|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Allele | Coverage | Depth | Diffs | Divergence | Length | maxMAF | Clusterid | Annotation |
| ail\_CVF037\_VFG023567 | 100 | 174,009 |  | 0 | 537 | 0,013 | 387 | (ail) attachment invasion locus protein [Ail (CVF037)] [Yersinia enterocolitica subsp. palearctica 105.5R(r)] |
| cheA\_AI145\_VFG043211 | 100 | 175,268 | 32snp | 1,557 | 2055 | 0,068 | 40 | (cheA) chemotaxis protein CheA [peritrichous flagella (AI145)] [Yersinia enterocolitica subsp. enterocolitica 8081] |
| cheB\_AI145\_VFG043207 | 100 | 150,833 | 6snp | 0,571 | 1050 | 0,013 | 199 | (cheB) chemotaxis-specific methylesterase CheB [peritrichous flagella (AI145)] [Yersinia enterocolitica subsp. enterocolitica 8081] |
| cheD\_AI145\_VFG043209 | 99,881 | 175,069 | 23snp2holes | 1,376 | 1674 | 0,32 | 66 | (cheD) methyl-accepting chemotaxis protein CheD [peritrichous flagella (AI145)] [Yersinia enterocolitica subsp. enterocolitica 8081] |
| cheR\_AI145\_VFG043208 | 100 | 164,391 | 6snp | 0,725 | 828 | 0,371 | 284 | (cheR) chemotaxis methyltransferase CheR [peritrichous flagella (AI145)] [Yersinia enterocolitica subsp. enterocolitica 8081] |
| cheW\_AI145\_VFG043210 | 100 | 154,184 | 3snp | 0,602 | 498 | 0,013 | 400 | (cheW) purine-binding chemotaxis protein CheW [peritrichous flagella (AI145)] [Yersinia enterocolitica subsp. enterocolitica 8081] |
| cheY\_AI145\_VFG043206 | 100 | 171,847 |  | 0 | 390 | 0,066 | 457 | (cheY) chemotaxis regulatory protein CheY [peritrichous flagella (AI145)] [Yersinia enterocolitica subsp. enterocolitica 8081] |
| cheZ\_AI145\_VFG043205 | 99,845 | 159,74 | 2snp1holes | 0,311 | 645 | 0,013 | 355 | (cheZ) chemotaxis regulator CheZ [peritrichous flagella (AI145)] [Yersinia enterocolitica subsp. enterocolitica 8081] |
| flgA\_CVF039\_VFG023682 | 100 | 157,949 | 1snp | 0,147 | 681 | 0,231 | 341 | (flgA) flagellar basal body P-ring biosynthesis protein FlgA [Flagella (cluster I) (CVF039)] [Yersinia enterocolitica subsp. palearctica 105.5R(r)] |
| flgB\_CVF039\_VFG002680 | 91,787 | 95,916 | 35snp34holes | 9,211 | 414 | 0,01 | 442 | (flgB) flagellar basal body rod protein [Flagella (cluster I) (CVF039)] [Yersinia pestis CO92] |
| flgB\_CVF039\_VFG023680 | 100 | 149,251 |  | 0 | 414 | 0,008 | 441 | (flgB) flagellar basal body rod protein FlgB [Flagella (cluster I) (CVF039)] [Yersinia enterocolitica subsp. palearctica 105.5R(r)] |
| flgC\_CVF039\_VFG023678 | 100 | 151,586 | 1snp | 0,247 | 405 | 0,01 | 446 | (flgC) flagellar basal body rod protein FlgC [Flagella (cluster I) (CVF039)] [Yersinia enterocolitica subsp. palearctica 105.5R(r)] |
| flgD\_CVF039\_VFG023676 | 100 | 154,222 | 1snp | 0,146 | 687 | 0,026 | 339 | (flgD) flagellar basal body rod modification protein [Flagella (cluster I) (CVF039)] [Yersinia enterocolitica subsp. palearctica 105.5R(r)] |
