**Additional file 1: Table S1 Details of transposon records available in The Transposon Registry**

| Transposon name | Origin | Type | Size (kb) | Accession number | Accessory Functions | References |
| --- | --- | --- | --- | --- | --- | --- |
| Tn*1* | *Escherichia coli* | Unit transposon | 3.6 | L10085.1 | AMR  | (1) |
| Tn*2* | *Escherichia coli* | Unit transposon | 5 | HM749967.1 | AMR  | (2) |
| Tn*3* | *Escherichia coli* | Unit transposon | 4.96 | V00613.1 | AMR  | (3) |
| Tn*4* | *Escherichia coli* | Unit transposon | - | HM749966.1, HQ201416.1 | AMR, Heavy metal resistance | (4) |
| Tn*5* | *Escherichia coli*  | Composite transposon | 5.8 | U00004.1 | AMR  | (5) |
| Tn*6* | *Escherichia coli* | Composite transposon | 5 | - | AMR | (6) |
| Tn*7* | *Escherichia coli* | Unit transposon | 14 | KX159450.1 | AMR  | (7) |
| Tn*9* | *Escherichia coli* | Composite transposon | 2.6 | V00622.1 | AMR | (8) |
| Tn*10* | *Shigella flexneri* | Composite transposon | 9.3 | AF162223.1 | AMR  | (9) |
| Tn*21* | *Escherichia coli* | Unit transposon | 19.7 | AF071413.3 | AMR, Heavy metal resistance | (10) |
| Tn*45* | *Corynebacterium glutamicum* | Unit transposon | 2.4 | U85507.1 | AMR | (11) |
| Tn*55* | *-* | Unit transposon | - | - | AMR | (12) |
| Tn*71* | *Escherichia coli* | Unit transposon |   | AP002527.1 | AMR | (13) |
| Tn*72* | *-* | Unit transposon | - | - | AMR | (13) |
| Tn*76* | *Klebsiella aerogenes* | Unit transposon |   | - | AMR | (14) |
| Tn*125* | *Acinetobacter baumannii* | Composite transposon | 10 | JN872328.1 | AMR | (15) |
| Tn*163* | *Rhizobium leguminosarum*  | Unit transposon | 4.6 | L14931.1 | - | (16) |
| Tn*501* | *Pseudomonas aeruginosa* | Unit transposon | 8.3 | Z00027.1 | Heavy metal resistance | (17) |
| Tn*502* | *Pseudomonas aeruginosa* | Unit transposon | 9.6 | EU306743.1 | Heavy metal resistance | (18) |
| Tn*510* | *Bordetella bronchiseptica* | Unit transposon | 13.3 | DQ471307.1 | AMR, Heavy metal resistance | (19) |
| Tn*511* | *Proteus mirabilis* | Unit transposon | 19 | EU287476.1 | AMR, Heavy metal resistance | (19) |
| Tn*512* | *Pseudomonas sp* | Unit transposon | 8.4 | EU306744.1 | Heavy metal resistance | (20) |
| Tn*536* | *Shigella flexneri*  | Not specified | 16 |  - | AMR, Heavy metal resistance | (21) |
| Tn*551* | *Staphylococcus aureus* | Unit transposon | 5.2 | Y13600.1 | AMR | (22) |
| Tn*552* | *Staphylococcus aureus* | Unit transposon | 6.5 | X52734.1 | AMR | (23) |
| Tn*554* | *Staphylococcus aureus* | Unit transposon | 6.7 | X03216.1 | AMR | (24) |
| Tn*558* | *Staphylococcus lentus* | Unit transposon | 6.6 | AJ715531.1 | AMR | (25) |
| Tn*559* | *Staphylococcus aureus* | Unit transposon | 4.2 | FN677369.2 | AMR | (26) |
| Tn*601* | *Escherichia coli* | Composite transposon | - | - | AMR | (27) |
| Tn*602* | *Escherichia coli* | Composite transposon | 3 | AH000951.1 | AMR | (28) |
| Tn*610* | *Mycobacterium smegmatis* | Composite transposon | 3.97 | X53635.1 | AMR | (29) |
| Tn*611* | *Mycobacterium smegmatis* | Composite transposon | - | - | AMR | (30) |
| Tn*654* | *Escherichia coli* | Unit transposon | - | - | AMR | (31) |
| Tn*679* | *Escherichia coli*  | Composite transposon | - | - | AMR | (32) |
| Tn*701* | *Morganella morganii* | Unit transposon | 8.5 | - | AMR | (33) |
| Tn*732* | *Klebsiella sp.* | Not specified | - | - | AMR | (34) |
| Tn*733* | *-* | Not specified | - | - | AMR | (35) |
| Tn*734* | *-* | Not specified | - | - | AMR | (35) |
| Tn*735* | *Escherichia coli* | Unit transposon | 15 | - | AMR, Heavy metal resistance | (36) |
| Tn*800* | *Escherichia coli* | Not specified | - | - | AMR | (36) |
| Tn*801* | *Pseudomonas aeruginosa* | Unit transposon | 4.95 | AF080442.1 | AMR | (37) |
| Tn*802* | *Escherichia coli* | Unit transposon | - | - | AMR | (38) |
| Tn*804* | *Escherichia coli* | Not specified | - | - | AMR | (39) |
| Tn*813* | *-* | Unit transposon | - | - | AMR, Heavy metal resistance | (40) |
| Tn*841* | *Klebsiella oxytoca* | Unit transposon | 7 | M88143.1 | AMR | (41) |
| Tn*901* | *Salmonella panama* | Unit transposon | - | - | AMR | (42) |
| Tn*902* | *Escherichia coli*  | Unit transposon | - | - | AMR | (43) |
| Tn*903* | *Escherichia coli* | Composite transposon | 3 | V00359.1 | AMR | (44) |
| Tn*904* | *Pseudomonas sp.* | Not specified | 5.2 |   | AMR | (45) |
| Tn*916* | *Enterococcus faecalis* | Conjugative transposon | 18 | KM516885.1 | AMR | (46) |
| Tn*917* | *Enterococcus faecalis*  | Unit transposon | 5.2 | M11180.2 | AMR | (47) |
| Tn*918* | *Enterococcus faecalis* | Conjugative transposon | 16.8 | - | AMR | (48) |
| Tn*919* | *Streptococcus sanguis* | Conjugative transposon | - | - | AMR | (49) |
| Tn*924* | *Enterococcus faecalis* | Composite transposon | 27 | - | AMR | (50) |
| Tn*925* | *Enterococcus faecalis* | Conjugative transposon | 18 | AY855841.2 | AMR | (51) |
| Tn*950* | *Enterococcus faecium* | Conjugative transposon | 47 | - | AMR | (52) |
| Tn*951* | *Yersinia enterocolitica* | Unit transposon | 16.6 | - | Metabolism | (53) |
| Tn*981* | *Escherichia coli*  | Composite transposon | 2.3 | - | AMR | (54) |
| Tn*1000* | *Escherichia coli* | Unit transposon | 5.9 | X60200.1 | - | (55) |
| Tn*1013* | *Pseudomonas aeruginosa* | Unit transposon | 8.2 | AM261760.1 | Efflux function | (56) |
| Tn*1021* | *Escherichia coli* | Not specified | 6 | - | AMR | (57) |
| Tn*1022* | *Escherichia coli* | Not specified | 10 | - | AMR | (57) |
| Tn*1116* | *Streptococcus pyogenes* | Conjugative transposon | 23 | AM411377.1 | AMR | (58) |
| Tn*1213* | *Pseudomonas aeruginosa* | Unit transposon | 4.2 | AY779042.1 | AMR | (59) |
| Tn*1207.1* | *Streptococcus pneumoniae* | Composite transposon | 7.2 | AF227520.1 | AMR, Efflux function | (60) |
| Tn*1331* | *Klebsiella pneumoniae* | Unit transposon | 8 | NC\_003486.1 | AMR | (61) |
| Tn*1332* | *Pseudomonas putida* | Unit transposon | 11 | DQ174113.1 | AMR | (62) |
| Tn*1401* | *Salmonella typhimurium* | Unit transposon | 15.9 | - | AMR, Heavy metal resistance | (63) |
| Tn*1402* | *-* | Unit transposon | - | - | AMR, Heavy metal resistance | (63) |
| Tn*1403* | *Pseudomonas aeruginosa* | Unit transposon | 19.6 | AF313472 | AMR | (64) |
| Tn*1404* | *Pseudomonas sp.* | Unit transposon | 19 | AH008062.3 | AMR | (65) |
| Tn*1405* | *Pseudomonas aeruginosa*  | Not specified | 8 | - | AMR | (66) |
| Tn*1523* | *Escherichia coli* | Not specified | 10.8 | - | AMR | (67) |
| Tn*1525* | *Salmonella panama* | Composite transposon | 4.44 | - | AMR | (68) |
| Tn*1527* | *Vibrio cholerae* | Not specified | 14 | - | AMR | (69) |
| Tn*1528* | *Providencia stuartii* | Composite transposon | 5.2 | - | AMR | (70) |
| Tn*1545* | *Streptococcus pneumoniae* | Conjugative transposon | 25.3 | X61025.1 | AMR | (71) |
| Tn*1546* | *Enterococcus faecium* | Unit transposon | 10.8 | M97297.1 | AMR | (72) |
| Tn*1547* | *Enterococcus faecalis* | Composite transposon | 64 | - | AMR | (73) |
| Tn*1548* | *Klebsiella pneumoniae* | Composite transposon | 16.6 | - | AMR | (74) |
| Tn*1549* | *Enterococcus faecalis* | Conjugative transposon | 33.8 | AF192329.1 | AMR | (75) |
| Tn*1681* | *Escherichia coli* | Composite transposon | 25 | L36547.1 | Virulence determinants | (76) |
| Tn*1696* | *Pseudomonas aeruginosa* | Unit transposon | 13.6 | U12338.3 | AMR, Heavy metal resistance | (77) |
