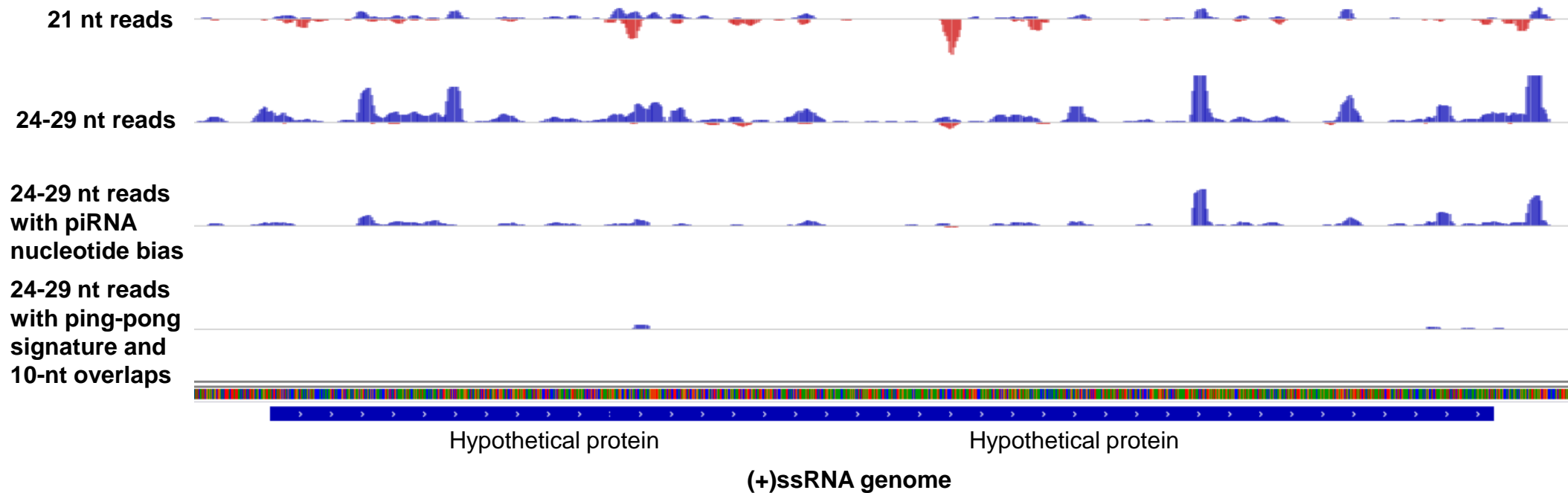
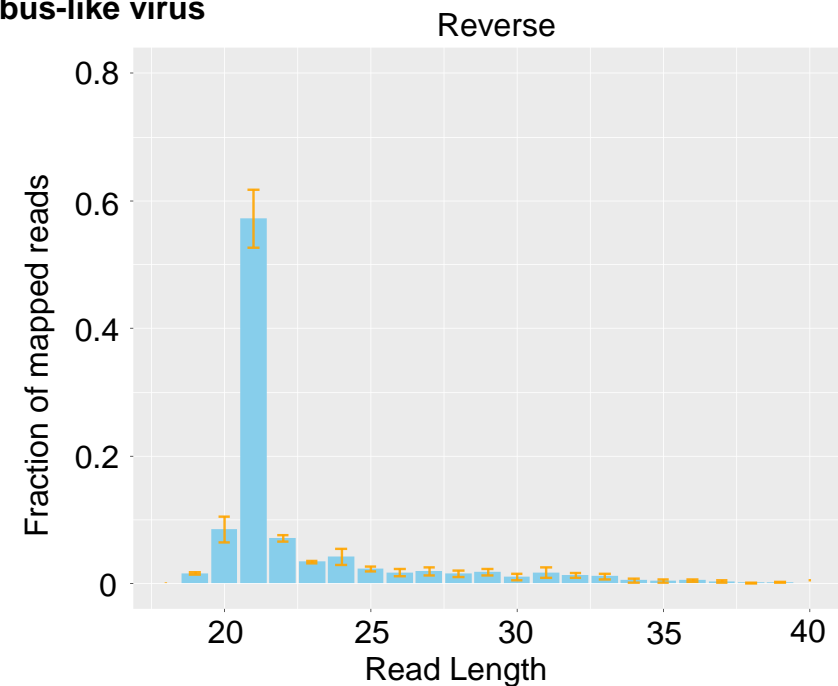
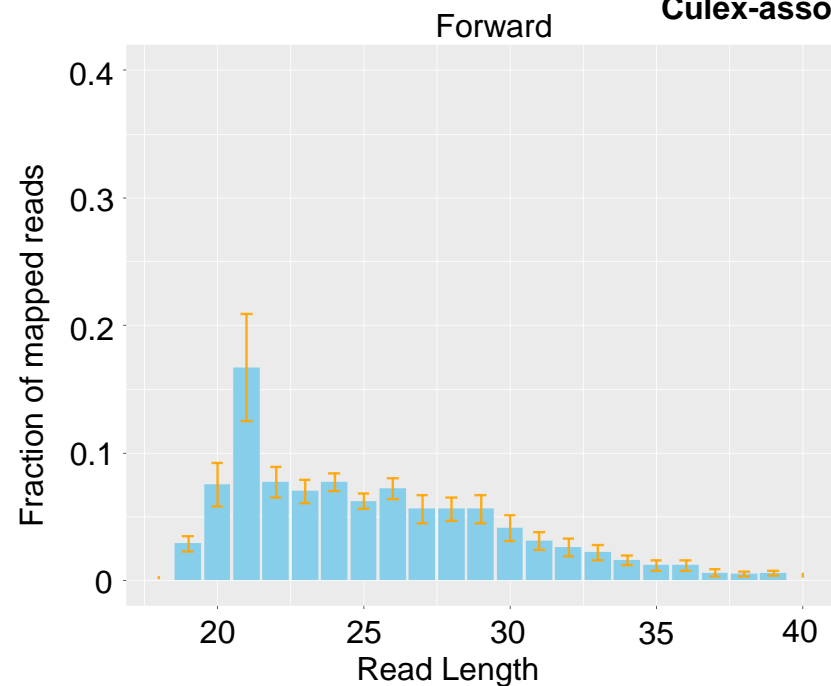


Fig. S2: Small RNA size profiles and genome coverage plots for all viruses not shown in main figures.

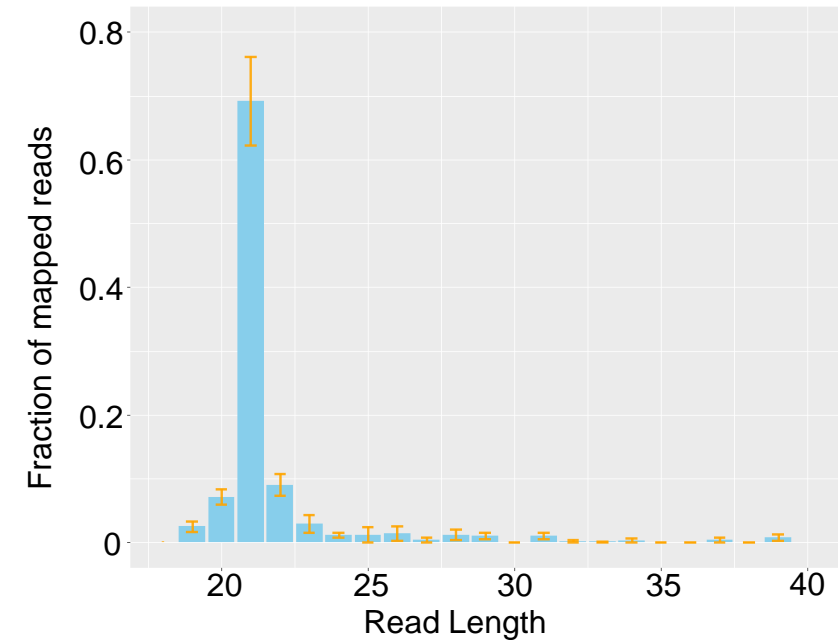
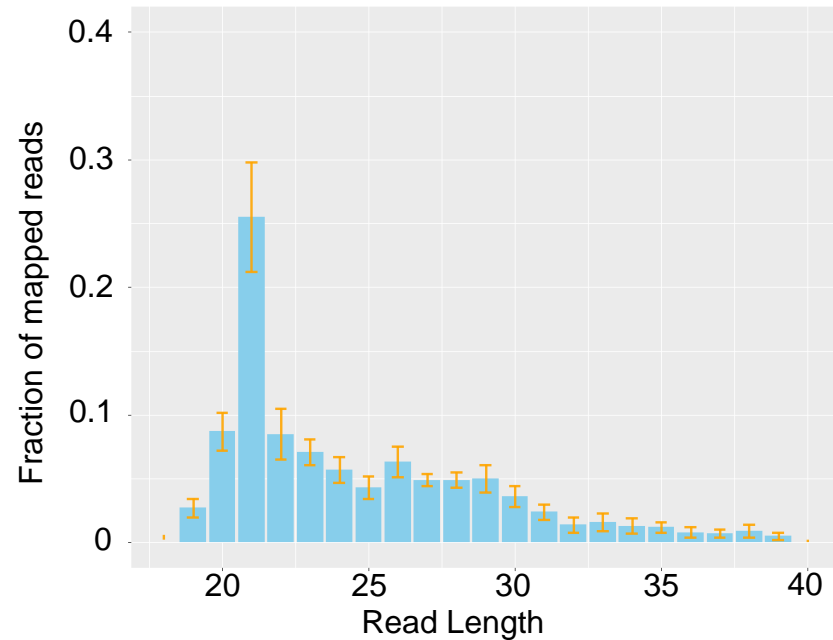
Culex-associated tombus-like virus



Forward

Culex-originated Tymoviridae-like virus

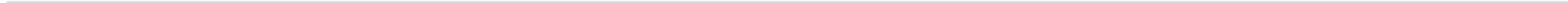
Reverse



21 nt reads



24-29 nt reads

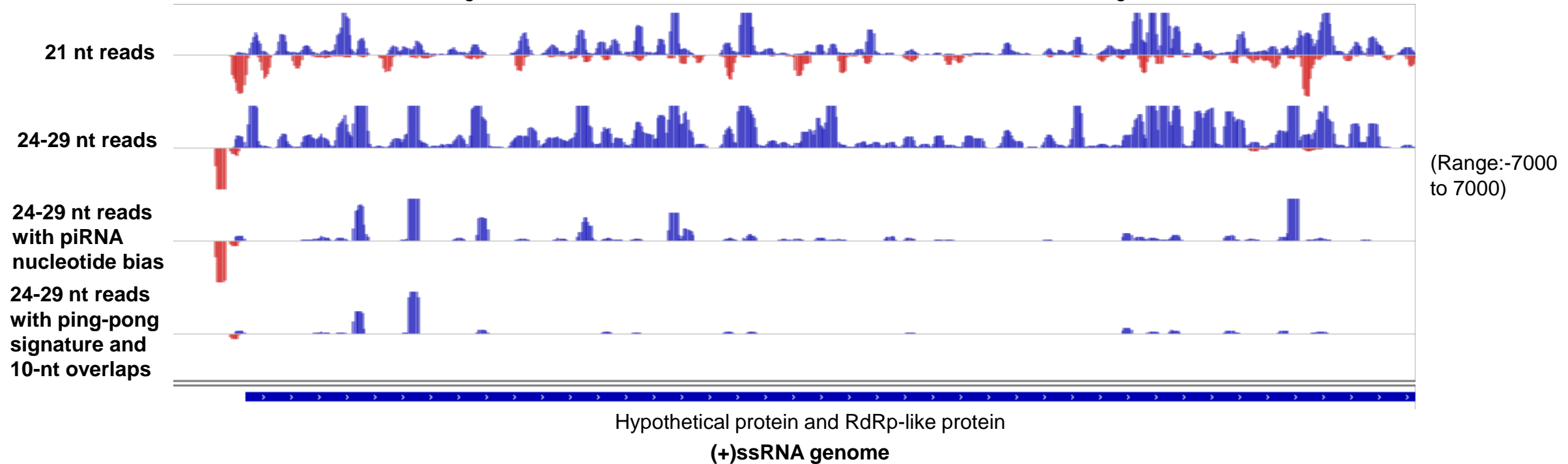
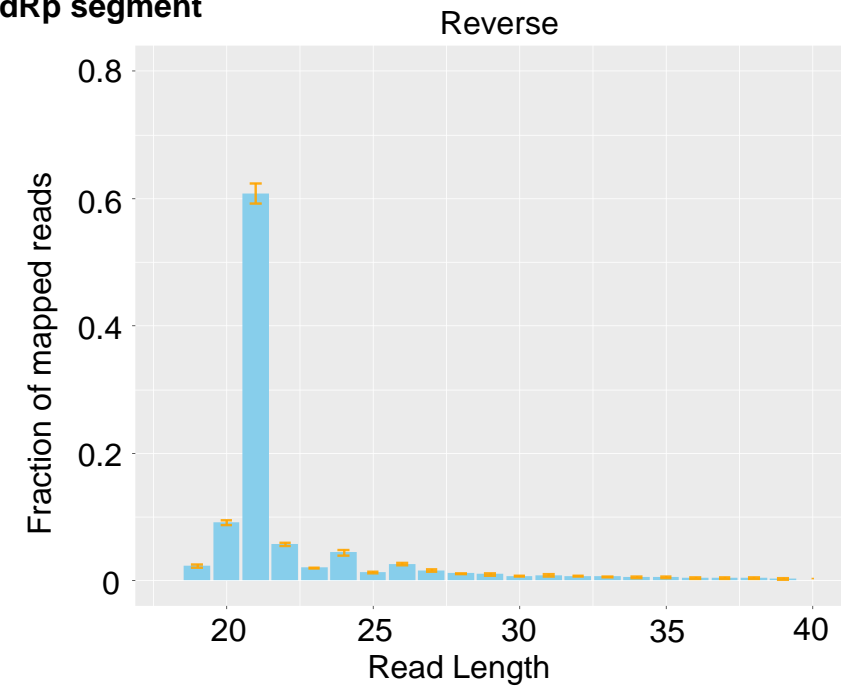
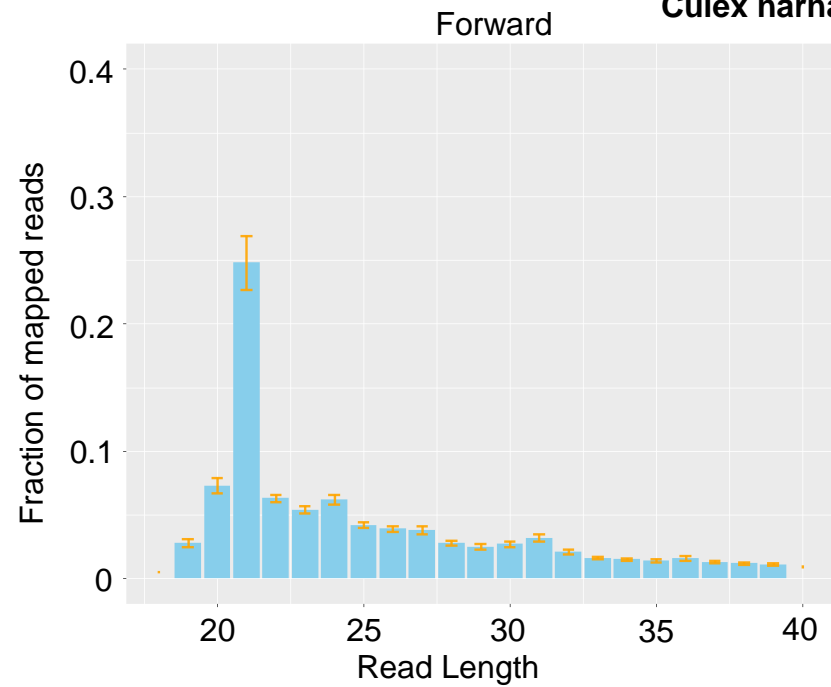
24-29 nt reads
with piRNA
nucleotide bias24-29 nt reads
with ping-pong
signature and
10-nt overlaps

Movement protein RNA polymerase Capsid protein

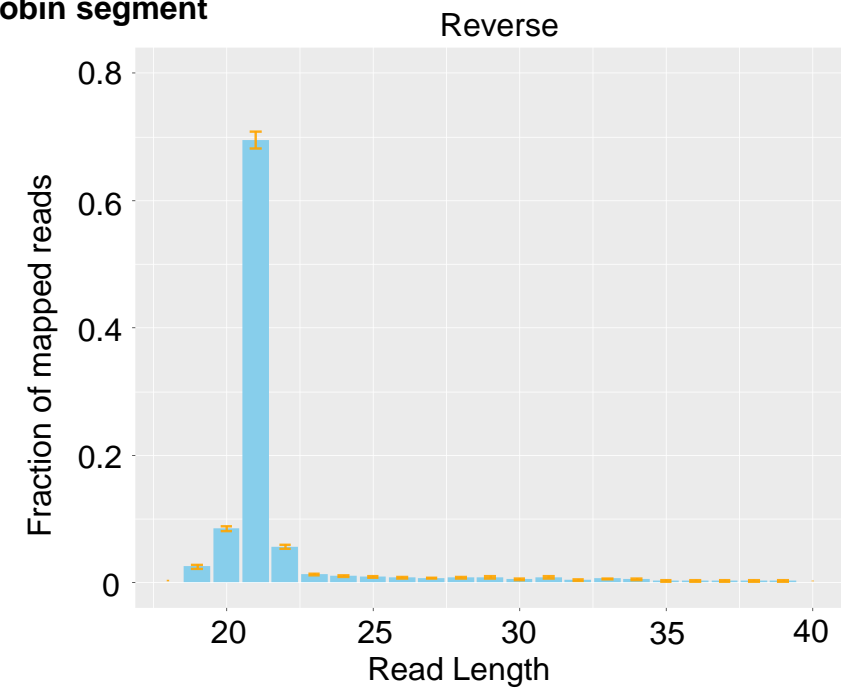
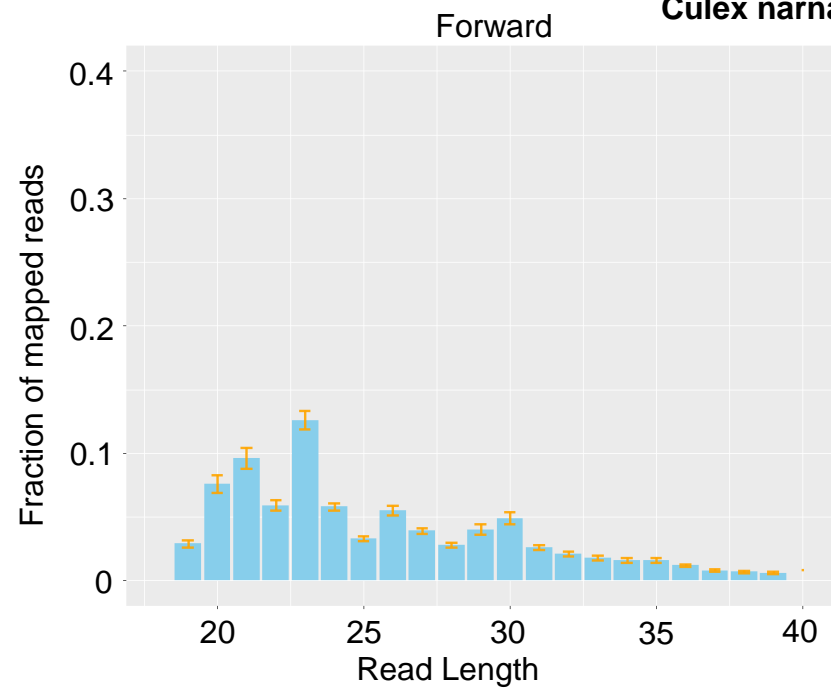
(+)ssRNA genome

(Range:-75
to 75)

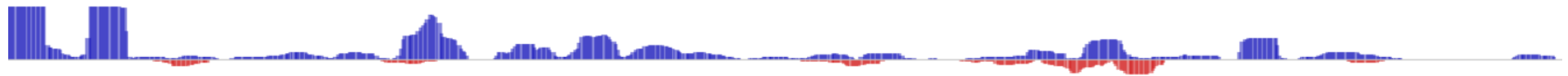
Culex narnavirus 1, RdRp segment



Culex narnavirus 1, Robin segment



21 nt reads



24-29 nt reads



24-29 nt reads
with piRNA
nucleotide bias



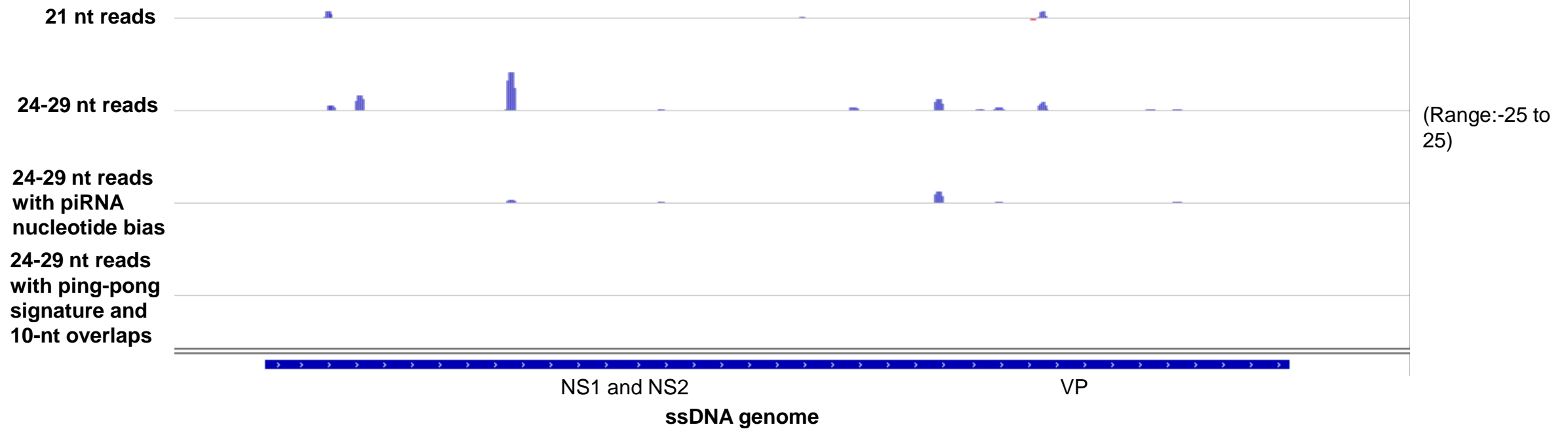
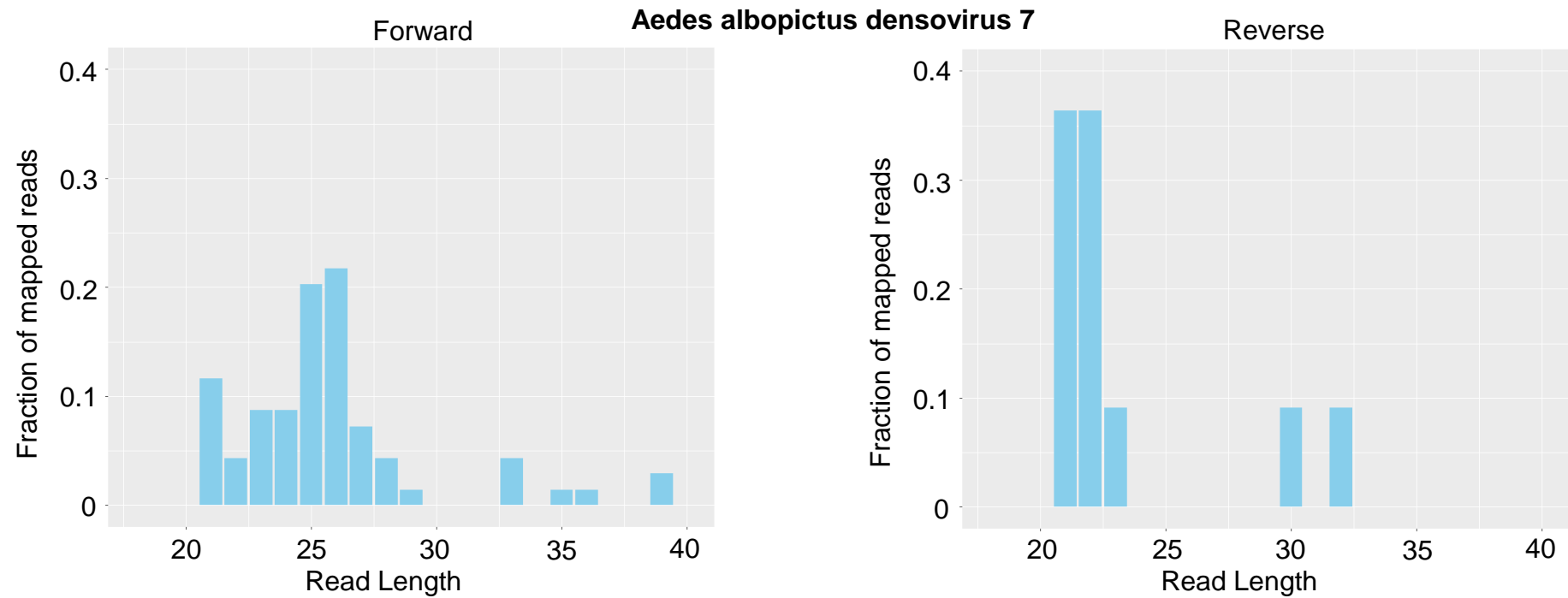
24-29 nt reads
with ping-pong
signature and
10-nt overlaps



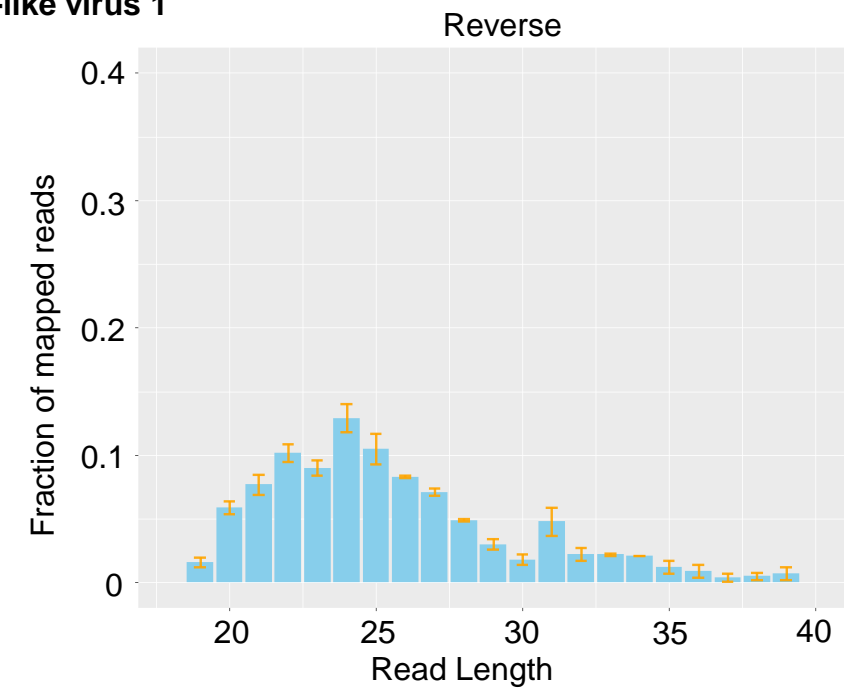
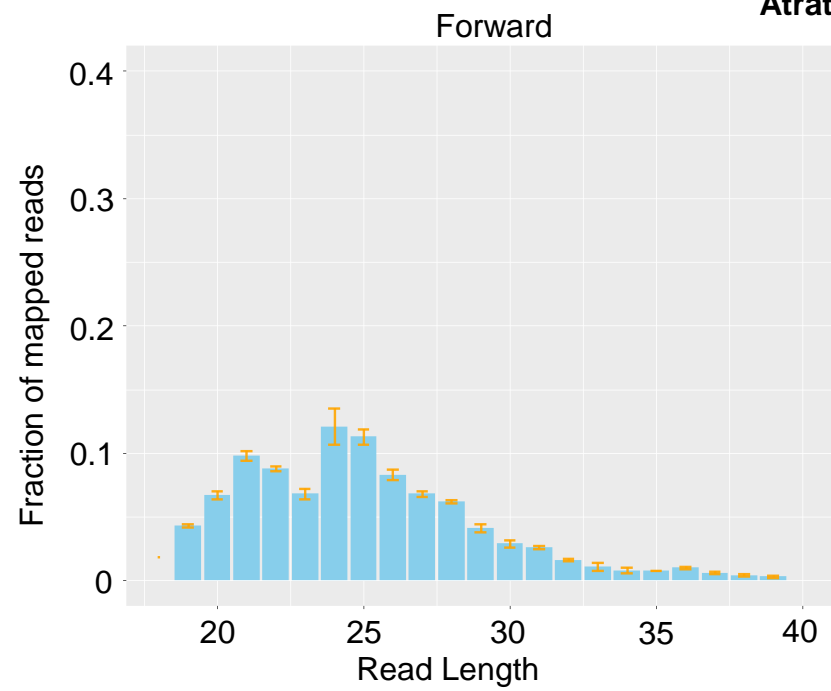
(Range:-20000
to 20000)

Putative Robin and hypothetical protein
(+)ssRNA genome





Atrato picorna-like virus 1



21 nt reads

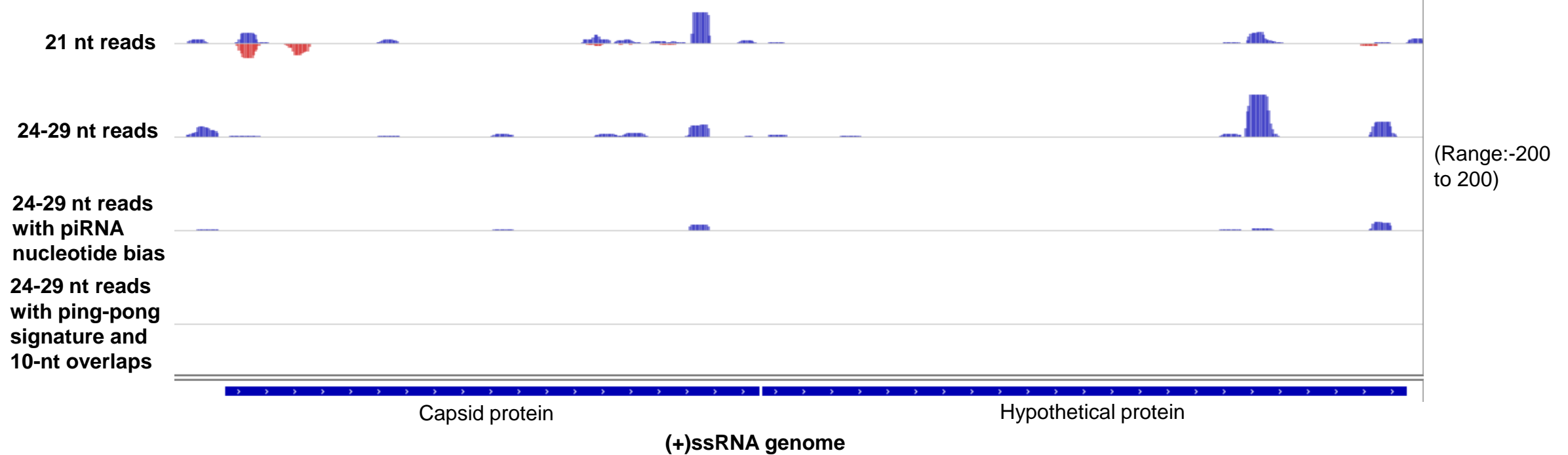
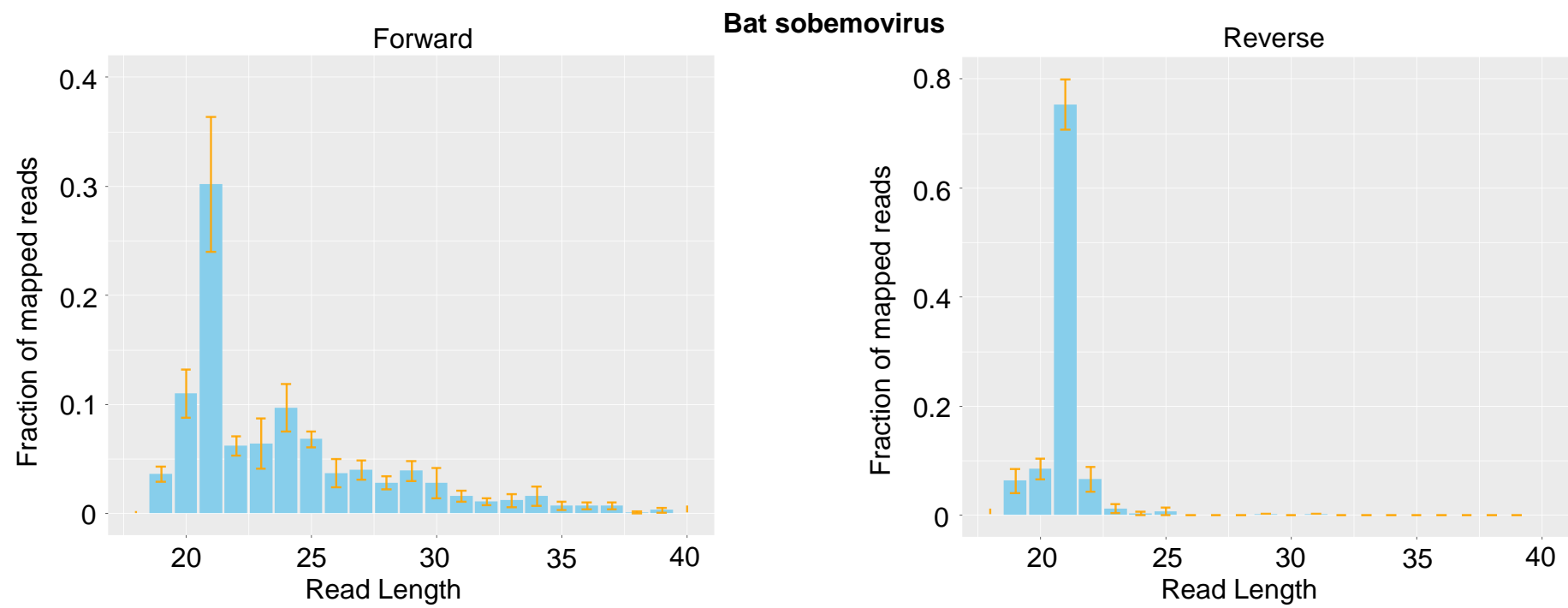
24-29 nt reads

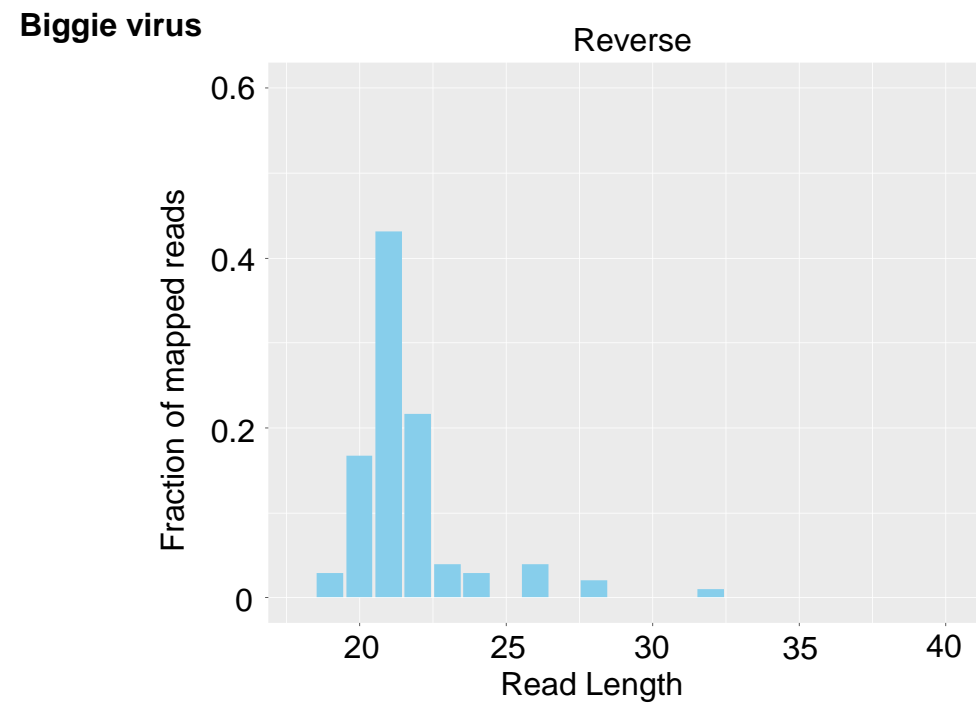
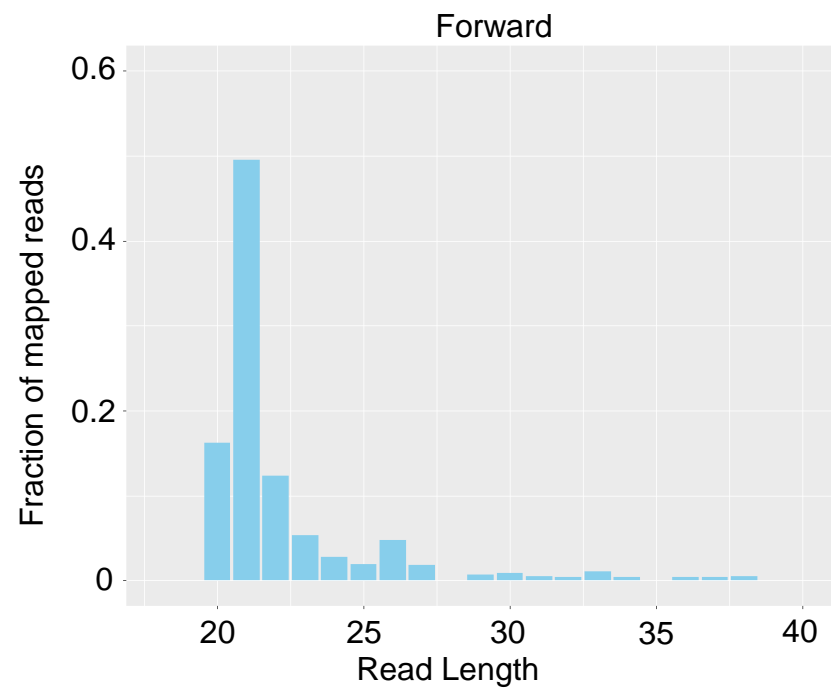
24-29 nt reads
with piRNA
nucleotide bias

24-29 nt reads
with ping-pong
signature and
10-nt overlaps

(Range:-250
to 250)

Polyprotein
(+)ssRNA genome





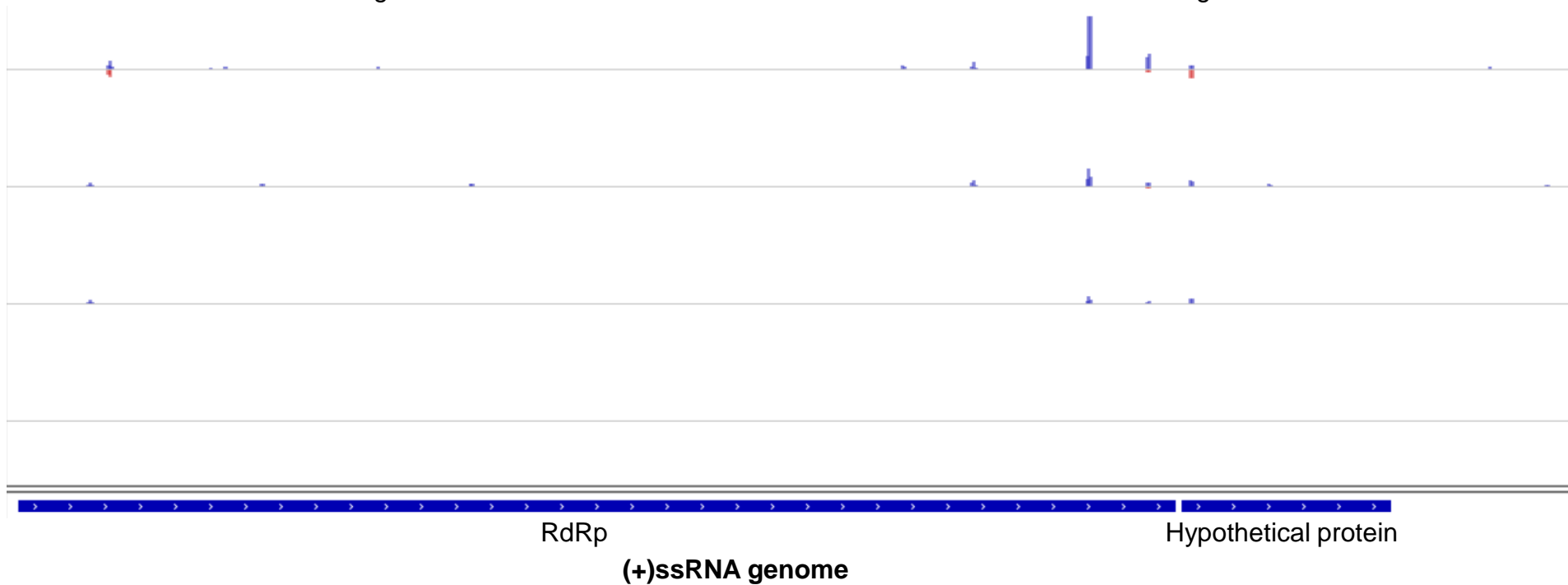
21 nt reads

24-29 nt reads

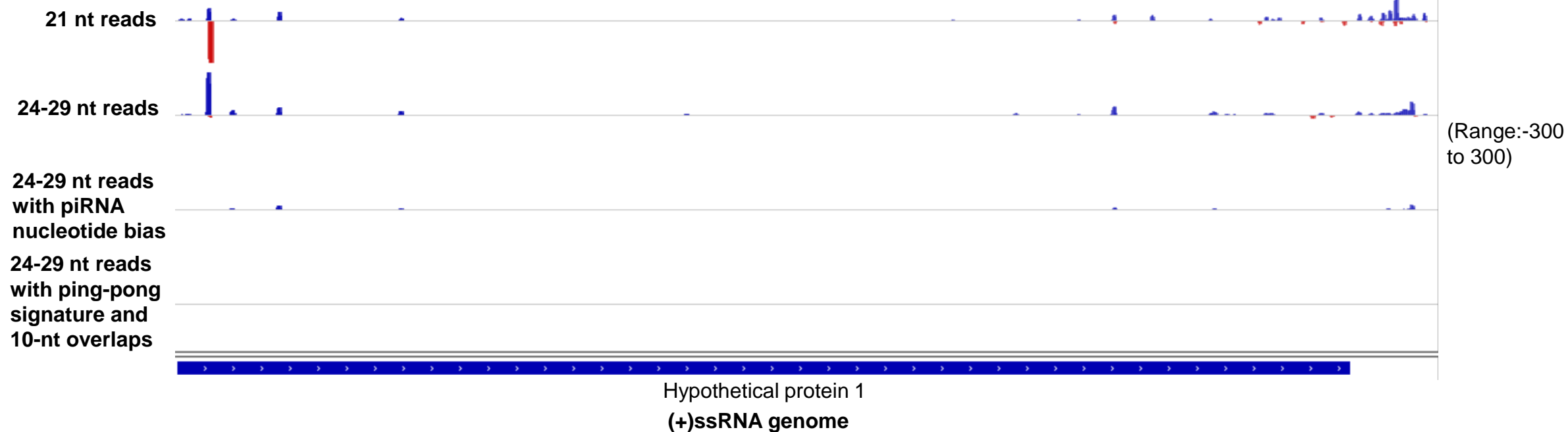
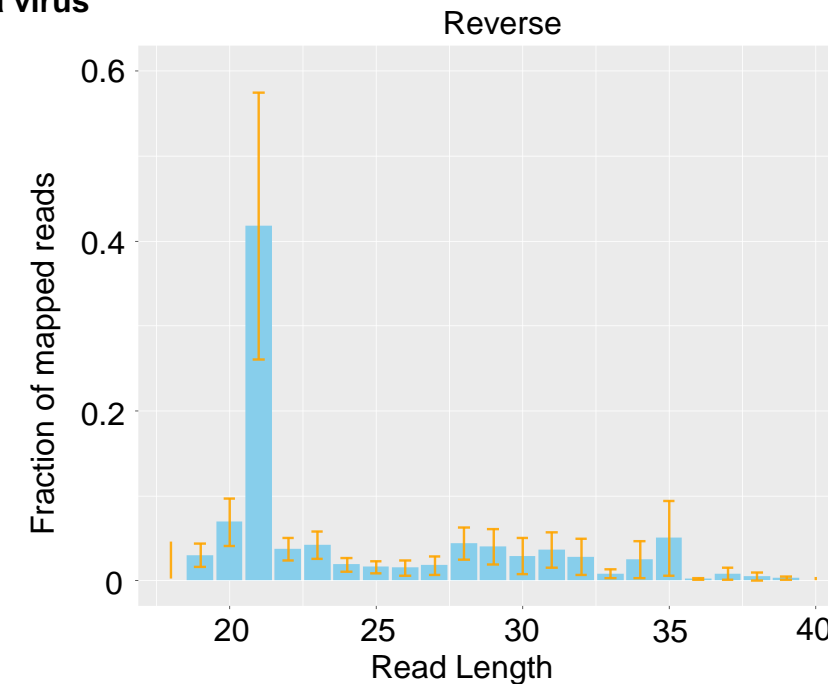
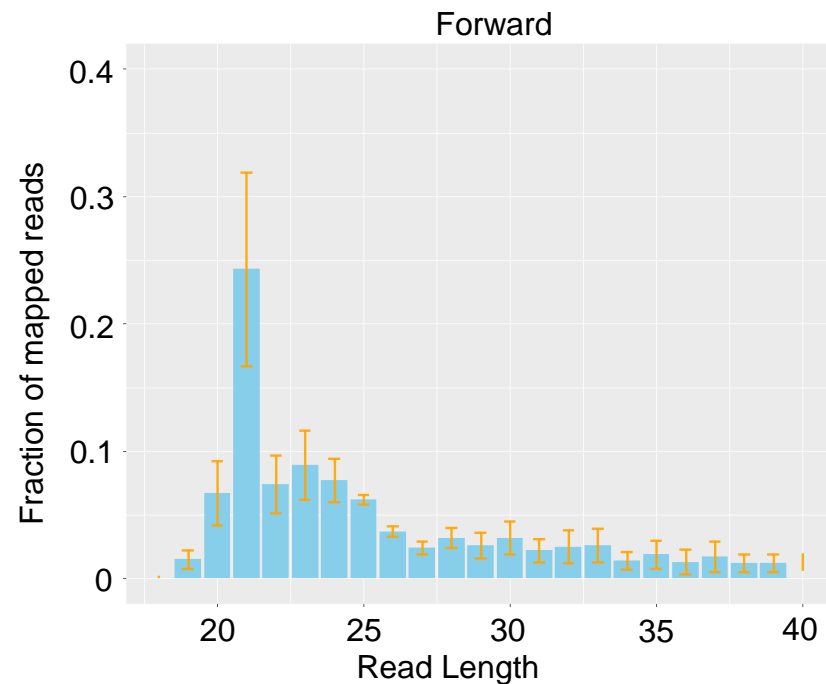
**24-29 nt reads
with piRNA
nucleotide bias**

