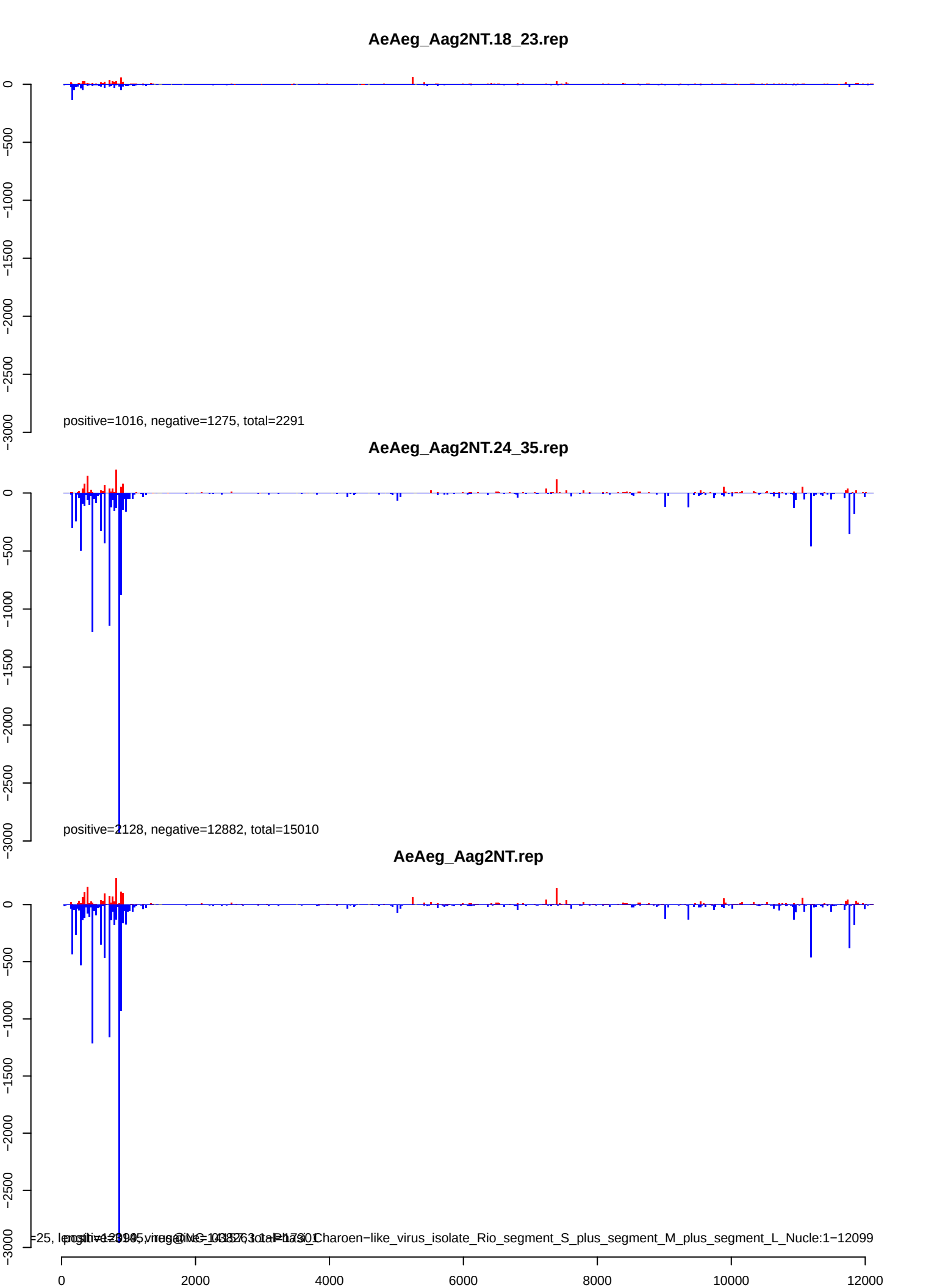
AeAeg_Aag2NT.18_23.rep
positive=1016, negative=1275, total=2291
AeAeg_Aag2NT.24_35.rep
positive=2128, negative=12882, total=15010
AeAeg_Aag2NT.rep
0
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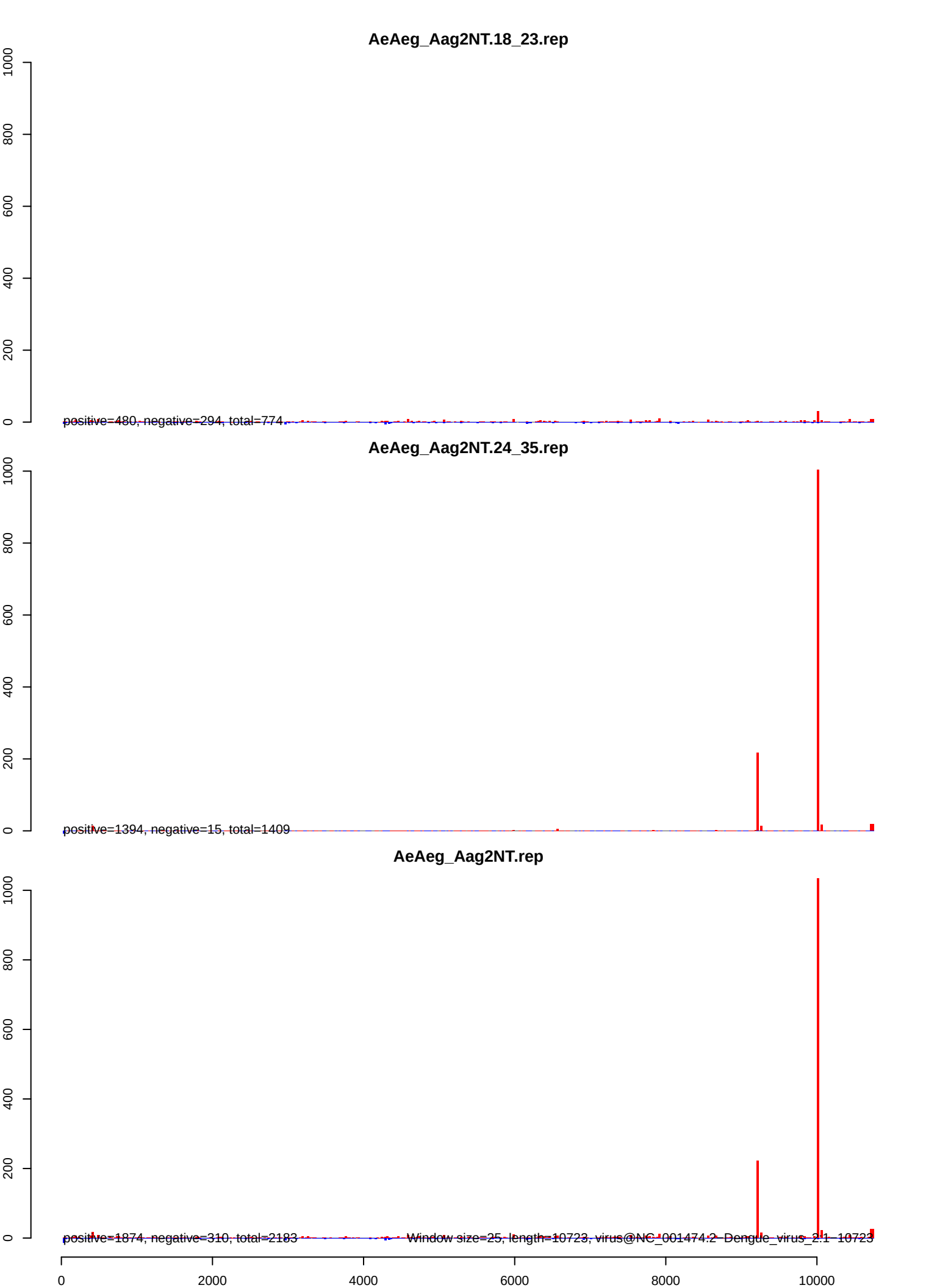
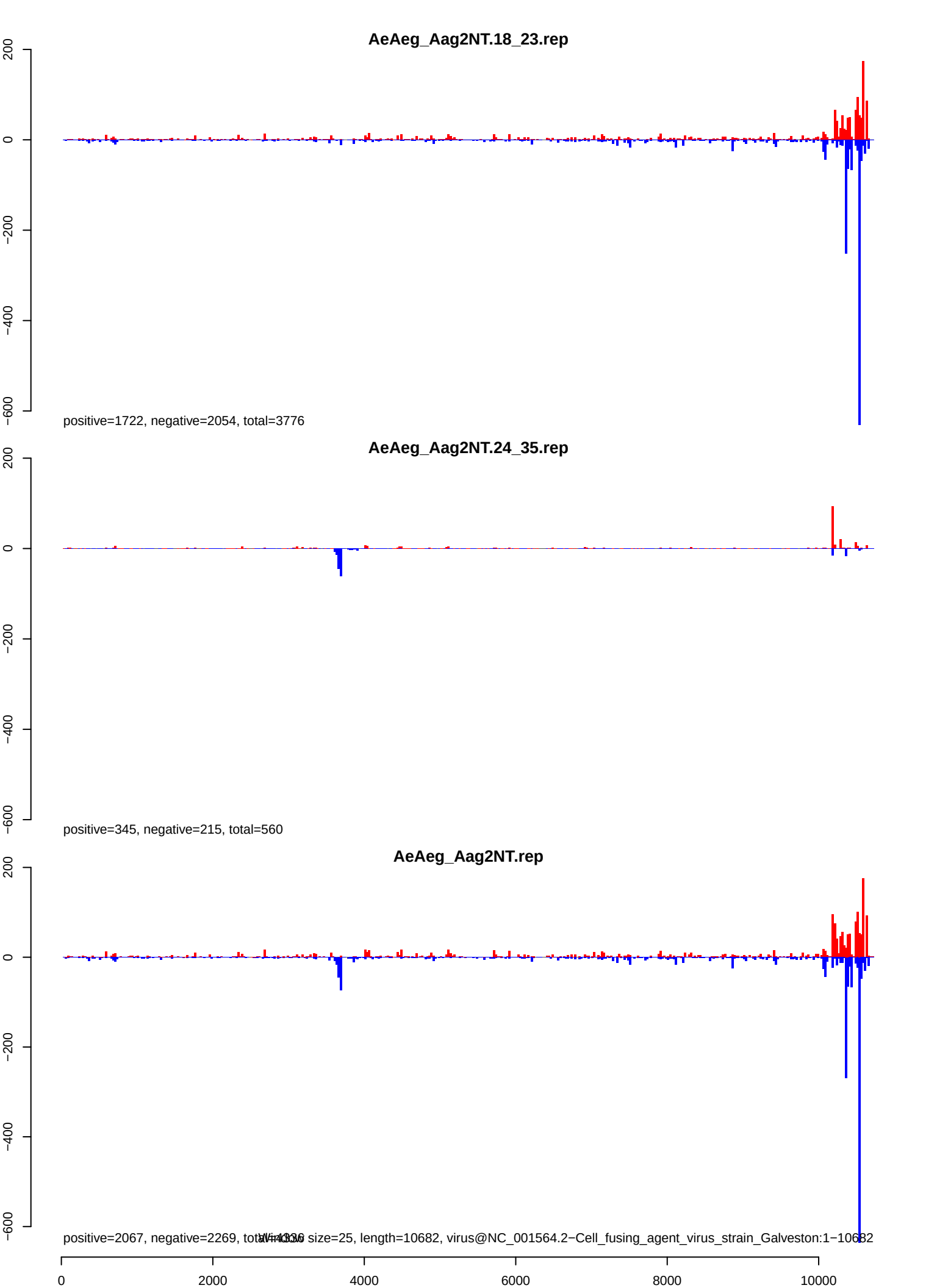
−1000
−1500
−2000
−2500
−3000
0
2000
4000
6000
8000
10000
12000


AeAeg_Aag2NT.18_23.rep
positive=480, negative=294, total=774
AeAeg_Aag2NT.24_35.rep
positive=1394, negative=15, total=1409
AeAeg_Aag2NT.rep
positive=1874, negative=310, total=2183
Window size=25, length=10723, virus@NC_001474.2 Dengue_virus_2 1 10723
0
200
400
600
800
1000
0
2000
4000
6000
8000
10000


AeAeg_Aag2NT.18_23.rep
200
0
−200
−400
−600
positive=1722, negative=2054, total=3776
AeAeg_Aag2NT.24_35.rep
200
0
−200
−400
−600
positive=345, negative=215, total=560
AeAeg_Aag2NT.rep
200
0
−200
−400
−600
positive=2067, negative=2269, total=4336
W=4336 size=25, length=10682, virus@NC_001564.2−Cell_fusing_agent_virus_strain_Galveston:1−10682
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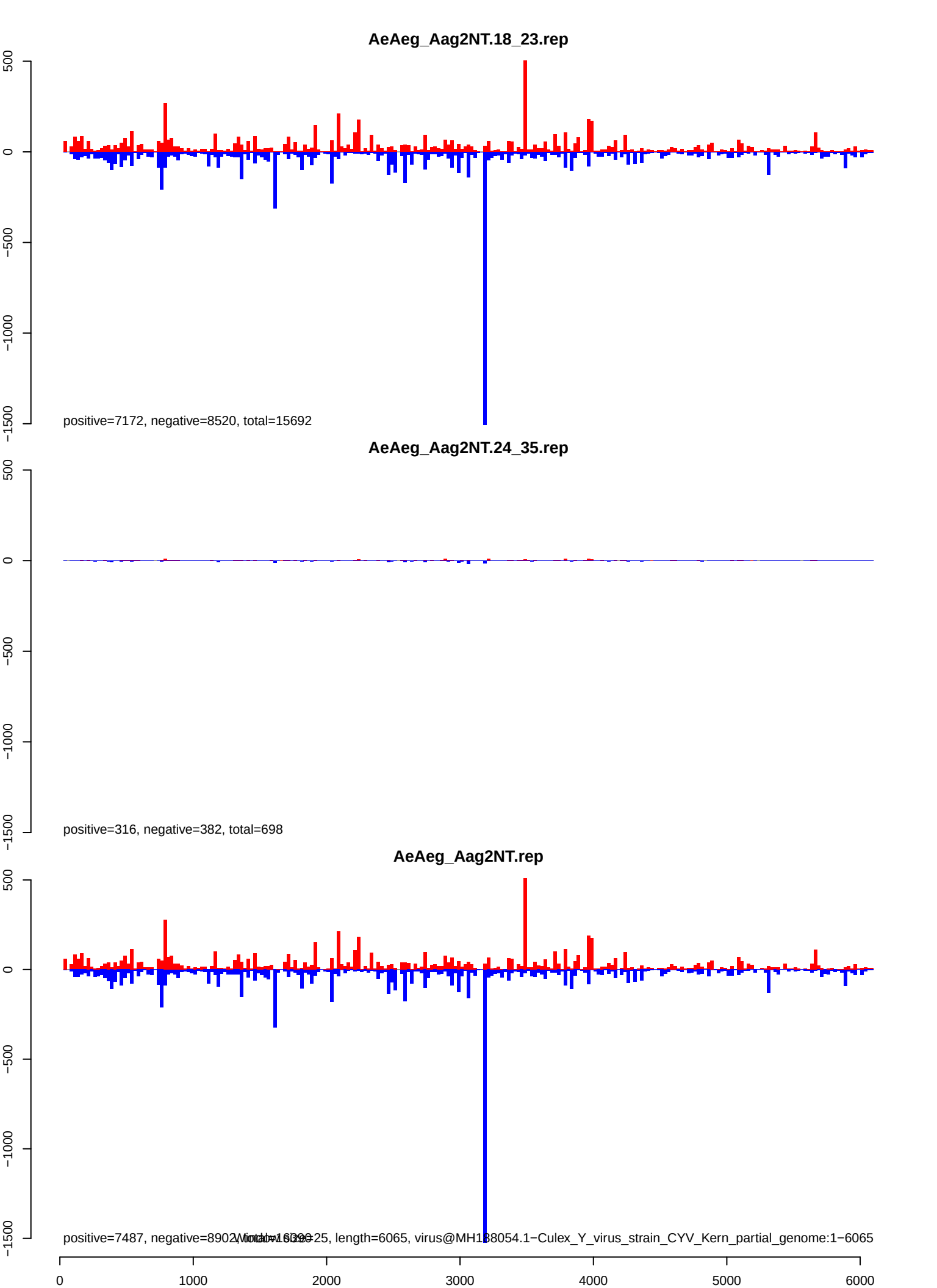
2000
4000
6000
8000
10000


