Supplementary Table 1. Primer list for semi-quantitative RT-PCR

Gene annotation	**gi number**	**Primer sequence 5'-3'**	**DNA base quantity (mer)**	**Tm (50mM NaCl)**	**Fragment Size (bp)**
TonB-dependent receptor	gi|84625831|ref| YP_453203.1|	Forward : AAAGATACCGCGGATGCTGA	20	52.3	2900
		Reverse : GTGAATAACAGCTACGCACG	20	53.6	
Hypothetical protein WOO_1491	gi|84623148|ref| YP_450520.1|	Forward : GGTCTCATCAGCCAGCTGAG	20	53.7	1140
		Reverse : GAGTTCACTCTCATCTCTCC	20	54.1	
Aminotransferase and dihydrorhizobitoxine synthase	gi|84622935|ref| YP_450307.1|	Forward : ATGTCGTATCTCAATCATGA	20	56.3	1320
		Reverse : AACGTCATCAAGGCTGCGTT	20	56.7	
Porin O	gi|84622659|ref| YP_450031.1|	Forward : GTGAGCAACGACACTTTGCG	20	55.1	1190
		Reverse : GAAGTCGTATTGGAAGCGGC	20	52.3	
3-ketoacyl-ACP reductase	gi|84622657|ref| YP_450029.1|	Forward : GACCATGTGGAGCTCACCAT	20	54.6	738
		Reverse : ATGACTCTCCGCATCGCATA	20	55.2	
HrpF protein	gi|84621766|ref| YP_449138.1|	Forward : GTCTCACTCGAAGTTGTCGG	20	55	2330
		Reverse : ATGTCGCTCAACATGCTTTC	20	53.2	
Hhypothetical protein XOO_2904	gi|84624561|ref| YP_451933.1|	Forward : ATGGCTTTCGATATGCATCT	20	54.7	500
		Reverse : GGACTTCTTCACTTCCTGCA	20	56	
Protease	gi|188578761|ref| YP_001915690.1|	Forward : GTGCTCGACACTACCACCTT	20	53	1860
		Reverse : CTGTCGAGCCATCAAGGACA	20	51.5	
16s rRNA	KY789442.1	Forward : CAGCAGCCGCGGTAATAC	18	58	410
		Reverse : CCGTCAATTCCTTTGAGTTT	19	58	

Supplementary Table 2. Quality of raw data

Sample	Raw reads	N Include Reads No (%)	Total N No (%)	Q30	Q20	GC
In vitro -R1	26,646,901	108,305 (0.41)	149,288 (0.01)	94.75%	98.48%	53.61%
In vitro -R2	26,646,901	27,673 (0.10)	532,163 (0.02)	92.34%	96.42%	53.68%
In vitro -summary	53,293,802	135,978 (0.26)	681,451 (0.01)	93.55%	97.45%	53.64%
In planta (R)-R1	30,055,628	125,206 (0.42)	172,086 (0.01)	95.17%	98.66%	53.78%
In planta (R)-R2	30,055,628	32,192 (0.11)	607,670 (0.02)	92.80%	96.76%	53.85%
In planta (R)-summary	60,111,256	157,398 (0.26)	779,756 (0.01)	93.98%	97.71%	53.82%
In planta (S)-R1	29,834,022	1,215,010 (0.41)	167,362 (0.01)	95.22%	98.69%	53.72%
In planta (S)-R2	29,834,022	31,069 (0.10)	594,035 (0.02)	93.41%	97.16%	53.78%
In planta (S)-summary	59,668,044	152,579 (0.26)	761,397 (0.01)	94.31%	97.92%	53.75%
Summary	242,897,730	756,374 (0.26)	3,780,623 (0.01)	93.72%	97.43%	

R1: Reads sequencing from the left.

R2: Reads sequencing from the right.

Q20: The percentage of bases with a Phred value N20.

Q30: The percentage of bases with a Phred value N30.

Supplementary Table 3. Mapped information of *Xoo* transcriptome.

Sample		**Raw**		**Quality trim**							
		Reads No	**Reads Length**	**Clear NO**	**Clear Length**	**%**	**Mapped Reads**		**Mapped nucleotides**		**Average coverage**
In planta	**Susceptible (S)**	94,542,634	9,548,806,034	54,406,402	5,235,181,135	54.83%	51,316,263	94.32%	4,899,612,529	93.59%	92.33
	Resistant (R)	104,550,144	10,559,564,544	49,565,710	4,697,020,133	44.48%	46,227,949	93.27%	4,347,491,854	92.56%	81.92
In vitro		92,620,466	9,354,667,066	45,734,982	4,468,510,187	47.77%	45,001,417	98.40%	4,329,164,062	96.88%	81.57

Supplementary Table 4. Up-regulated genes during in planta [susceptible and resistant] growth as compared to the *in vitro*

nearest_ref_id	Dongjin	Samgwang	*in vitro*	Description
ACD56668	7.704028117	7.805498835	7.333039035	chromosomal replication initiator protein DnaA
ACD56669	8.720815408	9.041097842	9.509448431	DNA polymerase III, beta subunit
ACD56670	7.058078336	7.537358197	6.068993189	DNA replication and repair RecF protein
ACD56671	8.50085781	8.626665453	8.010500133	DNA gyrase, B subunit
ACD56672	8.74021251	8.607108344	8.716538267	caax amino terminal protease family
ACD56673	9.008039182	9.834101243	9.952961056	peptidase M48, Ste24p
ACD56674	7.763199085	7.933047347	8.245362553	tetratricopeptide repeat domain protein
ACD56675	8.406566431	9.168779909	9.515163655	TonB protein
ACD56676	9.79171804	9.895770658	10.20268708	biopolymer transport ExbB protein
ACD56677	9.787058564	10.01275023	10.04354683	biopolymer transport ExbD1 protein
ACD56678	9.370942362	9.387080306	9.248193249	biopolymer transport ExbD2 protein
ACD56684	7.147204925	7.224648088	7.353155649	TonB-dependent outer membrane Receptor
ACD56685	7.497835873	7.980939266	7.228145276	conserved hypothetical protein
ACD56692	7.494943563	7.138517562	8.003163695	trans-2-enoyl-CoA reductase
ACD56696	9.554726975	9.60292708	9.105795916	TonB-dependent receptor
ACD56702	0	0	0	conserved hypothetical protein
ACD56710	6.907239205	7.882086649	8.012764193	conserved hypothetical protein
ACD56711	7.434169494	6.715097143	6.112120437	neutral protease A
ACD56712	9.33238347	9.085121868	9.542803601	conserved domain protein
ACD56713	10.1769585	10.22209451	8.67175688	conserved hypothetical protein
ACD56716	13.62086129	14.33001351	12.78700672	conserved hypothetical protein
ACD56717	13.67350784	14.27720021	13.49498055	conserved hypothetical protein
ACD56718	11.22344668	11.9495094	9.655450223	putative secreted protein
ACD56720	7.582036575	8.159513141	5.477152734	conserved hypothetical protein
ACD56721	6.88869455	7.251804289	7.472000292	cell division inhibitor
ACD56724	7.138783757	7.076452206	8.19015555	protease do
ACD56725	9.888408407	10.75749002	10.43719028	conserved hypothetical protein
ACD56726	9.528723675	10.19746245	8.934286492	putative membrane protein
ACD56727	9.357545407	10.34241918	8.16371508	conserved hypothetical protein
ACD56732	0	0	6.149846682	transposase
ACD56733	4.37422573	3.928521928	1.798440436	ISXo8 transposase
ACD56734	8.279201972	7.896786486	7.606353389	Hpa3
ACD56735	6.97472432	6.894356997	6.516086082	XopF1 effector
ACD56744	9.387515485	9.276610651	8.254282237	hypothetical protein
ACD56747	9.309053374	9.650807633	9.600678606	type III secretion protein HrpB1/HrpK
ACD56748	8.731729716	8.606142376	8.197000396	type III secretion protein HrpB2
ACD56749	8.23148041	8.437548188	7.402952354	type III secretion apparatus lipoprotein, YscJ/HrcJ family
ACD56750	7.719025962	8.201908261	7.137247341	type III secretion protein HrpB4
ACD56751	7.524306634	7.17447633	6.494041127	type III secretion apparatus protein, HrpE/YscL family
ACD56752	6.956951088	7.215756242	6.226776313	type III secretion apparatus H+-transporting two-sector ATPase
ACD56753	6.608646635	6.851024389	5.664428795	type III secretion protein HrpB7
ACD56755	7.620337143	7.535765265	7.039631932	type III secretion apparatus protein SpaR/YscT/HrcT
ACD56756	7.314633089	7.627577657	8.38011469	HrpA type III secretion outer membrane pore, YscC/HrcC family
ACD56759	7.875190285	7.634586008	6.509634092	Hpa2
ACD56761	9.232934114	9.128004635	7.826078105	hypothetical protein
ACD56767	7.029486015	7.180277179	6.330432912	small-conductance mechanosensitive channel
ACD56770	8.512527153	8.254872722	9.80890949	ISXoo11 transposase
ACD56772	8.256397418	8.788594365	7.528071165	inner membrane protein YedI
ACD56774	7.239063834	7.272555141	7.017131326	YngK protein
ACD56777	8.996046902	10.07195837	9.32254111	glycogen synthase
ACD56778	8.986342667	9.708463165	7.735887679	1,4-alpha-glucan branching enzyme
ACD56779	7.518346292	7.964000011	6.684608376	malto-oligosyltrehalose trehalohydrolase
ACD56780	7.866413481	8.140016828	6.843720096	4-alpha-glucanotransferase
ACD56781	6.844561409	7.359187305	6.320269846	malto-oligosyltrehalose synthase
ACD56782	6.608625938	9.595906408	7.816081257	hypothetical protein
ACD56783	7.310730919	7.262771391	6.780703794	glycogen debranching enzyme GlgX
ACD56784	6.932132057	6.801016346	5.783671419	NAD-binding domain 4, putative
ACD56787	9.80150467	9.082886171	10.42898821	bacterial pre-peptidase C-terminal domain protein
ACD56789	7.151950119	6.814704221	7.218800538	Rhs family protein
ACD56790	-0.478165293	0	0	ISXo8 transposase

ACD56791	9.272415173	9.194146165	8.279568797	hypothetical protein
ACD56793	7.618532334	7.817488958	7.034468852	putative secreted protein
ACD56794	8.744484051	8.861682476	10.00424856	VirK
ACD56795	9.604214059	9.420692923	10.23340398	conserved hypothetical protein
ACD56798	8.200354274	8.222954255	8.574911358	ISXoo7 transposase
ACD56799	10.33423976	10.98311474	10.33007655	conserved hypothetical protein
ACD56800	11.50367669	12.03748518	10.95639068	hypothetical protein
ACD56804	6.235053032	6.709524999	6.948682604	putative ISXoo5 transposase
ACD56805	7.197491934	6.540312506	7.261023	ISXoo4 transposase
ACD56806	0	0	0	transposase
ACD56811	0	0	0	hypothetical protein
ACD56812	8.590388689	8.908050297	7.412231097	acriflavin resistance protein
ACD56814	8.478632117	7.696265128	8.225361702	ABC transporter ATP-binding protein
ACD56815	7.572055938	7.063815694	7.471520777	ABC transporter permease
ACD56816	7.169914983	7.314596839	6.453945517	ABC transporter permease
ACD56823	7.114419084	7.088374845	7.37172438	ATP-dependent RNA helicase
ACD56824	6.832864704	6.619358718	6.166564822	conserved hypothetical protein
ACD56829	6.355541387	6.376792197	8.65837217	TonB-dependent receptor
ACD56830	6.754687114	7.24216422	10.44122201	conserved hypothetical protein
ACD56832	0	0	9.05638031	lipoprotein, putative
ACD56833	10.90363334	11.75923491	9.402423744	conserved hypothetical protein
ACD56834	8.277454794	7.843330666	7.610463845	lipoprotein, putative
ACD56836	7.766045169	7.713895106	9.14863419	conserved hypothetical protein
ACD56838	7.145157747	7.067606452	8.206955732	glutamate synthase [NADPH] large chain
ACD56839	6.921043516	6.732309907	6.94373383	glutamate synthase [NADPH] small chain
ACD56840	7.820083205	8.377657371	7.560447481	ISxac1 transposase
ACD56841	0	0	4.313398241	transposase
ACD56845	7.36677681	6.545755284	6.775392996	transposase (IS4 family)
ACD56846	5.728731402	5.573722918	6.924004843	ISxac1 transposase
ACD56853	9.314096033	8.292533305	8.599912842	hypothetical protein
ACD56855	0	0	6.692106328	hypothetical protein
ACD56861	11.77353486	10.95875569	10.93329969	hypothetical protein
ACD56862	0	0	0	putative transposase
ACD56864	8.134128509	7.650204487	8.464974513	IS1113 transposase
ACD56865	0	0	0	hypothetical protein
ACD56866	5.051215468	4.921241127	3.35119014	ISXoo5 transposase
ACD56867	6.763650587	6.216146348	6.339078578	transposase
ACD56871	6.60786734	6.86273653	6.388310101	nitrogen regulatory protein P-II
ACD56872	6.88156674	6.553469562	6.001295589	conserved hypothetical protein
ACD56873	2.389698961	3.421438762	3.804962187	ISXo2 putative transposase
ACD56874	7.356187837	7.781359714	6.923565191	conserved hypothetical protein
ACD56875	7.25707664	6.879031796	7.271360308	conserved hypothetical protein
ACD56878	6.912074971	6.459080739	7.292395261	biosynthetic arginine decarboxylase
ACD56880	2.889037358	3.96597817	3.607176418	transposase
ACD56881	6.013200943	5.792941225	6.58684279	Rhs element Vgr protein
ACD56882	6.520547968	6.068715948	6.662561571	conserved hypothetical protein
ACD56883	7.379976117	7.171887335	7.860726963	conserved hypothetical protein
ACD56885	7.09926364	6.730639956	7.025017717	conserved hypothetical protein
ACD56886	6.753965486	6.620980752	7.327588571	conserved hypothetical protein
ACD56890	6.656181712	6.919125522	6.204663083	threonine dehydratase
ACD56891	7.401894941	7.600344099	6.864532845	conserved hypothetical protein
ACD56892	7.921710047	8.42161885	9.611701709	conserved hypothetical protein
ACD56898	10.33339019	9.643809301	10.34913745	transposase
ACD56899	7.913332253	8.106829863	7.173966895	conserved hypothetical protein
ACD56900	7.029430799	7.216425763	6.870894843	periplasmic glucan biosynthesis protein
ACD56904	7.348338663	7.49212558	6.64679629	ATP-dependent DNA helicase Rep
ACD56905	9.831604937	0	8.341096238	conserved domain protein
ACD56906	10.41140506	9.566999664	8.637425493	conserved hypothetical protein
ACD56907	9.871112076	9.069205381	9.053917738	hypothetical protein
ACD56910	6.930725512	6.417072743	6.722534332	5'-nucleotidase, lipoprotein e(P4) family
ACD56911	6.562361499	6.74192534	5.879041601	orotidine 5'-phosphate decarboxylase
ACD56916	7.249748715	7.525787008	6.923315599	conserved hypothetical protein
ACD56917	7.674863133	7.953701754	7.127622963	glycerol-3-phosphate acyltransferase
ACD56918	7.445933573	7.505922679	6.830610274	NADPH quinone reductase or zn-dependent oxidoreductase

ACD56919	6.080659795	5.541431204	5.327299336	NADPH quinone reductase or zn-dependent oxidoreductase
ACD56921	8.22134061	7.344260395	8.027126399	conserved hypothetical protein
ACD56923	3.637621838	5.321650349	4.102044982	ISXoo3 transposase ORF B
ACD56924	0.979601023	1.591909158	1.245842452	ISXo2 putative transposase
ACD56925	8.417033912	7.752072839	9.514410297	transposase
ACD56930	7.963427883	8.131435149	8.601284238	fatty acid desaturase
ACD56931	8.632020958	8.335104467	7.941587599	EF hand domain protein
ACD56932	7.217977079	7.016329167	6.879730268	ABC transporter ATP-binding protein
ACD56933	7.217773564	7.48094365	6.793752854	ABC transporter amino acid permease
ACD56935	7.631460837	8.513443371	7.488322191	conserved hypothetical protein
ACD56936	7.012043433	7.092154571	6.572826019	conserved hypothetical protein
ACD56940	8.843362075	9.026639628	7.464537582	conserved hypothetical protein
ACD56941	9.046799337	8.946993974	7.71168762	conserved hypothetical protein
ACD56942	7.565262052	7.566465091	6.849711592	possible malate permease
ACD56943	9.655160387	9.90708144	10.25561875	partition protein
ACD56944	7.368986552	7.944032641	7.224204313	putative phosphoglycerate mutase family protein
ACD56945	8.816138872	8.809112136	8.856366388	YceI like family
ACD56946	7.379724919	7.643661413	7.242126102	cardiolipin synthase
ACD56947	8.050452722	8.28965467	7.948116052	esterase YdiI
ACD56948	8.039741585	8.292818552	6.93479954	acetyltransferase
ACD56949	6.95986287	6.909137045	6.413081209	hydrolase, alpha/beta fold family protein
ACD56950	6.581888994	6.487524937	6.280832002	tetratricopeptide repeat family
ACD56951	6.923648379	6.828365012	7.7478573	conserved hypothetical protein
ACD56952	7.103885747	7.119075995	6.772941338	alcohol dehydrogenase
ACD56954	9.340753631	8.936799865	9.021302045	hypothetical protein
ACD56956	7.545999248	7.458053843	8.38610822	glutamine synthetase, type I
ACD56957	7.43970624	6.043217625	6.215263121	nitrogen regulatory protein P-II
ACD56958	7.292100725	7.457093543	6.74823311	ammonium transporter
ACD56959	8.034413826	8.408669408	8.402116721	two-component system sensor protein
ACD56960	7.253128912	7.346309836	6.638553207	nitrogen regulation protein NR(I)
ACD56961	7.534645275	7.654457023	6.264406943	superoxide dismutase
ACD56962	8.201726967	7.904351624	7.449487092	superoxide dismutase
ACD56968	7.32297367	6.76008785	5.651800837	hemagglutinin
ACD56969	6.283149487	5.887939499	6.477664377	hemagglutinin-like protein
ACD56972	6.996467839	6.940178499	7.022556461	exodeoxyribonuclease V, gamma subunit
ACD56973	6.85127431	6.727280627	6.887890772	exodeoxyribonuclease V beta chain
ACD56974	6.571124622	6.190334353	6.74582892	exodeoxyribonuclease V, alpha subunit
ACD56975	8.131198468	8.898404883	9.536892155	plasmid maintenance system killer protein
ACD56976	6.950293432	7.72463663	8.372133735	addiction module antidote protein, HigA family
ACD56977	7.368934187	9.385942189	10.22491815	hypothetical protein
ACD56978	7.017465428	6.923101629	7.309912848	XopQ effector
ACD56980	7.6960286	8.532036373	7.4563462	paar motif family
ACD56981	8.388714778	7.752293664	9.308759944	conserved hypothetical protein
ACD56982	7.72396805	7.583729672	8.195446032	hypothetical protein
ACD56985	6.528041462	6.065259941	6.112975303	hypothetical protein
ACD56987	7.390392546	7.631853672	7.219352477	conserved hypothetical protein
ACD56990	7.291999464	6.74910515	6.477623905	conserved hypothetical protein
ACD56991	6.612979044	6.715824748	6.837085441	conserved hypothetical protein
ACD56992	0	10.49782191	10.46813526	conserved hypothetical protein
ACD56995	8.419471474	8.439880739	9.081858876	ISXo3 transposase ORF B
ACD56997	8.439905665	9.825784038	10.16460529	oxidoreductase
ACD56998	8.995207486	9.695257876	10.02197934	DesA3_2
ACD57003	0	0	0	hypothetical protein
ACD57004	10.39843375	10.76199162	9.917518281	conserved hypothetical protein
ACD57009	6.935789738	6.904893486	6.555877493	hexuranate transporter
ACD57010	9.274138169	8.77825458	8.712344718	xylanase
ACD57011	7.749775591	6.971853901	7.218044911	glycosyl hydrolase family 10
ACD57012	10.80491348	10.50472962	9.677342624	lipoprotein, putative
ACD57013	7.52994585	7.250127843	13.5828829	glycosyl hydrolase family 10
ACD57014	7.762667726	7.071977136	9.883193125	glucuronate isomerase
ACD57015	9.164361414	8.995201831	11.00108443	conserved hypothetical protein
ACD57016	8.597929633	9.117588561	7.32898901	bleomycin resistance protein
ACD57025	6.842991399	6.915114518	6.262803331	sal operon transcriptional repressor
ACD57027	7.975847968	7.672213165	6.598427738	hypothetical protein

ACD57028	7.666018016	7.878418822	7.960795486	ATPase of the PP-loop superfamily
ACD57029	7.132813297	6.84067723	6.585754263	recombination associated protein RdgC
ACD57030	8.560936538	8.264883552	9.793780486	protein of unknown function
ACD57033	7.984674789	8.343598807	9.345899737	conserved hypothetical protein
ACD57034	11.12393385	11.43299593	13.73007735	conserved domain protein
ACD57035	9.187891436	9.284766276	10.33239466	sec-independent protein translocase
ACD57036	7.914086097	7.921477987	7.219323432	twin arginine-targeting protein translocase TatC
ACD57041	6.520499253	6.158290569	6.555648996	skwp protein 4
ACD57043	6.978138415	7.229011037	7.312156888	glycyl-tRNA synthetase, alpha subunit
ACD57045	6.623897581	6.342465854	6.785929746	glycyl-tRNA synthetase, beta subunit
ACD57046	7.348843211	7.02219024	7.29525466	tetratricopeptide repeat family
ACD57048	9.201241771	7.777840495	8.003242417	hypothetical protein
ACD57053	8.385569088	8.365167596	8.550211927	conserved hypothetical protein
ACD57055	8.175280073	8.629560623	7.063697072	conserved hypothetical protein
ACD57058	6.925928231	8.048579509	5.605218735	putative secreted protein
ACD57059	5.569418178	6.086495062	5.935631824	conserved hypothetical protein
ACD57060	11.00886277	9.914694568	9.347670085	putative membrane protein
ACD57061	8.842447777	9.003728714	8.000450772	conserved hypothetical protein
ACD57062	8.750603155	6.884964165	7.1854305	hypothetical protein
ACD57064	7.553276016	7.488932693	7.794409368	acyl-CoA dehydrogenase
ACD57065	7.181838026	7.236942195	7.21172285	acyl-CoA carboxyltransferase beta chain
ACD57066	6.798556044	6.696188608	6.592243233	biotin carboxylase
ACD57067	6.662832127	6.456186827	6.661136757	dipeptidyl anminopeptidase
ACD57071	0	0	0	transposase
ACD57074	9.064917871	8.050469047	8.811522408	ISxac1 transposase
ACD57087	6.212427319	6.728015724	6.305051221	alpha/beta hydrolase fold
ACD57088	8.146268269	8.241158517	8.094246628	conserved hypothetical protein
ACD57090	6.927019385	6.885122841	7.059398544	deoxyribonuclease TatD
ACD57095	7.641596603	7.20982374	7.745338188	MFS transporter
ACD57098	6.985375191	6.77276983	6.036411019	NAD-dependent deacetylase
ACD57099	7.383445102	6.989604538	6.21985388	FMN oxidoreductase
ACD57100	7.474379256	7.396365026	6.731033858	dehydrogenase
ACD57101	7.505041382	7.377748458	7.322270694	conserved hypothetical protein
ACD57102	7.615879719	7.479262902	7.088014355	formyltetrahydrofolate deformylase
ACD57109	7.526507064	8.36732301	7.92150179	FMN reductase
ACD57110	8.871427853	9.438307408	9.564869705	conserved hypothetical protein
ACD57111	7.85232975	8.355787143	7.931635786	5-methyltetrahydropteroyltriglutamate-homocysteine methyltransferase
ACD57112	10.57858026	8.499738279	8.723640468	hypothetical protein
ACD57114	6.740725224	7.050958725	6.617311708	hypothetical protein
ACD57117	10.69569809	10.58909868	8.747410898	hypothetical protein
ACD57119	8.792292503	8.550235019	8.571790559	transcriptional regulatory protein
ACD57123	9.678473381	9.719455563	7.961768007	amino acid transporter
ACD57125	7.094299419	7.134539267	6.865522959	AMP-ligase
ACD57130	8.778569994	9.131638354	7.994217647	xanthomonadin biosynthesis acyl carrier protein
ACD57131	7.927463912	8.417046574	6.751825207	ketosynthase
ACD57132	7.69341726	8.221036037	7.212744413	acyltransferase
ACD57133	7.460726184	8.015961361	7.35264378	xanthomonadin biosynthesis dehydratase
ACD57134	7.209628818	7.723367427	7.530320495	xanthomonadin biosynthesis acyltransferase
ACD57135	7.438101522	8.078951341	9.464419139	fatty acyl CoA synthetase
ACD57136	7.093222111	6.942397208	6.960604378	membrane protein involved in xanthomonadin export
ACD57137	7.377904593	7.101345421	6.965703491	xanthomonadin biosynthesis phosphotransferase/dehydratase
ACD57139	9.367432225	9.184394364	10.04334177	ISXoo2 transposase
ACD57140	9.057731852	9.496306548	9.046695676	transposase
ACD57145	0	1.827981573	0	transposase
ACD57147	15.61656894	15.87874545	16.64203759	hypothetical protein
ACD57149	7.698544937	8.00114919	8.004675539	ATP-dependent RNA helicase RhlB
ACD57150	6.45705249	7.29586075	6.621631399	cell division ATP-binding protein FtsE
ACD57151	7.073348967	7.363687985	6.834812326	cell division protein
ACD57152	7.44681037	8.220465395	7.183546063	response regulator protein
ACD57153	7.910612752	8.377427461	7.211849368	uracil-DNA glycosylase
ACD57154	9.662593613	10.43756483	11.65001954	alternative sigma factor RpoH
ACD57157	9.933855862	8.939514571	11.4491796	conserved hypothetical protein
ACD57158	10.27722927	10.36272192	11.68465659	protein of unknown function
ACD57159	0	0	0	ISxac1 transposase

ACD57160	7.325044554	7.437419184	8.592763484	ISxac1 transposase
ACD57161	10.4100909	11.01532445	12.4690974	chaperonin GroS
ACD57162	9.990813079	10.34540525	11.90646599	chaperonin GroL
ACD57164	6.493828236	6.595794545	6.635768899	TonB-dependent outer membrane receptor
ACD57165	6.805666496	6.345247329	6.689369057	TonB-dependent outer membrane receptor
ACD57166	8.041407274	7.609695873	9.473583998	phospho-2-dehydro-3-deoxyheptonate aldolase
ACD57168	7.225650904	7.485958079	5.537960722	conserved hypothetical protein
ACD57169	6.583800363	6.775814367	6.21990614	conserved hypothetical protein
ACD57171	7.029375581	7.043388254	6.985249941	conserved hypothetical protein
ACD57173	7.683710488	8.695190005	6.1462866	conserved hypothetical protein
ACD57174	6.448187354	5.242499616	5.834488748	conserved hypothetical protein
ACD57178	6.439313955	6.7083528	6.009006705	glutamate-ammonia-ligase adenylyltransferase
ACD57182	6.027695934	6.241607595	5.572471347	proteinase
ACD57183	6.522286489	6.192576886	6.137989122	proteinase
ACD57186	7.839588036	7.592823271	7.747273258	nitroreductase
ACD57187	8.124503911	8.140896218	7.969075643	YceI like family
ACD57192	0	0	9.131288514	hypothetical protein
ACD57193	10.16937387	8.489474698	9.361009447	conserved hypothetical protein
ACD57194	10.46473973	11.30982306	9.852245468	conserved hypothetical protein
ACD57195	10.48237438	11.67967802	11.47485174	transposase
ACD57196	7.435336892	6.42248027	8.509834373	ISPsy21, transposase OrfB
ACD57200	8.748444461	8.323518691	0	hypothetical protein
ACD57201	6.682938419	5.977199772	6.210079048	lipase family
ACD57202	7.936390599	8.100567733	7.619618424	conserved hypothetical protein
ACD57203	0	8.447393228	10.25054714	conserved hypothetical protein
ACD57205	7.482477238	6.78217264	7.038776358	arabinogalactan endo-1,4-beta-galactosidase
ACD57206	7.46562354	6.903689072	7.159205324	arabinogalactan endo-1,4-beta-galactosidase
ACD57207	8.026102883	8.129416975	8.044798454	pyruvate dehydrogenase E1 component
ACD57208	6.855279633	5.083804795	0	ISXoo3 transposase ORF A
ACD57209	6.105726262	5.480071198	5.289425053	ISXoo3 transposase ORF B
ACD57211	6.998319635	6.961924244	7.60783332	DNA polymerase I
ACD57213	4.401705548	4.55196506	4.712397685	transposase
ACD57214	6.939285356	6.417945317	6.604840813	ISXoo6 transposase
ACD57216	7.597508827	7.949966743	7.292800151	site-specific recombinase
ACD57218	9.176542192	9.370565361	8.871289228	proteinase inhibitor
ACD57220	7.621202064	7.61321485	7.103906723	MFS transporter
ACD57221	6.898933872	6.677268619	6.33756125	putative signal protein with HD-GYP domain
ACD57222	7.520846508	7.371811486	6.674997269	transcriptional regulator MarR family
ACD57227	0	8.524757173	7.530679438	hypothetical protein
ACD57228	7.423485731	7.672701125	8.551231449	ferredoxin
ACD57235	5.907231993	5.784090379	5.450647114	conserved hypothetical protein
ACD57236	7.381032402	7.703875896	6.819221104	hypothetical tRNA/rRNA methyltransferase YibK
ACD57244	11.00361629	11.8675915	13.62763647	conserved hypothetical protein
ACD57251	5.725776596	4.554736183	5.5377185	ISXo5 transposase
ACD57252	8.109355335	6.444450077	7.644281722	putative transposase
ACD57253	0	0	-0.459355699	ISXo5 transposase
ACD57254	4.429877032	5.457640254	6.018462817	transposase (IS4 family)
ACD57256	7.385327491	7.153116244	8.48756272	conserved hypothetical protein
ACD57261	6.082089416	6.557872615	5.619013837	N-acyl-L-amino acid amidohydrolase
ACD57263	8.157058873	8.131321958	9.14974712	7-cyano-7-deazaguanine reductase
ACD57265	0	0.638963514	-0.444768893	IS1113 transposase
ACD57270	8.395752612	8.211917489	8.62357061	isocitrate dehydrogenase, NADP-dependent
ACD57271	7.947110898	8.535232601	8.029143641	hypothetical protein
ACD57272	8.892764402	7.921263744	9.008661115	conserved domain protein
ACD57276	7.059658115	7.346150243	7.114533608	anthranilate synthase component II
ACD57277	10.67541901	11.14614223	10.63043095	molybdopterin biosynthesis
ACD57278	7.530203429	7.65881843	7.948449001	nitrilotriacetate monooxygenase component B
ACD57279	7.764108585	7.255519616	6.880073254	anthranilate phosphoribosyltransferase
ACD57280	7.81961071	8.044038867	8.540562041	indole-3-glycerol phosphate synthase
ACD57281	7.238987432	7.401144048	6.046746417	conserved hypothetical protein, putative
ACD57283	8.93619623	9.26728765	10.2820459	S-adenosylmethionine decarboxylase proenzyme (AdoMetDC)(SamDC)
ACD57284	8.923003548	8.168531727	8.572810106	SugE
ACD57286	11.50385058	12.04150516	11.59900623	ribosomal protein L13
ACD57287	9.649457386	10.17480088	9.912059997	ribosomal protein S9

ACD57288	9.046823888	9.61479817	8.047434781	pyrophosphatase, MutT/nudix family
ACD57289	8.001543309	8.743097524	10.91041038	bacterioferritin
ACD57293	9.540521359	10.32200699	7.532659824	putative membrane protein
ACD57294	9.344970488	9.822844845	7.303488527	cytochrome c oxidase, subunit II
ACD57295	8.757523355	9.188892929	7.497205173	cytochrome c oxidase, subunit I
ACD57296	11.16798884	11.62563579	10.72395952	conserved hypothetical protein
ACD57297	10.06688299	10.4148966	7.694601653	cytochrome C oxidase assembly protein CtaG
ACD57298	8.98031669	9.359338872	7.082276802	cytochrome C oxidase subunit III
ACD57300	7.860559373	8.340655728	7.311984394	conserved hypothetical protein
ACD57301	7.375777972	7.826262462	7.134005259	conserved hypothetical protein
ACD57302	8.056648552	8.220818446	7.047243904	cytochrome oxidase assembly protein
ACD57303	6.720538412	6.6441447	5.846954584	protoheme IX farnesyltransferase
ACD57306	6.423073879	6.619757796	6.513121181	hypothetical protein
ACD57307	10.92632565	10.07630789	11.51396441	hypothetical protein
ACD57308	0	0	-0.960457287	ISXo8 transposase
ACD57309	0	3.121325464	0	ISXo1 transposase
ACD57314	6.102513267	5.978850003	6.080700296	conserved hypothetical protein
ACD57315	7.210476536	7.830318715	6.885488952	conserved hypothetical protein
ACD57317	7.609969141	7.846881894	7.28213396	multidrug efflux protein
ACD57318	8.311852739	8.377908929	8.824035884	signal peptide peptidase SppA, 67K type
ACD57320	7.650405564	7.499080498	7.701743104	tropinone reductase-II
ACD57330	8.614963766	9.11914864	7.885812272	peptide deformylase
ACD57331	6.728519185	6.567816171	6.388282545	methionyl-tRNA formyltransferase
ACD57332	7.140512829	7.279276273	6.705162355	ribosomal RNA small subunit methyltransferase B
ACD57333	7.511879131	7.368200866	6.753444085	dolichyl-phosphate-mannose-protein mannosyltransferase
ACD57334	7.184240616	7.399717984	6.628385753	O-Antigen Polymerase family
ACD57336	7.083011207	7.259837401	7.151128194	CDP-Glycerol\x3aPoly(glycerophosphate) glycerophosphotransferase family
ACD57341	7.452463652	6.744228384	6.423068835	N-acetyltransferase
ACD57343	7.803252872	7.797227031	7.709001075	D-tyrosyl-tRNA(Tyr) deacylase
ACD57344	8.559377091	8.84350341	9.150072197	RNA polymerase sigma-70 factor
ACD57345	10.11467935	10.49555527	8.794961648	conserved hypothetical protein
PXO_rna2	0	0	0	XO_rna2 cdna:pseudogene chromosome:GCA_000019585.1:Chromosome:718477:718552:1 gene:PXO_rna2 transcript:PXO_rna
ACD57353	5.423621868	5.419319774	5.256312493	transposase
ACD57359	9.815605848	10.00244937	11.2981657	transposase
ACD57360	7.334630842	6.991521846	6.2239071	ABC transporter ATP-binding protein
ACD57361	7.293848655	7.287232171	6.087189128	membrane protein, putative
ACD57362	7.081659187	7.235315404	6.427711756	conserved hypothetical protein
ACD57363	6.441342377	6.556722155	5.762707584	TonB-dependent outer membrane Receptor
ACD57368	11.19926745	11.56222334	11.84555278	conserved hypothetical protein
ACD57372	0	0	0	ISXo8 transposase
ACD57375	0	0	0	ISXoo12 transposase
ACD57376	0	0	0	ISXoo12 transposase
ACD57377	3.424290603	4.629700494	5.087518002	ISXoo11 transposase
ACD57380	6.127373274	7.242002211	6.726354417	peptidase M22, glycoprotease
ACD57381	7.929234733	8.067869927	7.677346148	dihydroneopterin aldolase
ACD57382	6.63750302	6.57250318	6.031273878	periplasmic beta-glucosidase
ACD57389	9.234601909	9.361224439	7.865386859	membrane protein
ACD57392	0	0	0	putative ISXo8 transposase
ACD57404	7.046862076	6.553736796	6.0501904	N-acetylmuramoyl-L-alanine amidase
ACD57405	5.79607596	6.083264436	6.022154722	D-alanyl-D-alanine dipeptidase
ACD57406	9.357191286	9.251506081	9.202633209	conserved domain protein
ACD57407	7.769745297	7.893471428	7.556513718	conserved hypothetical protein
ACD57408	14.27246941	14.16405054	12.27680778	EF hand domain protein
ACD57409	8.616331964	9.10183914	7.278449458	conserved hypothetical protein
ACD57410	8.937041248	9.038433438	8.876974239	HAD superfamily hydrolase
ACD57411	6.763929386	6.838334129	7.100346961	conserved hypothetical protein
ACD57412	7.697627886	8.485696502	6.901965011	conserved hypothetical protein
ACD57413	5.570687576	5.904821249	5.730574748	ISXo3 transposase ORF B
ACD57415	6.906000659	6.85122433	5.647982163	uroporphyrinogen-III synthase
ACD57416	7.209092647	7.034666927	6.700939026	conserved hypothetical protein
ACD57417	7.153785073	7.2359472	6.912566041	porphyrin biosynthesis protein
ACD57418	10.46350394	10.93183077	9.366512375	hypothetical protein

ACD57421	7.526843489	7.589239157	7.60347057	conserved hypothetical protein
ACD57422	9.620388466	9.301891682	0	IS1478 transposase
ACD57429	7.115688751	6.837350404	6.562137081	tryptophan 2,3-dioxygenase
ACD57430	7.879816022	7.926527282	9.077170884	di-tripeptide transporter
ACD57431	7.936773369	8.106965923	8.865918815	lipoprotein, putative
ACD57433	7.763936023	7.595645381	7.797894932	4-hydroxyphenylpyruvate dioxygenase
ACD57434	6.882398504	7.220542783	6.903640874	homogentisate 1,2-dioxygenase
ACD57441	10.43274023	0	0	conserved hypothetical protein
ACD57447	8.499124359	8.163579238	8.424099087	hypothetical protein
ACD57448	0	0	0	ISXo7 transposase
ACD57450	7.467385461	6.276744166	5.750812819	DnaJ domain protein
ACD57451	0	10.39121136	9.006283996	hypothetical protein
ACD57452	7.093105882	6.717498217	7.345884217	ribulose-phosphate 3-epimerase
ACD57453	7.44805021	7.145779337	7.760959407	N-acetyltransferase
ACD57454	8.583974066	9.16304329	8.980833618	conserved hypothetical protein
ACD57455	6.77002292	6.562086696	6.449561375	anthranilate synthase component I
ACD57456	6.419795048	6.499823569	5.624524982	threonine aldolase
ACD57458	4.949684331	3.564012265	4.937871652	ISXoo3 transposase ORF B
ACD57459	7.173747083	6.770710138	6.750807461	putative secreted protein
ACD57463	8.642271962	8.033054021	7.598179079	conserved hypothetical protein
ACD57464	7.695722447	6.239909707	6.026636309	conserved hypothetical protein
ACD57465	7.107101969	6.516186961	6.671109344	conserved hypothetical protein
ACD57467	7.425131962	9.876687297	9.873687105	hypothetical protein
ACD57469	7.651101933	7.392635124	6.587972487	drug/metabolite transporter superfamily protein
ACD57475	8.224763833	8.267933683	7.033918499	D-serine/D-alanine/glycine transporter
ACD57477	8.252277508	8.48029744	7.269902767	magnesium and cobalt transport protein
ACD57480	11.05918896	11.6128685	10.28181414	avidin family
ACD57484	7.348312102	5.434995109	7.263963968	conserved hypothetical protein
ACD57486	11.0204522	9.798261173	7.494751603	endonuclease
ACD57487	0	9.522785515	0	conserved domain protein
ACD57488	10.03287225	7.293066948	8.148161316	endonuclease
ACD57490	3.387941488	5.003912509	3.026769966	ISXoo11 transposase
ACD57492	6.689802338	6.152777658	6.790120385	conserved hypothetical protein
ACD57495	6.724090873	7.658411446	7.419564172	Putative signal protein with GAF,PAS(PAC) and GGDEF domains
ACD57498	9.06087153	9.419288168	8.818121975	hypothetical protein
ACD57501	7.044634548	7.273842212	6.818991123	sulfate permease
ACD57502	10.73533601	10.20350707	8.449536614	hypothetical protein
ACD57503	5.48050749	6.593925895	6.546375922	hypothetical protein
ACD57504	6.238532761	5.939003197	6.271134299	Putative signal protein with GGDEF domain
ACD57505	0	9.154453593	0	hypothetical protein
ACD57506	6.762109587	6.896090168	7.326096865	aminopeptidase
ACD57508	0	3.640458974	5.192336218	ISXoo13 transposase
ACD57511	7.748467942	8.185757546	7.12188573	glucans biosynthesis glucosyltransferase H
ACD57512	6.828415791	6.673217192	6.532796947	carboxylesterase
ACD57513	6.802787754	7.333441624	6.164337779	two-component system sensor protein
ACD57514	7.429080294	7.662903317	7.163418223	two-component system regulatory protein
ACD57515	6.938826819	7.469617399	7.555417396	porphobilinogen deaminase
ACD57517	8.085945092	7.992082942	8.235698343	transcriptional regulator
ACD57519	6.713901978	6.490343889	6.365358347	conserved hypothetical protein
ACD57520	6.635091214	6.530654471	6.489647293	prolyl oligopeptidase family protein
ACD57521	8.893362211	8.963832441	7.532270199	hypothetical protein
ACD57522	9.473291752	10.34951346	8.74634972	conserved hypothetical protein
ACD57525	7.795546184	8.006511225	7.703536799	protease II
ACD57526	7.811432496	7.135493828	7.502807941	conserved hypothetical protein
ACD57527	9.489496775	10.21925324	10.58681165	lipoprotein, putative
ACD57528	7.070035051	7.679423798	6.92150774	diaminopimelate epimerase
ACD57529	7.085488393	6.920233743	6.016108494	protein of unknown function
ACD57530	7.10659958	6.770221189	6.125035246	tyrosine recombinase XerC
ACD57532	9.979653836	9.461385311	12.60431461	ATP-dependent protease HslV
ACD57533	7.324342588	7.277557081	8.660263364	heat shock protein HslVU, ATPase subunit HslU
ACD57537	11.16530902	11.38060176	13.71067731	hypothetical protein
ACD57540	6.143577091	5.85993974	6.010509084	multidrug resistance efflux pump
ACD57541	6.177433491	5.837824694	7.530125379	isrso5-transposase protein
ACD57542	9.414010764	9.022656323	8.980091011	isrso5-transposase protein

ACD57543	7.504739553	7.461070114	7.746668827	ElaA
ACD57544	7.75443993	8.06301211	7.839197488	cytosine deaminase
ACD57545	7.722623128	7.072234454	7.875374617	transposase
ACD57547	6.920317123	6.807625402	7.35146049	rod shape-determining protein
ACD57548	7.511270357	7.241611408	7.256916297	rod shape-determining protein
ACD57549	8.70215883	8.880936481	9.054780659	rod shape-determining protein MreD
ACD57550	6.83406647	6.898522789	6.317888308	penicillin-binding protein 2
ACD57551	7.141565626	6.809028508	6.434042692	rod shape-determining protein RodA
ACD57552	8.516834627	8.361316569	8.541534199	transposase
ACD57553	7.314877757	7.140359445	7.705791334	conserved hypothetical protein
ACD57554	6.778760522	6.608387902	7.303351528	conserved hypothetical protein
ACD57555	6.742855081	6.640664305	6.958517916	Rhs element Vgr protein
ACD57556	7.424989251	7.294510475	8.747921061	LysM domain protein
ACD57557	5.989995013	5.407947519	5.735405739	conserved hypothetical protein
ACD57558	6.298658316	6.005730081	6.42669079	endopolygalacturonase
ACD57559	8.039763514	8.312560808	9.424523243	lytic murein transglycosylase B
ACD57560	7.079122064	7.342972461	7.157842066	rare lipoprotein A
ACD57562	7.390263556	7.29469426	9.026484712	penicillin-binding protein 6
ACD57563	6.35901507	6.133832691	5.519167596	conserved hypothetical protein
ACD57564	10.04115261	10.06435207	13.02521917	putative secreted protein
ACD57565	8.711281515	8.559667704	8.327404437	lipoyltransferase
ACD57566	10.74523733	10.72799701	11.50351769	lipoic acid synthetase
ACD57567	9.861904202	9.958696253	10.64500087	tail-specific protease
ACD57569	8.761604418	9.180898738	7.378953728	bifunctional NMN adenylyltransferase/Nudix hydrolase
ACD57570	7.223219802	6.841646111	6.242987326	nicotinamide phosphoribosyltransferase
ACD57571	8.396750328	7.864718543	7.99287604	conserved hypothetical protein
ACD57572	6.846204949	6.933253945	5.636354906	conserved hypothetical protein
ACD57573	9.134546968	0	8.729233254	conserved hypothetical protein
ACD57574	6.409165179	6.872434796	6.804131021	conserved hypothetical protein
ACD57575	6.530184697	6.985910229	7.889467458	conserved hypothetical protein
ACD57576	7.370347396	8.038869619	8.971557923	rickettsia 17 kDa surface antigen family
ACD57577	6.128336711	5.91375589	5.982503089	conserved hypothetical protein
ACD57578	7.481064782	7.927007529	7.922239482	6-phosphogluconate dehydrogenase (decarboxylating)
ACD57580	13.00399393	13.93871584	13.54825599	putative phospholipid-binding domain family
ACD57581	7.542838417	7.952100554	7.520972191	two-component system sensor protein
ACD57582	7.684706549	7.988962975	7.327103486	two-component system regulatory protein
ACD57583	7.131805527	7.183198661	6.5700105	histidine kinase-response regulator hybrid protein
ACD57584	8.075436363	8.268420357	7.217579713	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase
ACD57586	6.95919055	6.818888897	6.811304042	conserved hypothetical protein
ACD57588	4.271410735	5.011916006	5.29408768	ISXoo13 transposase
ACD57590	0	0	6.662034554	transposase
ACD57592	6.661421833	6.097391679	6.062525427	TonB-dependent receptor
ACD57593	8.195736373	8.829411967	8.762441838	hypothetical protein
AGS47849	6.615738502	6.567251853	5.932840719	truncated beta-galactosidase
ACD57594	7.455047697	7.543070498	7.007711298	membrane protein, putative
ACD57595	7.649701673	8.105452849	8.760357357	transcriptional regulator GntR family
ACD57597	8.141110871	8.069868619	7.8987223	glucose-galactose transporter
ACD57598	7.775228365	7.308948747	7.731895994	transcriptional regulator LacI family
ACD57599	6.939026712	6.773442553	6.450600929	glucosamine-fructose-6-phosphate aminotransferase
ACD57600	6.925109324	7.186510462	6.274056613	N-acetylglucosamine-6-phosphate deacetylase
ACD57605	9.080271252	10.17806723	8.247486095	hypothetical protein
ACD57607	0	0	0	ISXo8 transposase
ACD57614	0	2.210292224	3.137047691	ISXo3 transposase ORF B
ACD57621	0	0	0	ISXoo3 transposase ORF A
ACD57622	0	1.930029534	0	ISXoo3 transposase ORF B
ACD57629	6.040511109	7.090747595	6.218172814	GTP-binding protein
ACD57632	7.413120146	7.497644297	7.226874552	glutamate--cysteine ligase
ACD57633	10.18116468	10.09693912	7.779325391	hypothetical protein
ACD57636	7.296714353	6.529639818	6.839266787	glutamate--cysteine ligase
ACD57638	8.515869325	8.936852855	6.085278051	conserved hypothetical protein
ACD57641	7.926853393	8.382204665	7.69407228	glycosyl transferase, group 1 family protein
ACD57642	0	0	0	conserved hypothetical protein
ACD57644	10.82442578	9.806430399	10.39921383	conserved hypothetical protein
ACD57645	6.929506975	6.784739527	6.28484908	S-(hydroxymethyl)glutathione dehydrogenase/class III alcohol dehydrogenase

ACD57647	8.07204147	8.270659751	6.935624753	glutathione-dependent formaldehyde-activating enzyme (S-(hydroxymethyl)glutathione synthase)
ACD57649	6.440131648	6.672411198	5.567372036	S-formylglutathione hydrolase
ACD57650	9.827447508	9.99703831	8.623534031	conserved hypothetical protein
ACD57651	8.483122472	8.188123944	7.893968869	lipoprotein, putative
ACD57654	6.144754079	6.639224927	6.994557097	conserved hypothetical protein
ACD57656	7.536643538	7.37340461	7.455713531	TonB-dependent outer membrane Receptor
ACD57657	8.666408656	8.835564113	8.367720513	serine hydroxymethyltransferase
ACD57658	8.820498107	9.217565173	8.768329911	conserved hypothetical protein
ACD57659	6.997439199	7.505970301	6.011533656	ATP cone domain protein
ACD57660	7.896683573	7.668424099	6.427366486	acetyltransferase
ACD57661	7.283329168	7.564637294	6.271138035	riboflavin biosynthesis protein RibD
ACD57663	7.95214716	7.760001331	6.369454269	riboflavin synthase, alpha subunit
ACD57664	7.069852511	7.281095456	6.449617497	riboflavin biosynthesis protein ribAB
ACD57665	7.033070544	7.954836074	6.594653046	6,7-dimethyl-8-ribityllumazine synthase
ACD57666	7.142597235	7.169273638	6.647760605	transcription antitermination factor NusB
ACD57667	6.488277197	6.86757528	5.936783968	thiamine-monophosphate kinase
ACD57668	11.15902615	10.72993508	10.47418251	hypothetical protein
ACD57669	5.668127636	6.219559641	5.7106687	hydrolase CocE/NonD family protein subfamily
ACD57670	6.423228547	5.855267173	6.024264265	conserved hypothetical protein
ACD57671	8.327247232	8.798040791	8.285046125	conserved hypothetical protein
ACD57673	6.584959495	6.314660277	6.203073877	conserved hypothetical protein
ACD57674	9.141854244	8.533933163	11.29526959	conserved hypothetical protein
ACD57675	6.764990981	6.646825085	7.60889793	K+-transporting ATPase, A subunit
ACD57676	7.028646501	6.71596199	7.709400929	K+-transporting ATPase, B subunit
ACD57677	7.149818237	7.354125938	8.289534795	K+-transporting ATPase, C subunit
ACD57678	6.648594866	6.780021321	6.205216545	sensor protein KdpD
ACD57679	7.161565256	7.256897432	7.179083035	two-component system regulatory protein
ACD57684	6.453102687	6.746823317	6.269753192	conserved hypothetical protein
ACD57686	8.308225248	8.631227995	8.029657172	MraZ protein
ACD57687	7.197216693	7.241172821	6.320798744	S-adenosyl-methyltransferase MraW
ACD57688	9.050575158	9.151734536	7.411663512	cell division protein FtsL
ACD57689	6.916464702	7.017688119	6.172109431	peptidoglycan synthetase FtsI
ACD57690	7.034732946	7.296044363	6.116187986	UDP-N-acetylmuramoylalanyl-D-glutamate--2, 6-diaminopimelate ligase
ACD57691	7.542366403	7.761198826	6.55810229	UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase
ACD57692	7.163377966	7.39752918	6.324445204	phospho-N-acetylmuramoyl-pentapeptide-transferase
ACD57693	7.799203898	7.365368846	6.673344414	cell division protein FtsW
ACD57694	6.881334249	6.71929298	5.800177725	undecaprenyldiphospho-muramoylpentapeptide beta-N-acetylglucosaminyltransferase
ACD57695	7.747138962	7.698760221	6.411616062	UDP-N-acetylmuramate--alanine ligase
ACD57696	7.250630034	6.779693094	6.020119897	D-alanine--D-alanine ligase
ACD57697	7.215426219	7.38451612	6.282999427	cell division protein FtsQ
ACD57698	7.442653269	6.698246265	5.520019872	cell division protein FtsA
ACD57699	8.230659356	8.314120964	7.178684767	cell division protein FtsZ
ACD57700	8.706344057	9.272944648	9.102755224	UDP-3-0-acyl N-acetylglucosamine deacetylase
ACD57702	7.554980168	8.008837561	6.661550098	peptidase
ACD57703	8.041894563	7.969144733	7.582608688	preprotein translocase, SecA subunit
ACD57704	7.670826176	8.077189581	7.24055285	glyoxalase family protein
ACD57705	7.120497098	6.724745757	6.075166777	dgtp-pyrophosphohydrolase\x3b thiamine phosphate synthase
ACD57706	9.352105238	9.94220658	9.8769144	hypothetical protein
ACD57710	7.724200041	7.418898301	6.929495139	quinone reductase
ACD57711	6.327940604	6.188044796	6.466297566	protease
ACD57713	0	0	8.425912426	hypothetical protein
ACD57715	7.633794454	7.067929068	7.659753342	galactose 1-dehydrogenase
ACD57717	7.407684152	7.339618441	6.388360046	conserved hypothetical protein
ACD57718	7.016451748	6.912733684	7.413196325	conserved hypothetical protein
ACD57719	7.59912435	7.378190796	7.117321024	conserved hypothetical protein
ACD57721	7.41153641	8.224879569	6.047001728	sulfotransferase
ACD57722	7.081403545	7.129715761	6.325841503	methyltransferase
ACD57724	7.866512394	7.261831659	8.202481392	hypothetical protein
ACD57725	7.364677479	7.096219678	7.636233082	phosphoenolpyruvate carboxylase
ACD57726	7.930122287	7.552138795	8.029552272	transcriptional regulator TetR/acrR family
ACD57730	6.787719763	6.10576397	8.137057736	TonB-dependent receptor
ACD57731	6.585109768	6.617069223	7.697252561	phosphoanhydride phosphohydrolase

ACD57733	7.671894842	8.170250573	7.850349386	integral membrane protein
ACD57734	6.937885772	7.374083112	6.532667615	conserved hypothetical protein
ACD57737	0	0	7.647976408	hypothetical protein
ACD57741	10.18837867	9.552574964	10.80207202	hypothetical protein
ACD57745	6.643186624	6.641717975	6.742855081	voltage-gated potassium channel beta subunit
ACD57746	8.255123015	9.300180937	6.89858325	conserved hypothetical protein
ACD57747	7.741015231	8.394282614	6.999075477	conserved hypothetical protein
ACD57754	8.303917706	8.417228056	8.646623508	acyl-CoA thioesterase I
ACD57755	8.670755376	9.553368184	10.09624077	two-component system regulatory protein
ACD57756	6.814076112	7.33596196	6.469395989	two-component system sensor protein
ACD57760	7.130961749	7.577088886	7.087685593	diacylglycerol kinase
ACD57761	7.873542545	8.129030523	7.750479218	LemA family protein
ACD57762	6.891565004	7.171517098	6.267093783	glycine rich protein
ACD57763	6.192227707	7.054620597	6.297321664	conserved hypothetical protein
ACD57764	7.367633159	7.351672494	6.974047416	prolipoprotein diacylglyceryl transferase
ACD57765	7.355139632	7.411316073	7.565627638	thymidylate synthase
ACD57766	11.19652221	11.75965104	11.43813688	hypothetical protein
ACD57767	7.555141267	7.582232324	7.607004746	dihydrofolate reductase
ACD57777	6.772901761	7.098284796	7.932143871	2-polyprenyl-6-methoxyphenol 4-hydroxylase
ACD57778	7.24830712	7.847414451	7.539856721	VisC
ACD57779	7.098726937	6.088684372	12.37142273	transposase
ACD57780	3.283874373	0.568207261	1.146870242	ISXo5 transposase
ACD57781	5.071299313	5.476874168	7.101692092	transposase
ACD57783	7.537327133	7.40933153	7.87635732	protocatechuate 3,4-dioxygenase beta chain
ACD57784	7.886257482	9.601297239	8.147851067	conserved domain protein
ACD57785	7.180287126	7.852104987	8.642524689	transcriptional regulator
ACD57793	6.830077816	7.556621006	6.711605032	glucose-fructose oxidoreductase
ACD57799	10.85457234	10.64591957	11.19479378	transposase
ACD57801	0	4.607762318	2.087520548	ISXoo11 transposase
ACD57802	8.431898703	8.377926277	8.546524095	transposase, IS30 family
ACD57805	9.06207043	10.29556233	8.709073471	cellulose biosynthesis protein
ACD57806	6.944097083	7.089360434	6.673443356	glutathione S-transferase
ACD57807	7.897319094	7.052883181	7.106316909	conserved hypothetical protein
ACD57815	6.853496704	6.543732498	6.298616163	conserved hypothetical protein
ACD57816	7.348382928	7.80133329	8.07936211	methionine-S-sulfoxide reductase
ACD57826	7.409161784	7.575448485	7.337666498	protein methyltransferase HemK (Protein-glutamine N-methyltransferase hemK) (Protein-(glutamine-N5) MTase hemK)
ACD57827	7.230990715	6.67067041	6.81905501	conserved hypothetical protein
ACD57828	7.925352671	7.461020986	7.26358846	2-succinyl-6-hydroxy-2, 4-cyclohexadiene-1-carboxylate synthase, putative
ACD57829	7.015771849	5.922395301	6.279432293	hypothetical protein
ACD57830	7.764447011	7.999932372	7.259338405	proline iminopeptidase
ACD57835	7.08329848	7.427103287	6.431907058	conserved hypothetical protein
ACD57836	6.83406647	7.037019745	5.863688236	pyridine nucleotide transhydrogenase
ACD57837	10.77959625	11.20584211	10.24989564	hypothetical protein
ACD57841	8.480757894	9.073338255	8.698228898	pyridine nucleotide transhydrogenase subunit alpha
ACD57842	7.26923891	7.221471121	6.988412026	pyridine nucleotide transhydrogenase subunit beta
ACD57845	8.162305721	8.495679175	8.809263298	domain of unknown function protein
ACD57846	8.10142947	8.568860565	8.402590022	branched-chain amino acid aminotransferase
ACD57847	0	0	0	extracellular protease
ACD57848	0	0	0	hypothetical protein
ACD57849	1.706349306	2.283898073	-1.422129881	extracellular protease
ACD57852	6.843506551	6.619663905	10.08881473	xylanase
ACD57855	7.574086366	7.492526197	6.729321638	tRNA-processing ribonuclease BN
ACD57856	6.386126331	6.788372501	6.866932699	thioredoxin
ACD57857	7.964675869	8.49882129	7.611039556	acylphosphatase
ACD57858	7.024563477	8.265418142	9.064869382	conserved hypothetical protein
ACD57864	7.21451341	7.584714516	7.907395451	tetratricopeptide repeat family
ACD57865	6.324900589	7.005613322	5.988243859	outer membrane lipoprotein LolB
ACD57866	8.860441427	9.301516772	8.4995629	4-diphosphocytidyl-2C-methyl-D-erythritol kinase
PXO_rna3	0	0	0	XO_rna3 cdna:pseudogene chromosome:GCA_000019585.1:Chromosome:1232205:1232281:1 gene:PXO_rna3 transcript:PXO_rna
ACD57867	7.669040943	7.975779198	7.942725616	ribose-phosphate pyrophosphokinase
ACD57868	8.925450592	8.722640203	9.360138179	50S ribosomal protein L25
ACD57869	6.551565235	6.691045553	6.177299931	peptidyl-tRNA hydrolase

ACD57870	7.191227046	7.045311906	7.003028732	GTP-binding protein YchF
PXO_rna4	0	0	0	XO_rna4 cdna:pseudogene chromosome:GCA_000019585.1:Chromosome:1236069:1236154:1 gene:PXO_rna4 transcript:PXO_rna
PXO_rna5	0	0	0	XO_rna5 cdna:pseudogene chromosome:GCA_000019585.1:Chromosome:1236184:1236257:1 gene:PXO_rna5 transcript:PXO_rna
PXO_rna6	0	0	0	XO_rna6 cdna:pseudogene chromosome:GCA_000019585.1:Chromosome:1236292:1236367:1 gene:PXO_rna6 transcript:PXO_rna
PXO_rna7	0	0	0	XO_rna7 cdna:pseudogene chromosome:GCA_000019585.1:Chromosome:1237710:1237785:1 gene:PXO_rna7 transcript:PXO_rna
ACD57872	9.470762574	9.635792475	9.561062596	preprotein translocase subunit SecE
ACD57873	8.949835463	9.045857931	8.780615222	transcription termination/antitermination factor NusG
ACD57874	10.51660617	10.72900887	11.472635	ribosomal protein L11
ACD57875	9.259274841	9.411208011	10.0725078	ribosomal protein L1
ACD57876	8.966834185	9.206631015	9.894369125	ribosomal protein L10, putative
ACD57877	9.193503184	9.776000324	10.11800665	ribosomal protein L7/L12
ACD57878	9.015080476	8.912434307	9.229402864	DNA-directed RNA polymerase, beta subunit
ACD57879	8.767843464	8.660808851	8.138471485	DNA-directed RNA polymerase, beta' subunit
ACD57880	11.84155649	12.29105843	13.16950071	ribosomal protein S12
ACD57881	10.21939846	10.51747255	11.28842778	ribosomal protein S7
ACD57882	9.185829388	9.259856227	10.04201499	translation elongation factor G
ACD57885	9.09255367	0	6.656424863	putative phenylacetaldehyde dehydrogenase
ACD57886	11.38225655	11.7088511	11.58752908	ribosomal protein S10
ACD57887	9.695558907	9.988088174	9.973453429	ribosomal protein L3
ACD57888	9.781412174	10.0423297	9.835380941	ribosomal protein L4/L1 family
ACD57889	11.50253349	11.52668018	11.74692994	ribosomal protein L23
ACD57890	9.198445041	9.111091319	9.005978163	ribosomal protein L2
ACD57891	10.70866146	10.75941386	10.3719073	ribosomal protein S19
ACD57892	10.82603201	10.99894295	10.064635	ribosomal protein L22
ACD57893	8.893987065	8.634952591	8.375469568	ribosomal protein S3
ACD57894	9.630407292	9.047107549	9.282136277	ribosomal protein L16
ACD57895	11.31498535	11.29420143	10.61942218	ribosomal protein L29
ACD57896	10.05417016	10.03754695	9.091369267	ribosomal protein S17
ACD57897	9.810635896	9.670965997	9.295330435	ribosomal protein L14
ACD57898	10.07666865	10.28118821	9.600464902	ribosomal protein L24
ACD57899	10.6091695	10.46821673	10.83608192	50S ribosomal protein L5
ACD57900	10.43910364	10.34743313	10.14960742	30S ribosomal protein S14
ACD57901	11.78033881	12.06867753	12.05246616	ribosomal protein S8
ACD57902	10.04555491	9.918702266	10.3488056	50S ribosomal protein L6
ACD57903	10.98710765	11.20584822	11.31017536	ribosomal protein L18
ACD57904	10.1411492	10.20336024	10.48007322	ribosomal protein S5
ACD57905	11.74662348	11.91601752	12.47785943	ribosomal protein L30
ACD57906	10.70155772	10.27792665	11.62439795	ribosomal protein L15
ACD57907	8.534139439	8.996145791	7.753785022	preprotein translocase, SecY subunit
ACD57908	11.35873361	11.49858996	12.05274804	ribosomal protein S13p/S18e
ACD57909	11.10177218	10.95152514	11.54495478	ribosomal protein S11
ACD57910	9.463395628	9.513737464	9.816506911	ribosomal protein S4
ACD57911	9.404707313	9.406224142	8.837240009	DNA-directed RNA polymerase, alpha subunit
ACD57912	9.737440028	9.875720175	9.76376676	ribosomal protein L17
ACD57916	0	0	0	transposase, IS30 family
ACD57917	5.787798107	6.286175148	5.088773401	transposase
ACD57919	7.643935536	7.165640655	7.357639971	transposase
ACD57928	7.068079597	7.658597102	7.37086174	putative sulfotransferase required for AvrXa21 activity ST (raxST)
ACD57929	7.349869467	7.285993972	7.503666755	putative membrane fusion protein/putative ABC transporter protein required for AvrXa21 activity A (raxA)
ACD57930	7.210603164	7.010410616	6.87601345	colicin V secretion/processing ATP-binding protein CvaB/putative ABC transporter protein required for AvrXa21 activity B (raxB)
ACD57931	7.406102939	6.861856138	6.124818188	conserved hypothetical protein
ACD57936	7.162300685	7.526788727	7.058381441	two-component system regulatory protein (response regulator) required for AvrXa21 activity R (raxR)
ACD57937	6.961044467	6.146510636	6.304144115	two-component system (histidine kinase) sensor protein requried for AvrXa21 activity H (raxH)
ACD57945	7.229049503	7.14291372	6.06233114	two-component system sensor protein
ACD57946	7.590661896	7.707276296	7.334729154	two-component system regulatory protein
ACD57947	9.096891693	9.699813605	9.26604158	conserved hypothetical protein

ACD57948	8.143102556	8.453406459	7.782755829	conserved hypothetical protein
ACD57949	7.439373802	7.596808454	7.185995352	DNA-3-methyladenine glycosylase
ACD57954	6.785445929	6.483270835	6.530613899	phosphoribosylglycinamide formyltransferase 2
ACD57956	0	0	0	conserved hypothetical protein
ACD57958	8.209195022	8.201599558	8.41444001	D-alanyl-D-alanine carboxypeptidase family
ACD57959	10.48797063	10.80597759	10.1489341	paar motif family
ACD57960	7.789272795	8.015877756	7.609422553	putative membrane protein
ACD57961	6.991499171	6.915903274	6.908308549	ImcF-related family
ACD57962	7.490874938	6.982001024	6.266531705	conserved hypothetical protein
ACD57963	7.03440282	7.21292919	6.689257221	OmpA family domain protein
ACD57965	6.641258444	6.550769868	6.472146553	Rhs element Vgr protein
ACD57966	6.195550365	6.203445892	6.48309183	ATPase involved in DNA repair
ACD57968	0	0	0	ATPase involved in DNA repair
ACD57970	0	0	0	ATPase involved in DNA repair
ACD57973	4.798403107	4.046814068	3.600697931	ATPase involved in DNA repair
ACD57975	0	0	0	ATPase involved in DNA repair
ACD57977	6.431537719	7.118401258	6.58772502	Rhs element Vgr protein
ACD57978	6.256487999	6.175434779	7.032508638	Rhs element Vgr protein
ACD57979	8.009739058	8.09502773	7.707731838	conserved hypothetical protein
ACD57980	10.58864906	8.437281846	12.1343108	conserved hypothetical protein
ACD57982	0	0	0.610558337	ISXo8 transposase
ACD57984	10.10670688	9.602899251	10.104887	conserved hypothetical protein
ACD57985	13.44576498	12.80689596	13.0926531	conserved hypothetical protein
ACD57991	8.193421867	7.656017204	8.270080366	conserved hypothetical protein
ACD57992	7.2235577	7.389971136	6.742248796	conserved hypothetical protein
ACD57997	7.310794527	7.869439619	8.997834333	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase
ACD57998	9.44119711	9.860432115	8.630882301	hypothetical protein
ACD57999	8.460033982	8.937750446	7.274634403	conserved hypothetical protein
ACD58000	8.409798228	6.541346015	7.46135666	hypothetical protein
ACD58001	6.560747048	6.170051232	6.128643968	metallopeptidase
ACD58002	6.74262607	6.260187536	5.720240153	cardiolipin synthase
ACD58008	10.11665586	10.9388812	9.662134275	hypothetical protein
ACD58014	7.070657661	7.191473822	6.712760839	sensor protein CreC
ACD58015	3.44343426	3.689120211	4.00267552	ISXoo2 transposase
ACD58019	0	0	0	conserved hypothetical protein
ACD58020	5.953016076	6.02446153	5.668842447	ISXoo6 transposase
ACD58021	0	0	0	DNA (cytosine-5)-methyltransferase PliMCI
ACD58023	0	0	0	conserved hypothetical protein
ACD58024	0	0	0	transposase TnpA, ISL3 family
ACD58027	8.801785947	7.410951597	6.154844432	transposase
ACD58028	6.146926028	5.474984332	5.125667631	ISXoo6 transposase
ACD58030	7.532823435	7.119843772	6.249684253	conserved hypothetical protein
ACD58031	6.634384167	6.504712544	5.984869569	carbon-nitrogen hydrolase family protein
ACD58032	6.946847805	7.064106815	7.030104293	glutamyl-tRNA synthetase
ACD58033	7.472617738	7.750693589	6.810507371	transcriptional regulator, Fur family
ACD58034	6.866969778	5.922480935	5.817546516	cupin domain
ACD58035	6.674587763	9.129878006	9.291467728	conserved hypothetical protein
ACD58036	9.609356062	7.99859043	9.605336908	transposase
ACD58038	8.975363645	8.126818026	10.20105794	hypothetical protein
ACD58041	13.50882229	14.90847706	12.67204296	conserved domain protein
ACD58044	6.562677457	6.866376387	6.72374967	molybdopterin biosynthesis protein
ACD58047	9.797170278	10.84323015	12.99463983	outer membrane protein
ACD58048	9.540815795	10.42642202	10.78830235	hypothetical protein
ACD58049	6.864161377	6.70887696	6.745640714	acyl-CoA dehydrogenase 1
ACD58050	8.117923562	8.262790179	7.86333142	conserved hypothetical protein
ACD58051	6.391853625	5.283555127	6.173515246	conserved hypothetical protein
ACD58052	9.989209982	9.326024936	9.341967962	hypothetical protein
ACD58053	10.50834942	10.45975947	10.30896467	conserved hypothetical protein
ACD58054	7.308584768	7.229587923	6.518042512	conserved hypothetical protein
ACD58055	6.996919716	6.33292987	6.112727235	glutathione S-transferase
ACD58056	6.492135196	6.588344359	5.813560602	asparagine synthase (glutamine-hydrolyzing)
ACD58057	7.436977989	7.317891925	7.350470727	NADPH-dependent fmn reductase
ACD58058	7.180824165	7.401374477	6.53700868	replicative DNA helicase
ACD58059	6.929980315	6.950491743	6.130065982	photolyase

ACD58060	9.276803708	9.599990924	8.104284235	hypothetical protein
ACD58061	8.916046638	9.418571574	10.39330464	OmpA family protein
ACD58062	7.473072529	6.966372784	6.934693407	short chain dehydrogenase
ACD58063	3.739912893	2.590499026	4.037698491	IS1112 transposase
ACD58068	9.071703685	9.173352337	9.025795687	conserved hypothetical protein
ACD58069	9.475946172	9.411720704	8.072416693	conserved hypothetical protein
ACD58073	10.53694653	10.41949676	11.48066905	hypothetical protein
ACD58076	6.144515496	6.511572404	5.438928216	conserved hypothetical protein
ACD58077	5.770120736	6.453481363	7.67308996	conserved hypothetical protein
ACD58078	9.196931567	9.307660759	8.773429365	conserved hypothetical protein
ACD58079	6.70149361	7.053849877	7.781766234	conserved hypothetical protein
ACD58080	6.853983176	8.425769792	7.27351589	inner membrane protein
ACD58086	7.243116846	7.489021033	7.630383628	ATP-dependent RNA helicase
ACD58087	6.734655433	6.604839331	5.995152073	Putative signal protein with PAS(PAC), GGDEF and EAL domains
ACD58088	11.01959073	9.757901654	8.808385051	hypothetical protein
ACD58089	7.775709036	7.570440161	8.457323416	ribosomal large subunit pseudouridine synthase F
ACD58093	10.68582629	9.706508105	8.523162023	hypothetical protein
ACD58094	6.096291375	6.768250502	6.572788131	regulator of ribonuclease activity A
ACD58095	6.900069786	6.378877453	6.002495506	beta-lactamase
ACD58096	6.900468352	7.16491698	6.028193401	transporter, monovalent cation\x3aproton antiporter-2 (CPA2) family
ACD58099	6.903749317	6.08805677	6.662262477	outer membrane channel protein
ACD58100	6.022492101	5.694582154	5.741059738	outer membrane protein V
ACD58101	5.919709529	6.123188171	6.36151748	RND efflux membrane fusion protein
ACD58102	6.720962434	6.314977425	5.805349213	acriflavin resistance protein
ACD58103	6.956788504	6.474551234	5.970296895	conserved hypothetical protein
ACD58104	7.175754121	6.958552715	6.158819703	ABC transporter ATP-binding protein
ACD58111	6.438903273	6.592125104	6.429185769	ISXoo6 transposase
ACD58112	5.850744426	5.640644063	5.547890887	RhsD protein
ACD58114	6.547102748	5.301390104	6.25588024	ISXo8 transposase
ACD58115	0	0	0	ISxac1 transposase
ACD58116	3.719588697	2.147270875	2.561990808	IS1112 transposase
ACD58122	11.07736986	11.49504053	11.08682622	pilin
ACD58123	7.17178728	6.858901042	6.057580239	sulfatase domain protein
ACD58124	7.589074328	7.255850035	7.404528507	spermine/spermidine synthase family protein
ACD58125	7.559552995	7.919596322	6.906373537	putative integral membrane protein
ACD58126	7.159689727	7.697662633	7.253431513	type IV-A pilus assembly ATPase PilB
ACD58132	9.239125907	9.161827233	9.688862232	succinyl-CoA synthetase beta chain
ACD58133	9.113182167	8.940748176	9.830160233	chain A, Succinyl-Coa Synthetase (Succinate-Coa Ligase) (Adp-Forming) (E.C.)
ACD58134	0	0	0	hypothetical protein
ACD58135	7.014288335	6.776169803	6.24549186	glutamine-dependent NAD(+) synthetase (NAD(+) synthase[glutamine hydrolyzing])
ACD58136	9.89492384	9.450623609	8.452710735	hypothetical protein
ACD58138	7.130766169	7.024519153	7.356742461	ribosomal large subunit pseudouridine synthase D
ACD58139	6.865065116	6.947572654	6.318618727	conserved hypothetical protein
ACD58140	6.587782016	6.938297555	6.063207384	conserved hypothetical protein
ACD58141	6.960998148	6.945139463	6.006385553	protein of unknown function
ACD58148	7.336569042	7.983352778	7.076217022	lipoprotein, putative
ACD58150	7.720846182	8.133912814	6.924171163	inorganic anion transporter, sulfate permease (SulP) family protein
ACD58151	10.28564496	10.35777191	11.5333346	conserved domain protein
ACD58154	8.910789616	9.269907441	10.81609566	EF hand domain protein
ACD58160	8.794370375	9.074877344	8.403212325	conserved hypothetical protein
ACD58163	11.89272494	12.65833423	13.3068734	ribosomal protein L21
ACD58164	10.72140684	11.68952194	11.08668029	ribosomal protein L27
ACD58165	7.772914953	7.7501442	8.142209191	GTP-binding protein Obg/CgtA
ACD58167	7.054175583	7.189725741	6.216722581	integral membrane protein MviN
ACD58168	6.643734998	7.175494661	7.007969128	riboflavin biosynthesis protein RibF
ACD58169	6.782644451	7.153025016	6.224937434	isoleucyl-tRNA synthetase
ACD58170	6.620925052	6.774510352	6.007928775	signal peptidase II
ACD58171	7.114533608	7.201859265	7.204091796	4-hydroxy-3-methylbut-2-enyl diphosphate reductase
PXO_rna8	0	0	0	XO_rna8 cdna:pseudogene chromosome:GCA_000019585.1:Chromosome:1542126:1542201:1 gene:PXO_rna8 transcript:PXO_rna
ACD58173	7.887263271	7.891990222	10.36738199	ubiquinol oxidase, subunit II
ACD58174	8.115797973	7.912871377	9.56349565	cytOchrome o ubiquinol oxidase, subunit I
ACD58175	7.816030042	7.829545162	8.939579214	cytOchrome o ubiquinol oxidase, subunit III

ACD58176	8.454332199	8.7968216	8.783892043	cytOchrome o ubiquinol oxidase subunit IV
ACD58177	7.099852731	6.940507412	7.382355995	PDZ domain family protein
ACD58178	7.450270993	7.828682351	6.851711568	Rhs element Vgr protein, putative
ACD58179	6.706046995	6.850736926	5.533479251	tetratricopeptide repeat domain protein
ACD58181	0	0	0	RHS Repeat family
ACD58182	0	0	0	hypothetical protein
ACD58183	5.976808108	6.478664472	4.142290893	RHS Repeat family
ACD58185	0	0	0	transposase
ACD58187	5.80400708	5.74819285	5.987179864	RhsD protein
ACD58189	4.194591403	3.746871676	3.261088461	RhsD protein
ACD58190	2.175336168	0	0	transposase
ACD58202	4.140705047	3.818022246	4.644600428	isrso17-ISXo8 transposase protein
ACD58203	0	0	0	ISXo8 transposase
ACD58205	10.55424348	11.22278887	5.783941138	conserved hypothetical protein
ACD58206	9.641175699	10.22602678	5.988305219	SciI protein
ACD58207	10.1691734	10.83929041	6.368518684	conserved hypothetical protein
ACD58208	9.006171771	9.715306539	5.398189591	ImpE protein
ACD58209	9.000780309	9.445010706	5.829725272	conserved hypothetical protein
ACD58210	8.130560267	8.442719612	6.006753564	SciC protein
ACD58211	7.456921114	7.821238252	5.752023316	conserved hypothetical protein
ACD58212	7.886653785	8.178580204	5.507553642	ClpB
ACD58213	9.930347048	10.43295941	7.50458067	transposase
ACD58214	10.49777202	11.1399286	9.733842388	hypothetical protein
ACD58215	8.523060062	9.167658993	5.713503369	Rhs-family protein
ACD58216	8.078294937	8.828939345	5.352253578	conserved hypothetical protein
ACD58217	9.186636735	9.865747187	6.93515326	FHA domain protein
ACD58218	7.612293516	8.080449813	5.796618518	ImpJ
ACD58219	8.134344172	8.621355936	6.721181235	OmpA family membrane protein
ACD58220	6.892536745	7.27254581	6.03088118	SciS protein
ACD58221	7.348427193	7.469381335	6.63144774	conserved hypothetical protein
ACD58222	8.717367975	9.133419676	7.481524991	phosphoprotein phosphatase
ACD58223	7.063686288	7.712279365	5.96945905	protein kinase
ACD58224	6.77059122	7.473673284	7.173896959	putative membrane protein
ACD58231	7.115719958	6.952904287	6.011025935	transposase, Mutator family
ACD58239	6.079881537	6.388780205	6.62072129	membrane fusion protein
ACD58240	6.597756112	6.370997705	6.942056993	RND superfamily protein
ACD58241	3.293504388	2.517414286	1.895985025	ISXoo5 transposase
ACD58242	7.659011171	7.503722401	6.577667495	cation/multidrug efflux pump
ACD58244	9.875148807	8.593816865	8.313400055	putative membrane protein
ACD58261	7.092535171	6.557607677	6.353753777	NDP-hexose isomerase
ACD58262	6.977325723	6.19061091	6.351783784	transferase hexapeptide repeat
ACD58263	7.174366467	6.411043148	6.174712008	conserved hypothetical protein
ACD58264	6.913870753	6.866339292	5.977131066	conserved hypothetical protein
ACD58265	6.733598385	6.697926686	6.243865169	aminotransferase
ACD58266	7.522228415	7.043967806	6.290229013	lipopolysaccharide biosynthesis protein
ACD58267	6.599006783	6.358709215	5.635905269	glycosyl transferase
ACD58268	7.242802549	6.861608044	6.403744905	lipoprotein, putative
ACD58269	6.716250157	6.405224873	6.317117713	chain length determinant protein
ACD58270	6.391322651	6.876909797	5.88650869	methyltransferase
ACD58271	6.333758248	6.363234167	5.338620517	amidohydrolase family protein
ACD58272	6.568738986	6.354631993	5.793112953	biotin synthesis protein
ACD58273	6.767813677	6.229382193	5.884439187	glycosyltransferase
ACD58274	6.544259716	6.257112479	5.943128986	hexosyltransferase
ACD58277	6.178439778	5.820288756	4.902652471	conserved hypothetical protein
ACD58278	6.262773269	6.407910141	6.023324114	ABC transporter ATP-binding protein
ACD58281	7.698614387	7.905639718	7.237066521	flavin-dependent oxidoreductase
ACD58282	7.018912308	7.522393213	6.192470366	general stress protein
ACD58285	7.248383029	7.079474117	6.823545575	conserved hypothetical protein
ACD58286	7.100515171	7.247338926	7.908374606	transport protein
ACD58287	7.347532789	7.308939649	7.366934137	transmembrane
ACD58291	0	0	0	hypothetical protein
ACD58292	10.07582674	10.9295839	11.82288945	conserved hypothetical protein
ACD58293	7.850124314	7.945707185	8.462011407	CTP synthase
ACD58294	6.945830064	6.79492267	6.889935871	3-deoxy-8-phosphooctulonate synthase

ACD58295	9.124705511	9.398098075	8.341950177	conserved hypothetical protein
ACD58296	8.271477035	8.477252324	9.796477706	phosphopyruvate hydratase
ACD58297	7.73806523	8.831842414	8.213021569	septum formation initiator protein FtsB
ACD58298	7.191503432	7.104881761	5.900890953	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase
ACD58299	6.724254622	6.728954469	6.26632368	2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase
ACD58300	6.610788634	7.132772177	6.11188891	tRNA pseudouridine synthase D
ACD58302	7.364397337	7.627854853	7.684545261	5'/3'-nucleotidase SurE
ACD58303	6.818927233	6.973576838	6.397864556	protein-L-isoaspartate O-methyltransferase
ACD58304	8.096082602	8.011143375	8.258876916	lipoprotein
ACD58305	7.582766732	7.953829773	7.916613981	lipoprotein
ACD58308	8.33860269	8.728917067	8.724176162	ribosomal RNA large subunit methyltransferase J
ACD58309	8.713431196	9.215964894	9.805540752	cell division protease FtsH
ACD58310	6.89575097	7.069132863	6.603307359	dihydropteroate synthase
ACD58311	6.82671372	6.532284227	5.865322516	tRNA delta(2)-isopentenylpyrophosphate transferase
ACD58312	9.927112747	9.583359242	8.167975044	RNA chaperone Hfq, putative
ACD58313	6.904736969	7.163367902	5.893252985	GTP-binding protein
ACD58314	6.564466581	6.768700426	6.454029444	competence/damage-inducible protein CinA domain protein
ACD58316	6.970669625	6.874046904	6.260742684	2-polyprenylphenol 6-hydroxylase
ACD58317	9.155172412	9.605966507	9.216001284	LexA repressor
ACD58318	8.585691178	8.587762517	9.40790292	protein RecA
ACD58319	8.299166798	8.16899296	8.661664103	regulatory protein RecX
ACD58320	7.716428518	7.906794413	8.084351329	alanyl-tRNA synthetase
ACD58321	12.84065206	13.7210244	13.12167111	carbon storage regulator
PXO_rna9	0	0	0	XO_rna9 cdna:pseudogene chromosome:GCA_000019585.1:Chromosome:1727365:1727457:1 gene:PXO_rna9 transcript:PXO_rna
ACD58322	9.379406528	9.382386259	9.633073326	hypothetical protein
ACD58323	7.135750322	6.750124097	7.022955869	hypothetical protein
ACD58324	8.353790821	7.504326421	7.818543833	hypothetical protein
ACD58326	8.24455412	8.441599671	9.789965574	replicative DNA helicase
ACD58327	8.757720016	9.801936262	9.096997078	isopentenyl transferase
ACD58328	9.817575295	9.056477858	8.26006801	conserved domain protein
ACD58330	7.520972191	7.597315141	6.96151915	endolysin
ACD58331	7.368969097	8.299730042	7.805247306	hypothetical protein
ACD58333	6.280911786	6.557826675	5.781058028	transcriptional regulator
ACD58334	7.841859932	7.924699696	7.284874984	DedA family protein
ACD58343	7.912895323	8.466027504	8.349236991	dihydrodipicolinate synthase
ACD58344	7.928382168	8.322788947	8.406366595	conserved hypothetical protein
ACD58346	11.31719212	9.788403499	10.58598593	hypothetical protein
ACD58351	7.016953107	7.62811741	6.865485842	galactose-binding protein regulator
ACD58353	6.704000442	5.916287935	5.970140411	alpha-xylosidase
ACD58354	8.406579186	8.730694294	6.972531835	expressed protein
ACD58355	7.956387774	7.417253377	6.60675312	conserved hypothetical protein
ACD58356	7.753878599	7.982685615	9.817679212	xylulokinase
ACD58359	7.97499958	8.816100462	8.463700102	conserved hypothetical protein
ACD58360	12.52313555	12.13260255	13.51365358	hypothetical protein
ACD58368	7.571722311	7.596555044	7.108127138	ferrous iron transport protein
ACD58369	7.15383573	7.197246186	6.573245752	ferrous iron transport protein B
ACD58370	6.732540561	8.083250605	6.325255078	conserved hypothetical protein
ACD58371	8.015983655	8.631147947	8.350050756	conserved hypothetical protein
ACD58372	7.045290061	7.084319436	7.042316017	conserved hypothetical protein
ACD58373	7.80931797	7.579858968	7.713668324	valine-pyruvate aminotransferase
ACD58374	6.514753498	6.235054947	6.397613031	mosc domain protein
ACD58377	7.632348201	8.183362447	7.784778781	dihydrodipicolinate reductase
ACD58379	7.247262961	6.957984225	7.702962228	carbamoyl-phosphate synthase, small subunit
ACD58380	7.25370569	7.767158191	8.359169731	putative secreted protein
ACD58381	6.686108285	6.70763522	6.982377589	carbamoyl-phosphate synthase, large subunit
ACD58382	7.032762074	7.024231015	7.488153454	transcriptional elongation factor
ACD58383	6.496516677	6.235181351	5.306440888	RpfE regulatory protein
ACD58384	7.299116416	7.060609475	6.225261432	single-stranded-DNA-specific exonuclease RecJ
ACD58386	8.167282652	8.670560656	8.900842662	hypothetical protein
ACD58387	9.976463883	9.999873195	10.651563	conserved hypothetical protein
ACD58389	8.769447784	8.913194605	7.975601528	RpfD regulatory protein
ACD58390	7.806601175	8.157281242	8.160083186	peptide chain release factor 2

ACD58391	7.175055469	7.271855164	7.765852953	lysyl-tRNA synthetase
ACD58392	7.815857178	8.06769249	7.818869729	Two-component system response regulator RpfG
ACD58393	7.558734475	7.81677888	6.849448889	two component sensor-regulator hybrid protein RpfC
ACD58396	8.574998371	8.25363006	8.32284752	hypothetical protein
ACD58397	6.870697611	7.60295862	5.438984753	conserved hypothetical protein
ACD58399	9.341961293	8.724097697	9.223217388	SpoVT / AbrB like domain protein
ACD58400	7.935783846	7.87099345	8.453431153	PIN domain, putative
ACD58401	7.290903551	7.367982544	7.708063051	aconitate hydratase 2
ACD58402	9.271467697	0	7.985033574	hypothetical protein
ACD58403	8.34978987	8.599235955	8.670054263	beta-ketoadipate enol-lactone hydrolase
ACD58414	0	0	0	ISXo3 transposase ORF B
ACD58426	11.46290098	10.05851944	10.43933224	hypothetical protein
ACD58435	8.043278879	9.281614801	6.86246379	hypothetical protein
ACD58436	0	0	7.371933427	hypothetical protein
ACD58443	7.694392713	7.643769625	7.225583429	TonB-dependent receptor
ACD58449	3.582026034	3.524853531	3.48595486	Tal3a, TAL effector AvrBs3/PthA family
ACD58452	0	0	7.04384754	hypothetical protein
ACD58455	5.703277924	5.622602428	6.089301106	Tal3b, TAL effector AvrBs3/PthA family
ACD58458	4.689953258	5.121661981	5.44957458	Rhs element Vgr protein
ACD58459	1.171232452	0	-0.487196656	conserved hypothetical protein
ACD58460	5.543972166	5.423480688	5.681775325	conserved hypothetical protein
ACD58461	0	0	0	conserved hypothetical protein
ACD58462	6.891917336	6.407245667	6.863653549	conserved hypothetical protein
ACD58463	10.90531178	0	12.04211078	conserved hypothetical protein
ACD58467	5.723457537	5.73276304	5.335247418	conserved hypothetical protein
ACD58473	7.777630121	7.907527645	7.666820489	transcriptional regulator LacI family
ACD58476	2.965477708	3.368377246	1.871977663	ISXo5 transposase
ACD58482	7.055260741	7.054588039	7.014768134	NAD-glutamate dehydrogenase
ACD58483	7.626168971	8.644598986	6.383049316	hypothetical protein
ACD58484	7.634615048	7.376290383	7.336470855	ISXoo6 transposase
ACD58489	7.593719777	7.730918415	7.282171035	conserved hypothetical protein
ACD58491	6.668374456	6.502123706	6.305199005	integral membrane transporter
ACD58492	7.169925001	7.353199767	5.864780437	formate dehydrogenase family accessory protein FdhD
ACD58493	6.786544089	6.823813037	6.331492049	oxidoreductase alpha (molybdopterin) subunit
ACD58494	7.405345724	6.713805772	6.694434504	conserved hypothetical protein
ACD58495	7.388792257	7.369911368	6.216709002	metabolite transport protein
ACD58500	8.842256047	9.381906283	8.69368906	glutamine amidotransferase
ACD58501	7.134323634	7.203299056	6.170021178	glutamine synthetase
ACD58503	9.491833059	10.92953212	0	periplasmic putrescine-binding protein\x3b permease protein
ACD58504	7.760460488	7.786831565	6.540603885	transport protein
ACD58505	6.916201933	7.08390476	5.799434465	transport protein
ACD58506	6.500999582	6.573454815	5.572337944	outer membrane protein OprN
ACD58507	7.76670116	7.531599798	6.905314793	ATP-binding component of putrescine transport system
ACD58508	8.071698323	8.083585697	7.606012791	polyamine transport protein
ACD58509	7.538351917	7.457364461	6.751316423	putrescine transport protein\x3b permease
ACD58511	6.699676553	6.812998718	6.682025441	aldehyde-dehydrogenase like protein YneI
ACD58522	6.894247847	6.852261076	5.738600323	repressor
ACD58523	7.881107841	8.02017436	7.59324171	soluble lytic murein transglycosylase
ACD58524	8.068547213	8.394642752	6.57535923	ubiquinol-Cytochrome c reductase, iron-sulfur subunit
ACD58525	7.588302378	7.882025493	5.957993508	ubiquinol cytochrome C oxidoreductase, cytochrome B subunit
ACD58526	7.403838619	7.65442838	5.382432087	ubiquinol cytochrome C oxidoreductase, cytochrome C1 subunit
ACD58527	8.101024938	8.041127967	6.526386558	stringent starvation protein A
ACD58528	9.583917671	9.971500445	10.25728176	stringent starvation protein B
ACD58529	8.890902631	8.141713774	7.635544007	hypothetical protein
ACD58530	0	10.24748847	0	hypothetical protein
ACD58533	5.754978336	6.286530039	5.501735297	ATP-dependent DNA helicase
ACD58534	6.302871016	5.808240877	6.004528358	ATP-dependent DNA helicase
ACD58535	9.841383508	7.147255813	7.687319689	conserved domain protein
ACD58536	5.316536781	5.288576353	5.466039743	ATP-dependent DNA helicase
ACD58539	10.1974133	9.258158489	8.170070266	conserved domain protein
ACD58540	11.2777872	12.17431403	11.54741512	transcriptional regulator, HTH motif containing
ACD58541	10.07694917	10.76054532	10.42175979	conserved hypothetical protein
ACD58542	10.28343567	11.06469562	8.747635795	hypothetical protein
ACD58543	12.44859385	13.39973187	13.18453291	TlpA

ACD58546	7.935866332	7.064408657	6.03336353	ATP-dependent DNA ligase
ACD58549	6.45751878	6.679311189	6.356730138	conserved hypothetical protein
ACD58550	6.159290106	6.659724804	7.154645988	ISXo3 transposase ORF B
ACD58551	8.103864771	8.935159155	10.62542575	virulence protein
ACD58555	7.064494885	7.433810747	7.159800714	YjeF family protein
ACD58556	6.666799191	7.459111895	7.313880701	conserved hypothetical protein
ACD58557	7.741669219	7.983392684	7.058933363	N-acetylmuramoyl-L-alanine amidase
ACD58558	6.814332516	6.386436777	6.307954867	DNA mismatch repair protein MutL
ACD58559	6.471231365	6.857993432	6.31210605	lipoprotein, putative
ACD58560	6.857719794	7.279369144	6.125136529	GumN protein
ACD58564	7.827050483	7.935612967	9.75329699	putative Probable protease HtpX homolog
ACD58569	12.06212036	12.91015925	11.76324142	major cold shock protein
ACD58570	9.103114675	9.042502074	8.429335599	glutathione S-transferase
ACD58572	7.057634388	7.457709193	7.166635114	conserved hypothetical protein
ACD58573	8.075580763	8.083239966	9.260357396	adenine phosphoribosyltransferase
ACD58575	7.15171678	7.321693638	7.347904787	ABC transporter ATP-binding protein
ACD58576	9.58979906	8.697770345	8.939576276	hypothetical protein
ACD58579	8.302876498	8.845443006	9.232135478	superoxide dismutase
ACD58581	6.660766075	6.557488209	6.656052968	tRNA/rRNA methyltransferase
ACD58583	7.213425053	7.650448648	6.23988871	phosphate-binding protein
ACD58584	6.72975668	6.53488179	5.850771925	Putative signal protein with GGDEF and EAL domains
ACD58586	7.823354501	7.636885587	8.149081497	translation elongation factor P
ACD58587	6.560105042	6.983233054	6.260159302	conserved hypothetical protein
ACD58588	7.163196797	6.672015106	6.344911918	Amidohydrolase family protein
ACD58589	7.367161356	7.053621838	5.962618426	ubiquinone biosynthesis O-methyltransferase
ACD58590	7.119117507	7.488233808	6.110014472	phosphoglycolate phosphatase, bacterial
ACD58591	6.975435301	6.713503369	6.39516565	conserved hypothetical protein
ACD58593	8.393879496	7.833427761	8.665321703	transposase
ACD58594	9.917298973	9.970220956	8.711570619	hypothetical protein
ACD58600	0	0	-1.001631167	ISXo8 transposase
ACD58601	8.712791785	9.363247749	8.15522808	general stress protein
ACD58603	12.30727482	12.09000984	12.51934631	conserved hypothetical protein
ACD58605	9.915259454	10.53028928	9.259703254	hypothetical protein
ACD58608	8.11816243	8.515404174	8.364458623	DnaK supressor
ACD58609	6.10772971	5.330518962	5.264040936	peptidase, S41 family
ACD58613	0	7.278737504	6.893155889	hypothetical protein
ACD58614	9.668064152	10.16764394	10.03659949	conserved hypothetical protein
ACD58615	7.625299717	7.494895575	7.595048569	ornithine carbamoyltransferase
ACD58616	7.149574392	7.219149155	7.117476877	argininosuccinate synthase
ACD58617	8.540147416	8.072513163	8.205695519	acetyltransferase, gnat family
ACD58618	7.223827961	7.160587462	6.112251827	acetylornithine deacetylase
ACD58619	7.190387693	6.994217647	6.760101161	acetylglutamate kinase
ACD58620	7.996919716	7.436211821	6.496719586	amino-acid acetyltransferase
ACD58621	7.945268244	7.00929118	6.391302027	N-acetyl-gamma-glutamyl-phosphate reductase
ACD58622	7.198317342	6.976157391	6.016777094	argininosuccinate lyase
ACD58623	7.443465756	7.126838671	6.682095691	cupin domain protein
ACD58624	9.034433085	8.375643325	7.956893024	conserved hypothetical protein
ACD58625	6.965668864	7.141718882	6.270730756	glutamate 5-kinase
ACD58626	6.97260076	6.750110694	5.174893733	gamma-glutamyl phosphate reductase
ACD58627	6.954963992	6.845665673	6.898075301	alpha-amino acid ester hydrolase
ACD58632	0	0	0	hypothetical protein
ACD58633	6.839695103	7.244582661	6.157514693	ABC transporter, CydDC cysteine exporter (CydDC-E) family, permease/ATP-binding protein CydD
ACD58634	6.699745948	6.663216513	5.803888292	ABC transporter, CydDC cysteine exporter (CydDC-E) family, permease/ATP-binding protein CydC
ACD58638	8.831772759	8.790283326	6.518209363	conserved hypothetical protein
ACD58639	8.570884111	8.578874575	4.802736065	hypothetical protein
ACD58640	8.042660751	0	7.925477296	hypothetical protein
ACD58643	7.301313274	7.291032526	5.907904934	cation efflux system protein
ACD58644	7.29351763	7.426583454	6.31344722	cation efflux system protein
ACD58645	6.540808435	6.382445921	5.537159371	RND superfamily protein
ACD58646	6.774997849	6.053745635	5.435531922	RND superfamily protein
ACD58647	7.558129849	7.813075701	6.367519591	transport protein
ACD58654	5.876212414	6.136730737	8.111052185	ISXoo2 transposase

ACD58655	8.73420154	8.247566795	8.941338171	transposase
ACD58657	5.575248788	6.155532699	5.940368808	putative methyltransferase
ACD58658	7.834698576	8.138333245	8.270094387	pantetheine-phosphate adenylyltransferase
ACD58659	8.249217769	8.891416149	8.489406456	lipoprotein, putative
ACD58660	8.219700961	8.534046035	7.194658374	ferredoxin
ACD58661	7.507136558	7.652443472	6.673796665	gamma-glutamyltransferase
ACD58669	6.822717403	6.532865503	6.014658798	TonB-dependent outer membrane receptor
ACD58670	7.227105676	7.085265302	7.183565912	TonB-dependent receptor
ACD58671	6.702283524	6.791944272	6.091752718	putative phytase
ACD58675	0	0	0.828785916	ISXo8 transposase
ACD58678	7.600782659	6.755728829	7.786544089	conserved hypothetical protein
ACD58681	6.333835158	6.338864715	6.709649059	transcriptional regulator AsnC/lrp family
ACD58682	6.283945842	6.741938819	6.271343499	S-adenosylmethionine\x3atRNA ribosyltransferase-isomerase
ACD58683	7.430628173	7.197845738	7.429615964	queuine tRNA-ribosyltransferase
ACD58684	8.242783498	8.405745651	8.305537392	preprotein translocase, YajC subunit
ACD58686	7.545651818	7.553083981	7.235219653	protein-export membrane protein SecD
ACD58687	7.309549112	7.532792272	7.157063927	protein-export membrane protein SecF
ACD58689	6.138232884	5.310561889	5.730131799	ISXoo6 transposase
ACD58691	8.775277756	8.081206457	8.547850796	transposase
ACD58694	7.420793962	7.454299294	7.266496099	putative ISXoo14 transposase
ACD58697	0	8.829332679	9.35549646	putative transcriptional regulator, ArsR family
ACD58700	0	8.448863793	9.973424728	hypothetical protein
ACD58707	14.06746797	15.06427122	14.89240051	conserved hypothetical protein
ACD58710	7.877449792	7.322054325	6.851761532	carbonic anhydrase
ACD58714	9.069551806	9.022978055	9.562459957	peptidyl-prolyl cis-trans isomerase
ACD58715	8.091440676	7.827888872	7.067939821	MutT/nudix family protein
ACD58716	6.972003304	7.153774942	6.574443668	3-mercaptopyruvate sulfurtransferase
ACD58717	7.264799125	7.018344858	7.274820737	lipoprotein, putative
ACD58719	7.781812124	7.538297591	7.265089908	mosc
ACD58720	7.031902415	7.300370866	6.497307381	conserved hypothetical protein
ACD58721	6.666870185	6.569592862	5.902879141	acetyltransferase
ACD58722	6.898982227	6.336754686	8.374174424	hypothetical protein
ACD58723	6.472252177	6.54223483	6.018033223	methyltransferase
ACD58724	7.339778757	7.701348053	7.28118821	NAD(+) kinase
ACD58725	7.285920016	7.315113325	6.708670077	cytosolic 5'-nucleotidase 1A
ACD58732	10.69128988	9.45093079	0	hypothetical protein
ACD58744	8.776321166	9.226009916	10.27289801	HesB protein family
ACD58745	11.67494697	11.80640462	11.68909382	30S ribosomal protein S6
ACD58746	11.61398279	12.2732915	11.80491348	ribosomal protein S18
ACD58747	8.55677426	8.96923109	8.493078866	ribosomal protein L9
ACD58748	7.214552265	7.097199924	7.069766602	chromosome segregation protein SMC
ACD58749	7.179958837	7.541445144	6.439269069	cell division protein ZipA
ACD58750	7.539019189	9.305995593	0	putative membrane protein
ACD58753	7.390366749	7.071955691	6.070249775	DNA ligase
ACD58754	6.822653678	6.94963998	6.065281486	tRNA synthetases class II (D, K and N) subfamily
ACD58755	7.150366736	7.959718	6.575442434	conserved hypothetical protein
ACD58756	6.323580837	6.960407452	7.027120868	IDI2
ACD58757	7.940613118	8.167021664	7.08537154	DNA gyrase, A subunit
ACD58758	7.495831048	7.692922314	7.627212845	ISXoo3 transposase ORF A
ACD58759	9.363712074	9.229969983	9.03140071	transposase
ACD58766	6.798789305	7.126714796	6.2449213	formiminoglutamate deiminase
ACD58767	6.204979931	6.355349334	5.781464633	histidine utilization repressor
ACD58771	8.926411643	9.154714333	7.725618473	FHA domain protein
ACD58772	9.425616655	9.334836396	8.938256382	hypothetical protein
ACD58775	7.946824417	8.00445083	7.858534337	phosphoserine aminotransferase
ACD58776	8.028966899	7.990143684	8.255052182	P-protein
ACD58777	6.665478048	6.894514644	5.783650467	3-phosphoshikimate 1-carboxyvinyltransferase
ACD58782	6.45679301	6.417763082	5.810710435	YapH protein
ACD58783	10.42005495	11.22231191	10.45457691	hypothetical protein
ACD58789	9.922327207	8.538949372	10.00277283	choline dehydrogenase
ACD58792	6.4128882	6.466291039	6.006798436	putative ISXoo4 transposase
ACD58796	5.212071235	7.949213909	4.097492814	transposase
ACD58797	6.706157536	7.035700881	5.952067929	N-acetylmuramoyl-L-alanine amidase
ACD58798	7.018745434	6.971486075	5.899325501	conserved hypothetical protein

ACD58799	11.03999512	9.611959848	10.05177992	hypothetical protein
ACD58800	7.856998135	7.843066798	7.762275722	poly(A) polymerase (PAP) (Plasmid copy number protein)
ACD58801	6.959480382	6.945326777	6.050725877	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase
ACD58802	7.835305138	8.031207701	8.095729306	3-methyl-2-oxobutanoate hydroxymethyltransferase
ACD58803	7.445544634	7.667033461	7.231374804	pantoate--beta-alanine ligase
ACD58804	10.15579223	10.37619052	12.32808303	aspartate 1-decarboxylase
ACD58805	7.461954128	7.757616689	8.471756491	glucose-6-phosphate isomerase
ACD58806	9.17029815	9.514260367	10.05612286	addiction module antitoxin, Axe family, putative
ACD58807	8.075425666	8.191898177	8.58784126	conserved hypothetical protein
ACD58809	10.03838405	8.756442904	9.569834727	putative helicase
ACD58811	6.736618404	6.703668295	6.250743713	glucan 1,4-beta-glucosidase
ACD58812	7.138599474	7.027928107	6.691687694	sodium/glucose cotransport protein
ACD58814	0	10.37932421	9.554803705	hypothetical protein
ACD58815	6.686668598	6.536149284	7.422359164	IS1112 transposase
ACD58817	10.99665708	11.69461906	9.955495896	hypothetical protein
ACD58819	7.621033518	7.206496712	7.037656765	oligopeptide transporter
ACD58820	7.617188266	7.955086086	7.482638574	peptidase, S54 (rhomboid) family
ACD58822	6.743299528	7.774180869	7.516787362	conserved hypothetical protein
ACD58823	7.16413259	7.710413857	7.359327889	conserved hypothetical protein
ACD58824	9.212654447	8.835930389	9.83218273	transcriptional regulator MarR family
ACD58827	6.552830455	6.23109635	5.838263525	extracellular protease
ACD58828	7.447637049	8.6360409	9.878233346	hypothetical protein
ACD58829	8.416476659	7.501359524	7.352899737	hypothetical protein
ACD58830	0	9.650956585	10.39175913	biotin acetyl-CoA-carboxylase synthetase
ACD58833	7.230308706	5.555402057	6.313628609	hypothetical protein
ACD58834	6.195717675	7.160879862	6.467390352	glutathione peroxidase
ACD58837	6.957752124	6.79199635	6.682587342	fumarate hydratase
ACD58838	6.304989184	5.752159835	5.777088265	glutathione S-transferase
ACD58839	4.210856386	3.233605873	4.046002047	isrso5-transposase protein
ACD58840	9.108989599	8.430268544	9.337010801	isrso5-transposase protein
ACD58841	5.260507478	4.43956995	4.861528644	IS1112 transposase
ACD58843	0	0	0	conserved hypothetical protein
ACD58847	6.265268102	5.630513227	6.916082477	transposase
ACD58849	0	0	0	phosphinothricin N-acetyltransferase
ACD58853	0	0	0	ATPase, AAA family
ACD58854	0	0	0	peptidase S8 and S53, subtilisin, kexin, sedolisin
ACD58857	3.437241058	2.819588486	5.647400861	transposase
ACD58859	0	0	0	conserved hypothetical protein
ACD58860	0	0	0	conserved hypothetical protein
ACD58861	0	0	0	transcriptional regulator, ArsR family
ACD58862	0	0	0	arsenate reductase
ACD58863	0	0	0	arsenate reductase
ACD58864	0	0	0	arsenical resistance protein ArsH
ACD58865	0	0	0	arsenical membrane pump
ACD58866	0	0	0	cointegrase
ACD58867	0	0	0	transposase
ACD58868	0	0	0	transposase
PXO_rna20	0	0	0	XO_rna20 cdna:pseudogene chromosome:GCA_000019585.1:Chromosome:2311816:2311902:1 gene:PXO_rna20 transcript:PXO_rna2
ACD58874	8.753517628	9.12869036	8.032398434	hypothetical protein
ACD58875	7.89284635	9.303189396	8.136903984	conserved hypothetical protein
ACD58885	7.81677888	7.819227491	8.189063485	sugar ABC transporter ATP-binding protein
ACD58887	12.70447647	13.19870593	13.89785491	conserved hypothetical protein
ACD58888	8.741001743	8.655412655	8.267769861	succinate dehydrogenase, cytochrome b556 subunit
ACD58889	8.591593404	8.932793486	8.47208155	succinate dehydrogenase, hydrophobic membrane anchor protein
ACD58890	8.700984094	8.582119395	8.201393719	succinate dehydrogenase, flavoprotein subunit
ACD58891	10.44233188	10.27494883	7.639152558	putative secreted protein
ACD58892	8.118987778	7.940196121	7.33948483	succinate dehydrogenase iron-sulfur protein
ACD58893	9.108202951	8.910037046	8.564263834	TPR repeat region superfamily
ACD58894	8.712189931	8.190975291	6.588552745	putative membrane protein
ACD58895	6.959665843	7.137196099	6.644966637	lipoprotein releasing system transmembrane protein
ACD58896	6.947537589	7.164434329	6.704097304	lipoprotein releasing system, ATP-binding protein
ACD58897	8.986792039	8.313454476	8.668104938	hypothetical protein

ACD58901	7.107311247	7.449371534	6.433373455	DNA internalization-related competence protein ComEC/Rec2
ACD58902	8.390143155	8.646778293	7.678839541	biopolymer transport protein
ACD58903	8.24339299	8.044180978	7.417439052	biopolymer transport protein
ACD58904	7.281104732	7.373500315	6.05381513	lipid A export permease/ATP-binding protein MsbA
ACD58905	7.081222438	7.109308317	5.691375035	tetraacyldisaccharide 4'-kinase
ACD58907	6.931375766	6.524044864	5.421815743	3-deoxy-D-manno-octulosonate cytidylyltransferase
ACD58908	6.876737938	6.668246796	5.98627212	low molecular weight phosphotyrosine protein phosphatase
ACD58909	7.288672318	7.246968562	7.386664394	conserved hypothetical protein
ACD58910	6.940636607	6.519699148	5.908070718	excinuclease ABC, C subunit
ACD58911	8.993181832	9.214382268	7.256142627	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase
PXO_rna21	0	0	0	XO_rna21 cdna:pseudogene chromosome:GCA_000019585.1:Chromosome:2344873:2344948:1 gene:PXO_rna21 transcript:PXO_rna2
PXO_rna22	0	0	0	XO_rna22 cdna:pseudogene chromosome:GCA_000019585.1:Chromosome:2345017:2345090:1 gene:PXO_rna22 transcript:PXO_rna2
PXO_rna23	0	0	0	XO_rna23 cdna:pseudogene chromosome:GCA_000019585.1:Chromosome:2345173:2345248:1 gene:PXO_rna23 transcript:PXO_rna2
ACD58914	0	0	0	IS1113 transposase
ACD58915	6.805008636	6.452826026	7.077264366	RhsD protein
ACD58916	7.608447045	7.442935204	8.591810296	RhsD protein
ACD58929	8.99214244	7.990336592	8.759951414	hypothetical protein
ACD58930	6.409877976	6.443359662	7.055846386	phage replication protein
ACD58931	8.598878788	8.507247581	8.616328288	helix-destabilizing protein
ACD58932	10.33233871	8.891094082	10.58275356	hypothetical protein
ACD58933	7.83161127	7.311612098	6.812357029	hypothetical protein
ACD58934	7.919661864	7.162814256	7.684930918	phage-related protein
ACD58935	6.928950601	6.54389022	6.566360055	phage-related protein
ACD58939	0	0	0	hypothetical protein
ACD58940	0	0	0	hypothetical protein
ACD58941	0	0	0	hypothetical protein
ACD58943	0	0	0	transposase
ACD58946	4.193692905	3.555607587	4.079924192	ISXo8
ACD58948	5.334768477	4.936524874	5.467677276	Tal6a, TAL effector AvrBs3/PthA
ACD58963	6.067464478	6.097486494	5.900770223	putative transposase
ACD58968	7.874194488	7.681898983	6.256457806	ethyl tert-butyl ether degradation EthD
ACD58971	9.818141153	9.371750512	8.100436325	hypothetical protein
ACD58977	9.977480284	11.18482576	11.45481335	hypothetical protein
ACD58978	7.343487772	7.64653711	7.826510354	piperideine-6-carboxylate dehydrogenase
ACD58979	9.054978678	8.667462857	9.870130417	conserved hypothetical protein
ACD58980	7.689655596	7.614400662	7.752206676	conserved hypothetical protein
ACD58981	7.220832953	7.227201967	7.188628405	dihydroorotate oxidase
ACD58982	6.843091931	6.312367485	5.861342535	UDP-N-acetylenolpyruvoylglucosamine reductase
ACD58983	7.045257292	6.799216853	5.74728803	integral membrane protein
ACD58984	9.444174236	8.841935391	9.207092434	pyridoxal phosphate biosynthetic protein
ACD58985	10.88053248	7.855198638	10.72082567	aspartate racemase
ACD58989	7.457175645	7.503515704	8.40955217	prop transport protein
ACD58992	0	0	0	hypothetical protein
ACD58993	7.426524752	7.238404739	8.649626236	two-component system sensor protein
ACD58994	8.262094845	8.062002951	9.746883765	two-component system regulatory protein
ACD58998	6.031154756	6.003102963	6.338456506	FAD dependent oxidoreductase, putative
ACD59004	6.701077692	6.006827603	5.991428876	D-beta-hydroxybutyrate dehydrogenase
ACD59008	8.410154514	8.441010316	8.206179219	phosphoenolpyruvate synthase
ACD59009	7.771892179	7.704118059	5.906279725	small conductance mechanosensitive ion channel
ACD59013	7.459685707	7.427178731	6.707138224	manganese transport protein
ACD59015	9.853390656	10.93318164	10.15488138	methyl-accepting chemotaxis protein
ACD59016	9.845292451	11.01415301	9.726488959	conserved hypothetical protein
ACD59018	8.427040414	8.579685522	7.915837561	inner membrane protein YeiH
ACD59021	6.851074377	6.625733679	6.294911097	NADH dehydrogenase
ACD59022	5.895094152	6.264643391	5.738311181	conserved hypothetical protein
ACD59026	8.486070744	7.60295862	7.456666537	conserved hypothetical protein
ACD59027	7.847790256	7.647638302	8.180645174	transposase
ACD59039	11.03172188	11.72054782	8.767492592	ribosomal protein L36
ACD59040	8.121253758	8.778954311	8.982448897	conserved hypothetical protein
ACD59041	9.527435953	12.28080846	10.40195679	hypothetical protein

ACD59042	10.16931122	11.55967344	10.89091783	hypothetical protein
ACD59043	7.343336752	7.102931025	7.307701737	porphyromonas-type peptidyl-arginine deiminase
ACD59044	7.299931474	6.93376146	9.158493561	beta-alanine synthetase
ACD59045	7.903490247	7.99150484	8.517267818	phosphinothricin N-acetyltransferase
ACD59046	6.811162729	6.709483644	6.586231814	pheromone shutdown protein
ACD59057	9.225985824	9.254780622	9.078217536	segregation and condensation protein A
ACD59058	8.823701601	8.870084168	7.368192134	segregation and condensation protein B, putative
ACD59059	7.890829691	7.981139119	6.716071775	ribosomal large subunit pseudouridine synthase B
ACD59061	6.506878	6.813575993	6.790772038	glutamine cyclotransferase
ACD59062	0	0	0	ISXo5 transposase
ACD59253	0	0	-0.43555354	ISXo5 transposase
ACD59391	0	0	0	conserved hypothetical protein
ACD59445	0	0	0	ISXo5 transposase
ACD59449	0	0	0	ISXoo13 transposase
PXO_rna27	0	0	0	XO_rna27 cdna:pseudogene chromosome:GCA_000019585.1:Chromosome:2937879:2937965:1 gene:PXO_rna27 transcript:PXO_rna2
ACD59456	6.69047297	6.624473806	7.668643924	transcriptional regulator
ACD59457	6.57218027	6.788542165	6.449520107	methionine synthase
ACD59458	7.095787315	6.702754495	6.609121103	methionine synthase
ACD59469	7.981881187	8.565787553	7.89624157	transcriptional regulator GntR family
ACD59470	7.087473449	6.806955549	6.83406647	ABC transporter ATP-binding protein
ACD59471	7.275593768	7.805937293	6.991691898	membrane protein, putative
ACD59472	6.260735158	6.385110019	5.543338119	conserved hypothetical protein
ACD59473	8.099731777	8.684643438	7.949686665	conserved hypothetical protein
ACD59475	8.165911939	7.716648008	8.85055567	conserved hypothetical protein
ACD59477	11.01586103	11.64760233	11.25655074	glycine dehydrogenase
ACD59479	4.795855244	4.327435876	5.318013084	transposase, IS30 family
ACD59485	7.886452599	8.060885037	8.009839812	adenylosuccinate lyase
ACD59486	7.458283564	7.40721677	7.164544951	conserved hypothetical protein
ACD59487	0	0	0	hypothetical protein
ACD59489	9.095518341	8.370739709	9.151145957	hypothetical protein
ACD59490	7.92633158	7.564332436	8.486074767	transcription factor jumonji, JmjC
ACD59491	7.234338449	6.949184722	6.728573603	acetyltransferase, gnat family
ACD59492	7.792783788	8.04930948	9.199137369	2-oxoglutarate dehydrogenase, E1 component
ACD59493	8.228592651	8.372085838	9.002283398	2-oxoglutarate dehydrogenase, E2 component, dihydrolipoamide succinyltransferase
ACD59494	7.380616907	7.479731769	7.112731405	dihydrolipoamide dehydrogenase
ACD59495	6.750606505	6.510025129	6.966165106	conserved hypothetical protein
ACD59496	6.919828685	6.896114394	5.976175725	thymidylate synthase
ACD59497	6.76016771	6.491829051	6.409854221	ABC transporter, permease/ATP-binding protein
ACD59498	7.142168339	6.628343463	6.557537223	hydrogen peroxide-inducible genes activator
ACD59500	6.240323871	6.133964173	5.741499346	outer membrane component of multidrug efflux pump
ACD59501	0	0	0	ISXo8 transposase
ACD59508	6.757023247	6.814088933	6.751731497	DNA repair protein RecN
ACD59510	10.21170582	10.65761321	11.28922353	outer membrane protein
ACD59513	9.16768157	8.799767296	9.997588798	SsrA-binding protein
ACD59516	6.713943207	5.98287268	7.128169651	lipoprotein, putative
ACD59517	6.358531649	5.903978223	6.079941254	acyl-CoA dehydrogenase
ACD59518	8.32984566	8.616732615	9.385402994	HNH endonuclease family protein
ACD59519	8.401587805	8.544983746	9.195556762	1-deoxy-D-xylulose-5-phosphate synthase
ACD59525	0	3.721503907	0	transposase, IS30 family
ACD59526	0	0	0	conserved domain protein
ACD59528	0	0	0	transposase
ACD59529	1.829399028	4.783399029	3.286304546	transposase
ACD59537	6.553589362	6.839732889	6.119005422	transcriptional regulator
ACD59538	6.836302884	6.775169093	6.916106369	DNA topoisomerase IV, A subunit
ACD59540	7.334335864	7.263541514	7.103675972	penicillin acylase II
ACD59542	7.153987688	6.696160782	6.415246562	TonB-dependent outer membrane Receptor
ACD59543	7.366409648	6.196634582	6.084225878	hypothetical protein
ACD59544	9.7748447	9.843486136	10.75409414	conserved hypothetical protein
ACD59553	8.791638281	8.705445775	8.449895599	protein U
ACD59554	8.084845584	8.013562754	7.846436901	pili assembly chaperone
ACD59555	6.92132921	7.27561239	6.932238378	outer membrane usher protein FasD
ACD59556	7.628503866	7.67468662	7.218878016	spore Coat Protein U domain family

ACD59557	8.180853995	8.73047693	10.3261598	conserved hypothetical protein
ACD59558	7.354875259	7.28872768	8.451388346	pili assembly chaperone
ACD59559	9.026719846	8.808024589	9.28529355	ribosomal protein S2
ACD59560	6.891321967	6.917813623	6.890227791	translation elongation factor Ts
ACD59561	9.536552238	9.668156363	9.136862981	conserved hypothetical protein
ACD59562	8.287453825	8.749678396	8.082596154	uridylate kinase
ACD59563	9.075931007	8.994039404	10.04515898	ribosome recycling factor
ACD59564	7.351248455	7.70559092	6.289137289	undecaprenyl diphosphate synthase
ACD59565	8.26218413	8.469576701	8.192371729	phosphatidate cytidylyltransferase
ACD59566	7.691883072	7.752614804	7.389704467	1-deoxy-D-xylulose 5-phosphate reductoisomerase
ACD59567	7.917061725	8.128231527	7.112741829	membrane-associated Zn-dependent protease
ACD59568	7.916727422	7.972876425	7.869748051	outer membrane antigen
ACD59570	6.950480079	7.217162846	6.525713417	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase
ACD59571	7.487019996	7.27659902	7.343381171	beta-hydroxyacyl-(acyl-carrier-protein) dehydratase FabZ
ACD59572	7.259526726	7.265924413	6.709166545	acyl-[acyl-carrier-protein]--UDP-N-acetylglucosamine O-acyltransferase
ACD59573	6.938438711	6.901132384	6.571869419	lipid-A-disaccharide synthase
ACD59574	7.314043903	7.450204997	6.999819652	ribonuclease HII
ACD59575	7.26441445	7.179331897	6.755822279	DNA polymerase III, alpha subunit subfamily, putative
ACD59576	7.95247918	8.553533303	7.675300793	acetyl-CoA carboxylase, carboxyl transferase, alpha subunit
ACD59578	7.220716892	7.410620946	9.323421863	outer membrane receptor protein, mostly Fe transport
ACD59579	6.332783109	6.822946791	6.769507291	ABC transporter ATP-binding protein
ACD59580	7.163518859	7.082436487	7.45925127	membrane protein, putative
ACD59581	7.037876361	7.205656425	6.442573654	conserved hypothetical protein
ACD59582	6.172155446	6.826001812	6.806169364	transposase
ACD59583	7.659938825	7.237936504	6.779942553	hypothetical protein
ACD59585	7.023854133	7.650017748	7.564202852	conserved hypothetical protein
ACD59586	7.851986348	8.311512198	8.817421803	PHB depolymerase
ACD59587	7.978001091	7.313635864	7.708152741	conserved hypothetical protein
ACD59588	0	0	0	transposase
ACD59589	0	5.5987225	6.95575451	transposase
ACD59591	4.990696241	5.298874557	4.694083427	transposase
ACD59592	0	1.847872669	-0.130003868	ISXoo5 transposase
ACD59593	7.566175844	7.489647293	7.515944209	conserved hypothetical protein
ACD59597	7.626300409	7.468436694	7.46586838	conserved hypothetical protein
ACD59598	7.461487633	7.516157013	7.329204342	conserved hypothetical integral membrane protein
ACD59600	7.12361447	6.451122074	6.525799534	hypothetical protein
ACD59604	9.285101626	8.641444875	8.74130518	glyoxylase I family protein
ACD59605	9.106128431	9.669854136	8.865024893	conserved hypothetical protein
ACD59606	6.99304027	6.82315066	7.038523977	methionyl-tRNA synthetase
ACD59607	6.467111526	7.46479894	6.899381094	phosphotransferase
ACD59608	6.512947422	5.754470663	6.979522372	ferredoxin II
ACD59611	6.053309042	6.380852369	6.40959799	conserved hypothetical protein
ACD59612	8.189345228	8.180794335	9.261497907	conserved hypothetical protein
ACD59613	8.75217991	9.089482261	8.511301988	RNA polymerase sigma factor
ACD59614	8.349705846	8.788653088	7.755535234	conserved hypothetical protein
ACD59615	8.866558757	8.925815511	7.509711675	delta 9 acyl-lipid fatty acid desaturase
ACD59616	8.000495841	7.759235745	6.691436456	dehydrogenase
ACD59617	8.493687358	8.485740772	6.759395553	conserved hypothetical protein
ACD59618	8.369034553	8.350576805	7.279722	cyclopropane-fatty-acyl-phospholipid synthase
ACD59619	8.147484786	8.279424864	6.928121561	conserved hypothetical protein
ACD59620	7.818831392	8.057493596	6.729212857	membrane protein, putative
ACD59621	7.505390789	7.836738391	6.5449119	cyclopropane-fatty-acyl-phospholipid synthase
ACD59625	6.715055947	6.6794801	6.607103904	oxacillin resistance-associated protein fmtc
ACD59632	7.913410049	8.363157933	9.887184053	GTN Reductase
ACD59633	6.750405521	7.208614799	5.969647838	conserved hypothetical protein
ACD59635	7.208478242	7.420313963	7.147479698	cation transport protein
ACD59636	9.197042183	10.23149721	11.78141709	hypothetical protein
ACD59638	8.441251068	8.63956501	9.689884438	fkbp-type peptidyl-prolyl cis-trans isomerase slyd
ACD59639	7.718012213	7.45173863	7.233610091	heat shock protein
ACD59640	11.46509189	12.06747134	11.77911195	conserved hypothetical protein
ACD59643	0	0.997776537	-0.986336224	ISXo8 transposase
ACD59646	8.299862808	9.023299715	8.787794843	conserved hypothetical protein
ACD59649	8.389343094	7.860466259	8.042972583	protein of unknown function
ACD59650	6.440819347	6.455797355	5.88468827	leucine dehydrogenase

ACD59652	8.222881824	8.654166987	10.36464903	acetoacetyl-CoA thiolase
ACD59653	12.05829958	12.57563142	13.98384867	outer membrane protein
ACD59654	7.991476495	9.276296588	8.291359515	conserved hypothetical protein
ACD59655	5.983928457	5.785179107	6.159590842	Putative signal protein with CHASE3 and GGDEF domains
ACD59656	8.551423731	9.405530811	7.925679048	protein of unknown function
ACD59657	8.639470952	9.186574838	6.636106897	conserved hypothetical protein
ACD59658	7.193249362	7.537940538	6.838863549	mRNA 3'-end processing factor
ACD59659	6.302869188	6.960789695	7.043202311	conserved hypothetical protein
ACD59660	6.812318519	6.529674171	6.408232921	DNA ligase
ACD59661	7.152548509	7.012635712	6.996750279	ATP-dependent helicase
ACD59662	6.521694653	6.863703102	7.290700855	Ser/Thr protein phosphatase family protein
ACD59671	0	0	0	ISXo5 transposase
ACD59675	10.31710731	10.43160207	8.462608605	lipoprotein, putative
ACD59676	9.226734896	9.451903439	8.796948107	response regulator
ACD59686	7.349595281	7.713414011	7.56553625	fatty oxidation complex alpha subunit
ACD59694	6.94358147	7.534458526	6.58926313	transcriptional regulator
ACD59695	6.544626026	6.521027174	5.902059104	TonB-dependent receptor plug domain protein
ACD59696	7.548559927	6.974644026	7.673302008	TonB-dependent receptor
ACD59697	7.019279362	6.55210036	5.946539049	beta-galactosidase
ACD59698	10.64357664	9.621526275	0	hypothetical protein
ACD59701	9.004526673	8.664045443	9.44240031	hypothetical protein
ACD59703	9.051461832	9.576833877	7.529524258	DNA polymerase III alpha subunit
ACD59704	9.240657787	9.692979834	8.8175689	major facilitator superfamily protein
ACD59708	6.75919579	6.386169453	6.550380487	YceI like family
ACD59709	8.177105549	7.860484882	7.410646383	cytochrome B561
ACD59710	9.060971476	9.700526416	9.281253134	YceI like family
ACD59711	6.651898398	6.225941976	6.516905522	cold shock domain protein
ACD59713	7.81622849	7.402543125	7.311167034	L-serine ammonia-lyase
ACD59717	6.903255237	6.920972084	7.571494793	peptidase
ACD59718	7.30874857	7.461127428	7.05318738	peptide chain release factor 3
ACD59719	6.74970856	7.371358474	6.115241373	hemolysin III
ACD59720	8.761674222	8.206765306	8.679687692	AsmA family membrane protein
ACD59721	6.367516097	6.258336127	5.894405506	AsmA family membrane protein
ACD59722	10.30210195	9.551815907	10.20936807	isrso5-transposase protein
ACD59724	11.66826453	10.59382993	7.906902618	AsmA family membrane protein
ACD59728	9.431821417	9.590280141	10.10272374	chaperonin HslO
ACD59729	8.356020528	8.769196503	9.238232752	conserved hypothetical protein
ACD59730	9.258149064	9.217940739	9.573768354	TonB-dependent outer membrane Receptor
ACD59732	7.575387973	7.711818375	8.401587805	hydrolase, alpha/beta fold family, putative
ACD59733	7.735799696	7.792041916	8.412684157	acyl-coenzyme A dehydrogenase
ACD59736	7.462371391	7.920906601	8.29245048	beta-lactamase
AGS47850	5.76147145	5.680917855	7.271827157	ribonuclease HII fragment
ACD59738	7.056789427	7.822762009	6.687256693	IS1389 transposase
ACD59747	6.921591047	6.840777924	6.810584487	adenosylmethionine-8-amino-7-oxononanoate transaminase
ACD59748	6.806427177	6.893143751	6.155741139	conserved hypothetical protein
ACD59750	10.46715719	10.42641153	8.974291253	TonB-dependent receptor
ACD59751	7.676500146	7.794961648	6.052265895	alpha-L-fucosidase
ACD59752	7.783378074	8.165339168	5.968848774	glycosyl hydrolase, family 18
ACD59753	6.687662619	6.718087584	6.129179964	beta-hexosaminidase
ACD59754	6.820638509	6.528991627	5.931021119	beta-mannosidase
ACD59755	6.446408433	6.137796541	5.647685786	glucan 1,4-beta-glucosidase
ACD59759	0	0	0	hypothetical protein
ACD59765	7.805176354	8.108796243	6.555566177	conserved hypothetical protein
AGS47851	7.4134333	7.20513833	6.102500669	antigen
ACD59766	6.892548888	7.019924261	6.02888294	beta-galactosidase
ACD59768	9.218391289	9.869735715	10.67108988	conserved hypothetical protein
ACD59770	6.365164096	6.053411143	6.277049295	BNR/Asp-box repeat domain protein
ACD59771	7.794994128	7.658390023	8.322459991	leucin rich protein
ACD59775	6.053148272	5.857279376	5.967553675	von Willebrand factor type A domain protein
ACD59776	7.486722417	6.677818284	6.22342255	conserved hypothetical protein
ACD59777	7.749648231	7.325386415	7.665939875	hypothetical protein
ACD59778	10.97066675	0	8.687134193	translation initiation factor IF-2
ACD59779	2.015490433	0.995441102	1.607394235	ISXo8 transposase
ACD59784	9.383797158	11.34508917	10.14113642	hypothetical protein

ACD59789	6.856027059	7.110217062	6.779088962	glutathione synthase
ACD59790	6.380772731	7.25296813	6.512266399	TonB protein
ACD59796	7.112157978	7.321053196	6.580153024	glycosyltransferase
ACD59799	9.716003161	9.678976828	9.799995506	coenzyme PQQ biosynthesis protein B
ACD59800	9.228746554	9.002455	9.5465839	coenzyme PQQ biosynthesis protein C
ACD59801	8.238108526	7.828510997	8.192243491	bifunctional coenzyme PQQ synthesis protein C/D (Pyrroloquinolinequinone biosynthesis protein C/D)
ACD59802	7.508254327	7.08664579	6.572595644	coenzyme PQQ biosynthesis protein E
ACD59803	7.491965302	7.733896605	7.030589896	conserved hypothetical protein
ACD59804	6.970186438	6.720716243	6.833522636	PhoPQ-regulated protein
ACD59805	10.41872757	0	8.196956149	hypothetical protein
ACD59806	7.580039932	6.675293735	6.658568541	glucose kinase
ACD59808	7.561150448	7.465109241	7.266046267	glucose kinase
ACD59809	8.587312479	8.344122774	7.866561848	glucose kinase
ACD59810	7.376420628	6.798141264	6.814319697	TonB-dependent receptor
ACD59812	9.880434525	10.16839634	10.7221586	DNA-binding related protein
ACD59813	6.791241046	6.868945989	6.722575315	ATP-dependent DNA helicase RecQ
ACD59814	9.618082615	10.35547223	9.853181657	hypothetical protein
ACD59815	9.303977051	9.620179495	10.00229465	conserved hypothetical protein
ACD59816	8.604227034	9.270157475	9.256859701	response regulator
ACD59818	7.475717221	7.102763097	7.638696553	transposase
ACD59838	7.103896235	7.04187814	7.667019263	conserved hypothetical protein
ACD59841	9.466561868	7.743784223	9.331723128	hypothetical protein
ACD59842	7.702650618	7.573616894	7.121025765	transmembrane transport protein
ACD59843	6.960720204	6.452173687	7.365036331	Non-hemolytic phospholipase C
ACD59844	6.908644808	7.494983552	8.169388901	Non-hemolytic phospholipase C
ACD59845	6.709593923	6.569358932	5.871604658	phospholipase C
ACD59848	7.363258702	7.101692092	7.320168738	ISXoo3 transposase ORF A
ACD59849	0	0	0	transposase
ACD59850	6.527553635	6.672609203	6.155237189	DNA repair protein RadA
ACD59853	7.269538151	6.74359575	6.841356773	DNA mismatch repair protein MutS
ACD59854	0	0	0	conserved hypothetical protein
ACD59855	6.62892812	6.324925784	6.793804866	conserved hypothetical protein
ACD59857	0	0	0	ISXoo11 transposase
ACD59858	0	0	0	conserved hypothetical protein
ACD59859	5.192935842	4.879852773	5.251075227	Rhs element Vgr protein
ACD59861	6.344288805	5.738916421	6.632724803	conserved hypothetical protein
ACD59863	7.57145687	7.266739699	7.940624863	conserved hypothetical protein
ACD59866	10.17040081	9.922759805	10.96097933	transcriptional coactivator/pterin dehydratase
ACD59867	7.456477629	6.710544728	6.919471187	TonB protein
ACD59868	8.582699001	7.485475131	8.759165823	zinc transporter ZupT
ACD59869	6.169299698	5.726675934	6.765799923	zinc transporter ZupT
ACD59870	8.002455	8.454286954	10.95541743	conserved hypothetical protein
ACD59872	7.592315003	7.477653045	7.536037354	ribonuclease E
ACD59878	7.639514364	6.968182934	6.813268142	fkbp-type peptidyl-prolyl cis-trans isomerase
ACD59879	6.655409077	6.696494662	5.885222921	pyridine nucleotide-disulfide oxidoreductase
PXO_rna29	0	0	0	XO_rna29 cdna:pseudogene chromosome:GCA_000019585.1:Chromosome:3409594:3409677:1 gene:PXO_rna29 transcript:PXO_rna2
ACD59883	7.354522686	6.919447351	6.272245326	phosphopantetheinyl transferase
ACD59886	5.27003924	5.738021981	5.755995814	isrso17-ISXo8 transposase protein
ACD59888	0	0	0	ISXo8 transposase
ACD59890	8.154934532	8.026324246	7.390125954	ISXoo6 transposase
ACD59892	0	0	0	ISXo8 transposase
ACD59896	0	4.654716216	1.229403344	ISXo2 putative transposase
ACD59902	6.647242546	6.625079033	6.168102448	siroheme synthase
ACD59903	7.897077024	7.771872377	7.49255023	FAD containing monooxygenase
ACD59904	8.56708145	8.077381877	7.850586923	FAD containing monooxygenase
ACD59905	6.181082668	6.87296416	7.130755875	short chain dehydrogenase
ACD59913	7.744706041	7.274112538	6.619807673	conserved hypothetical protein
ACD59914	8.014505938	8.141008659	7.708518345	hypothetical protein
ACD59916	0	0	0	ISXo5 transposase
ACD59917	10.76957341	8.67116597	10.43642006	putative lipoprotein
ACD59921	8.701302996	9.042895999	7.496973581	hypothetical protein
ACD59929	0	0	0	hypothetical protein

ACD59930	0	0	0	hypothetical protein
ACD59932	8.955655719	8.176322773	9.97272137	hypothetical protein
ACD59933	9.942713888	9.394824931	9.638995144	hypothetical protein
ACD59934	7.070163889	7.004849664	8.191375117	peptidase
ACD59947	0	7.862562974	10.96275144	hypothetical protein
ACD59948	7.130920577	6.831167877	7.559629468	transcriptional regulator
ACD59950	7.862284001	8.028519426	6.895641925	signal recognition particle-docking protein FtsY
ACD59951	6.632426729	6.408971645	6.104707771	A/G-specific adenine glycosylase
ACD59952	9.027115338	8.946102117	8.977460249	Fe(II) trafficking protein YggX
ACD59953	6.81271641	7.389231222	7.678755051	hypothetical protein
ACD59956	10.84740975	11.07864452	9.534374869	hypothetical protein
ACD59957	10.56891565	10.87011038	10.91293423	conserved hypothetical protein
ACD59958	6.971899873	7.116011193	6.565559097	transposase
ACD59959	8.020929951	7.473592115	5.979997872	conserved hypothetical protein
ACD59960	0	9.9261403	8.83810087	conserved hypothetical protein
ACD59962	11.4415644	11.26360372	11.83095484	hypothetical protein
ACD59965	9.224250144	9.04089517	9.59411369	hypothetical protein
ACD59968	7.896744111	7.59273359	8.526647902	conserved hypothetical protein
ACD59969	8.184389405	8.120673342	8.651937851	hypothetical protein
ACD59972	9.929854599	7.80886767	10.34027295	hypothetical protein
ACD59985	10.01934053	9.712121132	8.274042631	hypothetical protein
ACD59997	8.119589621	10.6123525	8.500718414	transcriptional regulator, LacI family
ACD59999	9.116336163	6.696021643	7.238156307	conserved domain protein
ACD60000	10.43372105	9.557992051	9.453764482	transposase
ACD60001	7.842111446	7.90542311	6.999312302	transposase
ACD60006	9.261389773	8.065976139	9.388019439	fimbrial biogenesis protein
ACD60012	0	0	0	conserved hypothetical protein
ACD60017	5.787004022	5.522667835	5.667968742	phage capsid scaffolding protein (GPO)
ACD60018	6.55527627	5.660275488	6.255959528	phage major capsid protein, P2 family
ACD60019	5.5127926	5.6178891	5.822623089	phage-related terminase
ACD60020	7.110029093	7.125702755	7.610264507	phage head completion protein (GPL)
ACD60021	8.737801664	8.024773996	8.035898787	phage Tail Protein X
ACD60022	7.258773296	7.447951062	7.226961228	phage-related protein
ACD60023	0	0	0	phage-related protein
ACD60024	6.939520448	6.38777093	5.497663456	phage-related lytic enzyme
ACD60025	8.381006437	7.685267407	8.165575338	lipoprotein, putative
ACD60026	7.16103108	6.707883653	6.554381641	P2 phage tail completion protein R (GpR)
ACD60027	7.356064558	6.878026382	7.899598611	phage virion morphogenesis protein
ACD60028	8.872822605	9.405205298	9.424844427	conserved hypothetical protein
ACD60029	7.305031151	6.457495798	7.378702352	phage-related baseplate assembly protein
ACD60030	7.185787274	6.99354983	7.797441052	phage tail protein I
ACD60031	7.042688108	6.483356298	6.279764708	phage-related protein
ACD60032	7.931275292	7.806491623	8.332143991	probable tail fiber assembly protein, putative
ACD60033	6.853122383	5.455593539	6.189510294	phage-related baseplate protein
ACD60034	7.773805166	7.461757728	8.768875726	phage-related baseplate protein
ACD60035	5.187898363	4.507306261	5.480924268	phage tail sheath protein
ACD60036	8.158200677	7.578048072	8.574911358	phage major tail tube protein
ACD60037	0	0	0	phage tail protein E
ACD60038	0	0	9.031659854	phage tail protein, P2 GpE family
ACD60039	4.905952539	4.21130818	5.355696421	phage-related tail protein
ACD60040	0	0	0	gpU
ACD60041	0	0	0	bacteriophage P2 gpD protein
ACD60044	0	0	0	hypothetical protein
ACD60045	0	0	0	N-acetylglucosamine-6-phosphate deacetylase
ACD60046	0	0	0	conserved hypothetical protein
ACD60047	0	0	0	phage-related protein
ACD60048	0	0	0	hypothetical protein
ACD60049	0	0	0	conserved hypothetical protein
ACD60050	0	0	0	conserved hypothetical protein
ACD60051	0	0	0	conserved hypothetical protein
ACD60052	0	0	0	conserved hypothetical protein
ACD60053	0	0	0	conserved hypothetical protein
ACD60054	0	0	0	conserved hypothetical protein
ACD60055	0	0	0	site-specific recombinase, phage integrase family

ACD60067	7.942344422	7.938891493	7.441915002	superoxide dismutase
ACD60070	8.481214164	8.53485145	8.451709786	conserved hypothetical protein
ACD60071	6.846919492	6.716812604	6.001914808	nicotinate-nucleotide pyrophosphorylase
ACD60072	6.79956657	6.586856297	5.925588856	conserved hypothetical protein
ACD60096	7.020079883	7.227789201	7.476462699	dehydrogenase
ACD60106	9.306373898	10.57942909	10.88193222	hypothetical protein
ACD60112	6.356907926	6.616897254	6.968413363	transcriptional regulator
ACD60118	5.342512078	6.936732153	6.966049716	2-ketoacid dehydrogenase\x3b malate dehydrogenase\x3b lactate dehydrogenase
ACD60123	8.02683325	8.218384023	8.335131272	SCO1/SenC superfamily
ACD60124	6.677592806	6.680042993	6.238857541	phosphatidylserine decarboxylase
ACD60126	10.17785552	10.11441908	9.561045407	cath1
ACD60127	5.379343707	7.098337439	6.442484082	conserved hypothetical protein
ACD60130	6.623291858	6.620196361	5.962678573	transcription elongation factor GreB
ACD60132	8.36744533	8.164228147	7.279201972	carboxymethylenebutenolidase
ACD60133	8.052932075	8.053877022	6.926888964	diadenosine tetraphosphate hydrolase and other HIT family hydrolase
ACD60134	12.13055769	12.92810009	12.59213931	conserved hypothetical protein
ACD60135	9.953028011	10.0259147	9.807483728	conserved hypothetical protein
ACD60139	6.16256857	6.344056179	6.522766686	metallopeptidase
ACD60149	9.060398717	9.071250501	9.967255084	lipoprotein
ACD60150	8.593518112	9.143196965	6.52166482	outer membrane lipoprotein
ACD60151	9.009419959	9.011825458	8.9203201	hypothetical protein
ACD60156	8.170766328	8.386910077	8.699551633	alkaline phosphatase, placental type
ACD60157	6.701341121	6.592918925	6.234957264	tRNA(Ile)-lysidine synthase (tRNA(Ile)-lysidinesynthetase) (tRNA(Ile)-2-lysyl-cytidine synthase)
ACD60158	7.871313873	7.768257119	8.366247892	exodeoxyribonuclease VII, small subunit
ACD60159	7.066229147	7.143179105	5.650956944	polyprenyl synthetase ,gene\x3a ispa or
ACD60160	12.21770632	11.32849542	11.55747806	hypothetical protein
ACD60161	7.567385727	6.91353571	7.151706634	extracellular protease
ACD60165	8.828260274	8.997532348	9.560292706	conserved hypothetical protein
ACD60168	7.939849511	6.960592795	8.320814085	conserved hypothetical protein
ACD60172	7.007677665	7.662191255	8.354434529	outer membrane protein
ACD60173	3.573507834	3.203991994	2.695486109	ISXo3 transposase ORF B
ACD60174	7.447562667	6.939861262	10.18856412	TonB-dependent Receptor/Oar-like
ACD60175	7.989593185	7.990722332	8.556122818	TonB family C-terminal domain protein
ACD60177	10.24987194	10.32996447	11.04185077	conserved hypothetical protein
ACD60185	6.918386234	6.756089247	6.901277224	thioredoxin
ACD60186	7.792133043	7.480628659	7.270827916	lipoprotein, putative
ACD60191	9.181964709	8.293195729	7.925061837	conserved hypothetical protein
ACD60192	7.112637587	6.932781677	6.359691588	peptidyl-prolyl cis-trans isomerase
ACD60200	6.640752502	6.201179027	5.788724857	glycogen debranching enzyme GlgX
ACD60202	0	0	0	ISXo5 transposase
ACD60203	8.854572336	10.64591957	11.51672434	transposase
ACD60211	6.412727339	5.670021678	4.977467691	transposase
ACD60213	7.186866969	6.44458425	6.629366821	conserved hypothetical protein
ACD60214	7.551016063	5.937391477	6.007785289	transposase
ACD60215	5.702139432	6.157508629	5.647855563	transposase
ACD60217	10.12921861	10.42194909	9.880711541	thiamine biosynthesis protein ThiS
ACD60218	8.159386994	8.448599532	8.82314429	thiazole biosynthesis protein ThiG
ACD60219	7.192243491	6.860404179	6.235893603	tRNA (guanine-N(7)-)-methyltransferase
ACD60220	7.090916928	7.155941455	6.298366888	sulfur deprivation response regulator
ACD60222	11.48500913	11.99776166	9.564578233	conserved hypothetical protein
ACD60223	4.754834068	5.312015263	5.44290038	putative ISXoo4 transposase
ACD60226	7.285254243	7.45852145	7.733998257	fumarylacetoacetate hydrolase
ACD60227	8.650689177	9.556427499	8.810732282	large conductance mechanosensitive channel protein
ACD60230	10.87121221	0	10.36385003	hypothetical protein
ACD60231	5.649678683	5.624606861	5.798662312	putative transposase
ACD60238	7.62118008	6.247564896	6.455828583	conserved hypothetical protein
ACD60246	6.26387761	6.551186836	5.517124486	sulfite reductase [NADPH] flavoprotein, alpha-component
ACD60247	6.934245204	6.731427653	5.804502782	sulfite reductase (NADPH) hemoprotein, beta-component
ACD60248	7.734465764	8.045006042	6.751396769	phosphoadenosine phosphosulfate reductase
ACD60252	7.430134706	7.594205152	7.251368789	sensor histidine kinase
ACD60255	6.9721412	7.017120188	6.661564349	siroheme synthase
ACD60256	7.330459803	7.187935962	7.06714391	cysteine synthase A
ACD60257	12.49080325	12.63613065	11.57750908	conserved hypothetical protein

ACD60258	14.10542567	14.2045253	13.20241925	hypothetical protein
ACD60259	7.632457266	8.58866592	8.768869111	appr-1-p processing
ACD60266	8.908650812	9.333689831	8.327974725	hypothetical protein
ACD60268	9.02471306	9.930774291	9.413071475	morphine 6-dehydrogenase (Naloxone reductase)
ACD60269	9.512294057	9.47623383	7.869279207	catalase
ACD60270	6.883510851	6.771238544	5.940317121	conserved hypothetical protein
ACD60274	9.743080689	10.36584124	11.15814891	hypothetical protein
ACD60277	6.549815466	7.003725904	6.91858898	transposase
ACD60280	7.827641217	5.259600164	6.219213059	hypothetical protein
ACD60282	7.269846678	6.714204297	8.639630123	lipoprotein, putative
ACD60283	7.13137341	6.363395385	7.05940936	endoproteinase Arg-C
ACD60286	10.38743578	7.891279431	8.340059268	hypothetical protein
ACD60290	9.589042484	9.188598736	9.219529149	putative addiction module antidote
ACD60291	9.252407616	8.364594318	9.432942709	death-on-curing protein
ACD60295	7.966799585	7.82156354	6.544496205	transcriptional regulator uid family
ACD60299	6.647760605	5.743531125	6.460013498	serine/threonine kinase
ACD60310	7.050469047	6.907094963	6.695743323	type I restriction enzyme EcoKI R protein
ACD60311	7.709063129	7.260759617	7.834641698	abortive infection bacteriophage resistance protein
ACD60312	7.506129031	7.101219338	7.929489221	type I restriction enzyme EcoKI M protein
ACD60313	0	0	0	type I restriction-modification system, S subunit
ACD60316	7.05382816	7.319464394	7.238309193	Rhs element Vgr protein
ACD60334	9.308614345	9.859390354	8.008041984	lipoprotein, putative
ACD60335	8.754122537	8.782765656	7.840683524	conserved hypothetical protein
ACD60336	9.092413601	9.358583075	9.016301306	conserved hypothetical protein
ACD60337	6.588594718	6.894175075	5.945146488	Rhs element Vgr protein
ACD60338	0	0	0	EF hand domain protein
ACD60339	6.355331714	6.073770972	6.607916151	Rhs element Vgr protein
ACD60340	0	0	0	conserved hypothetical protein
ACD60341	3.509151087	4.759464797	3.526707363	Rhs element Vgr protein
ACD60351	7.5538059	7.428619793	6.976890572	carbon starvation protein A
ACD60352	9.298754529	8.573764567	8.908482693	conserved domain protein
ACD60357	7.270024285	6.980665137	7.067316036	Putative signal protein with GGDEF domain
ACD60359	7.325791144	7.455524498	7.069197324	polyprenyl synthetase , gene\x3a ispb or
ACD60366	8.702650618	9.111018267	10.4639943	phenazine biosynthesis PhzF family protein
ACD60373	11.12707865	11.10917117	9.042272235	conserved hypothetical protein
ACD60374	11.48649316	10.87511194	10.69696753	hypothetical protein
ACD60375	7.510938191	7.385663989	6.928382168	DNA-3-methyladenine glycosylase I
ACD60376	10.19288457	9.823238252	10.08679969	conserved hypothetical protein
ACD60380	6.486510052	6.352984458	5.869691305	conserved hypothetical protein
ACD60381	6.574457293	6.745223884	5.775232316	pyrroline-5-carboxylate reductase
ACD60382	0	2.880848101	2.188926251	isrso17-transposase protein
ACD60383	4.894900201	4.541694484	3.105646234	ISXo8 transposase
ACD60384	9.937250218	11.16795122	10.6381191	bacterial DNA-binding protein
ACD60385	7.415657274	7.584970015	7.53239489	peptidase
ACD60386	8.939229517	9.102335315	9.383388938	conserved hypothetical protein
ACD60387	9.608077362	10.16255498	9.428944252	conserved hypothetical protein
ACD60388	8.572404647	8.977737849	9.730188194	conserved hypothetical protein
ACD60392	8.543426283	8.903716182	7.45479279	Rrf2 family protein
ACD60393	8.047941844	8.088290032	7.884683386	FeS assembly protein SufB
ACD60394	8.076238404	7.96953618	7.605531373	FeS assembly ATPase SufC
ACD60395	7.34394962	7.252665432	6.254697964	FeS assembly protein SufD
ACD60396	7.601629668	7.420970763	6.733001759	cysteine desulfurase
ACD60397	7.781149852	7.679043706	7.205822567	acetyltransferase
ACD60398	7.100105125	6.937238446	6.124069601	benzene 1,2-dioxygenase ferredoxin protein
ACD60400	6.179769789	4.815027142	5.518277042	ISXo8 transposase
ACD60401	0	0	0	IS66 family element, Orf1 protein
ACD60402	6.768488715	6.58697786	6.553911854	transposase
ACD60404	0	0	5.077409651	conserved domain protein
ACD60405	0	0	0	ISXo2 putative transposase
ACD60406	10.41357504	10.67259329	8.138814469	putative serine-pyruvate aminotransferase
ACD60407	9.761266987	10.0197575	7.640779972	O-acetylhomoserine sulfhydrylase , gene\x3a MetY
ACD60408	8.426575069	8.651105522	7.549053029	glutamine synthetase family protein
ACD60411	6.416404031	6.29304303	6.3565893	transposase
ACD60413	6.035161997	5.836578089	5.822806614	transposase

ACD60414	0	0	1.921497267	transposase (IS4 family)
ACD60420	7.381672723	7.979676698	9.350232021	HrpG
ACD60424	10.49877941	0	10.82954833	hypothetical protein
ACD60425	8.51101333	8.169779723	8.602019572	transcriptional regulator, LysR family
ACD60428	6.655695287	6.403715938	6.719073892	TonB-dependent outer membrane receptor
ACD60429	7.438084884	7.423107504	7.930867411	glyoxalase family protein
ACD60430	7.000067625	6.815959618	6.045379624	TonB-dependent outer membrane receptor
ACD60431	7.709662843	7.650994269	8.298534604	TonB-dependent outer membrane Receptor
ACD60433	8.187005587	7.925417952	8.205583121	cation\x3aproton antiporter
ACD60435	6.376948435	6.890446693	5.624589316	4-hydroxy-2-oxovalerate aldolase
ACD60436	7.554796032	7.462543171	7.69309661	TonB-dependent outer membrane Receptor
ACD60437	8.043590577	8.075516587	7.70938025	vibrioferrin biosynthesis protein PvsA
ACD60438	7.725747972	7.540244302	7.446603626	vibrioferrin biosynthesis protein PvsB
ACD60439	7.256652164	7.556912175	7.611570778	transport protein
ACD60440	7.478114344	7.61007991	7.167096954	iron transporter
ACD60441	7.642484978	7.220426699	7.355007452	diaminopimelate decarboxylase
ACD60450	9.153754679	9.087133954	8.274336217	hypothetical protein
ACD60451	0	0	-0.882480485	ISXo8 transposase
ACD60457	2.170319284	3.813750413	0	transposase
ACD60460	7.478599762	6.664710377	8.005978163	conserved hypothetical protein
ACD60461	8.210554462	8.682524139	7.600953587	glutathione transferase
ACD60466	7.781162969	7.558573776	7.722493348	multi antimicrobial extrusion family protein
ACD60477	7.614577346	7.50989374	6.625472149	putative cytochrome C assembly protein
ACD60479	6.712403188	6.357127931	7.586066641	alpha-N-arabinofuranosidase 2
ACD60481	9.938157856	9.26462791	9.558068607	conserved domain protein
ACD60483	8.907596742	8.36046963	7.99983656	transposase
ACD60485	8.964511266	8.242435782	8.415205146	conserved domain protein
ACD60486	6.346552736	5.831294575	5.198230893	ISPsy21, transposase OrfB
ACD60487	9.632190043	8.953073131	9.980482356	transposase
ACD60489	6.700189999	6.337461346	6.198910558	succinyl-diaminopimelate desuccinylase
ACD60491	9.341752304	9.045535801	10.11125306	transglycosylase-associated protein
ACD60492	6.691073479	6.884243797	6.485521823	aminoglycoside phosphotransferase
ACD60493	6.5153198	7.098411136	6.073987282	nucleotidyl transferase
ACD60497	7.603188649	7.991119309	8.257109649	phosphoribosylformylglycinamidine cyclo-ligase
ACD60498	7.169955057	7.30088332	6.271024083	conserved hypothetical protein
ACD60499	6.761910199	6.440639979	6.35338152	membrane protein, putative
ACD60500	6.918672455	6.87280414	5.947511875	phosphoribosylglycinamide formyltransferase
ACD60501	6.923624611	6.442084256	8.406353839	conserved hypothetical protein
ACD60502	7.062963557	7.409866099	8.560558297	conserved hypothetical protein
ACD60506	7.16537937	6.962618426	9.119690768	arabinose 5-phosphate isomerase
ACD60507	7.579210325	7.770908313	9.105803772	phosphatase, YrbI family
ACD60508	7.784294578	7.503825738	8.169960067	conserved hypothetical protein
ACD60509	8.279907678	8.583428822	9.175507136	conserved hypothetical protein
ACD60510	7.378459602	7.208985389	7.63784206	ABC transporter ATP-binding protein
ACD60511	7.052774523	7.192421048	6.496219451	RNA polymerase sigma-54 factor
ACD60512	10.82476785	11.10802126	10.16154762	ribosomal subunit interface protein
ACD60513	7.90032947	8.507061216	8.499606747	nitrogen regulatory IIA protein
ACD60514	8.112830428	8.274513272	8.029375581	HPr kinase/phosphorylase (HPrK/P) (HPr(Ser)kinase/phosphorylase)
ACD60515	7.591799078	7.577459041	6.6877186	conserved hypothetical protein
ACD60516	10.70791988	10.25901349	8.029988386	hypothetical protein
ACD60517	8.124028232	8.160824411	7.144841754	sugar transport protein
ACD60518	7.926349372	7.669983425	6.522371241	phosphotransferase system HPr enzyme
ACD60519	7.432115919	7.481355457	6.65696823	phosphoenolpyruvate-protein phosphotransferase
ACD60521	6.855242251	6.607191216	6.691227057	magnesium transporter
ACD60522	7.061948965	6.926319718	8.061349589	phospholipase/carboxylesterase superfamily
ACD60530	7.572950285	7.429599228	6.600666714	amino acid transporter
ACD60531	11.30123324	11.28618231	10.43944653	hypothetical protein
ACD60532	9.661172395	9.880931891	8.734591084	endoproteinase Arg-C
ACD60534	7.180247337	6.1784836	6.953661018	conserved hypothetical protein
ACD60535	6.91353571	6.546198404	5.955849808	hydrolase
ACD60539	8.500479418	6.609645645	6.444998287	putative anaerobic transcriptional regulatory protein
ACD60552	7.880942602	8.41460068	7.714630185	shikimate kinase
ACD60553	7.057331126	7.395979621	7.605331352	3-dehydroquinate synthase
ACD60554	10.62703223	11.55584012	13.41098127	conserved hypothetical protein

ACD60555	7.013138399	7.328118384	8.447380829	uroporphyrinogen decarboxylase
ACD60557	3.17754631	3.492404421	3.537581844	Tal9a, TAL effector AvrBs3/PthA
ACD60559	8.185212428	7.421349551	8.672138896	filamentous phage phiLf related protein
ACD60561	5.780651308	5.800648862	5.990757497	Tal9b, TAL effector AvrBs3/PthA
ACD60562	8.702051445	0	8.44001783	probable transmembrane protein
ACD60565	5.269990634	4.962002935	5.561436122	Tal9c, also AvrXa27, TAL effector AvrBs3/PthA
ACD60566	8.872542531	9.359035722	7.816426911	Chloride channel protein EriC
ACD60569	5.791347854	5.350430061	5.32886518	Tal9d, TAL effector AvrBs3/PthA
ACD60570	10.2564446	0	10.65860424	similar to membrane-bound transport protein
ACD60573	4.995778455	5.171154775	5.036463771	Tal9e, TAL effector AvrBs3/PthA
ACD60575	1.792318145	0	0.317280911	transposase
ACD60576	4.972426144	2.401037868	4.957519985	transposase
ACD60578	6.713929464	6.561326136	7.10431569	glutamate-1-semialdehyde-2,1-aminomutase
ACD60579	9.971241763	9.619480874	9.777953887	hypothetical protein
ACD60580	0	9.946915045	9.773709577	hypothetical protein
ACD60585	6.521198392	7.194382591	6.525069725	hypothetical protein
ACD60586	6.916201933	7.054685709	6.321013497	hydrolase
ACD60588	7.157165008	6.599334161	5.924221056	ion transporter
ACD60594	7.762574717	7.795370848	6.302448836	PAP2 superfamily protein
ACD60595	0	0	0	ISXoo6 transposase
ACD60597	7.120465994	7.387517639	6.332143991	ribosomal protein S6 modification protein
ACD60598	7.903098542	8.078385677	8.500343969	two-component system regulatory protein
ACD60600	7.794539335	8.136155491	7.522644298	two-component system sensor protein
ACD60606	8.653196195	0	6.884036167	hypothetical protein
ACD60610	7.492998782	7.268247232	6.983882867	endonuclease
ACD60611	7.805621359	7.452686029	6.841809624	beta-lactamase
ACD60612	6.534167459	7.085297174	6.319363229	molybdate ABC transporter, periplasmic molybdate-binding protein
ACD60613	7.429138892	7.274997733	6.840966704	molybdate ABC transporter, permease protein
ACD60614	7.38025325	7.396750328	6.220742039	molybdenum import ATP-binding protein ModC
ACD60627	6.691450415	6.341631788	6.815319246	conserved hypothetical protein
ACD60628	6.601778215	6.072588191	7.787504294	TonB-dependent receptor
ACD60630	6.221239093	6.253197003	6.375214978	ErfK/YbiS/YcfS/YnhG
ACD60631	7.493407164	7.318569924	7.122558839	M23 peptidase domain protein
ACD60641	7.829526135	7.072609626	7.66254733	transposase
ACD60642	6.886281873	6.327953175	7.220649185	ISXoo2 transposase
ACD60648	7.436528331	7.608210459	7.036041703	penicillin-binding protein 1A (PBP-1a) (PBP1a)
ACD60649	6.709442287	7.483598148	7.250611086	conserved hypothetical protein
ACD60660	7.591679417	7.366663175	6.965680407	ribonuclease PH
ACD60661	7.34807304	7.68552673	6.947409011	glyoxalase family protein
ACD60662	7.725175363	7.457003225	6.555394387	non-canonical purine NTP pyrophosphatase, RdgB/HAM1 family
ACD60663	7.129468494	7.01278095	6.300129217	putative oxygen-independent coproporphyrinogen III oxidase
ACD60664	6.683710488	6.850174333	6.327757414	conserved hypothetical protein
ACD60665	7.921840937	8.33487661	7.231499611	type IV pilus assembly protein PilZ
ACD60666	7.068821263	6.900673631	7.232161866	Xaa-Pro dipeptidase
ACD60667	10.21996711	9.968306794	10.16827097	conserved hypothetical protein
ACD60668	8.916981141	0	9.388906314	conserved hypothetical protein
ACD60671	9.628789996	9.80917003	10.41464296	conserved hypothetical protein
ACD60672	10.15100385	10.31227036	10.41263335	conserved hypothetical protein
ACD60673	7.077969292	7.50719207	7.46828191	5,10-methenyltetrahydrofolate synthetase
ACD60674	6.489892906	6.899199804	6.914719978	conserved hypothetical protein
ACD60675	8.749433705	9.022745084	8.572772217	ribose 5-phosphate isomerase A
ACD60676	10.42563554	10.90792716	10.05597379	conserved hypothetical protein
ACD60677	9.155850406	9.425473991	9.863264817	tetratricopeptide repeat domain protein
ACD60679	8.604078739	9.15533688	9.31439971	thiamine-phosphate pyrophosphorylase
ACD60680	0	8.537160148	0	transposase
ACD60681	5.055004717	4.652297183	6.121902303	ISPsy21, transposase OrfB
ACD60684	7.744927996	9.922026839	7.600849546	alpha-1,2-mannosidase
ACD60687	8.080359203	8.575573281	9.143036211	polyphosphate-selective porin O
ACD60688	6.379575912	6.305695157	6.06945299	sensor histidine kinase
ACD60689	6.735603408	6.661949074	6.666373148	citrate carrier protein
ACD60690	6.424734015	5.793050509	6.04100856	extracellular solute-binding protein, family 1
ACD60692	6.66392807	5.77173507	6.057549914	rhizopine catabolism protein MocA
ACD60693	7.194727311	6.235382426	7.383306849	conserved hypothetical protein
ACD60698	8.064936728	8.333052457	6.389038438	porin O

ACD60699	7.731963856	7.882905889	6.637558083	Mg++/citrate complex transporter
ACD60700	7.50698587	7.925673114	5.68898878	acetoacetyl-CoA reductase
ACD60701	7.42832667	7.497532533	6.679972643	transcriptional regulator
ACD60703	7.80042755	7.56968855	6.398536784	TonB-dependent receptor
ACD60704	7.905844262	7.876142411	6.373707365	alpha-amlyase
ACD60708	8.871335438	8.980933556	8.16521353	aspartate aminotransferase
ACD60709	7.214668823	7.101954667	5.998608481	conserved hypothetical protein, putative
ACD60710	7.046327346	6.994183698	6.55168058	conserved hypothetical protein
ACD60712	9.11046765	9.152294984	10.69004164	putative glutaredoxin homolog, putative
ACD60715	9.13225294	8.923181871	7.857788208	conserved hypothetical protein
ACD60716	9.191631736	9.902414309	9.165967194	conserved hypothetical protein
ACD60717	8.912344481	9.968652395	7.136375978	conserved hypothetical protein
ACD60718	6.688054439	6.944612511	7.727314668	rhamnogalacturonase B
ACD60725	6.714602712	6.72583657	6.056951958	methanol dehydrogenase regulator
ACD60726	6.490454608	6.520118905	6.107564432	protein of unknown function
ACD60727	6.910636735	6.728940868	5.902104942	membrane protein, putative
ACD60728	9.286881148	9.805363402	11.87954496	outer membrane protein Slp
ACD60733	11.12236212	11.49852514	10.97432137	hypothetical protein
PXO_rna37	0	0	0	XO_rna37 cdna:pseudogene chromosome:GCA_000019585.1:Chromosome:4294922:4295014:1 gene:PXO_rna37 transcript:PXO_rna3
ACD60741	7.72354491	7.581735372	8.004074363	heptosyl transferase, glycosyltransferase family 9 protein
ACD60743	6.371236485	6.09848904	6.061577489	integrase
ACD60750	0	0	8.755221421	hypothetical protein
ACD60757	7.014433407	7.431748304	7.406502657	protein phosphatase
ACD60761	10.60924339	11.53737373	8.727971492	hydroxyacylglutathione hydrolase
ACD60762	8.526115774	8.943827581	7.820715086	murein hydrolase D
ACD60763	11.42179134	10.03190793	11.7608904	hypothetical protein
ACD60774	8.634752978	8.944659359	8.539848968	membrane protein, putative
ACD60776	4.425325019	3.73684296	4.138830848	ISXo5 transposase
ACD60780	6.750847648	6.952648073	7.211314022	protease
ACD60781	6.910828583	7.611792063	8.599990924	phosphate regulon transcriptional regulatory protein PhoB
ACD60782	6.753310363	6.960986569	6.316362999	two-component system sensor protein
ACD60784	7.510677149	7.25016575	7.046065366	polyphosphate kinase
ACD60785	6.406898863	6.939684988	6.301966195	exopolyphosphatase
ACD60786	7.194313638	6.579202781	11.98721071	glycosyl transferase
ACD60787	7.164293525	7.278802538	11.38565213	PAP2 superfamily, putative
ACD60788	11.64239021	0	12.19126592	hypothetical protein
ACD60789	7.250099412	7.513245959	7.719984259	UDP-2,3-diacylglucosamine hydrolase
ACD60790	8.811076008	9.805698737	9.592210338	hypothetical protein
ACD60799	10.01159068	9.994254425	10.17968521	hypothetical protein
ACD60803	6.601672749	6.159051895	6.127979881	TonB-dependent receptor
ACD60804	7.761478099	8.129993884	8.152061702	L-threonine 3-dehydrogenase
ACD60810	6.294701611	6.318546425	6.774931981	2-amino-3-ketobutyrate coenzyme A ligase
ACD60811	7.553598578	7.20982374	6.470128467	HNH endonuclease domain protein
ACD60815	7.466178451	7.456822573	7.334550399	oxidoreductase
ACD60816	6.237248209	6.646421904	6.548407339	2,4-dienoyl-CoA reductase
ACD60817	6.812600905	6.908740867	6.127352637	membrane protein, putative
ACD60819	0	0	0	transposase
ACD60820	5.075143239	5.440134971	4.198116929	ISXoo3 transposase ORF B
ACD60821	6.889437037	6.263453253	5.735906628	glycerophosphodiester phosphodiesterase
ACD60823	4.988184769	5.047403152	4.081092453	ISXoo11 transposase
ACD60824	9.179476217	8.472154678	7.962213527	glycerophosphodiester phosphodiesterase
ACD60826	8.364204708	8.571119311	7.864012763	cell Wall Hydrolase superfamily
ACD60828	0	0	-1.083003697	ISXo8 transposase
ACD60830	7.645644023	7.144525692	7.738727311	glutathione S-transferase GST-4.5
ACD60833	8.736033177	9.092278806	9.408862558	GTP-binding protein TypA
ACD60834	7.865745641	8.227837324	8.026661758	putative membrane protein
ACD60835	7.611548648	6.436505012	6.937073626	glu-trnAgln amidotransferase a subunit
ACD60838	9.62153177	9.624223381	10.47123828	TonB-dependent outer membrane Receptor
ACD60840	6.531531181	6.723367427	9.209041456	transposase
ACD60841	0	4.090472387	3.123778747	ISXoo3 transposase ORF A
ACD60842	0	0	0	transposase
ACD60843	7.54525024	9.028453122	7.992915683	transposase

ACD60844	0	0	2.243638618	transposase
ACD60845	9.015624123	8.647800172	9.530732102	transposase (IS4 family)
ACD60862	0.962719286	0	0.551136991	ISXo5 transposase
ACD60863	8.551435268	7.787778521	10.77784707	conserved hypothetical protein
ACD60866	5.536481914	5.1769251	4.799791899	ISXoo8 transposase
ACD60874	7.150427667	7.102952015	7.373308898	6-phosphofructokinase
ACD60875	4.253043795	0	3.272305428	ISXo8 transposase
ACD60880	8.448335223	9.43998252	10.17530004	inorganic pyrophosphatase
ACD60881	9.394252599	9.872887229	9.065857695	response regulator
ACD60887	8.755421735	9.078388346	10.62435682	ketol-acid reductoisomerase
ACD60888	7.839600632	8.204742301	8.27714324	acetolactate synthase, large subunit, biosynthetic type
ACD60889	8.797466992	8.899698295	7.839997367	acetolactate synthase isozyme II small subunit
ACD60890	8.186084518	8.493483222	7.728117791	threonine dehydratase
ACD60891	8.574809206	8.786354586	8.979911014	2-isopropylmalate synthase
ACD60892	10.55294762	11.46189889	10.29817715	Urease accessory protein UreD
ACD60897	7.065970755	6.583162518	6.085312048	transcriptional regulator LysR family
ACD60899	0	1.552229498	-0.453994082	ISXo5 transposase
ACD60902	8.899081954	8.990693972	8.7826379	transcriptional regulator
ACD60903	8.778658691	8.769110529	9.43995344	L-isoaspartate protein carboxylmethyltransferase
ACD60904	7.613877846	7.53806474	7.57027317	outer membrane protein required for AvrXa21 activity C (raxC)
ACD60906	6.973197968	6.87541148	6.227076787	lipid A biosynthesis lauroyl acyltransferase
ACD60912	8.565357265	8.045415667	7.76897825	transposase
ACD60913	6.990886807	6.767191303	6.346221175	IS1595 transposase
ACD60922	6.947034898	5.573423003	6.501085594	peroxiredoxin
ACD60923	6.33189507	6.01822689	7.080241933	bacterioferritin
ACD60938	10.98630427	9.840600132	11.80642476	hypothetical protein
ACD60939	11.7989618	11.1857241	10.52931342	hypothetical protein
ACD60941	8.385836522	8.676873858	8.665044506	hypothetical protein
ACD60943	0	8.532223437	8.42769416	hypothetical protein
ACD60949	7.660972814	7.301194363	7.32713044	propionate catabolism operon regulatory protein PrpR
ACD60963	6.086554506	5.891550423	5.909326692	septum formation protein Maf
ACD60965	7.338513555	7.551969672	6.78501428	crispr-associated helicase Cas3 domain protein
ACD60966	7.607744567	8.078865972	6.983791683	crispr-associated protein Cas5, dvulg subtype
ACD60967	7.68258032	7.830641962	7.461168365	crispr-associated protein, Csd1 family
ACD60968	7.861198594	7.974873426	7.684362915	crispr-associated protein, Csd2 family
ACD60969	7.621656306	8.031075336	6.578312303	crispr-associated protein Cas4
ACD60970	7.79377886	7.955045389	7.415530524	crispr-associated protein Cas1
ACD60971	8.581837035	7.955405806	7.628912085	crispr-associated protein Cas2
ACD60975	6.851436736	6.429264453	5.882254203	aminoglycoside phosphotransferase
ACD60976	6.73202493	6.364680981	6.072463857	TonB-dependent outer membrane Receptor
ACD60977	7.196607044	7.162975338	6.602633548	PnuC protein
ACD60978	7.424367874	6.606859696	7.485853454	transcriptional regulator
ACD60990	10.29654918	10.87086557	11.87117755	hypothetical protein
ACD60994	10.6697886	10.37703696	9.020966053	hypothetical protein
ACD60997	8.612739515	8.166208284	7.458472235	hypothetical protein
ACD61001	6.699440583	7.25260867	6.436231813	RDD family, putative
ACD61005	7.066013824	6.871252259	7.116697443	cytosol aminopeptidase
ACD61006	8.604808944	9.437265198	8.065119891	putative membrane protein
ACD61007	6.307902059	6.114223331	5.179889191	DNA polymerase III holoenzyme chi subunit
ACD61008	6.84289086	6.630868472	6.240375394	valyl-tRNA synthetase
ACD61009	8.176876245	8.195224547	6.100220791	conserved hypothetical protein
ACD61010	0	8.377223547	8.090218302	conserved hypothetical protein
ACD61011	6.165530117	5.756775129	5.130860874	transposase
ACD61012	7.141228406	7.273907468	7.088109787	ISXoo3 transposase ORF B
ACD61013	0.424728641	-0.001837721	-0.974812411	ISXo8 transposase
ACD61015	5.377703349	5.70645872	4.937174875	ISXo8 transposase
ACD61016	7.368131006	7.131229342	6.640921651	pectate lyase
ACD61018	0.38901606	-0.031772083	0.582218773	ISXo8 transposase
ACD61026	8.774101781	9.0045351	9.709826514	conserved hypothetical protein
ACD61027	7.043628851	7.029739983	6.676887959	prolyl-tRNA synthetase
ACD61028	9.050795518	9.646618109	10.08915913	DNA-binding protein
ACD61030	7.726899318	7.695576306	7.038008103	ABC transporter permease
ACD61031	10.61106169	11.99308699	11.34510026	hypothetical protein
ACD61032	6.886452599	7.216716762	7.043027284	ABC transporter ATP-binding protein

ACD61033	7.026224637	7.200172785	6.592817292	ABC transporter substrate-binding protein
ACD61034	9.054989528	9.197545993	8.742339755	lipoprotein, putative
ACD61036	7.463736879	7.203328424	7.234520481	electron transfer flavoprotein-ubiquinone oxidoreductase
ACD61037	7.173247387	6.714575239	6.488678884	conserved hypothetical protein
ACD61040	7.605272081	7.811798528	7.576537254	phosphohexose mutase
ACD61041	7.670691652	7.605005332	8.199068642	mannose-1-phosphate guanylyltransferase/mannose-6-phosphate isomerase
ACD61046	7.683029685	7.507762932	8.004866514	electron transfer flavoprotein beta subunit
ACD61047	8.227794013	7.994228964	8.340629026	electron transfer flavoprotein alpha subunit
ACD61048	8.909317091	9.24410691	9.960734681	ABC transporter
ACD61049	7.896520109	8.012842393	7.767866632	ABC transporter, ATP binding protein
ACD61059	10.99755352	12.41274713	11.36325323	hypothetical protein
ACD61064	11.55853073	11.44571843	9.503968808	hypothetical protein
ACD61068	8.184379486	8.216658566	7.230327922	Tfp pilus assembly protein
ACD61071	7.854338571	7.769051005	8.197732727	ATP-dependent RNA helicase
ACD61073	7.615975327	8.061090322	8.013194242	putative 6-pyruvoyl tetrahydrobiopterin synthase
ACD61074	8.94966624	9.2598021	12.68379732	conserved hypothetical protein
ACD61076	7.720853021	8.043311692	8.852972627	possible Sensor with GAF domain
ACD61077	8.085052802	8.167729233	7.17429655	TfoX C-terminal domain family
ACD61080	6.7950396	6.994568411	6.850949404	beta-hydroxyacyl-(acyl-carrier-protein) dehydratase FabA
ACD61081	6.884463608	6.667409633	7.280529528	beta-ketoacyl-synthase I
ACD61085	8.238141973	8.246902076	8.016563176	conserved hypothetical protein
ACD61086	7.588812061	7.0393797	7.207385321	copper resistance protein A
ACD61087	7.428703531	6.994081845	6.845490051	copper resistance protein B
ACD61088	8.181614442	8.242121337	8.151255065	lactoylglutathione lyase
ACD61089	0	0	0	hypothetical protein
ACD61095	6.005736817	5.684549469	5.956611965	ABC transporter permease
ACD61096	6.412452987	7.025361072	7.605612855	conserved domain protein
ACD61100	0	0.556856091	0.549718451	ISXo5 transposase
ACD61102	0	8.822217084	7.794032396	conserved domain protein
ACD61104	7.422729178	8.104058788	7.095966603	conserved hypothetical protein
ACD61116	6.702740646	6.982799682	8.048868273	conserved hypothetical protein
ACD61123	9.330143799	9.814226755	12.13177016	outer membrane protein
ACD61129	7.714540896	7.41933663	7.245429109	protein YajQ
ACD61130	0	10.02627444	9.198373826	hypothetical protein
ACD61131	6.579207307	5.647677153	5.877282906	conserved hypothetical protein
ACD61132	8.034479857	8.382948191	7.631853672	conserved hypothetical protein
ACD61133	6.829494422	6.596516283	6.536666848	3-oxoacyl-[acyl-carrier protein] reductase
ACD61137	11.44307822	11.27425584	10.56170799	conserved hypothetical protein
ACD61143	8.314433699	8.278969757	10.4048861	conserved hypothetical protein
ACD61146	7.192006713	6.837173768	7.822462485	leucine responsive regulatory protein
ACD61148	6.934669821	6.357342623	8.430398188	methionine-R-sulfoxide reductase
ACD61149	6.599697165	7.114564841	7.085350293	putative secreted protein
ACD61150	7.527336248	7.64316353	8.473446001	flagellar motor component MotA
ACD61151	7.250544768	7.328971064	7.966672711	chemotaxis MotB protein
ACD61152	7.667870842	7.861434352	7.762534855	conserved hypothetical protein
ACD61153	8.530761358	8.718594521	7.660915785	conserved hypothetical protein
ACD61154	7.010511322	7.03865566	6.545956017	probable two-component response regulator
ACD61157	6.593939336	5.887098735	5.918806005	Xanthomonas adhesin-like protein B
ACD61158	7.352705567	6.777248739	7.43131373	protease
ACD61160	6.831167877	7.917527232	7.735867376	conserved hypothetical protein
ACD61167	11.83525302	11.41490189	9.690244222	beta-Ig-H3/fasciclin repeat containing protein
ACD61168	12.92167732	12.61726312	11.1445053	hypothetical protein
ACD61173	9.720244258	9.890132011	9.838187559	tryptophan repressor binding protein
ACD61175	7.240438365	7.680971286	6.26471094	oxidoreductase
ACD61177	7.825404046	7.941863386	6.64793325	glycosyl transferase, group 2 family protein
ACD61178	7.136878357	7.091541171	7.917306433	metallopeptidase
ACD61180	10.08399781	10.63468401	9.235169382	conserved hypothetical protein
ACD61187	8.224701139	7.794383373	8.143592396	D-amino acid oxidase
ACD61189	4.122482224	3.584637858	2.344041616	ISXo8 transposase
ACD61194	9.419134341	9.580222759	8.838857248	regulatory protein
ACD61197	11.17434524	10.71880683	11.14217089	hypothetical protein
ACD61198	8.656760917	8.817661627	8.125268806	cytochrome D ubiquinol oxidase subunit I
ACD61201	6.132525434	4.896218558	5.256486112	transposase
ACD61202	1.777110364	2.642073071	0.270672457	ISXo8 transposase

ACD61203	0	0	0	ISXo5 transposase
ACD61204	8.496410418	8.377292968	8.410048485	periplasmic divalent cation tolerance protein
ACD61206	6.606553269	6.874944473	6.150514998	C-type cytochrome biogenesis protein
ACD61207	8.924043455	9.514577963	7.566244355	hypothetical protein
ACD61208	7.780953079	8.339564998	7.473332346	3-dehydroquinate dehydratase, type II
ACD61209	6.771225336	7.597784413	6.456901406	acetyl-CoA carboxylase, biotin carboxyl carrier protein
ACD61210	8.01619543	8.710348417	7.08512718	conserved hypothetical protein
ACD61211	7.286696365	7.381785182	7.012825636	acetyl-CoA carboxylase, biotin carboxylase
ACD61215	6.938873855	6.88082019	6.636787005	ribosomal protein L11 methyltransferase
ACD61217	7.180774447	6.950736678	6.469482278	transcriptional regulator PbsX family
ACD61218	5.808086389	6.135941125	5.644926273	conserved hypothetical protein
ACD61219	9.322775429	9.488535093	8.856223195	Putative fis-like DNA-binding protein
ACD61221	6.607416133	0	7.27414982	isrso17-ISXo8 transposase protein
ACD61222	1.963122655	0.56222044	1.152864846	ISXo5 transposase
ACD61228	0	0	0	hypothetical protein
ACD61229	0	0	0	radical SAM domain protein
ACD61230	0	0	0	hypothetical gene
ACD61231	0	0	0	putative secretion protein
ACD61232	0	0	0	ABC transporter, ATP-binding protein
ACD61233	0	0	0	TPR repeat
ACD61234	0	0	0	transposase
ACD61236	0	0	0	transposase IS3
ACD61237	0	0	0	putative transposase
ACD61243	0	0	0	hypothetical protein
ACD61247	0.968798559	1.570764068	-0.430993128	ISXo5 transposase
ACD61252	8.073600685	7.999103673	9.333815037	bifunctional purine biosynthesis protein PurH
ACD61253	6.494884378	6.540693766	5.072916124	phosphoribosylamine--glycine ligase
ACD61254	7.864644267	7.539941997	8.268336137	conserved hypothetical protein
ACD61255	7.000383165	6.836504874	6.200718165	hypothetical membrane protein
ACD61257	7.06530303	6.84289086	6.50933639	2-acylglycerophosphoethanolamine acyltransferase
ACD61258	8.757963306	8.639810978	8.477988917	hypothetical protein
ACD61259	8.91135004	9.726361229	9.981781316	transmembrane protein
ACD61263	11.09410408	8.962664693	9.406685469	hypothetical protein
ACD61264	11.30871445	10.60282875	11.7387214	hypothetical protein
ACD61269	8.766442775	9.228260741	8.963572381	conserved hypothetical protein
ACD61270	7.051698368	7.235392	6.959700615	Putative two-component system regulatory protein with GGDEF and EAL domains
ACD61271	7.330379128	7.130333741	7.18582691	two-component system sensor protein
ACD61275	8.049091617	7.866833814	6.440560252	membrane-bound metalloendopeptidase
ACD61276	8.286950435	6.849811657	7.700203874	hypothetical protein
ACD61277	6.814012004	7.249663398	6.779128369	conserved hypothetical protein
ACD61280	9.83081148	8.923773151	8.831319913	multi-sensor hybrid histidine kinase
ACD61282	6.868217576	6.447238649	6.947853143	orotate phosphoribosyltransferase
ACD61283	8.471463875	9.498647793	9.068649316	conserved hypothetical protein
ACD61284	7.275994091	7.497237114	6.713420885	chromosome partitioning protein
ACD61285	7.24413546	7.558833946	7.511831703	chromosome partitioning protein
ACD61286	8.193944186	8.673517558	8.604223327	mitomycin resistance protein
ACD61287	9.925079645	9.676182767	8.876876041	hypothetical protein
ACD61288	6.955452304	6.540864216	6.423737827	nucleotide sugar epimerase
ACD61289	6.933029637	7.238805963	6.932049357	dolichol-phosphate mannosyltransferase
ACD61290	7.723230887	8.118027423	7.460750753	lipid A Biosynthesis N-terminal domain family
ACD61292	7.229116817	7.398709494	7.190634612	conserved hypothetical protein
ACD61296	5.940991248	5.960449156	5.715212486	DNA repair protein
ACD61297	7.976008418	8.300531027	9.00307091	arginyl-tRNA synthetase
ACD61298	7.463924839	7.755722154	7.511863322	conserved hypothetical protein
ACD61299	7.355914849	7.76242855	7.161827233	conserved hypothetical protein
ACD61300	7.154149759	7.16010336	6.530478129	serine 3-dehydrogenase
ACD61303	10.07438234	9.901191227	10.42913471	transcriptional regulator
ACD61304	7.283625501	6.753684755	6.726190906	transcriptional regulator
ACD61313	9.81871318	8.947406088	8.37816478	hypothetical protein
ACD61319	0	0	0	hypothetical protein
ACD61325	7.481960843	7.564774459	7.417725957	glutathione-regulated potassium-efflux system protein
ACD61332	6.931801228	7.395499862	7.017576778	beta-ketoacyl-synthase II
ACD61333	5.587340986	6.616115051	5.937191357	conserved hypothetical protein
ACD61334	7.220871638	7.472374041	6.739821106	glycosyltransferase

ACD61335	7.729151664	7.746010382	7.746628523	halogenase
ACD61336	8.931880989	8.190999975	7.68218701	hypothetical protein
ACD61343	6.460600056	6.643551749	6.584069557	hypothetical protein
ACD61344	5.814170987	7.251103639	5.907936171	competence protein F
PXO_rna53	0	0	0	XO_rna53 cdna:pseudogene chromosome:GCA_000019585.1:Chromosome:4935878:4935954:1 gene:PXO_rna53 transcript:PXO_rna5
ACD61346	8.2095216	8.294331262	8.459902877	transport protein
ACD61347	8.212248315	8.238672234	8.949952157	hydrolase
ACD61348	6.36291343	7.036876927	6.755435088	leucine aminopeptidase
ACD61351	7.564774459	7.652988339	8.658357887	catalase
ACD61352	7.486239724	8.115537906	8.956259982	cytochrome B561
ACD61353	7.11049897	7.662782291	6.907203146	transposase
ACD61354	7.17254752	6.480350763	7.537404793	hydrolase, alpha/beta fold family protein
ACD61358	6.92544169	6.114997858	6.944600799	conserved hypothetical protein
ACD61367	6.701327257	6.303417289	7.187708372	conserved hypothetical protein
ACD61368	7.693019923	7.040289721	8.039604518	conserved hypothetical protein
ACD61369	8.931092055	9.161555179	10.95153243	conserved hypothetical protein
ACD61371	7.163297449	6.800213972	7.616703213	thymidylate kinase
ACD61375	9.107711405	9.476924378	9.728650124	putative secreted protein
ACD61376	6.927007529	6.693863264	6.864334741	conserved hypothetical protein
ACD61388	8.477887759	8.770782805	10.05316565	hypothetical protein
ACD61395	6.638544519	6.482951513	7.020791085	conserved hypothetical protein
ACD61397	6.750405521	6.443273454	7.774398336	DNA/RNA non-specific endonuclease
ACD61399	5.457275803	5.090192891	5.604388658	NAD-dependent epimerase/dehydratase
ACD61400	7.913038986	6.991646553	7.445726703	NAD-dependent epimerase/dehydratase
ACD61403	7.616784067	8.428414613	10.27106612	lipoprotein, putative
ACD61406	11.76150137	11.46672907	11.41641226	hypothetical protein
ACD61409	8.267208046	8.672800111	6.236351021	TonB-dependent receptor
ACD61410	7.450402976	7.702872214	6.447349418	SapC
ACD61411	7.005557184	7.330809344	6.060808317	pass1 domain protein
ACD61412	7.616365049	7.980905003	6.706862041	tryptophan halogenase
ACD61413	8.283361582	8.583477715	8.132021537	TonB protein
ACD61421	7.005006921	6.815677889	7.237248209	heavy metal transporter
ACD61423	7.835260919	7.754125879	7.967197433	ABC transporter ATP-binding protein
ACD61424	7.764533264	8.052149581	7.394557013	permease
ACD61425	6.73020518	7.147082787	6.616106227	conserved hypothetical protein
ACD61426	7.006802924	6.988014303	6.038899241	2-dehydropantoate 2-reductase
ACD61427	8.847862274	8.084813702	8.278728213	hypothetical protein
ACD61430	0	0	1.633738085	ISXo8 transposase
ACD61435	9.050564275	8.733564492	9.87617465	hypothetical protein
ACD61438	7.746534475	7.497340917	7.967295437	ISXo3 transposase ORF B
ACD61440	7.114668943	6.953323449	6.967860271	transposase
ACD61442	6.091549634	5.79585005	5.839168508	hypothetical protein
ACD61443	6.738970448	6.643411771	7.456986803	conserved hypothetical protein
ACD61444	7.336872487	7.237860043	6.544745018	2-polyprenylphenol 6-hydroxylase
ACD61445	7.400486697	6.807638281	6.361878873	cupin region
ACD61446	6.969634025	6.380686164	6.553303667	tRNA pseudouridine synthase C
ACD61448	6.395469015	7.35696249	6.922923296	peptidyl-tRNA hydrolase domain, putative
ACD61449	8.295250068	8.560420731	8.591556006	acyltransferase
ACD61450	9.845938471	10.45703196	10.04691936	hypothetical protein
ACD61452	8.183471627	8.028977946	8.99150484	peptidyl-dipeptidase dcp
ACD61458	6.37389699	6.006906126	6.449992138	transcriptional regulator
ACD61461	8.363736162	9.185903702	7.023665655	membrane protein YebN
ACD61463	7.171096715	6.633973136	6.330106591	hypothetical protein
ACD61464	6.853733723	6.221774635	5.952354536	conserved hypothetical protein
ACD61467	9.749168855	9.737443408	10.11774698	shikimate kinase
ACD61468	8.494063534	8.845352047	9.277103709	polyvinylalcohol dehydrogenase
ACD61472	7.33084519	6.894090171	6.138017802	ISXoo3 transposase ORF A
ACD61475	0	0	0	putative transposase
ACD61476	0	0	-1.002625207	ISXo8 transposase
ACD61478	8.097842519	8.142260256	10.22271039	transposase
ACD61480	6.92677039	6.520070175	5.815045079	acetyltransferase
ACD61482	7.69128988	8.425597773	7.986757914	ABC transporter ATP-binding protein