| flgE\_CVF039\_VFG023674 | 100 | 159,002 |  | 0 | 1260 | 0,256 | 136 | (flgE) flagellar hook protein FlgE [Flagella (cluster I) (CVF039)] [Yersinia enterocolitica subsp. palearctica 105.5R(r)] |
| flgF\_CVF039\_VFG023672 | 100 | 150,952 | 1snp | 0,132 | 756 | 0,259 | 311 | (flgF) flagellar basal body rod protein FlgF [Flagella (cluster I) (CVF039)] [Yersinia enterocolitica subsp. palearctica 105.5R(r)] |
| flgG\_CVF039\_VFG023670 | 100 | 157,684 |  | 0 | 783 | 0,201 | 306 | (flgG) flagellar basal-body rod protein FlgG [Flagella (cluster I) (CVF039)] [Yersinia enterocolitica subsp. palearctica 105.5R(r)] |
| flgH\_CVF039\_VFG023668 | 100 | 157,164 | 1snp | 0,139 | 717 | 0,022 | 329 | (flgH) flagellar basal body L-ring protein [Flagella (cluster I) (CVF039)] [Yersinia enterocolitica subsp. palearctica 105.5R(r)] |
| flgI\_CVF039\_VFG023666 | 100 | 162,873 | 2snp | 0,178 | 1122 | 0,223 | 172 | (flgI) flagellar basal body P-ring protein [Flagella (cluster I) (CVF039)] [Yersinia enterocolitica subsp. palearctica 105.5R(r)] |
| flgJ\_CVF039\_VFG023664 | 100 | 154,374 | 2snp | 0,208 | 963 | 0,014 | 241 | (flgJ) flagellar rod assembly protein/muramidase FlgJ [Flagella (cluster I) (CVF039)] [Yersinia enterocolitica subsp. palearctica 105.5R(r)] |
| flgK\_CVF039\_VFG023662 | 100 | 180,248 | 3snp | 0,18 | 1665 | 0,155 | 68 | (flgK) flagellar hook-associated protein FlgK [Flagella (cluster I) (CVF039)] [Yersinia enterocolitica subsp. palearctica 105.5R(r)] |
| flgL\_CVF039\_VFG023660 | 100 | 175,626 |  | 0 | 981 | 0,018 | 231 | (flgL) flagellar hook-associated protein FlgL [Flagella (cluster I) (CVF039)] [Yersinia enterocolitica subsp. palearctica 105.5R(r)] |
| flgM\_CVF039\_VFG023684 | 100 | 134,787 |  | 0 | 300 | 0,013 | 481 | (flgM) anti-sigma28 factor FlgM [Flagella (cluster I) (CVF039)] [Yersinia enterocolitica subsp. palearctica 105.5R(r)] |
| flgN\_CVF039\_VFG023686 | 100 | 152,579 | 2snp | 0,454 | 441 | 0,011 | 429 | (flgN) flagella synthesis protein FlgN [Flagella (cluster I) (CVF039)] [Yersinia enterocolitica subsp. palearctica 105.5R(r)] |
| flhA\_CVF039\_VFG023690 | 100 | 172,165 | 3snp1indel | 0,144 | 2079 | 0,029 | 36 | (flhA) flagellar biosynthesis protein FlhA [Flagella (cluster I) (CVF039)] [Yersinia enterocolitica subsp. palearctica 105.5R(r)] |
| flhB\_CVF039\_VFG023692 | 100 | 171,169 | 1snp | 0,087 | 1152 | 0,064 | 164 | (flhB) flagellar biosynthesis protein FlhB [Flagella (cluster I) (CVF039)] [Yersinia enterocolitica subsp. palearctica 105.5R(r)] |
| flhC\_CVF039\_VFG002942 | 90,206 | 75,498 | 55snp57holes | 10,476 | 582 | 0,037 | 371 | (flhC) flagellum biosynthesis transcription activator [Flagella (cluster I) (CVF039)] [Yersinia pestis Antiqua] |
| flhC\_CVF039\_VFG023694 | 100 | 160,712 | 1snp | 0,172 | 582 | 0,049 | 373 | (flhC) transcriptional activator FlhC [Flagella (cluster I) (CVF039)] [Yersinia enterocolitica subsp. palearctica 105.5R(r)] |