AeAeg_Aag2NT.18_23.rep
500
0
−500
−1000
−1500
positive=7172, negative=8520, total=15692
AeAeg_Aag2NT.24_35.rep
500
0
−500
−1000
−1500
positive=316, negative=382, total=698
AeAeg_Aag2NT.rep
500
0
−500
−1000
−1500
positive=7487, negative=8902, total=16389
length=6065, virus@MH188054.1−Culex_Y_virus_strain_CYV_Kern_partial_genome:1−6065
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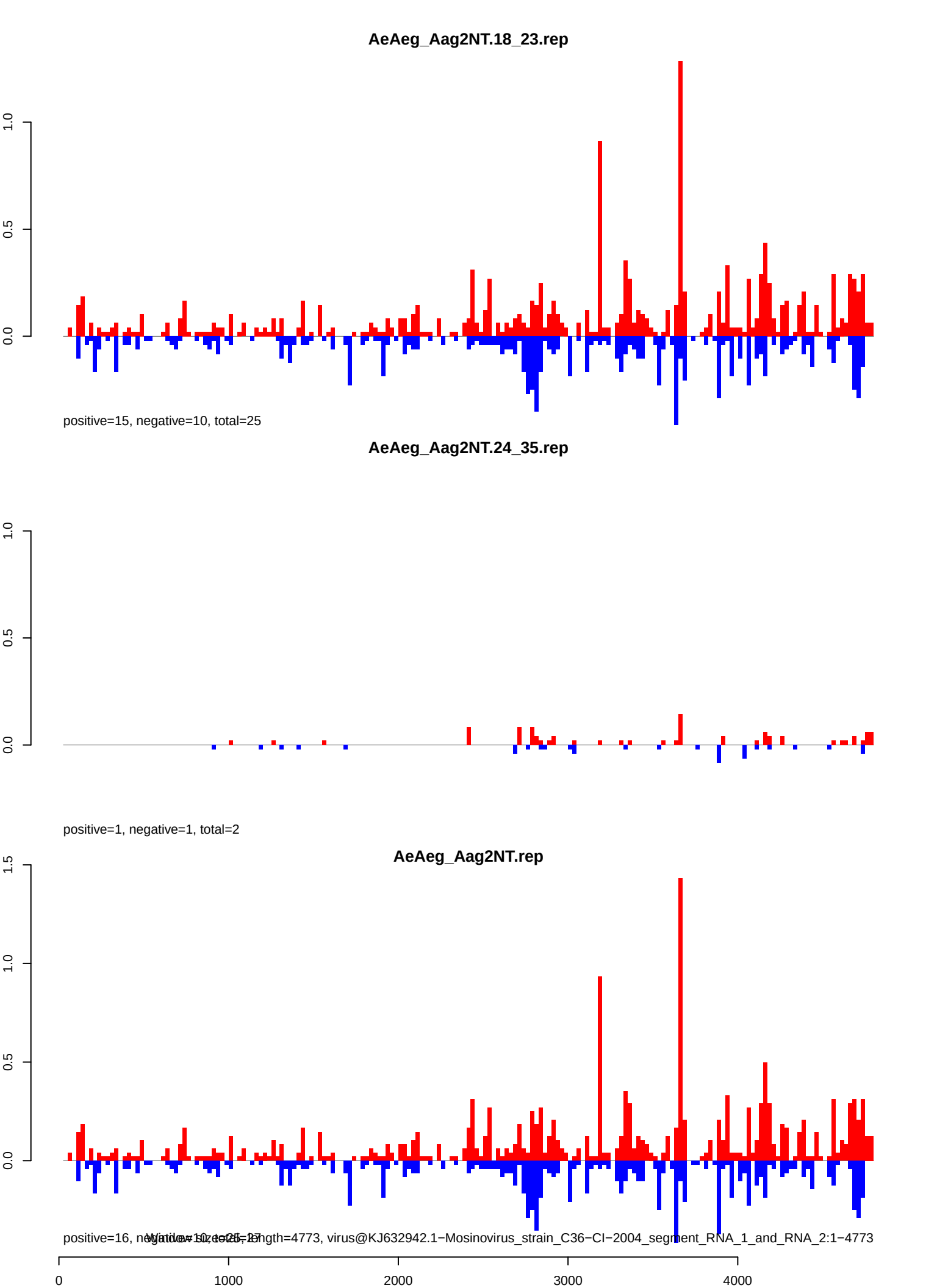
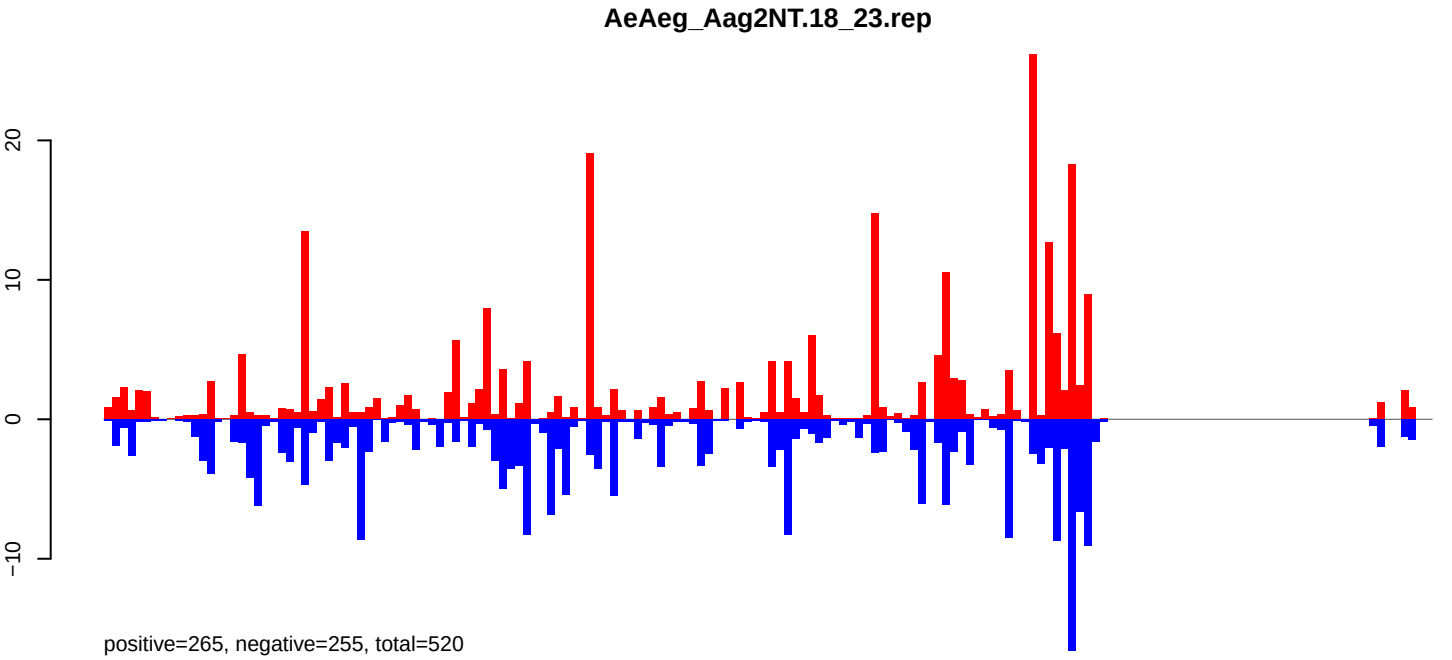
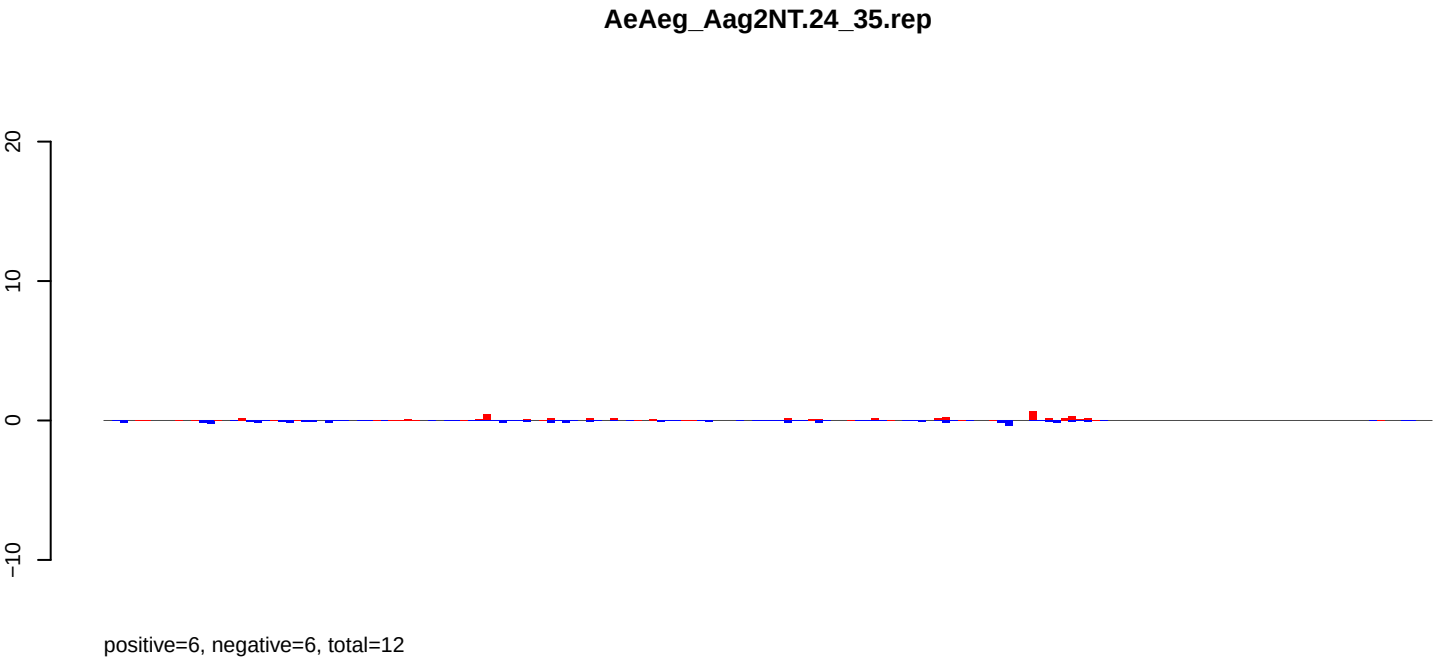
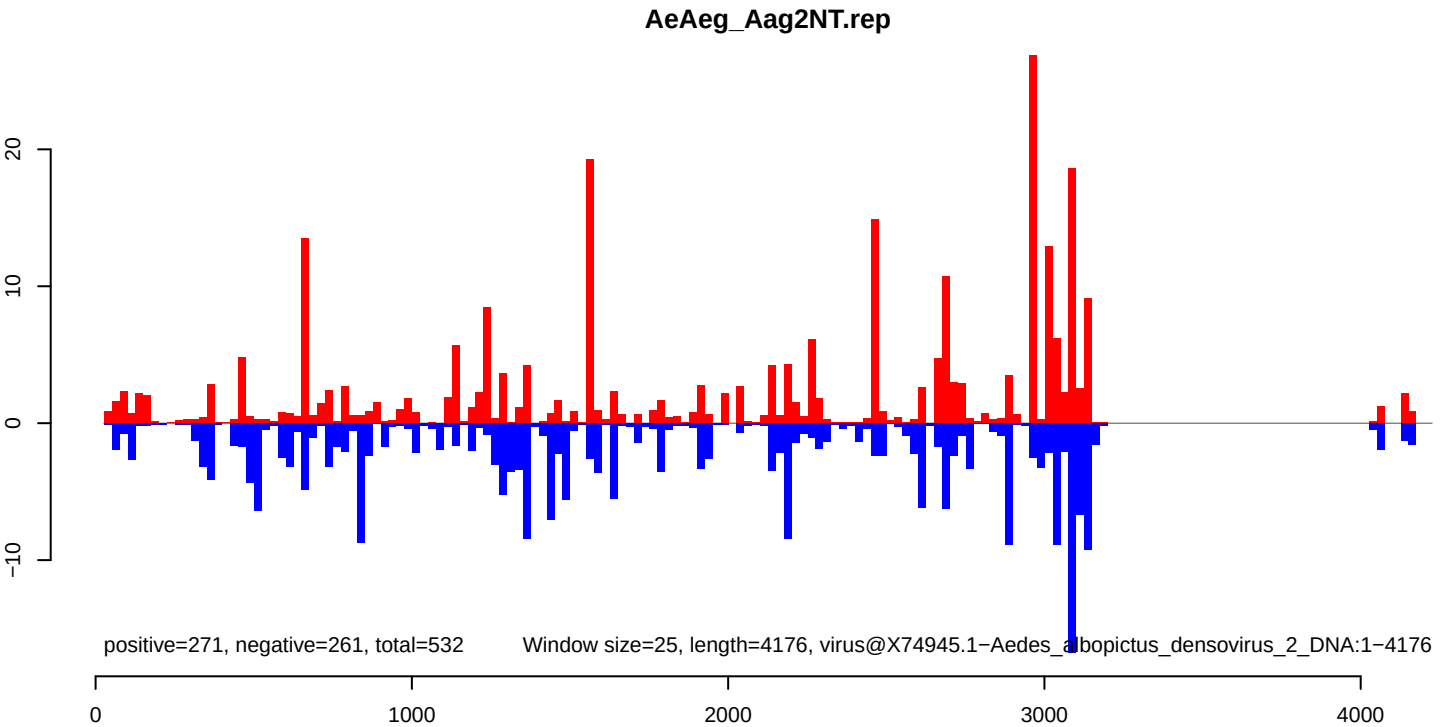
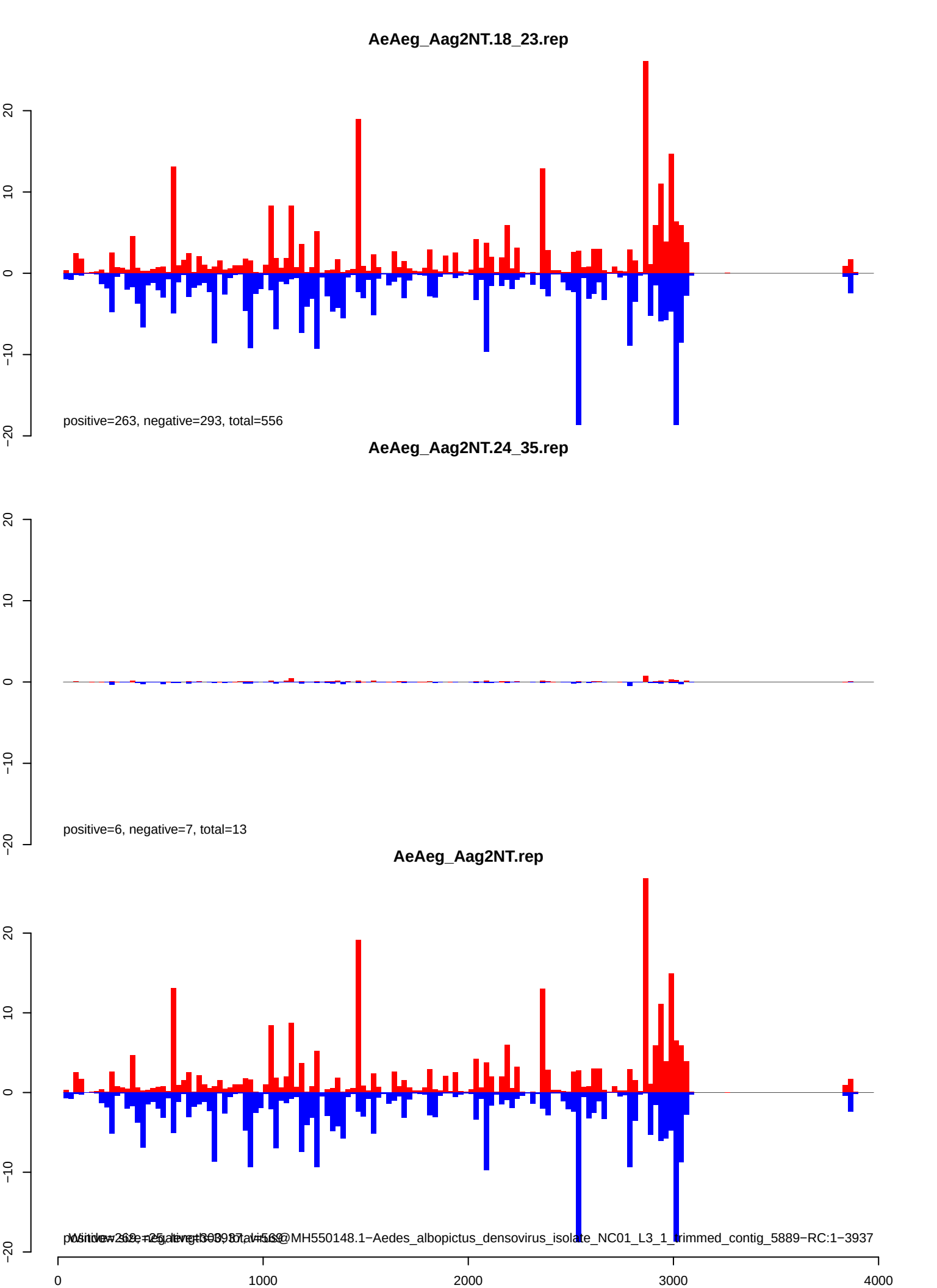
3000
4000
5000
6000

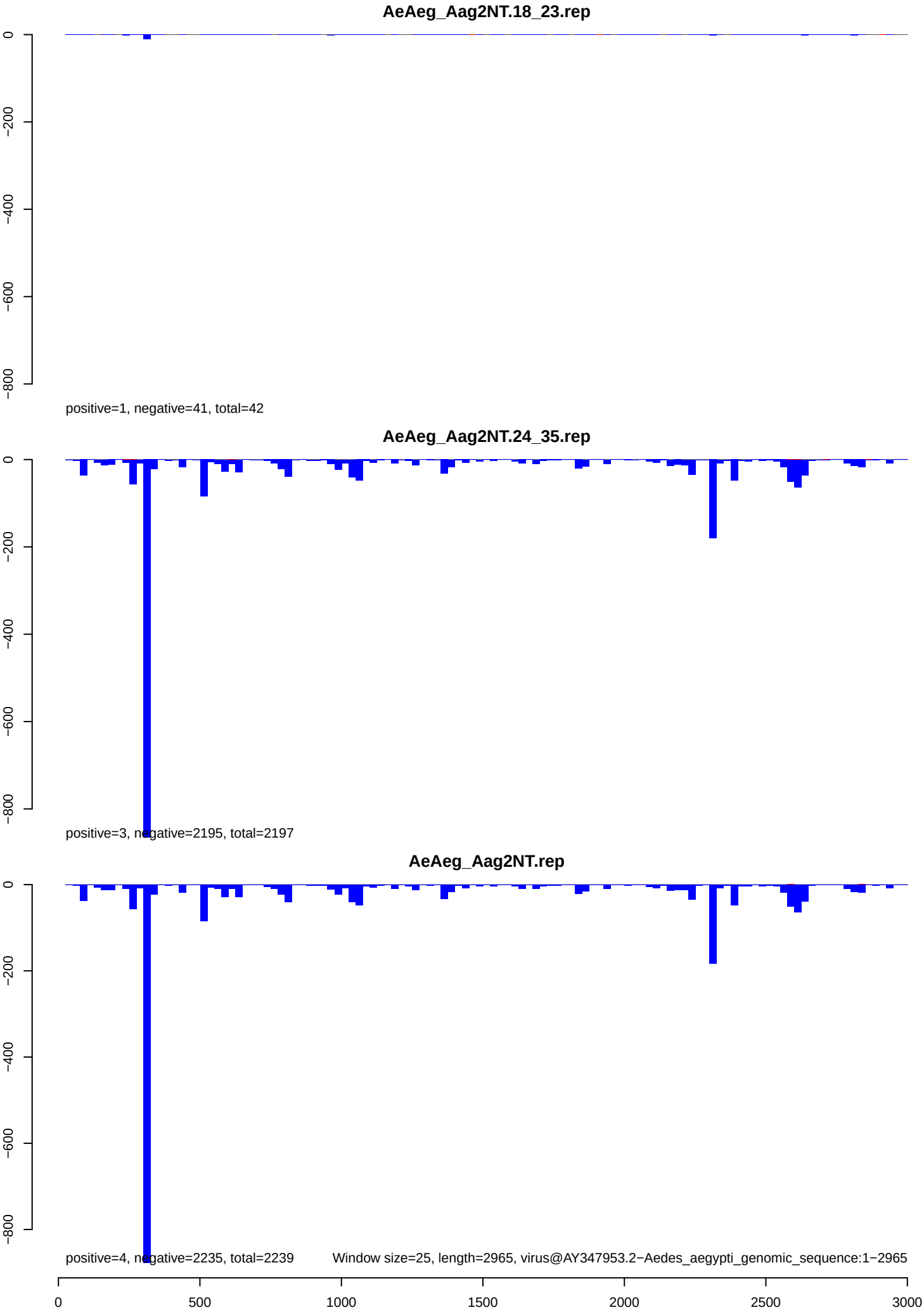

AeAeg_Aag2NT.18_23.rep
1.0
0.5
0.0
positive=15, negative=10, total=25
AeAeg_Aag2NT.24_35.rep
1.0
0.5
0.0
positive=1, negative=1, total=2
AeAeg_Aag2NT.rep
1.5
1.0
0.5
0.0
positive=16, negative=10, total=25, length=4773, virus@KJ632942.1−Mosinovirus_strain_C36−CI−2004_segment_RNA_1_and_RNA_2:1−4773
0
1000
2000
3000
4000

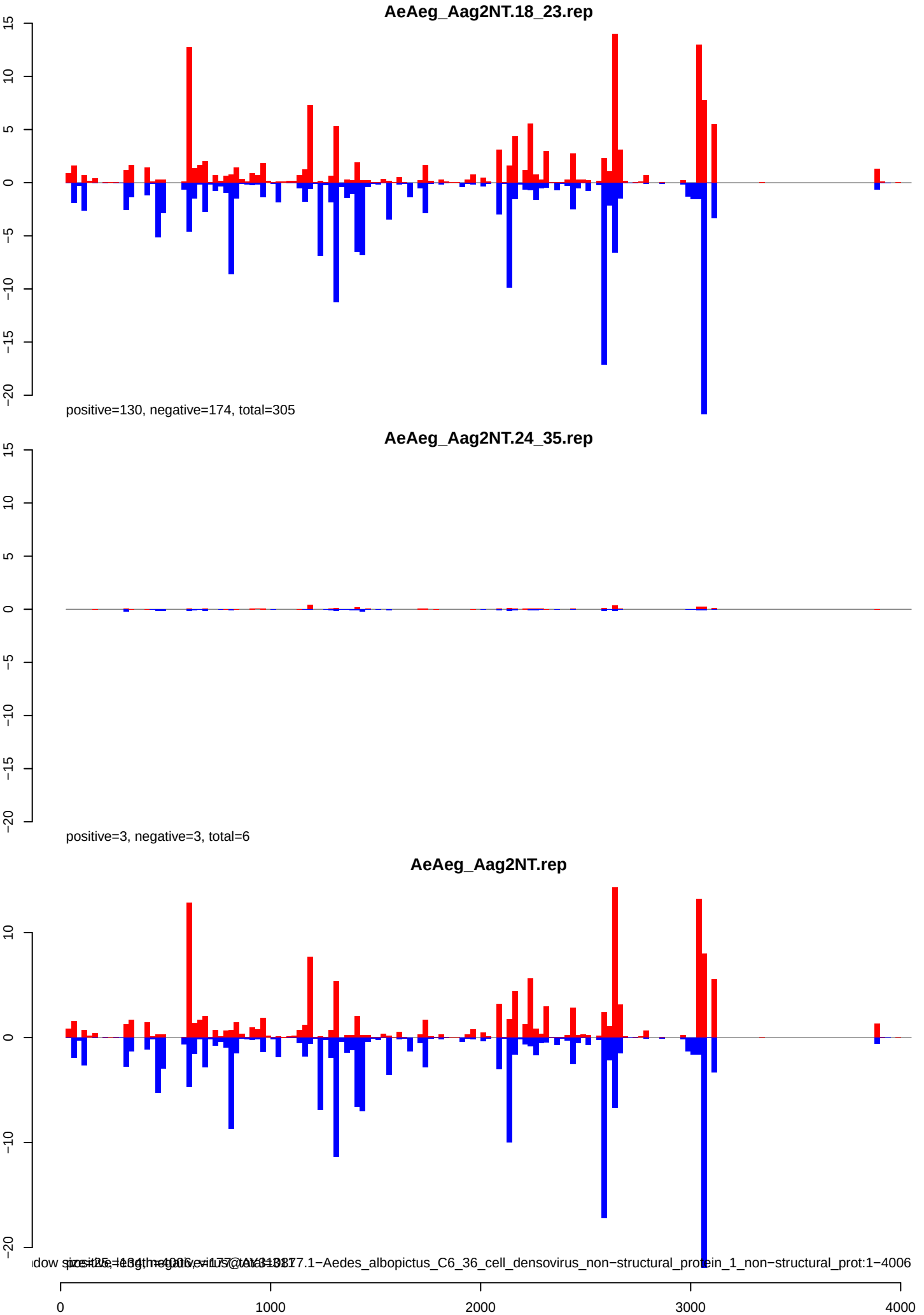

AeAeg_Aag2NT.18_23.rep
20
10
0
−10
positive=265, negative=255, total=520

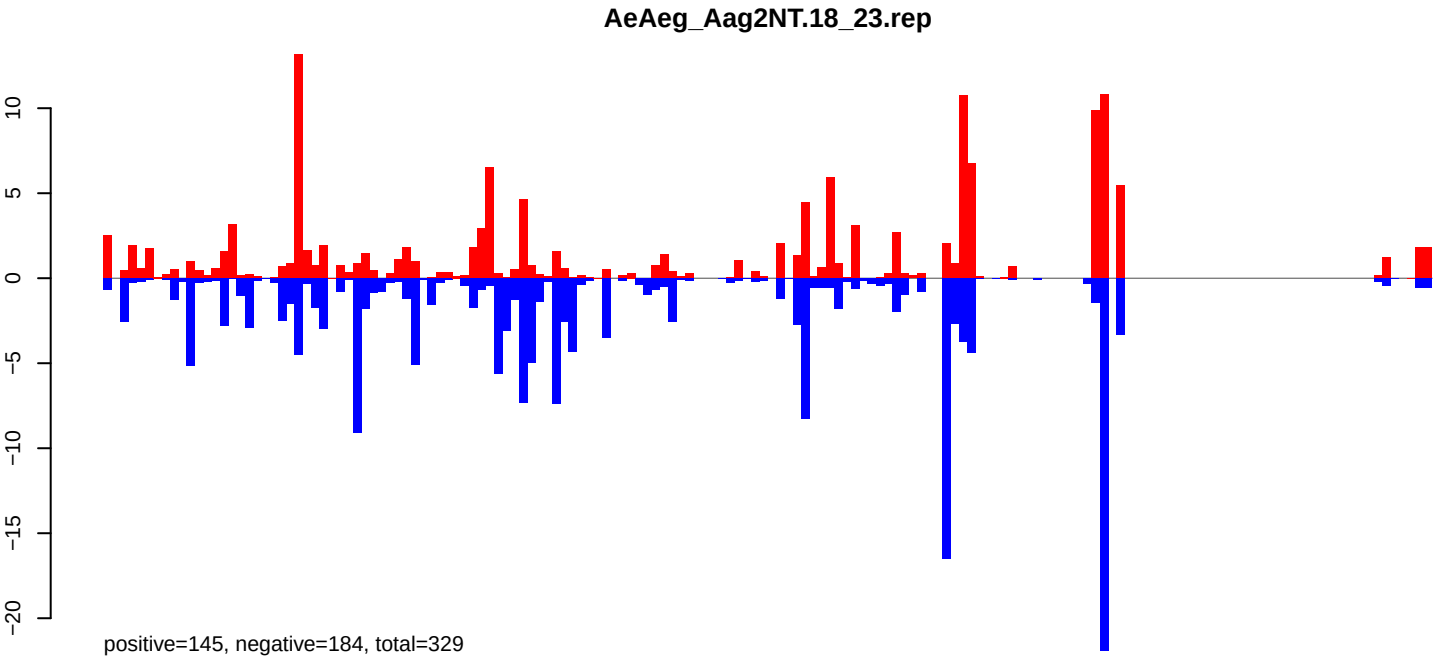

AeAeg_Aag2NT.24_35.rep
20
10
0
−10
positive=6, negative=6, total=12

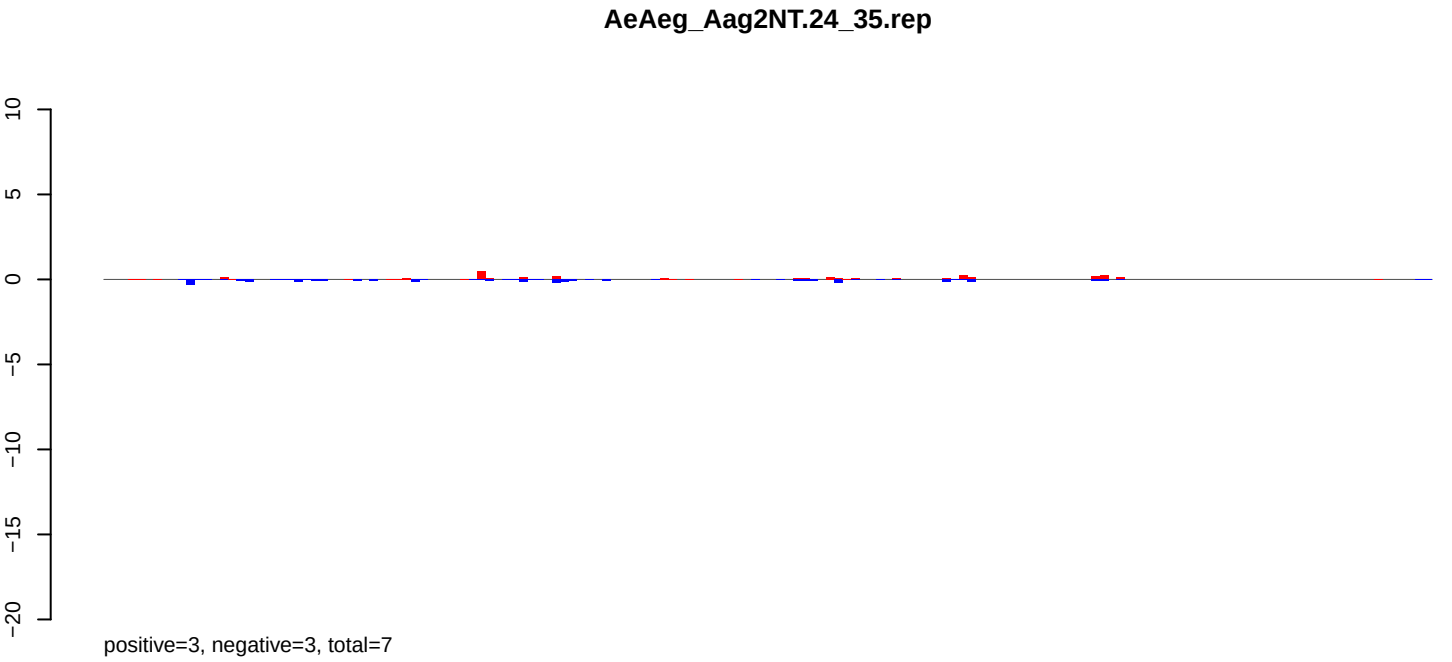

AeAeg_Aag2NT.rep
20
10
0
−10
positive=271, negative=261, total=532
Window size=25, length=4176, virus@X74945.1−Aedes_albopictus_densovirus_2_DNA:1−4176
0
1000
2000
3000
4000

