213	0.4565	0.935679	0.662	fdxA putative ferredoxin 1938621:1938848 reverse MW:8147
RPA1734	0.915649	0.788	0.807909	0.9795	0.837053	0.9235	0.60337	0.9915	0.611677	0.998	CDS putative amidotransferase, subunit A 1938948:1940381 reverse MW:50316
RPA1735	0.76379	0.9705	1.034781	0.325	0.938134	0.7665	0.883956	0.894	0.706267	0.9955	CDS pseudogene of fused ABC transporter ATPase and permease domains 1940520:1941632 forward MW:41277
RPA1736	0.802141	0.965	0.916996	0.7135	1.123566	0.1295	0.73658	0.9925	0.34559	1	bglA putative beta-glucosidase 1941645:1943021 reverse MW:51738
RPA1737	1.127544	0.0645	0.961978	0.6475	1.006407	0.4655	0.92364	0.7735	0.703981	0.9995	CDS possible dehydrogenase 1943207:1943986 reverse MW:27337
RPA1738	1.188354	0.353			2.159395	0.038					CDS putative branched-chain amino acid transport system ATPase 1944029:1945513 reverse MW:53670
RPA1739	1.798233	0.045	1.078128	0.2785	1.495764	0.005	1.180385	0.128	1.164457	0.286	CDS putative branched-chain amino acid transport system permease protein 1945513:1946436 reverse MW:31893
RPA1740			0.729728	0.8455	1.936578	0.015			0.482253	0.98	CDS possible branched-chain amino acid transport system permease protein 1946438:1947313 reverse MW:30592
RPA1741	1.982714	0.071	0.624055	0.9685	2.46234	0.0035	1.263083	0.2315	0.963556	0.572	CDS possible branched-chain amino acid transport system substrate-binding protein 1947510:1948760 reverse MW:44690
RPA1742	1.114258	0.228	0.829717	0.918	1.195955	0.053	0.583258	0.9955	0.507804	0.9995	yeaU putative tartrate dehydrogenase 1948929:1950047 forward MW:41347
RPA1743	1.033499	0.3475	0.924158	0.8615	1.419819	0.013	0.860992	0.85	0.909557	0.787	CDS hypothetical protein 1950081:1950920 reverse MW:30610
RPA1744	1.02989	0.36	1.38905	0.005	1.198186	0.0425	0.975013	0.563	0.781615	0.965	serA possible phosphoglycerate dehydrogenase (serA), Nter fragment 1951061:1951975 reverse MW:32854
RPA1745	0.881149	0.8965	0.958622	0.609	1.476781	0.004	0.872349	0.8915	0.817551	0.971	CDS N-carbamoyl-beta-alanine amidohydrolase 1952010:1953260 reverse MW:44232
RPA1746	1.648531	0.0005	1.909836	0.0025	1.624157	0.0045	2.708183	0	3.776244	0	CDS transcriptional regulator, LysR family 1953330:1954280 reverse MW:34750
RPA1747	1.098482	0.168	1.986287	0.0015	1.518651	0.0065	2.189188	0.0545	2.435516	0.0195	CDS conserved hypothetical protein 1954396:1955214 forward MW:29494
RPA1748	1.796689	0.0155	1.947888	0.0005	2.555748	0.0005	1.204231	0.1495	2.257584	0.0005	CDS putative branched-chain amino acid transport system substrate-binding protein 1955272:1956519 forward MW:45278
RPA1749	1.253964	0.098	1.510369	0.002	1.408912	0.037	1.050913	0.3965	1.1211	0.2105	CDS putative branched-chain amino acid transport system permease protein 1956692:1957525 forward MW:29392
RPA1750	1.26844	0.175	1.833201	0.001	0.873982	0.6445	0.887855	0.636	1.47503	0.0505	CDS putative branched-chain amino acid transport system permease protein 1957525:1958511 forward MW:35659
RPA1751	0.723454	0.9805	1.324601	0.095	0.62312	0.9645	0.788526	0.9185	0.700492	0.8415	CDS putative branched-chain amino acid transport system ATP-binding protein 1958508:1959242 forward MW:26252
RPA1752	1.252312	0.291	2.332475	0.005	1.786356	0.0035	1.306369	0.147	2.159385	0.0235	CDS branched-chain amino acid transport system ATP-binding protein 1959226:1959930 forward MW:26027
RPA1753	1.438014	0.0115	0.810941	0.9765	1.16404	0.1315	0.975432	0.552	1.002428	0.4925	CDS conserved hypothetical protein 1960124:1960903 forward MW:29027
RPA1754	1.29439	0.164	0.801599	0.9425	1.328125	0.008	0.773482	0.9885	0.761027	0.9965	ragC putative cation efflux system protein 1961116:1964310 forward MW:113661
RPA1755	1.076762	0.296	0.673488	0.9755	1.138572	0.093	0.548158	0.9935	0.573119	0.997	ragD possible cation/heavy metal efflux pump, HlyD family secretion protein 1964300:1965502 forward MW:41847
RPA1756	0.999278	0.4855	0.85061	0.8685	1.087171	0.2995	0.989994	0.5225	0.612781	0.9985	CDS possible acetyl-CoA acetyltransferase 1965670:1967184 reverse MW:53583
RPA1757	0.810528	0.8595	0.618839	0.998	0.588169	0.998	0.398625	0.9995	0.339765	1	CDS possible oxoacyl carrier protein reductase 1967224:1968003 reverse MW:27014
RPA1758	0.916172	0.728	0.787126	0.9855	0.799095	0.9605	0.58859	0.997	0.47584	1	CDS putative enoyl-CoA hydratase paaG 1968171:1968971 forward MW:28971
RPA1759	0.748705	0.944	0.798929	0.92	0.640209	0.9945	0.42413	0.997	0.391765	1	CDS Tyrosine protein kinase:Aminoglycoside phosphotransferase 1968979:1969974 forward MW:36113
RPA1760							0.766302	0.9305	0.587109	0.9735	CDS conserved unknown protein 1969993:1970367 forward MW:13627
RPA1761	1.042286	0.362	0.727264	0.995	0.952512	0.7175	0.886429	0.8185	0.594849	0.999	CDS putative enoyl-CoA hydratase 1970699:1971478 reverse MW:27701
RPA1762	1.010354	0.4865	0.645419	0.9985	0.721096	0.9795	0.729078	0.966	0.561336	0.9995	CDS putative acyl-CoA dehydrogenase 1971547:1972878 forward MW:50487
RPA1763	1.133463	0.2665	0.675153	0.9885	0.966641	0.6395	1.05657	0.377	0.843304	0.961	CDS putative long-chain-fatty-acid CoA ligase 1973251:1974828 reverse MW:57703
RPA1764	1.103433	0.2165	0.814952	0.9885	0.703621	0.929	0.880867	0.883	1.160781	0.0845	CDS putative 2, 4-dienoyl-CoA reductase (NADPH) 1975165:1976037 reverse MW:31192
RPA1765	1.135082	0.1545	0.855003	0.9635	0.738749	0.9725	0.875695	0.9355	1.021926	0.395	CDS putative enoyl-CoA hydratase 1976145:1976957 forward MW:28773
RPA1766	0.994015	0.5425	0.960353	0.681	1.114219	0.1065	0.726747	0.9665	0.630471	0.997	CDS putative long-chain-fatty-acid-CoA ligase 1977106:1978650 forward MW:56368
RPA1767	0.743714	0.959	0.521925	0.9985	0.804603	0.924	0.584774	0.998	0.690464	0.9875	CDS sensor histidine kinase with a PAC motif and a response regulator receiver domain 1978647:1980956 reverse MW:83025
RPA1768	2.122912	0.1255	0.561032	0.9525	2.097278	0.001	0.874599	0.751	1.122031	0.267	CDS hypothetical protein 1981208:1981402 reverse MW:6715
RPA1769	0.691022	0.9035	0.595038	0.993			1.123107	0.2025	0.836943	0.7935	CDS transcriptional regulator, LysR family 1981608:1982498 reverse MW:31727
RPA1770	0.806266	0.903	0.704448	0.996	0.726738	0.903	0.832283	0.925	0.720863	0.9565	CDS conserved hypothetical membrane protein 1982495:1983559 reverse MW:36902
RPA1771	1.370301	0.0095	1.071213	0.343	1.211556	0.0855	1.255614	0.273	1.496408	0.0165	CDS hypothetical protein 1983838:1984620 forward MW:27789
RPA1772	1.181184	0.0525	2.480579	0.001	1.139275	0.1165	3.007599	0.0025	1.535854	0.001	ppc putative phosphoenolpyruvate carboxylase 1984721:1987531 forward MW:104140
RPA1773	1.020739	0.4435	1.242302	0.033			1.480325	0.0105	1.109677	0.159	CDS putative DMT superfamily multidrug-efflux transporter 1987669:1987998 forward MW:11366
RPA1774											CDS OmpA/MotB domain, possible porin 1988407:1989732 forward MW:44811
RPA1775	0.671837	0.989	0.828005	0.9575	0.705425	0.995	0.430202	1	0.311373	1	CDS putative dehydrogenase 1989978:1990892 reverse MW:32539
RPA1776	0.85866	0.961	0.891848	0.8895	0.841576	0.9815	0.681682	0.9865	0.533261	1	CDS possible lipid transfer protein 1991177:1992316 reverse MW:40431
RPA1777	0.891698	0.9015	0.920043	0.7605	0.903168	0.872	0.609819	0.996	0.488992	1	CDS DUF35 1992322:1992735 reverse MW:15397

RPA1778	0.813124	0.983	0.825483	0.935	0.942022	0.79	0.700639	0.9935	0.632598	0.996	CDS putative Glu-tRNA amidotransferase 1993022:1994380 forward MW:47209
RPA1779	0.810256	0.9725	0.955602	0.673	1.014079	0.4475	0.820026	0.9015	0.674384	0.994	CDS conserved hypothetical protein 1994373:1995059 forward MW:24287
RPA1780											CDS Phenylacetic acid degradation-related protein 1995247:1995837 reverse MW:20619
RPA1781	1.507797	0.0115	1.141512	0.124	1.008649	0.465	1.379256	0.0185	1.008213	0.4565	phbH 4-hydroxybenzoate hydroxylase (4-hydroxybenzoate-3-monooxygenase) 1996035:1997207 reverse MW:43046
RPA1782	1.694724	0.0465	0.935426	0.688	1.216789	0.0595	1.43296	0.0265	1.039073	0.321	CDS TrapT family, dctP subunit, C4-dicarboxylate periplasmic binding protein 1997376:1998386 forward MW:37078
RPA1783					1.178389	0.3745			0.394645	0.997	CDS possible TrapT family, dctQ subunit, C4-dicarboxylate transport 1998472:1999125 forward MW:24819
RPA1784	1.294133	0.0945	0.931623	0.7325	0.831099	0.969	1.440871	0.0385	0.82188	0.958	CDS TrapT family, dctM subunit, C4-dicarboxylate transport 1999132:2000439 forward MW:45877
RPA1785	1.22494	0.064	0.942671	0.7175	0.943753	0.6305	0.790255	0.849	0.412237	1	CDS conserved hypothetical protein 2000607:2001068 forward MW:17115
RPA1786	0.94631	0.6975	0.643628	0.991	0.700358	0.993	0.583522	0.987	0.68095	0.999	CDS putative 3-hydroxybutyryl-CoA dehydratase 2001366:2002172 forward MW:28495
RPA1787			0.70602	0.92			0.919718	0.655			fcs2 putative feruloyl-CoA synthetase 2002181:2004079 forward MW:68282
RPA1788	1.198326	0.1165	0.962762	0.6505	0.973528	0.6015	1.167106	0.099	0.958871	0.683	CDS possible 4-hydroxybenzoyl-CoA thioesterase 2004318:2004737 forward MW:15854
RPA1789	1.484827	0.1035	0.772862	0.962	1.394929	0.005	1.211118	0.146	0.86513	0.852	CDS putative branched-chain amino acid transport system substrate-binding protein 2004817:2005974 forward MW:40884
RPA1790	1.389329	0.009	1.459389	0.0045	1.147353	0.058	1.62172	0.003	1.459463	0.0015	CDS putative diguanylate cyclase (GGDEF) 2006289:2007107 forward MW:29328
RPA1791	1.133408	0.221	0.876782	0.9435	1.065618	0.183	0.971076	0.5945	0.805817	0.9695	CDS branched-chain amino acid transport system ATP-binding protein 2007080:2007799 reverse MW:25355
RPA1792	0.983688	0.553	0.800663	0.969	0.975002	0.66	1.00371	0.4975	0.979806	0.5895	CDS putative branched-chain amino acid transport system ATP-binding protein 2007796:2009568 reverse MW:62826
RPA1793	1.022961	0.3865	0.705588	0.997	0.879697	0.93	0.755075	0.937	0.955149	0.6925	CDS branched-chain amino acid transport system permease protein 2009574:2010614 reverse MW:36304
RPA1794	0.923986	0.7195	1.09807	0.2495	1.201	0.1335	1.784095	0.003	1.54284	0.0025	CDS transcriptional regulator, MarR family 2010746:2011297 forward MW:19992
RPA1795	0.853315	0.9285	0.781541	0.9905	0.975217	0.626	0.751445	0.9785	0.75282	0.9815	CDS possible potassium-efflux system protein 2011435:2013261 reverse MW:65118
RPA1796	1.155043	0.0575	0.905654	0.87	0.987763	0.546	1.080587	0.2075	1.066571	0.172	CDS putative Adenylate/Guanylate cyclase 2013917:2015491 forward MW:57886
RPA1797	1.133473	0.099	1.0477	0.2285	0.891602	0.853	0.958679	0.642	0.922498	0.8335	CDS conserved hypothetical protein 2015733:2017013 reverse MW:43763
RPA1799	0.754781	0.9855	0.925803	0.6845	0.998033	0.5075	0.581543	0.989	0.896757	0.9145	ung Uracil-DNA glycosylase:Phage SPO1 DNA polymerase-related protein 2018690:2020177 reverse MW:55537
RPA1800	0.538521	0.9995	0.6194	0.992	0.861695	0.892	0.444056	0.9995	0.849498	0.978	CDS Elongator protein 3/MiaB/NifB 2020274:2021524 reverse MW:46629
RPA1801					0.833035	0.748			0.549196	0.995	CDS conserved hypothetical protein 2021694:2022479 forward MW:28211
RPA1802	0.262207	1	0.32495	0.9995	0.767229	0.973	0.274192	0.9995	0.410666	1	CDS conserved hypothetical protein 2022532:2023968 forward MW:51415
RPA1803			0.599957	0.9815	0.857135	0.93	0.526329	0.9985	0.586501	1	dnaE2 putative DNA polymerase III alpha chain 2024122:2027709 forward MW:133398
RPA1804	1.170883	0.0605	1.249829	0.0545	1.177784	0.039	2.133389	0	3.880637	0	CDS conserved hypothetical protein 2027715:2028668 reverse MW:33811
RPA1805	0.867418	0.866	0.758459	0.972	0.677738	0.98	0.915741	0.7535	0.914194	0.9045	CDS transcriptional regulator, LysR family 2028745:2029695 forward MW:34885
RPA1806	0.940039	0.794	0.941748	0.7245	0.921619	0.7415	0.908267	0.728	0.821795	0.965	CDS L-carnitine dehydratase/bile acid-inducible protein F 2029742:2031139 forward MW:49448
RPA1807	1.006095	0.4635	0.899294	0.8875	0.955247	0.687	0.898962	0.7765	1.091968	0.179	CDS possible heavy metal efflux pump, HlyD family secretion protein 2031359:2032597 forward MW:44742
RPA1808	0.831371	0.885	0.714199	0.9365	0.793747	0.922	0.769947	0.8955	0.742795	0.98	czcA1 putative RND divalent metal cation efflux transporter CzcA 2032754:2035876 forward MW:112520
RPA1809	1.183524	0.218	1.561694	0.0045	1.203086	0.204	1.503014	0.0085	0.819265	0.6655	CDS hypothetical protein 2036076:2036393 forward MW:11563
RPA1810	0.99654	0.5175	0.849176	0.939	1.009892	0.455	1.260396	0.0805	1.303368	0.0505	CDS putative outer membrane protein 2036488:2037930 reverse MW:50757
RPA1811	0.927758	0.6675	0.76199	0.9825	0.897098	0.8365	0.605387	0.9975	0.623161	0.998	CDS enoyl CoA hydratase 2038105:2038884 reverse MW:27791
RPA1812	1.033647	0.3405	1.087383	0.224	1.76784	0.023	0.610692	0.998	0.662866	0.9985	CDS conserved hypothetical protein 2038968:2039705 reverse MW:24472
RPA1813	1.113117	0.1365	1.106726	0.265	2.231439	0.0115	0.426346	0.9985	0.644947	0.9965	CDS RNA polymerase ECF-type sigma factor 2039897:2040505 forward MW:22148
RPA1814			0.760139	0.7665							CDS conserved hypothetical protein 2040502:2041146 forward MW:22334
RPA1815	1.997837	0.003	1.197895	0.0525	1.77647	0.005	1.805386	0.006	2.144633	0.0005	CDS hypothetical protein 2041227:2041607 forward MW:12990
RPA1816	1.139557	0.0605	1.177492	0.356	1.071789	0.2805			1.377768	0.0135	CDS putative outer membrane receptor for iron transport 2041668:2043896 forward MW:80721
RPA1817	1.054165	0.2005	1.231968	0.026	1.01356	0.445	1.211986	0.0545	1.032149	0.324	CDS conserved hypothetical protein 2043919:2045028 reverse MW:40591
RPA1818	1.184223	0.025	1.09326	0.1485	0.953157	0.7	0.962078	0.659	1.08517	0.1415	CDS putative diguanylate cyclase (GGDEF) 2045066:2046355 reverse MW:47926
RPA1819	0.870552	0.825			1.112815	0.2195	1.431568	0.2145	0.999865	0.5205	CDS RNA polymerase ECF-type sigma factor, possible FecI 2046600:2047169 forward MW:21373
RPA1820	0.857436	0.951	1.090608	0.315	1.111292	0.115	1.303269	0.0645	1.168497	0.089	CDS hypothetical protein 2047166:2047999 forward MW:28804
RPA1821	1.285298	0.0045	1.114877	0.148	1.035773	0.3365	1.306294	0.0285	1.33381	0.001	CDS conserved hypothetical protein 2048486:2048995 forward MW:19179
RPA1822	0.651636	0.9835	0.679548	0.973	0.981105	0.5655	0.909966	0.688	0.865402	0.851	CDS methyl-accepting chemotaxis receptor/sensory transducer 2049434:2051500 forward MW:72869
RPA1823	0.890024	0.815	0.852179	0.9265	0.553792	0.987	0.849656	0.9075	0.641771	0.9975	CDS TonB dependent receptor 2051982:2054615 forward MW:94990
RPA1824	0.841005	0.919	0.878853	0.8375	1.009305	0.4765	0.870639	0.9225	0.81919	0.973	CDS unknown protein 2054711:2055226 forward MW:17579
RPA1825	0.949998	0.704	1.001899	0.498	1.034266	0.4055	1.193384	0.1645	1.206265	0.0285	CDS conserved hypothetical protein 2055318:2055557 reverse MW:8920
RPA1826	1.060922	0.201	0.827917	0.99	0.858735	0.8965	0.742869	0.974	0.849233	0.941	CDS conserved hypothetical protein 2055690:2057048 reverse MW:46556
RPA1827	0.924671	0.6615	1.12952	0.388	0.767114	0.8465	2.807741	0.105	1.915583	0.054	CDS hypothetical protein 2057154:2057414 reverse MW:9757
RPA1828	0.827898	0.903	0.974137	0.616	0.939676	0.727	0.953588	0.718	0.842061	0.976	CDS Pyrrolidone-carboxylate/pyroglutamyl peptidase I (C15) 2057481:2058131 reverse MW:23817
RPA1829	0.665555	0.996	0.70431	0.9965	0.503716	0.9995	0.588042	0.9975	0.600514	0.9995	argK LAO/AO transport system kinase 2058128:2059117 reverse MW:35000
RPA1830	0.270068	0.999	0.5133	0.997	0.256044	1	0.436281	0.992	0.102438	1	CDS hypothetical protein 2059204:2059533 reverse MW:11978
RPA1831	0.177706	1	0.49382	0.9965	0.237928	1	0.47736	0.9975	0.083958	1	CDS conserved hypothetical protein 2059524:2059796 reverse MW:9551
RPA1832	0.89911	0.8915	0.802748	0.991	0.735153	0.994	0.728752	0.9805	0.908888	0.8135	CDS unknown protein 2059995:2060753 reverse MW:27520
RPA1833	0.998974	0.5035	1.071986	0.145	0.869075	0.921	1.203296	0.0325	0.904782	0.9065	CDS PilT protein, N-terminal 2060841:2061242 reverse MW:14987
RPA1834	1.539012	0.0085	1.302735	0.028	1.184104	0.037	2.160136	0	1.478809	0.0045	CDS hypothetical protein 2061248:2061505 reverse MW:9585
RPA1835	1.001586	0.491	0.881142	0.917	0.942146	0.7205	0.881854	0.8425	0.835153	0.9075	mutB methylmalonyl-CoA mutase, subunit alpha, N-terminus 2061569:2063728 reverse MW:78104
RPA1836	1.126035	0.169	0.964528	0.6295	0.89804	0.874	0.89441	0.8155	1.001864	0.487	CDS DUF636 2063791:2064255 reverse MW:16687
RPA1837	0.9357	0.776	0.78015	0.972	0.906541	0.8185	0.808301	0.8905	0.820651	0.9485	CDS possible methylmalonyl-CoA small subunit 2064252:2066123 reverse MW:65276
RPA1838	0.872548	0.767			0.86049	0.86			0.735799	0.9675	folK putative 2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase 2066281:2066772 reverse MW:18017
RPA1839									0.660421	0.7755	folB putative dihydroneopterin aldolase 2066774:2067139 reverse MW:13209
RPA1840	0.850769	0.872	0.944655	0.6375	1.024952	0.4565	0.896409	0.639	0.722578	0.972	folP dihydropteroate synthase 2067136:2067993 reverse MW:29872
RPA1841	1.163518	0.2655	0.828646	0.7895	1.106913	0.126	1.078	0.3605	1.128887	0.1405	CDS conserved unknown protein 2068059:2068466 reverse MW:14836
RPA1842	1.293371	0.177	0.765207	0.991	1.5705	0.0055	1.270363	0.051	1.157808	0.1925	CDS conserved unknown protein 2068484:2068852 reverse MW:12571
RPA1843	0.943322	0.8025	0.773702	0.991	0.987859	0.569	0.754793	0.992	0.875314	0.9495	CDS conserved unknown protein 2069189:2070799 forward MW:57304
RPA1844	0.758158	0.992	0.820807	0.978	0.739677	0.992	0.617132	0.9955	0.647828	0.9935	CDS putative peptidase 2071008:2072414 forward MW:50332
RPA1845	1.351207	0.0175	2.700903	0.0005	1.079866	0.242	2.034825	0.042	1.714202	0.0025	CDS putative tonB-dependent receptor protein 2072749:2075049 forward MW:81582
RPA1846	1.396381	0.0295	2.147915	0.006	1.342728	0.0055	1.372556	0.0985	1.48738	0.019	CDS unknown protein 2075163:2075897 forward MW:26087
RPA1847									0.896725	0.5465	CDS conserved hypothetical protein 2075894:2076175 forward MW:9430
RPA1848	1.297445	0.046	2.417675	0.004	1.426773	0.051	1.369658	0.2365	1.412703	0.066	CDS Uncharacterized iron-regulated membrane protein DUF337 2076237:2077811 forward MW:58431
RPA1849	1.40139	0.029	2.673419	0.0025	1.337864	0.0665			1.367716	0.2795	CDS conserved hypothetical protein 2077808:2078095 forward MW:10153
RPA1850	0.848374	0.9855	0.929516	0.8485	0.889878	0.9045	0.835284	0.9685	0.842488	0.9685	CDS methyl-accepting chemotaxis receptor/sensory transducer 2078135:2080132 reverse MW:71547
RPA1851	1.74661	0.02	1.29586	0.0745	2.03776	0.0005	1.616215	0.009	1.1451	0.2035	CDS putative aldolase 2080588:2081661 reverse MW:39645
RPA1852	0.781205	0.857	1.26104	0.011	0.704954	0.955	0.813206	0.7745	0.805034	0.944	mucR putative transcriptional regulator MucR 2082702:2083118 forward MW:15466
RPA1853	0.723238	0.9945	0.776256	0.9705	0.666979	0.9975	0.806676	0.954	0.873102	0.9585	CDS putative short-chain dehydrogenase 2083126:2083866 reverse MW:24773
RPA1854	0.983055	0.59	0.97269	0.6505	0.952978	0.7505	1.140054	0.1015	1.458579	0.001	CDS possible transcriptional regulator, TetR family 2083944:2084579 forward MW:22643
RPA1855	0.421465	0.996	0.394656	0.995	0.969617	0.596	0.332705	1	0.695162	0.989	CDS conserved hypothetical protein 2084701:2085312 forward MW:22282

RPA1856	1.090723	0.1545	1.238202	0.0135	0.981212	0.569	1.737521	0.0055	1.74483	0.002	CDS Protein of unknown function UPF0050 2085342:2085770 reverse MW:15979
RPA1857									1.012958	0.4845	CDS conserved hypothetical protein 2085886:2086308 reverse MW:14855
RPA1858	1.053745	0.3295	1.082851	0.2055	0.779512	0.9845	1.037903	0.3595	0.906118	0.816	CDS sensor histidine kinase with a PAS domain 2086715:2088547 forward MW:65197
RPA1859	0.923208	0.751	0.864163	0.835	0.719353	0.9745	0.773847	0.9765	0.634555	0.995	CDS conserved hypothetical protein 2088540:2089325 forward MW:27658
RPA1860	1.036822	0.44	1.411842	0.063			1.395208	0.0295	0.929234	0.74	CDS conserved unknown protein 2089478:2089819 forward MW:12651
RPA1861	0.998869	0.4995	0.765708	0.9895	0.763922	0.934	0.899235	0.731	1.141891	0.08	CDS hypothetical protein 2089994:2090968 reverse MW:35719
RPA1862	0.954474	0.723	0.788557	0.9935	0.766307	0.9845	0.661909	0.9685	0.62257	0.9995	CDS possible polysaccharide deacetylase 2091120:2092193 reverse MW:37669
RPA1863	1.493637	0.001	1.466858	0.0025	1.77977	0	2.136063	0.001	2.708015	0	CDS conserved hypothetical protein 2092273:2092803 reverse MW:19030
RPA1864	0.942138	0.678	1.137226	0.192	0.690768	0.992	1.151739	0.387	0.953816	0.665	CDS hypothetical protein 2093201:2093983 forward MW:28896
RPA1865	0.990874	0.548	0.927733	0.798	0.850959	0.8875	0.658331	0.963	0.814998	0.9715	CDS conserved hypothetical protein 2093990:2094556 reverse MW:19942
RPA1866	0.771093	0.9735	0.838189	0.973	0.819625	0.9605	0.585154	0.9975	0.723547	0.991	CDS conserved hypothetical protein 2094553:2095131 reverse MW:20554
RPA1867	0.90536	0.9175	0.899978	0.901	1.03177	0.328	0.71872	0.9965	0.935638	0.754	CDS putative penicillin-binding protein 2095175:2097448 reverse MW:82594
RPA1868	0.814879	0.881			0.662384	0.9765	0.612342	0.9345	0.670445	0.9715	CDS conserved hypothetical protein 2097623:2098231 forward MW:22836
RPA1869	0.75587	0.962	1.091602	0.1935	0.809336	0.974	0.839746	0.9105	0.657475	0.9915	CDS DUF81 2098286:2099029 forward MW:25454
RPA1870	1.282664	0.017	0.986969	0.557	1.115164	0.138	1.43433	0.0095	1.259201	0.018	CDS possible transcriptional regulator, MarR/EmrR family 2099324:2099839 reverse MW:18548
RPA1871	1.086932	0.333	0.735611	0.9635	1.023797	0.4015	0.748376	0.892	0.707985	0.881	CDS putative cytochrome P450 2099919:2101157 forward MW:44623
RPA1872											thcC Rhodocoxin 2101167:2101487 forward MW:11168
RPA1873	0.988832	0.526	1.042849	0.328	1.272978	0.068	0.954086	0.623	1.022615	0.4405	CDS possible urea/short-chain binding protein of ABC transporter 2101563:2102777 forward MW:42896
RPA1874	0.891592	0.7515	1.970938	0.009	1.051364	0.395			0.586824	0.987	CDS hypothetical protein 2102977:2103183 reverse MW:7297
RPA1875	0.886003	0.9195	1.227588	0.0255	1.087016	0.1405	0.640687	0.9705	0.630559	0.9975	CDS possible uncharacterized iron-regulated membrane protein 2103180:2104325 reverse MW:42268
RPA1876	0.913212	0.6475	2.390578	0.002	0.761811	0.9705	0.546414	0.8905	0.640088	0.9295	CDS putative TonB-dependent iron siderophore receptor 2104322:2106625 reverse MW:83366
RPA1877	0.874223	0.9615	1.212926	0.0135	1.347299	0.0275	1.139408	0.12	1.150474	0.114	CDS conserved hypothetical protein 2107191:2108096 forward MW:32646
RPA1878	1.092612	0.226	1.482859	0.0025	1.260367	0.087	1.957204	0.001	2.694058	0.0005	CDS putative 6-aminohexanoate-dimer hydrolase 2108394:2109569 reverse MW:42815
RPA1879	1.355751	0.038	1.088066	0.177	1.601814	0.005	1.113193	0.1865	1.503796	0.0035	CDS Choloylglycine hydrolase 2109685:2110752 reverse MW:38585
RPA1880	0.886947	0.906	1.073195	0.316	1.547412	0.0025	1.003921	0.4955	0.824415	0.9005	CDS putative membrane transport protein-major facilitator superfamily 2110908:2112551 forward MW:57935
RPA1881	1.2632	0.007	0.990326	0.5325	1.207246	0.0135	1.004996	0.469	1.275102	0.005	CDS hypothetical protein 2112675:2114075 forward MW:49950
RPA1882	1.351886	0.0105	1.568791	0.0065	1.092967	0.2745	1.388404	0.1225	1.042097	0.3695	CDS Flp/Fap pilin component 2114160:2114351 forward MW:6775
RPA1883	1.146626	0.088	1.018088	0.444	0.742788	0.977	0.786765	0.961	0.994404	0.5195	CDS hypothetical protein 2114647:2116200 forward MW:54757
RPA1884	0.6463	0.9905	0.60081	0.999	0.907854	0.7835	0.380906	1	0.95134	0.7135	CDS methyl-accepting chemotaxis receptor/sensory transducer 2116794:2118473 forward MW:60570
RPA1885	0.310718	0.998	0.221779	1	0.876228	0.772	0.087418	1	0.962241	0.6765	CDS putative portal protein, R. capsulatus GTA orfg3 homologue 2118601:2119788 forward MW:42991
RPA1886	1.662023	0.005	2.287584	0.001	2.057207	0	2.180238	0.0015	1.964572	0.004	CDS hypothetical protein 2119814:2120014 forward MW:7730
RPA1887	0.244467	1			0.816798	0.8185			0.742788	0.9945	CDS possible phage protease, R. capsulatus GTA orfg4 homologue 2120319:2120996 forward MW:24376
RPA1888	0.350904	0.998	0.260823	0.999	0.871449	0.815	0.122758	1	0.7988	0.9715	CDS putative major capsid protein, R. capsulatus GTA orfg5 homologue 2121168:2122421 forward MW:44524
RPA1889	0.586266	0.999	0.367066	0.9375	0.968042	0.595			0.893948	0.6585	CDS hypothetical protein 2122753:2123124 forward MW:13653
RPA1890	1.184099	0.059	1.683852	0.0015	1.111252	0.215	1.374827	0.0565	2.049675	0.012	CDS hypothetical protein 2123340:2126441 reverse MW:115123
RPA1891					0.848802	0.908	0.203706	0.998	0.631908	0.9995	CDS conserved hypothetical protein 2127296:2128252 forward MW:34878
RPA1892	0.400398	0.9665			0.834529	0.924	0.18277	1	0.595133	0.9915	CDS probable large terminase, Rhodobacter capsulatus GTA orfg2 homologue 2128329:2129489 forward MW:42051
RPA1893	0.994735	0.514	1.236765	0.0255	1.037115	0.3915	0.707328	0.991	0.963976	0.676	CDS hypothetical protein 2129587:2129865 forward MW:9780
RPA1894	0.609324	0.999	0.458155	0.9965	0.785017	0.9265	0.311691	1	0.7571	0.9905	CDS hypothetical protein 2129885:2130196 reverse MW:11570
RPA1895	1.384118	0.025			1.336137	0.0455			1.475105	0.0265	CDS possible peptidase 2130278:2130982 reverse MW:23439
RPA1896	0.427986	0.9865			0.747049	0.9425			0.765218	0.9825	GTA orfg6 homologue of Rhodobacter capsulatus gene transfer agent (GTA) orfg6 (21% idenity) 2131110:2131670 forward MW:19843
RPA1897	0.729568	0.987	0.895581	0.7055	0.956233	0.6275	0.887673	0.608	0.778062	0.9725	GTA orfg7 homologue of Rhodobacter capsulatus gene transfer agent (GTA) orfg7 2131667:2131987 forward MW:11420
RPA1898	0.382079	0.9945			0.825314	0.9385			0.779297	0.8295	GTA orfg8 homologue of Rhodobacter capsulatus gene transfer agent (GTA) orfg8 (32% identity) 2131984:2132394 forward MW:14681
RPA1899	0.497113	0.9995	0.497896	1	0.853205	0.9055	0.329213	1	0.826708	0.9845	GTA orfg9 homologue of Rhodobacter capsulatus gene transfer agent (GTA) orfg9 (56% identity) 2132407:2132814 forward MW:14269
RPA1900											GTA orfg10 homologue of Rhodobacter capsulatus gene transfer agent (GTA) orfg10 2132824:2133141 forward MW:10586
RPA1901	0.839118	0.924	0.736743	0.6125	0.938015	0.75			0.997507	0.4925	GTA orfg10.1 homologue of Rhodobacter capsulatus gene transfer agent (GTA) orfg10.1; translated by translational frameshift with GTA orfg10 2133135:2133326 forward MW:6903
RPA1902					0.832569	0.943			0.610385	0.9955	GTA orfg11 homologue of Rhodobacter capsulatus gene transfer agent (GTA) orfg11 2133338:2133931 forward MW:19811
RPA1903	3.356039	0.0015	2.985094	0.002	2.674552	0	4.135309	0	4.240538	0.0005	GTA orfg12 homologue of Rhodobacter capsulatus gene transfer agent (GTA) orfg12 2134093:2134731 forward MW:22521
RPA1904	1.280492	0.025	1.152024	0.107	1.259787	0.0245	1.13411	0.167	1.55009	0.005	CDS DUF262 2134844:2136670 forward MW:69374
RPA1905											GTA orfg13 homologue of Rhodobacter capsulatus gene transfer agent (GTA) orfg13 (37% identity) 2136963:2137874 forward MW:31856
RPA1906					0.72759	0.8665	0.256512	0.99	0.55619	0.952	GTA ofrg14 homologue of Rhodobacter capsulatus gene transfer agent (GTA) orfg14 2137914:2138366 forward MW:16236
RPA1907	0.940035	0.784	0.654281	0.9985	0.981418	0.557	0.571685	0.997	0.71016	0.9895	CDS putative protein 2138431:2138856 forward MW:15687
RPA1908	1.770231	0.092	2.47578	0.0075	1.011689	0.448	1.594058	0.036	1.243977	0.0205	CDS hypothetical protein 2138895:2139362 reverse MW:16763
RPA1909	0.767105	0.956	0.928823	0.6335	0.812003	0.9245	1.058334	0.3605	1.641931	0.0045	CDS transcriptional regulator, MarR family 2139516:2139989 forward MW:17123
RPA1910	0.864386	0.6885			0.837535	0.7065	0.462263	0.9975	0.918324	0.6555	CDS conserved hypothetical protein 2139991:2140443 forward MW:15922
RPA1911			0.530784	0.9745	0.852209	0.867	0.491038	0.9895	1.171484	0.242	CDS Nickel-dependent hydrogenase b-type cytochrome subunit 2140469:2141014 forward MW:19752
RPA1912	0.16191	0.9975			0.773601	0.9595			0.71748	0.82	CDS homologue of Rhodobacter capsulatus gene transfer agent (GTA) orfg15 2141169:2145041 forward MW:135879
RPA1913	0.995503	0.5275	0.836786	0.953	0.972641	0.591	1.284621	0.0195	0.848153	0.9375	CDS conserved hypothetical protein 2145051:2146418 forward MW:47204
RPA1914	0.72172	0.981			0.878305	0.823			0.741525	0.895	CDS possible glycohydrolase 2146542:2147303 forward MW:27307
RPA1915	0.734605	0.9885	0.755278	0.981	0.823199	0.9445	0.735037	0.963	0.894557	0.907	feuP two-component transcriptional regulator FeuP, winged helix family 2147990:2148664 forward MW:24990
RPA1916	0.775545	0.9935	0.898702	0.833	0.923689	0.8595	0.807143	0.974	1.057826	0.2	feuQ two-component sensor histidine kinase, FeuQ 2148680:2150071 forward MW:50603
RPA1917	0.765568	0.9815	0.743486	0.97	0.931615	0.797	0.574148	0.993	0.66403	0.999	lipA1 LipA a lipoprotein 2150168:2150632 forward MW:15832
RPA1918	0.790231	0.9945	0.793972	0.967	0.843424	0.9695	0.750891	0.981	0.921545	0.8385	CDS unknown protein 2150801:2152258 forward MW:54004
RPA1919	0.817966	0.959	0.992293	0.548	0.905008	0.843	0.880906	0.9	0.811892	0.946	cycH cytochrome c-type biogenesis protein cycH 2152421:2153527 forward MW:39211
RPA1920	0.786537	0.964	0.973152	0.619	0.933338	0.7635	0.703808	0.9875	0.75511	0.9895	cycJ CycJ cytochrome-c biosynthesis protein 2153641:2154144 forward MW:17836
RPA1921	0.955064	0.623	0.79036	0.9705	1.024644	0.4585	0.58878	0.992	0.656736	0.9945	cycK CycK cytochrome c-type synthesis protein 2154141:2156123 forward MW:71040
RPA1922	1.144619	0.0915	1.09131	0.1435	1.01822	0.417	0.860071	0.8955	0.95849	0.665	cycL CycL cytochrome C-type biogenesis protein 2156125:2156634 forward MW:18876
RPA1923	0.958744	0.666	1.028244	0.3935	0.923924	0.811	0.896318	0.8025	1.33873	0.002	aimE aliphatic amidase 2156945:2157967 reverse MW:38253
RPA1924											CDS Cobalamin synthesis protein/P47K 2158087:2158764 reverse MW:25602
RPA1925	1.269761	0.0155	1.272876	0.0055	1.171508	0.045	1.465055	0.0035	1.207774	0.0315	CDS putative transmembrane protein 2159007:2160473 reverse MW:50524
RPA1926	1.655488	0.011	1.361727	0.004	1.304061	0.048	2.561044	0.0005	3.403181	0.0005	CDS possible transcriptional regulator, XRE family 2160548:2161399 forward MW:32479
RPA1927	88.93854	0	46.46757	0	52.14828	0	143.582	0	117.46	0	CDS hypothetical protein 2161591:2162175 reverse MW:21488
RPA1928	91.10034	0	59.15753	0	29.33864	0	113.0707	0	101.8076	0	CDS ferredoxin-like protein [2Fe-2S] 2162133:2163041 reverse MW:33018
RPA1929	0.953614	0.7045	0.74709	0.934	1.008968	0.4755	1.023994	0.4395	1.325345	0.009	CDS htrA-like serine protease 2163410:2164981 forward MW:53823
RPA1930	1.071134	0.2865	0.930875	0.7245	1.56146	0.0065	1.302483	0.0595	1.752145	0.005	CDS two-component transcriptional regulator, winged helix family 2165214:2165939 forward MW:27227
RPA1931	1.143999	0.22	1.252111	0.044	0.981199	0.546	1.412967	0.108	1.414986	0.1225	CDS methyl-accepting chemotaxis receptor/sensory transducer 2166162:2167460 forward MW:46554
RPA1932	1.051002	0.3165	0.890618	0.9115	0.920268	0.797	0.926496	0.7185	1.061726	0.2295	CDS sensor histidine kinase 2167673:2169121 forward MW:52145

RPA1933	0.990367	0.544	0.785485	0.9905	0.951445	0.6795	0.711004	0.9835	0.832229	0.954	glnE putative glutamate-ammonia-ligase adenylyltransferase 2169118:2172090 forward MW:109349
RPA1934	1.566737	0.023	2.646805	0.001	1.102479	0.185	1.794308	0.1345	1.230681	0.087	CDS hypothetical protein 2172149:2172400 reverse MW:8701
RPA1935	0.957793	0.751	0.949174	0.653	1.016905	0.415	0.916275	0.8015	0.925798	0.753	CDS possible transcriptional regulator, AraC family 2172501:2173523 reverse MW:37152
RPA1936	1.232005	0.2775	0.723566	0.896			0.886848	0.6845	0.978188	0.5325	CDS possible serine protease/outer membrane autotransporter 2173925:2177401 forward MW:119867
RPA1938	0.923347	0.8195	0.663031	0.9965	0.635423	0.9865	0.685102	0.9915	0.70174	0.998	CDS sensor histidine kinase, possible pleC 2178903:2181242 reverse MW:85848
RPA1939	0.919401	0.8765	0.939928	0.791	0.698586	0.988	0.74687	0.984	1.076416	0.2255	CDS possible cation efflux protein 2181428:2182810 reverse MW:49453
RPA1940	0.960522	0.759	0.925156	0.883	1.024229	0.3655	0.852347	0.9395	0.648911	0.9985	CDS putative quinone oxidoreductase 2182941:2183909 reverse MW:33691
RPA1941	0.923891	0.8335	0.692038	0.992	0.974553	0.5515	0.679052	0.964	0.547697	0.9965	CDS possible 2-nitropropane dioxygenase 2183952:2184950 reverse MW:35592
RPA1942	1.140218	0.0555	0.958086	0.67	0.929851	0.8115	0.706954	0.987	0.739961	0.9875	CDS putative 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase 2185188:2185973 reverse MW:27828
RPA1943	1.181942	0.0655	0.919872	0.794	0.956769	0.684	0.621338	0.991	0.72474	0.994	panE putative ketopantoate reductase 2186129:2187121 reverse MW:35769
RPA1944	1.941606	0.0375	0.869773	0.875	1.608692	0.0095	0.87097	0.8005	0.959453	0.621	oxlT possible oxalate/formate antiporter 2187210:2188550 reverse MW:48364
RPA1945	1.182253	0.0765	1.021868	0.4155	0.971926	0.61	0.987139	0.541	1.088255	0.133	CDS putative acyl-CoA transferase 2188671:2189996 reverse MW:48355
RPA1946	0.958801	0.665	0.937918	0.76	0.72026	0.9945	0.972259	0.5795	0.996122	0.5255	CDS possible transcriptional regulator, GntR family 2190065:2191039 reverse MW:36772
RPA1947	1.418891	0.247	0.624922	0.9625	1.927694	0.001	0.748044	0.91	0.478655	0.991	pqqB pyrroloquinoline quinone biosynthesis protein B 2191349:2192275 forward MW:32195
RPA1948	0.869663	0.597	0.548883	0.9875	1.06519	0.312	0.661296	0.9685	0.421996	0.997	pqqC pyrroloquinoline quinone biosynthesis protein C 2192272:2193036 forward MW:28618
RPA1949	0.90581	0.709	0.730616	0.9925	0.969893	0.632	0.693033	0.981	0.649733	0.9995	pqqD pyrroloquinoline quinone biosynthesis protein D 2193041:2193349 forward MW:11303
RPA1950	1.031605	0.4435	0.742347	0.8715	1.340343	0.055	0.799401	0.9165	0.494622	0.9565	pqqE putative pyrroloquinoline quinone biosynthesis protein E 2193391:2194524 forward MW:40890
RPA1951											CDS possible FusE-MFP/HlyD family membrane fusion protein 2194774:2195664 reverse MW:32272
RPA1952	1.086146	0.195	1.105991	0.114	1.125959	0.097	1.206377	0.0325	1.330957	0.0115	CDS conserved hypothetical membrane protein 2195661:2195870 reverse MW:7724
RPA1953	1.146628	0.2635							0.933956	0.6985	CDS possible FusB/FusC Fusaric Acid resistance pump 2195870:2197882 reverse MW:71846
RPA1954											CDS probable transcriptional regulator, TetR family 2198048:2198734 forward MW:25460
RPA1955	1.042982	0.385	0.769727	0.951	0.807188	0.933	0.78626	0.976	0.884434	0.886	CDS glutathione dependent formaldehyde dehydrogenase 2198871:2199980 reverse MW:39631
RPA1957	1.12351	0.236	1.085038	0.1475	1.252344	0.03	1.150063	0.095	1.531786	0.0025	CDS alkanal monooxygenase (LuxA-like protein) 2201728:2202744 reverse MW:37373
RPA1959	0.864832	0.893	1.218228	0.0275	0.914001	0.7435	1.429648	0.0075	2.089484	0	CDS putative RND efflux membrane protein 2203559:2204647 forward MW:38155
RPA1960	0.860346	0.904	0.886792	0.913	0.788206	0.9725	0.585964	0.997	0.847796	0.92	CDS putative RND efflux membrane protein 2204644:2205717 forward MW:37685
RPA1961	1.047057	0.357	0.889061	0.7925	0.870545	0.954	0.722826	0.8905	0.811677	0.949	CDS RND efflux transporter 2205714:2208764 forward MW:110782
RPA1962	0.826981	0.902	0.995815	0.496	0.824797	0.9485	0.807781	0.874	0.907264	0.866	CDS unknown protein 2208766:2209047 forward MW:10544
RPA1963	0.735501	0.991	0.87664	0.8415	0.820059	0.9075	0.611018	0.9955	0.818075	0.9145	CDS Patatin-like phospholipase domain 2209076:2210269 forward MW:43247
RPA1964	0.543029	0.998	0.745423	0.995	0.566211	0.997	0.575663	0.997	0.545299	0.9855	CDS hypothetical protein 2210328:2210885 forward MW:19829
RPA1965	0.981784	0.5575	1.107194	0.0725	0.899889	0.8385	1.1098	0.1595	0.946754	0.7785	CDS putative Adenylate/Guanylate cyclase 2210911:2212899 reverse MW:72626
RPA1966	0.90296	0.8765	0.713222	0.9855	0.957781	0.6045	0.928886	0.6755	1.090706	0.154	CDS probable transcriptional regulator, TetR family 2213166:2213798 reverse MW:22774
RPA1967	0.815328	0.988	0.865654	0.965	0.753467	0.988	0.717158	0.9945	0.743313	0.994	CDS putative component of multidrug efflux system 2213962:2215077 forward MW:39782
RPA1968											CDS RND efflux transporter 2215077:2218232 forward MW:114010
RPA1969	1.065665	0.332	0.715114	0.9585	0.908623	0.7475	0.882268	0.795	1.059206	0.343	yjbN NifR3/Smm1 family protein 2218343:2219338 forward MW:36248
RPA1970	0.980989	0.5905	1.052573	0.3195	0.995479	0.524	1.19279	0.089	1.28005	0.013	CDS conserved hypothetical protein 2219352:2219888 reverse MW:18657
RPA1971	1.16718	0.158	1.169474	0.234	0.850457	0.917	1.196744	0.274	1.095818	0.2575	CDS hypothetical protein 2219911:2220183 reverse MW:9748
RPA1972	1.146201	0.0175	1.060254	0.171	0.974189	0.6555	0.918825	0.8555	1.081858	0.1725	CDS sensor histidine kinase 2220180:2221778 reverse MW:57793
RPA1973	0.922473	0.7235	0.75087	0.986	0.945121	0.7275	0.741539	0.973	0.580968	0.9995	CDS 3-hydroxyisobutyrate dehydrogenase 2221944:2222813 reverse MW:30320
RPA1974	1.040382	0.3725	0.904547	0.835	0.853885	0.912	0.798083	0.886	0.765098	0.983	CDS MRP protein(ATP/GTP-binding protein) homolog 2223122:2224234 forward MW:38670
RPA1975	1.211503	0.04	1.010781	0.4385	1.155339	0.144	1.057135	0.3375	0.973353	0.6295	CDS periplasmic mannitol-binding protein, SmoM; possible Trap-T transport system, dctP subunit 2224485:2225576 forward MW:40120
RPA1976	1.268715	0.015	1.062447	0.2915	1.076032	0.3195	0.836511	0.9735	1.202258	0.0205	CDS possible TrapT family, dctM subunit, glutamate transport 2225766:2227607 reverse MW:66137
RPA1977	1.888004	0	1.771414	0.0025	1.76861	0	1.199665	0.0525	1.659835	0	CDS possible TrapT family, dctQ subunit, glutamate transport 2227645:2228241 reverse MW:22150
RPA1978	1.140535	0.2525	0.846871	0.9485	1.058576	0.3135	0.770765	0.985	1.040537	0.31	moaA molybdenum biosynthetic protein A 2228415:2229449 reverse MW:37860
RPA1979	1.308498	0.004	1.193844	0.038	1.188761	0.1285	1.209327	0.0705	1.288617	0.035	CDS unknown protein 2229556:2230005 reverse MW:15140
RPA1980	0.954037	0.6785	1.304764	0.052	0.985534	0.5735	0.864032	0.914	0.832969	0.9665	cbbZ phosphoglycolate phosphatase 2230169:2230846 reverse MW:24193
RPA1981	0.962308	0.6475	1.025967	0.3665	0.922404	0.8035	0.706067	0.995	0.932841	0.7325	cbbI, rpiA, ppi ribose 5-phosphate isomerase 2230997:2231695 forward MW:24676
RPA1982	0.93982	0.6815	1.061217	0.231	0.973019	0.5945	0.665557	0.997	0.806114	0.889	CDS conserved unknown protein 2231692:2232231 forward MW:19915
RPA1983	0.919667	0.7525	1.056536	0.1945	1.000997	0.492	0.657039	0.996	0.794297	0.971	gor putative glutathione reductase 2232249:2233634 forward MW:49426
RPA1984	0.902299	0.938	0.957286	0.7175	0.841414	0.971	0.987844	0.54	0.995208	0.5285	aroG2 2-dehydro-3-deoxyphosphoheptonate aldolase 2233823:2235211 forward MW:50463
RPA1985	1.065882	0.181	0.8833	0.904	0.884439	0.8535	0.828252	0.842	0.659787	0.991	CDS probable diacylglycerol kinase 2235342:2235695 forward MW:12811
RPA1986	1.14547	0.051	0.959656	0.7215	0.888064	0.894	0.984214	0.5915	1.090915	0.115	nadE NH3-dependent NAD synthetase 2235739:2237493 forward MW:62867
RPA1987	0.729547	0.9945	0.783668	0.9835	0.762913	0.961	0.731978	0.9785	0.683553	0.9975	CDS hypothetical protein 2237747:2238076 reverse MW:12041
RPA1988	0.854197	0.981	0.61586	0.9995	0.824875	0.9475	0.50181	0.9995	0.968006	0.638	CDS probable transcriptional regulator, AraC family 2238302:2239309 reverse MW:36821
RPA1989											CDS hypothetical protein 2239874:2240200 forward MW:11950
RPA1990	0.840704	0.9155	0.858374	0.915	0.841689	0.929	0.845568	0.8845	0.800382	0.989	CDS possible sulfatase 2240367:2242157 forward MW:66473
RPA1991	0.949271	0.787	0.649646	0.999	0.802294	0.981	0.67923	0.9945	0.914293	0.823	CDS conserved hypothetical protein 2242169:2243230 forward MW:37085
RPA1992	1.087206	0.1365	0.844177	0.9255	1.028182	0.383	0.938112	0.7055	1.088364	0.1655	CDS possible NtrR protein 2243485:2243895 reverse MW:15136
RPA1993	1.528052	0.051	1.032754	0.4035	1.056308	0.402	1.365526	0.109	0.981734	0.536	CDS possible virulence-associated protein 2243892:2244155 reverse MW:9921
RPA1994	1.454675	0.0425	0.930833	0.8275	1.686774	0.003	1.066327	0.329	0.996837	0.494	CDS conserved unknown protein 2244336:2244761 forward MW:14423
RPA1995	0.790937	0.9945	0.965758	0.7045	0.839339	0.924	0.73827	0.983	0.868533	0.9445	CDS conserved hypothetical protein 2244858:2246027 reverse MW:41116
RPA1996	0.852611	0.936	0.966014	0.642	0.821535	0.9405	0.796757	0.962	0.871559	0.963	CDS hypothetical protein 2246213:2246521 reverse MW:10619
RPA1997	0.804155	0.968	0.897654	0.8485	0.719262	0.99	0.756425	0.9635	0.883206	0.744	cysS cysteine-tRNA ligase 2246922:2248313 forward MW:51727
RPA1998	0.695529	0.983	0.840197	0.98	0.759308	0.9905	0.751812	0.987	0.739789	0.959	CDS hypothetical protein 2248843:2248974 forward MW:4920
RPA1999	0.641229	0.9855	0.744377	0.9165	0.721642	0.9765	0.688451	0.99	0.6561	0.9475	CDS GCN5-related N-acetyltransferase:Aminotransferase, class-II 2248971:2249474 forward MW:17622
RPA2000	0.705905	0.9985	0.669769	0.9945	0.65695	0.9915	0.642759	0.988	0.634828	0.97	leuA putative isopropyl malate synthase 2249471:2251069 forward MW:58014
RPA2001	1.033263	0.461			0.989222	0.5205			0.547361	0.98	CDS putative acetolactate synthase large subunit 2251263:2252807 forward MW:53370
RPA2002	0.954273	0.737	0.769898	0.984	0.961421	0.713	0.735692	0.994	0.636688	0.993	CDS FAD linked oxidase, C-terminal:FAD linked oxidase, N-terminal 2252819:2254228 forward MW:50636
RPA2003	0.630599	0.9615	1.06038	0.2355	0.814329	0.78	0.682964	0.965	0.345642	0.9845	CDS probable cytochrome c precursor 2254253:2256322 reverse MW:73887
RPA2004	0.643261	0.9975	0.8183	0.879	0.693609	0.9985	0.545522	0.9995	0.647345	0.997	CDS conserved hypothetical protein 2256505:2257140 reverse MW:22456
RPA2005	0.587396	0.998	0.622349	0.999	0.694399	0.9965	0.510348	0.999	0.449912	1	CDS ABC transporter, fused ATPase and permease domain 2257299:2259254 forward MW:72099
RPA2006	0.775893	0.987	0.890179	0.942	0.776179	0.996	0.748869	0.994	0.884619	0.914	psd putative phosphatidylserine decarboxylase 2259270:2260001 forward MW:26640
RPA2007	0.856137	0.9145	0.812628	0.9375	1.069729	0.1725	0.668479	0.9915	0.932334	0.7955	pssA possible phosphatidylserine synthase 2260031:2260945 forward MW:32769
RPA2008	0.881798	0.9575	0.828978	0.9535	0.874896	0.927	0.696553	0.9825	0.622381	0.9965	CDS conserved unknown protein 2261081:2261800 forward MW:25017
RPA2009	0.971172	0.688	1.133876	0.1575	0.810892	0.9825	0.831507	0.7995	0.869428	0.956	CDS possible chemotaxis protein motA 2262032:2262805 forward MW:28083
RPA2010											motB1 putative chemotaxis protein motB1 2262836:2263660 forward MW:30184
RPA2011	1.119035	0.2585			1.186721	0.1465			0.830839	0.8005	CDS puative potassium uptake protein Kup 2263810:2265765 forward MW:70151
RPA2012	1.281168	0.01	1.269708	0.022	1.249832	0.064	1.349019	0.014	0.82814	0.8395	CDS conserved unknown protein 2265975:2266301 forward MW:11249

RPA2013	1.091491	0.1345	0.997332	0.513	0.917522	0.79	1.158487	0.1585	0.850014	0.8875	CDS possible aminotransferase 2266324:2267481 forward MW:42555
RPA2014	0.950701	0.773	0.987807	0.5595	0.932656	0.6985	0.895484	0.8485	1.029035	0.376	CDS ABC transporter, polyamine transport protein 2267489:2268604 forward MW:41176
RPA2015											CDS hypothetical protein 2268717:2269856 forward MW:40846
RPA2016	1.121051	0.1295	0.775666	0.9845	1.072322	0.2475	0.781266	0.967	1.133582	0.0935	CDS possible methyltransferase related protein 2269872:2271830 reverse MW:73022
RPA2017	0.656695	0.9975	0.760288	0.9895	0.505045	0.9975	0.495976	0.9995	0.602422	0.9995	CDS putative lipid A biosynthesis lauroyl acyltransferase 2272117:2273049 reverse MW:34635
RPA2018	0.900902	0.852	0.943931	0.7615	0.870002	0.8965	0.874143	0.881	0.96114	0.658	CDS alcohol dehydrogenase 2273049:2274071 reverse MW:36217
RPA2019	0.910519	0.7175	0.830237	0.9595	0.968684	0.65	0.666632	0.994	0.753916	0.905	CDS 3-oxoacyl-acyl carrier protein synthase II 2274168:2275448 reverse MW:44398
RPA2020	0.944631	0.6485	0.771577	0.9065	0.852068	0.907	0.700872	0.9165	0.807976	0.952	CDS 3-oxoacyl-acyl carrier protein synthase 2275459:2276667 reverse MW:42291
RPA2021	0.81362	0.8815	1.206642	0.0155	0.704745	0.9955	0.901492	0.724	1.10944	0.1335	CDS 3-hydroxymyristoyl-acyl carrier protein dehydratase 2276660:2277130 reverse MW:17352
RPA2022	0.899913	0.878	1.117846	0.1365	0.804021	0.9645	0.719177	0.943	0.981128	0.5725	CDS specialized acyl carrier protein 2277156:2277437 reverse MW:10228
RPA2023	0.864021	0.9595	1.0388	0.3675	1.379209	0.1055	0.877443	0.712	0.739801	0.84	CDS conserved hypothetical protein 2277604:2277957 reverse MW:13048
RPA2024	0.887794	0.8925	0.668416	0.9925	1.279411	0.025	0.925719	0.663	0.956251	0.702	CDS conserved unknown protein 2278154:2278777 forward MW:23719
RPA2025											CDS possible MgtC Mg2+ transport protein 2278805:2279266 reverse MW:16103
RPA2026	1.198813	0.0325	1.370913	0.004	0.899435	0.8525	1.475336	0.038	1.907058	0.0025	CDS ferric siderophore receptor 2279693:2282260 forward MW:91199
RPA2027	0.97826	0.5815	0.968203	0.644	0.792531	0.972	0.796327	0.9515	1.03332	0.365	CDS ATPase:Protein of unknown function DUF87 2282020:2283771 reverse MW:63484
RPA2028	1.222331	0.1645	1.049617	0.392	0.608618	0.974	0.892537	0.727	1.270264	0.0415	CDS conserved hypothetical protein 2284104:2284685 forward MW:21868
RPA2029	0.770561	0.9555	0.931722	0.716	0.738921	0.99	0.695586	0.9965	0.741228	0.9915	serB putative phosphoserine phosphatase 2284710:2285441 reverse MW:26006
RPA2030											miaA tRNA isopentenyltransferase 2285587:2286552 forward MW:34399
RPA2031	0.784672	0.892	0.776342	0.993	0.6317	0.994	0.479768	0.999	0.581749	0.986	ilvI acetolactate synthase (large subunit) 2286918:2288696 forward MW:64487
RPA2032	0.641942	0.9885	0.670534	0.9985	0.453161	1	0.372953	1	0.348392	0.9855	ilvH acetolactate synthase (small subunit) 2288912:2289454 forward MW:19942
RPA2033	0.856164	0.7245	2.0506	0.0215	0.854948	0.7935	0.866124	0.8765	0.81454	0.857	CDS possible AtsE 2289458:2289856 reverse MW:14450
RPA2034	0.610093	0.9995	0.598286	0.996	0.728313	0.9965	0.463905	0.995	0.44739	1	CDS Permeases of the drug/metabolite transporter (DMT) superfamily 2290068:2290943 forward MW:30724
RPA2035	1.060325	0.3175	1.089828	0.0885	0.82439	0.989	0.804182	0.9785	0.747212	0.984	ilvC ketol-acid reductoisomerase 2291138:2292157 forward MW:37107
RPA2036	0.861691	0.94	1.104939	0.2645	0.832395	0.875	1.132265	0.3945	0.965989	0.551	CDS possible transcriptional regulator, GntR family 2292447:2293175 forward MW:26913
RPA2037	0.507482	0.9905			0.441679	0.996			0.21691	0.9635	CDS possible periplasmic binding protein 2293274:2294506 forward MW:44359
RPA2038	0.876614	0.9535	0.759661	0.98	0.724805	0.9775	0.895512	0.7955	0.770153	0.9935	CDS putative oxidoreductase 2294633:2295487 forward MW:30436
RPA2039	1.294959	0.0925	0.898726	0.812	1.126882	0.12	1.142456	0.2655	0.864789	0.866	CDS possible choline ABC transporter permease and substrate binding protein 2295590:2297137 reverse MW:54974
RPA2040											CDS possible choline ABC transporter ATP-binding subunit 2297134:2297742 reverse MW:22305
RPA2041	1.01166	0.4845			0.956225	0.536	0.866837	0.711	0.638693	0.99	CDS ABC-transport protein, ATP-binding protein 2297977:2298837 forward MW:30924
RPA2042	1.047406	0.223	0.991563	0.546	0.891964	0.9395	0.9921	0.527	0.811335	0.9825	CDS putative ABC transporter, permease protein 2299064:2299858 forward MW:29024
RPA2043	1.149627	0.0395	0.857962	0.922	0.950562	0.69	1.120802	0.1865	1.041516	0.326	CDS putative ABC transporter, periplasmic substrate-binding protein 2299917:2300939 forward MW:35299
RPA2044	1.124491	0.095	1.119036	0.159	1.132525	0.1275	1.082689	0.261	0.933213	0.7375	CDS conserved unknown protein 2300947:2301663 forward MW:26990
RPA2045	0.964052	0.6555	1.142648	0.078	0.931514	0.7845	0.997618	0.513	0.974642	0.6055	bioB biotin synthetase 2301725:2302735 reverse MW:36446
RPA2046	0.659801	0.987	0.776898	0.9925	0.641496	0.997	0.750677	0.9925	0.712979	0.9515	leuI 2-isopropylmalate synthase 2303251:2304825 forward MW:57551
RPA2047	1.437908	0.0915	1.753767	0.0075	0.930372	0.673	1.182112	0.1695	1.292546	0.051	dctP1 TrapT family, dctP subunit, C4-dicarboxylate periplasmic binding protein 2305049:2306053 forward MW:36473
RPA2048	1.053911	0.4145	1.487038	0.01	0.781961	0.962	0.669979	0.9595	0.816962	0.8605	dctQ1 possible TrapT family, dctQ subunit, C4-dicarboxylate transport 2306192:2306776 forward MW:21916
RPA2049	1.121149	0.292	1.28587	0.029	0.835777	0.8975	0.839904	0.9595	0.972262	0.542	dctM1 TrapT family, dctM subunit, C4-dicarboxylate transport 2306773:2308098 forward MW:47067
RPA2050	0.85299	0.9345	0.781079	0.9375	1.053608	0.3265	1.052563	0.4025	1.321859	0.022	CDS conserved hypothetical protein 2308231:2308830 forward MW:22113
RPA2051	0.82358	0.8185	0.989669	0.527	0.779986	0.9865	0.558308	1	0.833413	0.817	CDS putative ornithine decarboxylase 2309647:2312004 forward MW:88522
RPA2052			1.428295	0.1125					0.936494	0.5615	CDS putative phophinothricin N-acetyltransferase 2311958:2312569 forward MW:22501
RPA2053	1.02054	0.3975	1.049297	0.3145	0.857128	0.904	1.13648	0.2075	1.005264	0.4925	CDS conserved hypothetical protein 2312691:2313050 forward MW:12661
RPA2054											CDS possible outer membrane protein precursor CzcC 2313105:2314376 forward MW:45096
RPA2055			0.648751	0.99	0.381118	0.99	0.715092	0.972	0.327066	0.999	CDS possible RND divalent metal cation efflux membrane fusion protein CzcB precursor 2314373:2315368 forward MW:35300
RPA2056	0.614989	0.982	0.70709	0.9995	0.682034	0.997	0.694116	0.9685	0.527173	0.9985	czcA2 RND divalent metal cation efflux transporter CzcA 2315398:2318613 forward MW:114943
RPA2057	0.812786	0.834	0.701919	0.9955	0.823811	0.9385	0.76149	0.9195	0.657909	0.982	CDS hypothetical protein 2318610:2318978 forward MW:12538
RPA2058											CDS conserved hypothetical protein 2319039:2319308 reverse MW:10363
RPA2059	1.333233	0.046	1.102987	0.128	1.376896	0.0215	1.857445	0.002	1.485693	0.0045	CDS conserved hypothetical protein 2319382:2320281 reverse MW:32821
RPA2060	0.95251	0.572	1.931688	0					0.764496	0.71	nosR regulatory protein NosR 2320449:2322716 forward MW:82108
RPA2061	1.095311	0.338	1.296263	0.023	0.980123	0.5315	0.735191	0.9345	0.943455	0.6635	nosZ nitrous-oxide reductase precursor NosZ 2322735:2324672 forward MW:71470
RPA2062	0.973977	0.625	0.852081	0.937	0.763915	0.987	0.815834	0.866	0.898421	0.82	nosD putative periplasmic ABC transport copper binding protein 2324675:2326039 forward MW:48587
RPA2063	0.967871	0.656	0.911846	0.8795	0.910878	0.783	0.661729	0.994	0.686543	0.9985	nosF putative NosF protein (an ABC transporter) 2326036:2326941 forward MW:32543
RPA2065											nosL putative nosL (possibly a disulfide isomerase) 2327762:2328313 forward MW:19369
RPA2066											nosX putative nosX 2328326:2329324 forward MW:35165
RPA2069	0.766256	0.823	1.097477	0.1775	1.052661	0.4015	0.93715	0.637	0.94183	0.7005	CDS conserved hypothetical protein 2330201:2331484 forward MW:43584
RPA2070											CDS hypothetical protein 2331496:2332005 forward MW:18902
RPA2071			1.486049	0.034	2.077596	0.044	1.255697	0.1715			CDS hypothetical protein 2332157:2332408 reverse MW:8727
RPA2072	1.017293	0.401	1.000665	0.505	1.075166	0.15	0.958211	0.665	0.899841	0.834	CDS possible 3-oxoacyl-acyl carrier protein reductase 2332505:2332651 reverse MW:4942
RPA2073	1.696071	0.089	2.994636	0.004			1.798237	0.0235	2.517329	0	CDS putative oxidoreductase 2332713:2333363 reverse MW:23326
RPA2074											CDS response regulator receiver (CheY-like protein) 2333431:2333799 reverse MW:13497
RPA2075									2.067383	0.005	CDS putative signal transduction histidine kinase with GAF and PAS/PAC domains 2333796:2335697 reverse MW:70432
RPA2076	1.092323	0.195	1.158379	0.072	1.185115	0.05	1.014068	0.439	1.135463	0.1025	CDS putative signal transduction histidine kinase 2336125:2336811 reverse MW:25207
RPA2077	1.787393	0.007	2.858769	0.001	1.723729	0.001	1.721448	0.0005	2.681612	0	CDS probable transcriptional regulator, Crp/Fnr family 2336808:2337734 reverse MW:34484
RPA2080	1.172708	0.0715	1.37021	0.0095	1.416903	0.005	2.022269	0.0005	2.269316	0.0005	CDS zinc-containing dehydrogenase 2338535:2339704 reverse MW:42178
RPA2081	0.768196	0.991	1.024058	0.3645	0.549616	0.9995	0.526616	0.991	0.889351	0.927	CDS possible Fe ABC Transporter 2340151:2341086 forward MW:33624
RPA2082			0.903135	0.7			0.736748	0.913	1.003495	0.4945	cobA putative uroporphyrin III methylase 2341120:2341869 reverse MW:25821
RPA2083	0.705801	0.969	0.680526	0.996	0.839087	0.932	0.431291	0.9995	0.464182	0.997	cobB putative cobyrinic acid a,c-diamide synthase 2341869:2343230 reverse MW:47801
RPA2084	0.782726	0.819	0.729039	0.9715	0.871977	0.9415	0.429966	0.992	0.55864	0.975	cobM precorrin 3 or 4 methylase 2343217:2343996 reverse MW:27593
RPA2085	1.24597	0.111	1.042877	0.3705	1.101653	0.375	0.937496	0.601	0.593198	0.9925	CbiG cobalamin biosynthesis protein G; CbiG 2343993:2344385 reverse MW:12912
RPA2086	0.760353	0.947	0.565768	0.997	0.832101	0.972	0.300951	0.9985	0.53178	0.979	cobL putative precorrin 6y methylase 2344382:2345605 reverse MW:42847
RPA2087	0.891346	0.61							0.684268	0.833	cobK putative precorrin 6x reductase 2345604:2346386 forward MW:27455
RPA2088	0.849738	0.8145	0.924096	0.826	0.704435	0.9965	0.338611	1	0.563751	0.9815	cobJ precorrin 3 methylase 2346353:2347114 reverse MW:27013
RPA2089	1.004327	0.4975	1.27718	0.0265	0.930342	0.7085	1.521787	0.0355	1.313884	0.0755	cobI precorrin 2 methylase 2347111:2347839 reverse MW:25808
RPA2090	0.735362	0.9955	1.128073	0.2135	0.503807	0.995	0.236993	0.984	0.715481	0.9615	cobH precorrin isomerase CobH 2347836:2348465 reverse MW:21791
RPA2091	0.726213	0.9775	1.337802	0.036	0.600767	0.961	0.477999	0.9815	0.798876	0.919	CDS hypothetical protein 2348462:2349025 reverse MW:19740
RPA2092	0.781227	0.9935	0.731562	0.991	0.801464	0.9865	0.697885	0.9925	0.799149	0.9615	CDS conserved hypothetical protein 2349426:2350562 reverse MW:39717
RPA2093	1.048169	0.3485	1.178268	0.2795	1.272105	0.0125	2.114984	0.089	1.11103	0.161	CDS conserved hypothetical protein 2350549:2351847 reverse MW:45279
RPA2094	0.502735	0.964	0.830929	0.938	0.639312	0.988	0.230501	1	0.839661	0.8785	cobT1 putative nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase 2352419:2353483 forward MW:36744