| flhD\_CVF039\_VFG002943 | 99,612 | 58,452 | 25snp1indel | 9,69 | 258 | 0,013 | 494 | (flhD) hypothetical protein [Flagella (cluster I) (CVF039)] [Yersinia pestis Antiqua] |
| flhD\_VF0394\_VFG002359 | 100 | 150,241 | trun | 0 | 360 | 0,014 | 468 | (flhD) flagellar transcriptional activator FlhD [Flagella (VF0394)] [Yersinia enterocolitica subsp. enterocolitica 8081] |
| flhE\_CVF039\_VFG023688 | 100 | 166,03 |  | 0 | 393 | 0,01 | 436 | (flhE) flagellar protein FlhE precursor [Flagella (cluster I) (CVF039)] [Yersinia enterocolitica subsp. palearctica 105.5R(r)] |
| fliA\_CVF039\_VFG023620 | 100 | 160,641 | 1snp | 0,138 | 723 | 0,129 | 324 | (fliA) flagellar biosynthesis sigma factor [Flagella (cluster I) (CVF039)] [Yersinia enterocolitica subsp. palearctica 105.5R(r)] |
| fliB\_CVF039\_VFG023622 | 100 | 171,963 |  | 0 | 1206 | 0,019 | 150 | (fliB) flagellin lysine-N-methylase [Flagella (cluster I) (CVF039)] [Yersinia enterocolitica subsp. palearctica 105.5R(r)] |
| fliC\_CVF039\_VFG023626 | 100 | 404,361 | 12snp | 1,081 | 1110 | 0,494 | 177 | (fliC) flagellin [Flagella (cluster I) (CVF039)] [Yersinia enterocolitica subsp. palearctica 105.5R(r)] |
| fliC\_CVF039\_VFG023624 | 100 | 374,822 | 12snp | 1,047 | 1146 | 0,46 | 167 | (fliC) flagellin [Flagella (cluster I) (CVF039)] [Yersinia enterocolitica subsp. palearctica 105.5R(r)] |
| fliD\_CVF039\_VFG023628 | 100 | 180,561 | 4snp | 0,286 | 1401 | 0,292 | 95 | (fliD) flagellar capping protein [Flagella (cluster I) (CVF039)] [Yersinia enterocolitica subsp. palearctica 105.5R(r)] |
| fliE\_CVF039\_VFG023633 | 100 | 133,928 |  | 0 | 318 | 0,014 | 476 | (fliE) flagellar hook-basal body protein FliE [Flagella (cluster I) (CVF039)] [Yersinia enterocolitica subsp. palearctica 105.5R(r)] |
| fliF\_VF0394\_VFG002328 | 99,353 | 181,325 | 19snp11holes | 1,124 | 1701 | 0,041 | 59 | (fliF) flagellar M-ring protein FliF [Flagella (VF0394)] [Yersinia enterocolitica subsp. enterocolitica 8081] |
| fliF\_CVF039\_VFG023635 | 100 | 184,522 | 2snp | 0,119 | 1680 | 0,022 | 65 | (fliF) flagellar MS-ring protein [Flagella (cluster I) (CVF039)] [Yersinia enterocolitica subsp. palearctica 105.5R(r)] |
| fliG\_CVF039\_VFG023637 | 100 | 172,851 |  | 0 | 993 | 0,014 | 223 | (fliG) flagellar motor switch protein G [Flagella (cluster I) (CVF039)] [Yersinia enterocolitica subsp. palearctica 105.5R(r)] |
| fliG\_CVF039\_VFG003416 | 90,332 | 50,442 | 100snp96holes | 11,148 | 993 | 0,036 | 224 | (fliG) flagellar motor protein [Flagella (cluster I) (CVF039)] [Yersinia pseudotuberculosis IP 32953] |
| fliH\_CVF039\_VFG023639 | 100 | 167,952 | 2snp | 0,277 | 723 | 0,013 | 325 | (fliH) flagellar assembly protein H [Flagella (cluster I) (CVF039)] [Yersinia enterocolitica subsp. palearctica 105.5R(r)] |