ACD61483	7.727267011	8.416835521	8.050224146	toluene tolerance protein
ACD61484	8.559063469	8.769976653	9.527983229	toluene tolerance protein
ACD61485	8.21273955	8.537435856	9.997814579	toluene tolerance protein Ttg2D
ACD61486	9.708063051	10.07412808	10.56566381	conserved hypothetical protein
ACD61487	7.960476958	8.421008647	8.799764058	lipoprotein
ACD61492	5.17892175	4.624621481	5.308459174	ISXo2 putative transposase
ACD61494	0	8.79179454	0	transposase
ACD61496	4.535001589	5.288325337	6.641340823	ISXo8 transposase
ACD61497	5.316410067	0	4.970651221	transposase
ACD61500	9.473275515	0	10.10313041	hypothetical protein
ACD61501	7.373639512	7.502338559	6.754433249	benzoate transporter
ACD61502	8.675646591	8.379620962	7.440503777	benzoate transporter
ACD61507	11.53297437	11.2061841	11.46090123	hypothetical protein
ACD61517	9.827042542	9.781595772	9.153250542	alcohol dehydrogenase
ACD61520	0	0	0	transposase (IS4 family)
ACD61521	9.614424589	9.525875077	7.731936712	outer membrane lipoprotein\x3b lipocalin
ACD61522	11.29917367	9.218379179	10.08557868	conserved hypothetical protein
ACD61523	5.054926599	5.232568667	3.301836366	transposase
ACD61528	9.853613659	10.74899785	8.779374643	phenylalanine-4-hydroxylase
ACD61529	7.634854603	8.128020106	6.030969436	conserved hypothetical protein
ACD61531	0	7.803272249	7.850580672	hypothetical protein
ACD61535	4.755074506	0	3.22836619	transposase (IS4 family)
ACD61541	7.90312265	7.868976845	8.776837654	conserved hypothetical protein
ACD61542	6.614927704	6.471498016	5.746471325	ribosomal large subunit pseudouridine synthase E
ACD61546	7.365193848	6.476665208	7.261972658	hypothetical protein
ACD61548	0	0	7.659417985	hypothetical protein
ACD61554	10.1283166	6.646263481	8.067574186	hypothetical protein
ACD61555	7.02001319	6.263164017	6.711384773	xylosidase
ACD61560	8.049521865	8.170495955	6.60633414	conserved hypothetical protein
ACD61561	7.808552377	7.78630884	7.533890347	secreted protein of porin family
ACD61562	8.693898102	8.360447682	8.717025179	protein of unknown function
ACD61563	7.664546839	7.727988505	6.93429239	solute\x3aNa+ symporter
ACD61564	9.196378359	0	8.362636452	hypothetical protein
ACD61566	6.920186095	7.221674115	7.090070065	exodeoxyribonuclease III
ACD61567	7.731658449	7.672255603	7.684110398	conserved hypothetical protein
ACD61569	0	10.09349679	9.68554425	hypothetical protein
ACD61570	6.985762259	6.633742153	8.476960821	HetI
ACD61573	7.186540174	6.852785411	7.76586621	methyltransferase GidB
ACD61575	9.127024463	9.921973302	9.054645014	conserved hypothetical protein
ACD61576	11.75271515	11.92095571	12.74943999	ribosomal protein L28
ACD61577	9.275337689	10.02310285	9.595746069	ribosomal protein L33
ACD61581	6.173141429	6.558168124	6.182859119	transcriptional regulator
ACD61582	7.698690778	7.36274164	6.659282393	cardiolipin synthase
ACD61584	7.292864555	7.125124128	6.462053955	conserved hypothetical protein
ACD61585	7.042786586	7.231259588	7.160295003	DNA helicase II
ACD61589	8.499200117	8.46515823	7.5107879	hypothetical protein
ACD61590	6.873788596	6.658182914	6.121305569	zinc-binding alcohol dehydrogenase family protein, putative
ACD61591	5.532301373	6.83047084	6.216722581	conserved hypothetical protein
ACD61592	6.828047603	7.371532727	6.920221831	hypothetical protein
ACD61593	6.996377447	7.426734393	7.744134179	glutathione peroxidase
ACD61595	0	0	-0.012148	ISXo8 transposase
ACD61598	7.718258866	8.011674533	7.306772606	peptidase, S54 (rhomboid) family
ACD61599	8.879172743	9.056030707	10.1676314	conserved hypothetical protein
ACD61600	7.29117991	7.422148886	6.7473874	D-3-phosphoglycerate dehydrogenase
ACD61603	7.404034547	7.272611124	7.177578998	conserved hypothetical protein
ACD61604	6.793063518	6.479901494	6.029382207	peptidase
ACD61607	2.491740241	1.201564861	1.081905413	transposase
ACD61615	7.030258821	7.063492157	7.698517156	transcriptional regulator for cryptic hemolysin
ACD61616	5.115412017	6.044623621	5.700744871	outer membrane efflux protein
ACD61617	7.237018704	7.163498732	6.427232378	conserved hypothetical protein
ACD61621	7.077093423	6.522245681	7.045541261	phospholipase D active site domain protein
ACD61623	10.00677488	9.615331688	10.89880542	conserved hypothetical protein
ACD61624	6.617114784	6.008816277	6.455429151	plasmid stabilization system protein, RelE/ParE family
ACD61625	8.639952029	9.655691709	10.2008128	hypothetical protein

ACD61635	0	0	0	prophage Lp2 protein 6
ACD61647	7.726865268	7.665506472	6.885330315	export protein
ACD61648	6.855989697	6.890239953	6.266683487	peptidase, S54 (rhomboid) family, putative
ACD61650	8.18070484	8.423590776	8.758593004	phosphatase
ACD56679	7.104116464	7.735109185	7.677028956	pyridoxal phosphate biosynthesis protein PdxJ
ACD56680	9.210442442	10.04550031	10.01884	conserved hypothetical protein
ACD56681	7.006129685	6.848522793	6.203714076	cardiolipin synthetase
ACD56682	7.826167108	7.581953751	8.027917052	fructose-1,6-bisphosphatase
ACD56683	7.863064989	8.143189311	9.240958246	aspartate aminotransferase
ACD56686	8.606360793	7.994455271	7.844467257	hypothetical protein
ACD56687	7.388800865	7.599942588	7.281503529	ISXoo7 transposase
ACD56688	7.62391806	7.98638818	7.877909856	L-lactate dehydrogenase
ACD56689	8.482089959	8.330361199	7.627490111	isoprenylcysteine carboxyl methyltransferase (icmt) family
ACD56690	6.708297614	5.981889177	7.558971664	transcriptional regulator
ACD56691	0	8.206828784	10.23515262	transcriptional regulator
ACD56693	10.70980756	10.3003068	10.22770017	hypothetical protein
ACD56694	9.990742183	9.60519058	9.538132659	hypothetical protein
ACD56695	7.280158307	7.21229696	7.510202406	2-keto-3-deoxygluconate kinase
ACD56698	0	0	0	transposase
ACD56699	0	0	0	conserved hypothetical protein
ACD56700	0	0	0	LasA
ACD56701	0	0	0	hypothetical protein
ACD56703	0	0	0	proline-betaine transporter
ACD56704	0	0	0	proline/betaine transporter
ACD56705	0	0	0	ISXo2 putative transposase
ACD56706	10.16259274	10.14956931	8.509529587	thioredoxin
ACD56707	8.915422304	9.489749637	8.590231478	AtsE
ACD56708	7.053057017	6.536424409	5.697670973	conserved hypothetical protein
ACD56709	6.604734087	6.565254434	6.870475692	MutT-nudix family protein
ACD56714	7.175055469	7.879675138	8.000760596	ISXoo15 transposase
ACD56715	6.336083396	6.102775692	5.975185351	ISXoo2 transposase
ACD56719	2.096170754	0	0.688672738	ISXoo6 transposase
ACD56722	0	9.082143718	9.059558077	hypothetical protein
ACD56723	7.487944515	8.349856202	8.851355525	histone H1
ACD56728	6.738889407	7.097758261	6.484441078	HpaF leucine rich hrp associated protein
ACD56729	9.87771358	9.808674642	9.214268116	conserved hypothetical protein
ACD56730	12.77329789	13.81949057	10.37485474	hypothetical protein
ACD56731	9.406068916	9.728568501	8.980028157	HrpF/NolX/HrpK
ACD56736	10.9090155	9.797160548	8.83039161	HpaB
ACD56737	12.33302953	13.1931172	12.29640578	HrpE type III pilin
ACD56738	12.15719217	12.63290207	12.4319363	HrpD6
ACD56739	8.262179431	8.234649805	6.687214695	HrpD5
ACD56740	7.561723266	7.546346595	6.959549933	HpaA
ACD56741	9.26751239	9.680876375	8.555624458	HrcS
ACD56742	8.185638629	8.752407409	8.236707859	type III secretion apparatus protein, YscR/HrcR family
ACD56743	7.552907286	7.52767248	7.111970261	type III secretion apparatus protein, YscQ/HrcQ family
ACD56745	7.289576291	7.028149189	6.395074799	HrcV
ACD56746	6.810263141	6.683724522	6.743286062	HrcU
ACD56754	7.815428129	8.984785851	7.206555319	hypothetical protein
ACD56757	11.23625941	11.78699243	10.88816484	Hpa1
ACD56758	9.680271605	10.06623722	9.734839999	hypothetical protein
ACD56760	7.800188081	7.719429894	6.828174575	putative protein
ACD56762	11.777769	10.77704157	11.24304304	hypothetical protein
ACD56763	10.43050482	9.9259134	10.19483071	ISXoo2 transposase
ACD56764	8.218597139	7.944676926	8.892621742	transposase
ACD56765	11.06312539	11.32438309	10.35518589	putative transposase
ACD56766	9.302915328	10.12453493	9.809662032	conserved hypothetical protein
ACD56768	8.767098586	7.669111828	7.984384278	conserved hypothetical protein
ACD56771	7.415403762	7.636878339	7.085743313	ABC transporter substrate binding protein
ACD56773	10.46941797	10.33361381	9.001608047	hypothetical protein
ACD56775	7.175674292	7.69642511	7.383289566	Putative signal protein with GGDEF domain
ACD56776	11.21090264	12.20657791	11.70703984	hypothetical protein
ACD56785	9.762247481	9.199662531	8.95886297	methylamine utilization protein
ACD56786	5.23457796	3.954084614	4.431308715	ISXo8 transposase

ACD56788	2.543265727	4.140713226	3.864354552	ISXo5 transposase
ACD56792	8.282828969	7.061484606	8.295750571	putative secreted protein
ACD56796	7.433034546	6.916715481	6.625654787	ATP-dependent RNA helicase
ACD56797	9.220138866	8.749688451	7.202545059	hypothetical protein
ACD56801	9.196112744	8.821920635	7.456641899	dihydrolipoamide acyltransferase
ACD56802	0	0	0.571744757	ISXo5 transposase
ACD56803	7.547557793	6.501295824	7.595958608	dihydrolipoamide acyltransferase
ACD56807	10.07371314	9.962343686	10.6953066	membrane protein, putative
ACD56810	0	0	0	conserved hypothetical protein
ACD56818	0	0	0	ISXo5 transposase
ACD56819	9.145389601	8.835298821	9.56502018	transposase
ACD56820	7.352467231	6.745022149	7.20030032	plasmid stabilization system protein, RelE/ParE family
ACD56821	9.195003027	9.051124634	9.263100152	antitoxin of toxin-antitoxin stability system
ACD56822	8.243050183	7.82000021	7.882801982	hemolysin III
ACD56825	9.356559811	9.441995898	8.652812714	conserved hypothetical protein
ACD56826	7.274708939	7.153339222	7.891741181	avirulence protein AvrBs2
ACD56827	6.921840937	8.479966146	8.088729947	hypothetical protein
ACD56828	7.284560401	6.843468863	7.089900632	ROK family protein
ACD56831	6.358267896	6.053919367	5.95623326	saccharopine dehydrogenase
ACD56835	6.150435791	6.28156473	6.330983187	DNA topoisomerase
ACD56837	8.722414791	10.5789953	10.07474358	hypothetical protein
ACD56843	0	0	-0.447390778	ISXo5 transposase
ACD56848	10.9981814	11.34027852	11.88094566	putative transposase
ACD56849	5.839004695	4.187348114	5.22282774	putative ISXoo4 transposase
ACD56850	7.503324881	8.038095925	8.170531006	4-deoxy-L-threo-5-hexosulose-uronate ketol-isomerase
ACD56851	8.457623018	8.71404971	10.38766195	4-deoxy-L-threo-5-hexosulose-uronate ketol-isomerase
ACD56852	6.750472519	7.123003954	6.373378507	transcriptional regulator LacI family
ACD56854	10.8618856	9.911218195	10.01897905	conserved domain protein
ACD56856	9.634055933	10.04265802	6.978435906	conserved hypothetical protein
ACD56857	9.712937912	9.033541386	6.795598132	conserved hypothetical protein
ACD56858	7.548868136	7.865454911	6.441913342	1,4-alpha-glucan branching enzyme
ACD56859	7.92991524	7.932657681	6.54836418	alpha-amylase family protein
ACD56860	7.759761713	8.084829643	6.88787859	alpha-amylase
ACD56868	0	0	0	ISXo8 transposase
ACD56869	6.888877164	7.115210155	6.731305453	ComM
ACD56870	7.778280867	8.332502075	8.226638575	conserved hypothetical protein
ACD56876	6.243916566	5.987086614	7.097663464	spermidine synthase
ACD56877	9.40319954	8.142030452	8.189379824	hypothetical protein
ACD56888	7.71101301	7.810970008	8.288723066	glucose-inhibited division protein A
ACD56889	8.45030399	8.787719763	9.260769025	lipoprotein, putative
ACD56893	7.821856875	7.614518454	7.588444808	aspartyl-asparaginyl beta-hydroxylase
ACD56894	6.725482146	6.520186495	6.707248682	biotin biosynthesis protein BioC
ACD56895	6.846204949	7.029927669	6.809530205	oxidoreductase
ACD56896	7.113992142	6.843506551	6.807342041	putative pimeloyl-BioC--CoA transferase BioH
ACD56897	4.900205069	6.852660587	6.305768106	conserved hypothetical protein
ACD56901	7.058738591	6.843694975	6.390997784	sensor histidine kinase
ACD56902	7.625570045	7.876596753	7.37321318	thymidine kinase
ACD56903	9.740666203	8.537000912	9.71636678	hypothetical protein
ACD56908	9.354330938	8.91861283	8.372355784	hypothetical protein
ACD56909	6.446145376	5.943044569	6.311850015	protein of unknown function
ACD56912	6.632160591	6.235326894	6.584457469	tryptophan halogenase
ACD56913	6.913320284	6.601631154	6.720552092	TonB-dependent outer membrane receptor
ACD56914	7.024773996	7.351787316	7.109130679	TonB-dependent outer membrane receptor
ACD56915	7.411282172	7.255916109	6.190928885	transcriptional regulator LacI family
ACD56920	8.093243242	9.153359491	8.481621858	conserved hypothetical protein
ACD56926	0	0.57128848	-0.441362065	ISXo5 transposase
ACD56927	6.65487944	6.172261477	5.987370895	lipoprotein
ACD56928	7.659610647	7.225284571	7.99051813	conserved hypothetical protein
ACD56929	7.338139128	7.131260215	7.252324822	ABC transporter ATP-binding protein
ACD56934	6.988184769	6.795130538	6.113990059	aminotransferase, class V superfamily
ACD56937	7.205353411	7.28437532	6.71168762	HipA
ACD56938	7.392274485	6.562272957	7.17851547	transcriptional regulator
ACD56939	7.383341413	7.326447465	6.59552753	indolepyruvate ferredoxin oxidoreductase chain alpha
ACD56953	7.282699259	7.556590353	6.269936419	domain of unknown function (306) family

ACD56955	7.845697031	7.887969952	7.577134216	undecaprenyl-diphosphatase
ACD56963	8.242845412	6.455895966	6.830977809	transposase
ACD56964	3.267424933	0.554539738	2.874616003	ISXo5 transposase
ACD56965	8.028668599	8.092323739	6.623442581	microcystin dependent protein
ACD56966	7.141003548	7.65047737	6.523460023	microcystin dependent protein
ACD56967	6.342752064	6.815818761	6.150908935	microcystin dependent protein
ACD56970	6.239724536	6.185924014	7.795883809	RecF/RecN/SMC N terminal domain protein
ACD56971	8.939247151	8.909689112	9.475046366	hypothetical protein
ACD56979	9.233250568	10.30755375	11.33127527	lipoprotein, putative
ACD56983	7.070088735	6.760620161	7.053589259	ISXo2 putative transposase
ACD56984	8.90618711	7.953905415	7.438284533	DNA-binding protein
ACD56986	13.53827382	14.15327493	13.94393414	hypothetical protein
ACD56988	12.80805718	13.37548749	14.1125291	organic hydroperoxide resistance protein
ACD56989	9.777927594	10.01381117	9.56752073	transcriptional regulator MarR family
ACD56993	2.739418254	2.617606457	6.888073488	IS1112 transposase
ACD56994	0	0	0	ISXo8 transposase
ACD56996	9.110715584	9.576658178	9.370255841	transcriptional regulator TetR family
ACD56999	7.077616872	6.634571488	7.190407448	Putative signal protein with EAL domain
ACD57002	7.162008574	7.726068261	6.420057899	putative signal transduction protein
ACD57005	5.38263613	5.537997983	8.457590188	ISXo3 transposase ORF B
ACD57006	6.626601212	6.364059344	6.020057652	beta-xylosidase (1,4-beta-D-xylan xylohydrolase) (Xylan1,4-beta-xylosidase) (Exo-beta-(1,4)-xylanase)
ACD57007	7.866864716	7.749675044	8.296048953	transport protein
ACD57008	7.844360543	7.480030794	6.504224709	TonB-dependent receptor
ACD57017	7.179779739	6.597306201	6.427487172	D-mannonate oxidoreductase
ACD57018	6.566512278	6.239808534	5.890342111	glucan 1,4-beta-glucosidase
ACD57019	7.497700176	7.018467268	6.916034692	xylosidase\x3b arabinosidase
ACD57020	7.317855756	6.745170091	6.446027895	starvation sensing protein
ACD57021	6.421533016	6.148334212	5.932373041	sialic acid-specific 9-O-acetylesterase
ACD57022	6.581405483	6.391332963	6.409435065	alpha-glucuronidase
ACD57023	10.75991314	10.1670041	8.954301018	hypothetical protein
ACD57024	8.743679893	9.342616966	9.830515207	hypothetical protein
ACD57031	6.742140985	7.246560102	6.535057595	hydrolase
ACD57032	7.654048807	7.249644437	7.647976408	ferrochelatase
ACD57037	8.608775983	8.580575153	8.081334301	membrane protein, putative
ACD57038	7.705487247	7.862209599	7.66797016	GMP synthase
ACD57039	11.5057421	12.15522302	11.99434283	hypothetical protein
ACD57042	7.142045773	7.085881375	7.131270505	type II secretory pathway ATPase
ACD57044	13.03478005	12.93526268	14.05529091	hypothetical protein
ACD57047	8.428020922	8.662415592	7.986723789	TonB-dependent receptor
ACD57049	11.5551499	10.75404401	10.6439734	putative ISXo8 transposase
ACD57050	7.408576008	7.465117406	8.29349464	colicin V secretion/processing ATP-binding protein CvaB
ACD57051	7.174186674	7.158902489	7.176701749	ATPase
ACD57052	7.454891469	8.045262754	7.930908795	conserved hypothetical protein
ACD57054	7.246902076	7.346088175	6.368914985	nitrile hydratase activator
ACD57056	6.807908708	7.19313106	6.245778956	nuclease
ACD57057	7.291842956	7.887525271	6.007433239	cytochrome C5
ACD57063	6.510767332	7.322306753	6.700398101	transcriptional regulator, TetR family
ACD57070	0	0	9.565063987	transposase
ACD57072	9.412436473	9.953694479	9.645791709	hypothetical protein
ACD57073	7.593951284	7.208097765	8.231077144	putative secreted protein
ACD57078	7.27518402	6.847984383	6.958599113	monoxygenase
ACD57079	6.450091146	6.701549057	6.302344643	chitooligosaccharide deacetylase
ACD57080	6.998274497	6.871535663	6.402696599	conserved hypothetical protein
ACD57081	6.686808643	6.216000799	6.381672723	polysaccharide deacetylase family protein
ACD57082	6.275571421	6.360827775	6.493195781	purine catabolism protein PucG
ACD57083	4.210147252	4.515270908	5.737232468	ISXoo2 transposase
ACD57089	10.72691634	10.9532143	11.72702274	gas vesicle protein
ACD57091	9.877669108	10.36404708	11.8484156	conserved hypothetical protein
ACD57092	10.2188417	11.15059775	11.09570689	conserved hypothetical protein
ACD57093	0	0	0	hypothetical protein
ACD57094	7.283106879	7.071322913	7.867179879	transcriptional regulator LysR family
ACD57096	9.357032893	9.517417436	8.045819716	conserved domain protein
ACD57097	0	10.00641024	10.18036919	hypothetical protein

ACD57103	7.245970956	6.170115344	5.799791899	two-component system regulatory protein
ACD57104	6.823354501	7.027253596	5.843225125	sensor protein BaeS
ACD57105	8.42311591	8.663458482	7.980362393	sensor protein BaeS
ACD57106	7.47253651	7.276561801	6.764314304	5,10-methylenetetrahydrofolate reductase
ACD57107	7.578636862	7.503857533	6.971313624	conserved hypothetical protein
ACD57108	7.629371193	7.760254219	7.365937444	transcriptional regulator, LysR family
ACD57113	6.619638964	6.927695012	6.205638832	2-keto-3-deoxy-D-gluconate transport system
ACD57115	7.732099572	8.061948965	7.438492473	phosphate-selective porin O and P
ACD57116	5.902621121	5.696408417	6.893374346	phosphate-selective porin O and P
ACD57118	7.766866768	7.944671071	8.282523206	oxidoreductase
ACD57120	9.361035774	10.44973675	8.839080933	conserved hypothetical protein
ACD57121	7.507667804	7.638320059	7.374326599	conserved hypothetical protein
ACD57122	7.561471254	7.332636334	7.776452773	conserved hypothetical protein
ACD57124	6.918481648	6.35983915	6.32083123	dipeptidyl peptidase
ACD57126	8.967468369	9.360245745	8.837962158	hypothetical protein
ACD57127	8.586370695	8.436116021	7.499997322	conserved domain protein
ACD57128	7.411477092	7.579202781	6.688320256	xanthomonadin biosynthesis pteridine-dependent deoxygenase like protein
ACD57129	7.970968661	8.245181884	7.479222476	hydroxylase
ACD57138	0	10.40822358	9.34698569	conserved hypothetical protein
ACD57141	6.842161743	6.970669625	6.46308782	pathogenicity protein
ACD57142	6.941129792	6.643779725	6.543109174	pathogenicity protein
ACD57146	9.340519988	9.315355647	8.793886131	transcription termination factor Rho
ACD57148	10.73345603	11.02740152	11.41842716	thioredoxin
ACD57155	9.581912337	9.401496078	11.26261168	YghA protein
ACD57156	6.824462381	6.408766199	8.987843816	NADH dehydrogenase
ACD57163	7.556168812	7.651022981	8.595451444	XopX effector protein
ACD57167	12.78810451	12.37754134	8.394514142	hypothetical protein
ACD57172	0	9.289809111	8.950211767	hypothetical protein
ACD57175	6.960951828	6.898026916	5.696500226	gluconolactonase
ACD57176	6.671010241	6.546937663	6.890884396	conserved hypothetical protein
ACD57177	0	0	9.285300487	hypothetical protein
ACD57184	6.132550111	5.010793263	6.233728953	hypothetical protein
ACD57185	6.760420568	7.129416975	6.245727625	conserved hypothetical protein
ACD57188	9.733179756	9.934653605	7.876983445	putative carboxypeptidase
ACD57189	10.3836395	10.50193668	9.085857481	anti-sigma F factor antagonist
ACD57190	10.54142578	10.93360214	7.492750494	conserved hypothetical protein
ACD57191	7.62399851	7.908134384	6.470558014	IcfG protein
ACD57197	6.048929287	6.450711441	4.358086758	transposase
ACD57198	4.381324908	3.563951273	4.182898836	Tal1, also PthXo7, TAL effector AvrBs3/PthA family
ACD57204	8.0361901	8.444774722	8.964389968	hypothetical protein
ACD57210	9.785746699	10.41108723	11.06041223	conserved hypothetical protein
ACD57212	7.543542282	7.462502273	8.674372373	coproporphyrinogen III oxidase, aerobic
ACD57215	5.907712698	4.841766861	5.026494671	transposase
ACD57217	7.332108178	6.950993232	7.06684264	dihydroxy-acid dehydratase
ACD57219	7.324648615	6.955545297	8.483106345	transferase
ACD57223	6.676352044	5.666742392	6.158290569	ISXoo4 transposase
ACD57224	10.14562651	10.43535773	10.55977858	conserved domain protein
ACD57225	6.487741975	6.469812733	6.44411376	NAD(P)H steroid dehydrogenase
ACD57226	6.361878873	6.423606742	5.647176336	AMP-ligase
ACD57229	7.28424575	6.974357225	6.468400851	haloalkane dehalogenase
ACD57230	7.318136041	7.364064598	6.441123226	conserved hypothetical protein
ACD57231	7.01995761	6.783103009	7.509616675	methyltransferase
ACD57232	7.595264942	6.8738255	7.861093111	Fic protein family
ACD57233	7.085275926	7.08390476	6.876038015	3-oxoacyl-synthase III
ACD57234	7.943376346	8.528172772	9.294758579	lipoprotein, putative
ACD57237	10.07996471	12.22868944	9.286472283	hypothetical protein
ACD57238	7.260242119	8.024823852	6.712155532	MFS transporter
ACD57239	8.705228031	9.388036665	8.123898944	conserved hypothetical protein
ACD57240	9.642474148	10.75839813	8.574525412	conserved hypothetical protein
ACD57241	6.932510053	7.546786447	6.59302055	two-component system regulatory protein
ACD57242	6.829862242	7.108587181	6.828910793	two-component system sensor protein
ACD57243	7.817546516	8.073563198	7.15171678	pyruvate dehydrogenase
ACD57245	7.916948309	7.954841888	8.122066983	glycerol-3-phosphate dehydrogenase [NAD(P)+] (NAD(P)H-dependent glycerol-3-phosphate dehydrogenase)

ACD57246	9.38178302	9.437117438	10.9134654	protein-export chaperone SecB
ACD57247	8.197634449	8.204752081	7.997077839	conserved hypothetical protein
ACD57248	6.733354341	7.46727948	7.585954013	conserved hypothetical protein
ACD57249	6.992247263	6.438756928	6.673598822	thioesterase domain, putative subfamily
ACD57250	9.078649859	8.860270699	9.977981063	hypothetical protein
ACD57255	5.852348478	6.453881335	7.978144137	hypothetical protein
ACD57257	6.715316836	6.429207533	6.425521408	acriflavin resistance protein
ACD57258	6.951401292	6.653561662	6.651166528	acriflavin resistance protein D
ACD57259	7.356980091	6.925916366	7.093919284	membrane fusion protein
ACD57262	5.842732497	5.464857739	6.004040645	transposase (IS4 family)
ACD57266	3.45995614	3.927375018	3.270095321	IS1112 transposase
ACD57268	6.596739888	5.281943005	5.904308266	transposase
ACD57269	7.463295486	7.084648965	6.806092011	conserved hypothetical protein
ACD57273	5.920493396	5.797036331	4.642701572	ISXoo3 transposase ORF B
ACD57275	6.819527688	6.876885247	6.838510624	conserved hypothetical protein
ACD57282	8.078172161	8.54331801	7.466047903	cAMP-regulatory protein
ACD57285	9.006432681	8.981393178	9.249390822	ubiquinone biosynthesis protein
PXO_rna0	0	0	0	XO_rna0 cdna:pseudogene chromosome:GCA_000019585.1:Chromosome:654845:654918:-1 gene:PXO_rna0 transcript:PXO_rna
PXO_rna1	0	0	0	XO_rna1 cdna:pseudogene chromosome:GCA_000019585.1:Chromosome:654971:655047:-1 gene:PXO_rna1 transcript:PXO_rna
ACD57290	1.95320563	2.152037357	0.557424795	ISXo5 transposase
ACD57291	0	4.097400107	0	ISXoo3 transposase ORF A
ACD57292	7.276980461	7.385431037	9.96699564	bifunctional PutA protein
ACD57299	10.65457338	11.23452407	9.966591968	putative membrane protein
ACD57304	6.83852323	6.433617153	6.87958325	disulphide-isomerase
ACD57305	7.636291095	7.733442472	6.726463414	bile acid/sodium symporter
ACD57310	3.892925258	3.464759739	4.07288612	ISXo8 transposase
ACD57311	9.621383411	0	0	conserved domain protein
ACD57312	5.905726352	6.072943984	5.890505061	conserved hypothetical protein
ACD57313	6.971520563	6.746997938	6.574891685	primosomal protein N'
ACD57316	7.762076358	7.005310153	8.087897706	conserved hypothetical protein
ACD57319	9.248076995	9.586293749	9.508862394	conserved hypothetical protein
ACD57321	8.064564943	8.379711925	7.795383837	conserved hypothetical protein
ACD57322	7.462952086	7.418468271	7.492726464	conserved hypothetical protein
ACD57323	6.790224669	7.338183708	6.600833196	Sua5/YciO/YrdC family protein
ACD57324	7.440761221	7.707027757	8.140829771	DNA topoisomerase I
ACD57325	6.636468018	7.030126369	6.87115367	RDD family protein
ACD57326	8.083910077	8.082420519	8.204082012	fimbrial protein
ACD57327	8.106453017	8.437506575	8.18103793	smg protein
ACD57328	6.52433798	6.485397844	5.889544118	DNA protecting protein DprA
ACD57329	10.60933575	11.30143903	10.01938223	LysM domain protein
ACD57335	7.531529622	7.488306122	7.811785687	lipopolysaccharide core biosynthesis glycosyl transferase
ACD57337	10.78208907	11.45919593	10.05403445	hypothetical protein
ACD57338	7.00299499	6.80308493	6.830698998	bacterial membrane flanked domain family
ACD57339	6.718169802	6.477991345	5.729215577	bacterial membrane flanked domain family
ACD57340	6.99317617	7.324351589	7.830464502	riboflavin biosynthesis protein
ACD57342	7.089932402	7.067466629	6.767535628	lipid A biosynthesis lauroyl acyltransferase
ACD57346	10.9575374	11.42180712	11.00386923	hypothetical protein
ACD57347	7.248980676	7.196685723	8.000743698	site-specific recombinase, phage integrase family
ACD57348	0	0	6.778602845	conserved hypothetical protein
ACD57349	7.200996661	6.170904499	7.366304727	conserved hypothetical protein
ACD57350	8.811965459	10.03691538	9.125343723	hypothetical protein
ACD57351	0	0	8.943297219	conserved hypothetical protein
ACD57352	0	9.215882408	8.362833673	conserved hypothetical protein
ACD57364	7.572836627	7.252286971	6.458150658	conserved hypothetical protein
ACD57365	6.331251975	6.344235535	5.933506545	OmpA family protein
ACD57366	7.03411665	6.61636799	6.658025777	conserved hypothetical protein
ACD57367	6.822296765	6.774549885	6.38097701	conserved hypothetical protein
ACD57369	9.405700984	10.01530354	10.33168954	hypothetical protein
ACD57370	9.546892531	10.10771402	10.0152896	conserved hypothetical protein
ACD57371	10.52158081	10.55683173	9.567324877	conserved hypothetical protein
ACD57373	6.862922459	7.347320176	6.943229811	DNA primase

ACD57374	8.264466058	8.423347059	6.739834604	ribonuclease BN
ACD57378	7.744786756	7.603025406	7.96891442	GatB/Yqey
ACD57379	11.08351922	12.08039118	12.63289526	ribosomal protein S21
ACD57385	4.887042667	5.223851124	5.986069563	transposase
ACD57386	4.063036925	5.021062138	5.874206786	ISXo2 putative transposase
ACD57387	6.964537257	7.787647944	8.287195225	transposase
ACD57388	8.520265084	8.147026803	7.073102562	dehydrogenase
ACD57390	9.966822651	10.03891899	7.910522813	conserved hypothetical protein
ACD57391	8.674188736	8.697044004	8.004967609	conserved hypothetical protein
ACD57396	7.331069204	7.011674533	6.236262993	cationic amino acid transporter
ACD57397	7.366811773	7.313254923	6.933490021	conserved hypothetical protein
ACD57400	2.785542182	1.394925655	3.185084742	hypothetical protein
ACD57402	6.86318272	5.989806599	5.640811779	chloromuconate cycloisomerase
ACD57403	6.520750668	6.500563071	5.783807594	NlpC/P60 family protein
ACD57414	6.741547883	6.423993239	7.183744541	glycosyltransferase
ACD57419	7.580899204	7.056897783	6.164794322	conserved hypothetical protein
ACD57420	7.000698636	6.797583715	6.627544098	3-ketoacyl-CoA thiolase
ACD57423	7.252684353	7.215164089	6.99859043	variant SH3 domain protein
ACD57424	6.798789305	6.909437108	6.277743038	2-oxoacid dehydrogenase E1 component, beta subunit
ACD57425	4.273993228	2.875290564	2.548860739	ISXo5 transposase
ACD57426	6.361129671	6.7740886	6.587057395	2-oxoacid dehydrogenase E1 component, beta subunit
ACD57427	6.518288059	6.335063366	5.758127254	pyruvate dehydrogenase E1 component, alpha subunit
ACD57428	5.749882832	5.737624575	6.726299915	nuclease
ACD57432	6.382644775	7.116770208	6.96176222	transcriptional regulator MarR/emrR family
ACD57435	8.404554052	8.106636218	6.30534495	Na+/H+ antiporter subunit
ACD57436	8.469633678	7.092038257	6.901023745	PhaF
ACD57437	7.733225523	7.695353586	6.910840572	PhaE
ACD57438	7.144454314	7.070432265	5.788753564	PhaD
ACD57439	7.077926579	7.389790495	7.058316496	PhaC
ACD57440	7.01664117	7.247044542	6.072716801	NADH dehydrogenase subunit 5
ACD57442	9.001340632	8.771159296	7.533010396	conserved hypothetical protein
ACD57443	6.314769021	6.893277258	7.100935611	zinc metalloprotease
ACD57444	6.669650438	5.973850021	6.099987347	neutral protease A
ACD57445	7.643488256	6.740914072	6.403739794	zinc metalloprotease
ACD57446	7.056323404	7.008775948	6.779075825	lytic enzyme
ACD57449	7.359670506	7.051176307	6.912949198	phosphoribosylaminoimidazole-succinocarboxamide synthase
ACD57460	6.555909694	6.211545705	6.145475708	oxidoreductase
ACD57461	8.028668599	7.54690989	8.148161316	conserved hypothetical protein
ACD57462	7.092947374	6.672481917	7.072427412	dipeptidyl peptidase IV
ACD57466	6.759115877	6.295588959	6.283564387	lipoprotein, putative
ACD57468	7.083862222	7.039324862	5.990178863	conserved hypothetical protein
ACD57470	8.017866247	7.883730774	7.663017215	cellulase
ACD57471	11.60126938	9.585174757	10.5908677	hypothetical protein
ACD57472	10.41856947	10.46287031	11.58399944	exoglucanase A
ACD57473	12.60805841	12.62351574	12.85580871	hypothetical protein
ACD57474	0	0	0	hypothetical protein
ACD57476	8.892227074	9.404996761	9.563146688	conserved hypothetical protein
ACD57478	7.781982561	7.330665953	7.224840992	conserved hypothetical protein
ACD57479	7.990172054	5.779855904	7.75557529	conserved hypothetical protein
ACD57482	0	0	0	ISXo8 transposase
ACD57483	7.184746437	7.251586555	7.255387428	trehalase
ACD57485	6.958610712	6.742774258	5.659935972	protein of unknown function
ACD57491	9.878523046	11.10589542	9.268698717	hypothetical protein
ACD57493	6.981795584	7.101303394	7.232775861	histidine kinase-response regulator hybrid protein
ACD57494	6.486194665	6.3407118	6.618839164	zinc protease
ACD57496	10.3007415	12.43567807	12.36684674	hypothetical protein
ACD57497	7.430017587	8.694887156	7.770796017	conserved domain protein
ACD57499	7.661101119	8.775383119	8.156634255	histidine kinase, hamp region\x3abacterial chemotaxis sensory transducer
ACD57500	9.515506678	10.1708264	11.18558164	major extracellular endoglucanase
ACD57509	7.49111553	7.152974331	6.98753689	transposase
ACD57510	10.59346582	11.26947153	10.64689167	hypothetical protein
ACD57516	8.006011836	7.884713908	9.714722902	protein of unknown function
ACD57518	9.521645585	9.653224863	9.994975642	outer membrane lipoprotein
ACD57523	8.6921726	8.96188374	7.493959496	aminotransferase

ACD57524	10.03945373	9.796931889	9.174438878	hypothetical protein
ACD57531	6.764725656	6.421127341	7.958071253	hypothetical protein
ACD57534	7.468860231	6.86810643	6.787954783	HAD-superfamily hydrolase subfamily IA, variant 1 and 3
ACD57535	7.250222609	7.787112451	7.594421651	lipoprotein, putative
ACD57536	7.484919541	7.867136626	8.00851266	aminopeptidase
ACD57538	7.641806107	7.774622359	6.408682993	Putative signal protein with HAMP and GGDEF domains
ACD57539	7.440229673	7.586044116	7.501797386	ubiquinone/menaquinone biosynthesis methyltransferase UbiE
ACD57546	7.907473567	7.429113779	7.883962878	sugar kinase
ACD57561	8.134292826	8.362842438	8.908530729	hypothetical protein
ACD57568	7.804105201	7.53459859	7.55086989	endonuclease/exonuclease/phosphatase family
ACD57579	7.125960997	6.999131868	6.533848308	oxidoreductase YvaA
ACD57585	6.343288777	6.750164304	6.679142258	pteridine reductase 1
ACD57587	7.309985584	7.023166623	6.582298571	ISXoo3 transposase ORF B
ACD57589	0	6.394325493	3.862739009	transposase
ACD57591	8.119288731	7.777551222	7.212569339	hypothetical protein
ACD57596	10.88054779	8.546898317	11.62786671	hypothetical protein
ACD57601	8.156770753	8.505402699	7.208322161	conserved hypothetical protein
ACD57602	8.602928936	8.572696437	7.804731212	biofilm PGA synthesis N-glycosyltransferase PgaC
ACD57603	8.120326018	7.733706836	7.277873194	biofilm PGA synthesis lipoprotein PgaB
ACD57604	7.899223977	7.771918583	7.26425492	HmsH
ACD57606	0	0	0	ISXo5 transposase
ACD57608	10.5758701	10.27065742	10.36587403	hypothetical protein
ACD57612	7.082127747	6.767389962	6.108869408	tRNA nucleotidyltransferase
ACD57616	1.171328542	1.816214663	3.129845146	ISXo8 transposase
ACD57617	7.63382351	7.208400204	6.905362935	isrso16-transposase orfa protein
ACD57618	7.25500968	7.138148903	6.715838472	putative cystathionine gamma-synthase protein
ACD57619	3.285134371	2.896647734	4.469202227	ISXo2 putative transposase
ACD57620	8.181206932	7.968591921	7.909791102	ISXoo6 transposase
ACD57623	9.866632935	10.1284455	10.99215236	high-affinity choline transport
ACD57624	7.522487375	6.984464032	6.822564458	high-affinity choline transport
ACD57625	7.177628826	6.913092856	6.649989017	endonuclease/exonuclease/phosphatase
ACD57626	7.358835784	7.653138859	7.610655774	thiol\x3adisulfide interchange protein
ACD57627	7.17028563	7.058457208	7.412171807	disulfide oxidoreductase
ACD57628	7.561700358	7.900595145	6.227671773	cytochrome C4
ACD57631	7.458390207	8.574847041	8.504362178	conserved mebrane associated protein
ACD57634	7.383963436	6.388458209	5.986581591	two-component system sensor protein
ACD57635	0	0	0	two-component system regulatory protein, EnvZ family
ACD57637	8.944015066	9.243535802	7.771013995	conserved hypothetical protein
ACD57639	8.313835364	8.259507895	7.531654377	two-component system sensor protein
ACD57640	8.560795187	8.712987764	8.443909115	two-component system regulatory protein
ACD57643	8.762202625	8.047582011	8.09154646	hypothetical protein
ACD57646	8.338045506	6.978904902	9.410160875	hypothetical protein
ACD57652	7.963612838	5.389604668	7.475311908	conserved hypothetical protein
ACD57653	8.636323726	8.515132109	9.852835338	ABC transporter ATP-binding protein
ACD57655	9.113229059	8.524400671	9.575662145	hypothetical protein
ACD57662	7.177917792	7.877909856	7.694775747	conserved hypothetical protein
ACD57672	7.029684776	6.006257624	7.399111265	hypothetical protein
ACD57680	6.29303935	6.568284494	5.925377597	D-lactate dehydrogenase
ACD57681	7.312084262	7.043453875	6.680591602	inner membrane protein YbcI
ACD57682	7.852092499	8.041100581	7.888091758	conserved hypothetical protein
ACD57683	6.089648565	6.485856673	6.675180802	LppC superfamily
ACD57685	7.114075458	6.719977416	6.752654942	conserved hypothetical protein
ACD57701	8.537459153	9.035513944	8.066288355	conserved hypothetical protein
ACD57707	7.607123143	8.129952684	7.598581081	conserved hypothetical protein
ACD57708	8.482287646	8.232516864	8.241630474	conserved hypothetical protein
ACD57709	6.864173761	6.666628788	7.192450639	5,10-methylenetetrahydrofolate reductase
ACD57712	8.873757842	9.090239477	7.987531206	glyoxalase/bleomycin resistance protein/dioxygenase
ACD57714	10.16874732	11.52042716	9.983136126	conserved hypothetical protein
ACD57716	7.537606691	6.51949001	8.207448772	hypothetical protein
ACD57720	11.01233122	12.01689532	9.634094061	hypothetical protein
ACD57723	8.370482538	8.28686729	9.011545955	adenosylhomocysteinase
ACD57727	10.23005647	9.018901183	11.60297717	conserved hypothetical protein
ACD57729	5.598064414	5.607256327	4.843054232	ISXo8 transposase
ACD57732	8.14973188	8.200991758	8.863656647	S-adenosylmethionine synthetase

ACD57735	5.902249684	4.008235876	-5.381585412	methyltransferase
ACD57736	3.983340236	0	3.061631057	tRNA-dihydrouridine synthase B
ACD57738	6.752092915	5.981770472	7.242183278	putative secreted protein
ACD57739	7.337398903	7.694727003	8.230668962	ribokinase
ACD57740	6.884756638	7.048530468	5.996488177	nucleoside transporter
ACD57743	6.157342893	6.693556651	6.460347767	ISXo8 transposase
ACD57744	9.018931775	7.941393929	9.389003149	hypothetical protein
ACD57748	9.216983459	8.471524841	8.450967894	transmembrane signal peptide protein
ACD57749	10.45649816	10.10050466	9.582461918	ABC transporter permease
ACD57750	7.777616971	7.573154845	6.418621747	permease
ACD57751	7.29259772	6.72902247	6.685407587	taurine dioxygenase
ACD57752	7.158377425	6.879129847	6.332505656	oxidoreductase
ACD57753	6.489197698	6.936378819	6.8483976	ABC transporter ATP-binding protein
ACD57757	7.207160779	6.709924709	7.207404845	ISXoo8 transposase
ACD57758	12.55734164	11.07645488	11.99982036	conserved hypothetical protein
ACD57759	7.050741111	7.22318118	6.398001421	conserved hypothetical protein
ACD57768	7.585563498	6.973163521	6.359819827	bis(5'-nucleosyl)-tetraphosphatase (symmetrical)
ACD57769	7.183814002	7.444103818	6.681603872	ApaG protein
ACD57770	8.174925683	8.052366983	7.95419631	dimethyladenosine transferase
ACD57771	7.146940279	7.25124569	6.18549988	4-hydroxythreonine-4-phosphate dehydrogenase
ACD57772	8.719867928	9.164283467	8.448859665	peptidyl-prolyl cis-trans isomerase
ACD57773	8.661289992	8.903854738	9.124113555	organic solvent tolerance protein
ACD57774	7.157801654	7.138107936	6.515072169	acetoin utilization family protein
ACD57775	8.293549817	8.855189293	8.632319116	ATP\x3acob(I)alamin adenosyltransferase, putative
ACD57776	8.712637047	9.204040428	8.741632145	conserved hypothetical protein
ACD57782	8.805624583	8.973060173	9.257677767	VanR
ACD57786	6.75966186	6.571582771	5.918806005	acid-CoA ligase
ACD57787	6.324452405	6.418151147	5.666875865	aldehyde dehydrogenase
ACD57788	7.4852497	7.673224261	7.553391225	P-hydroxycinnamoyl CoA hydratase
ACD57789	7.17173725	7.475068666	6.385339572	transcriptional regulator MarR family
ACD57790	8.281276321	8.098353231	8.273455279	conserved hypothetical protein
ACD57791	7.564179983	7.711377889	7.481153605	conserved hypothetical protein
ACD57792	7.360531083	7.199593829	7.196813567	gluconolactonase
ACD57794	6.72222009	6.390573112	5.852273562	conserved hypothetical protein
ACD57795	6.523005157	6.880477382	6.553977879	cytidine and deoxycytidylate deaminase zinc-binding region
ACD57796	8.946488169	8.465876541	8.454648871	conserved hypothetical protein
ACD57797	6.911955173	6.872077673	6.102002976	integral membrane protein
ACD57803	8.922495207	6.968332717	7.699544692	hypothetical protein
ACD57804	7.115158125	6.893070924	6.90408664	glutaminyl-tRNA synthetase
ACD57808	7.107572801	6.141876208	6.041196977	two-component system regulatory protein
ACD57809	6.541305743	6.627504702	5.864364458	two-component system sensor protein
ACD57810	0	0	0	transposase
ACD57813	0	0	0	two-component system sensor protein
ACD57814	7.428544424	7.041889088	8.265183697	two-component system regulatory protein
ACD57817	5.75360721	6.808475152	6.086964177	DJ-1/PfpI family
ACD57818	0.803317977	0	1.337779586	ISXo8 transposase
ACD57820	6.550225013	7.484371793	8.18968127	ISXo8 transposase
ACD57821	7.888158748	7.600492778	8.828507823	transaldolase superfamily
ACD57822	7.518220381	7.403216586	8.541681321	regulator of nucleoside diphosphate kinase
ACD57823	7.444658785	7.629924843	6.887768949	oxidative stress transcriptional regulator
ACD57824	7.821659199	7.928932841	7.415209373	alkyl hydroperoxide reductase subunit F
ACD57825	9.264060177	9.670142806	10.55165059	alkyl hydroperoxide reductase subunit C
ACD57831	7.173976886	6.971830915	5.873380128	N-formylglutamate amidohydrolase
ACD57832	8.082856906	7.23628213	7.039357765	nudix hydrolase family protein
ACD57833	7.533578921	7.39149279	6.848497755	exodeoxyribonuclease IX
ACD57834	7.0431148	7.502577247	7.577285307	nitroreductase family
ACD57838	8.209857848	8.484158276	10.41296143	putative secreted protein
ACD57839	5.617251458	6.674149887	7.036821993	conserved hypothetical protein
ACD57840	8.104656408	8.473174026	9.310578702	ECF sigma factor
ACD57843	0	0	0	putative transposase
ACD57844	8.813178339	9.283199503	8.481008255	conserved hypothetical protein
ACD57850	7.413814071	7.673718944	6.696411199	YbaK/ebsC protein
ACD57851	7.752654942	7.649866903	7.016741443	asparaginase
ACD57853	10.35634192	10.37073099	9.62021066	hypothetical protein

ACD57854	7.690291371	8.080140648	8.28318561	tryptophan repressor binding protein
ACD57859	7.464619262	7.280863545	7.899683192	transcriptional regulator
ACD57860	8.218970015	7.990523802	7.898117637	molybdenum cofactor biosynthesis protein B
ACD57861	7.139981027	7.127323744	6.466193137	tetratricopeptide repeat domain protein
ACD57862	6.914002356	6.627497406	6.491420223	peptide chain release factor 1
ACD57863	7.458792101	7.413010103	8.016852849	glutamyl-tRNA reductase
ACD57884	6.244245846	7.791214994	7.573957655	ISxac3 transposase
ACD57913	6.00720223	6.100506761	7.457873322	ISXoo2 transposase
ACD57920	8.821541219	5.66443164	8.321098307	hypothetical protein
ACD57921	6.395636952	6.073972291	6.421541431	conserved hypothetical protein
ACD57922	7.196420165	6.525606938	7.096251309	conserved hypothetical protein
ACD57923	5.93696766	6.125861837	6.383985893	conserved hypothetical protein
ACD57924	7.542018097	8.232267415	7.981327526	conserved hypothetical protein
ACD57925	7.499224039	5.951911787	7.598543864	hypothetical protein
ACD57926	7.374439632	7.13154833	7.992298255	glycine dehydrogenase
ACD57927	8.56817655	8.791726179	9.510293411	hypothetical protein
ACD57932	6.380641147	6.546521008	6.332738362	angiotensin-converting enzyme, testis-specific isoform (ACE-T) (Dipeptidyl carboxypeptidase I)(Kininase II)
ACD57933	8.047751035	8.143969867	7.59724809	inner membrane protein
ACD57934	8.726460008	9.28503225	8.280914569	transmembrane protein
ACD57935	7.577043554	7.385405151	6.102332691	dolichyl-phosphate-mannose-protein mannosyltransferase
ACD57938	10.67484548	0	9.513865741	hypothetical protein
ACD57939	7.520846508	6.712293124	6.063056345	conserved hypothetical protein
ACD57940	9.909180558	9.873933131	9.149371157	cell division topological specificity factor MinE
ACD57941	8.104525372	8.226720449	8.043749134	septum site-determining protein MinD
ACD57942	7.517559164	7.826891643	8.273646428	septum site-determining protein MinC
ACD57943	8.724268267	9.115046252	9.164668133	acetyltransferase, gnat family
ACD57944	9.739100442	0	9.769333721	hypothetical protein
ACD57950	6.761232076	7.43345191	7.305633148	D-alanyl-D-alanine carboxypeptidase family
ACD57951	10.06548345	9.151366702	9.59462319	conserved hypothetical protein
ACD57952	8.917052771	8.583101577	8.023549229	conserved hypothetical protein
ACD57953	8.343345636	8.329863595	8.091028042	spfh domain/band 7 family protein
ACD57955	8.573431335	8.595235099	8.292997953	transposase
ACD57957	10.35484441	10.53868365	10.47690818	conserved hypothetical protein
ACD57964	6.59119768	7.126250172	7.299702572	ImpA, N-terminal
ACD57967	0	0	0	lipoprotein, putative
ACD57969	5.731039291	5.546622868	7.070872292	similar to Sulfatase modifying factor 1 precursor (C-alpha-formyglycine-generating enzyme 1)
ACD57972	0	0	0	lipoprotein, putative
ACD57976	7.313944171	7.501415259	9.760189337	lipoprotein, putative
ACD57986	0	0	0	ISXo8 transposase
ACD57988	6.126638402	5.543529909	6.065255632	RhsD protein
ACD57989	0	-0.000943831	0	ISXo8 transposase
ACD57993	12.20075151	11.72787792	10.78366127	hypothetical protein
ACD57994	8.344118335	9.141458337	8.83942427	conserved hypothetical protein
ACD57995	6.207389226	6.214103429	5.70395616	pirin, N-terminal\x3aPirin, C-terminal
ACD57996	7.595220178	8.061311782	7.476827195	endonuclease V
ACD58003	6.929282083	7.986723789	6.09741275	chemotaxis response regulator protein-glutamate methylesterase group 2operon
ACD58004	7.717498217	8.665854626	7.155718879	CheR methyltransferase, SAM binding domain
ACD58005	7.578750064	8.785171258	6.583851498	Response regulator with EAL domain
ACD58006	9.413469266	10.47548013	9.101203577	chemotaxis protein
ACD58007	8.609441022	9.590122918	8.759485437	chemotaxis protein
ACD58010	7.931718509	9.088385447	7.745163367	stas domain, putative
ACD58011	6.834900792	6.888451028	6.316457134	transcription-repair coupling factor
ACD58012	6.950608384	6.882838656	7.569764488	N-acetyltransferase family protein
ACD58013	6.307758194	6.810635896	6.492120772	conserved hypothetical protein
ACD58016	2.013237128	0.008486889	1.350435012	ISXo8 transposase
ACD58017	8.430030136	8.353517378	8.419050045	cysteine protease
ACD58025	7.284884235	7.857508311	8.129143893	ISXoo2 transposase
ACD58026	9.905283199	10.69372216	9.123138497	cysteine protease
ACD58037	7.526522713	7.142055988	7.308475556	transposase
ACD58039	9.510509029	7.843142194	9.547764058	transposase
ACD58040	7.834951342	8.000298652	7.40730176	conserved hypothetical protein
ACD58042	7.450683401	8.57534637	10.74977727	peptidoglycan-associated outer membrane lipoprotein

ACD58043	7.032552717	6.414981143	6.665719637	conserved hypothetical protein
ACD58045	8.152619488	8.197010228	7.745069223	putative deoxyribonuclease YjjV
ACD58046	9.60554804	9.75976837	9.335879359	conserved hypothetical protein
ACD58064	8.973364453	7.379335042	9.239080546	hypothetical protein
ACD58065	6.793817869	6.700841952	5.766857494	TonB-dependent receptor
ACD58066	6.41580936	6.075628893	5.415004813	TonB-dependent outer membrane Receptor
ACD58067	9.195970079	8.152528229	7.368235794	conserved domain protein
ACD58070	7.248762516	7.339787663	7.346141377	alcohol dehydrogenase
ACD58071	6.972175672	6.988400664	6.532795388	chloride channel
ACD58072	6.517385939	6.070996764	5.927555171	type I phosphodiesterase/nucleotide pyrophosphatase family protein
ACD58074	7.780953079	7.979590964	7.914193757	6-O-methylguanine-DNA methyltransferase
ACD58075	6.451303441	6.063884706	6.29525466	DNA methylation and regulatory protein
ACD58081	8.418286945	7.878099973	7.905723946	conserved hypothetical protein
ACD58082	9.029140879	8.913565628	10.48062866	conserved hypothetical protein
ACD58083	6.020093221	6.412110821	5.967551369	conserved hypothetical protein
ACD58084	6.562897213	8.618998426	7.362198087	RNA polymerase ECF-type sigma factor
ACD58085	8.848992173	0	0	conserved domain protein
ACD58090	7.452900137	7.343603248	7.228203009	integral membrane protein DUF6
ACD58091	6.727185309	6.470331867	6.161724463	DUF72
ACD58092	9.229933943	8.518212511	7.991283739	conserved hypothetical protein
ACD58097	6.649888453	6.427713432	6.040653569	two-component system sensor protein
ACD58098	6.867427018	6.626574931	6.2732697	two-component system regulatory protein
ACD58106	0	0	6.377909797	ISXoo12 transposase
ACD58108	0	0	5.86273653	transposase
ACD58109	2.915966356	2.793723206	2.078824993	ISXo8 transposase
ACD58117	0	0.010493419	0	ISXo8 transposase
ACD58119	7.943862736	7.758776197	7.319473426	dephospho-CoA kinase
ACD58120	8.070909849	8.368624317	6.579712671	type IV prepilin peptidase
ACD58121	8.590658154	9.045877038	8.481468482	pilin biogenesis protein
ACD58127	9.272702093	9.84898748	9.252566096	hypothetical protein
ACD58128	10.50861682	10.93610051	11.76181299	hypothetical protein
ACD58129	7.025438593	7.259592632	6.603522497	two-component system regulatory protein
ACD58130	0	10.66810494	10.56737622	hypothetical protein
ACD58131	6.444088906	6.020017636	5.490765856	two-component system sensor protein
ACD58137	8.553890357	8.112350883	8.726531532	competence lipoprotein
ACD58142	9.981053471	0	0	hypothetical protein
ACD58143	7.995133978	7.959457197	6.991011569	alpha,alpha-trehalose-phosphate synthase
ACD58144	8.015755126	7.795312398	7.372046648	glycosyl hydrolase, family 15
ACD58145	7.961901099	7.87296416	8.108294444	trehalose-phosphatase
ACD58146	8.471508584	8.446165231	7.1476832	hypothetical protein
ACD58147	9.915849509	9.827207718	9.85417803	TonB-dependent outer membrane Receptor
ACD58149	8.473027869	8.732421847	8.796169429	conserved hypothetical protein
ACD58152	7.062888026	6.75281548	7.680999407	phytase
ACD58153	6.806349838	6.913044971	6.727171692	putative arginyl-tRNA--protein transferase
ACD58155	9.958135071	10.08192277	10.69176096	conserved hypothetical protein
ACD58156	6.9013255	6.458716652	6.393356133	RNA polymerase sigma factor
ACD58157	7.765010879	8.185341293	8.261220505	pathogenicity-related protein
ACD58158	7.618304738	7.683317487	7.094172718	acyl-CoA thioesterase II
ACD58159	5.993721907	6.326357575	5.621169822	enoyl-CoA hydratase/isomerase family protein
ACD58161	7.636472368	7.271873834	6.597888675	putative thioesterase
ACD58162	7.272097861	7.029927669	6.289520962	excinuclease ABC, A subunit
ACD58166	9.089818556	10.01395071	10.12791696	ribosomal protein S20
ACD58172	0	0	7.610035603	hypothetical protein
ACD58184	8.306143736	5.649879833	8.517303255	transposase
ACD58192	5.929682129	5.116061113	6.874551087	conserved hypothetical protein
ACD58194	0	0	0	ISXo2 putative transposase
ACD58195	0	0	0	conserved hypothetical protein
ACD58197	8.032756565	7.392961339	7.837224237	conserved hypothetical protein
ACD58198	0	0	0	conserved hypothetical protein
ACD58199	7.462265042	6.973266861	7.382900652	conserved hypothetical protein
ACD58200	1.170803175	2.28527792	1.516186646	conserved hypothetical protein
ACD58201	5.205908563	5.126233649	5.096658236	Rhs element Vgr protein
ACD58225	8.3323499	9.066094574	7.259592632	ImpA-related N-terminal family
ACD58226	8.189814677	9.359696858	7.55444304	transcriptional regulator, LysR family

ACD58227	7.298951516	6.741480469	6.434232892	VirA-like protein
ACD58228	6.911619685	6.590637946	5.892677593	cytochrome C peroxidase
ACD58229	6.63119161	7.130714696	5.408664314	VirG
ACD58230	6.684510197	5.017659171	6.731631298	transposase
ACD58232	6.500266678	0	6.806195147	transposase
ACD58233	8.783292941	8.190116033	8.720637589	transposase
ACD58234	8.075404272	8.198454864	8.258787426	hypothetical protein
ACD58235	3.950244434	2.959529068	3.737102644	putative ISXoo14 transposase
ACD58236	6.62000863	6.526793421	7.188321793	early chlorosis factor protein
ACD58238	6.854855919	7.338103463	6.77615664	conserved hypothetical protein
ACD58243	5.042530528	4.663708948	5.243375851	Tal2b, also PthXo1, TAL effector AvrBs3/PthA family
ACD58246	5.273698639	4.654166271	4.855805363	Tal2a, TAL effector AvrBs3/PthA family
ACD58247	7.590706802	7.142352167	6.654449862	tetratricopeptide repeat domain protein
ACD58248	7.854033061	7.594078224	6.57616535	C-type cytochrome biogenesis protein
ACD58249	7.367065229	5.232223278	6.882997566	C-type cytochrome biogenesis protein/thioredoxin
ACD58250	7.174716002	7.237114336	6.444935361	cytochrome c-type biogenesis protein CcmF
ACD58251	6.268767481	6.347001198	6.56633722	C-type cytochrome biogenesis protein
ACD58252	7.359591448	8.31579263	7.94687704	conserved domain protein
ACD58253	7.185143035	7.114314964	6.498276402	heme exporter protein C\x3b cytochrome C-type biogenesis protein
ACD58254	6.159483876	5.831378189	5.730661691	serine protease
ACD58255	5.644914739	5.665293275	7.182930609	conserved hypothetical protein
ACD58256	7.065852311	6.185127173	7.599734353	RNA polymerase sigma-E factor
ACD58257	6.29788838	6.37326017	6.335465391	conserved hypothetical protein
ACD58258	7.158256229	5.728217129	7.064494885	cytochrome C2
ACD58259	7.207765986	6.626075497	6.742949369	cytochrome C
ACD58260	6.399887136	6.470667008	6.268720703	cytochrome like B561
ACD58275	6.248707497	6.114700172	6.348499783	conserved hypothetical protein
ACD58276	7.08961467	6.312247667	6.789285839	Mg-protoporphyrin IX monomethyl ester oxidative cyclase
ACD58279	7.370853024	7.451161647	6.925690915	MFS transporter
ACD58280	8.251804289	8.763428174	7.980133864	hypothetical protein
ACD58283	8.092344883	8.371567575	7.584331184	ExoD protein
ACD58284	6.826904351	7.03998279	5.787361937	hemolysin
ACD58288	5.91032013	5.49276331	5.97188838	serine carboxypeptidase
ACD58290	7.530172209	7.573919797	7.114564841	DNA topoisomerase IV, B subunit
ACD58301	7.505343148	7.591342817	7.232209844	Smr domain protein
ACD58306	8.656238928	8.258085448	8.044377725	conserved hypothetical protein
ACD58307	10.26886945	10.74815091	9.908200449	conserved hypothetical protein
ACD58315	9.749385097	7.632479078	11.05521464	hypothetical protein
ACD58325	8.694535492	8.935282936	8.238954005	hypothetical protein
ACD58332	7.118245505	7.630252561	7.506954144	pirin, N-terminal
PXO_rna10	0	0	0	XO_rna10 cdna:pseudogene chromosome:GCA_000019585.1:Chromosome:1735706:1735782:-1 gene:PXO_rna10 transcript:PXO_rna1
PXO_rna11	0	0	0	XO_rna11 cdna:pseudogene chromosome:GCA_000019585.1:Chromosome:1735876:1735952:-1 gene:PXO_rna11 transcript:PXO_rna1
ACD58335	7.338451158	7.194096904	5.957782299	conserved hypothetical protein
ACD58336	8.544415834	10.26550957	9.257178024	conserved hypothetical protein
ACD58337	7.541359956	7.426734393	6.979590964	phosphomethylpyrimidine kinase
ACD58338	7.3870092	7.3587391	6.391783183	putative secreted protein
ACD58339	7.523679562	7.111052185	6.555843757	PhoH family protein
ACD58340	7.970968661	7.717128026	7.79273174	bacterioferritin comigratory protein
ACD58341	9.270867618	9.559009917	9.023366256	conserved hypothetical protein
ACD58342	8.510554522	8.518082652	8.674199332	glycine cleavage system transcriptional repressor
ACD58345	8.961084995	8.884665073	9.865389952	ferredoxin
ACD58347	6.795572158	6.591888817	6.453096101	2-oxo-3-deoxygalactonate kinase
ACD58348	6.453669018	6.706143719	6.285827566	regucalcin
ACD58349	7.138261559	6.89285242	6.287193378	galactonate dehydratase
ACD58350	6.750016873	6.635249418	6.149320344	2-dehydro-3-deoxy-6-phosphogalactonate aldolase
ACD58352	8.596827085	8.728577004	7.76614458	relaxation protein
ACD58358	5.77538246	5.758700258	6.594733652	transposase
ACD58361	10.95237725	11.34378533	11.81121813	conserved hypothetical protein
ACD58362	11.53562531	11.37610911	9.784759154	lipoprotein, putative
ACD58363	7.152345693	7.247035044	7.113856744	elongation factor P
ACD58364	7.423351261	7.161010918	6.899211891	3-hydroxyacyl-CoA dehydrogenase type II

ACD58365	6.577250557	6.13544868	5.776838312	hydroxymethylglutaryl-CoA lyase
ACD58366	6.698107326	7.385362007	6.784608674	glyoxalase family protein
ACD58367	7.056095756	6.951238082	6.41706599	enoyl-CoA hydratase
ACD58378	11.08282099	10.96895473	13.21730646	hypothetical protein
ACD58385	6.25222073	6.089015025	8.080700296	ISXo8 transposase
ACD58388	6.459267667	6.910240968	5.689997971	transposase subfamily, putative
ACD58394	7.29953774	7.827603112	7.612831646	RpfF protein
ACD58395	7.594473905	7.661856464	6.613966223	long-chain-fatty-acid--CoA ligase
ACD58398	7.277259499	7.747931128	7.414456923	aconitate hydratase 1
ACD58404	7.022523172	7.804840898	6.72492307	C-di-GMP phosphodiesterase A
ACD58405	7.158791434	7.938109326	7.000067625	chemotaxis response regulator protein-glutamate methylesterase group 1operon
ACD58406	8.456354415	9.700923425	7.45292484	chemotaxis protein
ACD58407	7.889309259	8.794802483	9.696084257	chemotaxis protein methyltransferase 2
ACD58408	6.486683807	5.920043142	5.712727829	methyl-accepting chemotaxis protein
ACD58409	8.169018023	7.821876003	7.275947548	conserved hypothetical protein
ACD58412	8.057856379	8.439398738	8.518999282	chemotaxis signal transduction protein
ACD58413	7.816574108	8.558034157	8.52509009	type IV pilus assembly protein PilZ
ACD58415	7.509814584	7.930388447	9.005004113	chemotaxis protein
ACD58416	7.437602282	8.477321143	9.536771737	chemotaxis protein
ACD58417	11.11160519	9.791898703	10.54501271	hypothetical protein
ACD58418	6.985432119	6.40040472	6.342168918	chemotaxis protein
ACD58419	7.374622206	8.254943564	8.56069203	chemotaxis protein
ACD58420	7.422804851	7.878369773	8.152158062	chemotaxis protein
ACD58421	3.281819891	0.560313878	2.134707233	ISXo5 transposase
ACD58422	7.123904116	7.782428224	7.150579985	chemotaxis protein
ACD58423	7.162874664	8.167894784	6.922483314	conserved hypothetical protein
ACD58424	0	10.81000119	10.66273957	hypothetical protein
ACD58425	6.134929379	6.710448298	6.576470742	chemotaxis protein
ACD58427	9.689727222	11.41607442	10.50676378	transposition helper protein
ACD58428	7.751878752	8.712791785	8.775284341	chemotaxis protein CheA
ACD58429	8.288266268	9.687835803	10.00430475	chemotaxis response regulator
ACD58430	9.046515616	10.51774811	11.46047125	conserved hypothetical protein
ACD58431	7.628248671	8.385638108	8.08717109	chemotaxis protein
ACD58432	6.427850847	7.691973774	7.319654059	chromosome partioning protein
ACD58433	7.451903439	8.172247473	8.129133587	OmpA family protein
ACD58434	8.295070947	9.146326827	8.804750569	MotA protein
ACD58437	7.02357695	6.204209202	6.64508196	TonB-dependent receptor
ACD58438	8.534306774	8.018361551	8.837482868	TonB-dependent siderophore receptor, putative
ACD58439	9.696343382	10.00309622	8.507326878	superoxide dismutase
ACD58440	7.802303095	8.686801641	6.757236647	PepSY-associated membrane protein
ACD58441	6.43367223	6.082862227	5.77298619	TonB-dependent outer membrane Receptor
ACD58442	8.380660193	7.688208339	7.221152072	hypothetical protein
ACD58444	0	0	0	ISXo8 transposase
ACD58445	7.598268423	8.657875767	7.396793133	transposase
ACD58446	6.548401173	7.028204454	6.051613546	isrso17-transposase protein
ACD58450	6.393577513	6.270941883	6.233316727	ISxac3 transposase
ACD58456	0	0	-0.293885905	ISxac3 transposase
ACD58465	0	0	11.69134223	putative transposase
ACD58469	7.69405138	7.617158874	8.56220044	regulator of pathogenicity factors
ACD58470	6.627354403	6.709979832	7.328127362	pts system fructose-specific eiibc component (eiibc-fru) (eii-fru)
ACD58471	6.624874395	6.859273866	6.83791802	1-phosphofructokinase
ACD58472	6.740779183	7.071247819	7.508745554	multiphosphoryl transfer protein (MTP)
ACD58477	6.773178777	6.520115761	6.513132238	transposase and inactivated derivative
ACD58478	7.486609803	7.388990238	7.044995117	AcrB protein
ACD58479	6.897119389	6.633031537	6.377606187	multidrug resistance protein
ACD58480	9.025676665	8.972235996	8.040717123	transcriptional regulator TetR/acrR family
ACD58481	8.759971381	0	10.36285339	hypothetical protein
ACD58485	7.303369795	7.62529241	5.407012774	two-component system regulatory protein with HD-GYP domain
ACD58486	7.973215192	8.090620582	6.48773233	two-component system sensor histidine kinase-response regulator hybridprotein
ACD58487	7.733340781	7.668608471	7.310040134	conserved hypothetical protein
ACD58488	6.39342993	6.566690359	6.811329734	conserved hypothetical protein
ACD58490	7.003523534	6.961252884	6.700731002	omega-amino acid-pyruvate aminotransferase
ACD58496	0	0	0	hypothetical protein
ACD58497	6.698579663	7.386310882	7.252201803	Putative two-component system regulatory protein with GGDEF domain

ACD58498	6.681575763	6.33558151	6.659739073	oxidoreductase
ACD58499	7.219623527	6.824144112	7.329455522	gamma-glutamylputrescine synthetase
ACD58502	0	-0.087137099	2.12460275	ISXo8 transposase
ACD58510	8.472049047	7.573548733	8.092699009	conserved hypothetical protein
ACD58512	7.624861239	6.891844447	5.953754126	magnesium and cobalt transport protein
ACD58513	7.714149335	7.953550443	6.352147623	membrane protein, putative
ACD58514	8.666149425	9.157531366	8.311784637	polar amino acid transporter
ACD58515	7.062218873	7.077584829	7.027253596	conserved hypothetical protein
ACD58516	8.190279035	8.576643063	9.233703552	conserved hypothetical protein, putative
ACD58517	6.506509911	6.860503505	5.909084228	conserved hypothetical protein
ACD58518	7.240056682	6.82671372	6.306856434	ATP-binding protein
ACD58519	7.084468265	6.902145954	6.864520464	tRNA-I(6)A37 thiotransferase enzyme MiaB
ACD58520	7.36252249	8.481638002	7.208975638	glutathione S-transferase
ACD58521	7.322496044	6.239749354	7.067767769	glutathione S-transferase
ACD58531	7.707421256	7.661877836	7.651661657	conserved hypothetical protein
ACD58532	7.893538168	8.387797634	8.624620019	hypothetical protein
PXO_rna12	0	0	0	XO_rna12 cdna:pseudogene chromosome:GCA_000019585.1:Chromosome:1976131:1976206:-1 gene:PXO_rna12 transcript:PXO_rna1
ACD58545	8.175943696	8.206516248	8.267503026	virulence regulator
ACD58547	8.092302594	8.15904382	7.161978352	ribonuclease D
ACD58548	9.373830885	0	9.327310116	hypothetical protein
ACD58552	8.786011455	10.90155328	10.66993915	hypothetical protein
ACD58553	6.555971028	6.556930562	8.078124116	exodeoxyribonuclease VII, large subunit
ACD58554	7.540972674	7.687655621	8.633623741	iron-sulfur cluster binding protein, putative
ACD58561	9.958507766	10.00019723	10.79518737	polyhydroxyalkanoate synthesis repressor PhaR
ACD58562	7.128747059	7.296521648	6.927659461	acetoacetyl-CoA reductase
ACD58563	6.390397705	6.054284136	5.415265157	glutamyl-Q tRNA(Asp) synthetase
ACD58565	7.476981066	7.916984126	6.598851997	Putative signal protein with PAS, GGDEF and EAL domains
ACD58566	6.919065916	6.924064246	5.807579038	conserved hypothetical protein
ACD58567	7.413611006	7.810359553	6.539549682	YaeQ family protein
ACD58568	7.838233265	7.367851534	7.221171411	EMG2
ACD58571	6.428304893	6.537061501	6.329398113	carboxylesterase
ACD58574	6.521328756	6.80472476	7.214863065	ATP-dependent RNA helicase
ACD58577	7.276273321	7.30241959	7.892749226	conserved hypothetical protein
ACD58578	6.671491531	6.457756793	8.055385481	ribonuclease
ACD58580	6.564893325	6.988968654	7.019501773	inositol-1-monophosphatase
ACD58582	0	8.715512472	8.94018731	hypothetical protein
ACD58585	7.271378985	7.484871218	7.521726057	lysine 2,3-aminomutase
ACD58592	8.490100761	8.310040134	8.239202301	polygalacturonase
ACD58595	7.758436438	7.796188901	7.338673994	pectinesterase
ACD58598	5.693144015	5.556944353	5.769695054	ISXo8 transposase
ACD58599	8.775518103	8.796010398	7.384878704	ISXo1 transposase
ACD58602	0	0	9.910752146	hypothetical protein
ACD58604	8.036360464	6.52530155	7.71290525	ethanolamine ammonia-lyase light chain
ACD58606	7.171797286	7.365526327	6.126221257	peptidase
ACD58607	8.13126536	7.841778181	8.327723287	dihydroorotase
ACD58610	7.158589493	6.982252078	5.817262539	drug\x3aproton antiporter
ACD58611	7.556942821	7.736726628	7.943048087	SufE protein probably involved in Fe-S center assembly
ACD58612	8.902405265	8.812863987	8.141115981	cysteinyl-tRNA synthetase
ACD58628	6.363829884	6.176907153	5.635333592	MFS transporter
PXO_rna13	0	0	0	XO_rna13 cdna:pseudogene chromosome:GCA_000019585.1:Chromosome:2061380:2061456:-1 gene:PXO_rna13 transcript:PXO_rna1
ACD58629	9.034072619	8.669898414	9.245383946	cytochrome D ubiquinol oxidase subunit II
ACD58630	9.549189758	9.02500664	9.501520752	cytochrome D ubiquinol oxidase subunit I
ACD58631	7.671951438	7.236014192	7.474484716	cytochrome D ubiquinol oxidase subunit I
ACD58635	2.536552782	2.693939628	2.670992119	ISXo8 transposase
ACD58636	0	0.565392455	1.155289414	ISXo5 transposase
ACD58637	9.570982748	8.468538517	6.507859639	lipoprotein, putative
PXO_rna14	0	0	0	XO_rna14 cdna:pseudogene chromosome:GCA_000019585.1:Chromosome:2070700:2070775:-1 gene:PXO_rna14 transcript:PXO_rna1
PXO_rna15	0	0	0	XO_rna15 cdna:pseudogene chromosome:GCA_000019585.1:Chromosome:2070823:2070898:-1 gene:PXO_rna15 transcript:PXO_rna1

PXO_rna16	0	0	0	XO_rna16 cdna:pseudogene chromosome:GCA_000019585.1:Chromosome:2071658:2071733:-1 gene:PXO_rna16 transcript:PXO_rna1
PXO_rna17	0	0	0	XO_rna17 cdna:pseudogene chromosome:GCA_000019585.1:Chromosome:2071781:2071856:-1 gene:PXO_rna17 transcript:PXO_rna1
ACD58641	7.075179615	6.924384975	6.232353768	cytochrome C552
ACD58642	9.087619302	8.850693177	9.527064469	cytochrome C4
ACD58648	7.666855987	7.798724514	7.09751599	ISXoo5 transposase
ACD58649	2.28137778	2.934778786	2.454523362	transposase
ACD58650	6.165572323	4.547005551	6.731997787	Tal4, TAL effector AvrBs3/PthA family
ACD58656	6.983974046	7.176233	8.712048889	albxxii protein
ACD58662	6.896695681	7.167106992	6.750606505	ISXoo2 transposase
ACD58663	9.047391154	10.30439696	10.16499489	hypothetical protein
ACD58667	8.402479172	10.25337478	11.13166407	hypothetical protein
ACD58668	6.600144845	6.751061964	7.025139562	uracil phosphoribosyltransferase
ACD58672	6.14537992	6.680915043	5.89447099	transposase (IS4 family)
ACD58677	3.367077464	1.009612323	0	IS1478 transposase
ACD58679	0	9.330397056	9.047920038	hypothetical protein
ACD58680	7.700835018	7.828276144	8.892321197	L-lysine 6-aminotransferase
ACD58685	8.796662641	10.5324923	10.21416124	hypothetical protein
ACD58688	5.622669776	6.133351857	5.57244103	site-specific recombinase
ACD58692	0	0.931947747	0.955721968	ISXo8 transposase
ACD58693	4.829753174	4.463916668	5.210018635	IS1113 tranposase
ACD58696	7.705853526	8.037069179	6.489419302	ribonuclease T
ACD58698	7.438866688	6.797765266	7.219720318	conserved hypothetical protein
ACD58699	7.735115956	7.464831606	9.882179907	phosphate transport system regulatory protein PhoU
ACD58701	5.212946694	6.300220755	7.744981799	phosphate import ATP-binding protein PstB
ACD58702	3.344075714	5.622611213	-6.028731851	phosphate ABC transporter, permease protein PstA
ACD58703	-3.627261816	-6.332399576	0	phosphate ABC transporter, permease protein PstC
ACD58704	6.737713798	7.161535025	9.936157942	phosphate ABC transporter, phosphate-binding protein PstS
ACD58705	8.717553052	8.918693323	10.2733527	phosphate ABC transporter, phosphate-binding protein PstS
ACD58706	6.62986803	6.737335237	9.341830123	polyphosphate-selective porin O
ACD58711	8.110358023	7.507318948	8.335296554	endonuclease III
ACD58712	6.411439805	4.99699878	6.979659552	conserved hypothetical protein
ACD58713	8.084781819	7.549214792	8.067025562	3-hydroxybutyryl-CoA dehydratase
ACD58718	7.620982218	7.020113228	7.485298009	N-acetylmuramoyl-L-alanine amidase, putative
ACD58726	7.124017889	6.966499684	6.337771738	conserved hypothetical protein
ACD58727	7.159245697	6.757103275	6.263286104	putative oxidoreductase
ACD58728	7.648875241	7.471455745	7.187599513	conserved hypothetical protein
ACD58729	6.823303543	6.629108863	5.987836996	exodeoxyribonuclease I
ACD58730	0	9.019421153	7.98123618	hypothetical protein
ACD58731	7.800013308	7.355492055	7.661970444	kynurenine 3-monooxygenase
ACD58733	7.404698799	7.170556042	7.581788087	kynureninase
ACD58734	6.919709529	6.377149784	5.735736075	conserved hypothetical protein
ACD58735	6.976707312	6.966603503	5.562105018	conserved hypothetical protein
ACD58736	7.301230952	6.483978575	6.890702036	3-hydroxyanthranilate 3,4-dioxygenase
ACD58737	6.355287661	6.471265512	6.815152702	carbonic anhydrase
ACD58738	7.93667327	6.880905879	8.005910814	transcriptional regulator protein Pai2
ACD58739	7.902634384	7.895181422	6.430930862	transcriptional regulator protein Pai2
ACD58740	7.766051796	7.2773153	7.405447844	conserved hypothetical protein
ACD58741	7.707925055	8.29556692	6.72807016	putative membrane protein
ACD58742	9.24055285	8.823768464	8.908947974	conserved hypothetical protein
ACD58743	7.876713385	7.818262608	8.574260487	asparaginyl-tRNA synthetase
ACD58751	11.23438635	11.65442122	9.771953236	conserved domain protein
ACD58752	10.39958769	0	9.10939974	hypothetical protein
ACD58760	9.633216854	9.286070235	8.611795751	conserved hypothetical protein
ACD58761	10.01904857	9.911980631	8.632279123	acyltransferase, putative
ACD58762	7.210086843	7.314479018	6.210757051	urocanate hydratase
ACD58763	6.952636426	6.886440405	6.195524774	N-formylglutamate amidohydrolase
ACD58764	7.516874014	7.582412991	6.835090344	histidine ammonia-lyase
ACD58765	6.603277682	6.808294944	6.543463404	imidazolonepropionase
ACD58768	7.50831772	7.891595381	6.829430996	conserved hypothetical protein
ACD58769	7.935607074	9.016220506	8.48979579	poly(hydroxyalcanoate) granule associated protein
ACD58770	8.039346797	8.166635114	9.678895866	putative polyhydroxyalkanoic acid system protein

ACD58773	9.726385073	10.34496161	9.787109185	NapD
ACD58774	8.574052297	8.787141843	9.902254508	twin-arginine translocation pathway signal
ACD58778	6.639185848	5.904281769	6.188351468	transposase
ACD58780	12.1643193	11.81748336	9.701904212	IS1595 transposase
ACD58781	9.270236917	0	9.108273531	transposase
ACD58784	6.556443211	6.280759637	6.467589248	nodulation protein
ACD58785	6.70683442	6.544027826	6.354362236	nodulation protein
ACD58786	5.875721096	5.835009471	6.042484564	cation efflux system protein
ACD58787	6.494135557	5.93936059	5.664212594	cation efflux system protein
ACD58788	7.341051748	6.29356545	6.838195439	cation efflux system protein
ACD58790	6.248912386	6.017271658	6.258707352	serine protease
ACD58793	5.061136778	0	2.509591974	transposase
ACD58794	6.842815451	5.035412768	4.998502427	ISXoo3 transposase ORF A
PXO_rna18	0	0	0	XO_rna18 cdna:pseudogene chromosome:GCA_000019585.1:Chromosome:2235296:2235370:-1 gene:PXO_rna18 transcript:PXO_rna1
ACD58808	7.915479073	7.667232205	9.111002613	alkaline phosphatase
ACD58810	9.623045618	8.502565313	9.902794144	hypothetical protein
ACD58813	8.488864426	9.660539698	10.73345603	Putative signal protein with GAF, GGDEF and EAL domains
PXO_rna19	0	0	0	XO_rna19 cdna:pseudogene chromosome:GCA_000019585.1:Chromosome:2252421:2252507:-1 gene:PXO_rna19 transcript:PXO_rna1
ACD58816	7.590437346	7.779620874	5.550254261	beta-glucosidase
ACD58818	8.193283864	8.575871993	5.888382834	zinc carboxypeptidase family
ACD58821	10.5539844	11.95774052	12.72727595	conserved hypothetical protein
ACD58825	7.739443098	7.540066028	8.213415332	conserved hypothetical protein
ACD58826	7.965132039	7.980630867	8.52431447	putative DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog
ACD58831	6.479426215	6.050125085	6.558391629	peptidyl-dipeptidase dcp
ACD58832	6.696188608	6.603986788	6.78719736	peptidyl-dipeptidase dcp
ACD58835	7.474801051	7.703280693	7.280074769	ferredoxin--NADP reductase
ACD58836	6.535905203	6.67116597	6.561908047	ABC transporter ATP-binding protein
ACD58842	6.999628007	7.391063107	6.293716254	Putative signal protein with GGDEF domain
ACD58845	0	0	0	transposase
ACD58848	0	0	0	hypothetical protein
ACD58850	7.577338185	7.180187653	7.965322548	transposase
ACD58851	0	0	-0.974554408	ISXo8 transposase
ACD58852	0	0	0	conserved hypothetical protein
ACD58855	4.912951592	4.554944877	5.361287615	ISXoo8 transposase
ACD58858	0	0	0	cointegrate resolution protein T
ACD58872	6.891066733	6.734438666	6.282565831	two-component system sensor protein
ACD58873	8.496266596	9.097558127	8.637432738	two-component system regulatory protein
ACD58878	0	0	0	transposase
ACD58879	7.387431475	7.105091361	7.088258226	khg/kdpg aldolase
ACD58880	6.965553435	6.846944558	6.602755273	phosphogluconate dehydratase
ACD58881	7.875952036	7.508729711	6.879068566	6-phosphogluconolactonase
ACD58882	7.45322124	8.277157191	6.49937554	glucokinase
ACD58883	7.343247909	6.818812223	6.882166148	glucose-6-phosphate 1-dehydrogenase
ACD58884	8.825502631	0	9.131864676	hypothetical protein
ACD58886	7.952339391	7.845878899	7.041921934	glycine cleavage T-protein (aminomethyl transferase)
ACD58898	6.943382207	6.622395975	6.076334619	aldo-keto reductase family protein
ACD58899	9.781531843	10.79427776	8.650786096	conserved hypothetical protein
ACD58900	2.959812805	1.565026809	1.866405568	ISXo5 transposase
ACD58906	9.956573634	7.006993618	7.889722975	hypothetical protein
ACD58912	6.06212819	6.512901609	5.436038544	glyoxalase family protein
ACD58913	6.685856073	5.442999876	5.656204599	transposase
ACD58917	8.149772519	6.949126345	7.631810029	transposase
ACD58918	7.194668222	7.086847443	7.499909651	transposase
ACD58920	4.923182466	4.560568232	5.572919977	Tal5b, also PthXo6, TAL effector AvrBs3/PthA
ACD58925	4.939588617	4.158345107	5.576098821	Tal5a, TAL effector AvrBs3/PthA
ACD58928	8.357402449	8.439652224	8.735451097	pectate lyase L
ACD58936	9.731006696	9.889966282	8.598502923	conserved domain protein
ACD58942	0	0	0	hypothetical protein
ACD58944	0	0	0	transposase
ACD58945	6.359601989	5.282020873	4.781763612	transposase

ACD58953	7.550385104	7.914821612	7.935730817	hypothetical protein
ACD58954	6.879999764	7.289354962	6.198010817	phosphoribosyl-AMP cyclohydrolase domain protein
ACD58955	7.615695839	7.318569924	6.560791366	imidazoleglycerol phosphate synthase, cyclase subunit
ACD58956	7.47770161	5.995934443	5.942788943	phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase
ACD58957	6.867896464	7.029198868	6.35713849	imidazole glycerol phosphate synthase, glutamine amidotransferase subunit
ACD58958	6.562598092	6.011945069	6.116418823	histidine biosynthesis bifunctional protein HisB
ACD58959	6.673697747	6.415555875	6.39781665	histidinol-phosphate aminotransferase
ACD58960	6.771753554	6.647501599	6.252483783	histidinol dehydrogenase
ACD58961	5.762000592	6.437012957	6.201908261	ATP phosphoribosyltransferase
ACD58962	7.490401656	7.811182	9.476472825	putative TrpR homolog YerC/YecD
ACD58965	6.682390702	6.800589331	6.891674358	histidyl-tRNA synthetase
ACD58966	7.863994185	7.927866832	6.968712867	conserved hypothetical protein
ACD58967	7.122041091	7.272499155	6.449846914	threonine synthase
ACD58969	8.563207715	9.671197822	10.02808563	NOL1/NOP2/sun family protein
ACD58970	0	0	0	ISXo7 transposase
ACD58972	6.996784168	6.766833648	5.93202809	homoserine kinase
ACD58973	7.075029825	6.885928162	6.929293921	bifunctional aspartokinase/homoserine dehydrogenase 2, (ak-hd 2) (ak-hsdh 2)
ACD58974	11.4184746	11.2371502	11.21887802	hypothetical protein
ACD58975	0	8.106787996	7.981413158	hypothetical protein
ACD58976	10.29973462	11.17278376	9.303168843	tryptophan-rich sensory protein
PXO_rna24	0	0	0	XO_rna24 cdna:pseudogene chromosome:GCA_000019585.1:Chromosome:2416949:2417025:-1 gene:PXO_rna24 transcript:PXO_rna2
ACD58986	8.436257636	8.83960693	8.358413845	hypothetical protein
ACD58987	0	0	0	hypothetical protein
ACD58988	6.975905274	5.987721054	6.882202838	IS1112 transposase
ACD58990	7.868149655	7.912673814	7.642275573	phosphatidylglycerophosphatase B
ACD58991	7.450609176	7.976512572	8.770617647	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase
ACD58995	6.723258196	6.380305207	7.72644979	ISXoo2 transposase
ACD58996	6.942995324	7.336595819	7.244810966	S1 RNA binding domain protein
ACD58997	9.242876367	9.983335675	11.26370347	conserved hypothetical protein
ACD58999	6.71090284	7.582194682	5.96349262	hypothetical protein
ACD59000	10.95017677	10.73365092	11.1581931	PspC domain superfamily
ACD59001	7.254934119	6.646997842	6.471198843	poly-beta-hydroxybutyrate polymerase (Poly(3-hydroxybutyrate) polymerase) (PHB polymerase) (PHB synthase) (Poly(3-hydroxyalkanoate) polymerase)
ACD59002	6.80538275	6.98100779	6.520865361	PHA synthase subunit
ACD59003	7.575039984	8.026894097	6.598944275	CDP-diacylglycerol--serine O-phosphatidyltransferase
ACD59005	7.819463821	7.793733349	7.426843394	7,8-dihydro-8-oxoguanine-triphosphatase
ACD59006	9.172057411	8.925204293	9.62942766	conserved hypothetical protein
ACD59007	8.574483784	8.800576389	8.615419976	GTP-binding protein
ACD59010	7.432633762	6.831915233	5.587310979	oligoribonuclease
ACD59011	6.66860138	6.734614792	5.624776451	tRNA-specific adenosine deaminase
ACD59012	8.393467685	8.490401656	7.213755534	iron dependent repressor
ACD59014	8.71027953	9.25988682	8.687263693	hypothetical protein
ACD59017	10.53819863	9.268382927	9.590160353	conserved domain protein
ACD59019	10.98294368	11.08638174	11.17492568	conserved hypothetical protein
ACD59020	7.799838514	7.88006713	6.866178536	transcriptional regulator LysR family
ACD59023	6.894199333	7.315973724	6.132712552	GMP synthase
ACD59024	7.723271851	7.901952948	7.61579146	inosine-5'-monophosphate dehydrogenase
ACD59025	6.223795147	6.374363118	5.76212022	FolD bifunctional protein
ACD59028	6.887171865	6.160851633	6.450148897	transport protein
ACD59029	9.095774131	9.268010907	8.630434595	transport protein
ACD59030	10.39489137	9.889356416	8.757259986	hypothetical protein
ACD59031	9.092934164	9.233516623	9.289255814	UTP-glucose-1-phosphate uridylyltransferase
ACD59032	8.112632375	8.24701605	7.381075676	epimerase
ACD59033	8.00291063	8.162215073	7.668012723	lipopolysaccharide core biosynthesis protein
ACD59034	6.415243181	6.471673589	5.94535019	heat shock protein
ACD59035	9.154924409	9.279636115	9.101474119	conserved hypothetical protein
ACD59036	8.560485694	8.770987575	8.462853957	integration host factor, beta subunit
ACD59037	10.14015235	10.39466633	9.761333482	ribosomal protein S1
ACD59038	7.798944791	8.399594097	7.54814374	cytidylate kinase
ACD59047	6.301260223	6.446878175	5.846688871	discoidin domain protein
ACD59048	7.48039439	7.687634628	6.49869446	L-arabinose transport system permease protein AraQ
ACD59049	7.302712028	7.059733814	6.282866027	ABC transporter sugar permease
ACD59050	6.844385653	6.510408147	5.919828685	ABC transporter sugar binding protein

ACD59051	7.353790821	7.224078873	7.006623424	conserved hypothetical protein
ACD59052	6.996727686	6.699162923	7.40921271	TonB-dependent outer membrane receptor
ACD59053	8.216095893	7.970548844	8.319956568	transcriptional regulator LacI family
ACD59054	8.603659723	8.668615562	9.79757561	transcriptional regulator, LacI family
ACD59055	9.215637346	8.380733777	9.476772527	morphogene BolA protein
ACD59056	9.336992955	8.753440742	8.992459718	protein YciI
ACD59060	8.763527766	9.951822347	11.78481885	conserved hypothetical protein
PXO_rna25	0	0	0	XO_rna25 cdna:pseudogene chromosome:GCA_000019585.1:Chromosome:2691992:2692081:-1 gene:PXO_rna25 transcript:PXO_rna2
ACD59345	0	0	0	UDP-N-acetylglucosamine 1-carboxyvinyltransferase protein
PXO_rna26	0	0	0	XO_rna26 cdna:pseudogene chromosome:GCA_000019585.1:Chromosome:2904079:2904168:-1 gene:PXO_rna26 transcript:PXO_rna2
ACD59446	2.839623054	0	0	transposase (IS4 family)
ACD59448	0.946992804	1.536356332	0	ISXo1 transposase
ACD59450	7.390272156	7.321134394	8.002921878	RNA methyltransferase, TrmH family, group 3
ACD59451	8.020807749	7.754072416	6.072515306	conserved hypothetical protein
ACD59452	7.264799125	7.494623615	6.01732066	ribonuclease R
ACD59453	6.7380382	6.6779451	6.522292767	acetylhydrolase
ACD59454	9.251420867	8.988017144	8.256052968	conserved domain protein
ACD59455	7.460505043	7.263400669	8.009100789	acyl-CoA dehydrogenase, short-chain specific
ACD59459	8.206242724	8.207385321	7.080892125	N-acylglucosamine 2-epimerase
ACD59460	9.285256555	9.05604697	8.21158172	fructokinase
ACD59461	9.047432054	9.034196453	7.967341555	glucose-galactose transporter
ACD59462	8.35123962	8.558956363	6.578239833	transcriptional regulator
ACD59463	7.206975262	7.660181344	6.585970532	conserved hypothetical protein
ACD59464	7.79565657	8.039527755	6.509458329	nucleoprotein/polynucleotide-associated enzyme
ACD59465	9.688657704	10.30548039	9.039758032	conserved domain protein
ACD59466	8.365696911	8.65442838	7.713139027	UDP-glucose dehydrogenase
ACD59467	8.967266613	9.404281548	8.80116189	fkbp-type peptidyl-prolyl cis-trans isomerase\x3b rotamase
ACD59468	8.952732512	9.198567819	9.419109053	ABC transporter vitamin B12 uptake permease
ACD59474	8.300050489	8.433393486	7.73603656	hypothetical protein
ACD59476	8.024513613	8.455799821	7.299849074	fumarate hydratase class II
ACD59482	7.282689994	7.917604802	9.038587076	ISXoo2 transposase
ACD59483	6.737213536	7.408091926	7.036876927	conserved hypothetical protein
ACD59484	10.73697687	11.45401134	10.83624765	hypothetical protein
ACD59488	7.580032392	8.172122435	6.480425089	putative serine protease
ACD59499	0	0	8.310181045	hypothetical protein
ACD59502	6.759502082	6.600733606	6.633994925	prephenate dehydrogenase
ACD59503	6.079104993	6.077272912	6.084772254	pyridoxal kinase
ACD59504	7.268088126	7.692420223	7.008899172	chaperone protein DnaJ
ACD59505	9.513449293	10.09976859	11.29642299	chaperone protein DnaK
ACD59506	7.438850058	8.528856485	10.09138249	co-chaperone GrpE
ACD59507	7.187708372	7.467181645	7.193968819	heat-inducible transcription repressor HrcA
ACD59509	8.387220353	9.292280215	8.751818513	ferric uptake regulator Fur
ACD59511	7.927594281	7.165218555	7.134703537	conserved hypothetical protein
ACD59512	7.385310232	7.774892458	6.896065942	streptomyces cyclase/dehydrase superfamily
ACD59514	8.419656864	8.349953482	9.174988081	serine peptidase
ACD59515	9.432640025	9.595296649	8.236607417	conserved domain protein
ACD59520	6.930382533	6.772914953	6.745802035	glycosyltransferase
ACD59521	9.55749625	9.147408465	8.835905131	glycosyltransferase
ACD59522	7.924984667	9.978181326	10.81202484	glycosyltransferase
ACD59523	10.22755578	9.9391193	9.441016543	conserved hypothetical protein
ACD59527	6.230018514	6.269695227	5.18464132	putative PAS/PAC sensor protein
ACD59530	7.310558254	8.215309723	7.043650721	conserved hypothetical protein
ACD59533	7.224175366	7.30492167	6.436944686	multidrug resistance membrane translocase
ACD59534	7.835734632	7.216949518	7.815133485	multidrug resistance efflux pump
ACD59535	7.626322315	7.203445892	7.934646235	outer membrane efflux protein
ACD59536	7.733801724	7.923363144	7.489237846	transcriptional regulator MarR family
ACD59539	9.554822887	10.35770594	11.96443834	bacterioferritin
ACD59545	7.578274558	7.32978737	9.380999946	asparagine synthase (glutamine-hydrolyzing)
ACD59546	7.378017346	7.168912756	6.940108008	succinyl-diaminopimelate desuccinylase
ACD59547	7.367406014	7.484242881	6.535465131	histone acetyltransferase HPA2-related acetyltransferase
ACD59548	7.725632105	7.861756906	7.1248554	ArsC family protein

ACD59549	8.521329541	9.201606908	7.35838747	conserved hypothetical protein
ACD59550	7.752206676	7.96374576	7.569802455	2,3,4,5-tetrahydropyridine-2-carboxylate N-succin
ACD59551	7.529750684	7.539174324	7.061797795	protein-P-II uridylyltransferase
ACD59552	9.111018267	9.36965405	10.27052894	methionine aminopeptidase, type I
ACD59577	6.472361043	6.954487147	6.650692767	transposase
ACD59584	7.956376157	8.572976803	8.080812199	conserved hypothetical protein
ACD59594	6.730490516	6.442188786	7.191394858	putative ISXoo4 transposase
ACD59595	6.924848125	4.005310153	2.66982275	ISXoo8 transposase
ACD59596	6.650017748	6.096871142	7.095829503	conserved hypothetical protein
ACD59601	7.359854959	7.757643355	7.440395803	homocysteine S-methyltransferase
ACD59602	7.684292776	7.487647126	6.824016784	S-methylmethionine permease
ACD59603	3.709434016	5.926065857	6.092509801	ISXoo2 transposase
ACD59609	7.547411269	6.151010448	8.419323988	hypothetical protein
ACD59610	7.386328128	8.739557861	8.768243884	hypothetical protein
ACD59622	6.781464633	8.480228763	7.105688553	endoribonuclease L-PSP family
ACD59623	7.335801219	7.980116723	7.110822574	conserved hypothetical protein
ACD59624	7.558168124	7.557264563	7.718806834	conserved hypothetical protein
ACD59626	7.450246245	7.570713377	7.37503074	virulence protein
ACD59627	7.575274508	8.068821263	7.552461611	conserved hypothetical protein
ACD59628	7.814159448	8.34894056	6.397725966	2'-5' RNA ligase
ACD59629	12.22926345	12.89075827	11.53423478	conserved hypothetical protein
ACD59630	8.822338197	9.106866496	9.749324753	probable acyl-CoA dehydrogenase
ACD59631	7.80870038	7.991107968	8.018077746	MFS transporter
ACD59634	8.121243395	8.366199799	8.270566317	alkylphosphonate utilization operon protein PhnA
ACD59644	0	0	8.160295003	ISXo1 transposase
ACD59645	6.987912013	7.037371239	5.411765185	DnaK suppressor protein
ACD59647	9.314524334	8.964571912	10.12897383	hypothetical protein
ACD59648	9.488199658	10.66092291	10.95515585	conserved hypothetical protein
ACD59651	7.03178114	7.136488772	6.496190684	serine protease
ACD59663	6.984441246	6.689564749	6.764858325	oxidoreductase
ACD59664	5.827778385	5.350299217	6.370792009	oxidoreductase
ACD59665	9.519223434	9.739790734	8.550550566	conserved domain protein
ACD59666	10.23848834	10.47951756	8.502923275	purine phosphorylase, family 2
ACD59667	7.693626342	7.044689186	6.380041941	hypoxanthine-guanine phosphoribosyltransferase
ACD59668	7.221790099	7.472520264	8.05265499	beta-hexosaminidase
ACD59669	6.470728821	6.52501333	5.872621942	deoxyribodipyrimidine photolyase-related protein
ACD59670	6.679409722	6.963959565	5.724230061	lipoprotein, putative
ACD59672	6.694545939	6.581494365	5.537684337	polyketide synthase
ACD59673	7.850574422	6.856450429	7.51812594	adenylate cyclase
ACD59674	6.617299952	6.805073145	6.342014202	23S rRNA (uracil-5-)-methyltransferase RumA
ACD59677	6.633743605	7.051807107	7.459669316	DNA repair protein RecO
ACD59678	7.030722305	7.088120391	6.214536723	GTP-binding protein Era
ACD59679	7.995902795	8.031053274	6.4051687	ribonuclease III
ACD59680	7.753343794	7.579956993	6.747749908	conserved hypothetical protein
ACD59681	7.110300596	7.213045879	6.235941457	signal peptidase I
ACD59682	7.538615759	7.806388508	7.496821828	GTP-binding protein LepA
ACD59683	6.890860083	7.069100632	8.903785462	periplasmic protease
ACD59684	7.909821097	8.339279937	11.33218204	regulatory protein
ACD59685	8.56722599	8.5905122	11.66601091	RNA polymerase sigma-H factor
ACD59687	8.275081565	7.927090519	8.699444054	cobalt-zinc-cadmium resistance protein
ACD59688	0	0	7.085148431	hypothetical protein
ACD59689	6.27358489	6.51155343	5.539084348	3-hydroxyisobutyrate dehydrogenase
ACD59690	6.94646185	7.30058136	6.722520671	enoyl-CoA hydratase
ACD59691	7.323451137	7.794428864	7.889461374	enoyl-CoA hydratase
ACD59692	6.57075132	6.906698223	7.043771003	acyl-CoA dehydrogenase family member 8
ACD59693	6.683064786	7.093739741	7.392051187	methylmalonate-semialdehyde dehydrogenase
ACD59699	7.53439627	7.842934847	6.94716351	conserved hypothetical protein
ACD59700	6.616223879	6.709331997	6.087865891	F5/8 type C domain protein
ACD59702	8.627949671	7.909173056	7.589621188	TnpB
ACD59705	6.993923393	6.721591399	6.156091169	histidine kinase-response regulator hybrid protein
ACD59706	6.774404925	6.786544089	5.91750575	histidine kinase/response regulator hybrid protein
ACD59707	6.737740834	6.591716812	5.755632702	histidine kinase-response regulator hybrid protein
ACD59712	8.68116812	9.440163216	7.931334395	conserved hypothetical protein
ACD59714	7.55628379	7.888852817	6.713200903	homoserine dehydrogenase

ACD59715	7.169083184	7.461520374	6.142047816	O-succinylhomoserine (thiol)-lyase
ACD59716	7.590070506	7.723701896	6.572365232	homoserine O-acetyltransferase
ACD59725	9.262552958	9.461313681	7.967358848	CBS domain protein
ACD59726	7.264939834	6.935176839	6.288245963	SfII prophage-derived bactoprenol glucosyl transferase
ACD59727	7.515534274	7.350815454	6.472726576	monofunctional biosynthetic peptidoglycan transglycosylase
ACD59731	6.745802035	7.331812684	6.82822536	transcriptional regulator
ACD59734	7.565155405	8.239803762	7.137667457	conserved hypothetical protein
ACD59735	7.177180315	6.996004519	6.393790281	membrane protein, putative
ACD59737	11.98215223	12.2998176	12.74955941	hypothetical protein
ACD59739	8.377340692	8.05646973	8.936838136	glycine cleavage system H protein
ACD59740	7.259018204	7.520956481	6.989422885	glycine cleavage system T protein
ACD59741	9.163214412	9.8371091	8.021973793	nodulation protein nfed, C-terminal only
ACD59742	6.726027377	6.836050355	6.093887602	inner membrane protein
ACD59743	8.983891416	8.712179611	6.996851944	membrane protein YnfA
ACD59744	6.861434352	7.070936675	6.244736771	MazG family protein
ACD59745	7.729138065	7.437427507	6.70354372	3'(2'),5'-bisphosphate nucleotidase
ACD59746	8.319496007	8.361829757	6.591253043	ADP compounds hydrolase NudE
ACD59749	6.962687826	7.344721995	6.405456353	glucokinase
ACD59756	7.049064381	7.03115255	6.202735064	colicin V secretion/processing ATP-binding protein CvaB
ACD59757	3.915865041	4.381511804	5.217381959	peptidase, S54 (rhomboid) family, putative
ACD59760	11.849925	8.785364187	12.72231659	hypothetical protein
ACD59761	0	0	0	hypothetical protein
ACD59762	6.645038715	6.4180398	6.565853037	membrane-fusion protein
ACD59763	8.220165475	8.415306571	7.871572625	hypothetical protein
ACD59764	7.718724652	8.303680304	6.241491287	membrane-fusion protein
ACD59767	6.803627442	7.285929261	8.367628792	conserved hypothetical protein
ACD59769	7.544864001	7.093993207	7.406740734	RebB protein
ACD59772	8.979753855	8.685708929	8.479877249	copper homeostasis protein
ACD59773	7.347196137	7.321414043	7.3763338	N(4)-(Beta-N-acetylglucosaminyl)-L-asparaginase (Glycosylasparaginase) (Aspartylglucosaminidase) (N4-(N-acetyl-beta-glucosaminyl)-L-asparagine amidase) (AGA)
ACD59774	4.541874106	5.164150696	3.104425567	ISXo2 putative transposase
ACD59780	7.849661557	7.347373332	6.351912727	ribosomal protein alanine acetyltransferase
ACD59781	4.053033116	7.045868849	0	conserved hypothetical protein, putative
ACD59782	5.949000243	6.636249036	-4.370268689	glutamate methyltransferase
ACD59783	8.193382439	8.378442261	6.965022341	PilL protein
ACD59785	7.184181096	7.525035261	6.666373148	pilus biogenesis protein
ACD59786	7.61225665	7.760939453	6.570472039	pilus biogenesis protein
ACD59787	9.921775494	10.55754029	7.07480511	PilH
ACD59788	10.6454603	11.46971812	10.05540446	type IV pilus response regulator PilG
ACD59791	8.04094721	7.870081085	8.444033397	dinitrogenase reductase activationg glycohydrolase
ACD59792	7.525638256	7.430360551	8.810089585	glycoprotease family protein
ACD59793	6.766131326	6.654449862	6.27306078	ATP-dependent helicase
ACD59794	6.46280489	6.482474011	5.475927939	lipoprotein, putative
ACD59795	6.811252657	7.001036565	6.684229648	penicillin-binding protein 1B
ACD59797	7.542296748	7.519219501	7.854513119	tetratricopeptide repeat domain protein
ACD59798	7.168802469	7.569946723	6.868625039	GTP pyrophosphokinase (ATP\x3aGTP 3'-pyrophosphotransferase)(ppGpp synthetase I) ((P)ppGpp synthetase)
ACD59807	5.86537696	7.288496992	5.958448316	putative chemotaxis protein CheX
ACD59811	6.816394909	6.821340311	6.212544049	ATP-dependent helicase HrpA
PXO_rna28	0	0	0	XO_rna28 cdna:pseudogene chromosome:GCA_000019585.1:Chromosome:3342212:3342287:-1 gene:PXO_rna28 transcript:PXO_rna2
ACD59817	6.433692257	6.9912724	6.434551504	ExsB protein
ACD59821	4.367091446	0	0	ISXoo13 transposase
ACD59822	8.23329851	8.417371536	8.217405225	radical activating enzyme
ACD59823	9.222410938	9.300871883	8.794253392	tol-pal system protein YbgF, putative
ACD59824	9.473425706	10.12639474	9.891192837	outer membrane protein P6
ACD59825	7.985893156	8.700002682	9.281204441	Tol-Pal system beta propeller repeat protein TolB
ACD59826	7.876197677	7.913685293	9.259818574	protein TolA
ACD59827	7.016407174	7.20630134	7.988474515	protein TolR
ACD59828	7.499925592	7.569111289	8.731906173	protein TolQ
ACD59829	9.172294985	9.956345662	11.50507216	thioesterase family protein
ACD59830	6.067647321	6.508539576	5.847859143	holliday junction DNA helicase RuvB
ACD59831	7.585413272	7.550631365	6.441380559	potassium uptake protein

ACD59832	7.961310772	8.166449333	7.194993181	holliday junction DNA helicase RuvA
ACD59833	7.557425408	7.554780687	7.054522922	crossover junction endodeoxyribonuclease RuvC
ACD59834	7.847777731	8.232065906	8.350086127	conserved hypothetical protein
ACD59835	6.681814672	7.121212307	6.358834026	conserved hypothetical protein
ACD59836	8.242612032	7.73752453	8.069385318	acetyltransferase
ACD59837	7.409815196	7.16629366	7.785158177	aspartyl-tRNA synthetase
ACD59839	10.50872575	10.43878146	11.3276593	hypothetical protein
ACD59840	8.941379256	8.350046334	9.714367455	putative regulatory protein, FmdB family
ACD59846	7.043289817	7.083266564	6.340320138	membrane protein, putative
ACD59847	0	0	0	hypothetical protein
ACD59851	0	4.009409881	3.932458085	ISXo8 transposase
ACD59864	7.474517164	7.334890015	7.410968551	conserved hypothetical protein
ACD59865	10.00894678	10.13210125	11.24029048	protein GntY
ACD59871	6.982594355	7.218296831	6.892148128	ribosomal large subunit pseudouridine synthase C
ACD59873	6.746433703	6.365940943	6.086932341	ISXoo11 transposase
ACD59874	6.794142898	6.739834604	8.264320611	ISXoo12 transposase
ACD59875	7.493190976	7.471472004	6.701978697	transcriptional regulator LuxR/uhpA family
ACD59876	7.46760555	7.313563311	7.83622713	rhodanese domain protein
ACD59877	8.589044357	8.394522716	8.2526134	conserved hypothetical protein
ACD59880	6.26283527	6.327595756	5.463190839	VI polysaccharide biosynthesis protein VipA/tviB
ACD59881	9.321425318	0	7.860969004	hypothetical protein
ACD59887	5.324454205	1.196808453	2.085849516	ISXoo13 transposase
ACD59889	10.30562859	10.87239016	10.04401154	conserved hypothetical protein
ACD59891	0	0	2.984736984	ISXo1 transposase
ACD59897	10.19262571	10.5881993	9.417806112	conserved domain protein
ACD59898	0	0	2.722065949	transposase
ACD59899	7.841935391	7.865974473	7.576559928	nitrate transport ATP-binding protein
ACD59900	6.398278535	7.954940735	6.815882789	histidine kinase/response regulator hybrid protein
ACD59901	10.17758149	9.919828685	8.291502262	conserved domain protein
ACD59906	0	0	10.25731712	transcriptional regulator, AraC family
ACD59907	5.424404828	5.777603822	5.122656155	AraC-type DNA-binding domain-containing protein
ACD59908	7.301679092	7.100620293	7.515928444	transcriptional regulator, AraC family
ACD59909	7.216309347	6.709924709	6.533092963	conserved hypothetical protein
ACD59910	6.375788395	6.497481438	5.801021521	molybdopterin guanine dinucleotide synthase
ACD59911	6.802348337	6.873800897	5.961125522	molybdopterin biosynthesis
ACD59912	9.013534839	7.787693647	10.17033821	hypothetical protein
ACD59915	9.224787946	10.2595432	7.16919345	exodeoxyribonuclease III
ACD59920	7.365465086	7.10867081	6.747159107	conserved hypothetical protein
ACD59924	9.987022358	8.646648707	10.11318217	lipoprotein, putative
ACD59925	7.30543251	6.732459158	6.568541398	peptidase
ACD59926	7.179958837	7.164102412	6.475200022	xylosidase\x3b arabinosidase
ACD59927	6.84393361	6.663045687	6.13029461	conserved hypothetical protein
ACD59928	7.136191386	6.769599854	6.875386905	TonB-dependent outer membrane receptor
ACD59931	6.609765303	6.273403991	6.38407399	conserved hypothetical protein
ACD59935	7.930382533	8.624908747	8.747182609	conserved hypothetical protein
ACD59936	7.222002712	6.89251246	6.921019706	peptidase
ACD59937	7.353358582	7.459464407	6.798024585	amino acid permease
ACD59938	6.394250026	6.191479744	6.404637496	conserved hypothetical protein
ACD59939	7.301989965	6.277190675	7.150204239	lipoprotein, putative
ACD59940	6.622781038	6.072174417	6.90480921	proline dipeptidase
ACD59941	6.415229658	6.546226191	7.526131427	ketoglutarate semialdehyde dehydrogenase
ACD59942	7.017855115	6.759821621	8.597136331	dihydrodipicolinate synthetase
ACD59943	6.131048208	5.785553167	7.064494885	oxidoreductase
ACD59944	8.131877534	8.238017739	8.453970202	sarcosine oxidase alpha subunit
ACD59945	6.114035883	5.781094758	7.175514621	D-amino acid oxidase
ACD59946	6.602194065	6.470051981	7.739699614	proline racemase
ACD59949	7.507961095	7.100410042	7.977995369	hypothetical protein
ACD59954	11.24299542	8.781720342	9.465731683	hypothetical protein
ACD59955	6.147320947	6.457259384	6.444496459	sensor histidine kinase
ACD59961	7.213590303	7.465811254	6.879632258	conserved hypothetical protein
ACD59963	10.64844747	9.782223433	11.75084095	hypothetical protein
ACD59964	8.613483769	8.587297476	8.751540712	conserved hypothetical protein
ACD59966	7.077296415	7.023743266	6.433625498	conserved hypothetical protein
ACD59967	7.537932775	8.068407482	7.315403201	conserved hypothetical protein

ACD59971	7.602305433	7.403881215	8.764038899	ISXoo2 transposase
PXO_rna30	0	0	0	XO_rna30 cdna:pseudogene chromosome:GCA_000019585.1:Chromosome:3494266:3494341:-1 gene:PXO_rna30 transcript:PXO_rna3
ACD59973	7.530804267	7.154463719	7.173657151	serine peptidase
ACD59974	6.95182089	6.632982115	7.432642113	GumN Protein
ACD59975	8.349060024	8.214702817	8.75033852	conserved hypothetical protein
ACD59976	8.707790496	8.606246036	7.568693391	exopolysaccharide xanthan biosynthesis glycosyltransferase GumM
ACD59977	8.261643639	8.296994188	7.76059355	exopolysaccharide xanthan biosynthesis pyruvyltransferase GumL
ACD59978	7.906289347	7.909515114	7.193929406	exopolysaccharide xanthan biosynthesis glucuronosyltransferase GumK
ACD59979	8.366483962	8.469124878	6.71781349	exopolysaccharide xanthan biosynthesis protein GumJ
ACD59980	7.739659115	7.7420736	6.642077694	exopolysaccharide xanthan biosynthesis glycosyltransferase GumI
ACD59981	7.763132676	7.897676073	6.843908492	exopolysaccharide xanthan biosynthesis glycosyltransferase GumH
ACD59982	8.027043438	8.298768273	7.066035358	exopolysaccharide xanthan biosynthesis acetyltransferase GumG
ACD59983	8.348533422	8.264428525	7.604404968	exopolysaccharide xanthan biosynthesis acetyltransferase GumF
ACD59984	7.821378582	8.244596931	7.096788934	exopolysaccharide xanthan biosynthesis polymerase GumE
ACD59986	9.662855264	9.719601017	9.716864036	exopolysaccharide xanthan biosynthesis glycosyltransferase GumD
ACD59987	8.416379539	8.85640374	7.851923903	exopolysaccharide xanthan biosynthesis chain length determinant protein GumC
ACD59988	8.776360649	9.410659102	8.874932181	exopolysaccharide xanthan biosynthesis export protein GumB
PXO_rna31	0	0	0	XO_rna31 cdna:pseudogene chromosome:GCA_000019585.1:Chromosome:3515163:3515239:-1 gene:PXO_rna31 transcript:PXO_rna3
ACD59989	8.771264959	9.124028232	7.641285904	transcription regulator protein
ACD59990	9.508488077	10.17155212	7.982942253	integration host factor, alpha subunit
ACD59991	7.054240716	6.746877049	6.060438709	phenylalanyl-tRNA synthetase, beta subunit
ACD59992	7.26516494	7.318931393	6.869674034	phenylalanyl-tRNA synthetase, alpha subunit
ACD59993	7.51843285	8.619471703	8.465509267	ribosomal protein L20
ACD59994	11.0115767	11.76590764	11.40504571	ribosomal protein L35
ACD59995	9.95434319	10.92878483	8.581193048	translation initiation factor IF-3
ACD59996	7.514816607	7.865949736	7.128128399	threonyl-tRNA synthetase
ACD59998	9.826313315	9.82767297	9.720550382	integrase core domain protein
ACD60002	9.358385272	9.125444468	7.224725253	conserved domain protein
PXO_rna32	0	0	0	XO_rna32 cdna:pseudogene chromosome:GCA_000019585.1:Chromosome:3526449:3526523:-1 gene:PXO_rna32 transcript:PXO_rna3
ACD60004	6.931293023	6.993832841	6.134896531	excinuclease ABC, B subunit
ACD60005	11.14588121	8.513617071	0	hypothetical protein
ACD60007	7.740414919	7.438018327	7.931943021	conserved hypothetical protein
ACD60008	0	0	0	conserved hypothetical protein
ACD60009	3.350200191	2.584505575	2.948892347	ISXoo6 transposase
ACD60010	6.143321984	6.010003241	6.111265063	conserved hypothetical protein
ACD60011	7.282541739	7.544763562	7.37313486	conserved hypothetical protein
ACD60014	0	0	0	DNA methylase
ACD60015	7.247937005	6.05022088	7.037327307	phage portal protein, pbsx family
ACD60016	6.044098992	5.437267695	5.408249907	phage terminase, ATPase subunit
ACD60042	0	0	0	phage-related protei
ACD60043	0	0	0	hypothetical protein
PXO_rna33	0	0	0	XO_rna33 cdna:pseudogene chromosome:GCA_000019585.1:Chromosome:3571806:3571882:-1 gene:PXO_rna33 transcript:PXO_rna3
ACD60056	11.41639115	11.33343492	9.713097775	type IV pilin
ACD60057	9.054389967	9.15763494	7.595660298	PilY1
ACD60058	9.178166855	9.421246446	7.151219542	PilX
ACD60059	9.596694797	9.810092799	7.209775012	prepilin-type N-terminal cleavage/methylation domain protein
ACD60060	8.669622095	9.336477549	6.626789546	type IV pilus modification protein PilV
ACD60061	9.613010365	9.805516569	7.401041624	pre-pilin like leader sequence
ACD60062	7.390616101	7.657411351	6.660281193	decarboxylase family protein
ACD60063	6.459682429	6.191416574	6.792191622	TonB-dependent outer membrane Receptor/Oar-like
ACD60064	7.317801501	7.729430411	7.006455123	multiple antibiotic resistance protein MarC
ACD60065	6.447362644	7.297787524	6.236178789	short chain dehydrogenase
ACD60066	8.501363505	8.052111533	7.553859646	putative glutaredoxin homolog
ACD60068	7.327552644	7.531771325	6.527195477	phosphoribosylaminoimidazole carboxylase, ATPase subunit
ACD60069	7.140901329	7.443192215	7.782402012	phosphoribosylaminoimidazole carboxylase, catalytic subunit
ACD60073	8.368096075	8.396805974	7.898208353	polyribonucleotide nucleotidyltransferase
ACD60074	11.31936165	11.76082804	12.09673821	ribosomal protein S15
ACD60075	6.725113999	6.797804167	6.115376641	tRNA pseudouridine synthase B

ACD60076	7.435370233	6.962063107	5.141162996	ribosome-binding factor A
ACD60077	8.209253519	8.37390047	7.945830064	translation initiation factor IF-2
ACD60078	7.827876172	8.153739481	7.569491092	N utilization substance protein A
ACD60079	8.431948833	8.44872754	7.599481457	YhbC family protein
PXO_rna34	0	0	0	XO_rna34 cdna:pseudogene chromosome:GCA_000019585.1:Chromosome:3600803:3600879:-1 gene:PXO_rna34 transcript:PXO_rna3
ACD60080	8.57219998	8.454480262	7.477952501	NADH-ubiquinone oxidoreductase Nqo14 subunit
ACD60081	8.056518502	7.950474247	6.039149363	NADH-ubiquinone oxidoreductase Nqo13 subunit
ACD60082	9.439257431	9.395587687	8.933327723	NADH-quinone oxidoreductase chain l
ACD60083	9.379917652	9.047042093	8.308461904	NADH-quinone oxidoreductase chain 11
ACD60084	8.529653091	8.772891866	7.460169172	NADH-ubiquinone oxidoreductase Nqo10 subunit
ACD60085	7.821901507	7.912404366	7.345094718	NADH-quinone oxidoreductase chain 9
ACD60086	9.387866548	9.527664662	8.886675122	NADH-ubiquinone oxidoreductase chain 1
ACD60087	8.05435469	8.097616063	7.507120697	NADH-quinone oxidoreductase, chain g
ACD60088	7.959236927	7.862934854	7.728240262	NADH-quinone oxidoreductase, f subunit
ACD60089	8.918484629	8.824522844	9.540207486	NADH-ubiquinone oxidoreductase Nqo2 subunit
ACD60090	7.809079972	7.870050252	7.813178339	NADH dehydrogenase i, d subunit
ACD60091	7.911290112	7.538910584	7.952665544	NADH-quinone oxidoreductase chain c
ACD60092	8.160365602	8.937011814	8.373191425	NADH-ubiquinone oxidoreductase 20 kda subunit
ACD60093	10.59164389	10.89471168	11.34911533	NADH-quinone oxidoreductase chain a
PXO_rna35	0	0	0	XO_rna35 cdna:pseudogene chromosome:GCA_000019585.1:Chromosome:3616006:3616090:-1 gene:PXO_rna35 transcript:PXO_rna3
ACD60094	8.874723207	9.55661909	9.050469047	preprotein translocase subunit SecG
ACD60095	7.461160177	7.636769608	6.543737137	triosephosphate isomerase
ACD60097	6.81548577	7.311503115	7.39516565	cyanoglobin
ACD60098	9.699648794	11.4260498	10.09821636	conserved hypothetical protein
ACD60102	11.61886265	11.72496569	8.519140856	hypothetical protein
ACD60103	8.052350679	8.451660338	5.985511815	Putative signal protein with HAMP, GGDEF and EAL domains
ACD60104	9.232459303	9.943852483	7.377653034	conserved hypothetical protein
ACD60105	8.311766476	8.338455615	7.344979361	oxidoreductase
ACD60107	7.460578761	7.704194159	4.248671449	phosphoglucosamine mutase
ACD60108	7.80830138	8.313259459	7.824379638	acetyl-CoA carboxylase, carboxyl transferase, beta subunit
ACD60109	6.863442934	6.42786928	6.725318537	tryptophan synthase, alpha subunit
ACD60110	7.984800089	9.183672596	8.524996097	putative membrane protein
ACD60111	8.540306306	8.464986762	9.250158643	tryptophan synthase, beta subunit
ACD60113	8.718094436	9.780401971	9.953829773	N-(5'phosphoribosyl)anthranilate isomerase
ACD60114	7.915831587	8.317783416	8.215426219	tRNA pseudouridine synthase A
ACD60115	10.06501215	10.87318262	10.14296221	glyoxalase family protein
ACD60116	9.661013801	9.892705215	9.272844366	conserved hypothetical protein
ACD60117	6.79301148	7.200437653	6.666614587	FimV
ACD60119	7.301477904	7.385292974	6.6574971	aspartate-semialdehyde dehydrogenase
ACD60120	7.242202337	7.061743801	6.47938741	glyoxylate reductase
ACD60121	7.386604044	7.670401321	6.772175989	chorismate synthase
ACD60122	7.08329848	6.842061147	7.238719996	modification methylase, HemK family
ACD60125	6.878259406	7.000811288	6.83960693	membrane-bound lytic murein transglycosylase D
ACD60128	4.672425342	5.023530379	4.448689552	transposase
ACD60129	0	2.179794466	-0.427139428	IS1112 transposase
ACD60131	7.08676254	6.365389845	6.332525348	conserved hypothetical protein
ACD60136	7.231432408	7.166132948	6.850024271	deoxycytidine triphosphate deaminase
ACD60137	6.789716212	7.049271356	6.139209567	conserved hypothetical protein
ACD60138	6.095394913	5.760867619	6.133043546	transposase
ACD60140	7.986211811	8.664457951	8.891829261	peptidase, S54 (rhomboid) family, putative
ACD60141	4.435495252	5.5127926	5.169772709	methylated-DNA-protein-cysteine S-methyltransferase related protein
ACD60142	10.17507544	8.621916332	8.08418654	glutathione reductase
ACD60143	2.08971847	2.675858828	1.093174775	ISXoo10 transposase
ACD60144	7.643387238	7.083692059	7.398367474	reductase
ACD60145	8.773182075	7.570015055	7.820600219	reductase
ACD60146	7.598447093	6.98414499	6.295552227	D-amino acid dehydrogenase subunit
ACD60147	7.72389981	7.725229907	6.461183102	transport protein
ACD60148	7.267339156	8.574370247	7.614113505	peptidyl-prolyl cis-trans isomerase
ACD60152	6.486065915	6.448578885	6.120548937	acyl-CoA thioester hydrolase
ACD60153	7.349515668	6.792048425	6.410746432	conserved hypothetical protein
ACD60154	8.527883562	8.850402522	8.146232623	conserved hypothetical protein

ACD60155	7.010052491	6.949593293	7.611541271	glutamate symport protein
ACD60162	7.595503661	7.566023585	7.989564803	conserved hypothetical protein
ACD60163	9.819639447	10.23981331	9.561033947	conserved hypothetical protein
ACD60164	7.486086838	7.161283075	6.754647033	PmbA
ACD60166	11.78357534	12.37972492	13.06953368	conserved hypothetical protein
ACD60167	8.814399814	8.72316944	10.10227757	TldD
ACD60169	6.350357568	6.238471618	6.000085657	conserved hypothetical protein
ACD60170	7.637733402	7.735434172	7.508872295	ribonuclease G
ACD60171	8.063848043	7.386216022	7.578636862	septum formation protein Maf
ACD60176	6.776025006	7.193239504	6.780388847	conserved hypothetical protein
ACD60178	8.413259804	8.45450905	7.678987388	DnaJ domain protein
ACD60179	9.320491447	9.557115192	8.868350323	domain of unknown function superfamily
ACD60180	6.342686294	6.268571006	6.114227497	nicotinate (nicotinamide) nucleotide adenylyltransferase
ACD60181	6.753577796	6.93228563	6.16654072	DNA polymerase III, delta subunit
ACD60182	7.776321166	8.244663523	8.668544652	lipoprotein
ACD60183	7.413678697	7.469991766	7.934080042	leucyl-tRNA synthetase
ACD60184	7.54280747	7.552845822	6.684608376	membrane protein, putative
ACD60187	2.964766422	2.566386543	2.544646116	ISXo5 transposase
ACD60190	9.599155972	8.011557136	9.570658359	hypothetical protein
ACD60193	9.047612	8.550596737	7.747971396	conserved hypothetical protein
ACD60195	0	0	-0.975280337	ISXo8 transposase
ACD60197	3.956251849	2.872458437	2.138109984	ISXo5 transposase
ACD60208	8.351681327	9.015440143	8.627876735	virulence regulator
ACD60209	8.982625726	9.141141533	10.32110507	conserved hypothetical protein
ACD60210	10.34219693	9.864457012	9.387739486	transposase
ACD60212	7.066971764	8.092545742	7.747655933	ISXoo3 transposase ORF A
PXO_rna36	0	0	0	XO_rna36 cdna:pseudogene chromosome:GCA_000019585.1:Chromosome:3730177:3730250:-1 gene:PXO_rna36 transcript:PXO_rna3
ACD60216	9.221625786	9.450557629	8.577500583	lipase\x3b esterase
ACD60221	8.335001713	8.70752134	8.482021368	rieske [2Fe-2S] domain, putative
ACD60232	6.407288162	6.280408891	5.88448803	carboxylesterase
ACD60233	7.197246186	7.537187333	6.537212187	tRNA/rRNA methyltransferase
ACD60234	11.09669539	10.56672955	10.83016657	conserved domain protein
ACD60235	0	9.378442261	8.864167569	acetyltransferase
ACD60236	8.979782431	9.056542887	0	acetyltransferase
ACD60237	0	0	0	ISXo5 transposase
ACD60239	6.798063479	6.776196128	5.909300287	aminopeptidase N
ACD60240	6.896308182	7.01108186	5.90408664	acriflavin resistance protein
ACD60241	6.910552793	6.682573297	5.818559171	RND efflux membrane fusion protein
ACD60244	6.843745217	7.285522438	6.35910119	CysN/CysC bifunctional enzyme required for AvrXa21 activity Q (raxQ)
ACD60245	7.02986143	6.781267903	6.066138715	sulfate adenylyltransferase subunit 2 required for AvrXa21 activity P (raxP)/ATP sulfurylase small subunit RaxP
ACD60249	7.198189631	7.387939765	6.76915021	sulfite reductase [NADPH] flavoprotein alpha-component
ACD60250	6.74387845	6.847270367	6.393568933	TonB-dependent receptor
ACD60251	8.476410042	9.27290267	8.926998637	conserved hypothetical protein
ACD60253	8.926859322	9.117910579	9.319315354	conserved hypothetical protein
ACD60254	8.044558053	8.799349626	8.819684148	transcriptional regulator LysR family
ACD60260	8.646223872	8.618029373	8.844225571	fructose-bisphosphate aldolase class-I
ACD60261	7.626862538	7.680127408	7.857178584	pyruvate kinase
ACD60262	7.426541524	7.719197133	6.494356404	indigoidine synthesis like protein
ACD60263	7.420347653	7.415674173	7.760227601	phosphoglycerate kinase
ACD60264	6.779285989	6.618201942	5.875917643	conserved hypothetical protein
ACD60265	7.454652983	7.400239045	6.542163621	membrane protein, putative
ACD60267	7.284384575	6.679719356	6.362650477	isrso5-transposase protein
ACD60271	6.761524639	5.996639569	6.381996237	conserved hypothetical protein
ACD60272	7.67093945	7.457265951	6.755501853	transcriptional regulator AraC/xylS family
ACD60273	6.689620656	7.786027797	7.587934995	conserved hypothetical protein
ACD60275	6.930512638	7.814665773	6.835671479	transposase
ACD60276	9.213043448	9.569350577	9.313787758	conserved domain protein
ACD60278	7.759408869	7.936184449	7.534092738	alanyl dipeptidyl peptidase
ACD60279	7.128221215	5.985302319	7.537715394	conserved hypothetical protein
ACD60281	6.86139713	6.910864551	6.17511337	oligopeptide transporter, OPT family
ACD60284	8.215867851	9.010077674	9.020816082	HD domain protein
ACD60285	6.435370233	5.898950796	5.472653477	error-prone DNA polymerase

ACD60287	6.257870546	5.772202387	4.779380553	conserved hypothetical protein
ACD60288	5.519736884	5.809679394	5.300914427	conserved hypothetical protein
ACD60289	6.961843235	7.14201513	7.054837626	LexA repressor
ACD60292	8.59840615	8.432470912	9.394722056	conserved hypothetical protein
ACD60293	6.818326528	6.765415401	7.080593713	carbohydrate kinase superfamily
ACD60294	7.469837148	7.19913246	6.365849982	phosphoglycerate mutase family protein, putative
ACD60296	8.23175879	9.200275795	8.449722307	conserved hypothetical protein
ACD60297	8.343643218	9.029566075	7.043705396	synthetase/amidase
ACD60298	7.066541308	7.203269687	7.165982264	conserved hypothetical protein
ACD60300	0	0	0	conserved hypothetical protein
ACD60301	0	0	0	conserved hypothetical protein
ACD60303	0	0	0	HsdS polypeptide, part of CfrA family
ACD60304	0	0	0	type I restriction enzyme EcoEI M protein
ACD60305	0	0	0	conserved hypothetical protein
ACD60306	0	0	0	conserved hypothetical protein
ACD60307	0	0	0	type I restriction enzyme EcoAI R protein
ACD60308	0	0	2.400611702	plasmid stabilization system
ACD60309	0	0	0	conserved hypothetical protein
AGS47854	8.017860681	0	0	Putative DNA-entry nuclease precursor (N-terminal fragment), authentic frameshift
ACD60314	8.827987287	9.485203401	9.843829997	plasmid stabilization system
ACD60315	6.871966824	7.205363186	7.118235121	conserved hypothetical protein
ACD60317	8.964026011	8.68267863	8.719501768	conserved hypothetical protein
ACD60318	7.418485137	6.619993963	6.999729469	conserved hypothetical protein
ACD60319	7.697044004	7.665577531	7.503475951	conserved hypothetical protein
ACD60320	6.861409537	6.29556692	7.329796338	conserved hypothetical protein
ACD60322	4.77367991	5.093002325	5.457068911	Rhs element Vgr protein
ACD60323	10.32921331	9.943732365	10.11538184	putative VGR-related protein
ACD60324	9.554134101	9.958330857	9.601267521	hypothetical protein
ACD60325	7.913858789	7.483356298	7.486609803	type VI secretion ATPase, ClpV1 family
ACD60326	7.484009198	7.088692851	6.507791469	conserved hypothetical protein
ACD60327	7.351999272	7.374882986	6.69631382	EvpF
ACD60328	9.561140899	9.577980119	7.180346807	conserved hypothetical protein
ACD60329	13.10104661	12.9889793	10.28437301	hypothetical protein
ACD60390	7.969162005	7.571365851	6.844234988	protease
ACD60391	7.60829179	7.618025701	7.721762266	nuclear protein SET
ACD60399	9.237045004	0	8.498378534	conserved domain protein
ACD60415	0	0	7.961304984	hypothetical protein
ACD60416	7.362136705	7.126776735	7.416265521	tetratricopeptide repeat family
ACD60417	6.506971594	6.483106345	6.130253418	Hsp90xo protein
ACD60418	8.521337394	8.992595673	9.82793808	HrpX/HrpB
ACD60419	0	6.555336097	7.869248357	Rfc5 protein
ACD60421	8.504262852	9.401359543	8.592886792	conserved hypothetical protein
ACD60422	5.040826693	4.237020617	4.598234175	ISXoo5 transposase
ACD60423	7.061765399	6.11047809	6.15163764	xylanase
ACD60426	7.848015692	7.863504883	7.653826747	conserved hypothetical protein
ACD60427	6.365302349	6.341784766	6.429729769	ABC transporter ATP-binding protein
ACD60432	8.120662976	8.117637907	8.332882443	cytochrome P-450 hydroxylase
ACD60434	5.769930385	4.827727583	5.058874934	ISXoo3 transposase ORF A
ACD60442	8.549399641	8.596085371	8.52483943	cobalamin 5'-phosphate synthase
ACD60443	6.330683877	5.963578161	6.627532425	alpha-ribazole-5'""-phosphate phosphatase
ACD60444	6.858727024	6.912398377	7.632980661	nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase (NN\x3aDBI PRT) (N(1)-alpha-phosphoribosyltransferase)
ACD60445	8.700727535	8.182304958	8.785373996	cobinamide kinase / cobinamide phosphate guanyltransferase superfamily
ACD60446	8.144632753	8.053100473	8.080572395	adenosyl cobinamide kinase\x3b adenosyl cobinamide phosphate guanylyltransferase
ACD60447	8.699919422	8.421038111	8.930891059	cob(I)alamin adenosyltransferase
ACD60448	6.972508859	6.561072527	7.694267335	conserved hypothetical protein
ACD60449	8.575626222	7.841721581	8.604201083	conserved hypothetical protein
ACD60452	6.260462314	6.082634472	5.443500567	TonB-dependent outer membrane Receptor
ACD60453	7.237391631	6.76655541	6.965530348	ISxac3 transposase
ACD60454	3.986465547	3.813083399	4.12384826	transposase
ACD60458	7.668161683	7.998703246	7.259479648	conserved hypothetical protein
ACD60459	7.697280366	7.902115798	8.441159753	ATP-dependent chaperone ClpB
ACD60463	3.858965671	2.913733874	2.887642241	ISXo8 transposase

ACD60464	5.546227734	4.30898696	0	ISXo8 transposase
ACD60465	7.082564222	7.028823281	7.688061435	putative heat shock protein 15 homolog
ACD60467	9.949320439	10.41324711	11.61541354	ribosomal protein L19
ACD60468	7.777735312	8.115953991	8.252215998	tRNA (guanine-N1)-methyltransferase
ACD60469	8.660323984	9.693976485	9.37271926	16S rRNA processing protein RimM
ACD60470	10.50716035	11.71160245	12.01203435	ribosomal protein S16
ACD60471	7.466537397	7.361996394	6.100346961	conserved hypothetical protein
ACD60472	6.30983829	6.206861987	6.007392872	2-nitropropane dioxygenase
ACD60473	7.439298993	7.106463486	6.375282757	conserved hypothetical protein
ACD60474	7.149045921	7.329437582	7.078332301	signal recognition particle protein
ACD60475	1.583384291	2.772402997	1.838040091	ISXo5 transposase transposase
ACD60476	5.662649863	6.860280012	4.031906825	transposase
ACD60478	7.455746404	7.23308276	6.838535836	aldose 1-epimerase
ACD60480	8.674474776	8.464484488	10.39534133	transposase
ACD60482	6.003570756	5.686685404	6.327121455	transposase
ACD60484	7.982725539	7.614746647	7.884951958	conserved hypothetical protein
ACD60488	9.393845183	10.66031685	11.58935153	DNA transport competence protein
ACD60490	6.26761632	5.727974895	5.850251859	ISXoo2 transposase
ACD60494	7.087441625	7.071816289	5.746318142	replication related protein
ACD60495	7.528039899	7.349825247	6.431273609	permease
ACD60496	6.43301117	7.062909607	6.36346197	conserved hypothetical protein
ACD60503	8.009190388	7.713469001	8.464688685	conserved hypothetical protein
ACD60504	6.404835017	6.344757496	6.819872517	UDP-N-acetylglucosamine 1-carboxyvinyltransferase
ACD60505	8.545234792	9.296269257	10.92069525	BolA superfamily transcriptional regulator
ACD60520	8.877808655	7.821314797	8.589969422	hypothetical protein
ACD60523	8.149985856	8.29327851	8.264428525	cytochrome D ubiquinol oxidase, subunit II
ACD60524	6.909557116	6.881175155	8.883083126	cytochrome D ubiquinol oxidase subunit I
ACD60525	7.791462469	9.595731152	8.483275673	conserved hypothetical protein
ACD60527	6.870512681	7.185658449	5.744938757	amino acid transporter
ACD60528	6.233797966	6.407444531	5.738362528	proline imino-peptidase
ACD60529	8.443055425	8.578833073	8.502656801	transcriptional regulator AhyR/AsaR family
ACD60533	9.954779379	9.684159502	7.959381846	hypothetical protein
ACD60536	7.783882223	7.805098948	6.007774078	tryptophan halogenase
ACD60537	7.117923562	6.54773206	6.432717268	pass1 domain protein
ACD60538	7.380209952	7.399393293	6.775590529	SapC superfamily
ACD60540	6.912386401	6.495714347	5.821051976	TonB-dependent receptor
ACD60541	10.73018989	11.05459075	9.248449447	hypothetical protein
ACD60542	7.274634403	6.768091672	6.644577357	peptidase
ACD60543	7.891650058	7.518039363	6.818428793	redox-sensitive transcriptional activator SoxR
ACD60544	6.827260126	7.164283467	6.052485453	synthetase/amidase
ACD60545	6.574030341	7.066369089	6.386581628	lipoprotein, putative
ACD60546	8.481222238	9.013819539	8.475437567	conserved hypothetical protein
ACD60547	7.829266074	7.971865394	7.789540166	conserved hypothetical protein
ACD60548	7.207687909	6.74046889	6.613419675	voltage-gated ion channel superfamily protein
ACD60549	7.302940453	7.337193713	7.504056233	PspA/IM30 family protein
ACD60550	8.035722872	8.027336545	8.556762766	conserved hypothetical protein
ACD60551	7.089826499	7.466472141	7.386647151	pyridoxamine 5'-phosphate oxidase
ACD60556	4.992070476	5.473640817	6.315673095	transposase, IS30 family
ACD60567	0	0	0	hypothetical protein
ACD60577	6.872213144	6.949418205	6.826891643	TonB-dependent outer membrane Receptor
ACD60581	7.142566604	7.181331185	6.349839398	azurin
ACD60582	8.058543793	7.665016072	7.089243894	TdcF
ACD60583	8.698367825	9.226756568	8.136150363	cytochrome C6
ACD60584	6.212398135	6.680507214	6.237318966	TonB-dependent receptor
ACD60587	6.521353885	6.95176262	6.758849468	acetylornithine aminotransferase
ACD60589	6.524620067	6.616579719	6.551918932	conserved hypothetical protein
ACD60590	6.687102692	6.268541065	5.842795341	conserved hypothetical protein
ACD60591	8.068557961	7.759675174	8.638345403	lipoprotein, putative
ACD60593	7.553183842	7.886245286	7.705024081	conserved hypothetical protein
ACD60596	9.07642281	8.382835822	0	hypothetical protein
ACD60601	5.817116691	5.412581702	5.334217856	ISXo5 transposase
ACD60604	9.453287098	9.319130162	8.794565327	glyceraldehyde-3-phosphate dehydrogenase, type I
ACD60605	8.640487173	8.217477931	6.939485186	hypothetical protein
ACD60607	4.090811097	3.660369625	0	Transposase

ACD60609	1.929446376	1.539024774	1.12841879	ISXo8 transposase
ACD60615	7.168862627	7.808681077	7.019746386	lipoprotein, putative
ACD60616	8.977122478	8.531397057	7.362347146	TonB-like protein
ACD60617	7.390994346	7.2345588	6.425853696	peptidase, M56 family protein
ACD60618	7.512218984	8.32652836	7.917998553	transcriptional regulator BlaI family
ACD60619	6.661592851	6.81971927	5.384661164	signal transduction histidine kinase
ACD60620	6.824004051	6.84323015	5.601429106	DNA-binding response regulator
ACD60621	6.115545189	6.641363947	5.622441368	TPR repeat protein
ACD60622	7.954324286	7.572957861	7.464382379	TPR repeats containing protein
ACD60623	6.60320794	6.668076565	6.361585906	dehydrogenase with different specificities
ACD60624	6.816113265	6.321980392	6.299770331	possible Transcriptional activator, TenA family
ACD60625	6.117281538	5.96929787	5.748106956	long-chain acyl-CoA synthetase
ACD60626	6.212156859	5.335000819	5.685802822	putative thermostable hemolysin
ACD60629	8.019685237	7.69516564	8.79262113	hypothetical protein
ACD60632	6.783404268	7.157811757	7.284893487	outer membrane receptor for ferric iron uptake
ACD60633	8.205328971	8.263349022	8.73770028	transketolase
ACD60634	7.540593037	7.644130276	7.10912023	proton glutamate symport protein
ACD60635	7.23202752	7.002072385	6.96897776	putative membrane protein
ACD60636	7.906301375	7.909071023	8.463928925	tetratricopeptide repeat domain protein
ACD60637	7.277566379	7.637124765	7.742033167	von Willebrand factor type A domain protein
ACD60638	8.028287348	8.469251077	8.20030032	conserved hypothetical protein
ACD60639	7.005051848	7.632559052	7.870173581	protein of unknown function
ACD60640	9.077670274	9.255673034	10.90242034	methanol dehydrogenase regulatory protein
ACD60643	8.777906231	9.883972039	8.020068768	fimbrial assembly protein
ACD60644	9.093774067	10.22632789	8.033098083	fimbrial assembly protein
ACD60645	9.417405294	10.1912073	9.206335532	fimbrial assembly membrane protein
ACD60646	10.04907255	10.73002002	9.426235397	fimbrial assembly membrane protein
ACD60647	9.286049437	10.31890429	9.099113699	fimbrial assembly membrane protein
ACD60650	8.497708159	8.552496194	9.573440803	citrate synthase I
ACD60651	10.51884983	11.65080943	11.11326683	ribosomal protein L31
ACD60652	6.886403822	7.199368071	6.687270693	inosine-uridine preferring nucleoside hydrolase
ACD60653	7.054718264	7.196321797	6.351138892	ATP-dependent DNA helicase RecG
ACD60654	8.702151902	8.71829312	8.899900664	endoribonuclease L-PSP, putative
ACD60655	7.324558614	7.450675154	7.041790549	guanosine-3',5'-bis(diphosphate) 3'-pyrophosphohydrolase ((ppGpp)ase)
ACD60656	11.20090473	11.68838146	11.18218327	DNA-directed RNA polymerase omega chain
ACD60658	8.282203476	8.025211557	7.384352064	guanylate kinase
ACD60659	6.700620044	7.045530341	6.262034693	conserved hypothetical protein
ACD60669	6.873665575	6.961982105	6.275876799	aminopeptidase P
ACD60670	8.41090921	8.767366787	7.207492698	conserved hypothetical protein
ACD60678	9.511630118	7.913828877	9.47273551	conserved domain protein
ACD60682	5.241035497	3.976858503	4.818272836	ISXoo3 transposase ORF B
ACD60685	7.605990575	7.890519652	8.501009139	NADP-dependent malic enzyme
ACD60686	7.333692067	7.534746421	7.082436487	C4-dicarboxylate transport protein
ACD60691	7.214824219	6.881101721	6.765919237	transcriptional regulator
ACD60694	7.614113505	7.336015536	7.01720929	transcriptional regulator LuxR/uhpA family
ACD60695	6.868625039	6.616362108	6.323984273	periplasmic iron-binding protein
ACD60696	7.002252452	6.840463234	6.238767756	two-component system sensor protein
ACD60697	8.111610403	7.781018673	7.925489165	two-component system regulatory protein
ACD60702	7.378173452	7.718587672	6.096514876	sugar transporter
ACD60705	7.662768052	7.281392248	8.114033801	ThiJ/PfpI family protein
ACD60706	7.337684336	7.425408949	6.301704696	conserved hypothetical protein
ACD60707	7.086412262	6.946859499	6.522415185	GTPase
ACD60711	8.382649962	8.418101379	7.574722182	acetylxylan esterase
ACD60713	2.09546876	0	1.856216844	ISXo3 transposase ORF B
ACD60714	2.564275725	1.189748667	1.866053381	ISXoo13 transposase
ACD60719	9.837251049	10.34725594	10.52932318	cellulase S
ACD60720	6.874649444	6.487258016	7.175065452	cellulase S
ACD60721	9.001199868	9.571718519	11.26641762	peptide deformylase
ACD60722	8.106311674	7.028513901	7.161605564	arsenate reductase
ACD60723	10.19989315	9.989039637	8.9956428	hypothetical protein
ACD60724	6.951377977	7.021390889	5.967650502	membrane protein, putative
ACD60729	7.370329958	7.678522677	7.24052423	HIT domain, putative
ACD60730	7.446165231	6.951529515	6.440811043	recombination protein RecR
ACD60731	8.692859562	8.71751878	8.579636501	conserved hypothetical protein

ACD60732	7.413534849	7.645031507	7.222640363	DNA polymerase III subunit gamma/tau
ACD60734	7.491885156	7.208487997	7.313409125	molybdopterin converting factor, subunit 2
ACD60735	9.058294846	8.226262858	8.889132785	molybdopterin converting factor, subunit 1
ACD60736	7.230241448	6.935730817	7.146186791	molybdenum cofactor biosynthesis protein C
ACD60737	7.455458742	7.260449141	6.819923596	conserved hypothetical protein
ACD60738	7.521875213	7.313735617	6.267470254	molybdenum cofactor biosynthesis protein A
ACD60739	6.99688583	6.767906348	6.849699084	molybdenum cofactor biosynthesis protein A
ACD60740	7.356337518	7.598826694	7.360601311	3-deoxy-D-manno-octulosonic acid kinase
ACD60742	7.881071123	6.963982677	7.404545537	conserved hypothetical protein
ACD60744	2.960493176	1.567053757	2.72644325	ISXo5 transposase
ACD60745	7.212306688	6.050379799	7.28049241	conserved hypothetical protein
ACD60746	12.94777572	12.08851001	12.76602984	paar motif family
ACD60747	8.397606186	8.354892885	9.00098588	conserved hypothetical protein
ACD60748	6.907659828	6.300392832	7.406613197	conserved hypothetical protein
ACD60749	0	9.660541481	7.600693471	hypothetical protein
ACD60751	5.91634049	5.927377388	6.911284119	conserved hypothetical protein
ACD60752	6.937344392	6.367671596	7.415496722	conserved hypothetical protein
ACD60753	5.122105302	4.771341561	5.662433396	Rhs element Vgr protein
ACD60754	9.243992707	9.157432838	8.331557436	hypothetical protein
ACD60755	10.44753787	9.738637813	11.13887333	site-specific DNA methylase
ACD60756	10.24757154	10.57668274	11.55340371	hypothetical protein
PXO_rna38	0	0	0	XO_rna38 cdna:pseudogene chromosome:GCA_000019585.1:Chromosome:4317461:4317551:-1 gene:PXO_rna38 transcript:PXO_rna3
ACD60758	7.956155416	8.083213368	7.616115051	DNA polymerase III, epsilon subunit
ACD60759	7.266205598	8.015782997	7.585443319	RNase H
ACD60760	8.397914171	8.891725994	7.923226449	conserved hypothetical protein
ACD60764	7.456313341	7.366129842	6.947759653	peptidyl-prolyl cis-trans isomerase
PXO_rna39	0	0	0	XO_rna39 cdna:pseudogene chromosome:GCA_000019585.1:Chromosome:4325889:4325965:-1 gene:PXO_rna39 transcript:PXO_rna3
PXO_rna40	0	0	0	XO_rna40 cdna:pseudogene chromosome:GCA_000019585.1:Chromosome:4326060:4326136:-1 gene:PXO_rna40 transcript:PXO_rna4
PXO_rna41	0	0	0	XO_rna41 cdna:pseudogene chromosome:GCA_000019585.1:Chromosome:4326165:4326239:-1 gene:PXO_rna41 transcript:PXO_rna4
ACD60765	9.809840463	10.35077347	9.868527814	DNA-binding protein HU
ACD60766	8.459034003	8.824764671	9.615853977	ATP-dependent protease La
ACD60767	8.75423948	9.261942109	8.311389583	ATP-dependent Clp protease, ATP-binding subunit ClpX
ACD60768	9.031370382	9.107614645	8.931204364	ATP-dependent Clp protease, proteolytic subunit ClpP
ACD60769	8.554895775	8.833443574	8.819639447	trigger factor
PXO_rna42	0	0	0	XO_rna42 cdna:pseudogene chromosome:GCA_000019585.1:Chromosome:4332977:4333061:-1 gene:PXO_rna42 transcript:PXO_rna4
ACD60770	7.717964248	7.716785172	6.537097232	transposase
ACD60771	8.395602681	8.992638156	8.649482535	conserved domain protein
ACD60772	9.264416796	9.379571147	8.625252222	transposase
ACD60773	7.703626771	7.890069675	7.501701864	ISXoo3 transposase ORF A
PXO_rna43	0	0	0	XO_rna43 cdna:pseudogene chromosome:GCA_000019585.1:Chromosome:4335467:4335542:-1 gene:PXO_rna43 transcript:PXO_rna4
PXO_rna44	0	0	0	XO_rna44 cdna:pseudogene chromosome:GCA_000019585.1:Chromosome:4335636:4335712:-1 gene:PXO_rna44 transcript:PXO_rna4
PXO_rna45	0	0	0	XO_rna45 cdna:pseudogene chromosome:GCA_000019585.1:Chromosome:4335745:4335821:-1 gene:PXO_rna45 transcript:PXO_rna4
PXO_rna46	0	0	0	XO_rna46 cdna:pseudogene chromosome:GCA_000019585.1:Chromosome:4335864:4335940:-1 gene:PXO_rna46 transcript:PXO_rna4
ACD60775	8.677250998	9.03552769	9.555125925	isocitrate dehydrogenase [NAD] subunit alpha, (isocitric dehydrogenase) (nad(+)-specific icdh)
ACD60777	2.839623054	2.512702227	0	transposase (IS4 family)
ACD60778	8.406523915	8.258043036	8.555888993	carboxymuconolactone decarboxylase
ACD60779	8.139929882	8.048911855	10.17284001	glutaredoxin 3
ACD60783	11.49029434	12.75039924	11.30035256	hypothetical protein
ACD60791	7.173157423	6.167215402	6.155623768	conserved hypothetical protein
ACD60792	11.06666777	8.747420969	11.96637206	hypothetical protein
ACD60793	7.807921584	7.409127832	7.601570245	conserved hypothetical protein

ACD60794	7.857514531	7.899296495	9.07281593	amidophosphoribosyltransferase
ACD60795	8.010276329	7.906926663	8.54340695	colicin V production protein
ACD60796	6.329701276	6.730368236	7.986314221	conserved hypothetical protein
ACD60797	6.795000624	6.312859364	6.2351622	folylpolyglutamate synthase\x3b dihydrofolate synthase
ACD60798	0	0	7.239025633	hypothetical protein
ACD60800	7.347479639	7.961166047	7.068703052	phosphoglycerate mutase
ACD60801	6.95541743	7.022212438	5.865186397	conserved hypothetical protein
ACD60802	6.850124314	5.813442599	5.897765607	Non-hemolytic phospholipase C
ACD60805	10.37883671	10.53929454	11.12362999	conserved hypothetical protein
ACD60806	7.261690646	7.429490434	6.725427612	sulfate/thiosulfate import ATP-binding protein CysA
ACD60807	7.95419631	8.09318513	6.935389026	sulfate ABC transporter, permease protein CysW
ACD60808	7.406885261	7.769441172	6.976993646	sulfate ABC transporter, permease protein CysT
ACD60809	7.714973551	7.717964248	7.8622158	ABC transporter sulfate binding protein
ACD60812	6.473816129	6.666600386	6.065929839	pseudouridylate synthase
ACD60813	6.68385082	6.155739115	6.512451302	conserved hypothetical protein
ACD60814	10.26801559	11.0004719	13.35770319	OmpA family outer membrane protein
ACD60825	10.8051312	10.3527828	10.7076611	hypothetical protein
ACD60829	0	0	0	putative transposase
ACD60831	8.683026175	8.531619291	9.721341897	malate dehydrogenase
ACD60832	9.024339074	9.535469797	10.36946648	peptidyl-prolyl cis-trans isomerase
ACD60836	7.020679983	7.29200867	6.462974982	membrane protein
ACD60837	7.100494146	7.478947544	7.05883598	3-deoxy-7-phosphoheptulonate synthase
ACD60839	7.860956592	7.892639954	6.992757103	disulfide bond formation protein B
ACD60846	8.98251735	9.006331689	9.06301211	conserved hypothetical protein
ACD60847	9.797192979	9.703808429	9.777450949	transposase
ACD60848	3.181407918	2.856597335	4.706149246	transposase
ACD60849	6.865238371	5.232449709	5.47518867	transposase
ACD60851	0	0	0	transposase
ACD60853	8.088608056	7.878590481	7.942356152	transposase
ACD60854	4.04199638	4.119613482	3.045214037	ISXo8 transposase
ACD60855	9.540536857	9.881081832	11.96457552	transposase
ACD60856	8.363004576	8.3459862	8.065739241	ISXoo3 transposase ORF A
ACD60858	7.62902141	7.405158486	7.499128346	pseudouridylate synthase
ACD60859	0	8.579100932	9.93801079	pseudouridylate synthase
ACD60864	0	0	0	ISXoo11 transposase
ACD60867	0.66829162	2.220147285	1.522226532	ISXo8 transposase
ACD60870	8.712035128	9.353773181	8.202985754	conserved hypothetical protein
ACD60871	6.880281455	6.712582025	5.832705236	ATP-dependent protease La (LON) domain subfamily
ACD60872	7.631511766	8.086783766	7.338468986	UDP-N-acetylmuramate\x3aL-alanyl-gamma-D-glutamyl-meso-diaminopimelate ligase
ACD60873	8.311398666	8.828015858	8.403391294	adenylate kinase
ACD60877	7.687004682	7.680985347	8.232339376	conserved hypothetical protein
ACD60878	3.962872876	3.150939796	3.023384887	ISXo5 transposase
ACD60879	7.089243894	7.143036211	6.5358881	conserved hypothetical protein
ACD60882	6.924088006	6.652041858	9.386216022	TonB-dependent receptor
ACD60883	5.982053521	6.164277433	7.370730992	transcriptional regulator
ACD60884	6.746863616	6.999143145	7.585428296	transcriptional regulatory protein, C terminal
ACD60885	7.088226419	6.946496941	6.989218499	thiamine biosynthesis protein ThiC
ACD60886	10.62315905	9.42980633	0	hypothetical protein
ACD60893	7.636530371	7.497189202	6.901168595	3-isopropylmalate dehydrogenase
ACD60894	8.065410749	8.453373533	7.78359416	methyltransferase in menaquinone/biotin biosynthesis
ACD60895	8.138696737	8.369025826	8.477972733	3-isopropylmalate dehydratase, small subunit
ACD60896	8.755929073	9.021807273	9.766696192	3-isopropylmalate dehydratase, large subunit
ACD60898	7.68044392	7.132000966	7.540407055	Putative signal protein with GGDEF domain
ACD60900	0	0	11.82976237	conserved hypothetical protein
ACD60901	0	0	0	conserved hypothetical protein
ACD60905	7.456321556	7.245001192	6.24071693	3-deoxy-D-manno-octulosonic-acid transferase
ACD60907	7.478340892	7.451244087	6.759701802	membrane protein
ACD60908	7.275779979	7.090228889	6.870389381	glycosyltransferase
ACD60909	10.06369168	10.49271445	10.51606441	conserved hypothetical protein
ACD60910	7.080401844	7.779226884	7.301660804	conserved hypothetical protein
ACD60911	8.051861473	7.932403752	7.567256417	conserved hypothetical protein
ACD60914	6.851424242	6.402012659	6.881187394	aminopeptidase N
ACD60915	7.481266646	7.760021298	9.011431343	adenylosuccinate synthetase

ACD60916	9.886856468	9.497225136	9.571191381	conserved hypothetical protein
ACD60917	8.535551445	7.943599051	8.485455005	HflC protein
ACD60918	7.754553506	7.819968288	7.539864473	integral membrane protease subunit
ACD60919	8.675466645	9.163254673	9.609332051	regulatory protein PilH family
ACD60920	7.520445822	7.87374554	9.100478377	curved DNA binding protein
ACD60921	8.521977258	9.014302285	10.35623186	low molecular weight heat shock protein
ACD60925	0	2.759477581	1.70577005	ISXo3 transposase ORF A
ACD60926	0	2.1842549	0	ISXo8 transposase
ACD60928	7.28872768	0	5.412869574	ISXo8 transposase
ACD60929	6.023601345	5.692800992	5.222387269	conserved hypothetical protein
ACD60930	6.876074862	7.034105642	8.465007176	glycerophosphodiester phosphodiesterase
ACD60931	6.831801255	6.480342684	10.25286645	TonB-dependent outer membrane receptor
ACD60932	9.046463776	9.02142698	8.297150138	hypothetical protein
ACD60933	6.517337117	6.112426996	5.019128102	conserved hypothetical protein
ACD60934	8.821276525	7.809768129	8.064106815	hypothetical protein
ACD60936	6.974345752	6.493077265	6.218992288	inosine-uridine preferring nucleoside hydrolase
ACD60937	6.136644619	5.802684374	5.97647133	TonB-dependent outer membrane receptor
ACD60940	5.749089055	6.265474403	5.658091491	probable AcnD-accessory protein PrpF
ACD60942	11.17220871	10.5430705	9.597013386	conserved hypothetical protein
ACD60944	7.751149021	8.687025685	6.621076023	conserved hypothetical protein
ACD60945	6.783823306	6.817789516	6.062663571	2-methylisocitrate dehydratase, Fe/S-dependent
ACD60946	0	0	0	aconitate hydratase 1
ACD60947	7.653088687	7.868168179	7.603559586	2-methylcitrate synthase
ACD60948	7.252741113	7.489896116	5.953435204	methylisocitrate lyase
ACD60950	9.416843963	8.491612627	9.649696285	lipoprotein, putative
PXO_rna47	0	0	0	XO_rna47 cdna:pseudogene chromosome:GCA_000019585.1:Chromosome:4520331:4520405:-1 gene:PXO_rna47 transcript:PXO_rna4
ACD60951	7.608543147	7.478826234	7.677923965	type IV fimbriae assembly protein
ACD60952	6.690431064	6.997642424	6.471758116	DNA polymerase III delta' subunit
ACD60953	6.639802297	6.822972276	6.088616536	conserved hypothetical protein
ACD60954	6.43107633	6.253384236	6.136964462	para-aminobenzoate synthase component I
ACD60955	7.212335874	7.36927453	7.53039073	3-oxoacyl-[acyl-carrier-protein] synthase II
ACD60956	11.78649018	12.14201768	13.32353333	acyl carrier protein
ACD60957	7.316453513	7.535135378	8.033802898	3-oxoacyl-(acyl-carrier-protein) reductase
ACD60958	6.46746861	6.702297379	6.656467768	malonyl CoA-acyl carrier protein transacylase
ACD60959	7.239999421	7.499255935	6.999470163	conserved hypothetical protein
ACD60960	7.649536425	8.283870855	8.24008054	3-oxoacyl-[acyl-carrier-protein] synthase III
ACD60961	11.16960562	11.26492928	12.47758627	ribosomal protein L32
ACD60962	8.254149935	8.299157638	8.010321093	conserved hypothetical protein
ACD60964	6.461687344	5.653770868	6.354406317	ISXo5 transposase
ACD60972	8.303438296	7.32998465	8.64292896	transposase
ACD60973	7.808565248	7.361715731	8.132335208	transposase
ACD60974	7.220039684	6.779653702	6.318063715	glycosyl transferase
ACD60979	7.95095242	7.909017003	6.092957942	conserved hypothetical protein
ACD60980	7.707165839	7.641293131	7.597724832	general secretion pathway protein D
ACD60981	7.009559924	7.382502986	6.752588045	general secretion pathway protein N
ACD60982	6.53233878	6.793362705	6.535088709	general secretion pathway protein M
ACD60983	7.230808237	7.867816175	6.503372589	general secretion pathway protein L
ACD60984	6.161073418	6.78501428	6.258786484	general secretion pathway protein K
ACD60985	7.400102391	7.168742308	6.745923014	general secretion pathway protein J
ACD60986	8.316050682	7.803246413	7.426575069	general secretion pathway protein I
ACD60987	5.844483577	7.312538119	6.836403883	general secretion pathway protein H
ACD60988	7.420591877	7.111114799	7.391776311	general secretion pathway protein G
ACD60989	7.38921401	7.821984393	6.623757146	general secretion pathway protein F
ACD60991	7.52277767	7.25306271	7.398333267	general secretory pathway protein E
ACD60992	8.220397676	8.645521541	8.775932855	protease
ACD60993	8.619123181	8.530261963	8.728036138	extracellular protease
AGS47856	8.219613848	8.527602112	7.420162352	truncated serine protease
ACD60995	8.220697548	8.558807166	6.950351762	Xanthomonas adhesin-like protein A
ACD60996	6.948904492	7.013484592	6.483606209	phosphoribosylformylglycinamidine synthase
ACD60998	6.775076887	7.239846713	6.193521418	disulfide isomerase
ACD60999	9.327963501	10.12092471	9.090938093	hypothetical protein
ACD61000	6.498477468	6.852123719	6.019492878	tyrosine recombinase XerD

ACD61002	9.756614696	9.685488185	9.965145029	conserved hypothetical protein
ACD61003	6.747937839	7.127509473	6.285910772	putative permease, YjgP/YjgQ family
ACD61004	6.767125077	6.548499818	6.625418083	putative permease, YjgP/YjgQ family
ACD61014	3.939339431	3.702535652	2.287126503	ISXo1 transposase
ACD61017	6.893811163	6.919077837	6.931801228	soluble lytic murein transglycosylase
ACD61020	0.625364016	0	0	ISXo8 transposase
ACD61022	0	0	0	ISXo8 transposase
ACD61023	7.932462809	7.345289915	6.490799544	ribosomal-protein-alanine acetyltransferase
ACD61024	7.479190134	7.413924053	6.693068724	conserved hypothetical protein
ACD61025	7.339030462	7.346983474	6.728029333	phosphatidylserine synthase
ACD61029	7.388172313	7.563249669	6.65047737	membrane protein, putative
ACD61035	6.357757838	6.635394543	6.188112072	DNA repair system specific for alkylated DNA
ACD61038	7.288183198	7.283773644	6.275118822	succinyl-CoA\x3a3-ketoacid-coenzyme A transferase subunit B
ACD61039	6.172255475	6.804569895	6.042022654	succinyl-CoA\x3a3-ketoacid-coenzyme A transferase subunit A
ACD61042	6.728042942	6.853035027	6.170423847	dTDP-4-dehydrorhamnose reductase
ACD61043	7.371689536	7.527258044	7.419741124	dTDP-4-dehydrorhamnose 3,5-epimerase
ACD61044	7.56192179	7.76773424	7.28213396	glucose-1-phosphate thymidylyltransferase
ACD61045	7.650843526	7.435961895	7.323424115	dTDP-glucose 4,6-dehydratase
ACD61050	7.33655119	7.539127785	6.840765337	transposase
ACD61052	10.70689311	9.523683482	9.997828689	conserved domain protein
ACD61053	0	0	0	ISXo8 transposase
ACD61054	7.848779406	8.159260837	8.118167622	putative O-antigen acetylase
ACD61055	8.850436904	8.711253978	8.588594718	putative glycosyl transferase
ACD61056	10.43187364	10.11612299	9.54706225	hypothetical protein
ACD61057	8.615129342	8.575943825	8.13187239	putative glycosyltransferase
ACD61058	8.635402525	8.442425193	7.922477367	sugar nucleotide epimerase/dehydratase
ACD61060	8.709304423	8.862355299	8.393742239	putative methyltransferase
ACD61061	9.094774446	9.477337335	9.865440991	cystathionine gamma-synthase (CGS) (O-succinylhomoserine(Thiol)-lyase)
ACD61062	10.47766721	10.24727483	10.05173915	hypothetical protein
ACD61063	8.518409244	8.768667348	8.22527493	cystathionine beta-synthase
ACD61065	14.95884721	15.05912473	15.43318116	UptF
ACD61066	7.026700483	7.69642511	7.978395863	outer membrane protein
ACD61067	8.062191884	8.584864815	10.03624231	outer membran protein
ACD61069	7.214260829	7.030987087	6.759368919	maleylacetoacetate isomerase
ACD61070	7.402022895	6.962155675	6.916727422	fumarylacetoacetate hydrolase
ACD61072	8.43934471	6.091665988	8.816065252	spo0B-associated GTP-binding protein
ACD61075	6.823774831	6.916655776	7.301569357	dethiobiotin synthase
ACD61078	7.912440295	7.030413332	7.742188154	phosphoglycolate phosphatase, bacterial
ACD61079	6.754326345	6.66715413	6.568900076	ImpB/MucB/SamB family
ACD61082	6.372605656	6.331929098	7.877462063	conserved hypothetical protein
ACD61083	7.421383216	7.332842173	7.883297004	oligopeptidase A
ACD61084	6.923184843	6.854033061	7.2773525	cysteine synthase
ACD61090	7.512527153	7.045421127	8.15390158	ISXoo11 transposase
ACD61092	9.340557818	11.03052231	9.438791853	conserved hypothetical protein
ACD61093	7.99760291	7.883034236	8.538774817	conserved hypothetical protein
ACD61094	7.055651198	7.031097398	7.044601765	glucosamine--fructose-6-phosphate aminotransferase, isomerizing
ACD61097	3.304277388	0.648493054	3.294566348	transposase
ACD61099	4.431549419	7.288902977	5.677477234	ISXoo12 transposase
ACD61101	7.755081184	8.054767095	8.155567104	transposase
ACD61103	7.704726747	7.54335668	7.727552929	UDP-N-acetylglucosamine pyrophosphorylase
ACD61105	6.889899376	7.971807928	7.408839212	chorismate mutase\x3b prephenate dehydratase
ACD61106	9.360667147	10.18115226	9.369968059	hypothetical protein
ACD61107	7.431280296	8.351835892	6.137601886	ATP synthase F1, epsilon subunit
ACD61108	8.031726011	8.015989228	7.825677523	ATP synthase F1, beta subunit
ACD61109	7.71363396	8.151432665	7.256576688	ATP synthase F1, gamma subunit
ACD61110	7.882104995	8.05800255	8.177509236	ATP synthase F1, alpha subunit
ACD61111	7.29614534	7.587800014	7.421458959	ATP synthase F1, delta subunit
ACD61112	8.204028198	8.8832359	8.749041441	ATP synthase F0, B subunit
ACD61113	12.04856861	11.8652345	12.65757972	ATP synthase C chain
ACD61114	9.312966883	9.311148865	8.989045315	ATP synthase F0, A subunit
ACD61115	10.50433238	10.40654517	10.63190459	conserved hypothetical protein
ACD61117	7.541816815	7.696598984	6.81258807	conserved hypothetical protein
ACD61118	7.486231678	7.741804025	7.1248554	dihydrolipoamide dehydrogenase
ACD61119	6.675717152	7.41493042	6.468415514	conserved hypothetical protein

ACD61120	7.208429469	7.394265463	7.995919749	pyruvate dehydrogenase complex dihydrolipoamide acetyltransferase
ACD61121	6.697579238	6.099065819	5.794223494	putative secreted protein
ACD61122	7.706758459	7.049434736	6.833307576	T/U mismatch-specific DNA glycosylase
ACD61124	8.232914933	7.833307576	8.243987948	conserved hypothetical protein
ACD61125	8.249345783	8.060090629	8.570937224	outer membrane protein
ACD61126	6.396846209	6.484499082	6.216668266	ABC transporter permease
ACD61127	6.802787754	6.435621927	6.390024464	ABC transporter ATP-binding protein
ACD61128	7.120870295	6.785968967	7.050664938	integral membrane protein DUF6
ACD61134	7.571934628	6.960523294	6.501542646	HAD superfamily hydrolase
ACD61135	6.785380536	6.768872419	6.525732206	ribosomal small subunit pseudouridylate synthase
ACD61136	7.285198748	6.870327727	6.360969955	ribosomal RNA small subunit methyltransferase C
ACD61138	9.309060197	9.219763872	8.808253107	L-sorbosone dehydrogenase
ACD61139	9.049867604	8.618429553	8.49820698	conserved hypothetical protein
ACD61140	7.671901916	8.336301243	8.318714522	sensor histidine kinase
ACD61141	9.154866198	9.809502873	9.186681299	conserved hypothetical protein
ACD61142	9.214765947	9.796234335	10.7927659	conserved hypothetical protein
ACD61144	7.079602115	7.408346726	7.985813481	alanine racemase
ACD61145	7.989632919	7.637479834	9.06176	D-amino acid dehydrogenase small subunit
ACD61147	7.958401913	8.103293055	10.14411012	conserved hypothetical protein
ACD61155	7.159861248	6.653747943	6.047119549	histidine kinase/response regulator hybrid protein
ACD61156	8.14550424	8.136401614	8.436049374	hypothetical protein
ACD61159	7.738821869	7.323865415	7.657261277	conserved hypothetical protein
ACD61161	11.96899072	10.97467987	10.57154409	hypothetical protein
ACD61162	7.742033167	6.63611415	6.663899614	ABC-2 type transporter
ACD61163	7.205089443	7.141228406	6.350118844	ABC transporter ATP-binding protein
ACD61164	7.307073272	7.183625457	6.273810516	Na+/H+ antiporter
ACD61165	8.814220345	8.675681872	7.538724386	hypothetical protein
ACD61166	7.648134644	7.336015536	6.771251752	hypothetical protein
ACD61169	7.08061503	6.860230342	6.485061277	uracil DNA glycosylase superfamily protein
ACD61170	7.434945085	7.468852087	7.569680956	elongator protein 3/MiaB/NifB
ACD61171	7.774681653	7.033555151	6.996117538	4,5-dopa dioxygenase extradiol
ACD61172	8.891340196	8.967355966	8.447289901	DoxX subfamily
ACD61174	10.00102812	10.70234587	9.408482601	hypothetical protein
ACD61176	8.191607063	6.721919446	7.146023823	hypothetical protein
ACD61179	6.778852493	6.771700741	6.346425086	conserved hypothetical protein
ACD61181	7.305943169	7.475368659	6.565406774	amino acid transporter
ACD61182	8.125966161	7.908446665	7.56285296	lipoprotein, putative
ACD61183	7.543843833	7.326887841	8.282453706	transcriptional regulator protein
ACD61184	6.669310286	6.046191996	6.859199309	transcriptional regulator protein
ACD61185	7.846461974	7.445569463	8.068106476	histidine kinase family
ACD61186	7.827857123	8.24306923	7.310412835	conserved hypothetical protein
ACD61188	10.07875125	9.23556672	10.79899824	conserved hypothetical protein
ACD61190	4.438778548	0	1.937020409	transposase
ACD61192	0	0	0	methyltransferase
ACD61193	8.02504541	7.635232002	7.569787269	methyltransferase
ACD61195	9.301690523	9.130910283	7.312647024	conserved hypothetical protein
ACD61196	8.071049339	8.551416041	6.71189407	transcriptional regulator NtrC family
ACD61205	9.879875741	9.241368295	8.722213257	hypothetical protein
ACD61212	6.750472519	6.869748051	6.752935873	conserved hypothetical protein
ACD61213	7.064710435	7.55007722	5.921681488	conserved hypothetical protein
ACD61214	6.412690084	7.099253118	6.141479795	conserved hypothetical protein
ACD61216	7.187728164	6.782198856	6.97157804	conserved hypothetical protein
ACD61220	11.74940437	10.33798978	11.0283136	hypothetical protein
ACD61223	0	0	0	Rhs family protein
ACD61225	0	0	0	filamentous haemagglutinin, N-terminal\x3aAdhesin HecA 20-residue repeat x2
ACD61226	0	0	0	ISxac3 transposase
ACD61235	0	0	0	integrase core domain protein
ACD61238	0	0	0	ISXoo9 transposase orfB
ACD61240	0	0	0	filamentous haemagglutinin
ACD61242	0	0	0	filamentous haemagglutinin
ACD61244	0	0	0	filamentous haemagglutinin\x3b haemagglutination activity domain protein
ACD61245	0	0	0	outer membrane hemolysin activator protein
ACD61246	0	0	0	ice nucleation protein
ACD61248	7.752668321	7.761644307	7.13017927	dual specificity phosphatase, catalytic domain protein

ACD61249	4.79006824	5.10912232	3.470601938	alpha/beta hydrolase fold
ACD61250	7.098611151	7.303598117	7.631853672	alpha/beta hydrolase
ACD61251	7.502927251	8.06452722	8.268429715	CDP-alcohol phosphatidyltransferase
ACD61256	0	7.879969142	8.776933036	hypothetical protein
ACD61260	8.158382474	8.098211092	7.01180869	transmembrane protein
ACD61261	7.127468202	7.326977697	6.436661578	NADH pyrophosphatase
ACD61262	9.817432996	9.75580893	10.70210341	conserved hypothetical protein
ACD61265	9.291341095	9.221676532	9.124581453	HesB/YadR/YfhF
ACD61266	8.639619271	8.410955836	9.120849564	conserved hypothetical protein
ACD61267	7.843324384	7.712664557	7.657854336	conserved hypothetical protein
ACD61268	6.896174955	6.829494422	6.440154909	conserved hypothetical protein
PXO_rna50	0	0	0	XO_rna50 cdna:pseudogene chromosome:GCA_000019585.1:Chromosome:4861134:4861210:-1 gene:PXO_rna50 transcript:PXO_rna5
PXO_rna51	0	0	0	XO_rna51 cdna:pseudogene chromosome:GCA_000019585.1:Chromosome:4861230:4861305:-1 gene:PXO_rna51 transcript:PXO_rna5
ACD61274	8.197103633	8.344540036	7.821097909	tyrosyl-tRNA synthetase
ACD61278	10.07542567	10.31841853	10.0344551	conserved hypothetical protein
ACD61279	7.413357134	7.623698627	6.649514869	signal transducer
ACD61281	7.114544019	7.541259272	8.395932508	exodeoxyribonuclease III
ACD61291	10.73183661	10.77152248	10.07470344	conserved hypothetical protein
ACD61293	7.89372017	8.214668823	8.115215358	phosphomannomutase
ACD61294	8.333168771	7.57562244	7.449998739	deoxyuridine 5'-triphosphate nucleotidohydrolase
ACD61295	6.794415866	6.665094263	7.078129454	phosphopantothenoylcysteine decarboxylase/phosphopantothenate--cysteine ligase
ACD61301	7.39096856	7.423485731	7.218839277	transposase
ACD61302	8.49077468	8.628540319	9.616859403	RIO1//family protein
ACD61305	6.320383585	6.424645008	5.555104446	hydrolase
ACD61306	8.871621906	8.659275257	8.901005638	4-carboxymuconolactone decarboxylase
ACD61307	7.380971816	8.054219005	7.329311996	3-oxoadipate enol-lactonase
ACD61308	7.405473372	7.568579398	7.314098299	3-carboxy-cis,cis-muconate cycloisomerase
ACD61309	5.942507468	6.877597029	6.484141354	protocatechuate 3,4-dioxygenase, alpha subunit
ACD61310	6.483107958	7.259818574	7.314243347	protocatechuate 3,4-dioxygenase, beta subunit
ACD61311	6.332468061	6.740779183	5.999594185	beta-ketoadipyl CoA thiolase
ACD61312	9.691089186	9.229592729	9.229191339	glutaconate CoA transferase subunit B
ACD61315	7.085244053	6.799074351	6.062417493	thioredoxin
ACD61316	7.211391903	7.859379483	7.295869931	ribonucleotide reductase-associated flavodoxin, putative
ACD61317	8.73753129	8.363455838	9.268046007	ribonucleoside-diphosphate reductase, beta subunit
ACD61318	9.017106265	8.763633991	10.03945373	ribonucleoside-diphosphate reductase, alpha subunit
ACD61320	0	0	0	hypothetical protein
ACD61321	8.171381989	7.981201924	7.497189202	integral membrane protein
ACD61322	7.180794335	7.055239046	7.437901847	acetyltransferase, gnat family
ACD61323	7.028900616	7.029971827	7.871424773	conserved hypothetical protein
ACD61324	7.028955852	6.584771632	8.509616675	magnesium transporter
ACD61326	0.339479485	0	-1.055657269	ISXo8 transposase
ACD61327	6.329677958	6.3626084	5.843905981	glucose-6-phosphate 1-dehydrogenase
ACD61328	6.999007806	7.136058056	6.500795681	glycosyl hydrolase, family 15
ACD61329	6.851786514	6.153550005	6.915461146	phosphatase
ACD61330	6.266550444	6.589679607	5.632242037	ankyrin-like protein
ACD61331	8.031714985	7.948530767	7.732119929	conserved hypothetical protein
ACD61337	6.714204297	6.894126559	5.793185802	3-oxoacyl-[acyl-carrier-protein] reductase
ACD61338	9.604844148	0	9.871316954	hypothetical protein
ACD61339	8.100147187	7.660117152	8.372003102	ISXoo2 transposase
ACD61340	9.480194424	10.13189553	9.545317821	hypothetical protein
ACD61341	6.920733951	7.012769779	6.715220725	8-amino-7-oxononanoate synthase
ACD61342	7.767456176	7.834654338	8.157437891	biotin synthase
ACD61345	7.941669754	7.944249388	7.506819302	4-hydroxybenzoate polyprenyl transferase
ACD61349	7.654127595	7.659696266	7.165309016	transmembrane regulator protein PrtR
ACD61350	7.575206424	7.68692767	8.125248139	ECF sigma factor
ACD61355	7.467369157	7.717649008	7.5116736	RarD protein
ACD61356	6.917801691	6.585112774	6.376033332	integral membrane protein
ACD61357	8.071553534	8.506299646	8.194333339	drug/metabolite transporter superfamily protein
ACD61359	10.78391495	8.915750934	0	hypothetical protein
ACD61360	6.879472976	6.797843067	6.728940868	peptidase

ACD61361	7.657797184	7.638863048	7.468762502	metallo-beta-lactamase superfamily protein
ACD61362	6.933950258	6.938132856	7.039862192	tryptophanyl-tRNA synthetase
ACD61363	12.13958972	13.39748747	12.15090551	conserved domain protein
ACD61364	12.18898439	13.22168831	13.41390555	entericidin EcnA/B family
ACD61365	11.47218312	12.97327045	14.27514968	conserved domain protein
ACD61366	6.372624809	5.710500646	6.7416827	arginase
ACD61370	0	9.137677702	7.378589652	hypothetical protein
PXO_rna54	0	0	0	XO_rna54 cdna:pseudogene chromosome:GCA_000019585.1:Chromosome:4957642:4957717:-1 gene:PXO_rna54 transcript:PXO_rna5
ACD61372	6.486714373	6.928701939	6.074882159	conserved hypothetical protein
ACD61373	7.037832445	7.424980856	6.850411899	transcriptional regulator
ACD61374	6.697926686	7.254943564	6.204600487	biotin-[acetyl-CoA-carboxylase] ligase
ACD61377	7.329859111	7.082798374	6.716126664	conserved hypothetical protein
ACD61378	6.776538311	7.091043915	7.093623555	conserved hypothetical protein
ACD61379	7.593002617	7.967992802	8.227668885	two-component system sensor protein required for AvrXa21activity H2 (raxH2)
ACD61380	9.889494837	10.27639198	11.43527438	two-component system regulatory protein (response regulator) required for AvrXa21 activity R2 (raxR2)
ACD61381	9.888916727	11.34640846	11.7592141	conserved hypothetical protein
ACD61382	7.265502533	7.643560407	7.710730682	tRNA-dihydrouridine synthase A
ACD61383	10.06545653	11.50912673	12.70451538	putative membrane protein
ACD61384	6.958053848	6.733191621	6.074584642	ankyrin AnkB
ACD61385	7.780598819	7.696918856	6.273819838	catalase
ACD61386	9.706566813	9.890657962	9.524106784	hypothetical protein
ACD61387	7.127158631	7.029331405	6.99424028	membrane-fusion protein
ACD61389	-11.14728381	0	-8.454609773	ISXo5 transposase
ACD61390	6.583174555	5.21848671	5.933341298	membrane-fusion protein
ACD61391	7.04785462	6.821455119	6.615698782	ATP-dependent helicase
ACD61392	0	10.63797425	8.48614719	conserved hypothetical protein
ACD61393	7.635805169	7.779929425	6.277421317	conserved hypothetical protein
ACD61394	7.605427662	7.938720982	7.096620289	shikimate dehydrogenase
ACD61396	7.680936135	7.857396336	8.309767365	iron-uptake factor
ACD61398	6.333085562	6.011457621	6.074580361	transcriptional regulator LysR family
ACD61401	7.555854491	7.990858451	8.434799173	delta-aminolevulinic acid dehydratase
ACD61402	9.660741122	9.627433567	10.0880064	conserved hypothetical protein
ACD61404	7.498011462	7.057731852	7.884152199	conserved hypothetical protein
ACD61405	7.549399641	7.204228769	7.475587533	dipeptidyl peptidase IV
ACD61407	8.23878686	8.24104408	8.281508165	glutathione S-transferase
ACD61408	9.176784014	8.271687118	9.007122602	hypothetical protein
ACD61414	7.606782726	7.543209729	6.980093868	ABC transporter sodium permease
ACD61415	7.60533876	7.056149961	7.200722088	sodium ABC transporter ATP-binding protein
ACD61416	6.652816298	6.725972863	6.715673766	cysteine proteinase
ACD61417	9.669746091	9.456512538	8.314333994	helix-turn-helix, putative
ACD61418	8.276394304	8.096815283	8.063724032	membrane protein, putative
ACD61419	0	7.765932493	8.203196261	hypothetical protein
ACD61420	8.701205946	8.327206805	8.415543199	conserved hypothetical protein
ACD61422	7.706972521	7.091054496	6.6289908	phenol hydroxylase
ACD61428	4.809347556	9.428464864	3.600091309	ISXoo13 transposase
ACD61429	8.013724646	8.406630203	7.514035443	putative ISXoo14 transposase
ACD61433	7.361742045	7.287379944	7.265849421	IS66 family element, Orf1 protein, putative
ACD61439	6.500934273	7.691771431	9.6571094	conserved hypothetical protein
ACD61441	7.255462966	6.805060244	6.976191767	D-alanine--D-alanine ligase A
ACD61447	7.288496992	6.961600178	7.476098111	conserved hypothetical protein
ACD61451	8.446024586	4.917484268	7.813595232	hypothetical protein
ACD61453	8.519388575	8.588714636	7.700210811	XopN effector
ACD61454	0	0	0	ISXo5 transposase
ACD61455	4.872523447	4.853776133	4.995081955	ISXoo5 transposase
ACD61456	7.500786122	7.520367243	6.677719642	conserved hypothetical protein
ACD61457	7.252116631	7.473786912	6.630194306	L-fucose\x3aH+ symporter permease
ACD61462	7.059084833	6.995032192	6.51191233	two-component system sensor protein
ACD61465	6.827399871	6.49562002	5.872080137	NdvB protein
ACD61466	7.544779014	7.209082896	6.569671843	cation symporter
ACD61469	8.687708104	7.738274697	8.235324979	conserved hypothetical protein
ACD61470	7.293030151	7.375708478	7.547673459	3-dehydroquinate dehydratase
ACD61471	7.367598216	7.074687389	7.444783002	conserved hypothetical protein

