

| Table S1. Genes affected by the big deletion of 37390 bp from 233143 to 270532 | | | | |
|--|--|-------------------|---------|-----------------------|
| Gene name | Annotation | Location | COG(s) | COG function category |
| DVU_tRNA-Pseudo-1 | pseudogene tRNA with anticodon TTT | 233143-233215 (-) | - | - |
| DVU0189 | P4 family phage/plasmid primase | 233752-235437 (+) | COG3378 | R |
| DVU0190 | hypothetical protein | 235434-235646 (-) | - | S |
| DVU0191 | hypothetical protein | 235704-237263 (+) | COG0358 | L |
| DVU0192 | adenine specific DNA methyltransferase, putative | 237390-238748 (+) | COG0863 | LK |
| DVU0193 | hypothetical protein | 238741-239472 (+) | COG1428 | F |
| DVU0194 | terminase, large subunit, putative | 239489-241447 (+) | COG5525 | R |
| DVU0195 | hypothetical protein | 241444-241662 (+) | - | S |
| DVU0196 | hypothetical protein | 242446-242586 (+) | - | S |
| DVU0197 | lambda family phage portal protein | 242590-244290 (+) | COG5511 | R |
| DVU0198 | minor capsid protein C, degenerate | 244274-245593 (+) | COG0616 | OU |
| DVU0199 | hypothetical protein | 245603-245986 (+) | - | S |
| DVU0200 | major head protein | 245998-247002 (+) | - | S |
| DVU0201 | hypothetical protein | 247011-247331 (+) | - | S |
| DVU0202 | holin | 247334-247822 (+) | COG4824 | R |
| DVU0203 | hypothetical protein | 247843-248391 (+) | COG3926 | R |
| DVU0204 | putative lipoprotein | 248409-248819 (+) | - | S |
| DVU0205 | hypothetical protein | 248812-248979 (+) | - | S |
| DVU0206 | hypothetical protein | 248982-249575 (+) | - | S |
| DVU0207 | hypothetical protein | 249572-249898 (+) | - | S |
| DVU0208 | hypothetical protein | 249895-250452 (+) | - | S |
| DVU0209 | hypothetical protein | 250436-250627 (+) | - | S |
| DVU0210 | tail sheath protein, putative | 250631-252094 (+) | COG4386 | R |
| DVU0211 | tail tube protein, putative | 252144-252509 (+) | - | S |
| DVU0212 | hypothetical protein | 252509-252769 (+) | - | S |
| DVU0213 | hypothetical protein | 252969-254459 (+) | COG3941 | R |
| DVU0214 | tail/DNA circulation protein, putative | 254468-255667 (+) | COG4228 | R |
| DVU0215 | tail protein, putative | 255790-256923 (+) | COG4379 | R |
| DVU0216 | phage baseplate assembly protein V, putative | 256925-257563 (+) | COG4384 | S |
| DVU0217 | tail protein, putative | 257565-258041 (+) | COG4381 | S |
| DVU0218 | tail protein, putative | 258050-259111 (+) | COG3299 | S |
| DVU0219 | tail protein, putative | 259120-259746 (+) | COG3778 | S |
| DVU0220 | tail fiber protein, putative | 259739-260755 (+) | - | S |
| DVU0221 | tail fiber assembly protein, putative | 260765-261208 (+) | - | S |
| DVU0222 | hypothetical protein | 261220-261549 (+) | - | S |
| DVU0223 | hypothetical protein | 261649-261831 (+) | COG1724 | N |
| DVU0224 | hypothetical protein | 261875-262270 (+) | COG1598 | S |
| DVU0225 | hypothetical protein | 262334-262510 (+) | - | S |
| DVU0226 | hypothetical protein | 262657-263796 (-) | - | S |
| DVU0227 | hypothetical protein | 263799-264329 (-) | COG3013 | S |
| DVU0228 | hypothetical protein | 264667-264765 (+) | - | S |
| DVU0230 | transcriptional regulator cII, putative | 265802-266266 (+) | - | S |
| DVU0231 | hypothetical protein | 266347-266571 (+) | - | S |
| DVU0232 | hypothetical protein | 266564-266812 (+) | COG0376 | P |
| DVU0233 | hypothetical protein | 266937-267239 (-) | - | S |
| DVU0234 | hypothetical protein | 267982-268305 (+) | - | S |
| DVU0235 | hypothetical protein | 268308-268871 (+) | - | S |
| DVU0236 | phage integrase family site specific recombinase | 269283-270425 (-) | COG0582 | L |

R: general function prediction only; S: function unknown; N: cell motility; P: inorganic ion transport and metabolism; L: replication, recombination and repair; K: transcription; O: posttranslational modification, protein turnover, chaperones; U: intercellular tracking, secretion, and vesicular transport.
(+): positive strand; (-): negative strand