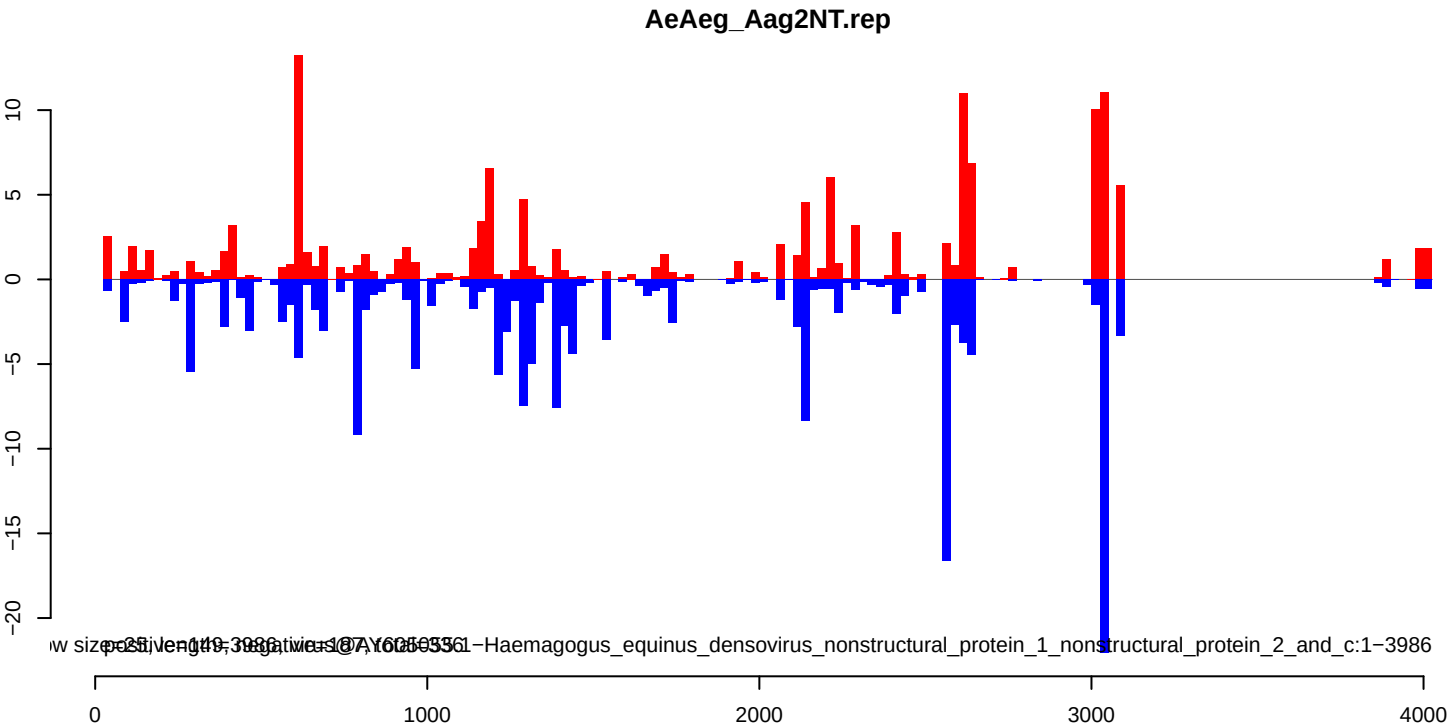

AeAeg_Aag2NT.18_23.rep
positive=263, negative=293, total=556
AeAeg_Aag2NT.24_35.rep
positive=6, negative=7, total=13
AeAeg_Aag2NT.rep
positive=269, negative=300, total=569@MH550148.1−Aedes_albopictus_densovirus_isolate_NC01_L3_1_trimmed_contig_5889−RC:1−3937
20
10
0
−10
−20
0
1000
2000
3000
4000

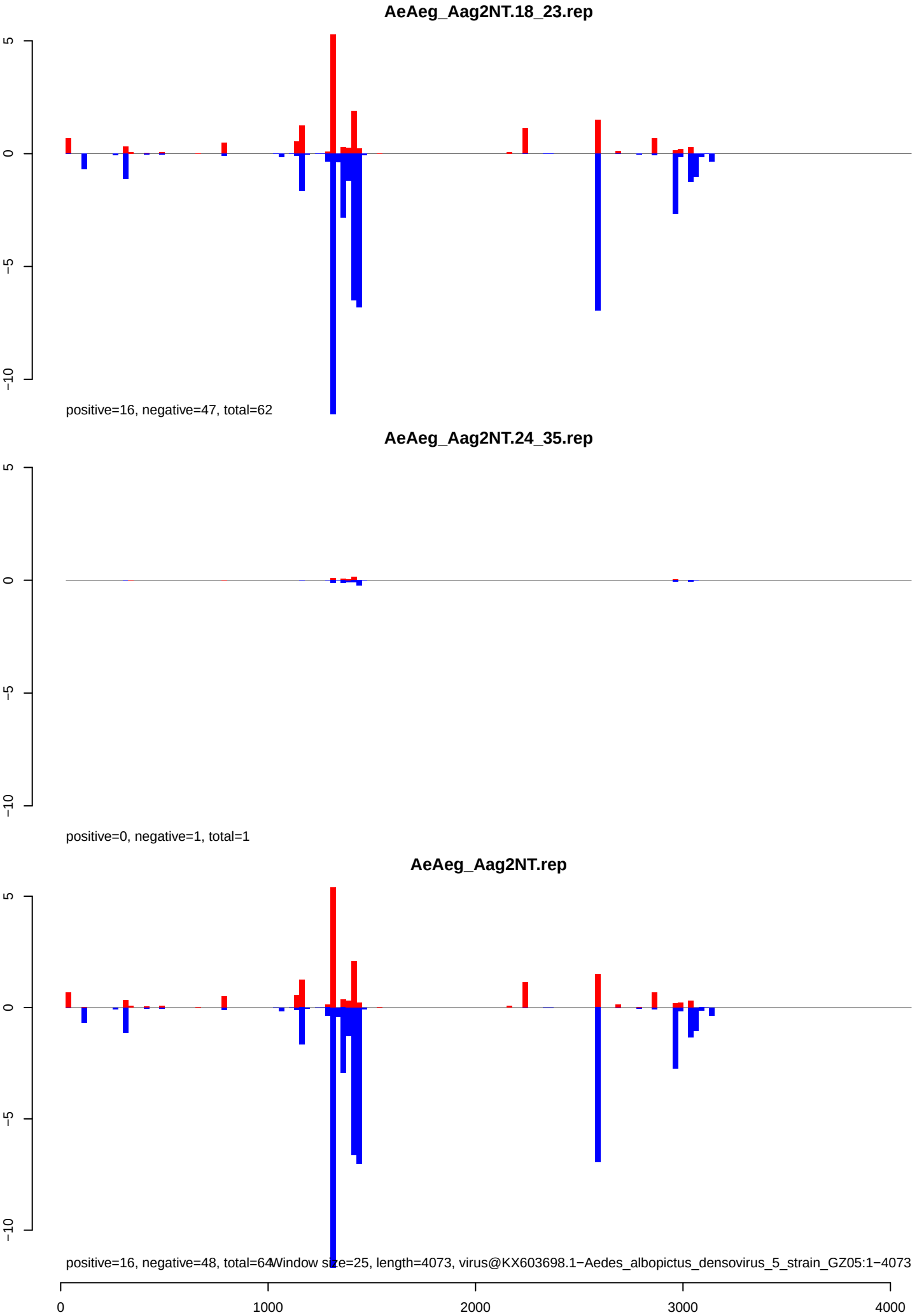

AeAeg_Aag2NT.18_23.rep
0
−200
−400
−600
−800
positive=1, negative=41, total=42
AeAeg_Aag2NT.24_35.rep
0
−200
−400
−600
−800
positive=3, negative=2195, total=2197
AeAeg_Aag2NT.rep
0
−200
−400
−600
−800
positive=4, negative=2235, total=2239
Window size=25, length=2965, virus@AY347953.2−Aedes_aegypti_genomic_sequence:1−2965
0
500
1000
1500
2000
2500
3000

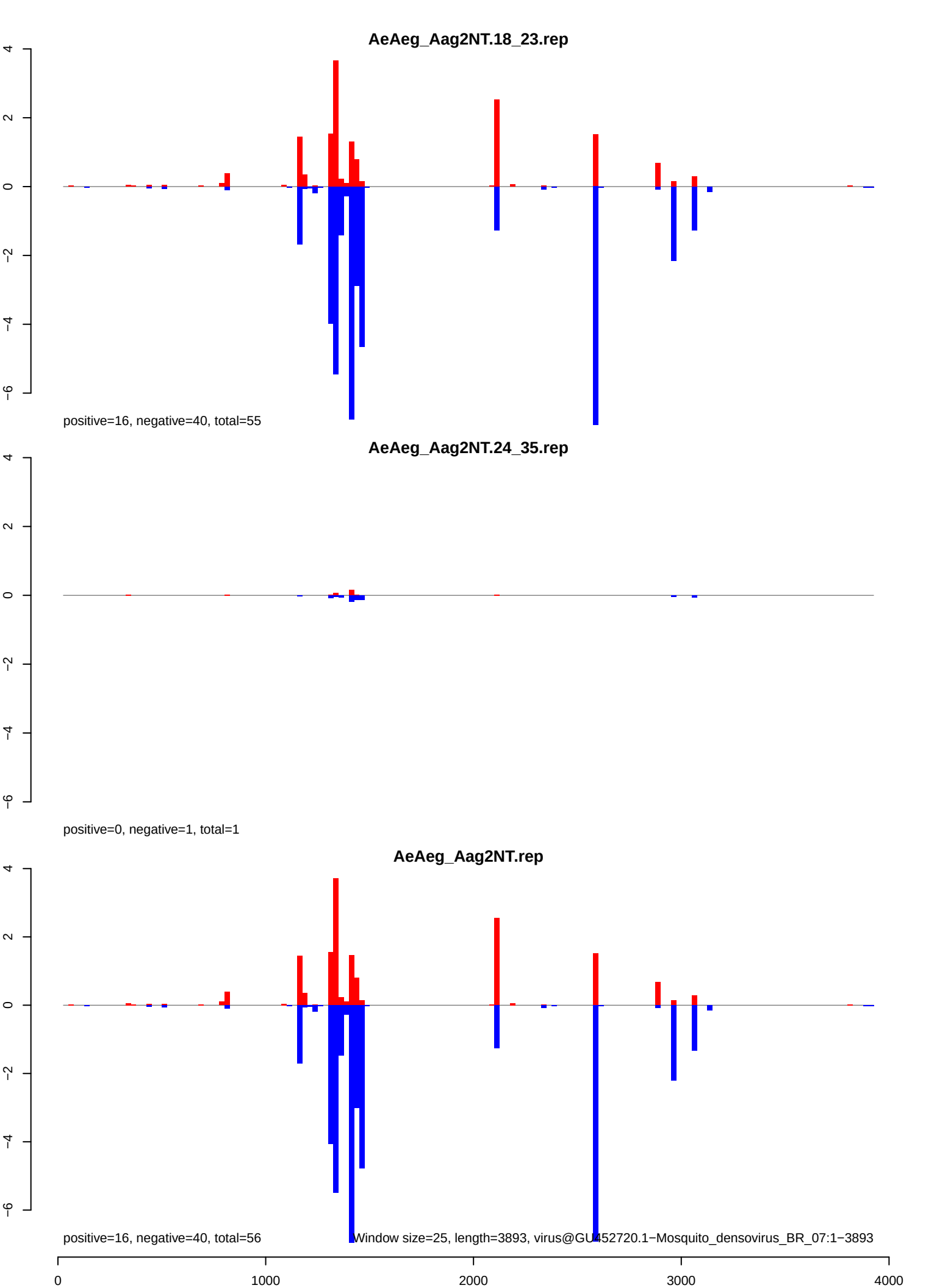

AeAeg_Aag2NT.18_23.rep
positive=130, negative=174, total=305
AeAeg_Aag2NT.24_35.rep
positive=3, negative=3, total=6
AeAeg_Aag2NT.rep
0
1000
2000
3000
4000

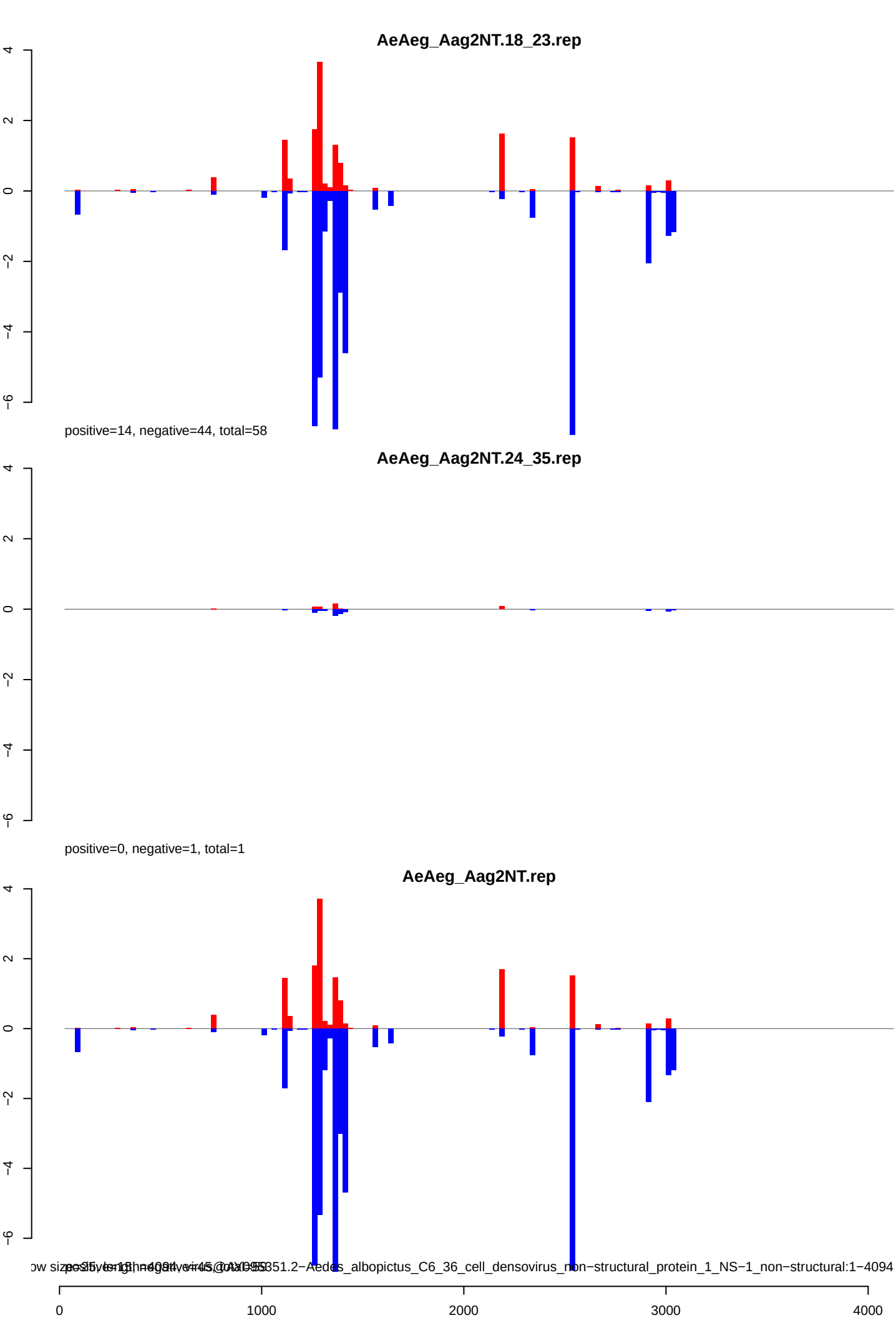

AeAeg_Aag2NT.18_23.rep
positive=145, negative=184, total=329

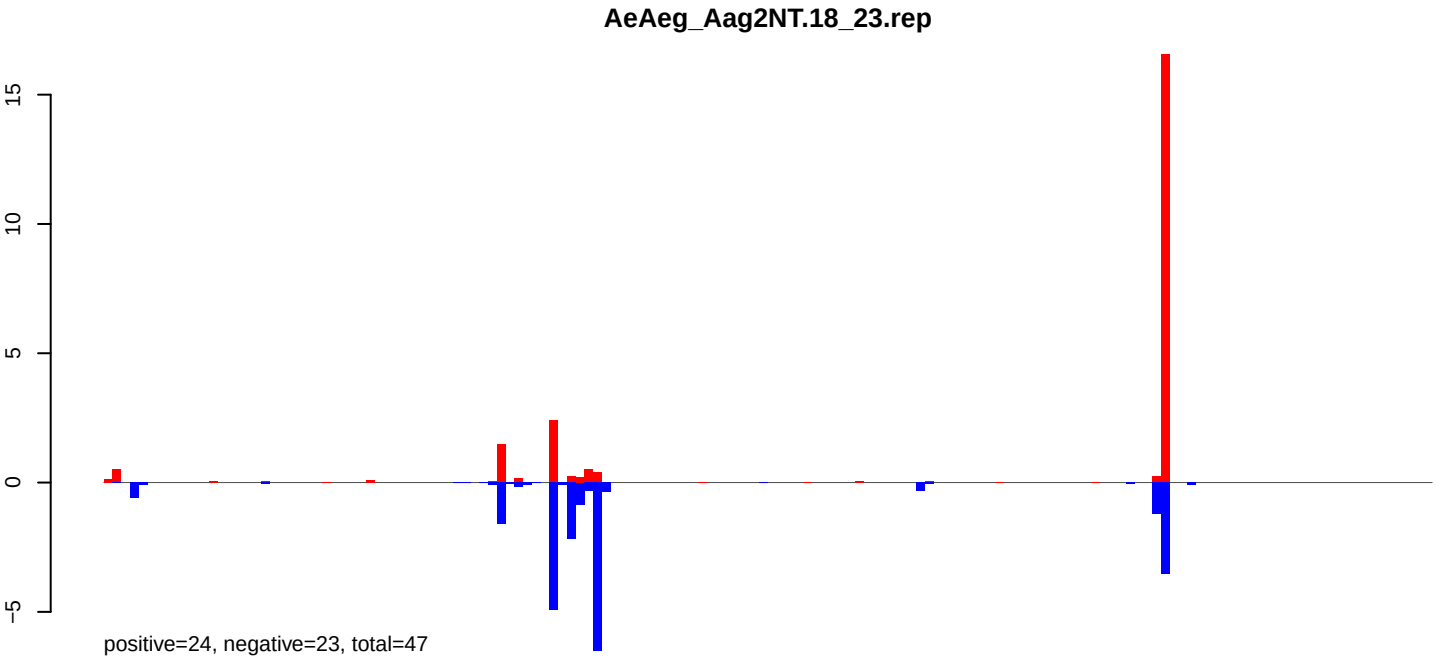

AeAeg_Aag2NT.24_35.rep
positive=3, negative=3, total=7

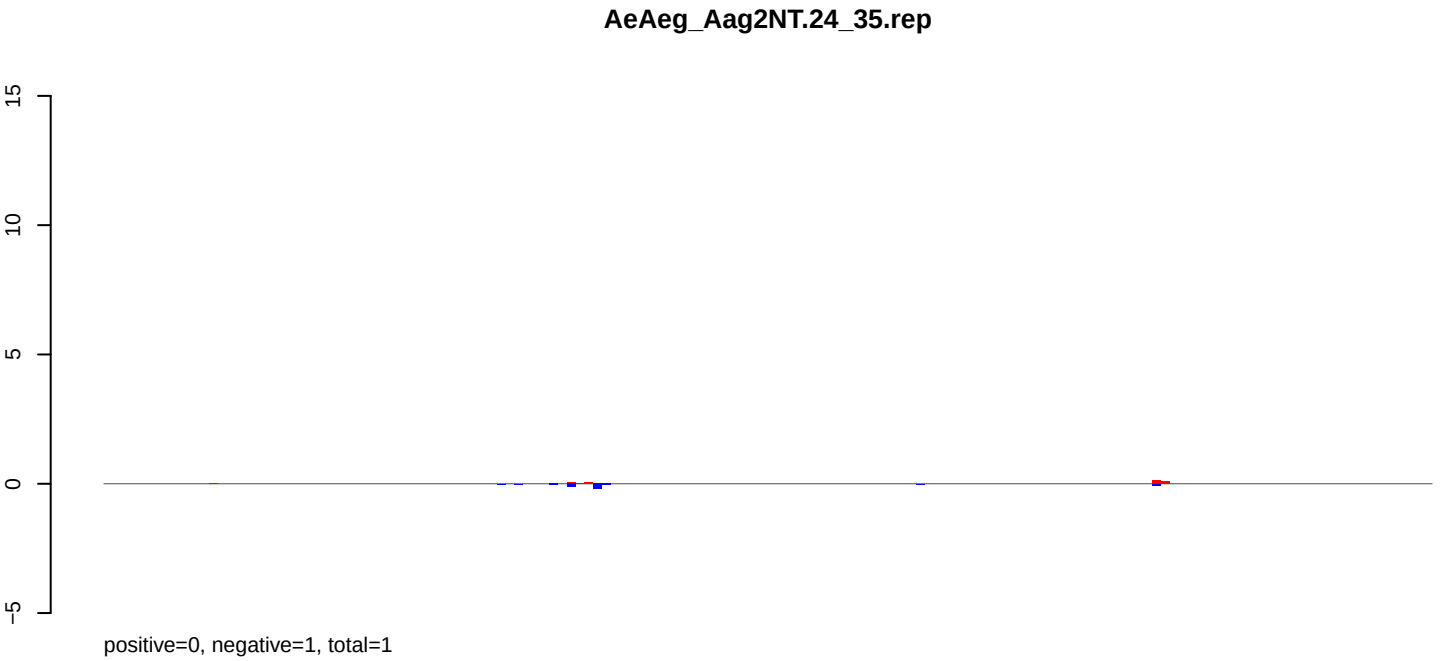

AeAeg_Aag2NT.rep
0
1000
2000
3000
4000

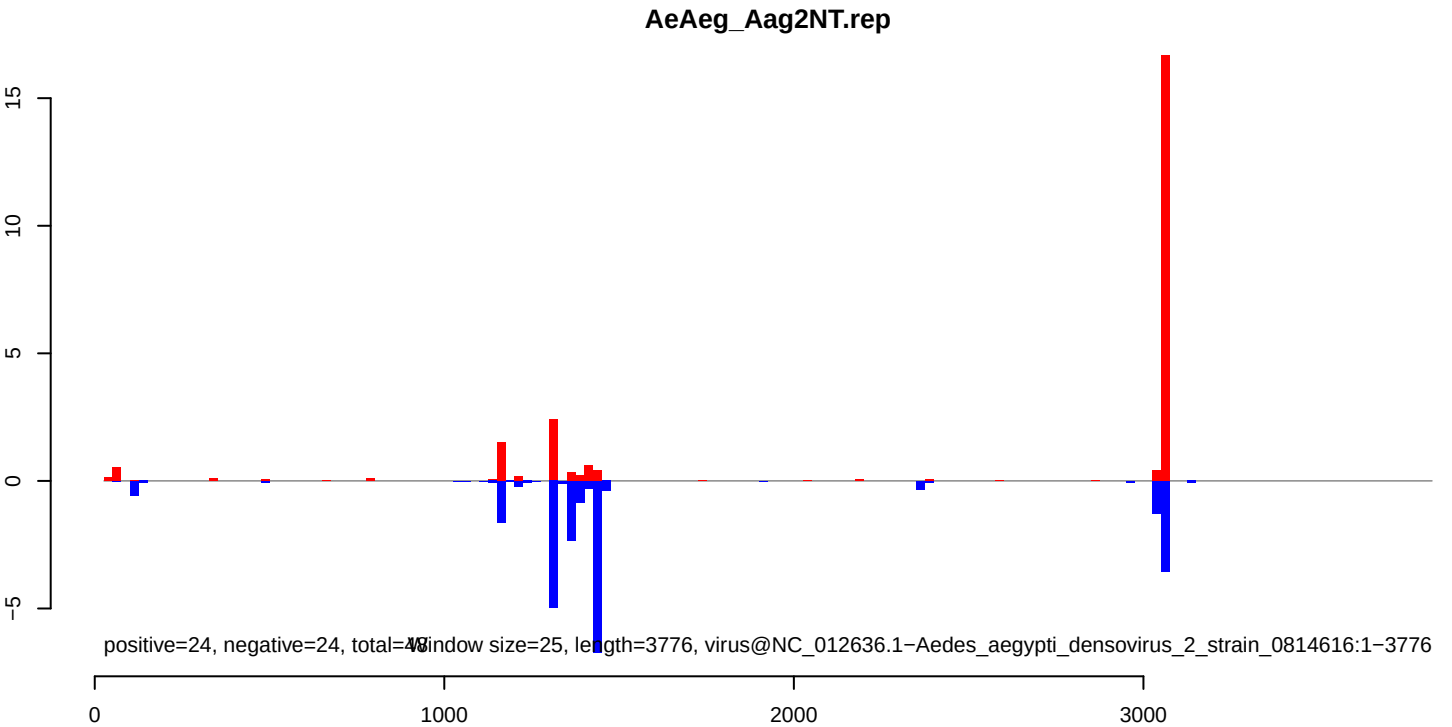

AeAeg_Aag2NT.18_23.rep
5
0
−5
−10
positive=16, negative=47, total=62
AeAeg_Aag2NT.24_35.rep
5
0
−5
−10
positive=0, negative=1, total=1
AeAeg_Aag2NT.rep
5
0
−5
−10
positive=16, negative=48, total=64
Window size=25, length=4073, virus@KX603698.1−Aedes_albopictus_densovirus_5_strain_GZ05:1−4073
0
1000
2000
3000
4000

