

**Table S1.** Summary of the best BLASTP hits at order level for SFB proteins

<b>Order</b>	<b>Number of gene</b>
<i>Clostridiales</i>	987
<i>Bacillales</i>	55
<i>Erysipelotrichales</i>	50
<i>Fusobacteriales</i>	33
<i>Lactobacillales</i>	27
<i>Thermoanaerobacterales</i>	15
<i>Selenomonadales</i>	8
<i>Prochlorales</i>	6
<i>Thermotogales</i>	5
others	55
No hit	250
Total	1,491

Table S2. Putative transport activities in SFB

Gene ID	Annotation	Pfam	
		ID number	Family
<b>1. ABC transporter</b>			
SFBM_0171	antimicrobial peptide ABC transporter protein	PF00005	ABC_tran
SFBM_0172	ABC transporter permease protein	PF02687	FtsX
SFBM_0174	ABC transporter, permease	no motif	
SFBM_0179	amino acid ABC transporter, ATP-binding protein	PF00005	ABC_tran
SFBM_0180	amino acid ABC transporter, inner membrane subunit	PF00528	BPD_transp_1
SFBM_0181	amino acid ABC transporter, amino acid-binding protein	PF00497	SBP_bac_3
SFBM_0283	ABC transporter ATP-binding protein	PF00005	ABC_tran
SFBM_0291	ABC-type iron (III) transport system, ATPase component	PF00005	ABC_tran
SFBM_0292	ABC transporter, substrate-binding protein	PF01297	SBP_bac_9
SFBM_0359	iron compound ABC transporter, iron-binding protein	PF01497	Peripla_BP_2
SFBM_0360	iron compound ABC transporter, periplasmic iron compound-binding protein	PF01032	FecCD
SFBM_0361	iron compound ABC transporter, ATP-binding protein	PF00005	ABC_tran
SFBM_0399	ABC transporter, ATP-binding protein	PF00005	ABC_tran
SFBM_0400	ABC transporter permease protein	PF02687	FtsX
SFBM_0445	oligopeptide ABC transporter, permease protein	PF00528	BPD_transp_1
SFBM_0446	oligopeptide ABC transporter, permease component	PF00528	BPD_transp_1
SFBM_0447	oligopeptide ABC transporter, ATPase subunit	PF00005	ABC_tran
SFBM_0448	oligopeptide ABC transporter, ATPase subunit	PF08352	oligo_HPY
		PF00005	ABC_tran
SFBM_0449	ABC transporter, extracellular solute-binding protein	PF08352	oligo_HPY
		PF00496	SBP_bac_5
SFBM_0450	ABC transporter, extracellular solute-binding protein	PF00496	SBP_bac_5
SFBM_0643	phosphonate ABC transporter, periplasmic phosphonate-binding protein	no motif	
SFBM_0644	phosphonate ABC transporter, ATPase subunit	PF00005	ABC_tran
SFBM_0645	phosphonate ABC transporter, inner membrane subunit	PF00528	BPD_transp_1
SFBM_0646	phosphonate ABC transporter permease	PF00528	BPD_transp_1
SFBM_0683	ABC-type sugar transport system	PF00532	Peripla_BP_1
SFBM_0684	ribose ABC transporter, permease protein RbsC	PF02653	BPD_transp_2
SFBM_0685	ribose ABC transporter, ATP-binding protein, pseudogene	PF00005	ABC_tran
SFBM_0758	ABC transporter, ATP-binding protein	PF00005	ABC_tran
SFBM_0786	sugar ABC transporter ATP-binding protein	PF00005	ABC_tran
SFBM_0789	ABC transporter, extracellular solute-binding protein	PF12010	DUF3502
SFBM_0791	sugar ABC transporter	PF00528	BPD_transp_1
SFBM_0792	ABC transporter	PF00528	BPD_transp_1
SFBM_0815	phosphate ABC transporter, regulatory protein PhoU	PF01895	PhoU
SFBM_0816	phosphate ABC transporter, ATPase component	PF00005	ABC_tran
SFBM_0817	phosphate ABC transporter, inner membrane subunit PstA	PF11812	DUF3333
SFBM_0818	phosphate ABC transporter, inner membrane subunit PstC	PF00528	BPD_transp_1
		PF00528	BPD_transp_1
SFBM_0819	phosphate ABC transporter, phosphate binding protein	PF11184	DUF2969
SFBM_0912	ABC transporter related protein	PF00664	ABC_membrane
SFBM_0913	ABC transporter related protein	PF00005	ABC_tran
		PF00664	ABC_membrane
SFBM_0989	iron compound ABC transporter, ATP-binding protein	PF00005	ABC_tran
SFBM_0990	iron compound ABC transporter, permease protein	PF01032	FecCD
SFBM_0991	ABC transporter, iron(III) dicitrate-binding periplasmic protein	PF01497	Peripla_BP_2
SFBM_1086	ABC transporter related protein	PF00005	ABC_tran
SFBM_1098	ABC transporter related protein	PF00005	ABC_tran
SFBM_1139	ABC transporter ATP-binding protein	PF00664	ABC_membrane
SFBM_1140	iron compound ABC transporter, substrate-binding protein	PF00005	ABC_tran
		PF01497	Peripla_BP_2
SFBM_1141	ABC transporter, ATP-binding protein	PF00005	ABC_tran
SFBM_1142	iron compound ABC transporter, permease protein	PF01032	FecCD
SFBM_1143	iron compound ABC transporter, permease protein	PF01032	FecCD
SFBM_1144	iron compound ABC transporter, iron compound-binding protein	PF01497	Peripla_BP_2
SFBM_1145	ferrichrome ABC transporter, permease protein	PF01032	FecCD
SFBM_1146	ferrichrome ABC transporter, permease protein	PF01032	FecCD
SFBM_1147	ferrichrome ABC transporter, ATP-binding protein	PF00005	ABC_tran
SFBM_1148	ABC transporter, permease protein	PF07690	MFS_1
SFBM_1193	ABC transporter related protein	PF02463	SMC_N
SFBM_1365	cobalt ABC transporter, permease protein	PF02361	CbiQ
SFBM_1366	cobalt ABC transporter, ATP-binding protein	PF00005	ABC_tran
SFBM_1367	cobalt ABC transporter protein CbiO	PF00005	ABC_tran
		PF12370	CoABC_C
SFBM_1477	cobalt ABC transporter, ATP-binding protein	PF00005	ABC_tran
SFBM_1478	cobalt ABC transporter, permease	PF12558	DUF3744
		PF02361	CbiQ
<b>2. PTS system</b>			
SFBM_0209	PTS system, mannitol-specific IIBC component	PF02302	PTS_IIB
SFBM_0345	PTS system, mannose-specific IIB component	PF02378	PTS_EIIC
		PF00359	PTS_EIIA_2
SFBM_0346	PTS system, mannose-specific IIC component	PF03609	EII-Sor
SFBM_0347	PTS system, mannose-specific IID component	PF03613	EIID-AGA
SFBM_0650	PTS system, IIBC component	PF00359	PTS_EIIA_2
		PF02302	PTS_IIB
		PF02378	PTS_EIIC

