S3 Text – Supplementary Genome Analysis

## Within-Patient Evolution

Within-patient *E. faecium* populations were genetically diverse and evolved over time. Phylogenies for isolates from individual patients are shown in Figures A to D with data on daptomycin susceptibility for each isolate. Tables A to D list coding mutations detected among isolates within a patient. In several cases, variation was detected in genes previously associated with daptomycin susceptibility; however, in many cases, the evolution of increased daptomycin resistance occurred through previously undescribed genetic pathways. In addition to the variants listed in Tables A to D, many annotated genes were present in some genomes but not others. There were 215, 635, 280, and 2094 annotated genes present in some but not all isolates from Patient 4, 86, 87, and 150, respectively.

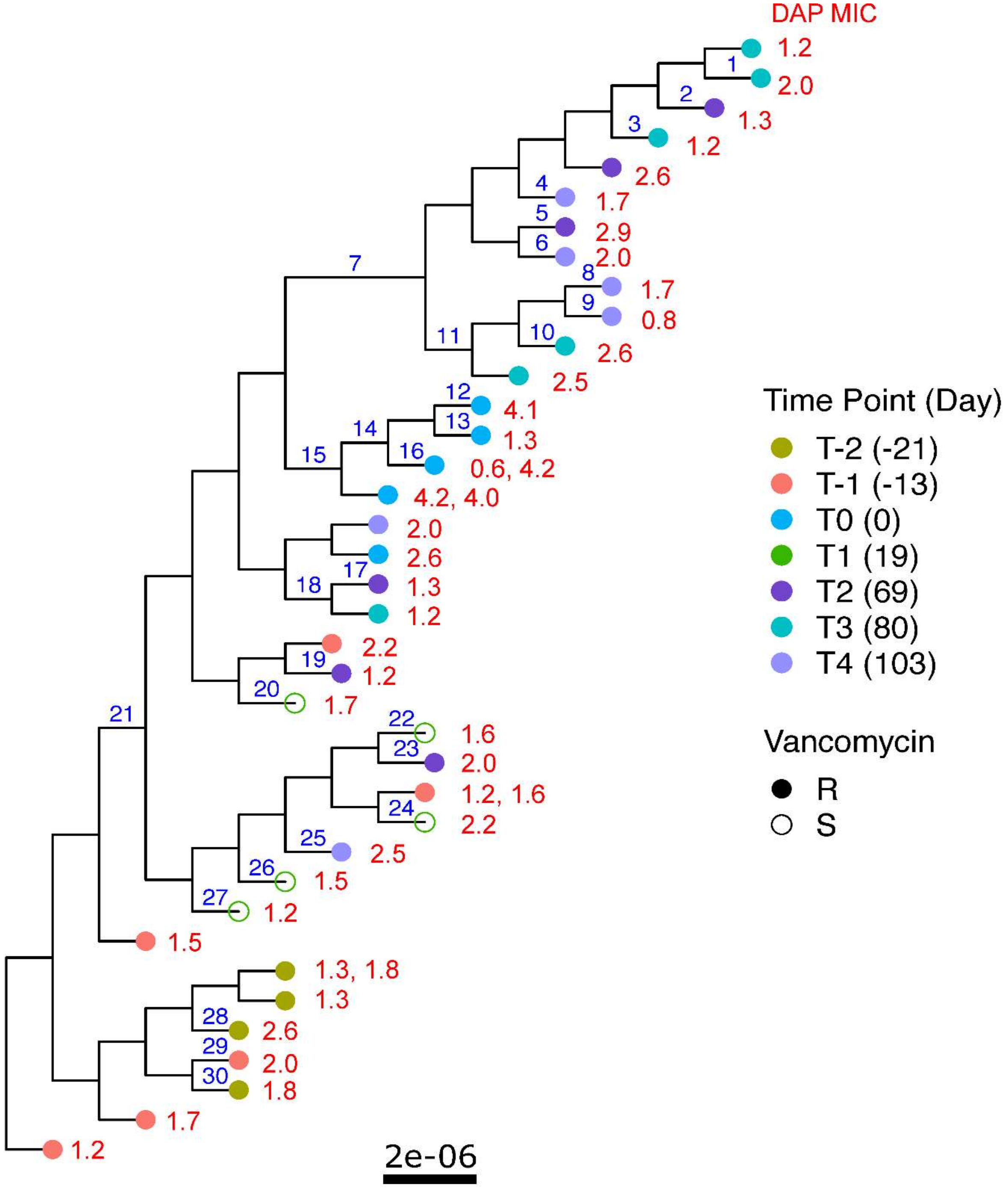

**Figure A:** Phylogeny for *E. faecium* strains isolated from Patient 4. Branch labels (blue) correspond to variants in Table A. For tips representing two isolates with identical core genomes, the daptomycin MICs for both isolates are listed (red). The index sample is labelled T0 and timepoints are labelled in order from that timepoint. The number of days between the index sample and the other timepoints are in brackets after the timepoint number.