RPA2095	0.350193	0.969	0.668701	0.987	0.472489	0.995	0.121176	1	0.402698	0.9985	CDS possible cobalamin (5`-phosphate) synthase 2353480:2354250 forward MW:25962
RPA2096	0.425628	0.978	0.396832	0.9995	0.545592	0.9995	0.126774	1	0.341688	0.997	cobQ2 cobyric acid synthase 2354337:2355911 forward MW:56464
RPA2097	0.475739	0.988	0.371806	1	0.584415	0.9995	0.154891	1	0.369297	0.9985	cobF putative cobF protein 2355943:2356707 forward MW:28331
RPA2098	0.541749	0.999	0.742928	0.883	0.650633	0.9485	0.631769	0.952	0.806099	0.958	CDS Glutamine amidotransferase class-I 2356827:2357591 forward MW:27549
RPA2099			0.874194	0.7315			1.272301	0.195	1.087636	0.324	CDS Putative diterpenoid Major Facilitator Superfamily (MFS) transporter 2357596:2359245 reverse MW:58269
RPA2100											CDS possible hydrolase 2359573:2360223 forward MW:24005
RPA2101											CDS conserved hypothetical protein 2360535:2362415 forward MW:68859
RPA2102											CDS conserved hypothetical protein 2362417:2362842 forward MW:15250
RPA2103	1.201534	0.064	1.039373	0.297	1.113532	0.1265	1.290224	0.051	1.282097	0.0145	CDS conserved hypothetical protein 2362862:2363782 forward MW:32574
RPA2104	1.225979	0.0045	1.080271	0.1515	1.085587	0.134	1.353696	0.0095	1.362031	0.004	CDS conserved hypothetical protein 2363779:2365212 forward MW:52783
RPA2105	1.442919	0.107	1.175495	0.0915	1.969718	0.0025	0.989147	0.525	0.878584	0.8305	CDS non-heme chloroperoxidase 2365285:2366127 reverse MW:30652
RPA2106			0.793341	0.952			1.129356	0.3115			CDS conserved unknown protein 2366342:2367043 reverse MW:24489
RPA2107	1.059953	0.3635	0.973605	0.5165	1.04139	0.363	2.636325	0.099	1.474956	0.019	CDS sensor histidine kinase with a GAF, a Ser/Thr protein kinase, and an unknown domain 2367208:2372346 reverse MW:188250
RPA2108									1.370759	0.076	CDS response regulator receiver (CheY-like protein) 2372333:2372719 reverse MW:13631
RPA2109	1.109788	0.2855	0.984895	0.5375	1.395774	0.0425	1.686572	0.0115	1.629844	0.005	CDS two-component transcriptional regulator, LuxR family 2372808:2373443 reverse MW:23124
RPA2110	2.099293	0.0015	2.052192	0	1.695263	0.0035	4.69119	0	2.816664	0	CDS probable transcriptional regulator, AraC family 2373680:2374288 forward MW:22495
RPA2111	1.67203	0.0015	1.660466	0	1.849652	0	3.10358	0	2.29944	0.002	CDS PAS domain:sigma-54-dependent transcriptional regulator, Fis family 2374328:2376253 reverse MW:71593
RPA2112	4.345633	0	2.662791	0.0005	3.607547	0	24.25549	0	9.777549	0	nrtA putative nitrate transporter component, nrtA 2376415:2377803 forward MW:50670
RPA2113	3.492947	0	2.231835	0	2.63308	0.0005	16.74364	0	6.203917	0	nrtB possible nitrate transport system permease protein 2377950:2378789 forward MW:30224
RPA2114	2.035734	0.0025	1.52426	0.0105	1.585309	0.0265	5.811403	0	3.778009	0	nrtC1 putative nitrate transport system ATP-binding protein 2378795:2379682 forward MW:32495
RPA2115	2.752213	0.001	2.786121	0	2.946884	0	17.10252	0	9.011498	0	cynS putative cyanate lyase 2379725:2380213 forward MW:18275
RPA2116	4.393949	0.006	11.36711	0	5.780614	0	5.816651	0.0245	4.274989	0.0005	CDS hypothetical protein 2380320:2380736 reverse MW:15079
RPA2117	4.583191	0.006	8.444618	0	5.563819	0.0005	5.898601	0.0245	5.354624	0	CDS putative flavodoxin 2380715:2381197 reverse MW:17214
RPA2118	2.339037	0.0025	3.282865	0	2.135207	0.0005	2.020868	0.0015	2.251941	0.0005	CDS putative ATP-binding protein of ABC transporter 2381400:2382206 reverse MW:28338
RPA2119	2.219791	0.0015	2.631661	0	2.225974	0.0005	1.269784	0.03	2.104767	0	CDS putative permease protein of ABC transporter 2382203:2383285 reverse MW:36658
RPA2120	3.050605	0.0005	4.804055	0	3.208175	0.0005	2.750737	0.007	3.014047	0	CDS putative hemin binding protein 2383282:2384253 reverse MW:33387
RPA2121	3.270665	0	4.752652	0.0175	3.366015	0	2.325284	0.0155	2.058169	0.008	CDS conserved unknown protein 2384250:2384453 reverse MW:7285
RPA2122	4.753111	0.002	8.332628	0	4.453506	0	5.165175	0.0025	4.672131	0	CDS putative oxygen independent coproporphyrinogen III oxidase 2384786:2386246 forward MW:51638
RPA2123	1.289181	0.108	1.283545	0.016	1.134166	0.1935	1.202681	0.1145	1.397536	0.0255	CDS conserved unknown protein 2386234:2386905 forward MW:22707
RPA2124	11.14166	0	22.08869	0	8.123684	0.0005	6.938171	0.001	17.44175	0	CDS tonB dependent iron siderophore receptor 2387123:2389462 forward MW:82872
RPA2125	5.313687	0	7.325377	0	3.981246	0.0035	4.071402	0	4.736799	0	CDS conserved unknown protein 2389539:2389871 forward MW:12587
RPA2126	2.88072	0.0055	3.337598	0.001	3.268986	0	1.728761	0.065	2.32155	0	CDS conserved unknown protein 2389888:2390424 forward MW:19257
RPA2127	5.393454	0			5.648004	0			5.67188	0.0025	exbB3 putative exbB, uptake of enterochelin; tonB-dependent uptake of B colicins 2390417:2391214 forward MW:27621
RPA2128	7.120607	0.0005			6.361492	0.0005	7.48204	0.0005	4.181383	0	exbD3 biopolymer transport protein ExbD/TolR 2391220:2391657 forward MW:15345
RPA2129	0.947126	0.6885	0.964385	0.5915	1.061151	0.3485	1.083496	0.278	0.910867	0.6715	CDS possible energy transducer TonB, C-terminal region 2391654:2392511 forward MW:29965
RPA2130	1.699049	0.0495	3.207909	0	2.231388	0	1.317359	0.0905	1.605806	0.0015	CDS DUF81 2393564:2394370 reverse MW:27388
RPA2131	0.864644	0.906			1.011723	0.462			0.758129	0.8255	CDS hypothetical protein 2394921:2396003 forward MW:38915
RPA2132	0.911003	0.791	0.946702	0.732	0.877828	0.789	0.914387	0.6925	1.070047	0.337	CDS hypothetical protein 2396132:2397517 forward MW:47911
RPA2133	1.293847	0.0205	1.03439	0.3145	1.251625	0.0135	1.112655	0.233	0.994558	0.509	CDS conserved hypothetical protein 2397522:2398313 forward MW:28162
RPA2134	1.443703	0.0145	1.710744	0.0185	2.151756	0.0005	1.820262	0.0045	1.879806	0.003	CDS hypothetical protein 2398474:2398917 forward MW:15728
RPA2135	0.96926	0.6555	1.039147	0.3965	1.324674	0.008			1.293612	0.0575	CDS sensor histidine kinase with a response regulator receiver domain 2398973:2401096 reverse MW:77273
RPA2136	0.970157	0.628	1.02778	0.393	0.995414	0.5425	1.089454	0.21	1.197719	0.078	CDS possible cytochrome C precursor 2401317:2401631 forward MW:11231
RPA2137	0.792399	0.9895	0.774697	0.9755	0.915205	0.8765	0.815174	0.799	0.685461	0.9965	CDS probable acyl-CoA dehydrogenase 2401734:2402873 forward MW:40818
RPA2138	0.89547	0.7715	1.279888	0.021	0.793127	0.8435	1.217803	0.111	0.877944	0.7845	CDS putative acyl-CoA dehydrogenase 2403023:2404177 forward MW:41993
RPA2139	0.743741	0.969	1.026422	0.351	0.910258	0.8145	0.890131	0.905	0.807801	0.9465	CDS possible glutathione S-transferase 2404371:2405069 forward MW:26171
RPA2140	1.116675	0.0915	0.969583	0.6345	1.043891	0.3195	1.502986	0.015	1.035131	0.361	CDS probable transcriptional regulator, AraC family 2405234:2406058 forward MW:30172
RPA2141	0.97427	0.5445	0.850378	0.9055	1.119825	0.1325	1.010893	0.4645	0.999166	0.4975	CDS conserved hypothetical protein 2406179:2407045 forward MW:31427
RPA2142	1.137183	0.177	1.322413	0.0165	1.026244	0.4065	1.209778	0.042	0.998451	0.4915	CDS putative fatty-acid--CoA ligase 2407213:2408817 forward MW:58292
RPA2143	0.757645	0.9015	1.264209	0.0135	1.004249	0.4765	0.836406	0.9305	0.778434	0.9825	CDS putative acetyl/propionyl-CoA carboxylase 2409057:2410679 forward MW:57762
RPA2144	0.896704	0.9185	0.997308	0.5095	0.926797	0.7865	0.81983	0.9085	0.800167	0.958	CDS possible biotin carboxylase 2410676:2412658 forward MW:70309
RPA2145	0.891598	0.9005	0.916866	0.7015	0.940894	0.6955	0.747546	0.934	0.686953	0.973	CDS putative enoyl-CoA hydratase/isomerase 2412778:2413557 forward MW:27947
RPA2146	0.938419	0.687	0.853068	0.8915	1.047479	0.289	0.743284	0.9635	0.705312	0.991	CDS putative long-chain-fatty-acid--CoA ligase 2413733:2415271 forward MW:56251
RPA2147									0.890942	0.6955	CDS unknown protein 2415426:2416820 forward MW:49953
RPA2148	1.111533	0.121	0.981144	0.594	0.957155	0.681	1.056102	0.311	1.188483	0.036	CDS Beta-lactamase 2416916:2418184 reverse MW:45662
RPA2149	0.923448	0.79	0.95519	0.7295	1.087938	0.1395	1.096244	0.1915	0.905709	0.833	CDS putative hydroxyquinol 1,2-dioxygenase 2418328:2419320 forward MW:36655
RPA2150	1.008247	0.483	1.254177	0.0905	1.115505	0.2025	1.309073	0.1825	1.236671	0.0455	CDS putative oxidoreductase 2419351:2420184 forward MW:29913
RPA2151	0.893899	0.7295			0.980905	0.5285			0.896083	0.6625	CDS Permeases of the drug/metabolite transporter (DMT) superfamily 2420403:2421317 forward MW:32945
RPA2152	1.400419	0.002	1.195004	0.025	1.092326	0.1105	1.493451	0.0045	1.067337	0.1825	CDS putative diguanylate cyclase (GGDEF)/phosphodiesterase (EAL) with PAS domain 2421412:2423541 forward MW:76840
RPA2153	0.755769	0.9955	0.665854	0.998	0.768238	0.9975	0.699133	0.9865	0.517223	0.9995	CDS aldehyde dehydrogenase 2423788:2425218 forward MW:50503
RPA2154	1.102156	0.123	1.177858	0.029	1.147879	0.0635	1.386213	0.008	1.173898	0.0355	CDS putative acyltransferase 2425291:2426538 forward MW:45055
RPA2155	1.446152	0.0025	1.100349	0.1225	0.963792	0.658	2.83969	0	1.864121	0.001	ilvD3 dihydroxy-acid dehydratase 2426865:2428571 forward MW:60025
RPA2156	7.885586	0.0005	4.060692	0	3.112003	0	26.12883	0	8.946249	0	CDS hypothetical protein 2428576:2428854 reverse MW:11016
RPA2157	0.987821	0.5555	0.925876	0.8525	1.004485	0.474	0.787581	0.9835	1.06227	0.234	CDS conserved hypothetical protein 2429253:2430449 forward MW:43019
RPA2158	1.446119	0.0965	2.632752	0.0005	1.729346	0.004	1.349553	0.064	2.411254	0.0005	CDS hypothetical protein 2430585:2430914 forward MW:11918
RPA2159	1.167108	0.043	1.603807	0.0865	1.483959	0.0005	0.718297	0.9335	0.970127	0.5935	CDS hypothetical protein 2431025:2431339 reverse MW:11306
RPA2160											CDS short chain dehydrogenase 2431465:2432214 reverse MW:25236
RPA2161	0.806013	0.7765	1.210972	0.0365	0.921155	0.844	1.446872	0.011	1.559772	0.004	CDS possible transcriptional regulator, arsR family 2432327:2432641 forward MW:11365
RPA2162	0.231749	0.9995	0.193162	1	0.246531	1	0.108395	1	0.073617	0.9995	CDS possible serine protease/outer membrane autotransporter 2433296:2436136 forward MW:94530
RPA2163	0.887221	0.8835	0.912597	0.8475	0.67622	0.987	0.837145	0.875	0.746062	0.9855	CDS SEC-C motif 2436196:2436882 reverse MW:24911
RPA2164	0.989784	0.5185	0.747672	0.983	0.870491	0.9625	0.64584	0.991	0.639932	0.9995	groEL2 chaperonin GroEL2, cpn60 2437219:2438862 reverse MW:57796
RPA2165	1.149279	0.341	0.878375	0.6775	0.899439	0.8065	0.717923	0.845	0.722079	0.9675	groES2 chaperonin GroES2, cpn10 2439028:2439342 reverse MW:11164
RPA2166	1.038796	0.4305	1.01737	0.463	1.441209	0.0095	2.053336	0	1.567639	0.009	CDS conserved hypothetical protein 2439785:2440069 forward MW:10928
RPA2167			0.68372	0.8175			1.247206	0.1755	1.133318	0.3625	CDS conserved hypothetical protein 2440210:2441895 reverse MW:61346
RPA2168	1.10461	0.2595	1.034354	0.3935	0.643735	0.9815	0.714261	0.972	0.851006	0.9215	CDS putative H+/nucleoside symporter 2442142:2443392 reverse MW:43097
RPA2169									0.904715	0.7135	rlp1 ribulose-bisphosphate carboxylase-like protein; rubisco-like protein 2443567:2444673 forward MW:38755
RPA2170	1.237451	0.027	1.057455	0.1995	1.161391	0.0805	1.291784	0.034	1.339831	0.0175	CDS hypothetical protein 2444663:2445160 forward MW:18239
RPA2171	1.221005	0.0185	0.888129	0.877	1.050746	0.4	0.962585	0.592	1.149891	0.152	CDS unknown protein 2445677:2446480 forward MW:27643

RPA2172	1.31044	0.0045	0.963	0.722	1.04561	0.3995	0.958174	0.6025	0.914418	0.873	CDS putative oxidoreductase 2446500:2447258 reverse MW:26420
RPA2173	1.244972	0.056	1.109131	0.21	1.091095	0.1945	1.31024	0.0405	1.210698	0.0435	CDS GCN5-related N-acetyltransferase 2447291:2447791 reverse MW:17655
RPA2174	1.619537	0.004	1.643391	0.018	1.084963	0.2595	1.847872	0.0035	1.931057	0.002	CDS conserved hypothetical protein 2447810:2448556 reverse MW:27425
RPA2175	1.137155	0.0685	1.200918	0.087	1.319438	0.039	1.88667	0.001	1.577019	0.0035	CDS Transglutaminase-like domain 2448770:2449597 reverse MW:29561
RPA2176	1.91862	0	1.439103	0.0045	1.723043	0.003	2.479174	0	1.687	0.0005	CDS DUF403 2449647:2450591 reverse MW:36053
RPA2177	1.58111	0.009	1.309966	0.01	1.70011	0	1.898786	0	1.60459	0.004	CDS DUF404 2450743:2452161 reverse MW:52783
RPA2178	1.324058	0.0165	1.087792	0.1895	1.409675	0.006	1.824685	0.003	1.941203	0.001	CDS possible competence damage protein 2452385:2453122 forward MW:26593
RPA2179	1.348019	0.0105	1.045602	0.266	1.564523	0.001	1.609267	0.0045	1.364168	0.03	CDS xanthine-guanine phosphoribosyltransferase 2453243:2453797 forward MW:20109
RPA2180	0.948475	0.768	1.073773	0.146	1.060152	0.227	0.952797	0.634	1.099776	0.099	CDS conserved hypothetical protein 2454102:2454776 forward MW:24780
RPA2181	1.061952	0.1945	0.824469	0.9795	0.886043	0.8705	0.800686	0.8395	0.820792	0.977	CDS possible metE (5-methyltetrahydropteroyltriglutamate-homocysteine methyltransferase) 2454971:2455993 reverse MW:37454
RPA2182	1.03869	0.3335	0.754679	0.9935	1.087391	0.199	1.221326	0.1045	0.964992	0.618	CDS putative glutathione S-transferase 2456070:2456864 forward MW:29324
RPA2183	0.701006	0.9835	0.607623	0.9895	0.649838	0.992	0.487804	0.995	0.379408	1	CDS DSBA oxidoreductase 2457284:2457904 forward MW:23056
RPA2184	0.581767	0.98	0.79866	0.883	0.680277	0.9755	0.799082	0.863	0.492452	1	CDS putative oxidoreductase 2457904:2458878 forward MW:34221
RPA2185	0.79655	0.9645	0.971971	0.6255	0.650981	0.991	0.67262	0.9835	0.682065	0.9875	CDS nodN-like protein 2458970:2459437 forward MW:17564
RPA2186	0.841528	0.8375	1.031714	0.337	0.655039	0.998	0.582471	0.997	0.628869	0.9995	CDS possible 3-oxo-(acyl) acyl carrier protein reductase 2459456:2460373 forward MW:31988
RPA2187	0.971024	0.6885	1.046849	0.2695	0.741768	0.992	0.844939	0.89	0.898501	0.8615	CDS conserved unknown protein 2460577:2461812 forward MW:42871
RPA2188	1.054402	0.3315	1.000507	0.5015	0.796078	0.954	0.950635	0.678	0.907437	0.807	CDS hypothetical protein 2461819:2462145 reverse MW:11577
RPA2189											CDS possible transcriptional regulator, TetR family 2462142:2462798 reverse MW:23471
RPA2190	1.089575	0.1455	1.027839	0.3525	1.051734	0.288	1.144513	0.245	1.049066	0.2755	CDS ABC transporter, with duplicated ATPase domains 2462902:2464719 reverse MW:66012
RPA2191	0.957996	0.654	0.777426	0.9585	1.128192	0.0885	0.987659	0.5355	0.913266	0.748	CDS DUF188 2464730:2465206 reverse MW:16962
RPA2192											CDS hypothetical protein 2465309:2466109 forward MW:28919
RPA2193	1.244481	0.3135	0.744516	0.7815	1.197307	0.0695	0.901234	0.5945	0.627184	0.974	CDS putative ABC transporter, perplasmic binding protein, branched chain amino acids 2466304:2467518 forward MW:43967
RPA2194	0.815021	0.9125	0.892549	0.93	0.936858	0.8	0.701814	0.994	0.634707	0.9875	CDS possible carbon-monoxide dehydrogenase large subunit 2467751:2470255 reverse MW:88204
RPA2195	1.175297	0.0245	1.241108	0.039	1.129482	0.098	1.571553	0.0015	1.332751	0.019	CDS possible exopolyphosphatase 2470320:2471435 forward MW:39850
RPA2196	0.976473	0.5625	1.402823	0.003	1.094006	0.293	1.310953	0.022	1.033367	0.442	CDS conserved hypothetical protein 2471462:2472175 reverse MW:24961
RPA2197	1.059604	0.2515	0.985792	0.53	0.96449	0.6845	1.126333	0.1805	1.186969	0.053	CDS cell division protein FtsJ 2472235:2472948 forward MW:25386
RPA2198	0.895577	0.9445	0.748985	0.9925	0.867258	0.9185	0.587219	0.998	0.757476	0.9795	CDS possible multidrug efflux protein 2473309:2474886 reverse MW:54985
RPA2199	1.021282	0.4445	1.010499	0.4765	1.10473	0.174	1.132729	0.1395	0.807069	0.916	CDS hypothetical protein 2474976:2475224 forward MW:9239
RPA2200	0.669613	0.9905	0.810575	0.977	0.693471	0.998	0.540646	0.999	0.596782	0.996	guaB inosine monophosphate dehydrogenase 2475578:2477074 forward MW:52395
RPA2201	0.744821	0.996	0.607474	0.992	0.792923	0.976	0.536765	0.993	0.403187	1	CDS quinone oxidoreductase 2477373:2478398 forward MW:36423
RPA2202	0.983306	0.5875	1.007855	0.474	1.039229	0.32	1.355651	0.0595	1.012244	0.482	CDS SUN-family protein, putative RNA methyltransferase 2478589:2479890 forward MW:45798
RPA2203	0.858594	0.957	0.936815	0.779	0.783478	0.979	0.694965	0.994	0.822866	0.982	guaA GMP synthetase 2480182:2481804 forward MW:58431
RPA2204	1.030374	0.37	0.900423	0.891	1.257739	0.039	1.347256	0.0615	1.383525	0.018	CDS integrase 2482087:2483343 forward MW:47563
RPA2205	0.975383	0.6145	1.223698	0.0185	1.244939	0.0345	1.632736	0.0025	1.748119	0.0035	CDS hypothetical protein 2483315:2483662 reverse MW:13399
RPA2206	1.058395	0.2975	1.22535	0.247	0.953266	0.6905	2.230293	0.046	1.145699	0.0675	CDS conserved hypothetical protein 2483746:2484126 reverse MW:13603
RPA2207	1.292507	0.0035	1.188587	0.048	1.199801	0.0205	1.537801	0.0045	1.882856	0	CDS putative recombinase 2484202:2485770 forward MW:59137
RPA2208	1.246485	0.0485	1.364304	0.0295	1.088938	0.3025	1.632574	0.0275	2.343824	0.0005	parB2 possible ParB-like partioning protein 2485767:2486651 forward MW:32547
RPA2209	1.232381	0.0155	1.392996	0.002	1.221634	0.0155	1.498673	0.005	1.232761	0.0615	CDS ParB-like nuclease 2486653:2487543 forward MW:32834
RPA2210	1.000574	0.4905	0.91283	0.8305	0.887091	0.8415	0.940354	0.6575	1.012136	0.431	CDS conserved unknown protein 2487834:2489702 forward MW:67945
RPA2211	1.033447	0.328	1.071639	0.202	0.98805	0.552	0.971622	0.59	1.039255	0.2925	CDS DEAD/DEAH box helicase:Helicase, C-terminal 2489714:2492842 reverse MW:117800
RPA2212	1.055233	0.1855	1.031198	0.3525	0.947763	0.695	0.853725	0.926	1.048979	0.272	CDS hypothetical protein 2492832:2494688 reverse MW:67305
RPA2213	0.981845	0.564	0.90984	0.705	0.904211	0.804	0.998509	0.4945	0.842705	0.952	CDS hypothetical protein 2494678:2495862 reverse MW:44132
RPA2214	1.109891	0.069	1.130269	0.088	0.907731	0.893	0.979632	0.588	1.320067	0.0055	CDS possible helicase 2495915:2499256 reverse MW:123400
RPA2215	1.320782	0.061	1.242471	0.009	1.063345	0.197	1.784625	0.0005	1.712198	0	CDS possible ATP-dependent exodeoxyribonuclease (subunit A) 2499276:2502677 reverse MW:122200
RPA2216	1.3002	0.047	1.22807	0.0245	0.952424	0.7075	1.256627	0.015	1.742088	0.0015	CDS hypothetical protein 2502677:2505340 reverse MW:95300
RPA2217	1.098845	0.11	1.156521	0.0545	1.075922	0.2135	1.27348	0.0135	1.966292	0.0005	CDS conserved unknown protein 2505626:2506510 reverse MW:33367
RPA2218	1.051652	0.271	1.012501	0.419	0.771491	0.9935	1.022992	0.3955	1.338197	0.0045	CDS possible ATP-dependent RNA helicase 2506544:2510062 forward MW:132644
RPA2219	1.09293	0.0735	1.16486	0.026	0.969423	0.664	0.968996	0.5775	1.138624	0.09	CDS Possible ATPase 2510059:2514300 forward MW:158247
RPA2220	1.324628	0.0135	1.329995	0.0035	1.126889	0.0535	1.414295	0.0025	1.514977	0.002	CDS conserved unknown protein 2514284:2517118 forward MW:102931
RPA2221	1.15848	0.1165	1.029356	0.374	1.000016	0.5155	1.054496	0.335	0.920416	0.8125	CDS conserved unknown protein 2517132:2520431 forward MW:121403
RPA2222	1.483392	0.0025	1.71511	0	1.359878	0.013	1.889792	0.0035	1.715426	0	CDS transcriptional regulator, LysR family 2520519:2521466 forward MW:33529
RPA2223	1.337916	0.211			0.975053	0.511			1.349715	0.3325	CDS conserved hypothetical protein 2521433:2521681 reverse MW:8840
RPA2224	1.670833	0.001	1.690305	0.001	1.67578	0.0015	2.676868	0	2.301474	0.001	trbI1 possible trbI, a component on a type IV secretion system (Y10832) 2521686:2522930 reverse MW:43450
RPA2225	1.363471	0.0155	1.211072	0.1125	1.101367	0.3415	1.493616	0.0525	1.387995	0.0135	trbG1 probable conjugal transfer protein trbG 2522927:2523928 reverse MW:36594
RPA2226	1.632169	0.048	0.965449	0.599			1.18211	0.249	1.18294	0.1585	trbF1 putative conjugal transfer protein trbF 2523928:2524614 reverse MW:25718
RPA2227											trbL putative CONJUGAL TRANSFER protein trbL 2524611:2525909 reverse MW:43497
RPA2228			0.849852	0.7775			0.914265	0.664			trbK probable trbK 2525909:2526256 reverse MW:12545
RPA2229	1.383506	0.014	1.285796	0.043	1.200484	0.032	1.384851	0.092	1.306102	0.009	trbJ putative conjugal transfer protein trbJ 2526265:2527008 reverse MW:26713
RPA2230			1.278719	0.094			0.93981	0.5455	1.624636	0.0965	trbE1 conjugal transfer protein trbE 2527005:2529452 reverse MW:89771
RPA2232	0.874682	0.7545			0.937978	0.5955			0.854633	0.6515	trbC1 putative conjugal transfer protein; TrbC 2529721:2530038 reverse MW:10870
RPA2233											trbB1 conjugal transfer protein trbB 2530035:2531018 reverse MW:34644
RPA2234											CDS conserved hypothetical protein 2531155:2531598 reverse MW:16494
RPA2235	1.199452	0.0275	1.336737	0.1715	1.120792	0.178			2.230001	0.0025	traG2 plasmid transfer factor, traG protein 2531595:2533598 reverse MW:73853
RPA2236	1.416818	0.0045	1.276427	0.0105	1.322471	0.0385	2.871647	0.0005	3.271824	0.0005	CDS conserved hypothetical protein 2533709:2535463 reverse MW:63858
RPA2237	1.405462	0.0155	1.191122	0.1215	1.265692	0.073	1.554326	0.0125	1.770994	0.0005	CDS possible lytic transglycosylase 2535732:2536574 reverse MW:29696
RPA2238	1.244914	0.053	0.948734	0.605	1.408718	0.034	1.613117	0.0115	1.646293	0.015	CDS conserved hypothetical protein 2537089:2537562 reverse MW:18144
RPA2239									1.776695	0.008	CDS putative partition protein 2537801:2538439 reverse MW:22913
RPA2240	1.288339	0.0725	1.137958	0.2045	1.381017	0.0435	1.465784	0.005	1.768431	0.002	CDS possible replication protein A 2538642:2539544 reverse MW:34171
RPA2241			1.184254	0.118	1.060501	0.393	1.889187	0.0015	3.446347	0	CDS conserved hypothetical protein 2539976:2540539 reverse MW:20370
RPA2242	1.281124	0.0185	1.164861	0.074	1.162881	0.138	1.807108	0.0005	2.275469	0.001	CDS conserved hypothetical protein 2540885:2541145 reverse MW:9596
RPA2243	1.368781	0.0305	1.358989	0.2415	1.270636	0.067			1.506822	0.031	CDS possible transcriptional regulator, XRE family 2541339:2541584 forward MW:9057
RPA2244	1.065298	0.176	1.453376	0.0025	1.291531	0.0085	1.767356	0.002	1.584167	0.0005	CDS conserved hypothetical protein 2541653:2541976 reverse MW:11641
RPA2245	0.905867	0.9065	0.94102	0.7415	1.245669	0.0305	1.204043	0.0395	1.741362	0	CDS hypothetical protein 2542604:2543107 reverse MW:17008
RPA2246	1.035637	0.422	1.174622	0.1225	1.018943	0.4475	1.17152	0.1595	1.182944	0.0925	CDS hypothetical protein 2543519:2543944 forward MW:15197
RPA2247	1.031103	0.321	0.994694	0.539	1.13649	0.0725	1.152563	0.1195	1.132178	0.1875	CDS conserved hypothetical protein 2543965:2545224 reverse MW:46377
RPA2248	1.026227	0.401	1.029938	0.3555	0.963319	0.654	1.160794	0.1055	1.194333	0.053	CDS conserved hypothetical protein 2545228:2546292 reverse MW:39000
RPA2249	1.033163	0.441	0.902889	0.731	1.013971	0.4905	1.357016	0.065	1.220464	0.179	CDS putative methylase/helicase 2546279:2550634 reverse MW:156497

RPA2250							1.004406	0.491			CDS hypothetical protein 2550722:2551054 reverse MW:11887
RPA2251	0.928171	0.7205	0.844309	0.7425	0.776701	0.878	1.12452	0.3895	1.116704	0.2505	CDS putative plasmid stabilization protein 2551051:2553156 reverse MW:76632
RPA2252			1.202621	0.0695	1.578876	0.133	3.060702	0	2.439962	0	CDS putative ardC antirestriction protein 2553276:2554220 reverse MW:34135
RPA2253			0.98691	0.523	0.829246	0.8675			1.095538	0.2515	CDS hypothetical protein 2554308:2555078 forward MW:28446
RPA2254	1.388427	0.003	1.535306	0.001	1.210251	0.0175	1.637363	0.0025	1.821281	0	CDS hypothetical protein 2555371:2556099 reverse MW:27655
RPA2255	1.30639	0.0665	1.5108	0.0015	0.914166	0.7815	1.323653	0.0665	1.231687	0.0805	CDS hypothetical protein 2556144:2556767 reverse MW:23450
RPA2256	0.814745	0.982	0.915376	0.7805	0.829811	0.9635	0.743459	0.9705	1.036172	0.299	CDS transcriptional regulator, ArsR family, ArsR1 2557368:2557700 forward MW:11751
RPA2257	0.880794	0.874	0.668484	0.984	0.871066	0.915	0.580754	0.9925	0.670523	0.9965	arsC1 arsenate reductase pump modifier 2557712:2558140 forward MW:15318
RPA2258	0.999976	0.5	1.245521	0.043	0.769933	0.97	1.010333	0.459	1.103961	0.149	arsB arsenical pump membrane protein 2558140:2559423 forward MW:44452
RPA2259			1.277362	0.069	1.489207	0.13	0.979574	0.5485	1.173777	0.237	arsH possible arsH protein 2559423:2560178 forward MW:28040
RPA2260	1.223059	0.0205	1.184127	0.0745	1.196762	0.026	1.07619	0.269	1.200317	0.0265	CDS possible Viral (Superfamily 1) RNA helicase 2560618:2564379 forward MW:138716
RPA2261	0.864049	0.5825			1.394309	0.308					CDS GMP synthetase: N-terminal fragment 2564583:2564822 forward MW:8643
RPA2262	0.575008	0.9995	0.673985	0.997	0.333567	0.9995	0.407085	1	0.528767	0.9985	gltS putative glutamate permease 2565446:2566642 reverse MW:42019
RPA2263	1.081313	0.2015	1.064288	0.284	0.892064	0.749	1.222622	0.1115	1.131247	0.065	CDS possible plasmid stabilization protein 2566820:2567248 reverse MW:15264
RPA2264	1.114115	0.155	0.932895	0.7855	0.868855	0.903	1.302501	0.0485	1.07633	0.2115	CDS conserved hypothetical protein 2567248:2567742 reverse MW:17864
RPA2265	0.748731	0.9355	0.656792	0.9905	0.978113	0.579	0.720887	0.952	0.740125	0.99	CDS conserved hypothetical protein 2567739:2568734 reverse MW:36019
RPA2266	1.197126	0.0525	0.93767	0.736	1.166827	0.1195	1.354338	0.027	1.808002	0	gst1, parB putative glutathione S-transferase 2568791:2569447 forward MW:23788
RPA2267	1.093423	0.0965	0.945179	0.769	0.821369	0.8655	1.180695	0.108	0.916105	0.8975	CDS hypothetical protein 2569676:2570119 forward MW:15528
RPA2268	0.961088	0.6765	0.873525	0.9235	0.770039	0.9345	0.922156	0.6795	0.747877	0.996	CDS Flavin reductase-like 2570195:2570755 forward MW:20357
RPA2269	1.224221	0.164	0.661458	0.996	1.436743	0.0035	0.815696	0.9315	0.709609	0.9905	CDS conserved unknown protein 2570803:2572605 reverse MW:66996
RPA2270	1.052989	0.365	0.801229	0.903	0.969328	0.5875	1.282336	0.1175	1.001245	0.505	CDS hypothetical protein 2572793:2573764 reverse MW:34918
RPA2271											CDS putative Pyruvate kinase 2573878:2575062 reverse MW:43214
RPA2272	1.045006	0.3465	0.89055	0.895	1.13973	0.101	1.015177	0.4425	0.810936	0.946	CDS conserved unknown protein 2575540:2575887 forward MW:12963
RPA2273											CDS hypothetical protein 2576083:2576379 forward MW:11101
RPA2274	1.134231	0.286	1.001702	0.489	1.316276	0.1785	1.646433	0.0035	1.468081	0.106	CDS hypothetical protein 2576370:2576729 forward MW:13336
RPA2275	1.33188	0.092	0.806498	0.968	1.007931	0.472	1.062928	0.23	1.029042	0.38	CDS putative branched-chain amino acid transport system ATP-binding protein 2576915:2577670 forward MW:27608
RPA2276	1.093202	0.3335	0.736607	0.992	0.844482	0.932	0.778994	0.922	0.925204	0.766	CDS putative branched-chain amino acid transport system ATP-binding protein 2577663:2578409 forward MW:27169
RPA2277	1.008396	0.478	0.68113	0.9955	0.930128	0.8285	0.701892	0.9815	0.811862	0.97	CDS possible ABC transporter, permease protein 2578448:2579323 forward MW:31408
RPA2278	1.011079	0.472	0.744285	0.986	1.062938	0.2275	1.153521	0.163	0.86854	0.857	CDS possible ABC transporter, permease protein 2579325:2580296 forward MW:34716
RPA2279	1.125708	0.1165	0.686033	0.9935	1.471614	0.0105	0.926003	0.703	1.149524	0.1145	CDS unknown protein 2580448:2583054 reverse MW:96485
RPA2280	1.05723	0.2875	1.34365	0.0125	0.814465	0.9395	1.156108	0.1525	1.276189	0.034	CDS putative low-affinity phosphate transport accessory protein 2583631:2584275 forward MW:24519
RPA2281	0.850744	0.8585	1.079427	0.185	0.721465	0.995	0.704568	0.9925	0.925512	0.7795	CDS putative low-affinity phosphate transport protein 2584290:2585306 forward MW:35255
RPA2282	1.146026	0.125	1.24567	0.099	1.134843	0.1235	1.758604	0.006	1.816009	0	CDS conserved hypothetical protein 2585324:2585635 reverse MW:11430
RPA2283	1.239441	0.0025	1.262886	0.0175	1.401319	0.001	1.994619	0.0005	2.227778	0.0005	CDS putative proteic killer suppression protein {plasmid Rts1) 2585678:2585953 reverse MW:10550
RPA2284	1.250654	0.079	1.406553	0.0105	1.186594	0.0665	1.846869	0.006	1.453306	0.0085	CDS SugE homolog, probable drug efflux protein 2586042:2586356 reverse MW:10510
RPA2285	0.866657	0.936	0.881901	0.9375	0.720127	0.9935	0.627505	0.996	0.89803	0.8745	prfC peptide chain release factor 3 2586587:2588212 forward MW:59638
RPA2286	1.675946	0.001	1.87769	0	1.58229	0.003	2.378795	0.002	3.294724	0	CDS hypothetical protein 2589207:2590193 reverse MW:37454
RPA2287	1.920605	0.0025	2.047698	0	1.686157	0.017	2.67129	0.004	4.12882	0	CDS hypothetical protein 2590350:2591336 forward MW:37335
RPA2288	2.230186	0.002	2.295102	0.0135	2.209999	0.0095			1.139009	0.292	CDS Streptomyces cyclase/dehydrase 2591445:2591903 reverse MW:17102
RPA2289	2.16515	0.075	0.831837	0.9515	2.200934	0.0025	1.950352	0.012	2.577953	0.006	CDS hypothetical protein 2592184:2593512 forward MW:49027
RPA2290	1.573012	0	1.111957	0.146	1.34416	0.0065	2.255023	0.0005	2.085441	0.028	CDS conserved hypothetical protein 2593524:2595245 forward MW:58397
RPA2291	1.178492	0.0315	1.066447	0.2665	1.10044	0.2185	1.115708	0.2315	1.216457	0.1265	CDS putative Adenylate/Guanylate cyclase 2595381:2597675 forward MW:82107
RPA2292	1.409993	0.0085	1.695337	0.005	1.075349	0.2	2.117586	0.003	2.118005	0.001	CDS sensor histidine kinase 2597690:2599114 reverse MW:51934
RPA2293	0.977788	0.591	1.106538	0.206	1.020417	0.4065	1.378406	0.016	1.352537	0.008	CDS hypothetical protein 2599302:2599898 reverse MW:22169
RPA2294	1.475316	0.009	1.294783	0.0545	1.162408	0.1315	1.754183	0.0385	1.391336	0.0225	CDS probable transcriptional regulator, TetR family 2600118:2600813 forward MW:25744
RPA2295	0.963926	0.669	1.054631	0.298	0.828785	0.976	1.167565	0.239	1.283258	0.028	CDS unknown protein 2601286:2601942 forward MW:22659
RPA2296			0.682931	0.9595	0.727828	0.9155	0.848136	0.834	0.921805	0.718	CDS conserved hypothetical protein 2601939:2602415 forward MW:17488
RPA2297	1.132741	0.3215			0.879163	0.652	1.736721	0.004	0.857138	0.5995	CDS conserved unknown protein 2602665:2605472 forward MW:93059
RPA2298			0.731542	0.9765	1.248892	0.1855	1.616996	0.006	1.042271	0.441	CDS hypothetical protein 2605541:2606095 forward MW:20530
RPA2299	0.772106	0.9305	0.75641	0.9505	1.494996	0.021	1.036842	0.3475	0.871572	0.919	CDS possible two-component transcriptional regulator, LuxR family 2606224:2606970 forward MW:26641
RPA2300	0.838181	0.9185	0.769153	0.987	0.755103	0.9655	1.016458	0.462	0.758452	0.977	CDS Bacterial regulatory protein, LuxR family 2607195:2607848 forward MW:22872
RPA2301	0.827554	0.9585	1.170559	0.142	1.003667	0.4865	0.848708	0.792	0.97054	0.6125	CDS probable transcriptional regulator, AraC family 2607873:2608865 reverse MW:36725
RPA2302	0.725554	0.9605	0.894397	0.8515	0.693595	0.9385	0.661736	0.946	0.526606	0.9975	CDS acyl-CoA synthetase 2609019:2610710 forward MW:60776
RPA2303	0.805447	0.946	0.741134	0.9885	0.936119	0.7585	0.599231	0.999	0.444156	1	CDS putative 3-hydroxyacyl-CoA dehydrogenase 2610729:2611496 forward MW:26329
RPA2304	0.987663	0.5415	0.799224	0.983	0.888617	0.836	0.741595	0.971	0.620832	0.9995	CDS putative acyl-CoA thiolase 2611555:2612742 forward MW:40814
RPA2305	0.971777	0.6205	0.910685	0.9075	1.064177	0.22	0.72674	0.9925	0.534023	0.9995	CDS acyl-CoA dehydrogenase 2612750:2613877 forward MW:40257
RPA2306	1.264684	0.0225	1.240771	0.0595	1.280271	0.039	1.196209	0.172	1.19198	0.0655	CDS Nickel-dependent hydrogenase b-type cytochrome subunit 2614239:2614787 forward MW:20221
RPA2307	1.283935	0.2205	3.746692	0	1.498894	0.042	0.800483	0.755	1.021143	0.47	CDS possible tonB-dependent receptor precursor 2614856:2617183 reverse MW:83375
RPA2308	1.029902	0.436	2.508124	0.0165	0.98738	0.5195	1.220356	0.325	0.656293	0.8905	CDS possible periplasmic iron siderophore binding protein of ABC transporter 2617418:2618596 forward MW:42682
RPA2309	0.840361	0.7935	1.548913	0.001	0.829772	0.976	1.058952	0.314	0.786222	0.9875	CDS putative iron chelatin ABC transporter, permease subunit 2618593:2619684 forward MW:37333
RPA2310					0.550956	0.964					CDS putative iron ABC transporter ATP-binding protein 2619681:2620451 forward MW:27928
RPA2311	0.56901	0.929	1.404333	0.042	0.689604	0.981	0.402135	0.9895	0.345919	0.9955	CDS hypothetical protein 2620446:2621075 reverse MW:23598
RPA2312	0.507154	0.9725	1.430451	0.0365	0.568858	0.998	0.198189	0.9755	0.287742	0.9785	CDS hypothetical protein 2621072:2621737 reverse MW:24032
RPA2313	0.449562	0.9645	1.313185	0.0185	0.601376	0.9985	0.295968	0.9865	0.237194	0.9985	CDS unknown protein 2621691:2622218 reverse MW:19205
RPA2314	0.405788	1	0.410527	1	0.61391	0.9995	0.38921	0.9995	0.267569	1	CDS cytochrome c556 2622816:2623256 forward MW:15200
RPA2315	0.460359	0.9985	0.517296	0.999	0.642092	0.9985	0.495817	0.9995	0.356782	0.997	CDS putative nickel-dependent hydrogenase, b-type cytochrome subunit 2623260:2623934 forward MW:24178
RPA2316	0.611713	0.999	0.795836	0.98	0.554704	0.9995	0.771454	0.8	0.47022	0.991	CDS enoyl-CoA hydratase 2623966:2624751 reverse MW:27653
RPA2317	0.671515	0.992	0.855417	0.9435	0.610263	0.9965	0.745346	0.894	0.592745	0.9915	gctB putative CoA transferase, small subunit B 2624776:2625570 reverse MW:28269
RPA2318	0.59141	0.946	1.002532	0.4825	0.46763	0.9975	0.704633	0.8705	0.379421	1	gctA possible glutaconate CoA-transferase, subunit A 2625567:2626562 reverse MW:36403
RPA2319	0.524229	0.928	1.182389	0.159	0.370679	0.9935	0.767621	0.7425	0.302647	0.999	CDS Uncharacterized protein family UPF0065 2626690:2627682 reverse MW:34093
RPA2320	0.723777	0.914	1.080743	0.347	0.453965	0.9845	0.952743	0.649	0.391201	1	CDS possible TctA subunit of the Tripartite Tricarboxylate Transport(TTT) Family 2627760:2629262 reverse MW:52350
RPA2321	0.765283	0.963	0.9664	0.5935	0.533181	0.998	1.174924	0.1185	0.475158	0.9985	CDS possible TctB subunit of the Tripartite Tricarboxylate Transporter(TTT) Family 2629262:2629738 reverse MW:16234
RPA2322	1.017959	0.413	1.193332	0.047	1.148213	0.071	0.923383	0.804	0.93034	0.824	CDS transcriptional regulator, LysR family 2630453:2631346 forward MW:32849
RPA2323									0.69413	0.6695	goaT 4-aminobutyrate aminotransferase 2631514:2632788 forward MW:44855
RPA2324									0.885558	0.831	gabD2 succinate-semialdehyde dehydrogenase 2632826:2634277 forward MW:51499
RPA2325	1.296958	0.054	1.075658	0.2175	1.530055	0.0025	1.843784	0.0025	1.144226	0.179	CDS possible acetylornithine deacetylase 2634327:2635625 forward MW:46918
RPA2326	0.758831	0.9955	0.878271	0.787	0.681472	0.9985			0.646243	0.998	CDS acetolactate synthase I 2635625:2637214 forward MW:56649

RPA2327			1.774259	0.0125			3.641891	0.0095	1.249856	0.1515	CDS putative ABC transporter oligopeptide-binding protein 2637293:2638882 forward MW:59230
RPA2328	1.255781	0.1775	1.320544	0.0875	1.287452	0.096	2.151156	0.026	0.973167	0.6115	CDS putative ABC transporter permease protein 2638879:2639901 forward MW:36761
RPA2329	1.080247	0.205	1.199022	0.047	0.993629	0.527	1.486832	0.0065	1.168961	0.0255	CDS putative ABC transporter permease protein 2639914:2640753 forward MW:29628
RPA2330	1.114621	0.1585	1.210453	0.251	1.214134	0.0275	1.409516	0.0135	1.064175	0.3315	CDS putative ABC transporter ATP-binding protein 2640750:2642408 forward MW:59249
RPA2331	0.770802	0.983			0.785263	0.9675			0.777592	0.9365	ggt2 possible gamma-glutamyltranspeptidase 2642483:2644060 forward MW:56102
RPA2332	0.914531	0.876	0.954349	0.725	0.840591	0.936	0.733986	0.9905	0.788127	0.9885	CDS Rare lipoprotein A:Staphylococcus nuclease (SNase-like) 2644354:2645508 forward MW:41055
RPA2333	1.095757	0.138	1.069902	0.195	1.129471	0.133	0.998946	0.5105	0.702967	0.99	ctpC putative cation transport ATPase, possible copper transporter 2645744:2647840 reverse MW:73612
RPA2334	1.079739	0.179	1.322376	0.009	1.056758	0.2985	1.285038	0.0765	0.747598	0.9885	CDS unknown protein 2647837:2648175 reverse MW:12089
RPA2335	3.456201	0.003	1.609293	0.002	2.426442	0.0005	4.399243	0	7.937943	0.0005	CDS unknown protein 2648168:2648509 reverse MW:11443
RPA2336	1.325003	0.0225	1.376423	0.015	1.256983	0.0075	1.457622	0.047	0.867902	0.871	CDS unknown protein 2648496:2648819 reverse MW:10907
RPA2337	1.344333	0.047	1.362235	0.026	1.376303	0.069	1.152386	0.3075	0.87554	0.855	CDS hypothetical protein 2648837:2649169 reverse MW:11910
RPA2338	1.189359	0.01	1.31938	0.016	1.46603	0.0105	1.367981	0.0525	0.878657	0.8215	CDS unknown protein 2649177:2649677 reverse MW:17883
RPA2339	2.491495	0.001	1.858519	0.0165	2.174132	0.003	2.881848	0.0005	2.541037	0.0005	CDS transcriptional regulator, FUR family; possible iron response regulator IRR 2650175:2650666 forward MW:18274
RPA2340	0.980555	0.623	1.085401	0.129	1.013971	0.429	1.06091	0.27	0.914046	0.865	CDS putative membrane protein 2650793:2652166 reverse MW:49183
RPA2341	1.02746	0.389	0.988768	0.5705	0.941676	0.754	0.902068	0.834	0.85646	0.9745	ilvD putative dihydroxy-acid dehydratase 2652218:2653897 reverse MW:59253
RPA2342	1.038262	0.323	1.129971	0.107	1.107598	0.1865	1.475465	0.0095	1.110279	0.1985	CDS putative transmembrane transport protein 2653962:2655269 reverse MW:47050
RPA2343	0.781867	0.9165	1.401797	0.016	0.675425	0.9615	1.45918	0.016	1.021045	0.4195	CDS transcriptional regulator, GntR family 2655678:2656355 forward MW:25645
RPA2344	0.651303	0.9055	1.45025	0.032	0.367598	0.9945	1.036783	0.376	0.363375	0.999	CDS conserved unknown protein 2656394:2657014 reverse MW:22287
RPA2345	0.613546	1	0.807024	0.814	0.372558	1	0.821372	0.98	0.314824	1	CDS unknown protein 2657015:2658025 reverse MW:35635
RPA2346	0.325696	0.981			0.486546	0.9885	0.713209	0.756	0.2207	0.9995	CDS hypothetical protein 2658270:2659448 reverse MW:41201
RPA2347	0.371842	0.952	1.443022	0.025	0.284668	0.9825	2.923297	0.004	0.412375	0.998	CDS possible vanadium nitrogenase associated protein N (U51863) 2659490:2660881 reverse MW:49919
RPA2348	0.415868	0.938	1.663869	0.038	0.259928	0.977	1.734858	0.0295	0.317606	0.9985	CDS possible nitrogenase molybdenum-iron protein alpha chain (nitrogenase component I) (dinitrogenase) 2660881:2662416 reverse MW:55375
RPA2349	0.555985	0.949	1.13315	0.253	0.496917	0.9805	1.558644	0.0095	0.362279	1	metY putative homocysteine synthase 2662641:2663834 reverse MW:41958
RPA2350	0.528904	0.9635	1.011914	0.4675	0.638872	0.9565	1.520537	0.005	0.414846	0.999	metC putative O-acetylhomoserine sulfhydrylase 2664108:2665409 forward MW:46335
RPA2351	0.521602	0.9935	0.391438	0.978	0.457305	0.9995	1.502291	0.002	0.51504	0.9895	CDS transcriptional regulator, AsnC family 2665574:2666062 reverse MW:18216
RPA2352	0.196522	0.941	0.842296	0.715	0.233871	0.9875	1.040934	0.456	0.183188	1	CDS conserved hypothetical protein 2666343:2666840 reverse MW:18060
RPA2354	0.388693	0.992	0.794828	0.731	0.303109	0.9775	1.583022	0.0125	0.153592	1	nifB2 putative nitrogenase iron-molybdenum cofactor biosynthesis protein NifB 2667804:2668727 reverse MW:32895
RPA2355	0.22238	1	0.305648	0.975	0.17726	1	1.133089	0.2505	0.133803	1	CDS possible nitrogenase NifB 2668724:2669107 reverse MW:13520
RPA2356	0.57016	0.968	0.586735	0.94	0.349166	1	0.956971	0.6165	0.213885	1	CDS putative cystathionine beta-synthase 2669577:2670974 forward MW:50427
RPA2357	0.527094	0.86	1.863872	0.049	0.403851	0.985	1.561489	0.0735	0.272764	0.991	CDS cystathionine gamma-lyase 2670976:2672148 forward MW:41844
RPA2358	0.514707	0.979	0.788702	0.977	0.425011	1	1.088286	0.2125	0.391617	1	CDS 2OG-Fe(II) oxygenase superfamily 2672250:2673296 reverse MW:38594
RPA2359	0.194747	1	0.525179	0.9795	0.22151	0.9915	0.886958	0.8345	0.16709	1	CDS putative periplasmic protein 2673702:2674571 forward MW:30763
RPA2360											CDS ABC transporter, ATP-binding protein 2674580:2675713 forward MW:39781
RPA2361	0.497103	0.8805	1.529509	0.018	0.319675	0.9875	1.030841	0.442	0.378704	0.9905	CDS putative ABC transporter, permease protein 2675667:2676368 forward MW:24039
RPA2362	0.332652	0.972	1.206853	0.0435	0.452357	0.991	1.019643	0.4665	0.397463	0.9975	CDS putative O-acetylhomoserine sulfhydrylase 2676404:2677717 forward MW:46651
RPA2363	0.983987	0.5785	1.048255	0.2485	0.982364	0.597	1.049419	0.3245	0.958431	0.743	NifD1 possible nitrogenase molybdenum-iron protein alpha chain (nitrogenase component I) (dinitrogenase) 2677746:2679251 forward MW:54625
RPA2364	0.248905	0.9975	0.618167	0.9035	0.486025	0.9665	1.245602	0.083	0.697784	0.879	CDS possible nitrogenase iron-molybdenum cofactor biosynthesis protein NifE homolog 2679264:2680643 forward MW:49727
RPA2365	0.573568	0.997	0.617013	0.95	0.572221	0.99	1.568787	0.0025	0.416315	0.995	CDS putative L-allo-threonine aldolase 2680655:2681755 reverse MW:38483
RPA2366	1.437007	0.099	1.502754	0.0135	1.371861	0.191	2.478603	0.0005			CDS hypothetical protein 2682058:2682309 forward MW:8602
RPA2367	1.074601	0.2545	1.072262	0.196	1.170056	0.0485	1.338998	0.0115	1.061778	0.2805	CDS two component sensor histidine kinase, possible AdeS 2682429:2683532 reverse MW:39505
RPA2368	1.222557	0.0855	1.038348	0.3565	1.029391	0.359	1.087711	0.1585	1.282366	0.04	CDS pseudogene-two-component transcriptional regulator, winged helix family 2683529:2683762 reverse MW:8366
RPA2369											CDS pseudogene-two-component transcriptional regulator, winged helix family 2683800:2684213 reverse MW:15283
RPA2370	0.952485	0.6355	1.165752	0.2415	0.94663	0.604	0.736317	0.6385	0.92522	0.5515	CDS hypothetical protein 2684472:2684612 reverse MW:4866
RPA2371	1.094097	0.3835			1.00934	0.5135			0.890562	0.662	mexA putative RND multidrug efflux membrane fusion protein MexA precursor 2684924:2686141 forward MW:42596
RPA2372											mexB RND multidrug efflux transporter MexB 2686138:2689305 forward MW:111866
RPA2373											CDS possible outer membrane protein 2689314:2690843 forward MW:53510
RPA2374	1.010259	0.444	0.903531	0.8615	0.912491	0.818	1.032709	0.4065	1.07888	0.225	CDS hypothetical protein 2690837:2691043 forward MW:7243
RPA2375	1.139381	0.211	1.464556	0.0275	0.881168	0.8425	1.340386	0.073	1.064632	0.3885	CDS conserved hypothetical protein 2691216:2692823 forward MW:57698
RPA2376	1.221741	0.187			0.964836	0.5655			1.225867	0.2415	CDS conserved hypothetical protein 2692943:2693468 forward MW:18979
RPA2377	5.985494	0	5.704046	0	3.80715	0.0015	5.358756	0	3.839857	0	CDS conserved hypothetical protein 2693666:2693968 reverse MW:11229
RPA2378	12.59882	0	14.01393	0	7.50326	0	14.36514	0	7.355683	0	CDS putative tonB-dependent receptor protein 2694083:2696398 reverse MW:83219
RPA2379	7.406431	0	11.82279	0	4.348475	0			3.269279	0.001	CDS probable acetyltransferase 2696546:2697043 reverse MW:18629
RPA2380	2.884895	0	8.246089	0.0005	2.10839	0.005	10.40255	0.0015	2.539733	0.001	CDS probable tonB dependent iron siderophore receptor 2697057:2699288 reverse MW:79606
RPA2381	1.745991	0	1.420323	0.003	1.306652	0.0175	1.186863	0.1	1.192995	0.041	fecR4 probable FecR, iron siderophore sensor protein 2699387:2700403 reverse MW:36801
RPA2382	2.715532	0.0065	2.575408	0	1.491874	0.107			1.425828	0.0515	CDS putative iron(III) ABC transporter, ATP-binding protein 2700496:2701254 reverse MW:27522
RPA2383	0.894229	0.923	0.902565	0.816	1.323787	0.0145	0.803277	0.9595	0.871874	0.946	CDS putative iron(III) ABC transporter, permease protein 2701251:2702201 reverse MW:33340
RPA2384	1.532615	0.0025	1.62668	0.004	1.194605	0.014	0.941356	0.6625	0.896013	0.904	CDS putative ironIII transport permease protein 2702194:2703171 reverse MW:34080
RPA2385	3.987971	0	3.813327	0	2.335226	0.002	3.033856	0	1.87185	0.001	CDS putative ABC transporter, periplasmic Fe+3 siderophore binding protein, 2703168:2704073 reverse MW:31963
RPA2386	7.819284	0	8.119644	0.0005	4.572945	0	5.793326	0	5.718011	0	CDS conserved hypothetical protein 2704064:2704981 reverse MW:33691
RPA2387	6.962817	0	7.698356	0	4.693578	0.001	5.251701	0	4.845772	0.0005	CDS conserved hypothetical protein 2704981:2706291 reverse MW:49311
RPA2388	1.205683	0.074	2.256005	0.0005	1.037055	0.364	2.033068	0.001	1.388631	0.1235	CDS possible acyl-CoA ligase for activation during siderophore synthesis 2706288:2707556 reverse MW:45450
RPA2389	1.925125	0.016	1.655938	0.0165	1.451904	0.0225	2.769128	0.0005	2.219177	0.0025	CDS possible Rhizobactin siderophore biosynthesis protein RhsF 2707553:2709241 reverse MW:63208
RPA2390	5.793993	0	9.09153	0.0005	4.322898	0.0005	5.031112	0	3.830663	0.0005	CDS possible Rhizobactin siderophore biosynthesis protein rhbC 2709270:2711051 reverse MW:66376
RPA2391	1.677714	0.0045	2.032708	0.001	1.643346	0.0165	2.09835	0.0095	1.951444	0	CDS RNA polymerase ECF-type sigma factor, possible FecI 2711220:2711837 forward MW:23417
RPA2393											CDS pseudogene with part of ABC ATPase and transcriptional regulator 2712025:2713205 reverse MW:43759
RPA2394											prpC putative 2-methylcitrate synthase 2713351:2714226 forward MW:32286
RPA2395	1.122044	0.0575	1.090617	0.2395	1.055061	0.2825	1.147568	0.23	1.002364	0.4925	prpB putative carboxyphosphonoenolpyruvate phosphonomutase 2714237:2715154 forward MW:32729
RPA2396											CDS DUF208 2715184:2715783 forward MW:22464
RPA2397	0.87202	0.9045	0.883081	0.936	0.800096	0.98	0.776208	0.976	0.910684	0.719	metE 5-methyltetrahydropteroyltriglutamate-homocystein e methyltransferase 2716133:2718499 forward MW:86303
RPA2398	1.144134	0.2565	1.303518	0.0715	0.991496	0.5145	0.88954	0.692	1.273837	0.181	CDS iron siderophore uptake receptor family, probable Mg/Co uptake 2719364:2721757 forward MW:87725
RPA2399	0.904595	0.778	0.736724	0.9295	0.676471	0.8515	0.7659	0.74	0.829891	0.8865	CDS CobN/Magnesium chelatase family 2721766:2725668 forward MW:141441
RPA2400			0.686423	0.9565							CDS conserved hypothetical protein 2725671:2726141 forward MW:17273
RPA2401											CDS conserved unknown protein 2726141:2726476 forward MW:12335
RPA2402											CDS hypothetical protein 2726837:2727190 forward MW:13003
RPA2403	0.694616	0.916	0.818212	0.965	0.79765	0.9045	0.765831	0.89	0.75711	0.978	CDS possible iron-chelator utilization protein 2727725:2728216 forward MW:16981
RPA2404	0.573144	0.9995	0.518478	1	0.762263	0.9945	0.214438	1	0.30933	1	CDS probable transcriptional regulator, AraC family 2728872:2729876 forward MW:36812
RPA2405	1.038621	0.404	1.226164	0.025	0.812001	0.8735	0.823317	0.871	0.796426	0.9685	draT2 NAD+ ADP-ribosyltransferase 2729949:2730821 forward MW:32341

RPA2406	0.976471	0.575			0.932883	0.7255			0.884713	0.7055	draG dinitrogenase reductase activating glycohydrolase 2730833:2731723 forward MW:31629
RPA2407							1.181164	0.3275			CDS hypothetical protein 2732218:2732553 reverse MW:12201
RPA2408											amiC1 putative aliphatic amidase expression-regulating protein, AmiC 2732949:2734106 forward MW:41316
RPA2409	2.17769	0.0005	2.880985	0.01	2.489723	0.0015	5.955716	0.007	4.266905	0.003	CDS possible AmiR antitermination protein 2734103:2734768 forward MW:24278
RPA2410	3.360671	0.001	4.002783	0	3.31318	0	11.10708	0.0005	7.55581	0	CDS putative urea/short-chain amide transport system substrate-binding protein 2734780:2736018 forward MW:45493
RPA2411									1.279087	0.2535	CDS putative permease of ABC transporter 2736137:2737009 forward MW:30148
RPA2412	2.828258	0.04	2.514271	0.002	2.146328	0.002			1.828925	0.0015	CDS possible permease of ABC transporter 2737021:2738085 forward MW:37776
RPA2413	1.00193	0.496	0.882181	0.9545	0.919557	0.767	0.895224	0.8285	0.835433	0.9685	CDS putative urea/short-chain amide transport system ATP-binding protein 2738085:2738807 forward MW:26159
RPA2414							2.430681	0.01			CDS putative urea/short-chain amide transport system ATP-binding protein 2738800:2739513 forward MW:25911
RPA2415									1.618251	0.059	CDS Acetamidase/Formamidase 2739539:2740528 forward MW:35782
RPA2416	2.01746	0	1.865907	0.006	1.585087	0.0025	3.499025	0	2.949124	0	CDS Nitrilase/cyanide hydratase and apolipoprotein N-acyltransferase 2740543:2742282 forward MW:62940
RPA2417	1.033585	0.383	1.084703	0.184	0.992891	0.5245	1.035284	0.3955	1.203285	0.027	CDS putative 3-ketoacyl-CoA reductase 2742298:2743059 forward MW:25761
RPA2418					1.278945	0.0545	1.325135	0.0835	1.925622	0.0005	CDS pseudogene of ABC transporter, ATPase subunit 2743363:2743983 reverse MW:22470
RPA2420	0.885315	0.9345	0.85257	0.98	0.94013	0.752	0.747168	0.9855	0.792585	0.9825	CDS putative soluble lytic murein transglycosylase precursor 2747337:2749574 reverse MW:81065
RPA2422	0.924832	0.7845	0.861508	0.909	0.899384	0.928	0.967885	0.6005	1.160709	0.0475	CDS Family of unknown function ThiJ/PfpI 2751142:2751831 reverse MW:24545
RPA2423	0.891021	0.7725	1.182848	0.021	1.124111	0.173	1.266018	0.0385	0.954143	0.642	CDS probable transcriptional regulator, AraC family 2751955:2752893 forward MW:33683
RPA2425	0.803174	0.977	0.657325	0.999	0.882087	0.8625	0.491712	0.998	0.533916	0.9995	CDS putative lipase/esterase 2754356:2755300 reverse MW:33752
RPA2426	0.835296	0.978	0.803393	0.984	0.879487	0.944	0.718927	0.996	0.827227	0.981	CDS hypothetical protein 2755533:2756522 forward MW:34573
RPA2427	1.003638	0.4935	0.805511	0.99	0.673947	0.979	0.871379	0.9335	1.238467	0.01	CDS Serine protease, trypsin family 2756723:2757967 reverse MW:43873
RPA2428			0.632626	0.986			0.944559	0.65	0.92278	0.6095	CDS hypothetical protein 2758031:2758351 reverse MW:11064
RPA2429	1.086135	0.357	0.659991	0.9685	1.142826	0.2395	0.968934	0.5675	0.958869	0.6415	aat putative leucyl/phenylalanyl-tRNA-protein transferase 2758475:2759158 reverse MW:24909
RPA2430	1.121638	0.281	1.545867	0.0025	0.707639	0.996	0.769058	0.976	1.138	0.152	CDS conserved hypothetical protein 2759213:2760640 reverse MW:50332
RPA2431	0.779089	0.959	0.689696	0.9935	1.037213	0.285	0.809405	0.818	0.686942	0.992	CDS conserved hypothetical protein 2760673:2761344 reverse MW:24108
RPA2432	1.174814	0.021	1.347941	0.0305	1.386858	0.004	1.053137	0.318	1.187631	0.073	CDS putative signal transduction histidine kinase with response regulator receiver domain 2761477:2762568 reverse MW:39311
RPA2433	1.008873	0.4355	1.397916	0.038	0.889548	0.915	0.951123	0.6605	1.077766	0.2095	CDS response regulator receiver (CheY-like protein) 2762565:2763008 reverse MW:16338
RPA2434	1.43112	0.0355	2.294843	0.014	1.54732	0.0215	1.300727	0.2115	1.845513	0.004	CDS sensor histidine kinase 2763005:2764537 reverse MW:56851
RPA2435	0.907606	0.8015	0.928825	0.812	0.759889	0.9555	0.798588	0.961	1.05186	0.316	accC biotin carboxylase 2764725:2766077 reverse MW:48662
RPA2436	0.676852	0.962	0.918565	0.8665	0.562391	0.9965	0.506214	0.9975	0.746205	0.9825	accB putative biotin carboxyl carrier protein of acetyl-CoA carboxylase 2766195:2766689 reverse MW:17010
RPA2437	1.050986	0.351	1.634451	0.003	0.612118	0.9965	1.161481	0.2345	1.27044	0.0795	aroQ2 3-dehydroquinate dehydratase type 2 2766728:2767183 reverse MW:16014
RPA2438	0.878861	0.7485	0.87578	0.9175	1.116115	0.1105	1.127333	0.239	1.344968	0.008	CDS hypothetical protein 2767477:2768148 reverse MW:23795
RPA2439	0.609371	0.988	0.851223	0.943	0.860956	0.774	0.677308	0.978	0.571766	0.9975	CDS conserved hypothetical protein 2768379:2768627 forward MW:9355
RPA2440	0.823829	0.9615	0.834819	0.9505	1.022417	0.4045	0.804706	0.9495	1.235244	0.0385	CDS Cation efflux protein 2768965:2769918 forward MW:34229
RPA2441	0.658012	0.9855	0.803198	0.944	0.598847	0.9985	0.826835	0.827	1.044303	0.3585	CDS possible transcriptional regulator, TetR family 2769906:2770598 forward MW:25343
RPA2442	0.911011	0.932	0.877983	0.924	0.982505	0.597	0.939536	0.7825	0.903917	0.9015	CDS putative outer membrane protein 2770683:2771450 reverse MW:27686
RPA2443	0.559964	0.9985	0.591077	0.9985	0.682045	0.9965	0.553819	0.997	0.510054	1	CDS probable antioxidant protein 2771641:2772330 reverse MW:25740
RPA2444	1.025916	0.396	0.77727	0.993	1.414168	0.0045	1.005136	0.478	0.893928	0.885	CDS unknown protein 2772482:2772871 reverse MW:13348
RPA2445	1.146418	0.092	0.858866	0.8565	1.084227	0.2675	1.105512	0.3395	1.10386	0.147	CDS conserved hypothetical protein 2773057:2774484 reverse MW:50980
RPA2446	1.197462	0.0355	1.029103	0.379	1.099589	0.2785	1.102519	0.2575	1.171481	0.0235	CDS putative aminotransferase 2774592:2775782 forward MW:43057
RPA2448	0.800415	0.9775	0.90972	0.9005	0.554183	0.99	0.697511	0.967	1.099058	0.138	dctA2 C4-dicarboxylic acid transport protein 2776597:2777934 forward MW:46844
RPA2449	1.226166	0.0725	1.350442	0.013	0.815502	0.98	1.399539	0.0255	1.308733	0.0135	CDS hypothetical protein 2778036:2779055 reverse MW:38636
RPA2450	1.12669	0.05	1.050617	0.2115	1.135795	0.042	1.113914	0.139	1.051223	0.2545	rne putative ribonuclease E 2779169:2782324 reverse MW:115619
RPA2451	0.990554	0.5495	0.856104	0.9635	0.925513	0.8415	0.931206	0.7465	1.01269	0.4305	CDS putative N-acetylmuramoyl-L-alanine amidase 2782905:2784335 forward MW:51257
RPA2452	0.800928	0.9425	0.839484	0.9585	0.962667	0.6585	0.662338	0.9975	0.832054	0.9325	CDS putative penicillin-binding protein 1A 2784555:2787053 forward MW:91473
RPA2453	0.702567	0.9815	0.791103	0.9905	0.523468	0.9985	0.691231	0.993	0.701698	0.9995	prfB translation peptide releasing factor RF-2 2787334:2788302 forward MW:35502
RPA2454	1.040979	0.4005	0.879698	0.7585	0.842796	0.729	1.344172	0.0295	0.910277	0.6885	CDS putative dehydrogenase 2788309:2789202 forward MW:31199
RPA2455	1.057405	0.2055	0.886345	0.9315	0.721602	0.9925	0.872605	0.926	0.825594	0.9885	CDS Peptidase M23/M37 2789329:2790699 reverse MW:49615
RPA2456	0.788506	0.9895	0.831024	0.982	0.990896	0.542	0.919655	0.779	0.86217	0.9655	CDS possible bacterioferritin co-migratory protein 2790796:2791485 reverse MW:23830
RPA2458	0.963809	0.7105	0.90357	0.83	1.120388	0.127	0.629255	0.9975	0.561278	0.997	CDS putative cytochrome b561 2795551:2796111 reverse MW:20300
RPA2459	0.904547	0.922	0.928084	0.825	1.422617	0.01	0.706716	0.989	0.599816	0.9945	CDS putative permease 2796332:2797549 reverse MW:43336
RPA2460	1.166479	0.021	1.071722	0.183	0.795773	0.981	1.133581	0.124	1.232076	0.019	tyrS tyrosyl-tRNA synthetase 2797634:2798890 reverse MW:46039
RPA2461	1.41075	0.0095	1.157069	0.113	0.974938	0.5795	1.78988	0.011	1.43461	0.0045	CDS Protein of unknown function UPF0075 2799048:2800151 forward MW:38390
RPA2462	0.858562	0.936	1.094504	0.0955	0.765471	0.9835	1.055246	0.316	0.941946	0.8335	CDS conserved unknown protein 2800206:2800853 reverse MW:23976
RPA2463	0.917121	0.8405	0.812231	0.923	1.056365	0.34	0.895801	0.8005	0.957896	0.615	nifS1 putative cysteine desulfurase, nifS homolog 2801091:2802263 forward MW:40148
RPA2464	2.924913	0.002	1.594674	0.004	2.135065	0.0015	3.251337	0	4.846944	0	sufB sufB, needed for fhuF Fe-S center stability 2802346:2803827 forward MW:54960
RPA2465	2.773754	0.0005	2.010907	0	1.882838	0.0005	5.542223	0	5.01671	0	sufC sufC, related to ABC transporter ATP-binding protein 2803960:2804718 forward MW:27404
RPA2466	1.3543	0.058	1.280215	0.0255	1.073519	0.253	2.16729	0.002	1.722971	0.008	sufD sufD, needed for fhuF Fe-S center production/stability 2804742:2806055 forward MW:46403
RPA2467	2.99536	0.0005	1.894545	0	2.10054	0	4.732188	0	6.348527	0	sufS sufS, putative selenosysteine lyase 2806052:2807299 forward MW:45681
RPA2468	2.10889	0.002	1.578247	0.001	1.997759	0	3.642126	0	3.863163	0	CDS DUF59 2807296:2807664 forward MW:13425
RPA2469	1.735741	0.002	2.079778	0	2.001377	0.0005	5.046322	0	4.01925	0	CDS putative lactoylglutathione lyase 2807693:2808088 forward MW:14613
RPA2470	1.521959	0.0025	1.557138	0.0015	2.013237	0.001	3.371227	0	3.562517	0	CDS Protein of unknown function, HesB/YadR/YfhF 2808218:2808589 forward MW:13325
RPA2471	1.171423	0.2715	0.568564	0.9295	0.676024	0.9545			0.714977	0.914	CDS unknown protein 2808744:2810708 forward MW:71688
RPA2472											CDS hypothetical protein 2810714:2811814 forward MW:38700
RPA2473	0.722805	0.969	0.538954	0.9955	0.674941	0.9795	0.63654	0.938	0.432132	0.9995	CDS possible translation initiation inhibitor 2811811:2812284 forward MW:16492
RPA2474									2.678743	0	CDS possible o-linked GlcNac transferase 2812370:2814040 forward MW:60118
RPA2475	1.120137	0.208	0.880864	0.756	1.168832	0.2455	1.417294	0.107	1.298007	0.06	CDS TfoX, N-terminal 2814065:2814661 forward MW:21564
RPA2476	1.38479	0.0075	1.379612	0.002	0.954037	0.7235	1.631579	0.0165	1.356807	0.0035	CDS putative diguanylate cyclase (GGDEF) 2814670:2815737 reverse MW:39169
RPA2477	1.204126	0.033	1.435863	0.005	1.101779	0.2455	1.640416	0.0105	1.604505	0.001	CDS possible ATP-dependent RNA helicase 2815836:2817254 reverse MW:51467
RPA2478	1.249173	0.034	1.600708	0.0045	1.273829	0.0925	1.717643	0.0115	1.881577	0.001	CDS probable transcriptional regulator, AraC family 2817528:2818619 reverse MW:40970
RPA2479	1.450738	0.001	1.555389	0.0025	1.342685	0.0025	2.768522	0	3.609832	0	CDS methyl-accepting chemotaxis receptor/sensory transducer 2818822:2820561 forward MW:62024
RPA2480	1.291068	0.0275	0.910557	0.8445	1.195095	0.112	1.346607	0.073	1.13405	0.173	CDS unknown protein 2820739:2822244 forward MW:54636
RPA2481	1.06548	0.2555	1.015084	0.412	1.163083	0.0725	1.61288	0.0005	2.577722	0	CDS possible transcriptional regulator, XRE family 2822299:2823135 reverse MW:30636
RPA2482									0.979762	0.504	CDS probable epimerase/dehydratase 2823234:2824139 forward MW:31884
RPA2483											CDS hypothetical protein 2824175:2824552 reverse MW:13717
RPA2484	1.023029	0.409	0.918551	0.8115	1.105707	0.12	0.987796	0.5255	1.365677	0.0245	CDS conserved hypothetical protein 2824583:2825053 reverse MW:17067
RPA2485	0.804347	0.9895	0.735062	0.9945	0.861158	0.9205	0.868543	0.8245	0.865713	0.8785	aqpZ aquaporin Z (water channel) 2825375:2826097 forward MW:24508
RPA2486	0.660073	0.984	0.656738	0.9975	0.756289	0.9715	0.620733	0.998	0.739668	0.993	parE DNA topoisomerase 2826143:2828194 reverse MW:74364
RPA2487	0.760144	0.943	0.821363	0.8695	1.061896	0.4015	0.816978	0.9085	0.770261	0.941	CDS possible DedA family. Putative integral membrane protein. 2828652:2829182 forward MW:19299