| fliI\_CVF039\_VFG023641 | 100 | 168,474 |  | 0 | 1365 | 0,149 | 104 | (fliI) flagellum-specific ATP synthase [Flagella (cluster I) (CVF039)] [Yersinia enterocolitica subsp. palearctica 105.5R(r)] |
| fliJ\_CVF039\_VFG023643 | 100 | 156,478 |  | 0 | 447 | 0,015 | 422 | (fliJ) flagellar biosynthesis chaperone [Flagella (cluster I) (CVF039)] [Yersinia enterocolitica subsp. palearctica 105.5R(r)] |
| fliK\_CVF039\_VFG023645 | 100 | 153,704 | 2snp | 0,147 | 1359 | 0,257 | 107 | (fliK) flagellar hook-length control protein FliK [Flagella (cluster I) (CVF039)] [Yersinia enterocolitica subsp. palearctica 105.5R(r)] |
| fliL\_CVF039\_VFG023647 | 100 | 163,786 |  | 0 | 471 | 0,113 | 413 | (fliL) flagellar basal body-associated protein FliL [Flagella (cluster I) (CVF039)] [Yersinia enterocolitica subsp. palearctica 105.5R(r)] |
| fliM\_CVF039\_VFG023649 | 100 | 173,324 |  | 0 | 1005 | 0,017 | 218 | (fliM) flagellar motor switch protein FliM [Flagella (cluster I) (CVF039)] [Yersinia enterocolitica subsp. palearctica 105.5R(r)] |
| fliN\_CVF039\_VFG023651 | 100 | 143,396 |  | 0 | 375 | 0,051 | 438 | (fliN) flagellar motor switch protein FliN [Flagella (cluster I) (CVF039)] [Yersinia enterocolitica subsp. palearctica 105.5R(r)] |
| fliO\_CVF039\_VFG023653 | 100 | 160,96 | 2snp | 0,353 | 567 | 0,024 | 381 | (fliO) flagellar protein FliO [Flagella (cluster I) (CVF039)] [Yersinia enterocolitica subsp. palearctica 105.5R(r)] |
| fliP\_CVF039\_VFG023655 | 99,867 | 166,952 | 1indel | 0 | 753 | 0,311 | 313 | (fliP) flagellar biosynthesis protein FliP [Flagella (cluster I) (CVF039)] [Yersinia enterocolitica subsp. palearctica 105.5R(r)] |
| fliQ\_CVF039\_VFG023657 | 100 | 121,561 |  | 0 | 270 | 0,098 | 487 | (fliQ) flagellar biosynthesis protein FliQ [Flagella (cluster I) (CVF039)] [Yersinia enterocolitica subsp. palearctica 105.5R(r)] |
| fliR\_CVF039\_VFG023658 | 100 | 160,205 | 6snp | 0,766 | 783 | 0,037 | 304 | (fliR) flagellar biosynthesis protein FliR [Flagella (cluster I) (CVF039)] [Yersinia enterocolitica subsp. palearctica 105.5R(r)] |
| fliS\_CVF039\_VFG023630 | 100 | 138,557 | 1snp | 0,292 | 342 | 0,014 | 451 | (fliS) flagellar protein FliS [Flagella (cluster I) (CVF039)] [Yersinia enterocolitica subsp. palearctica 105.5R(r)] |
| fliT\_CVF039\_VFG023632 | 100 | 147,011 |  | 0 | 363 | 0,012 | 466 | (fliT) flagellar biosynthesis protein FliT [Flagella (cluster I) (CVF039)] [Yersinia enterocolitica subsp. palearctica 105.5R(r)] |
| fliZ\_CVF039\_VFG023618 | 100 | 148,523 |  | 0 | 510 | 0,015 | 394 | (fliZ) flagella biosynthesis protein FliZ [Flagella (cluster I) (CVF039)] [Yersinia enterocolitica subsp. palearctica 105.5R(r)] |
| hemP\_IA059\_VFG044241 | 100 | 191,802 | 7snp | 2,846 | 246 | 0,013 | 499 | (hemP) hemin uptake protein [direct heme uptake system (IA059)] [Yersinia enterocolitica subsp. enterocolitica 8081] |