**Table A: Nonsynonymous mutations within Patient 4.** Branch numbers correspond to Figure A. Asterisks indicates loci known to be associated with variation in daptomycin susceptibility [1].

| Branch | Locus | Contig | Position | Mutation |
|---|---|---|---|---|
| 1 | hypothetical protein | 1 | 2733759 | S85F |
| 1 | *norG* | 1 | 1200265 | R87G |
| 2 | hypothetical protein | 1 | 2142365 | H140R |
| 2 | hypothetical protein | 6 | 3320 | I89ILG |
| 3 | *ctpE_2* | 1 | 1780334 | frameshift |
| 4 | 5.5kb sequence | 1 | 2636227 | deleted: *yurK_1*, phosphorylated carbohydrates phosphatase, *manZ_5, levE*, hypothetical protein, *frlB_2* |
| 5 | 5.2kb sequence | 5 | 13746 | deleted: 6 hypothetical proteins |
| 6 | hypothetical protein | 4 | 40556 | deleted |
| 7 | *fabD_2* | 1 | 947147 | Q162K |
| 7 | hypothetical protein | 1 | 2324634 | E264K |
| 7 | *murJ_1* | 1 | 1395230 | S144N |
| 7 | *rnpA* | 1 | 2791463 | E34D |
| 7 | *ybiT_1* | 1 | 18596 | TT359T |
| 8 | *potA* | 1 | 689615 | D167Y |
| 9 | *gmuR* | 1 | 1026782 | L211P |
| 10 | hypothetical protein | 4 | 22620 | 18aa insertion |
| 11 | hypothetical protein | 1 | 1966884 | frameshift |
| 12 | hypothetical protein | 1 | 1900362 | frameshift |
| 12 | *pstB3_2* | 1 | 1898781 | frameshift |
| 13 | *rapA* | 1 | 2355585 | K488E |
| 14 | IS30 family transposase IS1062 | 1 | 1786098 | frameshift |
| 14 | hypothetical protein | 1 | 1900362 | frameshift |
| 15 | *cls** | 1 | 1036195 | N13S |
| 15 | hypothetical protein | 1 | 1521249 | altered stop |
| 15 | ISL3 family transposase ISEfa5 | 2 | 199879 | K429N |
| 16 | IS30 family transposase IS1062 | 1 | 1786098 | frameshift |
| 17 | hypothetical protein | 1 | 639610 | frameshift |
| 17 | 2.5kb sequence | 1 | 930541 | deleted: *prfC*, hypothetical protein |
| 18 | hypothetical protein | 2 | 97613 | deleted |
| 18 | hypothetical protein | 2 | 99596 | deleted |
| 18 | IS256 family transposase ISEfa13 | 2 | 106570 | deleted |
| 18 | 3.2kb sequence | 2 | 101024 | deleted: *panD, panC, panB*, IS256 family transposase ISEfa13, IS3 family transposase ISEfa8 |
| 19 | *gshAB* | 1 | 128400 | E319K |
| 19 | hypothetical protein | 1 | 1076147 | Q259L |
| 20 | *rsmD* | 1 | 1219512 | G54D |
| 20 | *truA_1* | 1 | 104779 | A6V |
| 20 | *vanA* cassette | 5 | 19816 | deleted: *vanR, vanS, vanH, vanA, vanX* |
| 21 | *bceB_2* | 1 | 744561 | G352V |
| 22 | *vanA* plasmid | 5 | 0 | loss of *vanA*-containing plasmid |
| 22 | IS30 family transposase IS1062 | 1 | 1786098 | frameshift |
| 22 | hypothetical protein | 4 | 50960 | frameshift |
| 23 | *comGA* | 1 | 2389377 | T148I |
| 23 | hypothetical protein | 1 | 2539971 | 12aa insertion |
| 23 | *rihB* | 1 | 1936471 | S287N |

| | | | | |
|---|---|---|---|---|
| 23 | *rplA* | 1 | 2320420 | P138A |
| 24 | *vanA* plasmid | 5 | 0 | loss of *vanA*-containing plasmid |
| 25 | *graS* | 1 | 530930 | Q110R |
| 25 | hypothetical protein | 5 | 33751 | deleted |
| 25 | *nylA* | 1 | 1410475 | F119S |
| 25 | *rex_2* | 1 | 2101769 | H102Q |
| 26 | 1.5kb sequence | 5 | 19818 | deleted: *vanR, vanS* |
| 27 | 1.5kb sequence | 5 | 19818 | deleted: *vanR, vanS* |
| 28 | hypothetical protein | 1 | 1834542 | frameshift |
| 28 | hypothetical protein | 1 | 2558795 | altered stop |
| 29 | hypothetical protein | 4 | 50960 | frameshift |
| 30 | IS3 family transposase ISPa31 | 2 | 115091 | frameshift |

