Figure S1: Pairwise genome collinearity alignment of the Xanthomonas strains sequenced in this study performed using BRIG 0.95. The genomes of X. theicola CFBP 4691 (A) and X. translucens pv. translucens DSM 18974 (B) were used as reference for the three strains FX1, FX4, and AmX2. Circular mapping against the reference genomes confirmed the absence of a large portion of the T3SS and Xops in the three sequences obtained in this study.

Figure S2: Visualization of genomic islands in the whole genome sequences of the three Xanthomonas strains sequenced in this study against the genomes of two reference strains X. theicola CFBP 4691 and X. translucens pv. translucens DSM 18974.

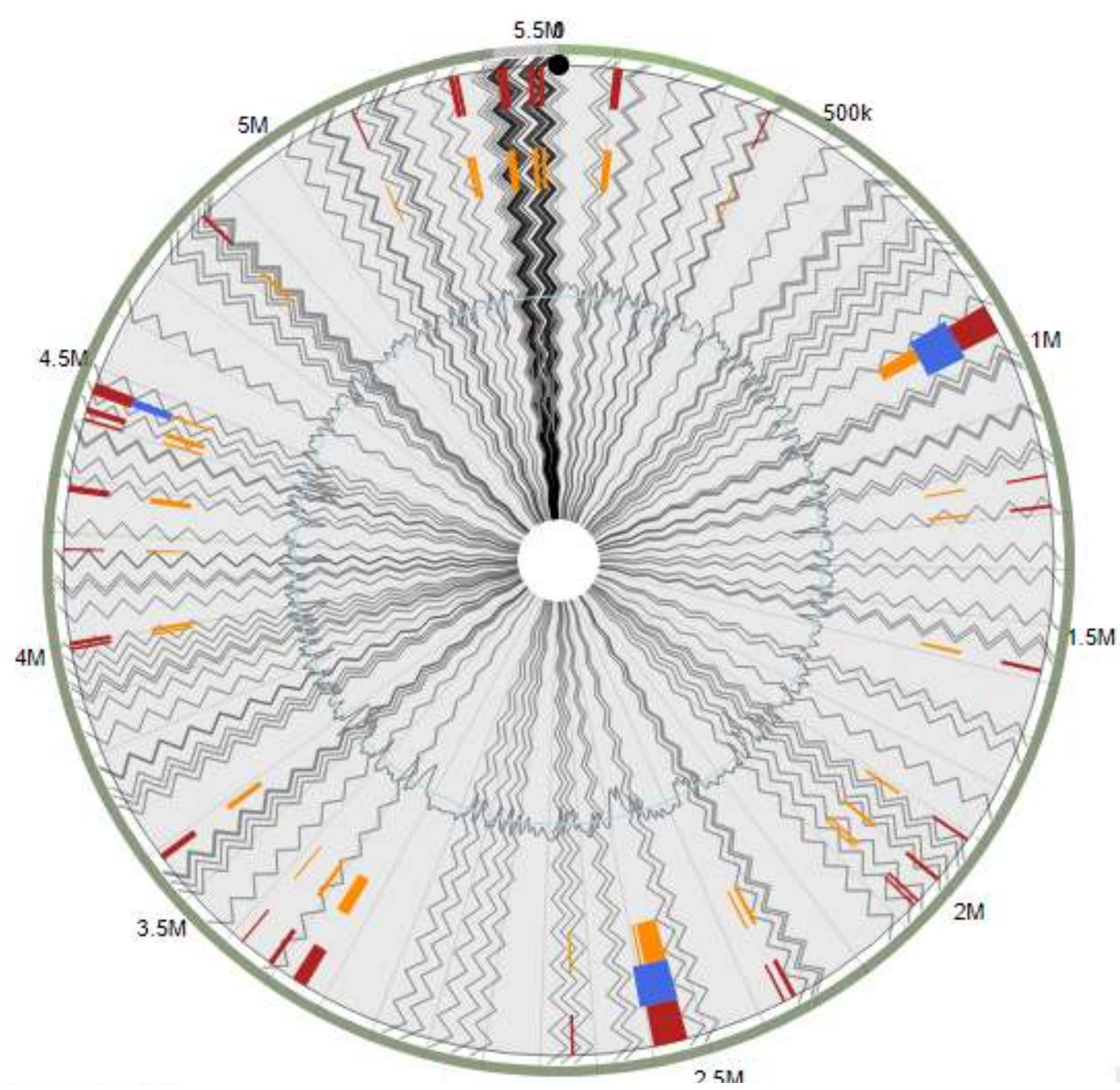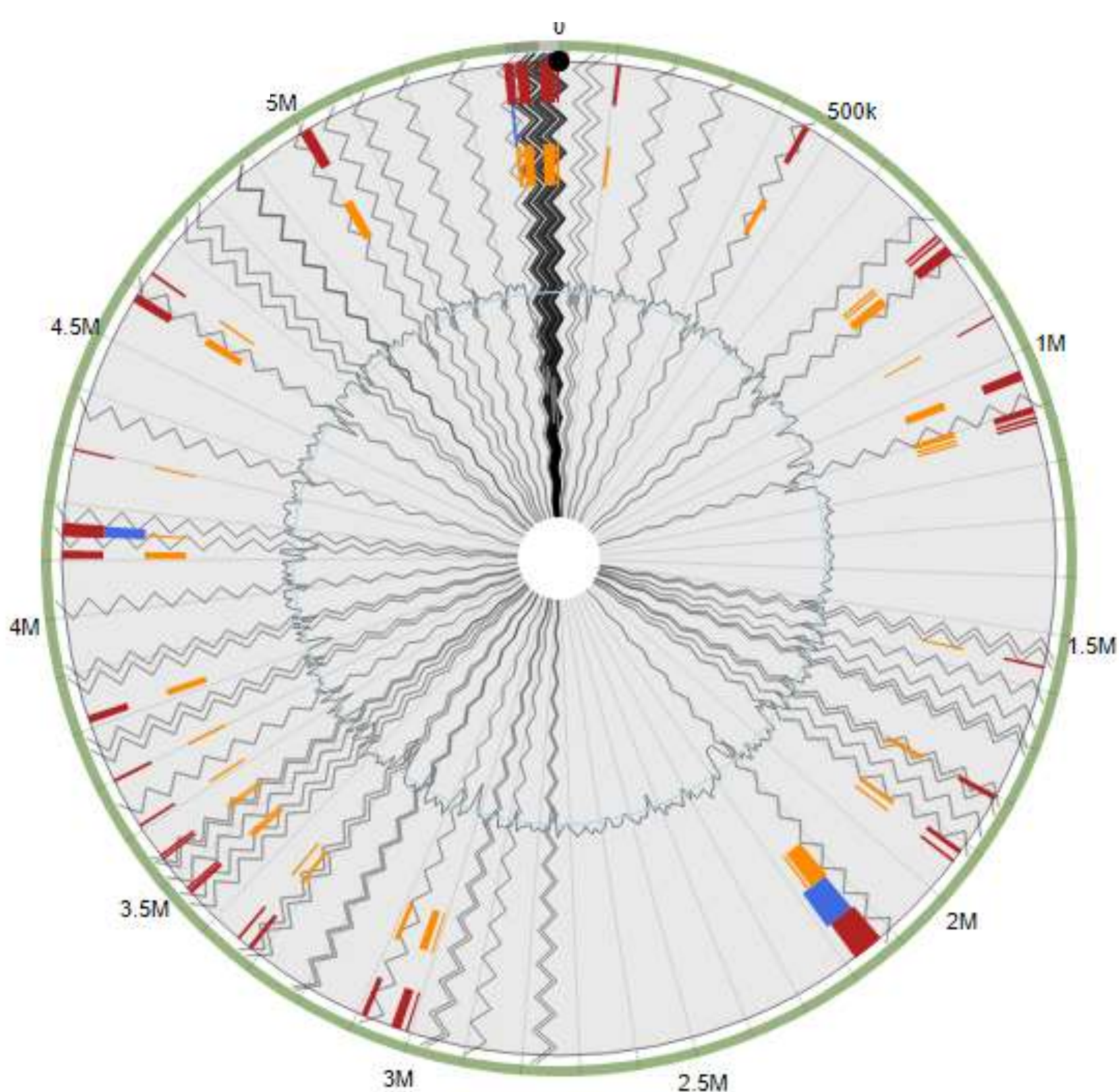**Xanthomonas theicola CFBP 4691**
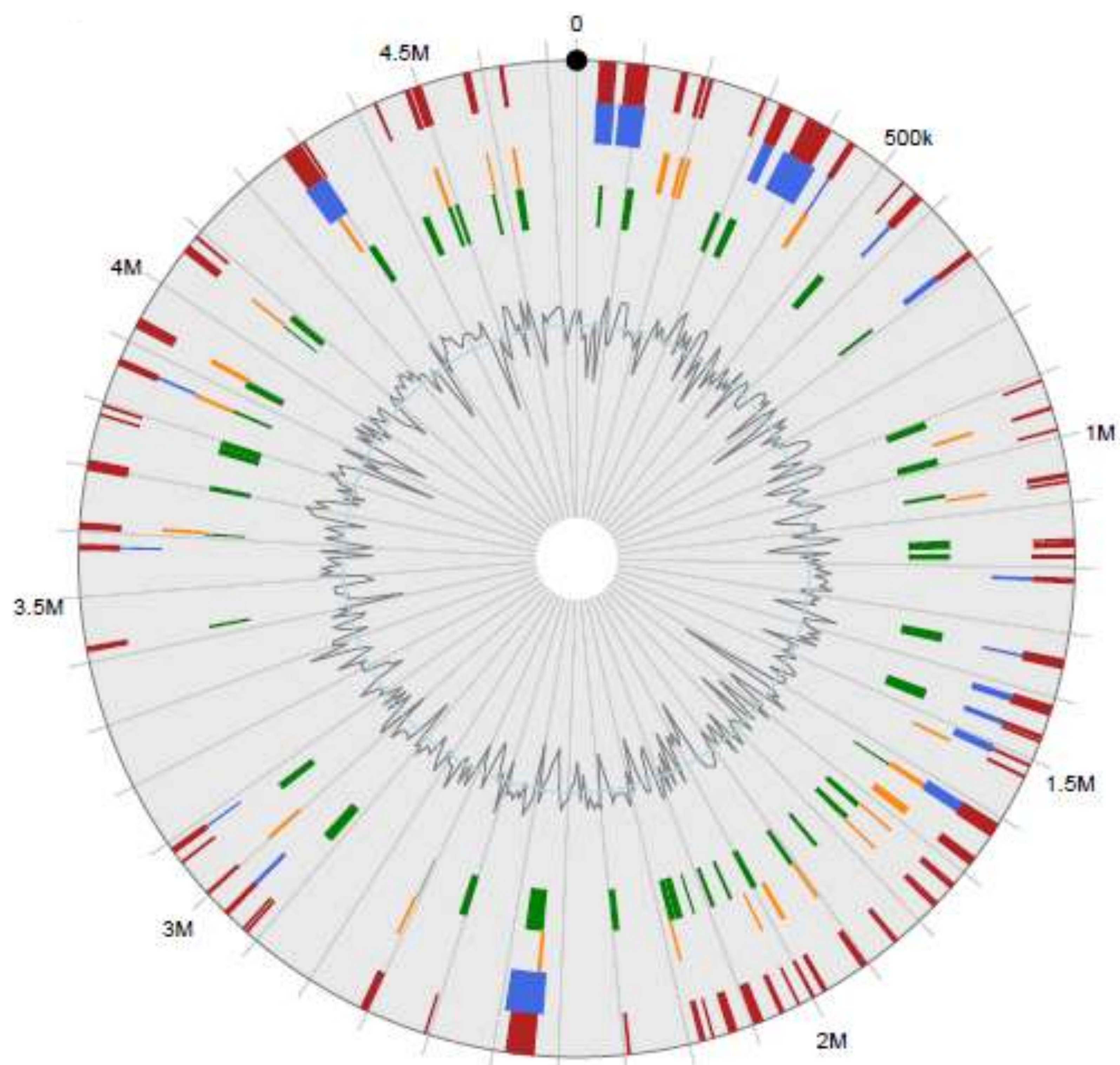
X. translucens pv. translucens DSM 18974