SFBM_0696	PTS system, IIabc component	PF02378 PF00367 PF00358	PTS_EIIC PTS_EIIB PTS_EIIA_1
SFBM_0706	PTS system, beta-glucoside-specific IIABC component	PF02378 PF00367 PF00358	PTS_EIIC PTS_EIIB PTS_EIIA_1
SFBM_0710	PTS system IIA component	PF00359	PTS_EIIA_2
SFBM_0711	PTS system IIC component	PF03611	EIIC-GAT
SFBM_0712	PTS system IIB component	PF02302	PTS_IIB
SFBM_0966	PTS system, IIA component	PF02255	PTS_IIA
SFBM_0998	PTS system, IIC component	PF02378	PTS_EIIC
SFBM_0999	PTS system IIB component	PF02302	PTS_IIB
SFBM_1004	PTS system IIB subunit	PF02302	PTS_IIB
SFBM_1005	PTS system IIC subunit	PF03611	EIIC-GAT
SFBM_1006	PTS system IIA subunit	PF00359	PTS_EIIA_2
SFBM_1013	PTS system cellobiose-specific IIC component	PF02378	PTS_EIIC
<b>3. MATE efflux family protein</b>			
SFBM_0213	MATE efflux family protein	PF01554	MatE
SFBM_0516	MATE efflux family protein	PF01554	MatE
SFBM_1096	MATE efflux family protein	PF01554	MatE
SFBM_1157	MATE efflux family protein	PF01554	MatE
<b>4. Other transporter</b>			
SFBM_0022	chromate transporter	PF02417	Chromate_transp
SFBM_0023	chromate transporter	PF02417	Chromate_transp
SFBM_0341	magnesium and cobalt transporter	PF01544	CorA
SFBM_0357	transporter, major facilitator family	PF07690	MFS_1
SFBM_0552	amino acid permease-associated protein	PF00324	AA_permease
SFBM_0639	xanthine/uracil/vitamin C permease	PF00860	Xan_ur_permease
SFBM_0778	uracil permease	PF00860	Xan_ur_permease
SFBM_0781	C4-dicarboxylate transporter/malic acid transport protein	PF03595	C4dic_mal_trans
SFBM_0964	sodium:dicarboxylate symporter family protein	PF00375	SDF
SFBM_0993	putative transporter	PF00892	EamA
SFBM_1016	sodium:dicarboxylate symporter family protein	PF00375	SDF
SFBM_1022	putative transporter	PF00496	SBP_bac_5
SFBM_1029	sodium/calcium exchanger protein	PF01699	Na_Ca_ex
SFBM_1215	ferrous iron transport protein A	PF04023	FeoA
SFBM_1216	ferrous iron transport protein B	PF02421 PF07670 PF07664	FeoB_N Gate FeoB_C
SFBM_1248	purine and pyrimidine permease	PF02133	Transp_cyt_pur
SFBM_1253	Na(+)/H(+) antiporter	PF00999	Na_H_Exchange
SFBM_1310	magnesium transporter	PF05239 PF03448 PF00571	PRC MgtE_N CBS
SFBM_1315	thiamin transport protein	PF09515	Thia_YuaJ
SFBM_1346	aminobenzoyl-glutamate transport protein	PF03806	ABG_transport
SFBM_1426	magnesium and cobalt transporter	PF01544	CorA
SFBM_1468	putative transporter	PF03180	Lipoprotein_9

**Table S3. Predicted polysaccharide degradation and proteolytic activities in SFB**

Gene name	Predicted function	pfam motif	PSORT prediction
<b>Polysaccharide degradation</b>			
SFBM_0066	$\alpha$ -N-acetylglucosaminidase family protein	$\alpha$ -N-acetylglucosaminidase (NAGLU)	Extracellular
SFBM_0558	glycoside hydrolase	Glycosyl hydrolase family 3 N terminal domain	Cytoplasm
SFBM_0697	$\beta$ -D-glucosidase	Glycosyl hydrolase family 1	Cytoplasm
SFBM_0784	endo- $\beta$ -N-acetylglucosaminidase	Glycosyl hydrolase family 85	Cytoplasmic membrane
SFBM_0790	$\alpha$ -mannosidase	Glycosyl hydrolase family 38 C-terminal domain	Cytoplasm
SFBM_0797	$\alpha$ -glucosidase	Glycosyl hydrolase family 31	Cytoplasm
SFBM_0996	$\beta$ -D-glucosidase	Glycosyl hydrolase family 1	Cytoplasm
SFBM_1000	6-phospho- $\beta$ -glucosidase	Family 4 glycosyl hydrolase	Cytoplasm
<b>Proteolysis</b>			
SFBM_0069	Carboxyl-terminal protease	Peptidase family S41	Cytoplasmic membrane
SFBM_0156	Aminopeptidase	Aminopeptidase I zinc metalloprotease (M18)	Cytoplasm
SFBM_0176	CAAX amino terminal protease family protein		Cytoplasmic membrane
SFBM_0254	Xaa-pro aminopeptidase	Metallopeptidase family M24	Cytoplasm
SFBM_0258	Aminoacyl-histidine dipeptidase	Peptidase family M20/M25/M40	Cytoplasm
SFBM_0261	Amidohydrolase family protein	Amidohydrolase family	Cytoplasm
SFBM_0280	O-sialoglycoprotein endopeptidase	Glycoprotease family	Cytoplasm
SFBM_0282	Serine protease	Trypsin	Cytoplasmic membrane
SFBM_0299	Peptidase	Peptidase family M23	Extracellular
SFBM_0302	ATP-dependent Clp protease, proteolytic subunit ClpP	Clp protease	Cytoplasmic membrane
SFBM_0303	ATP-dependent protease ATP-binding subunit ClpX	AAA domain (Cdc48 subfamily)	Cytoplasmic membrane
SFBM_0311	Thermostable carboxypeptidase	Peptidase family M20/M25/M40	Cytoplasmic membrane
SFBM_0342	Aminopeptidase	Aminopeptidase I zinc metalloprotease (M18)	Cytoplasm
SFBM_0421	Peptidase		Cytoplasmic membrane
SFBM_0436	Aminopeptidase	Peptidase family M28	Cytoplasmic membrane
SFBM_0470	Peptidase	Peptidase family M23	Cytoplasmic membrane
SFBM_0522	U32 family peptidase	Peptidase family U32	Cytoplasm
SFBM_0724	Membrane-associated zinc metalloprotease	Peptidase family M50	Cytoplasmic membrane
SFBM_0739	Clp protease	Clp protease	Cytoplasm
SFBM_0812	Peptidase	Peptidase family M28	Extracellular
SFBM_0833	Peptidase	Peptidase family U32	Cytoplasmic membrane
SFBM_0888	Serine protease	Trypsin	Extracellular
SFBM_0903	Peptidase	Insulinase (Peptidase family M16)	Cytoplasm
SFBM_0904	Peptidase	Peptidase M16 inactive domain	Cytoplasm
SFBM_1021	Peptidase	Peptidase family M28	Cytoplasmic membrane
SFBM_1035	Subtilisin like protease	Subtilase family	Cytoplasmic membrane
SFBM_1063	Putative cysteine protease	Transglutaminase-like superfamily	Cytoplasmic membrane
SFBM_1065	Peptidase	Insulinase (Peptidase family M16)	Cytoplasm
SFBM_1260	Glycoprotease family protein	Glycoprotease family	Cytoplasm
SFBM_1273	Peptidase	Peptidase family M23	Extracellular
SFBM_1325	Oligoendopeptidase F	Peptidase family M3	Cytoplasm
SFBM_1327	PepF/M3 family oligoendopeptidase	Peptidase family M3	Cytoplasmic membrane
SFBM_1358	isoaspartyl dipeptidase	Amidohydrolase family	Cytoplasm
SFBM_1374	Methionine aminopeptidase	Metallopeptidase family M24	Cytoplasm
SFBM_1427	LD-carboxypeptidase family protein	LD-carboxypeptidase	Cytoplasm
SFBM_1430	ATP-dependent Clp protease, ATPase subunit	AAA domain (Cdc48 subfamily)	Cytoplasm
SFBM_1450	Serine protease		Cytoplasmic membrane
SFBM_1459	Leucyl aminopeptidase	Cytosol aminopeptidase family, catalytic dom	Cytoplasmic membrane
SFBM_1485	ATP-dependent protease	Lon protease (S16) C-terminal proteolytic do	Cytoplasmic membrane
SFBM_1496	Subtilase family protein	Subtilase family	Cytoplasmic membrane
SFBM_1497	Peptidase	Peptidase family M23	Cytoplasmic membrane