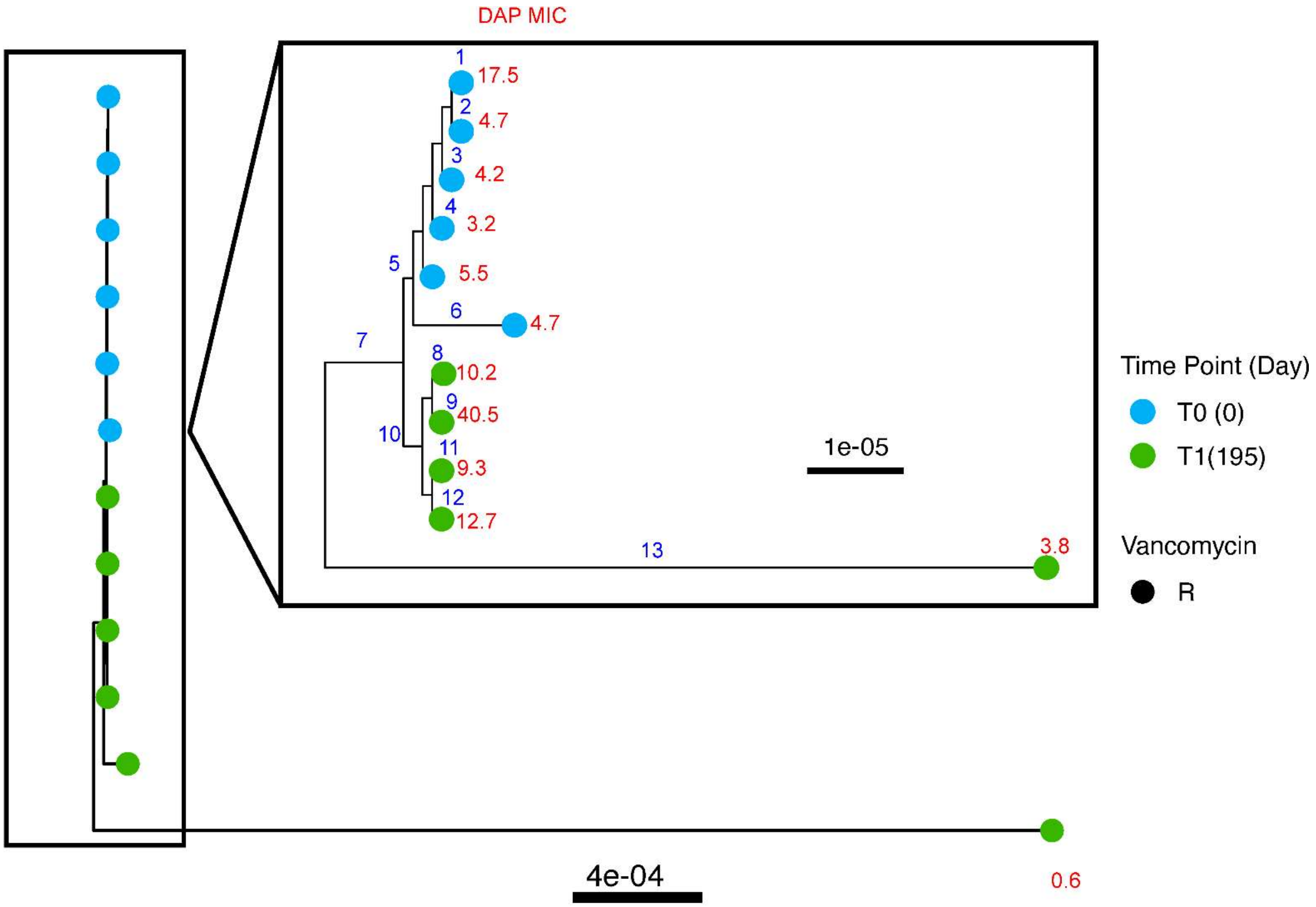

**Figure B:** Phylogeny for *E. faecium* strains isolated from Patient 86. Rectangle shows detailed structure of indicated group. Branch numbers (blue) correspond to mutations listed in Table B. The index sample is labelled T0 and timepoints are labelled in order from that timepoint. The number of days between the index sample and the other timepoints are in brackets after the timepoint number.

**Table B: Nonsynonymous mutations within Patient 86.** Branch numbers correspond to Figure B. Asterisks indicates loci known to be associated with variation in daptomycin susceptibility [1].

