Part 5: Pathogen Detection (RG3/4 Species) − Neg_Control_W

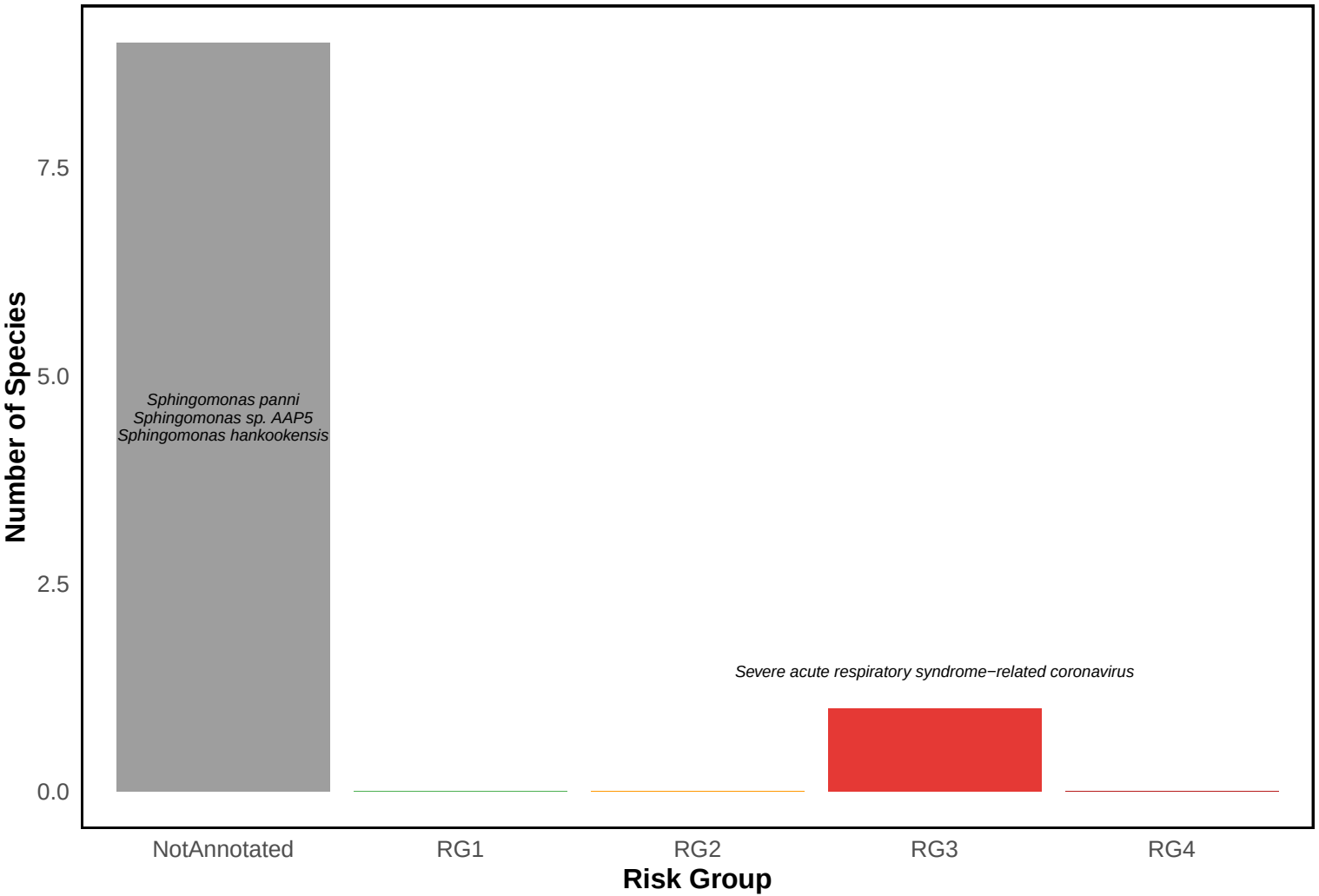
Pathogen detection analysis for sample Neg_Control_W:

Filtering criteria:
− Include: RG3, RG4 risk groups
− Exclude: RG1, RG2 risk groups
− Exclude: Species annotated as 'Microbiome' in HOMD.Category

Key findings:
− Total species in sample: 27
− Potential pathogenic species identified: 10
− Most abundant pathogen: Sphingomonas panni
− Average pathogen reads: 2734.7

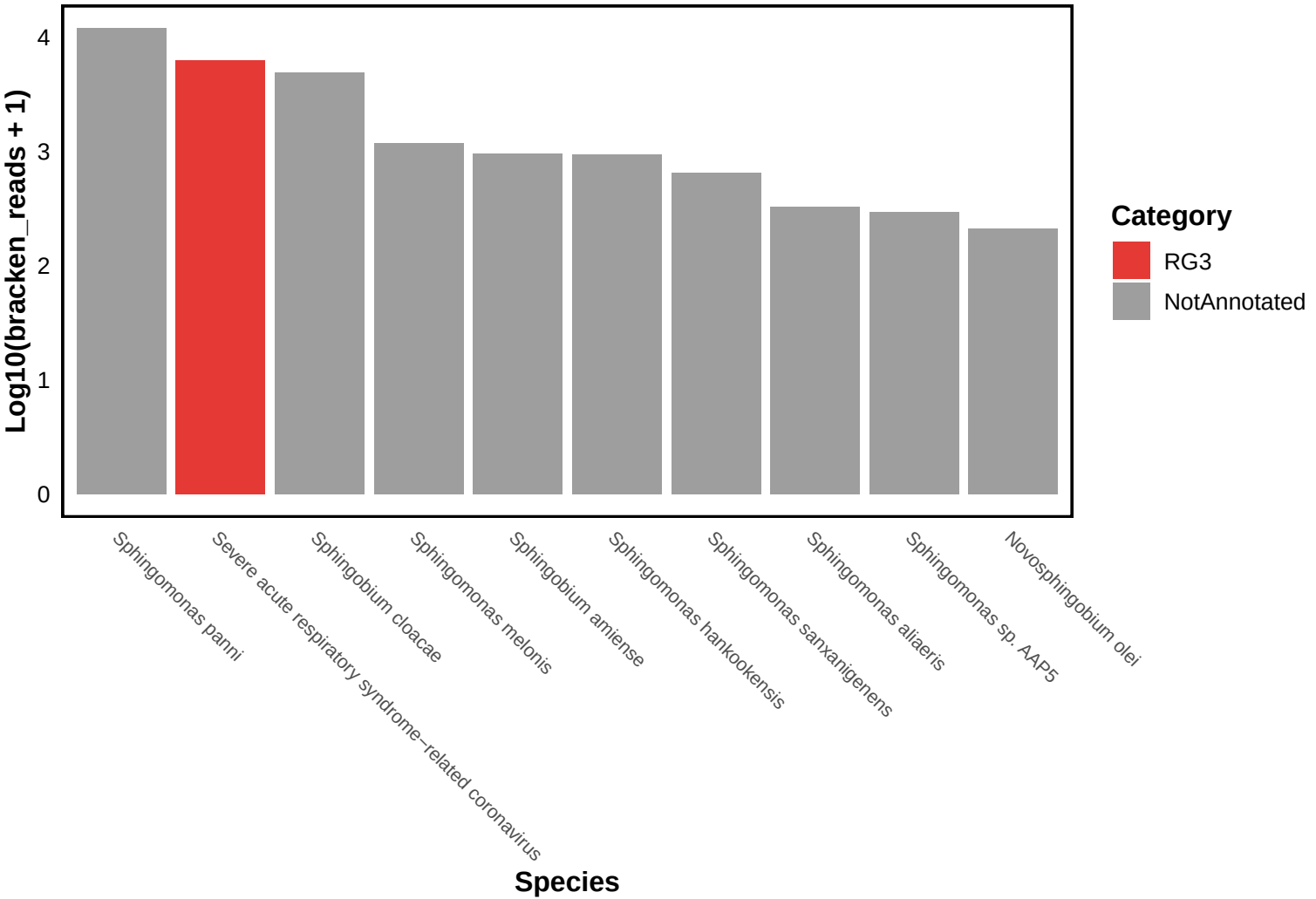
Species per Risk Group − Neg_Control_W − Pathogens

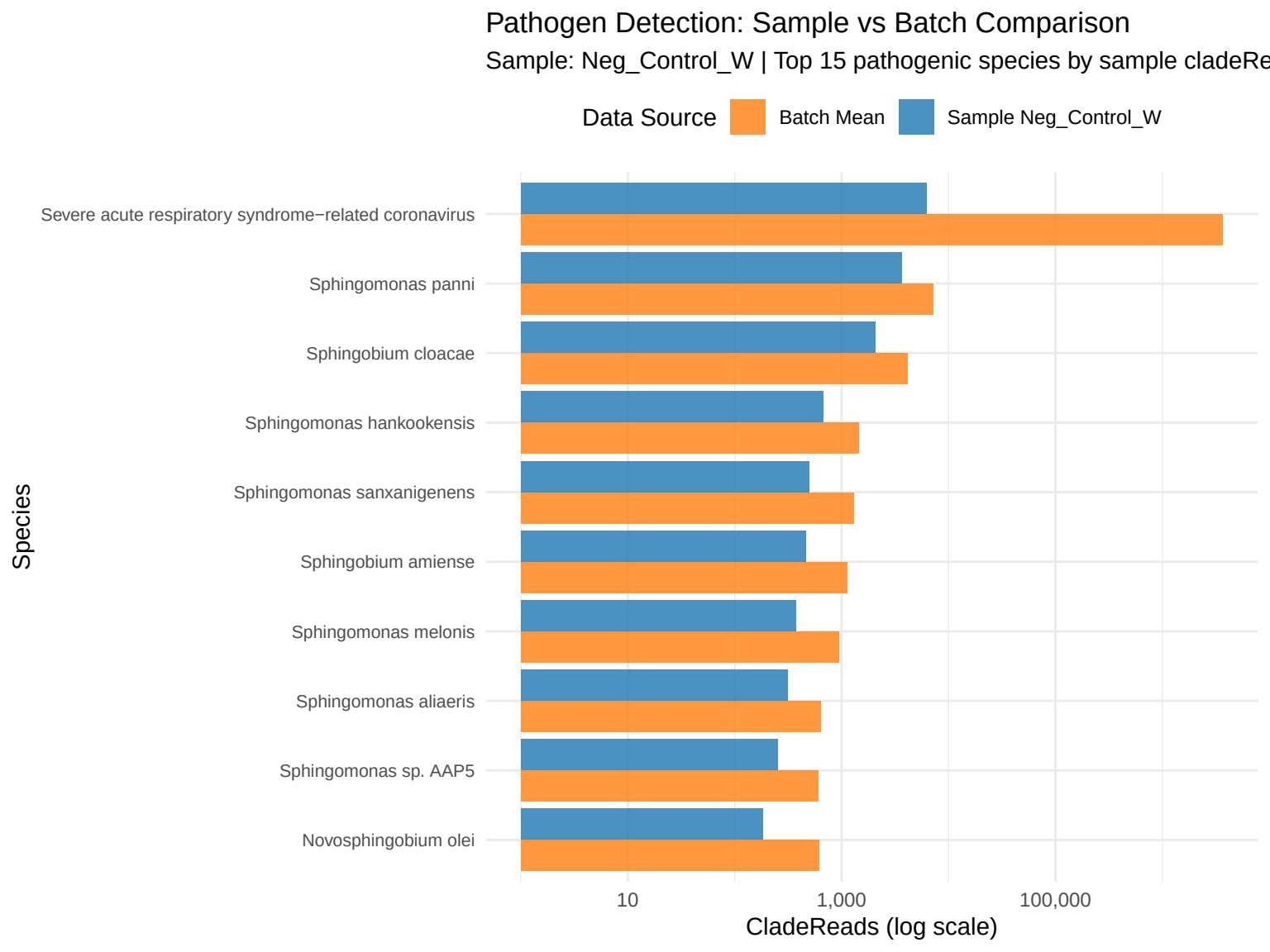
Total species: 10



Species by Risk Group − Neg_Control_W − Pathogens

Top 10 species by Log10(bracken_reads + 1)




Pathogen Detection: Sample vs Batch Comparison
Sample: Neg_Control_W | Top 15 pathogenic species by sample cladeRe
Data Source
Batch Mean
Sample Neg_Control_W
Species
Severe acute respiratory syndrome−related coronavirus
Sphingomonas panni
Sphingobium cloacae
Sphingomonas hankookensis
Sphingomonas sanxanigenens
Sphingobium amiense
Sphingomonas melonis
Sphingomonas aliaeris
Sphingomonas sp. AAP5
Novosphingobium olei
10
1,000
100,000
CladeReads (log scale)

Part 5: Pathogen Detection (RG3/4 Species) − W61303224

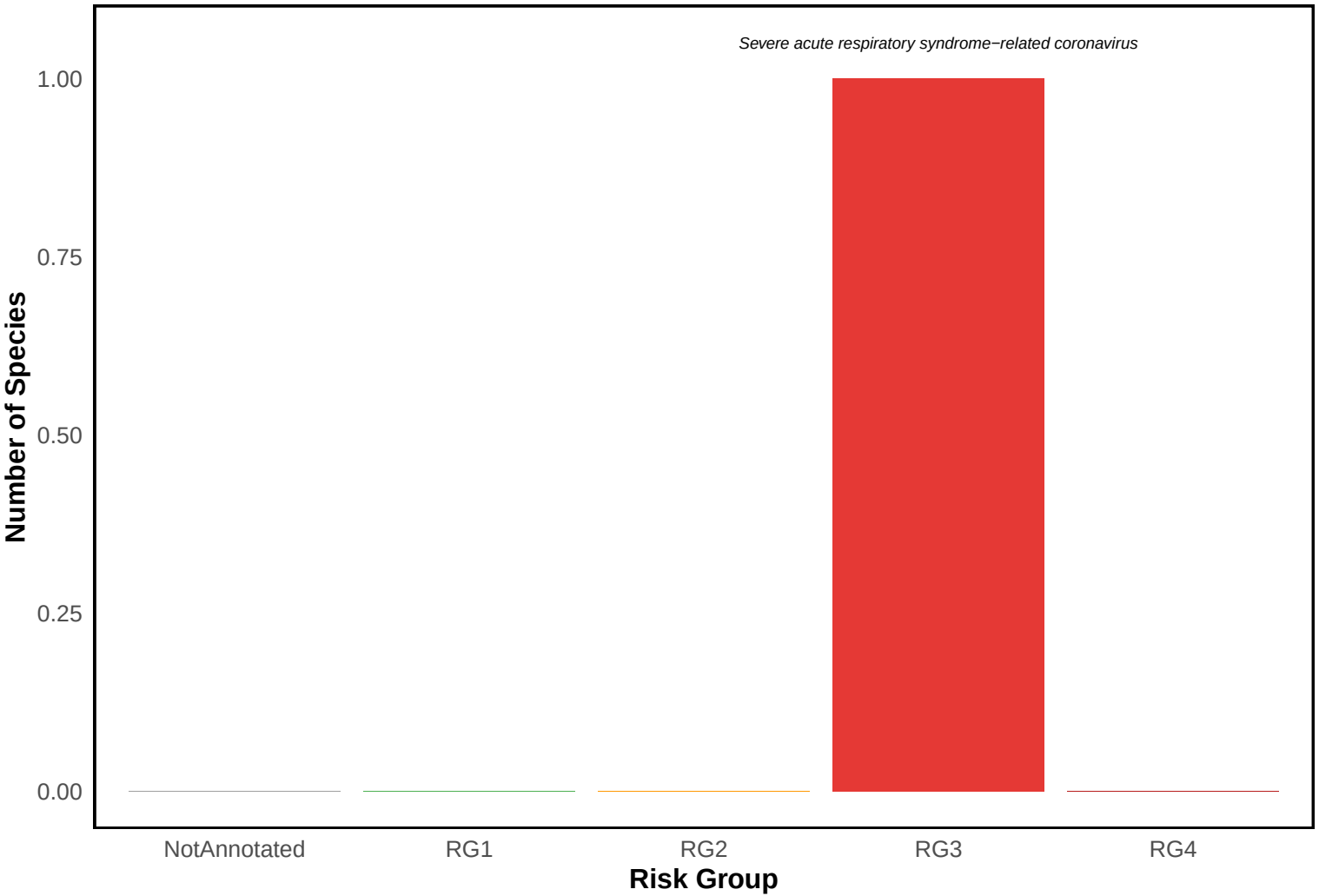
Pathogen detection analysis for sample W61303224:

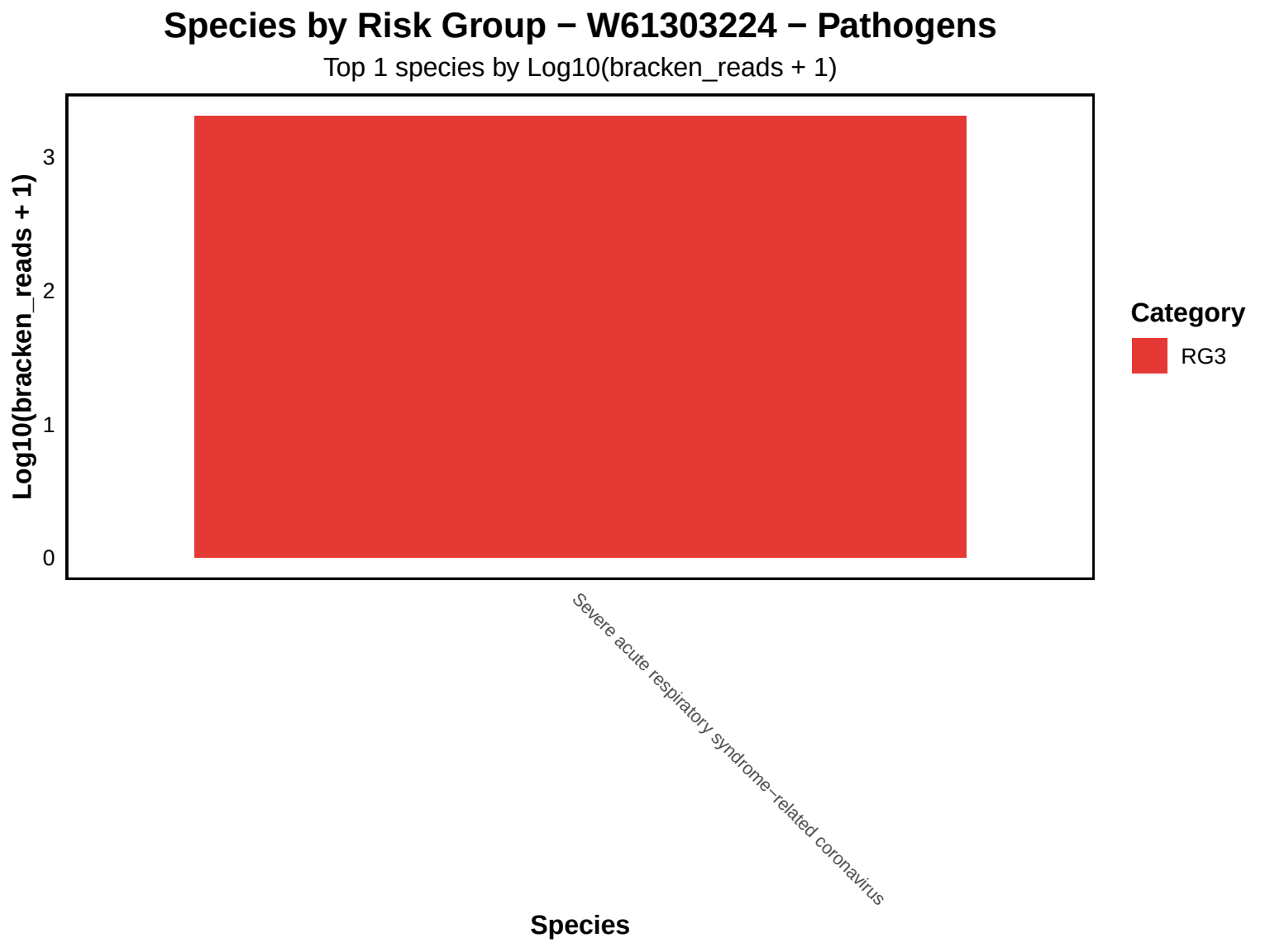
Filtering criteria:
− Include: RG3, RG4 risk groups
− Exclude: RG1, RG2 risk groups
− Exclude: Species annotated as 'Microbiome' in HOMD.Category

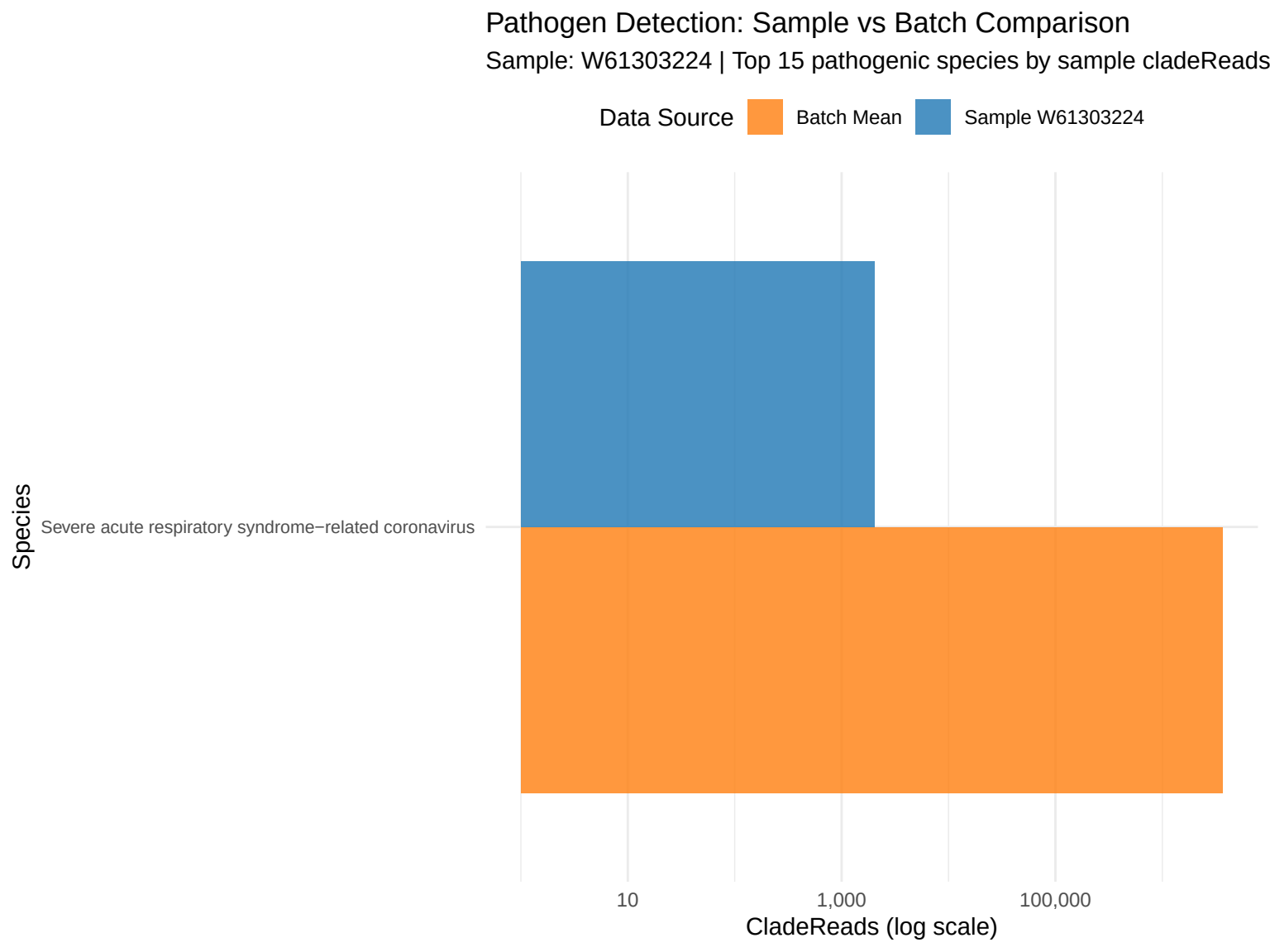
Key findings:
− Total species in sample: 12
− Potential pathogenic species identified: 1
− Most abundant pathogen: Severe acute respiratory syndrome−related coronavirus
− Average pathogen reads: 2012

Species per Risk Group − W61303224 − Pathogens

Total species: 1




Species by Risk Group − W61303224 − Pathogens
Top 1 species by Log10(bracken_reads + 1)
Log10(bracken_reads + 1)
3
2
1
0
Severe acute respiratory syndrome−related coronavirus
Species
Category
RG3


Pathogen Detection: Sample vs Batch Comparison
Sample: W61303224 | Top 15 pathogenic species by sample cladeReads
Data Source
Batch Mean
Sample W61303224
Species
Severe acute respiratory syndrome−related coronavirus
10
1,000
100,000
CladeReads (log scale)

Part 5: Pathogen Detection (RG3/4 Species) − W61304616

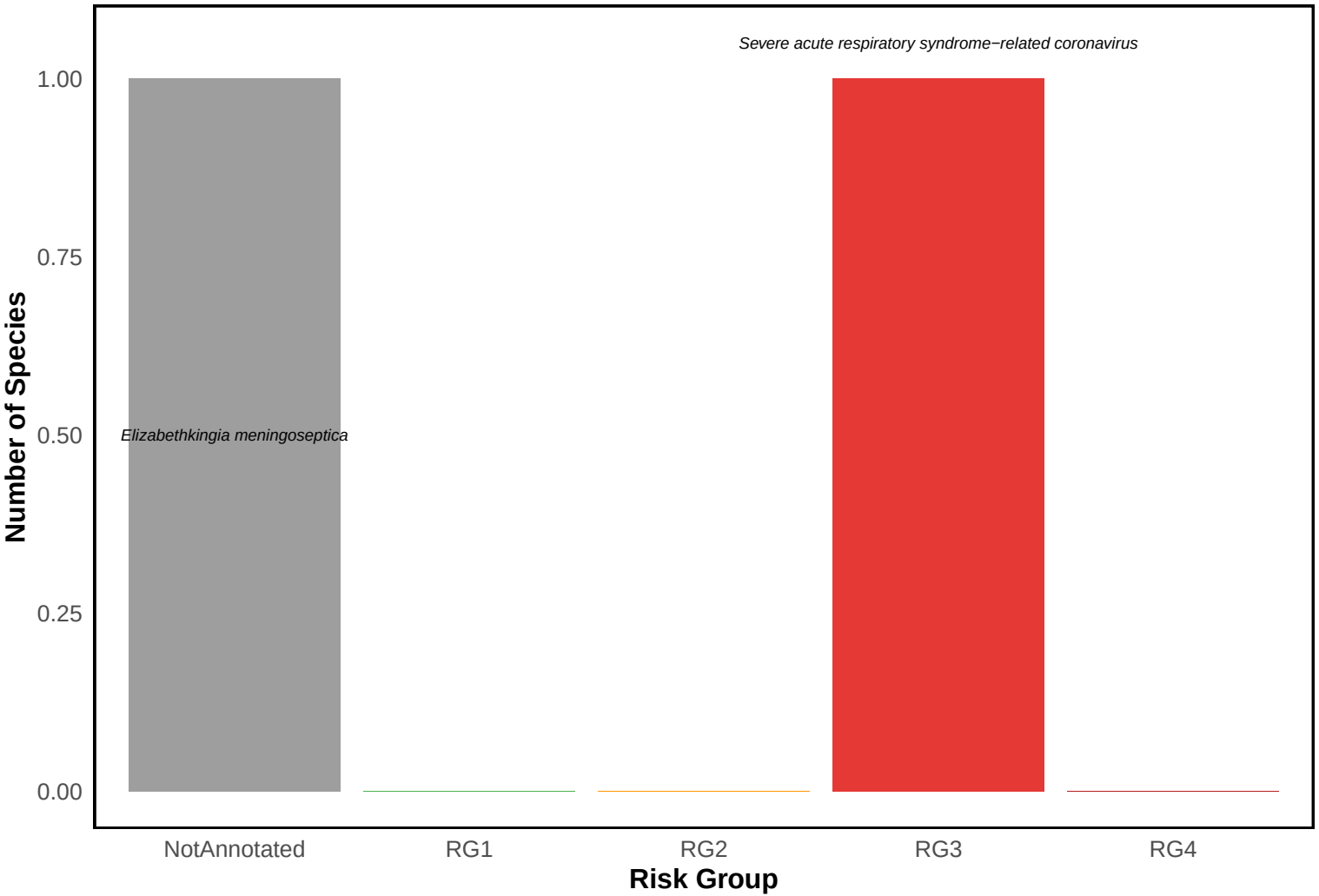
Pathogen detection analysis for sample W61304616:

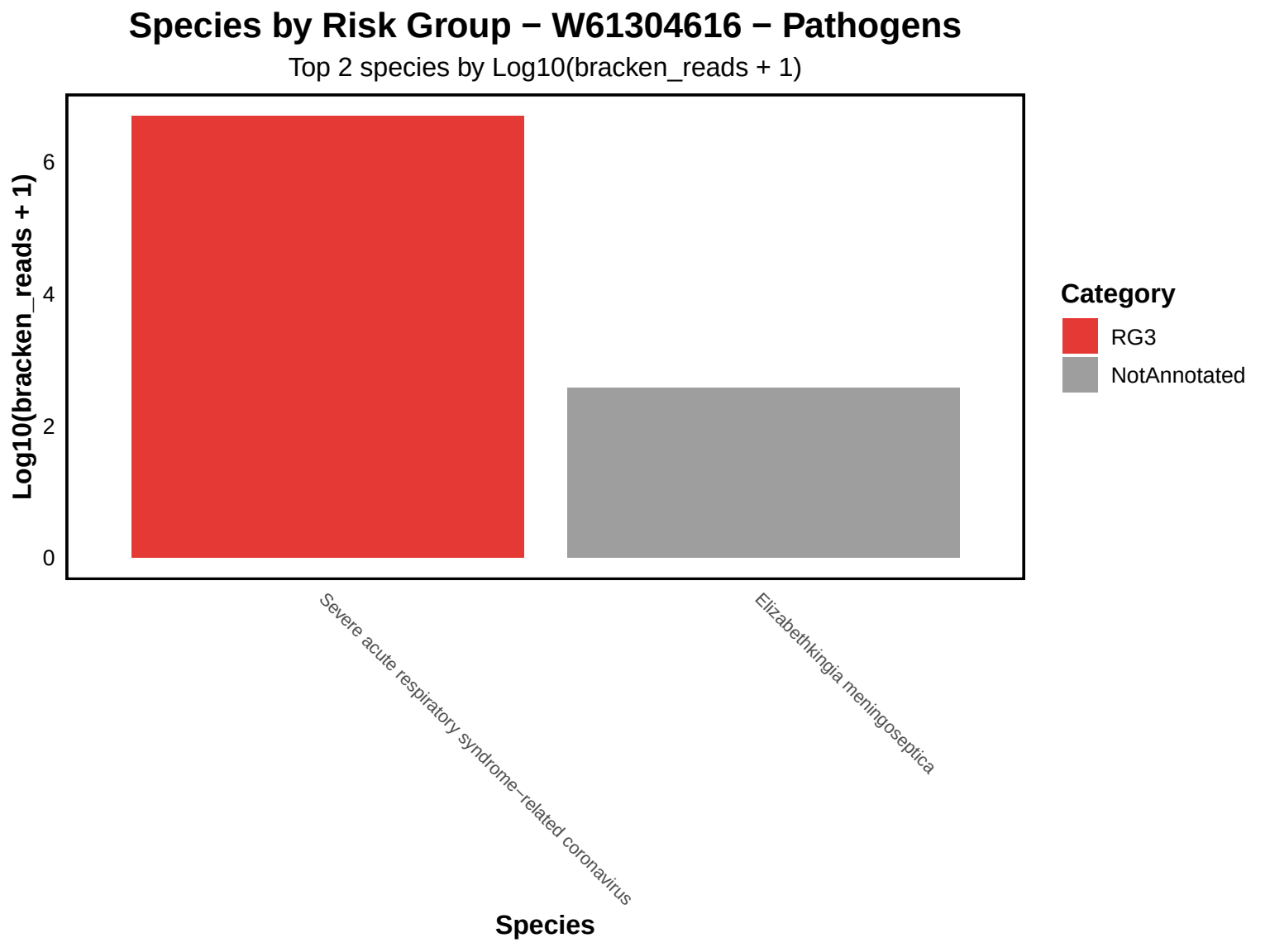
Filtering criteria:
− Include: RG3, RG4 risk groups
− Exclude: RG1, RG2 risk groups
− Exclude: Species annotated as 'Microbiome' in HOMD.Category

