G2JD G9JD/ G3T7
9185 MED Ag2/ S3545
97

99
T136P2 G3T1
BovineT3552B^T
Porcine T3552B / DD3F (3)

DD3

98
Ovine / G819CB/ T354A
G3ST1/ T354A
T3551C/ T184F2/ T18D2

G10JD
ELK22AF/ ELK22F/ ELK23F/ ELK24F
T2723/ T380A2F45/ T354b
99
T116B/ T645C3/ T200/
T323CF1/ T167LAB2/ T122A
W35/ G187/ G169A/ T100A
T119A / T52A/ T320A^T / T2721
G2S3R1/ S2331/ S32R
S3R/ S4R/ S5R
1A/ 2LC/ 6LD/ 10C/ 11A

DD2

G23F1/ 3F2/ G26F1
C2F/ C2R/ C2RA
K/ P
G2S1F/ G2S4F/ G2F3
G2SL1/ SL2/ SL4/ G2SL5
G2ST24/ ST25/ ST26/ ST27
DD1F/ DD1R/ DD2F/ DD2R/ DD3F/ DD4F/ DD5F
V1/ 4A
T354B/ T296A/ T257/ T136

1498 MED AGg
74
T. phagedenis CIP 62.29
T. phagedenis ATCC 27087
T. phagedenis biovar Reiter
F4021

T. medium ATCC 700293^T
ELK22R/ ELK23AR/ ELK24R
T296/ T56/ T184Y
T3202F/ T200BA1 / T200BA2
99
T19^T / T54/ T380/ T3551
OV11F/ G1OV11
MED1985 AG3
2c/ 2D / 3E
S2R

DD1

ST12/ ST27
85
2F/ 6F/ G1F7C5 / G1F9
DD3F (1)
7.45g
T136E/ T18A/ T52R2G/ T35B1
T. vincentii OMZ 838 (CP009227)

Brachyspira hyodysenteriae (EF517531)

0.05

Figure S1. Treponeme phylogenetic tree based on 16S rRNA gene sequences. A

maximum likelihood tree (bootstrapped 10,000 times) for comparison of the 16S

5   rRNA gene of the treponeme sequences isolated in this study. (For clarity, bootstrap

6   values below 65 were removed). Genbank numbers for each individual isolate can be

7   found in Tables 1, 2 and 3. For simplicity, due to the large number of samples in this

8   study, sequences which have an identical 16S rRNA gene and from the same host

9   species have been grouped together.

10 Key: DD1, DD2 and DD3 refer to the DD treponeme phylogroups, where DD1 is

11 *Treponema medium*/*Treponema vincentii* phylogroup, DD2 is *Treponema*

12 *phagedenis* phylogroup and DD3 is *T. pedis* phylogroup.