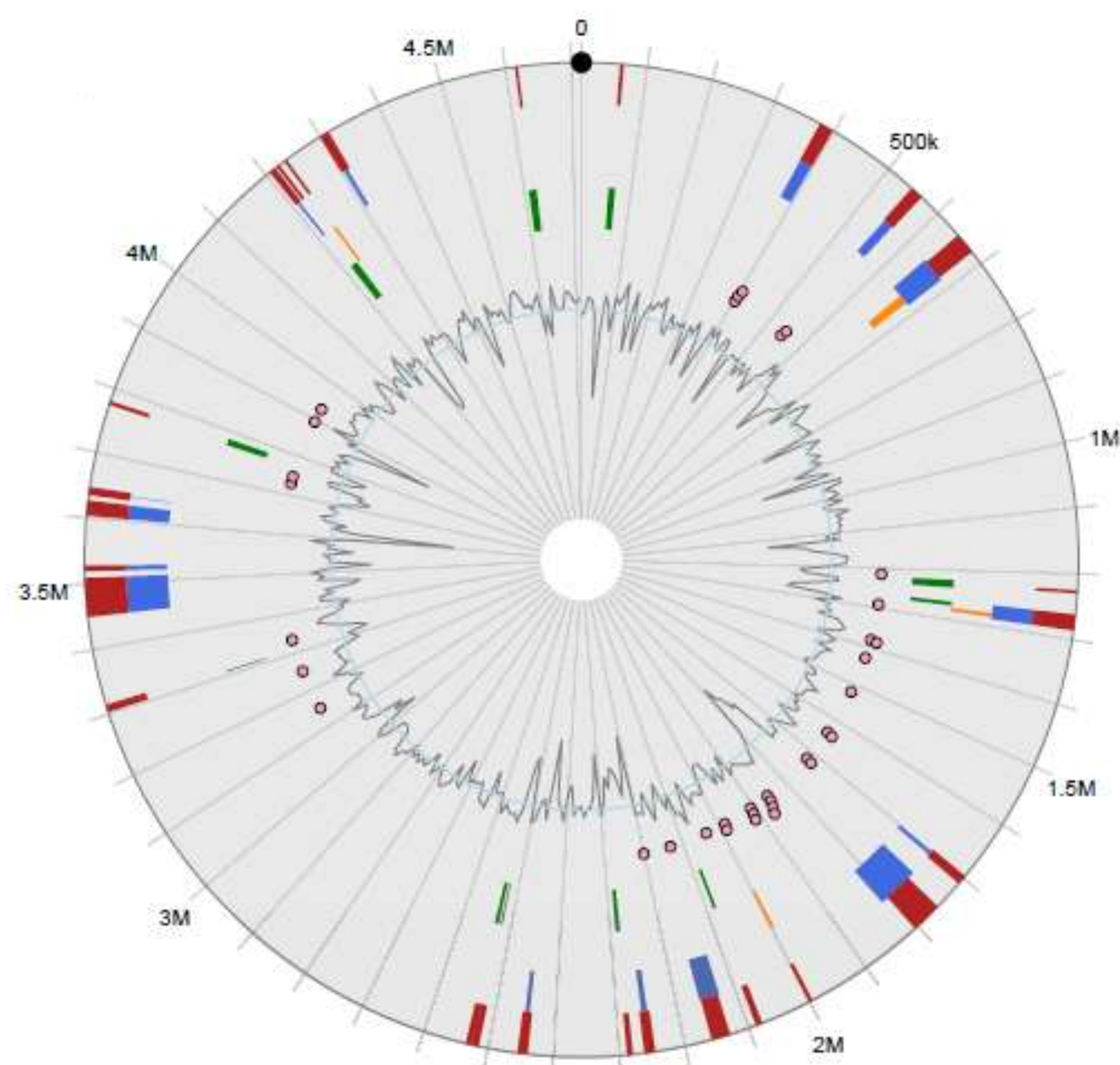
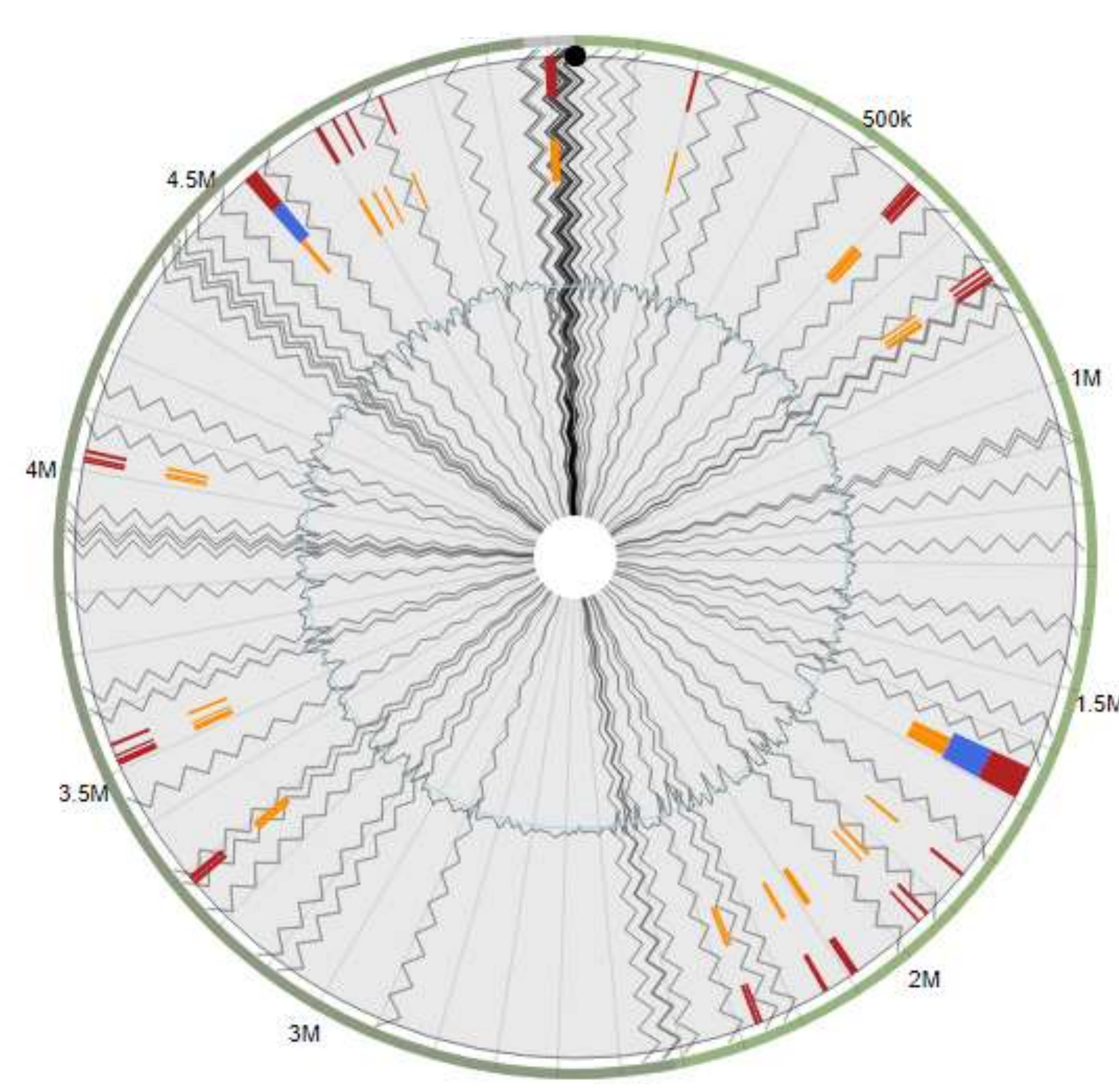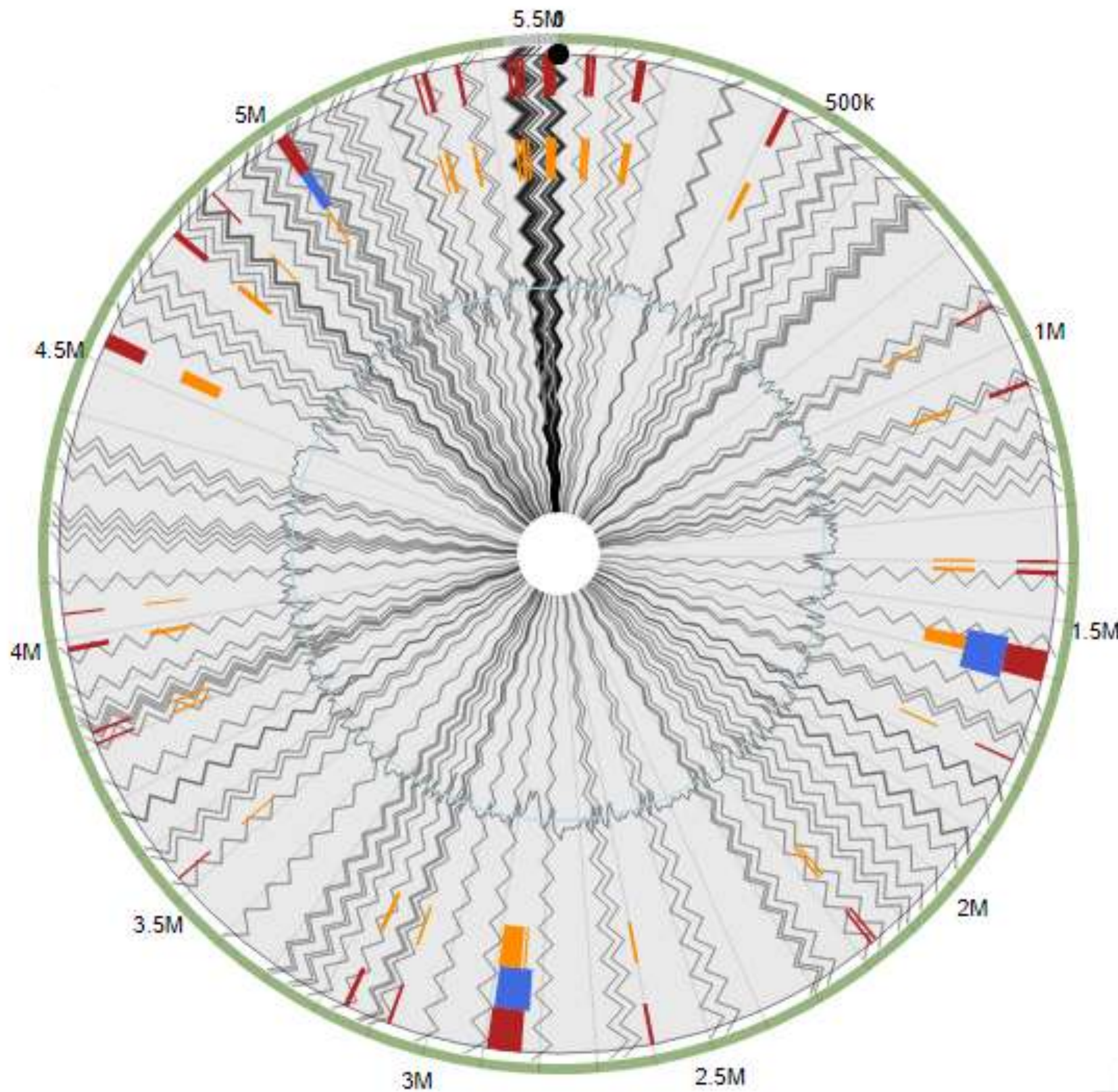**FX1 vs. CFBP 4691**
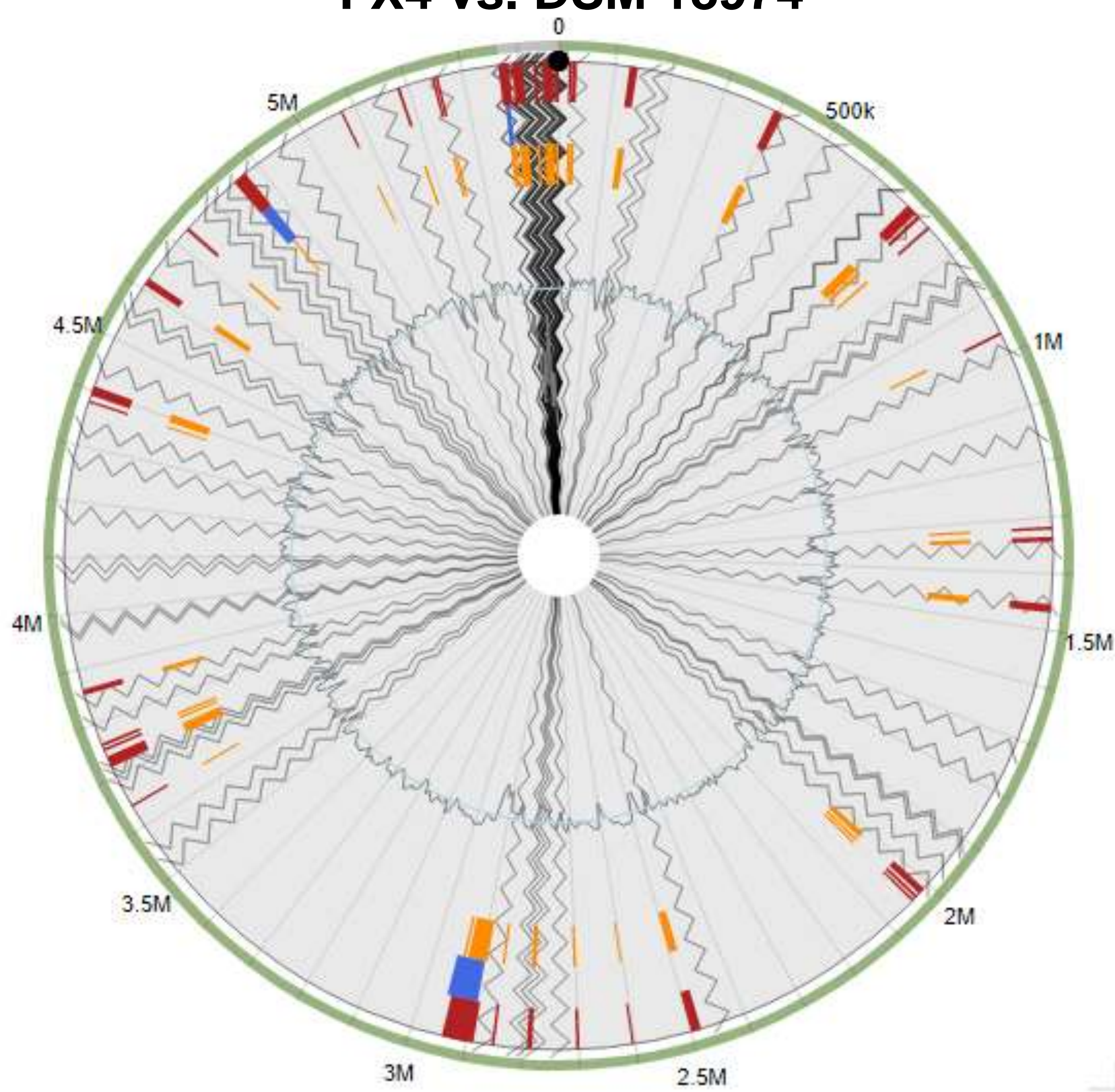
FX4 vs. CFBP 4691