**Table S4. The germination/sporulation-related genes and chemotaxis/motility-related genes in SFB**

Gene ID	Predicted function	Pfam description (e-value <10 <sup>-8</sup> )
<b>Germination</b>		
SFBM_0401	spore cortex-lytic enzyme	Putative peptidoglycan binding domain
SFBM_0605	serine/threonine protein kinase PrkC	Protein kinase domain
SFBM_0945	spore protease	Germination protease
SFBM_0949	stage V sporulation protein AE	SpoVA protein
SFBM_0950	stage V sporulation protein AD	Stage V sporulation protein AD (SpoVAD)
SFBM_0951	stage V sporulation protein AC	SpoVA protein
SFBM_1035	serine protease Csp	Subtilase family
SFBM_1289	spore germination protein GerAC	Spore germination B3/ GerAC like, C-terminal
SFBM_1290	spore germination protein GerAB	Spore germination protein
SFBM_1291	spore germination protein GerAA	Bacillus/Clostridium GerA spore germination protein
SFBM_1470	pre-pro-form spore cortex-lytic enzyme	Putative peptidoglycan binding domain
SFBM_1496	serine protease Csp	Subtilase family
<b>Sporulation</b>		
SFBM_0041	AbrB family transcriptional regulator	SpoVT / AbrB like domain
SFBM_0249	spore maturation protein A	Nucleoside recognition
SFBM_0250	spore maturation protein B	
SFBM_0298	small acid-soluble spore protein	Small, acid-soluble spore proteins, alpha/bet type
SFBM_0313	stage V sporulation protein B	Polysaccharide biosynthesis protein
SFBM_0314	stage V sporulation protein B	Polysaccharide biosynthesis protein
SFBM_0471	sporulation protein YtxC	YtxC-like family
SFBM_0490	small acid-soluble spore protein	Small, acid-soluble spore proteins, alpha/beta type
SFBM_0495	CotS family spore coat protein	Phosphotransferase enzyme family
SFBM_0496	spore coat protein	
SFBM_0524	sporulation protein YqfC	YabP family
SFBM_0525	stage IV sporulation protein	Putative stage IV sporulation protein YqfD
SFBM_0534	CotS family spore coat protein	Phosphotransferase enzyme family
SFBM_0588	sporulation protein YtfJ	Sporulation protein YtfJ (Spore_YtfJ)
SFBM_0632	stage V sporulation protein S	Stage V sporulation protein S (SpoVS)
SFBM_0660	stage IV sporulation protein B	SpoVB peptidase S55
SFBM_0661	sporulation transcription factor Spo0A	Sporulation initiation factor Spo0A C terminal
SFBM_0737	sporulation protein	
SFBM_0740	DNA translocase FtsK/SpoIIIE	FtsK/SpoIIIE family
SFBM_0745	stage V sporulation protein S	Stage V sporulation protein S (SpoVS)
SFBM_0809	stage IV sporulation protein A	Stage IV sporulation protein A (spore_IV_A)
SFBM_0825	RNA polymerase sigma-G factor	Sigma-70 region 2
SFBM_0826	sporulation sigma factor SigE	Sigma-70 region 2
SFBM_0827	sporulation factor SpoIIIGA	Sporulation factor SpoIIIGA
SFBM_0828	cell division protein FtsZ	Tubulin/FtsZ family, GTPase domain
SFBM_0831	sporulation sigma factor SigK	Sigma-70, region 4
SFBM_0896	cell division protein FtsW	Cell cycle protein
SFBM_0900	stage V sporulation protein D	Penicillin binding protein transpeptidase domain
SFBM_0944	stage II sporulation protein P	Stage II sporulation protein P (SpoIIP)
SFBM_0969	stage III sporulation protein AG	
SFBM_0970	stage III sporulation protein AF	Stage III sporulation protein AF (Spore_III_AF)
SFBM_0971	stage III sporulation protein AE	Stage III sporulation protein AE (spore_III_AE)
SFBM_0972	stage III sporulation protein AD	Stage III sporulation protein AC/AD protein family
SFBM_0973	stage III sporulation protein AC	Stage III sporulation protein AC/AD protein family
SFBM_0974	stage III sporulation protein AB	Stage III sporulation protein AB (spore_III_AB)
SFBM_0975	stage III sporulation protein AA	Protein of unknown function, DUF265
SFBM_1017	sporulation sigma factor SigF	Sigma-70 region 2
SFBM_1018	anti-sigma F factor	Histidine kinase-, DNA gyrase B-, and HSP90-like A
SFBM_1019	anti-sigma factor antagonist	STAS domain
SFBM_1127	stage II sporulation protein M	
SFBM_1272	sporulation transcriptional regulator spoIIID	Stage III sporulation protein D
SFBM_1274	stage II sporulation protein D	Stage II sporulation protein
SFBM_1288	stage II sporulation protein R	Stage II sporulation protein R (spore_II_R)
SFBM_1298	sporulation peptidase YabG	YabG peptidase U57
SFBM_1300	spore coat protein	Choline/ethanolamine kinase
SFBM_1437	stage II sporulation protein E	Stage II sporulation protein E (SpoIIE)
SFBM_1440	spore cortex biosynthesis protein	Spore cortex protein YabQ (Spore_YabQ)
SFBM_1441	sporulation protein	YabP family
SFBM_1444	stage V sporulation protein B	Polysaccharide biosynthesis protein
SFBM_1445	stage V sporulation protein T	SpoVT / AbrB like domain
SFBM_1458	septation protein spoVG	SpoVG
SFBM_1505	sporulation initiation inhibitor protein Soj	CobQ/CobB/MinD/ParA nucleotide binding domain
SFBM_1506	stage 0 sporulation protein J	ParB-like nuclease domain
SFBM_1512	stage III sporulation protein J	60Kd inner membrane protein
<b>Chemotaxis</b>		
SFBM_0442	methyl-accepting chemotaxis protein without membrane domain (probably intracellular type)	Methyl-accepting chemotaxis protein (MCP) signaling domain
SFBM_0564	chemotaxis protein CheW	CheW-like domain
SFBM_0565	chemoreceptor glutamine deamidase CheD	CheD
SFBM_0566	protein-glutamate methyltransferase CheB	CheB methyltransferase
SFBM_0567	chemotaxis protein methyltransferase CheR	CheR methyltransferase, SAM binding domain
SFBM_0568	chemotaxis protein CheA	CheW-like domain
SFBM_0569	chemotaxis protein CheC	CheC-like family
SFBM_0570	chemotaxis protein CheY	Response regulator receiver domain
SFBM_0571	chemotaxis signal transduction protein CheW	CheW-like domain
SFBM_1032	methyl-accepting chemotaxis protein (chemotaxis sensory transducer)	Methyl-accepting chemotaxis protein (MCP) signaling domain
SFBM_1114	chemotaxis protein MotB	OmpA family
SFBM_1115	chemotaxis protein MotA	MotA/TolQ/ExbB proton channel family
<b>Motility</b>		
SFBM_0572	flagellar switch protein FliM	Flagellar motor switch protein FliM
SFBM_0573	flagellar motor switch phosphatase FliY	CheC-like family
SFBM_0574	FigN family protein	FigN protein