13

14

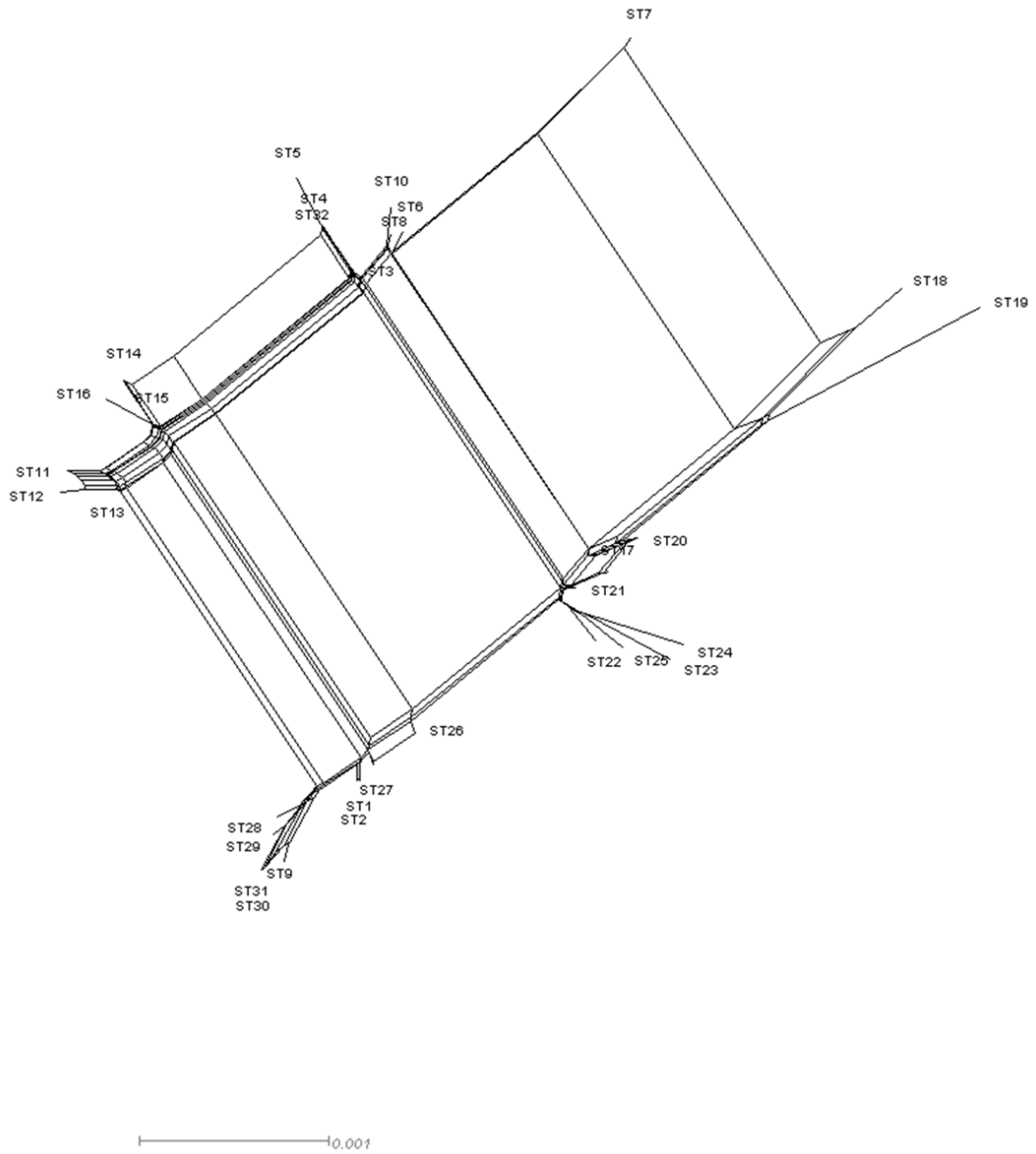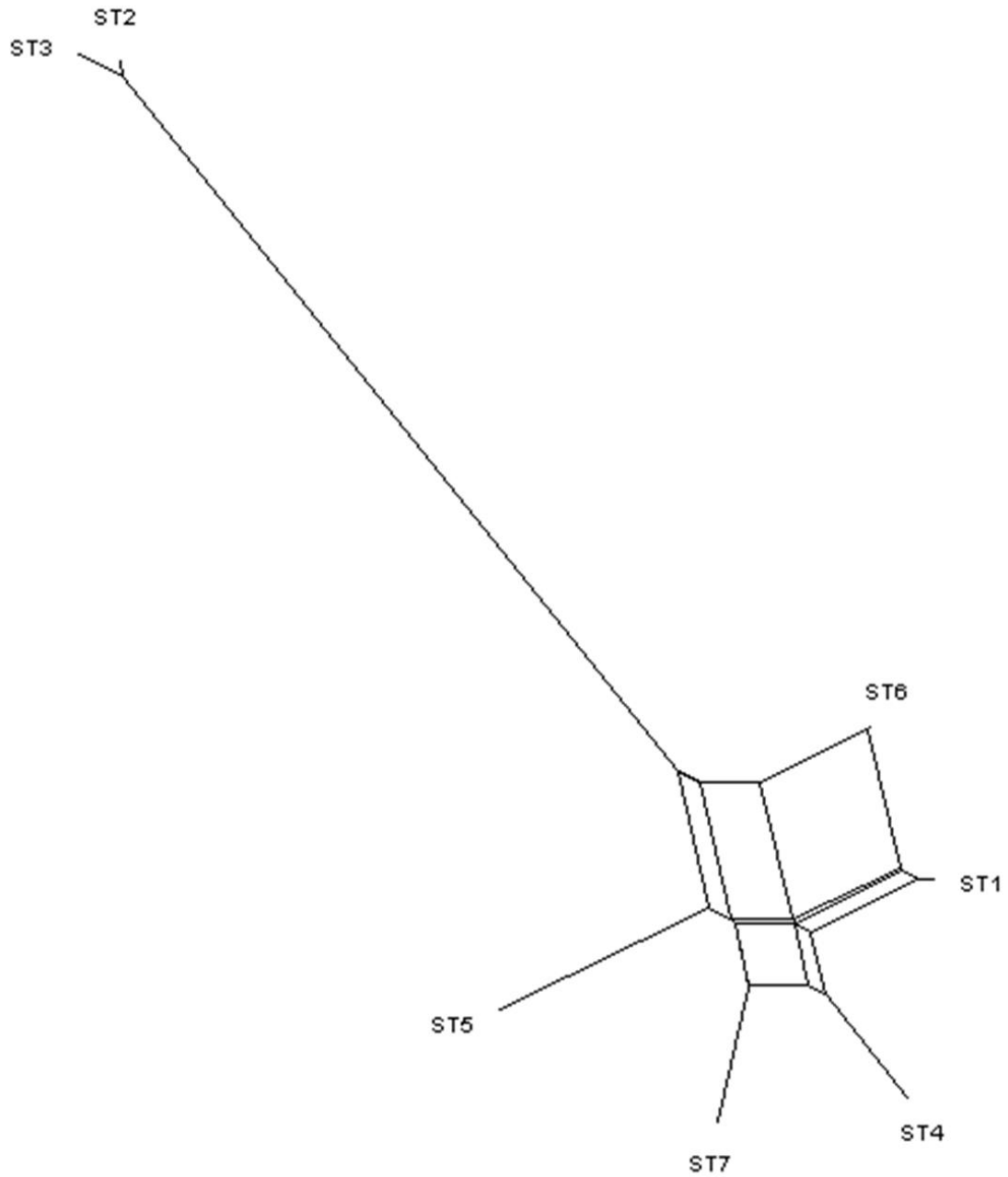15