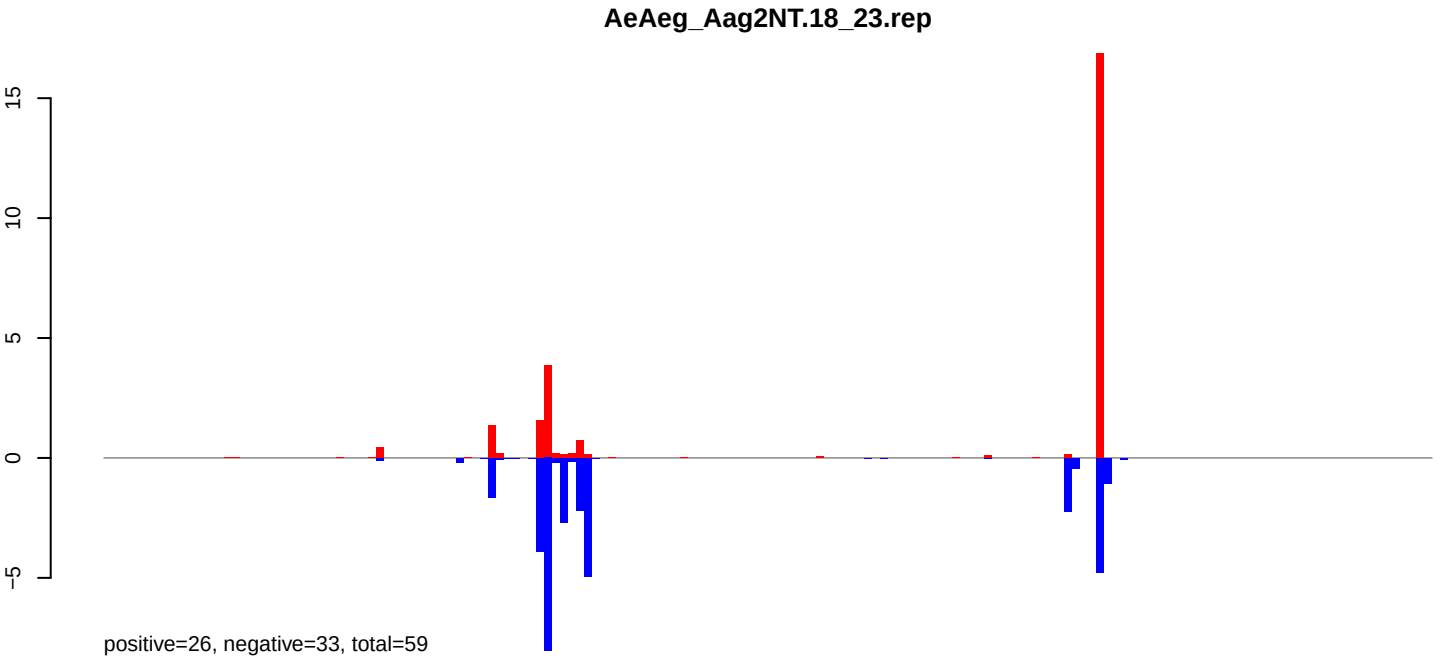

AeAeg_Aag2NT.18_23.rep
positive=16, negative=40, total=55
AeAeg_Aag2NT.24_35.rep
positive=0, negative=1, total=1
AeAeg_Aag2NT.rep
positive=16, negative=40, total=56
Window size=25, length=3893, virus@GU452720.1−Mosquito_densovirus_BR_07:1−3893
4
2
0
−2
−4
−6
0
1000
2000
3000
4000

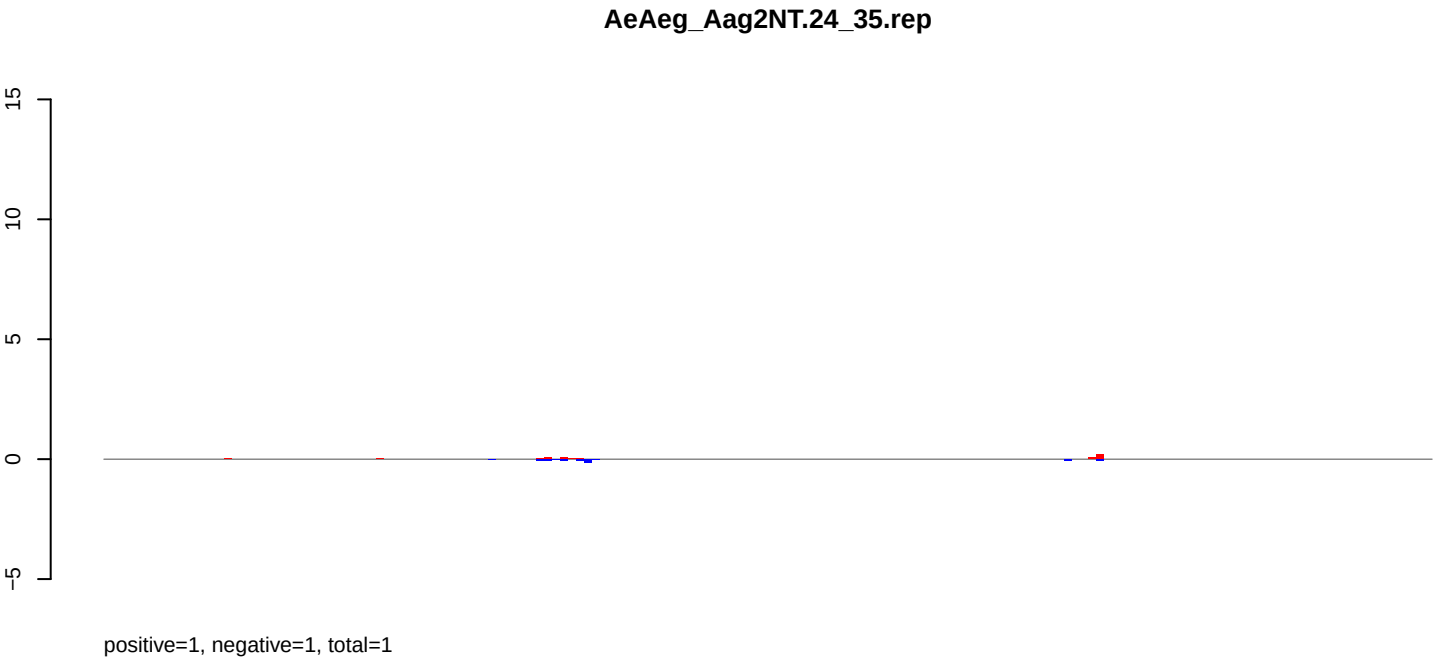

AeAeg_Aag2NT.18_23.rep
positive=14, negative=44, total=58
AeAeg_Aag2NT.24_35.rep
positive=0, negative=1, total=1
AeAeg_Aag2NT.rep
positive=58, negative=45, total=103
gi|1355351.2-Aedes_albopictus_C6_36_cell_densovirus_non-structural_protein_1_NS-1_non-structural:1-4094
0
1000
2000
3000
4000

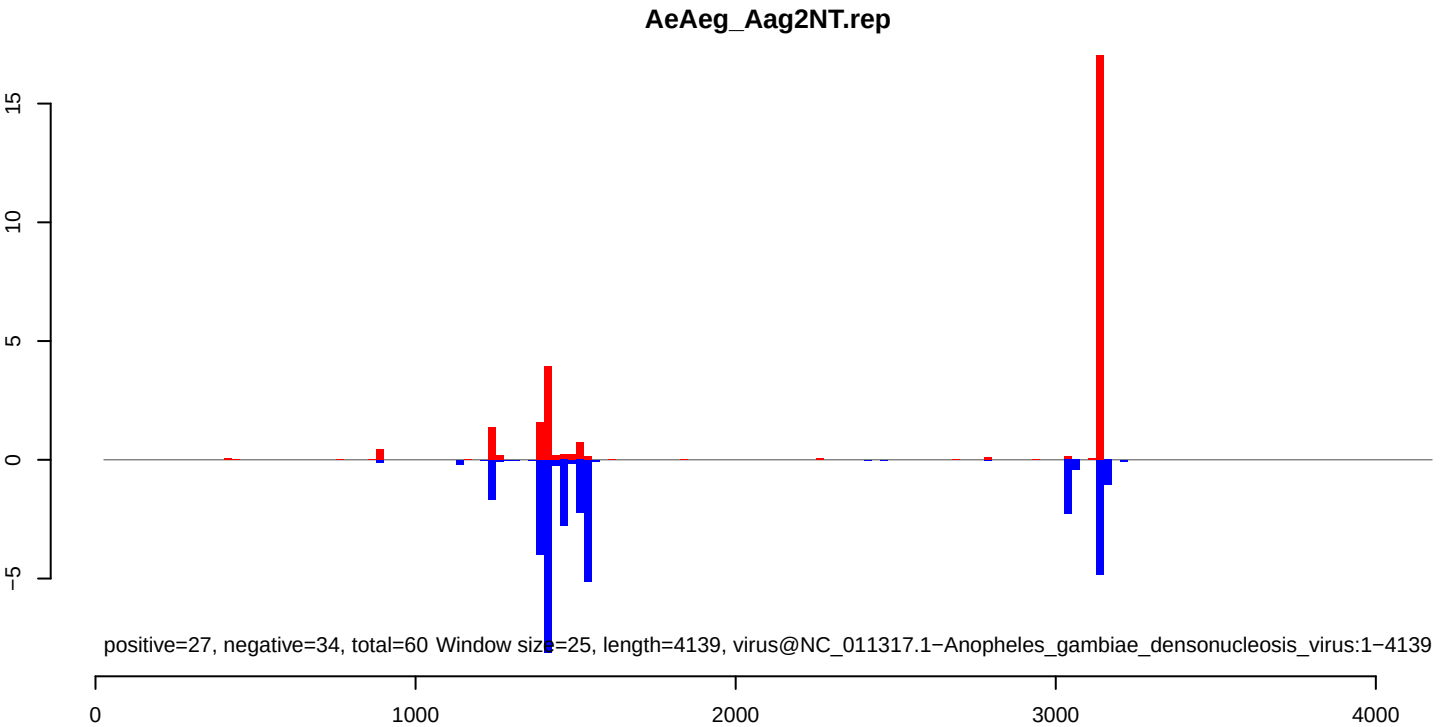

AeAeg_Aag2NT.18_23.rep
15
10
5
0
−5
positive=24, negative=23, total=47

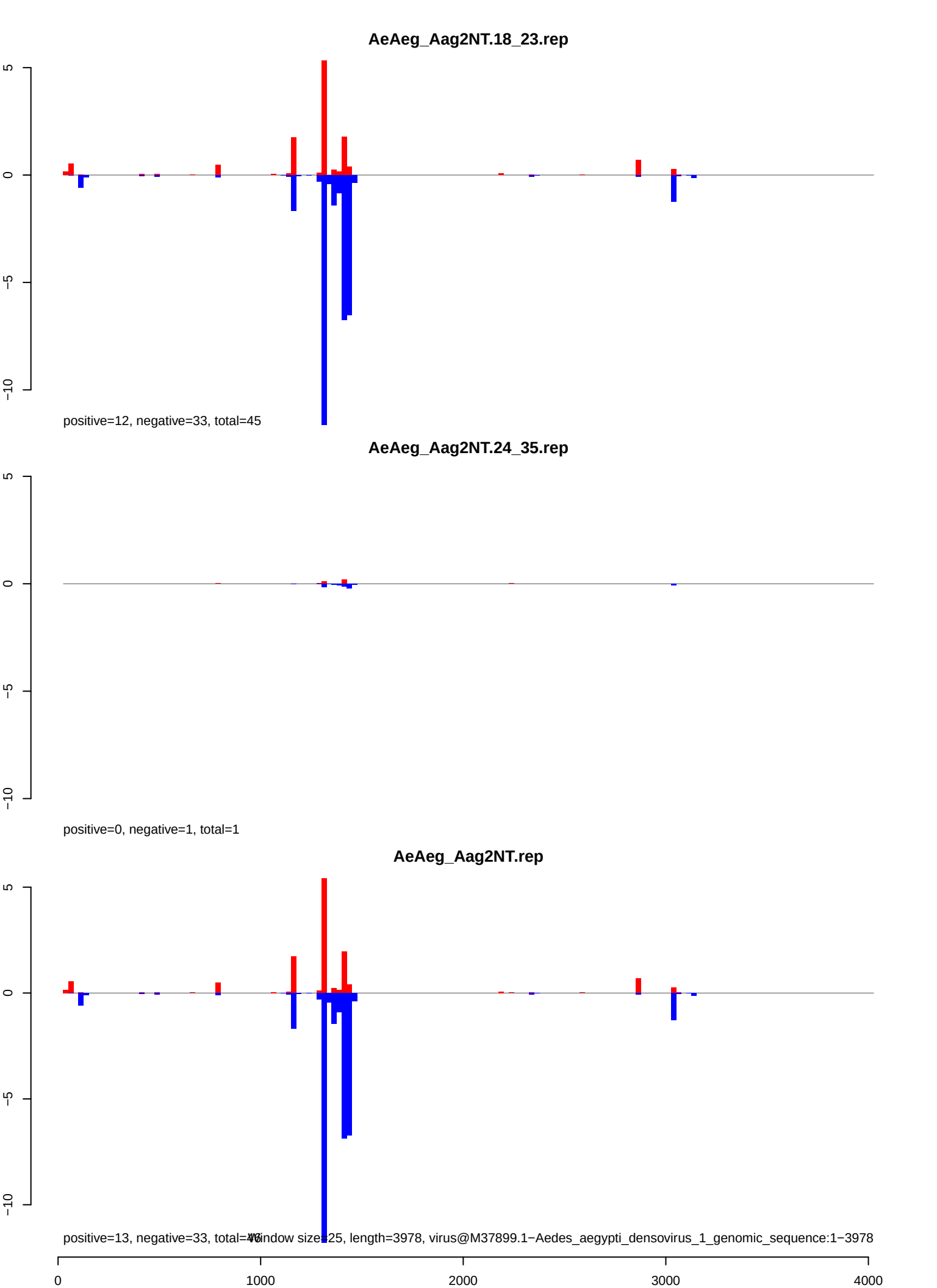

AeAeg_Aag2NT.24_35.rep
15
10
5
0
−5
positive=0, negative=1, total=1

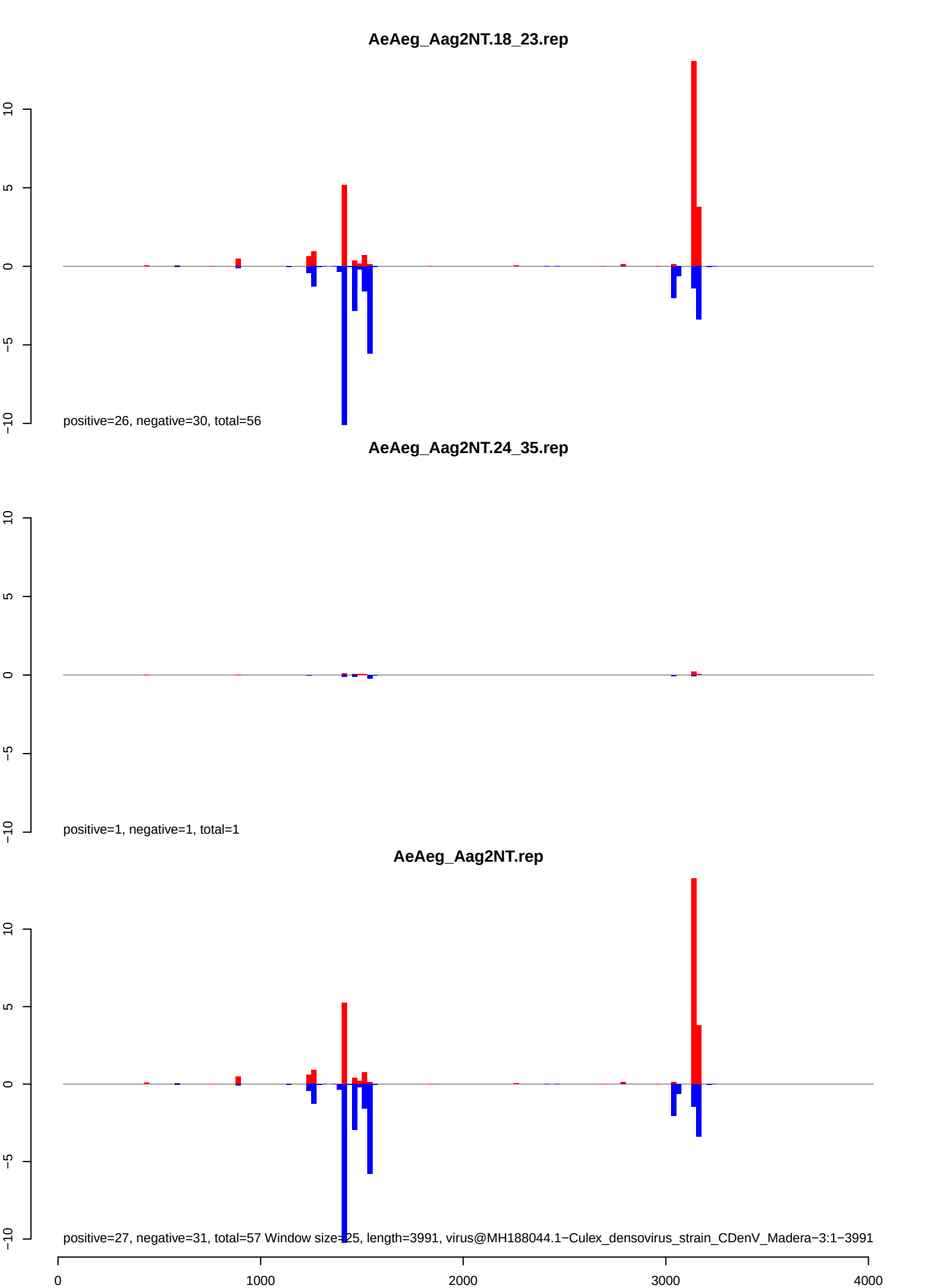

AeAeg_Aag2NT.rep
15
10
5
0
−5
positive=24, negative=24, total=48
window size=25, length=3776, virus@NC_012636.1−Aedes_aegypti_densovirus_2_strain_0814616:1−3776
0
1000
2000
3000