SFBM_0575	flagellar hook-associated protein	Domain of unknown function (DUF1078)
SFBM_0576	flagellar hook-associated protein	Bacterial flagellin N-terminal helical region
SFBM_0577	flagellar assembly protein FliW	FliW protein
SFBM_0578	carbon storage regulator	Global regulator protein family
SFBM_0579	flagellar protein FliS	Flagellar protein FliS
SFBM_0580	flagellar hook-associated protein	Flagellar hook-associated protein 2 C-terminus
SFBM_0582	flagellar hook protein FlgE	Flagella basal body rod protein
SFBM_0583	flagellin domain-containing protein FliC3	Bacterial flagellin N-terminal helical region
SFBM_0584	flagellin domain-containing protein FliC4	Bacterial flagellin N-terminal helical region
SFBM_0642	flagellin domain-containing protein FliC2	Bacterial flagellin N-terminal helical region
SFBM_0953	flagellar FliD family protein	Flagellar protein (FliD)
SFBM_0954	flagellar hook assembly protein FlgD	Flagellar hook capping protein
SFBM_0955	flagellar hook-length control protein FliK	Flagellar hook-length control protein FliK
SFBM_0956	flagellar protein FliJ	Flagellar FliJ protein
SFBM_0957	flagellar protein export ATPase FliI	ATP synthase alpha/beta family, nucleotide-binding domain
SFBM_0958	flagellar assembly protein FliH	
SFBM_0959	flagellar motor switch protein FliG	FliG C-terminal domain
SFBM_0960	flagellar basal-body rod protein FlgC	
SFBM_0961	flagellar basal-body rod protein FlgB	
SFBM_0962	flagellin domain-containing protein FliC1	Bacterial flagellin N-terminal helical region
SFBM_1102	flagellar basal body rod protein FlgG	Domain of unknown function (DUF1078)
SFBM_1103	flagellar basal-body rod protein FlgG	Flagella basal body rod protein
SFBM_1105	RNA polymerase sigma factor for flagellar operon fliA	Sigma-70, region 4
SFBM_1107	flagellar biosynthesis protein	SRP54-type protein, GTPase domain
SFBM_1108	flagellar biosynthesis protein FliA	FHIPEP family
SFBM_1109	flagellar biosynthetic protein FliR/FliB	FliB HrpN YscU SpaS Family
SFBM_1110	flagellar biosynthetic protein FliQ	Bacterial export proteins, family 3
SFBM_1111	flagellar biosynthetic protein FliP	FliP family
SFBM_1112	flagellar biosynthesis protein	
SFBM_1113	flagellar basal body-associated protein	Flagellar basal body-associated protein FliL
SFBM_1316	flagellar hook-basal body complex protein FliE	Flagellar hook-basal body complex protein FliE
SFBM_1317	flagellar MS-ring protein FliF	Secretory protein of YscJ/FliF family

**Table S5. Sensor kinases in SFB**

<b>Gene name</b>	<b>Gene annotation</b>	<b>Cognate response regulator</b>	<b>Note</b>
SFBM_0276	sensor protein	SFBM_0275	no His kinase domain
SFBM_0368	two-component system, sensor histidine kinase	SFBM_0367	
SFBM_0465	two-component sensor protein	SFBM_0464	
SFBM_0504	histidine kinase	Orphan	PAS domain (E-value 0.15)
SFBM_0568	chemotaxis protein CheA	SFBM_0566 SFBM_0570	
SFBM_0794	sensor histidine kinase	SFBM_0793	
SFBM_0820	phosphate regulon sensor protein	SFBM_0821	PAS domain (E-value 0.034)
SFBM_1099	two component sensor histidine kinase	SFBM_1100	
SFBM_1134	two-component sensor histidine kinase	SFBM_1135	
SFBM_1451	two component sensor histidine kinase	SFBM_1452	

Table S6. The 277 human gut metagenome sequence reads that are highly homologous to the mouse SFB genome sequence

ID	length	identity	difference of the BLAST bit score between the top (to SFB) and the second hits	position in the SFB genome sequence		CDS
I85_1_FC30JGUAAXX:2:39:1519:918/1	44	95.24	11.9	29141	29182	SFBM_0021
I77_1_FC30JKTAAXX:6:45:886:1975/1	44	97.73	15.9	29340	29383	SFBM_0021
I77_1_FC30JKTAAXX:6:78:1609:1659/1	44	97.73	15.9	29340	29383	SFBM_0021
I85_1_FC30JGUAAXX:7:74:674:47/1	44	97.73	15.9	29340	29383	SFBM_0021
I85_1_FC30JGUAAXX:7:74:420:322/1	44	97.73	15.9	29341	29384	SFBM_0021
I85_1_FC30JGUAAXX:8:88:373:634/1	44	95.24	7.9	29342	29383	SFBM_0021
I360_1_FC30VNMAAXX:7:50:333:1378/1	45	97.67	13.9	29343	29385	SFBM_0021
I85_1_FC30JGUAAXX:8:67:1134:257/2	44	95.24	29.7	29360	29401	SFBM_0021
I77_1_FC30JKTAAXX:7:26:905:214/1	44	95.24	7.9	29383	29342	SFBM_0021
I352_1_FC30DVNAAXX:1:82:80:1255/1	44	95.45	15.9	29406	29363	SFBM_0021
I352_1_FC30DVNAAXX:6:43:818:1536/1	44	95.45	2	33450	33493	SFBM_0025
I85_1_FC30JGUAAXX:7:48:365:242/2	44	95.35	8	87657	87699	SFBM_0071
I352_1_FC30DVNAAXX:6:1:678:1742/1	44	95.24	7.9	87699	87658	SFBM_0071
I352_1_FC30DVNAAXX:3:1:589:1015/2	44	100	4	90983	91024	SFBM_0072
I361_2_FC30JAPAAXX:1:85:1094:125/1	44	100	4	90983	91024	SFBM_0072
I358_1_FC30JBRAAXX:7:47:1118:1274/2	44	95.45	4	91031	90988	SFBM_0072
I352_1_FC30DVNAAXX:4:39:425:870/1	44	95.24	13.9	210064	210023	SFBM_0194
I361_2_FC30JAPAAXX:4:25:715:352/1	44	95.24	13.9	210064	210023	SFBM_0194
I352_1_FC30DVNAAXX:8:50:49:1121/1	44	95.24	9.9	211972	211931	SFBM_0196
I361_2_FC30JAPAAXX:1:95:591:1698/1	44	95.35	13.9	212350	212392	SFBM_0197
I326_1_FC30GA4AAXX:1:54:1166:817/2	44	95.45	8	261022	261065	SFBM_0236
I358_1_FC30JBRAAXX:7:60:893:374/2	44	95.24	4	272732	272691	SFBM_0247
I330_1_FC30JM6AAXX:4:92:821:1784/2	44	95.45	15.9	273679	273722	SFBM_0247
I361_1_FC30VWMAAXX:7:1:1587:1547/1	65	95.38	23.2	273717	273781	SFBM_0247
I326_1_FC30VVEAAXX:5:51:1307:795/2	75	97.26	33.4	387338	387410	SFBM_0351
I328_1_FC30MD2AAXX:6:60:46:594/2	75	97.3	33.4	387338	387411	SFBM_0351
I328_3_FC30VVTAAAX:3:43:1789:1285/2	75	95.95	33.3	387338	387411	SFBM_0351
I330_1_FC30MKYAAXX:3:63:1755:2028/2	75	97.33	35.4	387338	387412	SFBM_0351
I85_2_FC30MG0AAXX:5:70:483:415/1	72	95.83	31.3	387339	387410	SFBM_0351
I330_1_FC30W0RAAXX:4:74:945:212/1	75	97.33	37.4	387340	387414	SFBM_0351
I361_1_FC30VWMAAXX:2:58:1725:1392/1	75	97.33	37.4	387340	387414	SFBM_0351
I85_2_FC30MG0AAXX:4:34:1331:2036/2	75	97.33	37.4	387340	387414	SFBM_0351
I85_1_FC30VW3AAXX:8:42:1637:1928/1	75	96	31.3	387345	387419	SFBM_0351
I328_1_FC30DVI1AAXX:2:10:221:1734/2	75	96	31.3	387346	387420	SFBM_0351
I330_1_FC30MKYAAXX:4:81:994:1321/2	75	95.83	25.3	387349	387420	SFBM_0351
I85_2_FC30MG0AAXX:8:44:295:286/1	75	95.83	25.3	387349	387420	SFBM_0351
I77_1_FC30JKTAAXX:7:19:298:1065/2	44	95.45	13.9	387383	387426	SFBM_0351
I361_1_FC30VWMAAXX:2:59:17873/1	61	96.72	31.2	387401	387411	SFBM_0351
I328_1_FC30MD2AAXX:5:75:1781:841/1	75	95.83	25.3	387409	387338	SFBM_0351
I360_1_FC30NG5AAXX:2:47:149:71/2	75	97.33	35.4	387413	387339	SFBM_0351
I326_1_FC30VVEAAXX:7:13:1466:923/1	75	97.22	33.3	387414	387343	SFBM_0351
FC30Y35AAXX:2:81:1183:1049#0/1	71	95.77	43.2	387432	387362	SFBM_0351
I85_1_FC30JGUAAXX:7:22:890:1508/1	44	95.24	17.8	387691	387650	SFBM_0351
I358_1_FC30JBRAAXX:1:13:1741:807/1	44	95.35	19.8	387692	387650	SFBM_0351
I85_1_FC30JGUAAXX:7:19:1070:1629/2	44	95.45	25.8	388075	388118	SFBM_0351
I77_1_FC30JKTAAXX:6:43:1378:848/2	44	95.45	11.9	388091	388134	SFBM_0351
I330_1_FC30JM6AAXX:4:78:1623:885/1	44	95.24	13.9	474016	473975	SFBM_0439
I360_1_FC30VNMAAXX:7:35:1689:1644/1	45	95.45	8	475104	475147	SFBM_0441
I77_1_FC30JKTAAXX:7:19:1335:490/2	44	97.73	6	475164	475207	SFBM_0441
I361_2_FC30JAPAAXX:6:97:1599:629/1	44	95.45	8	481614	481657	SFBM_0447
I352_1_FC30DVNAAXX:3:97:701:1677/1	44	95.35	13.9	481618	481660	SFBM_0447
I361_2_FC30JAPAAXX:6:46:1053:491/1	44	95.24	11.9	481619	481660	SFBM_0447
I352_1_FC30DVNAAXX:3:44:544:1567/1	44	95.24	2	481655	481614	SFBM_0447
I352_1_FC30DVNAAXX:3:59:285:141/1	44	95.45	8	481657	481614	SFBM_0447
I352_1_FC30DVNAAXX:2:74:253:1372/1	44	95.24	6	582874	582833	SFBM_0533
I361_2_FC30JAPAAXX:7:38:805:337/2	44	95.35	9.9	583495	583453	SFBM_0533
I358_1_FC30JBRAAXX:7:88:254:239/1	44	95.24	7.9	584478	584519	SFBM_0533
I352_1_FC30DVNAAXX:6:69:1040:905/2	44	95.45	8	584521	584478	SFBM_0533
I326_1_FC30VYFAAXX:5:40:243:1417/1	75	97.22	2	584867	584796	SFBM_0533
I330_2_FC30VY5AAXX:4:33:830:1877/2	75	97.22	2	584867	584796	SFBM_0533
I352_1_FC30DVNAAXX:3:38:436:1140/1	44	95.35	6	585015	585057	SFBM_0533
I352_1_FC30DVNAAXX:3:35:1290:246/2	44	95.24	2	585056	585015	SFBM_0533
I352_1_FC30DVNAAXX:1:86:168:905/1	44	95.35	25.8	588693	588735	SFBM_0536



