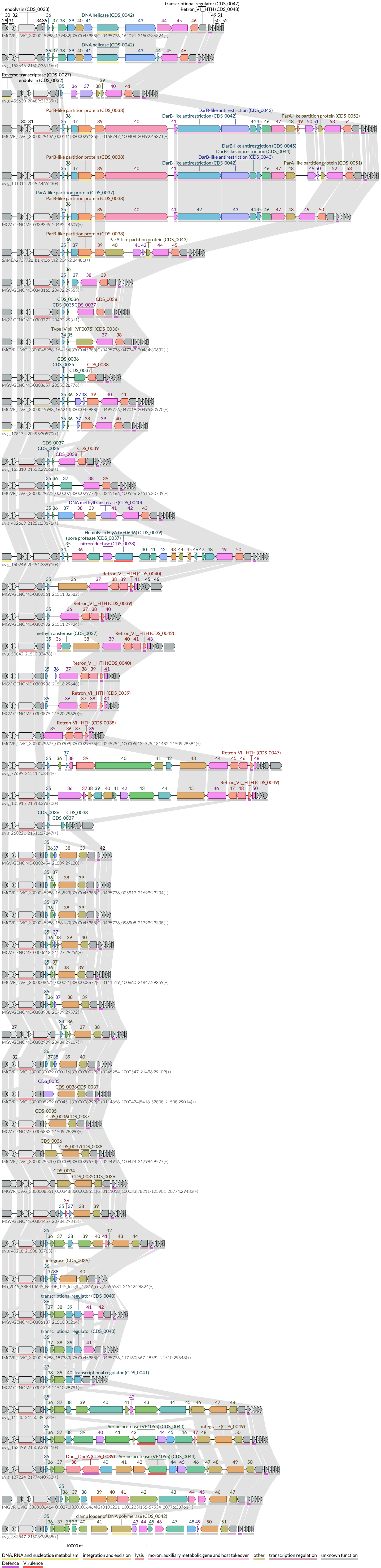
endolysin (CDS_0033)
transcriptional regulator (CDS_0047)
Retron_VI__HTH (CDS_0048)
DNA helicase (CDS_0042)
IMGVR_UViG_3300045988_179482|3300045988|Ga0495776_164091 21507:36824(+)
DNA helicase (CDS_0042)
uvig_153646 21507:36116(+)
Reverse transcriptase (CDS_0027)
endolysin (CDS_0032)
uvig_455630 20489:31239(+)
ParB-like partition protein (CDS_0038)
DarB-like antirestriction (CDS_0043)
DarB-like antirestriction (CDS_0042)
ParA-like partition protein (CDS_0052)
IMGVR_UViG_3300029136_000111|3300029136|Ga0168747_100408 20492:46371(+)
DarB-like antirestriction (CDS_0045)
DarB-like antirestriction (CDS_0044)
DarB-like antirestriction (CDS_0043)
ParB-like partition protein (CDS_0038)
DarB-like antirestriction (CDS_0042)
ParA-like partition protein (CDS_0051)
uvig_131314 20492:46523(+)
ParA-like partition protein (CDS_0037)
ParB-like partition protein (CDS_0038)
MGV-GENOME-0339349 20492:44609(+)
ParB-like partition protein (CDS_0038)
ParA-like partition protein (CDS_0043)
SAMEA2737728_b1_ct36_vs2 20492:34481(+)
MGV-GENOME-0343165 20492:29553(+)
CDS_0036
CDS_0035
CDS_0037
CDS_0038
MGV-GENOME-0303772 20492:29311(+)
Type IV pili (VF0075) (CDS_0036)
IMGVR_UViG_3300045988_164154|3300045988|Ga0495776_047247 20484:30632(+)
CDS_0036
CDS_0035
CDS_0037
CDS_0038
MGV-GENOME-0303657 20553:28776(+)
IMGVR_UViG_3300045988_166213|3300045988|Ga0495776_047019 20495:30970(+)
uvig_178174 20495:30570(+)
CDS_0037
CDS_0036
CDS_0038
CDS_0039
uvig_163810 21532:29068(+)
IMGVR_UViG_3300029772_000007|3300029772|Ga0245166_100526 21515:30739(+)
DNA methyltransferase (CDS_0040)
uvig_402669 21251:33176(+)
Hemolysin HlyA (VF0646) (CDS_0039)
spore protease (CDS_0037)
nitroreductase (CDS_0038)
uvig_160249 20491:38891(+)
Retron_VI__HTH (CDS_0040)
MGV-GENOME-0309361 21511:32582(+)
Retron_VI__HTH (CDS_0039)
MGV-GENOME-0302992 21511:29724(+)
methyltransferase (CDS_0037)
Retron_VI__HTH (CDS_0042)
uvig_50842 21510:33478(+)
Retron_VI__HTH (CDS_0040)
MGV-GENOME-0303936 21516:29648(+)
Retron_VI__HTH (CDS_0039)
