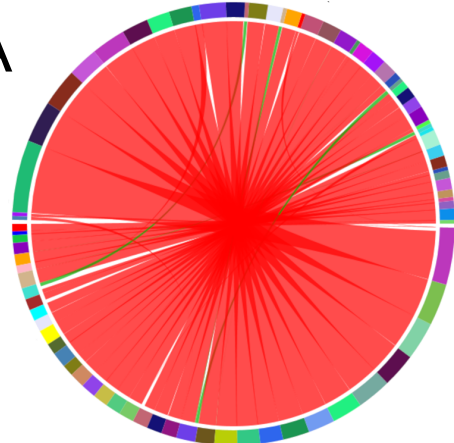
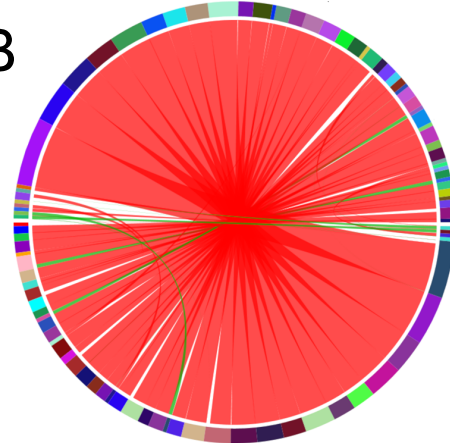


E. monterogei ATCC30507 (this study)*E. monterogei* ATCC30507 (this study)*E. monterogei* ATCC30507 (this study)

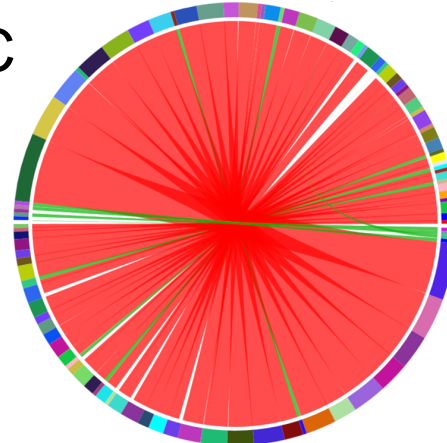
A

*L. major* Friedlin (TriTrypDB)

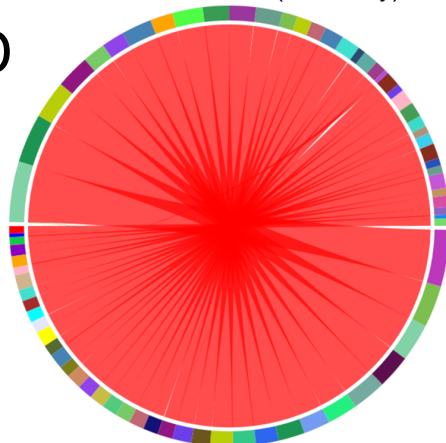
B

*P. deanei* TCC258 (this study)

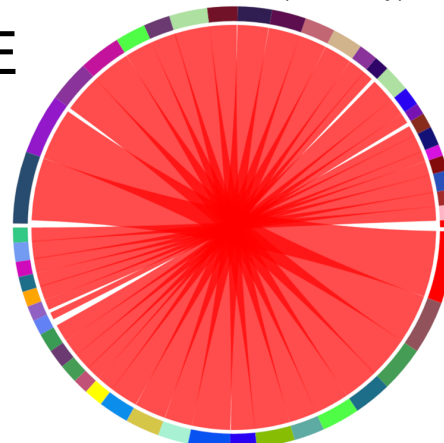
C

*P. hertigi* TCC260 (this study)*P. deanei* TCC258 (this study)

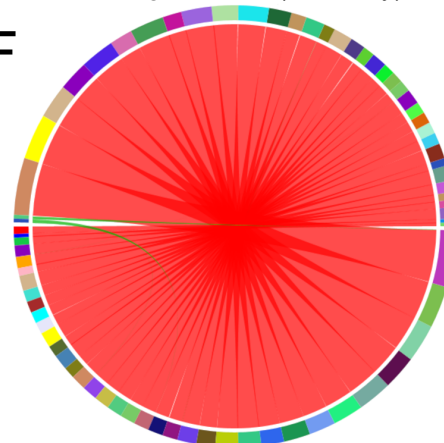
D

*L. major* Friedlin (TriTrypDB)*P. deanei* TCC258 (this study)

E

*P. hertigi* TCC260 (this study)*P. hertigi* TCC260 (this study)

F

*L. major* Friedlin (TriTrypDB)

	Species	Chromosomes	Total kb	# genes	% of sequence covered by genes	# of anchors	% of anchors in blocks	% of anchors annotated	% of coverage by anchors	# of blocks	% double coverage	# of inverted blocks	% of genes within syntenic blocks
A	<i>Endotrypanum monterogei</i> ATCC30507	35	30,584	7,695	46	7,186	55	94	46	155	0	53	82
	<i>Leishmania major</i> Friedlin	36	32,855	10,354	50	7,186	55	97	42	155	0	53	50
B	<i>Endotrypanum monterogei</i> ATCC30507	35	30,584	7,695	46	7,768	35	92	51	113	0	39	56
	<i>Porcisia deanei</i> TCC258	37	29,784	7,802	48	7,768	35	94	52	113	0	39	47
C	<i>Endotrypanum monterogei</i> ATCC30507	35	30,584	7,695	46	7,761	34	93	51	114	0	37	54
	<i>Porcisia hertigi</i> TCC260	37	29,350	7,818	49	7,761	34	94	53	114	0	37	50
D	<i>Porcisia deanei</i> TCC258	37	29,784	7,802	48	7,580	52	96	49	68	0	20	84
	<i>Leishmania major</i> Friedlin	36	32,855	10,354	50	7,580	52	97	46	68	0	20	41
E	<i>Porcisia deanei</i> TCC258	37	29,784	7,802	48	8,425	55	71	72	37	0	0	46
	<i>Porcisia hertigi</i> TCC260	37	29,350	7,818	49	8,425	55	71	73	37	0	0	46
F	<i>Porcisia hertigi</i> TCC260	37	29,350	7,818	49	7,565	52	96	50	71	0	16	85
	<i>Leishmania major</i> Friedlin	36	32,855	10,354	50	7,565	52	98	46	71	0	16	42