

**Table 1. Cluster analysis of MRSA isolates analyzed by Whole Genome Sequencing.**

Characteristic	Number of Isolates (%)		
	Cluster A Isolates = 73	Cluster B Isolates = 18	Cluster C Isolates = 6
<b>Sequence Type</b>			
5	55 (75.3%)	0	0
105	14 (19.2%)	0	0
1866	1 (1.4%)	0	0
4234	1 (1.4%)	0	0
other/ unknown	2 (2.7%)	0	0
8	0	14 (77.8%)	0
3	0	2 (11.1%)	0
1750	0	1 (5.6%)	0
2253	0	1 (5.6%)	0
59	0	0	2 (33.3%)
15	0	0	1 (16.7%)
87	0	0	1 (16.7%)
97	0	0	1 (16.7%)
398	0	0	1 (16.7%)
<b>SCCmec</b>			

II	69 (94.5%)	0	0
IV	3 (4.1%)	18 (100%)	3 (50%)
Not detected	1 (1.4%)	0	3 (50%)
<b>Toxin</b>			
SEG	71 (97.3%)	0	0
SEI	71 (97.3%)	0	0
SEM	73 (100%)	0	0
SEN	72 (98.6%)	0	0
SEO	73 (100%)	0	0
LukF	0	9 (50%)	0
LukS	0	9 (50%)	0