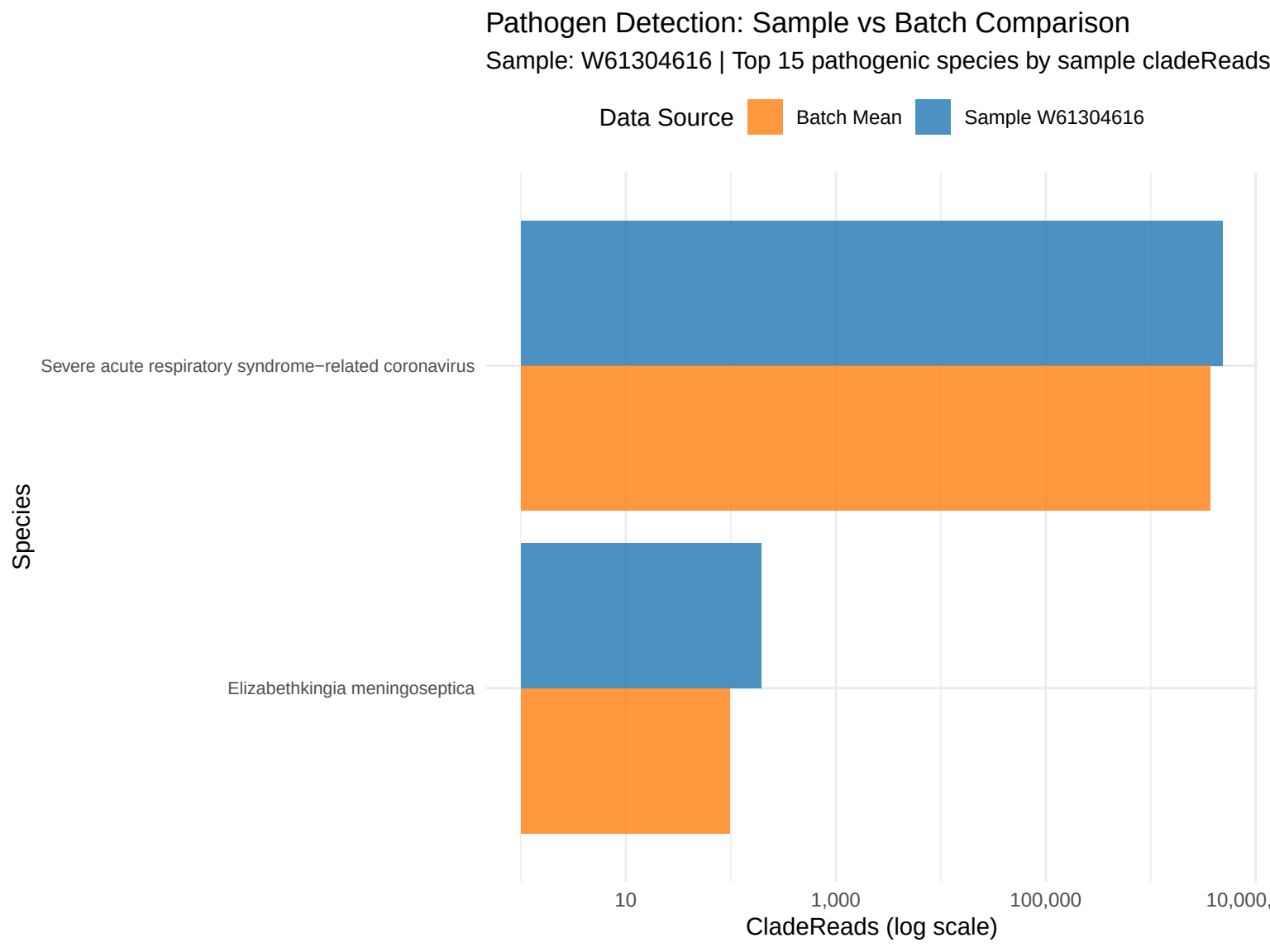
Key findings:
− Total species in sample: 26
− Potential pathogenic species identified: 2
− Most abundant pathogen: Severe acute respiratory syndrome−related coronavirus
− Average pathogen reads: 2429167.5

Species per Risk Group − W61304616 − Pathogens

Total species: 2




Species by Risk Group − W61304616 − Pathogens
Top 2 species by Log10(bracken_reads + 1)
Log10(bracken_reads + 1)
0
2
4
6
Severe acute respiratory syndrome−related coronavirus
Elizabethkingia meningoseptica
Species
Category
RG3
NotAnnotated


Pathogen Detection: Sample vs Batch Comparison
Sample: W61304616 | Top 15 pathogenic species by sample cladeReads
Data Source
Batch Mean
Sample W61304616
Species
Severe acute respiratory syndrome−related coronavirus
Elizabethkingia meningoseptica
10
1,000
100,000
10,000,
CladeReads (log scale)

Part 5: Pathogen Detection (RG3/4 Species) − W61402281

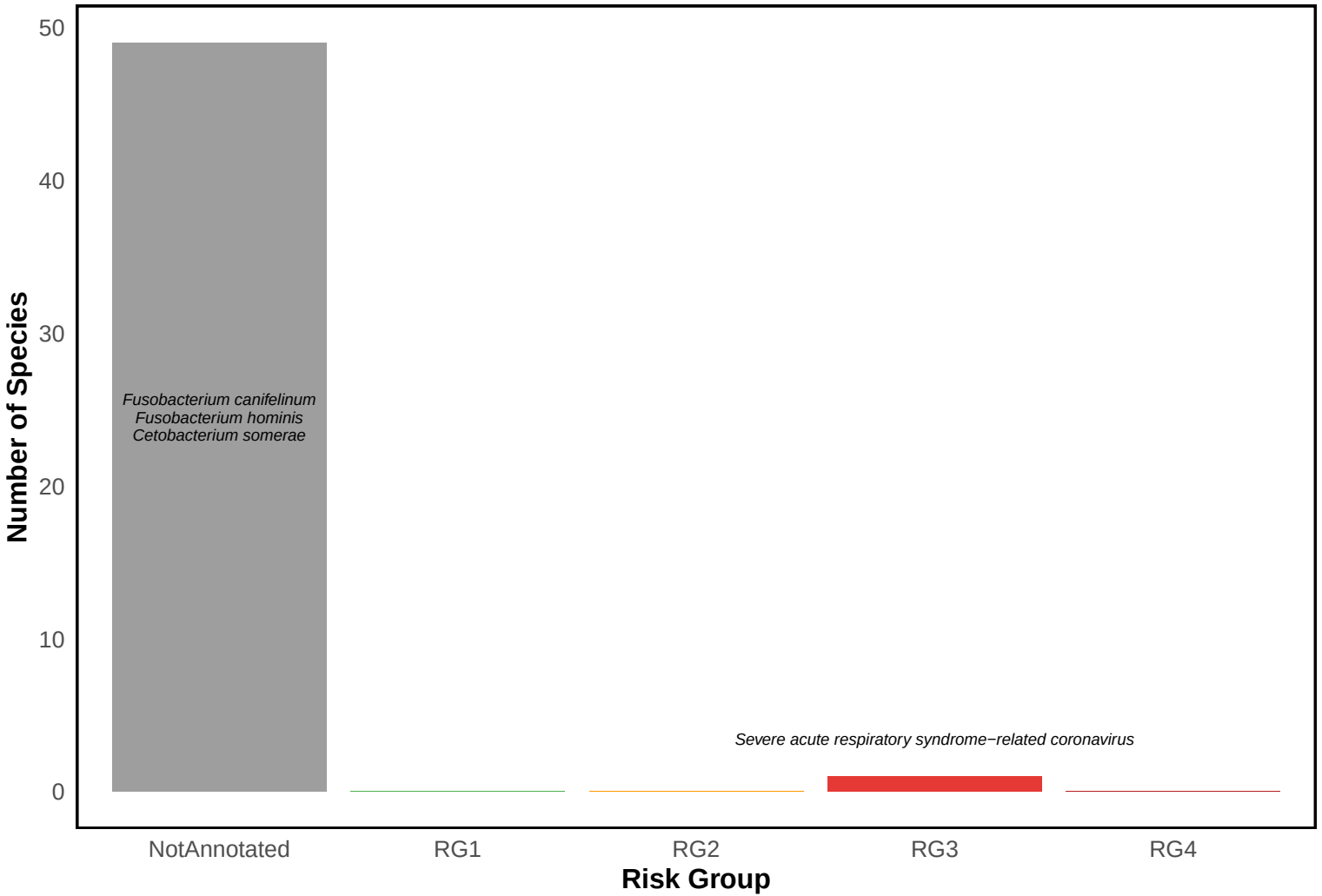
Pathogen detection analysis for sample W61402281:

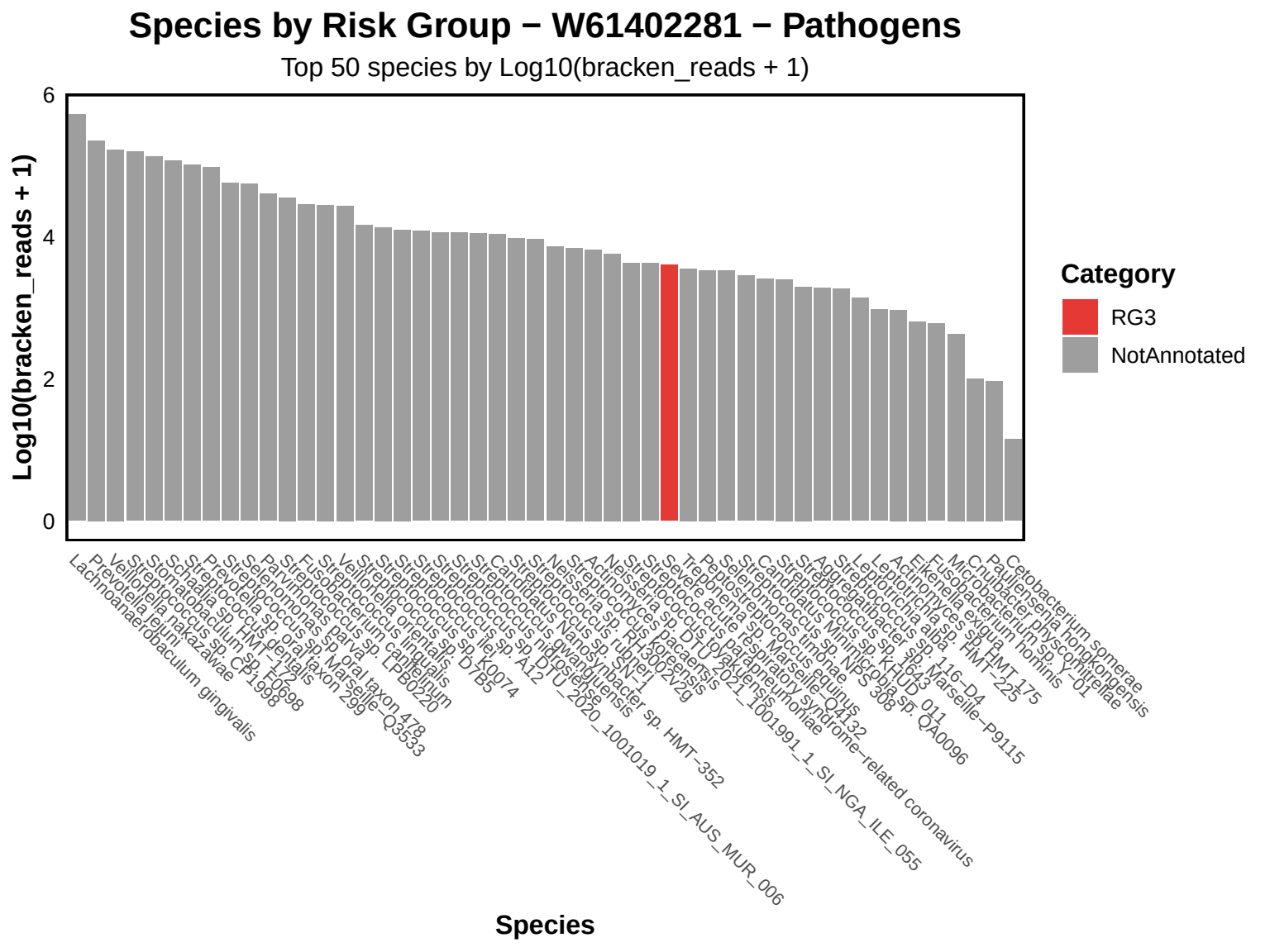
Filtering criteria:
− Include: RG3, RG4 risk groups
− Exclude: RG1, RG2 risk groups
− Exclude: Species annotated as 'Microbiome' in HOMD.Category

Key findings:
− Total species in sample: 193
− Potential pathogenic species identified: 50
− Most abundant pathogen: Lachnoanaerobaculum gingivalis
− Average pathogen reads: 39342.8

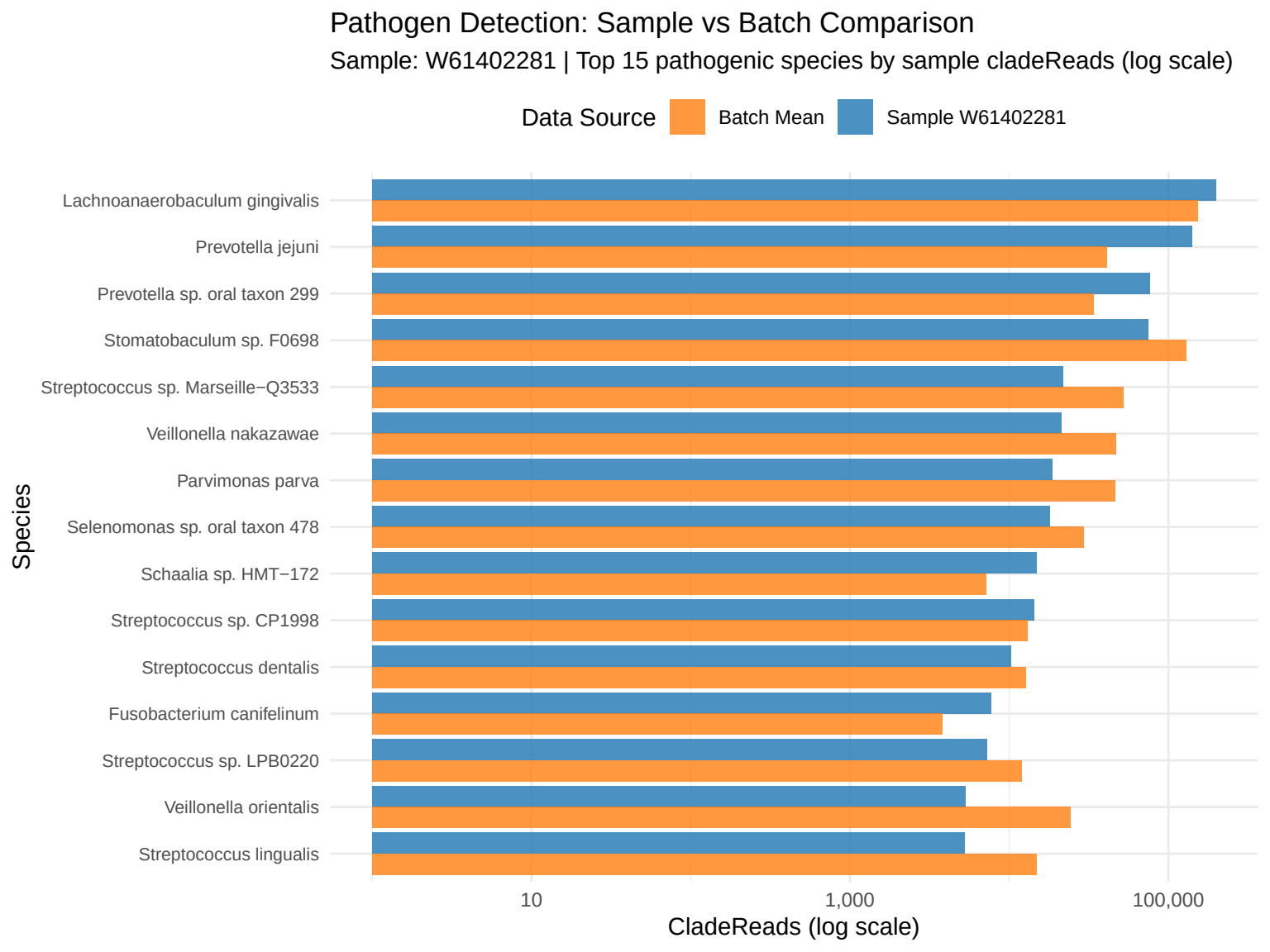
Species per Risk Group − W61402281 − Pathogens

Total species: 50





Species by Risk Group − W61402281 − Pathogens
Top 50 species by Log10(bracken_reads + 1)
Log10(bracken_reads + 1)
0
2
4
6
Category
RG3
NotAnnotated
Species
Lachnoanaerobaculum gingivalis
Prevotella rejuni
Veillonella nakazawae
Streptococcus sp. CP1998
Stomatobaculum sp. E0698
Schaalia sp. HMT−175
Streptococcus dentalis
Prevotella sp. oral taxon 299
Streptococcus sp. Marseille−Q3533
Selenomonas sp. oral taxon 478
Parvimonas parva
Streptococcus sp. LPB0220
Fusobacterium canifelinum
Streptococcus lingualis
Veillonella orientalis
Streptococcus sp. D7B5
Streptococcus sp. K0074
Streptococcus ile
Streptococcus sp. A12
Streptococcus nidrosense
Candidatus Nanosynbacter sp. HMT−352
Streptococcus gwangjuensis
Streptococcus sp. SN−1
Neisseria sp. RH3002v2g
Actinomyces pacaensis
Neisseria sp. DTU−2021_1001991_1_SI_NGA_ILE_055
Streptococcus rubneri
Streptococcus sp. DTU−2020_1001019_1_SI_AUS_MUR_006
Streptococcus toyakuensis
Severe acute respiratory syndrome−related coronavirus
Treponema sp. Marseille−Q4132
Peptostreptococcus equinus
Selenomonas sp. NPS 308
Streptococcus sp. KHUD_011
Candidatus Minimicrobia sp. QA0096
Streptococcus sp. 116−D4
Aggregatibacter sp. 1643
Streptococcus sp. Marseille−P9115
Leptotrichia alba
Leptotrichia sp. HMT−225
Actinomyces sp. HMT−175
Eikenella exigua
Fusobacterium hominis
Microbacterium sp. Y−01
Cnuibacter physcomitrellae
Paulensenia hongkongensis
Cetobacterium somerae


Pathogen Detection: Sample vs Batch Comparison
Sample: W61402281 | Top 15 pathogenic species by sample cladeReads (log scale)
Data Source
Batch Mean
Sample W61402281
Species
Lachnoanaerobaculum gingivalis
Prevotella jejuni
Prevotella sp. oral taxon 299
Stomatobaculum sp. F0698
Streptococcus sp. Marseille−Q3533
Veillonella nakazawae
Parvimonas parva
Selenomonas sp. oral taxon 478
Schaalia sp. HMT−172
Streptococcus sp. CP1998
Streptococcus dentalis
Fusobacterium canifelinum
Streptococcus sp. LPB0220
Veillonella orientalis
Streptococcus lingualis
10
1,000
100,000
CladeReads (log scale)

Part 5: Pathogen Detection (RG3/4 Species) − W61402322

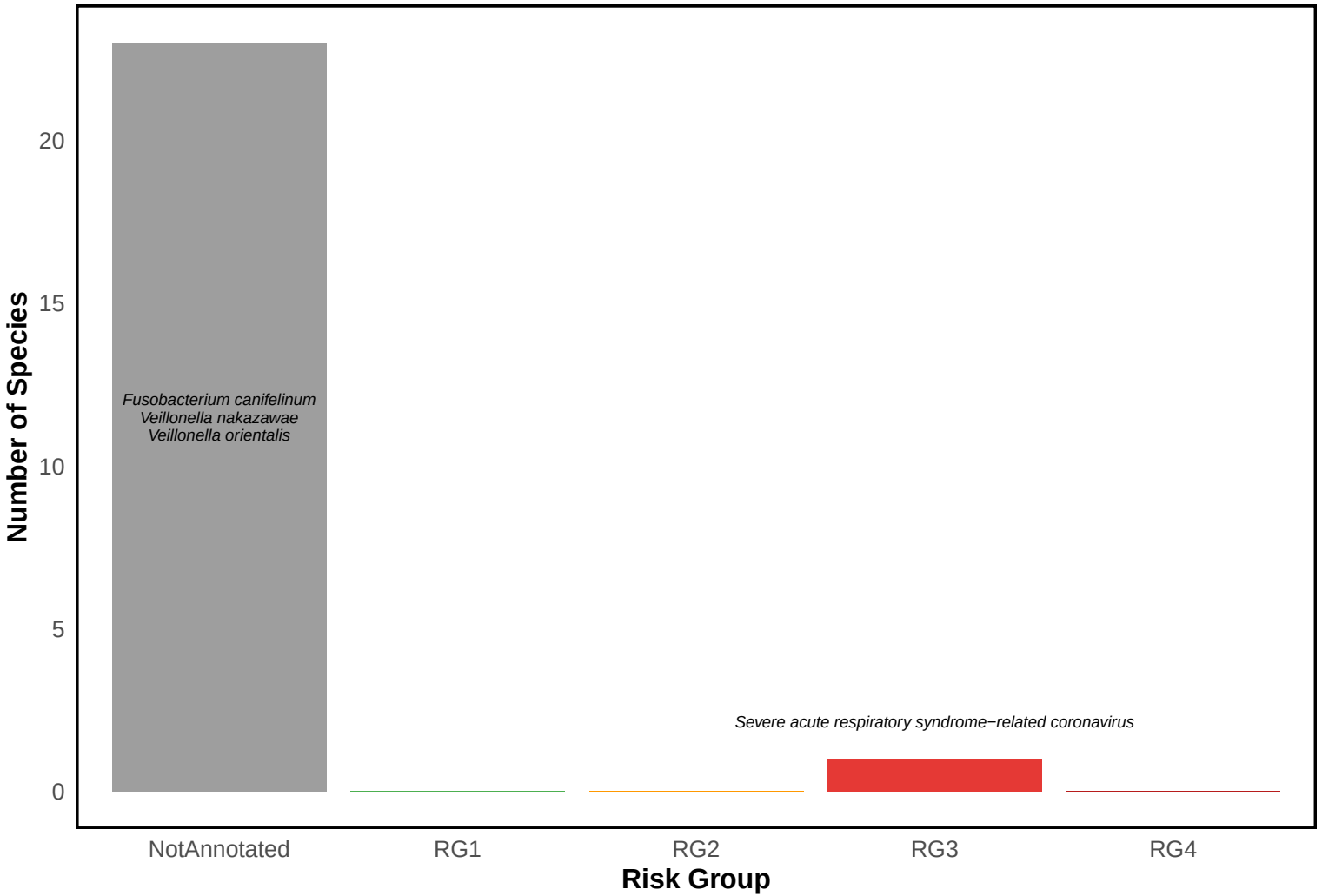
Pathogen detection analysis for sample W61402322:

Filtering criteria:
− Include: RG3, RG4 risk groups
− Exclude: RG1, RG2 risk groups
− Exclude: Species annotated as 'Microbiome' in HOMD.Category

Key findings:
− Total species in sample: 114
− Potential pathogenic species identified: 24
− Most abundant pathogen: Lachnoanaerobaculum gingivalis
− Average pathogen reads: 18341.8

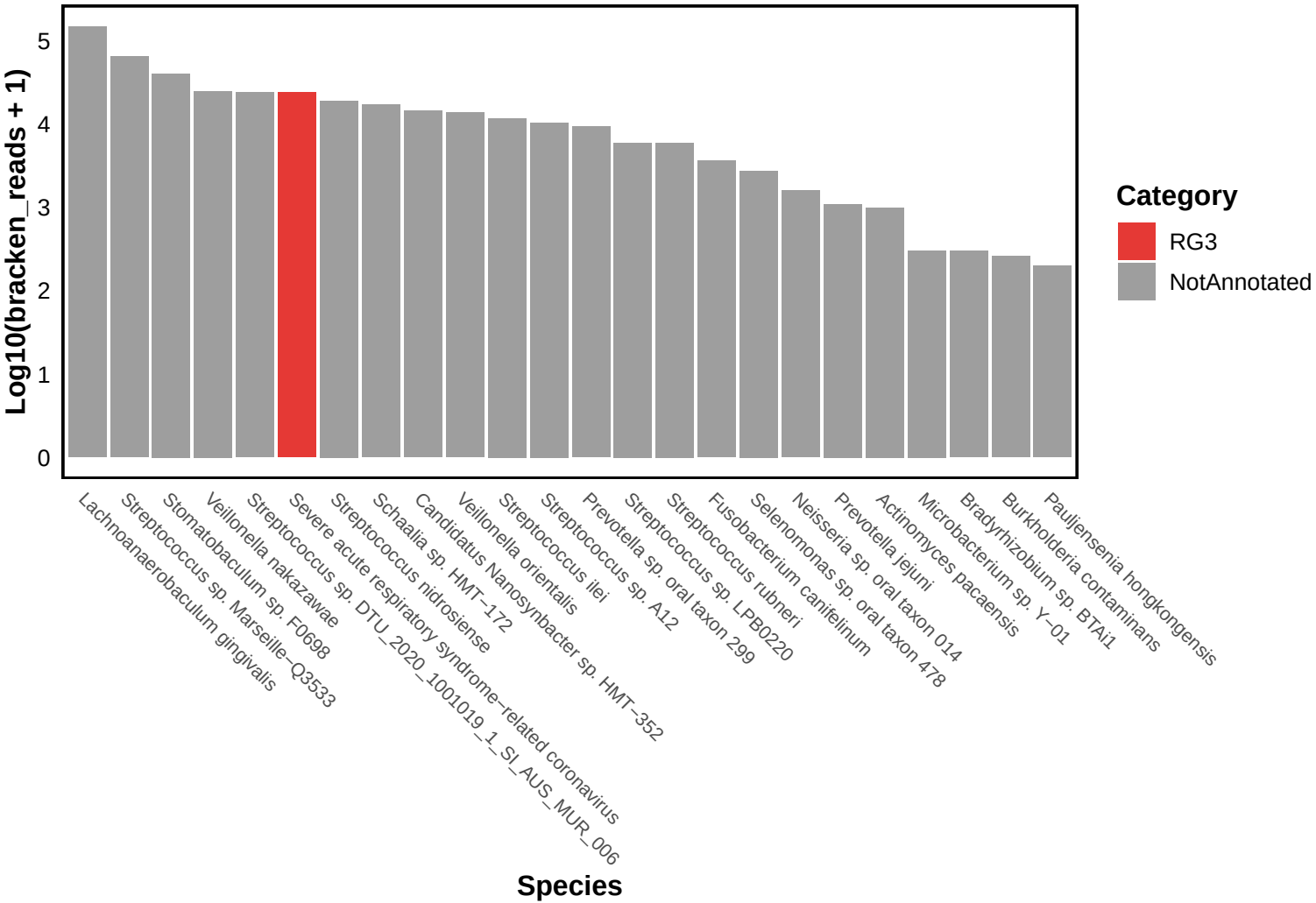
Species per Risk Group − W61402322 − Pathogens

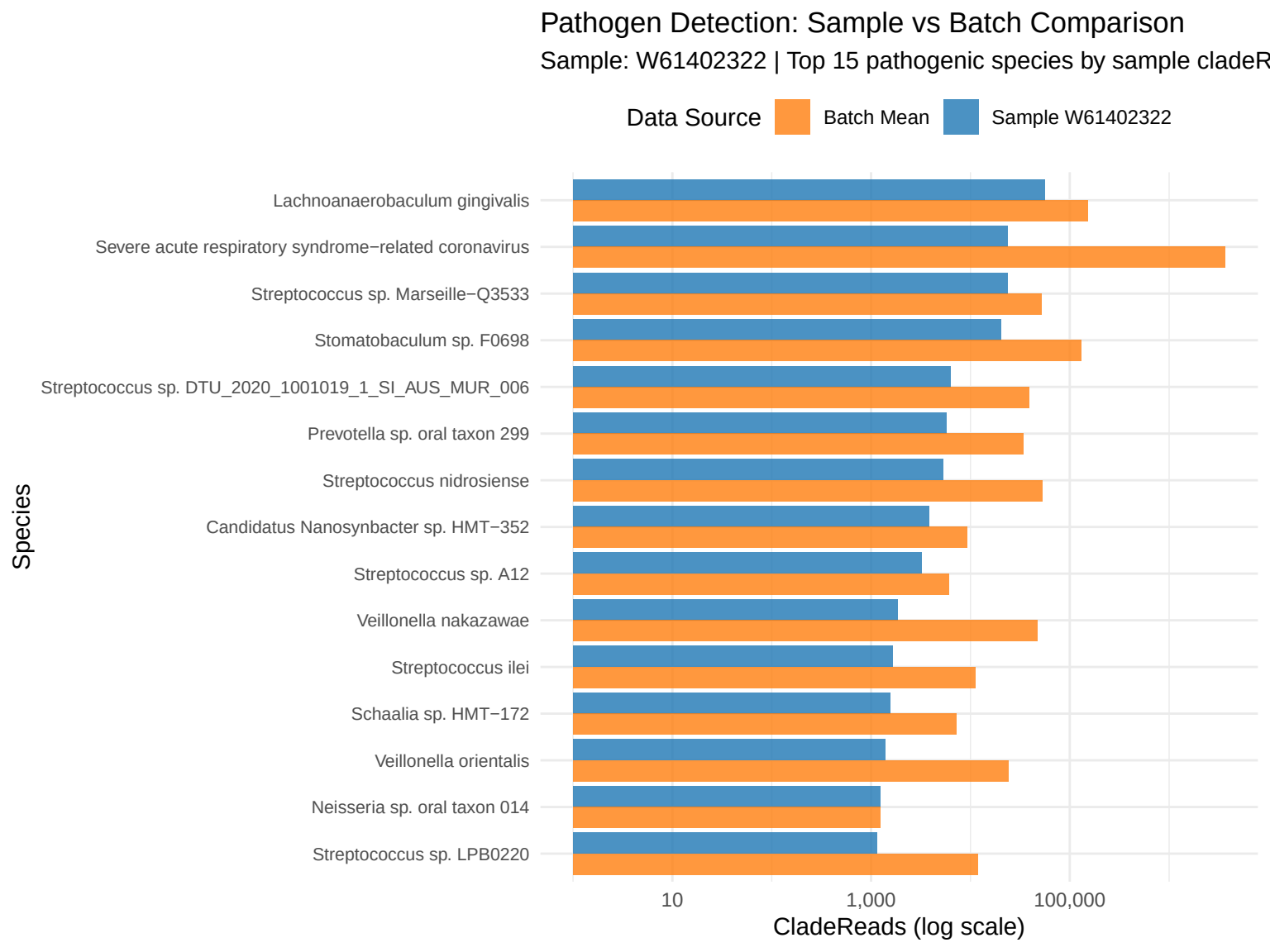
Total species: 24



Species by Risk Group − W61402322 − Pathogens

Top 24 species by Log10(bracken_reads + 1)




Pathogen Detection: Sample vs Batch Comparison
Sample: W61402322 | Top 15 pathogenic species by sample cladeR
Data Source
Batch Mean
Sample W61402322
Species
Lachnoanaerobaculum gingivalis
Severe acute respiratory syndrome−related coronavirus
Streptococcus sp. Marseille−Q3533
Stomatobaculum sp. F0698
Streptococcus sp. DTU_2020_1001019_1_SI_AUS_MUR_006
Prevotella sp. oral taxon 299
Streptococcus nidrosiense
Candidatus Nanosynbacter sp. HMT−352
Streptococcus sp. A12
Veillonella nakazawae
Streptococcus ilei
Schaalia sp. HMT−172
Veillonella orientalis
Neisseria sp. oral taxon 014
Streptococcus sp. LPB0220
10
1,000
100,000
CladeReads (log scale)

Part 5: Pathogen Detection (RG3/4 Species) − W61501463

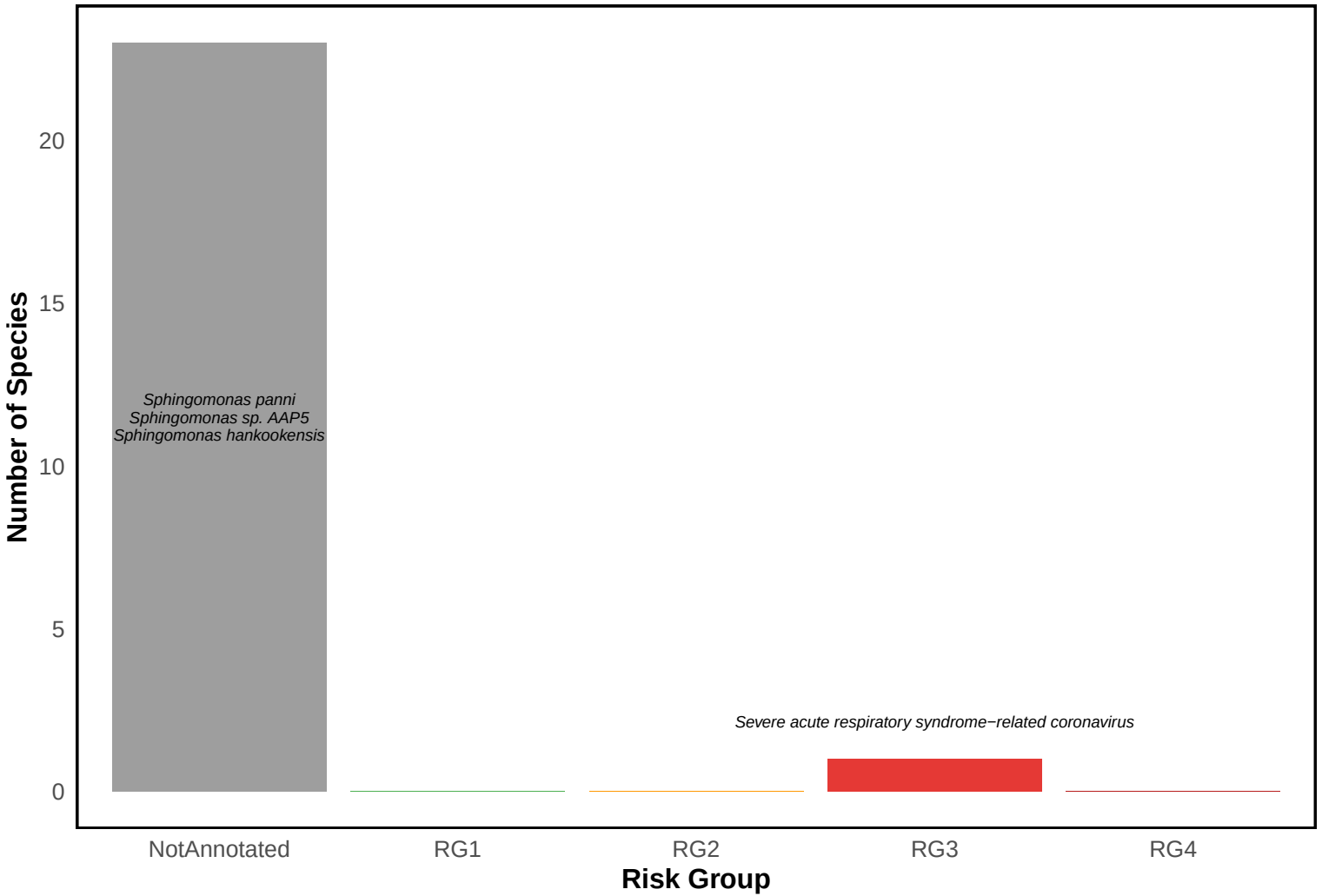
Pathogen detection analysis for sample W61501463:

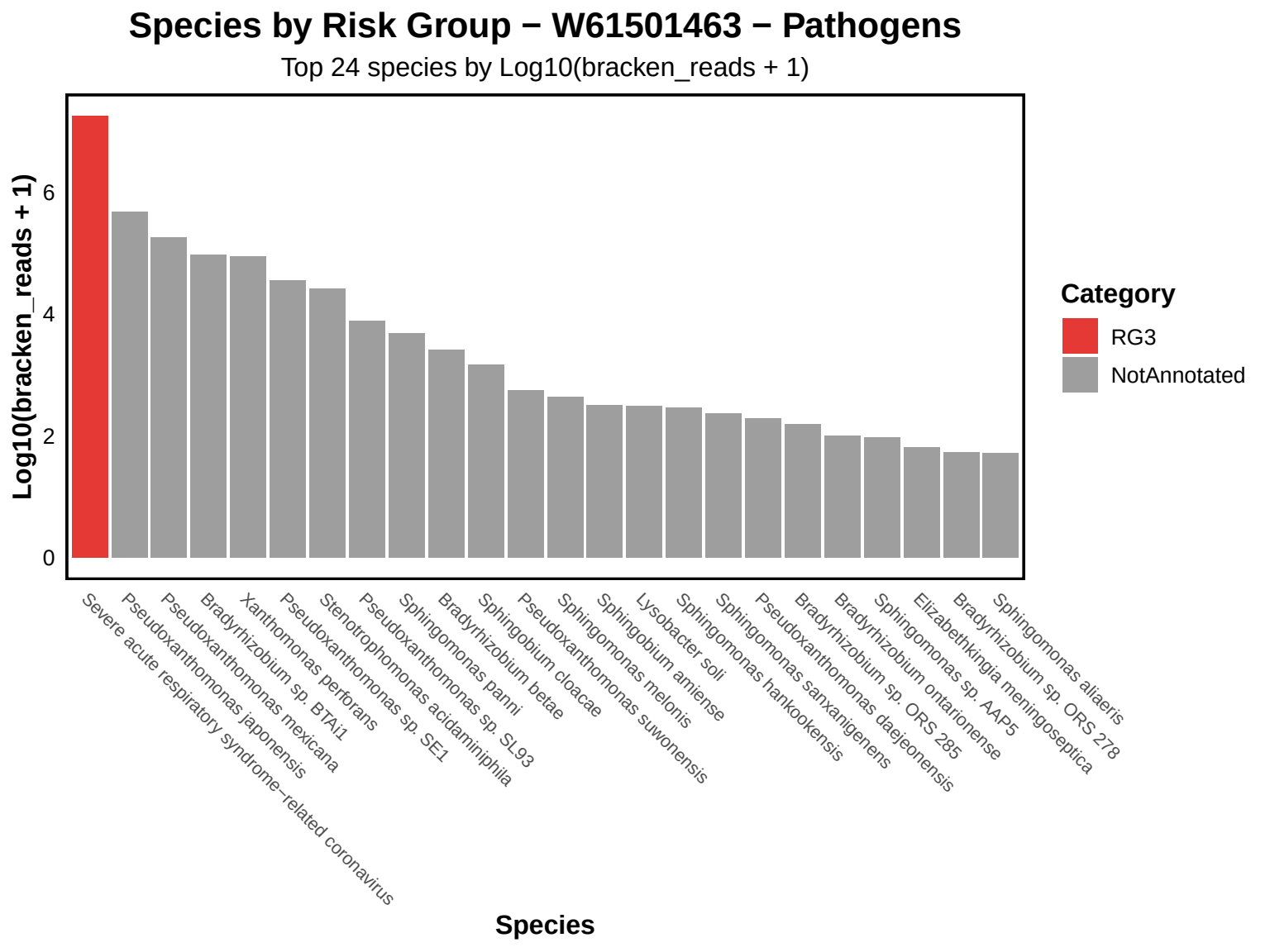
Filtering criteria:
− Include: RG3, RG4 risk groups
− Exclude: RG1, RG2 risk groups
− Exclude: Species annotated as 'Microbiome' in HOMD.Category

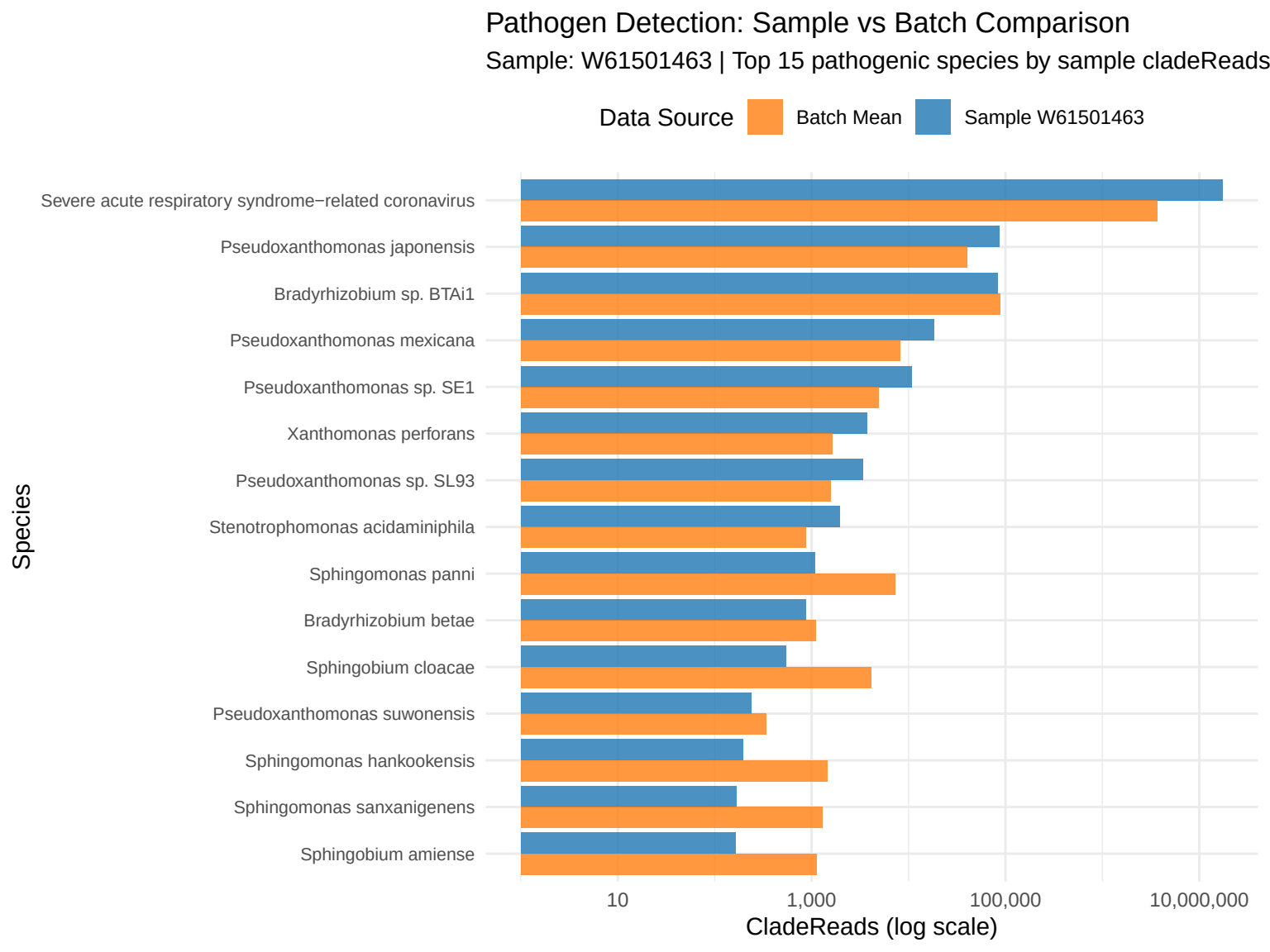
Key findings:
− Total species in sample: 45
− Potential pathogenic species identified: 24
− Most abundant pathogen: Severe acute respiratory syndrome−related coronavirus
− Average pathogen reads: 766097.3

Species per Risk Group − W61501463 − Pathogens

Total species: 24




Species by Risk Group − W61501463 − Pathogens
Top 24 species by Log10(bracken_reads + 1)
Log10(bracken_reads + 1)
0
2
4
6
Severe acute respiratory syndrome−related coronavirus
Pseudoxanthomonas japonensis
Pseudoxanthomonas mexicana
Bradyrhizobium sp. BTAi1
Xanthomonas perforans
Pseudoxanthomonas sp. SE1
Stenotrophomonas acidaminiphila
Pseudoxanthomonas sp. SL93
Sphingomonas panni
Bradyrhizobium betae
Sphingobium cloacae
Pseudoxanthomonas suwonensis
Sphingomonas melonis
Sphingobium amiense
Lysobacter soli
Sphingomonas hankookensis
Pseudoxanthomonas sanxanigenens
Bradyrhizobium sp. ORS 285
Bradyrhizobium daejeonensis
Sphingomonas sp. AAP5
Bradyrhizobium ontariense
Elizabethkingia meningoseptica
Bradyrhizobium sp. ORS 278
Sphingomonas aliaeris
Species
Category
RG3
NotAnnotated


Pathogen Detection: Sample vs Batch Comparison
Sample: W61501463 | Top 15 pathogenic species by sample cladeReads
Data Source
Batch Mean
Sample W61501463
Severe acute respiratory syndrome−related coronavirus
Pseudoxanthomonas japonensis
Bradyrhizobium sp. BTAi1
Pseudoxanthomonas mexicana
Pseudoxanthomonas sp. SE1
Xanthomonas perforans
Pseudoxanthomonas sp. SL93
Stenotrophomonas acidaminiphila
Sphingomonas panni
Bradyrhizobium betae
Sphingobium cloacae
Pseudoxanthomonas suwonensis
Sphingomonas hankookensis
Sphingomonas sanxanigenens
Sphingobium amiense
Species
10
1,000
100,000
10,000,000
CladeReads (log scale)

Part 5: Pathogen Detection (RG3/4 Species) − W71607201

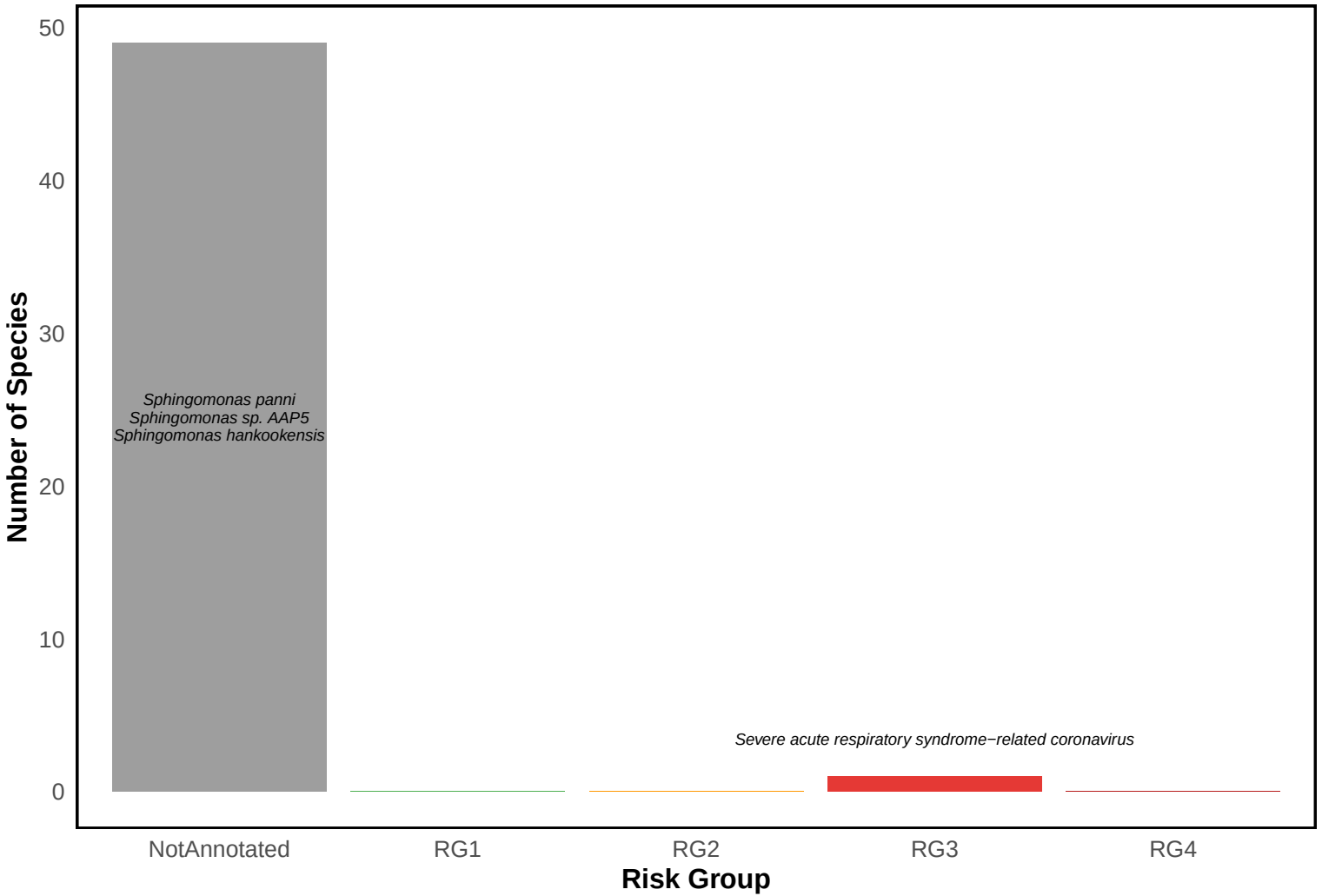
Pathogen detection analysis for sample W71607201:

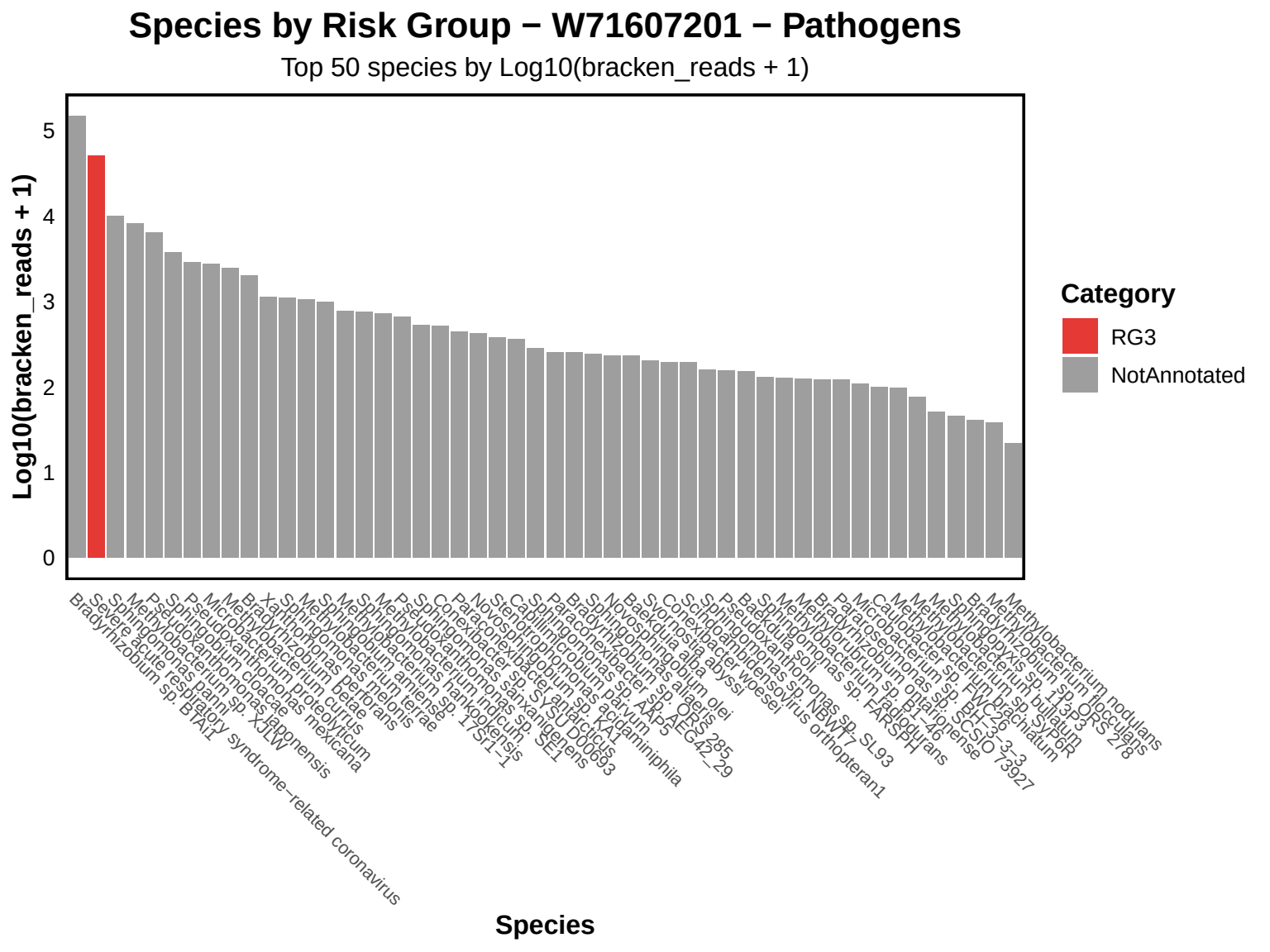
Filtering criteria:
− Include: RG3, RG4 risk groups
− Exclude: RG1, RG2 risk groups
− Exclude: Species annotated as 'Microbiome' in HOMD.Category

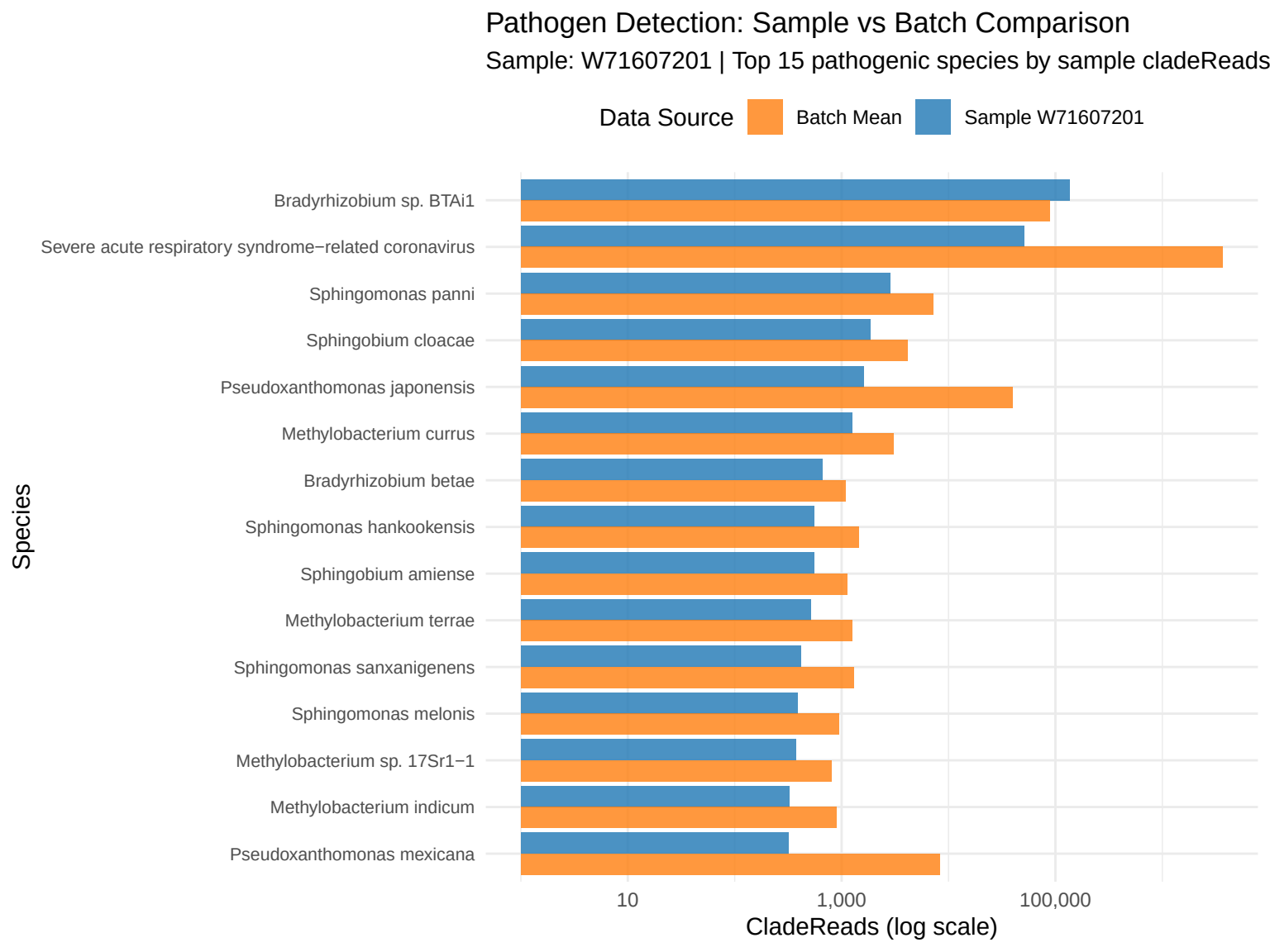
Key findings:
− Total species in sample: 77
− Potential pathogenic species identified: 50
− Most abundant pathogen: Bradyrhizobium sp. BTAi1
− Average pathogen reads: 4966.1

Species per Risk Group − W71607201 − Pathogens

Total species: 50




Species by Risk Group − W71607201 − Pathogens
Top 50 species by Log10(bracken_reads + 1)
Log10(bracken_reads + 1)
0
1
2
3
4
5
Category
RG3
NotAnnotated
Bradyrhizobium sp. BTAi1
Severe acute respiratory syndrome−related coronavirus
Sphingomonas panni
Methylobacterium sp. XJLW
Pseudoxanthomonas japonensis
Sphingobium cloacae
Pseudoxanthomonas mexicana
Microbacterium proteolyticum
Methylobacterium currus
Bradyrhizobium betae
Xanthomonas perforans
Sphingomonas melonis
Methylobacterium terrae
Sphingobium amiense
Methylobacterium sp. 17Sr1-1
Sphingomonas hankookensis
Pseudoxanthomonas sp. SE1
Conexibacter sp. SYSU0006 63
Paracoccus sanxanigenens
Novosphingobium sp. AXP5
Stenotrophomonas sp. AEG42_29
Caulimicrobium parvum
Sphingomonas acidaminiphila
Paracoccus sp. AXP5
Bradyrhizobium sp. ORS 285
Novosphingobium olei
Baekduia alba
Svornostia abyssi
Conexibacter woesei
Scindoambidensovirus orthopteran1
Sphingomonas sp. NBWT7
Pseudoxanthomonas sp. SL93
Baekduia soli
Sphingomonas sp. FARSPH
Methylobacterium radiodurans
Methylorubrum sp. FARSPH
Bradyrhizobium sp. BTA46
Pararoseomonas sp. SCSIO 73927
Microbacterium sp. FWC26-3-3
Caulobacter sp. FWC26-3-3
Methylobacterium sp. SCSIO 73927
Methylobacterium sp. FWC26-3-3
Sphingopyxis sp. SYP6R
Bradyrhizobium sp. ORS 278
Methylobacterium nodulans
Methylobacterium flocculans
Species


Pathogen Detection: Sample vs Batch Comparison
Sample: W71607201 | Top 15 pathogenic species by sample cladeReads
Data Source
Batch Mean
Sample W71607201
Species
Bradyrhizobium sp. BTAi1
Severe acute respiratory syndrome−related coronavirus
Sphingomonas panni
Sphingobium cloacae
Pseudoxanthomonas japonensis
Methylobacterium currus
Bradyrhizobium betae
Sphingomonas hankookensis
Sphingobium amiense
Methylobacterium terrae
Sphingomonas sanxanigenens
Sphingomonas melonis
Methylobacterium sp. 17Sr1−1
Methylobacterium indicum
Pseudoxanthomonas mexicana
10
1,000
100,000
CladeReads (log scale)

Part 5: Pathogen Detection (RG3/4 Species) − W72504187

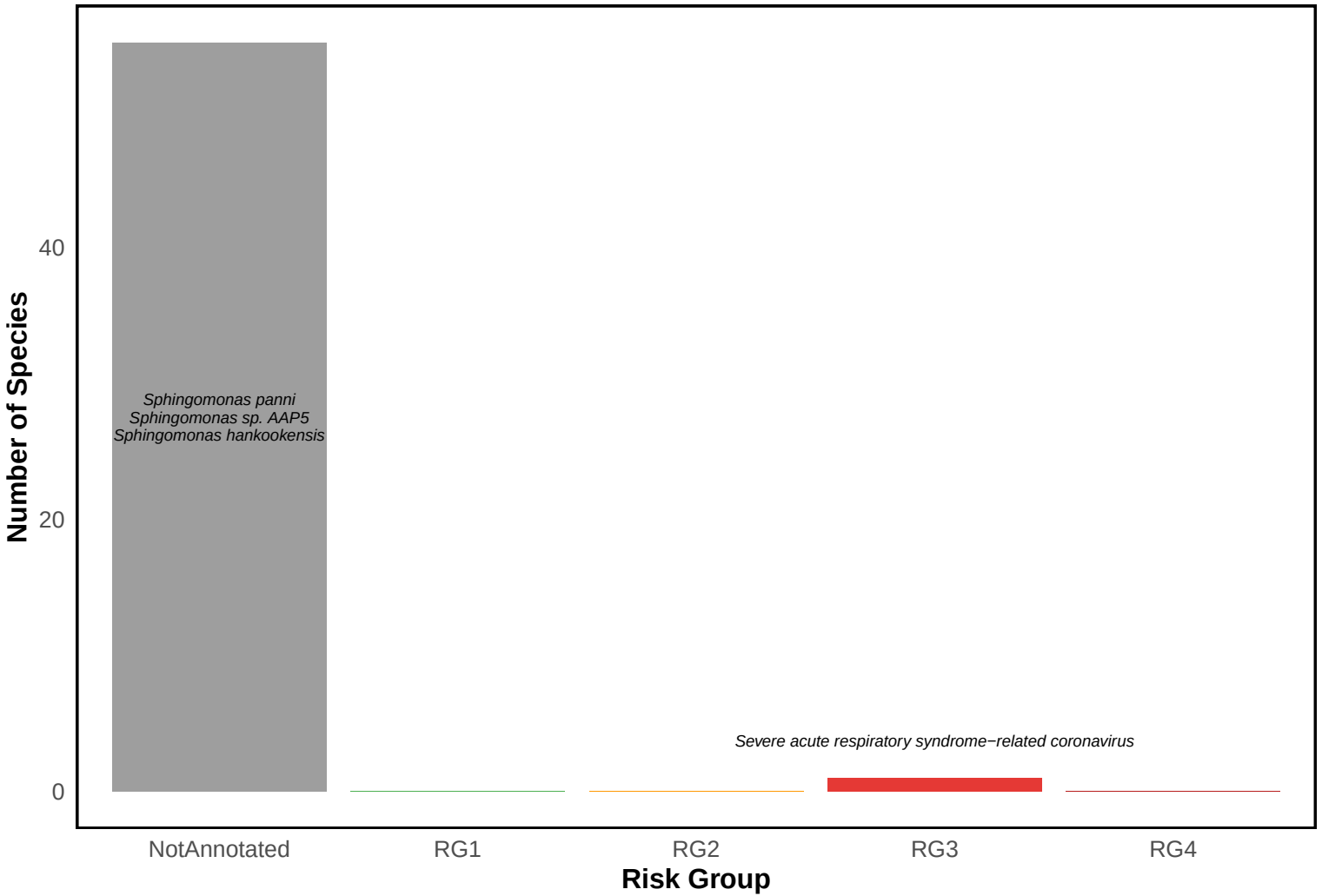
Pathogen detection analysis for sample W72504187:

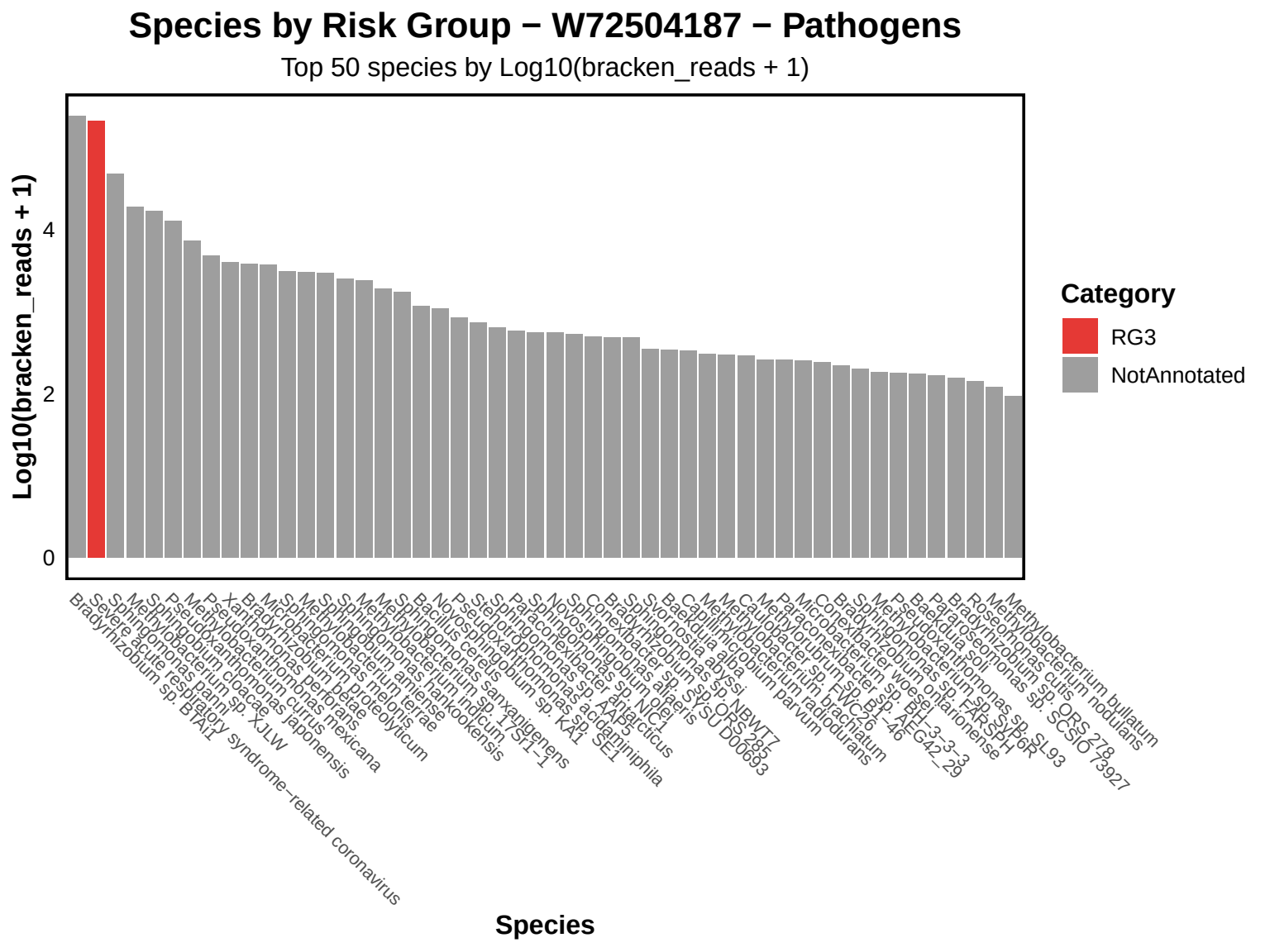
Filtering criteria:
− Include: RG3, RG4 risk groups
− Exclude: RG1, RG2 risk groups
− Exclude: Species annotated as 'Microbiome' in HOMD.Category