ACD61474	0.420401554	-0.002545716	0	ISXo8 transposase
ACD61477	0	0	0	IS1112 transposase
ACD61481	8.051431923	8.835112456	8.403991956	conserved hypothetical protein
ACD61488	9.508416767	8.192312543	8.844457841	extracellular protease
ACD61489	4.325954803	4.335890521	4.053267765	transposase
ACD61490	10.21176665	9.916836378	10.28726219	ISXoo11 transposase
ACD61491	0	0	1.537017691	ISXoo12 transposase
ACD61495	7.123790333	6.7924129	7.275379596	formamidopyrimidine-DNA glycosylase
PXO_rna57	0	0	0	XO_rna57 cdna:pseudogene chromosome:GCA_000019585.1:Chromosome:5086533:5086609:-1 gene:PXO_rna57 transcript:PXO_rna5
PXO_rna58	0	0	0	XO_rna58 cdna:pseudogene chromosome:GCA_000019585.1:Chromosome:5086629:5086704:-1 gene:PXO_rna58 transcript:PXO_rna5
ACD61503	7.627548475	7.427036222	7.171316931	GAF domain protein
ACD61504	7.403778984	8.286506937	6.638790661	conserved hypothetical protein
ACD61505	7.086433493	7.047898232	6.401041624	tetracycline-efflux transporter
ACD61506	6.14811046	6.47740534	6.264239905	transglycolase
ACD61508	7.302474427	9.612936669	9.915000949	conserved hypothetical protein
ACD61509	8.014996819	7.740428412	7.887665391	SEC-C motif
ACD61510	7.861880945	7.45149138	7.989763465	transposase
ACD61511	7.127065747	7.41100246	7.903182918	transposase, IS30 family
ACD61512	8.129416975	8.749353249	7.597151232	endoglucanase
ACD61513	10.11681179	10.09189814	6.539717166	hypothetical protein
ACD61514	9.862280901	9.421469479	7.99791899	endoglucanase
ACD61515	8.060787786	8.378039029	10.41301434	endoglucanase
ACD61516	9.469128949	9.462571798	7.834629058	conserved hypothetical protein
ACD61518	0	0	0	ISXo8 transposase
ACD61519	5.80095683	5.483483677	5.483409509	ISXo8 transposase
ACD61524	6.485743992	5.764120531	5.298255067	TonB-dependent Receptor
ACD61525	5.931274109	5.908563152	6.335233124	ferripyoverdine receptor
ACD61526	7.263015621	8.387961299	6.739942587	ferripyoverdine receptor
ACD61527	7.086401646	7.607485673	6.343247909	transcriptional regulator AsnC family
ACD61530	7.666926979	6.930512638	6.359236511	rhamnogalacturonan acetylesterase
ACD61532	7.205793249	7.386414358	6.782696865	sugar-phosphate isomerase
ACD61533	0	0	0	transposase
ACD61534	0	0	0	ISXoo3 transposase ORF A
ACD61536	11.19574744	11.15180936	9.268336137	hypothetical protein
ACD61537	9.997687581	9.711537925	7.936402378	conserved hypothetical protein
ACD61538	7.538972645	7.131877534	6.833838844	2,5-diketo-D-gluconic acid reductase B
ACD61539	6.70104996	7.104787432	7.208000191	quinone oxidoreductase
ACD61540	7.925738381	8.105389988	9.340277405	oxidoreductase
ACD61543	11.0214242	10.25860136	11.39064189	hypothetical protein
ACD61544	10.13428512	11.37526212	11.98789994	conserved hypothetical protein
ACD61545	6.193566756	6.194284085	5.894812914	ATP-dependent RNA helicase
ACD61547	8.629986751	8.673312609	9.604388287	YehS
ACD61549	8.018127834	8.069605508	7.432182748	RTS beta protein
ACD61550	8.284814848	8.694187226	7.645953785	2-hydroxyhepta-2,4-diene-1, 7-dioateisomerase/5-carboxymethyl-2-oxo-hex-3-ene-1, 7-dioatedecarboxylase
ACD61551	8.812495016	8.857561184	8.971549302	dehydrogenase/reductase SDR family member 6
ACD61552	7.584391321	8.153673623	7.212005068	hydrolase
ACD61553	7.367100185	7.705770603	6.650276303	oxidoreductase
ACD61556	8.724796907	8.289147436	8.36055303	putative secreted protein
ACD61557	7.25772726	7.767595214	7.053893309	hypothetical protein
ACD61558	8.269954179	8.543364414	9.237592398	two-component system regulatory protein
ACD61559	7.82498419	8.231153965	9.879760895	acetate--CoA ligase
ACD61565	6.427292728	6.285466954	6.092552084	transcriptional regulator
ACD61568	11.47697398	11.30700722	11.02570019	transglycosylase associated protein
ACD61571	6.488688523	6.273073838	9.271355639	alkaline phosphatase
ACD61572	6.708394188	6.327857992	9.017056143	alkaline phosphatase D
ACD61574	7.649356785	6.655022605	8.706534006	hypothetical protein
ACD61578	8.374530922	8.20012373	8.258745035	4-oxalomesaconate hydratase
ACD61579	6.866796731	6.733666168	6.644332201	FldA
ACD61580	7.524659241	7.102458676	7.346797369	4-carboxy-4-hydroxy-2-oxoadipate aldolase/oxaloacetate decarboxylase
ACD61583	12.41153482	12.41084351	12.20013231	lactoylglutathione lyase-related lyase

ACD61586	9.295243179	8.546840454	8.856276116	putative secreted protein
ACD61587	4.281631491	4.026454833	3.721886644	ISXo5 transposase
ACD61588	6.989638595	7.113033665	6.537510405	amino acid transporter
ACD61594	7.341354252	7.266383654	7.383324131	transposase
ACD61596	6.83673208	6.740252994	6.570642042	radical SAM domain protein
ACD61597	8.823762096	8.784939055	9.206474734	outer membrane protein
ACD61601	7.120092693	7.191710687	7.444807845	carboxyl-terminal protease
ACD61602	6.208318259	6.767535628	6.433133055	M23 peptidase domain protein
ACD61605	8.124322965	7.421273801	8.390431241	conserved hypothetical protein
ACD61606	0	0	0	ISXo8 transposase
ACD61608	6.529959901	6.599966385	5.874351894	conserved hypothetical protein
ACD61609	6.830039776	6.795000624	6.799255714	putative ATP-binding protein
ACD61610	7.251548685	6.98232054	7.206281802	conserved hypothetical protein
ACD61611	7.66835318	7.276198865	7.161635793	conserved hypothetical protein
ACD61612	7.661193777	6.832687516	6.646479508	hypothetical protein
ACD61613	8.694424056	8.336118218	8.795413061	conserved hypothetical protein
ACD61614	6.381683104	6.425966119	7.21451341	GTP cyclohydrolase I
ACD61618	6.983563697	7.081414198	6.72816542	dicarboxylate transport protein
ACD61619	7.858944543	7.830990481	8.303780748	conserved hypothetical protein
ACD61622	7.335211682	6.878676303	7.702241961	conserved hypothetical protein
ACD61626	0	6.06894806	0	transposase
ACD61627	9.994296859	9.633574703	8.831741096	transposase
ACD61628	4.314029397	4.298628992	4.155797797	IS1112 transposase
ACD61629	0	0	0	hypothetical protein
ACD61630	9.122564016	8.904423884	8.349860624	conserved hypothetical protein
ACD61631	10.3614065	10.09699181	9.787678957	conserved hypothetical protein
ACD61632	11.72531939	11.87474318	10.78060538	paar motif family
ACD61633	3.915903274	2.947153689	3.620398731	transposase
ACD61634	0	0	0.309804828	transposase
ACD61636	0	0	0	bleomycin resistance protein
ACD61637	12.0709796	11.99174858	11.06993305	putative secreted protein
ACD61638	9.082556239	9.357945613	8.267507708	conserved hypothetical protein
ACD61639	10.06239698	8.59458587	10.4910213	conserved hypothetical protein
ACD61640	8.426868547	7.086815605	7.035810832	conserved hypothetical protein
ACD61641	7.006701958	6.31242376	5.899782266	sugar diacide regulator
ACD61642	5.953581871	5.910684699	5.861139028	glycerate kinase
ACD61643	6.568816494	6.804750569	6.521829682	MFS transporter
ACD61644	6.521016177	6.587671021	5.903016572	dipeptidase
ACD61645	8.49097118	8.517208754	7.732839	conserved hypothetical protein
ACD61646	8.053540388	7.946567121	8.266753752	oxidoreductase
ACD61649	7.11904486	6.855728135	6.593531557	glycerophosphoryl diester phosphodiesterase
ACD61651	6.345644752	6.422125333	6.109722024	tRNA modification GTPase TrmE
ACD61652	7.293664762	6.903737268	7.121906446	polysaccharide deacetylase
ACD61653	8.056843606	8.114877126	7.957467749	60 kDa inner-membrane protein
ACD61654	10.43502429	10.42720807	9.962483954	ribonuclease P protein component
ACD61655	14.60409565	15.56079853	14.80180938	ribosomal protein L34
ACD59187	0	0	0.813787347	flagellar basal body-associated protein FliL
ACD59442	1.185955324	0	0	ISXoo5 transposase
ACD60331	9.844581808	9.902494204	8.693190722	EvpB
ACD59156	0	0	0	flagellar L-ring protein FlgH
ACD59143	0	0	0	sensory box histidine kinase
ACD59112	0	0	0	type IV pilus biogenesis/stability protein PilW
ACD60342	8.315226564	8.039692242	8.897924091	Rhs element Vgr protein
ACD60354	7.632748064	8.486050626	8.397032817	hydrolase
ACD59124	0	0	0	putative secreted protein
ACD59153	0	0	7.163408158	flagellar biosynthesis hook protein
ACD59073	0	0	0	C-type cytochrome biogenesis protein
ACD59089	0	0	-1.757262148	ISXo8 transposase
ACD59087	0	0	0	conserved hypothetical protein
ACD59218	6.694852341	6.068184958	4.682247418	ISXoo5 transposase
ACD58795	0	0	0	ISXoo5 transposase
ACD59082	0	0	0	sugar aldolase
ACD59110	0	0	0	conserved hypothetical protein
ACD60332	10.35868416	10.63627115	9.907096466	EvpA

ACD59210	0	0	2.561985922	transposase
ACD59127	0	0	0	DNA translocase FtsK
ACD59181	0	0	6.127874672	flagellar M-ring protein FliF
ACD59114	0	0	0	nucleoside diphosphate kinase
ACD58018	0	0	0	hypothetical protein
ACD59150	0	0	0	flagellar basal-body rod protein FlgB
ACD60364	9.70860111	9.981938254	9.214678535	conserved hypothetical protein
ACD59162	0	0	7.004467684	flagellar protein
ACD59216	0	0	0	RHS Repeat family
ACD60560	10.44077575	12.36467365	12.6672535	putative membrane protein
ACD59418	9.873653273	9.590379332	0	putative membrane protein
ACD58180	0	0	0	hypothetical protein
ACD59246	0	0	-0.792292025	ISXo8 transposase
ACD57075	0	0	0	ISXo8 transposase
ACD59444	0	0	0	ISXo8 transposase
ACD59201	0	0	0	conserved hypothetical protein
ACD59229	0	0	0	transcriptional regulator
ACD59091	0	0	0	ISXo8 transposase
ACD59138	0	0	0	conserved hypothetical protein
ACD60379	8.54382837	8.999157243	7.954289384	twitching motility protein
ACD59209	0	0	0	ISXo2 putative transposase
ACD59223	0	-2.097949581	2.99787226	Tal7a, TAL effector AvrBs3/PthA
ACD59227	-1.47903372	-2.256941803	-3.020996102	Tal7b, TAL effector AvrBs3/PthA
ACD57395	0	0	4.174078787	ISXoo11 transposase
ACD60356	2.570679076	1.595599137	3.893964017	ISXo8 transposase
ACD59105	0	0	0	transposase
ACD61091	0	0	0	ISXoo12 transposase
ACD60229	0	0	0	ISXoo12 transposase
ACD59922	0	0	0	putative transposase
ACD59758	0	0	0	IS1112 transposase
ACD58791	0	0	1.180345215	IS1112 transposase
ACD59175	0	0	0	acetyltransferase
ACD59236	0	0	0	TonB family C-terminal domain protein
ACD59121	0	0	0	conserved hypothetical protein
ACD57143	4.544077299	4.183438874	3.182218736	IS66 family element, Orf1 protein, putative
ACD57355	0	0	0	conserved hypothetical protein
ACD59076	0	0	0	conserved hypothetical protein
ACD59195	0	0	0	Putative signal protein with GGDEF domain
ACD59081	0	0	0	cationic amino acid transporter
ACD59241	0	0	0	ISXo3 transposase ORF B
ACD59074	0	0	0	conserved domain protein
ACD59071	0	0	0	C-type cytochrome biogenesis protein/thioredoxin
ACD59251	3.343507315	1.651104517	2.373486743	IS1113 transposase
ACD58538	8.591200673	8.634938074	9.390863261	IS1113 transposase
ACD59923	0	0	0	IS1113 transposase
ACD59433	0	0	0	ISXo8 transposase
ACD59197	0	0	0	Putative signal protein with GGDEF domain
ACD60368	8.065469991	8.661977568	8.034672429	peroxiredoxin OsmC
ACD59192	0	0	0	hypothetical protein
ACD60367	8.735874143	9.084114771	11.47870896	rickettsia 17 kDa surface antigen family
ACD58665	0	0	0	ISXoo12 transposase
ACD59098	0	4.751099466	4.979604681	conserved domain protein
ACD59290	0	4.686511733	1.394503167	transposase, IS30 family
ACD59064	0	0	0	succinyldiaminopimelate transaminase
ACD60353	12.71699089	11.91724899	12.15607992	hypothetical protein
ACD59176	0	0	0	ring hydroxylating dioxygenase alpha-subunit
ACD59219	0	0	0	transposase
ACD59133	0	0	0	translation initiation factor IF-1
ACD59065	0	0	0	heme ABC exporter, ATP-binding protein CcmA
ACD59190	0	0	0	flagellar protein
ACD60347	6.61845011	6.102597248	6.570046943	conserved hypothetical protein
ACD59189	0	0	0	flagellar protein
ACD59220	6.196841101	0	6.462117775	transposase
ACD59111	0	0	0	conserved hypothetical protein

ACD58674	0	0	0	ISXo3 transposase ORF A
ACD60935	0	0	0	ISXo3 transposase ORF B
ACD60592	0	0	0	ISXo3 transposase ORF B
ACD61272	0	0	0	ISXoo3 transposase ORF A
ACD56922	0	0	0	ISXoo3 transposase ORF A
ACD60683	0	4.093560176	0	ISXoo3 transposase ORF A
ACD59430	0	0	0	ISXoo3 transposase ORF A
ACD59230	0	0	0	acyl carrier protein phosphodiesterase
ACD59200	0	0	0	flagellar biosynthesis protein FlhA
ACD59239	0	0	0	transposase
ACD59182	0	0	6.300652738	flagellar motor switch protein FliG
ACD59177	0	0	0	conserved hypothetical protein
ACD59167	0	0	13.6291289	RNA polymerase sigma-54 factor
ACD59228	0	0	0	phage-related integrase
ACD60349	8.418413454	8.282916979	6.997326284	conserved hypothetical protein
ACD59234	0	0	0	seryl-tRNA synthetase
ACD59101	0	0	0	hypothetical protein
ACD60361	10.25083133	9.465609257	9.01664117	AsmA family protein
ACD59144	0	0	0	Putative signal protein with GGDEF, EAL and two component receiver domains
ACD58690	0	0	0	transposase
ACD59126	0	0	0	conserved hypothetical protein
ACD60346	4.744263373	4.775456209	4.487389875	conserved hypothetical protein
ACD59070	0	0	0	cytochrome c-type biogenesis protein CcmF
ACD59108	0.331510322	0	0	GTP-binding protein
ACD60389	8.197511592	8.048672137	7.334943631	intracellular protease I
ACD59113	0	0	0	radical SAM enzyme, Cfr family
ACD59142	0	0	0	Putative signal protein with PAS(PAC), GGDEF and EAL domains
ACD59096	0	0	0	ISXo8 transposase
ACD59232	0	0	-0.968116459	ISXo8 transposase
ACD57812	0.42183459	0	0	ISXo8 transposase
ACD60243	0	0	0	ISXo8 transposase
ACD58196	0	0	0	ISXo8 transposase
ACD59212	0	0	0	ISXo8 transposase
ACD59860	0	0	0	conserved hypothetical protein
ACD59080	0	0	0	cationic amino acid transporter
ACD60348	6.321780211	6.432799099	6.799022528	Rhs element Vgr protein
ACD59191	0	0	0	flagellar biosynthetic protein
ACD59088	0	0	0	conserved hypothetical protein
ACD59723	0	0	0	ISXo7 transposase
ACD60343	6.801973435	6.389269088	6.884512451	conserved hypothetical protein
ACD60345	5.254132924	5.264074725	5.905849075	conserved hypothetical protein
ACD59206	0	0	0	chemotaxis phosphatase CheZ
ACD59183	0	0	0	flagellar assembly protein FliH
ACD59146	0	0	0	conserved hypothetical protein
ACD59173	0	0	0	3-oxoacyl-reductase
ACD59205	0	0	0	chemotaxis response regulator CheY
ACD59157	0	0	4.544411197	flagellar P-ring protein FlgI
ACD59186	0.548495811	3.014291013	2.627174899	flagellar protein
ACD59069	0	0	0	C-type cytochrome biogenesis protein
ACD59155	0	0	8.511179414	flagellar basal-body rod protein FlgG
ACD59204	0	0	0	RNA polymerase sigma factor FliA
ACD57871	0.691587763	0	0	translation elongation factor Tu
ACD59067	0	0	0	ABC transporter heme permease
ACD59129	0	0	0	protein of unknown function
ACD60344	7.412154867	6.06707075	8.440262901	conserved hypothetical protein
ACD59235	0	0	0	TonB protein
ACD59132	0	0	0	leucyl/phenylalanyl-tRNA--protein transferase
ACD59179	0	0	0	O-antigen biosynthesis protein
ACD60371	9.542441858	10.29050274	6.430517785	conserved hypothetical protein
ACD56842	0	0	0	conserved domain protein
ACD59104	0	0	0	ISXo3 transposase ORF B
ACD59170	0	0	6.250135424	nucleotide sugar transaminase
ACD59115	0	0	0	transcriptional regulator TetR family

ACD59086	0	0	0	hypothetical protein
ACD61021	2.991841981	0	-0.894260247	ISXoo8 transposase
ACD59172	0	0	0	3-oxoacyl-synthase
ACD59106	3.330085073	0	2.28681315	ISXoo2 transposase
ACD59141	0	0	0	conserved hypothetical protein
ACD59208	0	0	0	transposase
ACD59095	3.077526724	0	-0.142663884	transposase (IS4 family) protein
ACD60330	12.23968504	12.55618989	11.68046062	Hcp family protein
ACD57610	0	0	0	ISXoo12 transposase
ACD60370	8.32925817	8.322784441	8.32152228	aspartate carbamoyltransferase
ACD58009	0	0.536251879	0	ISXo1 transposase
ACD58193	0	0	-0.499226495	ISXo1 transposase
ACD57481	0	2.855144557	0	ISXo1 transposase
ACD59281	0	0	0	ISXo1 transposase
ACD60599	0	0	0	ISXo1 transposase
ACD60360	7.146023823	7.475311908	7.106620516	dienelactone hydrolase
ACD59185	0	0	0	flagellar export protein FliJ
ACD59164	0	0	9.463608153	conserved hypothetical protein
ACD59203	0	0	0	flagellar synthesis regulator FleN
ACD59242	0	0	0	ISXo5 transposase
ACD57356	0.961401073	0	0	ISXo5 transposase
ACD59214	0	0	0	ISXo5 transposase
ACD59094	0	0	0	ISXo5 transposase
ACD60355	5.602492512	5.41986919	6.300409306	ISXo5 transposase
ACD59249	0	0	0	hypothetical protein
ACD57358	9.062774724	9.836449645	12.20458948	transposase
ACD59102	0	0	0	putative transposase
ACD59119	0	0	0	conserved hypothetical protein
ACD59158	0	0	0	flagellar rod assembly protein/muramidase FlgJ
ACD60362	7.505446369	7.701798541	6.923886032	UDP-N-acetylmuramoylalanine--D-glutamate ligase
ACD59148	0	0	0	flagella basal body P-ring formation protein FlgA
ACD60369	9.429446496	9.132695075	9.331597741	hypothetical protein
ACD59196	0	0	0	hypothetical protein
ACD59221	11.38429809	0	0	conserved hypothetical protein
ACD59202	0	0	6.651754923	flagellar biosynthetic protein FlhF
ACD59166	0	0	8.686976678	response regulator
ACD59139	0	0	10.97557574	chemotaxis protein
ACD59440	0	0	0	integral membrane protein
ACD60363	7.318488581	7.68210974	6.76879304	conserved hypothetical protein
ACD59184	0	0	0	flagellum-specific ATP synthase
ACD59128	0	0	0	thioredoxin-disulfide reductase
ACD59207	0	0	0	chemotaxis protein CheA
ACD59180	0	0	0	flagellar hook-basal body complex protein (FliE)
ACD59199	0	0	0	flagellar biosynthetic protein FlhB
ACD59169	0	0	0	transcriptional regulator
ACD59125	0	0	0	outer membrane lipoprotein carrier protein LolA
ACD59154	0	0	0	flagellar basal-body rod protein FlgF
ACD59159	0	0	0.883886654	flagellar hook-associated protein FlgK
ACD59168	0	0	11.91588685	response regulator
ACD59117	0	0	0	3-ketoacyl-CoA thiolase
ACD59122	0	0	0	ATPase
ACD60358	8.75420941	8.894005261	9.408718229	single-stranded DNA binding protein
ACD59066	0	0	0	heme exporter protein CcmB
ACD60377	7.246759597	7.876467833	6.583025585	conserved hypothetical protein, putative
ACD59161	8.480834622	11.74486747	15.5482319	flagellar protein
ACD59075	0	0	0	conserved hypothetical protein
ACD59123	0	0	0	hypothetical protein
ACD59085	0	0	0	conserved hypothetical protein
ACD59174	0	0	0	dehydrogenase with different specificities
ACD59151	0	8.443904972	10.78416041	flagellar basal-body rod protein FlgC
ACD59116	0	0	0	3-hydroxyacyl-CoA dehydrogenase
ACD58357	0	0.045834347	-0.058201061	xylose isomerase
ACD59193	0	0	0	flagellar biosynthesis pathway component FliQ
ACD59078	0	0	0	D-3-phosphoglycerate dehydrogenase

ACD60333	11.75480401	11.91568148	11.64798	TPR repeat protein
ACD56884	0	0	0	paar motif family
ACD59118	0	0	0	Cl-channel, voltage gated
ACD59083	0	4.072671789	0	dioxygenase
ACD60365	8.488972848	8.49228584	8.961715924	bifunctional diaminopimelate decarboxylase/asparta
ACD59092	0	0	0	molybdopterin biosynthesis protein
ACD61227	0	0	0	ISxac3 transposase
ACD59152	0	0	11.71765072	flagellar protein
ACD60378	8.594361931	8.693389381	7.414727512	twitching motility protein
ACD59165	0	0	0	conserved hypothetical protein
ACD59137	0	0	0	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase
ACD60350	7.646479508	7.556567363	8.587526265	pirin
ACD60372	7.949978412	8.074628524	7.51465883	conserved hypothetical protein
ACD59188	0	0	5.147416606	flagellar motor switch protein FliM
ACD59068	0	0	8.674227585	conserved domain protein
ACD58949	0	0	0	probable transmembrane protein
ACD60558	0	0	0	similar to membrane-bound transport protein
ACD59145	0	0	0	histidine kinase
ACD58022	0	0	0	ISXoo13 transposase
ACD59637	0	4.517483578	7.504985787	ISXoo13 transposase
ACD59103	0	0	0	ISXoo13 transposase
ACD60003	0	0	0	ISXoo13 transposase
ACD60526	4.156064869	4.885745174	4.215476698	ISXoo13 transposase
ACD59063	0	0	0	hydrolase, carbon-nitrogen family
ACD59077	0	0	0	oxidoreductase
ACD58451	0	0	0	conserved domain protein
ACD59160	0	0	0	flagellar hook-associated protein 3
ACD59107	0	0	0	molybdopterin biosynthesis
ACD59439	0	0	0	homoserine O-acetyltransferase
ACD59149	0	0	0	chemotaxis protein
ACD59140	0	0	0	conserved hypothetical protein
ACD58871	3.433627167	0	0	ISXoo11 transposase
ACD59480	0	0	0	ISXoo11 transposase
ACD61459	0	0	0	ISXoo11 transposase
ACD59097	0	0	0	transposase
ACD59171	0	0	0	acyl carrier protein
ACD59147	0	0	0	flagellar protein
ACD59072	0	0	0	C-type cytochrome biogenesis protein
ACD59084	0	0	0	2,3-diketo-5-methylthio-1-phosphopentane phosphatase
ACD59134	0	0	0	ATP-dependent Clp protease ATP-binding subunit ClpA
ACD59079	0	0	0	hydrolase, nudix family protein
ACD59135	0	0	0	ATP-dependent Clp protease adaptor protein ClpS
ACD59198	0	0	0	Putative signal protein with GGDEF and EAL domains
ACD59120	0	0	0	putative Protein CrcB homolog
ACD59178	0	0	0	methyltransferase, FkbM family protein
ACD59194	0	0	0	flagellar biosynthetic protein FliR
ACD59217	0	0	0	glutamate synthase domain 2
ACD59136	0	0	0	7,8-dihydro-8-oxoguanine-triphosphatase
ACD59431	0	0	0	ISXoo3 transposase ORF B
ACD61273	0	0	-0.120159379	ISXoo3 transposase ORF B
ACD58447	0	0	0	probable vgr-related protein
ACD59215	0	0	0	hypothetical protein
ACD61431	0	0	0	transposase
ACD59163	0	0	11.59386261	flagellar protein FliS
ACD59109	0	0	0	serine/threonine protein kinase
ACD59093	0	0	0	conserved domain protein
ACD59100	0	0	0	transposase
ACD59213	0	0	0	Rhs family protein

Supplementary Table 5. Gene ontology analysis of enriched up-regulated genes of Xoo during in planta growth on [susceptible (S) and resistant (R)] hosts

Dongjin (susceptible)

Biological process (Dongjin 2UP)

GOBPID	Pvalue	Count	Size	Term
GO:0044699	0.049822672	111	854	single-organism process
GO:0044763	0.024923796	92	675	single-organism cellular process
GO:0055085	0.003805717	20	93	transmembrane transport
GO:0006811	0.018376485	12	54	ion transport
GO:0022900	0.001861278	7	17	electron transport chain
GO:0006091	0.002748574	7	18	generation of precursor metabolites and energy
GO:0022904	0.003156084	6	14	respiratory electron transport chain
GO:0015980	0.0068811	6	16	energy derivation by oxidation of organic compounds
GO:0045333	0.0068811	6	16	cellular respiration
GO:0042773	0.008651732	4	8	ATP synthesis coupled electron transport
GO:0006119	0.008651732	4	8	oxidative phosphorylation
GO:0000105	0.013586307	2	2	histidine biosynthetic process
GO:0052803	0.013586307	2	2	imidazole-containing compound metabolic process
GO:0006547	0.013586307	2	2	histidine metabolic process

Molecular function (Dongjin 2UP)

GO:0005215	0.043896526	32	203	transporter activity
GO:0043169	0.001315858	23	103	cation binding
GO:0022857	0.006700711	19	90	transmembrane transporter activity
GO:0046872	0.012152936	19	95	metal ion binding
GO:0022892	0.042652682	16	87	substrate-specific transporter activity
GO:0046914	0.018261914	14	66	transition metal ion binding
GO:0022891	0.026391758	14	69	substrate-specific transmembrane transporter activity
GO:0015075	0.01444729	13	58	ion transmembrane transporter activity
GO:0016746	0.027794462	10	44	transferase activity, transferring acyl groups
GO:0016747	0.023089679	8	31	transferase activity, transferring acyl groups other than amino-acyl groups
GO:0022890	0.045581024	8	35	inorganic cation transmembrane transporter activity
GO:0008080	0.002904536	7	18	N-acetyltransferase activity
GO:0016410	0.002904536	7	18	N-acyltransferase activity
GO:0016407	0.002904536	7	18	acetyltransferase activity
GO:0015077	0.00777801	7	21	monovalent inorganic cation transmembrane transporter activity
GO:0009055	0.016999046	7	24	electron carrier activity
GO:0015078	0.01005246	6	17	hydrogen ion transmembrane transporter activity
GO:0016651	0.031764142	5	16	oxidoreductase activity, acting on NAD(P)H
GO:0046906	0.022124728	4	10	tetrapyrrole binding
GO:0020037	0.022124728	4	10	heme binding
GO:0003954	0.031622083	4	11	NADH dehydrogenase activity
GO:0008137	0.031622083	4	11	NADH dehydrogenase (ubiquinone) activity
GO:0016655	0.031622083	4	11	oxidoreductase activity, acting on NAD(P)H, quinone or similar compound as acceptor
GO:0050136	0.031622083	4	11	NADH dehydrogenase (quinone) activity
GO:0004129	0.03820029	2	3	cytochrome-c oxidase activity
GO:0016675	0.03820029	2	3	oxidoreductase activity, acting on a heme group of donors
GO:0016676	0.03820029	2	3	oxidoreductase activity, acting on a heme group of donors, oxygen as acceptor

Samgwang (resistant)

Biological process (Samgwang 2UP)

GO:0005975	0.010648185	19	79	carbohydrate metabolic process
GO:0022900	0.005608886	7	17	electron transport chain
GO:0006091	0.008095887	7	18	generation of precursor metabolites and energy
GO:0022904	0.008246657	6	14	respiratory electron transport chain
GO:0015980	0.017199638	6	16	energy derivation by oxidation of organic compounds
GO:0045333	0.017199638	6	16	cellular respiration

GO:0042773	0.016969694	4	8	ATP synthesis coupled electron transport
GO:0006119	0.016969694	4	8	oxidative phosphorylation
Molecular function (Samgwang 2UP)				
GO:0043169	0.000364365	27	103	cation binding
GO:0046872	0.014211064	21	95	metal ion binding
GO:0046914	0.028357657	15	66	transition metal ion binding
GO:0015077	0.017314143	7	21	monovalent inorganic cation transmembrane transporter activity
GO:0009055	0.035938369	7	24	electron carrier activity
GO:0015078	0.020375979	6	17	hydrogen ion transmembrane transporter activity
GO:0003954	0.0104944	5	11	NADH dehydrogenase activity
GO:0008137	0.0104944	5	11	NADH dehydrogenase (ubiquinone) activity
GO:0016655	0.0104944	5	11	oxidoreductase activity, acting on NAD(P)H, quinone or similar compound as acceptor
GO:0050136	0.0104944	5	11	NADH dehydrogenase (quinone) activity
GO:0046906	0.036466265	4	10	tetrapyrrole binding
GO:0020037	0.036466265	4	10	heme binding
GO:0046983	0.036711569	3	6	protein dimerization activity

Supplementary Table 6. Enriched KEGG pathways of up-regulated Xoo genes during in planta growth on [susceptible (S) and resistant (R)] hosts.

Dongjin (susceptible)			
Kegg Pathway	Discription	Gene number	(%) of genes
01100	Metabolic pathways	60	19.67213115
01110	Biosynthesis of secondary metabolites	25	8.196721311
01130	Biosynthesis of antibiotics	16	5.245901639
00190	Oxidative phosphorylation	13	4.262295082
02020	Two-component system	11	3.606557377
01230	Biosynthesis of amino acids	9	2.950819672
00500	Starch and sucrose metabolism	8	2.62295082
00230	Purine metabolism	7	2.295081967
01120	Microbial metabolism in diverse environments	6	1.967213115
03070	Bacterial secretion system	6	1.967213115
00564	Glycerophospholipid metabolism	5	1.639344262
01502	Vancomycin resistance	4	1.31147541
00920	Sulfur metabolism	4	1.31147541
00550	Peptidoglycan biosynthesis	4	1.31147541
00270	Cysteine and methionine metabolism	4	1.31147541
04112	Cell cycle - Caulobacter	4	1.31147541
01503	Cationic antimicrobial peptide (CAMP) resistance	4	1.31147541
00330	Arginine and proline metabolism	4	1.31147541
05014	Amyotrophic lateral sclerosis (ALS)	4	1.31147541
02010	ABC transporters	4	1.31147541
00900	Terpenoid backbone biosynthesis	3	0.983606557
04146	Peroxisome	3	0.983606557
00511	Other glycan degradation	3	0.983606557
03430	Mismatch repair	3	0.983606557
00540	Lipopolysaccharide biosynthesis	3	0.983606557
03440	Homologous recombination	3	0.983606557
00630	Glyoxylate and dicarboxylate metabolism	3	0.983606557
04260	Cardiac muscle contraction	3	0.983606557
01200	Carbon metabolism	3	0.983606557
03018	RNA degradation	2	0.655737705
03008	Ribosome biogenesis in eukaryotes	2	0.655737705
00740	Riboflavin metabolism	2	0.655737705
00860	Porphyrin and chlorophyll metabolism	2	0.655737705
00360	Phenylalanine metabolism	2	0.655737705
03420	Nucleotide excision repair	2	0.655737705
00340	Histidine metabolism	2	0.655737705
04068	FoxO signaling pathway	2	0.655737705
00790	Folate biosynthesis	2	0.655737705
03030	DNA replication	2	0.655737705
05204	Chemical carcinogenesis	2	0.655737705
00650	Butanoate metabolism	2	0.655737705
01501	beta-Lactam resistance	2	0.655737705
03410	Base excision repair	2	0.655737705
00520	Amino sugar and nucleotide sugar metabolism	2	0.655737705
01210	2-Oxocarboxylic acid metabolism	2	0.655737705
05111	Vibrio cholerae pathogenic cycle	1	0.327868852
00280	Valine, leucine and isoleucine degradation	1	0.327868852
00130	Ubiquinone and other terpenoid-quinone biosynthesis	1	0.327868852
00380	Tryptophan metabolism	1	0.327868852
00623	Toluene degradation	1	0.327868852

00072	Synthesis and degradation of ketone bodies	1	0.327868852
04122	Sulfur relay system	1	0.327868852
00600	Sphingolipid metabolism	1	0.327868852
00450	Selenocompound metabolism	1	0.327868852
03010	Ribosome	1	0.327868852
05211	Renal cell carcinoma	1	0.327868852
00240	Pyrimidine metabolism	1	0.327868852
00640	Propanoate metabolism	1	0.327868852
05340	Primary immunodeficiency	1	0.327868852
03320	PPAR signaling pathway	1	0.327868852
00195	Photosynthesis	1	0.327868852
00440	Phosphonate and phosphinate metabolism	1	0.327868852
00940	Phenylpropanoid biosynthesis	1	0.327868852
00400	Phenylalanine, tyrosine and tryptophan biosynthesis	1	0.327868852
00030	Pentose phosphate pathway	1	0.327868852
05200	Pathways in cancer	1	0.327868852
00910	Nitrogen metabolism	1	0.327868852
00760	Nicotinate and nicotinamide metabolism	1	0.327868852
00260	Glycine, serine and threonine metabolism	1	0.327868852
00561	Glycerolipid metabolism	1	0.327868852
04724	Glutamatergic synapse	1	0.327868852
00052	Galactose metabolism	1	0.327868852
04727	GABAergic synapse	1	0.327868852
00051	Fructose and mannose metabolism	1	0.327868852
00364	Fluorobenzoate degradation	1	0.327868852
01212	Fatty acid metabolism	1	0.327868852
00983	Drug metabolism - other enzymes	1	0.327868852
00471	D-Glutamine and D-glutamate metabolism	1	0.327868852
01220	Degradation of aromatic compounds	1	0.327868852
00473	D-Alanine metabolism	1	0.327868852
00460	Cyanoamino acid metabolism	1	0.327868852
00361	Chlorocyclohexane and chlorobenzene degradation	1	0.327868852
00332	Carbapenem biosynthesis	1	0.327868852
00930	Caprolactam degradation	1	0.327868852
01040	Biosynthesis of unsaturated fatty acids	1	0.327868852
02030	Bacterial chemotaxis	1	0.327868852
00053	Ascorbate and aldarate metabolism	1	0.327868852
04152	AMPK signaling pathway	1	0.327868852
00250	Alanine, aspartate and glutamate metabolism	1	0.327868852

Samgwang (resistant)			
01100	Metabolic pathways	70	17.76649746
01110	Biosynthesis of secondary metabolites	31	7.868020305
02020	Two-component system	19	4.822335025
01130	Biosynthesis of antibiotics	18	4.568527919
01120	Microbial metabolism in diverse environments	14	3.553299492
00190	Oxidative phosphorylation	11	2.791878173
03070	Bacterial secretion system	11	2.791878173
00500	Starch and sucrose metabolism	10	2.538071066
01200	Carbon metabolism	9	2.284263959
01230	Biosynthesis of amino acids	9	2.284263959
02010	ABC transporters	6	1.52284264
05016	Huntington's disease	5	1.269035533
00630	Glyoxylate and dicarboxylate metabolism	5	1.269035533
00920	Sulfur metabolism	4	1.015228426

00230	Purine metabolism	4	1.015228426
04146	Peroxisome	4	1.015228426
00550	Peptidoglycan biosynthesis	4	1.015228426
00564	Glycerophospholipid metabolism	4	1.015228426
01212	Fatty acid metabolism	4	1.015228426
00270	Cysteine and methionine metabolism	4	1.015228426
04112	Cell cycle - Caulobacter	4	1.015228426
02030	Bacterial chemotaxis	4	1.015228426
00900	Terpenoid backbone biosynthesis	3	0.76142132
03018	RNA degradation	3	0.76142132
00740	Riboflavin metabolism	3	0.76142132
00640	Propanoate metabolism	3	0.76142132
05012	Parkinson's disease	3	0.76142132
04932	Non-alcoholic fatty liver disease (NAFLD)	3	0.76142132
00540	Lipopolysaccharide biosynthesis	3	0.76142132
00790	Folate biosynthesis	3	0.76142132
00061	Fatty acid biosynthesis	3	0.76142132
04260	Cardiac muscle contraction	3	0.76142132
00720	Carbon fixation pathways in prokaryotes	3	0.76142132
00650	Butanoate metabolism	3	0.76142132
00053	Ascorbate and aldarate metabolism	3	0.76142132
00330	Arginine and proline metabolism	3	0.76142132
05010	Alzheimer's disease	3	0.76142132
01502	Vancomycin resistance	2	0.507614213
00280	Valine, leucine and isoleucine degradation	2	0.507614213
03008	Ribosome biogenesis in eukaryotes	2	0.507614213
00620	Pyruvate metabolism	2	0.507614213
03060	Protein export	2	0.507614213
03320	PPAR signaling pathway	2	0.507614213
00860	Porphyrin and chlorophyll metabolism	2	0.507614213
00400	Phenylalanine, tyrosine and tryptophan biosynthesis	2	0.507614213
00511	Other glycan degradation	2	0.507614213
00760	Nicotinate and nicotinamide metabolism	2	0.507614213
00300	Lysine biosynthesis	2	0.507614213
00340	Histidine metabolism	2	0.507614213
00010	Glycolysis / Gluconeogenesis	2	0.507614213
00051	Fructose and mannose metabolism	2	0.507614213
04068	FoxO signaling pathway	2	0.507614213
01503	Cationic antimicrobial peptide (CAMP) resistance	2	0.507614213
00780	Biotin metabolism	2	0.507614213
01040	Biosynthesis of unsaturated fatty acids	2	0.507614213
03410	Base excision repair	2	0.507614213
05014	Amyotrophic lateral sclerosis (ALS)	2	0.507614213
00520	Amino sugar and nucleotide sugar metabolism	2	0.507614213
01210	2-Oxocarboxylic acid metabolism	2	0.507614213
00750	Vitamin B6 metabolism	1	0.253807107
05111	Vibrio cholerae pathogenic cycle	1	0.253807107
00290	Valine, leucine and isoleucine biosynthesis	1	0.253807107
00130	Ubiquinone and other terpenoid-quinone biosynthesis	1	0.253807107
00350	Tyrosine metabolism	1	0.253807107
00380	Tryptophan metabolism	1	0.253807107
00253	Tetracycline biosynthesis	1	0.253807107
00072	Synthesis and degradation of ketone bodies	1	0.253807107
04122	Sulfur relay system	1	0.253807107
00521	Streptomycin biosynthesis	1	0.253807107

00450	Selenocompound metabolism	1	0.253807107
03010	Ribosome	1	0.253807107
05211	Renal cell carcinoma	1	0.253807107
05205	Proteoglycans in cancer	1	0.253807107
05020	Prion diseases	1	0.253807107
05340	Primary immunodeficiency	1	0.253807107
00195	Photosynthesis	1	0.253807107
02060	Phosphotransferase system (PTS)	1	0.253807107
00940	Phenylpropanoid biosynthesis	1	0.253807107
00360	Phenylalanine metabolism	1	0.253807107
00030	Pentose phosphate pathway	1	0.253807107
05200	Pathways in cancer	1	0.253807107
00770	Pantothenate and CoA biosynthesis	1	0.253807107
03420	Nucleotide excision repair	1	0.253807107
00910	Nitrogen metabolism	1	0.253807107
03430	Mismatch repair	1	0.253807107
00680	Methane metabolism	1	0.253807107
00562	Inositol phosphate metabolism	1	0.253807107
03440	Homologous recombination	1	0.253807107
00260	Glycine, serine and threonine metabolism	1	0.253807107
00561	Glycerolipid metabolism	1	0.253807107
04724	Glutamatergic synapse	1	0.253807107
00052	Galactose metabolism	1	0.253807107
04727	GABAergic synapse	1	0.253807107
00071	Fatty acid degradation	1	0.253807107
00983	Drug metabolism - other enzymes	1	0.253807107
03030	DNA replication	1	0.253807107
00471	D-Glutamine and D-glutamate metabolism	1	0.253807107
01220	Degradation of aromatic compounds	1	0.253807107
00460	Cyanoamino acid metabolism	1	0.253807107
00020	Citrate cycle (TCA cycle)	1	0.253807107
05204	Chemical carcinogenesis	1	0.253807107
00710	Carbon fixation in photosynthetic organisms	1	0.253807107
00332	Carbapenem biosynthesis	1	0.253807107
00930	Caprolactam degradation	1	0.253807107
00660	C5-Branched dibasic acid metabolism	1	0.253807107
00524	Butirosin and neomycin biosynthesis	1	0.253807107
01501	beta-Lactam resistance	1	0.253807107
04152	AMPK signaling pathway	1	0.253807107
00250	Alanine, aspartate and glutamate metabolism	1	0.253807107
04920	Adipocytokine signaling pathway	1	0.253807107

Supplementary Table 7. Analysis of putative secretory proteins

Signal P											
# name	Cmax	pos	Ymax	pos	Smax	pos	Smean	D	?	Dmaxcut	Networks-used
gi_188518723_gb_ACD56668.1_	0.108	23	0.103	57	0.122	45	0.084	0.094	N	0.57	SignalP-noTM
gi_188518724_gb_ACD56669.1_	0.167	32	0.149	32	0.228	1	0.153	0.151	N	0.57	SignalP-noTM
gi_188518725_gb_ACD56670.1_	0.128	32	0.174	15	0.391	11	0.302	0.234	N	0.57	SignalP-noTM
gi_188518726_gb_ACD56671.1_	0.104	67	0.125	12	0.184	6	0.161	0.142	N	0.57	SignalP-noTM
gi_188518727_gb_ACD56672.1_	0.134	50	0.114	13	0.17	10	0.135	0.122	N	0.51	SignalP-TM
gi_188518728_gb_ACD56673.1_	0.26	19	0.492	19	0.961	10	0.936	0.701	Y	0.57	SignalP-noTM
gi_188518729_gb_ACD56674.1_	0.219	30	0.356	23	0.946	15	0.903	0.613	Y	0.57	SignalP-noTM
gi_188518730_gb_ACD56675.1_	0.106	14	0.138	14	0.266	7	0.176	0.156	N	0.57	SignalP-noTM
gi_188518731_gb_ACD56676.1_	0.171	20	0.211	20	0.443	1	0.311	0.248	N	0.51	SignalP-TM
gi_188518732_gb_ACD56677.1_	0.122	25	0.123	31	0.207	23	0.109	0.118	N	0.51	SignalP-TM
gi_188518733_gb_ACD56678.1_	0.198	25	0.135	33	0.209	1	0.121	0.13	N	0.51	SignalP-TM
gi_188518739_gb_ACD56684.1_	0.834	25	0.844	25	0.958	8	0.883	0.862	Y	0.57	SignalP-noTM
gi_188518740_gb_ACD56685.1_	0.206	49	0.19	49	0.33	39	0.118	0.156	N	0.57	SignalP-noTM
gi_188518747_gb_ACD56692.1_	0.12	57	0.141	11	0.28	1	0.184	0.161	N	0.57	SignalP-noTM
gi_188518751_gb_ACD56696.1_	0.196	20	0.282	20	0.617	10	0.407	0.341	N	0.57	SignalP-noTM
gi_188518757_gb_ACD56702.1_	0.13	25	0.144	18	0.221	9	0.162	0.152	N	0.57	SignalP-noTM
gi_188518765_gb_ACD56710.1_	0.131	25	0.128	25	0.202	37	0.118	0.124	N	0.51	SignalP-TM
gi_188518766_gb_ACD56711.1_	0.135	21	0.112	11	0.206	2	0.116	0.114	N	0.57	SignalP-noTM
gi_188518767_gb_ACD56712.1_	0.229	17	0.269	17	0.485	13	0.315	0.29	N	0.57	SignalP-noTM
gi_188518768_gb_ACD56713.1_	0.142	40	0.115	40	0.128	36	0.089	0.103	N	0.57	SignalP-noTM
gi_188518771_gb_ACD56716.1_	0.107	42	0.118	18	0.156	13	0.122	0.12	N	0.57	SignalP-noTM
gi_188518772_gb_ACD56717.1_	0.148	49	0.12	11	0.231	1	0.133	0.126	N	0.57	SignalP-noTM
gi_188518773_gb_ACD56718.1_	0.203	19	0.407	19	0.934	1	0.837	0.609	Y	0.57	SignalP-noTM
gi_188518775_gb_ACD56720.1_	0.152	17	0.103	17	0.151	6	0.069	0.087	N	0.57	SignalP-noTM
gi_188518776_gb_ACD56721.1_	0.121	68	0.16	18	0.308	9	0.245	0.2	N	0.57	SignalP-noTM
gi_188518779_gb_ACD56724.1_	0.34	21	0.471	21	0.823	2	0.709	0.559	Y	0.51	SignalP-TM
gi_188518780_gb_ACD56725.1_	0.158	38	0.114	11	0.169	3	0.133	0.123	N	0.57	SignalP-noTM
gi_188518781_gb_ACD56726.1_	0.223	19	0.107	42	0.131	41	0.065	0.087	N	0.57	SignalP-noTM
gi_188518782_gb_ACD56727.1_	0.127	33	0.144	16	0.247	5	0.211	0.169	N	0.51	SignalP-TM
gi_188518787_gb_ACD56732.1_	0.105	21	0.138	13	0.25	9	0.186	0.161	N	0.57	SignalP-noTM
gi_188518788_gb_ACD56733.1_	0.129	25	0.109	25	0.137	14	0.098	0.104	N	0.57	SignalP-noTM
gi_188518789_gb_ACD56734.1_	0.131	29	0.181	29	0.346	19	0.227	0.198	N	0.51	SignalP-TM
gi_188518790_gb_ACD56735.1_	0.172	28	0.144	28	0.265	25	0.132	0.138	N	0.57	SignalP-noTM
gi_188518799_gb_ACD56744.1_	0.114	25	0.152	25	0.352	13	0.193	0.171	N	0.57	SignalP-noTM
gi_188518802_gb_ACD56747.1_	0.151	37	0.123	37	0.167	35	0.092	0.108	N	0.57	SignalP-noTM
gi_188518803_gb_ACD56748.1_	0.178	31	0.289	17	0.78	8	0.633	0.451	N	0.57	SignalP-noTM
gi_188518804_gb_ACD56749.1_	0.28	18	0.444	18	0.831	12	0.666	0.549	N	0.57	SignalP-noTM
gi_188518805_gb_ACD56750.1_	0.136	27	0.116	27	0.187	21	0.096	0.108	N	0.51	SignalP-TM
gi_188518806_gb_ACD56751.1_	0.267	26	0.175	26	0.162	31	0.108	0.143	N	0.57	SignalP-noTM
gi_188518807_gb_ACD56752.1_	0.11	23	0.117	47	0.157	43	0.109	0.113	N	0.57	SignalP-noTM
gi_188518808_gb_ACD56753.1_	0.101	22	0.12	11	0.188	2	0.147	0.132	N	0.57	SignalP-noTM
gi_188518810_gb_ACD56755.1_	0.563	41	0.345	41	0.342	37	0.146	0.271	N	0.51	SignalP-TM
gi_188518811_gb_ACD56756.1_	0.852	20	0.823	20	0.925	13	0.813	0.819	Y	0.57	SignalP-noTM
gi_188518814_gb_ACD56759.1_	0.123	52	0.122	52	0.139	44	0.101	0.112	N	0.57	SignalP-noTM
gi_188518816_gb_ACD56761.1_	0.139	35	0.115	12	0.169	2	0.133	0.124	N	0.57	SignalP-noTM
gi_188518822_gb_ACD56767.1_	0.796	17	0.741	17	0.808	13	0.675	0.71	Y	0.57	SignalP-noTM
gi_188518825_gb_ACD56770.1_	0.111	9	0.106	68	0.124	62	0.09	0.098	N	0.57	SignalP-noTM
gi_188518827_gb_ACD56772.1_	0.121	46	0.129	11	0.223	1	0.16	0.143	N	0.57	SignalP-noTM
gi_188518829_gb_ACD56774.1_	0.149	24	0.119	13	0.189	11	0.125	0.122	N	0.57	SignalP-noTM
gi_188518832_gb_ACD56777.1_	0.117	44	0.105	30	0.134	6	0.106	0.106	N	0.57	SignalP-noTM
gi_188518833_gb_ACD56778.1_	0.213	18	0.137	18	0.115	1	0.092	0.116	N	0.57	SignalP-noTM
gi_188518834_gb_ACD56779.1_	0.111	37	0.106	43	0.138	41	0.092	0.099	N	0.57	SignalP-noTM
gi_188518835_gb_ACD56780.1_	0.221	49	0.158	38	0.202	31	0.103	0.132	N	0.57	SignalP-noTM
gi_188518836_gb_ACD56781.1_	0.226	30	0.195	45	0.373	42	0.187	0.192	N	0.57	SignalP-noTM
gi_188518837_gb_ACD56782.1_	0.104	26	0.097	55	0.104	45	0.075	0.087	N	0.57	SignalP-noTM
gi_188518838_gb_ACD56783.1_	0.131	41	0.154	11	0.306	2	0.237	0.193	N	0.57	SignalP-noTM
gi_188518839_gb_ACD56784.1_	0.112	39	0.113	48	0.157	47	0.092	0.103	N	0.57	SignalP-noTM
gi_188518842_gb_ACD56787.1_	0.164	10	0.15	14	0.324	9	0.218	0.182	N	0.57	SignalP-noTM
gi_188518844_gb_ACD56789.1_	0.112	57	0.101	57	0.117	1	0.093	0.098	N	0.57	SignalP-noTM
gi_188518845_gb_ACD56790.1_	0.158	39	0.171	11	0.358	1	0.291	0.227	N	0.57	SignalP-noTM
gi_188518846_gb_ACD56791.1_	0.202	29	0.254	29	0.564	25	0.216	0.236	N	0.57	SignalP-noTM
gi_188518848_gb_ACD56793.1_	0.307	30	0.288	30	0.48	20	0.26	0.275	N	0.57	SignalP-noTM
gi_188518849_gb_ACD56794.1_	0.781	23	0.837	23	0.957	15	0.912	0.872	Y	0.57	SignalP-noTM
gi_188518850_gb_ACD56795.1_	0.102	43	0.125	11	0.253	1	0.143	0.134	N	0.57	SignalP-noTM
gi_188518853_gb_ACD56798.1_	0.112	48	0.106	35	0.129	5	0.1	0.103	N	0.57	SignalP-noTM
gi_188518854_gb_ACD56799.1_	0.102	60	0.106	14	0.151	13	0.115	0.11	N	0.57	SignalP-noTM
gi_188518855_gb_ACD56800.1_	0.151	35	0.294	27	0.887	17	0.661	0.467	N	0.57	SignalP-noTM
gi_188518859_gb_ACD56804.1_	0.128	29	0.123	29	0.141	26	0.098	0.111	N	0.57	SignalP-noTM
gi_188518860_gb_ACD56805.1_	0.122	43	0.109	43	0.129	23	0.092	0.101	N	0.57	SignalP-noTM
gi_188518861_gb_ACD56806.1_	0.12	13	0.112	33	0.155	27	0.1	0.106	N	0.57	SignalP-noTM
gi_188518866_gb_ACD56811.1_	0.1	22	0.111	12	0.148	6	0.128	0.119	N	0.57	SignalP-noTM
gi_188518867_gb_ACD56812.1_	0.104	50	0.101	68	0.123	57	0.069	0.089	N	0.51	SignalP-TM

Secretome P				
Network 1	Network 2	Network 3	SecP score	Sequence name
0.126198	0.067926	0.13717	0.110431	gi_188518723_gb_ACD56668.1_
0.112346	0.328716	0.079585	0.173549	gi_188518724_gb_ACD56669.1_
0.140397	0.096129	0.123901	0.120142	gi_188518725_gb_ACD56670.1_
0.082944	0.007994	0.103958	0.064965	gi_188518726_gb_ACD56671.1_
0.193879	0.265612	0.317562	0.259018	gi_188518727_gb_ACD56672.1_
0.942622	0.988581	0.907711	0.946305	gi_188518728_gb_ACD56673.1_
0.947599	0.983127	0.899076	0.943267	gi_188518729_gb_ACD56674.1_
0.739043	0.979688	0.792161	0.836964	gi_188518730_gb_ACD56675.1_
0.1034	0.002924	0.185126	0.09715	gi_188518731_gb_ACD56676.1_
0.220458	0.012742	0.239577	0.157592	gi_188518732_gb_ACD56677.1_
0.929367	0.994223	0.875773	0.933121	gi_188518804_gb_ACD56749.1_
0.193411	0.088105	0.248431	0.176649	gi_188518805_gb_ACD56750.1_
0.198611	0.143687	0.26386	0.202053	gi_188518806_gb_ACD56751.1_
0.138955	0.450661	0.100924	0.23018	gi_188518807_gb_ACD56752.1_
0.231475	0.123251	0.263278	0.206001	gi_188518808_gb_ACD56753.1_
0.064767	0.061399	0.194818	0.106995	gi_188518810_gb_ACD56755.1_
0.931502	0.995023	0.875447	0.933991	gi_188518811_gb_ACD56756.1_
0.165619	0.654527	0.105647	0.308598	gi_188518814_gb_ACD56759.1_
0.144798	0.090052	0.349554	0.194801	gi_188518816_gb_ACD56761.1_
0.124881	0.079585	0.159092	0.121186	gi_188518822_gb_ACD56767.1_
0.235772	0.954436	0.115373	0.435194	gi_188518825_gb_ACD56770.1_
0.072426	0.032609	0.171505	0.09218	gi_188518827_gb_ACD56772.1_
0.185126	0.159494	0.19201	0.178877	gi_188518829_gb_ACD56774.1_
0.11847	0.145542	0.107072	0.123695	gi_188518832_gb_ACD56777.1_
0.118784	0.064767	0.141122	0.108224	gi_188518833_gb_ACD56778.1_
0.528469	0.120045	0.5015	0.383338	gi_188518834_gb_ACD56779.1_
0.146665	0.066051	0.169806	0.127507	gi_188518835_gb_ACD56780.1_
0.171931	0.085021	0.163557	0.14017	gi_188518836_gb_ACD56781.1_
0.86283	0.812144	0.864947	0.84664	gi_188518879_gb_ACD56824.1_
0.928176	0.962637	0.889437	0.92675	gi_188518884_gb_ACD56829.1_
0.368886	0.463316	0.436593	0.422932	gi_188518885_gb_ACD56830.1_
0.872138	0.998417	0.932264	0.934273	gi_188518887_gb_ACD56832.1_
0.149313	0.053454	0.143318	0.115362	gi_188518888_gb_ACD56833.1_
0.082262	0.0298	0.138596	0.083553	gi_188518889_gb_ACD56834.1_
0.898803	0.988649	0.897982	0.928478	gi_188518891_gb_ACD56836.1_
0.09639	0.051956	0.119098	0.089148	gi_188518893_gb_ACD56838.1_
0.1065	0.07024	0.145916	0.107552	gi_188518894_gb_ACD56839.1_
0.147041	0.048108	0.122927	0.106025	gi_188518895_gb_ACD56840.1_
0.679832	0.97682	0.86807	0.841574	gi_188518896_gb_ACD56841.1_
0.090298	0.005692	0.197658	0.097883	gi_188518897_gb_ACD56842.1_
0.527722	0.967105	0.753803	0.749543	gi_188518900_gb_ACD56845.1_
0.250678	0.316912	0.176245	0.247945	gi_188518901_gb_ACD56846.1_
0.919753	0.82977	0.765846	0.838456	gi_188518908_gb_ACD56853.1_
0.24122	0.0602	0.232009	0.17781	gi_188518910_gb_ACD56855.1_
0.937556	0.999846	0.79413	0.910511	gi_188518916_gb_ACD56861.1_
0.930345	0.944065	0.908212	0.927541	gi_188518917_gb_ACD56862.1_
0.141486	0.086669	0.174942	0.134366	gi_188518919_gb_ACD56864.1_
0.721919	0.949069	0.770122	0.813703	gi_188518920_gb_ACD56865.1_
0.16645	0.144056	0.150077	0.153528	gi_188518921_gb_ACD56866.1_
0.152775	0.254074	0.108806	0.171885	gi_188518922_gb_ACD56867.1_
0.094833	0.007355	0.080691	0.06096	gi_188518926_gb_ACD56871.1_
0.444727	0.130903	0.50675	0.360793	gi_188518927_gb_ACD56872.1_
0.160704	0.037363	0.134703	0.110923	gi_188518928_gb_ACD56873.1_
0.917511	0.940139	0.828069	0.89524	gi_188518929_gb_ACD56874.1_
0.109681	0.077845	0.204403	0.130643	gi_188518930_gb_ACD56875.1_
0.07871	0.006225	0.100924	0.061953	gi_188518933_gb_ACD56878.1_
0.238486	0.597005	0.252372	0.362621	gi_188518935_gb_ACD56880.1_
0.797057	0.445468	0.770653	0.671059	gi_188518936_gb_ACD56881.1_
0.945782	0.924072	0.893785	0.921213	gi_188518937_gb_ACD56882.1_
0.878681	0.686326	0.816678	0.793895	gi_188518938_gb_ACD56883.1_
0.534445	0.949213	0.609926	0.697861	gi_188518939_gb_ACD56884.1_
0.922371	0.904909	0.887953	0.905078	gi_188518940_gb_ACD56885.1_
0.817127	0.578105	0.75547	0.716901	gi_188518941_gb_ACD56886.1_
0.112047	0.001434	0.172787	0.095423	gi_188518945_gb_ACD56890.1_
0.186943	0.048246	0.155119	0.130103	gi_188518946_gb_ACD56891.1_
0.155513	0.010922	0.181532	0.115989	gi_188518947_gb_ACD56892.1_
0.089562	0.03059	0.099034	0.073062	gi_188518953_gb_ACD56898.1_
0.23308	0.653849	0.321475	0.402801	gi_188518954_gb_ACD56899.1_
0.638071	0.917738	0.609926	0.721912	gi_188518955_gb_ACD56900.1_
0.916138	0.521736	0.883088	0.773654	gi_188518998_gb_ACD56943.1_
0.130562	0.105647	0.108806	0.115005	gi_188518999_gb_ACD56944.1_
0.063151	0.166034	0.044532	0.091239	gi_188519000_gb_ACD56945.1_

Tat P						
max. C	max. Y	max. S	mean S	max. D	signal peptide	Sequence name
0.682	0.645	0.859	0.723	0.684	YES	gi_188518885_gb_ACD5 length = 100
0.905	0.704	0.878	0.687	0.696	YES	gi_188518955_gb_ACD5 length = 100
0.739	0.419	0.765	0.319	0.369	YES	gi_188519070_gb_ACD5 length = 100
0.511	0.541	0.878	0.547	0.544	YES	gi_188519082_gb_ACD5 length = 100
0.831	0.627	0.773	0.319	0.473	YES	gi_188519122_gb_ACD5 length = 100
0.569	0.41	0.783	0.437	0.423	YES	gi_188519530_gb_ACD5 length = 100
0.616	0.6	0.834	0.657	0.629	YES	gi_188519848_gb_ACD5 length = 100
0.787	0.5	0.767	0.303	0.401	YES	gi_188519911_gb_ACD5 length = 100
0.631	0.576	0.854	0.574	0.575	YES	gi_188520134_gb_ACD5 length = 100
0.875	0.685	0.829	0.419	0.552	YES	gi_188520498_gb_ACD5 length = 100
0.612	0.587	0.894	0.722	0.654	YES	gi_188520615_gb_ACD5 length = 100
0.839	0.585	0.885	0.559	0.572	YES	gi_188520988_gb_ACD5 length = 79
0.596	0.465	0.752	0.374	0.42	YES	gi_188521047_gb_ACD5 length = 48
0.659	0.399	0.825	0.377	0.388	YES	gi_188521495_gb_ACD5 length = 60
0.698	0.416	0.872	0.342	0.379	YES	gi_188521633_gb_ACD5 length = 100
0.761	0.431	0.889	0.645	0.538	YES	gi_188521820_gb_ACD5 length = 100
0.571	0.581	0.885	0.748	0.664	YES	gi_528897485_gb_AGS4 length = 100
0.537	0.524	0.789	0.582	0.553	YES	gi_188521893_gb_ACD5 length = 100
0.813	0.715	0.823	0.651	0.683	YES	gi_188521898_gb_ACD5 length = 100
0.727	0.654	0.883	0.589	0.621	YES	gi_188521925_gb_ACD5 length = 100
0.874	0.494	0.841	0.433	0.463	YES	gi_188521934_gb_ACD5 length = 100
0.519	0.461	0.812	0.409	0.435	YES	gi_188522241_gb_ACD6 length = 100
0.568	0.453	0.862	0.336	0.395	YES	gi_188522556_gb_ACD6 length = 100
0.621	0.621	0.867	0.702	0.661	YES	gi_188522590_gb_ACD6 length = 100
0.517	0.492	0.872	0.409	0.451	YES	gi_188523140_gb_ACD6 length = 100
0.721	0.574	0.84	0.518	0.546	YES	gi_188523141_gb_ACD6 length = 100
0.84	0.742	0.834	0.359	0.55	YES	gi_188523222_gb_ACD6 length = 100
0.74	0.583	0.885	0.611	0.597	YES	gi_188523353_gb_ACD6 length = 100
0.543	0.381	0.791	0.438	0.41	YES	gi_188523355_gb_ACD6 length = 100
0.659	0.399	0.825	0.377	0.388	YES	gi_188521303_gb_ACD5 length = 60
0.548	0.39	0.797	0.536	0.463	YES	gi_188518831_gb_ACD5 length = 37
0.544	0.395	0.833	0.385	0.39	YES	gi_188518950_gb_ACD5 length = 100
0.675	0.545	0.869	0.542	0.543	YES	gi_188519443_gb_ACD5 length = 100
0.726	0.56	0.903	0.333	0.447	YES	gi_188519681_gb_ACD5 length = 100
0.636	0.451	0.825	0.522	0.487	YES	gi_188519980_gb_ACD5 length = 60
0.642	0.54	0.813	0.572	0.556	YES	gi_188520119_gb_ACD5 length = 63
0.611	0.394	0.755	0.333	0.363	YES	gi_188520603_gb_ACD5 length = 39
0.753	0.416	0.768	0.34	0.378	YES	gi_188521021_gb_ACD5 length = 100
0.652	0.438	0.842	0.375	0.406	YES	gi_188519063_gb_ACD5 length = 100
0.543	0.426	0.758	0.379	0.402	YES	gi_188520753_gb_ACD5 length = 100
0.74	0.641	0.834	0.493	0.567	YES	gi_188521522_gb_ACD5 length = 100
0.629	0.456	0.851	0.391	0.423	YES	gi_188521703_gb_ACD5 length = 57
0.586	0.588	0.904	0.603	0.596	YES	gi_188521706_gb_ACD5 length = 100
0.579	0.376	0.807	0.371	0.374	YES	gi_188521725_gb_ACD5 length = 100
0.519	0.418	0.796	0.534	0.476	YES	gi_188521862_gb_ACD5 length = 67
0.647	0.447	0.863	0.341	0.394	YES	gi_188522114_gb_ACD6 length = 100
0.719	0.371	0.878	0.359	0.365	YES	gi_188522149_gb_ACD6 length = 100
0.569	0.447	0.862	0.499	0.473	YES	gi_188522287_gb_ACD6 length = 100
0.839	0.629	0.827	0.319	0.474	YES	gi_188522399_gb_ACD6 length = 100
0.592	0.446	0.773	0.362	0.404	YES	gi_188522597_gb_ACD6 length = 100
0.778	0.578	0.854	0.532	0.555	YES	gi_188522698_gb_ACD6 length = 100
0.714	0.461	0.808	0.478	0.47	YES	gi_188522867_gb_ACD6 length = 100
0.575	0.453	0.788	0.408	0.43	YES	gi_528897497_gb_AGS4 length = 100
0.845	0.618	0.834	0.438	0.528	YES	gi_188523317_gb_ACD6 length = 100
0.687	0.449	0.76	0.339	0.394	YES	gi_188523373_gb_ACD6 length = 100
0.52	0.366	0.765	0.377	0.371	YES	gi_188523411_gb_ACD6 length = 100
0.566	0.433	0.798	0.323	0.378	YES	gi_188523502_gb_ACD6 length = 100
0.527	0.388	0.885	0.593	0.49	YES	gi_188523611_gb_ACD6 length = 67
0.753	0.611	0.829	0.494	0.553	YES	gi_188523626_gb_ACD6 length = 100
0.577	0.48	0.835	0.515	0.498	YES	gi_188523629_gb_ACD6 length = 97
0.709	0.405	0.817	0.538	0.472	YES	gi_188521975_gb_ACD5 length = 100
0.839	0.629	0.827	0.319	0.474	YES	gi_188522399_gb_ACD6 length = 100
0.746	0.535	0.767	0.5	0.517	YES	gi_188523229_gb_ACD6 length = 44

gi_188518869_gb_ACD56814.1_	0.109	64	0.118	17	0.159	10	0.132	0.124	N	0.57	SignalP-noTM
gi_188518870_gb_ACD56815.1_	0.123	42	0.143	14	0.233	10	0.208	0.167	N	0.51	SignalP-TM
gi_188518871_gb_ACD56816.1_	0.127	32	0.109	48	0.163	43	0.062	0.091	N	0.51	SignalP-TM
gi_188518878_gb_ACD56823.1_	0.116	8	0.104	35	0.124	2	0.099	0.102	N	0.57	SignalP-noTM
gi_188518879_gb_ACD56824.1_	0.225	25	0.151	25	0.205	1	0.129	0.141	N	0.57	SignalP-noTM
gi_188518884_gb_ACD56829.1_	0.792	20	0.805	20	0.917	16	0.815	0.81	Y	0.57	SignalP-noTM
gi_188518885_gb_ACD56830.1_	0.814	32	0.749	32	0.788	28	0.627	0.692	Y	0.57	SignalP-noTM
gi_188518887_gb_ACD56832.1_	0.138	31	0.248	18	0.76	15	0.559	0.394	N	0.57	SignalP-noTM
gi_188518888_gb_ACD56833.1_	0.138	33	0.112	19	0.143	11	0.115	0.113	N	0.57	SignalP-noTM
gi_188518889_gb_ACD56834.1_	0.407	33	0.569	33	0.985	14	0.897	0.723	Y	0.57	SignalP-noTM
gi_188518891_gb_ACD56836.1_	0.11	38	0.103	69	0.123	6	0.08	0.092	N	0.57	SignalP-noTM
gi_188518893_gb_ACD56838.1_	0.237	32	0.166	32	0.16	1	0.114	0.142	N	0.57	SignalP-noTM
gi_188518894_gb_ACD56839.1_	0.118	66	0.137	13	0.24	6	0.193	0.164	N	0.57	SignalP-noTM
gi_188518895_gb_ACD56840.1_	0.128	51	0.132	51	0.181	47	0.131	0.132	N	0.57	SignalP-noTM
gi_188518896_gb_ACD56841.1_	0.11	57	0.178	32	0.467	25	0.246	0.21	N	0.57	SignalP-noTM
gi_188518897_gb_ACD56842.1_	0.1	25	0.1	25	0.121	3	0.098	0.099	N	0.57	SignalP-noTM
gi_188518900_gb_ACD56845.1_	0.151	23	0.142	23	0.206	17	0.129	0.136	N	0.57	SignalP-noTM
gi_188518901_gb_ACD56846.1_	0.135	40	0.12	24	0.16	38	0.11	0.117	N	0.51	SignalP-TM
gi_188518908_gb_ACD56853.1_	0.165	49	0.21	49	0.417	37	0.164	0.188	N	0.57	SignalP-noTM
gi_188518910_gb_ACD56855.1_	0.11	33	0.126	26	0.197	1	0.132	0.128	N	0.51	SignalP-TM
gi_188518916_gb_ACD56861.1_	0.136	22	0.144	22	0.27	1	0.158	0.15	N	0.57	SignalP-noTM
gi_188518917_gb_ACD56862.1_	0.11	20	0.112	11	0.182	2	0.121	0.116	N	0.57	SignalP-noTM
gi_188518919_gb_ACD56864.1_	0.106	43	0.106	43	0.136	10	0.1	0.104	N	0.57	SignalP-noTM
gi_188518920_gb_ACD56865.1_	0.166	10	0.107	20	0.229	8	0.106	0.107	N	0.57	SignalP-noTM
gi_188518921_gb_ACD56866.1_	0.128	29	0.123	29	0.141	26	0.098	0.111	N	0.57	SignalP-noTM
gi_188518922_gb_ACD56867.1_	0.107	27	0.129	11	0.22	5	0.18	0.148	N	0.51	SignalP-TM
gi_188518926_gb_ACD56871.1_	0.288	34	0.181	34	0.416	4	0.19	0.185	N	0.57	SignalP-noTM
gi_188518927_gb_ACD56872.1_	0.79	28	0.876	28	0.985	18	0.949	0.91	Y	0.57	SignalP-noTM
gi_188518928_gb_ACD56873.1_	0.199	22	0.261	22	0.47	8	0.359	0.307	N	0.57	SignalP-noTM
gi_188518929_gb_ACD56874.1_	0.127	44	0.114	42	0.154	22	0.105	0.109	N	0.57	SignalP-noTM
gi_188518930_gb_ACD56875.1_	0.107	52	0.114	52	0.172	49	0.093	0.104	N	0.57	SignalP-noTM
gi_188518933_gb_ACD56878.1_	0.192	20	0.127	20	0.12	2	0.089	0.109	N	0.57	SignalP-noTM
gi_188518935_gb_ACD56880.1_	0.109	57	0.138	11	0.252	2	0.193	0.164	N	0.57	SignalP-noTM
gi_188518936_gb_ACD56881.1_	0.155	49	0.155	49	0.229	47	0.125	0.141	N	0.57	SignalP-noTM
gi_188518937_gb_ACD56882.1_	0.117	48	0.138	11	0.257	1	0.184	0.16	N	0.57	SignalP-noTM
gi_188518938_gb_ACD56883.1_	0.124	36	0.123	11	0.273	35	0.169	0.14	N	0.51	SignalP-TM
gi_188518939_gb_ACD56884.1_	0.114	26	0.096	47	0.099	45	0.07	0.084	N	0.57	SignalP-noTM
gi_188518940_gb_ACD56885.1_	0.142	63	0.129	15	0.269	12	0.165	0.146	N	0.57	SignalP-noTM
gi_188518941_gb_ACD56886.1_	0.121	36	0.122	38	0.278	35	0.104	0.115	N	0.51	SignalP-TM
gi_188518945_gb_ACD56890.1_	0.112	65	0.12	11	0.227	1	0.134	0.127	N	0.57	SignalP-noTM
gi_188518946_gb_ACD56891.1_	0.133	34	0.125	11	0.188	4	0.163	0.139	N	0.51	SignalP-TM
gi_188518947_gb_ACD56892.1_	0.117	34	0.102	70	0.116	69	0.079	0.091	N	0.57	SignalP-noTM
gi_188518953_gb_ACD56898.1_	0.149	24	0.169	24	0.292	1	0.201	0.181	N	0.51	SignalP-TM
gi_188518954_gb_ACD56899.1_	0.295	21	0.246	21	0.279	20	0.193	0.221	N	0.57	SignalP-noTM
gi_188518955_gb_ACD56900.1_	0.383	31	0.529	31	0.968	14	0.847	0.678	Y	0.57	SignalP-noTM
gi_188518959_gb_ACD56904.1_	0.133	35	0.132	35	0.157	29	0.114	0.124	N	0.57	SignalP-noTM
gi_188518960_gb_ACD56905.1_	0.102	27	0.098	11	0.129	8	0.096	0.097	N	0.57	SignalP-noTM
gi_188518961_gb_ACD56906.1_	0.134	18	0.153	18	0.246	5	0.184	0.168	N	0.57	SignalP-noTM
gi_188518962_gb_ACD56907.1_	0.103	10	0.095	39	0.1	41	0.078	0.087	N	0.57	SignalP-noTM
gi_188518965_gb_ACD56910.1_	0.223	39	0.404	39	0.898	38	0.533	0.465	N	0.57	SignalP-noTM
gi_188518966_gb_ACD56911.1_	0.147	61	0.139	11	0.339	1	0.17	0.153	N	0.57	SignalP-noTM
gi_188518971_gb_ACD56916.1_	0.166	30	0.311	30	0.838	8	0.644	0.468	N	0.57	SignalP-noTM
gi_188518972_gb_ACD56917.1_	0.136	26	0.118	26	0.153	51	0.104	0.111	N	0.57	SignalP-noTM
gi_188518973_gb_ACD56918.1_	0.105	30	0.109	30	0.123	27	0.092	0.101	N	0.57	SignalP-noTM
gi_188518974_gb_ACD56919.1_	0.162	33	0.132	33	0.203	19	0.123	0.128	N	0.57	SignalP-noTM
gi_188518976_gb_ACD56921.1_	0.82	22	0.84	22	0.962	18	0.878	0.858	Y	0.57	SignalP-noTM
gi_188518977_gb_ACD56922.1_	0.105	20	0.102	64	0.138	1	0.095	0.099	N	0.57	SignalP-noTM
gi_188518978_gb_ACD56923.1_	0.168	27	0.176	27	0.35	34	0.183	0.179	N	0.57	SignalP-noTM
gi_188518979_gb_ACD56924.1_	0.109	29	0.131	11	0.274	1	0.162	0.146	N	0.57	SignalP-noTM
gi_188518980_gb_ACD56925.1_	0.129	42	0.126	11	0.209	5	0.171	0.142	N	0.51	SignalP-TM
gi_188518985_gb_ACD56930.1_	0.192	53	0.138	53	0.133	50	0.068	0.112	N	0.51	SignalP-TM
gi_188518986_gb_ACD56931.1_	0.732	22	0.794	22	0.942	18	0.883	0.836	Y	0.57	SignalP-noTM
gi_188518987_gb_ACD56932.1_	0.127	49	0.142	32	0.227	28	0.15	0.145	N	0.51	SignalP-TM
gi_188518988_gb_ACD56933.1_	0.901	20	0.935	20	0.983	18	0.959	0.946	Y	0.57	SignalP-noTM
gi_188518990_gb_ACD56935.1_	0.141	24	0.151	24	0.252	3	0.173	0.162	N	0.57	SignalP-noTM
gi_188518991_gb_ACD56936.1_	0.154	14	0.128	14	0.291	1	0.12	0.124	N	0.57	SignalP-noTM
gi_188518995_gb_ACD56940.1_	0.127	66	0.107	53	0.118	13	0.091	0.099	N	0.57	SignalP-noTM
gi_188518996_gb_ACD56941.1_	0.148	29	0.13	29	0.139	28	0.118	0.125	N	0.57	SignalP-noTM
gi_188518997_gb_ACD56942.1_	0.149	21	0.143	30	0.211	2	0.128	0.137	N	0.51	SignalP-TM
gi_188518998_gb_ACD56943.1_	0.279	27	0.258	27	0.377	11	0.279	0.267	N	0.57	SignalP-noTM
gi_188518999_gb_ACD56944.1_	0.114	60	0.108	60	0.13	10	0.076	0.093	N	0.57	SignalP-noTM
gi_188519000_gb_ACD56945.1_	0.107	32	0.109	38	0.17	31	0.102	0.106	N	0.57	SignalP-noTM
gi_188519001_gb_ACD56946.1_	0.162	23	0.221	23	0.503	11	0.309	0.262	N	0.57	SignalP-noTM
gi_188519002_gb_ACD56947.1_	0.129	45	0.118	45	0.148	1	0.103	0.111	N	0.57	SignalP-noTM
gi_188519003_gb_ACD56948.1_	0.13	26	0.166	26	0.31	1	0.216	0.185	N	0.51	SignalP-TM
gi_188519004_gb_ACD56949.1_	0.163	37	0.162	37	0.27	23	0.16	0.161	N	0.57	SignalP-noTM
gi_188519005_gb_ACD56950.1_	0.224	28	0.136	28	0.123	9	0.088	0.113	N	0.57	SignalP-noTM
gi_188519006_gb_ACD56951.1_	0.118	28	0.116	11	0.187	1	0.135	0.125	N	0.57	SignalP-noTM

0.341414	0.907711	0.412413	0.553846	gi_188519001_gb_ACD56946.1_
0.11847	0.072024	0.094833	0.095109	gi_188519002_gb_ACD56947.1_
0.145916	0.0527	0.126861	0.108492	gi_188519003_gb_ACD56948.1_
0.154727	0.047291	0.156699	0.119572	gi_188519004_gb_ACD56949.1_
0.132274	0.061572	0.158291	0.117379	gi_188519005_gb_ACD56950.1_
0.927169	0.998445	0.825491	0.917035	gi_188519006_gb_ACD56951.1_
0.105931	0.031038	0.142583	0.093184	gi_188519007_gb_ACD56952.1_
0.722521	0.013321	0.752129	0.49599	gi_188519009_gb_ACD56954.1_
0.299643	0.224088	0.267371	0.263701	gi_188519011_gb_ACD56956.1_
0.13193	0.005051	0.087384	0.074788	gi_188519012_gb_ACD56957.1_
0.072426	0.035468	0.164379	0.090758	gi_188519013_gb_ACD56958.1_
0.135755	0.132964	0.105647	0.124789	gi_188519014_gb_ACD56959.1_
0.153944	0.564882	0.108225	0.275684	gi_188519015_gb_ACD56960.1_
0.931884	0.999023	0.862475	0.931127	gi_188519016_gb_ACD56961.1_
0.743645	0.997006	0.779542	0.840064	gi_188519017_gb_ACD56962.1_
0.746494	0.999176	0.882467	0.876046	gi_188519023_gb_ACD56968.1_
0.950781	0.999833	0.908462	0.953025	gi_188519024_gb_ACD56969.1_
0.16645	0.048939	0.163557	0.126315	gi_188519027_gb_ACD56972.1_
0.317562	0.194348	0.279891	0.263934	gi_188518837_gb_ACD56782.1_
0.179314	0.822882	0.161515	0.387904	gi_188518838_gb_ACD56783.1_
0.126198	0.191081	0.099034	0.138771	gi_188518839_gb_ACD56784.1_
0.876099	0.974618	0.789182	0.879966	gi_188518842_gb_ACD56787.1_
0.910194	0.889141	0.865646	0.888327	gi_188518844_gb_ACD56789.1_
0.9398	0.636684	0.913568	0.830017	gi_188518845_gb_ACD56790.1_
0.184673	0.118157	0.229878	0.177569	gi_188518846_gb_ACD56791.1_
0.174078	0.947	0.088588	0.403222	gi_188518848_gb_ACD56793.1_
0.333366	0.854458	0.389361	0.525728	gi_188518849_gb_ACD56794.1_
0.144798	0.846447	0.079805	0.357017	gi_188518850_gb_ACD56795.1_
0.13331	0.130222	0.108806	0.124113	gi_188518853_gb_ACD56798.1_
0.928176	0.738464	0.830194	0.832278	gi_188518854_gb_ACD56799.1_
0.210818	0.768525	0.266784	0.415376	gi_188518855_gb_ACD56800.1_
0.155513	0.123251	0.153944	0.144236	gi_188518859_gb_ACD56804.1_
0.167702	0.132964	0.113548	0.138071	gi_188518860_gb_ACD56805.1_
0.176245	0.63599	0.085489	0.299241	gi_188518861_gb_ACD56806.1_
0.148932	0.021668	0.186943	0.119181	gi_188518866_gb_ACD56811.1_
0.328054	0.061399	0.432907	0.27412	gi_188518867_gb_ACD56812.1_
0.053151	0.034757	0.095609	0.061172	gi_188518869_gb_ACD56814.1_
0.108515	0.052252	0.147418	0.102728	gi_188518870_gb_ACD56815.1_
0.151614	0.093299	0.174078	0.139664	gi_188518871_gb_ACD56816.1_
0.115986	0.039696	0.148932	0.101538	gi_188518878_gb_ACD56823.1_
0.116603	0.055619	0.128532	0.100251	gi_188518959_gb_ACD56904.1_
0.106786	0.678525	0.076775	0.287362	gi_188518960_gb_ACD56905.1_
0.612777	0.949069	0.529964	0.69727	gi_188518961_gb_ACD56906.1_
0.351603	0.008285	0.291523	0.217137	gi_188518962_gb_ACD56907.1_
0.888251	0.50375	0.856313	0.749438	gi_188518965_gb_ACD56910.1_
0.092541	0.053454	0.1034	0.083132	gi_188518966_gb_ACD56911.1_
0.432907	0.301535	0.561192	0.431878	gi_188518971_gb_ACD56916.1_
0.131587	0.053911	0.150077	0.111858	gi_188518972_gb_ACD56917.1_
0.179756	0.028609	0.23308	0.147148	gi_188518973_gb_ACD56918.1_
0.071625	0.01743	0.141122	0.076726	gi_188518974_gb_ACD56919.1_
0.950781	0.985571	0.884321	0.940224	gi_188518976_gb_ACD56921.1_
0.064949	0.025456	0.100924	0.063776	gi_188518977_gb_ACD56922.1_
0.174942	0.926355	0.082716	0.394671	gi_188518978_gb_ACD56923.1_
0.200047	0.064224	0.151614	0.138628	gi_188518979_gb_ACD56924.1_
0.154335	0.265612	0.105931	0.175293	gi_188518980_gb_ACD56925.1_
0.148552	0.102293	0.152	0.134282	gi_188518985_gb_ACD56930.1_
0.216361	0.059357	0.192943	0.15622	gi_188518986_gb_ACD56931.1_
0.153944	0.183772	0.143318	0.160345	gi_188518987_gb_ACD56932.1_
0.132274	0.092793	0.147795	0.124287	gi_188518988_gb_ACD56933.1_
0.461824	0.097704	0.520988	0.360172	gi_188518990_gb_ACD56935.1_
0.10147	0.017327	0.123251	0.080683	gi_188518991_gb_ACD56936.1_
0.553791	0.213829	0.679179	0.482266	gi_188518995_gb_ACD56940.1_
0.687617	0.913568	0.819357	0.806847	gi_188518996_gb_ACD56941.1_
0.095349	0.535938	0.176681	0.269323	gi_188518997_gb_ACD56942.1_
0.888251	0.986836	0.872138	0.915742	gi_188518733_gb_ACD56678.1_
0.845273	0.792654	0.866342	0.834756	gi_188518739_gb_ACD56684.1_
0.168121	0.008334	0.27032	0.148925	gi_188518740_gb_ACD56685.1_
0.090298	0.010857	0.126861	0.076005	gi_188518747_gb_ACD56692.1_
0.556014	0.00967	0.51949	0.361725	gi_188518751_gb_ACD56696.1_
0.115067	0.019551	0.186487	0.107035	gi_188518757_gb_ACD56702.1_
0.757128	0.998487	0.686326	0.81398	gi_188518765_gb_ACD56710.1_
0.888548	0.981675	0.80799	0.892738	gi_188518766_gb_ACD56711.1_
0.965041	0.999812	0.951061	0.971971	gi_188518767_gb_ACD56712.1_
0.121639	0.025382	0.095868	0.080963	gi_188518768_gb_ACD56713.1_
0.141122	0.029029	0.130222	0.100124	gi_188518771_gb_ACD56716.1_
0.099302	0.026211	0.103679	0.076397	gi_188518772_gb_ACD56717.1_
0.840104	0.975059	0.915444	0.910202	gi_188518773_gb_ACD56718.1_
0.094319	0.001412	0.184222	0.093318	gi_188518775_gb_ACD56720.1_

gi_188519007_gb_ACD56952.1_	0.294	38	0.203	38	0.226	36	0.144	0.181	N	0.51	SignalP-TM
gi_188519009_gb_ACD56954.1_	0.115	25	0.098	39	0.111	39	0.084	0.091	N	0.57	SignalP-noTM
gi_188519011_gb_ACD56956.1_	0.112	37	0.103	11	0.124	1	0.106	0.104	N	0.57	SignalP-noTM
gi_188519012_gb_ACD56957.1_	0.116	24	0.138	17	0.223	13	0.19	0.163	N	0.57	SignalP-noTM
gi_188519013_gb_ACD56958.1_	0.6	36	0.734	36	0.982	15	0.913	0.818	Y	0.57	SignalP-noTM
gi_188519014_gb_ACD56959.1_	0.296	29	0.164	29	0.205	44	0.084	0.127	N	0.57	SignalP-noTM
gi_188519015_gb_ACD56960.1_	0.202	38	0.154	38	0.249	29	0.106	0.131	N	0.57	SignalP-noTM
gi_188519016_gb_ACD56961.1_	0.241	25	0.457	25	0.976	17	0.906	0.668	Y	0.57	SignalP-noTM
gi_188519017_gb_ACD56962.1_	0.272	28	0.134	50	0.156	41	0.082	0.109	N	0.57	SignalP-noTM
gi_188519023_gb_ACD56968.1_	0.795	33	0.883	33	0.993	20	0.941	0.91	Y	0.57	SignalP-noTM
gi_188519024_gb_ACD56969.1_	0.188	44	0.244	44	0.578	40	0.291	0.266	N	0.57	SignalP-noTM
gi_188519027_gb_ACD56972.1_	0.134	35	0.132	17	0.216	5	0.164	0.147	N	0.57	SignalP-noTM
gi_188519028_gb_ACD56973.1_	0.13	60	0.127	60	0.21	5	0.119	0.123	N	0.57	SignalP-noTM
gi_188519029_gb_ACD56974.1_	0.287	55	0.183	55	0.297	10	0.15	0.167	N	0.57	SignalP-noTM
gi_188519030_gb_ACD56975.1_	0.107	44	0.114	42	0.197	39	0.113	0.113	N	0.57	SignalP-noTM
gi_188519031_gb_ACD56976.1_	0.262	30	0.18	30	0.228	29	0.093	0.139	N	0.57	SignalP-noTM
gi_188519032_gb_ACD56977.1_	0.146	30	0.136	30	0.196	20	0.123	0.13	N	0.57	SignalP-noTM
gi_188519033_gb_ACD56978.1_	0.14	26	0.139	26	0.192	25	0.133	0.136	N	0.57	SignalP-noTM
gi_188519035_gb_ACD56980.1_	0.107	17	0.112	33	0.143	30	0.109	0.11	N	0.57	SignalP-noTM
gi_188519036_gb_ACD56981.1_	0.123	21	0.109	21	0.114	14	0.096	0.103	N	0.57	SignalP-noTM
gi_188519037_gb_ACD56982.1_	0.132	46	0.103	26	0.101	20	0.081	0.092	N	0.57	SignalP-noTM
gi_188519040_gb_ACD56985.1_	0.114	55	0.157	11	0.334	2	0.243	0.197	N	0.57	SignalP-noTM
gi_188519042_gb_ACD56987.1_	0.637	23	0.736	23	0.966	10	0.89	0.808	Y	0.57	SignalP-noTM
gi_188519045_gb_ACD56990.1_	0.111	62	0.099	41	0.103	29	0.084	0.092	N	0.57	SignalP-noTM
gi_188519046_gb_ACD56991.1_	0.146	20	0.139	20	0.177	19	0.12	0.13	N	0.57	SignalP-noTM
gi_188519047_gb_ACD56992.1_	0.105	32	0.099	32	0.101	24	0.087	0.093	N	0.57	SignalP-noTM
gi_188519050_gb_ACD56995.1_	0.105	45	0.105	51	0.184	42	0.087	0.096	N	0.57	SignalP-noTM
gi_188519052_gb_ACD56997.1_	0.113	18	0.18	18	0.362	2	0.299	0.236	N	0.57	SignalP-noTM
gi_188519053_gb_ACD56998.1_	0.104	19	0.121	11	0.273	1	0.128	0.124	N	0.51	SignalP-TM
gi_188519058_gb_ACD57003.1_	0.147	41	0.144	18	0.263	15	0.214	0.17	N	0.51	SignalP-TM
gi_188519059_gb_ACD57004.1_	0.13	51	0.111	51	0.137	23	0.106	0.108	N	0.57	SignalP-noTM
gi_188519064_gb_ACD57009.1_	0.126	35	0.18	32	0.348	30	0.245	0.204	N	0.51	SignalP-TM
gi_188519065_gb_ACD57010.1_	0.315	12	0.473	12	0.871	11	0.711	0.585	Y	0.57	SignalP-noTM
gi_188519066_gb_ACD57011.1_	0.146	26	0.111	41	0.158	33	0.09	0.101	N	0.57	SignalP-noTM
gi_188519067_gb_ACD57012.1_	0.178	45	0.26	19	0.741	15	0.554	0.398	N	0.57	SignalP-noTM
gi_188519068_gb_ACD57013.1_	0.676	23	0.793	23	0.98	19	0.943	0.864	Y	0.57	SignalP-noTM
gi_188519069_gb_ACD57014.1_	0.156	51	0.162	37	0.36	29	0.166	0.164	N	0.57	SignalP-noTM
gi_188519070_gb_ACD57015.1_	0.382	25	0.581	25	0.957	21	0.862	0.713	Y	0.57	SignalP-noTM
gi_188519071_gb_ACD57016.1_	0.115	55	0.104	55	0.1	44	0.078	0.092	N	0.57	SignalP-noTM
gi_188519080_gb_ACD57025.1_	0.12	45	0.187	45	0.504	43	0.23	0.207	N	0.57	SignalP-noTM
gi_188519082_gb_ACD57027.1_	0.136	41	0.212	36	0.49	26	0.326	0.265	N	0.57	SignalP-noTM
gi_188519083_gb_ACD57028.1_	0.115	44	0.108	18	0.185	10	0.1	0.104	N	0.57	SignalP-noTM
gi_188519084_gb_ACD57029.1_	0.104	30	0.163	11	0.335	1	0.258	0.208	N	0.57	SignalP-noTM
gi_188519085_gb_ACD57030.1_	0.112	29	0.171	11	0.439	1	0.271	0.218	N	0.57	SignalP-noTM
gi_188519088_gb_ACD57033.1_	0.75	20	0.75	20	0.876	1	0.758	0.754	Y	0.57	SignalP-noTM
gi_188519089_gb_ACD57034.1_	0.154	30	0.153	30	0.245	24	0.125	0.142	N	0.51	SignalP-TM
gi_188519090_gb_ACD57035.1_	0.1	57	0.102	29	0.114	22	0.097	0.099	N	0.57	SignalP-noTM
gi_188519091_gb_ACD57036.1_	0.125	51	0.113	65	0.157	59	0.071	0.097	N	0.51	SignalP-TM
gi_188519096_gb_ACD57041.1_	0.2	29	0.15	29	0.222	4	0.123	0.137	N	0.57	SignalP-noTM
gi_188519098_gb_ACD57043.1_	0.276	59	0.163	59	0.298	1	0.123	0.144	N	0.57	SignalP-noTM
gi_188519100_gb_ACD57045.1_	0.148	21	0.11	53	0.15	47	0.087	0.099	N	0.57	SignalP-noTM
gi_188519101_gb_ACD57046.1_	0.223	53	0.17	16	0.39	30	0.181	0.176	N	0.57	SignalP-noTM
gi_188519103_gb_ACD57048.1_	0.189	35	0.145	35	0.15	34	0.1	0.124	N	0.57	SignalP-noTM
gi_188519108_gb_ACD57053.1_	0.132	24	0.172	11	0.381	8	0.303	0.234	N	0.57	SignalP-noTM
gi_188519110_gb_ACD57055.1_	0.539	31	0.299	31	0.358	7	0.22	0.269	N	0.51	SignalP-TM
gi_188519113_gb_ACD57058.1_	0.127	6	0.108	52	0.146	5	0.1	0.105	N	0.57	SignalP-noTM
gi_188519114_gb_ACD57059.1_	0.153	21	0.184	32	0.496	28	0.265	0.222	N	0.57	SignalP-noTM
gi_188519115_gb_ACD57060.1_	0.185	20	0.296	18	0.737	2	0.53	0.382	N	0.51	SignalP-TM
gi_188519116_gb_ACD57061.1_	0.187	58	0.313	19	0.708	8	0.573	0.409	N	0.51	SignalP-TM
gi_188519117_gb_ACD57062.1_	0.194	54	0.204	54	0.337	52	0.12	0.173	N	0.51	SignalP-TM
gi_188519119_gb_ACD57064.1_	0.208	36	0.165	36	0.268	33	0.093	0.131	N	0.57	SignalP-noTM
gi_188519120_gb_ACD57065.1_	0.137	47	0.114	47	0.125	43	0.085	0.101	N	0.57	SignalP-noTM
gi_188519121_gb_ACD57066.1_	0.123	49	0.161	49	0.367	42	0.145	0.154	N	0.57	SignalP-noTM
gi_188519122_gb_ACD57067.1_	0.314	37	0.379	19	0.943	15	0.903	0.625	Y	0.57	SignalP-noTM
gi_188519126_gb_ACD57071.1_	0.106	56	0.106	11	0.152	1	0.108	0.107	N	0.57	SignalP-noTM
gi_188519129_gb_ACD57074.1_	0.11	50	0.169	38	0.383	31	0.198	0.183	N	0.57	SignalP-noTM
gi_188519130_gb_ACD57075.1_	0.118	65	0.179	11	0.427	3	0.325	0.248	N	0.57	SignalP-noTM
gi_188519142_gb_ACD57087.1_	0.15	29	0.137	29	0.203	28	0.1	0.119	N	0.57	SignalP-noTM
gi_188519143_gb_ACD57088.1_	0.726	54	0.416	54	0.497	51	0.156	0.32	N	0.51	SignalP-TM
gi_188519145_gb_ACD57090.1_	0.125	61	0.099	61	0.107	21	0.079	0.09	N	0.57	SignalP-noTM
gi_188519150_gb_ACD57095.1_	0.172	23	0.172	23	0.316	20	0.193	0.18	N	0.51	SignalP-TM
gi_188519153_gb_ACD57098.1_	0.106	37	0.105	46	0.127	39	0.087	0.096	N	0.57	SignalP-noTM
gi_188519154_gb_ACD57099.1_	0.24	24	0.255	24	0.486	34	0.297	0.275	N	0.57	SignalP-noTM
gi_188519155_gb_ACD57100.1_	0.153	27	0.128	27	0.147	1	0.102	0.116	N	0.57	SignalP-noTM
gi_188519156_gb_ACD57101.1_	0.127	46	0.133	46	0.213	5	0.14	0.136	N	0.57	SignalP-noTM
gi_188519157_gb_ACD57102.1_	0.132	20	0.122	20	0.153	13	0.103	0.113	N	0.57	SignalP-noTM
gi_188519164_gb_ACD57109.1_	0.12	42	0.176	11	0.52	2	0.314	0.241	N	0.57	SignalP-noTM
gi_188519165_gb_ACD57110.1_	0.103	59	0.117	25	0.159	21	0.114	0.116	N	0.57	SignalP-noTM

0.145542	0.368886	0.107647	0.207358	gi_188518776_gb_ACD56721.1_
0.753246	0.855573	0.741925	0.783581	gi_188518779_gb_ACD56724.1_
0.669295	0.969587	0.693387	0.777423	gi_188518780_gb_ACD56725.1_
0.188314	0.017225	0.246197	0.150579	gi_188518781_gb_ACD56726.1_
0.193411	0.001906	0.287819	0.161045	gi_188518782_gb_ACD56727.1_
0.13193	0.712181	0.076139	0.30675	gi_188518787_gb_ACD56732.1_
0.885238	0.919753	0.890903	0.898631	gi_188518788_gb_ACD56733.1_
0.052252	0.00277	0.109975	0.054999	gi_188518789_gb_ACD56734.1_
0.334701	0.134354	0.450661	0.306572	gi_188518790_gb_ACD56735.1_
0.106215	0.823319	0.068881	0.332805	gi_188518799_gb_ACD56744.1_
0.077201	0.036827	0.127527	0.080518	gi_188518802_gb_ACD56747.1_
0.944065	0.999071	0.933205	0.95878	gi_188518803_gb_ACD56748.1_
0.150077	0.055148	0.197182	0.134136	gi_188519028_gb_ACD56973.1_
0.56193	0.109389	0.657911	0.443077	gi_188519029_gb_ACD56974.1_
0.24453	0.970886	0.086432	0.433949	gi_188519030_gb_ACD56975.1_
0.109681	0.053911	0.108515	0.090702	gi_188519031_gb_ACD56976.1_
0.400832	0.031219	0.511998	0.314683	gi_188519032_gb_ACD56977.1_
0.156699	0.012407	0.189233	0.119446	gi_188519033_gb_ACD56978.1_
0.201491	0.112346	0.317562	0.210466	gi_188519035_gb_ACD56980.1_
0.120999	0.066608	0.095091	0.094233	gi_188519036_gb_ACD56981.1_
0.14295	0.03506	0.171931	0.116647	gi_188519037_gb_ACD56982.1_
0.204891	0.901233	0.131244	0.412456	gi_188519040_gb_ACD56985.1_
0.159896	0.041567	0.213829	0.138431	gi_188519042_gb_ACD56987.1_
0.43807	0.373788	0.310454	0.374104	gi_188519045_gb_ACD56990.1_
0.108225	0.152775	0.126529	0.129176	gi_188519046_gb_ACD56991.1_
0.120681	0.022643	0.211318	0.118214	gi_188519047_gb_ACD56992.1_
0.111749	0.031493	0.152	0.098414	gi_188519050_gb_ACD56995.1_
0.121319	0.044788	0.141851	0.102653	gi_188519052_gb_ACD56997.1_
0.133658	0.062444	0.129882	0.108661	gi_188519053_gb_ACD56998.1_
0.225133	0.181979	0.125868	0.17766	gi_188519058_gb_ACD57003.1_
0.955468	0.905424	0.860686	0.907193	gi_188519059_gb_ACD57004.1_
0.114762	0.201009	0.187856	0.167876	gi_188519064_gb_ACD57009.1_
0.951616	0.697833	0.956102	0.868517	gi_188519065_gb_ACD57010.1_
0.546366	0.6972	0.593391	0.612319	gi_188519066_gb_ACD57011.1_
0.109975	0.019608	0.201491	0.110358	gi_188519067_gb_ACD57012.1_
0.426291	0.827213	0.486503	0.580002	gi_188519068_gb_ACD57013.1_
0.115986	0.11847	0.107936	0.114131	gi_188519069_gb_ACD57014.1_
0.906954	0.999708	0.887054	0.931239	gi_188519070_gb_ACD57015.1_
0.106786	0.010793	0.074468	0.064016	gi_188519071_gb_ACD57016.1_
0.132619	0.007076	0.156303	0.098666	gi_188519080_gb_ACD57025.1_
0.916369	0.916369	0.873471	0.90207	gi_188519082_gb_ACD57027.1_
0.140397	0.034456	0.187399	0.120751	gi_188519083_gb_ACD57028.1_
0.051222	0.033472	0.074261	0.052985	gi_188519084_gb_ACD57029.1_
0.20538	0.853335	0.09639	0.385035	gi_188519085_gb_ACD57030.1_
0.924909	0.986797	0.867036	0.926247	gi_188519088_gb_ACD57033.1_
0.13193	0.002005	0.272693	0.135543	gi_188519089_gb_ACD57034.1_
0.881843	0.989829	0.932264	0.934645	gi_188519090_gb_ACD57035.1_
0.056733	0.761514	0.147418	0.321888	gi_188519091_gb_ACD57036.1_
0.279287	0.057867	0.370983	0.236046	gi_188519096_gb_ACD57041.1_
0.203915	0.070437	0.256927	0.177093	gi_188519098_gb_ACD57043.1_
0.074883	0.04936	0.125538	0.08326	gi_188519100_gb_ACD57045.1_
0.16645	0.096914	0.198134	0.153833	gi_188519101_gb_ACD57046.1_
0.921507	0.998248	0.842108	0.920621	gi_188519103_gb_ACD57048.1_
0.953911	0.997699	0.879319	0.943643	gi_188519108_gb_ACD57053.1_
0.07806	0.042168	0.109097	0.076442	gi_188519110_gb_ACD57055.1_
0.146665	0.038791	0.155119	0.113525	gi_188519113_gb_ACD57058.1_
0.751009	0.953247	0.848	0.850752	gi_188519114_gb_ACD57059.1_
0.14629	0.336038	0.311739	0.264689	gi_188519115_gb_ACD57060.1_
0.164792	0.284754	0.276278	0.241941	gi_188519116_gb_ACD57061.1_
0.165619	0.074675	0.181979	0.140758	gi_188519117_gb_ACD57062.1_
0.094576	0.022843	0.137525	0.084981	gi_188519119_gb_ACD57064.1_
0.083862	0.041447	0.107647	0.077652	gi_188519120_gb_ACD57065.1_
0.104238	0.036615	0.137525	0.092793	gi_188519121_gb_ACD57066.1_
0.952979	0.962745	0.887654	0.934459	gi_188519122_gb_ACD57067.1_
0.333366	0.862475	0.129882	0.441908	gi_188519126_gb_ACD57071.1_
0.236313	0.284754	0.138238	0.219768	gi_188519129_gb_ACD57074.1_
0.825058	0.276878	0.828921	0.643619	gi_188519130_gb_ACD57075.1_
0.109097	0.047156	0.164379	0.106877	gi_188519142_gb_ACD57087.1_
0.912376	0.934502	0.855573	0.900817	gi_188519143_gb_ACD57088.1_
0.118157	0.062797	0.115373	0.098776	gi_188519145_gb_ACD57090.1_
0.126198	0.087384	0.193411	0.135664	gi_188519150_gb_ACD57095.1_
0.141122	0.102293	0.143318	0.128911	gi_188519153_gb_ACD57098.1_
0.085255	0.033182	0.148173	0.08887	gi_188519154_gb_ACD57099.1_
0.121319	0.005205	0.184222	0.103582	gi_188519155_gb_ACD57100.1_
0.115679	0.033961	0.184673	0.111438	gi_188519156_gb_ACD57101.1_
0.120363	0.057216	0.152775	0.110118	gi_188519157_gb_ACD57102.1_
0.091788	0.039128	0.118157	0.083024	gi_188519164_gb_ACD57109.1_
0.152775	0.335369	0.177555	0.2219	gi_188519165_gb_ACD57110.1_

gi_188519166_gb_ACD57111.1_	0.177	20	0.165	20	0.241	8	0.171	0.168	N	0.57	SignalP-noTM
gi_188519167_gb_ACD57112.1_	0.113	27	0.135	11	0.312	1	0.159	0.146	N	0.57	SignalP-noTM
gi_188519169_gb_ACD57114.1_	0.12	57	0.107	14	0.159	4	0.114	0.11	N	0.57	SignalP-noTM
gi_188519172_gb_ACD57117.1_	0.131	25	0.157	11	0.373	4	0.254	0.202	N	0.57	SignalP-noTM
gi_188519174_gb_ACD57119.1_	0.16	30	0.168	30	0.337	27	0.148	0.161	N	0.51	SignalP-TM
gi_188519178_gb_ACD57123.1_	0.243	20	0.431	20	0.864	1	0.767	0.589	Y	0.57	SignalP-noTM
gi_188519180_gb_ACD57125.1_	0.205	29	0.22	29	0.382	2	0.256	0.237	N	0.57	SignalP-noTM
gi_188519185_gb_ACD57130.1_	0.145	50	0.187	16	0.434	10	0.239	0.211	N	0.57	SignalP-noTM
gi_188519186_gb_ACD57131.1_	0.273	19	0.329	19	0.483	16	0.389	0.351	N	0.51	SignalP-TM
gi_188519187_gb_ACD57132.1_	0.182	28	0.2	14	0.44	10	0.355	0.258	N	0.51	SignalP-TM
gi_188519188_gb_ACD57133.1_	0.12	45	0.124	45	0.176	34	0.099	0.112	N	0.57	SignalP-noTM
gi_188519189_gb_ACD57134.1_	0.133	53	0.113	53	0.129	7	0.088	0.104	N	0.51	SignalP-TM
gi_188519190_gb_ACD57135.1_	0.617	23	0.767	23	0.979	10	0.953	0.854	Y	0.57	SignalP-noTM
gi_188519191_gb_ACD57136.1_	0.128	43	0.138	11	0.254	2	0.196	0.159	N	0.51	SignalP-TM
gi_188519192_gb_ACD57137.1_	0.113	22	0.109	38	0.159	37	0.096	0.103	N	0.57	SignalP-noTM
gi_188519194_gb_ACD57139.1_	0.113	27	0.145	11	0.274	5	0.213	0.177	N	0.57	SignalP-noTM
gi_188519195_gb_ACD57140.1_	0.113	20	0.133	11	0.288	1	0.16	0.146	N	0.57	SignalP-noTM
gi_188519198_gb_ACD57143.1_	0.107	22	0.103	22	0.134	1	0.1	0.101	N	0.57	SignalP-noTM
gi_188519200_gb_ACD57145.1_	0.198	21	0.139	21	0.136	9	0.106	0.124	N	0.57	SignalP-noTM
gi_188519202_gb_ACD57147.1_	0.101	35	0.128	16	0.218	9	0.165	0.146	N	0.57	SignalP-noTM
gi_188519204_gb_ACD57149.1_	0.183	38	0.15	38	0.25	21	0.134	0.143	N	0.57	SignalP-noTM
gi_188519205_gb_ACD57150.1_	0.15	60	0.115	60	0.134	5	0.086	0.102	N	0.57	SignalP-noTM
gi_188519206_gb_ACD57151.1_	0.147	53	0.1	40	0.115	58	0.086	0.095	N	0.51	SignalP-TM
gi_188519207_gb_ACD57152.1_	0.242	52	0.153	52	0.144	49	0.097	0.127	N	0.57	SignalP-noTM
gi_188519208_gb_ACD57153.1_	0.139	54	0.133	54	0.192	51	0.111	0.122	N	0.57	SignalP-noTM
gi_188519209_gb_ACD57154.1_	0.129	24	0.121	11	0.217	1	0.146	0.133	N	0.57	SignalP-noTM
gi_188519212_gb_ACD57157.1_	0.112	44	0.108	11	0.145	4	0.118	0.113	N	0.57	SignalP-noTM
gi_188519213_gb_ACD57158.1_	0.129	44	0.122	44	0.16	43	0.087	0.106	N	0.57	SignalP-noTM
gi_188519214_gb_ACD57159.1_	0.103	67	0.144	34	0.286	27	0.168	0.155	N	0.57	SignalP-noTM
gi_188519215_gb_ACD57160.1_	0.136	40	0.122	24	0.173	38	0.115	0.12	N	0.51	SignalP-TM
gi_188519216_gb_ACD57161.1_	0.123	18	0.107	32	0.104	25	0.085	0.097	N	0.57	SignalP-noTM
gi_188519217_gb_ACD57162.1_	0.122	30	0.133	30	0.212	12	0.154	0.143	N	0.57	SignalP-noTM
gi_188519219_gb_ACD57164.1_	0.239	13	0.23	13	0.354	12	0.221	0.226	N	0.57	SignalP-noTM
gi_188519220_gb_ACD57165.1_	0.122	67	0.112	67	0.116	1	0.089	0.101	N	0.57	SignalP-noTM
gi_188519221_gb_ACD57166.1_	0.135	67	0.143	30	0.221	19	0.135	0.139	N	0.57	SignalP-noTM
gi_188519223_gb_ACD57168.1_	0.328	33	0.2	33	0.227	31	0.138	0.177	N	0.51	SignalP-TM
gi_188519224_gb_ACD57169.1_	0.141	51	0.12	51	0.138	31	0.104	0.113	N	0.57	SignalP-noTM
gi_188519226_gb_ACD57171.1_	0.126	47	0.136	21	0.18	25	0.137	0.137	N	0.51	SignalP-TM
gi_188519228_gb_ACD57173.1_	0.102	44	0.104	53	0.113	44	0.086	0.095	N	0.57	SignalP-noTM
gi_188519229_gb_ACD57174.1_	0.144	23	0.223	18	0.45	14	0.347	0.281	N	0.57	SignalP-noTM
gi_188519233_gb_ACD57178.1_	0.152	18	0.121	27	0.172	28	0.092	0.107	N	0.57	SignalP-noTM
gi_188519237_gb_ACD57182.1_	0.705	28	0.791	28	0.976	19	0.905	0.845	Y	0.57	SignalP-noTM
gi_188519238_gb_ACD57183.1_	0.127	55	0.111	31	0.144	30	0.104	0.108	N	0.57	SignalP-noTM
gi_188519241_gb_ACD57186.1_	0.4	25	0.225	25	0.187	19	0.123	0.177	N	0.57	SignalP-noTM
gi_188519242_gb_ACD57187.1_	0.235	25	0.463	25	0.98	12	0.93	0.683	Y	0.57	SignalP-noTM
gi_188519247_gb_ACD57192.1_	0.109	19	0.175	11	0.427	3	0.311	0.239	N	0.57	SignalP-noTM
gi_188519248_gb_ACD57193.1_	0.101	48	0.109	27	0.14	21	0.102	0.106	N	0.57	SignalP-noTM
gi_188519249_gb_ACD57194.1_	0.11	31	0.106	31	0.113	25	0.094	0.1	N	0.57	SignalP-noTM
gi_188519250_gb_ACD57195.1_	0.102	36	0.107	27	0.154	1	0.11	0.109	N	0.57	SignalP-noTM
gi_188519251_gb_ACD57196.1_	0.332	33	0.192	33	0.185	32	0.095	0.147	N	0.57	SignalP-noTM
gi_188519255_gb_ACD57200.1_	0.159	22	0.177	17	0.439	1	0.264	0.218	N	0.57	SignalP-noTM
gi_188519256_gb_ACD57201.1_	0.128	40	0.118	40	0.153	1	0.11	0.114	N	0.57	SignalP-noTM
gi_188519257_gb_ACD57202.1_	0.113	27	0.107	46	0.151	18	0.099	0.103	N	0.57	SignalP-noTM
gi_188519258_gb_ACD57203.1_	0.152	22	0.166	11	0.337	1	0.268	0.214	N	0.57	SignalP-noTM
gi_188519260_gb_ACD57205.1_	0.27	41	0.197	41	0.207	35	0.102	0.152	N	0.57	SignalP-noTM
gi_188519261_gb_ACD57206.1_	0.165	22	0.17	22	0.245	20	0.141	0.156	N	0.57	SignalP-noTM
gi_188519262_gb_ACD57207.1_	0.112	37	0.105	37	0.116	24	0.087	0.097	N	0.57	SignalP-noTM
gi_188519263_gb_ACD57208.1_	0.105	20	0.102	62	0.136	1	0.094	0.098	N	0.57	SignalP-noTM
gi_188519264_gb_ACD57209.1_	0.167	35	0.145	35	0.337	34	0.109	0.128	N	0.57	SignalP-noTM
gi_188519266_gb_ACD57211.1_	0.169	27	0.189	20	0.374	15	0.243	0.214	N	0.57	SignalP-noTM
gi_188519268_gb_ACD57213.1_	0.118	62	0.14	11	0.271	3	0.194	0.166	N	0.57	SignalP-noTM
gi_188519269_gb_ACD57214.1_	0.104	36	0.12	20	0.186	31	0.139	0.129	N	0.57	SignalP-noTM
gi_188519271_gb_ACD57216.1_	0.196	31	0.142	31	0.157	49	0.093	0.119	N	0.57	SignalP-noTM
gi_188519273_gb_ACD57218.1_	0.114	31	0.127	31	0.186	17	0.14	0.133	N	0.57	SignalP-noTM
gi_188519275_gb_ACD57220.1_	0.142	51	0.158	43	0.302	35	0.142	0.152	N	0.51	SignalP-TM
gi_188519276_gb_ACD57221.1_	0.131	38	0.11	38	0.141	5	0.1	0.105	N	0.57	SignalP-noTM
gi_188519277_gb_ACD57222.1_	0.127	69	0.157	31	0.288	25	0.194	0.174	N	0.57	SignalP-noTM
gi_188519282_gb_ACD57227.1_	0.107	26	0.099	37	0.118	1	0.094	0.097	N	0.57	SignalP-noTM
gi_188519283_gb_ACD57228.1_	0.155	24	0.201	24	0.465	20	0.259	0.228	N	0.57	SignalP-noTM
gi_188519290_gb_ACD57235.1_	0.659	27	0.785	27	0.983	11	0.942	0.859	Y	0.57	SignalP-noTM
gi_188519291_gb_ACD57236.1_	0.113	21	0.119	21	0.159	12	0.111	0.115	N	0.57	SignalP-noTM
gi_188519299_gb_ACD57244.1_	0.556	17	0.702	17	0.933	13	0.889	0.79	Y	0.57	SignalP-noTM
gi_188519306_gb_ACD57251.1_	0.156	42	0.144	42	0.211	19	0.138	0.141	N	0.57	SignalP-noTM
gi_188519307_gb_ACD57252.1_	0.174	25	0.214	25	0.403	23	0.245	0.229	N	0.57	SignalP-noTM
gi_188519308_gb_ACD57253.1_	0.155	42	0.145	42	0.21	19	0.138	0.141	N	0.57	SignalP-noTM
gi_188519309_gb_ACD57254.1_	0.112	28	0.114	11	0.184	25	0.131	0.122	N	0.57	SignalP-noTM
gi_188519311_gb_ACD57256.1_	0.296	20	0.156	20	0.155	1	0.094	0.127	N	0.57	SignalP-noTM
gi_188519316_gb_ACD57261.1_	0.481	22	0.672	22	0.973	18	0.937	0.797	Y	0.57	SignalP-noTM

0.06985	0.012932	0.120999	0.067927	gi_188519166_gb_ACD57111.1_
0.312383	0.97592	0.134005	0.474103	gi_188519167_gb_ACD57112.1_
0.771182	0.997076	0.674586	0.814281	gi_188519169_gb_ACD57114.1_
0.149313	0.02795	0.183772	0.120345	gi_188519172_gb_ACD57117.1_
0.193879	0.150844	0.136108	0.160277	gi_188519174_gb_ACD57119.1_
0.3327	0.186487	0.34074	0.286642	gi_188519178_gb_ACD57123.1_
0.163967	0.109389	0.206853	0.16007	gi_188519180_gb_ACD57125.1_
0.299013	0.057867	0.354344	0.237075	gi_188519185_gb_ACD57130.1_
0.177118	0.048522	0.201974	0.142538	gi_188519186_gb_ACD57131.1_
0.139314	0.183322	0.098767	0.140468	gi_188519187_gb_ACD57132.1_
0.389361	0.314967	0.41314	0.372489	gi_188519188_gb_ACD57133.1_
0.168541	0.156699	0.14295	0.156063	gi_188519189_gb_ACD57134.1_
0.426291	0.177555	0.578837	0.394228	gi_188519190_gb_ACD57135.1_
0.110563	0.065314	0.169384	0.115087	gi_188519191_gb_ACD57136.1_
0.090052	0.003477	0.103123	0.065551	gi_188519192_gb_ACD57137.1_
0.807524	0.395082	0.863892	0.688833	gi_188519194_gb_ACD57139.1_
0.456609	0.904391	0.529964	0.630321	gi_188519195_gb_ACD57140.1_
0.140035	0.568565	0.115679	0.27476	gi_188519198_gb_ACD57143.1_
0.118784	0.516494	0.096651	0.243976	gi_188519200_gb_ACD57145.1_
0.29463	0.988097	0.167284	0.483337	gi_188519202_gb_ACD57147.1_
0.125538	0.076988	0.172787	0.125104	gi_188519204_gb_ACD57149.1_
0.101197	0.531458	0.072024	0.234893	gi_188519205_gb_ACD57150.1_
0.105364	0.022053	0.15046	0.092626	gi_188519206_gb_ACD57151.1_
0.139674	0.455121	0.106786	0.23386	gi_188519207_gb_ACD57152.1_
0.252372	0.086907	0.304068	0.214449	gi_188519208_gb_ACD57153.1_
0.094319	0.043898	0.11385	0.084022	gi_188519209_gb_ACD57154.1_
0.203915	0.135755	0.277479	0.205716	gi_188519212_gb_ACD57157.1_
0.822445	0.679179	0.840506	0.78071	gi_188519213_gb_ACD57158.1_
0.640146	0.979984	0.834795	0.818308	gi_188519214_gb_ACD57159.1_
0.217891	0.428494	0.125538	0.257308	gi_188519215_gb_ACD57160.1_
0.695932	0.534445	0.45289	0.561089	gi_188519216_gb_ACD57161.1_
0.144798	0.020075	0.216361	0.127078	gi_188519217_gb_ACD57162.1_
0.956851	0.999875	0.884933	0.94722	gi_188519219_gb_ACD57164.1_
0.776953	0.779026	0.810306	0.788762	gi_188519220_gb_ACD57165.1_
0.096129	0.011151	0.120045	0.075775	gi_188519221_gb_ACD57166.1_
0.506	0.939118	0.564882	0.67	gi_188519223_gb_ACD57168.1_
0.250115	0.231475	0.353658	0.278416	gi_188519224_gb_ACD57169.1_
0.945474	0.898256	0.918415	0.920715	gi_188519226_gb_ACD57171.1_
0.072225	0.030948	0.090298	0.06449	gi_188519228_gb_ACD57173.1_
0.228818	0.931119	0.125209	0.428382	gi_188519229_gb_ACD57174.1_
0.179756	0.120363	0.161515	0.153878	gi_188519233_gb_ACD57178.1_
0.354344	0.161515	0.464808	0.326889	gi_188519237_gb_ACD57182.1_
0.947599	0.999793	0.888251	0.945214	gi_188519238_gb_ACD57183.1_
0.865995	0.958672	0.804711	0.876459	gi_188519241_gb_ACD57186.1_
0.831879	0.994342	0.870456	0.898892	gi_188519242_gb_ACD57187.1_
0.348191	0.237941	0.29713	0.294421	gi_188519247_gb_ACD57192.1_
0.797057	0.638071	0.58904	0.674723	gi_188519248_gb_ACD57193.1_
0.821127	0.124553	0.880271	0.60865	gi_188519249_gb_ACD57194.1_
0.130903	0.001513	0.34344	0.158619	gi_188519250_gb_ACD57195.1_
0.236313	0.863539	0.29463	0.464827	gi_188519251_gb_ACD57196.1_
0.220458	0.05869	0.20538	0.161509	gi_188519255_gb_ACD57200.1_
0.844881	0.935956	0.863892	0.881576	gi_188519256_gb_ACD57201.1_
0.964736	0.988513	0.954436	0.969228	gi_188519257_gb_ACD57202.1_
0.225133	0.034959	0.279287	0.179793	gi_188519258_gb_ACD57203.1_
0.952979	0.999449	0.911412	0.954613	gi_188519260_gb_ACD57205.1_
0.948632	0.905424	0.836033	0.896696	gi_188519261_gb_ACD57206.1_
0.185126	0.228289	0.221491	0.211635	gi_188519262_gb_ACD57207.1_
0.068689	0.025681	0.108225	0.067532	gi_188519263_gb_ACD57208.1_
0.208829	0.944538	0.094833	0.416067	gi_188519264_gb_ACD57209.1_
0.110269	0.054837	0.130562	0.098556	gi_188519266_gb_ACD57211.1_
0.762602	0.357094	0.832716	0.650804	gi_188519268_gb_ACD57213.1_
0.141486	0.072024	0.157493	0.123668	gi_188519269_gb_ACD57214.1_
0.141486	0.533699	0.094319	0.256501	gi_188519271_gb_ACD57216.1_
0.793147	0.075508	0.812601	0.560419	gi_188519273_gb_ACD57218.1_
0.099571	0.199567	0.184222	0.16112	gi_188519275_gb_ACD57220.1_
0.10147	0.029369	0.164379	0.098406	gi_188519276_gb_ACD57221.1_
0.268548	0.865297	0.143687	0.425844	gi_188519277_gb_ACD57222.1_
0.154335	0.805652	0.334033	0.43134	gi_188519282_gb_ACD57227.1_
0.258649	0.544135	0.356405	0.386396	gi_188519283_gb_ACD57228.1_
0.32213	0.05255	0.466301	0.280327	gi_188519290_gb_ACD57235.1_
0.274482	0.174509	0.319515	0.256169	gi_188519291_gb_ACD57236.1_
0.931119	0.580299	0.8397	0.783706	gi_188519299_gb_ACD57244.1_
0.270912	0.818021	0.300273	0.463069	gi_188519306_gb_ACD57251.1_
0.164792	0.034357	0.163147	0.120765	gi_188519307_gb_ACD57252.1_
0.26386	0.730271	0.29463	0.429587	gi_188519308_gb_ACD57253.1_
0.16645	0.034059	0.14295	0.114486	gi_188519309_gb_ACD57254.1_
0.106215	0.040388	0.14295	0.096518	gi_188519311_gb_ACD57256.1_
0.451404	0.186943	0.432171	0.356839	gi_188519316_gb_ACD57261.1_

gi_188519318_gb_ACD57263.1_	0.144	53	0.121	32	0.136	30	0.093	0.108	N	0.57	SignalP-noTM
gi_188519320_gb_ACD57265.1_	0.114	67	0.106	43	0.137	10	0.101	0.104	N	0.57	SignalP-noTM
gi_188519325_gb_ACD57270.1_	0.147	35	0.133	35	0.152	9	0.116	0.125	N	0.57	SignalP-noTM
gi_188519326_gb_ACD57271.1_	0.172	60	0.245	50	0.752	46	0.29	0.266	N	0.57	SignalP-noTM
gi_188519327_gb_ACD57272.1_	0.152	38	0.143	38	0.232	36	0.099	0.122	N	0.57	SignalP-noTM
gi_188519331_gb_ACD57276.1_	0.124	21	0.124	33	0.17	1	0.129	0.126	N	0.57	SignalP-noTM
gi_188519332_gb_ACD57277.1_	0.122	47	0.203	11	0.606	1	0.386	0.289	N	0.57	SignalP-noTM
gi_188519333_gb_ACD57278.1_	0.183	42	0.138	42	0.176	41	0.086	0.113	N	0.57	SignalP-noTM
gi_188519334_gb_ACD57279.1_	0.107	42	0.106	42	0.12	41	0.091	0.099	N	0.57	SignalP-noTM
gi_188519335_gb_ACD57280.1_	0.127	59	0.135	51	0.264	42	0.108	0.122	N	0.57	SignalP-noTM
gi_188519336_gb_ACD57281.1_	0.124	59	0.128	59	0.203	55	0.09	0.114	N	0.51	SignalP-TM
gi_188519338_gb_ACD57283.1_	0.14	31	0.152	11	0.296	2	0.231	0.189	N	0.57	SignalP-noTM
gi_188519339_gb_ACD57284.1_	0.136	18	0.122	18	0.181	1	0.115	0.119	N	0.51	SignalP-TM
gi_188519341_gb_ACD57286.1_	0.112	21	0.117	21	0.151	6	0.123	0.12	N	0.57	SignalP-noTM
gi_188519342_gb_ACD57287.1_	0.103	29	0.17	11	0.37	4	0.296	0.229	N	0.57	SignalP-noTM
gi_188519343_gb_ACD57288.1_	0.125	45	0.12	45	0.178	46	0.11	0.115	N	0.57	SignalP-noTM
gi_188519344_gb_ACD57289.1_	0.131	30	0.115	30	0.157	2	0.113	0.114	N	0.57	SignalP-noTM
gi_188519348_gb_ACD57293.1_	0.196	56	0.12	26	0.148	8	0.118	0.119	N	0.51	SignalP-TM
gi_188519349_gb_ACD57294.1_	0.698	23	0.713	23	0.825	10	0.731	0.72	Y	0.51	SignalP-TM
gi_188519350_gb_ACD57295.1_	0.127	49	0.105	30	0.123	52	0.081	0.096	N	0.51	SignalP-TM
gi_188519351_gb_ACD57296.1_	0.104	13	0.122	18	0.171	12	0.134	0.126	N	0.51	SignalP-TM
gi_188519352_gb_ACD57297.1_	0.184	39	0.149	11	0.269	2	0.226	0.177	N	0.51	SignalP-TM
gi_188519353_gb_ACD57298.1_	0.155	42	0.146	36	0.225	24	0.119	0.136	N	0.51	SignalP-TM
gi_188519355_gb_ACD57300.1_	0.18	23	0.271	23	0.668	5	0.5	0.356	N	0.51	SignalP-TM
gi_188519356_gb_ACD57301.1_	0.239	34	0.166	34	0.324	7	0.18	0.171	N	0.51	SignalP-TM
gi_188519357_gb_ACD57302.1_	0.159	21	0.257	21	0.642	8	0.432	0.322	N	0.51	SignalP-TM
gi_188519358_gb_ACD57303.1_	0.144	62	0.149	62	0.228	59	0.121	0.139	N	0.51	SignalP-TM
gi_188519361_gb_ACD57306.1_	0.251	32	0.368	32	0.739	17	0.565	0.461	N	0.57	SignalP-noTM
gi_188519362_gb_ACD57307.1_	0.125	30	0.103	39	0.123	1	0.09	0.096	N	0.57	SignalP-noTM
gi_188519363_gb_ACD57308.1_	0.113	54	0.135	13	0.233	9	0.177	0.155	N	0.57	SignalP-noTM
gi_188519364_gb_ACD57309.1_	0.108	48	0.103	48	0.139	6	0.103	0.103	N	0.57	SignalP-noTM
gi_188519369_gb_ACD57314.1_	0.126	16	0.182	11	0.514	1	0.303	0.239	N	0.57	SignalP-noTM
gi_188519370_gb_ACD57315.1_	0.26	22	0.477	22	0.912	14	0.878	0.665	Y	0.57	SignalP-noTM
gi_188519372_gb_ACD57317.1_	0.169	30	0.182	22	0.407	1	0.28	0.218	N	0.51	SignalP-TM
gi_188519373_gb_ACD57318.1_	0.267	46	0.186	46	0.169	45	0.09	0.15	N	0.51	SignalP-TM
gi_188519375_gb_ACD57320.1_	0.137	21	0.122	11	0.209	2	0.151	0.133	N	0.51	SignalP-TM
gi_188519385_gb_ACD57330.1_	0.121	27	0.104	60	0.134	14	0.089	0.097	N	0.57	SignalP-noTM
gi_188519386_gb_ACD57331.1_	0.15	21	0.173	11	0.409	1	0.285	0.225	N	0.57	SignalP-noTM
gi_188519387_gb_ACD57332.1_	0.132	23	0.166	18	0.325	4	0.244	0.203	N	0.57	SignalP-noTM
gi_188519388_gb_ACD57333.1_	0.132	34	0.192	11	0.482	2	0.383	0.263	N	0.51	SignalP-TM
gi_188519389_gb_ACD57334.1_	0.194	22	0.167	22	0.486	1	0.189	0.175	N	0.51	SignalP-TM
gi_188519391_gb_ACD57336.1_	0.183	24	0.265	24	0.542	23	0.332	0.296	N	0.57	SignalP-noTM
gi_188519396_gb_ACD57341.1_	0.16	25	0.149	25	0.207	23	0.134	0.142	N	0.57	SignalP-noTM
gi_188519398_gb_ACD57343.1_	0.138	43	0.129	43	0.246	12	0.123	0.126	N	0.57	SignalP-noTM
gi_188519399_gb_ACD57344.1_	0.113	29	0.108	29	0.164	1	0.094	0.101	N	0.57	SignalP-noTM
gi_188519400_gb_ACD57345.1_	0.124	49	0.132	11	0.26	5	0.184	0.156	N	0.57	SignalP-noTM
gi_188519408_gb_ACD57353.1_	0.107	26	0.107	11	0.153	1	0.113	0.11	N	0.57	SignalP-noTM
gi_188519410_gb_ACD57355.1_	0.192	22	0.379	22	0.9	6	0.796	0.575	Y	0.57	SignalP-noTM
gi_188519414_gb_ACD57359.1_	0.135	21	0.127	44	0.211	37	0.12	0.123	N	0.57	SignalP-noTM
gi_188519415_gb_ACD57360.1_	0.331	35	0.229	35	0.217	32	0.158	0.196	N	0.57	SignalP-noTM
gi_188519416_gb_ACD57361.1_	0.148	40	0.281	37	0.733	31	0.32	0.295	N	0.51	SignalP-TM
gi_188519417_gb_ACD57362.1_	0.315	41	0.281	41	0.333	31	0.205	0.253	N	0.51	SignalP-TM
gi_188519418_gb_ACD57363.1_	0.395	29	0.603	29	0.966	17	0.919	0.752	Y	0.57	SignalP-noTM
gi_188519423_gb_ACD57368.1_	0.164	52	0.121	52	0.138	49	0.079	0.105	N	0.51	SignalP-TM
gi_188519427_gb_ACD57372.1_	0.113	54	0.169	11	0.431	1	0.268	0.216	N	0.57	SignalP-noTM
gi_188519430_gb_ACD57375.1_	0.124	20	0.132	25	0.178	34	0.125	0.129	N	0.57	SignalP-noTM
gi_188519431_gb_ACD57376.1_	0.124	20	0.116	20	0.125	13	0.103	0.11	N	0.57	SignalP-noTM
gi_188519432_gb_ACD57377.1_	0.111	9	0.106	68	0.124	62	0.09	0.098	N	0.57	SignalP-noTM
gi_188519435_gb_ACD57380.1_	0.216	33	0.139	33	0.182	40	0.086	0.114	N	0.57	SignalP-noTM
gi_188519436_gb_ACD57381.1_	0.109	64	0.103	33	0.128	10	0.097	0.1	N	0.57	SignalP-noTM
gi_188519437_gb_ACD57382.1_	0.124	27	0.118	27	0.135	26	0.102	0.11	N	0.57	SignalP-noTM
gi_188519444_gb_ACD57389.1_	0.134	33	0.195	12	0.476	5	0.377	0.263	N	0.51	SignalP-TM
gi_188519447_gb_ACD57392.1_	0.122	18	0.178	11	0.496	1	0.297	0.234	N	0.57	SignalP-noTM
gi_188519450_gb_ACD57395.1_	0.12	30	0.118	41	0.162	33	0.108	0.113	N	0.57	SignalP-noTM
gi_188519459_gb_ACD57404.1_	0.472	29	0.642	29	0.954	25	0.871	0.75	Y	0.57	SignalP-noTM
gi_188519460_gb_ACD57405.1_	0.336	34	0.559	34	0.978	26	0.803	0.674	Y	0.57	SignalP-noTM
gi_188519461_gb_ACD57406.1_	0.109	33	0.115	33	0.189	22	0.103	0.109	N	0.57	SignalP-noTM
gi_188519462_gb_ACD57407.1_	0.18	29	0.12	11	0.225	1	0.136	0.126	N	0.51	SignalP-TM
gi_188519463_gb_ACD57408.1_	0.813	27	0.885	27	0.993	17	0.966	0.923	Y	0.57	SignalP-noTM
gi_188519464_gb_ACD57409.1_	0.148	23	0.135	11	0.287	1	0.165	0.149	N	0.57	SignalP-noTM
gi_188519465_gb_ACD57410.1_	0.118	6	0.102	58	0.112	51	0.081	0.092	N	0.57	SignalP-noTM
gi_188519466_gb_ACD57411.1_	0.482	30	0.664	30	0.978	14	0.902	0.776	Y	0.57	SignalP-noTM
gi_188519467_gb_ACD57412.1_	0.217	22	0.351	21	0.9	9	0.682	0.507	N	0.57	SignalP-noTM
gi_188519468_gb_ACD57413.1_	0.105	45	0.105	51	0.184	42	0.087	0.096	N	0.57	SignalP-noTM
gi_188519470_gb_ACD57415.1_	0.139	33	0.123	33	0.179	31	0.107	0.116	N	0.57	SignalP-noTM
gi_188519471_gb_ACD57416.1_	0.224	23	0.324	23	0.725	14	0.474	0.395	N	0.57	SignalP-noTM
gi_188519472_gb_ACD57417.1_	0.142	18	0.193	18	0.374	17	0.267	0.221	N	0.51	SignalP-TM
gi_188519473_gb_ACD57418.1_	0.105	10	0.12	11	0.206	1	0.139	0.129	N	0.57	SignalP-noTM

0.198134	0.453634	0.263278	0.305015	gi_188519318_gb_ACD57263.1_
0.129882	0.083862	0.17581	0.129851	gi_188519320_gb_ACD57265.1_
0.759876	0.75823	0.690829	0.736312	gi_188519325_gb_ACD57270.1_
0.550824	0.105647	0.83355	0.496674	gi_188519326_gb_ACD57271.1_
0.16645	0.002713	0.188773	0.119312	gi_188519327_gb_ACD57272.1_
0.150844	0.294007	0.155119	0.19999	gi_188519331_gb_ACD57276.1_
0.941144	0.998284	0.854084	0.931171	gi_188519332_gb_ACD57277.1_
0.449918	0.033862	0.439547	0.307776	gi_188519333_gb_ACD57278.1_
0.099571	0.061226	0.14517	0.101989	gi_188519334_gb_ACD57279.1_
0.086432	0.007994	0.093808	0.062745	gi_188519335_gb_ACD57280.1_
0.136108	0.186487	0.095091	0.139229	gi_188519336_gb_ACD57281.1_
0.059861	0.033278	0.106215	0.066451	gi_188519338_gb_ACD57283.1_
0.061054	0.016824	0.125209	0.067696	gi_188519339_gb_ACD57284.1_
0.777992	0.069267	0.710333	0.519197	gi_188519341_gb_ACD57286.1_
0.188314	0.05869	0.196234	0.147746	gi_188519342_gb_ACD57287.1_
0.173217	0.535192	0.238486	0.315632	gi_188519343_gb_ACD57288.1_
0.069074	0.013361	0.126529	0.069655	gi_188519344_gb_ACD57289.1_
0.132964	0.047562	0.145542	0.108689	gi_188519348_gb_ACD57293.1_
0.770122	0.805182	0.679832	0.751712	gi_188519349_gb_ACD57294.1_
0.046353	0.75547	0.129206	0.310343	gi_188519350_gb_ACD57295.1_
0.341414	0.733802	0.27032	0.448512	gi_188519351_gb_ACD57296.1_
0.833134	0.983176	0.760423	0.858911	gi_188519352_gb_ACD57297.1_
0.075091	0.79413	0.17023	0.346484	gi_188519353_gb_ACD57298.1_
0.210818	0.232009	0.208829	0.217219	gi_188519355_gb_ACD57300.1_
0.331369	0.067736	0.41096	0.270022	gi_188519356_gb_ACD57301.1_
0.140035	0.097704	0.207839	0.148526	gi_188519357_gb_ACD57302.1_
0.0985	0.458099	0.176681	0.244427	gi_188519358_gb_ACD57303.1_
0.960189	0.977817	0.933949	0.957318	gi_188519361_gb_ACD57306.1_
0.867726	0.998747	0.884321	0.916931	gi_188519362_gb_ACD57307.1_
0.791666	0.891194	0.849156	0.844005	gi_188519363_gb_ACD57308.1_
0.101744	0.042411	0.112645	0.0856	gi_188519364_gb_ACD57309.1_
0.780057	0.072628	0.77539	0.542692	gi_188519369_gb_ACD57314.1_
0.482757	0.080025	0.654527	0.40577	gi_188519370_gb_ACD57315.1_
0.090545	0.089074	0.138238	0.105952	gi_188519372_gb_ACD57317.1_
0.178873	0.027545	0.220458	0.142292	gi_188519373_gb_ACD57318.1_
0.111452	0.039241	0.109975	0.086889	gi_188519375_gb_ACD57320.1_
0.061745	0.005127	0.136108	0.06766	gi_188519385_gb_ACD57330.1_
0.114153	0.046353	0.132619	0.097708	gi_188519386_gb_ACD57331.1_
0.174942	0.059524	0.193879	0.142782	gi_188519387_gb_ACD57332.1_
0.15046	0.041927	0.197658	0.130015	gi_188519388_gb_ACD57333.1_
0.128869	0.080691	0.181087	0.130216	gi_188519389_gb_ACD57334.1_
0.138596	0.062797	0.13331	0.111568	gi_188519391_gb_ACD57336.1_
0.076562	0.041447	0.131587	0.083199	gi_188519396_gb_ACD57341.1_
0.179314	0.085489	0.152775	0.139193	gi_188519398_gb_ACD57343.1_
0.078493	0.006151	0.117222	0.067289	gi_188519399_gb_ACD57344.1_
0.118784	0.906954	0.246754	0.424164	gi_188519400_gb_ACD57345.1_
0.224088	0.930926	0.093046	0.41602	gi_188519408_gb_ACD57353.1_
0.610639	0.941144	0.823755	0.791846	gi_188519410_gb_ACD57355.1_
0.095349	0.041927	0.139674	0.092317	gi_188519414_gb_ACD57359.1_
0.180643	0.103679	0.155513	0.146612	gi_188519415_gb_ACD57360.1_
0.163557	0.08883	0.20538	0.152589	gi_188519416_gb_ACD57361.1_
0.189694	0.073237	0.222527	0.161819	gi_188519417_gb_ACD57362.1_
0.640146	0.965941	0.737303	0.78113	gi_188519418_gb_ACD57363.1_
0.103123	0.021353	0.162329	0.095602	gi_188519423_gb_ACD57368.1_
0.793639	0.741925	0.829346	0.788303	gi_188519427_gb_ACD57372.1_
0.088588	0.035778	0.080247	0.068204	gi_188519430_gb_ACD57375.1_
0.864245	0.999712	0.745357	0.869771	gi_188519431_gb_ACD57376.1_
0.187399	0.894353	0.102845	0.394866	gi_188519432_gb_ACD57377.1_
0.119413	0.033375	0.169806	0.107531	gi_188519435_gb_ACD57380.1_
0.175375	0.563407	0.13717	0.291984	gi_188519436_gb_ACD57381.1_
0.111155	0.034656	0.150077	0.098629	gi_188519437_gb_ACD57382.1_
0.095868	0.093046	0.171931	0.120282	gi_188519444_gb_ACD57389.1_
0.82419	0.99549	0.855202	0.891627	gi_188519447_gb_ACD57392.1_
0.21687	0.983809	0.076139	0.425606	gi_188519450_gb_ACD57395.1_
0.567829	0.034757	0.574443	0.392343	gi_188519459_gb_ACD57404.1_
0.259225	0.216361	0.336038	0.270541	gi_188519460_gb_ACD57405.1_
0.081361	0.096914	0.129206	0.102494	gi_188519461_gb_ACD57406.1_
0.075299	0.276878	0.134354	0.162177	gi_188519462_gb_ACD57407.1_
0.865646	0.894919	0.93808	0.899548	gi_188519463_gb_ACD57408.1_
0.752688	0.836853	0.728495	0.772679	gi_188519464_gb_ACD57409.1_
0.091788	0.053151	0.111452	0.085464	gi_188519465_gb_ACD57410.1_
0.118784	0.69211	0.155119	0.322004	gi_188519466_gb_ACD57411.1_
0.213325	0.158691	0.23308	0.201699	gi_188519467_gb_ACD57412.1_
0.136108	0.033086	0.165619	0.111604	gi_188519468_gb_ACD57413.1_
0.168541	0.045304	0.216361	0.143402	gi_188519470_gb_ACD57415.1_
0.299013	0.1065	0.267371	0.224295	gi_188519471_gb_ACD57416.1_
0.150077	0.088105	0.207839	0.148674	gi_188519472_gb_ACD57417.1_
0.402274	0.940139	0.388648	0.57702	gi_188519473_gb_ACD57418.1_

gi_188519476_gb_ACD57421.1_	0.176	30	0.195	30	0.313	9	0.216	0.205	N	0.57	SignalP-noTM
gi_188519477_gb_ACD57422.1_	0.121	19	0.172	13	0.412	1	0.259	0.213	N	0.57	SignalP-noTM
gi_188519484_gb_ACD57429.1_	0.141	47	0.108	47	0.107	40	0.08	0.095	N	0.57	SignalP-noTM
gi_188519485_gb_ACD57430.1_	0.107	21	0.113	21	0.143	11	0.114	0.113	N	0.51	SignalP-TM
gi_188519486_gb_ACD57431.1_	0.169	22	0.325	22	0.898	11	0.682	0.493	N	0.57	SignalP-noTM
gi_188519488_gb_ACD57433.1_	0.115	37	0.11	11	0.159	5	0.123	0.116	N	0.57	SignalP-noTM
gi_188519489_gb_ACD57434.1_	0.168	22	0.131	50	0.235	49	0.1	0.117	N	0.57	SignalP-noTM
gi_188519496_gb_ACD57441.1_	0.101	20	0.213	11	0.576	1	0.466	0.332	N	0.57	SignalP-noTM
gi_188519502_gb_ACD57447.1_	0.103	54	0.105	54	0.116	49	0.088	0.097	N	0.57	SignalP-noTM
gi_188519503_gb_ACD57448.1_	0.102	37	0.116	16	0.163	10	0.131	0.123	N	0.57	SignalP-noTM
gi_188519505_gb_ACD57450.1_	0.138	35	0.162	11	0.37	3	0.276	0.204	N	0.51	SignalP-TM
gi_188519506_gb_ACD57451.1_	0.121	38	0.195	11	0.442	1	0.374	0.279	N	0.57	SignalP-noTM
gi_188519507_gb_ACD57452.1_	0.127	54	0.201	48	0.481	34	0.265	0.231	N	0.57	SignalP-noTM
gi_188519508_gb_ACD57453.1_	0.118	39	0.108	39	0.123	7	0.094	0.101	N	0.57	SignalP-noTM
gi_188519509_gb_ACD57454.1_	0.129	19	0.113	19	0.124	1	0.098	0.106	N	0.57	SignalP-noTM
gi_188519510_gb_ACD57455.1_	0.109	12	0.107	12	0.126	9	0.104	0.106	N	0.57	SignalP-noTM
gi_188519511_gb_ACD57456.1_	0.131	66	0.131	39	0.216	6	0.123	0.127	N	0.57	SignalP-noTM
gi_188519513_gb_ACD57458.1_	0.161	35	0.141	35	0.333	34	0.108	0.126	N	0.57	SignalP-noTM
gi_188519514_gb_ACD57459.1_	0.477	20	0.419	20	0.704	13	0.419	0.419	N	0.57	SignalP-noTM
gi_188519518_gb_ACD57463.1_	0.114	63	0.143	11	0.345	2	0.186	0.163	N	0.57	SignalP-noTM
gi_188519519_gb_ACD57464.1_	0.294	43	0.169	43	0.159	1	0.089	0.131	N	0.57	SignalP-noTM
gi_188519520_gb_ACD57465.1_	0.115	62	0.136	11	0.24	1	0.182	0.158	N	0.57	SignalP-noTM
gi_188519522_gb_ACD57467.1_	0.134	20	0.146	20	0.259	30	0.169	0.157	N	0.57	SignalP-noTM
gi_188519524_gb_ACD57469.1_	0.165	21	0.184	21	0.382	2	0.237	0.204	N	0.51	SignalP-TM
gi_188519530_gb_ACD57475.1_	0.13	26	0.108	12	0.138	8	0.122	0.113	N	0.51	SignalP-TM
gi_188519532_gb_ACD57477.1_	0.123	10	0.11	23	0.155	34	0.092	0.102	N	0.57	SignalP-noTM
gi_188519535_gb_ACD57480.1_	0.261	13	0.382	13	0.799	10	0.559	0.465	N	0.57	SignalP-noTM
gi_188519536_gb_ACD57481.1_	0.108	48	0.103	48	0.139	6	0.103	0.103	N	0.57	SignalP-noTM
gi_188519539_gb_ACD57484.1_	0.132	63	0.153	54	0.336	51	0.126	0.14	N	0.57	SignalP-noTM
gi_188519541_gb_ACD57486.1_	0.114	26	0.114	26	0.154	22	0.109	0.111	N	0.57	SignalP-noTM
gi_188519542_gb_ACD57487.1_	0.116	23	0.144	23	0.271	19	0.167	0.155	N	0.57	SignalP-noTM
gi_188519543_gb_ACD57488.1_	0.104	46	0.119	11	0.199	3	0.143	0.131	N	0.57	SignalP-noTM
gi_188519545_gb_ACD57490.1_	0.111	9	0.106	37	0.126	33	0.08	0.094	N	0.57	SignalP-noTM
gi_188519547_gb_ACD57492.1_	0.117	18	0.112	18	0.132	31	0.107	0.11	N	0.57	SignalP-noTM
gi_188519550_gb_ACD57495.1_	0.127	34	0.107	34	0.15	1	0.093	0.1	N	0.57	SignalP-noTM
gi_188519553_gb_ACD57498.1_	0.139	61	0.125	61	0.188	33	0.111	0.118	N	0.57	SignalP-noTM
gi_188519556_gb_ACD57501.1_	0.18	38	0.154	38	0.192	27	0.135	0.147	N	0.51	SignalP-TM
gi_188519557_gb_ACD57502.1_	0.108	25	0.214	11	0.574	2	0.463	0.331	N	0.57	SignalP-noTM
gi_188519558_gb_ACD57503.1_	0.241	36	0.15	36	0.142	44	0.085	0.12	N	0.57	SignalP-noTM
gi_188519559_gb_ACD57504.1_	0.118	20	0.122	20	0.163	1	0.122	0.122	N	0.57	SignalP-noTM
gi_188519560_gb_ACD57505.1_	0.109	6	0.146	14	0.289	27	0.22	0.173	N	0.51	SignalP-TM
gi_188519561_gb_ACD57506.1_	0.613	20	0.759	20	0.962	10	0.935	0.842	Y	0.57	SignalP-noTM
gi_188519563_gb_ACD57508.1_	0.411	21	0.358	21	0.512	16	0.275	0.319	N	0.57	SignalP-noTM
gi_188519566_gb_ACD57511.1_	0.136	37	0.114	26	0.153	23	0.115	0.114	N	0.51	SignalP-TM
gi_188519567_gb_ACD57512.1_	0.14	33	0.125	33	0.271	6	0.122	0.124	N	0.57	SignalP-noTM
gi_188519568_gb_ACD57513.1_	0.131	43	0.129	28	0.203	25	0.138	0.132	N	0.51	SignalP-TM
gi_188519569_gb_ACD57514.1_	0.1	68	0.103	43	0.124	35	0.096	0.1	N	0.57	SignalP-noTM
gi_188519570_gb_ACD57515.1_	0.121	24	0.167	11	0.327	1	0.279	0.219	N	0.57	SignalP-noTM
gi_188519572_gb_ACD57517.1_	0.112	24	0.146	11	0.251	1	0.21	0.176	N	0.57	SignalP-noTM
gi_188519574_gb_ACD57519.1_	0.124	40	0.124	40	0.184	35	0.127	0.125	N	0.51	SignalP-TM
gi_188519575_gb_ACD57520.1_	0.578	22	0.697	22	0.905	15	0.839	0.764	Y	0.57	SignalP-noTM
gi_188519576_gb_ACD57521.1_	0.164	22	0.267	22	0.749	10	0.496	0.375	N	0.57	SignalP-noTM
gi_188519577_gb_ACD57522.1_	0.108	32	0.101	47	0.118	34	0.091	0.097	N	0.57	SignalP-noTM
gi_188519580_gb_ACD57525.1_	0.198	39	0.135	39	0.115	55	0.092	0.115	N	0.57	SignalP-noTM
gi_188519581_gb_ACD57526.1_	0.142	29	0.214	22	0.443	18	0.363	0.269	N	0.51	SignalP-TM
gi_188519582_gb_ACD57527.1_	0.381	23	0.458	23	0.716	8	0.588	0.506	N	0.51	SignalP-TM
gi_188519583_gb_ACD57528.1_	0.134	23	0.102	54	0.109	69	0.073	0.088	N	0.57	SignalP-noTM
gi_188519584_gb_ACD57529.1_	0.11	51	0.109	15	0.139	8	0.114	0.111	N	0.57	SignalP-noTM
gi_188519585_gb_ACD57530.1_	0.214	42	0.144	42	0.133	39	0.105	0.126	N	0.57	SignalP-noTM
gi_188519587_gb_ACD57532.1_	0.115	25	0.219	25	0.633	24	0.408	0.308	N	0.57	SignalP-noTM
gi_188519588_gb_ACD57533.1_	0.139	26	0.346	26	0.917	16	0.858	0.586	Y	0.57	SignalP-noTM
gi_188519592_gb_ACD57537.1_	0.115	19	0.117	48	0.146	40	0.107	0.112	N	0.57	SignalP-noTM
gi_188519595_gb_ACD57540.1_	0.162	51	0.124	14	0.183	5	0.15	0.134	N	0.51	SignalP-TM
gi_188519596_gb_ACD57541.1_	0.136	23	0.115	23	0.158	41	0.094	0.105	N	0.57	SignalP-noTM
gi_188519597_gb_ACD57542.1_	0.116	42	0.111	42	0.12	38	0.086	0.099	N	0.57	SignalP-noTM
gi_188519598_gb_ACD57543.1_	0.131	61	0.192	14	0.456	9	0.363	0.272	N	0.57	SignalP-noTM
gi_188519599_gb_ACD57544.1_	0.16	24	0.117	24	0.185	1	0.094	0.106	N	0.57	SignalP-noTM
gi_188519600_gb_ACD57545.1_	0.103	49	0.108	35	0.157	1	0.11	0.109	N	0.57	SignalP-noTM
gi_188519602_gb_ACD57547.1_	0.131	41	0.146	11	0.246	1	0.213	0.177	N	0.57	SignalP-noTM
gi_188519603_gb_ACD57548.1_	0.136	6	0.121	15	0.182	10	0.146	0.13	N	0.51	SignalP-TM
gi_188519604_gb_ACD57549.1_	0.129	30	0.144	12	0.261	2	0.221	0.173	N	0.51	SignalP-TM
gi_188519605_gb_ACD57550.1_	0.112	47	0.12	17	0.178	7	0.135	0.125	N	0.51	SignalP-TM
gi_188519606_gb_ACD57551.1_	0.174	42	0.167	42	0.213	32	0.115	0.148	N	0.51	SignalP-TM
gi_188519607_gb_ACD57552.1_	0.101	66	0.11	28	0.139	19	0.105	0.107	N	0.57	SignalP-noTM
gi_188519608_gb_ACD57553.1_	0.148	9	0.106	63	0.142	1	0.097	0.102	N	0.57	SignalP-noTM
gi_188519609_gb_ACD57554.1_	0.143	45	0.121	45	0.122	41	0.094	0.108	N	0.57	SignalP-noTM
gi_188519610_gb_ACD57555.1_	0.126	34	0.119	11	0.193	1	0.139	0.128	N	0.57	SignalP-noTM
gi_188519611_gb_ACD57556.1_	0.105	20	0.107	33	0.125	30	0.092	0.1	N	0.57	SignalP-noTM

0.064044	0.041091	0.126861	0.077332	gi_188519476_gb_ACD57421.1_
0.148932	0.102293	0.195289	0.148838	gi_188519477_gb_ACD57422.1_
0.117845	0.057055	0.124881	0.099927	gi_188519484_gb_ACD57429.1_
0.074675	0.827641	0.165619	0.355978	gi_188519485_gb_ACD57430.1_
0.916827	0.989207	0.894919	0.933651	gi_188519486_gb_ACD57431.1_
0.071625	0.071226	0.077629	0.073493	gi_188519488_gb_ACD57433.1_
0.657236	0.114457	0.617039	0.462911	gi_188519489_gb_ACD57434.1_
0.93738	0.985443	0.814874	0.912566	gi_188519496_gb_ACD57441.1_
0.049642	0.01904	0.080468	0.049717	gi_188519502_gb_ACD57447.1_
0.157493	0.105931	0.124227	0.129217	gi_188519503_gb_ACD57448.1_
0.197658	0.066795	0.183772	0.149408	gi_188519505_gb_ACD57450.1_
0.426291	0.981072	0.387935	0.598433	gi_188519506_gb_ACD57451.1_
0.062797	0.019436	0.09104	0.057758	gi_188519507_gb_ACD57452.1_
0.152387	0.100652	0.122282	0.125107	gi_188519508_gb_ACD57453.1_
0.084788	0.008187	0.107647	0.066874	gi_188519509_gb_ACD57454.1_
0.097969	0.191081	0.086432	0.125161	gi_188519510_gb_ACD57455.1_
0.093046	0.002091	0.184673	0.09327	gi_188519511_gb_ACD57456.1_
0.218915	0.942945	0.096651	0.419504	gi_188519513_gb_ACD57458.1_
0.938946	0.999741	0.888251	0.942313	gi_188519514_gb_ACD57459.1_
0.293385	0.06717	0.326073	0.228876	gi_188519518_gb_ACD57463.1_
0.120999	0.000934	0.200047	0.107327	gi_188519519_gb_ACD57464.1_
0.129544	0.235772	0.140035	0.16845	gi_188519520_gb_ACD57465.1_
0.250678	0.053151	0.30789	0.203906	gi_188519522_gb_ACD57467.1_
0.092038	0.425557	0.196708	0.238101	gi_188519524_gb_ACD57469.1_
0.081137	0.833966	0.165619	0.360241	gi_188519530_gb_ACD57475.1_
0.087864	0.064044	0.128869	0.093592	gi_188519532_gb_ACD57477.1_
0.851448	0.995938	0.832716	0.893367	gi_188519535_gb_ACD57480.1_
0.098767	0.041091	0.110563	0.083474	gi_188519536_gb_ACD57481.1_
0.902031	0.999587	0.61491	0.838843	gi_188519539_gb_ACD57484.1_
0.165205	0.065681	0.130562	0.120483	gi_188519541_gb_ACD57486.1_
0.076139	0.002517	0.134354	0.071003	gi_188519542_gb_ACD57487.1_
0.497	0.025382	0.663962	0.395448	gi_188519543_gb_ACD57488.1_
0.212822	0.921507	0.110563	0.414964	gi_188519545_gb_ACD57490.1_
0.923225	0.470783	0.915908	0.769972	gi_188519547_gb_ACD57492.1_
0.106215	0.070633	0.15046	0.109103	gi_188519550_gb_ACD57495.1_
0.17023	0.083402	0.206361	0.153331	gi_188519553_gb_ACD57498.1_
0.091788	0.091289	0.137525	0.106867	gi_188519556_gb_ACD57501.1_
0.82419	0.98352	0.728495	0.845402	gi_188519557_gb_ACD57502.1_
0.201491	0.200047	0.116912	0.172817	gi_188519558_gb_ACD57503.1_
0.20587	0.147418	0.178873	0.177387	gi_188519559_gb_ACD57504.1_
0.282925	0.371684	0.467795	0.374135	gi_188519560_gb_ACD57505.1_
0.91117	0.954305	0.860326	0.9086	gi_188519561_gb_ACD57506.1_
0.135755	0.018164	0.126529	0.093483	gi_188519563_gb_ACD57508.1_
0.101197	0.038346	0.125538	0.08836	gi_188519566_gb_ACD57511.1_
0.095091	0.031676	0.150077	0.092281	gi_188519567_gb_ACD57512.1_
0.136815	0.049784	0.163967	0.116855	gi_188519568_gb_ACD57513.1_
0.164379	0.117533	0.122282	0.134731	gi_188519569_gb_ACD57514.1_
0.102569	0.055619	0.111452	0.08988	gi_188519570_gb_ACD57515.1_
0.162737	0.394365	0.144427	0.233843	gi_188519572_gb_ACD57517.1_
0.3327	0.262697	0.307252	0.300883	gi_188519574_gb_ACD57519.1_
0.941805	0.968962	0.887953	0.932907	gi_188519575_gb_ACD57520.1_
0.178873	0.085021	0.227761	0.163885	gi_188519576_gb_ACD57521.1_
0.306613	0.989646	0.085255	0.460505	gi_188519577_gb_ACD57522.1_
0.90016	0.918639	0.849923	0.889574	gi_188519580_gb_ACD57525.1_
0.16645	0.045695	0.232009	0.148051	gi_188519581_gb_ACD57526.1_
0.491751	0.997915	0.663292	0.717653	gi_188519582_gb_ACD57527.1_
0.102293	0.080025	0.113247	0.098522	gi_188519583_gb_ACD57528.1_
0.111155	0.052252	0.142217	0.101875	gi_188519584_gb_ACD57529.1_
0.14295	0.048522	0.148173	0.113215	gi_188519585_gb_ACD57530.1_
0.115067	0.003122	0.140035	0.086075	gi_188519587_gb_ACD57532.1_
0.074468	0.044277	0.089806	0.069517	gi_188519588_gb_ACD57533.1_
0.188314	0.978959	0.398672	0.521982	gi_188519592_gb_ACD57537.1_
0.467795	0.791666	0.604201	0.621221	gi_188519595_gb_ACD57540.1_
0.279891	0.962852	0.361237	0.53466	gi_188519596_gb_ACD57541.1_
0.132274	0.048246	0.144056	0.108192	gi_188519597_gb_ACD57542.1_
0.089562	0.026135	0.127862	0.081186	gi_188519598_gb_ACD57543.1_
0.05869	0.048384	0.073645	0.06024	gi_188519599_gb_ACD57544.1_
0.200047	0.471531	0.090545	0.254041	gi_188519600_gb_ACD57545.1_
0.072024	0.028945	0.091538	0.064169	gi_188519602_gb_ACD57547.1_
0.957344	0.999565	0.905681	0.954197	gi_188519603_gb_ACD57548.1_
0.109975	0.0527	0.136108	0.099594	gi_188519604_gb_ACD57549.1_
0.214333	0.389361	0.265027	0.289574	gi_188519605_gb_ACD57550.1_
0.089317	0.572241	0.169384	0.276981	gi_188519606_gb_ACD57551.1_
0.153944	0.075299	0.135053	0.121432	gi_188519607_gb_ACD57552.1_
0.203915	0.059357	0.246754	0.170009	gi_188519608_gb_ACD57553.1_
0.212822	0.148552	0.282316	0.214563	gi_188519609_gb_ACD57554.1_
0.953113	0.999138	0.909208	0.95382	gi_188519610_gb_ACD57555.1_
0.905167	0.532205	0.847613	0.761662	gi_188519611_gb_ACD57556.1_

gi_188519612_gb_ACD57557.1_	0.141	21	0.202	11	0.571	3	0.403	0.297	N	0.57	SignalP-noTM
gi_188519613_gb_ACD57558.1_	0.228	38	0.301	38	0.9	37	0.347	0.322	N	0.57	SignalP-noTM
gi_188519614_gb_ACD57559.1_	0.136	33	0.113	33	0.145	46	0.087	0.101	N	0.57	SignalP-noTM
gi_188519615_gb_ACD57560.1_	0.188	65	0.386	25	0.969	20	0.91	0.632	Y	0.57	SignalP-noTM
gi_188519617_gb_ACD57562.1_	0.474	21	0.668	21	0.972	19	0.945	0.799	Y	0.57	SignalP-noTM
gi_188519618_gb_ACD57563.1_	0.177	22	0.161	38	0.202	36	0.127	0.149	N	0.51	SignalP-TM
gi_188519619_gb_ACD57564.1_	0.109	40	0.103	40	0.118	52	0.084	0.094	N	0.57	SignalP-noTM
gi_188519620_gb_ACD57565.1_	0.119	26	0.111	34	0.144	1	0.096	0.104	N	0.57	SignalP-noTM
gi_188519621_gb_ACD57566.1_	0.104	41	0.109	57	0.147	33	0.098	0.104	N	0.57	SignalP-noTM
gi_188519622_gb_ACD57567.1_	0.421	21	0.609	21	0.952	17	0.871	0.732	Y	0.57	SignalP-noTM
gi_188519624_gb_ACD57569.1_	0.215	23	0.159	23	0.223	41	0.116	0.139	N	0.57	SignalP-noTM
gi_188519625_gb_ACD57570.1_	0.124	29	0.109	64	0.109	66	0.088	0.099	N	0.57	SignalP-noTM
gi_188519626_gb_ACD57571.1_	0.202	38	0.181	19	0.256	34	0.194	0.187	N	0.57	SignalP-noTM
gi_188519627_gb_ACD57572.1_	0.117	29	0.146	11	0.281	3	0.215	0.179	N	0.57	SignalP-noTM
gi_188519628_gb_ACD57573.1_	0.105	24	0.131	11	0.289	1	0.157	0.143	N	0.57	SignalP-noTM
gi_188519629_gb_ACD57574.1_	0.164	60	0.124	60	0.172	15	0.092	0.109	N	0.57	SignalP-noTM
gi_188519630_gb_ACD57575.1_	0.341	21	0.513	21	0.897	1	0.814	0.654	Y	0.57	SignalP-noTM
gi_188519631_gb_ACD57576.1_	0.795	25	0.814	25	0.942	9	0.876	0.843	Y	0.57	SignalP-noTM
gi_188519632_gb_ACD57577.1_	0.312	18	0.223	18	0.268	5	0.179	0.203	N	0.57	SignalP-noTM
gi_188519633_gb_ACD57578.1_	0.148	42	0.123	42	0.177	15	0.112	0.119	N	0.51	SignalP-TM
gi_188519635_gb_ACD57580.1_	0.883	26	0.89	26	0.962	11	0.919	0.904	Y	0.57	SignalP-noTM
gi_188519636_gb_ACD57581.1_	0.138	40	0.165	40	0.316	32	0.145	0.158	N	0.51	SignalP-TM
gi_188519637_gb_ACD57582.1_	0.123	21	0.124	21	0.196	14	0.114	0.119	N	0.57	SignalP-noTM
gi_188519638_gb_ACD57583.1_	0.108	24	0.093	70	0.096	69	0.073	0.084	N	0.57	SignalP-noTM
gi_188519639_gb_ACD57584.1_	0.122	37	0.165	15	0.32	4	0.263	0.211	N	0.57	SignalP-noTM
gi_188519641_gb_ACD57586.1_	0.123	21	0.121	57	0.184	51	0.081	0.102	N	0.57	SignalP-noTM
gi_188519643_gb_ACD57588.1_	0.411	21	0.358	21	0.512	16	0.275	0.319	N	0.57	SignalP-noTM
gi_188519645_gb_ACD57590.1_	0.106	39	0.14	11	0.246	1	0.191	0.164	N	0.57	SignalP-noTM
gi_188519647_gb_ACD57592.1_	0.104	31	0.106	58	0.123	39	0.091	0.099	N	0.57	SignalP-noTM
gi_188519648_gb_ACD57593.1_	0.149	45	0.149	11	0.317	2	0.23	0.187	N	0.57	SignalP-noTM
gi_528897472_gb_AGS47849.1_	0.116	18	0.146	12	0.324	1	0.202	0.173	N	0.57	SignalP-noTM
gi_188519649_gb_ACD57594.1_	0.166	51	0.166	51	0.366	1	0.153	0.161	N	0.51	SignalP-TM
gi_188519650_gb_ACD57595.1_	0.115	34	0.109	58	0.143	5	0.095	0.102	N	0.57	SignalP-noTM
gi_188519652_gb_ACD57597.1_	0.139	46	0.116	70	0.153	13	0.079	0.102	N	0.51	SignalP-TM
gi_188519653_gb_ACD57598.1_	0.114	33	0.136	12	0.241	3	0.188	0.161	N	0.57	SignalP-noTM
gi_188519654_gb_ACD57599.1_	0.141	38	0.128	38	0.133	29	0.103	0.116	N	0.57	SignalP-noTM
gi_188519655_gb_ACD57600.1_	0.177	40	0.139	40	0.183	26	0.113	0.127	N	0.57	SignalP-noTM
gi_188519660_gb_ACD57605.1_	0.152	27	0.149	27	0.222	32	0.134	0.142	N	0.57	SignalP-noTM
gi_188519662_gb_ACD57607.1_	0.122	31	0.146	11	0.316	1	0.203	0.173	N	0.57	SignalP-noTM
gi_188519665_gb_ACD57610.1_	0.125	20	0.145	20	0.211	17	0.154	0.15	N	0.57	SignalP-noTM
gi_188519669_gb_ACD57614.1_	0.105	45	0.105	51	0.184	42	0.087	0.096	N	0.57	SignalP-noTM
gi_188519676_gb_ACD57621.1_	0.106	22	0.103	64	0.126	1	0.094	0.098	N	0.57	SignalP-noTM
gi_188519677_gb_ACD57622.1_	0.168	27	0.169	35	0.37	34	0.167	0.168	N	0.57	SignalP-noTM
gi_188519684_gb_ACD57629.1_	0.13	53	0.114	53	0.127	49	0.086	0.101	N	0.57	SignalP-noTM
gi_188519687_gb_ACD57632.1_	0.131	8	0.099	33	0.12	6	0.091	0.095	N	0.57	SignalP-noTM
gi_188519688_gb_ACD57633.1_	0.183	26	0.275	26	0.615	3	0.487	0.375	N	0.57	SignalP-noTM
gi_188519691_gb_ACD57636.1_	0.102	35	0.102	35	0.119	13	0.093	0.098	N	0.57	SignalP-noTM
gi_188519693_gb_ACD57638.1_	0.606	32	0.644	26	0.881	12	0.768	0.703	Y	0.57	SignalP-noTM
gi_188519696_gb_ACD57641.1_	0.128	27	0.136	12	0.217	6	0.187	0.16	N	0.57	SignalP-noTM
gi_188519697_gb_ACD57642.1_	0.274	25	0.175	25	0.217	23	0.108	0.143	N	0.57	SignalP-noTM
gi_188519699_gb_ACD57644.1_	0.102	24	0.098	38	0.102	33	0.073	0.086	N	0.57	SignalP-noTM
gi_188519700_gb_ACD57645.1_	0.114	43	0.106	12	0.143	3	0.113	0.109	N	0.57	SignalP-noTM
gi_188519702_gb_ACD57647.1_	0.213	37	0.143	37	0.189	45	0.088	0.117	N	0.57	SignalP-noTM
gi_188519704_gb_ACD57649.1_	0.219	39	0.194	39	0.489	38	0.123	0.16	N	0.57	SignalP-noTM
gi_188519705_gb_ACD57650.1_	0.184	56	0.164	31	0.291	29	0.133	0.153	N	0.51	SignalP-TM
gi_188519706_gb_ACD57651.1_	0.179	26	0.239	26	0.385	15	0.292	0.259	N	0.51	SignalP-TM
gi_188519709_gb_ACD57654.1_	0.807	27	0.818	27	0.954	13	0.88	0.847	Y	0.57	SignalP-noTM
gi_188519711_gb_ACD57656.1_	0.172	14	0.363	14	0.853	13	0.767	0.553	N	0.57	SignalP-noTM
gi_188519712_gb_ACD57657.1_	0.108	24	0.107	57	0.115	54	0.091	0.099	N	0.57	SignalP-noTM
gi_188519713_gb_ACD57658.1_	0.129	18	0.14	18	0.206	9	0.154	0.147	N	0.57	SignalP-noTM
gi_188519714_gb_ACD57659.1_	0.11	43	0.132	12	0.206	9	0.178	0.154	N	0.57	SignalP-noTM
gi_188519715_gb_ACD57660.1_	0.248	20	0.195	20	0.196	12	0.148	0.173	N	0.57	SignalP-noTM
gi_188519716_gb_ACD57661.1_	0.113	20	0.113	30	0.186	27	0.095	0.105	N	0.57	SignalP-noTM
gi_188519718_gb_ACD57663.1_	0.272	64	0.199	64	0.29	53	0.118	0.161	N	0.57	SignalP-noTM
gi_188519719_gb_ACD57664.1_	0.121	67	0.106	32	0.135	1	0.097	0.102	N	0.57	SignalP-noTM
gi_188519720_gb_ACD57665.1_	0.221	40	0.188	40	0.259	2	0.171	0.18	N	0.57	SignalP-noTM
gi_188519721_gb_ACD57666.1_	0.142	43	0.177	43	0.34	42	0.165	0.171	N	0.57	SignalP-noTM
gi_188519722_gb_ACD57667.1_	0.143	20	0.171	20	0.297	1	0.216	0.192	N	0.57	SignalP-noTM
gi_188519723_gb_ACD57668.1_	0.189	43	0.201	43	0.469	3	0.202	0.202	N	0.51	SignalP-TM
gi_188519724_gb_ACD57669.1_	0.244	27	0.2	27	0.353	11	0.194	0.197	N	0.57	SignalP-noTM
gi_188519725_gb_ACD57670.1_	0.116	29	0.171	29	0.381	26	0.218	0.193	N	0.57	SignalP-noTM
gi_188519726_gb_ACD57671.1_	0.107	41	0.108	28	0.127	20	0.086	0.098	N	0.57	SignalP-noTM
gi_188519728_gb_ACD57673.1_	0.169	55	0.122	55	0.12	23	0.09	0.107	N	0.57	SignalP-noTM
gi_188519729_gb_ACD57674.1_	0.368	23	0.401	23	0.649	22	0.397	0.4	N	0.51	SignalP-TM
gi_188519730_gb_ACD57675.1_	0.165	24	0.166	24	0.318	22	0.139	0.156	N	0.51	SignalP-TM
gi_188519731_gb_ACD57676.1_	0.447	67	0.243	67	0.187	55	0.106	0.192	N	0.51	SignalP-TM
gi_188519732_gb_ACD57677.1_	0.127	42	0.137	11	0.301	1	0.177	0.152	N	0.51	SignalP-TM
gi_188519733_gb_ACD57678.1_	0.161	40	0.125	40	0.135	44	0.088	0.107	N	0.57	SignalP-noTM

0.698465	0.94131	0.776433	0.805403	gi_188519612_gb_ACD57557.1_
0.913093	0.990185	0.804239	0.902506	gi_188519613_gb_ACD57558.1_
0.272693	0.414595	0.331369	0.339552	gi_188519614_gb_ACD57559.1_
0.954696	0.99976	0.890025	0.94816	gi_188519615_gb_ACD57560.1_
0.923438	0.686972	0.871804	0.827405	gi_188519617_gb_ACD57562.1_
0.956353	0.999857	0.91117	0.955793	gi_188519618_gb_ACD57563.1_
0.456609	0.160704	0.508999	0.375437	gi_188519619_gb_ACD57564.1_
0.090545	0.107936	0.109975	0.102819	gi_188519620_gb_ACD57565.1_
0.490251	0.185126	0.491001	0.388793	gi_188519621_gb_ACD57566.1_
0.647028	0.78313	0.692748	0.707635	gi_188519622_gb_ACD57567.1_
0.089317	0.050931	0.082716	0.074321	gi_188519624_gb_ACD57569.1_
0.151614	0.02401	0.17023	0.115285	gi_188519625_gb_ACD57570.1_
0.163147	0.022183	0.135404	0.106911	gi_188519626_gb_ACD57571.1_
0.228818	0.4985	0.165205	0.297508	gi_188519627_gb_ACD57572.1_
0.844093	0.985867	0.850687	0.893549	gi_188519628_gb_ACD57573.1_
0.133658	0.024435	0.210818	0.12297	gi_188519629_gb_ACD57574.1_
0.90016	0.985006	0.929367	0.938178	gi_188519630_gb_ACD57575.1_
0.791666	0.371684	0.867381	0.67691	gi_188519631_gb_ACD57576.1_
0.237398	0.135404	0.290285	0.221029	gi_188519632_gb_ACD57577.1_
0.191081	0.016774	0.24453	0.150795	gi_188519633_gb_ACD57578.1_
0.942133	0.998487	0.917056	0.952559	gi_188519635_gb_ACD57580.1_
0.179314	0.075508	0.166866	0.140563	gi_188519636_gb_ACD57581.1_
0.080247	0.060711	0.084788	0.075249	gi_188519637_gb_ACD57582.1_
0.074675	0.04004	0.117845	0.07752	gi_188519638_gb_ACD57583.1_
0.178873	0.021165	0.20538	0.135139	gi_188519639_gb_ACD57584.1_
0.125209	0.102018	0.128869	0.118699	gi_188519641_gb_ACD57586.1_
0.129206	0.008689	0.128869	0.088921	gi_188519643_gb_ACD57588.1_
0.461079	0.945474	0.705993	0.704182	gi_188519645_gb_ACD57590.1_
0.925117	0.895762	0.876749	0.899209	gi_188519647_gb_ACD57592.1_
0.311096	0.051661	0.449176	0.270644	gi_188519648_gb_ACD57593.1_
0.143687	0.117845	0.206361	0.155964	gi_188519649_gb_ACD57594.1_
0.129882	0.040855	0.122927	0.097888	gi_188519650_gb_ACD57595.1_
0.061572	0.803292	0.175375	0.346746	gi_188519652_gb_ACD57597.1_
0.185579	0.057541	0.240672	0.161264	gi_188519653_gb_ACD57598.1_
0.801866	0.136815	0.707857	0.548846	gi_188519654_gb_ACD57599.1_
0.109975	0.003648	0.144056	0.085893	gi_188519655_gb_ACD57600.1_
0.119098	0.017688	0.239031	0.125272	gi_188519660_gb_ACD57605.1_
0.810767	0.901766	0.861762	0.858098	gi_188519662_gb_ACD57607.1_
0.585405	0.623399	0.594114	0.600973	gi_188519665_gb_ACD57610.1_
0.117222	0.034556	0.134703	0.095494	gi_188519669_gb_ACD57614.1_
0.063864	0.026059	0.100924	0.063616	gi_188519676_gb_ACD57621.1_
0.198134	0.92129	0.088105	0.40251	gi_188519677_gb_ACD57622.1_
0.227233	0.261536	0.261536	0.250102	gi_188519684_gb_ACD57629.1_
0.123251	0.11847	0.138238	0.126653	gi_188519687_gb_ACD57632.1_
0.311096	0.980449	0.330041	0.540529	gi_188519688_gb_ACD57633.1_
0.087384	0.071824	0.094833	0.08468	gi_188519691_gb_ACD57636.1_
0.116912	0.047291	0.10011	0.088104	gi_188519693_gb_ACD57638.1_
0.154727	0.336708	0.124881	0.205439	gi_188519696_gb_ACD57641.1_
0.63599	0.97814	0.778509	0.797546	gi_188519697_gb_ACD57642.1_
0.155907	0.125209	0.232009	0.171042	gi_188519699_gb_ACD57644.1_
0.142583	0.009527	0.136108	0.096073	gi_188519700_gb_ACD57645.1_
0.803292	0.582489	0.721919	0.702567	gi_188519702_gb_ACD57647.1_
0.282316	0.048108	0.287205	0.205876	gi_188519704_gb_ACD57649.1_
0.092038	0.179314	0.144056	0.138469	gi_188519705_gb_ACD57650.1_
0.084324	0.025756	0.159896	0.089992	gi_188519706_gb_ACD57651.1_
0.400112	0.990038	0.114762	0.501637	gi_188519709_gb_ACD57654.1_
0.368886	0.67787	0.43807	0.494942	gi_528897472_gb_AGS47849.1_
0.956727	0.99902	0.906192	0.95398	gi_188519711_gb_ACD57656.1_
0.396517	0.035674	0.394365	0.275519	gi_188519712_gb_ACD57657.1_
0.057216	0.030149	0.115679	0.067681	gi_188519713_gb_ACD57658.1_
0.150077	0.110859	0.081137	0.114024	gi_188519714_gb_ACD57659.1_
0.068116	0.045304	0.129206	0.080875	gi_188519715_gb_ACD57660.1_
0.134703	0.111749	0.130222	0.125558	gi_188519716_gb_ACD57661.1_
0.085489	0.001085	0.118784	0.068453	gi_188519718_gb_ACD57663.1_
0.08181	0.008689	0.089074	0.059858	gi_188519719_gb_ACD57664.1_
0.061399	0.041447	0.081361	0.061402	gi_188519720_gb_ACD57665.1_
0.172787	0.260957	0.131244	0.188329	gi_188519721_gb_ACD57666.1_
0.167702	0.041567	0.22461	0.144626	gi_188519722_gb_ACD57667.1_
0.897431	0.99883	0.885543	0.927268	gi_188519723_gb_ACD57668.1_
0.906192	0.688904	0.858514	0.81787	gi_188519724_gb_ACD57669.1_
0.888845	0.995517	0.807524	0.897295	gi_188519725_gb_ACD57670.1_
0.104238	0.961654	0.226707	0.430866	gi_188519726_gb_ACD57671.1_
0.168121	0.177994	0.232544	0.192886	gi_188519728_gb_ACD57673.1_
0.209822	0.155119	0.145916	0.170286	gi_188519729_gb_ACD57674.1_
0.167702	0.34344	0.249553	0.253565	gi_188519730_gb_ACD57675.1_
0.100381	0.005051	0.12196	0.075797	gi_188519731_gb_ACD57676.1_
0.858878	0.467048	0.848	0.724642	gi_188519732_gb_ACD57677.1_
0.212822	0.348872	0.163967	0.241887	gi_188519733_gb_ACD57678.1_

gi_188519734_gb_ACD57679.1_	0.112	29	0.105	67	0.156	1	0.096	0.1	N	0.57	SignalP-noTM
gi_188519739_gb_ACD57684.1_	0.115	52	0.104	70	0.124	8	0.091	0.098	N	0.57	SignalP-noTM
gi_188519741_gb_ACD57686.1_	0.13	29	0.146	11	0.292	2	0.219	0.181	N	0.57	SignalP-noTM
gi_188519742_gb_ACD57687.1_	0.108	35	0.109	35	0.131	32	0.095	0.103	N	0.57	SignalP-noTM
gi_188519743_gb_ACD57688.1_	0.305	18	0.285	18	0.678	1	0.35	0.309	N	0.51	SignalP-TM
gi_188519744_gb_ACD57689.1_	0.158	37	0.191	14	0.417	11	0.375	0.259	N	0.51	SignalP-TM
gi_188519745_gb_ACD57690.1_	0.17	58	0.155	11	0.412	1	0.22	0.186	N	0.57	SignalP-noTM
gi_188519746_gb_ACD57691.1_	0.125	19	0.153	19	0.392	12	0.185	0.168	N	0.57	SignalP-noTM
gi_188519747_gb_ACD57692.1_	0.179	30	0.12	46	0.163	42	0.082	0.106	N	0.51	SignalP-TM
gi_188519748_gb_ACD57693.1_	0.152	47	0.146	47	0.179	40	0.095	0.128	N	0.51	SignalP-TM
gi_188519749_gb_ACD57694.1_	0.296	19	0.236	19	0.333	30	0.179	0.209	N	0.57	SignalP-noTM
gi_188519750_gb_ACD57695.1_	0.118	49	0.133	49	0.214	9	0.141	0.137	N	0.57	SignalP-noTM
gi_188519751_gb_ACD57696.1_	0.145	52	0.158	12	0.345	6	0.256	0.204	N	0.57	SignalP-noTM
gi_188519752_gb_ACD57697.1_	0.497	24	0.338	24	0.467	1	0.295	0.322	N	0.51	SignalP-TM
gi_188519753_gb_ACD57698.1_	0.169	23	0.158	23	0.222	22	0.147	0.153	N	0.57	SignalP-noTM
gi_188519754_gb_ACD57699.1_	0.107	22	0.11	33	0.158	12	0.109	0.11	N	0.57	SignalP-noTM
gi_188519755_gb_ACD57700.1_	0.104	25	0.162	11	0.374	1	0.244	0.201	N	0.57	SignalP-noTM
gi_188519757_gb_ACD57702.1_	0.121	52	0.209	16	0.477	10	0.398	0.279	N	0.51	SignalP-TM
gi_188519758_gb_ACD57703.1_	0.112	70	0.139	16	0.249	7	0.18	0.158	N	0.57	SignalP-noTM
gi_188519759_gb_ACD57704.1_	0.117	20	0.119	20	0.17	10	0.114	0.117	N	0.57	SignalP-noTM
gi_188519760_gb_ACD57705.1_	0.102	18	0.121	11	0.205	1	0.139	0.13	N	0.57	SignalP-noTM
gi_188519761_gb_ACD57706.1_	0.111	3	0.172	11	0.449	1	0.278	0.222	N	0.57	SignalP-noTM
gi_188519765_gb_ACD57710.1_	0.111	33	0.104	33	0.119	50	0.081	0.093	N	0.57	SignalP-noTM
gi_188519766_gb_ACD57711.1_	0.239	23	0.459	23	0.954	7	0.905	0.669	Y	0.57	SignalP-noTM
gi_188519768_gb_ACD57713.1_	0.113	38	0.152	27	0.293	21	0.184	0.167	N	0.57	SignalP-noTM
gi_188519770_gb_ACD57715.1_	0.115	59	0.114	11	0.24	1	0.116	0.115	N	0.57	SignalP-noTM
gi_188519772_gb_ACD57717.1_	0.102	34	0.105	67	0.12	1	0.082	0.094	N	0.57	SignalP-noTM
gi_188519773_gb_ACD57718.1_	0.103	23	0.122	12	0.175	4	0.149	0.135	N	0.57	SignalP-noTM
gi_188519774_gb_ACD57719.1_	0.173	40	0.174	40	0.456	38	0.213	0.193	N	0.57	SignalP-noTM
gi_188519776_gb_ACD57721.1_	0.151	39	0.127	11	0.204	6	0.166	0.145	N	0.57	SignalP-noTM
gi_188519777_gb_ACD57722.1_	0.26	38	0.364	38	0.573	34	0.273	0.321	N	0.57	SignalP-noTM
gi_188519779_gb_ACD57724.1_	0.104	25	0.195	13	0.511	10	0.382	0.283	N	0.57	SignalP-noTM
gi_188519780_gb_ACD57725.1_	0.208	31	0.152	31	0.207	1	0.104	0.129	N	0.57	SignalP-noTM
gi_188519781_gb_ACD57726.1_	0.112	17	0.108	17	0.146	8	0.1	0.104	N	0.57	SignalP-noTM
gi_188519785_gb_ACD57730.1_	0.437	26	0.637	26	0.979	13	0.946	0.782	Y	0.57	SignalP-noTM
gi_188519786_gb_ACD57731.1_	0.183	57	0.15	57	0.247	50	0.081	0.117	N	0.57	SignalP-noTM
gi_188519788_gb_ACD57733.1_	0.279	26	0.272	26	0.556	37	0.239	0.256	N	0.57	SignalP-noTM
gi_188519789_gb_ACD57734.1_	0.156	31	0.201	18	0.368	1	0.292	0.244	N	0.57	SignalP-noTM
gi_188519792_gb_ACD57737.1_	0.151	23	0.26	13	0.749	9	0.69	0.462	N	0.57	SignalP-noTM
gi_188519796_gb_ACD57741.1_	0.113	7	0.1	63	0.105	61	0.084	0.092	N	0.57	SignalP-noTM
gi_188519800_gb_ACD57745.1_	0.136	21	0.216	21	0.556	2	0.383	0.278	N	0.51	SignalP-TM
gi_188519801_gb_ACD57746.1_	0.158	25	0.132	25	0.173	2	0.107	0.12	N	0.57	SignalP-noTM
gi_188519802_gb_ACD57747.1_	0.173	28	0.221	28	0.525	1	0.343	0.266	N	0.51	SignalP-TM
gi_188519809_gb_ACD57754.1_	0.586	29	0.528	29	0.585	24	0.394	0.478	N	0.51	SignalP-TM
gi_188519810_gb_ACD57755.1_	0.127	49	0.114	49	0.118	30	0.099	0.107	N	0.57	SignalP-noTM
gi_188519811_gb_ACD57756.1_	0.173	28	0.181	28	0.279	26	0.197	0.187	N	0.51	SignalP-TM
gi_188519815_gb_ACD57760.1_	0.112	29	0.11	29	0.172	27	0.089	0.102	N	0.51	SignalP-TM
gi_188519816_gb_ACD57761.1_	0.121	24	0.239	22	0.626	17	0.473	0.326	N	0.51	SignalP-TM
gi_188519817_gb_ACD57762.1_	0.267	16	0.497	16	0.95	10	0.922	0.697	Y	0.57	SignalP-noTM
gi_188519818_gb_ACD57763.1_	0.128	22	0.103	22	0.113	21	0.08	0.092	N	0.57	SignalP-noTM
gi_188519819_gb_ACD57764.1_	0.145	22	0.098	50	0.119	1	0.071	0.088	N	0.51	SignalP-TM
gi_188519820_gb_ACD57765.1_	0.102	70	0.105	49	0.126	43	0.091	0.098	N	0.57	SignalP-noTM
gi_188519821_gb_ACD57766.1_	0.111	34	0.1	12	0.121	6	0.1	0.1	N	0.51	SignalP-TM
gi_188519822_gb_ACD57767.1_	0.115	49	0.126	55	0.266	48	0.11	0.118	N	0.57	SignalP-noTM
gi_188519832_gb_ACD57777.1_	0.352	23	0.209	23	0.213	20	0.13	0.18	N	0.51	SignalP-TM
gi_188519833_gb_ACD57778.1_	0.17	25	0.225	25	0.37	19	0.271	0.242	N	0.51	SignalP-TM
gi_188519834_gb_ACD57779.1_	0.11	36	0.135	12	0.261	3	0.182	0.158	N	0.57	SignalP-noTM
gi_188519835_gb_ACD57780.1_	0.156	42	0.146	42	0.219	19	0.143	0.145	N	0.57	SignalP-noTM
gi_188519836_gb_ACD57781.1_	0.116	41	0.124	54	0.17	49	0.114	0.119	N	0.57	SignalP-noTM
gi_188519838_gb_ACD57783.1_	0.164	20	0.156	20	0.211	13	0.133	0.145	N	0.57	SignalP-noTM
gi_188519839_gb_ACD57784.1_	0.12	27	0.132	13	0.218	3	0.179	0.154	N	0.57	SignalP-noTM
gi_188519840_gb_ACD57785.1_	0.108	40	0.116	19	0.178	39	0.132	0.123	N	0.57	SignalP-noTM
gi_188519848_gb_ACD57793.1_	0.493	29	0.448	29	0.692	23	0.341	0.408	N	0.51	SignalP-TM
gi_188519854_gb_ACD57799.1_	0.11	17	0.119	11	0.22	1	0.13	0.124	N	0.57	SignalP-noTM
gi_188519856_gb_ACD57801.1_	0.111	9	0.108	41	0.124	62	0.083	0.096	N	0.57	SignalP-noTM
gi_188519857_gb_ACD57802.1_	0.197	26	0.193	26	0.369	22	0.219	0.205	N	0.57	SignalP-noTM
gi_188519860_gb_ACD57805.1_	0.261	28	0.339	28	0.649	13	0.519	0.423	N	0.57	SignalP-noTM
gi_188519861_gb_ACD57806.1_	0.135	36	0.147	18	0.269	9	0.201	0.172	N	0.57	SignalP-noTM
gi_188519862_gb_ACD57807.1_	0.174	62	0.135	62	0.184	51	0.098	0.118	N	0.57	SignalP-noTM
gi_188519867_gb_ACD57812.1_	0.133	22	0.158	22	0.292	11	0.194	0.175	N	0.57	SignalP-noTM
gi_188519870_gb_ACD57815.1_	0.188	31	0.153	31	0.186	26	0.128	0.141	N	0.57	SignalP-noTM
gi_188519871_gb_ACD57816.1_	0.157	18	0.125	18	0.117	18	0.097	0.112	N	0.57	SignalP-noTM
gi_188519881_gb_ACD57826.1_	0.117	67	0.105	67	0.106	69	0.077	0.092	N	0.57	SignalP-noTM
gi_188519882_gb_ACD57827.1_	0.168	21	0.143	21	0.172	20	0.116	0.13	N	0.57	SignalP-noTM
gi_188519883_gb_ACD57828.1_	0.115	32	0.128	13	0.193	2	0.167	0.146	N	0.57	SignalP-noTM
gi_188519884_gb_ACD57829.1_	0.17	18	0.128	18	0.238	26	0.102	0.116	N	0.57	SignalP-noTM
gi_188519885_gb_ACD57830.1_	0.102	48	0.104	29	0.133	1	0.096	0.1	N	0.57	SignalP-noTM
gi_188519890_gb_ACD57835.1_	0.143	25	0.16	23	0.338	18	0.188	0.173	N	0.57	SignalP-noTM

