

Supplementary Information

Table S1. DNA FISH and immunostaining foci counts.

Species	ori foci per cell (%)				ter foci per cell (%)			
	1	2	3	>4	1	2	3	>4
Candidatus T. hypermnestrae (n _{ori} =413; n _{ter} =576)	76	20	5	-	90	10	-	-
A. filiformis (n _{ori} =748; n _{ter} =447)	95	5	-	-	90	10	-	-
S. muelleri (n _{ori} =188; n _{ter} =293)	28	43	21	8	25	32	21	22
C. steedae (n _{ori} =215; n _{ter} =236)	27	43	22	8	25	32	22	21
	left arm foci per cell (%)				right arm foci per cell (%)			
	1	2	3	>4	1	2	3	>4
A. filiformis (n _{left} =373, n _{right} =519)	95	5	-	-	81	16	3	-
	5XparS_c foci per cell (%)							
	1		2		3		>4	
S. muelleri (n=331)	20		57		18		5	
	ParB foci per cell (%)							
	1		2		3		>4	
A. filiformis (n=611)	87		13		-		-	
S. muelleri (n=277)	29		35		21		15	
C. steedae (n=399)	5		15		23		57	

Table S2. Description of *A. filiformis* chromatin frontiers.

LIQUID MEDIUM, EXPONENTIAL PHASE						
# ¹	start	end	type	Growth condition specificity ² (± 1 bin)	Proteins encoded by CAT4 genes ³ , rRNA genes ⁴ and <i>parS</i> sites ⁵ (contained in ± 1 bin)	Membrane, periplasmic or extracellular proteins ⁶ (contained in ± 1 bin)
1	1	1	down	exponential and stationary	ND	Ppk
2	42	42	down	exponential	Anr, unknown function	PurK, 2X unknown function, cytochrome c5, PlsY
3	44	46	up & down	exponential and solid	Unknown function	FtsN, colicin V production protein, RarD, Lgt, HisJ, 1x unknown function
4	58	58	down	exponential	Csd2	ND
5	76	78	up & down	exponential and stationary	Unknown function, LipA, ferredoxin	Unknown function, aerotaxis receptor, Atp FEBA, FixG
6	141	142	up & down	all conditions	ND	Ppi, PetCBA, unknown function
7	159	162	up & down	exponential and stationary	Fructokinase, EngB, 2X unknown function, multidrug transporter, YahK, 5S/16S/23S rRNA	Amidase, PgsBA, cytochrome c oxidase cbb3-type, 2X unknown function,
8	167	167	up	exponential and stationary	LysR-family transcriptional regulator, Tmk, YciO, 2X unknown function, LysA	Psd, SEL1 repeat-containing protein
9	189	190	down	exponential and stationary	ND	Nuo NMLKJH, 3X unknown function
10	196	197	up	exponential and stationary	Unknown function	Tpx, 4X unknown function, BamA
11	219	221	up & down	exponential and stationary	Nicotinamidase/pyrazinamidase, ErfK/SrfK, HexR	Thiamine transport system permease protein, unknown function
12	229	229	up & down	exponential and stationary	Unknown function (membrane protein), Ser tRNA	Unknown function, ABC-type Fe3+/spermidine/putrescine transport system, PIIY1
13	243	243	up	exponential	ND	2X unknown function, SecE, CpdB, recombinase
14	259	262	up & down	exponential and stationary	Peptide/bleomycin uptake transporter, LTXXQ-motif family protein; 5S/16S/23S rRNA; parS_7 (dialect g)	LutA, ComEA , peptide/bleomycin uptake transporter, LTXXQ-motif family protein
15	266	266	up	exponential	TamA, unknown function, 5S/16S/23S rRNA	TamA, unknown function, AqpZ
16	281	281	up & down	exponential	YceF, unknown function, 5S/16S/23S rRNA	DltB, unknown function, RnhB
17	340	340	up	exponential	ND	NqrBD, RxA, unknown function, LptD
18	370	370	down	exponential	TilS, phosphohistidine phosphatase; 5S/16S/23S rRNA	Unknown function, 2X amino acid ABC transporter, GltL, polar amino acid transporter
19	373	375	up & down	exponential	PyrL, putative ABC transport system substrate-binding protein, unknown function	Dual specificity phosphatase, unknown function
20	377	378	up	exponential	MurU, YdzA, unknown function, PykA, 5-formyltetrahydrofolate cyclo-ligase, LysR-family transcriptional regulator; 5S/16S/23S rRNA	MurU, YdzA, FtsK
21	418	418	up & down	exponential and stationary	Pcp, unknown function, HTH-type transcriptional regulator, haloacid dehalogenase-like hydrolase, phosphoglycolate phosphatase	TPR repeat-containing protein, SodA, Pcp, SpuE, autotransporter barrel domain-containing protein
22	448	449	up & down	exponential	Transposase, transglutaminase-like superfamily protein	2X unknown function, phospholipase A1, Sdh ABCD, transglutaminase-like protein

LIQUID MEDIUM, STATIONARY PHASE						
# ¹	start	end	type	Growth condition specificity ² (± 1 bin)	Proteins encoded by CAT4 genes ³ , rRNA genes ⁴ and <i>parS</i> sites ⁵ (contained in ± 1 bin)	Membrane, periplasmic or extracellular proteins ⁶ (contained in ± 1 bin)
1	1	3	up & down	exponential and stationary	ND	Ppk, DgkA, OmpR, O-antigen ligase, unknown function
5	76	79	up & down	exponential and stationary	2X unknown function, LipA, ferredoxin	2X Unknown function, aerotaxis receptor, AtpFEBA, FixG, FtsH
23	109	111	up & down	stationary	5X unknown function, PpiB	3X unknown function, thiol:disulfide interchange protein
24	124	124	down	stationary	PrfA, 2X unknown function, YafQ, RelB	Transporter, unknown function, Era
6	141	141	up	all conditions	ND	Ppi , PetCBA
7	161	162	down	exponential and stationary	EngB, 2X unknown function, multidrug transporter, YahK; 5S/16S/23S rRNA	Cytochrome c oxidase cbb3-type, 2X unknown function
8	167	167	up	exponential and stationary	LysR, unknown function, LysA	Psd, SEL1
9	188	188	down	exponential and stationary	ND	3X unknown function, NuoNMLKJH
10	196	197	up	exponential and stationary	2X unknown function	Tpx, 4X unknown function, BamA
25	203	203	down	stationary	Unknown function, RNaseP, IspU	3X unknown function, serine protease, SCO1/2, CdsA
26	216	216	down	stationary	Eda, RDD family protein, YrdA, MviN, Nicotinamidase/pyrazinamidase	RDD family protein, MviN, RTX-toxin related
11	220	222	up & down	exponential and stationary	ErfK/SrfK, HexR	Thiamine transport system permease, unknown function
27	225	225	up	stationary	TsaC	OmpA
12	228	228	up & down	exponential and stationary	ND	ND
28	251	252	down	stationary	RuvA; parS_1-4 (dialects f, e, b, f)	ABC transporter, 2X unknown function
14	256	263	up & down	exponential and stationary	Unknown function, LldF, peptide/bleomycin uptake transporter, LTXXQ motif family protein, 5S/16S/23S rRNA ; parS_7 (dialect g)	LutA, ComEA , peptide/bleomycin uptake transporter, LTXXQ motif family protein, RhtA
29	386	386	down	stationary	TldD, serine aminopeptidase, alpha/beta hydrolase	Alpha/beta hydrolase, pertactin
21	417	418	up & down	exponential and stationary	haloacid dehalogenase-like hydrolase, phosphoglycolate phosphatase	TPR repeat-containing protein, Soda, pcp, SpuA, autotransporter barrel domain-containing protein
30	486	486	down	stationary	IscA, TatD, 3X unknown function, CysE	IscU, 2X unknown function, NhaD, UbiA

