

**Table S1.** Primary recombination analysis in the tryptophan operon for global *C. trachomatis* strains (n=595) using RDP4.

	Daughter	Major parent	Minor parent	Beginning	Ending	Uncorrected	MC corrected	Identified by (Av. P-Val)	Recombinant score
1	<b>B_9</b>	A_HAR13	L3_404LN	1090	1450	6.163X10 <sup>-6</sup>	7.396X10 <sup>-3</sup>	GENECONV (1.123X10 <sup>-2</sup> ) Bootscan (1.124X10 <sup>-2</sup> ) Maxchi (2.381X10 <sup>-2</sup> ) 3Seq (3.223X10 <sup>-2</sup> )	0.549 (B_9) 0.196 (A_HAR13) 0.255 (L3_404LN)
2	<b>A_8</b>	A_HAR13	L3_404LN	971	1555	8.421X10 <sup>-6</sup>	1.011X10 <sup>-3</sup>	GENECONV (1.123X10 <sup>-2</sup> ) Bootscan (1.124X10 <sup>-2</sup> ) Maxchi (2.381X10 <sup>-2</sup> ) 3Seq (3.223X10 <sup>-2</sup> )	0.549 (B_9) 0.196 (A_HAR13) 0.255 (L3_404LN)
		A_HAR13	B_9	971	1555	8.431X10 <sup>-6</sup>	1.011X10 <sup>-3</sup>	MaxChi (2.629X10 <sup>-2</sup> ) 3Seq (1.360X10 <sup>-2</sup> )	0.549 (B_9) 0.196 (A_HAR13) 0.255 (L3_404LN)
	<b>A_15</b>	A_HAR13 (99.8%)	L3_404LN	1012	1438	5.575X10 <sup>-6</sup>	6.908X10 <sup>-6</sup>	GENECONV (1.123X10 <sup>-2</sup> ) Bootscan (1.124X10 <sup>-2</sup> ) Maxchi (2.381X10 <sup>-2</sup> ) 3Seq (3.223X10 <sup>-2</sup> )	0.549 (B_9) 0.196 (A_HAR13) 0.255 (L3_404LN)
		A_HAR13 (99.8%)	B_9 (92.9%)	1090	1206	5.604X10 <sup>-6</sup>	6.725X10 <sup>-3</sup>	MaxChi (2.629X10 <sup>-2</sup> ) 3Seq (1.360X10 <sup>-2</sup> )	0.446 (A_15) 0.215 (A_HAR13) 0.339 (B_9)
	<b>A_S45</b>	A_HAR13	B_9 (99.6%)	1339	1206	1.567X10 <sup>-4</sup>	1.881X10 <sup>-2</sup>	MaxChi (2.629X10 <sup>-2</sup> ) 3Seq (1.360 X10 <sup>-2</sup> )	0.446 (A_S45) 0.215 (A_HAR13) 0.339 (B_9)
3	<b>B_QH111L</b>	D_Fin163 (99.3%)	E_UK769748	332	1912	1.182X10 <sup>-4</sup>	1.418X10 <sup>-2</sup>	3Seq (1.418X10 <sup>-2</sup> )	0.452 (B_QH111L) 0.305 (D_Fin163) 0.242 (E_UK769748)
4	<b>I_UK913341</b>	L3_404LN (99.3%)	E_UK769748	433	2486	4.014X10 <sup>-4</sup>	4.817X10 <sup>-2</sup>	3Seq (7.766X10 <sup>-2</sup> )	0.537 (I_UK913341) 0.253 (L3_404LN) 0.210 (E_UK769748)
	<b>Ia_SF16</b>	L3_404LN (98.9%)	E_UK769748 (99.8%)	433	2486	7.87 X 10 <sup>-3</sup>	0.944	3Seq (7.766X10 <sup>-2</sup> )	0.537 (Ia_SF16) 0.253 (L3404LN) 0.210 (EUK769748)

<b>Ia_SF27</b>	L3_404LN (98.9%)	E_UK769748 (99.8%)	433	2486	$7.87 \times 10^{-3}$	0.944	3Seq (7.766X10 <sup>-3</sup> )	0.537 (Ia_SF27) 0.253 (L3_404LN) 0.210 (E_UK769748)
<b>I_NL58</b>	L3_404LN (98.9%)	E_UK769748 (99.8%)	433	2486	$6.597 \times 10^{-3}$	0.791	3Seq (7.766X10 <sup>-3</sup> )	0.537 (I_NL58) 0.253 (L3_404LN) 0.210 (E_UK769748)
<b>I_NL63</b>	L3_404LN (98.9%)	E_UK769748 (99.8%)	433	2486	$6.597 \times 10^{-3}$	0.791	3Seq (7.766X10 <sup>-3</sup> )	0.537 (I_NL63) 0.253 (L3_404LN) 0.210 (E_UK769748)
<b>I_NL69</b>	L3_404LN (98.9%)	E_UK769748 (99.8%)	433	2486	$6.597 \times 10^{-3}$	0.791	3Seq (7.766X10 <sup>-3</sup> )	0.537 (I_NL69) 0.253 (L3_404LN) 0.210 (E_UK769748)
<b>I_NL70</b>	L3_404LN (98.9%)	E_UK769748 (99.8%)	433	2486	$6.597 \times 10^{-3}$	0.791	3Seq (7.766X10 <sup>-3</sup> )	0.537 (I_NL70) 0.253 (L3_404LN) 0.210 (E_UK769748)
<b>I_S2459</b>	L3_404LN (98.9%)	E_UK769748 (99.8%)	433	2486	$6.597 \times 10^{-3}$	0.791	3Seq (7.766X10 <sup>-3</sup> )	0.537 (I_S2459) 0.253 (L3_404LN) 0.210 (E_UK769748)
<b>Ia_20-97</b>	L3_404LN (98.9%)	E_UK769748 (99.8%)	433	2486	$6.597 \times 10^{-3}$	0.791	3Seq (7.766X10 <sup>-3</sup> )	0.537 (Ia_20-97) 0.253 (L3_404LN) 0.210 (E_UK769748)
<b>Ia_Soton1</b>	L3_404LN (98.9%)	E_UK769748 (99.8%)	433	2486	$6.597 \times 10^{-3}$	0.791	3Seq (7.766X10 <sup>-3</sup> )	0.537 (Ia_Soton1) 0.253 (L3_404LN) 0.210 (E_UK769748)
<b>Ia_Soton3</b>	L3_404LN (98.9%)	E_UK769748 (99.8%)	433	2486	$6.597 \times 10^{-3}$	0.791	3Seq (7.766X10 <sup>-3</sup> )	0.537 (Ia_Soton2) 0.253 (L3_404LN) 0.210 (E_UK769748)
<b>Ia_UW202</b>	L3_404LN (98.9%)	E_UK769748 (99.8%)	433	2486	$8.33 \times 10^{-3}$	1	3Seq (7.766X10 <sup>-3</sup> )	0.537 (Ia_UW202) 0.253 (L3_404LN) 0.210 (E_UK769748)