RPA2488	0.917879	0.8335	0.577255	0.999	1.215861	0.026	0.613054	0.9935	0.546701	0.999	CDS conserved unknown protein 2829268:2830257 forward MW:35328
RPA2489											CDS hypothetical protein 2830404:2830949 reverse MW:20764
RPA2490	0.338842	1	0.490534	0.9985	0.426129	0.999	0.400624	0.9925	0.450244	0.995	CDS conserved hypothetical protein 2831398:2832063 forward MW:23406
RPA2491	0.594198	0.9415	1.057632	0.2265	0.65762	0.967	0.766819	0.889	0.560415	0.999	argC N-acetylglutamate semialdehyde dehydrogenase 2832078:2833073 forward MW:34521
RPA2492			0.940248	0.636	0.426618	0.9785	0.775174	0.8915	0.486379	0.997	CDS Conserved hypothetical protein 2833129:2833740 forward MW:22471
RPA2493											CDS possible P-methylase 2833995:2835791 forward MW:67535
RPA2494	1.719333	0.0035	1.512527	0.012	1.614262	0.0165	2.412882	0.002	1.622277	0.017	CDS hypothetical protein 2836026:2836388 forward MW:12121
RPA2495	1.695614	0.0105	1.725711	0.001	1.572853	0.0015	1.855769	0.003	1.366586	0.008	CDS possible translation initiation inhibitor 2836393:2836791 reverse MW:14362
RPA2496	1.632048	0.003	1.114233	0.1645	1.319143	0.0225	1.741823	0.0095	1.742044	0.0005	CDS transcriptional regulator, GntR family 2837138:2837836 reverse MW:25893
RPA2497			3.890066	0	5.666893	0	23.87371	0	6.816901	0.0005	CDS putative anion ABC transporter, ATP-binding protein 2838147:2838935 forward MW:29176
RPA2498	1.31012	0.008	1.46248	0.0035	1.295499	0.064	2.744435	0.0005	1.771353	0.0065	CDS possible ABC transporter, permease protein 2838935:2839813 forward MW:31741
RPA2499			1.92721	0.0095					4.700337	0.0095	CDS possible ABC transporter, periplasmic protein 2839879:2840856 forward MW:34629
RPA2500	2.272794	0.0065			2.155103	0.0065			2.697802	0.0075	CDS possible amidase 2840927:2842204 forward MW:44183
RPA2501	1.792107	0.0205	1.056234	0.324	1.570027	0.005	1.363352	0.015	1.237367	0.0305	phbC poly-beta-hydroxybutyrate synthase 2842246:2844051 reverse MW:66772
RPA2502	1.088264	0.2765	1.205337	0.0355	1.043245	0.357	1.314044	0.111	1.303746	0.033	CDS unknown protein 2844378:2844683 forward MW:10023
RPA2503	0.876742	0.864	0.872638	0.9315	0.763628	0.994	0.712144	0.9825	0.784242	0.98	CDS possible aminotransferase 2844868:2846088 forward MW:44402
RPA2504	0.751113	0.9815	0.859303	0.973	0.722497	0.997	0.576554	0.9985	0.716647	0.9945	HDH putative homoserine dehydrogenase 2846167:2847492 forward MW:46114
RPA2505	1.078464	0.1655	1.198337	0.027	1.042731	0.2915	0.799503	0.987	0.758827	0.9835	glpX Fructose-1,6-bisphosphatase/sedoheptulose 1,7-bisphosphatase related protein 2847555:2848559 forward MW:35497
RPA2506	1.018022	0.4215	1.172144	0.051	1.016591	0.4265	0.790504	0.977	0.754475	0.9285	CDS possible acetyltransferase 2848668:2849111 forward MW:16588
RPA2507	1.251351	0.0595	0.800575	0.747	1.017869	0.4535	0.752555	0.845	0.563812	0.9885	CDS possible haloacid dehalogenase 2849176:2849901 forward MW:26732
RPA2508	0.953487	0.7605	0.940813	0.7775	0.90397	0.862	0.927055	0.8135	0.865726	0.954	recJ putative single-strand DNA-specific exonuclease 2849930:2851867 forward MW:68646
RPA2509	1.039863	0.4045	1.407888	0.004	0.918026	0.799	1.237471	0.111	1.489443	0.002	CDS hypothetical protein 2852031:2852321 reverse MW:11029
RPA2510	0.608524	0.9935	0.753737	0.95	0.923928	0.8065	0.639878	0.995	0.581251	1	CDS conserved hypothetical protein 2852406:2853524 reverse MW:40696
RPA2511	0.755924	0.994	0.637917	0.9975	0.994897	0.5185	0.66087	0.981	0.740884	0.9855	CDS possible membrane-bound lytic transglycosylase 2853542:2854771 reverse MW:45268
RPA2512			1.744536	0.05	1.85229	0.0045	1.308022	0.1165	1.583908	0.0125	CDS Diacylglycerol kinase related protein 2854994:2855974 forward MW:34614
RPA2513	1.055936	0.2805	1.319617	0.009	0.770178	0.9685	1.057084	0.3595	1.055666	0.309	efp elongation factor P 2856053:2856619 reverse MW:20717
RPA2514			1.332693	0.1475			0.828609	0.888			CDS putative lysyl-tRNA synthetase 2856757:2857812 forward MW:39013
RPA2515	0.867486	0.912	0.851024	0.9285	0.89308	0.9015	0.701631	0.9845	0.70978	0.998	kamA putative L-lysine 2,3-aminomutase 2857809:2858900 forward MW:39554
RPA2516	1.204858	0.0745	1.016324	0.472	1.279104	0.0255	1.416276	0.1015	1.090208	0.23	CDS unknown protein 2859061:2859321 forward MW:8827
RPA2517	1.089354	0.128	1.258165	0.016	1.288882	0.0185	0.889117	0.843	0.98443	0.5535	CDS conserved hypothetical protein 2859349:2859939 reverse MW:21204
RPA2518	1.04844	0.3235	1.140914	0.2285	1.081003	0.2405	5.879725	0.0175	2.526428	0.0025	CDS hypothetical protein 2860251:2860388 forward MW:5097
RPA2519	1.577604	0.015	1.811378	0.011	1.781398	0.005	2.672299	0.0005	3.074412	0.0005	CDS hypothetical protein 2860446:2860673 forward MW:8051
RPA2520	1.317228	0.006	1.181645	0.082	1.435195	0.015	2.185254	0.001	2.569449	0	CDS hypothetical protein 2861230:2861799 reverse MW:20540
RPA2521	0.819059	0.933	0.852032	0.8665	0.849063	0.862	0.651442	0.9975	0.375687	1	CDS hypothetical protein 2862192:2862401 forward MW:7958
RPA2522	1.28272	0.0755	1.264227	0.109	1.049895	0.3765	1.406294	0.128	0.985319	0.5555	CDS hypothetical protein 2862889:2863146 forward MW:9435
RPA2523	1.089139	0.2255	1.050034	0.303	1.257164	0.0155	1.221446	0.0655	0.999004	0.506	CDS putative lactoylglutathione lyase 2863487:2863936 reverse MW:17161
RPA2524	0.952274	0.7145	1.0122	0.457	1.101256	0.104	1.309031	0.023	1.305329	0.0195	CDS Sir2 family, possible ADP ribosyltransferase 2864429:2865190 forward MW:27721
RPA2525	0.894703	0.902	0.63739	0.99	1.066061	0.316	0.8383	0.8615	0.846009	0.916	cspA2 cold shock DNA binding protein 2865394:2866101 forward MW:25412
RPA2526	0.946177	0.748	1.2841	0.004	0.974364	0.656	1.891246	0	2.381908	0	CDS DUF192 2866285:2866770 forward MW:17542
RPA2527					0.834817	0.733			0.571176	0.996	CDS possible DNA-dependent RNA polymerase 2867308:2868930 reverse MW:60007
RPA2528											CDS hypothetical protein 2869057:2869569 forward MW:19042
RPA2529											CDS hypothetical protein 2869607:2869996 forward MW:14234
RPA2530	1.615188	0.035	2.127683	0.0095	1.411965	0.0535			1.746747	0.015	CDS hypothetical protein 2870046:2870819 forward MW:29430
RPA2531	2.674281	0.0005	2.378258	0	2.602532	0.0065	2.473125	0.0015	2.542178	0.002	CDS hypothetical protein 2870915:2871193 forward MW:10203
RPA2532	0.990283	0.5535	1.237937	0.0335	1.045123	0.312	0.488128	1	0.727817	0.986	CDS hypothetical protein 2871455:2872216 forward MW:27412
RPA2533	1.507082	0.01	1.263671	0.037	0.94928	0.664	1.471574	0.016	1.356804	0.003	CDS unknown protein 2872381:2872800 forward MW:15458
RPA2534	1.235792	0.0785	0.886994	0.8915	0.824494	0.956	1.205528	0.04	1.459735	0.001	CDS hypothetical protein 2872797:2873579 forward MW:29022
RPA2535	0.939205	0.808	0.973883	0.61	0.86232	0.9585	0.784292	0.975	0.808378	0.9855	waaG putative UDP-glucose:(heptosyl) LPS alpha 1,3-glucosyltransferase 2874172:2875290 forward MW:39764
RPA2536	1.205867	0.067	1.066729	0.259	1.24764	0.0375	1.103176	0.182	1.422781	0.029	CDS putative opgC protein 2875224:2876498 reverse MW:47549
RPA2537	1.0959	0.0905	1.125407	0.159	0.968329	0.6905	0.987892	0.549	0.793723	0.9725	CDS possible NADH dehydrogenase (ubiquinone) Fe-S protein 4 (18kD) (NADH-coenzyme Q reductase) 2876741:2877046 forward MW:11918
RPA2538	0.919655	0.7525	0.633606	0.997	0.921308	0.752	0.64059	0.9875	0.709191	0.9975	CDS putative acyl-CoA carboxylase, beta chain 2877195:2878850 forward MW:59093
RPA2539	0.872574	0.823	0.578023	0.9965	0.669878	0.981	0.472531	0.998	0.444711	0.999	CDS putative acyl-CoA carboxylase biotin-carrying subunit 2878864:2880879 forward MW:71555
RPA2540	1.179144	0.3255	0.747606	0.962	1.088149	0.3065	0.896903	0.777	0.850714	0.7845	hmgL 3-hydroxy-3-methylglutaryl-CoA lyase 2881000:2881905 forward MW:31410
RPA2541	1.16455	0.3425	0.42405	0.988	1.238136	0.1015			0.507488	0.9195	CDS TrapT family, dctM subunit, C4-dicarboxylate transport 2882000:2883358 reverse MW:47654
RPA2542	1.29709	0.1945	0.460907	0.995	1.279208	0.155	0.825752	0.6715	0.522298	0.999	CDS possible TrapT family, dctQ subunit, C4-dicarboxylate transport 2883355:2883906 reverse MW:19465
RPA2543	1.511489	0.174	0.439182	0.9985	1.297612	0.129	0.659338	0.9225	0.567528	0.9995	CDS TrapT family, dctP subunit, C4-dicarboxylate periplasmic binding protein 2883903:2884922 reverse MW:36194
RPA2544	1.063118	0.332	0.622293	0.9995	1.454524	0.0115	0.629308	0.9985	0.444279	0.9985	CDS conserved hypothetical protein 2885193:2885432 forward MW:8676
RPA2545	1.045804	0.332	0.899178	0.931	0.986429	0.569	0.963063	0.6845	0.85374	0.979	CDS possible outer membrane protein 2885963:2888956 forward MW:104836
RPA2546	1.015863	0.4355	0.905026	0.8595	0.973069	0.626	0.894185	0.846	0.77569	0.9935	CDS FKBP-type peptidyl-prolyl cis-trans isomerase 2889133:2889591 forward MW:15826
RPA2547	1.03853	0.2705	1.123963	0.0985	0.811613	0.9775	1.171038	0.0755	1.2498	0.0215	CDS hypothetical protein 2889640:2889981 reverse MW:11368
RPA2548	0.603658	0.996	0.721377	0.972	1.087273	0.1705	0.570004	0.9955	0.618694	0.9985	CDS conserved hypothetical protein 2890202:2891008 forward MW:28368
RPA2549	0.809019	0.978	0.790606	0.9765	0.782676	0.971	0.619458	0.975	0.629948	0.997	CDS conserved hypothetical protein 2891005:2891484 forward MW:16135
RPA2550	0.965024	0.705	1.136284	0.407	0.913338	0.8555			1.005057	0.472	CDS hypothetical protein 2891485:2892042 reverse MW:20136
RPA2551	0.912632	0.881	1.054368	0.377	0.826715	0.9805	0.993218	0.5205	0.901284	0.803	CDS hypothetical protein 2892078:2892521 forward MW:14818
RPA2552	0.970442	0.6325	0.90378	0.798	1.08276	0.271	1.293094	0.117	1.634651	0.0025	CDS unknown protein 2893377:2893697 reverse MW:11666
RPA2553	0.678558	0.948	0.696919	0.9665	0.858509	0.904	0.600806	0.9605	0.541315	0.9925	CDS conserved unknown protein 2894171:2899384 forward MW:185531
RPA2554	0.897852	0.8975	0.815064	0.9705	1.065957	0.214	0.820044	0.967	0.81581	0.9795	CDS penicillin binding protein 2899381:2901576 forward MW:77886
RPA2555	1.255148	0.141	0.944576	0.805	0.978631	0.6385	1.126547	0.2395	1.093733	0.2145	CDS Glycosyl transferase, family 39 2901627:2903372 forward MW:63758
RPA2556	0.837547	0.9665	0.909129	0.86	0.83744	0.909	1.005355	0.487	0.998899	0.513	CDS PA-phosphatase related phosphoesterase 2903374:2904222 forward MW:30291
RPA2557	0.834932	0.8545	1.302105	0.005	0.609857	0.993	0.905436	0.745	1.119953	0.125	CDS Glycosyl transferase, family 2 2904286:2905038 forward MW:27337
RPA2558	0.90438	0.903	1.097418	0.2095	0.773758	0.988	1.071303	0.3	1.192813	0.164	CDS conserved hypothetical protein 2905038:2905376 forward MW:12660
RPA2559	0.799185	0.976	0.711744	0.9895	0.768798	0.946	0.682927	0.949	0.676088	0.996	metC cystathionine beta-lyase 2905539:2906735 reverse MW:42197
RPA2560	1.135772	0.0265	1.07985	0.115	1.175977	0.034	1.538342	0.002	1.329588	0.0035	aapJ-1 ABC transporter, periplasmic amino acid binding protein aapJ-1 2907057:2908073 forward MW:36524
RPA2561	1.029167	0.378	1.170808	0.075	1.002395	0.4805	1.35359	0.005	1.51668	0.002	aapQ-1 polar amino acid ABC transport permease protein aapQ-1 2908094:2909299 forward MW:43177
RPA2562	0.938736	0.7945	0.969031	0.655	0.882777	0.927	0.899302	0.8725	0.953478	0.712	aapM-1 polar amino acid ABC transport permease protein aapM-1 2909296:2910801 forward MW:53984
RPA2563	1.035213	0.4045	1.063574	0.3405	1.115772	0.381	1.385655	0.0915	0.901286	0.732	aapP-1 amino acid ABC transporter, ATP-binding protein aapP-1 2910817:2911557 forward MW:27531
RPA2564	1.956235	0.012	1.104226	0.2935			2.07761	0.002	1.017765	0.487	CDS hypothetical protein 2911582:2911851 reverse MW:9917

RPA2566	1.468706	0.0755	2.958707	0.0015	0.745329	0.989	1.771989	0.0635	1.99535	0.015	CDS putative EA59 gene protein, phage lambda 2912351:2913934 forward MW:59202
RPA2567	1.047339	0.3515	1.858583	0.0045	0.876618	0.917	1.58866	0.0625	1.532975	0.006	CDS possible EA31 gene protein, phage lambda 2913943:2914782 forward MW:31038
RPA2568	0.904859	0.7975	0.829511	0.914	0.770822	0.9395	0.973127	0.5635	0.727594	0.9945	CDS O-acetylserine (thiol) lyase 2914922:2915959 reverse MW:36592
RPA2569	0.959259	0.6725	0.906003	0.831	0.939336	0.757	1.040022	0.427	0.942061	0.714	cfa1 cyclopropane-fatty-acyl-phospholipid synthase 2916070:2917299 reverse MW:47015
RPA2570	0.842327	0.9215	0.790284	0.9185	0.756439	0.987	0.883128	0.817	0.68306	0.9665	CDS conserved hypothetical protein 2917359:2918204 reverse MW:30645
RPA2571	1.009088	0.467	0.849766	0.9605	0.995144	0.523	0.871151	0.9165	0.667661	0.9985	CDS possible NADPH-dependent oxidoreductase 2918206:2919519 reverse MW:48580
RPA2572	0.949109	0.6015			1.035281	0.446			0.89515	0.751	CDS possible outer membrane efflux protein. 2919954:2921402 forward MW:51665
RPA2573	0.927335	0.716	0.775311	0.9735	0.871812	0.941	0.727411	0.947	0.812933	0.93	CDS possible membrane protein, permease. 2921392:2922762 forward MW:47411
RPA2574	1.101398	0.1795	0.795312	0.9315	0.993764	0.5265	0.939913	0.6945	0.869079	0.9125	CDS possible RND efflux transporter 2922833:2925964 forward MW:110863
RPA2575	0.949806	0.7505	0.790078	0.9835	0.984199	0.595	0.881476	0.8945	0.791342	0.9785	CDS possible RND efflux transporter 2925964:2929071 forward MW:110638
RPA2577	1.04542	0.3085	1.251082	0.014	0.904284	0.839	1.036258	0.3895	0.895362	0.922	CDS putative alginate o-acetyltransferase AlgI 2930223:2931692 forward MW:54752
RPA2578	1.135124	0.0775	1.026459	0.377	0.895606	0.7785	1.666645	0.0055	1.925564	0	CDS possible alginate o-acetyltransferase AlgJ 2931695:2932828 forward MW:42396
RPA2579	1.25232	0.082	2.520647	0.0025	1.8228	0	1.389911	0.0325	1.751447	0.001	CDS hypothetical protein 2933211:2933600 reverse MW:13892
RPA2580	0.905598	0.9015	1.031619	0.431	0.901467	0.864	0.785612	0.9395	0.842912	0.916	CDS possible protein-L-isoaspartate O-methyltransferase 2934119:2934784 forward MW:24367
RPA2581	0.912376	0.816	0.783854	0.963	1.057615	0.299	1.086268	0.2095	1.071947	0.3005	CDS putative outer membrane protein 2934830:2936386 forward MW:55473
RPA2582	0.786683	0.9945	0.730165	0.9865	0.926439	0.848	0.807707	0.9655	0.841	0.885	CDS unknown protein 2936679:2937467 forward MW:27564
RPA2583	1.020542	0.446	1.051163	0.233	0.79975	0.9395	0.771131	0.98	0.906113	0.871	valS valyl-tRNA synthetase 2937609:2940482 forward MW:107230
RPA2584											CDS possible glyoxalase 2940486:2940872 forward MW:13952
RPA2585	0.868247	0.963	0.836515	0.9785	1.00735	0.472	0.80242	0.904	0.730935	0.9795	CDS hypothetical protein 2941074:2941634 forward MW:20394
RPA2586	0.968808	0.5795	1.136406	0.1675	1.215844	0.2335	1.279016	0.043	1.201526	0.1225	3mg possible DNA-3-methyladenine glycosidase 2941820:2942497 reverse MW:24163
RPA2587	1.05904	0.2125	0.912888	0.8765	1.006129	0.4775	0.930448	0.743	1.238396	0.034	lipA2 lipoic acid synthetase 2942590:2943549 forward MW:35108
RPA2588	0.647597	0.9775	0.810896	0.937	0.447704	0.985	0.715613	0.981	0.687032	0.9935	CDS Protein of unknown function UPF0083 2943576:2944049 forward MW:18126
RPA2589							0.760191	0.7805			cinA possible competence-damaged protein 2944131:2944751 reverse MW:21615
RPA2590	0.759499	0.9655	0.789674	0.9855	0.663847	0.999	0.514394	0.9995	0.668809	0.997	ispD 4-diphosphocytidyl-2C-methyl-D-erythritol synthase:YgbB 2944754:2945950 reverse MW:41660
RPA2591	1.800106	0.001	2.682792	0.0005	2.493555	0	3.914092	0	3.260431	0.001	nifR3 putative nitrogen regulation protein nifR3 2946224:2947225 forward MW:35876
RPA2592	1.905987	0	2.371581	0	1.574168	0.0055	2.974432	0.0005	2.866263	0	ntrB nitrogen regulatory signal transduction histidine kinase NtrB 2947222:2948394 forward MW:42312
RPA2593	1.13271	0.208	1.622169	0.0015	1.033862	0.36	1.849729	0.006	1.389629	0.0245	ntrC nitrogen assimilation regulatory protein ntrC Response regulator 2948404:2949846 forward MW:52855
RPA2594	1.10269	0.112	0.97028	0.663	0.921128	0.7445	1.027976	0.3795	1.215146	0.0245	ntrY nitrogen regulatory signal transduction histidine kinase NtrY 2950006:2952297 forward MW:83700
RPA2595	0.917116	0.7885	0.807308	0.9165	1.012809	0.4675	0.868605	0.7795	1.009301	0.467	ntrX nitrogen assimilation regulatory protein ntrX-Response regulator 2952314:2953681 forward MW:50069
RPA2596	0.754272	0.9895	0.837735	0.969	0.80268	0.958	0.58182	0.999	0.751349	0.993	CDS D-alanine aminotransferase 2953722:2954579 forward MW:31170
RPA2597	1.472726	0.0765	1.44554	0.025	1.466807	0.045	1.393705	0.045	1.096493	0.337	CDS probable nfrA protein 2954761:2955009 forward MW:9196
RPA2598	0.88802	0.6975	1.151198	0.103	0.685859	0.9885	1.012259	0.48	0.805172	0.976	CDS GTP binding protein-like 2955114:2956388 forward MW:46997
RPA2599	0.58881	0.99	0.628355	0.9975	0.70377	0.99	0.608397	0.998	0.589947	0.9955	gyrA DNA gyrase subunit A 2956669:2959332 forward MW:98000
RPA2600	0.884208	0.8865	1.2661	0.058	0.624097	0.9925	1.928129	0.019	1.184119	0.0735	CDS hypothetical protein 2959517:2959936 forward MW:15314
RPA2601	1.288775	0.0125	1.403017	0.0175	0.915141	0.7995	1.383834	0.081	1.125998	0.1925	kdtB phosphopantetheine adenylyltransferase 2960110:2960619 forward MW:17673
RPA2602	0.937912	0.735	1.041482	0.3005	0.886803	0.8675	0.677601	0.9925	0.760391	0.9715	CDS peptidyl prolyl cis-trans isomerase 2960636:2961199 forward MW:20009
RPA2603	1.170453	0.0495	1.130783	0.2205	1.120853	0.105	0.926995	0.5975	1.310557	0.054	CDS conserved hypothetical protein 2961209:2961652 forward MW:15982
RPA2604	0.931611	0.828	0.849681	0.9265	1.04413	0.344	0.544839	1	0.603823	0.9915	CDS peptidyl prolyl cis-trans isomerase 2961628:2962095 forward MW:16926
RPA2605	0.867686	0.8925	0.884585	0.9435	0.950657	0.605	0.551348	0.9995	0.706004	0.949	queA S-adenosylmethionine tRNA ribosyltransferase 2962252:2963346 forward MW:39147
RPA2606	0.827859	0.992	0.723864	0.9975	0.817188	0.98	0.489892	0.9995	0.538993	0.9735	tgt tRNA guanine transglycosylase 2963343:2964476 forward MW:41644
RPA2607	0.47716	0.979	0.384732	0.991	0.422212	0.9995	1.47997	0.03	0.451897	0.9925	CDS possible transcriptional regulator, XRE family, CUPIN domain 2965553:2966176 reverse MW:22664
RPA2608	0.613293	0.996	1.215899	0.0505	0.624468	0.9945	1.38227	0.052	0.577073	0.996	CDS possible sulfonate binding protein 2966741:2967694 reverse MW:33411
RPA2609	0.474936	0.878	1.693203	0.0015	0.812958	0.844	0.980491	0.5085	0.949801	0.593	CDS possible monooxygenase 2967856:2968425 reverse MW:19614
RPA2610	0.413985	0.854	2.232775	0	0.692263	0.8785	1.34927	0.258	0.822376	0.9135	ssuB aliphatic sulfonate transport ATP-binding protein, Subunit of ABC transporter 2968436:2969281 reverse MW:30386
RPA2611	0.496103	0.832	2.533611	0	0.368916	0.9615	1.425204	0.211	0.642885	0.8715	CDS putative aliphatic sulfonate transport membrane component. Permease subunit of an ABC transporter 2969286:2970092 reverse MW:29502
RPA2612	0.657024	0.974	1.32333	0.067	0.690819	0.9815	1.141753	0.229	0.689908	0.966	msuD methanesulfonate sulfonatase MsuD (monooxygenase) 2970089:2971264 reverse MW:42480
RPA2613	0.439201	0.946	1.248775	0.1635	0.360785	0.9695	1.589586	0.02	0.351035	1	CDS putative aliphatic sulfonate binding protein, subunit of ABC transporter 2971309:2972256 reverse MW:33863
RPA2614	0.344867	0.996	0.761974	0.8095	0.274645	0.988	2.025233	0.0005	0.340298	0.9995	CDS conserved hypothetical protein 2972643:2973920 forward MW:47316
RPA2615	0.663813	0.945	0.410462	0.9905	0.582027	0.94	1.192266	0.2835	0.384118	0.999	nifH2 putative nitrogenase iron protein (nitrogenase component II) (nitrogenase reductase) 2973960:2974832 forward MW:30281
RPA2616			0.800986	0.7725			0.985889	0.5465	0.889756	0.6785	CDS possible nitrogenase iron-molybdenum cofactor biosynthesis protein NifE homolog 2974834:2976192 forward MW:47946
RPA2617	0.551822	0.9725	1.554845	0.003	0.469377	0.973	1.313993	0.1195	0.582355	0.9905	CDS possible vanadium nitrogenase associated protein vnfN (U51863) 2976189:2977439 forward MW:43436
RPA2618	0.460143	0.9855	0.965817	0.553	0.289379	0.9965	1.023809	0.4055	0.24037	1	CDS putative sulfonate transport system substrate-binding protein 2977601:2978587 reverse MW:35607
RPA2619	0.968017	0.5575	1.527608	0.037	0.616429	0.9925	1.71365	0.006	0.805179	0.901	CDS possible GMC-type oxidoreductase 2978920:2980524 forward MW:57577
RPA2620	0.775122	0.851	1.324177	0.025	0.695373	0.972	1.128301	0.328	0.808188	0.98	CDS unknown protein 2980614:2980940 reverse MW:12000
RPA2621	0.73169	0.849	1.217421	0.0865	0.714243	0.9555	1.048861	0.416	0.783282	0.988	CDS conserved unknown protein 2980972:2981481 reverse MW:17949
RPA2622	0.539593	0.861	1.687645	0.0315	0.331053	0.9985	1.016801	0.488	0.353764	0.988	CDS putative sulfonate transport system, ATP-binding protein. Subunit of ABC transporter 2981510:2982289 reverse MW:28060
RPA2623	0.801517	0.8045	1.405128	0.0175	0.738962	0.9105	1.023766	0.4275	0.644649	0.9795	CDS possible sulfonate transport system permease protein. Subunit of an ABC transporter 2982289:2983131 reverse MW:29869
RPA2624	0.5733	0.944	1.160149	0.2235	0.336989	0.9995	1.079202	0.275	0.260148	0.9995	CDS putative sulfonate transport system substrate-binding protein 2983255:2984229 reverse MW:35243
RPA2625	0.948397	0.598	0.653791	0.917	0.83091	0.809	0.990664	0.5405	0.737332	0.9545	CDS putative cystathionine or methionine gamma-lyase 2984782:2985990 reverse MW:42429
RPA2626	0.167371	0.9965	0.49399	0.984	0.164293	0.999	0.922805	0.776	0.120525	1	CDS possible hydrolase 2986232:2987266 reverse MW:37460
RPA2627	0.293268	0.975	0.88831	0.718	0.215784	0.9965	0.955202	0.662	0.140369	1	CDS putative carboxylesterase 2987649:2989346 forward MW:59931
RPA2628	0.329274	0.9295	1.391467	0.091	0.223322	0.9965	1.292222	0.2085	0.196247	0.9965	aapJ-2 polar amino acid ABC transport substrate-binding protein, aapJ-2 2989377:2990399 forward MW:37064
RPA2629	0.449765	0.967	0.947269	0.7515	0.520766	0.988	0.787718	0.8465	0.322107	0.9985	aapQ-2 polar amino acid ABC transpor permease protein, aapQ-2 2990420:2991589 forward MW:41738
RPA2630	0.515392	0.9815	1.09174	0.2615	0.705617	0.9725	1.053176	0.424	0.954871	0.6575	aapM-2 polar amino acid ABC transport system protein, aapM-2 2991586:2992668 forward MW:39462
RPA2631											CDS possible ABC transport substrate-binding periplasmic protein 2993216:2994244 forward MW:35973
RPA2632	0.53222	0.9975	0.990901	0.5275	0.545009	0.948	0.944086	0.6855	0.57355	0.995	CDS ABC transport permease protein, possibly for nitrate 2994255:2995253 forward MW:35799
RPA2633	0.310975	0.99	1.135494	0.327			1.157175	0.197	0.800676	0.761	CDS putative ATP-binding protein of ABC transporter, possibly for nitrate 2995253:2996065 forward MW:29214
RPA2634	1.036907	0.3955	1.232319	0.055	0.757373	0.961	1.636376	0.017	0.902662	0.79	nifB1 putative nitrogenase iron-molybdenum cofactor biosynthesis protein NifB 2996908:2997804 forward MW:32104
RPA2635	2.451574	0.0055			2.941691	0.003	2.507189	0.2015	1.354067	0.095	nifH3 putative nitrogenase reductase NifH subunit 2997843:2998712 forward MW:31163
RPA2636	0.531791	0.867	1.394437	0.006	0.458435	0.9355	2.51265	0.0195	0.70457	0.985	NifD2 possible nitrogenase molybdenum-iron protein alpha chain (nitrogenase component I) (dinitrogenase) 2998778:3000286 forward MW:55393
RPA2637	0.45839	0.977	1.386137	0.0315	0.590915	0.9475	1.835811	0.041	0.995188	0.518	CDS possible nitrogenase iron-molybdenum protein subunit nifK homolog 3000298:3001680 forward MW:50833
RPA2638	1.084494	0.175	1.134657	0.0785	1.016256	0.448	1.433009	0.004	1.308212	0.015	CDS possible oxidoreductase 3001975:3003279 forward MW:47092
RPA2639	1.003689	0.482	1.187627	0.039	0.852421	0.926	1.015406	0.4325	0.704927	0.998	CDS probable L-2-amino-thiazoline-4-carboxylic acid hydrolase 3003327:3003812 reverse MW:17887
RPA2640	1.015942	0.4695	1.174669	0.1735	0.83071	0.899	0.939967	0.601	0.623076	0.9995	CDS Isochorismatase hydrolase family 3003809:3004531 reverse MW:25909
RPA2641	1.08676	0.213	1.21252	0.2095	0.864788	0.792	1.633673	0.0005	0.868393	0.9065	CDS putative ABC transporter oligopeptide-binding protein 3004528:3006129 reverse MW:60483
RPA2642	0.948028	0.643	1.215408	0.0195	0.808883	0.953	1.874455	0.006	1.388625	0.0105	CDS transcriptional regulator, LysR family 3006354:3007244 forward MW:33183
RPA2643	0.865913	0.7515	1.045564	0.2845	0.706726	0.9845	1.135223	0.2115	0.686605	0.988	CDS putative ABC transporter ATP-binding protein 3007305:3008927 reverse MW:57761

RPA2644	0.850212	0.8025	1.095888	0.2915	0.65893	0.985	1.06873	0.414	0.766929	0.967	CDS putative ABC transporter permease protein 3008924:3009754 reverse MW:29525
RPA2645	0.883253	0.791	1.119748	0.104	0.801562	0.9235	1.393856	0.0415	0.805207	0.9475	CDS putative ABC transporter permease protein 3009759:3010736 reverse MW:35191
RPA2646	1.030925	0.401	1.172454	0.0895	0.772076	0.9725	1.093832	0.219	0.8824	0.8905	CDS putative ABC transporter oligopeptide-binding protein 3010761:3012377 reverse MW:59989
RPA2647	1.169469	0.0305	1.077804	0.173	0.948734	0.7615	1.172842	0.0695	0.897536	0.9245	CDS putative hydrolase 3012547:3013713 reverse MW:41371
RPA2648	1.170914	0.114	0.993746	0.534	0.847354	0.9495	1.059656	0.2575	0.857329	0.9495	CDS unknown protein 3013743:3014525 reverse MW:27818
RPA2649	1.003338	0.486	0.688916	0.9915	1.175005	0.0705	1.403977	0.0075	0.931294	0.7425	CDS conserved unknown protein 3015504:3015860 forward MW:12921
RPA2650	0.85704	0.97	0.781406	0.9725	0.913084	0.8175	0.590348	0.9895	0.590024	0.999	CDS Permeases of the drug/metabolite transporter (DMT) superfamily 3015857:3016726 reverse MW:31437
RPA2651	1.511277	0.0305	1.252423	0.075	1.543985	0.008	2.329464	0.0265	1.254131	0.082	CDS Endoribonuclease, protein synthesis inhibitor 3016936:3017337 forward MW:14269
RPA2652	1.28833	0.0135	1.279702	0.0225	1.081317	0.2865	1.192422	0.0875	1.009697	0.474	CDS unknown protein 3017428:3017631 forward MW:7179
RPA2655	0.944127	0.769	0.839928	0.936	0.918774	0.7945	0.735651	0.9875	0.96878	0.607	CDS beta-(1-3)-glucosyl transferase 3018684:3021518 reverse MW:104582
RPA2656	1.042541	0.338	1.142202	0.036	1.07347	0.2005	0.955288	0.6975	0.880312	0.955	CDS hypothetical protein 3021706:3022284 reverse MW:20239
RPA2657	0.991184	0.544	1.045976	0.268	0.958486	0.6755	1.336552	0.008	1.59171	0	CDS putative beta (1-6) glucans synthase 3022547:3024181 forward MW:59947
RPA2658	0.913368	0.9115	0.663384	0.9995	1.137227	0.12	0.982317	0.5715	0.990105	0.5395	CDS hypothetical protein 3024595:3025986 reverse MW:48276
RPA2659	0.933062	0.801	0.930613	0.8085	0.681536	0.9875	0.76991	0.986	0.965989	0.6265	glmU UDP-N-acetylglucosamine pyrophosphorylase 3026154:3027512 forward MW:47047
RPA2660	0.916595	0.793	0.78508	0.9945	0.882135	0.932	0.626402	0.996	0.673266	0.992	glmS glucosamine-fructose-6-phosphate aminotransferase 3027638:3029464 forward MW:65642
RPA2661	0.960854	0.7275	1.026794	0.336	0.779153	0.976	1.044804	0.3625	1.05751	0.211	CDS DUF502 3029723:3030526 forward MW:29016
RPA2662	0.920696	0.853	0.844804	0.9665	0.835483	0.9465	0.789974	0.977	0.839325	0.987	recG ATP-dependent DNA helicase 3030557:3032659 reverse MW:76810
RPA2663	0.787865	0.9125	0.995191	0.506	0.776535	0.985	0.724756	0.9835	0.792167	0.877	Mfd transcription repair coupling factor 3033100:3036618 forward MW:129567
RPA2664	1.206151	0.019	1.121188	0.1075	1.022178	0.433	1.257923	0.035	1.277812	0.015	CDS hypothetical protein 3036761:3037993 reverse MW:43814
RPA2665	0.787586	0.963	0.657293	0.9325	0.789331	0.934	1.080459	0.2845	0.775158	0.8915	CDS possible acid-CoA ligase 3038042:3039577 reverse MW:53423
RPA2666	1.052452	0.22	0.965412	0.722	1.155405	0.0355	1.051511	0.271	1.032415	0.322	CDS possible binding protein component of ABC transporter 3039582:3041462 reverse MW:70315
RPA2667	0.81663	0.8955	0.89169	0.899	0.786535	0.9935	0.714457	0.99	0.752691	0.986	CDS conserved unknown protein 3041681:3042427 forward MW:26287
RPA2668	1.171801	0.1835	1.278748	0.012	0.947848	0.6355	1.295967	0.021	1.426011	0.03	CDS unknown protein 3042513:3043187 reverse MW:24645
RPA2669	1.081308	0.2265	1.104705	0.1265	1.000251	0.4935	1.132342	0.159	0.975863	0.582	CDS conserved hypothetical protein 3043229:3043561 reverse MW:12779
RPA2670	0.875532	0.941	0.956575	0.746	0.836564	0.924	1.001417	0.4905	1.079667	0.2035	CDS probable transporter 3043684:3044640 forward MW:34233
RPA2671	1.088829	0.104	0.891983	0.9365	1.21143	0.013	1.100124	0.14	1.06075	0.2515	CDS putative FAD-dependent monoxygenase 3044646:3045842 reverse MW:42818
RPA2672	1.287419	0.0075	1.179325	0.0555	1.277744	0.0395	1.25444	0.026	1.313122	0.009	CDS possible phosphatidylcholine synthase 3045976:3046710 forward MW:26435
RPA2673	1.267678	0.0065	1.236399	0.007	1.166569	0.0645	1.055002	0.2545	1.134506	0.108	CDS possibly involved in transport 3046707:3047429 forward MW:26186
RPA2674	1.236305	0.0065	1.023854	0.3675	1.109715	0.1265	1.166741	0.059	1.020638	0.3795	CDS quinone oxidoreductase 3047516:3048490 forward MW:34876
RPA2675	0.972135	0.611	1.202995	0.0195	0.722891	0.9925	1.040725	0.352	1.140856	0.1395	CDS Protein of unknown function UPF0004:Elongator protein 3/MiaB/NifB 3048669:3049994 reverse MW:48740
RPA2676	1.327092	0.0595	0.977037	0.554	1.039952	0.302	1.62834	0.0015	1.389626	0.022	CDS transcriptional regulator, LysR family 3050394:3051308 reverse MW:32527
RPA2677	1.389761	0.005	1.8634	0.0005	1.712147	0.0035	2.343398	0.001	2.053274	0.0005	CDS putative substrate-binding protein, subunit of ABC transporter 3051410:3052366 forward MW:34071
RPA2678	1.36167	0.0025	2.843093	0	1.053787	0.3805	2.613401	0.002	2.250987	0	CDS putative permease protein, subunit of ABC transporter 3052374:3053258 forward MW:31604
RPA2679	1.098836	0.344	3.129227	0.0035	0.333194	0.9915	3.004637	0.0035	1.81192	0.008	CDS putative transport system ATP-binding protein 3053251:3054069 forward MW:29687
RPA2680	0.929175	0.6715	1.205683	0.1445	0.952461	0.5795	1.1994	0.2275	1.23192	0.0575	CDS conserved hypothetical protein 3054071:3054922 forward MW:30664
RPA2681											CDS possible lactam utilization protein. 3054938:3055702 reverse MW:26516
RPA2682	0.906094	0.606	0.791234	0.972	1.112259	0.2765	0.822342	0.7505	1.128973	0.1365	uahA Urea amidolyase-related 3055730:3056740 reverse MW:34831
RPA2683	1.076781	0.1895	0.90273	0.861	1.128307	0.0985	0.98976	0.5385	1.321706	0.0135	dur1 DUF213 3056737:3057465 reverse MW:26154
RPA2684	0.903112	0.758	0.91371	0.861	1.001234	0.4935	0.80662	0.939	0.903894	0.9115	CDS conserved unknown protein 3057686:3058399 forward MW:25114
RPA2685	0.922206	0.7765	1.160094	0.069	1.034512	0.3805	1.035766	0.406	0.935633	0.8205	CDS conserved hypothetical protein 3058412:3058819 forward MW:14507
RPA2686	1.19842	0.0415	0.977328	0.6315	0.931896	0.757	0.981355	0.582	1.042437	0.268	dapA2 dihydrodipicolinate synthase 3058948:3059841 forward MW:31760
RPA2687	1.399156	0.002	1.397584	0.0055	1.244167	0.031	1.374767	0.0215	1.294348	0.022	mscL large-conductance mechanosensitive channel 3059852:3060331 forward MW:17004
RPA2688	1.091982	0.236	1.168559	0.2655	0.923153	0.7795	1.180228	0.1625	0.826106	0.926	SmpB small protein B 3060369:3060842 forward MW:18147
RPA2689	0.875854	0.663	1.523049	0.005	0.923668	0.596	1.548685	0.005	1.167269	0.296	CDS possible thiol-specific antioxidant related protein 3060865:3061443 forward MW:20763
RPA2690	1.521581	0.001	1.441056	0.016	1.14791	0.0905	1.478053	0.037	1.495454	0.007	CDS possible uracil-DNA glycosylase 3061557:3062231 reverse MW:24535
RPA2691	1.347156	0.001	1.322157	0.022	1.140745	0.046	1.293159	0.0115	1.388932	0.0045	CDS DUF88 3062237:3062887 reverse MW:24439
RPA2692	1.071461	0.256	1.283604	0.045	0.975761	0.6285	1.282502	0.013	1.126441	0.1075	rnpO RNA polymerase omega subunit 3063234:3063626 forward MW:14368
RPA2693	1.168273	0.0395	1.288792	0.0125	1.217743	0.0125	1.232102	0.028	1.07024	0.264	relA GTP pyrophosphokinase 3063892:3066174 forward MW:84504
RPA2694	0.927983	0.852	1.023683	0.3975	0.905157	0.803	1.005056	0.4805	0.832611	0.9745	pdxJ pyridoxal phosphate biosynthetic protein pdxJ 3066324:3067088 forward MW:27110
RPA2695	0.85417	0.9055	1.118543	0.1215	0.8734	0.9275	1.152797	0.1555	0.845251	0.9395	acpS acyl carrier protein synthase 3067085:3067525 forward MW:15786
RPA2696	0.837471	0.984	0.942444	0.738	0.741327	0.98	0.898331	0.711	0.852586	0.927	lepB2 putative signal peptidase I 3067767:3068525 forward MW:28456
RPA2697	0.717152	0.9835	0.630763	0.9915	0.599979	0.989	0.549185	0.972	0.594832	0.9985	CDS putative ribonuclease III 3068522:3069340 forward MW:29186
RPA2698	0.91786	0.9005	0.886778	0.9205	0.774387	0.989	0.825403	0.957	0.742036	0.982	era possible GTP-binding protein Era 3069330:3070256 forward MW:33978
RPA2699	0.840778	0.9305	0.953256	0.7555	0.904619	0.831	0.911691	0.7945	0.726476	0.983	CDS hypothetical protein 3070253:3070654 forward MW:14262
RPA2700	0.88251	0.8705	0.864757	0.919	0.861316	0.955	0.923973	0.704	0.84334	0.912	CDS putative DNA repair protein RecO 3070697:3071449 forward MW:27407
RPA2701	0.886278	0.7745	0.96922	0.624	1.115894	0.1985	1.186396	0.059	1.608248	0.005	CDS conserved hypothetical protein 3071489:3072358 reverse MW:29745
RPA2702			0.674275	0.9315					1.059205	0.364	CDS DUF24, predicted transcriptional regulator, related to MarR family 3072441:3072953 forward MW:18832
RPA2703	0.889332	0.888	0.851578	0.9455	0.899911	0.7885	0.892484	0.902	0.942626	0.798	parC DNA topoisomerase IV subunitA 3072963:3075224 forward MW:83967
RPA2704	1.056802	0.297	1.021874	0.406	0.972471	0.5935	1.48411	0.0095	1.130232	0.172	CDS possible Na+/? antiporter 3075310:3076740 forward MW:51047
RPA2705											CDS hypothetical protein 3076754:3077119 reverse MW:13137
RPA2706	2.357605	0	2.1756	0	3.283054	0	3.122914	0	2.197824	0.0015	CDS manganese transport protein 3077204:3078577 forward MW:48249
RPA2707	1.133123	0.2425	1.420048	0.016	0.852719	0.7775			1.234612	0.0455	CDS probable transcriptional regulator, AraC family 3078637:3079458 reverse MW:29875
RPA2708	0.99572	0.5085			1.208933	0.117			0.593033	0.962	CDS possible fusaric acid resistance pump 3079565:3081658 forward MW:75472
RPA2709			1.380693	0.0755			2.158977	0.0075	2.591296	0	CDS possible FusE-MFP/HlyD family membrane fusion protein 3081860:3082762 forward MW:32576
RPA2710	1.138294	0.1605	0.910765	0.9165	1.336251	0.007	1.294974	0.0115	1.194615	0.1165	CDS Arginine-tRNA-protein transferase, N terminus 3082855:3083631 reverse MW:29434
RPA2711	1.226445	0.0215	0.890683	0.8595	1.403344	0.008	1.156577	0.1425	1.061596	0.325	CDS conserved hypothetical protein 3083700:3084314 reverse MW:22382
RPA2712	0.986827	0.573	1.011531	0.455	1.20056	0.027	0.879091	0.889	0.624919	0.9805	hemB delta-aminolevulinic acid dehydratase 3084385:3085437 reverse MW:38416
RPA2713	1.426507	0.003	1.51827	0.0055	1.452566	0.002	1.35996	0.0545	1.362442	0.019	CDS conserved hypothetical protein 3085631:3086095 forward MW:16962
RPA2714	1.048116	0.377	0.735843	0.9905	0.829869	0.8815	0.616352	0.9825	0.528237	1	CDS putative long-chain-fatty-acid--CoA ligase 3086173:3087738 forward MW:56363
RPA2715	1.921812	0	1.507464	0.0105	1.500939	0.0245	2.224718	0.001	1.769115	0.0005	CDS possible transcriptional regulator, MarR family 3088091:3088609 forward MW:19653
RPA2716	0.904269	0.7635	1.204496	0.0395	0.909485	0.878	0.877714	0.853	0.780709	0.9745	CDS conserved hypothetical protein 3088824:3089051 forward MW:8314
RPA2717	1.372824	0.0015	1.134822	0.052	0.965972	0.709	1.165084	0.2205	0.914793	0.7595	CDS conserved hypothetical protein 3089068:3089283 forward MW:7898
RPA2718	1.9869	0	2.34613	0.002	2.026581	0.001	2.405304	0.0035	2.589536	0	CDS hypothetical protein 3089301:3089864 forward MW:21127
RPA2719	1.097855	0.1655	1.125522	0.0775	1.124462	0.093	1.184077	0.0465	1.196617	0.0375	CDS conserved hypothetical protein 3089902:3090321 forward MW:15826
RPA2720	0.931707	0.75	0.991307	0.5655	1.042344	0.276	1.121936	0.093	1.171787	0.082	CDS possible glutathione-S-transferase 3090492:3091364 reverse MW:32500
RPA2721	1.024829	0.3665	0.804674	0.9455	0.976287	0.5875	1.015605	0.4735	0.783226	0.9115	CDS hypothetical protein 3091573:3091842 forward MW:9883
RPA2722	1.088294	0.2115	0.81098	0.9755	1.207528	0.0275	0.97269	0.595	1.055122	0.29	CDS possible MutT-like domain 3092068:3092691 reverse MW:23166

RPA2723	1.090068	0.1255	0.912603	0.733	1.151083	0.051	1.295621	0.0405	1.092233	0.2945	CDS conserved hypothetical protein 3092917:3093480 reverse MW:20985
RPA2724	0.867864	0.7555	0.757068	0.983	0.998365	0.5115	0.714751	0.968	0.755584	0.9685	glyA1 glycine hydroxymethyltransferase 3093944:3095242 forward MW:46185
RPA2725	0.947986	0.776	0.957694	0.657	1.063071	0.231	0.855042	0.9215	0.878715	0.924	CDS DUF193:ATP cone domain 3095345:3095827 forward MW:18601
RPA2726	0.803686	0.986	0.923819	0.733	1.146879	0.1455	0.612456	0.9705	0.664783	0.9665	ribD putative riboflavin-specific deaminase / reductase 3095824:3096993 forward MW:40746
RPA2727	0.916229	0.794	0.705316	0.989	0.801805	0.9505	0.608786	0.993	0.646428	0.9945	ribC riboflavin synthase alpha chain 3097004:3097612 forward MW:21515
RPA2728	0.819356	0.9725	0.78782	0.9855	0.693301	0.9745	0.775238	0.9745	0.66938	0.9965	ribE riboflavin synthase, beta chain 3097743:3098234 forward MW:17087
RPA2729	0.854811	0.955	0.74235	0.9385	0.899095	0.8465	0.983276	0.546	0.763273	0.934	nusB antitermination factor, NusB 3098240:3098764 forward MW:19621
RPA2730	0.675291	0.9855	0.696971	0.9125	0.683846	0.9445	0.529261	0.997	0.53742	0.99	thiL putative thiamine-monophosphate kinase (thiamine-phosphate kinase). 3098958:3099938 forward MW:33513
RPA2731	1.217347	0.0275	1.031457	0.3775	1.023285	0.4425	1.09818	0.2775	1.137373	0.065	CDS H+ translocating pyrophosphate synthase 3100167:3102287 forward MW:71953
RPA2732	0.923479	0.875	1.113077	0.143	1.011844	0.4265	0.962632	0.6815	0.971816	0.632	CDS conserved hypothetical protein 3102449:3102691 forward MW:8528
RPA2733	0.880677	0.613	2.02466	0.0055			1.166257	0.2315	0.995919	0.5155	CDS unknown protein 3103016:3103174 forward MW:5608
RPA2734	1.110524	0.084	1.135612	0.104	1.137457	0.05	1.258829	0.0525	1.301203	0.0215	CDS possible epoxide hydrolase-related protein 3103212:3104075 forward MW:32047
RPA2735	2.383318	0	2.394909	0	2.290293	0.0005	3.025819	0	2.732914	0.0015	mexC2 putative RND multidrug efflux membrane fusion protein MexC precursor 3104271:3105464 forward MW:42470
RPA2736	1.752726	0.014	1.859692	0.006	1.482324	0.0585	2.40459	0.002	1.271341	0.0705	mexD2 RND multidrug efflux transporter MexD 3105483:3108614 forward MW:111201
RPA2737	0.82423	0.8725	1.193419	0.027	0.782595	0.9085	1.073649	0.3775	0.871237	0.8865	CDS unknown protein 3108667:3109152 reverse MW:17871
RPA2738	0.866491	0.84	1.154633	0.121	0.958662	0.6595	0.91716	0.741	0.908816	0.838	CDS conserved hypothetical protein 3109261:3109797 forward MW:19755
RPA2739	0.877303	0.8225	0.821573	0.945	0.772202	0.964	0.864469	0.767	0.954205	0.68	CDS conserved unknown protein 3109815:3110381 forward MW:20317
RPA2740	1.058972	0.242	1.142852	0.058	0.875489	0.8695	0.903137	0.8165	1.15097	0.1115	plsX fatty acid/phospholipid synthesis protein 3110622:3111683 forward MW:37469
RPA2741	1.03091	0.3625	1.08047	0.1475	0.889916	0.7905	1.025503	0.4225	1.090912	0.148	fabH 3-oxoacyl-acyl carrier protein synthase III 3111680:3112657 forward MW:34575
RPA2742	1.080529	0.114	0.892198	0.898	0.991148	0.534	1.293636	0.035	1.433593	0.0025	himA integration host factor alpha subunit 3112791:3113147 forward MW:12834
RPA2743	1.186964	0.019	0.994121	0.5155	1.119908	0.111	1.540792	0	1.424571	0.0055	CDS bacterial regulatory protein, MerR family 3113162:3113914 forward MW:27444
RPA2744	1.540224	0.013	2.919053	0	1.14866	0.1315	4.138186	0.0005	3.991085	0	CDS hypothetical protein 3114466:3114693 forward MW:7965
RPA2745	1.77742	0.0355	3.030407	0	1.513554	0.017	1.623162	0.014	1.822351	0.002	CDS possible ferric siderophore receptor protein 3115010:3117304 forward MW:80966
RPA2746	0.874338	0.9545	0.716817	0.991	1.034414	0.373	0.879022	0.795	0.80567	0.9555	CDS conserved hypothetical protein 3117464:3117901 forward MW:15179
RPA2747	1.044853	0.2765	0.904407	0.78	1.2601	0.0845	0.886005	0.814	0.927887	0.8445	CDS hypothetical protein 3118016:3118333 reverse MW:11022
RPA2748	1.486007	0.067	0.782191	0.97	1.669744	0.008	0.919351	0.675	0.655505	0.9795	CDS possible short-chain dehydrogenase 3118557:3119525 forward MW:34835
RPA2749	1.365925	0.0865	0.91828	0.782	1.297822	0.081	1.082934	0.3035	0.626423	0.971	CDS conserved unknown protein 3119564:3120349 forward MW:28025
RPA2750	1.540529	0.0005	1.428466	0.0025	1.159653	0.1005	1.638415	0.006	1.443218	0.001	CDS probable glycosyl transferase 3120549:3122105 reverse MW:57767
RPA2751	1.029441	0.397	1.092336	0.1995	1.055214	0.34	1.085722	0.337	0.940613	0.693	CDS possible transferase 3122216:3123391 reverse MW:42340
RPA2752	1.07711	0.151	1.065549	0.168	1.114398	0.09	1.028265	0.367	1.081562	0.1605	CDS possible succinoglycan biosynthesis transport protein exoP 3123858:3125993 forward MW:76295
RPA2753	1.541541	0.002	1.532188	0.0055	1.073687	0.2565	1.720545	0.0005	1.262231	0.0165	CDS conserved hypothetical protein 3126073:3127266 reverse MW:44158
RPA2754	1.122198	0.081	1.160055	0.0745	1.275748	0.0135	1.127098	0.1615	0.950776	0.6935	CDS Polysaccharide deacetylase 3127397:3128449 forward MW:38065
RPA2755	0.917619	0.6955	0.663803	1	1.060471	0.312	1.127677	0.227	0.628048	0.9915	CDS possible DNA-binding stress protein 3128515:3128997 reverse MW:18247
RPA2756	1.843033	0.0065	1.941713	0	1.90276	0.0035	1.529072	0.1425	1.068845	0.224	CDS hypothetical protein 3129278:3130285 forward MW:36542
RPA2757	2.499603	0	1.914878	0	4.369674	0.0015	0.904527	0.678	1.032442	0.4065	CDS conserved hypothetical protein 3130373:3130585 reverse MW:7727
RPA2758	1.257725	0.062	0.927926	0.8475	1.246242	0.031	0.856669	0.9325	0.802123	0.9795	CDS possible cytochrome c oxidase assembly protein 3130682:3131788 forward MW:40792
RPA2759	0.584664	0.9705	0.621959	0.996	0.705911	0.919	0.635223	0.986	0.64109	0.9925	CDS possible transcriptional regulator, TetR family 3131802:3132479 reverse MW:24631
RPA2760	0.756695	0.9765	0.524834	0.9995	0.74034	0.997	0.582881	0.983	0.577565	0.998	CDS possible benzaldehyde lyase 3132481:3134283 reverse MW:62398
RPA2761	0.827416	0.9115	0.754998	0.8475	1.079129	0.3455			0.642305	0.7325	CDS possible oxidoreductase 3134350:3134721 forward MW:12776
RPA2762	1.283929	0.01	1.330905	0.0075	1.155873	0.069	1.167957	0.1255	1.075677	0.15	CDS conserved hypothetical protein 3134810:3135382 reverse MW:21824
RPA2763	1.097249	0.188	0.972757	0.634	0.940968	0.7375	0.900052	0.879	0.847044	0.931	CDS putative O-acetylhomoserine sulfhydrylase 3135410:3136690 reverse MW:45155
RPA2764	1.188821	0.0575	1.356141	0.0045	1.243784	0.0735	1.11312	0.244	0.837394	0.9455	CDS CoA Binding Domain 3136785:3137369 reverse MW:21159
RPA2765	0.947604	0.754	0.90062	0.886	1.052884	0.2715	0.895528	0.835	0.999894	0.499	CDS putative enoyl-CoA hydratase 3137519:3138346 reverse MW:29211
RPA2766	1.191436	0.0255	1.227375	0.023	1.054132	0.2275	0.969146	0.55	0.961274	0.7205	CDS Phenylacetic acid degradation-related protein:Thioesterase superfamily 3138437:3138865 forward MW:15206
RPA2767	0.790579	0.9415	1.017824	0.414	0.780534	0.9315	0.787722	0.944	0.678911	0.9975	rplM, L13 ribosomal protein L13 3139021:3139485 forward MW:17173
RPA2768	0.748923	0.943	0.85531	0.971	0.734681	0.9885	0.718755	0.9855	0.635296	1	rpsI, S9 ribosomal protein S9 3139487:3139969 forward MW:17497
RPA2769	1.328183	0.014	1.44374	0.003	1.405102	0.002	1.834108	0.002	1.930159	0	CDS putative diguanylate cyclase (GGDEF) 3140244:3141479 forward MW:44015
RPA2770	0.944694	0.7115	1.012996	0.4515	0.860188	0.9345	0.939001	0.7365	0.840827	0.965	CDS conserved unknown protein 3141558:3141860 forward MW:11246
RPA2771	0.970404	0.689	0.709609	0.9925	1.26958	0.0265	0.791783	0.957	0.858523	0.926	CDS possible transport protein/permease 3141844:3143010 reverse MW:40291
RPA2772	1.215791	0.01	0.971306	0.6345	1.134179	0.057	1.003892	0.4735	1.206587	0.0285	rlpA2 rare lipoprotein A 3143257:3144204 forward MW:33430
RPA2773	1.174466	0.026	0.954048	0.693	1.255073	0.012	1.217907	0.081	1.072213	0.2205	CDS epoxide hydrolase 3144233:3145183 reverse MW:34681
RPA2774	1.066512	0.199	0.987362	0.558	1.114683	0.139	1.174928	0.0725	1.216003	0.1125	CDS penicillin binding protein 3145328:3146569 forward MW:44311
RPA2775	1.018146	0.4235	1.006055	0.4705	0.859491	0.9615	0.972486	0.6305	0.785297	0.991	CDS thymidylate kinase 3146572:3147264 forward MW:25143
RPA2776			0.839642	0.855	0.896456	0.669	0.914275	0.7095	0.953461	0.6025	CDS probable DNA polymerase III, delta prime subunit 3147261:3148316 forward MW:37438
RPA2777	0.802334	0.954	1.021948	0.405	0.784374	0.957	0.899051	0.852	0.848696	0.9415	metG methionyl-tRNA synthetase 3148397:3149941 forward MW:57551
RPA2778	0.773711	0.9745	0.938366	0.773	0.696659	0.99	0.65765	0.988	0.618184	0.9945	CDS possible deoxyribonuclease 3149945:3150733 forward MW:28613
RPA2779	0.9622	0.6795	0.973117	0.6465	0.955225	0.635	0.822857	0.9715	0.744555	0.9585	CDS possible hydrolase 3150759:3151562 forward MW:29330
RPA2780	1.564332	0.005	1.058366	0.22	1.520411	0.0015	1.210891	0.071	1.046318	0.3165	CDS possible AMP-binding enzyme 3151757:3153406 reverse MW:59425
RPA2781	1.301985	0.0035	1.115925	0.078	1.193022	0.07	0.916784	0.7795	0.959626	0.6185	dctQ2 TrapT dctQ-M fusion permease, dicarboxylate transport 3153461:3155344 reverse MW:65734
RPA2782	1.16821	0.0975	0.840251	0.972	0.838852	0.805	0.706409	0.9715	0.770754	0.9945	dctP2 TrapT family, dctP subunit, C4-dicarboxylate periplasmic binding protein 3155357:3156376 reverse MW:37341
RPA2783	1.031694	0.3955	1.04961	0.3885	0.979239	0.553	1.686103	0.0315	1.261714	0.146	CDS hypothetical protein 3156741:3157331 reverse MW:21688
RPA2784									1.123339	0.3825	CDS possible nodulin-related protein 3157632:3158327 forward MW:23370
RPA2785	1.65165	0.0095	1.794568	0.007	1.285441	0.094	2.339344	0.001	2.039243	0.001	CDS possible flavodoxin oxidoreductase 3158421:3159758 reverse MW:48822
RPA2786	1.944558	0.0005	2.559263	0.0045	1.793503	0.001	2.177384	0.0005	3.134375	0	CDS hypothetical protein 3159849:3160592 reverse MW:28423
RPA2787	2.158902	0.0005	1.518798	0.0035	1.51586	0.01	3.703651	0.0005	4.162086	0	CDS putative signal transduction histidine kinase with PAS/PAC domain 3160874:3161932 forward MW:38605
RPA2788	0.975828	0.643	0.991264	0.5615	0.829691	0.9325	1.055518	0.3115	0.801051	0.9875	CDS possible methyltransferase 3161963:3162709 reverse MW:27170
RPA2789	1.356319	0.0755	2.285757	0.0005	1.329349	0.105	3.423694	0.0055	3.257279	0	phaA pH adaptation potassium efflux system components phaA and phaB 3163151:3166078 forward MW:105345
RPA2790	0.858339	0.8005	0.89438	0.752					1.029191	0.418	phaC pH adaptation K efflux system component 3166069:3166410 forward MW:11992
RPA2791	1.034657	0.4335	0.71286	0.998	0.874066	0.94	0.821733	0.917	0.659054	0.9985	phaD putative component of pH adaptation K-efflux system phaD 3166407:3168041 forward MW:57101
RPA2792	1.01968	0.4295	0.811297	0.9845	1.088687	0.202	1.266357	0.0785	0.802944	0.988	phaE putative component of pH adaptation K-efflux system phaE 3168038:3168526 forward MW:17848
RPA2793	0.923564	0.641	0.869446	0.9145	1.163265	0.074	1.108318	0.1275	0.717406	0.9945	phaF pH adaptation potassium efflux system phaF 3168523:3168804 forward MW:10011
RPA2794					1.569065	0.0045	1.923353	0.006	2.061266	0	phaG putative pH adaptation potassium efflux system component phaG 3168843:3169172 forward MW:11662
RPA2795	1.663076	0.0615	0.824504	0.729	1.246155	0.1615			2.140716	0	CDS Protein of unknown function UPF0001 3169197:3169979 reverse MW:28742
RPA2796	0.593315	0.996	0.795245	0.9305	0.559831	0.994	0.912801	0.7075	0.721556	0.987	glyA2 glycine hydroxymethyltransferase 3170000:3171304 reverse MW:45360
RPA2797	1.38568	0.036	0.991256	0.5505	1.199904	0.067	1.927032	0.001	1.996581	0.0015	CDS transcriptional regulator, GntR family with aminotransferase domain 3171458:3172909 reverse MW:52829
RPA2798	0.986687	0.505	0.936036	0.5905	0.923533	0.597	1.677162	0.057	2.602861	0.0005	BenE probable Benzoate membrane transport protein 3173005:3174288 forward MW:44284
RPA2799	1.139934	0.1245	0.899758	0.9175	1.076662	0.207	1.416475	0.016	1.629754	0	pdxK putative pyridoxamine kinase 3174285:3175151 forward MW:30352

RPA2800	1.267115	0.0255	1.504298	0.006	1.375124	0.0065	1.942674	0	1.682635	0	CDS unknown protein 3175202:3176011 reverse MW:29460
RPA2801	0.950328	0.7145	0.711189	0.966	1.162808	0.2035	0.74763	0.9635	0.592996	0.996	CDS Collagen triple helix repeat 3176255:3176752 reverse MW:15559
RPA2802	0.786919	0.9615	0.58947	1	0.911337	0.8775	0.677272	0.9825	0.679535	0.9915	CDS ATP-dependent DNA helicase 3176999:3179062 forward MW:75848
RPA2803	1.201484	0.0605	1.010537	0.4335	1.333264	0.0315	1.517326	0.0175	1.426977	0.0035	CDS hypothetical protein 3179069:3179392 reverse MW:11737
RPA2804	0.989508	0.545	0.949718	0.6855	0.81221	0.962	0.898382	0.7605	0.844428	0.978	CDS conserved hypothetical protein 3179465:3180202 reverse MW:26427
RPA2805	1.347153	0.015	0.981122	0.6195	1.362483	0.005	1.323004	0.0075	1.145309	0.1595	nthA nitrile hydratase alpha subunit 3180266:3180907 forward MW:23715
RPA2806	1.593837	0.068	0.757757	0.952	1.280799	0.051	1.250355	0.232	0.917704	0.7505	nthB putative nitrile hydratase beta subunit 3180904:3181560 forward MW:24204
RPA2807	1.143647	0.2195	0.747014	0.952	0.872934	0.7535			0.965309	0.6145	CDS conserved hypothetical protein 3181560:3181982 forward MW:15381
RPA2808	1.086103	0.3535	0.673245	0.916	0.69844	0.78	1.248208	0.1445	1.124033	0.3185	CDS conserved hypothetical protein 3182106:3183239 forward MW:41019
RPA2809	0.991058	0.558	1.181062	0.0335	1.124938	0.115	1.546166	0.015	1.265925	0.022	CDS Beta-lactamase 3183212:3184504 reverse MW:47189
RPA2810	1.199242	0.0155	1.336697	0.007	1.128313	0.1375	1.562356	0.007	1.5751	0.004	CDS possible exsB protein 3184586:3185299 reverse MW:25921
RPA2811	1.328186	0.0065	1.124789	0.0485	0.995863	0.525	1.264876	0.054	1.240025	0.0175	mazG possible mazG 3185416:3186240 forward MW:30362
RPA2812	1.0252	0.4525	0.781212	0.988	1.105531	0.1025	1.093937	0.2045	1.256127	0.0265	CDS probable HlyC/CorC family of transporters with 2 CBS domains 3186319:3187614 forward MW:45891
RPA2813	0.869068	0.7755	0.787126	0.6205	0.951293	0.69			0.659989	0.9905	CDS hypothetical protein 3187611:3187973 forward MW:13682
RPA2814	0.756692	0.986	0.738565	0.996	0.924062	0.8445	0.732792	0.993	0.917416	0.786	ssb single-strand DNA-binding protein 3188088:3188591 reverse MW:17827
RPA2815	1.587066	0.1595	0.485561	0.9995	1.26854	0.145	1.163415	0.244	1.838112	0.0135	CDS possible outer membrane protein 3189020:3189886 forward MW:30951
RPA2816	1.000844	0.5025	0.99543	0.5155	0.885144	0.8545	0.939053	0.757	0.845834	0.936	uvrA excinuclease ABC subunit A 3190193:3193210 forward MW:110772
RPA2817	1.631736	0.015	1.480935	0.0035	1.460538	0.0005	1.978304	0.002	1.977174	0	CDS unknown protein 3193267:3194052 reverse MW:29157
RPA2818	0.988178	0.536	0.797287	0.968	1.140466	0.1275	0.972381	0.626	0.893669	0.865	CDS conserved hypothetical protein 3194397:3194771 forward MW:13908
RPA2819	1.418127	0.0115	1.109989	0.1385	1.165064	0.123	2.186306	0	2.310011	0	CDS conserved hypothetical protein 3194789:3195151 reverse MW:13194
RPA2820	1.19635	0.1015	0.905921	0.8	1.000706	0.4955	1.450317	0.0205	1.211286	0.1145	CDS DUF433 3195154:3195492 reverse MW:11791
RPA2821	1.272096	0.129	0.977558	0.5245	1.182334	0.1105	1.880161	0.1565	1.067967	0.367	CDS possible ion transporter 3195528:3196304 forward MW:28555
RPA2822	1.385967	0.0135	0.795088	0.871	0.979415	0.5265	1.192692	0.1145	0.714268	0.989	CDS conserved unknown protein 3196342:3196896 forward MW:19353
RPA2823	0.638077	0.9185	0.743938	0.861	1.03417	0.4465	0.727761	0.9075	0.340522	0.9935	CDS conserved hypothetical protein 3197176:3197466 forward MW:10207
RPA2824	0.868815	0.942	1.059958	0.266	0.768346	0.9755	0.97569	0.5945	0.976894	0.5615	CDS Thioesterase superfamily 3197599:3198006 forward MW:14498
RPA2825	2.16127	0.0125	3.671876	0.004	3.103538	0	1.317686	0.137	2.184681	0.0005	CDS conserved unknown protein 3198306:3198698 reverse MW:13431
RPA2826					1.229869	0.3405	1.065706	0.3755	0.971694	0.5315	CDS conserved hypothetical protein 3199080:3199976 forward MW:31212
RPA2827	0.894757	0.892	0.805179	0.985	0.868088	0.8845	0.950097	0.715	0.925196	0.8595	gid putative glucose-inhibited division protein (gid) 3200764:3202200 forward MW:51167
RPA2828	1.227995	0.087	0.728914	0.997	1.092693	0.1585	0.793846	0.9375	0.892171	0.92	CDS conserved hypothetical protein 3202230:3203102 reverse MW:31526
RPA2829											CDS conserved hypothetical protein 3203099:3203482 reverse MW:14101
RPA2830	0.966927	0.6745	0.892375	0.9005	0.856259	0.9495	0.769499	0.9905	0.790255	0.86	secF putative protein-export membrane protein secF 3203644:3204762 reverse MW:40525
RPA2831	0.895004	0.8825	0.969721	0.693	0.754453	0.989	0.845757	0.9465	0.928033	0.797	secD protein-export membrane protein secD 3204788:3206389 reverse MW:57161
RPA2832	0.90197	0.9195	1.139401	0.0955	0.715954	0.9885	0.94131	0.654	1.001995	0.4765	yajC putative membrane protein, possible preprotein translocase 3206434:3206871 reverse MW:15652
RPA2833	0.888008	0.901	0.718651	0.994	0.979359	0.6075	0.723692	0.993	0.718755	0.992	CDS possible ATPase family protein 3207035:3208051 forward MW:36648
RPA2834	0.933846	0.8595	0.84104	0.9785	1.049145	0.2595	0.859032	0.9445	0.919076	0.8625	CDS conserved hypothetical protein 3208220:3209920 forward MW:61121
RPA2835	1.635174	0.0035	1.343625	0.007	1.695993	0.008	2.393713	0	2.813565	0	CDS conserved hypothetical protein 3209967:3210767 reverse MW:29971
RPA2836	1.057175	0.318	0.968712	0.6365	1.029745	0.3275	11.16683	0	6.72783	0	CDS possible hydrolase 3211602:3212495 forward MW:32381
RPA2837	1.177624	0.04	0.872706	0.936	0.795261	0.9205	0.944893	0.6485	0.927402	0.77	lppB Peptidoglycan-binding LysM:Peptidase M23/M37 3212596:3214011 reverse MW:48714
RPA2838	0.921913	0.792	0.784301	0.917	1.026424	0.4275	0.901384	0.733	0.970957	0.6045	pimt2 putative D-aspartate protein carboxylmethyltransferase type II 3214132:3214785 reverse MW:23903
RPA2839	1.138847	0.122	1.083144	0.1935	1.158098	0.0735	1.381306	0.01	1.341189	0.018	CDS response regulator receiver (CheY-like protein) 3215009:3215383 forward MW:13416
RPA2840	1.029894	0.3695	1.213896	0.0295	0.933253	0.8105	1.72022	0.0035	2.105945	0	CDS conserved hypothetical protein 3215392:3215919 reverse MW:19442
RPA2841	0.907153	0.89	0.988371	0.5755	0.675779	0.997	0.833134	0.964	0.965871	0.666	surE survival protein surE 3216132:3216899 reverse MW:27694
RPA2843	1.675248	0.032	2.949925	0.001	1.496639	0.0095	1.6788	0.026	1.993173	0.001	CDS pseudogene of Fe+3 siderophore transport receptor 3217041:3219283 reverse MW:80547
RPA2844	0.99473	0.5145	0.948385	0.6915	0.932942	0.691	0.770761	0.8275	0.845154	0.95	CDS SCP-like extracellular protein 3219531:3220202 reverse MW:23164
RPA2845	0.782141	0.9335	0.995867	0.523	0.664148	0.998	0.669581	0.9965	0.767395	0.9865	serS seryl-tRNA synthetase 3220208:3221512 reverse MW:47329
RPA2846	1.288116	0.0375			1.268966	0.016			1.178343	0.134	CDS conserved hypothetical protein 3221637:3221942 reverse MW:10614
RPA2847	0.847784	0.9515	0.754838	0.99	0.801337	0.981	0.637316	0.9955	0.676962	0.9995	tatC putative sec-independent protein translocase component TatC 3222083:3222898 reverse MW:29739
RPA2848	0.929628	0.7865	0.918448	0.8955	1.024415	0.3795	1.078106	0.2225	1.020084	0.393	tatB possible sec-independent protein secretion pathway component TatB 3222895:3223404 reverse MW:17860
RPA2849	1.527489	0.0165	1.05083	0.277	1.352125	0.012	1.454032	0.005	1.316716	0.012	tatAE putative sec-independent protein translocase protein tatA/E 3223621:3223857 reverse MW:8366
RPA2850	0.808403	0.9715	0.730777	0.9975	1.059277	0.2555	0.580037	0.9985	0.696594	0.996	CDS conserved unknown protein 3224004:3225302 reverse MW:46430
RPA2851	0.917876	0.837	0.848839	0.9685	0.869367	0.919	0.728454	0.9805	0.746767	0.9905	CDS DUF173 3225323:3226156 reverse MW:31108
RPA2852	0.906833	0.941	0.873711	0.967	0.825806	0.909	0.690373	0.9985	0.901602	0.8885	CDS putative sugar hydrolase 3226153:3227178 reverse MW:35976
RPA2853	1.241023	0.0065	1.073572	0.1535	1.138558	0.0715	1.040156	0.328	1.207901	0.0265	CDS Proline-rich region 3227227:3228849 reverse MW:57489
RPA2854	1.323823	0.0285	1.297756	0.0445	1.333598	0.0135	2.431079	0.0005	2.514635	0.0015	argS arginyl-tRNA synthetase 3228952:3230745 reverse MW:65197
RPA2855	0.843761	0.8985	1.027029	0.382	0.761642	0.9805	0.874746	0.8345	0.802282	0.9765	CDS dGTP triphosphohydrolase 3230797:3232011 reverse MW:45370
RPA2856	0.936353	0.7195	0.769924	0.9835	1.203854	0.1965	1.07675	0.3665	1.624138	0.002	CDS Protein of unknown function, HesB/YadR/YfhF 3232118:3232450 forward MW:11483
RPA2857	0.976852	0.6185	1.103551	0.194	0.945668	0.762	1.192113	0.0925	1.517466	0.003	CDS unknown protein 3232645:3233694 forward MW:37061
RPA2858	1.346666	0.075	1.627732	0.024	1.055865	0.366	1.289365	0.142	2.252485	0	CDS hypothetical protein 3233691:3234755 forward MW:39246
RPA2859	1.226438	0.1315			1.180407	0.223			1.117193	0.3685	CDS hypothetical protein 3234782:3235519 reverse MW:25393
RPA2860	1.028928	0.3965	1.09579	0.157	1.044749	0.3375	1.27072	0.187	1.049257	0.3345	CDS hypothetical protein 3235643:3236602 reverse MW:33416
RPA2861	1.103878	0.1375	1.0348	0.3285	0.924576	0.8365	1.204391	0.034	1.166791	0.0415	xthA2 exodeoxyribonuclease III 3237166:3238077 forward MW:34374
RPA2862	1.673852	0.005	0.952879	0.7455	1.514572	0.0075	1.48714	0.0185	1.680231	0.0115	exoR putative exopolysaccharide regulatory protein exoR 3238277:3239098 reverse MW:29666
RPA2863	0.891921	0.9295	0.830384	0.9755	1.02248	0.3785	0.945605	0.7415	0.84124	0.86	CDS dihydrolipoamide dehydrogenase, E3 Component of Pyruvate dehydrogenase multienzyme complex 3239761:3241182 reverse MW:50406
RPA2864	0.759876	0.9895	0.71432	0.9925	0.915773	0.8845	1.028937	0.3675	0.764091	0.95	CDS dihydrolipoamide acetyltransferase 3241258:3242649 reverse MW:48330
RPA2865	0.755092	0.8955	0.56496	0.9995	0.720152	0.9975	0.825956	0.9775	0.709708	0.986	CDS conserved unknown protein 3242662:3242958 reverse MW:11042
RPA2866	0.662168	0.9735	0.54414	0.999	0.835294	0.975	0.82328	0.929	0.646264	0.99	CDS pyruvate dehydrogenase E1 beta subunit 3242963:3244372 reverse MW:49737
RPA2867	0.764659	0.9415	0.573427	0.9995	0.8109	0.9835	0.863529	0.8655	0.700198	0.986	CDS pyruvate dehydrogenase E1 alpha subunit 3244431:3245465 reverse MW:37698
RPA2868	1.050987	0.313	1.117503	0.205	1.070004	0.283	0.980769	0.56	0.760433	0.9865	CDS Septum formation initiator 3245618:3245935 reverse MW:11868
RPA2869	1.18376	0.0285	1.108917	0.1035	1.522657	0.0015	1.477063	0.0035	1.187696	0.0225	CDS possible flavin-dependent oxidoreductase 3246024:3246584 reverse MW:20152
RPA2870	1.258385	0.0085	0.924318	0.719	0.984938	0.5765	1.068101	0.3775	0.882716	0.9325	CDS L-carnitine dehydratase/bile acid-inducible protein F 3246724:3247866 reverse MW:40344
RPA2871	1.079936	0.326	0.746861	0.958	1.032737	0.4455	0.966272	0.558	1.138838	0.1415	CDS probable RhtB family transporter, amino acid efflux 3247959:3248573 forward MW:21792
RPA2872	1.748711	0.0015	1.114443	0.138	1.680664	0.002	2.403488	0	2.15353	0	CDS unknown protein 3248725:3249528 reverse MW:30009
RPA2873	0.892816	0.8675	0.757769	0.986	0.926559	0.7635	0.804434	0.9475	0.932052	0.6825	CDS possible NADH oxidoreductase 3249613:3250746 reverse MW:39430
RPA2874	1.05322	0.334	1.0546	0.2415	0.702373	0.9835	0.771362	0.976	0.925697	0.816	eno enolase 3250857:3252140 reverse MW:45001
RPA2875	1.184569	0.0975	1.023085	0.4025	0.929497	0.7845	0.935674	0.6325	0.989228	0.541	CDS GTP cyclohydrolase I 3252326:3252802 forward MW:17783
RPA2876	2.565264	0.005	3.757699	0.004	1.863069	0.002	1.670775	0.0235	2.677793	0	CDS periplasmic glucans biosynthesis protein OpgG 3253245:3254750 forward MW:56032
RPA2877	1.684438	0.008	2.412409	0.008	1.517805	0.002	2.389681	0.0025	2.20456	0	CDS putative glycosyltransferase family protein 3254738:3256903 forward MW:79058