SOLID MEDIUM								
# ¹	start	end	type	Growth condition specificity ² (± 1 bin)	RIF	CHL	Proteins encoded by CAT4 genes ³ , rRNA genes ⁴ and <i>parS</i> sites ⁵ (contained in ± 1 bin)	Membrane, periplasmic or extracellular proteins ⁶ (contained in ± 1 bin)
31	31	35	up & down	solid	N	N	AccA, Rpe, AcpS, 2X unknown function, MFS transporter, PBP7 , Apt, AroQ, Ung, Adk, UDP-glucose:protein N-beta-glucosyltransferase	MFS transporter, PBP7 , ArnT, FkpA, unknown function
3	47	47	down	exponential and solid	N	N	ND	HisJ, unknown function, MrdBA , MreD
32	54	56	up	solid	N	N	Ddc, unknown function, M23 peptidase , IlvA, Csd2	3X unknown function, LoiCD , DacA
33	61	61	up	solid	N	N	ND	4X unknown function, Signal transduction histidine kinase involved in nitrogen fixation, septation protein A
34	135	137	down	solid	N	N	hldE, YggH, 3',5'-nucleoside bisphosphate phosphatase	OppB , GltL, unknown function
6	143	144	up & down	all conditions	N	N	FAD/FMN-containing dehydrogenase	Ppi , PetCBA, 3X unknown function, EfeO/EfeM, EfeB, UraA
35	236	238	down	solid	N	N	ND	Unknown function, azaleucine resistance, CBS domain-containing protein, polar amino acid transport system substrate-binding protein
36	302	305	up & down	solid	N	N	2X unknown function, LysM, CysI	2X unknown function
37	354	355	up	solid	N	N	FHA	YrbEF, YidC, hemolysin activation/secretion protein, FHA
38	384	384	down	solid	N	N	Serine aminopeptidase, alpha/beta hydrolase	RmpM, MacB, Membrane fusion protein, macrolide-specific efflux system, alpha/beta hydrolase
39	391	391	up	solid	N	N	ND	Pertactin, 2X unknown function, Ydgl, HemYX
40	394	395	up	solid	N	N	put. DNA primase/helicase, unknown function, tmRNA	OmpR-family protein
41	420	420	up	solid	N	N	HTH-type transcriptional regulator, haloacid dehalogenase-like hydrolase, phosphoglycolate phosphatase, YiaA	SpuE , autotransporter barrel domain-containing protein, FabI , Hemoglobin/transferrin/lactoferrin receptor protein, YiaA, 2X unknown function, YciN
42	434	435	up	solid	N	N	PseF, RsmG	3X unknown function, MglBAC, polar amino acid transporter , GlnB
43	440	440	down	solid	N	N	PseB, membrane protein implicated in regulation of membrane protease activity, TrmH	3X unknown function, membrane protein implicated in regulation of membrane protease activity, YqiK
44	462	462	up	solid	N	N	MltG , MetF, TrpB, unknown function	NlpD, YhjE, holin-like protein, 2X unknown function
45	466	466	up	solid	N	N	3X unknown function, AroG, CtrD	3X unknown function, CtrBC

SOLID MEDIUM + RIFAMPICIN (RIF)					
# ¹	start	end	type	Present in solid medium?	Present in CHL?
1	2	2	up	N	Y
5	78	78	down	N	Y
46	119	120	up & down	N	N
24	124	124	up	N	N
6.II	139	140	up	N	Y
8	167	168	down	N	N
14	259	263	up & down	N	Y
47	338	338	up	N	N
48	350	351	up	N	N
49	366	367	up	N	Y
20	378	379	up	N	Y
29	384	386	up & down	N	N
50	402	404	up & down	N	N
51	414	414	down	N	N
21	417	419	up & down	N	Y
22	447	447	up	N	Y
30	486	486	down	N	Y

SOLID MEDIUM + CHLORAMPHENICOL (CHL)					
# ¹	start	end	type	Present in solid medium?	Present in RIF?
1	2	3	up	N	Y
5	76	78	up & down	N	Y
6.II	140	140	up	N	Y
7	161	162	down	N	N
10	196	196	up	N	N
14	259	263	up & down	N	Y
49	366	367	up	N	Y
20	378	379	up & down	N	Y
21	417	419	up & down	N	Y
52	444	444	down	N	N
22	447	449	up & down	N	Y
30	486	487	down	N	Y

¹Frontiers are numbered sequentially (from liquid medium exponential phase to liquid medium stationary phase, to solid medium). See Supplementary Data Set 1 for genomic position of frontiers, gene names, intracellular localization, category of expression and Supplementary Data Set 3 for annotation.

²All conditions frontiers: frontiers that share at least 1 bin irrespective of the growth condition. Exponential and solid frontiers: frontiers that share at least 1 bin in liquid medium exponential phase and on solid medium. Exponential and stationary frontiers: frontiers that share at least 1 bin in liquid medium exponential phase and stationary phase.

³Proteins encoded by genes that are CAT4 at least in the respective condition. See Supplementary Data Set 1 for genomic position of frontier-generating bins, gene names, intracellular localization category of expression.

⁴See Table S3 for rRNA genes genomic position.

⁵See Table S3 for *parS* genomic position.

⁶Proteins are defined as membrane proteins based on PSORTb. See Supplementary Data Set 1 for genomic position of frontier-generating bins, gene names, intracellular localization, category of expression.

RIF: rifampicin (25 µg/ml, 30 min); CHL: chloramphenicol (25 µg/ml, 30 min). Y: frontier present. N: frontier absent.

Table S3. Genomic positions and bins of *A. filiformis* rRNA genes and *parS* sites

rRNA operon #	rRNA gene	start	end	bin	
1	5S	793,150	793,260	159	
	23S	793,397	796,282	159 160	
	16S	797,108	798,634	160	
2	16S	1,300,206	1,301,732	261	
	23S	1,302,558	1,305,443	261 262	
	5S	1,305,580	1,305,690	262	
3	16S	1,318,439	1,319,965	264	
	23S	1,320,791	1,323,676	265	
	5S	1,323,813	1,323,923	265	
4	16S	1,392,778	1,394,304	279	
	23S	1,395,130	1,398,015	280	
	5S	1,398,152	1,398,262	280	
5	16S	1,854,102	1,855,628	371 372	
	23S	1,856,454	1,859,339	372	
	5S	1,859,476	1,859,586	372	
6	16S	1,877,147	1,878,673	376	
	23S	1,879,576	1,882,461	376 377	
	5S	1,882,598	1,882,708	377	
<i>parS</i> site #	dialect	start	end	bin	sequence
<i>parS1</i>	f	1,258,860	1,258,875	251	TGTTTCACGTGAAACA
<i>parS2</i>	e	1,258,901	1,258,916	251	TGTTTCACGTGAAACG
<i>parS3</i>	b	1,259,463	1,259,478	251	TGTTTCACATGAAACA
<i>parS4</i>	f	1,264,185	1,264,200	252	TGTTTCACATGAAACA
<i>parS5</i>	g	1,271,279	1,271,294	254	TGTTTCACATGAAACC
<i>parS6</i>	f	1,271,393	1,271,408	254	TGTTTCACATGAAACA
<i>parS7</i>	g	1,296,548	1,296,563	259	TGTTTCACATGAAACC

Table S4. Description of *C. steedae* chromatin frontiers.

LIQUID MEDIUM, EXPONENTIAL PHASE						
# ¹	start	end	type	Growth condition specificity ² (± 1 bin)	Products of CAT4 genes ³ , rRNA genes ⁴ and <i>parS</i> sites ⁵ (contained in ± 1 bin)	Membrane, periplasmic or extracellular proteins ⁶ (contained in ± 1 bin)
1	2	3	up	exponential	phosphate acetyltransferase	DUF2788 domain-containing protein, LplX, NhaC, phage holin family protein
2	26	26	up & down	exponential	SucAB, Sdh AB, AspC	Sdh ABCD
3	35	35	down	all conditions	PilY1 ; <i>parS_1</i> (dialect h)	Isoprenylcysteine carboxyl methyltransferase family protein; MFS transporter, PilY1
4	43	46	up & down	all conditions	LldD, 2X hemolysin, GatA; <i>parS_2</i> (dialect j)	OmpA, MotA/TolQ/ExbB proton channel family protein, Ubi B, 2X hemolysin, MrdAB, MreCD
5	181	181	up & down	exponential and solid	MetE, BamE ⁷ ; 5S rRNA , 16S rRNA , 23S rRNA	DUF1275 domain-containing protein, conserved membrane protein of unknown function, DUF4184 family protein, BamE ⁷
6	184	184	up & down	all conditions	BamE ⁷ , YadA-like adhesin, methyltransferase regulatory domain-containing protein	BamE ⁷ , YadA-like adhesin ⁸ , energy-coupling factor ABC transporter permease, LspA
7	190	191	up & down	exponential and solid	25 ribosomal proteins, InfA, SecY	nonpolar-amino-acid-transporting ATPase, SecY, polar amino acid transporter
8	210	210	down	exponential	HemL, 1 ribosomal protein, YceD, TetR/AcrR, NmoA	conserved membrane protein of unknown function
9	218	218	up & down	exponential	5S rRNA , 16S rRNA , 23S rRNA	Zinc/Manganese transport system permease protein, Uncharacterized transporter HI_0223, conserved membrane protein of unknown function, Zinc/Manganese transport system ATP-binding protein, DUF2339 domain-containing protein
10	246	249	up & down	all conditions	2 ribosomal proteins, TrmD, alpha-glucan phosphorylase, peptidase M23, roadblock/LC7 domain-containing protein; 5S rRNA , 16S rRNA , 23S rRNA	Azu, alpha-glucan phosphorylase, CcpA, FabF, polar amino acid transport system substrate-binding protein
11	272	274	up & down	exponential	Nuo AH, LolA, HsdM	Nuo HJKLN, Nqo, DUF2818 family protein, LolA
12	300	302	up & down	all conditions	1 ribosomal protein; 5S rRNA , 16S rRNA , 23S rRNA	CstA, ComEA , UraA, conserved protein of unknown function, conserved membrane protein of unknown function, AMP-binding protein, conserved membrane protein of unknown function, 1-acyl-sn-glycerol-3-phosphate acyltransferase
13	332	333	up & down	all conditions	Tig	EpsL, polysaccharide biosynthesis protein, MrcA
14	364	365	up & down	exponential	Zn ribbon domain-containing protein, Mtn	Ppi , DUF485 domain-containing protein, acetate/glycolate:cation symporter membrane-associated protein, anhydro-N-acetylmuramic acid kinase, conserved exported protein of unknown function (extracellular)
15	369	369	up	exponential	L-lactate permease, Adh	L-lactate permease, tyrosine-protein kinase Etk/Wzc
16	386	387	up & down	exponential and solid	Atp EFHEGDC	ATP F0F1 synthase subunit I, Atp ACB, P-type Cu ²⁺ transporter
17	405	405	up	exponential	3 ribosomal proteins, PriB, HemY, CopA	ferredoxin/ferredoxin---NADP ⁺ reductase, YgjV, CobA, Prepilin-type N-terminal cleavage/methylation domain-containing protein
18	418	418	up & down	all conditions	Lpd	Kdo2-lipid IVA lauroyltransferase/acyltransferase, choline dehydrogenase, BetT