0.10011	0.055619	0.102569	0.086099	gi_188519734_gb_ACD57679.1_
0.128869	0.004918	0.134005	0.089264	gi_188519739_gb_ACD57684.1_
0.117222	0.022118	0.106215	0.081852	gi_188519741_gb_ACD57686.1_
0.198611	0.176681	0.262116	0.212469	gi_188519742_gb_ACD57687.1_
0.191545	0.243977	0.147795	0.194439	gi_188519743_gb_ACD57688.1_
0.913805	0.945936	0.863539	0.90776	gi_188519744_gb_ACD57689.1_
0.114762	0.001227	0.154335	0.090108	gi_188519745_gb_ACD57690.1_
0.135404	0.002023	0.208829	0.115419	gi_188519746_gb_ACD57691.1_
0.089806	0.793147	0.168541	0.350498	gi_188519747_gb_ACD57692.1_
0.074055	0.047426	0.132964	0.084815	gi_188519748_gb_ACD57693.1_
0.143687	0.057704	0.185579	0.12899	gi_188519749_gb_ACD57694.1_
0.127194	0.228289	0.112946	0.156143	gi_188519750_gb_ACD57695.1_
0.114153	0.001866	0.156699	0.090906	gi_188519751_gb_ACD57696.1_
0.291523	0.977882	0.334033	0.534479	gi_188519752_gb_ACD57697.1_
0.075718	0.031954	0.124553	0.077408	gi_188519753_gb_ACD57698.1_
0.541901	0.031861	0.574443	0.382735	gi_188519754_gb_ACD57699.1_
0.05869	0.074468	0.080691	0.071283	gi_188519755_gb_ACD57700.1_
0.757128	0.358473	0.823755	0.646452	gi_188519757_gb_ACD57702.1_
0.085724	0.016286	0.110563	0.070858	gi_188519758_gb_ACD57703.1_
0.080468	0.034059	0.117845	0.077457	gi_188519759_gb_ACD57704.1_
0.105647	0.031768	0.112346	0.083254	gi_188519760_gb_ACD57705.1_
0.804711	0.980449	0.733802	0.839654	gi_188519761_gb_ACD57706.1_
0.105081	0.00277	0.143687	0.083846	gi_188519765_gb_ACD57710.1_
0.960189	0.998625	0.910438	0.956417	gi_188519766_gb_ACD57711.1_
0.171079	0.245641	0.405886	0.274202	gi_188519768_gb_ACD57713.1_
0.058525	0.032704	0.115067	0.068765	gi_188519770_gb_ACD57715.1_
0.336708	0.281709	0.523982	0.3808	gi_188519772_gb_ACD57717.1_
0.10011	0.036827	0.077415	0.071451	gi_188519773_gb_ACD57718.1_
0.209325	0.211318	0.195761	0.205468	gi_188519774_gb_ACD57719.1_
0.196708	0.242872	0.17023	0.20327	gi_188519776_gb_ACD57721.1_
0.145916	0.13331	0.163557	0.147594	gi_188519777_gb_ACD57722.1_
0.228289	0.938255	0.136815	0.434453	gi_188519779_gb_ACD57724.1_
0.183322	0.203915	0.137881	0.175039	gi_188519780_gb_ACD57725.1_
0.136815	0.08181	0.118784	0.11247	gi_188519781_gb_ACD57726.1_
0.953779	0.95996	0.903086	0.938942	gi_188519785_gb_ACD57730.1_
0.762602	0.280496	0.763687	0.602262	gi_188519786_gb_ACD57731.1_
0.122282	0.049784	0.20538	0.125815	gi_188519788_gb_ACD57733.1_
0.30789	0.587587	0.338721	0.411399	gi_188519789_gb_ACD57734.1_
0.803292	0.714634	0.868756	0.795561	gi_188519792_gb_ACD57737.1_
0.617748	0.983617	0.488752	0.696706	gi_188519796_gb_ACD57741.1_
0.144798	0.089562	0.132964	0.122441	gi_188519800_gb_ACD57745.1_
0.108806	0.919532	0.083173	0.370504	gi_188519801_gb_ACD57746.1_
0.17023	0.045826	0.159896	0.125317	gi_188519802_gb_ACD57747.1_
0.772767	0.399392	0.681788	0.617982	gi_188519809_gb_ACD57754.1_
0.151228	0.799953	0.074261	0.341814	gi_188519810_gb_ACD57755.1_
0.153553	0.560453	0.0985	0.270835	gi_188519811_gb_ACD57756.1_
0.128196	0.07806	0.169806	0.125354	gi_188519815_gb_ACD57760.1_
0.891485	0.266198	0.881216	0.679633	gi_188519816_gb_ACD57761.1_
0.21032	0.043025	0.256355	0.1699	gi_188519817_gb_ACD57762.1_
0.109681	0.053454	0.136108	0.099748	gi_188519818_gb_ACD57763.1_
0.085959	0.139314	0.156303	0.127192	gi_188519819_gb_ACD57764.1_
0.092793	0.304068	0.113548	0.170136	gi_188519820_gb_ACD57765.1_
0.088105	0.031129	0.181087	0.100107	gi_188519821_gb_ACD57766.1_
0.128869	0.538921	0.096651	0.254814	gi_188519822_gb_ACD57767.1_
0.156699	0.324098	0.11847	0.199756	gi_188519832_gb_ACD57777.1_
0.16645	0.112645	0.142583	0.140559	gi_188519833_gb_ACD57778.1_
0.620578	0.640837	0.771711	0.677709	gi_188519834_gb_ACD57779.1_
0.312383	0.740775	0.391503	0.481554	gi_188519835_gb_ACD57780.1_
0.411686	0.64497	0.553791	0.536816	gi_188519836_gb_ACD57781.1_
0.07635	0.033375	0.119098	0.076274	gi_188519838_gb_ACD57783.1_
0.21687	0.961543	0.074468	0.417627	gi_188519839_gb_ACD57784.1_
0.164379	0.140397	0.141122	0.148633	gi_188519840_gb_ACD57785.1_
0.219428	0.49325	0.284754	0.332477	gi_188519848_gb_ACD57793.1_
0.167702	0.143318	0.335369	0.215463	gi_188519854_gb_ACD57799.1_
0.202458	0.867036	0.105364	0.391619	gi_188519856_gb_ACD57801.1_
0.194818	0.156303	0.23308	0.194734	gi_188519857_gb_ACD57802.1_
0.311739	0.754359	0.120045	0.395381	gi_188519860_gb_ACD57805.1_
0.159896	0.036721	0.181532	0.12605	gi_188519861_gb_ACD57806.1_
0.047834	0.015398	0.103123	0.055452	gi_188519862_gb_ACD57807.1_
0.743073	0.841309	0.827213	0.803865	gi_188519867_gb_ACD57812.1_
0.951754	0.971887	0.906192	0.943278	gi_188519870_gb_ACD57815.1_
0.90361	0.993294	0.849156	0.915353	gi_188519871_gb_ACD57816.1_
0.121319	0.091788	0.117845	0.110317	gi_188519881_gb_ACD57826.1_
0.486503	0.850306	0.530711	0.622507	gi_188519882_gb_ACD57827.1_
0.927169	0.947	0.877396	0.917188	gi_188519883_gb_ACD57828.1_
0.906701	0.861045	0.933018	0.900255	gi_188519884_gb_ACD57829.1_
0.075508	0.042411	0.097704	0.071874	gi_188519885_gb_ACD57830.1_
0.104518	0.055619	0.138955	0.099697	gi_188519890_gb_ACD57835.1_

gi_188519891_gb_ACD57836.1_	0.116	63	0.125	20	0.187	17	0.124	0.125	N	0.57	SignalP-noTM
gi_188519892_gb_ACD57837.1_	0.168	22	0.137	22	0.173	32	0.111	0.127	N	0.51	SignalP-TM
gi_188519896_gb_ACD57841.1_	0.164	33	0.105	18	0.153	15	0.108	0.106	N	0.51	SignalP-TM
gi_188519897_gb_ACD57842.1_	0.254	21	0.221	21	0.262	20	0.18	0.206	N	0.51	SignalP-TM
gi_188519900_gb_ACD57845.1_	0.202	24	0.152	24	0.152	23	0.109	0.132	N	0.57	SignalP-noTM
gi_188519901_gb_ACD57846.1_	0.131	15	0.169	15	0.362	27	0.212	0.189	N	0.57	SignalP-noTM
gi_188519902_gb_ACD57847.1_	0.702	33	0.785	33	0.973	23	0.887	0.833	Y	0.57	SignalP-noTM
gi_188519903_gb_ACD57848.1_	0.1	26	0.133	13	0.219	3	0.179	0.155	N	0.57	SignalP-noTM
gi_188519904_gb_ACD57849.1_	0.425	20	0.608	20	0.962	18	0.863	0.728	Y	0.57	SignalP-noTM
gi_188519907_gb_ACD57852.1_	0.718	26	0.824	26	0.985	16	0.952	0.885	Y	0.57	SignalP-noTM
gi_188519910_gb_ACD57855.1_	0.153	51	0.136	70	0.189	6	0.104	0.124	N	0.51	SignalP-TM
gi_188519911_gb_ACD57856.1_	0.66	21	0.801	21	0.987	19	0.966	0.879	Y	0.57	SignalP-noTM
gi_188519912_gb_ACD57857.1_	0.117	67	0.153	22	0.281	17	0.213	0.181	N	0.57	SignalP-noTM
gi_188519913_gb_ACD57858.1_	0.122	35	0.126	30	0.166	3	0.125	0.126	N	0.51	SignalP-TM
gi_188519919_gb_ACD57864.1_	0.204	12	0.26	12	0.475	8	0.34	0.298	N	0.57	SignalP-noTM
gi_188519920_gb_ACD57865.1_	0.178	23	0.375	23	0.922	4	0.837	0.592	Y	0.57	SignalP-noTM
gi_188519921_gb_ACD57866.1_	0.171	29	0.144	29	0.199	26	0.122	0.134	N	0.57	SignalP-noTM
gi_188519922_gb_ACD57867.1_	0.118	22	0.109	47	0.155	8	0.106	0.108	N	0.57	SignalP-noTM
gi_188519923_gb_ACD57868.1_	0.124	22	0.105	22	0.123	20	0.082	0.094	N	0.57	SignalP-noTM
gi_188519924_gb_ACD57869.1_	0.424	19	0.255	19	0.201	16	0.139	0.201	N	0.57	SignalP-noTM
gi_188519925_gb_ACD57870.1_	0.184	31	0.266	22	0.613	20	0.375	0.317	N	0.57	SignalP-noTM
gi_188519926_gb_ACD57871.1_	0.107	19	0.108	11	0.158	3	0.119	0.113	N	0.57	SignalP-noTM
gi_188519927_gb_ACD57872.1_	0.115	26	0.122	12	0.154	8	0.133	0.126	N	0.51	SignalP-TM
gi_188519928_gb_ACD57873.1_	0.227	21	0.164	21	0.212	1	0.132	0.149	N	0.57	SignalP-noTM
gi_188519929_gb_ACD57874.1_	0.141	21	0.198	21	0.411	12	0.279	0.236	N	0.57	SignalP-noTM
gi_188519930_gb_ACD57875.1_	0.474	22	0.369	22	0.597	2	0.354	0.362	N	0.57	SignalP-noTM
gi_188519931_gb_ACD57876.1_	0.163	28	0.137	46	0.201	40	0.114	0.126	N	0.57	SignalP-noTM
gi_188519932_gb_ACD57877.1_	0.141	27	0.184	51	0.52	41	0.146	0.166	N	0.57	SignalP-noTM
gi_188519933_gb_ACD57878.1_	0.112	36	0.163	20	0.336	15	0.234	0.196	N	0.57	SignalP-noTM
gi_188519934_gb_ACD57879.1_	0.127	37	0.122	37	0.177	36	0.098	0.111	N	0.57	SignalP-noTM
gi_188519935_gb_ACD57880.1_	0.109	26	0.144	12	0.255	7	0.207	0.173	N	0.57	SignalP-noTM
gi_188519936_gb_ACD57881.1_	0.104	58	0.118	13	0.172	9	0.14	0.128	N	0.57	SignalP-noTM
gi_188519937_gb_ACD57882.1_	0.118	25	0.111	11	0.196	2	0.117	0.114	N	0.57	SignalP-noTM
gi_188519940_gb_ACD57885.1_	0.115	42	0.163	23	0.341	17	0.222	0.191	N	0.57	SignalP-noTM
gi_188519941_gb_ACD57886.1_	0.101	17	0.125	11	0.219	2	0.152	0.137	N	0.57	SignalP-noTM
gi_188519942_gb_ACD57887.1_	0.204	32	0.153	32	0.153	1	0.122	0.139	N	0.57	SignalP-noTM
gi_188519943_gb_ACD57888.1_	0.124	21	0.114	11	0.158	3	0.132	0.122	N	0.57	SignalP-noTM
gi_188519944_gb_ACD57889.1_	0.118	41	0.118	11	0.162	3	0.14	0.128	N	0.57	SignalP-noTM
gi_188519945_gb_ACD57890.1_	0.179	29	0.16	11	0.335	1	0.25	0.202	N	0.57	SignalP-noTM
gi_188519946_gb_ACD57891.1_	0.108	23	0.134	51	0.243	45	0.109	0.122	N	0.57	SignalP-noTM
gi_188519947_gb_ACD57892.1_	0.151	59	0.118	59	0.187	3	0.104	0.112	N	0.57	SignalP-noTM
gi_188519948_gb_ACD57893.1_	0.128	51	0.107	51	0.129	1	0.086	0.097	N	0.57	SignalP-noTM
gi_188519949_gb_ACD57894.1_	0.122	41	0.182	17	0.43	14	0.323	0.248	N	0.57	SignalP-noTM
gi_188519950_gb_ACD57895.1_	0.101	32	0.109	50	0.137	41	0.091	0.101	N	0.57	SignalP-noTM
gi_188519951_gb_ACD57896.1_	0.157	52	0.125	11	0.212	1	0.151	0.137	N	0.57	SignalP-noTM
gi_188519952_gb_ACD57897.1_	0.173	31	0.137	31	0.161	29	0.098	0.118	N	0.57	SignalP-noTM
gi_188519953_gb_ACD57898.1_	0.111	52	0.104	39	0.115	8	0.103	0.103	N	0.57	SignalP-noTM
gi_188519954_gb_ACD57899.1_	0.13	27	0.13	27	0.168	1	0.132	0.131	N	0.57	SignalP-noTM
gi_188519955_gb_ACD57900.1_	0.115	39	0.114	11	0.196	2	0.13	0.122	N	0.57	SignalP-noTM
gi_188519956_gb_ACD57901.1_	0.11	30	0.117	30	0.218	1	0.116	0.117	N	0.57	SignalP-noTM
gi_188519957_gb_ACD57902.1_	0.116	23	0.105	37	0.115	20	0.087	0.097	N	0.57	SignalP-noTM
gi_188519958_gb_ACD57903.1_	0.165	59	0.197	21	0.415	14	0.313	0.252	N	0.57	SignalP-noTM
gi_188519959_gb_ACD57904.1_	0.105	3	0.119	25	0.154	18	0.127	0.122	N	0.57	SignalP-noTM
gi_188519960_gb_ACD57905.1_	0.11	3	0.156	11	0.37	2	0.244	0.197	N	0.57	SignalP-noTM
gi_188519961_gb_ACD57906.1_	0.104	43	0.117	14	0.164	8	0.136	0.126	N	0.57	SignalP-noTM
gi_188519962_gb_ACD57907.1_	0.113	5	0.102	58	0.126	37	0.096	0.1	N	0.51	SignalP-TM
gi_188519963_gb_ACD57908.1_	0.102	14	0.111	14	0.195	2	0.122	0.117	N	0.57	SignalP-noTM
gi_188519964_gb_ACD57909.1_	0.116	27	0.164	11	0.336	2	0.272	0.215	N	0.57	SignalP-noTM
gi_188519965_gb_ACD57910.1_	0.152	28	0.122	28	0.201	1	0.115	0.119	N	0.57	SignalP-noTM
gi_188519966_gb_ACD57911.1_	0.164	56	0.143	56	0.279	54	0.12	0.132	N	0.57	SignalP-noTM
gi_188519967_gb_ACD57912.1_	0.113	26	0.182	17	0.431	13	0.309	0.242	N	0.57	SignalP-noTM
gi_188519971_gb_ACD57916.1_	0.175	33	0.15	33	0.225	32	0.115	0.134	N	0.57	SignalP-noTM
gi_188519972_gb_ACD57917.1_	0.106	6	0.122	42	0.173	41	0.115	0.118	N	0.57	SignalP-noTM
gi_188519974_gb_ACD57919.1_	0.119	30	0.107	30	0.171	1	0.088	0.098	N	0.57	SignalP-noTM
gi_188519983_gb_ACD57928.1_	0.566	43	0.303	43	0.28	40	0.158	0.235	N	0.57	SignalP-noTM
gi_188519984_gb_ACD57929.1_	0.112	54	0.12	19	0.179	12	0.14	0.128	N	0.51	SignalP-TM
gi_188519985_gb_ACD57930.1_	0.137	40	0.219	17	0.512	9	0.403	0.305	N	0.57	SignalP-noTM
gi_188519986_gb_ACD57931.1_	0.104	38	0.116	13	0.151	1	0.133	0.124	N	0.57	SignalP-noTM
gi_188519991_gb_ACD57936.1_	0.118	41	0.104	69	0.114	3	0.088	0.097	N	0.57	SignalP-noTM
gi_188519992_gb_ACD57937.1_	0.15	21	0.218	21	0.372	13	0.306	0.251	N	0.51	SignalP-TM
gi_188520000_gb_ACD57945.1_	0.124	53	0.115	53	0.13	68	0.075	0.1	N	0.51	SignalP-TM
gi_188520001_gb_ACD57946.1_	0.176	34	0.137	34	0.22	3	0.118	0.128	N	0.57	SignalP-noTM
gi_188520002_gb_ACD57947.1_	0.133	33	0.124	33	0.182	1	0.096	0.114	N	0.51	SignalP-TM
gi_188520003_gb_ACD57948.1_	0.226	33	0.344	33	0.771	21	0.53	0.413	N	0.51	SignalP-TM
gi_188520004_gb_ACD57949.1_	0.118	26	0.108	42	0.148	32	0.092	0.1	N	0.57	SignalP-noTM
gi_188520009_gb_ACD57954.1_	0.135	41	0.181	11	0.511	1	0.304	0.239	N	0.57	SignalP-noTM
gi_188520011_gb_ACD57956.1_	0.153	26	0.12	26	0.137	1	0.097	0.109	N	0.57	SignalP-noTM
gi_188520013_gb_ACD57958.1_	0.126	30	0.128	30	0.235	1	0.112	0.122	N	0.51	SignalP-TM

0.163557	0.014994	0.202458	0.127003	gi_188519891_gb_ACD57836.1_
0.083862	0.061399	0.0985	0.081254	gi_188519892_gb_ACD57837.1_
0.059023	0.002378	0.086907	0.049436	gi_188519896_gb_ACD57841.1_
0.067926	0.262697	0.149313	0.159979	gi_188519897_gb_ACD57842.1_
0.062444	0.10147	0.090052	0.084655	gi_188519900_gb_ACD57845.1_
0.136108	0.032233	0.188314	0.118885	gi_188519901_gb_ACD57846.1_
0.960985	0.999686	0.920195	0.960289	gi_188519902_gb_ACD57847.1_
0.774343	0.984373	0.834381	0.864366	gi_188519903_gb_ACD57848.1_
0.955976	0.989271	0.915212	0.953486	gi_188519904_gb_ACD57849.1_
0.954566	0.974169	0.902824	0.943853	gi_188519907_gb_ACD57852.1_
0.204891	0.181979	0.215853	0.200908	gi_188519910_gb_ACD57855.1_
0.890319	0.990613	0.875773	0.918902	gi_188519911_gb_ACD57856.1_
0.930539	0.987666	0.912616	0.943607	gi_188519912_gb_ACD57857.1_
0.162329	0.049219	0.203915	0.138488	gi_188519913_gb_ACD57858.1_
0.193411	0.159494	0.177994	0.176966	gi_188519919_gb_ACD57864.1_
0.842108	0.318863	0.884321	0.681764	gi_188519920_gb_ACD57865.1_
0.11847	0.050787	0.148932	0.106063	gi_188519921_gb_ACD57866.1_
0.099302	0.057216	0.113247	0.089922	gi_188519922_gb_ACD57867.1_
0.088105	0.983761	0.107072	0.392979	gi_188519923_gb_ACD57868.1_
0.072628	0.007013	0.095609	0.058417	gi_188519924_gb_ACD57869.1_
0.07024	0.003861	0.089806	0.054636	gi_188519925_gb_ACD57870.1_
0.057055	0.00455	0.074261	0.045289	gi_188519926_gb_ACD57871.1_
0.191081	0.138596	0.154727	0.161468	gi_188519927_gb_ACD57872.1_
0.086907	0.080247	0.06985	0.079001	gi_188519928_gb_ACD57873.1_
0.955212	0.999499	0.889141	0.947951	gi_188519929_gb_ACD57874.1_
0.957467	0.999952	0.916827	0.958082	gi_188519930_gb_ACD57875.1_
0.204403	0.002011	0.351603	0.186006	gi_188519931_gb_ACD57876.1_
0.23041	0.144056	0.248431	0.207632	gi_188519932_gb_ACD57877.1_
0.075718	0.059861	0.089074	0.074884	gi_188519933_gb_ACD57878.1_
0.075299	0.067547	0.080247	0.074364	gi_188519934_gb_ACD57879.1_
0.948632	0.674586	0.873471	0.83223	gi_188519935_gb_ACD57880.1_
0.359163	0.861045	0.570036	0.596748	gi_188519936_gb_ACD57881.1_
0.110563	0.053911	0.16645	0.110308	gi_188519937_gb_ACD57882.1_
0.109097	0.040973	0.130903	0.093658	gi_188519940_gb_ACD57885.1_
0.133658	0.055148	0.075718	0.088175	gi_188519941_gb_ACD57886.1_
0.799953	0.98096	0.733802	0.838238	gi_188519942_gb_ACD57887.1_
0.38509	0.506	0.527722	0.472937	gi_188519943_gb_ACD57888.1_
0.76959	0.802818	0.898256	0.823555	gi_188519944_gb_ACD57889.1_
0.735557	0.681137	0.710333	0.709009	gi_188519945_gb_ACD57890.1_
0.816678	0.981513	0.612065	0.803419	gi_188519946_gb_ACD57891.1_
0.265027	0.107936	0.232009	0.201657	gi_188519947_gb_ACD57892.1_
0.155907	0.929169	0.084324	0.3898	gi_188519948_gb_ACD57893.1_
0.339393	0.813513	0.515745	0.556217	gi_188519949_gb_ACD57894.1_
0.225133	0.675244	0.136461	0.345613	gi_188519950_gb_ACD57895.1_
0.882778	0.846836	0.882467	0.870694	gi_188519951_gb_ACD57896.1_
0.135404	0.222527	0.098234	0.152055	gi_188519952_gb_ACD57897.1_
0.69147	0.019096	0.526226	0.412264	gi_188519953_gb_ACD57898.1_
0.245641	0.85371	0.260957	0.453436	gi_188519954_gb_ACD57899.1_
0.784654	0.379422	0.809844	0.657973	gi_188519955_gb_ACD57900.1_
0.082489	0.002795	0.103679	0.062988	gi_188519956_gb_ACD57901.1_
0.594837	0.897707	0.589766	0.694103	gi_188519957_gb_ACD57902.1_
0.348872	0.729088	0.363316	0.480425	gi_188519958_gb_ACD57903.1_
0.510498	0.455121	0.741351	0.56899	gi_188519959_gb_ACD57904.1_
0.267371	0.0488	0.440286	0.252152	gi_188519960_gb_ACD57905.1_
0.852205	0.723122	0.786171	0.787166	gi_188519961_gb_ACD57906.1_
0.087624	0.051809	0.17581	0.105081	gi_188519962_gb_ACD57907.1_
0.225133	0.987955	0.071226	0.428105	gi_188519963_gb_ACD57908.1_
0.936136	0.819801	0.916598	0.890845	gi_188519964_gb_ACD57909.1_
0.842108	0.618456	0.874462	0.778342	gi_188519965_gb_ACD57910.1_
0.069267	0.043025	0.073645	0.061979	gi_188519966_gb_ACD57911.1_
0.202943	0.822445	0.077845	0.367744	gi_188519967_gb_ACD57912.1_
0.150077	0.196234	0.26386	0.20339	gi_188519971_gb_ACD57916.1_
0.186943	0.375897	0.094319	0.219053	gi_188519972_gb_ACD57917.1_
0.119413	0.213325	0.079585	0.137441	gi_188519974_gb_ACD57919.1_
0.151228	0.02886	0.161921	0.114003	gi_188519983_gb_ACD57928.1_
0.21687	0.082036	0.179314	0.159407	gi_188519984_gb_ACD57929.1_
0.164379	0.092793	0.203915	0.153696	gi_188519985_gb_ACD57930.1_
0.164792	0.05836	0.185126	0.136093	gi_188519986_gb_ACD57931.1_
0.130222	0.033278	0.136815	0.100105	gi_188519991_gb_ACD57936.1_
0.099571	0.059189	0.125868	0.094876	gi_188519992_gb_ACD57937.1_
0.131587	0.067547	0.164379	0.121171	gi_188520000_gb_ACD57945.1_
0.082716	0.014344	0.113548	0.070203	gi_188520001_gb_ACD57946.1_
0.905937	0.871804	0.859965	0.879235	gi_188520002_gb_ACD57947.1_
0.10147	0.101197	0.21738	0.140016	gi_188520003_gb_ACD57948.1_
0.186487	0.467795	0.108806	0.254363	gi_188520004_gb_ACD57949.1_
0.079365	0.039696	0.111155	0.076739	gi_188520009_gb_ACD57954.1_
0.296504	0.985356	0.06054	0.447467	gi_188520011_gb_ACD57956.1_
0.152775	0.042168	0.119413	0.104785	gi_188520013_gb_ACD57958.1_

gi_188520014_gb_ACD57959.1_	0.108	46	0.109	26	0.144	21	0.101	0.105	N	0.57	SignalP-noTM
gi_188520015_gb_ACD57960.1_	0.14	68	0.168	11	0.403	1	0.273	0.207	N	0.51	SignalP-TM
gi_188520016_gb_ACD57961.1_	0.12	32	0.153	13	0.296	1	0.213	0.175	N	0.51	SignalP-TM
gi_188520017_gb_ACD57962.1_	0.139	25	0.126	25	0.163	5	0.124	0.125	N	0.57	SignalP-noTM
gi_188520018_gb_ACD57963.1_	0.393	25	0.617	25	0.99	17	0.948	0.772	Y	0.57	SignalP-noTM
gi_188520020_gb_ACD57965.1_	0.154	46	0.117	46	0.123	1	0.092	0.106	N	0.57	SignalP-noTM
gi_188520021_gb_ACD57966.1_	0.124	20	0.12	42	0.177	1	0.12	0.12	N	0.57	SignalP-noTM
gi_188520023_gb_ACD57968.1_	0.11	19	0.104	28	0.129	17	0.089	0.097	N	0.57	SignalP-noTM
gi_188520025_gb_ACD57970.1_	0.11	28	0.109	28	0.15	26	0.094	0.102	N	0.57	SignalP-noTM
gi_188520028_gb_ACD57973.1_	0.133	45	0.103	45	0.106	64	0.077	0.091	N	0.57	SignalP-noTM
gi_188520030_gb_ACD57975.1_	0.109	28	0.121	41	0.238	38	0.122	0.122	N	0.57	SignalP-noTM
gi_188520032_gb_ACD57977.1_	0.198	62	0.264	19	0.513	17	0.337	0.291	N	0.51	SignalP-TM
gi_188520033_gb_ACD57978.1_	0.14	22	0.132	11	0.264	1	0.159	0.144	N	0.57	SignalP-noTM
gi_188520034_gb_ACD57979.1_	0.126	38	0.111	38	0.122	36	0.086	0.099	N	0.57	SignalP-noTM
gi_188520035_gb_ACD57980.1_	0.142	44	0.123	44	0.213	2	0.121	0.122	N	0.57	SignalP-noTM
gi_188520037_gb_ACD57982.1_	0.133	22	0.158	22	0.292	11	0.194	0.175	N	0.57	SignalP-noTM
gi_188520039_gb_ACD57984.1_	0.104	40	0.137	11	0.275	3	0.197	0.165	N	0.57	SignalP-noTM
gi_188520040_gb_ACD57985.1_	0.1	10	0.11	36	0.18	1	0.102	0.107	N	0.57	SignalP-noTM
gi_188520046_gb_ACD57991.1_	0.222	50	0.35	42	0.801	37	0.354	0.352	N	0.51	SignalP-TM
gi_188520047_gb_ACD57992.1_	0.103	52	0.114	36	0.187	1	0.107	0.11	N	0.57	SignalP-noTM
gi_188520052_gb_ACD57997.1_	0.132	40	0.123	11	0.184	1	0.146	0.134	N	0.57	SignalP-noTM
gi_188520053_gb_ACD57998.1_	0.102	21	0.123	11	0.251	2	0.143	0.132	N	0.57	SignalP-noTM
gi_188520054_gb_ACD57999.1_	0.267	18	0.332	18	0.592	2	0.448	0.375	N	0.51	SignalP-TM
gi_188520055_gb_ACD58000.1_	0.275	28	0.158	28	0.153	3	0.088	0.125	N	0.57	SignalP-noTM
gi_188520056_gb_ACD58001.1_	0.168	51	0.16	11	0.45	7	0.286	0.219	N	0.57	SignalP-noTM
gi_188520057_gb_ACD58002.1_	0.117	32	0.178	19	0.361	10	0.263	0.218	N	0.57	SignalP-noTM
gi_188520063_gb_ACD58008.1_	0.113	44	0.142	11	0.27	4	0.2	0.169	N	0.57	SignalP-noTM
gi_188520069_gb_ACD58014.1_	0.104	48	0.106	38	0.126	37	0.089	0.098	N	0.57	SignalP-noTM
gi_188520070_gb_ACD58015.1_	0.11	36	0.148	11	0.3	3	0.218	0.181	N	0.57	SignalP-noTM
gi_188520074_gb_ACD58019.1_	0.122	18	0.108	18	0.114	4	0.098	0.103	N	0.57	SignalP-noTM
gi_188520075_gb_ACD58020.1_	0.113	28	0.124	51	0.287	48	0.112	0.118	N	0.57	SignalP-noTM
gi_188520076_gb_ACD58021.1_	0.251	31	0.16	31	0.154	30	0.086	0.125	N	0.57	SignalP-noTM
gi_188520077_gb_ACD58022.1_	0.411	21	0.358	21	0.512	16	0.275	0.319	N	0.57	SignalP-noTM
gi_188520078_gb_ACD58023.1_	0.115	25	0.101	21	0.107	41	0.076	0.089	N	0.57	SignalP-noTM
gi_188520079_gb_ACD58024.1_	0.119	38	0.108	51	0.129	50	0.087	0.098	N	0.57	SignalP-noTM
gi_188520082_gb_ACD58027.1_	0.106	13	0.116	19	0.226	12	0.113	0.115	N	0.57	SignalP-noTM
gi_188520083_gb_ACD58028.1_	0.157	33	0.12	21	0.225	10	0.116	0.118	N	0.57	SignalP-noTM
gi_188520085_gb_ACD58030.1_	0.134	25	0.226	11	0.641	3	0.502	0.356	N	0.57	SignalP-noTM
gi_188520086_gb_ACD58031.1_	0.156	33	0.203	21	0.398	15	0.284	0.241	N	0.57	SignalP-noTM
gi_188520087_gb_ACD58032.1_	0.119	23	0.164	12	0.37	4	0.277	0.217	N	0.57	SignalP-noTM
gi_188520088_gb_ACD58033.1_	0.166	61	0.127	61	0.125	40	0.086	0.107	N	0.57	SignalP-noTM
gi_188520089_gb_ACD58034.1_	0.114	19	0.113	11	0.152	2	0.122	0.118	N	0.57	SignalP-noTM
gi_188520090_gb_ACD58035.1_	0.187	27	0.123	27	0.168	38	0.087	0.106	N	0.57	SignalP-noTM
gi_188520091_gb_ACD58036.1_	0.107	41	0.109	24	0.132	3	0.114	0.112	N	0.57	SignalP-noTM
gi_188520093_gb_ACD58038.1_	0.111	30	0.115	55	0.167	53	0.122	0.118	N	0.57	SignalP-noTM
gi_188520096_gb_ACD58041.1_	0.102	58	0.097	58	0.105	10	0.089	0.093	N	0.57	SignalP-noTM
gi_188520099_gb_ACD58044.1_	0.14	45	0.153	45	0.228	43	0.147	0.15	N	0.57	SignalP-noTM
gi_188520102_gb_ACD58047.1_	0.63	24	0.763	24	0.946	22	0.913	0.833	Y	0.57	SignalP-noTM
gi_188520103_gb_ACD58048.1_	0.14	20	0.202	11	0.55	1	0.386	0.289	N	0.57	SignalP-noTM
gi_188520104_gb_ACD58049.1_	0.101	41	0.099	11	0.152	1	0.091	0.095	N	0.57	SignalP-noTM
gi_188520105_gb_ACD58050.1_	0.116	25	0.176	11	0.371	9	0.307	0.237	N	0.57	SignalP-noTM
gi_188520106_gb_ACD58051.1_	0.105	42	0.108	51	0.137	18	0.099	0.104	N	0.57	SignalP-noTM
gi_188520107_gb_ACD58052.1_	0.117	28	0.116	28	0.15	1	0.097	0.109	N	0.51	SignalP-TM
gi_188520108_gb_ACD58053.1_	0.207	37	0.145	17	0.266	3	0.17	0.154	N	0.51	SignalP-TM
gi_188520109_gb_ACD58054.1_	0.144	16	0.202	16	0.348	11	0.283	0.232	N	0.51	SignalP-TM
gi_188520110_gb_ACD58055.1_	0.129	34	0.135	11	0.213	8	0.183	0.157	N	0.57	SignalP-noTM
gi_188520111_gb_ACD58056.1_	0.183	17	0.191	17	0.272	14	0.195	0.193	N	0.57	SignalP-noTM
gi_188520112_gb_ACD58057.1_	0.132	18	0.158	18	0.278	14	0.183	0.17	N	0.57	SignalP-noTM
gi_188520113_gb_ACD58058.1_	0.109	56	0.113	25	0.148	49	0.102	0.108	N	0.57	SignalP-noTM
gi_188520114_gb_ACD58059.1_	0.113	22	0.124	12	0.207	6	0.158	0.14	N	0.57	SignalP-noTM
gi_188520115_gb_ACD58060.1_	0.172	20	0.246	20	0.515	11	0.331	0.286	N	0.57	SignalP-noTM
gi_188520116_gb_ACD58061.1_	0.657	24	0.737	24	0.928	10	0.859	0.783	Y	0.51	SignalP-TM
gi_188520117_gb_ACD58062.1_	0.136	41	0.139	13	0.299	11	0.169	0.153	N	0.57	SignalP-noTM
gi_188520118_gb_ACD58063.1_	0.277	33	0.179	33	0.167	32	0.109	0.146	N	0.57	SignalP-noTM
gi_188520123_gb_ACD58068.1_	0.125	34	0.13	12	0.216	32	0.178	0.148	N	0.51	SignalP-TM
gi_188520124_gb_ACD58069.1_	0.127	26	0.226	26	0.575	20	0.288	0.255	N	0.57	SignalP-noTM
gi_188520128_gb_ACD58073.1_	0.143	37	0.213	12	0.624	1	0.413	0.307	N	0.57	SignalP-noTM
gi_188520131_gb_ACD58076.1_	0.11	35	0.108	11	0.154	2	0.115	0.111	N	0.57	SignalP-noTM
gi_188520132_gb_ACD58077.1_	0.114	38	0.101	25	0.122	23	0.098	0.099	N	0.57	SignalP-noTM
gi_188520133_gb_ACD58078.1_	0.167	27	0.18	11	0.399	2	0.333	0.237	N	0.51	SignalP-TM
gi_188520134_gb_ACD58079.1_	0.158	25	0.21	25	0.617	10	0.326	0.264	N	0.57	SignalP-noTM
gi_188520135_gb_ACD58080.1_	0.195	31	0.281	31	0.521	23	0.329	0.299	N	0.51	SignalP-TM
gi_188520141_gb_ACD58086.1_	0.228	18	0.208	18	0.243	6	0.193	0.201	N	0.57	SignalP-noTM
gi_188520142_gb_ACD58087.1_	0.177	49	0.147	49	0.195	4	0.126	0.139	N	0.51	SignalP-TM
gi_188520143_gb_ACD58088.1_	0.176	32	0.13	32	0.112	14	0.09	0.111	N	0.57	SignalP-noTM
gi_188520144_gb_ACD58089.1_	0.151	21	0.15	21	0.252	1	0.161	0.155	N	0.57	SignalP-noTM
gi_188520148_gb_ACD58093.1_	0.115	31	0.107	18	0.129	6	0.111	0.109	N	0.57	SignalP-noTM
gi_188520149_gb_ACD58094.1_	0.116	52	0.128	52	0.186	47	0.12	0.124	N	0.57	SignalP-noTM

0.732041	0.321475	0.490251	0.514589	gi_188520014_gb_ACD57959.1_
0.256355	0.073237	0.339393	0.222995	gi_188520015_gb_ACD57960.1_
0.248431	0.041806	0.318863	0.203033	gi_188520016_gb_ACD57961.1_
0.141122	0.062269	0.179756	0.127716	gi_188520017_gb_ACD57962.1_
0.895201	0.513497	0.890903	0.766534	gi_188520018_gb_ACD57963.1_
0.945628	0.981403	0.907459	0.94483	gi_188520020_gb_ACD57965.1_
0.945163	0.997327	0.899348	0.947279	gi_188520021_gb_ACD57966.1_
0.881843	0.999605	0.826353	0.9026	gi_188520023_gb_ACD57968.1_
0.901766	0.99975	0.82419	0.908569	gi_188520025_gb_ACD57970.1_
0.925739	0.761514	0.899348	0.8622	gi_188520028_gb_ACD57973.1_
0.94715	0.999746	0.908462	0.951786	gi_188520030_gb_ACD57975.1_
0.9512	0.996297	0.914979	0.954159	gi_188520032_gb_ACD57977.1_
0.951339	0.99947	0.925532	0.95878	gi_188520033_gb_ACD57978.1_
0.135053	0.055462	0.114457	0.101657	gi_188520034_gb_ACD57979.1_
0.06037	0.009815	0.152	0.074062	gi_188520035_gb_ACD57980.1_
0.781597	0.867381	0.845273	0.831417	gi_188520037_gb_ACD57982.1_
0.739043	0.870456	0.463316	0.690938	gi_188520039_gb_ACD57984.1_
0.376601	0.344117	0.467048	0.395922	gi_188520040_gb_ACD57985.1_
0.893785	0.99935	0.836033	0.909723	gi_188520046_gb_ACD57991.1_
0.6972	0.214333	0.780057	0.563863	gi_188520047_gb_ACD57992.1_
0.327393	0.051515	0.400112	0.259673	gi_188520052_gb_ACD57997.1_
0.52473	0.304703	0.747061	0.525498	gi_188520053_gb_ACD57998.1_
0.07806	0.157493	0.168962	0.134838	gi_188520054_gb_ACD57999.1_
0.357094	0.988132	0.276278	0.540501	gi_188520055_gb_ACD58000.1_
0.907207	0.792654	0.846056	0.848639	gi_188520056_gb_ACD58001.1_
0.576641	0.38438	0.604918	0.52198	gi_188520057_gb_ACD58002.1_
0.806589	0.85371	0.855202	0.8385	gi_188520063_gb_ACD58008.1_
0.074261	0.039468	0.116912	0.07688	gi_188520069_gb_ACD58014.1_
0.49925	0.847613	0.655883	0.667582	gi_188520070_gb_ACD58015.1_
0.220974	0.082716	0.136108	0.146599	gi_188520074_gb_ACD58019.1_
0.10011	0.066982	0.138238	0.101777	gi_188520075_gb_ACD58020.1_
0.190618	0.516494	0.219943	0.309018	gi_188520076_gb_ACD58021.1_
0.132964	0.01473	0.124881	0.090858	gi_188520077_gb_ACD58022.1_
0.119413	0.24232	0.149313	0.170349	gi_188520078_gb_ACD58023.1_
0.114762	0.377306	0.099034	0.197034	gi_188520079_gb_ACD58024.1_
0.087384	0.036934	0.218403	0.11424	gi_188520082_gb_ACD58027.1_
0.090052	0.026909	0.134703	0.083888	gi_188520083_gb_ACD58028.1_
0.157892	0.352287	0.172359	0.227513	gi_188520085_gb_ACD58030.1_
0.091538	0.010666	0.141851	0.081352	gi_188520086_gb_ACD58031.1_
0.103679	0.031401	0.140397	0.091826	gi_188520087_gb_ACD58032.1_
0.061745	0.000992	0.096129	0.052955	gi_188520088_gb_ACD58033.1_
0.852959	0.999534	0.790178	0.88089	gi_188520089_gb_ACD58034.1_
0.247312	0.025456	0.29713	0.189966	gi_188520090_gb_ACD58035.1_
0.143687	0.054372	0.112946	0.103668	gi_188520091_gb_ACD58036.1_
0.400112	0.98016	0.581759	0.65401	gi_188520093_gb_ACD58038.1_
0.78262	0.983374	0.69147	0.819155	gi_188520096_gb_ACD58041.1_
0.138955	0.12196	0.111749	0.124221	gi_188520099_gb_ACD58044.1_
0.957832	0.907711	0.871468	0.912337	gi_188520102_gb_ACD58047.1_
0.312383	0.966722	0.44695	0.575352	gi_188520103_gb_ACD58048.1_
0.090792	0.072628	0.096651	0.08669	gi_188520104_gb_ACD58049.1_
0.927976	0.997946	0.749885	0.891936	gi_188520105_gb_ACD58050.1_
0.159896	0.174942	0.102018	0.145619	gi_188520106_gb_ACD58051.1_
0.197658	0.045695	0.132274	0.125209	gi_188520107_gb_ACD58052.1_
0.102845	0.552308	0.255784	0.303646	gi_188520108_gb_ACD58053.1_
0.132619	0.0238	0.248991	0.135137	gi_188520109_gb_ACD58054.1_
0.239577	0.31432	0.284754	0.27955	gi_188520110_gb_ACD58055.1_
0.178873	0.156699	0.174509	0.170027	gi_188520111_gb_ACD58056.1_
0.110563	0.056253	0.153553	0.10679	gi_188520112_gb_ACD58057.1_
0.092289	0.063506	0.096129	0.083975	gi_188520113_gb_ACD58058.1_
0.186032	0.397953	0.185579	0.256521	gi_188520114_gb_ACD58059.1_
0.153164	0.020674	0.203915	0.125918	gi_188520115_gb_ACD58060.1_
0.427759	0.296504	0.597005	0.440423	gi_188520116_gb_ACD58061.1_
0.893214	0.998858	0.883397	0.925156	gi_188520117_gb_ACD58062.1_
0.177118	0.178433	0.082262	0.145938	gi_188520118_gb_ACD58063.1_
0.057216	0.415324	0.126198	0.199579	gi_188520123_gb_ACD58068.1_
0.935595	0.994409	0.874462	0.934822	gi_188520124_gb_ACD58069.1_
0.140035	0.10736	0.230942	0.159446	gi_188520128_gb_ACD58073.1_
0.183772	0.256355	0.11847	0.186199	gi_188520131_gb_ACD58076.1_
0.271505	0.018057	0.572975	0.287512	gi_188520132_gb_ACD58077.1_
0.157493	0.019379	0.181532	0.119468	gi_188520133_gb_ACD58078.1_
0.968139	0.997343	0.932074	0.965852	gi_188520134_gb_ACD58079.1_
0.190156	0.007622	0.297757	0.165178	gi_188520135_gb_ACD58080.1_
0.139314	0.570036	0.136108	0.281819	gi_188520141_gb_ACD58086.1_
0.093299	0.046619	0.148552	0.096157	gi_188520142_gb_ACD58087.1_
0.44695	0.977817	0.408783	0.611183	gi_188520143_gb_ACD58088.1_
0.141122	0.942622	0.061572	0.381772	gi_188520144_gb_ACD58089.1_
0.141486	0.201974	0.201974	0.181811	gi_188520148_gb_ACD58093.1_
0.360545	0.820244	0.363316	0.514702	gi_188520149_gb_ACD58094.1_

gi_188520150_gb_ACD58095.1_	0.619	22	0.741	22	0.929	17	0.865	0.8	Y	0.57	SignalP-noTM
gi_188520151_gb_ACD58096.1_	0.282	61	0.191	61	0.277	1	0.151	0.177	N	0.51	SignalP-TM
gi_188520154_gb_ACD58099.1_	0.181	22	0.361	12	0.91	10	0.85	0.591	Y	0.57	SignalP-noTM
gi_188520155_gb_ACD58100.1_	0.128	35	0.134	35	0.197	31	0.132	0.133	N	0.57	SignalP-noTM
gi_188520156_gb_ACD58101.1_	0.239	26	0.428	20	0.928	12	0.89	0.645	Y	0.57	SignalP-noTM
gi_188520157_gb_ACD58102.1_	0.159	29	0.241	11	0.722	1	0.589	0.37	N	0.51	SignalP-TM
gi_188520158_gb_ACD58103.1_	0.124	44	0.18	17	0.441	13	0.295	0.234	N	0.57	SignalP-noTM
gi_188520159_gb_ACD58104.1_	0.114	51	0.1	31	0.121	21	0.084	0.094	N	0.51	SignalP-TM
gi_188520166_gb_ACD58111.1_	0.124	23	0.151	11	0.325	4	0.217	0.182	N	0.57	SignalP-noTM
gi_188520167_gb_ACD58112.1_	0.132	34	0.128	34	0.171	24	0.119	0.124	N	0.57	SignalP-noTM
gi_188520169_gb_ACD58114.1_	0.112	54	0.16	13	0.319	9	0.254	0.204	N	0.57	SignalP-noTM
gi_188520170_gb_ACD58115.1_	0.17	31	0.146	31	0.257	1	0.145	0.146	N	0.57	SignalP-noTM
gi_188520171_gb_ACD58116.1_	0.234	33	0.157	33	0.183	32	0.098	0.129	N	0.57	SignalP-noTM
gi_188520177_gb_ACD58122.1_	0.206	32	0.191	32	0.297	23	0.182	0.188	N	0.51	SignalP-TM
gi_188520178_gb_ACD58123.1_	0.14	43	0.191	22	0.496	3	0.363	0.254	N	0.51	SignalP-TM
gi_188520179_gb_ACD58124.1_	0.122	17	0.137	11	0.293	1	0.182	0.154	N	0.51	SignalP-TM
gi_188520180_gb_ACD58125.1_	0.115	37	0.123	21	0.193	1	0.139	0.129	N	0.51	SignalP-TM
gi_188520181_gb_ACD58126.1_	0.11	30	0.155	11	0.367	1	0.222	0.186	N	0.57	SignalP-noTM
gi_188520187_gb_ACD58132.1_	0.199	26	0.154	26	0.156	25	0.11	0.133	N	0.57	SignalP-noTM
gi_188520188_gb_ACD58133.1_	0.121	26	0.152	11	0.28	1	0.229	0.188	N	0.57	SignalP-noTM
gi_188520189_gb_ACD58134.1_	0.211	17	0.187	17	0.254	16	0.165	0.176	N	0.57	SignalP-noTM
gi_188520190_gb_ACD58135.1_	0.181	20	0.205	20	0.457	10	0.242	0.223	N	0.57	SignalP-noTM
gi_188520191_gb_ACD58136.1_	0.232	18	0.209	18	0.407	4	0.243	0.225	N	0.57	SignalP-noTM
gi_188520193_gb_ACD58138.1_	0.127	19	0.099	19	0.102	52	0.077	0.089	N	0.57	SignalP-noTM
gi_188520194_gb_ACD58139.1_	0.116	45	0.152	13	0.272	11	0.234	0.19	N	0.57	SignalP-noTM
gi_188520195_gb_ACD58140.1_	0.174	61	0.165	61	0.262	40	0.151	0.159	N	0.57	SignalP-noTM
gi_188520196_gb_ACD58141.1_	0.111	51	0.138	21	0.257	13	0.161	0.149	N	0.57	SignalP-noTM
gi_188520203_gb_ACD58148.1_	0.393	24	0.61	24	0.983	12	0.943	0.766	Y	0.57	SignalP-noTM
gi_188520205_gb_ACD58150.1_	0.145	41	0.113	11	0.162	1	0.13	0.12	N	0.51	SignalP-TM
gi_188520206_gb_ACD58151.1_	0.106	43	0.173	11	0.365	5	0.305	0.235	N	0.57	SignalP-noTM
gi_188520209_gb_ACD58154.1_	0.846	24	0.907	24	0.986	13	0.967	0.935	Y	0.57	SignalP-noTM
gi_188520215_gb_ACD58160.1_	0.267	16	0.445	16	0.866	1	0.756	0.591	Y	0.57	SignalP-noTM
gi_188520218_gb_ACD58163.1_	0.111	44	0.099	66	0.115	3	0.083	0.092	N	0.57	SignalP-noTM
gi_188520219_gb_ACD58164.1_	0.104	31	0.113	18	0.154	13	0.122	0.117	N	0.57	SignalP-noTM
gi_188520220_gb_ACD58165.1_	0.101	56	0.105	69	0.138	8	0.096	0.101	N	0.57	SignalP-noTM
gi_188520222_gb_ACD58167.1_	0.119	52	0.166	14	0.379	49	0.279	0.219	N	0.57	SignalP-noTM
gi_188520223_gb_ACD58168.1_	0.284	35	0.265	35	0.457	34	0.197	0.233	N	0.57	SignalP-noTM
gi_188520224_gb_ACD58169.1_	0.199	45	0.137	45	0.133	2	0.097	0.118	N	0.57	SignalP-noTM
gi_188520225_gb_ACD58170.1_	0.242	29	0.195	29	0.419	1	0.216	0.203	N	0.51	SignalP-TM
gi_188520226_gb_ACD58171.1_	0.154	19	0.128	19	0.21	1	0.112	0.12	N	0.57	SignalP-noTM
gi_188520228_gb_ACD58173.1_	0.159	31	0.247	31	0.528	23	0.335	0.28	N	0.51	SignalP-TM
gi_188520229_gb_ACD58174.1_	0.109	35	0.1	16	0.12	7	0.097	0.099	N	0.51	SignalP-TM
gi_188520230_gb_ACD58175.1_	0.157	16	0.177	16	0.287	1	0.212	0.19	N	0.51	SignalP-TM
gi_188520231_gb_ACD58176.1_	0.147	46	0.124	46	0.133	37	0.071	0.104	N	0.51	SignalP-TM
gi_188520232_gb_ACD58177.1_	0.612	22	0.764	22	0.975	11	0.954	0.854	Y	0.57	SignalP-noTM
gi_188520233_gb_ACD58178.1_	0.119	18	0.115	18	0.123	25	0.105	0.11	N	0.57	SignalP-noTM
gi_188520234_gb_ACD58179.1_	0.157	38	0.167	50	0.395	45	0.148	0.158	N	0.57	SignalP-noTM
gi_188520235_gb_ACD58180.1_	0.106	19	0.095	36	0.107	1	0.07	0.086	N	0.51	SignalP-TM
gi_188520236_gb_ACD58181.1_	0.121	46	0.117	46	0.164	18	0.109	0.113	N	0.57	SignalP-noTM
gi_188520237_gb_ACD58182.1_	0.128	36	0.115	36	0.117	31	0.092	0.104	N	0.57	SignalP-noTM
gi_188520238_gb_ACD58183.1_	0.107	21	0.105	40	0.119	20	0.096	0.101	N	0.57	SignalP-noTM
gi_188520240_gb_ACD58185.1_	0.139	19	0.19	19	0.459	11	0.219	0.204	N	0.57	SignalP-noTM
gi_188520242_gb_ACD58187.1_	0.121	46	0.117	46	0.164	18	0.109	0.113	N	0.57	SignalP-noTM
gi_188520244_gb_ACD58189.1_	0.116	19	0.107	67	0.127	40	0.094	0.101	N	0.57	SignalP-noTM
gi_188520245_gb_ACD58190.1_	0.148	21	0.12	21	0.149	9	0.106	0.113	N	0.57	SignalP-noTM
gi_188520251_gb_ACD58196.1_	0.133	22	0.158	22	0.292	11	0.194	0.175	N	0.57	SignalP-noTM
gi_188520257_gb_ACD58202.1_	0.111	27	0.131	18	0.216	1	0.161	0.145	N	0.57	SignalP-noTM
gi_188520258_gb_ACD58203.1_	0.115	63	0.131	12	0.233	4	0.178	0.153	N	0.57	SignalP-noTM
gi_188520260_gb_ACD58205.1_	0.131	32	0.146	32	0.298	30	0.151	0.148	N	0.57	SignalP-noTM
gi_188520261_gb_ACD58206.1_	0.124	40	0.117	40	0.129	38	0.081	0.1	N	0.57	SignalP-noTM
gi_188520262_gb_ACD58207.1_	0.145	52	0.12	52	0.114	41	0.086	0.104	N	0.57	SignalP-noTM
gi_188520263_gb_ACD58208.1_	0.131	25	0.118	51	0.17	47	0.087	0.104	N	0.57	SignalP-noTM
gi_188520264_gb_ACD58209.1_	0.108	59	0.101	30	0.12	2	0.088	0.095	N	0.57	SignalP-noTM
gi_188520265_gb_ACD58210.1_	0.214	43	0.137	43	0.115	41	0.084	0.112	N	0.57	SignalP-noTM
gi_188520266_gb_ACD58211.1_	0.123	25	0.109	11	0.168	1	0.114	0.111	N	0.57	SignalP-noTM
gi_188520267_gb_ACD58212.1_	0.157	49	0.119	49	0.124	12	0.094	0.107	N	0.57	SignalP-noTM
gi_188520268_gb_ACD58213.1_	0.101	26	0.136	14	0.268	6	0.185	0.159	N	0.57	SignalP-noTM
gi_188520269_gb_ACD58214.1_	0.12	32	0.134	11	0.251	5	0.191	0.16	N	0.57	SignalP-noTM
gi_188520270_gb_ACD58215.1_	0.214	34	0.165	34	0.239	2	0.147	0.157	N	0.57	SignalP-noTM
gi_188520271_gb_ACD58216.1_	0.718	20	0.608	20	0.721	19	0.514	0.564	N	0.57	SignalP-noTM
gi_188520272_gb_ACD58217.1_	0.244	30	0.185	18	0.26	1	0.17	0.178	N	0.57	SignalP-noTM
gi_188520273_gb_ACD58218.1_	0.124	23	0.115	23	0.199	1	0.105	0.111	N	0.57	SignalP-noTM
gi_188520274_gb_ACD58219.1_	0.125	34	0.126	34	0.194	32	0.108	0.117	N	0.57	SignalP-noTM
gi_188520275_gb_ACD58220.1_	0.141	29	0.137	11	0.229	5	0.198	0.159	N	0.51	SignalP-TM
gi_188520276_gb_ACD58221.1_	0.225	43	0.215	43	0.513	42	0.147	0.183	N	0.57	SignalP-noTM
gi_188520277_gb_ACD58222.1_	0.161	25	0.106	25	0.105	47	0.067	0.087	N	0.57	SignalP-noTM
gi_188520278_gb_ACD58223.1_	0.126	57	0.108	21	0.142	9	0.113	0.11	N	0.57	SignalP-noTM
gi_188520279_gb_ACD58224.1_	0.105	47	0.127	52	0.209	43	0.117	0.122	N	0.57	SignalP-noTM

0.390788	0.22461	0.427025	0.347474	gi_188520150_gb_ACD58095.1_
0.097704	0.431435	0.222527	0.250555	gi_188520151_gb_ACD58096.1_
0.199567	0.073441	0.230942	0.167983	gi_188520154_gb_ACD58099.1_
0.641527	0.928972	0.788182	0.786227	gi_188520155_gb_ACD58100.1_
0.27508	0.096129	0.352287	0.241165	gi_188520156_gb_ACD58101.1_
0.112645	0.054526	0.136108	0.101093	gi_188520157_gb_ACD58102.1_
0.234693	0.109975	0.30789	0.217519	gi_188520158_gb_ACD58103.1_
0.121639	0.1034	0.14517	0.123403	gi_188520159_gb_ACD58104.1_
0.120363	0.069655	0.167702	0.11924	gi_188520166_gb_ACD58111.1_
0.958194	0.92365	0.894069	0.925304	gi_188520167_gb_ACD58112.1_
0.152775	0.830194	0.084788	0.355919	gi_188520169_gb_ACD58114.1_
0.366793	0.359854	0.246197	0.324281	gi_188520170_gb_ACD58115.1_
0.177118	0.182873	0.081137	0.147043	gi_188520171_gb_ACD58116.1_
0.918639	0.990613	0.896877	0.935376	gi_188520177_gb_ACD58122.1_
0.105364	0.386511	0.088346	0.193407	gi_188520178_gb_ACD58123.1_
0.093046	0.585405	0.186487	0.288313	gi_188520179_gb_ACD58124.1_
0.111452	0.057378	0.148932	0.105921	gi_188520180_gb_ACD58125.1_
0.089317	0.014175	0.119413	0.074302	gi_188520181_gb_ACD58126.1_
0.109389	0.053	0.141851	0.101413	gi_188520187_gb_ACD58132.1_
0.368188	0.884933	0.266784	0.506635	gi_188520188_gb_ACD58133.1_
0.669959	0.999607	0.622694	0.764087	gi_188520189_gb_ACD58134.1_
0.123575	0.163557	0.144798	0.143977	gi_188520190_gb_ACD58135.1_
0.234154	0.751009	0.37449	0.453218	gi_188520191_gb_ACD58136.1_
0.137525	0.222527	0.124227	0.161426	gi_188520193_gb_ACD58138.1_
0.507499	0.085724	0.586133	0.393119	gi_188520194_gb_ACD58139.1_
0.148173	0.215853	0.088588	0.150871	gi_188520195_gb_ACD58140.1_
0.234693	0.913568	0.216361	0.454874	gi_188520196_gb_ACD58141.1_
0.811227	0.276878	0.796085	0.628063	gi_188520203_gb_ACD58148.1_
0.083402	0.611352	0.168541	0.287765	gi_188520205_gb_ACD58150.1_
0.341414	0.988716	0.120363	0.483498	gi_188520206_gb_ACD58151.1_
0.953381	0.994933	0.813057	0.920457	gi_188520209_gb_ACD58154.1_
0.902031	0.967391	0.867381	0.912268	gi_188520215_gb_ACD58160.1_
0.08181	0.000199	0.186032	0.089347	gi_188520218_gb_ACD58163.1_
0.88615	0.988849	0.649764	0.841588	gi_188520219_gb_ACD58164.1_
0.103123	0.026988	0.101197	0.077103	gi_188520220_gb_ACD58165.1_
0.11847	0.147795	0.204891	0.157052	gi_188520222_gb_ACD58167.1_
0.077201	0.130562	0.092289	0.100017	gi_188520223_gb_ACD58168.1_
0.079365	0.044659	0.120363	0.081462	gi_188520224_gb_ACD58169.1_
0.130222	0.707857	0.235772	0.35795	gi_188520225_gb_ACD58170.1_
0.078928	0.113548	0.076562	0.089679	gi_188520226_gb_ACD58171.1_
0.509749	0.065314	0.3858	0.320288	gi_188520228_gb_ACD58173.1_
0.062444	0.711566	0.132964	0.302325	gi_188520229_gb_ACD58174.1_
0.051809	0.196234	0.180643	0.142895	gi_188520230_gb_ACD58175.1_
0.053911	0.122927	0.178433	0.118424	gi_188520231_gb_ACD58176.1_
0.919753	0.844093	0.850306	0.871384	gi_188520232_gb_ACD58177.1_
0.602047	0.337378	0.65656	0.531995	gi_188520233_gb_ACD58178.1_
0.174942	0.051368	0.246754	0.157688	gi_188520234_gb_ACD58179.1_
0.330041	0.954305	0.352972	0.545773	gi_188520235_gb_ACD58180.1_
0.168541	0.829346	0.181532	0.39314	gi_188520236_gb_ACD58181.1_
0.128196	0.001518	0.124227	0.084647	gi_188520237_gb_ACD58182.1_
0.392933	0.78262	0.489502	0.555018	gi_188520238_gb_ACD58183.1_
0.147418	0.258649	0.069074	0.15838	gi_188520240_gb_ACD58185.1_
0.169806	0.603483	0.183322	0.31887	gi_188520242_gb_ACD58187.1_
0.176681	0.673927	0.102018	0.317542	gi_188520244_gb_ACD58189.1_
0.1065	0.387223	0.090545	0.194756	gi_188520245_gb_ACD58190.1_
0.757128	0.79462	0.832716	0.794821	gi_188520251_gb_ACD58196.1_
0.776953	0.239031	0.810306	0.608763	gi_188520257_gb_ACD58202.1_
0.841309	0.93283	0.85705	0.877063	gi_188520258_gb_ACD58203.1_
0.375897	0.033375	0.409508	0.272927	gi_188520260_gb_ACD58205.1_
0.369584	0.044277	0.429228	0.28103	gi_188520261_gb_ACD58206.1_
0.910438	0.99963	0.907962	0.939343	gi_188520262_gb_ACD58207.1_
0.102569	0.032799	0.164379	0.099916	gi_188520263_gb_ACD58208.1_
0.115067	0.054681	0.102293	0.09068	gi_188520264_gb_ACD58209.1_
0.109975	0.045174	0.100924	0.085358	gi_188520265_gb_ACD58210.1_
0.160704	0.122604	0.103123	0.12881	gi_188520266_gb_ACD58211.1_
0.112645	0.076562	0.113548	0.100918	gi_188520267_gb_ACD58212.1_
0.838485	0.963911	0.773293	0.858563	gi_188520268_gb_ACD58213.1_
0.41096	0.34074	0.320168	0.357289	gi_188520269_gb_ACD58214.1_
0.290904	0.251242	0.387223	0.30979	gi_188520270_gb_ACD58215.1_
0.180199	0.171505	0.277479	0.209728	gi_188520271_gb_ACD58216.1_
0.894069	0.965643	0.853335	0.904349	gi_188520272_gb_ACD58217.1_
0.102293	0.045826	0.118784	0.088968	gi_188520273_gb_ACD58218.1_
0.159092	0.229878	0.155513	0.181494	gi_188520274_gb_ACD58219.1_
0.227761	0.117533	0.246754	0.197349	gi_188520275_gb_ACD58220.1_
0.888251	0.829346	0.822882	0.846826	gi_188520276_gb_ACD58221.1_
0.19201	0.418971	0.138238	0.24974	gi_188520277_gb_ACD58222.1_
0.195761	0.119729	0.163557	0.159682	gi_188520278_gb_ACD58223.1_
0.330705	0.024435	0.309171	0.221437	gi_188520279_gb_ACD58224.1_

gi_188520286_gb_ACD58231.1_	0.159	53	0.148	53	0.212	51	0.106	0.128	N	0.57	SignalP-noTM
gi_188520294_gb_ACD58239.1_	0.174	24	0.267	19	0.742	7	0.577	0.413	N	0.57	SignalP-noTM
gi_188520295_gb_ACD58240.1_	0.156	35	0.16	35	0.268	24	0.164	0.162	N	0.51	SignalP-TM
gi_188520296_gb_ACD58241.1_	0.128	29	0.123	29	0.141	26	0.098	0.111	N	0.57	SignalP-noTM
gi_188520297_gb_ACD58242.1_	0.182	22	0.15	22	0.173	18	0.098	0.131	N	0.51	SignalP-TM
gi_188520299_gb_ACD58244.1_	0.145	28	0.119	28	0.126	1	0.097	0.109	N	0.57	SignalP-noTM
gi_188520316_gb_ACD58261.1_	0.105	51	0.11	51	0.134	46	0.095	0.103	N	0.57	SignalP-noTM
gi_188520317_gb_ACD58262.1_	0.131	54	0.119	22	0.196	16	0.118	0.118	N	0.57	SignalP-noTM
gi_188520318_gb_ACD58263.1_	0.118	49	0.123	26	0.301	24	0.13	0.126	N	0.57	SignalP-noTM
gi_188520319_gb_ACD58264.1_	0.11	26	0.118	11	0.174	1	0.138	0.127	N	0.57	SignalP-noTM
gi_188520320_gb_ACD58265.1_	0.134	17	0.11	40	0.168	38	0.088	0.1	N	0.57	SignalP-noTM
gi_188520321_gb_ACD58266.1_	0.163	33	0.177	11	0.451	18	0.322	0.231	N	0.51	SignalP-TM
gi_188520322_gb_ACD58267.1_	0.119	32	0.169	11	0.405	6	0.307	0.234	N	0.57	SignalP-noTM
gi_188520323_gb_ACD58268.1_	0.141	42	0.219	27	0.453	17	0.364	0.272	N	0.51	SignalP-TM
gi_188520324_gb_ACD58269.1_	0.342	42	0.255	42	0.32	36	0.118	0.204	N	0.51	SignalP-TM
gi_188520325_gb_ACD58270.1_	0.13	9	0.121	55	0.204	48	0.104	0.113	N	0.57	SignalP-noTM
gi_188520326_gb_ACD58271.1_	0.146	24	0.186	24	0.33	9	0.232	0.208	N	0.57	SignalP-noTM
gi_188520327_gb_ACD58272.1_	0.351	20	0.292	20	0.412	16	0.24	0.268	N	0.57	SignalP-noTM
gi_188520328_gb_ACD58273.1_	0.187	21	0.229	21	0.433	2	0.289	0.257	N	0.57	SignalP-noTM
gi_188520329_gb_ACD58274.1_	0.136	34	0.135	34	0.213	30	0.119	0.128	N	0.57	SignalP-noTM
gi_188520332_gb_ACD58277.1_	0.2	31	0.19	24	0.453	14	0.257	0.222	N	0.57	SignalP-noTM
gi_188520333_gb_ACD58278.1_	0.15	22	0.177	22	0.246	3	0.215	0.191	N	0.51	SignalP-TM
gi_188520336_gb_ACD58281.1_	0.277	19	0.152	50	0.184	48	0.096	0.126	N	0.57	SignalP-noTM
gi_188520337_gb_ACD58282.1_	0.355	31	0.211	31	0.193	5	0.137	0.176	N	0.57	SignalP-noTM
gi_188520340_gb_ACD58285.1_	0.282	25	0.227	25	0.324	21	0.174	0.202	N	0.57	SignalP-noTM
gi_188520341_gb_ACD58286.1_	0.123	55	0.179	19	0.337	8	0.275	0.215	N	0.51	SignalP-TM
gi_188520342_gb_ACD58287.1_	0.133	39	0.112	39	0.21	1	0.095	0.106	N	0.51	SignalP-TM
gi_188520346_gb_ACD58291.1_	0.525	21	0.529	21	0.641	17	0.537	0.533	N	0.57	SignalP-noTM
gi_188520347_gb_ACD58292.1_	0.575	26	0.701	26	0.989	11	0.909	0.799	Y	0.57	SignalP-noTM
gi_188520348_gb_ACD58293.1_	0.162	26	0.251	23	0.526	13	0.409	0.325	N	0.57	SignalP-noTM
gi_188520349_gb_ACD58294.1_	0.136	19	0.135	19	0.175	15	0.138	0.136	N	0.57	SignalP-noTM
gi_188520350_gb_ACD58295.1_	0.134	33	0.156	18	0.308	13	0.221	0.18	N	0.51	SignalP-TM
gi_188520351_gb_ACD58296.1_	0.125	24	0.119	24	0.141	21	0.113	0.116	N	0.57	SignalP-noTM
gi_188520352_gb_ACD58297.1_	0.14	30	0.148	24	0.378	1	0.183	0.161	N	0.51	SignalP-TM
gi_188520353_gb_ACD58298.1_	0.214	55	0.247	55	0.407	51	0.182	0.223	N	0.51	SignalP-TM
gi_188520354_gb_ACD58299.1_	0.162	38	0.113	38	0.109	7	0.085	0.1	N	0.57	SignalP-noTM
gi_188520355_gb_ACD58300.1_	0.142	32	0.125	47	0.251	46	0.103	0.115	N	0.57	SignalP-noTM
gi_188520357_gb_ACD58302.1_	0.102	27	0.102	45	0.118	43	0.087	0.095	N	0.57	SignalP-noTM
gi_188520358_gb_ACD58303.1_	0.108	58	0.117	11	0.174	1	0.131	0.124	N	0.57	SignalP-noTM
gi_188520359_gb_ACD58304.1_	0.116	21	0.138	21	0.193	11	0.146	0.141	N	0.51	SignalP-TM
gi_188520360_gb_ACD58305.1_	0.158	35	0.369	35	0.927	24	0.701	0.525	N	0.57	SignalP-noTM
gi_188520363_gb_ACD58308.1_	0.116	27	0.103	45	0.152	2	0.096	0.1	N	0.57	SignalP-noTM
gi_188520364_gb_ACD58309.1_	0.343	31	0.347	31	0.479	23	0.239	0.307	N	0.51	SignalP-TM
gi_188520365_gb_ACD58310.1_	0.126	32	0.121	32	0.188	1	0.124	0.122	N	0.57	SignalP-noTM
gi_188520366_gb_ACD58311.1_	0.156	25	0.185	25	0.34	17	0.225	0.204	N	0.57	SignalP-noTM
gi_188520367_gb_ACD58312.1_	0.12	43	0.132	43	0.221	33	0.135	0.133	N	0.57	SignalP-noTM
gi_188520368_gb_ACD58313.1_	0.107	32	0.095	64	0.096	62	0.075	0.085	N	0.57	SignalP-noTM
gi_188520369_gb_ACD58314.1_	0.121	23	0.106	42	0.135	38	0.085	0.096	N	0.57	SignalP-noTM
gi_188520371_gb_ACD58316.1_	0.105	54	0.105	44	0.123	33	0.094	0.1	N	0.57	SignalP-noTM
gi_188520372_gb_ACD58317.1_	0.124	21	0.098	70	0.103	20	0.081	0.09	N	0.57	SignalP-noTM
gi_188520373_gb_ACD58318.1_	0.104	22	0.104	39	0.125	46	0.089	0.097	N	0.57	SignalP-noTM
gi_188520374_gb_ACD58319.1_	0.126	54	0.127	18	0.2	8	0.154	0.139	N	0.57	SignalP-noTM
gi_188520375_gb_ACD58320.1_	0.134	67	0.138	11	0.278	1	0.175	0.155	N	0.57	SignalP-noTM
gi_188520376_gb_ACD58321.1_	0.109	23	0.129	11	0.191	5	0.171	0.149	N	0.57	SignalP-noTM
gi_188520377_gb_ACD58322.1_	0.236	34	0.205	34	0.27	30	0.151	0.18	N	0.57	SignalP-noTM
gi_188520378_gb_ACD58323.1_	0.137	27	0.135	11	0.282	6	0.202	0.166	N	0.57	SignalP-noTM
gi_188520379_gb_ACD58324.1_	0.116	26	0.149	11	0.351	1	0.199	0.172	N	0.57	SignalP-noTM
gi_188520381_gb_ACD58326.1_	0.178	48	0.141	48	0.189	3	0.098	0.121	N	0.57	SignalP-noTM
gi_188520382_gb_ACD58327.1_	0.159	39	0.14	11	0.242	5	0.197	0.167	N	0.57	SignalP-noTM
gi_188520383_gb_ACD58328.1_	0.2	25	0.175	25	0.214	24	0.147	0.162	N	0.57	SignalP-noTM
gi_188520385_gb_ACD58330.1_	0.149	62	0.13	31	0.182	36	0.111	0.121	N	0.57	SignalP-noTM
gi_188520386_gb_ACD58331.1_	0.16	46	0.17	18	0.382	1	0.257	0.21	N	0.57	SignalP-noTM
gi_188520388_gb_ACD58333.1_	0.136	22	0.133	40	0.222	21	0.125	0.129	N	0.57	SignalP-noTM
gi_188520389_gb_ACD58334.1_	0.159	20	0.136	41	0.189	29	0.122	0.131	N	0.51	SignalP-TM
gi_188520398_gb_ACD58343.1_	0.171	20	0.171	20	0.252	9	0.183	0.177	N	0.57	SignalP-noTM
gi_188520399_gb_ACD58344.1_	0.136	22	0.328	14	0.912	1	0.837	0.568	N	0.57	SignalP-noTM
gi_188520401_gb_ACD58346.1_	0.131	37	0.164	20	0.324	14	0.263	0.211	N	0.57	SignalP-noTM
gi_188520406_gb_ACD58351.1_	0.128	24	0.111	24	0.198	23	0.096	0.104	N	0.57	SignalP-noTM
gi_188520408_gb_ACD58353.1_	0.786	39	0.796	39	0.953	32	0.698	0.75	Y	0.57	SignalP-noTM
gi_188520409_gb_ACD58354.1_	0.155	30	0.223	30	0.556	25	0.291	0.255	N	0.57	SignalP-noTM
gi_188520410_gb_ACD58355.1_	0.114	38	0.104	38	0.126	30	0.09	0.097	N	0.57	SignalP-noTM
gi_188520411_gb_ACD58356.1_	0.174	19	0.135	19	0.176	42	0.101	0.119	N	0.57	SignalP-noTM
gi_188520412_gb_ACD58357.1_	0.113	65	0.109	11	0.159	2	0.119	0.114	N	0.57	SignalP-noTM
gi_188520414_gb_ACD58359.1_	0.224	57	0.146	57	0.32	1	0.109	0.129	N	0.57	SignalP-noTM
gi_188520415_gb_ACD58360.1_	0.106	39	0.102	20	0.133	11	0.092	0.097	N	0.57	SignalP-noTM
gi_188520423_gb_ACD58368.1_	0.126	46	0.115	46	0.145	18	0.104	0.11	N	0.57	SignalP-noTM
gi_188520424_gb_ACD58369.1_	0.151	38	0.225	11	0.693	1	0.491	0.35	N	0.57	SignalP-noTM
gi_188520425_gb_ACD58370.1_	0.112	25	0.122	41	0.25	1	0.119	0.121	N	0.51	SignalP-TM

0.115679	0.033961	0.146665	0.098768	gi_188520286_gb_ACD58231.1_
0.191081	0.10011	0.198134	0.163108	gi_188520294_gb_ACD58239.1_
0.141851	0.065681	0.208829	0.138787	gi_188520295_gb_ACD58240.1_
0.164792	0.153164	0.147795	0.15525	gi_188520296_gb_ACD58241.1_
0.084092	0.009699	0.158291	0.084027	gi_188520297_gb_ACD58242.1_
0.939118	0.99952	0.906701	0.948446	gi_188520299_gb_ACD58244.1_
0.07871	0.0527	0.086669	0.072693	gi_188520316_gb_ACD58261.1_
0.08181	0.046353	0.113247	0.08047	gi_188520317_gb_ACD58262.1_
0.11847	0.575176	0.115067	0.269571	gi_188520318_gb_ACD58263.1_
0.140397	0.045695	0.167284	0.117792	gi_188520319_gb_ACD58264.1_
0.072225	0.045826	0.121319	0.07979	gi_188520320_gb_ACD58265.1_
0.194818	0.424091	0.307252	0.30872	gi_188520321_gb_ACD58266.1_
0.141486	0.3028	0.085021	0.176436	gi_188520322_gb_ACD58267.1_
0.111452	0.036509	0.162329	0.10343	gi_188520323_gb_ACD58268.1_
0.289667	0.889141	0.253506	0.477438	gi_188520324_gb_ACD58269.1_
0.181979	0.78768	0.111749	0.360469	gi_188520325_gb_ACD58270.1_
0.097704	0.069655	0.108806	0.092055	gi_188520326_gb_ACD58271.1_
0.078276	0.026442	0.140397	0.081705	gi_188520327_gb_ACD58272.1_
0.172359	0.046619	0.158691	0.12589	gi_188520328_gb_ACD58273.1_
0.158291	0.112946	0.143318	0.138185	gi_188520329_gb_ACD58274.1_
0.075091	0.043647	0.128869	0.082536	gi_188520332_gb_ACD58277.1_
0.128532	0.043149	0.162737	0.111473	gi_188520333_gb_ACD58278.1_
0.099034	0.047562	0.145916	0.097504	gi_188520336_gb_ACD58281.1_
0.712181	0.75878	0.685033	0.718665	gi_188520337_gb_ACD58282.1_
0.181087	0.052104	0.24453	0.15924	gi_188520340_gb_ACD58285.1_
0.065131	0.066982	0.167284	0.099799	gi_188520341_gb_ACD58286.1_
0.128869	0.380836	0.109389	0.206365	gi_188520342_gb_ACD58287.1_
0.771711	0.972374	0.737303	0.827129	gi_188520346_gb_ACD58291.1_
0.917284	0.397953	0.927574	0.747604	gi_188520347_gb_ACD58292.1_
0.090545	0.018707	0.08181	0.063687	gi_188520348_gb_ACD58293.1_
0.739621	0.979265	0.645656	0.788181	gi_188520349_gb_ACD58294.1_
0.130903	0.269729	0.248431	0.216354	gi_188520350_gb_ACD58295.1_
0.100381	0.008951	0.141851	0.083728	gi_188520351_gb_ACD58296.1_
0.623399	0.638763	0.644282	0.635481	gi_188520352_gb_ACD58297.1_
0.148552	0.073441	0.167702	0.129898	gi_188520353_gb_ACD58298.1_
0.086432	0.001231	0.099302	0.062322	gi_188520354_gb_ACD58299.1_
0.151614	0.050787	0.203429	0.135277	gi_188520355_gb_ACD58300.1_
0.167702	0.173217	0.220974	0.187298	gi_188520357_gb_ACD58302.1_
0.105647	0.061745	0.10736	0.091584	gi_188520358_gb_ACD58303.1_
0.086669	0.064767	0.177118	0.109518	gi_188520359_gb_ACD58304.1_
0.958553	0.999617	0.899076	0.952415	gi_188520360_gb_ACD58305.1_
0.162329	0.127527	0.194348	0.161401	gi_188520363_gb_ACD58308.1_
0.099034	0.007055	0.134005	0.080031	gi_188520364_gb_ACD58309.1_
0.067736	0.03704	0.114153	0.072976	gi_188520365_gb_ACD58310.1_
0.202458	0.727307	0.136815	0.355527	gi_188520366_gb_ACD58311.1_
0.931311	0.994492	0.876749	0.934184	gi_188520367_gb_ACD58312.1_
0.125209	0.120681	0.096651	0.11418	gi_188520368_gb_ACD58313.1_
0.195289	0.077415	0.291523	0.188076	gi_188520369_gb_ACD58314.1_
0.195761	0.31432	0.14517	0.218417	gi_188520371_gb_ACD58316.1_
0.115373	0.378716	0.07635	0.190146	gi_188520372_gb_ACD58317.1_
0.06717	0.011184	0.115373	0.064576	gi_188520373_gb_ACD58318.1_
0.213325	0.795597	0.104518	0.371147	gi_188520374_gb_ACD58319.1_
0.080247	0.036615	0.107072	0.074645	gi_188520375_gb_ACD58320.1_
0.105931	0.000445	0.243424	0.1166	gi_188520376_gb_ACD58321.1_
0.17023	0.042901	0.141851	0.118327	gi_188520377_gb_ACD58322.1_
0.226181	0.223567	0.288434	0.246061	gi_188520378_gb_ACD58323.1_
0.094319	0.029114	0.131587	0.085007	gi_188520379_gb_ACD58324.1_
0.114153	0.108806	0.105364	0.109441	gi_188520381_gb_ACD58326.1_
0.149313	0.123251	0.098767	0.123777	gi_188520382_gb_ACD58327.1_
0.597005	0.979807	0.604918	0.727243	gi_188520383_gb_ACD58328.1_
0.156699	0.030325	0.204891	0.130638	gi_188520385_gb_ACD58330.1_
0.960418	0.963701	0.947	0.95704	gi_188520386_gb_ACD58331.1_
0.132274	0.056893	0.128869	0.106012	gi_188520388_gb_ACD58333.1_
0.147041	0.051956	0.164792	0.121263	gi_188520389_gb_ACD58334.1_
0.122282	0.095349	0.208829	0.142153	gi_188520398_gb_ACD58343.1_
0.934686	0.999894	0.899619	0.944733	gi_188520399_gb_ACD58344.1_
0.840908	0.984094	0.800911	0.875304	gi_188520401_gb_ACD58346.1_
0.093553	0.037363	0.098234	0.076383	gi_188520406_gb_ACD58351.1_
0.891485	0.984187	0.835621	0.903764	gi_188520408_gb_ACD58353.1_
0.643595	0.066051	0.665967	0.458538	gi_188520409_gb_ACD58354.1_
0.324098	0.837671	0.362622	0.50813	gi_188520410_gb_ACD58355.1_
0.332034	0.071625	0.365401	0.256353	gi_188520411_gb_ACD58356.1_
0.551566	0.178873	0.521736	0.417392	gi_188520412_gb_ACD58357.1_
0.943747	0.86807	0.923012	0.91161	gi_188520414_gb_ACD58359.1_
0.119413	0.002135	0.163557	0.095035	gi_188520415_gb_ACD58360.1_
0.168541	0.975277	0.064044	0.402621	gi_188520423_gb_ACD58368.1_
0.102845	0.091538	0.169806	0.121396	gi_188520424_gb_ACD58369.1_
0.258649	0.022511	0.275678	0.185613	gi_188520425_gb_ACD58370.1_

gi_188520426_gb_ACD58371.1_	0.137	21	0.199	12	0.432	10	0.302	0.247	N	0.57	SignalP-noTM
gi_188520427_gb_ACD58372.1_	0.107	28	0.116	55	0.174	50	0.094	0.106	N	0.57	SignalP-noTM
gi_188520428_gb_ACD58373.1_	0.295	31	0.265	31	0.52	5	0.285	0.274	N	0.57	SignalP-noTM
gi_188520429_gb_ACD58374.1_	0.148	34	0.126	34	0.132	57	0.087	0.107	N	0.57	SignalP-noTM
gi_188520432_gb_ACD58377.1_	0.159	20	0.128	20	0.133	19	0.096	0.113	N	0.57	SignalP-noTM
gi_188520434_gb_ACD58379.1_	0.127	33	0.117	33	0.182	10	0.104	0.111	N	0.57	SignalP-noTM
gi_188520435_gb_ACD58380.1_	0.16	34	0.202	19	0.501	8	0.349	0.256	N	0.51	SignalP-TM
gi_188520436_gb_ACD58381.1_	0.16	24	0.218	24	0.486	19	0.315	0.264	N	0.57	SignalP-noTM
gi_188520437_gb_ACD58382.1_	0.111	34	0.102	65	0.105	56	0.085	0.094	N	0.57	SignalP-noTM
gi_188520438_gb_ACD58383.1_	0.143	38	0.146	11	0.258	4	0.211	0.177	N	0.57	SignalP-noTM
gi_188520439_gb_ACD58384.1_	0.121	41	0.134	11	0.3	10	0.173	0.152	N	0.57	SignalP-noTM
gi_188520441_gb_ACD58386.1_	0.127	29	0.103	42	0.125	33	0.081	0.093	N	0.57	SignalP-noTM
gi_188520442_gb_ACD58387.1_	0.154	47	0.126	47	0.153	46	0.079	0.104	N	0.57	SignalP-noTM
gi_188520444_gb_ACD58389.1_	0.151	38	0.122	46	0.166	44	0.105	0.116	N	0.51	SignalP-TM
gi_188520445_gb_ACD58390.1_	0.239	36	0.189	36	0.251	35	0.109	0.152	N	0.57	SignalP-noTM
gi_188520446_gb_ACD58391.1_	0.114	35	0.101	69	0.111	15	0.088	0.095	N	0.57	SignalP-noTM
gi_188520447_gb_ACD58392.1_	0.144	43	0.106	43	0.126	3	0.083	0.096	N	0.57	SignalP-noTM
gi_188520448_gb_ACD58393.1_	0.112	40	0.112	15	0.162	8	0.114	0.113	N	0.51	SignalP-TM
gi_188520451_gb_ACD58396.1_	0.14	26	0.179	11	0.446	2	0.315	0.243	N	0.57	SignalP-noTM
gi_188520452_gb_ACD58397.1_	0.113	53	0.154	15	0.295	3	0.246	0.197	N	0.57	SignalP-noTM
gi_188520454_gb_ACD58399.1_	0.112	31	0.104	11	0.12	3	0.111	0.107	N	0.57	SignalP-noTM
gi_188520455_gb_ACD58400.1_	0.243	21	0.156	21	0.124	19	0.092	0.126	N	0.57	SignalP-noTM
gi_188520456_gb_ACD58401.1_	0.189	25	0.159	25	0.227	23	0.127	0.144	N	0.57	SignalP-noTM
gi_188520457_gb_ACD58402.1_	0.305	37	0.173	37	0.26	19	0.153	0.164	N	0.57	SignalP-noTM
gi_188520458_gb_ACD58403.1_	0.118	68	0.104	68	0.105	24	0.082	0.094	N	0.57	SignalP-noTM
gi_188520469_gb_ACD58414.1_	0.105	45	0.105	51	0.184	42	0.087	0.096	N	0.57	SignalP-noTM
gi_188520481_gb_ACD58426.1_	0.119	29	0.244	19	0.722	16	0.494	0.361	N	0.57	SignalP-noTM
gi_188520490_gb_ACD58435.1_	0.103	28	0.147	11	0.339	1	0.2	0.172	N	0.57	SignalP-noTM
gi_188520491_gb_ACD58436.1_	0.111	22	0.117	22	0.179	21	0.116	0.116	N	0.57	SignalP-noTM
gi_188520498_gb_ACD58443.1_	0.455	36	0.62	36	0.975	25	0.828	0.718	Y	0.57	SignalP-noTM
gi_188520502_gb_ACD58447.1_	0.145	27	0.136	27	0.186	13	0.128	0.133	N	0.57	SignalP-noTM
gi_528897474_gb_ACD58449.2_	0.113	66	0.122	56	0.198	47	0.111	0.117	N	0.57	SignalP-noTM
gi_188520507_gb_ACD58452.1_	0.117	32	0.128	18	0.206	8	0.157	0.142	N	0.57	SignalP-noTM
gi_528897475_gb_ACD58455.2_	0.113	66	0.122	56	0.198	47	0.111	0.117	N	0.57	SignalP-noTM
gi_188520513_gb_ACD58458.1_	0.121	61	0.12	19	0.157	13	0.122	0.121	N	0.57	SignalP-noTM
gi_188520514_gb_ACD58459.1_	0.225	29	0.172	29	0.3	28	0.134	0.155	N	0.57	SignalP-noTM
gi_188520515_gb_ACD58460.1_	0.122	31	0.16	26	0.289	3	0.201	0.179	N	0.57	SignalP-noTM
gi_188520516_gb_ACD58461.1_	0.105	3	0.099	32	0.11	20	0.092	0.096	N	0.57	SignalP-noTM
gi_188520517_gb_ACD58462.1_	0.175	39	0.128	39	0.128	2	0.092	0.111	N	0.57	SignalP-noTM
gi_188520518_gb_ACD58463.1_	0.105	3	0.1	18	0.117	12	0.096	0.098	N	0.57	SignalP-noTM
gi_188520522_gb_ACD58467.1_	0.128	26	0.104	26	0.126	2	0.09	0.097	N	0.57	SignalP-noTM
gi_188520528_gb_ACD58473.1_	0.149	23	0.138	23	0.21	6	0.15	0.143	N	0.57	SignalP-noTM
gi_188520531_gb_ACD58476.1_	0.156	42	0.146	42	0.211	19	0.139	0.142	N	0.57	SignalP-noTM
gi_188520537_gb_ACD58482.1_	0.171	41	0.14	41	0.208	8	0.144	0.142	N	0.57	SignalP-noTM
gi_188520538_gb_ACD58483.1_	0.117	33	0.223	19	0.586	15	0.469	0.339	N	0.57	SignalP-noTM
gi_188520539_gb_ACD58484.1_	0.106	48	0.137	14	0.269	6	0.186	0.16	N	0.57	SignalP-noTM
gi_188520544_gb_ACD58489.1_	0.113	13	0.107	35	0.143	29	0.085	0.096	N	0.57	SignalP-noTM
gi_188520546_gb_ACD58491.1_	0.157	35	0.131	35	0.14	53	0.093	0.117	N	0.51	SignalP-TM
gi_188520547_gb_ACD58492.1_	0.139	20	0.175	20	0.351	1	0.229	0.201	N	0.57	SignalP-noTM
gi_188520548_gb_ACD58493.1_	0.112	24	0.129	11	0.227	3	0.172	0.149	N	0.57	SignalP-noTM
gi_188520549_gb_ACD58494.1_	0.149	26	0.15	46	0.28	42	0.123	0.137	N	0.57	SignalP-noTM
gi_188520550_gb_ACD58495.1_	0.142	42	0.151	42	0.24	35	0.134	0.144	N	0.51	SignalP-TM
gi_188520555_gb_ACD58500.1_	0.131	37	0.145	11	0.336	1	0.189	0.166	N	0.57	SignalP-noTM
gi_188520556_gb_ACD58501.1_	0.109	45	0.151	12	0.325	6	0.237	0.191	N	0.57	SignalP-noTM
gi_188520558_gb_ACD58503.1_	0.1	25	0.12	12	0.178	2	0.144	0.131	N	0.57	SignalP-noTM
gi_188520559_gb_ACD58504.1_	0.16	24	0.11	39	0.147	36	0.095	0.104	N	0.51	SignalP-TM
gi_188520560_gb_ACD58505.1_	0.192	48	0.167	48	0.242	37	0.111	0.146	N	0.51	SignalP-TM
gi_188520561_gb_ACD58506.1_	0.168	23	0.384	23	0.949	17	0.901	0.627	Y	0.57	SignalP-noTM
gi_188520562_gb_ACD58507.1_	0.108	7	0.098	43	0.134	6	0.093	0.095	N	0.57	SignalP-noTM
gi_188520563_gb_ACD58508.1_	0.209	26	0.189	26	0.293	6	0.202	0.194	N	0.51	SignalP-TM
gi_188520564_gb_ACD58509.1_	0.143	58	0.157	11	0.376	2	0.237	0.187	N	0.51	SignalP-TM
gi_188520566_gb_ACD58511.1_	0.423	41	0.235	41	0.211	27	0.118	0.18	N	0.57	SignalP-noTM
gi_188520577_gb_ACD58522.1_	0.144	15	0.112	41	0.136	25	0.097	0.105	N	0.57	SignalP-noTM
gi_188520578_gb_ACD58523.1_	0.706	23	0.789	23	0.961	16	0.905	0.843	Y	0.57	SignalP-noTM
gi_188520579_gb_ACD58524.1_	0.122	20	0.199	11	0.501	4	0.384	0.286	N	0.57	SignalP-noTM
gi_188520580_gb_ACD58525.1_	0.1	21	0.109	12	0.132	6	0.12	0.113	N	0.51	SignalP-TM
gi_188520581_gb_ACD58526.1_	0.895	24	0.919	24	0.953	18	0.932	0.925	Y	0.57	SignalP-noTM
gi_188520582_gb_ACD58527.1_	0.148	21	0.145	21	0.279	4	0.17	0.157	N	0.57	SignalP-noTM
gi_188520583_gb_ACD58528.1_	0.127	48	0.148	11	0.32	2	0.206	0.175	N	0.57	SignalP-noTM
gi_188520584_gb_ACD58529.1_	0.112	50	0.11	50	0.118	41	0.085	0.098	N	0.57	SignalP-noTM
gi_188520585_gb_ACD58530.1_	0.111	40	0.113	14	0.154	2	0.129	0.121	N	0.57	SignalP-noTM
gi_188520588_gb_ACD58533.1_	0.147	60	0.111	11	0.139	4	0.123	0.117	N	0.57	SignalP-noTM
gi_188520589_gb_ACD58534.1_	0.107	21	0.108	40	0.136	34	0.1	0.104	N	0.57	SignalP-noTM
gi_188520590_gb_ACD58535.1_	0.207	27	0.175	27	0.238	22	0.146	0.161	N	0.57	SignalP-noTM
gi_188520591_gb_ACD58536.1_	0.11	63	0.129	24	0.194	17	0.152	0.139	N	0.57	SignalP-noTM
gi_188520593_gb_ACD58538.1_	0.114	67	0.106	43	0.137	10	0.101	0.104	N	0.57	SignalP-noTM
gi_188520594_gb_ACD58539.1_	0.106	10	0.123	20	0.19	9	0.143	0.132	N	0.57	SignalP-noTM
gi_188520595_gb_ACD58540.1_	0.101	50	0.114	15	0.152	13	0.126	0.12	N	0.57	SignalP-noTM

0.102845	0.000711	0.157095	0.086884	gi_188520426_gb_ACD58371.1_
0.675244	0.287205	0.6673	0.54325	gi_188520427_gb_ACD58372.1_
0.179314	0.046619	0.235772	0.153902	gi_188520428_gb_ACD58373.1_
0.13717	0.064405	0.134703	0.112093	gi_188520429_gb_ACD58374.1_
0.089074	0.006587	0.111155	0.068939	gi_188520432_gb_ACD58377.1_
0.416052	0.219428	0.456609	0.36403	gi_188520434_gb_ACD58379.1_
0.362622	0.21738	0.437331	0.339111	gi_188520435_gb_ACD58380.1_
0.068116	0.027787	0.097704	0.064536	gi_188520436_gb_ACD58381.1_
0.060711	0.000809	0.097969	0.053163	gi_188520437_gb_ACD58382.1_
0.189233	0.156303	0.233617	0.193051	gi_188520438_gb_ACD58383.1_
0.105647	0.068498	0.123251	0.099132	gi_188520439_gb_ACD58384.1_
0.047834	0.027305	0.088588	0.054576	gi_188520441_gb_ACD58386.1_
0.201491	0.010825	0.254643	0.155653	gi_188520442_gb_ACD58387.1_
0.124881	0.037148	0.174509	0.112179	gi_188520444_gb_ACD58389.1_
0.075928	0.033862	0.118157	0.075982	gi_188520445_gb_ACD58390.1_
0.091788	0.126529	0.087145	0.101821	gi_188520446_gb_ACD58391.1_
0.163557	0.214839	0.122282	0.166893	gi_188520447_gb_ACD58392.1_
0.126861	0.076988	0.144427	0.116092	gi_188520448_gb_ACD58393.1_
0.915444	0.965243	0.830616	0.903768	gi_188520451_gb_ACD58396.1_
0.795597	0.348191	0.806121	0.64997	gi_188520452_gb_ACD58397.1_
0.135755	0.000385	0.108806	0.081649	gi_188520454_gb_ACD58399.1_
0.105931	0.014644	0.095868	0.072148	gi_188520455_gb_ACD58400.1_
0.221491	0.1065	0.234154	0.187382	gi_188520456_gb_ACD58401.1_
0.247871	0.629017	0.175375	0.350754	gi_188520457_gb_ACD58402.1_
0.067547	0.086907	0.156303	0.103586	gi_188520458_gb_ACD58403.1_
0.097176	0.029199	0.119413	0.081929	gi_188520469_gb_ACD58414.1_
0.324098	0.029627	0.282316	0.212014	gi_188520481_gb_ACD58426.1_
0.392218	0.973635	0.509749	0.625201	gi_188520490_gb_ACD58435.1_
0.08883	0.832716	0.157892	0.359813	gi_188520491_gb_ACD58436.1_
0.955596	0.988816	0.898803	0.947738	gi_188520498_gb_ACD58443.1_
0.134005	0.14629	0.092289	0.124195	gi_188520502_gb_ACD58447.1_
0.880587	0.976546	0.901766	0.919633	gi_188520507_gb_ACD58452.1_
0.932642	0.974093	0.890319	0.932351	gi_188520513_gb_ACD58458.1_
0.138238	0.069267	0.21687	0.141458	gi_188520514_gb_ACD58459.1_
0.255213	0.108515	0.349554	0.237761	gi_188520515_gb_ACD58460.1_
0.826353	0.970631	0.470783	0.755922	gi_188520516_gb_ACD58461.1_
0.229878	0.043772	0.315614	0.196421	gi_188520517_gb_ACD58462.1_
0.864245	0.915908	0.529217	0.76979	gi_188520518_gb_ACD58463.1_
0.172787	0.047834	0.251807	0.157476	gi_188520522_gb_ACD58467.1_
0.163967	0.284144	0.130903	0.193005	gi_188520528_gb_ACD58473.1_
0.250115	0.527722	0.284754	0.354197	gi_188520531_gb_ACD58476.1_
0.115067	0.082489	0.119413	0.105656	gi_188520537_gb_ACD58482.1_
0.487253	0.020613	0.506	0.337955	gi_528897474_gb_ACD58449.2_
0.488752	0.023385	0.483506	0.331881	gi_528897475_gb_ACD58455.2_
0.637378	0.825491	0.642217	0.701695	gi_188520538_gb_ACD58483.1_
0.1034	0.070831	0.145916	0.106716	gi_188520539_gb_ACD58484.1_
0.284144	0.04936	0.337378	0.223627	gi_188520544_gb_ACD58489.1_
0.061745	0.618456	0.136461	0.272221	gi_188520546_gb_ACD58491.1_
0.102569	0.042778	0.137881	0.094409	gi_188520547_gb_ACD58492.1_
0.104518	0.035468	0.120681	0.086889	gi_188520548_gb_ACD58493.1_
0.491001	0.3327	0.694024	0.505908	gi_188520549_gb_ACD58494.1_
0.108806	0.597005	0.196708	0.30084	gi_188520550_gb_ACD58495.1_
0.638071	0.378716	0.607067	0.541285	gi_188520555_gb_ACD58500.1_
0.156303	0.029713	0.208334	0.13145	gi_188520556_gb_ACD58501.1_
0.967105	0.989799	0.790178	0.915694	gi_188520558_gb_ACD58503.1_
0.922799	0.967485	0.909455	0.933246	gi_188520559_gb_ACD58504.1_
0.062973	0.376601	0.17023	0.203268	gi_188520560_gb_ACD58505.1_
0.489502	0.149694	0.619871	0.419689	gi_188520561_gb_ACD58506.1_
0.074261	0.035571	0.123251	0.077694	gi_188520562_gb_ACD58507.1_
0.101197	0.4955	0.075091	0.223929	gi_188520563_gb_ACD58508.1_
0.105081	0.289051	0.218403	0.204178	gi_188520564_gb_ACD58509.1_
0.106215	0.072426	0.180643	0.119761	gi_188520566_gb_ACD58511.1_
0.242872	0.044788	0.171079	0.152913	gi_188520577_gb_ACD58522.1_
0.907711	0.818021	0.900429	0.875387	gi_188520578_gb_ACD58523.1_
0.904391	0.999827	0.854084	0.919434	gi_188520579_gb_ACD58524.1_
0.071028	0.472278	0.109975	0.21776	gi_188520580_gb_ACD58525.1_
0.831459	0.299013	0.743073	0.624515	gi_188520581_gb_ACD58526.1_
0.112645	0.238486	0.129544	0.160225	gi_188520582_gb_ACD58527.1_
0.93808	0.999923	0.858878	0.932294	gi_188520583_gb_ACD58528.1_
0.120681	0.127194	0.141486	0.129787	gi_188520584_gb_ACD58529.1_
0.192476	0.98737	0.319515	0.499787	gi_188520585_gb_ACD58530.1_
0.129882	0.029541	0.112946	0.09079	gi_188520588_gb_ACD58533.1_
0.075718	0.026442	0.129882	0.077347	gi_188520589_gb_ACD58534.1_
0.446209	0.89264	0.38367	0.574173	gi_188520590_gb_ACD58535.1_
0.204403	0.045695	0.132274	0.127457	gi_188520591_gb_ACD58536.1_
0.136815	0.078276	0.177555	0.130882	gi_188520593_gb_ACD58538.1_
0.174078	0.02271	0.087384	0.094724	gi_188520594_gb_ACD58539.1_
0.057378	0.094319	0.136108	0.095935	gi_188520595_gb_ACD58540.1_

gi_188520596_gb_ACD58541.1_	0.102	27	0.117	11	0.198	1	0.128	0.122	N	0.57	SignalP-noTM
gi_188520597_gb_ACD58542.1_	0.109	9	0.104	24	0.123	14	0.09	0.097	N	0.57	SignalP-noTM
gi_188520598_gb_ACD58543.1_	0.104	36	0.106	11	0.178	1	0.104	0.105	N	0.57	SignalP-noTM
gi_188520601_gb_ACD58546.1_	0.112	29	0.108	55	0.137	49	0.093	0.101	N	0.57	SignalP-noTM
gi_188520604_gb_ACD58549.1_	0.108	43	0.097	64	0.098	61	0.081	0.089	N	0.57	SignalP-noTM
gi_188520605_gb_ACD58550.1_	0.105	45	0.105	51	0.184	42	0.087	0.096	N	0.57	SignalP-noTM
gi_188520606_gb_ACD58551.1_	0.599	26	0.427	26	0.47	25	0.246	0.36	N	0.51	SignalP-TM
gi_188520610_gb_ACD58555.1_	0.17	39	0.147	39	0.21	38	0.109	0.129	N	0.57	SignalP-noTM
gi_188520611_gb_ACD58556.1_	0.126	48	0.11	48	0.117	28	0.085	0.098	N	0.57	SignalP-noTM
gi_188520612_gb_ACD58557.1_	0.23	30	0.315	30	0.586	26	0.407	0.349	N	0.51	SignalP-TM
gi_188520613_gb_ACD58558.1_	0.117	40	0.108	40	0.12	1	0.095	0.102	N	0.57	SignalP-noTM
gi_188520614_gb_ACD58559.1_	0.184	32	0.232	32	0.428	27	0.24	0.235	N	0.51	SignalP-TM
gi_188520615_gb_ACD58560.1_	0.236	37	0.348	37	0.664	28	0.474	0.395	N	0.51	SignalP-TM
gi_188520619_gb_ACD58564.1_	0.267	34	0.194	25	0.45	1	0.257	0.217	N	0.51	SignalP-TM
gi_188520624_gb_ACD58569.1_	0.106	61	0.1	61	0.114	10	0.09	0.096	N	0.57	SignalP-noTM
gi_188520625_gb_ACD58570.1_	0.107	46	0.147	11	0.284	1	0.211	0.177	N	0.57	SignalP-noTM
gi_188520627_gb_ACD58572.1_	0.17	49	0.21	49	0.447	40	0.17	0.191	N	0.57	SignalP-noTM
gi_188520628_gb_ACD58573.1_	0.153	52	0.127	52	0.164	8	0.105	0.117	N	0.57	SignalP-noTM
gi_188520630_gb_ACD58575.1_	0.102	24	0.102	24	0.12	3	0.101	0.102	N	0.57	SignalP-noTM
gi_188520631_gb_ACD58576.1_	0.159	37	0.121	51	0.132	45	0.089	0.106	N	0.57	SignalP-noTM
gi_188520634_gb_ACD58579.1_	0.116	42	0.11	22	0.216	11	0.104	0.107	N	0.57	SignalP-noTM
gi_188520636_gb_ACD58581.1_	0.129	48	0.128	11	0.291	1	0.147	0.137	N	0.57	SignalP-noTM
gi_188520638_gb_ACD58583.1_	0.104	29	0.104	46	0.13	38	0.093	0.099	N	0.57	SignalP-noTM
gi_188520639_gb_ACD58584.1_	0.23	29	0.178	29	0.264	3	0.153	0.169	N	0.51	SignalP-TM
gi_188520641_gb_ACD58586.1_	0.113	33	0.114	33	0.138	1	0.107	0.111	N	0.57	SignalP-noTM
gi_188520642_gb_ACD58587.1_	0.391	23	0.552	23	0.886	18	0.777	0.658	Y	0.57	SignalP-noTM
gi_188520643_gb_ACD58588.1_	0.134	30	0.111	30	0.174	53	0.081	0.097	N	0.57	SignalP-noTM
gi_188520644_gb_ACD58589.1_	0.107	30	0.101	11	0.133	1	0.098	0.099	N	0.57	SignalP-noTM
gi_188520645_gb_ACD58590.1_	0.127	20	0.113	20	0.141	9	0.097	0.106	N	0.57	SignalP-noTM
gi_188520646_gb_ACD58591.1_	0.11	62	0.117	38	0.156	30	0.107	0.112	N	0.57	SignalP-noTM
gi_188520648_gb_ACD58593.1_	0.138	47	0.145	47	0.205	37	0.12	0.133	N	0.57	SignalP-noTM
gi_188520649_gb_ACD58594.1_	0.114	31	0.144	15	0.335	13	0.19	0.166	N	0.57	SignalP-noTM
gi_188520655_gb_ACD58600.1_	0.113	22	0.144	13	0.284	11	0.208	0.174	N	0.57	SignalP-noTM
gi_188520656_gb_ACD58601.1_	0.126	39	0.106	39	0.12	8	0.088	0.097	N	0.57	SignalP-noTM
gi_188520658_gb_ACD58603.1_	0.119	39	0.107	39	0.108	17	0.085	0.097	N	0.57	SignalP-noTM
gi_188520660_gb_ACD58605.1_	0.155	31	0.144	31	0.192	6	0.149	0.146	N	0.57	SignalP-noTM
gi_188520663_gb_ACD58608.1_	0.106	38	0.106	66	0.129	1	0.105	0.106	N	0.57	SignalP-noTM
gi_188520664_gb_ACD58609.1_	0.776	17	0.722	17	0.821	15	0.687	0.706	Y	0.57	SignalP-noTM
gi_188520668_gb_ACD58613.1_	0.128	36	0.191	36	0.438	21	0.302	0.243	N	0.57	SignalP-noTM
gi_188520669_gb_ACD58614.1_	0.661	17	0.6	17	0.66	7	0.536	0.57	N	0.57	SignalP-noTM
gi_188520670_gb_ACD58615.1_	0.108	22	0.114	50	0.183	1	0.103	0.108	N	0.57	SignalP-noTM
gi_188520671_gb_ACD58616.1_	0.164	59	0.132	59	0.21	6	0.11	0.122	N	0.57	SignalP-noTM
gi_188520672_gb_ACD58617.1_	0.148	27	0.116	27	0.128	40	0.093	0.105	N	0.57	SignalP-noTM
gi_188520673_gb_ACD58618.1_	0.355	29	0.183	29	0.174	12	0.103	0.145	N	0.57	SignalP-noTM
gi_188520674_gb_ACD58619.1_	0.274	26	0.221	26	0.367	3	0.238	0.229	N	0.57	SignalP-noTM
gi_188520675_gb_ACD58620.1_	0.15	32	0.129	11	0.256	2	0.163	0.145	N	0.57	SignalP-noTM
gi_188520676_gb_ACD58621.1_	0.158	40	0.2	45	0.508	38	0.154	0.178	N	0.57	SignalP-noTM
gi_188520677_gb_ACD58622.1_	0.232	45	0.125	45	0.155	21	0.079	0.103	N	0.57	SignalP-noTM
gi_188520678_gb_ACD58623.1_	0.113	59	0.101	43	0.11	30	0.085	0.093	N	0.57	SignalP-noTM
gi_188520679_gb_ACD58624.1_	0.119	67	0.108	67	0.12	11	0.082	0.096	N	0.57	SignalP-noTM
gi_188520680_gb_ACD58625.1_	0.251	70	0.183	33	0.54	31	0.211	0.196	N	0.57	SignalP-noTM
gi_188520681_gb_ACD58626.1_	0.205	49	0.255	41	0.661	33	0.347	0.298	N	0.57	SignalP-noTM
gi_188520682_gb_ACD58627.1_	0.492	23	0.67	23	0.96	13	0.914	0.785	Y	0.57	SignalP-noTM
gi_188520687_gb_ACD58632.1_	0.101	44	0.1	44	0.102	35	0.089	0.094	N	0.57	SignalP-noTM
gi_188520688_gb_ACD58633.1_	0.133	51	0.135	32	0.205	25	0.134	0.135	N	0.51	SignalP-TM
gi_188520689_gb_ACD58634.1_	0.147	48	0.147	18	0.248	14	0.205	0.168	N	0.51	SignalP-TM
gi_188520693_gb_ACD58638.1_	0.104	34	0.101	34	0.109	22	0.086	0.094	N	0.57	SignalP-noTM
gi_188520694_gb_ACD58639.1_	0.139	17	0.208	11	0.651	1	0.409	0.303	N	0.57	SignalP-noTM
gi_188520695_gb_ACD58640.1_	0.251	41	0.168	24	0.336	1	0.215	0.19	N	0.57	SignalP-noTM
gi_188520698_gb_ACD58643.1_	0.175	22	0.333	22	0.866	19	0.701	0.506	N	0.57	SignalP-noTM
gi_188520699_gb_ACD58644.1_	0.106	25	0.132	13	0.24	5	0.178	0.153	N	0.57	SignalP-noTM
gi_188520700_gb_ACD58645.1_	0.107	33	0.104	68	0.134	58	0.077	0.094	N	0.51	SignalP-TM
gi_188520701_gb_ACD58646.1_	0.171	37	0.163	37	0.289	3	0.185	0.171	N	0.51	SignalP-TM
gi_188520702_gb_ACD58647.1_	0.15	17	0.138	17	0.245	2	0.15	0.143	N	0.51	SignalP-TM
gi_188520709_gb_ACD58654.1_	0.109	36	0.138	12	0.275	3	0.188	0.162	N	0.57	SignalP-noTM
gi_188520710_gb_ACD58655.1_	0.109	19	0.117	12	0.163	4	0.137	0.126	N	0.57	SignalP-noTM
gi_188520712_gb_ACD58657.1_	0.151	23	0.17	11	0.405	1	0.269	0.217	N	0.57	SignalP-noTM
gi_188520713_gb_ACD58658.1_	0.161	60	0.128	60	0.179	1	0.113	0.121	N	0.57	SignalP-noTM
gi_188520714_gb_ACD58659.1_	0.185	22	0.392	22	0.95	10	0.832	0.599	Y	0.57	SignalP-noTM
gi_188520715_gb_ACD58660.1_	0.14	24	0.14	24	0.236	1	0.159	0.149	N	0.57	SignalP-noTM
gi_188520716_gb_ACD58661.1_	0.543	27	0.72	27	0.982	23	0.939	0.823	Y	0.57	SignalP-noTM
gi_188520724_gb_ACD58669.1_	0.875	27	0.866	27	0.966	15	0.884	0.875	Y	0.57	SignalP-noTM
gi_188520725_gb_ACD58670.1_	0.104	70	0.108	35	0.131	13	0.107	0.108	N	0.57	SignalP-noTM
gi_188520726_gb_ACD58671.1_	0.217	26	0.392	26	0.858	8	0.76	0.565	N	0.57	SignalP-noTM
gi_188520729_gb_ACD58674.1_	0.105	45	0.105	51	0.184	42	0.087	0.096	N	0.57	SignalP-noTM
gi_188520730_gb_ACD58675.1_	0.127	48	0.126	42	0.193	41	0.101	0.114	N	0.57	SignalP-noTM
gi_188520733_gb_ACD58678.1_	0.151	31	0.131	31	0.13	25	0.095	0.114	N	0.57	SignalP-noTM
gi_188520736_gb_ACD58681.1_	0.125	21	0.12	21	0.159	1	0.107	0.114	N	0.57	SignalP-noTM

0.709715	0.899619	0.561192	0.723509	gi_188520596_gb_ACD58541.1_
0.153553	0.063328	0.230942	0.149274	gi_188520597_gb_ACD58542.1_
0.066982	0.00054	0.138955	0.068826	gi_188520598_gb_ACD58543.1_
0.266784	0.97902	0.248991	0.498265	gi_188520601_gb_ACD58546.1_
0.359163	0.879001	0.461824	0.566663	gi_188520604_gb_ACD58549.1_
0.109097	0.031401	0.129544	0.090014	gi_188520605_gb_ACD58550.1_
0.184673	0.042656	0.262116	0.163148	gi_188520606_gb_ACD58551.1_
0.170654	0.031129	0.224088	0.141957	gi_188520610_gb_ACD58555.1_
0.109975	0.022843	0.144056	0.092291	gi_188520611_gb_ACD58556.1_
0.95585	0.991049	0.921507	0.956135	gi_188520612_gb_ACD58557.1_
0.114762	0.114457	0.107072	0.112097	gi_188520613_gb_ACD58558.1_
0.736722	0.842108	0.697833	0.758888	gi_188520614_gb_ACD58559.1_
0.401553	0.228289	0.520988	0.38361	gi_188520615_gb_ACD58560.1_
0.125868	0.110563	0.199089	0.145173	gi_188520619_gb_ACD58564.1_
0.881843	0.999063	0.829346	0.903417	gi_188520624_gb_ACD58569.1_
0.091289	0.02186	0.140397	0.084515	gi_188520625_gb_ACD58570.1_
0.191081	0.177994	0.180643	0.183239	gi_188520627_gb_ACD58572.1_
0.094576	0.103123	0.074675	0.090791	gi_188520628_gb_ACD58573.1_
0.119413	0.066422	0.121639	0.102491	gi_188520630_gb_ACD58575.1_
0.564145	0.488002	0.617039	0.556395	gi_188520631_gb_ACD58576.1_
0.894636	0.990529	0.840506	0.908557	gi_188520634_gb_ACD58579.1_
0.099571	0.043647	0.130903	0.091374	gi_188520636_gb_ACD58581.1_
0.150077	0.227233	0.087864	0.155058	gi_188520638_gb_ACD58583.1_
0.154335	0.117533	0.172787	0.148218	gi_188520639_gb_ACD58584.1_
0.929955	0.996942	0.806121	0.911006	gi_188520641_gb_ACD58586.1_
0.466301	0.869097	0.611352	0.648917	gi_188520642_gb_ACD58587.1_
0.066982	0.003714	0.100924	0.057207	gi_188520643_gb_ACD58588.1_
0.187399	0.119729	0.228818	0.178649	gi_188520644_gb_ACD58589.1_
0.112946	0.115679	0.145916	0.124847	gi_188520645_gb_ACD58590.1_
0.461079	0.06985	0.559714	0.363548	gi_188520646_gb_ACD58591.1_
0.115373	0.348191	0.101197	0.188254	gi_188520648_gb_ACD58593.1_
0.936672	0.836443	0.934869	0.902661	gi_188520649_gb_ACD58594.1_
0.668631	0.863539	0.78968	0.77395	gi_188520655_gb_ACD58600.1_
0.255213	0.018487	0.289051	0.187584	gi_188520656_gb_ACD58601.1_
0.926763	0.997254	0.739621	0.887879	gi_188520658_gb_ACD58603.1_
0.442505	0.095609	0.712181	0.416765	gi_188520660_gb_ACD58605.1_
0.134354	0.039925	0.156303	0.110194	gi_188520663_gb_ACD58608.1_
0.424824	0.593391	0.540412	0.519542	gi_188520664_gb_ACD58609.1_
0.90256	0.669295	0.887953	0.819936	gi_188520668_gb_ACD58613.1_
0.578837	0.347511	0.689546	0.538631	gi_188520669_gb_ACD58614.1_
0.209822	0.145916	0.245085	0.200274	gi_188520670_gb_ACD58615.1_
0.144427	0.016824	0.188314	0.116522	gi_188520671_gb_ACD58616.1_
0.09104	0.02795	0.108806	0.075932	gi_188520672_gb_ACD58617.1_
0.106786	0.010857	0.15046	0.089368	gi_188520673_gb_ACD58618.1_
0.069267	0.043025	0.108225	0.073506	gi_188520674_gb_ACD58619.1_
0.174509	0.804239	0.169806	0.382851	gi_188520675_gb_ACD58620.1_
0.809382	0.535192	0.701615	0.682063	gi_188520676_gb_ACD58621.1_
0.085489	0.051368	0.140397	0.092418	gi_188520677_gb_ACD58622.1_
0.121639	0.039128	0.196234	0.119	gi_188520678_gb_ACD58623.1_
0.087624	0.013009	0.12196	0.074198	gi_188520679_gb_ACD58624.1_
0.157892	0.411686	0.123901	0.23116	gi_188520680_gb_ACD58625.1_
0.1603	0.125538	0.17023	0.152023	gi_188520681_gb_ACD58626.1_
0.943906	0.998345	0.875119	0.939123	gi_188520682_gb_ACD58627.1_
0.168541	0.956727	0.297757	0.474342	gi_188520687_gb_ACD58632.1_
0.164379	0.123251	0.187399	0.158343	gi_188520688_gb_ACD58633.1_
0.174942	0.144798	0.21738	0.17904	gi_188520689_gb_ACD58634.1_
0.717684	0.899348	0.534445	0.717159	gi_188520693_gb_ACD58638.1_
0.184222	0.983809	0.048522	0.405518	gi_188520694_gb_ACD58639.1_
0.177118	0.334033	0.248431	0.253194	gi_188520695_gb_ACD58640.1_
0.587587	0.63251	0.707857	0.642651	gi_188520698_gb_ACD58643.1_
0.713409	0.993994	0.581029	0.762811	gi_188520699_gb_ACD58644.1_
0.087864	0.038457	0.132619	0.086313	gi_188520700_gb_ACD58645.1_
0.10011	0.087145	0.094576	0.093944	gi_188520701_gb_ACD58646.1_
0.141122	0.086669	0.227761	0.151851	gi_188520702_gb_ACD58647.1_
0.4985	0.979984	0.763687	0.74739	gi_188520709_gb_ACD58654.1_
0.266784	0.940977	0.418241	0.542001	gi_188520710_gb_ACD58655.1_
0.182873	0.114457	0.135755	0.144362	gi_188520712_gb_ACD58657.1_
0.131244	0.063506	0.157493	0.117414	gi_188520713_gb_ACD58658.1_
0.949358	0.98722	0.926967	0.954515	gi_188520714_gb_ACD58659.1_
0.226707	0.997934	0.158291	0.460977	gi_188520715_gb_ACD58660.1_
0.918863	0.996979	0.860326	0.925389	gi_188520716_gb_ACD58661.1_
0.147418	0.012518	0.207839	0.122592	gi_188520724_gb_ACD58669.1_
0.913805	0.943428	0.826783	0.894672	gi_188520725_gb_ACD58670.1_
0.312383	0.874462	0.399392	0.528746	gi_188520726_gb_ACD58671.1_
0.810767	0.528469	0.764768	0.701335	gi_188520729_gb_ACD58674.1_
0.748758	0.807057	0.845665	0.800493	gi_188520730_gb_ACD58675.1_
0.097176	0.425557	0.07385	0.198861	gi_188520733_gb_ACD58678.1_
0.135053	0.817127	0.077201	0.343127	gi_188520736_gb_ACD58681.1_

gi_188520737_gb_ACD58682.1_	0.324	51	0.201	51	0.214	47	0.084	0.146	N	0.57	SignalP-noTM
gi_188520738_gb_ACD58683.1_	0.114	34	0.121	15	0.183	7	0.145	0.132	N	0.57	SignalP-noTM
gi_188520739_gb_ACD58684.1_	0.162	22	0.227	16	0.431	1	0.371	0.28	N	0.51	SignalP-TM
gi_188520741_gb_ACD58686.1_	0.239	24	0.26	24	0.414	22	0.263	0.262	N	0.51	SignalP-TM
gi_188520742_gb_ACD58687.1_	0.123	48	0.129	24	0.235	19	0.143	0.134	N	0.51	SignalP-TM
gi_188520744_gb_ACD58689.1_	0.113	28	0.124	51	0.287	48	0.112	0.118	N	0.57	SignalP-noTM
gi_188520745_gb_ACD58690.1_	0.138	31	0.157	17	0.246	2	0.195	0.175	N	0.57	SignalP-noTM
gi_188520746_gb_ACD58691.1_	0.105	25	0.106	32	0.16	1	0.108	0.107	N	0.57	SignalP-noTM
gi_188520749_gb_ACD58694.1_	0.11	24	0.129	54	0.232	49	0.101	0.116	N	0.57	SignalP-noTM
gi_188520752_gb_ACD58697.1_	0.26	33	0.251	33	0.507	6	0.338	0.292	N	0.57	SignalP-noTM
gi_188520755_gb_ACD58700.1_	0.386	19	0.374	19	0.501	3	0.396	0.385	N	0.57	SignalP-noTM
gi_188520762_gb_ACD58707.1_	0.34	20	0.407	20	0.69	1	0.534	0.467	N	0.57	SignalP-noTM
gi_188520765_gb_ACD58710.1_	0.165	37	0.147	37	0.16	35	0.111	0.13	N	0.57	SignalP-noTM
gi_188520769_gb_ACD58714.1_	0.856	22	0.856	22	0.922	2	0.876	0.866	Y	0.57	SignalP-noTM
gi_188520770_gb_ACD58715.1_	0.118	46	0.103	28	0.117	20	0.072	0.088	N	0.57	SignalP-noTM
gi_188520771_gb_ACD58716.1_	0.145	33	0.138	33	0.29	1	0.136	0.137	N	0.57	SignalP-noTM
gi_188520772_gb_ACD58717.1_	0.329	27	0.487	27	0.947	17	0.812	0.64	Y	0.57	SignalP-noTM
gi_188520774_gb_ACD58719.1_	0.131	64	0.125	11	0.195	1	0.155	0.139	N	0.57	SignalP-noTM
gi_188520775_gb_ACD58720.1_	0.118	26	0.11	50	0.135	38	0.095	0.103	N	0.57	SignalP-noTM
gi_188520776_gb_ACD58721.1_	0.12	28	0.118	28	0.207	25	0.102	0.11	N	0.57	SignalP-noTM
gi_188520777_gb_ACD58722.1_	0.16	20	0.116	11	0.236	2	0.131	0.123	N	0.57	SignalP-noTM
gi_188520778_gb_ACD58723.1_	0.352	30	0.277	30	0.464	15	0.284	0.28	N	0.57	SignalP-noTM
gi_188520779_gb_ACD58724.1_	0.233	20	0.206	20	0.408	4	0.247	0.225	N	0.57	SignalP-noTM
gi_188520780_gb_ACD58725.1_	0.117	24	0.101	70	0.117	33	0.084	0.093	N	0.57	SignalP-noTM
gi_188520787_gb_ACD58732.1_	0.104	18	0.226	11	0.674	1	0.516	0.333	N	0.51	SignalP-TM
gi_188520799_gb_ACD58744.1_	0.115	20	0.129	20	0.183	9	0.136	0.132	N	0.57	SignalP-noTM
gi_188520800_gb_ACD58745.1_	0.12	22	0.106	22	0.119	16	0.082	0.095	N	0.57	SignalP-noTM
gi_188520801_gb_ACD58746.1_	0.102	60	0.133	11	0.34	1	0.153	0.142	N	0.57	SignalP-noTM
gi_188520802_gb_ACD58747.1_	0.178	42	0.14	42	0.168	41	0.103	0.122	N	0.57	SignalP-noTM
gi_188520803_gb_ACD58748.1_	0.128	54	0.159	16	0.298	11	0.254	0.203	N	0.57	SignalP-noTM
gi_188520804_gb_ACD58749.1_	0.123	27	0.129	32	0.22	1	0.119	0.125	N	0.51	SignalP-TM
gi_188520805_gb_ACD58750.1_	0.142	29	0.245	12	0.645	10	0.609	0.416	N	0.57	SignalP-noTM
gi_188520808_gb_ACD58753.1_	0.123	28	0.145	11	0.298	1	0.197	0.169	N	0.57	SignalP-noTM
gi_188520809_gb_ACD58754.1_	0.137	27	0.145	12	0.265	1	0.209	0.175	N	0.57	SignalP-noTM
gi_188520810_gb_ACD58755.1_	0.277	24	0.488	24	0.969	9	0.899	0.681	Y	0.57	SignalP-noTM
gi_188520811_gb_ACD58756.1_	0.109	67	0.107	12	0.149	2	0.116	0.111	N	0.57	SignalP-noTM
gi_188520812_gb_ACD58757.1_	0.108	63	0.111	38	0.185	37	0.097	0.104	N	0.57	SignalP-noTM
gi_188520813_gb_ACD58758.1_	0.106	25	0.103	11	0.141	2	0.104	0.103	N	0.57	SignalP-noTM
gi_188520814_gb_ACD58759.1_	0.17	35	0.147	35	0.333	34	0.109	0.129	N	0.57	SignalP-noTM
gi_188520821_gb_ACD58766.1_	0.288	28	0.203	28	0.268	8	0.184	0.194	N	0.57	SignalP-noTM
gi_188520822_gb_ACD58767.1_	0.101	52	0.1	70	0.117	33	0.092	0.096	N	0.57	SignalP-noTM
gi_188520826_gb_ACD58771.1_	0.123	40	0.122	40	0.144	44	0.107	0.115	N	0.57	SignalP-noTM
gi_188520827_gb_ACD58772.1_	0.141	25	0.189	18	0.456	5	0.34	0.26	N	0.57	SignalP-noTM
gi_188520830_gb_ACD58775.1_	0.158	25	0.139	25	0.22	2	0.142	0.14	N	0.57	SignalP-noTM
gi_188520831_gb_ACD58776.1_	0.206	49	0.136	49	0.207	11	0.119	0.128	N	0.57	SignalP-noTM
gi_188520832_gb_ACD58777.1_	0.125	40	0.154	11	0.347	1	0.235	0.192	N	0.57	SignalP-noTM
gi_188520837_gb_ACD58782.1_	0.151	55	0.226	55	0.424	46	0.219	0.224	N	0.51	SignalP-TM
gi_188520838_gb_ACD58783.1_	0.119	18	0.275	18	0.773	1	0.649	0.451	N	0.57	SignalP-noTM
gi_188520844_gb_ACD58789.1_	0.131	24	0.127	13	0.168	10	0.137	0.132	N	0.57	SignalP-noTM
gi_188520847_gb_ACD58792.1_	0.117	25	0.152	18	0.238	16	0.202	0.175	N	0.57	SignalP-noTM
gi_188520850_gb_ACD58795.1_	0.128	29	0.122	29	0.165	50	0.097	0.11	N	0.57	SignalP-noTM
gi_188520851_gb_ACD58796.1_	0.136	38	0.111	38	0.128	37	0.079	0.096	N	0.57	SignalP-noTM
gi_188520852_gb_ACD58797.1_	0.168	47	0.141	47	0.368	7	0.135	0.138	N	0.57	SignalP-noTM
gi_188520853_gb_ACD58798.1_	0.199	35	0.166	35	0.31	25	0.122	0.145	N	0.57	SignalP-noTM
gi_188520854_gb_ACD58799.1_	0.098	25	0.162	11	0.348	5	0.276	0.204	N	0.51	SignalP-TM
gi_188520855_gb_ACD58800.1_	0.114	21	0.118	37	0.171	30	0.108	0.113	N	0.57	SignalP-noTM
gi_188520856_gb_ACD58801.1_	0.219	37	0.269	18	0.409	14	0.298	0.283	N	0.57	SignalP-noTM
gi_188520857_gb_ACD58802.1_	0.147	17	0.159	39	0.405	32	0.179	0.168	N	0.57	SignalP-noTM
gi_188520858_gb_ACD58803.1_	0.123	46	0.134	46	0.229	44	0.135	0.135	N	0.57	SignalP-noTM
gi_188520859_gb_ACD58804.1_	0.246	30	0.237	13	0.734	12	0.518	0.369	N	0.57	SignalP-noTM
gi_188520860_gb_ACD58805.1_	0.172	28	0.161	28	0.278	26	0.166	0.163	N	0.57	SignalP-noTM
gi_188520861_gb_ACD58806.1_	0.107	35	0.106	47	0.138	44	0.09	0.098	N	0.57	SignalP-noTM
gi_188520862_gb_ACD58807.1_	0.199	38	0.134	13	0.211	2	0.179	0.155	N	0.57	SignalP-noTM
gi_188520864_gb_ACD58809.1_	0.109	36	0.119	25	0.186	19	0.138	0.128	N	0.57	SignalP-noTM
gi_188520866_gb_ACD58811.1_	0.126	25	0.142	17	0.24	9	0.189	0.164	N	0.57	SignalP-noTM
gi_188520867_gb_ACD58812.1_	0.125	52	0.24	11	0.691	4	0.6	0.41	N	0.57	SignalP-noTM
gi_188520869_gb_ACD58814.1_	0.104	27	0.138	12	0.231	2	0.189	0.162	N	0.57	SignalP-noTM
gi_188520870_gb_ACD58815.1_	0.277	33	0.179	33	0.168	32	0.109	0.146	N	0.57	SignalP-noTM
gi_188520872_gb_ACD58817.1_	0.102	41	0.131	19	0.249	12	0.134	0.133	N	0.57	SignalP-noTM
gi_188520874_gb_ACD58819.1_	0.116	12	0.134	12	0.18	9	0.152	0.141	N	0.51	SignalP-TM
gi_188520875_gb_ACD58820.1_	0.128	20	0.134	20	0.197	1	0.143	0.137	N	0.51	SignalP-TM
gi_188520877_gb_ACD58822.1_	0.141	7	0.1	44	0.119	40	0.087	0.095	N	0.51	SignalP-TM
gi_188520878_gb_ACD58823.1_	0.226	38	0.139	38	0.141	17	0.089	0.116	N	0.57	SignalP-noTM
gi_188520879_gb_ACD58824.1_	0.103	44	0.11	30	0.154	1	0.12	0.115	N	0.57	SignalP-noTM
gi_188520882_gb_ACD58827.1_	0.116	41	0.139	41	0.3	35	0.108	0.125	N	0.57	SignalP-noTM
gi_188520883_gb_ACD58828.1_	0.49	26	0.67	26	0.967	16	0.932	0.793	Y	0.57	SignalP-noTM
gi_188520884_gb_ACD58829.1_	0.356	24	0.288	24	0.453	14	0.237	0.264	N	0.57	SignalP-noTM
gi_188520885_gb_ACD58830.1_	0.105	40	0.1	11	0.165	2	0.095	0.098	N	0.57	SignalP-noTM

0.116294	0.29713	0.080913	0.164779	gi_188520737_gb_ACD58682.1_
0.077629	0.027305	0.090298	0.065077	gi_188520738_gb_ACD58683.1_
0.091538	0.003113	0.126529	0.073727	gi_188520739_gb_ACD58684.1_
0.106786	0.021796	0.13193	0.086837	gi_188520741_gb_ACD58686.1_
0.101744	0.125538	0.113247	0.11351	gi_188520742_gb_ACD58687.1_
0.095349	0.048939	0.128869	0.091052	gi_188520744_gb_ACD58689.1_
0.271505	0.246754	0.352287	0.290182	gi_188520745_gb_ACD58690.1_
0.752688	0.606351	0.907459	0.755499	gi_188520746_gb_ACD58691.1_
0.129882	0.008535	0.137525	0.091981	gi_188520749_gb_ACD58694.1_
0.658586	0.408783	0.737884	0.601751	gi_188520752_gb_ACD58697.1_
0.236855	0.021227	0.341414	0.199832	gi_188520755_gb_ACD58700.1_
0.653849	0.215853	0.660607	0.510103	gi_188520762_gb_ACD58707.1_
0.068881	0.051077	0.116912	0.078957	gi_188520765_gb_ACD58710.1_
0.955212	0.999564	0.931884	0.96222	gi_188520769_gb_ACD58714.1_
0.129206	0.026211	0.184222	0.113213	gi_188520770_gb_ACD58715.1_
0.630416	0.094319	0.647713	0.457483	gi_188520771_gb_ACD58716.1_
0.624806	0.344117	0.734973	0.567965	gi_188520772_gb_ACD58717.1_
0.091538	0.040272	0.116912	0.082907	gi_188520774_gb_ACD58719.1_
0.124227	0.073237	0.129206	0.10889	gi_188520775_gb_ACD58720.1_
0.069655	0.038679	0.117222	0.075185	gi_188520776_gb_ACD58721.1_
0.837671	0.999731	0.68568	0.841027	gi_188520777_gb_ACD58722.1_
0.145542	0.169806	0.128532	0.14796	gi_188520778_gb_ACD58723.1_
0.103958	0.155907	0.102569	0.120811	gi_188520779_gb_ACD58724.1_
0.080247	0.047156	0.096914	0.074772	gi_188520780_gb_ACD58725.1_
0.427759	0.969851	0.331369	0.576326	gi_188520787_gb_ACD58732.1_
0.392218	0.729088	0.364705	0.495337	gi_188520799_gb_ACD58744.1_
0.049784	0.020016	0.091788	0.053863	gi_188520800_gb_ACD58745.1_
0.600608	0.727307	0.737884	0.6886	gi_188520801_gb_ACD58746.1_
0.357094	0.92129	0.369584	0.549323	gi_188520802_gb_ACD58747.1_
0.165205	0.069074	0.177555	0.137278	gi_188520803_gb_ACD58748.1_
0.062973	0.03131	0.081361	0.058548	gi_188520804_gb_ACD58749.1_
0.036615	0.047021	0.075928	0.053188	gi_188520805_gb_ACD58750.1_
0.084324	0.024435	0.120681	0.07648	gi_188520808_gb_ACD58753.1_
0.164792	0.552308	0.109681	0.275594	gi_188520809_gb_ACD58754.1_
0.126198	0.925532	0.08181	0.377847	gi_188520810_gb_ACD58755.1_
0.120045	0.008163	0.159092	0.095767	gi_188520811_gb_ACD58756.1_
0.08883	0.030413	0.083402	0.067548	gi_188520812_gb_ACD58757.1_
0.073237	0.043397	0.109975	0.075536	gi_188520813_gb_ACD58758.1_
0.24232	0.951478	0.102569	0.432122	gi_188520814_gb_ACD58759.1_
0.123251	0.059693	0.153944	0.112296	gi_188520821_gb_ACD58766.1_
0.138955	0.077415	0.086195	0.100855	gi_188520822_gb_ACD58767.1_
0.119098	0.167702	0.0985	0.128433	gi_188520826_gb_ACD58771.1_
0.922799	0.999649	0.80799	0.910146	gi_188520827_gb_ACD58772.1_
0.137881	0.05869	0.198611	0.131727	gi_188520830_gb_ACD58775.1_
0.119729	0.001311	0.193879	0.104973	gi_188520831_gb_ACD58776.1_
0.177994	0.002458	0.259225	0.146559	gi_188520832_gb_ACD58777.1_
0.948485	0.999929	0.895482	0.947965	gi_188520837_gb_ACD58782.1_
0.56193	0.929169	0.75547	0.748856	gi_188520838_gb_ACD58783.1_
0.090298	0.022643	0.239031	0.117324	gi_188520844_gb_ACD58789.1_
0.169384	0.134005	0.112047	0.138479	gi_188520847_gb_ACD58792.1_
0.192476	0.963173	0.151614	0.435754	gi_188520850_gb_ACD58795.1_
0.149694	0.085021	0.153553	0.129423	gi_188520851_gb_ACD58796.1_
0.153553	0.056572	0.217891	0.142672	gi_188520852_gb_ACD58797.1_
0.091538	0.047021	0.179756	0.106105	gi_188520853_gb_ACD58798.1_
0.919087	0.999755	0.802818	0.90722	gi_188520854_gb_ACD58799.1_
0.141851	0.088346	0.087384	0.10586	gi_188520855_gb_ACD58800.1_
0.064224	0.03214	0.096651	0.064338	gi_188520856_gb_ACD58801.1_
0.110859	0.002161	0.181979	0.098333	gi_188520857_gb_ACD58802.1_
0.086669	0.038568	0.127527	0.084255	gi_188520858_gb_ACD58803.1_
0.072628	0.000578	0.109975	0.06106	gi_188520859_gb_ACD58804.1_
0.1603	0.004962	0.21738	0.127547	gi_188520860_gb_ACD58805.1_
0.937027	0.877396	0.920195	0.911539	gi_188520861_gb_ACD58806.1_
0.090545	0.125868	0.173647	0.13002	gi_188520862_gb_ACD58807.1_
0.955468	0.999791	0.823319	0.926193	gi_188520864_gb_ACD58809.1_
0.932264	0.999222	0.885543	0.93901	gi_188520866_gb_ACD58811.1_
0.119729	0.415324	0.187399	0.240817	gi_188520867_gb_ACD58812.1_
0.102845	0.021353	0.136815	0.087004	gi_188520869_gb_ACD58814.1_
0.254643	0.039925	0.100381	0.13165	gi_188520870_gb_ACD58815.1_
0.177994	0.002042	0.279891	0.153309	gi_188520872_gb_ACD58817.1_
0.085724	0.032799	0.110269	0.076264	gi_188520874_gb_ACD58819.1_
0.06054	0.56193	0.113548	0.245339	gi_188520875_gb_ACD58820.1_
0.074261	0.033961	0.11385	0.074024	gi_188520877_gb_ACD58822.1_
0.201009	0.02408	0.247312	0.157467	gi_188520878_gb_ACD58823.1_
0.054064	0.026831	0.098234	0.05971	gi_188520879_gb_ACD58824.1_
0.339393	0.074883	0.432171	0.282149	gi_188520882_gb_ACD58827.1_
0.936494	0.922585	0.926763	0.928614	gi_188520883_gb_ACD58828.1_
0.316912	0.188773	0.428494	0.311393	gi_188520884_gb_ACD58829.1_
0.266198	0.985825	0.083173	0.445065	gi_188520885_gb_ACD58830.1_

gi_188520888_gb_ACD58833.1_	0.112	21	0.146	11	0.288	1	0.205	0.174	N	0.57	SignalP-noTM
gi_188520889_gb_ACD58834.1_	0.24	44	0.216	44	0.331	42	0.147	0.184	N	0.57	SignalP-noTM
gi_188520892_gb_ACD58837.1_	0.112	60	0.103	38	0.119	35	0.081	0.092	N	0.57	SignalP-noTM
gi_188520893_gb_ACD58838.1_	0.148	23	0.172	23	0.393	11	0.209	0.189	N	0.57	SignalP-noTM
gi_188520894_gb_ACD58839.1_	0.136	23	0.115	23	0.161	41	0.092	0.104	N	0.57	SignalP-noTM
gi_188520895_gb_ACD58840.1_	0.131	21	0.104	42	0.129	40	0.077	0.091	N	0.57	SignalP-noTM
gi_188520896_gb_ACD58841.1_	0.175	33	0.147	33	0.215	32	0.11	0.13	N	0.57	SignalP-noTM
gi_188520898_gb_ACD58843.1_	0.133	43	0.103	43	0.1	39	0.059	0.082	N	0.57	SignalP-noTM
gi_188520902_gb_ACD58847.1_	0.125	53	0.147	11	0.282	5	0.22	0.181	N	0.57	SignalP-noTM
gi_188520904_gb_ACD58849.1_	0.202	12	0.188	12	0.349	10	0.175	0.182	N	0.57	SignalP-noTM
gi_188520908_gb_ACD58853.1_	0.099	65	0.102	16	0.147	10	0.103	0.102	N	0.57	SignalP-noTM
gi_188520909_gb_ACD58854.1_	0.127	60	0.106	38	0.136	1	0.088	0.098	N	0.57	SignalP-noTM
gi_188520912_gb_ACD58857.1_	0.136	38	0.112	38	0.129	37	0.093	0.103	N	0.57	SignalP-noTM
gi_188520914_gb_ACD58859.1_	0.117	67	0.114	27	0.144	11	0.123	0.118	N	0.57	SignalP-noTM
gi_188520915_gb_ACD58860.1_	0.171	23	0.346	23	0.831	18	0.701	0.513	N	0.57	SignalP-noTM
gi_188520916_gb_ACD58861.1_	0.134	21	0.112	21	0.135	30	0.096	0.105	N	0.57	SignalP-noTM
gi_188520917_gb_ACD58862.1_	0.152	24	0.174	11	0.433	1	0.281	0.224	N	0.57	SignalP-noTM
gi_188520918_gb_ACD58863.1_	0.125	59	0.118	11	0.215	1	0.139	0.128	N	0.57	SignalP-noTM
gi_188520919_gb_ACD58864.1_	0.16	27	0.124	27	0.129	53	0.08	0.103	N	0.57	SignalP-noTM
gi_188520920_gb_ACD58865.1_	0.185	37	0.211	37	0.4	29	0.167	0.195	N	0.51	SignalP-TM
gi_188520921_gb_ACD58866.1_	0.204	24	0.13	24	0.105	23	0.081	0.107	N	0.57	SignalP-noTM
gi_188520922_gb_ACD58867.1_	0.125	31	0.14	11	0.303	4	0.211	0.174	N	0.57	SignalP-noTM
gi_188520923_gb_ACD58868.1_	0.129	41	0.109	41	0.117	23	0.087	0.099	N	0.57	SignalP-noTM
gi_188520926_gb_ACD58871.1_	0.113	44	0.106	68	0.124	62	0.088	0.098	N	0.57	SignalP-noTM
gi_188520929_gb_ACD58874.1_	0.157	21	0.143	21	0.227	1	0.146	0.144	N	0.57	SignalP-noTM
gi_188520930_gb_ACD58875.1_	0.146	31	0.166	31	0.277	35	0.155	0.162	N	0.51	SignalP-TM
gi_188520940_gb_ACD58885.1_	0.103	54	0.104	19	0.153	8	0.101	0.103	N	0.57	SignalP-noTM
gi_188520942_gb_ACD58887.1_	0.223	43	0.152	43	0.138	5	0.106	0.13	N	0.57	SignalP-noTM
gi_188520943_gb_ACD58888.1_	0.141	43	0.158	17	0.323	14	0.238	0.187	N	0.51	SignalP-TM
gi_188520944_gb_ACD58889.1_	0.198	55	0.239	55	0.418	50	0.178	0.216	N	0.51	SignalP-TM
gi_188520945_gb_ACD58890.1_	0.131	31	0.139	11	0.241	3	0.199	0.167	N	0.57	SignalP-noTM
gi_188520946_gb_ACD58891.1_	0.22	24	0.293	24	0.686	4	0.497	0.369	N	0.51	SignalP-TM
gi_188520947_gb_ACD58892.1_	0.115	41	0.107	41	0.113	38	0.09	0.099	N	0.57	SignalP-noTM
gi_188520948_gb_ACD58893.1_	0.116	37	0.159	11	0.335	1	0.244	0.199	N	0.57	SignalP-noTM
gi_188520949_gb_ACD58894.1_	0.446	22	0.293	22	0.361	6	0.244	0.275	N	0.51	SignalP-TM
gi_188520950_gb_ACD58895.1_	0.127	33	0.134	33	0.247	15	0.158	0.143	N	0.51	SignalP-TM
gi_188520951_gb_ACD58896.1_	0.111	24	0.105	24	0.142	1	0.096	0.101	N	0.57	SignalP-noTM
gi_188520952_gb_ACD58897.1_	0.253	29	0.151	29	0.191	35	0.087	0.121	N	0.57	SignalP-noTM
gi_188520956_gb_ACD58901.1_	0.181	22	0.209	22	0.371	7	0.277	0.234	N	0.51	SignalP-TM
gi_188520957_gb_ACD58902.1_	0.151	25	0.111	11	0.153	4	0.128	0.117	N	0.51	SignalP-TM
gi_188520958_gb_ACD58903.1_	0.12	38	0.114	52	0.167	49	0.086	0.104	N	0.51	SignalP-TM
gi_188520959_gb_ACD58904.1_	0.157	23	0.257	23	0.717	8	0.509	0.35	N	0.51	SignalP-TM
gi_188520960_gb_ACD58905.1_	0.117	64	0.129	19	0.191	6	0.161	0.141	N	0.51	SignalP-TM
gi_188520962_gb_ACD58907.1_	0.133	20	0.156	11	0.297	2	0.235	0.193	N	0.57	SignalP-noTM
gi_188520963_gb_ACD58908.1_	0.143	20	0.17	20	0.253	12	0.204	0.186	N	0.57	SignalP-noTM
gi_188520964_gb_ACD58909.1_	0.241	45	0.216	45	0.474	43	0.146	0.183	N	0.57	SignalP-noTM
gi_188520965_gb_ACD58910.1_	0.123	16	0.115	43	0.145	52	0.088	0.102	N	0.57	SignalP-noTM
gi_188520966_gb_ACD58911.1_	0.24	37	0.196	37	0.264	2	0.127	0.17	N	0.51	SignalP-TM
gi_188520969_gb_ACD58914.1_	0.114	67	0.106	43	0.137	10	0.101	0.104	N	0.57	SignalP-noTM
gi_188520970_gb_ACD58915.1_	0.147	40	0.139	40	0.171	26	0.11	0.125	N	0.57	SignalP-noTM
gi_188520971_gb_ACD58916.1_	0.119	19	0.139	19	0.2	48	0.151	0.145	N	0.57	SignalP-noTM
gi_188520984_gb_ACD58929.1_	0.115	61	0.182	12	0.485	1	0.286	0.221	N	0.51	SignalP-TM
gi_188520985_gb_ACD58930.1_	0.348	34	0.237	34	0.231	33	0.154	0.198	N	0.57	SignalP-noTM
gi_188520986_gb_ACD58931.1_	0.106	22	0.12	29	0.165	19	0.115	0.117	N	0.57	SignalP-noTM
gi_188520987_gb_ACD58932.1_	0.109	39	0.111	16	0.159	8	0.114	0.113	N	0.57	SignalP-noTM
gi_188520988_gb_ACD58933.1_	0.788	35	0.796	35	0.862	26	0.726	0.77	Y	0.51	SignalP-TM
gi_188520989_gb_ACD58934.1_	0.132	14	0.154	14	0.281	12	0.185	0.169	N	0.57	SignalP-noTM
gi_188520990_gb_ACD58935.1_	0.107	18	0.104	50	0.144	2	0.094	0.099	N	0.57	SignalP-noTM
gi_188520994_gb_ACD58939.1_	0.111	50	0.13	50	0.2	48	0.125	0.128	N	0.57	SignalP-noTM
gi_188520995_gb_ACD58940.1_	0.147	63	0.168	11	0.443	1	0.256	0.21	N	0.57	SignalP-noTM
gi_188520996_gb_ACD58941.1_	0.115	26	0.107	48	0.13	36	0.09	0.099	N	0.57	SignalP-noTM
gi_188520998_gb_ACD58943.1_	0.104	26	0.106	11	0.138	5	0.116	0.109	N	0.51	SignalP-TM
gi_188521001_gb_ACD58946.1_	0.169	49	0.143	49	0.195	12	0.13	0.137	N	0.57	SignalP-noTM
gi_528897479_gb_ACD58948.2_	0.116	66	0.12	58	0.201	1	0.109	0.115	N	0.57	SignalP-noTM
gi_188521004_gb_ACD58949.1_	0.29	32	0.144	32	0.246	14	0.131	0.14	N	0.51	SignalP-TM
gi_188521018_gb_ACD58963.1_	0.128	56	0.146	56	0.204	46	0.139	0.143	N	0.57	SignalP-noTM
gi_188521023_gb_ACD58968.1_	0.155	35	0.159	35	0.326	2	0.177	0.168	N	0.57	SignalP-noTM
gi_188521026_gb_ACD58971.1_	0.103	29	0.147	18	0.31	17	0.213	0.178	N	0.57	SignalP-noTM
gi_188521032_gb_ACD58977.1_	0.18	46	0.143	11	0.278	2	0.201	0.17	N	0.57	SignalP-noTM
gi_188521033_gb_ACD58978.1_	0.14	45	0.147	11	0.325	2	0.213	0.178	N	0.57	SignalP-noTM
gi_188521034_gb_ACD58979.1_	0.136	45	0.17	11	0.429	1	0.276	0.209	N	0.51	SignalP-TM
gi_188521035_gb_ACD58980.1_	0.138	54	0.182	11	0.442	3	0.32	0.247	N	0.57	SignalP-noTM
gi_188521036_gb_ACD58981.1_	0.316	20	0.252	20	0.354	1	0.219	0.236	N	0.57	SignalP-noTM
gi_188521037_gb_ACD58982.1_	0.182	47	0.16	47	0.213	37	0.116	0.139	N	0.57	SignalP-noTM
gi_188521038_gb_ACD58983.1_	0.196	24	0.198	24	0.419	3	0.243	0.215	N	0.51	SignalP-TM
gi_188521039_gb_ACD58984.1_	0.165	37	0.137	37	0.156	20	0.114	0.126	N	0.57	SignalP-noTM
gi_188521040_gb_ACD58985.1_	0.214	39	0.22	21	0.381	20	0.257	0.237	N	0.57	SignalP-noTM
gi_188521044_gb_ACD58989.1_	0.147	65	0.134	65	0.222	64	0.082	0.115	N	0.51	SignalP-TM

0.749885	0.987029	0.769058	0.835324	gi_188520888_gb_ACD58833.1_
0.095868	0.006587	0.118784	0.073746	gi_188520889_gb_ACD58834.1_
0.170654	0.061226	0.212822	0.148234	gi_188520892_gb_ACD58837.1_
0.78262	0.111155	0.781597	0.558457	gi_188520893_gb_ACD58838.1_
0.323442	0.958194	0.41314	0.564925	gi_188520894_gb_ACD58839.1_
0.148932	0.029455	0.181087	0.119825	gi_188520895_gb_ACD58840.1_
0.218915	0.103123	0.079365	0.133801	gi_188520896_gb_ACD58841.1_
0.104799	0.074261	0.182873	0.120644	gi_188520898_gb_ACD58843.1_
0.465555	0.930733	0.650446	0.682245	gi_188520902_gb_ACD58847.1_
0.097704	0.005378	0.166866	0.089983	gi_188520904_gb_ACD58849.1_
0.126198	0.232009	0.10736	0.155189	gi_188520908_gb_ACD58853.1_
0.35503	0.302167	0.392933	0.350043	gi_188520909_gb_ACD58854.1_
0.158691	0.084092	0.161515	0.134766	gi_188520912_gb_ACD58857.1_
0.070045	0.053454	0.138955	0.087485	gi_188520914_gb_ACD58859.1_
0.197182	0.070633	0.212822	0.160212	gi_188520915_gb_ACD58860.1_
0.092038	0.039241	0.136815	0.089365	gi_188520916_gb_ACD58861.1_
0.186032	0.030325	0.237398	0.151252	gi_188520917_gb_ACD58862.1_
0.193879	0.06985	0.240124	0.167951	gi_188520918_gb_ACD58863.1_
0.127527	0.101197	0.135755	0.121493	gi_188520919_gb_ACD58864.1_
0.1034	0.362622	0.193411	0.219811	gi_188520920_gb_ACD58865.1_
0.15046	0.867381	0.100652	0.372831	gi_188520921_gb_ACD58866.1_
0.140035	0.105647	0.129544	0.125075	gi_188520922_gb_ACD58867.1_
0.23041	0.818021	0.427759	0.492063	gi_188520923_gb_ACD58868.1_
0.21738	0.874462	0.118784	0.403542	gi_188520926_gb_ACD58871.1_
0.174509	0.890319	0.087864	0.384231	gi_188520929_gb_ACD58874.1_
0.218403	0.106786	0.273289	0.199493	gi_188520930_gb_ACD58875.1_
0.073237	0.057541	0.088346	0.073041	gi_188520940_gb_ACD58885.1_
0.642217	0.990969	0.56193	0.731705	gi_188520942_gb_ACD58887.1_
0.141851	0.409508	0.250678	0.267346	gi_188520943_gb_ACD58888.1_
0.107936	0.057704	0.162737	0.109459	gi_188520944_gb_ACD58889.1_
0.126198	0.035881	0.164792	0.108957	gi_188520945_gb_ACD58890.1_
0.240124	0.473774	0.287205	0.333701	gi_188520946_gb_ACD58891.1_
0.216361	0.040504	0.250115	0.168993	gi_188520947_gb_ACD58892.1_
0.249553	0.181979	0.169384	0.200305	gi_188520948_gb_ACD58893.1_
0.276278	0.07635	0.214839	0.189156	gi_188520949_gb_ACD58894.1_
0.091788	0.062094	0.131244	0.095042	gi_188520950_gb_ACD58895.1_
0.108515	0.001455	0.142217	0.084062	gi_188520951_gb_ACD58896.1_
0.160704	0.029455	0.261536	0.150565	gi_188520952_gb_ACD58897.1_
0.162737	0.077629	0.165205	0.13519	gi_188520956_gb_ACD58901.1_
0.103679	0.074675	0.117533	0.098629	gi_188520957_gb_ACD58902.1_
0.36401	0.049784	0.450661	0.288152	gi_188520958_gb_ACD58903.1_
0.115679	0.069267	0.163557	0.116168	gi_188520959_gb_ACD58904.1_
0.219428	0.959844	0.214839	0.464704	gi_188520960_gb_ACD58905.1_
0.102018	0.050642	0.134005	0.095555	gi_188520962_gb_ACD58907.1_
0.182873	0.958433	0.07871	0.406672	gi_188520963_gb_ACD58908.1_
0.136815	0.098767	0.162737	0.132773	gi_188520964_gb_ACD58909.1_
0.135755	0.073237	0.129544	0.112845	gi_188520965_gb_ACD58910.1_
0.118784	0.046753	0.211318	0.125618	gi_188520966_gb_ACD58911.1_
0.138596	0.082036	0.172787	0.13114	gi_188520969_gb_ACD58914.1_
0.963066	0.990214	0.90016	0.951147	gi_188520970_gb_ACD58915.1_
0.956228	0.8966	0.878681	0.910503	gi_188520971_gb_ACD58916.1_
0.188773	0.151614	0.189233	0.17654	gi_188520984_gb_ACD58929.1_
0.094319	0.005127	0.120999	0.073482	gi_188520985_gb_ACD58930.1_
0.94164	0.998987	0.781597	0.907408	gi_188520986_gb_ACD58931.1_
0.952574	0.998709	0.863892	0.938392	gi_188520987_gb_ACD58932.1_
0.350919	0.529217	0.414595	0.431577	gi_188520988_gb_ACD58933.1_
0.822445	0.948044	0.860686	0.877058	gi_188520989_gb_ACD58934.1_
0.618456	0.905681	0.612777	0.712305	gi_188520990_gb_ACD58935.1_
0.122927	0.851448	0.070633	0.348336	gi_188520994_gb_ACD58939.1_
0.186943	0.248431	0.130903	0.188759	gi_188520995_gb_ACD58940.1_
0.135053	0.427025	0.111749	0.224609	gi_188520996_gb_ACD58941.1_
0.132964	0.019322	0.130222	0.094169	gi_188520998_gb_ACD58943.1_
0.956353	0.999729	0.907962	0.954681	gi_188521001_gb_ACD58946.1_
0.448434	0.162737	0.468542	0.359904	gi_188521004_gb_ACD58949.1_
0.158291	0.150844	0.143687	0.150941	gi_188521018_gb_ACD58963.1_
0.24453	0.066982	0.24453	0.185347	gi_188521023_gb_ACD58968.1_
0.310454	0.994811	0.50525	0.603505	gi_188521026_gb_ACD58971.1_
0.813968	0.416052	0.840908	0.690309	gi_188521032_gb_ACD58977.1_
0.318212	0.057867	0.32213	0.232736	gi_188521033_gb_ACD58978.1_
0.089317	0.491001	0.181979	0.254099	gi_188521034_gb_ACD58979.1_
0.181979	0.15046	0.201491	0.177977	gi_188521035_gb_ACD58980.1_
0.768525	0.092038	0.734388	0.53165	gi_528897479_gb_ACD58948.2_
0.181532	0.38438	0.170654	0.245522	gi_188521036_gb_ACD58981.1_
0.066608	0.0527	0.117533	0.078947	gi_188521037_gb_ACD58982.1_
0.114153	0.086432	0.180643	0.127076	gi_188521038_gb_ACD58983.1_
0.810767	0.981072	0.812144	0.867994	gi_188521039_gb_ACD58984.1_
0.052401	0.033961	0.069267	0.051876	gi_188521040_gb_ACD58985.1_
0.11385	0.074675	0.171079	0.119868	gi_188521044_gb_ACD58989.1_

gi_188521047_gb_ACD58992.1_	0.133	47	0.11	47	0.104	46	0.07	0.091	N	0.57	SignalP-noTM
gi_188521048_gb_ACD58993.1_	0.19	46	0.275	22	0.494	24	0.403	0.322	N	0.51	SignalP-TM
gi_188521049_gb_ACD58994.1_	0.132	45	0.157	27	0.334	26	0.193	0.174	N	0.57	SignalP-noTM
gi_188521053_gb_ACD58998.1_	0.114	55	0.11	34	0.141	24	0.096	0.104	N	0.57	SignalP-noTM
gi_188521059_gb_ACD59004.1_	0.137	23	0.175	11	0.367	1	0.295	0.231	N	0.57	SignalP-noTM
gi_188521063_gb_ACD59008.1_	0.149	51	0.134	51	0.161	44	0.098	0.117	N	0.57	SignalP-noTM
gi_188521064_gb_ACD59009.1_	0.215	18	0.369	18	0.707	14	0.631	0.466	N	0.51	SignalP-TM
gi_188521068_gb_ACD59013.1_	0.136	16	0.171	11	0.442	1	0.279	0.211	N	0.51	SignalP-TM
gi_188521070_gb_ACD59015.1_	0.117	50	0.118	50	0.163	41	0.094	0.107	N	0.57	SignalP-noTM
gi_188521071_gb_ACD59016.1_	0.113	23	0.114	11	0.185	2	0.123	0.118	N	0.57	SignalP-noTM
gi_188521073_gb_ACD59018.1_	0.131	30	0.168	11	0.394	2	0.284	0.211	N	0.51	SignalP-TM
gi_188521076_gb_ACD59021.1_	0.133	26	0.102	56	0.128	47	0.074	0.092	N	0.51	SignalP-TM
gi_188521077_gb_ACD59022.1_	0.134	28	0.248	22	0.66	19	0.517	0.374	N	0.57	SignalP-noTM
gi_188521081_gb_ACD59026.1_	0.13	39	0.121	45	0.153	44	0.108	0.115	N	0.57	SignalP-noTM
gi_188521082_gb_ACD59027.1_	0.112	42	0.125	11	0.206	5	0.169	0.141	N	0.51	SignalP-TM
gi_188521094_gb_ACD59039.1_	0.116	38	0.138	18	0.293	10	0.177	0.157	N	0.57	SignalP-noTM
gi_188521095_gb_ACD59040.1_	0.646	27	0.749	27	0.955	12	0.895	0.817	Y	0.57	SignalP-noTM
gi_188521096_gb_ACD59041.1_	0.146	36	0.186	20	0.424	10	0.285	0.232	N	0.57	SignalP-noTM
gi_188521097_gb_ACD59042.1_	0.104	42	0.137	23	0.221	14	0.167	0.151	N	0.57	SignalP-noTM
gi_188521098_gb_ACD59043.1_	0.124	42	0.113	50	0.146	38	0.088	0.102	N	0.57	SignalP-noTM
gi_188521099_gb_ACD59044.1_	0.182	39	0.122	39	0.275	1	0.101	0.112	N	0.57	SignalP-noTM
gi_188521100_gb_ACD59045.1_	0.314	70	0.174	70	0.244	20	0.119	0.148	N	0.57	SignalP-noTM
gi_188521101_gb_ACD59046.1_	0.146	43	0.158	43	0.254	41	0.118	0.139	N	0.57	SignalP-noTM
gi_188521112_gb_ACD59057.1_	0.108	34	0.1	65	0.103	55	0.084	0.092	N	0.57	SignalP-noTM
gi_188521113_gb_ACD59058.1_	0.204	25	0.275	25	0.594	22	0.287	0.28	N	0.57	SignalP-noTM
gi_188521114_gb_ACD59059.1_	0.104	38	0.115	11	0.206	1	0.123	0.119	N	0.57	SignalP-noTM
gi_188521116_gb_ACD59061.1_	0.453	38	0.459	38	0.765	35	0.243	0.379	N	0.51	SignalP-TM
gi_188521117_gb_ACD59062.1_	0.156	42	0.146	42	0.219	19	0.143	0.145	N	0.57	SignalP-noTM
gi_188521120_gb_ACD59065.1_	0.117	14	0.162	14	0.405	2	0.235	0.197	N	0.57	SignalP-noTM
gi_188521121_gb_ACD59066.1_	0.137	61	0.111	12	0.166	1	0.117	0.113	N	0.51	SignalP-TM
gi_188521122_gb_ACD59067.1_	0.156	44	0.186	46	0.391	42	0.174	0.181	N	0.51	SignalP-TM
gi_188521123_gb_ACD59068.1_	0.104	25	0.103	11	0.159	2	0.105	0.104	N	0.51	SignalP-TM
gi_188521124_gb_ACD59069.1_	0.215	30	0.256	30	0.462	1	0.354	0.292	N	0.51	SignalP-TM
gi_188521125_gb_ACD59070.1_	0.302	29	0.205	29	0.252	1	0.165	0.19	N	0.51	SignalP-TM
gi_188521126_gb_ACD59071.1_	0.442	18	0.408	18	0.46	13	0.342	0.384	N	0.51	SignalP-TM
gi_188521127_gb_ACD59072.1_	0.336	18	0.385	18	0.557	17	0.398	0.39	N	0.51	SignalP-TM
gi_188521128_gb_ACD59073.1_	0.15	28	0.124	28	0.204	1	0.094	0.113	N	0.51	SignalP-TM
gi_188521133_gb_ACD59078.1_	0.116	28	0.158	11	0.333	2	0.255	0.204	N	0.57	SignalP-noTM
gi_188521135_gb_ACD59080.1_	0.145	61	0.117	61	0.138	58	0.09	0.107	N	0.51	SignalP-TM
gi_188521136_gb_ACD59081.1_	0.14	55	0.13	11	0.223	2	0.174	0.147	N	0.51	SignalP-TM
gi_188521137_gb_ACD59082.1_	0.164	16	0.169	16	0.227	13	0.17	0.169	N	0.57	SignalP-noTM
gi_188521138_gb_ACD59083.1_	0.109	57	0.104	69	0.114	68	0.089	0.097	N	0.57	SignalP-noTM
gi_188521139_gb_ACD59084.1_	0.147	38	0.138	38	0.172	31	0.112	0.126	N	0.57	SignalP-noTM
gi_188521140_gb_ACD59085.1_	0.488	36	0.642	36	0.952	26	0.803	0.718	Y	0.57	SignalP-noTM
gi_188521144_gb_ACD59089.1_	0.11	27	0.163	14	0.318	7	0.268	0.213	N	0.57	SignalP-noTM
gi_188521146_gb_ACD59091.1_	0.102	21	0.138	11	0.308	1	0.178	0.157	N	0.57	SignalP-noTM
gi_188521147_gb_ACD59092.1_	0.109	59	0.102	59	0.127	4	0.082	0.092	N	0.57	SignalP-noTM
gi_188521149_gb_ACD59094.1_	0.156	42	0.146	42	0.219	19	0.143	0.145	N	0.57	SignalP-noTM
gi_188521157_gb_ACD59102.1_	0.137	56	0.144	56	0.175	52	0.129	0.137	N	0.57	SignalP-noTM
gi_188521158_gb_ACD59103.1_	0.411	21	0.358	21	0.512	16	0.275	0.319	N	0.57	SignalP-noTM
gi_188521159_gb_ACD59104.1_	0.117	42	0.113	42	0.127	12	0.099	0.106	N	0.57	SignalP-noTM
gi_188521161_gb_ACD59106.1_	0.109	36	0.138	12	0.278	3	0.191	0.163	N	0.57	SignalP-noTM
gi_188521170_gb_ACD59115.1_	0.181	28	0.126	28	0.154	2	0.1	0.114	N	0.57	SignalP-noTM
gi_188521171_gb_ACD59116.1_	0.213	30	0.367	24	0.893	19	0.684	0.516	N	0.57	SignalP-noTM
gi_188521172_gb_ACD59117.1_	0.136	47	0.124	11	0.211	1	0.152	0.137	N	0.57	SignalP-noTM
gi_188521173_gb_ACD59118.1_	0.3	36	0.192	36	0.29	18	0.147	0.175	N	0.51	SignalP-TM
gi_188521174_gb_ACD59119.1_	0.116	25	0.096	40	0.096	29	0.076	0.086	N	0.57	SignalP-noTM
gi_188521175_gb_ACD59120.1_	0.148	29	0.127	29	0.158	27	0.106	0.119	N	0.51	SignalP-TM
gi_188521176_gb_ACD59121.1_	0.169	25	0.115	25	0.123	29	0.077	0.097	N	0.57	SignalP-noTM
gi_188521179_gb_ACD59124.1_	0.126	37	0.101	64	0.119	3	0.085	0.093	N	0.57	SignalP-noTM
gi_188521183_gb_ACD59128.1_	0.338	31	0.355	31	0.668	24	0.418	0.385	N	0.57	SignalP-noTM
gi_188521184_gb_ACD59129.1_	0.15	49	0.146	21	0.251	17	0.18	0.162	N	0.57	SignalP-noTM
gi_188521187_gb_ACD59132.1_	0.298	39	0.298	39	0.617	16	0.388	0.34	N	0.57	SignalP-noTM
gi_188521188_gb_ACD59133.1_	0.101	37	0.111	23	0.144	19	0.098	0.105	N	0.57	SignalP-noTM
gi_188521191_gb_ACD59136.1_	0.109	28	0.117	11	0.195	2	0.135	0.125	N	0.57	SignalP-noTM
gi_188521192_gb_ACD59137.1_	0.201	20	0.161	20	0.186	19	0.129	0.146	N	0.57	SignalP-noTM
gi_188521193_gb_ACD59138.1_	0.146	45	0.126	30	0.226	1	0.124	0.125	N	0.57	SignalP-noTM
gi_188521194_gb_ACD59139.1_	0.258	33	0.266	18	0.501	17	0.349	0.297	N	0.51	SignalP-TM
gi_188521195_gb_ACD59140.1_	0.215	35	0.153	35	0.215	34	0.116	0.135	N	0.57	SignalP-noTM
gi_188521196_gb_ACD59141.1_	0.192	31	0.153	31	0.175	30	0.124	0.139	N	0.57	SignalP-noTM
gi_188521198_gb_ACD59143.1_	0.142	20	0.202	20	0.338	14	0.25	0.22	N	0.51	SignalP-TM
gi_188521199_gb_ACD59144.1_	0.123	27	0.113	27	0.181	15	0.106	0.11	N	0.57	SignalP-noTM
gi_188521204_gb_ACD59149.1_	0.118	36	0.169	20	0.366	13	0.246	0.205	N	0.57	SignalP-noTM
gi_188521205_gb_ACD59150.1_	0.183	26	0.145	26	0.26	2	0.129	0.137	N	0.57	SignalP-noTM
gi_188521206_gb_ACD59151.1_	0.403	32	0.3	32	0.327	27	0.213	0.259	N	0.57	SignalP-noTM
gi_188521207_gb_ACD59152.1_	0.116	43	0.118	11	0.233	1	0.129	0.123	N	0.57	SignalP-noTM
gi_188521208_gb_ACD59153.1_	0.182	26	0.232	16	0.557	11	0.369	0.296	N	0.57	SignalP-noTM
gi_188521209_gb_ACD59154.1_	0.114	25	0.115	11	0.187	3	0.132	0.123	N	0.57	SignalP-noTM

0.604918	0.971055	0.654527	0.7435	gi_188521047_gb_ACD58992.1_
0.102845	0.066422	0.147041	0.105436	gi_188521048_gb_ACD58993.1_
0.120681	0.032515	0.159494	0.10423	gi_188521049_gb_ACD58994.1_
0.13193	0.150077	0.122282	0.134763	gi_188521053_gb_ACD58998.1_
0.099571	0.001607	0.150844	0.084007	gi_188521059_gb_ACD59004.1_
0.074675	0.006262	0.103679	0.061539	gi_188521063_gb_ACD59008.1_
0.108515	0.03214	0.150844	0.097166	gi_188521064_gb_ACD59009.1_
0.091289	0.120999	0.161515	0.124601	gi_188521068_gb_ACD59013.1_
0.094063	0.064224	0.103958	0.087415	gi_188521070_gb_ACD59015.1_
0.094063	0.050354	0.187856	0.110758	gi_188521071_gb_ACD59016.1_
0.103123	0.086907	0.201009	0.130346	gi_188521073_gb_ACD59018.1_
0.125868	0.249553	0.24122	0.205547	gi_188521076_gb_ACD59021.1_
0.120363	0.054372	0.155513	0.110083	gi_188521077_gb_ACD59022.1_
0.110269	0.259802	0.224088	0.198053	gi_188521081_gb_ACD59026.1_
0.228289	0.655205	0.219943	0.367812	gi_188521082_gb_ACD59027.1_
0.394365	0.114457	0.539666	0.349496	gi_188521094_gb_ACD59039.1_
0.904651	0.923438	0.816678	0.881589	gi_188521095_gb_ACD59040.1_
0.166866	0.975779	0.283534	0.475393	gi_188521096_gb_ACD59041.1_
0.122927	0.968507	0.135755	0.409063	gi_188521097_gb_ACD59042.1_
0.087624	0.0298	0.117533	0.078319	gi_188521098_gb_ACD59043.1_
0.071625	0.038791	0.102569	0.070995	gi_188521099_gb_ACD59044.1_
0.169806	0.144056	0.173647	0.162503	gi_188521100_gb_ACD59045.1_
0.129544	0.047426	0.137881	0.10495	gi_188521101_gb_ACD59046.1_
0.059189	0.033086	0.107936	0.066737	gi_188521112_gb_ACD59057.1_
0.731452	0.100381	0.705993	0.512609	gi_188521113_gb_ACD59058.1_
0.956727	0.999835	0.850306	0.935623	gi_188521114_gb_ACD59059.1_
0.78313	0.735557	0.698465	0.739051	gi_188521116_gb_ACD59061.1_
0.268548	0.550824	0.313674	0.377682	gi_188521117_gb_ACD59062.1_
0.082944	0.04121	0.115373	0.079842	gi_188521120_gb_ACD59065.1_
0.094833	0.274482	0.253506	0.207607	gi_188521121_gb_ACD59066.1_
0.111452	0.083173	0.173217	0.122614	gi_188521122_gb_ACD59067.1_
0.309171	0.045045	0.234693	0.196303	gi_188521123_gb_ACD59068.1_
0.24232	0.237398	0.336708	0.272142	gi_188521124_gb_ACD59069.1_
0.136108	0.094063	0.206853	0.145675	gi_188521125_gb_ACD59070.1_
0.063506	0.039582	0.073237	0.058775	gi_188521126_gb_ACD59071.1_
0.124881	0.040855	0.123901	0.096546	gi_188521127_gb_ACD59072.1_
0.127194	0.049501	0.147041	0.107912	gi_188521128_gb_ACD59073.1_
0.055777	0.027787	0.092793	0.058786	gi_188521133_gb_ACD59078.1_
0.046887	0.24232	0.119729	0.136312	gi_188521135_gb_ACD59080.1_
0.069267	0.454377	0.156699	0.226781	gi_188521136_gb_ACD59081.1_
0.083631	0.052252	0.109681	0.081855	gi_188521137_gb_ACD59082.1_
0.071226	0.02516	0.109097	0.068494	gi_188521138_gb_ACD59083.1_
0.075091	0.040272	0.12196	0.079108	gi_188521139_gb_ACD59084.1_
0.822882	0.166866	0.778509	0.589419	gi_188521140_gb_ACD59085.1_
0.814421	0.858878	0.855202	0.842834	gi_188521144_gb_ACD59089.1_
0.683737	0.964326	0.837263	0.828442	gi_188521146_gb_ACD59091.1_
0.105647	0.050642	0.122604	0.092964	gi_188521147_gb_ACD59092.1_
0.32213	0.85371	0.396517	0.524119	gi_188521149_gb_ACD59094.1_
0.226707	0.901233	0.172787	0.433576	gi_188521157_gb_ACD59102.1_
0.126529	0.011868	0.12196	0.086786	gi_188521158_gb_ACD59103.1_
0.222527	0.098234	0.318212	0.212991	gi_188521159_gb_ACD59104.1_
0.484255	0.786171	0.675244	0.648557	gi_188521161_gb_ACD59106.1_
0.142217	0.081585	0.169384	0.131062	gi_188521170_gb_ACD59115.1_
0.09984	0.008767	0.150844	0.086484	gi_188521171_gb_ACD59116.1_
0.095349	0.00277	0.159092	0.085737	gi_188521172_gb_ACD59117.1_
0.104238	0.114457	0.135053	0.117916	gi_188521173_gb_ACD59118.1_
0.295254	0.949646	0.187856	0.477585	gi_188521174_gb_ACD59119.1_
0.070831	0.03214	0.115986	0.072986	gi_188521175_gb_ACD59120.1_
0.085724	0.000636	0.137525	0.074628	gi_188521176_gb_ACD59121.1_
0.195761	0.046221	0.275678	0.172553	gi_188521179_gb_ACD59124.1_
0.108806	0.004496	0.161109	0.09147	gi_188521183_gb_ACD59128.1_
0.120999	0.042778	0.142217	0.101998	gi_188521184_gb_ACD59129.1_
0.182873	0.222527	0.24453	0.216643	gi_188521187_gb_ACD59132.1_
0.074883	0.002548	0.176681	0.084704	gi_188521188_gb_ACD59133.1_
0.088588	0.279287	0.07871	0.148862	gi_188521191_gb_ACD59136.1_
0.223047	0.128532	0.328716	0.226765	gi_188521192_gb_ACD59137.1_
0.185126	0.090545	0.234693	0.170121	gi_188521193_gb_ACD59138.1_
0.175375	0.127194	0.21032	0.170963	gi_188521194_gb_ACD59139.1_
0.096914	0.053606	0.130903	0.093808	gi_188521195_gb_ACD59140.1_
0.154335	0.580299	0.102569	0.279068	gi_188521196_gb_ACD59141.1_
0.113548	0.031493	0.13193	0.092324	gi_188521198_gb_ACD59143.1_
0.138596	0.111452	0.118784	0.122944	gi_188521199_gb_ACD59144.1_
0.103958	0.091538	0.106786	0.100761	gi_188521204_gb_ACD59149.1_
0.952029	0.999171	0.920195	0.957132	gi_188521205_gb_ACD59150.1_
0.942133	0.992966	0.921507	0.952202	gi_188521206_gb_ACD59151.1_
0.913093	0.999938	0.905681	0.939571	gi_188521207_gb_ACD59152.1_
0.933949	0.999777	0.897707	0.943811	gi_188521208_gb_ACD59153.1_
0.949069	0.999829	0.905167	0.951355	gi_188521209_gb_ACD59154.1_

gi_188521210_gb_ACD59155.1_	0.144	28	0.142	28	0.192	27	0.146	0.144	N	0.57	SignalP-noTM
gi_188521211_gb_ACD59156.1_	0.225	33	0.21	33	0.406	6	0.274	0.24	N	0.57	SignalP-noTM
gi_188521212_gb_ACD59157.1_	0.369	27	0.519	27	0.925	7	0.815	0.658	Y	0.57	SignalP-noTM
gi_188521213_gb_ACD59158.1_	0.132	44	0.115	44	0.133	42	0.085	0.101	N	0.57	SignalP-noTM
gi_188521214_gb_ACD59159.1_	0.132	26	0.24	20	0.607	14	0.506	0.365	N	0.57	SignalP-noTM
gi_188521215_gb_ACD59160.1_	0.113	23	0.157	11	0.421	3	0.248	0.2	N	0.57	SignalP-noTM
gi_188521216_gb_ACD59161.1_	0.185	43	0.18	11	0.4	5	0.335	0.253	N	0.57	SignalP-noTM
gi_188521217_gb_ACD59162.1_	0.117	32	0.156	12	0.311	8	0.231	0.191	N	0.57	SignalP-noTM
gi_188521218_gb_ACD59163.1_	0.17	47	0.145	47	0.29	2	0.15	0.148	N	0.57	SignalP-noTM
gi_188521219_gb_ACD59164.1_	0.112	17	0.099	65	0.109	70	0.078	0.089	N	0.57	SignalP-noTM
gi_188521220_gb_ACD59165.1_	0.176	42	0.121	42	0.183	10	0.091	0.107	N	0.57	SignalP-noTM
gi_188521221_gb_ACD59166.1_	0.145	25	0.144	25	0.245	3	0.165	0.154	N	0.57	SignalP-noTM
gi_188521222_gb_ACD59167.1_	0.104	22	0.12	12	0.171	1	0.145	0.131	N	0.57	SignalP-noTM
gi_188521223_gb_ACD59168.1_	0.173	19	0.137	19	0.157	35	0.099	0.119	N	0.57	SignalP-noTM
gi_188521224_gb_ACD59169.1_	0.128	17	0.115	34	0.138	33	0.101	0.108	N	0.57	SignalP-noTM
gi_188521225_gb_ACD59170.1_	0.109	62	0.103	38	0.132	2	0.094	0.1	N	0.51	SignalP-TM
gi_188521226_gb_ACD59171.1_	0.143	39	0.114	57	0.122	51	0.095	0.105	N	0.57	SignalP-noTM
gi_188521227_gb_ACD59172.1_	0.105	25	0.153	11	0.34	1	0.224	0.186	N	0.57	SignalP-noTM
gi_188521228_gb_ACD59173.1_	0.122	66	0.128	41	0.194	30	0.122	0.125	N	0.57	SignalP-noTM
gi_188521229_gb_ACD59174.1_	0.115	24	0.167	11	0.391	4	0.288	0.224	N	0.57	SignalP-noTM
gi_188521230_gb_ACD59175.1_	0.103	46	0.101	61	0.113	51	0.086	0.094	N	0.57	SignalP-noTM
gi_188521231_gb_ACD59176.1_	0.141	61	0.151	19	0.33	8	0.206	0.177	N	0.57	SignalP-noTM
gi_188521232_gb_ACD59177.1_	0.115	26	0.109	22	0.159	18	0.108	0.109	N	0.57	SignalP-noTM
gi_188521233_gb_ACD59178.1_	0.197	65	0.131	65	0.122	1	0.073	0.104	N	0.57	SignalP-noTM
gi_188521234_gb_ACD59179.1_	0.113	36	0.114	11	0.172	1	0.127	0.12	N	0.57	SignalP-noTM
gi_188521235_gb_ACD59180.1_	0.115	20	0.127	20	0.171	11	0.129	0.128	N	0.57	SignalP-noTM
gi_188521236_gb_ACD59181.1_	0.124	43	0.141	43	0.213	44	0.126	0.136	N	0.51	SignalP-TM
gi_188521237_gb_ACD59182.1_	0.26	27	0.26	27	0.415	22	0.222	0.242	N	0.57	SignalP-noTM
gi_188521238_gb_ACD59183.1_	0.117	24	0.105	24	0.195	1	0.096	0.101	N	0.57	SignalP-noTM
gi_188521239_gb_ACD59184.1_	0.121	22	0.121	13	0.201	9	0.145	0.132	N	0.57	SignalP-noTM
gi_188521240_gb_ACD59185.1_	0.105	69	0.105	51	0.119	41	0.097	0.101	N	0.57	SignalP-noTM
gi_188521241_gb_ACD59186.1_	0.194	9	0.196	11	0.61	1	0.356	0.271	N	0.57	SignalP-noTM
gi_188521242_gb_ACD59187.1_	0.135	41	0.149	47	0.326	40	0.14	0.146	N	0.51	SignalP-TM
gi_188521243_gb_ACD59188.1_	0.121	27	0.107	58	0.127	54	0.087	0.097	N	0.57	SignalP-noTM
gi_188521244_gb_ACD59189.1_	0.128	26	0.107	50	0.131	46	0.078	0.093	N	0.57	SignalP-noTM
gi_188521245_gb_ACD59190.1_	0.245	24	0.273	24	0.609	10	0.403	0.321	N	0.51	SignalP-TM
gi_188521246_gb_ACD59191.1_	0.583	28	0.761	28	0.999	24	0.938	0.844	Y	0.57	SignalP-noTM
gi_188521248_gb_ACD59193.1_	0.42	41	0.23	41	0.247	40	0.087	0.177	N	0.51	SignalP-TM
gi_188521249_gb_ACD59194.1_	0.111	24	0.14	28	0.312	23	0.16	0.147	N	0.51	SignalP-TM
gi_188521250_gb_ACD59195.1_	0.267	40	0.218	40	0.363	1	0.208	0.214	N	0.51	SignalP-TM
gi_188521252_gb_ACD59197.1_	0.261	33	0.328	33	0.615	28	0.395	0.353	N	0.51	SignalP-TM
gi_188521253_gb_ACD59198.1_	0.233	40	0.175	40	0.297	1	0.155	0.167	N	0.51	SignalP-TM
gi_188521254_gb_ACD59199.1_	0.184	52	0.144	52	0.135	48	0.099	0.128	N	0.51	SignalP-TM
gi_188521255_gb_ACD59200.1_	0.168	27	0.22	27	0.46	9	0.359	0.272	N	0.51	SignalP-TM
gi_188521256_gb_ACD59201.1_	0.107	8	0.114	36	0.151	12	0.122	0.118	N	0.57	SignalP-noTM
gi_188521257_gb_ACD59202.1_	0.113	26	0.106	26	0.121	8	0.104	0.105	N	0.57	SignalP-noTM
gi_188521258_gb_ACD59203.1_	0.118	18	0.146	11	0.294	3	0.209	0.176	N	0.57	SignalP-noTM
gi_188521259_gb_ACD59204.1_	0.121	18	0.118	26	0.181	1	0.125	0.121	N	0.57	SignalP-noTM
gi_188521260_gb_ACD59205.1_	0.374	36	0.228	36	0.275	11	0.174	0.203	N	0.57	SignalP-noTM
gi_188521261_gb_ACD59206.1_	0.127	57	0.108	57	0.105	55	0.082	0.096	N	0.57	SignalP-noTM
gi_188521262_gb_ACD59207.1_	0.153	69	0.115	69	0.119	32	0.078	0.097	N	0.57	SignalP-noTM
gi_188521263_gb_ACD59208.1_	0.111	27	0.119	11	0.191	5	0.153	0.132	N	0.51	SignalP-TM
gi_188521265_gb_ACD59210.1_	0.11	57	0.168	34	0.444	25	0.228	0.196	N	0.57	SignalP-noTM
gi_188521267_gb_ACD59212.1_	0.134	22	0.162	22	0.318	11	0.201	0.18	N	0.57	SignalP-noTM
gi_188521273_gb_ACD59218.1_	0.127	29	0.118	29	0.126	26	0.093	0.106	N	0.57	SignalP-noTM
gi_528897480_gb_ACD59223.2_	0.116	66	0.12	58	0.201	1	0.109	0.115	N	0.57	SignalP-noTM
gi_528897481_gb_ACD59227.2_	0.116	66	0.118	59	0.197	1	0.108	0.113	N	0.57	SignalP-noTM
gi_188521285_gb_ACD59230.1_	0.198	23	0.173	23	0.281	1	0.175	0.174	N	0.57	SignalP-noTM
gi_188521290_gb_ACD59235.1_	0.189	30	0.128	30	0.189	4	0.126	0.127	N	0.51	SignalP-TM
gi_188521291_gb_ACD59236.1_	0.22	42	0.187	42	0.357	31	0.106	0.157	N	0.51	SignalP-TM
gi_188521446_gb_ACD59391.1_	0.123	9	0.138	11	0.261	6	0.199	0.166	N	0.57	SignalP-noTM
gi_188521485_gb_ACD59430.1_	0.103	20	0.102	62	0.131	1	0.095	0.099	N	0.57	SignalP-noTM
gi_188521486_gb_ACD59431.1_	0.167	35	0.167	35	0.329	34	0.17	0.169	N	0.57	SignalP-noTM
gi_188521488_gb_ACD59433.1_	0.158	24	0.161	24	0.241	21	0.172	0.166	N	0.57	SignalP-noTM
gi_188521494_gb_ACD59439.1_	0.585	60	0.321	60	0.296	59	0.133	0.233	N	0.57	SignalP-noTM
gi_188521495_gb_ACD59440.1_	0.135	37	0.119	11	0.186	3	0.142	0.13	N	0.57	SignalP-noTM
gi_188521497_gb_ACD59442.1_	0.124	33	0.126	42	0.203	32	0.123	0.125	N	0.57	SignalP-noTM
gi_188521499_gb_ACD59444.1_	0.118	65	0.181	11	0.43	3	0.33	0.251	N	0.57	SignalP-noTM
gi_188521500_gb_ACD59445.1_	0.155	42	0.145	42	0.21	19	0.138	0.141	N	0.57	SignalP-noTM
gi_188521504_gb_ACD59449.1_	0.411	21	0.358	21	0.512	16	0.275	0.319	N	0.57	SignalP-noTM
gi_188521511_gb_ACD59456.1_	0.116	43	0.112	33	0.153	25	0.108	0.11	N	0.57	SignalP-noTM
gi_188521512_gb_ACD59457.1_	0.116	26	0.125	48	0.209	44	0.122	0.124	N	0.57	SignalP-noTM
gi_188521513_gb_ACD59458.1_	0.111	25	0.158	11	0.304	1	0.247	0.2	N	0.57	SignalP-noTM
gi_188521524_gb_ACD59469.1_	0.161	20	0.116	33	0.165	32	0.084	0.101	N	0.57	SignalP-noTM
gi_188521525_gb_ACD59470.1_	0.11	47	0.118	13	0.158	2	0.139	0.128	N	0.57	SignalP-noTM
gi_188521526_gb_ACD59471.1_	0.139	33	0.121	11	0.247	1	0.13	0.124	N	0.51	SignalP-TM
gi_188521527_gb_ACD59472.1_	0.298	21	0.536	21	0.988	10	0.959	0.735	Y	0.57	SignalP-noTM
gi_188521528_gb_ACD59473.1_	0.151	27	0.221	16	0.594	8	0.408	0.309	N	0.57	SignalP-noTM