RPA2878	1.246163	0.031	1.47872	0.0025	1.018165	0.44	1.146807	0.124	0.894906	0.853	CDS possible MDR related permease 3256900:3258126 reverse MW:41948
RPA2879	0.998927	0.489	0.929756	0.669	0.805511	0.771	1.02558	0.4635	0.737199	0.9735	kdsA 2-dehydro-3-deoxyphosphooctonate aldolase 3258126:3258989 reverse MW:30067
RPA2880	0.88417	0.8885	0.870874	0.914	0.80609	0.9745	0.707763	0.9935	0.711099	0.9895	CDS conserved hypothetical protein 3258986:3259906 reverse MW:33286
RPA2881	1.210043	0.036	0.972717	0.654	1.527475	0.0215	0.887574	0.8205	0.837013	0.787	CDS conserved hypothetical protein 3260002:3260532 reverse MW:19740
RPA2882											CDS conserved hypothetical protein 3260682:3260957 forward MW:10151
RPA2883	1.015523	0.4095	0.949238	0.7305	1.167722	0.0385	1.202186	0.0875	1.486103	0.004	CDS hypothetical protein 3260992:3261849 reverse MW:30250
RPA2884	0.968341	0.6165	0.852247	0.8485	1.094752	0.1405	0.811107	0.8435	0.80632	0.9545	CDS conserved hypothetical protein 3261980:3262357 forward MW:11954
RPA2885	1.1166	0.1105	1.212863	0.018	1.081119	0.162	1.27934	0.018	1.207125	0.018	CDS hypothetical protein 3262467:3262613 forward MW:5409
RPA2886	1.006488	0.491	1.118721	0.086	0.956071	0.678	0.972396	0.6115	1.142283	0.07	pyrG CTP synthase 3262627:3264258 reverse MW:60118
RPA2887	1.032581	0.328	1.188064	0.0285	0.96781	0.6865	0.976705	0.6055	1.120618	0.149	secG possible secG: preprotein translocase 3264425:3264829 reverse MW:13666
RPA2888	0.851217	0.8465	0.795897	0.8665	0.48257	0.9965	0.504573	0.998	0.726544	0.9865	cbbJ, tpi, tim triose-phosphate isomerase 3265005:3265841 reverse MW:28165
RPA2889	1.007568	0.475	1.060183	0.247	0.844046	0.8985	1.174141	0.182	1.213351	0.045	CDS putative peptidyl-prolyl cis-trans isomerse D 3266039:3267940 forward MW:68656
RPA2890	0.834662	0.909	0.866336	0.9455	0.869823	0.9315	0.754633	0.977	0.779516	0.962	trpD anthranilate phosphoribosyltransferase 3267977:3268993 forward MW:34425
RPA2891	0.925619	0.877	1.008472	0.472	0.838847	0.921	0.841782	0.877	0.72522	0.9535	trpC indole-3-glycerol phosphate synthase 3269058:3269921 forward MW:30822
RPA2892	0.927274	0.8425	0.785699	0.992	0.742569	0.9935	0.681831	0.999	0.764827	0.976	moaC molybdenum cofactor biosynthesis protein C 3269932:3270462 forward MW:18172
RPA2893			0.675223	0.96			0.676343	0.9365			CDS putative cation-transporting ATPase 3270500:3273058 forward MW:90764
RPA2894	0.83578	0.944	1.173226	0.1175	0.997051	0.5185	1.145545	0.221	2.450366	0.0005	CDS conserved hypothetical protein 3273186:3273662 reverse MW:17493
RPA2895	1.121956	0.221	0.985404	0.596	1.618177	0	1.210906	0.0465	2.072803	0.002	CDS possible small heat shock protein 3273901:3274401 forward MW:18479
RPA2896	1.422083	0.029	2.135576	0.043	1.351559	0.008			1.785048	0.0045	CDS hypothetical protein 3274570:3274818 forward MW:9007
RPA2897	1.389306	0.0145	1.157238	0.064	1.100559	0.33	1.407544	0.0395	1.504323	0.0025	motB2 possible chemotaxis protein MotB2 3274858:3275838 reverse MW:34677
RPA2898	1.03912	0.307	1.065054	0.1755	0.718901	0.996	0.848825	0.908	1.039755	0.316	CDS Haloacid dehalogenase-like hydrolase 3275975:3276601 forward MW:23037
RPA2899	1.062171	0.189	1.007226	0.466	0.90879	0.904	1.190203	0.1245	1.264966	0.008	CDS conserved hypothetical protein 3276632:3277120 forward MW:18096
RPA2900	1.329937	0.0555	2.305818	0	1.005974	0.4715	1.840412	0.013	2.592072	0.0005	CDS possible rifampin ADP-ribosyl transferase 3277268:3277681 forward MW:15014
RPA2901											CDS hypothetical protein 3277725:3278066 reverse MW:11781
RPA2902	1.110799	0.1005	0.957549	0.7415	0.769646	0.931	0.787907	0.9485	0.94883	0.686	moeA molybdenum cofactor biosynthesis protein A 3278266:3279477 forward MW:42037
RPA2903	0.666722	0.9995	0.64631	0.986	1.002541	0.4905	0.84735	0.9305	1.121557	0.1105	lexA SOS response transcriptional repressor, lexA 3279537:3280364 forward MW:30187
RPA2904					0.886899	0.838	1.189843	0.21	1.890719	0.0005	CDS possible DNA uptake protein, ComEC 3280435:3282702 reverse MW:79249
RPA2905	1.040804	0.3385	0.959977	0.6955	0.722612	0.989	0.852725	0.961	0.950574	0.7505	glnS glutaminyl-tRNA synthetase 3282795:3284477 reverse MW:63661
RPA2906	0.850943	0.904	0.843932	0.944	0.69533	0.9855	0.8047	0.97	0.848683	0.906	gltX glutamyl-tRNA synthetase 3284639:3286060 forward MW:52180
RPA2907	1.401242	0.0075	1.376404	0.0935	1.010666	0.457	1.191491	0.0305	1.353178	0.006	cisY citrate synthase 3286211:3287515 forward MW:48027
RPA2908	1.550758	0	1.709441	0.0005	1.495333	0.003	2.109196	0.0005	1.651696	0.0035	CDS Cytidine/deoxycytidylate deaminase:Tat pathway signal 3287610:3288254 reverse MW:23198
RPA2909	0.877483	0.9275	1.02242	0.4405	0.946252	0.6815	0.656457	0.822	0.753841	0.9395	lpxB lipid-A-disaccharide synthase 3288404:3289585 reverse MW:42699
RPA2910	0.628685	0.983	0.860431	0.8575	0.802318	0.956	0.693533	0.991	0.677482	0.992	CDS conserved hypothetical protein 3289582:3290439 reverse MW:29860
RPA2911	0.819764	0.94	0.785767	0.987	0.743038	0.982	0.662386	0.989	0.689358	0.996	lpxA acyl-acyl carrier protein-UDP-N-acetylglucosamine O-acyltransferase 3290458:3291300 reverse MW:29232
RPA2912	0.712551	0.972	0.769626	0.991	0.638737	0.999	0.591389	0.993	0.629145	0.999	CDS possible (3R)-hydroxymyristoyl-acyl carrier protein dehydratase 3291309:3291764 reverse MW:17017
RPA2913	0.70683	0.971	0.905719	0.932	0.955966	0.616	0.825652	0.889	0.783339	0.9845	lpxD UDP-3-o-[3-hydroxymyristoyl] glucosamine n-acyltransferase 3291764:3292846 reverse MW:37746
RPA2914	0.880962	0.894	0.911522	0.778	0.834169	0.981	0.720439	0.982	0.860995	0.906	CDS putative outer membrane protein 3292876:3295401 reverse MW:92516
RPA2915	1.063128	0.205	1.007613	0.452	1.056749	0.2745	0.873848	0.905	1.021676	0.423	CDS Zinc metalloprotease 3295574:3296725 reverse MW:41069
RPA2916	1.072801	0.1845	0.959446	0.748	1.098809	0.1645	0.860552	0.9005	1.108854	0.0935	dxr 1-deoxy-d-xylulose 5-phosphate reductoisomerase 3296771:3297994 reverse MW:42364
RPA2917	0.879679	0.917	0.852548	0.9725	0.9885	0.538	0.780006	0.988	0.731289	0.99	cdsA Phosphatidate cytidylyltransferase 3297999:3298847 reverse MW:28633
RPA2918	1.095445	0.2135	1.082482	0.22	1.120966	0.0815	1.138907	0.1205	0.701833	0.9905	uppS undecaprenyl pyrophosphate synthetase 3298853:3299611 reverse MW:28088
RPA2919	0.861522	0.917	0.802849	0.9255	0.836415	0.8875	0.604878	0.999	0.694962	0.8865	rrf ribosome releasing factor 3299823:3300383 reverse MW:20764
RPA2920	0.784426	0.8305	0.819009	0.914	0.666244	0.995	0.424535	1	0.672304	0.9095	pyrH uridylate kinase 3300449:3301165 reverse MW:24644
RPA2921	0.70119	0.837	1.000367	0.504	0.506271	0.9975	0.533468	0.999	0.777583	0.914	tsf elongation factor Ts 3301233:3302159 reverse MW:32206
RPA2922	0.789403	0.893	1.097414	0.0935	0.463698	0.999	0.715665	0.9865	0.869195	0.8005	rpsB 30S ribosomal protein S2 3302284:3303279 reverse MW:36044
RPA2923	0.997234	0.4935	0.887732	0.7985	0.934154	0.7515	0.895144	0.7465	1.057998	0.375	CDS conserved hypothetical protein 3303514:3306003 reverse MW:85717
RPA2924	0.559446	0.999	0.579583	0.9985	0.945497	0.7175	0.52787	0.9985	0.769754	0.9895	dnaE DNA polymerase III alpha subunit 3306165:3309620 reverse MW:126012
RPA2925	0.791644	0.9815	0.740529	0.9935	1.18013	0.0345	0.952478	0.655	0.80184	0.956	CDS hypothetical protein 3310205:3310714 forward MW:19053
RPA2926	0.786394	0.9695	0.730096	0.996	0.978322	0.584	0.72837	0.988	0.778449	0.9895	CDS ATP-binding protein of ABC transporter, possibly involved in lipoprotein release 3310911:3311609 reverse MW:25382
RPA2927	0.81451	0.977	0.735489	0.9935	0.906881	0.8815	0.73316	0.987	0.837516	0.9575	CDS possible ABC type permease; lipoprotein releasing factor 3311621:3312901 reverse MW:46696
RPA2928	0.844027	0.972	0.796177	0.9925	0.665452	0.988	0.769719	0.993	0.68554	0.997	proS proline-tRNA ligase 3312981:3314297 reverse MW:49309
RPA2929			0.842441	0.785	1.382057	0.2515	0.813987	0.8615	0.972941	0.5585	CDS conserved hypothetical protein 3314473:3316053 reverse MW:54601
RPA2930	0.924162	0.81	0.897384	0.843	1.011968	0.4525	0.785532	0.9235	0.780078	0.979	CDS conserved unknown protein 3316071:3316598 reverse MW:18588
RPA2931	0.856345	0.8835	1.004985	0.4885	1.122021	0.087	0.571556	0.999	0.740843	0.9975	CDS DUF461 3316598:3317137 reverse MW:18666
RPA2932	1.121949	0.079	1.237669	0.0995	1.22405	0.0605	0.842554	0.653	0.927402	0.7835	CDS hypothetical protein 3317263:3317679 reverse MW:14248
RPA2933	1.082127	0.13	0.998075	0.5115	0.993797	0.5305	1.22646	0.041	1.128837	0.0595	CDS conserved hypothetical protein 3318298:3318579 reverse MW:10055
RPA2934	1.035885	0.339	1.143006	0.1095	0.995277	0.516	1.328761	0.088	0.971614	0.585	CDS conserved unknown protein 3318583:3318987 reverse MW:14330
RPA2935	1.014159	0.4155	1.157556	0.0275	0.745614	0.978	1.141598	0.079	1.072757	0.2405	CDS Beta-lactamase-like 3319029:3320699 reverse MW:59833
RPA2936	0.989494	0.557	1.149825	0.104	0.920217	0.822	1.015703	0.4455	0.89222	0.927	birA putative biotin-protein ligase birA 3320699:3321505 reverse MW:27923
RPA2937	0.845625	0.967	0.771093	0.9925	0.830721	0.955	0.87062	0.8605	0.746942	0.9895	nuoN1 NADH-ubiquinone dehydrogenase chain N 3321506:3322945 reverse MW:50574
RPA2938	0.919261	0.821	0.833482	0.9735	0.919291	0.8465	0.907463	0.8535	0.898331	0.933	nuoM1 NADH-ubiquinone dehydrogenase chain M 3322965:3324482 reverse MW:55181
RPA2939	0.973413	0.623	0.963928	0.7245	0.835577	0.8985	1.148851	0.0965	1.105383	0.0835	nuoL1 NADH-ubiquinone dehydrogenase chain L 3324483:3326576 reverse MW:76711
RPA2940	0.906503	0.889	0.87772	0.9185	0.866618	0.918	1.116086	0.139	0.926199	0.8695	nuoK1 NADH-ubiquinone dehydrogenase chain K 3326636:3326947 reverse MW:11043
RPA2941	0.852646	0.9645	0.921319	0.877	0.904307	0.8835	1.005793	0.4745	0.815395	0.982	nuoJ1 NADH-ubiquinone dehydrogenase chain J 3326944:3327582 reverse MW:23131
RPA2942	1.13309	0.188	0.955352	0.695	0.789933	0.9805	1.083749	0.2385	1.052649	0.3495	nuoI1 NADH-ubiquinone dehydrogenase chain I 3327592:3328080 reverse MW:18649
RPA2944	0.928855	0.87	0.982133	0.616	0.904786	0.82	1.137331	0.111	1.170988	0.035	nuoG1 NADH-ubiquinone dehydrogenase chain G 3329123:3331207 reverse MW:73832
RPA2945	0.857761	0.968	1.027652	0.404	1.003603	0.507	1.155403	0.1155	1.183877	0.076	nuoF1 NADH-ubiquinone dehydrogenase chain F 3331204:3332529 reverse MW:48335
RPA2946	1.01278	0.434	0.976246	0.611	0.89083	0.8685	0.861699	0.897	1.105747	0.166	CDS conserved hypothetical protein 3332548:3332763 reverse MW:7470
RPA2947	0.911392	0.63	1.143903	0.042	0.95387	0.6095	1.180469	0.0655	1.358088	0.0155	nuoE1 NADH-ubiquinone dehydrogenase chain E 3332760:3333509 reverse MW:26960
RPA2948	1.029476	0.4145	1.183192	0.068	0.786468	0.962	1.311333	0.1005	1.306682	0.0195	fkbM possible methyltransferase, FkbM family 3333512:3334483 reverse MW:35248
RPA2949	1.195452	0.0905	1.28741	0.0545	0.774781	0.9255	1.397697	0.009	1.361216	0.025	nuoD NADH-ubiquinone dehydrogenase chain D 3334480:3335688 reverse MW:45192
RPA2950	1.037179	0.317	1.44518	0.001	1.352362	0.043	1.154502	0.112	1.165434	0.0765	nuoC NADH-ubiquinone dehydrogenase chain C 3335740:3336354 reverse MW:23141
RPA2951	1.01165	0.4585	1.166852	0.029	1.261961	0.047	1.052329	0.289	1.072016	0.1795	nuoB1 NADH-ubiquinone dehydrogenase chain B 3336368:3336964 reverse MW:21799
RPA2952	0.948605	0.664	0.863351	0.936	1.204107	0.0325	1.13744	0.2175	1.356994	0.0065	nuoA1 NADH-ubiquinone dehydrogenase chain A 3336976:3337341 reverse MW:13528
RPA2953	0.870933	0.9535	0.816484	0.9285	1.030702	0.409	0.962781	0.62	0.621959	0.976	hupA possible DNA-binding protein hu-alpha (NS2) (HU-2) 3338656:3338967 forward MW:11220
RPA2954	0.888418	0.892	0.737339	0.9965	0.849793	0.862	0.762672	0.976	0.740011	0.995	pepT putative peptidase T (aminotripeptidase) (tripeptidase) 3339219:3340517 forward MW:46858
RPA2955	0.902703	0.904	0.718299	0.9765	1.002477	0.507	0.919566	0.73	0.614367	0.998	mex possible RND efflux membrane fusion protein precursor 3340667:3341911 forward MW:43537

RPA2956	0.925462	0.7255	0.892155	0.8885	0.824369	0.9045	0.749102	0.9605	0.630014	0.997	mexF putative RND multidrug efflux transporter MexF 3341940:3345080 forward MW:110277
RPA2957	1.097827	0.1945	1.447315	0	0.88466	0.8975	1.873532	0.002	2.358805	0	CDS putative diguanylate cyclase (GGDEF)/phosphodiesterase (EAL) 3345579:3348227 forward MW:97011
RPA2958	0.957677	0.6575	1.195149	0.0525	0.984507	0.563	1.030713	0.415	1.119026	0.1095	CDS putative DNA-binding protein 3348336:3349376 reverse MW:39528
RPA2959	1.031328	0.3225	0.948191	0.7935	1.185613	0.0705	0.940119	0.7785	0.877754	0.909	lon ATP-dependent protease Lon 3349571:3352003 reverse MW:89360
RPA2960	1.139811	0.0785	0.886985	0.8295	1.06821	0.3205	1.074525	0.3485	1.175531	0.027	clpX ATP-dependent Clp protease ATP binding subunit ClpX 3352313:3353587 reverse MW:46681
RPA2961	0.674871	1	0.688655	0.996	0.901444	0.871	0.552847	0.999	0.523092	0.9995	clpP ATP-dependent Clp protease proteolytic subunit 3353980:3354618 reverse MW:23590
RPA2962	0.856249	0.828	0.887064	0.9545	0.610747	0.9955	0.731661	0.9925	1.027086	0.45	tig putative trigger factor 3354932:3356290 reverse MW:50097
RPA2963	0.742238	0.988	0.919328	0.876	0.881738	0.8155	0.946357	0.695	0.660824	0.9995	CDS hypothetical protein 3356681:3357154 reverse MW:17365
RPA2964	0.752799	0.9235	0.59929	0.9835	0.702603	0.9015	0.435429	0.999	0.541147	0.999	CDS Multicopper oxidase, type 1 3357277:3358482 forward MW:42758
RPA2965	1.137186	0.229	0.867727	0.871	0.972787	0.601	1.162642	0.143	0.949164	0.772	yjeF Protein of unknown function UPF0031:YjeF-related protein, N-terminal 3358531:3360030 reverse MW:51441
RPA2966	3.964615	0.0005	3.385533	0	3.602707	0	4.069247	0	3.115796	0.001	glnB nitrogen regulatory protein P-II 3360442:3360780 forward MW:12335
RPA2967	2.75525	0.0005	2.323507	0	2.969293	0	2.475683	0	2.324909	0.0005	glnA glutamine synthetase I 3360870:3362279 forward MW:52362
RPA2968	0.982524	0.5905	0.917623	0.829	1.106152	0.1645	1.17303	0.159	1.242634	0.115	CDS probable transcriptional regulator, TetR family 3362578:3363327 forward MW:27098
RPA2969	0.928422	0.886	0.864874	0.917	1.281846	0.018	0.879607	0.7925	0.739043	0.986	CDS unknown protein 3363340:3363951 forward MW:21776
RPA2970	0.898129	0.9005	0.823653	0.9835	0.886214	0.934	0.645779	0.9945	0.56778	0.9995	bioA adenosylmethionine-8-amino-7-oxononanoate aminotransferase 3364094:3365371 reverse MW:46244
RPA2971			0.52066	0.978							bioD dethiobiotin synthetase 3365368:3366006 reverse MW:22562
RPA2972					1.05931	0.428					bioF 8-amino-7-oxononanoate synthase 3366003:3367133 reverse MW:40074
RPA2973			0.957034	0.5975					1.146404	0.235	CDS hypothetical protein 3367274:3367837 reverse MW:20303
RPA2974	0.752168	0.932	0.642757	0.987	0.991288	0.506	0.6178	0.9785	0.489428	0.9965	CDS putative 6-aminohexanoate-cyclic-dimer hydrolase 3367926:3369356 reverse MW:50290
RPA2975	1.097405	0.3355	0.532418	0.994			0.750027	0.8605	0.775749	0.933	serA1 putative phosphoglycerate dehydrogenase 3369556:3370545 reverse MW:35241
RPA2976	0.881476	0.8965	0.943114	0.647	0.809504	0.963	0.846827	0.6065	0.87192	0.8785	CDS Permeases of the drug/metabolite transporter (DMT) superfamily 3370654:3371553 reverse MW:31019
RPA2977	0.301581	0.999	0.164477	0.9995	1.657727	0.034	0.180819	0.9985	0.181628	0.9985	nrd ribonucleotide reductase 3372218:3375991 forward MW:138043
RPA2978	0.628439	0.985	0.535932	0.999	1.873808	0.069	0.61063	0.951	0.583936	0.9955	CDS unknown protein 3376115:3377209 forward MW:40555
RPA2979	0.68576	0.986	0.616601	0.9915	1.618851	0.048	0.799911	0.8175	0.738042	0.993	CDS conserved hypothetical protein 3377373:3377621 forward MW:8922
RPA2983	0.439363	0.9745	0.716407	0.909	0.635381	0.834			0.643194	0.9115	CDS hypothetical protein 3379718:3380197 forward MW:16502
RPA2984	1.108884	0.3	1.220184	0.023			1.363983	0.034	1.178596	0.1045	CDS putative diguanylate cyclase (GGDEF) 3380294:3381445 reverse MW:41733
RPA2985											CDS conserved unknownl protein 3381693:3382379 forward MW:24913
RPA2986	1.203621	0.211							0.587935	0.9765	CDS probable 5-carboxymethyl-2-hydroxymuconate delta isomerase 3383055:3383399 reverse MW:12708
RPA2987	1.064189	0.3355	0.975508	0.5625	1.172352	0.1225	1.194499	0.352	0.797051	0.911	CDS conserved hypothetical protein 3383593:3384438 forward MW:29877
RPA2988	1.157481	0.074	1.385345	0.0525	1.015655	0.4645			0.797009	0.8695	yrkN GCN5-related N-acetyltransferase 3384525:3385103 forward MW:21790
RPA2989			0.784455	0.7015	1.209782	0.2375	0.985059	0.5385	0.998055	0.5105	CDS putative quinone oxidoreductase 3385144:3386145 forward MW:34558
RPA2990			2.097742	0			1.405413	0.0985			CDS conserved hypothetical protein 3386280:3386771 reverse MW:18368
RPA2991											CDS hypothetical protein 3386893:3387189 reverse MW:10216
RPA2992	0.835888	0.7875	1.017111	0.4215	1.107804	0.238	0.875292	0.8585	0.761427	0.9835	CDS conserved hypothetical protein 3387497:3388180 reverse MW:24152
RPA2993											CDS Domain of unknown function UPF0126 3388210:3388863 reverse MW:22032
RPA2994	0.90793	0.653	0.779545	0.8865							CDS transcriptional regulator, LysR family 3388995:3389873 reverse MW:32463
RPA2995									0.111317	0.9995	nuoL3 possible NADH-Ubiquinone/plastoquinone (complex I) 3389982:3391553 forward MW:53796
RPA2996	1.271496	0.157	2.224472	0.1685	1.034109	0.4575			0.39126	0.98	CDS conserved hypothetical protein 3391575:3394001 forward MW:87125
RPA2997											CDS hypothetical protein 3394158:3394445 forward MW:10156
RPA2998	1.444362	0.0505	1.418724	0.0485	0.903532	0.7415	2.227019	0.0115	0.278914	1	dapA1 putative dihydrodipicolinate synthase 3394449:3395372 forward MW:31920
RPA2999											ptsN2 putative nitrogen regulatory IIA protein 3395404:3395850 reverse MW:15845
RPA3000	1.150946	0.0895	0.820916	0.9385	0.914045	0.777	0.838549	0.926	1.046139	0.364	kdpE two-component osmotic transcriptional regulator kdpE, winged helix family 3395874:3396557 reverse MW:25588
RPA3001	1.473384	0.004	1.232115	0.0235	1.352228	0.005	1.621164	0.0025	1.356907	0.007	kdpD two component osmosensitive K+channel and sensor histidine kinase, KdpD 3396563:3399286 reverse MW:98425
RPA3002	1.25638	0.0075	1.258192	0.023	1.379606	0.0025	1.934274	0.0025	1.416152	0.0315	kdpC potassium-transporting atpase c chain, KdpC 3399332:3399937 reverse MW:20616
RPA3003											kdpB potassium-transporting atpase b chain, KdpB 3399950:3402079 reverse MW:74205
RPA3004											kdpA potassium-transporting ATPase, A chain, KdpA 3402089:3403792 reverse MW:59738
RPA3005											CDS hypothetical protein 3404124:3404417 forward MW:10163
RPA3006											CDS hypothetical protein 3404723:3405283 forward MW:20458
RPA3007	1.354238	0.0575	1.324186	0.058			1.493111	0.0395	1.346266	0.035	CDS hypothetical protein 3405291:3406031 forward MW:27184
RPA3008	1.419361	0.107	1.599127	0.001			0.950101	0.5745	1.202033	0.112	kup2 potassium uptake protein Kup 3406021:3407925 reverse MW:69017
RPA3011	5.416241	0.007	11.13499	0	2.038891	0.0015	3.259192	0.004	2.138528	0.0015	CDS unknown protein 3409321:3409959 reverse MW:22235
RPA3014	1.359631	0.089	1.404876	0.006	1.58933	0.0045	1.233689	0.1745	0.872274	0.7305	CDS two-component transcriptional regulator, LuxR family 3410877:3411584 forward MW:25547
RPA3015	1.474966	0.1405	2.123376	0.0075	2.093597	0.0165	1.200007	0.279	0.686651	0.8335	phyB1 Bacteriophytochrome (light-regulated signal transduction histidine kinase), PhyB1 3411808:3414084 forward MW:83425
RPA3016	1.68566	0.0085	1.785303	0.0055	1.714873	0.0015	1.02736	0.447	0.879192	0.941	phyB2 Bacteriophytochrome (light-regulated signal transduction histidine kinase), PhyB2 3414088:3416415 forward MW:85703
RPA3017	2.555612	0.0025	1.546315	0.032			1.125837	0.2715	1.118668	0.2185	rphyB response regulator receiver (CheY-like protein) 3416416:3416880 forward MW:17589
RPA3018	1.04224	0.3965	1.45829	0.011	1.05743	0.323	1.313881	0.0645	1.314746	0.0375	CDS response regulator receiver:histidine kinase 3416877:3418013 forward MW:41968
RPA3019	1.14134	0.1645	1.142111	0.1485	1.07071	0.29	1.127321	0.139	1.112635	0.165	mexF pseudogene pseudogene of RND multidrug efflux transporter MexF; AcrB/AcrD/AcrF family 3418120:3421349 reverse MW:116235
RPA3020	1.31863	0.0305	1.235793	0.056	1.197049	0.054	1.243049	0.0525	1.373122	0.0225	mexE RND multidrug efflux membrane fusion protein MexE precursor 3421479:3422678 reverse MW:41854
RPA3021	1.467412	0.009	1.109169	0.083	1.286601	0.0555	1.454769	0.02	1.702598	0.001	CDS probable transcriptional regulator TetR family 3422874:3423461 forward MW:21083
RPA3022	1.469346	0.002	1.473696	0.001	1.223786	0.02	1.873514	0.0015	1.611031	0.0005	CDS putative diguanylate cyclase (GGDEF) 3423592:3424758 forward MW:41561
RPA3023	1.406708	0.038	1.07969	0.1525	1.417934	0.002	1.093775	0.267	1.187434	0.0875	CDS aldo/keto reductase 3424892:3425878 forward MW:35315
RPA3024	0.955583	0.75	1.065349	0.2685	0.95628	0.675	0.562165	0.9995	0.553773	0.9985	CDS unknown protein 3425900:3426310 reverse MW:14190
RPA3025	0.93454	0.6425			1.043578	0.3925			1.119324	0.258	CDS hypothetical protein 3426447:3426773 forward MW:11292
RPA3026	0.782894	0.9765	1.088444	0.224	0.757984	0.9515	0.788918	0.9385	1.252704	0.0085	CDS similar to abortive infection protein 3426819:3427469 forward MW:23663
RPA3027	0.586503	0.9965	0.738508	0.977	0.433388	0.999	0.453393	1	0.639486	0.963	kup1 potassium uptake protein Kup 3427479:3429341 reverse MW:67621
RPA3028	1.097471	0.069	1.043137	0.345	1.291187	0.0055	1.61896	0.0025	1.655827	0.0035	CDS conserved unknown protein 3429602:3430441 reverse MW:28167
RPA3029	1.908099	0.0035	8.440516	0.004	2.14785	0.012			2.179064	0.113	CDS conserved hypothetical protein 3430730:3430912 forward MW:6625
RPA3030	0.987531	0.545	1.115536	0.1085	1.030398	0.333	1.009661	0.464	0.89497	0.904	CDS hypothetical protein 3431088:3431384 forward MW:10930
RPA3031	0.663818	0.847	1.704696	0.0155	1.118113	0.315	1.559764	0.011	1.431008	0.0485	CDS possible Acetyltransferase (GNAT) family 3431503:3432126 reverse MW:22752
RPA3032	1.0849	0.273	1.356551	0.0065	1.188833	0.0285	1.906725	0.0005	1.669252	0.0005	CDS Phenylacetic acid degradation-related protein 3432381:3432779 reverse MW:13810
RPA3033	1.268239	0.009	1.247049	0.0285	1.579327	0.0035	1.319468	0.045	1.003855	0.4765	argE possible acetylornitine deacetylase 3432927:3434207 reverse MW:46433
RPA3034	0.781137	0.9645	0.688549	0.9275	1.125398	0.2205	0.609637	0.9905	0.613446	0.999	CDS unknown protein 3434340:3434603 forward MW:9316
RPA3035	0.706908	0.9985	0.763866	0.947	1.132944	0.251	0.831532	0.922	0.852093	0.907	CDS hypothetical protein 3434632:3435048 reverse MW:15293
RPA3036	0.896689	0.9305	1.278374	0.0285	0.920329	0.768	1.551358	0.0035	1.426724	0.045	CDS hypothetical protein 3435160:3435408 reverse MW:9249
RPA3037	0.797899	0.953	0.713216	0.998	1.090927	0.183	0.781284	0.9695	1.069372	0.3025	CDS conserved unknown protein 3436290:3436868 reverse MW:21270
RPA3038	0.971271	0.6715	0.802489	0.935	1.065758	0.248	0.89882	0.857	0.979019	0.58	CDS ErfK/YbiS/YcfS/YnhG 3437018:3438631 forward MW:56907
RPA3039	1.032033	0.306	0.789991	0.98	1.095649	0.1935	0.949013	0.688	0.953324	0.7175	CDS possible polysaccharide deacetylase 3438785:3439723 forward MW:33372

RPA3040	1.043818	0.368	0.758558	0.98	1.000156	0.4855	0.969796	0.5405	0.919153	0.744	CDS unknown protein 3439761:3440324 forward MW:20141
RPA3041	1.007315	0.439	0.872068	0.9055	1.172581	0.094	0.986732	0.5445	1.112304	0.1295	CDS conserved hypothetical protein 3440328:3440777 reverse MW:15385
RPA3042	0.967867	0.7175	0.810224	0.9865	0.913906	0.823	0.698411	0.9935	0.698258	0.977	mao malate oxidoreductase 3440872:3443196 reverse MW:82696
RPA3043	0.757087	0.9615	0.861055	0.922	0.695428	0.9985	0.704268	0.992	0.696014	0.9895	aspS aspartate-tRNA ligase 3443227:3445002 reverse MW:66654
RPA3044	1.25444	0.0075	1.203785	0.027	1.543167	0.0005	1.442833	0.016	1.336248	0.013	CDS Protein of unknown function UPF0061 3445262:3446740 forward MW:53500
RPA3045	0.813386	0.9885	0.692706	0.9945	0.939885	0.787	0.655808	0.9955	0.678855	0.999	rnd ribonuclease D 3446844:3448022 forward MW:43712
RPA3046	0.581625	0.9985	0.752329	0.987	0.62852	0.9815	0.671846	0.9845	0.532139	1	CDS conserved hypothetical protein 3448019:3448942 forward MW:34075
RPA3047	0.876537	0.785	0.634335	0.9765	0.850731	0.77	0.786627	0.8345	0.828167	0.9585	CDS putative exopolyphosphatase 3448964:3450469 reverse MW:54914
RPA3048	1.031564	0.291	0.888975	0.9325	1.187787	0.0485	0.851164	0.946	0.891871	0.9105	CDS putative polyphosphate kinase 3450482:3452773 reverse MW:85669
RPA3049	0.915256	0.798	1.08874	0.263	0.927798	0.782	0.974351	0.6145	1.000853	0.493	CDS conserved hypothetical protein 3452843:3453532 reverse MW:24862
RPA3050	1.189448	0.121	1.617976	0.0005	1.101209	0.112	1.1495	0.1895	1.196234	0.1225	CDS CDP-alcohol phosphatidyltransferase 3453563:3454192 reverse MW:23005
RPA3051	0.847003	0.9485	1.118886	0.062	0.646331	0.995	0.773612	0.964	0.992536	0.5335	purM 5'-phosphoribosyl-5-aminoimidazole synthetase 3454375:3455448 forward MW:37032
RPA3052	1.254817	0.052	1.155939	0.076	1.083585	0.222	1.539391	0.007	1.942035	0.0115	purN phosphoribosylglycinamide formyltransferase 3455457:3456110 forward MW:22896
RPA3053	2.202845	0.001	2.103827	0.0015	2.840652	0.002	3.619895	0.0005	2.766445	0.005	cspA3 cold shock DNA binding protein 3456174:3456377 reverse MW:7526
RPA3054	0.847318	0.9665	0.717351	0.9975	0.980013	0.5855	1.008604	0.4565	0.75011	0.9905	CDS possible transcriptional regulator, Crp/Fnr family 3456869:3457642 forward MW:28442
RPA3055	0.889314	0.779	1.322964	0.0075	0.666767	0.988	0.862669	0.8945	0.882767	0.806	CDS Integral membrane protein TerC family 3457725:3458546 reverse MW:28680
RPA3056	0.876259	0.811	1.134393	0.1975	0.611519	0.999	0.759765	0.9755	0.759931	0.9555	CDS nucleoside-diphosphate-kinase 3458619:3459041 reverse MW:15219
RPA3057	0.93187	0.7775	0.991913	0.5555	0.625672	0.995	0.840026	0.945	0.980773	0.564	CDS ABC transporter, duplicated ATPase domains 3459188:3461065 forward MW:67961
RPA3058	0.95501	0.688	0.970804	0.674	1.022494	0.3505	0.740745	0.996	0.857018	0.866	CDS unknown protein 3461069:3461608 reverse MW:19077
RPA3059	1.387935	0.024	1.342255	0.0045	1.320961	0.0025	1.23942	0.0205	1.003126	0.487	CDS hypothetical protein 3461736:3462188 reverse MW:17105
RPA3060	1.275499	0.003	1.025317	0.362	1.102089	0.209	0.968476	0.63	0.9306	0.772	CDS leucine aminopeptidase 3462199:3463701 reverse MW:52289
RPA3061	0.840261	0.985	0.923149	0.8995	0.888244	0.7735	0.676211	0.9975	0.7605	0.977	CDS possible permease 3464110:3465276 forward MW:42760
RPA3062	1.016621	0.391	1.011177	0.4315	0.928887	0.717	0.612015	0.9845	0.712781	0.9445	CDS predicted permease 3465290:3466375 forward MW:39682
RPA3063	0.96015	0.74	0.815971	0.9865	0.8647	0.91	0.967388	0.6675	0.982776	0.6145	CDS organic solvent tolerance protein homolog 3466375:3468888 forward MW:92162
RPA3064	0.802299	0.9445	0.891629	0.937	0.94854	0.749	0.955341	0.663	0.810409	0.988	CDS conserved unknown protein 3468967:3469893 forward MW:34307
RPA3065	0.695911	0.9965	0.70784	0.9955	0.794591	0.973	0.568874	0.9985	0.651288	0.9985	pdxA pyridoxal phosphate biosynthetic protein PdxA 3469954:3470967 forward MW:34927
RPA3066	0.750537	0.988	0.900135	0.844	0.833936	0.935	0.585033	0.981	0.54892	0.999	ksgA dimethyladenosine transferase 3470964:3471827 forward MW:31208
RPA3067	0.84782	0.898	0.676461	0.9915	0.945955	0.645	0.668378	0.9805	0.499253	1	CDS putative NAD-dependent alcohol dehydrogenase 3471844:3472902 forward MW:37794
RPA3068	1.195105	0.0675	1.044894	0.402	1.547733	0.006	0.541694	0.9915	0.727472	0.944	CDS conserved hypothetical protein 3472944:3474239 forward MW:44504
RPA3069	0.64591	0.991	0.66653	0.9965	0.694268	0.9955	0.529343	0.9995	0.570292	0.997	kguA putative guanylate kinase 3474243:3474905 reverse MW:24534
RPA3070	0.726073	0.9875	1.12838	0.206	0.709962	0.995	0.68414	0.96	0.551966	0.9995	CDS conserved unknown protein 3474908:3475795 reverse MW:32100
RPA3071	0.799282	0.9845	0.854022	0.981	0.928322	0.8325	0.733689	0.994	0.814691	0.985	CDS DUF175 3475897:3477153 reverse MW:45213
RPA3072	0.832632	0.97	0.965682	0.686	0.747219	0.9895	0.638278	0.993	0.779442	0.9455	fabF 3-oxoacyl-acyl carrier protein synthase II 3477356:3478621 reverse MW:43842
RPA3073	0.741213	0.968	0.955974	0.635	0.798591	0.9035	0.705849	0.943	0.57516	0.996	acpP constitutive acyl carrier protein 3478718:3478957 reverse MW:8572
RPA3074	1.174849	0.0205	1.257202	0.0105	1.155207	0.069	1.910007	0	1.67967	0	fabG2 3-oxoacyl-acyl carrier protein reductase fabG 3479262:3479999 reverse MW:25349
RPA3075	0.792569	0.9115	0.927391	0.7275	0.613748	0.998	0.769575	0.9445	0.841979	0.969	fabD putative malonyl CoA-acyl carrier protein transacylase 3480019:3480978 reverse MW:32288
RPA3076	0.90327	0.88	0.913214	0.8445	1.237064	0.0285	0.974221	0.573	1.214182	0.0775	CDS putative diguanylate cyclase (GGDEF) 3481244:3482593 forward MW:48032
RPA3077	0.736611	0.941	1.128223	0.123	0.509292	0.9915	0.703061	0.929	0.865323	0.8405	RPS6 possible 30S ribosomal protein S6 3482765:3483241 forward MW:17932
RPA3078	0.887333	0.9025	1.085373	0.178	0.429382	0.999	0.617375	0.993	0.819979	0.931	RPS18 30S ribosomal protein S18 3483247:3483486 forward MW:9094
RPA3079	0.844373	0.823	0.884834	0.804	0.661852	0.9845	0.770941	0.983	0.870518	0.7475	CDS hypothetical protein 3483613:3484563 forward MW:32768
RPA3080	0.74318	0.9865	0.723936	0.9815	0.956355	0.631	0.565648	0.99	0.487594	0.9715	RPL9 putative 50S ribosomal protein L9, cultivar specific nodulation protein Csn1 3484599:3485186 forward MW:21179
RPA3081	0.946653	0.6565	0.957998	0.7705	0.823043	0.967	0.902552	0.825	1.124586	0.0925	CDS unknown protein 3485351:3486322 reverse MW:32773
RPA3082	1.622419	0	1.591131	0.0015	1.782719	0.0045	5.517546	0	3.976683	0	cfa2 cyclopropane-fatty-acyl-phospholipid synthase 3486581:3487831 forward MW:47086
RPA3084	0.674377	0.9975	0.564997	0.9995	0.68052	0.996	0.473794	0.9975	0.619551	0.9855	dnaB replicative DNA helicase (dnaB) 3488450:3489946 forward MW:54629
RPA3085	0.839123	0.937	0.703856	0.9895	0.917351	0.8285	0.72048	0.9735	0.744621	0.988	CDS putative alanine racemase 3490014:3491255 forward MW:43075
RPA3086											CDS hypothetical protein 3491385:3491642 reverse MW:9355
RPA3087	1.119746	0.209			0.963675	0.631			0.972924	0.573	CDS conserved hypothetical protein 3491639:3493276 reverse MW:58116
RPA3088	0.955914	0.611	0.890243	0.8045	1.027046	0.406	1.050648	0.3445	0.809379	0.966	CDS conserved hypothetical protein 3493736:3494128 reverse MW:14432
RPA3089	0.774219	0.979	0.716091	0.944	0.924054	0.7655	1.05165	0.408	1.070979	0.2525	RadA DNA repair protein RadA 3494276:3495733 forward MW:50565
RPA3090	0.9396	0.768	0.805465	0.991	0.97161	0.6405	0.882442	0.875	0.934555	0.8175	CDS putative colicin V production protein 3495947:3496582 forward MW:23138
RPA3091	1.332285	0.027	1.084613	0.2325	1.133664	0.202	1.095726	0.196	1.194371	0.0625	purF amidophosphoribosyltransferase 3496606:3498135 forward MW:55173
RPA3092	0.931643	0.7985	0.92038	0.7435	0.960549	0.622	0.880482	0.824	0.887679	0.925	CDS putative oxidoreductase 3498265:3499008 forward MW:26130
RPA3093	1.899232	0.038	0.914113	0.699	1.658387	0.0065	1.165545	0.1075	1.429585	0.013	CDS possible urea/short-chain binding protein of ABC transporter 3499092:3500318 forward MW:42982
RPA3094	1.023468	0.3815	0.92774	0.8445	0.879136	0.9365	0.774321	0.988	0.917896	0.882	CDS putative tetracycline-efflux transporter 3500339:3501625 reverse MW:44688
RPA3095	1.078964	0.102	1.101276	0.081	0.929598	0.813	1.131512	0.095	1.124252	0.073	CDS GTP-binding protein 3501622:3503001 reverse MW:50746
RPA3097	0.80312	0.9775	0.914217	0.854	0.741198	0.9965	0.695453	0.994	0.761158	0.9925	CDS conserved unknown protein 3503672:3504361 reverse MW:25024
RPA3098	1.330338	0.022	1.199394	0.0305	0.856991	0.9175	1.10135	0.2415	1.163369	0.054	panB 3-methyl-2-oxobutanoate hydroxymethyltransferase 3504491:3505315 reverse MW:29240
RPA3099	1.189783	0.0245	1.235879	0.0175	0.889749	0.8005	0.998086	0.518	1.049151	0.2485	CDS conserved hypothetical protein 3505318:3505902 reverse MW:20706
RPA3100	1.06055	0.243	1.087437	0.1335	0.7715	0.991	0.935222	0.718	1.022812	0.425	CDS Uncharacterized protein family UPF0065 3506040:3507044 forward MW:34499
RPA3101	1.389626	0.051	1.305545	0.209	1.131705	0.3255	1.189391	0.1725	1.177168	0.0825	CDS conserved unknown protein 3507093:3507578 reverse MW:17266
RPA3102	0.994025	0.521	1.137303	0.1795	1.022836	0.4145	0.712577	0.9725	0.437719	0.997	CDS conserved hypothetical protein 3507682:3507948 reverse MW:9572
RPA3103	2.926766	0.001	2.356074	0.0005	2.189767	0.0005	4.719142	0	2.302942	0.0385	CDS hypothetical protein 3508623:3508823 reverse MW:6976
RPA3104	0.987212	0.5765	0.92297	0.842	0.815527	0.9375	1.006546	0.4775	0.957175	0.702	gatB Glu-tRNA(Gln) amidotransferase subunit B 3509284:3510768 reverse MW:54032
RPA3105	0.881453	0.918	0.930213	0.83	0.893654	0.921	0.735396	0.9885	0.768366	0.9925	CDS Patatin-like phospholipase domain 3510864:3512249 reverse MW:49280
RPA3106	0.954479	0.66	0.80032	0.9935	0.962971	0.642	0.882431	0.9115	0.981129	0.575	CDS putative signal transduction histidine kinase with PAS/PAC domain 3512391:3513497 reverse MW:39923
RPA3107	0.735255	0.981	0.788421	0.9785	0.55392	0.9995	0.611595	0.963	0.706841	0.9935	GatA2 Glu-tRNA(Gln) amidotransferase subunit A 3513574:3515052 reverse MW:51977
RPA3108	0.888438	0.931	0.757675	0.986	1.001527	0.4885	1.042384	0.4195	1.213203	0.038	CDS conserved hypothetical protein 3515232:3515519 forward MW:10998
RPA3110					0.868131	0.9465			0.609399	0.997	CDS hypothetical protein 3515755:3515961 reverse MW:7605
RPA3111	1.226263	0.0335	1.126447	0.1155	1.028298	0.432	1.405944	0.0105	1.384089	0.0055	gatC Glu-tRNA(Gln) amidotransferase subunit C 3515973:3516260 reverse MW:10383
RPA3112	0.611912	0.987	0.699581	0.935	0.610031	0.99	0.392074	0.989	0.52417	0.996	CDS 2-nitropropane dioxygenase 3516348:3517424 reverse MW:37481
RPA3113	1.098745	0.175	1.294515	0.0065	0.859519	0.8785	0.901242	0.7435	0.870673	0.8765	CDS conserved hypothetical protein 3517583:3518065 forward MW:17084
RPA3114											CDS SEC-C motif 3518087:3518473 forward MW:14638
RPA3115	0.771225	0.991	0.517372	0.999	0.738343	0.982	0.653764	0.99	0.531648	0.999	CDS probable acyl-CoA dehydrogenase 3518600:3520285 reverse MW:61077
RPA3116	0.851324	0.943	0.758826	0.9435	0.993242	0.5005	0.673184	0.849	0.696341	0.996	ipdC indole-3-pyruvate decarboxylase 3520331:3521962 reverse MW:58286
RPA3117	1.200139	0.011	1.034294	0.3105	0.748276	0.989	0.820105	0.945	1.074263	0.1705	pyrB aspartate carbamoyltransferase 3522153:3523106 forward MW:34421
RPA3118	0.980472	0.6125	0.806735	0.983	0.566243	0.9985	0.614405	0.996	0.855129	0.9255	pyr putative noncatalytic chain of dihydroorotase 3523126:3524436 forward MW:46133
RPA3119	0.996237	0.518	0.870546	0.9495	0.964481	0.672	0.805483	0.978	0.86815	0.923	CDS DUF205 3524580:3525191 forward MW:21525

RPA3120	1.078481	0.3115			0.924534	0.684	0.950895	0.647	0.9451	0.671	DprA DNA processing chain A 3525318:3526460 forward MW:39849
RPA3121	0.985482	0.583	1.132787	0.1135	0.722183	0.976	0.884589	0.836	1.096276	0.144	CDS putative alginate o-acetyltransferase AlgI 3526551:3527963 forward MW:52797
RPA3122	0.977737	0.6405	1.103038	0.1225	0.99315	0.5305	1.333368	0.0115	1.564368	0.001	CDS hypothetical protein 3527968:3529158 forward MW:44507
RPA3123	0.830961	0.9805	1.029024	0.3865	0.96668	0.6295	1.111779	0.3265	1.237473	0.0305	CDS hypothetical protein 3529411:3529704 reverse MW:11131
RPA3124	0.703553	0.9995	0.760242	0.996	0.713016	0.9725	0.611699	0.997	0.652197	0.999	TopA DNA topoisomerase I 3529873:3532608 forward MW:98943
RPA3125	1.171039	0.1525	0.97338	0.6305	1.504652	0.0025	1.26356	0.068	0.955826	0.6405	RNR ribonuclease R 3532611:3534956 forward MW:85197
RPA3126	0.898877	0.843	0.908225	0.8	1.396024	0.007	0.909929	0.7755	0.613741	0.997	CDS conserved hypothetical protein 3534956:3535384 forward MW:15923
RPA3127	0.672707	0.999	0.807274	0.9845	1.063445	0.266	0.714241	0.99	0.414934	1	CDS NUDIX hydrolase 3535454:3536209 forward MW:27284
RPA3128	0.840344	0.978	1.02301	0.3805	1.193248	0.054	0.716557	0.9885	0.755484	0.9925	CDS putative transport protein 3536244:3537392 reverse MW:39465
RPA3129	1.158312	0.048	1.451881	0.002	1.059199	0.216	1.435228	0.0135	1.469197	0.0045	RPL33 50S ribosomal protein L33 3537789:3537956 forward MW:6366
RPA3130	0.989691	0.5435	1.032648	0.3215	1.082843	0.1815	1.256104	0.026	1.386874	0.0005	CDS transcriptional regulator, XRE family 3538223:3538606 reverse MW:14259
RPA3131	1.065368	0.2765	1.100522	0.2645	1.144123	0.1135	0.963944	0.581	1.124511	0.3045	CDS conserved hypothetical protein 3538617:3538934 reverse MW:12023
RPA3132	1.408173	0.002	1.171111	0.055	1.027322	0.3675	1.218425	0.064	1.202273	0.026	CDS putative diguanylate cyclase (GGDEF) with response regulator receiver domain 3538970:3540343 reverse MW:50977
RPA3133	1.442029	0.0025	1.483604	0.001	1.066835	0.192	1.492829	0.005	1.258596	0.029	CDS response regulator receiver (CheY-like protein) 3540354:3540719 reverse MW:13646
RPA3134	0.774366	0.984	0.692617	0.989	0.948353	0.7725	0.791743	0.9325	0.687136	0.9975	CDS conserved unknown protein 3540845:3541144 forward MW:10871
RPA3135	0.908099	0.914	0.8502	0.9295	0.922402	0.781	0.967333	0.6255	1.160817	0.1105	dinP DNA damage inducible protein P 3541141:3542436 forward MW:47217
RPA3136	0.968921	0.635	1.021339	0.409	1.064164	0.242	1.107187	0.16	1.181066	0.0585	CDS conserved unknown protein 3542561:3543427 reverse MW:31297
RPA3137	0.945685	0.705	0.841433	0.9755	0.920209	0.8105	0.72492	0.9945	0.601692	0.9975	CDS Endoribonuclease L-PSP 3543689:3544168 forward MW:16199
RPA3138	1.284648	0.0345	1.191423	0.075	1.050052	0.283	0.943259	0.7565	1.023706	0.4245	CDS putative glycerophosphoryl diester phosphodiesterase 3544187:3544933 forward MW:27578
RPA3139	1.120327	0.222	0.890402	0.8115	1.285538	0.035	0.920849	0.745	0.788201	0.9745	CDS DUF482 3544936:3546255 forward MW:48563
RPA3140	0.967514	0.671	0.849001	0.8915	1.014235	0.4135	1.016996	0.4285	0.711911	0.9915	CDS probable Hit-like protein involved in cell-cycle regulation 3546263:3546733 forward MW:17100
RPA3141	1.060173	0.367	1.288255	0.05	0.926232	0.853	0.989389	0.5245	0.972254	0.644	CDS possible VirR protein 3546739:3547200 reverse MW:16817
RPA3142											CDS conserved hypothetical protein 3547249:3547593 reverse MW:12087
RPA3143	0.807725	0.986	0.99117	0.564	0.795446	0.977	0.736573	0.9955	0.596609	0.9995	CDS conserved hypothetical protein 3547590:3548333 reverse MW:26095
RPA3144									1.157408	0.36	CDS conserved hypothetical protein 3548486:3548845 forward MW:13766
RPA3145	0.92041	0.8425	0.89321	0.84	1.218051	0.0195	1.045224	0.3425	0.850573	0.924	CDS possible transglycosylase SLT domain 3548862:3549977 reverse MW:39786
RPA3146	1.068068	0.325	1.066022	0.227	1.023772	0.375	0.818519	0.9595	1.036326	0.3285	CDS conserved hypothetical protein 3550605:3552380 forward MW:61284
RPA3147	1.037227	0.346	1.184809	0.031	1.339032	0.0115	1.599112	0.0015	1.218832	0.077	clpA endopeptidase Clp: ATP-binding chain A 3552454:3554838 reverse MW:87506
RPA3148	0.954686	0.6835	1.05121	0.2245	1.079222	0.2385	1.239619	0.055	1.149716	0.1005	CDS DUF174 3555032:3555430 reverse MW:14742
RPA3149	1.451413	0.013	1.216157	0.0595	1.11745	0.128	1.895017	0	1.948489	0	CDS conserved hypothetical protein 3555834:3557201 forward MW:48636
RPA3150	1.047897	0.307	1.072541	0.165	1.099795	0.104	0.871795	0.9075	1.087595	0.111	CDS possible D-alanyl-D-alanine carboxypeptidase 3557558:3559315 forward MW:62391
RPA3151	1.094714	0.1725	1.013864	0.407	1.122177	0.0965	1.283376	0.011	1.457216	0.0005	CDS Heat shock protein DnaJ, N-terminal 3559644:3560372 reverse MW:25268
RPA3152	0.942015	0.6345	1.196734	0.1145	0.882136	0.845	2.945283	0.001	1.48969	0.015	CDS hypothetical protein 3560428:3561168 reverse MW:25939
RPA3153	0.804598	0.841	1.390097	0.0445	0.758255	0.8255	4.740913	0	2.040807	0.003	CDS conserved hypothetical protein 3561248:3562078 reverse MW:30364
RPA3154	0.852867	0.843	1.040568	0.3355	0.835753	0.935	2.74028	0	1.751104	0.0045	CDS possible chromosome partitioning protein ParA 3562350:3563273 reverse MW:33893
RPA3155	0.730199	0.996	0.627817	0.9985	0.711096	0.9945	0.810318	0.9785	0.757053	0.989	panC putative pantoate-beta-alanine ligase 3563540:3564391 forward MW:30809
RPA3156	0.647107	0.994	0.840458	0.807	0.847819	0.897	0.745559	0.966	0.808586	0.949	CDS conserved hypothetical protein 3564418:3564837 reverse MW:15528
RPA3157	0.841715	0.9735	0.983293	0.5585	1.144088	0.0995	0.678769	0.997	1.033413	0.34	CDS hypothetical protein 3564876:3565910 reverse MW:34860
RPA3158	0.871592	0.9155	0.958906	0.6175	1.174878	0.084	1.291047	0.0965	1.596346	0.0035	CDS hypothetical protein 3566090:3566281 reverse MW:7029
RPA3159	0.766291	0.9265	0.565109	0.997	0.878111	0.8015	0.589232	0.978	0.671819	0.9795	CDS probable glutathione S-transferase 3566494:3567150 reverse MW:24405
RPA3160			1.010349	0.4935	0.570502	0.992	0.885334	0.7965	0.676821	0.9895	CDS DUF218 3567559:3568353 reverse MW:28332
RPA3161	1.077331	0.1575	0.932193	0.847	1.034708	0.3	1.053068	0.2935	1.25655	0.011	yafB putative aldose reductase 3568428:3569261 reverse MW:30525
RPA3162	1.203327	0.0325	0.998476	0.508	1.032416	0.402	1.024064	0.43	0.935667	0.7235	CDS transcriptional regulator, XRE family 3569316:3569681 reverse MW:13186
RPA3163	0.9263	0.7825	1.030334	0.3335	0.696554	0.9975	0.778173	0.9485	1.002439	0.4895	mgtE putative magnesium transporter 3569726:3571147 reverse MW:51622
RPA3164	1.421337	0.027	0.97469	0.609	1.449052	0.0095	1.495988	0.0095	1.438202	0.047	CDS possible chitooligosaccharide deacetylase 3571310:3572113 forward MW:28885
RPA3165	1.067137	0.189	1.148512	0.039	1.396841	0.0185	1.215135	0.0615	0.969366	0.6425	CDS possible polysaccharide deacetylase 3572197:3573570 forward MW:49551
RPA3166	0.944389	0.7585	1.193059	0.0185	0.982999	0.5905	1.144656	0.0875	1.0825	0.1485	CDS conserved hypothetical protein 3573642:3574085 forward MW:16017
RPA3167	1.021271	0.409	1.222115	0.017	0.930782	0.7195	1.253439	0.075	1.13564	0.058	CDS conserved hypothetical protein 3574085:3574546 forward MW:17366
RPA3168	1.174435	0.151	1.18574	0.189	0.902959	0.659	1.217586	0.1055	0.809425	0.813	CDS possible flgaellar switch protein FliN 3574819:3575061 reverse MW:8837
RPA3169	0.927158	0.777	0.872736	0.822	1.07678	0.334	1.345947	0.037	1.356763	0.015	lipB lipoate biosynthesis protein B 3575128:3575865 forward MW:26792
RPA3170	1.254519	0.058	0.947601	0.735	1.009221	0.489	1.012124	0.465	1.153461	0.127	CDS putative diguanylate cyclase (GGDEF)/phosphodiesterase (EAL) with PAS and GAF domains 3576134:3578755 forward MW:95821
RPA3171			0.698736	0.9295	0.541892	0.987	0.727869	0.885	0.718231	0.8875	CDS conserved hypothetical protein 3578780:3579211 reverse MW:15416
RPA3172			1.199935	0.1325	0.742586	0.809	1.179984	0.1705	1.430415	0.076	CDS transcriptional regulator, LysR family 3579317:3580165 forward MW:30098
RPA3173	1.065483	0.2615	1.163405	0.0715	1.183101	0.0665	0.822568	0.9655	0.958206	0.6025	CDS putative protein 3580184:3580483 reverse MW:10781
RPA3174	1.068323	0.287	1.390337	0.0075	0.812182	0.931	0.950748	0.599	1.018735	0.439	CDS conserved unknown protein 3580483:3581349 reverse MW:30188
RPA3175	0.817838	0.826	0.933429	0.7615	0.746151	0.975	0.669781	0.9915	0.681202	0.9775	CDS propionyl-CoA carboxylase precursor, biotin carrier protein 3581356:3583371 reverse MW:72945
RPA3176	1.033977	0.4085			1.13978	0.296			0.56527	0.998	CDS hypothetical protein 3583525:3585375 forward MW:64435
RPA3177	0.621805	0.9795	0.8305	0.873	0.942713	0.664	0.4532	0.999	0.618998	0.9975	CDS unknown protein 3585412:3586218 reverse MW:28671
RPA3178	0.951422	0.728	0.875279	0.84	1.104825	0.198	1.047992	0.3095	0.98682	0.5625	CDS hypothetical protein 3586281:3586679 reverse MW:14668
RPA3179	0.906954	0.6835	1.199787	0.213	0.998946	0.4875	1.60551	0.186	0.703244	0.8905	CDS Deoxyribodipyrimidine photolyase 3586798:3588249 forward MW:53598
RPA3180	1.493097	0.0025	1.178809	0.0545	1.52991	0.0025	1.879252	0.0015	1.468514	0.074	CDS hypothetical protein 3588328:3588645 forward MW:11041
RPA3181	1.259494	0.0175	1.304836	0.006	1.164273	0.09	1.637755	0.0035	1.887009	0.002	CDS Permeases of the drug/metabolite transporter (DMT) superfamily 3588752:3589627 reverse MW:30667
RPA3182	1.056105	0.338	0.909514	0.8225	0.918286	0.7495	1.150642	0.1375	1.573776	0.0105	phzF Phenazine biosynthesis PhzC/PhzF protein 3589781:3590689 forward MW:31719
RPA3183	1.044112	0.2615	1.09255	0.1825	1.044554	0.335	1.070765	0.236	1.307974	0.005	CDS unknown protein 3590744:3591190 reverse MW:16860
RPA3184	2.909337	0	2.369169	0	1.168984	0.1835	3.350758	0	3.151331	0	CDS putative cylclic diguanylate phosphodiesterase (EAL) 3591608:3592957 reverse MW:49029
RPA3185	0.579776	0.9995	0.337821	1			0.733735	0.943	0.524137	0.9635	CDS methyl-accepting chemotaxis receptor/sensory transducer 3593862:3595880 forward MW:71126
RPA3186	1.179428	0.0955	1.12751	0.1225	1.098354	0.3095	1.391189	0.009	1.052686	0.369	CDS hypothetical protein 3596045:3596395 forward MW:12022
RPA3187	0.957943	0.666	0.925516	0.7025	0.969856	0.646	1.463615	0.087	1.527686	0.0055	CDS sensor histidine kinase with a PAS/PAC domain 3596427:3599180 reverse MW:100350
RPA3188	1.508304	0.1675	0.572221	0.9305	2.342055	0.001	0.751595	0.84	0.352571	0.992	CDS alcohol dehydrogenase 3599316:3601490 reverse MW:78144
RPA3189	0.990528	0.558	0.938689	0.747	0.956578	0.728	0.711895	0.9755	0.627892	0.998	CDS NUDIX hydrolase 3601644:3602435 reverse MW:28365
RPA3190	0.817522	0.9925	0.822409	0.9785	0.658497	0.9985	0.632996	0.992	0.4932	1	CDS possible dihydrodipicoline synthase related protein 3602440:3603393 reverse MW:34600
RPA3191	0.726512	0.972	0.568168	0.986	0.756483	0.9845	0.474073	0.9965	0.342908	0.9995	CDS putative short-chain dehydrogenases 3603496:3604374 reverse MW:30436
RPA3192	0.473503	0.998	0.564458	0.9985	0.522862	1	0.29299	0.9985	0.24884	1	CDS MaoC-like dehydratase:Asparaginase/glutaminase 3604521:3605381 reverse MW:31424
RPA3193	0.516718	0.999	0.624311	0.9985	0.481658	0.9995	0.283444	1	0.30534	0.9995	CDS DUF35 3605568:3605960 reverse MW:14243
RPA3194	0.551423	0.999	0.683018	0.998	0.536177	1	0.330728	1	0.32983	1	CDS conserved hypothetical protein 3605960:3607108 reverse MW:40303
RPA3195	0.721524	0.988	0.625886	0.968	0.823641	0.869	0.659207	0.978	0.397149	0.9835	CDS related to Pyruvate ferredoxin/flavodoxin oxidoreductase 3607397:3610882 reverse MW:126909
RPA3196	0.856209	0.9605	0.905843	0.8595	0.98082	0.5715	0.843673	0.9435	0.955862	0.698	CDS hypothetical protein 3611163:3611609 forward MW:15230

RPA3197	0.429406	0.9995	0.432878	0.9985	0.640746	0.998	0.588109	0.9985	0.448867	1	CDS hypothetical protein 3611854:3612141 forward MW:9970
RPA3198	0.848143	0.9405	0.886031	0.89	0.974756	0.604	0.924192	0.764	0.854511	0.962	CDS conserved hypothetical protein 3612206:3613015 reverse MW:30340
RPA3199	1.017943	0.4335	0.74167	0.9855	1.060875	0.289	0.968107	0.5815	0.906644	0.8	CDS unknown protein 3613121:3613669 reverse MW:20008
RPA3200			2.243247	0.0015					3.668428	0.011	CDS putative dual serine/threonine-protein kinase/phosphatase 3613758:3615554 reverse MW:65718
RPA3201	5.646314	0	6.259693	0.0005	3.110692	0	23.80291	0	19.34684	0.0005	CDS formate/nitrate transporter 3615559:3616398 reverse MW:30135
RPA3202	0.889839	0.804	1.066967	0.222	0.680196	0.9975	0.814834	0.9525	0.74417	0.994	CDS conserved hypothetical protein 3617129:3617986 reverse MW:30732
RPA3203	1.098723	0.144	1.136302	0.0545	0.773588	0.98	0.953026	0.7095	1.928129	0.0005	pccB propionyl-CoA carboxylase beta chain 3618197:3619729 reverse MW:56070
RPA3204	0.836939	0.927			0.960171	0.674			0.785456	0.9505	CDS conserved hypothetical protein 3620009:3620425 forward MW:14383
RPA3205					1.253691	0.092	1.429085	0.026	1.243555	0.2025	CDS Type III secretion proteins, related to flagellar biosynthesis protein FlhB 3620427:3620702 reverse MW:9751
RPA3206	1.514433	0.004	1.410941	0.0045	1.35043	0.0505	2.297434	0	1.975081	0	CDS conserved hypothetical protein 3620699:3622498 reverse MW:59492
RPA3207			1.097442	0.37					0.792573	0.862	CDS conserved hypothetical protein 3622568:3623353 reverse MW:27966
RPA3208	0.919565	0.89	1.049671	0.284	0.986256	0.5755	1.130224	0.0875	1.04339	0.3615	rluC possible ribosomal large subunit pseudouridine synthase C 3623771:3625138 reverse MW:49208
RPA3209											CDS hypothetical protein 3625343:3625648 reverse MW:10696
RPA3210	1.754866	0	1.39198	0.003	2.086686	0	2.031978	0.004	2.524108	0.0005	CDS possible prolyl oligopeptidase family Dienelactone hydrolase family 3625694:3626662 reverse MW:34701
RPA3211	2.669808	0	1.608396	0.0105	2.087945	0.0115	2.984091	0	4.121478	0	CDS TPR repeat 3626787:3630191 forward MW:120858
RPA3212							3.072168	0.003	4.033258	0.0005	CDS unknown protein 3630220:3630666 forward MW:15858
RPA3213	1.206859	0.1165	1.277947	0.0105	1.165927	0.0425	1.430958	0.0405	1.289264	0.0125	CDS hypothetical protein 3630667:3630882 forward MW:8077
RPA3214	1.663585	0.049	2.910241	0.001	1.580247	0.014	5.766071	0.002	5.862988	0.0005	CDS hypothetical protein 3630882:3631649 forward MW:27876
RPA3215	1.169133	0.3025	1.598704	0.0195					2.102732	0.0035	CDS putative nitroreductase 3631787:3632464 forward MW:25110
RPA3216	1.253427	0.028	0.972018	0.637	1.358755	0.0235	1.160227	0.153	0.796475	0.8975	CDS sensor histidine kinase with multiple PAS and a response regulator receiver domain 3632669:3634729 forward MW:74741
RPA3217	0.892939	0.7095	0.694847	0.9615	1.123373	0.1695	0.88064	0.778	0.620929	0.997	CDS possible branched-chain amino acid transport system substrate-binding protein 3634858:3636066 reverse MW:42851
RPA3218	1.089649	0.247	0.88248	0.9375	1.185252	0.033	1.080896	0.3175	0.861043	0.936	CDS Protein of unknown function UPF0047 3636172:3636591 reverse MW:15987
RPA3219	1.068891	0.2995	0.608037	0.9875	0.763449	0.8975			0.714913	0.9225	CDS putative diguanylate cyclase (GGDEF)/phosphodiesterase (EAL) 3636661:3638631 reverse MW:70745
RPA3220	0.913211	0.851	0.896427	0.8915	0.790588	0.9725	0.774906	0.978	0.765369	0.962	CDS AAA ATPase 3638930:3640261 reverse MW:48403
RPA3221	1.115327	0.1885	1.291225	0.0295	1.047758	0.3695	1.579483	0.0105	0.929745	0.716	CDS heat shock protein HtrA like 3640484:3641875 reverse MW:48765
RPA3222	0.92606	0.72			0.920439	0.72	1.568885	0.356	0.88415	0.7175	CDS DUF24, predicted transcriptional regulator, related to MarR family 3641958:3642434 reverse MW:18058
RPA3223	0.892676	0.947	0.863605	0.9115	0.624354	0.997	0.749326	0.9865	0.865161	0.8205	CDS putative alginate lyase 3642465:3643481 forward MW:35968
RPA3224	0.673867	0.996	0.611595	0.998	0.848533	0.98	0.457387	0.9995	0.451712	0.999	CDS putative short-chain dehydrogenase 3643705:3644499 reverse MW:27606
RPA3225	0.86632	0.892	1.013541	0.424	0.875782	0.947	0.767812	0.989	0.872333	0.827	rplQ 50S ribosomal protein L17 3644784:3645203 reverse MW:15675
RPA3226	0.733267	0.945	0.913718	0.8835	0.640254	0.9995	0.635975	1	0.840074	0.8865	rpoA DNA-directed RNA polymerase alpha subunit 3645359:3646378 reverse MW:37535
RPA3227	0.704899	0.977	1.11089	0.0885	0.585113	0.9985	0.7641	0.964	0.889815	0.7795	rpsK 30S ribosomal protein S11 3646512:3646901 reverse MW:13877
RPA3228	1.208415	0.0795	1.388347	0.005	1.053985	0.2745	1.671537	0.022	1.399926	0.0175	rpsM 30S ribosomal protein S13 3647032:3647418 reverse MW:14446
RPA3229	0.96083	0.6495	0.868983	0.901	0.89626	0.823	0.657694	0.9985	0.585306	0.9985	adk Adenylate kinase 3647585:3648700 reverse MW:37905
RPA3230	0.887302	0.832	0.822803	0.972	0.961998	0.651	0.713968	0.993	0.64655	0.9975	secY secretion protein SecY 3648697:3650028 reverse MW:48527
RPA3231	0.665515	0.9935	0.719164	0.979	0.768913	0.9905	0.628025	0.9735	0.406569	0.9995	rplO 50S ribosomal protein L15 3650181:3650666 reverse MW:16837
RPA3232	0.645681	0.9995	0.703467	0.994	0.787718	0.9765	0.581159	0.993	0.374606	1	rpmD ribosomal protein L30 3650679:3650873 reverse MW:7224
RPA3233	0.62483	0.9995	0.745762	0.995	0.71775	0.991	0.500014	0.9975	0.352463	1	rpsE ribosomal protein S5 3650932:3651507 reverse MW:20654
RPA3234	0.659789	1	0.721541	0.9885	0.721802	0.988	0.556911	0.998	0.418921	1	rplR 50S ribosomal protein L18 3651568:3651930 reverse MW:13037
RPA3235	0.680238	0.998	0.709075	0.989	0.721597	0.9905	0.597976	0.9835	0.444813	0.9985	rplF 50S ribosomal protein L6 3651942:3652475 reverse MW:19404
RPA3236	0.659426	0.999	0.757536	0.9805	0.72635	0.994	0.530272	0.9975	0.366656	0.9995	rpsH 30S ribosomal protein S8 3652588:3652986 reverse MW:14609
RPA3237	0.693913	0.9945	0.824437	0.938	0.764262	0.988	0.565562	0.9965	0.383937	1	rpsN 30S ribosomal protein S14 3653002:3653307 reverse MW:11463
RPA3238	0.762191	0.971	0.845193	0.935	0.836875	0.966	0.623962	0.987	0.412982	1	rplE 50S ribosomal protein L5 3653351:3653908 reverse MW:21038
RPA3239	0.728362	0.9745	0.873522	0.8945	0.887021	0.799	0.642413	0.9965	0.435166	1	rplX 50S ribosomal protein L24 3653901:3654215 reverse MW:11130
RPA3240	0.720039	0.985	0.903784	0.7755	0.850367	0.849	0.613249	0.9965	0.425996	0.9995	rplN 50S ribosomal protein L14 3654215:3654583 reverse MW:13489
RPA3241	0.91029	0.7415	0.90874	0.7795	0.838593	0.968	0.736623	0.986	0.432266	0.999	rpsQ 30S ribosomal protein S17 3654647:3654895 reverse MW:9685
RPA3242	1.160027	0.0335	1.118934	0.069	1.273717	0.0155	1.053839	0.284	0.825988	0.9815	rpmC 50S ribosomal protein L29 3654908:3655117 reverse MW:7981
RPA3243	0.804398	0.9765	0.84623	0.9025	0.786417	0.9745	0.648478	0.9955	0.38868	1	rplP 50S ribosomal protein L16 3655123:3655536 reverse MW:15282
RPA3244	0.834597	0.9585	0.768929	0.921	0.888626	0.7835	0.629247	0.999	0.388312	1	rpsC 30S ribosomal protein S3 3655572:3656279 reverse MW:26270
RPA3245	0.687774	0.9995	0.640495	0.987	0.671536	0.9965	0.5381	0.9975	0.366498	1	rplV 50S ribosomal protein L22 3656302:3656685 reverse MW:13957
RPA3246	0.757269	0.997	0.726449	0.933	0.767377	0.9925	0.665305	0.9935	0.484833	0.9965	rpsS 30S ribosomal protein S19 3656696:3656974 reverse MW:10219
RPA3247	0.781536	0.982	0.686904	0.977	0.719923	0.9975	0.64454	0.985	0.51741	0.9855	rplB 50S ribosomal protein L2 3656986:3657822 reverse MW:30644
RPA3248	0.750459	0.9325	0.728722	0.9765	0.728835	0.996	0.691707	0.9885	0.546419	0.969	rplW 50S ribosomal protein L23 3657836:3658135 reverse MW:10908
RPA3249	0.774979	0.9075	0.770325	0.9465	0.844418	0.9695	0.798854	0.888	0.665469	0.915	rplD 50S ribosomal protein L4 3658132:3658752 reverse MW:22247
RPA3250	0.693584	0.9575	0.664814	0.9595	0.781167	0.971	0.649751	0.949	0.552311	0.9315	rplC 50S ribosomal protein L3 3658754:3659479 reverse MW:25608
RPA3251	0.795447	0.857	0.705905	0.98	0.833535	0.941	0.67307	0.973	0.593264	0.901	rpsJ 30S ribosomal protein S10 3659530:3659838 reverse MW:11668
RPA3253	1.143518	0.219	1.022086	0.375	0.966081	0.6145	0.839654	0.9245	0.784717	0.8675	fusA, EF-G elongation factor G 3661155:3663227 reverse MW:75601
RPA3254	0.760736	0.9485	1.132031	0.1055	0.516338	0.9995	0.69696	0.99	0.951494	0.587	rpsG 30S ribosomal protein S7 3663258:3663728 reverse MW:17688
RPA3255	0.736314	0.959	1.253369	0.0185	0.463543	0.999	0.8016	0.9055	0.975487	0.523	rpsL 30S ribosomal protein S12 3663744:3664115 reverse MW:13875
RPA3256	0.853154	0.8735	0.734561	0.9875	0.992671	0.532	0.709392	0.9885	0.649169	0.9975	CDS hypothetical protein 3664980:3665966 forward MW:35593
RPA3257	1.537907	0.002	1.548524	0.001	1.417487	0.001	1.648861	0.002	1.66828	0.001	CDS probable transcriptional regulator, AraC family 3666065:3666901 reverse MW:29951
RPA3258	1.044052	0.2785	0.858015	0.875	1.292891	0.02	0.768927	0.98	0.842007	0.956	CDS conserved hypothetical protein 3667022:3667717 forward MW:25264
RPA3259	1.636907	0.0035	1.707938	0.0005	1.386925	0.017	2.128095	0.0005	1.848613	0.0025	CDS conserved hypothetical protein 3667935:3668468 reverse MW:19252
RPA3260			0.536136	0.9255	0.765216	0.9275	1.27616	0.124	0.907694	0.8355	CDS putative cation-transporting P-type ATPase 3668874:3671003 reverse MW:73866
RPA3261	1.120903	0.3265	0.812863	0.9675	1.058562	0.262	1.269498	0.024	1.151724	0.129	hmrR heavy metal resistance transcriptional regulator Hmrr, MerR family 3671069:3671470 forward MW:14993
RPA3262	0.938204	0.826	0.919806	0.776	0.99585	0.5305	1.343003	0.0575	1.271909	0.044	CDS putative transporter 3671513:3672721 reverse MW:41563
RPA3263	0.844988	0.7845	1.025386	0.392	0.991429	0.5095	0.835024	0.824	0.867903	0.769	phnB conserved hypothetical protein 3672938:3673366 reverse MW:15967
RPA3264											CDS Bacterial regulatory protein, MarR family 3673511:3673972 forward MW:16687
RPA3265	0.799681	0.991	0.687671	0.9975	0.755922	0.9835	0.752054	0.9505	0.839661	0.9595	CDS putative ABC transporter 3674048:3676186 reverse MW:77342
RPA3266	0.828492	0.9495	0.706744	0.9875	0.754753	0.9965	0.805956	0.9325	0.986806	0.5475	CDS possible pyridine nucleotide-disulphide oxidored 3676306:3678369 reverse MW:77399
RPA3267	1.122212	0.0785	1.060482	0.2465	1.171439	0.0365	0.940522	0.734	0.716496	0.9775	rpoC RNA polymerase beta' subunit 3678672:3682880 reverse MW:156058
RPA3268	1.097883	0.1125	1.084765	0.153	1.159351	0.0305	0.991854	0.5345	0.911332	0.6085	rpoB RNA polymerase beta subunit 3683017:3687141 reverse MW:153601
RPA3269	0.961886	0.61	1.190746	0.025	0.947001	0.761	0.877083	0.9135	1.023778	0.4515	rplL 50S ribosomal protein L7/L12 3687607:3687984 reverse MW:12843
RPA3270	0.767213	0.995	0.856343	0.934	0.795264	0.989	0.562964	0.9915	0.581151	0.98	rplJ 50S ribosomal protein L10 3688040:3688600 reverse MW:19171
RPA3271	0.930516	0.8545	0.84603	0.927	1.038129	0.3205	0.707315	0.9935	0.605913	0.984	CDS putative D-isomer specific 2-hydroxyacid dehydrogenase 3689460:3690422 reverse MW:33389
RPA3272	0.924525	0.832	0.794793	0.872	0.971621	0.5845	1.000569	0.489	0.932584	0.6815	rplA 50S ribosomal protein L1 3690510:3691199 reverse MW:24010
RPA3273	0.675195	0.997	0.789853	0.9905	0.667074	0.9955	0.658816	0.9865	0.743711	0.9385	rplK 50S ribosomal protein L11 3691207:3691635 reverse MW:15471
RPA3274	0.761176	0.9335	1.238939	0.0155	0.59711	0.997	1.03724	0.3885	1.093306	0.248	nusG transcription antitermination protein, NusG 3691858:3692388 reverse MW:19901