LIQUID MEDIUM, STATIONARY PHASE						
# ¹	start	end	Type	Growth condition specificity ²	Products of CAT4 genes ³ , rRNA genes ⁴ and <i>parS</i> sites ⁵ (contained in ± 1 bin)	Membrane, periplasmic or extracellular proteins ⁶ (contained in ± 1 bin)
3	34	34	down	all conditions	PilY1; <i>parS_1</i> (dialect h)	LysO; PilY1
4	44	46	up & down	all conditions	2X hemolysins, GatA; <i>parS_2</i> (dialect j)	UbiB , 2X hemolysins, MrdBA, MreDC
19	153	153	up	stationary	Nitroreductase family protein, GrpE, Odhl	YedIH, TatCBA, putative outer membrane protein NMB0088
20	170	170	down	stationary	Adhesin, NmoA	NarYG, RsfS, conserved membrane protein of unknown function
6	184	184	down	all conditions	BamE ⁷	BamE ⁷ , YadA-like adhesin ⁸ , energy-coupling factor ABC transporter permease, LspA
21	232	232	up	stationary	ND	conserved protein of unknown function, hemolysin, Blc, PotIHG, BamA , putative Zinc metalloprotease NMA0084, Ppi
10	248	248	up & down	all conditions	roadblock/LC7 domain-containing protein, 1 ribosomal protein, TrmD; <i>5S rRNA</i> , <i>16S rRNA</i> , <i>23S rRNA</i>	CcpA, FabF
12	302	302	up	all conditions	Unknown function; <i>23S rRNA</i> , <i>5S rRNA</i>	ComEA , UraA, conserved protein of unknown function, conserved membrane protein of unknown function, AMP-binding protein, conserved membrane protein of unknown function, PlsC
13	332	333	up & down	all conditions	Tig	EpsL, polysaccharide biosynthesis protein, MrcA
15	370	371	up	stationary	Adh, prepilin-type N-terminal cleavage/methylation domain containing protein, unknown function, PilVW, FimT, DnaB	L-lactate permease, tyrosine-protein kinase Etk/Wzc, GfcE, LoiDC , ParA, UshA
22	399	399	down	stationary	Mdh	Lnt, YegL, Rhomboid family intramembrane serine protease, phosphate:Na ⁺ symporter
18	417	419	down	all conditions	Lpd, Pcm	choline dehydrogenase, BetT, multiple antibiotic resistance protein

SOLID MEDIUM						
# ¹	start	end	Type	Growth condition specificity ²	Products of CAT4 genes ³ , rRNA genes ⁴ and <i>parS</i> sites ⁵ (contained in ± 1 bin)	Membrane, periplasmic or extracellular proteins ⁶ (contained in ± 1 bin)
3	31	37	down	all conditions	Unknown function, PilY1, PBP7 , unknown function; <i>parS_1</i> (dialect h)	NupX, FHA , LysO, Isoprenylcysteine carboxyl methyltransferase family protein, MFS transporter , S-adenosylmethionine uptake transporter, PBP7
4	44	45	up & down	all conditions	2X hemolysin ; <i>parS_2</i> (dialect j)	UbiB, 2X hemolysin , MrdBA
23	174	174	up	solid	ND	RecC, polar amino acid transporter , KefC, SpuD
5	181	181	down	exponential and solid	BamE ⁷ ; 5S rRNA , 16S rRNA , 23S rRNA	BamE ⁷ , DUF1275 domain-containing protein, conserved membrane protein of unknown function, DUF4184 family protein
6	185	185	down	all conditions	ND	YadA-like adhesin ⁸ , energy-coupling factor ABC transporter permease, LspA, Phage coat protein
7	190	190	down	exponential and solid	DUF4124, RpoA, SecY, 10 ribosomal proteins	nonpolar-amino-acid-transporting ATPase, SecY, polar amino acid transporter
24	193	194	up	solid	10 ribosomal proteins, TufB	YocR, ZupT, FtsX, FtsE, Recombinase
10	246	248	down	all conditions	Unknown function, alphasglucanphosphorylase, ATP/GTP binding protein, M23 peptidase ; 5S rRNA , 16S rRNA , 23S rRNA	metallophosphoesterase, Azu, Alpha-glucan phosphorylase, CcpA, FabF
25	258	259	down	solid	Unknown function	2X RDD family protein, OppA , CdiB, FHA
26	262	262	up	solid	ND	conserved membrane protein of unknown function, MitB
12	302	302	up	all conditions	Unknown function; 5S rRNA , 16S rRNA , 23S rRNA	ComEA, UraA , 3X unknown function, AMP-binding protein, PlsC
27	328	329	down	solid	PIN7 domain-containing protein	YqiK , YbjQ, 3X unknown function, WecA
13	334	334	up & down	all conditions	PiINOPQ	PiINOPQ, EpsL, polysaccharide biosynthesis protein, MrcA
28	338	338	up	solid	IgA peptidase, 2X unknown function	LepA, signal peptidase I, Iga
29	373	373	up	solid	ND	LoIC , ParA, UshA, Mtr, MFS transporter
16	388	388	up	exponential and solid	ND	P-type Cu ²⁺ transporter, Mg transporter, membrane protein of unknown function, cardiolipin synthase A/B
18a ¹	416	416	down	all conditions	PrpC	LysE, 2X membrane protein of unknown functionm, bacterial/archaeal transporter family-2 protein, Kdo2-lipid IVA lauroyltransferase/acyltransferase
18b ¹	419	419	up & down	all conditions	Lpd	choline dehydrogenase, BetT, multiple antibiotic resistance protein

¹Frontiers are numbered sequentially (from liquid medium exponential phase to liquid medium stationary phase, to solid medium). In liquid medium exponential phase, bin 418 is involved in one frontier (frontier #18); in liquid medium stationary phase, bins 417 through 419 are involved in one frontier (frontier #18); on solid medium, bin 416 is involved in frontier 18a and bin 419 is involved in frontier 18b. See Supplementary Data Set 2 for genomic position of frontiers, gene names, intracellular localization, category of expression and Supplementary Data Set 3 for annotation.

²All conditions frontiers: frontiers that share at least 1 bin irrespective of the growth condition. Exponential and solid frontiers: frontiers that share at least 1 bin condition in exponential phase and on solid medium. Exponential and stationary frontiers: frontiers that share at least 1 bin condition in exponential phase and stationary phase.

³Proteins encoded by genes that are CAT4 at least in the respective condition. See Supplementary Data Set 2 for genomic position of frontier-generating bins, gene names, intracellular localization, category of expression.

⁴See Table S3 for rRNA genes genomic position.

