Figure Legends

Fig S1. Pulsed-field gel electrophoresis analysis using *SpeI* of environmental and clinical *Burkholderia pseudomallei* isolates involved in a case cluster occurring in a remote island community. Note that both ST-125 and ST-126 isolates appear identical using this typing method and led to the original conclusion of a clonal outbreak (Currie *et al.,* 2001). A similar figure was published previously in the original study (Currie *et al*., 2001); however, strain names, environmental strains and some clinical strains were omitted from the original figure but have been included in this figure for clarity.

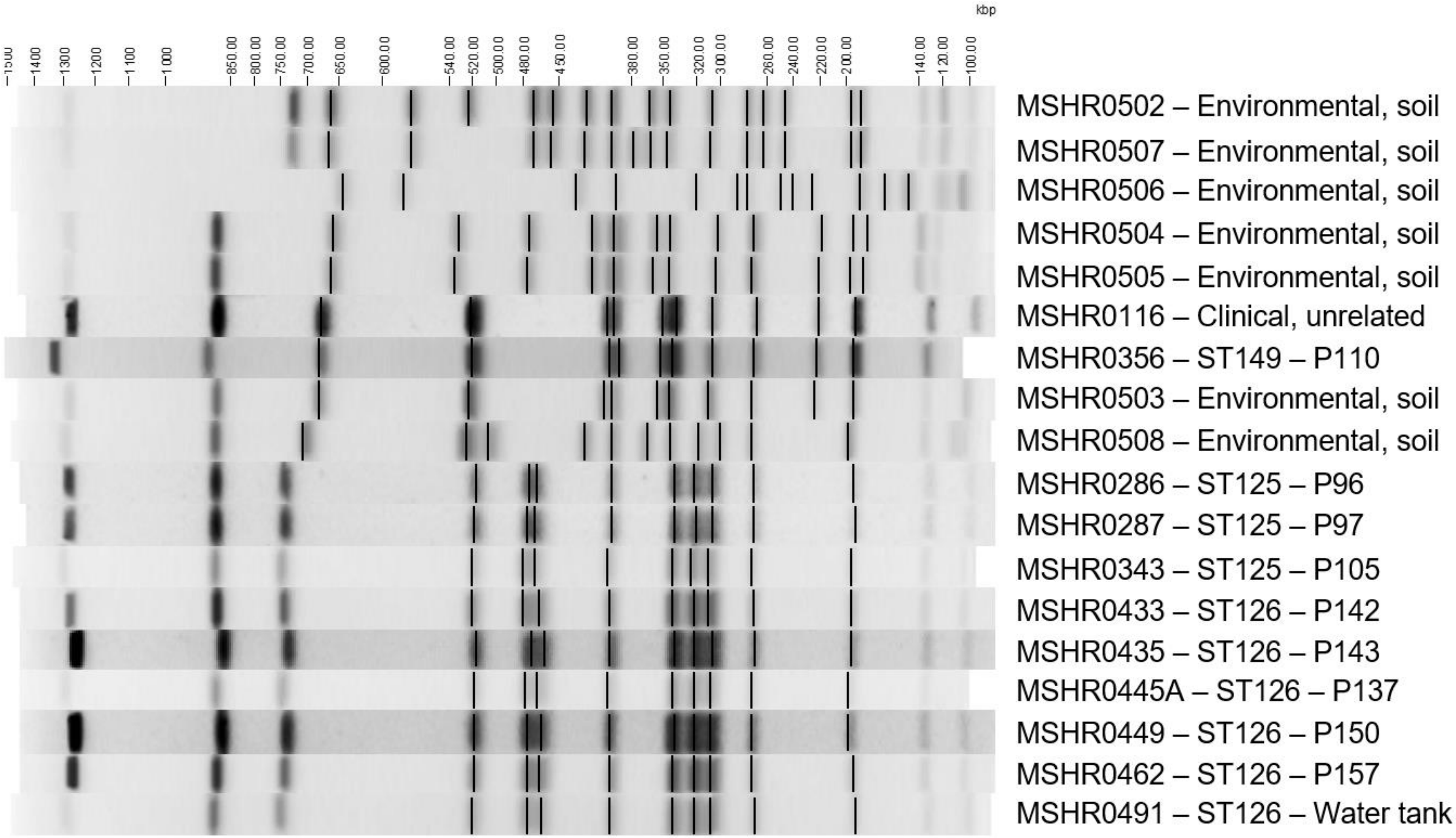
kbp
1500
1400
1300
1200
1100
1000
850.00
800.00
750.00
700.00
650.00
600.00
540.00
520.00
500.00
480.00
450.00
380.00
350.00
320.00
300.00
260.00
240.00
220.00
200.00
140.00
120.00
100.00
MSHR0502 – Environmental, soil
MSHR0507 – Environmental, soil
MSHR0506 – Environmental, soil
MSHR0504 – Environmental, soil
MSHR0505 – Environmental, soil
MSHR0116 – Clinical, unrelated
MSHR0356 – ST149 – P110
MSHR0503 – Environmental, soil
MSHR0508 – Environmental, soil
MSHR0286 – ST125 – P96
MSHR0287 – ST125 – P97
MSHR0343 – ST125 – P105
MSHR0433 – ST126 – P142
MSHR0435 – ST126 – P143
MSHR0445A – ST126 – P137
MSHR0449 – ST126 – P150
MSHR0462 – ST126 – P157
MSHR0491 – ST126 – Water tank

Fig S2. Phylogenetic reconstruction in comparison to predicted recombination block distribution of the ST-125 and ST-126 strains.