**24-29 nt reads
with ping-pong
signature and
10-nt overlaps**

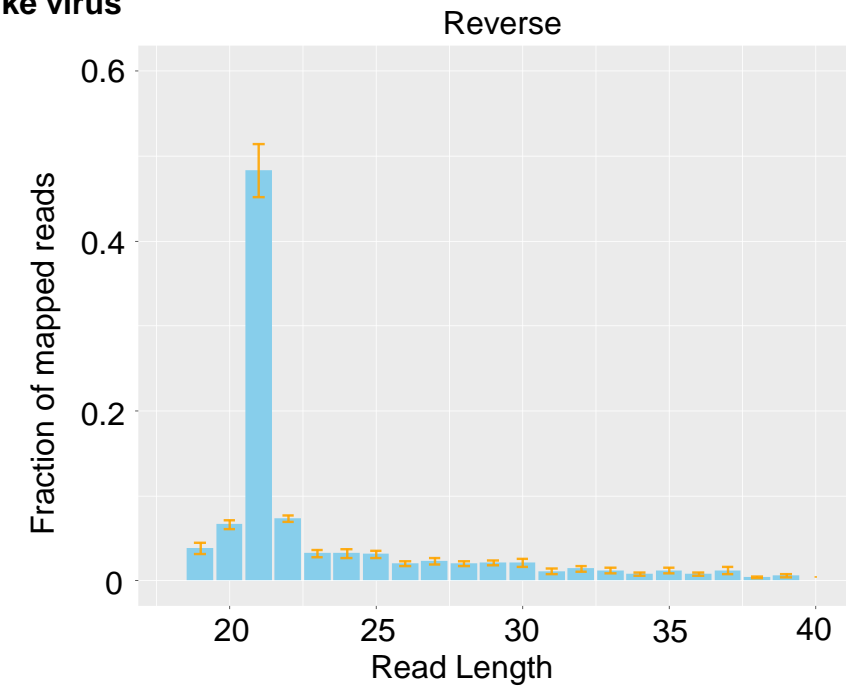
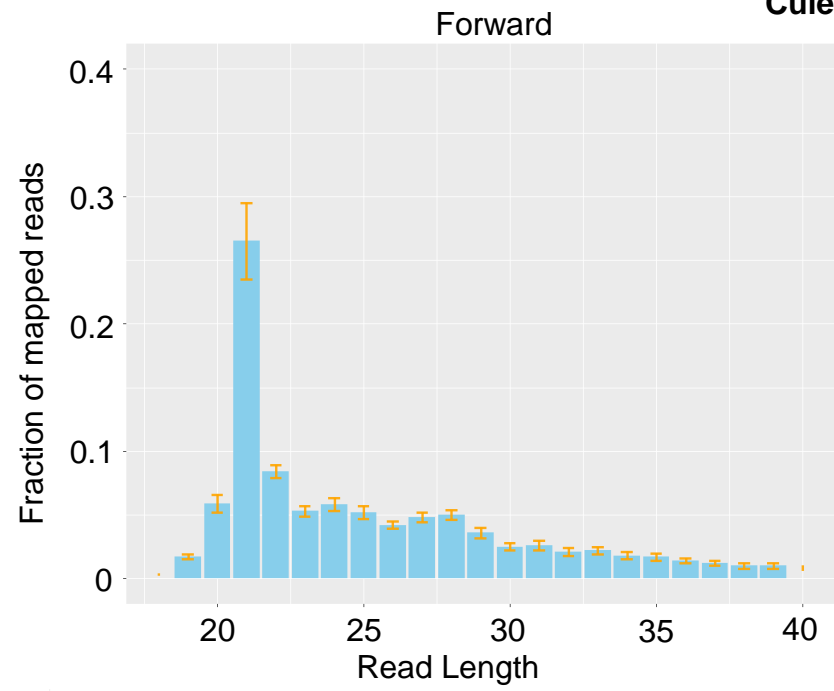
(Range:-60 to
60)



Cordoba virus



Culex Biggie-like virus



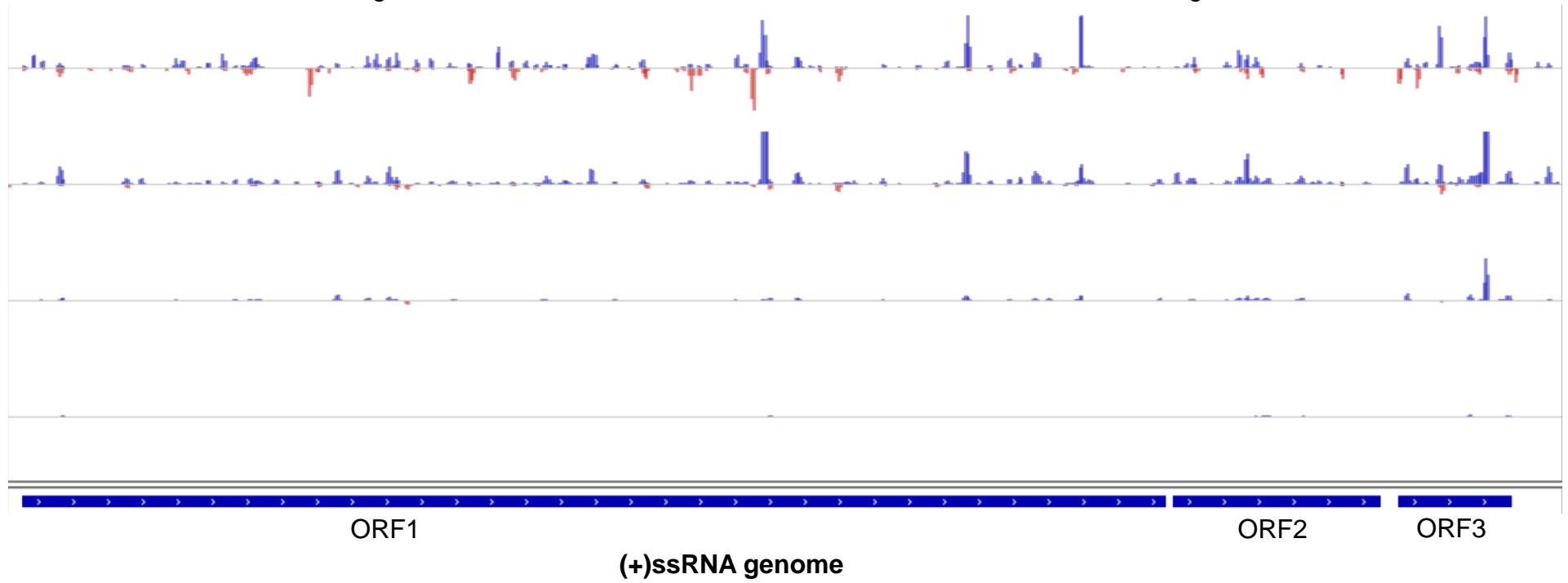
21 nt reads

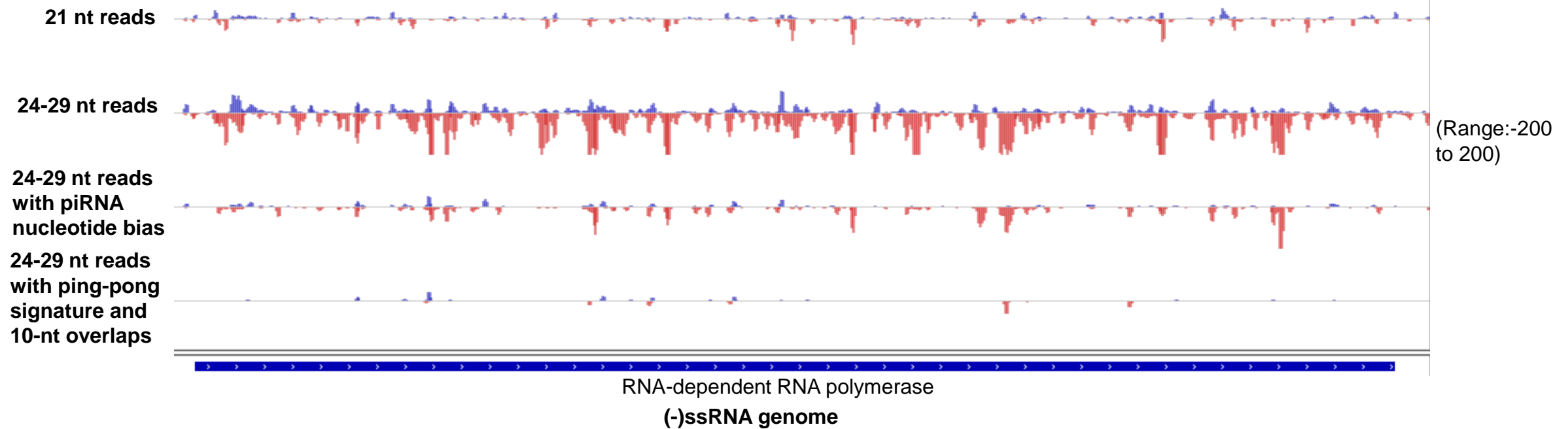
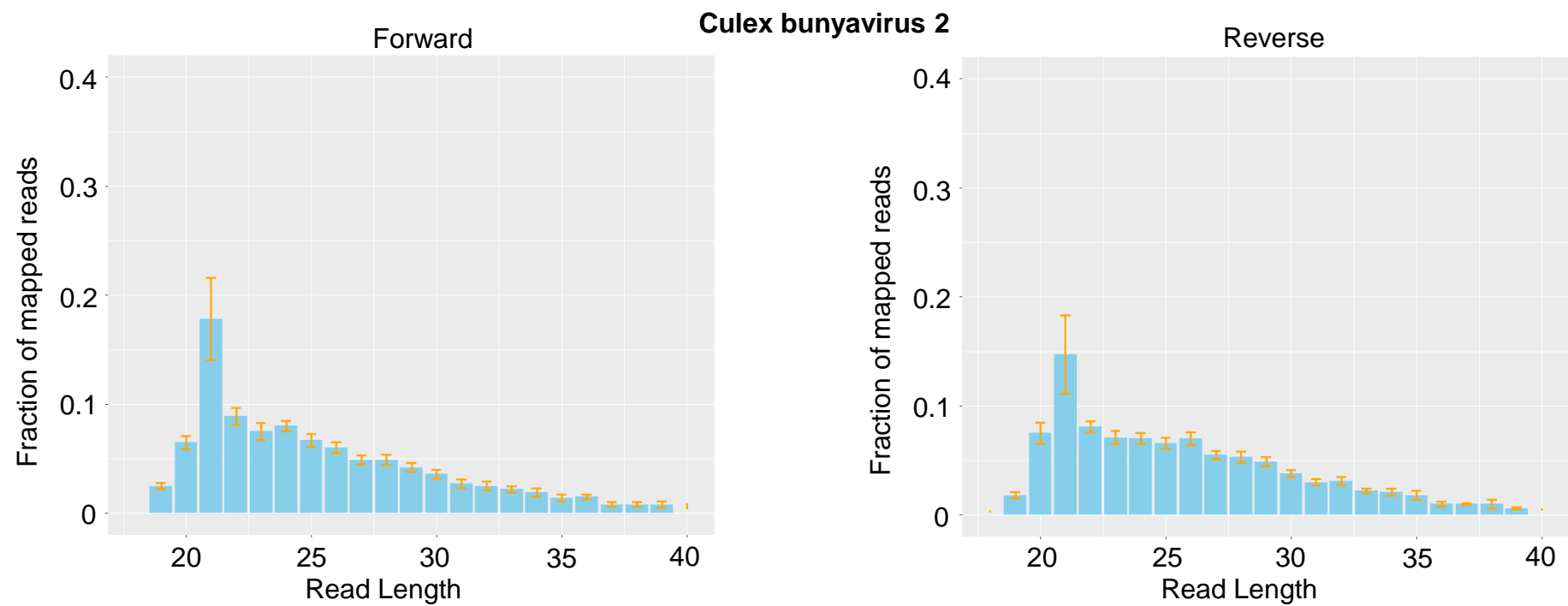
24-29 nt reads

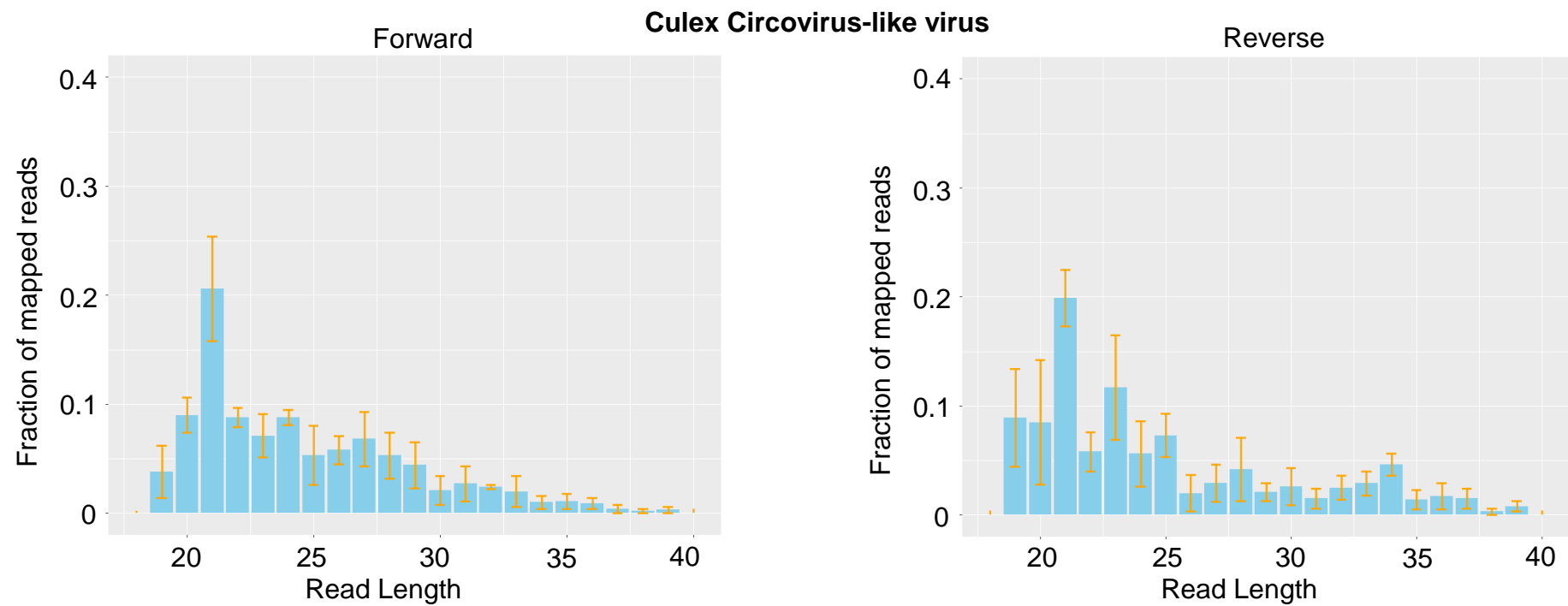
24-29 nt reads
with piRNA
nucleotide bias

24-29 nt reads
with ping-pong
signature and
10-nt overlaps

(Range:-800
to 800)







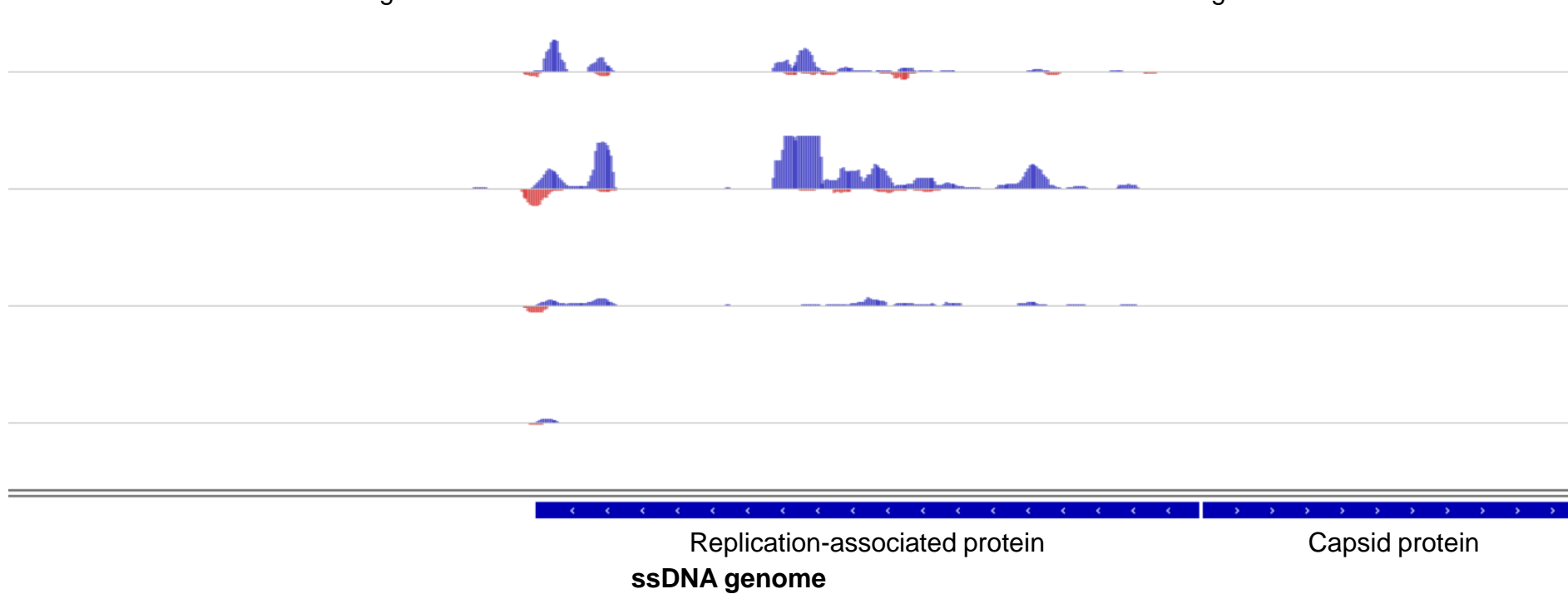
21 nt reads

24-29 nt reads

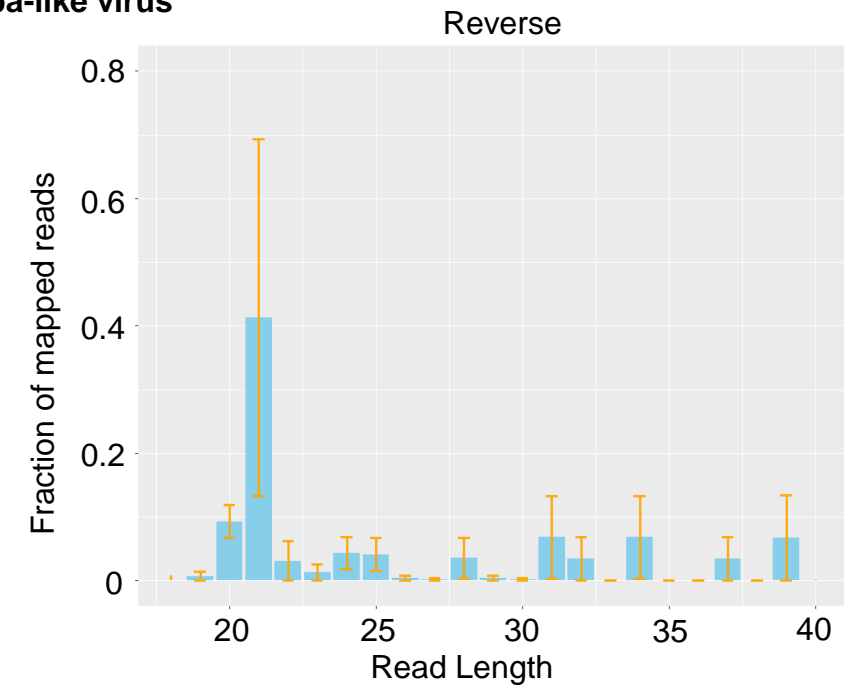
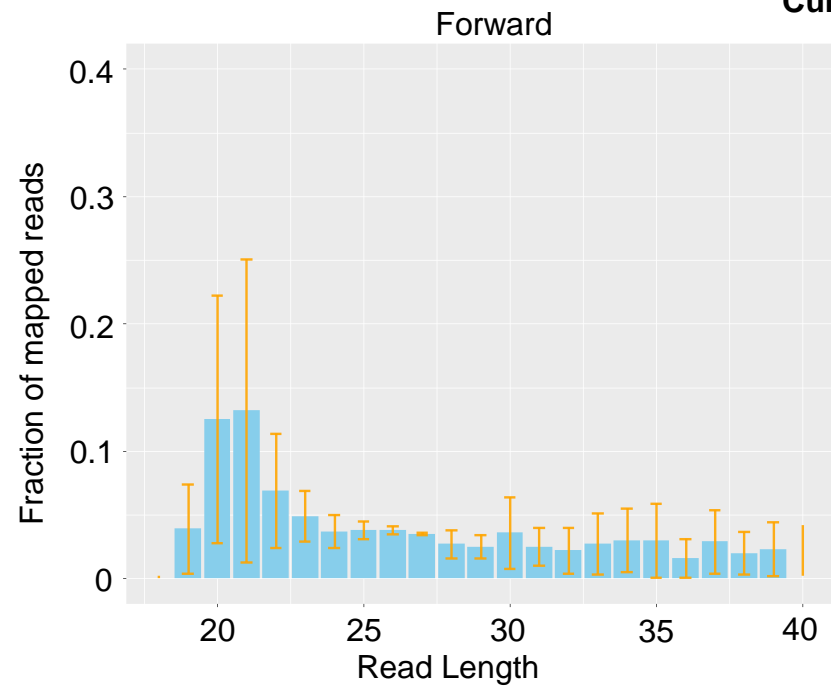
**24-29 nt reads
with piRNA
nucleotide bias**

**24-29 nt reads
with ping-pong
signature and
10-nt overlaps**

(Range:-150
to 150)



Culex Cordoba-like virus



21 nt reads

24-29 nt reads

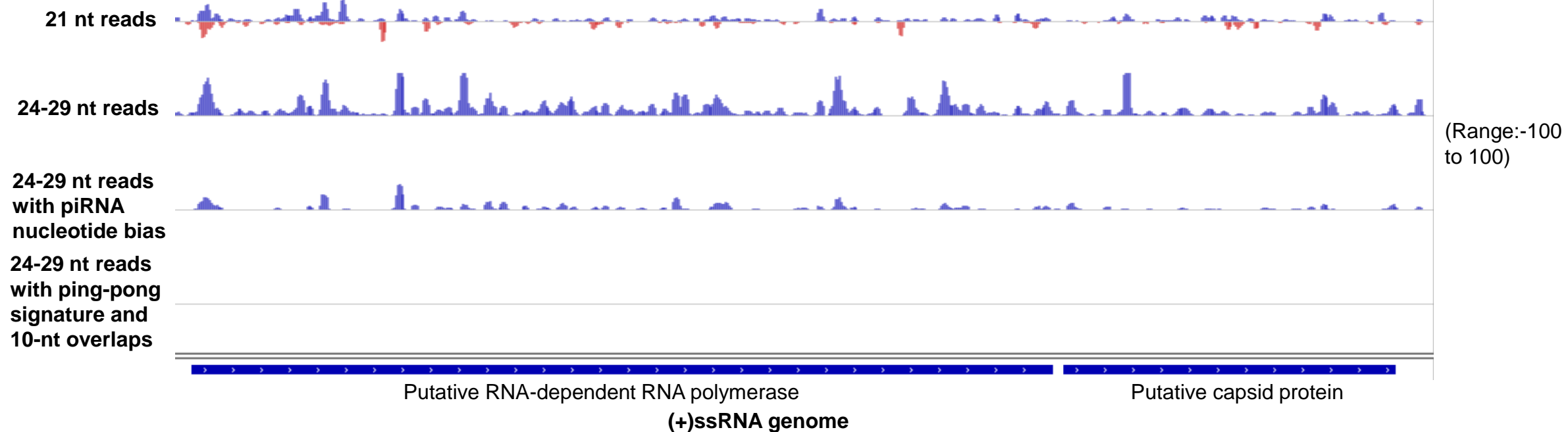
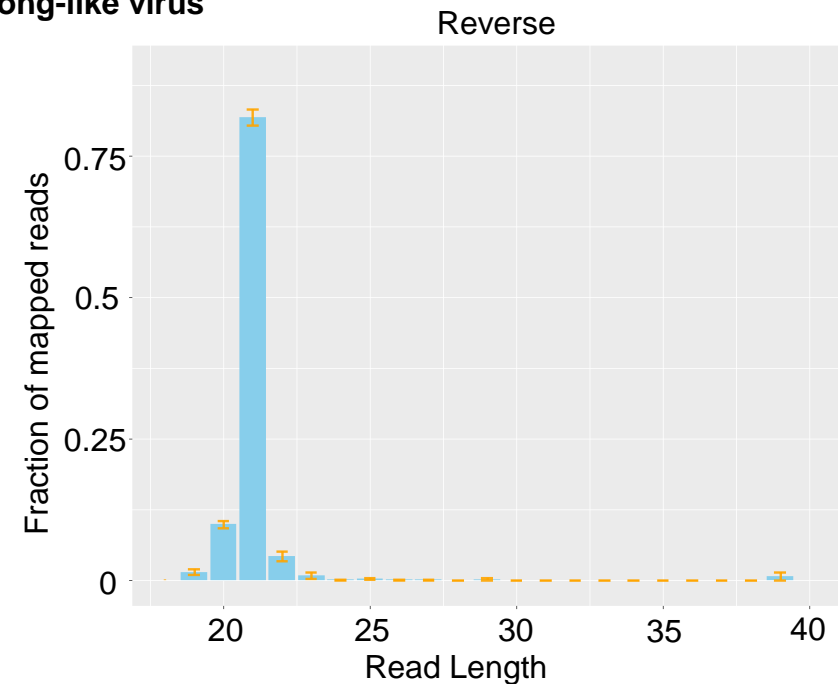
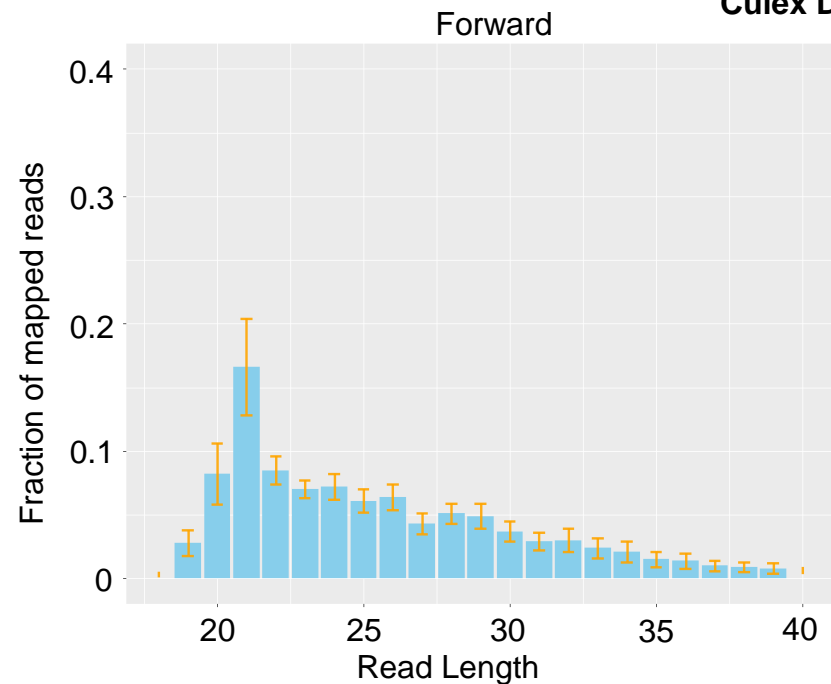
24-29 nt reads
with piRNA
nucleotide bias

24-29 nt reads
with ping-pong
signature and
10-nt overlaps

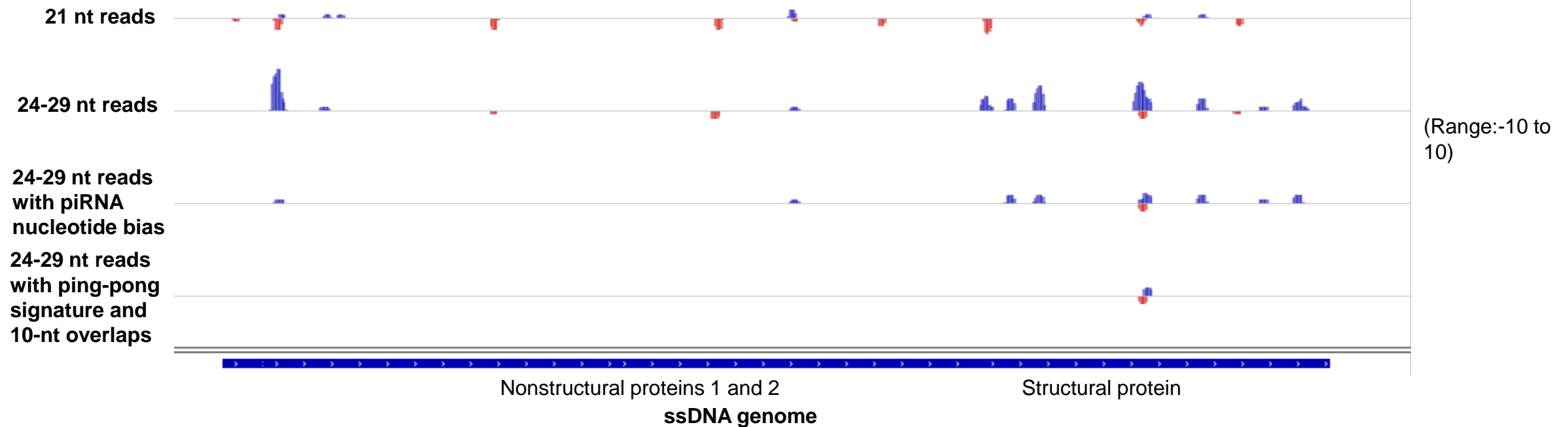
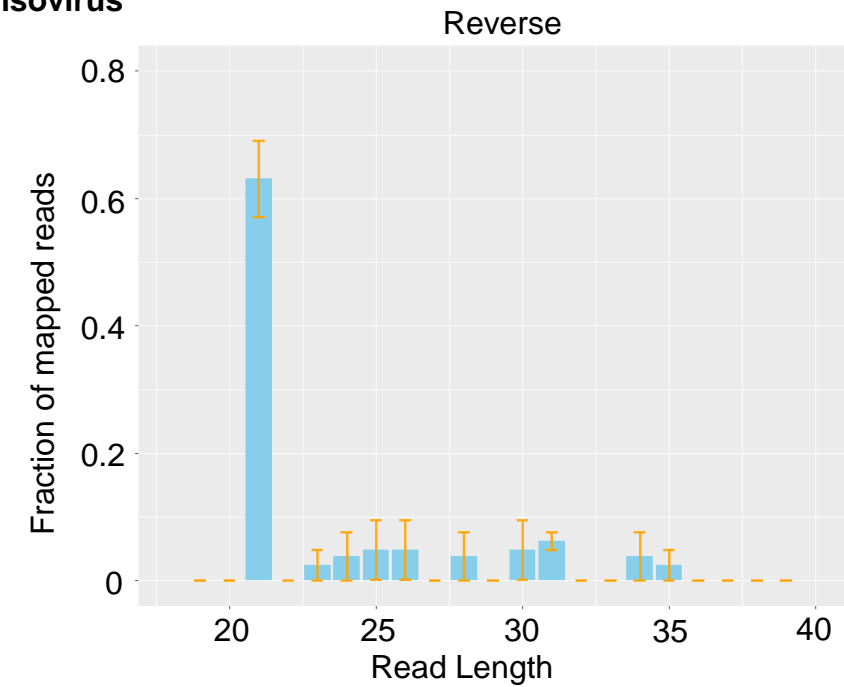
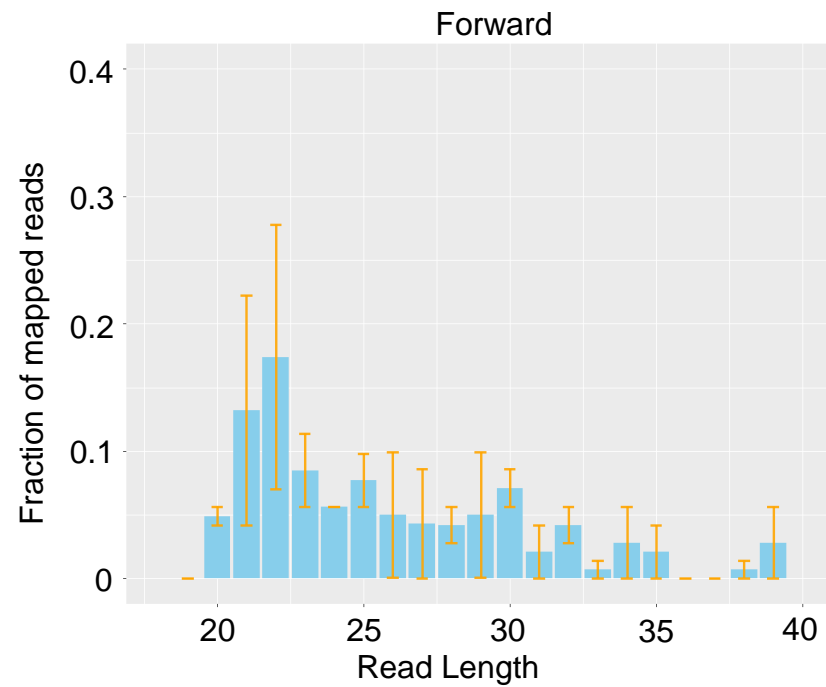
(Range:-150
to 150)

Hypothetical protein
(+)ssRNA genome

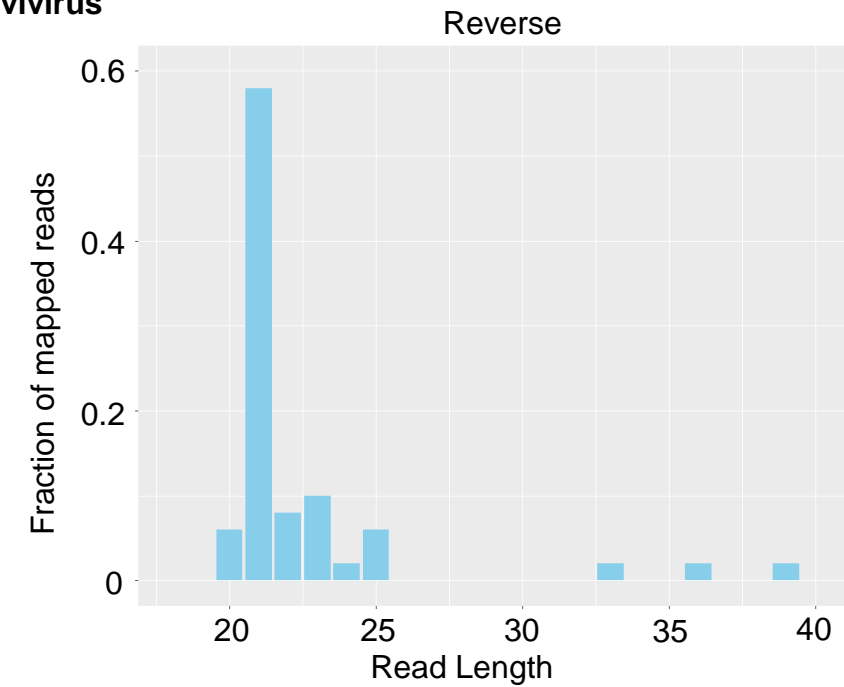
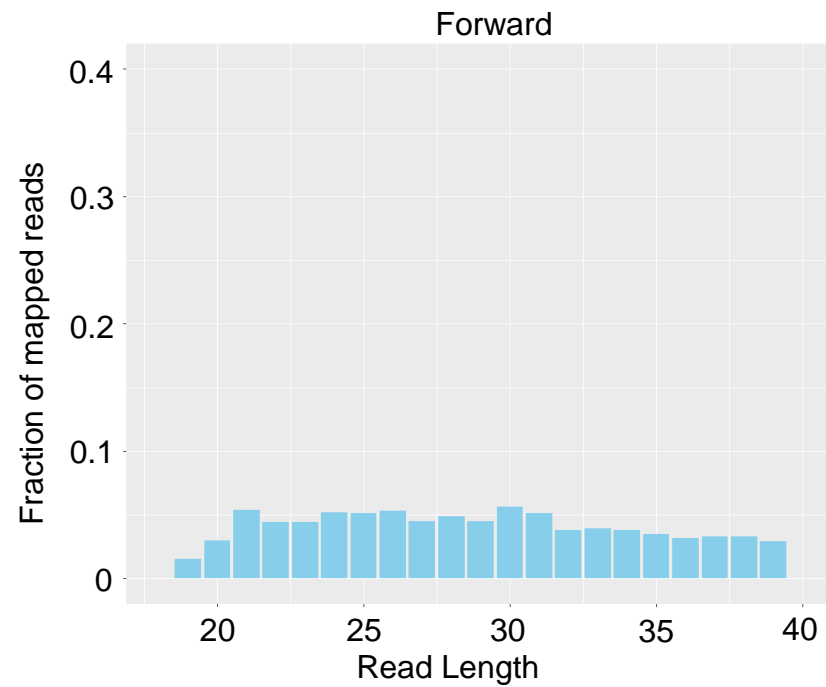
Culex Daeseongdong-like virus



Culex densovirus



Culex flavivirus



21 nt reads

24-29 nt reads

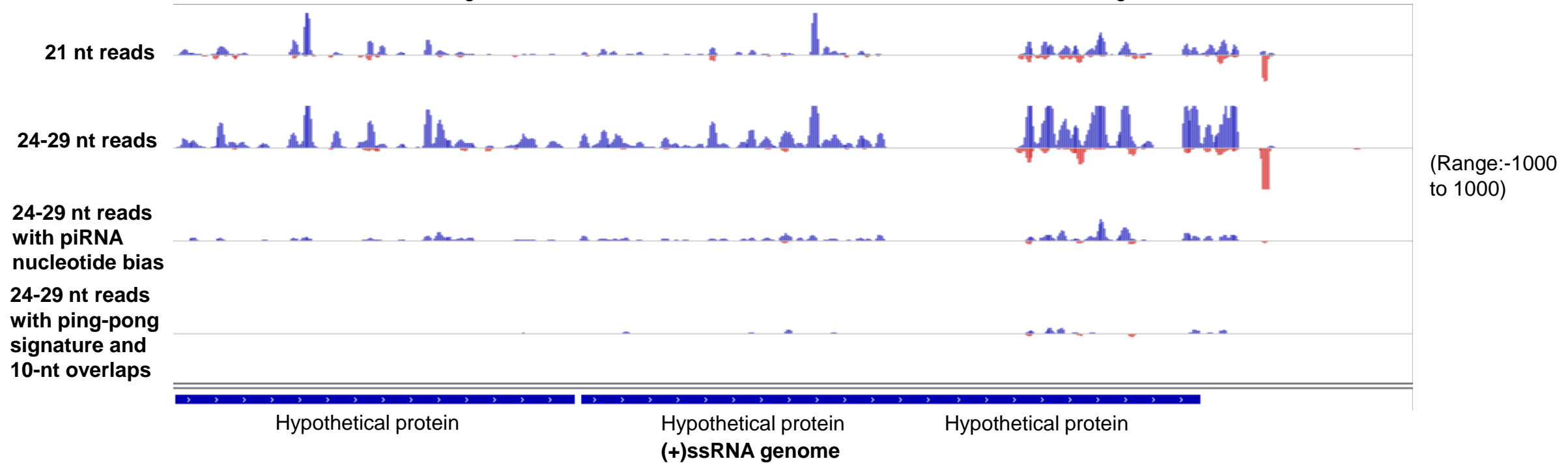
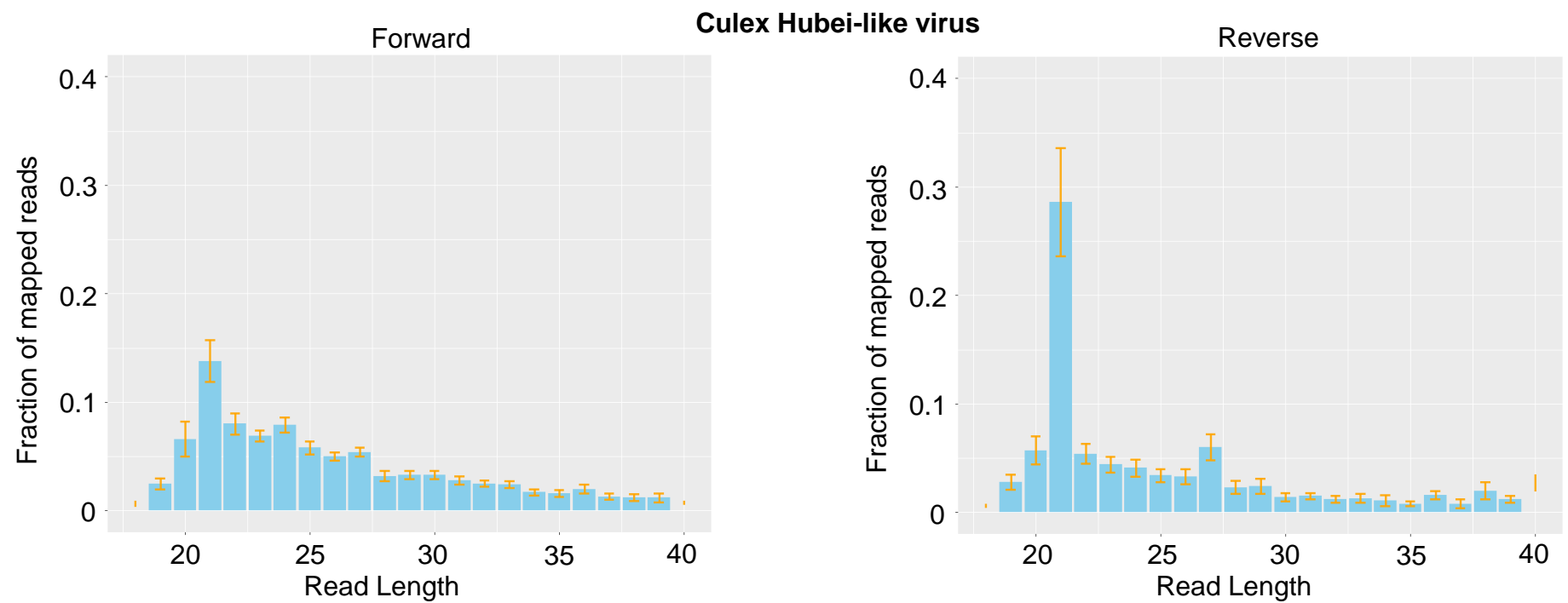
24-29 nt reads
with piRNA
nucleotide bias

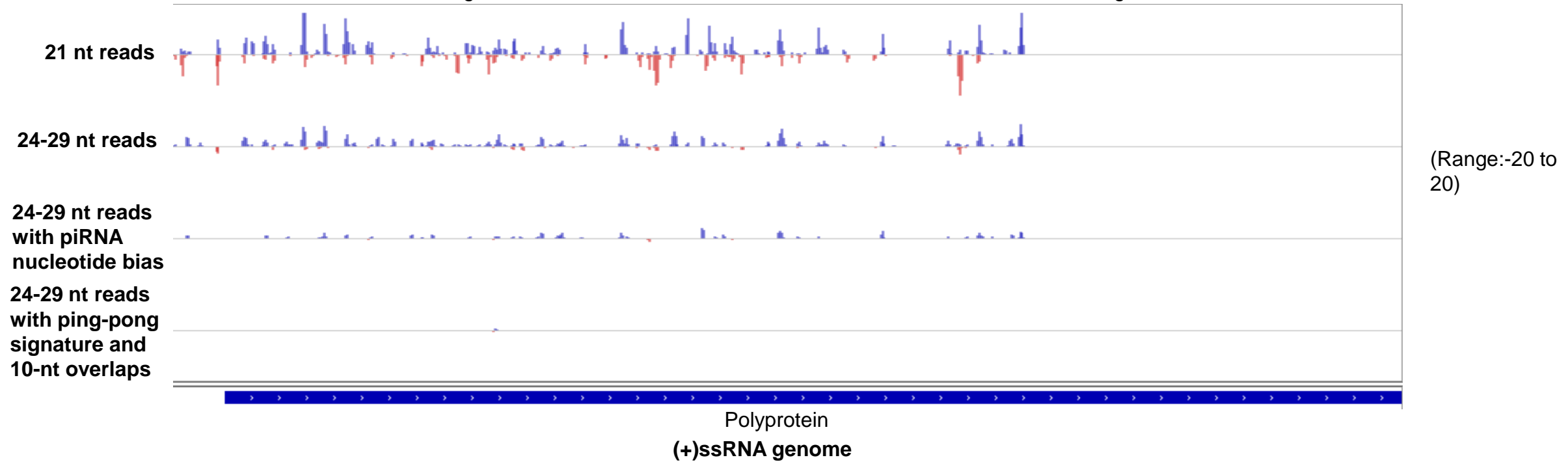
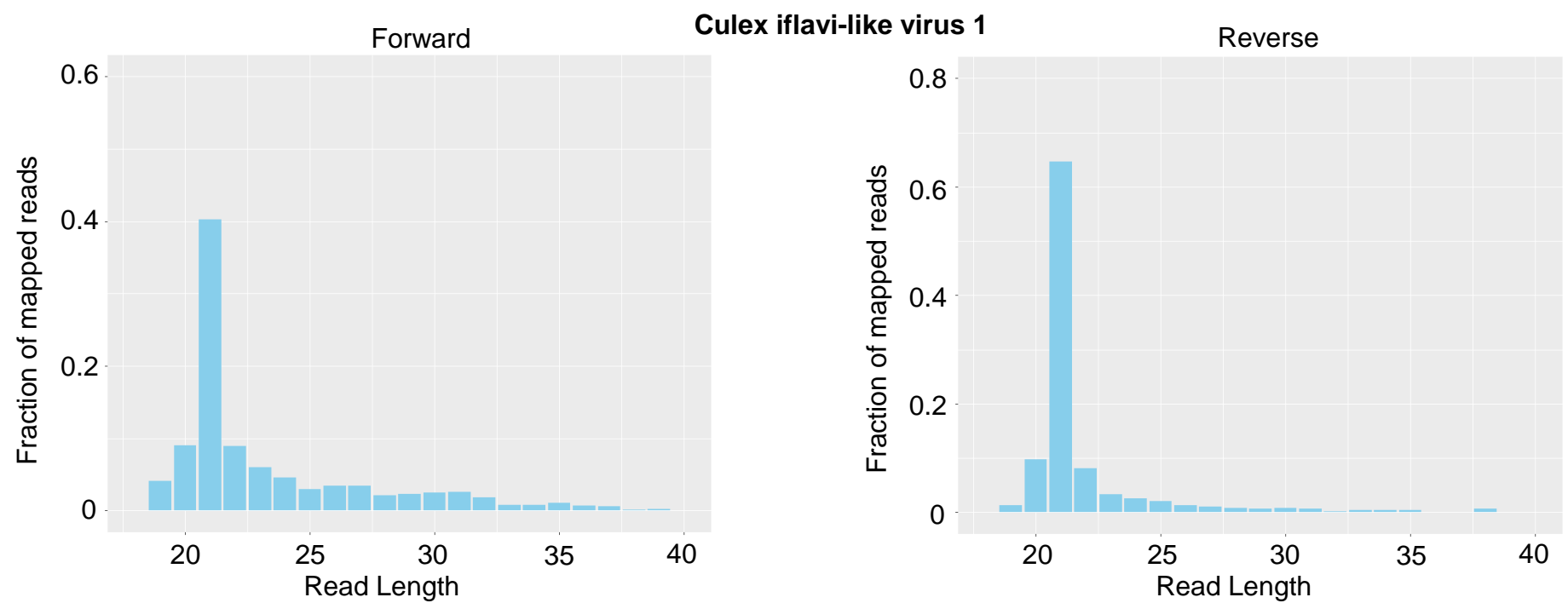
24-29 nt reads
with ping-pong
signature and
10-nt overlaps