⁵See Table S3 for *parS* genomic position.

⁶Proteins are defined as membrane proteins based on PSORTb. See Supplementary Data Set 2 for genomic position of bins, gene names, intracellular localization, category of expression.

⁷*bamE* spans across bins 182 and 183. Therefore, it matches frontier #5 (181) and frontier #6 (184) in liquid medium exponential *C. steedae*, but only #6 in stationary phase. On solid medium, *bamE* lies between frontier #5 (181) and frontier #6 (185).

⁸The *yadA*-like adhesin gene spans across bins 183 and 185.

Table S5. Genomic positions and bins of *C. steedae* rRNA genes and *parS* sites and genomic positions of *S. muelleri* *parS* sites.

<i>C. steedae</i> rRNA operon #	rRNA gene	start	end	bin	
1	5S	903740	903851	181	
	23S	903928	906811	181 182	
	16S	907406	908934	182	
2	16S	1079024	1080552	216 217	
	23S	1081147	1084031	217	
	5S	1084108	1084219	217	
3	16S	1231766	1233294	247	
	23S	1233889	1236773	247 248	
	5S	1236850	1236961	248	
4	16S	1498454	1499982	300	
	23S	1500610	1503495	301	
	5S	1503572	1503683	301	
<i>C. steedae</i> <i>parS</i> site #	dialect	start	end	bin	sequence
<i>parS1</i>	h	170,813	170,828	34	TGTTCCAAGTGGAAC
<i>parS2</i>	i	189,742	189,757	37	CGTTCCACCTGAAACG
<i>parS3</i>	j	226,624	226,639	45	AGTTTCATGTGAAACG
<i>parS4</i>	k	278,630	278,645	55	CGTTCCACCTGCAACA
<i>parS5</i>	e	1,023,430	1,023,445	204	TGTTTCACGTGAAACG
<i>parS6</i>	l	1,038,803	1,038,818	207	AGTTTCACGTGAAACG
<i>S. muelleri</i> <i>parS</i> site #	dialect	start	end		sequence
<i>parS1</i>	a	1,215,754	1,215,769		TGTTTCATGTGAAACA
<i>parS2</i>	b	1,215,793	1,215,808		TGTTTCACGTGAAACA
<i>parS3</i>	b	1,215,824	1,215,839		TGTTTCACGTGAAACA
<i>parS4</i>	c	1,447,496	1,447,511		CGTTCCAAGTGAAACA
<i>parS5</i>	c	1,448,045	1,448,060		CGTTCCAAGTGAAACA
<i>parS6</i>	c	1,448,594	1,448,609		CGTTCCAAGTGAAACA
<i>parS7</i>	c	1,449,143	1,449,158		CGTTCCAAGTGAAACA
<i>parS8</i>	c	1,449,692	1,449,707		CGTTCCAAGTGAAACA
<i>parS9</i>	d	2,178,556	2,178,571		TGTTGCAAGTGTAACA
<i>parS10</i>	a	2,345,466	2,345,481		TGTTTCATGTGAAACA

Table S6. Genomic position, gene content and *parS* site content of *A. filiformis* loop anchors. Only genes with predicted known functions and assigned EggNOG COG class (in parenthesis) are shown. Genes in eggNOG-based Clusters of Orthologous Groups (COG) Category *Metabolism* are in green, *Information processing* are in orange and *Cellular processes and signaling* are in black. See Supplementary Data Set 4 for additional information on genes with predicted function contained in loop anchors.

Exponential Loop 1 (Exp L1; anchor 2 + anchor 2')	Anchor 2'	
	Genomic position (Mbp; bins)	1.045–1.130; 210–226
	Genes	<i>polar aa transport permease</i> (P), <i>ribF</i> (H), <i>ubiG</i> (H), <i>truA</i> (J), <i>edd</i> (GE), <i>norM</i> (V), <i>murB</i> (M), <i>rlmD</i> (H), <i>ytfH</i> (K), <i>RTX toxin-related</i> (Q), <i>eda</i> (G), <i>asd</i> (E), <i>prmC</i> (J), <i>bioH</i> (I), <i>pncA</i> (Q), <i>lcbA</i> (M), <i>rlpA</i> (M), <i>yibK</i> (J), <i>thiamin transport</i> (P), <i>hexR</i> (K), <i>transpeptidase</i> (M), <i>nudE</i> (L), <i>trxA</i> (O), <i>valS</i> (J), <i>tsaC</i> (J), <i>recC</i> (L), <i>ompA</i> (JM), <i>adhesin</i> (W)
	Anchor 2 (Viewpoint 2; contains <i>parS1-6</i>)	
	Genomic position (Mbp; bins)	1.245–1.270; 251–254
Exponential Loop 2; Exp L2; anchor 3 + anchor 3')	Genes	<i>ruvA</i> (L), <i>hemerythrin-like</i> (P), <i>heptosyltransferase</i> (M), <i>etfB</i> (C), <i>etfA</i> (C), <i>ltaE</i> (E), <i>purD</i> (F), <i>ldh</i> (C)
	Anchor 3'	
	Genomic position (Mbp; bins)	1.020–1.135; 204–227
	Genes	<i>had</i> (O), <i>hisG</i> (E), <i>cdsA</i> (M), <i>dxr</i> (I), <i>proC</i> (E), <i>hisD</i> (E), <i>dtd</i> (J), <i>nagK</i> (Q), <i>truC</i> (J), <i>nnrD</i> (H), <i>gtrA</i> (U), <i>yfdH</i> (M), <i>transposase</i> (L), <i>polar aa transport permease</i> (P), <i>ribF</i> (H), <i>ubiG</i> (H), <i>truA</i> (J), <i>edd</i> (GE), <i>norM</i> (V), <i>murB</i> (M), <i>rlmD</i> (H), <i>ytfH</i> (K), <i>RTX toxin-related</i> (Q), <i>eda</i> (G), <i>asd</i> (E), <i>prmC</i> (J), <i>bioH</i> (I), <i>pncA</i> (Q), <i>lcbA</i> (M), <i>rlpA</i> (M), <i>yibK</i> (J), <i>thiamin transport</i> (P), <i>hexR</i> (K), <i>transpeptidase</i> (M), <i>nudE</i> (L), <i>trxA</i> (O), <i>valS</i> (J), <i>tsaC</i> (J), <i>recC</i> (L), <i>ompA</i> (JM), <i>adhesin</i> (W)
	Anchor 3 (Viewpoint 3)	
Stationary Loop 1 (Stat L1; anchor 2 + anchor 2')	Genomic position (Mbp; bins)	1.285–1.290; 257–258
	Genes	<i>csy1</i> (L), <i>cas3</i> (L), <i>cas1</i> (L), <i>lldF</i> (C)
	Anchor 2'	
	Genomic position (Mbp; bins)	1.030–1.135; 207–227
	Genes	<i>proC</i> (E), <i>hisD</i> (E), <i>dtd</i> (J), <i>nagK</i> (Q), <i>truC</i> (J), <i>nnrD</i> (H), <i>gtrA</i> (U), <i>yfdH</i> (M), <i>transposase</i> (L), <i>polar aa transport permease</i> (P), <i>ribF</i> (H), <i>ubiG</i> (H), <i>truA</i> (J), <i>edd</i> (GE), <i>norM</i> (V), <i>murB</i> (M), <i>rlmD</i> (H), <i>ytfH</i> (K), <i>RTX toxin-related</i> (Q), <i>eda</i> (G), <i>asd</i> (E), <i>prmC</i> (J), <i>bioH</i> (I), <i>pncA</i> (Q), <i>lcbA</i> (M), <i>rlpA</i> (M), <i>yibK</i> (J), <i>thiamin transport</i> (P), <i>hexR</i> (K), <i>transpeptidase</i> (M), <i>nudE</i> (L), <i>trxA</i> (O), <i>valS</i> (J), <i>tsaC</i> (J), <i>recC</i> (L), <i>ompA</i> (JM), <i>adhesin</i> (W)
Stationary Loop 2 (Stat L2; anchor 3 + anchor 3')	Anchor 2 (Viewpoint 2; contains <i>parS1-6</i>)	
	Genomic position (Mbp; bins)	1.245–1.270; 251–254
	Genes	<i>ruvA</i> (L), <i>hemerythrin-like</i> (P), <i>heptosyltransferase</i> (M), <i>etfB</i> (C), <i>etfA</i> (C), <i>ltaE</i> (E), <i>purD</i> (F), <i>ldh</i> (C)
	Anchor 3'	
	Genomic position (Mbp; bins)	1.065–1.090; 213–218
Stationary Loop 2 (Stat L2; anchor 3 + anchor 3')	Genes	<i>ytfH</i> (K), <i>RTX toxin-related</i> (Q), <i>eda</i> (G), <i>asd</i> (E), <i>prmC</i> (J), <i>bioH</i> (I), <i>pncA</i> (Q), <i>lcbA</i> (M), <i>CDP-glycerol glycerophosphotransferase</i> (M)
	Anchor 3 (Viewpoint 3)	
	Genomic position (Mbp; bins)	1.285–1.290; 257–258
	Genes	<i>csy1</i> (L), <i>cas3</i> (L), <i>cas1</i> (L), <i>lldF</i> (C)