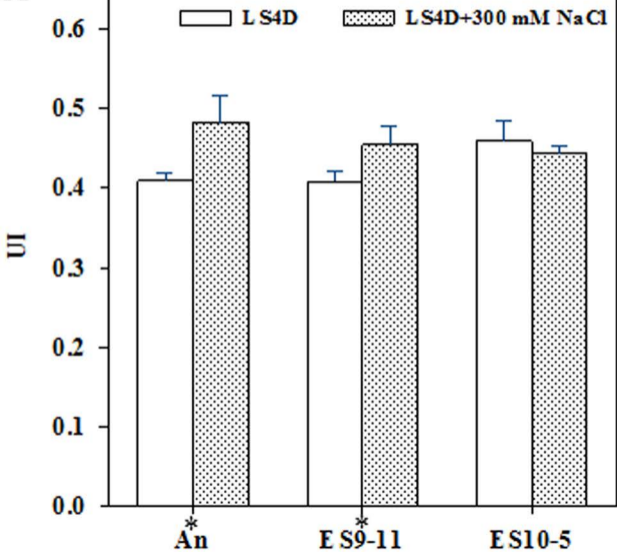
| Table S2. Details of the genes deleted in plasmid due to the deletion from 51979b to 157737 | | | | |
|---|---|------------------|---------|-----------------------|
| Gene name | Annotation | Location | COG(s) | COG function category |
| DVUA0043 | polysaccharide deacetylase family protein | 51965-52816(+) | | G |
| DVUA0044 | hypothetical protein | 52878-53855(+) | | S |
| DVUA0045 | aminotransférase | 53852-55468(+) | | M |
| DVUA0046 | glycosyl transférse, group 2 family protein | 55465-56913(+) | | M |
| DVUA0047 | hypothetical protein | 56989-58305(+) | | S |
| DVUA0048 | exopolysaccharide production protein | 58360-59757(+) | COG3307 | M |
| DVUA0049 | polysaccharide biosynthesis family protein | 59761-61230(+) | | M |
| DVUA0050 | hypothetical protein | 61246-62502(+) | | S |
| DVUA0051 | glycosyl transférse, group 1 family protein | 62499-63887(+) | | M |
| DVUA0052 | hypothetical protein | 64069-64737(+) | | S |
| DVUA0053 | hypothetical protein | 64988-65575(+) | | S |
| DVUA0054 | glycosyl transférse, group 1 family protein | 65572-66972(+) | | M |
| DVUA0055 | hypothetical protein | 66969-67922(+) | | S |
| DVUA0056 | hypothetical protein | 67912-68532(+) | | S |
| DVUA0057 | sigma-54 dependent transcriptional regulator/response regulator | 68687-70117(+) | | T |
| DVUA0058 | BNR/Asp-box repeat-containing protein | 70158-72893(+) | | S |
| DVUA0059 | hypothetical protein | 72938-74314(+) | | S |
| DVUA0060 | hypothetical protein | 74453-75838(+) | | S |
| DVUA0061 | hypothetical protein | 75835-77187(+) | | S |
| DVUA0062 | hypothetical protein | 77184-78479(+) | | S |
| DVUA0063 | Orn/DAP/Arg family decarboxylase | 78536-80092(+) | | E |
| DVUA0064 | hypothetical protein | 80843-82885(+) | | S |
| DVUA0065 | sensor histidine kinase | 82882-84918(+) | COG642 | T |
| DVUA0066 | patatin family phospholipase | 85372-86784(+) | COG1752 | S |
| DVUA0067 | hypothetical protein | 87157-88281(-) | | S |
| DVUA0068 | hypothetical protein | 88333-90315(-) | | S |
| DVUA0069 | GtrA family protein, selenocysteine-containing | 90871-92028(-) | | S |
| DVUA0070 | hypothetical protein | 92091-94022(-) | | S |
| DVUA0071 | glycosyl transférse, group 1/2 family protein | 94115-96271(-) | | M |
| DVUA0072 | glycosyl transférse, group 1 family protein | 96400-97737(-) | COG438 | M |
| DVUA0073 | asparagine synthase (glutamine-hydrolyzing) | 97846-100515(-) | COG0367 | E |
| DVUA0074 | sulfotransférase family protein | 100606-101295(-) | | EFHI |
| DVUA0075 | radical SAM domain-containing protein | 101383-102789(-) | | EFHI |
| DVUA0076 | ABC transporter ATP-binding protein | 102804-104198(-) | COG1134 | GM |
| DVUA0077 | ABC transporter permease | 104230-105114(-) | | GM |
| DVUA0078 | hypothetical protein | 105230-105388(-) | | S |
| DVUA0079(<i>cysC</i>) | adenylyl-sulfate kinase | 105582-106268(+) | COG529 | P |
| DVUA0080 | glycosyl transférse, group 2 family protein | 106366-107247(+) | | M |
| DVUA0081 | glycosyl transférse, group 1/2 family protein | 107247-109361(+) | COG438 | M |
| DVUA0082 | phage integrase family site specific recombinase | 109666-110697(-) | COG4973 | L |
| DVUA0083 | hypothetical protein | 110806-110934(+) | | S |
| DVUA0084 | AbrB family transcriptional regulator | 111110-111301(+) | | T |
| DVUA0085 | hypothetical protein | 111356-114886(+) | | S |
| DVUA0086 | response regulator | 114998-116089(-) | COG3437 | T |
| DVUA0087 | sensory box histidine kinase | 116475-119588(-) | | T |
| DVUA0088 | hypothetical protein | 119777-120796(-) | | S |
| DVUA0089 | hypothetical protein | 121289-121906(-) | | S |
| DVUA0090 | hypothetical protein | 122486-123358(+) | | S |
| DVUA0091(<i>katA</i>) | catalase | 123495-124952(+) | COG0753 | P |
| DVUA0092 | hypothetical protein | 125171-125650(-) | | S |
| DVUA0093 | chromate transport family protein | 125839-127176(-) | COG2059 | P |
| DVUA0094(<i>chrB</i>) | chrB protein (chromate resistance exported protein) | 127186-128190(-) | | P |
| DVUA0095 | hypothetical protein | 128594-129079(+) | | S |
| DVUA0096 | major facilitator superfamily protein | 129163-130374(+) | COG2814 | G |
| DVUA0097 | radical SAM domain-containing protein | 130707-132206(+) | | EFHI |
| DVUA0098 | dehydrogenase | 132351-133400(-) | COG0371 | C |
| DVUA0099 | HAMP domain-containing protein | 133570-135753(-) | COG2208 | T |
| DVUA0100(<i>flrC</i>) | sigma-54 dependent transcriptional regulator | 136112-137839(-) | COG2204 | T |
| DVUA0101(<i>flhB</i>) | hrpY/hrcU family type III secretion protein | 137887-138927(-) | COG1377 | N |
| DVUA0102(<i>escT</i>) | type III secretion inner membrane protein | 138924-139739(-) | | U |
| DVUA0103(<i>mvX</i>) | HrpO family type III secretion protein | 139746-140006(-) | COG4794 | U |
| DVUA0104(<i>scfI</i>) | type III secretion inner membrane protein HrcV family | 140328-142421(-) | | U |
| DVUA0105 | hypothetical protein | 143145-143519(-) | | S |
| DVUA0106 | YopN family type III secretion target protein | 143522-144646(-) | | U |
| DVUA0107 | hypothetical protein | 144885-144989(+) | | S |
| DVUA203 | hypothetical protein | 145353-145655(+) | | S |
| DVUA0108 | hypothetical protein | 145580-146200(+) | | S |
| DVUA0109 | LcrH/SycD family type III secretion system chaperone | 146209-146709(+) | | U |
| DVUA0110 | type III secretion system target, YopB family | 146706-147713(+) | | U |
| DVUA0111 | type III secretion system protein IpaC family | 147662-148558(+) | | U |
| DVUA201 | hypothetical protein | 148611-149066(+) | | S |
| DVUA0112 | type III secretion system protein YscC family | 149369-151243(+) | COG1450 | U |
| DVUA0113 | YscD family type III secretion protein | 151240-153048(+) | | U |
| DVUA0114 | hypothetical protein | 153041-153250(+) | | S |
| DVUA0115 | type III secretion system protein YscF family | 153276-153527(+) | | U |
| DVUA0116 | hypothetical protein | 153722-154087(+) | | S |
| DVUA0117(<i>escJ</i>) | type III secretion lipoprotein | 154970-155785(+) | COG4669 | U |
| DVUA200 | hypothetical protein | 155792-156715(+) | | S |
| DVUA0118 | type III secretion system protein | 156694-157311(+) | | U |
| DVUA0119(<i>scfN</i>) | type III secretion system ATPase | 157639-158955(+) | COG1157 | NU |

S: function unknown; U: intracellular trafficking, secretion, and vesicular transport; P: inorganic ion transport and metabolism; N: cell motility; M: cell wall/membrane/envelope biogenesis; T: signal transduction mechanisms; C: energy production and conversion; transport and metabolism of carbohydrate (G), amino acid (E), nucleotide (F), coenzyme (H), or lipid (L); (+): positive strand; (-): negative strand