(Range:-15 to
15)

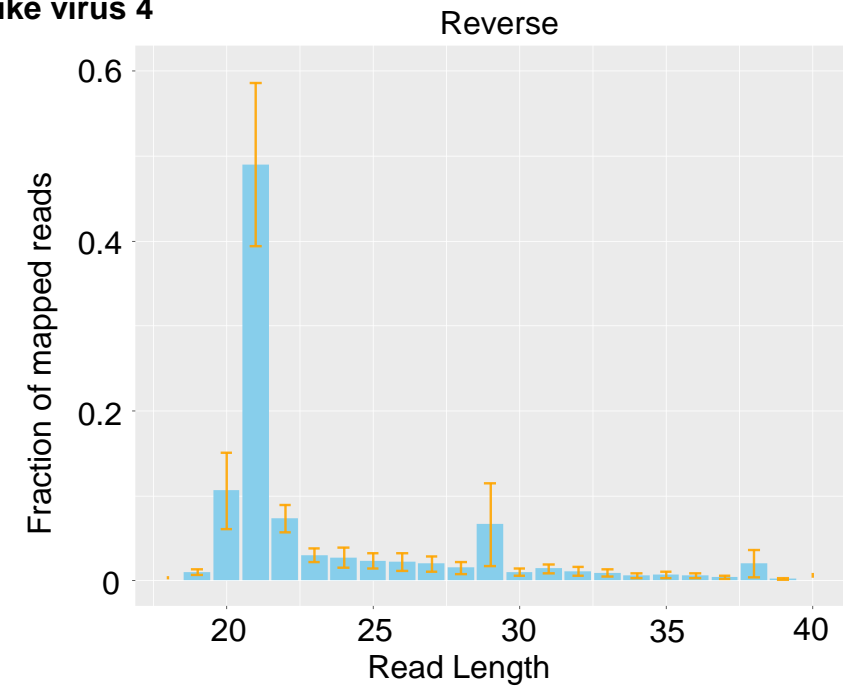
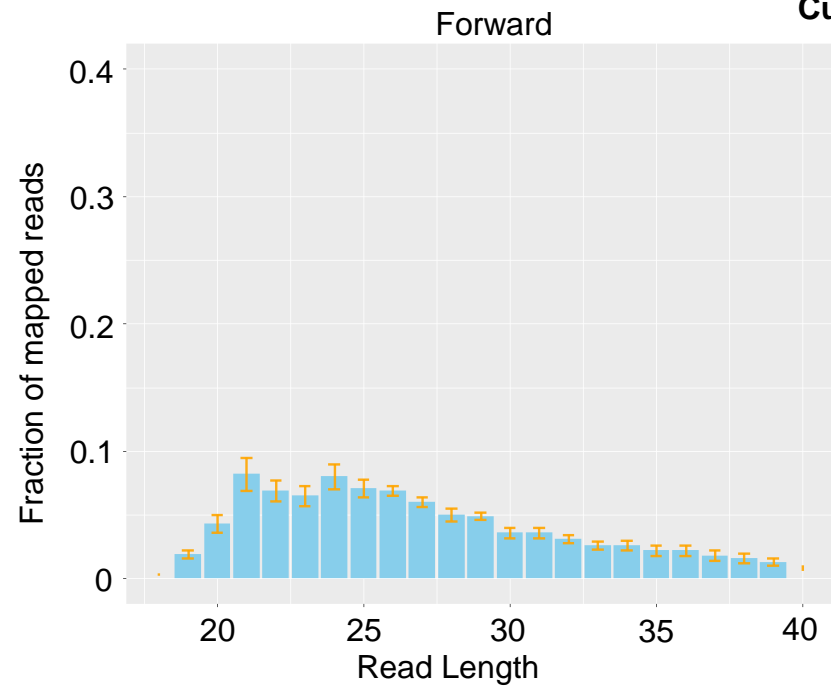
Polyprotein

(+)ssRNA genome





Culex iflavi-like virus 4



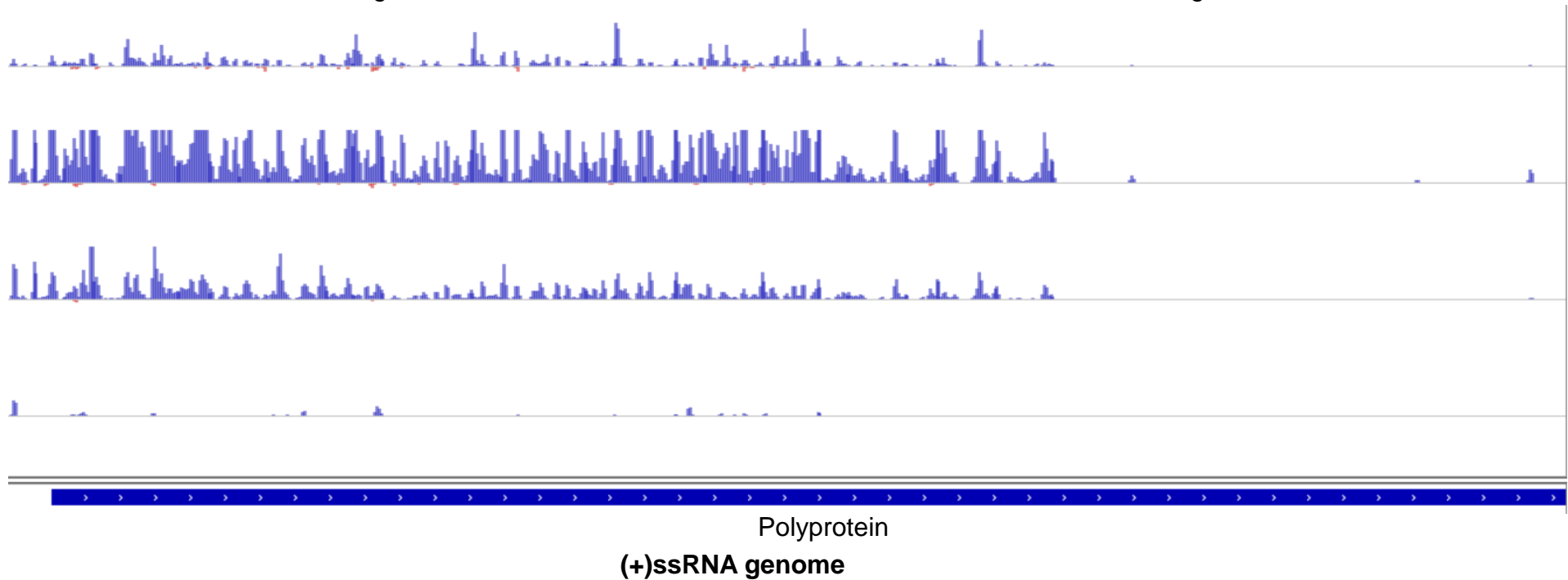
21 nt reads

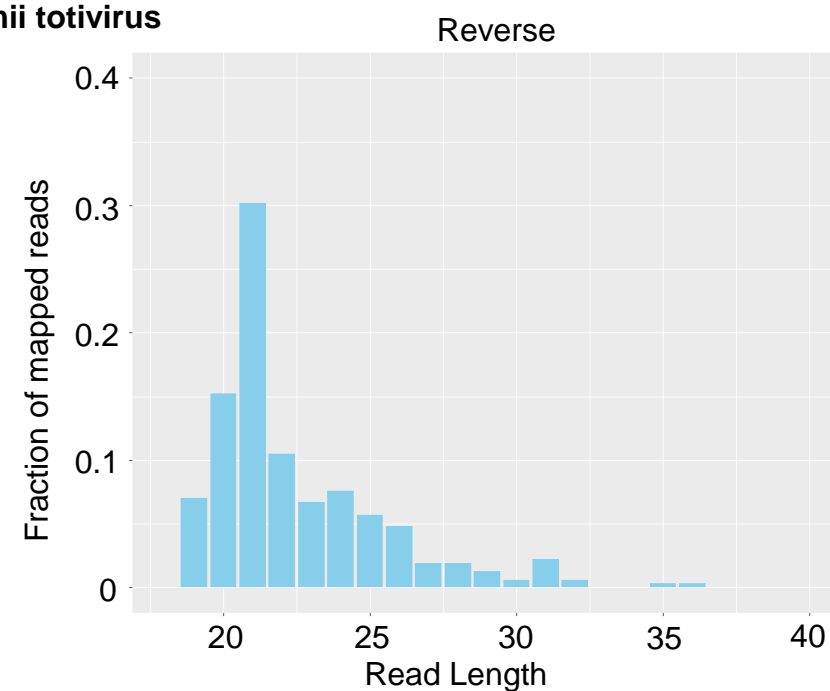
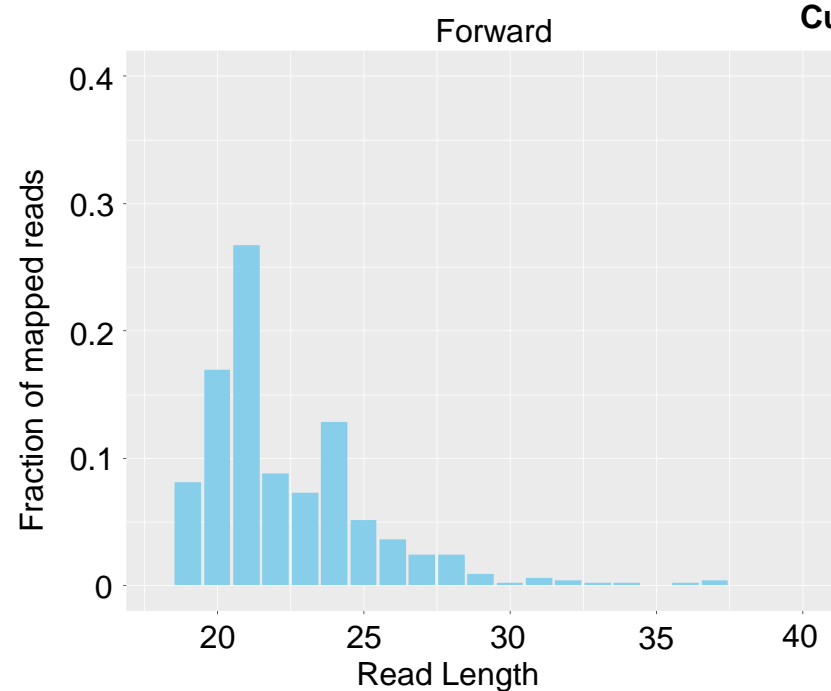
24-29 nt reads

**24-29 nt reads
with piRNA
nucleotide bias**

**24-29 nt reads
with ping-pong
signature and
10-nt overlaps**

(Range:-400
to 400)





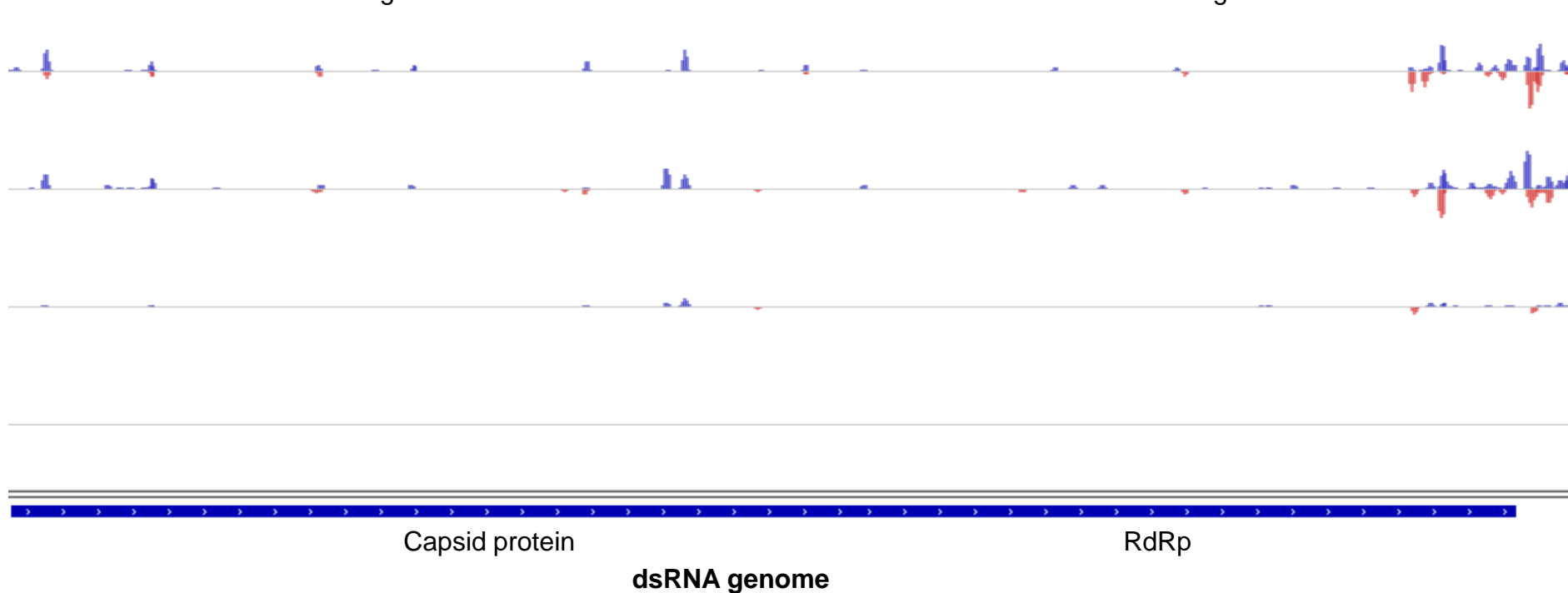
21 nt reads

24-29 nt reads

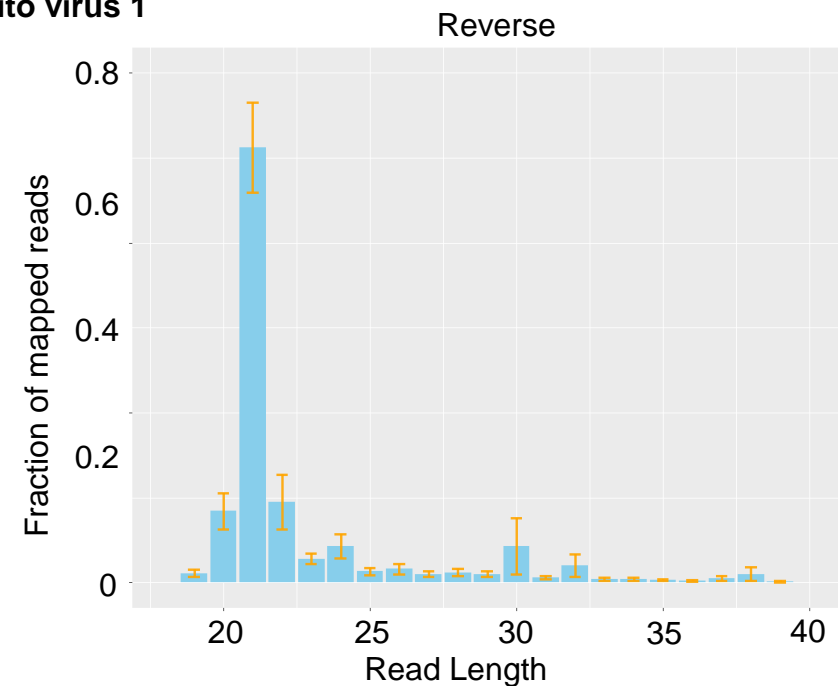
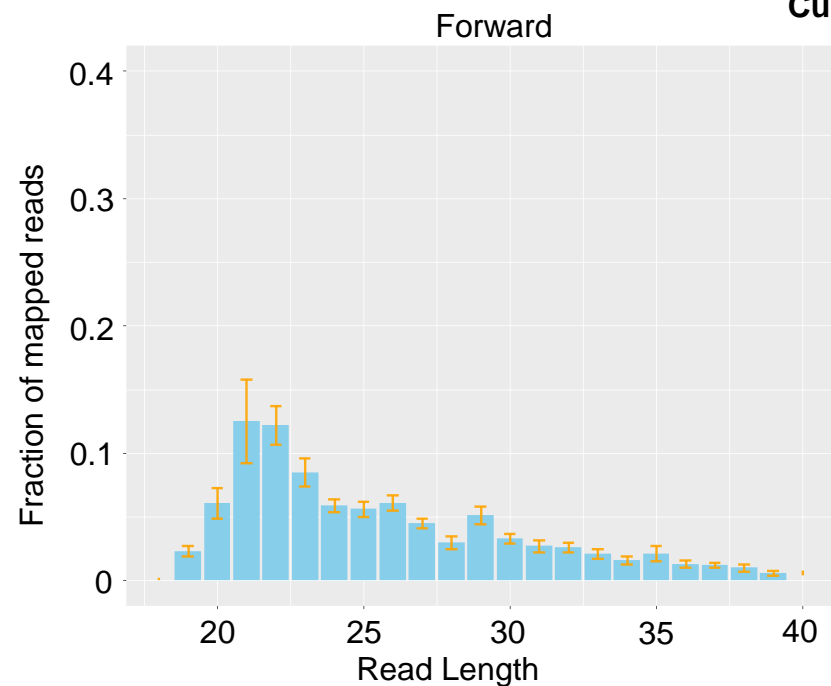
24-29 nt reads
with piRNA
nucleotide bias

24-29 nt reads
with ping-pong
signature and
10-nt overlaps

(Range:-25 to
25)



Culex mosquito virus 1



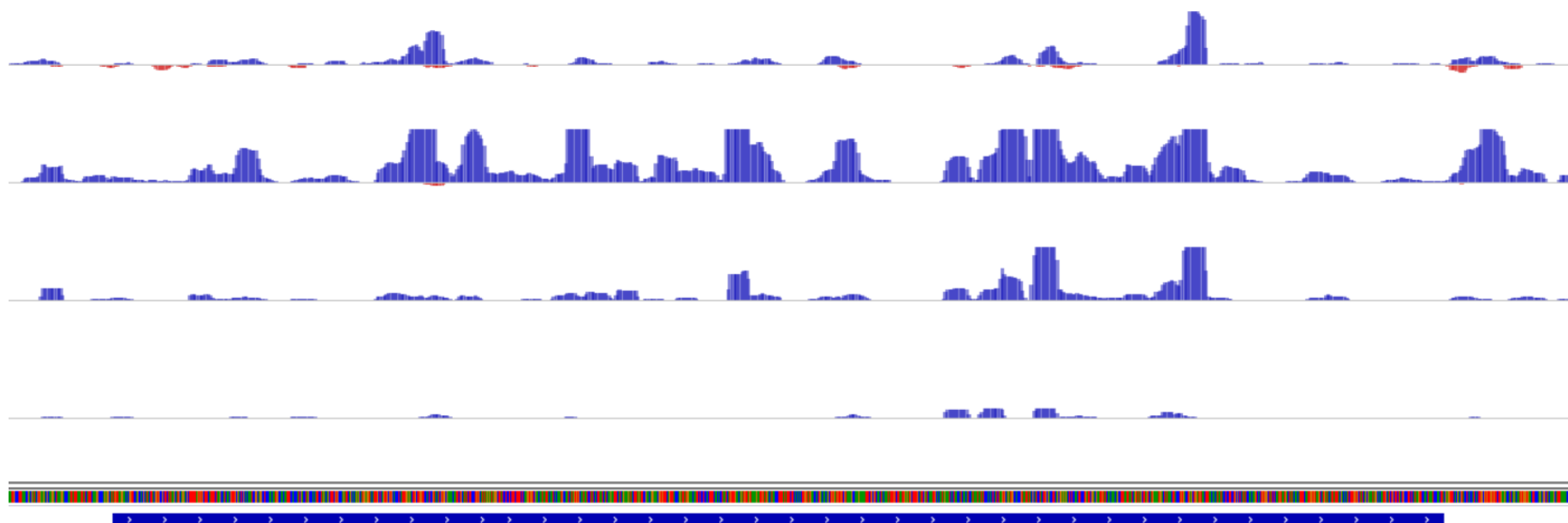
21 nt reads

24-29 nt reads

24-29 nt reads
with piRNA
nucleotide bias

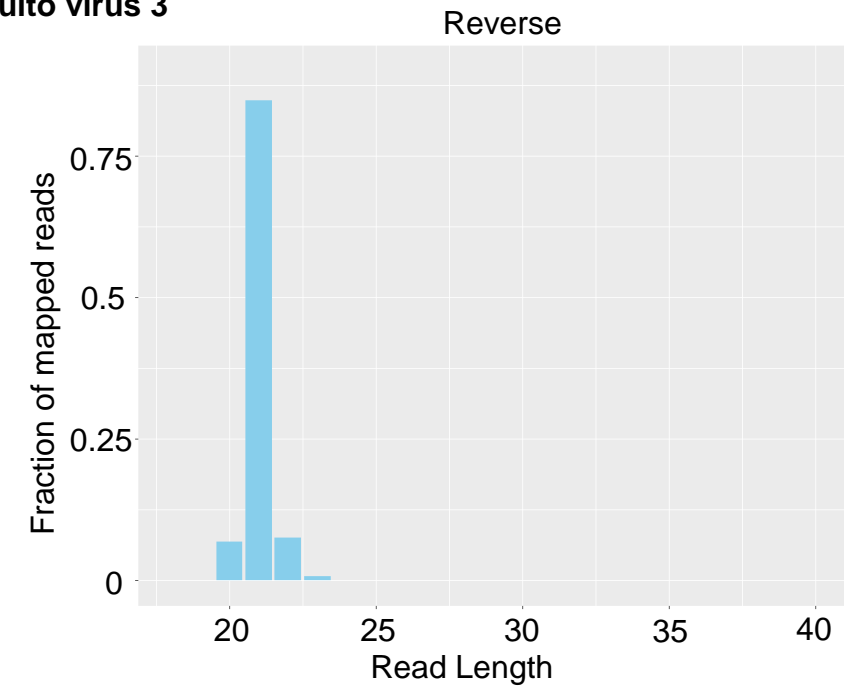
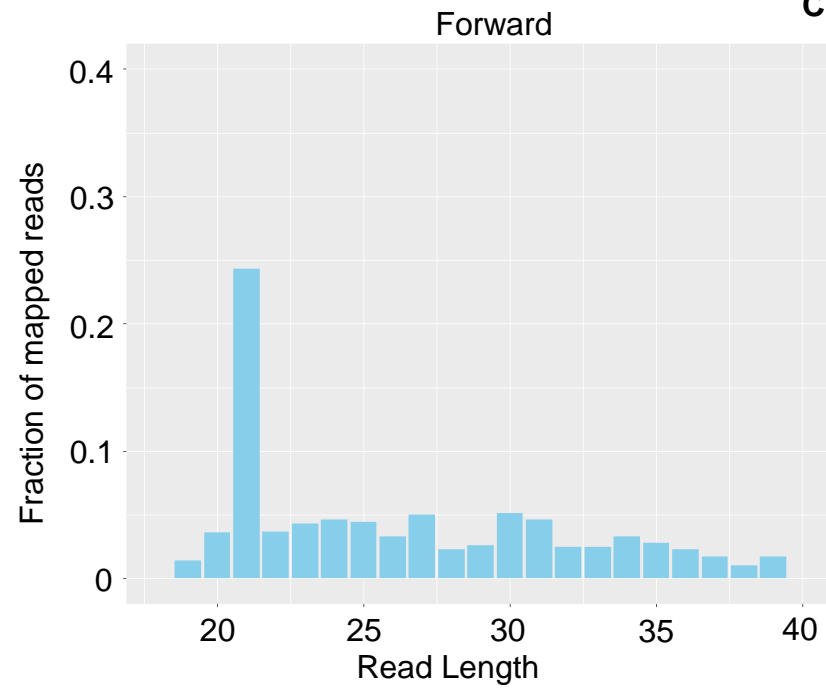
24-29 nt reads
with ping-pong
signature and
10-nt overlaps

(Range:-2000
to 2000)



(+)ssRNA genome

Culex mosquito virus 3

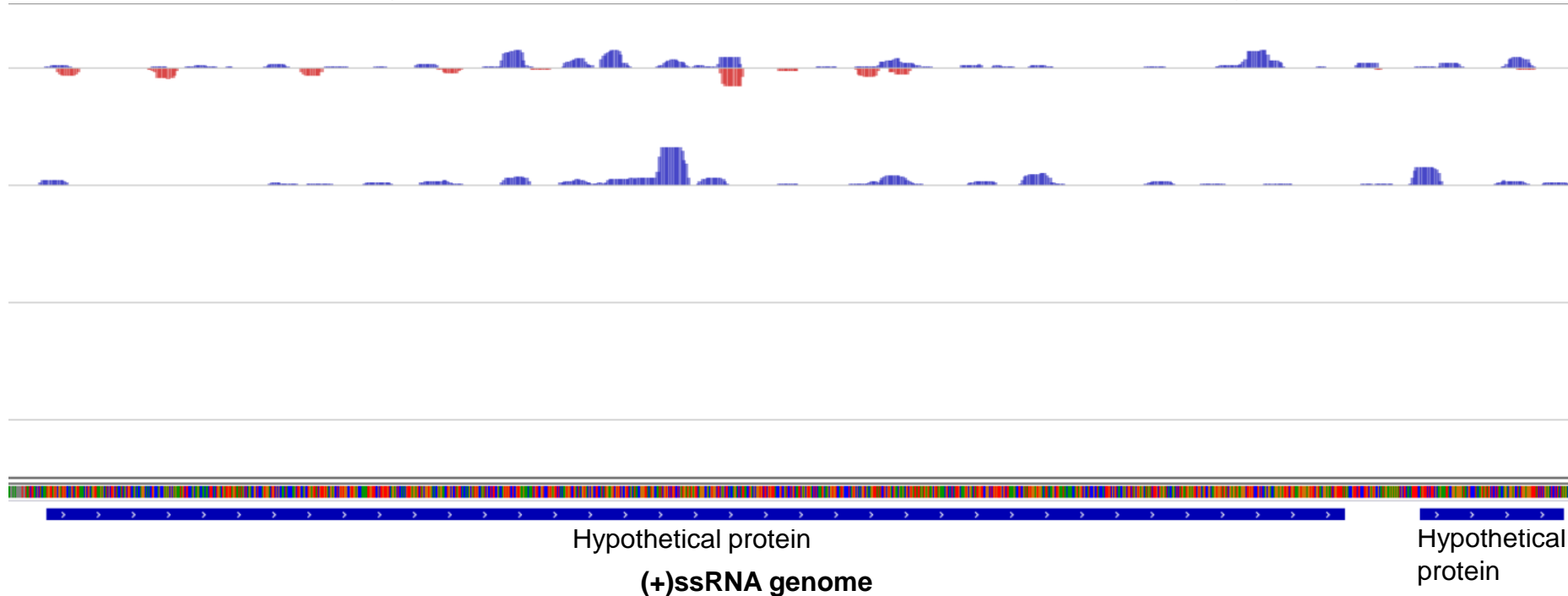


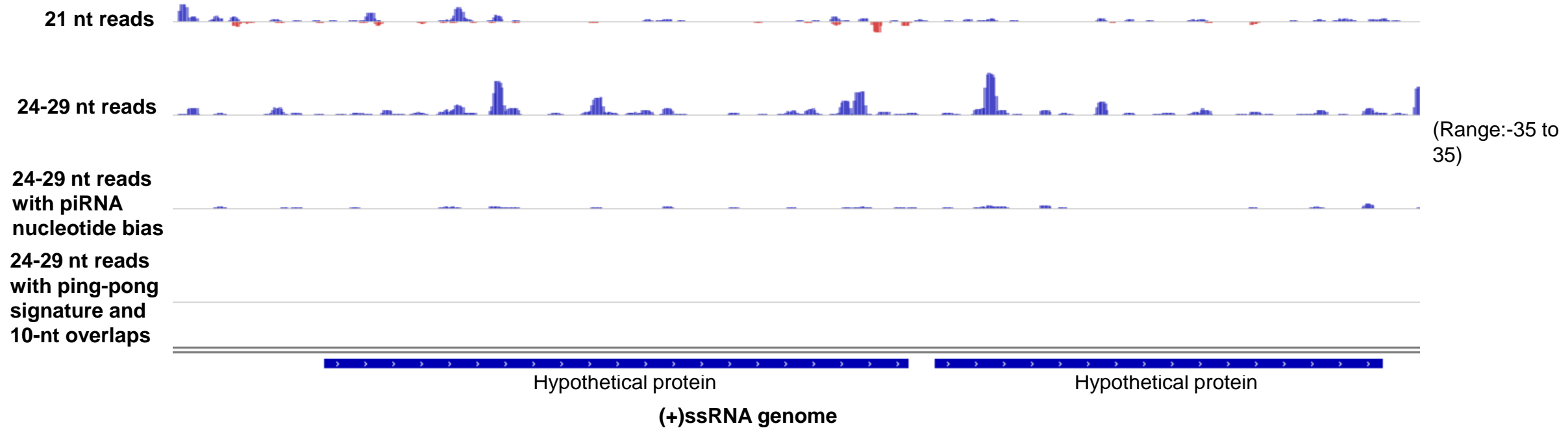
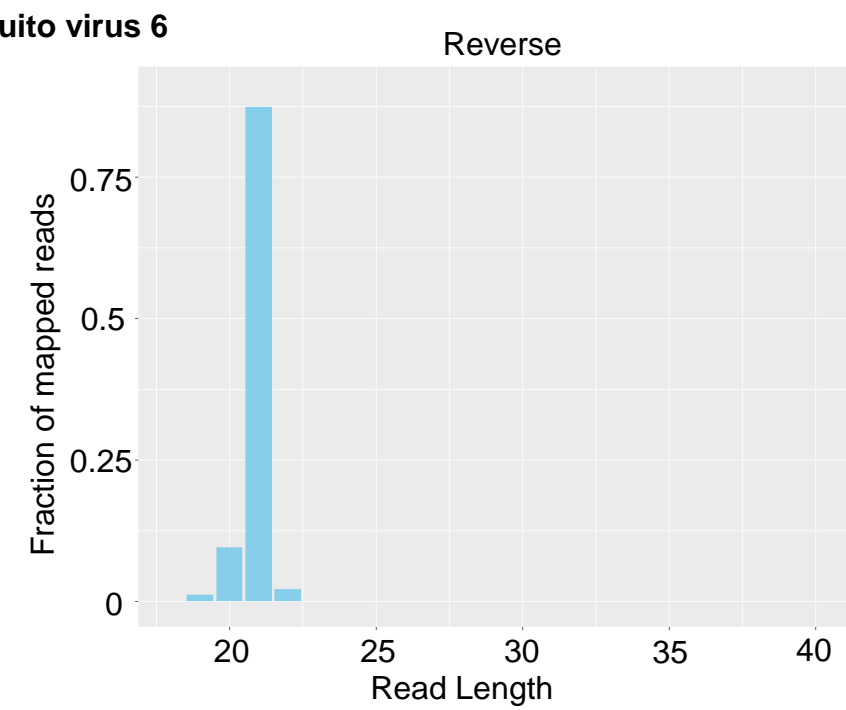
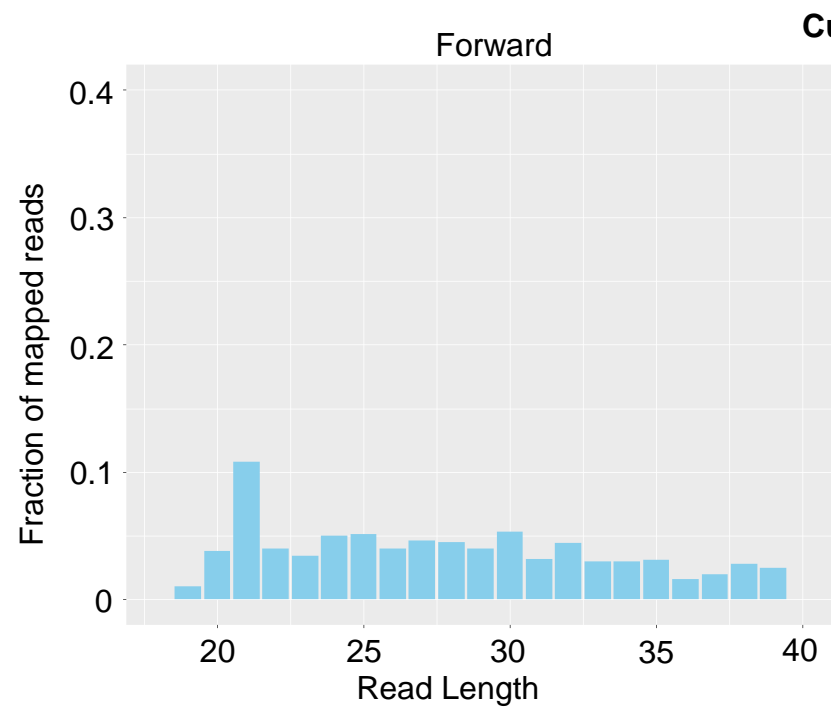
21 nt reads

24-29 nt reads

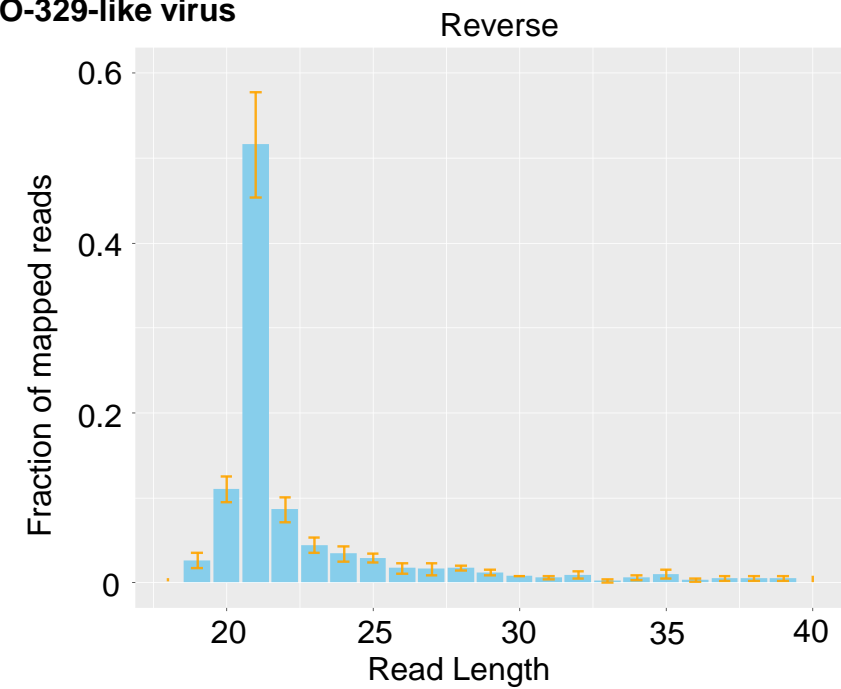
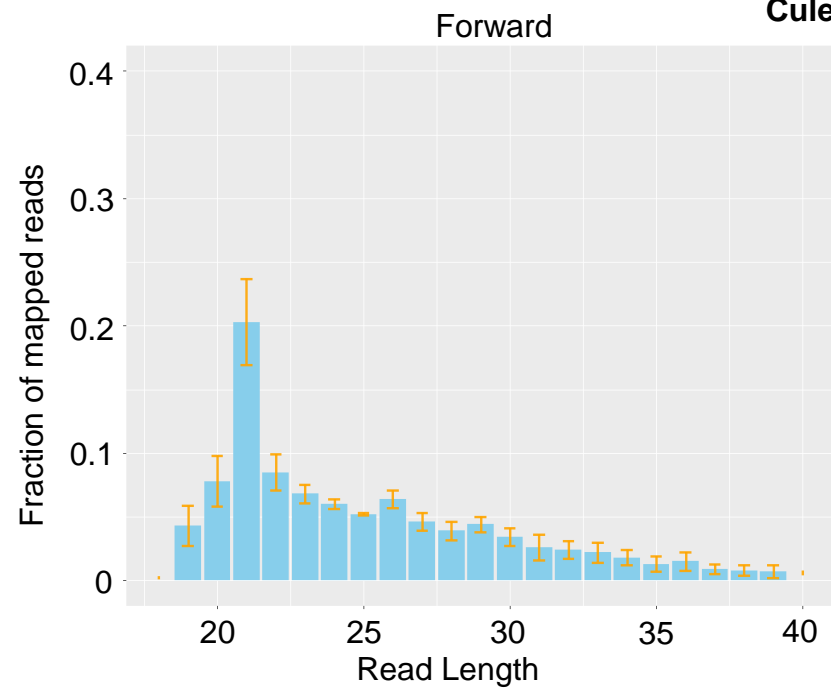
24-29 nt reads
with piRNA
nucleotide bias

24-29 nt reads
with ping-pong
signature and
10-nt overlaps





Culex Negev EO-329-like virus



21 nt reads



24-29 nt reads



24-29 nt reads
with piRNA
nucleotide bias

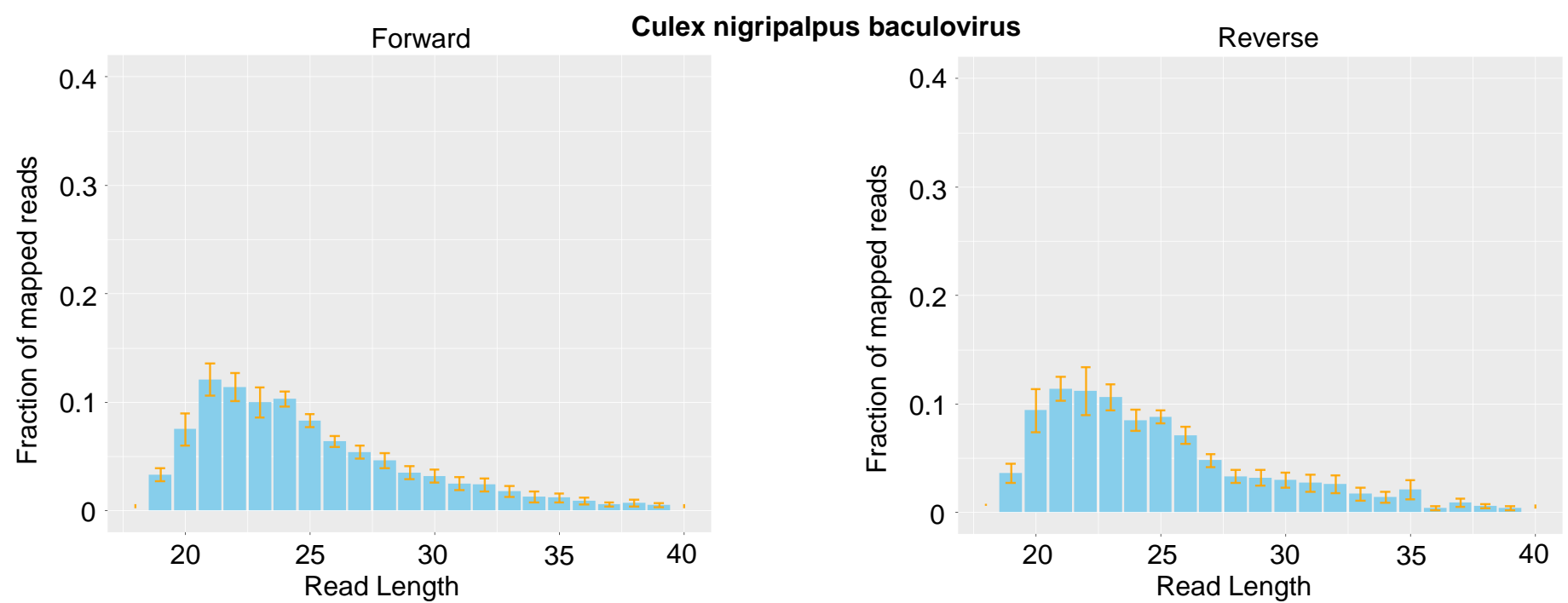


24-29 nt reads
with ping-pong
signature and
10-nt overlaps



(Range:-150
to 150)





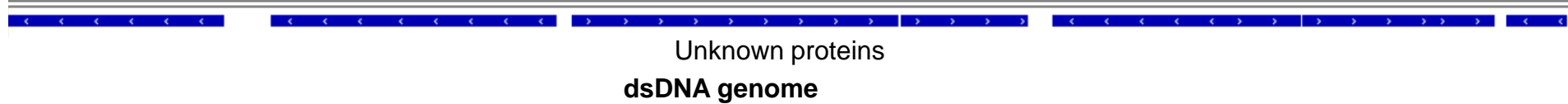
21 nt reads

24-29 nt reads

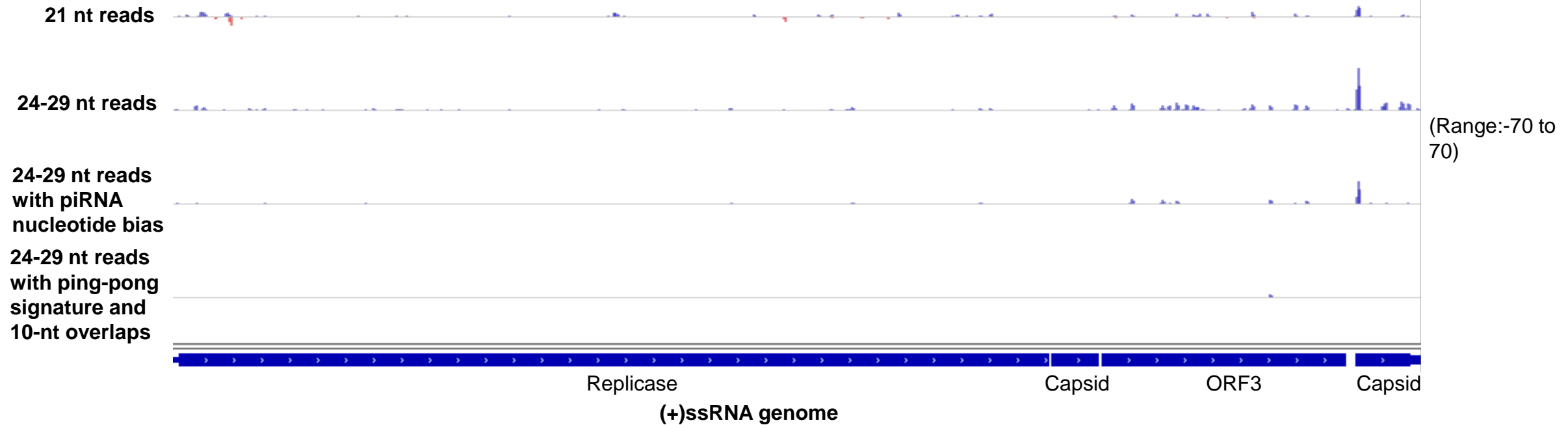
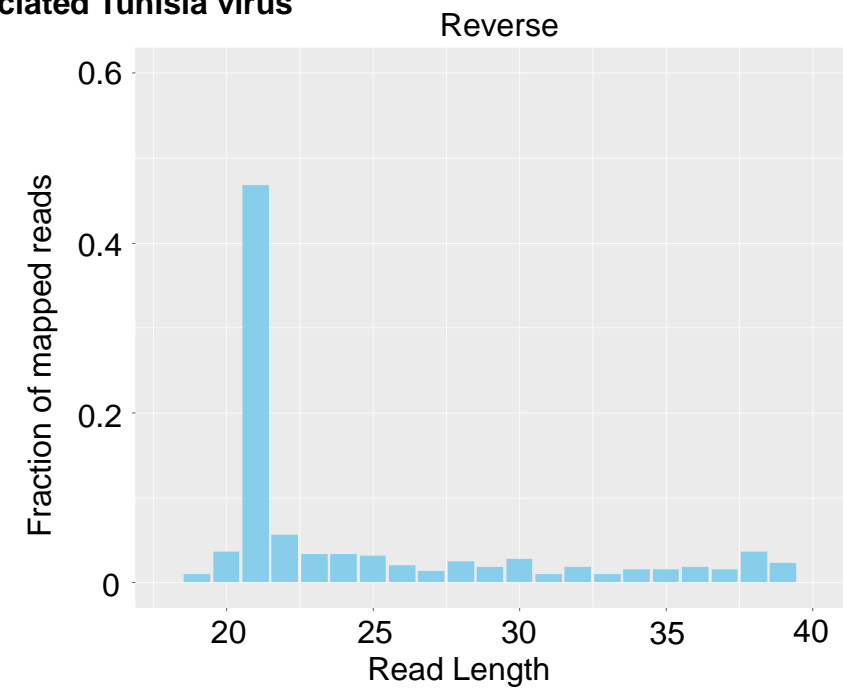
24-29 nt reads
with piRNA
nucleotide bias

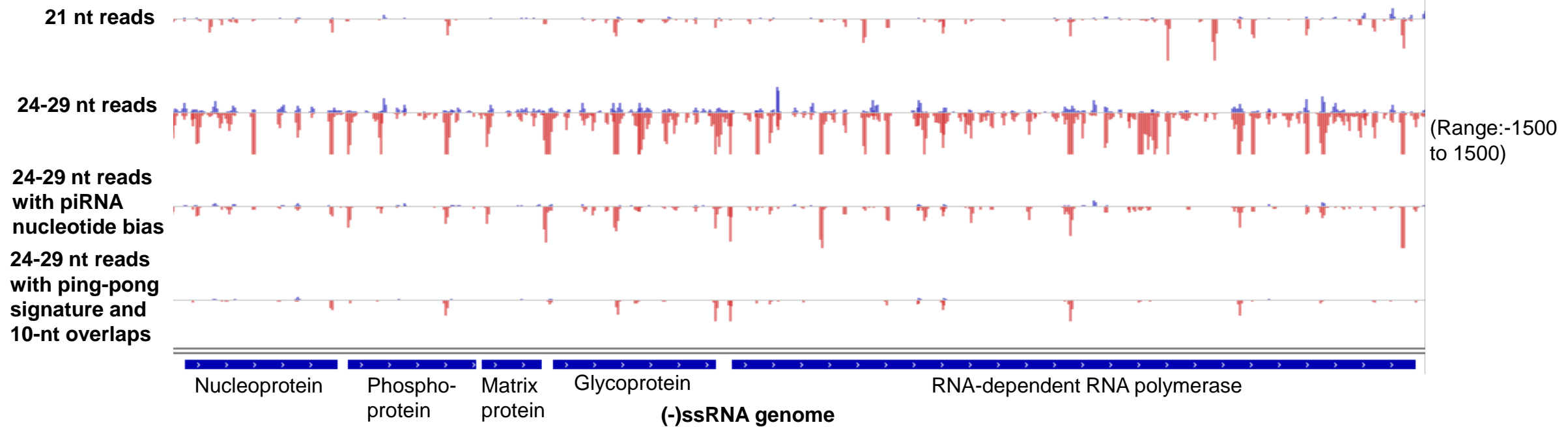
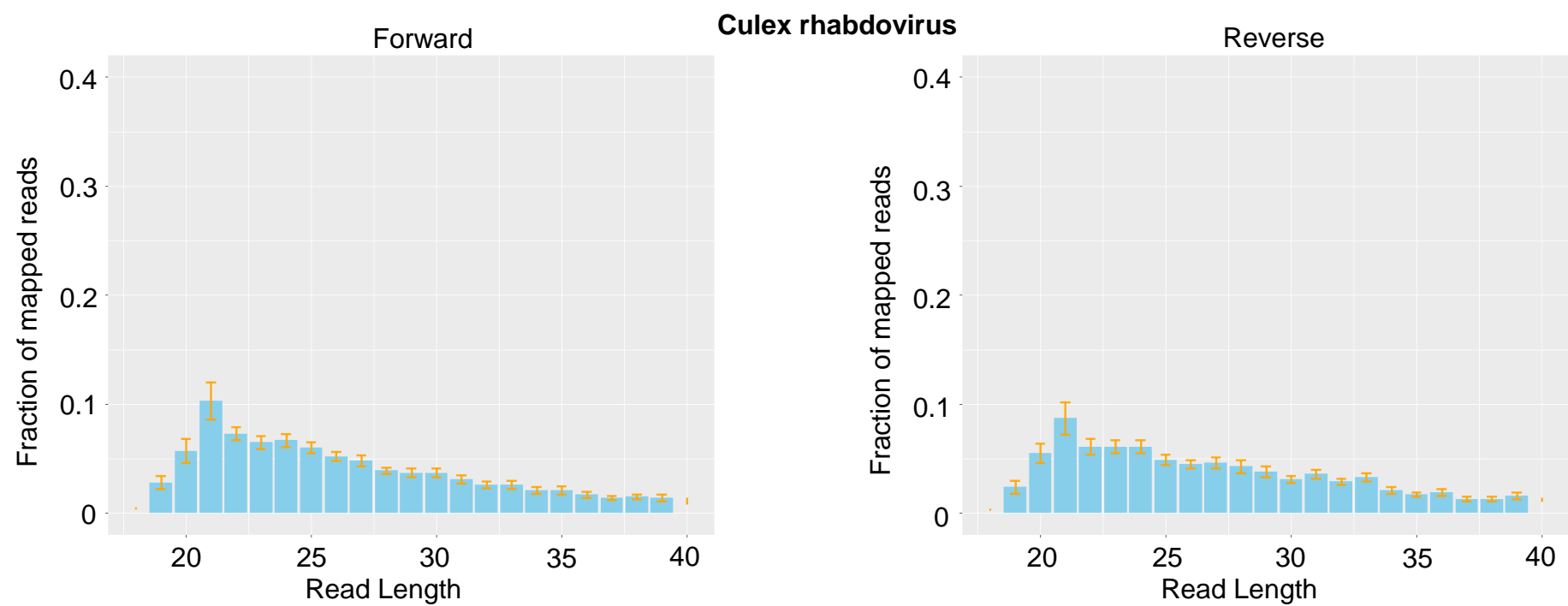
24-29 nt reads
with ping-pong
signature and
10-nt overlaps