0.953381	0.999908	0.908711	0.954	gi_188521210_gb_ACD59155.1_
0.958672	0.974544	0.899619	0.944278	gi_188521211_gb_ACD59156.1_
0.842507	0.827213	0.791666	0.820462	gi_188521212_gb_ACD59157.1_
0.963066	0.999861	0.933764	0.965564	gi_188521213_gb_ACD59158.1_
0.959728	0.999976	0.931119	0.963608	gi_188521214_gb_ACD59159.1_
0.956102	0.99981	0.928375	0.961429	gi_188521215_gb_ACD59160.1_
0.962529	0.99996	0.938601	0.96703	gi_188521216_gb_ACD59161.1_
0.954955	0.999972	0.924282	0.959736	gi_188521217_gb_ACD59162.1_
0.1065	0.000998	0.187856	0.098451	gi_188521218_gb_ACD59163.1_
0.252939	0.058856	0.276278	0.196024	gi_188521219_gb_ACD59164.1_
0.089562	0.025014	0.127527	0.080701	gi_188521220_gb_ACD59165.1_
0.117845	0.075718	0.116603	0.103389	gi_188521221_gb_ACD59166.1_
0.126198	0.054837	0.131587	0.104207	gi_188521222_gb_ACD59167.1_
0.057704	0.046353	0.087864	0.063974	gi_188521223_gb_ACD59168.1_
0.094833	0.08883	0.08883	0.090831	gi_188521224_gb_ACD59169.1_
0.065866	0.124881	0.091788	0.094178	gi_188521225_gb_ACD59170.1_
0.182873	0.001518	0.135404	0.106598	gi_188521226_gb_ACD59171.1_
0.065866	0.04229	0.111452	0.073203	gi_188521227_gb_ACD59172.1_
0.080691	0.010446	0.124227	0.071788	gi_188521228_gb_ACD59173.1_
0.135404	0.019096	0.1603	0.104933	gi_188521229_gb_ACD59174.1_
0.078276	0.534445	0.076562	0.229761	gi_188521230_gb_ACD59175.1_
0.063151	0.032233	0.087624	0.061003	gi_188521231_gb_ACD59176.1_
0.054064	0.105931	0.065681	0.075225	gi_188521232_gb_ACD59177.1_
0.059189	0.032421	0.103123	0.064911	gi_188521233_gb_ACD59178.1_
0.093553	0.051077	0.110859	0.085163	gi_188521234_gb_ACD59179.1_
0.952438	0.978959	0.943906	0.958434	gi_188521235_gb_ACD59180.1_
0.929955	0.829346	0.897431	0.885577	gi_188521236_gb_ACD59181.1_
0.104799	0.016529	0.103123	0.074817	gi_188521237_gb_ACD59182.1_
0.079805	0.030325	0.102569	0.0709	gi_188521238_gb_ACD59183.1_
0.127862	0.563407	0.092289	0.261186	gi_188521239_gb_ACD59184.1_
0.24453	0.028443	0.197658	0.156877	gi_188521240_gb_ACD59185.1_
0.877073	0.915444	0.899348	0.897288	gi_188521241_gb_ACD59186.1_
0.886452	0.999392	0.869438	0.918427	gi_188521242_gb_ACD59187.1_
0.06192	0.050211	0.069655	0.060595	gi_188521243_gb_ACD59188.1_
0.071425	0.539666	0.055148	0.22208	gi_188521244_gb_ACD59189.1_
0.818913	0.546366	0.749885	0.705055	gi_188521245_gb_ACD59190.1_
0.078276	0.247871	0.195289	0.173812	gi_188521246_gb_ACD59191.1_
0.068498	0.09984	0.206853	0.125064	gi_188521248_gb_ACD59193.1_
0.092038	0.108515	0.191081	0.130545	gi_188521249_gb_ACD59194.1_
0.13331	0.570036	0.099034	0.26746	gi_188521250_gb_ACD59195.1_
0.099302	0.061745	0.1034	0.088149	gi_188521252_gb_ACD59197.1_
0.138238	0.121639	0.198611	0.152829	gi_188521253_gb_ACD59198.1_
0.0985	0.026288	0.149694	0.091494	gi_188521254_gb_ACD59199.1_
0.075091	0.141122	0.153944	0.123386	gi_188521255_gb_ACD59200.1_
0.948923	0.999785	0.747061	0.89859	gi_188521256_gb_ACD59201.1_
0.232009	0.045434	0.340066	0.205836	gi_188521257_gb_ACD59202.1_
0.080247	0.046887	0.098234	0.075123	gi_188521258_gb_ACD59203.1_
0.133658	0.077845	0.122282	0.111262	gi_188521259_gb_ACD59204.1_
0.091538	0.006151	0.127527	0.075072	gi_188521260_gb_ACD59205.1_
0.07871	0.034556	0.11847	0.077245	gi_188521261_gb_ACD59206.1_
0.082944	0.041447	0.116912	0.080434	gi_188521262_gb_ACD59207.1_
0.086432	0.083402	0.082262	0.084032	gi_188521263_gb_ACD59208.1_
0.564145	0.917056	0.811227	0.764143	gi_188521265_gb_ACD59210.1_
0.716466	0.810306	0.815327	0.7807	gi_188521267_gb_ACD59212.1_
0.177994	0.197658	0.147795	0.174482	gi_188521273_gb_ACD59218.1_
0.094576	0.009058	0.144427	0.082687	gi_188521285_gb_ACD59230.1_
0.914511	0.998335	0.840104	0.91765	gi_188521290_gb_ACD59235.1_
0.775912	0.093046	0.734973	0.534644	gi_528897480_gb_ACD59223.2_
0.679179	0.071625	0.660607	0.47047	gi_528897481_gb_ACD59227.2_
0.952029	0.999897	0.869097	0.940341	gi_188521291_gb_ACD59236.1_
0.202458	0.049926	0.511998	0.254794	gi_188521446_gb_ACD59391.1_
0.062797	0.024941	0.096129	0.061289	gi_188521485_gb_ACD59430.1_
0.219943	0.949789	0.102018	0.423917	gi_188521486_gb_ACD59431.1_
0.757128	0.105364	0.767456	0.543316	gi_188521488_gb_ACD59433.1_
0.123251	0.043522	0.161921	0.109565	gi_188521494_gb_ACD59439.1_
0.360545	0.769058	0.350236	0.49328	gi_188521495_gb_ACD59440.1_
0.161109	0.068116	0.145542	0.124922	gi_188521497_gb_ACD59442.1_
0.93946	0.931694	0.893785	0.921646	gi_188521499_gb_ACD59444.1_
0.290285	0.643595	0.353658	0.429179	gi_188521500_gb_ACD59445.1_
0.130222	0.010603	0.125868	0.088898	gi_188521504_gb_ACD59449.1_
0.141486	0.087384	0.124553	0.117808	gi_188521511_gb_ACD59456.1_
0.084556	0.001115	0.127527	0.071066	gi_188521512_gb_ACD59457.1_
0.080913	0.043522	0.094319	0.072918	gi_188521513_gb_ACD59458.1_
0.112346	0.051956	0.107072	0.090458	gi_188521524_gb_ACD59469.1_
0.138596	0.132274	0.096651	0.122507	gi_188521525_gb_ACD59470.1_
0.108515	0.3028	0.235772	0.215696	gi_188521526_gb_ACD59471.1_
0.699727	0.940139	0.739621	0.793162	gi_188521527_gb_ACD59472.1_
0.798509	0.727307	0.814421	0.780079	gi_188521528_gb_ACD59473.1_

gi_188521530_gb_ACD59475.1_	0.248	41	0.199	41	0.28	37	0.137	0.17	N	0.57	SignalP-noTM
gi_188521532_gb_ACD59477.1_	0.128	27	0.207	27	0.443	15	0.307	0.254	N	0.57	SignalP-noTM
gi_188521534_gb_ACD59479.1_	0.197	26	0.19	26	0.369	22	0.212	0.2	N	0.57	SignalP-noTM
gi_188521540_gb_ACD59485.1_	0.135	23	0.139	55	0.297	48	0.104	0.123	N	0.57	SignalP-noTM
gi_188521541_gb_ACD59486.1_	0.241	19	0.282	19	0.484	18	0.317	0.299	N	0.57	SignalP-noTM
gi_188521542_gb_ACD59487.1_	0.101	32	0.13	18	0.214	17	0.158	0.143	N	0.57	SignalP-noTM
gi_188521544_gb_ACD59489.1_	0.113	23	0.276	17	0.853	14	0.738	0.493	N	0.57	SignalP-noTM
gi_188521545_gb_ACD59490.1_	0.134	49	0.124	49	0.168	34	0.117	0.121	N	0.57	SignalP-noTM
gi_188521546_gb_ACD59491.1_	0.141	36	0.154	36	0.257	15	0.169	0.161	N	0.57	SignalP-noTM
gi_188521547_gb_ACD59492.1_	0.117	23	0.103	33	0.144	1	0.093	0.099	N	0.57	SignalP-noTM
gi_188521548_gb_ACD59493.1_	0.111	21	0.106	21	0.134	2	0.103	0.105	N	0.57	SignalP-noTM
gi_188521549_gb_ACD59494.1_	0.17	20	0.138	20	0.18	32	0.107	0.123	N	0.57	SignalP-noTM
gi_188521550_gb_ACD59495.1_	0.221	56	0.204	56	0.32	51	0.164	0.185	N	0.57	SignalP-noTM
gi_188521551_gb_ACD59496.1_	0.179	49	0.207	11	0.58	5	0.441	0.317	N	0.57	SignalP-noTM
gi_188521552_gb_ACD59497.1_	0.13	52	0.178	46	0.447	43	0.201	0.187	N	0.51	SignalP-TM
gi_188521553_gb_ACD59498.1_	0.157	24	0.14	24	0.153	1	0.123	0.132	N	0.57	SignalP-noTM
gi_188521555_gb_ACD59500.1_	0.106	34	0.126	14	0.233	6	0.156	0.14	N	0.57	SignalP-noTM
gi_188521556_gb_ACD59501.1_	0.114	22	0.144	13	0.262	9	0.209	0.175	N	0.57	SignalP-noTM
gi_188521563_gb_ACD59508.1_	0.132	51	0.115	51	0.155	1	0.106	0.111	N	0.57	SignalP-noTM
gi_188521565_gb_ACD59510.1_	0.146	23	0.215	11	0.709	1	0.447	0.301	N	0.51	SignalP-TM
gi_188521568_gb_ACD59513.1_	0.102	26	0.123	12	0.195	3	0.153	0.137	N	0.57	SignalP-noTM
gi_188521571_gb_ACD59516.1_	0.138	18	0.246	18	0.573	10	0.428	0.332	N	0.57	SignalP-noTM
gi_188521572_gb_ACD59517.1_	0.156	36	0.121	11	0.222	1	0.135	0.127	N	0.57	SignalP-noTM
gi_188521573_gb_ACD59518.1_	0.161	35	0.138	35	0.147	7	0.112	0.126	N	0.57	SignalP-noTM
gi_188521574_gb_ACD59519.1_	0.169	51	0.11	51	0.124	1	0.085	0.101	N	0.51	SignalP-TM
gi_188521580_gb_ACD59525.1_	0.197	26	0.191	26	0.363	22	0.215	0.202	N	0.57	SignalP-noTM
gi_188521581_gb_ACD59526.1_	0.117	34	0.283	12	0.882	4	0.825	0.538	N	0.57	SignalP-noTM
gi_188521583_gb_ACD59528.1_	0.102	30	0.096	16	0.118	7	0.088	0.092	N	0.57	SignalP-noTM
gi_188521584_gb_ACD59529.1_	0.109	48	0.161	11	0.376	3	0.28	0.217	N	0.57	SignalP-noTM
gi_188521592_gb_ACD59537.1_	0.142	42	0.119	42	0.143	1	0.101	0.11	N	0.57	SignalP-noTM
gi_188521593_gb_ACD59538.1_	0.105	66	0.106	43	0.14	41	0.093	0.1	N	0.57	SignalP-noTM
gi_188521595_gb_ACD59540.1_	0.149	36	0.179	11	0.481	2	0.32	0.231	N	0.51	SignalP-TM
gi_188521597_gb_ACD59542.1_	0.861	20	0.861	20	0.927	19	0.828	0.845	Y	0.57	SignalP-noTM
gi_188521598_gb_ACD59543.1_	0.152	15	0.212	15	0.429	3	0.3	0.253	N	0.57	SignalP-noTM
gi_188521599_gb_ACD59544.1_	0.129	20	0.163	15	0.406	5	0.22	0.19	N	0.57	SignalP-noTM
gi_188521608_gb_ACD59553.1_	0.246	28	0.331	28	0.804	24	0.388	0.358	N	0.57	SignalP-noTM
gi_188521609_gb_ACD59554.1_	0.702	17	0.586	17	0.651	15	0.46	0.527	N	0.57	SignalP-noTM
gi_188521610_gb_ACD59555.1_	0.199	20	0.346	20	0.804	13	0.602	0.466	N	0.57	SignalP-noTM
gi_188521611_gb_ACD59556.1_	0.832	29	0.792	29	0.958	14	0.86	0.824	Y	0.57	SignalP-noTM
gi_188521612_gb_ACD59557.1_	0.119	37	0.132	11	0.283	4	0.183	0.156	N	0.57	SignalP-noTM
gi_188521613_gb_ACD59558.1_	0.771	29	0.822	29	0.977	18	0.903	0.86	Y	0.57	SignalP-noTM
gi_188521614_gb_ACD59559.1_	0.121	24	0.111	36	0.144	34	0.1	0.106	N	0.57	SignalP-noTM
gi_188521615_gb_ACD59560.1_	0.139	49	0.103	31	0.129	11	0.094	0.099	N	0.57	SignalP-noTM
gi_188521616_gb_ACD59561.1_	0.157	33	0.122	33	0.172	39	0.089	0.106	N	0.57	SignalP-noTM
gi_188521617_gb_ACD59562.1_	0.203	20	0.158	20	0.307	2	0.15	0.154	N	0.57	SignalP-noTM
gi_188521618_gb_ACD59563.1_	0.125	38	0.133	14	0.22	5	0.181	0.155	N	0.57	SignalP-noTM
gi_188521619_gb_ACD59564.1_	0.128	53	0.178	15	0.38	14	0.323	0.246	N	0.57	SignalP-noTM
gi_188521620_gb_ACD59565.1_	0.275	25	0.212	25	0.327	10	0.201	0.208	N	0.51	SignalP-TM
gi_188521621_gb_ACD59566.1_	0.276	23	0.25	23	0.474	3	0.268	0.258	N	0.57	SignalP-noTM
gi_188521622_gb_ACD59567.1_	0.114	33	0.108	33	0.136	31	0.094	0.103	N	0.51	SignalP-TM
gi_188521623_gb_ACD59568.1_	0.805	27	0.879	27	0.99	15	0.956	0.915	Y	0.57	SignalP-noTM
gi_188521625_gb_ACD59570.1_	0.157	34	0.183	11	0.539	1	0.305	0.24	N	0.57	SignalP-noTM
gi_188521626_gb_ACD59571.1_	0.105	18	0.105	39	0.119	8	0.093	0.099	N	0.57	SignalP-noTM
gi_188521627_gb_ACD59572.1_	0.18	22	0.133	22	0.164	1	0.106	0.12	N	0.57	SignalP-noTM
gi_188521628_gb_ACD59573.1_	0.133	27	0.107	27	0.108	55	0.08	0.094	N	0.57	SignalP-noTM
gi_188521629_gb_ACD59574.1_	0.152	21	0.116	21	0.131	20	0.088	0.103	N	0.57	SignalP-noTM
gi_188521630_gb_ACD59575.1_	0.149	55	0.125	32	0.239	1	0.113	0.119	N	0.57	SignalP-noTM
gi_188521631_gb_ACD59576.1_	0.103	33	0.103	40	0.112	38	0.086	0.095	N	0.57	SignalP-noTM
gi_188521633_gb_ACD59578.1_	0.562	38	0.7	38	0.923	29	0.819	0.756	Y	0.57	SignalP-noTM
gi_188521634_gb_ACD59579.1_	0.221	37	0.182	37	0.201	2	0.138	0.161	N	0.57	SignalP-noTM
gi_188521635_gb_ACD59580.1_	0.17	38	0.18	38	0.275	34	0.142	0.166	N	0.51	SignalP-TM
gi_188521636_gb_ACD59581.1_	0.313	51	0.238	51	0.25	45	0.131	0.199	N	0.51	SignalP-TM
gi_188521637_gb_ACD59582.1_	0.111	26	0.142	16	0.295	25	0.197	0.168	N	0.57	SignalP-noTM
gi_188521638_gb_ACD59583.1_	0.115	53	0.119	13	0.16	7	0.143	0.131	N	0.57	SignalP-noTM
gi_188521640_gb_ACD59585.1_	0.112	27	0.141	34	0.362	29	0.135	0.139	N	0.57	SignalP-noTM
gi_188521641_gb_ACD59586.1_	0.18	35	0.156	35	0.277	16	0.185	0.169	N	0.57	SignalP-noTM
gi_188521642_gb_ACD59587.1_	0.25	24	0.238	19	0.473	8	0.256	0.246	N	0.57	SignalP-noTM
gi_188521643_gb_ACD59588.1_	0.128	29	0.122	29	0.165	50	0.097	0.11	N	0.57	SignalP-noTM
gi_188521644_gb_ACD59589.1_	0.15	38	0.116	38	0.149	37	0.092	0.105	N	0.57	SignalP-noTM
gi_188521646_gb_ACD59591.1_	0.108	58	0.104	24	0.129	1	0.098	0.101	N	0.57	SignalP-noTM
gi_188521647_gb_ACD59592.1_	0.124	33	0.127	42	0.205	32	0.124	0.126	N	0.57	SignalP-noTM
gi_188521648_gb_ACD59593.1_	0.105	20	0.15	16	0.28	6	0.228	0.187	N	0.57	SignalP-noTM
gi_188521652_gb_ACD59597.1_	0.13	30	0.182	20	0.379	1	0.307	0.228	N	0.51	SignalP-TM
gi_188521653_gb_ACD59598.1_	0.549	30	0.353	30	0.386	12	0.232	0.308	N	0.51	SignalP-TM
gi_188521655_gb_ACD59600.1_	0.171	20	0.162	55	0.416	49	0.153	0.158	N	0.57	SignalP-noTM
gi_188521659_gb_ACD59604.1_	0.14	26	0.105	26	0.109	45	0.079	0.093	N	0.57	SignalP-noTM
gi_188521660_gb_ACD59605.1_	0.798	24	0.877	24	0.984	13	0.964	0.918	Y	0.57	SignalP-noTM
gi_188521661_gb_ACD59606.1_	0.241	30	0.187	30	0.448	1	0.233	0.209	N	0.57	SignalP-noTM

0.220974	0.079585	0.371684	0.224081	gi_188521530_gb_ACD59475.1_
0.916369	0.511998	0.879001	0.769123	gi_188521532_gb_ACD59477.1_
0.143687	0.020796	0.176681	0.113721	gi_188521534_gb_ACD59479.1_
0.092038	0.008359	0.142217	0.080871	gi_188521540_gb_ACD59485.1_
0.962421	0.999846	0.865646	0.942638	gi_188521541_gb_ACD59486.1_
0.873139	0.995517	0.567829	0.812162	gi_188521542_gb_ACD59487.1_
0.334701	0.867726	0.207839	0.470089	gi_188521544_gb_ACD59489.1_
0.115679	0.024364	0.169384	0.103142	gi_188521545_gb_ACD59490.1_
0.187399	0.375897	0.17023	0.244509	gi_188521546_gb_ACD59491.1_
0.090052	0.008689	0.137525	0.078755	gi_188521547_gb_ACD59492.1_
0.85483	0.963806	0.806589	0.875075	gi_188521548_gb_ACD59493.1_
0.067736	0.009359	0.109975	0.062357	gi_188521549_gb_ACD59494.1_
0.084324	0.074468	0.115679	0.09149	gi_188521550_gb_ACD59495.1_
0.129544	0.004185	0.138596	0.090775	gi_188521551_gb_ACD59496.1_
0.153944	0.112047	0.174942	0.146978	gi_188521552_gb_ACD59497.1_
0.138596	0.565619	0.093553	0.265923	gi_188521553_gb_ACD59498.1_
0.227761	0.937027	0.121639	0.428809	gi_188521555_gb_ACD59500.1_
0.733802	0.836443	0.821127	0.797124	gi_188521556_gb_ACD59501.1_
0.11847	0.065314	0.159092	0.114292	gi_188521563_gb_ACD59508.1_
0.948191	0.979508	0.896321	0.94134	gi_188521565_gb_ACD59510.1_
0.169384	0.412413	0.144427	0.242075	gi_188521568_gb_ACD59513.1_
0.938255	0.983761	0.851448	0.924488	gi_188521571_gb_ACD59516.1_
0.111155	0.003395	0.146665	0.087072	gi_188521572_gb_ACD59517.1_
0.257501	0.045957	0.359854	0.221104	gi_188521573_gb_ACD59518.1_
0.137881	0.008114	0.190618	0.112204	gi_188521574_gb_ACD59519.1_
0.607067	0.825058	0.72968	0.720602	gi_188521580_gb_ACD59525.1_
0.247871	0.472278	0.226181	0.315443	gi_188521581_gb_ACD59526.1_
0.317562	0.554532	0.455121	0.442405	gi_188521583_gb_ACD59528.1_
0.141486	0.892928	0.098767	0.377727	gi_188521584_gb_ACD59529.1_
0.214333	0.062797	0.266784	0.181305	gi_188521592_gb_ACD59537.1_
0.116912	0.036615	0.147418	0.100315	gi_188521593_gb_ACD59538.1_
0.528469	0.283534	0.597005	0.469669	gi_188521595_gb_ACD59540.1_
0.643595	0.990779	0.709715	0.781363	gi_188521597_gb_ACD59542.1_
0.302167	0.368188	0.094833	0.255063	gi_188521598_gb_ACD59543.1_
0.940139	0.99424	0.869097	0.934492	gi_188521599_gb_ACD59544.1_
0.950499	0.99906	0.873802	0.94112	gi_188521608_gb_ACD59553.1_
0.958553	0.998374	0.908212	0.955046	gi_188521609_gb_ACD59554.1_
0.667966	0.964429	0.743073	0.791823	gi_188521610_gb_ACD59555.1_
0.956228	0.998128	0.906701	0.953686	gi_188521611_gb_ACD59556.1_
0.771182	0.99932	0.513497	0.761333	gi_188521612_gb_ACD59557.1_
0.767456	0.209325	0.78768	0.588154	gi_188521613_gb_ACD59558.1_
0.080468	0.001111	0.1065	0.062693	gi_188521614_gb_ACD59559.1_
0.075091	0.002705	0.147041	0.074946	gi_188521615_gb_ACD59560.1_
0.24232	0.039354	0.362622	0.214765	gi_188521616_gb_ACD59561.1_
0.113548	0.090298	0.142217	0.115354	gi_188521617_gb_ACD59562.1_
0.276278	0.074675	0.420432	0.257128	gi_188521618_gb_ACD59563.1_
0.186487	0.181087	0.120681	0.162752	gi_188521619_gb_ACD59564.1_
0.079365	0.405163	0.20587	0.230133	gi_188521620_gb_ACD59565.1_
0.092793	0.011938	0.15046	0.085064	gi_188521621_gb_ACD59566.1_
0.080691	0.07024	0.093046	0.081326	gi_188521622_gb_ACD59567.1_
0.796085	0.916827	0.799953	0.837622	gi_188521623_gb_ACD59568.1_
0.088588	0.025382	0.107936	0.073969	gi_188521625_gb_ACD59570.1_
0.058031	0.072628	0.089806	0.073488	gi_188521626_gb_ACD59571.1_
0.083173	0.116603	0.080913	0.093563	gi_188521627_gb_ACD59572.1_
0.101197	0.054372	0.128869	0.094813	gi_188521628_gb_ACD59573.1_
0.085959	0.047698	0.09744	0.077032	gi_188521629_gb_ACD59574.1_
0.108225	0.074883	0.114457	0.099188	gi_188521630_gb_ACD59575.1_
0.124881	0.30853	0.083631	0.172347	gi_188521631_gb_ACD59576.1_
0.958073	0.973247	0.895482	0.942267	gi_188521633_gb_ACD59578.1_
0.129544	0.010761	0.138238	0.092848	gi_188521634_gb_ACD59579.1_
0.125868	0.095609	0.19201	0.137829	gi_188521635_gb_ACD59580.1_
0.14517	0.054992	0.21738	0.139181	gi_188521636_gb_ACD59581.1_
0.101744	0.031129	0.127862	0.086912	gi_188521803_gb_ACD59748.1_
0.955212	0.999663	0.875447	0.943441	gi_188521805_gb_ACD59750.1_
0.802818	0.966138	0.733802	0.834253	gi_188521806_gb_ACD59751.1_
0.836443	0.830616	0.712795	0.793285	gi_188521807_gb_ACD59752.1_
0.282316	0.225133	0.338721	0.282057	gi_188521808_gb_ACD59753.1_
0.772767	0.931311	0.762059	0.822046	gi_188521809_gb_ACD59754.1_
0.779542	0.652489	0.779542	0.737191	gi_188521810_gb_ACD59755.1_
0.64497	0.319515	0.6142	0.526228	gi_188521814_gb_ACD59759.1_
0.299643	0.227233	0.365401	0.297426	gi_188521820_gb_ACD59765.1_
0.890903	0.92365	0.830616	0.881723	gi_188521821_gb_ACD59766.1_
0.809844	0.972933	0.895482	0.892753	gi_188521823_gb_ACD59768.1_
0.935956	0.999881	0.869438	0.935092	gi_188521825_gb_ACD59770.1_
0.909455	0.189233	0.863539	0.654076	gi_188521826_gb_ACD59771.1_
0.869097	0.920415	0.837263	0.875592	gi_188521830_gb_ACD59775.1_
0.817574	0.228289	0.893785	0.646549	gi_188521831_gb_ACD59776.1_
0.612777	0.978647	0.851068	0.814164	gi_188521832_gb_ACD59777.1_

gi_188521662_gb_ACD59607.1_	0.142	53	0.161	53	0.31	37	0.15	0.156	N	0.57	SignalP-noTM
gi_188521663_gb_ACD59608.1_	0.118	39	0.108	39	0.144	2	0.091	0.1	N	0.57	SignalP-noTM
gi_188521666_gb_ACD59611.1_	0.1	33	0.107	68	0.121	57	0.087	0.098	N	0.57	SignalP-noTM
gi_188521667_gb_ACD59612.1_	0.289	31	0.373	31	0.784	12	0.515	0.426	N	0.51	SignalP-TM
gi_188521668_gb_ACD59613.1_	0.445	53	0.255	53	0.278	49	0.095	0.18	N	0.57	SignalP-noTM
gi_188521669_gb_ACD59614.1_	0.141	18	0.108	18	0.114	62	0.081	0.095	N	0.57	SignalP-noTM
gi_188521670_gb_ACD59615.1_	0.118	55	0.105	27	0.126	16	0.084	0.097	N	0.51	SignalP-TM
gi_188521671_gb_ACD59616.1_	0.141	27	0.144	27	0.231	14	0.157	0.15	N	0.57	SignalP-noTM
gi_188521672_gb_ACD59617.1_	0.117	46	0.189	26	0.487	25	0.27	0.227	N	0.57	SignalP-noTM
gi_188521673_gb_ACD59618.1_	0.128	11	0.108	11	0.134	18	0.091	0.1	N	0.57	SignalP-noTM
gi_188521674_gb_ACD59619.1_	0.502	25	0.398	25	0.462	12	0.346	0.379	N	0.51	SignalP-TM
gi_188521675_gb_ACD59620.1_	0.162	45	0.142	31	0.186	30	0.118	0.133	N	0.51	SignalP-TM
gi_188521676_gb_ACD59621.1_	0.114	41	0.116	11	0.182	4	0.135	0.125	N	0.57	SignalP-noTM
gi_188521680_gb_ACD59625.1_	0.167	37	0.238	37	0.53	34	0.179	0.216	N	0.51	SignalP-TM
gi_188521687_gb_ACD59632.1_	0.147	45	0.182	16	0.41	10	0.305	0.24	N	0.57	SignalP-noTM
gi_188521688_gb_ACD59633.1_	0.2	15	0.34	15	0.686	1	0.592	0.433	N	0.51	SignalP-TM
gi_188521690_gb_ACD59635.1_	0.135	28	0.228	20	0.543	9	0.375	0.283	N	0.51	SignalP-TM
gi_188521691_gb_ACD59636.1_	0.121	24	0.16	11	0.424	1	0.245	0.2	N	0.57	SignalP-noTM
gi_188521692_gb_ACD59637.1_	0.411	21	0.358	21	0.512	16	0.275	0.319	N	0.57	SignalP-noTM
gi_188521693_gb_ACD59638.1_	0.122	49	0.114	25	0.148	23	0.096	0.105	N	0.57	SignalP-noTM
gi_188521802_gb_ACD59747.1_	0.105	43	0.113	11	0.18	1	0.123	0.117	N	0.57	SignalP-noTM
gi_188521803_gb_ACD59748.1_	0.125	36	0.107	36	0.168	2	0.092	0.1	N	0.57	SignalP-noTM
gi_188521805_gb_ACD59750.1_	0.148	63	0.12	63	0.133	26	0.098	0.11	N	0.57	SignalP-noTM
gi_188521806_gb_ACD59751.1_	0.247	12	0.343	12	0.656	11	0.485	0.41	N	0.57	SignalP-noTM
gi_188521807_gb_ACD59752.1_	0.281	14	0.49	14	0.903	5	0.848	0.658	Y	0.57	SignalP-noTM
gi_188521808_gb_ACD59753.1_	0.113	40	0.105	40	0.115	18	0.09	0.098	N	0.57	SignalP-noTM
gi_188521809_gb_ACD59754.1_	0.188	19	0.139	19	0.238	34	0.091	0.116	N	0.57	SignalP-noTM
gi_188521810_gb_ACD59755.1_	0.425	25	0.634	25	0.989	10	0.939	0.777	Y	0.57	SignalP-noTM
gi_188521814_gb_ACD59759.1_	0.105	32	0.125	11	0.218	1	0.149	0.136	N	0.57	SignalP-noTM
gi_188521820_gb_ACD59765.1_	0.794	29	0.838	29	0.956	19	0.814	0.827	Y	0.57	SignalP-noTM
gi_528897485_gb_AGS47851.1_	0.308	29	0.332	29	0.489	8	0.387	0.352	N	0.51	SignalP-TM
gi_188521821_gb_ACD59766.1_	0.726	24	0.823	24	0.976	20	0.943	0.879	Y	0.57	SignalP-noTM
gi_188521823_gb_ACD59768.1_	0.306	24	0.162	24	0.134	43	0.091	0.128	N	0.57	SignalP-noTM
gi_188521825_gb_ACD59770.1_	0.426	36	0.22	36	0.263	5	0.125	0.176	N	0.57	SignalP-noTM
gi_188521826_gb_ACD59771.1_	0.133	29	0.16	11	0.345	4	0.262	0.208	N	0.57	SignalP-noTM
gi_188521830_gb_ACD59775.1_	0.133	28	0.128	17	0.188	5	0.136	0.132	N	0.57	SignalP-noTM
gi_188521831_gb_ACD59776.1_	0.164	29	0.148	19	0.334	14	0.196	0.171	N	0.57	SignalP-noTM
gi_188521832_gb_ACD59777.1_	0.193	22	0.121	22	0.113	29	0.073	0.098	N	0.57	SignalP-noTM
gi_188521833_gb_ACD59778.1_	0.1	29	0.162	11	0.309	6	0.273	0.214	N	0.57	SignalP-noTM
gi_188521834_gb_ACD59779.1_	0.115	22	0.145	13	0.276	9	0.212	0.177	N	0.57	SignalP-noTM
gi_188521839_gb_ACD59784.1_	0.111	23	0.177	11	0.466	2	0.287	0.229	N	0.57	SignalP-noTM
gi_188521844_gb_ACD59789.1_	0.153	19	0.14	19	0.156	18	0.131	0.136	N	0.57	SignalP-noTM
gi_188521845_gb_ACD59790.1_	0.196	39	0.15	39	0.156	8	0.105	0.133	N	0.51	SignalP-TM
gi_188521851_gb_ACD59796.1_	0.125	25	0.2	52	0.472	43	0.298	0.246	N	0.57	SignalP-noTM
gi_188521854_gb_ACD59799.1_	0.119	52	0.107	52	0.156	3	0.088	0.098	N	0.57	SignalP-noTM
gi_188521855_gb_ACD59800.1_	0.136	45	0.098	45	0.1	68	0.064	0.082	N	0.57	SignalP-noTM
gi_188521856_gb_ACD59801.1_	0.106	57	0.103	11	0.148	1	0.1	0.102	N	0.57	SignalP-noTM
gi_188521857_gb_ACD59802.1_	0.328	24	0.295	24	0.432	31	0.26	0.278	N	0.57	SignalP-noTM
gi_188521858_gb_ACD59803.1_	0.815	28	0.859	28	0.975	16	0.925	0.89	Y	0.57	SignalP-noTM
gi_188521859_gb_ACD59804.1_	0.479	22	0.672	22	0.976	14	0.943	0.799	Y	0.57	SignalP-noTM
gi_188521860_gb_ACD59805.1_	0.119	19	0.14	11	0.265	1	0.195	0.166	N	0.57	SignalP-noTM
gi_188521861_gb_ACD59806.1_	0.144	25	0.19	13	0.421	5	0.348	0.264	N	0.57	SignalP-noTM
gi_188521863_gb_ACD59808.1_	0.131	23	0.12	23	0.159	2	0.115	0.118	N	0.57	SignalP-noTM
gi_188521864_gb_ACD59809.1_	0.198	32	0.157	32	0.284	13	0.135	0.147	N	0.57	SignalP-noTM
gi_188521865_gb_ACD59810.1_	0.654	28	0.763	28	0.977	16	0.884	0.82	Y	0.57	SignalP-noTM
gi_188521867_gb_ACD59812.1_	0.132	21	0.24	21	0.698	8	0.501	0.363	N	0.57	SignalP-noTM
gi_188521868_gb_ACD59813.1_	0.153	25	0.119	25	0.127	24	0.076	0.103	N	0.51	SignalP-TM
gi_188521869_gb_ACD59814.1_	0.156	34	0.184	20	0.412	18	0.308	0.243	N	0.57	SignalP-noTM
gi_188521870_gb_ACD59815.1_	0.477	28	0.641	28	0.983	14	0.915	0.77	Y	0.57	SignalP-noTM
gi_188521871_gb_ACD59816.1_	0.147	21	0.116	21	0.137	1	0.098	0.108	N	0.57	SignalP-noTM
gi_188521873_gb_ACD59818.1_	0.11	63	0.138	11	0.257	1	0.189	0.162	N	0.57	SignalP-noTM
gi_188521893_gb_ACD59838.1_	0.474	28	0.543	28	0.915	20	0.751	0.641	Y	0.57	SignalP-noTM
gi_188521896_gb_ACD59841.1_	0.268	39	0.238	39	0.329	31	0.19	0.215	N	0.57	SignalP-noTM
gi_188521897_gb_ACD59842.1_	0.139	33	0.164	27	0.427	1	0.221	0.185	N	0.51	SignalP-TM
gi_188521898_gb_ACD59843.1_	0.358	29	0.486	29	0.834	26	0.635	0.556	N	0.57	SignalP-noTM
gi_188521899_gb_ACD59844.1_	0.173	34	0.13	34	0.207	15	0.119	0.125	N	0.57	SignalP-noTM
gi_188521900_gb_ACD59845.1_	0.118	36	0.124	20	0.187	11	0.13	0.127	N	0.57	SignalP-noTM
gi_188521903_gb_ACD59848.1_	0.105	20	0.102	62	0.139	1	0.095	0.098	N	0.57	SignalP-noTM
gi_188521904_gb_ACD59849.1_	0.147	31	0.129	31	0.146	18	0.115	0.123	N	0.57	SignalP-noTM
gi_188521905_gb_ACD59850.1_	0.106	54	0.122	11	0.23	1	0.136	0.129	N	0.57	SignalP-noTM
gi_188521908_gb_ACD59853.1_	0.231	63	0.141	63	0.247	6	0.114	0.129	N	0.57	SignalP-noTM
gi_188521909_gb_ACD59854.1_	0.149	24	0.113	24	0.166	30	0.088	0.101	N	0.57	SignalP-noTM
gi_188521910_gb_ACD59855.1_	0.122	31	0.16	26	0.289	3	0.201	0.179	N	0.57	SignalP-noTM
gi_188521912_gb_ACD59857.1_	0.113	44	0.106	68	0.124	62	0.088	0.098	N	0.57	SignalP-noTM
gi_188521913_gb_ACD59858.1_	0.16	23	0.099	11	0.167	3	0.097	0.098	N	0.51	SignalP-TM
gi_188521914_gb_ACD59859.1_	0.128	39	0.113	18	0.149	13	0.108	0.111	N	0.57	SignalP-noTM
gi_188521915_gb_ACD59860.1_	0.12	45	0.1	45	0.12	12	0.087	0.094	N	0.57	SignalP-noTM
gi_188521916_gb_ACD59861.1_	0.134	44	0.177	32	0.279	20	0.196	0.186	N	0.57	SignalP-noTM

0.382961	0.0527	0.681788	0.372483	gi_188521833_gb_ACD59778.1_
0.791171	0.828495	0.838891	0.819519	gi_188521834_gb_ACD59779.1_
0.255213	0.633904	0.215853	0.368323	gi_188521839_gb_ACD59784.1_
0.104518	0.125538	0.087624	0.105893	gi_188521844_gb_ACD59789.1_
0.925117	0.907459	0.897707	0.910094	gi_188521845_gb_ACD59790.1_
0.105647	0.053606	0.121319	0.093524	gi_188521851_gb_ACD59796.1_
0.458843	0.161109	0.432171	0.350708	gi_188521854_gb_ACD59799.1_
0.119413	0.026442	0.13717	0.094342	gi_188521855_gb_ACD59800.1_
0.168121	0.037255	0.185579	0.130318	gi_188521856_gb_ACD59801.1_
0.116912	0.053302	0.120363	0.096859	gi_188521857_gb_ACD59802.1_
0.769058	0.07871	0.756576	0.534781	gi_188521858_gb_ACD59803.1_
0.535938	0.683088	0.578105	0.599044	gi_528897485_gb_AGS47851.1_
0.924909	0.764228	0.875119	0.854752	gi_188521859_gb_ACD59804.1_
0.071028	0.002697	0.123575	0.065767	gi_188521860_gb_ACD59805.1_
0.940811	0.997607	0.875447	0.937955	gi_188521861_gb_ACD59806.1_
0.113247	0.075508	0.104238	0.097664	gi_188521863_gb_ACD59808.1_
0.060882	0.000672	0.08181	0.047788	gi_188521864_gb_ACD59809.1_
0.950499	0.9473	0.8966	0.931466	gi_188521865_gb_ACD59810.1_
0.35503	0.043397	0.44695	0.281792	gi_188521867_gb_ACD59812.1_
0.150844	0.13193	0.124881	0.135885	gi_188521868_gb_ACD59813.1_
0.940811	0.090792	0.808455	0.613353	gi_188521869_gb_ACD59814.1_
0.910683	0.99952	0.857783	0.922662	gi_188521870_gb_ACD59815.1_
0.078928	0.048246	0.126198	0.084457	gi_188521871_gb_ACD59816.1_
0.168121	0.079585	0.120999	0.122902	gi_188521873_gb_ACD59818.1_
0.318212	0.983905	0.320168	0.540762	gi_188521893_gb_ACD59838.1_
0.946849	0.998527	0.759328	0.901568	gi_188521896_gb_ACD59841.1_
0.10736	0.053911	0.170654	0.110642	gi_188521897_gb_ACD59842.1_
0.513497	0.206361	0.560453	0.42677	gi_188521898_gb_ACD59843.1_
0.94131	0.997163	0.8935	0.943991	gi_188521899_gb_ACD59844.1_
0.852205	0.876099	0.798991	0.842432	gi_188521900_gb_ACD59845.1_
0.063151	0.024292	0.1034	0.063614	gi_188521903_gb_ACD59848.1_
0.23041	0.057378	0.334033	0.207274	gi_188521904_gb_ACD59849.1_
0.089806	0.002029	0.123575	0.071803	gi_188521905_gb_ACD59850.1_
0.105081	0.07385	0.105081	0.094671	gi_188521908_gb_ACD59853.1_
0.375897	0.964222	0.420432	0.58685	gi_188521909_gb_ACD59854.1_
0.21032	0.09639	0.291523	0.199411	gi_188521910_gb_ACD59855.1_
0.223047	0.946698	0.116912	0.428886	gi_188521912_gb_ACD59857.1_
0.057055	0.084324	0.086195	0.075858	gi_188521913_gb_ACD59858.1_
0.960075	0.995241	0.931119	0.962145	gi_188521914_gb_ACD59859.1_
0.14629	0.09984	0.176681	0.140937	gi_188521915_gb_ACD59860.1_
0.219428	0.010354	0.304703	0.178162	gi_188521916_gb_ACD59861.1_
0.045957	0.050211	0.058525	0.051564	gi_188521918_gb_ACD59863.1_
0.075508	0.038679	0.073237	0.062475	gi_188521921_gb_ACD59866.1_
0.951478	0.998309	0.910438	0.953408	gi_188521922_gb_ACD59867.1_
0.034757	0.050931	0.070633	0.052107	gi_188521923_gb_ACD59868.1_
0.085489	0.020432	0.163147	0.089689	gi_188521924_gb_ACD59869.1_
0.932453	0.984465	0.916598	0.944505	gi_188521925_gb_ACD59870.1_
0.935051	0.994764	0.892353	0.940723	gi_188521927_gb_ACD59872.1_
0.600608	0.057867	0.483506	0.38066	gi_188521933_gb_ACD59878.1_
0.115067	0.067547	0.129206	0.10394	gi_188521934_gb_ACD59879.1_
0.526974	0.071028	0.617039	0.405014	gi_188521941_gb_ACD59886.1_
0.883397	0.864947	0.897155	0.881833	gi_188521943_gb_ACD59888.1_
0.115679	0.111155	0.156699	0.127844	gi_188521945_gb_ACD59890.1_
0.851448	0.407333	0.857417	0.705399	gi_188521947_gb_ACD59892.1_
0.195761	0.069461	0.14517	0.136797	gi_188521951_gb_ACD59896.1_
0.163557	0.098767	0.196234	0.152853	gi_188521957_gb_ACD59902.1_
0.788182	0.975849	0.684386	0.816139	gi_188521958_gb_ACD59903.1_
0.403717	0.807057	0.548596	0.586457	gi_188521959_gb_ACD59904.1_
0.70537	0.985138	0.861762	0.850757	gi_188521960_gb_ACD59905.1_
0.098767	0.001379	0.142583	0.08091	gi_528897486_gb_ACD59883.2_
0.150844	0.226181	0.097969	0.158331	gi_188521637_gb_ACD59582.1_
0.206853	0.058031	0.357094	0.207326	gi_188521638_gb_ACD59583.1_
0.118157	0.029029	0.135755	0.094314	gi_188521640_gb_ACD59585.1_
0.086195	0.046887	0.097176	0.076753	gi_188521641_gb_ACD59586.1_
0.898803	0.999732	0.812601	0.903712	gi_188521642_gb_ACD59587.1_
0.185579	0.862475	0.225657	0.42457	gi_188521643_gb_ACD59588.1_
0.06003	0.001752	0.089317	0.050366	gi_188521644_gb_ACD59589.1_
0.151614	0.083173	0.136108	0.123632	gi_188521646_gb_ACD59591.1_
0.186032	0.109097	0.159494	0.151541	gi_188521647_gb_ACD59592.1_
0.946546	0.97114	0.744787	0.887491	gi_188521648_gb_ACD59593.1_
0.104799	0.213829	0.108225	0.142284	gi_188521652_gb_ACD59597.1_
0.110563	0.099571	0.172359	0.127498	gi_188521653_gb_ACD59598.1_
0.828069	0.662622	0.827213	0.772635	gi_188521655_gb_ACD59600.1_
0.094576	0.014344	0.064224	0.057715	gi_188521659_gb_ACD59604.1_
0.930926	0.999366	0.855573	0.928622	gi_188521660_gb_ACD59605.1_
0.176245	0.016577	0.210818	0.134547	gi_188521661_gb_ACD59606.1_
0.123575	0.191545	0.106215	0.140445	gi_188521662_gb_ACD59607.1_
0.427759	0.980848	0.378716	0.595774	gi_188521663_gb_ACD59608.1_

gi_188521918_gb_ACD59863.1_	0.104	17	0.129	30	0.185	24	0.139	0.134	N	0.57	SignalP-noTM
gi_188521921_gb_ACD59866.1_	0.107	41	0.102	67	0.109	42	0.084	0.094	N	0.57	SignalP-noTM
gi_188521922_gb_ACD59867.1_	0.234	28	0.359	28	0.858	1	0.622	0.483	N	0.57	SignalP-noTM
gi_188521923_gb_ACD59868.1_	0.107	38	0.141	38	0.294	37	0.151	0.145	N	0.51	SignalP-TM
gi_188521924_gb_ACD59869.1_	0.121	33	0.111	16	0.136	6	0.107	0.109	N	0.51	SignalP-TM
gi_188521925_gb_ACD59870.1_	0.176	24	0.351	24	0.829	20	0.725	0.527	N	0.57	SignalP-noTM
gi_188521927_gb_ACD59872.1_	0.105	12	0.112	38	0.156	33	0.105	0.109	N	0.57	SignalP-noTM
gi_188521933_gb_ACD59878.1_	0.497	20	0.693	20	0.987	10	0.957	0.817	Y	0.57	SignalP-noTM
gi_188521934_gb_ACD59879.1_	0.351	28	0.429	28	0.762	21	0.524	0.473	N	0.57	SignalP-noTM
gi_528897486_gb_ACD59883.2_	0.163	56	0.138	31	0.189	17	0.142	0.14	N	0.57	SignalP-noTM
gi_188521941_gb_ACD59886.1_	0.109	33	0.153	11	0.322	3	0.227	0.188	N	0.57	SignalP-noTM
gi_188521943_gb_ACD59888.1_	0.169	49	0.143	49	0.195	12	0.13	0.137	N	0.57	SignalP-noTM
gi_188521945_gb_ACD59890.1_	0.109	52	0.128	18	0.225	10	0.144	0.135	N	0.57	SignalP-noTM
gi_188521947_gb_ACD59892.1_	0.133	22	0.158	22	0.292	11	0.194	0.175	N	0.57	SignalP-noTM
gi_188521951_gb_ACD59896.1_	0.109	29	0.131	11	0.274	1	0.162	0.146	N	0.57	SignalP-noTM
gi_188521957_gb_ACD59902.1_	0.227	46	0.189	11	0.42	6	0.349	0.264	N	0.57	SignalP-noTM
gi_188521958_gb_ACD59903.1_	0.136	31	0.164	31	0.298	28	0.187	0.175	N	0.57	SignalP-noTM
gi_188521959_gb_ACD59904.1_	0.238	26	0.175	26	0.179	1	0.125	0.151	N	0.57	SignalP-noTM
gi_188521960_gb_ACD59905.1_	0.121	20	0.178	11	0.576	1	0.282	0.227	N	0.57	SignalP-noTM
gi_188521968_gb_ACD59913.1_	0.105	32	0.103	32	0.126	2	0.086	0.097	N	0.51	SignalP-TM
gi_188521969_gb_ACD59914.1_	0.166	25	0.333	15	0.875	6	0.817	0.56	N	0.57	SignalP-noTM
gi_188521971_gb_ACD59916.1_	0.156	42	0.144	42	0.208	19	0.137	0.141	N	0.57	SignalP-noTM
gi_188521972_gb_ACD59917.1_	0.117	20	0.195	18	0.424	7	0.338	0.262	N	0.57	SignalP-noTM
gi_188521976_gb_ACD59921.1_	0.154	17	0.193	46	0.45	35	0.168	0.181	N	0.57	SignalP-noTM
gi_188521977_gb_ACD59922.1_	0.103	39	0.097	39	0.102	40	0.082	0.09	N	0.57	SignalP-noTM
gi_188521978_gb_ACD59923.1_	0.11	67	0.106	43	0.135	10	0.1	0.103	N	0.57	SignalP-noTM
gi_188521984_gb_ACD59929.1_	0.102	39	0.199	11	0.495	2	0.386	0.287	N	0.57	SignalP-noTM
gi_188521985_gb_ACD59930.1_	0.127	27	0.142	16	0.244	10	0.204	0.172	N	0.57	SignalP-noTM
gi_188521987_gb_ACD59932.1_	0.101	49	0.213	14	0.524	10	0.444	0.322	N	0.57	SignalP-noTM
gi_188521988_gb_ACD59933.1_	0.199	38	0.177	38	0.292	2	0.192	0.183	N	0.51	SignalP-TM
gi_188521989_gb_ACD59934.1_	0.14	44	0.218	44	0.687	40	0.177	0.199	N	0.57	SignalP-noTM
gi_188522002_gb_ACD59947.1_	0.104	8	0.1	44	0.113	42	0.086	0.093	N	0.57	SignalP-noTM
gi_188522003_gb_ACD59948.1_	0.116	17	0.159	17	0.272	14	0.215	0.185	N	0.57	SignalP-noTM
gi_188522005_gb_ACD59950.1_	0.112	61	0.124	12	0.191	9	0.159	0.141	N	0.57	SignalP-noTM
gi_188522006_gb_ACD59951.1_	0.13	26	0.114	55	0.165	51	0.088	0.101	N	0.57	SignalP-noTM
gi_188522007_gb_ACD59952.1_	0.114	40	0.105	48	0.13	50	0.089	0.098	N	0.57	SignalP-noTM
gi_188522008_gb_ACD59953.1_	0.169	36	0.202	11	0.558	1	0.392	0.291	N	0.57	SignalP-noTM
gi_188522011_gb_ACD59956.1_	0.192	30	0.186	30	0.411	12	0.271	0.226	N	0.57	SignalP-noTM
gi_188522012_gb_ACD59957.1_	0.149	25	0.127	25	0.163	2	0.12	0.124	N	0.57	SignalP-noTM
gi_188522013_gb_ACD59958.1_	0.111	27	0.124	11	0.206	5	0.167	0.14	N	0.51	SignalP-TM
gi_188522014_gb_ACD59959.1_	0.121	30	0.15	11	0.313	4	0.23	0.188	N	0.57	SignalP-noTM
gi_188522015_gb_ACD59960.1_	0.151	17	0.135	17	0.223	16	0.113	0.125	N	0.57	SignalP-noTM
gi_188522017_gb_ACD59962.1_	0.107	5	0.153	11	0.403	1	0.217	0.183	N	0.57	SignalP-noTM
gi_188522020_gb_ACD59965.1_	0.104	28	0.147	12	0.254	11	0.213	0.178	N	0.57	SignalP-noTM
gi_188522023_gb_ACD59968.1_	0.212	20	0.131	20	0.126	17	0.082	0.108	N	0.57	SignalP-noTM
gi_188522024_gb_ACD59969.1_	0.123	29	0.165	19	0.411	1	0.241	0.201	N	0.57	SignalP-noTM
gi_188522027_gb_ACD59972.1_	0.112	53	0.124	13	0.276	11	0.153	0.137	N	0.57	SignalP-noTM
gi_188522040_gb_ACD59985.1_	0.131	16	0.136	16	0.266	14	0.14	0.138	N	0.57	SignalP-noTM
gi_188522052_gb_ACD59997.1_	0.241	29	0.201	29	0.29	24	0.192	0.197	N	0.57	SignalP-noTM
gi_188522054_gb_ACD59999.1_	0.109	25	0.102	63	0.125	51	0.096	0.099	N	0.57	SignalP-noTM
gi_188522055_gb_ACD60000.1_	0.123	27	0.121	46	0.198	34	0.121	0.121	N	0.57	SignalP-noTM
gi_188522056_gb_ACD60001.1_	0.128	59	0.104	39	0.115	34	0.079	0.092	N	0.57	SignalP-noTM
gi_188522058_gb_ACD60003.1_	0.411	21	0.358	21	0.512	16	0.275	0.319	N	0.57	SignalP-noTM
gi_188522061_gb_ACD60006.1_	0.116	43	0.141	43	0.259	42	0.146	0.143	N	0.57	SignalP-noTM
gi_188522067_gb_ACD60012.1_	0.115	33	0.117	11	0.167	3	0.135	0.125	N	0.57	SignalP-noTM
gi_188522072_gb_ACD60017.1_	0.112	65	0.167	11	0.385	2	0.272	0.216	N	0.57	SignalP-noTM
gi_188522073_gb_ACD60018.1_	0.187	31	0.167	31	0.226	14	0.146	0.157	N	0.57	SignalP-noTM
gi_188522074_gb_ACD60019.1_	0.142	30	0.106	30	0.186	1	0.082	0.095	N	0.57	SignalP-noTM
gi_188522075_gb_ACD60020.1_	0.276	66	0.196	66	0.239	51	0.151	0.175	N	0.57	SignalP-noTM
gi_188522076_gb_ACD60021.1_	0.118	19	0.123	35	0.22	31	0.127	0.125	N	0.57	SignalP-noTM
gi_188522077_gb_ACD60022.1_	0.181	21	0.182	21	0.304	19	0.178	0.181	N	0.51	SignalP-TM
gi_188522078_gb_ACD60023.1_	0.276	35	0.235	35	0.337	2	0.207	0.224	N	0.51	SignalP-TM
gi_188522079_gb_ACD60024.1_	0.159	20	0.195	20	0.319	17	0.197	0.196	N	0.57	SignalP-noTM
gi_188522080_gb_ACD60025.1_	0.124	23	0.198	23	0.429	1	0.326	0.245	N	0.51	SignalP-TM
gi_188522081_gb_ACD60026.1_	0.197	20	0.192	11	0.567	2	0.341	0.262	N	0.57	SignalP-noTM
gi_188522082_gb_ACD60027.1_	0.113	12	0.111	33	0.145	24	0.097	0.104	N	0.57	SignalP-noTM
gi_188522083_gb_ACD60028.1_	0.138	57	0.11	57	0.102	22	0.087	0.099	N	0.57	SignalP-noTM
gi_188522084_gb_ACD60029.1_	0.15	33	0.111	33	0.134	43	0.082	0.098	N	0.57	SignalP-noTM
gi_188522085_gb_ACD60030.1_	0.127	40	0.122	24	0.201	20	0.12	0.121	N	0.57	SignalP-noTM
gi_188522086_gb_ACD60031.1_	0.232	44	0.244	44	0.413	40	0.219	0.235	N	0.51	SignalP-TM
gi_188522087_gb_ACD60032.1_	0.16	24	0.192	24	0.274	15	0.195	0.193	N	0.57	SignalP-noTM
gi_188522088_gb_ACD60033.1_	0.126	19	0.159	19	0.296	1	0.217	0.181	N	0.51	SignalP-TM
gi_188522089_gb_ACD60034.1_	0.108	34	0.111	34	0.13	31	0.091	0.102	N	0.57	SignalP-noTM
gi_188522090_gb_ACD60035.1_	0.171	41	0.243	41	0.613	35	0.252	0.247	N	0.57	SignalP-noTM
gi_188522091_gb_ACD60036.1_	0.106	21	0.105	21	0.141	13	0.104	0.104	N	0.57	SignalP-noTM
gi_188522092_gb_ACD60037.1_	0.186	67	0.142	67	0.134	52	0.107	0.125	N	0.57	SignalP-noTM
gi_188522093_gb_ACD60038.1_	0.107	16	0.102	28	0.111	15	0.083	0.093	N	0.57	SignalP-noTM
gi_188522094_gb_ACD60039.1_	0.106	29	0.13	11	0.264	1	0.157	0.143	N	0.57	SignalP-noTM

0.269138	0.985699	0.152775	0.469204	gi_188521666_gb_ACD59611.1_
0.10147	0.773293	0.254074	0.376279	gi_188521667_gb_ACD59612.1_
0.119098	0.157892	0.068881	0.11529	gi_188521668_gb_ACD59613.1_
0.937556	0.999435	0.885238	0.940743	gi_188521669_gb_ACD59614.1_
0.173217	0.328716	0.136108	0.21268	gi_188521670_gb_ACD59615.1_
0.172787	0.037906	0.200047	0.136913	gi_188521671_gb_ACD59616.1_
0.220458	0.542646	0.110563	0.291222	gi_188521672_gb_ACD59617.1_
0.143318	0.323442	0.109389	0.19205	gi_188521673_gb_ACD59618.1_
0.122927	0.127527	0.257501	0.169318	gi_188521674_gb_ACD59619.1_
0.239031	0.826353	0.242872	0.436085	gi_188521675_gb_ACD59620.1_
0.149313	0.049501	0.143318	0.114044	gi_188521676_gb_ACD59621.1_
0.13193	0.072831	0.179314	0.128025	gi_188521680_gb_ACD59625.1_
0.120681	0.080913	0.14629	0.115961	gi_188521687_gb_ACD59632.1_
0.206853	0.097176	0.240672	0.181567	gi_188521688_gb_ACD59633.1_
0.080025	0.007182	0.15046	0.079222	gi_188521690_gb_ACD59635.1_
0.242872	0.112645	0.270912	0.20881	gi_188521691_gb_ACD59636.1_
0.129544	0.010231	0.127527	0.089101	gi_188521692_gb_ACD59637.1_
0.530711	0.819357	0.443986	0.598018	gi_188521693_gb_ACD59638.1_
0.086195	0.053911	0.13331	0.091139	gi_188521802_gb_ACD59747.1_
0.13717	0.009194	0.180643	0.109002	gi_188521968_gb_ACD59913.1_
0.137881	0.001665	0.227761	0.122436	gi_188521969_gb_ACD59914.1_
0.300273	0.658586	0.36749	0.442116	gi_188521971_gb_ACD59916.1_
0.792654	0.990301	0.805182	0.862712	gi_188521972_gb_ACD59917.1_
0.915908	0.943588	0.830194	0.896563	gi_188521976_gb_ACD59921.1_
0.072831	0.089074	0.17023	0.110712	gi_188521977_gb_ACD59922.1_
0.144056	0.074883	0.177994	0.132311	gi_188521978_gb_ACD59923.1_
0.177555	0.791666	0.083173	0.350798	gi_188521984_gb_ACD59929.1_
0.424824	0.38509	0.560453	0.456789	gi_188521985_gb_ACD59930.1_
0.438808	0.988026	0.488002	0.638279	gi_188521987_gb_ACD59932.1_
0.135755	0.047562	0.220458	0.134592	gi_188521988_gb_ACD59933.1_
0.793147	0.158691	0.715856	0.555898	gi_188521989_gb_ACD59934.1_
0.143318	0.182426	0.295254	0.206999	gi_188522002_gb_ACD59947.1_
0.09744	0.050211	0.112645	0.086765	gi_188522003_gb_ACD59948.1_
0.115679	0.035881	0.110859	0.087473	gi_188522005_gb_ACD59950.1_
0.135755	0.038016	0.164792	0.112854	gi_188522006_gb_ACD59951.1_
0.232009	0.078276	0.266784	0.192356	gi_188522007_gb_ACD59952.1_
0.49925	0.093808	0.596283	0.396447	gi_188522008_gb_ACD59953.1_
0.153944	0.104238	0.212822	0.157001	gi_188522011_gb_ACD59956.1_
0.91819	0.954174	0.897707	0.923357	gi_188522012_gb_ACD59957.1_
0.174509	0.434381	0.108225	0.239038	gi_188522013_gb_ACD59958.1_
0.091788	0.071425	0.10147	0.088228	gi_188522014_gb_ACD59959.1_
0.193879	0.547853	0.137525	0.293086	gi_188522015_gb_ACD59960.1_
0.972132	0.998566	0.825922	0.932207	gi_188522017_gb_ACD59962.1_
0.091538	0.004274	0.176245	0.090686	gi_188522020_gb_ACD59965.1_
0.249553	0.643595	0.320168	0.404439	gi_188522023_gb_ACD59968.1_
0.069655	0.094063	0.163557	0.109092	gi_188522024_gb_ACD59969.1_
0.059861	0.007055	0.120681	0.062532	gi_188522027_gb_ACD59972.1_
0.948191	0.904132	0.9398	0.930708	gi_188522040_gb_ACD59985.1_
0.889731	0.984047	0.806589	0.893456	gi_188522052_gb_ACD59997.1_
0.119729	0.088346	0.07635	0.094808	gi_188522054_gb_ACD59999.1_
0.363316	0.986952	0.125209	0.491826	gi_188522055_gb_ACD60000.1_
0.901233	0.368188	0.856682	0.708701	gi_188522056_gb_ACD60001.1_
0.128196	0.01237	0.123575	0.088047	gi_188522058_gb_ACD60003.1_
0.844487	0.823755	0.813968	0.827403	gi_188522061_gb_ACD60006.1_
0.08181	0.072024	0.119098	0.090977	gi_188522067_gb_ACD60012.1_
0.464062	0.053302	0.532952	0.350105	gi_188522072_gb_ACD60017.1_
0.295879	0.037471	0.366096	0.233149	gi_188522073_gb_ACD60018.1_
0.112645	0.158291	0.240672	0.170536	gi_188522074_gb_ACD60019.1_
0.718898	0.972294	0.852959	0.84805	gi_188522075_gb_ACD60020.1_
0.804711	0.995827	0.627615	0.809384	gi_188522076_gb_ACD60021.1_
0.182426	0.304703	0.220458	0.235862	gi_188522077_gb_ACD60022.1_
0.148932	0.114762	0.174509	0.146068	gi_188522078_gb_ACD60023.1_
0.181979	0.779542	0.167702	0.376408	gi_188522079_gb_ACD60024.1_
0.158291	0.003583	0.258649	0.140174	gi_188522080_gb_ACD60025.1_
0.103958	0.001737	0.13193	0.079208	gi_188522081_gb_ACD60026.1_
0.326733	0.966914	0.338049	0.543899	gi_188522082_gb_ACD60027.1_
0.070831	0.063685	0.124553	0.086356	gi_188522083_gb_ACD60028.1_
0.089806	0.054992	0.116603	0.087134	gi_188522084_gb_ACD60029.1_
0.196708	0.482008	0.172787	0.283834	gi_188522085_gb_ACD60030.1_
0.82419	0.999552	0.736722	0.853488	gi_188522086_gb_ACD60031.1_
0.945936	0.979747	0.893785	0.939823	gi_188522087_gb_ACD60032.1_
0.887355	0.994918	0.795597	0.892623	gi_188522088_gb_ACD60033.1_
0.118157	0.820244	0.065866	0.334756	gi_188522089_gb_ACD60034.1_
0.218915	0.072628	0.269138	0.186894	gi_188522090_gb_ACD60035.1_
0.239577	0.116294	0.304068	0.21998	gi_188522091_gb_ACD60036.1_
0.50375	0.195289	0.432907	0.377315	gi_188522092_gb_ACD60037.1_
0.090545	0.277479	0.1034	0.157141	gi_188522093_gb_ACD60038.1_
0.176681	0.0488	0.260379	0.161953	gi_188522094_gb_ACD60039.1_

gi_188522095_gb_ACD60040.1_	0.159	30	0.207	12	0.506	1	0.409	0.302	N	0.57	SignalP-noTM
gi_188522096_gb_ACD60041.1_	0.101	33	0.109	11	0.165	1	0.114	0.111	N	0.57	SignalP-noTM
gi_188522099_gb_ACD60044.1_	0.106	25	0.113	11	0.209	3	0.127	0.119	N	0.57	SignalP-noTM
gi_188522100_gb_ACD60045.1_	0.233	37	0.166	37	0.156	35	0.103	0.137	N	0.57	SignalP-noTM
gi_188522101_gb_ACD60046.1_	0.134	19	0.111	63	0.147	39	0.098	0.105	N	0.57	SignalP-noTM
gi_188522102_gb_ACD60047.1_	0.108	59	0.134	18	0.248	13	0.165	0.149	N	0.57	SignalP-noTM
gi_188522103_gb_ACD60048.1_	0.144	25	0.114	25	0.163	23	0.091	0.103	N	0.57	SignalP-noTM
gi_188522104_gb_ACD60049.1_	0.395	25	0.457	25	0.717	20	0.451	0.454	N	0.57	SignalP-noTM
gi_188522105_gb_ACD60050.1_	0.123	36	0.107	36	0.109	9	0.086	0.097	N	0.57	SignalP-noTM
gi_188522106_gb_ACD60051.1_	0.137	16	0.159	16	0.351	16	0.168	0.163	N	0.57	SignalP-noTM
gi_188522107_gb_ACD60052.1_	0.11	26	0.158	11	0.345	7	0.253	0.203	N	0.57	SignalP-noTM
gi_188522108_gb_ACD60053.1_	0.124	41	0.127	41	0.195	39	0.106	0.117	N	0.57	SignalP-noTM
gi_188522109_gb_ACD60054.1_	0.143	42	0.115	25	0.14	23	0.113	0.114	N	0.57	SignalP-noTM
gi_188522110_gb_ACD60055.1_	0.106	49	0.11	30	0.155	8	0.115	0.112	N	0.57	SignalP-noTM
gi_188522122_gb_ACD60067.1_	0.144	29	0.113	29	0.124	10	0.098	0.106	N	0.57	SignalP-noTM
gi_188522125_gb_ACD60070.1_	0.117	41	0.119	41	0.155	40	0.101	0.111	N	0.57	SignalP-noTM
gi_188522126_gb_ACD60071.1_	0.175	38	0.114	38	0.113	6	0.074	0.095	N	0.57	SignalP-noTM
gi_188522127_gb_ACD60072.1_	0.11	17	0.158	11	0.344	1	0.238	0.196	N	0.57	SignalP-noTM
gi_188522151_gb_ACD60096.1_	0.152	27	0.158	27	0.394	1	0.179	0.168	N	0.57	SignalP-noTM
gi_188522161_gb_ACD60106.1_	0.101	33	0.103	21	0.138	10	0.092	0.098	N	0.57	SignalP-noTM
gi_188522167_gb_ACD60112.1_	0.137	35	0.176	22	0.417	25	0.235	0.204	N	0.57	SignalP-noTM
gi_188522173_gb_ACD60118.1_	0.108	23	0.127	11	0.244	1	0.144	0.135	N	0.57	SignalP-noTM
gi_188522178_gb_ACD60123.1_	0.119	28	0.185	11	0.508	1	0.329	0.238	N	0.51	SignalP-TM
gi_188522179_gb_ACD60124.1_	0.162	24	0.201	24	0.568	1	0.296	0.245	N	0.57	SignalP-noTM
gi_188522181_gb_ACD60126.1_	0.105	48	0.117	35	0.165	9	0.123	0.12	N	0.57	SignalP-noTM
gi_188522182_gb_ACD60127.1_	0.151	59	0.127	46	0.175	41	0.108	0.118	N	0.57	SignalP-noTM
gi_188522185_gb_ACD60130.1_	0.133	22	0.119	11	0.234	1	0.129	0.124	N	0.57	SignalP-noTM
gi_188522187_gb_ACD60132.1_	0.135	18	0.101	48	0.123	38	0.083	0.093	N	0.57	SignalP-noTM
gi_188522188_gb_ACD60133.1_	0.129	21	0.103	38	0.118	32	0.081	0.093	N	0.57	SignalP-noTM
gi_188522189_gb_ACD60134.1_	0.155	21	0.161	11	0.419	2	0.249	0.194	N	0.51	SignalP-TM
gi_188522190_gb_ACD60135.1_	0.177	27	0.154	27	0.315	1	0.157	0.155	N	0.51	SignalP-TM
gi_188522194_gb_ACD60139.1_	0.599	27	0.64	27	0.94	1	0.785	0.708	Y	0.57	SignalP-noTM
gi_188522204_gb_ACD60149.1_	0.153	32	0.165	32	0.393	29	0.205	0.184	N	0.57	SignalP-noTM
gi_188522205_gb_ACD60150.1_	0.192	10	0.266	19	0.719	8	0.424	0.34	N	0.57	SignalP-noTM
gi_188522206_gb_ACD60151.1_	0.118	32	0.104	32	0.119	2	0.093	0.099	N	0.57	SignalP-noTM
gi_188522211_gb_ACD60156.1_	0.245	23	0.491	23	0.992	19	0.977	0.72	Y	0.57	SignalP-noTM
gi_188522212_gb_ACD60157.1_	0.225	44	0.163	44	0.358	3	0.181	0.171	N	0.57	SignalP-noTM
gi_188522213_gb_ACD60158.1_	0.109	43	0.103	43	0.11	61	0.091	0.098	N	0.57	SignalP-noTM
gi_188522214_gb_ACD60159.1_	0.134	39	0.152	54	0.277	50	0.121	0.137	N	0.57	SignalP-noTM
gi_188522215_gb_ACD60160.1_	0.102	11	0.125	11	0.185	3	0.154	0.138	N	0.57	SignalP-noTM
gi_188522216_gb_ACD60161.1_	0.594	26	0.593	26	0.898	8	0.703	0.645	Y	0.57	SignalP-noTM
gi_188522220_gb_ACD60165.1_	0.105	43	0.111	16	0.162	7	0.115	0.113	N	0.57	SignalP-noTM
gi_188522223_gb_ACD60168.1_	0.109	19	0.11	14	0.147	4	0.12	0.115	N	0.57	SignalP-noTM
gi_188522227_gb_ACD60172.1_	0.824	25	0.863	25	0.976	10	0.925	0.892	Y	0.57	SignalP-noTM
gi_188522228_gb_ACD60173.1_	0.105	45	0.101	45	0.16	42	0.082	0.092	N	0.57	SignalP-noTM
gi_188522229_gb_ACD60174.1_	0.342	46	0.52	46	0.978	30	0.74	0.624	Y	0.57	SignalP-noTM
gi_188522230_gb_ACD60175.1_	0.169	47	0.184	47	0.317	45	0.165	0.177	N	0.51	SignalP-TM
gi_188522232_gb_ACD60177.1_	0.12	50	0.111	50	0.113	43	0.088	0.1	N	0.57	SignalP-noTM
gi_188522240_gb_ACD60185.1_	0.148	38	0.127	38	0.151	34	0.098	0.113	N	0.57	SignalP-noTM
gi_188522241_gb_ACD60186.1_	0.318	25	0.467	23	0.817	19	0.667	0.561	N	0.57	SignalP-noTM
gi_188522246_gb_ACD60191.1_	0.112	29	0.127	11	0.288	1	0.144	0.133	N	0.51	SignalP-TM
gi_188522247_gb_ACD60192.1_	0.598	49	0.532	49	0.725	44	0.349	0.464	N	0.51	SignalP-TM
gi_188522367_gb_ACD60312.1_	0.125	47	0.142	47	0.2	40	0.113	0.129	N	0.57	SignalP-noTM
gi_188522368_gb_ACD60313.1_	0.14	20	0.153	20	0.214	4	0.177	0.164	N	0.57	SignalP-noTM
gi_188522371_gb_ACD60316.1_	0.162	30	0.123	30	0.237	42	0.089	0.107	N	0.57	SignalP-noTM
gi_188522389_gb_ACD60334.1_	0.264	28	0.382	28	0.734	7	0.589	0.459	N	0.51	SignalP-TM
gi_188522390_gb_ACD60335.1_	0.12	66	0.175	51	0.392	38	0.157	0.167	N	0.57	SignalP-noTM
gi_188522391_gb_ACD60336.1_	0.128	19	0.139	11	0.298	1	0.178	0.157	N	0.57	SignalP-noTM
gi_188522392_gb_ACD60337.1_	0.34	21	0.247	21	0.286	19	0.193	0.222	N	0.57	SignalP-noTM
gi_188522393_gb_ACD60338.1_	0.158	31	0.131	31	0.221	23	0.112	0.122	N	0.57	SignalP-noTM
gi_188522394_gb_ACD60339.1_	0.121	24	0.136	24	0.185	14	0.136	0.136	N	0.57	SignalP-noTM
gi_188522395_gb_ACD60340.1_	0.257	16	0.319	16	0.642	12	0.4	0.357	N	0.57	SignalP-noTM
gi_188522396_gb_ACD60341.1_	0.12	61	0.109	13	0.174	11	0.113	0.111	N	0.57	SignalP-noTM
gi_188522406_gb_ACD60351.1_	0.132	27	0.244	11	0.698	4	0.608	0.379	N	0.51	SignalP-TM
gi_188522407_gb_ACD60352.1_	0.101	31	0.167	18	0.356	13	0.259	0.21	N	0.57	SignalP-noTM
gi_188522412_gb_ACD60357.1_	0.149	63	0.208	16	0.51	7	0.431	0.291	N	0.51	SignalP-TM
gi_188522414_gb_ACD60359.1_	0.213	21	0.173	21	0.227	19	0.128	0.152	N	0.57	SignalP-noTM
gi_188522421_gb_ACD60366.1_	0.167	24	0.174	24	0.338	11	0.219	0.195	N	0.57	SignalP-noTM
gi_188522428_gb_ACD60373.1_	0.109	51	0.176	11	0.386	5	0.315	0.241	N	0.57	SignalP-noTM
gi_188522429_gb_ACD60374.1_	0.1	26	0.106	42	0.15	4	0.099	0.103	N	0.57	SignalP-noTM
gi_188522430_gb_ACD60375.1_	0.113	61	0.107	37	0.126	33	0.09	0.099	N	0.57	SignalP-noTM
gi_188522431_gb_ACD60376.1_	0.117	37	0.109	37	0.109	41	0.088	0.099	N	0.57	SignalP-noTM
gi_188522435_gb_ACD60380.1_	0.156	22	0.138	22	0.219	1	0.137	0.138	N	0.57	SignalP-noTM
gi_188522436_gb_ACD60381.1_	0.15	29	0.143	11	0.253	4	0.205	0.172	N	0.57	SignalP-noTM
gi_188522437_gb_ACD60382.1_	0.111	27	0.14	18	0.24	16	0.179	0.159	N	0.57	SignalP-noTM
gi_188522438_gb_ACD60383.1_	0.127	59	0.122	59	0.144	49	0.108	0.115	N	0.57	SignalP-noTM
gi_188522439_gb_ACD60384.1_	0.132	30	0.232	30	0.556	17	0.356	0.29	N	0.57	SignalP-noTM
gi_188522440_gb_ACD60385.1_	0.183	41	0.196	41	0.307	38	0.168	0.186	N	0.51	SignalP-TM

0.103958	0.039354	0.168541	0.103951	gi_188522095_gb_ACD60040.1_
0.138238	0.208829	0.108225	0.151764	gi_188522096_gb_ACD60041.1_
0.297757	0.350236	0.415324	0.354439	gi_188522099_gb_ACD60044.1_
0.127527	0.0298	0.209822	0.122383	gi_188522100_gb_ACD60045.1_
0.961321	0.999377	0.869438	0.943379	gi_188522101_gb_ACD60046.1_
0.114153	0.054526	0.131244	0.099974	gi_188522102_gb_ACD60047.1_
0.092038	0.000929	0.23308	0.108682	gi_188522103_gb_ACD60048.1_
0.091289	0.077629	0.171931	0.113616	gi_188522104_gb_ACD60049.1_
0.056572	0.006356	0.112645	0.058524	gi_188522105_gb_ACD60050.1_
0.227233	0.357094	0.430699	0.338342	gi_188522106_gb_ACD60051.1_
0.36749	0.98016	0.187856	0.511835	gi_188522107_gb_ACD60052.1_
0.186487	0.753246	0.09744	0.345724	gi_188522108_gb_ACD60053.1_
0.182873	0.191545	0.132964	0.169127	gi_188522109_gb_ACD60054.1_
0.232009	0.58686	0.23308	0.35065	gi_188522110_gb_ACD60055.1_
0.07635	0.034656	0.126861	0.079289	gi_188522122_gb_ACD60067.1_
0.072426	0.002633	0.122282	0.06578	gi_188522125_gb_ACD60070.1_
0.113548	0.052252	0.136461	0.100754	gi_188522126_gb_ACD60071.1_
0.926967	0.653849	0.858149	0.812988	gi_188522127_gb_ACD60072.1_
0.186487	0.272693	0.171931	0.21037	gi_188522151_gb_ACD60096.1_
0.155119	0.996046	0.366793	0.505986	gi_188522161_gb_ACD60106.1_
0.129882	0.03704	0.195289	0.120737	gi_188522167_gb_ACD60112.1_
0.690829	0.987258	0.829346	0.835811	gi_188522173_gb_ACD60118.1_
0.918639	0.991886	0.850687	0.920404	gi_188522178_gb_ACD60123.1_
0.297757	0.508249	0.35503	0.387012	gi_188522179_gb_ACD60124.1_
0.955212	0.998721	0.802342	0.918758	gi_188522181_gb_ACD60126.1_
0.663962	0.816678	0.557495	0.679378	gi_188522182_gb_ACD60127.1_
0.157892	0.945008	0.109389	0.404096	gi_188522185_gb_ACD60130.1_
0.075718	0.003966	0.113247	0.06431	gi_188522187_gb_ACD60132.1_
0.216361	0.033862	0.282925	0.177716	gi_188522188_gb_ACD60133.1_
0.109097	0.149313	0.180643	0.146351	gi_188522189_gb_ACD60134.1_
0.130562	0.607782	0.153944	0.297429	gi_188522190_gb_ACD60135.1_
0.861404	0.209325	0.830616	0.633782	gi_188522194_gb_ACD60139.1_
0.846447	0.728495	0.665967	0.74697	gi_188522204_gb_ACD60149.1_
0.743645	0.067358	0.776953	0.529319	gi_188522205_gb_ACD60150.1_
0.442505	0.710333	0.640146	0.597661	gi_188522206_gb_ACD60151.1_
0.944223	0.994638	0.90361	0.94749	gi_188522211_gb_ACD60156.1_
0.171079	0.039015	0.195289	0.135128	gi_188522212_gb_ACD60157.1_
0.069267	0.011868	0.161515	0.080883	gi_188522213_gb_ACD60158.1_
0.106215	0.114762	0.202458	0.141145	gi_188522214_gb_ACD60159.1_
0.883088	0.992924	0.716466	0.864159	gi_188522215_gb_ACD60160.1_
0.959262	0.998732	0.891485	0.949826	gi_188522216_gb_ACD60161.1_
0.149694	0.046221	0.117222	0.104379	gi_188522220_gb_ACD60165.1_
0.313028	0.259802	0.382961	0.318597	gi_188522223_gb_ACD60168.1_
0.959612	0.999841	0.926763	0.962072	gi_188522227_gb_ACD60172.1_
0.093046	0.028609	0.112346	0.078	gi_188522228_gb_ACD60173.1_
0.957467	0.99549	0.891775	0.948244	gi_188522229_gb_ACD60174.1_
0.950358	0.72968	0.918639	0.866226	gi_188522230_gb_ACD60175.1_
0.21738	0.153553	0.228289	0.199741	gi_188522232_gb_ACD60177.1_
0.071625	0.00443	0.1065	0.060852	gi_188522240_gb_ACD60185.1_
0.126529	0.078276	0.11847	0.107758	gi_188522241_gb_ACD60186.1_
0.076775	0.00166	0.092793	0.057076	gi_188522246_gb_ACD60191.1_
0.287205	0.712795	0.370983	0.456994	gi_188522247_gb_ACD60192.1_
0.390788	0.107647	0.406609	0.301681	gi_188522367_gb_ACD60312.1_
0.106215	0.06054	0.127862	0.098206	gi_188522368_gb_ACD60313.1_
0.21232	0.084788	0.171505	0.156204	gi_188522371_gb_ACD60316.1_
0.100381	0.005795	0.162737	0.089638	gi_188522389_gb_ACD60334.1_
0.149694	0.046089	0.197658	0.131147	gi_188522390_gb_ACD60335.1_
0.103958	0.024868	0.1603	0.096375	gi_188522391_gb_ACD60336.1_
0.436593	0.043898	0.491001	0.323831	gi_188522392_gb_ACD60337.1_
0.944065	0.999578	0.897982	0.947208	gi_188522393_gb_ACD60338.1_
0.121639	0.02795	0.183772	0.11112	gi_188522475_gb_ACD60420.1_
0.218915	0.547853	0.492501	0.419756	gi_188522479_gb_ACD60424.1_
0.141122	0.058031	0.141851	0.113668	gi_188522480_gb_ACD60425.1_
0.956727	0.996543	0.899076	0.950782	gi_188522483_gb_ACD60428.1_
0.246754	0.316912	0.254074	0.27258	gi_188522484_gb_ACD60429.1_
0.956478	0.997733	0.891194	0.948468	gi_188522485_gb_ACD60430.1_
0.958314	0.995852	0.893785	0.949317	gi_188522486_gb_ACD60431.1_
0.074675	0.032327	0.174078	0.093693	gi_188522488_gb_ACD60433.1_
0.087624	0.046221	0.105931	0.079925	gi_188522490_gb_ACD60435.1_
0.546366	0.748758	0.68568	0.660268	gi_188522491_gb_ACD60436.1_
0.067736	0.041806	0.135755	0.081766	gi_188522492_gb_ACD60437.1_
0.137525	0.033764	0.192943	0.121411	gi_188522493_gb_ACD60438.1_
0.216361	0.207839	0.327393	0.250531	gi_188522494_gb_ACD60439.1_
0.142217	0.093046	0.158291	0.131185	gi_188522495_gb_ACD60440.1_
0.11847	0.032609	0.185126	0.112068	gi_188522496_gb_ACD60441.1_
0.21738	0.027225	0.279891	0.174832	gi_188522505_gb_ACD60450.1_
0.756576	0.886452	0.831459	0.824829	gi_188522506_gb_ACD60451.1_
0.115679	0.520239	0.093808	0.243242	gi_188522512_gb_ACD60457.1_

gi_188522441_gb_ACD60386.1_	0.104	56	0.136	11	0.215	5	0.185	0.159	N	0.57	SignalP-noTM
gi_188522442_gb_ACD60387.1_	0.296	18	0.367	18	0.626	13	0.443	0.402	N	0.57	SignalP-noTM
gi_188522443_gb_ACD60388.1_	0.589	16	0.644	16	0.87	12	0.715	0.678	Y	0.57	SignalP-noTM
gi_188522447_gb_ACD60392.1_	0.275	20	0.34	20	0.646	19	0.447	0.39	N	0.57	SignalP-noTM
gi_188522448_gb_ACD60393.1_	0.108	12	0.099	47	0.128	1	0.09	0.095	N	0.57	SignalP-noTM
gi_188522449_gb_ACD60394.1_	0.227	32	0.16	32	0.155	2	0.108	0.136	N	0.57	SignalP-noTM
gi_188522450_gb_ACD60395.1_	0.107	38	0.108	52	0.153	50	0.092	0.101	N	0.57	SignalP-noTM
gi_188522451_gb_ACD60396.1_	0.134	31	0.111	31	0.135	4	0.095	0.104	N	0.57	SignalP-noTM
gi_188522452_gb_ACD60397.1_	0.114	65	0.112	48	0.147	2	0.107	0.109	N	0.57	SignalP-noTM
gi_188522453_gb_ACD60398.1_	0.127	25	0.124	25	0.163	20	0.112	0.118	N	0.57	SignalP-noTM
gi_188522455_gb_ACD60400.1_	0.113	54	0.145	13	0.287	11	0.211	0.176	N	0.57	SignalP-noTM
gi_188522456_gb_ACD60401.1_	0.102	33	0.104	33	0.139	32	0.1	0.102	N	0.57	SignalP-noTM
gi_188522457_gb_ACD60402.1_	0.168	27	0.169	35	0.37	34	0.167	0.168	N	0.57	SignalP-noTM
gi_188522459_gb_ACD60404.1_	0.12	46	0.108	31	0.149	1	0.106	0.107	N	0.57	SignalP-noTM
gi_188522460_gb_ACD60405.1_	0.116	15	0.169	11	0.418	1	0.274	0.218	N	0.57	SignalP-noTM
gi_188522461_gb_ACD60406.1_	0.115	62	0.11	62	0.119	35	0.092	0.102	N	0.57	SignalP-noTM
gi_188522462_gb_ACD60407.1_	0.123	40	0.106	40	0.128	1	0.088	0.098	N	0.57	SignalP-noTM
gi_188522463_gb_ACD60408.1_	0.17	46	0.152	26	0.23	3	0.166	0.159	N	0.57	SignalP-noTM
gi_188522466_gb_ACD60411.1_	0.152	56	0.123	29	0.143	26	0.099	0.112	N	0.57	SignalP-noTM
gi_188522468_gb_ACD60413.1_	0.161	35	0.141	35	0.295	34	0.109	0.126	N	0.57	SignalP-noTM
gi_188522469_gb_ACD60414.1_	0.128	41	0.123	25	0.171	5	0.134	0.128	N	0.57	SignalP-noTM
gi_188522475_gb_ACD60420.1_	0.168	28	0.149	28	0.204	21	0.126	0.138	N	0.57	SignalP-noTM
gi_188522479_gb_ACD60424.1_	0.1	14	0.153	11	0.369	4	0.236	0.192	N	0.57	SignalP-noTM
gi_188522480_gb_ACD60425.1_	0.123	51	0.104	33	0.114	2	0.092	0.099	N	0.57	SignalP-noTM
gi_188522483_gb_ACD60428.1_	0.248	13	0.46	13	0.913	12	0.853	0.645	Y	0.57	SignalP-noTM
gi_188522484_gb_ACD60429.1_	0.127	51	0.131	27	0.209	20	0.131	0.131	N	0.57	SignalP-noTM
gi_188522485_gb_ACD60430.1_	0.574	26	0.74	26	0.984	22	0.955	0.841	Y	0.57	SignalP-noTM
gi_188522486_gb_ACD60431.1_	0.658	25	0.766	25	0.956	21	0.891	0.825	Y	0.57	SignalP-noTM
gi_188522488_gb_ACD60433.1_	0.143	26	0.135	53	0.189	43	0.108	0.125	N	0.51	SignalP-TM
gi_188522490_gb_ACD60435.1_	0.138	17	0.148	17	0.256	2	0.177	0.162	N	0.57	SignalP-noTM
gi_188522491_gb_ACD60436.1_	0.845	27	0.831	27	0.915	12	0.841	0.836	Y	0.57	SignalP-noTM
gi_188522492_gb_ACD60437.1_	0.194	48	0.175	22	0.239	19	0.186	0.18	N	0.57	SignalP-noTM
gi_188522493_gb_ACD60438.1_	0.169	42	0.136	42	0.236	1	0.131	0.134	N	0.57	SignalP-noTM
gi_188522494_gb_ACD60439.1_	0.199	22	0.243	22	0.567	3	0.371	0.291	N	0.51	SignalP-TM
gi_188522495_gb_ACD60440.1_	0.464	25	0.268	25	0.366	24	0.14	0.208	N	0.57	SignalP-noTM
gi_188522496_gb_ACD60441.1_	0.371	40	0.214	40	0.313	1	0.118	0.169	N	0.57	SignalP-noTM
gi_188522505_gb_ACD60450.1_	0.108	37	0.106	25	0.132	13	0.101	0.104	N	0.57	SignalP-noTM
gi_188522506_gb_ACD60451.1_	0.129	25	0.11	25	0.138	14	0.099	0.105	N	0.57	SignalP-noTM
gi_188522512_gb_ACD60457.1_	0.198	21	0.139	21	0.136	9	0.106	0.124	N	0.57	SignalP-noTM
gi_188522515_gb_ACD60460.1_	0.353	22	0.276	22	0.39	20	0.214	0.247	N	0.57	SignalP-noTM
gi_188522516_gb_ACD60461.1_	0.113	36	0.156	16	0.278	13	0.24	0.195	N	0.57	SignalP-noTM
gi_188522521_gb_ACD60466.1_	0.247	33	0.194	33	0.217	35	0.127	0.169	N	0.51	SignalP-TM
gi_188522532_gb_ACD60477.1_	0.139	22	0.236	22	0.521	1	0.369	0.285	N	0.51	SignalP-TM
gi_188522534_gb_ACD60479.1_	0.29	12	0.299	12	0.387	10	0.305	0.302	N	0.57	SignalP-noTM
gi_188522536_gb_ACD60481.1_	0.151	29	0.16	11	0.396	1	0.236	0.196	N	0.57	SignalP-noTM
gi_188522538_gb_ACD60483.1_	0.107	62	0.119	16	0.161	8	0.131	0.125	N	0.57	SignalP-noTM
gi_188522540_gb_ACD60485.1_	0.115	24	0.127	18	0.201	8	0.14	0.133	N	0.57	SignalP-noTM
gi_188522541_gb_ACD60486.1_	0.313	33	0.185	33	0.169	32	0.094	0.142	N	0.57	SignalP-noTM
gi_188522542_gb_ACD60487.1_	0.14	43	0.121	14	0.186	3	0.147	0.133	N	0.57	SignalP-noTM
gi_188522544_gb_ACD60489.1_	0.144	61	0.117	61	0.111	20	0.087	0.103	N	0.57	SignalP-noTM
gi_188522546_gb_ACD60491.1_	0.125	34	0.115	34	0.159	1	0.101	0.109	N	0.51	SignalP-TM
gi_188522547_gb_ACD60492.1_	0.126	24	0.103	58	0.138	1	0.082	0.093	N	0.57	SignalP-noTM
gi_188522548_gb_ACD60493.1_	0.162	43	0.163	43	0.329	41	0.144	0.154	N	0.57	SignalP-noTM
gi_188522552_gb_ACD60497.1_	0.106	35	0.11	43	0.17	41	0.102	0.106	N	0.57	SignalP-noTM
gi_188522553_gb_ACD60498.1_	0.118	13	0.131	13	0.293	1	0.144	0.136	N	0.51	SignalP-TM
gi_188522554_gb_ACD60499.1_	0.14	31	0.127	11	0.183	8	0.171	0.143	N	0.51	SignalP-TM
gi_188522555_gb_ACD60500.1_	0.192	25	0.143	25	0.192	36	0.118	0.132	N	0.57	SignalP-noTM
gi_188522556_gb_ACD60501.1_	0.418	25	0.555	20	0.899	2	0.848	0.692	Y	0.57	SignalP-noTM
gi_188522557_gb_ACD60502.1_	0.726	17	0.81	17	0.94	2	0.911	0.858	Y	0.57	SignalP-noTM
gi_188522561_gb_ACD60506.1_	0.15	59	0.164	11	0.407	1	0.25	0.204	N	0.57	SignalP-noTM
gi_188522562_gb_ACD60507.1_	0.112	24	0.109	13	0.13	5	0.119	0.113	N	0.57	SignalP-noTM
gi_188522563_gb_ACD60508.1_	0.162	35	0.207	25	0.386	24	0.32	0.249	N	0.51	SignalP-TM
gi_188522564_gb_ACD60509.1_	0.651	20	0.773	20	0.958	17	0.912	0.838	Y	0.57	SignalP-noTM
gi_188522565_gb_ACD60510.1_	0.112	54	0.12	15	0.183	6	0.144	0.131	N	0.57	SignalP-noTM
gi_188522566_gb_ACD60511.1_	0.195	27	0.17	27	0.236	1	0.145	0.158	N	0.57	SignalP-noTM
gi_188522567_gb_ACD60512.1_	0.134	53	0.108	12	0.158	1	0.114	0.111	N	0.57	SignalP-noTM
gi_188522568_gb_ACD60513.1_	0.267	39	0.166	39	0.278	1	0.129	0.148	N	0.57	SignalP-noTM
gi_188522569_gb_ACD60514.1_	0.114	47	0.107	47	0.142	6	0.094	0.101	N	0.57	SignalP-noTM
gi_188522570_gb_ACD60515.1_	0.133	23	0.193	23	0.518	1	0.296	0.242	N	0.57	SignalP-noTM
gi_188522571_gb_ACD60516.1_	0.142	19	0.173	11	0.443	1	0.282	0.224	N	0.57	SignalP-noTM
gi_188522572_gb_ACD60517.1_	0.117	35	0.18	16	0.378	5	0.296	0.223	N	0.51	SignalP-TM
gi_188522573_gb_ACD60518.1_	0.207	21	0.176	37	0.289	35	0.163	0.17	N	0.57	SignalP-noTM
gi_188522574_gb_ACD60519.1_	0.105	27	0.113	11	0.158	3	0.13	0.121	N	0.57	SignalP-noTM
gi_188522576_gb_ACD60521.1_	0.109	22	0.101	70	0.113	68	0.087	0.095	N	0.57	SignalP-noTM
gi_188522577_gb_ACD60522.1_	0.105	36	0.147	12	0.314	2	0.216	0.179	N	0.57	SignalP-noTM
gi_188522581_gb_ACD60526.1_	0.411	21	0.358	21	0.512	16	0.275	0.319	N	0.57	SignalP-noTM
gi_188522585_gb_ACD60530.1_	0.106	50	0.098	30	0.127	42	0.083	0.092	N	0.51	SignalP-TM
gi_188522586_gb_ACD60531.1_	0.129	22	0.159	11	0.387	1	0.239	0.197	N	0.57	SignalP-noTM

0.725518	0.925532	0.862119	0.837723	gi_188522515_gb_ACD60460.1_
0.095349	0.003305	0.155513	0.084722	gi_188522516_gb_ACD60461.1_
0.097704	0.236313	0.188773	0.174263	gi_188522521_gb_ACD60466.1_
0.159092	0.252372	0.261536	0.224333	gi_188522532_gb_ACD60477.1_
0.916369	0.935233	0.855573	0.902392	gi_188522534_gb_ACD60479.1_
0.964429	0.998145	0.919753	0.960776	gi_188522536_gb_ACD60481.1_
0.180199	0.257501	0.229347	0.222349	gi_188522538_gb_ACD60483.1_
0.449918	0.10011	0.526226	0.358751	gi_188522540_gb_ACD60485.1_
0.137525	0.875773	0.089806	0.367701	gi_188522541_gb_ACD60486.1_
0.917056	0.984047	0.786675	0.895926	gi_188522542_gb_ACD60487.1_
0.943428	0.984872	0.90896	0.945753	gi_188522394_gb_ACD60339.1_
0.867036	0.902296	0.786675	0.852002	gi_188522395_gb_ACD60340.1_
0.940139	0.988816	0.897982	0.942312	gi_188522396_gb_ACD60341.1_
0.079805	0.704746	0.17023	0.31826	gi_188522406_gb_ACD60351.1_
0.171079	0.90256	0.088346	0.387328	gi_188522407_gb_ACD60352.1_
0.154727	0.06192	0.157095	0.124581	gi_188522412_gb_ACD60357.1_
0.087624	0.120999	0.158691	0.122438	gi_188522414_gb_ACD60359.1_
0.206361	0.086195	0.258075	0.183544	gi_188522421_gb_ACD60366.1_
0.287819	0.75823	0.327393	0.457814	gi_188522428_gb_ACD60373.1_
0.087624	0.018597	0.285366	0.130529	gi_188522429_gb_ACD60374.1_
0.085959	0.040621	0.1034	0.07666	gi_188522430_gb_ACD60375.1_
0.966914	0.998902	0.764228	0.910015	gi_188522431_gb_ACD60376.1_
0.104799	0.115373	0.186032	0.135401	gi_188522435_gb_ACD60380.1_
0.299013	0.094063	0.40444	0.265839	gi_188522436_gb_ACD60381.1_
0.165619	0.047021	0.243977	0.152206	gi_188522437_gb_ACD60382.1_
0.907207	0.936494	0.897707	0.913803	gi_188522438_gb_ACD60383.1_
0.951616	0.99952	0.936672	0.962603	gi_188522439_gb_ACD60384.1_
0.944381	0.970631	0.875773	0.930262	gi_188522440_gb_ACD60385.1_
0.145916	0.059023	0.074261	0.093067	gi_188522441_gb_ACD60386.1_
0.951339	0.992645	0.921507	0.955164	gi_188522442_gb_ACD60387.1_
0.917738	0.760423	0.855202	0.844454	gi_188522443_gb_ACD60388.1_
0.087864	0.002414	0.109681	0.066653	gi_188522447_gb_ACD60392.1_
0.132274	0.0076	0.174509	0.104794	gi_188522448_gb_ACD60393.1_
0.065866	0.001917	0.099302	0.055695	gi_188522449_gb_ACD60394.1_
0.121319	0.071028	0.127194	0.106514	gi_188522450_gb_ACD60395.1_
0.093046	0.063151	0.11385	0.090016	gi_188522451_gb_ACD60396.1_
0.091289	0.232009	0.063151	0.128816	gi_188522452_gb_ACD60397.1_
0.221491	0.150844	0.227233	0.199856	gi_188522453_gb_ACD60398.1_
0.324098	0.056572	0.468542	0.283071	gi_188522455_gb_ACD60400.1_
0.17581	0.04004	0.271505	0.162452	gi_188522456_gb_ACD60401.1_
0.358473	0.975779	0.155119	0.496457	gi_188522457_gb_ACD60402.1_
0.090792	0.029713	0.144798	0.088434	gi_188522459_gb_ACD60404.1_
0.181087	0.045434	0.148173	0.124898	gi_188522460_gb_ACD60405.1_
0.039582	0.054681	0.066608	0.053624	gi_188522461_gb_ACD60406.1_
0.106786	0.047291	0.096651	0.083576	gi_188522462_gb_ACD60407.1_
0.099302	0.032233	0.141122	0.090886	gi_188522463_gb_ACD60408.1_
0.123575	0.268548	0.097704	0.163276	gi_188522466_gb_ACD60411.1_
0.232544	0.974017	0.109389	0.43865	gi_188522468_gb_ACD60413.1_
0.115986	0.027146	0.130222	0.091118	gi_188522469_gb_ACD60414.1_
0.151228	0.135053	0.170654	0.152312	gi_188522544_gb_ACD60489.1_
0.15046	0.098234	0.180643	0.143112	gi_188522546_gb_ACD60491.1_
0.122927	0.058525	0.148932	0.110128	gi_188522547_gb_ACD60492.1_
0.145916	0.148552	0.165205	0.153224	gi_188522548_gb_ACD60493.1_
0.069655	0.006042	0.09984	0.058512	gi_188522552_gb_ACD60497.1_
0.049642	0.474522	0.153164	0.225776	gi_188522553_gb_ACD60498.1_
0.070633	0.115986	0.138596	0.108405	gi_188522554_gb_ACD60499.1_
0.111155	0.077629	0.104238	0.097674	gi_188522555_gb_ACD60500.1_
0.955976	0.956102	0.909208	0.940429	gi_188522556_gb_ACD60501.1_
0.933392	0.899076	0.900698	0.911055	gi_188522557_gb_ACD60502.1_
0.104518	0.020432	0.120363	0.081771	gi_188522561_gb_ACD60506.1_
0.071824	0.048522	0.116912	0.079086	gi_188522562_gb_ACD60507.1_
0.957467	0.993794	0.899348	0.950203	gi_188522563_gb_ACD60508.1_
0.94164	0.999796	0.890903	0.944113	gi_188522564_gb_ACD60509.1_
0.107072	0.399392	0.079365	0.195276	gi_188522565_gb_ACD60510.1_
0.094319	0.046486	0.116912	0.085906	gi_188522566_gb_ACD60511.1_
0.168541	0.015353	0.207839	0.130578	gi_188522567_gb_ACD60512.1_
0.111155	0.059189	0.134354	0.101566	gi_188522568_gb_ACD60513.1_
0.072831	0.039354	0.096129	0.069438	gi_188522569_gb_ACD60514.1_
0.153164	0.187399	0.102845	0.147803	gi_188522570_gb_ACD60515.1_
0.4955	0.134005	0.638071	0.422525	gi_188522571_gb_ACD60516.1_
0.144056	0.036089	0.198134	0.126093	gi_188522572_gb_ACD60517.1_
0.153553	0.005251	0.14517	0.101325	gi_188522573_gb_ACD60518.1_
0.147418	0.239577	0.119729	0.168908	gi_188522574_gb_ACD60519.1_
0.07871	0.06985	0.109975	0.086178	gi_188522576_gb_ACD60521.1_
0.624806	0.541901	0.67787	0.614859	gi_188522577_gb_ACD60522.1_
0.129882	0.013762	0.12196	0.088535	gi_188522581_gb_ACD60526.1_
0.127862	0.228818	0.21032	0.189	gi_188522585_gb_ACD60530.1_
0.252939	0.871468	0.086195	0.403534	gi_188522586_gb_ACD60531.1_

gi_188522587_gb_ACD60532.1_	0.875	22	0.898	22	0.951	17	0.903	0.9	Y	0.57	SignalP-noTM
gi_188522589_gb_ACD60534.1_	0.518	25	0.63	25	0.932	19	0.779	0.7	Y	0.57	SignalP-noTM
gi_188522590_gb_ACD60535.1_	0.215	32	0.432	32	0.945	15	0.876	0.641	Y	0.57	SignalP-noTM
gi_188522594_gb_ACD60539.1_	0.107	19	0.114	58	0.159	51	0.116	0.115	N	0.57	SignalP-noTM
gi_188522607_gb_ACD60552.1_	0.118	26	0.133	11	0.279	1	0.163	0.147	N	0.57	SignalP-noTM
gi_188522608_gb_ACD60553.1_	0.163	56	0.127	12	0.236	11	0.157	0.141	N	0.57	SignalP-noTM
gi_188522609_gb_ACD60554.1_	0.104	29	0.104	65	0.118	55	0.094	0.099	N	0.57	SignalP-noTM
gi_188522610_gb_ACD60555.1_	0.194	55	0.149	55	0.175	32	0.129	0.139	N	0.57	SignalP-noTM
gi_528897493_gb_ACD60557.2_	0.122	66	0.115	66	0.198	1	0.104	0.11	N	0.57	SignalP-noTM
gi_188522613_gb_ACD60558.1_	0.128	24	0.166	24	0.278	1	0.233	0.191	N	0.51	SignalP-TM
gi_188522614_gb_ACD60559.1_	0.107	32	0.124	57	0.17	53	0.117	0.121	N	0.57	SignalP-noTM
gi_188522616_gb_ACD60561.1_	0.116	66	0.12	58	0.201	1	0.109	0.115	N	0.57	SignalP-noTM
gi_188522617_gb_ACD60562.1_	0.279	32	0.126	32	0.215	14	0.111	0.12	N	0.51	SignalP-TM
gi_528897494_gb_ACD60565.2_	0.116	66	0.119	58	0.201	1	0.108	0.114	N	0.57	SignalP-noTM
gi_188522621_gb_ACD60566.1_	0.214	32	0.122	49	0.207	47	0.1	0.114	N	0.51	SignalP-TM
gi_528897495_gb_ACD60569.2_	0.116	66	0.12	58	0.201	1	0.109	0.115	N	0.57	SignalP-noTM
gi_188522625_gb_ACD60570.1_	0.128	24	0.156	24	0.253	1	0.209	0.176	N	0.51	SignalP-TM
gi_528897496_gb_ACD60573.2_	0.116	66	0.12	58	0.201	1	0.109	0.115	N	0.57	SignalP-noTM
gi_188522630_gb_ACD60575.1_	0.283	32	0.272	32	0.565	13	0.338	0.303	N	0.57	SignalP-noTM
gi_188522631_gb_ACD60576.1_	0.175	33	0.146	33	0.213	32	0.109	0.129	N	0.57	SignalP-noTM
gi_188522633_gb_ACD60578.1_	0.221	26	0.204	26	0.252	14	0.192	0.198	N	0.57	SignalP-noTM
gi_188522634_gb_ACD60579.1_	0.102	41	0.133	17	0.215	12	0.18	0.155	N	0.57	SignalP-noTM
gi_188522635_gb_ACD60580.1_	0.15	36	0.149	11	0.28	4	0.221	0.183	N	0.57	SignalP-noTM
gi_188522640_gb_ACD60585.1_	0.146	54	0.221	11	0.653	1	0.472	0.339	N	0.57	SignalP-noTM
gi_188522641_gb_ACD60586.1_	0.232	19	0.218	19	0.386	18	0.205	0.212	N	0.57	SignalP-noTM
gi_188522643_gb_ACD60588.1_	0.15	64	0.127	64	0.152	59	0.084	0.111	N	0.51	SignalP-TM
gi_188522649_gb_ACD60594.1_	0.185	20	0.101	20	0.129	62	0.053	0.083	N	0.51	SignalP-TM
gi_188522650_gb_ACD60595.1_	0.106	48	0.137	14	0.269	6	0.186	0.16	N	0.57	SignalP-noTM
gi_188522652_gb_ACD60597.1_	0.126	53	0.197	11	0.608	2	0.396	0.291	N	0.57	SignalP-noTM
gi_188522653_gb_ACD60598.1_	0.137	31	0.105	31	0.109	61	0.07	0.089	N	0.57	SignalP-noTM
gi_188522654_gb_ACD60599.1_	0.105	48	0.104	48	0.139	6	0.103	0.103	N	0.57	SignalP-noTM
gi_188522655_gb_ACD60600.1_	0.129	21	0.167	11	0.385	1	0.278	0.208	N	0.51	SignalP-TM
gi_188522661_gb_ACD60606.1_	0.108	41	0.188	17	0.518	13	0.352	0.265	N	0.57	SignalP-noTM
gi_188522665_gb_ACD60610.1_	0.265	36	0.173	13	0.214	1	0.157	0.166	N	0.57	SignalP-noTM
gi_188522666_gb_ACD60611.1_	0.226	33	0.161	33	0.272	4	0.158	0.16	N	0.57	SignalP-noTM
gi_188522667_gb_ACD60612.1_	0.38	25	0.613	25	0.996	21	0.973	0.782	Y	0.57	SignalP-noTM
gi_188522668_gb_ACD60613.1_	0.154	35	0.124	26	0.17	31	0.116	0.121	N	0.51	SignalP-TM
gi_188522669_gb_ACD60614.1_	0.14	35	0.132	35	0.182	34	0.102	0.118	N	0.57	SignalP-noTM
gi_188522682_gb_ACD60627.1_	0.79	20	0.827	20	0.925	17	0.862	0.843	Y	0.57	SignalP-noTM
gi_188522683_gb_ACD60628.1_	0.257	12	0.382	12	0.766	9	0.574	0.472	N	0.57	SignalP-noTM
gi_188522685_gb_ACD60630.1_	0.107	58	0.097	25	0.102	13	0.082	0.09	N	0.57	SignalP-noTM
gi_188522686_gb_ACD60631.1_	0.581	49	0.264	49	0.497	1	0.181	0.233	N	0.51	SignalP-TM
gi_188522696_gb_ACD60641.1_	0.204	42	0.201	42	0.299	41	0.174	0.188	N	0.57	SignalP-noTM
gi_188522697_gb_ACD60642.1_	0.114	6	0.116	30	0.168	19	0.114	0.115	N	0.57	SignalP-noTM
gi_188522703_gb_ACD60648.1_	0.284	26	0.193	26	0.321	8	0.181	0.189	N	0.51	SignalP-TM
gi_188522704_gb_ACD60649.1_	0.119	60	0.107	60	0.115	40	0.077	0.093	N	0.57	SignalP-noTM
gi_188522715_gb_ACD60660.1_	0.122	28	0.141	12	0.235	4	0.201	0.169	N	0.57	SignalP-noTM
gi_188522716_gb_ACD60661.1_	0.225	26	0.204	26	0.337	11	0.217	0.209	N	0.51	SignalP-TM
gi_188522717_gb_ACD60662.1_	0.174	60	0.138	31	0.23	29	0.125	0.132	N	0.57	SignalP-noTM
gi_188522718_gb_ACD60663.1_	0.136	32	0.141	11	0.285	2	0.198	0.168	N	0.57	SignalP-noTM
gi_188522719_gb_ACD60664.1_	0.159	36	0.158	36	0.255	32	0.122	0.141	N	0.57	SignalP-noTM
gi_188522720_gb_ACD60665.1_	0.143	49	0.146	11	0.286	1	0.206	0.174	N	0.57	SignalP-noTM
gi_188522721_gb_ACD60666.1_	0.239	35	0.321	35	0.786	14	0.545	0.426	N	0.57	SignalP-noTM
gi_188522722_gb_ACD60667.1_	0.13	53	0.102	53	0.146	5	0.081	0.092	N	0.57	SignalP-noTM
gi_188522723_gb_ACD60668.1_	0.11	37	0.109	37	0.113	31	0.094	0.102	N	0.57	SignalP-noTM
gi_188522726_gb_ACD60671.1_	0.146	31	0.165	21	0.359	15	0.249	0.204	N	0.57	SignalP-noTM
gi_188522727_gb_ACD60672.1_	0.156	23	0.137	50	0.244	46	0.118	0.128	N	0.57	SignalP-noTM
gi_188522728_gb_ACD60673.1_	0.158	39	0.221	39	0.46	31	0.276	0.247	N	0.57	SignalP-noTM
gi_188522729_gb_ACD60674.1_	0.101	27	0.117	11	0.211	3	0.129	0.122	N	0.57	SignalP-noTM
gi_188522730_gb_ACD60675.1_	0.112	32	0.102	32	0.112	53	0.076	0.09	N	0.57	SignalP-noTM
gi_188522731_gb_ACD60676.1_	0.301	23	0.249	23	0.447	12	0.216	0.233	N	0.57	SignalP-noTM
gi_188522732_gb_ACD60677.1_	0.22	27	0.194	27	0.403	22	0.14	0.169	N	0.57	SignalP-noTM
gi_188522734_gb_ACD60679.1_	0.137	47	0.158	47	0.339	37	0.167	0.162	N	0.57	SignalP-noTM
gi_188522735_gb_ACD60680.1_	0.102	36	0.106	32	0.156	1	0.109	0.107	N	0.57	SignalP-noTM
gi_188522736_gb_ACD60681.1_	0.332	33	0.192	33	0.185	32	0.095	0.147	N	0.57	SignalP-noTM
gi_188522739_gb_ACD60684.1_	0.131	22	0.161	11	0.428	1	0.234	0.195	N	0.57	SignalP-noTM
gi_188522742_gb_ACD60687.1_	0.521	22	0.693	22	0.971	11	0.933	0.806	Y	0.57	SignalP-noTM
gi_188522743_gb_ACD60688.1_	0.139	27	0.236	27	0.57	23	0.356	0.28	N	0.51	SignalP-TM
gi_188522744_gb_ACD60689.1_	0.16	39	0.139	39	0.178	18	0.138	0.139	N	0.51	SignalP-TM
gi_188522745_gb_ACD60690.1_	0.658	26	0.796	26	0.99	14	0.96	0.873	Y	0.57	SignalP-noTM
gi_188522747_gb_ACD60692.1_	0.114	40	0.136	11	0.237	7	0.199	0.166	N	0.57	SignalP-noTM
gi_188522748_gb_ACD60693.1_	0.585	20	0.747	20	0.967	10	0.951	0.843	Y	0.57	SignalP-noTM
gi_188522753_gb_ACD60698.1_	0.887	26	0.867	26	0.952	25	0.796	0.834	Y	0.57	SignalP-noTM
gi_188522754_gb_ACD60699.1_	0.152	37	0.107	37	0.139	21	0.077	0.096	N	0.51	SignalP-TM
gi_188522755_gb_ACD60700.1_	0.137	21	0.199	21	0.484	1	0.32	0.256	N	0.57	SignalP-noTM
gi_188522756_gb_ACD60701.1_	0.158	36	0.142	36	0.224	6	0.146	0.144	N	0.57	SignalP-noTM
gi_188522758_gb_ACD60703.1_	0.769	28	0.854	28	0.98	20	0.946	0.898	Y	0.57	SignalP-noTM
gi_188522759_gb_ACD60704.1_	0.139	17	0.184	11	0.513	1	0.318	0.247	N	0.57	SignalP-noTM

0.952844	0.998579	0.917284	0.956236	gi_188522587_gb_ACD60532.1_
0.171505	0.454377	0.1603	0.262061	gi_188522589_gb_ACD60534.1_
0.187856	0.042533	0.260379	0.163589	gi_188522590_gb_ACD60535.1_
0.43807	0.97114	0.660607	0.689939	gi_188522594_gb_ACD60539.1_
0.119098	0.060711	0.135053	0.104954	gi_188522607_gb_ACD60552.1_
0.090298	0.040855	0.122282	0.084478	gi_188522608_gb_ACD60553.1_
0.096914	0.118157	0.090545	0.101872	gi_188522609_gb_ACD60554.1_
0.12196	0.085489	0.134354	0.113934	gi_188522610_gb_ACD60555.1_
0.798991	0.38367	0.741351	0.641337	gi_188522613_gb_ACD60558.1_
0.29713	0.950499	0.427025	0.558218	gi_188522614_gb_ACD60559.1_
0.675902	0.044916	0.635295	0.452038	gi_188522616_gb_ACD60561.1_
0.375194	0.13717	0.408058	0.306807	gi_188522617_gb_ACD60562.1_
0.40444	0.416781	0.38438	0.401867	gi_188522621_gb_ACD60566.1_
0.3028	0.09104	0.31432	0.236053	gi_188522625_gb_ACD60570.1_
0.291523	0.081361	0.245641	0.206175	gi_188522630_gb_ACD60575.1_
0.204403	0.331369	0.087864	0.207879	gi_188522631_gb_ACD60576.1_
0.111452	0.033764	0.173217	0.106144	gi_188522633_gb_ACD60578.1_
0.238486	0.969763	0.11385	0.4407	gi_188522634_gb_ACD60579.1_
0.63599	0.982155	0.825058	0.814401	gi_188522635_gb_ACD60580.1_
0.93946	0.999916	0.820686	0.920021	gi_188522640_gb_ACD60585.1_
0.174942	0.125209	0.179756	0.159969	gi_188522641_gb_ACD60586.1_
0.114153	0.035985	0.152	0.100713	gi_188522643_gb_ACD60588.1_
0.139674	0.047156	0.181532	0.122787	gi_188522649_gb_ACD60594.1_
0.104518	0.092541	0.136108	0.111056	gi_188522650_gb_ACD60595.1_
0.141122	0.228818	0.113247	0.161062	gi_188522652_gb_ACD60597.1_
0.092289	0.075299	0.090052	0.08588	gi_188522653_gb_ACD60598.1_
0.102569	0.042901	0.114457	0.086642	gi_188522654_gb_ACD60599.1_
0.163967	0.092541	0.154727	0.137078	gi_188522655_gb_ACD60600.1_
0.927372	0.922371	0.933764	0.927836	gi_188522661_gb_ACD60606.1_
0.775912	0.619164	0.707857	0.700978	gi_188522665_gb_ACD60610.1_
0.079585	0.033472	0.122282	0.078446	gi_188522666_gb_ACD60611.1_
0.563407	0.130562	0.665967	0.453312	gi_188522667_gb_ACD60612.1_
0.088346	0.14517	0.189694	0.14107	gi_188522668_gb_ACD60613.1_
0.168121	0.320821	0.081361	0.190101	gi_188522669_gb_ACD60614.1_
0.474522	0.059693	0.482757	0.338991	gi_188522682_gb_ACD60627.1_
0.654527	0.07871	0.634599	0.455945	gi_528897493_gb_ACD60557.2_
0.792161	0.113548	0.759328	0.555012	gi_528897494_gb_ACD60565.2_
0.777473	0.145542	0.748193	0.557069	gi_528897495_gb_ACD60569.2_
0.834795	0.096129	0.784147	0.57169	gi_528897496_gb_ACD60573.2_
0.94715	0.999662	0.900966	0.949259	gi_188522683_gb_ACD60628.1_
0.915444	0.999592	0.820686	0.911907	gi_188522685_gb_ACD60630.1_
0.886452	0.975205	0.887355	0.916337	gi_188522686_gb_ACD60631.1_
0.220458	0.313674	0.272099	0.268744	gi_188522696_gb_ACD60641.1_
0.366096	0.960418	0.50225	0.609588	gi_188522697_gb_ACD60642.1_
0.487253	0.831459	0.559714	0.626142	gi_188522703_gb_ACD60648.1_
0.120681	0.115986	0.091289	0.109319	gi_188522704_gb_ACD60649.1_
0.123901	0.657236	0.083862	0.288333	gi_188522715_gb_ACD60660.1_
0.09984	0.34074	0.105364	0.181981	gi_188522716_gb_ACD60661.1_
0.136108	0.038457	0.180643	0.118403	gi_188522717_gb_ACD60662.1_
0.091289	0.054218	0.113548	0.086352	gi_188522718_gb_ACD60663.1_
0.151228	0.063328	0.24122	0.151925	gi_188522719_gb_ACD60664.1_
0.091289	0.035366	0.08181	0.069488	gi_188522720_gb_ACD60665.1_
0.087384	0.036721	0.125209	0.083105	gi_188522721_gb_ACD60666.1_
0.686326	0.988948	0.72492	0.800065	gi_188522722_gb_ACD60667.1_
0.690829	0.979807	0.826353	0.83233	gi_188522723_gb_ACD60668.1_
0.339393	0.954826	0.207839	0.500686	gi_188522726_gb_ACD60671.1_
0.299643	0.982207	0.148932	0.476927	gi_188522727_gb_ACD60672.1_
0.161921	0.04229	0.14517	0.11646	gi_188522728_gb_ACD60673.1_
0.449918	0.855202	0.535938	0.613686	gi_188522729_gb_ACD60674.1_
0.054837	0.043647	0.07806	0.058848	gi_188522730_gb_ACD60675.1_
0.341414	0.097176	0.425557	0.288049	gi_188522731_gb_ACD60676.1_
0.135053	0.179314	0.107647	0.140671	gi_188522732_gb_ACD60677.1_
0.152775	0.042533	0.21232	0.135876	gi_188522734_gb_ACD60679.1_
0.185579	0.023454	0.430699	0.213244	gi_188522735_gb_ACD60680.1_
0.121639	0.68568	0.094833	0.300717	gi_188522736_gb_ACD60681.1_
0.490251	0.732041	0.581029	0.601107	gi_188522739_gb_ACD60684.1_
0.458099	0.846056	0.53743	0.613862	gi_188522742_gb_ACD60687.1_
0.162329	0.053606	0.141851	0.119262	gi_188522743_gb_ACD60688.1_
0.084556	0.50375	0.176245	0.25485	gi_188522744_gb_ACD60689.1_
0.673267	0.356405	0.665299	0.56499	gi_188522745_gb_ACD60690.1_
0.276878	0.179314	0.446209	0.3008	gi_188522747_gb_ACD60692.1_
0.336708	0.964119	0.444727	0.581851	gi_188522748_gb_ACD60693.1_
0.763687	0.516494	0.804239	0.694807	gi_188522753_gb_ACD60698.1_
0.059861	0.562669	0.125538	0.249356	gi_188522754_gb_ACD60699.1_
0.586133	0.317562	0.651809	0.518501	gi_188522755_gb_ACD60700.1_
0.107072	0.053151	0.127862	0.096028	gi_188522756_gb_ACD60701.1_
0.863185	0.976546	0.831879	0.890537	gi_188522758_gb_ACD60703.1_
0.187399	0.046753	0.24232	0.158824	gi_188522759_gb_ACD60704.1_

gi_188522763_gb_ACD60708.1_	0.102	36	0.115	36	0.184	1	0.113	0.114	N	0.57	SignalP-noTM
gi_188522764_gb_ACD60709.1_	0.157	27	0.144	27	0.254	2	0.154	0.149	N	0.57	SignalP-noTM
gi_188522765_gb_ACD60710.1_	0.112	29	0.186	11	0.406	8	0.363	0.269	N	0.57	SignalP-noTM
gi_188522767_gb_ACD60712.1_	0.132	58	0.121	32	0.183	6	0.135	0.128	N	0.57	SignalP-noTM
gi_188522770_gb_ACD60715.1_	0.28	31	0.263	31	0.447	10	0.292	0.277	N	0.57	SignalP-noTM
gi_188522771_gb_ACD60716.1_	0.117	52	0.103	52	0.112	5	0.094	0.099	N	0.57	SignalP-noTM
gi_188522772_gb_ACD60717.1_	0.132	32	0.245	15	0.708	12	0.578	0.402	N	0.57	SignalP-noTM
gi_188522773_gb_ACD60718.1_	0.809	26	0.812	26	0.918	19	0.834	0.823	Y	0.57	SignalP-noTM
gi_188522780_gb_ACD60725.1_	0.144	58	0.135	43	0.289	41	0.138	0.137	N	0.57	SignalP-noTM
gi_188522781_gb_ACD60726.1_	0.116	58	0.122	11	0.212	3	0.15	0.133	N	0.51	SignalP-TM
gi_188522782_gb_ACD60727.1_	0.425	28	0.342	22	0.556	13	0.369	0.352	N	0.51	SignalP-TM
gi_188522783_gb_ACD60728.1_	0.143	31	0.174	17	0.367	5	0.26	0.214	N	0.57	SignalP-noTM
gi_188522788_gb_ACD60733.1_	0.103	34	0.099	40	0.123	3	0.094	0.097	N	0.57	SignalP-noTM
gi_188522917_gb_ACD60862.1_	0.121	36	0.128	20	0.204	19	0.138	0.133	N	0.57	SignalP-noTM
gi_188522918_gb_ACD60863.1_	0.428	17	0.633	17	0.974	12	0.928	0.772	Y	0.57	SignalP-noTM
gi_188522921_gb_ACD60866.1_	0.133	51	0.145	23	0.262	4	0.2	0.171	N	0.57	SignalP-noTM
gi_188522929_gb_ACD60874.1_	0.237	23	0.237	23	0.352	22	0.263	0.249	N	0.57	SignalP-noTM
gi_188522930_gb_ACD60875.1_	0.112	19	0.154	19	0.284	1	0.204	0.178	N	0.57	SignalP-noTM
gi_188522935_gb_ACD60880.1_	0.103	52	0.108	59	0.128	30	0.1	0.104	N	0.57	SignalP-noTM
gi_188522936_gb_ACD60881.1_	0.13	30	0.128	11	0.276	1	0.144	0.135	N	0.57	SignalP-noTM
gi_188522942_gb_ACD60887.1_	0.257	23	0.17	23	0.178	20	0.121	0.147	N	0.57	SignalP-noTM
gi_188522943_gb_ACD60888.1_	0.123	63	0.137	11	0.271	5	0.188	0.161	N	0.57	SignalP-noTM
gi_188522944_gb_ACD60889.1_	0.107	22	0.224	14	0.598	10	0.5	0.354	N	0.57	SignalP-noTM
gi_188522945_gb_ACD60890.1_	0.181	27	0.147	27	0.161	25	0.117	0.133	N	0.57	SignalP-noTM
gi_188522946_gb_ACD60891.1_	0.131	66	0.113	66	0.15	1	0.099	0.106	N	0.57	SignalP-noTM
gi_188522947_gb_ACD60892.1_	0.125	17	0.159	17	0.306	2	0.222	0.182	N	0.51	SignalP-TM
gi_188522952_gb_ACD60897.1_	0.336	23	0.436	23	0.813	12	0.645	0.534	N	0.57	SignalP-noTM
gi_188522954_gb_ACD60899.1_	0.164	42	0.144	42	0.211	19	0.141	0.143	N	0.57	SignalP-noTM
gi_188522957_gb_ACD60902.1_	0.168	43	0.214	43	0.357	35	0.196	0.206	N	0.57	SignalP-noTM
gi_188522958_gb_ACD60903.1_	0.137	44	0.12	44	0.128	16	0.101	0.111	N	0.57	SignalP-noTM
gi_188522959_gb_ACD60904.1_	0.161	26	0.133	26	0.125	15	0.097	0.116	N	0.57	SignalP-noTM
gi_188522961_gb_ACD60906.1_	0.18	21	0.219	21	0.442	1	0.295	0.255	N	0.57	SignalP-noTM
gi_188522967_gb_ACD60912.1_	0.11	27	0.111	37	0.148	5	0.105	0.109	N	0.51	SignalP-TM
gi_188522968_gb_ACD60913.1_	0.195	26	0.174	26	0.333	43	0.163	0.169	N	0.57	SignalP-noTM
gi_188522977_gb_ACD60922.1_	0.173	51	0.171	51	0.262	42	0.135	0.154	N	0.57	SignalP-noTM
gi_188522978_gb_ACD60923.1_	0.165	53	0.129	11	0.217	1	0.163	0.145	N	0.57	SignalP-noTM
gi_188522993_gb_ACD60938.1_	0.11	44	0.16	32	0.369	24	0.224	0.19	N	0.57	SignalP-noTM
gi_188522994_gb_ACD60939.1_	0.106	9	0.103	45	0.117	30	0.097	0.1	N	0.57	SignalP-noTM
gi_188522996_gb_ACD60941.1_	0.397	40	0.37	40	0.555	27	0.312	0.343	N	0.57	SignalP-noTM
gi_188522998_gb_ACD60943.1_	0.101	26	0.142	12	0.274	1	0.196	0.167	N	0.57	SignalP-noTM
gi_188523004_gb_ACD60949.1_	0.139	15	0.14	42	0.188	34	0.118	0.13	N	0.57	SignalP-noTM
gi_188523018_gb_ACD60963.1_	0.114	15	0.176	15	0.377	8	0.273	0.222	N	0.57	SignalP-noTM
gi_188523020_gb_ACD60965.1_	0.119	60	0.109	60	0.114	47	0.089	0.099	N	0.57	SignalP-noTM
gi_188523021_gb_ACD60966.1_	0.112	31	0.124	12	0.208	3	0.157	0.139	N	0.57	SignalP-noTM
gi_188523022_gb_ACD60967.1_	0.117	8	0.114	53	0.164	50	0.104	0.109	N	0.57	SignalP-noTM
gi_188523023_gb_ACD60968.1_	0.118	24	0.125	24	0.155	22	0.123	0.124	N	0.57	SignalP-noTM
gi_188523024_gb_ACD60969.1_	0.135	33	0.127	33	0.14	31	0.084	0.107	N	0.57	SignalP-noTM
gi_188523025_gb_ACD60970.1_	0.12	59	0.118	11	0.206	1	0.136	0.127	N	0.57	SignalP-noTM
gi_188523026_gb_ACD60971.1_	0.105	16	0.124	16	0.172	7	0.136	0.129	N	0.57	SignalP-noTM
gi_188523030_gb_ACD60975.1_	0.133	56	0.14	56	0.197	52	0.106	0.124	N	0.57	SignalP-noTM
gi_188523031_gb_ACD60976.1_	0.203	11	0.197	11	0.415	10	0.204	0.2	N	0.57	SignalP-noTM
gi_188523032_gb_ACD60977.1_	0.109	21	0.107	11	0.165	3	0.112	0.109	N	0.51	SignalP-TM
gi_188523033_gb_ACD60978.1_	0.103	24	0.107	58	0.132	50	0.097	0.103	N	0.57	SignalP-noTM
gi_188523045_gb_ACD60990.1_	0.153	49	0.126	49	0.132	31	0.094	0.111	N	0.57	SignalP-noTM
gi_188523049_gb_ACD60994.1_	0.18	34	0.298	34	0.718	18	0.491	0.389	N	0.57	SignalP-noTM
gi_188523052_gb_ACD60997.1_	0.13	62	0.115	62	0.11	47	0.086	0.102	N	0.57	SignalP-noTM
gi_188523056_gb_ACD61001.1_	0.166	18	0.184	18	0.328	9	0.22	0.197	N	0.51	SignalP-TM
gi_188523060_gb_ACD61005.1_	0.322	37	0.215	37	0.252	6	0.158	0.188	N	0.57	SignalP-noTM
gi_188523061_gb_ACD61006.1_	0.278	23	0.386	23	0.727	18	0.458	0.413	N	0.51	SignalP-TM
gi_188523062_gb_ACD61007.1_	0.131	49	0.132	12	0.202	1	0.174	0.152	N	0.57	SignalP-noTM
gi_188523063_gb_ACD61008.1_	0.125	20	0.112	38	0.165	32	0.112	0.112	N	0.57	SignalP-noTM
gi_188523064_gb_ACD61009.1_	0.115	19	0.152	19	0.356	18	0.207	0.178	N	0.57	SignalP-noTM
gi_188523065_gb_ACD61010.1_	0.103	18	0.111	11	0.152	1	0.123	0.116	N	0.57	SignalP-noTM
gi_188523066_gb_ACD61011.1_	0.112	27	0.131	11	0.224	5	0.183	0.15	N	0.51	SignalP-TM
gi_188523067_gb_ACD61012.1_	0.161	35	0.141	35	0.333	34	0.108	0.126	N	0.57	SignalP-noTM
gi_188523068_gb_ACD61013.1_	0.133	22	0.159	22	0.295	11	0.196	0.176	N	0.57	SignalP-noTM
gi_188523070_gb_ACD61015.1_	0.133	22	0.157	22	0.289	11	0.192	0.173	N	0.57	SignalP-noTM
gi_188523071_gb_ACD61016.1_	0.133	31	0.184	31	0.361	29	0.186	0.185	N	0.57	SignalP-noTM
gi_188523073_gb_ACD61018.1_	0.124	20	0.163	20	0.41	1	0.223	0.191	N	0.57	SignalP-noTM
gi_188523081_gb_ACD61026.1_	0.712	21	0.775	21	0.948	16	0.869	0.819	Y	0.57	SignalP-noTM
gi_188523082_gb_ACD61027.1_	0.165	19	0.12	19	0.159	35	0.081	0.102	N	0.57	SignalP-noTM
gi_188523083_gb_ACD61028.1_	0.134	21	0.135	11	0.313	1	0.173	0.153	N	0.57	SignalP-noTM
gi_188523085_gb_ACD61030.1_	0.125	35	0.144	35	0.408	34	0.157	0.15	N	0.57	SignalP-noTM
gi_188523086_gb_ACD61031.1_	0.115	27	0.104	27	0.102	21	0.08	0.093	N	0.57	SignalP-noTM
gi_188523087_gb_ACD61032.1_	0.11	41	0.107	41	0.134	39	0.078	0.094	N	0.57	SignalP-noTM
gi_188523088_gb_ACD61033.1_	0.153	29	0.153	29	0.348	28	0.142	0.149	N	0.51	SignalP-TM
gi_188523089_gb_ACD61034.1_	0.193	23	0.411	23	0.929	2	0.888	0.636	Y	0.57	SignalP-noTM
gi_188523091_gb_ACD61036.1_	0.129	37	0.11	37	0.11	26	0.077	0.095	N	0.57	SignalP-noTM

0.130562	0.14517	0.112946	0.129559	gi_188522763_gb_ACD60708.1_
0.19201	0.091289	0.227761	0.170353	gi_188522764_gb_ACD60709.1_
0.580299	0.450661	0.673927	0.568296	gi_188522765_gb_ACD60710.1_
0.234154	0.021924	0.282925	0.179668	gi_188522767_gb_ACD60712.1_
0.245641	0.461824	0.372385	0.35995	gi_188522770_gb_ACD60715.1_
0.104799	0.03299	0.111749	0.083179	gi_188522771_gb_ACD60716.1_
0.166034	0.271505	0.099302	0.178947	gi_188522772_gb_ACD60717.1_
0.826783	0.889731	0.774867	0.83046	gi_188522773_gb_ACD60718.1_
0.090545	0.044532	0.147418	0.094165	gi_188522780_gb_ACD60725.1_
0.166034	0.420432	0.083862	0.223443	gi_188522781_gb_ACD60726.1_
0.234154	0.858514	0.17581	0.422826	gi_188522782_gb_ACD60727.1_
0.918415	0.999993	0.78968	0.902696	gi_188522783_gb_ACD60728.1_
0.090298	0.000831	0.213325	0.101485	gi_188522788_gb_ACD60733.1_
0.270912	0.655205	0.316263	0.414127	gi_188522917_gb_ACD60862.1_
0.946698	0.999851	0.904391	0.950313	gi_188522918_gb_ACD60863.1_
0.235232	0.118784	0.155119	0.169712	gi_188522921_gb_ACD60866.1_
0.676558	0.390074	0.630416	0.565683	gi_188522929_gb_ACD60874.1_
0.467048	0.706615	0.651809	0.608491	gi_188522930_gb_ACD60875.1_
0.091538	0.09104	0.107072	0.09655	gi_188522935_gb_ACD60880.1_
0.077629	0.043273	0.112047	0.07765	gi_188522936_gb_ACD60881.1_
0.182426	0.026211	0.236313	0.148317	gi_188522942_gb_ACD60887.1_
0.12196	0.023939	0.162329	0.102743	gi_188522943_gb_ACD60888.1_
0.182426	0.210818	0.092793	0.162012	gi_188522944_gb_ACD60889.1_
0.157892	0.261536	0.151614	0.190347	gi_188522945_gb_ACD60890.1_
0.105364	0.037363	0.130903	0.09121	gi_188522946_gb_ACD60891.1_
0.233617	0.041447	0.161109	0.145391	gi_188522947_gb_ACD60892.1_
0.134703	0.125868	0.184222	0.148264	gi_188522952_gb_ACD60897.1_
0.318863	0.840506	0.396517	0.518629	gi_188522954_gb_ACD60899.1_
0.196234	0.002941	0.281709	0.160295	gi_188522957_gb_ACD60902.1_
0.074675	0.069461	0.074468	0.072868	gi_188522958_gb_ACD60903.1_
0.687617	0.357094	0.791666	0.612126	gi_188522959_gb_ACD60904.1_
0.154335	0.119413	0.099571	0.12444	gi_188522961_gb_ACD60906.1_
0.14629	0.043647	0.161109	0.117015	gi_188522967_gb_ACD60912.1_
0.201491	0.49475	0.165205	0.287149	gi_188522968_gb_ACD60913.1_
0.049642	0.062797	0.06054	0.05766	gi_188522977_gb_ACD60922.1_
0.082036	0.029114	0.132619	0.081256	gi_188522978_gb_ACD60923.1_
0.725518	0.045957	0.840104	0.537193	gi_188522993_gb_ACD60938.1_
0.751009	0.978647	0.734388	0.821348	gi_188522994_gb_ACD60939.1_
0.242872	0.273289	0.269138	0.261766	gi_188522996_gb_ACD60941.1_
0.92129	0.999814	0.793639	0.904914	gi_188522998_gb_ACD60943.1_
0.157493	0.041091	0.167284	0.121956	gi_188523004_gb_ACD60949.1_
0.085021	0.03214	0.134005	0.083722	gi_188523018_gb_ACD60963.1_
0.146665	0.085724	0.118784	0.117058	gi_188523020_gb_ACD60965.1_
0.085959	0.397953	0.079585	0.187832	gi_188523021_gb_ACD60966.1_
0.421895	0.520988	0.523233	0.488705	gi_188523022_gb_ACD60967.1_
0.110269	0.010857	0.117845	0.079657	gi_188523023_gb_ACD60968.1_
0.118157	0.330705	0.082036	0.176966	gi_188523024_gb_ACD60969.1_
0.194348	0.649764	0.110269	0.318127	gi_188523025_gb_ACD60970.1_
0.09639	0.016048	0.124553	0.078997	gi_188523026_gb_ACD60971.1_
0.110563	0.052401	0.160704	0.107889	gi_188523030_gb_ACD60975.1_
0.304068	0.861045	0.353658	0.506257	gi_188523031_gb_ACD60976.1_
0.157493	0.07871	0.258649	0.164951	gi_188523032_gb_ACD60977.1_
0.181532	0.049079	0.159092	0.129901	gi_188523033_gb_ACD60978.1_
0.936672	0.99899	0.86669	0.934117	gi_188523045_gb_ACD60990.1_
0.58904	0.975849	0.775912	0.780267	gi_188523049_gb_ACD60994.1_
0.458843	0.471531	0.677215	0.535863	gi_188523052_gb_ACD60997.1_
0.204403	0.677215	0.15046	0.344026	gi_188523056_gb_ACD61001.1_
0.168541	0.037797	0.217891	0.14141	gi_188523060_gb_ACD61005.1_
0.34074	0.026988	0.350919	0.239549	gi_188523061_gb_ACD61006.1_
0.069074	0.030502	0.090052	0.063209	gi_188523062_gb_ACD61007.1_
0.0985	0.039582	0.112346	0.083476	gi_188523063_gb_ACD61008.1_
0.299013	0.988026	0.148173	0.478404	gi_188523064_gb_ACD61009.1_
0.3327	0.051661	0.316912	0.233758	gi_188523065_gb_ACD61010.1_
0.235232	0.040621	0.348872	0.208242	gi_188523066_gb_ACD61011.1_
0.203915	0.954696	0.088105	0.415572	gi_188523067_gb_ACD61012.1_
0.727307	0.849923	0.816678	0.797969	gi_188523068_gb_ACD61013.1_
0.779026	0.780572	0.840506	0.800035	gi_188523070_gb_ACD61015.1_
0.958553	0.999723	0.88615	0.948142	gi_188523071_gb_ACD61016.1_
0.830616	0.90016	0.869438	0.866738	gi_188523073_gb_ACD61018.1_
0.943267	0.999758	0.885238	0.942754	gi_188523081_gb_ACD61026.1_
0.115067	0.010922	0.117222	0.08107	gi_188523082_gb_ACD61027.1_
0.969763	0.997746	0.935051	0.96752	gi_188523083_gb_ACD61028.1_
0.097176	0.069655	0.129882	0.098904	gi_188523085_gb_ACD61030.1_
0.052104	0.000948	0.088346	0.047133	gi_188523086_gb_ACD61031.1_
0.076988	0.016675	0.095349	0.063004	gi_188523087_gb_ACD61032.1_
0.398672	0.79413	0.5015	0.564767	gi_188523088_gb_ACD61033.1_
0.911654	0.489502	0.868413	0.756523	gi_188523089_gb_ACD61034.1_
0.743645	0.572975	0.623399	0.646673	gi_188523091_gb_ACD61036.1_

gi_188523092_gb_ACD61037.1_	0.11	47	0.209	17	0.506	7	0.425	0.311	N	0.57	SignalP-noTM
gi_188523095_gb_ACD61040.1_	0.148	33	0.118	33	0.116	21	0.092	0.106	N	0.57	SignalP-noTM
gi_188523096_gb_ACD61041.1_	0.311	47	0.242	47	0.281	42	0.131	0.19	N	0.57	SignalP-noTM
gi_188523101_gb_ACD61046.1_	0.103	25	0.124	18	0.191	7	0.147	0.135	N	0.57	SignalP-noTM
gi_188523102_gb_ACD61047.1_	0.227	41	0.235	18	0.387	11	0.295	0.263	N	0.57	SignalP-noTM
gi_188523103_gb_ACD61048.1_	0.116	27	0.118	27	0.169	22	0.126	0.121	N	0.51	SignalP-TM
gi_188523104_gb_ACD61049.1_	0.116	21	0.129	41	0.216	36	0.115	0.123	N	0.57	SignalP-noTM
gi_188523114_gb_ACD61059.1_	0.123	34	0.169	18	0.366	14	0.253	0.208	N	0.57	SignalP-noTM
gi_188523119_gb_ACD61064.1_	0.11	19	0.179	11	0.502	2	0.3	0.236	N	0.57	SignalP-noTM
gi_188523123_gb_ACD61068.1_	0.116	29	0.111	16	0.139	8	0.113	0.112	N	0.57	SignalP-noTM
gi_188523126_gb_ACD61071.1_	0.176	46	0.207	18	0.467	13	0.272	0.238	N	0.57	SignalP-noTM
gi_188523128_gb_ACD61073.1_	0.107	15	0.108	11	0.146	1	0.116	0.112	N	0.57	SignalP-noTM
gi_188523129_gb_ACD61074.1_	0.275	27	0.244	27	0.35	26	0.204	0.225	N	0.57	SignalP-noTM
gi_188523131_gb_ACD61076.1_	0.162	39	0.177	56	0.369	53	0.13	0.155	N	0.57	SignalP-noTM
gi_188523132_gb_ACD61077.1_	0.11	56	0.136	11	0.305	2	0.174	0.154	N	0.57	SignalP-noTM
gi_188523135_gb_ACD61080.1_	0.122	29	0.129	11	0.21	3	0.173	0.15	N	0.57	SignalP-noTM
gi_188523136_gb_ACD61081.1_	0.132	46	0.104	33	0.108	12	0.087	0.096	N	0.57	SignalP-noTM
gi_188523140_gb_ACD61085.1_	0.66	25	0.732	25	0.934	9	0.861	0.78	Y	0.51	SignalP-TM
gi_188523141_gb_ACD61086.1_	0.211	44	0.188	44	0.248	31	0.146	0.172	N	0.51	SignalP-TM
gi_188523142_gb_ACD61087.1_	0.66	23	0.764	23	0.947	2	0.905	0.83	Y	0.57	SignalP-noTM
gi_188523143_gb_ACD61088.1_	0.198	26	0.153	26	0.17	14	0.122	0.138	N	0.57	SignalP-noTM
gi_188523144_gb_ACD61089.1_	0.111	5	0.139	28	0.3	25	0.172	0.154	N	0.57	SignalP-noTM
gi_188523150_gb_ACD61095.1_	0.154	16	0.219	16	0.398	15	0.308	0.252	N	0.51	SignalP-TM
gi_188523151_gb_ACD61096.1_	0.137	61	0.119	15	0.18	6	0.139	0.128	N	0.57	SignalP-noTM
gi_188523155_gb_ACD61100.1_	0.155	42	0.145	42	0.21	19	0.138	0.141	N	0.57	SignalP-noTM
gi_188523157_gb_ACD61102.1_	0.164	25	0.143	11	0.323	2	0.194	0.167	N	0.57	SignalP-noTM
gi_188523159_gb_ACD61104.1_	0.208	31	0.286	31	0.62	16	0.395	0.326	N	0.51	SignalP-TM
gi_188523171_gb_ACD61116.1_	0.832	24	0.782	24	0.901	12	0.805	0.793	Y	0.57	SignalP-noTM
gi_188523178_gb_ACD61123.1_	0.872	24	0.895	24	0.978	10	0.938	0.915	Y	0.57	SignalP-noTM
gi_188523184_gb_ACD61129.1_	0.11	20	0.119	20	0.177	1	0.124	0.122	N	0.57	SignalP-noTM
gi_188523185_gb_ACD61130.1_	0.116	19	0.141	19	0.257	1	0.171	0.155	N	0.57	SignalP-noTM
gi_188523186_gb_ACD61131.1_	0.23	44	0.211	44	0.3	33	0.165	0.189	N	0.57	SignalP-noTM
gi_188523187_gb_ACD61132.1_	0.152	34	0.171	34	0.507	31	0.167	0.169	N	0.57	SignalP-noTM
gi_188523188_gb_ACD61133.1_	0.175	19	0.152	19	0.287	27	0.136	0.144	N	0.57	SignalP-noTM
gi_188523192_gb_ACD61137.1_	0.116	30	0.116	30	0.137	21	0.096	0.107	N	0.57	SignalP-noTM
gi_188523198_gb_ACD61143.1_	0.339	25	0.444	25	0.883	17	0.691	0.56	N	0.57	SignalP-noTM
gi_188523201_gb_ACD61146.1_	0.103	69	0.115	11	0.194	4	0.137	0.125	N	0.57	SignalP-noTM
gi_188523203_gb_ACD61148.1_	0.105	13	0.102	11	0.178	2	0.102	0.102	N	0.57	SignalP-noTM
gi_188523204_gb_ACD61149.1_	0.194	25	0.285	12	0.824	7	0.768	0.512	N	0.57	SignalP-noTM
gi_188523205_gb_ACD61150.1_	0.12	28	0.099	28	0.146	1	0.08	0.092	N	0.51	SignalP-TM
gi_188523206_gb_ACD61151.1_	0.163	32	0.127	32	0.21	47	0.097	0.116	N	0.51	SignalP-TM
gi_188523207_gb_ACD61152.1_	0.119	46	0.193	21	0.457	15	0.336	0.26	N	0.57	SignalP-noTM
gi_188523208_gb_ACD61153.1_	0.252	33	0.145	33	0.135	2	0.081	0.115	N	0.57	SignalP-noTM
gi_188523209_gb_ACD61154.1_	0.133	24	0.103	35	0.114	31	0.085	0.096	N	0.51	SignalP-TM
gi_188523212_gb_ACD61157.1_	0.332	54	0.534	54	0.962	50	0.425	0.483	N	0.57	SignalP-noTM
gi_188523213_gb_ACD61158.1_	0.207	12	0.155	12	0.188	10	0.117	0.137	N	0.57	SignalP-noTM
gi_188523215_gb_ACD61160.1_	0.118	21	0.112	50	0.137	46	0.09	0.102	N	0.57	SignalP-noTM
gi_188523222_gb_ACD61167.1_	0.634	43	0.74	43	0.983	26	0.681	0.712	Y	0.57	SignalP-noTM
gi_188523223_gb_ACD61168.1_	0.102	20	0.109	11	0.179	1	0.112	0.111	N	0.57	SignalP-noTM
gi_188523228_gb_ACD61173.1_	0.192	22	0.209	22	0.328	10	0.218	0.213	N	0.57	SignalP-noTM
gi_188523230_gb_ACD61175.1_	0.128	33	0.116	33	0.142	32	0.088	0.103	N	0.57	SignalP-noTM
gi_188523232_gb_ACD61177.1_	0.192	29	0.136	29	0.158	23	0.094	0.116	N	0.57	SignalP-noTM
gi_188523233_gb_ACD61178.1_	0.281	22	0.502	22	0.933	3	0.897	0.688	Y	0.57	SignalP-noTM
gi_188523235_gb_ACD61180.1_	0.152	32	0.147	48	0.207	44	0.116	0.132	N	0.57	SignalP-noTM
gi_188523242_gb_ACD61187.1_	0.478	24	0.636	24	0.915	19	0.845	0.734	Y	0.57	SignalP-noTM
gi_188523244_gb_ACD61189.1_	0.115	22	0.146	13	0.28	9	0.215	0.178	N	0.57	SignalP-noTM
gi_188523249_gb_ACD61194.1_	0.121	32	0.117	32	0.137	23	0.096	0.107	N	0.57	SignalP-noTM
gi_188523252_gb_ACD61197.1_	0.101	63	0.112	30	0.142	20	0.103	0.108	N	0.57	SignalP-noTM
gi_188523253_gb_ACD61198.1_	0.18	56	0.12	12	0.202	1	0.141	0.128	N	0.51	SignalP-TM
gi_188523256_gb_ACD61201.1_	0.115	22	0.147	13	0.284	9	0.218	0.181	N	0.57	SignalP-noTM
gi_188523257_gb_ACD61202.1_	0.149	40	0.146	40	0.248	39	0.123	0.135	N	0.57	SignalP-noTM
gi_188523258_gb_ACD61203.1_	0.155	42	0.145	42	0.21	19	0.138	0.141	N	0.57	SignalP-noTM
gi_188523259_gb_ACD61204.1_	0.167	17	0.142	17	0.177	1	0.126	0.135	N	0.57	SignalP-noTM
gi_188523261_gb_ACD61206.1_	0.627	16	0.596	16	0.733	1	0.587	0.592	Y	0.57	SignalP-noTM
gi_188523262_gb_ACD61207.1_	0.127	28	0.176	28	0.447	1	0.254	0.212	N	0.57	SignalP-noTM
gi_188523263_gb_ACD61208.1_	0.165	42	0.13	14	0.265	12	0.17	0.148	N	0.57	SignalP-noTM
gi_188523264_gb_ACD61209.1_	0.107	58	0.144	55	0.363	48	0.119	0.133	N	0.57	SignalP-noTM
gi_188523265_gb_ACD61210.1_	0.126	61	0.123	11	0.184	6	0.156	0.138	N	0.57	SignalP-noTM
gi_188523266_gb_ACD61211.1_	0.14	46	0.141	12	0.235	4	0.203	0.17	N	0.57	SignalP-noTM
gi_188523270_gb_ACD61215.1_	0.226	26	0.177	26	0.203	20	0.143	0.161	N	0.57	SignalP-noTM
gi_188523272_gb_ACD61217.1_	0.25	35	0.176	35	0.241	2	0.15	0.164	N	0.57	SignalP-noTM
gi_188523273_gb_ACD61218.1_	0.16	26	0.147	11	0.337	1	0.203	0.174	N	0.57	SignalP-noTM
gi_188523274_gb_ACD61219.1_	0.109	70	0.107	70	0.118	43	0.095	0.101	N	0.57	SignalP-noTM
gi_188523276_gb_ACD61221.1_	0.121	18	0.152	18	0.311	1	0.205	0.172	N	0.51	SignalP-TM
gi_188523277_gb_ACD61222.1_	0.156	42	0.146	42	0.219	19	0.143	0.145	N	0.57	SignalP-noTM
gi_188523283_gb_ACD61228.1_	0.441	21	0.201	21	0.153	20	0.075	0.142	N	0.57	SignalP-noTM
gi_188523284_gb_ACD61229.1_	0.127	24	0.099	50	0.108	33	0.085	0.092	N	0.57	SignalP-noTM
gi_188523285_gb_ACD61230.1_	0.12	32	0.124	32	0.202	14	0.126	0.125	N	0.57	SignalP-noTM

0.141851	0.126198	0.113548	0.127199	gi_188523092_gb_ACD61037.1_
0.102293	0.004702	0.140035	0.082343	gi_188523095_gb_ACD61040.1_
0.278081	0.005283	0.333366	0.205577	gi_188523096_gb_ACD61041.1_
0.134354	0.039015	0.182873	0.118747	gi_188523101_gb_ACD61046.1_
0.3858	0.951339	0.349554	0.562231	gi_188523102_gb_ACD61047.1_
0.08181	0.52473	0.167284	0.257941	gi_188523103_gb_ACD61048.1_
0.0985	0.074261	0.10736	0.093374	gi_188523104_gb_ACD61049.1_
0.157892	0.457354	0.14295	0.252732	gi_188523114_gb_ACD61059.1_
0.696566	0.995889	0.589766	0.76074	gi_188523119_gb_ACD61064.1_
0.062444	0.046486	0.109097	0.072676	gi_188523123_gb_ACD61068.1_
0.163967	0.491751	0.242872	0.29953	gi_188523126_gb_ACD61071.1_
0.057216	0.019152	0.076562	0.050977	gi_188523128_gb_ACD61073.1_
0.715246	0.092289	0.736722	0.514752	gi_188523129_gb_ACD61074.1_
0.159092	0.130222	0.189694	0.159669	gi_188523131_gb_ACD61076.1_
0.27508	0.806589	0.3858	0.489156	gi_188523132_gb_ACD61077.1_
0.092541	0.168962	0.069655	0.110386	gi_188523135_gb_ACD61080.1_
0.147041	0.003681	0.199567	0.116763	gi_188523136_gb_ACD61081.1_
0.733216	0.998459	0.838485	0.85672	gi_188523140_gb_ACD61085.1_
0.236313	0.267959	0.304068	0.269447	gi_188523141_gb_ACD61086.1_
0.17581	0.065314	0.300903	0.180676	gi_188523142_gb_ACD61087.1_
0.106786	0.103123	0.137881	0.11593	gi_188523143_gb_ACD61088.1_
0.830616	0.951061	0.764768	0.848815	gi_188523144_gb_ACD61089.1_
0.52473	0.747628	0.679832	0.65073	gi_188523150_gb_ACD61095.1_
0.198134	0.161515	0.282925	0.214191	gi_188523151_gb_ACD61096.1_
0.278081	0.54711	0.336708	0.3873	gi_188523155_gb_ACD61100.1_
0.071625	0.009991	0.112645	0.064754	gi_188523157_gb_ACD61102.1_
0.159092	0.200047	0.166866	0.175335	gi_188523159_gb_ACD61104.1_
0.630416	0.490251	0.568565	0.563077	gi_188523171_gb_ACD61116.1_
0.9473	0.999896	0.8935	0.946899	gi_188523178_gb_ACD61123.1_
0.077201	0.001774	0.120363	0.066446	gi_188523184_gb_ACD61129.1_
0.296504	0.201974	0.20538	0.234619	gi_188523185_gb_ACD61130.1_
0.402995	0.284754	0.443246	0.376998	gi_188523186_gb_ACD61131.1_
0.071226	0.006413	0.09639	0.05801	gi_188523187_gb_ACD61132.1_
0.336038	0.064224	0.458099	0.28612	gi_188523188_gb_ACD61133.1_
0.882467	0.999948	0.694024	0.858813	gi_188523192_gb_ACD61137.1_
0.716466	0.377306	0.751009	0.614927	gi_188523198_gb_ACD61143.1_
0.125538	0.354344	0.089074	0.189652	gi_188523201_gb_ACD61146.1_
0.64497	0.812601	0.579568	0.679046	gi_188523203_gb_ACD61148.1_
0.935776	0.921724	0.913805	0.923768	gi_188523204_gb_ACD61149.1_
0.041806	0.026753	0.094833	0.054464	gi_188523205_gb_ACD61150.1_
0.958909	0.990669	0.934869	0.961482	gi_188523206_gb_ACD61151.1_
0.926355	0.908711	0.93015	0.921739	gi_188523207_gb_ACD61152.1_
0.204403	0.479012	0.165205	0.282873	gi_188523208_gb_ACD61153.1_
0.17023	0.424091	0.112346	0.235556	gi_188523209_gb_ACD61154.1_
0.960872	0.99993	0.936136	0.965646	gi_188523212_gb_ACD61157.1_
0.949932	0.999184	0.913093	0.95407	gi_188523213_gb_ACD61158.1_
0.959145	0.999206	0.839296	0.932549	gi_188523215_gb_ACD61160.1_
0.935051	0.999675	0.901233	0.94532	gi_188523222_gb_ACD61167.1_
0.266784	0.030325	0.099302	0.132137	gi_188523223_gb_ACD61168.1_
0.919309	0.999516	0.92194	0.946922	gi_188523228_gb_ACD61173.1_
0.082262	0.042168	0.10736	0.077263	gi_188523230_gb_ACD61175.1_
0.185579	0.102845	0.171079	0.153168	gi_188523232_gb_ACD61177.1_
0.400832	0.149694	0.448434	0.332987	gi_188523233_gb_ACD61178.1_
0.102293	0.055148	0.105931	0.087791	gi_188523235_gb_ACD61180.1_
0.24453	0.109975	0.286591	0.213699	gi_188523242_gb_ACD61187.1_
0.782109	0.90361	0.847225	0.844315	gi_188523244_gb_ACD61189.1_
0.083173	0.172787	0.094063	0.116674	gi_188523249_gb_ACD61194.1_
0.090298	0.75878	0.304068	0.384382	gi_188523252_gb_ACD61197.1_
0.102293	0.179314	0.159494	0.147034	gi_188523253_gb_ACD61198.1_
0.141486	0.157493	0.157095	0.152025	gi_188523256_gb_ACD61201.1_
0.917284	0.924909	0.898803	0.913665	gi_188523257_gb_ACD61202.1_
0.27508	0.627615	0.323442	0.408712	gi_188523258_gb_ACD61203.1_
0.069461	0.051222	0.144798	0.088494	gi_188523259_gb_ACD61204.1_
0.403717	0.103958	0.41314	0.306938	gi_188523261_gb_ACD61206.1_
0.320168	0.98841	0.150844	0.486474	gi_188523262_gb_ACD61207.1_
0.072628	0.004633	0.095868	0.05771	gi_188523263_gb_ACD61208.1_
0.639455	0.996988	0.756576	0.797673	gi_188523264_gb_ACD61209.1_
0.158691	0.054526	0.097969	0.103729	gi_188523265_gb_ACD61210.1_
0.065681	0.040621	0.089074	0.065125	gi_188523266_gb_ACD61211.1_
0.095609	0.066608	0.135404	0.099207	gi_188523270_gb_ACD61215.1_
0.180199	0.131587	0.105364	0.13905	gi_188523272_gb_ACD61217.1_
0.949213	0.994978	0.910194	0.951462	gi_188523273_gb_ACD61218.1_
0.14295	0.077629	0.161921	0.1275	gi_188523274_gb_ACD61219.1_
0.175375	0.103958	0.166866	0.148733	gi_188523276_gb_ACD61221.1_
0.302167	0.702243	0.375194	0.459868	gi_188523277_gb_ACD61222.1_
0.360545	0.018057	0.47527	0.284624	gi_188523283_gb_ACD61228.1_
0.064224	0.034959	0.080691	0.059958	gi_188523284_gb_ACD61229.1_
0.165205	0.158291	0.143318	0.155605	gi_188523285_gb_ACD61230.1_

gi_188523286_gb_ACD61231.1_	0.127	50	0.148	50	0.258	35	0.131	0.142	N	0.51	SignalP-TM
gi_188523287_gb_ACD61232.1_	0.137	33	0.126	33	0.165	30	0.106	0.117	N	0.57	SignalP-noTM
gi_188523288_gb_ACD61233.1_	0.117	27	0.127	17	0.201	4	0.152	0.139	N	0.57	SignalP-noTM
gi_188523289_gb_ACD61234.1_	0.105	69	0.112	14	0.16	6	0.126	0.119	N	0.57	SignalP-noTM
gi_188523291_gb_ACD61236.1_	0.245	30	0.227	30	0.448	10	0.287	0.255	N	0.57	SignalP-noTM
gi_188523292_gb_ACD61237.1_	0.117	20	0.16	11	0.407	1	0.243	0.199	N	0.57	SignalP-noTM
gi_188523298_gb_ACD61243.1_	0.102	26	0.103	41	0.116	30	0.087	0.096	N	0.57	SignalP-noTM
gi_188523302_gb_ACD61247.1_	0.156	42	0.146	42	0.219	19	0.143	0.145	N	0.57	SignalP-noTM
gi_188523307_gb_ACD61252.1_	0.141	43	0.129	43	0.232	2	0.132	0.13	N	0.57	SignalP-noTM
gi_188523308_gb_ACD61253.1_	0.139	38	0.135	38	0.18	35	0.121	0.128	N	0.57	SignalP-noTM
gi_188523309_gb_ACD61254.1_	0.126	37	0.132	13	0.199	2	0.17	0.15	N	0.57	SignalP-noTM
gi_188523310_gb_ACD61255.1_	0.182	59	0.173	59	0.226	46	0.128	0.156	N	0.51	SignalP-TM
gi_188523312_gb_ACD61257.1_	0.127	26	0.186	26	0.388	19	0.263	0.214	N	0.51	SignalP-TM
gi_188523313_gb_ACD61258.1_	0.218	41	0.335	41	0.639	37	0.326	0.331	N	0.57	SignalP-noTM
gi_188523314_gb_ACD61259.1_	0.116	43	0.122	18	0.159	11	0.133	0.126	N	0.51	SignalP-TM
gi_188523318_gb_ACD61263.1_	0.171	23	0.182	23	0.527	1	0.247	0.213	N	0.57	SignalP-noTM
gi_188523319_gb_ACD61264.1_	0.167	36	0.158	11	0.336	1	0.244	0.198	N	0.57	SignalP-noTM
gi_188523324_gb_ACD61269.1_	0.133	46	0.106	46	0.14	1	0.064	0.091	N	0.51	SignalP-TM
gi_188523325_gb_ACD61270.1_	0.153	61	0.119	25	0.155	9	0.127	0.123	N	0.57	SignalP-noTM
gi_188523326_gb_ACD61271.1_	0.364	29	0.435	21	0.913	12	0.746	0.581	Y	0.57	SignalP-noTM
gi_188523327_gb_ACD61272.1_	0.105	20	0.101	62	0.137	1	0.092	0.097	N	0.57	SignalP-noTM
gi_188523328_gb_ACD61273.1_	0.19	35	0.148	35	0.221	34	0.106	0.129	N	0.57	SignalP-noTM
gi_188523330_gb_ACD61275.1_	0.103	61	0.135	29	0.229	24	0.171	0.148	N	0.51	SignalP-TM
gi_188523331_gb_ACD61276.1_	0.102	21	0.097	37	0.13	1	0.085	0.091	N	0.57	SignalP-noTM
gi_188523332_gb_ACD61277.1_	0.138	18	0.11	34	0.124	28	0.086	0.099	N	0.57	SignalP-noTM
gi_188523335_gb_ACD61280.1_	0.118	25	0.144	11	0.282	3	0.202	0.171	N	0.57	SignalP-noTM
gi_188523337_gb_ACD61282.1_	0.112	62	0.147	15	0.27	14	0.212	0.177	N	0.57	SignalP-noTM
gi_188523338_gb_ACD61283.1_	0.151	8	0.113	36	0.143	33	0.103	0.109	N	0.57	SignalP-noTM
gi_188523339_gb_ACD61284.1_	0.117	37	0.155	20	0.296	8	0.213	0.182	N	0.57	SignalP-noTM
gi_188523340_gb_ACD61285.1_	0.134	28	0.292	28	0.824	25	0.529	0.403	N	0.57	SignalP-noTM
gi_188523341_gb_ACD61286.1_	0.156	26	0.115	26	0.168	1	0.091	0.104	N	0.57	SignalP-noTM
gi_188523342_gb_ACD61287.1_	0.142	48	0.123	48	0.131	38	0.094	0.11	N	0.57	SignalP-noTM
gi_188523343_gb_ACD61288.1_	0.478	22	0.396	22	0.443	19	0.33	0.365	N	0.57	SignalP-noTM
gi_188523344_gb_ACD61289.1_	0.131	36	0.128	36	0.2	35	0.123	0.125	N	0.57	SignalP-noTM
gi_188523345_gb_ACD61290.1_	0.105	32	0.101	70	0.144	64	0.074	0.091	N	0.51	SignalP-TM
gi_188523347_gb_ACD61292.1_	0.152	26	0.148	26	0.339	43	0.143	0.146	N	0.57	SignalP-noTM
gi_188523351_gb_ACD61296.1_	0.113	41	0.129	41	0.203	18	0.141	0.135	N	0.57	SignalP-noTM
gi_188523352_gb_ACD61297.1_	0.124	65	0.167	19	0.389	17	0.221	0.192	N	0.57	SignalP-noTM
gi_188523353_gb_ACD61298.1_	0.241	32	0.202	32	0.31	4	0.199	0.201	N	0.51	SignalP-TM
gi_188523354_gb_ACD61299.1_	0.574	15	0.507	15	0.636	7	0.446	0.478	N	0.57	SignalP-noTM
gi_188523355_gb_ACD61300.1_	0.21	44	0.219	18	0.487	1	0.329	0.271	N	0.57	SignalP-noTM
gi_188523358_gb_ACD61303.1_	0.153	46	0.178	46	0.59	44	0.118	0.15	N	0.57	SignalP-noTM
gi_188523359_gb_ACD61304.1_	0.365	50	0.276	50	0.613	49	0.162	0.222	N	0.57	SignalP-noTM
gi_188523368_gb_ACD61313.1_	0.111	23	0.157	11	0.31	4	0.243	0.197	N	0.57	SignalP-noTM
gi_188523374_gb_ACD61319.1_	0.104	36	0.129	11	0.217	3	0.167	0.147	N	0.57	SignalP-noTM
gi_188523380_gb_ACD61325.1_	0.137	43	0.14	43	0.287	1	0.121	0.133	N	0.51	SignalP-TM
gi_188523387_gb_ACD61332.1_	0.224	17	0.397	17	0.784	13	0.706	0.542	N	0.57	SignalP-noTM
gi_188523388_gb_ACD61333.1_	0.119	45	0.117	45	0.169	13	0.117	0.117	N	0.57	SignalP-noTM
gi_188523389_gb_ACD61334.1_	0.11	51	0.119	11	0.177	3	0.143	0.13	N	0.57	SignalP-noTM
gi_188523390_gb_ACD61335.1_	0.252	33	0.193	33	0.352	21	0.187	0.19	N	0.57	SignalP-noTM
gi_188523391_gb_ACD61336.1_	0.175	23	0.136	23	0.179	2	0.114	0.126	N	0.57	SignalP-noTM
gi_188521297_gb_ACD59242.1_	0.155	42	0.145	42	0.21	19	0.138	0.141	N	0.57	SignalP-noTM
gi_188521308_gb_ACD59253.1_	0.155	42	0.145	42	0.21	19	0.138	0.141	N	0.57	SignalP-noTM
gi_188521694_gb_ACD59639.1_	0.149	16	0.148	16	0.243	13	0.151	0.149	N	0.57	SignalP-noTM
gi_188521695_gb_ACD59640.1_	0.105	54	0.113	11	0.199	1	0.119	0.116	N	0.57	SignalP-noTM
gi_188521698_gb_ACD59643.1_	0.133	22	0.158	22	0.292	11	0.194	0.175	N	0.57	SignalP-noTM
gi_188521701_gb_ACD59646.1_	0.112	23	0.104	68	0.119	65	0.085	0.095	N	0.57	SignalP-noTM
gi_188521704_gb_ACD59649.1_	0.12	23	0.128	23	0.212	1	0.147	0.137	N	0.57	SignalP-noTM
gi_188521705_gb_ACD59650.1_	0.141	53	0.129	41	0.175	36	0.107	0.118	N	0.57	SignalP-noTM
gi_188521707_gb_ACD59652.1_	0.307	47	0.274	47	0.452	30	0.304	0.288	N	0.57	SignalP-noTM
gi_188521708_gb_ACD59653.1_	0.387	27	0.569	21	0.941	1	0.886	0.718	Y	0.57	SignalP-noTM
gi_188521709_gb_ACD59654.1_	0.149	19	0.367	19	0.95	1	0.915	0.625	Y	0.57	SignalP-noTM
gi_188521710_gb_ACD59655.1_	0.146	35	0.156	11	0.369	1	0.232	0.184	N	0.51	SignalP-TM
gi_188521711_gb_ACD59656.1_	0.119	42	0.122	11	0.209	4	0.152	0.136	N	0.57	SignalP-noTM
gi_188521712_gb_ACD59657.1_	0.114	31	0.149	16	0.292	14	0.224	0.184	N	0.57	SignalP-noTM
gi_188521713_gb_ACD59658.1_	0.11	52	0.111	11	0.179	1	0.115	0.113	N	0.57	SignalP-noTM
gi_188521714_gb_ACD59659.1_	0.188	40	0.34	31	0.809	17	0.646	0.484	N	0.57	SignalP-noTM
gi_188521715_gb_ACD59660.1_	0.131	45	0.152	11	0.349	1	0.225	0.179	N	0.51	SignalP-TM
gi_188521716_gb_ACD59661.1_	0.129	57	0.147	11	0.276	1	0.208	0.175	N	0.57	SignalP-noTM
gi_188521717_gb_ACD59662.1_	0.125	29	0.107	29	0.112	23	0.082	0.095	N	0.57	SignalP-noTM
gi_188521726_gb_ACD59671.1_	0.155	42	0.145	42	0.21	19	0.138	0.141	N	0.57	SignalP-noTM
gi_188521730_gb_ACD59675.1_	0.123	24	0.119	43	0.157	42	0.101	0.11	N	0.57	SignalP-noTM
gi_188521731_gb_ACD59676.1_	0.144	39	0.113	49	0.11	14	0.085	0.1	N	0.57	SignalP-noTM
gi_188521741_gb_ACD59686.1_	0.135	37	0.115	37	0.123	49	0.079	0.098	N	0.57	SignalP-noTM
gi_188521749_gb_ACD59694.1_	0.125	7	0.117	11	0.164	1	0.138	0.127	N	0.57	SignalP-noTM
gi_188521750_gb_ACD59695.1_	0.864	22	0.876	22	0.951	18	0.84	0.859	Y	0.57	SignalP-noTM
gi_188521751_gb_ACD59696.1_	0.109	35	0.119	12	0.183	2	0.146	0.132	N	0.57	SignalP-noTM
gi_188521752_gb_ACD59697.1_	0.103	41	0.119	27	0.164	18	0.112	0.116	N	0.57	SignalP-noTM

0.363316	0.111749	0.473774	0.31628	gi_188523286_gb_ACD61231.1_
0.130562	0.057867	0.151614	0.113348	gi_188523287_gb_ACD61232.1_
0.141851	0.731452	0.096129	0.323144	gi_188523288_gb_ACD61233.1_
0.056412	0.032609	0.081585	0.056869	gi_188523289_gb_ACD61234.1_
0.264443	0.06003	0.318863	0.214445	gi_188523291_gb_ACD61236.1_
0.497	0.979688	0.654527	0.710405	gi_188523292_gb_ACD61237.1_
0.690188	0.992147	0.903086	0.861807	gi_188523298_gb_ACD61243.1_
0.254074	0.644282	0.271505	0.389954	gi_188523302_gb_ACD61247.1_
0.168541	0.00576	0.232009	0.135437	gi_188523307_gb_ACD61252.1_
0.171931	0.004123	0.216361	0.130805	gi_188523308_gb_ACD61253.1_
0.073033	0.055619	0.092793	0.073815	gi_188523309_gb_ACD61254.1_
0.166866	0.096651	0.210818	0.158112	gi_188523310_gb_ACD61255.1_
0.119098	0.064949	0.152775	0.112274	gi_188523312_gb_ACD61257.1_
0.245641	0.046887	0.226707	0.173078	gi_188523313_gb_ACD61258.1_
0.074261	0.003104	0.208829	0.095398	gi_188523314_gb_ACD61259.1_
0.217891	0.193879	0.141486	0.184419	gi_188523318_gb_ACD61263.1_
0.931694	0.999988	0.657911	0.863198	gi_188523319_gb_ACD61264.1_
0.265612	0.047971	0.316912	0.210165	gi_188523324_gb_ACD61269.1_
0.101744	0.043522	0.153164	0.099477	gi_188523325_gb_ACD61270.1_
0.126198	0.05285	0.136461	0.10517	gi_188523326_gb_ACD61271.1_
0.053911	0.027225	0.097704	0.059613	gi_188523327_gb_ACD61272.1_
0.199567	0.957344	0.090052	0.415654	gi_188523328_gb_ACD61273.1_
0.317562	0.155907	0.406609	0.293359	gi_188523330_gb_ACD61275.1_
0.082262	0.0298	0.133658	0.081907	gi_188523331_gb_ACD61276.1_
0.132274	0.138238	0.135755	0.135422	gi_188523332_gb_ACD61277.1_
0.925739	0.925739	0.761514	0.870997	gi_188523335_gb_ACD61280.1_
0.118784	0.02795	0.121639	0.089458	gi_188523337_gb_ACD61282.1_
0.27508	0.07385	0.295254	0.214728	gi_188523338_gb_ACD61283.1_
0.075928	0.056412	0.088346	0.073562	gi_188523339_gb_ACD61284.1_
0.086669	0.036089	0.142583	0.088447	gi_188523340_gb_ACD61285.1_
0.072426	0.031676	0.117222	0.073775	gi_188523341_gb_ACD61286.1_
0.248991	0.98428	0.445468	0.55958	gi_188523342_gb_ACD61287.1_
0.235232	0.667966	0.267371	0.39019	gi_188523343_gb_ACD61288.1_
0.329378	0.942133	0.353658	0.541723	gi_188523344_gb_ACD61289.1_
0.281102	0.626914	0.330705	0.412907	gi_188523345_gb_ACD61290.1_
0.213325	0.036509	0.260957	0.170264	gi_188523347_gb_ACD61292.1_
0.279287	0.73614	0.324098	0.446508	gi_188521297_gb_ACD59242.1_
0.259802	0.491751	0.297757	0.34977	gi_188521308_gb_ACD59253.1_
0.161109	0.597005	0.102569	0.286894	gi_188523351_gb_ACD61296.1_
0.134005	0.01278	0.1603	0.102362	gi_188523352_gb_ACD61297.1_
0.933205	0.993867	0.90896	0.945344	gi_188523353_gb_ACD61298.1_
0.825491	0.939289	0.763687	0.842822	gi_188523354_gb_ACD61299.1_
0.143687	0.018928	0.210818	0.124478	gi_188523355_gb_ACD61300.1_
0.361929	0.253506	0.597726	0.404387	gi_188523358_gb_ACD61303.1_
0.164792	0.079147	0.151228	0.131722	gi_188523359_gb_ACD61304.1_
0.918863	0.998813	0.613489	0.843722	gi_188523368_gb_ACD61313.1_
0.805652	0.98527	0.704121	0.831681	gi_188523374_gb_ACD61319.1_
0.124553	0.114153	0.152387	0.130364	gi_188523380_gb_ACD61325.1_
0.338721	0.025831	0.397235	0.253929	gi_188523387_gb_ACD61332.1_
0.878681	0.942133	0.833134	0.884649	gi_188523388_gb_ACD61333.1_
0.116603	0.478264	0.082944	0.225937	gi_188523389_gb_ACD61334.1_
0.120999	0.124227	0.13193	0.125719	gi_188523390_gb_ACD61335.1_
0.902296	0.861045	0.82977	0.86437	gi_188523391_gb_ACD61336.1_
0.102569	0.043149	0.126861	0.09086	gi_188521694_gb_ACD59639.1_
0.892064	0.999176	0.650446	0.847229	gi_188521695_gb_ACD59640.1_
0.717684	0.91819	0.826783	0.820886	gi_188521698_gb_ACD59643.1_
0.139314	0.214839	0.173217	0.17579	gi_188521701_gb_ACD59646.1_
0.154335	0.069461	0.155907	0.126568	gi_188521704_gb_ACD59649.1_
0.097704	0.001923	0.116912	0.07218	gi_188521705_gb_ACD59650.1_
0.284754	0.028526	0.304068	0.205783	gi_188521707_gb_ACD59652.1_
0.93963	0.009085	0.972933	0.640549	gi_188521708_gb_ACD59653.1_
0.69211	0.037579	0.813057	0.514249	gi_188521709_gb_ACD59654.1_
0.162329	0.05836	0.197182	0.13929	gi_188521710_gb_ACD59655.1_
0.901766	0.999688	0.813513	0.904989	gi_188521711_gb_ACD59656.1_
0.50675	0.034959	0.551566	0.364425	gi_188521712_gb_ACD59657.1_
0.102293	0.084092	0.100652	0.095679	gi_188521713_gb_ACD59658.1_
0.339393	0.907459	0.096129	0.44766	gi_188521714_gb_ACD59659.1_
0.119413	0.055462	0.108806	0.09456	gi_188521715_gb_ACD59660.1_
0.176681	0.129544	0.148932	0.151719	gi_188521716_gb_ACD59661.1_
0.110563	0.058031	0.082036	0.083543	gi_188521717_gb_ACD59662.1_
0.277479	0.701615	0.322785	0.43396	gi_188521726_gb_ACD59671.1_
0.86807	0.981293	0.760423	0.869929	gi_188521730_gb_ACD59675.1_
0.1034	0.059861	0.155513	0.106258	gi_188521731_gb_ACD59676.1_
0.090298	0.054992	0.114457	0.086582	gi_188521741_gb_ACD59686.1_
0.165205	0.047834	0.156303	0.123114	gi_188521749_gb_ACD59694.1_
0.890319	0.826783	0.90016	0.872421	gi_188521750_gb_ACD59695.1_
0.953247	0.906701	0.881843	0.91393	gi_188521751_gb_ACD59696.1_
0.87804	0.692748	0.866342	0.812377	gi_188521752_gb_ACD59697.1_

gi_188521753_gb_ACD59698.1_	0.106	21	0.127	11	0.242	1	0.152	0.138	N	0.57	SignalP-noTM
gi_188521756_gb_ACD59701.1_	0.153	51	0.132	51	0.182	49	0.108	0.121	N	0.57	SignalP-noTM
gi_188521758_gb_ACD59703.1_	0.125	59	0.161	11	0.406	2	0.261	0.208	N	0.57	SignalP-noTM
gi_188521759_gb_ACD59704.1_	0.199	18	0.186	18	0.223	14	0.175	0.181	N	0.51	SignalP-TM
gi_188521763_gb_ACD59708.1_	0.16	9	0.132	15	0.204	5	0.135	0.133	N	0.57	SignalP-noTM
gi_188521764_gb_ACD59709.1_	0.122	36	0.096	11	0.118	32	0.096	0.096	N	0.51	SignalP-TM
gi_188521765_gb_ACD59710.1_	0.442	28	0.603	28	0.994	12	0.905	0.745	Y	0.57	SignalP-noTM
gi_188521766_gb_ACD59711.1_	0.128	23	0.182	11	0.476	4	0.345	0.242	N	0.51	SignalP-TM
gi_188521768_gb_ACD59713.1_	0.228	35	0.179	35	0.404	1	0.178	0.179	N	0.57	SignalP-noTM
gi_188521772_gb_ACD59717.1_	0.18	22	0.185	22	0.31	21	0.175	0.18	N	0.57	SignalP-noTM
gi_188521773_gb_ACD59718.1_	0.108	41	0.119	11	0.211	1	0.135	0.126	N	0.57	SignalP-noTM
gi_188521774_gb_ACD59719.1_	0.168	40	0.133	40	0.158	69	0.075	0.112	N	0.51	SignalP-TM
gi_188521775_gb_ACD59720.1_	0.099	11	0.12	11	0.262	1	0.121	0.12	N	0.51	SignalP-TM
gi_188521776_gb_ACD59721.1_	0.111	52	0.11	11	0.176	2	0.122	0.116	N	0.57	SignalP-noTM
gi_188521777_gb_ACD59722.1_	0.102	29	0.109	29	0.15	10	0.111	0.11	N	0.57	SignalP-noTM
gi_188521779_gb_ACD59724.1_	0.19	20	0.331	20	0.77	3	0.637	0.475	N	0.57	SignalP-noTM
gi_188521783_gb_ACD59728.1_	0.129	64	0.108	11	0.137	1	0.117	0.112	N	0.57	SignalP-noTM
gi_188521784_gb_ACD59729.1_	0.194	29	0.136	29	0.189	3	0.114	0.125	N	0.57	SignalP-noTM
gi_188521785_gb_ACD59730.1_	0.364	32	0.495	32	0.952	22	0.765	0.622	Y	0.57	SignalP-noTM
gi_188521787_gb_ACD59732.1_	0.237	25	0.166	25	0.245	1	0.129	0.149	N	0.57	SignalP-noTM
gi_188521788_gb_ACD59733.1_	0.221	32	0.243	23	0.576	14	0.403	0.302	N	0.51	SignalP-TM
gi_188521791_gb_ACD59736.1_	0.218	21	0.436	19	0.952	11	0.902	0.655	Y	0.57	SignalP-noTM
gi_528897484_gb_AGS47850.1_	0.193	44	0.224	44	0.523	28	0.259	0.24	N	0.57	SignalP-noTM
gi_188521793_gb_ACD59738.1_	0.103	29	0.158	14	0.319	13	0.255	0.204	N	0.57	SignalP-noTM
gi_188522255_gb_ACD60200.1_	0.117	42	0.16	11	0.291	1	0.235	0.195	N	0.57	SignalP-noTM
gi_188522257_gb_ACD60202.1_	0.156	42	0.146	42	0.219	19	0.143	0.145	N	0.57	SignalP-noTM
gi_188522258_gb_ACD60203.1_	0.11	17	0.118	11	0.217	1	0.129	0.123	N	0.57	SignalP-noTM
gi_188522266_gb_ACD60211.1_	0.132	25	0.15	25	0.233	16	0.175	0.162	N	0.57	SignalP-noTM
gi_188522268_gb_ACD60213.1_	0.112	45	0.108	45	0.126	1	0.099	0.104	N	0.57	SignalP-noTM
gi_188522269_gb_ACD60214.1_	0.109	29	0.133	11	0.28	1	0.166	0.148	N	0.57	SignalP-noTM
gi_188522270_gb_ACD60215.1_	0.275	33	0.316	33	0.649	10	0.462	0.385	N	0.57	SignalP-noTM
gi_188522272_gb_ACD60217.1_	0.134	34	0.134	11	0.242	4	0.184	0.158	N	0.57	SignalP-noTM
gi_188522273_gb_ACD60218.1_	0.11	43	0.121	11	0.186	6	0.153	0.136	N	0.57	SignalP-noTM
gi_188522274_gb_ACD60219.1_	0.128	44	0.128	44	0.169	37	0.111	0.12	N	0.57	SignalP-noTM
gi_188522275_gb_ACD60220.1_	0.147	33	0.116	33	0.161	1	0.092	0.107	N	0.51	SignalP-TM
gi_188522277_gb_ACD60222.1_	0.285	50	0.13	24	0.216	14	0.148	0.137	N	0.51	SignalP-TM
gi_188522278_gb_ACD60223.1_	0.111	27	0.12	11	0.194	5	0.157	0.134	N	0.51	SignalP-TM
gi_188522281_gb_ACD60226.1_	0.144	36	0.12	36	0.123	2	0.098	0.11	N	0.57	SignalP-noTM
gi_188522282_gb_ACD60227.1_	0.122	49	0.114	14	0.164	11	0.133	0.121	N	0.51	SignalP-TM
gi_188522285_gb_ACD60230.1_	0.104	35	0.194	18	0.502	11	0.357	0.27	N	0.57	SignalP-noTM
gi_188522286_gb_ACD60231.1_	0.144	35	0.233	24	0.491	18	0.412	0.317	N	0.57	SignalP-noTM
gi_188522293_gb_ACD60238.1_	0.131	35	0.137	11	0.25	3	0.184	0.159	N	0.57	SignalP-noTM
gi_188522298_gb_ACD60243.1_	0.133	22	0.158	22	0.292	11	0.194	0.175	N	0.57	SignalP-noTM
gi_188522301_gb_ACD60246.1_	0.118	54	0.104	65	0.126	60	0.086	0.097	N	0.51	SignalP-TM
gi_188522302_gb_ACD60247.1_	0.118	33	0.11	11	0.157	2	0.121	0.115	N	0.57	SignalP-noTM
gi_188522303_gb_ACD60248.1_	0.159	45	0.14	11	0.289	1	0.182	0.159	N	0.57	SignalP-noTM
gi_188522307_gb_ACD60252.1_	0.136	42	0.121	11	0.21	1	0.145	0.132	N	0.57	SignalP-noTM
gi_188522310_gb_ACD60255.1_	0.195	31	0.153	11	0.298	1	0.226	0.188	N	0.57	SignalP-noTM
gi_188522311_gb_ACD60256.1_	0.105	20	0.105	30	0.127	20	0.096	0.101	N	0.57	SignalP-noTM
gi_188522312_gb_ACD60257.1_	0.13	40	0.107	58	0.152	49	0.083	0.098	N	0.51	SignalP-TM
gi_188522313_gb_ACD60258.1_	0.125	19	0.133	11	0.246	2	0.171	0.151	N	0.57	SignalP-noTM
gi_188522314_gb_ACD60259.1_	0.145	22	0.115	22	0.117	13	0.082	0.1	N	0.57	SignalP-noTM
gi_188522321_gb_ACD60266.1_	0.151	60	0.224	11	0.681	1	0.479	0.344	N	0.57	SignalP-noTM
gi_188522323_gb_ACD60268.1_	0.118	18	0.122	11	0.189	6	0.154	0.137	N	0.57	SignalP-noTM
gi_188522324_gb_ACD60269.1_	0.117	21	0.126	11	0.227	2	0.154	0.139	N	0.57	SignalP-noTM
gi_188522325_gb_ACD60270.1_	0.177	30	0.135	30	0.168	29	0.107	0.122	N	0.57	SignalP-noTM
gi_188522329_gb_ACD60274.1_	0.116	30	0.1	11	0.141	1	0.097	0.099	N	0.57	SignalP-noTM
gi_188522332_gb_ACD60277.1_	0.111	27	0.126	11	0.21	5	0.171	0.142	N	0.51	SignalP-TM
gi_188522335_gb_ACD60280.1_	0.202	26	0.16	26	0.193	25	0.136	0.149	N	0.57	SignalP-noTM
gi_188522337_gb_ACD60282.1_	0.118	40	0.106	40	0.149	2	0.096	0.101	N	0.57	SignalP-noTM
gi_188522338_gb_ACD60283.1_	0.133	33	0.14	33	0.276	30	0.126	0.133	N	0.57	SignalP-noTM
gi_188522341_gb_ACD60286.1_	0.147	25	0.225	17	0.647	1	0.495	0.352	N	0.57	SignalP-noTM
gi_188522345_gb_ACD60290.1_	0.129	23	0.142	11	0.244	1	0.197	0.168	N	0.57	SignalP-noTM
gi_188522346_gb_ACD60291.1_	0.135	20	0.105	20	0.115	1	0.084	0.095	N	0.57	SignalP-noTM
gi_188522350_gb_ACD60295.1_	0.135	44	0.11	44	0.107	1	0.074	0.093	N	0.57	SignalP-noTM
gi_188522354_gb_ACD60299.1_	0.114	56	0.124	17	0.179	11	0.152	0.137	N	0.57	SignalP-noTM
gi_188522365_gb_ACD60310.1_	0.322	30	0.18	30	0.122	27	0.093	0.139	N	0.57	SignalP-noTM
gi_188522366_gb_ACD60311.1_	0.135	44	0.136	44	0.18	35	0.119	0.128	N	0.57	SignalP-noTM
gi_188522796_gb_ACD60741.1_	0.121	23	0.148	23	0.306	19	0.182	0.164	N	0.57	SignalP-noTM
gi_188522798_gb_ACD60743.1_	0.112	41	0.13	41	0.192	31	0.13	0.13	N	0.57	SignalP-noTM
gi_188522805_gb_ACD60750.1_	0.312	23	0.425	23	0.791	21	0.508	0.464	N	0.57	SignalP-noTM
gi_188522812_gb_ACD60757.1_	0.126	67	0.111	67	0.11	45	0.085	0.099	N	0.57	SignalP-noTM
gi_188522816_gb_ACD60761.1_	0.139	16	0.127	16	0.254	1	0.129	0.128	N	0.57	SignalP-noTM
gi_188522817_gb_ACD60762.1_	0.154	31	0.326	16	0.895	11	0.82	0.558	N	0.57	SignalP-noTM
gi_188522818_gb_ACD60763.1_	0.268	34	0.142	11	0.302	1	0.185	0.163	N	0.57	SignalP-noTM
gi_188522829_gb_ACD60774.1_	0.249	53	0.221	53	0.306	49	0.154	0.196	N	0.51	SignalP-TM
gi_188522831_gb_ACD60776.1_	0.155	42	0.145	42	0.21	19	0.138	0.141	N	0.57	SignalP-noTM
gi_188522835_gb_ACD60780.1_	0.158	29	0.119	29	0.132	5	0.091	0.106	N	0.57	SignalP-noTM