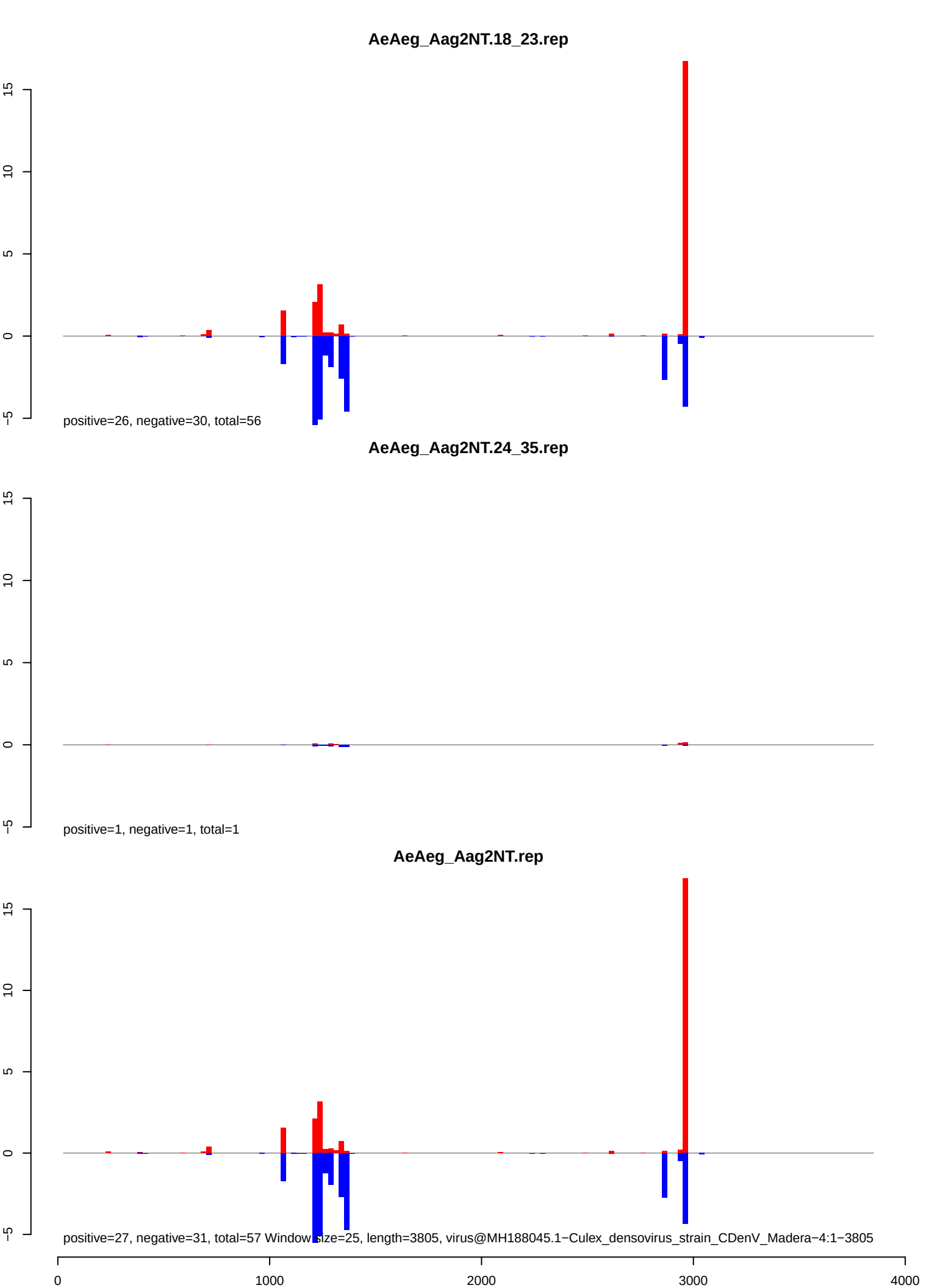

AeAeg_Aag2NT.18_23.rep
15
10
5
0
−5
positive=26, negative=33, total=59

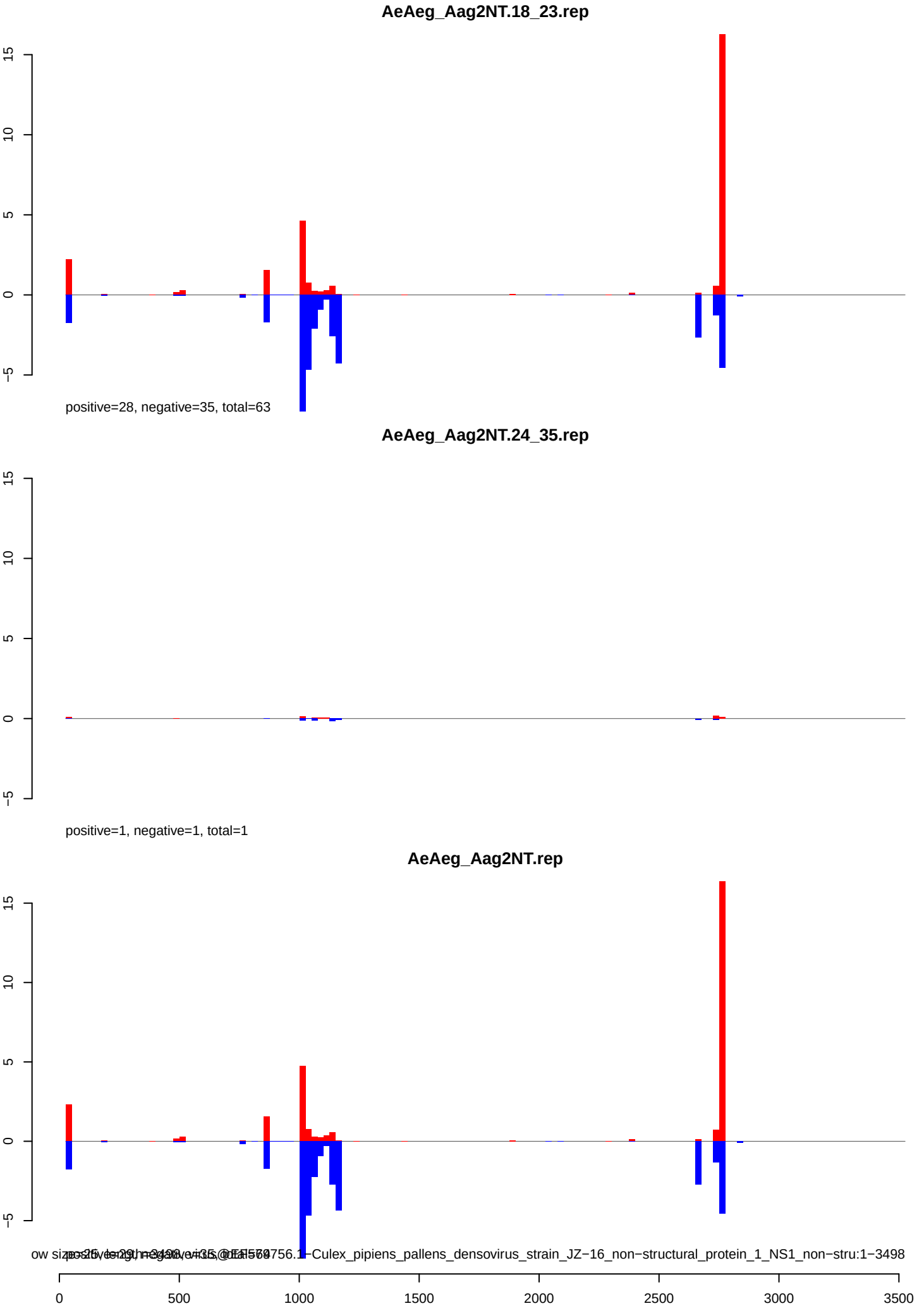

AeAeg_Aag2NT.24_35.rep
15
10
5
0
−5
positive=1, negative=1, total=1

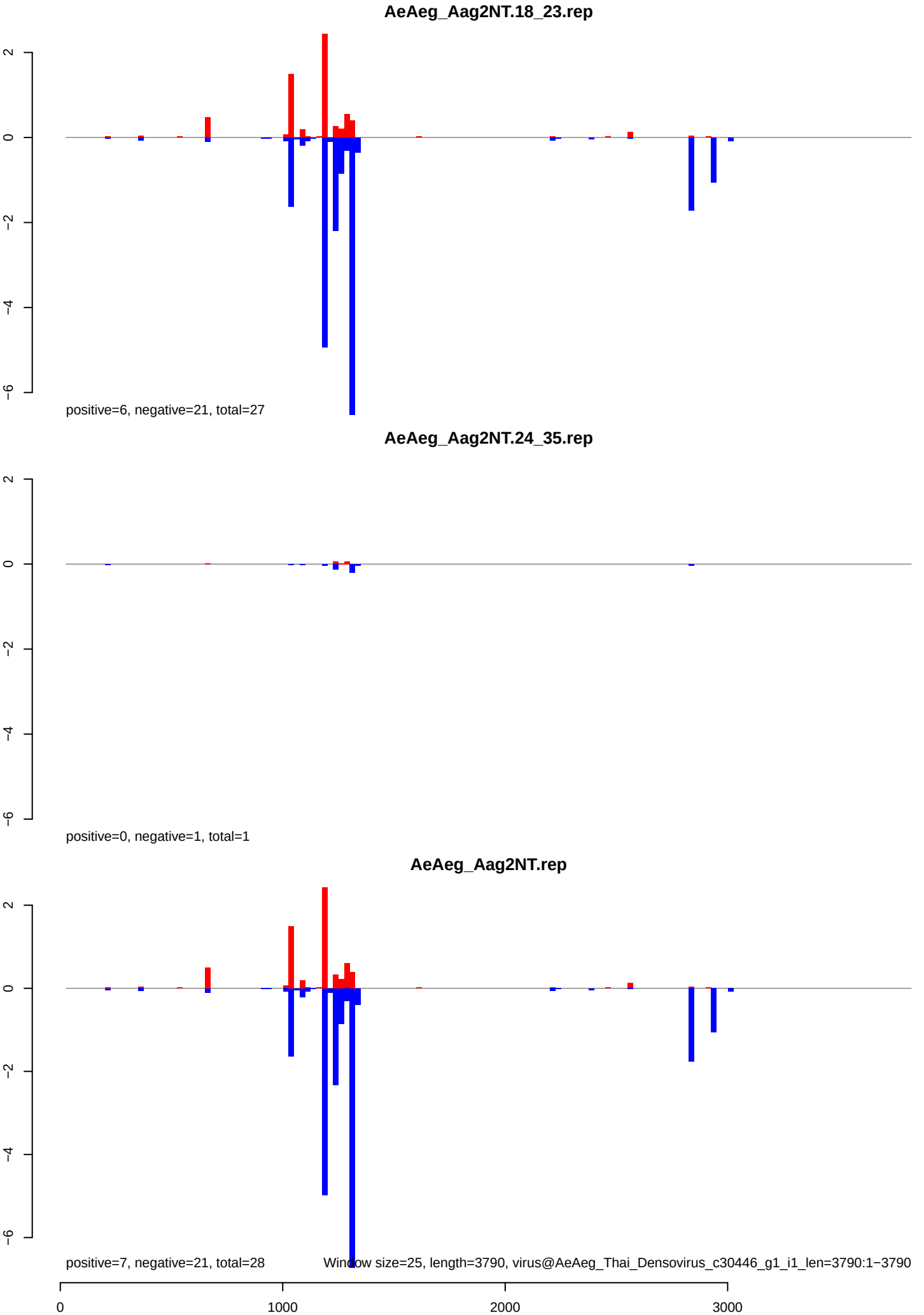

AeAeg_Aag2NT.rep
15
10
5
0
−5
positive=27, negative=34, total=60 Window size=25, length=4139, virus@NC_011317.1−Anopheles_gambiae_densonucleosis_virus:1−4139
0
1000
2000
3000
4000

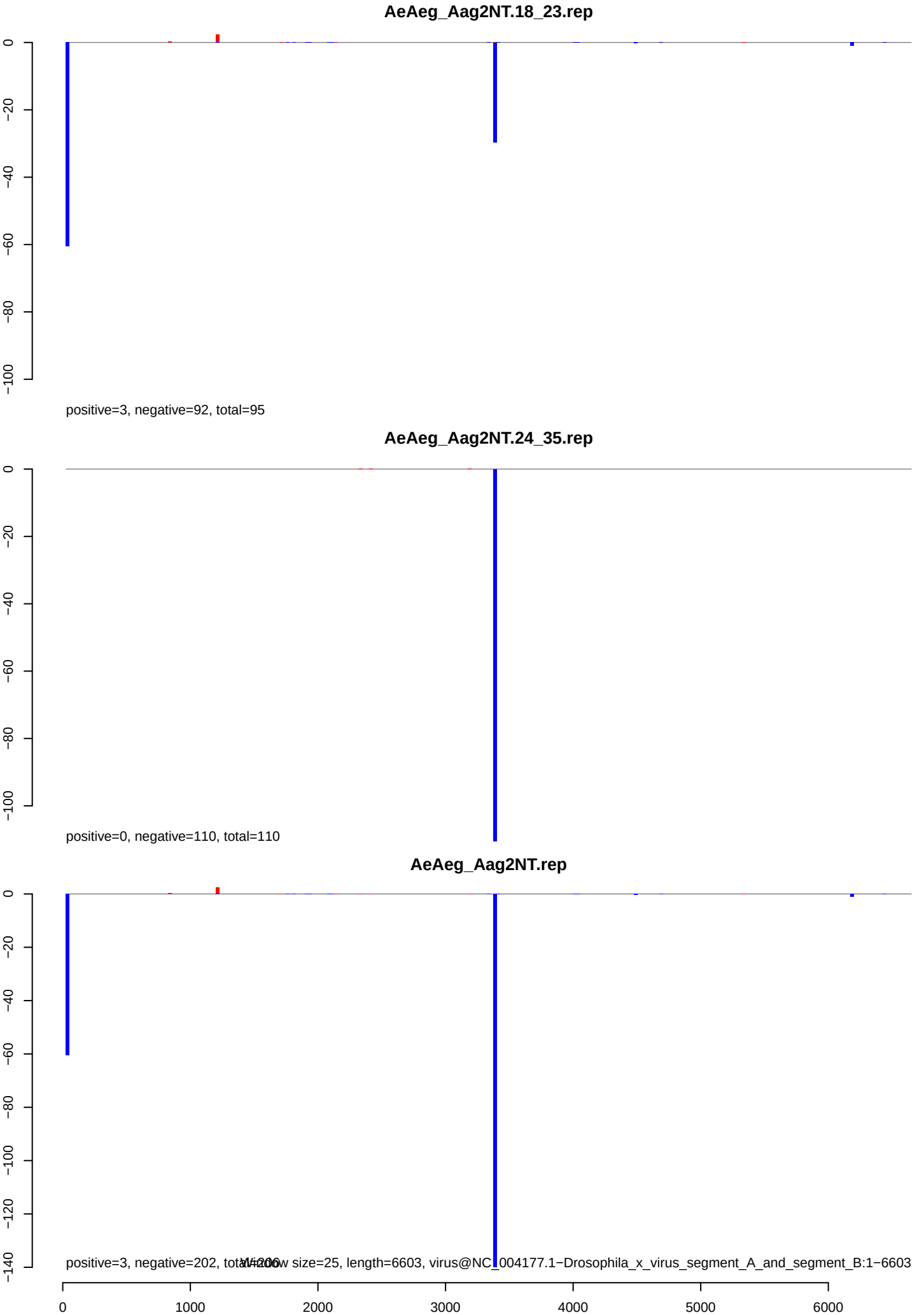

AeAeg_Aag2NT.18_23.rep
5
0
−5
−10
positive=12, negative=33, total=45
AeAeg_Aag2NT.24_35.rep
5
0
−5
−10
positive=0, negative=1, total=1
AeAeg_Aag2NT.rep
5
0
−5
−10
positive=13, negative=33, total=46
window size=25, length=3978, virus@M37899.1−Aedes_aegypti_densovirus_1_genomic_sequence:1−3978
0
1000
2000
3000
4000

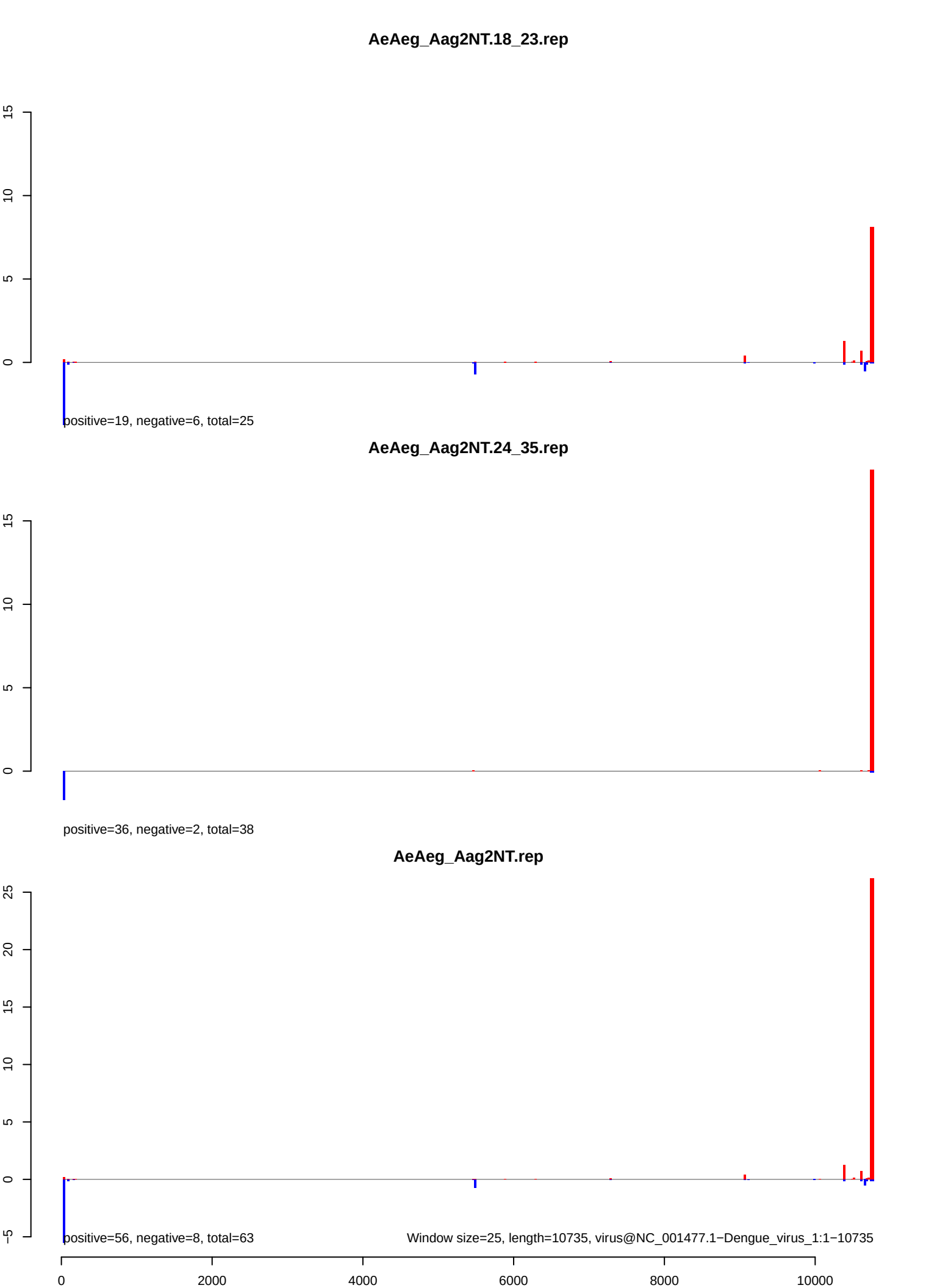

AeAeg_Aag2NT.18_23.rep
10
5
0
−5
−10
positive=26, negative=30, total=56
AeAeg_Aag2NT.24_35.rep
10
5
0
−5
−10
positive=1, negative=1, total=1
AeAeg_Aag2NT.rep
10
5
0
−5
−10
positive=27, negative=31, total=57 Window size=25, length=3991, virus@MH188044.1−Culex_densovirus_strain_CDenV_Madera−3:1−3991
0
1000
2000
3000
4000

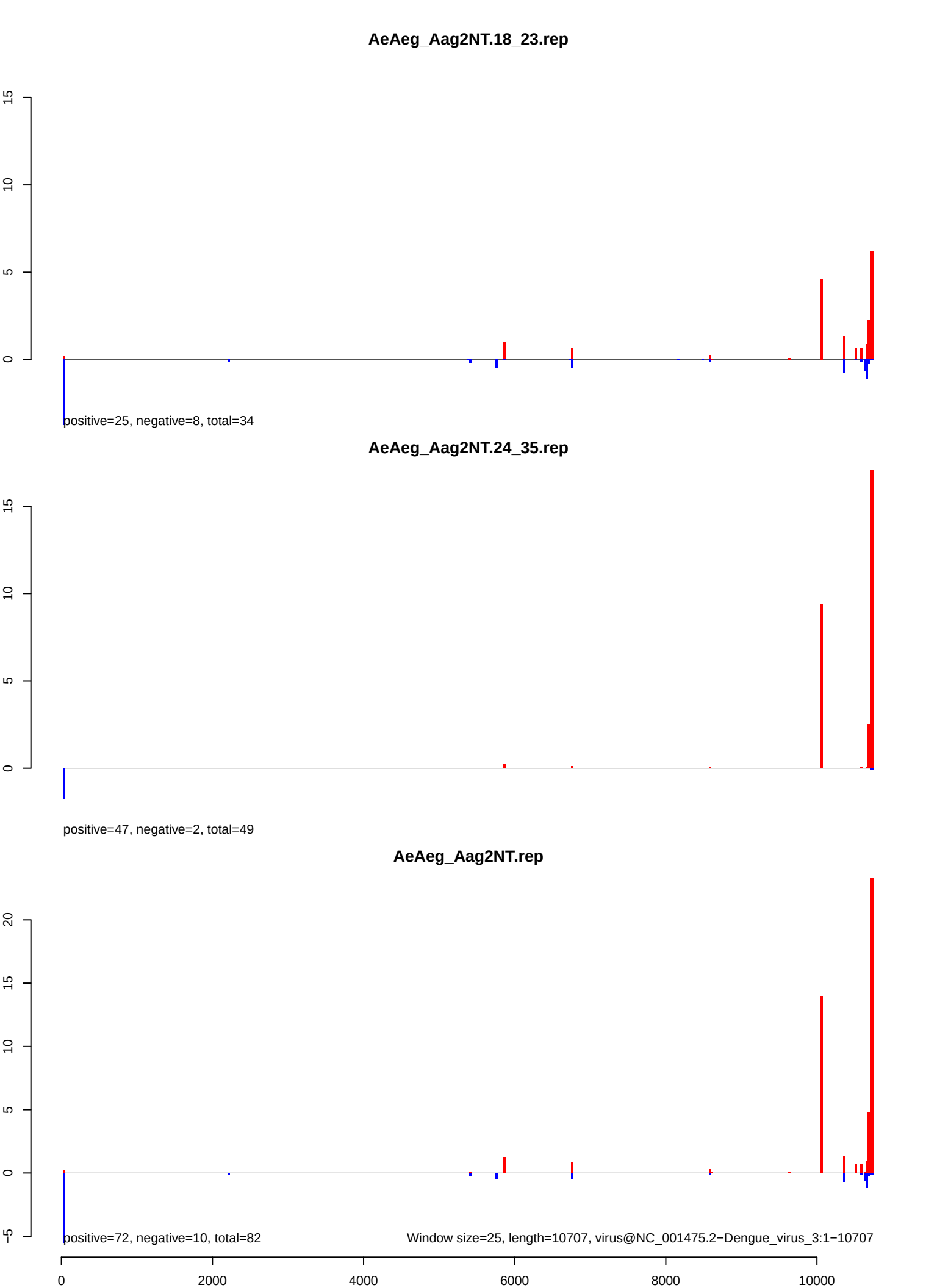

AeAeg_Aag2NT.18_23.rep
15
10
5
0
−5
positive=26, negative=30, total=56
AeAeg_Aag2NT.24_35.rep
15
10
5
0
−5
positive=1, negative=1, total=1
AeAeg_Aag2NT.rep
15
10
5
0
−5
positive=27, negative=31, total=57 Window size=25, length=3805, virus@MH188045.1−Culex_densovirus_strain_CDenV_Madera−4:1−3805
0
1000
2000
3000
4000