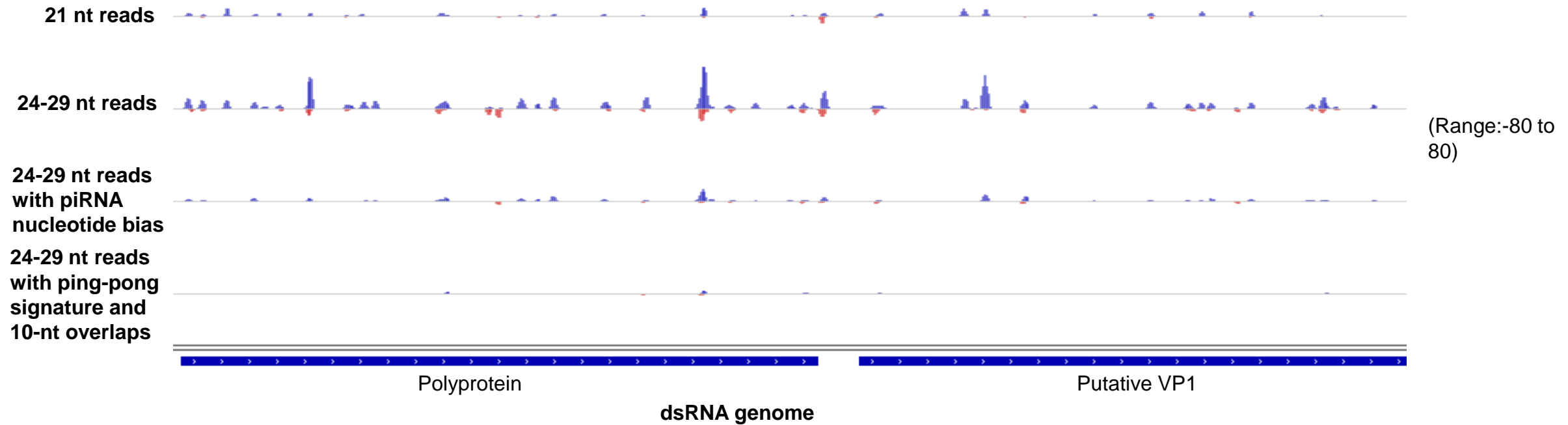
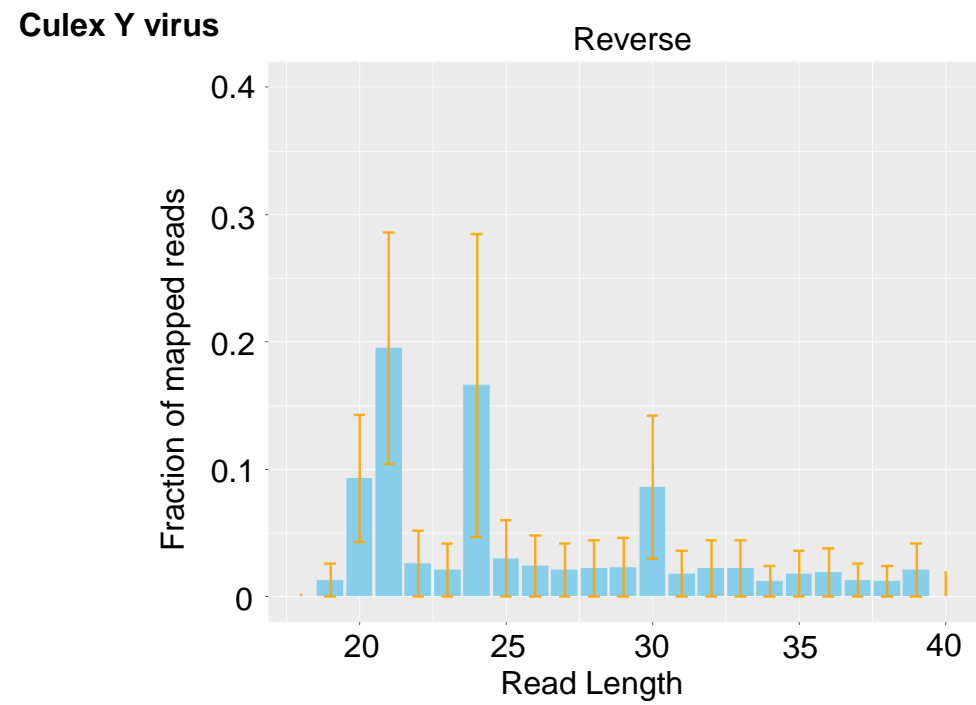
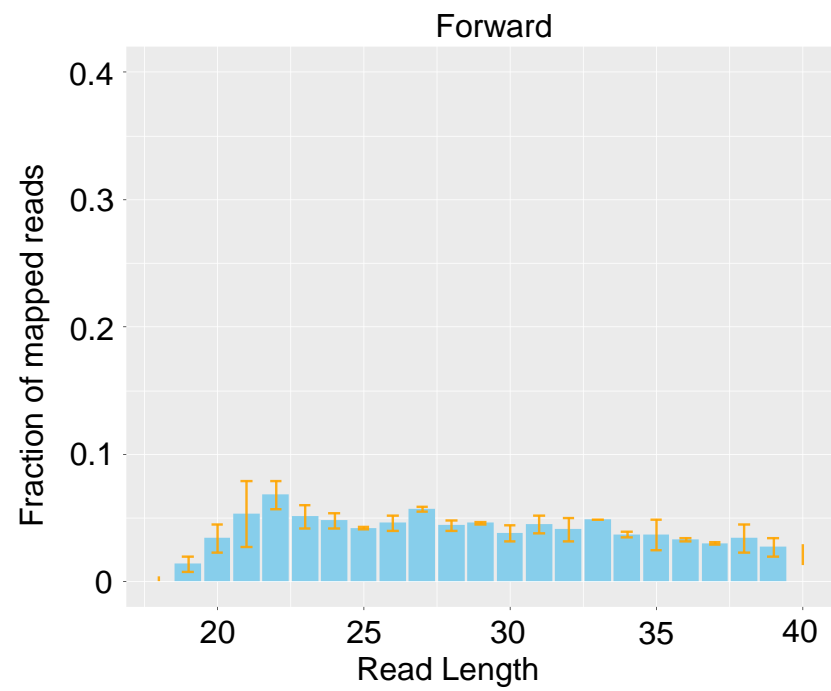
(Range:-250
to 250)

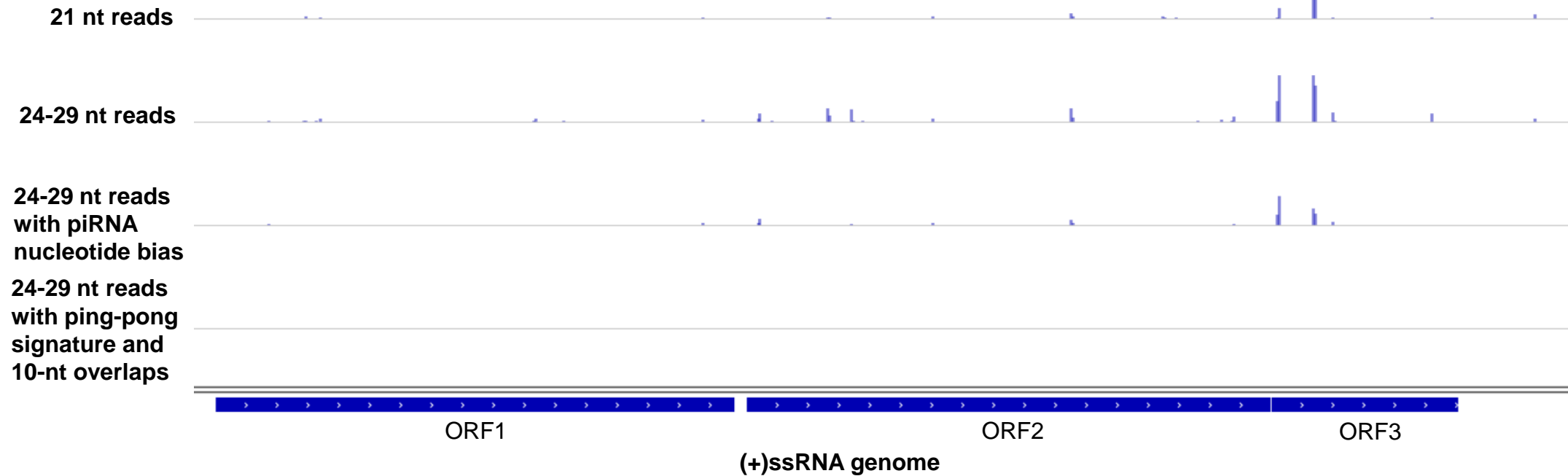
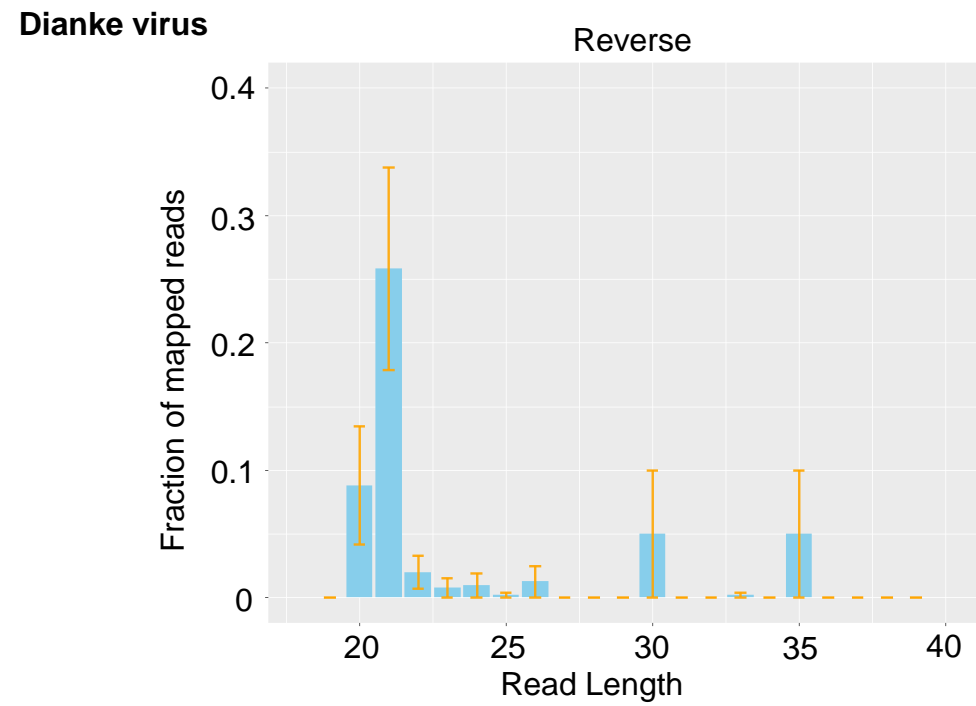
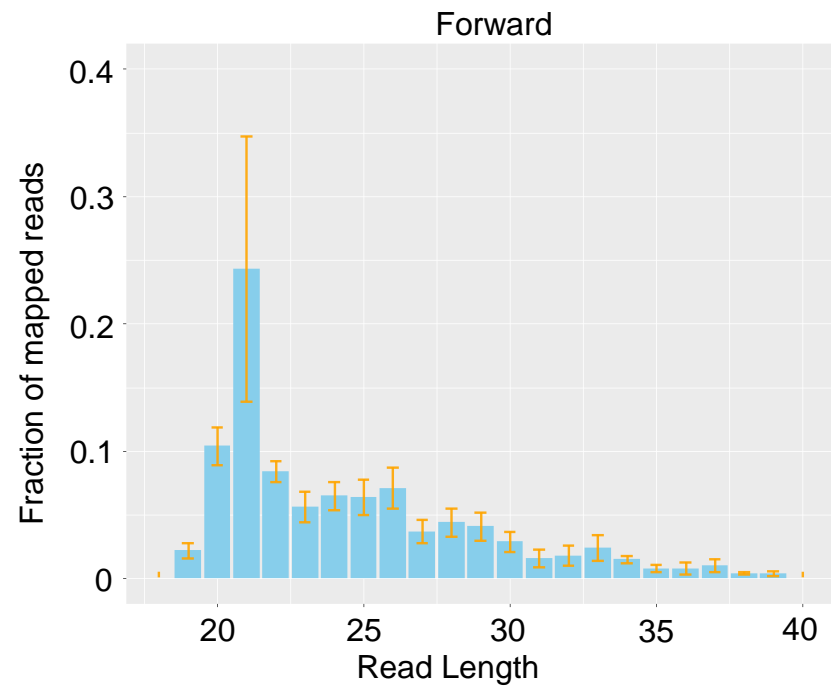


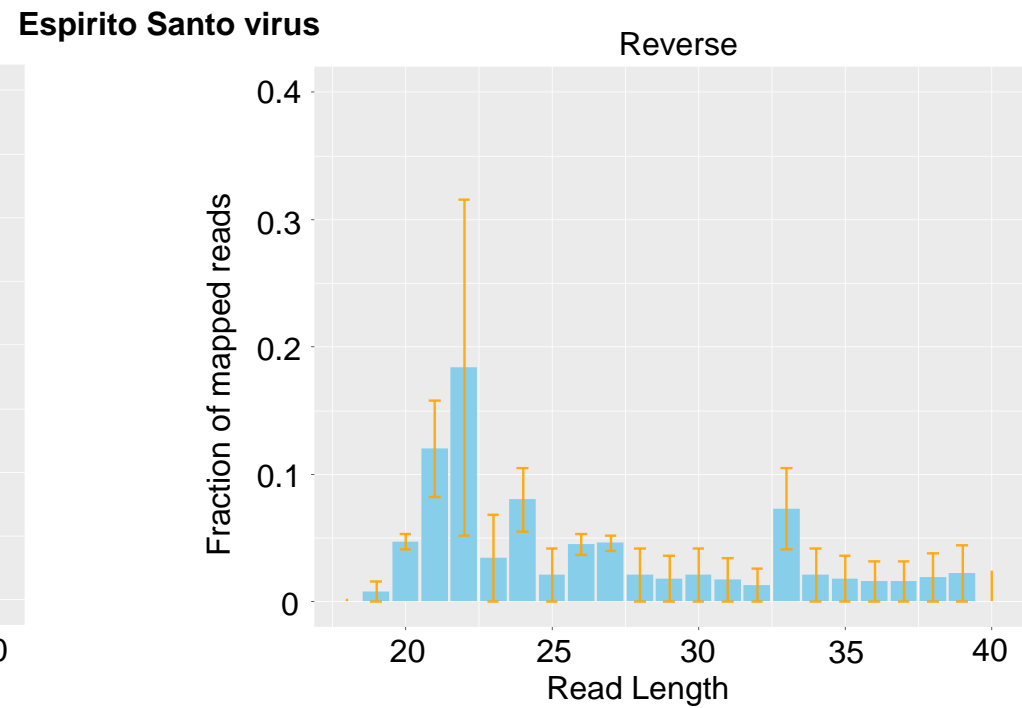
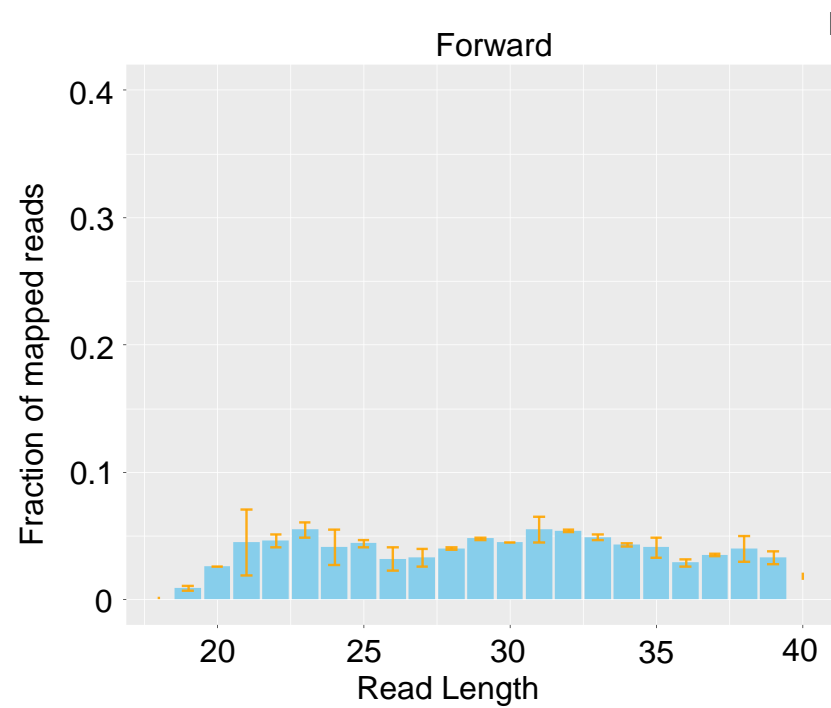
Culex pipiens associated Tunisia virus



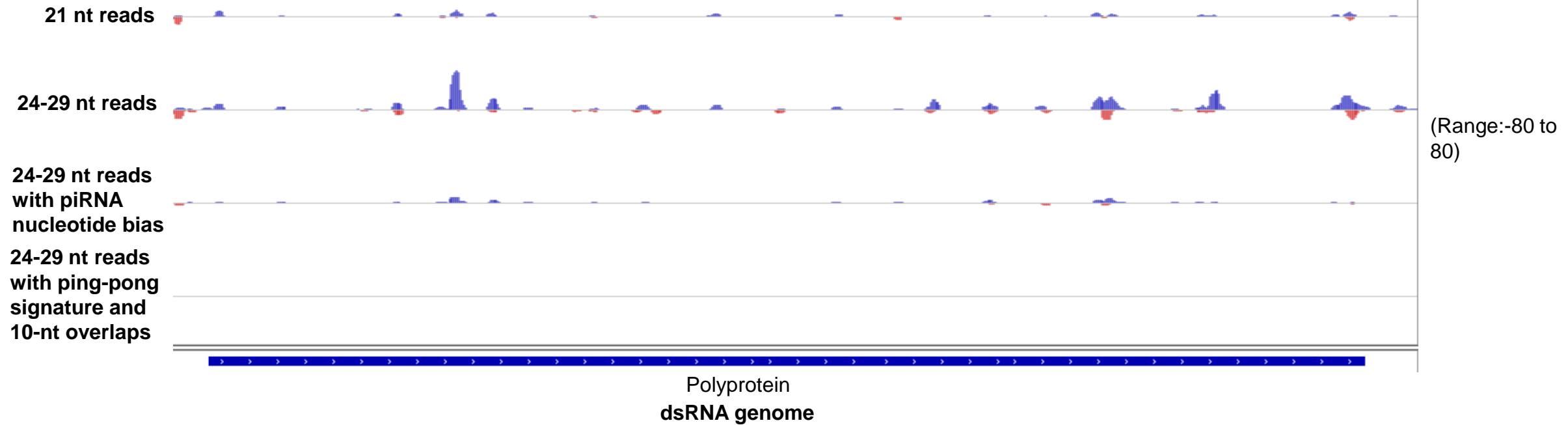


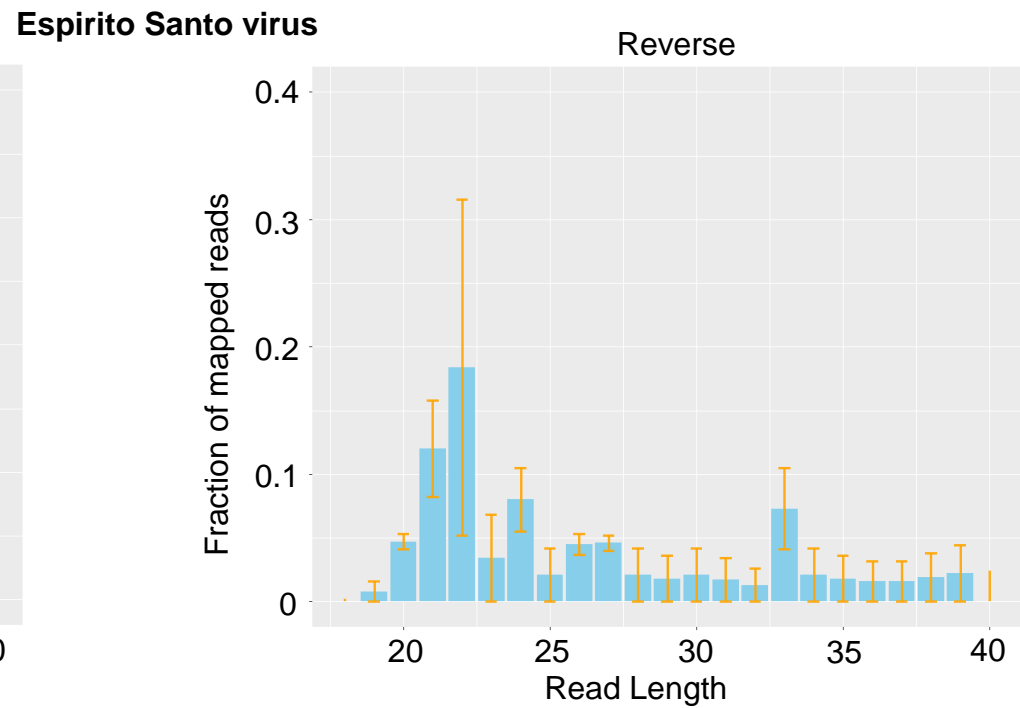
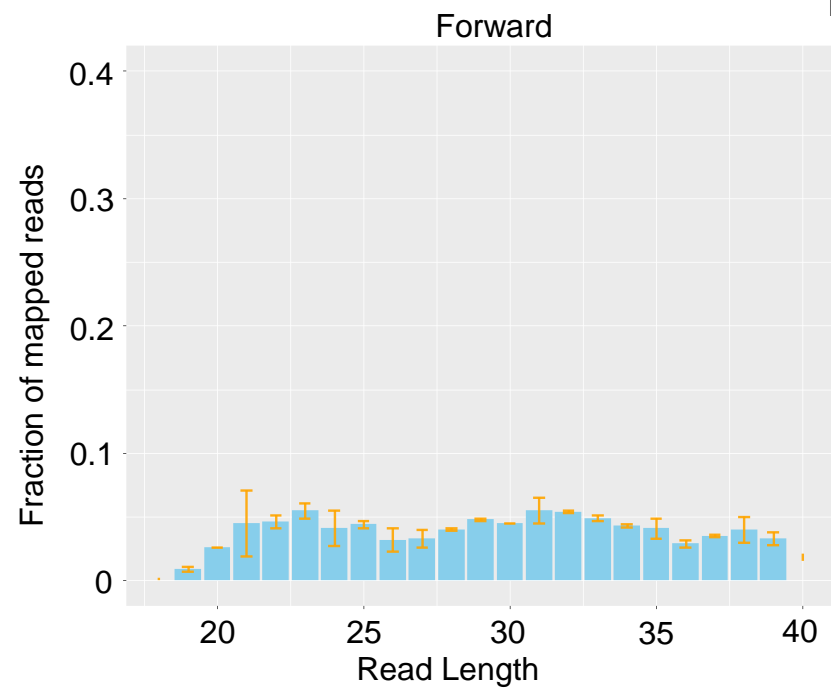




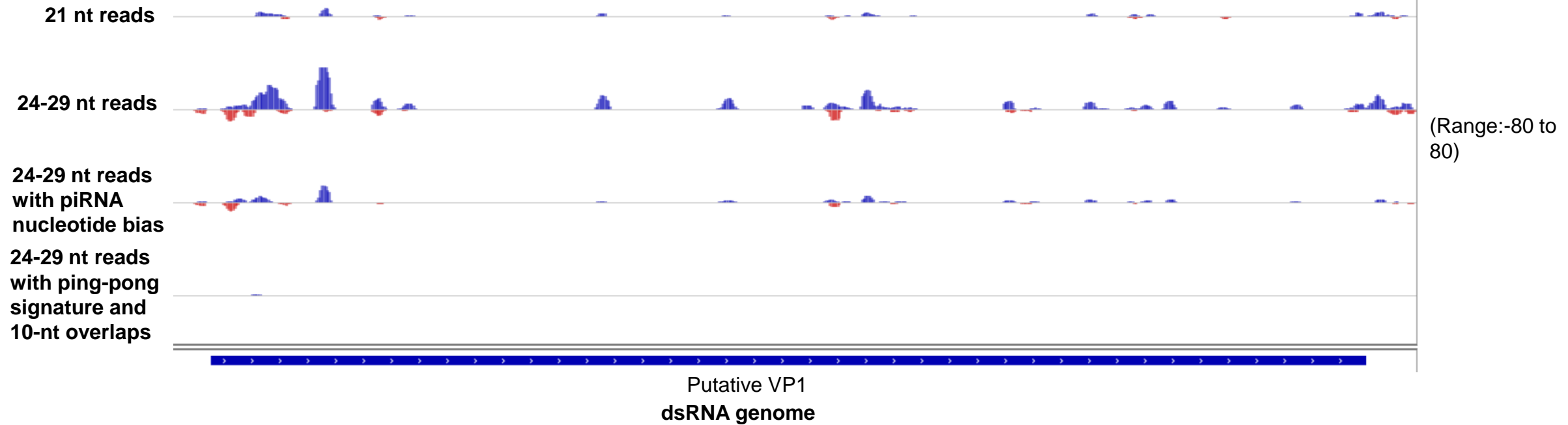


Coverage: Segment A

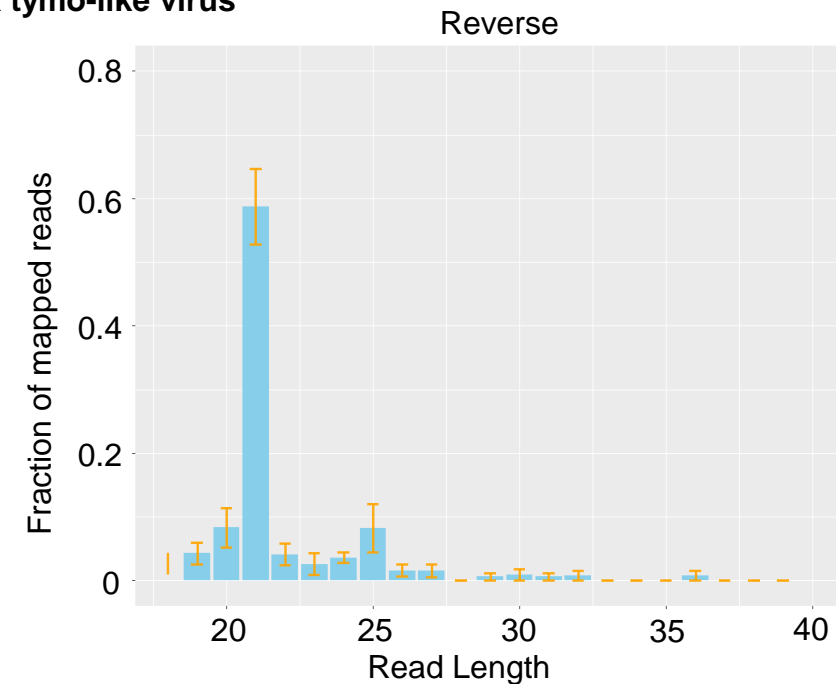
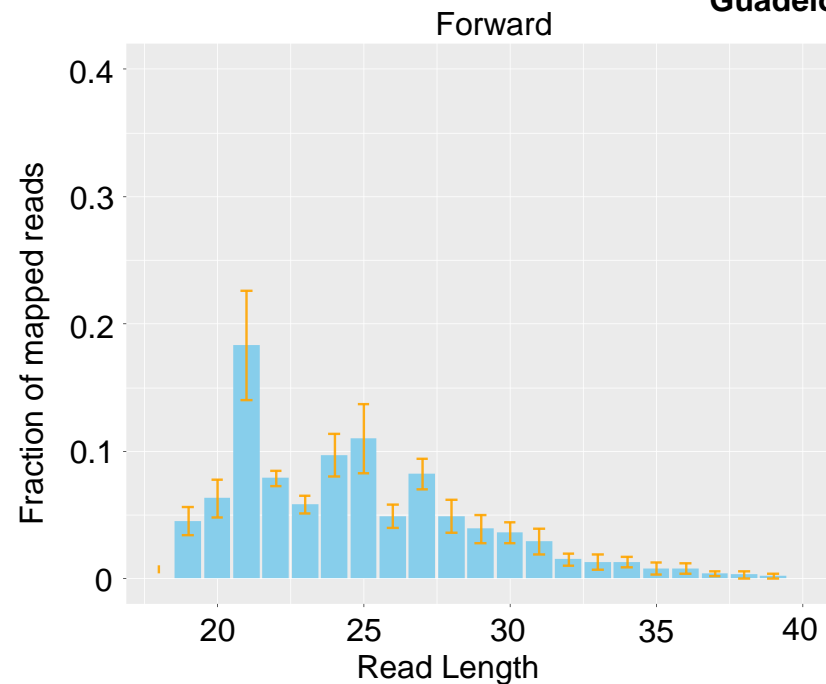




Coverage: Segment B



Guadeloupe Culex tymo-like virus



21 nt reads

24-29 nt reads

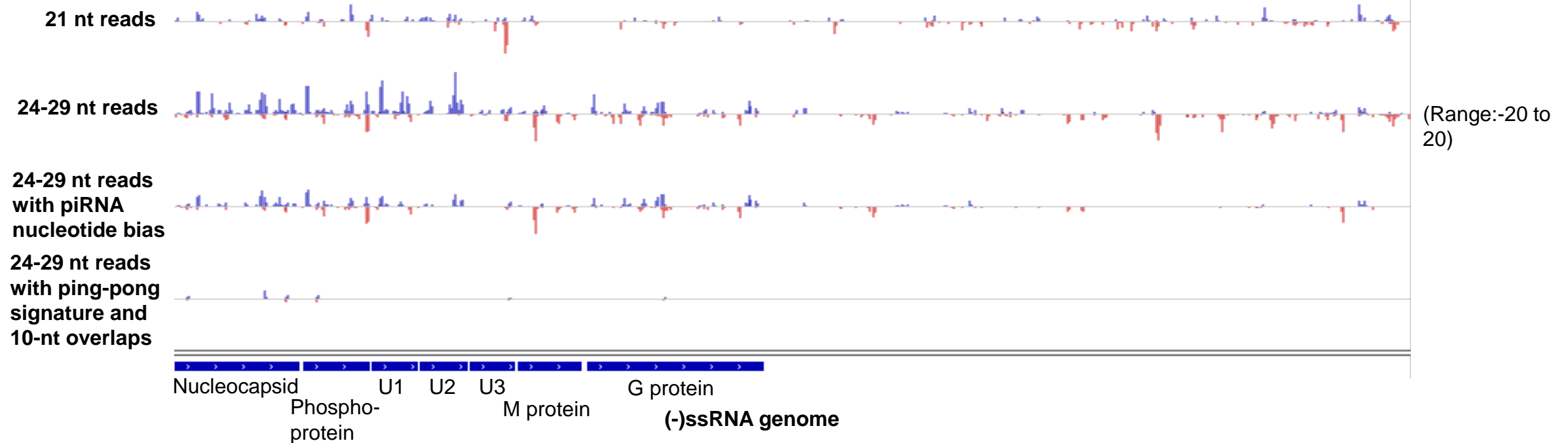
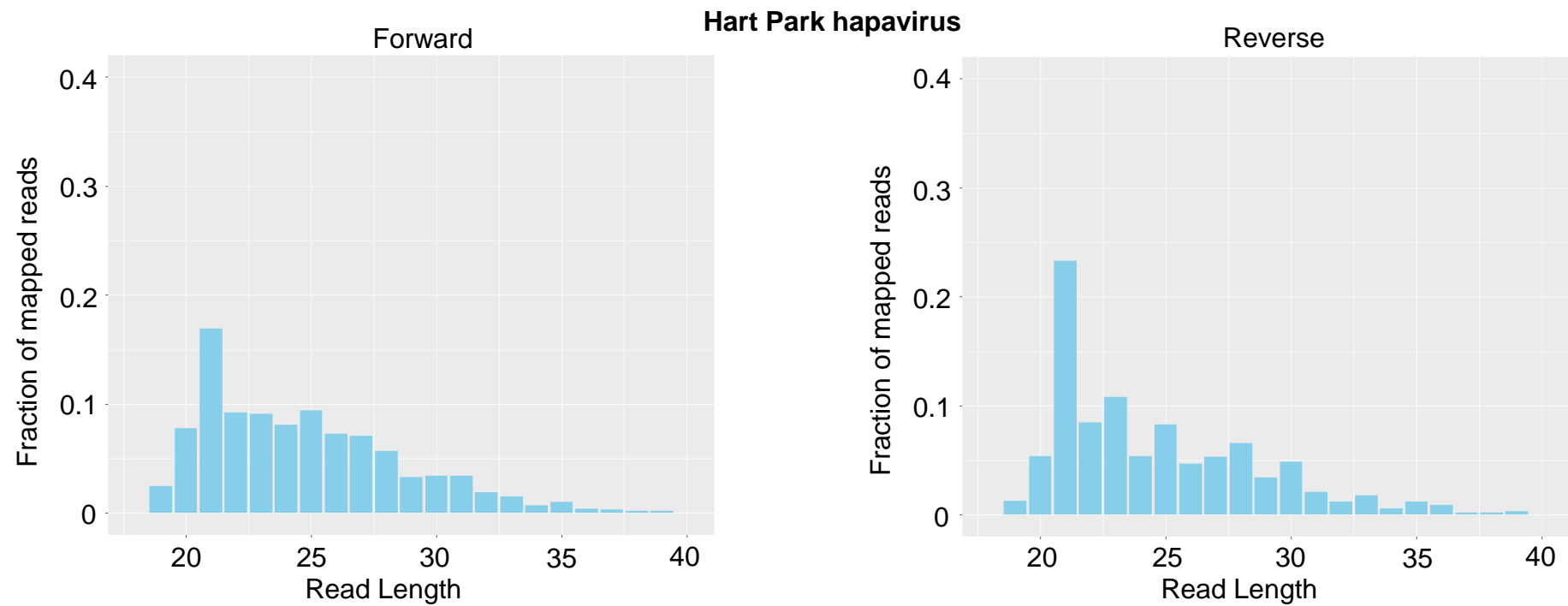
24-29 nt reads
with piRNA
nucleotide bias

24-29 nt reads
with ping-pong
signature and
10-nt overlaps

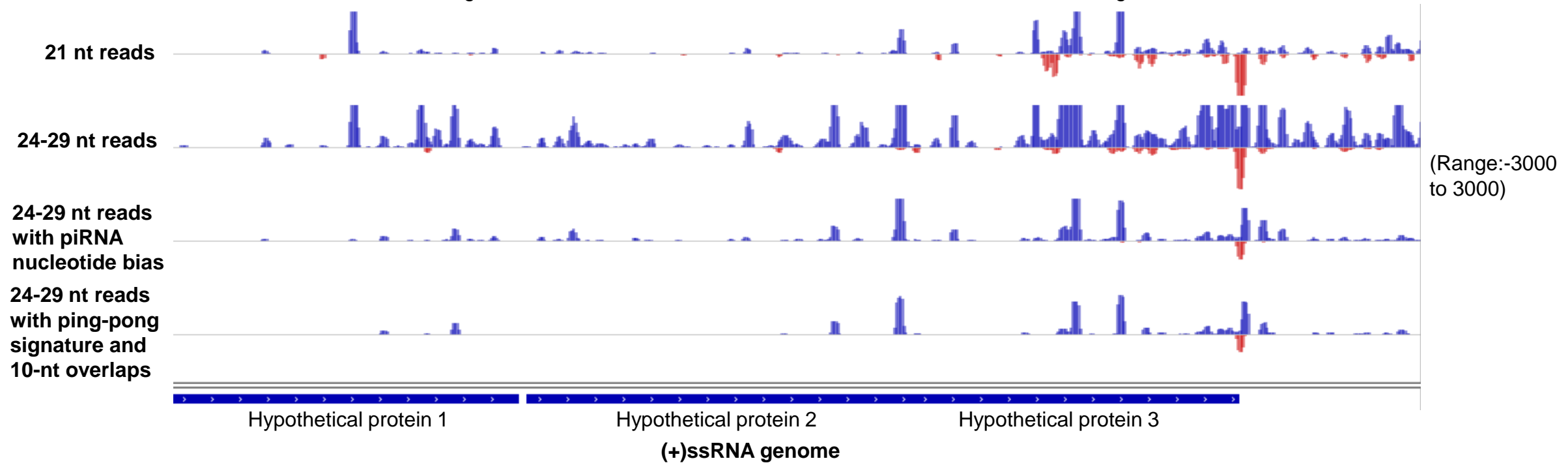
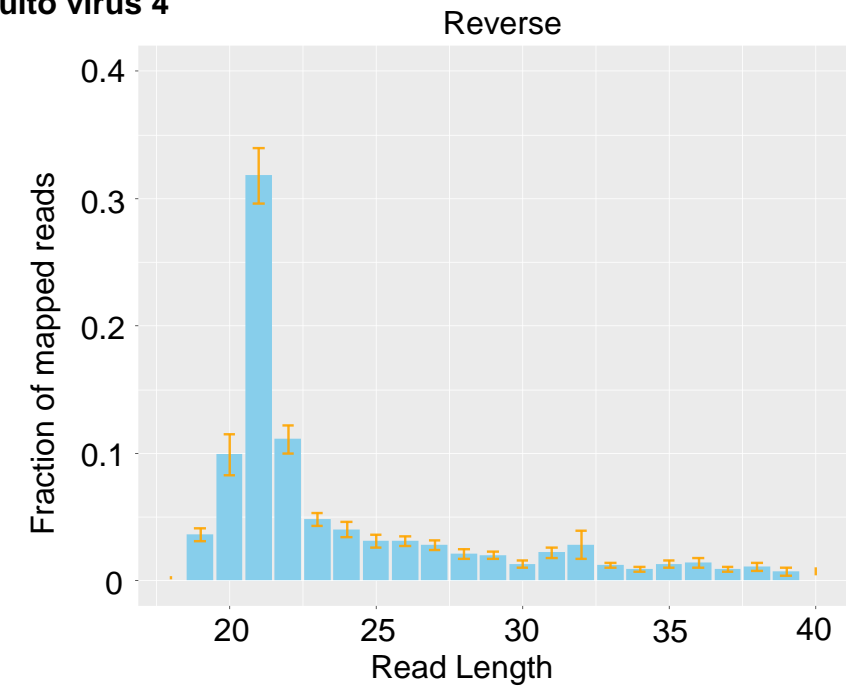
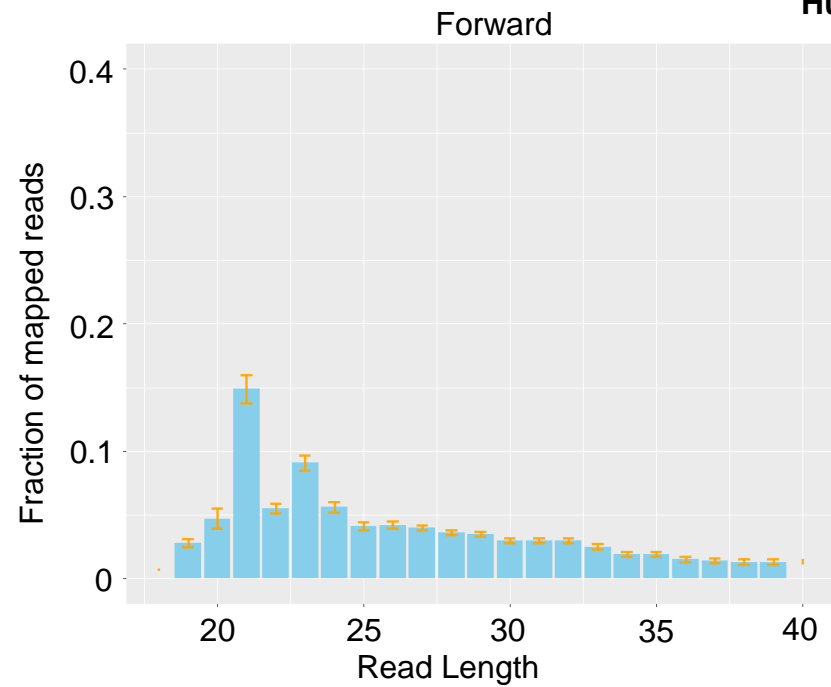
(Range:-100
to 100)



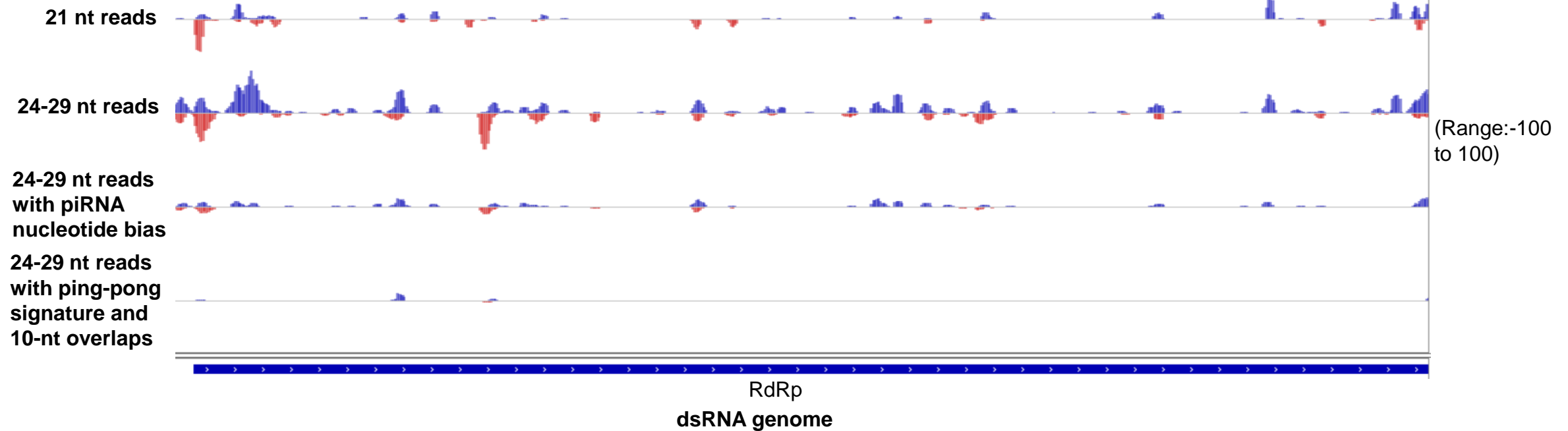
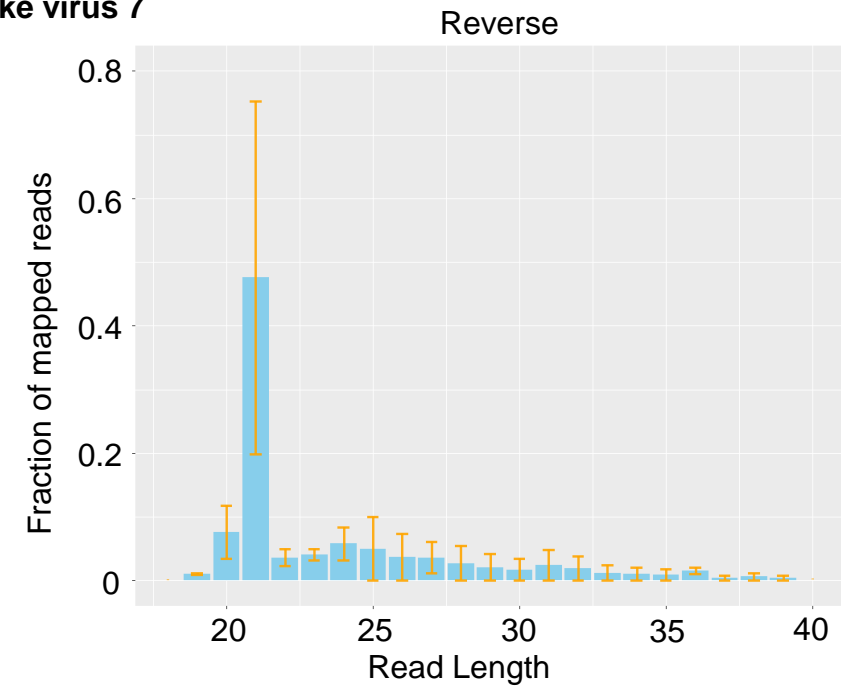
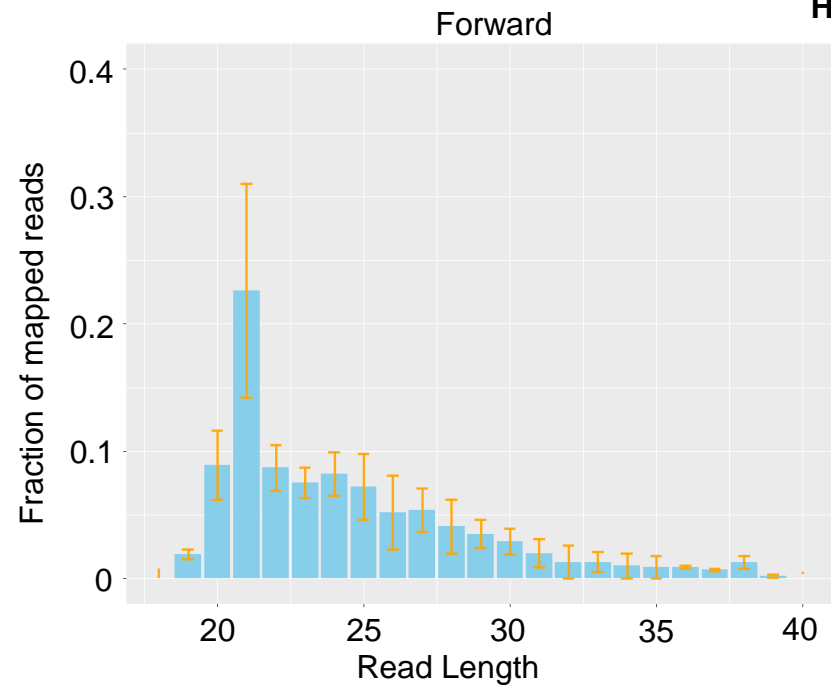
(+)ssRNA genome