T. medium (DD1) phylogroup

ST11

ST2

ST8
ST5
ST1
ST4
ST9
ST10
ST7
ST6
ST3

0.001

16

17

T. phagedenis (DD2) phylogroup

ST7

ST5

ST4
ST32

ST10
ST6
ST8

ST3

ST18

ST19

ST14

ST16
ST15

ST11
ST12
ST13

ST17 ST20

ST21

ST22 ST25 ST24
ST23

ST26

ST27
ST1
ST2

ST28
ST29

ST9

ST31
ST30

0.001
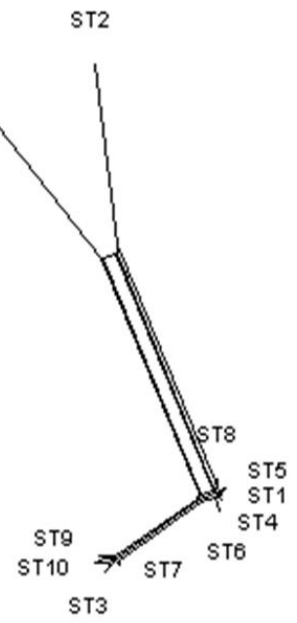
18

19

T. pedis phylogroup

20
21 **Figure S2**. Splits graphs showing recombination between isolates from the three

22 phylogroups examined in this study. Key: DD1, DD2 and DD3 refer to the DD

23 treponeme phylogroups, where DD1 is *Treponema medium* phylogroup, DD2 is

24 *Treponema phagedenis* phylogroup and DD3 is *T. pedis* phylogroup.

locus	T. medium (DD1) phylogroup (n= 34)			T. phagedenis (DD2) phylogroup (n=70)			T. pedis (DD3) phylogroup (n=17)		
	Number of positive selection sites	Number of negative selection sites	d_N/d_S	Number of positive selection sites	Number of negative selection sites	d_N/d_S	Number of positive selection sites	Number of negative selection sites	d_N/d_S
groEL	0	0	5.000E-09	0	0	6.950E-01	0	0	5.000E-09
recA	0	0	5.238E-03	0	0	1.682E-01	0	0	2.782E-02
glpK	0	0	7.409E-02	0	0	7.269E-01	0	0	5.000E-09
adK	0	2 (86, 92)	7.974E-02	0	0	2.532E-01	0	0	1.168E-01
gdh	0	0	5.639E-02	0	0	4.386E-02	0	1 (162)	8.778E-02
pyrG	0	2 (91, 96)	3.206E-02	0	0	1.094E-01	0	1 (142)	5.000E-09
rplB	0	1 (78)	1.071E-02	0	0	5.000E-09	0	1 (110)	5.000E-09

Table S1. Analysis of selection pressures on individual genes. d_N/d_S is the ratio of non-synonymous substitutions per non-synonymous site to synonymous substitutions per synonymous site.