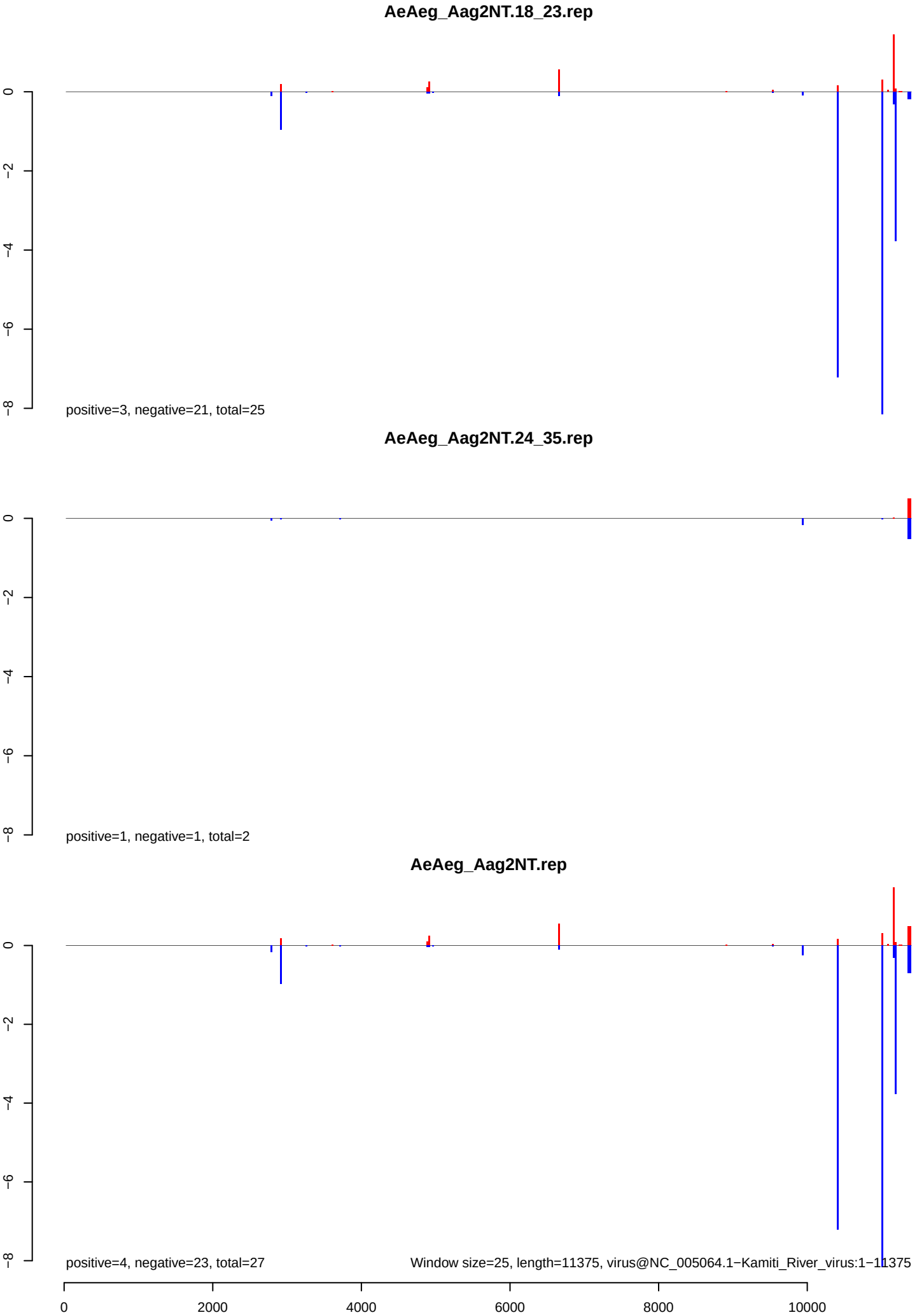

AeAeg_Aag2NT.18_23.rep
15
10
5
0
−5
positive=28, negative=35, total=63
AeAeg_Aag2NT.24_35.rep
15
10
5
0
−5
positive=1, negative=1, total=1
AeAeg_Aag2NT.rep
15
10
5
0
−5
0
500
1000
1500
2000
2500
3000
3500

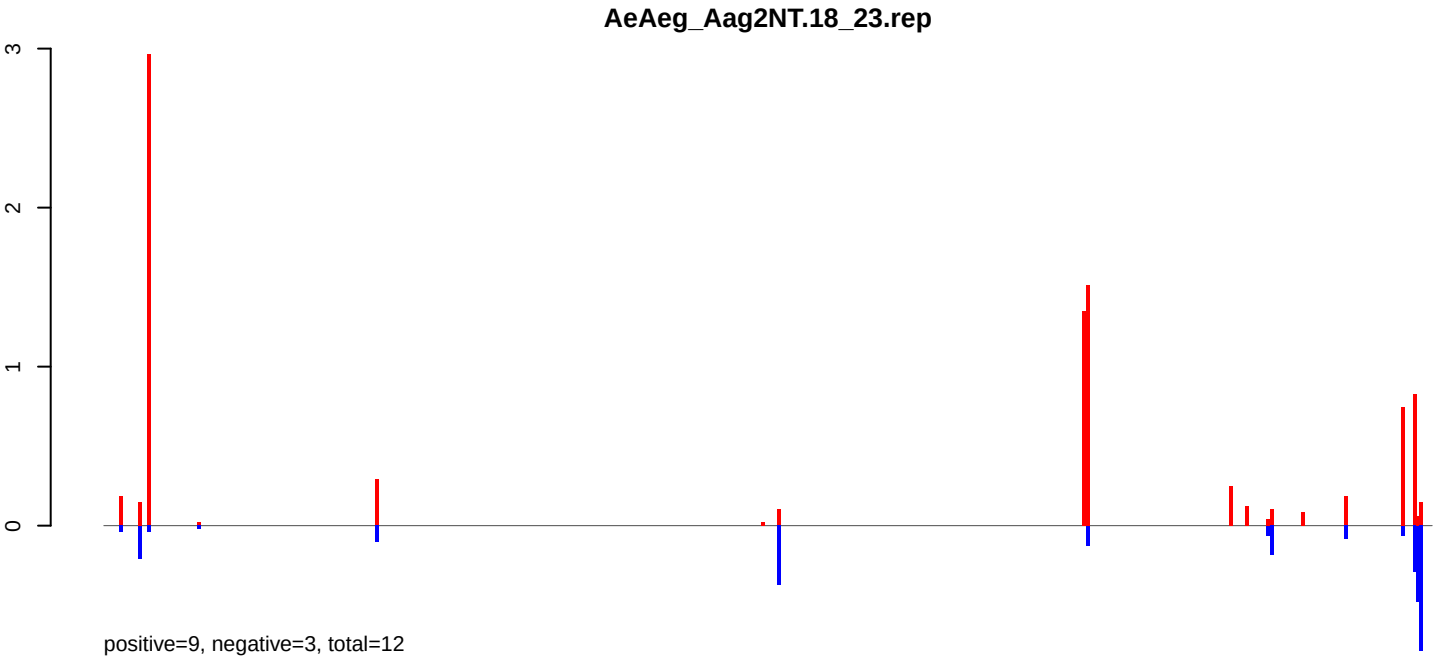

AeAeg_Aag2NT.18_23.rep
2
0
−2
−4
−6
positive=6, negative=21, total=27
AeAeg_Aag2NT.24_35.rep
2
0
−2
−4
−6
positive=0, negative=1, total=1
AeAeg_Aag2NT.rep
2
0
−2
−4
−6
positive=7, negative=21, total=28
Window size=25, length=3790, virus@AeAeg_Thai_Densovirus_c30446_g1_i1_len=3790:1−3790
0
1000
2000
3000

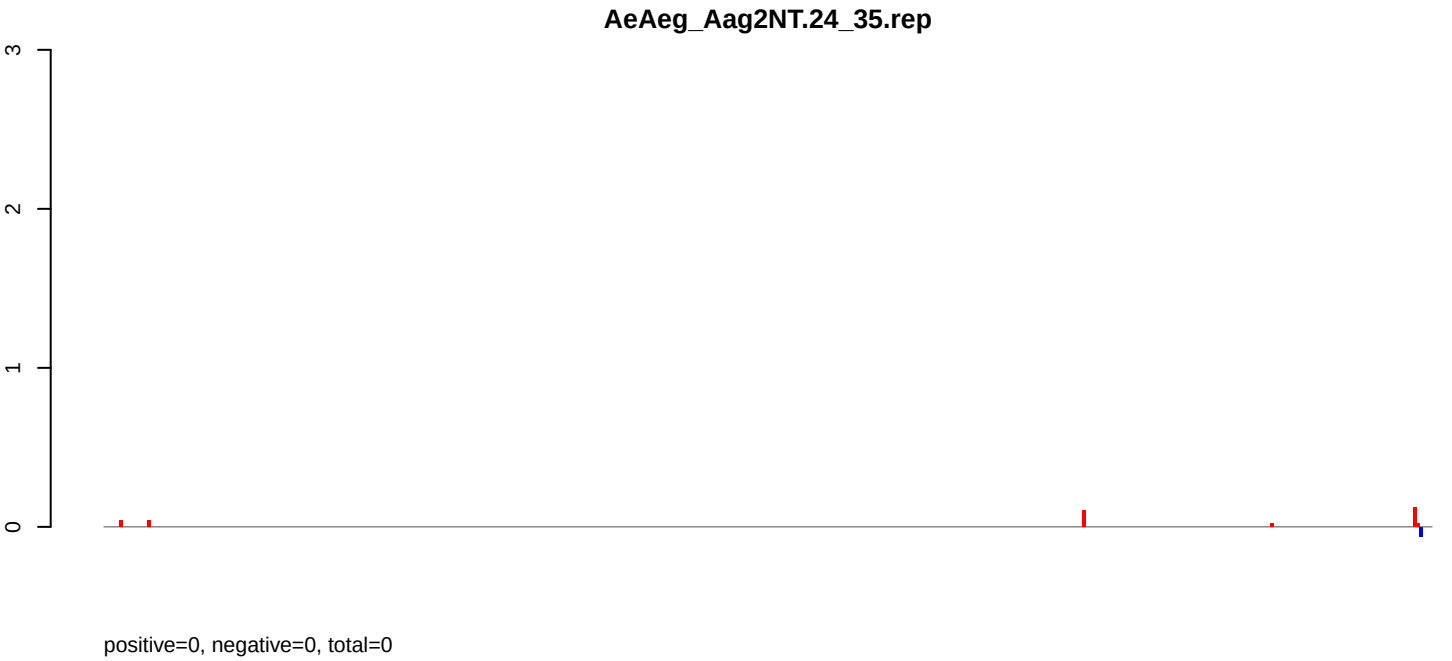

AeAeg_Aag2NT.18_23.rep
0
−20
−40
−60
−80
−100
positive=3, negative=92, total=95
AeAeg_Aag2NT.24_35.rep
0
−20
−40
−60
−80
−100
positive=0, negative=110, total=110
AeAeg_Aag2NT.rep
0
−20
−40
−60
−80
−100
−120
−140
positive=3, negative=202, total=206
window size=25, length=6603, virus@NC_004177.1−Drosophila_x_virus_segment_A_and_segment_B:1−6603
0
1000
2000
3000
4000
5000
6000

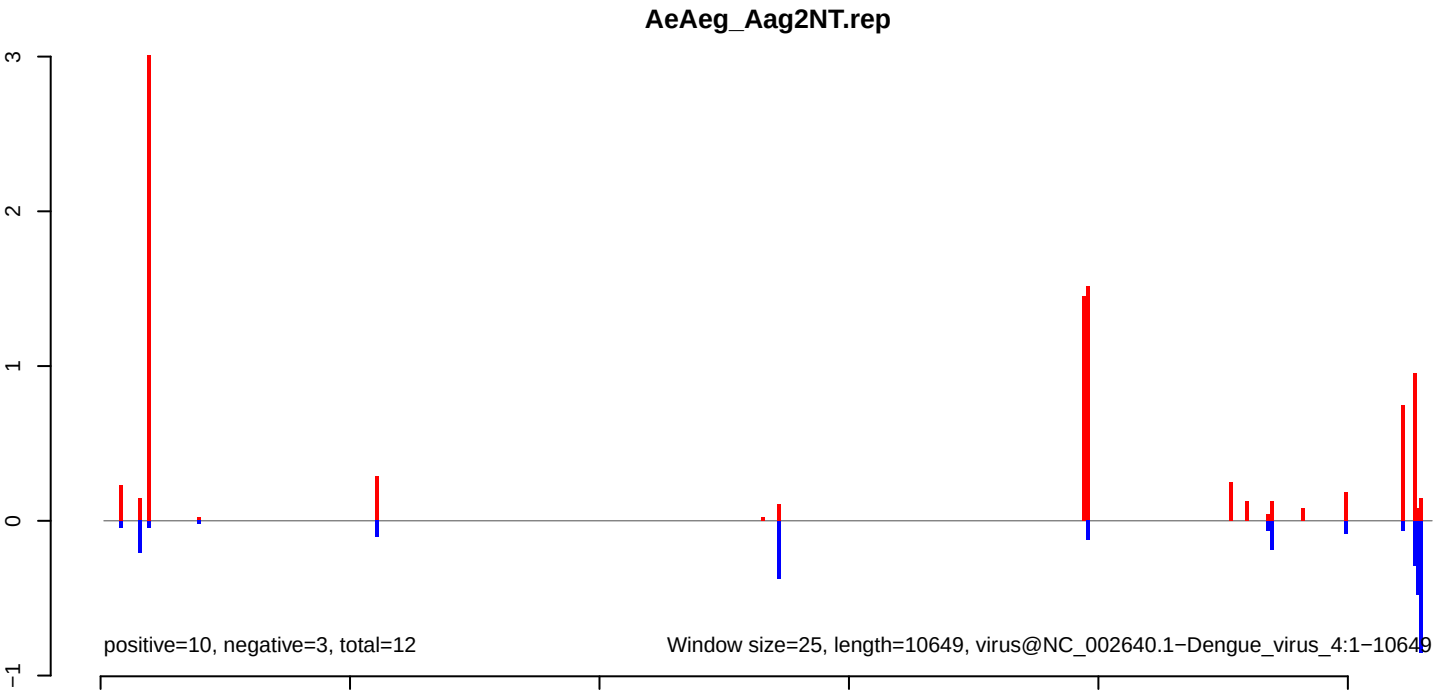

AeAeg_Aag2NT.18_23.rep
15
10
5
0
positive=19, negative=6, total=25
AeAeg_Aag2NT.24_35.rep
15
10
5
0
positive=36, negative=2, total=38
AeAeg_Aag2NT.rep
25
20
15
10
5
0
−5
positive=56, negative=8, total=63
Window size=25, length=10735, virus@NC_001477.1−Dengue_virus_1:1−10735
0
2000
4000
6000
8000
10000

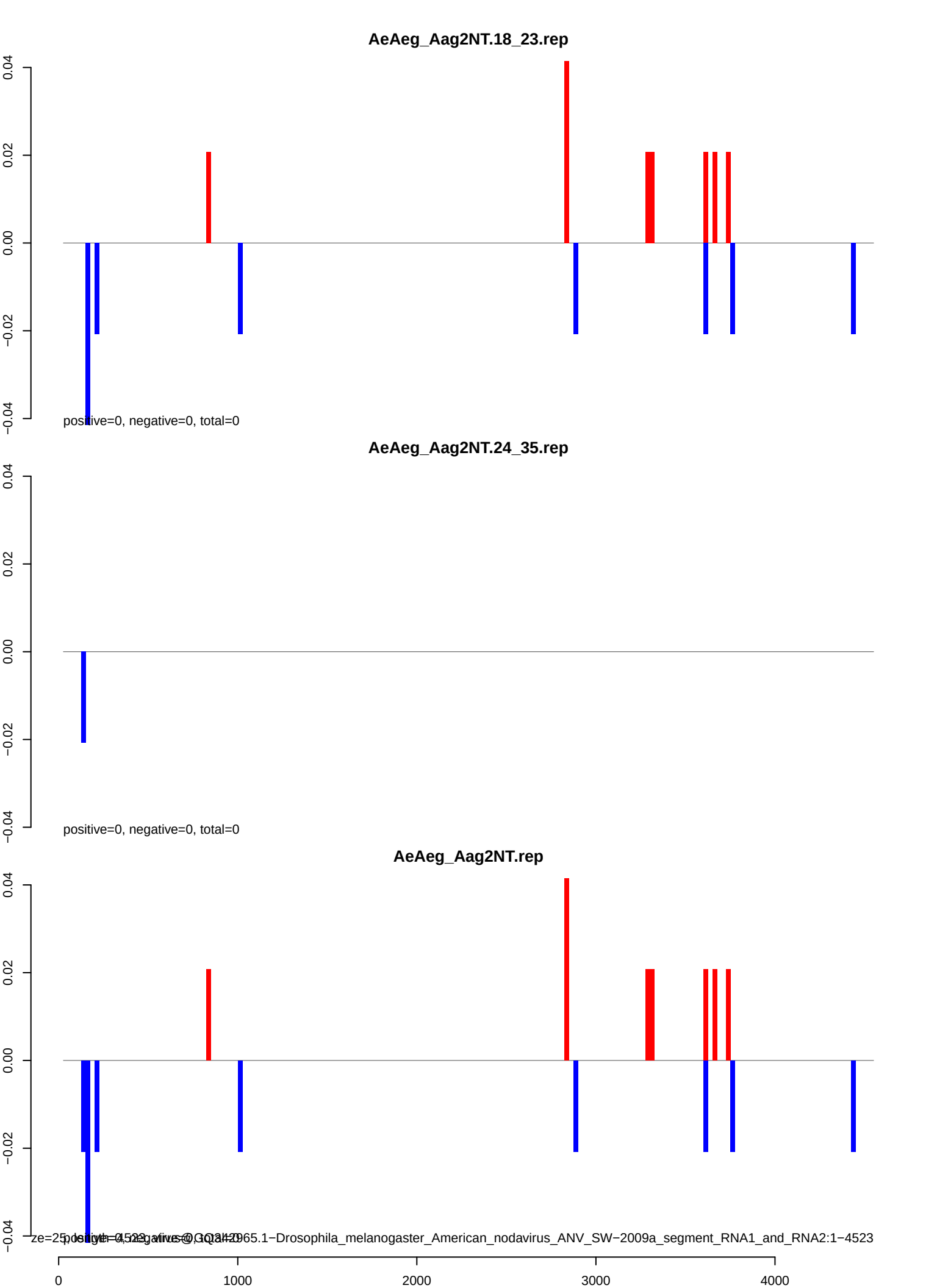

AeAeg_Aag2NT.18_23.rep
15
10
5
0
positive=25, negative=8, total=34
AeAeg_Aag2NT.24_35.rep
15
10
5
0
positive=47, negative=2, total=49
AeAeg_Aag2NT.rep
20
15
10
5
0
−5
positive=72, negative=10, total=82
Window size=25, length=10707, virus@NC_001475.2−Dengue_virus_3:1−10707
0
2000
4000
6000
8000
10000

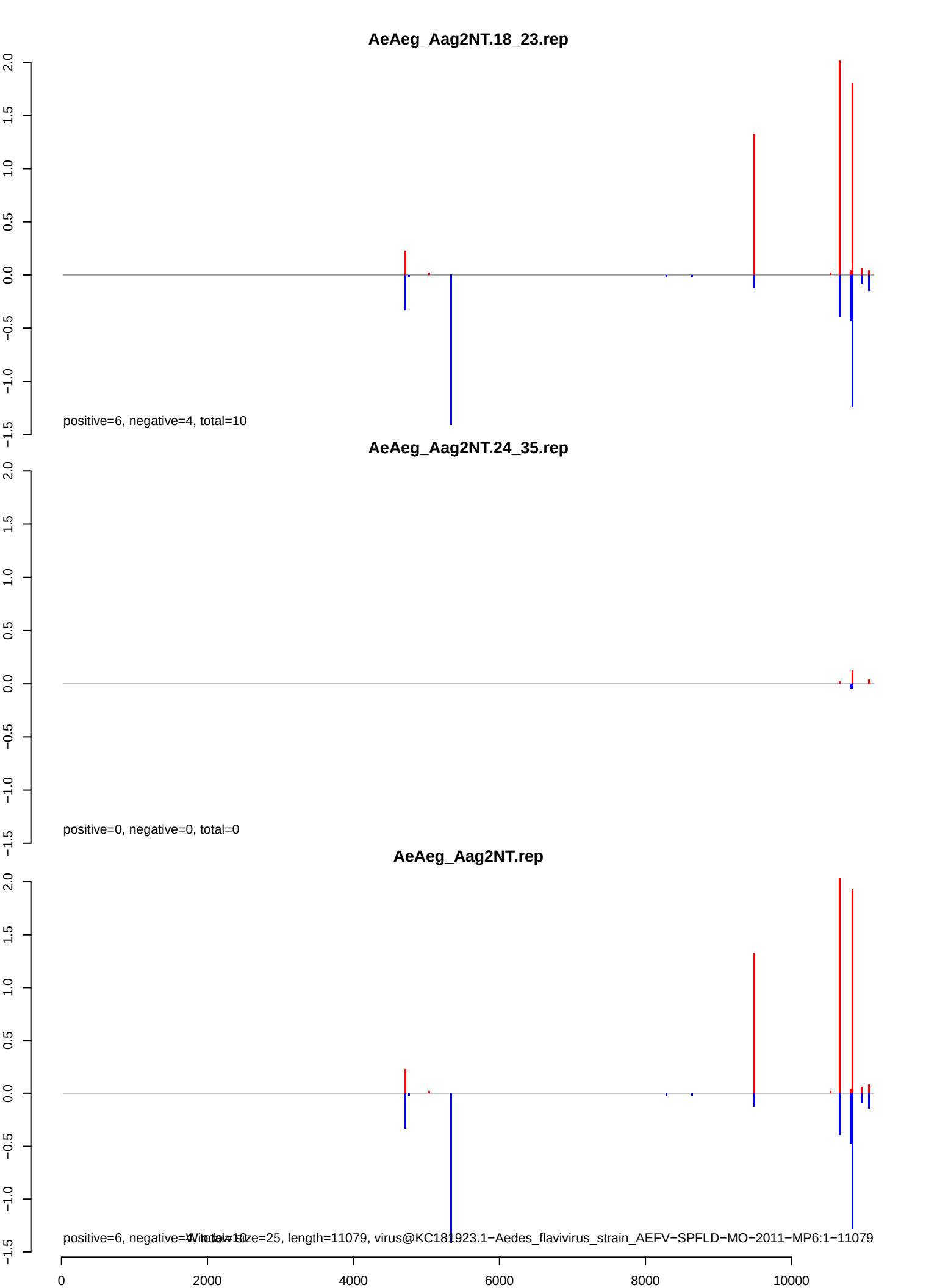

AeAeg_Aag2NT.18_23.rep
0
−2
−4
−6
−8
positive=3, negative=21, total=25
AeAeg_Aag2NT.24_35.rep
0
−2
−4
−6
−8
positive=1, negative=1, total=2
AeAeg_Aag2NT.rep
0
−2
−4
−6
−8
positive=4, negative=23, total=27
Window size=25, length=11375, virus@NC_005064.1−Kamiti_River_virus:1−11375
0
2000
4000
6000
8000
10000