| Tn*1699* | *Klebsiella pneumoniae* | Not specified | 9.3 | - | AMR | (78) |
| Tn*1700* | *Serratia marcescens* | Not specified | 12 | - | AMR | (78) |
| Tn*1701* | *Salmonella typhimurium* | Not specified | - | - | AMR | (79) |
| Tn*1720* | *Pseudomonas sp.* | Unit transposon | 9.3 | AH008063.2 | AMR | (65) |
| Tn*1721* | *Escherichia coli* | Unit transposon | 11.1 | X61367.1 | AMR | (80) |
| Tn*1722* | *Escherichia coli* | Unit transposon | 5.5 | - | - | (80) |
| Tn*1723* | *Escherichia coli* | Unit transposon | 3.9 | - | AMR | (81) |
| Tn*1725* | *Escherichia coli* | Unit transposon | 8.3 | - | AMR | (82) |
| Tn*1732* | *Halomonas elongata* | Unit transposon | - | - | AMR | (83) |
| Tn*1755* | *Escherichia coli* | Unit transposon | - | - | AMR | (84) |
| Tn*1756* | *Escherichia coli* | Unit transposon | - | - | AMR | (85) |
| Tn*1771* | *Escherichia coli* | Not specified | - | - | AMR | (86) |
| Tn*1792* | *Streptomyces lividans* | Composite transposon | 2.8 | AJ006518.1 | AMR | (87) |
| Tn*1806* | *Streptococcus pneumoniae* | Conjugative transposon | 52.4 | CP002121.1 | AMR | (88) |
| Tn*1822* | *-* | Unit transposon | - | - | AMR | (89) |
| Tn*1824* | *-* | Unit transposon | - | - | AMR | (89) |
| Tn*1825* | *Escherichia coli* | Unit transposon | 13.2 | - | AMR | (90) |
| Tn*1826* | *-* | Unit transposon | - | - | AMR | (91) |
| Tn*1831* | *Agrobacterium tumefaciens* | Not specified | - | - | AMR, Heavy metal resistance | (92) |
| Tn*1935* | *Salmonella wien* | Unit transposon | 23.5 | - | AMR, Heavy metal resistance | (93) |
| Tn*1999* | *Klebsiella pneumoniae* | Composite transposon | 4.9 | AY236073.2 | AMR | (94) |
| Tn*2000* | *Escherichia coli* | Composite transposon | 12 | AF205943.1 | AMR, Antiseptic resistance | (95) |
| Tn*2001* | *Pseudomonas aeruginosa* | Not specified | - | - | AMR | (96) |
| Tn*2003* | *Enterobacter cloacae* | Composite transposon | 9.5 | AY532647.1 | AMR | (97) |
| Tn*2006* | *Acinetobacter baumannii* | Composite transposon | 4.8 | EF127491.1 | AMR | (98) |
| Tn*2007* | *Acinetobacter baumannii* | Composite transposon | 2.5 | EF059914.1 | AMR | (98) |
| Tn*2008* | *Acinetobacter baumannii* | Unit transposon | 4 | GQ861438.1 | AMR | (99) |
| Tn*2009* | *Streptococcus pneumoniae* | Conjugative transposon | 23 | AF376746.2 | AMR | (100) |
| Tn*2010* | *Streptococcus pneumoniae* | Conjugative transposon | 26.4 | AB426620.1 | AMR | (101) |
| Tn*2011* | *Escherichia coli* | Not specified | - | - | AMR, Heavy metal resistance | (102) |
| Tn*2012* | *Escherichia coli*  | Unit transposon | 2.7 | EU523120.1 | AMR | (103) |
| Tn*2016* | *Klebsiella pneumoniae*  | Unit transposon | 4.4 | JQ809466.1 | AMR | (104) |
| Tn*2017* | *Streptococcus pneumoniae* | Conjugative transposon | 28.5 | FJ208941.1 | AMR | (105) |
| Tn*2020* | *Brucella abortus* | Composite transposon | 4.1 | AF118548.1 | - | (106) |
| Tn*2101* | *Enterobacter cloacae* | Not specified | - | - | AMR, Heavy metal resistance | (107) |
| Tn*2301* | *Escherichia coli* | Not specified | . | - | AMR | (108) |
| Tn*2350* | *Escherichia coli* | Composite transposon | 10.4 | - | AMR | (109) |
| Tn*2353* | *Escherichia coli* | Not specified | 13 | - | AMR, Heavy metal resistance | (110) |
| Tn*2354* | *Escherichia coli* | Not specified | 7.8 | - | - | (111) |
| Tn*2401* | *Pseudomonas aeruginosa* | Composite transposon | 7.1 | - | AMR | (112) |
| Tn*2410* | *Salmonella typhimurium* | Unit transposon | 18.5 | - | AMR, Heavy metal resistance | (113) |
| Tn*2411* | *Salmonella typhimurium* | Unit transposon | 18 | - | AMR, Heavy metal resistance | (113) |
| Tn*2424* | *Escherichia coli* | Unit transposon | 25 | AF047479.2 | AMR, Heavy metal resistance | (114) |
| Tn*2425* | *Escherichia coli* | Unit transposon | - | - | AMR, Heavy metal resistance | (115) |
| Tn*2426* | *Shigella sonnei* | Unit transposon | 3.5 | M86913.1 | AMR, Heavy metal resistance | (116) |
| Tn*2440* | *Escherichia coli* | Composite transposon | 4 | - | AMR | (117) |
| Tn*2501* | *Yersinia sp.* | Unit transposon | 6.3 | M15197.1 | - | (118) |
| Tn*2502* | *Yersinia enterocolitica* | Unit transposon | 4.6 | U58366.1 | Heavy metal resistance | (119) |
| Tn*2503* | *Yersinia pestis* | Unit transposon | 6.8 | CP002179.1 | Heavy metal resistance | (120) |
| Tn*2505* | *Escherichia coli* | Unit transposon | 8.2 | - | - | (121) |
| Tn*2506* | *Escherichia coli* | Unit transposon | 7.3 | - | AMR | (121) |
| Tn*2507* | *Yersinia enterocolitica* | Unit transposon | 9.1 | - | AMR | (122) |
| Tn*2515* | *Escherichia coli* | Unit transposon | - | - | AMR | (121) |
| Tn*2516* | *Escherichia coli* | Unit transposon | - |   | AMR | (121) |
| Tn*2521* | *Pseudomonas aeruginosa* | Not specified | 7 | AF313471.1 | AMR | (66) |
| Tn*2523* | *Pseudomonas aeruginosa* | Not specified | - | - | AMR | (123) |
| Tn*2601* | *Escherichia coli* | Unit transposon | 4.7 | - | AMR | (124) |
| Tn*2602* | *Escherichia coli* | Unit transposon | 4.7 | - | AMR | (124) |
| Tn*2603* | *Escherichia coli* | Unit transposon | 20 | - | AMR, Heavy metal resistance | (125) |
| Tn*2607* | *Escherichia coli* | Unit transposon | 24 |   | AMR | (126) |
| Tn*2608* | *Klebsiella pneumoniae* | Unit transposon | 13.5 |   | AMR, Heavy metal resistance | (126) |
| Tn*2610* | *Escherichia coli* | Unit transposon | 23.9 | AB207867.1 | AMR | (127) |
| Tn*2613* | *Proteus mirabilis* | Unit transposon | 7.2 | - | Heavy metal resistance | (126) |
| Tn*2653* | *Escherichia coli* | Composite transposon | 5.9 | - | AMR | (128) |
| Tn*2657* | *Escherichia coli* | Unit transposon | - | - | AMR | (129) |
| Tn*2660* | *Escherichia coli* | Unit transposon | 4.8 | - | AMR | (130) |
| Tn*2670* | *Shigella flexneri*  | Composite transposon and Unit transposon | 19.6 | AP000342.1 | AMR, Heavy metal resistance | (131) |
| Tn*2671* | *Shigella flexneri* | Composite transposon | 23 | AP000342.1 | AMR, Heavy metal resistance | (132) |
| Tn*2672* | *Escherichia coli* | Composite transposon and Unit transposon | 28 | - | AMR, Heavy metal resistance | (133) |
| Tn*2680* | *Proteus vulgaris* | Composite transposon | 5 | NC\_003905.1 | AMR | (134) |
| Tn*2681* | *Escherichia coli* | Composite transposon | - | - | AMR | (134) |
| Tn*2700* | *Salmonella typhimurium* | Composite transposon | - | - | AMR | (135) |
| Tn*2901* | *Escherichia coli* | Composite transposon | 11 | - | - | (136) |
| Tn*2921* | *Serratia marcescens* | Composite transposon | 12.4 | FJ829469.1 | AMR | (137) |
| Tn*2922* | *Escherichia coli* | Composite transposon | 27 | - | AMR | (138) |
| Tn*3000* | *Enterobacter hormaechei* | Composite transposon | 11.8 | KR822246.1 | AMR | (139) |
| Tn*3351* | *Salmonella naestved* | Not specified | - | - | AMR | (140) |
| Tn*3352* | *Salmonella naestved* | Not specified | - | - | AMR | (140) |
| Tn*3401* | *Pseudomonas fluorescens* | Not specified | - | - | Heavy metal resistance | (141) |
| Tn*3402* | *Citrobacter sp.* | Not specified | - | - | Heavy metal resistance | (141) |
| Tn*3403* | *Klebsiella sp.* | Not specified | - | - | Heavy metal resistance | (141) |
| Tn*3411* | *Escherichia coli* | Composite transposon | 7.4 | M19532.1, M22041.1 | Metabolism | (142) |
| Tn*3434* | *Paracoccus pantotrophus* | Unit transposon | 3.7 | AY232820.1 | - | (143) |
