

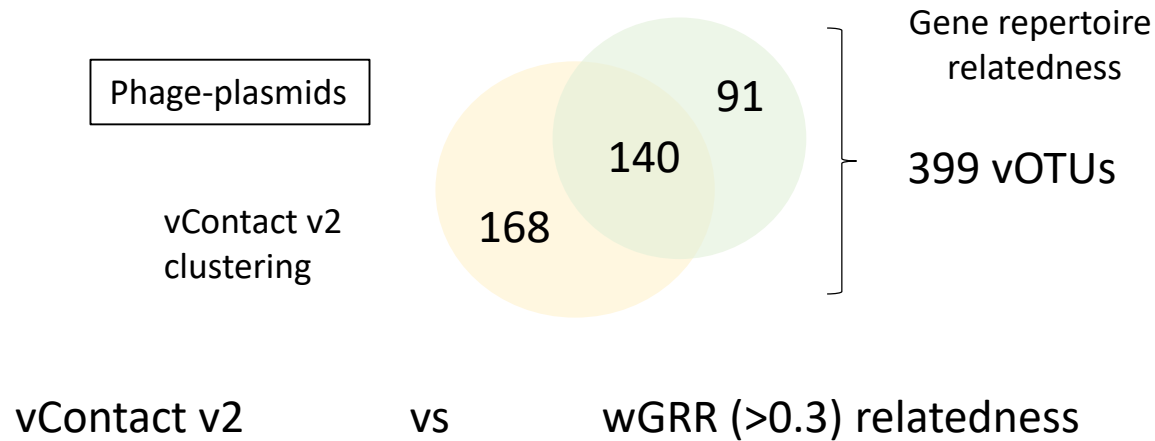
Supplemental file 1.

Slide 2: Comparison of detection methods and lists of vOTUs distinct for each method.

Slide 3: Networks of vOTUs and P-Ps based on genome relatedness scores. Genome similarity was computed using protein-sharing networks. P-Ps and vOTUs (nodes) were grouped using the wGRR metric (edges). Only edges >0.3 are shown.

Slide 4: vContact v2 was used to cluster P-Ps and vOTUs (nodes). Edges are weights from the vContact v2 generated network metric.

Slide 5-32: Genome-to-genome synteny plots generated with gggenomes (<https://github.com/thackl/gggenomes>). Gene-to-gene assignments are the best-bidirectional-hits as used to compute the wGRR. RefSeq accession number are indicating P-P sequences from PMID: 38378896.



N = 168 distinct

N = 61 related *Enterococcus faecium* p63-3, 18 kb
and *Clostridium beijerinckii* plasmid 18 kb
N = 41 related to a P-P of *Corynebacterium atypicum*;
were not detected by wGRR since far related (<0.3)
N = 32 related to vB_CpeS-CP51, similar Rep as *Carjivirus communis*

N = 8 related to CTC plasmid
N = 5 x *Selenomonas ruminantium lactilytica*, plasmid, 35 kb
N = 5 x *Sarcina* sp. (Clostridiaceae) plasmid p2 34 kb
N = 5 x related to *Carjivirus communis* (far related)

N = 3 x P-Ps of pBS32
N = 3 x *Cupriavidus oxalaticus*, plasmid 38 kb
N = 2 x *Klebsiella pneumoniae* plasmid, 40 kb
N = 2 x two P-Ps of IEBH
N = 1 x six PP of pLP39

N = 91 distinct

N = 72 related to CTC plasmid,
N = 5 related to *Carjivirus communis* (fragments)
N = 3 related to SSU5 (super) group

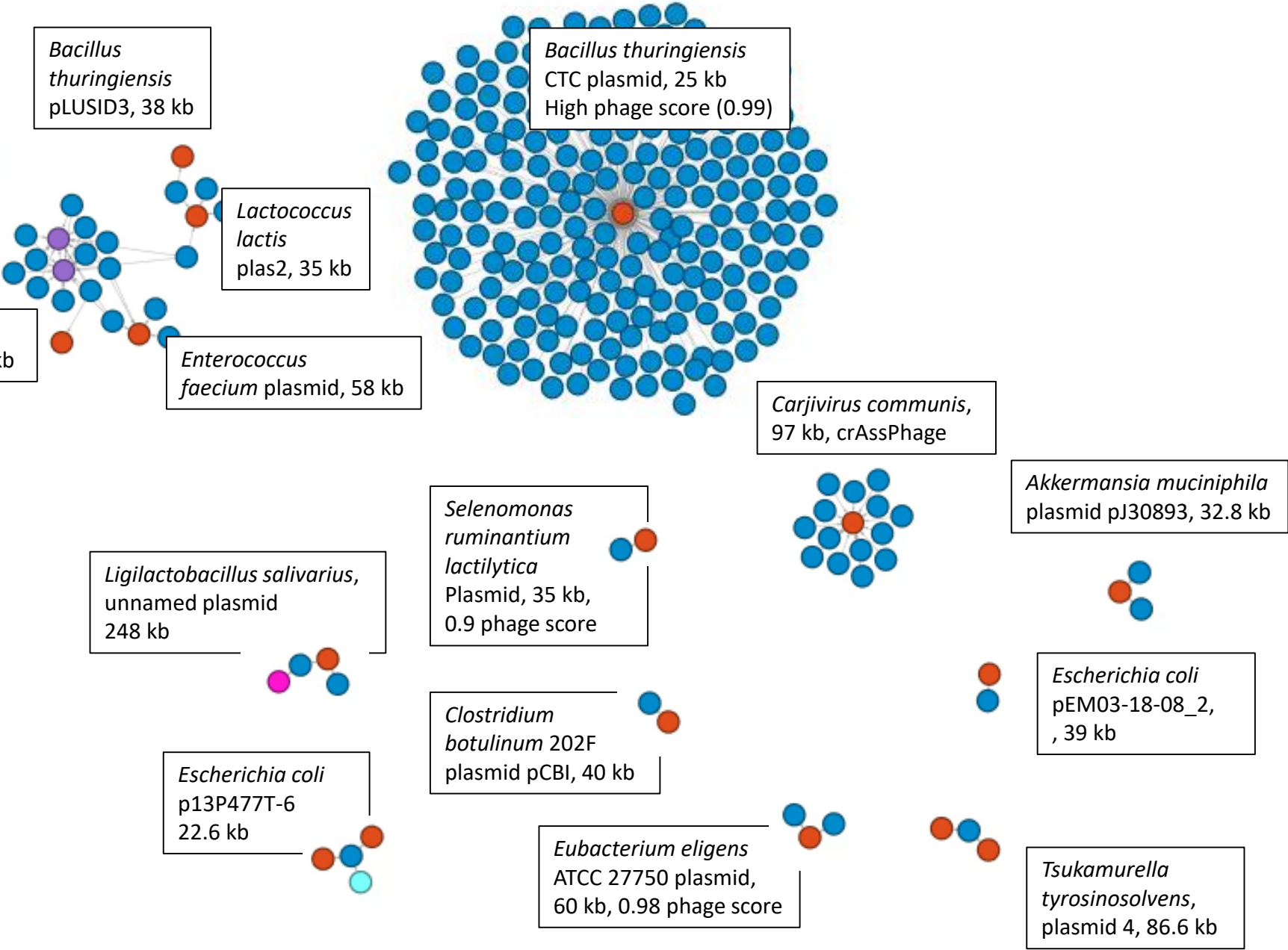
N = 2 related to a P-P of *Corynebacterium atypicum*
N = 2 x N15 (1xgroup,1xcomm)
N = 2 x F116 (community)
N = 2 x *Enterococcus faecium* plasmid, 58 kb

