

**Table S3.**

Mutation site	Number of mutants per treatment		Two-tailed <i>P</i> -value	Interpretation
	LL-37	LL-37+Fe <sup>2+</sup>		
G33 to D	1	0	> 0.9999	The groups are not significantly different.
L50 to P	0	0	> 0.9999	The groups are not significantly different.
R62 to H	0	0	> 0.9999	The groups are not significantly different.
deletion of 6 bp I74 - A75	6	0	0.0202	The groups are significantly different.
G77 to D	1	0	> 0.9999	The groups are not significantly different.
G84 to C	0	0	> 0.9999	The groups are not significantly different.
R93 to W	0	10	0.0004	The groups are significantly different.
Q134 to L	1	0	> 0.9999	The groups are not significantly different.
G135 to S	0	3	0.2308	The groups are not significantly different.
G137 to S	1	0	> 0.9999	The groups are not significantly different.
T299 frameshift	0	1	> 0.9999	The groups are not significantly different.
T144 to P	1	0	> 0.9999	The groups are not significantly different.
E153 to K	1	0	> 0.9999	The groups are not significantly different.
N166 to D	1	0	> 0.9999	The groups are not significantly different.
A164 to V	0	2	0.4872	The groups are not significantly different.
L175 to P	1	0	> 0.9999	The groups are not significantly different.
G216 to D	0	0	> 0.9999	The groups are not significantly different.
D274 to E	0	2	0.4872	The groups are not significantly different.
W275 to R	1	0	> 0.9999	The groups are not significantly different.
E282 to V	0	0	> 0.9999	The groups are not significantly different.
Y298 to stop, truncation	1	0	> 0.9999	The groups are not significantly different.
I303 to T	0	0	> 0.9999	The groups are not significantly different.
G305 to S	1	0	> 0.9999	The groups are not significantly different.
V332 to L	1	0	> 0.9999	The groups are not significantly different.
T336 to P	1	0	> 0.9999	The groups are not significantly different.
E374 to K	1	0	> 0.9999	The groups are not significantly different.
G395 to S	0	3	0.2308	The groups are not significantly different.