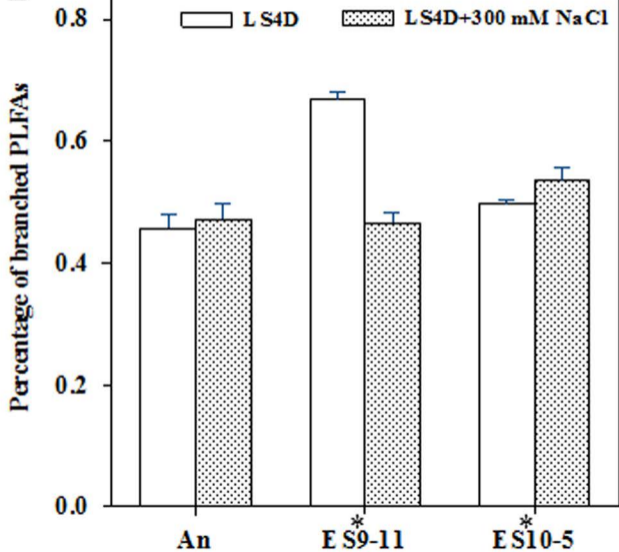
| Table S3. PCR primers used to confirm the mutations with Sanger sequencing | | | |
|---|-----------------------------------|-----------------------|-----------------------|
| Targeted gene | Targeted mutation position | Forward primer | Reverse primer |
| DVU0071 | 88598 | CGTGCCAGCTTCTGGTAGAC | G TTCACATCGGAGGCAATCT |
| DVU_tRNA-Pseudo-1 | 233143~270532 | CGCAGAGTTGGATGAATGGT | CGGTCTCGACGTTGTGTGT |
| DVU0201 | 233143~270533 | AGGCCGAGTTCTTCTCCAAG | ACAAAGCCCAGCACGTAGTC |
| DVU0236 | 233143~270534 | GCTCTTCTCGGCCCTTGTA | ATTGGCTCACAAACGCCTAC |
| DVU0829 | 919173 | CACCAACGACCTCATCCAGT | GACATAGCTGTTCGCGGAAGT |
| DVU1204 | 1296277 | CAGGCGAAGTGAAGGATTTC | GACCGAAGACCTGCTTGATG |
| DVU1260 | 1347079 | CAGCTTGAGGGTACCCATGT | AGCAGGGACATTGCTGAAGT |
| DVU1530 | 1599083 | TTGTAGATTCGGGCGAAGAC | AACAGTTCGCCGTTGATCTC |
| DVU1663 | 1743449 | TGTCATCCATCTGGAAGTGG | GGGGACTCTCACCGTAATGA |
| DVU1838 | 1909403 | GTGCTCATGACCTCCGAAAT | AGACCATCGAGTTCGAGGAA |
| DVU1862 | 1930032 | GTTGCCTGTGGAAATTGTCG | GTTCCCGGTGGACGTAGAT |
| DVU2001* | 2083308 | AAACATCAGGCTTGACGAC | GTTCCCGAGGTGAAGTTGAG |
| DVU2298 | 2392375 | CACCATGAGCACCATAGCC | GCTACCTGTTCGACGGAAGT |
| DVU2349 | 2444619 | GCATGAGCATGGTCTTTCTG | CAGGAGTATCTCCGCTCCA |
| DVU2394 | 2497747 | TTTTTGCGCAATGAGAACAG | AACACGTTGATGCGATGGTA |
| DVU2396 | 2499697 | GCTGGAGAGACTCAGCATCG | AGATGATGCGCAAATCCTTC |
| DVU2571 | 2685414 | GAAGCTTGCAAACTGCTCA | AGGAGAACGAACACCAGCAG |
| DVU2950* | 3056212 | CTCTTCATCGAACCGGAGTC | ATGCGGTACTCTGCCTCGTA |
| DVU3022* | 3140596 | ATCACCAAACGCAAGGAGAC | ATGAGGTTCGGTGAAGGTCAG |
| DVU3151 | 3304807 | TGCGTCGGTAAAATCCCTAC | AGAGTCTGCCGGGAGTGAC |
| *: pre-existing mutations in the DvH ancestor | | | |