Solid Loop (Solid L; anchor 1 + anchor 1')	Anchor 1'	
	Genomic position (Mbp; bins)	1–1.005; 200–201
	Genes	<i>dadA</i> (C), <i>serS</i> (J), <i>transposase</i> (L), <i>tetR</i> (K), <i>dusA</i> (H)
	Anchor 1 (Viewpoint 1)	
	Genomic position (Mbp; bins)	1.135–1.145; 227–229
	Genes	<i>adhesin</i> (W), <i>argF</i> (E), <i>pdxA</i> (H), <i>ftsY</i> (U), <i>cbiM</i> (H)

Table S7. Genes in loop anchors in liquid exponential, liquid stationary or solid medium *A. filiformis*.

Gene	Liquid Exponential	Liquid Stationary	Solid medium
Adhesin	✓	✓	✓
Transposase	✓	✓	✓
<i>recC/ruvA</i>	✓	✓	—
<i>cas</i> genes	✓	✓	—
<i>murB-lcbA</i> region ✓		✓	—
<i>tetR</i>	—	—	✓
<i>dusA</i>	—	—	✓
<i>ftsY</i>	—	—	✓
<i>cbiM</i>	—	—	✓

Table S8. DNA FISH probe primers.

Target	Probe No.	Primer	Sequence (5'-3')	Product (nt)
<i>A. filiformis ori</i> (9,232 nt)	1	Af_Ori1F	GGTTTTCAATGCCGTATCT	300
		Af_Ori1R	GACAATTTGTCCAAAGATGAG G	
	2	Af_Ori2F	CGCAGCCAATTCAATATGAC	300
		Af_Ori2R	CAACAAGCAGGTTTCAGAAG	
	3	Af_Ori3F	GTGGTGCAGTTTCAGATAGT	300
		Af_Ori3R	AAACTCTACAACGGTAGCG	
	4	Af_Ori4F	TGTCAAACCAATCATGACG	300
		Af_Ori4R	AAGACACGTCTTTGCGTAT	
	5	Af_Ori5F	GCAATCACATAGCGACCTT	300
		Af_Ori5R	AACCAATCCCTTGTCTGAA	
	6	Af_Ori6F	TTTAAGCCAGCCTTTTGGAT	300
		Af_Ori6R	GGATTTTGAGTTTGACCCG	
	7	Af_Ori7F	GCTTCAGCTTGAGATACTG	300
		Af_Ori7R	AGACATTTTGGAAGCGGTAA	
	8	Af_Ori8F	TGGAATAGAAGCCAACTCAG	300
		Af_Ori8R	TATCGCGGTATCAGTGTTG	
	9	Af_Ori9F	ACGCTAGATACATCTACGC	300
		Af_Ori9R	GATTTTGGGTCCTCGTGG	
	10	Af_Ori10F	ACACATCTACTGATTCGTCA	300
		Af_Ori10R	CAGTTCCAATTCTTTGACCAAC	

<i>A. filiformis</i> ter (6,778 nt)	1	Af_Ter1F	TTGGTTTACCCCATTAGCG	300
		Af_Ter1R	CATGTCAAGGCAGCTTTG	
	2	Af_Ter2F	ATGTGGCAGCAATTTTCAG	300
		Af_Ter2R	GAACACGAATTGCCCTTTTA	
	3	Af_Ter3F	ACGCAAATACGCCAAAAAC	300
		Af_Ter3R	TACATTTGGGGCGACAAA	
	4	Af_Ter4F	AACTTTGCACCACATATTCG	300
		Af_Ter4R	GCCGTTTTGTTC AAGTGT	
	5	Af_Ter5F	TTATAATGCGCCCAACAATG	300
		Af_Ter5R	GCACTTCGCATTAAAAACAC	
	6	Af_Ter6F	TGACGACAAAGTGGAACG	300
		Af_Ter6R	AACAACCACCAAGCCAAT	
	7	Af_Ter7F	CCTGAAACAAAATCCGCC	300
		Af_Ter7R	ATTCATGCGGATTTTGACC	
	8	Af_Ter8F	TGGAAGAGTCCACCAGTT	300
		Af_Ter8R	AAAACAACCACATTGGCG	
	9	Af_Ter9F	GCAACAACACGCCATTTT	300
		Af_Ter9R	TTCCCCTGCCCCATTATTA	
	10	Af_Ter10F	CGCACAGCAATTCAAAATCT	300
		Af_Ter10R	GTGTGAATGTGATACAAGCG	

A. filiformis left arm (6,718 nt)	1	Af_leftarm1F	TGCAGGTTTAGGAACATCTAC	300
		Af_leftarm1R	GCTGAAATTCCGGGTTTG	
	2	Af_leftarm2F	GATGGCAACCAAGTCTTTATC	300
		Af_leftarm2R	ATGGTGTTGTGTATCTGCA	
	3	Af_leftarm3F	AACCTGTATTGGGAATGGAAC	300
		Af_leftarm3R	AAGCCCTGATTATTGAGTCG	
	4	Af_leftarm4F	CACTCGGCTCACTTCCG	303
		Af_leftarm4R	CTAGACATCAGCCCCAGC	
	5	Af_leftarm5F	TTTATTCTTCTGATGGCGTG	282
		Af_leftarm5R	AGGCTTCATTGAATTTGCG	
	6	Af_leftarm6F	CACTTTGACCAAAGACCAAA	300
		Af_leftarm6R	CGTTCGTAAATCAATTCGGC	
	7	Af_leftarm7F	GCGCAATTTTCCATCAAAAG	300
		Af_leftarm7R	TGGGTAACATAAGGACGGT	
	8	Af_leftarm8F	GGCTACGATTTCCACAGTAA	300
		Af_leftarm8R	GAAACCAAAACGTTGCACA	
	9	Af_leftarm9F	GCGCTGGAAAAATTGCAA	314
		Af_leftarm9R	TTGCCCACATAATCTTGTG	
	10	Af_leftarm10F	TCAAATCCACATCGCGC	316
		Af_leftarm10R	TTTTTCTTGCGCGTGATG	

<i>A. filiformis</i> right arm (7,846 nt)	1	Af_rightarm1F	ACGATAAACCTTGATGTTGC	300
		Af_rightarm1R	TTGATGATGCGCTTGAAAC	
	2	Af_rightarm2F	AAAATCGGTCAAAATAGCCC	300
		Af_rightarm2R	CAAACGCATTATCCCAATCTC	
	3	Af_rightarm3F	GCAGCCTGAAAATTATTCTG	300
		Af_rightarm3R	TTGCAAAACGTGGACATC	
	4	Af_rightarm4F	CAAACGTGGCAAATTTCTG	317
		Af_rightarm4R	GGCACCAAATAGCGTACC	
	5	Af_rightarm5F	AATGTCGCTGATTGGTTTG	300
		Af_rightarm5R	GCCAAACTCAATGCAAACA	
	6	Af_rightarm6F	GCAGGCGAATTTGGTTTT	300
		Af_rightarm6R	GTGGTTGTCAATCACGGTA	
	7	Af_rightarm7F	CTGAAACGGCTTTTTAGGTG	300
		Af_rightarm7R	CAGCCGACTTAACCCAAG	
	8	Af_rightarm8F	GAATAAACGCAGGGTACG	283
		Af_rightarm8R	ATGAACACAATTTGCCCG	
	9	Af_rightarm9F	TTTGCCAAAATCGGGCG	280
		Af_rightarm9R	CAAACAAAATCACGCCAAAT	
	10	Af_rightarm10F	ACGGCTTTGAATGCTTTG	286
		Af_rightarm10R	GCGTATTGCCAAAATCCAC	