| Tn*3611* | *Pseudomonas aeruginosa* | Unit transposon | 9 | - | Heavy metal resistance | (144) |
| Tn*3613* | *Pseudomonas aeruginosa*  | Unit transposon | 24 | - | AMR, Heavy metal resistance | (144) |
| Tn*3614* | *Pseudomonas putida* | Unit transposon | 7.2 | - | - | (145) |
| Tn*3651* | *Escherichia coli* | Unit transposon | - | - | AMR | (146) |
| Tn*3701* | *Streptococcus pyogenes* | Conjugative transposon | 50 | - | AMR | (147) |
| Tn*3702* | *Enterococcus faecalis*  | Conjugative transposon | 18.5 | - | AMR | (148) |
| Tn*3703* | *Streptococcus pyogenes* | Conjugative transposon | 19.7 | - | AMR | (147) |
| Tn*3704* | *Streptococcus anginosus* | Conjugative transposon | 20.3 | - | AMR | (149) |
| Tn*3705* | *Streptococcus anginosus* | Conjugative transposon | 52 | - | AMR | (149) |
| Tn*3706* | *Streptococcus agalactiae* | Composite transposon | - | - | AMR | (150) |
| Tn*3707* | *Streptococcus agalactiae* | Conjugative transposon | - | - | AMR | (150) |
| Tn*3851* | *Staphylococcus aureus* | Not specified | 5.2 | - | AMR | (151) |
| Tn*3853* | *Staphylococcus aureus* | Unit transposon | - | - | AMR | (152) |
| Tn*3854* | *Staphylococcus aureus* | Not specified | 4.5 | - | AMR | (153) |
| Tn*3871* | *Streptococcus faecalis* | Unit transposon | 5.1 | - | AMR | (154) |
| Tn*3872* | *Streptococcus pneumoniae* | Conjugative transposon | 23.3 | - | AMR | (155) |
| Tn*3926* | *Yersinia enterocolitica* | Unit transposon | 7.8 | X78059.1 | Heavy metal resistance | (156) |
| Tn*3951* | *Streptococcus pneumoniae* | Conjugative transposon | 65 | - | AMR | (157) |
| Tn*4000* | *Klebsiella pneumoniae* | Unit transposon | - | X12618.1 | AMR, Heavy metal resistance | (158) |
| Tn*4001* | *Staphylococcus aureus* | Composite transposon | 4.7 | GU565967.1 | AMR | (159) |
| Tn*4002* | *Staphylococcus aureus* | Not specified | 6.7 | X16471.1 | AMR | (160) |
| Tn*4003* | *Staphylococcus aureus* | Composite transposon | 4.7 | GU565967.1 | AMR | (161)  |
| Tn*4031* | *Staphylococcus epidermidis* | Composite transposon | 5 | - | AMR | (162) |
| Tn*4132* | *Escherichia coli* | Unit transposon | 16 | - | AMR | (163) |
| Tn*4176* | *Alcaligenes faecalis* | Composite transposon | - | - | AMR | (164) |
| Tn*4201* | *Staphylococcus aureus* | Not specified | 6.7 | - | AMR | (165) |
| Tn*4291* | *Staphylococcus aureus* | Not specified | - | - | AMR | (166) |
| Tn*4321* | *Enterobacter aerogenases* | Composite transposon | 4.7 | U60777.1 | - | (167) |
| Tn*4351* | *Bacteroides fragilis* | Composite transposon | 5 | M17124.1 | AMR | (168) |
| Tn*4352* | *Salmonella typhimurium* | Composite transposon | 2.68 | M20306.1 | AMR | (169) |
| Tn*4371* | *Ralstonia eutropha* | Conjugative transposon | 55 | Y10831.1, Y10832.1 | Metabolism | (170) |
| Tn*4378* | *Ralstonia metallidurans* | Unit transposon | 8.2 | X90708.2 | Heavy metal resistance | (171) |
| Tn*4380* | *Ralstonia metallidurans* | Unit transposon |  | X71400.2 | Heavy metal resistance | (171) |
| Tn*4399* | *Bacteroides fragilis* | Conjugative transposon | 9.6 | L20975.1 | - | (172) |
| Tn*4400* | *Bacteroides fragilis* | Composite transposon | - | - | AMR | (173) |
| Tn*4401* | *Klebsiella pneumoniae* | Unit transposon | 10 | KT378596.1 | AMR | (174) |
| Tn*4411* | *Acinetobacter calcoaceticus* | Not specified | - | - | AMR | (175) |
| Tn*4430* | *Bacillus thuringiensis* | Unit transposon | 4.2 | X07651.1 | - | (176) |
| Tn*4431* | *Escherichia coli* | Unit transposon | - | - | AMR | (177) |
| Tn*4451* | *Clostridium perfringens* | Unit transposon | 6.3 | U15027.1 | AMR | (178) |
| Tn*4452* | *Clostridium perfringens* | Unit transposon | 6.2 | - | AMR | (179) |
| Tn*4521* | *Escherichia coli* | Composite transposon | - | M35123.1, AH000905.2 | Virulence determinants | (180) |
| Tn*4527* | *Salmonella typhimurium* | Composite transposon | 19.6 | - | AMR | (181) |
| Tn*4551* | *Bacteroides fragilis* | Composite transposon | 7.6 | M17808.1 | AMR | (182) |
| Tn*4555* | *Bacteroides vulgatus* | Unit transposon | 12.1 | U75371.3 | AMR | (183) |
| Tn*4556* | *Streptomyces fradiae* | Unit transposon | 6.8 | LC417441.1 | - | (184) |
| Tn*4560* | *Streptomyces fradiae* | Unit transposon | 8.6 | - | AMR | (185) |
| Tn*4563* | *Streptomyces coelicolor* | Unit transposon | 8.6 | - | AMR | (186) |
| Tn*4651* | *Pseudomonas putida* | Unit transposon | 56 | NC\_003350.1 | Metabolism | (187) |
| Tn*4652* | *Pseudomonas putida* | Unit transposon | 17 | AF151431.1 | Metabolism | (188) |
| Tn*4653* | *Pseudomonas putida* | Unit transposon | 70 | NC\_003350.1 | Metabolism | (188) |
| Tn*4654* | *-* | Unit transposon | - | - | - | (188) |
| Tn*4655* | *Pseudomonas putida* | Unit transposon | 39 | AB237655.1 | Metabolism | (189) |
| Tn*4656* | *Pseudomonas putida* | Unit transposon | 39 | AB062597.1 | Metabolism | (190) |
| Tn*4657* | *Pseudomonas putida* | Unit transposon | 86 | AB238971.1 | Metabolism | (191) |
| Tn*4658* | *Pseudomonas putida* | Unit transposon | 5.7 | AB238971.1 | - | (191) |
| Tn*4659* | *Pseudomonas putida* | Unit transposon | 3.7 | AB238971.1 | - | (191) |
| Tn*4660* | *Pseudomonas putida* | Unit transposon | 62 | AB238971.1 | Metabolism | (191) |
| Tn*4661* | *Pseudomonas aeruginosa* | Unit transposon | 13 | AB375440.1 | - | (192) |
| Tn*4671* | *Delftia acidovorans* | Unit transposon | 8.4 | AB063332.1 | Heavy metal resistance | (193) |
| Tn*4672* | *Delftia acidovorans* | Unit transposon | 11.9 | AB063332.1 | Heavy metal resistance | (193) |
| Tn*4676* | *Pseudomonas resinovorans* | Unit transposon | 73 | AB088420.3 | Metabolism | (194) |
| Tn*4731* | *Escherichia coli* | Composite transposon | - | - | AMR | (195) |
| Tn*4811* | *Streptomyces lividans* | Unit transposon | 5.4 | Z11519.1 | - | (196) |
| Tn*5030* | *Bacteroides sp.* | Conjugative transposon | 45 | - | AMR | (197) |
| Tn*5031* | *Enterococcus faecium* | Conjugative transposon | - | - | AMR | (198) |
| Tn*5032* | *Enterococcus faecium* | Conjugative transposon | - | - | AMR | (198) |
| Tn*5033* | *Enterococcus faecium* | Conjugative transposon | - | - | AMR | (198) |
| Tn*5036* | *Enterobacter cloacae* | Unit transposon | 8 | Y09025.1 | Heavy metal resistance | (199) |
| Tn*5037* | *Thiobacillus ferrooxidans* | Unit transposon | 6.6 | AJ251743.1 | Heavy metal resistance | (200) |
| Tn*5041* | *Pseudomonas sp.* | Unit transposon | 14.9 | X98999.3 | Heavy metal resistance | (201) |
| Tn*5042* | *Pseudomonas fluorescens* | Unit transposon | 7 | AJ563380.2 | Heavy metal resistance | (202) |
| Tn*5044* | *Xanthomonas campestris* | Unit transposon | 10 | Y17691.1 | Heavy metal resistance | (203) |
| Tn*5045* | *Pseudomonas sp.* | Unit transposon | 22 | FN821089.1 | AMR, Heavy metal resistance | (204) |
| Tn*5046* | *Pseudomonas sp.* | Unit transposon | 10 | Y18360.1 | Heavy metal resistance | (205) |
| Tn*5053* | *Xanthomonas sp.* | Unit transposon | 8.4 | L40585.1 | Heavy metal resistance | (206) |
| Tn*5056* | *Escherichia coli* | Unit transposon | - | AJ302763.1, AJ302764.1, AJ302765.1 | Heavy metal resistance | (202) |
| Tn*5058* | *Pseudomonas sp.* | Unit transposon | 12 | Y17897.1 | Heavy metal resistance | (207) |
| Tn*5060* | *Pseudomonas sp.* | Unit transposon | 8.7 | AJ551280.1 | Heavy metal resistance | (208) |