N = 1 x *Escherichia coli* pEM03-18-08_2, 39 kb
N = 1 x *Lactococcus lactis* plas2, 35 kb
N = 1 x *Pseudomonas luteola* plasmid, 120 kb

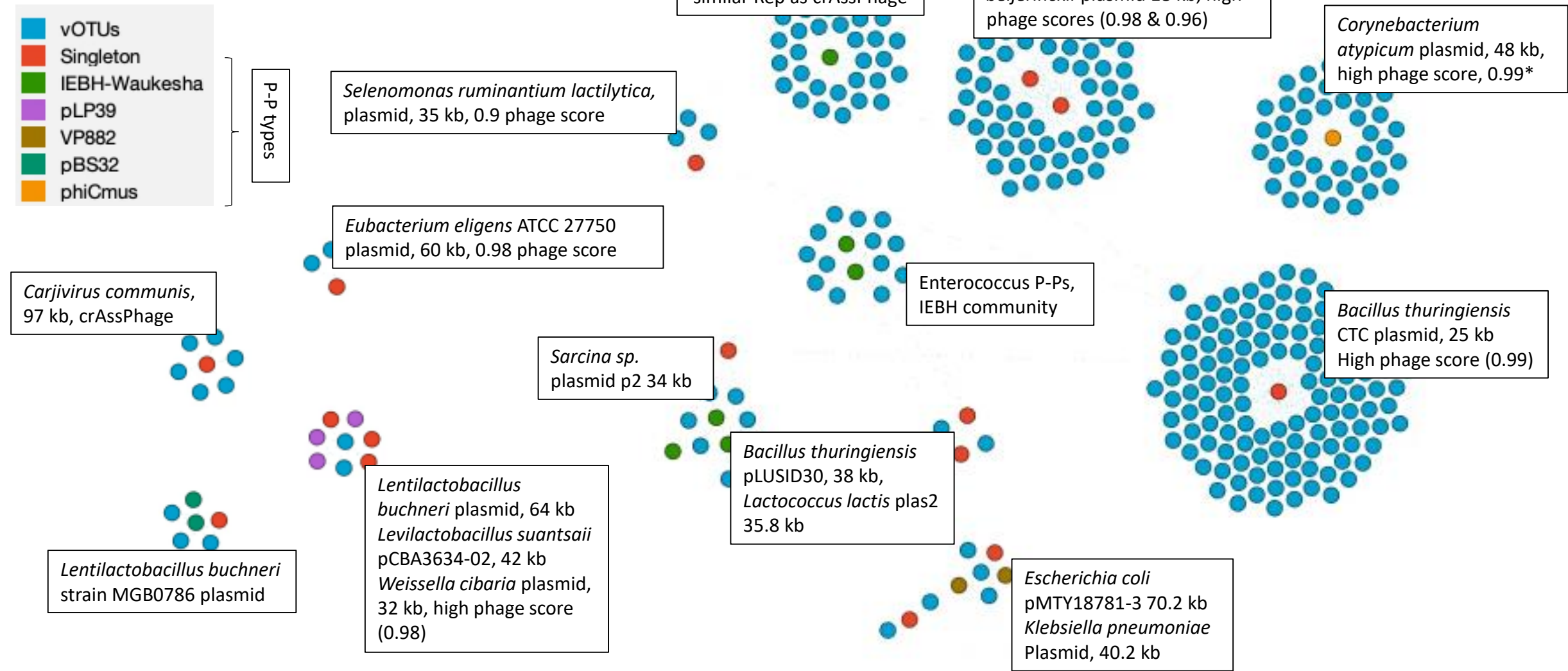
wGRR based clustering, (>0.3)
(up to three candidates)

- vOTUs
- Singleton
- SSU5_pHCM2
- F116
- IEBH-Waukesha
- N15
- pBS32
- PiSa
- pLP39
- VP882
- phiCmus

P-P types

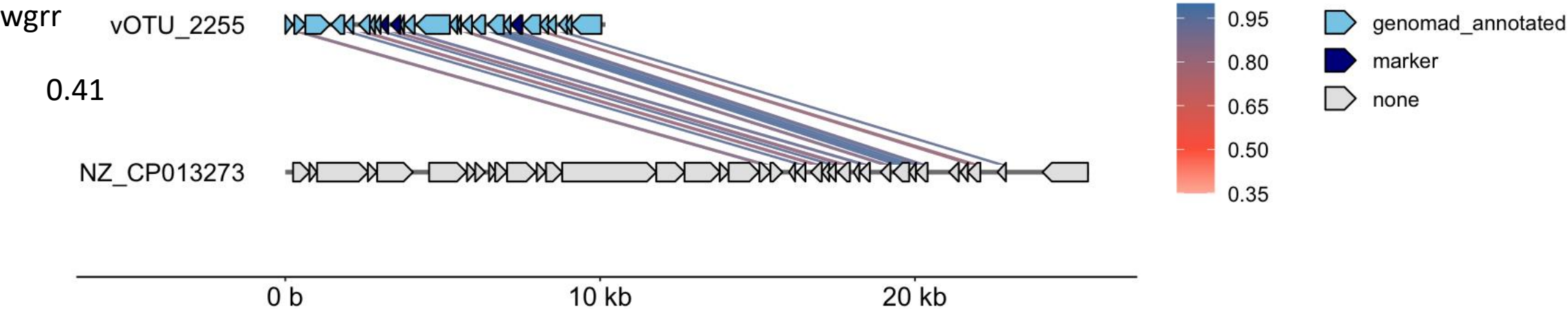


vContact_v2 clustering, (default)
Edge weights > 3



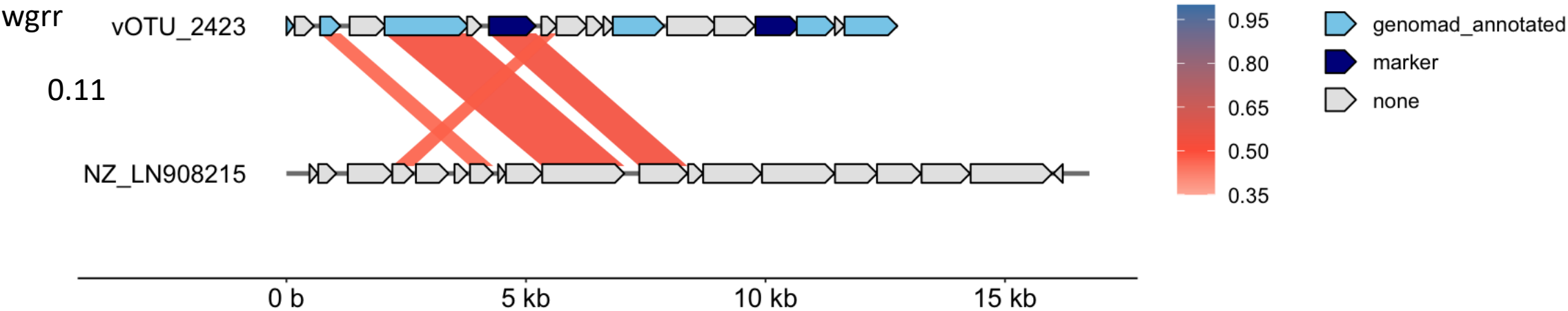
Bacillus thuringiensis strain CTC plasmid