I326_1_FC30GA4AAXX:6:100:627:1912/2	44	97.62	7.9	588830	588871	SFBM_0536
I358_1_FC30JBRAAXX:7:95:108:504/1	44	97.62	9.9	588830	588871	SFBM_0536
I360_1_FC30VNMAAXX:5:52:1605:1974/1	45	95.56	3.9	588840	588884	SFBM_0536
I77_1_FC30JKTAAXX:7:42:676:1034/2	44	95.35	6	589094	589136	SFBM_0536
I354_1_FC30VGDAAXX:7:8:724:1987/1	75	95.95	19.4	592356	592429	intergenic (SFBM_0540-SFBM_0541)
I85_1_FC30VW3AAXX:4:6:595:1210/1	66	96.92	23.2	592363	592427	intergenic (SFBM_0540-SFBM_0541)
I85_1_FC30VW3AAXX:4:22:1719:1823/2	65	96.77	21.8	592368	592429	intergenic (SFBM_0540-SFBM_0541)
I360_1_FC30VNMAAXX:8:50:256:1356/1	45	95.35	6	592585	592543	intergenic (SFBM_0540-SFBM_0541)
I326_1_FC30GA4AAXX:6:39:974:764/1	44	97.67	13.9	702775	702733	SFBM_0650
I352_1_FC30DVNAAXX:6:17:823:98/1	44	95.35	8	714256	714214	SFBM_0663
I360_1_FC30VNMAAXX:5:92:1784:1712/1	45	97.67	7.9	773175	773217	SFBM_0718
I360_1_FC30VNMAAXX:5:58:1200:1537/2	62	95.16	7.9	773176	773237	SFBM_0718
I330_2_FC30VY5AAXX:3:94:1046:1598/1	62	95.16	2	773178	773239	SFBM_0718
I360_1_FC30VNMAAXX:5:23:15:1683/2	60	96.67	7.4	773178	773237	SFBM_0718
I358_1_FC30JBRAAXX:1:83:1584:162/1	44	95.45	2	773197	773240	SFBM_0718
I352_1_FC30DVNAAXX:2:85:1323:1820/2	44	97.67	7.9	773217	773175	SFBM_0718
I360_1_FC30VNMAAXX:5:49:556:779/1	45	95.56	7.9	773225	773181	SFBM_0718
I361_2_FC30JAPAAXX:2:11:994:837/2	44	97.73	7.9	773225	773182	SFBM_0718
I361_2_FC30JAPAAXX:7:19:710:1183/1	44	95.35	6	773228	773186	SFBM_0718
I330_2_FC30VY5AAXX:6:62:1065:1523/2	61	98.28	6	773232	773175	SFBM_0718
I352_1_FC30DVNAAXX:3:71:1753:767/2	44	95.45	2	773237	773194	SFBM_0718
I85_1_FC30VW3AAXX:7:85:530:1311/1	75	100	4	773241	773169	SFBM_0718
I330_2_FC30VY5AAXX:3:61:1458:949/1	66	95.31	3.4	773242	773179	SFBM_0718
I330_2_FC30VY5AAXX:3:64:1481:676/2	71	95.59	2	773242	773175	SFBM_0718
I77_1_FC30JKTAAXX:6:25:1069:99/1	44	95.24	2	775323	775364	SFBM_0720
I361_2_FC30JAPAAXX:7:59:225:1027/1	44	95.24	11.9	775856	775897	SFBM_0721
I330_2_FC30VY5AAXX:3:75:1720:1989/1	65	95.16	15.8	782613	782674	SFBM_0726
I360_1_FC30VNMAAXX:5:45:1011:1115/1	45	95.56	9.9	782620	782664	SFBM_0726
I360_1_FC30VNMAAXX:6:27:350:1585/1	45	97.73	21.8	801647	801690	SFBM_0743
I360_1_FC30VNMAAXX:6:8:848:304/1	45	97.73	21.8	801690	801647	SFBM_0743
I360_1_FC30VNMAAXX:8:67:1519:212/1	45	95.56	29.7	801748	801792	SFBM_0743
I85_1_FC30JGUAAXX:8:17:1616:1857/2	44	95.35	4	862222	862264	SFBM_0799
I360_1_FC30VNMAAXX:3:57:1234:564/1	45	97.78	19.9	862224	862268	SFBM_0799
I326_1_FC30GA4AAXX:7:100:471:857/1	44	97.73	17.9	862267	862224	SFBM_0799
I326_1_FC30GA4AAXX:7:23:760:132/1	44	95.24	11.9	868401	868442	SFBM_0802
I77_1_FC30JKTAAXX:6:5:1329:1491/2	44	97.62	17.8	891685	891726	SFBM_0825
I77_1_FC30JKTAAXX:6:22:108:1427/2	44	95.45	13.9	891736	891693	SFBM_0825
I77_1_FC30JKTAAXX:6:65:216:1417/1	44	95.45	10	891738	891695	SFBM_0825
I361_2_FC30JAPAAXX:2:91:1370:1511/2	44	97.73	29.7	892653	892610	SFBM_0826
I326_1_FC30GA4AAXX:7:84:675:666/2	44	95.35	8	904143	904185	SFBM_0837
I77_1_FC30JKTAAXX:8:40:845:78/1	44	95.35	9.9	904143	904185	SFBM_0837
I361_2_FC30JAPAAXX:7:67:1717:1153/1	44	95.35	8	904185	904143	SFBM_0837
I352_1_FC30DVNAAXX:8:22:516:67/1	44	95.24	13.9	912879	912920	SFBM_0845
I361_2_FC30JAPAAXX:7:91:1192:787/1	44	95.24	4	917016	916975	SFBM_0850
I352_1_FC30DVNAAXX:3:13:1544:365/2	44	97.73	7.9	921504	921547	SFBM_0854
I358_1_FC30JBRAAXX:7:85:309:1767/1	44	97.73	4	924600	924643	SFBM_0856
I85_1_FC30JGUAAXX:2:29:1498:687/1	44	95.35	11.9	978657	978615	intergenic (SFBM_0911-SFBM_0912)
I354_1_FC30VGDAAXX:8:19:1588:637/1	75	97.33	17.9	1015071	1014997	SFBM_0942
I352_1_FC30DVNAAXX:4:17:1051:1956/1	44	95.45	4	1015368	1015411	SFBM_0942
I326_1_FC30GA4AAXX:2:86:885:1765/1	44	95.45	2	1015409	1015366	SFBM_0942
I361_2_FC30JAPAAXX:4:60:192:830/1	44	97.67	4	1015415	1015373	SFBM_0942
I352_1_FC30DVNAAXX:2:62:50:1823/1	44	95.24	2	1015418	1015377	SFBM_0942
I85_1_FC30JGUAAXX:2:57:980:1757/2	44	100	15.8	1054442	1054399	SFBM_0992
I77_1_FC30JKTAAXX:6:60:1511:1616/1	44	95.35	9.9	1108807	1108765	SFBM_1036
I360_1_FC30VNMAAXX:8:15:1337:2000/1	45	95.56	7.9	1132574	1132530	SFBM_1055
I326_1_FC30GA4AAXX:1:86:570:1746/1	44	95.24	4	1139207	1139248	SFBM_1061
I326_1_FC30GA4AAXX:1:96:906:1044/1	44	97.62	3.9	1139207	1139248	SFBM_1061
I330_1_FC30JM6AAXX:6:16:376:374/2	44	97.67	4	1139207	1139249	SFBM_1061
I326_1_FC30GA4AAXX:1:17:1255:1719/2	44	97.73	2	1139208	1139251	SFBM_1061
I330_1_FC30JM6AAXX:6:13:1335:859/1	44	97.73	2	1139208	1139251	SFBM_1061
I326_1_FC30GA4AAXX:1:64:1605:316/1	44	97.62	3.9	1139248	1139207	SFBM_1061
I330_1_FC30JM6AAXX:6:74:1741:1889/1	44	97.62	3.9	1139248	1139207	SFBM_1061
I330_1_FC30JM6AAXX:6:88:633:31/2	44	97.67	4	1139249	1139207	SFBM_1061
I326_1_FC30GA4AAXX:1:51:104:1046/1	44	97.73	4	1139250	1139207	SFBM_1061
I326_1_FC30GA4AAXX:7:61:1506:1700/2	44	97.73	7.9	1145589	1145632	SFBM_1067
I326_1_FC30GA4AAXX:1:1:1408:1617/1	44	97.62	7.9	1145829	1145788	SFBM_1067