AmX2 vs. CFBP 4691

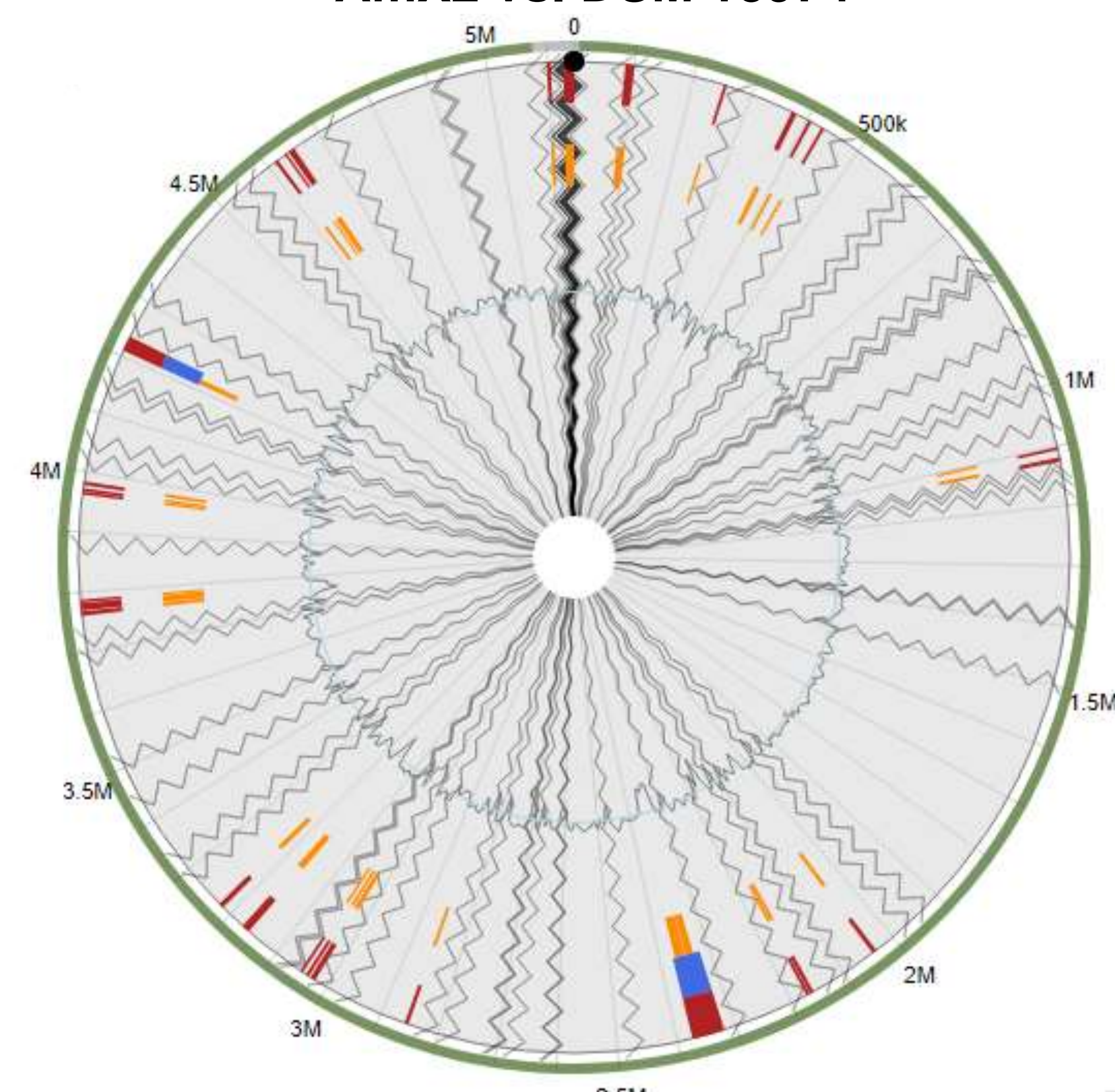**FX1 vs. DSM 18974**

FX4 vs. DSM 18974

AmX2 vs. DSM 18974

Table S1: Primer pairs used in this study.

Prime name	5´- 3´ sequence	Size of amplicon	Ann. Temp.	Target species/region	Reference
Xc-lip-F2	TATGTGATGGTGCCGACCATTC	777	57	*Xanthomonas sp.*	Lee et al. 2009
Xc-lip-R2	GGACTTCGCGGTCCACGTCGTAGC				
T1	CCGCCATAGGGCGGAGCACCCCGAT	139	53	*Xanthomonas translucens*	Maes et al. 1996
T2	GCAGGTGCGACGTTTGCAGAGGGATCTTCTGCAAA				
Bs-XeF	CATGAAGAACTCGGCGTATCG	173	64	*X. euvesicatoria* pv. euvesicatoria	Koenraadt et al. 2009
Bs-XeR	GTCGGACATAGTGGACACATAC				
Bs-XvF	CCATGTGCCGTTGAAATACTTG	138	64	*X. vesicatoria*	Koenraadt et al. 2009
Bs-XvR	ACAAGAGATGTTGCTATGATTTGC				
Bs-XgF	TCAGTGCTTAGTTCCTCATTGTC	154	64	*X. hortorum pv. gardnri*	Koenraadt et al. 2009
Bs-XgR	TGACCGATAAAGACTGCGAAAG				
Bs-XpF	GTCGTGTTGATGGAGCGTTC	197	64	*X. euvesicatoria* pv. perforans	Koenraadt et al. 2009
Bs-XpR	GTGCGAGTCAATTATCAGAATGTGG				
X-gyrB1F	ACGAGTACAACCCGGACAA	904	57	*gyrB*	Young et al. 2008
X-gyrB1R	CCCATCARGGTGCTGAAGAT				
P-X-ATPD-F	GGGCAAGATCGTTCAGAT	868	60	*atpD*	Boudon et al. 2005
P-X-ATPD-R	GCTCTTGGTCGAGGTGAT				
P-X-EFP-F	TCATCACCGAGACCGAATA	445	62	*efp*	Boudon et al. 2005
P-X-EFP-R	TCCTGGTTGACGAACAGC				
XtrpodF	TGGAACAGGGCTATCTGACC	674	54	*rpoD*	Young et al. 2008
XtrpodR	CATTCYAGGTTGGTCTGRTT				

A

Strain	Size	BUSCO notation assessment results				
AmX2	5,071 kbp	C:99.8%	[D:17%],	F:0.09%,	M:0.09%,	n:1152
FX1	5,387 kbp	C:99.6%	[D:17%],	F:0.26%,	M:0.09%,	n:1152
FX4	5,383 kbp	C:99.9%	[D:17%],	F:0.0%,	M:0.09%,	n:1152
DSM 18974	4,715 kbp	C:99.8%	[D:0%],	F:0.0%,	M:0.17%,	n:1152

C: Complete; D: Duplicated; F: Fragmented; M: Missing; n: No. of genes

B

ooxA	AmX2	FX1	FX4	*P. kilonensis*
Identity	27.1	25.8	25.8	35.8 and 29.3
Query coverage	73	66	66	85 and 84
Contig No.	5	15	1	17 and 23
ooxB	AmX2	FX1	FX4	
Identity	23.5	26 and 23	26 and 23	41.5 and 25.6
Query coverage	64	39 and 90	39 and 90	95 and 98
Contig No.	5	15 and 5	1 and 21	17 and 23
ooxAB	AmX2	FX1	FX4	
Identity	25	25	25	35.8 and 29.3
Query coverage	66	66	66	85 and 84
Contig No.	1	15	1	17 and 23

Table S2: Quality assessment of genome assembly and annotation using BUSCO online service confirmed the accuracy and completeness of all three genomes compared to the complete genome sequence of *X. translucens* DSM 18974 (A). BLAST-based in-silico analyses using the sequences of ooxA, ooxB, and ooxAB genes against the three genome sequences obtained in this study revealed the presence of these genes in the three strains (B).

Table S3: Genomic features of the gall-associated *Xanthomonas* strains sequenced in this study in comparison to the phylogenetically closely related reference strains.