MSHR0286
MSHR0436
MSHR0345
MSHR0462
MSHR0433
MSHR0449
MSHR0445A
MSHR0491
MSHR0435
MSHR0287
MSHR0344
7

Fig S3. Phylogenetic reconstruction in comparison to genome wide single-nucleotide polymorphism distribution of the ST-125 and ST-126 strains.

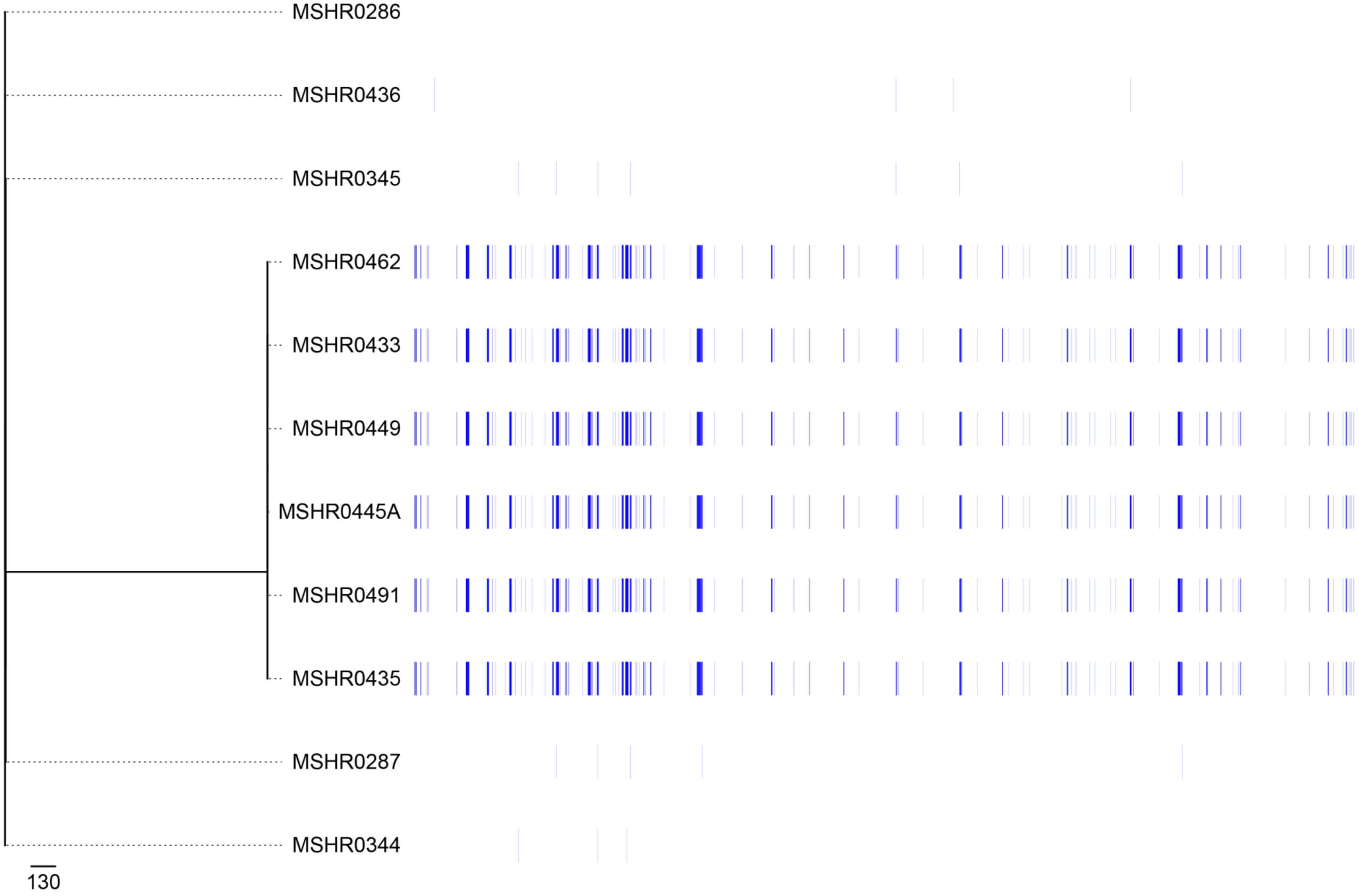
MSHR0286
MSHR0436
MSHR0345
MSHR0462
MSHR0433
MSHR0449
MSHR0445A
MSHR0491
MSHR0435
MSHR0287
MSHR0344
130

Table S1: Summary of recombination prediction for ST-125 and ST-126 strains using Gubbins

Node	Total SNPs	SNPs inside recombination blocks	SNPs outside recombination blocks	Recombination Blocks	Bases in Recombination blocks	Recombination to mutation ratio	Bases in Clonal Frame
MSHR0286	0	0	0	0	0	0	7356446
MSHR0287	2	0	2	0	0	0	7356446
MSHR0344	3	0	3	0	0	0	7356446
MSHR0345	4	0	4	0	0	0	7356446
MSHR0433	1	0	1	0	339312	0	7017098
MSHR0435	2	0	2	0	339312	0	7017098
MSHR0436	4	0	4	0	0	0	7356446
MSHR0445A	0	0	0	0	339312	0	7017098
MSHR0449	0	0	0	0	339312	0	7017098
MSHR0462	1	0	1	0	339312	0	7017098
MSHR0491	0	0	0	0	339312	0	7017098
Node5*	1343	1270	73	36	339312	17.4	7356446
Node3*	3	0	3	0	0	0	7356446

*Node 5= Separation between ST-125 and ST-126; Node 3= Node shared between MSHR0344 and MSHR0345. N.B. Nodes with no variation have been removed from this table. Abbreviations: SNP, single-nucleotide polymorphism.