0.915908	0.981183	0.796571	0.897887	gi_188521753_gb_ACD59698.1_
0.461079	0.924492	0.558974	0.648182	gi_188521756_gb_ACD59701.1_
0.709096	0.033278	0.743073	0.495149	gi_188521758_gb_ACD59703.1_
0.109389	0.012297	0.182873	0.10152	gi_188521759_gb_ACD59704.1_
0.786675	0.810306	0.745926	0.780969	gi_188521763_gb_ACD59708.1_
0.079585	0.044916	0.127862	0.084121	gi_188521764_gb_ACD59709.1_
0.946546	0.999792	0.881843	0.942727	gi_188521765_gb_ACD59710.1_
0.958553	0.999863	0.850306	0.936241	gi_188521766_gb_ACD59711.1_
0.083862	0.047021	0.10011	0.076998	gi_188521768_gb_ACD59713.1_
0.940476	0.990641	0.880902	0.93734	gi_188521772_gb_ACD59717.1_
0.08181	0.001334	0.105081	0.062742	gi_188521773_gb_ACD59718.1_
0.109097	0.07385	0.219428	0.134125	gi_188521774_gb_ACD59719.1_
0.254074	0.01811	0.368188	0.213457	gi_188521775_gb_ACD59720.1_
0.529217	0.832298	0.65656	0.672692	gi_188521776_gb_ACD59721.1_
0.562669	0.928176	0.647713	0.712853	gi_188521777_gb_ACD59722.1_
0.701615	0.952979	0.748193	0.800929	gi_188521779_gb_ACD59724.1_
0.085959	0.046887	0.139674	0.09084	gi_188521783_gb_ACD59728.1_
0.938255	0.996491	0.850687	0.928478	gi_188521784_gb_ACD59729.1_
0.949069	0.999583	0.887355	0.945336	gi_188521785_gb_ACD59730.1_
0.187856	0.022379	0.24453	0.151588	gi_188521787_gb_ACD59732.1_
0.072024	0.076562	0.10736	0.085315	gi_188521788_gb_ACD59733.1_
0.913093	0.940811	0.850687	0.90153	gi_188521791_gb_ACD59736.1_
0.899348	0.996574	0.718898	0.871607	gi_188521793_gb_ACD59738.1_
0.411686	0.545623	0.444727	0.467345	gi_188522255_gb_ACD60200.1_
0.266198	0.723122	0.299643	0.429654	gi_188522257_gb_ACD60202.1_
0.125868	0.104238	0.269729	0.166612	gi_188522258_gb_ACD60203.1_
0.094833	0.053758	0.082716	0.077102	gi_188522266_gb_ACD60211.1_
0.284754	0.661951	0.156303	0.367669	gi_188522268_gb_ACD60213.1_
0.380129	0.974986	0.517992	0.624369	gi_188522269_gb_ACD60214.1_
0.138955	0.067736	0.129882	0.112191	gi_188522270_gb_ACD60215.1_
0.089317	0.000211	0.185579	0.091702	gi_188522272_gb_ACD60217.1_
0.069461	0.181532	0.07635	0.109114	gi_188522273_gb_ACD60218.1_
0.14517	0.575909	0.156303	0.292461	gi_188522274_gb_ACD60219.1_
0.090052	0.168121	0.141486	0.13322	gi_188522275_gb_ACD60220.1_
0.098234	0.390788	0.069655	0.186226	gi_188522277_gb_ACD60222.1_
0.166866	0.129882	0.1065	0.134416	gi_188522278_gb_ACD60223.1_
0.080468	0.005378	0.120999	0.068948	gi_188522281_gb_ACD60226.1_
0.929367	0.998205	0.852582	0.926718	gi_528897484_gb_AGS47850.1_
0.072628	0.00466	0.077201	0.051496	gi_188522282_gb_ACD60227.1_
0.707857	0.59556	0.648397	0.650605	gi_188522285_gb_ACD60230.1_
0.38509	0.21232	0.523982	0.373797	gi_188522286_gb_ACD60231.1_
0.944065	0.999864	0.865297	0.936409	gi_188522293_gb_ACD60238.1_
0.791666	0.822882	0.842108	0.818885	gi_188522298_gb_ACD60243.1_
0.161109	0.046089	0.189694	0.132297	gi_188522301_gb_ACD60246.1_
0.127862	0.200047	0.112047	0.146652	gi_188522302_gb_ACD60247.1_
0.099302	0.100381	0.09744	0.099041	gi_188522303_gb_ACD60248.1_
0.100652	0.061572	0.095349	0.085858	gi_188522307_gb_ACD60252.1_
0.124881	0.043397	0.177118	0.115132	gi_188522310_gb_ACD60255.1_
0.107072	0.010292	0.130222	0.082529	gi_188522311_gb_ACD60256.1_
0.082489	0.020553	0.152775	0.085272	gi_188522312_gb_ACD60257.1_
0.126529	0.955468	0.317562	0.46652	gi_188522313_gb_ACD60258.1_
0.069461	0.041328	0.120999	0.077263	gi_188522314_gb_ACD60259.1_
0.318863	0.967767	0.066608	0.451079	gi_188522321_gb_ACD60266.1_
0.089317	0.029029	0.187856	0.102067	gi_188522323_gb_ACD60268.1_
0.3028	0.007268	0.352972	0.221013	gi_188522324_gb_ACD60269.1_
0.096129	0.039582	0.161921	0.099211	gi_188522325_gb_ACD60270.1_
0.837263	0.387935	0.812601	0.679266	gi_188522329_gb_ACD60274.1_
0.169806	0.583219	0.10011	0.284378	gi_188522332_gb_ACD60277.1_
0.567093	0.927169	0.649081	0.714448	gi_188522335_gb_ACD60280.1_
0.941805	0.998851	0.869778	0.936811	gi_188522337_gb_ACD60282.1_
0.945163	0.996034	0.893214	0.944804	gi_188522338_gb_ACD60283.1_
0.470783	0.0527	0.558974	0.360819	gi_188522341_gb_ACD60286.1_
0.086669	0.00224	0.100924	0.063278	gi_188522345_gb_ACD60290.1_
0.085021	0.028443	0.144056	0.08584	gi_188522346_gb_ACD60291.1_
0.210818	0.051077	0.258649	0.173515	gi_188522350_gb_ACD60295.1_
0.102018	0.061226	0.114153	0.092466	gi_188522354_gb_ACD60299.1_
0.142583	0.169384	0.125538	0.145835	gi_188522365_gb_ACD60310.1_
0.181979	0.061572	0.147418	0.130323	gi_188522366_gb_ACD60311.1_
0.133658	0.093808	0.10736	0.111609	gi_188522796_gb_ACD60741.1_
0.48051	0.567829	0.59556	0.547966	gi_188522798_gb_ACD60743.1_
0.078493	0.026831	0.142583	0.082636	gi_188522805_gb_ACD60750.1_
0.094319	0.069461	0.147795	0.103858	gi_188522812_gb_ACD60757.1_
0.114762	0.038903	0.134005	0.09589	gi_188522816_gb_ACD60761.1_
0.945163	0.843301	0.911412	0.899959	gi_188522817_gb_ACD60762.1_
0.800433	0.51949	0.92976	0.749894	gi_188522818_gb_ACD60763.1_
0.077629	0.263278	0.168962	0.169956	gi_188522829_gb_ACD60774.1_
0.306613	0.671946	0.371684	0.450081	gi_188522831_gb_ACD60776.1_
0.258649	0.14295	0.307252	0.236284	gi_188522835_gb_ACD60780.1_

gi_188522836_gb_ACD60781.1_	0.165	33	0.114	33	0.119	5	0.08	0.098	N	0.57	SignalP-noTM
gi_188522837_gb_ACD60782.1_	0.254	27	0.178	14	0.406	8	0.324	0.232	N	0.51	SignalP-TM
gi_188522839_gb_ACD60784.1_	0.117	46	0.112	46	0.152	42	0.079	0.097	N	0.57	SignalP-noTM
gi_188522840_gb_ACD60785.1_	0.125	31	0.113	51	0.143	26	0.095	0.105	N	0.57	SignalP-noTM
gi_188522841_gb_ACD60786.1_	0.126	24	0.136	11	0.27	4	0.193	0.163	N	0.57	SignalP-noTM
gi_188522842_gb_ACD60787.1_	0.176	24	0.238	24	0.483	12	0.32	0.268	N	0.51	SignalP-TM
gi_188522843_gb_ACD60788.1_	0.129	6	0.1	32	0.117	10	0.088	0.094	N	0.57	SignalP-noTM
gi_188522844_gb_ACD60789.1_	0.172	56	0.123	56	0.138	5	0.094	0.109	N	0.57	SignalP-noTM
gi_188522845_gb_ACD60790.1_	0.106	49	0.116	33	0.191	5	0.125	0.12	N	0.57	SignalP-noTM
gi_188522854_gb_ACD60799.1_	0.106	40	0.107	29	0.136	22	0.106	0.107	N	0.57	SignalP-noTM
gi_188522858_gb_ACD60803.1_	0.745	27	0.847	27	0.981	23	0.952	0.896	Y	0.57	SignalP-noTM
gi_188522859_gb_ACD60804.1_	0.105	3	0.109	14	0.175	4	0.121	0.115	N	0.57	SignalP-noTM
gi_188522865_gb_ACD60810.1_	0.116	24	0.136	13	0.334	12	0.188	0.161	N	0.57	SignalP-noTM
gi_188522866_gb_ACD60811.1_	0.24	20	0.227	20	0.502	1	0.263	0.244	N	0.57	SignalP-noTM
gi_188522870_gb_ACD60815.1_	0.151	51	0.119	51	0.154	17	0.112	0.116	N	0.57	SignalP-noTM
gi_188522871_gb_ACD60816.1_	0.122	23	0.144	11	0.311	2	0.205	0.172	N	0.57	SignalP-noTM
gi_188522872_gb_ACD60817.1_	0.201	22	0.232	22	0.56	4	0.37	0.283	N	0.51	SignalP-TM
gi_188522874_gb_ACD60819.1_	0.17	35	0.147	35	0.333	34	0.109	0.129	N	0.57	SignalP-noTM
gi_188522875_gb_ACD60820.1_	0.133	21	0.117	11	0.171	5	0.142	0.129	N	0.57	SignalP-noTM
gi_188522876_gb_ACD60821.1_	0.535	23	0.716	23	0.978	11	0.956	0.829	Y	0.57	SignalP-noTM
gi_188522878_gb_ACD60823.1_	0.111	9	0.106	68	0.124	62	0.089	0.098	N	0.57	SignalP-noTM
gi_188522879_gb_ACD60824.1_	0.113	9	0.115	11	0.191	1	0.131	0.123	N	0.57	SignalP-noTM
gi_188522881_gb_ACD60826.1_	0.417	18	0.534	18	0.827	17	0.668	0.597	Y	0.57	SignalP-noTM
gi_188522883_gb_ACD60828.1_	0.133	22	0.158	22	0.292	11	0.194	0.175	N	0.57	SignalP-noTM
gi_188522885_gb_ACD60830.1_	0.17	64	0.167	22	0.35	16	0.266	0.213	N	0.57	SignalP-noTM
gi_188522888_gb_ACD60833.1_	0.137	41	0.121	41	0.139	40	0.098	0.11	N	0.57	SignalP-noTM
gi_188522889_gb_ACD60834.1_	0.161	34	0.12	34	0.164	4	0.108	0.115	N	0.51	SignalP-TM
gi_188522890_gb_ACD60835.1_	0.133	26	0.154	26	0.266	5	0.198	0.175	N	0.57	SignalP-noTM
gi_188522893_gb_ACD60838.1_	0.79	25	0.852	25	0.964	21	0.926	0.886	Y	0.57	SignalP-noTM
gi_188522895_gb_ACD60840.1_	0.117	25	0.151	18	0.238	16	0.202	0.175	N	0.57	SignalP-noTM
gi_188522896_gb_ACD60841.1_	0.105	20	0.101	62	0.133	1	0.095	0.098	N	0.57	SignalP-noTM
gi_188522897_gb_ACD60842.1_	0.167	35	0.167	35	0.368	34	0.165	0.166	N	0.57	SignalP-noTM
gi_188522898_gb_ACD60843.1_	0.111	39	0.111	39	0.124	34	0.096	0.104	N	0.57	SignalP-noTM
gi_188522899_gb_ACD60844.1_	0.12	51	0.145	11	0.28	4	0.214	0.177	N	0.57	SignalP-noTM
gi_188522900_gb_ACD60845.1_	0.109	59	0.127	11	0.202	2	0.163	0.144	N	0.57	SignalP-noTM
gi_188523398_gb_ACD61343.1_	0.163	53	0.162	53	0.254	50	0.131	0.148	N	0.57	SignalP-noTM
gi_188523399_gb_ACD61344.1_	0.125	54	0.125	54	0.19	51	0.119	0.123	N	0.57	SignalP-noTM
gi_188523401_gb_ACD61346.1_	0.134	16	0.114	11	0.196	1	0.124	0.118	N	0.51	SignalP-TM
gi_188523402_gb_ACD61347.1_	0.133	43	0.118	43	0.12	42	0.089	0.105	N	0.57	SignalP-noTM
gi_188523403_gb_ACD61348.1_	0.121	31	0.128	48	0.238	42	0.122	0.125	N	0.57	SignalP-noTM
gi_188523406_gb_ACD61351.1_	0.199	34	0.183	12	0.409	2	0.337	0.24	N	0.51	SignalP-TM
gi_188523407_gb_ACD61352.1_	0.115	34	0.14	11	0.248	2	0.208	0.165	N	0.51	SignalP-TM
gi_188523408_gb_ACD61353.1_	0.126	48	0.125	11	0.228	1	0.154	0.138	N	0.57	SignalP-noTM
gi_188523409_gb_ACD61354.1_	0.182	24	0.383	24	0.956	13	0.859	0.607	Y	0.57	SignalP-noTM
gi_188523413_gb_ACD61358.1_	0.322	23	0.529	23	0.949	8	0.899	0.703	Y	0.57	SignalP-noTM
gi_188523422_gb_ACD61367.1_	0.117	23	0.11	11	0.158	1	0.119	0.114	N	0.57	SignalP-noTM
gi_188523423_gb_ACD61368.1_	0.144	25	0.161	11	0.371	1	0.252	0.204	N	0.57	SignalP-noTM
gi_188523424_gb_ACD61369.1_	0.154	23	0.153	23	0.341	33	0.147	0.151	N	0.57	SignalP-noTM
gi_188523426_gb_ACD61371.1_	0.118	36	0.118	36	0.144	25	0.111	0.115	N	0.57	SignalP-noTM
gi_188523430_gb_ACD61375.1_	0.773	33	0.866	33	0.994	21	0.918	0.89	Y	0.57	SignalP-noTM
gi_188523431_gb_ACD61376.1_	0.116	41	0.16	41	0.414	36	0.178	0.168	N	0.57	SignalP-noTM
gi_188523443_gb_ACD61388.1_	0.117	31	0.136	18	0.201	14	0.165	0.146	N	0.51	SignalP-TM
gi_188523450_gb_ACD61395.1_	0.113	26	0.113	11	0.157	1	0.114	0.113	N	0.57	SignalP-noTM
gi_188523452_gb_ACD61397.1_	0.137	50	0.22	14	0.722	12	0.432	0.32	N	0.57	SignalP-noTM
gi_188523454_gb_ACD61399.1_	0.148	22	0.16	22	0.418	1	0.183	0.17	N	0.57	SignalP-noTM
gi_188523455_gb_ACD61400.1_	0.173	26	0.196	11	0.464	1	0.385	0.285	N	0.57	SignalP-noTM
gi_188523458_gb_ACD61403.1_	0.134	33	0.298	26	0.88	19	0.746	0.509	N	0.57	SignalP-noTM
gi_188523461_gb_ACD61406.1_	0.155	31	0.128	31	0.192	4	0.118	0.124	N	0.57	SignalP-noTM
gi_188523464_gb_ACD61409.1_	0.218	26	0.17	26	0.41	6	0.191	0.18	N	0.57	SignalP-noTM
gi_188523465_gb_ACD61410.1_	0.159	33	0.117	33	0.167	4	0.091	0.105	N	0.57	SignalP-noTM
gi_188523466_gb_ACD61411.1_	0.175	45	0.219	45	0.413	44	0.153	0.188	N	0.57	SignalP-noTM
gi_188523467_gb_ACD61412.1_	0.113	34	0.143	34	0.331	31	0.14	0.142	N	0.51	SignalP-TM
gi_188523468_gb_ACD61413.1_	0.33	54	0.303	33	0.866	23	0.547	0.418	N	0.57	SignalP-noTM
gi_188523476_gb_ACD61421.1_	0.185	20	0.204	12	0.454	2	0.321	0.247	N	0.51	SignalP-TM
gi_188523478_gb_ACD61423.1_	0.124	42	0.12	11	0.263	1	0.125	0.122	N	0.57	SignalP-noTM
gi_188523479_gb_ACD61424.1_	0.111	18	0.116	11	0.193	2	0.129	0.12	N	0.51	SignalP-TM
gi_188523480_gb_ACD61425.1_	0.297	43	0.235	43	0.398	41	0.113	0.178	N	0.57	SignalP-noTM
gi_188523481_gb_ACD61426.1_	0.205	23	0.166	23	0.253	19	0.131	0.15	N	0.57	SignalP-noTM
gi_188523482_gb_ACD61427.1_	0.177	24	0.185	24	0.341	7	0.241	0.206	N	0.51	SignalP-TM
gi_188523485_gb_ACD61430.1_	0.133	22	0.157	22	0.289	11	0.192	0.173	N	0.57	SignalP-noTM
gi_188523486_gb_ACD61431.1_	0.117	34	0.285	12	0.887	4	0.831	0.541	N	0.57	SignalP-noTM
gi_188523490_gb_ACD61435.1_	0.122	35	0.13	11	0.187	3	0.169	0.149	N	0.57	SignalP-noTM
gi_188523493_gb_ACD61438.1_	0.105	45	0.105	51	0.184	42	0.087	0.096	N	0.57	SignalP-noTM
gi_188523495_gb_ACD61440.1_	0.112	42	0.118	11	0.185	5	0.149	0.129	N	0.51	SignalP-TM
gi_188523497_gb_ACD61442.1_	0.313	18	0.298	18	0.493	14	0.282	0.291	N	0.57	SignalP-noTM
gi_188523498_gb_ACD61443.1_	0.297	27	0.267	27	0.389	18	0.284	0.275	N	0.57	SignalP-noTM
gi_188523499_gb_ACD61444.1_	0.109	45	0.167	11	0.331	3	0.274	0.217	N	0.57	SignalP-noTM
gi_188523500_gb_ACD61445.1_	0.128	27	0.162	13	0.373	11	0.262	0.209	N	0.57	SignalP-noTM

0.178873	0.980848	0.064405	0.408042	gi_188522836_gb_ACD60781.1_
0.15046	0.054526	0.148552	0.117846	gi_188522837_gb_ACD60782.1_
0.107936	0.076562	0.102569	0.095689	gi_188522839_gb_ACD60784.1_
0.134703	0.064949	0.13717	0.112274	gi_188522840_gb_ACD60785.1_
0.181979	0.82977	0.123251	0.378333	gi_188522841_gb_ACD60786.1_
0.119413	0.068498	0.191545	0.126485	gi_188522842_gb_ACD60787.1_
0.431435	0.010231	0.485004	0.30889	gi_188522843_gb_ACD60788.1_
0.082944	0.001149	0.114153	0.066082	gi_188522844_gb_ACD60789.1_
0.576641	0.985356	0.859965	0.807321	gi_188522845_gb_ACD60790.1_
0.805182	0.998364	0.768525	0.857357	gi_188522854_gb_ACD60799.1_
0.949502	0.922585	0.89989	0.923992	gi_188522858_gb_ACD60803.1_
0.070045	0.00729	0.096914	0.058083	gi_188522859_gb_ACD60804.1_
0.082716	0.057704	0.142583	0.094334	gi_188522865_gb_ACD60810.1_
0.195289	0.21032	0.17581	0.193806	gi_188522866_gb_ACD60811.1_
0.082944	0.002657	0.113548	0.066383	gi_188522870_gb_ACD60815.1_
0.133658	0.038791	0.161921	0.111457	gi_188522871_gb_ACD60816.1_
0.137881	0.136815	0.275678	0.183458	gi_188522872_gb_ACD60817.1_
0.370983	0.950216	0.185126	0.502108	gi_188522874_gb_ACD60819.1_
0.16645	0.9512	0.10147	0.406373	gi_188522875_gb_ACD60820.1_
0.088588	0.140035	0.16645	0.131691	gi_188522876_gb_ACD60821.1_
0.195761	0.828921	0.115679	0.38012	gi_188522878_gb_ACD60823.1_
0.673927	0.380129	0.796571	0.616876	gi_188522879_gb_ACD60824.1_
0.891775	0.867381	0.875119	0.878092	gi_188522881_gb_ACD60826.1_
0.840506	0.804711	0.85483	0.833349	gi_188522883_gb_ACD60828.1_
0.189694	0.139314	0.237398	0.188802	gi_188522885_gb_ACD60830.1_
0.066051	0.009728	0.083631	0.053137	gi_188522888_gb_ACD60833.1_
0.129544	0.092038	0.197182	0.139588	gi_188522889_gb_ACD60834.1_
0.520988	0.854458	0.6972	0.690882	gi_188522890_gb_ACD60835.1_
0.949646	0.968324	0.88153	0.933167	gi_188522893_gb_ACD60838.1_
0.119413	0.035571	0.131587	0.095524	gi_188522895_gb_ACD60840.1_
0.054992	0.022118	0.095349	0.057486	gi_188522896_gb_ACD60841.1_
0.375194	0.973941	0.188314	0.512483	gi_188522897_gb_ACD60842.1_
0.312383	0.984647	0.127194	0.474741	gi_188522898_gb_ACD60843.1_
0.259802	0.885543	0.156303	0.433883	gi_188522899_gb_ACD60844.1_
0.134703	0.038791	0.10736	0.093618	gi_188522900_gb_ACD60845.1_
0.317562	0.144798	0.54711	0.33649	gi_188523398_gb_ACD61343.1_
0.258649	0.336038	0.150844	0.24851	gi_188523399_gb_ACD61344.1_
0.132619	0.300273	0.229878	0.220923	gi_188523401_gb_ACD61346.1_
0.066051	0.032515	0.115067	0.071211	gi_188523402_gb_ACD61347.1_
0.245641	0.058195	0.304703	0.202846	gi_188523403_gb_ACD61348.1_
0.955976	0.998844	0.906447	0.953756	gi_188523406_gb_ACD61351.1_
0.129882	0.033472	0.201974	0.121776	gi_188523407_gb_ACD61352.1_
0.355718	0.981403	0.089806	0.475642	gi_188523408_gb_ACD61353.1_
0.292763	0.088105	0.348872	0.243247	gi_188523409_gb_ACD61354.1_
0.780572	0.581029	0.743073	0.701558	gi_188523413_gb_ACD61358.1_
0.191545	0.02318	0.285978	0.166901	gi_188523422_gb_ACD61367.1_
0.49625	0.016529	0.470036	0.327605	gi_188523423_gb_ACD61368.1_
0.086669	0.090545	0.07871	0.085308	gi_188523424_gb_ACD61369.1_
0.093046	0.00533	0.095091	0.064489	gi_188523426_gb_ACD61371.1_
0.881843	0.619164	0.773819	0.758275	gi_188523430_gb_ACD61375.1_
0.114153	0.053302	0.163557	0.110337	gi_188523431_gb_ACD61376.1_
0.061572	0.174942	0.120681	0.119065	gi_188523443_gb_ACD61388.1_
0.94715	0.99974	0.867036	0.937975	gi_188523450_gb_ACD61395.1_
0.915212	0.998721	0.884933	0.932955	gi_188523452_gb_ACD61397.1_
0.225133	0.768525	0.201974	0.398544	gi_188523454_gb_ACD61399.1_
0.218403	0.068306	0.202943	0.163217	gi_188523455_gb_ACD61400.1_
0.956478	0.992903	0.919087	0.956156	gi_188523458_gb_ACD61403.1_
0.398672	0.038568	0.432171	0.289804	gi_188523461_gb_ACD61406.1_
0.951892	0.999562	0.885847	0.945767	gi_188523464_gb_ACD61409.1_
0.114762	0.057704	0.100924	0.09113	gi_188523465_gb_ACD61410.1_
0.152387	0.031129	0.1603	0.114605	gi_188523466_gb_ACD61411.1_
0.090298	0.044404	0.095091	0.076598	gi_188523467_gb_ACD61412.1_
0.949789	0.989859	0.933764	0.957804	gi_188523468_gb_ACD61413.1_
0.067926	0.015172	0.171079	0.084726	gi_188523476_gb_ACD61421.1_
0.071425	0.03131	0.098767	0.067167	gi_188523478_gb_ACD61423.1_
0.085255	0.13193	0.149313	0.122166	gi_188523479_gb_ACD61424.1_
0.095609	0.05285	0.094063	0.080841	gi_188523480_gb_ACD61425.1_
0.089074	0.083402	0.177555	0.116677	gi_188523481_gb_ACD61426.1_
0.58904	0.986319	0.777473	0.784277	gi_188523482_gb_ACD61427.1_
0.832716	0.393649	0.840506	0.688957	gi_188523485_gb_ACD61430.1_
0.260957	0.463316	0.255213	0.326495	gi_188523486_gb_ACD61431.1_
0.912376	0.986074	0.76959	0.889347	gi_188523490_gb_ACD61435.1_
0.148932	0.047021	0.153944	0.116632	gi_188523493_gb_ACD61438.1_
0.224088	0.185579	0.232009	0.213892	gi_188523495_gb_ACD61440.1_
0.73614	0.98505	0.735557	0.818916	gi_188523497_gb_ACD61442.1_
0.139674	0.061745	0.17581	0.125743	gi_188523498_gb_ACD61443.1_
0.172787	0.117222	0.136815	0.142275	gi_188523499_gb_ACD61444.1_
0.420432	0.538921	0.451404	0.470252	gi_188523500_gb_ACD61445.1_

gi_188523501_gb_ACD61446.1_	0.115	19	0.097	44	0.103	36	0.077	0.087	N	0.57	SignalP-noTM
gi_188523503_gb_ACD61448.1_	0.122	27	0.117	27	0.164	26	0.107	0.112	N	0.57	SignalP-noTM
gi_188523504_gb_ACD61449.1_	0.103	27	0.139	40	0.253	36	0.139	0.139	N	0.57	SignalP-noTM
gi_188523505_gb_ACD61450.1_	0.196	41	0.154	41	0.193	37	0.109	0.133	N	0.57	SignalP-noTM
gi_188523507_gb_ACD61452.1_	0.236	17	0.442	17	0.937	1	0.845	0.631	Y	0.57	SignalP-noTM
gi_188523513_gb_ACD61458.1_	0.115	25	0.102	67	0.147	5	0.09	0.096	N	0.57	SignalP-noTM
gi_188523516_gb_ACD61461.1_	0.406	58	0.264	58	0.32	52	0.195	0.239	N	0.51	SignalP-TM
gi_188523518_gb_ACD61463.1_	0.131	43	0.193	11	0.431	9	0.377	0.279	N	0.57	SignalP-noTM
gi_188523519_gb_ACD61464.1_	0.349	41	0.326	41	0.594	34	0.234	0.292	N	0.51	SignalP-TM
gi_188523522_gb_ACD61467.1_	0.172	19	0.177	19	0.242	3	0.197	0.187	N	0.57	SignalP-noTM
gi_188523523_gb_ACD61468.1_	0.136	25	0.131	12	0.232	4	0.155	0.142	N	0.57	SignalP-noTM
gi_188523527_gb_ACD61472.1_	0.105	20	0.102	62	0.134	1	0.091	0.097	N	0.57	SignalP-noTM
gi_188523530_gb_ACD61475.1_	0.11	17	0.103	59	0.116	47	0.089	0.097	N	0.57	SignalP-noTM
gi_188523531_gb_ACD61476.1_	0.125	29	0.149	29	0.345	1	0.183	0.165	N	0.57	SignalP-noTM
gi_188523533_gb_ACD61478.1_	0.124	33	0.122	11	0.223	3	0.156	0.138	N	0.57	SignalP-noTM
gi_188523535_gb_ACD61480.1_	0.124	58	0.119	11	0.211	3	0.144	0.13	N	0.57	SignalP-noTM
gi_188523537_gb_ACD61482.1_	0.137	6	0.123	53	0.196	1	0.124	0.123	N	0.57	SignalP-noTM
gi_188523538_gb_ACD61483.1_	0.113	23	0.134	12	0.217	8	0.188	0.154	N	0.51	SignalP-TM
gi_188523539_gb_ACD61484.1_	0.234	28	0.257	28	0.365	23	0.274	0.263	N	0.51	SignalP-TM
gi_188523540_gb_ACD61485.1_	0.478	25	0.672	25	0.987	17	0.951	0.803	Y	0.57	SignalP-noTM
gi_188523541_gb_ACD61486.1_	0.277	29	0.198	29	0.281	1	0.164	0.182	N	0.57	SignalP-noTM
gi_188523542_gb_ACD61487.1_	0.269	23	0.504	23	0.978	19	0.939	0.708	Y	0.57	SignalP-noTM
gi_188523547_gb_ACD61492.1_	0.106	26	0.14	11	0.331	1	0.172	0.155	N	0.57	SignalP-noTM
gi_188523549_gb_ACD61494.1_	0.104	38	0.163	19	0.345	18	0.24	0.199	N	0.57	SignalP-noTM
gi_188523551_gb_ACD61496.1_	0.115	22	0.145	13	0.273	9	0.21	0.175	N	0.57	SignalP-noTM
gi_188523552_gb_ACD61497.1_	0.121	36	0.13	20	0.213	19	0.146	0.138	N	0.57	SignalP-noTM
gi_188523555_gb_ACD61500.1_	0.193	20	0.242	11	0.752	3	0.575	0.398	N	0.57	SignalP-noTM
gi_188523556_gb_ACD61501.1_	0.499	32	0.262	32	0.301	5	0.198	0.239	N	0.51	SignalP-TM
gi_188523557_gb_ACD61502.1_	0.124	56	0.158	12	0.301	10	0.244	0.19	N	0.51	SignalP-TM
gi_188523562_gb_ACD61507.1_	0.133	18	0.12	18	0.212	32	0.11	0.115	N	0.57	SignalP-noTM
gi_188523572_gb_ACD61517.1_	0.145	12	0.148	12	0.238	6	0.149	0.149	N	0.57	SignalP-noTM
gi_188523575_gb_ACD61520.1_	0.116	53	0.114	53	0.136	45	0.098	0.106	N	0.57	SignalP-noTM
gi_188523576_gb_ACD61521.1_	0.41	16	0.557	16	0.886	11	0.738	0.642	Y	0.57	SignalP-noTM
gi_188523577_gb_ACD61522.1_	0.212	26	0.151	26	0.253	1	0.133	0.143	N	0.57	SignalP-noTM
gi_188523578_gb_ACD61523.1_	0.117	25	0.152	18	0.238	16	0.202	0.175	N	0.57	SignalP-noTM
gi_188523583_gb_ACD61528.1_	0.133	35	0.118	40	0.144	34	0.1	0.109	N	0.57	SignalP-noTM
gi_188523584_gb_ACD61529.1_	0.142	48	0.112	48	0.151	3	0.1	0.106	N	0.57	SignalP-noTM
gi_188523586_gb_ACD61531.1_	0.122	45	0.133	11	0.264	1	0.168	0.15	N	0.57	SignalP-noTM
gi_188523590_gb_ACD61535.1_	0.116	53	0.114	53	0.136	45	0.098	0.106	N	0.57	SignalP-noTM
gi_188523596_gb_ACD61541.1_	0.339	26	0.566	26	0.99	17	0.936	0.74	Y	0.57	SignalP-noTM
gi_188523597_gb_ACD61542.1_	0.17	48	0.163	24	0.379	1	0.222	0.191	N	0.57	SignalP-noTM
gi_188523601_gb_ACD61546.1_	0.123	44	0.151	44	0.241	43	0.164	0.157	N	0.57	SignalP-noTM
gi_188523603_gb_ACD61548.1_	0.159	22	0.172	22	0.304	26	0.169	0.171	N	0.57	SignalP-noTM
gi_188523609_gb_ACD61554.1_	0.127	48	0.145	31	0.262	3	0.181	0.162	N	0.57	SignalP-noTM
gi_188523610_gb_ACD61555.1_	0.479	21	0.617	21	0.949	6	0.843	0.723	Y	0.57	SignalP-noTM
gi_188523615_gb_ACD61560.1_	0.736	30	0.735	30	0.91	9	0.789	0.76	Y	0.57	SignalP-noTM
gi_188523616_gb_ACD61561.1_	0.108	34	0.121	34	0.191	31	0.122	0.121	N	0.57	SignalP-noTM
gi_188523617_gb_ACD61562.1_	0.114	21	0.11	21	0.148	20	0.092	0.104	N	0.51	SignalP-TM
gi_188523618_gb_ACD61563.1_	0.195	10	0.146	20	0.23	9	0.141	0.144	N	0.51	SignalP-TM
gi_188523619_gb_ACD61564.1_	0.105	17	0.1	43	0.126	32	0.077	0.089	N	0.57	SignalP-noTM
gi_188523621_gb_ACD61566.1_	0.249	27	0.214	27	0.374	7	0.249	0.23	N	0.57	SignalP-noTM
gi_188523622_gb_ACD61567.1_	0.114	31	0.121	11	0.172	50	0.146	0.133	N	0.57	SignalP-noTM
gi_188523624_gb_ACD61569.1_	0.155	17	0.302	17	0.754	7	0.591	0.438	N	0.57	SignalP-noTM
gi_188523625_gb_ACD61570.1_	0.136	51	0.119	11	0.247	20	0.131	0.125	N	0.57	SignalP-noTM
gi_188523628_gb_ACD61573.1_	0.185	29	0.159	50	0.296	45	0.13	0.145	N	0.57	SignalP-noTM
gi_188523630_gb_ACD61575.1_	0.327	20	0.257	20	0.394	2	0.245	0.253	N	0.51	SignalP-TM
gi_188523631_gb_ACD61576.1_	0.117	50	0.161	16	0.369	8	0.233	0.195	N	0.57	SignalP-noTM
gi_188523632_gb_ACD61577.1_	0.107	28	0.157	11	0.393	2	0.245	0.198	N	0.57	SignalP-noTM
gi_188523636_gb_ACD61581.1_	0.374	27	0.361	27	0.603	26	0.288	0.327	N	0.57	SignalP-noTM
gi_188523637_gb_ACD61582.1_	0.131	22	0.113	35	0.131	34	0.084	0.102	N	0.51	SignalP-TM
gi_188523639_gb_ACD61584.1_	0.125	26	0.116	41	0.172	30	0.101	0.111	N	0.51	SignalP-TM
gi_188523640_gb_ACD61585.1_	0.117	67	0.105	52	0.142	31	0.084	0.095	N	0.57	SignalP-noTM
gi_188523644_gb_ACD61589.1_	0.145	19	0.173	44	0.395	33	0.189	0.181	N	0.57	SignalP-noTM
gi_188523645_gb_ACD61590.1_	0.106	46	0.107	11	0.16	1	0.113	0.109	N	0.51	SignalP-TM
gi_188523646_gb_ACD61591.1_	0.196	18	0.412	18	0.963	7	0.872	0.629	Y	0.57	SignalP-noTM
gi_188523647_gb_ACD61592.1_	0.115	30	0.113	60	0.171	48	0.104	0.108	N	0.57	SignalP-noTM
gi_188523648_gb_ACD61593.1_	0.116	22	0.123	22	0.19	1	0.13	0.127	N	0.57	SignalP-noTM
gi_188523650_gb_ACD61595.1_	0.12	35	0.151	35	0.284	24	0.179	0.164	N	0.57	SignalP-noTM
gi_188523653_gb_ACD61598.1_	0.204	23	0.191	23	0.226	19	0.182	0.187	N	0.51	SignalP-TM
gi_188523654_gb_ACD61599.1_	0.131	22	0.126	22	0.149	2	0.127	0.126	N	0.57	SignalP-noTM
gi_188523655_gb_ACD61600.1_	0.142	42	0.105	62	0.116	57	0.075	0.091	N	0.57	SignalP-noTM
gi_188523658_gb_ACD61603.1_	0.122	33	0.122	33	0.155	29	0.122	0.122	N	0.57	SignalP-noTM
gi_188523659_gb_ACD61604.1_	0.186	17	0.385	17	0.882	12	0.798	0.579	Y	0.57	SignalP-noTM
gi_188523662_gb_ACD61607.1_	0.111	27	0.123	11	0.202	5	0.163	0.138	N	0.51	SignalP-TM
gi_188523670_gb_ACD61615.1_	0.187	44	0.148	44	0.15	41	0.104	0.127	N	0.57	SignalP-noTM
gi_188523671_gb_ACD61616.1_	0.313	25	0.153	25	0.111	52	0.067	0.113	N	0.57	SignalP-noTM
gi_188523672_gb_ACD61617.1_	0.321	40	0.259	40	0.321	14	0.22	0.245	N	0.51	SignalP-TM
gi_188523676_gb_ACD61621.1_	0.113	23	0.129	12	0.284	5	0.171	0.149	N	0.57	SignalP-noTM

0.13193	0.352972	0.096129	0.193677	gi_188523501_gb_ACD61446.1_
0.186943	0.942784	0.279287	0.469671	gi_188523503_gb_ACD61448.1_
0.440286	0.984872	0.539666	0.654941	gi_188523504_gb_ACD61449.1_
0.093808	0.009031	0.123901	0.07558	gi_188523505_gb_ACD61450.1_
0.805182	0.818468	0.78768	0.803777	gi_188523507_gb_ACD61452.1_
0.075299	0.028195	0.114457	0.07265	gi_188523513_gb_ACD61458.1_
0.120999	0.085959	0.152387	0.119782	gi_188523516_gb_ACD61461.1_
0.378011	0.883706	0.50675	0.589489	gi_188523518_gb_ACD61463.1_
0.77539	0.781085	0.773819	0.776765	gi_188523519_gb_ACD61464.1_
0.105931	0.013762	0.177118	0.098937	gi_188523522_gb_ACD61467.1_
0.939118	0.999767	0.873471	0.937452	gi_188523523_gb_ACD61468.1_
0.048246	0.022776	0.105647	0.05889	gi_188523527_gb_ACD61472.1_
0.088588	0.02098	0.117533	0.0757	gi_188523530_gb_ACD61475.1_
0.827641	0.913568	0.867726	0.869645	gi_188523531_gb_ACD61476.1_
0.441026	0.838891	0.611352	0.630423	gi_188523533_gb_ACD61478.1_
0.168541	0.024507	0.228289	0.140446	gi_188523535_gb_ACD61480.1_
0.087864	0.085959	0.105081	0.092968	gi_188523537_gb_ACD61482.1_
0.126529	0.344795	0.158691	0.210005	gi_188523538_gb_ACD61483.1_
0.936672	0.999524	0.888251	0.941482	gi_188523539_gb_ACD61484.1_
0.78262	0.631812	0.843301	0.752578	gi_188523540_gb_ACD61485.1_
0.16645	0.015307	0.131244	0.104334	gi_188523541_gb_ACD61486.1_
0.953514	0.991155	0.909948	0.951539	gi_188523542_gb_ACD61487.1_
0.189233	0.040973	0.149694	0.126633	gi_188523547_gb_ACD61492.1_
0.752129	0.954826	0.427025	0.711327	gi_188523549_gb_ACD61494.1_
0.111452	0.14629	0.115373	0.124372	gi_188523551_gb_ACD61496.1_
0.344117	0.713409	0.470036	0.509187	gi_188523552_gb_ACD61497.1_
0.299643	0.852582	0.136461	0.429562	gi_188523555_gb_ACD61500.1_
0.128869	0.062797	0.164792	0.118819	gi_188523556_gb_ACD61501.1_
0.102845	0.007268	0.140397	0.083503	gi_188523557_gb_ACD61502.1_
0.342089	0.922799	0.085959	0.450282	gi_188523562_gb_ACD61507.1_
0.159896	0.15046	0.213325	0.17456	gi_188523572_gb_ACD61517.1_
0.142583	0.038346	0.108806	0.096578	gi_188523575_gb_ACD61520.1_
0.711566	0.950216	0.79462	0.818801	gi_188523576_gb_ACD61521.1_
0.943588	0.999723	0.880902	0.941404	gi_188523577_gb_ACD61522.1_
0.124553	0.103123	0.11385	0.113842	gi_188523578_gb_ACD61523.1_
0.189694	0.203915	0.21738	0.203663	gi_188523583_gb_ACD61528.1_
0.177118	0.050931	0.125868	0.117972	gi_188523584_gb_ACD61529.1_
0.413867	0.748758	0.572975	0.578533	gi_188523586_gb_ACD61531.1_
0.129882	0.049784	0.1065	0.095389	gi_188523590_gb_ACD61535.1_
0.954436	0.995557	0.904391	0.951461	gi_188523596_gb_ACD61541.1_
0.687617	0.979143	0.769058	0.811939	gi_188523597_gb_ACD61542.1_
0.104518	0.084788	0.113247	0.100851	gi_188523601_gb_ACD61546.1_
0.928972	0.125868	0.914041	0.656294	gi_188523603_gb_ACD61548.1_
0.14295	0.016431	0.282316	0.147232	gi_188523609_gb_ACD61554.1_
0.734388	0.917056	0.701615	0.784353	gi_188523610_gb_ACD61555.1_
0.926559	0.867726	0.909948	0.901411	gi_188523615_gb_ACD61560.1_
0.904132	0.910926	0.859241	0.891433	gi_188523616_gb_ACD61561.1_
0.185579	0.303434	0.208334	0.232449	gi_188523617_gb_ACD61562.1_
0.083862	0.053151	0.204403	0.113805	gi_188523618_gb_ACD61563.1_
0.954436	0.985138	0.906192	0.948589	gi_188523619_gb_ACD61564.1_
0.088105	0.135755	0.087864	0.103908	gi_188523621_gb_ACD61566.1_
0.078928	0.02465	0.125868	0.076482	gi_188523622_gb_ACD61567.1_
0.116603	0.07806	0.237941	0.144201	gi_188523624_gb_ACD61569.1_
0.136461	0.274482	0.130562	0.180502	gi_188523625_gb_ACD61570.1_
0.095609	0.050642	0.118784	0.088345	gi_188523628_gb_ACD61573.1_
0.181532	0.257501	0.256355	0.231796	gi_188523630_gb_ACD61575.1_
0.359163	0.988062	0.34074	0.562655	gi_188523631_gb_ACD61576.1_
0.934869	0.976478	0.730862	0.880736	gi_188523632_gb_ACD61577.1_
0.147041	0.039128	0.150077	0.112082	gi_188523636_gb_ACD61581.1_
0.155907	0.05869	0.156699	0.123765	gi_188523637_gb_ACD61582.1_
0.13717	0.064044	0.1603	0.120505	gi_188523639_gb_ACD61584.1_
0.140397	0.133658	0.122927	0.132327	gi_188523640_gb_ACD61585.1_
0.265027	0.037148	0.236855	0.179677	gi_188523644_gb_ACD61589.1_
0.153944	0.060882	0.163147	0.125991	gi_188523645_gb_ACD61590.1_
0.830616	0.315614	0.850687	0.665639	gi_188523646_gb_ACD61591.1_
0.611352	0.20587	0.790675	0.535966	gi_188523647_gb_ACD61592.1_
0.184673	0.108515	0.206361	0.166516	gi_188523648_gb_ACD61593.1_
0.128532	0.004702	0.167284	0.100173	gi_188518734_gb_ACD56679.1_
0.185579	0.148552	0.154335	0.162822	gi_188518735_gb_ACD56680.1_
0.127194	0.06003	0.132274	0.106499	gi_188518736_gb_ACD56681.1_
0.174942	0.0136	0.220458	0.136333	gi_188518737_gb_ACD56682.1_
0.113548	0.008484	0.183772	0.101935	gi_188518738_gb_ACD56683.1_
0.188773	0.004523	0.314967	0.169421	gi_188518741_gb_ACD56686.1_
0.135755	0.122604	0.111452	0.12327	gi_188518742_gb_ACD56687.1_
0.125538	0.180643	0.119098	0.14176	gi_188518743_gb_ACD56688.1_
0.081361	0.024221	0.099034	0.068205	gi_188518744_gb_ACD56689.1_
0.176681	0.043898	0.1603	0.12696	gi_188518745_gb_ACD56690.1_
0.065681	0.000382	0.120999	0.062354	gi_188518746_gb_ACD56691.1_

gi_188523678_gb_ACD61623.1_	0.112	38	0.106	38	0.172	34	0.097	0.102	N	0.57	SignalP-noTM
gi_188523679_gb_ACD61624.1_	0.356	23	0.215	23	0.351	2	0.187	0.202	N	0.57	SignalP-noTM
gi_188523680_gb_ACD61625.1_	0.19	49	0.132	49	0.178	12	0.114	0.124	N	0.57	SignalP-noTM
gi_188523690_gb_ACD61635.1_	0.118	32	0.102	32	0.114	1	0.091	0.097	N	0.57	SignalP-noTM
gi_188523702_gb_ACD61647.1_	0.18	36	0.15	36	0.169	4	0.099	0.131	N	0.51	SignalP-TM
gi_188523703_gb_ACD61648.1_	0.175	24	0.227	11	0.606	5	0.495	0.326	N	0.51	SignalP-TM
gi_188523705_gb_ACD61650.1_	0.152	23	0.154	11	0.349	8	0.237	0.193	N	0.57	SignalP-noTM
gi_188518734_gb_ACD56679.1_	0.117	30	0.15	11	0.341	1	0.21	0.178	N	0.57	SignalP-noTM
gi_188518735_gb_ACD56680.1_	0.29	39	0.213	39	0.302	37	0.098	0.171	N	0.51	SignalP-TM
gi_188518736_gb_ACD56681.1_	0.113	6	0.086	11	0.115	7	0.08	0.084	N	0.51	SignalP-TM
gi_188518737_gb_ACD56682.1_	0.123	41	0.158	48	0.307	44	0.13	0.145	N	0.57	SignalP-noTM
gi_188518738_gb_ACD56683.1_	0.118	24	0.117	24	0.141	20	0.105	0.111	N	0.57	SignalP-noTM
gi_188518741_gb_ACD56686.1_	0.247	18	0.301	18	0.448	14	0.369	0.326	N	0.51	SignalP-TM
gi_188518742_gb_ACD56687.1_	0.112	48	0.112	14	0.2	6	0.125	0.118	N	0.57	SignalP-noTM
gi_188518743_gb_ACD56688.1_	0.21	32	0.162	32	0.216	5	0.126	0.145	N	0.57	SignalP-noTM
gi_188518744_gb_ACD56689.1_	0.196	48	0.129	29	0.201	23	0.117	0.125	N	0.51	SignalP-TM
gi_188518745_gb_ACD56690.1_	0.334	31	0.174	31	0.23	42	0.101	0.14	N	0.57	SignalP-noTM
gi_188518746_gb_ACD56691.1_	0.135	32	0.11	32	0.103	13	0.084	0.098	N	0.57	SignalP-noTM
gi_188518748_gb_ACD56693.1_	0.105	31	0.152	11	0.279	5	0.232	0.189	N	0.57	SignalP-noTM
gi_188518749_gb_ACD56694.1_	0.156	19	0.194	19	0.514	1	0.299	0.243	N	0.57	SignalP-noTM
gi_188518750_gb_ACD56695.1_	0.135	40	0.192	11	0.583	1	0.342	0.263	N	0.57	SignalP-noTM
gi_188518753_gb_ACD56698.1_	0.105	50	0.135	16	0.26	8	0.17	0.151	N	0.57	SignalP-noTM
gi_188518754_gb_ACD56699.1_	0.136	65	0.184	20	0.467	2	0.277	0.227	N	0.57	SignalP-noTM
gi_188518755_gb_ACD56700.1_	0.152	23	0.143	23	0.265	22	0.117	0.131	N	0.57	SignalP-noTM
gi_188518756_gb_ACD56701.1_	0.113	28	0.111	28	0.125	8	0.098	0.105	N	0.57	SignalP-noTM
gi_188518758_gb_ACD56703.1_	0.144	18	0.119	11	0.186	1	0.138	0.126	N	0.51	SignalP-TM
gi_188518759_gb_ACD56704.1_	0.105	45	0.113	29	0.188	3	0.128	0.119	N	0.51	SignalP-TM
gi_188518760_gb_ACD56705.1_	0.225	24	0.25	24	0.398	19	0.264	0.257	N	0.57	SignalP-noTM
gi_188518761_gb_ACD56706.1_	0.246	39	0.144	39	0.141	6	0.096	0.121	N	0.57	SignalP-noTM
gi_188518762_gb_ACD56707.1_	0.104	44	0.121	17	0.193	11	0.139	0.13	N	0.57	SignalP-noTM
gi_188518763_gb_ACD56708.1_	0.113	24	0.101	53	0.121	42	0.081	0.092	N	0.57	SignalP-noTM
gi_188518764_gb_ACD56709.1_	0.107	41	0.124	14	0.184	10	0.157	0.139	N	0.57	SignalP-noTM
gi_188518769_gb_ACD56714.1_	0.11	31	0.155	11	0.324	2	0.238	0.194	N	0.57	SignalP-noTM
gi_188518770_gb_ACD56715.1_	0.112	36	0.14	12	0.28	3	0.193	0.165	N	0.57	SignalP-noTM
gi_188518774_gb_ACD56719.1_	0.106	52	0.128	18	0.225	10	0.144	0.135	N	0.57	SignalP-noTM
gi_188518777_gb_ACD56722.1_	0.12	34	0.174	18	0.358	10	0.286	0.227	N	0.57	SignalP-noTM
gi_188518778_gb_ACD56723.1_	0.161	23	0.133	23	0.15	43	0.106	0.12	N	0.57	SignalP-noTM
gi_188518783_gb_ACD56728.1_	0.134	29	0.117	29	0.154	27	0.098	0.108	N	0.57	SignalP-noTM
gi_188518784_gb_ACD56729.1_	0.102	6	0.118	34	0.186	28	0.124	0.121	N	0.57	SignalP-noTM
gi_188518785_gb_ACD56730.1_	0.118	28	0.107	28	0.135	1	0.093	0.1	N	0.57	SignalP-noTM
gi_188518786_gb_ACD56731.1_	0.137	69	0.146	11	0.28	1	0.206	0.174	N	0.57	SignalP-noTM
gi_188518791_gb_ACD56736.1_	0.117	25	0.099	57	0.109	24	0.079	0.09	N	0.57	SignalP-noTM
gi_188518792_gb_ACD56737.1_	0.119	43	0.102	43	0.129	10	0.092	0.097	N	0.57	SignalP-noTM
gi_188518793_gb_ACD56738.1_	0.168	22	0.123	22	0.122	4	0.095	0.11	N	0.57	SignalP-noTM
gi_188518794_gb_ACD56739.1_	0.159	27	0.173	27	0.27	66	0.183	0.177	N	0.51	SignalP-TM
gi_188518795_gb_ACD56740.1_	0.111	25	0.113	11	0.204	1	0.119	0.116	N	0.57	SignalP-noTM
gi_188518796_gb_ACD56741.1_	0.194	22	0.248	22	0.4	1	0.3	0.267	N	0.51	SignalP-TM
gi_188518797_gb_ACD56742.1_	0.232	26	0.172	26	0.265	3	0.151	0.164	N	0.51	SignalP-TM
gi_188518798_gb_ACD56743.1_	0.229	45	0.142	45	0.243	48	0.084	0.121	N	0.51	SignalP-TM
gi_188518800_gb_ACD56745.1_	0.118	23	0.113	23	0.182	2	0.113	0.113	N	0.51	SignalP-TM
gi_188518801_gb_ACD56746.1_	0.115	48	0.112	48	0.138	44	0.094	0.105	N	0.51	SignalP-TM
gi_188518809_gb_ACD56754.1_	0.146	32	0.188	15	0.531	4	0.341	0.26	N	0.57	SignalP-noTM
gi_188518812_gb_ACD56757.1_	0.172	59	0.145	59	0.144	49	0.108	0.128	N	0.57	SignalP-noTM
gi_188518813_gb_ACD56758.1_	0.149	47	0.145	11	0.355	1	0.186	0.164	N	0.57	SignalP-noTM
gi_188518815_gb_ACD56760.1_	0.117	20	0.12	20	0.163	1	0.121	0.121	N	0.57	SignalP-noTM
gi_188518817_gb_ACD56762.1_	0.14	17	0.204	17	0.434	9	0.279	0.239	N	0.57	SignalP-noTM
gi_188518818_gb_ACD56763.1_	0.113	20	0.133	11	0.289	1	0.16	0.146	N	0.57	SignalP-noTM
gi_188518819_gb_ACD56764.1_	0.125	67	0.149	58	0.33	51	0.137	0.144	N	0.57	SignalP-noTM
gi_188518820_gb_ACD56765.1_	0.122	60	0.133	12	0.25	3	0.175	0.153	N	0.57	SignalP-noTM
gi_188518821_gb_ACD56766.1_	0.112	65	0.102	65	0.118	32	0.092	0.098	N	0.57	SignalP-noTM
gi_188518823_gb_ACD56768.1_	0.171	20	0.145	22	0.352	1	0.149	0.147	N	0.51	SignalP-TM
gi_188518826_gb_ACD56771.1_	0.162	48	0.204	48	0.521	47	0.132	0.17	N	0.57	SignalP-noTM
gi_188518828_gb_ACD56773.1_	0.275	41	0.223	33	0.557	24	0.337	0.277	N	0.57	SignalP-noTM
gi_188518830_gb_ACD56775.1_	0.378	46	0.303	46	0.631	45	0.125	0.219	N	0.57	SignalP-noTM
gi_188518831_gb_ACD56776.1_	0.126	21	0.185	11	0.43	3	0.351	0.263	N	0.57	SignalP-noTM
gi_188518840_gb_ACD56785.1_	0.123	33	0.119	33	0.131	12	0.104	0.112	N	0.57	SignalP-noTM
gi_188518841_gb_ACD56786.1_	0.124	29	0.144	29	0.235	1	0.15	0.147	N	0.57	SignalP-noTM
gi_188518843_gb_ACD56788.1_	0.123	42	0.129	20	0.212	35	0.139	0.133	N	0.57	SignalP-noTM
gi_188518847_gb_ACD56792.1_	0.316	27	0.537	27	0.971	15	0.905	0.71	Y	0.57	SignalP-noTM
gi_188518851_gb_ACD56796.1_	0.216	26	0.333	18	0.813	16	0.552	0.436	N	0.57	SignalP-noTM
gi_188518852_gb_ACD56797.1_	0.142	31	0.127	11	0.205	3	0.157	0.141	N	0.57	SignalP-noTM
gi_188518856_gb_ACD56801.1_	0.16	46	0.195	46	0.298	43	0.189	0.192	N	0.57	SignalP-noTM
gi_188518857_gb_ACD56802.1_	0.155	42	0.146	42	0.214	19	0.138	0.142	N	0.57	SignalP-noTM
gi_188518858_gb_ACD56803.1_	0.134	32	0.139	40	0.228	39	0.098	0.12	N	0.57	SignalP-noTM
gi_188518862_gb_ACD56807.1_	0.124	34	0.156	30	0.275	6	0.219	0.18	N	0.51	SignalP-TM
gi_188518865_gb_ACD56810.1_	0.134	52	0.207	11	0.573	1	0.41	0.302	N	0.57	SignalP-noTM
gi_188518873_gb_ACD56818.1_	0.155	42	0.145	42	0.21	19	0.138	0.141	N	0.57	SignalP-noTM
gi_188518874_gb_ACD56819.1_	0.102	44	0.131	51	0.206	42	0.116	0.124	N	0.57	SignalP-noTM

0.091538	0.004038	0.140759	0.078778	gi_188518748_gb_ACD56693.1_
0.868413	0.999444	0.829346	0.899068	gi_188518749_gb_ACD56694.1_
0.086907	0.046887	0.110269	0.081354	gi_188518750_gb_ACD56695.1_
0.237398	0.548596	0.344117	0.376704	gi_188518753_gb_ACD56698.1_
0.816678	0.088346	0.76692	0.557315	gi_188518754_gb_ACD56699.1_
0.159092	0.14295	0.23041	0.177484	gi_188518755_gb_ACD56700.1_
0.769058	0.897707	0.439547	0.702104	gi_188518756_gb_ACD56701.1_
0.074055	0.45289	0.136461	0.221135	gi_188518758_gb_ACD56703.1_
0.782109	0.872806	0.856313	0.837076	gi_188523650_gb_ACD61595.1_
0.136815	0.226707	0.191545	0.185022	gi_188523653_gb_ACD61598.1_
0.282925	0.023869	0.328716	0.211837	gi_188523654_gb_ACD61599.1_
0.150077	0.247871	0.123575	0.173841	gi_188523655_gb_ACD61600.1_
0.891775	0.784654	0.665299	0.780576	gi_188523658_gb_ACD61603.1_
0.950216	0.999683	0.904909	0.951603	gi_188523659_gb_ACD61604.1_
0.161921	0.360545	0.103123	0.20853	gi_188523662_gb_ACD61607.1_
0.161109	0.154727	0.120363	0.1454	gi_188523670_gb_ACD61615.1_
0.250115	0.054526	0.370983	0.225208	gi_188523671_gb_ACD61616.1_
0.334033	0.640837	0.380129	0.451666	gi_188523672_gb_ACD61617.1_
0.376601	0.303434	0.558974	0.413003	gi_188523676_gb_ACD61621.1_
0.768525	0.978585	0.732041	0.826384	gi_188523678_gb_ACD61623.1_
0.951616	0.999245	0.883706	0.944856	gi_188523679_gb_ACD61624.1_
0.85483	0.998999	0.756023	0.869951	gi_188523680_gb_ACD61625.1_
0.078276	0.046887	0.082036	0.069066	gi_188523690_gb_ACD61635.1_
0.085489	0.801389	0.158291	0.34839	gi_188523702_gb_ACD61647.1_
0.107647	0.050498	0.17023	0.109458	gi_188523703_gb_ACD61648.1_
0.797057	0.733802	0.800433	0.777097	gi_188523705_gb_ACD61650.1_
0.266198	0.675902	0.305976	0.416025	gi_188518843_gb_ACD56788.1_
0.573709	0.325414	0.75547	0.551531	gi_188518847_gb_ACD56792.1_
0.141851	0.14295	0.126529	0.13711	gi_188518851_gb_ACD56796.1_
0.653849	0.6972	0.61633	0.655793	gi_188518852_gb_ACD56797.1_
0.157892	0.138596	0.155119	0.150536	gi_188518856_gb_ACD56801.1_
0.266198	0.647028	0.299013	0.40408	gi_188518857_gb_ACD56802.1_
0.061745	0.018004	0.079147	0.052965	gi_188518858_gb_ACD56803.1_
0.144798	0.051809	0.194818	0.130475	gi_188518862_gb_ACD56807.1_
0.111155	0.029114	0.189694	0.109988	gi_188518865_gb_ACD56810.1_
0.288434	0.680485	0.353658	0.440859	gi_188518873_gb_ACD56818.1_
0.164379	0.401553	0.076139	0.214024	gi_188518874_gb_ACD56819.1_
0.156303	0.023661	0.089074	0.089679	gi_188518875_gb_ACD56820.1_
0.153553	0.013282	0.121639	0.096158	gi_188518876_gb_ACD56821.1_
0.105647	0.391503	0.216361	0.237837	gi_188518877_gb_ACD56822.1_
0.364705	0.996564	0.369584	0.576951	gi_188518880_gb_ACD56825.1_
0.267371	0.243424	0.36401	0.291602	gi_188518881_gb_ACD56826.1_
0.141486	0.961209	0.208829	0.437175	gi_188518882_gb_ACD56827.1_
0.122604	0.199089	0.10736	0.143018	gi_188518883_gb_ACD56828.1_
0.174078	0.074261	0.223567	0.157302	gi_188518886_gb_ACD56831.1_
0.371684	0.959027	0.407333	0.579348	gi_188518890_gb_ACD56835.1_
0.053758	0.000022	0.082944	0.045575	gi_188518892_gb_ACD56837.1_
0.284144	0.692748	0.333366	0.436753	gi_188518898_gb_ACD56843.1_
0.208829	0.030325	0.342089	0.193748	gi_188518903_gb_ACD56848.1_
0.197182	0.177555	0.127862	0.167533	gi_188518904_gb_ACD56849.1_
0.613489	0.876099	0.450661	0.64675	gi_188518905_gb_ACD56850.1_
0.88153	0.965743	0.817127	0.888133	gi_188518906_gb_ACD56851.1_
0.100652	0.122927	0.097969	0.107183	gi_188518907_gb_ACD56852.1_
0.186943	0.250678	0.260379	0.232667	gi_188518909_gb_ACD56854.1_
0.169384	0.044532	0.26386	0.159259	gi_188518911_gb_ACD56856.1_
0.051809	0.02886	0.070437	0.050369	gi_188518912_gb_ACD56857.1_
0.179314	0.666634	0.198134	0.348027	gi_188518913_gb_ACD56858.1_
0.098767	0.043772	0.101197	0.081245	gi_188518914_gb_ACD56859.1_
0.122604	0.089317	0.11847	0.11013	gi_188518915_gb_ACD56860.1_
0.773819	0.825491	0.836443	0.811918	gi_188518923_gb_ACD56868.1_
0.137881	0.092541	0.111155	0.113859	gi_188518924_gb_ACD56869.1_
0.168541	0.031493	0.271505	0.15718	gi_188518925_gb_ACD56870.1_
0.297757	0.567093	0.234154	0.366335	gi_188518931_gb_ACD56876.1_
0.8966	0.981943	0.76959	0.882711	gi_188518932_gb_ACD56877.1_
0.112346	0.110269	0.111749	0.111455	gi_188518943_gb_ACD56888.1_
0.953113	0.982155	0.784654	0.906641	gi_188518944_gb_ACD56889.1_
0.158691	0.328716	0.120363	0.20259	gi_188518948_gb_ACD56893.1_
0.200047	0.042047	0.223567	0.15522	gi_188518949_gb_ACD56894.1_
0.157493	0.161109	0.134703	0.151102	gi_188518950_gb_ACD56895.1_
0.095349	0.036299	0.140397	0.090682	gi_188518951_gb_ACD56896.1_
0.167284	0.038236	0.107072	0.104197	gi_188518952_gb_ACD56897.1_
0.110269	0.047834	0.125538	0.094547	gi_188518956_gb_ACD56901.1_
0.107647	0.075928	0.077201	0.086925	gi_188518957_gb_ACD56902.1_
0.184222	0.38367	0.102293	0.223395	gi_188518958_gb_ACD56903.1_
0.441026	0.024868	0.715246	0.393713	gi_188518963_gb_ACD56908.1_
0.149694	0.049079	0.180199	0.126324	gi_188519087_gb_ACD57032.1_
0.053302	0.210818	0.186943	0.150354	gi_188519092_gb_ACD57037.1_
0.094576	0.060882	0.0985	0.084653	gi_188519093_gb_ACD57038.1_

gi_188518875_gb_ACD56820.1_	0.161	26	0.113	47	0.148	38	0.087	0.101	N	0.57	SignalP-noTM
gi_188518876_gb_ACD56821.1_	0.115	19	0.146	11	0.367	1	0.191	0.167	N	0.57	SignalP-noTM
gi_188518877_gb_ACD56822.1_	0.145	46	0.151	20	0.2	67	0.158	0.153	N	0.51	SignalP-TM
gi_188518880_gb_ACD56825.1_	0.216	32	0.193	32	0.383	4	0.25	0.219	N	0.57	SignalP-noTM
gi_188518881_gb_ACD56826.1_	0.284	28	0.173	28	0.219	50	0.098	0.137	N	0.57	SignalP-noTM
gi_188518882_gb_ACD56827.1_	0.111	29	0.134	29	0.201	25	0.149	0.141	N	0.57	SignalP-noTM
gi_188518883_gb_ACD56828.1_	0.131	6	0.125	21	0.188	18	0.136	0.13	N	0.57	SignalP-noTM
gi_188518886_gb_ACD56831.1_	0.131	23	0.164	23	0.295	14	0.191	0.177	N	0.57	SignalP-noTM
gi_188518890_gb_ACD56835.1_	0.283	18	0.369	18	0.717	49	0.497	0.416	N	0.51	SignalP-TM
gi_188518892_gb_ACD56837.1_	0.149	34	0.126	21	0.182	2	0.138	0.132	N	0.57	SignalP-noTM
gi_188518898_gb_ACD56843.1_	0.155	42	0.145	42	0.21	19	0.138	0.141	N	0.57	SignalP-noTM
gi_188518903_gb_ACD56848.1_	0.106	31	0.137	12	0.265	3	0.186	0.16	N	0.57	SignalP-noTM
gi_188518904_gb_ACD56849.1_	0.109	57	0.138	11	0.252	2	0.193	0.164	N	0.57	SignalP-noTM
gi_188518905_gb_ACD56850.1_	0.131	45	0.167	45	0.32	33	0.174	0.17	N	0.57	SignalP-noTM
gi_188518906_gb_ACD56851.1_	0.105	20	0.117	20	0.198	17	0.127	0.122	N	0.57	SignalP-noTM
gi_188518907_gb_ACD56852.1_	0.108	24	0.11	38	0.128	37	0.108	0.109	N	0.57	SignalP-noTM
gi_188518909_gb_ACD56854.1_	0.178	26	0.205	26	0.461	24	0.252	0.227	N	0.57	SignalP-noTM
gi_188518911_gb_ACD56856.1_	0.131	14	0.16	47	0.48	40	0.13	0.146	N	0.57	SignalP-noTM
gi_188518912_gb_ACD56857.1_	0.415	35	0.195	35	0.178	21	0.108	0.154	N	0.57	SignalP-noTM
gi_188518913_gb_ACD56858.1_	0.173	27	0.125	11	0.258	1	0.147	0.135	N	0.57	SignalP-noTM
gi_188518914_gb_ACD56859.1_	0.106	26	0.105	70	0.151	4	0.092	0.099	N	0.57	SignalP-noTM
gi_188518915_gb_ACD56860.1_	0.199	35	0.143	35	0.249	1	0.139	0.141	N	0.57	SignalP-noTM
gi_188518923_gb_ACD56868.1_	0.133	22	0.158	22	0.292	11	0.194	0.175	N	0.57	SignalP-noTM
gi_188518924_gb_ACD56869.1_	0.134	17	0.123	41	0.156	1	0.103	0.114	N	0.57	SignalP-noTM
gi_188518925_gb_ACD56870.1_	0.112	40	0.101	65	0.111	24	0.086	0.094	N	0.57	SignalP-noTM
gi_188518931_gb_ACD56876.1_	0.105	18	0.109	11	0.15	1	0.12	0.114	N	0.57	SignalP-noTM
gi_188518932_gb_ACD56877.1_	0.115	23	0.133	56	0.227	48	0.13	0.131	N	0.57	SignalP-noTM
gi_188518943_gb_ACD56888.1_	0.142	32	0.134	19	0.188	43	0.143	0.138	N	0.57	SignalP-noTM
gi_188518944_gb_ACD56889.1_	0.419	21	0.588	21	0.915	1	0.849	0.711	Y	0.57	SignalP-noTM
gi_188518948_gb_ACD56893.1_	0.142	20	0.128	11	0.284	1	0.151	0.137	N	0.51	SignalP-TM
gi_188518949_gb_ACD56894.1_	0.127	26	0.212	18	0.561	9	0.403	0.302	N	0.57	SignalP-noTM
gi_188518950_gb_ACD56895.1_	0.216	27	0.321	27	0.659	7	0.534	0.421	N	0.57	SignalP-noTM
gi_188518951_gb_ACD56896.1_	0.128	49	0.11	24	0.141	5	0.11	0.11	N	0.51	SignalP-TM
gi_188518952_gb_ACD56897.1_	0.126	60	0.113	48	0.172	46	0.092	0.103	N	0.57	SignalP-noTM
gi_188518956_gb_ACD56901.1_	0.16	38	0.199	38	0.461	37	0.174	0.187	N	0.57	SignalP-noTM
gi_188518957_gb_ACD56902.1_	0.127	24	0.191	13	0.429	6	0.352	0.267	N	0.57	SignalP-noTM
gi_188518958_gb_ACD56903.1_	0.102	28	0.12	28	0.165	23	0.121	0.121	N	0.57	SignalP-noTM
gi_188518963_gb_ACD56908.1_	0.163	29	0.161	11	0.389	1	0.247	0.201	N	0.57	SignalP-noTM
gi_188519087_gb_ACD57032.1_	0.226	28	0.187	28	0.434	2	0.193	0.19	N	0.57	SignalP-noTM
gi_188519092_gb_ACD57037.1_	0.143	41	0.103	12	0.146	23	0.107	0.105	N	0.51	SignalP-TM
gi_188519093_gb_ACD57038.1_	0.116	42	0.122	42	0.196	40	0.12	0.121	N	0.57	SignalP-noTM
gi_188519094_gb_ACD57039.1_	0.107	29	0.107	12	0.141	4	0.118	0.112	N	0.57	SignalP-noTM
gi_188519097_gb_ACD57042.1_	0.147	29	0.188	29	0.424	15	0.235	0.21	N	0.57	SignalP-noTM
gi_188519099_gb_ACD57044.1_	0.134	21	0.19	11	0.47	3	0.334	0.258	N	0.57	SignalP-noTM
gi_188519102_gb_ACD57047.1_	0.142	23	0.145	23	0.204	7	0.161	0.152	N	0.57	SignalP-noTM
gi_188519104_gb_ACD57049.1_	0.106	33	0.143	11	0.278	2	0.2	0.17	N	0.57	SignalP-noTM
gi_188519105_gb_ACD57050.1_	0.118	27	0.105	17	0.138	1	0.102	0.104	N	0.57	SignalP-noTM
gi_188519106_gb_ACD57051.1_	0.133	9	0.1	54	0.117	1	0.087	0.094	N	0.57	SignalP-noTM
gi_188519107_gb_ACD57052.1_	0.113	51	0.114	11	0.177	1	0.127	0.12	N	0.57	SignalP-noTM
gi_188519109_gb_ACD57054.1_	0.116	23	0.192	11	0.482	3	0.384	0.282	N	0.57	SignalP-noTM
gi_188519111_gb_ACD57056.1_	0.685	27	0.792	27	0.978	18	0.927	0.855	Y	0.57	SignalP-noTM
gi_188519112_gb_ACD57057.1_	0.146	69	0.303	18	0.823	11	0.623	0.453	N	0.57	SignalP-noTM
gi_188519118_gb_ACD57063.1_	0.228	37	0.165	37	0.179	12	0.123	0.145	N	0.57	SignalP-noTM
gi_188519125_gb_ACD57070.1_	0.102	23	0.1	23	0.113	1	0.088	0.095	N	0.57	SignalP-noTM
gi_188519127_gb_ACD57072.1_	0.241	36	0.145	36	0.161	1	0.091	0.12	N	0.57	SignalP-noTM
gi_188519128_gb_ACD57073.1_	0.109	16	0.176	12	0.386	1	0.307	0.237	N	0.57	SignalP-noTM
gi_188519133_gb_ACD57078.1_	0.148	26	0.121	26	0.135	42	0.088	0.105	N	0.57	SignalP-noTM
gi_188519134_gb_ACD57079.1_	0.121	69	0.128	15	0.215	4	0.158	0.142	N	0.57	SignalP-noTM
gi_188519135_gb_ACD57080.1_	0.156	20	0.148	20	0.176	19	0.136	0.142	N	0.57	SignalP-noTM
gi_188519136_gb_ACD57081.1_	0.125	18	0.102	37	0.112	36	0.081	0.092	N	0.57	SignalP-noTM
gi_188519137_gb_ACD57082.1_	0.402	30	0.196	30	0.135	35	0.073	0.138	N	0.57	SignalP-noTM
gi_188519138_gb_ACD57083.1_	0.118	62	0.145	11	0.296	3	0.213	0.177	N	0.57	SignalP-noTM
gi_188519144_gb_ACD57089.1_	0.17	68	0.128	68	0.143	1	0.09	0.11	N	0.57	SignalP-noTM
gi_188519146_gb_ACD57091.1_	0.116	24	0.18	11	0.472	3	0.319	0.245	N	0.57	SignalP-noTM
gi_188519147_gb_ACD57092.1_	0.173	26	0.138	26	0.209	1	0.111	0.125	N	0.57	SignalP-noTM
gi_188519148_gb_ACD57093.1_	0.162	54	0.148	54	0.202	28	0.133	0.141	N	0.57	SignalP-noTM
gi_188519149_gb_ACD57094.1_	0.168	26	0.134	26	0.178	21	0.108	0.121	N	0.57	SignalP-noTM
gi_188519151_gb_ACD57096.1_	0.172	43	0.205	11	0.63	1	0.411	0.302	N	0.57	SignalP-noTM
gi_188519152_gb_ACD57097.1_	0.119	28	0.12	12	0.213	5	0.153	0.135	N	0.57	SignalP-noTM
gi_188519158_gb_ACD57103.1_	0.177	33	0.122	33	0.122	4	0.08	0.103	N	0.57	SignalP-noTM
gi_188519159_gb_ACD57104.1_	0.143	18	0.151	18	0.233	2	0.174	0.162	N	0.57	SignalP-noTM
gi_188519160_gb_ACD57105.1_	0.156	22	0.122	31	0.17	29	0.098	0.11	N	0.57	SignalP-noTM
gi_188519161_gb_ACD57106.1_	0.135	25	0.111	25	0.134	5	0.094	0.103	N	0.57	SignalP-noTM
gi_188519162_gb_ACD57107.1_	0.183	35	0.154	35	0.191	34	0.123	0.139	N	0.57	SignalP-noTM
gi_188519163_gb_ACD57108.1_	0.166	35	0.149	35	0.22	31	0.123	0.137	N	0.57	SignalP-noTM
gi_188519168_gb_ACD57113.1_	0.238	32	0.154	32	0.187	8	0.115	0.139	N	0.51	SignalP-TM
gi_188519170_gb_ACD57115.1_	0.156	65	0.13	65	0.195	49	0.12	0.125	N	0.57	SignalP-noTM
gi_188519171_gb_ACD57116.1_	0.815	22	0.771	22	0.889	2	0.775	0.773	Y	0.57	SignalP-noTM

0.631812	0.889731	0.581029	0.700857	gi_188519094_gb_ACD57039.1_
0.105647	0.095091	0.084556	0.095098	gi_188519097_gb_ACD57042.1_
0.554532	0.619871	0.709715	0.628039	gi_188519099_gb_ACD57044.1_
0.948632	0.996417	0.890319	0.945123	gi_188519102_gb_ACD57047.1_
0.054526	0.02129	0.135053	0.07029	gi_188519104_gb_ACD57049.1_
0.06192	0.001711	0.099571	0.054401	gi_188519105_gb_ACD57050.1_
0.163967	0.144056	0.135404	0.147809	gi_188519106_gb_ACD57051.1_
0.347511	0.029369	0.363316	0.246732	gi_188519107_gb_ACD57052.1_
0.09639	0.039015	0.105931	0.080445	gi_188519109_gb_ACD57054.1_
0.887054	0.714634	0.838485	0.813391	gi_188519111_gb_ACD57056.1_
0.953113	0.940811	0.933205	0.942376	gi_188519112_gb_ACD57057.1_
0.223567	0.154335	0.208334	0.195412	gi_188519240_gb_ACD57185.1_
0.31432	0.231475	0.427025	0.324273	gi_188519243_gb_ACD57188.1_
0.061226	0.001438	0.102018	0.054894	gi_188519244_gb_ACD57189.1_
0.05869	0.109097	0.059189	0.075659	gi_188519245_gb_ACD57190.1_
0.114762	0.057055	0.123575	0.098464	gi_188519246_gb_ACD57191.1_
0.148173	0.126198	0.110859	0.12841	gi_188519252_gb_ACD57197.1_
0.941475	0.992797	0.896877	0.943716	gi_188519259_gb_ACD57204.1_
0.851448	0.72492	0.767991	0.781453	gi_188519265_gb_ACD57210.1_
0.135404	0.084324	0.099571	0.106433	gi_188519267_gb_ACD57212.1_
0.163147	0.124227	0.20538	0.164251	gi_188519270_gb_ACD57215.1_
0.083402	0.001334	0.129206	0.071314	gi_188519272_gb_ACD57217.1_
0.076988	0.210818	0.087384	0.125063	gi_188519274_gb_ACD57219.1_
0.15046	0.096651	0.109097	0.118736	gi_188519278_gb_ACD57223.1_
0.14295	0.751569	0.286591	0.393703	gi_188519279_gb_ACD57224.1_
0.168962	0.731452	0.159494	0.353303	gi_188519280_gb_ACD57225.1_
0.138596	0.266784	0.137881	0.181087	gi_188519281_gb_ACD57226.1_
0.159092	0.358473	0.134005	0.21719	gi_188519284_gb_ACD57229.1_
0.112346	0.130222	0.103679	0.115416	gi_188519285_gb_ACD57230.1_
0.151228	0.327393	0.158291	0.212304	gi_188519286_gb_ACD57231.1_
0.126198	0.108806	0.130562	0.121855	gi_188519287_gb_ACD57232.1_
0.082036	0.006868	0.10147	0.063458	gi_188519288_gb_ACD57233.1_
0.953381	0.989013	0.929955	0.95745	gi_188519289_gb_ACD57234.1_
0.573709	0.999785	0.855573	0.809689	gi_188519292_gb_ACD57237.1_
0.124227	0.063151	0.226707	0.138028	gi_188519293_gb_ACD57238.1_
0.813968	0.991311	0.67787	0.827716	gi_188519294_gb_ACD57239.1_
0.915676	0.999679	0.851068	0.922141	gi_188519295_gb_ACD57240.1_
0.104799	0.056733	0.119413	0.093648	gi_188519296_gb_ACD57241.1_
0.134354	0.056412	0.175375	0.122047	gi_188519297_gb_ACD57242.1_
0.085959	0.071226	0.148552	0.101912	gi_188519298_gb_ACD57243.1_
0.093553	0.008334	0.134354	0.078747	gi_188519300_gb_ACD57245.1_
0.870456	0.998981	0.829346	0.899594	gi_188519301_gb_ACD57246.1_
0.087864	0.004261	0.129544	0.07389	gi_188519302_gb_ACD57247.1_
0.163557	0.642906	0.1603	0.322254	gi_188519303_gb_ACD57248.1_
0.434381	0.039354	0.415324	0.296353	gi_188519304_gb_ACD57249.1_
0.168962	0.034656	0.190618	0.131412	gi_188519305_gb_ACD57250.1_
0.49775	0.980848	0.554532	0.67771	gi_188519310_gb_ACD57255.1_
0.105931	0.066236	0.148173	0.10678	gi_188519312_gb_ACD57257.1_
0.529964	0.06003	0.538176	0.376057	gi_528897471_gb_ACD57198.2_
0.092289	0.015172	0.14629	0.084584	gi_188519313_gb_ACD57258.1_
0.954566	0.969587	0.913805	0.945986	gi_188519314_gb_ACD57259.1_
0.105931	0.038791	0.168541	0.104421	gi_188519317_gb_ACD57262.1_
0.183772	0.277479	0.083631	0.181627	gi_188519321_gb_ACD57266.1_
0.23041	0.051956	0.311739	0.198035	gi_188519323_gb_ACD57268.1_
0.154727	0.046753	0.194348	0.131943	gi_188519324_gb_ACD57269.1_
0.201491	0.780572	0.097704	0.359922	gi_188519328_gb_ACD57273.1_
0.070831	0.082944	0.107072	0.086949	gi_188519330_gb_ACD57275.1_
0.158691	0.838485	0.094063	0.363746	gi_188519337_gb_ACD57282.1_
0.105081	0.026059	0.13717	0.089437	gi_188519340_gb_ACD57285.1_
0.278684	0.585405	0.334701	0.399597	gi_188519345_gb_ACD57290.1_
0.066051	0.026831	0.096129	0.063004	gi_188519346_gb_ACD57291.1_
0.116294	0.007577	0.147041	0.090304	gi_188519347_gb_ACD57292.1_
0.110859	0.011085	0.085959	0.069301	gi_188519354_gb_ACD57299.1_
0.944695	0.842108	0.914745	0.900516	gi_188519359_gb_ACD57304.1_
0.067547	0.178873	0.141851	0.129424	gi_188519360_gb_ACD57305.1_
0.726711	0.858149	0.821127	0.801996	gi_188519365_gb_ACD57310.1_
0.805652	0.121639	0.351603	0.426298	gi_188519366_gb_ACD57311.1_
0.235232	0.016286	0.309812	0.18711	gi_188519367_gb_ACD57312.1_
0.145542	0.061399	0.173217	0.126719	gi_188519368_gb_ACD57313.1_
0.105931	0.053151	0.172787	0.110623	gi_188519371_gb_ACD57316.1_
0.896321	0.98096	0.946698	0.941326	gi_188519374_gb_ACD57319.1_
0.901766	0.983077	0.889437	0.92476	gi_188519376_gb_ACD57321.1_
0.958672	0.997527	0.890611	0.948937	gi_188519377_gb_ACD57322.1_
0.087145	0.117533	0.100381	0.101686	gi_188519378_gb_ACD57323.1_
0.366096	0.115373	0.50375	0.328406	gi_188519379_gb_ACD57324.1_
0.872138	0.888548	0.818468	0.859718	gi_188519380_gb_ACD57325.1_
0.570036	0.049642	0.526974	0.382217	gi_188519381_gb_ACD57326.1_
0.056094	0.059189	0.105931	0.073738	gi_188519382_gb_ACD57327.1_

gi_188519173_gb_ACD57118.1_	0.135	19	0.184	19	0.33	1	0.264	0.222	N	0.57	SignalP-noTM
gi_188519175_gb_ACD57120.1_	0.129	25	0.136	11	0.234	1	0.189	0.155	N	0.51	SignalP-TM
gi_188519176_gb_ACD57121.1_	0.256	31	0.21	31	0.313	13	0.192	0.203	N	0.51	SignalP-TM
gi_188519177_gb_ACD57122.1_	0.172	38	0.156	28	0.235	26	0.164	0.16	N	0.57	SignalP-noTM
gi_188519179_gb_ACD57124.1_	0.365	29	0.558	16	0.964	10	0.919	0.727	Y	0.57	SignalP-noTM
gi_188519181_gb_ACD57126.1_	0.107	49	0.118	14	0.167	9	0.138	0.127	N	0.57	SignalP-noTM
gi_188519182_gb_ACD57127.1_	0.127	39	0.149	11	0.307	1	0.215	0.18	N	0.57	SignalP-noTM
gi_188519183_gb_ACD57128.1_	0.168	33	0.128	33	0.177	2	0.094	0.112	N	0.57	SignalP-noTM
gi_188519184_gb_ACD57129.1_	0.143	45	0.157	11	0.393	2	0.231	0.192	N	0.57	SignalP-noTM
gi_188519193_gb_ACD57138.1_	0.111	5	0.12	14	0.201	4	0.142	0.13	N	0.57	SignalP-noTM
gi_188519196_gb_ACD57141.1_	0.123	50	0.124	24	0.189	21	0.149	0.133	N	0.51	SignalP-TM
gi_188519197_gb_ACD57142.1_	0.162	14	0.22	14	0.468	10	0.308	0.261	N	0.57	SignalP-noTM
gi_188519201_gb_ACD57146.1_	0.108	64	0.107	20	0.134	9	0.101	0.104	N	0.57	SignalP-noTM
gi_188519203_gb_ACD57148.1_	0.105	39	0.102	53	0.116	44	0.079	0.091	N	0.57	SignalP-noTM
gi_188519210_gb_ACD57155.1_	0.262	19	0.263	19	0.385	8	0.266	0.264	N	0.51	SignalP-TM
gi_188519211_gb_ACD57156.1_	0.195	52	0.153	52	0.173	13	0.106	0.131	N	0.57	SignalP-noTM
gi_188519218_gb_ACD57163.1_	0.325	39	0.211	39	0.218	45	0.108	0.163	N	0.57	SignalP-noTM
gi_188519222_gb_ACD57167.1_	0.119	22	0.181	11	0.406	9	0.337	0.254	N	0.57	SignalP-noTM
gi_188519227_gb_ACD57172.1_	0.103	33	0.17	13	0.334	11	0.29	0.226	N	0.57	SignalP-noTM
gi_188519230_gb_ACD57175.1_	0.215	34	0.156	34	0.16	27	0.104	0.131	N	0.57	SignalP-noTM
gi_188519231_gb_ACD57176.1_	0.127	22	0.117	22	0.223	1	0.117	0.117	N	0.57	SignalP-noTM
gi_188519232_gb_ACD57177.1_	0.101	30	0.112	11	0.164	1	0.122	0.116	N	0.57	SignalP-noTM
gi_188519239_gb_ACD57184.1_	0.168	24	0.156	14	0.313	6	0.235	0.193	N	0.57	SignalP-noTM
gi_188519240_gb_ACD57185.1_	0.124	38	0.124	11	0.193	7	0.155	0.138	N	0.57	SignalP-noTM
gi_188519243_gb_ACD57188.1_	0.153	63	0.204	13	0.579	7	0.42	0.305	N	0.57	SignalP-noTM
gi_188519244_gb_ACD57189.1_	0.099	61	0.105	31	0.15	7	0.105	0.105	N	0.51	SignalP-TM
gi_188519245_gb_ACD57190.1_	0.116	16	0.119	16	0.157	10	0.113	0.116	N	0.57	SignalP-noTM
gi_188519246_gb_ACD57191.1_	0.141	65	0.194	11	0.614	2	0.349	0.251	N	0.51	SignalP-TM
gi_188519252_gb_ACD57197.1_	0.111	27	0.122	11	0.198	5	0.161	0.137	N	0.51	SignalP-TM
gi_528897471_gb_ACD57198.2_	0.116	66	0.12	58	0.197	1	0.107	0.114	N	0.57	SignalP-noTM
gi_188519259_gb_ACD57204.1_	0.129	30	0.179	11	0.433	1	0.3	0.236	N	0.57	SignalP-noTM
gi_188519265_gb_ACD57210.1_	0.569	26	0.589	26	0.955	1	0.761	0.67	Y	0.57	SignalP-noTM
gi_188519267_gb_ACD57212.1_	0.154	25	0.11	25	0.15	2	0.097	0.104	N	0.57	SignalP-noTM
gi_188519270_gb_ACD57215.1_	0.101	20	0.123	11	0.201	5	0.162	0.137	N	0.51	SignalP-TM
gi_188519272_gb_ACD57217.1_	0.19	54	0.164	14	0.362	6	0.268	0.213	N	0.57	SignalP-noTM
gi_188519274_gb_ACD57219.1_	0.121	46	0.112	46	0.137	32	0.101	0.107	N	0.57	SignalP-noTM
gi_188519278_gb_ACD57223.1_	0.112	27	0.125	11	0.205	5	0.167	0.14	N	0.51	SignalP-TM
gi_188519279_gb_ACD57224.1_	0.662	27	0.241	27	0.267	11	0.134	0.201	N	0.51	SignalP-TM
gi_188519280_gb_ACD57225.1_	0.119	52	0.133	11	0.217	1	0.17	0.15	N	0.57	SignalP-noTM
gi_188519281_gb_ACD57226.1_	0.138	37	0.133	16	0.239	1	0.148	0.14	N	0.57	SignalP-noTM
gi_188519284_gb_ACD57229.1_	0.115	45	0.14	11	0.311	2	0.188	0.162	N	0.57	SignalP-noTM
gi_188519285_gb_ACD57230.1_	0.155	34	0.131	34	0.145	31	0.098	0.116	N	0.57	SignalP-noTM
gi_188519286_gb_ACD57231.1_	0.102	23	0.121	11	0.24	1	0.138	0.129	N	0.57	SignalP-noTM
gi_188519287_gb_ACD57232.1_	0.157	29	0.179	29	0.426	24	0.194	0.186	N	0.57	SignalP-noTM
gi_188519288_gb_ACD57233.1_	0.119	62	0.127	13	0.22	11	0.162	0.143	N	0.57	SignalP-noTM
gi_188519289_gb_ACD57234.1_	0.148	40	0.331	17	0.901	10	0.824	0.563	N	0.57	SignalP-noTM
gi_188519292_gb_ACD57237.1_	0.103	26	0.186	11	0.588	1	0.323	0.25	N	0.57	SignalP-noTM
gi_188519293_gb_ACD57238.1_	0.166	67	0.172	11	0.41	1	0.29	0.216	N	0.51	SignalP-TM
gi_188519294_gb_ACD57239.1_	0.171	60	0.126	11	0.228	1	0.153	0.139	N	0.57	SignalP-noTM
gi_188519295_gb_ACD57240.1_	0.33	20	0.568	20	0.984	12	0.965	0.755	Y	0.57	SignalP-noTM
gi_188519296_gb_ACD57241.1_	0.268	31	0.17	31	0.176	30	0.117	0.145	N	0.57	SignalP-noTM
gi_188519297_gb_ACD57242.1_	0.134	19	0.163	11	0.336	2	0.27	0.202	N	0.51	SignalP-TM
gi_188519298_gb_ACD57243.1_	0.118	64	0.175	11	0.47	3	0.302	0.235	N	0.57	SignalP-noTM
gi_188519300_gb_ACD57245.1_	0.29	26	0.241	26	0.379	25	0.171	0.215	N	0.51	SignalP-TM
gi_188519301_gb_ACD57246.1_	0.204	24	0.138	42	0.148	38	0.093	0.116	N	0.57	SignalP-noTM
gi_188519302_gb_ACD57247.1_	0.115	20	0.12	12	0.179	6	0.152	0.132	N	0.51	SignalP-TM
gi_188519303_gb_ACD57248.1_	0.465	21	0.567	15	0.862	11	0.737	0.646	Y	0.57	SignalP-noTM
gi_188519304_gb_ACD57249.1_	0.157	33	0.275	33	0.663	30	0.354	0.312	N	0.57	SignalP-noTM
gi_188519305_gb_ACD57250.1_	0.15	28	0.226	20	0.576	8	0.426	0.32	N	0.57	SignalP-noTM
gi_188519310_gb_ACD57255.1_	0.222	41	0.228	11	0.645	3	0.541	0.375	N	0.57	SignalP-noTM
gi_188519312_gb_ACD57257.1_	0.114	50	0.154	11	0.294	5	0.246	0.188	N	0.51	SignalP-TM
gi_188519313_gb_ACD57258.1_	0.14	37	0.169	11	0.343	2	0.295	0.215	N	0.51	SignalP-TM
gi_188519314_gb_ACD57259.1_	0.136	35	0.181	35	0.396	23	0.237	0.202	N	0.51	SignalP-TM
gi_188519317_gb_ACD57262.1_	0.117	40	0.12	40	0.153	8	0.115	0.117	N	0.57	SignalP-noTM
gi_188519321_gb_ACD57266.1_	0.175	33	0.148	33	0.218	32	0.113	0.132	N	0.57	SignalP-noTM
gi_188519323_gb_ACD57268.1_	0.103	36	0.132	11	0.222	5	0.185	0.152	N	0.51	SignalP-TM
gi_188519324_gb_ACD57269.1_	0.136	22	0.12	11	0.214	2	0.139	0.129	N	0.57	SignalP-noTM
gi_188519328_gb_ACD57273.1_	0.17	35	0.148	35	0.336	34	0.114	0.132	N	0.57	SignalP-noTM
gi_188519330_gb_ACD57275.1_	0.132	40	0.127	40	0.177	5	0.12	0.125	N	0.51	SignalP-TM
gi_188519337_gb_ACD57282.1_	0.118	60	0.15	11	0.368	1	0.202	0.174	N	0.57	SignalP-noTM
gi_188519340_gb_ACD57285.1_	0.178	70	0.139	11	0.323	1	0.175	0.156	N	0.57	SignalP-noTM
gi_188519345_gb_ACD57290.1_	0.156	42	0.146	42	0.219	19	0.143	0.145	N	0.57	SignalP-noTM
gi_188519346_gb_ACD57291.1_	0.105	20	0.102	62	0.136	1	0.094	0.098	N	0.57	SignalP-noTM
gi_188519347_gb_ACD57292.1_	0.157	61	0.141	11	0.296	1	0.188	0.163	N	0.57	SignalP-noTM
gi_188519354_gb_ACD57299.1_	0.162	24	0.105	11	0.156	1	0.11	0.107	N	0.51	SignalP-TM
gi_188519359_gb_ACD57304.1_	0.171	30	0.377	30	0.953	25	0.871	0.609	Y	0.57	SignalP-noTM
gi_188519360_gb_ACD57305.1_	0.214	36	0.37	36	0.766	31	0.446	0.398	N	0.51	SignalP-TM
gi_188519365_gb_ACD57310.1_	0.114	22	0.144	13	0.262	9	0.209	0.175	N	0.57	SignalP-noTM

0.117845	0.030858	0.167284	0.105329	gi_188519383_gb_ACD57328.1_
0.711566	0.935595	0.683737	0.776966	gi_188519384_gb_ACD57329.1_
0.216361	0.247312	0.154335	0.206003	gi_188519390_gb_ACD57335.1_
0.934869	0.995752	0.863185	0.931269	gi_188519392_gb_ACD57337.1_
0.161515	0.074468	0.144798	0.126927	gi_188519393_gb_ACD57338.1_
0.135755	0.049784	0.177118	0.120886	gi_188519394_gb_ACD57339.1_
0.125209	0.07024	0.139314	0.111588	gi_188519395_gb_ACD57340.1_
0.27032	0.829346	0.256355	0.452007	gi_188519397_gb_ACD57342.1_
0.274482	0.938946	0.460334	0.557921	gi_188519401_gb_ACD57346.1_
0.21738	0.649764	0.215853	0.360999	gi_188519402_gb_ACD57347.1_
0.203915	0.057704	0.282925	0.181515	gi_188519403_gb_ACD57348.1_
0.13331	0.026831	0.348191	0.169444	gi_188519404_gb_ACD57349.1_
0.088105	0.00118	0.104238	0.064508	gi_188519405_gb_ACD57350.1_
0.227233	0.07806	0.142217	0.14917	gi_188519406_gb_ACD57351.1_
0.116294	0.00695	0.255784	0.126343	gi_188519407_gb_ACD57352.1_
0.285366	0.730862	0.335369	0.450532	gi_188519411_gb_ACD57356.1_
0.50225	0.048522	0.676558	0.40911	gi_188519413_gb_ACD57358.1_
0.902824	0.548596	0.913331	0.78825	gi_188519419_gb_ACD57364.1_
0.135404	0.034357	0.16645	0.11207	gi_188519420_gb_ACD57365.1_
0.175375	0.033278	0.389361	0.199338	gi_188519421_gb_ACD57366.1_
0.184673	0.380836	0.147418	0.237642	gi_188519422_gb_ACD57367.1_
0.897431	0.998173	0.689546	0.861717	gi_188519424_gb_ACD57369.1_
0.878361	0.99975	0.678525	0.852212	gi_188519425_gb_ACD57370.1_
0.136108	0.956353	0.091289	0.394583	gi_188519426_gb_ACD57371.1_
0.123575	0.370983	0.09984	0.198133	gi_188519428_gb_ACD57373.1_
0.118157	0.275678	0.21032	0.201385	gi_188519429_gb_ACD57374.1_
0.059524	0.001569	0.151228	0.070774	gi_188519433_gb_ACD57378.1_
0.399392	0.889141	0.326073	0.538202	gi_188519434_gb_ACD57379.1_
0.369584	0.816228	0.530711	0.572174	gi_188519440_gb_ACD57385.1_
0.181979	0.203429	0.130562	0.17199	gi_188519441_gb_ACD57386.1_
0.682438	0.840506	0.810306	0.77775	gi_188519442_gb_ACD57387.1_
0.927976	0.993334	0.843697	0.921669	gi_188519443_gb_ACD57388.1_
0.676558	0.406609	0.827213	0.636793	gi_188519445_gb_ACD57390.1_
0.157493	0.629017	0.240672	0.342394	gi_188519446_gb_ACD57391.1_
0.143318	0.056094	0.208829	0.13608	gi_188519451_gb_ACD57396.1_
0.907711	0.879955	0.861762	0.883143	gi_188519452_gb_ACD57397.1_
0.19201	0.06054	0.165205	0.139252	gi_188519455_gb_ACD57400.1_
0.066422	0.04004	0.11847	0.074977	gi_188519457_gb_ACD57402.1_
0.223047	0.449176	0.225657	0.299293	gi_188519458_gb_ACD57403.1_
0.152775	0.045695	0.20587	0.13478	gi_188519469_gb_ACD57414.1_
0.116912	0.028609	0.1603	0.10194	gi_188519474_gb_ACD57419.1_
0.101197	0.001827	0.141122	0.081382	gi_188519475_gb_ACD57420.1_
0.304703	0.117845	0.436593	0.28638	gi_188519478_gb_ACD57423.1_
0.073645	0.017327	0.074055	0.055009	gi_188519479_gb_ACD57424.1_
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0.068306	0.039354	0.094319	0.067326	gi_188519481_gb_ACD57426.1_
0.148932	0.071824	0.232544	0.1511	gi_188519482_gb_ACD57427.1_
0.961874	0.999901	0.908212	0.956662	gi_188519483_gb_ACD57428.1_
0.159494	0.318863	0.104238	0.194198	gi_188519487_gb_ACD57432.1_
0.053758	0.012116	0.135755	0.06721	gi_188519490_gb_ACD57435.1_
0.125538	0.249553	0.258649	0.211247	gi_188519491_gb_ACD57436.1_
0.086432	0.053	0.106786	0.082073	gi_188519492_gb_ACD57437.1_
0.117533	0.088346	0.197182	0.134354	gi_188519493_gb_ACD57438.1_
0.092541	0.036089	0.144056	0.090895	gi_188519494_gb_ACD57439.1_
0.098234	0.178433	0.175375	0.150681	gi_188519495_gb_ACD57440.1_
0.103679	0.152387	0.133658	0.129908	gi_188519497_gb_ACD57442.1_
0.966333	0.998531	0.916598	0.960487	gi_188519498_gb_ACD57443.1_
0.952166	0.998042	0.897155	0.949121	gi_188519499_gb_ACD57444.1_
0.311096	0.920415	0.411686	0.547732	gi_188519500_gb_ACD57445.1_
0.174942	0.140397	0.131244	0.148861	gi_188519657_gb_ACD57602.1_
0.1603	0.128532	0.171079	0.153304	gi_188519658_gb_ACD57603.1_
0.315614	0.329378	0.364705	0.336566	gi_188519659_gb_ACD57604.1_
0.295254	0.770122	0.35503	0.473469	gi_188519661_gb_ACD57606.1_
0.27508	0.451404	0.085021	0.270502	gi_188519663_gb_ACD57608.1_
0.158291	0.302167	0.097704	0.186054	gi_188519667_gb_ACD57612.1_
0.793639	0.198134	0.797542	0.596438	gi_188519671_gb_ACD57616.1_
0.089317	0.030502	0.127527	0.082449	gi_188519672_gb_ACD57617.1_
0.057541	0.031954	0.115067	0.068187	gi_188519673_gb_ACD57618.1_
0.203429	0.085724	0.151614	0.146922	gi_188519674_gb_ACD57619.1_
0.115373	0.203915	0.147795	0.155694	gi_188519675_gb_ACD57620.1_
0.161515	0.041328	0.160704	0.121182	gi_188519678_gb_ACD57623.1_
0.188314	0.250678	0.24232	0.227104	gi_188519679_gb_ACD57624.1_
0.099571	0.045826	0.147041	0.097479	gi_188519680_gb_ACD57625.1_
0.92129	0.994492	0.919975	0.945252	gi_188519681_gb_ACD57626.1_
0.079805	0.035881	0.130222	0.081969	gi_188519682_gb_ACD57627.1_
0.944381	0.994525	0.906701	0.948536	gi_188519683_gb_ACD57628.1_
0.136108	0.105931	0.237398	0.159812	gi_188519686_gb_ACD57631.1_
0.153164	0.945319	0.069461	0.389315	gi_188519689_gb_ACD57634.1_

gi_188519366_gb_ACD57311.1_	0.113	17	0.108	32	0.129	24	0.093	0.101	N	0.57	SignalP-noTM
gi_188519367_gb_ACD57312.1_	0.226	56	0.199	37	0.262	35	0.155	0.178	N	0.57	SignalP-noTM
gi_188519368_gb_ACD57313.1_	0.112	29	0.2	11	0.524	1	0.387	0.288	N	0.57	SignalP-noTM
gi_188519371_gb_ACD57316.1_	0.36	22	0.574	22	0.949	13	0.921	0.737	Y	0.57	SignalP-noTM
gi_188519374_gb_ACD57319.1_	0.126	22	0.226	15	0.621	12	0.468	0.34	N	0.57	SignalP-noTM
gi_188519376_gb_ACD57321.1_	0.177	64	0.24	16	0.695	46	0.435	0.332	N	0.57	SignalP-noTM
gi_188519377_gb_ACD57322.1_	0.814	19	0.883	19	0.976	9	0.954	0.916	Y	0.57	SignalP-noTM
gi_188519378_gb_ACD57323.1_	0.237	22	0.175	22	0.189	12	0.138	0.158	N	0.57	SignalP-noTM
gi_188519379_gb_ACD57324.1_	0.145	15	0.121	15	0.152	12	0.098	0.11	N	0.57	SignalP-noTM
gi_188519380_gb_ACD57325.1_	0.157	64	0.123	13	0.209	9	0.155	0.138	N	0.57	SignalP-noTM
gi_188519381_gb_ACD57326.1_	0.21	37	0.202	37	0.315	23	0.18	0.191	N	0.57	SignalP-noTM
gi_188519382_gb_ACD57327.1_	0.179	22	0.152	22	0.17	16	0.105	0.13	N	0.57	SignalP-noTM
gi_188519383_gb_ACD57328.1_	0.161	58	0.116	33	0.156	32	0.081	0.1	N	0.57	SignalP-noTM
gi_188519384_gb_ACD57329.1_	0.12	49	0.14	11	0.345	10	0.192	0.164	N	0.57	SignalP-noTM
gi_188519390_gb_ACD57335.1_	0.183	52	0.156	11	0.374	3	0.24	0.195	N	0.57	SignalP-noTM
gi_188519392_gb_ACD57337.1_	0.284	21	0.345	21	0.697	1	0.463	0.4	N	0.57	SignalP-noTM
gi_188519393_gb_ACD57338.1_	0.114	51	0.111	51	0.178	35	0.094	0.105	N	0.51	SignalP-TM
gi_188519394_gb_ACD57339.1_	0.112	19	0.102	46	0.14	62	0.081	0.094	N	0.51	SignalP-TM
gi_188519395_gb_ACD57340.1_	0.133	46	0.126	46	0.186	1	0.107	0.117	N	0.57	SignalP-noTM
gi_188519397_gb_ACD57342.1_	0.127	6	0.165	11	0.412	3	0.275	0.217	N	0.57	SignalP-noTM
gi_188519401_gb_ACD57346.1_	0.102	44	0.112	18	0.168	9	0.109	0.111	N	0.57	SignalP-noTM
gi_188519402_gb_ACD57347.1_	0.104	22	0.122	27	0.173	21	0.138	0.129	N	0.57	SignalP-noTM
gi_188519403_gb_ACD57348.1_	0.214	40	0.15	40	0.154	31	0.092	0.123	N	0.57	SignalP-noTM
gi_188519404_gb_ACD57349.1_	0.108	50	0.096	60	0.113	49	0.081	0.089	N	0.57	SignalP-noTM
gi_188519405_gb_ACD57350.1_	0.114	19	0.101	44	0.105	35	0.075	0.089	N	0.57	SignalP-noTM
gi_188519406_gb_ACD57351.1_	0.132	33	0.117	15	0.182	9	0.134	0.125	N	0.57	SignalP-noTM
gi_188519407_gb_ACD57352.1_	0.114	17	0.118	11	0.158	1	0.14	0.128	N	0.57	SignalP-noTM
gi_188519411_gb_ACD57356.1_	0.155	42	0.145	42	0.21	19	0.138	0.141	N	0.57	SignalP-noTM
gi_188519413_gb_ACD57358.1_	0.116	17	0.117	11	0.206	1	0.126	0.121	N	0.57	SignalP-noTM
gi_188519419_gb_ACD57364.1_	0.132	39	0.116	39	0.162	1	0.111	0.114	N	0.57	SignalP-noTM
gi_188519420_gb_ACD57365.1_	0.113	30	0.103	60	0.109	49	0.063	0.088	N	0.51	SignalP-TM
gi_188519421_gb_ACD57366.1_	0.203	25	0.22	25	0.289	23	0.225	0.222	N	0.51	SignalP-TM
gi_188519422_gb_ACD57367.1_	0.204	36	0.207	12	0.635	2	0.431	0.312	N	0.57	SignalP-noTM
gi_188519424_gb_ACD57369.1_	0.17	18	0.128	18	0.184	1	0.106	0.117	N	0.57	SignalP-noTM
gi_188519425_gb_ACD57370.1_	0.11	19	0.124	11	0.245	2	0.148	0.135	N	0.57	SignalP-noTM
gi_188519426_gb_ACD57371.1_	0.11	25	0.121	52	0.166	49	0.097	0.11	N	0.57	SignalP-noTM
gi_188519428_gb_ACD57373.1_	0.107	33	0.11	33	0.143	47	0.095	0.103	N	0.57	SignalP-noTM
gi_188519429_gb_ACD57374.1_	0.17	67	0.152	67	0.208	7	0.099	0.132	N	0.51	SignalP-TM
gi_188519433_gb_ACD57378.1_	0.14	32	0.111	32	0.131	31	0.08	0.096	N	0.57	SignalP-noTM
gi_188519434_gb_ACD57379.1_	0.101	26	0.128	12	0.191	6	0.166	0.146	N	0.57	SignalP-noTM
gi_188519440_gb_ACD57385.1_	0.107	57	0.108	11	0.177	2	0.113	0.11	N	0.57	SignalP-noTM
gi_188519441_gb_ACD57386.1_	0.111	26	0.123	26	0.181	18	0.115	0.119	N	0.57	SignalP-noTM
gi_188519442_gb_ACD57387.1_	0.108	36	0.123	12	0.205	3	0.15	0.136	N	0.57	SignalP-noTM
gi_188519443_gb_ACD57388.1_	0.655	24	0.8	24	0.995	12	0.972	0.881	Y	0.57	SignalP-noTM
gi_188519445_gb_ACD57390.1_	0.114	53	0.139	11	0.25	3	0.191	0.163	N	0.57	SignalP-noTM
gi_188519446_gb_ACD57391.1_	0.184	18	0.308	18	0.657	14	0.547	0.42	N	0.57	SignalP-noTM
gi_188519451_gb_ACD57396.1_	0.363	60	0.233	60	0.248	59	0.11	0.188	N	0.51	SignalP-TM
gi_188519452_gb_ACD57397.1_	0.451	15	0.597	15	0.885	12	0.793	0.689	Y	0.57	SignalP-noTM
gi_188519455_gb_ACD57400.1_	0.125	29	0.113	29	0.158	42	0.091	0.102	N	0.57	SignalP-noTM
gi_188519457_gb_ACD57402.1_	0.162	20	0.177	20	0.416	1	0.232	0.203	N	0.57	SignalP-noTM
gi_188519458_gb_ACD57403.1_	0.414	24	0.64	24	0.995	14	0.974	0.797	Y	0.57	SignalP-noTM
gi_188519469_gb_ACD57414.1_	0.17	35	0.178	21	0.363	10	0.248	0.211	N	0.57	SignalP-noTM
gi_188519474_gb_ACD57419.1_	0.113	20	0.116	56	0.169	50	0.109	0.112	N	0.57	SignalP-noTM
gi_188519475_gb_ACD57420.1_	0.116	38	0.112	27	0.166	1	0.109	0.111	N	0.57	SignalP-noTM
gi_188519478_gb_ACD57423.1_	0.172	39	0.175	15	0.283	8	0.227	0.2	N	0.57	SignalP-noTM
gi_188519479_gb_ACD57424.1_	0.11	64	0.114	29	0.13	20	0.103	0.109	N	0.57	SignalP-noTM
gi_188519480_gb_ACD57425.1_	0.156	42	0.146	42	0.219	19	0.143	0.145	N	0.57	SignalP-noTM
gi_188519481_gb_ACD57426.1_	0.29	17	0.184	17	0.246	16	0.121	0.154	N	0.57	SignalP-noTM
gi_188519482_gb_ACD57427.1_	0.32	29	0.284	29	0.51	1	0.304	0.292	N	0.51	SignalP-TM
gi_188519483_gb_ACD57428.1_	0.279	69	0.273	24	0.769	1	0.472	0.367	N	0.57	SignalP-noTM
gi_188519487_gb_ACD57432.1_	0.157	54	0.162	54	0.246	53	0.13	0.147	N	0.57	SignalP-noTM
gi_188519490_gb_ACD57435.1_	0.119	40	0.117	40	0.208	1	0.084	0.105	N	0.51	SignalP-TM
gi_188519491_gb_ACD57436.1_	0.116	52	0.106	37	0.133	39	0.083	0.097	N	0.51	SignalP-TM
gi_188519492_gb_ACD57437.1_	0.141	52	0.163	11	0.411	1	0.25	0.195	N	0.51	SignalP-TM
gi_188519493_gb_ACD57438.1_	0.276	55	0.186	19	0.441	2	0.279	0.22	N	0.51	SignalP-TM
gi_188519494_gb_ACD57439.1_	0.142	39	0.103	57	0.17	1	0.077	0.093	N	0.51	SignalP-TM
gi_188519495_gb_ACD57440.1_	0.157	33	0.158	13	0.302	12	0.231	0.185	N	0.51	SignalP-TM
gi_188519497_gb_ACD57442.1_	0.159	63	0.124	63	0.177	22	0.093	0.112	N	0.51	SignalP-TM
gi_188519498_gb_ACD57443.1_	0.215	55	0.267	55	0.505	25	0.3	0.283	N	0.57	SignalP-noTM
gi_188519499_gb_ACD57444.1_	0.139	44	0.137	16	0.231	6	0.183	0.158	N	0.57	SignalP-noTM
gi_188519500_gb_ACD57445.1_	0.569	30	0.657	23	0.983	17	0.908	0.775	Y	0.57	SignalP-noTM
gi_188519657_gb_ACD57602.1_	0.144	23	0.122	50	0.179	46	0.093	0.111	N	0.51	SignalP-TM
gi_188519658_gb_ACD57603.1_	0.718	18	0.75	18	0.896	16	0.766	0.758	Y	0.57	SignalP-noTM
gi_188519659_gb_ACD57604.1_	0.549	26	0.622	26	0.894	1	0.766	0.69	Y	0.57	SignalP-noTM
gi_188519661_gb_ACD57606.1_	0.156	42	0.146	42	0.219	19	0.143	0.145	N	0.57	SignalP-noTM
gi_188519663_gb_ACD57608.1_	0.105	44	0.132	11	0.268	1	0.166	0.148	N	0.57	SignalP-noTM
gi_188519667_gb_ACD57612.1_	0.107	27	0.128	11	0.215	5	0.176	0.146	N	0.51	SignalP-TM
gi_188519671_gb_ACD57616.1_	0.133	30	0.209	14	0.557	10	0.436	0.316	N	0.57	SignalP-noTM

0.23041	0.211318	0.297757	0.246495	gi_188519690_gb_ACD57635.1_
0.624103	0.040504	0.704121	0.456243	gi_188519692_gb_ACD57637.1_
0.196234	0.356405	0.208334	0.253658	gi_188519694_gb_ACD57639.1_
0.189233	0.932453	0.085489	0.402392	gi_188519695_gb_ACD57640.1_
0.148552	0.936494	0.171505	0.41885	gi_188519698_gb_ACD57643.1_
0.906954	0.979807	0.896042	0.927601	gi_188519701_gb_ACD57646.1_
0.478264	0.351603	0.62551	0.485126	gi_188519707_gb_ACD57652.1_
0.075928	0.003615	0.103123	0.060889	gi_188519708_gb_ACD57653.1_
0.485004	0.962421	0.759876	0.735767	gi_188519710_gb_ACD57655.1_
0.938255	0.913568	0.873471	0.908431	gi_188519717_gb_ACD57662.1_
0.161921	0.157493	0.416781	0.245398	gi_188519727_gb_ACD57672.1_
0.158691	0.027787	0.201974	0.129484	gi_188519735_gb_ACD57680.1_
0.112645	0.073237	0.139314	0.108399	gi_188519736_gb_ACD57681.1_
0.235232	0.966818	0.117533	0.439861	gi_188519737_gb_ACD57682.1_
0.621284	0.523982	0.745926	0.630397	gi_188519738_gb_ACD57683.1_
0.281709	0.180199	0.353658	0.271855	gi_188519740_gb_ACD57685.1_
0.868413	0.429228	0.880271	0.725971	gi_188519756_gb_ACD57701.1_
0.935956	0.49925	0.870794	0.768667	gi_188519762_gb_ACD57707.1_
0.345473	0.985571	0.521736	0.617593	gi_188519763_gb_ACD57708.1_
0.107936	0.05255	0.135755	0.098747	gi_188519764_gb_ACD57709.1_
0.293385	0.59556	0.362622	0.417189	gi_188519767_gb_ACD57712.1_
0.084324	0.003954	0.119098	0.069125	gi_188519769_gb_ACD57714.1_
0.541157	0.95996	0.726711	0.742609	gi_188519771_gb_ACD57716.1_
0.353658	0.975277	0.600608	0.643181	gi_188519775_gb_ACD57720.1_
0.082262	0.007013	0.11847	0.069248	gi_188519778_gb_ACD57723.1_
0.079365	0.000108	0.132619	0.070697	gi_188519782_gb_ACD57727.1_
0.772239	0.827641	0.832716	0.810865	gi_188519784_gb_ACD57729.1_
0.689546	0.781597	0.651809	0.707651	gi_188519787_gb_ACD57732.1_
0.214333	0.035468	0.234154	0.161318	gi_188519790_gb_ACD57735.1_
0.110859	0.001421	0.144427	0.085569	gi_188519791_gb_ACD57736.1_
0.952438	0.973403	0.896321	0.940721	gi_188519793_gb_ACD57738.1_
0.187856	0.001732	0.256927	0.148838	gi_188519794_gb_ACD57739.1_
0.067547	0.10011	0.143687	0.103781	gi_188519795_gb_ACD57740.1_
0.800911	0.85705	0.848772	0.835578	gi_188519798_gb_ACD57743.1_
0.719504	0.043522	0.841709	0.534912	gi_188519799_gb_ACD57744.1_
0.055305	0.190156	0.183322	0.142928	gi_188519803_gb_ACD57748.1_
0.195761	0.906447	0.131244	0.411151	gi_188519804_gb_ACD57749.1_
0.144427	0.130903	0.220458	0.165263	gi_188519805_gb_ACD57750.1_
0.105931	0.034959	0.129882	0.090257	gi_188519806_gb_ACD57751.1_
0.154727	0.11847	0.172359	0.148519	gi_188519807_gb_ACD57752.1_
0.101744	0.097704	0.096651	0.0987	gi_188519808_gb_ACD57753.1_
0.228818	0.09104	0.158291	0.159383	gi_188519812_gb_ACD57757.1_
0.119098	0.125868	0.087145	0.110704	gi_188519813_gb_ACD57758.1_
0.563407	0.96869	0.705993	0.74603	gi_188519814_gb_ACD57759.1_
0.158291	0.688261	0.168962	0.338505	gi_188519823_gb_ACD57768.1_
0.082944	0.074055	0.126529	0.094509	gi_188519824_gb_ACD57769.1_
0.094319	0.147795	0.088346	0.110153	gi_188519825_gb_ACD57770.1_
0.088346	0.041927	0.122927	0.0844	gi_188519826_gb_ACD57771.1_
0.602765	0.094063	0.715246	0.470691	gi_188519827_gb_ACD57772.1_
0.915676	0.998354	0.851827	0.921952	gi_188519828_gb_ACD57773.1_
0.101744	0.064044	0.103679	0.089822	gi_188519829_gb_ACD57774.1_
0.157493	0.344795	0.108806	0.203698	gi_188519830_gb_ACD57775.1_
0.147795	0.059357	0.234693	0.147282	gi_188519831_gb_ACD57776.1_
0.122927	0.867381	0.094576	0.361628	gi_188519837_gb_ACD57782.1_
0.102293	0.056893	0.132619	0.097268	gi_188519841_gb_ACD57786.1_
0.090792	0.061054	0.108515	0.086787	gi_188519842_gb_ACD57787.1_
0.139674	0.238486	0.119413	0.165858	gi_188519843_gb_ACD57788.1_
0.147041	0.181532	0.213829	0.180801	gi_188519844_gb_ACD57789.1_
0.876425	0.983809	0.802342	0.887525	gi_188519845_gb_ACD57790.1_
0.126861	0.039696	0.147795	0.104784	gi_188519846_gb_ACD57791.1_
0.783639	0.947599	0.75823	0.829823	gi_188519847_gb_ACD57792.1_
0.117222	0.15046	0.107072	0.124918	gi_188519849_gb_ACD57794.1_
0.101744	0.051956	0.106215	0.086638	gi_188519850_gb_ACD57795.1_
0.70287	0.990806	0.686972	0.793549	gi_188519851_gb_ACD57796.1_
0.114153	0.057216	0.155907	0.109092	gi_188519852_gb_ACD57797.1_
0.884933	0.030502	0.850306	0.58858	gi_188519858_gb_ACD57803.1_
0.087624	0.237398	0.086195	0.137072	gi_188519859_gb_ACD57804.1_
0.089806	0.035571	0.095091	0.073489	gi_188519863_gb_ACD57808.1_
0.089317	0.028609	0.121639	0.079855	gi_188519864_gb_ACD57809.1_
0.119413	0.020735	0.144056	0.094735	gi_188519865_gb_ACD57810.1_
0.221491	0.967201	0.072831	0.420508	gi_188519868_gb_ACD57813.1_
0.183772	0.061399	0.288434	0.177868	gi_188519869_gb_ACD57814.1_
0.072628	0.030061	0.122604	0.075098	gi_188519872_gb_ACD57817.1_
0.907962	0.880902	0.899348	0.896071	gi_188519873_gb_ACD57818.1_
0.202943	0.843301	0.27508	0.440441	gi_188519875_gb_ACD57820.1_
0.105081	0.002977	0.153164	0.087074	gi_188519876_gb_ACD57821.1_
0.101744	0.028776	0.198134	0.109551	gi_188519877_gb_ACD57822.1_
0.080691	0.031493	0.100652	0.070945	gi_188519878_gb_ACD57823.1_

gi_188519672_gb_ACD57617.1_	0.105	37	0.111	14	0.17	5	0.122	0.116	N	0.57	SignalP-noTM
gi_188519673_gb_ACD57618.1_	0.151	18	0.132	18	0.182	36	0.116	0.124	N	0.57	SignalP-noTM
gi_188519674_gb_ACD57619.1_	0.109	29	0.131	11	0.274	1	0.162	0.146	N	0.57	SignalP-noTM
gi_188519675_gb_ACD57620.1_	0.106	48	0.137	14	0.269	6	0.186	0.16	N	0.57	SignalP-noTM
gi_188519678_gb_ACD57623.1_	0.138	25	0.291	16	0.78	12	0.639	0.455	N	0.57	SignalP-noTM
gi_188519679_gb_ACD57624.1_	0.17	18	0.203	18	0.333	1	0.264	0.226	N	0.51	SignalP-TM
gi_188519680_gb_ACD57625.1_	0.163	51	0.144	11	0.345	1	0.196	0.169	N	0.57	SignalP-noTM
gi_188519681_gb_ACD57626.1_	0.263	22	0.498	22	0.975	17	0.944	0.708	Y	0.57	SignalP-noTM
gi_188519682_gb_ACD57627.1_	0.811	22	0.88	22	0.966	18	0.952	0.914	Y	0.57	SignalP-noTM
gi_188519683_gb_ACD57628.1_	0.168	43	0.215	13	0.533	10	0.427	0.315	N	0.57	SignalP-noTM
gi_188519686_gb_ACD57631.1_	0.574	46	0.344	46	0.286	41	0.147	0.271	N	0.51	SignalP-TM
gi_188519689_gb_ACD57634.1_	0.133	21	0.126	21	0.183	1	0.126	0.126	N	0.57	SignalP-noTM
gi_188519690_gb_ACD57635.1_	0.29	40	0.205	40	0.298	11	0.154	0.186	N	0.51	SignalP-TM
gi_188519692_gb_ACD57637.1_	0.399	34	0.381	29	0.938	19	0.74	0.55	N	0.57	SignalP-noTM
gi_188519694_gb_ACD57639.1_	0.196	29	0.235	29	0.613	10	0.384	0.29	N	0.51	SignalP-TM
gi_188519695_gb_ACD57640.1_	0.235	27	0.136	27	0.129	1	0.073	0.106	N	0.57	SignalP-noTM
gi_188519698_gb_ACD57643.1_	0.143	48	0.115	48	0.133	26	0.097	0.106	N	0.57	SignalP-noTM
gi_188519701_gb_ACD57646.1_	0.149	45	0.124	45	0.202	27	0.127	0.125	N	0.57	SignalP-noTM
gi_188519707_gb_ACD57652.1_	0.12	8	0.1	47	0.112	7	0.087	0.094	N	0.57	SignalP-noTM
gi_188519708_gb_ACD57653.1_	0.11	34	0.196	26	0.471	24	0.328	0.258	N	0.57	SignalP-noTM
gi_188519710_gb_ACD57655.1_	0.114	19	0.165	19	0.319	9	0.229	0.195	N	0.57	SignalP-noTM
gi_188519717_gb_ACD57662.1_	0.705	21	0.802	21	0.984	8	0.93	0.862	Y	0.57	SignalP-noTM
gi_188519727_gb_ACD57672.1_	0.115	22	0.116	11	0.173	1	0.134	0.124	N	0.57	SignalP-noTM
gi_188519735_gb_ACD57680.1_	0.141	20	0.132	20	0.268	1	0.136	0.134	N	0.57	SignalP-noTM
gi_188519736_gb_ACD57681.1_	0.127	67	0.125	53	0.199	49	0.121	0.124	N	0.51	SignalP-TM
gi_188519737_gb_ACD57682.1_	0.136	35	0.125	35	0.161	11	0.117	0.121	N	0.57	SignalP-noTM
gi_188519738_gb_ACD57683.1_	0.323	25	0.557	25	0.992	18	0.958	0.745	Y	0.57	SignalP-noTM
gi_188519740_gb_ACD57685.1_	0.153	46	0.196	11	0.504	1	0.369	0.277	N	0.57	SignalP-noTM
gi_188519756_gb_ACD57701.1_	0.112	27	0.113	11	0.171	3	0.134	0.123	N	0.57	SignalP-noTM
gi_188519762_gb_ACD57707.1_	0.145	13	0.14	13	0.21	7	0.135	0.137	N	0.57	SignalP-noTM
gi_188519763_gb_ACD57708.1_	0.186	21	0.212	21	0.34	17	0.24	0.225	N	0.57	SignalP-noTM
gi_188519764_gb_ACD57709.1_	0.111	50	0.122	50	0.158	10	0.109	0.116	N	0.57	SignalP-noTM
gi_188519767_gb_ACD57712.1_	0.102	18	0.102	51	0.114	50	0.075	0.089	N	0.57	SignalP-noTM
gi_188519769_gb_ACD57714.1_	0.17	22	0.149	22	0.228	2	0.154	0.151	N	0.57	SignalP-noTM
gi_188519771_gb_ACD57716.1_	0.122	27	0.173	17	0.351	12	0.262	0.215	N	0.57	SignalP-noTM
gi_188519775_gb_ACD57720.1_	0.103	37	0.158	17	0.324	10	0.251	0.202	N	0.57	SignalP-noTM
gi_188519778_gb_ACD57723.1_	0.135	22	0.12	47	0.177	44	0.088	0.105	N	0.57	SignalP-noTM
gi_188519782_gb_ACD57727.1_	0.1	26	0.1	26	0.111	16	0.096	0.098	N	0.57	SignalP-noTM
gi_188519784_gb_ACD57729.1_	0.144	55	0.122	12	0.169	2	0.141	0.131	N	0.57	SignalP-noTM
gi_188519787_gb_ACD57732.1_	0.111	64	0.109	64	0.149	50	0.086	0.098	N	0.57	SignalP-noTM
gi_188519790_gb_ACD57735.1_	0.132	55	0.116	55	0.134	2	0.103	0.11	N	0.57	SignalP-noTM
gi_188519791_gb_ACD57736.1_	0.126	50	0.174	11	0.418	4	0.296	0.231	N	0.57	SignalP-noTM
gi_188519793_gb_ACD57738.1_	0.156	43	0.225	43	0.656	39	0.182	0.205	N	0.57	SignalP-noTM
gi_188519794_gb_ACD57739.1_	0.218	56	0.148	56	0.361	1	0.14	0.144	N	0.57	SignalP-noTM
gi_188519795_gb_ACD57740.1_	0.155	32	0.119	32	0.15	30	0.073	0.102	N	0.51	SignalP-TM
gi_188519798_gb_ACD57743.1_	0.14	20	0.19	20	0.465	1	0.269	0.227	N	0.57	SignalP-noTM
gi_188519799_gb_ACD57744.1_	0.16	42	0.177	42	0.383	3	0.223	0.194	N	0.51	SignalP-TM
gi_188519803_gb_ACD57748.1_	0.122	36	0.121	18	0.182	9	0.138	0.127	N	0.51	SignalP-TM
gi_188519804_gb_ACD57749.1_	0.111	33	0.106	15	0.128	14	0.114	0.109	N	0.51	SignalP-TM
gi_188519805_gb_ACD57750.1_	0.254	28	0.209	28	0.291	18	0.161	0.192	N	0.51	SignalP-TM
gi_188519806_gb_ACD57751.1_	0.128	50	0.118	23	0.154	7	0.115	0.117	N	0.57	SignalP-noTM
gi_188519807_gb_ACD57752.1_	0.164	23	0.156	23	0.299	2	0.183	0.166	N	0.51	SignalP-TM
gi_188519808_gb_ACD57753.1_	0.183	39	0.164	39	0.274	35	0.119	0.143	N	0.57	SignalP-noTM
gi_188519812_gb_ACD57757.1_	0.133	51	0.145	23	0.262	4	0.2	0.171	N	0.57	SignalP-noTM
gi_188519813_gb_ACD57758.1_	0.131	20	0.102	20	0.11	47	0.084	0.094	N	0.57	SignalP-noTM
gi_188519814_gb_ACD57759.1_	0.533	23	0.721	23	0.985	20	0.946	0.827	Y	0.57	SignalP-noTM
gi_188519823_gb_ACD57768.1_	0.137	60	0.116	60	0.118	49	0.094	0.105	N	0.57	SignalP-noTM
gi_188519824_gb_ACD57769.1_	0.114	43	0.112	11	0.168	1	0.121	0.116	N	0.57	SignalP-noTM
gi_188519825_gb_ACD57770.1_	0.185	31	0.125	31	0.232	2	0.09	0.108	N	0.57	SignalP-noTM
gi_188519826_gb_ACD57771.1_	0.14	65	0.115	65	0.129	1	0.087	0.102	N	0.57	SignalP-noTM
gi_188519827_gb_ACD57772.1_	0.55	26	0.654	26	0.909	12	0.824	0.734	Y	0.57	SignalP-noTM
gi_188519828_gb_ACD57773.1_	0.888	23	0.916	23	0.97	19	0.934	0.924	Y	0.57	SignalP-noTM
gi_188519829_gb_ACD57774.1_	0.128	20	0.101	70	0.128	10	0.08	0.091	N	0.57	SignalP-noTM
gi_188519830_gb_ACD57775.1_	0.115	52	0.114	11	0.183	1	0.122	0.118	N	0.57	SignalP-noTM
gi_188519831_gb_ACD57776.1_	0.152	27	0.175	17	0.374	8	0.263	0.207	N	0.51	SignalP-TM
gi_188519837_gb_ACD57782.1_	0.156	21	0.136	11	0.211	4	0.188	0.16	N	0.57	SignalP-noTM
gi_188519841_gb_ACD57786.1_	0.166	19	0.123	32	0.143	29	0.096	0.11	N	0.57	SignalP-noTM
gi_188519842_gb_ACD57787.1_	0.179	28	0.138	28	0.183	26	0.105	0.122	N	0.57	SignalP-noTM
gi_188519843_gb_ACD57788.1_	0.151	64	0.12	64	0.14	4	0.097	0.109	N	0.57	SignalP-noTM
gi_188519844_gb_ACD57789.1_	0.151	26	0.24	19	0.707	17	0.433	0.331	N	0.57	SignalP-noTM
gi_188519845_gb_ACD57790.1_	0.819	26	0.892	26	0.986	22	0.952	0.92	Y	0.57	SignalP-noTM
gi_188519846_gb_ACD57791.1_	0.111	60	0.106	54	0.124	9	0.095	0.101	N	0.57	SignalP-noTM
gi_188519847_gb_ACD57792.1_	0.636	15	0.578	15	0.781	12	0.54	0.56	N	0.57	SignalP-noTM
gi_188519849_gb_ACD57794.1_	0.166	18	0.152	18	0.185	14	0.125	0.139	N	0.57	SignalP-noTM
gi_188519850_gb_ACD57795.1_	0.135	17	0.103	24	0.133	1	0.084	0.094	N	0.57	SignalP-noTM
gi_188519851_gb_ACD57796.1_	0.267	29	0.213	29	0.462	1	0.253	0.232	N	0.57	SignalP-noTM
gi_188519852_gb_ACD57797.1_	0.14	45	0.114	45	0.166	1	0.092	0.106	N	0.51	SignalP-TM
gi_188519858_gb_ACD57803.1_	0.107	48	0.145	42	0.258	36	0.134	0.14	N	0.57	SignalP-noTM

0.080247	0.001621	0.128532	0.070133	gi_188519879_gb_ACD57824.1_
0.49775	0.95064	0.402995	0.617128	gi_188519880_gb_ACD57825.1_
0.088588	0.042778	0.106786	0.079384	gi_188519886_gb_ACD57831.1_
0.073237	0.001861	0.106215	0.060438	gi_188519887_gb_ACD57832.1_
0.103958	0.050068	0.119098	0.091041	gi_188519888_gb_ACD57833.1_
0.100652	0.055777	0.128532	0.094987	gi_188519889_gb_ACD57834.1_
0.334033	0.033569	0.375897	0.247833	gi_188519893_gb_ACD57838.1_
0.920853	0.831879	0.900429	0.884387	gi_188519894_gb_ACD57839.1_
0.160704	0.077415	0.142217	0.126779	gi_188519895_gb_ACD57840.1_
0.266198	0.868413	0.186032	0.440214	gi_188519898_gb_ACD57843.1_
0.138955	0.063151	0.250115	0.15074	gi_188519899_gb_ACD57844.1_
0.190618	0.005236	0.260957	0.15227	gi_188519905_gb_ACD57850.1_
0.074675	0.047698	0.077629	0.066667	gi_188519906_gb_ACD57851.1_
0.173217	0.178873	0.263278	0.205123	gi_188519908_gb_ACD57853.1_
0.900698	0.956478	0.851827	0.903001	gi_188519909_gb_ACD57854.1_
0.175375	0.597005	0.146665	0.306348	gi_188519914_gb_ACD57859.1_
0.093046	0.445468	0.077629	0.205381	gi_188519915_gb_ACD57860.1_
0.159896	0.055462	0.186487	0.133948	gi_188519916_gb_ACD57861.1_
0.107072	0.067358	0.106786	0.093739	gi_188519917_gb_ACD57862.1_
0.161109	0.085959	0.149313	0.132127	gi_188519918_gb_ACD57863.1_
0.092289	0.024292	0.104518	0.0737	gi_188519939_gb_ACD57884.1_
0.447692	0.953779	0.633904	0.678458	gi_188519968_gb_ACD57913.1_
0.061745	0.029627	0.093299	0.061557	gi_188519975_gb_ACD57920.1_
0.390074	0.573709	0.380836	0.448206	gi_188519976_gb_ACD57921.1_
0.289051	0.331369	0.313028	0.311149	gi_188519977_gb_ACD57922.1_
0.86283	0.871804	0.810306	0.848313	gi_188519978_gb_ACD57923.1_
0.631812	0.731452	0.600608	0.654624	gi_188519979_gb_ACD57924.1_
0.9015	0.018762	0.9015	0.607254	gi_188519980_gb_ACD57925.1_
0.074468	0.046089	0.132964	0.084507	gi_188519981_gb_ACD57926.1_
0.711566	0.031493	0.770122	0.504394	gi_188519982_gb_ACD57927.1_
0.883397	0.270912	0.832716	0.662342	gi_188519987_gb_ACD57932.1_
0.102569	0.055777	0.131587	0.096644	gi_188519988_gb_ACD57933.1_
0.095349	0.019379	0.140759	0.085162	gi_188519989_gb_ACD57934.1_
0.136461	0.048246	0.21232	0.132342	gi_188519990_gb_ACD57935.1_
0.825058	0.999887	0.599888	0.808278	gi_188519993_gb_ACD57938.1_
0.083173	0.035571	0.119098	0.079281	gi_188519994_gb_ACD57939.1_
0.071824	0.001934	0.074675	0.049478	gi_188519995_gb_ACD57940.1_
0.068306	0.002681	0.105081	0.058689	gi_188519996_gb_ACD57941.1_
0.127527	0.007971	0.166866	0.100788	gi_188519997_gb_ACD57942.1_
0.111749	0.452147	0.124227	0.229374	gi_188519998_gb_ACD57943.1_
0.079805	0.028609	0.138238	0.082217	gi_188519999_gb_ACD57944.1_
0.196234	0.599168	0.131244	0.308882	gi_188520005_gb_ACD57950.1_
0.473026	0.897155	0.649081	0.673087	gi_188520006_gb_ACD57951.1_
0.13193	0.090792	0.182873	0.135198	gi_188520007_gb_ACD57952.1_
0.079805	0.089074	0.160704	0.109861	gi_188520008_gb_ACD57953.1_
0.217891	0.980621	0.083631	0.427381	gi_188520010_gb_ACD57955.1_
0.790675	0.286591	0.868756	0.648674	gi_188520012_gb_ACD57957.1_
0.120999	0.036404	0.182873	0.113425	gi_188520019_gb_ACD57964.1_
0.944223	0.999765	0.890903	0.944964	gi_188520022_gb_ACD57967.1_
0.953911	0.999502	0.893785	0.949066	gi_188520024_gb_ACD57969.1_
0.951478	0.999772	0.898256	0.949835	gi_188520027_gb_ACD57972.1_
0.954174	0.999472	0.895482	0.949709	gi_188520031_gb_ACD57976.1_
0.770653	0.846056	0.836033	0.817581	gi_188520041_gb_ACD57986.1_
0.959379	0.948485	0.9015	0.936455	gi_188520043_gb_ACD57988.1_
0.721316	0.8397	0.813513	0.79151	gi_188520044_gb_ACD57989.1_
0.093808	0.020075	0.335369	0.149751	gi_188520048_gb_ACD57993.1_
0.798026	0.059693	0.779542	0.545754	gi_188520049_gb_ACD57994.1_
0.189694	0.066982	0.258649	0.171775	gi_188520050_gb_ACD57995.1_
0.147418	0.047562	0.197658	0.130879	gi_188520051_gb_ACD57996.1_
0.107647	0.022577	0.140397	0.090207	gi_188520058_gb_ACD58003.1_
0.124227	0.161109	0.104518	0.129951	gi_188520059_gb_ACD58004.1_
0.104238	0.06054	0.121639	0.095472	gi_188520060_gb_ACD58005.1_
0.040388	0.184222	0.07385	0.099487	gi_188520061_gb_ACD58006.1_
0.107072	0.004377	0.171505	0.094318	gi_188520062_gb_ACD58007.1_
0.105647	0.041328	0.118784	0.088586	gi_188520064_gb_ACD58009.1_
0.069655	0.226707	0.084788	0.12705	gi_188520065_gb_ACD58010.1_
0.092541	0.06192	0.095091	0.083184	gi_188520066_gb_ACD58011.1_
0.142217	0.033764	0.174078	0.116686	gi_188520067_gb_ACD58012.1_
0.123251	0.112047	0.129882	0.121727	gi_188520068_gb_ACD58013.1_
0.744216	0.897707	0.831038	0.82432	gi_188520071_gb_ACD58016.1_
0.93946	0.999859	0.8966	0.945306	gi_188520072_gb_ACD58017.1_
0.8935	0.970373	0.680485	0.848119	gi_188520073_gb_ACD58018.1_
0.467795	0.886753	0.647713	0.66742	gi_188520080_gb_ACD58025.1_
0.935414	0.99561	0.872473	0.934499	gi_188520081_gb_ACD58026.1_
0.197182	0.759328	0.108225	0.354912	gi_188520092_gb_ACD58037.1_
0.791171	0.989239	0.612777	0.797729	gi_188520094_gb_ACD58039.1_
0.069074	0.021103	0.168121	0.086099	gi_188520095_gb_ACD58040.1_
0.923861	0.841309	0.892064	0.885745	gi_188520097_gb_ACD58042.1_

gi_188519859_gb_ACD57804.1_	0.117	63	0.103	48	0.128	36	0.094	0.099	N	0.57	SignalP-noTM
gi_188519863_gb_ACD57808.1_	0.125	57	0.105	57	0.105	54	0.088	0.097	N	0.57	SignalP-noTM
gi_188519864_gb_ACD57809.1_	0.106	50	0.106	50	0.134	22	0.086	0.097	N	0.57	SignalP-noTM
gi_188519865_gb_ACD57810.1_	0.11	17	0.103	59	0.116	53	0.089	0.097	N	0.57	SignalP-noTM
gi_188519868_gb_ACD57813.1_	0.133	59	0.121	38	0.138	31	0.095	0.109	N	0.57	SignalP-noTM
gi_188519869_gb_ACD57814.1_	0.316	34	0.213	34	0.249	8	0.155	0.192	N	0.51	SignalP-TM
gi_188519872_gb_ACD57817.1_	0.125	37	0.106	37	0.126	15	0.095	0.101	N	0.57	SignalP-noTM
gi_188519873_gb_ACD57818.1_	0.163	24	0.15	33	0.239	31	0.139	0.145	N	0.57	SignalP-noTM
gi_188519875_gb_ACD57820.1_	0.115	22	0.146	13	0.28	9	0.215	0.178	N	0.57	SignalP-noTM
gi_188519876_gb_ACD57821.1_	0.122	67	0.127	11	0.253	1	0.145	0.135	N	0.57	SignalP-noTM
gi_188519877_gb_ACD57822.1_	0.229	65	0.162	36	0.261	33	0.172	0.166	N	0.57	SignalP-noTM
gi_188519878_gb_ACD57823.1_	0.136	25	0.156	22	0.232	14	0.167	0.161	N	0.57	SignalP-noTM
gi_188519879_gb_ACD57824.1_	0.125	26	0.114	26	0.146	25	0.098	0.107	N	0.57	SignalP-noTM
gi_188519880_gb_ACD57825.1_	0.121	55	0.176	50	0.437	41	0.173	0.175	N	0.57	SignalP-noTM
gi_188519886_gb_ACD57831.1_	0.119	26	0.097	69	0.102	66	0.072	0.085	N	0.57	SignalP-noTM
gi_188519887_gb_ACD57832.1_	0.197	34	0.173	34	0.201	42	0.147	0.161	N	0.57	SignalP-noTM
gi_188519888_gb_ACD57833.1_	0.126	33	0.141	36	0.306	35	0.14	0.141	N	0.57	SignalP-noTM
gi_188519889_gb_ACD57834.1_	0.391	62	0.189	62	0.12	48	0.088	0.142	N	0.57	SignalP-noTM
gi_188519893_gb_ACD57838.1_	0.102	59	0.112	18	0.17	10	0.11	0.111	N	0.57	SignalP-noTM
gi_188519894_gb_ACD57839.1_	0.161	32	0.187	32	0.346	29	0.2	0.191	N	0.51	SignalP-TM
gi_188519895_gb_ACD57840.1_	0.133	27	0.131	16	0.232	11	0.162	0.146	N	0.57	SignalP-noTM
gi_188519898_gb_ACD57843.1_	0.128	56	0.146	56	0.204	46	0.139	0.143	N	0.57	SignalP-noTM
gi_188519899_gb_ACD57844.1_	0.227	42	0.156	42	0.256	5	0.123	0.144	N	0.51	SignalP-TM
gi_188519905_gb_ACD57850.1_	0.142	23	0.151	11	0.375	1	0.214	0.18	N	0.57	SignalP-noTM
gi_188519906_gb_ACD57851.1_	0.105	53	0.1	31	0.112	22	0.075	0.088	N	0.57	SignalP-noTM
gi_188519908_gb_ACD57853.1_	0.144	23	0.217	21	0.58	2	0.387	0.28	N	0.51	SignalP-TM
gi_188519909_gb_ACD57854.1_	0.129	23	0.118	40	0.164	32	0.104	0.111	N	0.57	SignalP-noTM
gi_188519914_gb_ACD57859.1_	0.124	25	0.22	11	0.578	1	0.483	0.344	N	0.57	SignalP-noTM
gi_188519915_gb_ACD57860.1_	0.189	25	0.157	25	0.382	1	0.161	0.159	N	0.57	SignalP-noTM
gi_188519916_gb_ACD57861.1_	0.194	41	0.194	41	0.337	37	0.148	0.173	N	0.57	SignalP-noTM
gi_188519917_gb_ACD57862.1_	0.106	52	0.106	32	0.123	26	0.095	0.1	N	0.57	SignalP-noTM
gi_188519918_gb_ACD57863.1_	0.184	60	0.14	60	0.163	10	0.098	0.12	N	0.57	SignalP-noTM
gi_188519939_gb_ACD57884.1_	0.107	33	0.107	58	0.125	48	0.103	0.105	N	0.57	SignalP-noTM
gi_188519968_gb_ACD57913.1_	0.11	36	0.144	11	0.292	3	0.21	0.175	N	0.57	SignalP-noTM
gi_188519975_gb_ACD57920.1_	0.115	39	0.114	11	0.243	3	0.125	0.119	N	0.57	SignalP-noTM
gi_188519976_gb_ACD57921.1_	0.136	45	0.112	45	0.172	1	0.091	0.102	N	0.57	SignalP-noTM
gi_188519977_gb_ACD57922.1_	0.15	33	0.122	39	0.18	44	0.09	0.107	N	0.57	SignalP-noTM
gi_188519978_gb_ACD57923.1_	0.129	53	0.14	53	0.198	44	0.107	0.124	N	0.57	SignalP-noTM
gi_188519979_gb_ACD57924.1_	0.14	34	0.161	42	0.357	33	0.131	0.147	N	0.57	SignalP-noTM
gi_188519980_gb_ACD57925.1_	0.273	33	0.294	33	0.594	18	0.335	0.313	N	0.57	SignalP-noTM
gi_188519981_gb_ACD57926.1_	0.11	6	0.095	69	0.115	1	0.08	0.088	N	0.57	SignalP-noTM
gi_188519982_gb_ACD57927.1_	0.131	43	0.205	11	0.512	1	0.418	0.305	N	0.57	SignalP-noTM
gi_188519987_gb_ACD57932.1_	0.306	27	0.488	22	0.961	20	0.893	0.678	Y	0.57	SignalP-noTM
gi_188519988_gb_ACD57933.1_	0.206	29	0.181	29	0.284	13	0.184	0.182	N	0.51	SignalP-TM
gi_188519989_gb_ACD57934.1_	0.199	22	0.18	22	0.351	50	0.159	0.172	N	0.51	SignalP-TM
gi_188519990_gb_ACD57935.1_	0.184	29	0.213	29	0.532	27	0.246	0.225	N	0.51	SignalP-TM
gi_188519993_gb_ACD57938.1_	0.1	23	0.1	11	0.132	1	0.097	0.098	N	0.57	SignalP-noTM
gi_188519994_gb_ACD57939.1_	0.174	28	0.134	28	0.118	34	0.097	0.117	N	0.57	SignalP-noTM
gi_188519995_gb_ACD57940.1_	0.111	15	0.105	15	0.129	10	0.096	0.101	N	0.57	SignalP-noTM
gi_188519996_gb_ACD57941.1_	0.115	25	0.122	13	0.171	8	0.15	0.135	N	0.57	SignalP-noTM
gi_188519997_gb_ACD57942.1_	0.107	66	0.126	42	0.187	39	0.117	0.122	N	0.57	SignalP-noTM
gi_188519998_gb_ACD57943.1_	0.155	69	0.118	69	0.135	14	0.097	0.108	N	0.57	SignalP-noTM
gi_188519999_gb_ACD57944.1_	0.235	27	0.141	27	0.189	1	0.102	0.123	N	0.57	SignalP-noTM
gi_188520005_gb_ACD57950.1_	0.205	31	0.168	11	0.428	1	0.261	0.211	N	0.57	SignalP-noTM
gi_188520006_gb_ACD57951.1_	0.212	24	0.135	24	0.247	3	0.119	0.128	N	0.57	SignalP-noTM
gi_188520007_gb_ACD57952.1_	0.336	21	0.446	21	0.654	11	0.528	0.476	N	0.51	SignalP-TM
gi_188520008_gb_ACD57953.1_	0.166	55	0.124	70	0.12	2	0.085	0.105	N	0.57	SignalP-noTM
gi_188520010_gb_ACD57955.1_	0.113	20	0.102	11	0.157	1	0.099	0.101	N	0.57	SignalP-noTM
gi_188520012_gb_ACD57957.1_	0.284	21	0.381	21	0.672	14	0.501	0.438	N	0.57	SignalP-noTM
gi_188520019_gb_ACD57964.1_	0.126	20	0.104	47	0.119	45	0.08	0.093	N	0.57	SignalP-noTM
gi_188520022_gb_ACD57967.1_	0.424	27	0.591	27	0.931	19	0.852	0.714	Y	0.57	SignalP-noTM
gi_188520024_gb_ACD57969.1_	0.424	27	0.591	27	0.931	19	0.852	0.714	Y	0.57	SignalP-noTM
gi_188520027_gb_ACD57972.1_	0.398	27	0.523	27	0.844	19	0.721	0.616	Y	0.57	SignalP-noTM
gi_188520031_gb_ACD57976.1_	0.398	27	0.523	27	0.844	19	0.721	0.616	Y	0.57	SignalP-noTM
gi_188520041_gb_ACD57986.1_	0.134	22	0.162	22	0.318	11	0.201	0.18	N	0.57	SignalP-noTM
gi_188520043_gb_ACD57988.1_	0.132	34	0.128	34	0.171	24	0.119	0.124	N	0.57	SignalP-noTM
gi_188520044_gb_ACD57989.1_	0.133	22	0.158	22	0.292	11	0.194	0.175	N	0.57	SignalP-noTM
gi_188520048_gb_ACD57993.1_	0.104	32	0.115	32	0.143	24	0.108	0.111	N	0.57	SignalP-noTM
gi_188520049_gb_ACD57994.1_	0.874	22	0.908	22	0.97	17	0.937	0.922	Y	0.57	SignalP-noTM
gi_188520050_gb_ACD57995.1_	0.138	27	0.126	27	0.195	38	0.109	0.118	N	0.57	SignalP-noTM
gi_188520051_gb_ACD57996.1_	0.162	10	0.105	44	0.113	41	0.087	0.097	N	0.57	SignalP-noTM
gi_188520058_gb_ACD58003.1_	0.141	21	0.133	21	0.18	3	0.137	0.135	N	0.57	SignalP-noTM
gi_188520059_gb_ACD58004.1_	0.155	34	0.127	34	0.156	4	0.105	0.117	N	0.57	SignalP-noTM
gi_188520060_gb_ACD58005.1_	0.146	35	0.127	35	0.22	39	0.106	0.117	N	0.57	SignalP-noTM
gi_188520061_gb_ACD58006.1_	0.112	19	0.113	11	0.215	1	0.118	0.115	N	0.51	SignalP-TM
gi_188520062_gb_ACD58007.1_	0.185	34	0.211	14	0.518	11	0.447	0.298	N	0.51	SignalP-TM
gi_188520064_gb_ACD58009.1_	0.108	48	0.103	48	0.139	6	0.103	0.103	N	0.57	SignalP-noTM
gi_188520065_gb_ACD58010.1_	0.24	26	0.168	26	0.261	1	0.112	0.142	N	0.57	SignalP-noTM

0.129544	0.02408	0.144798	0.099474	gi_188520098_gb_ACD58043.1_
0.075508	0.039696	0.090052	0.068419	gi_188520100_gb_ACD58045.1_
0.213325	0.718291	0.181087	0.370901	gi_188520101_gb_ACD58046.1_
0.399392	0.965243	0.143687	0.502774	gi_188520119_gb_ACD58064.1_
0.922799	0.919309	0.866342	0.902817	gi_188520120_gb_ACD58065.1_
0.900429	0.875773	0.834795	0.870332	gi_188520121_gb_ACD58066.1_
0.77539	0.99351	0.689546	0.819482	gi_188520122_gb_ACD58067.1_
0.064949	0.002625	0.084556	0.05071	gi_188520125_gb_ACD58070.1_
0.120363	0.047698	0.173217	0.113759	gi_188520126_gb_ACD58071.1_
0.413867	0.891775	0.523982	0.609875	gi_188520127_gb_ACD58072.1_
0.723722	0.201491	0.683088	0.5361	gi_188520129_gb_ACD58074.1_
0.290904	0.053911	0.377306	0.240707	gi_188520130_gb_ACD58075.1_
0.098234	0.034959	0.255784	0.129659	gi_188520136_gb_ACD58081.1_
0.217891	0.064405	0.278081	0.186792	gi_188520137_gb_ACD58082.1_
0.259225	0.064044	0.259225	0.194165	gi_188520138_gb_ACD58083.1_
0.157493	0.03059	0.087384	0.091822	gi_188520139_gb_ACD58084.1_
0.083402	0.032233	0.112047	0.075894	gi_188520280_gb_ACD58225.1_
0.140397	0.076139	0.137525	0.11802	gi_188520281_gb_ACD58226.1_
0.144798	0.088588	0.17023	0.134539	gi_188520282_gb_ACD58227.1_
0.897155	0.96296	0.878361	0.912825	gi_188520283_gb_ACD58228.1_
0.129206	0.172787	0.075928	0.125974	gi_188520284_gb_ACD58229.1_
0.185579	0.941969	0.101744	0.409764	gi_188520285_gb_ACD58230.1_
0.161921	0.434381	0.079365	0.225222	gi_188520287_gb_ACD58232.1_
0.07024	0.00054	0.1065	0.059093	gi_188520288_gb_ACD58233.1_
0.130562	0.04229	0.203915	0.125589	gi_188520289_gb_ACD58234.1_
0.131244	0.06054	0.127527	0.106437	gi_188520290_gb_ACD58235.1_
0.427025	0.043647	0.488752	0.319808	gi_188520291_gb_ACD58236.1_
0.144427	0.448434	0.108225	0.233695	gi_188520293_gb_ACD58238.1_
0.825491	0.120045	0.787178	0.577571	gi_188520301_gb_ACD58246.1_
0.172359	0.23308	0.303434	0.236291	gi_188520302_gb_ACD58247.1_
0.619871	0.056733	0.597726	0.424777	gi_528897473_gb_ACD58243.2_
0.149313	0.065866	0.145916	0.120365	gi_188520303_gb_ACD58248.1_
0.146665	0.282925	0.150844	0.193478	gi_188520304_gb_ACD58249.1_
0.095609	0.178873	0.178873	0.151118	gi_188520305_gb_ACD58250.1_
0.373086	0.389361	0.45289	0.405112	gi_188520306_gb_ACD58251.1_
0.256355	0.021796	0.292763	0.190305	gi_188520307_gb_ACD58252.1_
0.112047	0.234693	0.171505	0.172748	gi_188520308_gb_ACD58253.1_
0.953647	0.999099	0.919975	0.957574	gi_188520309_gb_ACD58254.1_
0.877718	0.976955	0.838891	0.897855	gi_188520310_gb_ACD58255.1_
0.119098	0.455121	0.085021	0.219747	gi_188520311_gb_ACD58256.1_
0.959612	0.99965	0.889731	0.949664	gi_188520312_gb_ACD58257.1_
0.823319	0.994308	0.844487	0.887371	gi_188520313_gb_ACD58258.1_
0.959145	0.961764	0.884627	0.935179	gi_188520314_gb_ACD58259.1_
0.125209	0.051809	0.165205	0.114074	gi_188520315_gb_ACD58260.1_
0.135404	0.033764	0.145916	0.105028	gi_188520330_gb_ACD58275.1_
0.108806	0.057704	0.142217	0.102909	gi_188520331_gb_ACD58276.1_
0.115679	0.122604	0.22461	0.154298	gi_188520334_gb_ACD58279.1_
0.225133	0.083402	0.334033	0.214189	gi_188520335_gb_ACD58280.1_
0.190618	0.884014	0.128196	0.400943	gi_188520338_gb_ACD58283.1_
0.089562	0.031768	0.109975	0.077102	gi_188520339_gb_ACD58284.1_
0.932074	0.928176	0.890319	0.916856	gi_188520343_gb_ACD58288.1_
0.080247	0.003365	0.109389	0.064334	gi_188520345_gb_ACD58290.1_
0.166034	0.651809	0.123575	0.313806	gi_188520356_gb_ACD58301.1_
0.053151	0.036934	0.147795	0.079293	gi_188520361_gb_ACD58306.1_
0.165205	0.011385	0.165205	0.113932	gi_188520362_gb_ACD58307.1_
0.956727	0.99995	0.837263	0.931313	gi_188520370_gb_ACD58315.1_
0.346831	0.887654	0.522485	0.585657	gi_188520380_gb_ACD58325.1_
0.105081	0.054681	0.163557	0.107773	gi_188520387_gb_ACD58332.1_
0.167702	0.76959	0.229878	0.389057	gi_188520390_gb_ACD58335.1_
0.82977	0.994903	0.536684	0.787119	gi_188520391_gb_ACD58336.1_
0.07871	0.001811	0.130562	0.070361	gi_188520392_gb_ACD58337.1_
0.723722	0.231475	0.65656	0.537252	gi_188520393_gb_ACD58338.1_
0.073441	0.014514	0.085021	0.057659	gi_188520394_gb_ACD58339.1_
0.759876	0.669295	0.660607	0.696593	gi_188520395_gb_ACD58340.1_
0.050931	0.042901	0.129882	0.074571	gi_188520396_gb_ACD58341.1_
0.084556	0.043647	0.110859	0.079687	gi_188520397_gb_ACD58342.1_
0.338721	0.840104	0.284144	0.487656	gi_188520400_gb_ACD58345.1_
0.094063	0.023591	0.133658	0.083771	gi_188520402_gb_ACD58347.1_
0.157892	0.190156	0.23041	0.192819	gi_188520403_gb_ACD58348.1_
0.054218	0.070045	0.071824	0.065362	gi_188520404_gb_ACD58349.1_
0.065131	0.05285	0.128196	0.082059	gi_188520405_gb_ACD58350.1_
0.17581	0.092793	0.195761	0.154788	gi_188520407_gb_ACD58352.1_
0.153164	0.102293	0.092793	0.116083	gi_188520413_gb_ACD58358.1_
0.089562	0.022248	0.174078	0.095296	gi_188520416_gb_ACD58361.1_
0.746494	0.985783	0.887953	0.87341	gi_188520417_gb_ACD58362.1_
0.840908	0.046221	0.618456	0.501862	gi_188520418_gb_ACD58363.1_
0.299643	0.219943	0.362622	0.294069	gi_188520419_gb_ACD58364.1_
0.141486	0.017741	0.190156	0.116461	gi_188520420_gb_ACD58365.1_

gi_188520066_gb_ACD58011.1_	0.385	43	0.308	43	0.523	37	0.268	0.289	N	0.57	SignalP-noTM
gi_188520067_gb_ACD58012.1_	0.109	50	0.137	12	0.261	4	0.188	0.161	N	0.57	SignalP-noTM
gi_188520068_gb_ACD58013.1_	0.106	24	0.137	13	0.265	10	0.191	0.162	N	0.57	SignalP-noTM
gi_188520071_gb_ACD58016.1_	0.115	22	0.146	13	0.28	9	0.215	0.178	N	0.57	SignalP-noTM
gi_188520072_gb_ACD58017.1_	0.738	25	0.761	25	0.963	21	0.83	0.794	Y	0.57	SignalP-noTM
gi_188520073_gb_ACD58018.1_	0.105	23	0.117	11	0.162	3	0.135	0.126	N	0.57	SignalP-noTM
gi_188520080_gb_ACD58025.1_	0.11	36	0.139	11	0.286	3	0.196	0.166	N	0.57	SignalP-noTM
gi_188520081_gb_ACD58026.1_	0.399	67	0.342	67	0.51	1	0.253	0.309	N	0.51	SignalP-TM
gi_188520092_gb_ACD58037.1_	0.113	42	0.12	11	0.194	5	0.156	0.133	N	0.51	SignalP-TM
gi_188520094_gb_ACD58039.1_	0.138	8	0.117	41	0.162	33	0.105	0.111	N	0.57	SignalP-noTM
gi_188520095_gb_ACD58040.1_	0.154	29	0.139	44	0.263	40	0.096	0.123	N	0.51	SignalP-TM
gi_188520097_gb_ACD58042.1_	0.248	21	0.439	21	0.905	1	0.822	0.619	Y	0.57	SignalP-noTM
gi_188520098_gb_ACD58043.1_	0.275	18	0.412	18	0.732	14	0.617	0.508	N	0.57	SignalP-noTM
gi_188520100_gb_ACD58045.1_	0.126	29	0.144	49	0.438	40	0.102	0.124	N	0.57	SignalP-noTM
gi_188520101_gb_ACD58046.1_	0.116	26	0.13	26	0.204	25	0.133	0.131	N	0.51	SignalP-TM
gi_188520119_gb_ACD58064.1_	0.145	23	0.273	11	0.895	4	0.797	0.52	N	0.57	SignalP-noTM
gi_188520120_gb_ACD58065.1_	0.241	21	0.46	21	0.942	14	0.896	0.665	Y	0.57	SignalP-noTM
gi_188520121_gb_ACD58066.1_	0.114	27	0.111	27	0.136	17	0.104	0.108	N	0.57	SignalP-noTM
gi_188520122_gb_ACD58067.1_	0.127	23	0.104	23	0.121	22	0.075	0.09	N	0.57	SignalP-noTM
gi_188520125_gb_ACD58070.1_	0.116	61	0.098	24	0.107	25	0.077	0.088	N	0.57	SignalP-noTM
gi_188520126_gb_ACD58071.1_	0.13	42	0.137	11	0.295	1	0.18	0.153	N	0.51	SignalP-TM
gi_188520127_gb_ACD58072.1_	0.144	26	0.117	32	0.145	39	0.093	0.106	N	0.57	SignalP-noTM
gi_188520129_gb_ACD58074.1_	0.192	32	0.128	11	0.269	1	0.151	0.139	N	0.57	SignalP-noTM
gi_188520130_gb_ACD58075.1_	0.15	43	0.159	43	0.282	42	0.173	0.166	N	0.57	SignalP-noTM
gi_188520136_gb_ACD58081.1_	0.117	47	0.1	47	0.111	65	0.08	0.091	N	0.57	SignalP-noTM
gi_188520137_gb_ACD58082.1_	0.115	28	0.1	61	0.107	46	0.083	0.092	N	0.57	SignalP-noTM
gi_188520138_gb_ACD58083.1_	0.199	36	0.15	36	0.187	35	0.077	0.123	N	0.51	SignalP-TM
gi_188520139_gb_ACD58084.1_	0.126	35	0.119	35	0.154	25	0.102	0.111	N	0.57	SignalP-noTM
gi_188520280_gb_ACD58225.1_	0.105	24	0.11	36	0.125	29	0.09	0.101	N	0.57	SignalP-noTM
gi_188520281_gb_ACD58226.1_	0.157	28	0.131	28	0.184	27	0.1	0.116	N	0.57	SignalP-noTM
gi_188520282_gb_ACD58227.1_	0.237	66	0.335	15	0.851	12	0.599	0.459	N	0.57	SignalP-noTM
gi_188520283_gb_ACD58228.1_	0.493	41	0.666	41	0.982	28	0.669	0.668	Y	0.57	SignalP-noTM
gi_188520284_gb_ACD58229.1_	0.177	35	0.12	14	0.163	5	0.14	0.129	N	0.57	SignalP-noTM
gi_188520285_gb_ACD58230.1_	0.101	40	0.111	54	0.144	50	0.09	0.101	N	0.57	SignalP-noTM
gi_188520287_gb_ACD58232.1_	0.136	27	0.134	27	0.232	34	0.14	0.137	N	0.57	SignalP-noTM
gi_188520288_gb_ACD58233.1_	0.106	27	0.105	53	0.14	43	0.086	0.096	N	0.57	SignalP-noTM
gi_188520289_gb_ACD58234.1_	0.178	20	0.116	20	0.147	53	0.083	0.1	N	0.57	SignalP-noTM
gi_188520290_gb_ACD58235.1_	0.104	70	0.103	26	0.134	1	0.102	0.102	N	0.57	SignalP-noTM
gi_188520291_gb_ACD58236.1_	0.118	44	0.101	44	0.11	47	0.072	0.088	N	0.57	SignalP-noTM
gi_188520293_gb_ACD58238.1_	0.147	47	0.161	11	0.322	2	0.255	0.205	N	0.57	SignalP-noTM
gi_528897473_gb_ACD58243.2_	0.116	66	0.12	58	0.201	1	0.109	0.115	N	0.57	SignalP-noTM
gi_188520301_gb_ACD58246.1_	0.116	66	0.12	58	0.201	1	0.109	0.115	N	0.57	SignalP-noTM
gi_188520302_gb_ACD58247.1_	0.155	53	0.164	36	0.367	2	0.202	0.178	N	0.51	SignalP-TM
gi_188520303_gb_ACD58248.1_	0.544	43	0.51	43	0.811	39	0.264	0.419	N	0.51	SignalP-TM
gi_188520304_gb_ACD58249.1_	0.136	30	0.165	30	0.448	1	0.201	0.178	N	0.51	SignalP-TM
gi_188520305_gb_ACD58250.1_	0.159	20	0.137	20	0.254	2	0.15	0.142	N	0.51	SignalP-TM
gi_188520306_gb_ACD58251.1_	0.257	30	0.266	23	0.688	4	0.462	0.338	N	0.51	SignalP-TM
gi_188520307_gb_ACD58252.1_	0.14	20	0.105	58	0.137	49	0.084	0.098	N	0.51	SignalP-TM
gi_188520308_gb_ACD58253.1_	0.155	23	0.161	23	0.221	9	0.174	0.166	N	0.51	SignalP-TM
gi_188520309_gb_ACD58254.1_	0.656	25	0.758	25	0.967	10	0.894	0.822	Y	0.57	SignalP-noTM
gi_188520310_gb_ACD58255.1_	0.178	51	0.13	16	0.269	23	0.15	0.139	N	0.57	SignalP-noTM
gi_188520311_gb_ACD58256.1_	0.107	21	0.109	52	0.184	2	0.103	0.106	N	0.57	SignalP-noTM
gi_188520312_gb_ACD58257.1_	0.162	36	0.194	36	0.42	34	0.184	0.189	N	0.57	SignalP-noTM
gi_188520313_gb_ACD58258.1_	0.242	14	0.283	14	0.544	10	0.337	0.308	N	0.57	SignalP-noTM
gi_188520314_gb_ACD58259.1_	0.763	38	0.747	38	0.965	29	0.806	0.774	Y	0.57	SignalP-noTM
gi_188520315_gb_ACD58260.1_	0.158	39	0.127	39	0.192	38	0.088	0.113	N	0.51	SignalP-TM
gi_188520330_gb_ACD58275.1_	0.225	21	0.182	21	0.237	1	0.158	0.171	N	0.57	SignalP-noTM
gi_188520331_gb_ACD58276.1_	0.126	8	0.123	12	0.236	7	0.154	0.137	N	0.57	SignalP-noTM
gi_188520334_gb_ACD58279.1_	0.178	20	0.172	20	0.384	2	0.188	0.178	N	0.51	SignalP-TM
gi_188520335_gb_ACD58280.1_	0.126	35	0.144	11	0.274	3	0.206	0.173	N	0.57	SignalP-noTM
gi_188520338_gb_ACD58283.1_	0.122	58	0.115	11	0.218	1	0.122	0.118	N	0.51	SignalP-TM
gi_188520339_gb_ACD58284.1_	0.127	39	0.179	39	0.366	31	0.223	0.195	N	0.51	SignalP-TM
gi_188520343_gb_ACD58288.1_	0.234	10	0.126	12	0.309	8	0.157	0.141	N	0.57	SignalP-noTM
gi_188520345_gb_ACD58290.1_	0.111	37	0.109	31	0.172	1	0.103	0.106	N	0.57	SignalP-noTM
gi_188520356_gb_ACD58301.1_	0.324	35	0.185	35	0.157	31	0.081	0.136	N	0.57	SignalP-noTM
gi_188520361_gb_ACD58306.1_	0.111	23	0.098	49	0.107	40	0.076	0.088	N	0.57	SignalP-noTM
gi_188520362_gb_ACD58307.1_	0.133	37	0.113	37	0.149	36	0.101	0.107	N	0.57	SignalP-noTM
gi_188520370_gb_ACD58315.1_	0.111	13	0.132	13	0.188	6	0.156	0.144	N	0.57	SignalP-noTM
gi_188520380_gb_ACD58325.1_	0.1	38	0.12	11	0.227	1	0.132	0.126	N	0.57	SignalP-noTM
gi_188520387_gb_ACD58332.1_	0.127	28	0.123	12	0.206	7	0.158	0.14	N	0.57	SignalP-noTM
gi_188520390_gb_ACD58335.1_	0.138	19	0.178	11	0.465	1	0.297	0.234	N	0.57	SignalP-noTM
gi_188520391_gb_ACD58336.1_	0.105	38	0.1	12	0.109	8	0.102	0.101	N	0.57	SignalP-noTM
gi_188520392_gb_ACD58337.1_	0.124	43	0.163	11	0.429	1	0.242	0.2	N	0.57	SignalP-noTM
gi_188520393_gb_ACD58338.1_	0.298	23	0.515	23	0.944	14	0.903	0.697	Y	0.57	SignalP-noTM
gi_188520394_gb_ACD58339.1_	0.135	25	0.134	11	0.214	4	0.18	0.156	N	0.57	SignalP-noTM
gi_188520395_gb_ACD58340.1_	0.118	46	0.131	11	0.206	3	0.174	0.151	N	0.57	SignalP-noTM
gi_188520396_gb_ACD58341.1_	0.107	46	0.107	70	0.128	69	0.093	0.1	N	0.57	SignalP-noTM
gi_188520397_gb_ACD58342.1_	0.195	34	0.148	34	0.272	1	0.145	0.147	N	0.57	SignalP-noTM

0.741351	0.925739	0.685033	0.784041	gi_188520421_gb_ACD58366.1_
0.116912	0.062797	0.161921	0.113877	gi_188520422_gb_ACD58367.1_
0.886452	0.999742	0.544879	0.810358	gi_188520433_gb_ACD58378.1_
0.793639	0.671284	0.828921	0.764615	gi_188520440_gb_ACD58385.1_
0.14517	0.485754	0.092793	0.241239	gi_188520443_gb_ACD58388.1_
0.139314	0.141486	0.130562	0.137121	gi_188520449_gb_ACD58394.1_
0.144056	0.042047	0.177994	0.121366	gi_188520450_gb_ACD58395.1_
0.862475	0.631114	0.774867	0.756152	gi_188520453_gb_ACD58398.1_
0.083402	0.041091	0.13193	0.085474	gi_188520459_gb_ACD58404.1_
0.115373	0.063506	0.135404	0.104761	gi_188520460_gb_ACD58405.1_
0.082716	0.016577	0.087145	0.062146	gi_188520461_gb_ACD58406.1_
0.1603	0.733216	0.116912	0.336809	gi_188520462_gb_ACD58407.1_
0.107647	0.001473	0.206361	0.10516	gi_188520463_gb_ACD58408.1_
0.518741	0.817574	0.458099	0.598138	gi_188520464_gb_ACD58409.1_
0.065498	0.023112	0.065681	0.05143	gi_188520467_gb_ACD58412.1_
0.105647	0.072024	0.080247	0.085973	gi_188520468_gb_ACD58413.1_
0.272693	0.004236	0.406609	0.227846	gi_188520470_gb_ACD58415.1_
0.14517	0.068498	0.284754	0.166141	gi_188520471_gb_ACD58416.1_
0.36749	0.976131	0.392933	0.578851	gi_188520472_gb_ACD58417.1_
0.147041	0.174078	0.233617	0.184912	gi_188520473_gb_ACD58418.1_
0.144427	0.004325	0.272099	0.140284	gi_188520474_gb_ACD58419.1_
0.353658	0.005508	0.467048	0.275405	gi_188520475_gb_ACD58420.1_
0.273885	0.763145	0.314967	0.450666	gi_188520476_gb_ACD58421.1_
0.123901	0.071425	0.24177	0.145699	gi_188520477_gb_ACD58422.1_
0.285978	0.07635	0.375897	0.246075	gi_188520478_gb_ACD58423.1_
0.522485	0.978647	0.697833	0.732988	gi_188520479_gb_ACD58424.1_
0.954436	0.899076	0.937203	0.930238	gi_188520480_gb_ACD58425.1_
0.227233	0.036934	0.528469	0.264212	gi_188520482_gb_ACD58427.1_
0.061399	0.033961	0.094319	0.063226	gi_188520483_gb_ACD58428.1_
0.887654	0.996905	0.823319	0.902626	gi_188520484_gb_ACD58429.1_
0.080468	0.000977	0.126529	0.069325	gi_188520485_gb_ACD58430.1_
0.300903	0.147041	0.290285	0.246076	gi_188520486_gb_ACD58431.1_
0.148173	0.054218	0.180643	0.127678	gi_188520487_gb_ACD58432.1_
0.807524	0.628316	0.808919	0.748253	gi_188520488_gb_ACD58433.1_
0.105364	0.112645	0.179314	0.132441	gi_188520489_gb_ACD58434.1_
0.960985	0.994083	0.89989	0.951653	gi_188520492_gb_ACD58437.1_
0.839296	0.991337	0.750447	0.86036	gi_188520493_gb_ACD58438.1_
0.942133	0.776433	0.877073	0.865213	gi_188520494_gb_ACD58439.1_
0.136461	0.029369	0.115067	0.093632	gi_188520495_gb_ACD58440.1_
0.761514	0.772239	0.812144	0.781966	gi_188520496_gb_ACD58441.1_
0.209325	0.992194	0.248431	0.483317	gi_188520497_gb_ACD58442.1_
0.765846	0.798991	0.838079	0.800972	gi_188520499_gb_ACD58444.1_
0.07806	0.026753	0.129206	0.078006	gi_188520500_gb_ACD58445.1_
0.649081	0.178433	0.751569	0.526361	gi_188520501_gb_ACD58446.1_
0.203429	0.85483	0.115067	0.391109	gi_188520505_gb_ACD58450.1_
0.239031	0.284144	0.182426	0.2352	gi_188520506_gb_ACD58451.1_
0.200528	0.865297	0.108225	0.39135	gi_188520511_gb_ACD58456.1_
0.693387	0.892064	0.769058	0.784836	gi_188520520_gb_ACD58465.1_
0.954174	0.986238	0.898256	0.946223	gi_188520524_gb_ACD58469.1_
0.127862	0.01278	0.207839	0.11616	gi_188520525_gb_ACD58470.1_
0.137881	0.005097	0.168121	0.1037	gi_188520526_gb_ACD58471.1_
0.102845	0.055462	0.137525	0.098611	gi_188520527_gb_ACD58472.1_
0.196708	0.064224	0.290904	0.183945	gi_188520532_gb_ACD58477.1_
0.084788	0.168962	0.144798	0.132849	gi_188520533_gb_ACD58478.1_
0.946394	0.995986	0.92129	0.954557	gi_188520534_gb_ACD58479.1_
0.087624	0.056094	0.09984	0.081186	gi_188520535_gb_ACD58480.1_
0.946089	0.999953	0.769058	0.905033	gi_188520536_gb_ACD58481.1_
0.102018	0.034959	0.171931	0.102969	gi_188520540_gb_ACD58485.1_
0.082489	0.036299	0.115986	0.078258	gi_188520541_gb_ACD58486.1_
0.179314	0.167702	0.24177	0.196262	gi_188520542_gb_ACD58487.1_
0.13331	0.075299	0.194818	0.134476	gi_188520543_gb_ACD58488.1_
0.083631	0.051956	0.097176	0.077588	gi_188520545_gb_ACD58490.1_
0.084092	0.022843	0.105931	0.070955	gi_188520551_gb_ACD58496.1_
0.154727	0.0985	0.152775	0.135334	gi_188520552_gb_ACD58497.1_
0.209325	0.466301	0.182426	0.286017	gi_188520553_gb_ACD58498.1_
0.173647	0.061572	0.223047	0.152755	gi_188520554_gb_ACD58499.1_
0.857417	0.770122	0.852959	0.826833	gi_188520557_gb_ACD58502.1_
0.915908	0.99988	0.734973	0.883587	gi_188520565_gb_ACD58510.1_
0.107936	0.088346	0.120363	0.105548	gi_188520567_gb_ACD58512.1_
0.134354	0.038016	0.162329	0.111566	gi_188520568_gb_ACD58513.1_
0.054064	0.034757	0.082036	0.056952	gi_188520569_gb_ACD58514.1_
0.251242	0.035468	0.270912	0.185874	gi_188520570_gb_ACD58515.1_
0.06192	0.000447	0.105081	0.055816	gi_188520571_gb_ACD58516.1_
0.144056	0.005641	0.225133	0.124943	gi_188520572_gb_ACD58517.1_
0.088588	0.05285	0.094576	0.078671	gi_188520573_gb_ACD58518.1_
0.095868	0.049219	0.130562	0.091883	gi_188520574_gb_ACD58519.1_
0.905167	0.999632	0.810306	0.905035	gi_188520575_gb_ACD58520.1_
0.695932	0.045826	0.690188	0.477315	gi_188520576_gb_ACD58521.1_

gi_188520400_gb_ACD58345.1_	0.139	33	0.12	33	0.113	30	0.082	0.102	N	0.57	SignalP-noTM
gi_188520402_gb_ACD58347.1_	0.153	45	0.119	45	0.13	13	0.092	0.106	N	0.57	SignalP-noTM
gi_188520403_gb_ACD58348.1_	0.135	51	0.121	51	0.124	29	0.1	0.111	N	0.57	SignalP-noTM
gi_188520404_gb_ACD58349.1_	0.125	44	0.181	12	0.459	1	0.286	0.23	N	0.57	SignalP-noTM
gi_188520405_gb_ACD58350.1_	0.111	27	0.176	11	0.471	2	0.294	0.231	N	0.57	SignalP-noTM
gi_188520407_gb_ACD58352.1_	0.108	56	0.111	22	0.165	14	0.1	0.107	N	0.51	SignalP-TM
gi_188520413_gb_ACD58358.1_	0.176	33	0.148	33	0.218	32	0.111	0.131	N	0.57	SignalP-noTM
gi_188520416_gb_ACD58361.1_	0.133	46	0.107	46	0.115	45	0.087	0.098	N	0.57	SignalP-noTM
gi_188520417_gb_ACD58362.1_	0.3	21	0.525	21	0.952	14	0.899	0.701	Y	0.57	SignalP-noTM
gi_188520418_gb_ACD58363.1_	0.102	50	0.116	35	0.174	49	0.111	0.113	N	0.57	SignalP-noTM
gi_188520419_gb_ACD58364.1_	0.185	23	0.242	23	0.44	20	0.296	0.262	N	0.51	SignalP-TM
gi_188520420_gb_ACD58365.1_	0.168	61	0.125	61	0.165	37	0.094	0.111	N	0.57	SignalP-noTM
gi_188520421_gb_ACD58366.1_	0.208	48	0.176	48	0.299	30	0.174	0.175	N	0.51	SignalP-TM
gi_188520422_gb_ACD58367.1_	0.158	66	0.132	35	0.231	34	0.132	0.132	N	0.57	SignalP-noTM
gi_188520433_gb_ACD58378.1_	0.107	22	0.133	11	0.27	1	0.165	0.148	N	0.57	SignalP-noTM
gi_188520440_gb_ACD58385.1_	0.113	18	0.109	44	0.127	40	0.091	0.1	N	0.57	SignalP-noTM
gi_188520443_gb_ACD58388.1_	0.102	63	0.201	18	0.583	15	0.37	0.28	N	0.57	SignalP-noTM
gi_188520449_gb_ACD58394.1_	0.125	43	0.112	11	0.177	1	0.119	0.116	N	0.57	SignalP-noTM
gi_188520450_gb_ACD58395.1_	0.132	40	0.129	11	0.312	1	0.144	0.136	N	0.57	SignalP-noTM
gi_188520453_gb_ACD58398.1_	0.117	20	0.111	20	0.126	11	0.098	0.105	N	0.57	SignalP-noTM
gi_188520459_gb_ACD58404.1_	0.207	59	0.139	59	0.12	20	0.089	0.116	N	0.57	SignalP-noTM
gi_188520460_gb_ACD58405.1_	0.119	45	0.108	45	0.122	7	0.099	0.104	N	0.57	SignalP-noTM
gi_188520461_gb_ACD58406.1_	0.115	45	0.146	11	0.307	26	0.217	0.179	N	0.57	SignalP-noTM
gi_188520462_gb_ACD58407.1_	0.116	37	0.117	46	0.19	38	0.103	0.111	N	0.57	SignalP-noTM
gi_188520463_gb_ACD58408.1_	0.146	47	0.143	11	0.26	3	0.215	0.17	N	0.51	SignalP-TM
gi_188520464_gb_ACD58409.1_	0.11	56	0.105	11	0.164	2	0.11	0.107	N	0.57	SignalP-noTM
gi_188520467_gb_ACD58412.1_	0.12	21	0.107	48	0.142	1	0.092	0.1	N	0.57	SignalP-noTM
gi_188520468_gb_ACD58413.1_	0.108	21	0.112	51	0.147	46	0.093	0.103	N	0.57	SignalP-noTM
gi_188520470_gb_ACD58415.1_	0.252	49	0.305	20	0.478	11	0.357	0.33	N	0.57	SignalP-noTM
gi_188520471_gb_ACD58416.1_	0.295	40	0.288	40	0.42	37	0.276	0.284	N	0.51	SignalP-TM
gi_188520472_gb_ACD58417.1_	0.159	17	0.219	17	0.453	1	0.326	0.269	N	0.57	SignalP-noTM
gi_188520473_gb_ACD58418.1_	0.451	23	0.347	23	0.479	2	0.316	0.336	N	0.51	SignalP-TM
gi_188520474_gb_ACD58419.1_	0.12	25	0.134	13	0.252	4	0.18	0.156	N	0.57	SignalP-noTM
gi_188520475_gb_ACD58420.1_	0.154	40	0.164	16	0.297	7	0.237	0.191	N	0.51	SignalP-TM
gi_188520476_gb_ACD58421.1_	0.155	42	0.145	42	0.21	19	0.138	0.141	N	0.57	SignalP-noTM
gi_188520477_gb_ACD58422.1_	0.129	18	0.181	11	0.512	1	0.315	0.231	N	0.51	SignalP-TM
gi_188520478_gb_ACD58423.1_	0.64	18	0.562	18	0.751	15	0.463	0.515	N	0.57	SignalP-noTM
gi_188520479_gb_ACD58424.1_	0.147	26	0.11	26	0.142	5	0.095	0.103	N	0.57	SignalP-noTM
gi_188520480_gb_ACD58425.1_	0.162	41	0.171	41	0.255	32	0.138	0.155	N	0.57	SignalP-noTM
gi_188520482_gb_ACD58427.1_	0.156	36	0.128	36	0.208	2	0.11	0.12	N	0.57	SignalP-noTM
gi_188520483_gb_ACD58428.1_	0.106	64	0.1	36	0.106	25	0.083	0.092	N	0.57	SignalP-noTM
gi_188520484_gb_ACD58429.1_	0.134	24	0.157	11	0.34	5	0.251	0.201	N	0.57	SignalP-noTM
gi_188520485_gb_ACD58430.1_	0.165	58	0.133	58	0.154	53	0.084	0.11	N	0.57	SignalP-noTM
gi_188520486_gb_ACD58431.1_	0.39	54	0.222	54	0.229	41	0.092	0.161	N	0.57	SignalP-noTM
gi_188520487_gb_ACD58432.1_	0.117	48	0.166	19	0.353	10	0.253	0.207	N	0.57	SignalP-noTM
gi_188520488_gb_ACD58433.1_	0.129	64	0.128	64	0.187	63	0.086	0.112	N	0.51	SignalP-TM
gi_188520489_gb_ACD58434.1_	0.174	26	0.147	26	0.224	8	0.145	0.146	N	0.51	SignalP-TM
gi_188520492_gb_ACD58437.1_	0.141	45	0.162	45	0.331	34	0.143	0.153	N	0.57	SignalP-noTM
gi_188520493_gb_ACD58438.1_	0.728	25	0.8	25	0.949	9	0.906	0.85	Y	0.57	SignalP-noTM
gi_188520494_gb_ACD58439.1_	0.814	24	0.89	24	0.987	11	0.968	0.927	Y	0.57	SignalP-noTM
gi_188520495_gb_ACD58440.1_	0.21	38	0.166	24	0.398	19	0.217	0.185	N	0.51	SignalP-TM
gi_188520496_gb_ACD58441.1_	0.571	32	0.622	32	0.9	24	0.707	0.662	Y	0.57	SignalP-noTM
gi_188520497_gb_ACD58442.1_	0.426	32	0.615	18	0.976	12	0.923	0.759	Y	0.57	SignalP-noTM
gi_188520499_gb_ACD58444.1_	0.133	22	0.168	22	0.33	11	0.21	0.188	N	0.57	SignalP-noTM
gi_188520500_gb_ACD58445.1_	0.104	33	0.108	33	0.119	21	0.084	0.096	N	0.57	SignalP-noTM
gi_188520501_gb_ACD58446.1_	0.118	63	0.11	53	0.122	45	0.085	0.099	N	0.57	SignalP-noTM
gi_188520505_gb_ACD58450.1_	0.122	47	0.113	25	0.144	1	0.102	0.108	N	0.57	SignalP-noTM
gi_188520506_gb_ACD58451.1_	0.167	38	0.138	38	0.169	2	0.125	0.132	N	0.57	SignalP-noTM
gi_188520511_gb_ACD58456.1_	0.122	47	0.113	25	0.144	1	0.102	0.108	N	0.57	SignalP-noTM
gi_188520520_gb_ACD58465.1_	0.115	22	0.108	27	0.158	19	0.097	0.103	N	0.57	SignalP-noTM
gi_188520524_gb_ACD58469.1_	0.804	29	0.871	29	0.971	25	0.93	0.899	Y	0.57	SignalP-noTM
gi_188520525_gb_ACD58470.1_	0.212	21	0.165	21	0.179	1	0.135	0.151	N	0.57	SignalP-noTM
gi_188520526_gb_ACD58471.1_	0.121	58	0.126	14	0.206	7	0.164	0.14	N	0.51	SignalP-TM
gi_188520527_gb_ACD58472.1_	0.14	29	0.156	18	0.311	11	0.19	0.172	N	0.57	SignalP-noTM
gi_188520532_gb_ACD58477.1_	0.119	42	0.128	50	0.196	46	0.11	0.12	N	0.57	SignalP-noTM
gi_188520533_gb_ACD58478.1_	0.147	40	0.139	13	0.251	4	0.171	0.151	N	0.51	SignalP-TM
gi_188520534_gb_ACD58479.1_	0.645	20	0.746	20	0.916	7	0.869	0.804	Y	0.57	SignalP-noTM
gi_188520535_gb_ACD58480.1_	0.174	19	0.126	19	0.144	18	0.093	0.11	N	0.57	SignalP-noTM
gi_188520536_gb_ACD58481.1_	0.123	7	0.133	14	0.335	6	0.177	0.154	N	0.57	SignalP-noTM
gi_188520540_gb_ACD58485.1_	0.136	27	0.112	35	0.16	3	0.104	0.108	N	0.57	SignalP-noTM
gi_188520541_gb_ACD58486.1_	0.189	31	0.179	31	0.272	13	0.187	0.182	N	0.51	SignalP-TM
gi_188520542_gb_ACD58487.1_	0.308	40	0.211	19	0.393	14	0.293	0.241	N	0.51	SignalP-TM
gi_188520543_gb_ACD58488.1_	0.106	42	0.1	31	0.115	13	0.087	0.094	N	0.57	SignalP-noTM
gi_188520545_gb_ACD58490.1_	0.15	31	0.126	31	0.173	27	0.076	0.103	N	0.57	SignalP-noTM
gi_188520551_gb_ACD58496.1_	0.119	27	0.18	12	0.39	4	0.326	0.234	N	0.51	SignalP-TM
gi_188520552_gb_ACD58497.1_	0.23	36	0.178	36	0.271	35	0.128	0.155	N	0.57	SignalP-noTM
gi_188520553_gb_ACD58498.1_	0.11	32	0.11	43	0.13	1	0.091	0.103	N	0.51	SignalP-TM
gi_188520554_gb_ACD58499.1_	0.108	40	0.109	40	0.137	39	0.093	0.101	N	0.57	SignalP-noTM