| hemR\_IA059\_VFG044240 | 100 | 211,3 | 25snp | 1,211 | 2064 | 0,016 | 39 | (hemR) hemin receptor precursor [direct heme uptake system (IA059)] [Yersinia enterocolitica subsp. enterocolitica 8081] |
| hemS\_IA059\_VFG044239 | 100 | 213,098 | 17snp | 1,638 | 1038 | 0,021 | 205 | (hemS) hemin transport protein [direct heme uptake system (IA059)] [Yersinia enterocolitica subsp. enterocolitica 8081] |
| hemT\_IA059\_VFG044238 | 100 | 225,478 | 10snp | 1,19 | 840 | 0,055 | 281 | (hemT) hemin-binding periplasmic protein [direct heme uptake system (IA059)] [Yersinia enterocolitica subsp. enterocolitica 8081] |
| hemU\_IA059\_VFG044237 | 100 | 219,359 | 11snp | 1,095 | 1005 | 0,088 | 221 | (hemU) hemin transport system permease protein HmuU [direct heme uptake system (IA059)] [Yersinia enterocolitica subsp. enterocolitica 8081] |
| hmuV\_IA059\_VFG044236 | 98,502 | 209,294 | 22snp12holes | 2,788 | 801 | 0,016 | 295 | (hmuV) hemin importer ATP-binding subunit [direct heme uptake system (IA059)] [Yersinia enterocolitica subsp. enterocolitica 8081] |
| inv\_VF0131\_VFG000356 | 100 | 175,714 | 20snp | 0,797 | 2508 | 0,402 | 27 | (inv) invasin [Invasin (VF0131)] [Yersinia enterocolitica W1024] |
| motA\_AI145\_VFG043213 | 100 | 168,304 | 8snp | 0,901 | 888 | 0,213 | 266 | (motA) flagellar motor protein MotA [peritrichous flagella (AI145)] [Yersinia enterocolitica subsp. enterocolitica 8081] |
| motB\_AI145\_VFG043212 | 100 | 173,356 | 17snp | 1,365 | 1245 | 0,36 | 139 | (motB) flagellar motor protein MotB [peritrichous flagella (AI145)] [Yersinia enterocolitica subsp. enterocolitica 8081] |
| myfB\_AI049\_VFG042601 | 100 | 155,225 | 7snp | 0,871 | 804 | 0,022 | 291 | (myfB) chaperone protein [Mucoid Yersinia factor Myf fimbriae (AI049)] [Yersinia enterocolitica subsp. enterocolitica 8081] |
| myfC\_AI049\_VFG042602 | 99,829 | 153,939 | 79snp4holes | 3,386 | 2337 | 0,052 | 32 | (myfC) outer membrane usher protein [Mucoid Yersinia factor Myf fimbriae (AI049)] [Yersinia enterocolitica subsp. enterocolitica 8081] |
| myfE\_AI049\_VFG042599 | 100 | 163,472 | 3snp | 0,45 | 666 | 0,024 | 346 | (myfE) putative regulatory protein [Mucoid Yersinia factor Myf fimbriae (AI049)] [Yersinia enterocolitica subsp. enterocolitica 8081] |
| myfF\_AI049\_VFG042600 | 100 | 136,513 | 4snp | 0,813 | 492 | 0,02 | 406 | (myfF) hypothetical protein [Mucoid Yersinia factor Myf fimbriae (AI049)] [Yersinia enterocolitica subsp. enterocolitica 8081] |
| pla\_CVF044\_VFG023775 | 100 | 169,934 | 20snp | 2,137 | 936 | 0,097 | 255 | (pla) Peptidase A26 omptin [Pla (CVF044)] [Yersinia enterocolitica subsp. palearctica 105.5R(r)] |
| psaA\_CVF042\_VFG023569 | 100 | 145,11 |  | 0 | 480 | 0,122 | 410 | (psaA) pH 6 antigen precursor [Myf/pH6 antigen (CVF042)] [Yersinia enterocolitica subsp. palearctica 105.5R(r)] |