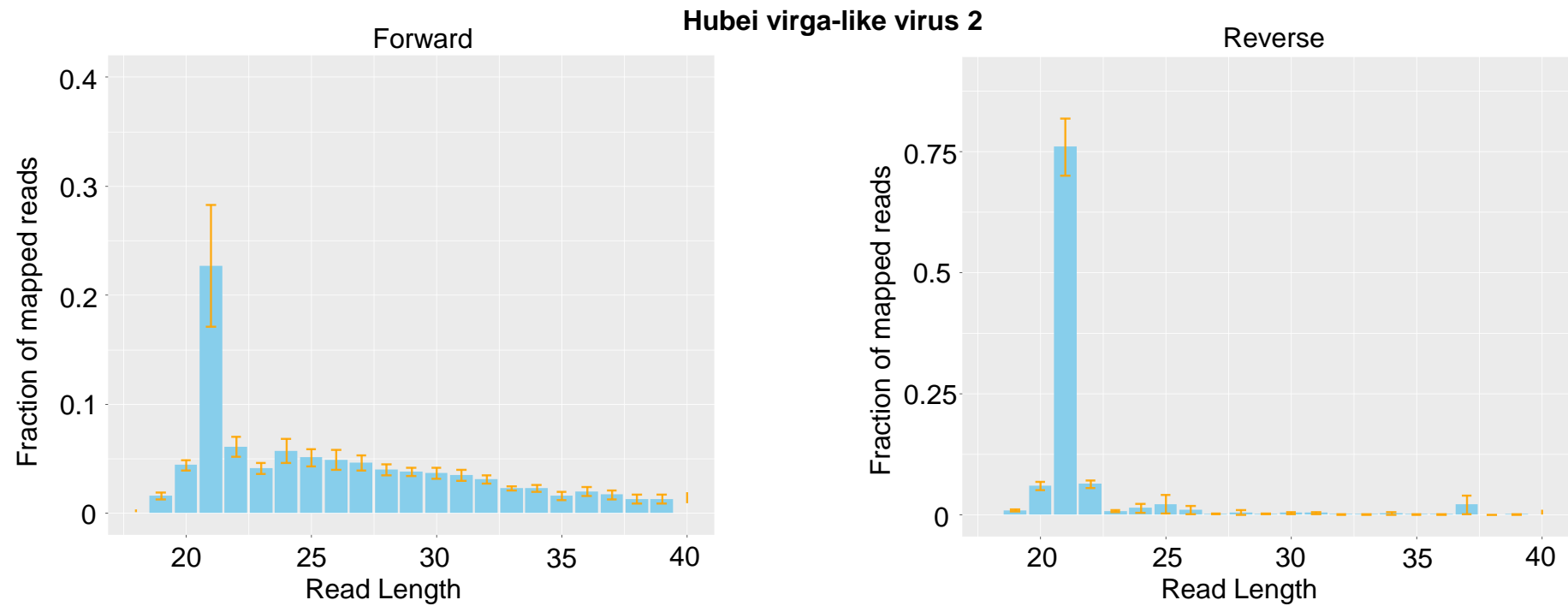


Hubei mosquito virus 4



Hubei reo-like virus 7





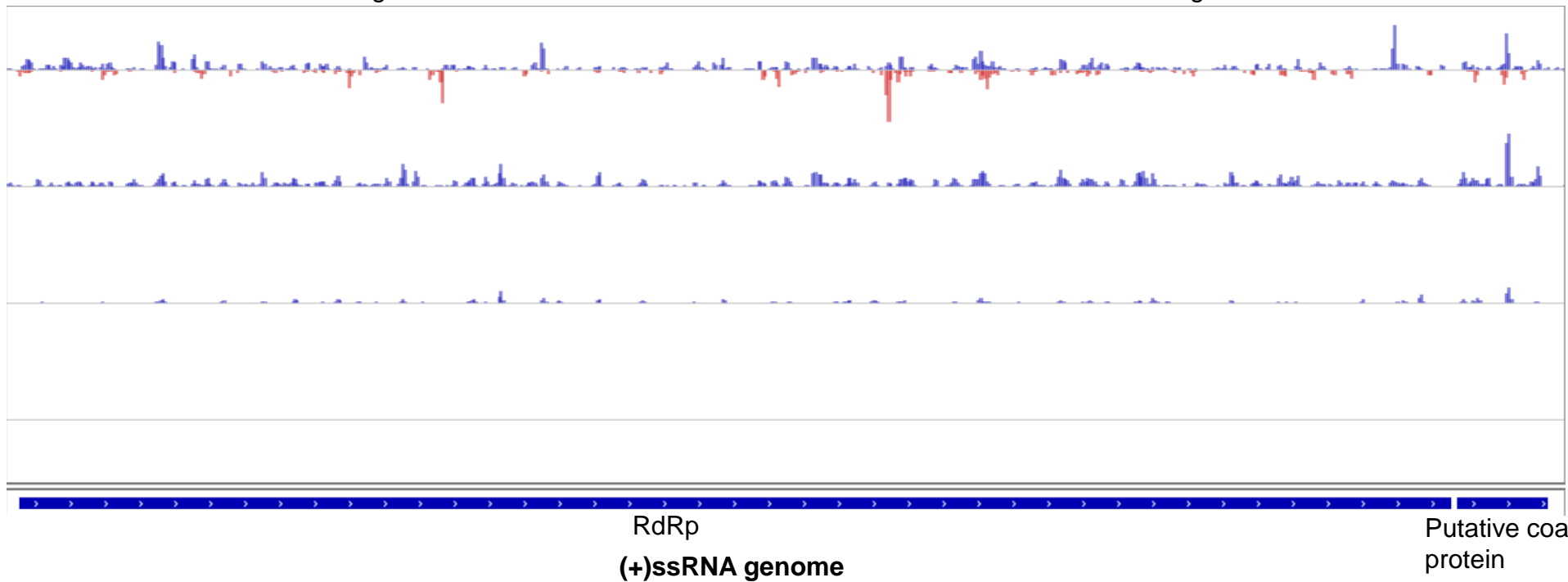
21 nt reads

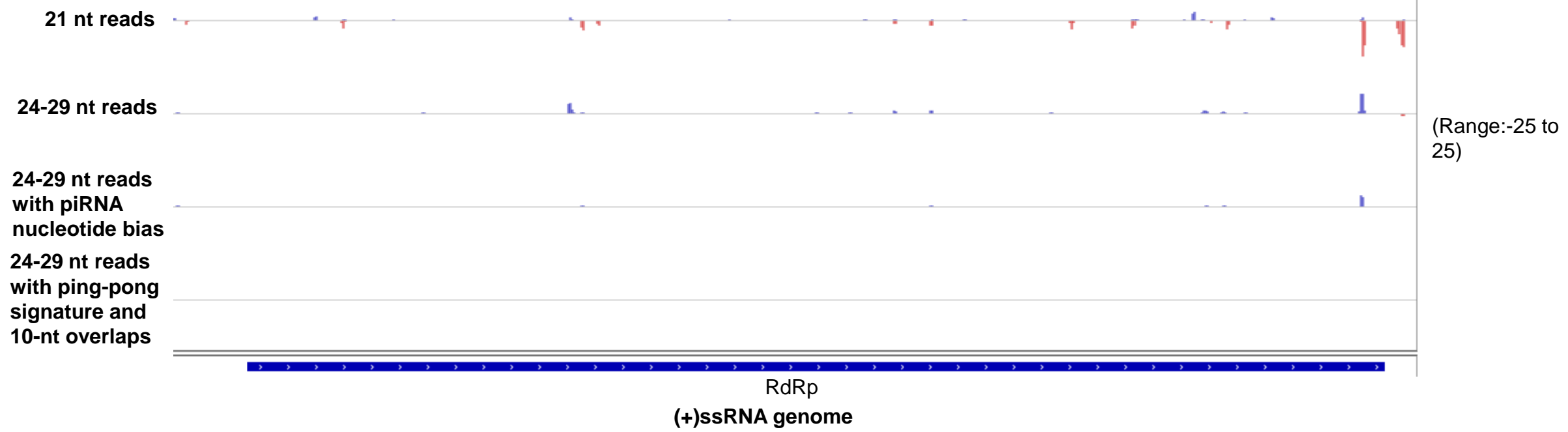
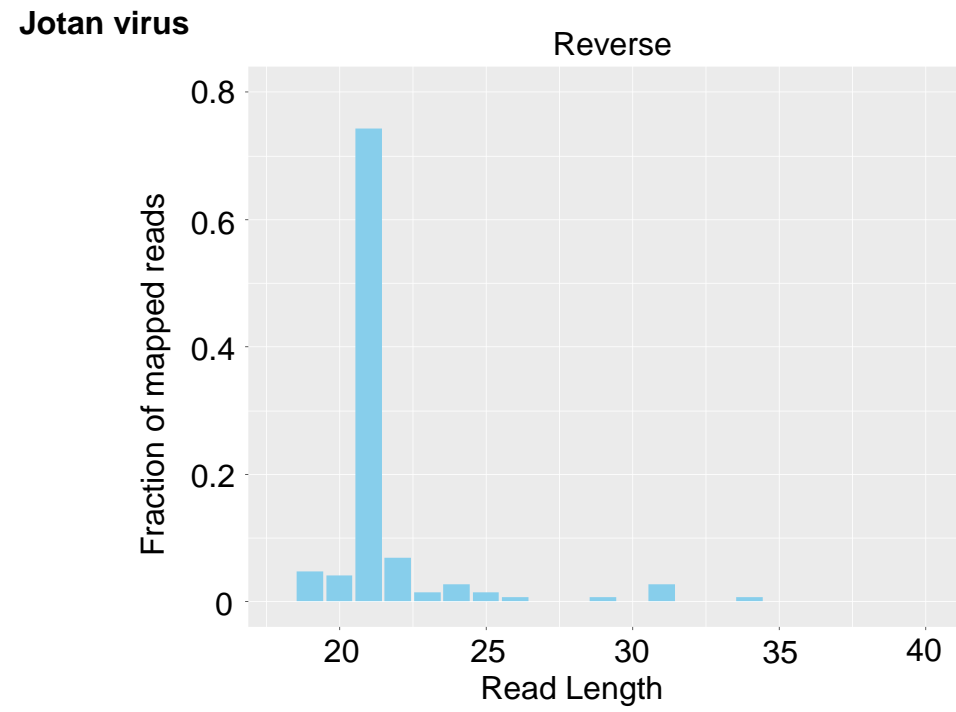
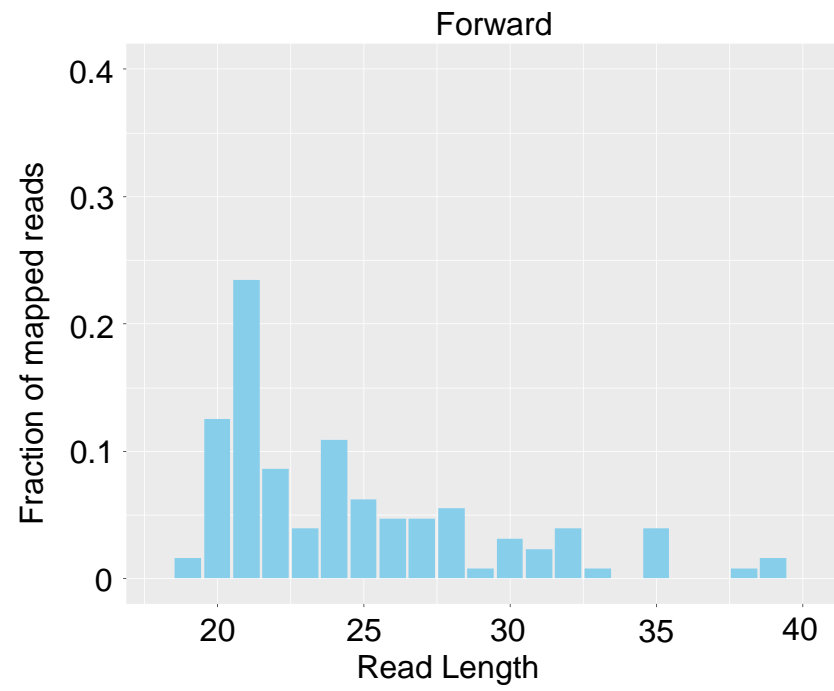
24-29 nt reads

24-29 nt reads
with piRNA
nucleotide bias

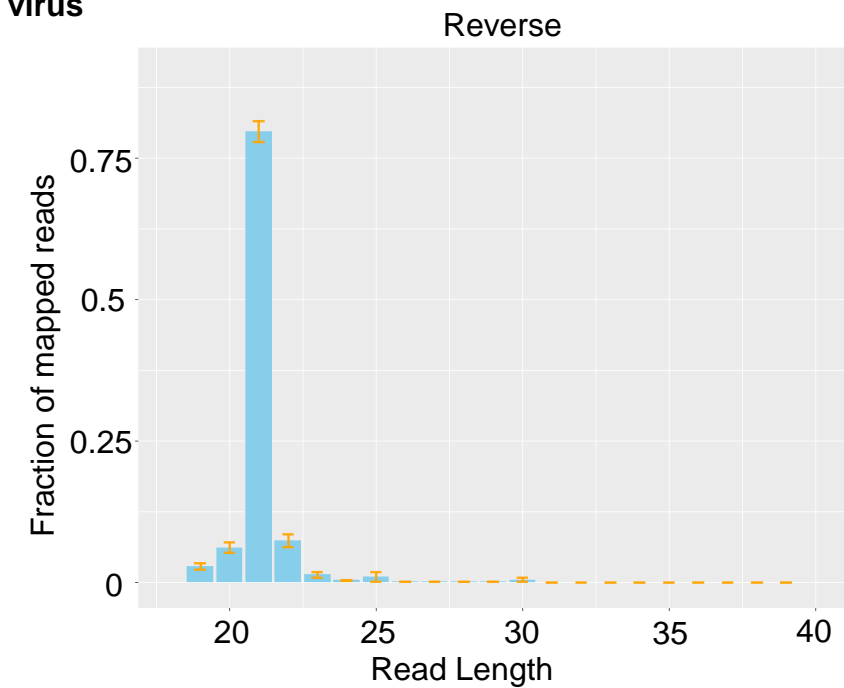
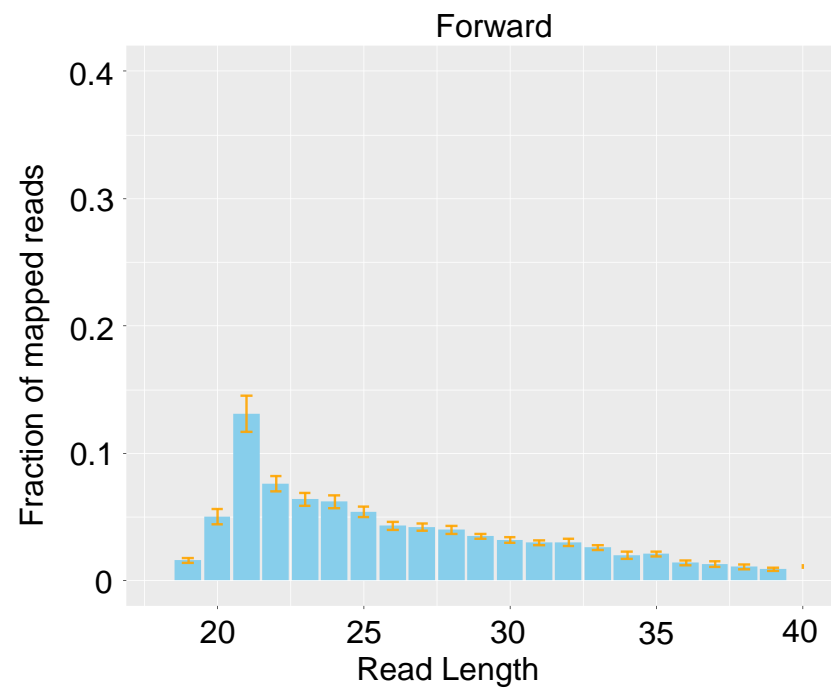
24-29 nt reads
with ping-pong
signature and
10-nt overlaps

(Range:-100
to 100)





Marma virus



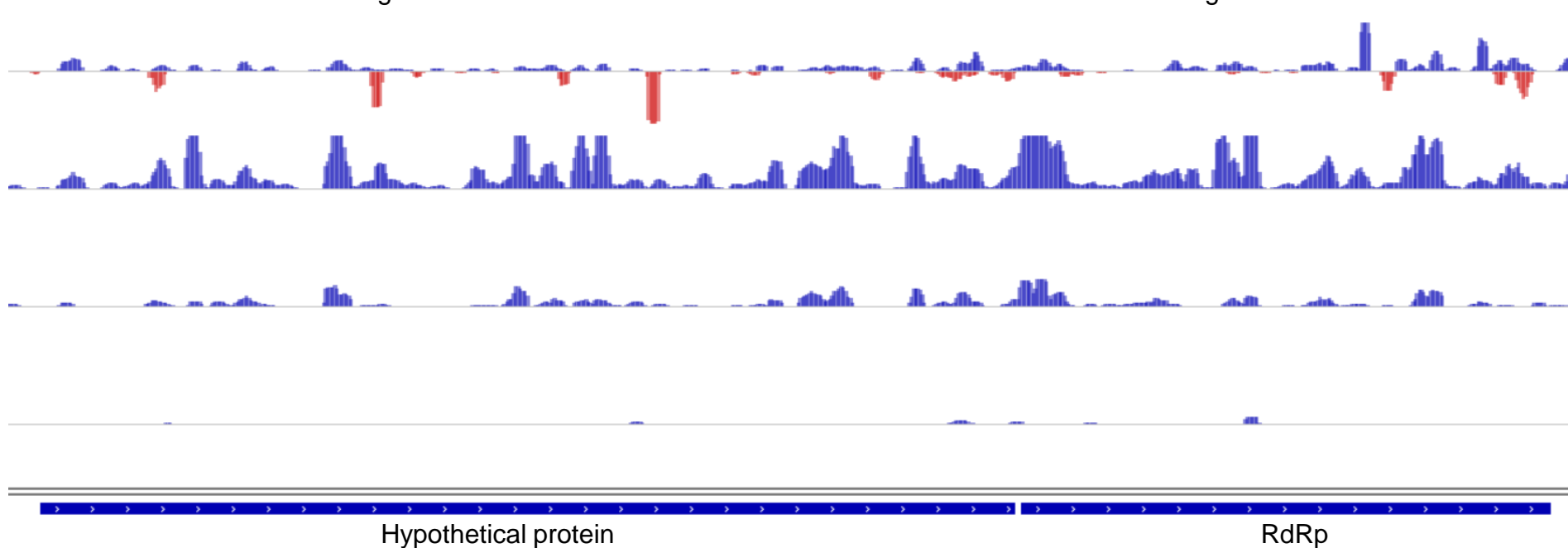
21 nt reads

24-29 nt reads

24-29 nt reads
with piRNA
nucleotide bias

24-29 nt reads
with ping-pong
signature and
10-nt overlaps

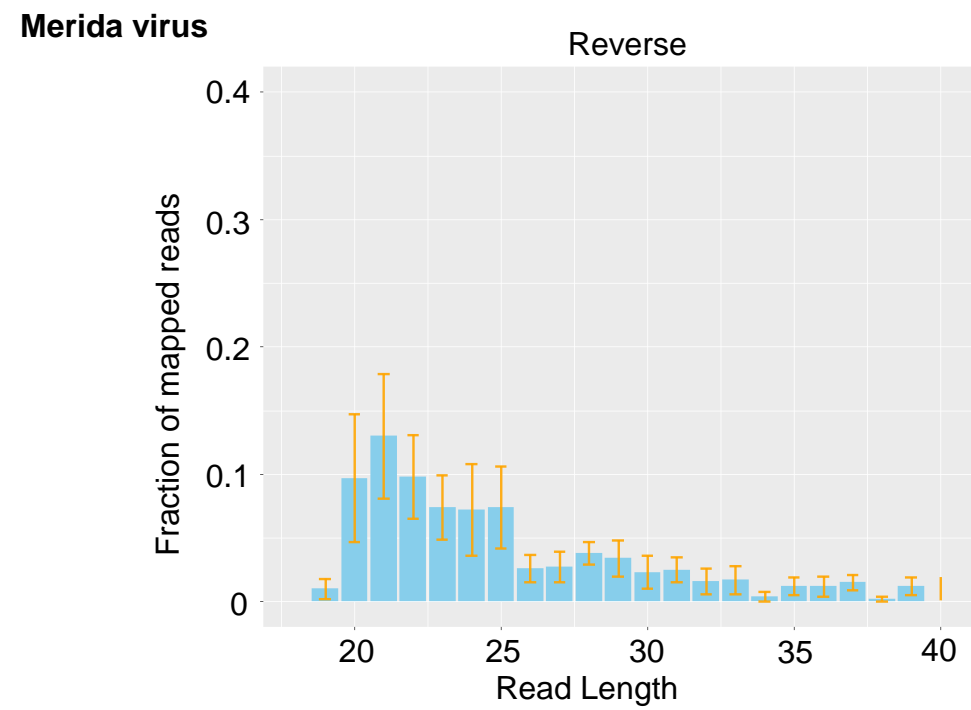
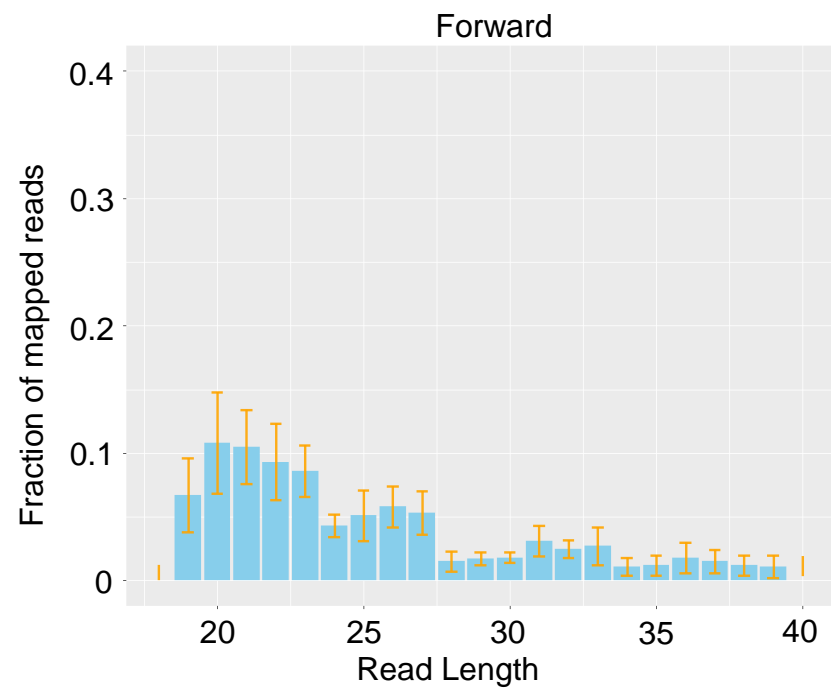
(Range:-3000
to 3000)



Hypothetical protein

RdRp

(+)ssRNA genome



21 nt reads



24-29 nt reads



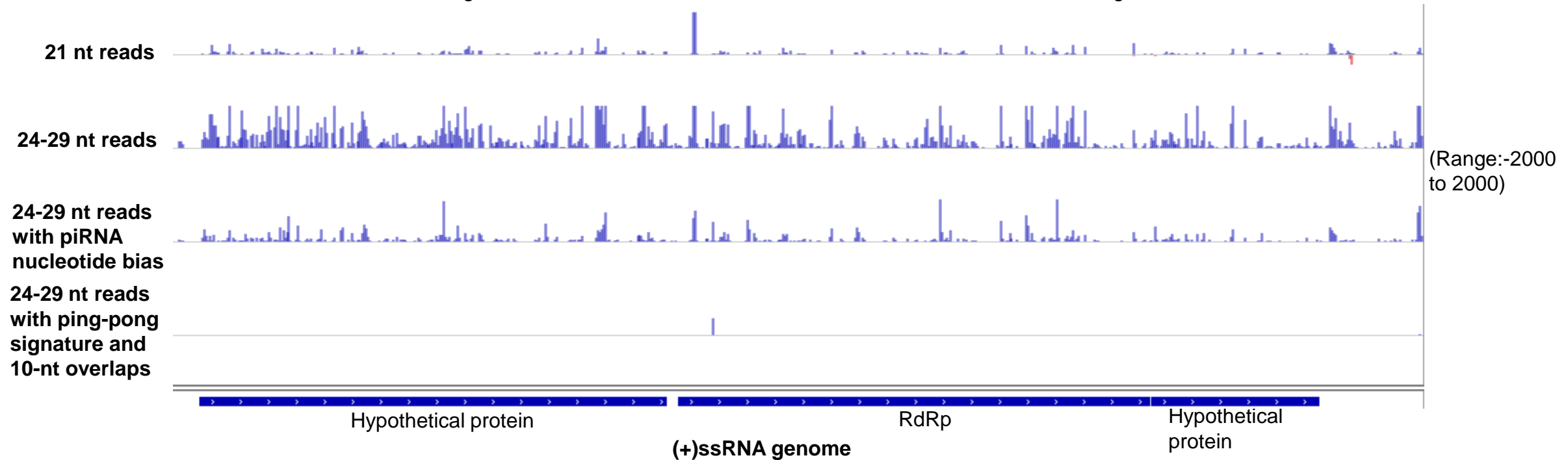
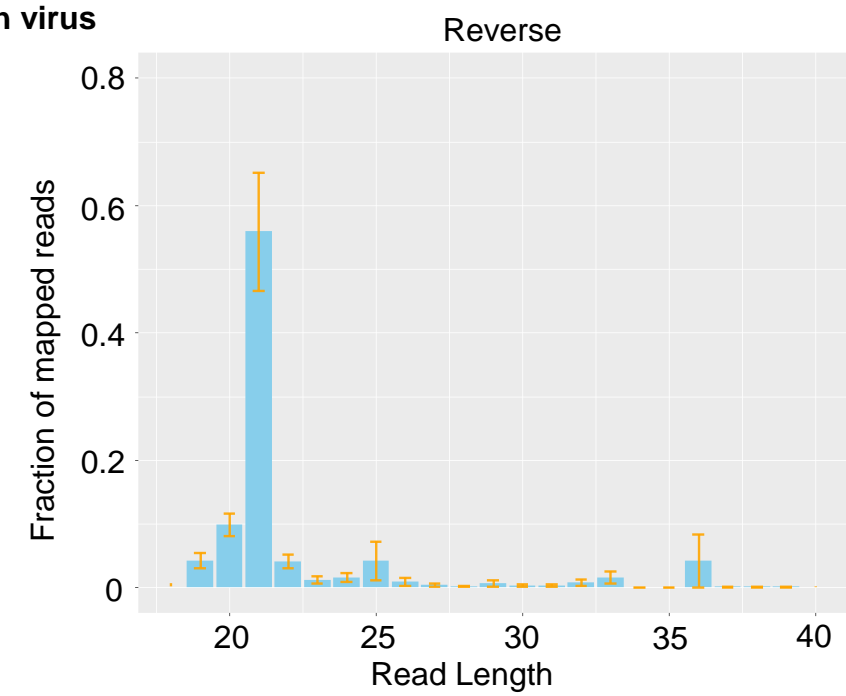
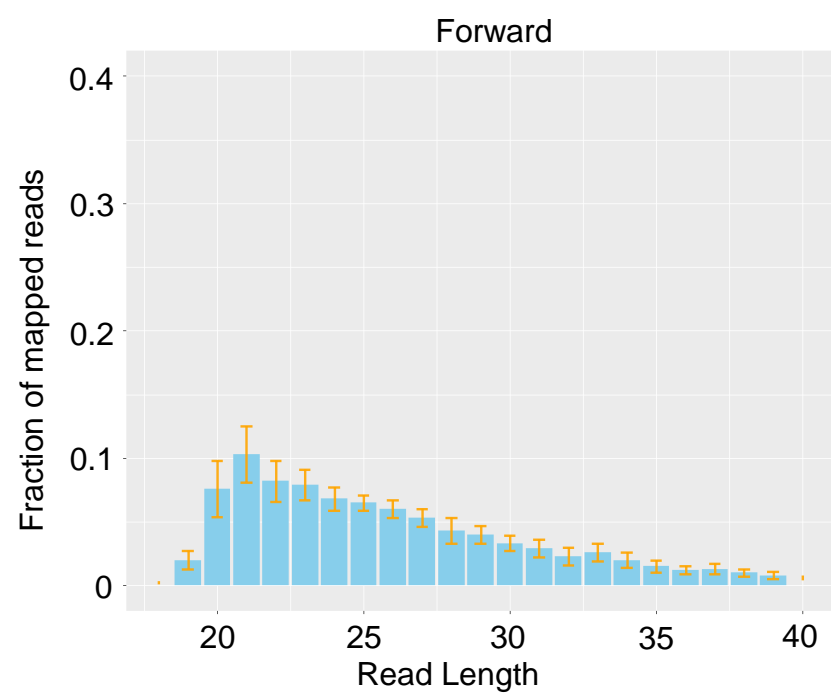
(Range:-20 to 20)

24-29 nt reads
with piRNA
nucleotide bias

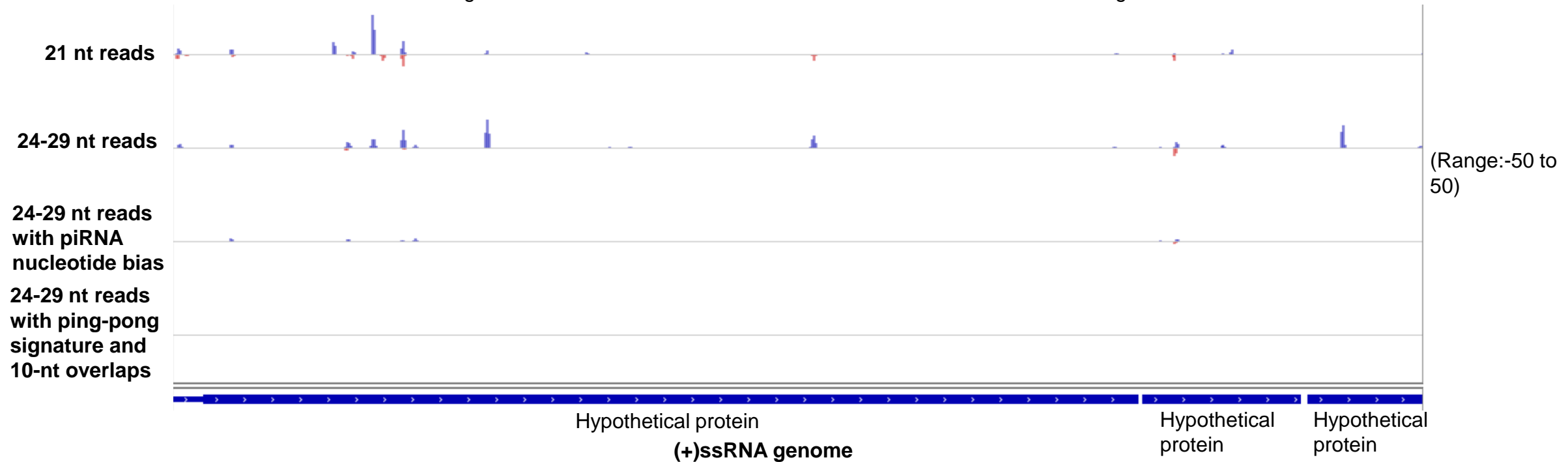
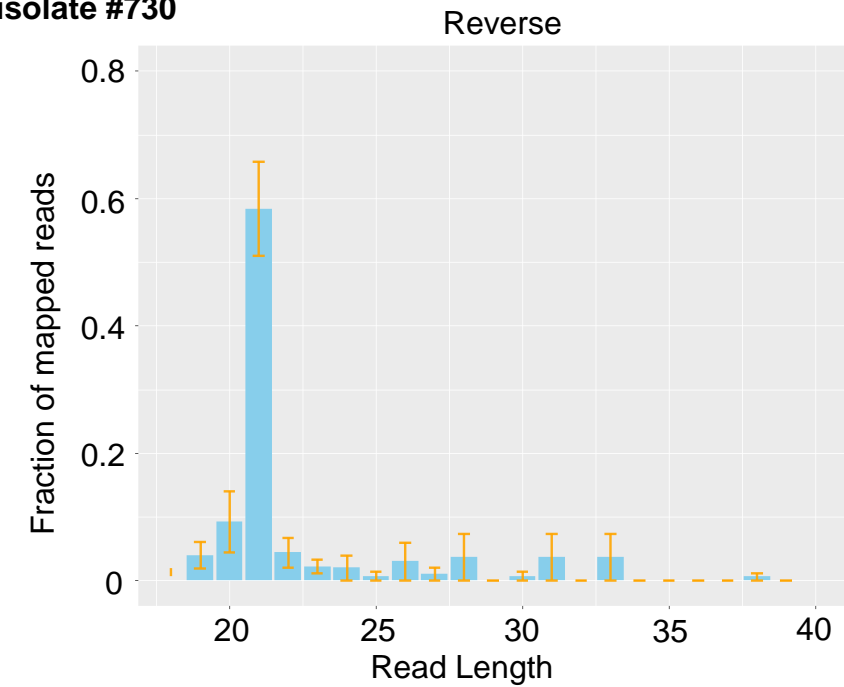
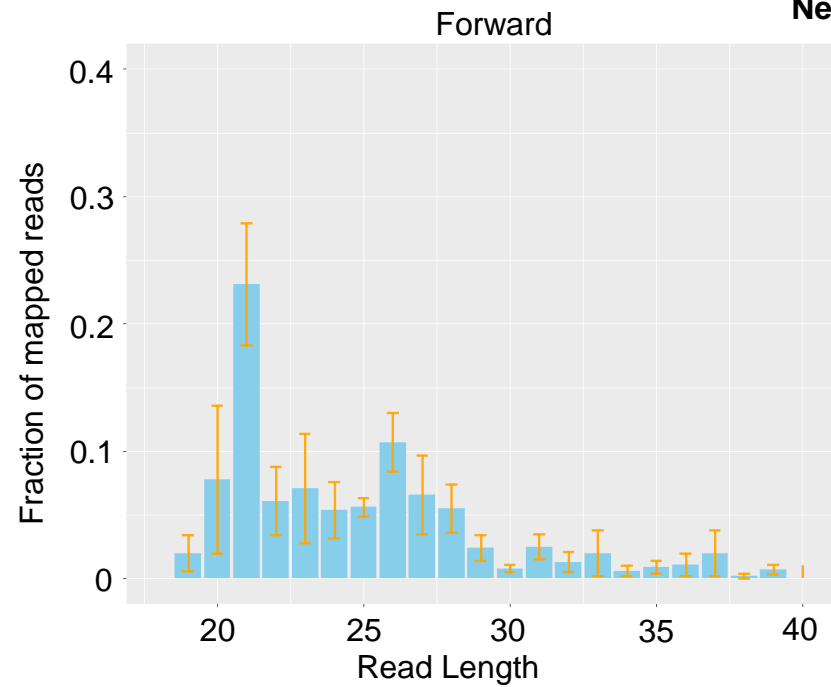


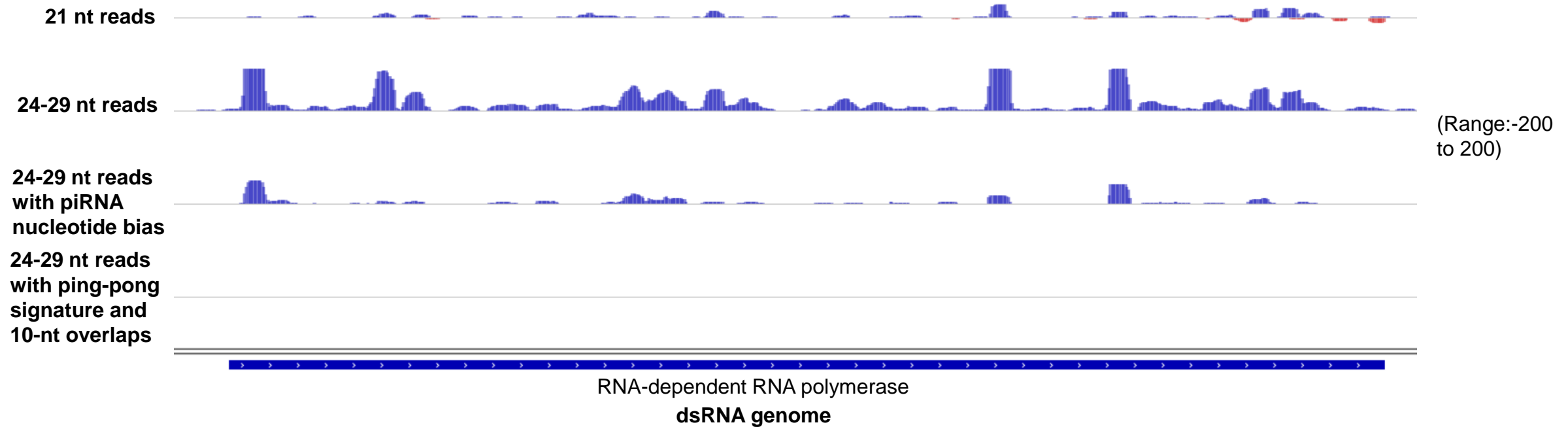
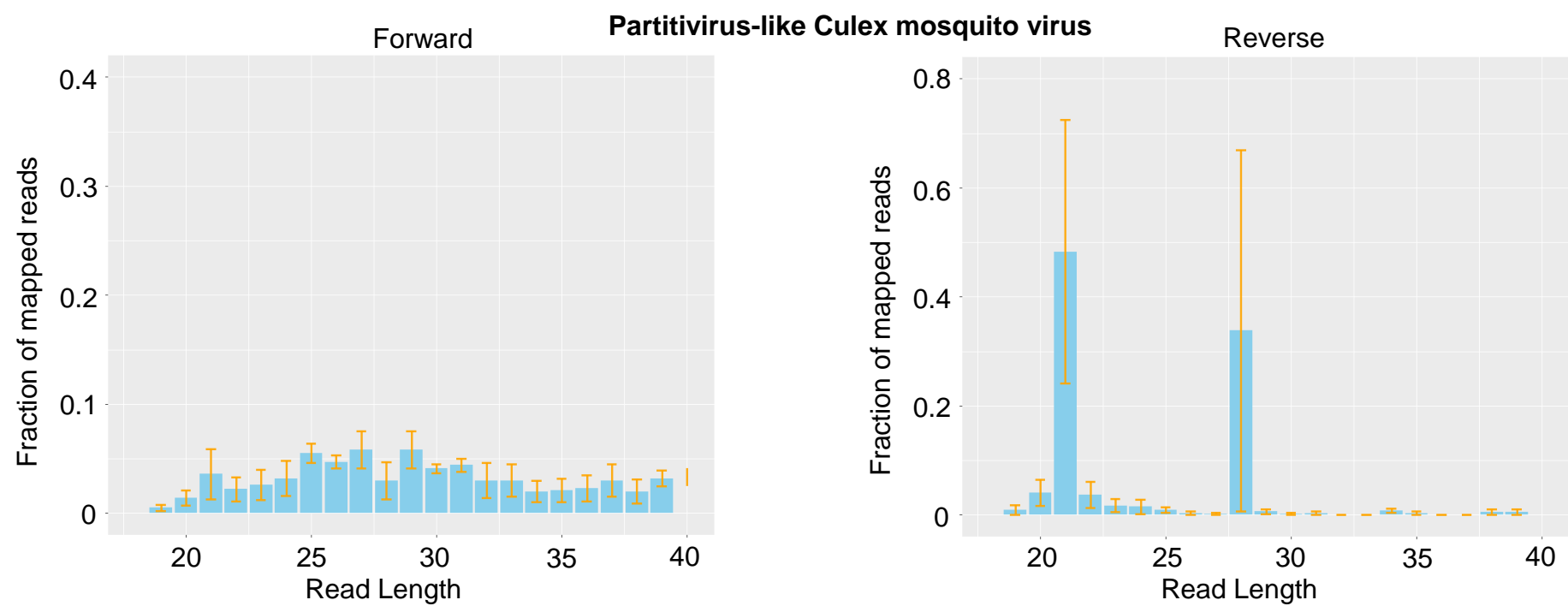
24-29 nt reads
with ping-pong
signature and
10-nt overlaps

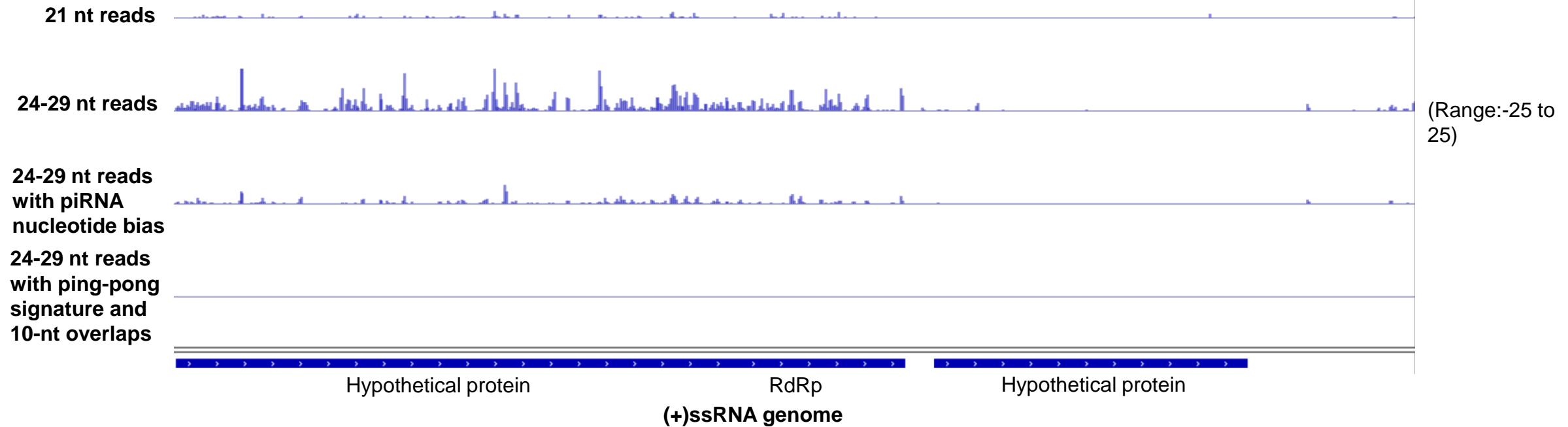
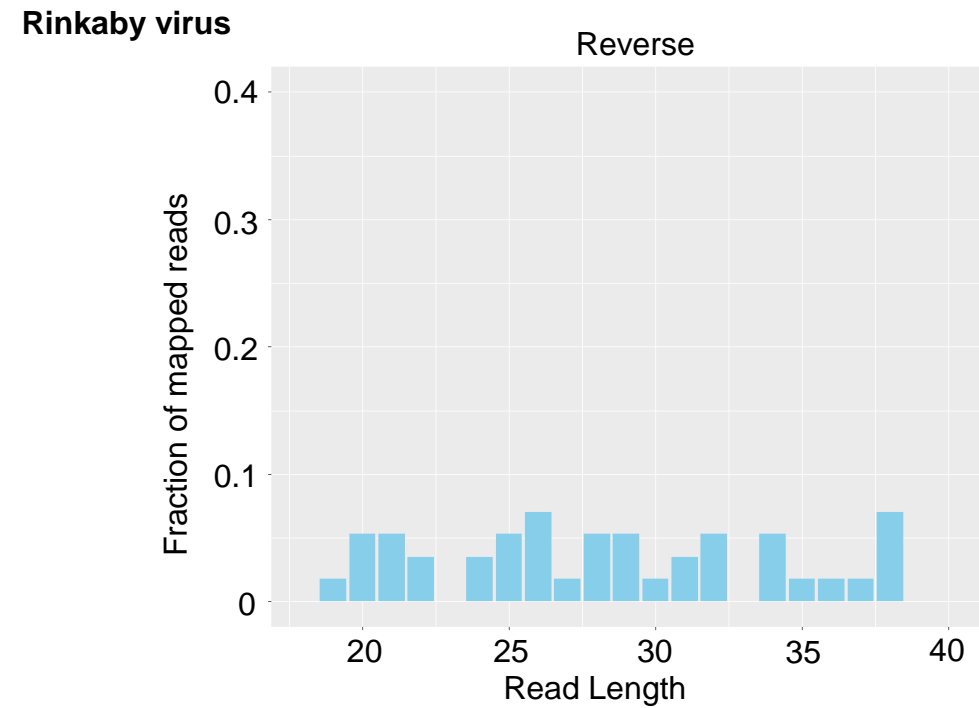
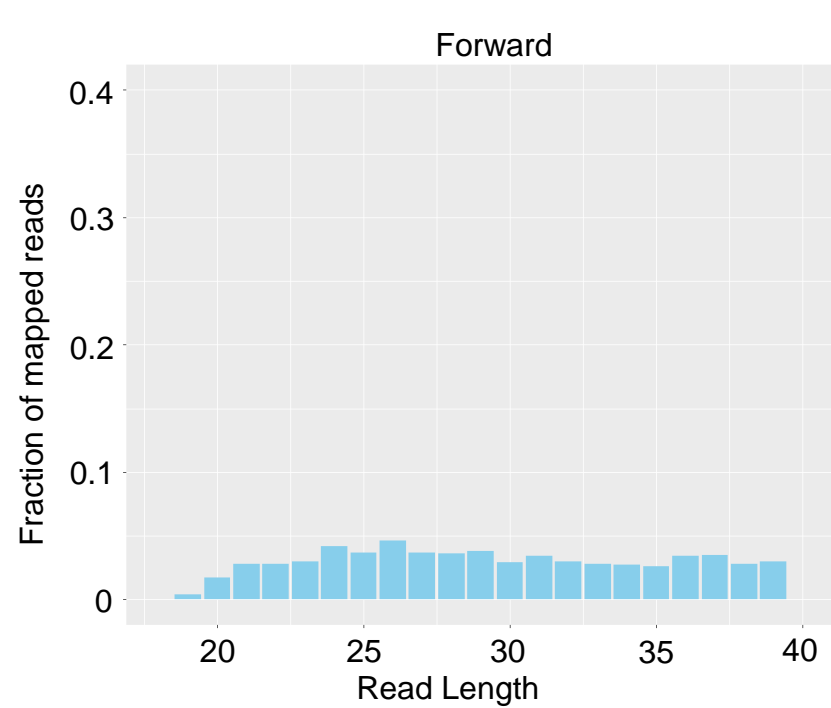