| Tn*5070* | *Pseudomonas sp.* | Unit transposon | 7 | Y17830.1 | Heavy metal resistance | (205) |
| Tn*5073* | *Klebsiella pneumoniae* | Unit transposon | 4.3 | AF461013.1 | Heavy metal resistance | (209) |
| Tn*5074* | *Morganella morganii* | Unit transposon | - | AF461012.1 | Heavy metal resistance | (209) |
| Tn*5075* | *Escherichia coli* | Composite transposon | 11.2 | AF457211.1 | Heavy metal resistance | (209) |
| Tn*5083* | *Bacillus megaterium* | Unit transposon | 5.5 | Y18009.2, Y09907.1 | Heavy metal resistance | (210) |
| Tn*5084* | *Bacillus cereus* | Unit transposon | 11.5 | AB066362.1 | Heavy metal resistance | (210) |
| Tn*5085* | *Exiguobacterium sp.* | Unit transposon | 11.8 | Y17750.1, Y17751.1, Y17752.1 | Heavy metal resistance | (210) |
| Tn*5086* | *Escherichia coli* | Unit transposon | 15.3 | X58425.1 | AMR, Heavy metal resistance | (211) |
| Tn*5090* | *Klebsiella aerogenes* | Unit transposon | 7.5 | X72585.1 | AMR, Antiseptic resistance | (212) |
| Tn*5096* | *Streptomyces spp.* | Unit transposon | 3 | - | AMR | (213) |
| Tn*5097* | *Streptomyces spp.* | Unit transposon | 3 | - | AMR | (214) |
| Tn*5098* | *Streptomyces fradiae* | Unit transposon | 5.3 | - | AMR, Metabolism | (215) |
| Tn*5099* | *Streptomyces spp.* | Unit transposon | 4.4 | - | AMR | (216) |
| Tn*5251* | *Streptococcus pneumoniae* | Conjugative transposon | 18 | FJ711160.1 | AMR | (217) |
| Tn*5252* | *Streptococcus pneumoniae* | Conjugative transposon | 47.5 | - | AMR | (218) |
| Tn*5253* | *Streptococcus pneumoniae* | Conjugative transposon | 66 | EU351020.1 | AMR | (219) |
| Tn*5271* | *Alcaligenes sp.* | Composite transposon | 17 | - | Metabolism | (220) |
| Tn*5276* | *Lactococcus lactis* | Conjugative transposon | 70 | CP001834.1 | Virulence determinants, Metabolism | (221) |
| Tn*5301* | *Lactococcus lactis* | Conjugative transposon | 70 | - | Virulence determinants, Metabolism | (222) |
| Tn*5306* | *Lactococcus lactis* | Conjugative transposon | - | - | Virulence determinants, Metabolism | (223) |
| Tn*5381* | *Enterococcus faecalis* | Conjugative transposon | 19 | - | AMR | (224) |
| Tn*5382* | *Enterococcus faecium* | Conjugative transposon | 27 | AF063010.1, AF063900.1 | AMR | (225) |
| Tn*5383* | *Enterococcus faecalis* | Conjugative transposon | 19 | - | AMR | (224) |
| Tn*5384* | *Enterococcus faecalis* | Composite transposon | 26 | - | AMR | (226) |
| Tn*5385* | *Enterococcus faecalis* | Composite transposon | 65 | - | AMR, Heavy metal resistance | (227) |
| Tn*5386* | *Enterococcus faecium* | Conjugative transposon | 29 | DQ321786.1 | AMR | (228) |
| Tn*5393* | *Erwinia amylovora* | Unit transposon | 6.7 | M96392.1 | AMR | (229) |
| Tn*5394* | *Erwinia pyrifoliae*  | Unit transposon | 6.3 | AY123045.1 | - | (230) |
| Tn*5396* | *Escherichia coli* | Unit transposon | - | - | - | (231) |
| Tn*5397* | *Clostridium difficile* | Conjugative transposon | 21 | AF333235.1 | AMR | (232) |
| Tn*5401* | *Bacillus thuringiensis* | Unit transposon | 4.8 | U03554.1 | - | (233) |
| Tn*5403* | *Klebsiella pneumoniae* | Unit transposon | 3.6 | X75779.1 | - | (234) |
| Tn*5404* | *Staphylococcus aureus* | Unit transposon | 16 | L43098.1 | AMR | (235) |
| Tn*5405* | *Staphylococcus aureus*  | Composite transposon | 12 | U73025.1, U73026.1, U73027.1 | AMR | (236) |
| Tn*5406* | *Staphylococcus aureus*  | Unit transposon | 5.5 | JQ319423.1 | AMR | (237) |
| Tn*5422* | *Listeria monocytogenes* | Unit transposon | 6.5 | L28104.1 | Heavy metal resistance | (238) |
| Tn*5431* | *Escherichia coli* | Unit transposon | 16 | X87813.1, X87814.1 | AMR | (239) |
| Tn*5432* | *Cutibacterium acnes* | Composite transposon | 4.5 | AF411029.1 | AMR | (240) |
| Tn*5466* | *Enterococcus hirae* | Composite transposon | 8.8 | X81655.1 | AMR | (241) |
| Tn*5467* | *Thiobacillus ferrooxidans* | Unit transposon | 3.5 | L37364.1 | - | (242) |
| Tn*5468* | *Thiobacillus ferrooxidans* | Unit transposon | 8 | AF032884.1 | - | (243) |
| Tn*5469* | *Fremyella diplosiphon* | Unit transposon | 4.9 | U33002.1 | - | (244) |
| Tn*5481* | *Lactococcus lactis* | Unit transposon | 5 | AJ000993.1 | - | (245) |
| Tn*5491* | *Streptomyces lividans*  | Unit transposon | - | - | AMR | (246) |
| Tn*5492* | *Streptomyces lividans* | Unit transposon | - | - | AMR | (247) |
| Tn*5493* | *Streptomyces lividans* | Unit transposon | - | - | AMR | (248) |
| Tn*5495* | *Pseudomonas veronii* | Unit transposon | - | - | AMR | (249) |
| Tn*5501* | *Pseudomonas putida* | Unit transposon | 5.6 | Y09450.1 | - | (250) |
| Tn*5502* | *Pseudomonas putida* | Unit transposon | 9 | Y09450.1, AF052749.1 | - | (250) |
| Tn*5506* |  *Enterococcus faecium* | Composite transposon | 39 | L40841.1 | AMR | (251) |
| Tn*5520* | *Bacteroides fragilis* | Unit transposon | 4.7 | AF038866.2 | - | (252) |
| Tn*5530* | *Burkholderia cepacia* | Composite transposon | 36 | AF029344.2 | Metabolism, Efflux functions | (253) |
| Tn*5531* | *Corynebacterium glutamicum* | Composite transposon | 4.5 | U53587.1 | AMR | (254) |
| Tn*5541* | *Fremyella diplosiphon* | Unit transposon | 4.7 | AF072896.1 | - | (255) |
| Tn*5542* | *Pseudomonas putida* | Composite transposon | 11.9 | AF148496.1 | Metabolism | (256) |
| Tn*5561* | *Rhodococcus erythropolis* | Unit transposon | - | AF002247.1 | - | (257) |
| Tn*5563* | *Pseudomonas alcaligenes* | Unit transposon | 6.3 | NC\_005909.1 | Efflux function | (258) |
| Tn*5564* | *Corynebacterium glutamicum* | Unit transposon | 4.2 | AF024666.2 | AMR | (259) |
| Tn*5565* | *Clostridium perfringens* | Composite transposon | 6.3 | - | Virulence determinants | (260) |
| Tn*5613* | *Acinetobacter sp.* | Composite transposon | 3.5 | AF091240.1 | - | (261) |
| Tn*5706* | *Pasteurella multocida* | Composite transposon | 4.4 | Y15510.1 | AMR | (262) |
| Tn*5707* | *Cupriavidus necator* | Composite transposon | 15 | D64144.1, AB019032.1 | Metabolism | (263) |
| Tn*5718* | Uncultured bacterium | Unit transposon | 10 | AJ304453.1 | Heavy metal resistance | (264) |
| Tn*5719* | Uncultured bacterium | Unit transposon | 8.4 | AJ431260.1 | Heavy metal resistance | (265) |
| Tn*5721* | *Lactococcus lactis* | Composite transposon | 11.5 | U91581.1 | Virulence determinants | (266) |
| Tn*5801* | *Staphylococcus aureus* | Conjugative transposon | 25.8 | BA000017.4 | AMR | (267) |
| Tn*6000* | *Enterococcus casseliflavus* | Conjugative transposon | 33.3 | FN555436.1 | AMR | (268) |
| Tn*6001* | *Pseudomonas aeruginosa* | Unit transposon | 12.1 | EF138817.1 | AMR | (269) |
| Tn*6002* | *Streptococcus cristatus* | Conjugative transposon | 20.9 | AY898750.1 | AMR | (270) |
| Tn*6003* | *Streptococcus pneumoniae* | Conjugative transposon | 25.1 | AM410044.5 | AMR | (271) |
| Tn*6004* | *Acinetobacter baumannii*  | Unit transposon | - | - | AMR | (272) |
| Tn*6005* | *Enterobacter cloacae* | Unit transposon | 23.7 | EU591509.1 | Antiseptic resistance, Heavy metal resistance | (273) |
| Tn*6006* | *Enterobacter cloacae* | Unit transposon | 15.7 | EU591509.1 | Antiseptic resistance | (273) |
| Tn*6007* | *Enterobacter cloacae* | Unit transposon | 7.2 | EU591509.1 | Antiseptic resistance | (273) |
| Tn*6008* | *Enterobacter cloacae* | Unit transposon | 6 | EU591509.1 | - | (273) |
| Tn*6009* | *Klebsiella pneumoniae* | Conjugative transposon | 19.7 | EU239355.1, EU399632.1 | AMR, Heavy metal resistance | (274) |
