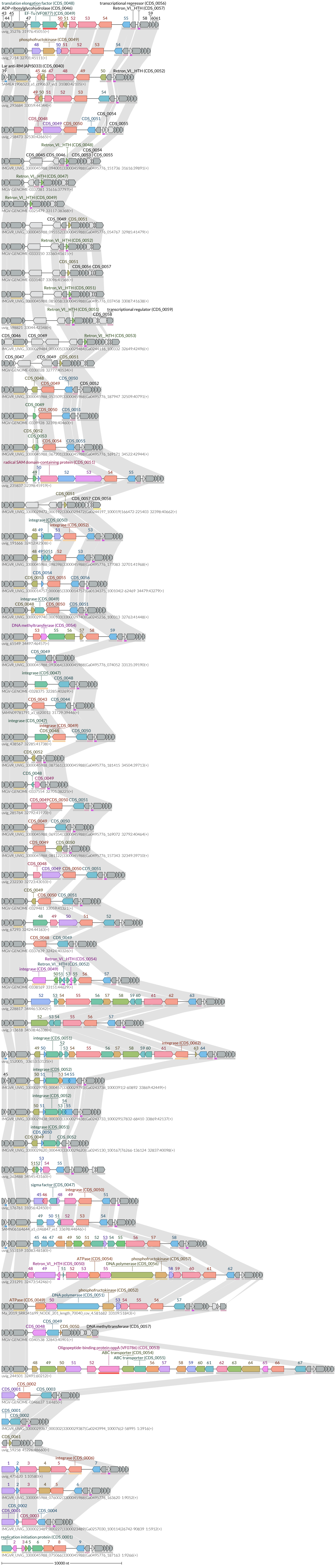
translation elongation factor (CDS_0048)
ADP-ribosylglycohydrolase (CDS_0046)
EF-Tu (VF0877) (CDS_0049)
transcriptional repressor (CDS_0056)
Retron_VI__HTH (CDS_0057)
uvig_35276 31976:45055(+)
phosphofructokinase (CDS_0049)
uvig_7214 32701:45111(+)
Lar anti-RM (APIS033) (CDS_0040)
Retron_VI__HTH (CDS_0052)
SAMEA1906523_a1_ct90637_vs1 31080:42105(+)
uvig_293684 33059:44344(+)
CDS_0048
CDS_0049
CDS_0050
CDS_0051
CDS_0054
CDS_0055
uvig_258473 32530:42665(+)
Retron_VI__HTH (CDS_0048)
CDS_0045
CDS_0046
CDS_0053
IMGVR_UViG_3300045988_094001|3300045988|Ga0495776_151736 31616:39891(+)
Retron_VI__HTH (CDS_0047)
MGV-GENOME-0337381 31616:37797(+)
Retron_VI__HTH (CDS_0049)
MGV-GENOME-0325479 33117:38368(+)
IMGVR_UViG_3300045988_095552|3300045988|Ga0495776_054767 32985:41479(+)
Retron_VI__HTH (CDS_0052)
MGV-GENOME-0333150 33360:41615(+)
CDS_0056
CDS_0057
MGV-GENOME-0331407 33096:41568(+)
Retron_VI__HTH (CDS_0051)
IMGVR_UViG_3300045988_085058|3300045988|Ga0495776_037458 33087:41638(+)
transcriptional regulator (CDS_0059)
CDS_0058
uvig_598821 33044:42348(+)
IMGVR_UViG_3300029484_000005|3300029484|Ga0244116_100332 32649:42496(+)
MGV-GENOME-0330028 32777:40534(+)
IMGVR_UViG_3300045988_053509|3300045988|Ga0495776_187947 32509:40791(+)
MGV-GENOME-0339928 32398:40460(+)
IMGVR_UViG_3300045988_067201|3300045988|Ga0495776_169171 34522:42944(+)
radical SAM domain-containing protein (CDS_0051)
uvig_235837 32398:45919(+)
IMGVR_UViG_3300029472_000192|3300029472|Ga0244197_100019|166472-225403 32398:40662(+)
integrase (CDS_0050)
integrase (CDS_0052)
uvig_191666 32412:42508(+)
IMGVR_UViG_3300045988_098398|3300045988|Ga0495776_177083 32701:41968(+)
IMGVR_UViG_3300014757_000085|3300014757|Ga0134375_100104|2-62469 34479:43279(+)
integrase (CDS_0049)
IMGVR_UViG_3300029740_000103|3300029740|Ga0245236_100313 32763:41448(+)
DNA methyltransferase (CDS_0054)
uvig_65549 34497:46457(+)
IMGVR_UViG_3300045988_093064|3300045988|Ga0495776_074052 33135:39190(+)
integrase (CDS_0047)
MGV-GENOME-0328375 32285:40269(+)
SAMN09781791_a1_ct20013 31729:39446(+)
uvig_438567 32285:41738(+)
IMGVR_UViG_3300045988_087361|3300045988|Ga0495776_181415 34504:39713(+)