Detection method,
vContact v2 = 8
wGRR + vcontact = 118
wGRR = 72



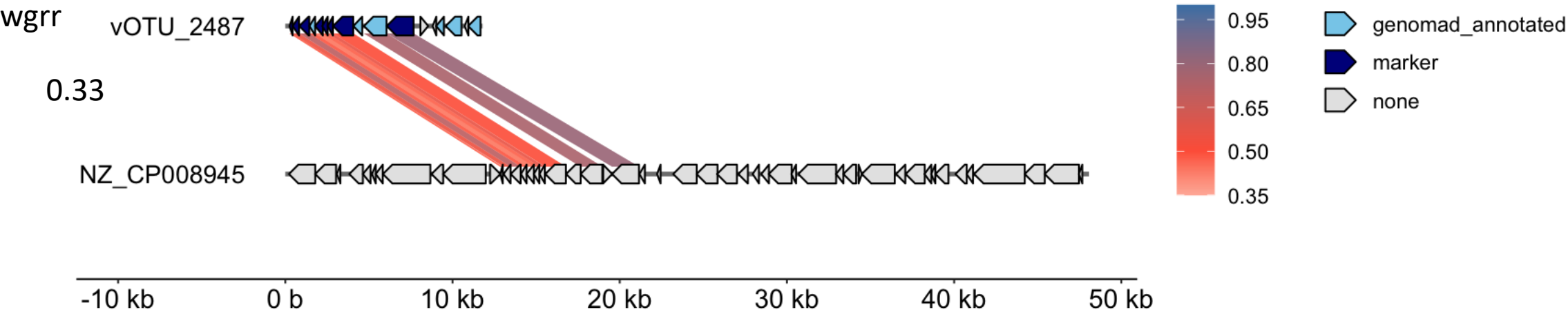
Detection method,
vContact v2 = 61

Enterococcus faecium isolate 2014-VREF-63 plasmid p63-3 sequence.



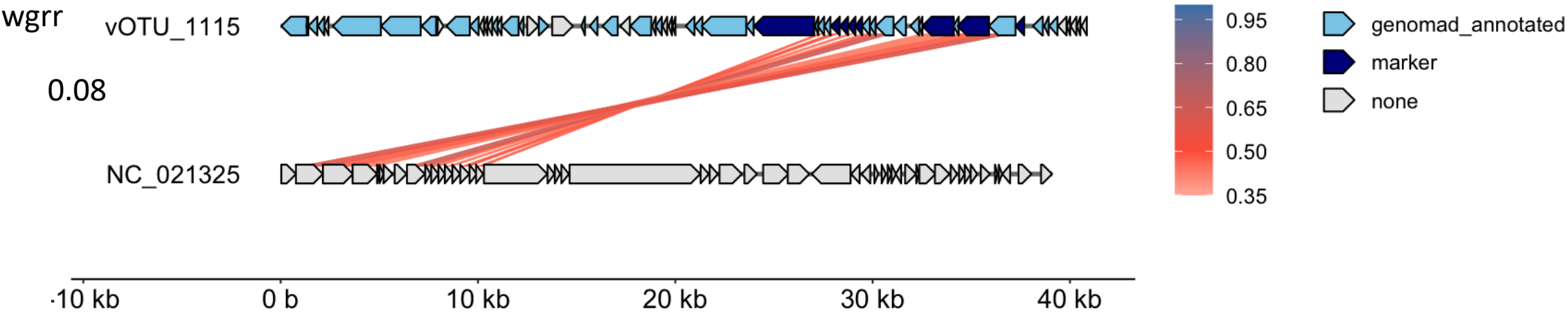
Corynebacterium atypicum strain R2070 plasmid phiCATYP2070I