| Table S4. Metabolites detected by Q-TOF | | | | | | | | | | | | | | | | |
|---|--------------------------------|----------|----------|-----------------|-----------|-----------|------------|-----------|------------|-----------|------------|-----------|------------|-----------|------------|-----------|
| RT | ID | m/z | Ion | Ion Formula | Peak area | | | | | | | | | | | |
| | | | | | An-C | | An-T | | ES9-11-C | | ES9-11-T | | ES10-5-C | | ES10-5-T | |
| | | | | | Average | Stdev | Average | Stdev | Average | Stdev | Average | Stdev | Average | Stdev | Average | Stdev |
| 28.335 | | 154.0963 | (M+H)+ | C7 H12 N3 O | 24,725 | 9,109 | 6,064 | 1,967 | 56,112 | 18,366 | 7,859 | 2,031 | 39,006 | 6,862 | 15,798 | 3,386 |
| 26.606 | | 554.2148 | (M+2H)+2 | > limit | 128,424 | 66,544 | 2,909 | 713 | 169,186 | 113,704 | 17,224 | 8,701 | 166,396 | 102,716 | 4,983 | 1,671 |
| 25.563 | | 575.2245 | (M+2H)+2 | > limit | 2,187,575 | 234,645 | 95,295 | 25,447 | 4,051,729 | 736,089 | 637,121 | 53,595 | 2,974,300 | 331,931 | 343,564 | 60,408 |
| 24.849 | | 184.1054 | (M+H)+ | C8 H14 N3 O2 | 1,063 | 800 | 12,718 | 5,128 | 1,571 | 1,178 | 84,034 | 47,535 | 4,518 | 5,628 | 178,852 | 46,783 |
| 24.684 | | 276.1540 | (M+H)+ | C7 H18 N9 O3 | 290 | 255 | 0 | 0 | 434 | 391 | 1,754 | 125 | 352 | 279 | 8,310 | 2,688 |
| 24.272 | | 539.7077 | (M+2H)+2 | > limit | 12,115 | 2,426 | 71 | 98 | 101,043 | 39,554 | 4,961 | 1,291 | 50,729 | 7,900 | 2,153 | 1,106 |
| 24.245 | | 304.1612 | (M+H)+ | C11 H22 N5 O5 | 518 | 352 | 545 | 443 | 404 | 298 | 7,082 | 1,096 | 782 | 534 | 23,148 | 7,433 |
| 22.433 | Piperazineethane sulfonic acid | 195.0812 | (M+H)+ | C6 H15 N2 O3 S | 1,322,347 | 418,597 | 1,995,537 | 695,786 | 1,374,564 | 564,310 | 1,651,593 | 316,699 | 1,430,536 | 452,362 | 1,698,778 | 202,925 |
| 21.911 | | 134.0811 | (M+H)+ | C5 H12 N O3 | 1,808 | 714 | 974 | 915 | 1,913 | 911 | 13,756 | 6,135 | 245 | 549 | 60,292 | 15,673 |
| 22.241 | | 539.7061 | (M+2H)+2 | > limit | 13,280 | 6,621 | 73 | 100 | 38,486 | 22,053 | 737 | 338 | 16,943 | 13,028 | 126 | 89 |
| 21.472 | citrulline | 176.1026 | (M+H)+ | C6 H14 N3 O3 | 160,516 | 25,240 | 9,970 | 7,275 | 516,958 | 76,468 | 442,094 | 121,226 | 409,182 | 67,024 | 404,934 | 33,529 |
| 21.362 | | 560.7057 | (M+2H)+2 | > limit | 161,312 | 30,673 | 5,659 | 2,183 | 497,126 | 106,115 | 34,961 | 9,264 | 241,241 | 32,802 | 8,618 | 2,427 |
| 20.896 | glutamine | 147.0772 | (M+H)+ | C5 H11 N2 O3 | 533,403 | 59,486 | 69,854 | 32,166 | 1,289,909 | 185,159 | 2,108,450 | 708,664 | 800,708 | 69,699 | 2,511,635 | 334,293 |
| 20.703 | C7 H13 N O5 | 192.0874 | (M+H)+ | C7 H14 N O5 | 1,952 | 285 | 3,651 | 1,441 | 1,796 | 1,445 | 71,316 | 10,919 | 3,539 | 1,923 | 55,734 | 10,058 |
| 20.456 | alanine | 90.0548 | (M+H)+ | C3 H8 N O2 | 88,800 | 6,225 | 102,428 | 20,421 | 1,031,693 | 89,253 | 1,052,130 | 247,669 | 98,242 | 13,330 | 124,471 | 30,430 |
| 20.346 | glutamate | 148.0599 | (M+H)+ | C5 H10 N O4 | 2,470,277 | 205,878 | 1,379,306 | 215,502 | 4,310,259 | 339,633 | 11,925,348 | 1,924,531 | 5,723,211 | 606,441 | 18,106,314 | 1,939,014 |
| 20.209 | threonine | 120.0638 | (M+H)+ | <none> | 27,794 | 8,201 | 2,580 | 312 | 121,352 | 25,231 | 85,573 | 31,938 | 81,065 | 15,311 | 17,104 | 4,176 |
| 20.072 | | 173.0249 | (M+H)+ | C4 H11 C2 N2 O | 66,234 | 37,914 | 7,938 | 5,966 | 60,011 | 39,328 | 1,941 | 1,355 | 76,535 | 34,494 | 5,011 | 2,975 |
| 20.044 | methanamine | 141.1132 | (M+H)+ | C6 H13 N4 | 63,106 | 124,229 | 3,334,028 | 1,167,795 | 4,219 | 6,422 | 173,723 | 116,245 | 175,645 | 239,842 | 133,916 | 84,249 |
| 19.962 | | 320.0738 | (M+H)+ | C10 H14 N3 O9 | 28,047 | 13,695 | 64 | 144 | 157,054 | 47,606 | 5,069 | 3,350 | 126,311 | 31,187 | 12,105 | 7,816 |
| 19.77 | AMP | 348.0713 | (M+H)+ | C12 H10 N7 O6 | 181,151 | 213,867 | 7,530 | 4,142 | 240,459 | 310,188 | 152,843 | 121,728 | 483,507 | 567,868 | 620,829 | 209,251 |
| 19.44 | | 263.1002 | (M+H)+ | C9 H11 N8 O2 | 85 | 77 | 2,615 | 2,379 | 26 | 57 | 14,496 | 6,965 | 26 | 58 | 9,968 | 5,832 |
| 18.287 | | 258.1724 | (M+H)+ | C14 H20 N5 | 10,891 | 5,506 | 20,172 | 14,204 | 12,225 | 4,732 | 17,550 | 6,666 | 17,518 | 7,295 | 12,034 | 6,810 |
| 18.205 | | 476.1849 | (M+H)+ | C19 H26 N9 O4 S | 35,243 | 3,937 | 26,917 | 34,857 | 24,278 | 8,120 | 12,776 | 5,770 | 22,282 | 2,434 | 8,375 | 5,046 |
| 18.205 | | 286.2883 | (M+H)+ | C16 H36 N3 O | 21,633 | 14,639 | 254,343 | 201,374 | 17,536 | 8,314 | 42,472 | 25,344 | 30,682 | 9,876 | 27,093 | 31,380 |
| 17.985 | valine | 118.0855 | (M+H)+ | C5 H12 N O2 | 40,720 | 7,389 | 10,490 | 6,475 | 338,597 | 110,694 | 236,033 | 69,825 | 99,504 | 26,440 | 169,280 | 107,327 |
| 17.601 | | 713.0721 | (M+H)+ | C21 H29 O25 S | 66,418 | 19,563 | 576,471 | 124,298 | 64,063 | 51,484 | 190,587 | 59,155 | 68,046 | 23,444 | 129,606 | 16,096 |
| 16.723 | | 895.4329 | (M+2H)+2 | > limit | 89 | 122 | 0 | 0 | 1,296 | 859 | 0 | 79 | 122 | 0 | 0 | |
| 16.064 | | 102.1277 | (M+H)+ | C6 H16 N | 593,765 | 56,853 | 1,061,987 | 82,886 | 545,078 | 49,074 | 618,410 | 31,092 | 577,230 | 47,351 | 547,740 | 42,809 |
| 16.5 | isoleucine | 132.1018 | (M+H)+ | C6 H14 N O2 | 16,885 | 4,203 | 9,731 | 6,429 | 170,251 | 56,915 | 69,601 | 22,480 | 65,276 | 10,713 | 41,665 | 23,591 |
| 16.064 | leucine | 132.1017 | (M+H)+ | C6 H14 N O2 | 61,143 | 15,844 | 10,810 | 6,679 | 362,972 | 111,871 | 179,812 | 50,507 | 230,073 | 73,345 | 280,908 | 158,885 |
| 15.268 | | 326.3204 | (M+H)+ | <none> | 9,459 | 4,118 | 10,953 | 5,558 | 109,249 | 21,777 | 82,844 | 29,133 | 11,649 | 5,824 | 453 | 342 |
| 15.185 | | 328.2980 | (M+H)+ | C23 H38 N | 17,007 | 2,852 | 17,797 | 2,535 | 82,445 | 15,424 | 66,141 | 8,833 | 13,555 | 1,887 | 189 | 164 |
| 15.158 | | 215.2119 | (M+H)+ | C12 H27 N2 O | 16,966 | 2,972 | 9,304 | 2,513 | 55,329 | 12,309 | 54,545 | 10,452 | 16,629 | 3,378 | 135 | 131 |
| 15.15 | | 342.3092 | (M+H)+ | C15 H36 N9 | 5,073 | 1,291 | 8,355 | 1,372 | 50,524 | 9,426 | 30,752 | 2,689 | 4,311 | 615 | 43 | 59 |
| 15.075 | | 606.2772 | (M+H)+ | C30 H48 N5 S4 | 2,561 | 754 | 9,987 | 2,669 | 473 | 277 | 16,910 | 5,165 | 479 | 236 | 4,117 | 2,389 |
| 14.636 | | 130.1575 | (M+H)+ | C8 H20 N | 398,578 | 70,720 | 815,375 | 302,708 | 352,040 | 37,651 | 327,327 | 106,690 | 362,695 | 141,481 | 309,119 | 73,870 |
| 14.114 | | 496.3019 | (M+H)+ | C21 H38 N9 O5 | 80,451 | 22,606 | 2,473 | 880 | 27,434 | 5,912 | 13,877 | 1,615 | 13,961 | 8,351 | 5,612 | 3,301 |
| 13.977 | | 440.2775 | (M+H)+ | C13 H30 N17 O | 1,035,993 | 275,735 | 122,168 | 75,687 | 614,612 | 137,715 | 311,675 | 64,744 | 985,294 | 350,582 | 285,959 | 209,163 |
| 13.95 | | 498.3193 | (M+H)+ | C18 H44 N9 O5 S | 147,010 | 41,874 | 7,115 | 1,184 | 14,876 | 1,713 | 30,804 | 6,600 | 10,639 | 5,230 | 8,625 | 4,448 |
| 13.84 | | 454.2930 | (M+H)+ | C14 H32 N17 O | 1,118,593 | 227,506 | 279,236 | 163,327 | 809,904 | 210,845 | 499,789 | 115,256 | 884,800 | 263,572 | 376,936 | 244,716 |
| 13.813 | | 466.2945 | (M+H)+ | C22 H48 N3 O S3 | 1,346,454 | 255,354 | 227,715 | 121,799 | 746,809 | 191,377 | 533,137 | 129,208 | 1,345,458 | 436,784 | 388,102 | 268,792 |
| 13.62 | | 482.3270 | (M+H)+ | C19 H44 N7 O7 | 917,747 | 126,125 | 151,586 | 78,326 | 152,958 | 36,749 | 244,155 | 60,179 | 193,736 | 67,149 | 100,135 | 63,989 |
| 13.593 | | 480.3098 | (M+H)+ | C16 H34 N17 O | 568,286 | 75,531 | 107,087 | 44,622 | 227,631 | 70,140 | 236,305 | 60,342 | 304,896 | 106,490 | 120,836 | 76,212 |
| 13.209 | | 818.4938 | (M+H)+ | > limit | 9,240 | 3,537 | 6,453 | 2,529 | 1,766 | 765 | 61,722 | 6,554 | 3,209 | 1,057 | 62,394 | 35,243 |
| 13.181 | | 256.3004 | (M+H)+ | C17 H38 N | 130,223 | 32,412 | 212,164 | 19,415 | 137,108 | 20,560 | 133,152 | 16,449 | 170,134 | 34,115 | 117,787 | 20,012 |
| 13.154 | | 844.5136 | (M+H)+ | > limit | 22,728 | 8,894 | 24,710 | 4,566 | 3,079 | 1,584 | 99,594 | 10,036 | 6,444 | 3,087 | 94,234 | 51,297 |
| 12.687 | | 512.3697 | (M+2H)+2 | > limit | 573 | 293 | 55,901 | 24,035 | 266 | 199 | 4,134 | 1,369 | 492 | 412 | 17,137 | 1,781 |
| 11.644 | hypoxanthine | 137.0458 | (M+H)+ | C5 H5 N4 O | 5,538,051 | 694,949 | 26,061 | 26,071 | 4,430,858 | 986,810 | 552,670 | 199,059 | 4,061,203 | 1,878,927 | 2,766,710 | 1,304,597 |
| 10.985 | | 330.3355 | (M+H)+ | C16 H40 N7 | 5,554,016 | 701,858 | 6,227,853 | 2,695,412 | 7,187,906 | 775,783 | 6,695,310 | 1,138,815 | 7,546,239 | 2,501,693 | 4,337,232 | 650,551 |
| 10.875 | | 164.9350 | (M+H)+ | C3 H2 C1 N2 S2 | 337 | 685 | 385,481 | 293,736 | 46 | 103 | 10,714 | 23,957 | 1,946 | 4,350 | 22,965 | 30,792 |
| 10.793 | | 358.3688 | (M+H)+ | C22 H48 N O2 | 9,830,026 | 1,147,336 | 12,574,662 | 5,335,974 | 11,893,371 | 1,485,476 | 11,543,308 | 1,696,027 | 13,852,739 | 4,048,381 | 8,380,317 | 583,432 |
| 9.228 | adenine | 136.0616 | (M+H)+ | C5 H6 N5 | 691,519 | 190,248 | 185,767 | 120,883 | 284,773 | 78,706 | 893,784 | 402,941 | 1,146,862 | 437,925 | 813,601 | 430,403 |
| 9.173 | | 678.5058 | (M+H)+ | C33 H68 N5 O9 | 1,147,322 | 171,736 | 845,190 | 182,298 | 1,389,594 | 318,612 | 1,059,217 | 265,006 | 1,991,854 | 318,233 | 1,524,591 | 304,036 |
| 8.596 | | 690.5014 | (M+H)+ | C32 H68 N9 O5 S | 2,010,420 | 240,744 | 1,755,935 | 255,025 | 3,744,518 | 246,894 | 2,301,790 | 335,114 | 2,975,132 | 497,794 | 2,338,841 | 396,846 |
| 8.075 | | 702.5063 | (M+H)+ | C26 H60 N19 O4 | 875,408 | 128,816 | 654,859 | 79,460 | 1,684,960 | 182,594 | 1,316,127 | 131,752 | 1,577,533 | 240,792 | 971,723 | 153,741 |
| 7.91 | | 688.4909 | (M+H)+ | C26 H54 N23 | 343,197 | 53,561 | 280,487 | 28,333 | 1,004,087 | 92,972 | 644,424 | 69,978 | 675,663 | 114,430 | 379,636 | 52,907 |
| 7.416 | | 738.5323 | (M+H)+ | C36 H80 N7 S4 | 46,185 | 5,671 | 37,130 | 6,502 | 109,561 | 8,487 | 81,431 | 21,207 | 84,087 | 18,553 | 70,039 | 27,401 |
| 7.388 | | 195.1241 | (M+H)+ | C9 H15 N4 O | 292,208 | 105,318 | 342,011 | | | | | | | | | |