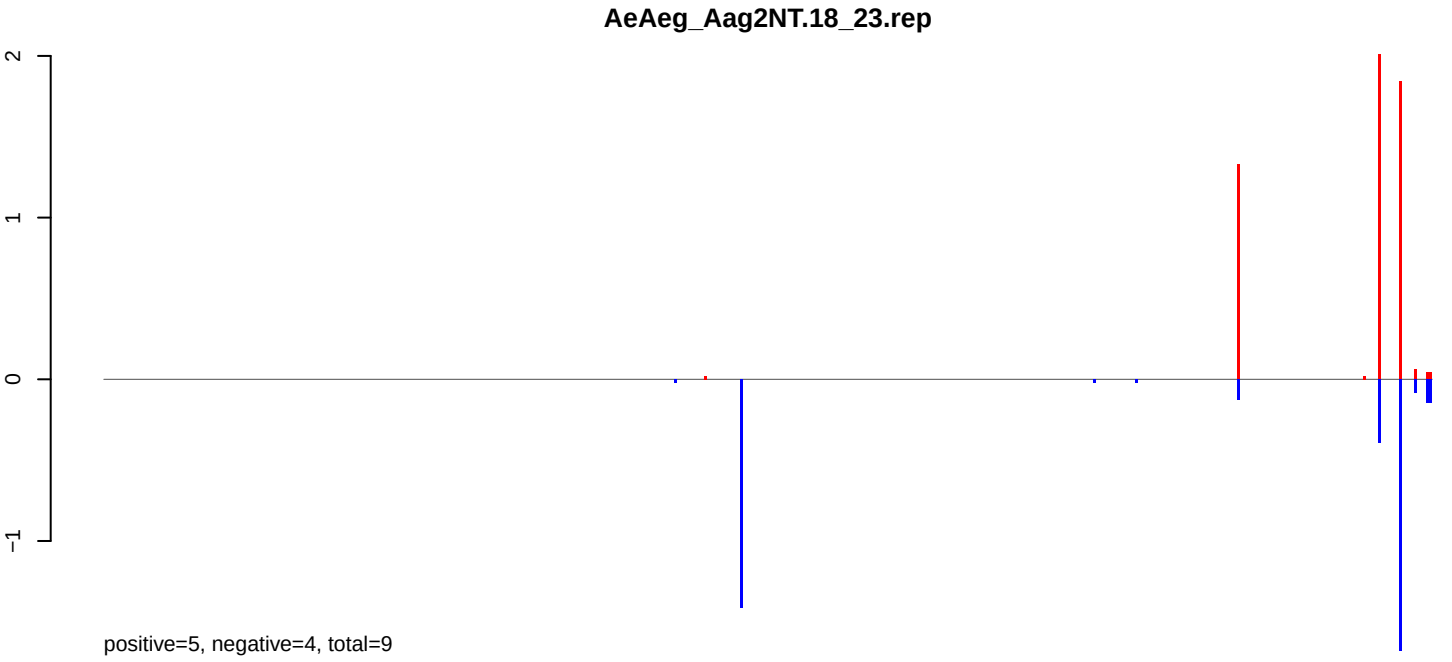

AeAeg_Aag2NT.18_23.rep
3
2
1
0
positive=9, negative=3, total=12

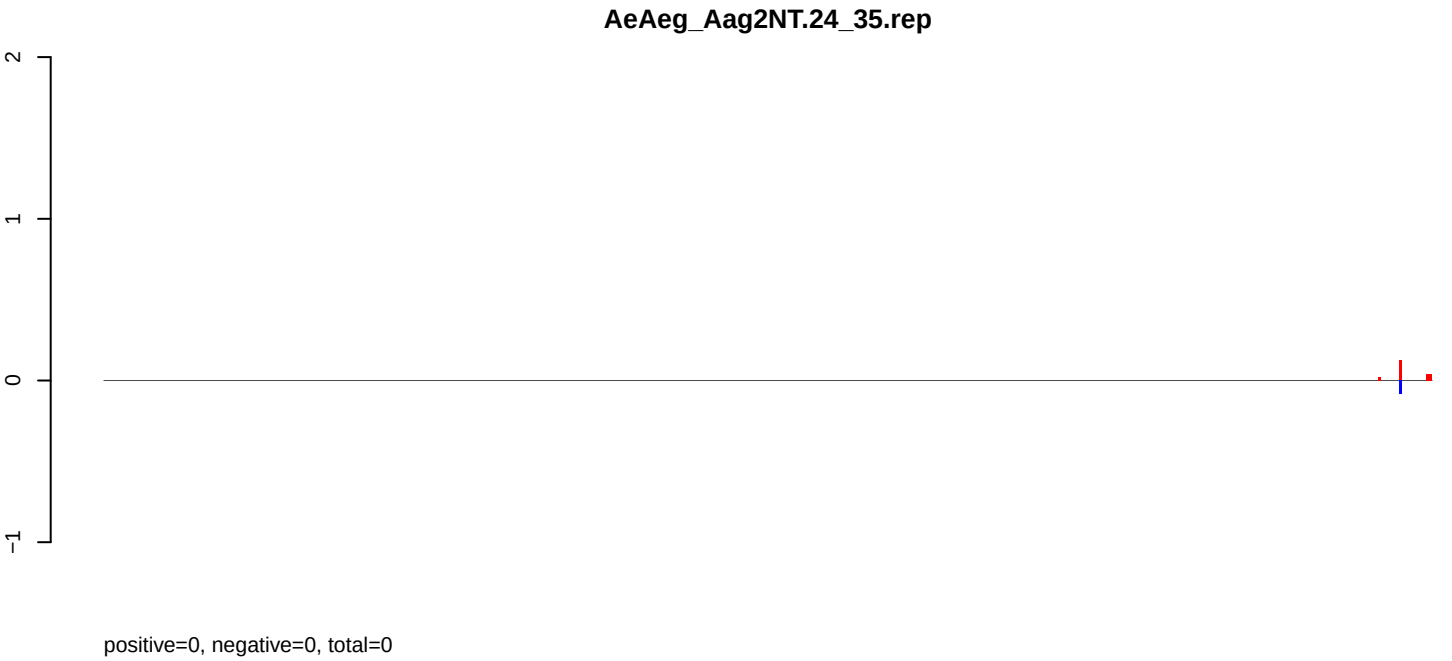

AeAeg_Aag2NT.24_35.rep
3
2
1
0
positive=0, negative=0, total=0

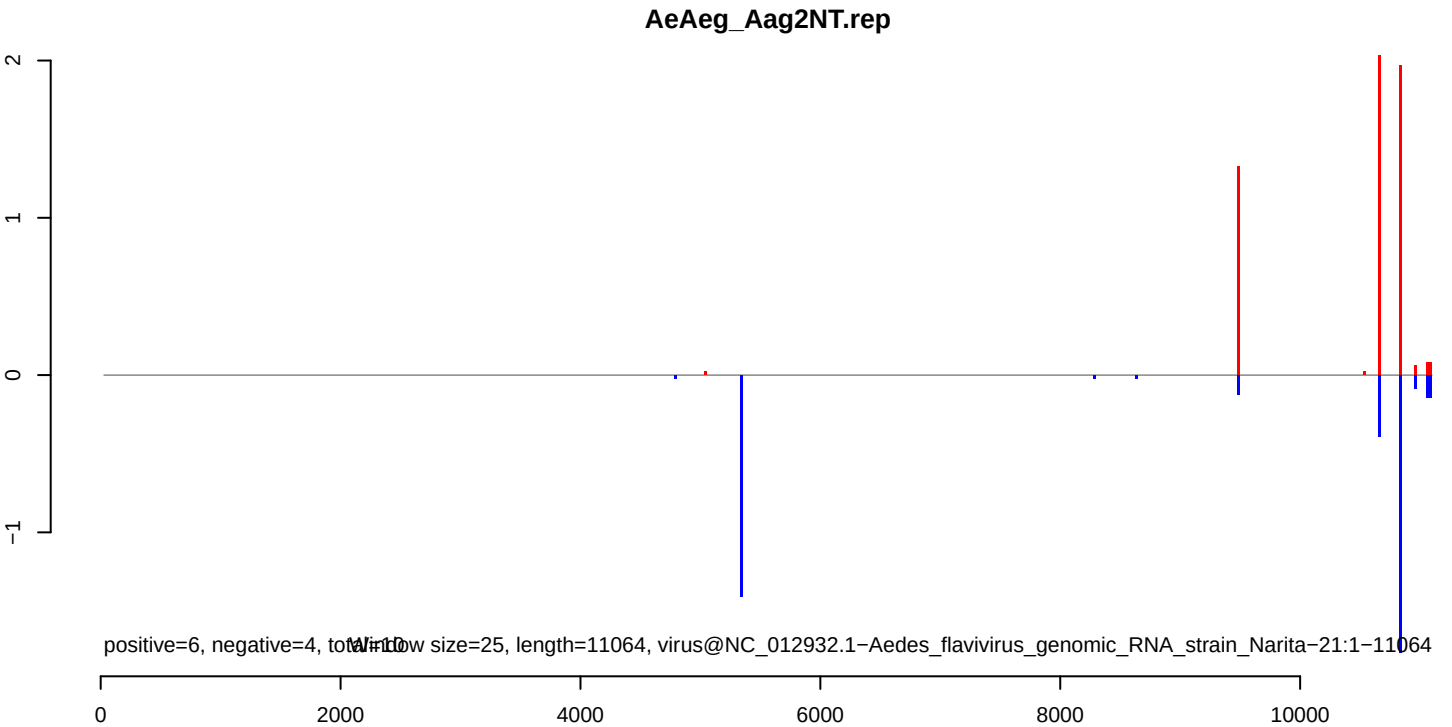

AeAeg_Aag2NT.rep
3
2
1
0
−1
positive=10, negative=3, total=12
Window size=25, length=10649, virus@NC_002640.1−Dengue_virus_4:1−10649
0
2000
4000
6000
8000
10000

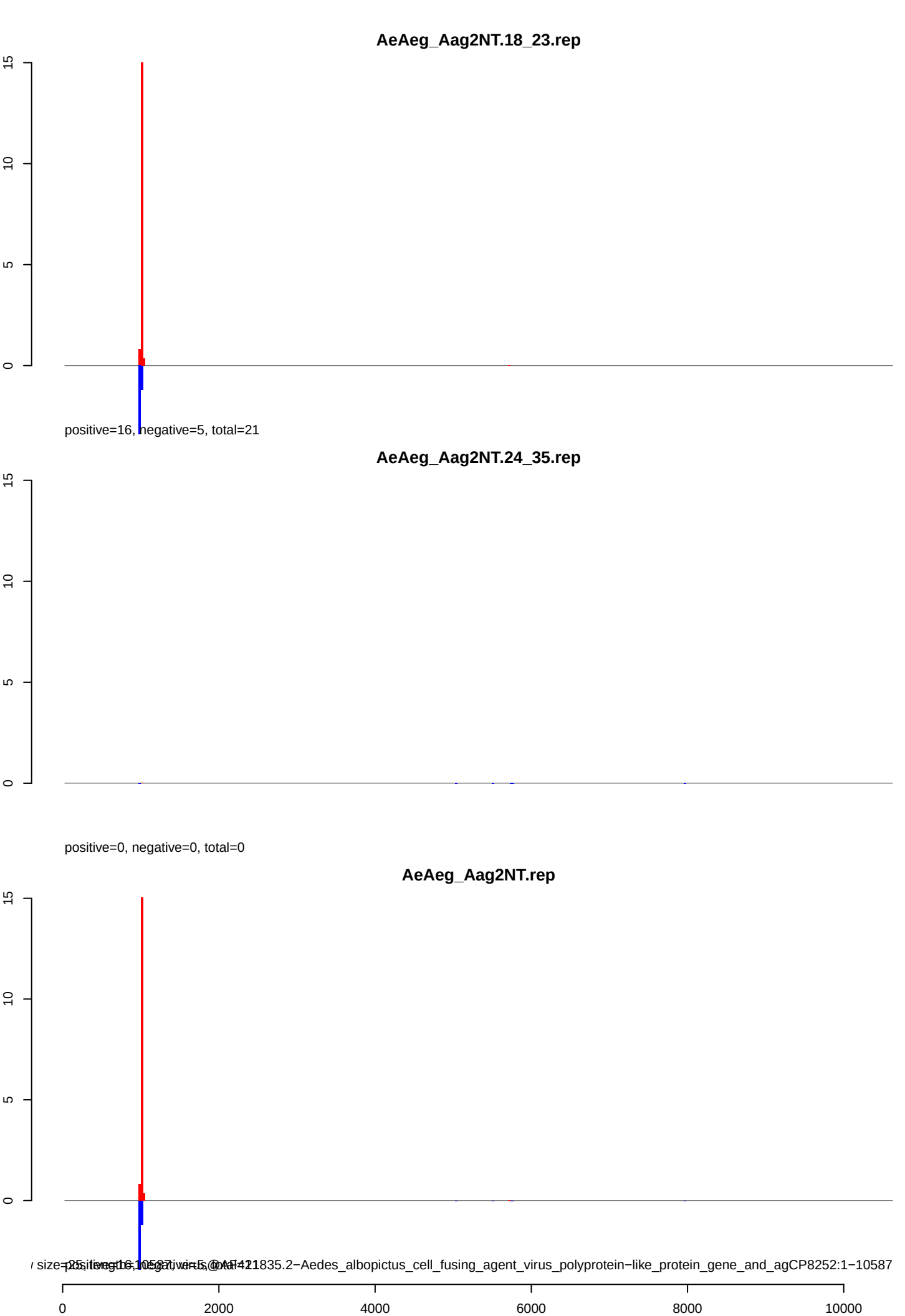

AeAeg_Aag2NT.18_23.rep
0.04
0.02
0.00
−0.02
−0.04
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
0.04
0.02
0.00
−0.02
−0.04
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.04
0.02
0.00
−0.02
−0.04
ze=25, positive=4523, negative=0, total=4523 NC_003142965.1−Drosophila_melanogaster_American_nodavirus_ANV_SW−2009a_segment_RNA1_and_RNA2:1−4523
0
1000
2000
3000
4000

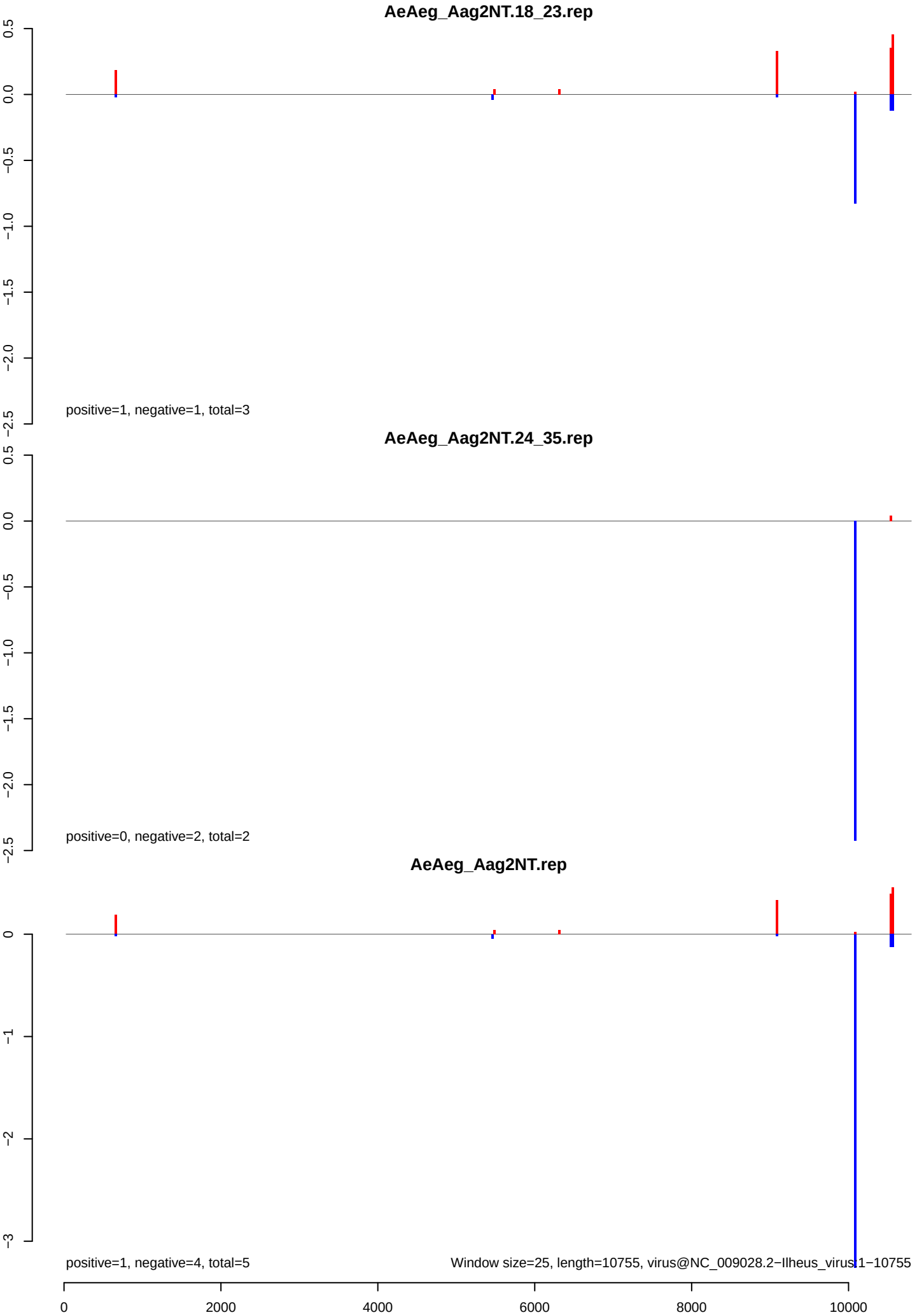

AeAeg_Aag2NT.18_23.rep
positive=6, negative=4, total=10
AeAeg_Aag2NT.24_35.rep
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
positive=6, negative=4, total=10
Window size=25, length=11079, virus@KC181923.1−Aedes_flavivirus_strain_AEFV−SPFLD−MO−2011−MP6:1−11079
2.0
1.5
1.0
0.5
0.0
−0.5
−1.0
−1.5
0
2000
4000
6000
8000
10000