0.105364	0.134703	0.123901	0.121323	gi_188520586_gb_ACD58531.1_
0.9512	0.957467	0.848	0.918889	gi_188520587_gb_ACD58532.1_
0.958909	0.999755	0.909702	0.956122	gi_188520600_gb_ACD58545.1_
0.093046	0.028278	0.112946	0.07809	gi_188520602_gb_ACD58547.1_
0.861404	0.798991	0.827213	0.829203	gi_188520603_gb_ACD58548.1_
0.61562	0.983617	0.715246	0.771494	gi_188520607_gb_ACD58552.1_
0.214333	0.180199	0.154335	0.182956	gi_188520608_gb_ACD58553.1_
0.119729	0.069074	0.076988	0.088597	gi_188520609_gb_ACD58554.1_
0.191545	0.234693	0.247312	0.224517	gi_188520616_gb_ACD58561.1_
0.113247	0.014818	0.152775	0.093613	gi_188520617_gb_ACD58562.1_
0.232009	0.079805	0.258075	0.189963	gi_188520618_gb_ACD58563.1_
0.105081	0.054681	0.159494	0.106419	gi_188520620_gb_ACD58565.1_
0.171079	0.010477	0.234693	0.13875	gi_188520621_gb_ACD58566.1_
0.134703	0.342089	0.102845	0.193212	gi_188520622_gb_ACD58567.1_
0.237398	0.072024	0.337378	0.2156	gi_188520623_gb_ACD58568.1_
0.265612	0.045564	0.339393	0.216856	gi_188520626_gb_ACD58571.1_
0.103679	0.020918	0.113247	0.079281	gi_188520629_gb_ACD58574.1_
0.17023	0.024941	0.243977	0.146383	gi_188520632_gb_ACD58577.1_
0.943107	0.999817	0.817127	0.920017	gi_188520633_gb_ACD58578.1_
0.137525	0.048108	0.120999	0.102211	gi_188520635_gb_ACD58580.1_
0.830616	0.999941	0.570772	0.800443	gi_188520637_gb_ACD58582.1_
0.138596	0.267959	0.117845	0.1748	gi_188520640_gb_ACD58585.1_
0.920415	0.999568	0.879001	0.932995	gi_188520647_gb_ACD58592.1_
0.962094	0.999852	0.907711	0.956552	gi_188520650_gb_ACD58595.1_
0.784654	0.226181	0.806121	0.605652	gi_188520653_gb_ACD58598.1_
0.109681	0.045174	0.114762	0.089872	gi_188520654_gb_ACD58599.1_
0.260957	0.085021	0.250115	0.198698	gi_188520657_gb_ACD58602.1_
0.139674	0.035571	0.219943	0.131729	gi_188520659_gb_ACD58604.1_
0.93738	0.997958	0.851827	0.929055	gi_188520661_gb_ACD58606.1_
0.107072	0.036934	0.143687	0.095898	gi_188520662_gb_ACD58607.1_
0.100381	0.07806	0.171079	0.116507	gi_188520665_gb_ACD58610.1_
0.063151	0.037255	0.114762	0.071723	gi_188520666_gb_ACD58611.1_
0.089074	0.028195	0.1603	0.092523	gi_188520667_gb_ACD58612.1_
0.150844	0.06717	0.24122	0.153078	gi_188520683_gb_ACD58628.1_
0.110269	0.109975	0.083402	0.101215	gi_188520684_gb_ACD58629.1_
0.095868	0.024868	0.080247	0.066994	gi_188520685_gb_ACD58630.1_
0.075508	0.14517	0.124553	0.115077	gi_188520686_gb_ACD58631.1_
0.841709	0.841709	0.88153	0.854983	gi_188520690_gb_ACD58635.1_
0.246754	0.581029	0.255784	0.361189	gi_188520691_gb_ACD58636.1_
0.700987	0.983952	0.61633	0.76709	gi_188520692_gb_ACD58637.1_
0.883706	0.887654	0.908212	0.893191	gi_188520696_gb_ACD58641.1_
0.948191	0.999824	0.908462	0.952159	gi_188520697_gb_ACD58642.1_
0.161921	0.375194	0.113247	0.216787	gi_188520703_gb_ACD58648.1_
0.144427	0.097176	0.141851	0.127818	gi_188520704_gb_ACD58649.1_
0.085021	0.003246	0.138596	0.075621	gi_188520711_gb_ACD58656.1_
0.290285	0.757128	0.366793	0.471402	gi_188520717_gb_ACD58662.1_
0.841709	0.997852	0.722521	0.854027	gi_188520718_gb_ACD58663.1_
0.408058	0.294007	0.453634	0.385233	gi_188520720_gb_ACD58665.1_
0.378716	0.350919	0.612065	0.447233	gi_188520806_gb_ACD58751.1_
0.752129	0.993008	0.744216	0.829784	gi_188520807_gb_ACD58752.1_
0.117222	0.304703	0.278684	0.233536	gi_188520815_gb_ACD58760.1_
0.0985	0.192476	0.1603	0.150425	gi_188520816_gb_ACD58761.1_
0.126198	0.00851	0.16645	0.100386	gi_188520817_gb_ACD58762.1_
0.171931	0.027305	0.222527	0.140588	gi_188520818_gb_ACD58763.1_
0.09744	0.016143	0.167702	0.093762	gi_188520819_gb_ACD58764.1_
0.085255	0.072831	0.147041	0.101709	gi_188520820_gb_ACD58765.1_
0.578105	0.127862	0.705993	0.470653	gi_188520823_gb_ACD58768.1_
0.875119	0.995962	0.927169	0.93275	gi_188520824_gb_ACD58769.1_
0.113247	0.002721	0.155513	0.090494	gi_188520825_gb_ACD58770.1_
0.11847	0.026988	0.112047	0.085835	gi_188520828_gb_ACD58773.1_
0.920195	0.990444	0.831038	0.913892	gi_188520829_gb_ACD58774.1_
0.162737	0.041567	0.133658	0.112654	gi_188520833_gb_ACD58778.1_
0.435855	0.022511	0.554532	0.337633	gi_188520835_gb_ACD58780.1_
0.240672	0.02318	0.29463	0.186161	gi_188520836_gb_ACD58781.1_
0.153553	0.043149	0.174078	0.123593	gi_188520839_gb_ACD58784.1_
0.132964	0.085959	0.176245	0.131723	gi_188520840_gb_ACD58785.1_
0.895201	0.903086	0.851068	0.883118	gi_188520841_gb_ACD58786.1_
0.101197	0.081361	0.123251	0.101936	gi_188520842_gb_ACD58787.1_
0.340066	0.192476	0.429228	0.32059	gi_188520843_gb_ACD58788.1_
0.955723	0.999559	0.921072	0.958785	gi_188520845_gb_ACD58790.1_
0.726711	0.08181	0.693387	0.500636	gi_528897476_gb_ACD58650.2_
0.183322	0.253506	0.079147	0.171992	gi_188520846_gb_ACD58791.1_
0.368886	0.90361	0.185126	0.485874	gi_188520848_gb_ACD58793.1_
0.06054	0.022248	0.105081	0.062623	gi_188520849_gb_ACD58794.1_
0.93997	0.999598	0.888845	0.942804	gi_188520863_gb_ACD58808.1_
0.757128	0.960304	0.852205	0.856546	gi_188520865_gb_ACD58810.1_
0.10147	0.05869	0.114457	0.091539	gi_188520868_gb_ACD58813.1_
0.889731	0.639455	0.831879	0.787022	gi_188520871_gb_ACD58816.1_

gi_188520557_gb_ACD58502.1_	0.107	36	0.137	11	0.253	5	0.205	0.162	N	0.51	SignalP-TM
gi_188520565_gb_ACD58510.1_	0.104	37	0.118	37	0.177	33	0.111	0.114	N	0.57	SignalP-noTM
gi_188520567_gb_ACD58512.1_	0.103	29	0.101	11	0.204	1	0.086	0.094	N	0.57	SignalP-noTM
gi_188520568_gb_ACD58513.1_	0.43	40	0.644	40	0.989	29	0.783	0.709	Y	0.57	SignalP-noTM
gi_188520569_gb_ACD58514.1_	0.124	34	0.107	14	0.144	5	0.112	0.109	N	0.57	SignalP-noTM
gi_188520570_gb_ACD58515.1_	0.845	20	0.883	20	0.956	16	0.915	0.898	Y	0.57	SignalP-noTM
gi_188520571_gb_ACD58516.1_	0.121	21	0.137	11	0.32	1	0.178	0.156	N	0.57	SignalP-noTM
gi_188520572_gb_ACD58517.1_	0.182	23	0.125	23	0.114	55	0.084	0.106	N	0.57	SignalP-noTM
gi_188520573_gb_ACD58518.1_	0.105	59	0.101	59	0.112	47	0.084	0.093	N	0.57	SignalP-noTM
gi_188520574_gb_ACD58519.1_	0.132	51	0.118	51	0.168	1	0.111	0.115	N	0.57	SignalP-noTM
gi_188520575_gb_ACD58520.1_	0.134	49	0.107	65	0.136	34	0.091	0.101	N	0.51	SignalP-TM
gi_188520576_gb_ACD58521.1_	0.117	32	0.105	17	0.127	14	0.109	0.107	N	0.57	SignalP-noTM
gi_188520586_gb_ACD58531.1_	0.214	17	0.235	17	0.46	16	0.272	0.253	N	0.57	SignalP-noTM
gi_188520587_gb_ACD58532.1_	0.107	42	0.107	42	0.123	39	0.086	0.097	N	0.57	SignalP-noTM
gi_188520600_gb_ACD58545.1_	0.128	43	0.104	43	0.145	2	0.083	0.094	N	0.57	SignalP-noTM
gi_188520602_gb_ACD58547.1_	0.111	63	0.103	63	0.122	50	0.087	0.095	N	0.57	SignalP-noTM
gi_188520603_gb_ACD58548.1_	0.164	21	0.22	21	0.607	2	0.38	0.295	N	0.57	SignalP-noTM
gi_188520607_gb_ACD58552.1_	0.1	21	0.098	40	0.116	14	0.093	0.096	N	0.57	SignalP-noTM
gi_188520608_gb_ACD58553.1_	0.11	32	0.119	11	0.192	2	0.142	0.129	N	0.57	SignalP-noTM
gi_188520609_gb_ACD58554.1_	0.122	14	0.11	14	0.158	5	0.1	0.105	N	0.57	SignalP-noTM
gi_188520616_gb_ACD58561.1_	0.106	25	0.121	11	0.209	4	0.149	0.134	N	0.57	SignalP-noTM
gi_188520617_gb_ACD58562.1_	0.121	25	0.142	11	0.294	1	0.186	0.163	N	0.57	SignalP-noTM
gi_188520618_gb_ACD58563.1_	0.156	37	0.196	37	0.368	33	0.229	0.208	N	0.51	SignalP-TM
gi_188520620_gb_ACD58565.1_	0.133	21	0.123	21	0.166	1	0.108	0.116	N	0.57	SignalP-noTM
gi_188520621_gb_ACD58566.1_	0.153	24	0.262	21	0.739	3	0.559	0.401	N	0.57	SignalP-noTM
gi_188520622_gb_ACD58567.1_	0.158	36	0.127	36	0.177	34	0.104	0.116	N	0.57	SignalP-noTM
gi_188520623_gb_ACD58568.1_	0.119	32	0.167	48	0.436	44	0.173	0.17	N	0.57	SignalP-noTM
gi_188520626_gb_ACD58571.1_	0.231	42	0.242	42	0.38	6	0.244	0.243	N	0.51	SignalP-TM
gi_188520629_gb_ACD58574.1_	0.362	31	0.233	31	0.364	3	0.186	0.211	N	0.57	SignalP-noTM
gi_188520632_gb_ACD58577.1_	0.124	34	0.104	57	0.172	45	0.081	0.093	N	0.57	SignalP-noTM
gi_188520633_gb_ACD58578.1_	0.153	62	0.234	26	0.535	20	0.359	0.28	N	0.51	SignalP-TM
gi_188520635_gb_ACD58580.1_	0.114	22	0.218	11	0.567	1	0.481	0.341	N	0.57	SignalP-noTM
gi_188520637_gb_ACD58582.1_	0.099	18	0.114	18	0.167	7	0.124	0.119	N	0.57	SignalP-noTM
gi_188520640_gb_ACD58585.1_	0.171	26	0.213	26	0.672	17	0.259	0.234	N	0.57	SignalP-noTM
gi_188520647_gb_ACD58592.1_	0.589	27	0.343	27	0.332	23	0.175	0.281	N	0.51	SignalP-TM
gi_188520650_gb_ACD58595.1_	0.789	26	0.853	26	0.971	21	0.886	0.869	Y	0.57	SignalP-noTM
gi_188520653_gb_ACD58598.1_	0.118	65	0.181	11	0.43	3	0.33	0.251	N	0.57	SignalP-noTM
gi_188520654_gb_ACD58599.1_	0.108	48	0.105	58	0.136	6	0.103	0.104	N	0.57	SignalP-noTM
gi_188520657_gb_ACD58602.1_	0.117	37	0.105	37	0.098	31	0.076	0.091	N	0.57	SignalP-noTM
gi_188520659_gb_ACD58604.1_	0.126	34	0.142	34	0.209	33	0.114	0.129	N	0.57	SignalP-noTM
gi_188520661_gb_ACD58606.1_	0.169	30	0.321	19	0.827	13	0.738	0.517	N	0.57	SignalP-noTM
gi_188520662_gb_ACD58607.1_	0.108	58	0.1	67	0.114	2	0.086	0.093	N	0.57	SignalP-noTM
gi_188520665_gb_ACD58610.1_	0.116	34	0.124	34	0.207	30	0.113	0.12	N	0.51	SignalP-TM
gi_188520666_gb_ACD58611.1_	0.24	18	0.125	18	0.125	34	0.07	0.099	N	0.57	SignalP-noTM
gi_188520667_gb_ACD58612.1_	0.139	38	0.135	38	0.204	2	0.131	0.133	N	0.57	SignalP-noTM
gi_188520683_gb_ACD58628.1_	0.236	23	0.226	23	0.39	32	0.224	0.225	N	0.51	SignalP-TM
gi_188520684_gb_ACD58629.1_	0.162	30	0.122	30	0.149	34	0.075	0.105	N	0.51	SignalP-TM
gi_188520685_gb_ACD58630.1_	0.226	32	0.146	32	0.184	60	0.087	0.124	N	0.51	SignalP-TM
gi_188520686_gb_ACD58631.1_	0.145	26	0.164	11	0.352	3	0.279	0.206	N	0.51	SignalP-TM
gi_188520690_gb_ACD58635.1_	0.146	44	0.141	44	0.191	42	0.092	0.118	N	0.57	SignalP-noTM
gi_188520691_gb_ACD58636.1_	0.156	42	0.146	42	0.219	19	0.143	0.145	N	0.57	SignalP-noTM
gi_188520692_gb_ACD58637.1_	0.137	20	0.18	11	0.428	2	0.322	0.247	N	0.57	SignalP-noTM
gi_188520696_gb_ACD58641.1_	0.248	29	0.441	29	0.934	20	0.85	0.633	Y	0.57	SignalP-noTM
gi_188520697_gb_ACD58642.1_	0.187	35	0.167	35	0.322	2	0.146	0.157	N	0.57	SignalP-noTM
gi_188520703_gb_ACD58648.1_	0.112	34	0.114	70	0.178	67	0.08	0.102	N	0.51	SignalP-TM
gi_188520704_gb_ACD58649.1_	0.128	29	0.123	29	0.141	26	0.098	0.111	N	0.57	SignalP-noTM
gi_528897476_gb_ACD58650.2_	0.116	66	0.12	58	0.197	1	0.107	0.114	N	0.57	SignalP-noTM
gi_188520711_gb_ACD58656.1_	0.269	46	0.166	46	0.128	41	0.097	0.134	N	0.57	SignalP-noTM
gi_188520717_gb_ACD58662.1_	0.122	27	0.158	11	0.341	5	0.258	0.205	N	0.57	SignalP-noTM
gi_188520718_gb_ACD58663.1_	0.109	20	0.138	11	0.202	6	0.184	0.159	N	0.57	SignalP-noTM
gi_188520720_gb_ACD58665.1_	0.123	22	0.131	27	0.178	36	0.128	0.13	N	0.57	SignalP-noTM
gi_188520806_gb_ACD58751.1_	0.106	43	0.108	12	0.157	9	0.12	0.114	N	0.57	SignalP-noTM
gi_188520807_gb_ACD58752.1_	0.104	13	0.138	11	0.253	3	0.187	0.161	N	0.57	SignalP-noTM
gi_188520815_gb_ACD58760.1_	0.302	23	0.236	23	0.501	2	0.258	0.244	N	0.51	SignalP-TM
gi_188520816_gb_ACD58761.1_	0.122	27	0.147	27	0.275	23	0.153	0.149	N	0.51	SignalP-TM
gi_188520817_gb_ACD58762.1_	0.111	28	0.164	11	0.369	3	0.263	0.211	N	0.57	SignalP-noTM
gi_188520818_gb_ACD58763.1_	0.153	26	0.121	26	0.203	24	0.08	0.102	N	0.57	SignalP-noTM
gi_188520819_gb_ACD58764.1_	0.156	46	0.134	12	0.215	3	0.179	0.155	N	0.57	SignalP-noTM
gi_188520820_gb_ACD58765.1_	0.115	54	0.114	11	0.21	1	0.122	0.117	N	0.57	SignalP-noTM
gi_188520823_gb_ACD58768.1_	0.162	22	0.175	22	0.273	11	0.179	0.176	N	0.51	SignalP-TM
gi_188520824_gb_ACD58769.1_	0.114	50	0.111	50	0.139	47	0.095	0.103	N	0.57	SignalP-noTM
gi_188520825_gb_ACD58770.1_	0.207	20	0.12	20	0.102	35	0.077	0.1	N	0.57	SignalP-noTM
gi_188520828_gb_ACD58773.1_	0.146	25	0.137	25	0.209	1	0.127	0.132	N	0.57	SignalP-noTM
gi_188520829_gb_ACD58774.1_	0.455	45	0.497	45	0.77	37	0.286	0.398	N	0.57	SignalP-noTM
gi_188520833_gb_ACD58778.1_	0.118	27	0.143	11	0.26	1	0.198	0.169	N	0.57	SignalP-noTM
gi_188520835_gb_ACD58780.1_	0.153	26	0.144	26	0.278	18	0.149	0.147	N	0.57	SignalP-noTM
gi_188520836_gb_ACD58781.1_	0.121	24	0.242	24	0.668	13	0.514	0.37	N	0.57	SignalP-noTM
gi_188520839_gb_ACD58784.1_	0.151	32	0.126	32	0.163	31	0.091	0.109	N	0.57	SignalP-noTM

0.674586	0.601328	0.752688	0.676201	gi_188520873_gb_ACD58818.1_
0.939289	0.999681	0.926763	0.955244	gi_188520876_gb_ACD58821.1_
0.207346	0.02836	0.326733	0.18748	gi_188520880_gb_ACD58825.1_
0.195289	0.037148	0.199567	0.144001	gi_188520881_gb_ACD58826.1_
0.93283	0.97814	0.883088	0.931353	gi_188520886_gb_ACD58831.1_
0.924909	0.949358	0.883088	0.919118	gi_188520887_gb_ACD58832.1_
0.095609	0.279287	0.08181	0.152235	gi_188520890_gb_ACD58835.1_
0.178873	0.203429	0.164792	0.182365	gi_188520891_gb_ACD58836.1_
0.13193	0.23308	0.115986	0.160332	gi_188520897_gb_ACD58842.1_
0.886753	0.998697	0.738464	0.874638	gi_188520900_gb_ACD58845.1_
0.561192	0.768525	0.665967	0.665228	gi_188520903_gb_ACD58848.1_
0.171079	0.547853	0.103123	0.274018	gi_188520905_gb_ACD58850.1_
0.803292	0.855202	0.849923	0.836139	gi_188520906_gb_ACD58851.1_
0.868413	0.998823	0.727307	0.864848	gi_188520907_gb_ACD58852.1_
0.221491	0.100652	0.145916	0.15602	gi_188520910_gb_ACD58855.1_
0.197658	0.316263	0.277479	0.2638	gi_188520913_gb_ACD58858.1_
0.096129	0.04415	0.127194	0.089158	gi_188520927_gb_ACD58872.1_
0.096129	0.006647	0.115679	0.072818	gi_188520928_gb_ACD58873.1_
0.15046	0.153164	0.110269	0.137964	gi_188520933_gb_ACD58878.1_
0.175375	0.159896	0.19201	0.17576	gi_188520934_gb_ACD58879.1_
0.186032	0.053606	0.239577	0.159738	gi_188520935_gb_ACD58880.1_
0.781597	0.083862	0.699097	0.521519	gi_188520936_gb_ACD58881.1_
0.083402	0.049079	0.106786	0.079756	gi_188520937_gb_ACD58882.1_
0.079365	0.032609	0.108225	0.0734	gi_188520938_gb_ACD58883.1_
0.06192	0.031768	0.095349	0.063012	gi_188520939_gb_ACD58884.1_
0.128532	0.007203	0.155119	0.096951	gi_188520941_gb_ACD58886.1_
0.122282	0.040504	0.162737	0.108508	gi_188520953_gb_ACD58898.1_
0.096914	0.246197	0.080468	0.141193	gi_188520954_gb_ACD58899.1_
0.284754	0.724322	0.331369	0.446815	gi_188520955_gb_ACD58900.1_
0.144798	0.887654	0.330705	0.454386	gi_188520961_gb_ACD58906.1_
0.073645	0.044916	0.121639	0.080067	gi_188520967_gb_ACD58912.1_
0.196234	0.178433	0.094063	0.156243	gi_188520968_gb_ACD58913.1_
0.276878	0.668631	0.086195	0.343901	gi_188520972_gb_ACD58917.1_
0.297757	0.096651	0.260957	0.218455	gi_188520973_gb_ACD58918.1_
0.899619	0.989738	0.796571	0.895309	gi_188520983_gb_ACD58928.1_
0.207839	0.726115	0.092289	0.342081	gi_188520991_gb_ACD58936.1_
0.655205	0.997746	0.790178	0.814376	gi_188520997_gb_ACD58942.1_
0.23041	0.753803	0.229878	0.404697	gi_188520999_gb_ACD58944.1_
0.3858	0.942459	0.559714	0.629324	gi_188521000_gb_ACD58945.1_
0.357094	0.942784	0.529217	0.609698	gi_188521008_gb_ACD58953.1_
0.094833	0.001371	0.135053	0.077086	gi_188521009_gb_ACD58954.1_
0.09639	0.225133	0.071824	0.131116	gi_188521010_gb_ACD58955.1_
0.115067	0.06262	0.179756	0.119148	gi_188521011_gb_ACD58956.1_
0.076988	0.046221	0.086195	0.069801	gi_188521012_gb_ACD58957.1_
0.072225	0.090545	0.07635	0.079707	gi_188521013_gb_ACD58958.1_
0.159896	0.057704	0.21687	0.144823	gi_188521014_gb_ACD58959.1_
0.112645	0.016675	0.192476	0.107265	gi_188521015_gb_ACD58960.1_
0.127194	0.076139	0.128532	0.110622	gi_188521016_gb_ACD58961.1_
0.135404	0.036404	0.153553	0.108454	gi_188521017_gb_ACD58962.1_
0.153944	0.08181	0.136461	0.124072	gi_188521020_gb_ACD58965.1_
0.281102	0.558235	0.303434	0.380924	gi_188521021_gb_ACD58966.1_
0.160704	0.066051	0.240672	0.155809	gi_188521022_gb_ACD58967.1_
0.663962	0.06192	0.636684	0.454189	gi_528897477_gb_ACD58920.2_
0.833966	0.164379	0.799472	0.599272	gi_528897478_gb_ACD58925.2_
0.355718	0.049219	0.682438	0.362458	gi_188521024_gb_ACD58969.1_
0.157493	0.089806	0.126529	0.124609	gi_188521025_gb_ACD58970.1_
0.120681	0.09744	0.195289	0.137803	gi_188521027_gb_ACD58972.1_
0.13193	0.010987	0.13193	0.091616	gi_188521028_gb_ACD58973.1_
0.106215	0.000664	0.15046	0.08578	gi_188521029_gb_ACD58974.1_
0.765307	0.980848	0.905424	0.88386	gi_188521030_gb_ACD58975.1_
0.206853	0.386511	0.299643	0.297669	gi_188521031_gb_ACD58976.1_
0.933764	0.996821	0.945474	0.958686	gi_188521041_gb_ACD58986.1_
0.90361	0.95996	0.741351	0.868307	gi_188521042_gb_ACD58987.1_
0.193411	0.361929	0.080913	0.212084	gi_188521043_gb_ACD58988.1_
0.086669	0.032895	0.129544	0.083036	gi_188521045_gb_ACD58990.1_
0.085255	0.013125	0.115986	0.071455	gi_188521046_gb_ACD58991.1_
0.514996	0.932453	0.683737	0.710395	gi_188521050_gb_ACD58995.1_
0.10147	0.014386	0.104518	0.073458	gi_188521051_gb_ACD58996.1_
0.114762	0.016675	0.187856	0.106431	gi_188521052_gb_ACD58997.1_
0.714022	0.971887	0.591217	0.759042	gi_188521054_gb_ACD58999.1_
0.086195	0.300273	0.153944	0.180137	gi_188521055_gb_ACD59000.1_
0.115373	0.107936	0.123251	0.11552	gi_188521056_gb_ACD59001.1_
0.965243	0.992861	0.950358	0.969487	gi_188521057_gb_ACD59002.1_
0.076139	0.08181	0.110859	0.089603	gi_188521058_gb_ACD59003.1_
0.108225	0.120363	0.128196	0.118928	gi_188521060_gb_ACD59005.1_
0.171505	0.131587	0.161109	0.154734	gi_188521061_gb_ACD59006.1_
0.124227	0.158691	0.097176	0.126698	gi_188521062_gb_ACD59007.1_
0.095091	0.084556	0.092289	0.090645	gi_188521065_gb_ACD59010.1_

gi_188520840_gb_ACD58785.1_	0.142	42	0.166	33	0.343	24	0.208	0.182	N	0.51	SignalP-TM
gi_188520841_gb_ACD58786.1_	0.125	40	0.167	16	0.432	6	0.267	0.214	N	0.57	SignalP-noTM
gi_188520842_gb_ACD58787.1_	0.148	39	0.165	39	0.258	30	0.15	0.159	N	0.51	SignalP-TM
gi_188520843_gb_ACD58788.1_	0.217	21	0.444	21	0.961	10	0.914	0.665	Y	0.57	SignalP-noTM
gi_188520845_gb_ACD58790.1_	0.178	21	0.369	21	0.937	1	0.811	0.577	Y	0.57	SignalP-noTM
gi_188520846_gb_ACD58791.1_	0.175	33	0.147	33	0.215	32	0.11	0.13	N	0.57	SignalP-noTM
gi_188520848_gb_ACD58793.1_	0.153	35	0.13	37	0.276	34	0.095	0.114	N	0.57	SignalP-noTM
gi_188520849_gb_ACD58794.1_	0.101	36	0.102	62	0.143	1	0.096	0.099	N	0.57	SignalP-noTM
gi_188520863_gb_ACD58808.1_	0.399	21	0.358	21	0.577	20	0.37	0.363	N	0.57	SignalP-noTM
gi_188520865_gb_ACD58810.1_	0.197	20	0.163	20	0.226	1	0.147	0.156	N	0.57	SignalP-noTM
gi_188520868_gb_ACD58813.1_	0.153	24	0.131	24	0.153	14	0.117	0.125	N	0.57	SignalP-noTM
gi_188520871_gb_ACD58816.1_	0.329	21	0.53	21	0.929	17	0.838	0.675	Y	0.57	SignalP-noTM
gi_188520873_gb_ACD58818.1_	0.853	23	0.914	23	0.988	19	0.97	0.94	Y	0.57	SignalP-noTM
gi_188520876_gb_ACD58821.1_	0.107	36	0.099	55	0.107	43	0.082	0.091	N	0.57	SignalP-noTM
gi_188520880_gb_ACD58825.1_	0.154	31	0.114	37	0.146	36	0.072	0.094	N	0.57	SignalP-noTM
gi_188520881_gb_ACD58826.1_	0.192	30	0.162	20	0.277	1	0.209	0.184	N	0.57	SignalP-noTM
gi_188520886_gb_ACD58831.1_	0.119	46	0.125	46	0.154	34	0.107	0.117	N	0.57	SignalP-noTM
gi_188520887_gb_ACD58832.1_	0.168	15	0.21	15	0.382	13	0.269	0.238	N	0.57	SignalP-noTM
gi_188520890_gb_ACD58835.1_	0.121	7	0.111	30	0.132	10	0.103	0.107	N	0.57	SignalP-noTM
gi_188520891_gb_ACD58836.1_	0.106	22	0.128	11	0.217	1	0.164	0.141	N	0.51	SignalP-TM
gi_188520897_gb_ACD58842.1_	0.273	41	0.163	41	0.165	5	0.115	0.145	N	0.51	SignalP-TM
gi_188520900_gb_ACD58845.1_	0.233	22	0.192	22	0.3	2	0.167	0.18	N	0.57	SignalP-noTM
gi_188520903_gb_ACD58848.1_	0.189	26	0.155	17	0.258	13	0.168	0.161	N	0.57	SignalP-noTM
gi_188520905_gb_ACD58850.1_	0.113	42	0.117	11	0.181	5	0.145	0.127	N	0.51	SignalP-TM
gi_188520906_gb_ACD58851.1_	0.115	22	0.153	22	0.298	11	0.205	0.177	N	0.57	SignalP-noTM
gi_188520907_gb_ACD58852.1_	0.212	20	0.13	20	0.105	30	0.076	0.105	N	0.57	SignalP-noTM
gi_188520910_gb_ACD58855.1_	0.143	51	0.182	23	0.283	20	0.24	0.209	N	0.57	SignalP-noTM
gi_188520913_gb_ACD58858.1_	0.109	30	0.103	56	0.12	52	0.088	0.096	N	0.57	SignalP-noTM
gi_188520927_gb_ACD58872.1_	0.549	29	0.303	29	0.436	28	0.152	0.232	N	0.57	SignalP-noTM
gi_188520928_gb_ACD58873.1_	0.135	24	0.13	11	0.281	10	0.171	0.149	N	0.57	SignalP-noTM
gi_188520933_gb_ACD58878.1_	0.112	27	0.123	11	0.201	5	0.164	0.138	N	0.51	SignalP-TM
gi_188520934_gb_ACD58879.1_	0.121	32	0.11	32	0.164	4	0.101	0.106	N	0.57	SignalP-noTM
gi_188520935_gb_ACD58880.1_	0.106	55	0.153	21	0.278	15	0.209	0.18	N	0.57	SignalP-noTM
gi_188520936_gb_ACD58881.1_	0.113	26	0.105	56	0.11	29	0.091	0.098	N	0.57	SignalP-noTM
gi_188520937_gb_ACD58882.1_	0.221	17	0.155	17	0.175	13	0.109	0.133	N	0.57	SignalP-noTM
gi_188520938_gb_ACD58883.1_	0.122	16	0.114	16	0.16	26	0.104	0.11	N	0.57	SignalP-noTM
gi_188520939_gb_ACD58884.1_	0.116	30	0.146	30	0.314	7	0.188	0.166	N	0.57	SignalP-noTM
gi_188520941_gb_ACD58886.1_	0.161	23	0.136	21	0.321	45	0.116	0.127	N	0.57	SignalP-noTM
gi_188520953_gb_ACD58898.1_	0.114	18	0.128	18	0.215	15	0.148	0.137	N	0.57	SignalP-noTM
gi_188520954_gb_ACD58899.1_	0.259	21	0.199	21	0.207	2	0.171	0.188	N	0.51	SignalP-TM
gi_188520955_gb_ACD58900.1_	0.155	42	0.145	42	0.224	19	0.146	0.146	N	0.57	SignalP-noTM
gi_188520961_gb_ACD58906.1_	0.101	39	0.105	43	0.125	1	0.097	0.101	N	0.57	SignalP-noTM
gi_188520967_gb_ACD58912.1_	0.12	35	0.101	58	0.125	4	0.084	0.093	N	0.57	SignalP-noTM
gi_188520968_gb_ACD58913.1_	0.11	30	0.123	13	0.181	6	0.151	0.136	N	0.57	SignalP-noTM
gi_188520972_gb_ACD58917.1_	0.277	33	0.182	33	0.179	29	0.109	0.148	N	0.57	SignalP-noTM
gi_188520973_gb_ACD58918.1_	0.284	32	0.274	32	0.572	13	0.343	0.306	N	0.57	SignalP-noTM
gi_528897477_gb_ACD58920.2_	0.116	66	0.12	58	0.201	1	0.109	0.115	N	0.57	SignalP-noTM
gi_528897478_gb_ACD58925.2_	0.107	66	0.117	58	0.201	1	0.107	0.112	N	0.57	SignalP-noTM
gi_188520983_gb_ACD58928.1_	0.119	34	0.171	34	0.311	32	0.183	0.177	N	0.57	SignalP-noTM
gi_188520991_gb_ACD58936.1_	0.113	33	0.105	58	0.115	45	0.088	0.097	N	0.57	SignalP-noTM
gi_188520997_gb_ACD58942.1_	0.109	27	0.099	43	0.106	38	0.081	0.091	N	0.57	SignalP-noTM
gi_188520999_gb_ACD58944.1_	0.131	22	0.139	11	0.242	2	0.201	0.168	N	0.57	SignalP-noTM
gi_188521000_gb_ACD58945.1_	0.155	42	0.145	42	0.21	19	0.138	0.141	N	0.57	SignalP-noTM
gi_188521008_gb_ACD58953.1_	0.449	24	0.336	13	0.632	6	0.503	0.415	N	0.57	SignalP-noTM
gi_188521009_gb_ACD58954.1_	0.259	49	0.189	49	0.193	44	0.091	0.143	N	0.57	SignalP-noTM
gi_188521010_gb_ACD58955.1_	0.118	33	0.106	57	0.122	49	0.088	0.098	N	0.57	SignalP-noTM
gi_188521011_gb_ACD58956.1_	0.111	43	0.143	11	0.34	2	0.206	0.173	N	0.57	SignalP-noTM
gi_188521012_gb_ACD58957.1_	0.139	21	0.108	29	0.12	31	0.083	0.096	N	0.57	SignalP-noTM
gi_188521013_gb_ACD58958.1_	0.113	21	0.101	21	0.117	19	0.079	0.091	N	0.57	SignalP-noTM
gi_188521014_gb_ACD58959.1_	0.124	34	0.125	11	0.201	3	0.15	0.137	N	0.57	SignalP-noTM
gi_188521015_gb_ACD58960.1_	0.142	27	0.123	27	0.123	14	0.107	0.115	N	0.57	SignalP-noTM
gi_188521016_gb_ACD58961.1_	0.11	33	0.137	25	0.263	21	0.149	0.143	N	0.57	SignalP-noTM
gi_188521017_gb_ACD58962.1_	0.255	36	0.203	22	0.46	16	0.308	0.253	N	0.57	SignalP-noTM
gi_188521020_gb_ACD58965.1_	0.103	49	0.111	11	0.167	1	0.118	0.114	N	0.57	SignalP-noTM
gi_188521021_gb_ACD58966.1_	0.768	20	0.823	20	0.916	14	0.883	0.851	Y	0.57	SignalP-noTM
gi_188521022_gb_ACD58967.1_	0.246	65	0.299	20	0.662	4	0.503	0.395	N	0.57	SignalP-noTM
gi_188521024_gb_ACD58969.1_	0.14	19	0.125	19	0.133	10	0.104	0.115	N	0.57	SignalP-noTM
gi_188521025_gb_ACD58970.1_	0.102	37	0.116	16	0.163	10	0.131	0.123	N	0.57	SignalP-noTM
gi_188521027_gb_ACD58972.1_	0.139	56	0.133	20	0.283	14	0.137	0.135	N	0.57	SignalP-noTM
gi_188521028_gb_ACD58973.1_	0.185	34	0.164	11	0.382	2	0.264	0.211	N	0.57	SignalP-noTM
gi_188521029_gb_ACD58974.1_	0.147	19	0.239	19	0.495	17	0.385	0.293	N	0.51	SignalP-TM
gi_188521030_gb_ACD58975.1_	0.135	38	0.161	20	0.307	11	0.229	0.193	N	0.57	SignalP-noTM
gi_188521031_gb_ACD58976.1_	0.13	22	0.113	22	0.133	20	0.096	0.107	N	0.51	SignalP-TM
gi_188521041_gb_ACD58986.1_	0.218	19	0.305	19	0.555	23	0.419	0.358	N	0.57	SignalP-noTM
gi_188521042_gb_ACD58987.1_	0.102	11	0.128	11	0.195	3	0.161	0.144	N	0.57	SignalP-noTM
gi_188521043_gb_ACD58988.1_	0.277	33	0.176	33	0.164	32	0.106	0.143	N	0.57	SignalP-noTM
gi_188521045_gb_ACD58990.1_	0.152	47	0.193	42	0.363	37	0.152	0.178	N	0.51	SignalP-TM
gi_188521046_gb_ACD58991.1_	0.114	34	0.117	37	0.164	36	0.094	0.107	N	0.57	SignalP-noTM

0.093553	0.074055	0.095868	0.087825	gi_188521066_gb_ACD59011.1_
0.166866	0.092541	0.1603	0.139902	gi_188521067_gb_ACD59012.1_
0.936136	0.991934	0.904909	0.944326	gi_188521069_gb_ACD59014.1_
0.16645	0.059023	0.112047	0.112507	gi_188521072_gb_ACD59017.1_
0.135053	0.018487	0.154727	0.102756	gi_188521074_gb_ACD59019.1_
0.157493	0.224088	0.127194	0.169592	gi_188521075_gb_ACD59020.1_
0.057378	0.086195	0.090792	0.078122	gi_188521078_gb_ACD59023.1_
0.083173	0.001911	0.114153	0.066412	gi_188521079_gb_ACD59024.1_
0.090298	0.106215	0.091289	0.095934	gi_188521080_gb_ACD59025.1_
0.110269	0.144798	0.091538	0.115535	gi_188521083_gb_ACD59028.1_
0.085021	0.032327	0.114762	0.07737	gi_188521084_gb_ACD59029.1_
0.185126	0.086669	0.251807	0.174534	gi_188521085_gb_ACD59030.1_
0.059189	0.004026	0.097969	0.053728	gi_188521086_gb_ACD59031.1_
0.128532	0.163147	0.115373	0.135684	gi_188521087_gb_ACD59032.1_
0.150077	0.209822	0.228289	0.196063	gi_188521088_gb_ACD59033.1_
0.120999	0.16645	0.1034	0.130283	gi_188521089_gb_ACD59034.1_
0.097704	0.006686	0.127527	0.077306	gi_188521090_gb_ACD59035.1_
0.240672	0.102845	0.405163	0.24956	gi_188521091_gb_ACD59036.1_
0.138596	0.171505	0.187399	0.165833	gi_188521092_gb_ACD59037.1_
0.148552	0.353658	0.114153	0.205454	gi_188521093_gb_ACD59038.1_
0.813513	0.938601	0.802342	0.851485	gi_188521102_gb_ACD59047.1_
0.091289	0.292143	0.209325	0.197586	gi_188521103_gb_ACD59048.1_
0.091538	0.730271	0.186943	0.336251	gi_188521104_gb_ACD59049.1_
0.322785	0.250115	0.378011	0.31697	gi_188521105_gb_ACD59050.1_
0.825058	0.890903	0.776953	0.830971	gi_188521106_gb_ACD59051.1_
0.954436	0.99975	0.89264	0.948942	gi_188521107_gb_ACD59052.1_
0.096129	0.04415	0.12196	0.087413	gi_188521108_gb_ACD59053.1_
0.162737	0.479012	0.097176	0.246308	gi_188521109_gb_ACD59054.1_
0.156303	0.002233	0.246754	0.135097	gi_188521110_gb_ACD59055.1_
0.223567	0.218403	0.345473	0.262481	gi_188521111_gb_ACD59056.1_
0.89264	0.996069	0.810767	0.899825	gi_188521115_gb_ACD59060.1_
0.125209	0.620578	0.082262	0.276016	gi_188521118_gb_ACD59063.1_
0.081137	0.043273	0.125868	0.083426	gi_188521119_gb_ACD59064.1_
0.086432	0.020193	0.163147	0.089924	gi_188521129_gb_ACD59074.1_
0.168962	0.045826	0.173217	0.129335	gi_188521130_gb_ACD59075.1_
0.906954	0.992903	0.901233	0.933697	gi_188521131_gb_ACD59076.1_
0.080468	0.041328	0.126529	0.082775	gi_188521132_gb_ACD59077.1_
0.142217	0.066982	0.144798	0.117999	gi_188521134_gb_ACD59079.1_
0.883397	0.998777	0.748758	0.876977	gi_188521141_gb_ACD59086.1_
0.50225	0.931884	0.711566	0.715233	gi_188521142_gb_ACD59087.1_
0.115679	0.34074	0.146665	0.201028	gi_188521143_gb_ACD59088.1_
0.373086	0.98898	0.204403	0.522156	gi_188521148_gb_ACD59093.1_
0.141122	0.122604	0.102293	0.122006	gi_188521150_gb_ACD59095.1_
0.751569	0.837263	0.831879	0.806904	gi_188521151_gb_ACD59096.1_
0.218403	0.008484	0.335369	0.187419	gi_188518964_gb_ACD56909.1_
0.077845	0.038679	0.106786	0.074437	gi_188518967_gb_ACD56912.1_
0.954174	0.999375	0.889437	0.947662	gi_188518968_gb_ACD56913.1_
0.956603	0.999479	0.893214	0.949765	gi_188518969_gb_ACD56914.1_
0.142217	0.047834	0.192476	0.127509	gi_188518970_gb_ACD56915.1_
0.127527	0.035468	0.122927	0.095307	gi_188518975_gb_ACD56920.1_
0.292763	0.730271	0.349554	0.457529	gi_188518981_gb_ACD56926.1_
0.458843	0.055305	0.549339	0.354496	gi_188518982_gb_ACD56927.1_
0.38438	0.087624	0.412413	0.294806	gi_188518983_gb_ACD56928.1_
0.149694	0.202458	0.131587	0.161246	gi_188518984_gb_ACD56929.1_
0.120045	0.037797	0.188314	0.115385	gi_188518989_gb_ACD56934.1_
0.083173	0.047971	0.150077	0.09374	gi_188518992_gb_ACD56937.1_
0.350236	0.912136	0.49775	0.586707	gi_188518993_gb_ACD56938.1_
0.119098	0.074675	0.147795	0.113856	gi_188518994_gb_ACD56939.1_
0.353658	0.293385	0.49775	0.381598	gi_188519008_gb_ACD56953.1_
0.119098	0.516494	0.209822	0.281805	gi_188519010_gb_ACD56955.1_
0.50525	0.134005	0.528469	0.389241	gi_188521152_gb_ACD59097.1_
0.896042	0.99924	0.629017	0.841433	gi_188521153_gb_ACD59098.1_
0.953514	0.996491	0.9015	0.950502	gi_188521155_gb_ACD59100.1_
0.102018	0.051661	0.157892	0.103857	gi_188521156_gb_ACD59101.1_
0.056893	0.022053	0.093808	0.057585	gi_188521160_gb_ACD59105.1_
0.13331	0.247312	0.124881	0.168501	gi_188521162_gb_ACD59107.1_
0.13331	0.148173	0.090052	0.123845	gi_188521163_gb_ACD59108.1_
0.902296	0.973865	0.856682	0.910948	gi_188521164_gb_ACD59109.1_
0.104238	0.001314	0.159494	0.088349	gi_188521165_gb_ACD59110.1_
0.940139	0.98352	0.904132	0.942597	gi_188521166_gb_ACD59111.1_
0.256355	0.06037	0.359854	0.225526	gi_188521167_gb_ACD59112.1_
0.171931	0.288434	0.146665	0.202343	gi_188521168_gb_ACD59113.1_
0.090298	0.001016	0.122604	0.071306	gi_188521169_gb_ACD59114.1_
0.130903	0.097704	0.126861	0.118489	gi_188521177_gb_ACD59122.1_
0.15046	0.058031	0.104518	0.104336	gi_188521178_gb_ACD59123.1_
0.92365	0.868756	0.880902	0.891103	gi_188521180_gb_ACD59125.1_
0.737303	0.873139	0.770653	0.793698	gi_188521181_gb_ACD59126.1_
0.086195	0.012667	0.123575	0.074146	gi_188521182_gb_ACD59127.1_

gi_188521050_gb_ACD58995.1_	0.11	36	0.144	11	0.292	3	0.21	0.175	N	0.57	SignalP-noTM
gi_188521051_gb_ACD58996.1_	0.18	28	0.115	43	0.148	41	0.078	0.098	N	0.57	SignalP-noTM
gi_188521052_gb_ACD58997.1_	0.102	15	0.104	50	0.131	29	0.096	0.1	N	0.57	SignalP-noTM
gi_188521054_gb_ACD58999.1_	0.595	38	0.331	38	0.359	23	0.186	0.277	N	0.51	SignalP-TM
gi_188521055_gb_ACD59000.1_	0.251	33	0.118	33	0.143	49	0.085	0.106	N	0.51	SignalP-TM
gi_188521056_gb_ACD59001.1_	0.101	20	0.107	14	0.165	10	0.114	0.11	N	0.57	SignalP-noTM
gi_188521057_gb_ACD59002.1_	0.221	45	0.14	35	0.251	34	0.091	0.117	N	0.57	SignalP-noTM
gi_188521058_gb_ACD59003.1_	0.263	32	0.216	32	0.295	13	0.202	0.211	N	0.51	SignalP-TM
gi_188521060_gb_ACD59005.1_	0.119	29	0.153	20	0.28	12	0.198	0.174	N	0.57	SignalP-noTM
gi_188521061_gb_ACD59006.1_	0.119	39	0.143	13	0.281	4	0.208	0.174	N	0.57	SignalP-noTM
gi_188521062_gb_ACD59007.1_	0.119	30	0.124	11	0.195	4	0.158	0.14	N	0.57	SignalP-noTM
gi_188521065_gb_ACD59010.1_	0.122	45	0.103	68	0.115	59	0.087	0.096	N	0.57	SignalP-noTM
gi_188521066_gb_ACD59011.1_	0.171	69	0.127	69	0.103	69	0.074	0.102	N	0.57	SignalP-noTM
gi_188521067_gb_ACD59012.1_	0.114	33	0.114	33	0.14	29	0.088	0.102	N	0.57	SignalP-noTM
gi_188521069_gb_ACD59014.1_	0.391	22	0.311	22	0.713	1	0.33	0.32	N	0.57	SignalP-noTM
gi_188521072_gb_ACD59017.1_	0.318	23	0.24	23	0.294	14	0.203	0.223	N	0.57	SignalP-noTM
gi_188521074_gb_ACD59019.1_	0.115	59	0.12	51	0.197	43	0.111	0.116	N	0.57	SignalP-noTM
gi_188521075_gb_ACD59020.1_	0.126	17	0.128	17	0.192	1	0.14	0.134	N	0.57	SignalP-noTM
gi_188521078_gb_ACD59023.1_	0.118	24	0.107	24	0.134	37	0.093	0.101	N	0.57	SignalP-noTM
gi_188521079_gb_ACD59024.1_	0.109	31	0.113	31	0.177	46	0.098	0.106	N	0.57	SignalP-noTM
gi_188521080_gb_ACD59025.1_	0.133	22	0.121	11	0.256	1	0.132	0.126	N	0.57	SignalP-noTM
gi_188521083_gb_ACD59028.1_	0.205	42	0.132	42	0.137	1	0.094	0.115	N	0.57	SignalP-noTM
gi_188521084_gb_ACD59029.1_	0.13	41	0.119	41	0.147	2	0.082	0.105	N	0.51	SignalP-TM
gi_188521085_gb_ACD59030.1_	0.155	39	0.104	39	0.124	14	0.087	0.096	N	0.57	SignalP-noTM
gi_188521086_gb_ACD59031.1_	0.124	18	0.102	59	0.111	41	0.086	0.095	N	0.57	SignalP-noTM
gi_188521087_gb_ACD59032.1_	0.15	44	0.127	44	0.144	5	0.092	0.114	N	0.51	SignalP-TM
gi_188521088_gb_ACD59033.1_	0.115	25	0.109	11	0.201	1	0.111	0.109	N	0.51	SignalP-TM
gi_188521089_gb_ACD59034.1_	0.119	21	0.112	39	0.145	33	0.091	0.105	N	0.51	SignalP-TM
gi_188521090_gb_ACD59035.1_	0.267	25	0.221	25	0.286	5	0.211	0.217	N	0.51	SignalP-TM
gi_188521091_gb_ACD59036.1_	0.154	39	0.117	39	0.112	58	0.078	0.099	N	0.57	SignalP-noTM
gi_188521092_gb_ACD59037.1_	0.113	17	0.107	69	0.12	59	0.096	0.102	N	0.57	SignalP-noTM
gi_188521093_gb_ACD59038.1_	0.123	17	0.141	42	0.223	40	0.114	0.128	N	0.57	SignalP-noTM
gi_188521102_gb_ACD59047.1_	0.183	13	0.155	13	0.23	5	0.131	0.144	N	0.57	SignalP-noTM
gi_188521103_gb_ACD59048.1_	0.125	45	0.137	45	0.189	5	0.119	0.13	N	0.51	SignalP-TM
gi_188521104_gb_ACD59049.1_	0.58	31	0.277	31	0.316	3	0.195	0.247	N	0.51	SignalP-TM
gi_188521105_gb_ACD59050.1_	0.137	62	0.111	28	0.158	2	0.111	0.111	N	0.57	SignalP-noTM
gi_188521106_gb_ACD59051.1_	0.131	14	0.134	14	0.209	10	0.132	0.133	N	0.57	SignalP-noTM
gi_188521107_gb_ACD59052.1_	0.88	34	0.917	34	0.979	28	0.84	0.881	Y	0.57	SignalP-noTM
gi_188521108_gb_ACD59053.1_	0.184	48	0.127	48	0.154	9	0.098	0.113	N	0.57	SignalP-noTM
gi_188521109_gb_ACD59054.1_	0.129	26	0.123	26	0.166	53	0.116	0.12	N	0.57	SignalP-noTM
gi_188521110_gb_ACD59055.1_	0.188	66	0.135	66	0.286	1	0.103	0.12	N	0.57	SignalP-noTM
gi_188521111_gb_ACD59056.1_	0.372	33	0.437	33	0.789	18	0.633	0.53	N	0.57	SignalP-noTM
gi_188521115_gb_ACD59060.1_	0.843	23	0.816	23	0.946	7	0.848	0.831	Y	0.57	SignalP-noTM
gi_188521118_gb_ACD59063.1_	0.114	53	0.106	53	0.113	53	0.089	0.098	N	0.57	SignalP-noTM
gi_188521119_gb_ACD59064.1_	0.154	30	0.179	14	0.46	13	0.276	0.225	N	0.57	SignalP-noTM
gi_188521129_gb_ACD59074.1_	0.124	38	0.111	38	0.133	25	0.103	0.107	N	0.57	SignalP-noTM
gi_188521130_gb_ACD59075.1_	0.835	23	0.871	23	0.937	17	0.895	0.882	Y	0.57	SignalP-noTM
gi_188521131_gb_ACD59076.1_	0.223	19	0.452	19	0.978	9	0.923	0.673	Y	0.57	SignalP-noTM
gi_188521132_gb_ACD59077.1_	0.111	55	0.121	11	0.235	3	0.135	0.128	N	0.57	SignalP-noTM
gi_188521134_gb_ACD59079.1_	0.128	25	0.126	25	0.175	27	0.133	0.13	N	0.57	SignalP-noTM
gi_188521141_gb_ACD59086.1_	0.153	31	0.16	15	0.334	6	0.254	0.194	N	0.51	SignalP-TM
gi_188521142_gb_ACD59087.1_	0.212	35	0.148	35	0.175	31	0.081	0.116	N	0.57	SignalP-noTM
gi_188521143_gb_ACD59088.1_	0.121	13	0.112	13	0.166	9	0.103	0.108	N	0.57	SignalP-noTM
gi_188521148_gb_ACD59093.1_	0.098	43	0.117	13	0.162	5	0.143	0.127	N	0.51	SignalP-TM
gi_188521150_gb_ACD59095.1_	0.105	36	0.129	11	0.219	5	0.18	0.148	N	0.51	SignalP-TM
gi_188521151_gb_ACD59096.1_	0.114	22	0.144	13	0.262	9	0.209	0.175	N	0.57	SignalP-noTM
gi_188521152_gb_ACD59097.1_	0.11	9	0.104	39	0.122	28	0.081	0.094	N	0.57	SignalP-noTM
gi_188521153_gb_ACD59098.1_	0.108	22	0.1	22	0.106	16	0.088	0.094	N	0.57	SignalP-noTM
gi_188521155_gb_ACD59100.1_	0.105	29	0.099	36	0.109	1	0.09	0.094	N	0.57	SignalP-noTM
gi_188521156_gb_ACD59101.1_	0.113	24	0.105	11	0.139	2	0.112	0.108	N	0.51	SignalP-TM
gi_188521160_gb_ACD59105.1_	0.12	20	0.127	25	0.163	34	0.12	0.124	N	0.57	SignalP-noTM
gi_188521162_gb_ACD59107.1_	0.161	58	0.16	11	0.351	2	0.263	0.208	N	0.57	SignalP-noTM
gi_188521163_gb_ACD59108.1_	0.156	22	0.16	22	0.266	5	0.191	0.175	N	0.57	SignalP-noTM
gi_188521164_gb_ACD59109.1_	0.155	17	0.362	17	0.929	15	0.852	0.592	Y	0.57	SignalP-noTM
gi_188521165_gb_ACD59110.1_	0.105	47	0.101	22	0.125	18	0.085	0.095	N	0.51	SignalP-TM
gi_188521166_gb_ACD59111.1_	0.106	45	0.098	60	0.106	44	0.089	0.093	N	0.57	SignalP-noTM
gi_188521167_gb_ACD59112.1_	0.343	21	0.323	21	0.547	1	0.317	0.32	N	0.57	SignalP-noTM
gi_188521168_gb_ACD59113.1_	0.1	69	0.108	11	0.133	1	0.114	0.111	N	0.57	SignalP-noTM
gi_188521169_gb_ACD59114.1_	0.135	17	0.106	17	0.129	46	0.084	0.096	N	0.57	SignalP-noTM
gi_188521177_gb_ACD59122.1_	0.107	27	0.129	11	0.21	2	0.165	0.146	N	0.57	SignalP-noTM
gi_188521178_gb_ACD59123.1_	0.272	21	0.293	21	0.517	9	0.35	0.32	N	0.57	SignalP-noTM
gi_188521180_gb_ACD59125.1_	0.613	29	0.748	29	0.972	14	0.886	0.813	Y	0.57	SignalP-noTM
gi_188521181_gb_ACD59126.1_	0.488	19	0.64	19	0.925	13	0.817	0.723	Y	0.57	SignalP-noTM
gi_188521182_gb_ACD59127.1_	0.131	58	0.129	58	0.169	56	0.105	0.12	N	0.51	SignalP-TM
gi_188521189_gb_ACD59134.1_	0.376	19	0.238	19	0.183	17	0.147	0.196	N	0.57	SignalP-noTM
gi_188521190_gb_ACD59135.1_	0.104	46	0.112	46	0.195	4	0.112	0.112	N	0.57	SignalP-noTM
gi_188521197_gb_ACD59142.1_	0.294	22	0.254	22	0.427	21	0.217	0.237	N	0.57	SignalP-noTM
gi_188521200_gb_ACD59145.1_	0.138	23	0.161	11	0.368	1	0.256	0.205	N	0.57	SignalP-noTM

0.066051	0.007246	0.091788	0.055028	gi_188521189_gb_ACD59134.1_
0.23041	0.19201	0.318212	0.246877	gi_188521190_gb_ACD59135.1_
0.115679	0.045564	0.127527	0.096257	gi_188521197_gb_ACD59142.1_
0.077201	0.043149	0.112946	0.077765	gi_188521200_gb_ACD59145.1_
0.207346	0.039128	0.210818	0.152431	gi_188521201_gb_ACD59146.1_
0.950358	0.995623	0.936849	0.960943	gi_188521202_gb_ACD59147.1_
0.130222	0.533699	0.157892	0.273938	gi_188521203_gb_ACD59148.1_
0.080025	0.000776	0.092793	0.057865	gi_188521247_gb_ACD59192.1_
0.148173	0.968046	0.147418	0.421212	gi_188521251_gb_ACD59196.1_
0.198134	0.073645	0.145542	0.139107	gi_188521264_gb_ACD59209.1_
0.951616	0.896321	0.899619	0.915852	gi_188521268_gb_ACD59213.1_
0.295879	0.773293	0.35503	0.474734	gi_188521269_gb_ACD59214.1_
0.236313	0.386511	0.188773	0.270532	gi_188521270_gb_ACD59215.1_
0.954566	0.902824	0.895201	0.91753	gi_188521271_gb_ACD59216.1_
0.936672	0.999926	0.895762	0.94412	gi_188521272_gb_ACD59217.1_
0.431435	0.267959	0.531458	0.410284	gi_188521274_gb_ACD59219.1_
0.333366	0.125868	0.265612	0.241615	gi_188521275_gb_ACD59220.1_
0.310454	0.424824	0.220458	0.318579	gi_188521276_gb_ACD59221.1_
0.262697	0.558974	0.083862	0.301844	gi_188521283_gb_ACD59228.1_
0.109097	0.039015	0.103123	0.083745	gi_188521284_gb_ACD59229.1_
0.345473	0.508249	0.49325	0.448991	gi_188519018_gb_ACD56963.1_
0.301535	0.745357	0.360545	0.469146	gi_188519019_gb_ACD56964.1_
0.835208	0.995865	0.842507	0.891193	gi_188519020_gb_ACD56965.1_
0.870794	0.998408	0.887355	0.918852	gi_188519021_gb_ACD56966.1_
0.893214	0.996439	0.870456	0.920036	gi_188519022_gb_ACD56967.1_
0.08883	0.005346	0.117222	0.070466	gi_188519025_gb_ACD56970.1_
0.368188	0.990097	0.087864	0.48205	gi_188519026_gb_ACD56971.1_
0.934134	0.995675	0.906447	0.945419	gi_188519034_gb_ACD56979.1_
0.136815	0.043898	0.111155	0.097289	gi_188519038_gb_ACD56983.1_
0.129544	0.02401	0.163967	0.10584	gi_188519039_gb_ACD56984.1_
0.272099	0.036299	0.204891	0.171096	gi_188519041_gb_ACD56986.1_
0.786675	0.992966	0.715856	0.831832	gi_188519043_gb_ACD56988.1_
0.153164	0.073237	0.197182	0.141194	gi_188519044_gb_ACD56989.1_
0.193879	0.204891	0.083173	0.160648	gi_188519048_gb_ACD56993.1_
0.760423	0.880587	0.840104	0.827038	gi_188519049_gb_ACD56994.1_
0.141486	0.082944	0.136815	0.120415	gi_188519051_gb_ACD56996.1_
0.066422	0.038126	0.094319	0.066289	gi_188519054_gb_ACD56999.1_
0.131244	0.059357	0.122282	0.104294	gi_188519057_gb_ACD57002.1_
0.184222	0.032799	0.236855	0.151292	gi_188519060_gb_ACD57005.1_
0.547853	0.76692	0.441026	0.585266	gi_188519061_gb_ACD57006.1_
0.091289	0.287819	0.165619	0.181576	gi_188519062_gb_ACD57007.1_
0.956851	0.962312	0.888845	0.936003	gi_188519063_gb_ACD57008.1_
0.119413	0.066236	0.139674	0.108441	gi_188519072_gb_ACD57017.1_
0.478264	0.804711	0.584676	0.62255	gi_188519073_gb_ACD57018.1_
0.934869	0.994795	0.857417	0.929027	gi_188519074_gb_ACD57019.1_
0.069655	0.089317	0.067926	0.075633	gi_188519075_gb_ACD57020.1_
0.779542	0.756576	0.771711	0.769276	gi_188519076_gb_ACD57021.1_
0.443246	0.813513	0.479012	0.57859	gi_188519077_gb_ACD57022.1_
0.967673	0.999775	0.84954	0.938996	gi_188519078_gb_ACD57023.1_
0.292763	0.482008	0.120681	0.298484	gi_188519079_gb_ACD57024.1_
0.103123	0.082262	0.157095	0.11416	gi_188519086_gb_ACD57031.1_
0.881216	0.596283	0.92615	0.801216	gi_188519501_gb_ACD57446.1_
0.197658	0.318212	0.247312	0.254394	gi_188519504_gb_ACD57449.1_
0.10736	0.139674	0.094319	0.113784	gi_188519515_gb_ACD57460.1_
0.309171	0.262116	0.356405	0.309231	gi_188519516_gb_ACD57461.1_
0.94745	0.908462	0.88615	0.914021	gi_188519517_gb_ACD57462.1_
0.299643	0.082036	0.391503	0.257727	gi_188519521_gb_ACD57466.1_
0.473774	0.892928	0.543391	0.636698	gi_188519523_gb_ACD57468.1_
0.929367	0.920195	0.869438	0.906333	gi_188519525_gb_ACD57470.1_
0.295254	0.051956	0.267371	0.20486	gi_188519526_gb_ACD57471.1_
0.943588	0.999705	0.900966	0.948086	gi_188519527_gb_ACD57472.1_
0.445468	0.035985	0.313028	0.264827	gi_188519528_gb_ACD57473.1_
0.910926	0.921724	0.811686	0.881445	gi_188519529_gb_ACD57474.1_
0.911412	0.998646	0.811227	0.907095	gi_188519531_gb_ACD57476.1_
0.729088	0.974017	0.655883	0.786329	gi_188519533_gb_ACD57478.1_
0.174078	0.024868	0.297757	0.165568	gi_188519534_gb_ACD57479.1_
0.699727	0.852205	0.811686	0.787873	gi_188519537_gb_ACD57482.1_
0.78968	0.346831	0.779026	0.638512	gi_188519538_gb_ACD57483.1_
0.223567	0.034556	0.214839	0.157654	gi_188519540_gb_ACD57485.1_
0.801389	0.974169	0.863185	0.879581	gi_188519546_gb_ACD57491.1_
0.120363	0.046353	0.126861	0.097859	gi_188519548_gb_ACD57493.1_
0.88615	0.883397	0.824625	0.864724	gi_188519549_gb_ACD57494.1_
0.278684	0.985783	0.468542	0.57767	gi_188519551_gb_ACD57496.1_
0.887654	0.995008	0.93808	0.940247	gi_188519552_gb_ACD57497.1_
0.923438	0.975779	0.819357	0.906191	gi_188519554_gb_ACD57499.1_
0.953779	0.999267	0.89989	0.950979	gi_188519555_gb_ACD57500.1_
0.3028	0.320821	0.386511	0.336711	gi_188519564_gb_ACD57509.1_
0.171505	0.713409	0.30853	0.397815	gi_188519565_gb_ACD57510.1_

gi_188521201_gb_ACD59146.1_	0.108	50	0.102	64	0.115	57	0.076	0.09	N	0.57	SignalP-noTM
gi_188521202_gb_ACD59147.1_	0.29	28	0.237	28	0.332	8	0.23	0.234	N	0.57	SignalP-noTM
gi_188521203_gb_ACD59148.1_	0.791	18	0.862	18	0.972	11	0.927	0.892	Y	0.57	SignalP-noTM
gi_188521247_gb_ACD59192.1_	0.473	37	0.292	37	0.328	34	0.09	0.217	N	0.51	SignalP-TM
gi_188521251_gb_ACD59196.1_	0.207	38	0.213	11	0.531	5	0.46	0.329	N	0.57	SignalP-noTM
gi_188521264_gb_ACD59209.1_	0.112	29	0.144	11	0.317	1	0.199	0.17	N	0.57	SignalP-noTM
gi_188521268_gb_ACD59213.1_	0.155	33	0.153	11	0.327	1	0.226	0.187	N	0.57	SignalP-noTM
gi_188521269_gb_ACD59214.1_	0.156	42	0.146	42	0.219	19	0.143	0.145	N	0.57	SignalP-noTM
gi_188521270_gb_ACD59215.1_	0.112	14	0.122	11	0.237	1	0.142	0.13	N	0.51	SignalP-TM
gi_188521271_gb_ACD59216.1_	0.189	22	0.183	22	0.319	20	0.195	0.189	N	0.57	SignalP-noTM
gi_188521272_gb_ACD59217.1_	0.164	50	0.224	12	0.476	9	0.378	0.297	N	0.57	SignalP-noTM
gi_188521274_gb_ACD59219.1_	0.107	38	0.108	12	0.159	1	0.115	0.111	N	0.57	SignalP-noTM
gi_188521275_gb_ACD59220.1_	0.283	32	0.272	32	0.565	13	0.338	0.303	N	0.57	SignalP-noTM
gi_188521276_gb_ACD59221.1_	0.1	43	0.116	37	0.146	33	0.107	0.111	N	0.57	SignalP-noTM
gi_188521283_gb_ACD59228.1_	0.357	10	0.099	28	0.114	9	0.094	0.097	N	0.57	SignalP-noTM
gi_188521284_gb_ACD59229.1_	0.132	28	0.119	28	0.18	25	0.091	0.106	N	0.57	SignalP-noTM
gi_188518964_gb_ACD56909.1_	0.14	27	0.127	40	0.207	39	0.102	0.115	N	0.57	SignalP-noTM
gi_188518967_gb_ACD56912.1_	0.19	27	0.248	27	0.512	21	0.266	0.255	N	0.51	SignalP-TM
gi_188518968_gb_ACD56913.1_	0.806	33	0.849	33	0.984	21	0.902	0.874	Y	0.57	SignalP-noTM
gi_188518969_gb_ACD56914.1_	0.854	33	0.891	33	0.995	19	0.949	0.918	Y	0.57	SignalP-noTM
gi_188518970_gb_ACD56915.1_	0.139	60	0.117	38	0.149	9	0.114	0.115	N	0.57	SignalP-noTM
gi_188518975_gb_ACD56920.1_	0.105	22	0.107	35	0.125	34	0.089	0.098	N	0.57	SignalP-noTM
gi_188518981_gb_ACD56926.1_	0.156	42	0.146	42	0.219	19	0.143	0.145	N	0.57	SignalP-noTM
gi_188518982_gb_ACD56927.1_	0.23	24	0.459	24	0.965	20	0.918	0.675	Y	0.57	SignalP-noTM
gi_188518983_gb_ACD56928.1_	0.154	28	0.111	28	0.155	1	0.081	0.097	N	0.57	SignalP-noTM
gi_188518984_gb_ACD56929.1_	0.135	18	0.149	18	0.253	1	0.17	0.159	N	0.57	SignalP-noTM
gi_188518989_gb_ACD56934.1_	0.163	25	0.149	25	0.258	7	0.171	0.159	N	0.57	SignalP-noTM
gi_188518992_gb_ACD56937.1_	0.142	29	0.117	29	0.129	27	0.091	0.105	N	0.57	SignalP-noTM
gi_188518993_gb_ACD56938.1_	0.117	63	0.131	11	0.229	4	0.181	0.155	N	0.57	SignalP-noTM
gi_188518994_gb_ACD56939.1_	0.105	60	0.111	46	0.155	52	0.096	0.104	N	0.57	SignalP-noTM
gi_188519008_gb_ACD56953.1_	0.22	20	0.357	20	0.863	1	0.654	0.497	N	0.57	SignalP-noTM
gi_188519010_gb_ACD56955.1_	0.11	31	0.1	70	0.128	1	0.072	0.09	N	0.51	SignalP-TM
gi_188519018_gb_ACD56963.1_	0.136	60	0.115	15	0.194	5	0.125	0.12	N	0.57	SignalP-noTM
gi_188519019_gb_ACD56964.1_	0.151	45	0.141	45	0.194	44	0.133	0.138	N	0.57	SignalP-noTM
gi_188519020_gb_ACD56965.1_	0.167	23	0.153	23	0.327	44	0.12	0.137	N	0.57	SignalP-noTM
gi_188519021_gb_ACD56966.1_	0.216	24	0.151	55	0.156	46	0.11	0.131	N	0.57	SignalP-noTM
gi_188519022_gb_ACD56967.1_	0.315	23	0.302	23	0.356	15	0.273	0.288	N	0.57	SignalP-noTM
gi_188519025_gb_ACD56970.1_	0.119	29	0.148	11	0.329	2	0.211	0.178	N	0.57	SignalP-noTM
gi_188519026_gb_ACD56971.1_	0.11	20	0.241	20	0.635	14	0.507	0.366	N	0.57	SignalP-noTM
gi_188519034_gb_ACD56979.1_	0.205	18	0.286	18	0.545	1	0.407	0.343	N	0.57	SignalP-noTM
gi_188519038_gb_ACD56983.1_	0.161	24	0.119	11	0.247	1	0.123	0.121	N	0.57	SignalP-noTM
gi_188519039_gb_ACD56984.1_	0.13	26	0.124	26	0.152	7	0.12	0.122	N	0.57	SignalP-noTM
gi_188519041_gb_ACD56986.1_	0.119	19	0.109	35	0.158	29	0.095	0.102	N	0.57	SignalP-noTM
gi_188519043_gb_ACD56988.1_	0.128	56	0.116	11	0.17	1	0.133	0.124	N	0.57	SignalP-noTM
gi_188519044_gb_ACD56989.1_	0.143	42	0.15	42	0.226	49	0.106	0.129	N	0.57	SignalP-noTM
gi_188519048_gb_ACD56993.1_	0.175	33	0.146	33	0.213	32	0.109	0.129	N	0.57	SignalP-noTM
gi_188519049_gb_ACD56994.1_	0.133	22	0.158	22	0.292	11	0.194	0.175	N	0.57	SignalP-noTM
gi_188519051_gb_ACD56996.1_	0.115	40	0.112	40	0.154	35	0.094	0.103	N	0.57	SignalP-noTM
gi_188519054_gb_ACD56999.1_	0.189	43	0.136	43	0.157	1	0.096	0.117	N	0.57	SignalP-noTM
gi_188519057_gb_ACD57002.1_	0.2	36	0.204	11	0.551	3	0.426	0.286	N	0.51	SignalP-TM
gi_188519060_gb_ACD57005.1_	0.105	45	0.105	51	0.184	42	0.087	0.096	N	0.57	SignalP-noTM
gi_188519061_gb_ACD57006.1_	0.173	36	0.185	36	0.344	24	0.184	0.184	N	0.57	SignalP-noTM
gi_188519062_gb_ACD57007.1_	0.143	42	0.16	11	0.327	2	0.257	0.196	N	0.51	SignalP-TM
gi_188519063_gb_ACD57008.1_	0.777	29	0.86	29	0.986	21	0.95	0.902	Y	0.57	SignalP-noTM
gi_188519072_gb_ACD57017.1_	0.136	29	0.097	29	0.098	40	0.057	0.078	N	0.57	SignalP-noTM
gi_188519073_gb_ACD57018.1_	0.729	32	0.806	32	0.979	28	0.789	0.798	Y	0.57	SignalP-noTM
gi_188519074_gb_ACD57019.1_	0.211	18	0.328	18	0.742	1	0.558	0.436	N	0.57	SignalP-noTM
gi_188519075_gb_ACD57020.1_	0.106	62	0.114	42	0.147	34	0.107	0.111	N	0.57	SignalP-noTM
gi_188519076_gb_ACD57021.1_	0.328	17	0.48	17	0.843	13	0.707	0.587	Y	0.57	SignalP-noTM
gi_188519077_gb_ACD57022.1_	0.702	35	0.488	35	0.517	27	0.233	0.394	N	0.51	SignalP-TM
gi_188519078_gb_ACD57023.1_	0.16	27	0.24	21	0.563	9	0.418	0.324	N	0.57	SignalP-noTM
gi_188519079_gb_ACD57024.1_	0.173	24	0.157	24	0.225	6	0.159	0.158	N	0.57	SignalP-noTM
gi_188519086_gb_ACD57031.1_	0.131	10	0.104	11	0.144	1	0.108	0.105	N	0.51	SignalP-TM
gi_188519501_gb_ACD57446.1_	0.175	26	0.154	26	0.205	22	0.131	0.143	N	0.57	SignalP-noTM
gi_188519504_gb_ACD57449.1_	0.118	37	0.103	37	0.113	2	0.09	0.097	N	0.57	SignalP-noTM
gi_188519515_gb_ACD57460.1_	0.104	21	0.103	70	0.134	2	0.091	0.098	N	0.57	SignalP-noTM
gi_188519516_gb_ACD57461.1_	0.205	21	0.255	21	0.459	8	0.356	0.293	N	0.51	SignalP-TM
gi_188519517_gb_ACD57462.1_	0.7	22	0.801	22	0.956	11	0.919	0.857	Y	0.57	SignalP-noTM
gi_188519521_gb_ACD57466.1_	0.263	24	0.49	24	0.96	17	0.918	0.691	Y	0.57	SignalP-noTM
gi_188519523_gb_ACD57468.1_	0.32	20	0.284	20	0.456	18	0.274	0.279	N	0.57	SignalP-noTM
gi_188519525_gb_ACD57470.1_	0.29	22	0.497	22	0.929	10	0.846	0.661	Y	0.57	SignalP-noTM
gi_188519526_gb_ACD57471.1_	0.106	22	0.12	12	0.18	7	0.149	0.131	N	0.51	SignalP-TM
gi_188519527_gb_ACD57472.1_	0.147	15	0.27	15	0.804	11	0.513	0.385	N	0.57	SignalP-noTM
gi_188519528_gb_ACD57473.1_	0.11	23	0.148	11	0.376	1	0.2	0.173	N	0.57	SignalP-noTM
gi_188519529_gb_ACD57474.1_	0.109	26	0.194	11	0.465	2	0.383	0.283	N	0.57	SignalP-noTM
gi_188519531_gb_ACD57476.1_	0.169	34	0.125	11	0.178	1	0.155	0.139	N	0.57	SignalP-noTM
gi_188519533_gb_ACD57478.1_	0.224	30	0.196	30	0.267	29	0.178	0.187	N	0.57	SignalP-noTM
gi_188519534_gb_ACD57479.1_	0.311	26	0.2	26	0.248	22	0.112	0.159	N	0.57	SignalP-noTM

0.961874	0.999549	0.888251	0.949891	gi_188519571_gb_ACD57516.1_
0.207346	0.512747	0.150077	0.290057	gi_188519573_gb_ACD57518.1_
0.093808	0.041806	0.157892	0.097835	gi_188519578_gb_ACD57523.1_
0.486503	0.467048	0.612065	0.521872	gi_188519579_gb_ACD57524.1_
0.919309	0.083862	0.891194	0.631455	gi_188519586_gb_ACD57531.1_
0.081137	0.062973	0.131587	0.091899	gi_188519589_gb_ACD57534.1_
0.705993	0.073033	0.773819	0.517615	gi_188519590_gb_ACD57535.1_
0.93015	0.998194	0.880902	0.936415	gi_188519591_gb_ACD57536.1_
0.147795	0.185126	0.131244	0.154722	gi_188519593_gb_ACD57538.1_
0.191081	0.26386	0.229347	0.228096	gi_188519594_gb_ACD57539.1_
0.279891	0.520239	0.287819	0.36265	gi_188519601_gb_ACD57546.1_
0.844881	0.984783	0.763145	0.86427	gi_188519616_gb_ACD57561.1_
0.161515	0.134354	0.185126	0.160332	gi_188519623_gb_ACD57568.1_
0.378716	0.256927	0.469289	0.368311	gi_188519634_gb_ACD57579.1_
0.097704	0.037579	0.126529	0.087271	gi_188519640_gb_ACD57585.1_
0.191081	0.884627	0.090545	0.388751	gi_188519642_gb_ACD57587.1_
0.075091	0.024941	0.111749	0.070594	gi_188519644_gb_ACD57589.1_
0.125209	0.00143	0.299643	0.142094	gi_188519646_gb_ACD57591.1_
0.302167	0.092541	0.199089	0.197932	gi_188519651_gb_ACD57596.1_
0.397235	0.134703	0.596283	0.376074	gi_188519656_gb_ACD57601.1_
0.348191	0.020432	0.443246	0.270623	gi_188520140_gb_ACD58085.1_
0.065131	0.189233	0.125868	0.126744	gi_188520145_gb_ACD58090.1_
0.150077	0.147041	0.14517	0.147429	gi_188520146_gb_ACD58091.1_
0.700987	0.998662	0.657236	0.785628	gi_188520147_gb_ACD58092.1_
0.179756	0.081361	0.159092	0.14007	gi_188520152_gb_ACD58097.1_
0.085724	0.054064	0.100924	0.080237	gi_188520153_gb_ACD58098.1_
0.842905	0.997006	0.694661	0.844857	gi_188520161_gb_ACD58106.1_
0.059861	0.019957	0.067358	0.049059	gi_188520163_gb_ACD58108.1_
0.949646	0.967105	0.907711	0.941487	gi_188520164_gb_ACD58109.1_
0.779026	0.897707	0.843301	0.840011	gi_188520172_gb_ACD58117.1_
0.181532	0.178433	0.157892	0.172619	gi_188520174_gb_ACD58119.1_
0.076988	0.492501	0.111155	0.226881	gi_188520175_gb_ACD58120.1_
0.082944	0.326733	0.159092	0.18959	gi_188520176_gb_ACD58121.1_
0.411686	0.985094	0.301535	0.566105	gi_188520182_gb_ACD58127.1_
0.129206	0.027465	0.100924	0.085865	gi_188520183_gb_ACD58128.1_
0.074261	0.038568	0.101744	0.071524	gi_188520184_gb_ACD58129.1_
0.721919	0.99845	0.586133	0.768834	gi_188520185_gb_ACD58130.1_
0.159092	0.073237	0.17023	0.134186	gi_188520186_gb_ACD58131.1_
0.774343	0.93738	0.833966	0.848563	gi_188520192_gb_ACD58137.1_
0.651809	0.979447	0.860326	0.830527	gi_188520197_gb_ACD58142.1_
0.148932	0.113548	0.145916	0.136132	gi_188520198_gb_ACD58143.1_
0.116294	0.430699	0.084788	0.210594	gi_188520199_gb_ACD58144.1_
0.099571	0.051368	0.124881	0.09194	gi_188520200_gb_ACD58145.1_
0.525478	0.947896	0.777473	0.750282	gi_188520201_gb_ACD58146.1_
0.933578	0.884627	0.875447	0.897884	gi_188520202_gb_ACD58147.1_
0.402274	0.482757	0.48051	0.45518	gi_188520204_gb_ACD58149.1_
0.706615	0.370284	0.690188	0.589029	gi_188520207_gb_ACD58152.1_
0.131244	0.148173	0.080025	0.119814	gi_188520208_gb_ACD58153.1_
0.916827	0.999278	0.88153	0.932545	gi_188520210_gb_ACD58155.1_
0.141486	0.043522	0.19201	0.125673	gi_188520211_gb_ACD58156.1_
0.266198	0.079805	0.345473	0.230492	gi_188520212_gb_ACD58157.1_
0.165205	0.047291	0.213325	0.14194	gi_188520213_gb_ACD58158.1_
0.130903	0.090298	0.148932	0.123378	gi_188520214_gb_ACD58159.1_
0.431435	0.833966	0.520239	0.595213	gi_188520216_gb_ACD58161.1_
0.090545	0.097969	0.102845	0.09712	gi_188520217_gb_ACD58162.1_
0.388648	0.259802	0.52473	0.39106	gi_188520221_gb_ACD58166.1_
0.286591	0.864245	0.177994	0.442943	gi_188520227_gb_ACD58172.1_
0.137881	0.305339	0.089562	0.177594	gi_188520239_gb_ACD58184.1_
0.393649	0.065866	0.516494	0.325336	gi_188520247_gb_ACD58192.1_
0.102018	0.041686	0.113548	0.085751	gi_188520248_gb_ACD58193.1_
0.153553	0.04415	0.170654	0.122786	gi_188520249_gb_ACD58194.1_
0.877396	0.795109	0.599888	0.757464	gi_188520250_gb_ACD58195.1_
0.269138	0.09984	0.347511	0.23883	gi_188520252_gb_ACD58197.1_
0.344795	0.064586	0.30789	0.23909	gi_188520253_gb_ACD58198.1_
0.228818	0.09639	0.314967	0.213392	gi_188520254_gb_ACD58199.1_
0.136815	0.074883	0.213325	0.141674	gi_188520255_gb_ACD58200.1_
0.935956	0.984602	0.894069	0.938209	gi_188520256_gb_ACD58201.1_
0.125209	0.000187	0.161921	0.095772	gi_188520722_gb_ACD58667.1_
0.075299	0.127527	0.070045	0.090957	gi_188520723_gb_ACD58668.1_
0.116912	0.034158	0.100652	0.083907	gi_188520727_gb_ACD58672.1_
0.175375	0.247871	0.112645	0.17863	gi_188520732_gb_ACD58677.1_
0.172787	0.023869	0.122604	0.10642	gi_188520734_gb_ACD58679.1_
0.126198	0.034858	0.14629	0.102449	gi_188520735_gb_ACD58680.1_
0.900966	0.999263	0.668631	0.856287	gi_188520740_gb_ACD58685.1_
0.157892	0.073645	0.189233	0.140257	gi_188520743_gb_ACD58688.1_
0.552308	0.75768	0.690188	0.666725	gi_188520747_gb_ACD58692.1_
0.138238	0.080691	0.171931	0.130287	gi_188520748_gb_ACD58693.1_
0.281102	0.08181	0.285978	0.216297	gi_188520751_gb_ACD58696.1_

gi_188519537_gb_ACD57482.1_	0.133	22	0.158	22	0.292	11	0.194	0.175	N	0.57	SignalP-noTM
gi_188519538_gb_ACD57483.1_	0.314	29	0.529	29	0.948	19	0.875	0.692	Y	0.57	SignalP-noTM
gi_188519540_gb_ACD57485.1_	0.141	26	0.118	39	0.148	36	0.095	0.107	N	0.57	SignalP-noTM
gi_188519546_gb_ACD57491.1_	0.102	36	0.138	21	0.236	2	0.188	0.161	N	0.57	SignalP-noTM
gi_188519548_gb_ACD57493.1_	0.118	46	0.103	46	0.13	43	0.088	0.096	N	0.57	SignalP-noTM
gi_188519549_gb_ACD57494.1_	0.206	21	0.439	21	0.959	16	0.928	0.669	Y	0.57	SignalP-noTM
gi_188519551_gb_ACD57496.1_	0.104	37	0.125	15	0.198	9	0.153	0.138	N	0.57	SignalP-noTM
gi_188519552_gb_ACD57497.1_	0.28	24	0.164	24	0.13	46	0.086	0.127	N	0.57	SignalP-noTM
gi_188519554_gb_ACD57499.1_	0.118	44	0.132	32	0.207	3	0.15	0.14	N	0.57	SignalP-noTM
gi_188519555_gb_ACD57500.1_	0.311	26	0.501	26	0.942	4	0.87	0.674	Y	0.57	SignalP-noTM
gi_188519564_gb_ACD57509.1_	0.124	20	0.132	25	0.178	34	0.125	0.129	N	0.57	SignalP-noTM
gi_188519565_gb_ACD57510.1_	0.106	7	0.132	11	0.23	3	0.18	0.155	N	0.57	SignalP-noTM
gi_188519571_gb_ACD57516.1_	0.349	21	0.476	21	0.925	11	0.642	0.554	N	0.57	SignalP-noTM
gi_188519573_gb_ACD57518.1_	0.874	23	0.903	23	0.967	19	0.922	0.912	Y	0.57	SignalP-noTM
gi_188519578_gb_ACD57523.1_	0.158	33	0.185	33	0.361	16	0.208	0.196	N	0.57	SignalP-noTM
gi_188519579_gb_ACD57524.1_	0.106	50	0.102	60	0.143	1	0.093	0.098	N	0.57	SignalP-noTM
gi_188519586_gb_ACD57531.1_	0.13	21	0.118	21	0.138	9	0.101	0.11	N	0.57	SignalP-noTM
gi_188519589_gb_ACD57534.1_	0.118	36	0.097	36	0.096	31	0.068	0.083	N	0.57	SignalP-noTM
gi_188519590_gb_ACD57535.1_	0.242	23	0.36	23	0.881	2	0.641	0.492	N	0.57	SignalP-noTM
gi_188519591_gb_ACD57536.1_	0.268	18	0.486	18	0.915	1	0.889	0.675	Y	0.57	SignalP-noTM
gi_188519593_gb_ACD57538.1_	0.135	22	0.153	18	0.25	4	0.202	0.171	N	0.51	SignalP-TM
gi_188519594_gb_ACD57539.1_	0.125	68	0.13	12	0.205	11	0.167	0.147	N	0.57	SignalP-noTM
gi_188519601_gb_ACD57546.1_	0.145	23	0.152	23	0.355	2	0.18	0.165	N	0.57	SignalP-noTM
gi_188519616_gb_ACD57561.1_	0.154	24	0.175	24	0.324	4	0.199	0.186	N	0.57	SignalP-noTM
gi_188519623_gb_ACD57568.1_	0.477	60	0.293	60	0.57	23	0.248	0.276	N	0.51	SignalP-TM
gi_188519634_gb_ACD57579.1_	0.135	22	0.195	22	0.358	20	0.253	0.222	N	0.57	SignalP-noTM
gi_188519640_gb_ACD57585.1_	0.231	43	0.176	43	0.218	42	0.11	0.145	N	0.57	SignalP-noTM
gi_188519642_gb_ACD57587.1_	0.17	37	0.159	37	0.371	34	0.144	0.152	N	0.57	SignalP-noTM
gi_188519644_gb_ACD57589.1_	0.103	24	0.108	11	0.163	2	0.114	0.111	N	0.57	SignalP-noTM
gi_188519646_gb_ACD57591.1_	0.506	24	0.452	24	0.529	15	0.401	0.428	N	0.57	SignalP-noTM
gi_188519651_gb_ACD57596.1_	0.127	23	0.183	23	0.338	17	0.239	0.209	N	0.57	SignalP-noTM
gi_188519656_gb_ACD57601.1_	0.107	52	0.107	69	0.143	67	0.086	0.099	N	0.51	SignalP-TM
gi_188520140_gb_ACD58085.1_	0.106	3	0.098	41	0.105	31	0.086	0.093	N	0.57	SignalP-noTM
gi_188520145_gb_ACD58090.1_	0.135	5	0.138	12	0.222	4	0.167	0.149	N	0.51	SignalP-TM
gi_188520146_gb_ACD58091.1_	0.104	49	0.126	13	0.196	6	0.161	0.143	N	0.57	SignalP-noTM
gi_188520147_gb_ACD58092.1_	0.157	22	0.185	22	0.247	16	0.207	0.195	N	0.57	SignalP-noTM
gi_188520152_gb_ACD58097.1_	0.142	29	0.12	17	0.184	9	0.141	0.128	N	0.51	SignalP-TM
gi_188520153_gb_ACD58098.1_	0.126	34	0.101	34	0.098	35	0.07	0.087	N	0.57	SignalP-noTM
gi_188520161_gb_ACD58106.1_	0.123	30	0.127	11	0.191	1	0.165	0.145	N	0.57	SignalP-noTM
gi_188520163_gb_ACD58108.1_	0.122	20	0.129	25	0.168	34	0.12	0.125	N	0.57	SignalP-noTM
gi_188520164_gb_ACD58109.1_	0.141	68	0.12	68	0.158	2	0.108	0.115	N	0.57	SignalP-noTM
gi_188520172_gb_ACD58117.1_	0.115	22	0.146	13	0.277	9	0.213	0.177	N	0.57	SignalP-noTM
gi_188520174_gb_ACD58119.1_	0.371	21	0.235	21	0.202	18	0.145	0.192	N	0.57	SignalP-noTM
gi_188520175_gb_ACD58120.1_	0.102	17	0.111	11	0.159	7	0.129	0.118	N	0.51	SignalP-TM
gi_188520176_gb_ACD58121.1_	0.11	28	0.123	11	0.184	9	0.163	0.142	N	0.57	SignalP-noTM
gi_188520182_gb_ACD58127.1_	0.151	24	0.242	24	0.665	23	0.432	0.332	N	0.57	SignalP-noTM
gi_188520183_gb_ACD58128.1_	0.1	3	0.1	36	0.118	1	0.087	0.094	N	0.57	SignalP-noTM
gi_188520184_gb_ACD58129.1_	0.19	41	0.199	41	0.409	40	0.132	0.167	N	0.57	SignalP-noTM
gi_188520185_gb_ACD58130.1_	0.108	34	0.112	11	0.181	4	0.126	0.119	N	0.57	SignalP-noTM
gi_188520186_gb_ACD58131.1_	0.183	45	0.171	45	0.242	41	0.109	0.148	N	0.51	SignalP-TM
gi_188520192_gb_ACD58137.1_	0.112	18	0.127	18	0.228	13	0.134	0.13	N	0.57	SignalP-noTM
gi_188520197_gb_ACD58142.1_	0.111	20	0.103	20	0.13	12	0.089	0.097	N	0.57	SignalP-noTM
gi_188520198_gb_ACD58143.1_	0.222	20	0.213	20	0.269	12	0.209	0.211	N	0.57	SignalP-noTM
gi_188520199_gb_ACD58144.1_	0.13	30	0.127	11	0.225	2	0.151	0.138	N	0.57	SignalP-noTM
gi_188520200_gb_ACD58145.1_	0.158	57	0.127	57	0.128	22	0.088	0.109	N	0.57	SignalP-noTM
gi_188520201_gb_ACD58146.1_	0.13	25	0.207	14	0.563	5	0.419	0.307	N	0.57	SignalP-noTM
gi_188520202_gb_ACD58147.1_	0.62	24	0.751	24	0.944	18	0.905	0.823	Y	0.57	SignalP-noTM
gi_188520204_gb_ACD58149.1_	0.887	22	0.907	22	0.974	11	0.924	0.915	Y	0.57	SignalP-noTM
gi_188520207_gb_ACD58152.1_	0.407	21	0.615	21	0.967	13	0.927	0.762	Y	0.57	SignalP-noTM
gi_188520208_gb_ACD58153.1_	0.144	21	0.101	21	0.107	70	0.065	0.084	N	0.57	SignalP-noTM
gi_188520210_gb_ACD58155.1_	0.294	10	0.11	16	0.172	9	0.116	0.112	N	0.57	SignalP-noTM
gi_188520211_gb_ACD58156.1_	0.18	44	0.132	44	0.185	5	0.106	0.12	N	0.57	SignalP-noTM
gi_188520212_gb_ACD58157.1_	0.196	54	0.137	54	0.185	3	0.106	0.122	N	0.57	SignalP-noTM
gi_188520213_gb_ACD58158.1_	0.124	23	0.128	23	0.247	49	0.134	0.131	N	0.57	SignalP-noTM
gi_188520214_gb_ACD58159.1_	0.199	24	0.177	24	0.315	31	0.14	0.16	N	0.57	SignalP-noTM
gi_188520216_gb_ACD58161.1_	0.117	60	0.12	60	0.193	2	0.115	0.118	N	0.57	SignalP-noTM
gi_188520217_gb_ACD58162.1_	0.154	44	0.127	44	0.18	42	0.1	0.114	N	0.57	SignalP-noTM
gi_188520221_gb_ACD58166.1_	0.132	50	0.176	41	0.422	40	0.222	0.198	N	0.57	SignalP-noTM
gi_188520227_gb_ACD58172.1_	0.101	32	0.152	24	0.272	18	0.215	0.182	N	0.57	SignalP-noTM
gi_188520239_gb_ACD58184.1_	0.108	32	0.13	53	0.207	43	0.145	0.137	N	0.57	SignalP-noTM
gi_188520247_gb_ACD58192.1_	0.128	26	0.104	26	0.126	2	0.09	0.097	N	0.57	SignalP-noTM
gi_188520248_gb_ACD58193.1_	0.108	48	0.103	48	0.139	6	0.103	0.103	N	0.57	SignalP-noTM
gi_188520249_gb_ACD58194.1_	0.178	22	0.23	41	0.573	35	0.247	0.236	N	0.51	SignalP-TM
gi_188520250_gb_ACD58195.1_	0.105	37	0.099	16	0.12	7	0.095	0.097	N	0.57	SignalP-noTM
gi_188520252_gb_ACD58197.1_	0.119	18	0.111	18	0.144	13	0.105	0.108	N	0.57	SignalP-noTM
gi_188520253_gb_ACD58198.1_	0.196	21	0.164	21	0.214	3	0.156	0.16	N	0.57	SignalP-noTM
gi_188520254_gb_ACD58199.1_	0.122	31	0.16	26	0.289	3	0.201	0.179	N	0.57	SignalP-noTM
gi_188520255_gb_ACD58200.1_	0.215	29	0.178	29	0.33	28	0.138	0.159	N	0.57	SignalP-noTM

0.447692	0.722521	0.603483	0.591232	gi_188520753_gb_ACD58698.1_
0.167702	0.138238	0.152387	0.152776	gi_188520754_gb_ACD58699.1_
0.078493	0.03068	0.124227	0.0778	gi_188520756_gb_ACD58701.1_
0.132964	0.400832	0.227233	0.253676	gi_188520757_gb_ACD58702.1_
0.094063	0.302167	0.149694	0.181975	gi_188520758_gb_ACD58703.1_
0.911412	0.994257	0.922799	0.942823	gi_188520759_gb_ACD58704.1_
0.946242	0.999962	0.915444	0.953883	gi_188520760_gb_ACD58705.1_
0.946698	0.896321	0.885543	0.909521	gi_188520761_gb_ACD58706.1_
0.144798	0.368188	0.155119	0.222702	gi_188520766_gb_ACD58711.1_
0.482008	0.187399	0.604201	0.424536	gi_188520767_gb_ACD58712.1_
0.123251	0.130562	0.177994	0.143936	gi_188520768_gb_ACD58713.1_
0.163147	0.026597	0.250115	0.14662	gi_188520773_gb_ACD58718.1_
0.200528	0.119413	0.257501	0.192481	gi_188520781_gb_ACD58726.1_
0.157493	0.14295	0.156699	0.152381	gi_188520782_gb_ACD58727.1_
0.200047	0.124227	0.227233	0.183836	gi_188520783_gb_ACD58728.1_
0.151228	0.140035	0.100381	0.130548	gi_188520784_gb_ACD58729.1_
0.737884	0.987519	0.894919	0.873441	gi_188520785_gb_ACD58730.1_
0.122927	0.067358	0.112946	0.101077	gi_188520786_gb_ACD58731.1_
0.113247	0.075718	0.116912	0.101959	gi_188520788_gb_ACD58733.1_
0.1603	0.137881	0.171505	0.156562	gi_188520789_gb_ACD58734.1_
0.229878	0.073033	0.224088	0.175666	gi_188520790_gb_ACD58735.1_
0.057055	0.02271	0.069655	0.049807	gi_188520791_gb_ACD58736.1_
0.114457	0.086669	0.112047	0.104391	gi_188520792_gb_ACD58737.1_
0.111452	0.062094	0.164379	0.112642	gi_188520793_gb_ACD58738.1_
0.186943	0.00809	0.238486	0.144506	gi_188520794_gb_ACD58739.1_
0.076988	0.032895	0.123251	0.077711	gi_188520795_gb_ACD58740.1_
0.134354	0.103123	0.185579	0.141019	gi_188520796_gb_ACD58741.1_
0.410234	0.079805	0.517992	0.33601	gi_188520797_gb_ACD58742.1_
0.072024	0.033569	0.082262	0.062618	gi_188520798_gb_ACD58743.1_
0.749885	0.930539	0.838485	0.839636	gi_188521287_gb_ACD59232.1_
0.087145	0.003375	0.130222	0.073581	gi_188521289_gb_ACD59234.1_
0.173647	0.050211	0.248991	0.157616	gi_188521294_gb_ACD59239.1_
0.13331	0.043025	0.158691	0.111675	gi_188521296_gb_ACD59241.1_
0.885543	0.906701	0.884627	0.89229	gi_188521301_gb_ACD59246.1_
0.947	0.982364	0.86283	0.930731	gi_188521304_gb_ACD59249.1_
0.137525	0.077845	0.174942	0.130104	gi_188521306_gb_ACD59251.1_
0.103123	0.042656	0.115067	0.086949	gi_188521336_gb_ACD59281.1_
0.192476	0.046887	0.247871	0.162411	gi_188521345_gb_ACD59290.1_
0.610639	0.995381	0.485754	0.697258	gi_188521400_gb_ACD59345.1_
0.566356	0.730862	0.799472	0.698897	gi_188521473_gb_ACD59418.1_
0.603483	0.767991	0.727307	0.699594	gi_188521501_gb_ACD59446.1_
0.103123	0.042533	0.114153	0.086603	gi_188521503_gb_ACD59448.1_
0.111749	0.056733	0.126529	0.098337	gi_188521505_gb_ACD59450.1_
0.915676	0.997343	0.799953	0.904324	gi_188521506_gb_ACD59451.1_
0.176245	0.127194	0.236313	0.179917	gi_188521507_gb_ACD59452.1_
0.300273	0.609212	0.387935	0.432473	gi_188521508_gb_ACD59453.1_
0.364705	0.740775	0.171505	0.425662	gi_188521509_gb_ACD59454.1_
0.076139	0.001004	0.130562	0.069235	gi_188521510_gb_ACD59455.1_
0.199567	0.175375	0.229347	0.20143	gi_188521514_gb_ACD59459.1_
0.135404	0.06192	0.223567	0.140297	gi_188521515_gb_ACD59460.1_
0.089806	0.621284	0.186032	0.299041	gi_188521516_gb_ACD59461.1_
0.193411	0.078276	0.272693	0.18146	gi_188521517_gb_ACD59462.1_
0.9473	0.995865	0.899348	0.947504	gi_188521518_gb_ACD59463.1_
0.796571	0.455865	0.809844	0.687427	gi_188521519_gb_ACD59464.1_
0.104238	0.02318	0.117533	0.08165	gi_188521520_gb_ACD59465.1_
0.094576	0.059693	0.112946	0.089072	gi_188521521_gb_ACD59466.1_
0.954696	0.998762	0.919975	0.957811	gi_188521522_gb_ACD59467.1_
0.638763	0.661951	0.569301	0.623338	gi_188521523_gb_ACD59468.1_
0.202458	0.799472	0.187399	0.396443	gi_188521529_gb_ACD59474.1_
0.134005	0.042901	0.196234	0.12438	gi_188521531_gb_ACD59476.1_
0.208334	0.949646	0.103123	0.420368	gi_188521535_gb_ACD59480.1_
0.412413	0.86669	0.607067	0.628723	gi_188521537_gb_ACD59482.1_
0.456609	0.917284	0.673267	0.682387	gi_188521538_gb_ACD59483.1_
0.950216	0.108806	0.869778	0.642933	gi_188521539_gb_ACD59484.1_
0.113247	0.001495	0.161515	0.092086	gi_188521543_gb_ACD59488.1_
0.840908	0.49475	0.901766	0.745808	gi_188521554_gb_ACD59499.1_
0.116294	0.087384	0.174078	0.125919	gi_188521557_gb_ACD59502.1_
0.138955	0.040272	0.204403	0.127877	gi_188521558_gb_ACD59503.1_
0.089806	0.048661	0.13331	0.090592	gi_188521559_gb_ACD59504.1_
0.572241	0.300273	0.578837	0.483784	gi_188521560_gb_ACD59505.1_
0.284754	0.050354	0.354344	0.229817	gi_188521561_gb_ACD59506.1_
0.14517	0.068116	0.139314	0.117533	gi_188521562_gb_ACD59507.1_
0.093553	0.001019	0.113548	0.069373	gi_188521564_gb_ACD59509.1_
0.089806	0.037688	0.144427	0.09064	gi_188521566_gb_ACD59511.1_
0.1034	0.089562	0.079585	0.090849	gi_188521567_gb_ACD59512.1_
0.103679	0.034059	0.151614	0.096451	gi_188521569_gb_ACD59514.1_
0.737303	0.961543	0.624806	0.774551	gi_188521570_gb_ACD59515.1_
0.135755	0.023522	0.208829	0.122702	gi_188521575_gb_ACD59520.1_

gi_188520256_gb_ACD58201.1_	0.121	61	0.121	19	0.159	13	0.124	0.122	N	0.57	SignalP-noTM
gi_188520722_gb_ACD58667.1_	0.121	23	0.113	23	0.128	11	0.1	0.107	N	0.57	SignalP-noTM
gi_188520723_gb_ACD58668.1_	0.131	7	0.214	22	0.482	14	0.332	0.269	N	0.57	SignalP-noTM
gi_188520727_gb_ACD58672.1_	0.121	41	0.12	15	0.185	5	0.141	0.13	N	0.57	SignalP-noTM
gi_188520732_gb_ACD58677.1_	0.132	25	0.154	25	0.244	16	0.186	0.169	N	0.57	SignalP-noTM
gi_188520734_gb_ACD58679.1_	0.145	30	0.195	20	0.392	16	0.31	0.249	N	0.57	SignalP-noTM
gi_188520735_gb_ACD58680.1_	0.183	15	0.153	15	0.253	1	0.144	0.149	N	0.57	SignalP-noTM
gi_188520740_gb_ACD58685.1_	0.101	41	0.137	11	0.286	2	0.18	0.157	N	0.57	SignalP-noTM
gi_188520743_gb_ACD58688.1_	0.112	50	0.12	41	0.179	36	0.12	0.12	N	0.57	SignalP-noTM
gi_188520747_gb_ACD58692.1_	0.115	22	0.146	13	0.28	9	0.215	0.178	N	0.57	SignalP-noTM
gi_188520748_gb_ACD58693.1_	0.114	67	0.106	43	0.137	10	0.101	0.104	N	0.57	SignalP-noTM
gi_188520751_gb_ACD58696.1_	0.112	42	0.126	12	0.231	4	0.163	0.143	N	0.57	SignalP-noTM
gi_188520753_gb_ACD58698.1_	0.827	22	0.849	22	0.934	7	0.893	0.87	Y	0.57	SignalP-noTM
gi_188520754_gb_ACD58699.1_	0.123	38	0.104	38	0.109	35	0.08	0.093	N	0.57	SignalP-noTM
gi_188520756_gb_ACD58701.1_	0.281	27	0.211	27	0.341	9	0.206	0.209	N	0.57	SignalP-noTM
gi_188520757_gb_ACD58702.1_	0.122	38	0.174	20	0.383	12	0.249	0.202	N	0.51	SignalP-TM
gi_188520758_gb_ACD58703.1_	0.141	57	0.113	33	0.155	25	0.096	0.107	N	0.51	SignalP-TM
gi_188520759_gb_ACD58704.1_	0.552	21	0.709	21	0.958	4	0.923	0.809	Y	0.57	SignalP-noTM
gi_188520760_gb_ACD58705.1_	0.854	25	0.904	25	0.974	21	0.944	0.923	Y	0.57	SignalP-noTM
gi_188520761_gb_ACD58706.1_	0.723	24	0.803	24	0.955	9	0.913	0.854	Y	0.57	SignalP-noTM
gi_188520766_gb_ACD58711.1_	0.206	58	0.166	58	0.179	54	0.121	0.145	N	0.57	SignalP-noTM
gi_188520767_gb_ACD58712.1_	0.135	50	0.114	50	0.165	49	0.081	0.098	N	0.57	SignalP-noTM
gi_188520768_gb_ACD58713.1_	0.122	67	0.112	11	0.158	1	0.12	0.116	N	0.57	SignalP-noTM
gi_188520773_gb_ACD58718.1_	0.157	47	0.146	47	0.182	44	0.125	0.136	N	0.57	SignalP-noTM
gi_188520781_gb_ACD58726.1_	0.149	20	0.159	11	0.375	1	0.247	0.192	N	0.51	SignalP-TM
gi_188520782_gb_ACD58727.1_	0.12	53	0.187	20	0.545	14	0.323	0.251	N	0.57	SignalP-noTM
gi_188520783_gb_ACD58728.1_	0.162	53	0.139	18	0.347	1	0.152	0.146	N	0.57	SignalP-noTM
gi_188520784_gb_ACD58729.1_	0.118	60	0.114	15	0.179	9	0.115	0.114	N	0.57	SignalP-noTM
gi_188520785_gb_ACD58730.1_	0.1	36	0.142	11	0.256	1	0.199	0.169	N	0.57	SignalP-noTM
gi_188520786_gb_ACD58731.1_	0.137	22	0.167	22	0.307	1	0.197	0.178	N	0.51	SignalP-TM
gi_188520788_gb_ACD58733.1_	0.151	54	0.112	54	0.108	32	0.074	0.094	N	0.57	SignalP-noTM
gi_188520789_gb_ACD58734.1_	0.117	54	0.12	20	0.169	9	0.122	0.121	N	0.51	SignalP-TM
gi_188520790_gb_ACD58735.1_	0.165	57	0.162	12	0.382	1	0.249	0.194	N	0.51	SignalP-TM
gi_188520791_gb_ACD58736.1_	0.235	22	0.151	22	0.14	19	0.09	0.123	N	0.57	SignalP-noTM
gi_188520792_gb_ACD58737.1_	0.105	49	0.104	34	0.128	5	0.102	0.103	N	0.57	SignalP-noTM
gi_188520793_gb_ACD58738.1_	0.112	25	0.113	37	0.149	28	0.09	0.102	N	0.57	SignalP-noTM
gi_188520794_gb_ACD58739.1_	0.156	26	0.178	26	0.309	18	0.192	0.185	N	0.57	SignalP-noTM
gi_188520795_gb_ACD58740.1_	0.133	34	0.135	34	0.212	31	0.12	0.128	N	0.57	SignalP-noTM
gi_188520796_gb_ACD58741.1_	0.173	16	0.17	11	0.58	1	0.25	0.2	N	0.51	SignalP-TM
gi_188520797_gb_ACD58742.1_	0.128	25	0.138	55	0.217	51	0.123	0.132	N	0.51	SignalP-TM
gi_188520798_gb_ACD58743.1_	0.205	48	0.193	48	0.235	40	0.126	0.162	N	0.57	SignalP-noTM
gi_188521287_gb_ACD59232.1_	0.115	22	0.146	13	0.278	9	0.213	0.178	N	0.57	SignalP-noTM
gi_188521289_gb_ACD59234.1_	0.159	26	0.113	26	0.131	41	0.075	0.096	N	0.57	SignalP-noTM
gi_188521294_gb_ACD59239.1_	0.116	53	0.129	11	0.219	1	0.165	0.146	N	0.57	SignalP-noTM
gi_188521296_gb_ACD59241.1_	0.104	47	0.104	53	0.179	44	0.089	0.097	N	0.57	SignalP-noTM
gi_188521301_gb_ACD59246.1_	0.118	65	0.179	11	0.427	3	0.325	0.248	N	0.57	SignalP-noTM
gi_188521304_gb_ACD59249.1_	0.131	21	0.17	21	0.392	3	0.249	0.207	N	0.57	SignalP-noTM
gi_188521306_gb_ACD59251.1_	0.114	67	0.106	43	0.137	10	0.101	0.104	N	0.57	SignalP-noTM
gi_188521336_gb_ACD59281.1_	0.108	48	0.103	48	0.139	6	0.103	0.103	N	0.57	SignalP-noTM
gi_188521345_gb_ACD59290.1_	0.197	26	0.191	26	0.363	22	0.215	0.202	N	0.57	SignalP-noTM
gi_188521400_gb_ACD59345.1_	0.131	40	0.104	64	0.126	9	0.091	0.098	N	0.57	SignalP-noTM
gi_188521473_gb_ACD59418.1_	0.184	28	0.134	28	0.12	1	0.098	0.117	N	0.57	SignalP-noTM
gi_188521501_gb_ACD59446.1_	0.105	45	0.105	51	0.172	42	0.087	0.097	N	0.57	SignalP-noTM
gi_188521503_gb_ACD59448.1_	0.108	48	0.103	35	0.14	6	0.104	0.103	N	0.57	SignalP-noTM
gi_188521505_gb_ACD59450.1_	0.147	23	0.13	23	0.207	1	0.124	0.127	N	0.57	SignalP-noTM
gi_188521506_gb_ACD59451.1_	0.128	46	0.181	14	0.38	10	0.327	0.25	N	0.57	SignalP-noTM
gi_188521507_gb_ACD59452.1_	0.136	56	0.172	11	0.436	3	0.285	0.226	N	0.57	SignalP-noTM
gi_188521508_gb_ACD59453.1_	0.121	31	0.123	11	0.243	4	0.152	0.136	N	0.57	SignalP-noTM
gi_188521509_gb_ACD59454.1_	0.105	4	0.143	11	0.25	1	0.207	0.173	N	0.57	SignalP-noTM
gi_188521510_gb_ACD59455.1_	0.105	21	0.102	45	0.112	30	0.092	0.097	N	0.57	SignalP-noTM
gi_188521514_gb_ACD59459.1_	0.105	30	0.106	11	0.158	1	0.104	0.105	N	0.57	SignalP-noTM
gi_188521515_gb_ACD59460.1_	0.391	30	0.281	30	0.346	19	0.222	0.253	N	0.57	SignalP-noTM
gi_188521516_gb_ACD59461.1_	0.11	51	0.144	11	0.278	2	0.211	0.169	N	0.51	SignalP-TM
gi_188521517_gb_ACD59462.1_	0.637	30	0.404	30	0.492	28	0.242	0.328	N	0.57	SignalP-noTM
gi_188521518_gb_ACD59463.1_	0.368	51	0.505	51	0.894	45	0.378	0.445	N	0.57	SignalP-noTM
gi_188521519_gb_ACD59464.1_	0.102	29	0.124	11	0.246	3	0.151	0.137	N	0.57	SignalP-noTM
gi_188521520_gb_ACD59465.1_	0.144	30	0.114	30	0.11	2	0.085	0.101	N	0.57	SignalP-noTM
gi_188521521_gb_ACD59466.1_	0.116	34	0.109	19	0.153	9	0.108	0.109	N	0.57	SignalP-noTM
gi_188521522_gb_ACD59467.1_	0.516	29	0.689	29	0.985	16	0.918	0.797	Y	0.57	SignalP-noTM
gi_188521523_gb_ACD59468.1_	0.87	22	0.898	22	0.941	18	0.911	0.904	Y	0.57	SignalP-noTM
gi_188521529_gb_ACD59474.1_	0.226	19	0.273	19	0.585	17	0.334	0.302	N	0.57	SignalP-noTM
gi_188521531_gb_ACD59476.1_	0.129	33	0.162	54	0.382	46	0.135	0.149	N	0.57	SignalP-noTM
gi_188521535_gb_ACD59480.1_	0.111	9	0.106	68	0.124	62	0.09	0.098	N	0.57	SignalP-noTM
gi_188521537_gb_ACD59482.1_	0.11	34	0.137	11	0.281	1	0.179	0.157	N	0.57	SignalP-noTM
gi_188521538_gb_ACD59483.1_	0.177	64	0.137	50	0.245	42	0.136	0.137	N	0.57	SignalP-noTM
gi_188521539_gb_ACD59484.1_	0.162	19	0.119	11	0.225	1	0.133	0.126	N	0.57	SignalP-noTM
gi_188521543_gb_ACD59488.1_	0.789	29	0.77	29	0.923	24	0.805	0.786	Y	0.57	SignalP-noTM
gi_188521554_gb_ACD59499.1_	0.148	18	0.172	11	0.441	1	0.277	0.211	N	0.51	SignalP-TM

0.442505	0.978773	0.647028	0.689435	gi_188521576_gb_ACD59521.1_
0.219428	0.128532	0.090052	0.146004	gi_188521577_gb_ACD59522.1_
0.194348	0.476767	0.10736	0.259492	gi_188521578_gb_ACD59523.1_
0.159896	0.222008	0.126529	0.169478	gi_188521582_gb_ACD59527.1_
0.128532	0.312383	0.219943	0.220286	gi_188521585_gb_ACD59530.1_
0.080913	0.50375	0.174509	0.253057	gi_188521588_gb_ACD59533.1_
0.361237	0.035778	0.481259	0.292758	gi_188521589_gb_ACD59534.1_
0.38367	0.141122	0.49325	0.339347	gi_188521590_gb_ACD59535.1_
0.179314	0.078928	0.143318	0.133853	gi_188521591_gb_ACD59536.1_
0.094063	0.061399	0.129882	0.095115	gi_188521594_gb_ACD59539.1_
0.09639	0.050931	0.130562	0.092628	gi_188521600_gb_ACD59545.1_
0.08883	0.051368	0.109097	0.083098	gi_188521601_gb_ACD59546.1_
0.171079	0.046486	0.210818	0.142794	gi_188521602_gb_ACD59547.1_
0.931502	0.852205	0.844487	0.876065	gi_188521603_gb_ACD59548.1_
0.201491	0.049642	0.118157	0.123097	gi_188521604_gb_ACD59549.1_
0.949069	0.999375	0.910926	0.953123	gi_188521605_gb_ACD59550.1_
0.201009	0.236855	0.145916	0.194593	gi_188521606_gb_ACD59551.1_
0.14629	0.02401	0.179756	0.116685	gi_188521607_gb_ACD59552.1_
0.139314	0.010761	0.143687	0.097921	gi_188521632_gb_ACD59577.1_
0.114153	0.057216	0.20538	0.125583	gi_188521639_gb_ACD59584.1_
0.163557	0.137525	0.111452	0.137511	gi_188521649_gb_ACD59594.1_
0.232544	0.139314	0.147795	0.173218	gi_188521650_gb_ACD59595.1_
0.332034	0.039925	0.400832	0.257597	gi_188521651_gb_ACD59596.1_
0.082944	0.097969	0.165619	0.115511	gi_188521656_gb_ACD59601.1_
0.095609	0.188314	0.188773	0.157565	gi_188521657_gb_ACD59602.1_
0.359854	0.958073	0.49325	0.603726	gi_188521658_gb_ACD59603.1_
0.350236	0.042778	0.234154	0.209056	gi_188521664_gb_ACD59609.1_
0.30789	0.974913	0.185126	0.48931	gi_188521665_gb_ACD59610.1_
0.076988	0.001287	0.119413	0.065896	gi_188521677_gb_ACD59622.1_
0.09639	0.09639	0.196708	0.129829	gi_188521678_gb_ACD59623.1_
0.704746	0.029974	0.671284	0.468668	gi_188521679_gb_ACD59624.1_
0.558235	0.041927	0.520988	0.373717	gi_188521681_gb_ACD59626.1_
0.094063	0.02795	0.143687	0.088567	gi_188521682_gb_ACD59627.1_
0.136815	0.049501	0.173647	0.119988	gi_188521683_gb_ACD59628.1_
0.129882	0.004148	0.186032	0.106687	gi_188521684_gb_ACD59629.1_
0.321475	0.975636	0.168962	0.488691	gi_188521685_gb_ACD59630.1_
0.127862	0.311739	0.243977	0.227859	gi_188521686_gb_ACD59631.1_
0.471531	0.005726	0.354344	0.2772	gi_188521689_gb_ACD59634.1_
0.10011	0.040973	0.111452	0.084178	gi_188521699_gb_ACD59644.1_
0.912616	0.974017	0.832716	0.90645	gi_188521700_gb_ACD59645.1_
0.801389	0.9866	0.761514	0.849834	gi_188521702_gb_ACD59647.1_
0.102569	0.004198	0.23308	0.113282	gi_188521703_gb_ACD59648.1_
0.946242	0.8397	0.904132	0.896691	gi_188521706_gb_ACD59651.1_
0.234154	0.890903	0.143687	0.422915	gi_188521718_gb_ACD59663.1_
0.776433	0.975493	0.777473	0.843133	gi_188521719_gb_ACD59664.1_
0.828495	0.99746	0.777473	0.867809	gi_188521720_gb_ACD59665.1_
0.110563	0.007377	0.158291	0.092077	gi_188521721_gb_ACD59666.1_
0.078276	0.248991	0.075299	0.134189	gi_188521722_gb_ACD59667.1_
0.119729	0.031768	0.173217	0.108238	gi_188521723_gb_ACD59668.1_
0.164792	0.079365	0.154727	0.132961	gi_188521724_gb_ACD59669.1_
0.733216	0.171079	0.604201	0.502832	gi_188521725_gb_ACD59670.1_
0.055462	0.122604	0.134703	0.104256	gi_188521727_gb_ACD59672.1_
0.077201	0.054064	0.093299	0.074855	gi_188521728_gb_ACD59673.1_
0.083631	0.078928	0.087624	0.083394	gi_188521729_gb_ACD59674.1_
0.165205	0.056094	0.118157	0.113152	gi_188521732_gb_ACD59677.1_
0.131587	0.212822	0.090052	0.14482	gi_188521733_gb_ACD59678.1_
0.122604	0.060882	0.133658	0.105715	gi_188521734_gb_ACD59679.1_
0.284144	0.991982	0.356405	0.544177	gi_188521735_gb_ACD59680.1_
0.138238	0.292763	0.138238	0.189746	gi_188521736_gb_ACD59681.1_
0.072225	0.015906	0.100381	0.062837	gi_188521737_gb_ACD59682.1_
0.936136	0.999437	0.864245	0.933273	gi_188521738_gb_ACD59683.1_
0.952302	0.981567	0.934319	0.956063	gi_188521739_gb_ACD59684.1_
0.208334	0.950216	0.09639	0.418313	gi_188521740_gb_ACD59685.1_
0.080913	0.006766	0.143318	0.076999	gi_188521742_gb_ACD59687.1_
0.073645	0.025531	0.132964	0.07738	gi_188521743_gb_ACD59688.1_
0.607067	0.885238	0.514996	0.6691	gi_188521744_gb_ACD59689.1_
0.092038	0.047021	0.162329	0.100463	gi_188521745_gb_ACD59690.1_
0.095868	0.01648	0.164379	0.092242	gi_188521746_gb_ACD59691.1_
0.122604	0.002985	0.155513	0.093701	gi_188521747_gb_ACD59692.1_
0.145542	0.023317	0.182873	0.117244	gi_188521748_gb_ACD59693.1_
0.202458	0.008978	0.232544	0.147993	gi_188521754_gb_ACD59699.1_
0.441026	0.939289	0.517243	0.632519	gi_188521755_gb_ACD59700.1_
0.131244	0.061399	0.125209	0.105951	gi_188521757_gb_ACD59702.1_
0.102293	0.088588	0.101744	0.097542	gi_188521760_gb_ACD59705.1_
0.134005	0.474522	0.105081	0.237869	gi_188521761_gb_ACD59706.1_
0.130222	0.139314	0.132619	0.134052	gi_188521762_gb_ACD59707.1_
0.069461	0.141486	0.081137	0.097361	gi_188521767_gb_ACD59712.1_
0.136461	0.034158	0.147418	0.106012	gi_188521769_gb_ACD59714.1_

gi_188521557_gb_ACD59502.1_	0.144	18	0.1	18	0.125	1	0.079	0.092	N	0.51	SignalP-TM
gi_188521558_gb_ACD59503.1_	0.13	43	0.124	43	0.144	47	0.094	0.11	N	0.57	SignalP-noTM
gi_188521559_gb_ACD59504.1_	0.101	39	0.104	70	0.126	9	0.092	0.098	N	0.57	SignalP-noTM
gi_188521560_gb_ACD59505.1_	0.11	20	0.113	27	0.144	2	0.119	0.116	N	0.57	SignalP-noTM
gi_188521561_gb_ACD59506.1_	0.102	47	0.104	61	0.118	52	0.087	0.096	N	0.57	SignalP-noTM
gi_188521562_gb_ACD59507.1_	0.138	63	0.132	11	0.3	1	0.16	0.145	N	0.57	SignalP-noTM
gi_188521564_gb_ACD59509.1_	0.107	64	0.114	11	0.161	5	0.134	0.123	N	0.57	SignalP-noTM
gi_188521566_gb_ACD59511.1_	0.24	46	0.186	46	0.228	42	0.098	0.145	N	0.57	SignalP-noTM
gi_188521567_gb_ACD59512.1_	0.144	27	0.138	11	0.316	2	0.185	0.16	N	0.57	SignalP-noTM
gi_188521569_gb_ACD59514.1_	0.261	34	0.165	34	0.208	47	0.082	0.126	N	0.57	SignalP-noTM
gi_188521570_gb_ACD59515.1_	0.386	25	0.222	25	0.286	15	0.147	0.187	N	0.57	SignalP-noTM
gi_188521575_gb_ACD59520.1_	0.153	33	0.14	33	0.21	41	0.109	0.129	N	0.51	SignalP-TM
gi_188521576_gb_ACD59521.1_	0.148	18	0.251	18	0.613	23	0.421	0.331	N	0.57	SignalP-noTM
gi_188521577_gb_ACD59522.1_	0.436	39	0.313	26	0.84	3	0.544	0.421	N	0.57	SignalP-noTM
gi_188521578_gb_ACD59523.1_	0.272	25	0.288	25	0.681	21	0.328	0.307	N	0.57	SignalP-noTM
gi_188521582_gb_ACD59527.1_	0.139	40	0.186	40	0.358	32	0.234	0.209	N	0.57	SignalP-noTM
gi_188521585_gb_ACD59530.1_	0.226	45	0.243	45	0.335	37	0.17	0.209	N	0.57	SignalP-noTM
gi_188521588_gb_ACD59533.1_	0.19	31	0.278	12	0.74	14	0.646	0.414	N	0.51	SignalP-TM
gi_188521589_gb_ACD59534.1_	0.116	25	0.14	25	0.216	22	0.131	0.137	N	0.51	SignalP-TM
gi_188521590_gb_ACD59535.1_	0.22	36	0.457	36	0.987	28	0.779	0.608	Y	0.57	SignalP-noTM
gi_188521591_gb_ACD59536.1_	0.23	57	0.158	57	0.401	1	0.124	0.142	N	0.57	SignalP-noTM
gi_188521594_gb_ACD59539.1_	0.107	26	0.107	63	0.126	53	0.09	0.099	N	0.57	SignalP-noTM
gi_188521600_gb_ACD59545.1_	0.114	18	0.106	18	0.124	8	0.09	0.098	N	0.57	SignalP-noTM
gi_188521601_gb_ACD59546.1_	0.154	23	0.126	35	0.197	34	0.091	0.11	N	0.57	SignalP-noTM
gi_188521602_gb_ACD59547.1_	0.185	41	0.179	41	0.427	39	0.141	0.161	N	0.57	SignalP-noTM
gi_188521603_gb_ACD59548.1_	0.105	65	0.132	15	0.234	10	0.174	0.152	N	0.57	SignalP-noTM
gi_188521604_gb_ACD59549.1_	0.185	46	0.188	46	0.266	36	0.159	0.174	N	0.57	SignalP-noTM
gi_188521605_gb_ACD59550.1_	0.109	26	0.194	35	0.459	28	0.277	0.233	N	0.57	SignalP-noTM
gi_188521606_gb_ACD59551.1_	0.128	24	0.127	24	0.222	4	0.142	0.134	N	0.57	SignalP-noTM
gi_188521607_gb_ACD59552.1_	0.124	40	0.124	40	0.179	2	0.127	0.125	N	0.57	SignalP-noTM
gi_188521632_gb_ACD59577.1_	0.14	54	0.16	12	0.398	6	0.257	0.206	N	0.57	SignalP-noTM
gi_188521639_gb_ACD59584.1_	0.243	21	0.184	36	0.207	29	0.113	0.158	N	0.51	SignalP-TM
gi_188521649_gb_ACD59594.1_	0.134	18	0.134	18	0.169	5	0.14	0.137	N	0.57	SignalP-noTM
gi_188521650_gb_ACD59595.1_	0.126	51	0.148	23	0.254	19	0.199	0.172	N	0.57	SignalP-noTM
gi_188521651_gb_ACD59596.1_	0.134	27	0.234	17	0.526	1	0.414	0.3	N	0.51	SignalP-TM
gi_188521656_gb_ACD59601.1_	0.115	32	0.11	14	0.145	1	0.123	0.116	N	0.57	SignalP-noTM
gi_188521657_gb_ACD59602.1_	0.148	44	0.124	16	0.187	6	0.148	0.133	N	0.51	SignalP-TM
gi_188521658_gb_ACD59603.1_	0.11	36	0.135	12	0.261	3	0.182	0.158	N	0.57	SignalP-noTM
gi_188521664_gb_ACD59609.1_	0.187	31	0.185	18	0.397	15	0.259	0.22	N	0.57	SignalP-noTM
gi_188521665_gb_ACD59610.1_	0.106	45	0.126	14	0.215	4	0.158	0.141	N	0.57	SignalP-noTM
gi_188521677_gb_ACD59622.1_	0.174	19	0.14	19	0.243	23	0.129	0.135	N	0.57	SignalP-noTM
gi_188521678_gb_ACD59623.1_	0.311	40	0.334	40	0.539	38	0.237	0.298	N	0.51	SignalP-TM
gi_188521679_gb_ACD59624.1_	0.12	43	0.152	11	0.423	1	0.203	0.171	N	0.51	SignalP-TM
gi_188521681_gb_ACD59626.1_	0.163	54	0.173	13	0.641	8	0.264	0.216	N	0.57	SignalP-noTM
gi_188521682_gb_ACD59627.1_	0.199	23	0.12	23	0.127	41	0.079	0.101	N	0.57	SignalP-noTM
gi_188521683_gb_ACD59628.1_	0.136	43	0.161	14	0.367	2	0.247	0.202	N	0.57	SignalP-noTM
gi_188521684_gb_ACD59629.1_	0.171	62	0.139	62	0.139	1	0.091	0.117	N	0.57	SignalP-noTM
gi_188521685_gb_ACD59630.1_	0.16	20	0.176	20	0.453	2	0.244	0.208	N	0.57	SignalP-noTM
gi_188521686_gb_ACD59631.1_	0.15	30	0.115	14	0.169	6	0.133	0.122	N	0.51	SignalP-TM
gi_188521689_gb_ACD59634.1_	0.221	38	0.207	38	0.341	35	0.165	0.187	N	0.57	SignalP-noTM
gi_188521699_gb_ACD59644.1_	0.108	48	0.103	48	0.139	6	0.103	0.103	N	0.57	SignalP-noTM
gi_188521700_gb_ACD59645.1_	0.107	33	0.107	51	0.138	43	0.082	0.096	N	0.57	SignalP-noTM
gi_188521702_gb_ACD59647.1_	0.132	18	0.129	15	0.217	1	0.157	0.142	N	0.57	SignalP-noTM
gi_188521703_gb_ACD59648.1_	0.188	27	0.142	20	0.225	2	0.155	0.147	N	0.51	SignalP-TM
gi_188521706_gb_ACD59651.1_	0.218	24	0.428	24	0.934	4	0.876	0.639	Y	0.57	SignalP-noTM
gi_188521718_gb_ACD59663.1_	0.112	36	0.131	18	0.274	12	0.163	0.146	N	0.57	SignalP-noTM
gi_188521719_gb_ACD59664.1_	0.157	61	0.141	12	0.252	1	0.145	0.143	N	0.57	SignalP-noTM
gi_188521720_gb_ACD59665.1_	0.12	26	0.108	62	0.156	1	0.093	0.101	N	0.57	SignalP-noTM
gi_188521721_gb_ACD59666.1_	0.118	51	0.126	16	0.248	12	0.134	0.13	N	0.57	SignalP-noTM
gi_188521722_gb_ACD59667.1_	0.148	39	0.165	12	0.394	11	0.211	0.187	N	0.57	SignalP-noTM
gi_188521723_gb_ACD59668.1_	0.124	40	0.188	11	0.504	1	0.325	0.252	N	0.57	SignalP-noTM
gi_188521724_gb_ACD59669.1_	0.111	36	0.128	13	0.257	9	0.166	0.146	N	0.57	SignalP-noTM
gi_188521725_gb_ACD59670.1_	0.395	32	0.506	32	0.814	14	0.633	0.565	N	0.57	SignalP-noTM
gi_188521727_gb_ACD59672.1_	0.16	35	0.184	35	0.331	42	0.146	0.166	N	0.57	SignalP-noTM
gi_188521728_gb_ACD59673.1_	0.235	23	0.15	23	0.195	35	0.098	0.126	N	0.57	SignalP-noTM
gi_188521729_gb_ACD59674.1_	0.123	26	0.11	26	0.145	2	0.103	0.107	N	0.57	SignalP-noTM
gi_188521732_gb_ACD59677.1_	0.12	66	0.102	13	0.148	6	0.106	0.104	N	0.57	SignalP-noTM
gi_188521733_gb_ACD59678.1_	0.109	31	0.164	11	0.323	2	0.27	0.214	N	0.57	SignalP-noTM
gi_188521734_gb_ACD59679.1_	0.126	18	0.099	63	0.103	66	0.083	0.091	N	0.57	SignalP-noTM
gi_188521735_gb_ACD59680.1_	0.122	57	0.163	11	0.37	2	0.269	0.203	N	0.51	SignalP-TM
gi_188521736_gb_ACD59681.1_	0.13	35	0.111	35	0.132	1	0.073	0.097	N	0.51	SignalP-TM
gi_188521737_gb_ACD59682.1_	0.201	34	0.134	34	0.154	33	0.096	0.116	N	0.57	SignalP-noTM
gi_188521738_gb_ACD59683.1_	0.473	24	0.661	24	0.976	20	0.895	0.771	Y	0.57	SignalP-noTM
gi_188521739_gb_ACD59684.1_	0.112	45	0.098	45	0.104	58	0.085	0.092	N	0.57	SignalP-noTM
gi_188521740_gb_ACD59685.1_	0.108	56	0.109	56	0.151	45	0.098	0.104	N	0.57	SignalP-noTM
gi_188521742_gb_ACD59687.1_	0.245	35	0.236	35	0.376	24	0.212	0.227	N	0.51	SignalP-TM
gi_188521743_gb_ACD59688.1_	0.153	27	0.197	11	0.543	4	0.394	0.289	N	0.57	SignalP-noTM
gi_188521744_gb_ACD59689.1_	0.408	35	0.236	35	0.31	34	0.127	0.185	N	0.57	SignalP-noTM

0.128196	0.003978	0.187856	0.106677	gi_188521770_gb_ACD59715.1_
0.14295	0.560453	0.102018	0.268474	gi_188521771_gb_ACD59716.1_
0.157493	0.092289	0.127194	0.125659	gi_188521778_gb_ACD59723.1_
0.108806	0.04004	0.125538	0.091461	gi_188521780_gb_ACD59725.1_
0.107936	0.194348	0.102569	0.134951	gi_188521781_gb_ACD59726.1_
0.216361	0.033472	0.285366	0.1784	gi_188521782_gb_ACD59727.1_
0.140035	0.075718	0.143318	0.11969	gi_188521786_gb_ACD59731.1_
0.159896	0.709096	0.270912	0.379968	gi_188521789_gb_ACD59734.1_
0.122604	0.089317	0.151614	0.121178	gi_188521790_gb_ACD59735.1_
0.924492	0.994622	0.939289	0.952801	gi_188521792_gb_ACD59737.1_
0.376601	0.004564	0.333366	0.238177	gi_188521794_gb_ACD59739.1_
0.093299	0.06192	0.107936	0.087718	gi_188521795_gb_ACD59740.1_
0.175375	0.433644	0.112047	0.240355	gi_188521796_gb_ACD59741.1_
0.107647	0.002959	0.13193	0.080845	gi_188521797_gb_ACD59742.1_
0.21232	0.591217	0.283534	0.362357	gi_188521798_gb_ACD59743.1_
0.177994	0.036934	0.292763	0.16923	gi_188521799_gb_ACD59744.1_
0.119413	0.641527	0.086669	0.282536	gi_188521800_gb_ACD59745.1_
0.121319	0.162737	0.078276	0.120777	gi_188521801_gb_ACD59746.1_
0.077629	0.090545	0.136461	0.101545	gi_188521804_gb_ACD59749.1_
0.077845	0.066422	0.134354	0.092874	gi_188521811_gb_ACD59756.1_
0.082036	0.75768	0.189694	0.343137	gi_188521812_gb_ACD59757.1_
0.188773	0.336038	0.078276	0.201029	gi_188521813_gb_ACD59758.1_
0.844093	0.998189	0.584676	0.808986	gi_188521815_gb_ACD59760.1_
0.151614	0.000245	0.161109	0.104323	gi_188521816_gb_ACD59761.1_
0.159494	0.074883	0.261536	0.165304	gi_188521817_gb_ACD59762.1_
0.056893	0.036615	0.112047	0.068518	gi_188521818_gb_ACD59763.1_
0.114762	0.04229	0.126861	0.094638	gi_188521819_gb_ACD59764.1_
0.890903	0.990068	0.86669	0.915887	gi_188521822_gb_ACD59767.1_
0.923012	0.999761	0.925945	0.949573	gi_188521824_gb_ACD59769.1_
0.161109	0.629716	0.10736	0.299395	gi_188521827_gb_ACD59772.1_
0.240672	0.080468	0.334033	0.218391	gi_188521828_gb_ACD59773.1_
0.291523	0.358473	0.43807	0.362689	gi_188521829_gb_ACD59774.1_
0.096914	0.041447	0.085021	0.074461	gi_188521835_gb_ACD59780.1_
0.132964	0.068498	0.185126	0.128863	gi_188521836_gb_ACD59781.1_
0.168962	0.136815	0.250678	0.185485	gi_188521837_gb_ACD59782.1_
0.10011	0.040388	0.176245	0.105581	gi_188521838_gb_ACD59783.1_
0.399392	0.011797	0.520988	0.310726	gi_188521840_gb_ACD59785.1_
0.127862	0.09639	0.079805	0.101352	gi_188521841_gb_ACD59786.1_
0.093299	0.076139	0.097969	0.089136	gi_188521842_gb_ACD59787.1_
0.064405	0.0238	0.069655	0.05262	gi_188521843_gb_ACD59788.1_
0.121319	0.010231	0.177994	0.103181	gi_188521846_gb_ACD59791.1_
0.127194	0.077629	0.168962	0.124595	gi_188521847_gb_ACD59792.1_
0.145542	0.08883	0.162329	0.132234	gi_188521848_gb_ACD59793.1_
0.688904	0.108515	0.763687	0.520369	gi_188521849_gb_ACD59794.1_
0.743073	0.735557	0.764228	0.747619	gi_188521850_gb_ACD59795.1_
0.27032	0.082489	0.263278	0.205362	gi_188521852_gb_ACD59797.1_
0.17581	0.463316	0.128869	0.255998	gi_188521853_gb_ACD59798.1_
0.854084	0.986156	0.49775	0.77933	gi_188521862_gb_ACD59807.1_
0.152387	0.209822	0.109975	0.157395	gi_188521866_gb_ACD59811.1_
0.106786	0.012894	0.145916	0.088532	gi_188521872_gb_ACD59817.1_
0.130903	0.015859	0.121319	0.08936	gi_188521876_gb_ACD59821.1_
0.094319	0.132964	0.085724	0.104336	gi_188521877_gb_ACD59822.1_
0.953113	0.831459	0.924909	0.90316	gi_188521878_gb_ACD59823.1_
0.913568	0.999043	0.821567	0.911393	gi_188521879_gb_ACD59824.1_
0.925117	0.715246	0.892353	0.844239	gi_188521880_gb_ACD59825.1_
0.954566	0.994442	0.949502	0.96617	gi_188521881_gb_ACD59826.1_
0.818021	0.987295	0.785667	0.863661	gi_188521882_gb_ACD59827.1_
0.941144	0.897707	0.893214	0.910688	gi_188521982_gb_ACD59927.1_
0.920853	0.887054	0.881216	0.896374	gi_188521983_gb_ACD59928.1_
0.271505	0.40444	0.315614	0.33052	gi_188521986_gb_ACD59931.1_
0.964532	0.936849	0.944223	0.948535	gi_188521990_gb_ACD59935.1_
0.408058	0.89853	0.518741	0.608443	gi_188521991_gb_ACD59936.1_
0.067358	0.324098	0.151228	0.180895	gi_188521992_gb_ACD59937.1_
0.336038	0.111452	0.413867	0.287119	gi_188521993_gb_ACD59938.1_
0.152775	0.038791	0.223567	0.138378	gi_188521994_gb_ACD59939.1_
0.074883	0.014175	0.10147	0.063509	gi_188521995_gb_ACD59940.1_
0.621284	0.031493	0.607782	0.420186	gi_188521996_gb_ACD59941.1_
0.068881	0.025087	0.115679	0.069882	gi_188521997_gb_ACD59942.1_
0.151228	0.016774	0.219943	0.129315	gi_188521998_gb_ACD59943.1_
0.107647	0.045304	0.226181	0.126377	gi_188521999_gb_ACD59944.1_
0.126198	0.057055	0.159092	0.114115	gi_188522000_gb_ACD59945.1_
0.087145	0.008459	0.08883	0.061478	gi_188522001_gb_ACD59946.1_
0.350919	0.969763	0.080025	0.466902	gi_188522004_gb_ACD59949.1_
0.32213	0.987144	0.119729	0.476334	gi_188522009_gb_ACD59954.1_
0.135404	0.011453	0.197658	0.114838	gi_188522010_gb_ACD59955.1_
0.094833	0.021989	0.153164	0.089995	gi_188522016_gb_ACD59961.1_
0.779542	0.547853	0.736722	0.688039	gi_188522018_gb_ACD59963.1_
0.594114	0.973403	0.507499	0.691672	gi_188522019_gb_ACD59964.1_

gi_188521745_gb_ACD59690.1_	0.169	21	0.123	56	0.136	51	0.1	0.112	N	0.57	SignalP-noTM
gi_188521746_gb_ACD59691.1_	0.145	33	0.125	33	0.159	30	0.093	0.11	N	0.57	SignalP-noTM
gi_188521747_gb_ACD59692.1_	0.109	12	0.095	70	0.118	11	0.073	0.085	N	0.57	SignalP-noTM
gi_188521748_gb_ACD59693.1_	0.186	38	0.133	38	0.151	11	0.097	0.116	N	0.57	SignalP-noTM
gi_188521754_gb_ACD59699.1_	0.201	46	0.162	46	0.311	2	0.119	0.142	N	0.57	SignalP-noTM
gi_188521755_gb_ACD59700.1_	0.105	48	0.101	68	0.126	47	0.086	0.094	N	0.57	SignalP-noTM
gi_188521757_gb_ACD59702.1_	0.132	34	0.118	34	0.195	1	0.111	0.114	N	0.57	SignalP-noTM
gi_188521760_gb_ACD59705.1_	0.346	48	0.189	48	0.194	45	0.098	0.146	N	0.57	SignalP-noTM
gi_188521761_gb_ACD59706.1_	0.51	21	0.692	21	0.97	20	0.932	0.805	Y	0.57	SignalP-noTM
gi_188521762_gb_ACD59707.1_	0.609	20	0.495	20	0.606	1	0.421	0.468	N	0.51	SignalP-TM
gi_188521767_gb_ACD59712.1_	0.143	27	0.1	27	0.106	61	0.065	0.083	N	0.57	SignalP-noTM
gi_188521769_gb_ACD59714.1_	0.17	22	0.157	22	0.238	31	0.152	0.155	N	0.57	SignalP-noTM
gi_188521770_gb_ACD59715.1_	0.154	30	0.142	30	0.262	1	0.129	0.136	N	0.57	SignalP-noTM
gi_188521771_gb_ACD59716.1_	0.105	61	0.099	29	0.125	38	0.079	0.092	N	0.51	SignalP-TM
gi_188521778_gb_ACD59723.1_	0.102	37	0.116	16	0.163	10	0.131	0.123	N	0.57	SignalP-noTM
gi_188521780_gb_ACD59725.1_	0.15	36	0.14	36	0.198	18	0.122	0.132	N	0.57	SignalP-noTM
gi_188521781_gb_ACD59726.1_	0.115	22	0.142	54	0.246	50	0.13	0.136	N	0.57	SignalP-noTM
gi_188521782_gb_ACD59727.1_	0.121	67	0.176	15	0.362	8	0.316	0.228	N	0.51	SignalP-TM
gi_188521786_gb_ACD59731.1_	0.12	45	0.13	11	0.237	3	0.174	0.151	N	0.57	SignalP-noTM
gi_188521789_gb_ACD59734.1_	0.137	51	0.116	51	0.249	1	0.092	0.107	N	0.51	SignalP-TM
gi_188521790_gb_ACD59735.1_	0.12	32	0.11	32	0.152	27	0.097	0.105	N	0.51	SignalP-TM
gi_188521792_gb_ACD59737.1_	0.101	7	0.138	12	0.284	4	0.198	0.167	N	0.57	SignalP-noTM
gi_188521794_gb_ACD59739.1_	0.113	18	0.1	67	0.102	55	0.089	0.095	N	0.57	SignalP-noTM
gi_188521795_gb_ACD59740.1_	0.108	32	0.112	11	0.161	1	0.122	0.117	N	0.57	SignalP-noTM
gi_188521796_gb_ACD59741.1_	0.198	36	0.125	11	0.218	2	0.158	0.138	N	0.51	SignalP-TM
gi_188521797_gb_ACD59742.1_	0.111	26	0.142	11	0.294	2	0.2	0.163	N	0.51	SignalP-TM
gi_188521798_gb_ACD59743.1_	0.44	18	0.29	18	0.573	1	0.267	0.282	N	0.51	SignalP-TM
gi_188521799_gb_ACD59744.1_	0.113	47	0.117	11	0.19	1	0.131	0.124	N	0.57	SignalP-noTM
gi_188521800_gb_ACD59745.1_	0.429	29	0.269	29	0.244	21	0.167	0.221	N	0.57	SignalP-noTM
gi_188521801_gb_ACD59746.1_	0.111	56	0.106	45	0.123	9	0.099	0.103	N	0.57	SignalP-noTM
gi_188521804_gb_ACD59749.1_	0.131	26	0.115	26	0.147	51	0.102	0.109	N	0.57	SignalP-noTM
gi_188521811_gb_ACD59756.1_	0.174	24	0.199	24	0.472	20	0.21	0.204	N	0.57	SignalP-noTM
gi_188521812_gb_ACD59757.1_	0.258	23	0.316	23	0.541	10	0.423	0.356	N	0.51	SignalP-TM
gi_188521813_gb_ACD59758.1_	0.169	33	0.127	33	0.159	32	0.096	0.112	N	0.57	SignalP-noTM
gi_188521815_gb_ACD59760.1_	0.105	35	0.105	12	0.141	6	0.114	0.109	N	0.57	SignalP-noTM
gi_188521816_gb_ACD59761.1_	0.101	25	0.141	11	0.253	4	0.201	0.169	N	0.57	SignalP-noTM
gi_188521817_gb_ACD59762.1_	0.173	29	0.193	29	0.259	27	0.186	0.19	N	0.51	SignalP-TM
gi_188521818_gb_ACD59763.1_	0.161	53	0.204	53	0.432	47	0.151	0.184	N	0.51	SignalP-TM
gi_188521819_gb_ACD59764.1_	0.143	45	0.138	45	0.175	43	0.113	0.129	N	0.51	SignalP-TM
gi_188521822_gb_ACD59767.1_	0.12	62	0.101	15	0.142	12	0.091	0.096	N	0.57	SignalP-noTM
gi_188521824_gb_ACD59769.1_	0.282	52	0.227	52	0.524	38	0.206	0.217	N	0.57	SignalP-noTM
gi_188521827_gb_ACD59772.1_	0.139	20	0.126	40	0.157	38	0.094	0.111	N	0.57	SignalP-noTM
gi_188521828_gb_ACD59773.1_	0.218	65	0.208	48	0.526	44	0.225	0.216	N	0.57	SignalP-noTM
gi_188521829_gb_ACD59774.1_	0.109	29	0.131	11	0.273	1	0.162	0.145	N	0.57	SignalP-noTM
gi_188521835_gb_ACD59780.1_	0.28	30	0.212	30	0.265	3	0.175	0.195	N	0.57	SignalP-noTM
gi_188521836_gb_ACD59781.1_	0.114	30	0.116	37	0.174	36	0.117	0.116	N	0.57	SignalP-noTM
gi_188521837_gb_ACD59782.1_	0.116	33	0.114	33	0.164	29	0.109	0.112	N	0.57	SignalP-noTM
gi_188521838_gb_ACD59783.1_	0.118	21	0.105	64	0.125	50	0.093	0.1	N	0.57	SignalP-noTM
gi_188521840_gb_ACD59785.1_	0.326	34	0.271	34	0.291	33	0.193	0.242	N	0.51	SignalP-TM
gi_188521841_gb_ACD59786.1_	0.131	20	0.115	20	0.148	51	0.1	0.108	N	0.57	SignalP-noTM
gi_188521842_gb_ACD59787.1_	0.184	69	0.134	69	0.103	38	0.09	0.113	N	0.57	SignalP-noTM
gi_188521843_gb_ACD59788.1_	0.127	28	0.12	11	0.184	2	0.144	0.131	N	0.57	SignalP-noTM
gi_188521846_gb_ACD59791.1_	0.191	59	0.171	59	0.245	52	0.093	0.134	N	0.57	SignalP-noTM
gi_188521847_gb_ACD59792.1_	0.116	6	0.106	36	0.12	30	0.096	0.101	N	0.57	SignalP-noTM
gi_188521848_gb_ACD59793.1_	0.29	20	0.18	20	0.148	19	0.113	0.149	N	0.57	SignalP-noTM
gi_188521849_gb_ACD59794.1_	0.158	23	0.363	23	0.967	11	0.864	0.599	Y	0.57	SignalP-noTM
gi_188521850_gb_ACD59795.1_	0.125	40	0.105	65	0.128	55	0.085	0.098	N	0.51	SignalP-TM
gi_188521852_gb_ACD59797.1_	0.144	28	0.19	11	0.505	2	0.369	0.256	N	0.51	SignalP-TM
gi_188521853_gb_ACD59798.1_	0.226	29	0.193	29	0.299	3	0.196	0.194	N	0.57	SignalP-noTM
gi_188521862_gb_ACD59807.1_	0.117	30	0.118	53	0.168	46	0.112	0.115	N	0.57	SignalP-noTM
gi_188521866_gb_ACD59811.1_	0.107	56	0.106	11	0.175	2	0.108	0.107	N	0.57	SignalP-noTM
gi_188521872_gb_ACD59817.1_	0.298	22	0.372	22	0.688	8	0.528	0.445	N	0.57	SignalP-noTM
gi_188521876_gb_ACD59821.1_	0.411	21	0.358	21	0.512	16	0.275	0.319	N	0.57	SignalP-noTM
gi_188521877_gb_ACD59822.1_	0.246	20	0.225	20	0.37	17	0.177	0.202	N	0.57	SignalP-noTM
gi_188521878_gb_ACD59823.1_	0.645	19	0.696	19	0.84	7	0.77	0.731	Y	0.57	SignalP-noTM
gi_188521879_gb_ACD59824.1_	0.107	25	0.128	11	0.214	1	0.158	0.142	N	0.57	SignalP-noTM
gi_188521880_gb_ACD59825.1_	0.853	23	0.911	23	0.984	19	0.963	0.935	Y	0.57	SignalP-noTM
gi_188521881_gb_ACD59826.1_	0.236	40	0.177	23	0.297	12	0.218	0.192	N	0.51	SignalP-TM
gi_188521882_gb_ACD59827.1_	0.13	38	0.11	11	0.148	5	0.129	0.117	N	0.51	SignalP-TM
gi_188521982_gb_ACD59927.1_	0.136	20	0.146	11	0.375	9	0.23	0.185	N	0.57	SignalP-noTM
gi_188521983_gb_ACD59928.1_	0.132	14	0.226	14	0.625	10	0.392	0.304	N	0.57	SignalP-noTM
gi_188521986_gb_ACD59931.1_	0.116	62	0.137	11	0.301	24	0.185	0.159	N	0.57	SignalP-noTM
gi_188521990_gb_ACD59935.1_	0.214	27	0.291	27	0.496	25	0.365	0.326	N	0.57	SignalP-noTM
gi_188521991_gb_ACD59936.1_	0.867	32	0.846	32	0.92	29	0.775	0.812	Y	0.57	SignalP-noTM
gi_188521992_gb_ACD59937.1_	0.137	6	0.129	11	0.227	5	0.179	0.148	N	0.51	SignalP-TM
gi_188521993_gb_ACD59938.1_	0.883	30	0.898	30	0.988	17	0.939	0.917	Y	0.57	SignalP-noTM
gi_188521994_gb_ACD59939.1_	0.216	32	0.348	32	0.959	18	0.771	0.547	N	0.57	SignalP-noTM
gi_188521995_gb_ACD59940.1_	0.166	25	0.138	25	0.173	13	0.113	0.128	N	0.51	SignalP-TM

0.101197	0.09984	0.103958	0.101665	gi_188522021_gb_ACD59966.1_
0.159896	0.925532	0.086669	0.390699	gi_188522022_gb_ACD59967.1_
0.63599	0.533699	0.770653	0.646781	gi_188522026_gb_ACD59971.1_
0.162737	0.199089	0.116603	0.159476	gi_188522028_gb_ACD59973.1_
0.180199	0.045564	0.224088	0.14995	gi_188522029_gb_ACD59974.1_
0.085959	0.087864	0.174078	0.115967	gi_188522030_gb_ACD59975.1_
0.161109	0.598447	0.120999	0.293518	gi_188522031_gb_ACD59976.1_
0.32213	0.07806	0.280496	0.226895	gi_188522032_gb_ACD59977.1_
0.163557	0.154335	0.188314	0.168735	gi_188522033_gb_ACD59978.1_
0.153553	0.324098	0.265612	0.247754	gi_188522034_gb_ACD59979.1_
0.162737	0.091289	0.181087	0.145038	gi_188522035_gb_ACD59980.1_
0.095349	0.059023	0.111155	0.088509	gi_188522036_gb_ACD59981.1_
0.135404	0.1065	0.20538	0.149095	gi_188522037_gb_ACD59982.1_
0.094319	0.053454	0.190156	0.112643	gi_188522038_gb_ACD59983.1_
0.103123	0.510498	0.164379	0.259333	gi_188522039_gb_ACD59984.1_
0.121319	0.077845	0.116603	0.105256	gi_188522041_gb_ACD59986.1_
0.135053	0.045695	0.204403	0.128384	gi_188522042_gb_ACD59987.1_
0.120681	0.160704	0.127862	0.136416	gi_188522043_gb_ACD59988.1_
0.127862	0.071625	0.076775	0.092087	gi_188522044_gb_ACD59989.1_
0.262697	0.211818	0.361929	0.278815	gi_188522045_gb_ACD59990.1_
0.08883	0.059189	0.096129	0.081383	gi_188522046_gb_ACD59991.1_
0.1065	0.109389	0.095609	0.103833	gi_188522047_gb_ACD59992.1_
0.342089	0.917511	0.32213	0.527243	gi_188522048_gb_ACD59993.1_
0.734388	0.732629	0.846836	0.771284	gi_188522049_gb_ACD59994.1_
0.069267	0.128869	0.07385	0.090662	gi_188522050_gb_ACD59995.1_
0.077629	0.047021	0.104238	0.076296	gi_188522051_gb_ACD59996.1_
0.153164	0.139314	0.21738	0.169953	gi_188522053_gb_ACD59998.1_
0.075718	0.02271	0.163967	0.087465	gi_188522057_gb_ACD60002.1_
0.080247	0.046089	0.099302	0.075213	gi_188522059_gb_ACD60004.1_
0.06985	0.00377	0.082489	0.052036	gi_188522060_gb_ACD60005.1_
0.934134	0.839296	0.871804	0.881745	gi_188522062_gb_ACD60007.1_
0.061226	0.017793	0.079365	0.052795	gi_188522063_gb_ACD60008.1_
0.096914	0.084324	0.128196	0.103145	gi_188522064_gb_ACD60009.1_
0.259802	0.10147	0.348191	0.236488	gi_188522065_gb_ACD60010.1_
0.115679	0.063328	0.192943	0.123983	gi_188522066_gb_ACD60011.1_
0.129882	0.070633	0.159092	0.119869	gi_188522069_gb_ACD60014.1_
0.479761	0.185579	0.484255	0.383198	gi_188522070_gb_ACD60015.1_
0.126861	0.137525	0.127527	0.130638	gi_188522071_gb_ACD60016.1_
0.820686	0.192476	0.848772	0.620645	gi_188522097_gb_ACD60042.1_
0.690188	0.020253	0.621284	0.443908	gi_188522098_gb_ACD60043.1_
0.948632	0.99904	0.917738	0.955137	gi_188522111_gb_ACD60056.1_
0.952166	0.993112	0.883088	0.942789	gi_188522112_gb_ACD60057.1_
0.282925	0.015128	0.346151	0.214735	gi_188522113_gb_ACD60058.1_
0.946242	0.981072	0.887355	0.938223	gi_188522114_gb_ACD60059.1_
0.858878	0.92365	0.863539	0.882022	gi_188522115_gb_ACD60060.1_
0.49325	0.730862	0.627615	0.617242	gi_188522116_gb_ACD60061.1_
0.086669	0.066982	0.087145	0.080265	gi_188522117_gb_ACD60062.1_
0.953381	0.897155	0.890903	0.913813	gi_188522118_gb_ACD60063.1_
0.071824	0.533699	0.136815	0.247446	gi_188522119_gb_ACD60064.1_
0.194348	0.046221	0.287819	0.176129	gi_188522120_gb_ACD60065.1_
0.049079	0.005988	0.074883	0.043317	gi_188522121_gb_ACD60066.1_
0.107936	0.003681	0.148552	0.086723	gi_188522123_gb_ACD60068.1_
0.649764	0.863539	0.554532	0.689278	gi_188522124_gb_ACD60069.1_
0.064949	0.003966	0.098767	0.055894	gi_188522128_gb_ACD60073.1_
0.231475	0.024292	0.307252	0.187673	gi_188522129_gb_ACD60074.1_
0.085489	0.056893	0.0985	0.080294	gi_188522130_gb_ACD60075.1_
0.120999	0.082944	0.111749	0.105231	gi_188522131_gb_ACD60076.1_
0.391503	0.027787	0.56193	0.327073	gi_188522132_gb_ACD60077.1_
0.109389	0.040156	0.126529	0.092025	gi_188522133_gb_ACD60078.1_
0.247312	0.03506	0.301535	0.194636	gi_188522134_gb_ACD60079.1_
0.076988	0.387223	0.181979	0.215397	gi_188522135_gb_ACD60080.1_
0.086907	0.694661	0.201009	0.327526	gi_188522136_gb_ACD60081.1_
0.063328	0.109097	0.174078	0.115501	gi_188522137_gb_ACD60082.1_
0.156303	0.237941	0.213325	0.202523	gi_188522138_gb_ACD60083.1_
0.083402	0.48051	0.199567	0.254493	gi_188522139_gb_ACD60084.1_
0.05869	0.024723	0.075091	0.052835	gi_188522140_gb_ACD60085.1_
0.06003	0.843697	0.172359	0.358695	gi_188522141_gb_ACD60086.1_
0.140035	0.03214	0.186032	0.119402	gi_188522142_gb_ACD60087.1_
0.464808	0.093553	0.382252	0.313538	gi_188522143_gb_ACD60088.1_
0.056094	0.194348	0.126198	0.125547	gi_188522144_gb_ACD60089.1_
0.105364	0.223047	0.102018	0.143476	gi_188522145_gb_ACD60090.1_
0.11385	0.053302	0.172787	0.113313	gi_188522146_gb_ACD60091.1_
0.348191	0.236855	0.377306	0.320784	gi_188522147_gb_ACD60092.1_
0.107647	0.474522	0.156699	0.246289	gi_188522148_gb_ACD60093.1_
0.815778	0.991789	0.923861	0.910476	gi_188522149_gb_ACD60094.1_
0.065681	0.00416	0.135404	0.068415	gi_188522150_gb_ACD60095.1_
0.107072	0.005143	0.102018	0.071411	gi_188522152_gb_ACD60097.1_
0.24453	0.767991	0.259802	0.424108	gi_188522153_gb_ACD60098.1_

gi_188521996_gb_ACD59941.1_	0.158	27	0.144	27	0.262	1	0.14	0.142	N	0.57	SignalP-noTM
gi_188521997_gb_ACD59942.1_	0.398	23	0.303	23	0.502	1	0.288	0.296	N	0.57	SignalP-noTM
gi_188521998_gb_ACD59943.1_	0.138	26	0.247	22	0.621	20	0.408	0.322	N	0.57	SignalP-noTM
gi_188521999_gb_ACD59944.1_	0.151	26	0.17	20	0.335	10	0.231	0.199	N	0.57	SignalP-noTM
gi_188522000_gb_ACD59945.1_	0.251	30	0.284	30	0.511	24	0.233	0.265	N	0.51	SignalP-TM
gi_188522001_gb_ACD59946.1_	0.112	26	0.149	11	0.265	1	0.219	0.182	N	0.57	SignalP-noTM
gi_188522004_gb_ACD59949.1_	0.101	49	0.125	49	0.185	19	0.133	0.129	N	0.57	SignalP-noTM
gi_188522009_gb_ACD59954.1_	0.103	20	0.176	11	0.432	2	0.308	0.238	N	0.57	SignalP-noTM
gi_188522010_gb_ACD59955.1_	0.141	24	0.121	24	0.156	8	0.115	0.118	N	0.57	SignalP-noTM
gi_188522016_gb_ACD59961.1_	0.104	38	0.121	52	0.184	40	0.094	0.108	N	0.57	SignalP-noTM
gi_188522018_gb_ACD59963.1_	0.426	47	0.348	47	0.374	44	0.17	0.282	N	0.51	SignalP-TM
gi_188522019_gb_ACD59964.1_	0.138	36	0.112	20	0.159	11	0.101	0.106	N	0.57	SignalP-noTM
gi_188522021_gb_ACD59966.1_	0.13	26	0.148	11	0.334	3	0.229	0.186	N	0.57	SignalP-noTM
gi_188522022_gb_ACD59967.1_	0.16	60	0.124	60	0.238	1	0.107	0.116	N	0.57	SignalP-noTM
gi_188522026_gb_ACD59971.1_	0.109	34	0.123	11	0.228	1	0.145	0.133	N	0.57	SignalP-noTM
gi_188522028_gb_ACD59973.1_	0.11	24	0.132	12	0.244	3	0.168	0.149	N	0.57	SignalP-noTM
gi_188522029_gb_ACD59974.1_	0.121	38	0.111	38	0.118	31	0.092	0.102	N	0.57	SignalP-noTM
gi_188522030_gb_ACD59975.1_	0.195	58	0.222	58	0.433	50	0.17	0.197	N	0.57	SignalP-noTM
gi_188522031_gb_ACD59976.1_	0.569	41	0.329	41	0.331	32	0.143	0.242	N	0.57	SignalP-noTM
gi_188522032_gb_ACD59977.1_	0.216	27	0.148	27	0.144	26	0.088	0.12	N	0.57	SignalP-noTM
gi_188522033_gb_ACD59978.1_	0.159	31	0.16	31	0.234	21	0.14	0.15	N	0.57	SignalP-noTM
gi_188522034_gb_ACD59979.1_	0.125	20	0.143	11	0.287	3	0.222	0.173	N	0.51	SignalP-TM
gi_188522035_gb_ACD59980.1_	0.125	32	0.179	13	0.407	10	0.288	0.23	N	0.57	SignalP-noTM
gi_188522036_gb_ACD59981.1_	0.119	34	0.12	11	0.208	1	0.14	0.129	N	0.57	SignalP-noTM
gi_188522037_gb_ACD59982.1_	0.155	33	0.138	33	0.203	1	0.145	0.14	N	0.51	SignalP-TM
gi_188522038_gb_ACD59983.1_	0.164	27	0.207	11	0.574	1	0.418	0.285	N	0.51	SignalP-TM
gi_188522039_gb_ACD59984.1_	0.199	38	0.118	14	0.197	6	0.142	0.127	N	0.51	SignalP-TM
gi_188522041_gb_ACD59986.1_	0.166	26	0.139	26	0.187	24	0.123	0.133	N	0.51	SignalP-TM
gi_188522042_gb_ACD59987.1_	0.15	44	0.099	70	0.115	5	0.06	0.085	N	0.51	SignalP-TM
gi_188522043_gb_ACD59988.1_	0.382	25	0.591	25	0.95	23	0.909	0.74	Y	0.57	SignalP-noTM
gi_188522044_gb_ACD59989.1_	0.101	22	0.113	54	0.145	50	0.107	0.11	N	0.57	SignalP-noTM
gi_188522045_gb_ACD59990.1_	0.101	3	0.103	65	0.119	42	0.094	0.099	N	0.57	SignalP-noTM
gi_188522046_gb_ACD59991.1_	0.113	23	0.117	13	0.161	10	0.14	0.127	N	0.57	SignalP-noTM
gi_188522047_gb_ACD59992.1_	0.197	41	0.141	41	0.17	39	0.085	0.115	N	0.57	SignalP-noTM
gi_188522048_gb_ACD59993.1_	0.11	47	0.185	11	0.456	4	0.352	0.263	N	0.57	SignalP-noTM
gi_188522049_gb_ACD59994.1_	0.101	53	0.148	11	0.332	2	0.22	0.182	N	0.57	SignalP-noTM
gi_188522050_gb_ACD59995.1_	0.123	25	0.105	41	0.112	52	0.09	0.098	N	0.57	SignalP-noTM
gi_188522051_gb_ACD59996.1_	0.119	50	0.136	11	0.299	3	0.197	0.165	N	0.57	SignalP-noTM
gi_188522053_gb_ACD59998.1_	0.252	56	0.167	56	0.201	2	0.119	0.144	N	0.57	SignalP-noTM
gi_188522057_gb_ACD60002.1_	0.111	27	0.121	11	0.196	5	0.158	0.134	N	0.51	SignalP-TM
gi_188522059_gb_ACD60004.1_	0.125	15	0.123	51	0.168	47	0.102	0.113	N	0.57	SignalP-noTM
gi_188522060_gb_ACD60005.1_	0.132	26	0.225	19	0.48	2	0.423	0.298	N	0.51	SignalP-TM
gi_188522062_gb_ACD60007.1_	0.119	18	0.106	18	0.12	8	0.098	0.102	N	0.57	SignalP-noTM
gi_188522063_gb_ACD60008.1_	0.186	22	0.178	22	0.372	1	0.218	0.193	N	0.51	SignalP-TM
gi_188522064_gb_ACD60009.1_	0.102	50	0.116	16	0.178	8	0.128	0.121	N	0.57	SignalP-noTM
gi_188522065_gb_ACD60010.1_	0.122	31	0.16	26	0.289	3	0.201	0.179	N	0.57	SignalP-noTM
gi_188522066_gb_ACD60011.1_	0.215	29	0.178	29	0.33	28	0.138	0.159	N	0.57	SignalP-noTM
gi_188522069_gb_ACD60014.1_	0.234	33	0.162	33	0.325	18	0.167	0.164	N	0.57	SignalP-noTM
gi_188522070_gb_ACD60015.1_	0.121	35	0.161	14	0.296	6	0.246	0.201	N	0.57	SignalP-noTM
gi_188522071_gb_ACD60016.1_	0.119	23	0.107	23	0.128	21	0.09	0.099	N	0.57	SignalP-noTM
gi_188522097_gb_ACD60042.1_	0.114	32	0.131	11	0.252	1	0.157	0.143	N	0.57	SignalP-noTM
gi_188522098_gb_ACD60043.1_	0.164	37	0.231	17	0.681	16	0.418	0.319	N	0.57	SignalP-noTM
gi_188522111_gb_ACD60056.1_	0.478	20	0.366	20	0.451	1	0.301	0.342	N	0.51	SignalP-TM
gi_188522112_gb_ACD60057.1_	0.142	30	0.188	11	0.533	1	0.335	0.243	N	0.51	SignalP-TM
gi_188522113_gb_ACD60058.1_	0.184	17	0.29	17	0.546	13	0.462	0.354	N	0.51	SignalP-TM
gi_188522114_gb_ACD60059.1_	0.374	54	0.197	54	0.266	1	0.112	0.166	N	0.51	SignalP-TM
gi_188522115_gb_ACD60060.1_	0.17	22	0.255	22	0.52	1	0.38	0.301	N	0.51	SignalP-TM
gi_188522116_gb_ACD60061.1_	0.216	20	0.269	20	0.418	1	0.309	0.284	N	0.51	SignalP-TM
gi_188522117_gb_ACD60062.1_	0.194	67	0.141	67	0.138	1	0.097	0.12	N	0.57	SignalP-noTM
gi_188522118_gb_ACD60063.1_	0.8	20	0.87	20	0.983	10	0.94	0.903	Y	0.57	SignalP-noTM
gi_188522119_gb_ACD60064.1_	0.119	25	0.122	11	0.263	1	0.138	0.128	N	0.51	SignalP-TM
gi_188522120_gb_ACD60065.1_	0.283	20	0.433	20	0.797	8	0.682	0.55	N	0.57	SignalP-noTM
gi_188522121_gb_ACD60066.1_	0.129	39	0.133	39	0.183	40	0.114	0.124	N	0.57	SignalP-noTM
gi_188522123_gb_ACD60068.1_	0.27	39	0.238	39	0.422	27	0.241	0.239	N	0.51	SignalP-TM
gi_188522124_gb_ACD60069.1_	0.135	27	0.126	27	0.282	1	0.121	0.124	N	0.57	SignalP-noTM
gi_188522128_gb_ACD60073.1_	0.121	29	0.129	12	0.28	2	0.166	0.146	N	0.57	SignalP-noTM
gi_188522129_gb_ACD60074.1_	0.112	45	0.111	45	0.135	47	0.096	0.104	N	0.57	SignalP-noTM
gi_188522130_gb_ACD60075.1_	0.167	22	0.139	22	0.181	2	0.124	0.132	N	0.57	SignalP-noTM
gi_188522131_gb_ACD60076.1_	0.194	36	0.13	36	0.138	2	0.091	0.112	N	0.57	SignalP-noTM
gi_188522132_gb_ACD60077.1_	0.136	29	0.138	29	0.206	25	0.152	0.144	N	0.57	SignalP-noTM
gi_188522133_gb_ACD60078.1_	0.134	27	0.108	27	0.122	56	0.082	0.096	N	0.57	SignalP-noTM
gi_188522134_gb_ACD60079.1_	0.141	27	0.12	27	0.126	37	0.094	0.108	N	0.57	SignalP-noTM
gi_188522135_gb_ACD60080.1_	0.161	31	0.157	11	0.368	1	0.239	0.187	N	0.51	SignalP-TM
gi_188522136_gb_ACD60081.1_	0.185	42	0.211	42	0.356	40	0.225	0.216	N	0.51	SignalP-TM
gi_188522137_gb_ACD60082.1_	0.177	25	0.147	11	0.268	1	0.218	0.173	N	0.51	SignalP-TM
gi_188522138_gb_ACD60083.1_	0.12	18	0.127	11	0.252	2	0.153	0.137	N	0.51	SignalP-TM
gi_188522139_gb_ACD60084.1_	0.246	33	0.222	17	0.386	13	0.303	0.252	N	0.51	SignalP-TM
gi_188522140_gb_ACD60085.1_	0.107	26	0.155	11	0.366	1	0.233	0.184	N	0.51	SignalP-TM

0.633207	0.027385	0.622694	0.427762	gi_188522157_gb_ACD60102.1_
0.125209	0.073441	0.140035	0.112895	gi_188522158_gb_ACD60103.1_
0.937556	0.750447	0.890319	0.859441	gi_188522159_gb_ACD60104.1_
0.129882	0.231475	0.152775	0.171377	gi_188522160_gb_ACD60105.1_
0.130222	0.012297	0.137881	0.093467	gi_188522162_gb_ACD60107.1_
0.084556	0.017124	0.121319	0.074333	gi_188522163_gb_ACD60108.1_
0.138596	0.076775	0.172787	0.129386	gi_188522164_gb_ACD60109.1_
0.14517	0.092038	0.178873	0.138694	gi_188522165_gb_ACD60110.1_
0.095091	0.002097	0.125209	0.074132	gi_188522166_gb_ACD60111.1_
0.183772	0.23308	0.255213	0.224022	gi_188522168_gb_ACD60113.1_
0.132274	0.066608	0.138238	0.112373	gi_188522169_gb_ACD60114.1_
0.236313	0.916138	0.311739	0.488063	gi_188522170_gb_ACD60115.1_
0.188314	0.037579	0.281709	0.169201	gi_188522171_gb_ACD60116.1_
0.777992	0.842905	0.798026	0.806308	gi_188522172_gb_ACD60117.1_
0.535192	0.162737	0.521736	0.406555	gi_188522174_gb_ACD60119.1_
0.109097	0.02186	0.153164	0.094707	gi_188522175_gb_ACD60120.1_
0.192476	0.027626	0.268548	0.162883	gi_188522176_gb_ACD60121.1_
0.05836	0.004802	0.084788	0.049317	gi_188522177_gb_ACD60122.1_
0.816678	0.506	0.833966	0.718881	gi_188522180_gb_ACD60125.1_
0.229878	0.381544	0.093299	0.234907	gi_188522183_gb_ACD60128.1_
0.180643	0.301535	0.078493	0.18689	gi_188522184_gb_ACD60129.1_
0.063328	0.035468	0.102018	0.066938	gi_188522186_gb_ACD60131.1_
0.218915	0.115373	0.262697	0.198995	gi_188522191_gb_ACD60136.1_
0.095609	0.002451	0.145916	0.081325	gi_188522192_gb_ACD60137.1_
0.157095	0.085021	0.123901	0.122006	gi_188522193_gb_ACD60138.1_
0.22461	0.571506	0.24122	0.345779	gi_188522195_gb_ACD60140.1_
0.681788	0.984141	0.852959	0.839629	gi_188522196_gb_ACD60141.1_
0.041567	0.182873	0.125868	0.116769	gi_188522197_gb_ACD60142.1_
0.203915	0.207839	0.1603	0.190685	gi_188522198_gb_ACD60143.1_
0.172787	0.508249	0.116294	0.265777	gi_188522199_gb_ACD60144.1_
0.305339	0.080691	0.287819	0.224616	gi_188522200_gb_ACD60145.1_
0.186032	0.567829	0.152775	0.302212	gi_188522201_gb_ACD60146.1_
0.146665	0.189694	0.214333	0.183564	gi_188522202_gb_ACD60147.1_
0.253506	0.033862	0.256355	0.181241	gi_188522203_gb_ACD60148.1_
0.109389	0.108806	0.133658	0.117284	gi_188522207_gb_ACD60152.1_
0.144056	0.032609	0.105081	0.093915	gi_188522208_gb_ACD60153.1_
0.09984	0.84954	0.195761	0.381714	gi_188522209_gb_ACD60154.1_
0.083402	0.048522	0.148552	0.093492	gi_188522210_gb_ACD60155.1_
0.054372	0.032609	0.177118	0.088033	gi_188522217_gb_ACD60162.1_
0.077415	0.094833	0.106215	0.092821	gi_188522218_gb_ACD60163.1_
0.129544	0.044788	0.181532	0.118621	gi_188522219_gb_ACD60164.1_
0.476767	0.914979	0.597726	0.663157	gi_188522221_gb_ACD60166.1_
0.172787	0.11385	0.223567	0.170068	gi_188522222_gb_ACD60167.1_
0.376601	0.702243	0.48051	0.519785	gi_188522224_gb_ACD60169.1_
0.09984	0.062797	0.099034	0.087224	gi_188522225_gb_ACD60170.1_
0.087384	0.00303	0.140035	0.076816	gi_188522226_gb_ACD60171.1_
0.119413	0.073441	0.124881	0.105912	gi_188522231_gb_ACD60176.1_
0.103123	0.026988	0.151228	0.09378	gi_188522233_gb_ACD60178.1_
0.087624	0.002274	0.091788	0.060562	gi_188522234_gb_ACD60179.1_
0.6142	0.260379	0.665967	0.513515	gi_188522235_gb_ACD60180.1_
0.158291	0.124881	0.144798	0.142657	gi_188522236_gb_ACD60181.1_
0.945008	0.909702	0.924282	0.926331	gi_188522237_gb_ACD60182.1_
0.149313	0.109975	0.177994	0.145761	gi_188522238_gb_ACD60183.1_
0.138238	0.074055	0.257501	0.156598	gi_188522239_gb_ACD60184.1_
0.30789	0.665299	0.397235	0.456808	gi_188522242_gb_ACD60187.1_
0.281709	0.988682	0.083402	0.451264	gi_188522245_gb_ACD60190.1_
0.230942	0.887054	0.169806	0.429267	gi_188522248_gb_ACD60193.1_
0.243977	0.50675	0.266198	0.338975	gi_188522252_gb_ACD60197.1_
0.962745	0.999818	0.906447	0.956337	gi_188522263_gb_ACD60208.1_
0.09104	0.023869	0.08883	0.067913	gi_188522264_gb_ACD60209.1_
0.145916	0.026135	0.117222	0.096424	gi_188522265_gb_ACD60210.1_
0.069461	0.037579	0.118784	0.075275	gi_188522267_gb_ACD60212.1_
0.953779	0.995367	0.904132	0.951093	gi_188522271_gb_ACD60216.1_
0.096914	0.033375	0.152387	0.094225	gi_188522276_gb_ACD60221.1_
0.455121	0.40444	0.49625	0.451937	gi_188522284_gb_ACD60229.1_
0.443986	0.044024	0.535938	0.341316	gi_188522287_gb_ACD60232.1_
0.126861	0.053606	0.203915	0.128127	gi_188522288_gb_ACD60233.1_
0.115679	0.041091	0.101197	0.085989	gi_188522289_gb_ACD60234.1_
0.423359	0.564882	0.481259	0.489833	gi_188522290_gb_ACD60235.1_
0.22461	0.97535	0.071824	0.423928	gi_188522291_gb_ACD60236.1_
0.279891	0.777992	0.320821	0.459568	gi_188522292_gb_ACD60237.1_
0.72492	0.565619	0.721316	0.670618	gi_188522294_gb_ACD60239.1_
0.106215	0.067358	0.124553	0.099375	gi_188522295_gb_ACD60240.1_
0.382252	0.351603	0.599168	0.444341	gi_188522296_gb_ACD60241.1_
0.112946	0.314967	0.092038	0.173317	gi_188522299_gb_ACD60244.1_
0.091289	0.185579	0.087624	0.121497	gi_188522300_gb_ACD60245.1_
0.148173	0.082489	0.168962	0.133208	gi_188522304_gb_ACD60249.1_
0.810306	0.746494	0.868413	0.808404	gi_188522305_gb_ACD60250.1_

gi_188522141_gb_ACD60086.1_	0.105	44	0.088	70	0.095	61	0.054	0.075	N	0.51	SignalP-TM
gi_188522142_gb_ACD60087.1_	0.151	31	0.12	31	0.173	30	0.084	0.103	N	0.57	SignalP-noTM
gi_188522143_gb_ACD60088.1_	0.114	57	0.106	44	0.123	32	0.084	0.095	N	0.57	SignalP-noTM
gi_188522144_gb_ACD60089.1_	0.105	28	0.098	69	0.103	62	0.082	0.091	N	0.57	SignalP-noTM
gi_188522145_gb_ACD60090.1_	0.137	55	0.115	55	0.109	27	0.086	0.102	N	0.57	SignalP-noTM
gi_188522146_gb_ACD60091.1_	0.149	20	0.138	37	0.24	6	0.135	0.137	N	0.57	SignalP-noTM
gi_188522147_gb_ACD60092.1_	0.114	63	0.112	53	0.162	47	0.11	0.111	N	0.57	SignalP-noTM
gi_188522148_gb_ACD60093.1_	0.113	31	0.117	37	0.212	28	0.089	0.107	N	0.51	SignalP-TM
gi_188522149_gb_ACD60094.1_	0.393	30	0.446	30	0.648	23	0.324	0.401	N	0.51	SignalP-TM
gi_188522150_gb_ACD60095.1_	0.48	20	0.45	20	0.472	15	0.404	0.428	N	0.57	SignalP-noTM
gi_188522152_gb_ACD60097.1_	0.121	40	0.113	12	0.207	7	0.126	0.119	N	0.57	SignalP-noTM
gi_188522153_gb_ACD60098.1_	0.123	27	0.13	27	0.236	22	0.141	0.135	N	0.57	SignalP-noTM
gi_188522157_gb_ACD60102.1_	0.594	24	0.579	24	0.734	15	0.595	0.585	Y	0.51	SignalP-TM
gi_188522158_gb_ACD60103.1_	0.239	26	0.353	26	0.724	19	0.52	0.415	N	0.51	SignalP-TM
gi_188522159_gb_ACD60104.1_	0.217	27	0.446	17	0.991	9	0.953	0.684	Y	0.57	SignalP-noTM
gi_188522160_gb_ACD60105.1_	0.171	45	0.112	45	0.144	2	0.082	0.098	N	0.57	SignalP-noTM
gi_188522162_gb_ACD60107.1_	0.113	35	0.126	14	0.2	5	0.16	0.142	N	0.57	SignalP-noTM
gi_188522163_gb_ACD60108.1_	0.112	22	0.121	22	0.179	12	0.125	0.122	N	0.57	SignalP-noTM
gi_188522164_gb_ACD60109.1_	0.134	33	0.154	15	0.349	10	0.231	0.19	N	0.57	SignalP-noTM
gi_188522165_gb_ACD60110.1_	0.312	35	0.165	35	0.124	62	0.083	0.134	N	0.51	SignalP-TM
gi_188522166_gb_ACD60111.1_	0.125	46	0.121	46	0.156	37	0.089	0.106	N	0.57	SignalP-noTM
gi_188522168_gb_ACD60113.1_	0.122	19	0.207	11	0.576	1	0.418	0.306	N	0.57	SignalP-noTM
gi_188522169_gb_ACD60114.1_	0.17	43	0.127	43	0.115	40	0.088	0.109	N	0.57	SignalP-noTM
gi_188522170_gb_ACD60115.1_	0.134	54	0.113	54	0.122	36	0.095	0.104	N	0.57	SignalP-noTM
gi_188522171_gb_ACD60116.1_	0.112	50	0.104	50	0.106	50	0.08	0.093	N	0.57	SignalP-noTM
gi_188522172_gb_ACD60117.1_	0.539	30	0.401	30	0.605	11	0.372	0.39	N	0.51	SignalP-TM
gi_188522174_gb_ACD60119.1_	0.149	49	0.167	11	0.373	1	0.271	0.216	N	0.57	SignalP-noTM
gi_188522175_gb_ACD60120.1_	0.15	64	0.12	45	0.198	1	0.106	0.113	N	0.57	SignalP-noTM
gi_188522176_gb_ACD60121.1_	0.138	25	0.121	11	0.208	1	0.145	0.132	N	0.57	SignalP-noTM
gi_188522177_gb_ACD60122.1_	0.148	26	0.132	38	0.216	33	0.105	0.119	N	0.57	SignalP-noTM
gi_188522180_gb_ACD60125.1_	0.172	14	0.208	14	0.493	10	0.251	0.228	N	0.57	SignalP-noTM
gi_188522183_gb_ACD60128.1_	0.175	33	0.148	33	0.218	32	0.113	0.132	N	0.57	SignalP-noTM
gi_188522184_gb_ACD60129.1_	0.175	33	0.147	33	0.215	32	0.11	0.13	N	0.57	SignalP-noTM
gi_188522186_gb_ACD60131.1_	0.117	24	0.171	11	0.397	1	0.287	0.225	N	0.57	SignalP-noTM
gi_188522191_gb_ACD60136.1_	0.108	46	0.111	11	0.16	2	0.126	0.118	N	0.57	SignalP-noTM
gi_188522192_gb_ACD60137.1_	0.12	32	0.159	11	0.402	2	0.263	0.208	N	0.57	SignalP-noTM
gi_188522193_gb_ACD60138.1_	0.12	27	0.128	11	0.273	1	0.151	0.139	N	0.57	SignalP-noTM
gi_188522195_gb_ACD60140.1_	0.142	31	0.161	25	0.269	4	0.2	0.176	N	0.51	SignalP-TM
gi_188522196_gb_ACD60141.1_	0.136	20	0.15	11	0.295	3	0.22	0.183	N	0.57	SignalP-noTM
gi_188522197_gb_ACD60142.1_	0.127	28	0.101	28	0.113	25	0.082	0.092	N	0.57	SignalP-noTM
gi_188522198_gb_ACD60143.1_	0.223	26	0.185	26	0.33	43	0.153	0.17	N	0.57	SignalP-noTM
gi_188522199_gb_ACD60144.1_	0.133	48	0.117	48	0.158	44	0.091	0.105	N	0.57	SignalP-noTM
gi_188522200_gb_ACD60145.1_	0.111	38	0.1	70	0.112	18	0.089	0.095	N	0.57	SignalP-noTM
gi_188522201_gb_ACD60146.1_	0.151	57	0.185	28	0.306	21	0.211	0.195	N	0.51	SignalP-TM
gi_188522202_gb_ACD60147.1_	0.199	35	0.186	35	0.256	30	0.126	0.164	N	0.51	SignalP-TM
gi_188522203_gb_ACD60148.1_	0.134	48	0.107	48	0.123	13	0.097	0.102	N	0.57	SignalP-noTM
gi_188522207_gb_ACD60152.1_	0.14	43	0.122	43	0.194	40	0.095	0.109	N	0.57	SignalP-noTM
gi_188522208_gb_ACD60153.1_	0.141	24	0.13	38	0.3	37	0.115	0.123	N	0.57	SignalP-noTM
gi_188522209_gb_ACD60154.1_	0.12	26	0.109	49	0.129	37	0.099	0.104	N	0.57	SignalP-noTM
gi_188522210_gb_ACD60155.1_	0.154	24	0.211	24	0.432	27	0.239	0.222	N	0.51	SignalP-TM
gi_188522217_gb_ACD60162.1_	0.161	10	0.117	61	0.153	50	0.093	0.108	N	0.51	SignalP-TM
gi_188522218_gb_ACD60163.1_	0.186	19	0.155	40	0.334	35	0.116	0.14	N	0.51	SignalP-TM
gi_188522219_gb_ACD60164.1_	0.106	41	0.11	61	0.144	34	0.095	0.103	N	0.57	SignalP-noTM
gi_188522221_gb_ACD60166.1_	0.107	11	0.149	11	0.337	1	0.182	0.165	N	0.57	SignalP-noTM
gi_188522222_gb_ACD60167.1_	0.185	22	0.143	22	0.204	2	0.119	0.132	N	0.57	SignalP-noTM
gi_188522224_gb_ACD60169.1_	0.206	34	0.34	34	0.674	19	0.498	0.398	N	0.51	SignalP-TM
gi_188522225_gb_ACD60170.1_	0.111	56	0.113	11	0.159	3	0.13	0.121	N	0.57	SignalP-noTM
gi_188522226_gb_ACD60171.1_	0.122	42	0.117	42	0.245	41	0.084	0.101	N	0.57	SignalP-noTM
gi_188522231_gb_ACD60176.1_	0.109	20	0.12	11	0.172	4	0.14	0.129	N	0.57	SignalP-noTM
gi_188522233_gb_ACD60178.1_	0.106	28	0.107	28	0.139	25	0.106	0.106	N	0.57	SignalP-noTM
gi_188522234_gb_ACD60179.1_	0.119	47	0.122	47	0.165	42	0.096	0.11	N	0.57	SignalP-noTM
gi_188522235_gb_ACD60180.1_	0.131	20	0.102	39	0.143	28	0.09	0.096	N	0.57	SignalP-noTM
gi_188522236_gb_ACD60181.1_	0.115	24	0.103	34	0.116	61	0.092	0.098	N	0.57	SignalP-noTM
gi_188522237_gb_ACD60182.1_	0.153	45	0.135	36	0.199	18	0.125	0.13	N	0.57	SignalP-noTM
gi_188522238_gb_ACD60183.1_	0.107	54	0.108	54	0.132	51	0.102	0.105	N	0.57	SignalP-noTM
gi_188522239_gb_ACD60184.1_	0.254	37	0.216	37	0.252	9	0.181	0.203	N	0.51	SignalP-TM
gi_188522242_gb_ACD60187.1_	0.156	42	0.146	42	0.219	19	0.143	0.145	N	0.57	SignalP-noTM
gi_188522245_gb_ACD60190.1_	0.139	26	0.193	26	0.35	22	0.245	0.217	N	0.57	SignalP-noTM
gi_188522248_gb_ACD60193.1_	0.133	26	0.159	11	0.357	1	0.247	0.191	N	0.51	SignalP-TM
gi_528897488_gb_ACD60195.2_	0.115	22	0.145	13	0.273	9	0.21	0.175	N	0.57	SignalP-noTM
gi_188522252_gb_ACD60197.1_	0.121	36	0.128	20	0.204	19	0.138	0.133	N	0.57	SignalP-noTM
gi_188522263_gb_ACD60208.1_	0.12	20	0.107	20	0.155	43	0.093	0.101	N	0.57	SignalP-noTM
gi_188522264_gb_ACD60209.1_	0.12	23	0.104	60	0.115	11	0.09	0.097	N	0.57	SignalP-noTM
gi_188522265_gb_ACD60210.1_	0.105	42	0.107	20	0.141	19	0.113	0.11	N	0.57	SignalP-noTM
gi_188522267_gb_ACD60212.1_	0.106	25	0.103	11	0.141	2	0.104	0.103	N	0.57	SignalP-noTM
gi_188522271_gb_ACD60216.1_	0.359	15	0.504	15	0.798	13	0.711	0.601	Y	0.57	SignalP-noTM
gi_188522276_gb_ACD60221.1_	0.112	26	0.128	11	0.268	1	0.142	0.135	N	0.57	SignalP-noTM
gi_188522284_gb_ACD60229.1_	0.124	20	0.132	25	0.178	34	0.125	0.129	N	0.57	SignalP-noTM