A



B



A

An

ES9-11

LS4D

ES10-5

B

An

ES9-11

LS4D+250mMNaCl

ES10-5

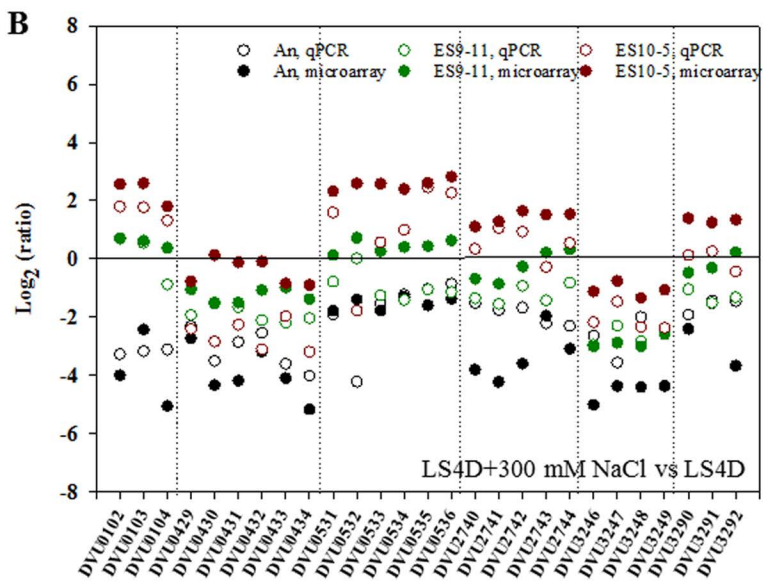
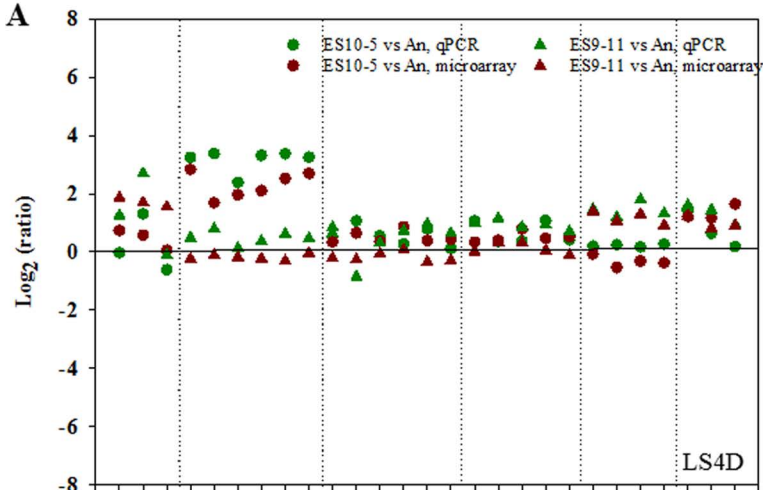
C