Detection method,
vContact v2 = 41
vContact v2+wGRR = 1
wGRR = 2



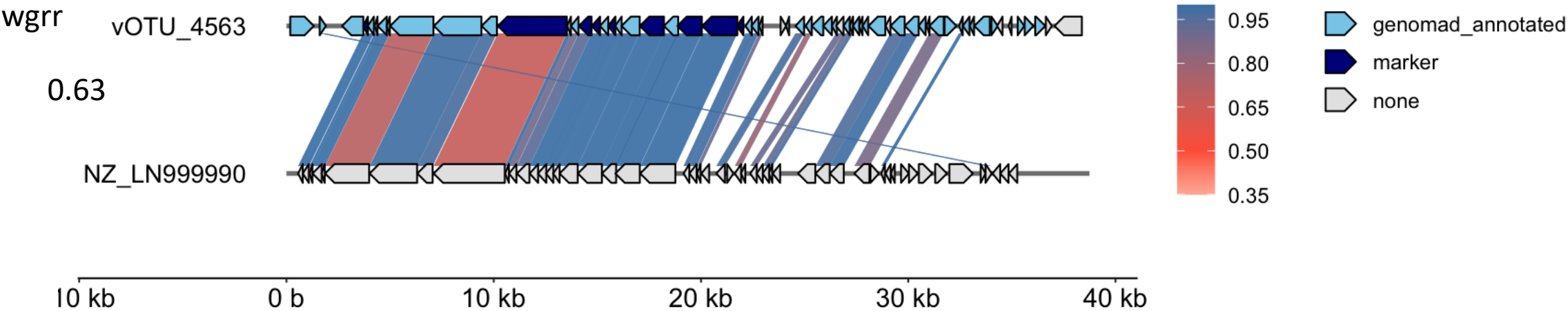
Detection method,
vContact v2 = 32

Clostridium phage vB_CpeS-CP51



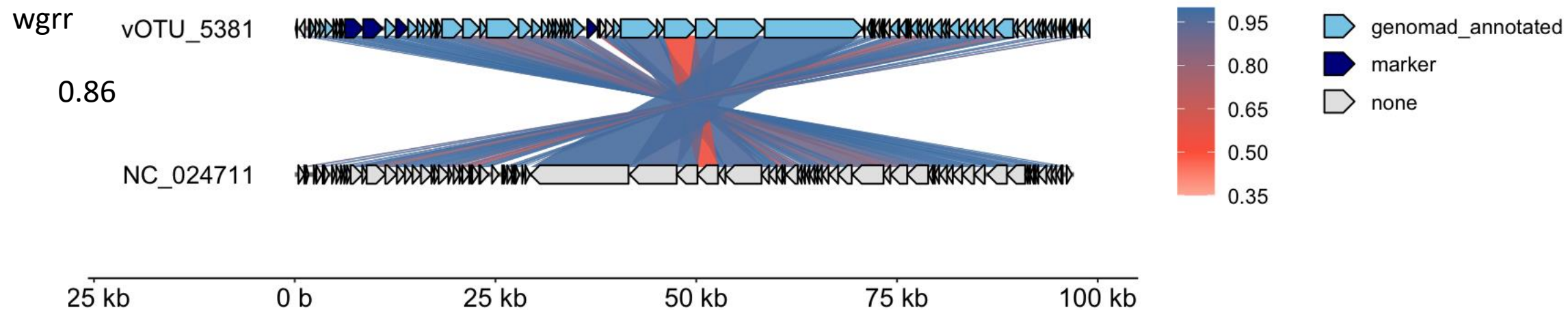
Detection method,
vContact v2+wGRR = 13

Enterococcus faecium isolate EFE11651 genome assembly, plasmid



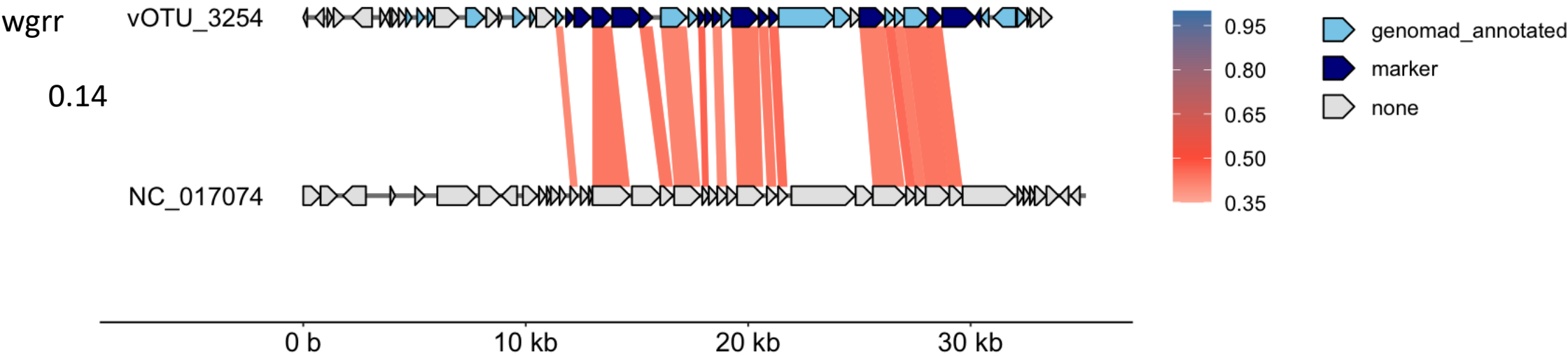
Carjivirus communis

Detection method,
vContact v2 = 5
vContact v2+wGRR = 1
wGRR = 5



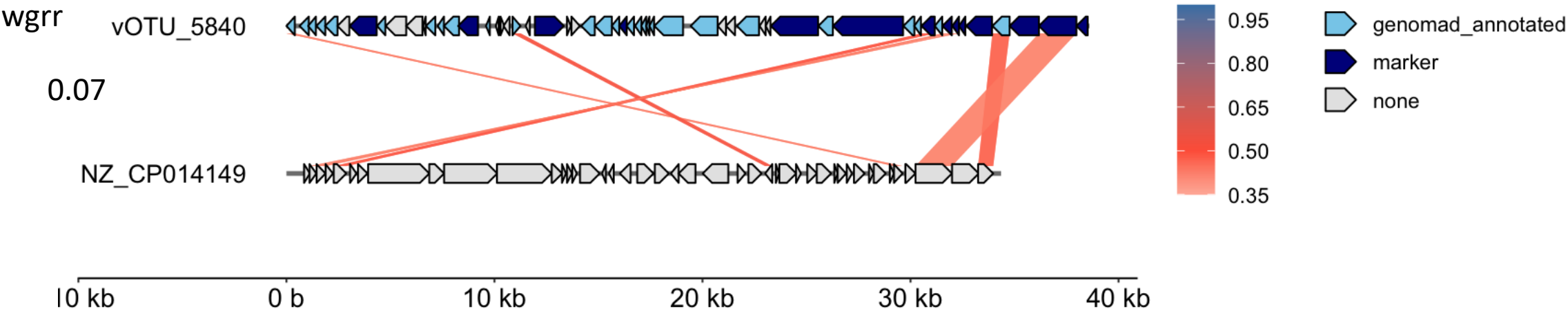
Detection method,
vContact v2 = 5

Selenomonas ruminantium subsp. lactilytica TAM6421 plasmid pSRC5 DNA