Key findings:
− Total species in sample: 79
− Potential pathogenic species identified: 56
− Most abundant pathogen: Bradyrhizobium sp. BTAi1
− Average pathogen reads: 10659.6

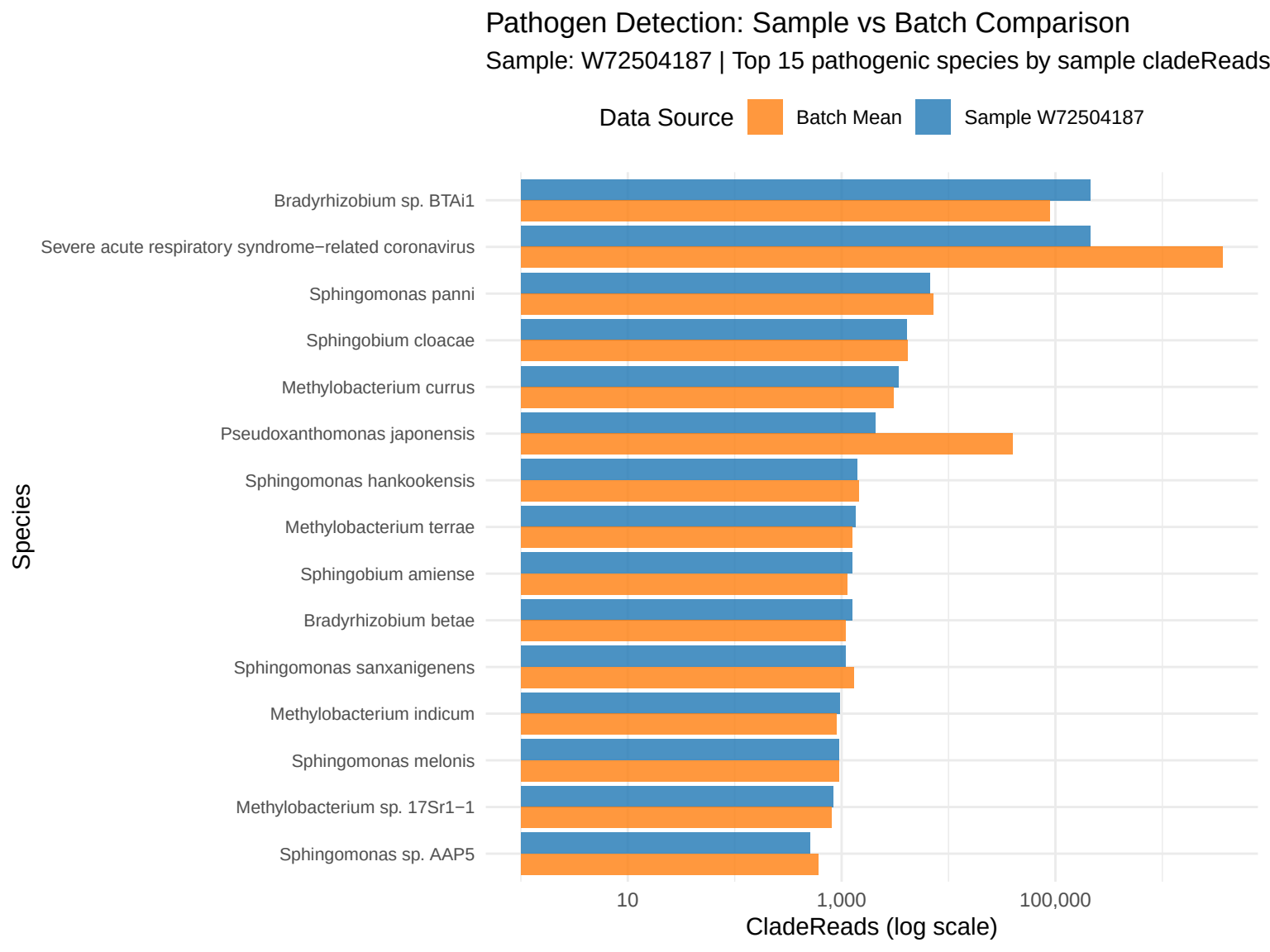
Species per Risk Group − W72504187 − Pathogens

Total species: 56





Species by Risk Group − W72504187 − Pathogens
Top 50 species by Log10(bracken_reads + 1)
Log10(bracken_reads + 1)
0
2
4
Category
RG3
NotAnnotated
Bradyrhizobium sp. BTAi1
Severe acute respiratory syndrome−related coronavirus
Sphingomonas panni
Methylobacterium sp. XJLW
Sphingobium cloacae
Pseudoxanthomonas japonensis
Methylobacterium currus
Xanthomonas perforans
Bradyrhizobium betae
Microbacterium proteolyticum
Sphingomonas melonis
Methylobacterium terrae
Sphingobium amiense
Sphingomonas hankookensis
Methylobacterium indicum
Sphingomonas sanxanigenens
Bacillus cereus
Novosphingobium sp. KA1
Pseudoxanthomonas sp. 1 SFL1
Stenotrophomonas sp. AAP5
Sphingomonas acidaminiphila
Paraconiexibacter antarcticus
Novosphingobium olei
Sphingomonas sp. NIC1
Conexibacter sp. SYSU D00693
Bradyrhizobium sp. ORS 285
Sphingomonas sp. NBWT7
Svornostia abyssi
Baekdulia alba
Capillimicrobium parvum
Methylobacterium radiodurans
Caulobacter sp. FWC26
Methylorubrum sp. BJ−46
Paraconexibacter sp. AEG42_29
Microbacterium sp. BH−3−3−3
Conexibacter woesei
Bradyrhizobium ontariense
Sphingomonas sp. FARSPH
Methylobacterium sp. SL93
Pseudoxanthomonas sp. SCSIO 73927
Baekdulia soli
Pararoseomonas sp. ORS 278
Bradyrhizobium sp. SCSIO 73927
Roseomonas cutis
Methylobacterium nodulans
Methylobacterium bullatum
Species


Pathogen Detection: Sample vs Batch Comparison
Sample: W72504187 | Top 15 pathogenic species by sample cladeReads
Data Source
Batch Mean
Sample W72504187
Species
Bradyrhizobium sp. BTAi1
Severe acute respiratory syndrome−related coronavirus
Sphingomonas panni
Sphingobium cloacae
Methylobacterium currus
Pseudoxanthomonas japonensis
Sphingomonas hankookensis
Methylobacterium terrae
Sphingobium amiense
Bradyrhizobium betae
Sphingomonas sanxanigenens
Methylobacterium indicum
Sphingomonas melonis
Methylobacterium sp. 17Sr1−1
Sphingomonas sp. AAP5
10
1,000
100,000
CladeReads (log scale)

Part 5: Pathogen Detection (RG3/4 Species) − W72803699

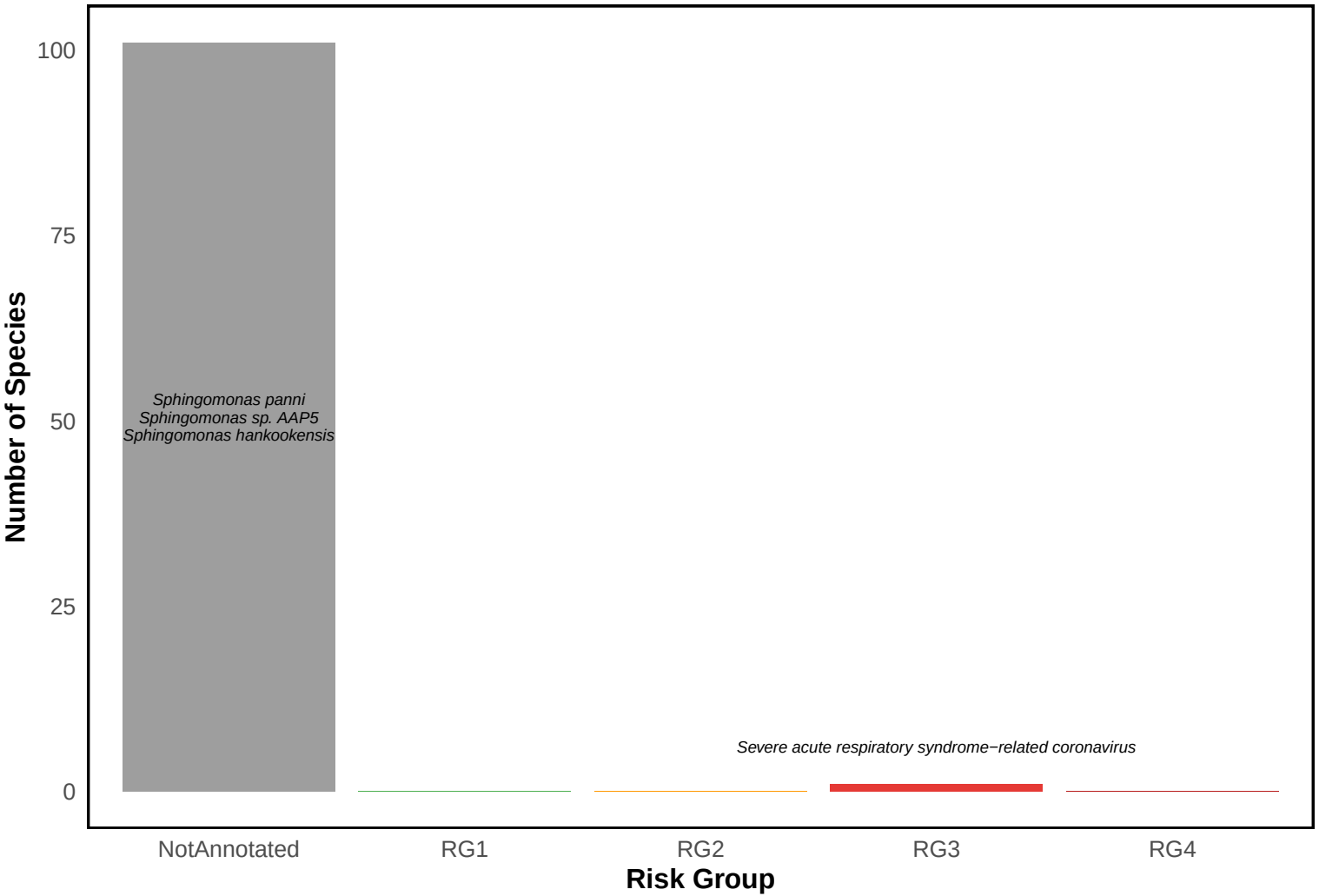
Pathogen detection analysis for sample W72803699:

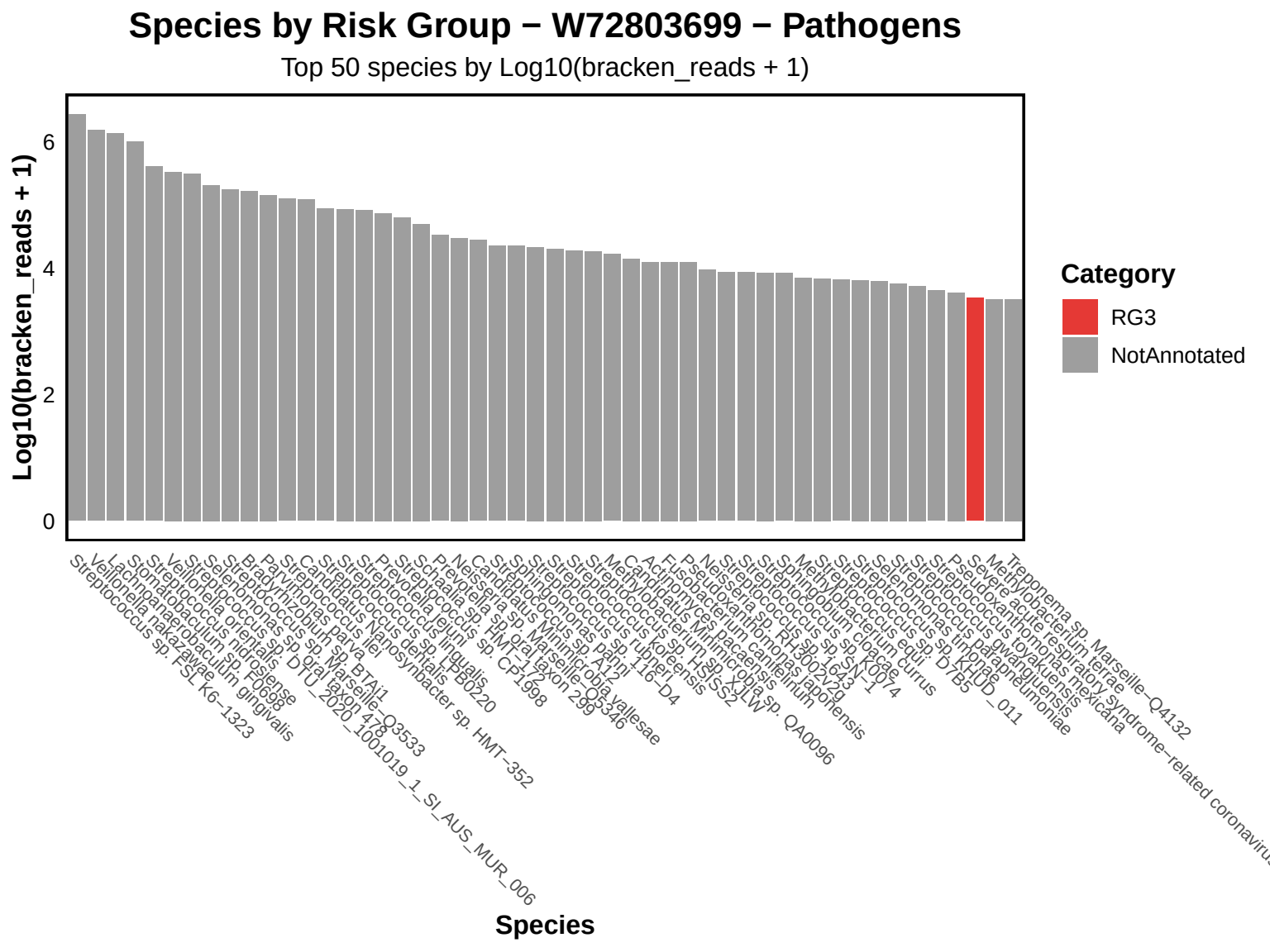
Filtering criteria:
− Include: RG3, RG4 risk groups
− Exclude: RG1, RG2 risk groups
− Exclude: Species annotated as 'Microbiome' in HOMD.Category

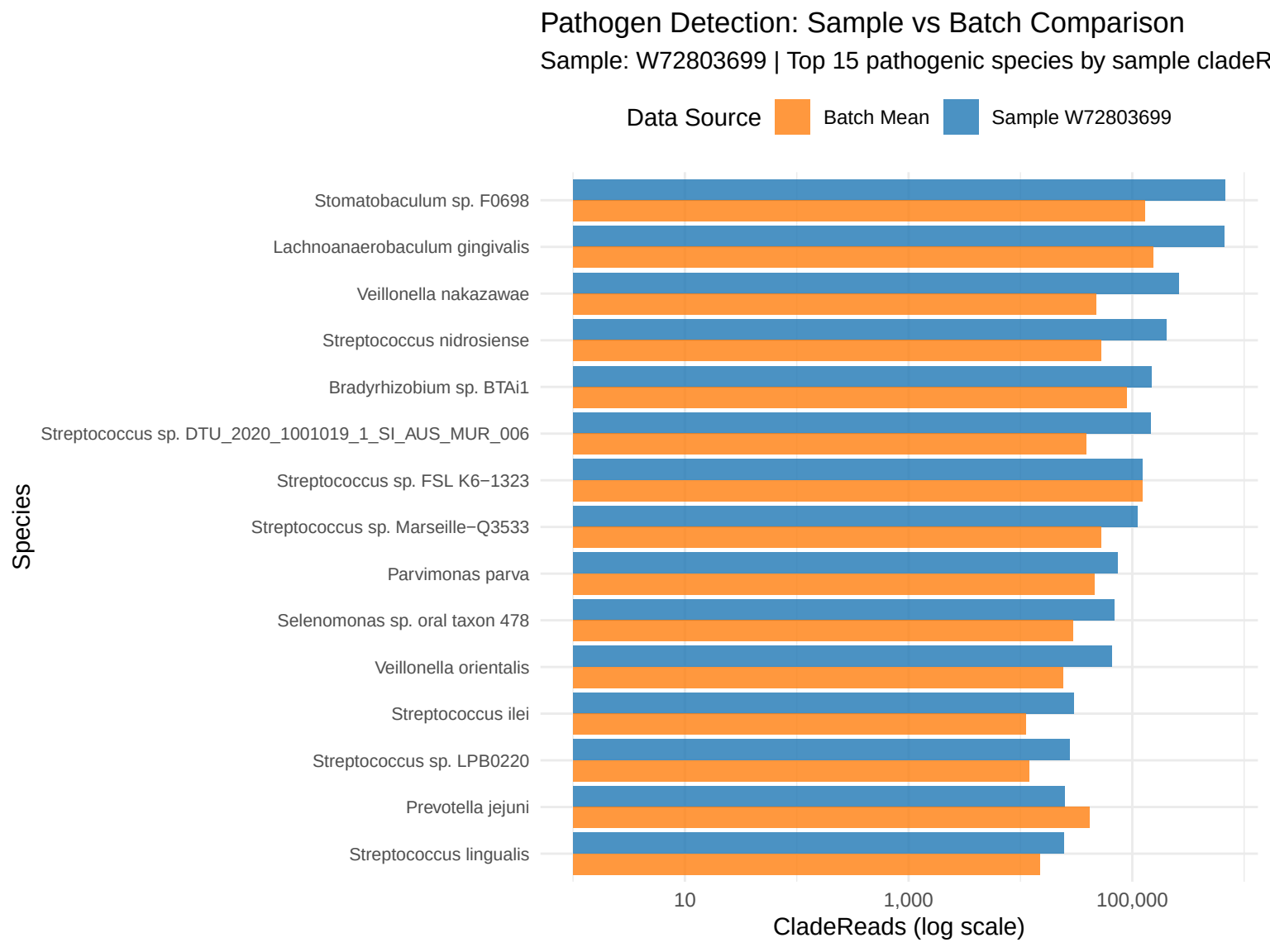
Key findings:
− Total species in sample: 254
− Potential pathogenic species identified: 102
− Most abundant pathogen: Streptococcus sp. FSL K6−1323
− Average pathogen reads: 91296.6

Species per Risk Group − W72803699 − Pathogens

Total species: 102




Species by Risk Group − W72803699 − Pathogens
Top 50 species by Log10(bracken_reads + 1)
Log10(bracken_reads + 1)
0
2
4
6
Category
RG3
NotAnnotated
Streptococcus sp. FSL K6−1323
Veillonella nakazawae
Lachnoanaerobaculum gingivalis
Stomatobaculum sp. F0698
Veillonella orientalis
Streptococcus nidrosiense
Selenomonas sp. DTU_2020_1001019_1_SI_AUS_MUR_006
Streptococcus oralis
Bradyrhizobium sp. BTAi1
Parvimonas parva
Streptococcus ilei
Candidatus Nanosynbacter sp. HMT−352
Streptococcus dentalis
Streptococcus lingualis
Prevotella jejuni
Schaalia sp. HPB0220
Neisseria sp. HMT−1198
Candidatus Marseille−Q3533
Streptococcus oralis taxon 478
Streptococcus sp. Marseille−Q4132
Sphingomonas sp. A12
Streptococcus Minimicrobia vallesae
Streptococcus sp. OH346
Streptococcus rubneri
Streptococcus sp. 116−D4
Methylobacterium sp. HS2
Candidatus Minimicrobia sp. XLW
Actinomyces koreensis
Fusobacterium sp. HS2
Pseudoxanthomonas pacaensis
Neisseria canifelini
Streptococcus sp. RH3002v29
Streptococcus sp. 1643−1
Streptococcus sp. SK074
Sphingobium cloacae
Methylobacterium currus
Streptococcus equi
Streptococcus sp. D7B5
Streptococcus thoraltonensis
Streptococcus pneumoniae
Pseudoxanthomonas mexicana
Streptococcus gwangjuensis
Streptococcus toyakuensis
Severe acute respiratory syndrome−related coronavirus
Methylobacterium terrae
Treponema sp. Marseille−Q4132
Species

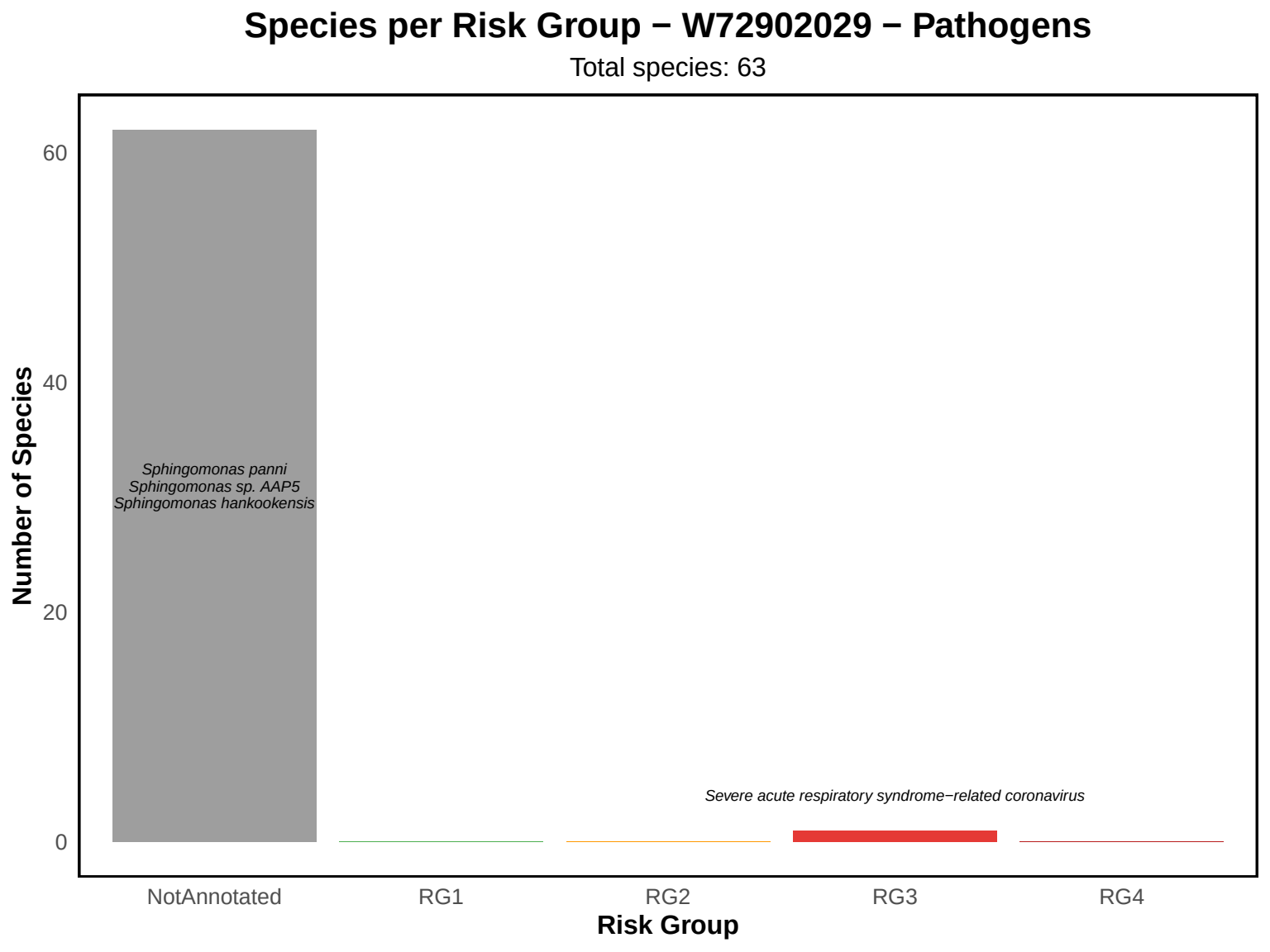

Pathogen Detection: Sample vs Batch Comparison
Sample: W72803699 | Top 15 pathogenic species by sample cladeR
Data Source
Batch Mean
Sample W72803699
Species
Stomatobaculum sp. F0698
Lachnoanaerobaculum gingivalis
Veillonella nakazawae
Streptococcus nidrosiense
Bradyrhizobium sp. BTAi1
Streptococcus sp. DTU_2020_1001019_1_SI_AUS_MUR_006
Streptococcus sp. FSL K6−1323
Streptococcus sp. Marseille−Q3533
Parvimonas parva
Selenomonas sp. oral taxon 478
Veillonella orientalis
Streptococcus ilei
Streptococcus sp. LPB0220
Prevotella jejuni
Streptococcus lingualis
10
1,000
100,000
CladeReads (log scale)

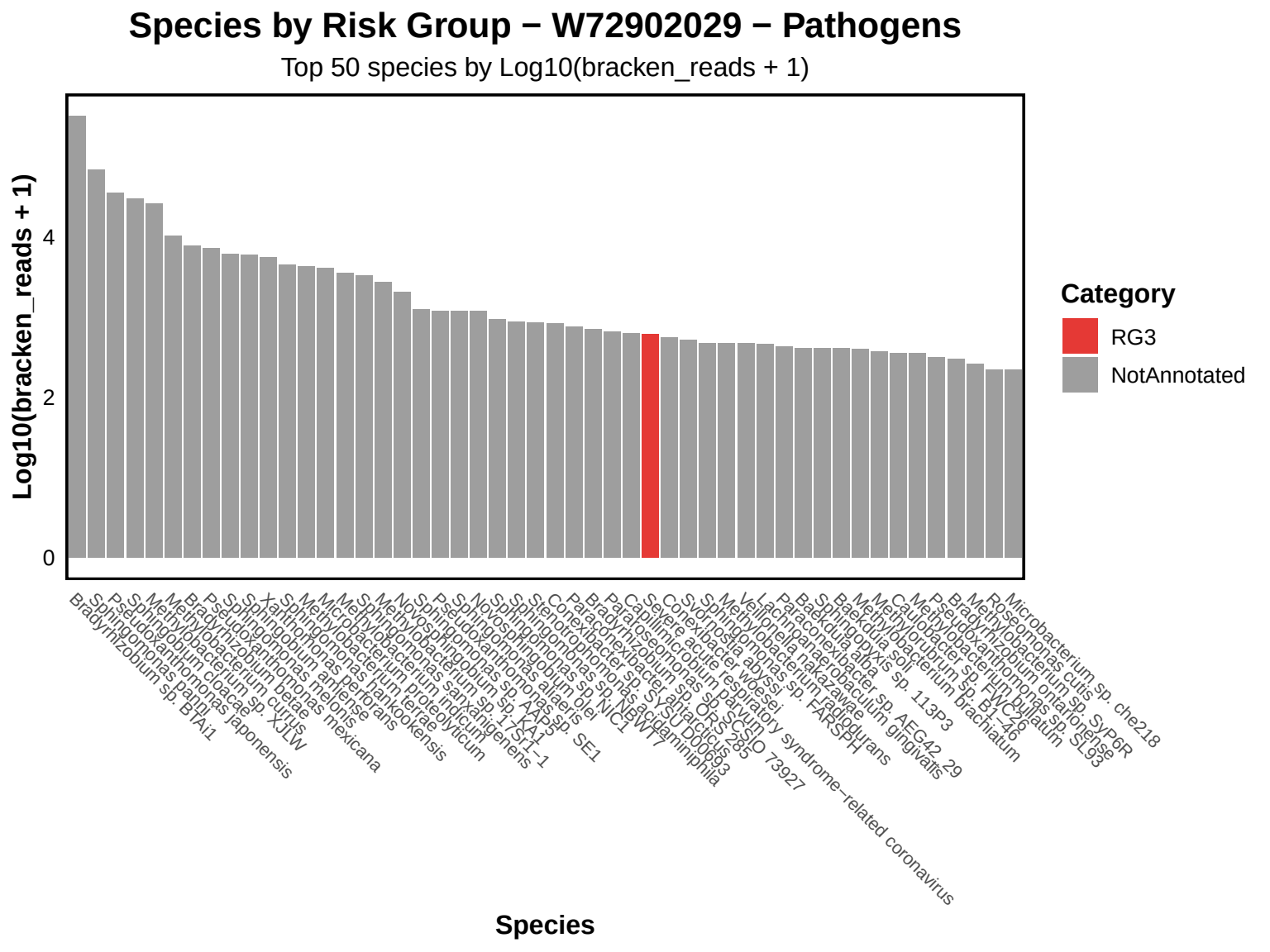
Part 5: Pathogen Detection (RG3/4 Species) − W72902029

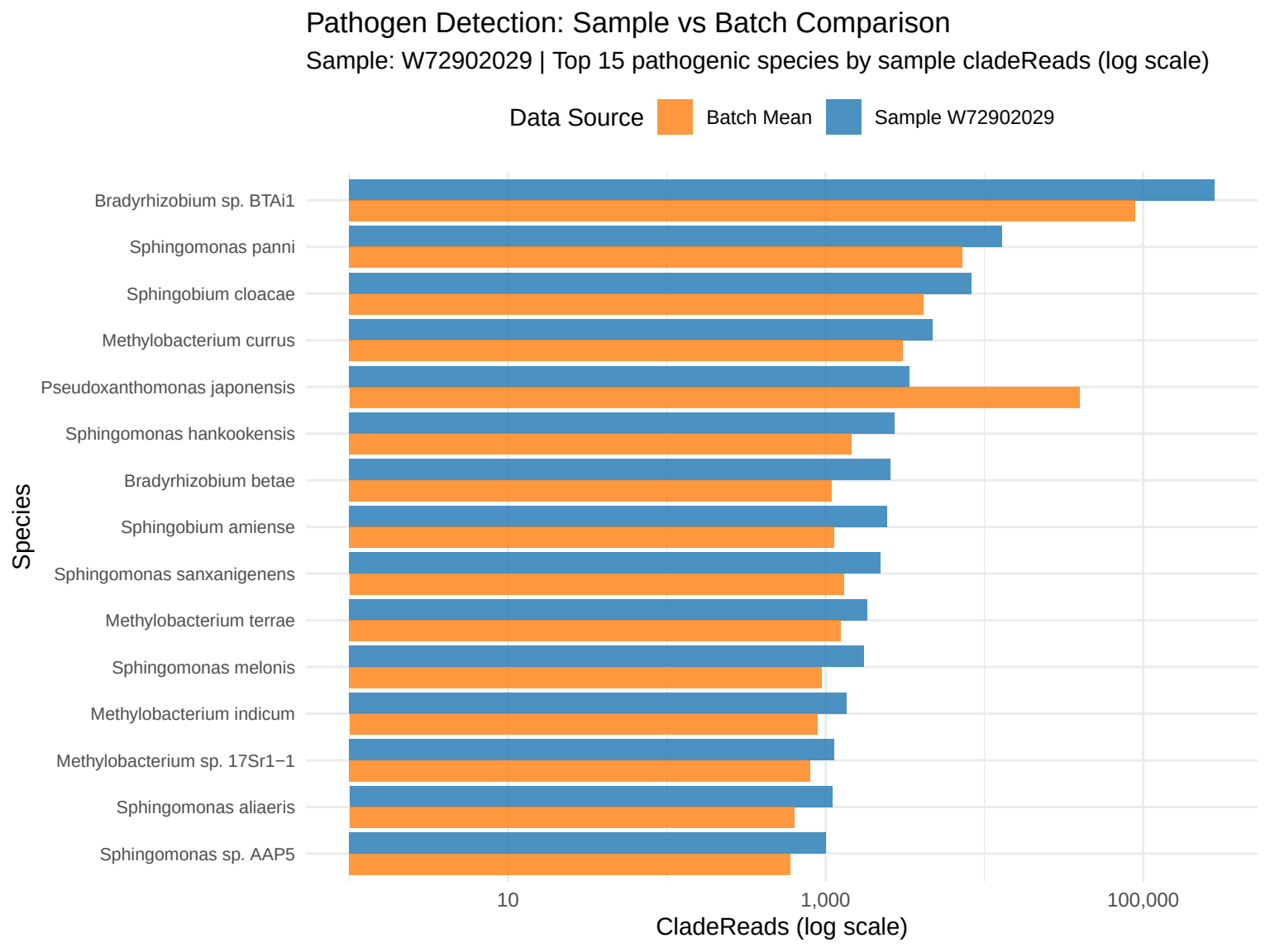
Pathogen detection analysis for sample W72902029:

Filtering criteria:
− Include: RG3, RG4 risk groups
− Exclude: RG1, RG2 risk groups
− Exclude: Species annotated as 'Microbiome' in HOMD.Category

Key findings:
− Total species in sample: 104
− Potential pathogenic species identified: 63
− Most abundant pathogen: Bradyrhizobium sp. BTAi1
− Average pathogen reads: 9015.3


Species per Risk Group − W72902029 − Pathogens
Total species: 63
Number of Species
60
40
20
0
Sphingomonas panni
Sphingomonas sp. AAP5
Sphingomonas hankookensis
Severe acute respiratory syndrome−related coronavirus
NotAnnotated
RG1
RG2
RG3
RG4
Risk Group