RPA3275	1.224817	0.046	2.63969	0	0.959551	0.5635	2.064962	0.013	2.609823	0.0005	secE preprotein translocase, SecE subunit 3692405:3692656 reverse MW:9332
RPA3276											CDS possible tonB protein 3692921:3693769 reverse MW:30394
RPA3277	1.545557	0.0435	1.346955	0.0145	1.307152	0.102	1.031991	0.4135	1.058898	0.2975	exbD putative exbD, uptake of enterochelin; tonB-dependent uptake of B colicins 3693766:3694215 reverse MW:16020
RPA3278											exbB putative exbB, uptake of enterochelin; tonB-dependent uptake of B colicins 3694230:3695165 reverse MW:32369
RPA3279											pigA possible iron-starvation protein 3695162:3695845 reverse MW:24683
RPA3280			1.502325	0.027			1.483194	0.032			hasR possible heme receptor 3695950:3699525 reverse MW:127509
RPA3281	1.042191	0.343	1.157768	0.1355	1.051327	0.3495	1.76631	0.0085	1.533155	0.0035	CDS probable FecR, iron siderophore sensor protein 3699586:3700551 reverse MW:34676
RPA3282	1.11804	0.173	1.55193	0.002	1.193506	0.043	1.333432	0.0365	1.376363	0.002	CDS RNA polymerase ECF-type sigma factor, possible FecI 3700694:3701215 reverse MW:19227
RPA3284	1.047357	0.347	0.663071	0.9975	1.058004	0.303	0.718277	0.9205	0.569904	0.997	CDS possible penicillin binding protein 3703437:3704660 forward MW:44312
RPA3285	0.932357	0.7275	0.699898	0.9925	0.790358	0.975	0.798604	0.8295	0.421901	0.9995	CDS putative dehydrogenase 3704783:3705550 reverse MW:26783
RPA3286	0.953976	0.6485	0.691963	0.9635	0.689095	0.947	0.587549	0.9225	0.519333	1	CDS possible phosphoglycerate mutase 3705733:3706488 reverse MW:27604
RPA3287	1.019956	0.424	0.695817	0.998	0.767998	0.975	0.682513	0.9465	0.536121	0.9995	CDS putative 3-oxoacyl-acyl carrier protein reductase 3706645:3707430 forward MW:26816
RPA3288	0.846592	0.956	0.660175	0.998	0.792107	0.981	0.828248	0.9075	0.642902	0.997	CDS Tyrosine protein kinase:Aminoglycoside phosphotransferase 3707777:3708835 reverse MW:39452
RPA3289	1.313957	0.132	0.625345	0.995	1.152771	0.1435	0.971233	0.55	0.834109	0.941	CDS acyl-CoA dehydrogenase 3708987:3710219 reverse MW:45921
RPA3290			0.743968	0.9095			0.943896	0.5895	1.506153	0.0635	CDS possible transcriptional regulator, TetR family 3710464:3711126 forward MW:23940
RPA3291	0.855544	0.6295			0.864392	0.613			1.239431	0.3675	CDS possible membrane transport protein 3711156:3712817 reverse MW:58164
RPA3292	1.087866	0.165	1.431545	0.0165	1.082438	0.2045	1.498132	0.0405	1.686499	0.0025	CDS hypothetical protein 3713027:3713293 reverse MW:9509
RPA3293	2.005603	0.0005	1.201855	0.3285	1.231902	0.2435	1.767824	0.0035	1.303644	0.2345	CDS putative branched-chain amino acid transport system ATP-binding protein 3713619:3714371 reverse MW:27338
RPA3294	1.888804	0.0005	1.339596	0.25	1.33385	0.192	1.867489	0.011	1.474908	0.185	CDS putative branched-chain amino acid transport system ATP-binding protein 3714368:3715138 reverse MW:27875
RPA3295	2.165948	0.0005	1.542219	0.139	1.034309	0.4485	1.938452	0.0155	1.917357	0.0395	CDS possible branched-chain amino acid ABC transporter, permease protein 3715135:3716358 reverse MW:43417
RPA3296	1.991847	0.0105	1.965907	0.0705	0.892498	0.6755	1.579025	0.0975	1.578389	0.0835	CDS possible ABC transporter subunit (U75364) 3716363:3717370 reverse MW:36133
RPA3297	2.580138	0.0005	1.623779	0.1345	1.19193	0.315	1.822754	0.0055	1.578182	0.0445	CDS possible branched-chain amino acid transport system substrate-binding protein 3717617:3718969 reverse MW:48306
RPA3298	0.989688	0.5605	0.782557	0.997	0.979782	0.598	0.877077	0.7855	0.752608	0.996	CDS hypothetical protein 3719415:3720800 reverse MW:49567
RPA3299	1.062381	0.402	0.473679	0.9975	1.181224	0.145	0.671602	0.9085	0.512619	0.996	CDS putative long-chain-fatty-acid CoA ligase 3720964:3722520 reverse MW:55682
RPA3300	1.215168	0.181	0.653129	0.9965	1.18501	0.0395	1.078972	0.211	0.994709	0.521	CDS possible transcriptional regulator, TetR family 3722438:3723184 reverse MW:27806
RPA3301	0.75342	0.775	0.554613	0.9985	0.967851	0.605	0.584233	0.9645	0.512287	0.9995	CDS putative lipid transfer protein 3723347:3724531 forward MW:41249
RPA3302	0.967546	0.548	0.531763	0.9995	1.050871	0.34	0.650856	0.986	0.535178	0.999	CDS conserved hypothetical protein 3724542:3724988 forward MW:16048
RPA3303	0.857176	0.766	0.509025	0.998	0.890728	0.6915			0.408099	0.999	CDS MaoC-like dehydratase 3724985:3725410 forward MW:15076
RPA3304	1.282112	0.01	0.94423	0.8035	1.119173	0.1235	1.291341	0.026	0.945164	0.7535	fabG3 putative 3-oxoacyl-acyl carrier protein reductase 3725434:3726261 forward MW:28950
RPA3305			0.762453	0.9315	0.96203	0.5405	0.731985	0.95	0.64566	0.9845	paaG2 enoyl-CoA hydratase/isomerase family 3726282:3727052 forward MW:26254
RPA3306	1.051763	0.3815	1.299858	0.2475	1.28092	0.117	2.309266	0.166	1.250956	0.0565	nirK1 nitrite reductase, major outer membrane copper-containing protein 3727317:3728423 forward MW:39946
RPA3307	0.882939	0.787	1.041434	0.3325	1.065831	0.238	1.369784	0.007	1.5639	0.013	xthA3 putative exonuclease III 3728453:3729235 reverse MW:28936
RPA3308	4.526057	0.003	7.924466	0.0005	4.063385	0	2.673173	0.0075	6.157026	0.0015	CDS ycfI, putative structural proteins 3729714:3730223 forward MW:18795
RPA3309	3.538262	0	5.320544	0.002	3.815698	0	2.363366	0.0025	5.692749	0.001	CDS conserved unknown protein 3730238:3730804 forward MW:20397
RPA3310							1.73362	0.1825	2.104849	0.0015	katE catalase 3730948:3733065 forward MW:78404
RPA3311	3.354849	0	5.107225	0.0025	3.678477	0.0005	2.567066	0.0065	4.943926	0	CDS glycosyl hydrolase 3733281:3735482 forward MW:82483
RPA3312	2.414243	0.01	3.026279	0.002			1.997883	0.002	3.514342	0.0015	CDS Transglutaminase-like domain 3735641:3736489 forward MW:31327
RPA3313	1.507554	0.0015	1.783508	0.009	1.452871	0.005	2.961795	0.005	3.396652	0	CDS hypothetical protein 3736702:3736914 reverse MW:7448
RPA3314	1.409636	0.0405	1.772458	0.013	1.104841	0.204	1.091799	0.228	1.000196	0.5005	degP putative DegP protease precursor 3736985:3738184 reverse MW:41611
RPA3315	1.261941	0.047	0.977719	0.591	1.152634	0.1305	0.948743	0.5965	0.993695	0.5355	CDS protease 3738485:3739159 forward MW:23914
RPA3316	1.123941	0.067	1.132887	0.111	1.058174	0.3135	1.304794	0.0605	1.230921	0.047	CDS possible chemotaxis cheB/cheR fusion protein 3740366:3743506 forward MW:115909
RPA3317			1.279225	0.0755			1.488802	0.0675	1.938662	0.0515	CDS hypothetical protein 3743574:3743972 reverse MW:14931
RPA3318	1.618274	0.0005	1.810719	0.0015	1.716066	0.0035	2.466454	0	3.340512	0	CDS transcriptional regulator, Crp/Fnr family 3743984:3744712 reverse MW:26763
RPA3319											CDS hypothetical protein 3744910:3745329 forward MW:15434
RPA3320	2.584187	0.0005	1.770052	0.0025	1.489323	0.0745	2.992816	0	2.981199	0	CDS hypothetical protein 3745839:3746519 forward MW:25010
RPA3321	1.137105	0.1025	1.111675	0.167	0.851132	0.911	0.901385	0.859	0.976952	0.572	algC possible phosphomannomutase AlgC 3746647:3748143 reverse MW:54355
RPA3322	1.075815	0.2305	1.047482	0.292	0.992812	0.5315	1.227464	0.1025	1.223559	0.02	manC, cpsB, rfbM putative mannose-1-phosphate guanylyltransferase (GDP) (GDP-mannose pyrophosphorylase) (GMP) 3748190:3749626 reverse MW:51995
RPA3323					1.229254	0.0745			1.03241	0.4465	CDS unknown protein 3749863:3751635 reverse MW:65847
RPA3324	1.68813	0.0005	1.715272	0.0005	1.53595	0.001	2.577039	0.0015	2.555136	0	CDS hypothetical protein 3751977:3752846 reverse MW:32370
RPA3325	1.093029	0.2125	1.073265	0.2145	1.08915	0.266	0.829433	0.8295	0.948443	0.7325	CDS hypothetical protein 3753666:3754148 forward MW:18220
RPA3326	1.373526	0	1.236515	0.013	1.679724	0.005	0.969025	0.6405	1.153327	0.116	CDS hypothetical protein 3754537:3755022 forward MW:17642
RPA3327	0.500677	1	0.653561	0.999	0.742987	0.9955	0.617467	0.9925	0.680622	0.9995	CDS hypothetical protein 3755308:3755592 forward MW:10137
RPA3328	2.883069	0.003	1.384102	0.005	3.007343	0.001	2.450547	0.0005	5.489793	0	CDS possible transcriptional regulator, XRE family 3755628:3756044 reverse MW:15532
RPA3329	2.182876	0.0005	2.104045	0.0005	1.488264	0.0055	3.650413	0	3.901387	0.0005	CDS conserved hypothetical protein 3756423:3758174 reverse MW:58262
RPA3330	1.362633	0.047	1.558167	0.024	1.27551	0.0685	1.576373	0.0245	1.519148	0.0565	CDS conserved hypothetical protein 3758733:3759116 forward MW:13216
RPA3331	1.858682	0.01	1.263319	0.0155	1.549287	0.006	1.753311	0	2.420026	0.0015	CDS hypothetical protein 3759101:3759631 forward MW:17582
RPA3332	2.761182	0.0225	1.174204	0.0965	2.191649	0.0035	2.569348	0.0015	4.312181	0	CDS hypothetical protein 3759664:3759948 forward MW:9328
RPA3333	2.229261	0.013	1.048992	0.254	1.809064	0.003	2.259847	0.004	3.704017	0	csgG putative curli production assembly/transport component csgg precursor 3760005:3760880 forward MW:30745
RPA3334	0.894617	0.932	1.004368	0.485	1.026632	0.39	1.042981	0.3525	0.890335	0.8505	CDS hypothetical protein 3761133:3761522 reverse MW:12892
RPA3335	0.990335	0.539	0.899783	0.7545	0.983922	0.544	0.884279	0.7685	0.733014	0.979	CDS hypothetical protein 3761657:3761998 reverse MW:11648
RPA3336	1.230123	0.023	0.858861	0.9325	1.068135	0.267	0.988435	0.5365	1.232363	0.0585	CDS possible lipopeptide antibiotics iturin a biosynthesis protein 3762564:3763271 reverse MW:25830
RPA3337	1.139958	0.0785	1.278663	0.05	0.952415	0.638	1.720303	0.005	1.617648	0.0015	CDS hypothetical protein 3763287:3764387 reverse MW:39981
RPA3338											CDS possible Condensation domain, peptide synthetase 3764459:3766768 reverse MW:85689
RPA3339											mcyE possible McyE polykeitde synthase and peptide synthetase (AF183408) 3766765:3774813 reverse MW:288444
RPA3340											CDS peptide synthetase (fragment) 3774836:3776749 reverse MW:67556
RPA3341	1.923269	0.021	1.514935	0.009	1.677343	0	2.063816	0.035	1.651064	0.0025	CDS putative acetyltransferase 3777237:3778376 forward MW:42550
RPA3342	1.631691	0.003	1.641599	0.001	1.089807	0.2055	2.056729	0.0005	2.301898	0.0015	CDS possible glycosyl hydrolase 3778452:3780284 forward MW:67342
RPA3343	1.634497	0.001	1.593768	0.002	1.375048	0.0025	1.728351	0.003	1.998766	0	mtfB possible mannosyltransferase B 3780347:3781483 forward MW:41468
RPA3344	1.175921	0.0775	0.958372	0.7	0.981833	0.5925	1.465197	0.0265	1.182286	0.0985	CDS possible oxidoreductase 3781605:3783353 forward MW:63943
RPA3345	1.381618	0.002	1.137231	0.0555	1.442205	0.002	1.316164	0.048	1.428118	0.0145	CDS conserved hypothetical protein 3783348:3784790 reverse MW:50800
RPA3346	1.492609	0.0795	3.378096	0.002					1.360708	0.081	CDS possible mannosyltransferase 3785284:3786384 forward MW:39905
RPA3347	1.56502	0.0295	1.708823	0.007	1.517169	0.111	1.895841	0.015	1.569105	0.001	CDS putative glycosyltransferase 3786407:3787297 forward MW:32414
RPA3348	1.269051	0.026	1.097693	0.127	0.995904	0.5045	1.187994	0.0935	1.257403	0.021	CDS possible polysaccharide export protein (AF040104) 3787401:3788894 reverse MW:53938
RPA3349	1.724277	0.0075	1.46345	0.007	1.757211	0.0025	2.13808	0.0005	1.921746	0.0005	CDS putative exopolysaccharide biosynthesis protein 3789036:3790172 reverse MW:40592
RPA3350	1.560666	0.0025	1.450067	0.006	1.42505	0.0055	1.658193	0.0025	1.680707	0	CDS putative aminotransferase 3790782:3791927 forward MW:42488
RPA3351	1.486949	0.004	1.715699	0.006	1.484243	0.014	2.189773	0	2.201243	0	CDS possible glycosyl transferase 3792003:3792809 forward MW:30719
RPA3352	2.04162	0	1.812308	0	1.561087	0.0005	2.250059	0.001	2.347118	0	CDS glycosyltransferase 3792840:3793958 forward MW:41419

RPA3353	1.40302	0.007	2.027767	0	1.395385	0.0105	1.968938	0.0015	1.874956	0	CDS putative serine/threonine protein phosphatase 3793955:3794671 reverse MW:26629
RPA3354	1.970085	0.0015	1.418832	0.0025	1.723654	0.005	1.866865	0.0015	2.695448	0	CDS hypothetical protein 3794981:3795619 forward MW:20658
RPA3355	2.171886	0.002	1.812091	0.0005	1.443348	0.006	2.102752	0.001	2.689825	0	CDS putative exopolysaccharide polymerization protein 3795678:3798026 forward MW:86547
RPA3356	1.681005	0.0015	1.609519	0.013	1.287292	0.0175	2.26871	0.0005	2.423991	0	CDS unknown protein 3798083:3798739 forward MW:24107
RPA3357	1.436422	0.001	1.297033	0.0265	1.265118	0.022	1.521346	0.0045	1.793808	0.0015	CDS putative glycosyltransferase 3799641:3800315 forward MW:25114
RPA3358	1.320143	0.01	1.447201	0.0135	1.226578	0.076	2.188694	0.003	2.198346	0.0005	CDS conserved hypothetical protein 3801039:3801755 forward MW:26359
RPA3359	1.311176	0.132	1.061649	0.2805	1.004011	0.4825	2.105344	0.0005	1.629941	0.001	CDS O-antigen polymerase 3801814:3803247 reverse MW:50834
RPA3360	1.498974	0.1765	0.758707	0.9925	1.311611	0.0125	1.844939	0.007	1.854223	0.008	pssN putative capsule polysaccharide export outer membrane protein 3803244:3804464 reverse MW:43834
RPA3361	1.203727	0.071	1.265296	0.0135	1.267068	0.0525	1.36311	0.034	1.848298	0.001	CDS hypothetical protein 3805215:3805466 forward MW:8953
RPA3362	1.408961	0.008	1.388152	0.0035	1.402617	0.007	1.699718	0.013	1.920879	0.0005	CDS unknown protein 3805695:3805976 forward MW:10280
RPA3363	0.680409	0.9685	0.917036	0.858	0.561815	0.999	0.732543	0.956	0.929293	0.7485	CDS hypothetical protein 3806489:3806956 reverse MW:16033
RPA3364	0.84872	0.941	1.01477	0.409	0.800635	0.982	0.78495	0.982	0.751713	0.9955	rrm1 putative rRNA methylase 3807406:3808233 forward MW:29739
RPA3365	0.835405	0.8745	1.019473	0.465	0.944729	0.648	0.893693	0.763	1.025219	0.4205	CDS unknown protein 3808306:3808806 reverse MW:17958
RPA3366	1.147877	0.0795	1.401884	0.009	1.156965	0.0445	1.354254	0.015	1.379685	0.003	CDS conserved hypothetical protein 3808864:3809337 reverse MW:17130
RPA3367	0.700052	0.91	1.328208	0.0375	0.897037	0.779	1.268887	0.048	0.85781	0.7005	CDS possible activator of photopigment and puc with BLUF domain 3809655:3810125 reverse MW:17239
RPA3368	0.880048	0.861	1.098408	0.195	0.945383	0.673	0.976603	0.624	1.119426	0.184	CDS hypothetical protein 3810250:3810849 reverse MW:22205
RPA3369	1.010844	0.4845	1.924093	0.0045	0.956218	0.5435	1.786632	0.0305	0.972887	0.5215	CDS hypothetical protein 3811211:3811423 forward MW:7925
RPA3370	0.493665	0.99	0.804813	0.896	0.910492	0.829	0.623169	0.9935	0.487329	0.985	CDS hypothetical protein 3811538:3812215 forward MW:25008
RPA3371	1.368015	0.019	1.670944	0.009	2.241842	0.0005	0.839304	0.9365	1.725997	0.0015	CDS putative outer membrane protein 3812381:3813103 reverse MW:25231
RPA3372	0.866024	0.97	1.029456	0.4	0.917607	0.8525	1.09945	0.155	1.04562	0.246	CDS hypothetical protein 3813283:3813702 reverse MW:15280
RPA3373	0.887795	0.8425	1.128568	0.138	1.089047	0.2975	1.83967	0.005	2.690327	0.004	CDS hypothetical protein 3813795:3814091 reverse MW:10172
RPA3374	0.888195	0.962	0.890589	0.9165	0.866535	0.958	0.962665	0.63	0.944961	0.7605	CDS DUF15 protein 3814236:3815222 forward MW:36480
RPA3375	0.9171	0.8655	0.879601	0.972	1.040999	0.31	0.988625	0.5475	0.985192	0.5925	CDS unknown protein 3815306:3815749 reverse MW:16864
RPA3376	0.947411	0.76	0.868143	0.9135	0.852164	0.949	0.791881	0.885	0.975206	0.608	CDS possible DNA methyltransferase 3815742:3819017 reverse MW:119299
RPA3377	1.013026	0.4245	0.71407	0.9915	0.904564	0.8525	0.68688	0.9845	0.612771	1	CDS 3-oxoacyl-acyl carrier protein reductase 3819486:3820190 reverse MW:24622
RPA3378	1.249501	0.2085	1.382114	0.0035	1.237841	0.045	1.580658	0.017	1.214057	0.109	CDS hypothetical protein 3820668:3820844 reverse MW:6373
RPA3379	1.215313	0.0325	1.152047	0.108	1.010385	0.456	1.32042	0.085	1.435172	0.013	CDS hypothetical protein 3821212:3821406 reverse MW:7354
RPA3380	0.862479	0.8805	0.69821	0.989	0.750589	0.9745	0.866769	0.901	0.846787	0.917	CDS response regulator receiver (CheY-like protein) 3821616:3822161 forward MW:20834
RPA3381	0.818206	0.8765	0.562387	0.9945	0.988573	0.529	0.738582	0.9635	0.694116	0.9905	CDS Hpt domain 3822179:3822769 forward MW:20888
RPA3382	1.148796	0.051	0.946923	0.788	0.834412	0.968	1.136427	0.1345	1.031058	0.347	CDS conserved hypothetical protein 3823066:3824235 reverse MW:41389
RPA3383			0.900828	0.6705	1.006476	0.4795	0.957317	0.577	1.152527	0.1505	CDS possible taurine transport system permease protein 3824681:3825466 forward MW:28348
RPA3384	1.589721	0.0355	1.135673	0.2295	1.21448	0.1465	1.807486	0.0035	1.75052	0.0095	CDS possible ABC related periplasmic binding protein 3825463:3826494 forward MW:36443
RPA3385			1.476162	0.002	1.248705	0.2215	1.826779	0.0025	1.619702	0.0095	nrtC2 putative nitrate transport system ATP-binding protein 3826491:3827327 forward MW:31690
RPA3386											CDS possible amidohydrolase 3827388:3829061 forward MW:60875
RPA3387	1.034872	0.303	0.949504	0.686	0.967306	0.6495	1.626387	0.0035	1.280315	0.026	CDS transcriptional regulator, LysR family 3829071:3830087 forward MW:38063
RPA3388	1.075358	0.16	0.894	0.8785	0.707722	0.97	1.006375	0.4805	1.034234	0.3495	CDS hypothetical protein 3830094:3831134 reverse MW:35916
RPA3389	1.195633	0.0295	0.913826	0.83	1.155424	0.164	1.421674	0.021	1.20442	0.0445	CDS hypothetical protein 3831331:3832029 forward MW:24398
RPA3390	0.824187	0.938	0.880803	0.9505	0.972371	0.6435	0.918858	0.8245	1.019819	0.4135	his3 phosphoribosyl c-AMP cyclohydrolase 3832039:3832494 reverse MW:16763
RPA3391	0.842786	0.9205	0.775222	0.987	0.866188	0.9305	0.885582	0.874	1.203229	0.017	gch1 possible GTP cyclohydrolase I 3832523:3833212 reverse MW:25702
RPA3392	0.766417	0.9765	0.572887	0.9995	0.790515	0.946	0.69762	0.981	0.894607	0.9175	CDS possible nifU homolog 3833480:3833932 forward MW:15989
RPA3393	2.0273	0.018	1.980081	0.003	2.87373	0.0015	4.447941	0.0015	3.859677	0.001	CDS conserved hypothetical protein 3834115:3835005 reverse MW:30814
RPA3394											CDS DUF37 3835177:3835635 forward MW:17292
RPA3395	1.084517	0.2825	0.728794	0.995	1.211804	0.0515	0.683778	0.9855	1.178921	0.151	CDS conserved hypothetical protein 3835622:3836413 reverse MW:28564
RPA3396	1.678394	0.0005	1.662934	0.0025	1.719507	0.001	2.290541	0.001	3.183171	0.002	CDS hypothetical protein 3836526:3837653 reverse MW:38755
RPA3397	1.699683	0.0005	1.561507	0.0025	1.818541	0.0015	2.13194	0.001	2.95915	0	CDS hypothetical protein 3837655:3838113 reverse MW:16575
RPA3398	1.10486	0.2075	1.174569	0.2845	1.115098	0.1275	1.681965	0.036	1.134566	0.123	CDS possible arsenite permease 3838266:3839531 reverse MW:43794
RPA3399	0.795439	0.978	0.962429	0.688	1.202179	0.0255	0.536824	0.999	0.83316	0.958	cspA4 cold shock DNA binding protein 3839779:3840006 forward MW:8078
RPA3400											CDS hypothetical protein 3840107:3840355 forward MW:9141
RPA3401	1.187023	0.1345	1.209086	0.1215	0.973417	0.546	1.905083	0.0135	1.423318	0.0235	CDS hypothetical protein 3840399:3840596 forward MW:7366
RPA3402			0.881352	0.7675	0.835576	0.7555	1.027612	0.4575	1.243602	0.131	CDS conserved hypothetical protein 3840586:3841008 reverse MW:15284
RPA3403	1.019841	0.4505	0.751613	0.958	0.868779	0.908	1.016481	0.462	0.894952	0.6775	CDS possible transcriptional regulator, TetR family 3841013:3841645 reverse MW:23140
RPA3404	0.874342	0.9325	0.869537	0.8425	1.007021	0.441	0.639268	0.9835	0.565859	0.9785	CDS putative O-methyltransferase 3841743:3842393 forward MW:23435
RPA3405	1.092798	0.153	1.09125	0.277	1.030393	0.3725	1.404371	0.1085	1.335934	0.03	CDS possible transporter 3842755:3843873 reverse MW:38156
RPA3406	1.190188	0.044	1.071078	0.151	1.159497	0.072	1.031388	0.3885	1.067699	0.2845	thrS threonyl-tRNA synthetase 3844183:3846159 forward MW:74111
RPA3407	1.083106	0.2045	0.883784	0.902	0.917717	0.7025	1.056301	0.3365	0.707579	0.995	CDS hypothetical protein 3846441:3847019 reverse MW:20553
RPA3408	0.936607	0.7405	0.698353	0.983	0.943536	0.703	1.087812	0.2285	0.797905	0.954	CDS Nitroreductase family 3847356:3847865 forward MW:18096
RPA3409			0.911818	0.617			1.24507	0.2365	1.268592	0.1865	CDS possible metal-dependent hydrolases 3847917:3849791 reverse MW:67452
RPA3410	1.301685	0.028	1.458912	0.005	1.158114	0.1585	0.961981	0.6215	0.997782	0.4865	CDS putative diguanylate cyclase (GGDEF)/phosphodiesterase (EAL) with PAS domains 3849886:3852360 reverse MW:90962
RPA3411	0.996988	0.5075	1.150026	0.0615	1.260428	0.0695	0.940525	0.7675	1.109402	0.11	CDS conserved hypothetical protein 3852571:3853734 reverse MW:40634
RPA3412	0.900319	0.837	0.760731	0.969	0.798658	0.968	0.670135	0.9655	0.732101	0.991	CDS Patatin-like phospholipase domain 3853863:3854894 forward MW:36418
RPA3413	1.139946	0.061	1.61272	0.003	1.081748	0.222	1.316816	0.1225	1.172846	0.103	CDS Uncharacterized iron-regulated membrane protein DUF337 3855126:3856241 reverse MW:40367
RPA3414	0.83741	0.7635			0.860411	0.705			1.086157	0.2925	CDS putative hydroxamate-type ferrisiderophore receptor 3856270:3858531 reverse MW:81447
RPA3415											CDS probable transcriptional regulator, TetR family 3858681:3859316 forward MW:22459
RPA3416	1.13459	0.0555	1.078038	0.2	1.963903	0	1.152853	0.1935	1.082843	0.1625	CDS protein with 2 CBS domains 3859338:3859766 reverse MW:15863
RPA3417	1.116009	0.0825	1.374634	0.004	0.995659	0.5115	1.080532	0.205	1.175829	0.032	CDS Lipocalin-related protein and Bos/Can/Equ allergen:Rhomboid-like protein 3860004:3860774 reverse MW:27566
RPA3418	0.783004	0.991	0.592708	0.999	0.791356	0.9795	0.798406	0.9485	0.763451	0.991	CDS conserved hypothetical protein 3861259:3861828 forward MW:20833
RPA3419	0.459553	0.9995	0.38292	1	0.537809	1	0.530438	0.9845	0.500092	0.998	CDS possible transcriptional regulator, Crp/Fnr family 3861798:3862562 reverse MW:27210
RPA3420	1.079409	0.227	1.04543	0.293	0.956648	0.7195	1.260489	0.02	1.153752	0.07	CDS conserved unknown protein 3863062:3863613 forward MW:20334
RPA3421	1.934617	0	1.683965	0	1.505418	0.0025	2.546766	0	2.928876	0	CDS conserved hypothetical protein 3863945:3864565 forward MW:23005
RPA3422	1.467442	0.046	1.51726	0.0345	1.169677	0.0425	2.492264	0.01	1.755157	0.0005	CDS possible transcriptional regulator, MarR family 3864703:3865290 reverse MW:22128
RPA3423	1.197497	0.0415	1.034707	0.3755	1.087413	0.2975	1.114539	0.2425	1.165214	0.0365	CDS conserved unknown protein 3865814:3867313 forward MW:52444
RPA3424	1.008794	0.489	2.264493	0.022	0.934864	0.672	1.986946	0.1335	1.456669	0.009	CDS hypothetical protein 3867737:3867904 forward MW:5968
RPA3425	0.920271	0.909	1.039469	0.2795	0.893031	0.8845	0.878892	0.8735	0.870264	0.963	CDS Bacterial transferase hexapeptide repeat 3867936:3868466 reverse MW:18181
RPA3426	1.227112	0.118	1.297941	0.0125	1.112329	0.3255	1.569286	0.0025	0.787213	0.9585	CDS conserved hypothetical protein 3868526:3868858 reverse MW:11637
RPA3427	0.814521	0.9375	1.426077	0.0045	0.722194	0.974	1.404595	0.0785	1.553642	0.0045	CDS conserved hypothetical protein 3869049:3869756 forward MW:26345
RPA3428	0.843841	0.7965	0.793142	0.943	0.942289	0.6865	0.697765	0.9905	0.557748	0.9975	CDS conserved unknown protein 3869773:3870003 reverse MW:8836
RPA3429	0.971332	0.7085	0.811193	0.989	0.976588	0.628	0.976888	0.6145	1.201126	0.036	cysE2 serine acetyltransferase 3870160:3870987 reverse MW:30069

RPA3430							0.893795	0.6705	0.459026	0.9975	CDS possible hydrolase 3871208:3871963 reverse MW:27180
RPA3431	1.091467	0.305	0.950187	0.565	0.978087	0.5685	0.75253	0.983	0.791003	0.9045	CDS hypothetical protein 3872133:3873281 reverse MW:39820
RPA3432	1.215328	0.179	0.906989	0.7845	1.224226	0.072	1.234961	0.0825	1.906514	0.0035	CDS conserved hypothetical protein 3873487:3873732 forward MW:8901
RPA3433	0.925951	0.6525	1.071809	0.339	0.837832	0.9705	0.778255	0.8955	0.886312	0.8525	CDS possible salicylate hydroxylase 3873751:3874944 forward MW:41653
RPA3434	0.940095	0.736	0.8323	0.973	1.120032	0.171	1.000787	0.514	1.20713	0.0345	CDS Universal stress protein (Usp) 3875337:3875981 forward MW:22709
RPA3435	1.14728	0.0385	1.338653	0.0135	0.898422	0.9235	1.109397	0.1085	1.14268	0.0855	CDS Glycosyl transferase, family 2 3876078:3876938 forward MW:32618
RPA3436	1.433521	0.0335	2.614105	0.001	1.140938	0.3015	2.250915	0.019	1.805826	0.0015	CDS GCN5-related N-acetyltransferase 3876964:3877473 forward MW:19003
RPA3437	1.183934	0.056	1.02233	0.3935	1.082469	0.1595	1.385517	0.0045	1.255422	0.0225	CDS conserved unknown protein 3878064:3879167 forward MW:41866
RPA3438											CDS hypothetical protein 3879239:3879502 reverse MW:9432
RPA3439	1.166677	0.0945	0.951807	0.691	1.182806	0.157	1.155227	0.1615	0.803595	0.965	CDS putative hydrolase 3880205:3881392 forward MW:42477
RPA3440	1.38891	0.003	1.383171	0.005	1.506198	0.0025	1.7444	0.0025	1.092041	0.2585	CDS probable amidase 3881385:3882800 forward MW:50243
RPA3441	0.773243	0.995	0.745303	0.9835	0.877089	0.918	0.660984	0.9605	0.386576	1	CDS enoyl-CoA hydratase/isomerase family protein 3882893:3883822 forward MW:34180
RPA3442	0.567302	0.9755	0.977422	0.5965	0.857192	0.855	0.564578	0.998	0.707535	0.998	CDS Putative cyclase 3883848:3884624 reverse MW:28727
RPA3443											CDS possible isomerase/decarboxylase 3884651:3885640 reverse MW:36176
RPA3444	0.625124	0.9955	0.542258	0.9985	0.706401	0.9925	0.491793	0.999	0.901057	0.791	CDS transcriptional regulator, GntR family 3885768:3886478 forward MW:26232
RPA3445	1.582425	0.009	1.105508	0.1915	1.333706	0.1195	1.571947	0.0045	1.335962	0.028	CDS probable acetyl-CoA synthetase 3886503:3888224 reverse MW:62539
RPA3446	0.891858	0.8385	0.849434	0.9235	1.033111	0.397	0.645145	0.986	0.543275	0.9985	CDS 3-hydroxyisobutyrate dehydrogenase 3888385:3889272 reverse MW:29541
RPA3447	0.944739	0.8205	1.00643	0.473	0.843911	0.934	0.801327	0.972	0.668507	0.9965	CDS putative enoyl-CoA hydratase/isomerase 3889306:3890379 reverse MW:38554
RPA3448	0.869048	0.8695	0.900467	0.918	0.78284	0.9605	0.679183	0.9955	0.545198	1	CDS acyl-CoA dehydrogenase 3890376:3891533 reverse MW:41809
RPA3449	1.137149	0.0375	1.13979	0.1125	1.093826	0.1385	0.946789	0.6755	0.729649	0.9905	CDS PilT protein, N-terminal 3891530:3891949 reverse MW:15504
RPA3450	0.943833	0.8195	0.923369	0.8785	1.053979	0.2465	0.759516	0.9765	0.605496	1	CDS putative malonic semialdehyde oxidative decarboxylase 3892228:3893724 reverse MW:53378
RPA3451	0.913066	0.732	0.844529	0.8605	0.954453	0.667	0.851201	0.8135	0.945074	0.696	CDS possible transcriptional regulator, TetR family 3893884:3894552 reverse MW:23867
RPA3452			0.358583	0.9965	0.480398	0.985					CDS Phenylacetic acid degradation-related protein 3894626:3895201 reverse MW:20006
RPA3453	0.869079	0.858	0.448241	0.9975	0.714123	0.928			0.472005	0.999	CDS putative enoyl-CoA hydratase 3895343:3896113 forward MW:27426
RPA3454	0.587864	0.9995	0.500548	0.9975	0.5495	0.999	0.457978	0.9985	0.500706	1	CDS putative transmembrane transport protein, MFS family 3896238:3897524 forward MW:45121
RPA3455	0.770169	0.9635	1.004247	0.4805	0.812319	0.969	0.648933	0.9855	0.727751	0.9845	CDS possible methylmalonyl-CoA decarboxylase alpha chain 3897573:3899132 reverse MW:56774
RPA3456	0.726721	0.974	0.892661	0.765	1.103555	0.123	0.494912	1	0.698549	0.9935	CDS possible transcriptional regulator 3899129:3900006 reverse MW:31827
RPA3457	0.593138	0.997	0.610252	0.9965	0.796705	0.964	0.434801	0.999	0.623412	0.9985	CDS Biotin/lipoyl attachment:Biotin-requiring enzyme, attachment site 3900286:3900507 forward MW:7490
RPA3458	0.86874	0.6575	0.437449	0.9995	0.965186	0.658	0.469585	0.9835	0.350455	0.999	CDS possible TrapT family, dctP subunit, C4-dicarboxylate periplasmic binding protein 3900691:3901851 forward MW:41090
RPA3459	0.859268	0.7305	0.602385	0.99	0.981888	0.6065	0.474795	0.9915	0.323625	0.995	CDS possible TrapT family, fused dctM-Q subunits, C4-dicarboxylate transport 3901879:3903945 forward MW:73436
RPA3460	0.870313	0.711	0.878279	0.8395	0.891951	0.815	1.024727	0.4085	0.730291	0.9315	CDS hypothetical protein 3904066:3904620 forward MW:20463
RPA3461					0.89952	0.7255	0.731452	0.905			CDS conserved hypothetical protein 3904676:3905041 reverse MW:12985
RPA3462	0.90967	0.873	0.791263	0.9215	0.823684	0.9705	0.604575	0.9985	0.548881	0.9985	CDS Thiolase 3905038:3906252 reverse MW:42316
RPA3463	0.939854	0.618	0.851398	0.899	1.021016	0.438	0.913469	0.7	0.907114	0.6975	CDS conserved hypothetical protein 3906356:3907573 reverse MW:44125
RPA3464	0.883362	0.8265	0.811288	0.956	0.584997	0.994	0.676958	0.977	0.623405	0.994	CDS conserved hypothetical protein 3907766:3908650 forward MW:32323
RPA3465	1.04454	0.314	0.938341	0.831	0.992911	0.5515	0.656844	0.9955	0.747775	0.987	CDS putative long-chain-fatty-acid CoA ligase 3908870:3910396 reverse MW:54291
RPA3466	1.133529	0.2215	0.946568	0.71	1.088051	0.189	0.82494	0.9365	0.882424	0.9525	CDS 3-ketoacyl-CoA thiolase 3910417:3911586 reverse MW:41057
RPA3467	1.243391	0.0065	1.065743	0.32	0.858756	0.9265	1.027658	0.4015	0.881891	0.941	CDS probable UDP-glucose 4-epimerase 3911835:3912899 reverse MW:37943
RPA3468	1.462433	0.002	1.298694	0.0305	1.267961	0.03	1.658735	0.0055	1.422935	0.02	CDS putative permease protein of sugar ABC transporter 3913033:3913959 reverse MW:34391
RPA3469	2.227594	0.0225	1.180114	0.3035	2.177113	0.0005	1.828652	0.005	1.124122	0.336	CDS probable permease protein of sugar ABC transporter 3913952:3914905 reverse MW:35406
RPA3470	2.827516	0.033	0.88567	0.7055	2.513096	0.0015	1.591384	0.023	1.03237	0.462	CDS putative sugar uptake ABC transporter periplasmic solute-binding protein precursor 3915123:3916448 reverse MW:47933
RPA3471	1.40888	0.03	1.066984	0.2545	1.33234	0.017	1.932836	0.0035	1.403735	0.0065	CDS ABC transporter, ATP-binding protein 3916525:3917589 reverse MW:38552
RPA3472	1.357129	0.2045	0.652977	0.982	1.259407	0.0395	1.029164	0.433	0.638852	0.987	ilvD1 dihydroxy-acid dehydratase 3917826:3919634 forward MW:64794
RPA3473	1.244099	0.193	0.736099	0.916	1.05291	0.315	0.853186	0.787	0.609888	0.9865	ucpA putative oxidoreductase 3919768:3920502 forward MW:25412
RPA3474	1.234881	0.0685	0.828918	0.802	1.271522	0.009	1.079172	0.337	0.73517	0.941	fabG4 putative 3-oxoacyl-acyl carrier protein reductase 3920586:3921335 forward MW:26315
RPA3476	1.482685	0.019	2.293216	0.0005	1.824786	0	2.017363	0.0035	1.929781	0	CDS possible energy transducer TonB 3922797:3923591 reverse MW:28187
RPA3477	1.740235	0.0005	2.673166	0.0005	1.708945	0.0015	1.967166	0.0385	2.036526	0.001	exbD5 exbD, uptake of enterochelin; tonB-dependent uptake of B colicins 3923696:3924145 reverse MW:16277
RPA3478	1.262383	0.0195	1.746232	0	1.372249	0.0165	1.47726	0.0415	1.227937	0.0325	exbB5 possible exbB, uptake of enterochelin; tonB-dependent uptake of B colicins 3924149:3924853 reverse MW:25092
RPA3479	2.678885	0	3.775226	0	2.78246	0	3.333412	0.0025	3.298633	0	CDS 2OG-Fe(II) oxygenase superfamily:Prolyl 4-hydroxylase, alpha subunit 3925057:3925746 reverse MW:25318
RPA3480	3.369628	0	3.673398	0	2.592298	0	4.571998	0.014	3.276325	0.0005	fiu putative outer membrane receptor for iron transport 3925772:3927973 reverse MW:79793
RPA3481	2.748552	0.0015	4.976511	0			5.180253	0.0185	2.613292	0.0005	CDS hypothetical protein 3928437:3928679 reverse MW:9117
RPA3482			0.977901	0.6375			1.316764	0.016			CDS putative membrane protein 3929016:3930239 forward MW:42852
RPA3483	1.138323	0.108	0.955967	0.7055	1.011003	0.435	1.066838	0.23	1.005927	0.4695	CDS RND efflux transporter 3930242:3933379 forward MW:113153
RPA3484											CDS PilT protein, N-terminal 3933422:3934063 reverse MW:23592
RPA3485	1.420473	0.1585	1.853318	0.0145	0.640659	0.949	0.952248	0.678	0.719156	0.828	CDS putative racemase 3934674:3935867 reverse MW:43068
RPA3486	1.10122	0.2515	0.640183	0.945	1.627935	0.0025	0.720727	0.8955	0.798611	0.909	CDS putative branched-chain amino acid transport system substrate-binding protein 3935977:3937188 reverse MW:43767
RPA3487	1.301236	0.0115	1.145967	0.263	1.133733	0.1065	1.843983	0.114	1.477485	0.0095	CDS conserved hypothetical protein 3937437:3938051 reverse MW:21691
RPA3488	0.704511	0.9985	0.655221	0.9855	0.81955	0.938	0.527702	0.9975	0.5825	0.9965	CDS probable serine protease 3938057:3939562 reverse MW:52201
RPA3489	0.79447	0.9085	0.974584	0.609	1.029461	0.441	0.868395	0.9305	0.676092	0.976	CDS conserved hypothetical protein 3939777:3939977 reverse MW:7152
RPA3490	1.218745	0.014	1.086114	0.172	1.211847	0.0195	1.128021	0.089	0.998174	0.51	hflC putative hflC protein 3940220:3941146 reverse MW:33979
RPA3491	1.05558	0.26	1.015501	0.4485	0.895857	0.901	0.935444	0.685	0.819408	0.9805	hflK putative protease subunit hflK 3941143:3942294 reverse MW:41772
RPA3492	0.698902	0.999	0.613231	1	0.789985	0.9525	0.498537	0.999	0.649841	0.9975	dyr dihydrofolate reductase 3942439:3942981 reverse MW:19506
RPA3493	0.644203	0.998	0.637639	0.9975	0.908999	0.8825	0.48322	0.9995	0.668319	0.9995	thyA thymidylate synthase 3942978:3943772 reverse MW:29662
RPA3494	1.065196	0.247	1.000695	0.507	1.015444	0.448	0.954322	0.672	1.296776	0.005	CDS possible TctC subunit of the Tripartite Tricarboxylate Transport(TTT) Family 3943944:3944951 reverse MW:35409
RPA3495	0.96699	0.592	0.942435	0.641	1.070967	0.3715	0.883219	0.707	0.897196	0.7755	CDS possible TctA subunit of the Tripartite Tricarboxylate Transport(TTT) Family 3945053:3946567 reverse MW:52650
RPA3496	1.06844	0.276	1.623267	0.086	1.178775	0.1395	1.125253	0.435	0.943713	0.637	CDS possible TctB subunit of the Tripartite Tricarboxylate Transport(TTT) Family 3946578:3947078 reverse MW:17534
RPA3498	0.838775	0.857	0.890724	0.842	1.207896	0.082	0.741785	0.913	0.885056	0.809	CDS possible chromate transport protein similar to chrA 3947678:3948274 reverse MW:21145
RPA3499	0.607518	1	0.591031	0.997	0.891486	0.853	0.712364	0.988	0.911965	0.9045	CDS conserved unknown protein 3949002:3949538 forward MW:19536
RPA3500	0.502366	0.999	0.679341	0.9955	0.665701	0.981	0.43253	0.9995	0.517242	0.9975	fumC2 fumarate hydratase C 3949644:3951077 forward MW:51087
RPA3501	1.167452	0.1295	1.53216	0.004	1.557439	0.002	1.43138	0.014	0.883584	0.8445	CDS conserved unknown protein 3951527:3951805 forward MW:10182
RPA3502	0.964025	0.6415	1.092924	0.234	1.036791	0.3275	0.795299	0.977	0.834393	0.9175	CDS unknown protein 3951826:3955641 reverse MW:131354
RPA3503	1.174935	0.059	1.160655	0.0715	0.87101	0.8535	0.92495	0.741	0.924616	0.816	CDS putative D-lactate dehydrogenase, oxidoreductase 3955777:3957240 reverse MW:51992
RPA3504	1.032739	0.43	0.791899	0.981	1.105756	0.113	0.787441	0.977	0.567138	0.999	CDS Thioesterase superfamily 3957325:3957804 forward MW:18096
RPA3505	1.086303	0.3635	0.97782	0.587	1.127999	0.144	0.952027	0.603	0.591223	0.999	CDS conserved hypothetical protein 3957801:3957974 reverse MW:6021
RPA3506	0.857824	0.9305	0.847153	0.882	0.711112	0.9775	0.813438	0.9635	0.473999	1	uvrD DNA helicase II 3958287:3960833 forward MW:93646
RPA3507	0.895662	0.907	0.99594	0.5285	0.860339	0.9125	0.914071	0.834	0.672549	0.995	CDS Protein of unknown function UPF0150 3960833:3961117 forward MW:9946
RPA3508	0.694522	0.9385	0.769595	0.9575	0.722394	0.9905	0.610056	0.9505	0.846073	0.849	CDS ATP-binding component of ABC transporter 3961413:3962333 forward MW:33429

RPA3509	0.694647	0.986	0.671273	0.998	0.863442	0.8835	0.603511	0.9965	0.708008	0.9905	CDS permease, ABC-2-type transport system 3962336:3963097 forward MW:27659
RPA3510	1.238838	0.059	1.751939	0.001	1.293344	0.062	1.125589	0.0925	1.324092	0.023	CDS conserved unknown protein 3963169:3963516 reverse MW:11853
RPA3511	0.853789	0.936	0.638255	0.9975	0.982509	0.548	0.782155	0.8705	1.188105	0.0575	CDS ErfK/YbiS/YcfS/YnhG 3963779:3964549 forward MW:27901
RPA3512	0.941984	0.788	0.843895	0.9705	1.03309	0.356	0.932014	0.7485	0.909568	0.8575	CDS conserved hypothetical protein 3964611:3966761 reverse MW:77032
RPA3513	0.905343	0.895	0.894355	0.897	0.917709	0.8645	0.805109	0.887	1.068285	0.2135	CDS phytoene dehydrogenase-related protein 3966889:3968661 forward MW:62784
RPA3514	1.014237	0.428	1.071497	0.2445	0.918912	0.857	0.933772	0.759	0.81938	0.986	CDS conserved hypothetical protein 3969431:3970366 forward MW:32988
RPA3515	1.365174	0.018	1.113408	0.095	0.935206	0.718	1.065798	0.2215	1.240632	0.022	CDS aminopeptidase P 3970781:3972610 forward MW:66140
RPA3516	0.709771	0.9895	0.610229	0.986	1.076958	0.2245	0.643742	0.979	0.832255	0.9325	CDS possible bcr efflux pump, Major Facilitator Superfamily (MFS) 3972983:3974269 forward MW:45038
RPA3517	0.806402	0.983	0.759997	0.9535	0.863	0.9565	0.754204	0.9465	0.710767	0.993	dnlJ DNA ligase 3974463:3976541 reverse MW:76072
RPA3518	1.143947	0.035	1.030396	0.357	1.297152	0.01	1.539948	0.008	1.310032	0.049	CDS Excinuclease ABC, C subunit, N-terminal 3976757:3977044 forward MW:11174
RPA3519	0.880456	0.9375	0.797572	0.9885	0.960056	0.742	0.711569	0.9875	0.783892	0.9865	recN putative DNA repair protein RecN 3977199:3978884 reverse MW:59513
RPA3520	0.852422	0.97	1.015975	0.432	0.806829	0.9335	0.828977	0.9505	1.076634	0.2285	CDS Protein of unknown function UPF0169 3978897:3979805 reverse MW:33633
RPA3521	1.614087	0.002	1.006573	0.463	1.705214	0.0005	1.534688	0.002	1.705957	0.0025	lpxC putative UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosmine deacetylase 3980032:3981087 reverse MW:37520
RPA3522	0.913922	0.917	0.826622	0.989	0.900675	0.905	0.757387	0.9925	0.730459	0.9975	ftsZ cell division protein FtsZ 3981341:3983119 reverse MW:62288
RPA3523	0.793308	0.995	0.802894	0.992	0.773524	0.9955	0.682353	0.996	0.91956	0.8605	ftsA putative cell division protein FtsA 3983213:3984535 reverse MW:46903
RPA3524	0.900315	0.8775	0.82144	0.9615	0.728434	0.99	0.726527	0.9515	0.901197	0.8445	ftsQ putative cell division protein FtsQ 3984532:3985521 reverse MW:36367
RPA3525	0.458455	0.999	0.399935	1	0.691786	0.998	0.356188	0.999	0.398042	1	ddlA putative D-alanyl-D-alanine ligase A 3985840:3986829 reverse MW:35057
RPA3526	0.878164	0.9195	0.862076	0.8085	1.16316	0.1515	0.943462	0.653	1.095452	0.2055	CDS conserved hypothetical protein 3986939:3988267 reverse MW:48347
RPA3527	0.642808	1	0.486085	0.9985	0.757867	0.989	0.521027	0.997	0.571558	0.9995	CDS hypothetical protein 3988434:3989318 forward MW:31558
RPA3528	0.932671	0.742	0.723424	0.9145	0.975749	0.62	0.713525	0.965	0.592596	0.9985	murB UDP-N-acetylenolpyruvoylglucosamine reductase 3989368:3990342 reverse MW:34585
RPA3529	0.718881	0.998	0.772755	0.993	0.658732	0.997	0.521804	1	0.638797	0.992	murC UDP-N-acetylmuramate-alanine ligase 3990383:3991786 reverse MW:49748
RPA3530	0.813361	0.9765	0.779137	0.951	0.82771	0.976	0.655347	0.98	0.881689	0.907	murG UDP-N-acetylglucosamine:N-acetylmuramyl-(pentapep tide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase 3991923:3993023 reverse MW:38444
RPA3531	0.763061	0.994	0.729447	0.9895	0.672506	0.9865	0.514848	0.9995	0.627522	0.999	ftsW putative cell division protein ftsW 3993028:3994170 reverse MW:41094
RPA3532	0.824755	0.9635	0.785248	0.982	0.894773	0.892	0.70669	0.9875	0.736517	0.9775	murD UDP-N-acetylmuramoylalanine-D-glutamate ligase 3994412:3995821 reverse MW:49063
RPA3533	0.840883	0.9135	0.89869	0.909	0.723249	0.991	0.614957	0.997	0.839795	0.9515	mraY phospho-N-acetylmuramoyl-pentapeptide- transferase 3996009:3997094 reverse MW:38717
RPA3534	0.755932	0.98	0.911606	0.8335	0.734891	0.9965	0.592595	0.995	0.794659	0.99	murF putative UDP-N-acetylmuramoylalanyl-D-glutamyl-2,6-diaminopimelate- D-alanyl-D-alanine ligase 3997105:3998544 reverse MW:49529
RPA3535	0.756964	0.991	0.656832	0.992	0.75123	0.985	0.632201	0.9895	0.797567	0.9675	murE UDP-N-acetylmuramoylalanyl-D-glutamate-2,6-diamin opimelate ligase 3998541:3999998 reverse MW:50119
RPA3537	0.87517	0.966	0.863834	0.964	0.808421	0.977	0.738802	0.9925	0.824609	0.986	CDS conserved hypothetical protein 4001862:4002245 reverse MW:14083
RPA3539	0.868765	0.93	0.678382	0.9745	0.983022	0.5475	0.820846	0.868	0.771744	0.9875	CDS Putative peptidoglycan binding domain 1:N-acetylmuramoyl-L-alanine amidase, family 2 4003820:4004605 forward MW:28455
RPA3540	1.198829	0.0295	1.224118	0.019	1.088891	0.117	1.681729	0.0005	2.116981	0.001	CDS putative cell filamentation protein 4005202:4005771 reverse MW:21494
RPA3541											CDS hypothetical protein 4005773:4005973 reverse MW:7785
RPA3542	0.891622	0.824	0.842328	0.98	0.810764	0.975	0.587337	0.9995	1.041571	0.3955	emrB1 putative multidrug resistance protein B (drug efflux transporter) 4006022:4007614 reverse MW:57751
RPA3543	0.918405	0.735	0.961705	0.7035	0.775222	0.968	0.949717	0.7245	1.345492	0.003	CDS possible multidrug resistance efflux pump 4007765:4009033 reverse MW:44537
RPA3544	0.856559	0.879	0.900485	0.8395	0.675769	0.9905	0.867643	0.897	1.775166	0	CDS transcriptional regulator, TetR family 4009215:4009865 forward MW:23264
RPA3546	1.007953	0.434	0.751697	0.9915	0.754095	0.9895	0.585774	0.9875	0.60877	0.995	CDS methyl-accepting chemotaxis receptor/sensory transducer 4011242:4013197 reverse MW:68350
RPA3547	1.022755	0.4375	1.202329	0.24	1.304998	0.0285					CDS hypothetical protein 4013379:4013627 reverse MW:8814
RPA3548	1.333638	0.0025	1.211185	0.0445	1.54728	0.0005	1.696778	0.003	1.163226	0.0945	CDS possible serine protease/outer membrane autotransporter 4013663:4016911 reverse MW:107610
RPA3549	0.862341	0.9435	0.879026	0.923	0.908156	0.882	0.821773	0.9445	0.721976	0.996	CDS possible hydrolase 4017089:4017727 forward MW:23190
RPA3550	0.512448	1	0.387497	0.9995	0.622022	0.979	0.261271	1	0.501359	0.9985	CDS Coenzyme B12-binding:Elongator protein 3/MiaB/NifB 4018092:4019861 forward MW:65641
RPA3551			0.901927	0.6345	1.105448	0.331	0.844681	0.745	1.0835	0.3065	CDS putative oxidoreductase, short-chain dehydrogenase/reductase family 4019858:4020577 forward MW:24926
RPA3552	0.626885	0.9725			0.920413	0.6525			0.625801	0.855	CDS putative short-chain dehydrogenase/reductase 4020574:4021392 forward MW:27696
RPA3553	1.011275	0.4555	0.929292	0.788	0.963913	0.651	0.910701	0.8065	1.193593	0.0535	CDS arsenite efflux pump ACR3 4021413:4022534 reverse MW:40264
RPA3554							0.685526	0.7465			arsC2 arsenate reductase 4022698:4023123 reverse MW:15434
RPA3555	1.063233	0.2355	0.963802	0.5835	0.902951	0.8485	0.80397	0.8145	0.897725	0.9015	arsC3 arsenate reductase 4023123:4023650 reverse MW:18919
RPA3556	1.277068	0.007	1.407191	0.0245	0.953098	0.7105	1.237922	0.09	1.537627	0.0055	arsR2 transcriptional regulator, ArsR family, ArsR2 4023643:4023999 reverse MW:12647
RPA3557	0.887959	0.841	0.710523	0.671	0.96626	0.5965			0.760596	0.7575	CDS Thiol-disulfide isomerase and thioredoxins 4024054:4024290 reverse MW:8079
RPA3558	0.86939	0.964	0.81948	0.9755	0.823326	0.953	0.711785	0.991	0.763235	0.997	CDS possible permease 4024302:4025351 reverse MW:36658
RPA3559	0.847276	0.8445			0.770811	0.9775			1.006912	0.4935	arsR3 transcriptional regulator, ArsR family, ArsR3 4025348:4025647 reverse MW:11223
RPA3560	1.336051	0.121			0.786915	0.75	0.960088	0.5565	1.266981	0.073	CDS DUF81 4025789:4026574 forward MW:26717
RPA3561	0.743166	0.93	0.715759	0.9815	0.742386	0.895	0.899518	0.7285	1.017824	0.4565	CDS transcriptional regulator, ArsR family 4026812:4027168 forward MW:13014
RPA3562	1.07847	0.1395	0.790109	0.973	1.121638	0.2325	0.964017	0.593	0.944946	0.739	CDS UbiE/COQ5 methyltransferase 4027158:4028009 forward MW:29656
RPA3563	1.137161	0.1215	1.373836	0.003	1.256681	0.0135	1.47676	0.006	1.284281	0.0305	CDS hypothetical protein 4028667:4029065 reverse MW:14404
RPA3564	0.82734	0.8995	1.055984	0.318	0.760412	0.978	0.55257	0.999	0.453751	0.992	CDS putative tyrosine phenol-lyase 4029316:4030764 reverse MW:53702
RPA3565	0.919088	0.784	1.723765	0.0035	0.483563	0.98	1.673655	0.038	0.84816	0.7705	CDS ErfK/YbiS/YcfS/YnhG 4031035:4031754 forward MW:25468
RPA3566	0.87364	0.771	0.426959	0.7785	1.067427	0.378			0.701515	0.947	CDS hypothetical protein 4031944:4032282 forward MW:11601
RPA3567	1.167336	0.0675	0.973571	0.5995	0.997573	0.5145	0.923428	0.789	1.074041	0.2265	CDS conserved hypothetical protein 4032439:4034001 forward MW:55899
RPA3568	2.721949	0.0005	3.139142	0.0125	3.235966	0	1.383898	0.023	3.315683	0.0015	CDS conserved unknown protein 4034096:4034635 reverse MW:18675
RPA3569											CDS hypothetical protein 4034923:4035465 reverse MW:18012
RPA3570	1.160053	0.096	0.919168	0.799	0.901287	0.744	1.08925	0.278	0.967791	0.6245	CDS two-component transcriptional regulator, winged helix family 4035633:4036355 forward MW:26563
RPA3571	0.8794	0.9275	1.130909	0.108	0.92413	0.8195	1.140765	0.3215	0.854143	0.9265	CDS two component sensor histidine kinase 4036352:4037686 forward MW:48262
RPA3572	1.071273	0.238	0.833188	0.976	0.965003	0.6915	0.72009	0.9925	0.68005	0.9985	CDS conserved hypothetical protein 4037705:4039183 reverse MW:52467
RPA3573	0.848731	0.91	1.087753	0.168	0.926532	0.7855	1.32049	0.0135	1.545098	0.001	thiO thiamine biosynthesis oxidoreductase thiO 4039635:4040612 forward MW:35908
RPA3574			1.021069	0.4325	0.886908	0.582	1.857	0.0015	1.202259	0.1365	thiS putative thiamin biosynthesis ThiS 4040603:4040800 forward MW:6958
RPA3575	0.894381	0.947	0.9985	0.5115	0.88142	0.8885	0.960337	0.6155	1.348541	0.0135	thiG thiamin biosynthesis ThiG 4041053:4041835 forward MW:27778
RPA3576	1.679179	0.002	1.878741	0.0025	1.633657	0.0035	2.181499	0.003	2.489459	0	thiE thiamin phosphate pyrophosphorylase 4041822:4042430 forward MW:21730
RPA3577	0.980646	0.574	1.030546	0.358	1.081078	0.202	1.248483	0.026	1.238339	0.0215	thiC thiamin biosynthesis protein thiC 4042665:4044665 forward MW:72751
RPA3578	1.352219	0.004	1.416172	0.002	1.296233	0.011	1.673335	0.0095	2.059482	0	CDS conserved hypothetical protein 4044836:4045711 forward MW:32879
RPA3579	1.42029	0.0115	1.81703	0.0025	1.406867	0.0055	2.451772	0.042	1.494242	0.005	CDS possible insertion element ISR1 hypothetical 10 KD protein A3 4045969:4046235 forward MW:9946
RPA3582			0.935801	0.69	0.723959	0.9705	1.012537	0.4565	0.696432	0.9705	CDS conserved hypothetical protein 4047439:4047969 reverse MW:18929
RPA3584	1.344015	0.0045	1.369065	0.005	1.422208	0.005	1.557471	0.0015	1.887713	0.0005	CDS hypothetical protein 4048474:4049253 forward MW:29192
RPA3585			0.741764	0.9715			0.936318	0.6015	1.475822	0.0495	CDS hypothetical protein 4049441:4049953 reverse MW:17344
RPA3586											CDS hypothetical protein 4050261:4050725 reverse MW:16768
RPA3587											CDS hypothetical protein 4051923:4052207 forward MW:10454
RPA3588	1.10134	0.1265	1.235592	0.0165	0.896382	0.845	1.069256	0.312	1.085543	0.1355	CDS possible FAD-dependent monooxygenase 4052583:4053875 reverse MW:45745
RPA3591	0.837834	0.965	0.77073	0.9595	1.042047	0.3525	0.638413	0.992	0.636744	0.9985	CDS Endoribonuclease L-PSP 4055350:4055733 forward MW:13647
RPA3592	0.894867	0.901	0.6846	0.999	0.880829	0.791	0.822293	0.948	0.983826	0.583	CDS hypothetical protein 4055953:4057032 forward MW:38262
RPA3593	0.822006	0.9125	0.932498	0.7595	1.177674	0.027	0.994216	0.5165	0.910805	0.8755	CDS Collagen triple helix repeat:Antifreeze protein, type I 4057138:4057776 forward MW:22070

RPA3595	1.092455	0.304	0.895427	0.894	1.318767	0.0145	1.006918	0.464	1.24196	0.013	CDS conserved hypothetical protein 4058240:4058869 forward MW:23099
RPA3596	0.852051	0.9665	0.792985	0.9945	0.921941	0.817	1.052421	0.2975	1.1577	0.083	CDS hypothetical protein 4058884:4060089 reverse MW:43359
RPA3597	1.101171	0.109	0.790642	0.975	0.716958	0.974	1.149034	0.2585	1.563605	0.0005	CDS conserved hypothetical protein 4060076:4061734 reverse MW:60237
RPA3598	0.845342	0.806	1.443876	0.014	0.827287	0.957	0.742925	0.988	0.675324	0.962	CDS methyl-accepting chemotaxis receptor/sensory transducer 4061895:4063706 forward MW:63004
RPA3599	1.014838	0.4575	1.061025	0.2765	1.006257	0.4745	1.900824	0.0165	1.929337	0	CDS hypothetical protein 4063844:4064386 forward MW:19312
RPA3600	1.524899	0.0155	1.203674	0.0335	1.715959	0.001	1.881408	0.0165	1.471414	0.0055	bfr bacterioferritin 4064442:4064924 reverse MW:18850
RPA3601	0.892358	0.8355	0.912145	0.7745	1.078414	0.2635	0.809373	0.8955	1.261598	0.016	CDS hypothetical protein 4065648:4066007 forward MW:12629
RPA3602	1.105074	0.183	1.093605	0.205	1.337042	0.069	0.851611	0.911	0.955029	0.6745	CDS unknown protein 4066228:4066512 forward MW:9663
RPA3603	0.726573	0.9975	0.742075	0.976	0.835728	0.9715	0.515282	0.999	0.724316	0.9895	CDS possible transglycosylase 4066589:4068463 reverse MW:68970
RPA3605	0.824848	0.9815	0.848901	0.925	1.139396	0.06	0.849911	0.884	0.863575	0.8715	CDS trans-aconitate methyltransferase 4068598:4069368 reverse MW:28758
RPA3606	1.142823	0.0355	0.995334	0.534	1.151673	0.039	1.087147	0.157	1.061282	0.2335	CDS hypothetical protein 4069410:4069688 forward MW:10488
RPA3608	1.010797	0.439	1.080107	0.17	1.093224	0.1075	1.325873	0.011	1.629998	0.0005	CDS PilT protein, N-terminal 4070229:4070630 forward MW:15016
RPA3609	0.783756	0.997	0.889784	0.9435	0.584086	0.995	0.734583	0.9925	0.917455	0.7865	CDS ABC transporter, ATPase component 4070637:4072286 reverse MW:61621
RPA3610	1.246837	0.1455	1.442942	0.02	1.705262	0.054	1.505834	0.009	1.093075	0.3095	CDS conserved hypothetical protein 4072527:4072727 forward MW:7765
RPA3611	0.87135	0.9045	0.847298	0.92	0.935473	0.689	0.668849	0.92	0.789074	0.9775	CDS ErfK/YbiS/YcfS/YnhG 4072807:4073691 reverse MW:30814
RPA3612	0.841924	0.9845	0.726829	0.998	0.945336	0.7185	0.799996	0.9005	0.90298	0.8755	CDS conserved hypothetical protein 4074440:4075474 forward MW:34382
RPA3613	0.808202	0.993	0.835969	0.9525	0.808939	0.981	0.697389	0.986	0.625288	0.9985	CDS putative thiosulfate sulfurtransferase 4075487:4076347 reverse MW:30216
RPA3614	0.711861	0.9935	0.896865	0.928	0.781831	0.9815	0.841953	0.813	0.581774	0.999	CDS conserved unknown protein 4076464:4076880 reverse MW:14979
RPA3615	1.216633	0.061	0.881817	0.9045	1.066048	0.268	1.202838	0.035	1.093041	0.147	CDS conserved unknown protein 4077026:4078201 reverse MW:45629
RPA3616	0.944133	0.817	0.951506	0.698	0.889048	0.8835	1.044751	0.3175	1.041668	0.324	CDS putative diguanylate cyclase (GGDEF) with PAS/PAC domain 4078368:4080302 forward MW:70310
RPA3617	1.086195	0.231	1.079979	0.3005	1.235803	0.0195	1.118843	0.2185	0.981731	0.5425	CDS conserved hypothetical protein 4080472:4080726 forward MW:8474
RPA3618	0.85625	0.9525	0.897757	0.921	0.883669	0.9355	0.769067	0.961	0.660925	0.999	CDS AAA ATPase 4080841:4081683 forward MW:32211
RPA3619	1.084866	0.2475	0.803655	0.9325	0.932453	0.7505	1.06838	0.318	0.954449	0.7425	vanA putative vanillate O-demethylase oxygenase, iron-sulfur subunit 4082101:4083144 forward MW:39031
RPA3620	0.864794	0.8295			0.898897	0.7565			1.014224	0.482	vanR transcriptional regulator VanR, GntR family 4083148:4083903 forward MW:27458
RPA3621	0.954464	0.661	0.865681	0.961	0.944596	0.735	0.790684	0.9315	0.746713	0.993	vanB putative vanillate O-demethylase oxidoreductase 4083934:4084926 forward MW:35685
RPA3622	0.79097	0.849	1.436402	0.004	1.27428	0.0785	1.25253	0.0525	0.754171	0.832	CDS hypothetical protein 4085029:4085313 reverse MW:10802
RPA3623	0.611809	0.9955	0.535725	0.9955	0.925542	0.7115	0.512355	0.987	0.50126	0.9995	CDS GCN5-related N-acetyltransferase 4085453:4086049 reverse MW:22387
RPA3624	0.874325	0.8915	0.68417	0.997	0.844339	0.951	0.706887	0.9875	0.543305	0.9965	CDS possible gluconolactonase precursor 4086198:4087127 reverse MW:32885
RPA3625	0.780419	0.982	0.675227	0.928	0.985327	0.5715	0.783036	0.851	0.630311	0.988	CDS Excinuclease ABC, C subunit, N-terminal 4087553:4088125 forward MW:21149
RPA3626	0.810414	0.983	0.756288	0.9975	0.861739	0.9125	0.55143	0.999	0.538445	1	CDS conserved unknown protein 4088910:4089164 reverse MW:9424
RPA3627	0.776471	0.9995	0.811103	0.9905	0.837358	0.955	1.330611	0.014	0.68188	0.9975	CDS putative glutathione peroxidase 4089161:4089637 reverse MW:17177
RPA3628	0.917462	0.788	0.718576	0.9915	0.937182	0.731	0.653361	0.977	0.614079	0.9995	CDS possible amidase 4089656:4091053 reverse MW:49305
RPA3629	0.656537	0.9595	0.439029	0.999	0.887242	0.74	0.577258	0.9655	0.705859	0.977	CDS conserved hypothetical protein 4091125:4091382 reverse MW:9824
RPA3630											CDS putative prolyl aminopeptidase 4091519:4092508 forward MW:35832
RPA3631	0.786725	0.985	0.636392	0.9995	0.786767	0.9925	0.609892	0.9985	0.71695	0.9985	CDS putative glucose dehydrogenase 4092518:4093291 reverse MW:26216
RPA3632	0.7872	0.8035	0.903424	0.778	1.039991	0.4145	1.072359	0.3375	0.66066	0.8725	CDS DUF24, predicted transcriptional regulator, related to MarR family 4093389:4093871 forward MW:17935
RPA3633	0.901265	0.884	0.890041	0.94	1.217088	0.0635	0.947532	0.7245	1.195151	0.027	CDS conserved hypothetical protein 4093891:4094565 forward MW:24131
RPA3634	0.988968	0.5915	1.031827	0.3115	1.089663	0.1825	0.891522	0.9005	0.784934	0.9925	tal putative Transaldolase Phosphoglucose isomerase 4094709:4097633 forward MW:104202
RPA3635	1.013381	0.452	1.121418	0.0545	1.209891	0.0885	1.047466	0.4105	0.903572	0.8835	gnd 6-phosphogluconate dehydrogenase 4097820:4098860 forward MW:37809
RPA3636	1.019033	0.438	1.07923	0.178	1.080104	0.16	0.894997	0.8485	0.795237	0.9	zwf putative glucose-6-phosphate 1-dehydrogenase 4098857:4100371 forward MW:56048
RPA3637	0.779482	0.9705	0.897851	0.878	1.029767	0.389	0.757928	0.9735	0.629122	0.999	pgl putative 6-phosphogluconolactonase 4100374:4101111 forward MW:26495
RPA3638	0.95025	0.669	0.971989	0.656	0.977481	0.575	0.596096	0.985	0.664526	0.9985	CDS thermoresistant gluconokinase 4101080:4101643 forward MW:20230
RPA3639	1.000708	0.495	0.992825	0.5255	0.843806	0.946	0.741087	0.981	0.678583	0.984	cof Cof-subfamily: Cof-like hydrolase 4101767:4102585 forward MW:29401
RPA3640	0.576383	0.998	0.806153	0.9675	0.680467	0.9785	0.715571	0.9835	0.732583	0.995	CDS Glycoside hydrolase, family 15 4102582:4104390 reverse MW:66781
RPA3641	0.706742	0.993	0.998271	0.514	1.031232	0.334	0.851385	0.8745	0.844447	0.92	malQ putative 4-alpha-glucanotransferase 4104395:4106347 reverse MW:72267
RPA3642	1.137585	0.1145	1.237005	0.022	1.173283	0.065	1.512492	0.005	1.623742	0.002	CDS putative alpha-amylase 4106445:4108511 forward MW:78391
RPA3643			1.251996	0.066	1.254402	0.1155	1.47503	0.023	1.664593	0.0045	CDS putative trehalose synthase 4108522:4111824 forward MW:125271
RPA3644	1.270267	0.0225	1.295848	0.02	1.224598	0.034	1.356732	0.0075	1.344798	0.008	glgB 1,4-alpha-glucan branching enzyme (glycogen branching enzyme) 4111821:4113971 forward MW:80566
RPA3645	1.43324	0.0015	1.756823	0.0095	1.408406	0.0035	1.591025	0.002	1.580957	0.0035	glgX probable glycosyl hydrolase 4114210:4116291 forward MW:78001
RPA3646	1.103558	0.18	1.291005	0.0255	0.98815	0.528	1.05723	0.3115	1.182951	0.0605	CDS putative maltooligosyltrehalose trehalohydrolase 4116288:4118054 forward MW:65632
RPA3647	1.722729	0.001	2.847764	0.004	1.781193	0.0045	1.502426	0.015	2.191962	0.0085	CDS putative glycosyl hydrolase 4118054:4120840 forward MW:103366
RPA3648	1.191365	0.301	1.060843	0.3625	1.145227	0.134	1.289829	0.105	0.803791	0.907	CDS conserved hypothetical protein 4121257:4121565 reverse MW:11538
RPA3649	0.579983	0.9495	1.291671	0.017	0.576508	0.975	1.165219	0.223	0.610815	0.9765	CDS conserved hypothetical protein 4121610:4121906 forward MW:10118
RPA3650	1.29484	0.0255	1.485761	0.003	1.351235	0.0045	1.659499	0.0005	1.770896	0.001	CDS ATP-dependent DNA ligase 4122046:4124790 reverse MW:99963
RPA3651	1.03673	0.3805	1.62443	0.002	1.239232	0.052	1.196801	0.131	1.580964	0.0005	CDS Ku domain 4124924:4125805 forward MW:32802
RPA3652	3.808115	0	8.859026	0.0005	3.564922	0.0005			1.884621	0.003	CDS conserved hypothetical protein 4126028:4126426 reverse MW:13802
RPA3653											CDS Protein of unknown function UPF0033 4126487:4126747 reverse MW:9240
RPA3654	1.153458	0.1385	0.897615	0.816	0.889008	0.747	0.866084	0.665	0.607753	0.9995	CDS putative molybdopterin-guanine dinucleotide biosynthesis protein A 4126878:4127498 forward MW:21766
RPA3655	1.144251	0.173	0.656448	0.98	1.161256	0.0445	0.824406	0.781	0.545132	0.998	CDS probable alcohol dehydrogenase 4127608:4128660 reverse MW:36512
RPA3656	0.988731	0.5405	0.550142	0.994	1.052655	0.2585	0.787735	0.8235	0.534274	0.9985	CDS conserved hypothetical protein 4128739:4129728 reverse MW:34837
RPA3657	1.147915	0.351	0.493085	0.975	0.711638	0.827			0.515149	0.995	fadD2 putative long-chain fatty acid-CoA ligase 4129813:4131375 forward MW:56600
RPA3658	1.179791	0.04	1.497852	0.003	1.017056	0.4505	1.141921	0.2045	0.858789	0.971	ureF possible urease accessory protein UreF 4131439:4132374 reverse MW:33012
RPA3659	1.029165	0.3605	0.963804	0.676	0.882339	0.9165	1.009848	0.4485	0.666259	1	CDS DUF176 4132804:4133103 reverse MW:10962
RPA3660	1.529266	0.0175	1.205299	0.0655	1.505927	0.013	1.580902	0.008	1.360918	0.058	ureC urease alpha subunit 4133317:4135029 reverse MW:60573
RPA3661					1.186956	0.2145	0.874444	0.6845			CDS Metal dependent phosphohydrolase 4135026:4135562 reverse MW:19637
RPA3662	1.206759	0.0345	0.978212	0.5755	1.04249	0.358	1.012278	0.4805	0.741811	0.994	ureB urease beta subunit 4135562:4135867 reverse MW:11195
RPA3663	1.191529	0.0405	0.948792	0.744	1.081332	0.2295	1.29952	0.0275	1.092054	0.1995	ureA urease gamma subunit 4136029:4136331 reverse MW:11088
RPA3664	1.493554	0.0035	1.575832	0.0035	1.735186	0.001	1.710244	0.003	1.697008	0.0015	ureD possible urease accessory protein D 4136378:4137295 reverse MW:32359
RPA3665	1.663608	0.0005	1.619235	0	1.428881	0.0045	1.737233	0.0005	1.51398	0.0035	CDS possible ATP-binding component of ABC transporter 4137494:4138189 reverse MW:25070
RPA3666	3.432519	0.0005	3.179069	0.0005	5.539097	0.0005			2.583009	0.002	CDS possible ATP-binding component of ABC transporter 4138409:4139173 reverse MW:28271
RPA3667	2.103008	0.0565	2.42292	0	2.448082	0	1.4562	0.02	1.49341	0.0055	CDS possible permease of ABC transporter 4139170:4140369 reverse MW:43144
RPA3668	4.039504	0	4.080741	0.0005	4.489759	0	5.813304	0	3.500685	0	CDS putative ABC transporter system permease component, possible fused protein 4140443:4142056 reverse MW:56502
RPA3669	9.023458	0	4.599853	0.0005	7.754146	0	10.17232	0	5.150483	0	CDS putative urea short-chain amide or branched-chain amino acid uptake ABC transporter periplasmic solute-binding protein precursor 4142166:4143488 reverse MW:48065
RPA3670	0.56607	0.982	1.185871	0.193	0.576929	0.9225	0.825544	0.7435	1.101638	0.339	CDS putative ATP-dependent RNA helicase 4143976:4145400 forward MW:51440
RPA3671	0.653577	0.9485	1.127311	0.0755	0.707073	0.9185	0.858728	0.828	0.923393	0.6975	infA translation initiation factor if-1 (infA) 4145425:4145703 forward MW:10577
RPA3672	0.960157	0.6575	0.949705	0.6295	0.968932	0.624	1.279626	0.034	0.903007	0.689	cspA5 cold shock DNA binding protein 4145943:4146197 forward MW:9073
RPA3673	1.205684	0.091	1.251235	0.0325	0.869758	0.9435	1.892561	0.0005	1.691792	0.0045	CDS conserved unknown protein 4146311:4146937 reverse MW:22563