| Branch | Locus | Contig | Position | Mutation |
|---|---|---|---|---|
| 1 | *kduD* | 1 | 2112219 | V128A |
| 2 | 13kb sequence | 2 | 70061 | deleted: *panD, panC, panB*, multiple hypothetical proteins |
| 2 | 208kb plasmid | 3 | 0 | plasmid lost |
| 2 | *gmuR* | 1 | 960027 | R14H |
| 2 | IS256 family transposase IS256, IS1595 family transposase ISCco2 | 9 | 3008 | IS256 family transposase IS256, IS1595 family transposase ISCco2 deleted |
| 3 | 208kb plasmid | 3 | 0 | plasmid lost |
| 3 | *MprF/FmtC** | 1 | 936171 | S455F |
| 4 | *pycA* | 1 | 770546 | D981E |
| 5 | 50.1kb sequence | 2 | 99381 | deleted: large region of plasmid |
| 5 | *aspS* | 1 | 1448994 | G362E |
| 5 | hypothetical protein | 1 | 1664819 | P166Q |
| 5 | hypothetical protein | 1 | 49743 | frameshift |
| 5 | *YycG/Walk/VicK** | 1 | 1375701 | V356G |
| 6 | 1.7kb sequence | 2 | 56825 | deleted: *licC_4*, IS1380 family transposase IS1678 |
| 6 | 2.4kb sequence | 2 | 86579 | deleted: IS3 family transposase ISPa31, *repN_1*, 2 hypothetical proteins |
| 6 | *citG_2* | 2 | 130597 | H233R |
| 6 | *dgaR_5* | 1 | 2670675 | V395G |
| 6 | hypothetical protein | 2 | 74313 | altered stop |
| 6 | hypothetical protein | 2 | 104206, 104530 | A18V, G126V |
| 6 | hypothetical protein | 1 | 767470 | hypothetical protein deleted |
| 6 | IS256 family transposase IS256 | 2 | 81564 | F25V |
| 6 | IS3 family transposase IS1485 | 2 | 81564 | R259K |
| 7 | *cls** | 1 | 951390, 951820, 952557 | F75V, R218Q, E464Q |
| 7 | hypothetical protein | 1 | 821682 | V227A |
| 7 | hypothetical protein | 1 | 855641 | D197G |
| 7 | hypothetical protein | 1 | 974050 | frameshift |
| 7 | hypothetical protein | 1 | 2459968 | A103E |
| 7 | *ohrB* | 1 | 2371395, 2371612 | A21E, L93F |
| 7 | *recQ_1* | 1 | 776003 | I289R |
| 7 | *scpA* | 1 | 919169 | S221G |
| 7 | *zosA* | 1 | 755705 | L245Q |
| 8 | 50.1kb sequence | 2 | 99381 | reversion to plasmid variant with 50.1kb region |
| 8 | 6-phosphogluconate dehydrogenase, NAD(+)-dependent, decarboxylating | 1 | 490941 | E220K |
| 8 | *citG_1* | 1 | 2199727 | frameshift |
| 8 | *ctpE_1* | 1 | 109404 | frameshift |
| 8 | *exuR_1* | 1 | 855008 | frameshift |
| 8 | *rpoC* | 1 | 1807953 | N675K |
| 9 | *exuR_1* | 1 | 855009 | altered stop |
| 9 | *lysA* | 1 | 2335824 | L253M |

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|---|---|---|---|---|
| 10 | *rpsJ* | 1 | 1948943 | Y58S |
| 10 | *wecA* | 1 | 18743 | frameshift |
| 11 | *yadH* | 1 | 1703267 | E94D |
| 12 | 42.5kb sequence | 1 | 421827 | 42.5kb deletion in chromosomal genome |
| 12 | 2kb sequence | 1 | 566851 | deleted: *cfa*, hypothetical protein |
| 12 | ISL3 family transposase ISEfa11 | 1 | 2825781 | frameshift |
| 12 | *ygaZ_1* | 1 | 586474 | V136G |
| 13 | *agrA* | 1 | 2311784 | S32N |
| 13 | *asd* | 1 | 2339953, 2340059 | K176E, T211N |
| 13 | *bceA_1* | 1 | 2292087 | G221V |
| 13 | *bglF_1* | 1 | 2219261, 2219983 | I283T, S524P |
| 13 | *bglH_2* | 1 | 2221306, 2221563 | W334L, K420E |
| 13 | *cysL* | 1 | 2428212, 2428277 | L104P, T126A |
| 13 | *galM* | 1 | 2351626 | H76R |
| 13 | *garK* | 1 | 2508631 | A215D |
| 13 | *glpE* | 1 | 2236403 | L20I |
| 13 | *gpmA_2* | 1 | 753085 | T14P |
| 13 | hypothetical protein | 1 | 794424 | N137I |
| 13 | hypothetical protein | 1 | 954110 | D18E |
| 13 | hypothetical protein | 1 | 1620289 | 12aa deletion |
| 13 | hypothetical protein | 1 | 2288116 | V81I |
| 13 | hypothetical protein | 1 | 2304272, 2305000 | E333G, T576P |
| 13 | hypothetical protein | 1 | 2348001 | frameshift |
| 13 | hypothetical protein | 1 | 2361366 | N228I |
| 13 | hypothetical protein | 1 | 2426032 | V99I |
| 13 | hypothetical protein | 1 | 2435462, 2435480 | A225T, E231K |
| 13 | hypothetical protein | 1 | 2442088, 2443170, 2443264, 2443492, 2443522, 2443621, 2443654, 2443655, 2443682, 2443683, 2443685, 2443696, 2443698, 2443746, 2443751, 2443762 | frameshift |
| 13 | hypothetical protein | 1 | 2443920, 2443977, 2443979, 2444109 | K26E, D69V, I70V, I89V |
| 13 | hypothetical protein | 1 | 2444486 | I58M |
| 13 | hypothetical protein | 1 | 2444598, 2444850, 2444921 | N12D, Q96K, MS119M |
| 13 | hypothetical protein | 1 | 2445046, 2445057, 2445081, 2445082, 2445129, 2445158, 2445190, 2445222, 2445249, 2445270 | R27K, S31T, V39I, V39E, T55S, D64E, T75M, V86I, V95I, T102A |
| 13 | hypothetical protein | 1 | 2445481, 2445483, 2445513, 2445523, 2445531, 2445535, 2445543, 2445544, 2446053 | A12V, I13F, F23L, Y26C, K29E, T30M, P33S, P33L, K203Q |
| 13 | hypothetical protein | 1 | 2446957, 2447175, 2447183, 2447316, 2448041, 2448184, 2448271 | altered stop |
| 13 | hypothetical protein | 1 | 2448279, 2448313, 2448315, 2448905, 2449409, 2449509 | frameshift |
| 13 | hypothetical protein | 1 | 2450022, 2450463, 2450755, 2451093, 2451159, 2451252, 2451373, 2451463, 2451513, 2451622, 2451831, 2452056, 2452497, 2452499, 2452571 | S167G, S314T, M411T, P524S, T546A, R577S, P617L, V647A, N664D, V700A, E770K, S845P, M992L, M992I, N1016K |
| 13 | hypothetical protein | 1 | 2456963, 2457420 | frameshift |
| 13 | hypothetical protein | 1 | 2513899 | L84F |