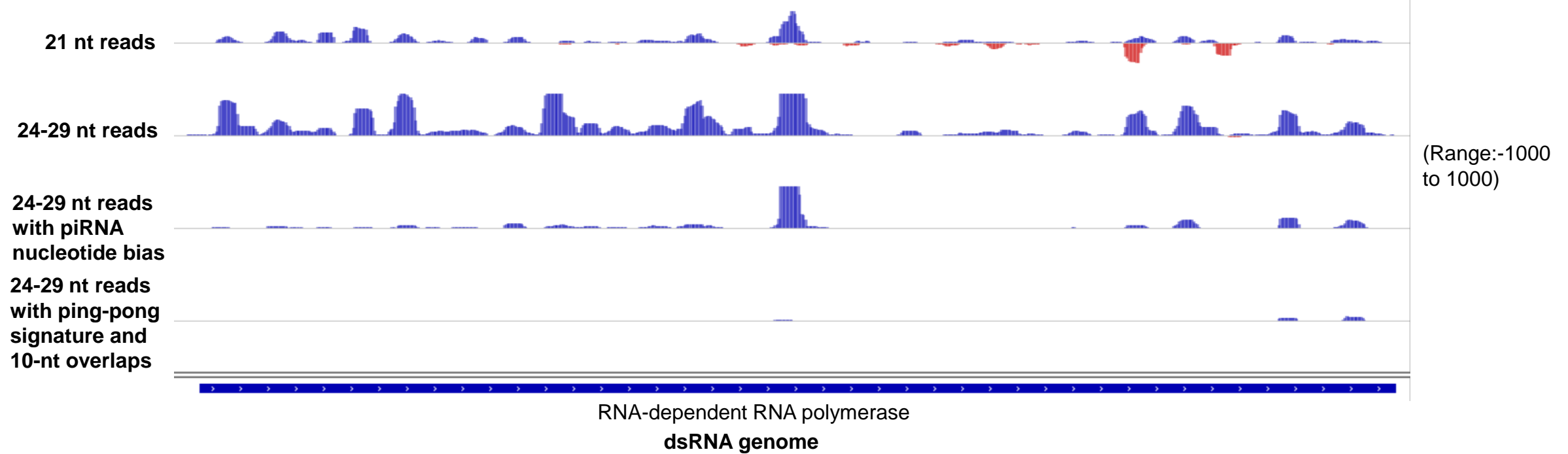
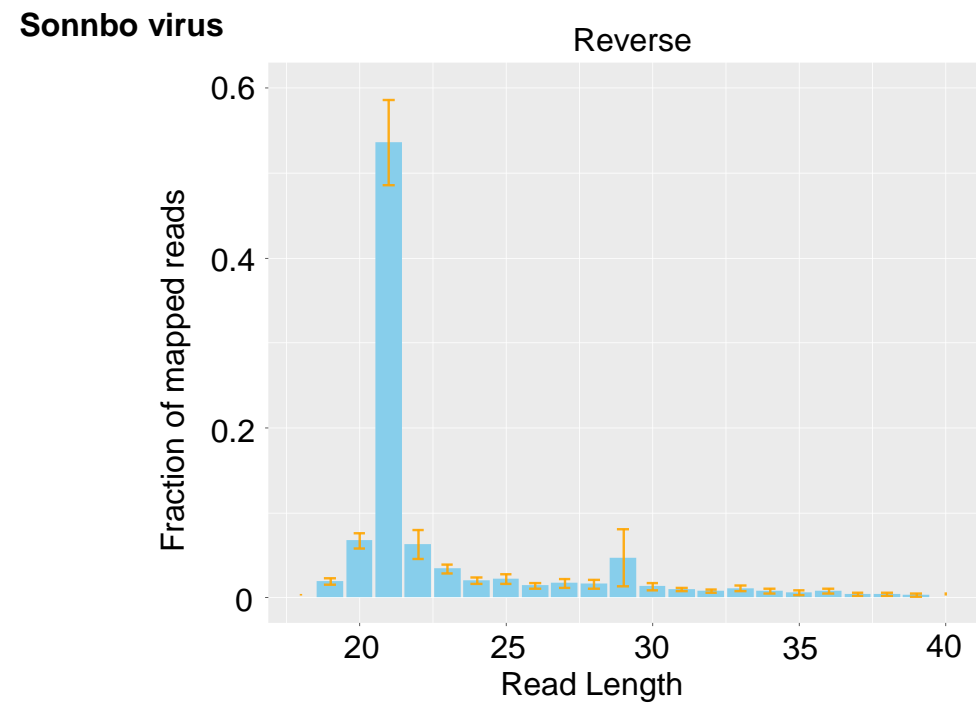
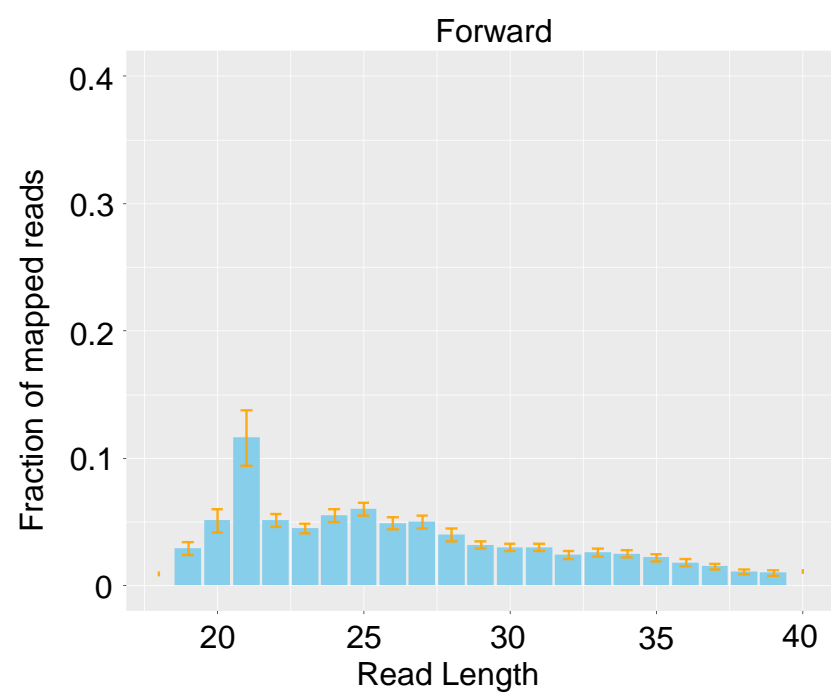


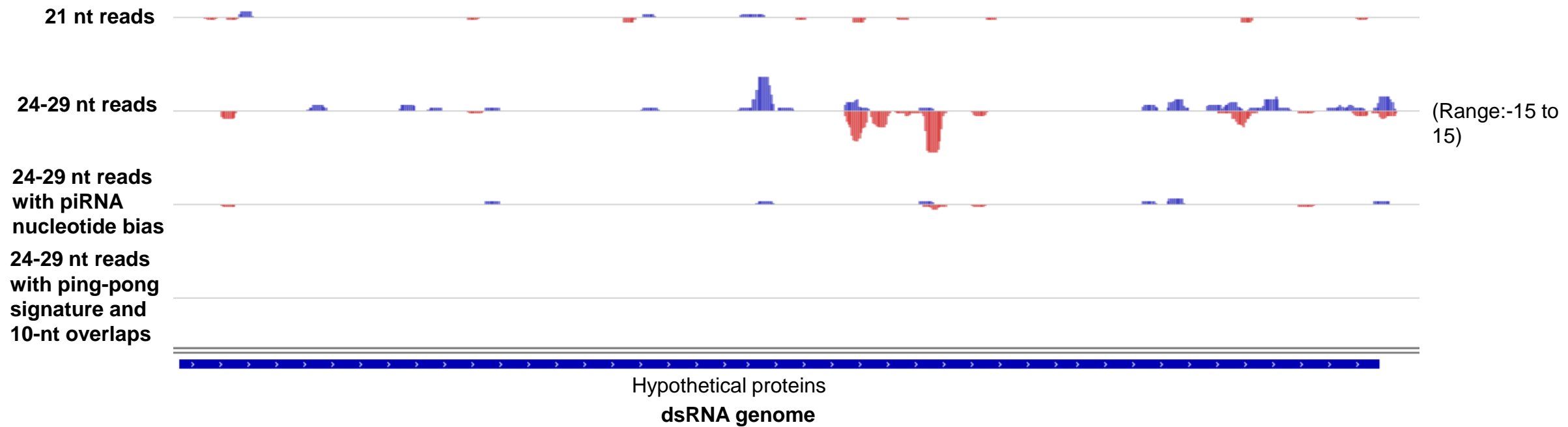
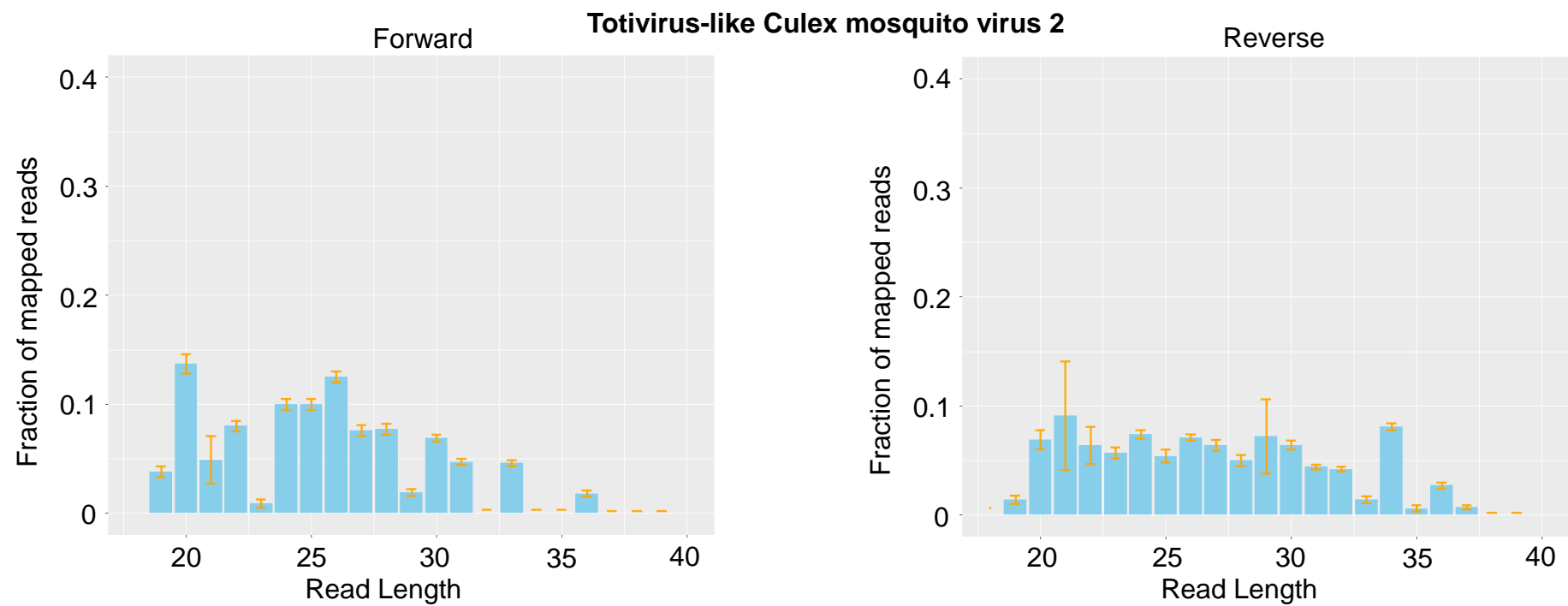
Negev virus isolate #730

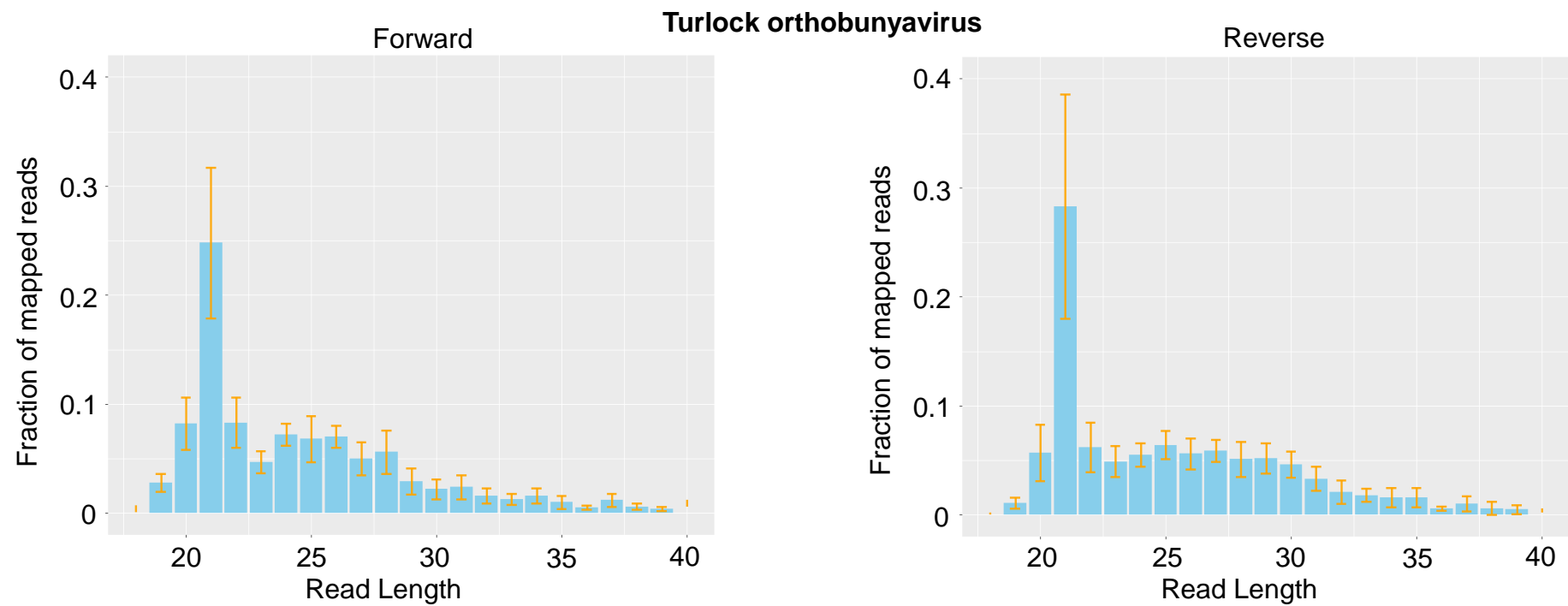




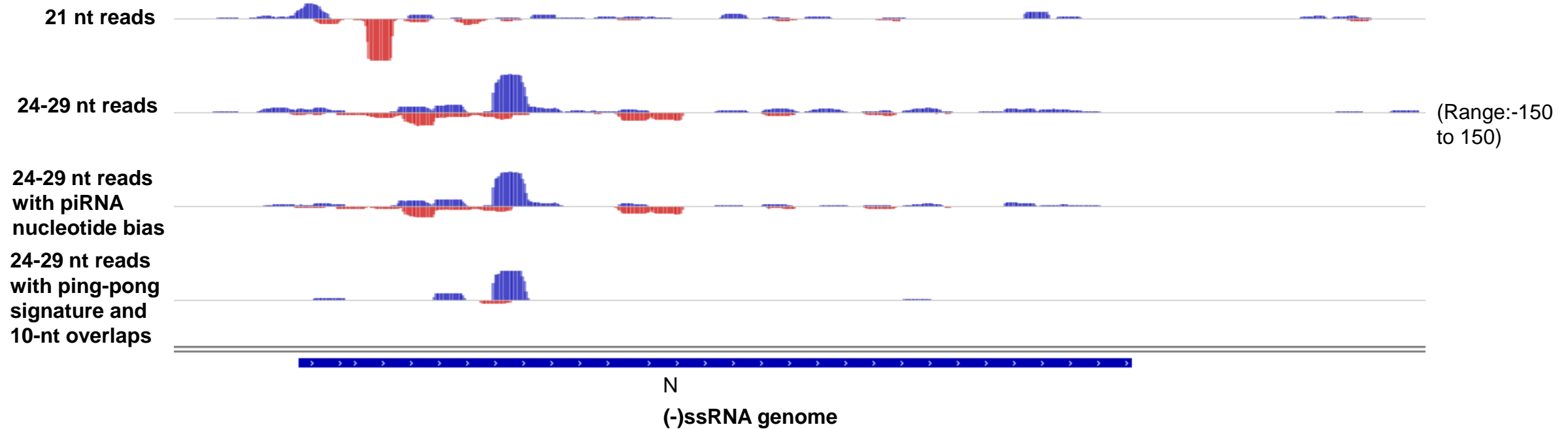


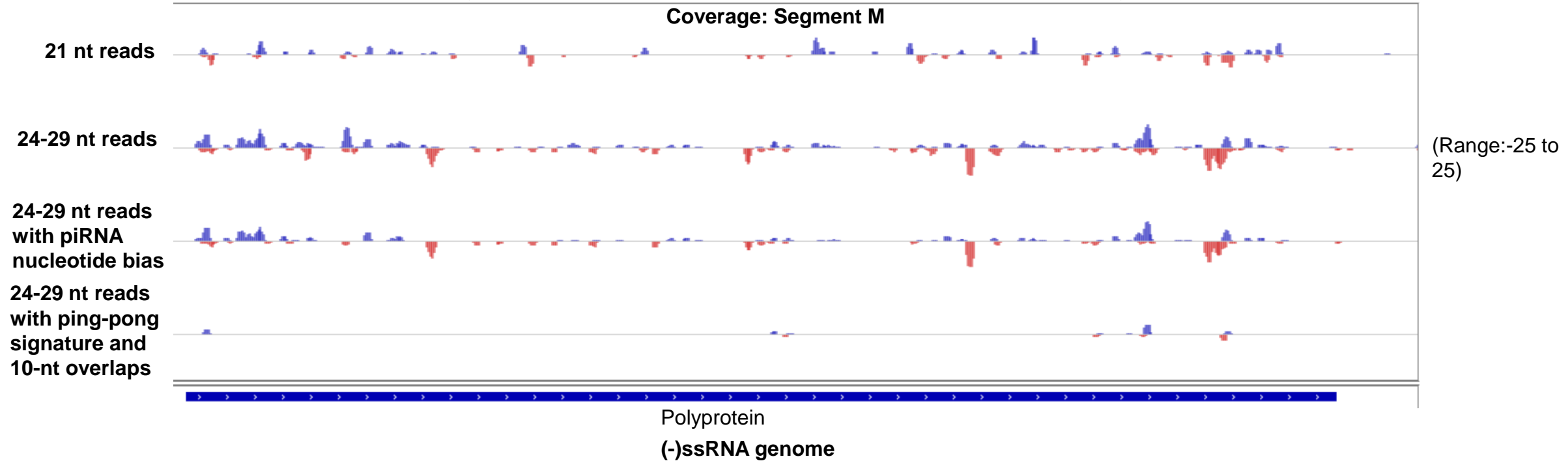
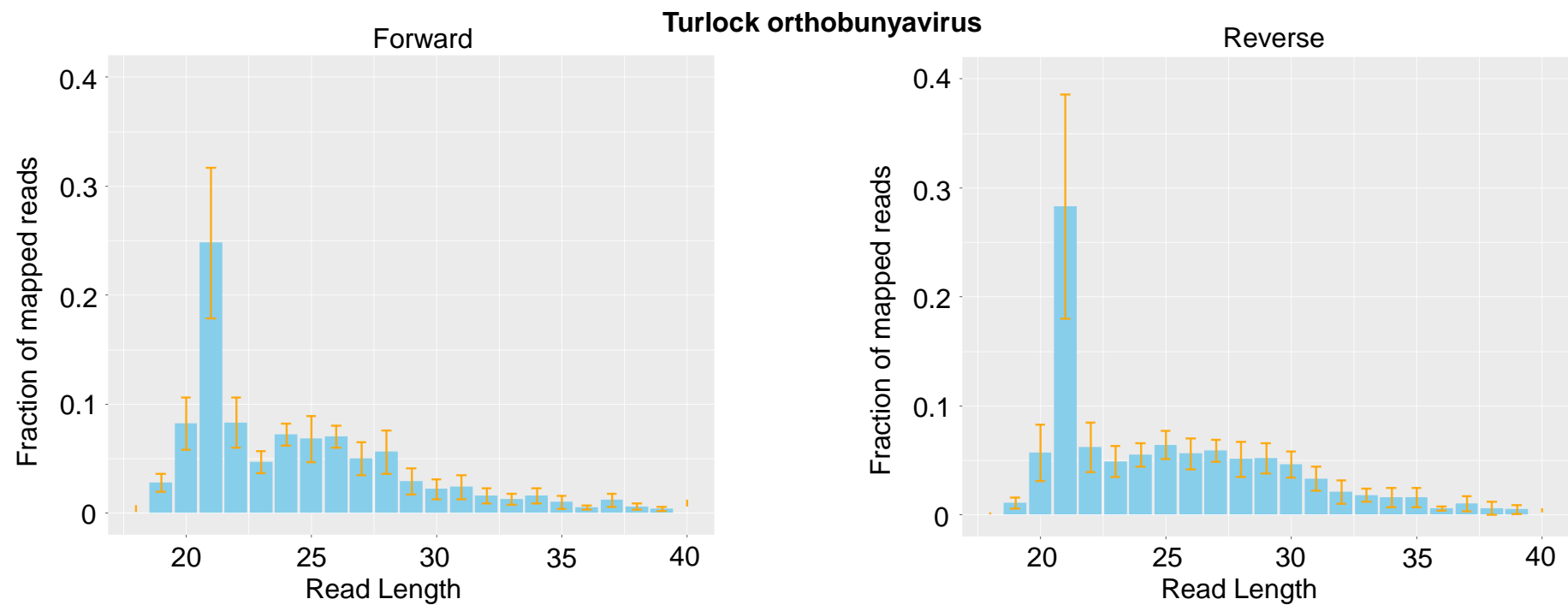