MGV-GENOME-0303875 21520:29620(+)
Retron_VI__HTH (CDS_0038)
IMGVR_UViG_3300029675_000309|3300029675|Ga0245254_100005|134725-181482 21509:28584(+)
Retron_VI__HTH (CDS_0047)
uvig_77699 21511:40842(+)
Retron_VI__HTH (CDS_0049)
uvig_105915 21513:39870(+)
CDS_0036
CDS_0038
CDS_0037
uvig_260221 21511:27847(+)
MGV-GENOME-0302454 21509:29120(+)
IMGVR_UViG_3300045988_163593|3300045988|Ga0495776_005917 21699:29234(+)
IMGVR_UViG_3300045988_158130|3300045988|Ga0495776_096908 21799:29338(+)
MGV-GENOME-0303618 21527:29256(+)
IMGVR_UViG_3300008672_000021|3300008672|Ga0111519_100660 21847:29359(+)
MGV-GENOME-0303908 21799:29572(+)
MGV-GENOME-0302999 20484:29107(+)
IMGVR_UViG_3300030029_000116|3300030029|Ga0245284_1000547 21496:29109(+)
CDS_0035
CDS_0036
CDS_0037
IMGVR_UViG_3300008299_000451|3300008299|Ga0114868_1000424|5418-52808 21508:29014(+)
CDS_0035
CDS_0036
CDS_0037
MGV-GENOME-0305883 21509:28390(+)
CDS_0036
CDS_0037
CDS_0038
IMGVR_UViG_3300029570_000009|3300029570|Ga0244916_100474 21798:29577(+)
CDS_0034
CDS_0035
CDS_0036
IMGVR_UViG_3300008551_000348|3300008551|Ga0111058_100033|78211-125901 20774:29433(+)
MGV-GENOME-0304457 20784:29343(+)
uvig_40218 21508:32763(+)
integrase (CDS_0039)
Ma_2019_SRR413645_NODE_145_length_47316_cov_6.596581 21542:28824(+)
transcriptional regulator (CDS_0040)
MGV-GENOME-0306137 21510:30214(+)
transcriptional regulator (CDS_0040)
IMGVR_UViG_3300045988_187383|3300045988|Ga0495776_117160|667-48592 21510:29548(+)
transcriptional regulator (CDS_0041)
MGV-GENOME-0301814 21510:28791(+)
uvig_11540 21550:39523(+)
Serine protease (VF1055) (CDS_0043)
integrase (CDS_0049)
uvig_163499 21509:39851(+)
Dnd__DndA (CDS_0039)
Serine protease (VF1055) (CDS_0043)
uvig_127224 21774:40952(+)
IMGVR_UViG_3300006464_000371|3300006464|Ga0100221_1000223|155-57534 20776:38761(+)
clamp loader of DNA polymerase (CDS_0042)
uvig_363847 21508:38888(+)
10000 nt
DNA, RNA and nucleotide metabolism
integration and excision
lysis
moron, auxiliary metabolic gene and host takeover
other
transcription regulation
unknown function
Defence
Virulence