An

ES9-11

LS4D+300mMNaCl

ES10-5



| Table S5 Selected genes and gene specific primers for reverse transcription real time PCR | | | |
|--|-------------------------|-------------------------|-------------------|
| Target gene | Forward primer sequence | Reverse primer sequence | Product size (bp) |
| DVU3246 | GACGCATTGTCAGCAACGTA | AACCTGTCTATGGCGTCCTC | 115 |
| DVU3247 | TCGAATCCGTGGACATCAC | ATAGGGTTCCGGCTCGAT | 116 |
| DVU3248 | GTGAAACGACAGGGCGTAAC | AGTGATGCGAAGTTGCTCAG | 116 |
| DVU3249 | CGGCTTTCTCCGTGACTATC | GACCCTGTTCGATGACGATG | 118 |
| DVU3290 | GTTCTTCATCGAAGGCGTGT | TCGGACTGGTAGCCCATGTA | 114 |
| DVU3291 | GTGCGGCCTACAACATCTC | CCATGATGGGAATCTCGTTC | 114 |
| DVU3292 | ATCCTCATCCACGGCAAC | CGGGTTCTGCTTGGTCAT | 114 |
| DVU1068 | GTGTTGCGTCTGCGTTTC | GAAGCTTGTCGGGTCCTTC | 117 |
| DVU1069 | CCCATCCTGTATGCCACTCT | AGGTGCAGGGCGAGAAAC | 116 |
| DVU1070 | CTGTCCTCGACCTTGTGGA | TGATTCGGCGAGAATGTCA | 118 |
| DVU2740 | TCAAGTCCATCATGCGTCTG | CAGCTTGCGTACCACATCAT | 116 |
| DVU2741 | GGCCTCAATTCCGTAGATGT | AGCGACATCACCACCTTC | 113 |
| DVU2742 | GGGAACGCTGTTCTCACTGT | GTGTCGACGCTCATGATTTC | 114 |
| DVU2743 | GGCAGATAGGGGGATTCTTC | GTCTGTAGGCCACCCGTTTC | 117 |
| DVU2744 | AACCGCTACGGCTACATCC | CATCTTGCGGACATCCTTCT | 114 |
| DVU0102 | GCTGGTCATCCTGATGCTCT | ACGTCCTTGACCACGTCCT | 114 |
| DVU0103 | CTCGAACGCACGGGTATC | AGCAGGATGTCGGGTTC | 116 |
| DVU0104 | CTGACAGGGGTGAGATTTCG | GTTCAGGGCCTCGGTCTT | 116 |
| DVU0429 | TCTGCAAGAGCTGCCAGATA | CATCGACGCATACAGAGCAG | 114 |
| DVU0430 | TGGTCATCTCCACCAACATC | GTCATCAGGGCACGGATTT | 115 |
| DVU0431 | CTGACCTTTGACGGTCTGGT | ATGCCTTCTTCTGGATGGTG | 115 |
| DVU0432 | TCAACCATCGCAACAAGAAG | TGTAGCACTCGCGGAACA | 117 |
| DVU0433 | TCGAAGTGCTCATCGACAAC | TGACGTACAGCCAAAGGATG | 114 |
| DVU0434 | CCCTGTCTGCTCTCGGAAT | GTAGAAAAGCAGCGCGAAAT | 116 |
| DVU2378 | CCACCATGCGTGAATACCT | AGGGCAGACTCTCGTAGCC | 118 |
| DVU2086 | GAGTGGTTCGAGAGGAC | CAACATCCCCGTGTCCAT | 116 |
| DVU0525 | CAGATGAAGAACGGCACCTA | CCATATTCCCCACCAGACT | 115 |
| DVU0531 | GCAGGACTCGTGCAACTACA | TAGTTGTGCTCGCGGTTG | 114 |
| DVU0532 | CCTGCATGTGGGCGACTA | CGACATGAAGAACAGCACGA | 115 |
| DVU0533 | CACGAGTTCATGCTCCACAC | ATTTGCGGATCTTCTCGTCA | 115 |
| DVU0534 | CTGGTGCTGACCATCTTCG | CAGGAACGACGAGTACCACA | 114 |
| DVU0535 | CTGCAACGAAGTGAACAAGC | GCGTTGTACCTGTTGACCAC | 117 |
| DVU0536 | ATGACATCCCCGAAAAGGTC | CCAGCTTGCTTTCACCGATA | 117 |
| DVU0094 | CCGTGTTGCTGTGGTTCAC | CATGAAGCGGAGACAGCAT | 117 |
| DVU0862 | TCATCAACGAACTCGACAGC | AGCTTCAGGTGGCACTGAG | 115 |
| DVU2444 | ACACCATCTCCACCCAGTCT | TGTTCTCAAGGCGGTTCTG | 115 |