| YE105\_C0173\_CVF043\_VFG023778 | 100 | 223,447 |  | 0 | 1077 | 0,014 | 190 | (YE105\_C0173) lipopolysaccharide biosynthesis protein WzzE [O-antigen (CVF043)] [Yersinia enterocolitica subsp. palearctica 105.5R(r)] |
| YE105\_C0309\_CVF046\_VFG023572 | 100 | 190,222 | 1snp | 0,158 | 633 | 0,144 | 358 | (YE105\_C0309) putative two-component response regulator [TTSS (chromosomally encoded) (CVF046)] [Yersinia enterocolitica subsp. palearctica 105.5R(r)] |
| YE105\_C0310\_CVF046\_VFG023574 | 100 | 228,54 | 3snp | 0,108 | 2781 | 0,015 | 23 | (YE105\_C0310) Multi-sensor hybrid histidine kinase [TTSS (chromosomally encoded) (CVF046)] [Yersinia enterocolitica subsp. palearctica 105.5R(r)] |
| YE105\_C0312\_CVF046\_VFG023576 | 100 | 225,972 | 2snp | 0,135 | 1482 | 0,177 | 88 | (YE105\_C0312) type III secretion outer membrane pore YscC/HrcC family [TTSS (chromosomally encoded) (CVF046)] [Yersinia enterocolitica subsp. palearctica 105.5R(r)] |
| YE105\_C0313\_CVF046\_VFG023578 | 100 | 229,2 |  | 0 | 1212 | 0,09 | 147 | (YE105\_C0313) type-III secretion protein [TTSS (chromosomally encoded) (CVF046)] [Yersinia enterocolitica subsp. palearctica 105.5R(r)] |
| YE105\_C0314\_CVF046\_VFG023580 | 100 | 156,143 | 2snp | 0,926 | 216 | 0,015 | 504 | (YE105\_C0314) type III secretion apparatus [TTSS (chromosomally encoded) (CVF046)] [Yersinia enterocolitica subsp. palearctica 105.5R(r)] |
| YE105\_C0323\_CVF046\_VFG023581 | 100 | 213,91 |  | 0 | 708 | 0,115 | 334 | (YE105\_C0323) AraC family transcriptional regulator [TTSS (chromosomally encoded) (CVF046)] [Yersinia enterocolitica subsp. palearctica 105.5R(r)] |
| YE105\_C0324\_CVF046\_VFG023583 | 100 | 161,332 |  | 0 | 216 | 0,012 | 505 | (YE105\_C0324) Secretion system apparatus [TTSS (chromosomally encoded) (CVF046)] [Yersinia enterocolitica subsp. palearctica 105.5R(r)] |
| YE105\_C0325\_CVF046\_VFG023584 | 100 | 166,69 |  | 0 | 276 | 0,131 | 486 | (YE105\_C0325) type III secretion apparatus [TTSS (chromosomally encoded) (CVF046)] [Yersinia enterocolitica subsp. palearctica 105.5R(r)] |
| YE105\_C0326\_CVF046\_VFG023585 | 100 | 179,144 |  | 0 | 249 | 0,058 | 498 | (YE105\_C0326) hypothetical protein [TTSS (chromosomally encoded) (CVF046)] [Yersinia enterocolitica subsp. palearctica 105.5R(r)] |
| YE105\_C0327\_CVF046\_VFG023586 | 100 | 208,849 |  | 0 | 732 | 0,017 | 323 | (YE105\_C0327) type III secretion system apparatus lipoprotein [TTSS (chromosomally encoded) (CVF046)] [Yersinia enterocolitica subsp. palearctica 105.5R(r)] |
| YE105\_C0328\_CVF046\_VFG023588 | 100 | 195,603 |  | 0 | 594 | 0,135 | 366 | (YE105\_C0328) hypothetical protein [TTSS (chromosomally encoded) (CVF046)] [Yersinia enterocolitica subsp. palearctica 105.5R(r)] |
| YE105\_C0332\_CVF046\_VFG023592 | 100 | 220,868 | 3snp | 0,147 | 2040 | 0,014 | 42 | (YE105\_C0332) Secretion system apparatus protein ssaV [TTSS (chromosomally encoded) (CVF046)] [Yersinia enterocolitica subsp. palearctica 105.5R(r)] |