Taxon	Strain	Host	Genome length (kbp)	G + C content (%)	No. of protein-coding genes	No. of RNAs	No. of pseudo-genes	Genome Coverage (x)	GenBank Accession Numbers
Xanthomonas sp.	FX1	*Ficus benjamina*	5,387	68.8	4,502	57	40	22	JAFJNT000000000
Xanthomonas sp.	FX4	*Ficus benjamina*	5,383	68.8	4,468	64	68	115	JAFIWB000000000
Xanthomonas sp.	AmX2	*Amaranthus* sp.	5,071	69.8	4,170	61	41	124	JAFIWC000000000
X. translucens pv. *graminis*	NCPPB 3709	Grass	4,187	68.8	3,337	59	233	ND	NZ_FLUK01000000
X. translucens pv. *undulosa*	ICMP 11055	*Triticum aestivum L.*	4,761	67.8	3,835	63	224	118	CP009750
X. translucens pv. *translucens*	UPB886	*Hordeum vulgare*	4,674	67.9	3,681	63	240	10	NZ_VCIH01000000
X. translucens pv. *translucens*	DSM 18974	*Hordeum vulgare*	4,715	67.7	3,804	64	190	ND	LT604072
X. translucens pv. *cerealis*	NCPPB 1943	*Hordeum vulgare*	4,410	67.3	3,583	58	358	197	NZ_MADM00000000
X. translucens pv. *arrhenatheri*	LMG 727	*Arrhenatherum elatius*	4,753	68.3	3,791	58	137	ND	NZ_CXOI00000000.1
X. translucens pv. *phlei*	LMG 730	*Phleum pratense*	4,396	68.4	3,545	58	212	ND	NZ_CXOJ01000000
X. translucens pv. *poae*	ATCC 33804	*Poa trivialis*	4,498	67.5	3,789	57	415	188	NZ_MADN00000000
X. hyacinthi	CFBP 1156	*Hyacinthus orientalis*	4,918	68.1	4,011	63	318	306	CP043476
X. translucens	569	Sorghum (*Sorghum bicolor*)	5,323	69.7	4,414	60	52	282	NZ_VIWM01000000
X. theicola	CFBP 4691	*Camellia sinensis*	4,744	68.4	3,766	61	665	264	CP049017
Xanthomonas sp.	NCPPB 1128	*Phaseolus vulgaris*	4,950	68.9	4,133	66	55	80	NZ_LFME00000000
X. sacchari	NCPPB 4393	Insect associated with banana plant	4,898	69.0	4,168	65	163	80	NZ_AGDB00000000
X. albilineans	CFBP 2523	*Saccharum officinarum*	3,684	63.1	2,996	81	168	100	NZ_MDCB00000000
X. sontii	PPL1	*Oryza sativa*	4,820	69.0	3,951	58	198	78	NQYO01000001

Taxon	Strain	Accession number	No. of contigs	Assembly Method	Annotation Method	Annotation Software revision	Annotation Method
Xanthomonas sp.	FX1	JAFJNT000000000	152	SPAdes v. 3.12	NCBI	5.1	Best-placed reference protein set-GeneMarkS-2+
Xanthomonas sp.	FX4	JAFIWB000000000	89	SPAdes v. 3.12	NCBI	5.1	Best-placed reference protein set-GeneMarkS-2+
Xanthomonas sp.	AmX2	JAFIWC000000000	75	SPAdes v. 3.12	NCBI	5.1	Best-placed reference protein set-GeneMarkS-2+
X. translucens pv. graminis	NCPPB 3709	NZ_FLUK01000000	300	ND	NCBI RefSeq	4.12	Best-placed reference protein set-GeneMarkS-2+
X. translucens pv. undulosa	ICMP11055	CP009750	1	HGAP3 v. SMRTAnalysis 2.2	NCBI	2.8 (rev. 449627)	Best-placed reference protein set; GeneMark-S+
X. translucens pv. translucens	UPB886	NZ_VCIH01000000	1	HGAP v. 4	NCBI RefSeq	5.1	Best-placed reference protein set-GeneMarkS-2+
X. translucens pv. translucens	DSM 18974	LT604072	1	ND	ND	ND	ND
X. translucens pv. cerealis	NCPPB1943	NZ_MADM00000000	251	Velvet v. 1.0.15	NCBI RefSeq	4.12	Best-placed reference protein set-GeneMarkS-2+
X. translucens pv. arrhenatheri	LMG 727	NZ_CXOI00000000.1	89	ND	NCBI RefSeq	4.12	Best-placed reference protein set-GeneMarkS-2+
X. translucens pv. phlei	LMG730	NZ_CXOJ01000000	142	ND	NCBI RefSeq	4.12	Best-placed reference protein set-GeneMarkS-2+
X. translucens pv. poae	ATCC 33804	NZ_MADN00000000	674	Velvet v. 1.0.15	NCBI RefSeq	4.12	Best-placed reference protein set-GeneMarkS-2+
X. hyacinthi	CFBP 1156	CP043476	1	HGAP v. 4.0	NCBI RefSeq	4.9	Best-placed reference protein set-GeneMarkS-2+
X. translucens	569	NZ_VIWM01000000	16	SPAdes v. 3.13.0	NCBI RefSeq	4.12	Best-placed reference protein set-GeneMarkS-2+
X. theicola	CFBP 4691	CP049017	435	HGAP v. 4.0	NCBI RefSeq	4.11	Best-placed reference protein set-GeneMarkS-2+
Xanthomonas sp.	NCPPB1128	NZ_LFME00000000	71	SPAdes v. 3.5.0	NCBI RefSeq	5.1	Best-placed reference protein set-GeneMarkS-2+
X. sacchari	NCPPB 4393	NZ_AGDB00000000	470	Velvet v. 1.1.03	NCBI RefSeq	5.0	Best-placed reference protein set-GeneMarkS-2+
X. albilineans	CFBP2523	NZ_MDCB00000000	148	Velvet v. 1.2.07;	NCBI RefSeq	4.11	Best-placed reference protein set-GeneMarkS-2+
X. sontii	PPL1	NQYO01000001	332	CLC NGS Cell v. 10	NCBI RefSeq	4.2	Best-placed reference protein set-GeneMarkS-2+
X. oryzae pv. oryzae	PXO99A	NC_010717	1	Celera Assembler v. 7.0; SVN revision	NCBI RefSeq	5.0	Best-placed reference protein set-GeneMarkS-2+

ND: Not determined

Table S4: Assembly and annotation information for the genome sequences of *Xanthomonas* strains used in this study.

Table S5: In silico screening for bacteriocins and antibiotic peptides among the clade-I xanthomonad genome sequences analyzed in this study.