| Tn*6010* | *Escherichia coli* | Composite transposon | 5.1 | EU370913.1  | AMR | (275) |
| Tn*6011* | *Escherichia coli* | Composite transposon | 5.6 | EU370913.1 | Virulence determinants | (275) |
| Tn*6012* | *Staphylococcus aureus* | Conjugative transposon | 13.3 | AB435014.1 | - | (276) |
| Tn*6013* | *Staphylococcus aureus* | Conjugative transposon | 13.4 | FJ231270.1 | AMR | (277) |
| Tn*6014* | *Staphylococcus aureus* | Conjugative transposon | - | EU918655.2 | AMR | (278) |
| Tn*6016* | *Pseudomonas aeruginosa* | Unit transposon | 8.8 | KC543497.1 | AMR, Heavy metal resistance | (279) |
| Tn*6017* | *Citrobacter freundii* | Unit transposon | 9 | CP016763.1 | AMR, Heavy metal resistance | (280) |
| Tn*6018* | *Acinetobacter baumannii*  | Unit transposon | 3.4 | FJ172370.5 | Heavy metal resistance | (281) |
| Tn*6019* | *Acinetobacter baumannii* | Unit transposon | 59 | FJ172370.5 | Heavy metal resistance | (282) |
| Tn*6020* | *Acinetobacter baumannii* | Composite transposon | 3 | FJ172370.5 | AMR | (281) |
| Tn*6021* | *Acinetobacter baumannii*  | Unit transposon | 13.1 | CP000521.1 | - | (282) |
| Tn*6022* | *Acinetobacter baumannii* | Unit transposon | 12 | JN107991.2 | - | (283) |
| Tn*6023* | *Salmonella enterica* | Composite transposon | 2.6 | GU562437.2 | AMR | (284) |
| Tn*6024* | *Serratia marcescens* | Unit transposon | 32.4 | BX664015.1 | Heavy metal resistance | - |
| Tn*6025* | *Salmonella enterica* | Unit transposon | 13.3 | GU562437.2 | AMR, Heavy metal resistance | (285) |
| Tn*6026* | *Salmonella enterica*  | Composite transposon and Unit transposon | 24.3 | GQ150541.1 | AMR, Heavy metal resistance | (285) |
| Tn*6027* | *Salmonella enterica*  | Composite transposon | 28 | HQ840942.1 | AMR | (286) |
| Tn*6028* | *-* | Unit transposon | - | - | AMR | - |
| Tn*6029* | *Salmonella enterica*  | Composite transposon | 8.8 | GQ150541.1 | AMR | (285) |
| Tn*6030* | *Hydrogenobacter thermophilus* | Unit transposon | 30.9 | AP011112.1 | - | (287) |
| Tn*6031* | *Sphingobacterium sp.* | Unit transposon | 13 | EU864422.1 | AMR | (288) |
| Tn*6032* | Uncultured bacterium | Unit transposon | 3.3 | AB266126.2  | - | (289) |
| Tn*6033* | *Ralstonia pickettii* | Conjugative transposon | 54.1 | CP001068.1 | - | (290) |
| Tn*6034* | *Shewanella sp.*  | Conjugative transposon | 45.2 | NC\_008577.1 | - | (290) |
| Tn*6035* | *Congregibacter litoralis* | Conjugative transposon | 50.7 | NZ\_AAOA01000008.1 | - | (290) |
| Tn*6036* | *Acidovorax avenae* | Conjugative transposon | 60 | NC\_008752.1 | - | (290) |
| Tn*6037* | *Delftia acidovorans* | Conjugative transposon | 57.9 | NC\_010002.1 | - | (290) |
| Tn*6038* | *Comamonas testosteroni* | Conjugative transposon | 52.5 | - | - | (290) |
| Tn*6039* | *Acidovorax sp.*  | Conjugative transposon | 53.5 | NC\_008782.1 | - | (290) |
| Tn*6040* | *Bordetella petrii* | Conjugative transposon | 47.1 | NC\_010170.1 | - | (290) |
| Tn*6041* | *Pseudomonas aeruginosa* | Conjugative transposon | 48.5 | NZ\_AAKW01000024.1 | - | (290) |
| Tn*6042* | *Pseudomonas aeruginosa* | Conjugative transposon | 55.3 | NC\_009656.1 | - | (290) |
| Tn*6045* | *Macrococcus caseolyticus*  | Unit transposon | 6.7 | AB498756.1 | AMR | (291) |
| Tn*6048* | *Cupriavidus metallidurans* | Unit transposon | 10.4 | CP000353.2 | - | (292) |
| Tn*6049* | *Cupriavidus metallidurans* | Unit transposon | 3.5 | CP000353.2 | - | (292) |
| Tn*6050* | *Cupriavidus metallidurans* | Unit transposon | 6.8 | CP000353.2 | - | (292) |
| Tn*6051* | *Delftia acidovorans* | Unit transposon | - | - | - | (292) |
| Tn*6052* | *Burkholderia xenovorans* | Unit transposon | - | - | - | (292) |
| Tn*6058* | *Streptococcus pneumoniae* | Conjugative transposon | 67.8 | FM201786.3 | AMR | (293) |
| Tn*6060* | *Pseudomonas aeruginosa* | Composite transposon | 25.4 | GQ161847.1 | AMR | (294) |
| Tn*6061* | *Pseudomonas aeruginosa* | Unit transposon | 26.6 | GU475047.1, GU475048.1, GU475049.1, GU475053.1 | AMR | (295) |
| Tn*6062* | *Salmonella enterica*  | Composite transposon | 4.9 | AM412236.1 | Efflux function | (296) |
| Tn*6063* | Delftia acidovorans | Composite transposon | 22.4 |  JF274990.2 | Metabolism | (297) |
| Tn*6072* | *Staphylococcus aureus*  | Composite transposon | 29.4 | GU235985.1 | AMR | (298) |
| Tn*6073* | *Clostridium difficile* | Conjugative transposon | 29.1 | BK008006.1 | Efflux function | (299) |
| Tn*6074* | *Salmonella bongori*  | Conjugative transposon | 109 | FN298494.1 | AMR, Efflux function | (300) |
| Tn*6075* | *Salmonella enterica* | Conjugative transposon | 104 | FN298495.1 | - | (300) |
| Tn*6076* | *Salmonella Senftenberg*  | Conjugative transposon | 114 | FN298496.1 | Metabolism | (300) |
| Tn*6077* | *Yersinia enterocolitica* | Conjugative transposon | 120 | FN298493.1 | Efflux function | (300) |
| Tn*6079* | Uncultured bacterium | Conjugative transposon | 28.4 | GU951538.1 | AMR | (301) |
| Tn*6080* | *Acinetobacter baumannii* | Unit transposon | 3.2 | GQ352402.1 | AMR | (302) |
| Tn*6082* | *Salmonella enterica* | Unit transposon | 3.6 | AP005147.1 | AMR | (303) |
| Tn*6083* | *Salmonella bongori* | Conjugative transposon | 84 | FN669609.1 | AMR | (300) |
| Tn*6084* | *Enterococcus faecium* | Conjugative transposon | 22.3 | HM243622.1 | AMR | (304) |
| Tn*6085* | *Enterococcus faecium* | Conjugative transposon | 20.8 | HM243621.1, HM243623.1 | AMR | (304) |
| Tn*6086* | *Enterococcus faecium* | Conjugative transposon | 24.5 | HM636636.1 | AMR | - |
| Tn*6087* | *Streptococcus oralis* | Conjugative transposon | 21.1 | HQ663849.2 | AMR, Antiseptic resistance | (305) |
| Tn*6088* | *Salmonella enterica*  | Composite transposon and Unit transposon | 43.3 | AY509004.1 | AMR, Antiseptic resistance, Efflux functions, Heavy metal resistance | (306) |
| Tn*6089* | *Salmonella enterica* | Composite transposon | 3 | AY509004.1 | AMR | (306) |
| Tn*6090* | *Salmonella enterica* | Composite transposon | 6 | AY509004.1 | - | (306) |
| Tn*6091* | *Salmonella enterica* | Composite transposon | 6.5 | AY509004.1 | - | (306) |
| Tn*6092* | *Salmonella enterica* | Unit transposon | 4.1 | AY509004.1 | AMR, Efflux function | (306) |
| Tn*6093* | *Proteus mirabilis* | Unit transposon | 6.3 | FM995219.1 | AMR, Antiseptic resistance, Efflux functions | (307) |
| Tn*6097* | *Paracoccus ferrooxidans*  | Composite transposon | 17.8 | JN122276.1 | AMR, Metabolism | (308) |
| Tn*6098* | *Lactococcus lactis* | Conjugative transposon | 51 | CP001834.1 | Efflux function, Metabolism, Virulence determinants | (309) |
| Tn*6099* | *Prevotella nigrescens* | Unit transposon | 7 | HM561907.1 | AMR | (310) |
| Tn*6100* | *Prevotella nigrescens* | Unit transposon | 6.3 | HM561908.1 | AMR | (310) |
| Tn*6101* | *Salmonella enterica* | Conjugative transposon | 84 | FR686852.1 | - | (300) |
| Tn*6103* | *Clostridium difficile*  | Conjugative transposon | 84.9 | BK008007.1 | Efflux function | (299) |
| Tn*6104* | *Clostridium difficile*  | Conjugative transposon | 15.6 | FN545816.1 | Efflux function | (299) |
| Tn*6105* | *Clostridium difficile*  | Conjugative transposon | 15.8 | FN545816.1 | - | (299) |
| Tn*6106* | *Clostridium difficile*  | Conjugative transposon | 11.3 | FN545816.1 | - | (299) |