<i>S. muelleri</i> ori (8,158 nt)	1	Sm_ori_1F	CAATGTAGATGCCGCTGAA	300
		Sm_ori_1R	CAACGATAGGTCACATTTGC	
	2	Sm_ori_2F	GATTTAGCAGCAGAACAACC	300
		Sm_ori_2R	GCCACAAATATCCACTACGT	
	3	Sm_ori_3F	CTATATATTCATTCGCTGGACG	300
		Sm_ori_3R	TTACCGCTTTTACGTGGG	
	4	Sm_ori_4F	ATTGATTACGTTGGCTCATG	300
		Sm_ori_4R	TTTTACGAGCAAGCTGTCT	
	5	Sm_ori_5F	GTGCTGATTTACGACGAAG	300
		Sm_ori_5R	CACCAATTGAGAAGTACGC	
	6	Sm_ori_6F	CCAAACCCACTACACATAAT	300
		Sm_ori_6R	GTTTTGGTGATCCTGAAAC	
	7	Sm_ori_7F	CAAAATTAGCCAGCGGAATC	300
		Sm_ori_7R	TTTTGGGGCAGATTGATTC	
	8	Sm_ori_8F	TATTACCTAACTTTGCTCCG	300
		Sm_ori_8R	AAAAAGGAGTGTGTACCGA	
	9	Sm_ori_9F	TACTATCCTGCATAC CTGCA	325
		Sm_ori_9R	AATTTGGTGGCTACGAATG	
	10	Sm_ori_10F	CATTTGTGCAGTTTGGTTAG	300
		Sm_ori_10R	GTGAAAATGTCCATGAATCC	

<i>S. muelleri</i> ter (8,187 nt)	1	Sm_ter_1F	GATTTGCGGTCAATCGTT	300
		Sm_ter_1R	GGGCAAATTCAATTCAGACC	
	2	Sm_ter_2F	ATGAAACCATCTGAACCGT	300
		Sm_ter_2R	CATTGATGCACTGGTTATTG	
	3	Sm_ter_3F	GATGATTTACG GATTTTAGCC	300
		Sm_ter_3R	CGTTCTCAATTTGTAGACCAAG	
	4	Sm_ter_4F	TCGTTAATTCAGGCGTGTC	300
		Sm_ter_4R	GGACGGTTGGACTTATTCG	
	5	Sm_ter_5F	TTGTCCGTCTAAATAAGGTGTC	300
		Sm_ter_5R	TTGGACAAACTCAAACATGG	
	6	Sm_ter_6F	CACCGAATGATCAGGAATG	300
		Sm_ter_6R	GGTTTAAAAGCGAGAGACG	
	7	Sm_ter_7F	TTCCTTGTGGGTCTAATACTTG	300
		Sm_ter_7R	CAGAGCCATTAAGTAAATCACG	
	8	Sm_ter_8F	AGCATCAACACGTACGAAA	300
		Sm_ter_8R	GATTATCGGCATGAGACGG	
	9	Sm_ter_9F	GCGTAGGATTATTCTCATTAGC	314
		Sm_ori_10R	GTGAAAATGTCCATGAATCC	

<i>S. muelleri</i> 5x parS_c (9,335 nt)	1	Sm_parS1F	AATACCCATCCTACGTCTGA	300
		Sm_parS1R	CTCTTGTTGGCGTTCTAAAATC	
	2	Sm_parS2F	TTATGCACGTGAGATTGAC	300
		Sm_parS2R	GCATTACGCAACAAGTCAT	
	3	Sm_parS3F	CAACATCACAAAGTACCAGTAC	300
		Sm_parS3R	CTACGGCTGTAGGTGATAAT	
	4	Sm_parS4F	TGGATATTCCTGTGGTACCA	300
		Sm_parS4R	CTGGGTCATAAGTGTAATTCAC	
	5	Sm_parS5F	GTAAAGCTAAAGACCACACAG	300
		Sm_parS5R	GTACACCTGTAACAGTTGT	
	6	Sm_parS6F	AGGCAATGTAACGACAGAAG	300
		Sm_parS6R	GTAACGTGTAAACCGCCTTA	
	7	Sm_parS7F	GGTAATACCAAAGGCACAAATC	300
		Sm_parS7R	CGGTTCTAATTGCAACGTC	
	8	Sm_parS8F	AGTTCTGGCGTGACTTTATT	300
		Sm_parS8R	AACTTTACCAGTCGTGTAAC	
	9	Sm_parS9F	TACTGATAGTTTACCAGTAGCG	300
		Sm_parS9R	AATTTTGCTGTTGAGGTATCG	

Ca. T. hypernestrae ori (2,858 nt)	1	Th_dnaA_start	TCCGTGGAAATCTGGAATCAATGT	306
		Th_ori_1R	TGTGGATTTTTCTTGAGGTGTGG	
	2	Th_ori_2F	CCGCGAGCAACTTAATTACCG	344
		Th_ori_2R	GCCTGCGAAGAACTGAATATCA	
	3	Th_ori_3F	TCGAATCCAAACAGCAAATCGT	315
		Th_ori_3R	GTACGTTTCTGGCAAATTCGAG	
	4	Th_ori_4F	GGACATGCTTGCTGCTCAG	315
		Th_ori_4R	CATTATGCTGTCAGGGTTCTGAAC	
	5	Th_ori_5F	TTCAGTGCCAGCAATTCGCC	310
		Th_ori_5R	CCGGATAAAGTCGTCCTTTGCC	
	6	Th_ori_6F	CGGAACCGATCTAGAAATAGAGG	304
		Th_ori_6R	CGCCATCGAAAATGCAGTCTT	
	7	Th_ori_7F	CAGGACGTTCGCTATTATCT	334
		Th_ori_7R	CATAGGCAACTTGCTCCGGA	
	8	Th_ori_8F	AGATACACTGAAGCAGGCATTG	317
		Th_ori_8R	GTCTCATCGGCATTACTACAAAG	
	9	Th_ori_9F	GACACATGATTTTGAAGGTAGAG	216
		Th_dnaA_stop	CAGCCTCTCAGTGTCACCGT	

Ca. T. hypernestrae ter (3,239 nt)	1	Th_dif_F1	GTAAGGGGATTGCCAGGCTTG	311
		Th_dif_R1	GTGGACGACACGGTGCATTT	
	2	Th_dif_F2	CACGATGCCCAGCGTCATG	333
		Th_dif_R2	CTCTCGACCAAGGAGGTACTTGC	
	3	Th_dif_F3	GTCGCCCCGCTTGTCTGATATCG	314
		Th_dif_R3	GAGAACCTGACCGGCGTTTATT	
	4	Th_dif_F4	ATGAAATCGGTATCCGTACGG	318
		Th_dif_R4	GAATTTCTCCGAGGCGCCG	
	5	Th_dif_F5	AGCGTCAGAAACCCGATGG	323
		Th_dif_R5	CTGCTGATCATTGTGGTCGCC	
	6	Th_dif_F6	GCCAGCGGCAGGAGATGC	324
		Th_dif_R6	GGTTGTCTGATCTGATTGAGGACCC	
	7	Th_dif_F7	GTCAGCGCATCCCCCTCG	319
		Th_dif_R7	GGCTGGTGATTGCAGGGACC	
	8	Th_dif_F8	AGCGATGGCCCAAATCCAAG	305
		Th_dif_R8	ATGATGTCCCCACGGGATAATTCG	
	9	Th_dif_F9	CATGCAGACCTTTGTCTGCGC	330
		Th_dif_R9	GGCTTCCTCCTTGATGTGCTCG	
	10	Th_dif_F10	GTGCTGGCGGCGATGGGA	326
		Th_dif_R10	GCCTGTGCTTAAGTGGCTGGT	
	11	Th_dif_F11	ACCGCGATCACGCGCTGA	325
		Th_dif_R11	AAACCGGAACCTGCTGACCA	
	12	Th_dif_F1.2	CGGATTACGCGGATGGGGTAA	
		Th_dif_R11.2	TATTAGCAGATTGCGACGCGCG	