Taxon	Strain	Start codon	End codon	gene ID	Class
Xanthomonas sp.	FX1	29117	49117	SU2U6DHN013	Sactipeptides
		4098	24404	SU2RDK4F016	Zoocin_A
Xanthomonas sp.	FX4	272837	293143	SU316SGK013	Zoocin_A
Xanthomonas sp.	AmX2	1	16792	SU25J9VB013	Zoocin_A
		59555	79909	SU2CS5MN013	Rhodanodin
X. translucens pv. *graminis*	NCPPB 3709	6493	13507	SU3F4TS1016	Sactipeptides
		1	14668	SU3FU8EM013	Zoocin_A
X. translucens pv. *undulosa*	ICMP 11055	3175859	3196165	SU3S1T6U016	Zoocin_A
X. translucens pv. *translucens*	UPB886	1556565	1576871	SU3WH7RE016	Zoocin_A
X. translucens pv. *translucens*	DSM 18974	2853584	2873890	SU8PDA47013	Zoocin_A
X. translucens pv. *cerealis*	NCPPB 1943	14585	34870	SU4ACKR701R	Zoocin_A
		428	20428	SU497DWS01R	Sactipeptides
X. translucens pv. *arrhenatheri*	LMG 727	15980	36286	SU4ACKR701R	Zoocin_A
		71606	91606	SU4ACKR701R	Sactipeptides
X. translucens pv. *poae*	ATCC 33804	-6589	13411	SU5MG31H013	Sactipeptides
		1522	18478	SU5PF8HV01R	Microcin
		0	7536	SU5PF8HV01R	Zoocin_A
		3934	16066	SU5PF8HV01R	Sactipeptides
X. hyacinthi	CFBP 1156	3858063	3878369	SU5WTNE1013	Zoocin_A
X. translucens	569	378461	398767	SU61CZRB013	Zoocin_A
X. theicola	CFBP 4691	35588	55588	SU6F10G2016	Sactipeptides
Xanthomonas sp.	NCPPB 1128	8891	28891	SU6S1F3901R	Sactipeptides
		464	20770	SU6TKGCX013	Zoocin_A
		8197	11803	SU6TKGCX013	Sactipeptides
X. sacchari	NCPPB 4393	0	14755	SU7CFRHR016	Zoocin_A
		6854	26854	SU7DUS55013	Sactipeptides
X. albilineans	CFBP 2523	70001	90307	SU7DUS55013	Zoocin_A
		269267	289267	SU7VAXPR01R	Lanthipeptide_class_IV
		303776	323776	SU8H1X8S013	Microcin

Table S6: Prophages within the genome sequences of clade-I xanthomonad strains detected using the online service PHASTER.

Taxon	Strain	Region Length (Kb)	Completeness	Total Protein	gene ID	Most Common Phage	GC %
Xanthomonas sp.	FX1	12.8	incomplete	12	SXHAS80N013	Escherichia phage 500465-1; NC_049342	68.9
Xanthomonas sp.	FX4	12.8	incomplete	12	SXHRWEJF01R	Escherichia phage 500465-1; NC_049342	68.9
Xanthomonas sp.	AmX2	11	incomplete	10	SXGGHMWK016	Escherichia phage 500465-1; NC_049342	69.8
		0.7	incomplete	11	SXGB4WXJ013	Ralstonia phage phiRSA1; NC_009382	63.7
X. translucens pv. *graminis*	NCPPB 3709	6.2	incomplete	8	SXJ587H6013	Escherichia phage 500465-1; NC_049342	68.9
X. translucens pv. *undulosa*	ICMP 11055	24.5	questionable	14	SXJFM2NJ016	Ralstonia phage phiRSA1; NC_009382	63.9
		33.7	intact	15	SXJED8BV013	Shigella phage SfIV; NC_022749	65.0
		13.5	incomplete	8	SXJBD8KU013	Stenotrophomonas phage phiSMA6 ; NC_043029	66.3
		44.5	intact	67	SXJ9R7KG013	Pseudomonas phage phiPSA1; NC_024365	67.2
X. translucens pv. *translucens*	UPB886	12.3	incomplete	10	SXJP44SE013	Paenibacillus phage Tripp; NC_028930	65.0
		9.1	incomplete	8	SXJRKK8B016	Synechococcus phage ACG-2014f; NC_047714	65.3
		10.6	questionable	10	SXJT2AG6013	Listeria phage LMTA-34; NC_042048	66.6
X. translucens pv. *translucens*	DSM 18974	12.3	incomplete	10	SXK3D14E013	Paenibacillus phage Tripp; NC_028930	65.0
X. translucens pv. *cerealis*	NCPPB 1943	6.1	incomplete	7	SXK72C59016	Agrobacterium phage Atu_ph07; NC_042013	63.2
X. translucens pv. *arrhenatheri*	LMG 727	9.3	incomplete	9	SXKGYC2N013	Escherichia phage 500465-1; NC_049342	69.1
X. translucens pv. *phlei*	LMG 730	5.2	questionable	6	SXKKGADM016	Coliphage phi-X174; NC_001422	44.8
X. translucens pv. *poae*	ATCC 33804	7.3	incomplete	7	SXKXT95Y013	Escherichia phage PA28; NC_041935	67.0
X. hyacinthi	CFBP 1156	11.7	incomplete	11	SXM3AX8A013	Escherichia phage 500465-1_NC_049342(6)	68.9
X. translucens	569	12.7	incomplete	13	SXMMNTAM013	Escherichia phage 500465-1_NC_049342(6)	69.6
X. theicola	CFBP 4691	4.4	incomplete	6	SXNNYR3W016	Synechococcus phage ACG-2014f; NC_047712	67.2
		24.5	intact	27	SXNTYE2H013	Xanthomonas phage Xp15; NC_007024	66.6
Xanthomonas sp.	NCPPB 1128	88.3	intact	111	SXPH7FS9013	Xylella phage Xfas53; NC_013599	67.8
X. sacchari	NCPPB 4393	7.6	intact	14	SXPMZ2W4013	Stenotrophomonas phage PSH1; NC_010429	62.4
X. albilineans	CFBP 2523	5.2	incomplete	9	SXR4BE1F013	Shigella phage SfIV; NC_022749	61.6
		9.6	incomplete	12	SXR6S4D4013	Escherichia phage 500465-1_NC_049342	63.2
		21.9	intact	27	SXR8XRZC013	Salmonella phage 118970_sal3; NC_031940	61.8
		6.7	incomplete	8	SXRDR02G013	Proteus phage Mydo; NC_048741	63.8
		7.9	intact	15	SXRG3EEA013	Stenotrophomonas phage phiSMA6 ; NC_043029	57.8
		8.5	questionable	18	SXRMUVS5016	Stx2-converting phage Stx2a_WGPS9;NC_049923	59.0

Reference for supplementary material:

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