| Tn*6107* | *Clostridium difficile*  | Conjugative transposon | 50.5 | BK008008.1 | Efflux function | (299) |
| Tn*6108* | *Salmonella enterica* | Composite transposon | 31 | JF274992.1 | AMR, Heavy metal resistance | - |
| Tn*6109* | *Salmonella enterica* | Composite transposon | 23 | JF274992.1 | - | - |
| Tn*6110* | *Clostridium difficile*  | Conjugative transposon | 58 | BK008009.1 | - | (299) |
| Tn*6111* | *Clostridium difficile*  | Conjugative transposon | 53.4 | JF422669.1 | - | (299) |
| Tn*6112* | *Pseudomonas sp.* | Unit transposon | 7.3 | HQ423158.1 | - | (311) |
| Tn*6113* | *Citrobacter freundii* | Unit transposon | - | FR716828.1 | AMR, Efflux function | (312) |
| Tn*6114* | *Klebsiella pneumoniae* | Unit transposon | 4 | EU331426.1 | AMR, Efflux function | (312) |
| Tn*6115* | *Clostridium difficile* | Unit transposon | 13.6 | - | Efflux function | (299) |
| Tn*6122* | *Paracoccus halophilus* | Unit transposon | 3.8 | JN127372.1 | - | (308) |
| Tn*6125* | *Delftia acidovorans* | Composite transposon | 32.8 | HQ891317.1 | Metabolism | - |
| Tn*6126* | *Delftia acidovorans* | Composite transposon | 35.9 | JF274988.1 | Metabolism | (313) |
| Tn*6127* | *Comamonas testosteroni* | Composite transposon | 37.8 | JF274987.1 | Metabolism | (297) |
| Tn*6130* | *Comamonas testosteroni* | Unit transposon | 15.6 | JF274989.1 | Heavy metal resistance | (313) |
| Tn*6133* | *Staphylococcus aureus* | Unit transposon | 11.5 | FR772051.1 | AMR | (314) |
| Tn*6134* | *Sphingobium japonicum* | Unit transposon | 4.6 | AB610645.1 | Metabolism | (315) |
| Tn*6135* | *Sphingobium japonicum* | Unit transposon | 4.3 | AB610646.1 | - | (315) |
| Tn*6136* | *Sphingobium japonicum* | Unit transposon | 3.8 | AB610647.1 | - | (315) |
| Tn*6137* | *Sphingobium japonicum* | Unit transposon | 3.8 | AB610648.1 | - | (315) |
| Tn*6138* | *Sphingobium japonicum* | Unit transposon | 4.6 | AB610649.1 | Metabolism | (315) |
| Tn*6161* | *Porphyromonas gingivalis* | Conjugative transposon | 44.3 | AP009380.1 | Efflux functions | (316) |
| Tn*6162* | *Pseudomonas aeruginosa* | Composite transposon and Unit transposon | 26 | JF826498.1 | AMR, Heavy metal resistance | (317) |
| Tn*6163* | *Pseudomonas aeruginosa* | Unit transposon | 21.2 | JF826499.1 | AMR, Heavy metal resistance | (317) |
| Tn*6164* | *Clostridium difficile* | Conjugative transposon | 106 | FN665653.1 | AMR | (318) |
| Tn*6166* | *Acinetobacter baumannii* | Unit transposon | 17.6 | JN247441.4 | AMR | (319) |
| Tn*6167* | *Acinetobacter baumannii* | Composite transposon and Unit transposon | 33 | JN968483.3 | AMR | (320) |
| Tn*6168* | *Acinetobacter baumannii* | Composite transposon | 5.5 | KC118540.6 | AMR | (321) |
| Tn*6170* | *Escherichia coli* | Unit transposon | 18.8 | AP012208.1 | - | (322) |
| Tn*6171* | *Acinetobacter baumannii* | Unit transposon | 49.9 | CP012952.1 | Metabolism | (323) |
| Tn*6172* | *Acinetobacter baumannii* | Unit transposon | 11.7 | KU744946.1, KT779035.1 | AMR | (324) |
| Tn*6176* | *Acinetobacter baumannii* | Unit transposon | 3.4 | KU549175.1 | Heavy metal resistance, Virulence determinants | - |
| Tn*6177* | *Acinetobacter baumannii* | Unit transposon | 35.6 | MG954377.1 | Heavy metal resistance | - |
| Tn*6178* | *Acinetobacter baumannii* | Composite transposon | 4.6 | KP054476.2 | AMR, Efflux function | - |
| Tn*6179* | *Acinetobacter baumannii* | Composite transposon | 2.7 | KX011025.2 | AMR | (325) |
| Tn*6180* | *Acinetobacter baumannii* | Composite transposon | 19 | KX011025.2 | AMR | (325) |
| Tn*6181* | *Escherichia coli* | Unit transposon | 19.4 | KX242350.1  | AMR | - |
| Tn*6182* | *Pseudomonas aeruginosa* | Unit transposon | 11.5 | KX709966.1 | Heavy metal resistance | (326) |
| Tn*6183* | *Acinetobacter baumannii* | Composite transposon and Unit transposon | 25.8 | MF399199.1 | AMR | - |
| Tn*6186* | *Bacteroides fragilis*  | Composite transposon | 8.5 | AB646744.1 | AMR, Efflux function | (327) |
| Tn*6187* | *Klebsiella pneumoniae* | Composite transposon and Unit transposon | 32.6 | JQ010984.1 | AMR, Heavy metal resistance | (328) |
| Tn*6188* | *Listeria monocytogenes* | Unit transposon | 5.1 | HG329628.1 | Antiseptic resistance | (329) |
| Tn*6190* | *Clostridium difficile* | Conjugative transposon | 17.9 | FN665653.1 | AMR | (318) |
| Tn*6191* | *Staphylococcus haemolyticus* | Composite transposon | 6.3 | JQ764731.1 | AMR | (330) |
| Tn*6192* | *Clostridium difficile* | Conjugative transposon | 37.5 | FN545816.1 | Efflux function | (331) |
| Tn*6194* | *Clostridium difficile* | Conjugative transposon | 28 | HG475346.1 | AMR | (332) |
| Tn*6196* | *Escherichia coli* | Unit transposon | 3.6 | KC999035.4 | - | (333) |
| Tn*6198* | *Listeria monocytogenes* | Conjugative transposon | 21.3 | JX120102.1 | AMR | (334) |
| Tn*6202* | *Enterococcus faecalis* | Conjugative transposon | 43.7 | FJ872411.1 | AMR | (335) |
| Tn*6203* | *Achromobacter xylosoxidans* | Unit transposon | 17.5 | JX448550.1 | AMR, Heavy metal resistance | (336) |
| Tn*6204* | *Mycobacterium abscessus* | Unit transposon | 11.5 | CP003505.2 | AMR | - |
| Tn*6205* | *Mycobacterium abscessus* | Unit transposon | 2.8 | CP003505.2 | AMR | - |
| Tn*6206* | *Acinetobacter baumannii* | Composite transposon | 7.8 | CP003849.1 | AMR | (337) |
| Tn*6207* | *Acinetobacter baumannii* | Unit transposon | 6.8 | CP001937.2 | AMR | (337) |
| Tn*6208* | *Acinetobacter baumannii* | Composite transposon | 9.2 | CP003846.1 | AMR | (337) |
| Tn*6209* | *Acinetobacter baumannii* | Unit transposon | 8.4 | CP003849.1 | AMR | (337) |
| Tn*6210* | *Acinetobacter baumannii* | Composite transposon | - | - | AMR | (337) |
| Tn*6211* | *Pseudomonas syringae* | Unit transposon | 4.9 | KX009065.1 | - | (338) |
| Tn*6212* | *Pseudomonas syringae* | Not specified | 16.3 | - | Heavy metal resistance, Efflux function | (338) |
| Tn*6213* | *Pseudomonas syringae* | Unit transposon | 4.8 | - | - | (338) |
| Tn*6214* | *Escherichia coli* | Unit transposon | 29 | KJ541071.1 | AMR, Heavy metal resistance | (339) |
| Tn*6215* | *Clostridioides difficile* | Conjugative transposon | 13 | KC166248.1 | AMR | (340) |
| Tn*6216* | *Enterobacter cloacae* | Unit transposon | 14 | KC511628.1 | AMR | (341) |
| Tn*6217* | *Pseudomonas aeruginosa* | Unit transposon | 6.9 | KC543497.1 | AMR | (279) |
| Tn*6218* | *Clostridium difficile* | Unit transposon | 14.2 | HG002387.1 | AMR | (342) |
| Tn*6222* | *Escherichia coli*  | Composite transposon | 7.8 | CP003297.1 | AMR | (343) |
| Tn*6223* | *Escherichia coli*  | Composite transposon | 1.5 | CP003289.1 | - | (343) |
| Tn*6224* | *Lactobacillus salivarius* | Conjugative transposon | 17 | CP007650.1 | AMR | (344) |
| Tn*6227* | *Streptococcus mitis* | Unit transposon | 7.9 | KJ690251.1 | AMR | - |
| Tn*6228* | *Sphingomonas sp.*  | Composite transposon | 32.5 | KF494257.1 | Metabolism | (345) |
| Tn*6229* | *Klebsiella pneumoniae* | Unit transposon | 16.8 | KF295829.1 | AMR | (346) |
| Tn*6230* | *Salmonella enterica*  | Unit transposon | 37 | - | Heavy metal resistance | (347) |
| Tn*6231* | *Pseudomonas moraviensis* | Unit transposon | - | - | - | (348) |
| Tn*6233* | *Burkholderia sp.* | Unit transposon | 8.8 | AB853026.1 | Heavy metal resistance | (349) |
| Tn*6234* | *Klebsiella pneumoniae* | Unit transposon | 29 | HG934082.1 | AMR, Heavy metal resistance | (350) |