0.1065	0.022183	0.201974	0.110219	gi_188522306_gb_ACD60251.1_
0.094319	0.000394	0.135053	0.076589	gi_188522308_gb_ACD60253.1_
0.134703	0.04229	0.181087	0.11936	gi_188522309_gb_ACD60254.1_
0.050498	0.14629	0.131244	0.109344	gi_188522315_gb_ACD60260.1_
0.109389	0.005427	0.121319	0.078712	gi_188522316_gb_ACD60261.1_
0.112047	0.053302	0.112946	0.092765	gi_188522317_gb_ACD60262.1_
0.129544	0.042533	0.178433	0.116837	gi_188522318_gb_ACD60263.1_
0.357094	0.445468	0.45289	0.418484	gi_188522319_gb_ACD60264.1_
0.113247	0.219943	0.23308	0.188757	gi_188522320_gb_ACD60265.1_
0.740775	0.869438	0.828069	0.812761	gi_528897488_gb_ACD60195.2_
0.163557	0.84954	0.123901	0.378999	gi_188522322_gb_ACD60267.1_
0.127862	0.042656	0.168962	0.11316	gi_188522326_gb_ACD60271.1_
0.136461	0.072225	0.183772	0.130819	gi_188522327_gb_ACD60272.1_
0.94745	0.999063	0.92194	0.956151	gi_188522385_gb_ACD60330.1_
0.123901	0.015217	0.183322	0.10748	gi_188522386_gb_ACD60331.1_
0.290904	0.558235	0.417511	0.422217	gi_188522387_gb_ACD60332.1_
0.917056	0.942622	0.919309	0.926329	gi_188522388_gb_ACD60333.1_
0.850306	0.98722	0.876099	0.904542	gi_188522397_gb_ACD60342.1_
0.239031	0.13193	0.311096	0.227352	gi_188522398_gb_ACD60343.1_
0.900966	0.999186	0.868756	0.922969	gi_188522399_gb_ACD60344.1_
0.125209	0.102569	0.115679	0.114486	gi_188522400_gb_ACD60345.1_
0.89853	0.999775	0.822445	0.906917	gi_188522401_gb_ACD60346.1_
0.100652	0.036509	0.161515	0.099559	gi_188522402_gb_ACD60347.1_
0.940476	0.963385	0.904391	0.936084	gi_188522403_gb_ACD60348.1_
0.138596	0.584676	0.086195	0.269822	gi_188522404_gb_ACD60349.1_
0.169384	0.148552	0.201491	0.173142	gi_188522405_gb_ACD60350.1_
0.330041	0.772239	0.446209	0.516163	gi_188522408_gb_ACD60353.1_
0.132619	0.050642	0.142217	0.108493	gi_188522409_gb_ACD60354.1_
0.271505	0.627615	0.313028	0.404049	gi_188522410_gb_ACD60355.1_
0.871468	0.469289	0.879955	0.740237	gi_188522411_gb_ACD60356.1_
0.913331	0.999613	0.815778	0.909574	gi_188522413_gb_ACD60358.1_
0.920635	0.999753	0.872138	0.930842	gi_188522415_gb_ACD60360.1_
0.08883	0.005641	0.114153	0.069541	gi_188522416_gb_ACD60361.1_
0.120363	0.048661	0.164792	0.111272	gi_188522417_gb_ACD60362.1_
0.073033	0.038236	0.120363	0.077211	gi_188522418_gb_ACD60363.1_
0.130222	0.026988	0.168541	0.108584	gi_188522419_gb_ACD60364.1_
0.093299	0.025014	0.119729	0.079347	gi_188522420_gb_ACD60365.1_
0.777473	0.507499	0.855573	0.713515	gi_188522422_gb_ACD60367.1_
0.894353	0.999336	0.831038	0.908242	gi_188522423_gb_ACD60368.1_
0.259225	0.957589	0.119413	0.445409	gi_188522424_gb_ACD60369.1_
0.129544	0.062094	0.100924	0.097521	gi_188522425_gb_ACD60370.1_
0.178433	0.096914	0.129544	0.134964	gi_188522426_gb_ACD60371.1_
0.098767	0.002697	0.142583	0.081349	gi_188522427_gb_ACD60372.1_
0.061745	0.40444	0.152	0.206062	gi_188522432_gb_ACD60377.1_
0.073645	0.046089	0.093046	0.070927	gi_188522433_gb_ACD60378.1_
0.085021	0.047562	0.105364	0.079316	gi_188522434_gb_ACD60379.1_
0.155119	0.035571	0.233617	0.141436	gi_188522444_gb_ACD60389.1_
0.814874	0.998491	0.877073	0.896813	gi_188522445_gb_ACD60390.1_
0.074261	0.193411	0.109389	0.125687	gi_188522446_gb_ACD60391.1_
0.208829	0.176245	0.157892	0.180989	gi_188522454_gb_ACD60399.1_
0.884933	0.987445	0.826783	0.89972	gi_188522470_gb_ACD60415.1_
0.123251	0.046089	0.169384	0.112908	gi_188522471_gb_ACD60416.1_
0.119098	0.039128	0.135404	0.097877	gi_188522472_gb_ACD60417.1_
0.168962	0.056733	0.202943	0.142879	gi_188522473_gb_ACD60418.1_
0.134703	0.000769	0.208829	0.114767	gi_188522474_gb_ACD60419.1_
0.057055	0.048108	0.128869	0.078011	gi_188522476_gb_ACD60421.1_
0.163557	0.153944	0.145542	0.154348	gi_188522477_gb_ACD60422.1_
0.940307	0.999356	0.849923	0.929862	gi_188522478_gb_ACD60423.1_
0.115986	0.110563	0.087145	0.104565	gi_188522481_gb_ACD60426.1_
0.115679	0.002079	0.173217	0.096992	gi_188522482_gb_ACD60427.1_
0.125538	0.041686	0.11847	0.095231	gi_188522487_gb_ACD60432.1_
0.189233	0.279891	0.09984	0.189655	gi_188522489_gb_ACD60434.1_
0.140035	0.248431	0.218403	0.20229	gi_188522497_gb_ACD60442.1_
0.236313	0.559714	0.345473	0.3805	gi_188522498_gb_ACD60443.1_
0.124881	0.068306	0.176681	0.123289	gi_188522499_gb_ACD60444.1_
0.087864	0.055935	0.124553	0.089451	gi_188522500_gb_ACD60445.1_
0.189694	0.124881	0.1603	0.158292	gi_188522501_gb_ACD60446.1_
0.116912	0.007097	0.120045	0.081351	gi_188522502_gb_ACD60447.1_
0.177555	0.059861	0.197658	0.145025	gi_188522503_gb_ACD60448.1_
0.223047	0.250678	0.250678	0.241468	gi_188522504_gb_ACD60449.1_
0.856682	0.959379	0.859965	0.892009	gi_188522507_gb_ACD60452.1_
0.270912	0.065131	0.342089	0.226044	gi_188522508_gb_ACD60453.1_
0.157095	0.091788	0.122604	0.123829	gi_188522509_gb_ACD60454.1_
0.224088	0.056893	0.269729	0.18357	gi_188522513_gb_ACD60458.1_
0.096914	0.052401	0.127862	0.092392	gi_188522514_gb_ACD60459.1_
0.843301	0.919753	0.889141	0.884065	gi_528897491_gb_ACD60463.2_
0.109975	0.08181	0.088588	0.093458	gi_188522519_gb_ACD60464.1_
0.223047	0.961764	0.103123	0.429311	gi_188522520_gb_ACD60465.1_

gi_188522287_gb_ACD60232.1_	0.223	49	0.26	12	0.732	2	0.669	0.452	N	0.57	SignalP-noTM
gi_188522288_gb_ACD60233.1_	0.128	22	0.144	22	0.207	19	0.167	0.155	N	0.57	SignalP-noTM
gi_188522289_gb_ACD60234.1_	0.144	34	0.14	12	0.274	1	0.191	0.164	N	0.57	SignalP-noTM
gi_188522290_gb_ACD60235.1_	0.11	24	0.098	40	0.105	39	0.073	0.086	N	0.57	SignalP-noTM
gi_188522291_gb_ACD60236.1_	0.123	30	0.108	30	0.118	1	0.084	0.097	N	0.57	SignalP-noTM
gi_188522292_gb_ACD60237.1_	0.156	42	0.146	42	0.234	19	0.152	0.149	N	0.57	SignalP-noTM
gi_188522294_gb_ACD60239.1_	0.832	39	0.874	39	0.951	29	0.672	0.779	Y	0.57	SignalP-noTM
gi_188522295_gb_ACD60240.1_	0.143	29	0.139	15	0.241	3	0.152	0.144	N	0.51	SignalP-TM
gi_188522296_gb_ACD60241.1_	0.136	30	0.17	21	0.418	15	0.285	0.224	N	0.57	SignalP-noTM
gi_188522299_gb_ACD60244.1_	0.108	21	0.101	70	0.111	70	0.083	0.093	N	0.57	SignalP-noTM
gi_188522300_gb_ACD60245.1_	0.113	25	0.127	55	0.21	50	0.098	0.113	N	0.57	SignalP-noTM
gi_188522304_gb_ACD60249.1_	0.11	52	0.104	58	0.165	48	0.083	0.096	N	0.51	SignalP-TM
gi_188522305_gb_ACD60250.1_	0.505	20	0.415	20	0.589	16	0.385	0.401	N	0.57	SignalP-noTM
gi_188522306_gb_ACD60251.1_	0.153	37	0.244	11	0.723	1	0.61	0.379	N	0.51	SignalP-TM
gi_188522308_gb_ACD60253.1_	0.127	39	0.104	39	0.103	55	0.078	0.092	N	0.57	SignalP-noTM
gi_188522309_gb_ACD60254.1_	0.333	29	0.25	29	0.401	21	0.212	0.232	N	0.57	SignalP-noTM
gi_188522315_gb_ACD60260.1_	0.128	32	0.112	51	0.139	48	0.094	0.104	N	0.57	SignalP-noTM
gi_188522316_gb_ACD60261.1_	0.114	27	0.108	11	0.165	1	0.113	0.11	N	0.57	SignalP-noTM
gi_188522317_gb_ACD60262.1_	0.244	29	0.15	29	0.171	38	0.087	0.121	N	0.57	SignalP-noTM
gi_188522318_gb_ACD60263.1_	0.11	30	0.11	53	0.141	1	0.106	0.108	N	0.57	SignalP-noTM
gi_188522319_gb_ACD60264.1_	0.795	19	0.778	19	0.928	15	0.785	0.781	Y	0.57	SignalP-noTM
gi_188522320_gb_ACD60265.1_	0.217	37	0.154	37	0.152	32	0.104	0.136	N	0.51	SignalP-TM
gi_188522322_gb_ACD60267.1_	0.144	23	0.123	52	0.138	41	0.1	0.112	N	0.57	SignalP-noTM
gi_188522326_gb_ACD60271.1_	0.11	51	0.132	12	0.258	4	0.176	0.153	N	0.57	SignalP-noTM
gi_188522327_gb_ACD60272.1_	0.11	70	0.119	34	0.189	26	0.098	0.109	N	0.57	SignalP-noTM
gi_188522385_gb_ACD60330.1_	0.115	42	0.101	42	0.109	39	0.076	0.089	N	0.57	SignalP-noTM
gi_188522386_gb_ACD60331.1_	0.178	19	0.117	19	0.169	2	0.099	0.108	N	0.57	SignalP-noTM
gi_188522387_gb_ACD60332.1_	0.117	56	0.127	11	0.227	2	0.169	0.147	N	0.57	SignalP-noTM
gi_188522388_gb_ACD60333.1_	0.132	51	0.115	51	0.131	23	0.092	0.104	N	0.57	SignalP-noTM
gi_188522397_gb_ACD60342.1_	0.149	55	0.14	11	0.265	4	0.209	0.173	N	0.57	SignalP-noTM
gi_188522398_gb_ACD60343.1_	0.11	33	0.12	33	0.189	2	0.122	0.121	N	0.57	SignalP-noTM
gi_188522399_gb_ACD60344.1_	0.476	34	0.484	34	0.977	17	0.783	0.624	Y	0.57	SignalP-noTM
gi_188522400_gb_ACD60345.1_	0.104	33	0.119	33	0.186	2	0.123	0.121	N	0.57	SignalP-noTM
gi_188522401_gb_ACD60346.1_	0.566	21	0.447	21	0.608	8	0.399	0.425	N	0.57	SignalP-noTM
gi_188522402_gb_ACD60347.1_	0.152	46	0.123	46	0.134	9	0.092	0.108	N	0.57	SignalP-noTM
gi_188522403_gb_ACD60348.1_	0.154	46	0.118	46	0.125	1	0.093	0.106	N	0.57	SignalP-noTM
gi_188522404_gb_ACD60349.1_	0.15	39	0.247	18	0.578	1	0.434	0.335	N	0.57	SignalP-noTM
gi_188522405_gb_ACD60350.1_	0.218	25	0.184	25	0.408	1	0.193	0.188	N	0.57	SignalP-noTM
gi_188522408_gb_ACD60353.1_	0.103	26	0.117	20	0.177	18	0.14	0.128	N	0.57	SignalP-noTM
gi_188522409_gb_ACD60354.1_	0.12	53	0.117	31	0.161	16	0.116	0.117	N	0.57	SignalP-noTM
gi_188522410_gb_ACD60355.1_	0.156	42	0.146	42	0.219	19	0.143	0.145	N	0.57	SignalP-noTM
gi_188522411_gb_ACD60356.1_	0.12	27	0.144	11	0.261	25	0.22	0.179	N	0.57	SignalP-noTM
gi_188522413_gb_ACD60358.1_	0.104	10	0.131	18	0.222	9	0.146	0.138	N	0.57	SignalP-noTM
gi_188522415_gb_ACD60360.1_	0.44	24	0.644	24	0.963	14	0.921	0.774	Y	0.57	SignalP-noTM
gi_188522416_gb_ACD60361.1_	0.378	24	0.456	24	0.763	20	0.511	0.482	N	0.57	SignalP-noTM
gi_188522417_gb_ACD60362.1_	0.157	43	0.134	43	0.169	23	0.109	0.122	N	0.57	SignalP-noTM
gi_188522418_gb_ACD60363.1_	0.227	32	0.219	32	0.384	1	0.234	0.226	N	0.57	SignalP-noTM
gi_188522419_gb_ACD60364.1_	0.13	40	0.115	18	0.171	8	0.125	0.119	N	0.51	SignalP-TM
gi_188522420_gb_ACD60365.1_	0.192	41	0.27	41	0.55	40	0.263	0.267	N	0.57	SignalP-noTM
gi_188522422_gb_ACD60367.1_	0.126	12	0.121	35	0.179	24	0.107	0.115	N	0.57	SignalP-noTM
gi_188522423_gb_ACD60368.1_	0.125	10	0.106	39	0.123	42	0.085	0.096	N	0.57	SignalP-noTM
gi_188522424_gb_ACD60369.1_	0.143	26	0.17	11	0.506	1	0.268	0.216	N	0.57	SignalP-noTM
gi_188522425_gb_ACD60370.1_	0.115	37	0.113	37	0.142	11	0.111	0.112	N	0.57	SignalP-noTM
gi_188522426_gb_ACD60371.1_	0.179	46	0.202	46	0.395	35	0.14	0.173	N	0.57	SignalP-noTM
gi_188522427_gb_ACD60372.1_	0.386	21	0.379	21	0.615	1	0.434	0.404	N	0.57	SignalP-noTM
gi_188522432_gb_ACD60377.1_	0.209	35	0.128	35	0.123	13	0.082	0.111	N	0.51	SignalP-TM
gi_188522433_gb_ACD60378.1_	0.122	33	0.145	18	0.32	16	0.189	0.166	N	0.57	SignalP-noTM
gi_188522434_gb_ACD60379.1_	0.113	50	0.106	70	0.12	69	0.085	0.096	N	0.57	SignalP-noTM
gi_188522444_gb_ACD60389.1_	0.178	27	0.187	27	0.399	26	0.154	0.171	N	0.57	SignalP-noTM
gi_188522445_gb_ACD60390.1_	0.12	25	0.167	12	0.411	1	0.264	0.213	N	0.57	SignalP-noTM
gi_188522446_gb_ACD60391.1_	0.11	41	0.2	11	0.494	3	0.401	0.294	N	0.57	SignalP-noTM
gi_188522454_gb_ACD60399.1_	0.107	54	0.194	47	0.523	40	0.177	0.186	N	0.57	SignalP-noTM
gi_188522470_gb_ACD60415.1_	0.139	15	0.195	15	0.55	1	0.301	0.245	N	0.57	SignalP-noTM
gi_188522471_gb_ACD60416.1_	0.114	53	0.103	53	0.125	13	0.082	0.093	N	0.57	SignalP-noTM
gi_188522472_gb_ACD60417.1_	0.263	40	0.197	40	0.233	39	0.107	0.155	N	0.57	SignalP-noTM
gi_188522473_gb_ACD60418.1_	0.114	50	0.106	61	0.12	52	0.075	0.091	N	0.57	SignalP-noTM
gi_188522474_gb_ACD60419.1_	0.157	20	0.128	20	0.148	1	0.108	0.119	N	0.57	SignalP-noTM
gi_188522476_gb_ACD60421.1_	0.211	26	0.308	21	0.694	13	0.577	0.408	N	0.51	SignalP-TM
gi_188522477_gb_ACD60422.1_	0.128	29	0.123	29	0.141	26	0.098	0.111	N	0.57	SignalP-noTM
gi_188522478_gb_ACD60423.1_	0.117	69	0.12	47	0.177	42	0.099	0.11	N	0.57	SignalP-noTM
gi_188522481_gb_ACD60426.1_	0.117	27	0.168	17	0.331	16	0.241	0.195	N	0.51	SignalP-TM
gi_188522482_gb_ACD60427.1_	0.199	38	0.138	38	0.244	1	0.128	0.134	N	0.57	SignalP-noTM
gi_188522487_gb_ACD60432.1_	0.269	43	0.206	43	0.365	41	0.123	0.167	N	0.57	SignalP-noTM
gi_188522489_gb_ACD60434.1_	0.148	24	0.164	11	0.379	2	0.279	0.218	N	0.57	SignalP-noTM
gi_188522497_gb_ACD60442.1_	0.281	24	0.174	24	0.144	23	0.098	0.146	N	0.51	SignalP-TM
gi_188522498_gb_ACD60443.1_	0.123	59	0.108	59	0.122	54	0.088	0.099	N	0.57	SignalP-noTM
gi_188522499_gb_ACD60444.1_	0.184	24	0.154	24	0.221	20	0.129	0.142	N	0.57	SignalP-noTM
gi_188522500_gb_ACD60445.1_	0.227	37	0.306	37	0.561	26	0.255	0.282	N	0.57	SignalP-noTM

0.324098	0.318863	0.45289	0.365284	gi_188522522_gb_ACD60467.1_
0.082489	0.029627	0.093553	0.068556	gi_188522523_gb_ACD60468.1_
0.198134	0.732041	0.245085	0.391753	gi_188522524_gb_ACD60469.1_
0.392218	0.491751	0.583948	0.489306	gi_188522525_gb_ACD60470.1_
0.10736	0.045045	0.132964	0.095123	gi_188522526_gb_ACD60471.1_
0.393649	0.082489	0.476018	0.317385	gi_188522527_gb_ACD60472.1_
0.208334	0.02836	0.272693	0.169796	gi_188522528_gb_ACD60473.1_
0.155513	0.072024	0.17581	0.134449	gi_188522529_gb_ACD60474.1_
0.256355	0.617039	0.309171	0.394188	gi_188522530_gb_ACD60475.1_
0.227233	0.344795	0.41314	0.328389	gi_188522531_gb_ACD60476.1_
0.194818	0.045304	0.225657	0.15526	gi_188522533_gb_ACD60478.1_
0.227233	0.024507	0.174942	0.142227	gi_188522535_gb_ACD60480.1_
0.20587	0.033862	0.285978	0.175237	gi_188522537_gb_ACD60482.1_
0.164792	0.084556	0.21738	0.155576	gi_188522539_gb_ACD60484.1_
0.589766	0.568565	0.700357	0.619563	gi_188522543_gb_ACD60488.1_
0.424824	0.929955	0.599168	0.651316	gi_188522545_gb_ACD60490.1_
0.20538	0.047834	0.183322	0.145512	gi_188522549_gb_ACD60494.1_
0.143318	0.345473	0.201491	0.230094	gi_188522550_gb_ACD60495.1_
0.703496	0.888251	0.823319	0.805022	gi_188522551_gb_ACD60496.1_
0.117845	0.459588	0.099571	0.225668	gi_188522558_gb_ACD60503.1_
0.071226	0.006909	0.097969	0.058701	gi_188522559_gb_ACD60504.1_
0.070045	0.000195	0.118157	0.062799	gi_188522560_gb_ACD60505.1_
0.609926	0.122604	0.651128	0.461219	gi_188522575_gb_ACD60520.1_
0.074675	0.5015	0.189233	0.255136	gi_188522578_gb_ACD60523.1_
0.076775	0.175375	0.13717	0.129773	gi_188522579_gb_ACD60524.1_
0.829346	0.229878	0.575176	0.5448	gi_188522580_gb_ACD60525.1_
0.111452	0.296504	0.215853	0.207936	gi_188522582_gb_ACD60527.1_
0.119098	0.050498	0.141851	0.103816	gi_188522583_gb_ACD60528.1_
0.125209	0.043898	0.132274	0.10046	gi_188522584_gb_ACD60529.1_
0.233617	0.35503	0.281102	0.289916	gi_188522588_gb_ACD60533.1_
0.063864	0.031038	0.10736	0.067421	gi_188522591_gb_ACD60536.1_
0.333366	0.030149	0.349554	0.23769	gi_188522592_gb_ACD60537.1_
0.082716	0.036934	0.134005	0.084552	gi_188522593_gb_ACD60538.1_
0.953647	0.988132	0.899619	0.947133	gi_188522595_gb_ACD60540.1_
0.855573	0.999761	0.700357	0.851897	gi_188522596_gb_ACD60541.1_
0.908711	0.987445	0.844487	0.913548	gi_188522597_gb_ACD60542.1_
0.247871	0.78968	0.132274	0.389942	gi_188522598_gb_ACD60543.1_
0.061745	0.040738	0.087145	0.063209	gi_188522599_gb_ACD60544.1_
0.93946	0.965142	0.896321	0.933641	gi_188522600_gb_ACD60545.1_
0.07385	0.01904	0.171079	0.08799	gi_188522601_gb_ACD60546.1_
0.528469	0.850306	0.441026	0.6066	gi_188522602_gb_ACD60547.1_
0.117845	0.068498	0.200047	0.128797	gi_188522603_gb_ACD60548.1_
0.276878	0.0079	0.449918	0.244899	gi_188522604_gb_ACD60549.1_
0.094063	0.087624	0.125538	0.102408	gi_188522605_gb_ACD60550.1_
0.146665	0.079147	0.170654	0.132155	gi_188522606_gb_ACD60551.1_
0.066608	0.320168	0.093046	0.159941	gi_188522611_gb_ACD60556.1_
0.492501	0.533699	0.762059	0.596086	gi_188522615_gb_ACD60560.1_
0.211818	0.054837	0.245085	0.17058	gi_188522622_gb_ACD60567.1_
0.955212	0.998237	0.88615	0.946533	gi_188522632_gb_ACD60577.1_
0.923225	0.999945	0.869438	0.930869	gi_188522636_gb_ACD60581.1_
0.902296	0.933949	0.828069	0.888105	gi_188522637_gb_ACD60582.1_
0.802342	0.930733	0.75878	0.830618	gi_188522638_gb_ACD60583.1_
0.9398	0.999845	0.872138	0.937261	gi_188522639_gb_ACD60584.1_
0.168962	0.007225	0.229347	0.135178	gi_188522642_gb_ACD60587.1_
0.513497	0.599168	0.69211	0.601592	gi_188522644_gb_ACD60589.1_
0.140759	0.003095	0.188773	0.110876	gi_188522645_gb_ACD60590.1_
0.0985	0.227761	0.217891	0.181384	gi_188522646_gb_ACD60591.1_
0.140759	0.035674	0.169806	0.115413	gi_188522647_gb_ACD60592.1_
0.230942	0.534445	0.115373	0.293587	gi_188522648_gb_ACD60593.1_
0.334701	0.807057	0.184673	0.442144	gi_188522651_gb_ACD60596.1_
0.246197	0.353658	0.265612	0.288489	gi_188522656_gb_ACD60601.1_
0.837671	0.570772	0.747061	0.718501	gi_188522659_gb_ACD60604.1_
0.251807	0.944852	0.083631	0.426763	gi_188522660_gb_ACD60605.1_
0.152	0.427025	0.214333	0.264453	gi_188522662_gb_ACD60607.1_
0.805652	0.489502	0.86807	0.721075	gi_188522664_gb_ACD60609.1_
0.945782	0.992861	0.883706	0.940783	gi_188522670_gb_ACD60615.1_
0.902824	0.98652	0.782109	0.890484	gi_188522671_gb_ACD60616.1_
0.151228	0.028195	0.212822	0.130748	gi_188522672_gb_ACD60617.1_
0.115986	0.078276	0.209325	0.134529	gi_188522673_gb_ACD60618.1_
0.139674	0.09984	0.115986	0.1185	gi_188522674_gb_ACD60619.1_
0.186032	0.101197	0.130222	0.13915	gi_188522675_gb_ACD60620.1_
0.406609	0.49325	0.520988	0.473616	gi_188522676_gb_ACD60621.1_
0.127527	0.031676	0.177118	0.112107	gi_188522677_gb_ACD60622.1_
0.141851	0.074675	0.193879	0.136802	gi_188522678_gb_ACD60623.1_
0.138596	0.228818	0.220458	0.195957	gi_188522679_gb_ACD60624.1_
0.174078	0.042656	0.239031	0.151922	gi_188522680_gb_ACD60625.1_
0.138955	0.045957	0.139314	0.108075	gi_188522681_gb_ACD60626.1_
0.93963	0.991789	0.840506	0.923975	gi_188522684_gb_ACD60629.1_

gi_188522501_gb_ACD60446.1_	0.294	23	0.259	23	0.424	1	0.252	0.256	N	0.51	SignalP-TM
gi_188522502_gb_ACD60447.1_	0.103	44	0.125	30	0.21	26	0.148	0.136	N	0.57	SignalP-noTM
gi_188522503_gb_ACD60448.1_	0.245	35	0.242	35	0.353	34	0.187	0.222	N	0.51	SignalP-TM
gi_188522504_gb_ACD60449.1_	0.186	36	0.19	36	0.343	13	0.217	0.2	N	0.51	SignalP-TM
gi_188522507_gb_ACD60452.1_	0.423	22	0.578	22	0.91	19	0.754	0.661	Y	0.57	SignalP-noTM
gi_188522508_gb_ACD60453.1_	0.114	37	0.123	26	0.182	34	0.128	0.125	N	0.57	SignalP-noTM
gi_188522509_gb_ACD60454.1_	0.117	57	0.201	11	0.526	4	0.404	0.297	N	0.57	SignalP-noTM
gi_188522513_gb_ACD60458.1_	0.118	19	0.104	70	0.12	31	0.085	0.095	N	0.57	SignalP-noTM
gi_188522514_gb_ACD60459.1_	0.137	30	0.146	14	0.241	1	0.211	0.177	N	0.57	SignalP-noTM
gi_528897491_gb_ACD60463.2_	0.169	49	0.143	49	0.195	12	0.13	0.137	N	0.57	SignalP-noTM
gi_188522519_gb_ACD60464.1_	0.115	22	0.144	22	0.268	11	0.186	0.163	N	0.57	SignalP-noTM
gi_188522520_gb_ACD60465.1_	0.136	30	0.124	30	0.238	29	0.092	0.109	N	0.57	SignalP-noTM
gi_188522522_gb_ACD60467.1_	0.115	50	0.116	50	0.212	1	0.114	0.115	N	0.57	SignalP-noTM
gi_188522523_gb_ACD60468.1_	0.139	43	0.14	11	0.268	2	0.199	0.168	N	0.57	SignalP-noTM
gi_188522524_gb_ACD60469.1_	0.105	32	0.155	13	0.325	4	0.249	0.199	N	0.57	SignalP-noTM
gi_188522525_gb_ACD60470.1_	0.11	46	0.136	13	0.25	7	0.187	0.16	N	0.57	SignalP-noTM
gi_188522526_gb_ACD60471.1_	0.125	19	0.207	14	0.42	12	0.343	0.271	N	0.57	SignalP-noTM
gi_188522527_gb_ACD60472.1_	0.32	29	0.482	29	0.928	26	0.573	0.525	N	0.57	SignalP-noTM
gi_188522528_gb_ACD60473.1_	0.197	19	0.118	19	0.123	1	0.082	0.101	N	0.57	SignalP-noTM
gi_188522529_gb_ACD60474.1_	0.11	53	0.128	11	0.187	8	0.171	0.148	N	0.57	SignalP-noTM
gi_188522530_gb_ACD60475.1_	0.172	29	0.236	29	0.536	2	0.346	0.288	N	0.57	SignalP-noTM
gi_188522531_gb_ACD60476.1_	0.154	42	0.144	42	0.21	19	0.138	0.141	N	0.57	SignalP-noTM
gi_188522533_gb_ACD60478.1_	0.701	59	0.329	59	0.229	49	0.11	0.226	N	0.57	SignalP-noTM
gi_188522535_gb_ACD60480.1_	0.116	18	0.167	37	0.376	32	0.198	0.181	N	0.57	SignalP-noTM
gi_188522537_gb_ACD60482.1_	0.126	43	0.139	43	0.19	42	0.124	0.133	N	0.51	SignalP-TM
gi_188522539_gb_ACD60484.1_	0.111	55	0.145	12	0.268	7	0.215	0.178	N	0.57	SignalP-noTM
gi_188522543_gb_ACD60488.1_	0.308	10	0.176	21	0.238	9	0.112	0.146	N	0.57	SignalP-noTM
gi_188522545_gb_ACD60490.1_	0.11	36	0.144	11	0.292	3	0.21	0.175	N	0.57	SignalP-noTM
gi_188522549_gb_ACD60494.1_	0.367	37	0.229	37	0.236	36	0.106	0.171	N	0.57	SignalP-noTM
gi_188522550_gb_ACD60495.1_	0.137	34	0.095	66	0.102	59	0.062	0.083	N	0.51	SignalP-TM
gi_188522551_gb_ACD60496.1_	0.111	9	0.103	70	0.119	39	0.085	0.095	N	0.57	SignalP-noTM
gi_188522558_gb_ACD60503.1_	0.292	29	0.237	29	0.334	5	0.235	0.236	N	0.51	SignalP-TM
gi_188522559_gb_ACD60504.1_	0.155	38	0.232	38	0.487	30	0.22	0.226	N	0.57	SignalP-noTM
gi_188522560_gb_ACD60505.1_	0.121	24	0.102	65	0.111	53	0.083	0.093	N	0.57	SignalP-noTM
gi_188522575_gb_ACD60520.1_	0.113	9	0.135	36	0.206	29	0.146	0.14	N	0.57	SignalP-noTM
gi_188522578_gb_ACD60523.1_	0.108	27	0.099	11	0.143	2	0.097	0.098	N	0.51	SignalP-TM
gi_188522579_gb_ACD60524.1_	0.121	36	0.102	17	0.126	9	0.093	0.099	N	0.51	SignalP-TM
gi_188522580_gb_ACD60525.1_	0.1	50	0.116	48	0.171	43	0.116	0.116	N	0.57	SignalP-noTM
gi_188522582_gb_ACD60527.1_	0.139	52	0.113	41	0.216	38	0.11	0.112	N	0.51	SignalP-TM
gi_188522583_gb_ACD60528.1_	0.127	41	0.15	28	0.267	20	0.185	0.167	N	0.57	SignalP-noTM
gi_188522584_gb_ACD60529.1_	0.127	32	0.123	21	0.183	38	0.117	0.12	N	0.57	SignalP-noTM
gi_188522588_gb_ACD60533.1_	0.169	23	0.192	23	0.418	35	0.243	0.216	N	0.57	SignalP-noTM
gi_188522591_gb_ACD60536.1_	0.109	21	0.143	11	0.26	1	0.198	0.169	N	0.57	SignalP-noTM
gi_188522592_gb_ACD60537.1_	0.233	18	0.194	18	0.431	1	0.194	0.194	N	0.57	SignalP-noTM
gi_188522593_gb_ACD60538.1_	0.174	20	0.173	20	0.289	18	0.163	0.168	N	0.57	SignalP-noTM
gi_188522595_gb_ACD60540.1_	0.819	25	0.841	25	0.909	20	0.843	0.842	Y	0.57	SignalP-noTM
gi_188522596_gb_ACD60541.1_	0.116	22	0.127	11	0.215	1	0.159	0.142	N	0.57	SignalP-noTM
gi_188522597_gb_ACD60542.1_	0.414	32	0.631	32	0.998	22	0.962	0.786	Y	0.57	SignalP-noTM
gi_188522598_gb_ACD60543.1_	0.135	44	0.158	44	0.294	4	0.153	0.155	N	0.57	SignalP-noTM
gi_188522599_gb_ACD60544.1_	0.101	33	0.102	62	0.126	5	0.086	0.094	N	0.57	SignalP-noTM
gi_188522600_gb_ACD60545.1_	0.136	23	0.335	23	0.934	2	0.87	0.586	Y	0.57	SignalP-noTM
gi_188522601_gb_ACD60546.1_	0.118	67	0.145	11	0.31	1	0.207	0.168	N	0.51	SignalP-TM
gi_188522602_gb_ACD60547.1_	0.125	56	0.127	12	0.19	10	0.158	0.141	N	0.57	SignalP-noTM
gi_188522603_gb_ACD60548.1_	0.238	28	0.191	28	0.443	2	0.204	0.196	N	0.51	SignalP-TM
gi_188522604_gb_ACD60549.1_	0.136	18	0.155	18	0.259	1	0.173	0.164	N	0.57	SignalP-noTM
gi_188522605_gb_ACD60550.1_	0.178	65	0.129	65	0.113	4	0.084	0.108	N	0.57	SignalP-noTM
gi_188522606_gb_ACD60551.1_	0.453	20	0.341	20	0.388	16	0.226	0.287	N	0.57	SignalP-noTM
gi_188522611_gb_ACD60556.1_	0.1	49	0.142	11	0.286	1	0.196	0.167	N	0.57	SignalP-noTM
gi_188522615_gb_ACD60560.1_	0.185	28	0.133	28	0.113	1	0.094	0.115	N	0.57	SignalP-noTM
gi_188522622_gb_ACD60567.1_	0.219	28	0.146	28	0.157	1	0.106	0.127	N	0.57	SignalP-noTM
gi_188522632_gb_ACD60577.1_	0.541	15	0.611	15	0.83	14	0.695	0.65	Y	0.57	SignalP-noTM
gi_188522636_gb_ACD60581.1_	0.869	22	0.916	22	0.984	10	0.957	0.935	Y	0.57	SignalP-noTM
gi_188522637_gb_ACD60582.1_	0.341	13	0.263	13	0.318	9	0.202	0.234	N	0.57	SignalP-noTM
gi_188522638_gb_ACD60583.1_	0.269	31	0.409	29	0.764	25	0.538	0.457	N	0.51	SignalP-TM
gi_188522639_gb_ACD60584.1_	0.108	30	0.132	11	0.25	2	0.17	0.15	N	0.57	SignalP-noTM
gi_188522642_gb_ACD60587.1_	0.14	64	0.113	21	0.144	12	0.105	0.109	N	0.57	SignalP-noTM
gi_188522644_gb_ACD60589.1_	0.136	34	0.104	34	0.103	70	0.075	0.09	N	0.57	SignalP-noTM
gi_188522645_gb_ACD60590.1_	0.33	45	0.221	45	0.279	35	0.13	0.178	N	0.57	SignalP-noTM
gi_188522646_gb_ACD60591.1_	0.234	29	0.417	29	0.948	16	0.843	0.618	Y	0.57	SignalP-noTM
gi_188522647_gb_ACD60592.1_	0.105	45	0.105	51	0.184	42	0.087	0.096	N	0.57	SignalP-noTM
gi_188522648_gb_ACD60593.1_	0.103	21	0.107	26	0.16	20	0.105	0.106	N	0.57	SignalP-noTM
gi_188522651_gb_ACD60596.1_	0.117	15	0.114	29	0.176	27	0.111	0.113	N	0.57	SignalP-noTM
gi_188522656_gb_ACD60601.1_	0.121	36	0.128	20	0.204	19	0.138	0.133	N	0.57	SignalP-noTM
gi_188522659_gb_ACD60604.1_	0.162	27	0.143	27	0.208	2	0.147	0.145	N	0.57	SignalP-noTM
gi_188522660_gb_ACD60605.1_	0.22	45	0.213	13	0.534	6	0.457	0.328	N	0.57	SignalP-noTM
gi_188522662_gb_ACD60607.1_	0.108	31	0.14	43	0.289	39	0.149	0.144	N	0.57	SignalP-noTM
gi_188522664_gb_ACD60609.1_	0.133	22	0.158	22	0.292	11	0.194	0.175	N	0.57	SignalP-noTM
gi_188522670_gb_ACD60615.1_	0.213	28	0.417	28	0.918	16	0.837	0.614	Y	0.57	SignalP-noTM

0.177994	0.131587	0.110859	0.140147	gi_188522687_gb_ACD60632.1_
0.305339	0.013242	0.342764	0.220448	gi_188522688_gb_ACD60633.1_
0.093046	0.117533	0.182426	0.131002	gi_188522689_gb_ACD60634.1_
0.920853	0.891775	0.8935	0.902043	gi_188522690_gb_ACD60635.1_
0.912855	0.284144	0.910926	0.702642	gi_188522691_gb_ACD60636.1_
0.172359	0.125209	0.17023	0.155933	gi_188522692_gb_ACD60637.1_
0.371684	0.291523	0.274482	0.312563	gi_188522693_gb_ACD60638.1_
0.215346	0.259802	0.218403	0.231184	gi_188522694_gb_ACD60639.1_
0.127194	0.069074	0.10736	0.101209	gi_188522695_gb_ACD60640.1_
0.663962	0.789182	0.666634	0.706593	gi_188522698_gb_ACD60643.1_
0.804711	0.971474	0.688904	0.821696	gi_188522699_gb_ACD60644.1_
0.199567	0.186943	0.238486	0.208332	gi_188522700_gb_ACD60645.1_
0.940139	0.592667	0.911412	0.814739	gi_188522701_gb_ACD60646.1_
0.051368	0.087864	0.121639	0.086957	gi_188522702_gb_ACD60647.1_
0.217891	0.136108	0.243977	0.199325	gi_188522705_gb_ACD60650.1_
0.844093	0.992775	0.666634	0.834501	gi_188522706_gb_ACD60651.1_
0.076562	0.01159	0.112645	0.066932	gi_188522707_gb_ACD60652.1_
0.112346	0.054526	0.126861	0.097911	gi_188522708_gb_ACD60653.1_
0.511998	0.897707	0.424091	0.611265	gi_188522709_gb_ACD60654.1_
0.109681	0.070437	0.112645	0.097588	gi_188522710_gb_ACD60655.1_
0.109975	0.000209	0.140035	0.083406	gi_188522711_gb_ACD60656.1_
0.104238	0.06985	0.164379	0.112822	gi_188522713_gb_ACD60658.1_
0.155513	0.087384	0.13193	0.124942	gi_188522714_gb_ACD60659.1_
0.127527	0.281709	0.094063	0.167766	gi_188522724_gb_ACD60669.1_
0.077845	0.079365	0.157095	0.104768	gi_188522725_gb_ACD60670.1_
0.470036	0.242872	0.366096	0.359668	gi_188522733_gb_ACD60678.1_
0.198134	0.773293	0.099302	0.35691	gi_188522737_gb_ACD60682.1_
0.064767	0.02516	0.099571	0.063166	gi_188522738_gb_ACD60683.1_
0.074675	0.025756	0.09104	0.063824	gi_188522740_gb_ACD60685.1_
0.065681	0.149694	0.166034	0.127136	gi_188522741_gb_ACD60686.1_
0.113247	0.066982	0.106215	0.095481	gi_188522746_gb_ACD60691.1_
0.090052	0.001322	0.156699	0.082691	gi_188522749_gb_ACD60694.1_
0.159494	0.320821	0.129882	0.203399	gi_188522750_gb_ACD60695.1_
0.140035	0.06717	0.136461	0.114555	gi_188522751_gb_ACD60696.1_
0.136815	0.910194	0.068689	0.371899	gi_188522752_gb_ACD60697.1_
0.112346	0.041686	0.201974	0.118669	gi_188522757_gb_ACD60702.1_
0.900698	0.998036	0.847613	0.915449	gi_188522760_gb_ACD60705.1_
0.140397	0.059524	0.155119	0.118347	gi_188522761_gb_ACD60706.1_
0.252939	0.247871	0.365401	0.288737	gi_188522762_gb_ACD60707.1_
0.164379	0.740198	0.115679	0.340085	gi_188522766_gb_ACD60711.1_
0.187399	0.108225	0.262697	0.186107	gi_188522768_gb_ACD60713.1_
0.135053	0.019724	0.124553	0.09311	gi_188522769_gb_ACD60714.1_
0.949502	0.962421	0.893214	0.935046	gi_188522774_gb_ACD60719.1_
0.916827	0.994749	0.801866	0.904481	gi_188522775_gb_ACD60720.1_
0.077201	0.065866	0.078928	0.073998	gi_188522776_gb_ACD60721.1_
0.064949	0.030237	0.10011	0.065099	gi_188522777_gb_ACD60722.1_
0.273289	0.954174	0.279891	0.502451	gi_188522778_gb_ACD60723.1_
0.112346	0.124881	0.133658	0.123628	gi_188522779_gb_ACD60724.1_
0.046221	0.029887	0.078276	0.051461	gi_188522784_gb_ACD60729.1_
0.936315	0.683737	0.895201	0.838418	gi_188522846_gb_ACD60791.1_
0.199567	0.660607	0.136815	0.33233	gi_188522847_gb_ACD60792.1_
0.12196	0.046887	0.130903	0.099917	gi_188522848_gb_ACD60793.1_
0.110563	0.194818	0.084556	0.129979	gi_188522849_gb_ACD60794.1_
0.165619	0.043273	0.225657	0.14485	gi_188522850_gb_ACD60795.1_
0.86669	0.694661	0.867036	0.809462	gi_188522851_gb_ACD60796.1_
0.087145	0.057216	0.181087	0.108483	gi_188522852_gb_ACD60797.1_
0.970545	0.998604	0.904132	0.95776	gi_188522853_gb_ACD60798.1_
0.085489	0.058525	0.087145	0.077053	gi_188522855_gb_ACD60800.1_
0.511998	0.754915	0.599168	0.622027	gi_188522856_gb_ACD60801.1_
0.648397	0.925117	0.748193	0.773902	gi_188522857_gb_ACD60802.1_
0.923012	0.999593	0.85705	0.926552	gi_188522860_gb_ACD60805.1_
0.109975	0.042047	0.102569	0.084864	gi_188522861_gb_ACD60806.1_
0.087624	0.13193	0.158691	0.126082	gi_188522862_gb_ACD60807.1_
0.115067	0.227233	0.184222	0.175507	gi_188522863_gb_ACD60808.1_
0.141486	0.00851	0.184222	0.111406	gi_188522864_gb_ACD60809.1_
0.279891	0.912136	0.387223	0.526417	gi_188522867_gb_ACD60812.1_
0.930733	0.999229	0.879637	0.936533	gi_188522868_gb_ACD60813.1_
0.941475	0.99997	0.864947	0.935464	gi_188522869_gb_ACD60814.1_
0.867726	0.99174	0.681137	0.846868	gi_188522880_gb_ACD60825.1_
0.27508	0.947748	0.190618	0.471149	gi_188522884_gb_ACD60829.1_
0.35503	0.427025	0.370983	0.384346	gi_188522886_gb_ACD60831.1_
0.72492	0.874462	0.633904	0.744429	gi_188522887_gb_ACD60832.1_
0.147795	0.454377	0.107647	0.236606	gi_188522891_gb_ACD60836.1_
0.158291	0.163967	0.199089	0.173782	gi_188522892_gb_ACD60837.1_
0.103958	0.077845	0.151228	0.11101	gi_188522894_gb_ACD60839.1_
0.937556	0.793639	0.887654	0.87295	gi_188522901_gb_ACD60846.1_
0.14295	0.027146	0.089074	0.08639	gi_188522902_gb_ACD60847.1_
0.113548	0.468542	0.093046	0.225045	gi_188522903_gb_ACD60848.1_

gi_188522671_gb_ACD60616.1_	0.116	31	0.099	70	0.103	62	0.077	0.089	N	0.57	SignalP-noTM
gi_188522672_gb_ACD60617.1_	0.182	21	0.176	38	0.311	27	0.155	0.168	N	0.51	SignalP-TM
gi_188522673_gb_ACD60618.1_	0.252	54	0.157	54	0.153	53	0.091	0.126	N	0.57	SignalP-noTM
gi_188522674_gb_ACD60619.1_	0.178	17	0.282	17	0.625	1	0.464	0.349	N	0.51	SignalP-TM
gi_188522675_gb_ACD60620.1_	0.131	56	0.111	56	0.136	36	0.091	0.102	N	0.57	SignalP-noTM
gi_188522676_gb_ACD60621.1_	0.113	51	0.109	35	0.19	34	0.107	0.108	N	0.57	SignalP-noTM
gi_188522677_gb_ACD60622.1_	0.372	26	0.593	26	0.967	17	0.927	0.75	Y	0.57	SignalP-noTM
gi_188522678_gb_ACD60623.1_	0.13	34	0.186	11	0.47	4	0.34	0.258	N	0.57	SignalP-noTM
gi_188522679_gb_ACD60624.1_	0.126	30	0.138	30	0.223	5	0.152	0.145	N	0.57	SignalP-noTM
gi_188522680_gb_ACD60625.1_	0.128	11	0.202	11	0.456	9	0.332	0.263	N	0.57	SignalP-noTM
gi_188522681_gb_ACD60626.1_	0.207	17	0.264	17	0.654	4	0.401	0.328	N	0.57	SignalP-noTM
gi_188522684_gb_ACD60629.1_	0.127	36	0.113	36	0.12	31	0.087	0.101	N	0.57	SignalP-noTM
gi_188522687_gb_ACD60632.1_	0.159	39	0.145	39	0.195	37	0.111	0.129	N	0.57	SignalP-noTM
gi_188522688_gb_ACD60633.1_	0.169	24	0.222	24	0.629	1	0.367	0.29	N	0.57	SignalP-noTM
gi_188522689_gb_ACD60634.1_	0.174	20	0.148	20	0.181	6	0.139	0.145	N	0.51	SignalP-TM
gi_188522690_gb_ACD60635.1_	0.499	29	0.671	29	0.961	19	0.892	0.775	Y	0.57	SignalP-noTM
gi_188522691_gb_ACD60636.1_	0.123	36	0.156	36	0.376	33	0.161	0.158	N	0.51	SignalP-TM
gi_188522692_gb_ACD60637.1_	0.151	42	0.143	42	0.186	37	0.101	0.128	N	0.51	SignalP-TM
gi_188522693_gb_ACD60638.1_	0.107	24	0.098	24	0.123	6	0.093	0.096	N	0.51	SignalP-TM
gi_188522694_gb_ACD60639.1_	0.155	21	0.259	21	0.528	4	0.457	0.352	N	0.57	SignalP-noTM
gi_188522695_gb_ACD60640.1_	0.126	14	0.133	54	0.324	50	0.106	0.12	N	0.57	SignalP-noTM
gi_188522698_gb_ACD60643.1_	0.774	43	0.861	43	0.987	32	0.718	0.794	Y	0.57	SignalP-noTM
gi_188522699_gb_ACD60644.1_	0.136	19	0.137	19	0.193	1	0.142	0.139	N	0.57	SignalP-noTM
gi_188522700_gb_ACD60645.1_	0.156	24	0.129	24	0.122	16	0.091	0.115	N	0.51	SignalP-TM
gi_188522701_gb_ACD60646.1_	0.128	46	0.115	22	0.155	11	0.118	0.116	N	0.51	SignalP-TM
gi_188522702_gb_ACD60647.1_	0.111	64	0.139	55	0.297	49	0.131	0.135	N	0.57	SignalP-noTM
gi_188522705_gb_ACD60650.1_	0.108	66	0.109	25	0.134	39	0.096	0.103	N	0.57	SignalP-noTM
gi_188522706_gb_ACD60651.1_	0.11	28	0.108	28	0.138	5	0.108	0.108	N	0.57	SignalP-noTM
gi_188522707_gb_ACD60652.1_	0.123	31	0.102	68	0.121	38	0.083	0.093	N	0.57	SignalP-noTM
gi_188522708_gb_ACD60653.1_	0.12	31	0.235	11	0.649	1	0.547	0.382	N	0.57	SignalP-noTM
gi_188522709_gb_ACD60654.1_	0.196	24	0.143	24	0.153	20	0.096	0.121	N	0.57	SignalP-noTM
gi_188522710_gb_ACD60655.1_	0.128	45	0.112	45	0.134	20	0.094	0.104	N	0.57	SignalP-noTM
gi_188522711_gb_ACD60656.1_	0.149	32	0.137	11	0.264	4	0.191	0.162	N	0.57	SignalP-noTM
gi_188522713_gb_ACD60658.1_	0.29	23	0.261	23	0.359	3	0.26	0.26	N	0.57	SignalP-noTM
gi_188522714_gb_ACD60659.1_	0.131	6	0.106	41	0.171	3	0.109	0.107	N	0.57	SignalP-noTM
gi_188522724_gb_ACD60669.1_	0.104	34	0.116	41	0.164	32	0.125	0.12	N	0.57	SignalP-noTM
gi_188522725_gb_ACD60670.1_	0.133	49	0.119	49	0.162	41	0.093	0.107	N	0.57	SignalP-noTM
gi_188522733_gb_ACD60678.1_	0.128	32	0.171	14	0.41	29	0.302	0.233	N	0.57	SignalP-noTM
gi_188522737_gb_ACD60682.1_	0.166	35	0.162	35	0.322	34	0.161	0.162	N	0.57	SignalP-noTM
gi_188522738_gb_ACD60683.1_	0.105	20	0.102	62	0.136	1	0.094	0.098	N	0.57	SignalP-noTM
gi_188522740_gb_ACD60685.1_	0.161	48	0.182	48	0.274	45	0.142	0.164	N	0.57	SignalP-noTM
gi_188522741_gb_ACD60686.1_	0.722	20	0.38	20	0.289	11	0.201	0.314	N	0.51	SignalP-TM
gi_188522746_gb_ACD60691.1_	0.137	18	0.11	37	0.177	25	0.101	0.106	N	0.57	SignalP-noTM
gi_188522749_gb_ACD60694.1_	0.178	24	0.176	24	0.245	1	0.175	0.175	N	0.57	SignalP-noTM
gi_188522750_gb_ACD60695.1_	0.423	14	0.344	14	0.458	9	0.268	0.308	N	0.57	SignalP-noTM
gi_188522751_gb_ACD60696.1_	0.146	34	0.15	34	0.228	2	0.154	0.151	N	0.51	SignalP-TM
gi_188522752_gb_ACD60697.1_	0.135	24	0.101	62	0.129	3	0.087	0.095	N	0.57	SignalP-noTM
gi_188522757_gb_ACD60702.1_	0.119	19	0.19	12	0.485	1	0.323	0.24	N	0.51	SignalP-TM
gi_188522760_gb_ACD60705.1_	0.131	46	0.153	21	0.415	1	0.202	0.176	N	0.57	SignalP-noTM
gi_188522761_gb_ACD60706.1_	0.212	34	0.193	34	0.352	39	0.182	0.188	N	0.57	SignalP-noTM
gi_188522762_gb_ACD60707.1_	0.127	26	0.105	54	0.151	1	0.084	0.095	N	0.57	SignalP-noTM
gi_188522766_gb_ACD60711.1_	0.149	30	0.124	15	0.183	7	0.144	0.131	N	0.51	SignalP-TM
gi_188522768_gb_ACD60713.1_	0.117	42	0.113	42	0.127	12	0.099	0.106	N	0.57	SignalP-noTM
gi_188522769_gb_ACD60714.1_	0.411	21	0.36	21	0.517	16	0.279	0.322	N	0.57	SignalP-noTM
gi_188522774_gb_ACD60719.1_	0.118	21	0.17	11	0.363	2	0.295	0.216	N	0.51	SignalP-TM
gi_188522775_gb_ACD60720.1_	0.125	31	0.138	11	0.29	1	0.18	0.157	N	0.57	SignalP-noTM
gi_188522776_gb_ACD60721.1_	0.126	31	0.148	31	0.264	10	0.191	0.168	N	0.57	SignalP-noTM
gi_188522777_gb_ACD60722.1_	0.226	26	0.294	26	0.585	19	0.359	0.318	N	0.51	SignalP-TM
gi_188522778_gb_ACD60723.1_	0.544	27	0.306	27	0.311	5	0.204	0.268	N	0.51	SignalP-TM
gi_188522779_gb_ACD60724.1_	0.123	34	0.165	34	0.307	26	0.168	0.166	N	0.51	SignalP-TM
gi_188522784_gb_ACD60729.1_	0.131	48	0.104	48	0.156	1	0.09	0.098	N	0.57	SignalP-noTM
gi_188522846_gb_ACD60791.1_	0.166	64	0.158	64	0.269	53	0.158	0.158	N	0.57	SignalP-noTM
gi_188522847_gb_ACD60792.1_	0.103	28	0.109	33	0.127	22	0.089	0.1	N	0.57	SignalP-noTM
gi_188522848_gb_ACD60793.1_	0.169	56	0.149	56	0.17	53	0.098	0.125	N	0.57	SignalP-noTM
gi_188522849_gb_ACD60794.1_	0.12	38	0.115	15	0.194	13	0.129	0.122	N	0.57	SignalP-noTM
gi_188522850_gb_ACD60795.1_	0.162	48	0.149	48	0.199	1	0.088	0.126	N	0.51	SignalP-TM
gi_188522851_gb_ACD60796.1_	0.245	19	0.399	19	0.841	11	0.657	0.52	N	0.57	SignalP-noTM
gi_188522852_gb_ACD60797.1_	0.129	46	0.114	46	0.129	30	0.102	0.109	N	0.57	SignalP-noTM
gi_188522853_gb_ACD60798.1_	0.119	46	0.14	14	0.269	8	0.197	0.167	N	0.57	SignalP-noTM
gi_188522855_gb_ACD60800.1_	0.12	65	0.102	65	0.099	22	0.082	0.093	N	0.57	SignalP-noTM
gi_188522856_gb_ACD60801.1_	0.288	14	0.347	14	0.576	10	0.415	0.379	N	0.57	SignalP-noTM
gi_188522857_gb_ACD60802.1_	0.38	26	0.249	26	0.312	6	0.215	0.233	N	0.57	SignalP-noTM
gi_188522860_gb_ACD60805.1_	0.252	13	0.251	13	0.414	9	0.251	0.251	N	0.57	SignalP-noTM
gi_188522861_gb_ACD60806.1_	0.147	57	0.112	57	0.182	3	0.093	0.103	N	0.57	SignalP-noTM
gi_188522862_gb_ACD60807.1_	0.141	51	0.106	12	0.176	2	0.105	0.106	N	0.51	SignalP-TM
gi_188522863_gb_ACD60808.1_	0.202	62	0.149	62	0.191	61	0.068	0.119	N	0.51	SignalP-TM
gi_188522864_gb_ACD60809.1_	0.357	52	0.288	52	0.351	48	0.192	0.253	N	0.51	SignalP-TM
gi_188522867_gb_ACD60812.1_	0.456	34	0.268	34	0.573	17	0.297	0.282	N	0.57	SignalP-noTM

0.166866	0.02373	0.137525	0.109374	gi_188522904_gb_ACD60849.1_
0.352287	0.852205	0.5015	0.568664	gi_188522906_gb_ACD60851.1_
0.143318	0.073237	0.123901	0.113485	gi_188522908_gb_ACD60853.1_
0.833134	0.923225	0.870794	0.875718	gi_188522909_gb_ACD60854.1_
0.184673	0.443986	0.092289	0.240316	gi_188522910_gb_ACD60855.1_
0.083862	0.03131	0.127862	0.081011	gi_188522911_gb_ACD60856.1_
0.129882	0.904391	0.072024	0.368766	gi_188522913_gb_ACD60858.1_
0.720713	0.995436	0.738464	0.818204	gi_188522914_gb_ACD60859.1_
0.208829	0.864596	0.111749	0.395058	gi_188522919_gb_ACD60864.1_
0.931311	0.919309	0.906447	0.919022	gi_188522922_gb_ACD60867.1_
0.115679	0.059189	0.152387	0.109085	gi_188522925_gb_ACD60870.1_
0.096129	0.064767	0.086669	0.082522	gi_188522926_gb_ACD60871.1_
0.101197	0.06262	0.152387	0.105401	gi_188522927_gb_ACD60872.1_
0.107647	0.013885	0.115986	0.079173	gi_188522928_gb_ACD60873.1_
0.949646	0.98946	0.917511	0.952206	gi_188522932_gb_ACD60877.1_
0.27508	0.76959	0.324098	0.456256	gi_188522933_gb_ACD60878.1_
0.166034	0.94164	0.213829	0.440501	gi_188522934_gb_ACD60879.1_
0.955212	0.995739	0.894353	0.948435	gi_188522937_gb_ACD60882.1_
0.380836	0.925739	0.470783	0.592453	gi_188522938_gb_ACD60883.1_
0.760969	0.395799	0.772767	0.643178	gi_188522939_gb_ACD60884.1_
0.072831	0.004496	0.104518	0.060615	gi_188522940_gb_ACD60885.1_
0.813968	0.950358	0.921724	0.89535	gi_188522941_gb_ACD60886.1_
0.090545	0.013844	0.13193	0.078773	gi_188522948_gb_ACD60893.1_
0.128532	0.002421	0.150844	0.093932	gi_188522949_gb_ACD60894.1_
0.103123	0.094833	0.094833	0.097596	gi_188522950_gb_ACD60895.1_
0.09984	0.000724	0.156699	0.085754	gi_188522951_gb_ACD60896.1_
0.264443	0.810306	0.135755	0.403501	gi_188522953_gb_ACD60898.1_
0.085021	0.152	0.099571	0.112197	gi_188522955_gb_ACD60900.1_
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0.130222	0.1603	0.115067	0.135196	gi_188522960_gb_ACD60905.1_
0.145542	0.125868	0.199567	0.156992	gi_188522962_gb_ACD60907.1_
0.140397	0.039468	0.147041	0.108969	gi_188522963_gb_ACD60908.1_
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0.111749	0.026059	0.127194	0.088334	gi_188522965_gb_ACD60910.1_
0.159896	0.454377	0.119413	0.244562	gi_188522966_gb_ACD60911.1_
0.879001	0.311739	0.829346	0.673362	gi_188522969_gb_ACD60914.1_
0.06717	0.024151	0.093299	0.06154	gi_188522970_gb_ACD60915.1_
0.153164	0.417511	0.272099	0.280925	gi_188522971_gb_ACD60916.1_
0.157095	0.128869	0.121639	0.135868	gi_188522972_gb_ACD60917.1_
0.94131	0.927574	0.889437	0.91944	gi_188522973_gb_ACD60918.1_
0.068116	0.000841	0.116912	0.061956	gi_188522974_gb_ACD60919.1_
0.905681	0.918639	0.837263	0.887194	gi_188522975_gb_ACD60920.1_
0.382252	0.45289	0.424824	0.419989	gi_188522976_gb_ACD60921.1_
0.681137	0.416052	0.705993	0.601061	gi_188522980_gb_ACD60925.1_
0.917964	0.559714	0.879955	0.785878	gi_188522981_gb_ACD60926.1_
0.130903	0.164379	0.102293	0.132525	gi_188522983_gb_ACD60928.1_
0.220458	0.30853	0.282316	0.270435	gi_188522984_gb_ACD60929.1_
0.1034	0.001194	0.149313	0.084636	gi_188522985_gb_ACD60930.1_
0.958073	0.940977	0.879001	0.926017	gi_188522986_gb_ACD60931.1_
0.44695	0.028693	0.473774	0.316472	gi_188522987_gb_ACD60932.1_
0.934502	0.912616	0.895201	0.914106	gi_188522988_gb_ACD60933.1_
0.942945	0.975636	0.842108	0.92023	gi_188522989_gb_ACD60934.1_
0.10736	0.033569	0.123575	0.088168	gi_188522990_gb_ACD60935.1_
0.329378	0.042901	0.372385	0.248221	gi_188522991_gb_ACD60936.1_
0.815327	0.872806	0.787178	0.825104	gi_188522992_gb_ACD60937.1_
0.663962	0.952166	0.601328	0.739152	gi_188522995_gb_ACD60940.1_
0.223567	0.318212	0.322785	0.288188	gi_188522997_gb_ACD60942.1_
0.126198	0.032704	0.206853	0.121918	gi_188522999_gb_ACD60944.1_
0.086195	0.072024	0.101197	0.086472	gi_188523000_gb_ACD60945.1_
0.116912	0.964119	0.254074	0.445035	gi_188523001_gb_ACD60946.1_
0.201974	0.090298	0.256927	0.183066	gi_188523002_gb_ACD60947.1_
0.095091	0.083631	0.150077	0.1096	gi_188523003_gb_ACD60948.1_
0.49325	0.327393	0.56193	0.460858	gi_188523005_gb_ACD60950.1_
0.904909	0.999565	0.830194	0.911556	gi_188523006_gb_ACD60951.1_
0.157095	0.134703	0.136461	0.142753	gi_188523007_gb_ACD60952.1_
0.181979	0.089317	0.21032	0.160539	gi_188523008_gb_ACD60953.1_
0.122927	0.201491	0.099034	0.141151	gi_188523009_gb_ACD60954.1_
0.543391	0.844093	0.456609	0.614698	gi_188523010_gb_ACD60955.1_
0.158291	0.422627	0.185126	0.255348	gi_188523011_gb_ACD60956.1_
0.127527	0.159896	0.179756	0.155726	gi_188523012_gb_ACD60957.1_
0.140397	0.00179	0.220458	0.120882	gi_188523013_gb_ACD60958.1_
0.105647	0.570772	0.087624	0.254681	gi_188523014_gb_ACD60959.1_
0.089074	0.026211	0.115679	0.076988	gi_188523015_gb_ACD60960.1_
0.951478	0.999972	0.807057	0.919502	gi_188523016_gb_ACD60961.1_
0.046221	0.02465	0.084324	0.051732	gi_188523017_gb_ACD60962.1_
0.260379	0.3858	0.310454	0.318878	gi_188523019_gb_ACD60964.1_
0.544879	0.870794	0.551566	0.655746	gi_188523027_gb_ACD60972.1_
0.4985	0.828495	0.684386	0.67046	gi_188523028_gb_ACD60973.1_

gi_188522868_gb_ACD60813.1_	0.311	35	0.211	35	0.51	1	0.205	0.208	N	0.57	SignalP-noTM
gi_188522869_gb_ACD60814.1_	0.609	23	0.678	23	0.925	19	0.802	0.736	Y	0.57	SignalP-noTM
gi_188522880_gb_ACD60825.1_	0.107	23	0.156	11	0.366	2	0.225	0.188	N	0.57	SignalP-noTM
gi_188522884_gb_ACD60829.1_	0.128	56	0.146	56	0.206	46	0.147	0.147	N	0.57	SignalP-noTM
gi_188522886_gb_ACD60831.1_	0.182	51	0.135	28	0.2	24	0.154	0.142	N	0.51	SignalP-TM
gi_188522887_gb_ACD60832.1_	0.134	29	0.135	29	0.189	1	0.143	0.139	N	0.57	SignalP-noTM
gi_188522891_gb_ACD60836.1_	0.105	22	0.117	47	0.186	45	0.079	0.103	N	0.51	SignalP-TM
gi_188522892_gb_ACD60837.1_	0.149	19	0.128	11	0.301	1	0.144	0.136	N	0.57	SignalP-noTM
gi_188522894_gb_ACD60839.1_	0.152	50	0.188	12	0.45	2	0.364	0.253	N	0.51	SignalP-TM
gi_188522901_gb_ACD60846.1_	0.466	60	0.534	60	0.915	43	0.449	0.494	N	0.57	SignalP-noTM
gi_188522902_gb_ACD60847.1_	0.104	36	0.115	14	0.16	10	0.137	0.125	N	0.57	SignalP-noTM
gi_188522903_gb_ACD60848.1_	0.128	21	0.109	21	0.135	9	0.1	0.105	N	0.57	SignalP-noTM
gi_188522904_gb_ACD60849.1_	0.11	26	0.134	12	0.226	9	0.185	0.158	N	0.57	SignalP-noTM
gi_188522906_gb_ACD60851.1_	0.156	42	0.146	42	0.219	19	0.143	0.145	N	0.57	SignalP-noTM
gi_188522908_gb_ACD60853.1_	0.122	43	0.111	43	0.141	1	0.098	0.105	N	0.57	SignalP-noTM
gi_188522909_gb_ACD60854.1_	0.118	65	0.179	11	0.418	3	0.323	0.247	N	0.57	SignalP-noTM
gi_188522910_gb_ACD60855.1_	0.169	37	0.172	35	0.366	34	0.18	0.176	N	0.57	SignalP-noTM
gi_188522911_gb_ACD60856.1_	0.103	25	0.102	62	0.139	2	0.096	0.099	N	0.57	SignalP-noTM
gi_188522913_gb_ACD60858.1_	0.158	20	0.115	42	0.165	25	0.1	0.108	N	0.57	SignalP-noTM
gi_188522914_gb_ACD60859.1_	0.178	39	0.144	23	0.253	19	0.18	0.16	N	0.57	SignalP-noTM
gi_188522919_gb_ACD60864.1_	0.111	9	0.106	68	0.124	62	0.09	0.098	N	0.57	SignalP-noTM
gi_188522922_gb_ACD60867.1_	0.125	37	0.102	15	0.12	5	0.102	0.102	N	0.57	SignalP-noTM
gi_188522925_gb_ACD60870.1_	0.154	36	0.12	47	0.141	46	0.073	0.103	N	0.51	SignalP-TM
gi_188522926_gb_ACD60871.1_	0.164	26	0.174	26	0.375	2	0.235	0.202	N	0.57	SignalP-noTM
gi_188522927_gb_ACD60872.1_	0.17	25	0.196	25	0.451	21	0.218	0.204	N	0.51	SignalP-TM
gi_188522928_gb_ACD60873.1_	0.155	50	0.111	50	0.112	2	0.085	0.099	N	0.57	SignalP-noTM
gi_188522932_gb_ACD60877.1_	0.599	14	0.58	14	0.848	11	0.557	0.569	N	0.57	SignalP-noTM
gi_188522933_gb_ACD60878.1_	0.156	42	0.146	42	0.234	19	0.152	0.149	N	0.57	SignalP-noTM
gi_188522934_gb_ACD60879.1_	0.333	19	0.469	19	0.948	9	0.694	0.575	Y	0.57	SignalP-noTM
gi_188522937_gb_ACD60882.1_	0.667	20	0.768	20	0.944	19	0.873	0.817	Y	0.57	SignalP-noTM
gi_188522938_gb_ACD60883.1_	0.29	40	0.219	40	0.338	39	0.125	0.174	N	0.57	SignalP-noTM
gi_188522939_gb_ACD60884.1_	0.144	33	0.186	41	0.548	32	0.178	0.183	N	0.57	SignalP-noTM
gi_188522940_gb_ACD60885.1_	0.109	4	0.111	56	0.156	1	0.106	0.109	N	0.57	SignalP-noTM
gi_188522941_gb_ACD60886.1_	0.576	27	0.549	27	0.737	17	0.538	0.544	N	0.57	SignalP-noTM
gi_188522948_gb_ACD60893.1_	0.128	20	0.108	20	0.139	19	0.085	0.098	N	0.57	SignalP-noTM
gi_188522949_gb_ACD60894.1_	0.248	28	0.129	28	0.149	2	0.081	0.106	N	0.57	SignalP-noTM
gi_188522950_gb_ACD60895.1_	0.108	18	0.111	60	0.137	49	0.097	0.104	N	0.57	SignalP-noTM
gi_188522951_gb_ACD60896.1_	0.117	42	0.105	44	0.125	3	0.095	0.1	N	0.57	SignalP-noTM
gi_188522953_gb_ACD60898.1_	0.101	49	0.117	31	0.165	9	0.127	0.122	N	0.57	SignalP-noTM
gi_188522955_gb_ACD60900.1_	0.115	25	0.115	43	0.146	34	0.079	0.102	N	0.51	SignalP-TM
gi_188522956_gb_ACD60901.1_	0.606	26	0.751	26	0.97	15	0.919	0.83	Y	0.57	SignalP-noTM
gi_188522960_gb_ACD60905.1_	0.13	29	0.117	11	0.171	4	0.143	0.127	N	0.51	SignalP-TM
gi_188522962_gb_ACD60907.1_	0.593	28	0.23	28	0.15	24	0.096	0.181	N	0.51	SignalP-TM
gi_188522963_gb_ACD60908.1_	0.141	21	0.152	21	0.327	1	0.181	0.166	N	0.57	SignalP-noTM
gi_188522964_gb_ACD60909.1_	0.158	33	0.153	12	0.242	5	0.171	0.161	N	0.57	SignalP-noTM
gi_188522965_gb_ACD60910.1_	0.134	33	0.135	21	0.226	19	0.137	0.136	N	0.57	SignalP-noTM
gi_188522966_gb_ACD60911.1_	0.119	61	0.121	40	0.172	36	0.123	0.122	N	0.57	SignalP-noTM
gi_188522969_gb_ACD60914.1_	0.53	21	0.724	21	0.993	10	0.976	0.842	Y	0.57	SignalP-noTM
gi_188522970_gb_ACD60915.1_	0.104	41	0.102	41	0.115	39	0.087	0.095	N	0.57	SignalP-noTM
gi_188522971_gb_ACD60916.1_	0.147	22	0.106	11	0.184	1	0.104	0.105	N	0.51	SignalP-TM
gi_188522972_gb_ACD60917.1_	0.169	19	0.198	19	0.292	18	0.224	0.208	N	0.51	SignalP-TM
gi_188522973_gb_ACD60918.1_	0.114	69	0.111	70	0.148	68	0.089	0.103	N	0.51	SignalP-TM
gi_188522974_gb_ACD60919.1_	0.104	32	0.102	66	0.131	31	0.089	0.096	N	0.57	SignalP-noTM
gi_188522975_gb_ACD60920.1_	0.11	43	0.101	20	0.116	9	0.086	0.094	N	0.57	SignalP-noTM
gi_188522976_gb_ACD60921.1_	0.105	36	0.107	11	0.132	1	0.117	0.112	N	0.57	SignalP-noTM
gi_188522980_gb_ACD60925.1_	0.105	45	0.105	51	0.184	42	0.087	0.096	N	0.57	SignalP-noTM
gi_188522981_gb_ACD60926.1_	0.179	22	0.166	22	0.231	20	0.168	0.167	N	0.57	SignalP-noTM
gi_188522983_gb_ACD60928.1_	0.112	22	0.143	13	0.257	9	0.207	0.173	N	0.57	SignalP-noTM
gi_188522984_gb_ACD60929.1_	0.199	35	0.166	35	0.21	33	0.134	0.151	N	0.57	SignalP-noTM
gi_188522985_gb_ACD60930.1_	0.293	13	0.493	13	0.895	9	0.828	0.651	Y	0.57	SignalP-noTM
gi_188522986_gb_ACD60931.1_	0.141	35	0.137	12	0.208	1	0.173	0.154	N	0.57	SignalP-noTM
gi_188522987_gb_ACD60932.1_	0.27	32	0.172	32	0.163	30	0.105	0.14	N	0.57	SignalP-noTM
gi_188522988_gb_ACD60933.1_	0.117	40	0.151	40	0.344	33	0.182	0.166	N	0.57	SignalP-noTM
gi_188522989_gb_ACD60934.1_	0.127	32	0.191	41	0.431	39	0.209	0.2	N	0.57	SignalP-noTM
gi_188522990_gb_ACD60935.1_	0.105	45	0.105	51	0.184	42	0.087	0.096	N	0.57	SignalP-noTM
gi_188522991_gb_ACD60936.1_	0.161	25	0.27	11	0.671	9	0.533	0.393	N	0.57	SignalP-noTM
gi_188522992_gb_ACD60937.1_	0.375	27	0.591	27	0.977	23	0.927	0.749	Y	0.57	SignalP-noTM
gi_188522995_gb_ACD60940.1_	0.176	21	0.174	21	0.229	1	0.175	0.174	N	0.57	SignalP-noTM
gi_188522997_gb_ACD60942.1_	0.128	19	0.162	11	0.434	1	0.252	0.204	N	0.57	SignalP-noTM
gi_188522999_gb_ACD60944.1_	0.103	35	0.101	40	0.118	33	0.079	0.091	N	0.57	SignalP-noTM
gi_188523000_gb_ACD60945.1_	0.199	43	0.136	43	0.177	1	0.101	0.12	N	0.57	SignalP-noTM
gi_188523001_gb_ACD60946.1_	0.101	26	0.103	21	0.115	14	0.101	0.102	N	0.57	SignalP-noTM
gi_188523002_gb_ACD60947.1_	0.124	29	0.187	15	0.432	11	0.343	0.26	N	0.57	SignalP-noTM
gi_188523003_gb_ACD60948.1_	0.176	19	0.202	19	0.383	1	0.258	0.229	N	0.57	SignalP-noTM
gi_188523005_gb_ACD60950.1_	0.198	24	0.383	24	0.919	1	0.804	0.581	Y	0.57	SignalP-noTM
gi_188523006_gb_ACD60951.1_	0.124	21	0.157	21	0.306	19	0.191	0.173	N	0.57	SignalP-noTM
gi_188523007_gb_ACD60952.1_	0.284	61	0.182	61	0.21	52	0.109	0.148	N	0.57	SignalP-noTM
gi_188523008_gb_ACD60953.1_	0.426	29	0.317	29	0.472	8	0.333	0.323	N	0.51	SignalP-TM

0.172359	0.12196	0.142583	0.145634	gi_188523029_gb_ACD60974.1_
0.180643	0.033278	0.246197	0.153373	gi_188523034_gb_ACD60979.1_
0.949789	0.999432	0.904132	0.951118	gi_188523035_gb_ACD60980.1_
0.921072	0.982102	0.906192	0.936455	gi_188523036_gb_ACD60981.1_
0.522485	0.818468	0.697833	0.679595	gi_188523037_gb_ACD60982.1_
0.223047	0.041927	0.215853	0.160276	gi_188523038_gb_ACD60983.1_
0.167702	0.120999	0.181532	0.156744	gi_188523039_gb_ACD60984.1_
0.095091	0.022776	0.162329	0.093399	gi_188523040_gb_ACD60985.1_
0.140397	0.040621	0.206361	0.129126	gi_188523041_gb_ACD60986.1_
0.148932	0.669959	0.176245	0.331712	gi_188523042_gb_ACD60987.1_
0.826353	0.989949	0.753803	0.856702	gi_188523043_gb_ACD60988.1_
0.146665	0.129544	0.17023	0.148813	gi_188523044_gb_ACD60989.1_
0.119729	0.054992	0.112346	0.095689	gi_188523046_gb_ACD60991.1_
0.945319	0.992903	0.926559	0.954927	gi_188523047_gb_ACD60992.1_
0.933578	0.999843	0.864245	0.932555	gi_188523048_gb_ACD60993.1_
0.958194	0.999976	0.932074	0.963415	gi_188523050_gb_ACD60995.1_
0.167702	0.048661	0.220974	0.145779	gi_188523051_gb_ACD60996.1_
0.923012	0.999642	0.848772	0.923809	gi_528897497_gb_AGS47856.1_
0.943747	0.995739	0.899348	0.946278	gi_188523053_gb_ACD60998.1_
0.398672	0.237941	0.634599	0.423737	gi_188523054_gb_ACD60999.1_
0.188773	0.03299	0.202943	0.141569	gi_188523055_gb_ACD61000.1_
0.247871	0.228818	0.201491	0.22606	gi_188523057_gb_ACD61002.1_
0.178433	0.085255	0.200047	0.154578	gi_188523058_gb_ACD61003.1_
0.157493	0.235772	0.156303	0.183189	gi_188523059_gb_ACD61004.1_
0.100652	0.040272	0.113548	0.084824	gi_188523069_gb_ACD61014.1_
0.443986	0.515745	0.54711	0.50228	gi_188523072_gb_ACD61017.1_
0.905424	0.894919	0.9015	0.900614	gi_188523075_gb_ACD61020.1_
0.230942	0.124553	0.147795	0.167763	gi_188523076_gb_ACD61021.1_
0.102018	0.027626	0.115986	0.081877	gi_188523077_gb_ACD61022.1_
0.073441	0.024578	0.080468	0.059496	gi_188523078_gb_ACD61023.1_
0.941969	0.10147	0.896321	0.646587	gi_188523079_gb_ACD61024.1_
0.155907	0.053911	0.182873	0.130897	gi_188523080_gb_ACD61025.1_
0.134354	0.044659	0.221491	0.133501	gi_188523084_gb_ACD61029.1_
0.154727	0.931119	0.111452	0.399099	gi_188523090_gb_ACD61035.1_
0.059524	0.006607	0.096129	0.054087	gi_188523093_gb_ACD61038.1_
0.089317	0.002174	0.102293	0.064595	gi_188523094_gb_ACD61039.1_
0.327393	0.064405	0.431435	0.274411	gi_188523097_gb_ACD61042.1_
0.609212	0.250678	0.488002	0.449297	gi_188523098_gb_ACD61043.1_
0.087145	0.225133	0.107072	0.139783	gi_188523099_gb_ACD61044.1_
0.392933	0.631812	0.427025	0.483923	gi_188523100_gb_ACD61045.1_
0.181532	0.026675	0.153553	0.120587	gi_188523105_gb_ACD61050.1_
0.065681	0.14629	0.074675	0.095549	gi_188523107_gb_ACD61052.1_
0.741351	0.805182	0.826783	0.791105	gi_188523108_gb_ACD61053.1_
0.077201	0.106786	0.13331	0.105766	gi_188523109_gb_ACD61054.1_
0.185579	0.635295	0.198134	0.339669	gi_188523110_gb_ACD61055.1_
0.213829	0.269729	0.1034	0.195653	gi_188523111_gb_ACD61056.1_
0.094319	0.032327	0.130222	0.085623	gi_188523112_gb_ACD61057.1_
0.208334	0.024292	0.254643	0.162423	gi_188523113_gb_ACD61058.1_
0.082489	0.165205	0.082489	0.110061	gi_188523115_gb_ACD61060.1_
0.090298	0.030237	0.138955	0.086497	gi_188523116_gb_ACD61061.1_
0.958672	0.997806	0.891775	0.949418	gi_188523117_gb_ACD61062.1_
0.100652	0.011555	0.135404	0.082537	gi_188523118_gb_ACD61063.1_
0.253506	0.836443	0.290904	0.460284	gi_188523120_gb_ACD61065.1_
0.201009	0.109097	0.24232	0.184142	gi_188523121_gb_ACD61066.1_
0.589766	0.321475	0.724322	0.545188	gi_188523122_gb_ACD61067.1_
0.088105	0.033375	0.148932	0.090137	gi_188523124_gb_ACD61069.1_
0.177994	0.059693	0.228289	0.155325	gi_188523125_gb_ACD61070.1_
0.093808	0.024578	0.122604	0.08033	gi_188523127_gb_ACD61072.1_
0.295879	0.044916	0.365401	0.235399	gi_188523130_gb_ACD61075.1_
0.103679	0.047156	0.181979	0.110938	gi_188523133_gb_ACD61078.1_
0.114457	0.167702	0.089317	0.123825	gi_188523134_gb_ACD61079.1_
0.946394	0.752129	0.935595	0.878039	gi_188523137_gb_ACD61082.1_
0.141122	0.065131	0.188314	0.131522	gi_188523138_gb_ACD61083.1_
0.080247	0.045174	0.099571	0.074997	gi_188523139_gb_ACD61084.1_
0.215346	0.943107	0.111155	0.423203	gi_188523145_gb_ACD61090.1_
0.412413	0.390788	0.470036	0.424412	gi_188523146_gb_ACD61091.1_
0.406609	0.936136	0.320821	0.554522	gi_188523147_gb_ACD61092.1_
0.189233	0.153944	0.148932	0.164036	gi_188523148_gb_ACD61093.1_
0.065681	0.043898	0.109389	0.072989	gi_188523149_gb_ACD61094.1_
0.131587	0.014994	0.170654	0.105745	gi_188523152_gb_ACD61097.1_
0.952302	0.997845	0.829346	0.926498	gi_188523154_gb_ACD61099.1_
0.066982	0.024221	0.081585	0.057596	gi_188523156_gb_ACD61101.1_
0.110859	0.010509	0.161515	0.094294	gi_188523158_gb_ACD61103.1_
0.197182	0.061745	0.250678	0.169868	gi_188523160_gb_ACD61105.1_
0.811686	0.987029	0.640837	0.813184	gi_188523161_gb_ACD61106.1_
0.107936	0.00405	0.10736	0.073115	gi_188523162_gb_ACD61107.1_
0.109681	0.082716	0.168962	0.120453	gi_188523163_gb_ACD61108.1_
0.13193	0.004816	0.192943	0.109896	gi_188523164_gb_ACD61109.1_

gi_188523009_gb_ACD60954.1_	0.147	39	0.123	26	0.163	1	0.107	0.116	N	0.57	SignalP-noTM
gi_188523010_gb_ACD60955.1_	0.131	53	0.11	53	0.119	28	0.086	0.099	N	0.57	SignalP-noTM
gi_188523011_gb_ACD60956.1_	0.119	47	0.112	66	0.135	57	0.101	0.107	N	0.57	SignalP-noTM
gi_188523012_gb_ACD60957.1_	0.19	44	0.203	25	0.361	21	0.223	0.212	N	0.57	SignalP-noTM
gi_188523013_gb_ACD60958.1_	0.141	23	0.125	23	0.148	21	0.115	0.12	N	0.57	SignalP-noTM
gi_188523014_gb_ACD60959.1_	0.293	22	0.188	22	0.208	19	0.113	0.153	N	0.57	SignalP-noTM
gi_188523015_gb_ACD60960.1_	0.117	23	0.126	12	0.217	1	0.155	0.14	N	0.57	SignalP-noTM
gi_188523016_gb_ACD60961.1_	0.102	32	0.163	11	0.367	2	0.268	0.212	N	0.57	SignalP-noTM
gi_188523017_gb_ACD60962.1_	0.105	26	0.157	12	0.356	5	0.25	0.201	N	0.57	SignalP-noTM
gi_188523019_gb_ACD60964.1_	0.144	42	0.143	42	0.229	35	0.144	0.144	N	0.57	SignalP-noTM
gi_188523027_gb_ACD60972.1_	0.14	60	0.113	60	0.161	5	0.096	0.105	N	0.57	SignalP-noTM
gi_188523028_gb_ACD60973.1_	0.112	36	0.136	12	0.255	3	0.184	0.158	N	0.57	SignalP-noTM
gi_188523029_gb_ACD60974.1_	0.149	22	0.175	22	0.34	5	0.234	0.203	N	0.57	SignalP-noTM
gi_188523034_gb_ACD60979.1_	0.134	45	0.117	11	0.18	1	0.135	0.126	N	0.57	SignalP-noTM
gi_188523035_gb_ACD60980.1_	0.137	22	0.303	22	0.923	1	0.732	0.505	N	0.57	SignalP-noTM
gi_188523036_gb_ACD60981.1_	0.304	26	0.248	26	0.373	21	0.19	0.226	N	0.51	SignalP-TM
gi_188523037_gb_ACD60982.1_	0.145	27	0.172	27	0.292	21	0.173	0.172	N	0.51	SignalP-TM
gi_188523038_gb_ACD60983.1_	0.136	33	0.136	33	0.188	2	0.146	0.141	N	0.57	SignalP-noTM
gi_188523039_gb_ACD60984.1_	0.251	28	0.243	28	0.422	3	0.253	0.247	N	0.51	SignalP-TM
gi_188523040_gb_ACD60985.1_	0.204	29	0.183	38	0.296	34	0.17	0.179	N	0.51	SignalP-TM
gi_188523041_gb_ACD60986.1_	0.397	40	0.393	40	0.706	32	0.282	0.352	N	0.51	SignalP-TM
gi_188523042_gb_ACD60987.1_	0.17	17	0.304	12	0.791	2	0.62	0.421	N	0.51	SignalP-TM
gi_188523043_gb_ACD60988.1_	0.111	44	0.161	11	0.367	4	0.262	0.198	N	0.51	SignalP-TM
gi_188523044_gb_ACD60989.1_	0.134	23	0.104	49	0.129	42	0.085	0.095	N	0.57	SignalP-noTM
gi_188523046_gb_ACD60991.1_	0.199	64	0.14	64	0.115	24	0.096	0.119	N	0.57	SignalP-noTM
gi_188523047_gb_ACD60992.1_	0.117	25	0.196	12	0.596	10	0.376	0.281	N	0.57	SignalP-noTM
gi_188523048_gb_ACD60993.1_	0.129	40	0.133	40	0.181	5	0.131	0.133	N	0.57	SignalP-noTM
gi_528897497_gb_AGS47856.1_	0.472	28	0.653	28	0.969	21	0.846	0.743	Y	0.57	SignalP-noTM
gi_188523050_gb_ACD60995.1_	0.403	67	0.268	67	0.509	12	0.233	0.255	N	0.51	SignalP-TM
gi_188523051_gb_ACD60996.1_	0.194	26	0.148	26	0.267	6	0.135	0.142	N	0.57	SignalP-noTM
gi_188523053_gb_ACD60998.1_	0.842	20	0.898	20	0.972	18	0.949	0.922	Y	0.57	SignalP-noTM
gi_188523054_gb_ACD60999.1_	0.251	26	0.236	26	0.405	9	0.276	0.255	N	0.57	SignalP-noTM
gi_188523055_gb_ACD61000.1_	0.213	23	0.226	23	0.622	1	0.308	0.265	N	0.57	SignalP-noTM
gi_188523057_gb_ACD61002.1_	0.21	46	0.192	46	0.394	16	0.226	0.204	N	0.51	SignalP-TM
gi_188523058_gb_ACD61003.1_	0.331	38	0.297	38	0.374	35	0.184	0.255	N	0.51	SignalP-TM
gi_188523059_gb_ACD61004.1_	0.117	34	0.1	11	0.13	1	0.1	0.1	N	0.51	SignalP-TM
gi_188523069_gb_ACD61014.1_	0.106	58	0.105	58	0.139	6	0.103	0.104	N	0.57	SignalP-noTM
gi_188523072_gb_ACD61017.1_	0.255	15	0.342	15	0.801	13	0.444	0.39	N	0.57	SignalP-noTM
gi_188523075_gb_ACD61020.1_	0.157	24	0.156	24	0.199	1	0.157	0.157	N	0.57	SignalP-noTM
gi_188523076_gb_ACD61021.1_	0.143	51	0.148	23	0.252	4	0.203	0.174	N	0.57	SignalP-noTM
gi_188523077_gb_ACD61022.1_	0.137	25	0.197	12	0.536	3	0.395	0.29	N	0.57	SignalP-noTM
gi_188523078_gb_ACD61023.1_	0.108	69	0.111	33	0.19	1	0.107	0.109	N	0.57	SignalP-noTM
gi_188523079_gb_ACD61024.1_	0.129	21	0.107	32	0.134	1	0.095	0.102	N	0.57	SignalP-noTM
gi_188523080_gb_ACD61025.1_	0.189	44	0.215	34	0.444	3	0.337	0.26	N	0.51	SignalP-TM
gi_188523084_gb_ACD61029.1_	0.168	17	0.248	17	0.548	12	0.37	0.305	N	0.57	SignalP-noTM
gi_188523090_gb_ACD61035.1_	0.17	36	0.124	25	0.136	22	0.105	0.115	N	0.57	SignalP-noTM
gi_188523093_gb_ACD61038.1_	0.129	36	0.129	36	0.208	31	0.118	0.124	N	0.57	SignalP-noTM
gi_188523094_gb_ACD61039.1_	0.154	49	0.131	49	0.197	47	0.096	0.115	N	0.57	SignalP-noTM
gi_188523097_gb_ACD61042.1_	0.165	29	0.15	29	0.248	1	0.158	0.154	N	0.57	SignalP-noTM
gi_188523098_gb_ACD61043.1_	0.128	21	0.12	21	0.211	1	0.118	0.119	N	0.57	SignalP-noTM
gi_188523099_gb_ACD61044.1_	0.1	22	0.107	11	0.164	1	0.114	0.11	N	0.51	SignalP-TM
gi_188523100_gb_ACD61045.1_	0.134	24	0.152	21	0.277	1	0.198	0.173	N	0.57	SignalP-noTM
gi_188523105_gb_ACD61050.1_	0.238	33	0.159	33	0.17	32	0.093	0.128	N	0.57	SignalP-noTM
gi_188523107_gb_ACD61052.1_	0.104	27	0.122	11	0.2	5	0.158	0.135	N	0.51	SignalP-TM
gi_188523108_gb_ACD61053.1_	0.133	22	0.158	22	0.292	11	0.194	0.175	N	0.57	SignalP-noTM
gi_188523109_gb_ACD61054.1_	0.222	34	0.208	34	0.258	27	0.149	0.186	N	0.51	SignalP-TM
gi_188523110_gb_ACD61055.1_	0.141	25	0.18	25	0.349	13	0.23	0.203	N	0.57	SignalP-noTM
gi_188523111_gb_ACD61056.1_	0.117	26	0.121	11	0.19	1	0.14	0.13	N	0.57	SignalP-noTM
gi_188523112_gb_ACD61057.1_	0.112	18	0.122	18	0.181	8	0.129	0.125	N	0.57	SignalP-noTM
gi_188523113_gb_ACD61058.1_	0.214	25	0.23	25	0.351	19	0.219	0.225	N	0.57	SignalP-noTM
gi_188523115_gb_ACD61060.1_	0.109	27	0.158	11	0.319	2	0.258	0.205	N	0.57	SignalP-noTM
gi_188523116_gb_ACD61061.1_	0.163	49	0.147	11	0.276	4	0.217	0.18	N	0.57	SignalP-noTM
gi_188523117_gb_ACD61062.1_	0.108	34	0.207	18	0.478	11	0.412	0.304	N	0.57	SignalP-noTM
gi_188523118_gb_ACD61063.1_	0.46	28	0.232	28	0.223	2	0.119	0.179	N	0.57	SignalP-noTM
gi_188523120_gb_ACD61065.1_	0.102	60	0.101	60	0.122	14	0.09	0.096	N	0.57	SignalP-noTM
gi_188523121_gb_ACD61066.1_	0.7	24	0.794	24	0.954	21	0.906	0.846	Y	0.57	SignalP-noTM
gi_188523122_gb_ACD61067.1_	0.653	21	0.774	21	0.964	18	0.89	0.829	Y	0.57	SignalP-noTM
gi_188523124_gb_ACD61069.1_	0.152	30	0.149	30	0.222	27	0.151	0.15	N	0.57	SignalP-noTM
gi_188523125_gb_ACD61070.1_	0.119	31	0.114	31	0.159	39	0.102	0.109	N	0.57	SignalP-noTM
gi_188523127_gb_ACD61072.1_	0.12	32	0.098	55	0.11	5	0.082	0.091	N	0.57	SignalP-noTM
gi_188523130_gb_ACD61075.1_	0.139	36	0.157	36	0.243	8	0.173	0.164	N	0.57	SignalP-noTM
gi_188523133_gb_ACD61078.1_	0.204	26	0.152	26	0.162	15	0.117	0.135	N	0.57	SignalP-noTM
gi_188523134_gb_ACD61079.1_	0.279	53	0.176	53	0.205	3	0.119	0.149	N	0.57	SignalP-noTM
gi_188523137_gb_ACD61082.1_	0.147	26	0.128	26	0.177	24	0.115	0.122	N	0.57	SignalP-noTM
gi_188523138_gb_ACD61083.1_	0.131	40	0.102	40	0.112	1	0.074	0.089	N	0.57	SignalP-noTM
gi_188523139_gb_ACD61084.1_	0.118	23	0.105	55	0.134	48	0.092	0.099	N	0.57	SignalP-noTM
gi_188523145_gb_ACD61090.1_	0.111	9	0.106	68	0.124	62	0.09	0.098	N	0.57	SignalP-noTM
gi_188523146_gb_ACD61091.1_	0.124	20	0.132	25	0.178	34	0.125	0.129	N	0.57	SignalP-noTM

0.113247	0.039925	0.155119	0.102764	gi_188523165_gb_ACD61110.1_
0.105364	0.002421	0.178873	0.095553	gi_188523166_gb_ACD61111.1_
0.153553	0.079147	0.321475	0.184725	gi_188523167_gb_ACD61112.1_
0.089562	0.056094	0.201009	0.115555	gi_188523168_gb_ACD61113.1_
0.042047	0.443246	0.12196	0.202418	gi_188523169_gb_ACD61114.1_
0.157493	0.16645	0.246754	0.190232	gi_188523170_gb_ACD61115.1_
0.248431	0.953113	0.283534	0.495026	gi_188523172_gb_ACD61117.1_
0.289051	0.351603	0.263278	0.301311	gi_188523173_gb_ACD61118.1_
0.873471	0.390074	0.852205	0.70525	gi_188523174_gb_ACD61119.1_
0.427759	0.991886	0.682438	0.700694	gi_188523260_gb_ACD61205.1_
0.94745	0.993775	0.905937	0.949054	gi_188523267_gb_ACD61212.1_
0.536684	0.07024	0.653849	0.420258	gi_188523268_gb_ACD61213.1_
0.95879	0.983999	0.946242	0.96301	gi_188523269_gb_ACD61214.1_
0.326073	0.983714	0.199089	0.502959	gi_188523271_gb_ACD61216.1_
0.054064	0.018487	0.126861	0.066471	gi_188523275_gb_ACD61220.1_
0.953113	0.999882	0.851827	0.934941	gi_188523278_gb_ACD61223.1_
0.932453	0.999868	0.926559	0.95296	gi_188523280_gb_ACD61225.1_
0.169384	0.540412	0.097969	0.269255	gi_188523281_gb_ACD61226.1_
0.236855	0.359854	0.159896	0.252202	gi_188523282_gb_ACD61227.1_
0.151614	0.378011	0.136461	0.222029	gi_188523290_gb_ACD61235.1_
0.198611	0.344795	0.062444	0.20195	gi_188523293_gb_ACD61238.1_
0.833134	0.990969	0.890611	0.904905	gi_188523295_gb_ACD61240.1_
0.93738	0.999902	0.924492	0.953925	gi_188523297_gb_ACD61242.1_
0.958194	0.999937	0.91819	0.958774	gi_188523299_gb_ACD61244.1_
0.270912	0.854084	0.328054	0.48435	gi_188523300_gb_ACD61245.1_
0.84954	0.998865	0.831038	0.893148	gi_188523301_gb_ACD61246.1_
0.142583	0.585405	0.143687	0.290558	gi_188523303_gb_ACD61248.1_
0.230942	0.771711	0.156699	0.386451	gi_188523304_gb_ACD61249.1_
0.349554	0.038457	0.364705	0.250905	gi_188523305_gb_ACD61250.1_
0.144056	0.071625	0.178873	0.131518	gi_188523306_gb_ACD61251.1_
0.798991	0.63599	0.618456	0.684479	gi_188523311_gb_ACD61256.1_
0.176245	0.059861	0.219943	0.152016	gi_188523315_gb_ACD61260.1_
0.07635	0.05285	0.084556	0.071252	gi_188523316_gb_ACD61261.1_
0.942945	0.998482	0.904391	0.948606	gi_188523317_gb_ACD61262.1_
0.147418	0.283534	0.181087	0.204013	gi_188523320_gb_ACD61265.1_
0.659934	0.990444	0.719504	0.789961	gi_188523321_gb_ACD61266.1_
0.095868	0.000177	0.156699	0.084248	gi_188523322_gb_ACD61267.1_
0.645656	0.594837	0.76692	0.669138	gi_188523323_gb_ACD61268.1_
0.088105	0.003838	0.115679	0.069207	gi_188523329_gb_ACD61274.1_
0.056412	0.000493	0.094063	0.050323	gi_188523333_gb_ACD61278.1_
0.126198	0.38367	0.202458	0.237442	gi_188523334_gb_ACD61279.1_
0.547853	0.905167	0.652489	0.701836	gi_188523336_gb_ACD61281.1_
0.944381	0.998769	0.877396	0.940182	gi_188523346_gb_ACD61291.1_
0.105364	0.035264	0.153944	0.098191	gi_188523348_gb_ACD61293.1_
0.127862	0.058856	0.155119	0.113946	gi_188523349_gb_ACD61294.1_
0.157892	0.002085	0.236855	0.132277	gi_188523350_gb_ACD61295.1_
0.240124	0.920635	0.074675	0.411811	gi_188523356_gb_ACD61301.1_
0.119098	0.016001	0.123251	0.086117	gi_188523357_gb_ACD61302.1_
0.895762	0.961209	0.875119	0.910697	gi_188523360_gb_ACD61305.1_
0.123575	0.040388	0.152	0.105321	gi_188523361_gb_ACD61306.1_
0.069267	0.022183	0.120999	0.070816	gi_188523362_gb_ACD61307.1_
0.104518	0.234154	0.243424	0.194032	gi_188523363_gb_ACD61308.1_
0.675902	0.931119	0.599888	0.735636	gi_188523364_gb_ACD61309.1_
0.309812	0.348191	0.38367	0.347224	gi_188523365_gb_ACD61310.1_
0.149694	0.054064	0.191545	0.131768	gi_188523366_gb_ACD61311.1_
0.903871	0.956603	0.816678	0.892384	gi_188523367_gb_ACD61312.1_
0.342764	0.085255	0.357783	0.261934	gi_188523370_gb_ACD61315.1_
0.080025	0.054526	0.090052	0.074868	gi_188523371_gb_ACD61316.1_
0.081361	0.018379	0.112946	0.070895	gi_188523372_gb_ACD61317.1_
0.133658	0.104238	0.157095	0.131664	gi_188523373_gb_ACD61318.1_
0.517243	0.973012	0.77539	0.755215	gi_188523375_gb_ACD61320.1_
0.069461	0.76692	0.186487	0.340956	gi_188523376_gb_ACD61321.1_
0.140759	0.451404	0.10736	0.233174	gi_188523377_gb_ACD61322.1_
0.223047	0.226707	0.258075	0.235943	gi_188523378_gb_ACD61323.1_
0.088105	0.128196	0.15046	0.122254	gi_188523379_gb_ACD61324.1_
0.461824	0.821127	0.621989	0.63498	gi_188523381_gb_ACD61326.1_
0.529964	0.584676	0.647713	0.587451	gi_188523382_gb_ACD61327.1_
0.097704	0.096651	0.095609	0.096655	gi_188523383_gb_ACD61328.1_
0.083862	0.02098	0.108806	0.071216	gi_188523384_gb_ACD61329.1_
0.140035	0.064224	0.17023	0.12483	gi_188523385_gb_ACD61330.1_
0.144427	0.054681	0.091289	0.096799	gi_188523386_gb_ACD61331.1_
0.110269	0.000983	0.166034	0.092429	gi_188523392_gb_ACD61337.1_
0.869438	0.998865	0.624103	0.830802	gi_188523393_gb_ACD61338.1_
0.494	0.726115	0.665299	0.628471	gi_188523394_gb_ACD61339.1_
0.429964	0.240124	0.368886	0.346325	gi_188523395_gb_ACD61340.1_
0.128869	0.138596	0.11847	0.128645	gi_188523396_gb_ACD61341.1_
0.085021	0.002915	0.125209	0.071048	gi_188523397_gb_ACD61342.1_
0.145542	0.1603	0.178873	0.161572	gi_188523400_gb_ACD61345.1_

gi_188523147_gb_ACD61092.1_	0.247	12	0.302	12	0.659	9	0.377	0.337	N	0.57	SignalP-noTM
gi_188523148_gb_ACD61093.1_	0.128	27	0.113	27	0.141	26	0.084	0.099	N	0.57	SignalP-noTM
gi_188523149_gb_ACD61094.1_	0.112	19	0.106	11	0.151	9	0.114	0.11	N	0.57	SignalP-noTM
gi_188523152_gb_ACD61097.1_	0.411	21	0.358	21	0.512	16	0.275	0.319	N	0.57	SignalP-noTM
gi_188523154_gb_ACD61099.1_	0.112	50	0.144	11	0.288	3	0.215	0.177	N	0.57	SignalP-noTM
gi_188523156_gb_ACD61101.1_	0.122	20	0.131	25	0.173	34	0.124	0.128	N	0.57	SignalP-noTM
gi_188523158_gb_ACD61103.1_	0.225	57	0.18	30	0.402	28	0.203	0.191	N	0.57	SignalP-noTM
gi_188523160_gb_ACD61105.1_	0.364	19	0.38	19	0.638	15	0.405	0.392	N	0.57	SignalP-noTM
gi_188523161_gb_ACD61106.1_	0.129	36	0.11	36	0.177	10	0.092	0.101	N	0.57	SignalP-noTM
gi_188523162_gb_ACD61107.1_	0.125	40	0.114	40	0.123	39	0.096	0.106	N	0.57	SignalP-noTM
gi_188523163_gb_ACD61108.1_	0.106	29	0.109	29	0.126	20	0.104	0.107	N	0.57	SignalP-noTM
gi_188523164_gb_ACD61109.1_	0.135	36	0.138	16	0.239	8	0.183	0.159	N	0.57	SignalP-noTM
gi_188523165_gb_ACD61110.1_	0.107	48	0.105	53	0.165	1	0.099	0.102	N	0.57	SignalP-noTM
gi_188523166_gb_ACD61111.1_	0.16	20	0.184	20	0.426	2	0.257	0.218	N	0.57	SignalP-noTM
gi_188523167_gb_ACD61112.1_	0.166	33	0.145	33	0.204	1	0.13	0.139	N	0.51	SignalP-TM
gi_188523168_gb_ACD61113.1_	0.133	25	0.155	25	0.266	1	0.195	0.17	N	0.51	SignalP-TM
gi_188523169_gb_ACD61114.1_	0.143	45	0.156	45	0.204	36	0.104	0.137	N	0.51	SignalP-TM
gi_188523170_gb_ACD61115.1_	0.216	28	0.193	28	0.433	1	0.216	0.202	N	0.51	SignalP-TM
gi_188523172_gb_ACD61117.1_	0.127	31	0.118	31	0.131	16	0.105	0.112	N	0.57	SignalP-noTM
gi_188523173_gb_ACD61118.1_	0.148	32	0.121	32	0.109	31	0.088	0.105	N	0.57	SignalP-noTM
gi_188523174_gb_ACD61119.1_	0.587	22	0.656	22	0.878	1	0.767	0.708	Y	0.57	SignalP-noTM
gi_188523260_gb_ACD61205.1_	0.101	22	0.101	11	0.138	1	0.099	0.1	N	0.57	SignalP-noTM
gi_188523267_gb_ACD61212.1_	0.154	21	0.287	21	0.637	13	0.518	0.373	N	0.51	SignalP-TM
gi_188523268_gb_ACD61213.1_	0.19	21	0.184	26	0.343	25	0.185	0.184	N	0.57	SignalP-noTM
gi_188523269_gb_ACD61214.1_	0.192	19	0.288	19	0.796	8	0.509	0.392	N	0.57	SignalP-noTM
gi_188523271_gb_ACD61216.1_	0.127	28	0.127	66	0.181	59	0.103	0.118	N	0.51	SignalP-TM
gi_188523275_gb_ACD61220.1_	0.101	36	0.133	19	0.27	17	0.165	0.148	N	0.57	SignalP-noTM
gi_188523278_gb_ACD61223.1_	0.114	26	0.185	11	0.454	5	0.351	0.263	N	0.57	SignalP-noTM
gi_188523280_gb_ACD61225.1_	0.14	46	0.166	11	0.41	1	0.264	0.212	N	0.57	SignalP-noTM
gi_188523281_gb_ACD61226.1_	0.126	44	0.11	22	0.141	20	0.119	0.114	N	0.57	SignalP-noTM
gi_188523282_gb_ACD61227.1_	0.14	55	0.116	55	0.148	9	0.104	0.11	N	0.57	SignalP-noTM
gi_188523290_gb_ACD61235.1_	0.115	21	0.11	38	0.149	36	0.095	0.103	N	0.57	SignalP-noTM
gi_188523293_gb_ACD61238.1_	0.123	22	0.153	11	0.348	3	0.236	0.192	N	0.57	SignalP-noTM
gi_188523295_gb_ACD61240.1_	0.141	27	0.109	48	0.107	43	0.077	0.094	N	0.57	SignalP-noTM
gi_188523297_gb_ACD61242.1_	0.156	27	0.118	48	0.15	53	0.076	0.098	N	0.57	SignalP-noTM
gi_188523299_gb_ACD61244.1_	0.241	19	0.364	19	0.732	9	0.547	0.45	N	0.57	SignalP-noTM
gi_188523300_gb_ACD61245.1_	0.542	20	0.541	20	0.623	17	0.495	0.52	N	0.57	SignalP-noTM
gi_188523301_gb_ACD61246.1_	0.134	58	0.133	11	0.219	1	0.167	0.149	N	0.57	SignalP-noTM
gi_188523303_gb_ACD61248.1_	0.166	30	0.218	30	0.416	2	0.278	0.24	N	0.51	SignalP-TM
gi_188523304_gb_ACD61249.1_	0.145	31	0.124	37	0.128	29	0.096	0.111	N	0.57	SignalP-noTM
gi_188523305_gb_ACD61250.1_	0.109	11	0.093	37	0.097	23	0.072	0.083	N	0.57	SignalP-noTM
gi_188523306_gb_ACD61251.1_	0.224	28	0.153	22	0.22	7	0.152	0.153	N	0.51	SignalP-TM
gi_188523311_gb_ACD61256.1_	0.134	35	0.151	35	0.319	28	0.136	0.144	N	0.57	SignalP-noTM
gi_188523315_gb_ACD61260.1_	0.139	23	0.162	11	0.35	1	0.265	0.2	N	0.51	SignalP-TM
gi_188523316_gb_ACD61261.1_	0.245	25	0.263	25	0.533	6	0.349	0.303	N	0.57	SignalP-noTM
gi_188523317_gb_ACD61262.1_	0.768	30	0.798	30	0.958	19	0.871	0.832	Y	0.57	SignalP-noTM
gi_188523320_gb_ACD61265.1_	0.117	37	0.112	46	0.141	40	0.092	0.103	N	0.57	SignalP-noTM
gi_188523321_gb_ACD61266.1_	0.13	47	0.201	47	0.476	38	0.18	0.191	N	0.57	SignalP-noTM
gi_188523322_gb_ACD61267.1_	0.118	47	0.124	12	0.193	10	0.155	0.139	N	0.57	SignalP-noTM
gi_188523323_gb_ACD61268.1_	0.121	59	0.116	32	0.158	28	0.119	0.117	N	0.51	SignalP-TM
gi_188523329_gb_ACD61274.1_	0.135	39	0.113	39	0.113	38	0.081	0.098	N	0.57	SignalP-noTM
gi_188523333_gb_ACD61278.1_	0.116	24	0.118	24	0.154	21	0.113	0.116	N	0.57	SignalP-noTM
gi_188523334_gb_ACD61279.1_	0.149	20	0.184	20	0.291	15	0.196	0.189	N	0.51	SignalP-TM
gi_188523336_gb_ACD61281.1_	0.139	28	0.251	15	0.723	10	0.589	0.41	N	0.57	SignalP-noTM
gi_188523346_gb_ACD61291.1_	0.107	29	0.184	11	0.426	1	0.338	0.257	N	0.57	SignalP-noTM
gi_188523348_gb_ACD61293.1_	0.231	39	0.178	39	0.35	2	0.193	0.184	N	0.51	SignalP-TM
gi_188523349_gb_ACD61294.1_	0.784	28	0.286	28	0.163	1	0.121	0.209	N	0.57	SignalP-noTM
gi_188523350_gb_ACD61295.1_	0.115	37	0.139	11	0.325	10	0.189	0.162	N	0.57	SignalP-noTM
gi_188523356_gb_ACD61301.1_	0.153	33	0.142	33	0.222	31	0.131	0.137	N	0.57	SignalP-noTM
gi_188523357_gb_ACD61302.1_	0.119	44	0.106	44	0.12	50	0.081	0.094	N	0.57	SignalP-noTM
gi_188523360_gb_ACD61305.1_	0.141	65	0.134	33	0.282	32	0.15	0.141	N	0.57	SignalP-noTM
gi_188523361_gb_ACD61306.1_	0.116	29	0.146	11	0.337	2	0.197	0.17	N	0.57	SignalP-noTM
gi_188523362_gb_ACD61307.1_	0.105	39	0.12	15	0.17	11	0.144	0.131	N	0.57	SignalP-noTM
gi_188523363_gb_ACD61308.1_	0.144	41	0.151	11	0.341	1	0.215	0.181	N	0.57	SignalP-noTM
gi_188523364_gb_ACD61309.1_	0.364	33	0.235	33	0.244	30	0.135	0.188	N	0.57	SignalP-noTM
gi_188523365_gb_ACD61310.1_	0.126	37	0.12	37	0.179	25	0.089	0.106	N	0.57	SignalP-noTM
gi_188523366_gb_ACD61311.1_	0.133	48	0.119	27	0.167	1	0.121	0.12	N	0.57	SignalP-noTM
gi_188523367_gb_ACD61312.1_	0.139	22	0.134	22	0.196	1	0.138	0.136	N	0.57	SignalP-noTM
gi_188523370_gb_ACD61315.1_	0.144	46	0.139	46	0.173	44	0.094	0.118	N	0.57	SignalP-noTM
gi_188523371_gb_ACD61316.1_	0.207	46	0.132	46	0.176	11	0.102	0.118	N	0.57	SignalP-noTM
gi_188523372_gb_ACD61317.1_	0.11	35	0.113	18	0.156	9	0.121	0.117	N	0.57	SignalP-noTM
gi_188523373_gb_ACD61318.1_	0.199	23	0.309	23	0.575	21	0.434	0.368	N	0.57	SignalP-noTM
gi_188523375_gb_ACD61320.1_	0.101	32	0.202	11	0.47	10	0.402	0.296	N	0.57	SignalP-noTM
gi_188523376_gb_ACD61321.1_	0.207	22	0.181	11	0.438	1	0.324	0.234	N	0.51	SignalP-TM
gi_188523377_gb_ACD61322.1_	0.14	53	0.141	11	0.312	1	0.183	0.161	N	0.57	SignalP-noTM
gi_188523378_gb_ACD61323.1_	0.336	43	0.164	43	0.1	55	0.074	0.122	N	0.57	SignalP-noTM
gi_188523379_gb_ACD61324.1_	0.145	28	0.124	28	0.149	19	0.089	0.107	N	0.57	SignalP-noTM
gi_188523381_gb_ACD61326.1_	0.115	22	0.146	13	0.28	9	0.215	0.178	N	0.57	SignalP-noTM

0.237398	0.881216	0.186032	0.434882	gi_188523404_gb_ACD61349.1_
0.235772	0.067358	0.158691	0.15394	gi_188523405_gb_ACD61350.1_
0.114457	0.09984	0.211318	0.141872	gi_188523410_gb_ACD61355.1_
0.102845	0.078928	0.187399	0.123057	gi_188523411_gb_ACD61356.1_
0.341414	0.078928	0.422627	0.28099	gi_188523412_gb_ACD61357.1_
0.898803	0.50675	0.869778	0.758444	gi_188523414_gb_ACD61359.1_
0.447692	0.159092	0.514246	0.373677	gi_188523415_gb_ACD61360.1_
0.071028	0.037906	0.107647	0.072194	gi_188523416_gb_ACD61361.1_
0.103123	0.066982	0.165619	0.111908	gi_188523417_gb_ACD61362.1_
0.966625	0.985741	0.876749	0.943038	gi_188523418_gb_ACD61363.1_
0.871804	0.997006	0.821127	0.896646	gi_188523419_gb_ACD61364.1_
0.87804	0.993867	0.83355	0.901819	gi_188523420_gb_ACD61365.1_
0.086669	0.031768	0.109975	0.076137	gi_188523421_gb_ACD61366.1_
0.507499	0.983665	0.707857	0.733007	gi_188523425_gb_ACD61370.1_
0.948339	0.954174	0.936672	0.946395	gi_188523427_gb_ACD61372.1_
0.115986	0.089806	0.190618	0.132137	gi_188523428_gb_ACD61373.1_
0.159896	0.186032	0.151228	0.165719	gi_188523429_gb_ACD61374.1_
0.551566	0.931311	0.684386	0.722421	gi_188523432_gb_ACD61377.1_
0.645656	0.567829	0.70537	0.639618	gi_188523433_gb_ACD61378.1_
0.096129	0.050787	0.108806	0.085241	gi_188523434_gb_ACD61379.1_
0.068689	0.051515	0.082944	0.067716	gi_188523435_gb_ACD61380.1_
0.944538	0.999977	0.811227	0.918581	gi_188523436_gb_ACD61381.1_
0.14295	0.081585	0.157892	0.127476	gi_188523437_gb_ACD61382.1_
0.086195	0.012481	0.177118	0.091931	gi_188523438_gb_ACD61383.1_
0.748758	0.184222	0.776953	0.569978	gi_188523439_gb_ACD61384.1_
0.953779	0.980334	0.89853	0.944214	gi_188523440_gb_ACD61385.1_
0.26386	0.029627	0.398672	0.23072	gi_188523441_gb_ACD61386.1_
0.089562	0.06262	0.174078	0.108753	gi_188523442_gb_ACD61387.1_
0.269138	0.633207	0.29713	0.399825	gi_188523444_gb_ACD61389.1_
0.141851	0.001417	0.161921	0.10173	gi_188523445_gb_ACD61390.1_
0.149313	0.040272	0.209325	0.13297	gi_188523446_gb_ACD61391.1_
0.190156	0.508999	0.154727	0.284627	gi_188523447_gb_ACD61392.1_
0.126198	0.078928	0.191545	0.132224	gi_188523448_gb_ACD61393.1_
0.150077	0.105647	0.154335	0.136686	gi_188523449_gb_ACD61394.1_
0.169384	0.093299	0.175375	0.146019	gi_188523451_gb_ACD61396.1_
0.120363	0.064586	0.148932	0.111294	gi_188523453_gb_ACD61398.1_
0.100652	0.065681	0.115679	0.094004	gi_188523456_gb_ACD61401.1_
0.085021	0.003256	0.064949	0.051075	gi_188523457_gb_ACD61402.1_
0.344117	0.360545	0.425557	0.37674	gi_188523459_gb_ACD61404.1_
0.698465	0.846447	0.703496	0.749469	gi_188523460_gb_ACD61405.1_
0.198611	0.096129	0.229878	0.174873	gi_188523462_gb_ACD61407.1_
0.088588	0.403717	0.158691	0.216999	gi_188523463_gb_ACD61408.1_
0.135404	0.128196	0.208334	0.157311	gi_188523469_gb_ACD61414.1_
0.094576	0.018271	0.102018	0.071622	gi_188523470_gb_ACD61415.1_
0.888251	0.807524	0.850306	0.848694	gi_188523471_gb_ACD61416.1_
0.078276	0.229347	0.076139	0.127921	gi_188523472_gb_ACD61417.1_
0.169384	0.047562	0.228818	0.148588	gi_188523473_gb_ACD61418.1_
0.645656	0.928774	0.878681	0.817704	gi_188523474_gb_ACD61419.1_
0.167284	0.001946	0.204403	0.124544	gi_188523475_gb_ACD61420.1_
0.35503	0.148552	0.326733	0.276772	gi_188523477_gb_ACD61422.1_
0.132964	0.017074	0.122927	0.090988	gi_188523483_gb_ACD61428.1_
0.147418	0.011521	0.162737	0.107225	gi_188523484_gb_ACD61429.1_
0.159092	0.550082	0.123251	0.277475	gi_188523488_gb_ACD61433.1_
0.13717	0.025234	0.23041	0.130938	gi_188523494_gb_ACD61439.1_
0.063685	0.041091	0.108515	0.071097	gi_188523496_gb_ACD61441.1_
0.299643	0.16645	0.424824	0.296972	gi_188523502_gb_ACD61447.1_
0.875773	0.980101	0.876099	0.910658	gi_188523506_gb_ACD61451.1_
0.907207	0.858878	0.879319	0.881801	gi_188523508_gb_ACD61453.1_
0.292763	0.642217	0.35503	0.430003	gi_188523509_gb_ACD61454.1_
0.155513	0.069074	0.149694	0.12476	gi_188523510_gb_ACD61455.1_
0.105081	0.062269	0.14295	0.103433	gi_188523511_gb_ACD61456.1_
0.107072	0.376601	0.263278	0.248984	gi_188523512_gb_ACD61457.1_
0.214333	0.942784	0.109681	0.422266	gi_188523514_gb_ACD61459.1_
0.16645	0.104238	0.1603	0.143663	gi_188523517_gb_ACD61462.1_
0.195761	0.084556	0.232544	0.170954	gi_188523520_gb_ACD61465.1_
0.151228	0.163557	0.21032	0.175035	gi_188523521_gb_ACD61466.1_
0.083862	0.056572	0.08883	0.076421	gi_188523524_gb_ACD61469.1_
0.067547	0.035571	0.081361	0.061493	gi_188523525_gb_ACD61470.1_
0.043025	0.094063	0.143687	0.093592	gi_188523526_gb_ACD61471.1_
0.721919	0.821567	0.810306	0.784597	gi_188523529_gb_ACD61474.1_
0.177994	0.184222	0.08181	0.148009	gi_188523532_gb_ACD61477.1_
0.098767	0.085021	0.096651	0.09348	gi_188523536_gb_ACD61481.1_
0.805652	0.999459	0.881843	0.895651	gi_188523543_gb_ACD61488.1_
0.166034	0.315614	0.1034	0.195016	gi_188523544_gb_ACD61489.1_
0.215346	0.943107	0.112346	0.4236	gi_188523545_gb_ACD61490.1_
0.44695	0.299013	0.48051	0.408824	gi_188523546_gb_ACD61491.1_
0.097176	0.041806	0.07871	0.072564	gi_188523550_gb_ACD61495.1_
0.179314	0.084092	0.185126	0.149511	gi_188521883_gb_ACD59828.1_

gi_188523382_gb_ACD61327.1_	0.136	28	0.162	26	0.265	6	0.216	0.188	N	0.57	SignalP-noTM
gi_188523383_gb_ACD61328.1_	0.143	42	0.106	42	0.153	2	0.082	0.095	N	0.57	SignalP-noTM
gi_188523384_gb_ACD61329.1_	0.174	27	0.16	20	0.271	1	0.182	0.17	N	0.57	SignalP-noTM
gi_188523385_gb_ACD61330.1_	0.375	38	0.268	38	0.49	1	0.223	0.251	N	0.51	SignalP-TM
gi_188523386_gb_ACD61331.1_	0.122	70	0.147	11	0.286	3	0.218	0.181	N	0.57	SignalP-noTM
gi_188523392_gb_ACD61337.1_	0.155	70	0.145	11	0.262	3	0.224	0.182	N	0.57	SignalP-noTM
gi_188523393_gb_ACD61338.1_	0.102	15	0.13	11	0.252	3	0.17	0.149	N	0.57	SignalP-noTM
gi_188523394_gb_ACD61339.1_	0.11	36	0.139	11	0.258	3	0.194	0.165	N	0.57	SignalP-noTM
gi_188523395_gb_ACD61340.1_	0.102	37	0.11	11	0.137	1	0.119	0.114	N	0.57	SignalP-noTM
gi_188523396_gb_ACD61341.1_	0.128	42	0.145	14	0.251	5	0.209	0.175	N	0.57	SignalP-noTM
gi_188523397_gb_ACD61342.1_	0.113	35	0.108	68	0.115	69	0.084	0.096	N	0.57	SignalP-noTM
gi_188523400_gb_ACD61345.1_	0.137	51	0.123	31	0.217	1	0.126	0.124	N	0.51	SignalP-TM
gi_188523404_gb_ACD61349.1_	0.178	25	0.212	40	0.518	44	0.249	0.23	N	0.57	SignalP-noTM
gi_188523405_gb_ACD61350.1_	0.26	31	0.163	31	0.148	3	0.093	0.13	N	0.57	SignalP-noTM
gi_188523410_gb_ACD61355.1_	0.11	24	0.121	11	0.21	3	0.154	0.133	N	0.51	SignalP-TM
gi_188523411_gb_ACD61356.1_	0.187	35	0.188	19	0.316	2	0.233	0.205	N	0.51	SignalP-TM
gi_188523412_gb_ACD61357.1_	0.161	24	0.164	24	0.259	13	0.167	0.165	N	0.51	SignalP-TM
gi_188523414_gb_ACD61359.1_	0.152	27	0.226	11	0.628	3	0.534	0.34	N	0.51	SignalP-TM
gi_188523415_gb_ACD61360.1_	0.524	44	0.447	44	0.495	28	0.262	0.379	N	0.51	SignalP-TM
gi_188523416_gb_ACD61361.1_	0.233	48	0.236	48	0.457	46	0.126	0.184	N	0.57	SignalP-noTM
gi_188523417_gb_ACD61362.1_	0.142	35	0.145	18	0.293	1	0.18	0.161	N	0.57	SignalP-noTM
gi_188523418_gb_ACD61363.1_	0.144	20	0.108	58	0.136	49	0.086	0.098	N	0.57	SignalP-noTM
gi_188523419_gb_ACD61364.1_	0.196	23	0.315	23	0.862	1	0.621	0.459	N	0.57	SignalP-noTM
gi_188523420_gb_ACD61365.1_	0.248	20	0.474	20	0.948	8	0.911	0.679	Y	0.57	SignalP-noTM
gi_188523421_gb_ACD61366.1_	0.145	20	0.132	20	0.216	2	0.13	0.131	N	0.57	SignalP-noTM
gi_188523425_gb_ACD61370.1_	0.114	27	0.179	27	0.339	21	0.262	0.218	N	0.57	SignalP-noTM
gi_188523427_gb_ACD61372.1_	0.34	69	0.289	21	0.495	15	0.339	0.307	N	0.51	SignalP-TM
gi_188523428_gb_ACD61373.1_	0.155	17	0.138	53	0.224	29	0.121	0.13	N	0.57	SignalP-noTM
gi_188523429_gb_ACD61374.1_	0.303	39	0.182	39	0.255	2	0.11	0.148	N	0.57	SignalP-noTM
gi_188523432_gb_ACD61377.1_	0.129	10	0.175	12	0.376	4	0.318	0.242	N	0.57	SignalP-noTM
gi_188523433_gb_ACD61378.1_	0.232	45	0.297	45	0.513	36	0.257	0.282	N	0.51	SignalP-TM
gi_188523434_gb_ACD61379.1_	0.531	21	0.713	21	0.971	13	0.943	0.821	Y	0.57	SignalP-noTM
gi_188523435_gb_ACD61380.1_	0.118	26	0.097	69	0.117	3	0.085	0.092	N	0.57	SignalP-noTM
gi_188523436_gb_ACD61381.1_	0.138	5	0.144	19	0.268	9	0.17	0.156	N	0.57	SignalP-noTM
gi_188523437_gb_ACD61382.1_	0.158	48	0.152	48	0.352	1	0.168	0.159	N	0.57	SignalP-noTM
gi_188523438_gb_ACD61383.1_	0.215	27	0.235	27	0.63	5	0.388	0.292	N	0.51	SignalP-TM
gi_188523439_gb_ACD61384.1_	0.301	15	0.524	15	0.976	9	0.901	0.701	Y	0.57	SignalP-noTM
gi_188523440_gb_ACD61385.1_	0.86	24	0.835	24	0.936	17	0.844	0.839	Y	0.57	SignalP-noTM
gi_188523441_gb_ACD61386.1_	0.125	29	0.13	11	0.239	2	0.173	0.15	N	0.57	SignalP-noTM
gi_188523442_gb_ACD61387.1_	0.107	28	0.095	68	0.103	10	0.085	0.09	N	0.57	SignalP-noTM
gi_188523444_gb_ACD61389.1_	0.156	42	0.146	42	0.234	19	0.152	0.149	N	0.57	SignalP-noTM
gi_188523445_gb_ACD61390.1_	0.189	44	0.214	44	0.481	11	0.223	0.218	N	0.57	SignalP-noTM
gi_188523446_gb_ACD61391.1_	0.127	34	0.137	54	0.241	48	0.123	0.131	N	0.57	SignalP-noTM
gi_188523447_gb_ACD61392.1_	0.252	32	0.11	32	0.147	1	0.081	0.099	N	0.51	SignalP-TM
gi_188523448_gb_ACD61393.1_	0.121	26	0.124	11	0.275	1	0.14	0.13	N	0.51	SignalP-TM
gi_188523449_gb_ACD61394.1_	0.14	23	0.128	56	0.221	49	0.09	0.11	N	0.57	SignalP-noTM
gi_188523451_gb_ACD61396.1_	0.151	33	0.141	33	0.269	1	0.151	0.145	N	0.51	SignalP-TM
gi_188523453_gb_ACD61398.1_	0.137	25	0.145	25	0.335	24	0.146	0.146	N	0.57	SignalP-noTM
gi_188523456_gb_ACD61401.1_	0.211	30	0.158	30	0.206	36	0.129	0.144	N	0.57	SignalP-noTM
gi_188523457_gb_ACD61402.1_	0.167	21	0.163	21	0.247	3	0.186	0.171	N	0.51	SignalP-TM
gi_188523459_gb_ACD61404.1_	0.836	21	0.867	21	0.943	19	0.883	0.875	Y	0.57	SignalP-noTM
gi_188523460_gb_ACD61405.1_	0.123	20	0.128	20	0.178	2	0.139	0.133	N	0.57	SignalP-noTM
gi_188523462_gb_ACD61407.1_	0.105	45	0.136	11	0.262	3	0.179	0.156	N	0.57	SignalP-noTM
gi_188523463_gb_ACD61408.1_	0.109	32	0.102	57	0.12	50	0.093	0.098	N	0.57	SignalP-noTM
gi_188523469_gb_ACD61414.1_	0.101	32	0.114	27	0.168	22	0.116	0.115	N	0.51	SignalP-TM
gi_188523470_gb_ACD61415.1_	0.135	21	0.141	21	0.278	27	0.154	0.147	N	0.57	SignalP-noTM
gi_188523471_gb_ACD61416.1_	0.353	26	0.589	26	0.993	15	0.977	0.771	Y	0.57	SignalP-noTM
gi_188523472_gb_ACD61417.1_	0.103	29	0.103	29	0.117	27	0.096	0.1	N	0.57	SignalP-noTM
gi_188523473_gb_ACD61418.1_	0.202	20	0.202	20	0.326	29	0.203	0.202	N	0.51	SignalP-TM
gi_188523474_gb_ACD61419.1_	0.143	20	0.156	11	0.445	2	0.229	0.19	N	0.57	SignalP-noTM
gi_188523475_gb_ACD61420.1_	0.106	31	0.116	11	0.198	2	0.134	0.124	N	0.57	SignalP-noTM
gi_188523477_gb_ACD61422.1_	0.119	30	0.102	30	0.108	29	0.075	0.089	N	0.57	SignalP-noTM
gi_188523483_gb_ACD61428.1_	0.411	21	0.358	21	0.512	16	0.275	0.319	N	0.57	SignalP-noTM
gi_188523484_gb_ACD61429.1_	0.108	30	0.116	11	0.2	2	0.129	0.122	N	0.57	SignalP-noTM
gi_188523488_gb_ACD61433.1_	0.105	20	0.102	62	0.136	1	0.094	0.098	N	0.57	SignalP-noTM
gi_188523494_gb_ACD61439.1_	0.311	26	0.199	26	0.243	22	0.109	0.157	N	0.57	SignalP-noTM
gi_188523496_gb_ACD61441.1_	0.109	62	0.105	18	0.134	14	0.109	0.107	N	0.57	SignalP-noTM
gi_188523502_gb_ACD61447.1_	0.655	33	0.794	33	0.99	18	0.929	0.858	Y	0.57	SignalP-noTM
gi_188523506_gb_ACD61451.1_	0.339	30	0.436	30	0.732	24	0.548	0.489	N	0.57	SignalP-noTM
gi_188523508_gb_ACD61453.1_	0.138	47	0.178	22	0.354	19	0.257	0.215	N	0.57	SignalP-noTM
gi_188523509_gb_ACD61454.1_	0.156	42	0.144	42	0.208	19	0.137	0.141	N	0.57	SignalP-noTM
gi_188523510_gb_ACD61455.1_	0.128	29	0.123	29	0.141	26	0.098	0.111	N	0.57	SignalP-noTM
gi_188523511_gb_ACD61456.1_	0.111	26	0.1	65	0.105	34	0.078	0.089	N	0.57	SignalP-noTM
gi_188523512_gb_ACD61457.1_	0.134	28	0.162	14	0.343	1	0.256	0.197	N	0.51	SignalP-TM
gi_188523514_gb_ACD61459.1_	0.111	9	0.106	68	0.124	62	0.09	0.098	N	0.57	SignalP-noTM
gi_188523517_gb_ACD61462.1_	0.166	17	0.139	17	0.335	1	0.151	0.144	N	0.51	SignalP-TM
gi_188523520_gb_ACD61465.1_	0.13	37	0.136	11	0.273	2	0.18	0.156	N	0.57	SignalP-noTM
gi_188523521_gb_ACD61466.1_	0.118	15	0.127	11	0.204	7	0.158	0.138	N	0.51	SignalP-TM

0.262697	0.935414	0.158291	0.452134	gi_188521884_gb_ACD59829.1_
0.106215	0.050642	0.109389	0.088749	gi_188521885_gb_ACD59830.1_
0.072831	0.363316	0.120045	0.185397	gi_188521886_gb_ACD59831.1_
0.097969	0.01356	0.102569	0.071366	gi_188521887_gb_ACD59832.1_
0.094063	0.00049	0.14295	0.079168	gi_188521888_gb_ACD59833.1_
0.105647	0.022183	0.126529	0.084786	gi_188521889_gb_ACD59834.1_
0.195289	0.028113	0.220974	0.148125	gi_188521890_gb_ACD59835.1_
0.120681	0.235772	0.093046	0.149833	gi_188521891_gb_ACD59836.1_
0.101744	0.053454	0.09639	0.083863	gi_188521892_gb_ACD59837.1_
0.186943	0.020075	0.090298	0.099105	gi_188521894_gb_ACD59839.1_
0.639455	0.681137	0.770653	0.697082	gi_188521895_gb_ACD59840.1_
0.120363	0.132274	0.207839	0.153492	gi_188521901_gb_ACD59846.1_
0.882155	0.973247	0.67787	0.844424	gi_188521902_gb_ACD59847.1_
0.949213	0.973325	0.893214	0.938584	gi_188521906_gb_ACD59851.1_
0.920853	0.995082	0.872806	0.92958	gi_188521919_gb_ACD59864.1_
0.144427	0.005006	0.225133	0.124855	gi_188521920_gb_ACD59865.1_
0.110563	0.424824	0.089806	0.208398	gi_188521926_gb_ACD59871.1_
0.186943	0.854458	0.105364	0.382255	gi_188521928_gb_ACD59873.1_
0.664631	0.638763	0.638071	0.647155	gi_188521929_gb_ACD59874.1_
0.092289	0.038126	0.092541	0.074319	gi_188521930_gb_ACD59875.1_
0.075091	0.010477	0.099034	0.061534	gi_188521931_gb_ACD59876.1_
0.138955	0.132964	0.124881	0.132267	gi_188521932_gb_ACD59877.1_
0.096651	0.009613	0.134354	0.080206	gi_188521935_gb_ACD59880.1_
0.195761	0.004456	0.271505	0.157241	gi_188521936_gb_ACD59881.1_
0.126198	0.007923	0.126861	0.086994	gi_188521942_gb_ACD59887.1_
0.924909	0.999549	0.782109	0.902189	gi_188521944_gb_ACD59889.1_
0.099302	0.040855	0.111749	0.083969	gi_188521946_gb_ACD59891.1_
0.230942	0.998431	0.198134	0.475836	gi_188521952_gb_ACD59897.1_
0.330041	0.844487	0.464808	0.546445	gi_188521953_gb_ACD59898.1_
0.085489	0.031861	0.10736	0.074903	gi_188523558_gb_ACD61503.1_
0.203429	0.033667	0.229878	0.155658	gi_188523559_gb_ACD61504.1_
0.156699	0.087864	0.15046	0.131674	gi_188523560_gb_ACD61505.1_
0.350919	0.797057	0.419701	0.522559	gi_188523561_gb_ACD61506.1_
0.144427	0.031129	0.248991	0.141516	gi_188523563_gb_ACD61508.1_
0.247871	0.751009	0.158291	0.385724	gi_188523564_gb_ACD61509.1_
0.594837	0.740775	0.781085	0.705566	gi_188523565_gb_ACD61510.1_
0.173647	0.792161	0.102018	0.355942	gi_188523566_gb_ACD61511.1_
0.930733	0.869438	0.890611	0.896927	gi_188523567_gb_ACD61512.1_
0.890319	0.557495	0.58686	0.678225	gi_188523568_gb_ACD61513.1_
0.86283	0.82977	0.774867	0.822489	gi_188523569_gb_ACD61514.1_
0.953514	0.994701	0.904132	0.950782	gi_188523570_gb_ACD61515.1_
0.123251	0.957344	0.198134	0.426243	gi_188523571_gb_ACD61516.1_
0.852582	0.956353	0.858514	0.88915	gi_188523573_gb_ACD61518.1_
0.461824	0.10736	0.603483	0.390889	gi_188523574_gb_ACD61519.1_
0.942945	0.640146	0.905937	0.829676	gi_188523579_gb_ACD61524.1_
0.870118	0.922799	0.744216	0.845711	gi_188523580_gb_ACD61525.1_
0.869097	0.977357	0.840104	0.895519	gi_188523581_gb_ACD61526.1_
0.165619	0.269138	0.132619	0.189125	gi_188523582_gb_ACD61527.1_
0.116294	0.041806	0.125209	0.094436	gi_188523585_gb_ACD61530.1_
0.107647	0.023454	0.155907	0.095669	gi_188523587_gb_ACD61532.1_
0.375897	0.954826	0.188773	0.506499	gi_188523588_gb_ACD61533.1_
0.090298	0.029455	0.105647	0.075133	gi_188523589_gb_ACD61534.1_
0.200047	0.149694	0.237941	0.195894	gi_188523591_gb_ACD61536.1_
0.121639	0.030502	0.159092	0.103744	gi_188523592_gb_ACD61537.1_
0.112346	0.003067	0.184673	0.100029	gi_188523593_gb_ACD61538.1_
0.112346	0.145916	0.114762	0.124341	gi_188523594_gb_ACD61539.1_
0.290285	0.021796	0.373788	0.228623	gi_188523595_gb_ACD61540.1_
0.929169	0.822006	0.882155	0.877777	gi_188523598_gb_ACD61543.1_
0.657236	0.330041	0.868756	0.618678	gi_188523599_gb_ACD61544.1_
0.156699	0.054526	0.144427	0.118551	gi_188523600_gb_ACD61545.1_
0.102569	0.397953	0.085021	0.195181	gi_188523602_gb_ACD61547.1_
0.106215	0.076775	0.123251	0.10208	gi_188523604_gb_ACD61549.1_
0.079805	0.01984	0.100652	0.066766	gi_188523605_gb_ACD61550.1_
0.087384	0.012297	0.132619	0.077433	gi_188523606_gb_ACD61551.1_
0.137881	0.016873	0.143687	0.09948	gi_188523607_gb_ACD61552.1_
0.140759	0.055305	0.172787	0.12295	gi_188523608_gb_ACD61553.1_
0.857417	0.040973	0.835208	0.577866	gi_188523611_gb_ACD61556.1_
0.392933	0.892064	0.638763	0.641253	gi_188523612_gb_ACD61557.1_
0.088588	0.044532	0.105931	0.079684	gi_188523613_gb_ACD61558.1_
0.178433	0.234154	0.207346	0.206644	gi_188523614_gb_ACD61559.1_
0.219943	0.186943	0.230942	0.212609	gi_188523620_gb_ACD61565.1_
0.21032	0.902031	0.208829	0.440393	gi_188523623_gb_ACD61568.1_
0.334033	0.961097	0.415324	0.570151	gi_188523626_gb_ACD61571.1_
0.635295	0.872806	0.718291	0.742131	gi_188523627_gb_ACD61572.1_
0.942459	0.992601	0.875773	0.936944	gi_188523629_gb_ACD61574.1_
0.065866	0.035778	0.094833	0.065492	gi_188523633_gb_ACD61578.1_
0.176245	0.02465	0.22461	0.141835	gi_188523634_gb_ACD61579.1_
0.152775	0.438808	0.122927	0.23817	gi_188521954_gb_ACD59899.1_

gi_188523524_gb_ACD61469.1_	0.125	40	0.1	40	0.11	12	0.084	0.092	N	0.57	SignalP-noTM
gi_188523525_gb_ACD61470.1_	0.13	45	0.128	25	0.185	20	0.143	0.135	N	0.57	SignalP-noTM
gi_188523526_gb_ACD61471.1_	0.185	19	0.143	19	0.193	18	0.112	0.128	N	0.57	SignalP-noTM
gi_188523529_gb_ACD61474.1_	0.115	22	0.146	13	0.28	9	0.215	0.178	N	0.57	SignalP-noTM
gi_188523532_gb_ACD61477.1_	0.277	33	0.179	33	0.167	32	0.109	0.146	N	0.57	SignalP-noTM
gi_188523536_gb_ACD61481.1_	0.159	19	0.132	19	0.161	38	0.104	0.119	N	0.57	SignalP-noTM
gi_188523543_gb_ACD61488.1_	0.115	23	0.151	13	0.338	12	0.214	0.18	N	0.57	SignalP-noTM
gi_188523544_gb_ACD61489.1_	0.111	27	0.123	11	0.202	5	0.163	0.138	N	0.51	SignalP-TM
gi_188523545_gb_ACD61490.1_	0.111	9	0.11	36	0.136	28	0.082	0.097	N	0.57	SignalP-noTM
gi_188523546_gb_ACD61491.1_	0.123	22	0.131	27	0.178	36	0.128	0.13	N	0.57	SignalP-noTM
gi_188523550_gb_ACD61495.1_	0.103	21	0.107	50	0.123	28	0.101	0.104	N	0.57	SignalP-noTM
gi_188523558_gb_ACD61503.1_	0.167	30	0.135	30	0.214	47	0.102	0.119	N	0.57	SignalP-noTM
gi_188523559_gb_ACD61504.1_	0.12	26	0.134	26	0.208	22	0.141	0.137	N	0.57	SignalP-noTM
gi_188523560_gb_ACD61505.1_	0.138	67	0.115	11	0.176	7	0.138	0.123	N	0.51	SignalP-TM
gi_188523561_gb_ACD61506.1_	0.603	22	0.72	22	0.963	18	0.87	0.79	Y	0.57	SignalP-noTM
gi_188523563_gb_ACD61508.1_	0.258	29	0.226	29	0.351	8	0.205	0.218	N	0.51	SignalP-TM
gi_188523564_gb_ACD61509.1_	0.135	56	0.179	11	0.428	4	0.323	0.247	N	0.57	SignalP-noTM
gi_188523565_gb_ACD61510.1_	0.101	55	0.191	11	0.395	4	0.37	0.275	N	0.57	SignalP-noTM
gi_188523566_gb_ACD61511.1_	0.175	33	0.148	33	0.218	32	0.113	0.132	N	0.57	SignalP-noTM
gi_188523567_gb_ACD61512.1_	0.522	30	0.512	30	0.641	27	0.449	0.488	N	0.51	SignalP-TM
gi_188523568_gb_ACD61513.1_	0.104	8	0.102	23	0.122	14	0.096	0.099	N	0.57	SignalP-noTM
gi_188523569_gb_ACD61514.1_	0.27	13	0.349	13	0.723	10	0.45	0.396	N	0.57	SignalP-noTM
gi_188523570_gb_ACD61515.1_	0.741	20	0.731	20	0.843	1	0.73	0.73	Y	0.57	SignalP-noTM
gi_188523571_gb_ACD61516.1_	0.167	54	0.182	54	0.319	44	0.156	0.17	N	0.57	SignalP-noTM
gi_188523573_gb_ACD61518.1_	0.115	63	0.131	12	0.233	4	0.178	0.153	N	0.57	SignalP-noTM
gi_188523574_gb_ACD61519.1_	0.115	22	0.145	13	0.273	9	0.21	0.175	N	0.57	SignalP-noTM
gi_188523579_gb_ACD61524.1_	0.122	60	0.116	42	0.159	8	0.12	0.118	N	0.57	SignalP-noTM
gi_188523580_gb_ACD61525.1_	0.108	17	0.112	17	0.153	11	0.114	0.113	N	0.57	SignalP-noTM
gi_188523581_gb_ACD61526.1_	0.79	20	0.872	20	0.975	16	0.952	0.909	Y	0.57	SignalP-noTM
gi_188523582_gb_ACD61527.1_	0.153	28	0.192	19	0.463	13	0.329	0.257	N	0.57	SignalP-noTM
gi_188523585_gb_ACD61530.1_	0.847	19	0.79	19	0.834	16	0.701	0.748	Y	0.57	SignalP-noTM
gi_188523587_gb_ACD61532.1_	0.14	50	0.166	30	0.352	27	0.192	0.176	N	0.51	SignalP-TM
gi_188523588_gb_ACD61533.1_	0.169	37	0.153	37	0.365	34	0.115	0.135	N	0.57	SignalP-noTM
gi_188523589_gb_ACD61534.1_	0.105	20	0.104	62	0.133	1	0.094	0.099	N	0.57	SignalP-noTM
gi_188523591_gb_ACD61536.1_	0.111	28	0.223	12	0.523	1	0.455	0.332	N	0.57	SignalP-noTM
gi_188523592_gb_ACD61537.1_	0.186	27	0.114	27	0.148	51	0.079	0.098	N	0.57	SignalP-noTM
gi_188523593_gb_ACD61538.1_	0.123	30	0.103	30	0.105	34	0.081	0.093	N	0.57	SignalP-noTM
gi_188523594_gb_ACD61539.1_	0.105	13	0.117	11	0.201	1	0.125	0.121	N	0.57	SignalP-noTM
gi_188523595_gb_ACD61540.1_	0.138	54	0.135	11	0.216	8	0.189	0.16	N	0.57	SignalP-noTM
gi_188523598_gb_ACD61543.1_	0.134	20	0.211	20	0.492	2	0.366	0.284	N	0.57	SignalP-noTM
gi_188523599_gb_ACD61544.1_	0.156	34	0.124	11	0.231	1	0.145	0.134	N	0.57	SignalP-noTM
gi_188523600_gb_ACD61545.1_	0.15	41	0.119	41	0.173	2	0.105	0.113	N	0.57	SignalP-noTM
gi_188523602_gb_ACD61547.1_	0.115	42	0.095	34	0.139	1	0.077	0.087	N	0.57	SignalP-noTM
gi_188523604_gb_ACD61549.1_	0.107	18	0.098	28	0.122	3	0.09	0.095	N	0.57	SignalP-noTM
gi_188523605_gb_ACD61550.1_	0.118	42	0.104	42	0.104	26	0.084	0.094	N	0.57	SignalP-noTM
gi_188523606_gb_ACD61551.1_	0.214	57	0.237	35	0.499	6	0.353	0.292	N	0.57	SignalP-noTM
gi_188523607_gb_ACD61552.1_	0.126	55	0.1	69	0.145	1	0.081	0.091	N	0.57	SignalP-noTM
gi_188523608_gb_ACD61553.1_	0.119	29	0.161	11	0.333	1	0.248	0.202	N	0.57	SignalP-noTM
gi_188523611_gb_ACD61556.1_	0.433	31	0.558	31	0.985	13	0.868	0.704	Y	0.57	SignalP-noTM
gi_188523612_gb_ACD61557.1_	0.12	21	0.139	51	0.26	43	0.15	0.145	N	0.57	SignalP-noTM
gi_188523613_gb_ACD61558.1_	0.144	46	0.111	46	0.172	30	0.088	0.1	N	0.57	SignalP-noTM
gi_188523614_gb_ACD61559.1_	0.147	13	0.105	24	0.112	31	0.074	0.091	N	0.57	SignalP-noTM
gi_188523620_gb_ACD61565.1_	0.129	41	0.218	27	0.63	15	0.327	0.269	N	0.57	SignalP-noTM
gi_188523623_gb_ACD61568.1_	0.176	26	0.134	26	0.195	23	0.075	0.112	N	0.51	SignalP-TM
gi_188523626_gb_ACD61571.1_	0.236	34	0.263	34	0.429	25	0.231	0.251	N	0.51	SignalP-TM
gi_188523627_gb_ACD61572.1_	0.35	65	0.354	25	0.866	18	0.718	0.489	N	0.51	SignalP-TM
gi_188523629_gb_ACD61574.1_	0.16	38	0.159	30	0.268	2	0.17	0.164	N	0.57	SignalP-noTM
gi_188523633_gb_ACD61578.1_	0.117	28	0.098	67	0.103	58	0.069	0.084	N	0.57	SignalP-noTM
gi_188523634_gb_ACD61579.1_	0.125	23	0.166	11	0.362	2	0.27	0.215	N	0.57	SignalP-noTM
gi_188521883_gb_ACD59828.1_	0.2	17	0.242	17	0.351	12	0.265	0.251	N	0.51	SignalP-TM
gi_188521884_gb_ACD59829.1_	0.107	21	0.117	11	0.203	5	0.143	0.129	N	0.57	SignalP-noTM
gi_188521885_gb_ACD59830.1_	0.105	66	0.097	50	0.104	42	0.077	0.088	N	0.57	SignalP-noTM
gi_188521886_gb_ACD59831.1_	0.111	65	0.116	12	0.159	29	0.128	0.12	N	0.51	SignalP-TM
gi_188521887_gb_ACD59832.1_	0.124	55	0.126	12	0.208	3	0.163	0.143	N	0.57	SignalP-noTM
gi_188521888_gb_ACD59833.1_	0.132	33	0.105	33	0.112	70	0.078	0.092	N	0.57	SignalP-noTM
gi_188521889_gb_ACD59834.1_	0.139	36	0.142	36	0.273	32	0.127	0.135	N	0.57	SignalP-noTM
gi_188521890_gb_ACD59835.1_	0.133	23	0.171	23	0.373	7	0.25	0.2	N	0.51	SignalP-TM
gi_188521891_gb_ACD59836.1_	0.113	31	0.137	11	0.296	19	0.194	0.164	N	0.57	SignalP-noTM
gi_188521892_gb_ACD59837.1_	0.154	22	0.151	22	0.161	11	0.139	0.145	N	0.57	SignalP-noTM
gi_188521894_gb_ACD59839.1_	0.115	19	0.249	11	0.74	4	0.611	0.419	N	0.57	SignalP-noTM
gi_188521895_gb_ACD59840.1_	0.155	23	0.135	23	0.16	1	0.111	0.124	N	0.57	SignalP-noTM
gi_188521901_gb_ACD59846.1_	0.114	25	0.126	14	0.184	7	0.154	0.136	N	0.51	SignalP-TM
gi_188521902_gb_ACD59847.1_	0.114	23	0.141	11	0.325	1	0.176	0.157	N	0.57	SignalP-noTM
gi_188521906_gb_ACD59851.1_	0.114	26	0.122	11	0.172	3	0.154	0.137	N	0.57	SignalP-noTM
gi_188521919_gb_ACD59864.1_	0.104	5	0.111	21	0.155	1	0.119	0.114	N	0.57	SignalP-noTM
gi_188521920_gb_ACD59865.1_	0.115	41	0.119	11	0.191	1	0.138	0.128	N	0.57	SignalP-noTM
gi_188521926_gb_ACD59871.1_	0.109	50	0.11	50	0.144	3	0.1	0.105	N	0.57	SignalP-noTM
gi_188521928_gb_ACD59873.1_	0.111	9	0.106	68	0.124	62	0.09	0.098	N	0.57	SignalP-noTM

0.214333	0.225657	0.295879	0.24529	gi_188521955_gb_ACD59900.1_
0.928972	0.935776	0.86807	0.910939	gi_188521956_gb_ACD59901.1_
0.284144	0.90896	0.313674	0.502259	gi_188521961_gb_ACD59906.1_
0.253506	0.105081	0.136108	0.164898	gi_188521962_gb_ACD59907.1_
0.115679	0.055619	0.192476	0.121258	gi_188521963_gb_ACD59908.1_
0.141486	0.427759	0.097704	0.222316	gi_188521964_gb_ACD59909.1_
0.104799	0.040156	0.162329	0.102428	gi_188521965_gb_ACD59910.1_
0.083173	0.036509	0.115679	0.078454	gi_188521966_gb_ACD59911.1_
0.841309	0.066236	0.771711	0.559752	gi_188521967_gb_ACD59912.1_
0.302167	0.989615	0.110859	0.467547	gi_188521970_gb_ACD59915.1_
0.24177	0.085255	0.299643	0.208889	gi_188521975_gb_ACD59920.1_
0.559714	0.322785	0.707237	0.529912	gi_188521979_gb_ACD59924.1_
0.556014	0.138238	0.58904	0.427764	gi_188521980_gb_ACD59925.1_
0.934686	0.999878	0.879001	0.937855	gi_188521981_gb_ACD59926.1_
0.940307	0.990301	0.900698	0.943769	gi_188522328_gb_ACD60273.1_
0.858514	0.927775	0.752129	0.846139	gi_188522330_gb_ACD60275.1_
0.135053	0.029369	0.17023	0.111551	gi_188522331_gb_ACD60276.1_
0.945936	0.998928	0.895201	0.946688	gi_188522333_gb_ACD60278.1_
0.951478	0.984556	0.897982	0.944672	gi_188522334_gb_ACD60279.1_
0.083402	0.117222	0.174078	0.124901	gi_188522336_gb_ACD60281.1_
0.080247	0.059357	0.127862	0.089155	gi_188522339_gb_ACD60284.1_
0.130222	0.058525	0.118784	0.10251	gi_188522340_gb_ACD60285.1_
0.219428	0.545623	0.112346	0.292466	gi_188522342_gb_ACD60287.1_
0.155513	0.033472	0.166866	0.118617	gi_188522343_gb_ACD60288.1_
0.111749	0.197658	0.087384	0.132264	gi_188522344_gb_ACD60289.1_
0.114153	0.031676	0.123251	0.089693	gi_188522347_gb_ACD60292.1_
0.709096	0.049642	0.775912	0.51155	gi_188522348_gb_ACD60293.1_
0.102018	0.136108	0.089317	0.109148	gi_188522349_gb_ACD60294.1_
0.924701	0.993922	0.883706	0.93411	gi_188522351_gb_ACD60296.1_
0.208829	0.43807	0.185579	0.277493	gi_188522352_gb_ACD60297.1_
0.254074	0.119413	0.208334	0.19394	gi_188522353_gb_ACD60298.1_
0.075508	0.031493	0.104238	0.070413	gi_188522355_gb_ACD60300.1_
0.10011	0.090792	0.163967	0.11829	gi_188522356_gb_ACD60301.1_
0.096651	0.009786	0.13717	0.081202	gi_188522358_gb_ACD60303.1_
0.062444	0.038457	0.088588	0.063163	gi_188522359_gb_ACD60304.1_
0.165205	0.486503	0.129882	0.26053	gi_188522360_gb_ACD60305.1_
0.170654	0.693387	0.104799	0.322947	gi_188522361_gb_ACD60306.1_
0.083402	0.068689	0.103123	0.085071	gi_188522362_gb_ACD60307.1_
0.196234	0.152387	0.220458	0.189693	gi_188522363_gb_ACD60308.1_
0.533699	0.056893	0.75768	0.449424	gi_188522364_gb_ACD60309.1_
0.115373	0.006243	0.109097	0.076904	gi_188522369_gb_ACD60314.1_
0.371684	0.429228	0.535938	0.445617	gi_188522370_gb_ACD60315.1_
0.056253	0.102569	0.07871	0.079177	gi_188522372_gb_ACD60317.1_
0.141851	0.002959	0.219428	0.121413	gi_188522373_gb_ACD60318.1_
0.055619	0.270912	0.06192	0.129484	gi_188522374_gb_ACD60319.1_
0.153553	0.003714	0.232544	0.129937	gi_188522375_gb_ACD60320.1_
0.946242	0.986279	0.908711	0.947077	gi_188522377_gb_ACD60322.1_
0.446209	0.749322	0.474522	0.556684	gi_188522378_gb_ACD60323.1_
0.173217	0.070045	0.186032	0.143098	gi_188522379_gb_ACD60324.1_
0.094576	0.011085	0.124881	0.076847	gi_188522380_gb_ACD60325.1_
0.157095	0.489502	0.122927	0.256508	gi_188522381_gb_ACD60326.1_
0.365401	0.896042	0.406609	0.556017	gi_528897490_gb_AGS47854.1_
0.914745	0.991049	0.902824	0.936206	gi_188523175_gb_ACD61120.1_
0.133658	0.50225	0.092793	0.2429	gi_188523176_gb_ACD61121.1_
0.31432	0.044916	0.395082	0.251439	gi_188523177_gb_ACD61122.1_
0.185579	0.087384	0.228818	0.16726	gi_188523179_gb_ACD61124.1_
0.908711	0.798991	0.844093	0.850598	gi_188523180_gb_ACD61125.1_
0.153164	0.087864	0.207346	0.149458	gi_188523181_gb_ACD61126.1_
0.117222	0.390074	0.080025	0.195774	gi_188523182_gb_ACD61127.1_
0.103958	0.239031	0.15046	0.164483	gi_188523183_gb_ACD61128.1_
0.093808	0.053758	0.136815	0.094794	gi_188523189_gb_ACD61134.1_
0.094576	0.035571	0.096129	0.075425	gi_188523190_gb_ACD61135.1_
0.16645	0.213829	0.128869	0.169716	gi_188523191_gb_ACD61136.1_
0.940643	0.99584	0.870794	0.935759	gi_188523193_gb_ACD61138.1_
0.10736	0.031401	0.157493	0.098751	gi_188523194_gb_ACD61139.1_
0.109975	0.054218	0.128869	0.097687	gi_188523195_gb_ACD61140.1_
0.188314	0.05255	0.172359	0.137741	gi_188523196_gb_ACD61141.1_
0.200047	0.031954	0.225657	0.152553	gi_188523197_gb_ACD61142.1_
0.119729	0.06003	0.131587	0.103782	gi_188523199_gb_ACD61144.1_
0.164792	0.176245	0.188773	0.176603	gi_188523200_gb_ACD61145.1_
0.892064	0.998724	0.809844	0.900211	gi_188523202_gb_ACD61147.1_
0.150077	0.045174	0.198611	0.131287	gi_188523210_gb_ACD61155.1_
0.831459	0.999981	0.514246	0.781895	gi_188523211_gb_ACD61156.1_
0.198611	0.034757	0.249553	0.160974	gi_188523214_gb_ACD61159.1_
0.575909	0.788682	0.626212	0.663601	gi_188523216_gb_ACD61161.1_
0.057704	0.695297	0.130562	0.294521	gi_188523217_gb_ACD61162.1_
0.096129	0.072024	0.105364	0.091172	gi_188523218_gb_ACD61163.1_
0.106215	0.136108	0.201491	0.147938	gi_188523219_gb_ACD61164.1_

gi_188521929_gb_ACD59874.1_	0.124	20	0.134	25	0.174	19	0.126	0.13	N	0.57	SignalP-noTM
gi_188521930_gb_ACD59875.1_	0.12	40	0.117	40	0.132	32	0.099	0.108	N	0.57	SignalP-noTM
gi_188521931_gb_ACD59876.1_	0.233	21	0.239	21	0.317	7	0.254	0.246	N	0.57	SignalP-noTM
gi_188521932_gb_ACD59877.1_	0.142	33	0.166	19	0.386	9	0.213	0.188	N	0.57	SignalP-noTM
gi_188521935_gb_ACD59880.1_	0.113	30	0.16	30	0.417	27	0.176	0.166	N	0.51	SignalP-TM
gi_188521936_gb_ACD59881.1_	0.108	36	0.103	29	0.135	9	0.1	0.102	N	0.57	SignalP-noTM
gi_188521942_gb_ACD59887.1_	0.411	21	0.358	21	0.512	16	0.275	0.319	N	0.57	SignalP-noTM
gi_188521944_gb_ACD59889.1_	0.131	42	0.118	11	0.198	1	0.133	0.125	N	0.57	SignalP-noTM
gi_188521946_gb_ACD59891.1_	0.108	48	0.103	48	0.139	6	0.103	0.103	N	0.57	SignalP-noTM
gi_188521952_gb_ACD59897.1_	0.11	36	0.129	17	0.242	6	0.155	0.141	N	0.57	SignalP-noTM
gi_188521953_gb_ACD59898.1_	0.156	42	0.146	42	0.219	19	0.143	0.145	N	0.57	SignalP-noTM
gi_188521954_gb_ACD59899.1_	0.206	21	0.145	21	0.18	20	0.107	0.131	N	0.51	SignalP-TM
gi_188521955_gb_ACD59900.1_	0.116	56	0.127	14	0.226	12	0.149	0.137	N	0.57	SignalP-noTM
gi_188521956_gb_ACD59901.1_	0.115	18	0.132	11	0.263	4	0.177	0.153	N	0.57	SignalP-noTM
gi_188521961_gb_ACD59906.1_	0.113	10	0.11	16	0.15	10	0.111	0.11	N	0.57	SignalP-noTM
gi_188521962_gb_ACD59907.1_	0.14	49	0.121	44	0.134	8	0.1	0.111	N	0.57	SignalP-noTM
gi_188521963_gb_ACD59908.1_	0.137	49	0.182	11	0.465	3	0.345	0.259	N	0.57	SignalP-noTM
gi_188521964_gb_ACD59909.1_	0.14	23	0.117	23	0.228	44	0.089	0.104	N	0.57	SignalP-noTM
gi_188521965_gb_ACD59910.1_	0.14	19	0.14	19	0.198	18	0.143	0.142	N	0.57	SignalP-noTM
gi_188521966_gb_ACD59911.1_	0.152	27	0.183	25	0.423	15	0.255	0.217	N	0.57	SignalP-noTM
gi_188521967_gb_ACD59912.1_	0.136	18	0.17	11	0.42	1	0.276	0.22	N	0.57	SignalP-noTM
gi_188521970_gb_ACD59915.1_	0.118	39	0.111	39	0.136	35	0.086	0.099	N	0.57	SignalP-noTM
gi_188521975_gb_ACD59920.1_	0.684	36	0.692	36	0.959	21	0.8	0.743	Y	0.57	SignalP-noTM
gi_188521979_gb_ACD59924.1_	0.246	29	0.223	29	0.481	11	0.298	0.259	N	0.57	SignalP-noTM
gi_188521980_gb_ACD59925.1_	0.397	20	0.385	20	0.655	4	0.458	0.419	N	0.57	SignalP-noTM
gi_188521981_gb_ACD59926.1_	0.729	24	0.814	24	0.973	17	0.927	0.867	Y	0.57	SignalP-noTM
gi_188522328_gb_ACD60273.1_	0.126	29	0.122	23	0.177	10	0.134	0.128	N	0.57	SignalP-noTM
gi_188522330_gb_ACD60275.1_	0.123	52	0.152	11	0.279	4	0.233	0.19	N	0.57	SignalP-noTM
gi_188522331_gb_ACD60276.1_	0.156	16	0.215	16	0.38	13	0.297	0.254	N	0.57	SignalP-noTM
gi_188522333_gb_ACD60278.1_	0.732	28	0.808	28	0.962	27	0.829	0.818	Y	0.57	SignalP-noTM
gi_188522334_gb_ACD60279.1_	0.183	32	0.224	32	0.592	14	0.385	0.3	N	0.57	SignalP-noTM
gi_188522336_gb_ACD60281.1_	0.179	31	0.195	31	0.373	27	0.223	0.205	N	0.51	SignalP-TM
gi_188522339_gb_ACD60284.1_	0.143	41	0.112	41	0.111	25	0.086	0.1	N	0.57	SignalP-noTM
gi_188522340_gb_ACD60285.1_	0.119	42	0.107	18	0.137	11	0.101	0.104	N	0.57	SignalP-noTM
gi_188522342_gb_ACD60287.1_	0.138	45	0.207	15	0.6	11	0.388	0.292	N	0.57	SignalP-noTM
gi_188522343_gb_ACD60288.1_	0.194	31	0.181	31	0.266	8	0.181	0.181	N	0.57	SignalP-noTM
gi_188522344_gb_ACD60289.1_	0.263	22	0.23	22	0.339	1	0.2	0.216	N	0.57	SignalP-noTM
gi_188522347_gb_ACD60292.1_	0.358	28	0.228	28	0.394	1	0.214	0.223	N	0.51	SignalP-TM
gi_188522348_gb_ACD60293.1_	0.171	48	0.203	12	0.506	1	0.396	0.293	N	0.57	SignalP-noTM
gi_188522349_gb_ACD60294.1_	0.116	30	0.111	11	0.146	10	0.127	0.119	N	0.57	SignalP-noTM
gi_188522351_gb_ACD60296.1_	0.161	68	0.117	68	0.134	6	0.083	0.101	N	0.57	SignalP-noTM
gi_188522352_gb_ACD60297.1_	0.118	52	0.108	52	0.16	51	0.087	0.098	N	0.57	SignalP-noTM
gi_188522353_gb_ACD60298.1_	0.207	38	0.172	28	0.273	10	0.191	0.181	N	0.57	SignalP-noTM
gi_188522355_gb_ACD60300.1_	0.149	45	0.125	45	0.143	43	0.097	0.112	N	0.57	SignalP-noTM
gi_188522356_gb_ACD60301.1_	0.127	20	0.207	14	0.446	13	0.342	0.27	N	0.57	SignalP-noTM
gi_188522358_gb_ACD60303.1_	0.111	35	0.108	46	0.13	34	0.095	0.102	N	0.57	SignalP-noTM
gi_188522359_gb_ACD60304.1_	0.102	44	0.108	57	0.129	46	0.091	0.1	N	0.57	SignalP-noTM
gi_188522360_gb_ACD60305.1_	0.131	33	0.121	52	0.185	41	0.108	0.115	N	0.57	SignalP-noTM
gi_188522361_gb_ACD60306.1_	0.119	61	0.121	40	0.175	36	0.118	0.12	N	0.57	SignalP-noTM
gi_188522362_gb_ACD60307.1_	0.13	24	0.133	24	0.269	21	0.142	0.137	N	0.57	SignalP-noTM
gi_188522363_gb_ACD60308.1_	0.123	60	0.117	12	0.154	11	0.12	0.119	N	0.57	SignalP-noTM
gi_188522364_gb_ACD60309.1_	0.125	40	0.119	11	0.214	1	0.13	0.124	N	0.57	SignalP-noTM
gi_528897490_gb_AGS47854.1_	0.121	43	0.141	43	0.217	33	0.149	0.145	N	0.57	SignalP-noTM
gi_188522369_gb_ACD60314.1_	0.124	45	0.117	45	0.174	40	0.092	0.105	N	0.57	SignalP-noTM
gi_188522370_gb_ACD60315.1_	0.113	14	0.106	66	0.116	36	0.09	0.098	N	0.57	SignalP-noTM
gi_188522372_gb_ACD60317.1_	0.101	67	0.168	11	0.311	2	0.286	0.223	N	0.57	SignalP-noTM
gi_188522373_gb_ACD60318.1_	0.141	39	0.157	17	0.331	16	0.228	0.191	N	0.57	SignalP-noTM
gi_188522374_gb_ACD60319.1_	0.111	17	0.128	11	0.276	2	0.152	0.137	N	0.51	SignalP-TM
gi_188522375_gb_ACD60320.1_	0.134	44	0.177	32	0.279	20	0.196	0.186	N	0.57	SignalP-noTM
gi_188522377_gb_ACD60322.1_	0.152	35	0.127	54	0.207	50	0.104	0.116	N	0.57	SignalP-noTM
gi_188522378_gb_ACD60323.1_	0.12	61	0.116	19	0.167	12	0.117	0.116	N	0.57	SignalP-noTM
gi_188522379_gb_ACD60324.1_	0.141	26	0.135	26	0.218	1	0.136	0.136	N	0.57	SignalP-noTM
gi_188522380_gb_ACD60325.1_	0.172	20	0.133	20	0.121	12	0.096	0.116	N	0.57	SignalP-noTM
gi_188522381_gb_ACD60326.1_	0.118	61	0.136	11	0.312	1	0.169	0.152	N	0.57	SignalP-noTM
gi_188522382_gb_ACD60327.1_	0.115	24	0.125	24	0.154	18	0.129	0.127	N	0.57	SignalP-noTM
gi_188522383_gb_ACD60328.1_	0.123	54	0.114	54	0.111	47	0.084	0.1	N	0.57	SignalP-noTM
gi_188522384_gb_ACD60329.1_	0.113	27	0.109	11	0.149	2	0.122	0.115	N	0.57	SignalP-noTM
gi_188523635_gb_ACD61580.1_	0.168	23	0.167	23	0.211	20	0.166	0.167	N	0.51	SignalP-TM
gi_188523638_gb_ACD61583.1_	0.183	21	0.245	21	0.543	12	0.315	0.278	N	0.57	SignalP-noTM
gi_188523641_gb_ACD61586.1_	0.112	55	0.112	55	0.159	40	0.1	0.106	N	0.57	SignalP-noTM
gi_188523642_gb_ACD61587.1_	0.157	42	0.145	42	0.219	19	0.142	0.143	N	0.57	SignalP-noTM
gi_188523643_gb_ACD61588.1_	0.194	32	0.155	32	0.336	3	0.154	0.155	N	0.57	SignalP-noTM
gi_188523649_gb_ACD61594.1_	0.111	27	0.122	11	0.197	5	0.159	0.136	N	0.51	SignalP-TM
gi_188523651_gb_ACD61596.1_	0.106	55	0.115	14	0.183	11	0.129	0.122	N	0.57	SignalP-noTM
gi_188523652_gb_ACD61597.1_	0.452	29	0.453	29	0.64	12	0.493	0.468	N	0.51	SignalP-TM
gi_188523656_gb_ACD61601.1_	0.643	22	0.768	22	0.961	11	0.915	0.837	Y	0.57	SignalP-noTM
gi_188523657_gb_ACD61602.1_	0.751	21	0.798	21	0.898	2	0.845	0.82	Y	0.57	SignalP-noTM
gi_188523660_gb_ACD61605.1_	0.812	26	0.846	26	0.965	11	0.902	0.872	Y	0.57	SignalP-noTM

0.831459	0.038126	0.83355	0.567712	gi_188523220_gb_ACD61165.1_
0.932264	0.999695	0.828495	0.920151	gi_188523221_gb_ACD61166.1_
0.196234	0.097969	0.162329	0.152177	gi_188523224_gb_ACD61169.1_
0.118157	0.139314	0.092038	0.116503	gi_188523225_gb_ACD61170.1_
0.135404	0.362622	0.184673	0.227566	gi_188523226_gb_ACD61171.1_
0.189233	0.002329	0.194818	0.128793	gi_188523227_gb_ACD61172.1_
0.87804	0.99723	0.781597	0.885622	gi_188523229_gb_ACD61174.1_
0.377306	0.908711	0.22461	0.503542	gi_188523231_gb_ACD61176.1_
0.167702	0.142217	0.137881	0.149267	gi_188523234_gb_ACD61179.1_
0.094576	0.649764	0.195761	0.313367	gi_188523236_gb_ACD61181.1_
0.126198	0.312383	0.248431	0.229004	gi_188523237_gb_ACD61182.1_
0.13331	0.094319	0.125209	0.117613	gi_188523238_gb_ACD61183.1_
0.129544	0.005899	0.300273	0.145239	gi_188523695_gb_ACD61640.1_
0.258649	0.486503	0.230942	0.325365	gi_188523696_gb_ACD61641.1_
0.092541	0.015172	0.153164	0.086959	gi_188523697_gb_ACD61642.1_
0.125868	0.091289	0.182426	0.133194	gi_188523698_gb_ACD61643.1_
0.460334	0.06717	0.548596	0.3587	gi_188523699_gb_ACD61644.1_
0.104238	0.049219	0.109097	0.087518	gi_188523700_gb_ACD61645.1_
0.082036	0.031129	0.082036	0.065067	gi_188523701_gb_ACD61646.1_
0.114153	0.011974	0.14629	0.090806	gi_188523704_gb_ACD61649.1_
0.163147	0.134354	0.144427	0.147309	gi_188523706_gb_ACD61651.1_
0.195761	0.037471	0.27032	0.167851	gi_188523707_gb_ACD61652.1_
0.686972	0.594114	0.633904	0.63833	gi_188523708_gb_ACD61653.1_
0.363316	0.98189	0.455865	0.600357	gi_188523709_gb_ACD61654.1_
0.50375	0.989397	0.373788	0.622312	gi_188523710_gb_ACD61655.1_
0.168541	0.027225	0.161109	0.118958	gi_188523239_gb_ACD61184.1_
0.083173	0.043772	0.119729	0.082225	gi_188523240_gb_ACD61185.1_
0.115679	0.039128	0.129544	0.094784	gi_188523241_gb_ACD61186.1_
0.116912	0.033961	0.178433	0.109769	gi_188523243_gb_ACD61188.1_
0.248431	0.972775	0.073441	0.431549	gi_188523245_gb_ACD61190.1_
0.087624	0.071226	0.211318	0.123389	gi_188523247_gb_ACD61192.1_
0.082036	0.050068	0.090052	0.074052	gi_188523248_gb_ACD61193.1_
0.390074	0.936672	0.651809	0.659518	gi_188523250_gb_ACD61195.1_
0.107072	0.123251	0.082944	0.104422	gi_188523251_gb_ACD61196.1_
0.112047	0.070831	0.093808	0.092229	gi_188523635_gb_ACD61580.1_
0.050068	0.026753	0.102018	0.059613	gi_188523638_gb_ACD61583.1_
0.414595	0.073237	0.363316	0.283716	gi_188523641_gb_ACD61586.1_
0.289667	0.6673	0.361237	0.439401	gi_188523642_gb_ACD61587.1_
0.102018	0.319515	0.181979	0.201171	gi_188523643_gb_ACD61588.1_
0.171505	0.435118	0.104518	0.237047	gi_188523649_gb_ACD61594.1_
0.129544	0.23041	0.111749	0.157234	gi_188523651_gb_ACD61596.1_
0.951892	0.999677	0.88615	0.945906	gi_188523652_gb_ACD61597.1_
0.945163	0.999764	0.897707	0.947545	gi_188523656_gb_ACD61601.1_
0.529217	0.613489	0.682438	0.608381	gi_188523657_gb_ACD61602.1_
0.952844	0.999875	0.914041	0.955587	gi_188523660_gb_ACD61605.1_
0.79413	0.90016	0.861045	0.851778	gi_188523661_gb_ACD61606.1_
0.194348	0.078928	0.144798	0.139358	gi_188523663_gb_ACD61608.1_
0.185579	0.063328	0.163147	0.137351	gi_188523664_gb_ACD61609.1_
0.114762	0.06054	0.123575	0.099626	gi_188523665_gb_ACD61610.1_
0.255213	0.264443	0.201491	0.240382	gi_188523666_gb_ACD61611.1_
0.157892	0.031584	0.137525	0.109	gi_188523667_gb_ACD61612.1_
0.087384	0.075299	0.085959	0.082881	gi_188523668_gb_ACD61613.1_
0.124881	0.082036	0.111452	0.106123	gi_188523669_gb_ACD61614.1_
0.095349	0.544879	0.190618	0.276949	gi_188523673_gb_ACD61618.1_
0.532205	0.1034	0.667966	0.434524	gi_188523674_gb_ACD61619.1_
0.215346	0.073645	0.262697	0.183896	gi_188523677_gb_ACD61622.1_
0.246197	0.906192	0.101197	0.417862	gi_188523681_gb_ACD61626.1_
0.300903	0.906192	0.424091	0.543729	gi_188523682_gb_ACD61627.1_
0.182426	0.262697	0.080913	0.175345	gi_188523683_gb_ACD61628.1_
0.076562	0.000362	0.153553	0.076826	gi_188523684_gb_ACD61629.1_
0.826353	0.488752	0.817127	0.710744	gi_188523685_gb_ACD61630.1_
0.054837	0.03704	0.122927	0.071601	gi_188523686_gb_ACD61631.1_
0.481259	0.984962	0.362622	0.609614	gi_188523687_gb_ACD61632.1_
0.144427	0.066608	0.110859	0.107298	gi_188523688_gb_ACD61633.1_
0.120363	0.054372	0.13331	0.102682	gi_188523689_gb_ACD61634.1_
0.082716	0.608497	0.116294	0.269169	gi_188523691_gb_ACD61636.1_
0.925117	0.990214	0.874791	0.930041	gi_188523692_gb_ACD61637.1_
0.069655	0.028195	0.134005	0.077285	gi_188523693_gb_ACD61638.1_
0.969052	0.280496	0.808919	0.686156	gi_188523694_gb_ACD61639.1_
0.114153	0.102293	0.138238	0.118228	gi_188518759_gb_ACD56704.1_
0.163967	0.043772	0.127194	0.111644	gi_188518760_gb_ACD56705.1_
0.100381	0.571506	0.059189	0.243692	gi_188518761_gb_ACD56706.1_
0.781597	0.075718	0.781597	0.546304	gi_188518762_gb_ACD56707.1_
0.139314	0.032704	0.127862	0.09996	gi_188518763_gb_ACD56708.1_
0.076988	0.037363	0.128532	0.080961	gi_188518764_gb_ACD56709.1_
0.186487	0.050642	0.182426	0.139852	gi_188518769_gb_ACD56714.1_
0.379422	0.949789	0.514246	0.614486	gi_188518770_gb_ACD56715.1_
0.118157	0.188314	0.158291	0.154921	gi_188518774_gb_ACD56719.1_

gi_188523661_gb_ACD61606.1_	0.12	35	0.145	35	0.258	5	0.172	0.157	N	0.57	SignalP-noTM
gi_188523663_gb_ACD61608.1_	0.173	21	0.168	21	0.365	1	0.203	0.184	N	0.57	SignalP-noTM
gi_188523664_gb_ACD61609.1_	0.127	11	0.124	21	0.236	9	0.121	0.122	N	0.57	SignalP-noTM
gi_188523665_gb_ACD61610.1_	0.161	20	0.101	45	0.106	52	0.056	0.08	N	0.57	SignalP-noTM
gi_188523666_gb_ACD61611.1_	0.124	48	0.164	14	0.345	7	0.265	0.211	N	0.57	SignalP-noTM
gi_188523667_gb_ACD61612.1_	0.123	22	0.132	22	0.178	21	0.141	0.136	N	0.57	SignalP-noTM
gi_188523668_gb_ACD61613.1_	0.131	60	0.187	21	0.561	17	0.288	0.234	N	0.57	SignalP-noTM
gi_188523669_gb_ACD61614.1_	0.109	7	0.111	62	0.141	52	0.099	0.106	N	0.57	SignalP-noTM
gi_188523673_gb_ACD61618.1_	0.124	26	0.105	67	0.145	56	0.083	0.097	N	0.51	SignalP-TM
gi_188523674_gb_ACD61619.1_	0.185	18	0.126	18	0.129	14	0.089	0.109	N	0.57	SignalP-noTM
gi_188523677_gb_ACD61622.1_	0.175	17	0.178	45	0.483	37	0.182	0.18	N	0.51	SignalP-TM
gi_188523681_gb_ACD61626.1_	0.215	40	0.191	40	0.274	36	0.169	0.18	N	0.57	SignalP-noTM
gi_188523682_gb_ACD61627.1_	0.12	28	0.142	11	0.272	2	0.194	0.166	N	0.57	SignalP-noTM
gi_188523683_gb_ACD61628.1_	0.277	33	0.179	33	0.168	32	0.109	0.146	N	0.57	SignalP-noTM
gi_188523684_gb_ACD61629.1_	0.104	3	0.094	16	0.104	4	0.088	0.091	N	0.57	SignalP-noTM
gi_188523685_gb_ACD61630.1_	0.273	26	0.169	26	0.156	9	0.114	0.143	N	0.57	SignalP-noTM
gi_188523686_gb_ACD61631.1_	0.122	28	0.102	70	0.112	65	0.084	0.094	N	0.57	SignalP-noTM
gi_188523687_gb_ACD61632.1_	0.102	68	0.108	32	0.132	30	0.105	0.107	N	0.57	SignalP-noTM
gi_188523688_gb_ACD61633.1_	0.127	42	0.122	11	0.202	5	0.164	0.138	N	0.51	SignalP-TM
gi_188523689_gb_ACD61634.1_	0.135	26	0.178	26	0.302	25	0.222	0.198	N	0.57	SignalP-noTM
gi_188523691_gb_ACD61636.1_	0.141	20	0.148	20	0.297	4	0.185	0.165	N	0.57	SignalP-noTM
gi_188523692_gb_ACD61637.1_	0.843	30	0.819	30	0.972	19	0.866	0.841	Y	0.57	SignalP-noTM
gi_188523693_gb_ACD61638.1_	0.118	53	0.118	37	0.161	9	0.124	0.121	N	0.57	SignalP-noTM
gi_188523694_gb_ACD61639.1_	0.1	18	0.101	42	0.113	14	0.097	0.099	N	0.57	SignalP-noTM
gi_188523695_gb_ACD61640.1_	0.163	40	0.108	40	0.188	1	0.087	0.098	N	0.57	SignalP-noTM
gi_188523696_gb_ACD61641.1_	0.141	66	0.188	12	0.442	13	0.354	0.266	N	0.57	SignalP-noTM
gi_188523697_gb_ACD61642.1_	0.121	63	0.115	11	0.179	2	0.132	0.123	N	0.57	SignalP-noTM
gi_188523698_gb_ACD61643.1_	0.106	24	0.133	24	0.239	21	0.165	0.145	N	0.51	SignalP-TM
gi_188523699_gb_ACD61644.1_	0.657	51	0.485	51	0.471	43	0.268	0.405	N	0.51	SignalP-TM
gi_188523700_gb_ACD61645.1_	0.107	46	0.101	64	0.137	58	0.079	0.093	N	0.51	SignalP-TM
gi_188523701_gb_ACD61646.1_	0.142	52	0.116	52	0.126	2	0.092	0.105	N	0.57	SignalP-noTM
gi_188523704_gb_ACD61649.1_	0.6	24	0.716	24	0.961	20	0.854	0.781	Y	0.57	SignalP-noTM
gi_188523706_gb_ACD61651.1_	0.115	50	0.166	11	0.47	1	0.257	0.2	N	0.51	SignalP-TM
gi_188523707_gb_ACD61652.1_	0.215	23	0.419	23	0.919	1	0.844	0.618	Y	0.57	SignalP-noTM
gi_188523708_gb_ACD61653.1_	0.216	29	0.268	29	0.511	1	0.334	0.293	N	0.51	SignalP-TM
gi_188523709_gb_ACD61654.1_	0.115	49	0.133	49	0.221	47	0.14	0.137	N	0.57	SignalP-noTM
gi_188523710_gb_ACD61655.1_	0.101	29	0.139	11	0.244	4	0.197	0.167	N	0.57	SignalP-noTM
gi_188523175_gb_ACD61120.1_	0.102	3	0.104	48	0.122	41	0.092	0.098	N	0.57	SignalP-noTM
gi_188523176_gb_ACD61121.1_	0.581	36	0.696	36	0.924	32	0.605	0.653	Y	0.57	SignalP-noTM
gi_188523177_gb_ACD61122.1_	0.108	18	0.116	70	0.179	1	0.102	0.111	N	0.51	SignalP-TM
gi_188523179_gb_ACD61124.1_	0.129	40	0.129	40	0.23	1	0.093	0.115	N	0.51	SignalP-TM
gi_188523180_gb_ACD61125.1_	0.231	19	0.459	19	0.956	10	0.922	0.677	Y	0.57	SignalP-noTM
gi_188523181_gb_ACD61126.1_	0.136	18	0.101	18	0.152	1	0.082	0.094	N	0.51	SignalP-TM
gi_188523182_gb_ACD61127.1_	0.145	36	0.107	36	0.132	8	0.095	0.101	N	0.57	SignalP-noTM
gi_188523183_gb_ACD61128.1_	0.165	48	0.172	11	0.357	1	0.304	0.221	N	0.51	SignalP-TM
gi_188523189_gb_ACD61134.1_	0.215	37	0.142	37	0.213	3	0.109	0.127	N	0.57	SignalP-noTM
gi_188523190_gb_ACD61135.1_	0.121	33	0.12	14	0.168	8	0.144	0.131	N	0.57	SignalP-noTM
gi_188523191_gb_ACD61136.1_	0.126	42	0.116	42	0.131	53	0.094	0.105	N	0.57	SignalP-noTM
gi_188523193_gb_ACD61138.1_	0.368	23	0.593	23	0.969	15	0.943	0.757	Y	0.57	SignalP-noTM
gi_188523194_gb_ACD61139.1_	0.103	21	0.103	53	0.153	1	0.098	0.1	N	0.57	SignalP-noTM
gi_188523195_gb_ACD61140.1_	0.168	16	0.257	16	0.526	6	0.411	0.329	N	0.57	SignalP-noTM
gi_188523196_gb_ACD61141.1_	0.116	56	0.106	56	0.134	51	0.086	0.096	N	0.57	SignalP-noTM
gi_188523197_gb_ACD61142.1_	0.103	25	0.122	11	0.197	2	0.145	0.132	N	0.57	SignalP-noTM
gi_188523199_gb_ACD61144.1_	0.154	31	0.131	31	0.195	33	0.111	0.121	N	0.57	SignalP-noTM
gi_188523200_gb_ACD61145.1_	0.356	23	0.434	23	0.808	18	0.522	0.475	N	0.57	SignalP-noTM
gi_188523202_gb_ACD61147.1_	0.341	27	0.576	27	0.992	19	0.964	0.759	Y	0.57	SignalP-noTM
gi_188523210_gb_ACD61155.1_	0.172	19	0.156	19	0.249	9	0.137	0.149	N	0.51	SignalP-TM
gi_188523211_gb_ACD61156.1_	0.136	47	0.145	11	0.329	3	0.196	0.169	N	0.57	SignalP-noTM
gi_188523214_gb_ACD61159.1_	0.11	45	0.101	65	0.11	55	0.082	0.092	N	0.57	SignalP-noTM
gi_188523216_gb_ACD61161.1_	0.111	22	0.109	22	0.125	11	0.099	0.105	N	0.57	SignalP-noTM
gi_188523217_gb_ACD61162.1_	0.119	25	0.157	18	0.296	13	0.212	0.178	N	0.51	SignalP-TM
gi_188523218_gb_ACD61163.1_	0.369	65	0.201	65	0.204	14	0.117	0.161	N	0.57	SignalP-noTM
gi_188523219_gb_ACD61164.1_	0.124	19	0.132	39	0.254	1	0.097	0.119	N	0.51	SignalP-TM
gi_188523220_gb_ACD61165.1_	0.533	41	0.364	41	0.403	38	0.17	0.273	N	0.57	SignalP-noTM
gi_188523221_gb_ACD61166.1_	0.114	28	0.15	31	0.365	27	0.187	0.167	N	0.57	SignalP-noTM
gi_188523224_gb_ACD61169.1_	0.163	23	0.123	23	0.229	2	0.116	0.12	N	0.57	SignalP-noTM
gi_188523225_gb_ACD61170.1_	0.141	22	0.142	12	0.249	10	0.201	0.169	N	0.57	SignalP-noTM
gi_188523226_gb_ACD61171.1_	0.129	43	0.149	43	0.272	40	0.131	0.14	N	0.57	SignalP-noTM
gi_188523227_gb_ACD61172.1_	0.208	41	0.216	21	0.453	14	0.341	0.262	N	0.51	SignalP-TM
gi_188523229_gb_ACD61174.1_	0.118	39	0.113	11	0.15	7	0.129	0.12	N	0.57	SignalP-noTM
gi_188523231_gb_ACD61176.1_	0.106	26	0.117	35	0.206	1	0.119	0.118	N	0.57	SignalP-noTM
gi_188523234_gb_ACD61179.1_	0.533	60	0.321	60	0.271	55	0.114	0.223	N	0.57	SignalP-noTM
gi_188523236_gb_ACD61181.1_	0.16	32	0.194	21	0.342	19	0.218	0.203	N	0.51	SignalP-TM
gi_188523237_gb_ACD61182.1_	0.155	16	0.338	16	0.85	13	0.743	0.528	N	0.57	SignalP-noTM
gi_188523238_gb_ACD61183.1_	0.117	20	0.124	20	0.154	12	0.13	0.127	N	0.57	SignalP-noTM
gi_188523239_gb_ACD61184.1_	0.126	33	0.124	33	0.202	30	0.12	0.122	N	0.57	SignalP-noTM
gi_188523240_gb_ACD61185.1_	0.108	18	0.11	39	0.142	35	0.104	0.107	N	0.57	SignalP-noTM
gi_188523241_gb_ACD61186.1_	0.327	29	0.165	29	0.323	1	0.133	0.153	N	0.51	SignalP-TM

0.805652	0.981403	0.843301	0.876785	gi_188518777_gb_ACD56722.1_
0.973789	0.753246	0.965444	0.897493	gi_188518778_gb_ACD56723.1_
0.112346	0.040272	0.149694	0.100771	gi_188518783_gb_ACD56728.1_
0.280496	0.419701	0.448434	0.382877	gi_188518784_gb_ACD56729.1_
0.165619	0.065498	0.257501	0.162873	gi_188518785_gb_ACD56730.1_
0.90016	0.99789	0.905424	0.934491	gi_188518786_gb_ACD56731.1_
0.054992	0.006647	0.061399	0.041013	gi_188518791_gb_ACD56736.1_
0.940476	0.999432	0.937203	0.959037	gi_188518792_gb_ACD56737.1_
0.182426	0.001923	0.295254	0.159868	gi_188518793_gb_ACD56738.1_
0.594837	0.458843	0.699097	0.584259	gi_188518794_gb_ACD56739.1_
0.099302	0.023939	0.140397	0.087879	gi_188518795_gb_ACD56740.1_
0.078493	0.007971	0.197182	0.094549	gi_188518796_gb_ACD56741.1_
0.07385	0.115679	0.140759	0.110096	gi_188518797_gb_ACD56742.1_
0.073237	0.033472	0.148552	0.085087	gi_188518798_gb_ACD56743.1_
0.091289	0.10147	0.166866	0.119875	gi_188518800_gb_ACD56745.1_
0.074468	0.019379	0.119413	0.071087	gi_188518801_gb_ACD56746.1_
0.6142	0.018057	0.795597	0.475951	gi_188518809_gb_ACD56754.1_
0.647028	0.960189	0.856313	0.821177	gi_188518812_gb_ACD56757.1_
0.195761	0.093808	0.105931	0.131833	gi_188518813_gb_ACD56758.1_
0.183322	0.079585	0.257501	0.173469	gi_188518815_gb_ACD56760.1_
0.902031	0.999903	0.731452	0.877795	gi_188518817_gb_ACD56762.1_
0.330705	0.935595	0.470036	0.578779	gi_188518818_gb_ACD56763.1_
0.96296	0.996792	0.913568	0.957773	gi_188518819_gb_ACD56764.1_
0.087145	0.057867	0.152387	0.099133	gi_188518820_gb_ACD56765.1_
0.891194	0.965842	0.801866	0.886301	gi_188518821_gb_ACD56766.1_
0.159494	0.053758	0.16645	0.126567	gi_188518823_gb_ACD56768.1_
0.13717	0.07806	0.136108	0.117113	gi_188518826_gb_ACD56771.1_
0.391503	0.591942	0.54711	0.510185	gi_188518828_gb_ACD56773.1_
0.172359	0.116912	0.194348	0.161206	gi_188518830_gb_ACD56775.1_
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0.05869	0.038346	0.112346	0.069794	gi_188518840_gb_ACD56785.1_
0.884321	0.85705	0.861045	0.867472	gi_188518841_gb_ACD56786.1_
0.191081	0.075091	0.23041	0.165527	gi_188519118_gb_ACD57063.1_
0.27032	0.370983	0.523233	0.388179	gi_188519125_gb_ACD57070.1_
0.47527	0.942459	0.40444	0.60739	gi_188519127_gb_ACD57072.1_
0.951478	0.998592	0.809382	0.919817	gi_188519128_gb_ACD57073.1_
0.222527	0.065314	0.26386	0.1839	gi_188519133_gb_ACD57078.1_
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0.854084	0.981675	0.798026	0.877928	gi_188519144_gb_ACD57089.1_
0.804239	0.982364	0.831459	0.872687	gi_188519146_gb_ACD57091.1_
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0.194818	0.97627	0.127527	0.432872	gi_188519148_gb_ACD57093.1_
0.141122	0.059189	0.126529	0.108947	gi_188519149_gb_ACD57094.1_
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0.897155	0.929169	0.879637	0.901987	gi_188519152_gb_ACD57097.1_
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0.141122	0.410234	0.093553	0.21497	gi_188519159_gb_ACD57104.1_
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0.114457	0.102293	0.119729	0.11216	gi_188519161_gb_ACD57106.1_
0.106215	0.670622	0.086432	0.287756	gi_188519162_gb_ACD57107.1_
0.09104	0.061399	0.137525	0.096655	gi_188519163_gb_ACD57108.1_
0.099302	0.517243	0.210818	0.275788	gi_188519168_gb_ACD57113.1_
0.934686	0.993008	0.875447	0.93438	gi_188519170_gb_ACD57115.1_
0.933392	0.976131	0.891194	0.933572	gi_188519171_gb_ACD57116.1_
0.156699	0.002227	0.246754	0.135227	gi_188519173_gb_ACD57118.1_
0.176245	0.076562	0.169806	0.140871	gi_188519175_gb_ACD57120.1_
0.105931	0.150077	0.197658	0.151222	gi_188519176_gb_ACD57121.1_
0.150844	0.068306	0.26386	0.161003	gi_188519177_gb_ACD57122.1_
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0.965544	0.999979	0.875447	0.94699	gi_188519181_gb_ACD57126.1_
0.894069	0.999747	0.748758	0.880858	gi_188519182_gb_ACD57127.1_
0.131244	0.086432	0.155513	0.124396	gi_188519183_gb_ACD57128.1_
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0.813968	0.998637	0.400832	0.737812	gi_188519193_gb_ACD57138.1_
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0.219943	0.920853	0.259225	0.466674	gi_188519197_gb_ACD57142.1_
0.862475	0.612065	0.838891	0.771144	gi_188519201_gb_ACD57146.1_
0.317562	0.852205	0.309812	0.493193	gi_188519203_gb_ACD57148.1_
0.072426	0.05285	0.138955	0.088077	gi_188519210_gb_ACD57155.1_
0.138596	0.104799	0.152	0.131798	gi_188519211_gb_ACD57156.1_
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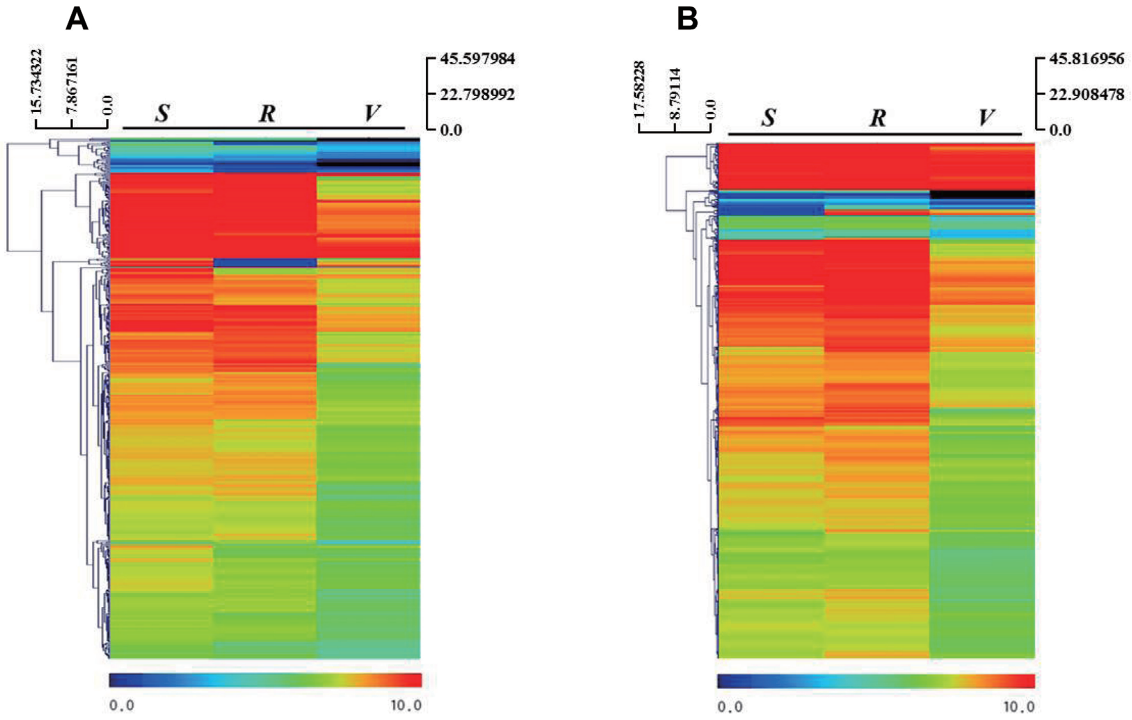
0.954043	0.919753	0.90361	0.925802	gi_188519222_gb_ACD57167.1_
0.348191	0.02291	0.109389	0.160163	gi_188519227_gb_ACD57172.1_
0.410234	0.108225	0.408783	0.309081	gi_188519230_gb_ACD57175.1_

gi_188523243_gb_ACD61188.1_	0.116	57	0.098	34	0.104	29	0.088	0.093	N	0.57	SignalP-noTM
gi_188523245_gb_ACD61190.1_	0.171	35	0.148	35	0.316	34	0.119	0.135	N	0.57	SignalP-noTM
gi_188523247_gb_ACD61192.1_	0.12	61	0.113	61	0.124	1	0.092	0.103	N	0.57	SignalP-noTM
gi_188523248_gb_ACD61193.1_	0.12	35	0.108	48	0.187	1	0.098	0.104	N	0.57	SignalP-noTM
gi_188523250_gb_ACD61195.1_	0.134	32	0.13	16	0.212	12	0.172	0.15	N	0.57	SignalP-noTM
gi_188523251_gb_ACD61196.1_	0.106	23	0.098	70	0.108	67	0.081	0.09	N	0.57	SignalP-noTM

0.716466	0.998496	0.757128	0.82403	gi_188519231_gb_ACD57176.1_
0.945628	0.999174	0.933578	0.95946	gi_188519232_gb_ACD57177.1_
0.844881	0.282316	0.868413	0.665203	gi_188519239_gb_ACD57184.1_
0.094063	0.073237	0.095868	0.087723	gi_188522382_gb_ACD60327.1_
0.086195	0.027868	0.148552	0.087538	gi_188522383_gb_ACD60328.1_
0.931694	0.981621	0.76959	0.894302	gi_188522384_gb_ACD60329.1_



Up-regulated genes in Dongjin cultivar

Up-regulated genes in Samgwang cultivar

Supplementary Fig. 1. Heat map of up-regulated genes during *in planta* [susceptible (S) and resistant (R)] growth as compared to *in vitro* (V) culture conditions.