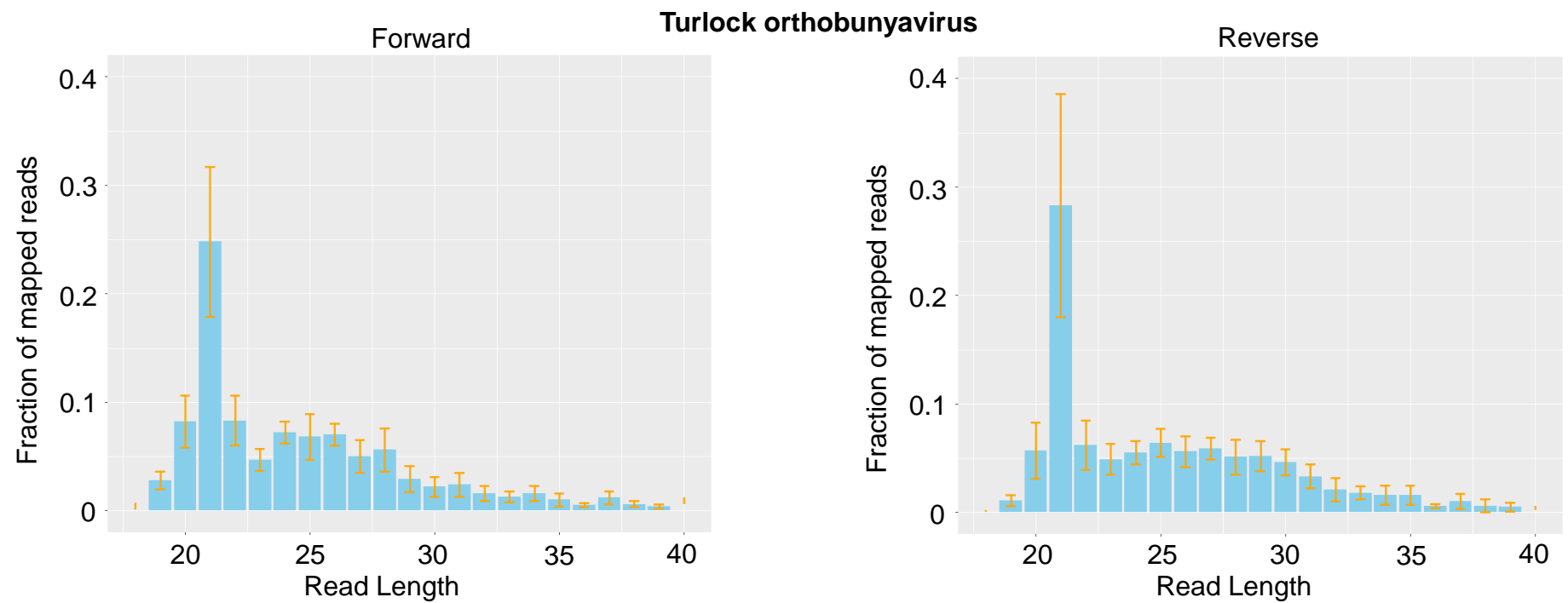




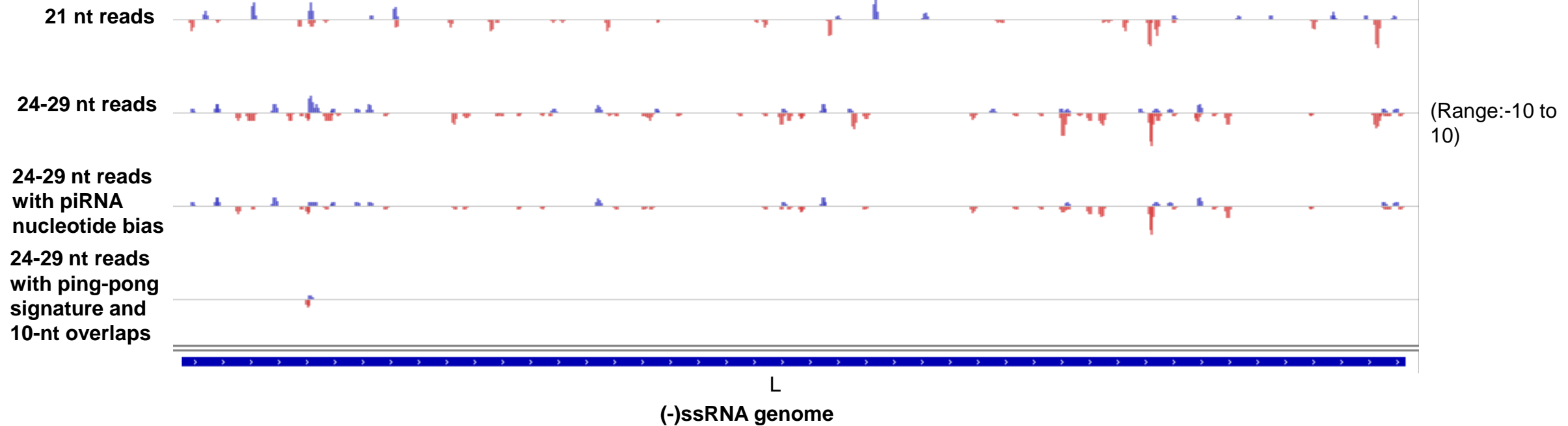
Coverage: Segment S

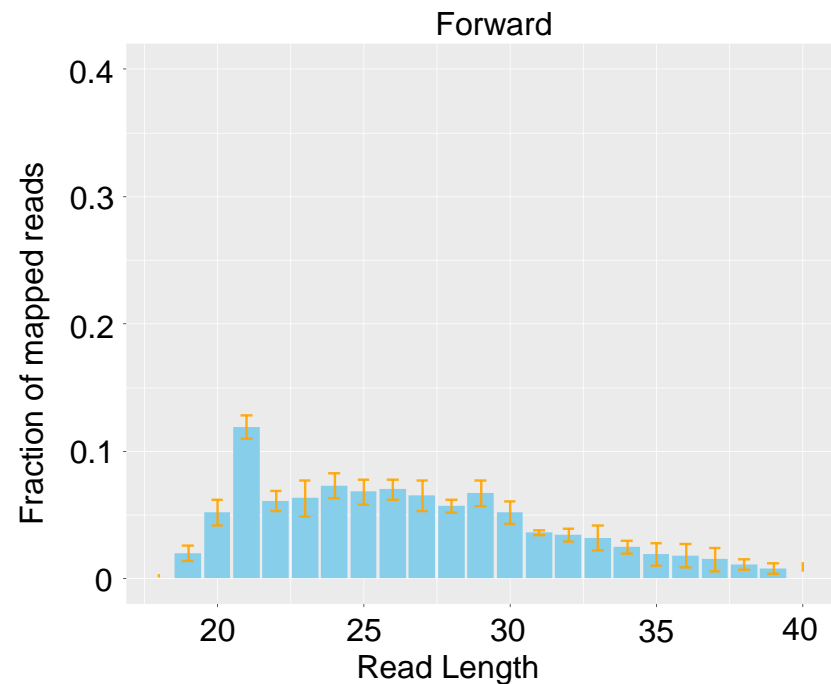




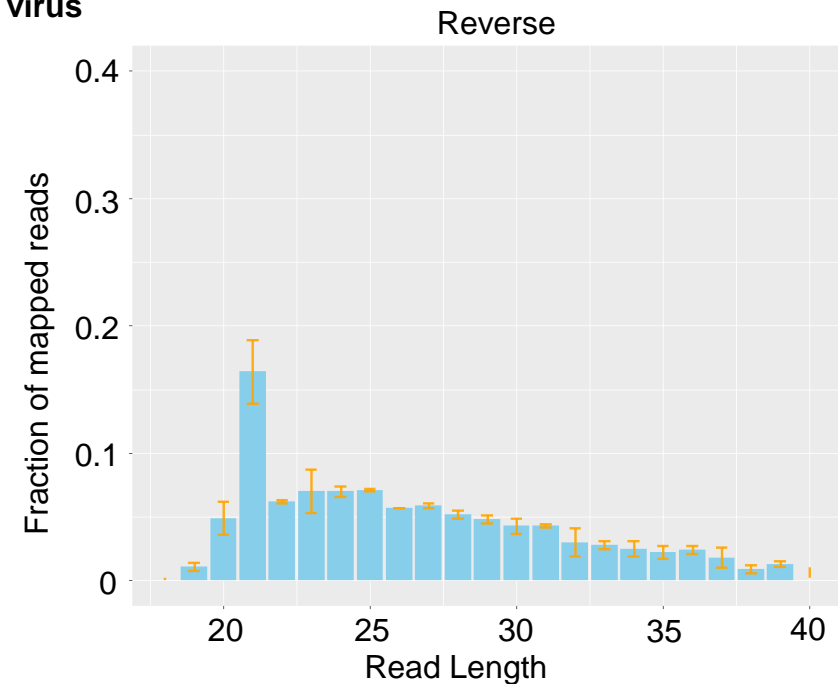


Coverage: Segment L

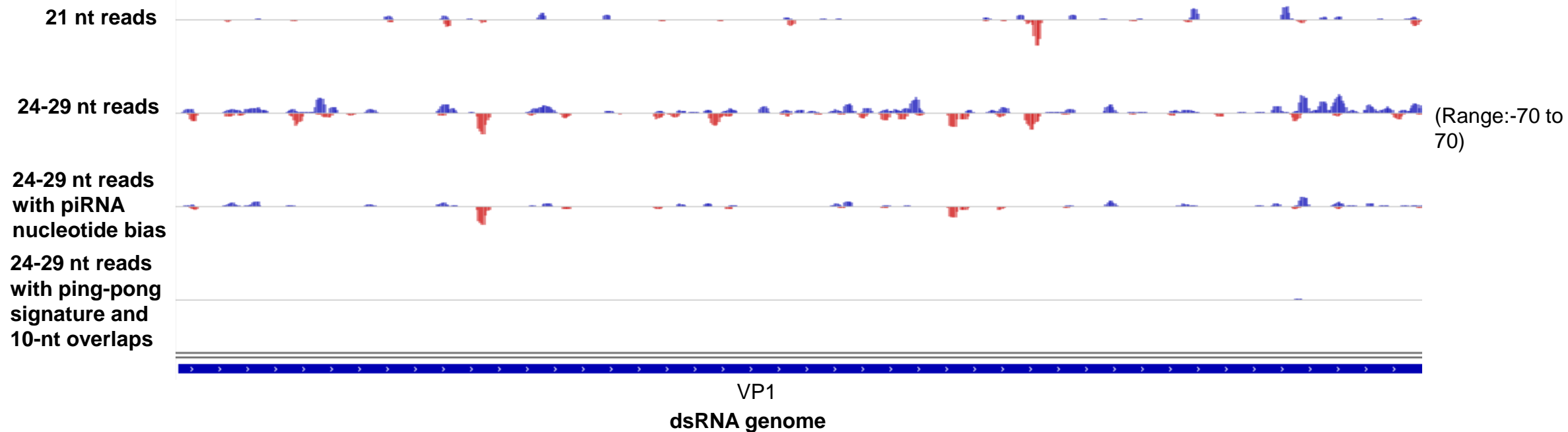


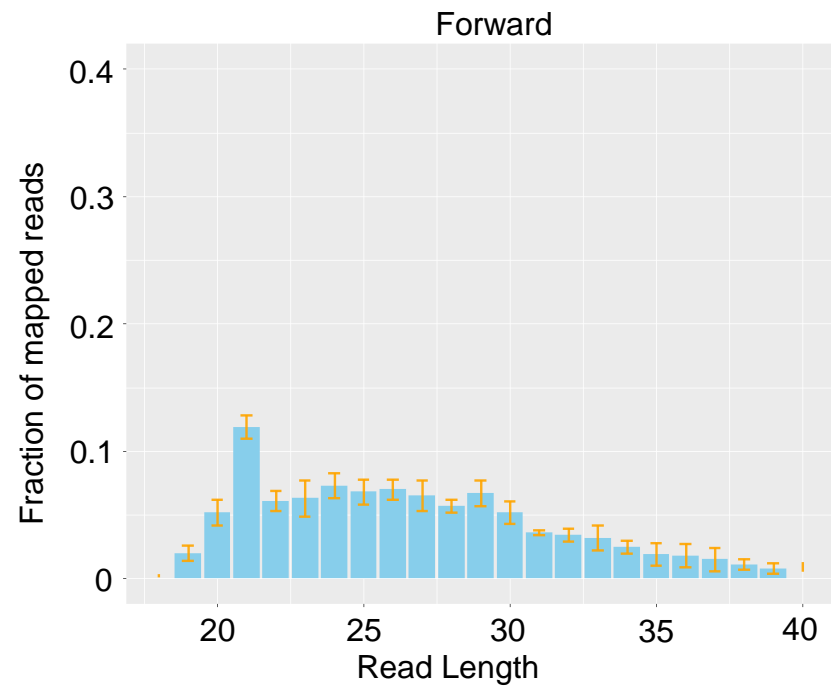


Umatilla virus

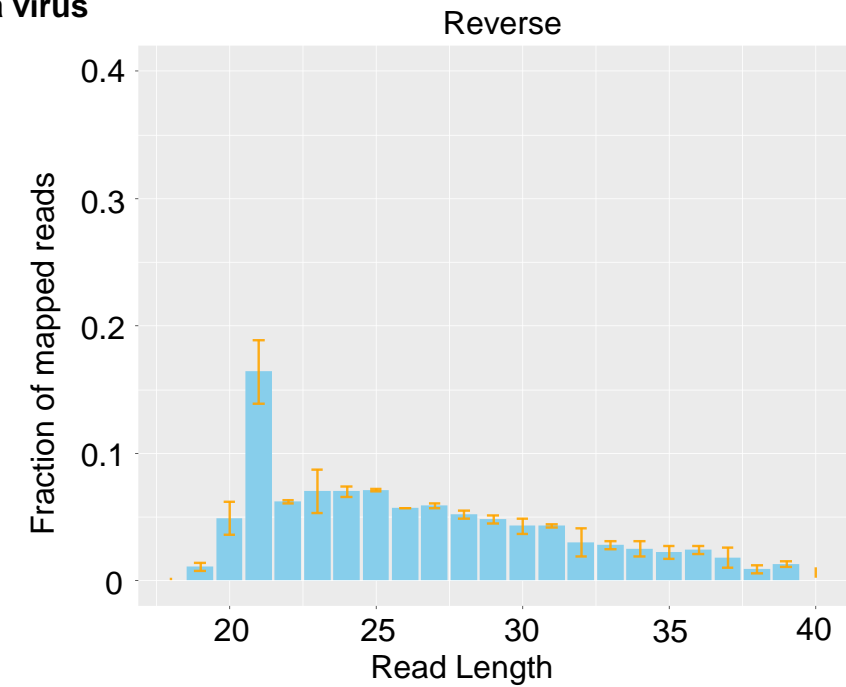


Coverage: Segment VP1

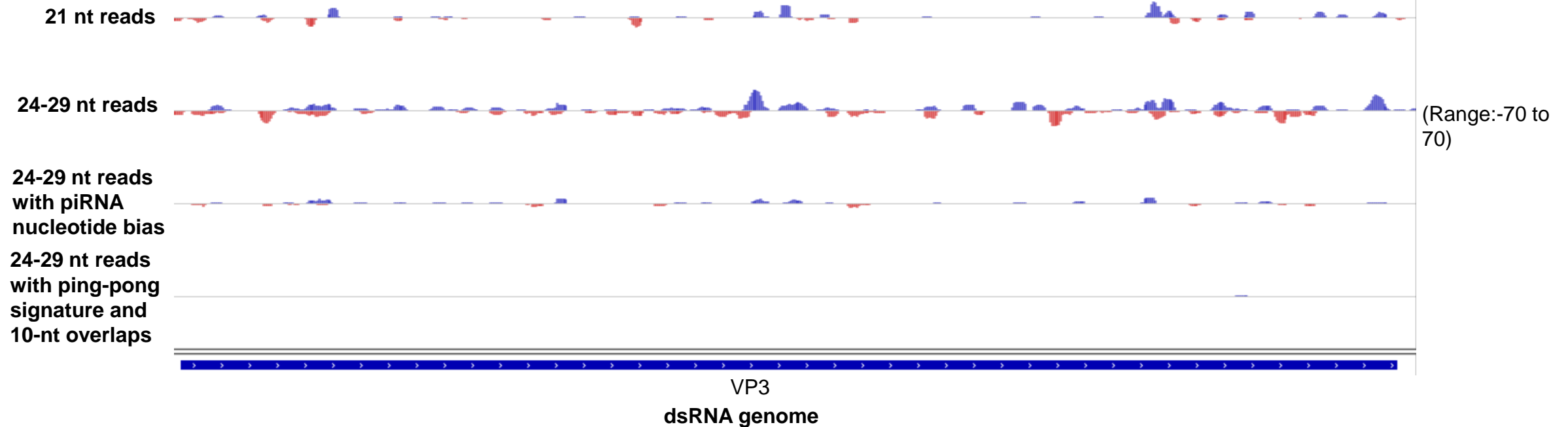


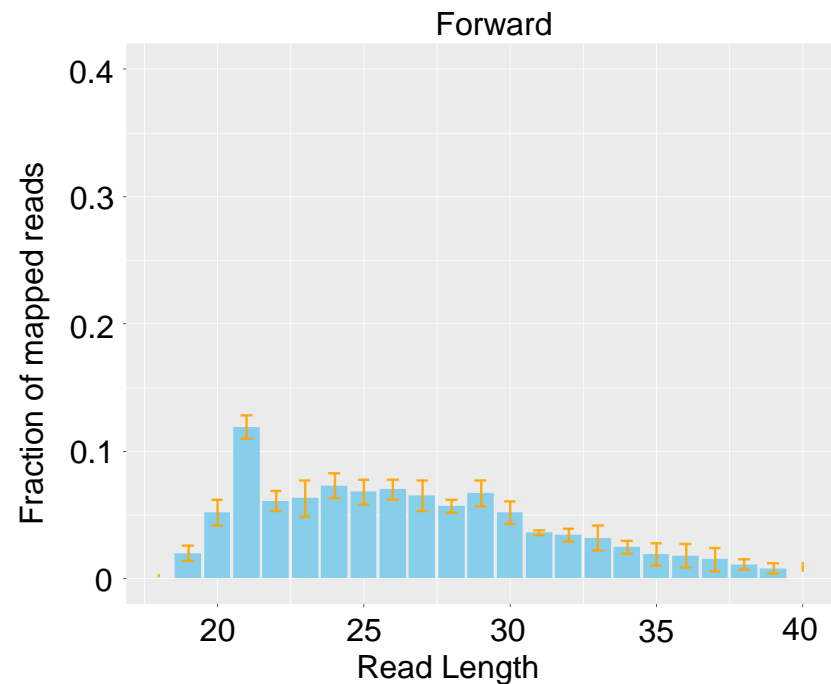


Umatilla virus

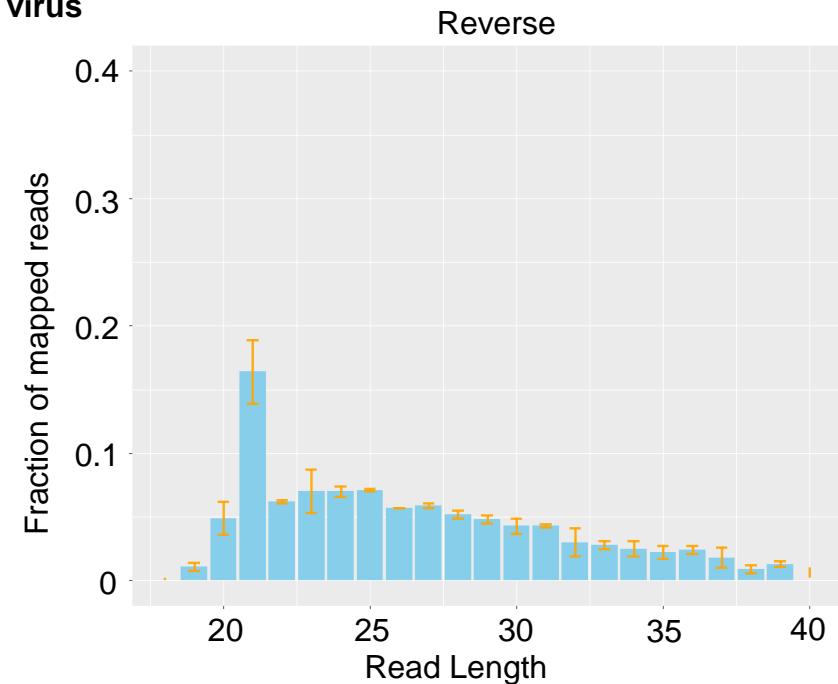


Coverage: Segment VP3

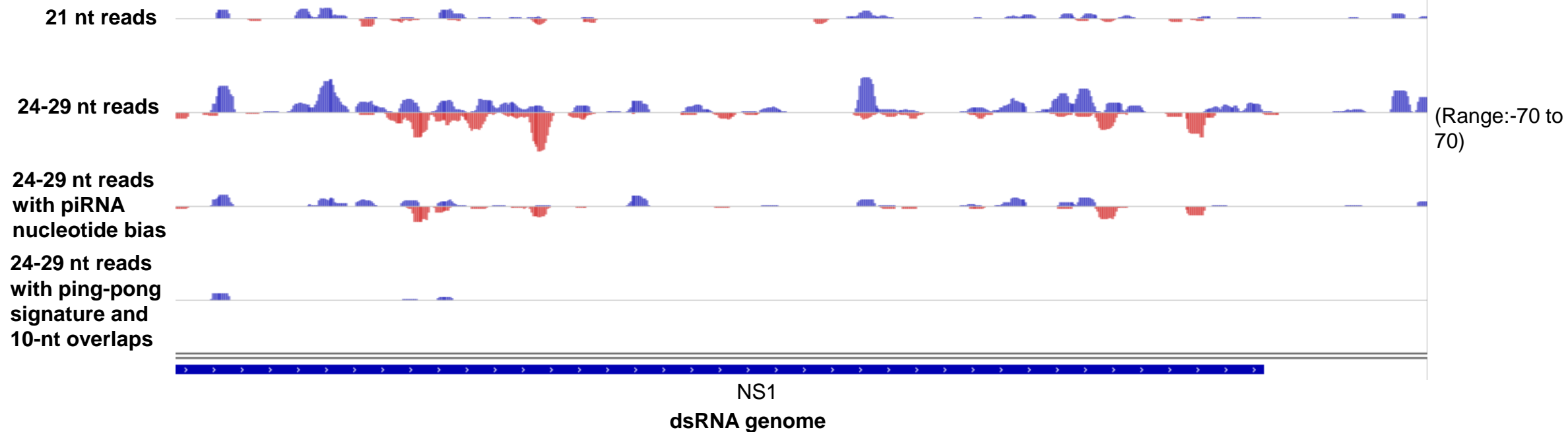


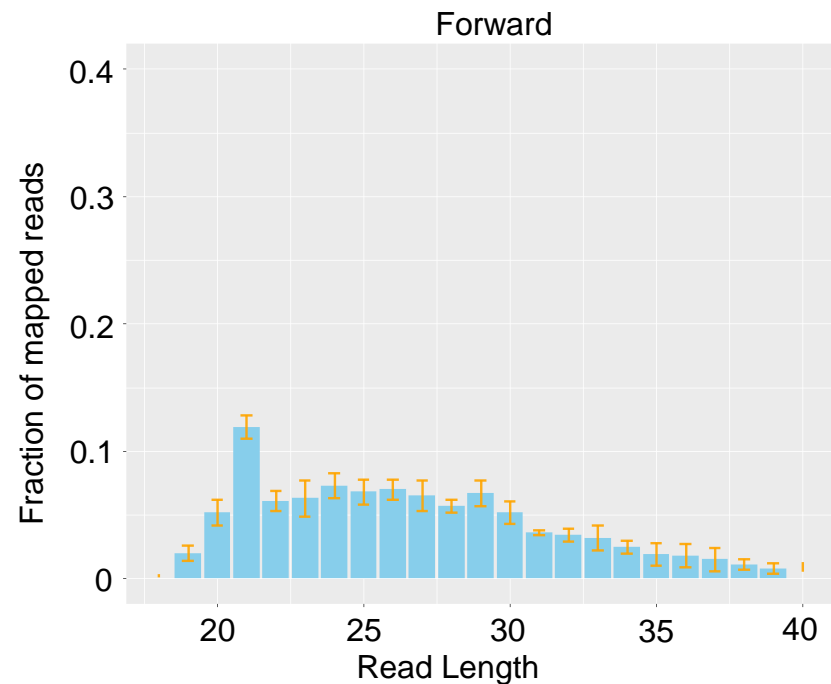


Umatilla virus

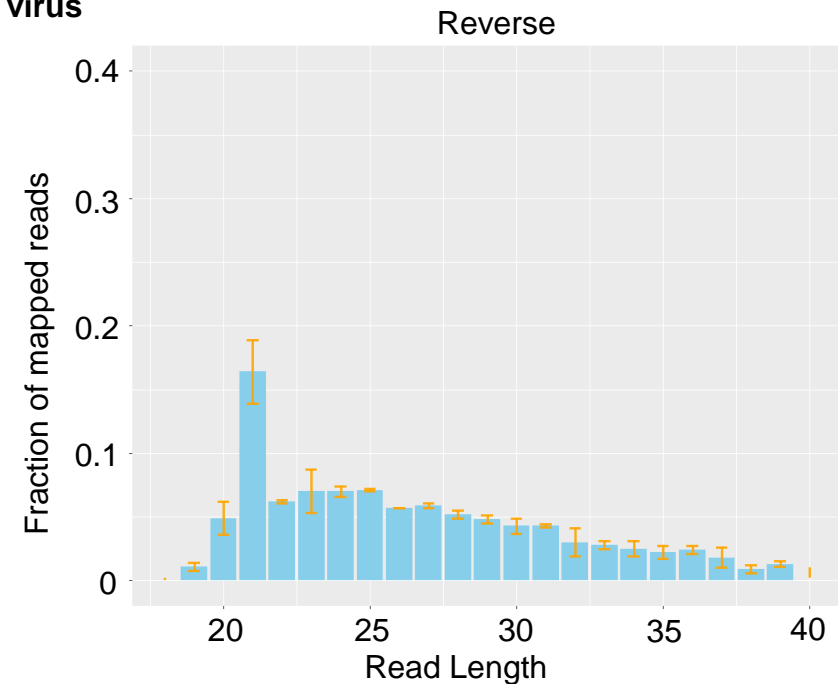


Coverage: Segment NS1

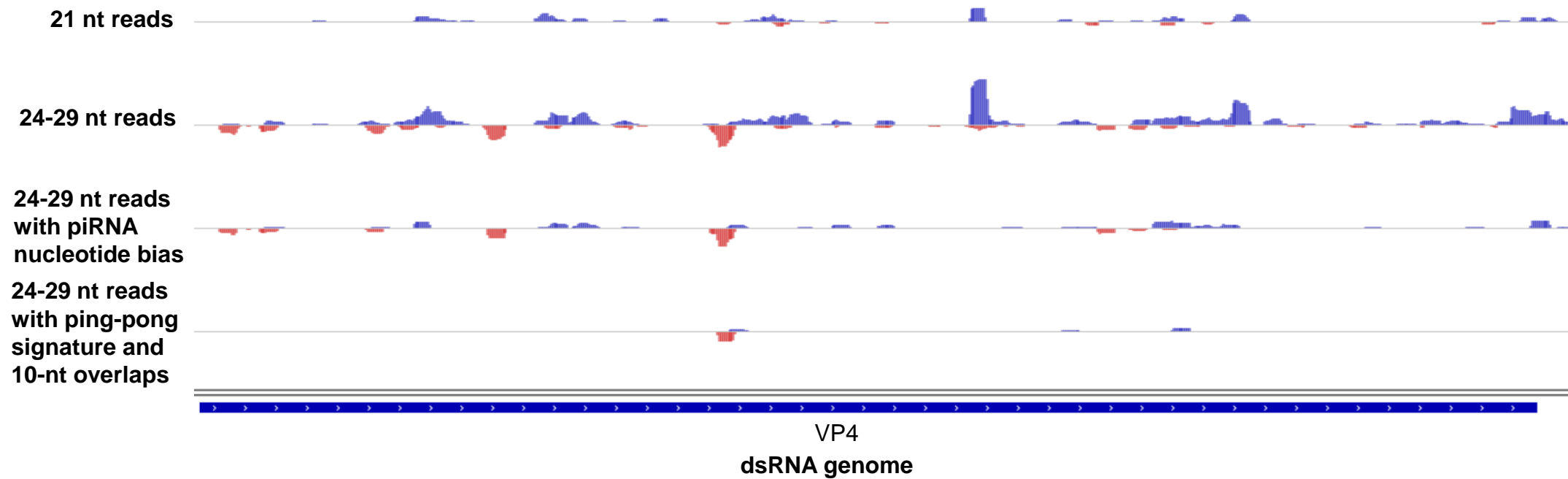


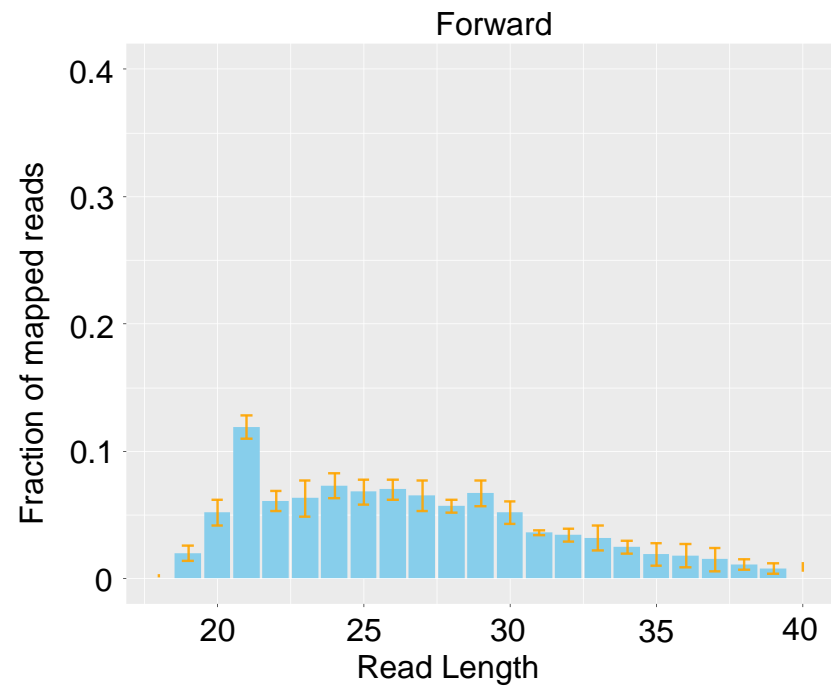


Umatilla virus

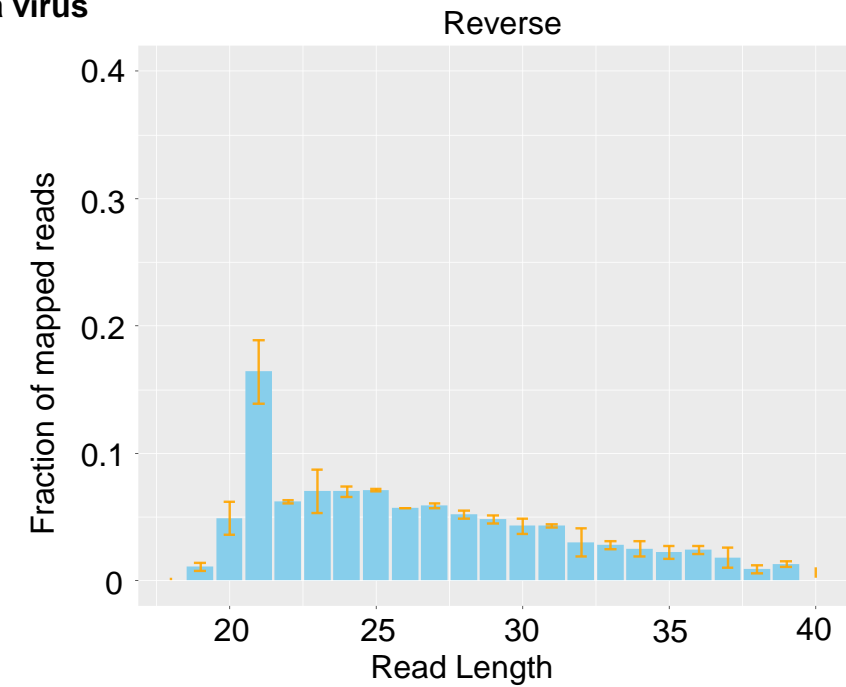


Coverage: Segment VP4

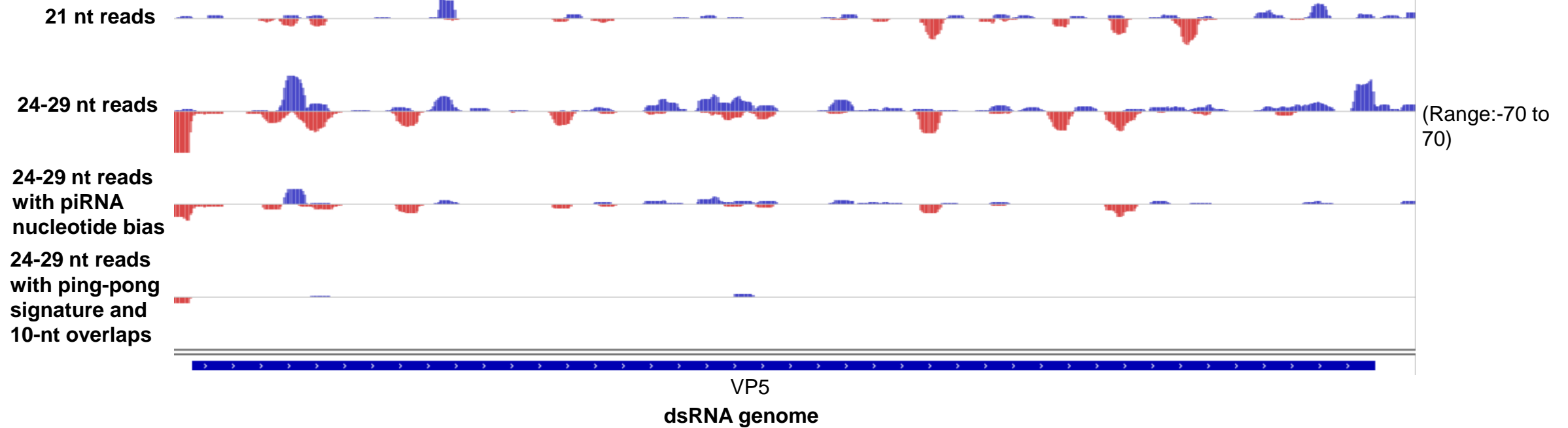


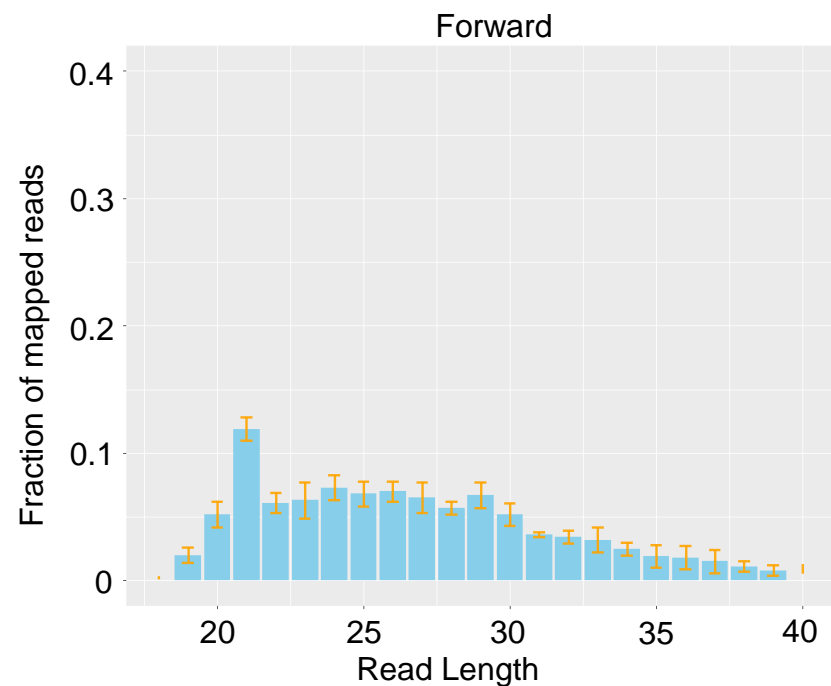


Umatilla virus

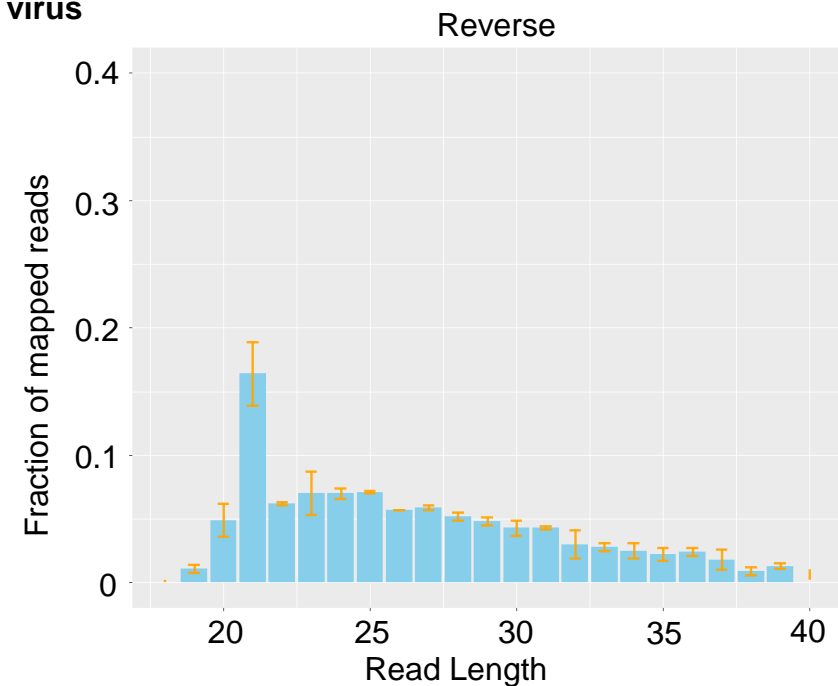


Coverage: Segment VP5

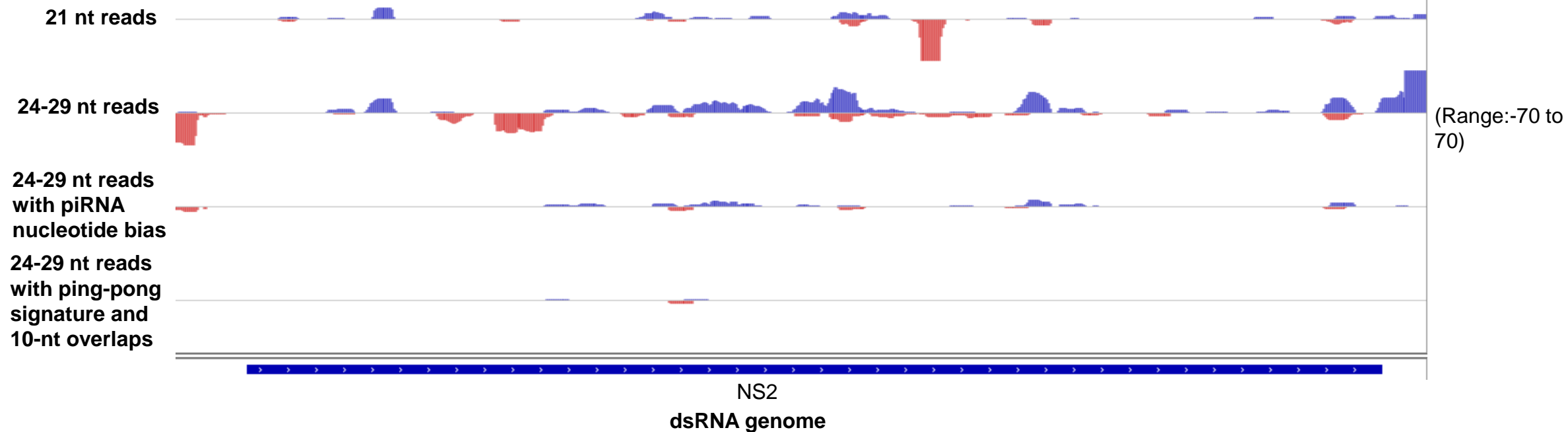


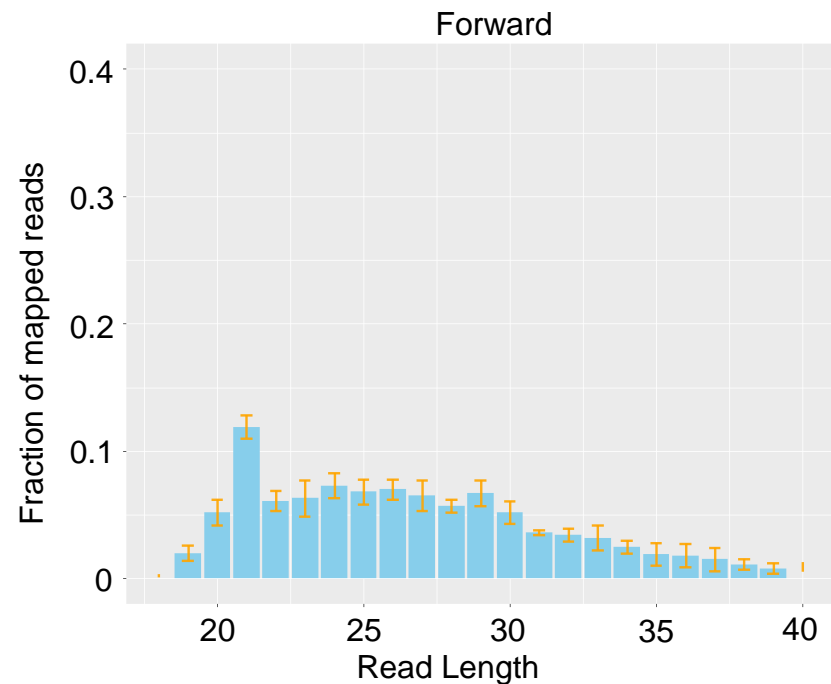


Umatilla virus

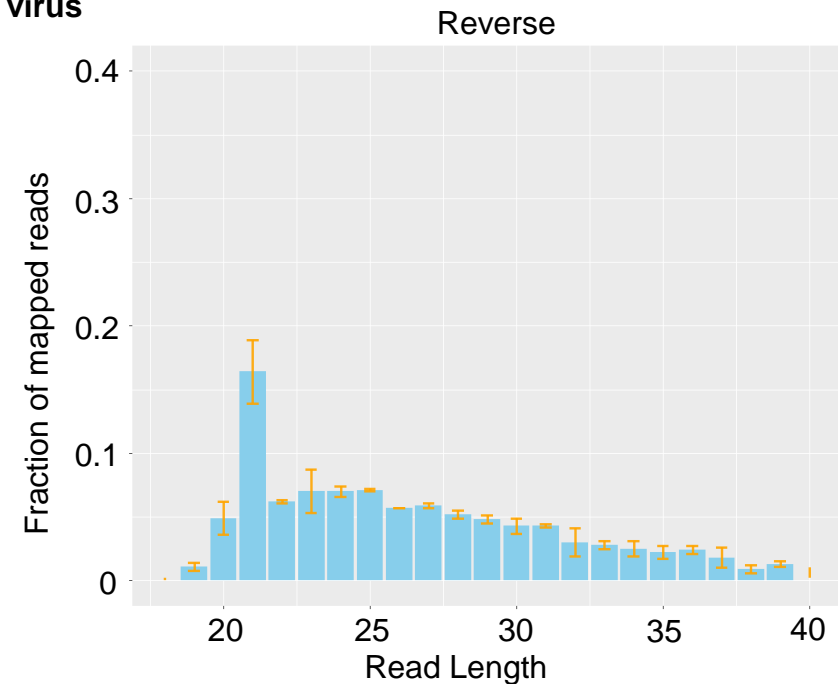


Coverage: Segment NS2

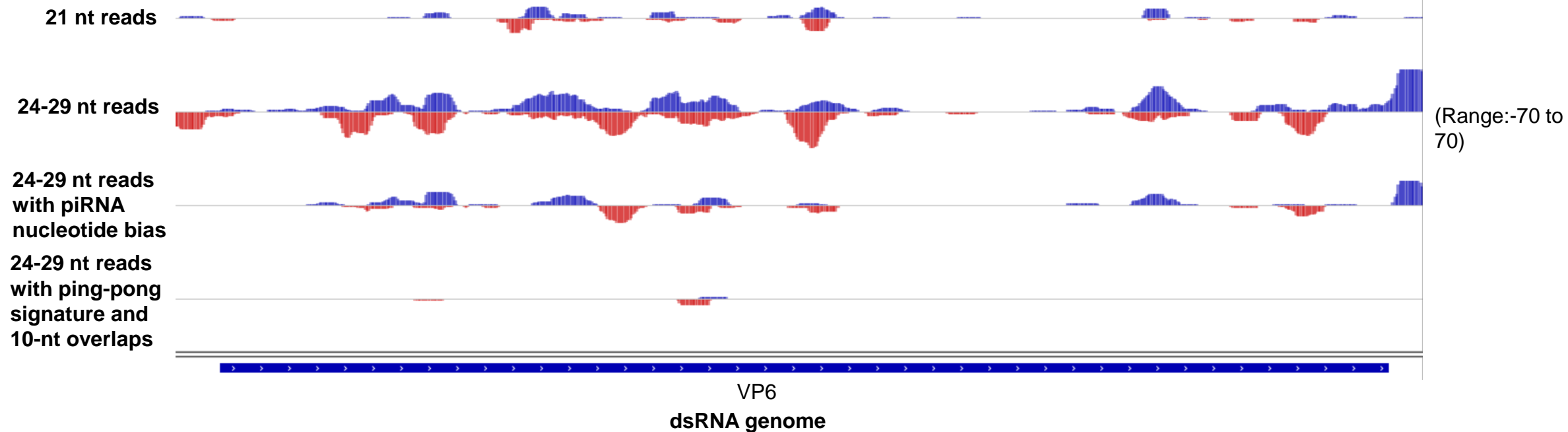


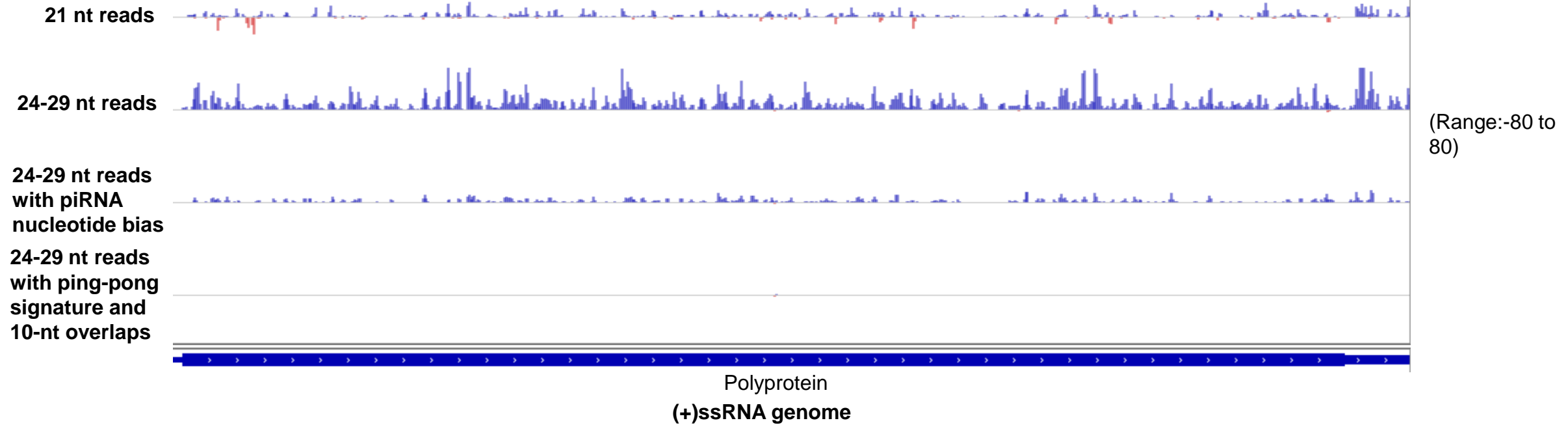
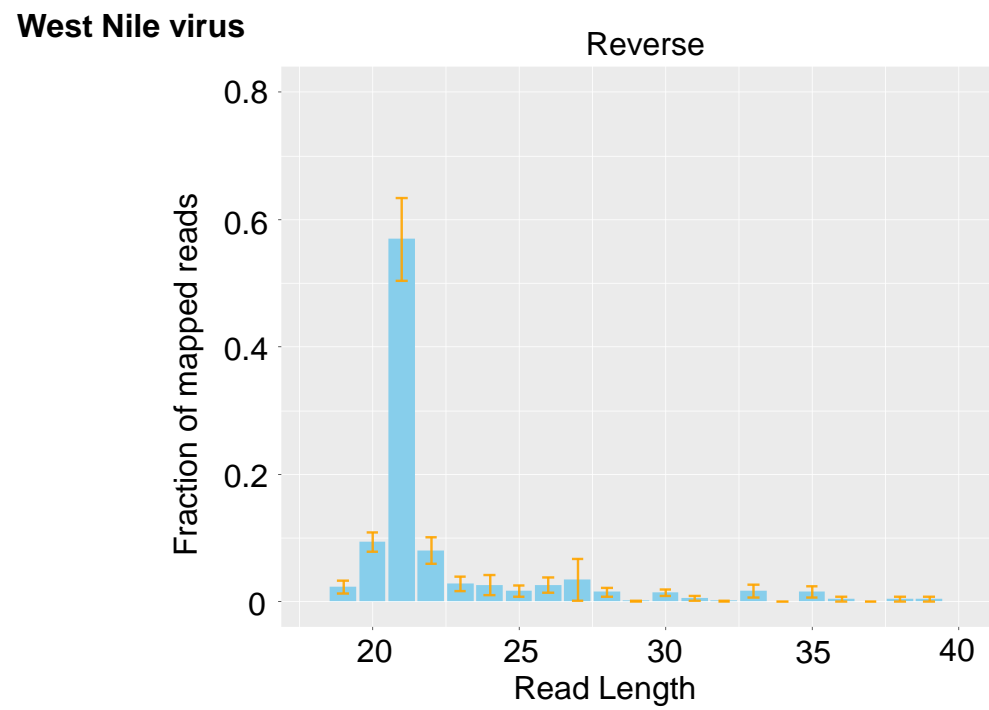
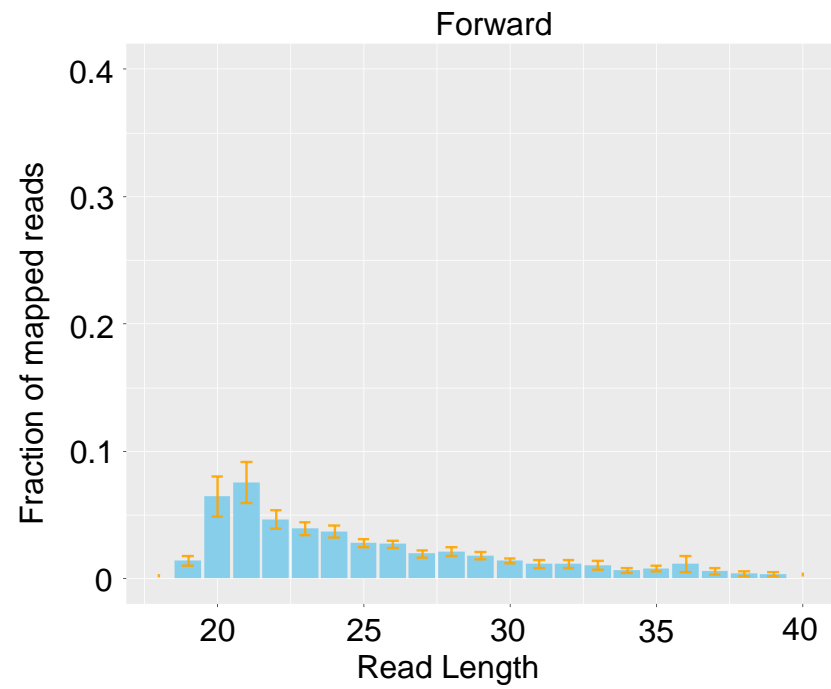


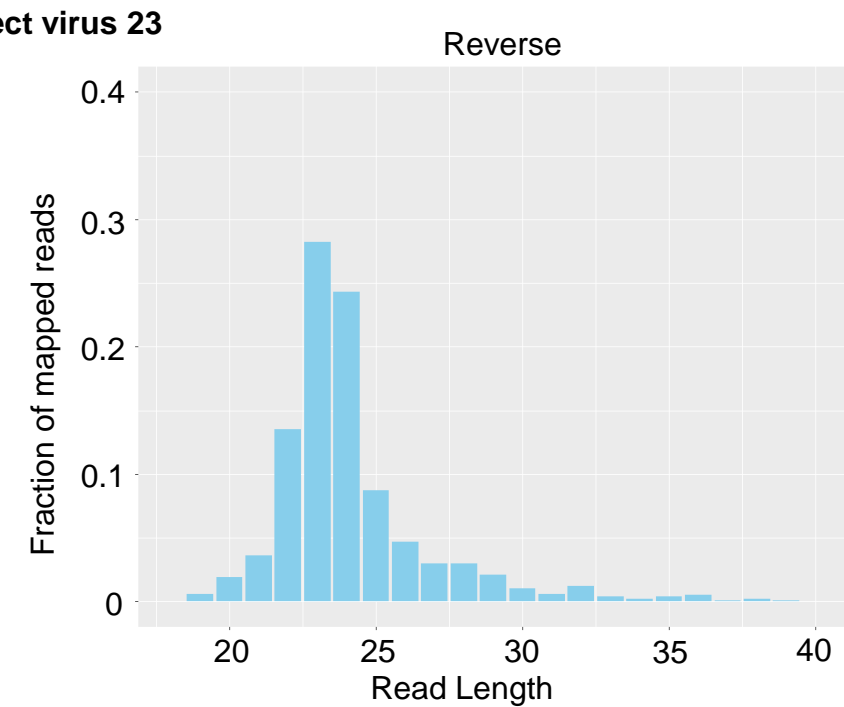
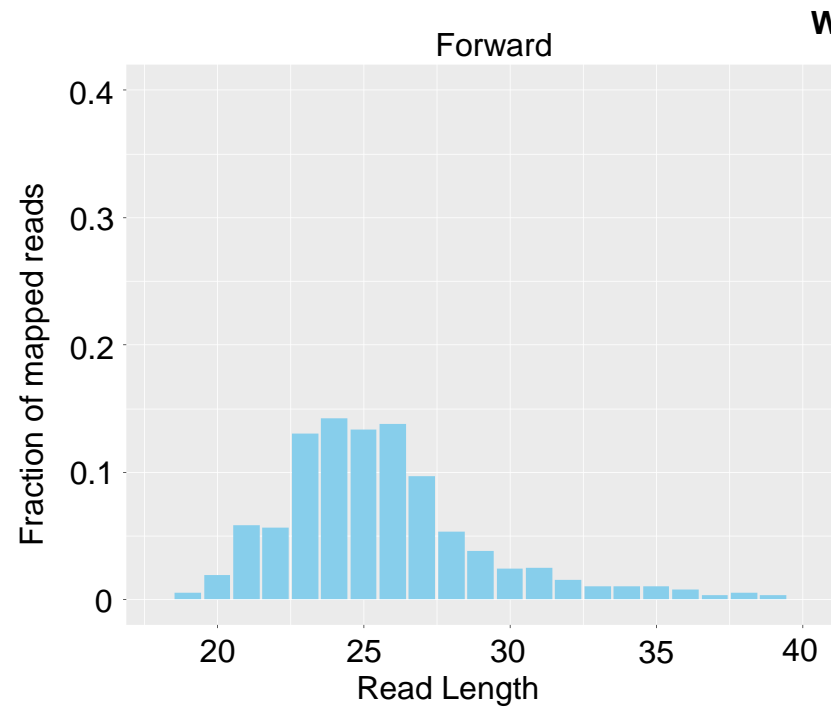
Umatilla virus



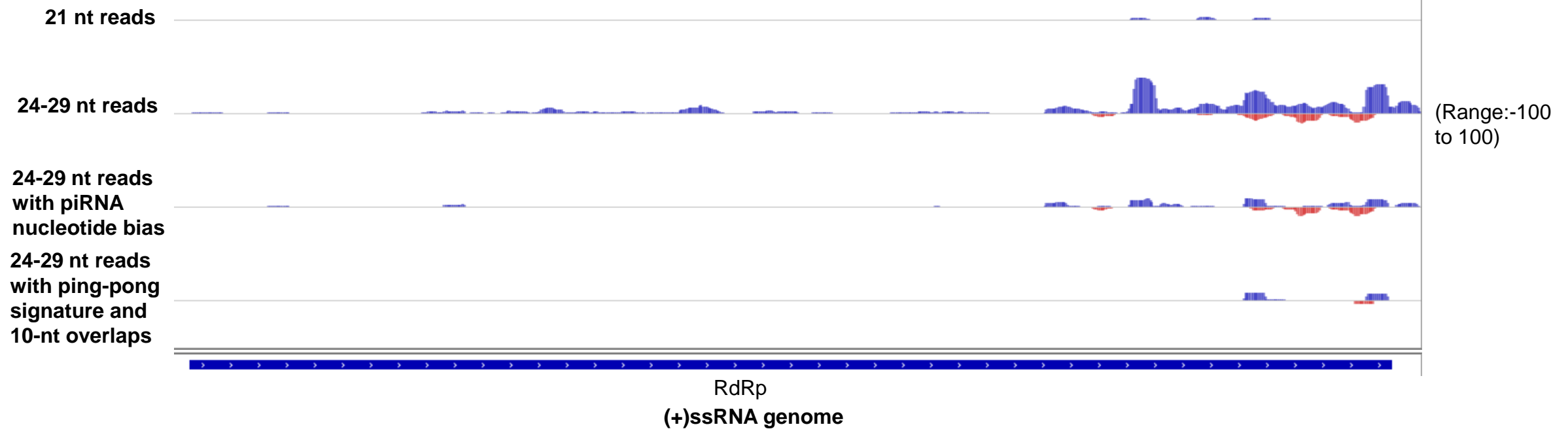
Coverage: Segment VP6

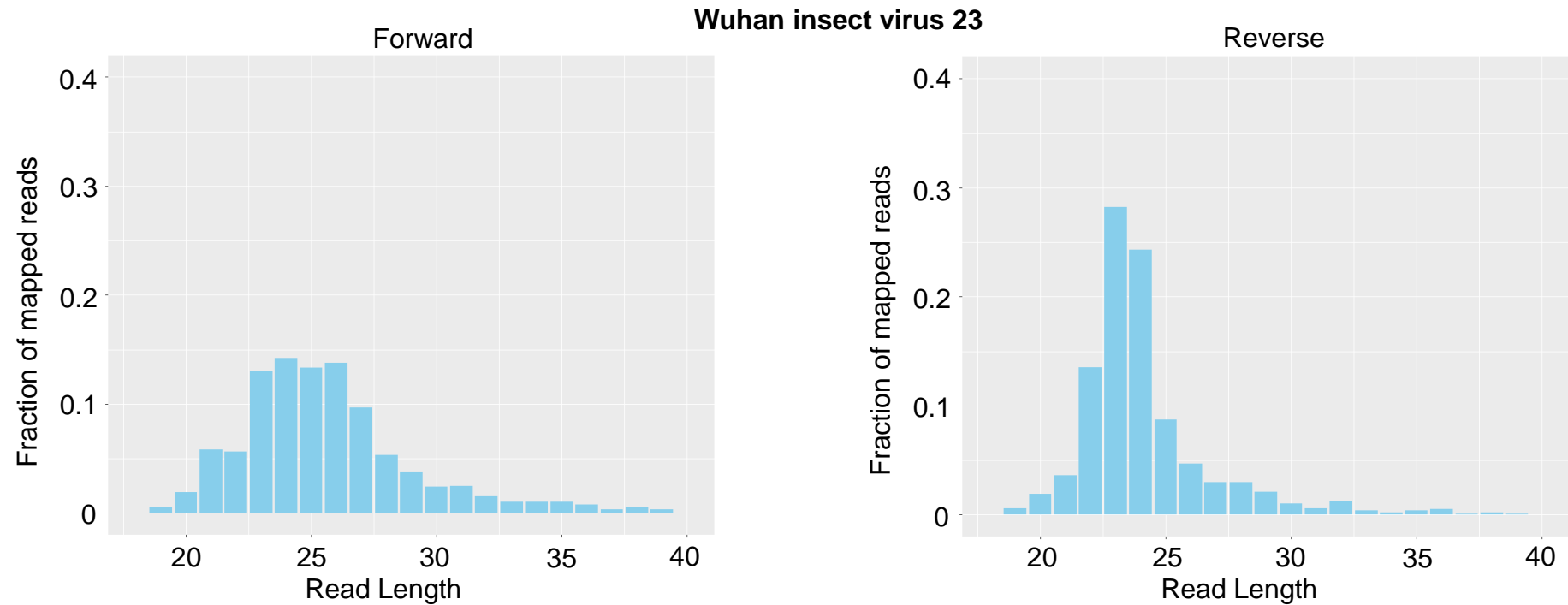




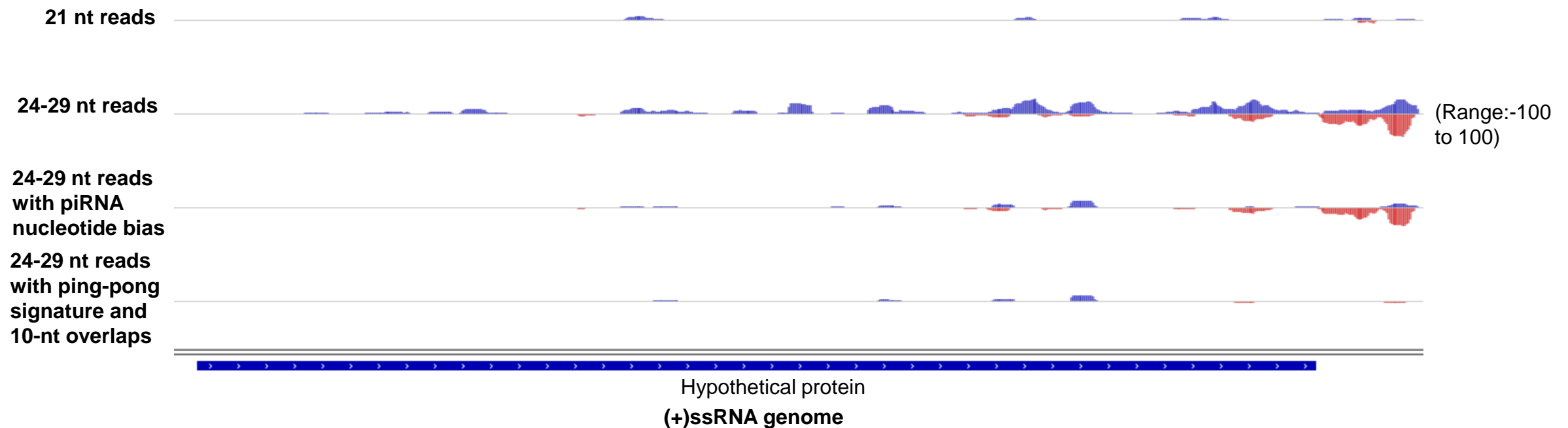


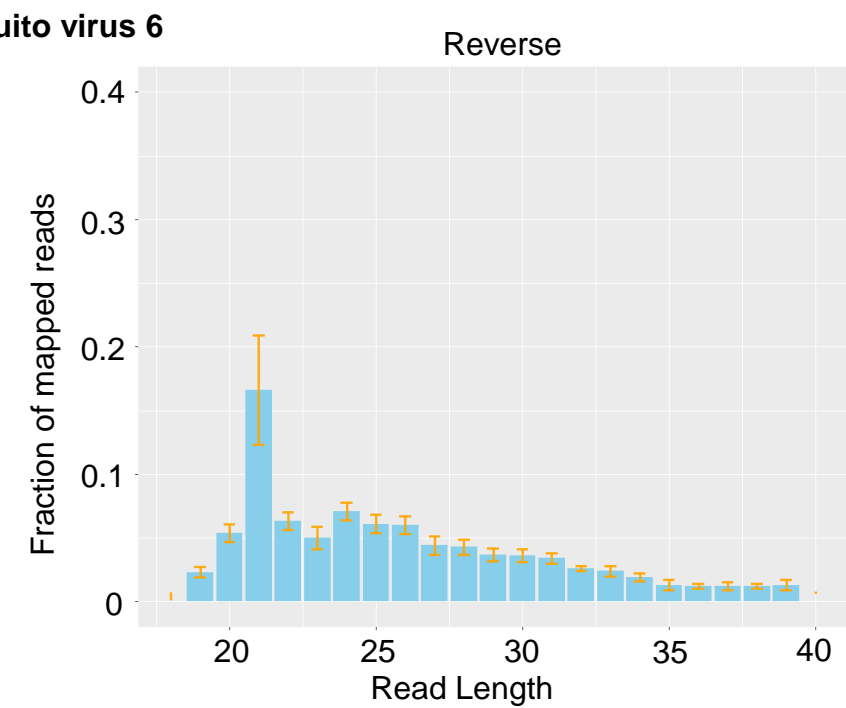
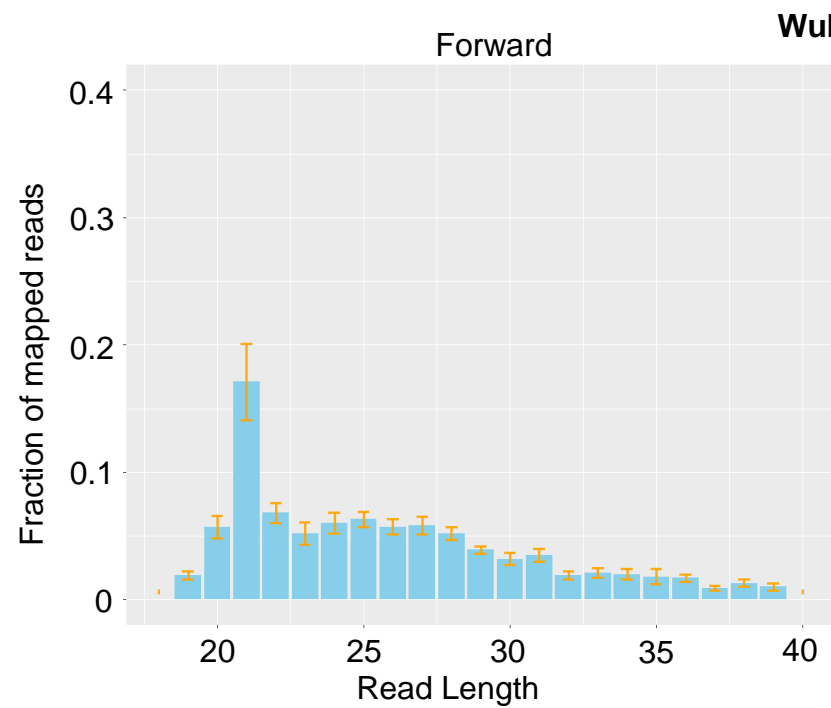
Coverage: Segment 1





Coverage: Segment 2





Coverage: Segment 1

21 nt reads

24-29 nt reads

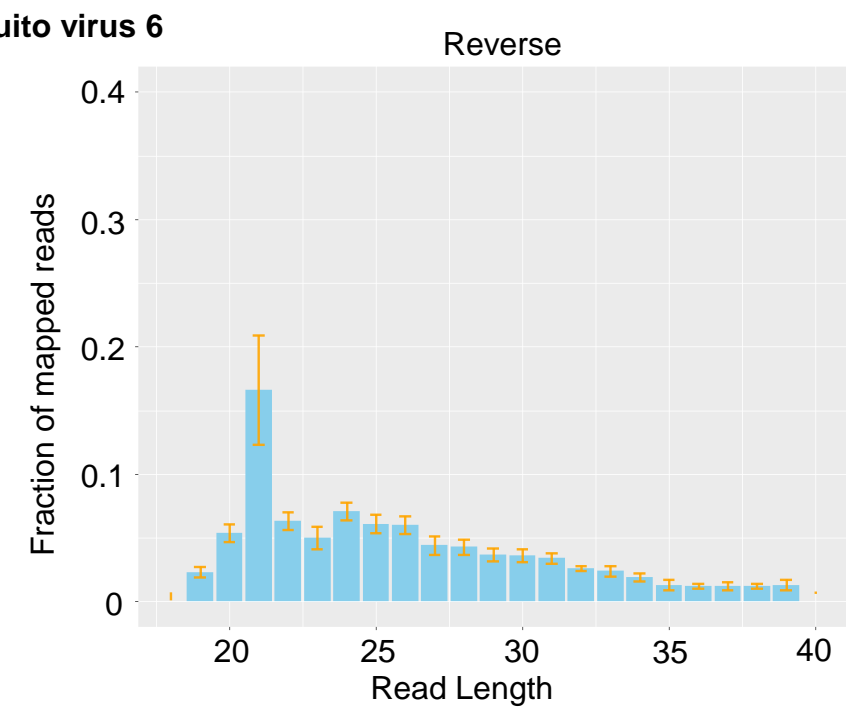
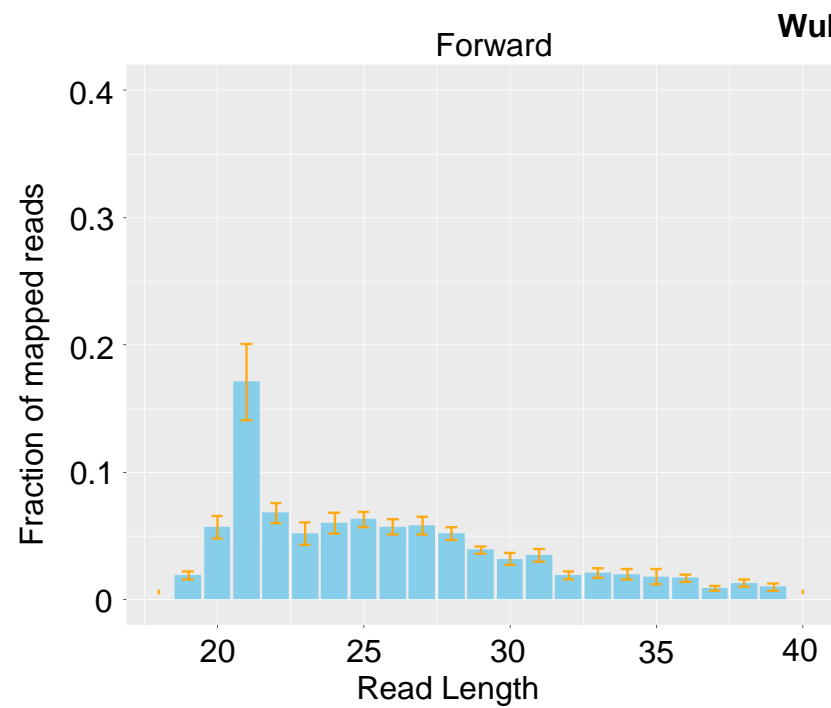
24-29 nt reads
with piRNA
nucleotide bias

24-29 nt reads
with ping-pong
signature and
10-nt overlaps

(Range:-300
to 300)

PB2

(-)ssRNA genome



Coverage: Segment 2

21 nt reads

24-29 nt reads

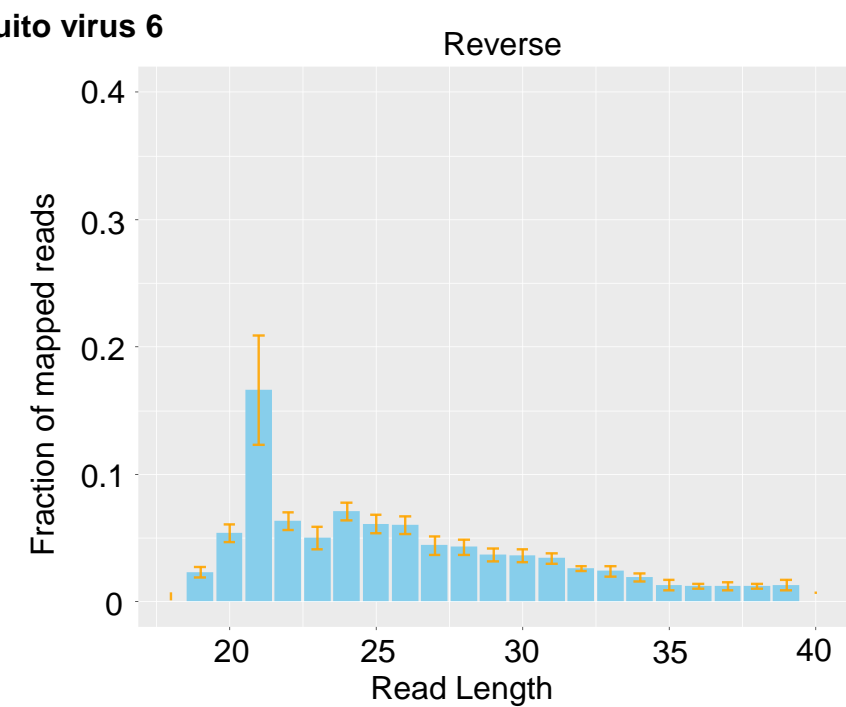
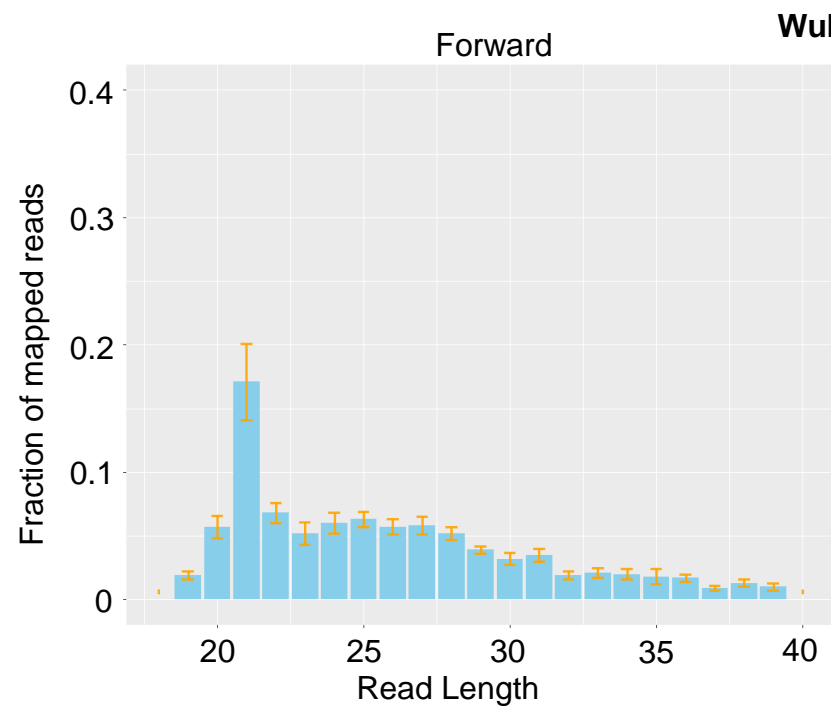
24-29 nt reads
with piRNA
nucleotide bias