| | | | | |
|---|---|---|---|---|
| 13 | hypothetical protein | 1 | 2524098 | H322R |
| 13 | hypothetical protein | 1 | 2541370 | H151Q |
| 13 | hypothetical protein | 2 | 167232, 167450, 167456, 167675, 167757, 167884, 167987 | A76S, V110A, E152D, E180K, Q253K, S255P, D327E |
| 13 | ISL3 family transposase ISEfa5 | 1 | 904571 | K429N |
| 13 | *lacS* | 1 | 2351881, 2352532 | A264V, D481V |
| 13 | *lpdC* | 1 | 2280438 | T57A |
| 13 | *malH* | 1 | 988842 | R79C |
| 13 | *malP* | 1 | 2262870 | K731E |
| 13 | *metB* | 1 | 2330242 | frameshift |
| 13 | *metN* | 1 | 2495987 | D32G |
| 13 | *metQ_1* | 1 | 2432982, 2433481 | F8L, D175N |
| 13 | *mutS2_1* | 1 | 2233684 | frameshift |
| 13 | *npr_1* | 1 | 2226194 | E395K |
| 13 | *ogt* | 1 | 2424863 | R36Q |
| 13 | *pckA* | 1 | 2364383 | V206A |
| 13 | *pdhB* | 1 | 784095 | T101A |
| 13 | *pgaC* | 1 | 2241447 | Y78D |
| 13 | *pgmB* | 1 | 2262578 | T66S |
| 13 | *pheT* | 1 | 725125 | G372E |
| 13 | plasmid | 9 | 0 | plasmid lost |
| 13 | *purK* | 1 | 810969 | V82I |
| 13 | putative ABC transporter ATP-binding protein | 1 | 2434196 | D65N |
| 13 | *rhaS_3* | 1 | 2354325, 2354382 | K277E, T296A |
| 13 | *ribZ_2* | 1 | 2367511 | I176F |
| 13 | *rodA* | 1 | 2429178, 2429808 | L81F, I291V |
| 13 | *sufS_1* | 1 | 2436202, 2436380, 2436607, 2436692, 2436773, 2436952 | Y44H, T103S, F179I, M207R, V234A, K294E |
| 13 | *tdh_2* | 1 | 2545115 | altered stop |
| 13 | *topB_2* | 1 | 2422422, 2422608, 2422631, 2423219 | R347Q, G409E, A417T, L613M |
| 13 | *yfdH* | 1 | 2424172, 2424178 | I112V, C114S |
| 13 | *yjcD* | 1 | 2317959 | S528A |
| 13 | *yknY* | 1 | 2459411, 2459412 | altered stop |