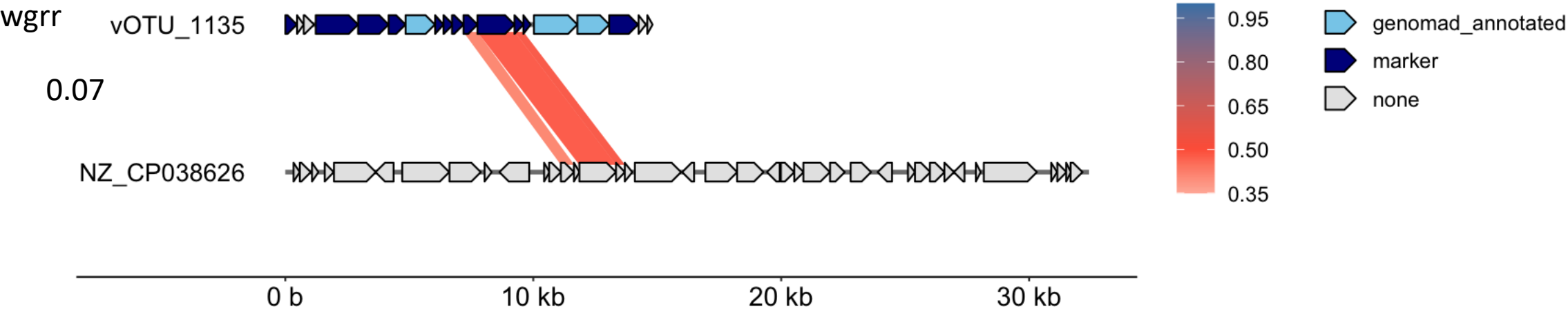
Detection method,
vContact v2 = 5

Paeniclostridium sordellii strain AM370 plasmid pRSJ16_1



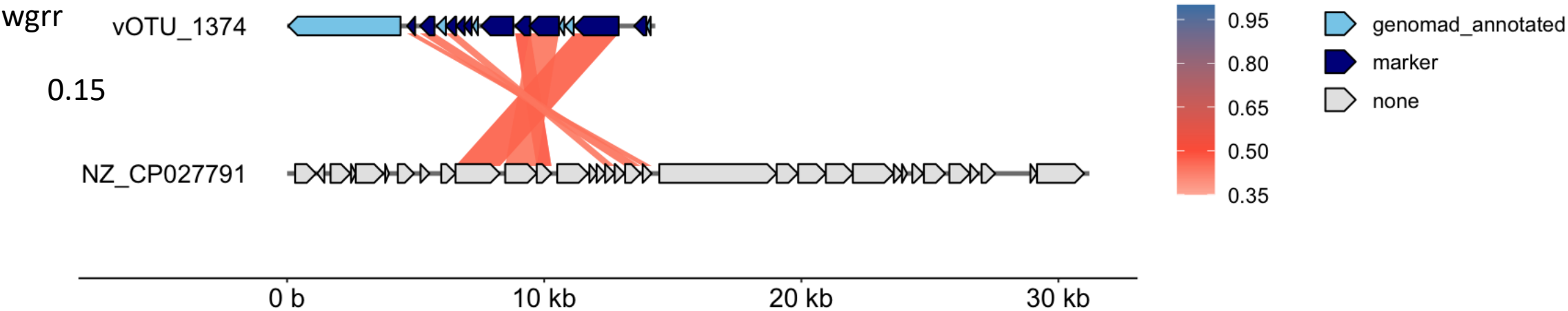
Detection method,
vContact v2 = 3

Arsenophonus nasoniae strain FIN plasmid pArsFIN14



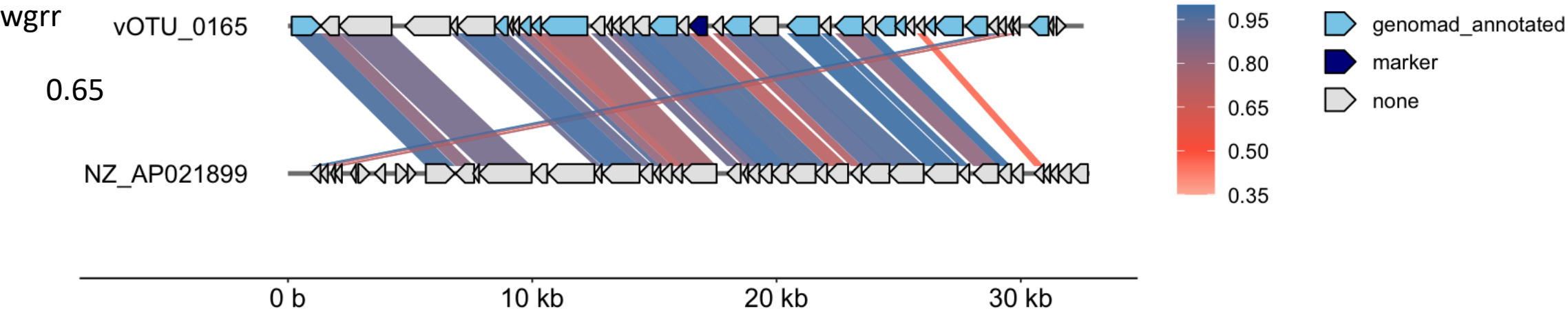
Detection method,
vContact v2 = 3

Bacillus licheniformis strain TAB7 plasmid pTAB7B



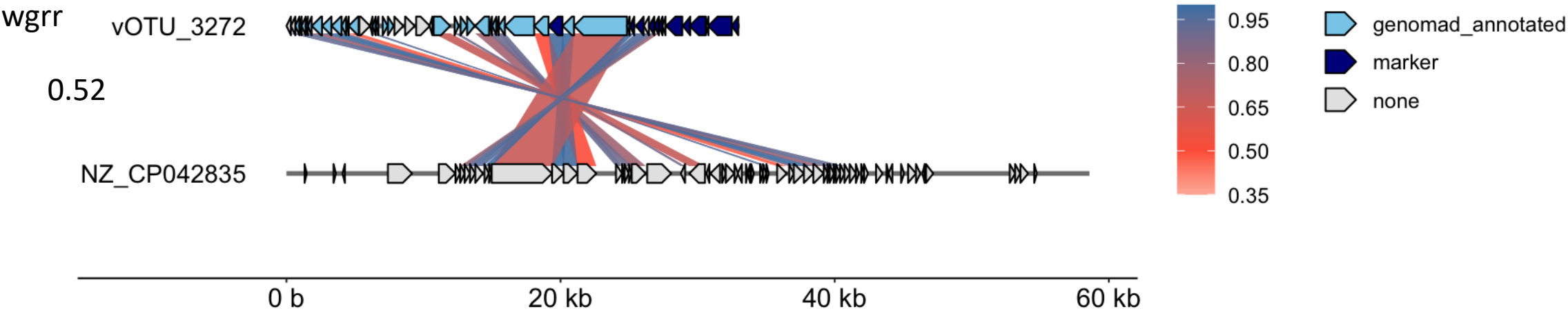
Detection method,
vContact v2+wGRR = 2

Akkermansia muciniphila plasmid pJ30893



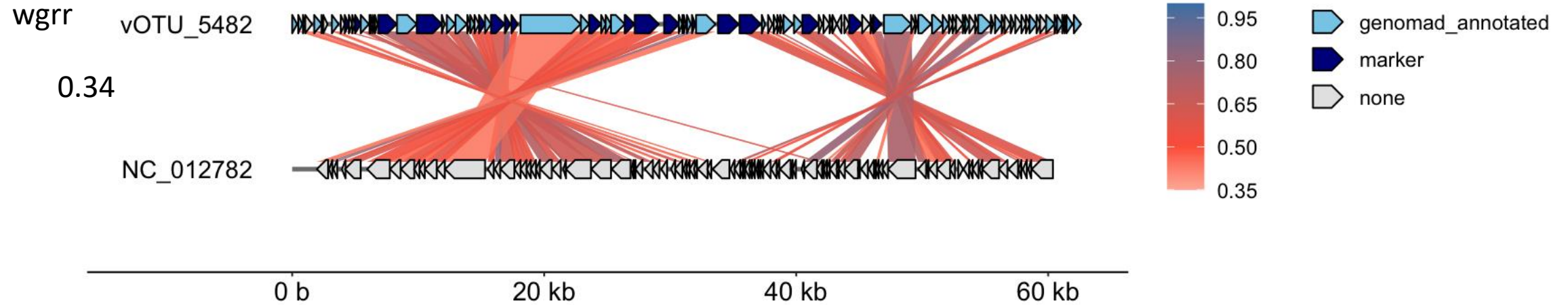
Detection method,
wGRR = 2

Enterococcus_faecium_strain_FA3_plasmid_unnamed2