| Tn*6235* | *Clostridium difficile* | Not specified | 40 | - | AMR | (351) |
| Tn*6237* | *Escherichia coli*  | Composite transposon | 21.9 | - | AMR | (352) |
| Tn*6238* | *Klebsiella pneumoniae* | Unit transposon | 8 | KJ511462.1 | AMR | (353) |
| Tn*6240* | *Klebsiella pneumoniae* | Unit transposon | 9.6 | HG934082.1 | AMR | (350) |
| Tn*6242* | *Escherichia coli*  | Composite transposon | 19.7 | - | AMR | (354) |
| Tn*6246* | *Enterococcus faecium* | Composite transposon | 5.1 | KP834591.1 | AMR | - |
| Tn*6247* | *Enterococcus faecium* | Conjugative transposon | 23.7 | KP345886.1 | AMR | - |
| Tn*6248* | *Enterococcus faecium* | Conjugative transposon | 26 | KP834592.1 | AMR | (355) |
| Tn*6249* | *Pseudomonas aeruginosa* | Composite transposon and Unit transposon | 26 | LK054503.1 | AMR | (356) |
| Tn*6250* | *Acinetobacter baumannii* | Composite transposon | 12.8 | CP007712.1 | AMR | (357) |
| Tn*6251* | *Acinetobacter baumannii* | Composite transposon | 5.2 | CP007712.1 | - | (357) |
| Tn*6252* | *Acinetobacter baumannii* | Composite transposon | 3.2 | CP007712.1 | AMR | (357) |
| Tn*6253* | *Streptococcus pyogenes* | Conjugative transposon | 20.2 | CP007024.1 | AMR | (358) |
| Tn*6254* | *Lactobacillus hokkaidonensis* | Conjugative transposon | 52 | AP014680.1 | Heavy metal resistance, Metabolism | (359) |
| Tn*6255* | *Citrobacter freundii* | Unit transposon | 4 | KP851978.1 | AMR | (360) |
| Tn*6256* | *Citrobacter freundii* | Composite transposon | 12.9 | KP851978.1 | AMR | (360) |
| Tn*6260* | *Enterococcus faecalis* | Unit transposon | 4.5 | KX470419.1 | AMR | (361) |
| Tn*6261* | *Enterococcus faecalis* | Unit transposon | 8.9 | KU354267.1 | AMR | (362) |
| Tn*6263* | *Streptococcus gallolyticus* | Conjugative transposon | 46 | JYKU01000013.1 | AMR | (363) |
| Tn*6264* | *Vibrio parahaemolyticus* | Composite transposon | 5.4 | KM067908.1 | Virulence determinants | (364) |
| Tn*6268* | *Sphingobium sp.* | Unit transposon | 4.1 | LC102249.1 | - | (365) |
| Tn*6269* | *Sphingobium sp.* | Unit transposon | 4.1 | LC102250.1 | - | (365) |
| Tn*6270* | *Sphingobium sp.* | Unit transposon | 4.2 | LC102251.1 | - | (365) |
| Tn*6271* | *Sphingobium sp.* | Unit transposon | 3.7 | LC102252.1 | - | (365) |
| Tn*6272* | *Sphingobium sp.* | Unit transposon | 3.8 | LC102253.1 | - | (365) |
| Tn*6273* | *Sphingobium sp.* | Unit transposon | 2.4 | LC102254.1 | - | (365) |
| Tn*6274* | *Sphingobium sp.* | Unit transposon | 4.6 | LC102255.1 | - | (365) |
| Tn*6275* | *Sphingobium sp.* | Unit transposon | 3.8 | LC102256.1 | - | (365) |
| Tn*6276* | *Sphingobium sp.* | Unit transposon | 4.6 | LC102257.1 | - | (365) |
| Tn*6277* | *Sphingobium sp.* | Unit transposon | 5.3 | LC102258.1 | - | (365) |
| Tn*6278* | *Sphingobium sp.* | Unit transposon | 3.9 | LC102259.1 | - | (365) |
| Tn*6279* | *Acinetobacter baumannii*  | Composite transposon | 21 | KT317075.1 | AMR | (366) |
| Tn*6283* | *Vibrio sp.*  | Unit transposon | 13.8 | LC081338.1 | Virulence determinants | (367) |
| Tn*6284* | *Pseudomonas aeruginosa* | Unit transposon | 22.6 | KU254577.1 | AMR, Heavy metal resistance | (368) |
| Tn*6285* | *Shigella boydii* | Composite transposon and Unit transposon | 25.8 | KX646543.1 | AMR, Antiseptic resistance, Heavy metal resistance | (368) |
| Tn*6286* | *Pseudomonas putida*  | Unit transposon | 23.7 | KU130294.1 | AMR | (369) |
| Tn*6290* | *Pseudomonas putida* | Not specified | 42 | BK010246.1 | - | (370) |
| Tn*6291* | *Pseudomonas fluorescens* | Not specified | 22.3 | BK010245.1 | - | (370) |
| Tn*6292* | *Pseudomonas aeruginosa* | Unit transposon | - | - | AMR | (371) |
| Tn*6293* | *Clostridium difficile* | Conjugative transposon | 104 | ERS1242839 | AMR | (372) |
| Tn*6294* | *Paenibacillus sp.* | Unit transposon | 8.6 | LC015492.1 | Heavy metal resistance | (373) |
| Tn*6295* | *Shigella boydii* | Composite transposon | 6.1 | KX646543.1 | AMR | (374) |
| Tn*6296* | *Klebsiella pneumoniae* | Unit transposon | 14.3 | FJ628167.2 | AMR | (375) |
| Tn*6297* | *Shewanella xiamenensis* | Composite transposon and Unit transposon | 78.2 | CP013115.1 | AMR, Antiseptic resistance, Heavy metal resistance | (376) |
| Tn*6298* | Uncultured bacterium | Unit transposon | 3 | KU736866.1 | AMR | (377) |
| Tn*6299* | Uncultured bacterium | Unit transposon | 21.4 | KU736875.1 | AMR | (377) |
| Tn*6300* | Uncultured bacterium | Unit transposon | 7.2 | KU736876.1 | AMR | (377) |
| Tn*6301* | Uncultured bacterium | Composite transposon and Unit transposon | 12.1 | KU736877.1 | AMR | (377) |
| Tn*6302* | Uncultured bacterium | Composite transposon | 11 | KU736878.1 | AMR | (377) |
| Tn*6303* | Uncultured bacterium | Unit transposon | 4.6 | KU736874.1 | AMR | (377) |
| Tn*6306* | *Raoultella ornithinolytica* | Composite transposon | 13.8 | KT225520.1 | AMR | (378) |
| Tn*6308* | *Leclercia adecarboxylata* | Composite transposon and Unit transposon | 30.6 | KX710094.1 | AMR, Heavy metal resistance | (379) |
| Tn*6309* | *Leclercia adecarboxylata* | Composite transposon | 5.4 | KX710094.1 | AMR | (379) |
| Tn*6310* | *Vibrio cholerae* | Unit transposon | 8.2 | AXDR01000001.1 | Heavy metal resistance | (380) |
| Tn*6317* | *Leclercia adecarboxylata* | Composite transposon | 21 | KX710093.1 | Heavy metal resistance | (379) |
| Tn*6320* | *Enterobacter cloacae* | Composite transposon and Unit transposon | 8.4 | MF062700.1 | AMR | - |
| Tn*6321* | *Enterobacter cloacae* | Unit transposon | 21.3 | KY270852.1 | AMR, Antiseptic resistance, Heavy metal resistance | - |
| Tn*6322* | *Leclercia adecarboxylata*  | Unit transposon | 9.3 | KX710093.1 | Heavy metal resistance | (379) |
| Tn*6325* | *Enterobacter hormaechei* | Unit transposon | 23.8 | CP010378.1 | AMR, Heavy metal resistance | (381) |
| Tn*6326* | *Actinotignum schaalii* | Composite transposon | 4 | KT897470.1 | AMR | (382) |
| Tn*6329* | *Klebsiella pneumoniae* | Composite transposon | 18 | LT576116.1 | AMR | (383) |
| Tn*6330* | *Escherichia coli* | Composite transposon | 4.7 | NZ\_CP029493.1 | AMR | (384) |
| Tn*6331* | *Streptococcus gallolyticus* | Conjugative transposon | - | - | AMR | (385) |
| Tn*6332* | *Bacillus sp.* | Unit transposon | 11.5 | LC155216.1 | Heavy metal resistance | - |
| Tn*6333* | *Escherichia coli* | Unit transposon | 11.5 | KX156773.1 | Heavy metal resistance | (386) |
| Tn*6338* | *Raoultella ornithinolytica* | Unit transposon | 33.2 | KY270853.1 | AMR, Antiseptic resistance, Efflux function, Heavy metal resistance | (387) |
| Tn*6339* | *Klebsiella pneumoniae* | Unit transposon | 8.5 | MF344565.1 | AMR | (387) |
| Tn*6340* | *Klebsiella pneumoniae* | Unit transposon | 13.3 | MF344565.1 | AMR, Heavy metal resistance | - |
| Tn*6344* | *Klebsiella pneumoniae* | Composite transposon | 7.4 | MF344567.1 | - | (387) |
| Tn*6345* | *Pseudomonas aeruginosa* | Unit transposon | 6 | KU961660.2 | AMR | - |
| Tn*6346* | *Achromobacter sp.* | Unit transposon | 8.2 | EU696790.1 | Heavy metal resistance | (388) |
| Tn*6347* | *Klebsiella pneumoniae* | Unit transposon | 3 | MF344562.1 | Efflux function | (387) |
| Tn*6350* | *Pseudomonas aeruginosa* | Unit transposon | 7.4 | KY347015.1 | Virulence determinants | (389) |
| Tn*6352* | *Pseudomonas aeruginosa* | Unit transposon | 11 | KX889311.1 | AMR | (390) |