| Table S6. Expression of genes affected by the big deletions in chromosome or plasmid DNA in LS4D | | | | | | | |
|--|---|--------------------|---------|--------------------|---------|--|--|
| Gene name | Annotation | ES9-11 | | ES10-5 | | location | |
| | | Log ₂ R | Z-score | Log ₂ R | Z-score | | |
| DVU0190 | hypothetical protein | -0.18 | -0.30 | -2.53 | -4.26 | deletion in the chromosome of ES10-5 (231343 to 270532) | |
| DVU0193 | hypothetical protein | -0.68 | -0.84 | -6.17 | -7.77 | | |
| DVU0194 | terminase, large subunit, putative | -0.53 | -0.77 | -2.66 | -3.95 | | |
| DVU0195 | hypothetical protein | -0.48 | -0.79 | -2.16 | -3.52 | | |
| DVU0213 | conserved domain protein | -0.41 | -0.47 | -6.35 | -7.60 | | |
| DVU0220 | tail fiber protein, putative | -0.40 | -0.46 | -5.37 | -6.25 | | |
| DVU0221 | tail fiber assembly protein, putative | -0.34 | -0.34 | -5.09 | -5.22 | | |
| DVU0223 | conserved hypothetical protein | 0.06 | 0.04 | -6.15 | -4.85 | | |
| DVU0224 | conserved hypothetical protein | -0.11 | -0.11 | -5.32 | -5.51 | | |
| DVU0226 | hypothetical protein | -0.44 | -0.39 | -6.26 | -5.88 | | |
| DVU0227 | conserved hypothetical protein | -0.57 | -0.42 | -4.24 | -3.17 | | |
| VIMSS11399146 | hypothetical protein | -0.01 | -0.01 | -7.01 | -6.51 | | |
| DVU0230 | transcriptional regulator cII, putative | -0.21 | -0.33 | -1.65 | -2.55 | | |
| DVU0231 | hypothetical protein | -0.83 | -1.11 | -6.55 | -8.97 | | |
| DVU0232 | hypothetical protein | -0.86 | -1.07 | -3.90 | -4.93 | | |
| VIMSS11399147 | hypothetical protein | -0.77 | -1.07 | -4.07 | -4.56 | | |
| DVU0234 | hypothetical protein | -0.84 | -0.87 | -4.44 | -4.66 | | |
| DVU0235 | hypothetical protein | -0.78 | -0.83 | -7.01 | -7.61 | | |
| DVU0236 | site-specific recombinase, phage integrase family | -0.30 | -0.34 | -4.07 | -4.57 | | |
| DVUA0043 | polysaccharide deacetylase family protein | 0.42 | 0.79 | -1.63 | -3.06 | | deletion in the plasmid of ES10-5 (51979 to 157737) |
| DVUA0044 | conserved hypothetical protein | 0.16 | 0.29 | -2.18 | -4.03 | | |
| DVUA0047 | hypothetical protein | 0.04 | 0.08 | -1.57 | -2.78 | | |
| DVUA0048 | exopolysaccharide production protein, putative | 0.26 | 0.50 | -2.55 | -4.79 | | |
| DVUA0049 | polysaccharide biosynthesis family protein | 0.18 | 0.33 | -2.13 | -3.89 | | |
| DVUA0051 | glycosyl transferase, group 1 family protein | 0.18 | 0.34 | -3.76 | -7.15 | | |
| DVUA0052 | conserved hypothetical protein | 0.04 | 0.07 | -4.52 | -7.71 | | |
| DVUA0053 | conserved hypothetical protein | 0.32 | 0.54 | -2.38 | -4.15 | | |
| DVUA0054 | glycosyl transferase, group 1 family protein | 0.02 | 0.04 | -1.07 | -1.73 | | |
| DVUA0055 | membrane protein, putative | 0.14 | 0.27 | -1.84 | -3.48 | | |
| DVUA0057 | sigma-54 dependent transcriptional regulator/response regulator | 0.20 | 0.36 | -1.82 | -3.19 | | |
| DVUA0058 | BNR/Asp-box repeat protein | 0.37 | 0.59 | -3.79 | -5.99 | | |
| DVUA0060 | membrane protein, putative | 0.05 | 0.09 | -1.19 | -2.16 | | |
| DVUA0061 | membrane protein, putative | 0.16 | 0.29 | -1.71 | -3.05 | | |
| DVUA0062 | conserved domain protein | 0.25 | 0.44 | -2.14 | -3.81 | | |
| DVUA0063 | Om/DAP/Arg family decarboxylase | 0.30 | 0.55 | -1.86 | -3.38 | | |
| DVUA0063.1 | hypothetical protein | 0.33 | 0.59 | -4.07 | -7.39 | | |
| DVUA0064 | gene conserved domain protein | 0.66 | 0.84 | -3.24 | -4.39 | | |
| DVUA0065 | sensor histidine kinase | 0.34 | 0.57 | -2.27 | -3.80 | | |
| DVUA0066 | phospholipase, putatin family | 0.07 | 0.11 | -4.37 | -7.08 | | |
| DVUA0067 | membrane protein, putative | -0.64 | -0.60 | -6.64 | -6.32 | | |
| DVUA0068 | membrane protein, putative | -0.20 | -0.16 | -4.94 | -3.96 | | |
| VIMSS11399254 | hypothetical protein | -0.19 | -0.19 | -5.04 | -5.10 | | |
| DVUA0069 | GtrA family protein, selenocysteine-containing | -0.29 | -0.27 | -6.80 | -6.52 | | |
| DVUA0070 | conserved domain protein | -0.22 | -0.21 | -5.86 | -5.60 | | |
| DVUA0071 | glycosyl transferase, group 1/2 family protein | -0.53 | -0.46 | -5.37 | -4.77 | | |
| DVUA0072 | glycosyl transferase, group 1 family protein | -0.48 | -0.35 | -7.33 | -5.51 | | |
| DVUA0073 | asparagine synthase (glutamine-hydrolyzing), putative | -0.52 | -0.52 | -5.92 | -5.83 | | |
| DVUA0074 | sulfotransferase family protein | -0.53 | -0.38 | -7.00 | -5.07 | | |
| DVUA0075 | radical SAM domain protein | -0.35 | -0.28 | -7.66 | -6.29 | | |
| DVUA0076 | ABC transporter, ATP-binding protein | -0.41 | -0.36 | -8.82 | -7.86 | | |
| DVUA0077 | ABC transporter, permease protein | -0.55 | -0.59 | -6.30 | -6.72 | | |
| DVUA0079(cysC) | adenylylsulfate kinase | -0.17 | -0.14 | -5.01 | -4.23 | | |
| DVUA0080 | glycosyl transferase, group 2 family protein | -0.22 | -0.19 | -6.57 | -5.88 | | |
| DVUA0081 | glycosyl transferase, group 1/2 family protein | -0.04 | -0.05 | -3.73 | -4.77 | | |
| DVUA0082 | site-specific recombinase, phage integrase family | -0.28 | -0.37 | -2.87 | -4.03 | | |
| DVUA0084 | transcriptional regulator, AbrB family | -0.52 | -0.56 | -5.31 | -5.98 | | |
| DVUA0085 | conserved hypothetical protein | -0.11 | -0.14 | -7.36 | -9.18 | | |
| DVUA0086 | response regulator | -0.15 | -0.15 | -6.44 | -6.94 | | |
| VIMSS11399255 | hypothetical protein | -0.51 | -0.44 | -6.45 | -5.55 | | |
| DVUA0087 | sensory box histidine kinase | -0.02 | -0.02 | -3.49 | -4.51 | | |
| DVUA0088 | conserved hypothetical protein | -0.05 | -0.07 | -5.64 | -7.53 | | |
| DVUA0089 | hypothetical protein | -0.22 | -0.40 | -1.90 | -3.45 | | |
| DVUA0090 | membrane protein, putative | 0.00 | 0.00 | -2.94 | -4.74 | | |
| DVUA0091 | catalsase | -0.18 | -0.16 | -4.87 | -4.29 | | |
| DVUA0092 | hypothetical protein | -2.22 | -2.51 | -6.76 | -7.75 | | |
| DVUA0093 | chromate transport family protein | -0.07 | -0.10 | -1.20 | -1.88 | | |
| DVUA0094(csrB) | chrB protein | 0.16 | 0.25 | -2.19 | -3.46 | | |
| VIMSS11399257 | hypothetical protein | -0.25 | -0.42 | -3.37 | -5.68 | | |
| DVUA0096 | major facilitator superfamily protein | 0.43 | 0.79 | -1.76 | -3.35 | | |
| DVUA0097 | radical SAM domain protein | -0.35 | -0.40 | -3.67 | -4.21 | | |
| DVUA0098 | dehydrogenase, putative | 0.27 | 0.30 | -5.97 | -7.28 | | |
| DVUA0099 | HAMP domain protein | -0.39 | -0.39 | -6.45 | -6.52 | | |
| DVUA0100(trC) | sigma-54 dependent transcriptional regulator | -0.20 | -0.21 | -5.14 | -5.42 | | |
| DVUA0101(fhbB) | type III secretion protein, hrpY/hrcU family | -0.35 | -0.43 | -4.91 | -6.09 | | |
| DVUA0102(escT) | type III secretion inner membrane protein | 0.09 | 0.13 | -2.07 | -3.08 | | |
| DVUA0103(mvX) | type III secretion protein, HrpO family | -0.01 | -0.01 | -4.90 | -7.15 | | |
| DVUA0104(escI') | type III secretion inner membrane protein, HrcV family | -0.26 | -0.34 | -3.97 | -5.18 | | |
| VIMSS11399261 | hypothetical protein | -0.30 | -0.39 | -4.14 | -5.57 | | |
| DVUA0105 | conserved hypothetical protein | -0.28 | -0.38 | -4.45 | -6.26 | | |
| DVUA0106 | type III secretion target, YopN family | -0.29 | -0.33 | -5.03 | -5.90 | | |
| DVUA203 | hypothetical protein | -0.39 | -0.37 | -4.72 | -4.46 | | |
| DVUA0108 | hypothetical protein | -0.66 | -0.61 | -5.65 | -5.41 | | |
| DVUA0109 | type III secretion system chaperone, LerH/SycD family | -0.34 | -0.30 | -6.65 | -6.00 | | |
| DVUA0110 | type III secretion system target, YopB family | -0.31 | -0.32 | -5.97 | -6.40 | | |
| DVUA0111 | type III secretion system protein, IpaC family, putative | -0.32 | -0.33 | -4.22 | -4.47 | | |
| DVUA201 | hypothetical protein | -0.29 | -0.26 | -3.96 | -3.62 | | |
| DVUA0112 | type III secretion system protein, YscC family | -0.24 | -0.26 | -2.90 | -3.07 | | |
| DVUA0113 | type III secretion protein, YscD family | -0.52 | -0.48 | -5.03 | -4.82 | | |
| DVUA0115 | type III secretion system protein, YscF family | -0.44 | -0.42 | -6.75 | -6.71 | | |
| DVUA0116 | conserved hypothetical protein | -0.30 | -0.28 | -4.55 | -4.34 | | |
| VIMSS11399264 | hypothetical protein | -0.28 | -0.31 | -6.79 | -7.93 | | |
| DVUA0117(escJ) | type III secretion lipoprotein | -0.47 | -0.60 | -4.88 | -6.44 | | |
| DVUA200 | hypothetical protein | -0.24 | -0.24 | -5.21 | -5.39 | | |
| DVUA0118 | type III secretion protein, YopL family | -0.21 | -0.21 | -4.60 | -4.82 | | |
| DVUA0119(escV) | type III secretion system ATPase | -0.19 | -0.22 | -3.60 | -4.37 | | |
| DVUA0119.1 | hypothetical protein | -0.23 | -0.24 | -2.75 | -3.03 | immediate downstream of the deletion in plasmid of ES10-5, to the last gene of the affected operon | |
| DVUA0120 | type III secretion protein, putative | -0.53 | -0.45 | -3.18 | -2.71 | | |
| DVUA0121 | type III secretion system protein, YopQ family | -0.38 | -0.48 | -1.96 | -2.56 | | |
| DVUA0122(yscR) | type III secretion system protein, YscR family | -0.36 | -0.45 | -1.84 | -2.34 | | |
| DVUA0123 | anti-sigma factor | -0.14 | -0.14 | -2.43 | -2.67 | | |
| DVUA0124 | sigma factor serine-protein kinase | -0.24 | -0.28 | -1.97 | -2.36 | | |
| DVUA0125(stl) | transglycosylase, SLT family | -0.22 | -0.30 | -1.12 | -1.58 | | |
| DVU1779 | hypothetical protein | -6.58 | -9.06 | 0.06 | 0.06 | | deletion in the chromosome of ES9-11 (1842155 to 1849967) |
| DVU1780 | conserved hypothetical protein | -7.78 | -8.39 | 0.06 | 0.04 | | |
| DVU1781 | conserved hypothetical protein | -4.94 | -3.91 | 0.66 | 0.82 | | |
| DVU1782 | iron-sulfur cluster-binding protein | -6.69 | -6.09 | -0.05 | -0.04 | | |
| DVU1783 | cysteine-rich domain protein | -7.25 | -5.69 | -0.21 | -0.17 | | |
| DVU1784 | oxalobredactase, short-chain dehydrogenase/reductase family | -7.16 | -6.16 | 0.14 | 0.11 | | |
| DVU1785 | membrane protein, MarC family | -5.13 | -5.74 | 0.03 | 0.02 | | |
| DVU1786 | GGDEF domain protein | -7.05 | -6.44 | -0.22 | -0.04 | | |