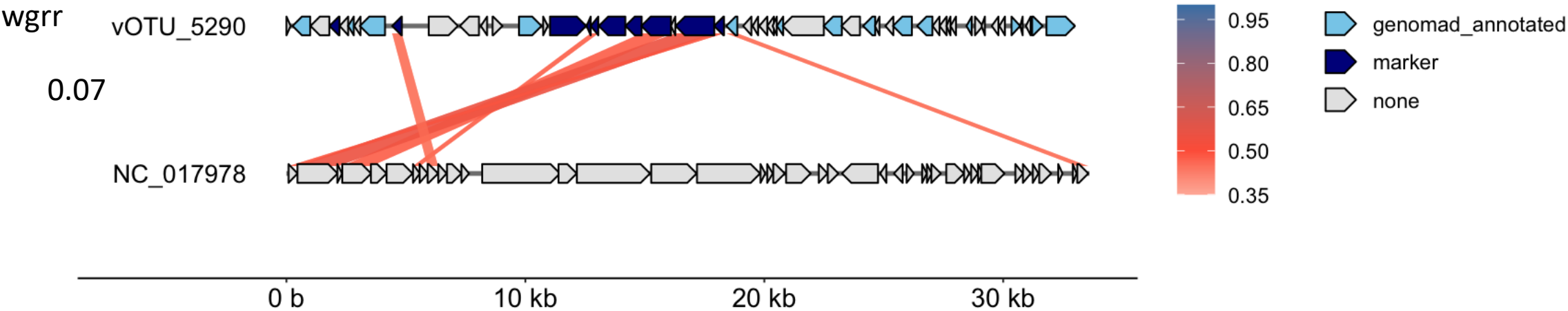
Detection method,
vContact v2+wGRR = 2

Eubacterium eligens ATCC 27750 plasmid unnamed



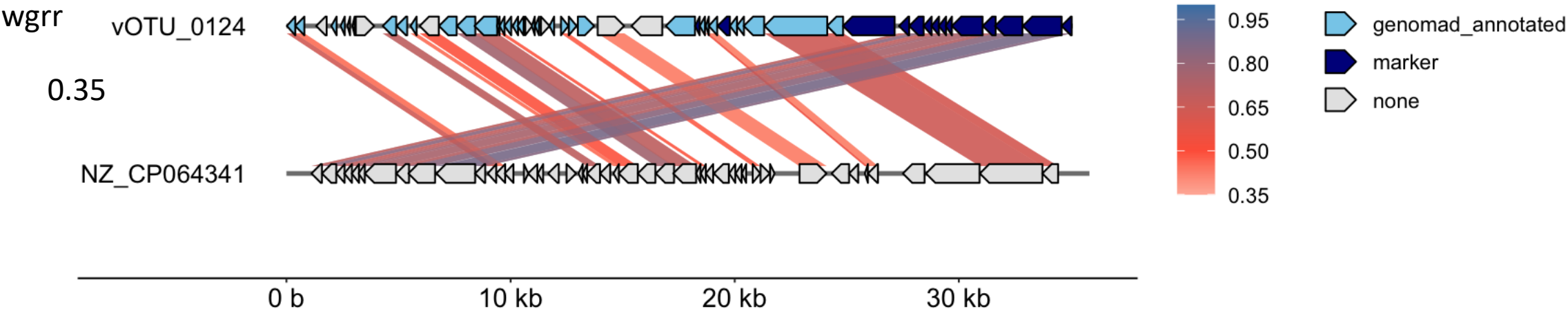
Detection method,
vContact v2 = 2

Clostridium phage PhiS63



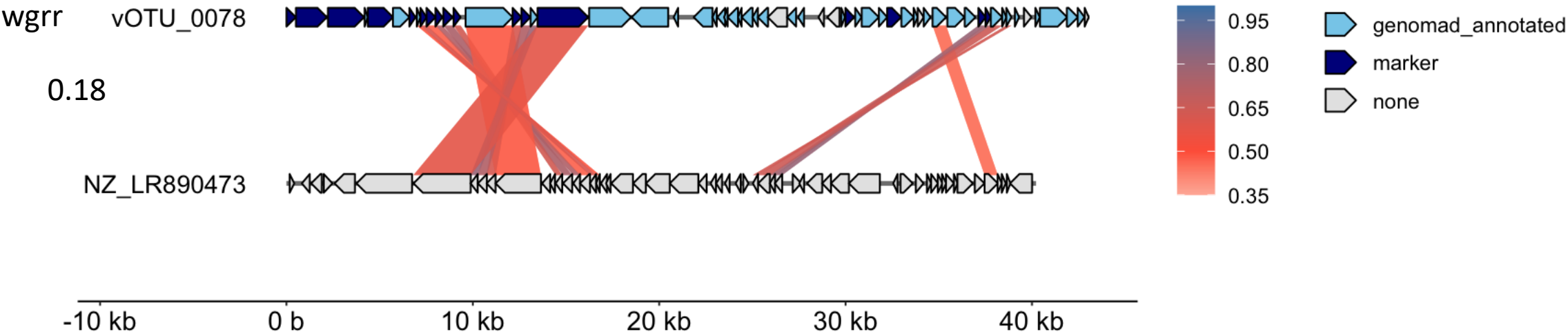
Detection method,
wGRR+vcontact = 2

Lactococcus lactis subsp. lactis strain L19 plasmid plas2, complete sequence



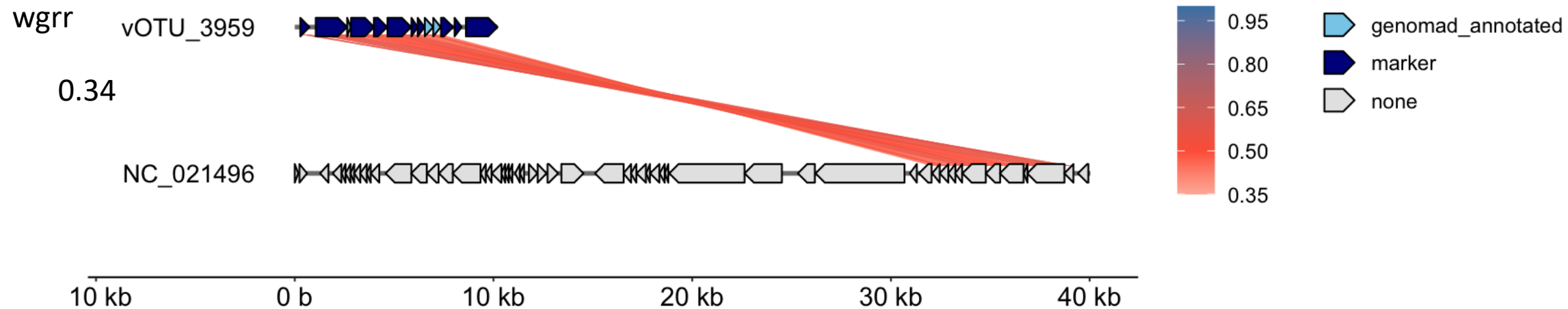
Detection method,
vContact v2 = 2

Klebsiella_pneumoniae_isolate_INF168-sc-2280023_plasmid_3,_complete



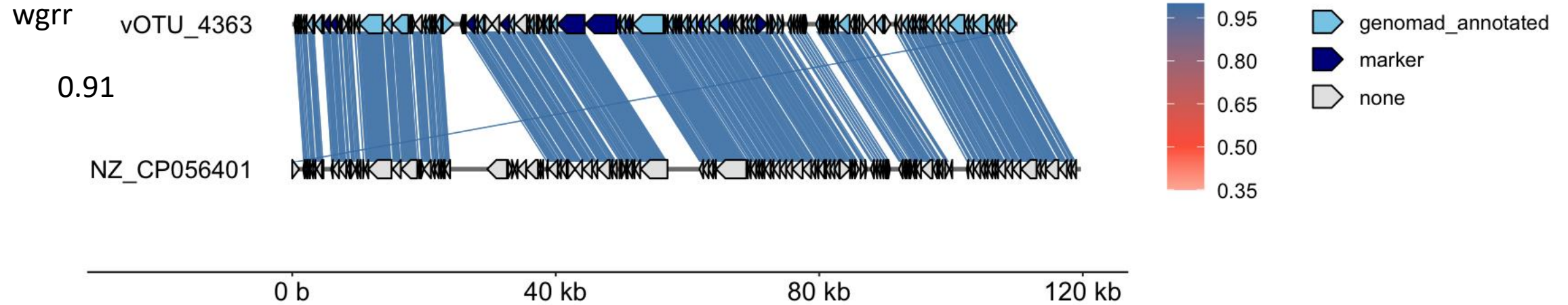
Lactobacillus reuteri I5007 plasmid pLRI02