| Tn*6356* | *Pseudomonas aeruginosa* | Unit transposon | 15.6 | KY494864.1 | AMR, Efflux function | (391) |
| Tn*6360* | *Escherichia coli* | Composite transposon | 17 | KF534788.2 | AMR | (392) |
| Tn*6361* | *Morganella morganii* | Composite transposon | 16.3 | KM660724.1 | AMR | (392) |
| Tn*6362* | *Cronobacter sakazakii* | Unit transposon | 10.7 | KY978628.1 | Efflux function, Heavy metal resistance | (393) |
| Tn*6363* | *Cronobacter sakazakii* | Composite transposon | 6.1 | KY978630.1 | AMR | (393) |
| Tn*6367* | *Klebsiella pneumoniae* | Composite transposon | 5.7 | MF168404.1 | AMR | (394) |
| Tn*6368* | *Providencia rettgeri* | Unit transposon | 2.8 | KX832928.1 | - | (395) |
| Tn*6369* | *Providencia rettgeri* | Unit transposon | 9.2 | CP017672.1 | Efflux functions | (395) |
| Tn*6374* | *Shewanella oneidensis* | Unit transposon | - | - | - | (396) |
| Tn*6375* | *Klebsiella pneumoniae* | Unit transposon | 18.8 | KY978631.1 | AMR | (397) |
| Tn*6376* | *Citrobacter freundii* | Unit transposon | 4.9 | MF072963.1 | - | (398) |
| Tn*6377* | *Klebsiella pneumoniae* | Unit transposon | 4 | MF133495.1 | AMR | - |
| Tn*6378* | *Enterobacter cloacae* | Unit transposon | - | CP021851.1 | AMR | (397) |
| Tn*6381* | *Klebsiella pneumoniae*  | Unit transposon | 22.8 | MF344566.1 | Heavy metal resistance | (387) |
| Tn*6382* | *Klebsiella pneumoniae* | Unit transposon | 20.4 | MF344566.1 | AMR, Antiseptic resistance, Heavy metal resistance | (387) |
| Tn*6383* | *Klebsiella pneumoniae* | Composite transposon and Unit transposon | 48.7 | MF344562.1 | AMR, Antiseptic resistance, Heavy metal resistance | (387) |
| Tn*6384* | *Klebsiella pneumoniae* | Composite transposon and Unit transposon | 26 | MF344563.1 | AMR, Antiseptic resistance, Heavy metal resistance | (387) |
| Tn*6390* | *Shigella flexneri* | Composite transposon | 4.5 | KY784668.1 | AMR | (399) |
| Tn*6391* | *Pseudomonas aeruginosa* | Unit transposon | 17.4 | MF168946.1 | AMR, Heavy metal resistance | - |
| Tn*6392* | *Pseudomonas aeruginosa* | Unit transposon | 14.5 | MF144194.1 | AMR, Heavy metal resistance | (400) |
| Tn*6393* | *Pseudomonas aeruginosa*  | Composite transposon and Unit transposon | 47.1 | MF144194.1 | AMR | (400) |
| Tn*6394* | *Pseudomonas aeruginosa* | Unit transposon | 7.2 | MF344578.1 | AMR | (397) |
| Tn*6397* | *Enterobacter cloacae* | Conjugative transposon | 114 | CP021851.1 | AMR, Metabolism, Heavy metal resistance | (397) |
| Tn*6399* | *Klebsiella pneumoniae*  | Unit transposon | 8.3 | MF344566.1 | - | - |
| Tn*6400* | *Klebsiella pneumoniae* | Unit transposon | 23.8 | KU318421.1 | AMR, Heavy metal resistance | (387) |
| Tn*6401* | *Raoultella planticola* | Composite transposon and Unit transposon | 39.3 | JX515588.1 | AMR | (387) |
| Tn*6402* | *Klebsiella pneumoniae* | Composite transposon | 9.4 | MF344563.1 | AMR | (387) |
| Tn*6403* | *Pseudomonas aeruginosa* | Composite transposon and Unit transposon | 30 | CP030075.1 | AMR, Heavy metal resistance | (400) |
| Tn*6404* | *Klebsiella pneumoniae* | Composite transposon | - | KX839207.1 | AMR, Antiseptic resistance, Heavy metal resistance | (401) |
| Tn*6411* | *Pseudomonas aeruginosa* | Composite transposon and Unit transposon | 37.6 | CP024477.1 | AMR | (397) |
| Tn*6413* | *Pseudomonas aeruginosa* | Conjugative transposon | 114.1 | CP030075.1 | AMR, Heavy metal resistance | (400) |
| Tn*6414* | *Escherichia coli* | Composite transposon and Unit transposon | 22.6 | KC340960.1 | AMR, Heavy metal resistance | (402) |
| Tn*6417* | *Pseudomonas aeruginosa* | Conjugative transposon | 108.2 | CP013993.1 | AMR, Heavy metal resistance | (400) |
| Tn*6431* | *Aeromonas caviae* | Composite transposon | 12.6 | CP025777.1 | AMR | (403) |
| Tn*6432* | *Aeromonas caviae* | Unit transposon | 9.5 | CP025777.1 | AMR | (404) |
| Tn*6435* | *Enterobacter hormaechei* | Composite transposon | 3.7 | KJ488943.1 | AMR | (404) |
| Tn*6450* | *Proteus mirabilis* | Composite transposon and Unit transposon | 65.8 | MF805806.1 | AMR | (405) |
| Tn*6451* | *Morganella morganii* | Composite transposon and Unit transposon | 111.2 | MG832661.1 | AMR | (406) |
| Tn*6452* | *Salmonella enterica* | Unit transposon | - | MK360094 | AMR | (407) |
| Tn*6456* | *Prevotella bivia* | Unit transposon | 7.8 | MG827401.1 | AMR, Efflux function | (408) |
| Tn*6497* | *Klebsiella pneumoniae* | Unit transposon | - | CP026021.1 | Virulence determinants | (409) |
| Tn*6498* | *Klebsiella pneumoniae* | Unit transposon | - | CP026021.1 | Virulence determinants | (409) |
| Tn*6499* | *Klebsiella pneumoniae* | Unit transposon | - | CP026021.1 | Efflux function | (409) |
| Tn*6501* | *Klebsiella pneumoniae* | Composite transposon | 6.9 | CP026022.1 | AMR | (409) |
| Tn*6505* | *Leclercia adecarboxylata* | Unit transposon | 16.9 | MK036884.1 | AMR, Heavy metal resistance | - |
| Tn*6516* | *Arthrobacter sp.* | Unit transposon | 14.9 | MH067970.1 | Efflux function, Heavy metal resistance | (410) |
| Tn*6517* | *Arthrobacter sp.* | Unit transposon | 7 | MH067971.1 | - | (410) |
| Tn*6518* | *Aeromonas veronii* | Not specified | - | MH481281 | AMR | - |
| Tn*6530* | *Pseudomonas aeruginosa* | Unit transposon | 35.1 | KX196168.1 | AMR, Heavy metal resistance | (400) |
| Tn*6531* | *Pseudomonas aeruginosa* | Unit transposon | 24.8 | AP014651.1 | AMR, Heavy metal resistance | (400) |
| Tn*6532* | *Pseudomonas aeruginosa* | Unit transposon | 21.2 | CP013993.1 | AMR, Heavy metal resistance | (400) |
| Tn*6533* | *Pseudomonas aeruginosa* | Conjugative transposon | 109 | AP014651.1 | AMR, Heavy metal resistance | (400) |
| Tn*6534* | *Pseudomonas aeruginosa* | Conjugative transposon | 118.7 | KX196168.1 | AMR, Heavy metal resistance | (400) |
| Tn*6535* | *Hafnia alvei* | Unit transposon | 14.3 | CP009706.1 | Heavy metal resistance | (387) |
| Tn*6539* | *Escherichia coli* | Composite transposon | 7.3 | KJ772290.2 | AMR | (411) |
| Tn*6540* | *Enterobacter cloacae* | Unit transposon | 16.1 | LT991958.1 | AMR | (412) |
| Tn*6628* | *Enterococcus faecium* | Composite transposon | 4.9 | MF580438.1 | AMR | (413) |
| Tn*6644* | *Streptococcus suis* | Composite transposon | 5.1 | KC844836.1 | AMR | (414) |
| Tn*6645* | *Acinetobacter baumannii* | Composite transposon | 8.4 | CP014234.1 | - | (415) |
| Tn*6647* | *Enterococcus faecalis* | Unit transposon | 32.8 | SAMN10475125  | - | (416) |
| Tn*6648* | *Enterococcus faecalis* | Unit transposon | 53.2 | SAMN10475125  | AMR | (416) |
| Tn*6649* | *Pseudomonas aeruginosa* | Unit transposon | 31.6 | CP033439.1 | AMR, Antiseptic resistance | - |
| Tn*6651* | *Escherichia coli* | Composite transposon | 3.9 | MH674341.1 | AMR | (417) |
| Tn*6652* | *Escherichia coli* | Composite transposon | 10.2 | MH674341.1 | AMR | (417) |
| Tn*6655* | *Acinetobacter baumannii* | Composite transposon | 3.2 | CP035186.1 | AMR | (418) |
| Tn*6656* | *Acinetobacter baumannii* | Composite transposon | 3.4 | CP035186.1 | AMR | (418) |
| Tn*6658* | *Acinetobacter baumannii* | Composite transposon | 3.9 | CP035186.1 | - | (418) |
| Tn*6674* | *Enterococcus faecalis* | Unit transposon | 12.9 | MK737778.1 | AMR | (419) |
| Tn*6677* | *Vibrio cholerae* | Unit transposon | - | - | Adaptive immune system | (420) |

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