| Table S7. High salinity induced gene expression changes | | | | | | |
|---|---|--------------------|--------------|--------------------|--------------|--|
| Locus Tag | Annotation | ES9-11 | | ES10-5 | | |
| | | Log ₂ R | Z-score | Log ₂ R | Z-score | |
| General stress response | | | | | | |
| DVU2986 | phage shock protein C | 1.69 | 2.13 | 0.98 | 1.00 | |
| DVU2987 | hypothetical protein | -0.82 | -0.28 | 0.18 | 0.17 | |
| DVU2988 | phage shock protein A | 1.65 | 1.34 | 0.79 | 0.53 | |
| DVU2441 | HSP20 family protein | 2.18 | 1.68 | 1.17 | 0.79 | |
| DVU2442 | HSP20 family protein | 1.19 | 1.17 | 0.61 | 0.46 | |
| Replication, recombination and repair | | | | | | |
| DVUA0004 | DNA-binding protein HU, putative | 0.30 | 0.53 | 1.65 | 1.63 | |
| DVU3256(<i>mutM</i>) | formamidopyrimidine-DNA glycosylase | -1.90 | -3.47 | -0.65 | -0.96 | |
| General function or function unknown | | | | | | |
| DVU0308 | hypothetical protein | 2.13 | 3.06 | 1.87 | 1.91 | |
| DVU1971 | hypothetical protein | 2.07 | 2.28 | 2.07 | 1.91 | |
| DVU0065 | hypothetical protein | 1.53 | 2.60 | 2.49 | 2.77 | |
| DVU1092 | sodium-dependent symporter family protein | -1.92 | -3.27 | -1.90 | -2.55 | |
| DVU2345 | hypothetical protein | -2.38 | -3.40 | -2.97 | -4.40 | |
| DVU2429 | hypothetical protein | -1.63 | -2.16 | -1.45 | -1.55 | |
| DVU2431 | hypothetical protein | -2.29 | -3.74 | -2.03 | -2.91 | |
| DVU2676 | hypothetical protein | -1.49 | -1.36 | -2.21 | -2.07 | |
| DVU2626 | hypothetical protein | -1.84 | -2.49 | -1.57 | -1.76 | |
| DVU3298 | hypothetical protein | -1.11 | -2.03 | -2.65 | -4.01 | |
| DVU3299 | hypothetical protein | -0.89 | -1.72 | -3.56 | -5.25 | |
| DVU3300 | hypothetical protein | -2.25 | -4.37 | -4.06 | -5.63 | |
| DVU3301 | hypothetical protein | -1.64 | -3.20 | -4.35 | -6.63 | |
| DVU3302 | hypothetical protein | -1.77 | -3.39 | -4.44 | -6.56 | |
| DVU0616 | hypothetical protein | -1.29 | -2.36 | -1.18 | -1.85 | |
| DVU0617 | hypothetical protein | -1.68 | -2.75 | -2.13 | -3.23 | |
| DVU2789 | Gpr1/Fun34/YaaH family protein | -2.41 | -4.27 | -1.97 | -2.60 | |
| DVU0729 | hypothetical protein DVU0729 | -1.00 | -1.62 | -1.92 | -2.32 | |
| DVU2631 | hypothetical protein | -0.24 | -0.47 | 1.60 | 2.40 | |
| DVU3130 | hypothetical protein | -0.31 | -0.49 | -2.03 | -2.27 | |
| DVU0475 | membrane protein, putative, truncation | -0.65 | -0.98 | -1.65 | -1.55 | |
| DVU3384(<i>zraP</i>) | zinc resistance-associated protein | 1.77 | 1.61 | 0.09 | 0.08 | |
| DVU0383 | hypothetical protein | -1.50 | -2.65 | -0.23 | -0.35 | |
| DVU0614 | hypothetical protein | -1.62 | -2.57 | -0.90 | -0.96 | |
| DVU1991 | hypothetical protein | -1.72 | -3.21 | -0.22 | -0.37 | |
| DVU2187 | hypothetical protein | -1.70 | -3.36 | -0.59 | -1.14 | |
| DVU2625 | hypothetical protein | -1.63 | -2.11 | -0.35 | -0.42 | |
| DVU3166 | alanyl-tRNA synthetase family protein, | -1.60 | -2.82 | -0.37 | -0.45 | |
| DVU3255 | CopG family transcriptional regulator | -1.71 | -2.82 | -0.84 | -0.95 | |
| DVU0008 | hypothetical protein DVU0008 | -1.75 | -3.32 | -0.58 | -1.02 | |

Operons are separated by lines. Bold font indicates more than two folds of significant expression changes.