**Table 2**. Mutations observed in *Enterococcus* genomes after culturing with individual phages. Each row indicates an *Enterococcus* gene in which one or more mutations were observed when that *Enterococcus* strain was cultured with the indicated phage. When more than one phage is listed, the mutation occurred separately for each phage host pair, the phages were not used in combinations. Locus ids refer to genomes in **Table S2**.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Enterococcus strain** | **Phage(s)** | **Mutated Host Gene** | **Locus id** | **Mutation Type** | **Exopolysaccharide Locus** | **AA change** |
| *E. faecalis* DP11 | Ump, SDS1 | NAD-dependent epimerase/dehydratase | HOCGOLEH\_00595 | SNP | Epa gene | G11V, G279E |
| *E. faecalis* DP11 | Ump | Bacterial sugar transferase | HOCGOLEH\_00585 | Nonsense | EpaR | E249\* |
| *E. faecalis* DP11 | SDS2 | TagF gene. glycerol glycerophosphotransferase | HOCGOLEH\_00593 | SNP | Epa gene | A113E |
| *E. faecalis* Yi6 | Bop | Bacterial sugar transferase | UMS\_01916 | SNP, Nonsense | EpaR | N705Y |
| *E. faecalis* Yi6 | Bop | UTP-glucose-1-phosphate uridylyltransferase | UMS\_01646 | DEL |  | K22\* |
| *E. faecalis* Yi6 | Bop | UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 | UMS\_01161 | SNP |  | A210T |
| *E. faecalis* Yi6 | Bop | isoleucyl-tRNA synthetase | UMS\_00984 | DEL |  | W31\* |
| *E. faecalis* Yi6 | phiV12 | 30S ribosomal protein S7 | UMS\_00243 | SNP |  | G82D |
| *E. faecalis* Yi6 | phiV12 | DNA-directed RNA polymerase subunit alpha | UMS\_00275 | SNP |  | G29V |
| *E. faecalis* B3286 | Bop, phiV12 | NAD-dependent epimerase/dehydratase | SQ1\_02166 | SNP, Nonsense | Epa gene | A123E, Q204\* |
| *E. faecalis* B3286 | Bop | Glucose-1-phosphate thymidylyltransferase; | SQ1\_02191 | SNP | EpaE | R217C |
| *E. faecalis* B3286 | Bop | endonuclease III | SQ1\_01204 | SNP |  | A130V |
| *E. faecalis* B3286 | phiV12 | Bacterial sugar transferase | SQ1\_02177 | SNP | EpaR | Y336\* |
| *E. faecalis* B3286 | phiV12 | ATP-dependent Clp protease ATP-binding subunit ClpE | SQ1\_00765 | SNP |  | I13F |
| *E. faecalis* TX2137 | Bop | Epimerase/dehydratase | HMPREF9494\_02361 | SNP | EpaW | D229Y, G192V |
| *E. faecalis* TX2137 | Bop | phosphocarrier protein HPr | HMPREF9494\_02513 | SNP |  | V209L |
| *E. faecalis* TX2137 | Bop, phiV12 | Bacterial sugar transferase | HMPREF9494\_02367 | SNP | EpaR | R400C, G251R |
| *E. faecalis* TX2137 | phiV12 | DNA ligase (NAD+) | HMPREF9494\_02501 | SNP |  | A434E |
| *E. faecium* TX1330 | Ben | DNA gyrase subunit A (EC 5.99.1.3) | HMPREF0352\_0587 | SNP |  | D116A |
| *E. faecium* TX1330 | Ben | DNA-directed RNA polymerase beta' subunit (EC 2.7.7.6) | HMPREF0352\_2730 | SNP |  | A924V |
| *E. faecium* TX1330 | Bob | response regulator transcription factor | D3Y30\_RS07660 | SNP |  | E192K |
| *E. faecium* TX1330 | Bop | polysaccharide biosynthesis protein | D3Y30\_RS11110 | SNP |  | L222S |
| *E. faecium* TX1330 | Bop, Ben, Bill, No phage | CpsD/CapB family tyrosine-protein kinase | D3Y30\_RS11120 | SNP | Yqw | P136S, P26Q, L62E |
| *E. faecium* TX1330 | Carl, phiV12, No phage | tyrosine protein kinase | D3Y30\_RS11125 | SNP | Yqw | A147T, V153A |