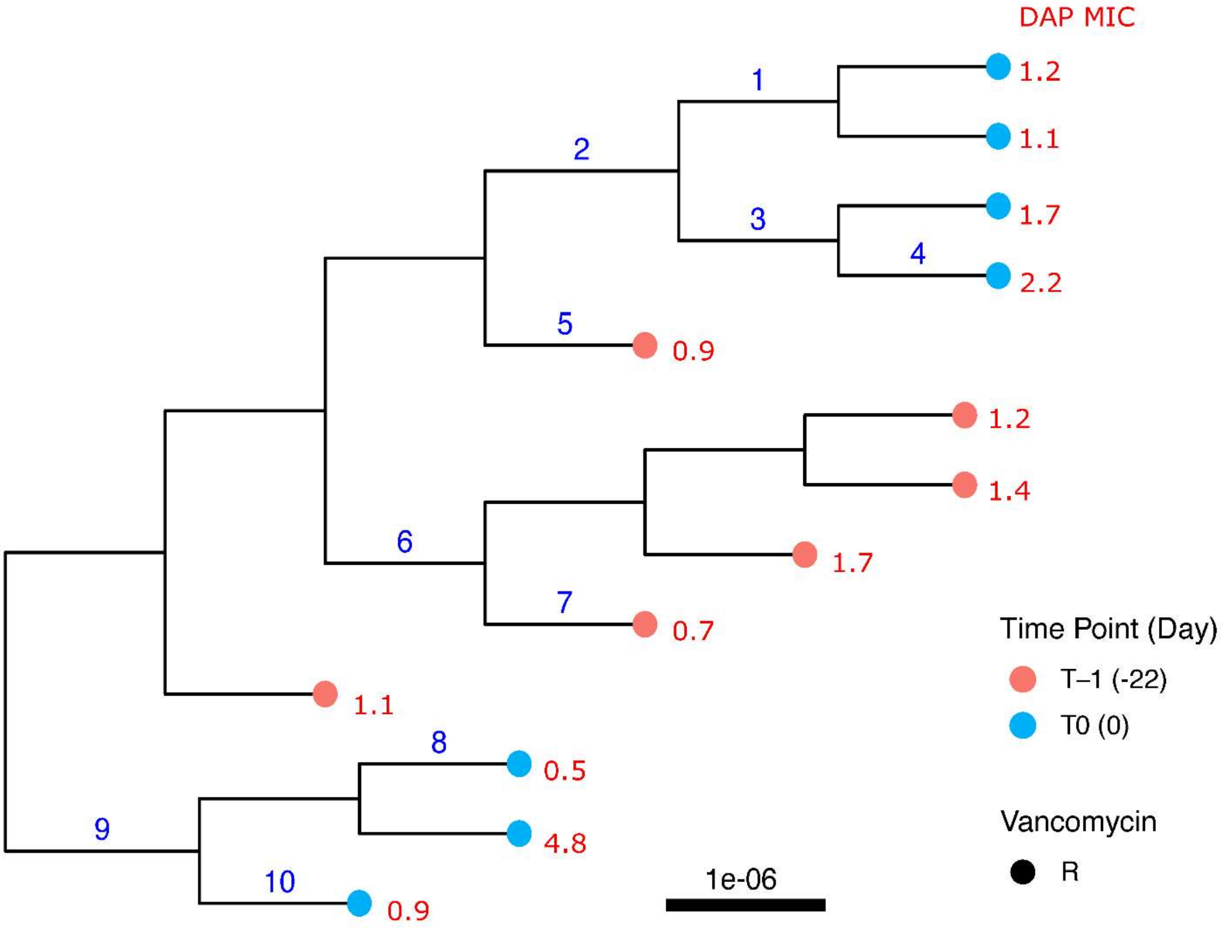

**Figure C:** Phylogeny for *E. faecium* strains isolated from Patient 87. Branch labels (blue) correspond to mutations listed in Table C. The index sample is labelled T0 and timepoints are labelled in order from that timepoint. The number of days between the index sample and the other timepoints are in brackets after the timepoint number.

**Table C: Nonsynonymous mutations within Patient 87.** Branch numbers correspond to Figure C. Asterisks indicates loci known to be associated with variation in daptomycin susceptibility [1].

| Branch | Locus | Contig | Position | Mutation |
|---|---|---|---|---|
| 1 | *dgaR_2* | 1 | 774236,<br>774239 | frameshift |
| 1 | IS1182 family transposase ISBpu1 | 1 | 1853455 | T43K |
| 2 | *cls** | 1 | 1043463 | R211Q |
| 2 | *rpoB* | 1 | 2797760 | G482D |
| 3 | *dgaR_2* | 1 | 774309 | L268Q |
| 3 | hypothetical protein | 2 | 38574 | I15M |
| 4 | 2.1kb sequence | 5 | 26621 | deleted: 3 hypothetical proteins |
| 5 | 3.2kb sequence | 2 | 10397 | deleted: 4 hypothetical proteins |
| 5 | 4.8kb sequence | 2 | 100691 | deleted: *bin3_1*, 4 hypothetical proteins |
| 5 | hypothetical protein | 5 | 33186 | L617S |
| 5 | hypothetical protein | 5 | 53745 | W10L |
| 5 | *topB_5* | 5 | 36699 | Q488K |
| 6 | 1.6kb sequence | 5 | 8212 | deletions: 5 hypothetical proteins |
| 6 | 5kb sequence | 6 | 2413 | deleted: *erm*, IS1182 family transposase IS1182, *COQ5_3, aadK*, 3 hypothetical proteins |
| 6 | hypothetical protein | 1 | 284855,<br>284911 | frameshift |
| 6 | hypothetical protein | 6 | 18062 | I78N |
| 6 | hypothetical protein | 6 | 24963 | frameshift |
| 6 | IS30 family transposase IS1252 | 6 | 20420 | D273E |
| 6 | plasmid | 2 | 0 | major structural changes in plasmid |
| 7 | *murI* | 1 | 1276709 | A258D |
| 8 | hypothetical protein | 6 | 22634 | deleted: hypothetical protein |
| 9 | *cls** | 1 | 1043295 | R267H |
| 9 | *rpoB* | 1 | 2797749 | H486Y |
| 10 | *cls** | 1 | 1042998 | P366L |