| YE105\_C0333\_CVF046\_VFG023594 | 100 | 215,317 | 7snp | 0,516 | 1356 | 0,222 | 109 | (YE105\_C0333) Secretion system apparatus ATP synthase ssaN [TTSS (chromosomally encoded) (CVF046)] [Yersinia enterocolitica subsp. palearctica 105.5R(r)] |
| YE105\_C0334\_CVF046\_VFG023596 | 100 | 199,298 | 3snp | 0,8 | 375 | 0,016 | 460 | (YE105\_C0334) type III secretion system apparatus protein [TTSS (chromosomally encoded) (CVF046)] [Yersinia enterocolitica subsp. palearctica 105.5R(r)] |
| YE105\_C0335\_CVF046\_VFG023598 | 100 | 169,803 | 3snp | 0,752 | 399 | 0,012 | 454 | (YE105\_C0335) hypothetical protein [TTSS (chromosomally encoded) (CVF046)] [Yersinia enterocolitica subsp. palearctica 105.5R(r)] |
| YE105\_C0336\_CVF046\_VFG023600 | 100 | 211,996 | 3snp | 0,316 | 948 | 0,206 | 249 | (YE105\_C0336) type III secretion system apparatus protein [TTSS (chromosomally encoded) (CVF046)] [Yersinia enterocolitica subsp. palearctica 105.5R(r)] |
| YE105\_C0338\_CVF046\_VFG023602 | 100 | 219,347 |  | 0 | 651 | 0,01 | 352 | (YE105\_C0338) type III secretion apparatus protein YscR/HrcR family [TTSS (chromosomally encoded) (CVF046)] [Yersinia enterocolitica subsp. palearctica 105.5R(r)] |
| YE105\_C0339\_CVF046\_VFG023604 | 100 | 179,694 |  | 0 | 270 | 0,076 | 490 | (YE105\_C0339) type III secretion system protein [TTSS (chromosomally encoded) (CVF046)] [Yersinia enterocolitica subsp. palearctica 105.5R(r)] |
| YE105\_C0340\_CVF046\_VFG023605 | 100 | 225,119 | 1snp | 0,126 | 795 | 0,208 | 298 | (YE105\_C0340) type III secretory pathway component EscT [TTSS (chromosomally encoded) (CVF046)] [Yersinia enterocolitica subsp. palearctica 105.5R(r)] |
| YE105\_C0341\_CVF046\_VFG023607 | 100 | 243,457 |  | 0 | 1077 | 0,03 | 189 | (YE105\_C0341) type III secretion protein YscU/HrpY family [TTSS (chromosomally encoded) (CVF046)] [Yersinia enterocolitica subsp. palearctica 105.5R(r)] |
| YE105\_C0912\_CVF045\_VFG023610 | 99,589 | 195,339 | 5snp8indel | 0,257 | 1947 | 0,232 | 47 | (YE105\_C0912) general secretion pathway protein D [T2SS (Yst1) (CVF045)] [Yersinia enterocolitica subsp. palearctica 105.5R(r)] |
| YE105\_C1175\_CVF043\_VFG023788 | 100 | 179,225 |  | 0 | 1257 | 0,028 | 138 | (YE105\_C1175) translocase [O-antigen (CVF043)] [Yersinia enterocolitica subsp. palearctica 105.5R(r)] |
| YE105\_C1176\_CVF043\_VFG023790 | 100 | 155,796 | 2snp | 0,209 | 957 | 0,016 | 246 | (YE105\_C1176) WbcK protein [O-antigen (CVF043)] [Yersinia enterocolitica subsp. palearctica 105.5R(r)] |
| YE105\_C1177\_CVF043\_VFG023792 | 100 | 163,01 |  | 0 | 879 | 0,021 | 270 | (YE105\_C1177) WbcL protein [O-antigen (CVF043)] [Yersinia enterocolitica subsp. palearctica 105.5R(r)] |
| YE105\_C1178\_CVF043\_VFG023794 | 100 | 182,392 | 1snp | 0,093 | 1077 | 0,085 | 191 | (YE105\_C1178) WbcM protein [O-antigen (CVF043)] [Yersinia enterocolitica subsp. palearctica 105.5R(r)] |