Detection method,
vContact v2+wGRR = 1
vContact v2 = 1



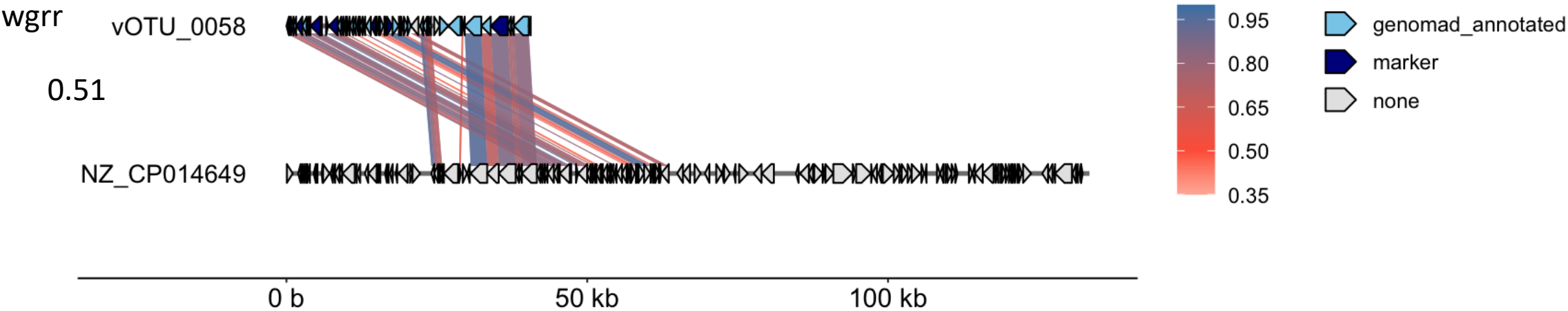
Detection method,
wGRR = 1

Citrobacter_sp._RHBSTW-00570_plasmid_pRHBSTW-00570_3,_complete



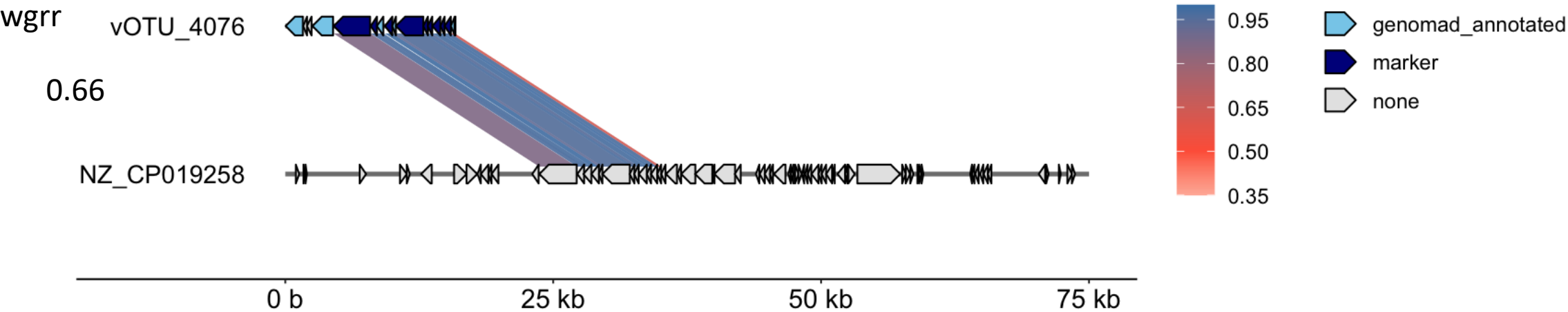
Detection method,
wGRR = 1

Klebsiella pneumoniae strain KPNIH36 plasmid pKPN-fff



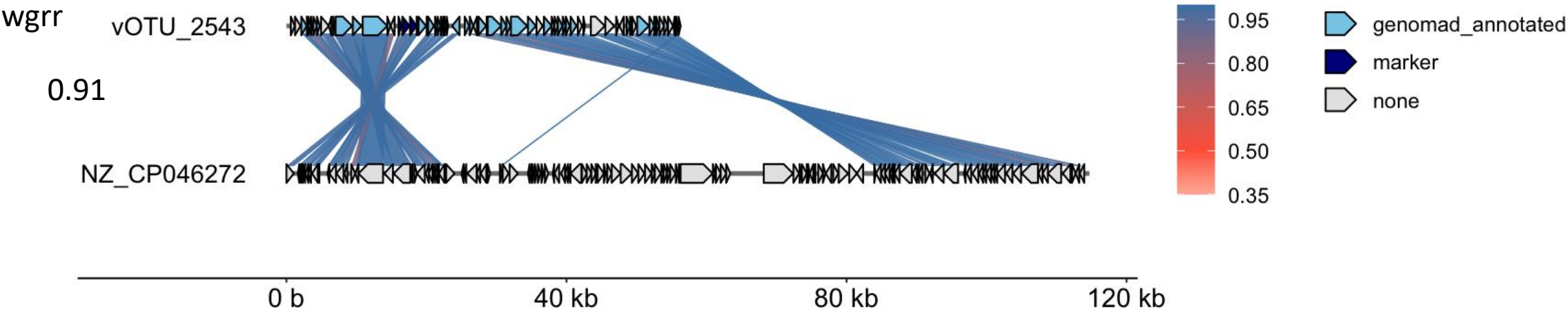
Detection method,
wGRR = 1

Escherichia_coli_strain_13TMH22_plasmid_p13TMH22-2,_complete



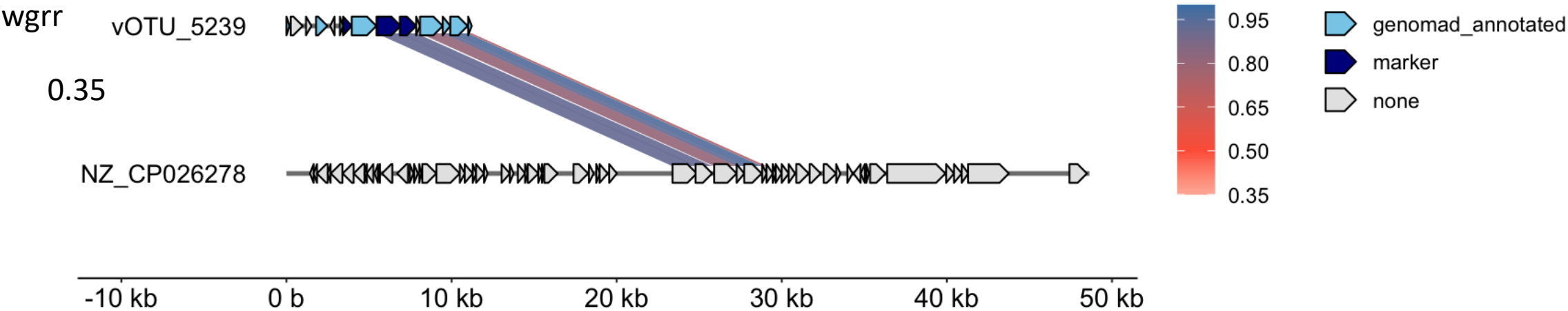
Detection method,
wGRR = 1

Enterobacter_hormaechei_strain_E70_plasmid_pE70



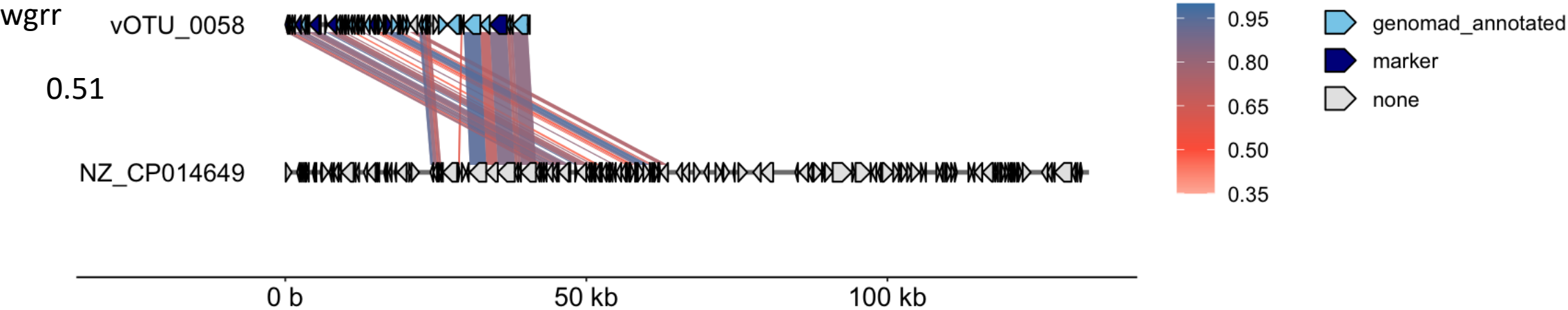
Detection method,
wGRR = 1

Klebsiella oxytoca strain KONIH2 plasmid pKOR-0e8e



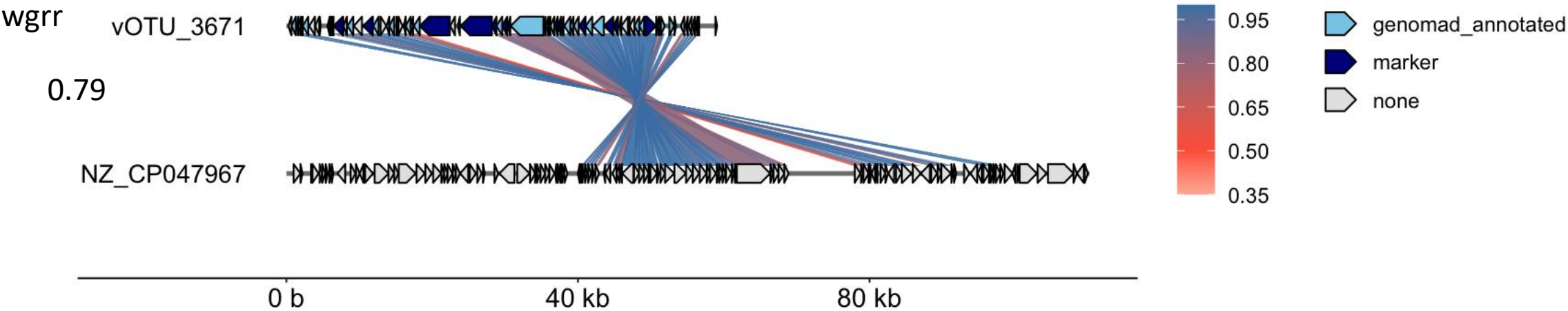