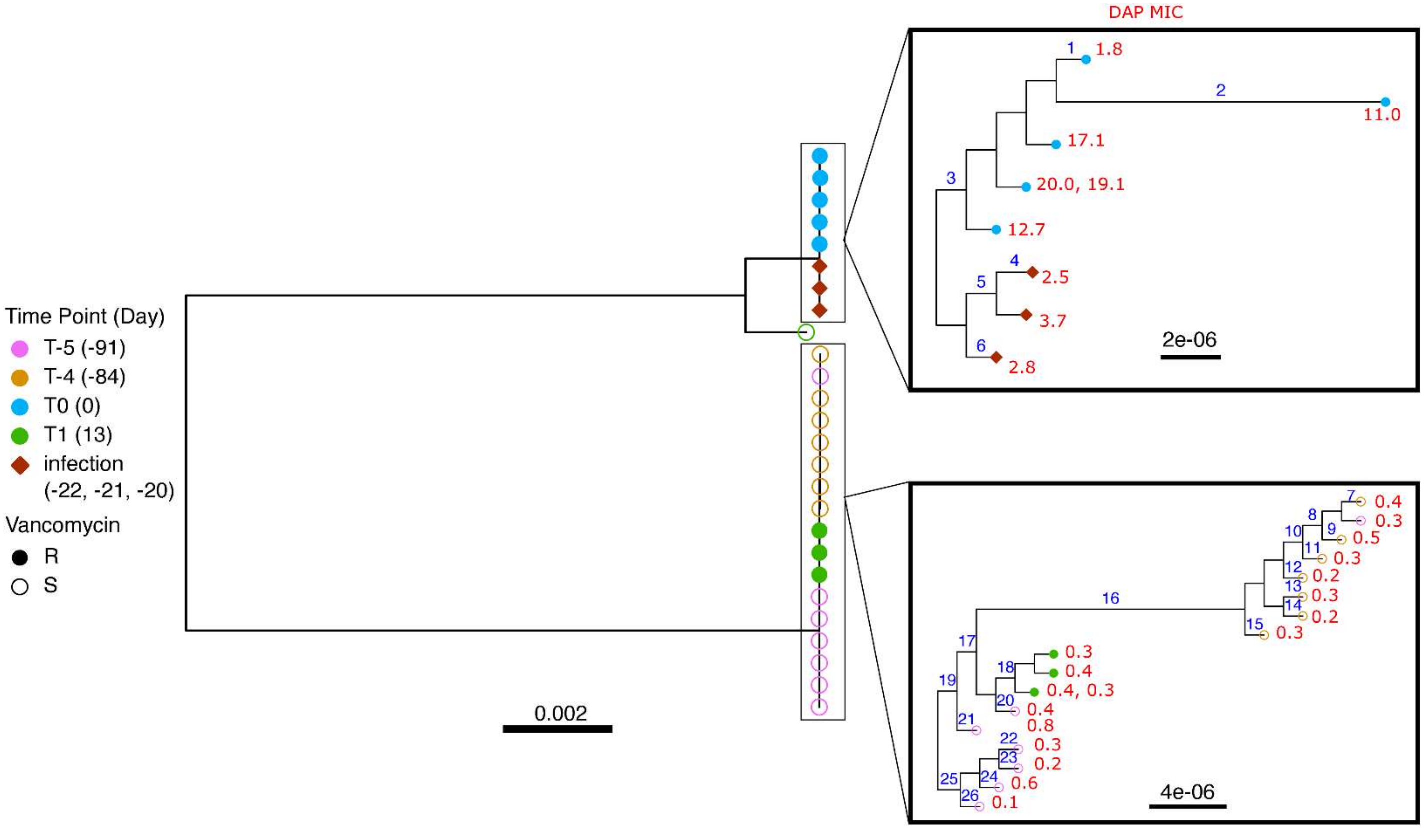

**Figure D:** Phylogeny for *E. faecium* strains isolated from Patient 150. Rectangle shows detailed structure of indicated group. Branch labels (blue) correspond to mutations listed in Table D. For tips representing two isolates with identical core genomes, the daptomycin MICs for both isolates are listed (red). The index sample is labelled T0 and timepoints are labelled in order from that timepoint. The number of days between the index sample and the other timepoints are in brackets after the timepoint number.

**Table D: Nonsynonymous mutations within Patient 150.** Branch numbers correspond to Figure D. Only variants for the upper box of Figure D are shown. The portion of the tree in the lower box included several apparent large recombinant regions and indels, which hindered assigning mutations to branches. Additionally, several large deletions were observed that are not listed in this table. Asterisks indicates loci known to be associated with variation in daptomycin susceptibility [1].