Species by Risk Group − W72902029 − Pathogens
Top 50 species by Log10(bracken_reads + 1)
Log10(bracken_reads + 1)
0
2
4
Category
RG3
NotAnnotated
Species
Bradyrhizobium sp. BTAi1
Sphingomonas panni
Pseudoxanthomonas japonensis
Sphingobium cloacae
Methylobacterium sp. XJLW
Methylobacterium curtus
Bradyrhizobium betae
Pseudoxanthomonas melonis
Sphingomonas mexicana
Sphingobium amiense
Xanthomonas perforans
Sphingomonas hankookensis
Microbacterium terrae
Methylobacterium proteolyticum
Sphingomonas sanxanigenens
Methylobacterium indicum
Novosphingobium sp. AAP5
Sphingomonas sp. KA1−1
Pseudoxanthomonas sp. SE1
Sphingomonas aliaeris
Novosphingobium oleiciens
Sphingomonas sp. NIC1
Stenotrophomonas sp. SU1
Conexibacter sp. SYSU DOC93
Paraconexibacter sp. ORS 285
Bradyrhizobium sp. ORS 285
Pararoseomonas sp. SCSIO 73927
Capillimicrobium parvum
Severe acute respiratory syndrome−related coronavirus
Conexibacter woesei
Svornostia abyssi
Sphingomonas sp. FARSPH
Methylobacterium radiodurans
Lachnoanaerobaculum gingivalis
Paraconexibacter sp. AEG42_29
Baekduia alba
Sphingopyxis sp. 113P3
Methylobacterium brachiatum
Caulobacter sp. FWC26
Methylobacterium sp. B1−46
Pseudoxanthomonas sp. SL93
Bradyrhizobium ontariense
Methylobacterium pulvatum
Roseomonas cutis SyP6R
Microbacterium sp. che218


Pathogen Detection: Sample vs Batch Comparison
Sample: W72902029 | Top 15 pathogenic species by sample cladeReads (log scale)
Data Source
Batch Mean
Sample W72902029
Species
Bradyrhizobium sp. BTAi1
Sphingomonas panni
Sphingobium cloacae
Methylobacterium currus
Pseudoxanthomonas japonensis
Sphingomonas hankookensis
Bradyrhizobium betae
Sphingobium amiense
Sphingomonas sanxanigenens
Methylobacterium terrae
Sphingomonas melonis
Methylobacterium indicum
Methylobacterium sp. 17Sr1−1
Sphingomonas aliaeris
Sphingomonas sp. AAP5
10
1,000
100,000
CladeReads (log scale)

Part 5: Pathogen Detection (RG3/4 Species) − W73007482

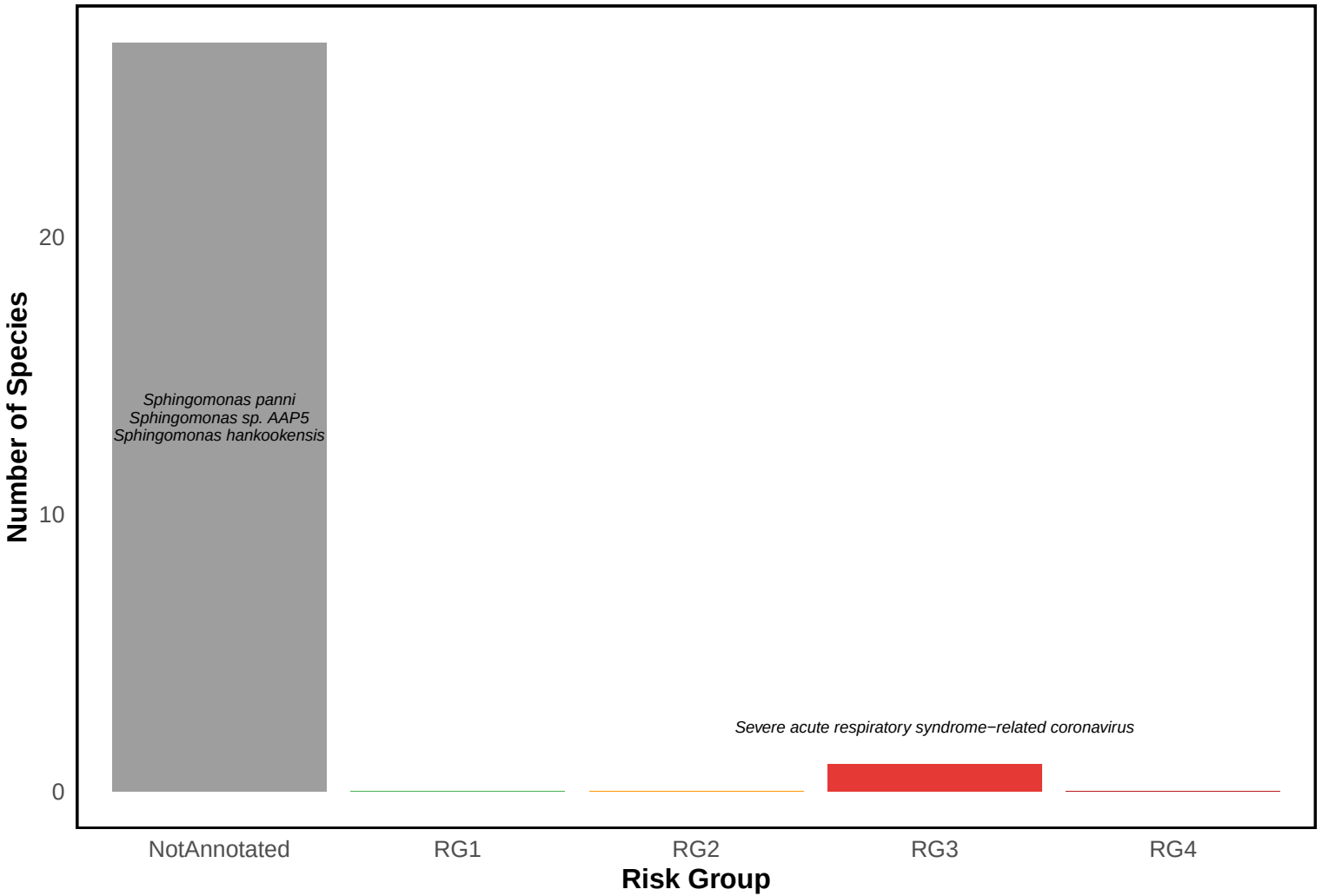
Pathogen detection analysis for sample W73007482:

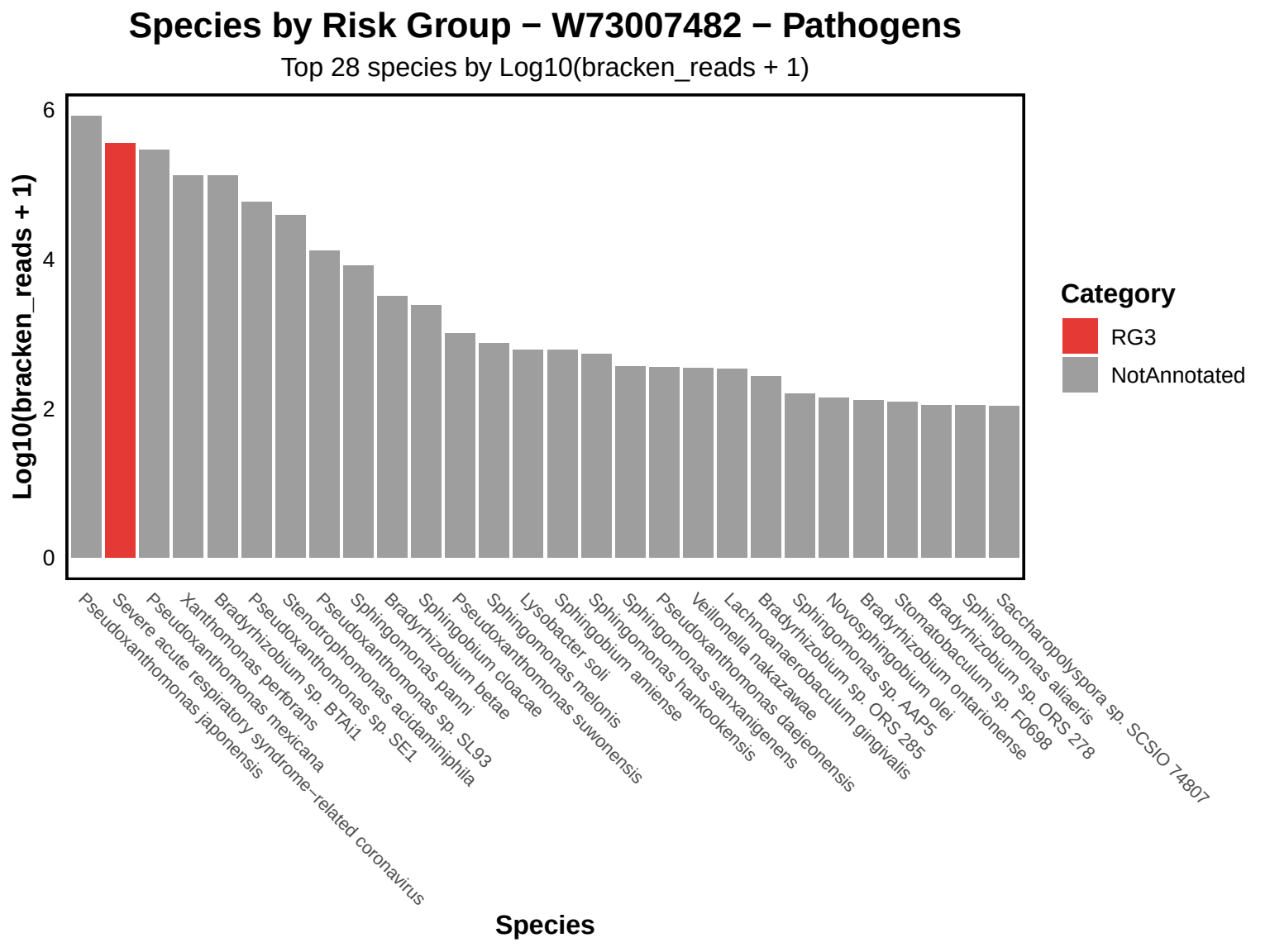
Filtering criteria:
− Include: RG3, RG4 risk groups
− Exclude: RG1, RG2 risk groups
− Exclude: Species annotated as 'Microbiome' in HOMD.Category

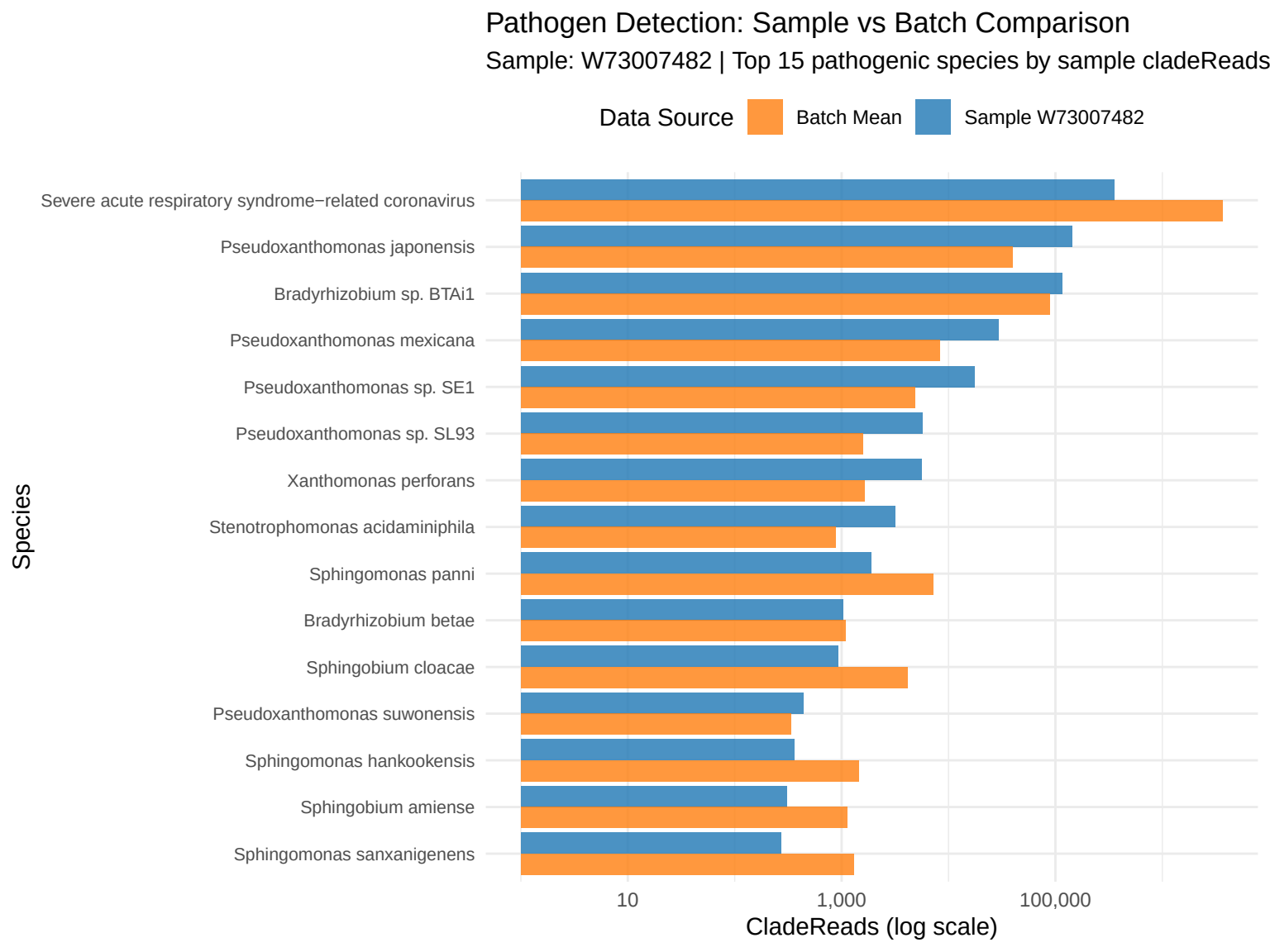
Key findings:
− Total species in sample: 60
− Potential pathogenic species identified: 28
− Most abundant pathogen: Pseudoxanthomonas japonensis
− Average pathogen reads: 65921.1

Species per Risk Group − W73007482 − Pathogens

Total species: 28




Species by Risk Group − W73007482 − Pathogens
Top 28 species by Log10(bracken_reads + 1)
Log10(bracken_reads + 1)
6
4
2
0
Category
RG3
NotAnnotated
Pseudoxanthomonas japonensis
Severe acute respiratory syndrome−related coronavirus
Pseudoxanthomonas mexicana
Xanthomonas perforans
Bradyrhizobium sp. BTAi1
Pseudoxanthomonas sp. SE1
Stenotrophomonas acidaminiphila
Pseudoxanthomonas sp. SL93
Sphingomonas panni
Bradyrhizobium betae
Sphingobium cloacae
Pseudoxanthomonas suwonensis
Sphingomonas melonis
Lysobacter soli
Sphingobium amiense
Sphingomonas hankookensis
Sphingomonas sanxanigenens
Pseudoxanthomonas daejeonensis
Veillonella nakazawae
Lachnoanaerobaculum gingivalis
Bradyrhizobium sp. ORS 285
Sphingomonas sp. AAP5
Novosphingobium olei
Stomatobaculum sp. F0698
Bradyrhizobium ontarionense
Bradyrhizobium sp. ORS 278
Sphingomonas aliaeris
Saccharopolyspora sp. SCSIO 74807
Species


Pathogen Detection: Sample vs Batch Comparison
Sample: W73007482 | Top 15 pathogenic species by sample cladeReads
Data Source
Batch Mean
Sample W73007482
Species
Severe acute respiratory syndrome−related coronavirus
Pseudoxanthomonas japonensis
Bradyrhizobium sp. BTAi1
Pseudoxanthomonas mexicana
Pseudoxanthomonas sp. SE1
Pseudoxanthomonas sp. SL93
Xanthomonas perforans
Stenotrophomonas acidaminiphila
Sphingomonas panni
Bradyrhizobium betae
Sphingobium cloacae
Pseudoxanthomonas suwonensis
Sphingomonas hankookensis
Sphingobium amiense
Sphingomonas sanxanigenens
10
1,000
100,000
CladeReads (log scale)

Part 5: Pathogen Detection (RG3/4 Species) − W73007677

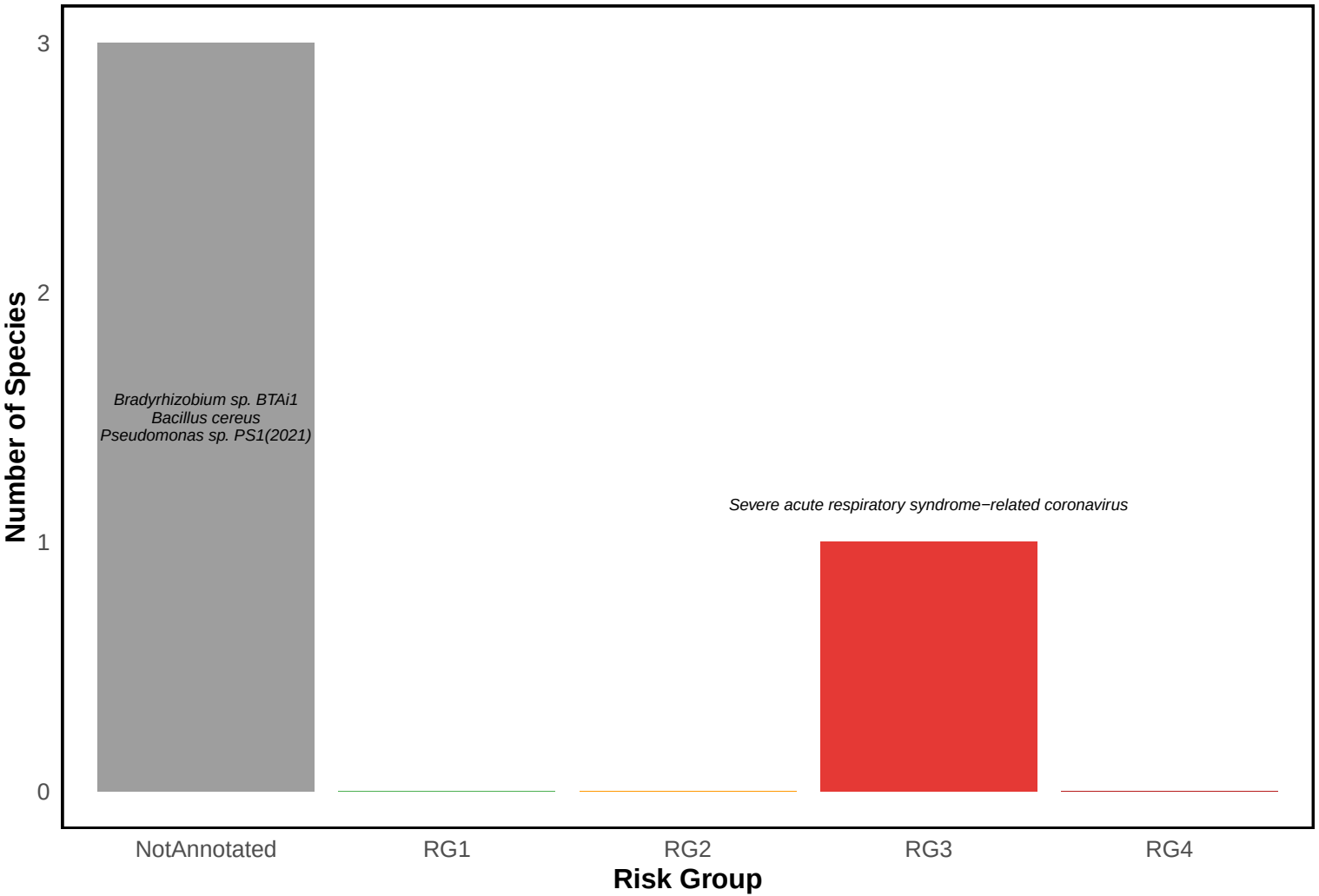
Pathogen detection analysis for sample W73007677:

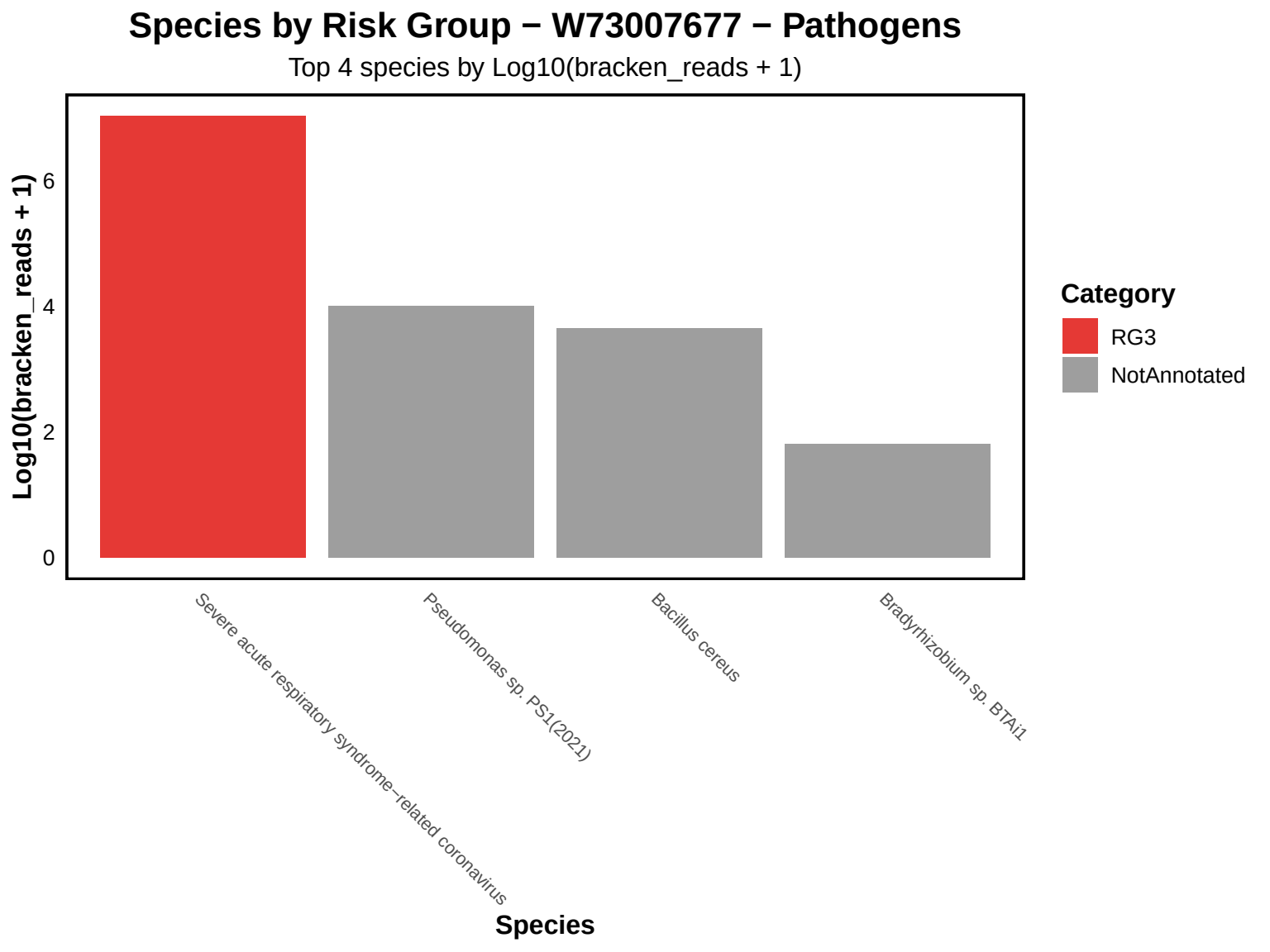
Filtering criteria:
− Include: RG3, RG4 risk groups
− Exclude: RG1, RG2 risk groups
− Exclude: Species annotated as 'Microbiome' in HOMD.Category

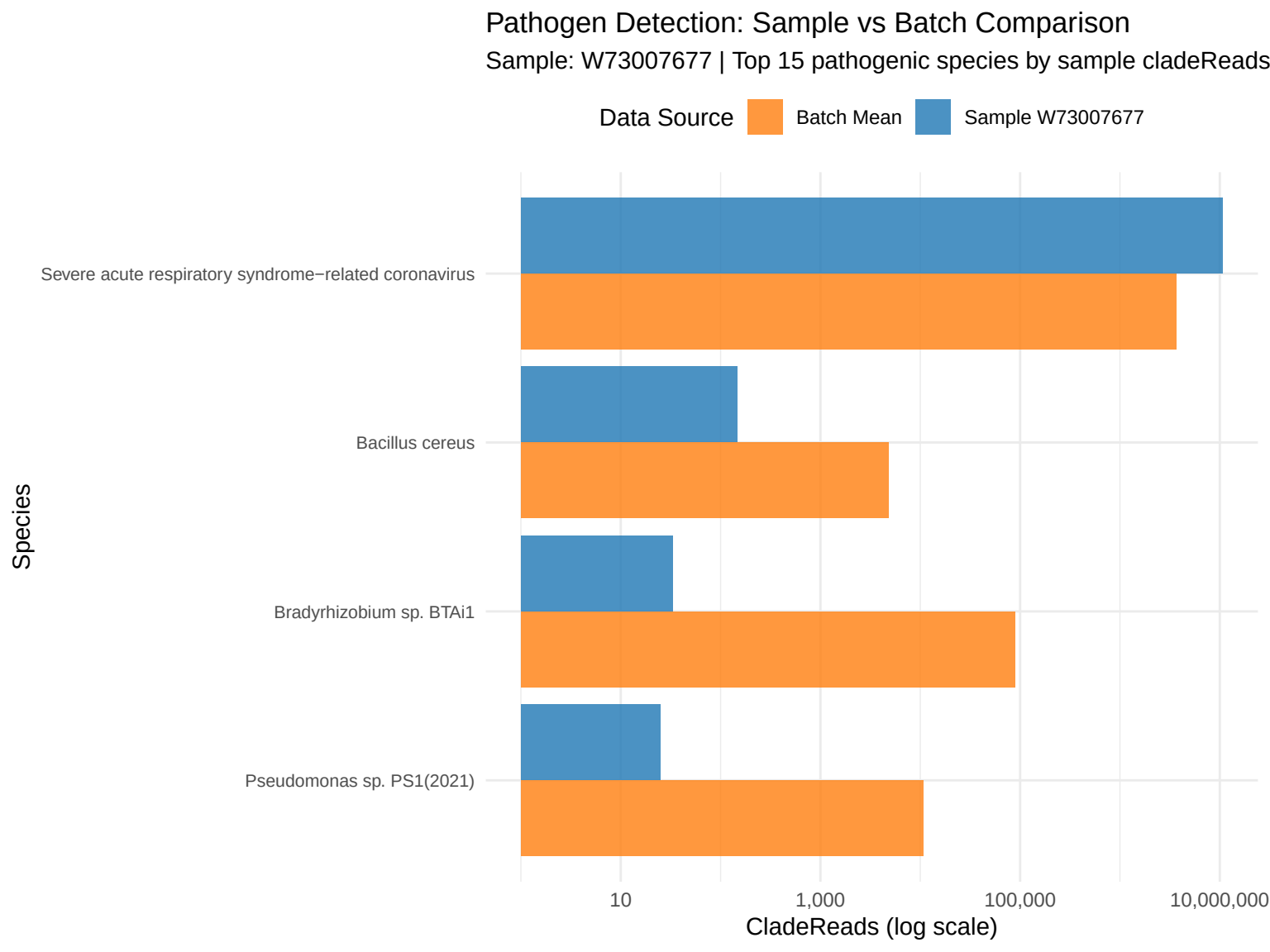
Key findings:
− Total species in sample: 26
− Potential pathogenic species identified: 4
− Most abundant pathogen: Severe acute respiratory syndrome−related coronavirus
− Average pathogen reads: 2684263.5

Species per Risk Group − W73007677 − Pathogens

Total species: 4




Species by Risk Group − W73007677 − Pathogens
Top 4 species by Log10(bracken_reads + 1)
Log10(bracken_reads + 1)
0
2
4
6
Severe acute respiratory syndrome−related coronavirus
Pseudomonas sp. PS1(2021)
Bacillus cereus
Bradyrhizobium sp. BTAi1
Species
Category
RG3
NotAnnotated


Pathogen Detection: Sample vs Batch Comparison
Sample: W73007677 | Top 15 pathogenic species by sample cladeReads
Data Source
Batch Mean
Sample W73007677
Species
Severe acute respiratory syndrome−related coronavirus
Bacillus cereus
Bradyrhizobium sp. BTAi1
Pseudomonas sp. PS1(2021)
10
1,000
100,000
10,000,000
CladeReads (log scale)

Part 5: Pathogen Detection (RG3/4 Species) − W73007934

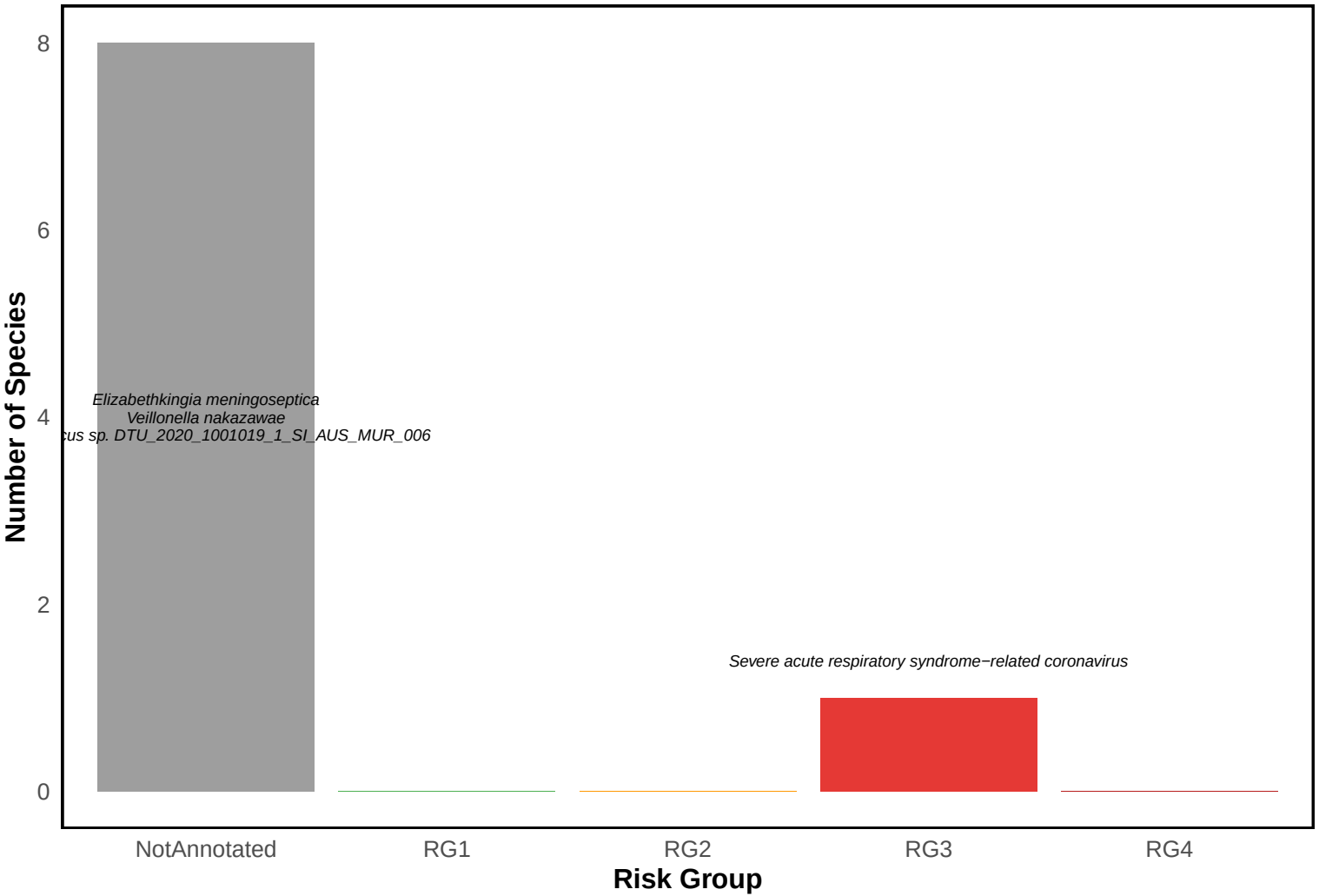
Pathogen detection analysis for sample W73007934:

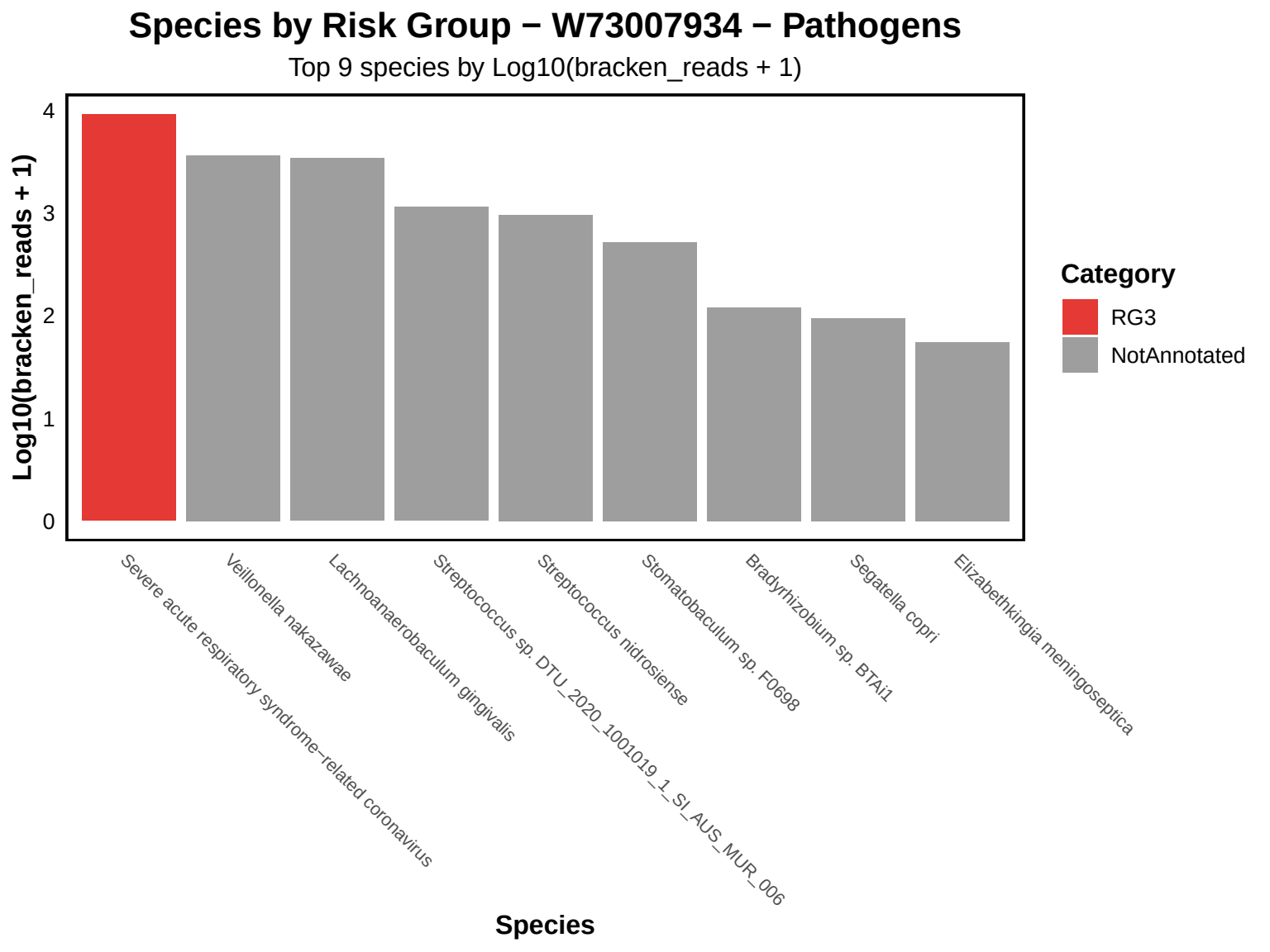
Filtering criteria:
− Include: RG3, RG4 risk groups
− Exclude: RG1, RG2 risk groups
− Exclude: Species annotated as 'Microbiome' in HOMD.Category

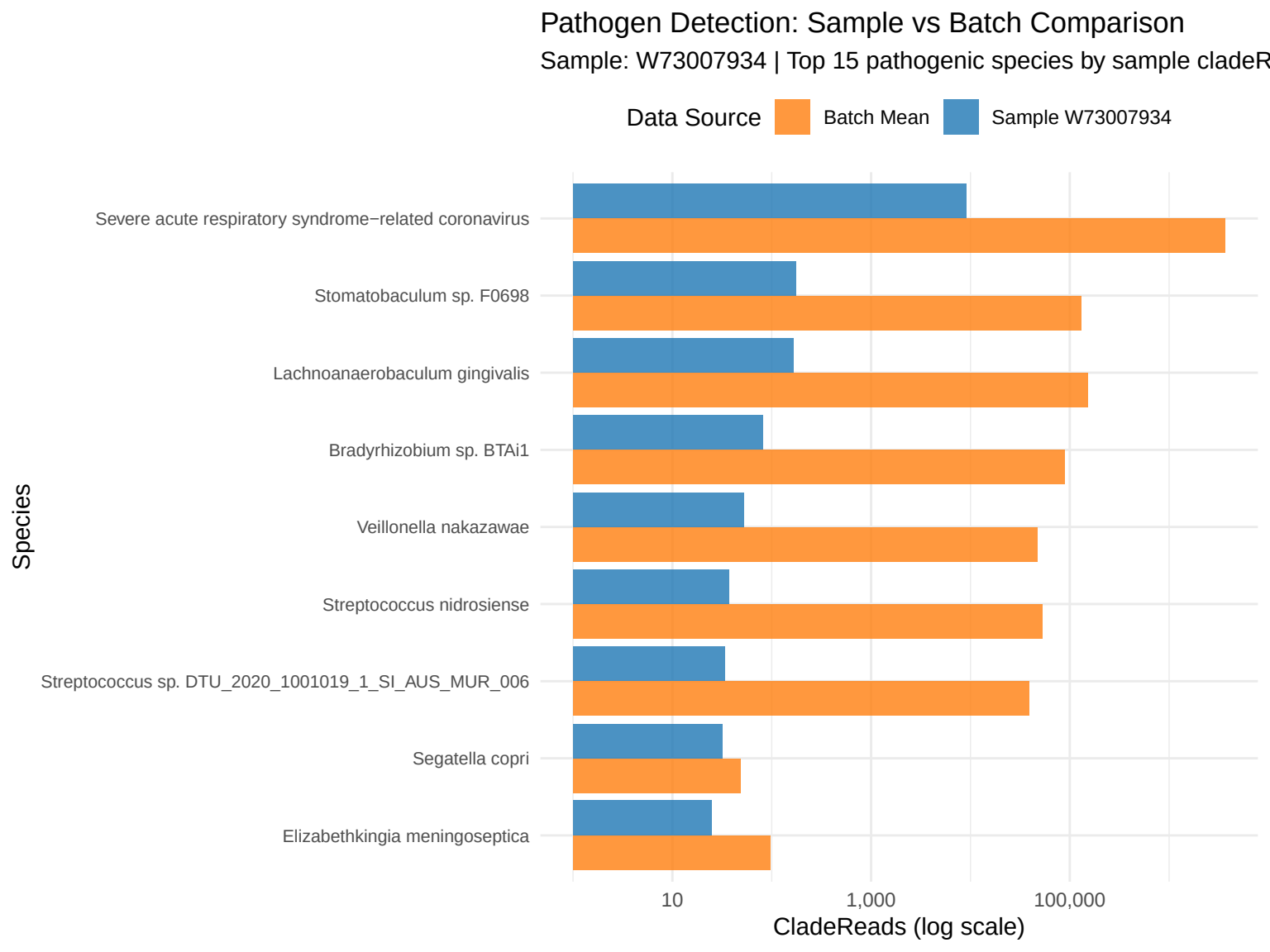
Key findings:
− Total species in sample: 40
− Potential pathogenic species identified: 9
− Most abundant pathogen: Severe acute respiratory syndrome−related coronavirus
− Average pathogen reads: 2104.7

Species per Risk Group − W73007934 − Pathogens

Total species: 9




Species by Risk Group − W73007934 − Pathogens
Top 9 species by Log10(bracken_reads + 1)
Log10(bracken_reads + 1)
0
1
2
3
4
Category
RG3
NotAnnotated
Severe acute respiratory syndrome−related coronavirus
Veillonella nakazawae
Lachnoanaerobaculum gingivalis
Streptococcus sp. DTU_2020_1001019_1_SI_AUS_MUR_006
Streptococcus nidrosiense
Stomatobaculum sp. F0698
Bradyrhizobium sp. BTAi1
Segatella copri
Elizabethkingia meningoseptica
Species


Pathogen Detection: Sample vs Batch Comparison
Sample: W73007934 | Top 15 pathogenic species by sample cladeR
Data Source
Batch Mean
Sample W73007934
Species
Severe acute respiratory syndrome−related coronavirus
Stomatobaculum sp. F0698
Lachnoanaerobaculum gingivalis
Bradyrhizobium sp. BTAi1
Veillonella nakazawae
Streptococcus nidrosiense
Streptococcus sp. DTU_2020_1001019_1_SI_AUS_MUR_006
Segatella copri
Elizabethkingia meningoseptica
10
1,000
100,000
CladeReads (log scale)

Part 5: Pathogen Detection (RG3/4 Species) − W73109775

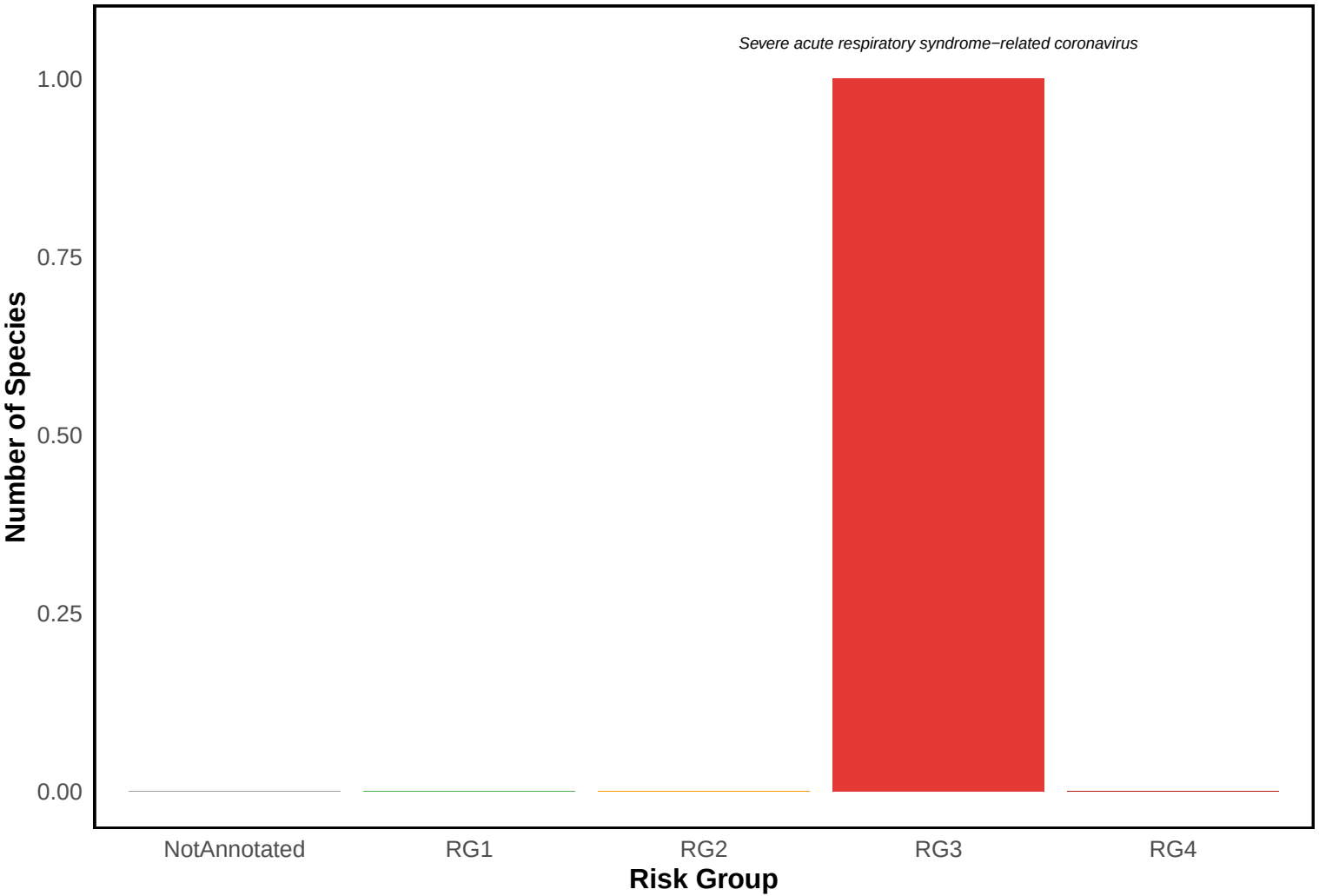
Pathogen detection analysis for sample W73109775:

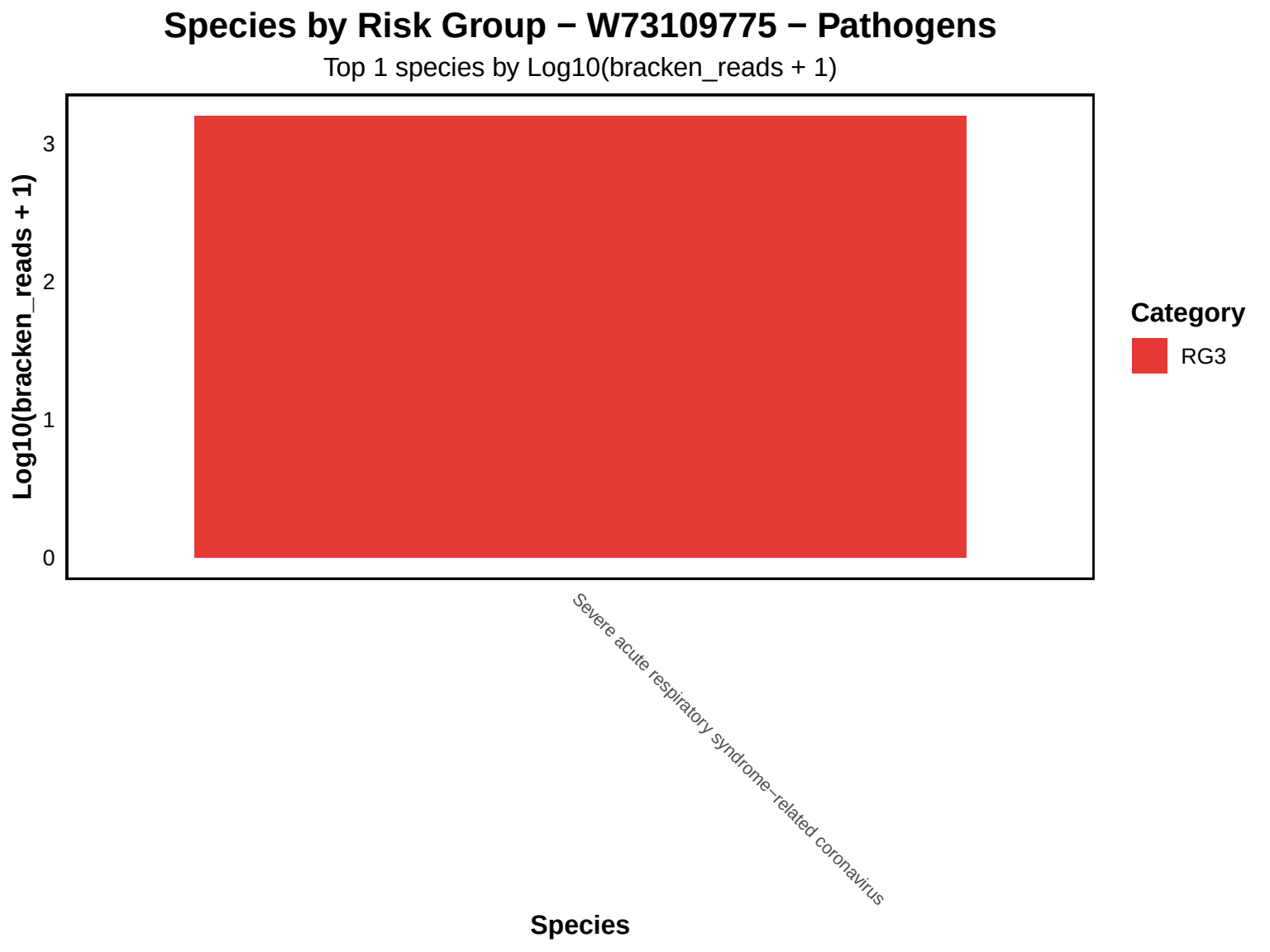
Filtering criteria:
− Include: RG3, RG4 risk groups
− Exclude: RG1, RG2 risk groups
− Exclude: Species annotated as 'Microbiome' in HOMD.Category

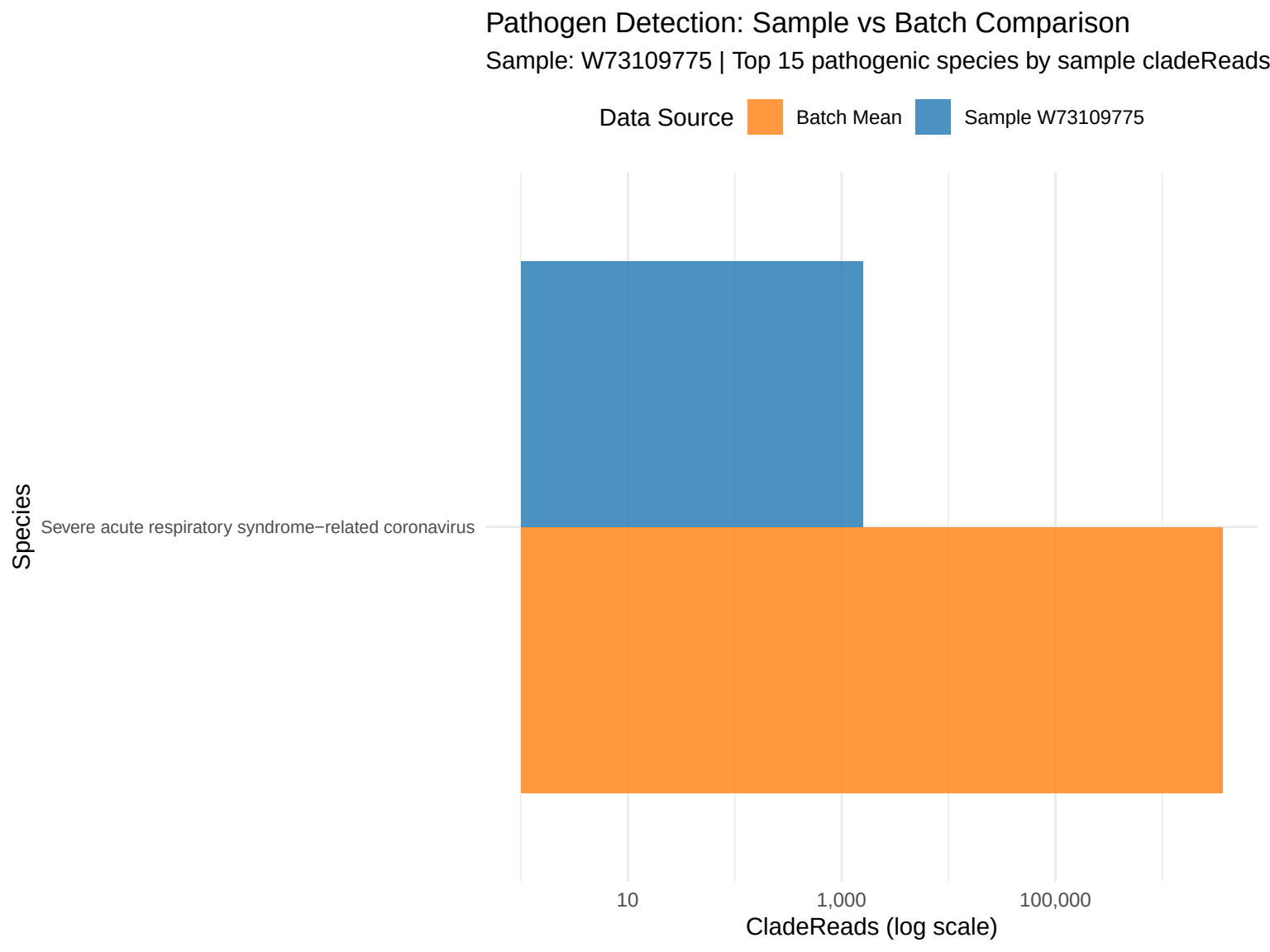
Key findings:
− Total species in sample: 22
− Potential pathogenic species identified: 1
− Most abundant pathogen: Severe acute respiratory syndrome−related coronavirus
− Average pathogen reads: 1564

Species per Risk Group − W73109775 − Pathogens

Total species: 1




Species by Risk Group − W73109775 − Pathogens
Top 1 species by Log10(bracken_reads + 1)
Log10(bracken_reads + 1)
0
1
2
3
Severe acute respiratory syndrome−related coronavirus
Species
Category
RG3


Pathogen Detection: Sample vs Batch Comparison
Sample: W73109775 | Top 15 pathogenic species by sample cladeReads
Data Source
Batch Mean
Sample W73109775
Species
Severe acute respiratory syndrome−related coronavirus
10
1,000
100,000
CladeReads (log scale)

Part 5: Pathogen Detection (RG3/4 Species) − W81802779

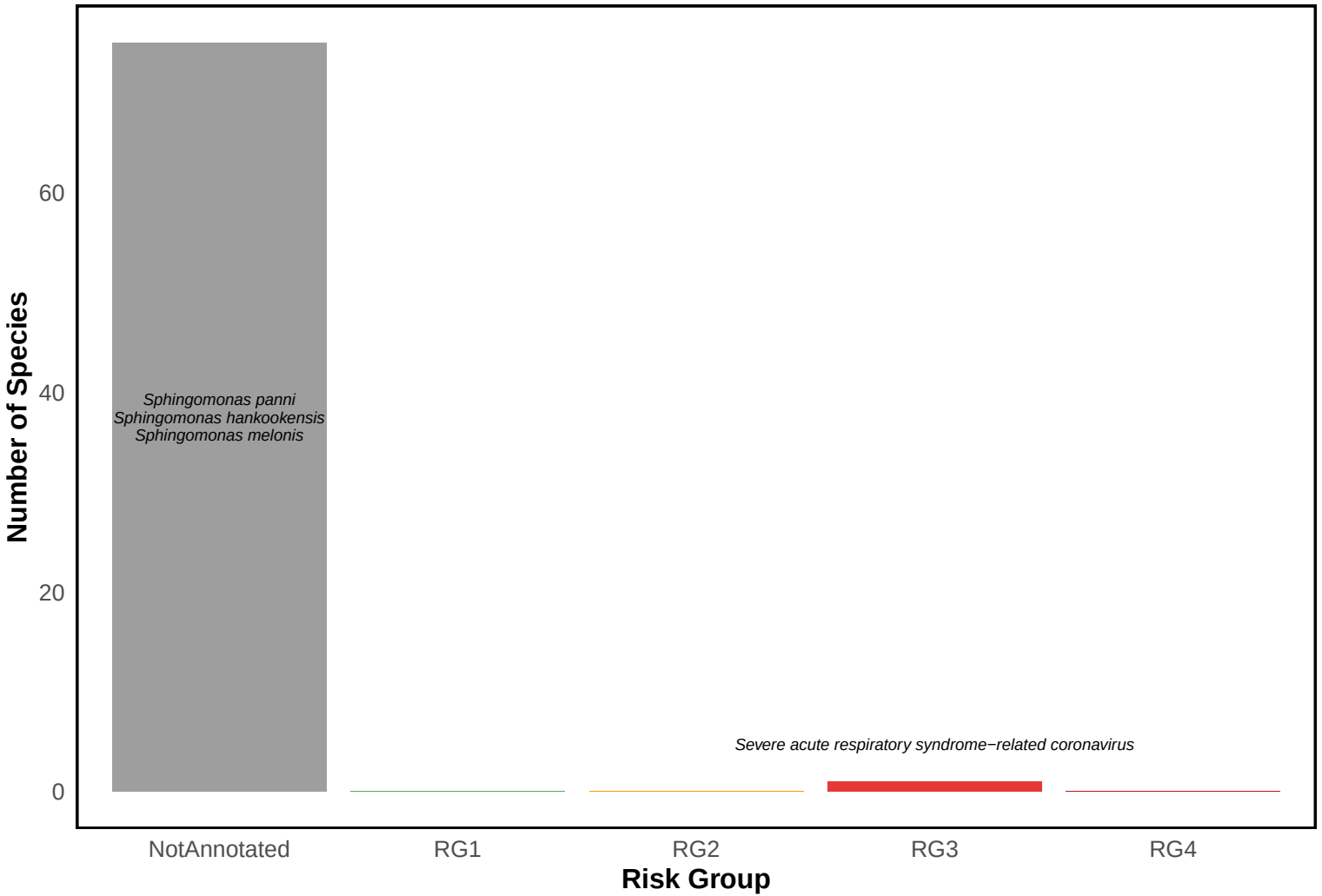
Pathogen detection analysis for sample W81802779:

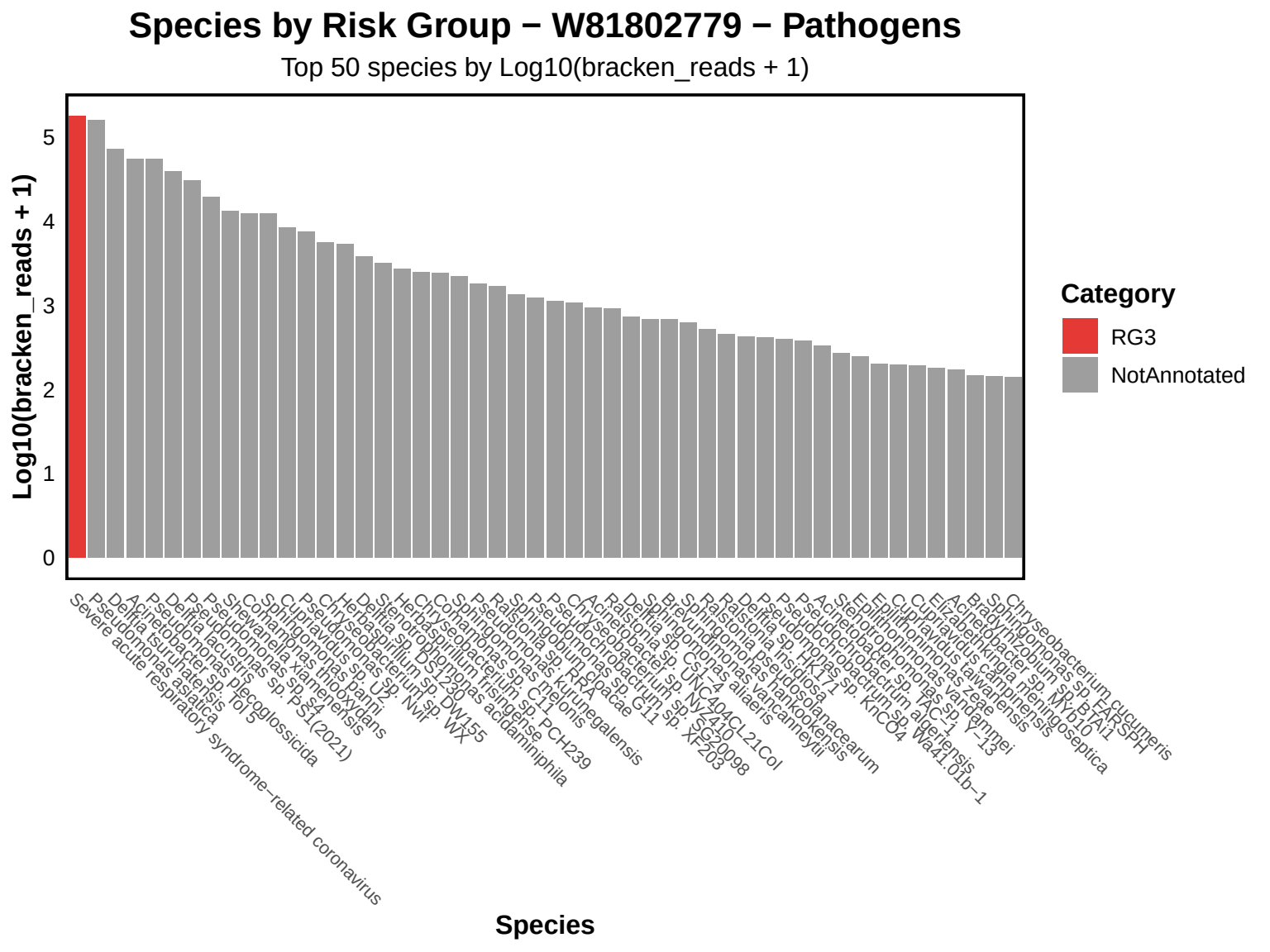
Filtering criteria:
− Include: RG3, RG4 risk groups
− Exclude: RG1, RG2 risk groups
− Exclude: Species annotated as 'Microbiome' in HOMD.Category

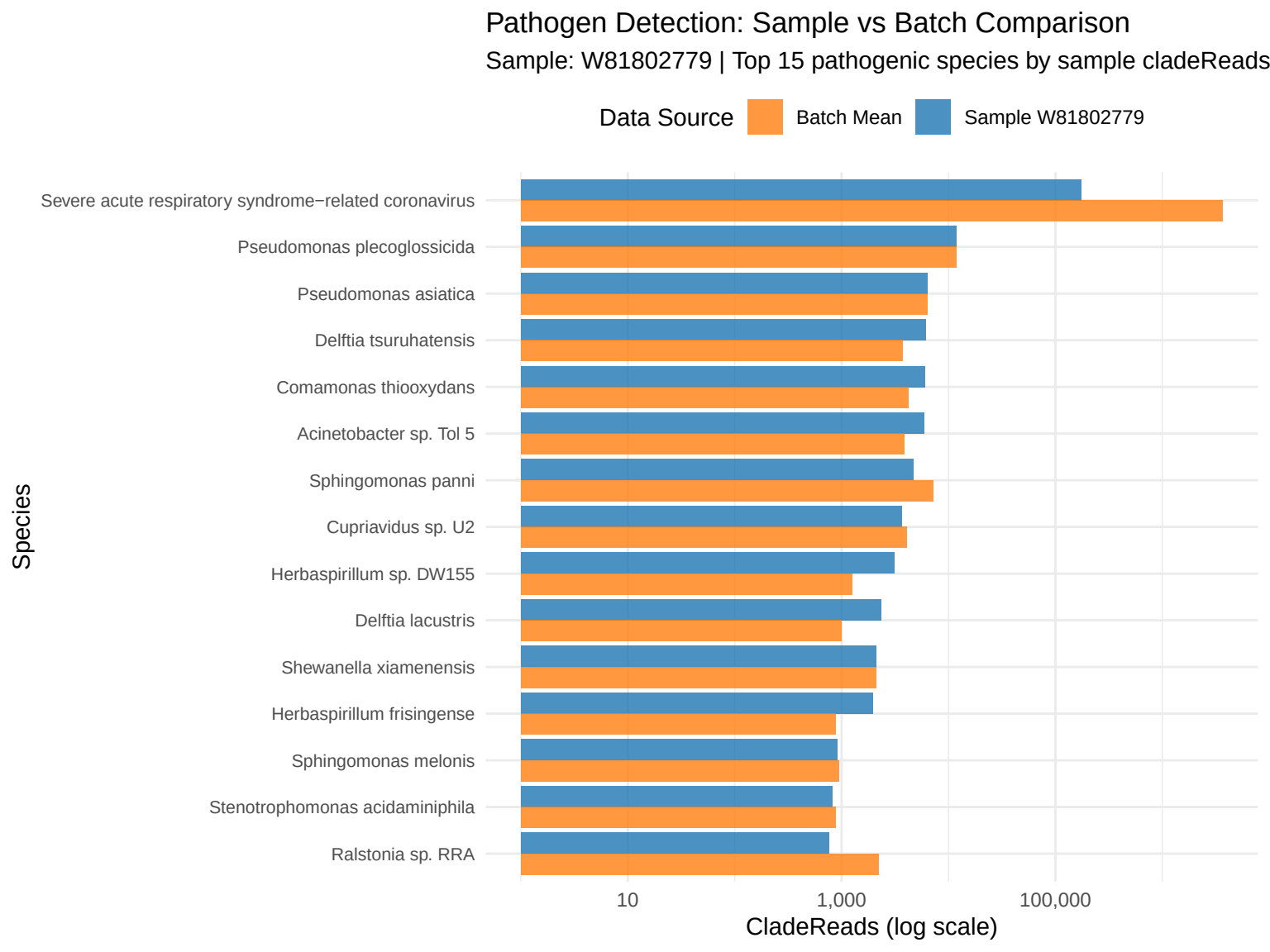
Key findings:
− Total species in sample: 132
− Potential pathogenic species identified: 76
− Most abundant pathogen: Severe acute respiratory syndrome−related coronavirus
− Average pathogen reads: 9181.6