Ca. T. hypermnestrae parS2 (3,524 nt)	1	Th_parS2_1f	CTCTACCTGTTTGATCGCGTTTCG	319
		Th_parS2_1r	CAAGGTCTTCAGCGAGATGTACG	
	2	Th_parS2_2f	TCGGCGGATTTCGAGCCACA	290
		Th_parS2_2r	CTGAGTCGTCTCCTCTCCATGG	
	3	Th_parS2_3f	GAGCCTCCCAGCATCATTTCC	313
		Th_parS2_3r	ATGCCGGCCATCAGGTCTTC	
	4	Th_parS2_4f	CCATCGGGTCCGTCCAGGA	321
		Th_parS2_4r	CGCTTGTTTCGAGCCTCTATTCC	
	5	Th_parS2_5f	GTTATTTATACTACAGCGCCGAGCG	330
		Th_parS2_5r	GCCAGGTTTTTCGCCACGG	
	6	Th_parS2_6f	CGAGGACAAAGCCAAGGTCG	316
		Th_parS2_6r	GGTGAGGAAGGTGCCGATG	
	7	Th_parS2_7f	GGATGGCCGACAGCGGTAAG	305
		Th_parS2_7r	AATGACGTGCTTGATGGTGCC	
	8	Th_parS2_8f	AACGACTCGATCGACGGCA	313
		Th_parS2_8r	GATCTTAATCATGCGCGATTCTCC	
	9	Th_parS2_9f	GACGACCACAAGCTGGTACG	320
		Th_parS2_9r	GCCTCGATCATCTCCTCGG	
	10	Th_parS2_10f	GATCCGCTCGGTCGTCAGTG	311
		Th_parS2_10r	CCGCTCAGGCATCCTCCTC	
	11	Th_parS2_11f	GGATGTCCCGGATTGTGCGG	333
		Th_parS2_11r	CTGAGCAGGACGTTATACCGG	

Ca. T. hypermnestrae <i>ftsQAZ</i> (3,690 nt)	1	Th_ftsQAZ_F1.2	CTGCCCCTGATCCGCCTGGA	335
		Th_ftsQAZ_R1.1	AATGGTTCAAGGCTGGTCTCC	
	2	Th_ftsQAZ_F2.1	CCGGACAAGCGATGAACAGG	329
		Th_ftsQAZ_R2.1	CAGGCGATCCGGCCAGTGA	
	3	Th_ftsQAZ_F3.1	GAGCTCCGGGTGGTGGAAAC	323
		Th_ftsQAZ_R3.1	GGGTAGACCCGGATAAACCTGGC	
	4	Th_ftsQAZ_F4.1	CCGTCCGGTGATCGATATGCG	319
		Th_ftsQAZ_R4.1	TCCTTCACCTCGCCCACCAG	
	5	Th_ftsQAZ_F5.1	CGACGAGGGGATCGAGATTATCG	312
		Th_ftsQAZ_R5.1	TGGGGCAGGATGTGCAGGAT	
	6	Th_ftsQAZ_F6.1	AATTCATCATCGACAATCAGGAAGGG	308
		Th_ftsQAZ_R6.1	GCCGGCGATGGGAATCACG	
	7	Th_ftsQAZ_F7.1	GATCAGGTGACCAACGATATCGCC	286
		Th_ftsQAZ_R7.1	AGCTGCCGCCGGTCATGAC	
	8	Th_ftsQAZ_F8.1	CCAAGATGGCGGGGCTCAT	361
		Th_ftsQAZ_R8.1	CCGTTTTGCTCGATGGTTATCTGATT	
	9	Th_ftsQAZ_F9.1	ATGTTTGAACATGGATACCAACGG	397
		Th_ftsQAZ_R9.1	TCACTACCGCCACGGTCAGG	
	10	Th_ftsQAZ_F10.1	CCAAGCCCTTTGCGTTTCGAG	349
		Th_ftsQAZ_R10.1	AAGGGGCTGTTGATGGCCG	
	11	Th_ftsQAZ_F11.1	GCTGGAGGATATCGACCTGGC	336
		Th_ftsQAZ_R11.1	CCCTTGTTGCGATAGACCGCC	

<i>C. steedae</i> ori (7,353 nt)	1	C_Ori1F	TCAATTTCAAAAACCGGCTC	300
		C_Ori1R	GATAGAACACATTATGTCTGCG	
	2	C_Ori2F	GCATGAGTGTGAAAGTAGC	300
		C_Ori2R	AAAAACCTGTGCATTCCAG	
	3	C_Ori3F	AACTGTGGTGTTC AACGTTA	300
		C_Ori3R	AGTTTGCCTTT CAGTTCAG	
	4	C_Ori4F	GTAGCCACGGGTT CATTGA	331
		C_Ori4R	ACCACTTAGCCTAATTATCGG	
	5	C_Ori5F	AGGTAAACAGTCAGTGGTAG	300
		C_Ori5R	TTTTTCGATCAAAGACGGG	
	6	C_Ori6F	TTTACCGAGCAATATGTCTG	300
		C_Ori6R	GCGTACAAAGCGGTTAATC	
	7	C_Ori7F	GTGGTGCTGATTTACGATGA	300
		C_Ori7R	CAGACGTTGACTCAATGTG	
	8	C_Ori8F	GCGTCCCACGGATAATTAAT	300
		C_Ori8R	CGAATATTACGCCAACGAAAG	
	9	C_Ori9F	GCTTACCATACCTTCAAGC	300
		C_Ori9R	CGGCAAAAAGAAAGTTTGAG	
	10	C_Ori10F	GTTAGACATAAACCCGACATGA	300
		C_Ori10R	CACCATGCTACTTGGTCTG	
	11	C_Ori11F	AGAAAGGAAACCCCATGTC	300
		C_Ori11R	GATTAAAGGTGGTAAATTCGCG	

<i>C. steedae</i> ter (4,498 nt)	1	C_Ter1F	TTGCCCCGACAACATTACTAC	300
		C_Ter1R	CTGTTTGC GGTT CATATAGG	
	2	C_Ter2F	GAAGGTTTTTGAACGCATTCA	300
		C_Ter2R	CGAACTTTACACCTTTCCTTC	
	3	C_Ter3F	CGTAGATTTAAACGCTGACCT	300
		C_Ter3R	TAAGCCATTTCCACACTCG	
	4	C_Ter4F	GCCGACAGTATTTGCTTAC	300
		C_Ter4R	CTTTGTGTTGCCCGATATAATC	
	5	C_Ter5F	CCAAAGAGCAACTGGGTAT	300
		C_Ter5R	TGTCCAGTTGAAAATCTTCC	
	6	C_Ter6F	GCTTACCTTATTAGATGTGG	300
		C_Ter6R	GTAGGTTTTGTAGGGCTTT	
	7	C_Ter7F	GGTGGCGTATTGCTTAACT	300
		C_Ter7R	GTGTAAAGGTTCTAAATGGGA C	
	8	C_Ter8F	ACACCTTTTTTATCGGTAGC	300
		C_Ter8R	TCGTCAAGGGGAATATCAG	
	9	C_Ter9F	AACAATGTGGACAAGCACT	300
		C_Ter9R	TACTGTGGGGGTCTAGTTG	
	10	C_Ter10F	CGGAATTACAGGTATCACAAC	300
		C_Ter10R	CAAGATGTTCTTTAACCAGTG	

Table S9. PCR cycling conditions for DNA FISH probe production.

Target	Primer	Product (nt)	Cycling conditions
<i>A. filiformis</i> <i>ori</i>	see Table S8	Initial 3,622 nt-long fragment	98°C for 5 min, followed by 31 cycles at 98°C for 20 s, 64°C (-0.3°C every cycle) for 20 s, 72°C for 120 s, followed by a final elongation step at 72°C for 5 min.
	see Table S8	~300 nt-long probes (P1-P11)	98°C for 5 min, followed by 31 cycles at 98°C for 20 s, 64°C (-0.3°C every cycle) for 20 s, 72°C for 15 s, followed by a final elongation step at 72°C for 5 min.
<i>A. filiformis</i> <i>ter</i>	see Table S8	Initial 3,583 nt-long fragment	98°C for 5 min, followed by 31 cycles at 98°C for 20 s, 63°C (-0.3°C every cycle) for 20 s, 72°C for 120 s, followed by a final elongation step at 72°C for 5 min.
	see Table S8	~300 nt-long probes (P1-P11)	98°C for 5 min, followed by 31 cycles at 98°C for 20 s, 62°C (-0.3°C every cycle) for 20 s, 72°C for 15 s, followed by a final elongation step at 72°C for 5 min.
<i>A. filiformis</i> left arm	see Table S8	Initial 6,718 nt-long fragment	98°C for 5 min, followed by 31 cycles at 98°C for 20 s, 63°C (-0.3°C every cycle) for 20 s, 72°C for 120 s, followed by a final elongation step at 72°C for 5 min.