I326_1_FC30GA4AAXX:1.95:1245:1447/1	44	97.62	7.9	1145829	1145788	SFBM_1067
I352_1_FC30DVNAAXX:6.97:1250:309/1	44	97.62	7.9	1145829	1145788	SFBM_1067
I85_1_FC30JGUAAXX:7.10:249:1425/2	44	97.62	7.9	1145829	1145788	SFBM_1067
I360_1_FC30VNMAAXX:8.70:1124:472/1	45	100	13.9	1145831	1145788	SFBM_1067
I354_1_FC30VW2AAXX:6.42:1716:278/2	75	96	8	1145863	1145789	SFBM_1067
I352_1_FC30DVNAAXX:7.42:789:1757/2	44	95.24	2	1246990	1247031	SFBM_1156
I361_2_FC30JAPAAXX:7.55:1311:1501/2	44	95.45	6	1247364	1247407	SFBM_1156
I80_1_FC30VGAAAXX:5.24:619:554/2	75	97.33	86.9	1260089	1260163	SFBM_1170
I352_2_FC30VYJAAXX:7.61:1227:1131/1	75	95.95	82.9	1260118	1260045	SFBM_1170
I80_1_FC30VGAAAXX:5.20:1172:1970/1	67	97.01	76.9	1260163	1260097	SFBM_1170
I321_1_FC30ML0AAXX:2.58:712:362/1	65	98.46	121	1260247	1260183	SFBM_1170
I326_1_FC30GA4AAXX:7.91:118:660/2	44	95.35	69.9	1262349	1262307	SFBM_1173
I352_1_FC30DVNAAXX:3.65:1012:633/1	44	95.24	27.8	1262887	1262846	SFBM_1173
I330_2_FC30VY5AAXX:6.1:1017:1849/2	75	97.22	80.9	1263261	1263190	SFBM_1173
I352_2_FC30VYJAAXX:4.64:381:769/2	68	95.59	70.9	1263317	1263384	SFBM_1173
I58_1_FC30VGCAAXX:3.2:307:613/1	70	95.52	68.9	1263317	1263383	SFBM_1173
I58_1_FC30VGCAAXX:4.14:1315:1987/1	66	95.38	64.9	1263344	1263408	SFBM_1173
I326_1_FC30MK7AAXX:5.7:1609:1320/1	62	95.16	59.5	1263345	1263406	SFBM_1173
I354_1_FC30VW2AAXX:7.89:1439:799/1	62	95.16	59.5	1263380	1263319	SFBM_1173
I80_1_FC30VGAAAXX:3.28:1071:208/2	70	95.59	70.9	1263392	1263325	SFBM_1173
I352_1_FC30DVNAAXX:3.57:1500:1706/2	44	95.24	27.8	1264325	1264366	SFBM_1173
I330_1_FC30JM6AAXX:4.55:1121:1227/2	44	97.73	17.9	1264992	1265035	SFBM_1174
I58_1_FC30DYKAAXX:1.41:706:530/1	75	95.83	6	1269378	1269307	SFBM_1179
I361_2_FC30JAPAAXX:4.25:216:1203/2	44	95.45	25.8	1283834	1283877	SFBM_1192
I77_1_FC30JKTAAXX:8.83:846:1694/1	44	95.35	23.8	1283835	1283877	SFBM_1192
I352_1_FC30DVNAAXX:6.66:1482:726/1	44	95.24	21.8	1283877	1283836	SFBM_1192
I361_2_FC30JAPAAXX:3.52:1115:1177/1	44	95.35	23.8	1283877	1283835	SFBM_1192
I352_1_FC30DVNAAXX:7.97:792:422/1	44	95.45	15.9	1365103	1365146	SFBM_1263
I352_1_FC30DVNAAXX:7.40:206:557/2	44	95.45	13.9	1365105	1365148	SFBM_1263
I361_2_FC30JAPAAXX:3.86:339:722/1	44	95.45	13.9	1365105	1365148	SFBM_1263
I361_2_FC30JAPAAXX:4.11:972:1102/2	44	95.45	13.9	1365105	1365148	SFBM_1263
I361_2_FC30JAPAAXX:4.75:154:510/1	44	95.45	13.9	1365105	1365148	SFBM_1263
I358_1_FC30JBRAAXX:7.89:464:670/1	44	95.24	11.9	1365143	1365102	SFBM_1263
I326_1_FC30GA4AAXX:6.34:278:93/1	44	95.45	15.9	1365146	1365103	SFBM_1263
I77_1_FC30JKTAAXX:8.40:1418:1344/2	44	95.35	9.9	1365148	1365106	SFBM_1263
I77_1_FC30JKTAAXX:7.48:244:73/1	44	97.62	11.9	1369065	1369106	SFBM_1265
I321_1_FC30VV6AAXX:2.68:492:827/2	75	95.83	12	1369612	1369683	SFBM_1265
I321_1_FC30VV6AAXX:6.34:1300:1615/1	75	95.83	74.9	1369612	1369683	SFBM_1265
I321_1_FC30VV6AAXX:6.34:1301:1613/1	64	96.83	64.9	1369612	1369674	SFBM_1265
I328_3_FC30VVTAAAXX:2.45:1706:1152/2	75	95.83	14	1369612	1369683	SFBM_1265
I328_3_FC30VVTAAAXX:2.71:205:584/2	75	95.83	12	1369612	1369683	SFBM_1265
I328_3_FC30VVTAAAXX:2.87:852:569/2	75	95.83	12	1369612	1369683	SFBM_1265
I330_1_FC30MKYAAXX:7.94:911:667/1	75	95.83	12	1369612	1369683	SFBM_1265
I330_2_FC30VY5AAXX:6.15:1622:795/1	75	95.83	12	1369612	1369683	SFBM_1265
I330_2_FC30VY5AAXX:6.21:1703:376/1	75	95.83	14	1369612	1369683	SFBM_1265
I352_1_FC30VWNAAXX:3.33:944:1089/2	75	95.83	14	1369612	1369683	SFBM_1265
I361_2_FC30W11AAXX:3.11:625:1674/1	74	97.18	80.9	1369612	1369682	SFBM_1265
I361_2_FC30W11AAXX:3.20:1135:1348/1	75	97.22	82.9	1369612	1369683	SFBM_1265
I361_2_FC30W11AAXX:3.37:1375:963/2	75	97.22	82.9	1369612	1369683	SFBM_1265
I361_2_FC30W11AAXX:3.43:796:194/2	75	97.22	82.9	1369612	1369683	SFBM_1265
I361_2_FC30W11AAXX:3.50:410:1324/1	75	97.22	82.9	1369612	1369683	SFBM_1265
I361_2_FC30W11AAXX:3.51:1728:246/2	75	97.22	82.9	1369612	1369683	SFBM_1265
I361_2_FC30W11AAXX:3.58:910:345/1	75	97.22	82.9	1369612	1369683	SFBM_1265
I361_2_FC30W11AAXX:3.84:1735:832/2	75	97.22	82.9	1369612	1369683	SFBM_1265
I361_2_FC30W11AAXX:3.84:343:847/2	75	97.22	82.9	1369612	1369683	SFBM_1265
I361_2_FC30W11AAXX:3.86:1082:2016/2	75	97.22	82.9	1369612	1369683	SFBM_1265
I361_2_FC30W11AAXX:5.10:412:1297/2	75	95.83	14	1369612	1369683	SFBM_1265
I321_1_FC30VV6AAXX:6.16:572:1900/1	66	96.88	23.3	1369617	1369680	SFBM_1265
I321_1_FC30VV6AAXX:6.6:1439:1339/1	61	98.36	68.9	1369618	1369678	SFBM_1265
I352_1_FC30DVNAAXX:8.67:1097:998/2	44	95.45	4	1369620	1369663	SFBM_1265
I352_1_FC30DVNAAXX:3.35:350:2017/1	44	95.24	29.7	1369653	1369612	SFBM_1265
I85_1_FC30JGUAAXX:7.100:675:1507/1	44	95.35	6	1369654	1369612	SFBM_1265
I352_1_FC30DVNAAXX:8.3:459:1254/2	44	95.45	4	1369663	1369620	SFBM_1265
I330_2_FC30VY5AAXX:2.55:1010:1552/1	67	95.38	66.8	1369676	1369612	SFBM_1265
I352_1_FC30DVNAAXX:8.97:556:1488/1	44	95.35	2	1369678	1369636	SFBM_1265
I321_1_FC30VV6AAXX:6.89:616:1688/1	75	97.22	82.9	1369683	1369612	SFBM_1265

