

1 **Table S1. Genome re-sequencing mapping statistics for eleven *M. abscessus* clinical isolates**  
 2 **from patients at NJH compared to the *M. abscessus* reference genome of type strain ATCC**  
 3 **19977<sup>T</sup>.**

<b>NJH <i>M. abscessus</i> isolates</b>											
<b>Mapping Statistic</b>	<b>1</b>	<b>2</b>	<b>3</b>	<b>4</b>	<b>5</b>	<b>6</b>	<b>7</b>	<b>8</b>	<b>9</b>	<b>10</b>	<b>11</b>
<b>Total Reads (M)<sup>a</sup></b>	17.8	10.3	17.3	21.3	23.6	23.2	24.6	21.4	17.0	18.7	19.2
<b>% Reads mapped to chromosome</b>	73.4	77.7	77.6	77.9	70.1	75.9	64.2	63.3	75.4	76.9	55.3
<b>No. Reads mapped to plasmid</b>	11	10	6	17	635	6	42	93	16.1K	8	25
<b>Coverage (x)</b>	158.4	96.6	160	201.6	198.8	214.4	190.8	161.6	115.6	171.6	123.6

4

5 <sup>a</sup> SOLiD5500, Single-end, 75bp reads