RPA3674	1.550394	0.001	1.537461	0.001	1.077132	0.169	1.696473	0.001	1.40293	0.02	CDS conserved hypothetical protein 4146950:4147483 reverse MW:19622
RPA3675	1.754858	0.0125	1.909968	0	1.787249	0.0005	3.162846	0	1.619772	0.038	CDS Flp/Fap pilin component 4148391:4148555 forward MW:5550
RPA3676	1.317808	0.0045	1.792941	0.007	1.077847	0.267	1.238277	0.024	1.292007	0.0385	CDS putative type IV prepilin peptidase, cpaA 4148883:4149407 forward MW:18714
RPA3677	1.009353	0.4385	0.829181	0.9805	0.753626	0.932	0.935926	0.748	0.916001	0.834	CDS conserved hypothetical protein 4149514:4150095 forward MW:19962
RPA3678	1.21811	0.0695	0.913219	0.88	0.75874	0.9935	0.942067	0.7665	1.10644	0.124	CDS putative exporter protein, cpaC 4150110:4151552 forward MW:50847
RPA3679	1.23018	0.035	0.990166	0.548	0.909659	0.8585	1.116952	0.125	1.037522	0.3205	CDS possible pilus assembly protein cpaD 4151572:4152300 forward MW:26174
RPA3680	1.294357	0.033	1.066117	0.16	0.890617	0.8955	1.043951	0.3025	1.158196	0.0305	CDS possible pilus assembly protein cpaE 4152297:4153568 forward MW:45209
RPA3681	0.993245	0.5215	0.858239	0.9215	0.733171	0.9785	1.004709	0.489	0.909409	0.8285	CDS secretory protein kinase, cpaF 4153661:4155043 forward MW:50573
RPA3682	1.218033	0.0205	1.209121	0.0115	0.895733	0.895	1.057692	0.2705	1.10454	0.0995	CDS conserved unknown protein 4155056:4156030 forward MW:35279
RPA3683	1.11945	0.094	1.007604	0.472	0.983248	0.5615	0.967872	0.6445	0.965845	0.6875	CDS conserved hypothetical protein 4156039:4157013 forward MW:36274
RPA3684	1.069153	0.294	0.639231	0.9755	0.717993	0.9545	0.766946	0.834	0.709506	0.9585	CDS TPR repeat 4157037:4157846 reverse MW:28561
RPA3685	0.705256	0.9715	0.580673	1	0.828435	0.952	0.519496	0.995	0.63927	0.9985	CDS leucine aminopeptidase 4157949:4159331 forward MW:48782
RPA3686	0.70571	0.9625	0.948186	0.703	0.967996	0.596	0.847645	0.8515	1.050953	0.347	CDS NLP/P60 4159324:4160169 forward MW:30204
RPA3687	0.809072	0.9555	0.865097	0.9545	0.938431	0.698	0.680146	0.9805	0.61623	0.9985	CDS putative MutT/ADP-ribose pyrophosphatase 4160153:4160791 reverse MW:23203
RPA3688	0.812074	0.9885	0.780053	0.989	0.947844	0.709	0.717399	0.9885	0.772981	0.9845	CDS peptide ABC transporter, ATP-binding protein 4160799:4162436 reverse MW:59259
RPA3689	0.884629	0.894	0.889473	0.874	1.040922	0.2975	0.676929	0.995	0.767383	0.9935	CDS peptide ABC transporter, permease protein 4162442:4163620 reverse MW:43430
RPA3690	0.710832	0.9935	0.92346	0.849	0.938755	0.718	0.800299	0.9655	0.811354	0.9885	CDS peptide ABC transporter, permease protein 4163620:4164729 reverse MW:40862
RPA3691	0.813325	0.9445	0.899936	0.925	0.907305	0.748	0.779537	0.978	0.843098	0.947	CDS putative ABC transporter, solute-binding protein 4164731:4166596 reverse MW:68919
RPA3692	0.798682	0.9735	0.713875	0.997	0.868516	0.9395	0.755974	0.9735	0.689744	0.997	CDS putative peptide ABC transporter, periplasmic peptide-binding protein 4166611:4168470 reverse MW:69716
RPA3693	1.71626	0.007	1.49878	0.001	2.08608	0.002	2.312033	0.019	2.007049	0.0005	CDS putative cytochrome c 4168719:4169273 reverse MW:19643
RPA3694	0.74676	0.972	1.011717	0.4255	0.636492	0.9995	0.781205	0.95	0.921863	0.833	kdsB 3-deoxy-manno-octulosonate cytidylyltransferase 4169473:4170210 forward MW:26269
RPA3695	0.716229	0.9925	1.032266	0.342	0.545924	0.997	0.635287	0.993	0.774066	0.9435	CDS chorismate mutase/prephenate dehydratase 4170282:4171124 forward MW:30620
RPA3696			0.695096	0.9875	0.754097	0.837	0.910138	0.7135	0.777297	0.9735	CDS transcriptional regulator, TetR family 4171164:4171790 reverse MW:22481
RPA3697											emrA putative multidrug resistance protein 4171914:4173092 forward MW:41564
RPA3698			0.949506	0.632	0.629661	0.978	0.755879	0.7915	0.752099	0.917	emrB2 putative drug efflux pump, Major Facilitator Superfamily (MFS) 4173089:4174621 forward MW:53965
RPA3699									1.084403	0.446	CDS possible iron-chelator utilization protein 4174638:4175366 forward MW:26576
RPA3700	1.209854	0.0225	1.278351	0.0095	1.161233	0.0675	1.058173	0.301	1.290114	0.0485	CDS Bacterial luciferase 4175434:4176450 reverse MW:37092
RPA3701	0.307569	1	0.432444	1	0.572321	0.962	0.524822	0.981	0.498493	0.999	metF putative 5,10-methylenetetrahydrofolate reductase 4176861:4177748 forward MW:32336
RPA3702	0.805429	0.929	1.012901	0.431	0.664141	0.999	1.024238	0.4195	0.636385	0.991	metH methionine synthase 4177761:4181642 forward MW:140068
RPA3703	0.587936	0.998	0.884856	0.798	0.758592	0.963	0.669642	0.9855	0.821647	0.911	CDS hypothetical protein 4181818:4182099 forward MW:9630
RPA3705			0.814429	0.876	1.058699	0.4185	1.083659	0.2565	0.906916	0.7835	glpK glycerol kinase 4183381:4184883 reverse MW:53763
RPA3706	1.047133	0.2425	1.176415	0.026	0.91837	0.8325	1.24016	0.033	1.293636	0.007	nasT putative two-component response regulator:antitermination factor NasT 4185092:4185676 forward MW:21640
RPA3707	0.98122	0.549	1.019033	0.4505	0.727981	0.9365	0.956186	0.627	0.919703	0.7955	CDS possible nitrate transporter component, nrtA 4185673:4186833 forward MW:41053
RPA3708					0.520074	0.99			0.790963	0.737	CDS Globin-like protein 4186852:4187292 forward MW:16517
RPA3709			1.13067	0.3155			4.824885	0.0005	1.37439	0.1	CDS possible hemoprotein 4187646:4188071 forward MW:15459
RPA3710	2.563321	0.0125	3.364279	0			13.9351	0.0005	6.323492	0.002	nirA possible ferredoxin-nitrite reductase 4188114:4189886 forward MW:63846
RPA3711							33.31271	0.002	4.273198	0.001	CDS possible sulfite reductase (NADPH) 4189883:4191502 forward MW:58387
RPA3712	0.874669	0.9025	0.92182	0.6755					0.601947	0.994	pimE pseudogene short chain dehydrogenase 4191642:4192413 reverse MW:26587
RPA3713	0.836025	0.9675	0.801972	0.947	0.957142	0.707	0.685714	0.932	0.803171	0.9835	pimD pimeloyl-CoA dehydrogenase (small subunit) 4192563:4193705 reverse MW:40482
RPA3714	0.972388	0.6445	1.001271	0.4965	1.028884	0.37	0.645836	0.994	0.912219	0.884	pimC pimeloyl-CoA dehydrogenase (large subunit) 4193874:4195064 reverse MW:44541
RPA3715	0.956183	0.6565	0.937151	0.745	0.924609	0.777	0.79598	0.8975	0.799594	0.989	pimB acetyl-CoA acetyltransferase 4195279:4196466 reverse MW:41126
RPA3716	1.287858	0.004	0.963462	0.5715	0.922565	0.8655	0.610748	0.997	1.090071	0.2075	pimA pimeloyl-CoA ligase 4196498:4198156 reverse MW:60028
RPA3717	0.896553	0.877	0.639196	0.971	0.817077	0.9825	0.486807	0.9925	0.651999	0.9925	pimF enoyl-CoA hydratase 4198335:4200434 reverse MW:73791
RPA3718	1.003944	0.48	0.504901	0.992	1.050445	0.2955	0.545199	0.9995	0.897577	0.833	CDS transcriptional regulator, IclR family 4200567:4201433 forward MW:31442
RPA3719	1.180289	0.2115	0.769359	0.9305	1.255658	0.019	0.764702	0.967	0.737879	0.999	ilvG putative high-affinity branched-chain amino acid transport system ATP-binding protein 4201464:4202264 forward MW:28914
RPA3720	1.067227	0.328	0.682735	0.9695	1.137766	0.0495	0.631034	0.9825	0.595204	1	ilvF putative branched-chain amino acid transport system ATP-binding protein 4202261:4202974 forward MW:25964
RPA3721	1.050256	0.3595	0.786885	0.8755	1.039511	0.329	0.636949	0.9725	0.579944	1	CDS possible ABC transporter, permease protein 4202985:4203863 forward MW:30842
RPA3722	0.951903	0.787	0.935019	0.8275	1.115682	0.0995	0.880116	0.911	0.888663	0.862	ilvM putative branched-chain amino acid transport system permease protein 4203866:4204885 forward MW:35921
RPA3723	1.593004	0.103	0.743142	0.9235	1.736017	0.0005	1.070634	0.3265	0.966781	0.602	CDS possible leucine/isoleucine/valine-binding protein precursor 4205084:4206319 forward MW:44336
RPA3724	1.094239	0.4025	0.728591	0.99	0.974513	0.589	1.005083	0.4715	0.776814	0.825	ilvK possible high-affinity leucine-isoleucine-valine transport system; periplasmic binding protein 4206500:4207732 forward MW:44975
RPA3725	0.898587	0.8595	0.81685	0.9445	0.797369	0.9695	0.899949	0.788	0.932438	0.753	ilvJ possible leucine/isoleucine/valine-binding protein precursor 4208080:4209309 forward MW:44653
RPA3726	3.051251	0.0015	4.324252	0.0055	2.652241	0.001	2.01597	0.002	2.628948	0.001	CDS conserved unknown protein 4209434:4209934 reverse MW:18433
RPA3727	0.995358	0.523	1.037231	0.3365	1.025349	0.3955	0.821888	0.955	0.897171	0.886	CDS CorA Metal Ion (Mg2+/Co2+) transporter (MIT) family protein, 4210179:4211219 forward MW:37743
RPA3728	1.004122	0.467	0.882767	0.908	0.944345	0.774	0.973697	0.602	1.00138	0.4955	CDS conserved unknown protein 4211408:4213420 forward MW:72032
RPA3729	0.978698	0.597	0.747837	0.9935	0.961478	0.6605	0.838188	0.821	0.711171	0.981	CDS hippurate hydrolase 4213681:4214853 reverse MW:41534
RPA3730	1.249799	0.0545	0.983806	0.5475	0.875675	0.9375	1.044545	0.403	0.850485	0.9615	CDS GMC-type oxidoreductase 4214978:4216597 forward MW:58983
RPA3731	0.89573	0.696	1.176216	0.1155	0.792197	0.7665	1.095276	0.325	1.168824	0.0795	CDS Alpha/beta hydrolase fold:Esterase/lipase/thioesterase, active site 4216597:4217499 forward MW:32817
RPA3732	0.755812	0.993	0.752412	0.9955	0.707532	0.9955	0.753069	0.9935	0.773362	0.9905	argD1 putative N-acetylornithine aminotransferase 4217524:4218915 reverse MW:50389
RPA3733	0.919083	0.725	1.139271	0.0405	0.854219	0.9295	0.796511	0.9745	1.000085	0.5125	CDS conserved unknown protein 4219247:4221859 reverse MW:92901
RPA3734	1.005744	0.4675	1.265348	0.011	0.844801	0.93	0.980033	0.5495	1.151456	0.0535	lytB1 penicillin tolerance protein 4222189:4223109 forward MW:32905
RPA3735	1.296119	0.0025	1.296809	0.0115	1.09586	0.115	1.129857	0.1845	1.321375	0.028	CDS conserved unknown protein 4223149:4224309 forward MW:43197
RPA3736	0.847708	0.9205	0.89981	0.8855	0.793239	0.969	0.818964	0.9125	0.834188	0.942	pstS2 putative phosphate transport system substrate-binding protein 4224384:4225388 reverse MW:35006
RPA3737	1.254068	0.018	1.15713	0.052	1.183479	0.0585	1.552984	0.005	1.556833	0.002	CDS putative phosphonoacetate hydrolase 4225422:4226666 reverse MW:44724
RPA3738	1.757754	0	2.102858	0.0095	1.956041	0.0005	3.621513	0.001	2.18359	0	CDS transcriptional regulator, LysR family 4226824:4227714 forward MW:33303
RPA3739	0.992448	0.535	0.894097	0.8745	1.221161	0.0205	1.221124	0.056	1.131298	0.213	CDS unknown protein 4227805:4228548 reverse MW:25770
RPA3740	1.072244	0.3375	0.843973	0.9815	1.10923	0.151	1.21314	0.0395	1.19192	0.085	sqhC squalene-hopene-cyclase 4228545:4230506 reverse MW:72648
RPA3741	0.837377	0.919	0.997694	0.489	0.52409	0.9885	0.617268	0.9405	0.945602	0.6055	CDS putative oxidoreductase 4230540:4231796 reverse MW:43828
RPA3742	0.762276	0.9185	1.08222	0.178	0.553952	0.997	0.662326	0.9875	0.907938	0.7325	CDS putative poly-isoprenyl transferase 4231796:4232635 reverse MW:30905
RPA3743	0.734832	0.9935	1.115656	0.103	0.527706	0.9975	0.615276	0.993	0.911276	0.7205	CDS possible phytoene synthase-related protein 4232632:4233510 reverse MW:32830
RPA3744	0.839947	0.9005	0.982389	0.5445	0.823544	0.9005	0.804212	0.9165	0.829368	0.9325	CDS conserved unknown protein 4233715:4233954 reverse MW:8668
RPA3745	0.691442	0.966	0.672905	0.958	0.757736	0.965	0.542028	0.997	0.584611	0.993	CDS unknown protein 4234344:4234847 forward MW:16958
RPA3746	0.631926	0.9985	0.644463	0.9955	0.870697	0.919	0.512407	0.999	0.594714	1	CDS possible RND Superfamily transporter 4234942:4237311 reverse MW:85216
RPA3747	0.883418	0.645			0.792062	0.928	0.951156	0.567	0.796155	0.887	eutC putative ethanolamine ammonia-lyase light chain 4237519:4238286 reverse MW:25917
RPA3748	1.718553	0.001	2.5181	0.002	1.934626	0	1.609652	0.031	2.36012	0	CDS Elongator protein 3/MiaB/NifB 4238294:4239877 reverse MW:60115
RPA3749	1.447445	0.007	1.16654	0.161	1.729585	0.0035	2.359815	0.006	1.492437	0.0195	eutB ethanolamine ammonia-lyase large subunit 4240105:4241487 reverse MW:49072
RPA3750											CDS methyl-accepting chemotaxis receptor/sensory transducer 4241549:4243252 reverse MW:58938
RPA3751	0.833687	0.921	0.401863	0.9625	0.803441	0.8475			0.77911	0.8915	CDS unknown protein 4243306:4243761 reverse MW:16293

RPA3752	0.921012	0.8275	0.892646	0.9215	1.033736	0.309	0.838866	0.935	0.929279	0.8265	CDS Transglutaminase-like domain 4243965:4244843 reverse MW:31882
RPA3753	1.239082	0.069	0.818086	0.962	1.154178	0.1215	1.076773	0.256	1.242009	0.0195	CDS DUF404 4244840:4247341 reverse MW:90965
RPA3754	1.240544	0.0385	1.161357	0.0715	1.702366	0.0005	2.56138	0	1.786368	0.016	CDS Transglutaminase-like domain 4247367:4250762 reverse MW:126232
RPA3755	0.636571	0.9975	0.788786	0.9755	0.856309	0.925	0.59509	1	0.287297	0.998	hpcH putative 2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase 4251014:4251790 reverse MW:27865
RPA3756	0.600071	0.9985	0.561349	0.993	1.122487	0.127	0.464265	0.998	0.262578	0.9995	CDS malate dehydrogenase-like protein 4251974:4253059 reverse MW:37744
RPA3757	0.447967	0.9935	0.331331	0.9945	0.930386	0.757	0.438634	0.987	0.186866	1	CDS transcriptional regulator, MarR family 4253100:4253639 reverse MW:19988
RPA3758											hpcG 2-oxo-hepta-3-ene-1,7-dioate hydratase 4253885:4254691 forward MW:28820
RPA3759	0.888569	0.8795	0.715802	0.995	0.980439	0.5865	0.688386	0.993	0.666073	0.999	hpcD putative 5-carboxymethyl-2-hydroxymuconate isomerase 4254712:4255110 forward MW:14728
RPA3760	1.021178	0.4655	0.458971	0.996	0.817992	0.9555	0.62996	0.961	0.530299	0.996	hpcC 5-carboxy-2-hydroxymuconate semialdehyde dehydrogenase 4255103:4256644 forward MW:54556
RPA3761	1.153075	0.2965	0.708331	0.98	1.000542	0.489	0.867925	0.906	0.657943	0.9965	CDS putative catechol 2,3-dioxygenase 4256841:4257818 forward MW:37237
RPA3762	1.782506	0.007	1.532124	0.0125	1.152271	0.119	1.516327	0.016	1.46487	0.0065	CDS putative 2-oxo-3-ene-1,7-dioic acid hydratase 4257949:4258821 forward MW:31685
RPA3763	0.935336	0.712	1.056033	0.3105	0.630282	0.9975	0.55577	0.995	0.625511	0.993	ilvB putative acetolactate synthase large subunit 4258850:4260475 forward MW:57644
RPA3764	1.135782	0.057	0.867102	0.8675	0.921202	0.8805	0.811557	0.938	0.794208	0.8585	CDS putative 2Fe:2S ferredoxin 4260666:4261754 reverse MW:39517
RPA3766	0.962103	0.5545							0.661706	0.977	paaC phenylacetic acid degradation protein paaC 4262260:4263036 reverse MW:28917
RPA3767	1.008732	0.463	0.661994	0.9955	1.255433	0.274	0.906295	0.72	0.811597	0.9025	paaB phenylacetic acid degradation protein paaB 4263153:4263440 reverse MW:10517
RPA3768	1.054971	0.259	0.849109	0.9005	1.055573	0.3885	1.190868	0.1505	1.189428	0.093	paaA phenylacetic acid degradation protein paaA 4263613:4264596 reverse MW:36958
RPA3769	0.945449	0.7735	0.753163	0.992	0.897047	0.862	1.2124	0.0625	0.94129	0.7805	CDS probable transcriptional regulator, TetR family 4264719:4265399 forward MW:24805
RPA3770	0.887411	0.5685	2.438737	0.0005	1.044339	0.3905	2.163027	0.0025	2.936101	0.001	CDS conserved unknown protein 4265634:4266137 reverse MW:18046
RPA3771	1.143433	0.0875	1.248011	0.188	1.100287	0.177	1.241196	0.264	1.132224	0.1655	CDS unknown protein 4266349:4266669 reverse MW:11317
RPA3772	0.931001	0.792	1.315649	0.0245	1.063756	0.2125	1.145773	0.132	1.195272	0.0335	CDS conserved hypothetical protein 4266718:4267509 reverse MW:28803
RPA3773	1.048561	0.3315	0.775366	0.979	1.023622	0.434	1.275026	0.037	1.000691	0.5045	CDS conserved unknown protein 4267528:4267782 reverse MW:9575
RPA3774	0.763941	0.9975	0.64316	0.992	1.440177	0.003	1.099722	0.284	0.759903	0.9495	CDS possible D-amino-acid dehydrogenase , 4267873:4269126 reverse MW:45422
RPA3775	0.708246	0.9975	0.725596	0.9965	0.808139	0.959	0.606465	0.9985	0.678616	0.936	CDS putative RND efflux transporter 4269405:4272509 reverse MW:111445
RPA3776	0.781437	0.983	0.848115	0.973	0.821254	0.9725	0.688979	0.9945	0.936423	0.742	CDS possible RND efflux membrane fusion protein precursor 4272651:4273844 reverse MW:42482
RPA3777	0.84913	0.872	1.333795	0.0085	0.854786	0.818	1.228019	0.0685	1.440851	0.004	CDS possible transcriptional regulator, TetR family 4273846:4274547 reverse MW:25511
RPA3778	1.036666	0.414	0.863903	0.952	0.946469	0.7775	0.747057	0.995	0.718719	0.9975	CDS putative cytochrome p450-like enzyme 4274767:4275987 forward MW:44208
RPA3779	0.813344	0.996	0.628268	0.999	0.961411	0.6445	0.643133	0.997	0.794997	0.9785	CDS conserved hypothetical protein 4276159:4277718 forward MW:56053
RPA3780	0.81918	0.9805	0.703333	0.9805	0.895379	0.78	0.854148	0.7965	1.002097	0.4925	CDS hypothetical protein 4277730:4278602 reverse MW:31423
RPA3781	1.017438	0.389	0.969416	0.6445	0.782159	0.956	1.290509	0.0325	1.074572	0.168	yihV possible sugar kinase 4278937:4279830 forward MW:32645
RPA3782	0.840985	0.944	0.896899	0.937	0.639342	0.9975	0.719543	0.9845	0.766329	0.9845	CDS putative rubredoxin reductase 4279934:4281151 reverse MW:43680
RPA3783	0.696633	0.977	0.760955	0.9715	0.525456	0.999	0.532405	0.999	0.569042	0.997	CDS Glycosyl transferase, family 39 4281276:4282772 reverse MW:53690
RPA3784	0.778402	0.979	0.956103	0.723	0.671072	0.9965	0.763349	0.989	0.791914	0.979	CDS putative dolichol-phosphate mannosyltransferase 4282780:4283916 reverse MW:41282
RPA3785	0.85455	0.9485	0.991631	0.5395	0.896889	0.7935	4.971918	0	2.761156	0.0005	CDS DUF72 4284169:4284975 forward MW:30316
RPA3786	0.648552	1	0.781583	0.9615	0.840652	0.885	0.832983	0.8835	0.409027	0.999	CDS unknown protein 4285121:4285378 forward MW:9335
RPA3787	0.581325	0.969	1.18737	0.0465	0.861742	0.7575	1.43289	0.0345	0.627917	0.999	CDS hypothetical protein 4285476:4286378 forward MW:32318
RPA3788	0.936715	0.755	1.165376	0.056	1.040228	0.2805	0.900779	0.776	0.999505	0.505	CDS putative ABC transporter, ATP-binding protein 4286411:4287583 reverse MW:42709
RPA3789	1.116842	0.075	1.207297	0.016	0.877498	0.884	1.080777	0.161	0.982838	0.576	CDS putative ATP-binding component of a transport system 4287580:4288533 reverse MW:34560
RPA3790	1.387177	0.002	1.199964	0.0315	0.776324	0.984	0.986907	0.551	0.923349	0.7865	CDS putative efflux protein 4288530:4289333 reverse MW:28841
RPA3791	1.389709	0.009	1.18778	0.1425	0.775433	0.9655	1.221915	0.11	1.373511	0.0115	CDS probable transcriptional regulator, TetR family 4289330:4290046 reverse MW:25498
RPA3792	0.696976	0.988	0.864925	0.9055	0.666616	0.997	0.750751	0.982	0.585635	0.996	CDS putative diguanylate cyclase (GGDEF) 4290117:4291256 reverse MW:41161
RPA3793	0.764386	0.9875	0.70602	0.996	0.61857	0.9995	0.618348	0.997	0.576812	0.999	CDS conserved hypothetical protein 4291644:4292054 reverse MW:14671
RPA3794			0.630263	0.9845			0.592777	0.9745			CDS conserved hypothetical protein 4292116:4292460 reverse MW:11820
RPA3795			0.662294	0.936			0.671625	0.9675	0.471651	0.969	CDS putative enoyl-CoA hydratase 4292609:4293361 reverse MW:26389
RPA3796											CDS transcriptional regulator, LysR family 4293461:4294291 forward MW:29349
RPA3797	0.879133	0.9225	0.547496	0.996	0.889526	0.7035	0.514399	0.9985	0.611791	0.994	CDS conserved hypothetical protein 4294303:4295904 reverse MW:54907
RPA3798	0.884924	0.935	0.753109	0.9955	0.972522	0.6425	0.612606	0.997	0.722201	0.9945	CDS conserved unknown protein 4295901:4296602 reverse MW:24649
RPA3799	0.899276	0.8165	0.813122	0.982	0.911876	0.8555	0.781999	0.9705	0.879183	0.9455	CDS DUF182 4296633:4296959 reverse MW:11293
RPA3800	0.989412	0.551	0.897206	0.891	0.93853	0.7275	0.902397	0.842	0.937666	0.7455	CDS conserved hypothetical protein 4296995:4298212 reverse MW:45509
RPA3801	0.861648	0.883	0.718112	0.992	0.961262	0.618	0.734669	0.982	0.659877	0.99	CDS MoxR-like ATPases 4298538:4299440 reverse MW:33063
RPA3802	0.832934	0.9655	0.650395	0.994	0.906407	0.8435	0.699786	0.993	0.612854	0.999	CDS carbon monoxide dehydrogenase medium subunit 4299460:4300266 reverse MW:28395
RPA3803	0.863283	0.9075	0.755089	0.9875	0.94708	0.6905	0.761223	0.9835	0.692779	0.9985	CDS carbon-monoxide dehydrogenase small subunit 4300342:4300827 reverse MW:17157
RPA3804	1.125334	0.2175	0.834758	0.968	1.238521	0.058	1.023676	0.4235	1.054959	0.283	CDS conserved unknown protein 4301003:4301467 reverse MW:16028
RPA3805	0.949463	0.7305	0.832969	0.926	0.949474	0.677	1.141574	0.2005	0.992195	0.5435	CDS hypothetical protein 4301663:4302190 reverse MW:18818
RPA3806	1.048964	0.249	1.0683	0.1715	0.994022	0.5105	1.13662	0.093	1.186187	0.031	livH permease of ABC transporter,putatively for branched chain amino acuds 4303024:4303941 forward MW:32972
RPA3807	1.526255	0.002	1.524667	0.0015	1.177862	0.0645	1.894227	0.0025	1.766412	0.001	livM putative permease of ABC transporter (high-affinity branched-chain amino acid transport) 4303954:4305285 forward MW:47373
RPA3808	1.37584	0.003	1.276277	0.0095	1.17337	0.0305	1.816235	0.0025	1.571155	0.002	livG ATP-binding component of ABC transporter (putative for high-affinity branched-chain amino acid transport) 4305282:4306118 forward MW:30451
RPA3809	1.322949	0.0695	0.981363	0.56	1.005611	0.4875	1.164715	0.2365	0.931787	0.707	livF ATP-binding component of ABC transporter (putatively for branched chain amino acids) 4306255:4306995 forward MW:26389
RPA3810	1.057318	0.332	0.862323	0.922	1.098231	0.1115	1.234843	0.0295	1.304277	0.019	livK putative periplasmic binding protein of ABC transporter 4307174:4308280 forward MW:39663
RPA3811	0.961326	0.6095	0.898393	0.8085	1.232899	0.114	1.439236	0.01	1.514115	0.0135	CDS Excinuclease ABC, C subunit, N-terminal 4308492:4308779 reverse MW:11282
RPA3812	0.841581	0.9335	0.781633	0.9845	0.907608	0.8505	0.564691	0.9985	0.619721	0.996	CDS putative holocytochrome c synthase 4309058:4309792 reverse MW:25390
RPA3813	0.648118	0.999	0.59147	0.998	0.781955	0.992	0.649231	0.995	0.560086	0.998	CDS Peptidase family T4 4309894:4310943 forward MW:35420
RPA3814	0.759025	0.998	0.761495	0.995	0.758744	0.9755	0.830116	0.865	0.779232	0.988	CDS Calcium-binding EF-hand 4311084:4311854 reverse MW:25351
RPA3815	0.95589	0.751	1.02865	0.361	0.737746	0.9905	0.801319	0.9705	0.853907	0.9585	cbbE, rpe, ppe ribulose-5-phosphate-3-epimerase 4312124:4312822 forward MW:24279
RPA3816	0.817425	0.957	0.823363	0.939	0.875552	0.7855	0.86248	0.8585	0.644617	0.9525	CDS hypothetical protein 4312829:4313380 reverse MW:20164
RPA3817	1.002378	0.4975	1.008647	0.455	0.70767	0.9885	0.902126	0.8615	1.054487	0.328	purB adenylosuccinate lyase 4313465:4314772 forward MW:48906
RPA3818	0.566518	0.997	0.710593	0.967	0.686341	0.9955	0.480905	0.998	0.533078	0.9985	purL phosphoribosylformylglycinamidine synthase I 4315019:4315720 reverse MW:24919
RPA3819	88.5972	0	82.77325	0	81.08864	0	155.6037	0	238.6162	0	CDS hypothetical protein 4315777:4316016 reverse MW:9203
RPA3820	0.911687	0.8845	1.049967	0.263	0.911594	0.8715	0.758244	0.8965	0.805072	0.9865	CDS Protein of unknown function UPF0062 4316040:4316285 reverse MW:8419
RPA3821	0.946669	0.775	0.938634	0.768	0.898083	0.915	1.045242	0.338	0.811683	0.9845	purC2 phosphoribosylaminoimidazole-succinocarboxamide synthase 4316467:4317234 reverse MW:29171
RPA3822	0.787387	0.961	0.972008	0.5855	0.898624	0.922	0.778587	0.9895	0.74037	0.986	CDS conserved unknown protein 4317533:4317856 forward MW:11940
RPA3823	0.579122	0.998	0.569102	0.999	0.951292	0.7025	0.309654	1	1.09728	0.174	CDS hypothetical protein 4318428:4319102 forward MW:25333
RPA3824	0.886294	0.8545	0.965268	0.6065	1.088511	0.1625	1.148201	0.097	0.874875	0.881	CDS conserved hypothetical protein 4319994:4320344 reverse MW:12703
RPA3825	0.843565	0.9035	0.725504	0.998	1.095915	0.202	0.904339	0.823	0.919541	0.8	CDS conserved hypothetical protein 4320433:4321281 reverse MW:29092
RPA3826	0.903258	0.8235	0.930783	0.7005	0.983955	0.569	1.571343	0.0095	2.240057	0	CDS conserved hypothetical protein 4321678:4322034 forward MW:13190
RPA3827			0.682549	0.9785	0.880601	0.763	1.205502	0.2255	1.148279	0.207	CDS conserved hypothetical protein 4322038:4322361 forward MW:11719
RPA3828	0.639898	0.9465			0.915714	0.751			1.134324	0.208	CDS transcriptional regulator, XRE family 4322486:4322683 forward MW:7248
RPA3829	0.846894	0.9705	0.734675	0.9825	0.963895	0.646	0.721098	0.907	0.673257	0.9885	CDS putative transcription elongation factor greA homologue 4323708:4324238 reverse MW:18641

RPA3830	1.060758	0.2585	1.047092	0.2395	1.001106	0.487	0.939401	0.755	0.791148	0.9815	CDS possible G/U mismatch-specific DNA glycosylase 4324251:4324745 reverse MW:18690
RPA3831	0.939799	0.8055	0.714669	0.9825	1.075857	0.2425	0.858967	0.795	0.786961	0.9755	CDS conserved unknown protein 4324785:4325186 reverse MW:13712
RPA3832	0.941664	0.691	0.956107	0.7255	0.763006	0.9955	0.677295	0.994	0.779581	0.9905	CDS putative diguanylate cyclase (GGDEF) with PAS/PAC domain 4325281:4326351 reverse MW:39596
RPA3833	0.744434	0.858	1.360407	0.086	0.813905	0.8965	1.223481	0.3045	0.856873	0.763	rrm2 tRNA/rRNA methyltransferase 4326454:4327668 reverse MW:44184
RPA3834	1.160574	0.199	1.128986	0.072	1.034173	0.3125	0.957977	0.711	1.045515	0.269	idh NADP-dependent isocitrate dehydrogenase 4328043:4329269 forward MW:45410
RPA3835	0.824267	0.9925	1.020382	0.378	0.884145	0.9425	1.163343	0.097	1.288063	0.0055	CDS unknown protein 4329349:4330659 reverse MW:48606
RPA3838			1.260146	0.073			1.106748	0.364			CDS Protein of unknown function UPF0060 4333101:4333433 forward MW:11839
RPA3839	1.134828	0.246	1.735318	0.005	1.911811	0.0045	1.376335	0.0305	1.709051	0.0165	pchR putative transcriptional regulator PchR, AraC family 4333604:4334443 forward MW:30143
RPA3840	1.159189	0.253	1.402194	0.048	1.158086	0.2065			1.729334	0.0115	CDS putative hydroxamate-type ferrisiderophore receptor 4334584:4336893 forward MW:83720
RPA3841											CDS hypothetical protein 4336914:4337444 forward MW:18963
RPA3842	0.86657	0.9655	0.831115	0.95	0.93408	0.8195	0.903737	0.811	0.926815	0.8595	CDS Uncharacterized iron-regulated membrane protein DUF337 4337441:4338550 forward MW:39668
RPA3843	1.051148	0.345			1.074825	0.373			0.893312	0.6885	kefC putative potassium efflux transporter 4338580:4340313 reverse MW:60079
RPA3844	0.943058	0.7075	1.110237	0.1115	0.935964	0.8075	0.764568	0.983	0.688584	0.9985	kefB possible glutathione-regulated potassium-efflux system protein kefB 4340497:4342275 forward MW:62402
RPA3845	0.98616	0.558	1.090056	0.3645	0.877489	0.704	1.022986	0.4565	0.946011	0.667	CDS possible membrane transport protein 4342505:4344463 forward MW:69842
RPA3846	0.735301	0.935	0.676686	0.9125	0.626348	0.9955			0.51423	0.9935	CDS GCN5-related N-acetyltransferase 4344559:4345320 reverse MW:27606
RPA3847	1.068168	0.149	1.056216	0.2145	0.935801	0.835	0.966618	0.637	0.998513	0.5095	alaS alanyl-tRNA synthetase 4345322:4347991 reverse MW:96168
RPA3848	0.76357	0.985	0.480218	0.999	0.800474	0.9845	0.549883	0.997	1.28218	0.01	gcvT2 glycine cleavage system protein T2 4348444:4349592 forward MW:40380
RPA3849	0.967355	0.605	1.0735	0.377	0.996676	0.5135	1.049079	0.3815	1.162844	0.2035	CDS glycine cleavage system protein H 4349602:4349967 forward MW:12927
RPA3850	0.930739	0.8215	1.013553	0.4295	1.015809	0.4115	0.954286	0.6645	1.309143	0.006	gcvP glycine cleavage system protein P 4350069:4353041 forward MW:106402
RPA3851	0.590463	0.996	0.682149	0.9975	1.079386	0.321	0.706026	0.9895	1.171447	0.034	recA recombination protein recA 4353490:4354581 reverse MW:38788
RPA3852	1.002173	0.4985	0.877283	0.9115	0.981742	0.5635	1.352555	0.027	1.667785	0.002	CDS hypothetical protein 4354998:4355564 reverse MW:20611
RPA3853	0.889599	0.7605	0.719141	0.9845	1.03423	0.337	1.133448	0.199	1.010211	0.4755	CDS hypothetical protein 4355837:4356952 forward MW:41388
RPA3854					0.944005	0.5645			1.007007	0.4885	CDS hypothetical protein 4357103:4357480 forward MW:13625
RPA3855	1.12002	0.124	0.839052	0.9755	1.210247	0.0265	1.108922	0.1625	1.201752	0.0865	CDS conserved hypothetical protein 4357821:4358735 forward MW:32232
RPA3856	1.205571	0.202	0.989971	0.5205	1.237286	0.04	1.199543	0.089	1.332662	0.015	CDS hypothetical protein 4358739:4359098 forward MW:13013
RPA3857	1.219463	0.031	1.6183	0.003	1.216764	0.0255	2.072245	0.002	1.757114	0.001	CDS possible esterase/lipase/outer membrane autotransporter 4359262:4361286 reverse MW:70533
RPA3858	1.447765	0.004	1.851876	0.008	1.158019	0.1125	1.891272	0.041	1.536211	0.053	CDS hypothetical protein 4361678:4361935 forward MW:9438
RPA3859	1.308453	0.1145	1.831602	0.004	1.157929	0.0485	1.229956	0.114	1.141487	0.067	CDS hypothetical protein 4361953:4362348 reverse MW:14362
RPA3860	2.525498	0.001	1.959571	0.0005	2.394622	0.0015	1.610386	0.026	1.9846	0.009	CDS hypothetical protein 4362408:4362581 forward MW:6656
RPA3861	0.887049	0.8745	0.901316	0.9265	0.781475	0.962	0.750881	0.9685	0.616976	0.994	CDS unknown protein 4362966:4363352 forward MW:12584
RPA3862	0.98925	0.5425	1.498932	0.0035	1.048287	0.3515	1.378653	0.014	1.631541	0.013	CDS hypothetical protein 4363538:4363834 reverse MW:11077
RPA3863	1.153614	0.1855	1.799981	0.0005	1.418721	0.0055	1.501132	0.0155	1.675329	0.0005	CDS transcriptional regulator, Crp/Fnr family 4363862:4364614 reverse MW:28110
RPA3864	0.888649	0.9495	0.990758	0.5345	1.163169	0.073	1.061863	0.264	1.032409	0.3475	CDS unknown protein 4364688:4364954 reverse MW:9463
RPA3865	0.847138	0.972	0.845213	0.8765	1.071546	0.155	1.038522	0.3235	0.761265	0.979	CDS Thioesterase superfamily 4365165:4365713 forward MW:19715
RPA3866	0.905308	0.842	1.191376	0.0515	0.90008	0.8845	1.604283	0.0055	1.144234	0.072	CDS conserved unknown protein 4365768:4367363 reverse MW:56191
RPA3867	1.096221	0.2145	1.077663	0.2255	1.269027	0.044	1.162069	0.1795	1.077934	0.287	CDS conserved hypothetical protein 4367449:4368609 forward MW:41873
RPA3868	1.221586	0.106	0.82514	0.951	1.603995	0.0055	1.106817	0.305	1.029349	0.372	CDS putatively similar to frnE protein 4368610:4369275 reverse MW:24551
RPA3869	1.044567	0.3155	0.746695	0.993	1.343099	0.0035	0.821086	0.8495	0.868137	0.872	CDS transcriptional regulator, XRE family 4369348:4370169 reverse MW:29943
RPA3870											CDS hypothetical protein 4370305:4370718 forward MW:14030
RPA3871	0.717122	0.9715	0.872769	0.952	0.759749	0.9325	0.706165	0.939	0.944976	0.7165	mes-4 Nuclear protein SET 4370841:4371578 reverse MW:26869
RPA3872	1.012771	0.465	1.181779	0.143	0.857258	0.852	1.259088	0.073	1.394081	0.04	CDS conserved hypothetical protein 4371720:4372349 forward MW:21696
RPA3873	0.854457	0.8465	0.847777	0.8525	1.449082	0.02	1.128001	0.2385	1.837655	0.0045	CDS hypothetical protein 4372500:4373093 forward MW:21114
RPA3874	0.781624	0.9945	0.82012	0.9115	0.876453	0.76	1.368157	0.073	2.286541	0	CDS hypothetical protein 4373101:4373811 reverse MW:24170
RPA3875	0.911042	0.8145	0.646913	0.9955	1.082062	0.3285	0.580478	0.997	0.35029	0.999	CDS conserved unknown protein 4374071:4374367 forward MW:10092
RPA3876	0.882831	0.7615	0.730447	0.9925	0.62277	0.996	0.79254	0.976	0.843277	0.9465	fumA fumarate hydratase, class I 4374559:4376214 reverse MW:59889
RPA3877	0.854493	0.8185	0.730617	0.99	0.984756	0.5475	1.187451	0.2145	1.337605	0.077	CDS hypothetical protein 4377765:4378049 reverse MW:10412
RPA3878	1.322276	0.041	1.104451	0.0715	1.188171	0.093	1.224681	0.038	1.481846	0.001	CDS conserved unknown protein 4378147:4378641 forward MW:17755
RPA3879	0.951024	0.72	1.062449	0.237	1.001602	0.4985	1.118553	0.1575	1.148045	0.096	CDS conserved hypothetical protein 4379170:4379529 forward MW:13038
RPA3880	1.21442	0.051	1.25845	0.0585	1.354625	0.0105	1.23193	0.0515	1.368873	0.003	CDS possible glutathione S-transferase P subunit 4379688:4380398 reverse MW:27055
RPA3881	0.945879	0.7335	0.963964	0.6425	1.055965	0.309	1.068856	0.2915	0.942739	0.6895	CDS conserved unknown protein 4380519:4381532 reverse MW:35422
RPA3882	0.771346	0.993	0.674281	0.999	0.679066	0.994	0.536833	0.9985	0.67982	0.9985	cckA sensor histidine kinase with multiple PAS and a response regulator receiver domain 4381871:4384519 reverse MW:94966
RPA3883	0.867936	0.828	0.690098	0.999	0.666148	0.999	0.721157	0.995	0.849491	0.9585	flhB putative flagellar biosynthetic protein flhB 4384623:4385696 reverse MW:39679
RPA3884	0.781815	0.9935	0.599624	0.996	0.790136	0.975	0.516801	0.9975	0.634572	0.996	fliR putative flagellar biosynthetic protein FliR 4385723:4386490 reverse MW:27118
RPA3885	0.627311	0.9975	0.61203	0.994	0.665059	0.9805	0.567127	0.9975	0.600441	0.9965	fliQ putative flagellar biosynthesis protein fliQ 4386597:4386860 reverse MW:9290
RPA3886	0.77137	0.9545	0.650739	0.9925	0.658769	0.995	0.592972	1	0.58479	0.9985	CDS Flagellar hook-basal body complex protein FliE 4387018:4387323 reverse MW:10404
RPA3887	0.878404	0.9065	0.644276	0.9925	0.624058	0.995	0.68185	0.962	0.685979	0.98	flgC flagellar basal-body rod protein flgC 4387359:4387784 reverse MW:15401
RPA3888	0.896122	0.867	0.721887	0.9875	0.649518	0.9865	0.740048	0.992	0.708208	0.9995	CDS possible flagellar basal-body rod protein FlgB 4387806:4388312 reverse MW:17880
RPA3889	1.39273	0.003	1.339362	0.017	1.166199	0.1075	3.496697	0.0015	1.236747	0.0665	CDS unknown protein 4388533:4389687 forward MW:41256
RPA3890	0.901418	0.903	1.074778	0.203	0.883982	0.8955	0.81535	0.8795	0.958764	0.6965	fliP putative flagellar biosynthesis protein fliP 4389684:4390448 forward MW:27126
RPA3891	0.976345	0.6055	1.050714	0.2625	0.92101	0.816	1.115372	0.137	1.10783	0.114	CDS unknown protein 4390618:4394346 reverse MW:132826
RPA3892	1.672492	0.055			1.295767	0.277			1.714763	0.2525	CDS hypothetical protein 4394823:4395152 forward MW:11748
RPA3893	1.047601	0.2675	1.064528	0.2145	1.05259	0.2725	1.270033	0.0185	1.433607	0.004	CDS putative carboxylesterase 4395182:4396705 reverse MW:55018
RPA3894							1.40272	0.279			CDS probable transcriptional regulator, TetR family 4396731:4397354 reverse MW:22973
RPA3895	1.109994	0.1165	0.965703	0.6995	0.956398	0.667	1.037904	0.3135	1.160571	0.0465	CDS conserved hypothetical protein 4397532:4398296 reverse MW:27947
RPA3896	1.005876	0.4715	0.823953	0.958	0.949207	0.635	0.859162	0.8815	1.041964	0.3555	CDS hypothetical protein 4398293:4398721 reverse MW:15090
RPA3897	0.891597	0.903	0.675702	0.989	0.713793	0.964	0.737262	0.9675	0.964626	0.5665	fliM possible flagellar motor switch protein FliM 4398718:4399920 reverse MW:44124
RPA3898	0.931889	0.751	0.881348	0.943	0.796911	0.989	1.152845	0.062	1.074508	0.1835	fliL Flagellar basal body-associated protein FliL 4399927:4400427 reverse MW:17989
RPA3899	0.931261	0.8655	0.990496	0.537	0.702999	0.983	1.198707	0.0685	1.065861	0.2255	flgF putative flagellar basal-body rod protein flgF 4400792:4401553 forward MW:27638
RPA3900	0.8874	0.7765	0.924484	0.688	0.661374	0.9505	1.057758	0.4315	0.932858	0.7305	flgG putative flagellar basal-body rod protein flgg (distal rod protein) 4401566:4402354 forward MW:27596
RPA3901	0.927992	0.882	1.039932	0.279	0.799727	0.97	0.987481	0.546	0.922471	0.7885	CDS Flageller protein FlgA 4402367:4403395 forward MW:36132
RPA3902	0.93253	0.8575	0.941972	0.7585	0.728115	0.977	0.891925	0.862	0.810748	0.98	flgH putative flagellar L-ring protein FlgH 4403401:4404159 forward MW:27024
RPA3903	0.962879	0.5755	0.948497	0.63	0.66898	0.9685	0.750267	0.9715	0.719679	0.972	mexD3 RND multidrug efflux transporter MexD 4404420:4407572 reverse MW:112018
RPA3904	0.920739	0.644	0.838993	0.886	0.898626	0.7845	1.072379	0.3775	1.049187	0.317	mexC3 putative RND multidrug efflux membrane fusion protein MexC precursor 4407585:4408778 reverse MW:42004
RPA3905	0.969986	0.6635	0.944054	0.731	1.009263	0.452	1.208974	0.1	1.329781	0.011	CDS possible transcriptional regulator, TetR family 4408925:4409488 forward MW:20513
RPA3906	0.533891	0.9935	0.714881	0.9885	0.884972	0.7895	0.508166	0.9915	0.52212	1	CDS unknown protein 4409685:4409966 forward MW:10059
RPA3907	1.079521	0.2265	1.388152	0.033	1.191241	0.0375	1.288244	0.0165	1.342184	0.051	dksA DnaK suppressor protein DksA 4410076:4410504 reverse MW:16804
RPA3908	1.01659	0.41	0.822332	0.9635	0.914356	0.7435	1.190173	0.085	1.07188	0.2295	CDS conserved unknown protein 4410625:4411035 reverse MW:14057

RPA3909	0.930122	0.861	0.941699	0.734	0.871693	0.9525	1.0995	0.1505	0.885257	0.94	flgI flagellar P-ring protein FlgI 4411334:4412455 forward MW:38615
RPA3910	1.03557	0.3195	0.952794	0.646	0.944182	0.744	0.975489	0.607	0.870318	0.926	CDS conserved hypothetical protein 4412452:4412790 forward MW:12117
RPA3911	1.142138	0.1505	1.140264	0.131	1.037629	0.4175	1.328761	0.0525	1.211017	0.0595	CDS hypothetical protein 4412808:4413299 forward MW:17814
RPA3912	1.309622	0.0655	1.541377	0.002	0.936088	0.6945	2.459943	0.002	1.89817	0.002	CDS hypothetical protein 4413479:4413850 forward MW:13030
RPA3913	1.200523	0.029	1.459365	0.006	1.118854	0.0805	1.737037	0.003	1.373919	0.002	CDS conserved hypothetical protein 4413967:4414335 reverse MW:13491
RPA3914	0.92621	0.761	0.884139	0.879	0.943263	0.67	0.899401	0.812	0.856912	0.9175	CDS putative flbT protein 4414339:4414719 reverse MW:14538
RPA3915	1.743894	0.005	1.115026	0.224	1.41379	0.016	1.258194	0.149	1.831863	0.0005	CDS conserved unknown protein 4414935:4417595 reverse MW:87557
RPA3916	0.73352	0.9965	0.625134	0.995	0.760966	0.9785	0.594106	0.9875	0.719171	0.992	CDS TPR repeat 4418117:4420264 forward MW:78650
RPA3917	0.877397	0.936	0.796414	0.986	0.902575	0.881	0.832487	0.9505	0.747928	0.9715	CDS possible acetolactate synthase large subunit 4420277:4422079 reverse MW:64373
RPA3918	0.817503	0.9865	0.685862	0.998	0.789182	0.981	0.795464	0.9695	0.635675	0.9945	CDS conserved hypothetical protein 4422103:4422909 reverse MW:28901
RPA3919	0.889646	0.9425	0.955912	0.749	0.889585	0.892	0.890266	0.818	0.839208	0.983	CDS possible mannose-1-phosphate guanyltransferase 4422906:4423826 reverse MW:32999
RPA3920	0.943785	0.6525	0.909766	0.6055	1.042007	0.365	1.491396	0.1865	0.814751	0.8655	CDS possible ADP-heptose synthase 4423823:4425307 reverse MW:53410
RPA3921	0.867482	0.969	0.777066	0.9955	0.865392	0.966	0.717353	0.992	0.782463	0.9935	CDS possible acetoin dehydrogenase (TPP-dependent) beta chain 4425313:4426368 reverse MW:37413
RPA3922	0.793411	0.9685	0.757515	0.954	0.770155	0.9115	0.771813	0.9525	0.726708	0.984	CDS putative acetoin dehydrogenase (TPP-dependent) beta chain 4426519:4427571 reverse MW:37561
RPA3923	0.899737	0.774	1.126647	0.2665	0.851722	0.9205	0.871726	0.6925	0.724298	0.9685	CDS putative acetoin dehydrogenase (TPP-dependent) alpha chain 4427582:4428559 reverse MW:34930
RPA3924	0.610534	0.999	0.484708	0.995	0.588747	0.9975	0.510587	0.9995	0.565239	1	CDS conserved hypothetical protein 4428556:4429215 reverse MW:25025
RPA3925	0.710922	0.997	0.77403	0.996	0.629132	0.998	0.7381	0.984	0.693538	0.9965	CDS putative dTDP-glucose 4,6-dehydratase 4429224:4430261 reverse MW:38892
RPA3926	0.831999	0.9545	0.764033	0.995	0.908857	0.8805	0.824003	0.947	0.85007	0.958	CDS putative sugar-nucleotide epimerase/dehydratase 4430258:4431196 reverse MW:34513
RPA3927	0.843861	0.9	0.521105	0.998	0.819682	0.973	1.209641	0.1365	0.703612	0.989	CDS possible phosphoheptose isomerase 4431338:4432006 reverse MW:23654
RPA3928	1.252094	0.0645	1.163721	0.0485	1.549744	0.0045	1.830075	0.001	1.233093	0.0165	CDS unknown protein 4432129:4433091 reverse MW:34344
RPA3929	1.365903	0.0045	1.376743	0.0115	1.495674	0.0185	1.677367	0.0005	1.333264	0.017	CDS conserved unknown protein 4433205:4435871 reverse MW:87791
RPA3930	0.777736	0.9045	0.893018	0.843	0.840741	0.9825	0.917531	0.8155	0.859387	0.877	CDS unknown protein 4436179:4437786 reverse MW:55018
RPA3931	0.952771	0.5795	0.903586	0.919	0.796418	0.97	0.89296	0.791	0.865724	0.8815	flgK2 possible flagellar hook-associated protein 1 FlgK 4437795:4439666 reverse MW:64722
RPA3932	0.891327	0.8345	0.836381	0.9835	0.822447	0.969	0.84183	0.9375	0.744477	0.998	CDS probable flagellar hook protein flgE 4439705:4441501 reverse MW:61449
RPA3933	1.368	0.005	1.735569	0.0075	1.507266	0.0065	1.314556	0.021	1.549901	0.0015	CDS sensor histidine kinase with multiple PAS and a response regulator receiver domain 4441771:4444836 forward MW:111336
RPA3934									1.447615	0.039	CDS sensor histidine kinase with a PAC motif and a response regulator receiver domain 4444803:4446011 forward MW:43708
RPA3935	0.736082	0.959	1.017618	0.437	1.0888	0.3275	0.755299	0.925	0.622494	0.869	CDS hypothetical protein 4446201:4446473 forward MW:9677
RPA3936	0.977601	0.625	0.916763	0.789	0.642013	0.991	0.630632	0.993	0.748759	0.97	CDS conserved hypothetical protein 4446510:4448003 reverse MW:54126
RPA3937	1.237779	0.074	0.853651	0.9645	1.202096	0.098	1.199063	0.1035	1.313757	0.0055	CDS putative methionine sulfoxide reductase, SelR 4448155:4448652 reverse MW:18578
RPA3938	1.003062	0.4855	1.082219	0.3265	0.854005	0.9515	1.065914	0.436	0.870439	0.825	CDS possible oxidoreductase 4448786:4450246 reverse MW:51574
RPA3939	1.039775	0.3265	0.952221	0.654	0.870014	0.9245	0.873568	0.852	0.865323	0.9195	CDS conserved unknown protein 4450387:4450917 forward MW:19505
RPA3940	1.117944	0.068	0.916112	0.7235	1.210724	0.1295	1.507246	0.02	2.043365	0	CDS Universal stress protein (Usp) 4450961:4451392 forward MW:15311
RPA3941	0.845466	0.957	0.879311	0.7895	0.887941	0.923	0.75257	0.9755	0.742976	0.9905	CDS hypothetical protein 4451414:4452010 reverse MW:21834
RPA3942	0.817931	0.9665	0.650658	0.989	0.928385	0.6845	0.789874	0.8865	0.797728	0.946	CDS conserved hypothetical protein 4452159:4452599 forward MW:14971
RPA3943	1.712679	0.0005	3.583059	0.0005	2.632534	0.0005	1.638921	0.0205	2.845843	0.0015	CDS conserved hypothetical protein 4452700:4453206 reverse MW:18680
RPA3944	1.003707	0.472	1.053985	0.259	1.049304	0.2555	1.132787	0.105	1.43965	0.0025	CDS conserved hypothetical protein 4453613:4454704 forward MW:39113
RPA3945	0.98915	0.5695	0.975935	0.585	1.219196	0.059	1.453885	0.0245	2.753512	0	CDS hypothetical protein 4454765:4456852 forward MW:73828
RPA3946	1.335949	0.024	1.115905	0.1195	1.280416	0.0065	1.605802	0.0035	1.99405	0	CDS conserved unknown protein 4456952:4458091 reverse MW:41910
RPA3947	0.990782	0.5215	0.971891	0.6095	1.206399	0.032	0.727227	0.9935	1.124537	0.065	CDS conserved unknown protein 4458271:4458933 reverse MW:23385
RPA3948	1.133393	0.0495	0.93332	0.7835	0.954003	0.71	0.861239	0.8735	1.091274	0.1625	CDS hypothetical protein 4459023:4460288 reverse MW:45062
RPA3949	1.070671	0.1265	1.067447	0.173	0.797655	0.979	0.841931	0.9435	1.097977	0.153	wbpX possible glycosyltransferase WbpX 4460299:4461624 reverse MW:47976
RPA3950	0.951917	0.732	0.876566	0.891	0.870817	0.9185	0.835716	0.94	0.936107	0.797	CDS possible glycosyl transferases 4461777:4462838 forward MW:38627
RPA3951	0.940971	0.777	0.865757	0.972	0.674511	0.9815	0.833471	0.84	0.944156	0.809	gmd GDP-mannose 4,6-dehydratase 4462907:4463893 forward MW:36595
RPA3952	0.859939	0.873	0.831732	0.9425	0.693675	0.9625	0.633557	0.956	0.819342	0.9225	CDS possible oxidoreductase Rmd 4463893:4464876 forward MW:34239
RPA3953			0.540363	0.995	0.678444	0.9225	0.806475	0.76	0.870433	0.8325	CDS putative chloride channel protein 4464910:4466172 reverse MW:43463
RPA3954	0.839492	0.9125	0.98052	0.5995	0.741443	0.983	0.645781	0.967	0.743557	0.9655	CDS thioredoxin reductase 4466340:4467368 reverse MW:37017
RPA3955	0.651568	0.9935	0.781955	0.97	0.607612	0.9815	0.941271	0.639	0.774205	0.985	CDS hypothetical protein 4467683:4467985 forward MW:11221
RPA3956	0.664551	0.999	0.892376	0.8485	0.545088	0.9995	0.674999	0.971	0.654049	0.9955	CDS ferredoxin 4468165:4468485 reverse MW:11488
RPA3957	1.075326	0.1645	1.156407	0.0705	1.044359	0.297	1.255216	0.0475	1.177781	0.029	CDS Hpt domain 4468582:4468941 reverse MW:12532
RPA3958	1.315219	0.017	1.241349	0.019	1.169637	0.045	1.389642	0.0045	1.154166	0.036	CDS conserved unknown protein 4469382:4475459 forward MW:215109
RPA3959	0.906326	0.797	0.866639	0.8145	1.18423	0.054	0.849925	0.8905	0.90621	0.8115	CDS putative amidase 4475883:4477367 forward MW:52209
RPA3960	0.861816	0.978	0.886306	0.9345	0.800088	0.9905	0.908996	0.8495	1.086227	0.149	CDS conserved unknown protein 4477612:4478415 forward MW:29233
RPA3961	0.908126	0.925	1.032519	0.345	0.777972	0.9885	0.811666	0.936	0.990133	0.5485	CDS putative periplasmic binding protein for ABC transporter 4478600:4479493 reverse MW:31898
RPA3962	0.954028	0.7005	1.088874	0.184	0.918535	0.838	0.938101	0.7035	0.898594	0.869	CDS ATP-binding component of ABC transporter 4479631:4480404 reverse MW:28139
RPA3963	1.042733	0.2895	1.039211	0.3135	1.231884	0.021	1.128183	0.114	1.221445	0.0225	CDS putative permease of ABC transporter 4480407:4481558 reverse MW:40953
RPA3964	1.160011	0.105	0.90718	0.839	1.104496	0.1445	1.122334	0.205	1.000093	0.494	CDS putative muconate cycloisomerase 4481663:4482658 forward MW:34596
RPA3965	0.507959	0.998	0.344231	0.9995	0.633769	0.9915	0.330774	0.9965	0.418912	1	CDS putative phenylpropionate transporter 4482628:4483836 reverse MW:42318
RPA3966	0.658058	0.9945	0.511852	0.999	0.8682	0.9195	0.630152	0.9975	0.593198	0.988	CDS hypothetical protein 4483913:4485370 forward MW:49104
RPA3967	1.079829	0.366	0.763973	0.9515	0.906444	0.798	0.851509	0.79	0.724473	0.991	CDS putative threonine dehydratase 4485400:4486395 reverse MW:33774
RPA3968			0.769931	0.9485	0.681285	0.963	0.419709	0.9995	0.805844	0.942	CDS putative glycosyl transferase 1 4486445:4487500 reverse MW:37996
RPA3969											CDS Metallo-phosphoesterase 4487500:4488297 reverse MW:30200
RPA3970											CDS putative phosphatidylethanolamine-N-methyltransferase 4488351:4489007 reverse MW:23911
RPA3971	0.77664	0.994	0.713676	0.9975	0.708845	0.983	0.634448	0.9965	0.78302	0.983	thiD phosphomethylpyrimidine kinase (hmp-phosphate kinase) 4489100:4489900 reverse MW:27138
RPA3972	0.893167	0.8415	0.984899	0.5885	1.283905	0.0125	0.649166	0.9895	0.726656	0.915	CDS putative diheme cytochrome c-553 4490291:4491220 reverse MW:33086
RPA3973	1.017578	0.429	0.799395	0.983	1.493637	0.001	0.660818	0.9935	0.630448	0.972	CDS cytochrome c556 4491254:4491703 reverse MW:16148
RPA3974	0.891229	0.904	0.716787	0.992	1.289039	0.0145	0.833706	0.883	0.579535	0.998	CDS putative dehydrogenase 4491815:4494136 reverse MW:82808
RPA3975	0.847177	0.936	0.717935	0.9875	1.339917	0.0305	0.732651	0.9425	0.687945	0.9905	CDS unknown protein 4494382:4494675 reverse MW:10576
RPA3976	0.723323	0.909	0.943935	0.7115	0.890488	0.792	0.941522	0.722	1.200187	0.0695	CDS putative nodulation protein 4495106:4496911 forward MW:67754
RPA3977	0.815211	0.94							0.953657	0.611	CDS putative virulence factor MviN-like protein, possible efflux protein 4496912:4498441 reverse MW:54187
RPA3978	1.014191	0.419	0.869634	0.9225	0.738348	0.9885	0.766796	0.941	0.790566	0.917	wpbE putative aminotransferase (aminosugar biosynthesis) 4498568:4499719 reverse MW:40571
RPA3979	0.876244	0.965	0.794467	0.988	0.785172	0.963	0.657484	0.9915	0.880152	0.943	CDS putative NADH-dependent dehydrogenase 4499777:4500772 reverse MW:34976
RPA3980	0.889529	0.9275	1.113882	0.1265	0.676745	0.998	0.771202	0.9755	0.976929	0.5915	wbnF nucleotide sugar epimerase 4500913:4501959 reverse MW:38688
RPA3981	0.843153	0.973	1.005596	0.475	0.703289	0.997	0.610787	0.994	0.976403	0.6115	CDS conserved hypothetical protein 4502087:4503046 forward MW:33907
RPA3982	0.865994	0.925	0.583618	0.9955	0.693381	0.9965	0.985538	0.532	1.646512	0.0005	CDS Glycosyl transferase, family 4 4503101:4504111 forward MW:35112
RPA3983	0.941776	0.7555	0.677908	0.9935	0.855902	0.9525	1.04904	0.343	0.978471	0.601	CDS putative nucleotide sugar epimerase/dehydratase 4504132:4506153 reverse MW:74298
RPA3984	0.677526	0.98	0.730877	0.9995	0.784415	0.9915	0.537979	0.9985	0.640894	0.997	rfaE putative ADP-heptose synthase 4506092:4507564 reverse MW:52131
RPA3985	0.780148	0.9775	0.758971	0.9925	0.683683	0.996	0.605975	0.9995	0.722346	0.9955	CDS ADP-L-glycero-D-mannoheptose-6-epimerase 4507589:4508569 reverse MW:36205

RPA3986	0.746646	0.978	0.868639	0.965	0.739076	0.9945	0.702079	0.995	0.711212	0.9955	CDS putative ADP-heptose--LPS heptosyltransferase II 4508639:4509829 forward MW:42971
RPA3987	0.835822	0.958	0.837979	0.8855	0.722379	0.98	1.084069	0.3325	0.764878	0.992	lpcA possible phosphoheptose isomerase 4509900:4510487 forward MW:19946
RPA3988	1.097151	0.2315	0.973159	0.611	0.805125	0.9565	0.843902	0.8635	0.796629	0.9475	CDS putative phosphatase 4510484:4511026 forward MW:20082
RPA3989	0.972142	0.6355	0.995454	0.528	0.825299	0.9805	0.925639	0.7295	0.930229	0.852	CDS putative lipopolysaccharide-heptosyl-transferase 4511023:4511967 reverse MW:34057
RPA3990	1.830366	0	1.601489	0.001	1.403156	0.0045	1.971592	0.0005	1.77336	0.001	galE1 UDP-galactose 4-epimerase 4512150:4513163 forward MW:35943
RPA3991	0.817075	0.9675	0.967013	0.714	0.71449	0.9935	0.756807	0.984	0.884772	0.861	CDS putative ABC transporter ATP-binding protein 4513285:4515087 forward MW:65237
RPA3992	0.987153	0.5505	0.864828	0.768	0.890823	0.806	0.789516	0.9475	0.803743	0.958	CDS Fumarylacetoacetate (FAA) hydrolase 4515148:4515849 forward MW:24984
RPA3993	0.860331	0.931	0.824372	0.9115	0.779408	0.9805	0.695916	0.985	0.75873	0.9825	CDS conserved unknown protein 4516059:4516916 reverse MW:30169
RPA3994	1.051299	0.2535	0.881084	0.84	0.906811	0.911	1.217441	0.15	1.246178	0.093	CDS putative diguanylate cyclase (GGDEF) 4517032:4518180 reverse MW:42030
RPA3995											CDS conserved hypothetical protein 4518385:4518843 forward MW:15553
RPA3996					1.492846	0.0905	1.566773	0.0375	2.094715	0.007	CDS probable transcriptional regulator, Crp/Fnr family 4518883:4519596 reverse MW:26063
RPA3997	1.299586	0.0085	1.253512	0.016	1.502225	0.0015	1.545148	0.003	1.928715	0.0045	CDS unknown protein 4519740:4520276 reverse MW:19652
RPA3998	1.669998	0.0075	1.437696	0.0085	1.577629	0.0165	2.33936	0.0005	2.222394	0.0015	CDS hypothetical protein 4520279:4520512 reverse MW:8844
RPA3999	1.423875	0.07	0.846778	0.8795	1.966962	0.0115	2.47411	0.0065	3.660395	0	CDS possible coenzyme PQQ synthesis protein E 4520517:4521560 reverse MW:38575
RPA4000											CDS Adenylate/Guanylate cyclase 4521683:4525000 forward MW:121034
RPA4001	0.653814	0.9575	0.695301	0.822	0.832335	0.678	0.704516	0.88	0.393711	0.996	CDS putative DEAD-box protein, ATP-independent RNA helicase 4525204:4527288 forward MW:76129
RPA4002	1.056154	0.4035	0.619958	0.996	0.942762	0.7395	0.744687	0.8885	0.513494	0.9995	CDS putative acyl-CoA dehydrogenase 4527500:4528882 reverse MW:51342
RPA4003	0.928525	0.6355	0.595574	0.759	0.879423	0.8175			1.109881	0.308	CDS conserved hypothetical protein 4529421:4529558 forward MW:4939
RPA4004			1.016601	0.418			1.240807	0.1345			CDS conserved hypothetical protein 4530050:4530211 forward MW:5700
RPA4005											rpsU, S21 possible ribosomal protein S21 4530423:4530698 reverse MW:10832
RPA4006	1.986141	0.0085	1.324933	0.224	1.208325	0.181	3.699508	0.0055	3.966797	0	CDS hypothetical protein 4530839:4531315 forward MW:17830
RPA4007											CDS hypothetical protein 4531480:4531812 forward MW:12319
RPA4008											CDS hypothetical protein 4532011:4532274 forward MW:9525
RPA4009	0.811135	0.773	1.094857	0.2145	1.063256	0.2815	1.036214	0.407	1.136289	0.252	CDS putative signal transduction histidine kinase with GAF domain 4532346:4534394 forward MW:74149
RPA4010	1.137245	0.2775	1.607426	0.027	0.95433	0.582	1.656525	0.0025	0.880391	0.9055	CDS response regulator receiver (CheY-like protein) 4534391:4534768 forward MW:13972
RPA4011	1.065225	0.2085	1.078487	0.3465	1.038828	0.35	1.245582	0.154	1.109653	0.1895	CDS possible serine protease/outer membrane autotransporter 4535113:4537245 forward MW:72618
RPA4012											CDS conserved hypothetical protein 4537981:4538667 forward MW:25635
RPA4013	0.991374	0.5255	1.09247	0.19	0.905192	0.809	1.033594	0.366	0.927947	0.7975	CDS putative ATP-binding component of ABC transporter 4538856:4540454 reverse MW:56334
RPA4014	0.765581	0.9715	1.102711	0.1565	0.763769	0.9915	0.768642	0.882	1.091522	0.1515	CDS hypothetical protein 4540989:4543007 forward MW:74260
RPA4015	0.596071	0.9955	0.781047	0.964	0.565958	0.997	0.423306	0.999	0.4187	0.998	ahcY S-adenosyl L-homocysteine hydrolase 4543091:4544500 reverse MW:51700
RPA4016	0.917496	0.8725	1.092991	0.1405	0.803125	0.9715	0.834245	0.895	0.822516	0.9775	metK methionine S-adenosyltransferase 4544761:4545957 reverse MW:43418
RPA4017	0.752089	0.996	0.815474	0.9845	0.864693	0.86	0.915915	0.78	0.968669	0.6	CDS hypothetical protein 4546021:4547427 reverse MW:52702
RPA4018	1.037947	0.296	1.002857	0.492	1.041599	0.2705	1.202322	0.0505	1.500676	0.001	CDS UDP-glucose-6-dehydrogenase 4547580:4548890 forward MW:46720
RPA4019	1.678657	0.0015	1.250926	0.027	1.190387	0.141	0.989667	0.5085	1.360893	0.0045	CDS putative branched-chain amino acid ABC transporter system substrate-binding protein 4549160:4550341 forward MW:41868
RPA4020	0.970768	0.563	0.822355	0.9315	0.949047	0.614	0.865128	0.8365	0.850241	0.94	CDS possible branched-chain amino acid transport system permease protein 4550491:4551363 forward MW:29603
RPA4021	1.09398	0.297	0.957106	0.6805	0.638425	0.986	0.640641	0.986	0.706487	0.9725	CDS putative branched-chain amino acid ABC transport system permease protein livm (liv-I protein m) 4551364:4552311 forward MW:33340
RPA4022	1.120642	0.0335	1.019239	0.395	0.870457	0.9495	0.819966	0.9705	0.937124	0.7485	CDS putative branched-chain amino acid ABC transport system, ATP-binding protein 4552308:4553090 forward MW:27904
RPA4023	0.969177	0.6385	0.900854	0.872	0.862327	0.959	0.851304	0.8665	0.882952	0.9345	CDS putative branched-chain amino acid ABC transport system ATP-binding protein 4553083:4553787 forward MW:25045
RPA4024	0.999618	0.497	0.769065	0.993	0.972527	0.6185	0.756133	0.9605	0.741908	0.987	CDS Methionine synthase, vitamin-B12 independent 4554023:4555144 reverse MW:42369
RPA4025	1.043496	0.246	0.843346	0.9665	0.998457	0.492	0.852017	0.927	0.725549	0.997	CDS putative branched-chain amino acid ABC transport system ATP-binding protein 4555160:4555876 reverse MW:25337
RPA4026	0.780223	0.9695	0.827827	0.8435	1.021924	0.4675			0.540031	1	CDS possible ABC transporter,ATP binding protein 4555897:4556514 reverse MW:22549
RPA4027	1.162973	0.1835	0.94956	0.6835	0.839147	0.9515	0.942221	0.704	0.779326	0.9885	CDS possible branched-chain amino acid ABC transport system permease protein 4556646:4557671 reverse MW:36846
RPA4028	1.212208	0.219	0.833272	0.9575	0.844456	0.8885	0.743541	0.953	0.556815	0.999	CDS possible ABC transport system permease protein 4557671:4558537 reverse MW:30750
RPA4029	1.182914	0.246	0.780362	0.979	1.120113	0.115	0.914841	0.755	0.591127	0.994	CDS possible branched-chain amino acid ABC transport system substrate-binding protein 4558688:4559866 reverse MW:41548
RPA4030	1.183091	0.0675	1.062399	0.1915	1.149597	0.137	1.380089	0.016	1.246627	0.0645	CDS hypothetical protein 4560104:4560502 forward MW:13923
RPA4031	0.835676	0.9515	0.873747	0.905	0.906079	0.8865	1.113294	0.196	1.728901	0	CDS hypothetical protein 4560558:4561145 forward MW:20768
RPA4032	1.064812	0.173	1.192331	0.058	1.241632	0.018	1.872096	0	2.666042	0	purU formyltetrahydrofolate deformylase 4561152:4562015 reverse MW:32565
RPA4033	1.024077	0.366	0.968127	0.661	1.210837	0.0255	1.058846	0.329	1.273433	0.014	hemD Uroporphyrinogen III synthase HEM4 4562147:4562992 forward MW:30418
RPA4034	0.958028	0.6025	0.840851	0.9295	1.052998	0.332	0.968361	0.588	1.070435	0.197	CDS ABC transporter, periplasmic branched chain amino acid binding protein 4563239:4564471 forward MW:44901
RPA4035	0.734614	0.9455	0.692878	0.995	0.81585	0.9905	0.431969	0.9985	0.553772	1	CDS possible ABC transport system permease protein 4564600:4565547 forward MW:33753
RPA4036	0.632998	0.995	0.603625	0.998	0.534087	0.9995	0.395138	1	0.516333	0.9995	CDS possible branched-chain amino acid ABC transporter, permease protein 4565544:4566845 forward MW:46419
RPA4037	0.745382	0.986	0.60386	0.999	0.687895	0.9935	0.430888	1	0.597027	0.9995	CDS putative ABC transport system ATP-binding protein 4566842:4567591 forward MW:27355
RPA4038	0.653729	0.9995	0.636996	0.998	0.698294	0.999	0.438701	1	0.475436	1	CDS possible ABC transport system ATP-binding protein 4567591:4568289 forward MW:25434
RPA4039	0.74357	0.991	0.587461	0.9985	0.983279	0.5495	0.706802	0.96	0.945732	0.732	CDS conserved hypothetical protein 4568455:4569033 forward MW:20718
RPA4040	1.031243	0.391	0.901362	0.811	0.797715	0.938	0.843559	0.936	1.142282	0.1215	CDS hypothetical protein 4569156:4571108 forward MW:70821
RPA4041	1.32594	0.0345	0.955423	0.7215	1.128286	0.067	0.887584	0.894	0.910727	0.8365	CDS putative branched-chain amino acid ABC transport system ATP-binding protein 4571291:4572217 forward MW:34552
RPA4042	1.277094	0.2235	0.743272	0.9925	0.904172	0.818	0.694732	0.9925	0.766477	0.9745	CDS putative long-chain-fatty-acid--CoA ligase 4572214:4574145 forward MW:71362
RPA4043	1.066191	0.2605	0.920053	0.878	1.096243	0.141	1.073604	0.2195	1.091381	0.185	CDS possible ABC transporter, permease protein 4574213:4575151 forward MW:33753
RPA4044	1.238136	0.113	0.833842	0.971	1.15635	0.047	0.778103	0.99	0.74151	0.9805	CDS putative branched-chain amino acid transport system permease protein 4575257:4576330 forward MW:38866
RPA4045	1.23901	0.0515	0.791205	0.988	1.305413	0.026	0.792167	0.9735	0.73288	0.929	CDS possible branched-chain amino acid ABC transport system substrate-binding protein 4576388:4577668 forward MW:44701
RPA4046	1.413351	0.012	1.088801	0.1595	1.373934	0.004	1.004188	0.478	0.973309	0.608	CDS putative branched-chain amino acid ABC transport system ATP-binding protein 4577938:4578780 forward MW:30816
RPA4048	1.063073	0.3085	1.075344	0.223	1.081302	0.25	0.935243	0.725	1.144285	0.114	rfbF alpha-D-glucose-1-phosphate cytidylyltransferase 4580288:4581055 forward MW:28855
RPA4049	0.932289	0.7955	0.886053	0.8615	0.872137	0.886	0.673487	0.9945	0.908192	0.764	rfbG cdp-glucose 4,6-dehydratase 4581052:4582146 forward MW:40538
RPA4050	1.027857	0.44	0.81027	0.951	0.846662	0.9555	0.644297	0.9935	0.610853	0.987	CDS unknown protein 4582156:4582953 forward MW:29985
RPA4051	1.08556	0.324	0.80406	0.969	0.834082	0.879	0.743521	0.985	0.826818	0.837	CDS possible oxo-acyl carrier protein dehydrogenase 4582978:4583694 forward MW:25432
RPA4052	0.886567	0.728	0.73077	0.975	0.77952	0.9695	0.756765	0.992	0.812644	0.9415	CDS possible 3-dehydroquinate synthase 4583678:4584796 forward MW:40911
RPA4053	0.903038	0.8095	0.817184	0.9375	0.89749	0.8465	0.663821	0.9975	0.600183	0.998	CDS possible dTDPglucose 4,6-dehydratase 4584793:4585872 forward MW:39543
RPA4054	1.002042	0.501	0.900571	0.802	0.751799	0.97	0.803021	0.975	0.848887	0.943	CDS possible acetolactate synthase large subunit 4585865:4587670 forward MW:65764
RPA4055	1.056934	0.253	1.155218	0.156	0.818687	0.917	0.93464	0.681	0.970661	0.5915	CDS hypothetical protein 4587670:4588125 forward MW:17397
RPA4056	1.083034	0.254	1.02153	0.4235	1.013355	0.46	0.934899	0.6995	0.875351	0.804	CDS unknown protein 4588115:4589041 forward MW:34716
RPA4057	1.073958	0.243	1.052201	0.262	0.942084	0.7195	0.968523	0.5985	0.93242	0.754	CDS possible dolichol phosphate mannose synthase 4589041:4589979 forward MW:35266
RPA4058	0.827694	0.9635	1.021467	0.417	0.757297	0.9885	0.714689	0.981	0.889109	0.814	CDS Glycosyl transferase, family 2:Mitochondrial substrate carrier 4590076:4591113 reverse MW:38462
RPA4059	0.749242	0.993	0.968352	0.687	0.749225	0.9935	0.756509	0.9795	0.889106	0.9315	CDS conserved unknown protein 4591214:4592116 reverse MW:31966
RPA4060	0.87444	0.9465	0.995989	0.512	0.794001	0.9885	0.756209	0.989	0.951751	0.728	CDS hypothetical protein 4592113:4593444 reverse MW:48827
RPA4061	0.828229	0.9825	0.969834	0.669	0.789214	0.971	0.974799	0.577	1.139117	0.0645	CDS putative glycosyltransferase 4593550:4594539 reverse MW:36424
RPA4062	0.698924	0.994	0.92701	0.727	0.545992	0.996	0.60531	0.9925	0.909661	0.7325	CDS conserved hypothetical protein 4594774:4596105 forward MW:48441
RPA4063	0.991943	0.5175	1.050359	0.39	0.777444	0.926	0.848947	0.855	0.920015	0.7005	CDS hypothetical protein 4597116:4599650 forward MW:92534