I361_2_FC30W11AAXX:3:31:106:228/2	75	97.22	82.9	1369683	1369612	SFBM_1265
I361_2_FC30W11AAXX:3:31:1717:1052/1	75	97.22	82.9	1369683	1369612	SFBM_1265
I58_1_FC30DYKAAXX:3:10:1639:1880/2	75	95.83	12	1369683	1369612	SFBM_1265
I85_1_FC30JGUAAAX:7:62:324:327/1	44	95.35	11.9	1390352	1390310	SFBM_1285
I361_2_FC30JAPAAXX:7:63:1549:1374/2	44	95.35	13.9	1467962	1468004	SFBM_1344
I352_1_FC30DVNAAXX:8:25:545:194/2	44	95.24	9.9	1472498	1472539	SFBM_1348
I85_1_FC30JGUAAAX:2:5:1598:1971/1	44	95.35	13.9	1499354	1499396	SFBM_1390
I77_1_FC30JKTAAXX:7:72:1714:1246/1	44	95.24	11.9	1499355	1499396	SFBM_1390
I85_1_FC30JGUAAAX:8:8:1451:429/1	44	95.24	11.9	1499355	1499396	SFBM_1390
I358_1_FC30JBRAAXX:1:30:1082:714/2	44	95.45	17.9	1499382	1499339	SFBM_1390
I77_1_FC30JKTAAXX:7:95:1660:775/1	44	95.45	13.9	1499384	1499341	SFBM_1390
I361_2_FC30JAPAAXX:8:29:850:535/2	44	95.35	13.9	1499396	1499354	SFBM_1390
I358_1_FC30JBRAAXX:1:86:945:237/2	44	100	23.8	1500429	1500470	SFBM_1392
I361_2_FC30JAPAAXX:7:98:1025:1790/2	44	95.45	8	1500430	1500473	SFBM_1392
I85_1_FC30JGUAAAX:1:8:1054:313/1	44	100	13.9	1500434	1500475	SFBM_1392
I352_1_FC30DVNAAXX:2:50:1570:560/1	44	95.24	2	1500440	1500481	SFBM_1392
I85_1_FC30JGUAAAX:1:55:355:2006/2	44	100	23.8	1500474	1500431	SFBM_1392
I77_1_FC30JKTAAXX:7:30:272:1004/1	44	95.24	11.9	1503274	1503233	SFBM_1397
I352_1_FC30DVNAAXX:7:94:87:1510/2	44	95.35	17.9	1510347	1510389	SFBM_1402
I361_2_FC30JAPAAXX:2:57:925:904/2	44	97.73	23.8	1510392	1510349	SFBM_1402
I352_1_FC30DVNAAXX:8:58:1223:1006/1	44	97.62	3.9	1510847	1510888	SFBM_1402
I361_2_FC30JAPAAXX:1:70:1362:1403/1	44	97.62	3.9	1510847	1510888	SFBM_1402
I361_2_FC30JAPAAXX:2:8:780:1293/1	44	97.67	4	1510887	1510845	SFBM_1402
I360_1_FC30VNMAAXX:5:84:1294:571/1	45	97.73	6	1510888	1510845	SFBM_1402
I328_1_FC30MD2AAXX:6:64:942:273/1	75	95.95	22	1511454	1511527	SFBM_1402
I361_2_FC30JAPAAXX:7:47:1033:388/1	44	95.35	6	1511508	1511550	SFBM_1402
I352_1_FC30DVNAAXX:6:95:865:1649/2	44	95.45	6	1512570	1512613	SFBM_1403
I361_2_FC30JAPAAXX:2:25:262:825/1	44	95.45	13.9	1512748	1512791	SFBM_1403
I361_2_FC30JAPAAXX:2:23:817:1474/1	44	95.45	15.9	1512752	1512795	SFBM_1403
I358_1_FC30JBRAAXX:8:42:471:1625/1	44	95.35	6	1512785	1512743	SFBM_1403
I361_2_FC30JAPAAXX:4:2:514:1349/2	44	95.24	9.9	1512808	1512767	SFBM_1403
I352_1_FC30DVNAAXX:6:79:1391:441/1	44	95.35	27.8	1515223	1515265	SFBM_1403
I77_1_FC30JKTAAXX:6:88:902:1981/1	44	95.35	27.8	1515223	1515265	SFBM_1403
I352_1_FC30DVNAAXX:6:25:119:230/1	44	95.24	23.8	1515264	1515223	SFBM_1403
I352_1_FC30DVNAAXX:6:99:1681:1565/2	44	95.35	27.8	1515265	1515223	SFBM_1403
I361_2_FC30JAPAAXX:7:73:639:197/2	44	95.35	4	1516967	1517009	SFBM_1406
I77_1_FC30JKTAAXX:8:5:1084:269/2	44	95.35	4	1517009	1516967	SFBM_1406
I358_1_FC30JBRAAXX:7:50:1348:995/2	44	95.45	13.9	1517789	1517746	SFBM_1407
I352_1_FC30DVNAAXX:3:80:548:1597/1	44	95.35	6	1525538	1525580	SFBM_1418
I358_1_FC30JBRAAXX:8:88:1260:59/1	44	95.35	6	1525538	1525580	SFBM_1418
I326_1_FC30GA4AAXX:2:90:1085:617/1	44	95.24	6	1525580	1525539	SFBM_1418
I77_1_FC30JKTAAXX:8:44:22:600/1	44	95.35	6	1525580	1525538	SFBM_1418
I352_1_FC30DVNAAXX:3:67:853:191/1	44	95.24	4	1537383	1537342	SFBM_1429
I330_1_FC30JM6AAXX:6:65:884:734/1	44	95.24	11.9	1537429	1537470	SFBM_1429
I352_1_FC30DVNAAXX:8:69:1096:1117/2	44	95.24	4	1537529	1537488	SFBM_1429
I358_1_FC30JBRAAXX:1:34:629:1822/2	44	95.35	4	1543440	1543482	SFBM_1434
I85_1_FC30JGUAAAX:1:79:141:116/2	44	95.45	4	1543440	1543483	SFBM_1434
I85_1_FC30JGUAAAX:1:96:1355:911/1	44	95.45	4	1543440	1543483	SFBM_1434
I85_1_FC30JGUAAAX:1:51:717:304/1	44	95.35	2	1543442	1543484	SFBM_1434
I85_1_FC30JGUAAAX:1:86:829:1245/1	44	95.45	4	1543483	1543440	SFBM_1434
I358_1_FC30JBRAAXX:1:53:1000:632/2	44	95.35	2	1543484	1543442	SFBM_1434
I358_1_FC30JBRAAXX:1:53:1128:1291/1	44	95.45	4	1543484	1543441	SFBM_1434
I358_1_FC30JBRAAXX:1:54:1290:218/2	44	95.35	2	1543484	1543442	SFBM_1434
I85_1_FC30JGUAAAX:1:46:503:1653/1	44	95.35	2	1543484	1543442	SFBM_1434
I358_1_FC30JBRAAXX:1:34:1026:219/2	44	95.35	6	1543502	1543544	SFBM_1434
I358_1_FC30JBRAAXX:1:92:354:353/2	44	95.45	8	1543502	1543545	SFBM_1434
I85_1_FC30JGUAAAX:1:37:1529:1288/1	44	95.45	8	1543502	1543545	SFBM_1434
I85_1_FC30JGUAAAX:1:49:672:371/2	44	95.35	6	1543502	1543544	SFBM_1434
I85_1_FC30JGUAAAX:1:84:186:1843/1	44	95.45	8	1543502	1543545	SFBM_1434
I85_1_FC30JGUAAAX:1:92:1288:1448/1	44	95.45	8	1543502	1543545	SFBM_1434
I358_1_FC30JBRAAXX:1:40:1507:492/2	44	95.45	8	1543503	1543546	SFBM_1434
I358_1_FC30JBRAAXX:1:67:834:1590/1	44	95.35	6	1543504	1543546	SFBM_1434
I85_1_FC30JGUAAAX:1:30:35:1907/2	44	95.35	6	1543504	1543546	SFBM_1434
I85_1_FC30JGUAAAX:1:38:1581:116/2	44	95.24	4	1543505	1543546	SFBM_1434
I85_1_FC30JGUAAAX:1:64:151:825/1	44	95.24	4	1543505	1543546	SFBM_1434
I361_2_FC30JAPAAXX:2:94:1311:603/2	44	95.45	8	1543529	1543486	SFBM_1434