MGV-GENOME-0337554 32701:38225(+)
uvig_285764 32792:41970(+)
IMGVR_UViG_3300045988_069354|3300045988|Ga0495776_169072 32792:40464(+)
IMGVR_UViG_3300045988_081122|3300045988|Ga0495776_157343 32349:39710(+)
uvig_232230 32723:43010(+)
MGV-GENOME-0329481 33059:41321(+)
uvig_67293 32424:44183(+)
MGV-GENOME-0337839 32424:40326(+)
Retron_VI__HTH (CDS_0054)
Retron_VI__HTH (CDS_0052)
integrase (CDS_0049)
MGV-GENOME-0338169 33151:44629(+)
uvig_228817 34446:53042(+)
uvig_313618 34508:46338(+)
integrase (CDS_0051)
integrase (CDS_0062)
uvig_152005_ 33653:53135(+)
integrase (CDS_0052)
IMGVR_UViG_3300029793_000457|3300029793|Ga0243738_1000391|2-60892 33869:42449(+)
IMGVR_UViG_3300029438_000303|3300029438|Ga0243733_1000295|7832-68410 33869:42137(+)
integrase (CDS_0051)
IMGVR_UViG_3300029620_000440|3300029620|Ga0245130_100167|76266-136124 32837:40098(+)
uvig_363488 34545:43160(+)
sigma factor (CDS_0047)
integrase (CDS_0050)
uvig_176761 31056:42450(+)
SAMN06164644_a1_ct46847_vs1 33698:44846(+)
uvig_553159 31083:48180(+)
ATPase (CDS_0054)
phosphofructokinase (CDS_0057)
Retron_VI__HTH (CDS_0050)
DNA polymerase (CDS_0056)
uvig_231291 32473:54246(+)
phosphofructokinase (CDS_0052)
DNA polymerase (CDS_0051)
ATPase (CDS_0049)
Ma_2019_SRR341699_NODE_201_length_70040_cov_4.581682 33109:51843(+)
DNA methyltransferase (CDS_0057)
MGV-GENOME-0340538 32843:40901(+)
Oligopeptide-binding protein oppA (VF0786) (CDS_0053)
ABC transporter (CDS_0054)
ABC transporter (CDS_0055)
uvig_244501 32491:60212(+)
MGV-GENOME-0346637 1:6485(+)
IMGVR_UViG_3300029387_000302|3300029387|Ga0243994_100076|2-58995 1:3916(+)
uvig_59258 45226:48660(+)
integrase (CDS_0006)
uvig_475620 1:10580(+)
IMGVR_UViG_3300045988_076002|3300045988|Ga0495776_163620 1:9052(+)
IMGVR_UViG_3300023489_000227|3300023489|Ga0257030_100114|26742-90839 1:5912(+)
replication initiation protein (CDS_0001)
IMGVR_UViG_3300045988_075066|3300045988|Ga0495776_187163 1:9266(+)
10000 nt
DNA, RNA and nucleotide metabolism
integration and excision
moron, auxiliary metabolic gene and host takeover
other
transcription regulation
unknown function
Defence
Virulence
Anti-defence