24-29 nt reads
with ping-pong
signature and
10-nt overlaps

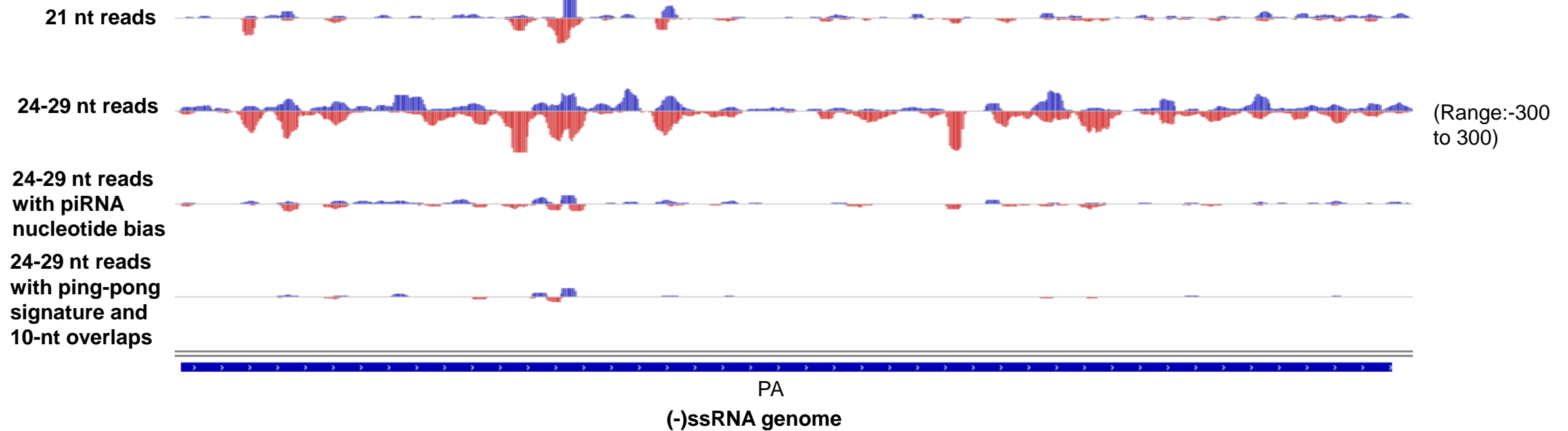
(Range:-300
to 300)

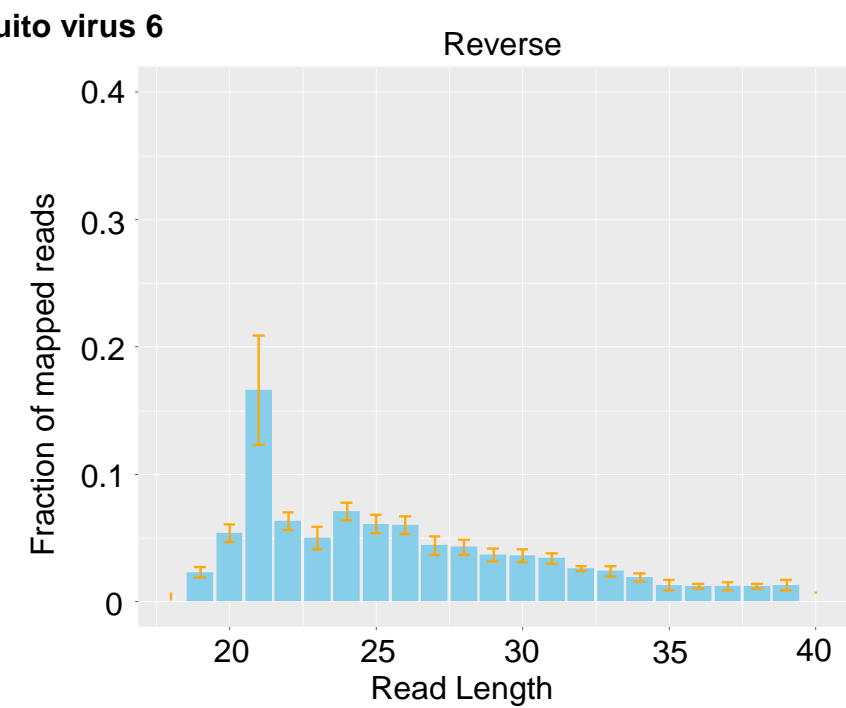
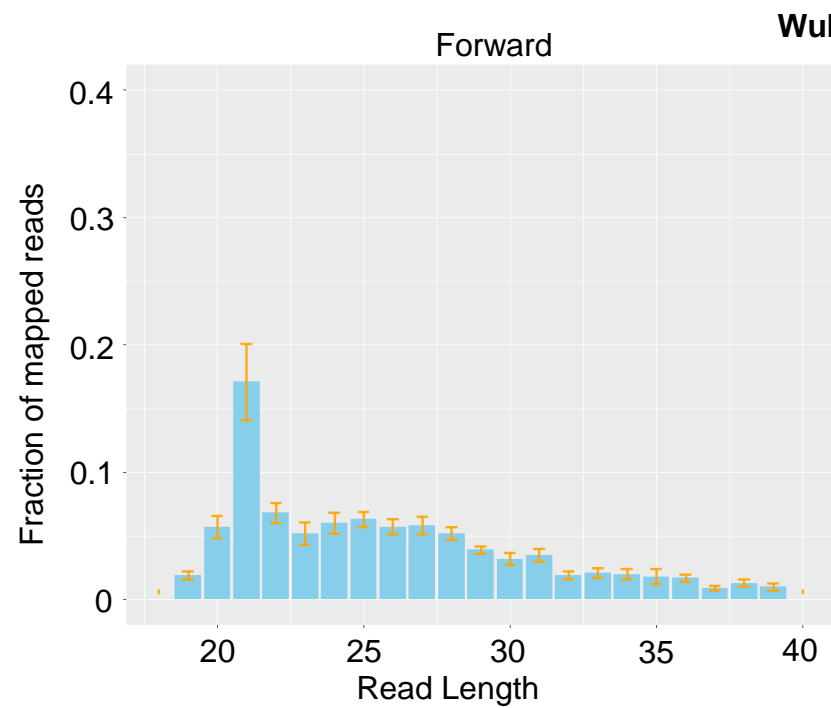
PB1

(-)ssRNA genome



Coverage: Segment 3





Coverage: Segment 4

21 nt reads

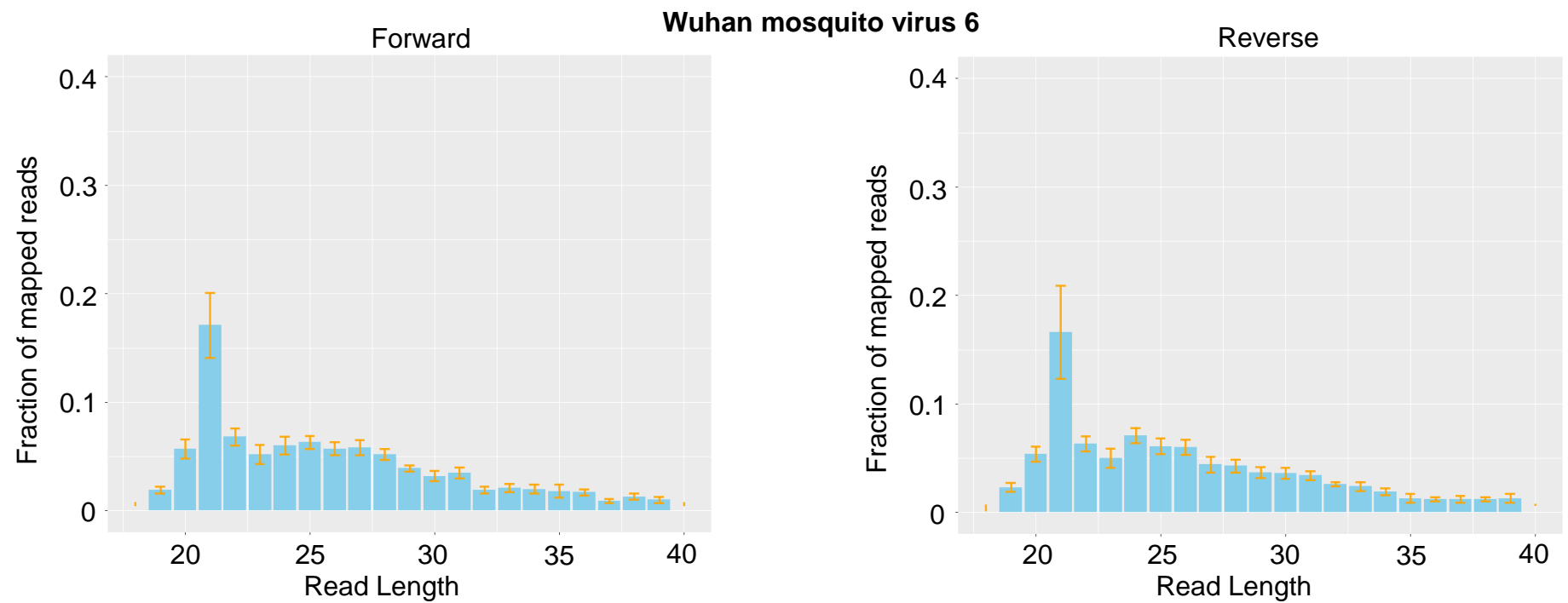
24-29 nt reads

24-29 nt reads
with piRNA
nucleotide bias

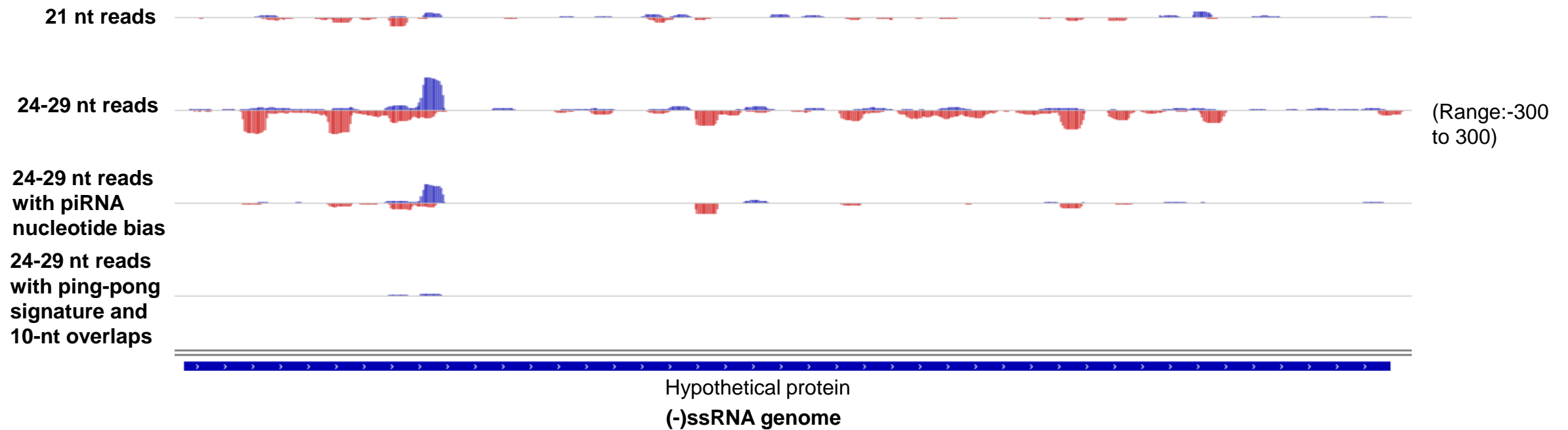
24-29 nt reads
with ping-pong
signature and
10-nt overlaps

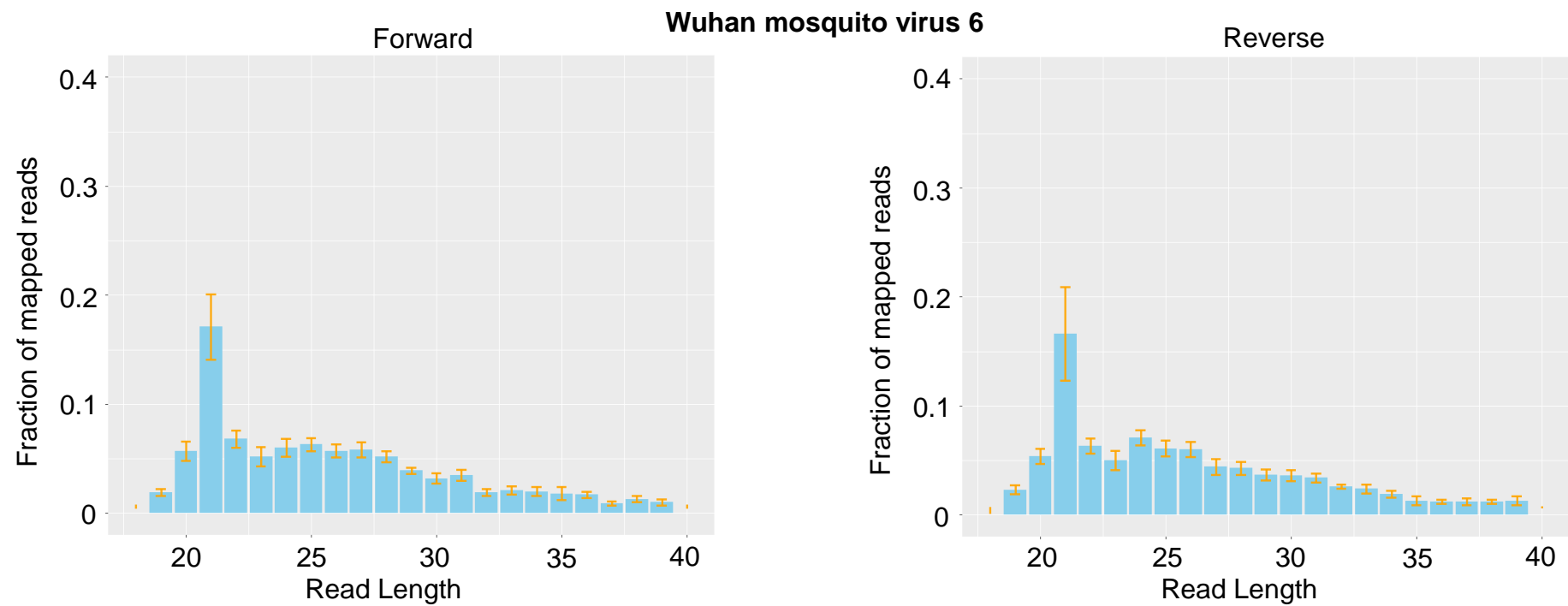
(Range:-300
to 300)

Nucleoprotein
(-)ssRNA genome

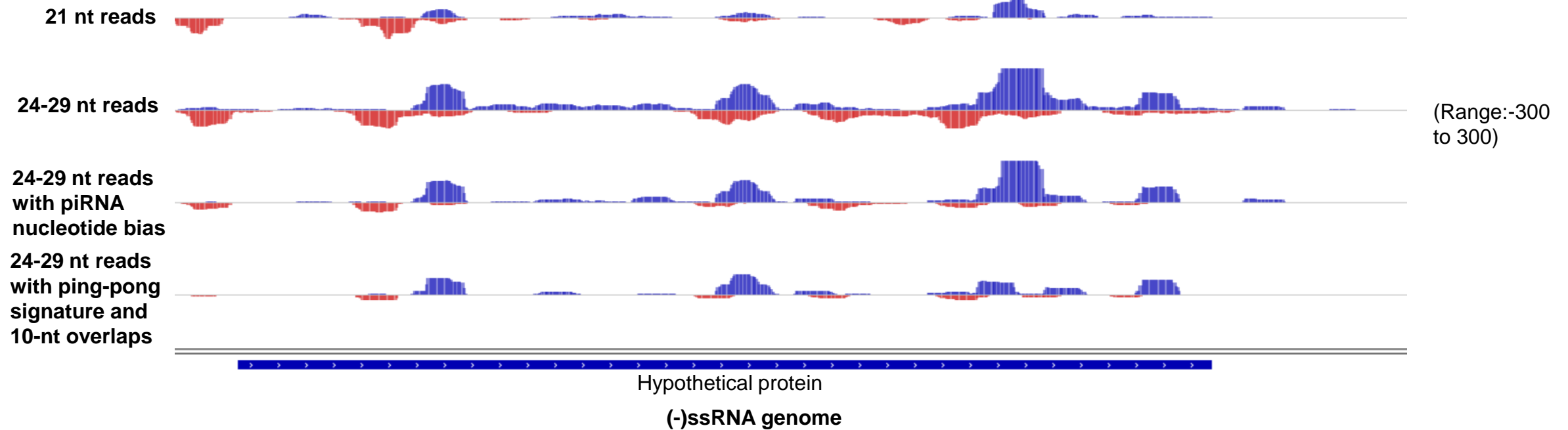


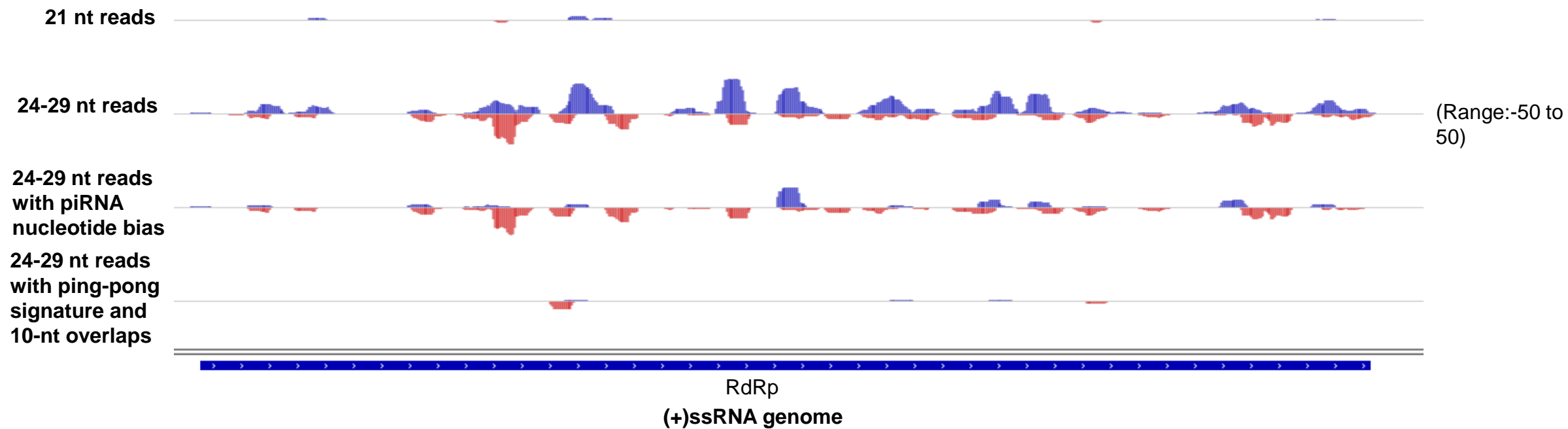
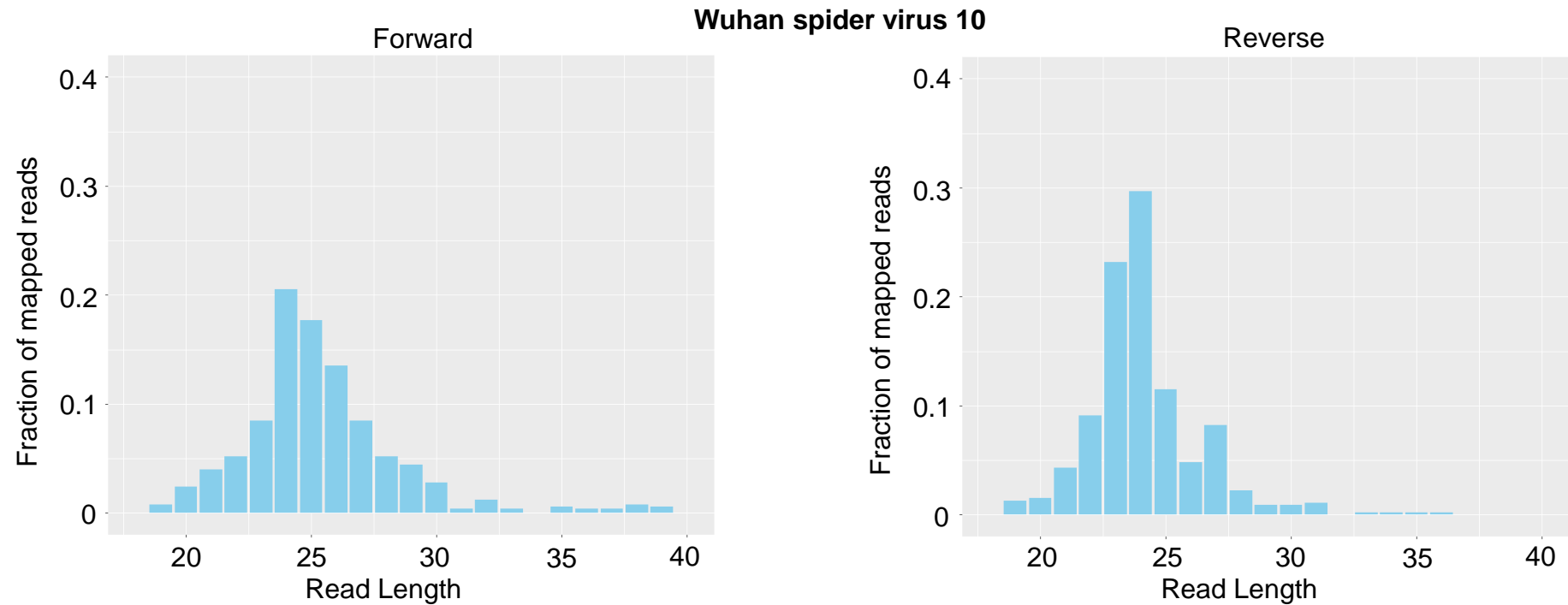
Coverage: Segment 5

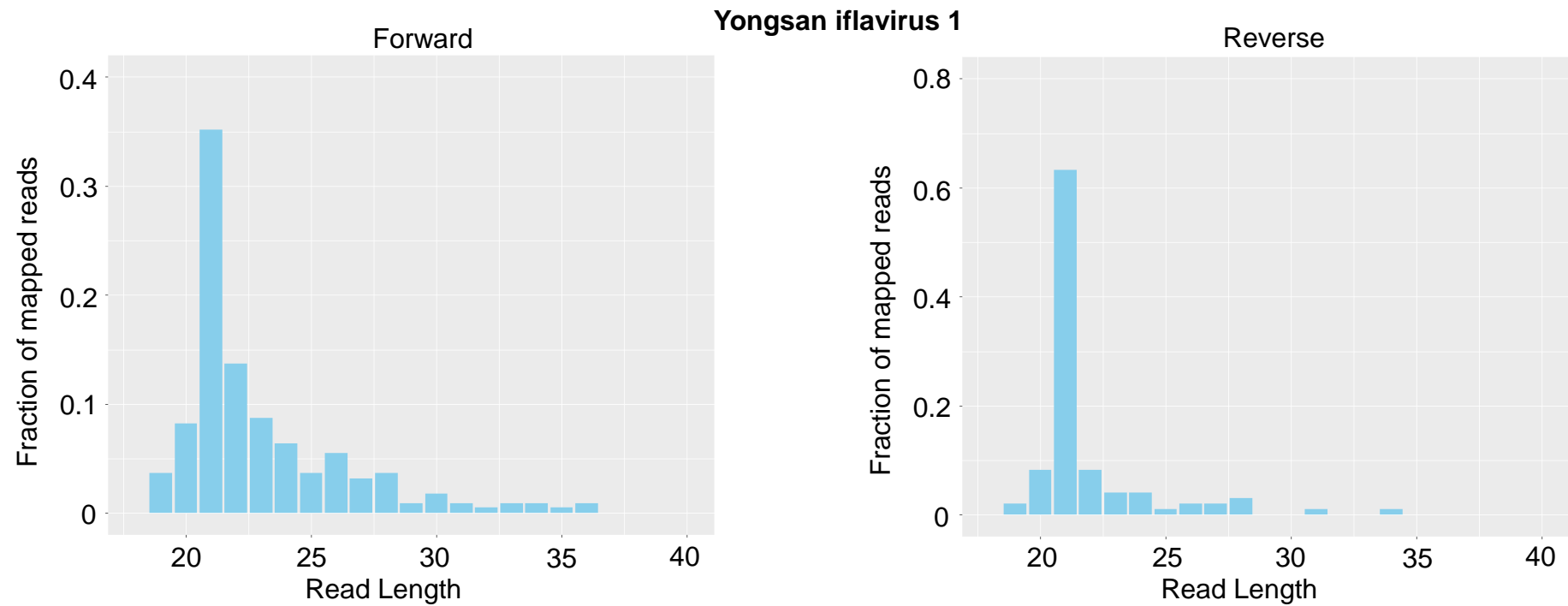




Coverage: Segment 6







21 nt reads

24-29 nt reads

**24-29 nt reads
with piRNA
nucleotide bias**

**24-29 nt reads
with ping-pong
signature and
10-nt overlaps**

(Range: -15 to
15)

Polyprotein
(+)ssRNA genome

Culex bunya-like virus (hypothetical protein 1 gene only)

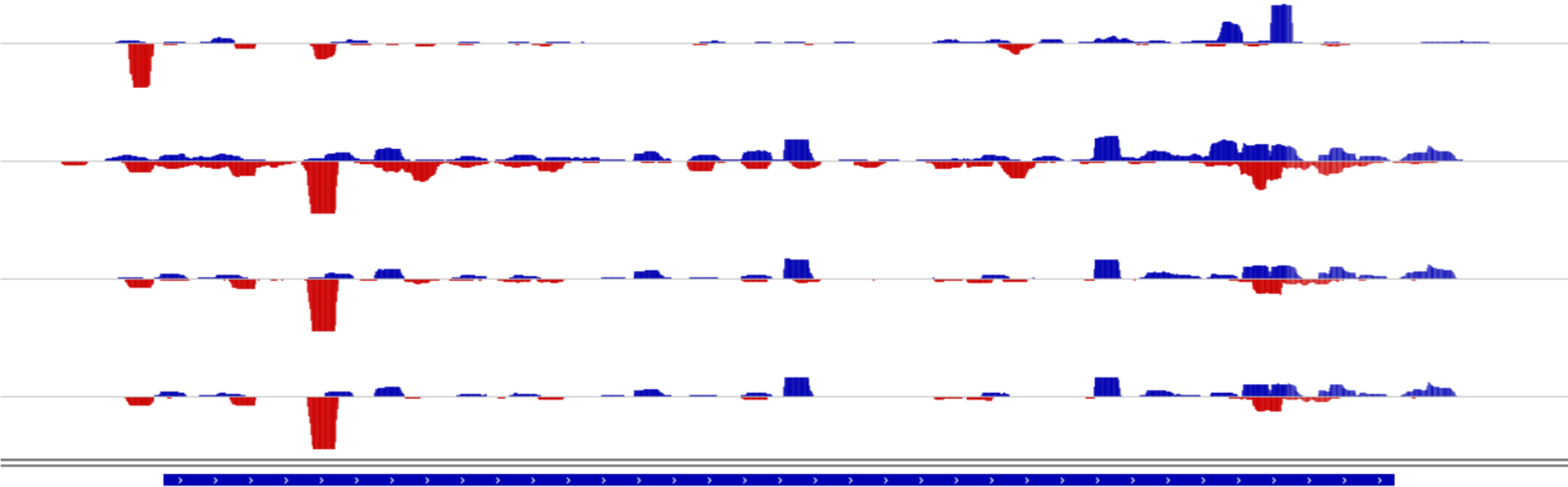
(Range:-2500 to 2500)

21 nt reads

24-29 nt reads

24-29 nt reads
with piRNA
nucleotide bias

24-29 nt reads
with ping-pong
signature and
10-nt overlaps

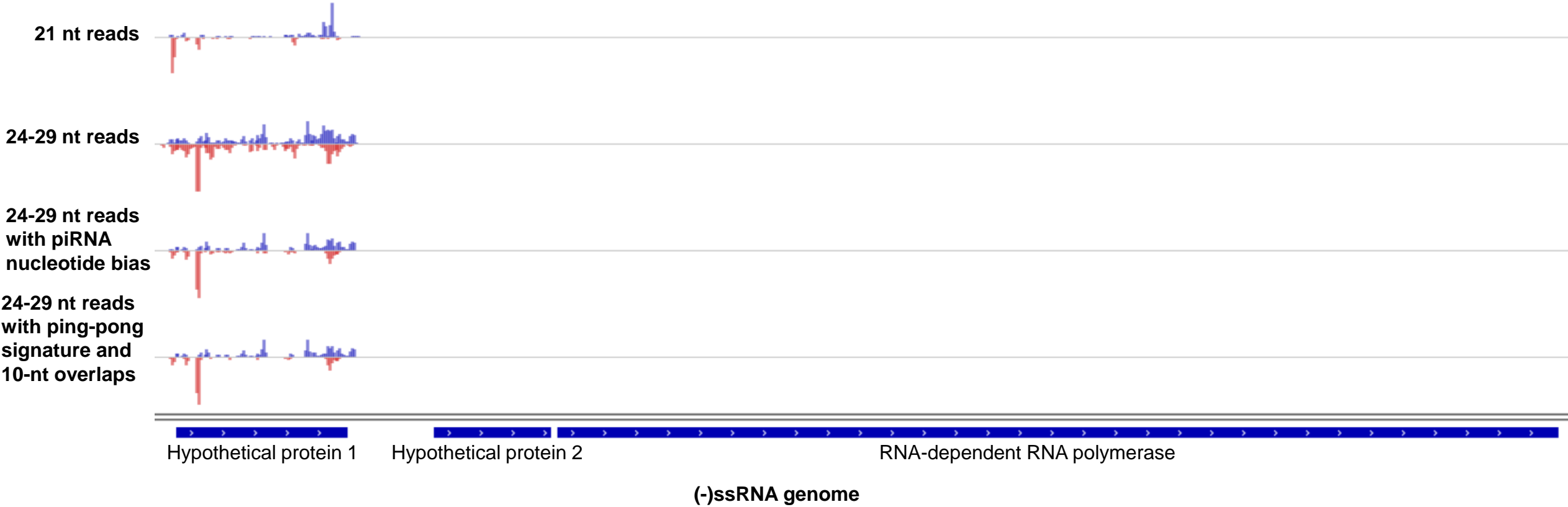


Hypothetical protein 1

(-)ssRNA genome

Culex bunya-like virus (full genome)

(Range:-2500 to 2500)



Culex phasma-like virus segment L

(Range:-5 to 5)

21 nt reads

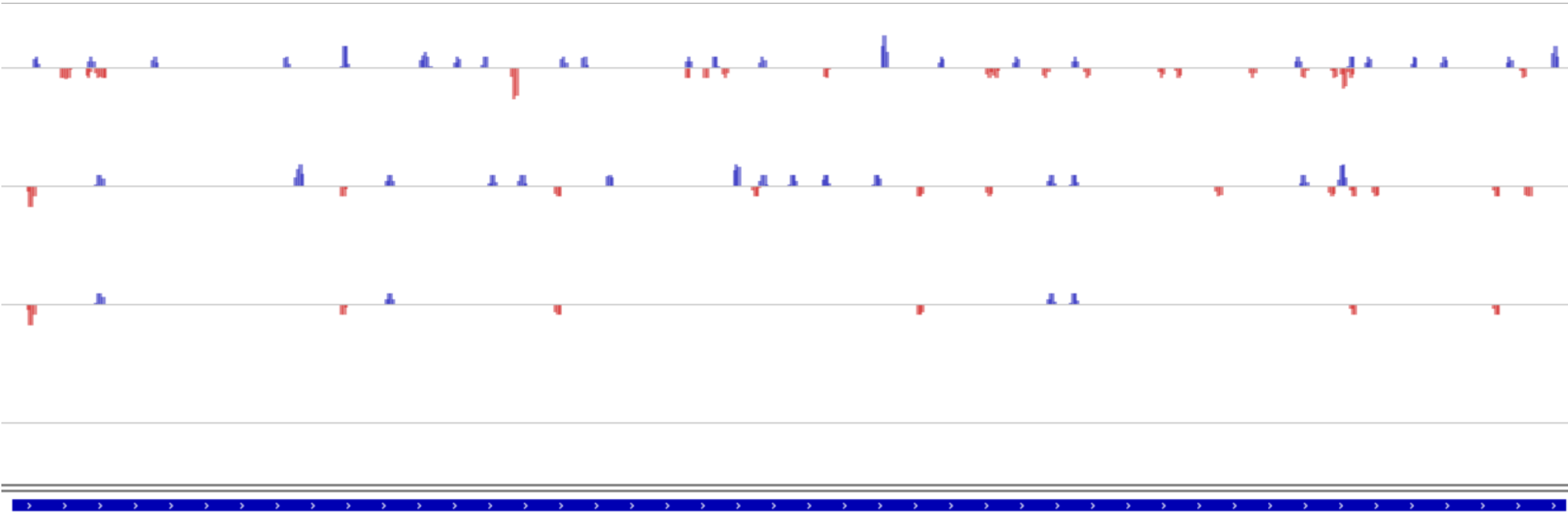
24-29 nt reads

24-29 nt reads
with piRNA
nucleotide bias

24-29 nt reads
with ping-pong
signature and
10-nt overlaps

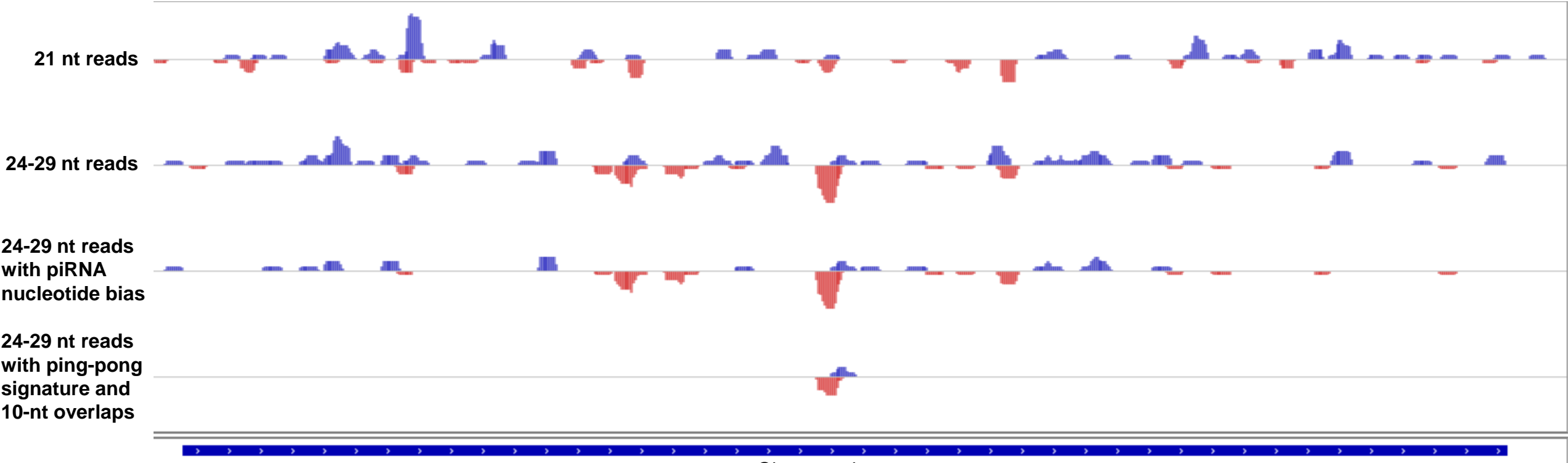
RNA-dependent RNA polymerase

(-)ssRNA genome



Culex phasma-like virus segment M

(Range:-10 to 10)



Glycoprotein

(-)ssRNA genome

Culex phasma-like virus segment S

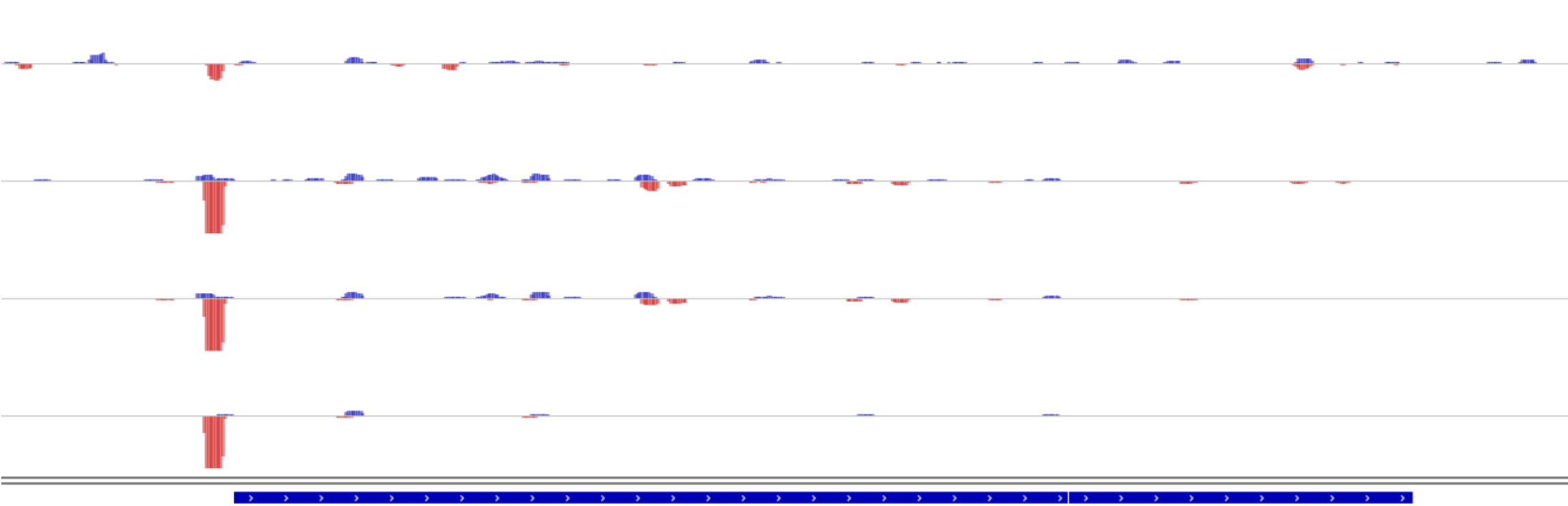
(Range:-80 to 80)

21 nt reads

24-29 nt reads

24-29 nt reads
with piRNA
nucleotide bias

24-29 nt reads
with ping-pong
signature and
10-nt overlaps



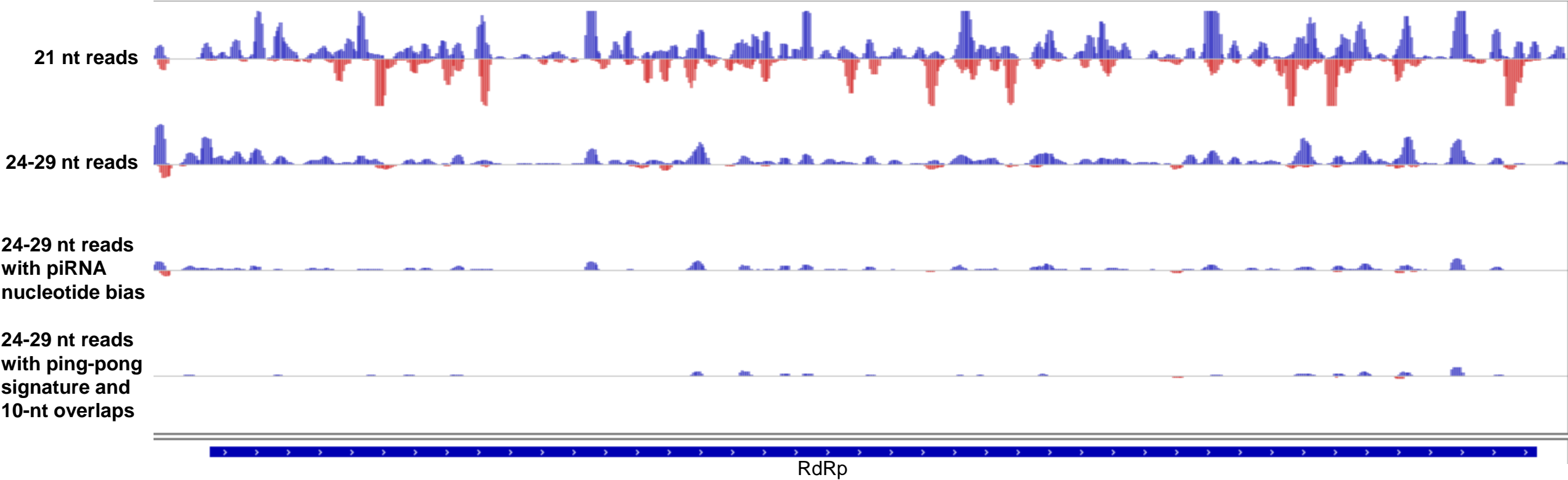
Nucleoprotein

Hypothetical protein

(-)ssRNA genome

Hubei chryso-like virus 1 segment A

(Range:-500 to 500)

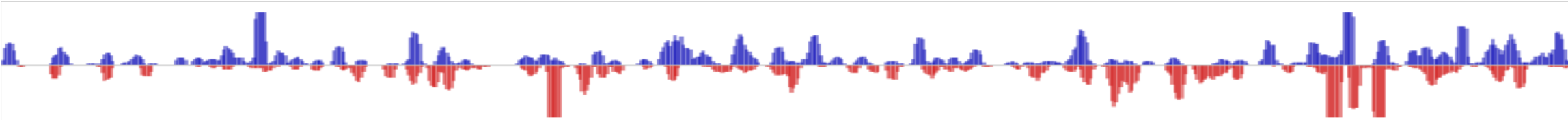


dsRNA genome

Hubei chryso-like virus 1 segment B

(Range:-500 to 500)

21 nt reads



24-29 nt reads



24-29 nt reads
with piRNA
nucleotide bias



24-29 nt reads
with ping-pong
signature and
10-nt overlaps

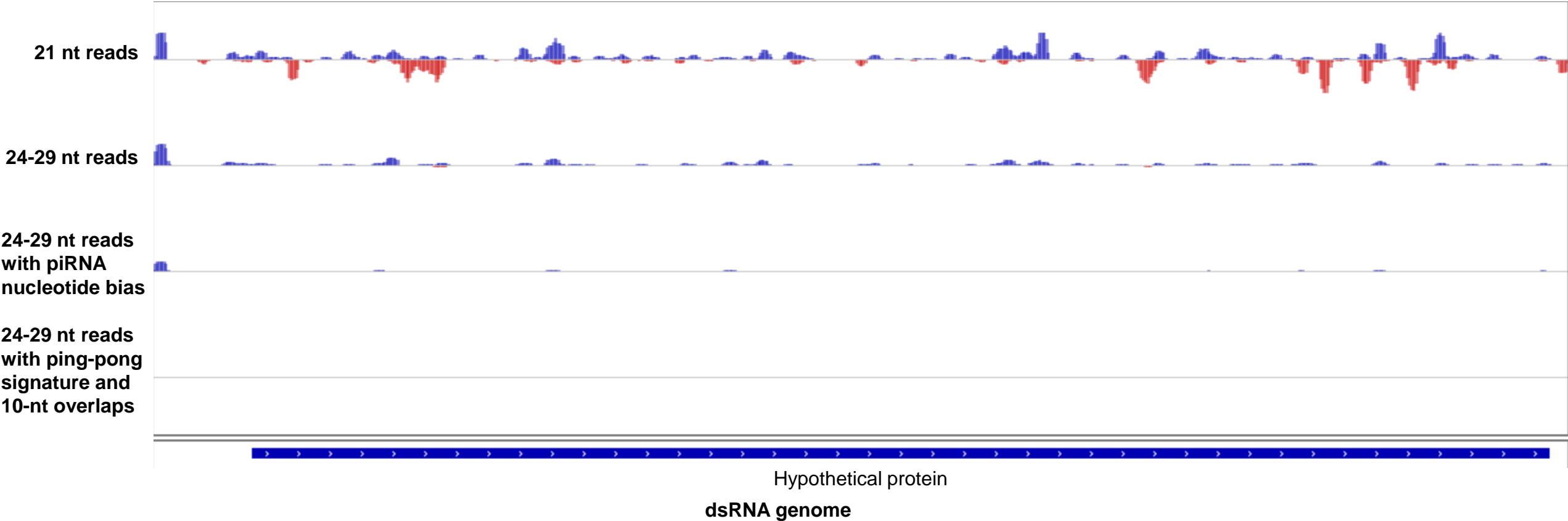


Putative protease

dsRNA genome

Hubei chryso-like virus 1 segment C

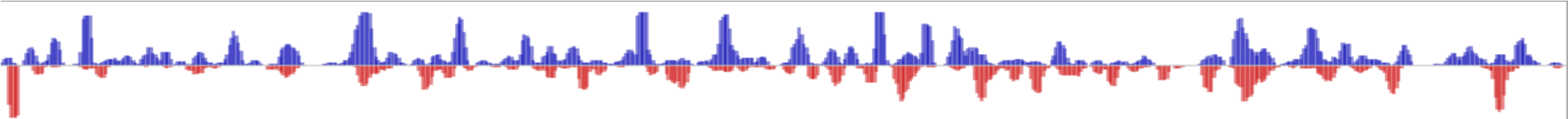
(Range:-500 to 500)



Hubei chryso-like virus 1 segment D

(Range:-500 to 500)

21 nt reads



24-29 nt reads



24-29 nt reads
with piRNA
nucleotide bias



24-29 nt reads
with ping-pong
signature and
10-nt overlaps



Hypothetical protein

dsRNA genome