I85_1_FC30JGUAAXX:1:39:1329:744/1	44	95.35	4	1543544	1543502	SFBM_1434
I85_1_FC30JGUAAXX:1:52:701:1206/1	44	95.45	8	1543545	1543502	SFBM_1434
I358_1_FC30JBRAAXX:1:3:1045:1379/1	44	95.24	4	1543546	1543505	SFBM_1434
I358_1_FC30JBRAAXX:1:3:437:935/2	44	95.24	4	1543546	1543505	SFBM_1434
I358_1_FC30JBRAAXX:1:37:196:1298/1	44	95.24	4	1543546	1543505	SFBM_1434
I358_1_FC30JBRAAXX:1:62:1047:1594/1	44	95.24	4	1543546	1543505	SFBM_1434
I85_1_FC30JGUAAXX:1:18:1619:1804/1	44	95.45	8	1543546	1543503	SFBM_1434
I85_1_FC30JGUAAXX:1:80:1411:655/1	44	95.45	8	1543546	1543503	SFBM_1434
I361_2_FC30W11AAXX:3:70:526:688/1	60	95	7.9	1543595	1543654	SFBM_1434
I85_1_FC30JGUAAXX:8:68:1302:1741/1	44	97.62	3.9	1543613	1543654	SFBM_1434
I352_1_FC30DVNAAXX:7:47:1734:1771/1	44	95.35	8	1543668	1543626	SFBM_1434
I330_2_FC30VY5AAXX:8:17:1503:1202/1	64	95.16	13.9	1557326	1557387	SFBM_1448
I360_1_FC30VNMAAXX:7:1:98:545/1	45	95.35	2	1566739	1566697	SFBM_1455
I358_1_FC30VV9AAXX:6:35:1459:1574/1	75	96	2	1577387	1577313	intergenic (SFBM_1465-SFBM_1466)
I360_1_FC30VNMAAXX:7:70:749:1162/1	45	97.73	39.7	1578184	1578227	SFBM_1466
I361_2_FC30JAPAAXX:4:77:1611:1829/2	44	95.24	6	1615296	1615337	SFBM_1510