| Branch | Locus | Contig | Position | Mutation |
|---|---|---|---|---|
| 1 | *murB* | 1 | 1725616 | P125S |
| 2 | 7kb sequence | 1 | 2549693 | deleted: *ydcF, yhgF, pphA, tcyP*, SprT-like protein, 3 hypothetical proteins |
| 3 | 7kb sequence | 1 | 498760 | inserted: 2 hypothetical proteins |
| 3 | 41.5kb sequence | 1 | 501602 | inserted: *clpP_2, lexA_2, xerC_1*, 69 hypothetical proteins |
| 3 | *cls** | 1 | 2030677 | K61E |
| 3 | hypothetical protein | 1 | 2519669 | A32P |
| 3 | hypothetical protein | 1 | 2529478 | altered stop |
| 3 | 35.8kb sequence | 1 | 2717996 | inserted: *xerC_9*, 57 hypothetical proteins |
| 4 | *ntpJ_2* | 1 | 433972 | G455C |
| 4 | *thrS* | 1 | 1962103 | R420H |
| 5 | *atpA* | 1 | 150355 | R279G |
| 5 | *gmuE_2* | 1 | 1753158, 1753161 | P259S, P260S |
| 6 | IMPDH | 1 | 351508 | V238I |
| 6 | IS30 family transposase IS1062 | 1 | 1333170 | frameshift |
| 7 | hypothetical protein | 1 | 2573572 | S36L |
| 8 | hypothetical protein | 2 | 113524 | S68L |
| 8 | IS6 family transposase IS1216E | 2 | 73619 | altered stop |
| 8 | plasmid | 2 | 0 | plasmid loss |
| 8 | plasmid | 5 | 0 | plasmid loss with a few genes retained |
| 8 | plasmid | 3 | 0 | plasmid loss with a few genes retained |
| 9 | hypothetical protein | 1 | 553389 | T225A |
| 9 | IS3 family transposase IS1485 | 1 | 553833 | F91S |
| 9 | *lipL* | 1 | 723312 | S93F |
| 9 | plasmid | 4 | 0 | plasmid loss with a few genes retained |
| 10 | hypothetical protein | 3 | 25676 | V145G |
| 10 | hypothetical protein | 3 | 34483 | frameshift |
| 11 | hypothetical protein | 3 | 31374 | frameshift |
| 12 | 14.4kb sequence | 3 | 22730 | deleted: 13 hypothetical proteins |
| 13 | 35.8kb sequence | 1 | 1024245 | deleted: *xerC_4*, 63 hypothetical proteins |
| 13 | *hdfR_1* | 1 | 895114 | R70K |
| 13 | hypothetical protein | 1 | 1843110 | V208I |
| 13 | hypothetical protein | 3 | 30581 | frameshift |
| 14 | hypothetical protein | 3 | 30349 | G454R |
| 14 | hypothetical protein | 1 | 544446 | frameshift |
| 15 | hypothetical protein | 3 | 31374 | frameshift |
| 15 | *rpoB* | 1 | 2563777 | I860V |
| 16 | 17.1kb sequence | 1 | 1238719 | deleted: *pepT*, Putative lipid kinase, *mdtD, slyA, clpB, eis_1, lepA, cspLA_2*, 12 hypothetical proteins |
| 16 | hypothetical protein | 3 | 25676 | G145V |
| 16 | hypothetical protein | 3 | 34483 | frameshift |

| | | | | |
|---|---|---|---|---|
| 16 | hypothetical protein | 2 | 113524 | L68S |
| 16 | IS6 family transposase IS1216E | 2 | 73619 | altered stop |
| 16 | *licC_4* | 1 | 2397251 | N298S |
| 16 | plasmid | 5 | 0 | plasmid acquired |
| 16 | plasmid | 3 | 0 | plasmid acquired |
| 16 | *rodA* | 1 | 491860 | M382V |
| 17 | hypothetical protein | 1 | 219232 | S107L |
| 18 | *vanA* plasmid | | | gain of *vanA*-containing plasmid, same plasmid that appears in upper part of tree |
| 18 | *glcR* | 1 | 1170490 | L4F |
| 18 | hypothetical protein | 1 | 544446 | frameshift |
| 18 | *lacE* | 1 | 547652, 547828 | T134M, F193L |
| 18 | *lacF_1* | 1 | 548265, 548287, 548290 | T86A, V87I, H94P |
| 18 | plasmid | 2 | 0 | variant/recombinant plasmid |
| 19 | *dprA* | 1 | 1635002 | altered stop |
| 19 | hypothetical protein | 1 | 859495 | altered stop |
| 19 | hypothetical protein | 1 | 2519750 | S101I |
| 20 | hypothetical protein | 3 | 30902 | frameshift |
| 20 | hypothetical protein | 3 | 25676 | G145V |
| 20 | hypothetical protein | 3 | 34483 | frameshift |
| 20 | hypothetical protein | 2 | 113524 | L68S |
| 20 | IS6 family transposase IS1216E | 2 | 73619 | altered stop |
| 20 | *pbpX_2* | 1 | 1879598 | T537A |
| 20 | plasmid | 5 | 0 | plasmid acquired |
| 20 | plasmid | 3 | 0 | plasmid acquired |
| 21 | plasmid | 2 | 0 | plasmid loss with a few genes retained |
| 21 | *ymdB* | 1 | 125726 | frameshift |
| 22 | hypothetical protein | 1 | 544446 | frameshift |
| 23 | hypothetical protein | 1 | 1810322 | frameshift |
| 24 | hypothetical protein | 1 | 1810322 | frameshift |
| 25 | hypothetical protein | 1 | 133787 | V83I |
| 25 | hypothetical protein | 1 | 1279975 | T15I |
| 25 | *pbpX_2* | 1 | 1880201 | G336R |
| 25 | plasmid | 5 | 0 | plasmid acquired |
| 25 | plasmid | 3 | 0 | plasmid acquired |
| 26 | *sasA_3* | 1 | 1735414 | L310S |

## References

1. Diaz L, Tran TT, Munita JM, Miller WR, Rincon S, Carvajal LP, et al. Whole-genome analyses of *Enterococcus faecium* isolates with diverse daptomycin MICs. Antimicrob Agents Chemother. 2014;58: 4527–4534. doi:10.1128/AAC.02686-14