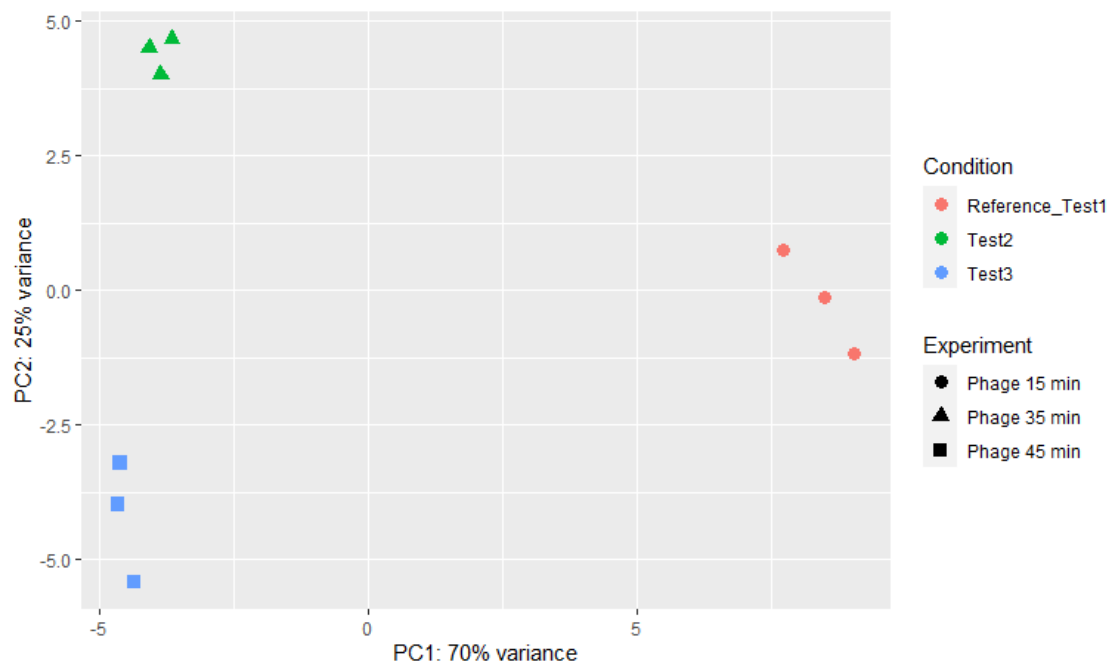
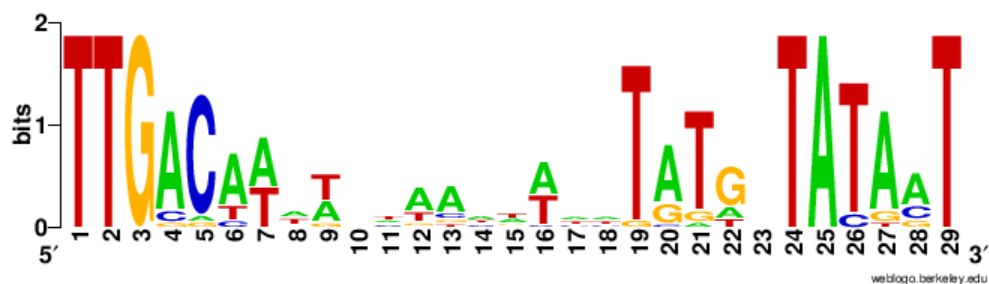


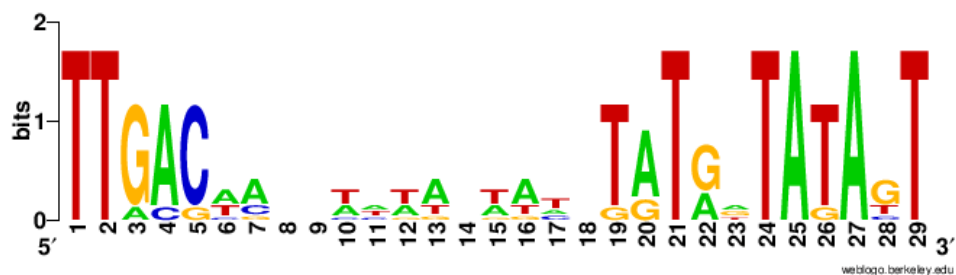
**Figure S1.** Percentage of unique reads mapping to the genomes of *Staphylococcus* phage SAM1 and *S. aureus* strain E1185(IV)ST12.



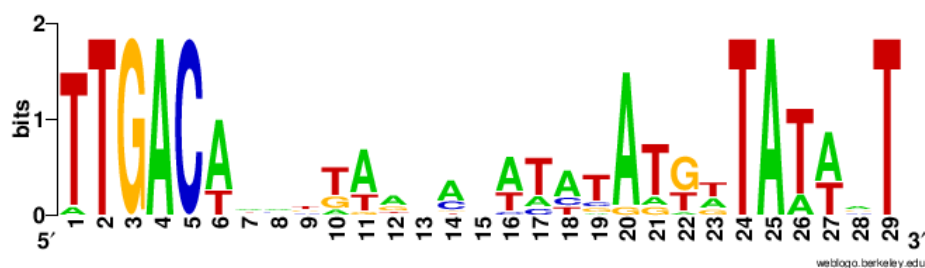
**Figure S2.** Principal component analysis (PCA) graph presenting the correlation between all the samples used in this study in relation to reads mapped to the genome of *Staphylococcus* phage SAM1



**Figure S3.** Consensus sequence logos for a putative promotor of *Staphylococcus* phage SAM1 among genes up regulated at 15 mins



**Figure S4.** Consensus sequence logos for a putative promotor of *Staphylococcus* phage SAM1 among genes up regulated at 35 mins



**Figure S5.** Consensus sequence logos for a putative promotor of *Staphylococcus* phage SAM1 among genes up regulated at 45 mins