Species per Risk Group − W81802779 − Pathogens

Total species: 76




Species by Risk Group − W81802779 − Pathogens
Top 50 species by Log10(bracken_reads + 1)
Log10(bracken_reads + 1)
0
1
2
3
4
5
Category
RG3
NotAnnotated
Severe acute respiratory syndrome−related coronavirus
Pseudomonas asiatica
Delftia isuruhatensis
Acinetobacter sp. Tol 5
Pseudomonas plecoglossicida
Delftia lacustris
Pseudomonas sp. PS1(2021)
Shewanella xiamenensis
Comamonas thiooxydans
Sphingomonas sp. U2
Cupriavidus panni
Pseudomonas sp. NvH
Chryseobacterium sp. DW155
Herbaspirillum sp. WX
Stenotrophomonas acidaminiphila
Herbaspirillum frisingense
Chryseobacterium sp. PCH239
Comamonas sp. C11
Raistonia sp. RHA
Sphingomonas melonis
Pseudomonas kurunegalensis
Sphingobium cloacae
Pseudochrobactrum sp. C11
Chryseobacterium sp. XF203
Acinetobacter sp. NyH410
Delftia sp. SG20098
Sphingomonas sp. UNC404CL21Col
Brevundimonas aliaeris
Raistonia vancanneytii
Raistonia pseudosolanacearum
Delftia sp. HK171
Raistonia insidiosa
Pseudochrobactrum sp. KnCO4
Pseudochrobactrum algeriensis
Stenotrophomonas sp. Wa41.01b−1
Epilithonimonas sp. PAC_1
Epilithonimonas vandammei
Cupriavidus zeae
Cupriavidus taiwanensis
Elizabethkingia meningoseptica
Acinetobacter sp. Y−13
Bradyrhizobium sp. MYb10
Sphingomonas sp. BHAI1
Sphingomonas sp. FARSPH
Chryseobacterium cucumeris
Species


Pathogen Detection: Sample vs Batch Comparison
Sample: W81802779 | Top 15 pathogenic species by sample cladeReads
Data Source
Batch Mean
Sample W81802779
Species
Severe acute respiratory syndrome−related coronavirus
Pseudomonas plecoglossicida
Pseudomonas asiatica
Delftia tsuruhatensis
Comamonas thiooxydans
Acinetobacter sp. Tol 5
Sphingomonas panni
Cupriavidus sp. U2
Herbaspirillum sp. DW155
Delftia lacustris
Shewanella xiamenensis
Herbaspirillum frisingense
Sphingomonas melonis
Stenotrophomonas acidaminiphila
Ralstonia sp. RRA
10
1,000
100,000
CladeReads (log scale)

Part 5: Pathogen Detection (RG3/4 Species) − W90303891

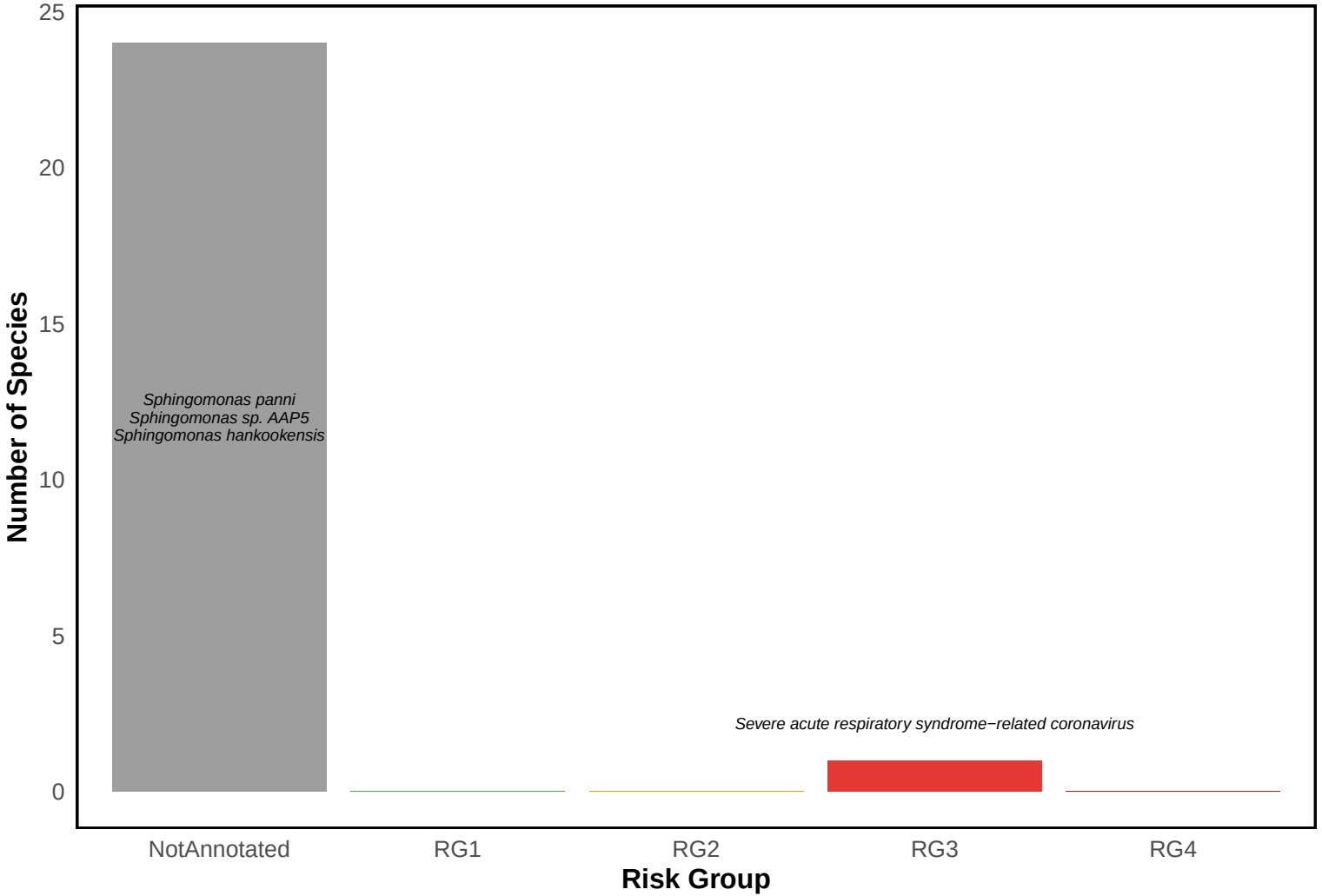
Pathogen detection analysis for sample W90303891:

Filtering criteria:
− Include: RG3, RG4 risk groups
− Exclude: RG1, RG2 risk groups
− Exclude: Species annotated as 'Microbiome' in HOMD.Category

Key findings:
− Total species in sample: 63
− Potential pathogenic species identified: 25
− Most abundant pathogen: Severe acute respiratory syndrome−related coronavirus
− Average pathogen reads: 1571745.3

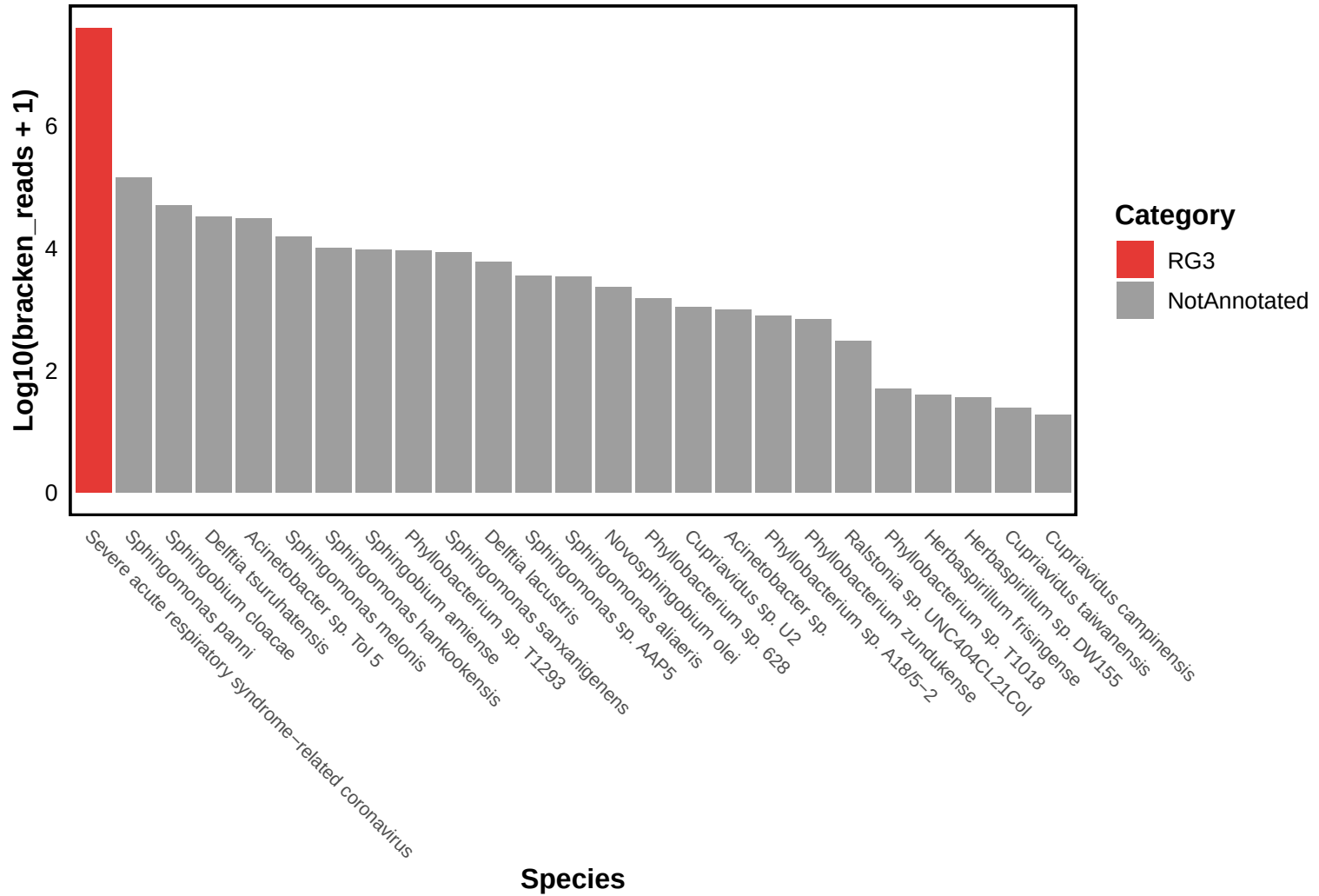
Species per Risk Group − W90303891 − Pathogens

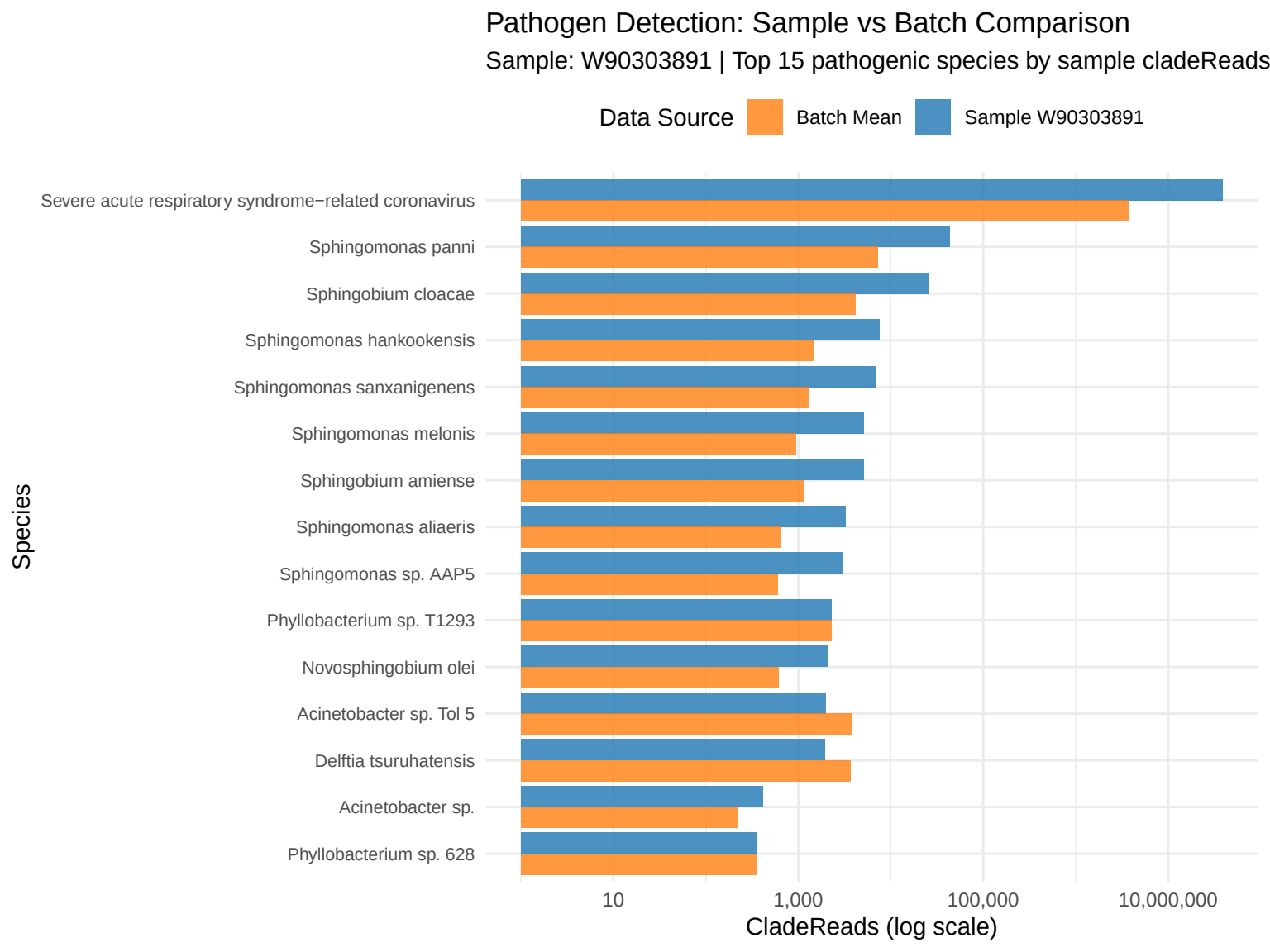
Total species: 25



Species by Risk Group − W90303891 − Pathogens

Top 25 species by Log10(bracken_reads + 1)




Pathogen Detection: Sample vs Batch Comparison
Sample: W90303891 | Top 15 pathogenic species by sample cladeReads
Data Source
Batch Mean
Sample W90303891
Species
Severe acute respiratory syndrome−related coronavirus
Sphingomonas panni
Sphingobium cloacae
Sphingomonas hankookensis
Sphingomonas sanxanigenens
Sphingomonas melonis
Sphingobium amiense
Sphingomonas aliaeris
Sphingomonas sp. AAP5
Phyllobacterium sp. T1293
Novosphingobium olei
Acinetobacter sp. Tol 5
Delftia tsuruhatensis
Acinetobacter sp.
Phyllobacterium sp. 628
10
1,000
100,000
10,000,000
CladeReads (log scale)

Part 5: Pathogen Detection (RG3/4 Species) − W90504037

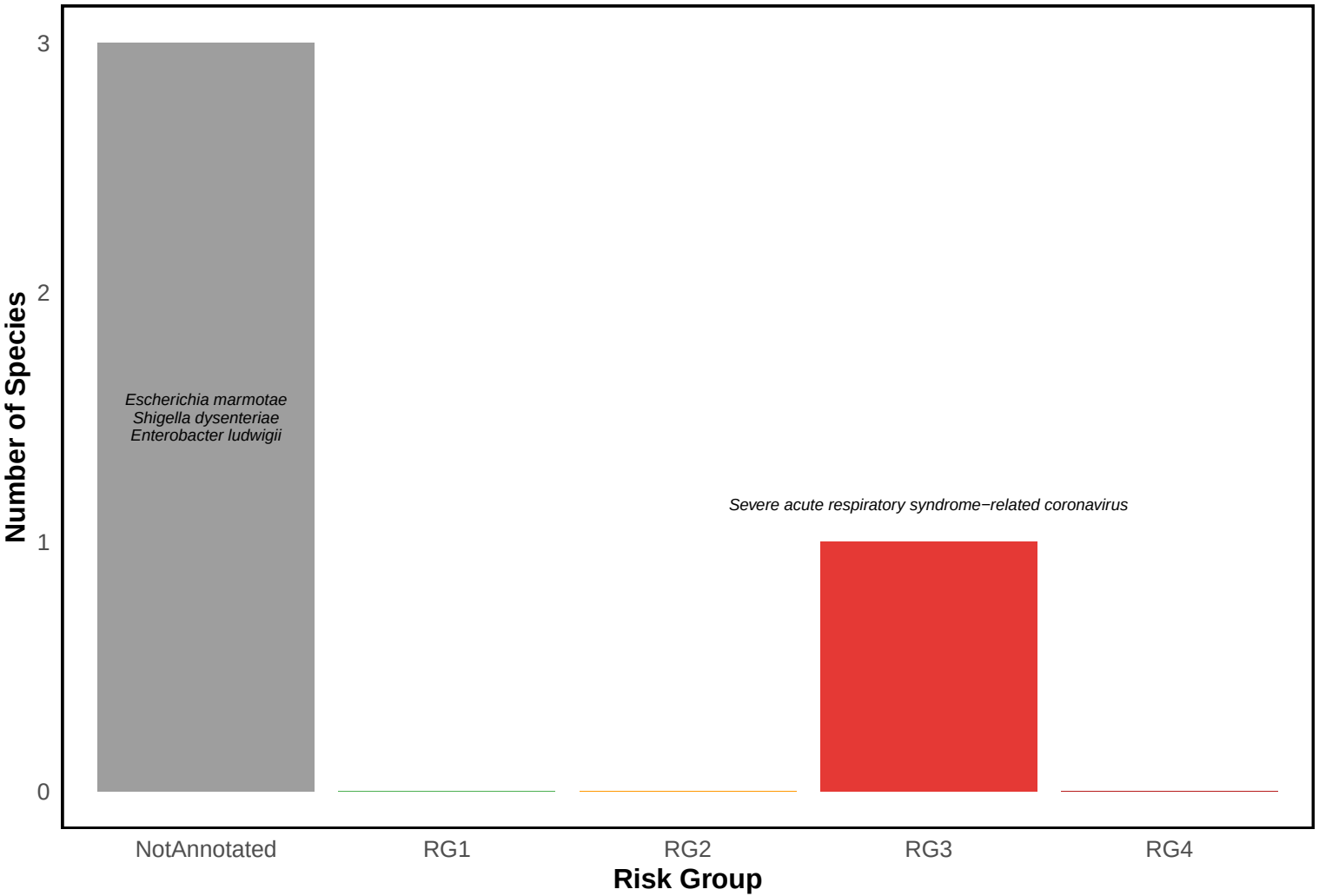
Pathogen detection analysis for sample W90504037:

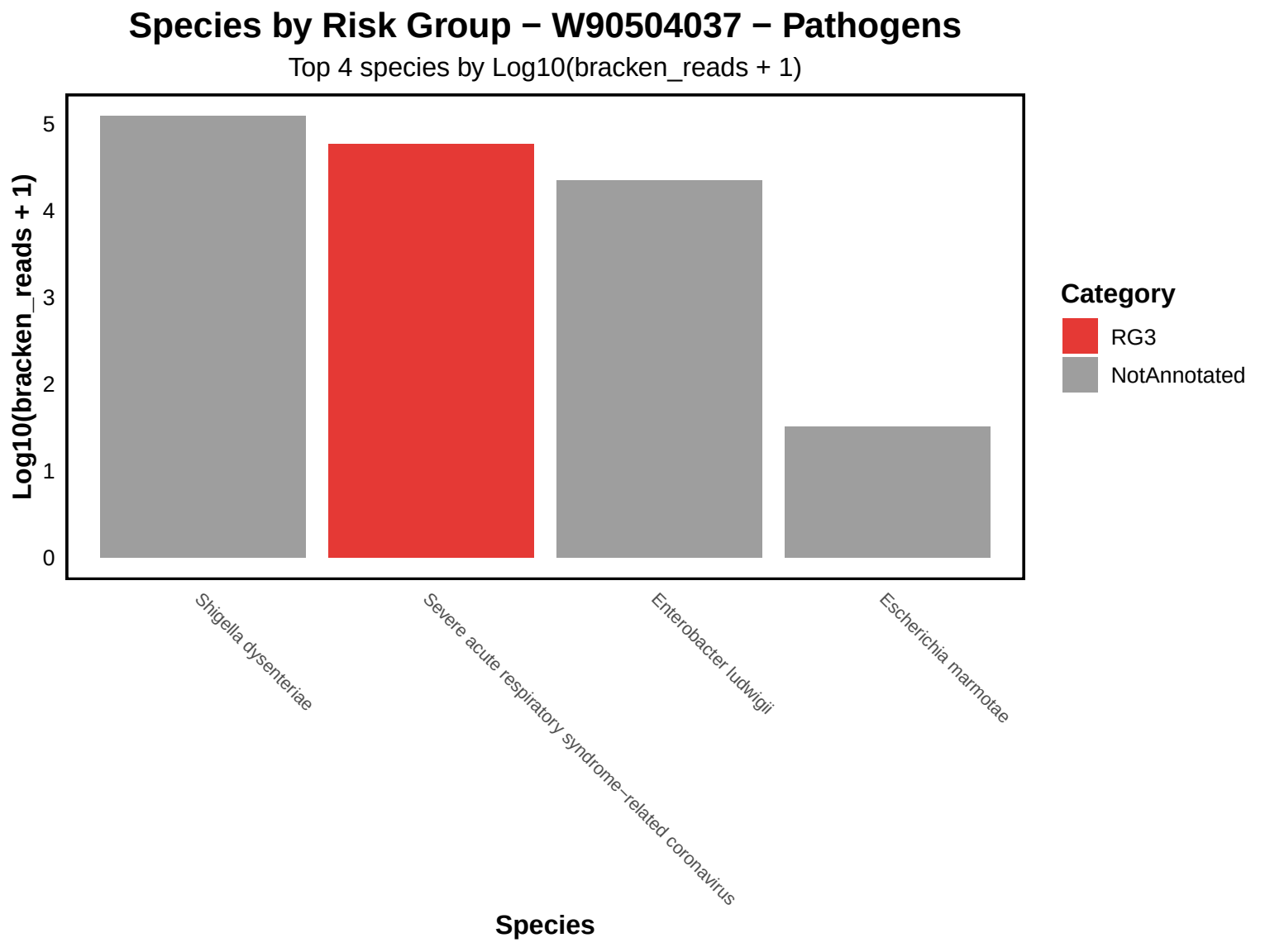
Filtering criteria:
− Include: RG3, RG4 risk groups
− Exclude: RG1, RG2 risk groups
− Exclude: Species annotated as 'Microbiome' in HOMD.Category

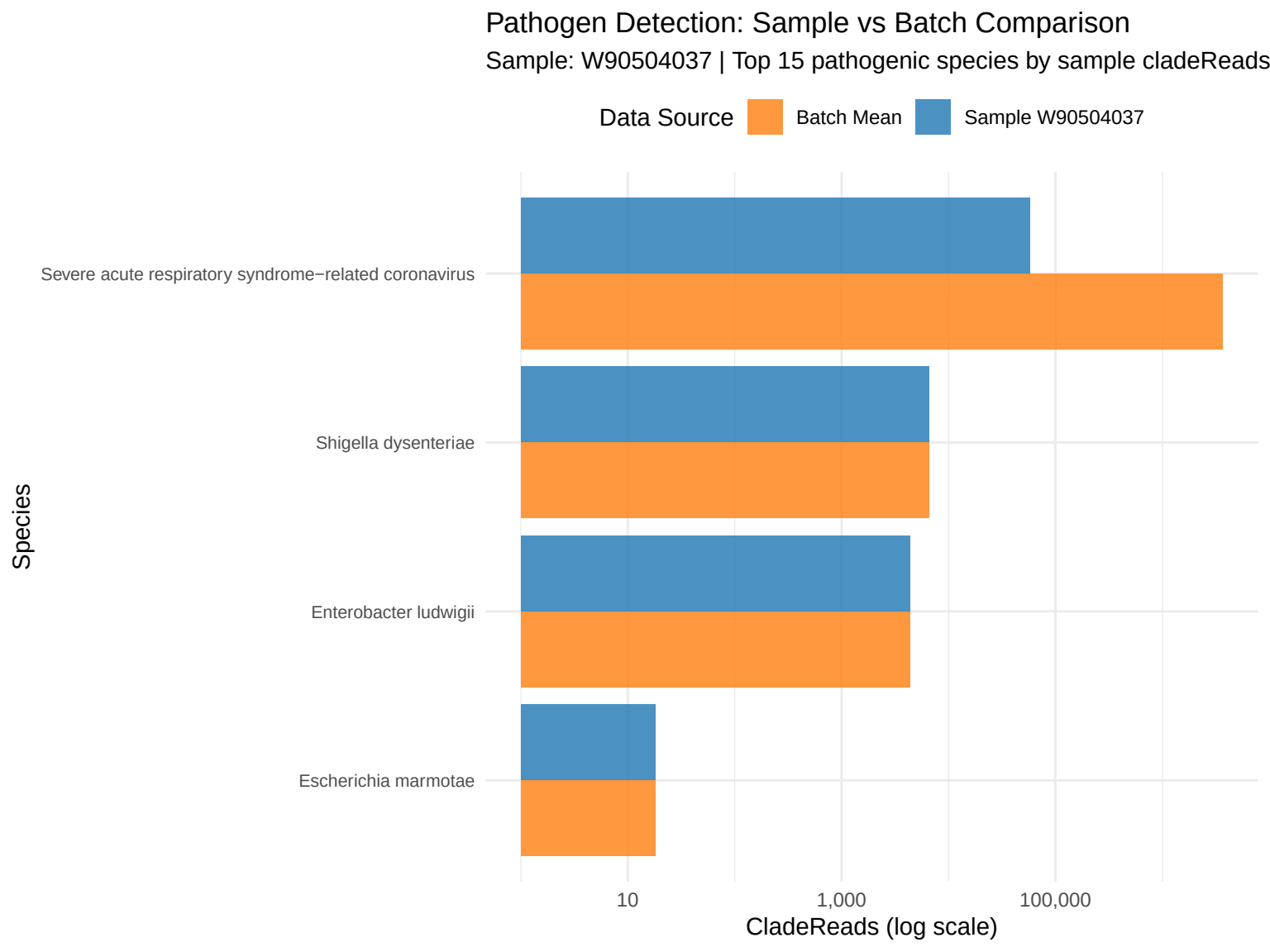
Key findings:
− Total species in sample: 30
− Potential pathogenic species identified: 4
− Most abundant pathogen: Shigella dysenteriae
− Average pathogen reads: 50176.2

Species per Risk Group − W90504037 − Pathogens

Total species: 4




Species by Risk Group − W90504037 − Pathogens
Top 4 species by Log10(bracken_reads + 1)
Log10(bracken_reads + 1)
0
1
2
3
4
5
Shigella dysenteriae
Severe acute respiratory syndrome−related coronavirus
Enterobacter ludwigii
Escherichia marmotae
Species
Category
RG3
NotAnnotated


Pathogen Detection: Sample vs Batch Comparison
Sample: W90504037 | Top 15 pathogenic species by sample cladeReads
Data Source
Batch Mean
Sample W90504037
Species
Severe acute respiratory syndrome−related coronavirus
Shigella dysenteriae
Enterobacter ludwigii
Escherichia marmotae
10
1,000
100,000
CladeReads (log scale)

Part 5: Pathogen Detection (RG3/4 Species) − X01703004

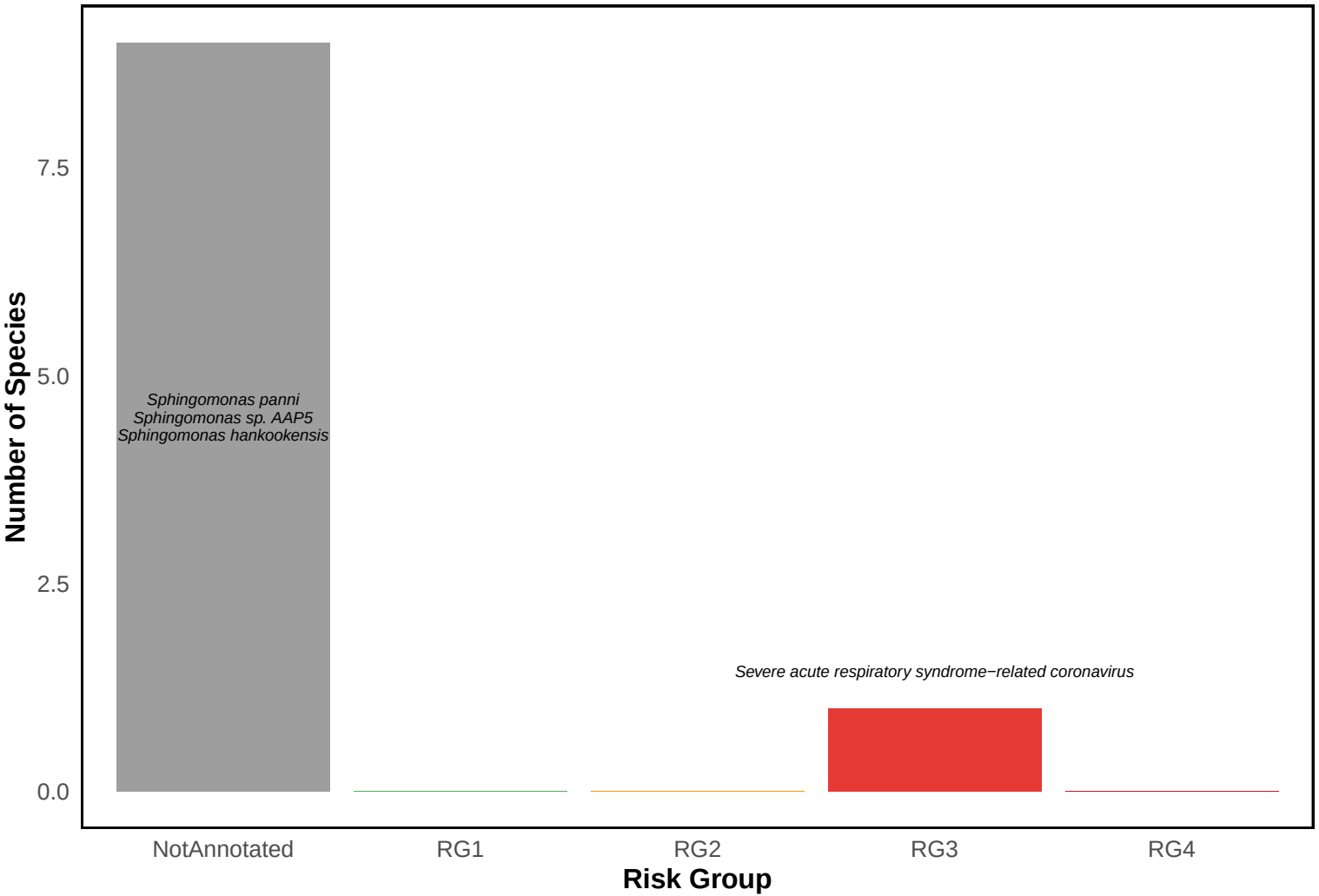
Pathogen detection analysis for sample X01703004:

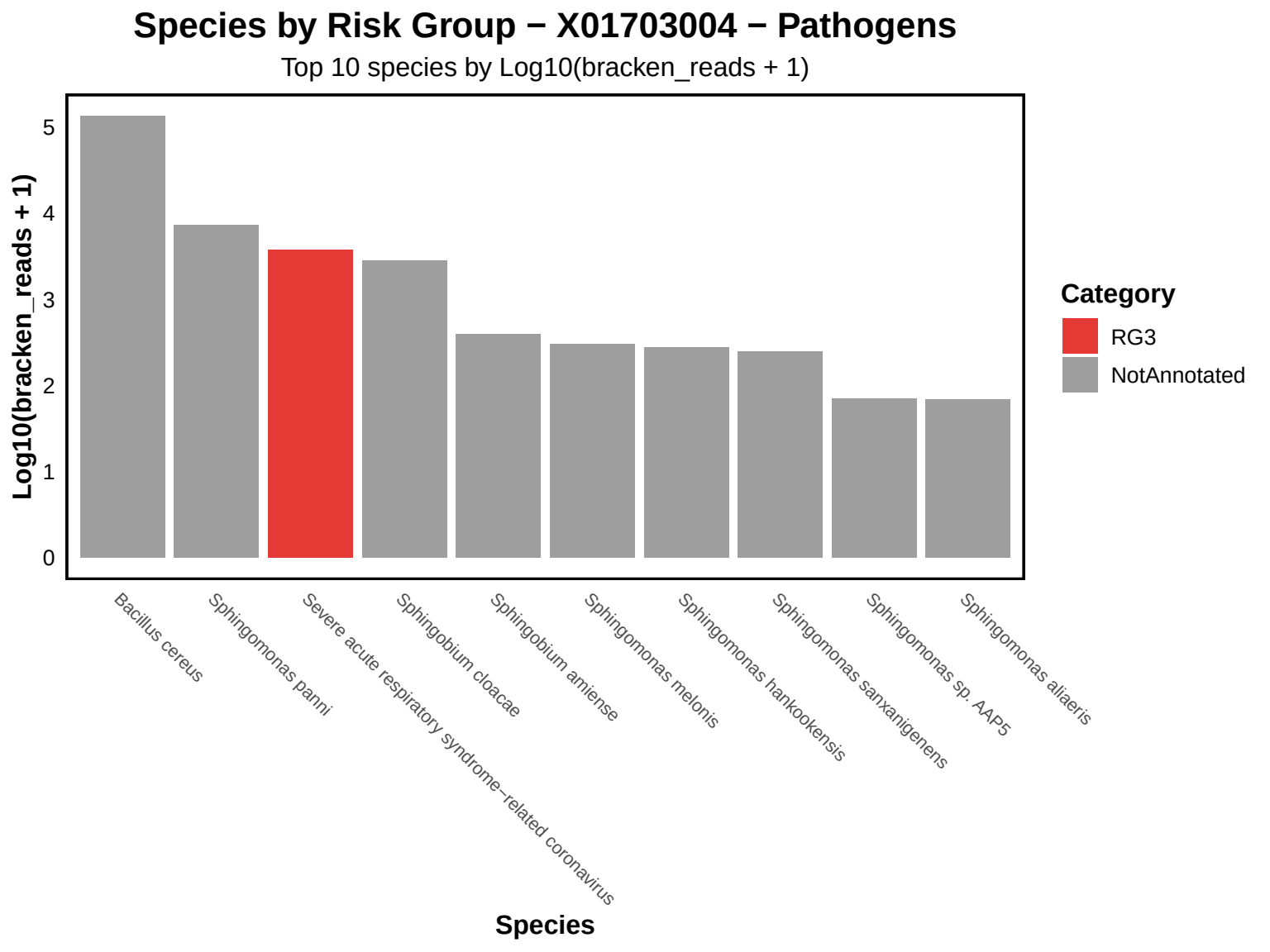
Filtering criteria:
− Include: RG3, RG4 risk groups
− Exclude: RG1, RG2 risk groups
− Exclude: Species annotated as 'Microbiome' in HOMD.Category

