Table S5: Mixed infection and lineage data from cohort two

ID	Fg/uL	Composite target coverage breadth %	Average coverage depth (x)	Species best match (main population (%)/min population (%))	SNP-based lineage (main (%)/min (%) if mixed)	Potential mixed infection
B1	46.8737	99.59	3506.66	Mycobacterium tuberculosis complex	Other than H37Rv	n/a
B2	0.9187	100	4422.03	Mycobacterium tuberculosis complex	Lineage 2 (M. tuberculosis)	n/a
B3	0.0075	99.99	1552.83	Mycobacterium tuberculosis complex : 87.6 / Mycobacterium bohemicum : 12.2	Lineage 2 (M. tuberculosis)	n/a
B4	1.9766	99.99	2265.29	Mycobacterium tuberculosis complex	Other than H37Rv	n/a
B5	1.7734	99.98	1338.48	Mycobacterium tuberculosis complex	Lineage 3 (M. tuberculosis)	n/a
B6	3.541	100	5108.63	Mycobacterium tuberculosis complex	Lineage 1 (M. tuberculosis)	n/a
B7	0.5198	100	1267.52	Mycobacterium tuberculosis complex : 93.6	Other than H37Rv	n/a
B8	93.5956	99.98	4664.92	Mycobacterium tuberculosis complex	Other than H37Rv	n/a
B9	919.4069	100	5384.32	Mycobacterium tuberculosis complex	Lineage 2 (M. tuberculosis)	n/a
B10	26.8838	99.99	3763.04	Mycobacterium tuberculosis complex	Lineage 2 (M. tuberculosis)	n/a
B11	3817.9069	99.9924282	4752.38	Mycobacterium tuberculosis complex	Other than H37Rv	n/a
B12	4.3692	99.98	783.88	Mycobacterium tuberculosis complex	Other than H37Rv	Yes
B13	0.00002	69.55	778.32	Mycobacterium tuberculosis complex	No lineage specific SNP detected	n/a
B14	0.0817	9.03	2.77			
B15	0.0124	56.78	213.53	Mycobacterium tuberculosis complex		
B16	0					
B17	0					
B18	0.0316					
B19	0	28.03	37.32			
B20	0	46.16	78.79			
B21	0	64.03	655.03	Mycobacterium tuberculosis complex		