RPA4064	1.05488	0.2415	1.09427	0.141	1.00954	0.4615	0.910889	0.7865	0.863858	0.9375	CDS hypothetical protein 4599852:4602869 reverse MW:109035
RPA4065	1.311013	0.0745	1.267503	0.097	1.174839	0.1115	1.274445	0.096	1.15144	0.108	CDS hypothetical protein 4602985:4605462 forward MW:90701
RPA4066	1.19897	0.17	1.051998	0.2935	1.2945	0.015	1.736701	0.002	2.078213	0.0015	CDS hypothetical protein 4605912:4605989 forward MW:2899
RPA4068	0.974354	0.545	0.845733	0.946	0.880871	0.714	1.326866	0.0375	1.275123	0.056	CDS hypothetical protein 4606504:4606749 reverse MW:9292
RPA4069	0.849707	0.88	0.639548	0.992	1.185548	0.073	0.792459	0.922	0.761937	0.9855	CDS DUF25 4606983:4607399 reverse MW:15218
RPA4070	0.957855	0.6235	0.730476	0.986	1.124498	0.2205	0.749219	0.949	0.74152	0.9965	msrA1 possible peptide methionine sulfoxide reductase 4607430:4608041 reverse MW:21843
RPA4071	0.790265	0.935	0.726422	0.9945	0.745178	0.9955	0.611456	0.999	0.70104	0.951	carB carbamoyl-phosphate synthase large subunit 4608699:4612028 forward MW:120100
RPA4072	0.785022	0.978	0.965515	0.6545	0.867818	0.856	1.284304	0.104	1.073092	0.1975	greA transcriptional elongation factor greA 4612252:4612728 forward MW:17160
RPA4073	0.938296	0.7385	0.85896	0.9005	0.869442	0.895	0.902906	0.72	1.160435	0.122	CDS DoxD-like family 4612907:4613317 forward MW:14880
RPA4074	0.952684	0.712	1.012047	0.4415	1.001698	0.4735	1.03661	0.3255	1.054573	0.222	CDS putative leucine responsive transcriptional regulator LRP/BkdR, AsnC family 4613354:4613836 reverse MW:17863
RPA4075	0.878597	0.9495	0.784907	0.991	0.847522	0.968	0.822419	0.9515	0.891689	0.9265	trxB thioredoxin reductase 4614093:4615058 forward MW:34404
RPA4077	1.317137	0.06	0.681488	0.9885	1.640035	0.0285	1.326075	0.1145	1.727993	0.003	CDS ATPase, ParA type 4616307:4616981 reverse MW:23979
RPA4078	0.839927	0.975	0.78463	0.9755	1.150147	0.081	0.821342	0.9485	1.021819	0.39	CDS conserved hypothetical protein 4617193:4617570 reverse MW:14328
RPA4079	1.693959	0.0195	0.861304	0.874	1.527207	0.0625	1.381354	0.055	1.873186	0.0025	CDS hypothetical protein 4617664:4617999 reverse MW:12148
RPA4080	1.426172	0.0035	1.334225	0.002	1.151352	0.0415	1.87623	0	1.581037	0.0035	CDS hypothetical protein 4618141:4618422 reverse MW:9727
RPA4081	1.548485	0.001	1.37864	0.001	1.138797	0.0845	2.016109	0.0005	1.873393	0	CDS possible pilus assembly protein cpaB 4618593:4619405 reverse MW:28831
RPA4082	1.084037	0.185	0.992036	0.544	1.206802	0.032	0.914528	0.802	1.797521	0.0035	CDS possible phage-like integrase 4619836:4621062 forward MW:45238
RPA4083	0.81539	0.9255	0.871766	0.9425	0.776097	0.9865	0.864785	0.9035	1.170207	0.0765	CDS hypothetical protein 4621775:4622530 forward MW:28237
RPA4084	0.835913	0.9735	0.728804	0.9685	0.817448	0.9845	0.640911	0.9985	0.839456	0.916	CDS AAA ATPase 4622490:4624481 forward MW:70803
RPA4085	1.114547	0.113	1.057171	0.281	1.112008	0.1595	1.273943	0.048	1.301191	0.0205	CDS transcriptional regulator, TetR family 4624551:4625177 forward MW:23225
RPA4086	0.859451	0.929	1.067348	0.2615	0.950499	0.628	1.210946	0.184	1.140953	0.1345	CDS probable permease of ABC transporter 4625458:4626570 reverse MW:40828
RPA4087	0.827809	0.964	0.758221	0.9955	0.882723	0.8715	0.760253	0.9855	0.840246	0.8615	CDS ABC-2 type transport system permease and double ATP-binding protein fusion 4626573:4629368 reverse MW:100738
RPA4088	0.780383	0.967	0.730809	0.998	0.758543	0.9975	0.615212	0.9965	0.71958	0.9845	CDS probable membrane fusion protein (HlyD family of secretion proteins) linked to ABC efflux pumps 4629365:4630441 reverse MW:38442
RPA4089	0.917495	0.8085	0.850451	0.9395	0.863497	0.9535	0.743894	0.986	0.785458	0.975	CDS Patatin-like phospholipase domain 4630485:4631675 reverse MW:42471
RPA4090	1.043925	0.311	0.957349	0.67	1.030423	0.3765	1.400871	0.0235	1.595042	0.0005	CDS conserved hypothetical protein 4631838:4632479 reverse MW:21768
RPA4091	0.846255	0.9565	1.012148	0.437	1.056453	0.2865	1.086286	0.2515	1.05951	0.2165	CDS transcriptional regulator, TetR family 4632585:4633280 forward MW:25550
RPA4092	0.864109	0.96	0.876487	0.833	1.280044	0.0125	0.891671	0.7615	0.948825	0.741	CDS unknown protein 4633402:4634001 reverse MW:21358
RPA4093	0.697961	0.9865	0.638547	0.981	1.166757	0.171	0.601091	0.9535	0.535966	0.9825	CDS hypothetical protein 4634191:4634442 reverse MW:9247
RPA4094	0.689371	0.9925	0.60841	0.999	0.948192	0.629	0.565821	0.9885	0.54849	0.9985	CDS conserved hypothetical protein 4634535:4635371 reverse MW:29728
RPA4095	1.171361	0.04	0.900338	0.9345	1.08346	0.2945	1.126058	0.1755	1.306315	0.018	CDS putative multidrug-efflux transport protein mexF 4635409:4638561 reverse MW:111776
RPA4096	0.960555	0.581	1.054491	0.428	1.217677	0.171	1.542705	0.306	1.515626	0.119	CDS possible multidrug efflux membrane fusion protein mexE 4638566:4639741 reverse MW:41530
RPA4097	1.117069	0.0805	0.814597	0.835	1.094909	0.154	1.302891	0.0495	2.308963	0	CDS transcriptional regulator, TetR family 4639835:4640461 forward MW:23583
RPA4098	1.367508	0.059	0.893416	0.89	1.260837	0.025	1.217378	0.104	3.091356	0.0005	CDS putative RNA polymerase ECF-type sigma factor 4640831:4641529 forward MW:26403
RPA4099	0.694752	0.917	1.062363	0.3135	0.996574	0.512	0.665227	0.981	0.432105	0.9975	CDS hypothetical protein 4641574:4641816 forward MW:9145
RPA4100	1.127043	0.174	0.864177	0.933	1.239471	0.16	1.232684	0.0265	1.894829	0	CDS hypothetical protein 4641838:4642200 forward MW:12818
RPA4101	0.946161	0.605	0.808018	0.9685	0.93221	0.72	0.963322	0.6315	1.457495	0.005	CDS putative organic hydroperoxide resistance protein 4642335:4642760 forward MW:14095
RPA4102	1.004123	0.493	0.802644	0.99	0.791947	0.9835	0.883255	0.8985	1.310944	0.007	CDS transcriptional regulator, MarR family 4642801:4643262 forward MW:17148
RPA4103	0.840021	0.9245	0.777523	0.995	0.783009	0.992	0.767766	0.978	1.106617	0.098	CDS possible glutathione S-transferase 4643266:4643931 forward MW:24591
RPA4104	1.407029	0.0045	1.642748	0.002	1.3224	0.0055	3.182175	0	4.990028	0	CDS hypothetical protein 4644066:4644707 reverse MW:22789
RPA4105	1.183609	0.02	1.477369	0.001	1.176707	0.076	2.032254	0.002	2.854855	0	rmrA putative hlyD family multidrug secretion protein 4645025:4646239 forward MW:44067
RPA4106	0.809331	0.9625	0.944031	0.69	1.041742	0.351	0.937517	0.6255	1.257466	0.0265	rmrB putative multidrug efflux pump, Major Facilitator Superfamily (MFS) 4646236:4647786 forward MW:55025
RPA4107	0.949721	0.75	0.89545	0.774	1.105505	0.098	1.145449	0.237	1.066984	0.296	oprN putative outer membrane efflux protein OprN precursor 4647970:4649298 forward MW:47391
RPA4108	0.917588	0.8315	0.82839	0.978	0.944023	0.715	0.780011	0.969	0.779997	0.9795	CDS probable transcriptional regulator, TetR family 4649318:4649986 forward MW:24405
RPA4109	0.798714	0.9455	0.882392	0.9295	0.860781	0.942	0.992583	0.534	0.809297	0.9555	CDS conserved hypothetical protein 4650058:4650372 forward MW:11816
RPA4110	0.747908	0.9655	0.719779	0.992	0.83834	0.951	0.840749	0.9625	0.856131	0.9355	mycA myosin-crossreactive antigen 4650930:4652696 forward MW:66560
RPA4111	1.203265	0.0765	1.048735	0.4185	1.150892	0.126	1.701704	0.2185	1.174048	0.16	CDS hypothetical protein 4652962:4653267 forward MW:11191
RPA4112	1.255343	0.014	1.048004	0.297	1.075169	0.2465	0.98086	0.573	1.159106	0.039	CDS putative diguanylate cyclase (GGDEF) 4654732:4655625 forward MW:32741
RPA4113											CDS putative conjugal transfer protein trbB 4656317:4657198 forward MW:31357
RPA4114	1.327578	0.003	1.305636	0.0485	1.51167	0.001	0.803903	0.959	1.553871	0.005	CDS transcriptional regulator, LysR family 4657318:4658322 forward MW:36429
RPA4115	1.103019	0.081	1.068608	0.2125	1.061775	0.294	1.139425	0.093	1.146124	0.079	trbI2 putative conjugal transfer protein trbI 4658541:4659776 reverse MW:43732
RPA4116	1.037103	0.373	1.007175	0.475	1.01819	0.45	0.874554	0.8655	0.918243	0.7555	trbG2 conjugal transfer protein trbG 4659776:4660816 reverse MW:37546
RPA4117			1.034027	0.4145			1.368141	0.191			trbF2 conjugal transfer protein trbF 4660813:4661496 reverse MW:25398
RPA4118											CDS conjugal transfer protein trbL 4661500:4662795 reverse MW:42783
RPA4119											CDS hypothetical protein, possible TrbK 4662799:4663185 reverse MW:13696
RPA4120											CDS possible conjugal transfer protein trbJ 4663182:4663919 reverse MW:26137
RPA4121	0.995372	0.527	0.882819	0.9015	0.854365	0.9545	0.760191	0.9845	0.852999	0.955	trbE2 conjugal transfer protein trbE 4663916:4666357 reverse MW:90089
RPA4123	0.704009	0.956	0.682546	0.9145	0.836047	0.918	0.690588	0.7035	0.76954	0.968	trbC2 conjugal transfer protein trbC 4666630:4666974 reverse MW:12085
RPA4124											trbB2 conjugal transfer protein trbB 4666971:4667939 reverse MW:33626
RPA4125	1.127582	0.135	1.104595	0.2205	1.163567	0.0745	0.859069	0.794	1.349876	0.0315	CDS conserved hypothetical protein 4668297:4668737 reverse MW:16642
RPA4126	1.223338	0.024	1.223757	0.0325	1.583649	0.0015	1.182847	0.1175	1.902068	0.0025	CDS hypothetical protein 4668694:4669896 reverse MW:44471
RPA4127	1.246019	0.0685	1.035191	0.3695	1.483259	0.0055	0.924647	0.7205	2.027025	0.0025	CDS conserved hypothetical protein 4669871:4670587 reverse MW:26576
RPA4128	1.020297	0.378	0.993486	0.5335	1.286776	0.036	0.855055	0.9205	1.447072	0.003	CDS conserved hypothetical protein 4670603:4670845 reverse MW:8996
RPA4129	0.951492	0.712	0.831336	0.9085	0.851946	0.9415	0.699868	0.98	0.849184	0.887	CDS possible transcriptional regulator, XRE family 4670965:4671315 forward MW:12706
RPA4130	1.035278	0.3265	0.99479	0.5215	0.948053	0.743	0.905488	0.747	1.173045	0.1055	CDS unknown protein 4671312:4672205 forward MW:32201
RPA4131	0.879086	0.767	1.031247	0.401	1.136865	0.193	1.668507	0	2.429327	0	CDS Helix-turn-helix protein, CopG family 4672420:4672884 reverse MW:17168
RPA4132	0.917639	0.784	0.884165	0.8395	0.869985	0.848	1.011466	0.457	1.007478	0.472	traG1 plasmid transfer factor, traG 4672894:4674888 reverse MW:73112
RPA4133	0.959314	0.6715	1.116274	0.1205	1.132005	0.0715	1.413136	0.015	1.54353	0.0015	CDS conserved hypothetical protein 4675022:4675321 reverse MW:11583
RPA4134	1.071038	0.3305	1.194629	0.1295	1.001431	0.494	1.934421	0.131	1.144594	0.1785	CDS transcriptional regulatorf, XRE family 4675429:4675707 reverse MW:10161
RPA4135	0.950665	0.668	1.070178	0.1785	0.685979	0.9735	1.158789	0.162	1.125421	0.098	CDS GCN5-related N-acetyltransferase 4675844:4676341 reverse MW:18315
RPA4136	0.931267	0.7955	1.119384	0.135	0.973282	0.612	1.208734	0.0465	1.345588	0.006	CDS possible DNA topoisomerase 4676616:4678526 forward MW:68588
RPA4137	0.979579	0.5175	1.908157	0.001	1.078553	0.1905	2.214726	0.005	3.734333	0	CDS conserved unknown protein 4679131:4679562 reverse MW:15512
RPA4139	0.920704	0.842	0.733816	0.989	1.017269	0.4515	0.743067	0.964	0.832967	0.9175	CDS conserved hypothetical protein 4680511:4681149 reverse MW:21784
RPA4140	1.032044	0.4	0.802193	0.973	0.983163	0.5885	1.038472	0.375	0.923827	0.796	CDS sensor histidine kinase with a PAS domain 4683029:4684075 forward MW:37635
RPA4141	0.825853	0.859	0.806908	0.9585	0.932457	0.69	1.119927	0.2085	1.060369	0.3925	CDS conserved hypothetical protein 4684624:4684875 forward MW:9293
RPA4142	1.207223	0.2235	0.63465	0.985			0.99336	0.5035	1.186541	0.1445	CDS PilT protein, N-terminal 4684872:4685276 forward MW:14438
RPA4143	1.05258	0.383	1.098162	0.221	0.947063	0.645	1.142452	0.219	0.997501	0.496	nnrR putative nitric oxide responsive transcriptional regulator NnrR, Crp/Fnr family 4685360:4686070 forward MW:25765
RPA4144	0.87485	0.886	0.8288	0.8865	1.390631	0.052	0.65805	0.997	0.702432	0.997	CDS conserved hypothetical protein 4686043:4686267 reverse MW:8058

RPA4145	7.636828	0	7.939205	0	9.122524	0	1.079619	0.277	2.082097	0	nirK2 dissimilatory nitrite reductase 4686505:4687617 forward MW:40059
RPA4146	0.878837	0.661			1.190391	0.281			0.842472	0.653	CDS DUF323 4687786:4688667 forward MW:31677
RPA4147	0.647836	0.9235	1.095289	0.216	1.128131	0.277	0.628161	0.9955	0.361973	0.997	CDS putative nucleoside phosphorylase 4688895:4690361 forward MW:51823
RPA4148	0.723258	0.9005	1.065055	0.3065	0.898741	0.785	0.585278	0.992	0.370465	0.9995	prsA putative ribose-phosphate pyrophosphokinase 4690358:4691269 forward MW:32265
RPA4149	0.701568	0.9845	0.994623	0.5155	0.906885	0.758	0.760535	0.9245	0.464666	0.999	CDS Beta-lactamase-like 4691266:4692894 forward MW:59606
RPA4150	0.691213	0.967	0.702537	0.989	0.92307	0.792	0.899542	0.672	0.971091	0.6045	CDS conserved hypothetical protein 4693308:4693706 reverse MW:14540
RPA4151	0.693707	0.992	0.892105	0.77	0.894003	0.8175	1.477294	0.089	1.198804	0.1665	CDS transcriptional regulator, LysR family 4693809:4694681 forward MW:31476
RPA4152	1.405976	0.001	1.502914	0.003	1.420313	0.0235	1.894157	0.0275	1.571068	0.003	fbpA periplasmic iron binding protein FbpA precursor 4694801:4695811 forward MW:36170
RPA4153	0.951601	0.6995	1.223109	0.099	0.979272	0.5955	0.844254	0.9175	0.831681	0.974	fpbB putative iron transport system permease protein 4695889:4697601 forward MW:60707
RPA4154	0.79679	0.99	0.762372	0.986	1.138904	0.0555	0.862851	0.9435	1.090418	0.122	CDS unknown protein 4697718:4698356 forward MW:21848
RPA4155	1.038839	0.3405	0.859979	0.9585	0.719088	0.9835	0.802221	0.968	0.95839	0.7125	CDS 3-oxoadipate CoA-transferase subunit B 4698521:4699171 reverse MW:23101
RPA4156	1.063455	0.3025	1.000681	0.4935	0.889261	0.8695	0.970245	0.632	1.003104	0.492	CDS 3-oxoadipate CoA-transferase subunit A 4699183:4699899 reverse MW:25768
RPA4157	0.805787	0.974	0.725437	0.9915	0.89357	0.893	0.561816	0.9975	0.722785	0.982	CDS possible asmA protein, assembly of outer membrane proteins 4700050:4702053 forward MW:70147
RPA4158	0.93841	0.7985	0.877415	0.924	0.948043	0.749	0.840109	0.952	0.701434	0.9835	potI ABC transporter, polyamine transport protein, permease protein 4702211:4703011 reverse MW:28719
RPA4159	0.974281	0.57	1.195832	0.1585	0.988259	0.52	1.392009	0.056	1.258043	0.0785	potH polyamine ABC transporter permease protein 4703319:4704233 reverse MW:33667
RPA4160	0.954302	0.6755	0.737191	0.9605	0.948437	0.712	0.812798	0.951	0.730116	0.9785	CDS polyamine ABC transporter, ATP-binding protein 4704230:4705372 reverse MW:41019
RPA4161	0.919091	0.7335	0.881404	0.85	0.950351	0.618	0.923887	0.6765	0.883448	0.8195	CDS unknown protein 4705473:4706279 reverse MW:29806
RPA4162	1.520821	0.0425	1.288454	0.0945	1.23325	0.2225	2.467601	0	1.68085	0.0065	CDS putative taurine ABC transport system permease protein 4706510:4707343 forward MW:30118
RPA4163									1.658078	0.128	CDS putative taurine transport system ATP-binding protein 4707355:4708209 forward MW:30838
RPA4164	1.325489	0.019	1.285254	0.0165	1.532911	0.0105	5.973048	0.0005	3.305598	0	CDS possible aliphatic sulfonate binding protein of ABC transporter system 4708273:4709268 forward MW:35415
RPA4165	1.024167	0.4225	1.168326	0.091	1.021795	0.4065	1.991301	0.0025	1.815148	0	CDS conserved hypothetical protein 4709325:4710020 forward MW:25345
RPA4166	0.969167	0.6255	0.971151	0.6295	1.107264	0.1215	1.784432	0.0035	1.514914	0.004	CDS putative nitrilase 4710032:4710985 forward MW:33711
RPA4167	0.894598	0.938	0.853077	0.9675	0.85362	0.9635	1.115248	0.125	1.101134	0.11	CDS putative diguanylate cyclase (GGDEF)/phosphodiesterase (EAL) with PAS domains 4711028:4713766 reverse MW:99709
RPA4168	0.721842	0.98	0.751452	0.926	0.672283	0.962	0.6432	0.9905	0.68869	0.9985	CDS NAD binding site:FAD dependent oxidoreductase 4713876:4714976 forward MW:38010
RPA4169									1.000845	0.5075	CDS Bacterial regulatory protein, GntR family 4715067:4715798 forward MW:26811
RPA4170	0.911684	0.7135	1.004276	0.4965	1.102512	0.1105	1.658452	0.0085	2.129703	0	CDS possible branched-chain amino acid ABC transport system substrate-binding protein 4716074:4717276 forward MW:43977
RPA4171	1.045564	0.3245	0.776778	0.9385	1.769738	0.005	1.213028	0.0525	0.926165	0.615	CDS conserved unknown protein 4717693:4718007 reverse MW:12298
RPA4172	1.003757	0.4785	0.888639	0.9515	1.182955	0.077	1.154721	0.101	1.279573	0.044	CDS hypothetical protein 4718090:4718449 reverse MW:13455
RPA4173	0.552495	0.988	0.670544	0.962	0.739164	0.997	0.510277	0.9995	0.486743	0.999	CDS putative diguanylate cyclase (GGDEF) 4718430:4719182 reverse MW:26932
RPA4174	0.629154	0.999	0.642365	0.9985	0.673868	0.992	0.558277	1	0.683202	0.9975	purE phosphoribosylaminoimidazole carboxylase catalytic subunit 4719311:4719799 forward MW:16380
RPA4175	0.620187	0.9985	0.653179	0.9985	0.637261	0.996	0.520253	0.9995	0.685422	0.999	purK phosphoribosylaminoimidazole carboxylase ATPase subunit 4719796:4720896 forward MW:39372
RPA4176	1.037729	0.441	1.794548	0.01	1.116355	0.2675	1.798188	0.035	1.239741	0.225	rpsU, S21 ribosomal protein S21 4721053:4721316 forward MW:10064
RPA4177	0.649974	0.9795	0.73198	0.9925	0.89564	0.8345	0.508735	1	0.630025	0.999	CDS conserved hypothetical protein 4721493:4722368 reverse MW:30360
RPA4178	0.750864	0.9625	0.701429	0.941	0.921679	0.7385	0.792178	0.839	0.619574	0.9955	CDS conserved unknown protein 4722518:4722805 reverse MW:10402
RPA4179	0.706181	0.9755	0.557272	0.997	0.919697	0.784	0.671549	0.9865	0.358696	0.999	CDS conserved unknown protein 4723009:4723383 forward MW:13394
RPA4180	1.103971	0.1695	1.053362	0.303	0.984699	0.5365	0.654262	0.976	0.793423	0.806	pntB nicotinamide nucleotide transhydrogenase, subunit beta 4723562:4724965 reverse MW:48113
RPA4181	0.880843	0.7775	1.138587	0.1635	0.851766	0.951	0.471181	0.9995	0.771173	0.9415	pntA beta nicotinamide nucleotide transhydrogenase, subunit alpha2 4724979:4725302 reverse MW:11651
RPA4182	0.97107	0.6105	1.130518	0.2265	0.80703	0.979	0.555505	0.996	0.880978	0.948	pntA alpha nicotinamide nucleotide transhydrogenase, subunit alpha1 4725328:4726455 reverse MW:39220
RPA4183	1.518672	0.024	2.14109	0.004	1.073923	0.228	1.045707	0.4335	1.287428	0.077	CDS hypothetical protein 4726655:4726807 reverse MW:5522
RPA4184	0.777694	0.8175			0.98707	0.5015			0.839215	0.676	CDS hypothetical protein 4727027:4727329 forward MW:11003
RPA4185	0.884592	0.945	0.772193	0.9855	1.136337	0.1015	0.920829	0.772	0.653672	0.9945	CDS putative oligoendopeptidase F 4727285:4729201 reverse MW:70787
RPA4186	0.853122	0.9785	0.865698	0.922	0.808634	0.989	0.811624	0.964	1.049743	0.2355	CDS Integral membrane protein TerC family 4729537:4730202 forward MW:23595
RPA4187	0.771418	0.9935	0.652687	0.9985	0.627766	0.999	0.620696	0.997	0.873583	0.9055	CDS two component sigma-54-dependent transcriptional regulator, Fis family 4730298:4731785 forward MW:53715
RPA4188	0.968207	0.621	0.805502	0.983	0.805619	0.9615	0.838539	0.9605	0.890533	0.8715	CDS conserved unknown protein 4732135:4734309 forward MW:78899
RPA4189	1.052263	0.2965	0.841709	0.982	1.034845	0.369	0.800954	0.9705	0.958616	0.6865	CDS conserved hypothetical protein 4734594:4736255 forward MW:58338
RPA4190	0.761586	0.976	0.921631	0.799	0.925814	0.796	0.76651	0.972	0.755484	0.9945	CDS conserved unknown protein 4736383:4736772 reverse MW:14762
RPA4191	0.852881	0.936	0.815236	0.972	0.991499	0.5405	0.750278	0.976	0.813891	0.982	CDS conserved unknown protein 4736843:4737142 reverse MW:11245
RPA4192	0.795818	0.9785	0.865688	0.919	0.919705	0.799	0.731132	0.9585	0.893602	0.8645	CDS conserved hypothetical protein 4737334:4737918 forward MW:20944
RPA4193	0.604516	0.999	0.701793	0.995	0.71685	0.992	0.562981	0.999	0.603555	0.9985	pyk pyruvate kinase 4737915:4739348 forward MW:51438
RPA4194	0.886748	0.89	0.822608	0.8185	1.006699	0.476	0.630291	0.953	0.736561	0.985	osmC osmotically inducible protein OsmC 4739575:4740003 reverse MW:14582
RPA4195	0.885981	0.752	0.783437	0.8555	0.80689	0.908	0.815247	0.823	0.805414	0.9345	CDS putative hydrolase 4740000:4741004 reverse MW:35374
RPA4196	1.525619	0.0035	0.874508	0.887	1.891843	0.002	1.262417	0.079	1.417017	0.0395	CDS TPR repeat 4741075:4741737 reverse MW:24183
RPA4197	1.137337	0.0385	1.467807	0.003	1.120979	0.168	2.069317	0.0025	1.498028	0.0195	rpmJ, L36 50S ribosomal protein L36 4741835:4741960 reverse MW:5065
RPA4198	1.073334	0.239	0.998034	0.513	0.858464	0.9535	0.872002	0.898	0.858463	0.9705	CDS Amidohydrolase 2 4742272:4743141 forward MW:32642
RPA4199			0.793239	0.806			0.903317	0.674	0.607356	0.995	CDS putative 2-haloacid halidohydrolase Iva 4743290:4744027 forward MW:27079
RPA4200	0.862339	0.948	1.034615	0.326	0.995503	0.514	0.868402	0.9145	0.950884	0.7165	CDS YbaK / prolyl-tRNA synthetases associated domain 4744104:4744586 forward MW:16797
RPA4201	0.814487	0.871	0.66559	0.9965	0.786003	0.9505	0.565469	0.9885	1.230589	0.0505	CDS hypothetical protein 4744660:4744950 reverse MW:10544
RPA4202	1.080414	0.21	1.586861	0.0025	0.957508	0.7085	1.352281	0.0205	1.376886	0.0115	CDS methyl-accepting chemotaxis sensory transducer 4745124:4746449 reverse MW:45858
RPA4203	1.45341	0.073	2.005155	0.01			2.289017	0.003	1.736969	0.0015	CDS putative sensor (PAS) domain for methyl-accepting chemotaxis sensory transducer 4746424:4746945 reverse MW:19687
RPA4204	2.029617	0.004	6.079754	0.0025	2.55333	0.0005	3.030324	0.03	3.958786	0.0005	CDS hypothetical protein 4747181:4747441 reverse MW:8972
RPA4205	1.136363	0.274	1.038832	0.3975	0.864305	0.852	1.044605	0.4135	1.057643	0.313	CDS possible polysaccharide export protein, PST family 4747662:4749023 forward MW:48738
RPA4206	0.894997	0.9075	0.860536	0.947	1.100725	0.2025	0.53248	1	0.726236	0.984	CDS D-beta-hydroxybutyrate dehydrogenase 4749468:4750256 reverse MW:27536
RPA4207			0.522636	0.999							CDS Patatin-like phospholipase domain 4750305:4751444 reverse MW:42862
RPA4208	0.69372	0.999	0.843043	0.9455	0.879308	0.922	0.646365	0.9935	0.892985	0.8855	CDS SCP-like extracellular protein 4751539:4752054 reverse MW:18110
RPA4209	35.2858	0	23.06057	0	43.22351	0	84.0369	0	36.74092	0	glnA II glutamine synthetase II 4752301:4753338 reverse MW:38677
RPA4210	0.909656	0.634	1.982864	0.0025	1.056608	0.295	1.097053	0.289	1.383299	0.0245	CDS hypothetical protein 4753765:4754016 forward MW:9212
RPA4211	0.926718	0.615	0.972615	0.5665	1.157459	0.215	1.089021	0.2655	0.918844	0.76	glsA glutaminase A 4754118:4755053 reverse MW:32985
RPA4212	0.782559	0.6605	1.399658	0.044	0.8187	0.8855	0.76392	0.8615	0.643259	0.9985	CDS conserved hypothetical protein 4755200:4755709 reverse MW:19007
RPA4213	0.852679	0.6125	1.463575	0.0335	0.581227	0.9765	0.820079	0.877	0.658617	0.932	CDS sulfite reductase hemoprotein subunit 4755696:4757351 reverse MW:61125
RPA4214	0.81151	0.783	1.093444	0.19	0.609743	0.9805	0.804913	0.906	0.522344	0.997	CDS conserved hypothetical protein 4757362:4757676 reverse MW:10704
RPA4215	0.823953	0.93	0.475508	0.9925	0.780984	0.9955	0.562423	0.961	0.579534	0.999	cysG putative siroheme synthase 4757673:4759109 reverse MW:50799
RPA4216	0.689525	0.982	0.647295	0.999	0.499852	1	0.465723	0.9995	0.508295	0.997	glcB malate synthase G 4759508:4761682 forward MW:78627
RPA4217	1.480499	0.0035	1.777841	0.0015	1.503734	0.001	2.241677	0	2.079486	0	CDS conserved unknown protein 4761873:4762073 forward MW:7991
RPA4218							1.167408	0.2725			CDS conserved hypothetical protein 4762211:4762372 reverse MW:5866
RPA4219	1.601073	0.0475	1.282647	0.042	0.902829	0.7615	2.459003	0.0005	1.548075	0.02	CDS conserved hypothetical protein 4762529:4763191 reverse MW:23305
RPA4220	1.255188	0.24	1.245631	0.2285			0.689727	0.983			CDS ErfK/YbiS/YcfS/YnhG 4763214:4763981 reverse MW:27174
RPA4221	1.217895	0.094			1.167504	0.1445	1.321941	0.067	0.871383	0.762	CDS putative permease 4764203:4765318 forward MW:40343

RPA4222			3.19821	0.0005			1.542222	0.094	2.083512	0.0025	CDS hypothetical protein 4765452:4765847 reverse MW:13176
RPA4223	1.224137	0.0375	1.819299	0.01	1.630073	0.008	0.935991	0.6385	1.652361	0.0005	CDS response regulator receiver (CheY-like protein) with unknown domain 4766223:4767029 reverse MW:29317
RPA4224	1.609837	0.0035	2.771558	0.008	2.336555	0.0015	1.578447	0.093	2.321534	0	CDS unknown protein 4767160:4767444 forward MW:10375
RPA4225	1.874235	0.001	3.206328	0.0035	2.454206	0.0015	1.562651	0.0765	2.868171	0	CDS RNA polymerase ECF-type sigma factor 4767444:4767989 forward MW:19690
RPA4226	0.890048	0.9245	1.116615	0.1635	1.052742	0.2755	0.819726	0.916	0.989147	0.558	CDS putative signal transduction histidine kinase with Chase domain 4768147:4769913 reverse MW:64832
RPA4227	0.792509	0.961	1.017171	0.418	0.726358	0.9965	0.529179	0.995	0.736175	0.9965	ureG urease accessory protein UreG 4770066:4770695 reverse MW:22330
RPA4228	0.979515	0.5875	0.910552	0.8405	1.025064	0.3845	1.227331	0.08	1.14522	0.0835	CDS hypothetical protein 4770919:4771263 forward MW:12625
RPA4229	1.222926	0.0235	1.213783	0.038	1.29185	0.015	1.220084	0.038	1.234122	0.0395	CDS hypothetical protein 4771282:4771632 forward MW:12786
RPA4230	0.970331	0.654	0.954756	0.6345	1.039337	0.3675	1.010898	0.4365	0.912961	0.7345	CDS conserved unknown protein 4772098:4772382 forward MW:10163
RPA4231	1.226727	0.0065	1.365787	0.007	1.452737	0.0035	1.545852	0.003	1.583062	0	CDS putative oxidoreductase 4772451:4774562 reverse MW:76660
RPA4232	2.033747	0.0485	7.139881	0.004	2.41015	0.0035	2.262091	0.066	2.260003	0.0025	CDS hypothetical protein 4774697:4775023 forward MW:12085
RPA4233	1.084303	0.333	1.714143	0.0005	1.578091	0.001	1.364335	0.0065	1.277341	0.0145	CDS Cyclic nucleotide regulated K+ channel 4775037:4776275 reverse MW:46121
RPA4234	1.093427	0.3495	1.770932	0.0045	1.148807	0.295	1.450638	0.0305	0.935213	0.5905	aadR anaerobic aromatic degradation regulator aadR, Crp/Fnr family 4776328:4777047 reverse MW:26711
RPA4235	0.71679	0.889	1.615861	0.029	1.06453	0.403	1.393593	0.047	0.841692	0.694	CDS putative cytochrome c, class I 4777176:4777559 forward MW:14147
RPA4236	0.848155	0.964	0.937161	0.8295	0.84647	0.909	0.786325	0.968	1.255918	0.0765	CDS Mce4/Rv3499c/MTV023.06c protein 4777519:4778715 reverse MW:42015
RPA4237	0.809609	0.989	0.77953	0.992	0.94724	0.7405	0.67528	0.9905	1.221444	0.0275	CDS ATP-binding component of ABC transporter 4778728:4779507 reverse MW:28087
RPA4238	0.842634	0.964	0.698955	0.9825	1.035598	0.314	1.241727	0.0615	1.916046	0.0015	CDS putative permease of ABC transporter 4779510:4780646 reverse MW:40575
RPA4239	1.318026	0.008	1.485895	0.006	1.682422	0.013	1.392942	0.0235	1.177006	0.263	CDS conserved unknown protein 4780758:4781219 forward MW:17228
RPA4240	0.614598	0.997	0.720789	0.9745	0.852322	0.923	0.725544	0.981	0.700163	0.998	CDS GCN5-related N-acetyltransferase:CoA Binding Domain 4781248:4783971 reverse MW:97617
RPA4241	0.661729	0.9165	1.440864	0.0125	1.132222	0.3265	1.224791	0.023	0.68679	0.796	CDS CBS domain 4784111:4784503 reverse MW:15098
RPA4242	0.968504	0.5775	0.848272	0.871	0.942086	0.7405	1.044534	0.3755	0.808313	0.9645	CDS conserved hypothetical protein 4784794:4786353 forward MW:54810
RPA4243	0.967364	0.6185	1.032638	0.331	1.075657	0.2225	0.908756	0.8255	0.728742	0.95	phaC putative poly-beta-hydroxyalkanoate synthase 4786335:4788101 reverse MW:65505
RPA4244	0.904171	0.709	1.06336	0.276	1.356313	0.013	0.973482	0.632	0.693185	0.9515	CDS conserved unknown protein 4788368:4789204 reverse MW:30363
RPA4245	1.204131	0.26	1.662566	0.0025	1.653309	0.0345	1.307793	0.0445	0.993082	0.5025	CDS conserved unknown protein 4789394:4790227 forward MW:29180
RPA4246	1.026821	0.4405	1.466425	0.005	1.758272	0.001	1.045723	0.3035	0.817425	0.9175	CDS CBS domain:Transport-associated domain 4790314:4791045 forward MW:27066
RPA4247	0.863883	0.943	0.954278	0.7355	0.880176	0.901	0.926432	0.799	0.885963	0.9135	fixL two component low oxygen sensor histidine kinase with PAS domains, fixL 4791190:4792716 forward MW:55967
RPA4248	0.970259	0.678	0.891212	0.787	0.912849	0.7855	0.931921	0.681	0.891562	0.8815	fixJ two-component nitrogen fixation transcriptional regulator fixJ, LuxR family 4792709:4793320 forward MW:22255
RPA4249	0.941602	0.608	1.452653	0.0035	1.104373	0.3015	1.376731	0.008	1.007381	0.48	CDS response regulator receiver (CheY-like protein) 4793406:4793798 forward MW:14057
RPA4250	1.155468	0.152	1.895457	0.0035	1.805211	0.0735	1.525183	0.211	0.574639	0.8655	fixK2 nitrogen fixation transcriptional regulator fixK2, Crp/Fnr family 4793997:4794689 forward MW:25420
RPA4251	1.022511	0.48	2.167654	0.019	0.437834	0.964	1.010123	0.477	0.390268	0.993	oahs O-acetylhomoserine sulfhydrylase 4795019:4796326 forward MW:46820
RPA4252	0.691866	0.813	1.385658	0.047	0.524791	0.8915	0.993508	0.514	0.476881	0.987	nuoN2 NADH-ubiquinone dehydrogenase chain N 4796479:4797843 reverse MW:46273
RPA4253	0.793515	0.9515	0.765958	0.9425	0.866554	0.785	0.918943	0.7825	0.811068	0.854	nuoM2 NADH-ubiquinone dehydrogenase chain M 4797854:4799296 reverse MW:50857
RPA4254	0.515312	1	0.480847	0.997	0.646657	0.9885	0.386572	0.998	0.32292	0.9995	nuoL2 NADH-ubiquinone dehydrogenase chain L 4799287:4801356 reverse MW:72136
RPA4255			0.575554	0.8745	0.86899	0.7635	0.68977	0.855			nuoK2 NADH-ubiquinone dehydrogenase chain K 4801359:4801667 reverse MW:10374
RPA4256	0.539747	0.9955	0.53059	0.992	0.732128	0.972	0.352579	1	0.310427	0.9995	nuoJ2 NADH-ubiquinone dehydrogenase chain J 4801664:4802170 reverse MW:17693
RPA4257	0.542042	0.993	0.374241	0.9965	0.602038	0.9965	0.380379	0.9955	0.235561	1	nuoI2 NADH-ubiquinone dehydrogenase chain I 4802167:4802688 reverse MW:19493
RPA4258	0.5627	0.9995	0.600685	0.9785	0.817425	0.9595	0.464009	0.9995	0.350865	0.9995	nuoH2 NADH-ubiquinone dehydrogenase chain H 4802685:4803644 reverse MW:34127
RPA4259	0.689228	0.987	0.452108	0.999	0.927572	0.7625	0.555323	0.995	0.425359	0.999	nuoG2 NADH-ubiquinone dehydrogenase chain G 4803641:4806274 reverse MW:92692
RPA4260	0.490692	0.996	0.648222	0.999	0.747808	0.9935	0.414734	1	0.394347	0.998	nuoF2 NADH-ubiquinone dehydrogenase chain F 4806271:4807557 reverse MW:45342
RPA4261	0.490657	0.999	0.594462	0.9995	0.550633	0.9975	0.400917	1	0.371913	1	nuoE2 NADH-ubiquinone dehydrogenase chain E 4807554:4808042 reverse MW:16493
RPA4262	0.534535	0.9985	0.588958	0.9995	0.531454	0.997	0.396815	1	0.396686	0.999	nuoCD NADH-ubiquinone dehydrogenase chain C,D 4808039:4809784 reverse MW:65863
RPA4263	0.535773	0.9955	0.568659	0.998	0.890271	0.795	0.441393	0.9995	0.383451	0.9995	nuoB2 NADH-ubiquinone dehydrogenase chain B 4809781:4810407 reverse MW:23238
RPA4264	0.592854	0.9975	0.712625	0.9975	0.799958	0.945	0.629963	0.999	0.890437	0.7635	nuoA2 NADH-ubiquinone dehydrogenase chain A 4810404:4810793 reverse MW:13690
RPA4265	0.825034	0.9515	0.715494	0.998	0.842791	0.9315	0.548262	0.9935	0.616625	0.9985	ndvA putative beta-1,2-glucan ABC export system ATP-binding protein ndvA 4811238:4813037 forward MW:65674
RPA4266	0.98155	0.573	0.778368	0.9835	1.000448	0.4895	0.767174	0.9825	0.923343	0.852	CDS possible D-alanyl-D-alanine carboxypeptidase (penicillin-binding protein) 4813207:4814661 forward MW:50863
RPA4267	1.04532	0.3845	0.837008	0.9785	1.023303	0.383	0.827104	0.9195	0.873288	0.954	CDS long-chain-fatty-acid-CoA-ligase 4814933:4816624 forward MW:61345
RPA4268	0.818538	0.932	0.70462	0.999	0.925963	0.7235	0.633673	0.997	0.539574	0.9995	CDS peroxiredoxin-like protein 4816864:4817349 forward MW:17396
RPA4269	0.867716	0.971	0.928336	0.792	0.754262	0.9885	0.810859	0.952	1.051034	0.2665	CDS ribonuclease H 4817500:4817967 reverse MW:17289
RPA4270	0.857548	0.974	0.920425	0.8345	0.761865	0.9805	0.775765	0.9555	0.957284	0.6485	thrB homoserine kinase 4817964:4818947 reverse MW:35821
RPA4271	0.811886	0.95	0.993089	0.538	0.818399	0.9805	0.76436	0.9885	1.106187	0.142	lytB2 penicillin tolerance protein (lytB) , control of stringent response 4819047:4820009 reverse MW:34613
RPA4272	0.903075	0.794	1.029958	0.415	0.64023	0.977	0.832129	0.931	1.108593	0.2145	CDS conserved unknown protein 4820269:4820985 forward MW:26110
RPA4273	0.427713	0.971			0.895365	0.77			1.313963	0.2345	CDS hypothetical protein 4821237:4821614 reverse MW:14497
RPA4274	1.510769	0.001	1.558684	0.005	1.177034	0.057	1.784703	0.0125	1.909418	0.0005	CDS conserved hypothetical protein 4822209:4823204 reverse MW:37017
RPA4275	1.562705	0.084	2.351321	0.0005	1.03452	0.4265	0.936049	0.586			CDS hypothetical protein 4823656:4824075 forward MW:14848
RPA4276	1.400471	0.0095	2.198452	0.0005	1.11192	0.176	2.492648	0.0265	1.753578	0.003	CDS hypothetical protein 4824214:4824513 forward MW:10273
RPA4277	0.809202	0.9855	0.751379	0.9935	0.89671	0.909	0.806548	0.9385	0.73861	0.995	CDS conserved hypothetical protein 4826624:4827253 forward MW:23238
RPA4278	0.988314	0.5495	0.960576	0.714	1.032168	0.367	1.708571	0.0015	1.320207	0.016	CDS hypothetical protein 4827318:4827884 forward MW:20864
RPA4279							2.043412	0.009	1.413039	0.0595	CDS hypothetical protein 4828105:4828641 forward MW:18757
RPA4280	0.945941	0.786	0.9061	0.819	1.030562	0.359	1.347243	0.0095	1.270182	0.0325	CDS probable transcriptional regulator, AraC family 4828657:4829655 reverse MW:36728
RPA4281	0.879664	0.8225	0.873974	0.9195	0.948769	0.6945	0.906352	0.7175	0.838286	0.878	CDS conserved hypothetical protein 4830173:4831345 forward MW:39594
RPA4282	0.900874	0.91	0.804359	0.993	0.999691	0.484	0.882902	0.888	0.851028	0.9435	CDS possible activator of photopigment and puc with BLUF domain 4831532:4832005 forward MW:17944
RPA4283	0.953718	0.6975	0.772012	0.99	0.740348	0.983	0.976843	0.5735	1.01104	0.4445	CDS transcriptional regulator, LysR family 4832018:4832923 reverse MW:32743
RPA4284	0.374663	1	0.444401	0.9945	0.471706	0.9975	0.41459	1	0.481376	0.9995	CDS YceI like family 4833016:4833657 forward MW:22807
RPA4285	0.552526	0.998	0.589726	0.986	0.572441	0.9995	0.522046	0.932	0.622684	0.972	CDS Nitroreductase family 4833734:4834324 forward MW:21551
RPA4286	0.579237	0.9995	0.646557	0.997	0.613614	0.9995	0.5595	0.9985	0.597323	0.9995	CDS Catalytic LigB subunit of aromatic ring-opening dioxygenase 4834367:4835170 forward MW:28564
RPA4287											CDS conserved hypothetical protein 4835541:4836173 reverse MW:23582
RPA4288	1.032562	0.3275	1.002849	0.497	1.107355	0.0805	0.916735	0.7875	1.052998	0.297	CDS conserved hypothetical protein 4836310:4837083 forward MW:26803
RPA4289	1.097172	0.276			0.958456	0.6265			0.916446	0.6585	CDS putative dual use protein Tyr:Ser/Thr phosphatase 4837083:4837640 forward MW:20230
RPA4290	0.638181	0.9985	0.84034	0.919	0.698406	0.982	0.617379	0.986	0.425834	1	CDS conserved hypothetical protein 4837773:4838222 forward MW:16522
RPA4292	1.194848	0.065	1.417741	0.0145	1.275534	0.03	1.194653	0.1045	1.18985	0.028	pucAb light harvesting protein B-800-850, alpha chain B (antenna pigment protein, alpha chain B) (LH II-B alpha) 4838726:4838926 forward MW:6824
RPA4293	3.02231	0.0075	7.523432	0.0005	3.003067	0	3.080811	0.0385	3.545243	0.002	CDS hypothetical protein 4839395:4839613 forward MW:7683
RPA4294	0.895794	0.9245	0.856737	0.946	0.722334	0.982	0.822196	0.959	1.047589	0.287	CDS unknown protein 4840036:4841637 reverse MW:57276
RPA4295	0.726586	0.993	0.8291	0.975	0.560999	0.9985	0.606699	0.998	0.828068	0.97	purA adenylosuccinate synthetase 4841675:4842967 reverse MW:46536
RPA4296	1.373599	0.01	1.215584	0.04	1.75707	0.0015	1.63268	0.0015	1.303137	0.058	CDS unknown protein 4843263:4843796 reverse MW:19775
RPA4297	0.994788	0.5265	0.865677	0.908	1.065406	0.29	0.641356	0.994	0.674185	0.9985	CDS putative aldose reductase 4843966:4844790 forward MW:30120
RPA4298	0.867378	0.6225			1.020377	0.482			0.638785	0.669	CDS ATP/GTP-binding site motif A (P-loop) 4845043:4845702 forward MW:22762
RPA4299	0.828221	0.9705	0.841776	0.9355	0.738103	0.994	0.608006	0.9975	0.689165	0.9965	CDS Permeases of the drug/metabolite transporter (DMT) superfamily 4845862:4846791 forward MW:33756

RPA4300	0.693718	0.9975	0.8964	0.869	0.941191	0.653	0.655955	0.996	0.443098	0.999	CDS Permeases of the drug/metabolite transporter (DMT) superfamily 4847325:4848356 forward MW:37591
RPA4301			0.732801	0.927	1.148644	0.2875	0.895287	0.6545	0.711133	0.9625	CDS hypothetical protein 4848372:4848566 reverse MW:6497
RPA4302	0.980531	0.5635	0.619316	0.9945	0.87322	0.664	0.762479	0.887	1.231842	0.1255	CDS methyl-accepting chemotaxis receptor/sensory transducer 4848828:4851020 reverse MW:77138
RPA4303	0.910399	0.9005	0.666124	0.998	0.94629	0.7785	0.705843	0.981	0.793526	0.9835	CDS conserved hypothetical protein 4851150:4852121 reverse MW:35996
RPA4304	0.695649	0.992	0.873018	0.865	0.815599	0.9665	0.724554	0.967	0.577919	0.999	CDS conserved hypothetical protein 4852302:4853657 forward MW:49430
RPA4305	0.644208	0.987	0.591713	0.9995	0.622484	0.9965	0.555898	0.998	0.627844	0.999	CDS hypothetical protein 4853852:4854190 reverse MW:12171
RPA4306	0.750357	0.9515	0.51966	1	0.840711	0.9165	0.416019	0.9995	0.588463	0.9975	CDS methyl-accepting chemotaxis receptor/sensory transducer 4854274:4855959 reverse MW:58534
RPA4307	1.236601	0.0105	1.661564	0.0175	1.022978	0.3905	1.536194	0.0755	1.413715	0.016	CDS methyl-accepting chemotaxis receptor/sensory transducer 4856166:4857851 reverse MW:58967
RPA4308	0.957448	0.663	1.237174	0.071	0.835915	0.981	0.996272	0.509	0.853839	0.8835	serA2 putative phosphoglycerate dehydrogenase 4858096:4859685 reverse MW:56215
RPA4309	1.206712	0.039	1.036364	0.362	1.079167	0.3105	1.113433	0.236	1.169932	0.035	serC phosphoserine aminotransferase, 4859855:4861027 reverse MW:41933
RPA4310	0.860204	0.759	1.019286	0.4195							CDS hypothetical protein 4861265:4861714 reverse MW:13506
RPA4311	1.16968	0.024	1.071348	0.264	1.161059	0.172	1.356266	0.035	1.238146	0.107	CDS methyl-accepting chemotaxis sensory transducer 4861753:4863057 reverse MW:44029
RPA4312	1.246468	0.0345	1.004792	0.4905	0.807913	0.891	1.570164	0.032	1.519998	0.0015	CDS putative sensor (PAS) domain for methyl-accepting chemotaxis sensory transducer 4863032:4863556 reverse MW:20231
RPA4313	1.032797	0.3845	1.129154	0.243	0.870836	0.8235	2.114424	0.0155	1.728956	0.001	CDS putative acetyltransfersase 4863729:4864199 reverse MW:17290
RPA4314	1.034339	0.372	0.877843	0.769	0.912801	0.85	1.254353	0.121	1.407372	0.03	gstA2 possible glutathione S-transferase 4864211:4864804 reverse MW:22040
RPA4315	1.189562	0.0635	0.894031	0.8675	0.789862	0.912	0.998859	0.5	1.011507	0.445	CDS conserved hypothetical protein 4864870:4865697 reverse MW:28548
RPA4316	1.295356	0.05	1.05309	0.301	0.934785	0.6985	1.10327	0.212	1.130054	0.0855	CDS conserved hypothetical protein 4865804:4866679 reverse MW:31257
RPA4317	0.775422	0.987	0.760515	0.9545	1.195092	0.048	0.669585	0.952	0.654027	0.997	CDS putative fosmidomycin resistance protein 4866990:4868342 reverse MW:47549
RPA4318	0.871484	0.87	0.753897	0.9905	0.816903	0.9085	0.612047	0.9845	0.752187	0.9835	mrsA phosphoglucomutase/phosphomannomutase family protein MrsA 4868426:4869778 reverse MW:48364
RPA4319	1.067653	0.318	1.532495	0.0365	1.106883	0.2065	1.043801	0.324	1.415087	0.004	CDS hypothetical protein 4869980:4870141 reverse MW:5751
RPA4320	0.955344	0.6915	0.853061	0.9375	0.852358	0.9245	0.740919	0.9885	0.7627	0.9955	lldA L-lactate dehydrogenase 4870306:4871445 forward MW:41483
RPA4321	0.90119	0.7925	0.657204	0.9955	0.921581	0.8665	0.521521	0.9985	0.521926	0.999	paaG3 putative enoyl-CoA hydratase paaG 4871637:4872452 forward MW:29129
RPA4322	0.913894	0.74	0.592339	0.993	0.84979	0.9245	0.971481	0.545	0.903834	0.689	CDS response regulator receiver (CheY-like protein) 4872601:4873059 forward MW:16603
RPA4323	1.300316	0.013	1.509246	0.0045	1.031584	0.348	1.46243	0.103	1.381847	0.0185	CDS hypothetical protein 4873169:4874002 forward MW:31104
RPA4324	1.226402	0.0445	1.37966	0.004	0.838732	0.891	1.174261	0.1905	1.624187	0.007	CDS hypothetical protein 4873999:4874490 forward MW:18135
RPA4325	1.227072	0.0535	1.198537	0.0715	0.870207	0.9255	1.156146	0.081	1.27638	0.0195	aroE putative shikimate 5-dehydrogenase 4874622:4875458 reverse MW:29554
RPA4326	1.032219	0.431	0.62148	0.9965	1.86171	0.0015	0.8564	0.814	0.862781	0.7075	sulP sulfate transporter family protein 4875560:4877311 reverse MW:60976
RPA4327	0.703061	0.9775	0.41352	0.9465	0.685705	0.987	0.981314	0.5115	0.872189	0.69	CDS transcriptional regulator, XRE family 4877353:4877622 reverse MW:9447
RPA4328	0.765001	0.9485	1.038514	0.3935	1.543139	0.036	0.777759	0.966	0.623095	0.9655	CDS elongation factor G, EF-G 4877790:4879841 reverse MW:73379
RPA4329	0.699465	0.9945	0.621775	0.9805	0.757467	0.8535	0.51999	0.997	0.494252	0.9945	CDS conserved unknown protein 4880054:4880527 reverse MW:15828
RPA4330	0.643558	0.981	0.70561	0.946	0.857602	0.7845	0.522814	0.992	0.474962	0.999	CDS conserved unknown protein 4880757:4881272 reverse MW:17905
RPA4331	1.128707	0.0815	0.979703	0.6005	1.042131	0.3675	1.118416	0.2255	1.179488	0.0305	aatA aspartate aminotransferase A 4881397:4882632 reverse MW:44426
RPA4332	0.920098	0.783	0.767346	0.99	1.138384	0.056	0.756187	0.9685	0.744079	0.9945	gstA1 possible glutathione S-transferase 4883013:4883666 forward MW:24379
RPA4333	0.819523	0.9785	0.901737	0.849	1.04223	0.304	0.795998	0.962	0.920592	0.8275	CDS conserved hypothetical protein 4884085:4885248 forward MW:41416
RPA4334	0.798594	0.954	0.777075	0.976	1.187008	0.0695	0.961743	0.5955	1.193146	0.1085	CDS possible acyltransferase 4885462:4886310 forward MW:30679
RPA4335	0.609704	0.9995	0.558516	0.997	1.190605	0.071	0.705201	0.974	0.97284	0.6265	CDS DnaB helicase 4886317:4887036 reverse MW:26041
RPA4336	0.567431	1	0.584238	0.997	0.834012	0.955	0.440403	1	0.44099	1	CDS putative oxidoreductase, 4887317:4888258 forward MW:34556
RPA4337	0.826986	0.8035	0.928914	0.6565	0.847693	0.853	1.544141	0.3115	0.768688	0.9775	CDS putative phosphoglycolate phosphatase 4888708:4889451 forward MW:26094
RPA4338											CDS transcriptional regulator, TetR family 4889378:4890058 reverse MW:24577
RPA4339	0.823747	0.684							0.727016	0.746	CDS possible crotonase, 3-hydroxbutyryl-CoA dehydratase 4890140:4890931 forward MW:28169
RPA4340	0.91315	0.824	0.912566	0.8365	0.828927	0.933	0.824778	0.894	0.82155	0.9835	ligE putative lignin beta-ether hydrolase 4890919:4891722 reverse MW:29653
RPA4341	0.592497	0.995	0.520275	0.9955	0.619066	0.989	0.496294	1	0.380686	1	CDS Beta-lactamase-like 4891911:4893896 reverse MW:72124
RPA4342	1.402675	0.0005	1.352101	0.0085	1.151215	0.0905	1.306878	0.012	1.765562	0	CDS conserved hypothetical protein 4894128:4895180 forward MW:38104
RPA4343	0.782806	0.978	0.67734	0.997	0.832383	0.9485	0.682843	0.9735	0.646797	0.9855	uvrB possible excinuclease ABC subunit B 4895687:4898275 forward MW:95790
RPA4344											CDS hypothetical protein 4898366:4898599 forward MW:8539
RPA4345	0.795672	0.9625	1.015539	0.457	0.859103	0.9215	1.5819	0.0195	1.900435	0	CDS hypothetical protein 4898852:4899241 reverse MW:13795
RPA4346	0.612991	0.996	0.688554	0.9925	0.684461	0.995	0.474825	1	0.414555	1	CDS putative acetyl-CoA acyltransferase 4899588:4900841 reverse MW:43835
RPA4347	0.808103	0.9545	0.745171	0.993	0.69781	0.9915	0.621209	0.9985	0.581689	1	CDS unknown protein 4901055:4901489 forward MW:14695
RPA4348					0.602515	0.982	0.819115	0.882	1.014489	0.49	CDS conserved hypothetical protein 4901974:4902405 forward MW:16340
RPA4349	0.92583	0.803	0.857441	0.8195	1.00266	0.5025	0.921577	0.709	0.942425	0.6935	CDS conserved unknown protein 4902523:4903053 forward MW:18984
RPA4350	0.978592	0.547	0.907925	0.7565	1.06897	0.2835	1.00661	0.4895	0.839404	0.9515	CDS hypothetical protein 4903203:4903349 reverse MW:4996
RPA4351	0.455487	0.86	0.452378	1	0.785438	0.688	0.353204	0.988	0.484846	0.9895	CDS conserved unknown protein 4903498:4903980 reverse MW:17667
RPA4352	1.140391	0.1225	1.043613	0.2655	1.138312	0.071	1.143189	0.0905	1.139919	0.0605	CDS conserved unknown protein 4903989:4904468 reverse MW:17588
RPA4353	0.553269	0.994	0.632579	0.9925	0.736784	0.9885	0.242369	0.9995	0.364924	0.9965	CDS conserved hypothetical protein 4904554:4904847 forward MW:10904
RPA4354	0.658694	0.9625	0.822194	0.9835	0.618206	0.9995	0.503101	1	0.642098	0.9635	CDS putative GTP-binding protein 4905007:4906104 reverse MW:39794
RPA4355	0.721059	0.9235	1.021214	0.3885	0.553137	0.998	0.591066	0.9945	0.763634	0.9075	pth putative peptidyl-tRNA hydrolase 4906232:4906852 reverse MW:22567
RPA4356	0.736891	0.9775	0.915502	0.8695	0.632777	0.9995	0.816531	0.966	0.822704	0.97	ctc, rplY, L25 putative 50S ribosomal protein L25 4906874:4907566 reverse MW:23969
RPA4357	1.012362	0.426	1.02695	0.411	0.960202	0.647	0.946513	0.6655	0.839986	0.8875	CDS conserved unknown protein 4907864:4908142 reverse MW:10212
RPA4358	0.979407	0.618	0.939333	0.7955	0.816577	0.944	0.966657	0.633	1.103568	0.096	lgt prolipoprotein diacylglyceryl transferase 4908396:4909256 forward MW:31226
RPA4359	0.854662	0.966	0.776018	0.9645	0.942988	0.7425	0.864642	0.7875	0.70964	0.996	CDS DUF185 4909253:4910392 forward MW:41325
RPA4360	0.828992	0.879	0.8348	0.9405	0.962904	0.648	1.038286	0.385	0.921015	0.6815	CDS DUF152 4910389:4911162 forward MW:27417
RPA4361	1.006346	0.4815	1.032961	0.373	0.942974	0.7195	1.900509	0.0045	1.074349	0.315	CDS conserved hypothetical protein 4911395:4912003 forward MW:20820
RPA4362	0.772122	0.934	0.893441	0.9265	0.766149	0.992	0.735025	0.9955	0.921305	0.834	ribP ribose-phosphate pyrophosphokinase 4912172:4913125 forward MW:34096
RPA4363	0.819588	0.9725	0.857115	0.787	0.772245	0.956	0.632212	0.9925	0.628436	0.9995	CDS putative 6,7-dimethyl-8-ribityllumazine synthase 4913326:4913871 reverse MW:19759
RPA4364	0.591432	0.9995	0.707276	0.9985	0.468814	0.9995	0.553511	0.9995	0.544036	0.9985	CDS conserved hypothetical protein 4914215:4914715 forward MW:18371
RPA4365	0.792759	0.964	0.793959	0.986	0.588261	0.9975	0.581673	0.995	0.77739	0.9355	CDS GCN5-related N-acetyltransferase 4914712:4915140 forward MW:15935
RPA4366	0.809172	0.981	0.805618	0.979	0.663176	0.994	0.697124	0.9785	0.745748	0.9945	proC pyrroline-5-carboxylate reductase 4915228:4916070 forward MW:27919
RPA4367	0.85292	0.939	0.91875	0.8725	0.78768	0.984	0.779225	0.9825	0.854378	0.963	CDS sensor histidine kinase 4916339:4917727 reverse MW:50972
RPA4368	0.756535	0.991	0.80909	0.99	0.838339	0.9375	0.715733	0.9845	0.731018	0.9945	CDS two-component transcriptional regulator, winged helix family 4918006:4918728 reverse MW:26633
RPA4369	0.975091	0.615	0.893995	0.917	1.018818	0.4175	0.879559	0.8	0.798833	0.981	CDS transcriptional regulator, MarR family 4918725:4919276 reverse MW:20399
RPA4370	1.329606	0.0385	0.9523	0.7915	0.919761	0.717	1.270314	0.0135	1.313267	0.0095	ilvE putative branched-chain amino acid aminotransferase 4919559:4920671 forward MW:40119
RPA4371	0.463624	1	0.425017	0.9995	0.874245	0.847	0.397888	0.9855	0.499358	1	mutL DNA mismatch repair protein MutL 4920918:4922705 reverse MW:64360
RPA4372	0.984681	0.5965	0.994743	0.512	0.840141	0.974	1.043926	0.3395	1.049876	0.2815	CDS Class I peptide chain release factor domain 4922941:4923360 reverse MW:15436
RPA4373	0.846436	0.9875	0.79942	0.975	0.931915	0.806	0.575375	0.994	0.693948	0.9975	CDS possible protease 4923703:4925136 reverse MW:51373
RPA4374	0.650429	0.9875	0.751391	0.9925	0.883163	0.854	0.509074	0.999	0.584292	0.993	CDS putative protease 4925133:4926614 reverse MW:53935
RPA4375	0.916377	0.824	0.809137	0.974	1.154284	0.0325	0.815459	0.942	1.095472	0.1165	CDS unknown protein 4926693:4927427 reverse MW:26058
RPA4376	0.951276	0.7425	1.020793	0.4255	0.877948	0.8165	0.796643	0.897	0.732431	0.8345	lspA Signal peptidase II, family A8 4927491:4928039 reverse MW:19519

RPA4377	0.812224	0.9185	0.833174	0.9815	0.736612	0.989	0.725312	0.981	0.741819	0.969	ileS isoleucyl-tRNA synthetase 4928148:4931165 reverse MW:111556
RPA4378	1.488216	0.007	1.589	0.0085	1.326835	0.05	2.12412	0.0055	1.230732	0.0715	CDS maltose O-acetyltransferase 4931347:4931919 reverse MW:19966
RPA4379	0.894319	0.9285	0.762183	0.9905	0.842803	0.9655	0.671386	0.994	0.748537	0.994	ribF putative riboflavin kinase ribF 4931916:4932884 reverse MW:34783
RPA4380	0.727567	0.957	0.782701	0.98	0.925278	0.7405	0.777786	0.909	0.858627	0.941	CDS Ribonuclease T2 4933007:4933702 reverse MW:26028
RPA4381	0.82835	0.9205	0.683011	0.949	1.104655	0.2655	0.573086	0.9805	0.605561	0.996	CDS conserved unknown protein 4933807:4934268 reverse MW:16744
RPA4382	0.840246	0.895	0.575887	0.9945	1.087214	0.2655	0.710389	0.952	0.860396	0.8585	CDS conserved hypothetical protein 4934435:4934725 forward MW:10234
RPA4383	0.908674	0.807	0.550197	0.999	1.093271	0.236	0.648986	0.98	0.899397	0.7805	CDS conserved unknown protein 4934735:4935268 forward MW:18894
RPA4384			0.706827	0.979	0.772547	0.926	0.768063	0.8635	0.806533	0.938	CDS hypothetical protein 4935410:4935790 forward MW:13104
RPA4385	0.779345	0.7845	0.764939	0.9885	0.505997	0.999	0.393292	0.996	0.531338	0.9895	PA0781 putative outer membrane hemin/siderophore receptor protein 4935808:4938261 forward MW:86551
RPA4386	0.997951	0.4945			1.053612	0.3385			0.77319	0.9605	CDS conserved hypothetical protein 4938474:4938836 forward MW:12624
RPA4387	0.867416	0.845	0.77656	0.8075	0.727984	0.917			1.022782	0.4395	CDS possible ferrichrome-iron receptor 4938984:4941257 forward MW:80898
RPA4388	0.779371	0.936	0.811082	0.958	0.730691	0.9885	0.477523	0.935	0.822579	0.9165	CDS GCN5-related N-acetyltransferase 4941280:4941831 reverse MW:20227
RPA4389	0.704252	0.9995	0.662734	0.9895	0.706579	0.9945	0.45509	1	0.702619	0.9895	CDS Small Conductance Mechanosensitive (MscS) Ion Channel 4941839:4943701 reverse MW:67252
RPA4390	0.787874	0.9875	0.969431	0.638	0.74894	0.99	0.629493	0.9905	0.531259	0.999	CDS NUDIX hydrolase 4943753:4944241 reverse MW:18144
RPA4391	0.725023	0.902	0.765526	0.9585	0.902708	0.612	1.289309	0.077	1.479531	0.006	CDS Metallo-phosphoesterase 4944376:4945257 forward MW:32541
RPA4392	0.836915	0.9575	0.628494	0.995	1.010243	0.4735	0.862163	0.791	0.951695	0.6775	CDS conserved hypothetical protein 4945303:4945851 reverse MW:19900
RPA4393	1.153009	0.057	1.04704	0.3225	1.349659	0.0125	1.223845	0.071	1.191038	0.089	CDS unknown protein 4946115:4946330 reverse MW:7935
RPA4394	1.032761	0.403	1.03712	0.3445	1.177704	0.087	0.633321	0.9965	0.851267	0.928	aceA isocitrate lyase 4946355:4947989 reverse MW:60704
RPA4395	1.390494	0.0965	2.022987	0.0115	1.242841	0.0315	1.831994	0.0015	0.855809	0.8975	CDS transcriptional regulator, XRE family 4948203:4949645 forward MW:54468
RPA4396	0.795682	0.9735	0.624374	0.999	0.910659	0.821	0.723464	0.99	0.657641	1	CDS possible transglycolase 4950947:4952305 forward MW:48905
RPA4397	1.459375	0.018	1.162445	0.0995	1.0933	0.2335	1.225977	0.053	1.315703	0.015	CDS possible substrate binding protein of ABC transporter system 4952405:4953571 forward MW:42024
RPA4398	1.192534	0.0255	1.263389	0.024	0.92035	0.859	1.009033	0.47	1.256886	0.076	CDS putative branched-chain amino acid ABC transporter, ATP-binding protein 4953733:4954497 forward MW:27397
RPA4399	1.221829	0.0215	1.275273	0.0285	0.9285	0.7385	0.855286	0.8955	0.904918	0.7605	CDS possible branched-chain amino acid transport system ATP-binding protein 4954639:4955631 forward MW:35480
RPA4400	1.091979	0.233	1.311593	0.0115	0.846822	0.919	1.003588	0.491	1.106451	0.1515	CDS possible branched-chain amino acid ABC transport system permease 4955628:4956653 forward MW:35929
RPA4401	0.911921	0.774	1.385179	0.1785	0.927124	0.7815			0.865944	0.7775	CDS possible branched-chain amino acid ABC transporter, permease protein 4956650:4957717 forward MW:37606
RPA4402	0.369431	0.996	0.813571	0.9025	0.550369	0.9995	0.470512	1	0.468892	1	CDS hypothetical protein 4958088:4958396 forward MW:10497
RPA4403	0.789005	0.9945	0.828015	0.9705	0.88279	0.934	0.82421	0.9395	0.742202	0.9975	CDS morphinone reductase 4958641:4959741 forward MW:39393
RPA4404	1.400951	0.0015	1.074363	0.3125	1.571137	0.0205	0.692134	0.979	0.448508	0.9995	CDS putative periplasmic binding ABC transporter protein, probable sugar binding 4960215:4962005 reverse MW:66714
RPA4405			0.901722	0.734							CDS conserved hypothetical protein 4962078:4962407 reverse MW:11737
RPA4406	0.948509	0.7305	0.687057	0.9645	0.858201	0.9215	0.647357	0.938	0.486952	0.997	CDS sugar ABC transport system, permease component 4962415:4963221 reverse MW:30130
RPA4407	0.939338	0.6665	0.706859	0.9665	0.943906	0.6705	0.704497	0.9265	0.483065	0.998	CDS permease protein of sugar ABC transporter 4963221:4964123 reverse MW:33383
RPA4408	0.942976	0.7015	0.60023	0.9905	1.015547	0.4425	0.623244	0.9435	0.509743	0.9995	CDS ATP-binding protein of sugar ABC transporter 4964123:4965223 reverse MW:40095
RPA4409	1.002879	0.487	0.545715	0.996	1.157031	0.0905	0.701334	0.9085	0.612932	0.992	CDS ATP-binding protein of sugar ABC transporter 4965236:4966315 reverse MW:39069
RPA4410	0.720107	0.8455	0.388888	0.9995	1.013048	0.4565	0.587364	0.952	0.443467	0.9985	glpD glycerol-3-phosphate dehydrogenase 4966312:4967847 reverse MW:56044
RPA4411	1.033584	0.3685	0.655985	0.9975	1.054488	0.363	0.892205	0.7775	0.895268	0.8365	glpR glycerol-3-phosphate regulon repressor glpR, DeoR family 4968043:4968840 reverse MW:28282
RPA4412	1.302828	0.09	0.94631	0.712	1.146668	0.067	1.136683	0.123	0.973273	0.646	CDS conserved unknown protein 4969028:4969645 reverse MW:22773
RPA4413	1.19653	0.106	0.929713	0.8515	1.071989	0.226	1.09819	0.186	0.869641	0.952	CDS possible transcriptional regulator, TetR family 4969663:4970277 reverse MW:22709
RPA4414	0.948336	0.674	0.895143	0.915	0.860592	0.8755	0.790064	0.951	0.916169	0.837	CDS putative RND efflux transporter 4970295:4973432 reverse MW:113438
RPA4415	0.75914	0.7545	0.818233	0.927	0.996419	0.507	0.81951	0.8315	0.583276	0.9855	CDS putative component of multidrug efflux system 4973454:4974557 reverse MW:39081
RPA4416											CDS conserved hypothetical protein 4974669:4975148 reverse MW:17226
RPA4417	1.241699	0.0175	1.308585	0.016	1.099788	0.162	1.304623	0.013	1.197206	0.0465	CDS sensor histidine kinase with PAS/PAC and response regulator receiver domains 4975255:4977876 reverse MW:95306
RPA4418											CDS conserved unknown protein 4978268:4978483 forward MW:7116
RPA4419	1.036542	0.293	1.043236	0.382	1.00128	0.4905	1.021275	0.4225	1.335639	0.0085	ggt3 putative gamma-glutamyltranspeptidase 4978588:4980174 reverse MW:56429
RPA4420	0.939623	0.694	1.736269	0.1215	0.962525	0.628			1.187276	0.1555	CDS conserved hypothetical protein 4980422:4980637 forward MW:7894
RPA4421	0.778153	0.9775	0.675952	0.9945	0.736309	0.9955	0.570489	0.9935	0.581957	1	CDS putative 4-coumarate:CoA ligase 2 4980789:4982339 reverse MW:56403
RPA4422	0.477172	0.9965	0.486673	1	0.901382	0.795	0.608188	0.996	1.165742	0.2	CDS transcriptional regulator, Crp/Fnr family 4982674:4983387 reverse MW:26257
RPA4423	1.051786	0.363	0.997855	0.507	1.48009	0.001	0.928343	0.7305	1.587446	0.0065	CDS conserved unknown protein 4983518:4983931 reverse MW:14984
RPA4424	0.95738	0.7095	0.848667	0.947	0.991848	0.526	0.908536	0.7075	0.796897	0.96	CDS Beta-lactamase-like 4984072:4984920 forward MW:31117
RPA4425	1.103878	0.21	0.864693	0.903	1.256338	0.058	0.759892	0.922	0.609032	0.9995	CDS 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase 4985030:4985872 forward MW:29610
RPA4426	0.841181	0.9305	0.839132	0.889	0.960586	0.5985	0.708415	0.92	0.499127	0.998	CDS Glutathione S-transferase, N-terminal 4985991:4986608 forward MW:23119
RPA4427	0.746746	0.9765	0.796086	0.942	0.70498	0.9945	0.927598	0.6895	0.86715	0.9435	ogt1 putative methylated-DNA-protein-cystein methyltransferase 4986620:4987168 reverse MW:19118
RPA4428	1.105234	0.2095	1.89994	0.0005	1.037162	0.3895	2.848538	0.0005	2.737575	0	CDS putative glucosyltransferase I; lipopolysaccharide core biosynthesis 4987215:4987754 reverse MW:20308
RPA4429	1.307465	0.242	4.267102	0.0035	1.102908	0.3585	1.290598	0.1375	1.868069	0.0015	CDS Uncharacterized iron-regulated membrane protein DUF337 4987875:4989020 reverse MW:41533
RPA4430											CDS putative TonB-dependent receptor 4989025:4991355 reverse MW:83973
RPA4431	0.784753	0.9965	0.74059	0.9875	0.833517	0.98	0.645703	0.998	0.77512	0.9975	CDS Peptidase M23/M37 4998672:5000702 forward MW:72400
RPA4432	1.058156	0.454	0.388162	0.995	1.387858	0.0085	0.407637	0.9855	0.318617	0.999	CDS NHL repeat 5000844:5002478 forward MW:56271
RPA4433	0.727448	0.964	0.700079	0.994	0.913204	0.822	0.637222	0.991	0.692245	0.991	clpB endopeptidase Clp: ATP-binding subunit B, clpB 5002756:5005395 reverse MW:96672
RPA4434	0.80139	0.987	0.833298	0.9585	0.952957	0.7125	0.61383	0.9935	0.669142	0.998	CDS MOSC domain 5005622:5006410 forward MW:28284
RPA4435	0.940265	0.735	0.913216	0.834	1.012967	0.4235	0.998069	0.5145	0.995799	0.5205	CDS hypothetical protein 5006617:5007360 reverse MW:26489
RPA4436	0.654764	0.996	0.649881	0.9975	0.829647	0.8975	0.48867	0.9875	0.764068	0.989	CDS conserved hypothetical protein 5007582:5008277 reverse MW:26074
RPA4437	0.662276	0.99	0.601279	0.9995	0.827623	0.872	0.606636	0.9705	0.968771	0.68	metX homoserine O-acetyltransferase 5008280:5009482 reverse MW:43777
RPA4438	0.759815	0.9915	0.836126	0.9855	0.819781	0.992	0.720835	0.998	0.770719	0.9935	aro Chorismate mutase 5009734:5010681 forward MW:33904
RPA4439	0.666368	0.9925	0.896971	0.889	0.692846	0.997	0.622758	0.998	0.739171	0.966	hisC putative histidinol-phosphate aminotransferase 5010724:5011821 forward MW:39354
RPA4440	0.709833	0.9685	0.997737	0.5225	0.814984	0.946	0.695392	0.983	0.682364	0.975	tyrC putative cyclohexadienyl dehydrogenase 5011818:5012759 forward MW:33536
RPA4441	0.75367	0.98	0.710358	0.9975	0.880788	0.9095	0.78456	0.9735	0.883037	0.9215	corA putative magnesium/cobalt transport protein 5013079:5014059 reverse MW:36321
RPA4442	1.387526	0.218	0.768445	0.964	1.590406	0.008	1.398569	0.082	1.661108	0.0175	CDS ErfK/YbiS/YcfS/YnhG 5014406:5015089 forward MW:24509
RPA4443	1.083155	0.2795	0.838079	0.9735	1.268653	0.0095	1.123674	0.0985	1.008992	0.4775	CDS acyl-CoA synthetase 5016593:5018221 forward MW:59960
RPA4444	0.618634	0.9995	0.632719	0.9995	0.728855	0.9955	0.623268	0.993	0.635504	1	CDS conserved hypothetical protein 5019052:5019897 forward MW:31046
RPA4445	0.912732	0.6385	0.969783	0.564	0.963058	0.5505	1.172277	0.1845	0.824029	0.8575	CDS hypothetical protein 5019977:5020276 reverse MW:10493
RPA4446	0.996166	0.527	0.801747	0.749	1.164748	0.0955			0.903249	0.75	CDS hypothetical protein 5020355:5020798 reverse MW:16520
RPA4447	1.121848	0.232	0.978447	0.5035	1.23478	0.1155			0.966411	0.55	CDS conserved hypothetical protein 5020795:5021214 reverse MW:14732
RPA4449	1.300984	0.0805	1.698404	0.0015	1.175016	0.121	1.496067	0.048	1.19576	0.1425	CDS pmethyl-accepting chemotaxis receptor/sensory transducer 5022729:5024420 forward MW:60404
RPA4450	0.926153	0.724	0.536101	0.9965	0.660141	0.9425	0.664148	0.9265	0.551858	0.9735	CDS hypothetical protein 5024628:5026223 forward MW:56178
RPA4451	0.929613	0.725	0.735299	0.994	0.811479	0.982	0.643582	0.9865	0.729197	0.8355	CDS unknown protein 5026213:5027448 forward MW:45526
RPA4452	0.811683	0.981	0.7602	0.991	0.648076	0.995	0.670369	0.9955	0.555501	0.994	CDS putative aromatic-L-amino-acid decarboxylase 5027445:5028905 forward MW:52309
RPA4453	0.741411	0.9975	0.791281	0.9855	0.684665	0.997	0.699455	0.995	0.765725	0.9935	CDS Metallo-phosphoesterase:Conserved hypothetical protein 282 5029184:5030011 reverse MW:29392
RPA4454	0.850957	0.8935	0.946143	0.743	0.79701	0.9685	1.088023	0.2575	1.249494	0.0225	CDS Antifreeze protein, type I:5-formyltetrahydrofolate cyclo-ligase 5030013:5030606 reverse MW:20498