Detection method,
wGRR = 1

Klebsiella pneumoniae strain KPNIH36 plasmid pKPN-fff



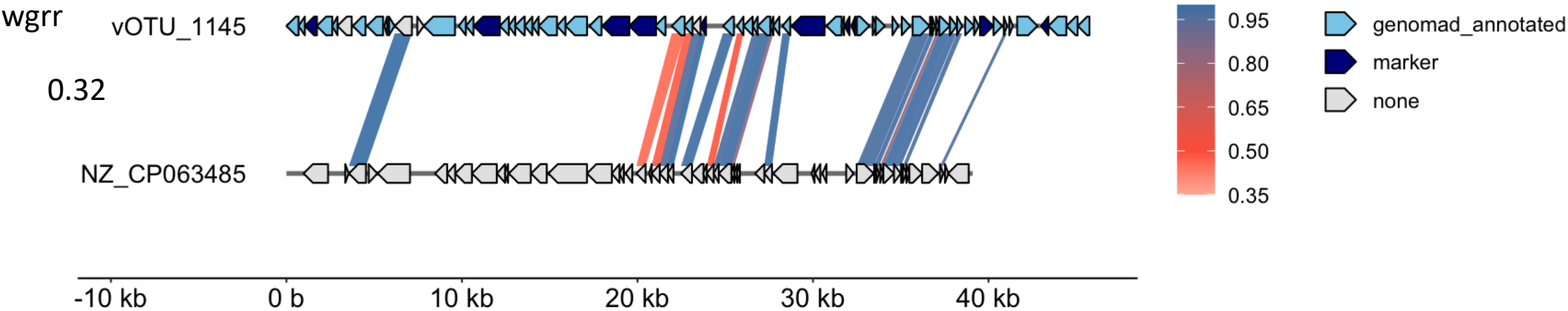
Detection method,
wGRR = 1

Enterobacter_hormaechei_strain_189_plasmid_pECL189-2,_complete



Detection method,
wGRR = 1

Escherichia_coli_strain_EM03-18-08_plasmid_pEM03-18-08_2,_complete



Detection method,
wGRR = 1

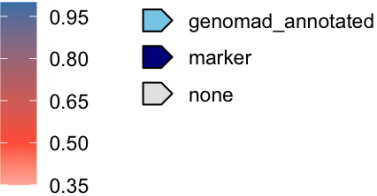
Escherichia_coli_O145_strain_RM9154-C1_plasmid_p1RM9154-C1

wgrr

vOTU_4335

0.36

NZ_CP031350



0 b

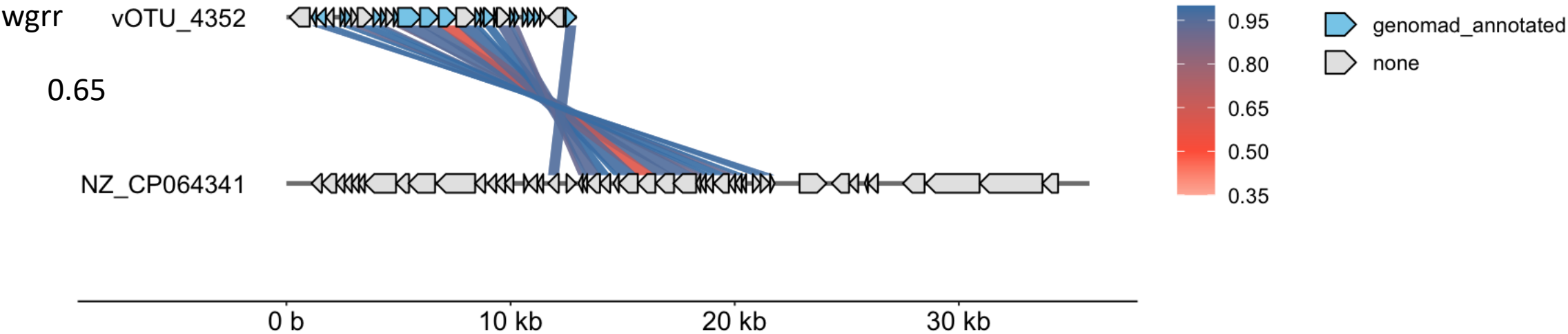
50 kb

100 kb

150 kb

Detection method,
wGRR = 1

Lactococcus_lactis_subsp._lactis_strain_L19_plasmid_plas2,_complete



Detection method,
wGRR = 1

Pseudomonas_luteola_strain_FDAARGOS_637_plasmid_unnamed2