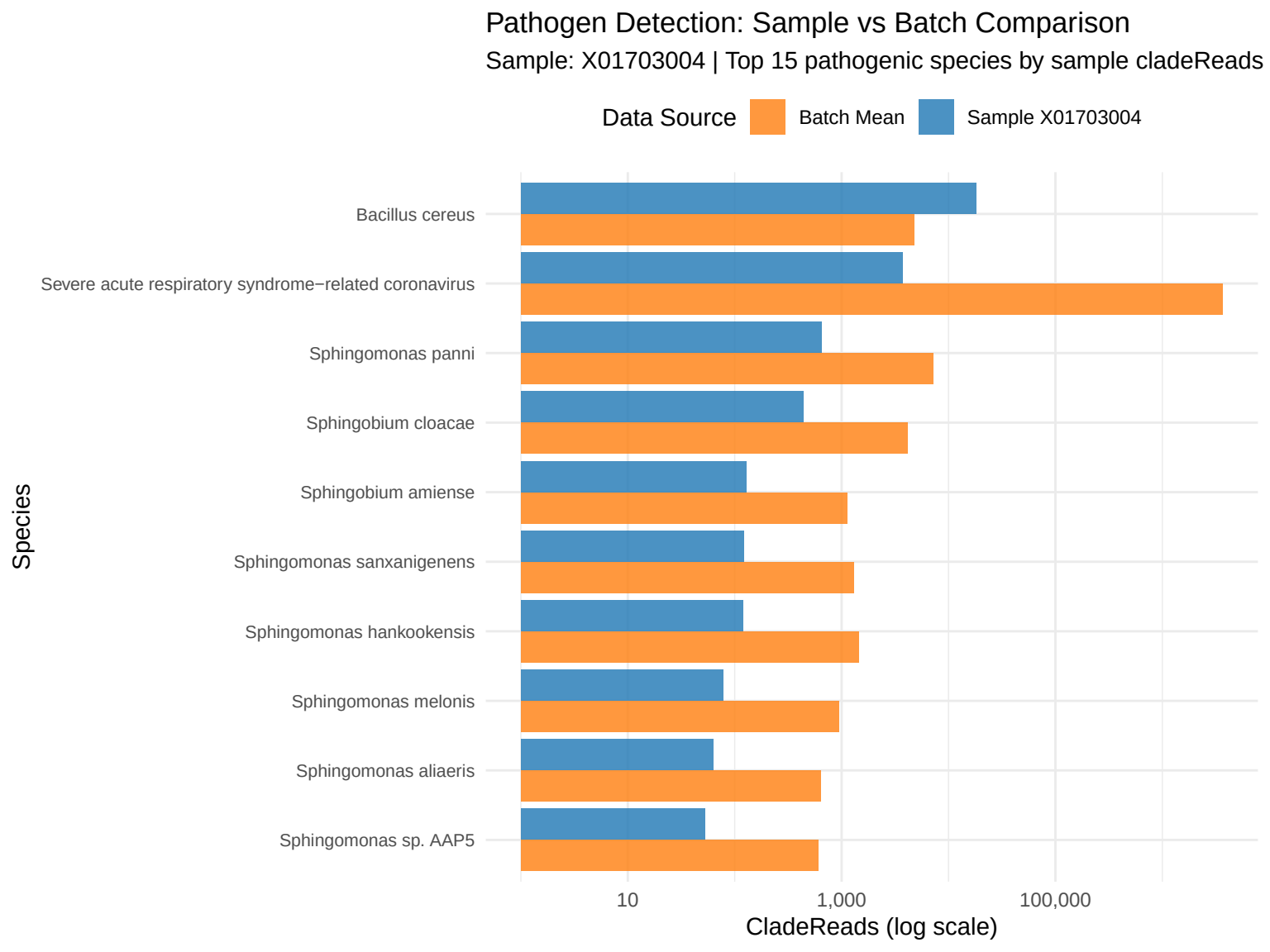
Key findings:
− Total species in sample: 28
− Potential pathogenic species identified: 10
− Most abundant pathogen: Bacillus cereus
− Average pathogen reads: 14869.1

Species per Risk Group − X01703004 − Pathogens

Total species: 10




Species by Risk Group − X01703004 − Pathogens
Top 10 species by Log10(bracken_reads + 1)
Log10(bracken_reads + 1)
0
1
2
3
4
5
Bacillus cereus
Sphingomonas panni
Severe acute respiratory syndrome−related coronavirus
Sphingobium cloacae
Sphingobium amiense
Sphingomonas melonis
Sphingomonas hankookensis
Sphingomonas sanxanigenens
Sphingomonas sp. AAP5
Sphingomonas aliaeris
Species
Category
RG3
NotAnnotated


Pathogen Detection: Sample vs Batch Comparison
Sample: X01703004 | Top 15 pathogenic species by sample cladeReads
Data Source
Batch Mean
Sample X01703004
Species
Bacillus cereus
Severe acute respiratory syndrome−related coronavirus
Sphingomonas panni
Sphingobium cloacae
Sphingobium amiense
Sphingomonas sanxanigenens
Sphingomonas hankookensis
Sphingomonas melonis
Sphingomonas aliaeris
Sphingomonas sp. AAP5
10
1,000
100,000
CladeReads (log scale)

Part 5: Pathogen Detection (RG3/4 Species) − X22106916

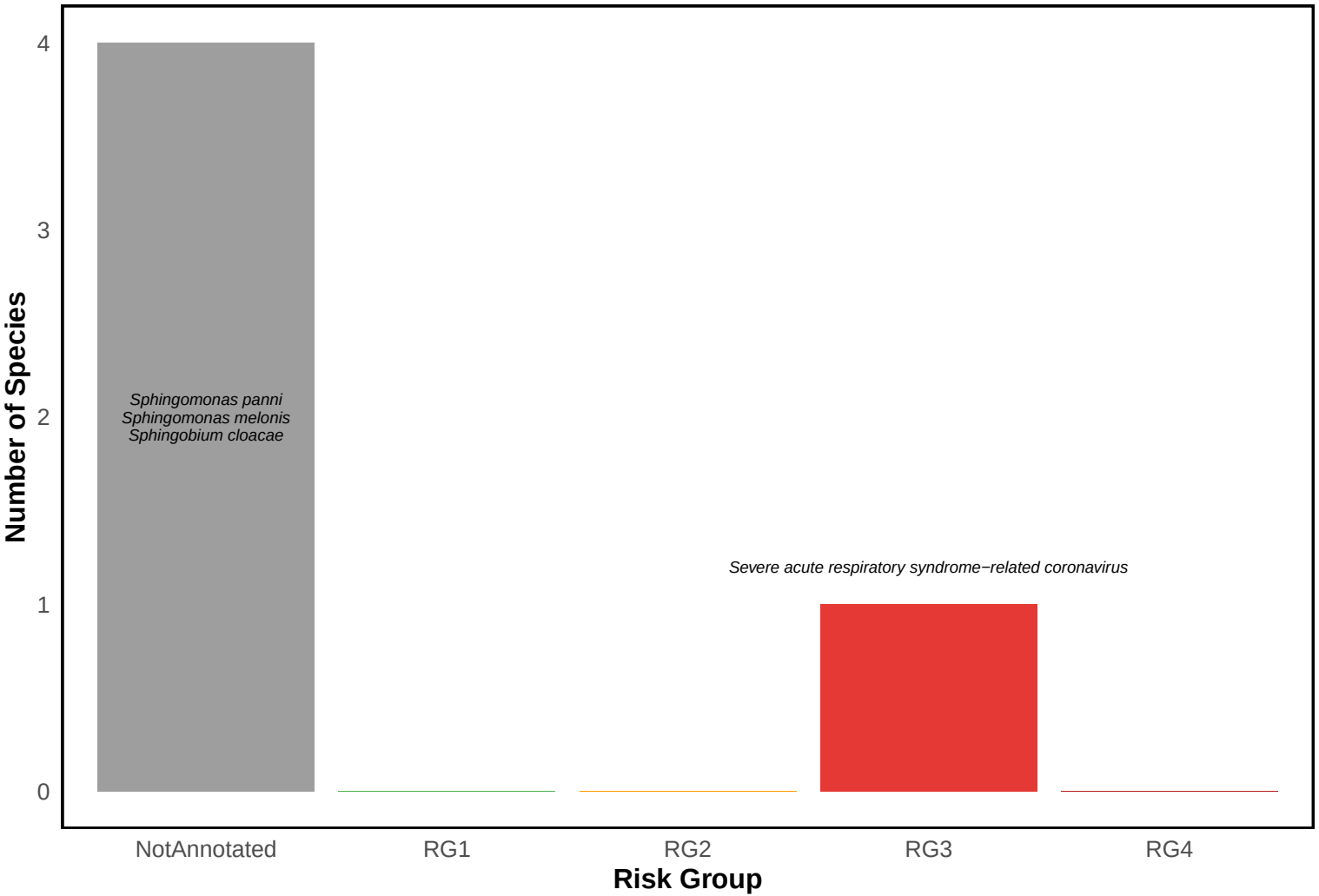
Pathogen detection analysis for sample X22106916:

Filtering criteria:
− Include: RG3, RG4 risk groups
− Exclude: RG1, RG2 risk groups
− Exclude: Species annotated as 'Microbiome' in HOMD.Category

Key findings:
− Total species in sample: 15
− Potential pathogenic species identified: 5
− Most abundant pathogen: Severe acute respiratory syndrome−related coronavirus
− Average pathogen reads: 39614.6

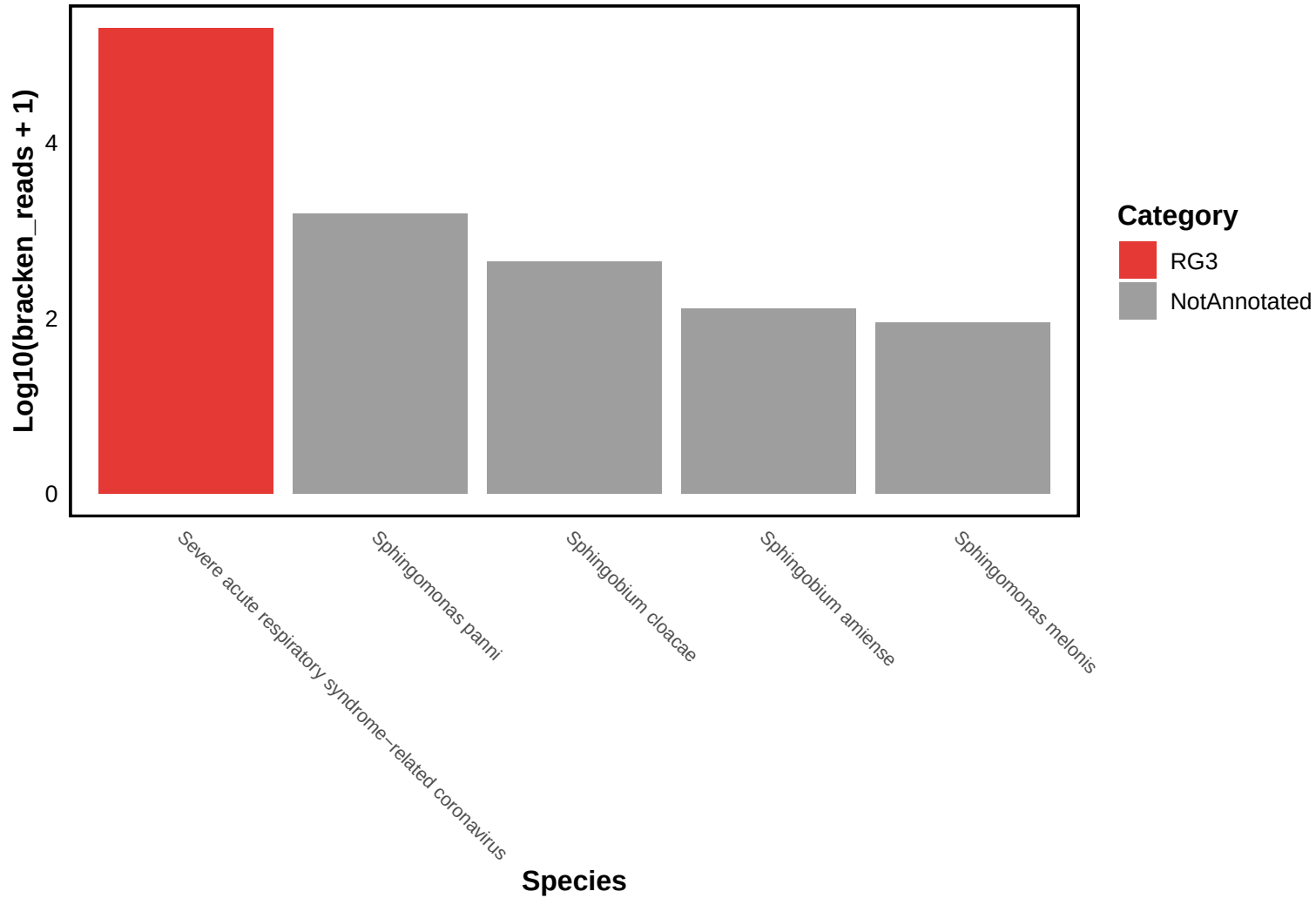
Species per Risk Group − X22106916 − Pathogens

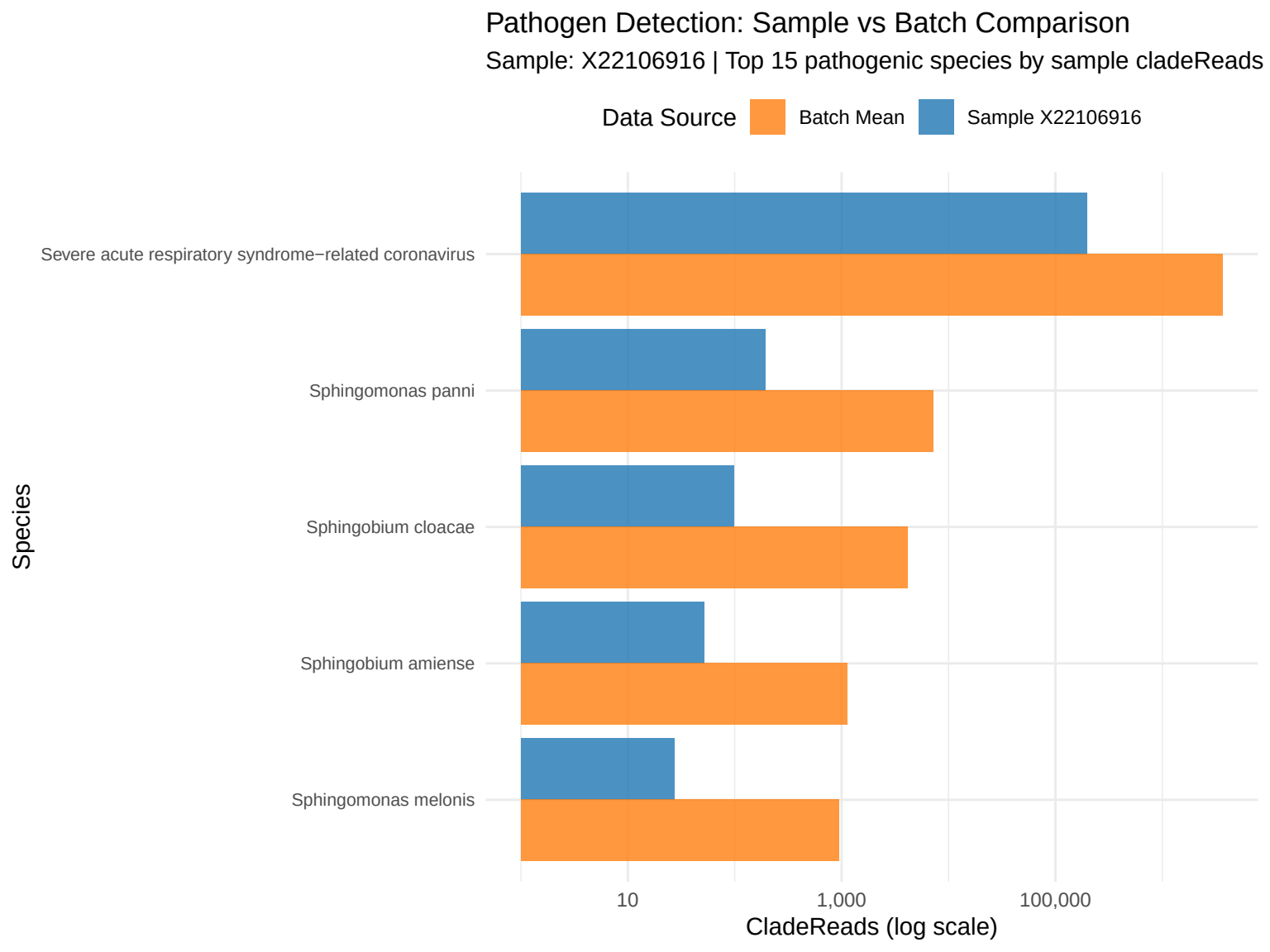
Total species: 5



Species by Risk Group − X22106916 − Pathogens

Top 5 species by Log10(bracken_reads + 1)




Pathogen Detection: Sample vs Batch Comparison
Sample: X22106916 | Top 15 pathogenic species by sample cladeReads
Data Source
Batch Mean
Sample X22106916
Species
Severe acute respiratory syndrome−related coronavirus
Sphingomonas panni
Sphingobium cloacae
Sphingobium amiense
Sphingomonas melonis
10
1,000
100,000
CladeReads (log scale)

Part 5: Pathogen Detection (RG3/4 Species) − X30306045

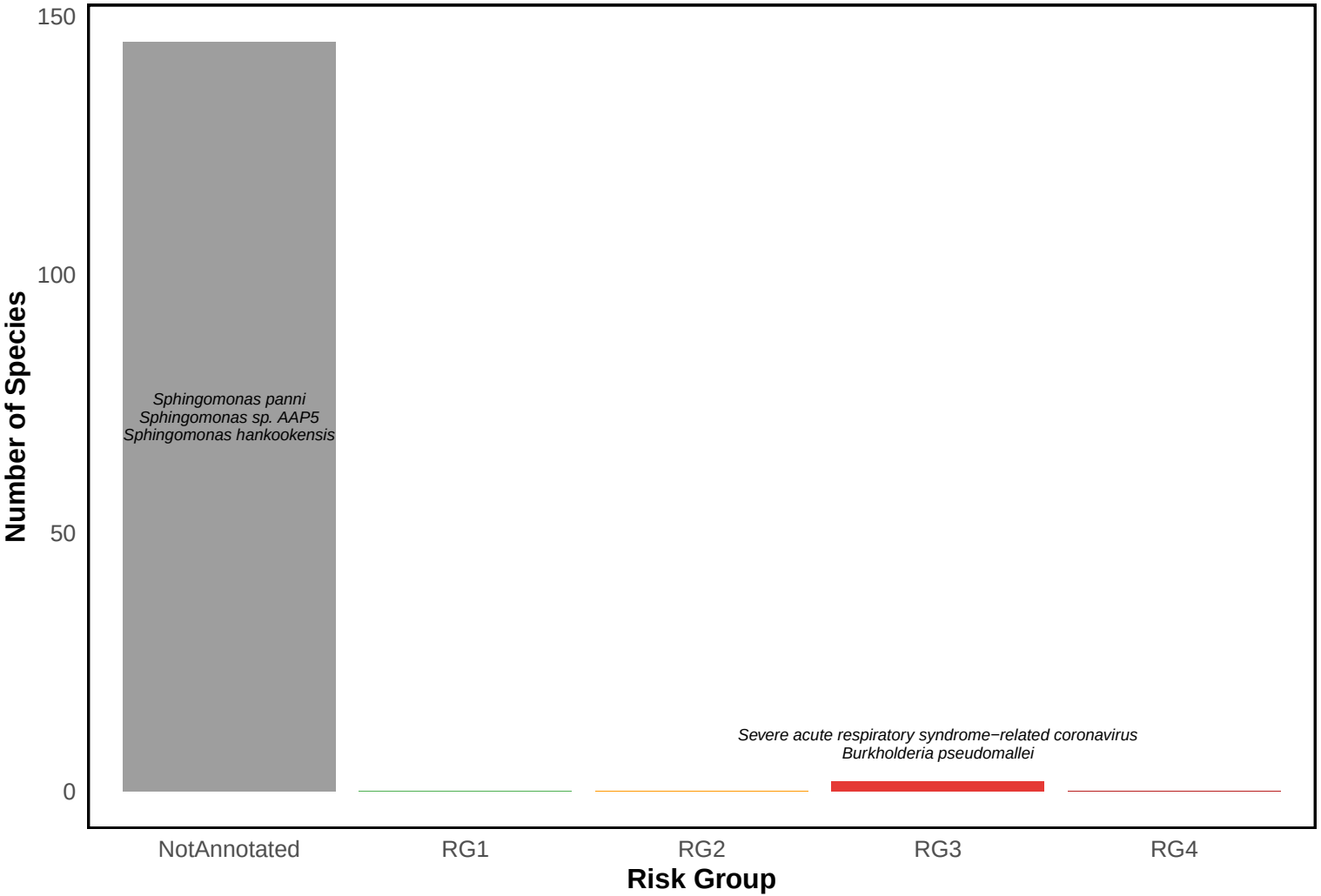
Pathogen detection analysis for sample X30306045:

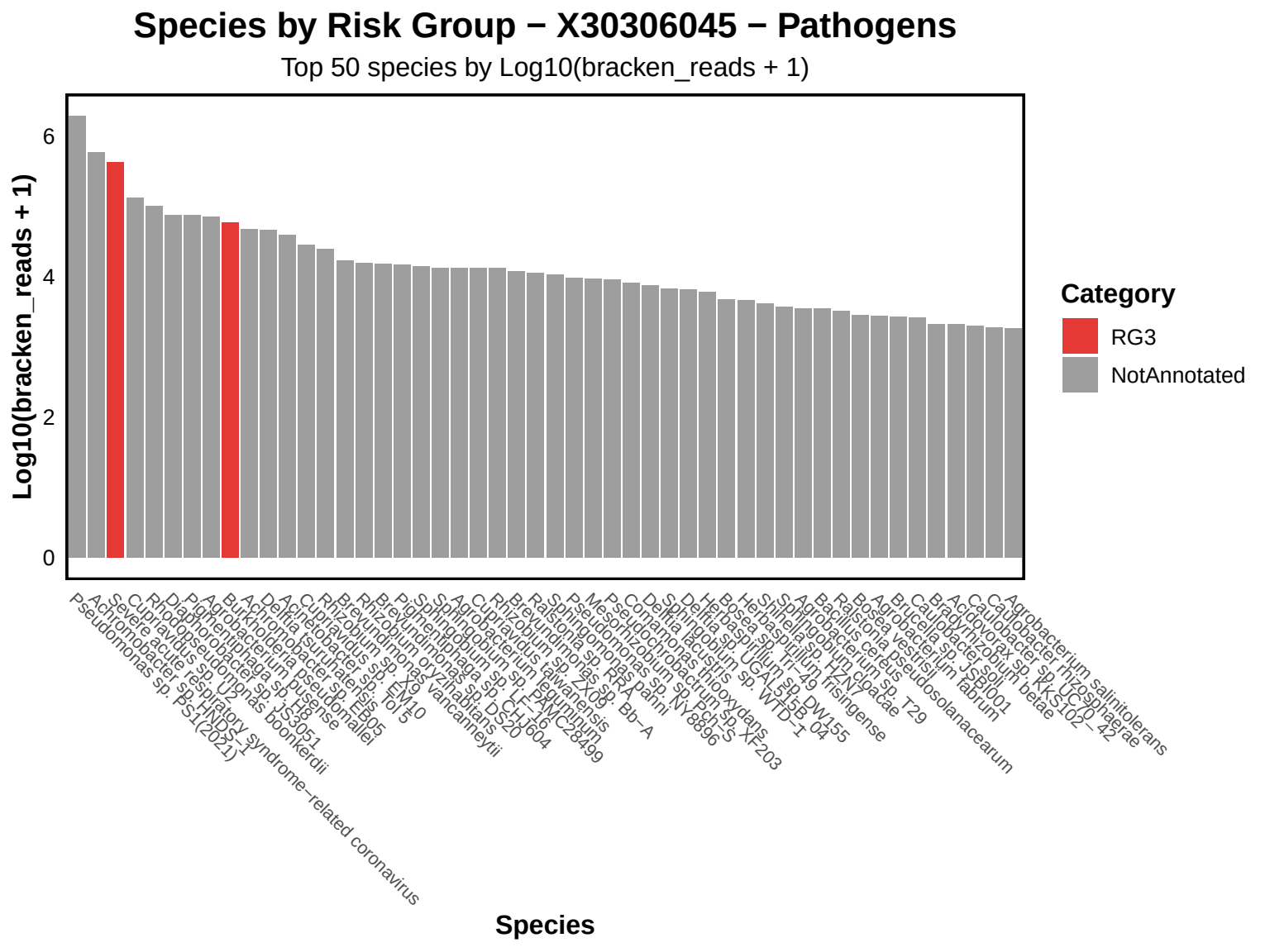
Filtering criteria:
− Include: RG3, RG4 risk groups
− Exclude: RG1, RG2 risk groups
− Exclude: Species annotated as 'Microbiome' in HOMD.Category

Key findings:
− Total species in sample: 224
− Potential pathogenic species identified: 147
− Most abundant pathogen: Pseudomonas sp. PS1(2021)
− Average pathogen reads: 26834.1

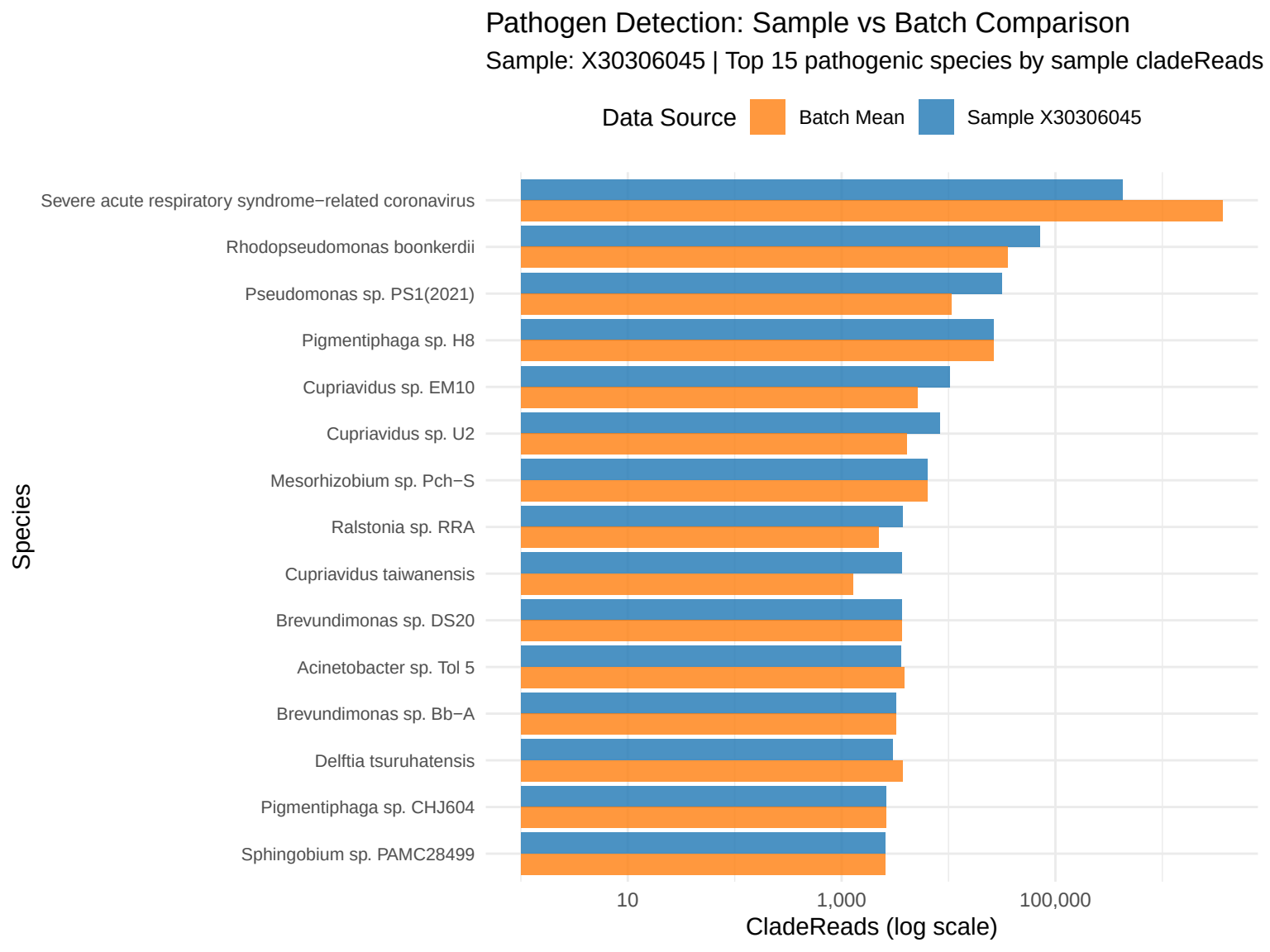
Species per Risk Group − X30306045 − Pathogens

Total species: 147





Species by Risk Group − X30306045 − Pathogens
Top 50 species by Log10(bracken_reads + 1)
Log10(bracken_reads + 1)
0
2
4
6
Category
RG3
NotAnnotated
Pseudomonas sp. PS1(2021)
Achromobacter sp. HNDY−1
Severe acute respiratory syndrome−related coronavirus
Cupriavidus sp. U2
Rhodopseudomonas boonkerdii
Diaphorobacter sp. JS3051
Pigmentiphaga sp. H8
Agrobacterium pusense
Burkholderia pseudomallei
Achromobacter sp. EB05
Delftia tsuruhatensis
Acinetobacter sp. Tol 5
Cupriavidus sp. EM10
Rhizobium sp. Tol 5
Brevundimonas vancanneytii
Rhizobium oryzinabitans
Brevundimonas sp. DS20
Pigmentiphaga sp. CH1604
Sphingobium sp. CF−16
Agrobacterium sp. PAMC28499
Cupriavidus taiwanensis
Rhizobium sp. ZX09
Brevundimonas sp. Bb−A
Ralstonia sp. RRA
Sphingomonas sp. Pahni
Pseudomonas sp. NY8896
Mesorhizobium sp. PCH5
Pseudochrobactrum sp. XF203
Comamonas thiooxydans
Delftia lacustris
Sphingobium sp. WTD−1
Delftia sp. UGA15B−04
Herbaspirillum sp. DW155
Bosea sp. HZN−1
Herbaspirillum frisingense
Shinella sp. HZN−1
Sphingobium rhizogenes
Agrobacterium sp. T29
Bacillus cereus
Ralstonia pseudosolanacearum
Bosea vestrisii
Agrobacterium fabrum
Brucella sp. JSB001
Caulobacter soli
Bradyrhizobium betae
Acidovorax sp. KKS102−42
Caulobacter rhizosphaerae
Caulobacter sp. UCC−42
Agrobacterium salinitolerans
Species


Pathogen Detection: Sample vs Batch Comparison
Sample: X30306045 | Top 15 pathogenic species by sample cladeReads
Data Source
Batch Mean
Sample X30306045
Species
Severe acute respiratory syndrome−related coronavirus
Rhodopseudomonas boonkerdii
Pseudomonas sp. PS1(2021)
Pigmentiphaga sp. H8
Cupriavidus sp. EM10
Cupriavidus sp. U2
Mesorhizobium sp. Pch−S
Ralstonia sp. RRA
Cupriavidus taiwanensis
Brevundimonas sp. DS20
Acinetobacter sp. Tol 5
Brevundimonas sp. Bb−A
Delftia tsuruhatensis
Pigmentiphaga sp. CHJ604
Sphingobium sp. PAMC28499
10
1,000
100,000
CladeReads (log scale)