RPA4455	1.005193	0.465	1.097274	0.173	1.08497	0.1135	1.223147	0.068	1.160687	0.074	CDS hypothetical protein 5030895:5031479 forward MW:21412
RPA4456	1.03521	0.4215	1.161863	0.0945	0.869189	0.7535	1.242815	0.175	1.137899	0.19	CDS unknown protein 5031753:5032292 forward MW:18079
RPA4457	0.915995	0.65					0.785771	0.914	1.055747	0.365	CDS putative sulfide dehydrogenase 5032374:5032763 reverse MW:13770
RPA4458	0.978946	0.572	0.856749	0.753	0.886578	0.873	1.28841	0.2455	1.244964	0.135	CDS hypothetical protein 5032787:5033263 reverse MW:17396
RPA4459	0.801251	0.8645	0.949803	0.6885	1.027609	0.4605	0.68639	0.9805	0.59113	0.9325	dhsU2 putative flavocytochrome C sulfide dehydrogenase, flavoprotein subunit 5033288:5034580 reverse MW:46330
RPA4460	1.4705	0.0255	0.91592	0.8185	1.332407	0.0125	0.854507	0.9395	0.911295	0.817	dhsU1 putative flavocytochrome C sulfide dehydrogenase, flavoprotein subunit 5034620:5035885 reverse MW:45339
RPA4461	1.17343	0.1445	0.878298	0.8515	1.403421	0.012	0.869827	0.7925	0.513607	0.978	CDS possible cytochrome subunit of sulfide dehydrogenase 5035913:5036335 reverse MW:15329
RPA4462	0.701984	0.95	0.880533	0.915	0.965348	0.579	0.787749	0.891	0.635824	0.9475	CDS Lipocalin-related protein and Bos/Can/Equ allergen 5036372:5037511 reverse MW:38557
RPA4463			0.350503	0.9935							CDS possible cytochrome 5037696:5038451 reverse MW:26706
RPA4464					0.743343	0.907			0.670828	0.9855	soxC sulfite dehydrogenase 5038435:5039730 reverse MW:47801
RPA4465	0.603894	0.993	0.49921	0.998	0.457596	0.999	0.272147	0.9995	0.540655	0.9985	soxB sulfur/thiosulfate oxidation protein SoxB 5039800:5041497 reverse MW:61530
RPA4466	1.072768	0.299	0.716623	0.9955	1.139905	0.163	0.525483	0.9985	0.845348	0.937	soxZ2 putative sulfur oxidation protein soxZ 5041640:5041969 reverse MW:12256
RPA4467											soxY2 putative sulfur oxidation protein soxY 5042008:5042472 reverse MW:16280
RPA4468	1.204641	0.2015	0.687453	0.9935	0.954862	0.6405	0.549423	0.9945	0.805139	0.9855	CDS conserved unknown protein 5042658:5043479 forward MW:30383
RPA4469	1.237903	0.189	0.701433	0.999	0.967039	0.563	0.595506	0.9935	0.897729	0.92	CDS conserved unknown protein 5043493:5044236 forward MW:26643
RPA4470	0.783325	0.887	0.625755	0.9985	1.013789	0.4365	0.401988	0.998	0.432678	1	CDS DUF336 5044401:5044898 forward MW:16477
RPA4471	0.981532	0.5945	0.894526	0.9085	1.077756	0.251	0.909338	0.8285	0.821216	0.9105	CDS conserved hypothetical protein 5045047:5045640 reverse MW:21979
RPA4472			0.451353	0.9825			0.879671	0.6555	1.01499	0.4745	CDS putative c-type cytochrome biogenesis protein 5045669:5046412 reverse MW:25292
RPA4473	1.547081	0.036	1.105909	0.3575	1.286122	0.0345	1.894907	0.0275	1.836251	0.002	CDS conserved hypothetical protein 5046561:5046857 forward MW:10984
RPA4474	1.333847	0.003	1.230311	0.0095	1.405225	0.007	1.464256	0.002	1.326087	0.0075	CDS transcriptional regulator, ArsR family 5046896:5047270 forward MW:14277
RPA4475	0.981064	0.539	1.01217	0.4345	0.873351	0.88	0.974748	0.615	0.890975	0.879	CDS conserved hypothetical protein 5047347:5048549 forward MW:41694
RPA4476	1.14864	0.065	1.170599	0.055	0.908927	0.887	1.045803	0.3465	0.892565	0.8595	CDS conserved unknown protein 5048464:5048976 reverse MW:17985
RPA4477	1.05366	0.3175	0.715866	0.9715	0.720183	0.983	0.606701	0.9435	0.715146	0.999	CDS Possible membrane protein with ATP/GTP-binding site motif A (P-loop) 5049148:5050203 reverse MW:35480
RPA4478	0.941732	0.63	1.274427	0.3595	1.052959	0.394			0.940031	0.552	CDS conserved hypothetical protein 5050403:5050708 reverse MW:10778
RPA4479	1.253342	0.0345	0.928358	0.773	1.024447	0.4015	1.080379	0.2705	1.023516	0.396	czcA3 putative heavy metal cation efflux system protein 5050705:5053800 reverse MW:110784
RPA4480			0.698064	0.969			0.882358	0.749			czcB possible RND divalent metal cation efflux membrane fusion protein CzcB precursor 5053801:5054907 reverse MW:39455
RPA4482			0.987212	0.559			1.490099	0.008			CDS putative sensor (PAS) domain for methyl-accepting chemotaxis sensory transducer 5056386:5056922 reverse MW:19671
RPA4483	1.448622	0.01	3.971522	0.0005	1.540866	0.004	4.356894	0.0095	1.473506	0.091	CDS methyl-accepting chemotaxis sensory transducer 5057092:5058342 reverse MW:43115
RPA4484	1.706377	0.0025	4.11721	0.001	1.6638	0.009	6.003382	0.009	2.239134	0.0025	CDS putative sensor (PAS) domain for methyl-accepting chemotaxis sensory transducer 5058377:5058910 reverse MW:19812
RPA4485	0.745614	0.993	0.682695	0.988	1.153369	0.083	0.690466	0.9915	0.640233	0.9925	mutY adenine glycosylase mutY 5059087:5060136 reverse MW:37801
RPA4486	0.843851	0.982	0.833394	0.972	0.993054	0.541	0.878697	0.8885	0.831417	0.9725	CDS conserved hypothetical protein 5060243:5060722 forward MW:17168
RPA4487	1.015603	0.4485	0.931569	0.7865	1.073761	0.226	0.711813	0.991	0.848156	0.8865	CDS DSBA oxidoreductase:Tat pathway signal 5060865:5061539 forward MW:24556
RPA4489	0.989244	0.555	1.025148	0.3665	1.048231	0.2445	0.877687	0.84	0.843423	0.973	CDS putative chromosome segregation SMC protein 5063290:5066823 forward MW:129213
RPA4490	1.025553	0.375	0.788824	0.9215	0.907755	0.8045	0.870004	0.782	0.817206	0.97	CDS conserved hypothetical protein 5067098:5068078 forward MW:34931
RPA4491					0.946271	0.5955			1.152233	0.162	CDS conserved hypothetical protein 5068489:5071404 reverse MW:97173
RPA4492	0.571348	0.825									apt adenine phosphoribosyltransferase 5071736:5072281 forward MW:19339
RPA4493	0.766554	0.9625	0.845709	0.8945	0.601674	0.9665	0.781397	0.923	0.779721	0.9135	CDS conserved unknown protein 5072490:5073155 reverse MW:25280
RPA4494	0.834809	0.9725	0.873689	0.9095	0.804639	0.9795	0.642019	0.998	0.810191	0.977	CDS conserved unknown protein 5073214:5073987 reverse MW:28342
RPA4495	0.908709	0.8145	0.933877	0.7	1.153244	0.17	1.104175	0.262	0.841742	0.944	htpX possible protease htpX homolog 5074168:5075364 reverse MW:41969
RPA4498	0.96483	0.631			0.949991	0.6165			1.081563	0.3095	trpG anthranilate synthase 5076071:5078230 reverse MW:78299
RPA4499	0.917204	0.8085	0.995044	0.5075	0.857642	0.952	0.765863	0.9855	0.757555	0.947	CDS unknown protein 5078463:5079113 reverse MW:23861
RPA4500	3.206018	0	2.644746	0.001	2.722344	0.0005	2.816307	0.002	1.929297	0.017	CDS hypothetical protein 5079891:5080097 forward MW:7589
RPA4501	1.320474	0.018	1.490143	0.0055	1.213679	0.0185	1.916929	0.0015	1.981408	0.0005	CDS phnA-like protein 5080134:5080352 reverse MW:7933
RPA4502	1.318421	0.0085	1.839497	0.026	1.203343	0.081	2.242327	0.0025	1.929505	0.002	CDS putative outer membrane protein 5080486:5081175 reverse MW:24724
RPA4503	1.140406	0.0665	1.043005	0.3225	1.028842	0.3475	1.134366	0.104	1.007841	0.463	CDS conserved hypothetical protein 5081408:5081668 reverse MW:9417
RPA4504	0.779638	0.923	1.034095	0.406	0.707884	0.959	0.739471	0.9815	0.68357	0.976	CDS acetyl-CoA synthetase 5081847:5083757 reverse MW:69381
RPA4505	1.24193	0.217	1.603799	0.0175	1.084164	0.3015	0.767107	0.9675	0.921907	0.762	CDS TPR repeat 5083938:5084684 reverse MW:26127
RPA4506	0.688281	0.9025	0.87061	0.8285	0.541968	0.989	0.564132	0.998	0.602117	0.9945	CDS putative short-chain alcohol dehydrogenase 5084870:5085673 reverse MW:27872
RPA4507	1.120197	0.08	1.290152	0.0145	0.946686	0.6705	1.386855	0.017	1.714846	0.0045	CDS Elongator protein 3/MiaB/NifB 5085773:5087557 reverse MW:65901
RPA4508	1.022102	0.428	0.967246	0.5465	1.202716	0.0665	1.569961	0.288	0.850534	0.926	CDS conserved hypothetical protein 5088621:5088992 reverse MW:13529
RPA4509	0.886672	0.9435	0.834254	0.8825	0.842425	0.9405	0.649453	0.9955	0.699079	0.998	CDS possible TrapT family, fused dctQ-M subunits, C4-dicarboxylate transport 5088989:5091109 reverse MW:75428
RPA4510	1.044751	0.352	0.789153	0.9865	1.018013	0.3915	0.770951	0.99	0.723279	0.9965	CDS conserved unknown protein 5091256:5092203 reverse MW:32889
RPA4511	1.821499	0.1115	2.372827	0.004					1.181575	0.1775	CDS Major Facilitator Superfamily (MFS) transporter 5092359:5093624 forward MW:42669
RPA4512	1.256293	0.0075	1.243536	0.015	1.196887	0.058	1.694509	0.002	1.236999	0.0275	CDS possible response regulator receiver 5093642:5093953 reverse MW:11027
RPA4513	1.230079	0.0195	0.939396	0.707	1.209287	0.085	1.081698	0.3065	0.948602	0.68	CDS putative signal transduction histidine kinase 5094008:5095012 reverse MW:36455
RPA4514	1.06412	0.2295	0.883387	0.95	1.06665	0.227	1.133572	0.102	1.134036	0.1	CDS possible alkaline phosphatase D precursor 5095094:5096794 forward MW:62425
RPA4515	1.045026	0.3105	0.826391	0.9705	1.444615	0.0035	1.060108	0.2435	1.034403	0.3945	CDS Uncharacterized protein family UPF0065:Tat pathway signal 5096930:5097937 forward MW:35819
RPA4516	1.038271	0.33	0.872247	0.815	1.038035	0.37	0.723812	0.948	0.838315	0.9245	vieA putative cylclic diguanylate phosphodiesterase (EAL) 5098179:5099393 forward MW:44280
RPA4517	0.467846	0.999	0.432613	0.9995	0.609968	0.983	0.521765	0.9995	1.076406	0.394	CDS conserved hypothetical protein 5099410:5099970 reverse MW:20161
RPA4518	1.179984	0.0265	1.011109	0.436	1.206165	0.0775	1.44971	0.014	1.521539	0.009	CDS hypothetical protein 5100110:5100445 forward MW:11870
RPA4519	0.952484	0.745	0.793283	0.9795	0.906775	0.737	0.936822	0.723	0.907823	0.9195	CDS unknown protein 5100464:5101675 reverse MW:44529
RPA4520	0.994149	0.512	1.056746	0.342	1.10386	0.274	0.995265	0.5015	0.913245	0.734	CDS NUDIX hydrolase 5101811:5102437 reverse MW:22519
RPA4521	0.94799	0.7235	0.905736	0.8085	0.89094	0.8725	1.012019	0.4535	0.859512	0.8415	CDS Thioesterase superfamily 5102565:5102942 forward MW:13775
RPA4522	0.881494	0.9065	1.06135	0.184	0.900439	0.87	1.071639	0.3035	1.3468	0.003	cbbY Haloacid dehalogenase-like hydrolase 5102958:5103704 reverse MW:26137
RPA4523	0.679764	0.999	0.595664	0.991	1.033858	0.329	0.920846	0.7485	0.926057	0.7435	CDS response regulator receiver (CheY-like protein) 5103980:5104369 reverse MW:13422
RPA4524											CDS sensor histidine kinase 5104629:5106185 reverse MW:56099
RPA4525	1.81947	0.004	1.629397	0.0065	2.087983	0	2.409578	0.002	2.292562	0	CDS hypothetical protein 5106564:5106995 forward MW:16334
RPA4526											CDS hypothetical protein 5107465:5107899 forward MW:16245
RPA4527	0.700926	0.9895	0.909683	0.896	0.816586	0.9625	0.686256	0.996	0.725538	0.9965	maf2 putative septum formation maf protein 5108324:5109043 reverse MW:25604
RPA4528	0.98498	0.564	0.858507	0.956	1.097323	0.101	1.157941	0.1185	1.406294	0.004	CDS conserved hypothetical protein 5109044:5110210 reverse MW:42547
RPA4529	0.950517	0.645			1.102621	0.225			0.752884	0.945	arsC4 putative arsenate reductase 5110793:5111263 reverse MW:17480
RPA4530	0.903635	0.902	0.952874	0.7145	0.885677	0.9585	0.842033	0.945	0.896005	0.8925	CDS conserved hypothetical protein 5111319:5111810 reverse MW:18439
RPA4531	0.760803	0.9855	0.824966	0.9665	0.745173	0.9905	0.715983	0.9805	0.913912	0.8755	hisD histidinol dehydrogenase 5111807:5113102 reverse MW:45117
RPA4532	1.08187	0.147	0.942381	0.7465	1.021225	0.4155	0.889015	0.7775	1.157252	0.084	CDS conserved hypothetical protein 5113226:5113681 reverse MW:16266
RPA4533	0.786522	0.991	0.811946	0.943	0.951916	0.734	0.75631	0.981	0.988175	0.568	murA UDP-N-acetylglucosamine 1-carboxyvinyltransferase 5113701:5114990 reverse MW:44906
RPA4534	1.123615	0.052	1.184369	0.0245	1.428042	0.0055	1.123693	0.089	1.214625	0.016	CDS hypothetical protein 5115149:5115622 reverse MW:17303
RPA4535											CDS hypothetical protein 5115658:5115945 forward MW:9145

RPA4536	0.965055	0.5545	0.810583	0.837	1.36979	0.058	0.812619	0.7585	0.589048	0.9835	CDS cyclic nucleotide regulated pyridine nucleotide-disulphide oxidoreductase 5116011:5117702 reverse MW:59169
RPA4537	0.570537	0.9955	0.468905	0.999	0.746428	0.76	0.765567	0.809	1.296266	0.0615	CDS conserved hypothetical protein 5118019:5118465 forward MW:16570
RPA4538	1.041238	0.326	1.480441	0.013	1.044501	0.3325	2.200164	0.001	3.755891	0	CDS conserved unknown protein 5118975:5119751 reverse MW:25986
RPA4539	1.046482	0.423	0.814163	0.7525	1.154282	0.228	2.073633	0.001	7.401504	0	CDS hypothetical protein 5119758:5120303 reverse MW:18779
RPA4540	1.116741	0.203	1.11398	0.153	1.113967	0.2005	2.516344	0.0005	4.47735	0.0005	CDS hypothetical protein 5120345:5120974 forward MW:21571
RPA4541											rlgA DNA invertase gene rlgA 5121110:5121649 reverse MW:19376
RPA4542	0.871968	0.731	0.951129	0.587	1.53578	0.1535	0.847091	0.742	0.796076	0.9495	CDS unknown protein 5122393:5122692 forward MW:11319
RPA4543	1.127273	0.2695	0.965705	0.622	0.917565	0.63	1.114319	0.1555	0.89738	0.7325	CDS conserved hypothetical protein 5122780:5123184 reverse MW:14941
RPA4544											CDS conserved unknown protein 5123181:5123774 reverse MW:21828
RPA4545											CDS hypothetical protein 5123771:5124109 reverse MW:12640
RPA4546									2.140124	0.067	CDS conserved hypothetical protein 5124106:5126418 reverse MW:83317
RPA4547							2.162813	0.0005	1.77679	0.0025	CDS hypothetical protein 5126565:5127233 reverse MW:24394
RPA4548					1.615753	0.127					CDS hypothetical protein 5127230:5127577 reverse MW:12709
RPA4549											CDS Phage integrase 5127998:5129380 reverse MW:50156
RPA4550	0.991906	0.552	1.002504	0.495	1.108631	0.162	1.052397	0.314	1.156841	0.0665	CDS conserved hypothetical protein 5129811:5130200 forward MW:14071
RPA4551	0.796123	0.996	0.711713	0.9935	1.187747	0.024	0.897238	0.86	0.872944	0.8545	CDS conserved unknown protein 5130324:5131613 forward MW:47673
RPA4552	0.855269	0.837	0.953905	0.673	0.88595	0.8115	0.713374	0.9725	0.414003	1	CDS possible 4-hydroxybutyrate-CoA transferase/hydrolase 5131650:5132891 reverse MW:43444
RPA4553	0.771168	0.9885	0.9098	0.815	0.750442	0.991	0.79111	0.976	0.438841	1	CDS putative acyl-CoA dehydrogenase 5132918:5134084 reverse MW:42703
RPA4554	0.975904	0.5545	0.880292	0.8605	0.822252	0.919	0.637914	0.9945	0.232036	1	dctM2 TrapT family, dctM subunit, C4-dicarboxylate transport 5134138:5135427 reverse MW:44785
RPA4555									0.354223	0.997	CDS possible TrapT family, dctQ subunit, C4-dicarboxylate transport 5135439:5135990 reverse MW:19940
RPA4556	0.755569	0.9875	0.684168	0.9885	0.868662	0.903	0.578785	0.9995	0.343344	0.9995	CDS possible TrapT family, dctP subunit, C4-dicarboxylate periplasmic binding protein 5136024:5137049 reverse MW:36835
RPA4557							1.326902	0.2285			CDS conserved hypothetical protein 5137253:5138449 forward MW:43375
RPA4558	0.837735	0.89	0.874632	0.868	1.023562	0.3995	0.713374	0.9915	0.373999	1	CDS possible dehydratase, MaoC family 5138494:5138946 forward MW:16950
RPA4559	0.849495	0.9665	0.75519	0.988	0.745223	0.9935	0.532237	0.999	0.394987	1	CDS putative citrate lyase beta chain 5138946:5139794 forward MW:29961
RPA4560	1.008642	0.456	1.023385	0.429	0.753593	0.934	1.21424	0.189	0.918221	0.7055	CDS transcriptional regulator, IclR family 5139835:5140566 forward MW:26965
RPA4561	1.072053	0.1945	0.893526	0.912	0.95518	0.6045	0.910331	0.7875	0.947511	0.706	CDS GMP reductase 5140697:5141761 reverse MW:37974
RPA4562			1.130216	0.2245			1.911851	0.01	1.277868	0.157	apbA/panE putative 2-dehydropantoate 2-reductase 5141828:5142733 forward MW:30809
RPA4563	0.946384	0.747	0.907903	0.866	0.937338	0.773	0.938465	0.6915	0.940188	0.739	exoI2 Staphylococcus nuclease (SNase-like) 5142735:5143484 reverse MW:27132
RPA4564	0.843188	0.896	0.682722	0.9785	1.061114	0.4125	0.912953	0.6625	0.838113	0.9535	CDS Phenylacetic acid degradation-related protein:Thioesterase superfamily 5143612:5144526 forward MW:32667
RPA4565	1.458687	0.005	1.787059	0.0025	1.219938	0.021	1.721952	0.0115	1.347401	0.009	CDS putative diguanylate cyclase (GGDEF) 5144704:5145906 forward MW:42887
RPA4566	1.040044	0.3085	1.015609	0.491	0.94934	0.6465	1.057881	0.3425	0.727597	0.9635	ackA putative acetate kinase 5145907:5147103 reverse MW:42662
RPA4567	0.859015	0.8615	0.958953	0.7085	0.984981	0.5435	0.750055	0.9935	0.849058	0.9115	pta putative phosphate acetyltransferase 5147100:5148515 reverse MW:50043
RPA4568	0.81977	0.929	1.010241	0.4435	0.991685	0.519	0.630408	0.998	0.718262	0.9915	CDS putative enoyl-acyl carrier protein reductase 5148539:5149300 reverse MW:27174
RPA4569	1.42842	0.002	1.34996	0.002	1.518322	0.0005	1.507051	0.002	1.432792	0.0025	CDS DUF344 5149383:5150252 reverse MW:34057
RPA4570	1.320645	0.0045	1.285515	0.0265	1.028274	0.4065	1.112809	0.205	1.848353	0.0005	CDS hypothetical protein 5150634:5152016 forward MW:50471
RPA4571	1.419528	0.0535	2.423779	0.0085	2.234755	0.001	1.178499	0.1655	1.841175	0	CDS hypothetical protein 5152095:5152499 reverse MW:13697
RPA4572	0.480735	0.9975	0.500545	0.9635	0.920741	0.612	0.77658	0.7575	2.037061	0.0005	htrA/degQ/degS putative serine protease htrA/degQ/degS family 5152730:5154292 reverse MW:53919
RPA4573	1.165287	0.2085	2.448849	0.0045	1.23316	0.05	0.980289	0.5385	1.668653	0.005	CDS conserved unknown protein 5154547:5155035 reverse MW:16557
RPA4574	1.270191	0.1865	1.706444	0.002	1.285583	0.0605	0.95161	0.5895	0.850186	0.7775	CDS hypothetical protein 5155144:5155428 reverse MW:9862
RPA4575	0.926299	0.867	0.910459	0.9165	1.022738	0.3765	0.901878	0.8505	0.951577	0.727	CDS putative ATP-binding protein of sugar ABC transporter 5155586:5157151 forward MW:55250
RPA4576	0.932658	0.773	0.902719	0.87	0.924653	0.832	0.711307	0.9845	0.871352	0.898	CDS putative permease protein of sugar ABC transporter 5157135:5158226 forward MW:37782
RPA4577			0.748543	0.972			0.782654	0.8765	0.822498	0.739	CDS putative permease protein of sugar ABC transporter 5158213:5159130 forward MW:30469
RPA4578	0.888879	0.913	1.206169	0.0185	0.9485	0.6625	1.071843	0.304	1.199796	0.0195	CDS Basic membrane lipoprotein 5159212:5160309 forward MW:39678
RPA4579	0.976349	0.6425	0.700603	0.9955	1.110105	0.2015	0.829963	0.8785	1.161701	0.094	CDS possible serine protease, htrA-like 5160505:5161548 reverse MW:37275
RPA4580	1.394341	0.016	1.025439	0.359	1.257537	0.0135	1.218056	0.091	1.126867	0.128	CDS Uncharacterized protein family UPF0065:Tat pathway signal 5161590:5162597 reverse MW:34728
RPA4581	1.047608	0.316	1.099396	0.121	0.824068	0.954	0.978891	0.588	1.160542	0.04	CDS conserved hypothetical protein 5162843:5164102 forward MW:45364
RPA4582	0.886234	0.9375	0.934175	0.771	0.683524	0.9985	0.724902	0.95	0.845673	0.9535	galE2 UDP-galactose 4-epimerase 5164133:5165116 forward MW:35393
RPA4583	1.085033	0.162	1.029683	0.4075	0.95613	0.692	1.084745	0.2845	1.227302	0.0205	CDS possible UDP-N-acetyl-D-mannosamine transferase 5165344:5166261 forward MW:34761
RPA4584	1.152693	0.1075	0.784354	0.956	0.874421	0.8	1.027938	0.453	0.930916	0.633	CDS possible endoglucanase 5166277:5167413 reverse MW:41753
RPA4585	0.979469	0.579	0.798926	0.981	0.935795	0.7265	0.836943	0.934	0.912286	0.8695	CDS Lipopolysaccharide biosynthesis 5167429:5169585 reverse MW:77146
RPA4586	0.976687	0.584	0.939369	0.7445	0.986364	0.5715	0.923139	0.728	1.217065	0.0395	CDS possible Glycosyl transferases group 1 5169889:5171088 forward MW:43585
RPA4587	1.170463	0.11	0.970487	0.6615	1.079171	0.1765	1.076468	0.225	1.122835	0.115	CDS conserved unknown protein 5171110:5172639 forward MW:56017
RPA4588			0.959322	0.6505	1.012289	0.474	1.066953	0.2965	1.080318	0.3435	CDS conserved hypothetical protein 5172657:5173022 reverse MW:12680
RPA4589	1.28187	0.049	0.967784	0.6035	1.26552	0.009	1.246835	0.0515	1.395902	0.0115	CDS possible membrane protein involved in export of O-antigen 5173165:5174634 forward MW:52299
RPA4590	1.198245	0.0165	1.100936	0.1105	1.262874	0.023	1.359261	0.0175	1.360667	0.0145	CDS possible homoserine O-succinyltransferase 5174703:5175704 reverse MW:36979
RPA4591	1.4366	0.022	1.064439	0.188	1.087258	0.1635	1.310485	0.065	1.236196	0.0795	metY homocysteine synthase 5175717:5177021 reverse MW:46947
RPA4592	1.372167	0.023	0.91036	0.8295	1.083079	0.245	1.200464	0.1245	1.107011	0.219	CDS putative fatty acid metabolism AMP-binding protein 5177281:5179104 forward MW:66071
RPA4593	1.046503	0.258	0.892474	0.933	1.253796	0.0335	0.950913	0.709	0.794506	0.9565	CDS possible branched-chain amino acid aminotransferase 5179104:5179988 forward MW:32580
RPA4594	1.429927	0.022	0.982633	0.5345	1.252932	0.0745	1.330957	0.071	1.044093	0.353	CDS conserved hypothetical protein 5180009:5180893 reverse MW:32932
RPA4595	0.928053	0.6375	0.842174	0.8075	1.069594	0.365	0.801043	0.9125	0.892282	0.647	CDS conserved unknown protein 5181226:5182605 forward MW:48331
RPA4596	1.222248	0.118	1.030726	0.4225	1.287318	0.057			0.76302	0.9445	fabG5 putative 3-oxoacyl-acyl carrier protein reductase 5182598:5183329 forward MW:25154
RPA4597	1.136333	0.0485	0.748999	0.9985	1.354453	0.005	0.916941	0.7645	0.863554	0.786	CDS possible seryl-tRNA synthetase 5183551:5184492 reverse MW:34379
RPA4598	1.058663	0.326	0.672134	0.9995	0.967626	0.656	0.809369	0.908	0.73872	0.9615	CDS possible acyl-CoA dehydrogenase 5184527:5185756 reverse MW:43675
RPA4599	1.201626	0.115	0.949038	0.649	0.970712	0.6115	1.179094	0.247	1.150101	0.1255	CDS conserved hypothetical protein 5186123:5186395 forward MW:9478
RPA4600	1.214517	0.013	0.942914	0.8005	1.318873	0.0135	1.041669	0.294	0.869462	0.949	CDS conserved unknown protein 5186469:5186924 forward MW:16650
RPA4601	1.047201	0.248	1.044081	0.3065	1.477009	0.009	1.404223	0.0655	0.965072	0.552	CDS conserved hypothetical protein 5187101:5187688 forward MW:20884
RPA4602	49.81843	0	41.70902	0	52.93708	0	185.0333	0	105.3853	0	fixX ferredoxin like protein, fixX 5188040:5188336 reverse MW:10736
RPA4603	58.99701	0.001	43.92684	0	30.05107	0	248.3019	0	181.8235	0	fixC nitrogen fixation protein,fixC 5188370:5189677 reverse MW:48312
RPA4604	22.21723	0.0005	15.95695	0	13.83152	0	70.24574	0	62.56767	0	fixB electron transfer flavoprotein alpha chain protein fixB 5189690:5190796 reverse MW:39490
RPA4605	51.52998	0	68.83511	0	39.44664	0	118.0973	0	180.6758	0	fixA electron trnasfer flavoprotein beta chain fixA 5190821:5191666 reverse MW:30505
RPA4606	15.03488	0.0005	14.02426	0	9.356038	0	15.79174	0	21.96393	0	nifW nitrogenase stabilizer NifW 5191999:5192349 reverse MW:12663
RPA4607	134.0726	0.0005	131.58	0	121.4759	0	342.0818	0	437.8748	0	nifV putative homocitrate synthase 5192378:5193571 reverse MW:41693
RPA4608	34.37637	0	40.76055	0	23.90562	0	142.5148	0	83.63345	0	nifS2 nitrogenase cofactor synthesis protein nifS 5193564:5194796 reverse MW:43543
RPA4609	248.422	0	140.9841	0	138.6947	0	384.1846	0	443.435	0	nifU putative nifU protein 5194793:5195779 reverse MW:34392
RPA4610	32.94428	0	53.13492	0	29.28802	0	307.0506	0.0005	50.77501	0	CDS Protein of unknown function, HesB/YadR/YfhF 5195807:5196127 reverse MW:10877
RPA4611	32.04055	0	109.3705	0	34.32259	0			4.127347	0.0005	nifQ putative nitrogen fixation protein nifQ 5196535:5197245 reverse MW:25769
RPA4612	13.88609	0	23.15794	0	13.223	0	1.451256	0.1535	1.973459	0.0015	fdxB ferredoxin 2[4Fe-4S] III, fdxB 5197263:5197574 reverse MW:11211

RPA4613	48.26697	0	70.55536	0.0005	52.43726	0			16.29071	0.0005	CDS DUF683 5197635:5197841 reverse MW:7575
RPA4614	76.46453	0	63.69128	0	72.09913	0	1.509079	0.0425	40.75585	0	CDS DUF269 5197860:5198324 reverse MW:17484
RPA4615	134.0849	0	158.3945	0	124.8418	0			26.60296	0.0005	nifX nitrogenase molybdenum-iron protein nifX 5198326:5198724 reverse MW:14621
RPA4616	12.05424	0	16.76718	0	9.365005	0			3.685412	0	nifN nitrogenase reductase-associated ferredoxin, nifN 5198780:5200153 reverse MW:48344
RPA4617	81.35795	0	54.37509	0	96.02847	0	1.612234	0.028	43.76632	0	nifE nitrogenase molybdenum-cofactor synthesis protein nifE 5200164:5201627 reverse MW:53557
RPA4618	311.444	0	184.7651	0	207.8643	0	1.299164	0.025	220.6226	0	nifK nitrogenase molybdenum-iron protein beta chain, nifK 5201667:5203226 reverse MW:57630
RPA4619	334.2489	0	176.0557	0	230.2714	0	Mutated		258.0358	0	nifD nitrogenase molybdenum-iron protein alpha chain, nifD 5203315:5204778 reverse MW:54592
RPA4621	53.15082	0	44.07071	0	59.61012	0	96.91255	0	111.0683	0	CDS conserved hypothetical protein 5206323:5207225 reverse MW:33478
RPA4622	6.763321	0	8.543444	0	4.685468	0	23.55266	0.0005	16.9754	0	CDS hypothetical protein 5207241:5207519 reverse MW:9934
RPA4623	24.09905	0	111.694	0	21.96292	0	277.1916	0	61.85431	0	fixU, nifT conserved hypothetical protein 5207522:5207722 reverse MW:7247
RPA4625	96.15459	0	74.06278	0	78.02971	0	237.4105	0	212.4712	0	nifZ NifZ domain 5207993:5208292 reverse MW:11072
RPA4626	119.1983	0	70.41254	0.0005	96.52726	0	256.2595	0	287.8525	0	CDS Protein of unknown function from Deinococcus and Synechococcus 5208289:5209074 reverse MW:29708
RPA4627	16.31473	0.003	16.37948	0	17.61124	0	49.30035	0	53.01149	0	CDS conserved hypothetical protein 5209064:5209603 reverse MW:19822
RPA4628	80.07556	0	63.819	0	69.99226	0	276.4904	0	108.1907	0	hesB Protein of unknown function, HesB/YadR/YfhF 5209607:5209963 reverse MW:12517
RPA4629	8.988371	0.001	4.8788	0.0005	4.578782	0.0005	25.9394	0	15.19358	0.0005	ferN ferredoxin 2[4Fe-4S], fdxN 5209974:5210195 reverse MW:7733
RPA4630	146.7473	0	75.32341	0	123.7286	0	529.5537	0	202.465	0	nifB nitrogen fixation protein nifB 5210219:5211775 reverse MW:56353
RPA4631	65.38378	0			55.9951	0	227.7299	0.0025	88.61352	0.0005	fer1 ferredoxin 2[4Fe-4S], fdxN 5211934:5212128 reverse MW:6859
RPA4632	1.823505	0.0005	2.084419	0	2.009884	0	3.732966	0	3.03619	0	nifA Mo/Fe nitrogenase specific transcriptional regulator, NifA 5212401:5214155 reverse MW:64773
RPA4633	9.553973	0	5.141076	0.0005	9.253968	0	52.46504	0	12.03289	0	fixR2 short-chain dehydrogenase 5214468:5215364 reverse MW:31646
RPA4634	2.542348	0.002	2.044081	0.0005	2.100995	0.001	7.677574	0.0005	4.10792	0.0005	CDS hypothetical protein 5215621:5216475 forward MW:30264
RPA4635	0.962912	0.595	1.272846	0.0135	1.108345	0.11	1.122911	0.23	0.925893	0.783	feoB ferrous iron transport protein B 5216625:5218511 reverse MW:68133
RPA4636	1.337655	0.006	1.543771	0.0025	1.73543	0.0005	1.786677	0.0035	1.585182	0.002	CDS FeoA family 5218549:5218839 reverse MW:10629
RPA4637	1.225217	0.032	1.170885	0.1005	1.079897	0.2485	1.519361	0.0135	1.281534	0.0145	CDS hypothetical protein 5219202:5219363 forward MW:5660
RPA4638	0.494049	1	0.462966	0.998	0.446837	1	0.406534	1	0.304119	0.9995	CDS methyl-accepting chemotaxis receptor/sensory transducer 5219533:5221230 reverse MW:59272
RPA4639	0.50204	0.999	0.298443	1	0.42567	1	0.37679	0.9995	0.644974	0.992	CDS methyl-accepting chemotaxis receptor/sensory transducer 5221609:5223303 reverse MW:59591
RPA4640	0.599592	0.992	0.631341	0.9925	0.839271	0.843	1.121154	0.1375	1.566224	0.081	CDS hypothetical protein 5223509:5223895 reverse MW:14295
RPA4641	0.635318	0.9775	1.128152	0.185	0.776623	0.969	0.561246	0.9945	0.43352	0.991	cbbM ribulose-bisphosphate carboxylase form II 5224192:5225577 reverse MW:50485
RPA4642	0.684964	0.944	1.259033	0.071	0.76373	0.976	0.613885	0.986	0.442216	0.995	cbbA fructose-bisphosphate aldolase 5225636:5226721 reverse MW:39341
RPA4643	0.648833	0.991	0.974038	0.622	0.62435	0.999	0.625974	0.9845	0.433671	1	cbbT1 transketolase 5226783:5228750 reverse MW:68864
RPA4644	0.867535	0.7	1.151326	0.112	1.053104	0.3545	0.979848	0.548	0.662641	0.9885	cbbP phosphoribulokinase (phosphopentokinase) (PRK) 5228833:5229708 reverse MW:33245
RPA4645	0.539015	1	1.122445	0.113	1.026436	0.37	0.934366	0.7385	0.573173	0.9945	cbbF fructose-1,6-bisphosphatase 5229746:5230777 reverse MW:36633
RPA4646	0.658431	0.979	0.535915	0.998	0.76023	0.9225	0.355504	0.998	0.349379	1	CDS putative carboxylesterase 5231249:5231998 forward MW:26151
RPA4647	0.832162	0.947	1.186762	0.165	0.857198	0.8385	1.088469	0.3695	0.614553	0.9935	kdgR probable transcriptional regulator KdgR, IclR family 5232127:5232882 reverse MW:27910
RPA4648	0.968349	0.6145	0.984782	0.535	0.993525	0.509	0.650351	0.9955	0.393067	1	CDS possible ABC transporter binding protein component 5232963:5234051 reverse MW:39941
RPA4649	0.630873	0.969	0.572986	0.998	0.763083	0.9705	0.463768	1	0.355673	1	CDS probable ABC transporter permease protein 5234085:5235878 reverse MW:63530
RPA4650	0.809331	0.918	0.621773	0.999	0.91297	0.8535	0.764112	0.952	0.467316	0.9995	potA putative spermidine/putrescine transport system ATP-binding protein 5235875:5237020 reverse MW:41465
RPA4651	0.782451	0.954	0.540019	0.998	0.895377	0.771	0.811302	0.8135	0.557104	0.9975	CDS possible glutaconate CoA-transferase, subunit A 5237135:5238082 forward MW:33750
RPA4652							0.994355	0.51			CDS possible CoA transferase, subunit B 5238082:5238849 forward MW:27870
RPA4653	0.801216	0.928	0.579291	0.9345	0.910908	0.767	1.924983	0.1565	0.432833	1	bisC biotin sulfoxide reductase 5238882:5241191 forward MW:83980
RPA4654	0.710731	0.9965	0.910307	0.7975	0.713354	0.99	0.608859	0.9725	0.344406	1	CDS conserved unknown protein 5241208:5241777 forward MW:21206
RPA4655	0.917827	0.6945	0.767726	0.86	0.849053	0.957	0.943697	0.6125	0.816776	0.972	fucA L-fuculose phosphate aldolase 5241859:5242545 forward MW:24844
RPA4656	0.588357	0.999	0.677039	0.9985	0.712975	0.9945	0.580656	0.991	0.543742	0.9995	CDS possible sugar kinase 5242576:5243535 forward MW:32863
RPA4657	0.558196	0.9995	0.613385	0.9995	0.64157	0.9905	0.416375	0.999	0.272359	0.9995	kduD putative 2-keto-3-deoxygluconate dehydrogenase 5243582:5244328 forward MW:26709
RPA4658	1.249863	0.036	1.063391	0.33	1.35706	0.0145	0.979088	0.5975	0.73398	0.991	CDS zinc-binding dehydrogenases (related to alcohol dehydrogenase, NADPH quinone oxidoreductase) 5244361:5245347 forward MW:34340
RPA4660	1.056409	0.241	1.123526	0.183	1.528372	0.003	0.700069	0.962	1.139254	0.0805	otsA putative alpha,alpha-trehalose-phosphate synthase (UDP-forming) (trehalose-6-phosphate synthase) 5252629:5254110 reverse MW:54099
RPA4661	1.130841	0.1145	1.565904	0.0205	1.529217	0.0005	1.167711	0.1985	1.384197	0.0045	otsB putative trehalose-6-phosphate phophatase, biosynthetic 5254267:5255064 reverse MW:28672
RPA4662	1.552459	0.021	1.852977	0.0065	1.525281	0.0035	1.063129	0.2565	1.215189	0.0455	CDS putative suar transport protein 5255061:5256548 reverse MW:53154
RPA4663	1.088887	0.256	1.142086	0.1275	0.744729	0.985	1.000042	0.501	1.071618	0.262	CDS methyl-accepting chemotaxis receptor/sensory transducer 5256729:5258771 reverse MW:71147
RPA4664			1.216189	0.2115					0.991194	0.504	CDS CUPIN domain:transcriptional regulator, AraC family 5258890:5259636 reverse MW:27143
RPA4665	1.001982	0.51	0.803681	0.976	1.014065	0.4635	0.719393	0.9505	0.809991	0.9715	leuA 2-isopropylmalate synthase 5259974:5261635 forward MW:61037
RPA4666	1.991407	0.1295	0.53284	0.9925	1.85674	0.007	1.011875	0.476	0.757918	0.9495	coxS, cutS carbon-monoxide dehydrogenase small subunit 5261956:5262426 forward MW:16733
RPA4667	1.772993	0.1865	0.547414	0.962	1.835342	0.0005	1.017386	0.4775	0.610042	0.957	coxL, cutL putative carbon-monoxide dehydrogenase large subunit 5262537:5264891 forward MW:83925
RPA4668	1.172968	0.2635	0.662523	0.9215	1.604283	0.0055	0.920729	0.6495	0.506567	0.954	coxM, cutM carbon monoxide dehydrogenase chain C 5265000:5265800 forward MW:28018
RPA4669	1.011899	0.4405	0.635837	0.987	0.942918	0.7065	0.644757	0.9855	0.727031	0.9965	CDS putative racemase 5265985:5267100 forward MW:39165
RPA4670	1.064927	0.171	0.908435	0.898	0.807488	0.985	0.913866	0.8365	0.778067	0.991	fahA fumarylacetoacetate hydrolase 5267227:5268492 reverse MW:46231
RPA4671	0.924659	0.746	1.113581	0.173	0.802022	0.902	0.903923	0.7205	0.781846	0.92	maiA putative maleylacetoacetate isomerase 5268784:5269440 reverse MW:24687
RPA4672	0.915882	0.7975	0.877366	0.9075	0.862928	0.9235	0.824293	0.9085	0.719485	0.9945	hmgA homogentisate 1,2-dioxygenase 5269437:5270783 reverse MW:49761
RPA4673	0.859757	0.8605	0.790959	0.975	0.867675	0.9225	0.97899	0.564	0.71773	0.958	cphA1 putative beta lactamase precursor 5270840:5271793 reverse MW:34975
RPA4674	1.097783	0.3025	0.977301	0.594	0.96253	0.617	1.159788	0.287	0.994268	0.5355	CDS conserved hypothetical protein 5272020:5272238 reverse MW:7562
RPA4675	0.961676	0.6275	0.566105	0.999	1.007385	0.476	0.849456	0.7945	0.819111	0.9695	CDS possible 3-(3-hydroxy-phenyl)propionate hydroxylase 5272528:5274135 reverse MW:59536
RPA4676									1.27246	0.124	CDS probable transcriptional regulator, MarR family 5274265:5274762 forward MW:18931
RPA4677	0.963529	0.712	0.962106	0.7095	1.19615	0.04	1.162626	0.052	1.11312	0.1035	CDS Caspase-1, p20:TPR repeat 5274933:5276363 forward MW:50807
RPA4678	1.75658	0.006	0.999973	0.5065	1.319292	0.161	1.872682	0.005	1.577924	0.005	CDS possible outer membrane protein OprF (AF117972) 5276468:5277118 forward MW:22865
RPA4679			0.450955	0.9935	0.678018	0.87	0.682287	0.9365	0.663861	0.9475	CDS possible component of multidrug efflux system 5277277:5278164 forward MW:30781
RPA4680	0.927924	0.8405	0.659008	0.991	0.608754	0.984	0.693528	0.9515	0.631542	0.9985	CDS putative efflux transporter 5278164:5281316 forward MW:112400
RPA4681	0.982332	0.5875	0.868824	0.9425	1.101448	0.0915	1.03785	0.4015	1.03561	0.385	CDS possible asmA protein 5281358:5283175 forward MW:62794
RPA4682	0.870851	0.896	0.88345	0.9355	0.818213	0.9625	0.789956	0.9825	0.760486	0.9955	CDS possible RND efflux membrane fusion protein precursor 5283182:5284153 forward MW:33468
RPA4683	1.746542	0.21	0.420014	0.993	1.992861	0.0245	0.768084	0.744	0.377279	0.9965	CDS hypothetical protein 5284215:5284469 reverse MW:9435
RPA4684	0.725443	0.8785	0.166013	1	0.744497	0.9525	0.455856	0.9985	0.340906	0.999	CDS methyl-accepting chemotaxis receptor/sensory transducer 5285027:5286706 forward MW:59105
RPA4685	0.801341	0.961	0.824886	0.986	0.87257	0.921	0.865474	0.9065	0.833895	0.9595	lysS lysyl tRNA synthetase 5286747:5288384 reverse MW:60877
RPA4686	0.836657	0.973	0.793668	0.9865	0.776219	0.965	0.800163	0.8725	1.056606	0.2435	CDS possible ABC transporter, periplasmic amino acid-binding protein 5288418:5289173 reverse MW:28338
RPA4687	0.642271	0.9915	0.62223	0.979	0.704575	0.977	1.075753	0.3595	1.290239	0.016	CDS possible Glycosyl transferases 5289415:5291466 forward MW:75488
RPA4688	0.757872	0.9625	0.641697	0.994	0.784818	0.965	0.681207	0.9885	0.67313	0.984	CDS possible inner mitochondrial membrane protein Sco1p 5291468:5292067 reverse MW:21777
RPA4689	0.789207	0.731	0.347041	0.9985	1.218158	0.23	0.569517	0.9365	0.627144	0.9465	CDS conserved hypothetical protein 5292243:5292701 reverse MW:16624
RPA4690	0.781856	0.8325			1.204945	0.23			0.599184	0.9355	CDS hypothetical protein 5292915:5293253 forward MW:12491
RPA4691	0.971741	0.6395	0.753585	0.959	0.719114	0.981	1.217365	0.0635	1.55193	0.001	CDS methyl-accepting chemotaxis receptor/sensory transducer 5293431:5295401 forward MW:70249
RPA4692	1.57198	0	1.298916	0.008	1.433768	0.002	2.500046	0	1.473971	0.0035	CDS unknown protein 5295550:5295927 forward MW:13564

RPA4693	0.938219	0.858	0.738159	0.983	1.12533	0.1545	0.836762	0.869	0.76623	0.9755	CDS putative FMN oxidoreductase 5296118:5297281 reverse MW:42544
RPA4694	0.867713	0.9265	0.761826	0.971	0.927529	0.661	1.017983	0.476	1.096056	0.224	CDS Uncharacterized protein family UPF0065:Tat pathway signal 5297448:5298446 forward MW:34897
RPA4695	0.765865	0.9775	0.802924	0.928	0.654213	0.997	0.919469	0.622	0.684644	0.996	ligR transcriptional regulator ligR, LysR family 5298468:5299370 forward MW:32575
RPA4696	1.230635	0.0775	1.689367	0.062	0.884247	0.833	2.774764	0	1.402103	0.028	FldA conserved unknown protein 5299497:5300615 forward MW:38993
RPA4697	0.894672	0.701	0.983518	0.5595	0.863628	0.887	1.060895	0.369	0.625904	0.999	ligJ 4-oxalomesaconate hydratase 5300785:5301813 forward MW:38469
RPA4698	1.023779	0.474	0.785601	0.8965	0.493052	0.999	0.88634	0.6395	0.452977	0.9925	FldZ possible acyl transferase 5301816:5302511 forward MW:24479
RPA4699	1.006413	0.4925	1.179716	0.0965	0.873555	0.8055	1.315697	0.1415	0.825059	0.939	FldX possible dehydrogenase 5302511:5303440 forward MW:33027
RPA4700	0.906462	0.712	1.197821	0.0985	0.833863	0.961	0.905097	0.693	0.664329	0.996	ligI 2-pyrone-4,6-dicarboxylic acid hydrolase 5303694:5304608 forward MW:34470
RPA4701	0.984509	0.5615	0.980106	0.5935	0.970932	0.664	0.86529	0.8795	0.712131	0.993	ligA Protocatechuate 4,5-dioxygenase, alpha chain 5304715:5305104 forward MW:14674
RPA4702	0.958381	0.6735	0.980472	0.59	1.018295	0.3995	0.870916	0.8185	0.778069	0.92	ligB Protocatechuate 4,5-dioxygenase, beta chain 5305104:5305958 forward MW:31265
RPA4703	0.991605	0.5075	1.044975	0.283	1.041144	0.3055	0.966397	0.5945	0.803445	0.8765	ligC 4-carboxy-2-hydroxymuconate-6-semialdehyde dehydrogenase 5305960:5306919 forward MW:35011
RPA4704	1.083433	0.23	1.342261	0.0155	1.483925	0.037	1.058011	0.308	1.62837	0.0005	CDS conserved hypothetical protein 5307112:5307510 forward MW:13877
RPA4705	0.779661	0.983	0.841743	0.962	1.00128	0.4815	1.040881	0.368	1.219894	0.012	hisE2 phosphoribosyl-AMP cyclohydrolase / phosphoribosyl-ATP pyrophosphohydrolase 5307616:5308011 forward MW:14605
RPA4706	1.130638	0.065	1.350035	0.0425	0.949937	0.751	1.042248	0.322	1.077945	0.2055	CDS DedA family 5308113:5308694 forward MW:21531
RPA4708	0.974278	0.634	0.961581	0.6825	0.913627	0.8945	0.926992	0.699	0.846728	0.9725	CDS conserved unknown protein 5309570:5310538 forward MW:34331
RPA4709	0.82416	0.968	0.829611	0.9655	0.787269	0.974	0.757138	0.9635	0.64869	0.999	CDS conserved hypothetical protein 5310696:5311469 forward MW:27875
RPA4710	0.752213	0.992	0.611723	0.998	0.665229	0.9865	0.609075	0.997	0.703108	0.996	CDS hypothetical protein 5311592:5311912 forward MW:11837
RPA4711	0.847741	0.9775	0.695827	0.9915	1.016958	0.4385	0.780734	0.976	1.228007	0.0325	CDS hypothetical protein 5312066:5312764 forward MW:24602
RPA4712	1.064049	0.2925	0.925612	0.792	1.314598	0.002	1.25848	0.041	1.336171	0.026	CDS TPR repeat 5312818:5314566 reverse MW:64678
RPA4713	4.355339	0	6.536345	0	3.325271	0.0005	23.88911	0	7.315584	0	CDS hypothetical protein 5314811:5315782 forward MW:33157
RPA4714	20.78979	0.001	10.37743	0	13.96497	0	38.33452	0	40.40452	0	CDS hypothetical protein 5315755:5316345 reverse MW:20098
RPA4715	1.291832	0.0305	0.929227	0.737	1.23006	0.043	1.339159	0.0435	1.163323	0.0725	modC molybdate transport system ATP-binding protein 5316493:5317614 reverse MW:40000
RPA4716	0.785863	0.9385	0.656059	0.9335	1.160251	0.195	0.689885	0.941	0.573403	0.999	modB molybdate transport system permease protein 5317611:5318297 reverse MW:24438
RPA4717	0.876483	0.8705	0.853272	0.9525	1.099203	0.1705	1.108441	0.1765	0.946348	0.715	modA molybdate transport system substrate-binding protein 5318535:5319308 reverse MW:27037
RPA4718	0.971445	0.654	0.768817	0.9915	0.956905	0.626	1.052918	0.3015	1.094337	0.114	modE putative molybdate transport system transcriptional regulator, ModE 5319453:5320244 reverse MW:27327
RPA4719	0.788361	0.8485	0.759381	0.977	0.99252	0.522	0.97765	0.5765	0.5785	0.988	CDS molybdo-pterin binding protein 5320343:5320552 forward MW:7087
RPA4720	0.992781	0.534	1.000773	0.508	1.031595	0.3425	1.396442	0.0115	1.207256	0.0355	CDS conserved hypothetical protein 5320597:5321166 reverse MW:20730
RPA4722	0.793836	0.832	0.76955	0.8885	0.850972	0.8265	0.703753	0.9625	0.419499	0.9975	CDS possible glutamate synthase, small subunit 5326633:5329467 forward MW:103832
RPA4723	0.961143	0.712	0.76994	0.988	0.861033	0.953	0.804699	0.948	0.917342	0.8585	polA DNA polymerase I 5330466:5333543 forward MW:111144
RPA4724	0.963665	0.7105	0.840483	0.9305	0.914332	0.6945	0.957449	0.61	1.033199	0.3525	pyrE putative uridine 5-monophosphate synthase 5333861:5334424 forward MW:20066
RPA4725	0.900006	0.9205	0.871584	0.9325	0.923767	0.808	0.901801	0.804	1.019257	0.4085	CDS conserved hypothetical protein 5334527:5335330 forward MW:28208
RPA4726	0.494643	0.9995	0.481738	0.9995	0.831835	0.9285	0.456717	0.9915	0.816949	0.9715	CDS conserved hypothetical protein 5335598:5336029 reverse MW:16157
RPA4727	1.098558	0.2025	0.884211	0.9145	1.030678	0.3695	2.071023	0.004	1.498504	0.002	glgA2 glycogen phosphorylase 5336312:5338858 forward MW:94541
RPA4728	0.814906	0.9065	0.563958	1	0.734181	0.98	0.7146	0.977	0.848802	0.917	CDS conserved hypothetical protein 5339139:5339972 forward MW:30124
RPA4729	0.765805	0.979	0.624695	0.9965	0.77307	0.9795	0.833881	0.8435	0.898674	0.858	rocF putative arginase 5340028:5341011 forward MW:34835
RPA4730	0.907926	0.8685	1.193031	0.028	0.603512	0.998	0.913644	0.853	1.162376	0.1705	CDS ATP-binding protein of ABC transporter, duplicated ATPase domains 5341259:5342878 forward MW:59773
RPA4731	0.723606	0.995	0.782137	0.989	0.740266	0.9945	0.637683	0.997	0.698752	0.992	CDS conserved unknown protein 5343026:5344219 reverse MW:42717
RPA4732	0.921406	0.872	0.919655	0.8425	1.052159	0.3825	0.942888	0.648	0.960854	0.7325	CDS uncharacterized cation transport protein chaC 5344380:5344958 forward MW:21632
RPA4733	0.884701	0.9085	1.024725	0.392	0.937609	0.707	1.537216	0.014	1.236879	0.013	plsC putative 1-acyl-SN-glycerol-3-phosphate acyltransferase 5344975:5345784 reverse MW:30327
RPA4734	0.969377	0.666	0.977707	0.593	0.939043	0.789	1.24664	0.053	1.247751	0.018	CDS conserved hypothetical protein 5345798:5346565 reverse MW:27802
RPA4735	0.824406	0.775	0.714802	0.808	0.528571	0.9845	0.756824	0.7845	0.673401	0.9635	CDS hypothetical protein 5346668:5347444 reverse MW:29215
RPA4736	0.604295	0.974	0.552561	0.995	0.511091	0.914	0.525635	0.9945	0.531092	0.9955	ftsE putative cell division ATP-binding protein FtsE, ABC type transporter 5347658:5348317 reverse MW:24472
RPA4737	1.057448	0.1775	0.934905	0.841	0.762437	0.988	1.080346	0.17	1.1578	0.0275	CDS conserved hypothetical protein 5348461:5349357 forward MW:32871
RPA4738	0.750183	0.904	1.049637	0.371	0.938927	0.607	1.202939	0.197	1.117184	0.312	CDS response regulator receiver (CheY-like protein) 5349417:5349797 forward MW:13486
RPA4739	1.024216	0.408	0.944443	0.7195	0.971408	0.595	1.001301	0.515	1.038018	0.3595	CDS conserved hypothetical protein 5349996:5352557 reverse MW:92429
RPA4740	0.931303	0.6375			0.986344	0.532			0.617844	0.854	pcaC putative 4-carboxymuconolactone decarboxylase 5352717:5353097 forward MW:14148
RPA4741	0.58377	0.998	0.804292	0.993	0.578802	0.9975	0.501552	0.9975	0.620836	0.994	lysA diaminopimelate decarboxylase 5353332:5354597 reverse MW:45333
RPA4742	0.795034	0.9645	0.882812	0.902	0.858808	0.962	0.791256	0.9765	0.944849	0.7705	CDS conserved hypothetical protein 5354606:5354887 reverse MW:9632
RPA4743	0.965059	0.729	1.061808	0.2955	0.854777	0.8505	0.990002	0.547	1.04085	0.345	argH argininosuccinate lyase, (ASAL) 5354942:5356339 reverse MW:50714
RPA4744	0.989162	0.5825	1.112535	0.101	0.906614	0.882	1.184101	0.0775	0.962629	0.629	CDS possible thioredoxin-like protein 5356435:5357121 forward MW:24059
RPA4745											CDS hypothetical protein 5357277:5357507 reverse MW:7617
RPA4746					1.002573	0.474			1.27185	0.103	CDS putative NAD(P)H quinone reductase 5357574:5358392 reverse MW:29994
RPA4747	1.052619	0.415	0.788403	0.831	0.712646	0.813	1.007431	0.4735	0.919457	0.697	CDS transcriptional regulator, LysR family 5358469:5359383 forward MW:32984
RPA4748	1.216965	0.088	1.146026	0.029	1.063119	0.217	1.075311	0.2495	1.074356	0.2495	hbdA 3-hydroxybutyryl-CoA dehydrogenase 5359398:5360279 reverse MW:31829
RPA4749	1.179561	0.1715	1.109588	0.1865	0.787753	0.969	0.832507	0.942	0.820898	0.942	etfA electron transfer flavoprotein alpha-subunit, (ETFLS) 5360445:5361389 reverse MW:32417
RPA4750	1.130114	0.197	1.086642	0.1665	0.724494	0.9925	0.812802	0.908	0.790478	0.9895	etfB electron transfer flavoprotein beta chain, (ETFSS) 5361389:5362138 reverse MW:26364
RPA4751	1.192255	0.0235	1.364706	0.0065	1.093414	0.183	1.054331	0.2885	1.147641	0.123	CDS DUF80 5362244:5362816 reverse MW:20774
RPA4752	1.18098	0.023	1.049581	0.3145	1.223386	0.056	0.848582	0.8425	1.173385	0.03	rbn1 putative ribonuclease RNAse BN (RBN) transmembrane protein 5363202:5364095 forward MW:32079
RPA4753	1.267795	0.018	1.259082	0.01	1.358661	0.005	0.962081	0.6045	1.050789	0.276	CDS histidine kinase with a response regulator receiver domain 5364022:5365239 reverse MW:42590
RPA4754	1.026304	0.3525	0.973205	0.648	0.988095	0.5445	1.045286	0.313	1.018377	0.3845	CDS possible glutamyl-tRNA synthetase 5365339:5366262 reverse MW:33531
RPA4755	0.964247	0.5785			1.180402	0.105	0.686071	0.85	0.791158	0.9485	CDS possible DNA-3-methyladenine glycosidase II 5366291:5367061 forward MW:27689
RPA4756	1.276824	0.0215	1.041687	0.304	1.108917	0.1395	1.289582	0.018	1.44173	0.0105	CDS Helix-turn-helix protein, CopG family 5367193:5367639 reverse MW:16764
RPA4757	1.373166	0.009	1.267121	0.016	1.290452	0.0135	1.310093	0.0125	1.519407	0.0025	CDS possible outer membrane receptor for iron transport 5367760:5369976 forward MW:79451
RPA4758	1.832179	0.036	4.014431	0.006	3.059159	0.002	1.312067	0.161	2.4048	0	CDS conserved hypothetical protein 5370412:5370765 forward MW:12873
RPA4759	0.736311	0.994	0.916856	0.869	0.876697	0.946	0.818553	0.945	0.948702	0.763	CDS glycosyl hydrolase, family 13 5370812:5372428 reverse MW:60111
RPA4760	0.722111	0.888	1.433966	0.094	1.069295	0.269	0.714335	0.9415	1.097689	0.21	CDS unknown protein 5372942:5373475 forward MW:18442
RPA4761	0.42913	0.9955	0.526241	0.98	1.028534	0.4745	0.709579	0.8115	1.290812	0.0275	CDS conserved hypothetical protein 5373755:5374279 forward MW:18177
RPA4762	1.228125	0.1275	0.938588	0.723	1.157144	0.2125	1.269141	0.018	1.147247	0.1565	ogt2 putative O-6-methylguanine-DNA methyltransferase 5374977:5375570 forward MW:21070
RPA4763	0.901964	0.9225	0.966631	0.6095	1.655503	0.011	0.631441	0.9825	0.572432	0.9875	CDS possible cation efflux pump 5375567:5377003 reverse MW:48996
RPA4764					0.875514	0.6965	1.145076	0.318	1.025889	0.447	CDS Metallo-phosphoesterase:Tat pathway signal 5377514:5379493 forward MW:72480
RPA4765	0.773053	0.975	0.755807	0.986	0.507304	0.997	0.580691	0.9955	0.664329	0.9985	CDS unknown protein 5379553:5380686 reverse MW:41262
RPA4766	1.123221	0.2655	1.643857	0.004	1.052101	0.3825	1.419842	0.028	1.77769	0.003	metZ O-succinylhomoserine sulfhydrylase 5380923:5382134 forward MW:43496
RPA4767	0.907886	0.8125	0.92128	0.713	1.096674	0.229	0.884459	0.854	0.92887	0.7595	CDS Lipolytic enzyme, G-D-S-L family 5382282:5383250 reverse MW:34309
RPA4768	0.923419	0.865	0.96528	0.7085	1.131664	0.085	0.885852	0.915	0.959632	0.731	CDS conserved hypothetical protein 5383250:5384029 reverse MW:28095
RPA4769	0.941642	0.7095	0.888783	0.865	1.003871	0.496	0.706601	0.9705	0.932228	0.761	opgC putative opgC protein 5384026:5385291 reverse MW:47101
RPA4770	1.002581	0.485	0.955499	0.714	1.155611	0.044	1.355377	0.0315	1.639699	0.001	apaG DUF525 5385542:5385934 forward MW:14691
RPA4771	0.706331	0.9625	0.695482	0.9955	0.980039	0.585	0.641495	0.975	0.849829	0.9445	CDS possible heat shock protein HSP33 5386010:5387011 reverse MW:36398

RPA4772	0.783803	0.9925	0.971869	0.674	0.715107	0.9965	0.980926	0.5715	1.214101	0.0595	argF ornithine carbamoyltransferase 5387283:5388215 reverse MW:33943
RPA4773	0.791067	0.99	0.896177	0.8855	0.799474	0.992	0.914448	0.7285	1.102297	0.126	argD2 putative acetylornithine aminotransferase 5388212:5389474 reverse MW:44380
RPA4774	0.923331	0.6135	0.535522	0.9985	1.018434	0.412	0.75798	0.9825	0.802846	0.969	CDS conserved unknown protein 5389767:5390408 forward MW:23379
RPA4775	0.688925	0.9985	0.697697	0.9335	0.770449	0.9885	0.65704	0.996	0.732008	0.9715	phoB two-component phosphate transcriptional regulator PhoB 5390650:5391363 reverse MW:26936
RPA4776	0.969672	0.63	0.930264	0.6695	0.924463	0.738	0.6941	0.9825	0.868477	0.8935	phoU phosphate regulon transcriptional regulator, phoU 5391441:5392157 reverse MW:26662
RPA4777	1.065419	0.409	1.147886	0.2065	0.970866	0.6765	0.994409	0.517	1.375327	0.01	pstB phosphate ABC transporter ATP-binding protein, PstB 5392181:5393002 reverse MW:30242
RPA4778	0.865707	0.614	1.094031	0.3135	0.732165	0.9955	0.527791	0.973	0.813163	0.9155	pstA phosphate transport system permease protein PstA 5392999:5393862 reverse MW:30669
RPA4779	0.70741	0.776	1.175493	0.1915	0.739716	0.962	0.561063	0.9535	0.721956	0.994	pstC phosphate ABC transporter, permease protein, PstC 5393864:5394865 reverse MW:35282
RPA4780	0.768582	0.794	0.989716	0.5545	0.910723	0.826	0.708949	0.908	0.970078	0.626	pstS1 periplasmic phosphate-binding protein, (PBP) 5395079:5396089 reverse MW:35626
RPA4781	0.88699	0.884	1.013741	0.4215	0.802369	0.9735	0.879958	0.922	0.970759	0.645	phoR two component sensor histidine kinase phoR 5396238:5397587 reverse MW:48576
RPA4782	1.023639	0.371	0.946912	0.7815	1.041681	0.282	1.043756	0.3135	1.041196	0.2825	CDS conserved hypothetical protein 5397591:5398625 reverse MW:36769
RPA4783	0.869337	0.9355	0.92993	0.82	0.800478	0.9795	0.81525	0.969	0.804367	0.97	CDS conserved hypothetical protein 5398873:5399169 reverse MW:10590
RPA4784	0.779649	0.984	0.824112	0.9535	0.754892	0.9925	0.757684	0.991	0.831346	0.9745	CDS OmpA/MotB domain 5399173:5400567 reverse MW:49142
RPA4785	1.321962	0.0155	1.260329	0.0605	1.291169	0.0435	1.165494	0.2275	0.994659	0.527	CDS Polysaccharide deacetylase 5400723:5401781 forward MW:39578
RPA4786	1.134641	0.1265	1.030118	0.33	0.860694	0.9185	0.828775	0.9325	0.860074	0.944	rhlG putative beta-ketoacyl reductase 5401842:5402648 forward MW:28140
RPA4787	0.903208	0.8405	1.065945	0.2055	0.779136	0.977	0.768507	0.965	1.031129	0.346	CDS possible Shikimate kinase with a Helix-turn-helix domain 5402871:5403788 forward MW:33251
RPA4788	1.14527	0.0785	1.124691	0.104	0.985998	0.574	1.426737	0.013	1.938697	0	ugpB2 putative sn-glycerol 3-phosphate transport system; periplasmic binding protein 5403795:5405123 reverse MW:47972
RPA4789	1.219129	0.0865	1.031977	0.3615	1.068253	0.235	1.221374	0.0475	1.270132	0.01	CDS sensor histidine kinase 5405300:5407411 forward MW:76842
RPA4790	1.35837	0.0105	0.925411	0.8085	1.221929	0.025	1.20913	0.035	1.325272	0.0075	CDS response regulator receiver:histidine kinase 5407468:5409120 forward MW:60377
RPA4791	1.228545	0.0185	1.083167	0.123	1.140294	0.042	1.110038	0.1105	1.000284	0.488	CDS two-component transcriptional regulator, winged helix family 5409117:5409857 forward MW:26966
RPA4792	1.238577	0.11	3.882997	0	0.341558	0.9515	4.963808	0.009	3.536568	0.003	CDS RNA polymerase ECF-type sigma factor 5410062:5410673 forward MW:22901
RPA4793	0.732318	0.993	0.563324	0.9995	0.805117	0.9755	0.493739	0.9995	0.461359	1	QxtA cytochrome bd-quinol oxidase subunit I 5411181:5412587 forward MW:51449
RPA4794	0.726606	0.9775	0.678417	0.9845	0.82677	0.927	0.564979	0.998	0.417898	0.999	qxtB putative cytochrome bd-quinol oxidase subunit II 5412601:5413611 forward MW:37246
RPA4795	0.91094	0.647	0.90431	0.841	0.966066	0.5735	0.708866	0.839	0.651565	0.9585	CDS conserved hypothetical protein 5413608:5413739 forward MW:4768
RPA4796	0.891992	0.959	0.82816	0.9795	0.773093	0.9825	0.66276	0.9965	0.695023	0.9905	CDS ErfK/YbiS/YcfS/YnhG 5413781:5414374 forward MW:21924
RPA4797	0.809926	0.9885	0.827827	0.9425	0.664111	0.997	0.666604	0.9855	0.722169	0.9805	CDS ABC transporter, amino acid binding protein 5414421:5415455 forward MW:38493
RPA4798	0.834954	0.982	0.775336	0.9765	0.798442	0.993	0.761328	0.987	0.676583	0.998	CDS putative acyl-CoA dehydrogenase 5415801:5416940 reverse MW:39968
RPA4799	0.820951	0.979	0.79919	0.978	0.915345	0.781	0.629003	0.998	0.579193	1	CDS possible acyl-CoA dehydrogenase 5417107:5418291 reverse MW:43453
RPA4800	1.290747	0.023	1.173139	0.0965	1.122365	0.1665	1.161557	0.207	0.823369	0.9765	CDS possible transporter 5419057:5420268 reverse MW:41779
RPA4801	0.865464	0.969	0.858875	0.9235	0.999355	0.5095	0.832751	0.934	0.794098	0.9815	CDS MFS permease family 5420357:5421604 reverse MW:43320
RPA4802	1.030377	0.396	1.381809	0.1615	0.948006	0.677	1.36349	0.081	0.863174	0.842	CDS conserved unknown protein 5421680:5422411 reverse MW:25749
RPA4803	0.582441	0.9885	0.460734	0.9985	0.319914	1	0.252155	1	0.61586	0.991	CDS putative outer membrane hemin/siderophore receptor protein 5422839:5424950 forward MW:75633
RPA4804	0.794266	0.9885	0.888844	0.771	0.551476	0.9995	0.837736	0.7005	0.852571	0.8765	CDS conserved hypothetical protein 5425107:5425394 forward MW:10330
RPA4805	1.069766	0.336	1.160882	0.1585	0.99266	0.527	1.148947	0.359	1.214346	0.0955	CDS conserved hypothetical protein 5425568:5425762 forward MW:6964
RPA4806											CDS hypothetical protein 5425793:5427049 reverse MW:44481
RPA4807	1.119011	0.391	0.503185	0.996	1.096069	0.1715	0.681948	0.929	0.454417	0.998	CDS possible branched-chain amino acid transport system substrate-binding protein 5427284:5428504 forward MW:44059
RPA4808	1.072683	0.389	0.526072	0.995	1.529012	0.039	0.708109	0.782	0.429031	0.999	CDS possible hexuronate transporter 5428619:5429905 reverse MW:45754
RPA4809	0.870511	0.906	0.711127	0.997	0.97681	0.609	0.725544	0.993	0.765052	0.994	CDS putative ABC transporter, ATP-binding protein 5430178:5430831 forward MW:23357
RPA4810	0.856985	0.7045	0.51131	0.985	0.962048	0.594			0.647896	0.8955	CDS predicted permease 5430828:5433293 forward MW:87963
RPA4811	0.884419	0.8715	0.764026	0.977	0.853798	0.966	0.68029	0.9945	0.580124	0.996	CDS conserved hypothetical protein 5433283:5434368 forward MW:39491
RPA4812	1.382522	0.0145	0.856099	0.9495	1.431209	0.0125	1.015444	0.4535	1.030658	0.356	CDS possible glutathione S-transferase 5434435:5434827 forward MW:14512
RPA4813	1.12281	0.3035	0.774549	0.981	0.988987	0.552	0.99515	0.506	0.855748	0.933	CDS possible branched chain amino acid periplasmic binding protein of ABC transporter 5435015:5436208 reverse MW:42244
RPA4814	1.185851	0.1155	0.775545	0.995	0.832987	0.874	1.121232	0.1905	1.379253	0.008	CDS conserved hypothetical protein 5436294:5437979 reverse MW:59569
RPA4815	0.648708	0.995	0.622451	0.9995	0.54588	0.9995	0.527298	1	0.730727	0.9835	htpG heat shock protein HtpG 5438067:5439953 reverse MW:69468
RPA4816			0.750749	0.8355	0.821435	0.788			0.7828	0.958	CDS two component sensor histidine kinase 5440041:5441417 reverse MW:48823
RPA4817	0.776401	0.9075	1.144016	0.3025	0.978062	0.5895	1.366784	0.3575	0.89214	0.7735	CDS two-component transcriptional regulator, winged helix family 5441414:5442079 reverse MW:24401
RPA4818			0.864382	0.8165	1.348416	0.21	0.829814	0.891	0.638406	0.9765	CDS conserved hypothetical protein 5442079:5442417 reverse MW:12866
RPA4819	0.895567	0.7005	0.932343	0.7285	1.211273	0.1315	1.173685	0.1305	1.29631	0.038	CDS hypothetical protein 5442515:5442823 reverse MW:10908
RPA4820	0.912762	0.7415	1.095207	0.1195	0.802886	0.966	0.864976	0.886	1.022761	0.401	eIF-2B translation initiation factor, aIF-2B alpha subunit 5443007:5444131 reverse MW:40046
RPA4821	1.081058	0.333	1.369326	0.011	0.842144	0.876	0.886068	0.8775	0.964739	0.6705	CDS putative 5'-methylthioadenosine phosphorylase 5444305:5445180 reverse MW:31642
RPA4822	1.21941	0.2935	0.608265	0.9945	1.367971	0.0115	0.926424	0.6585	0.656346	0.958	CDS possible alcohol dehydrogenase 5445459:5446601 forward MW:39953
RPA4823	1.26998	0.2485	0.823454	0.9155	1.333475	0.0095	1.156349	0.133	0.815675	0.8885	CDS putative long-chain-fatty-acid-CoA ligase 5446767:5448317 forward MW:57146
RPA4824	0.914596	0.8705	0.695405	0.926	1.016704	0.4205	0.852143	0.796	0.586609	0.9825	CDS conserved hypothetical protein 5448369:5448743 reverse MW:14414
RPA4825	0.596392	0.959	0.575505	0.9805	0.744465	0.762	0.73424	0.9525			CDS transcriptional regulator, MerR family 5448815:5449168 forward MW:13059
RPA4826	0.814275	0.991	0.842825	0.9725	0.866254	0.9665	0.892379	0.8975	0.874446	0.962	recQ DNA helicase 5449244:5451094 forward MW:66876
RPA4827	12.7688	0			8.721416	0	34.77603	0	11.67616	0	CDS conserved hypothetical protein 5451162:5451389 forward MW:8301
RPA4828	1.32318	0.0585	0.889405	0.8175	1.234753	0.0895	1.447725	0.0215	0.970676	0.622	CDS conserved hypothetical protein 5451413:5451691 reverse MW:9529
RPA4829	1.260254	0.0345	0.928493	0.7355	1.329517	0.006	0.976269	0.574	0.697837	0.9915	caiC putative crotonobetaine/carnitine-CoA ligase 5451971:5453557 forward MW:57552
RPA4830	1.476685	0.0295	1.07661	0.1765	1.051656	0.23	1.451303	0.004	1.305074	0.0065	CDS Metal dependent phosphohydrolase with a response regulator receiver domain 5453665:5454777 reverse MW:40772
RPA4831	1.310651	0.0715	0.751905	0.9895	1.355708	0.0335	1.111246	0.196	1.06675	0.1925	CDS conserved hypothetical protein 5454965:5455354 forward MW:13901
RPA4832	1.059219	0.2305	0.895815	0.8475	0.72475	0.987	1.093071	0.26	1.238045	0.0185	clcD putative dienelactone hydrolase 5455410:5456081 forward MW:23872
RPA4833	0.993708	0.543	0.858082	0.933	0.723254	0.977	0.829299	0.883	0.836852	0.9625	CDS possible polysaccharide export protein 5456108:5456749 reverse MW:22412
RPA4834	1.027432	0.3765	0.977426	0.64	1.65479	0.0005	1.005457	0.4785	1.164005	0.0265	msrA2, pms peptide methionine sulfoxide reductase 5456885:5457541 reverse MW:23576
RPA4835	0.827604	0.9735	1.058234	0.394	0.691415	0.993	0.962957	0.541	0.820703	0.8835	CDS conserved hypothetical protein 5457709:5458026 reverse MW:12042
RPA4836	0.930966	0.679	1.819709	0.0025	0.836364	0.928	1.815211	0.008	1.802374	0.003	rpsT 30S ribosomal protein S20 5458392:5458658 forward MW:9709