| YE105\_C1179\_CVF043\_VFG023796 | 100 | 177,75 |  | 0 | 744 | 0,016 | 317 | (YE105\_C1179) WbcN protein [O-antigen (CVF043)] [Yersinia enterocolitica subsp. palearctica 105.5R(r)] |
| YE105\_C1180\_CVF043\_VFG023798 | 100 | 184,861 |  | 0 | 1026 | 0,04 | 211 | (YE105\_C1180) Polyprenol phosphate:N-acetyl-hexosamine 1-phosphate transferase [O-antigen (CVF043)] [Yersinia enterocolitica subsp. palearctica 105.5R(r)] |
| YE105\_C1181\_CVF043\_VFG023800 | 100 | 191 | 1snp | 0,07 | 1437 | 0,014 | 90 | (YE105\_C1181) TrsG protein-like protein [O-antigen (CVF043)] [Yersinia enterocolitica subsp. palearctica 105.5R(r)] |
| YE105\_C1182\_CVF043\_VFG023802 | 100 | 161,571 |  | 0 | 1017 | 0,012 | 213 | (YE105\_C1182) putative glycosyl transferase [O-antigen (CVF043)] [Yersinia enterocolitica subsp. palearctica 105.5R(r)] |
| yplA\_CVF053\_VFG003624 | 99,795 | 176,08 | 27snp3indel | 2,769 | 975 | 0,172 | 233 | (yplA) phospholipase A [YplA (CVF053)] [Yersinia enterocolitica subsp. enterocolitica 8081] |
| yst1C\_CVF045\_VFG023609 | 100 | 155,654 | 2snp | 0,383 | 522 | 0,02 | 391 | (yst1C) general secretion pathway protein C [T2SS (Yst1) (CVF045)] [Yersinia enterocolitica subsp. palearctica 105.5R(r)] |
| yst1E\_CVF045\_VFG023611 | 100 | 207,409 | 1snp | 0,066 | 1506 | 0,013 | 85 | (yst1E) general secretion pathway protein E [T2SS (Yst1) (CVF045)] [Yersinia enterocolitica subsp. palearctica 105.5R(r)] |
| yst1F\_CVF045\_VFG023612 | 99,421 | 171,689 | 3snp7indel | 0,248 | 1209 | 0,18 | 148 | (yst1F) general secretion pathway protein F [T2SS (Yst1) (CVF045)] [Yersinia enterocolitica subsp. palearctica 105.5R(r)] |
| yst1G\_CVF045\_VFG023613 | 100 | 161,806 |  | 0 | 354 | 0,018 | 469 | (yst1G) general secretion pathway protein G [T2SS (Yst1) (CVF045)] [Yersinia enterocolitica subsp. palearctica 105.5R(r)] |
| yst1J\_CVF045\_VFG023614 | 100 | 185,234 | 4snp | 0,673 | 594 | 0,019 | 367 | (yst1J) general secretion pathway protein J precursor [T2SS (Yst1) (CVF045)] [Yersinia enterocolitica subsp. palearctica 105.5R(r)] |
| yst1K\_CVF045\_VFG023615 | 100 | 189,74 | 2snp1indel | 0,211 | 948 | 0,016 | 250 | (yst1K) general secretion pathway protein K [T2SS (Yst1) (CVF045)] [Yersinia enterocolitica subsp. palearctica 105.5R(r)] |
| yst1L\_CVF045\_VFG023616 | 100 | 177,099 | 4snp | 0,388 | 1032 | 0,008 | 208 | (yst1L) General secretion pathway protein L [T2SS (Yst1) (CVF045)] [Yersinia enterocolitica subsp. palearctica 105.5R(r)] |
| yst1O\_CVF045\_VFG023617 | 100 | 183,638 | 1snp | 0,12 | 834 | 0,325 | 283 | (yst1O) prepilin peptidase [T2SS (Yst1) (CVF045)] [Yersinia enterocolitica subsp. palearctica 105.5R(r)] |
| ystA\_VF0135\_VFG002155 | 100 | 131,747 |  | 0 | 216 | 0,014 | 502 | (ystA) enterotoxin [Yst (VF0135)] [Yersinia enterocolitica W1024] |