	see Table S8	~300 nt- long probes (P1-P10)	98°C for 5 min, followed by 31 cycles at 98°C for 20 s, 63°C (-0.3°C every cycle) for 20 s, 72°C for 30 s, followed by a final elongation step at 72°C for 5 min.
<i>A. filiformis</i> right arm	see Table S8	Initial 7,846 nt-long fragment	98°C for 5 min, followed by 31 cycles at 98°C for 20 s, 63°C (-0.3°C every cycle) for 20 s, 72°C for 120 s, followed by a final elongation step at 72°C for 5 min.
	see Table S8	~300 nt- long probes (P1-P10)	98°C for 5 min, followed by 31 cycles at 98°C for 20 s, 63°C (-0.3°C every cycle) for 20 s, 72°C for 30 s, followed by a final elongation step at 72°C for 5 min.
<i>S. muelleri</i> <i>ori</i>	see Table S8	Initial 8,158 nt-long fragment	98°C for 5 min, followed by 31 cycles at 98°C for 20 s, 58°C (-0.3°C every cycle) for 20 s, 72°C for 240s, followed by a final elongation step at 72°C for 5 min.
	see Table S8	~300 nt- long probes (P1-P10)	98°C for 5 min, followed by 31 cycles at 98°C for 20 s, 58°C (-0.3°C every cycle) for 20 s, 72°C for 15s, followed by a final elongation step at 72°C for 5 min.
<i>S. muelleri</i> <i>ter</i>	see Table S8	Initial 8,187 nt-long fragment	98°C for 5 min, followed by 31 cycles at 98°C for 20 s, 58°C (-0.3°C every cycle) for 20 s, 72°C for 240s, followed by a final elongation step at 72°C for 5 min.

	see Table S8	~300 nt- long probes (P1-P9)	98°C for 5 min, followed by 31 cycles at 98°C for 20 s, 58°C (-0.3°C every cycle) for 20 s, 72°C for 15s, followed by a final elongation step at 72°C for 5 min.
<i>S. muelleri</i> <i>5xparS_c</i>	see Table S8	Initial 9,335 nt-long fragment	98°C for 5 min, followed by 31 cycles at 98°C for 20 s, 63°C (-0.3°C every cycle) for 20 s, 72°C for 120 s, followed by a final elongation step at 72°C for 5 min.
	see Table S8	~300 nt- long probes (P1-P9)	98°C for 5 min, followed by 31 cycles at 98°C for 20 s, 63°C (-0.3°C every cycle) for 20 s, 72°C for 30 s, followed by a final elongation step at 72°C for 5 min.
<i>C. steedae</i> <i>ori</i>	see Table S8	Initial 7,353 nt-long fragment	95°C for 5 min, followed by 31 cycles at 95°C for 20 s, 58°C (-0.3°C every cycle) for 20 s, 72°C for 270s, followed by a final elongation step at 72°C for 5 min.
	see Table S8	300 nt-long probes (P1- P11)	95°C for 5 min, followed by 31 cycles at 95°C for 20 s, 58°C (-0.3°C every cycle) for 20 s, 72°C for 30s, followed by a final elongation step at 72°C for 5 min.
<i>C. steedae</i> <i>ter</i>	see Table S8	Initial 4, 498 nt-long fragment	95°C for 5 min, followed by 31 cycles at 95°C for 20 s, 58°C (-0.3°C every cycle) for 20 s, 72°C for 270s, followed by a final elongation step at 72°C for 5 min.

	see Table S8	300 nt-long probes (P1- P10)	95°C for 5 min, followed by 31 cycles at 95°C for 20 s, 58°C (-0.3°C every cycle) for 20 s, 72°C for 30s, followed by a final elongation step at 72°C for 5 min.
<i>Ca. T. hypermnestrae ori</i>	see Table S8	Initial 2,858 nt-long fragment	95°C for 5 min, followed by 31 cycles at 98°C for 45 s, 57°C for 45 s, 72°C for 180 s, followed by a final elongation step at 72°C for 5 min.
	see Table S8	~300 nt- long probes (P1-P9)	95°C for 5 min, followed by 31 cycles at 98°C for 45 s, 57°C for 45 s, 72°C for 30 s, followed by a final elongation step at 72°C for 5 min.
<i>Ca. T. hypermnestrae ter</i>	see Table S8	Initial 3,239 nt-long fragment	98°C for 5 min, followed by 31 cycles at 98°C for 20 s, 63°C (-0.3°C every cycle) for 20 s, 72°C for 125 s, followed by a final elongation step at 72°C for 5 min.
	see Table S8	~300 nt- long probes (P1-P10)	98°C for 5 min, followed by 31 cycles at 98°C for 20 s, 58°C for 20 s, 72°C for 15 s, followed by a final elongation step at 72°C for 5 min.
<i>Ca. T. hypermnestrae ftsQAZ</i>	see Table S8	Initial 4,010 nt-long fragment	98°C for 5 min, followed by 31 cycles at 98°C for 20 s, 65°C (-0.3°C every cycle) for 20 s, 72°C for 120 s, followed by a final elongation step at 72°C for 5 min.

	see Table S8	~300 nt- long probes (P1-P11)	95°C for 5 min, followed by 31 cycles at 94°C for 60 s, 57°C for 30 s, 72°C for 30 s, followed by a final elongation step at 72°C for 5 min.
<i>Ca. T. hypermnestrae</i> <i>parS2</i>	see Table S8	Initial 3,632 nt-long fragment	95°C for 5 min, followed by 31 cycles at 98°C for 20 s, 64°C (-0.3°C every cycle) for 20 s, 72°C for 120 s, followed by a final elongation step at 72°C for 5 min.
	see Table S8	~300 nt- long probes (P1-P10)	98°C for 5 min, followed by 31 cycles at 98°C for 20 s, 64°C (-0.2°C every cycle) for 20 s, 72°C for 20 s, followed by a final elongation step at 72°C for 5 min.

Table S10. SRA accession numbers

	Sample name	NCBI accession number
Genome sequencing	<i>A. filiformis</i> long reads	fast5: SRR13289602, fastq: SRR16893507
	<i>A. filiformis</i> short reads	SRR15998661
	<i>C. steedae</i> , long reads	fast5: SRR16896741, fastq: SRR16947409
	<i>C. steedae</i> , short reads	SRR19164917
	<i>A. filiformis</i> assembly	GCF_020162295.1
	<i>C. steedae</i> , assembly	GCF_023547005.1
Marker frequency analysis	<i>A. filiformis</i> , late exponential phase	SRR17498973
	<i>A. filiformis</i> , stationary phase	SRR17498972
	<i>C. steedae</i> , late exponential phase	SRR17498976
	<i>C. steedae</i> , stationary phase	SRR17498975
	<i>E. coli</i> , exponential phase*	ERR902995
	<i>E. coli</i> , stationary phase*	ERR902996
	<i>A. filiformis</i> 1kb-binned raw counts	GSE194131
	<i>C. steedae</i> 1kb-binned raw counts	GSE205139
RNA-Seq	<i>A. filiformis</i> , exponential phase (3 biological replicates)	SRR17498971, SRR17498970, SRR17498961
	<i>A. filiformis</i> , stationary phase (3 biological replicates)	SRR17498969, SRR17498968, SRR17498954
	<i>A. filiformis</i> , plate (3 biological replicates)	SRR17498958, SRR17498959, SRR17498960
	<i>A. filiformis</i> raw count table	GSE194132
	<i>C. steedae</i> raw count table	GSE250250
	<i>C. steedae</i> , plate (3 biological replicates)	SRR17498948, SRR17498950, SRR17498939
	<i>C. steedae</i> , exponential phase (3 biological replicates)	SRR17498951, SRR17498952, SRR17498953
	<i>C. steedae</i> , stationary phase (3 biological replicates)	SRR17498945, SRR17498946, SRR17498947
3C-Seq	<i>A. filiformis</i> , exponential phase (replicate 1)	SRR19164944
	<i>A. filiformis</i> , exponential phase (replicate 2)	SRR19164943
	<i>A. filiformis</i> , stationary phase	SRR19164942
	<i>A. filiformis</i> , plate (replicate 1)	SRR27205587
	<i>A. filiformis</i> , plate (replicate 2)	SRR27206238
	<i>A. filiformis</i> , exponential phase with 25 µg/ml rifampicin for 30 min	SRR27206238

ChIP-seq	<i>A. filiformis</i> , exponential phase with 25 µg/ml Chloramphenicol for 30 min	SRR27206240
	<i>C. steedae</i> , plate	SRR27206419
	<i>C. steedae</i> , exponential phase	SRR27206418
	<i>C. steedae</i> , stationary phase	SRR27206420
	<i>A. filiformis</i> 3C-seq matrices	GSE250400
	<i>C. steedae</i> 3C-seq matrices	GSE250401
	<i>A. filiformis</i> ChIP-seq reads	SRX32354318, SRX32354319
	<i>A. filiformis</i> ChIP-seq counts	GSE322725
	<i>S. muelleri</i> ChIP-seq reads	SRX32354384, SRX32354385
	<i>S. muelleri</i> ChIP-seq counts	GSE322727

* From Ivanova et al., 2015