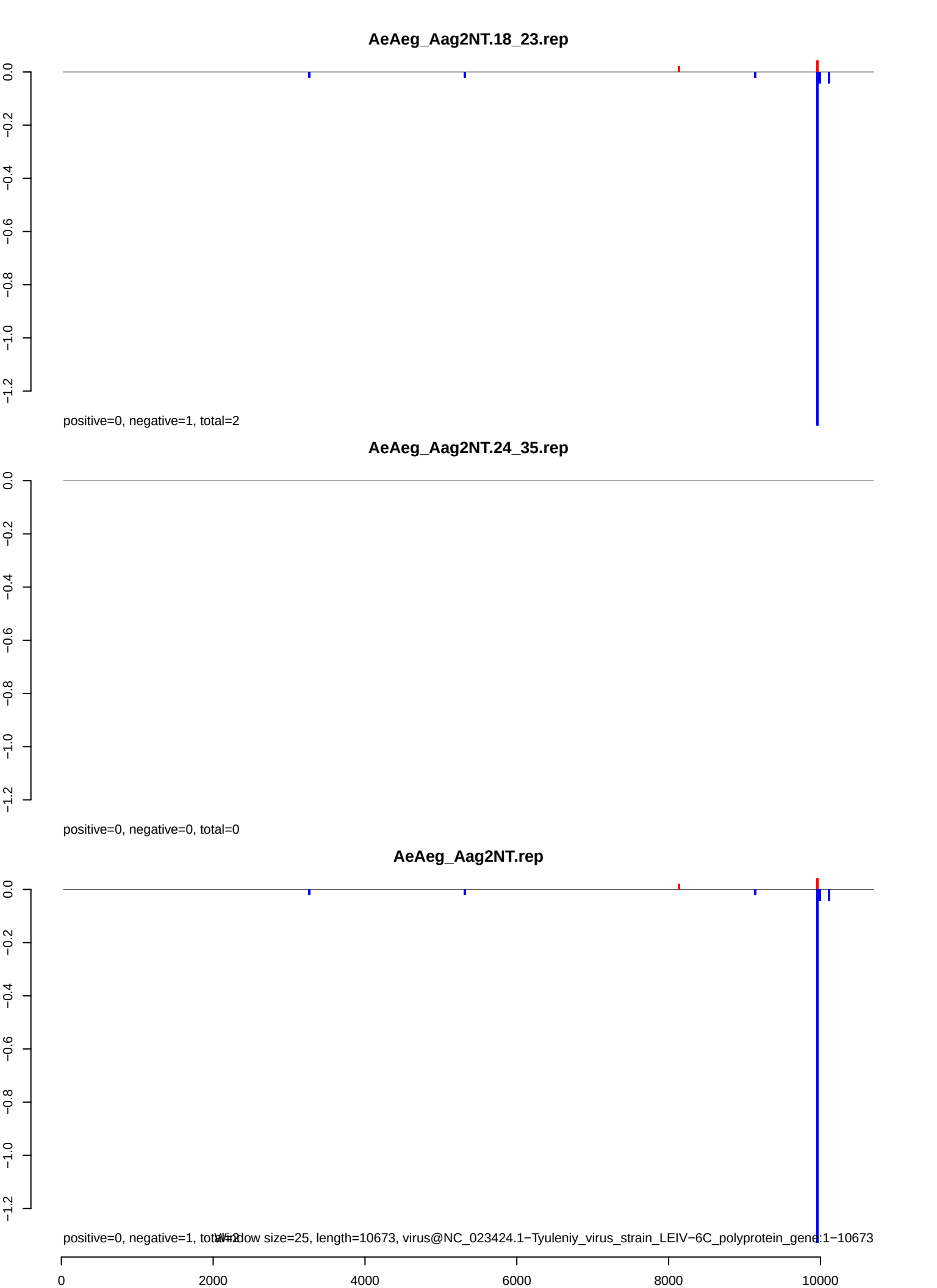

AeAeg_Aag2NT.18_23.rep
2
1
0
−1
positive=5, negative=4, total=9

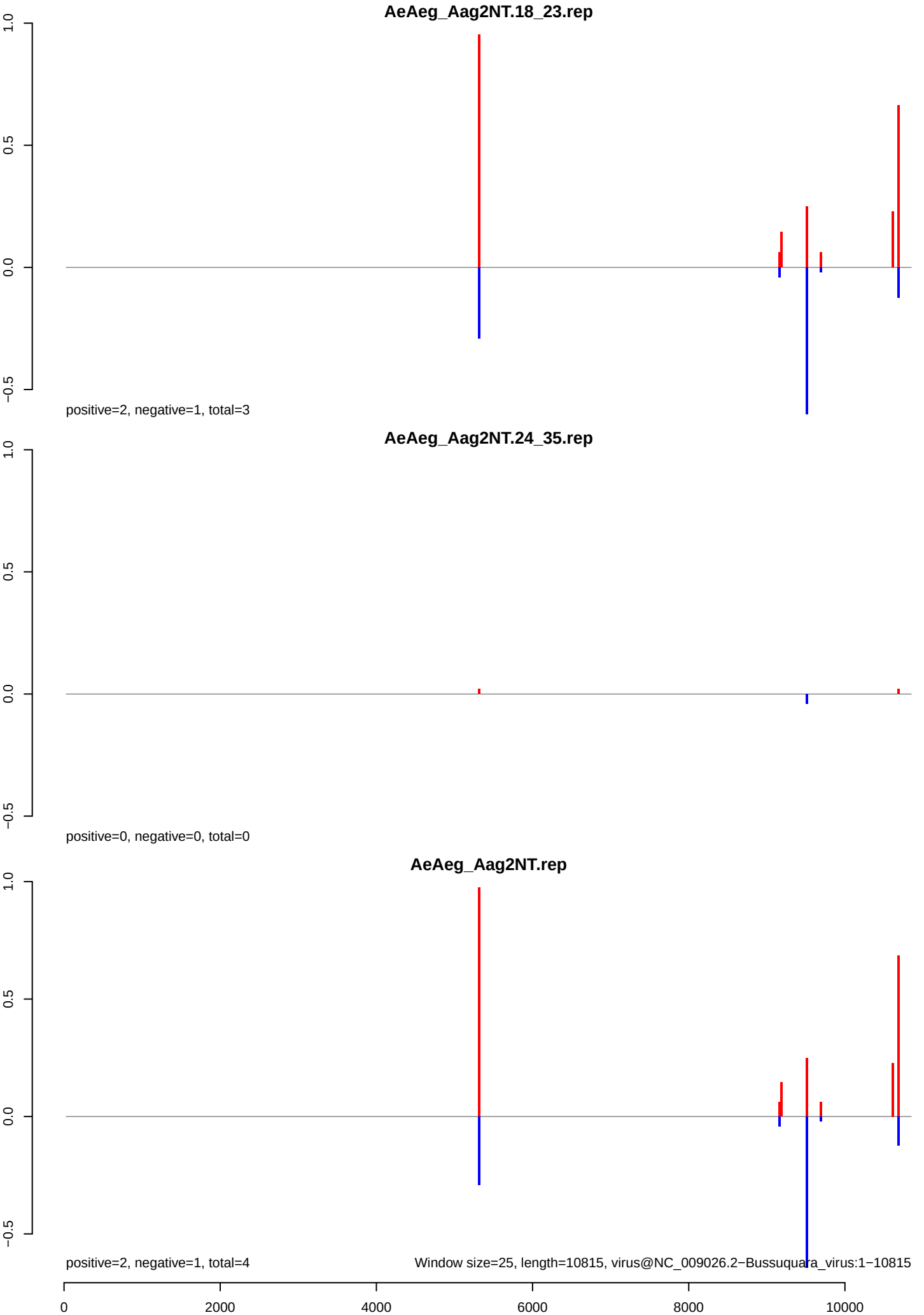

AeAeg_Aag2NT.24_35.rep
2
1
0
−1
positive=0, negative=0, total=0

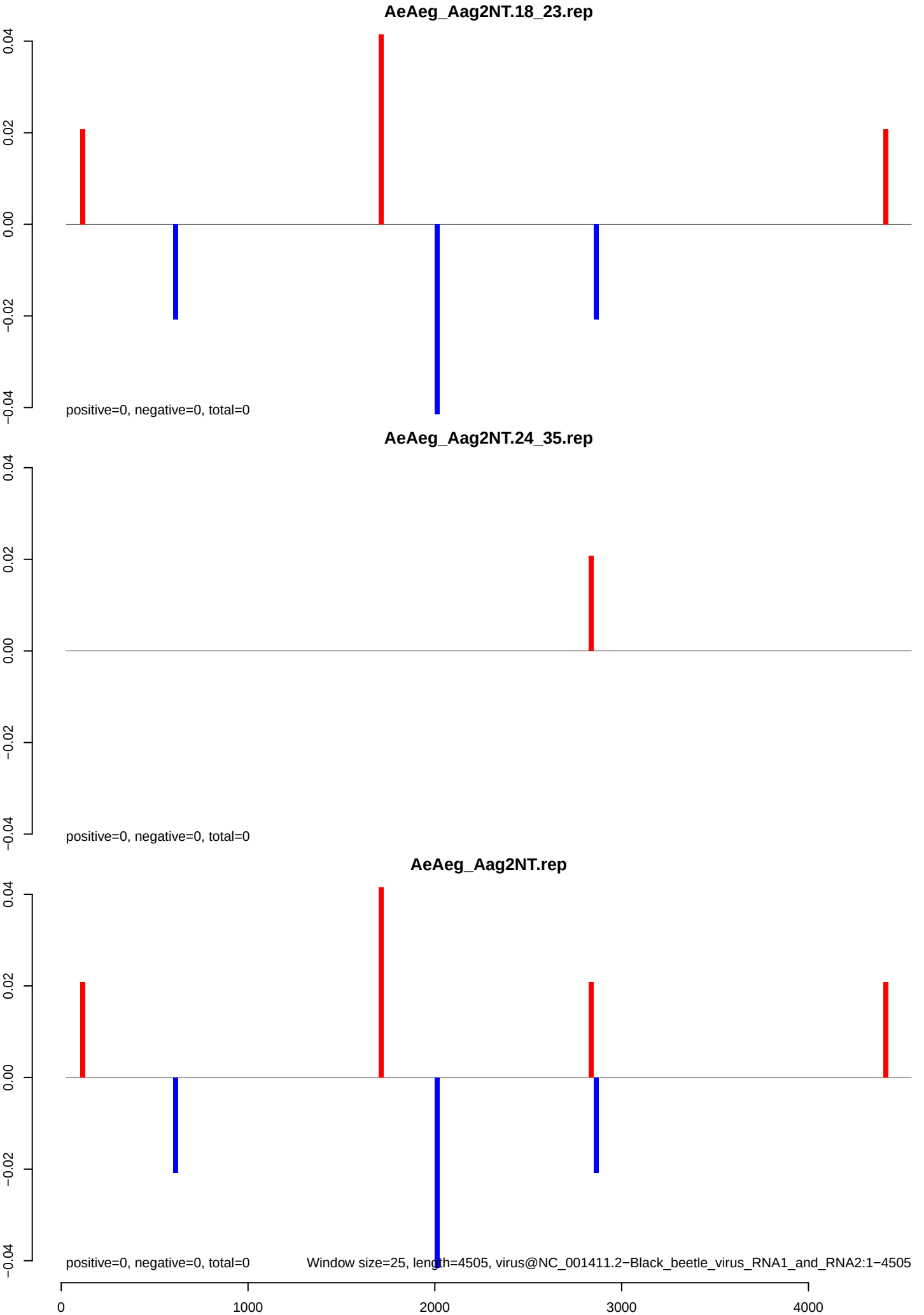

AeAeg_Aag2NT.rep
2
1
0
−1
positive=6, negative=4, total=10
window size=25, length=11064, virus@NC_012932.1−Aedes_flavivirus_genomic_RNA_strain_Narita−21:1−11064
0
2000
4000
6000
8000
10000

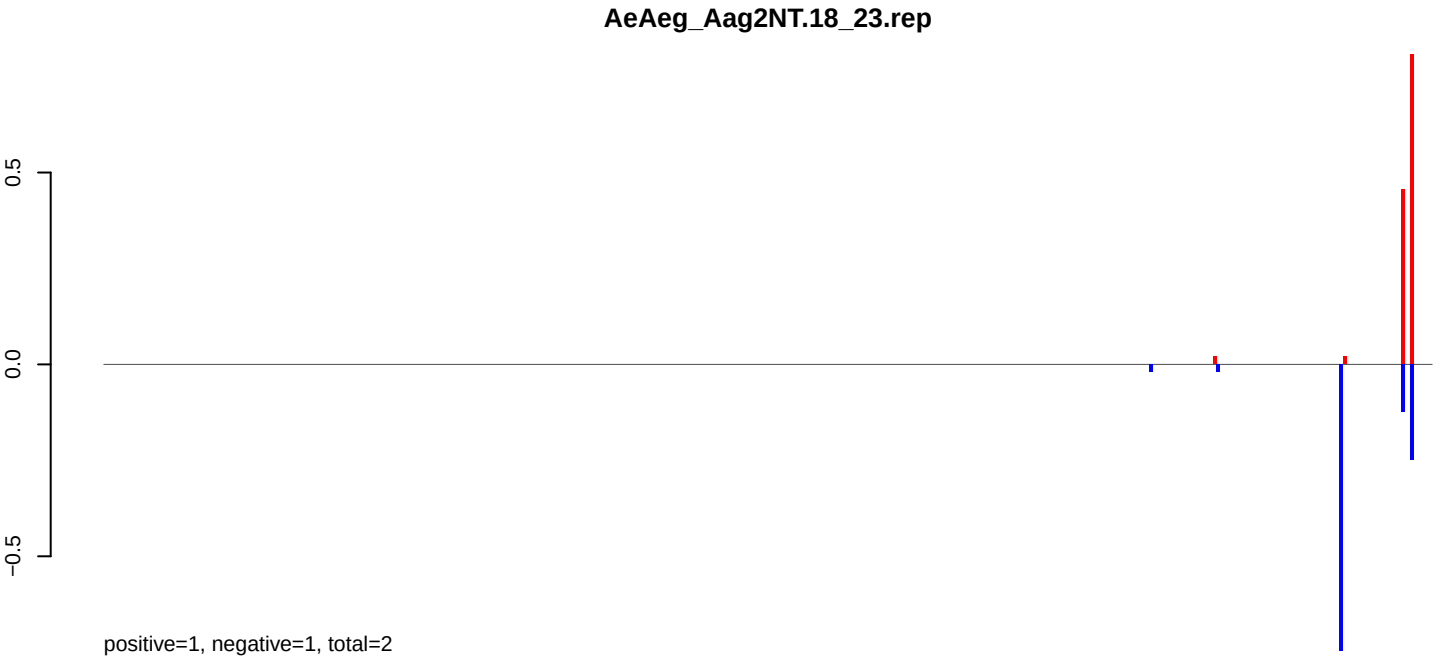

AeAeg_Aag2NT.18_23.rep
15
10
5
0
positive=16, negative=5, total=21
AeAeg_Aag2NT.24_35.rep
15
10
5
0
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
15
10
5
0
0
2000
4000
6000
8000
10000


AeAeg_Aag2NT.18_23.rep
0.5
0.0
−0.5
−1.0
−1.5
−2.0
−2.5
positive=1, negative=1, total=3
AeAeg_Aag2NT.24_35.rep
0.5
0.0
−0.5
−1.0
−1.5
−2.0
−2.5
positive=0, negative=2, total=2
AeAeg_Aag2NT.rep
0
−1
−2
−3
positive=1, negative=4, total=5
Window size=25, length=10755, virus@NC_009028.2−Ilheus_virus:1−10755
0
2000
4000
6000
8000
10000


AeAeg_Aag2NT.18_23.rep
0.0
−0.2
−0.4
−0.6
−0.8
−1.0
−1.2
positive=0, negative=1, total=2
AeAeg_Aag2NT.24_35.rep
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
positive=0, negative=1, total=2
window size=25, length=10673, virus@NC_023424.1−Tyuleniy_virus_strain_LEIV−6C_polyprotein_gene:1−10673
0
2000
4000
6000
8000
10000

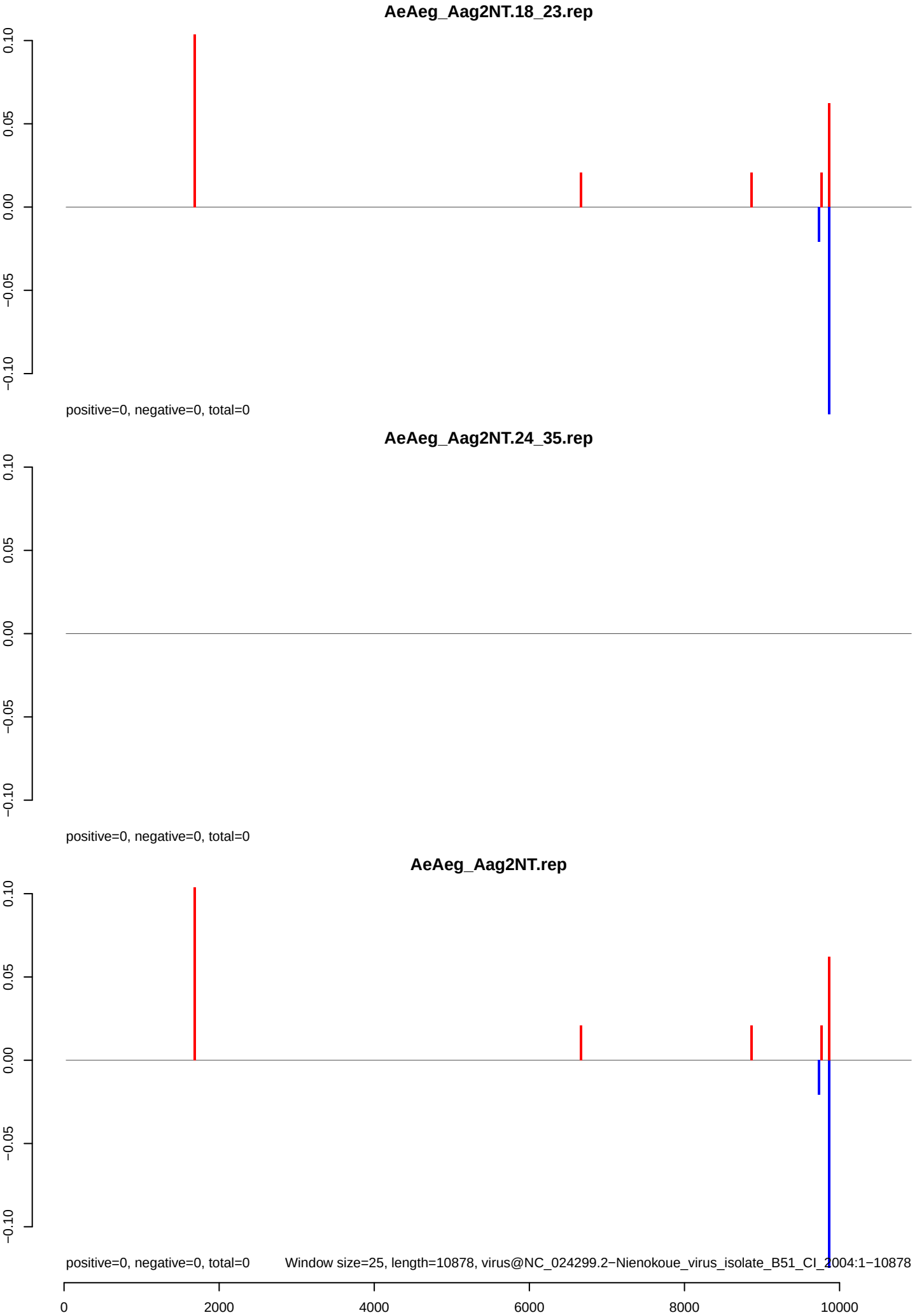

AeAeg_Aag2NT.18_23.rep
1.0
0.5
0.0
−0.5
positive=2, negative=1, total=3
AeAeg_Aag2NT.24_35.rep
1.0
0.5
0.0
−0.5
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
1.0
0.5
0.0
−0.5
positive=2, negative=1, total=4
Window size=25, length=10815, virus@NC_009026.2−Bussuquara_virus:1−10815
0
2000
4000
6000
8000
10000

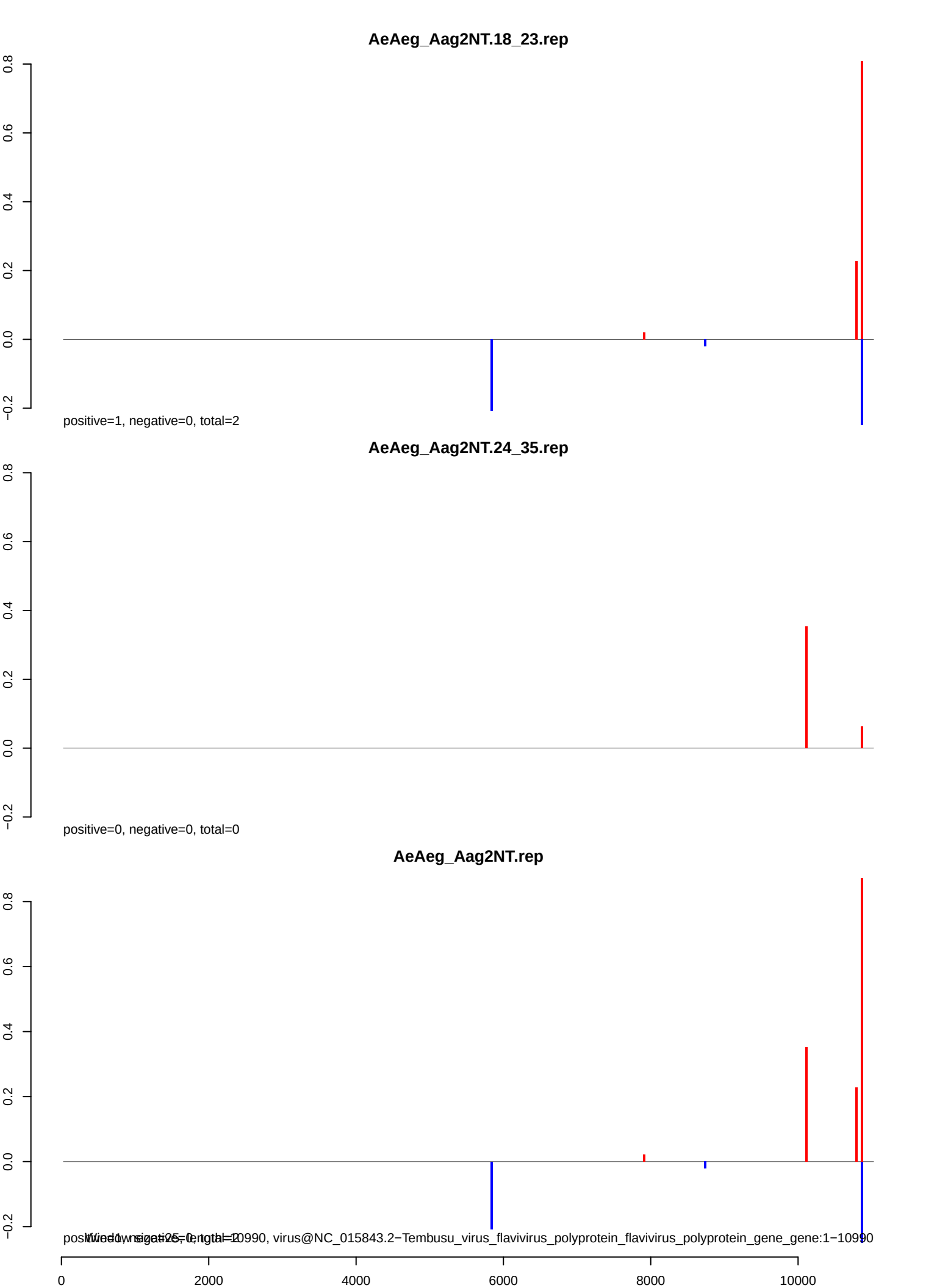

AeAeg_Aag2NT.18_23.rep
0.04
0.02
0.00
−0.02
−0.04
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
0.04
0.02
0.00
−0.02
−0.04
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.04
0.02
0.00
−0.02
−0.04
positive=0, negative=0, total=0
Window size=25, length=4505, virus@NC_001411.2−Black_beetle_virus_RNA1_and_RNA2:1−4505
0
1000
2000
3000
4000

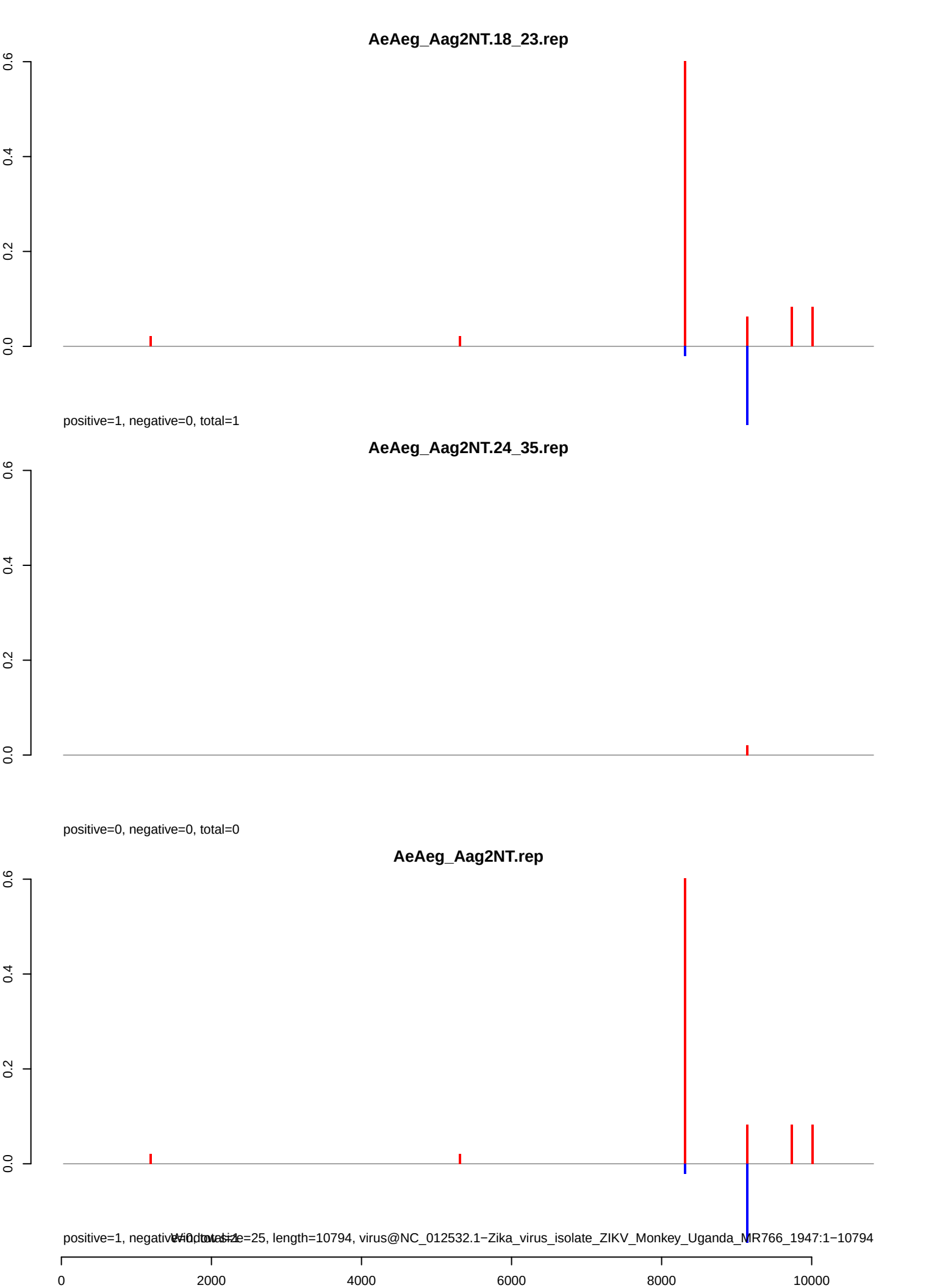

AeAeg_Aag2NT.18_23.rep
0.5
0.0
−0.5
positive=1, negative=1, total=2

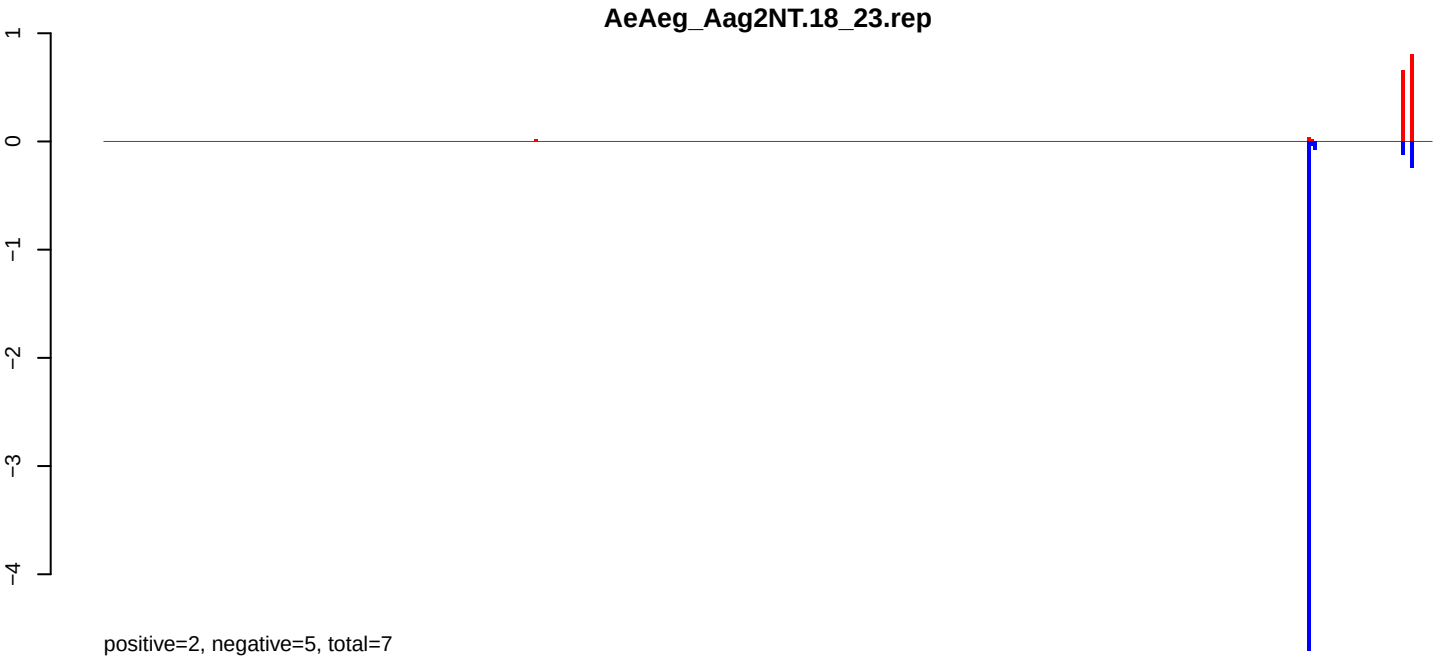
AeAeg_Aag2NT.24_35.rep
0.5
0.0
−0.5
positive=0, negative=0, total=0

AeAeg_Aag2NT.rep
0.5
0.0
−0.5
positive=1, negative=1, total=3
Window size=25, length=10794, virus@AY632542.4−Rocio_virus_strain_SPH_34675:1−10794
0
2000
4000
6000
8000
10000

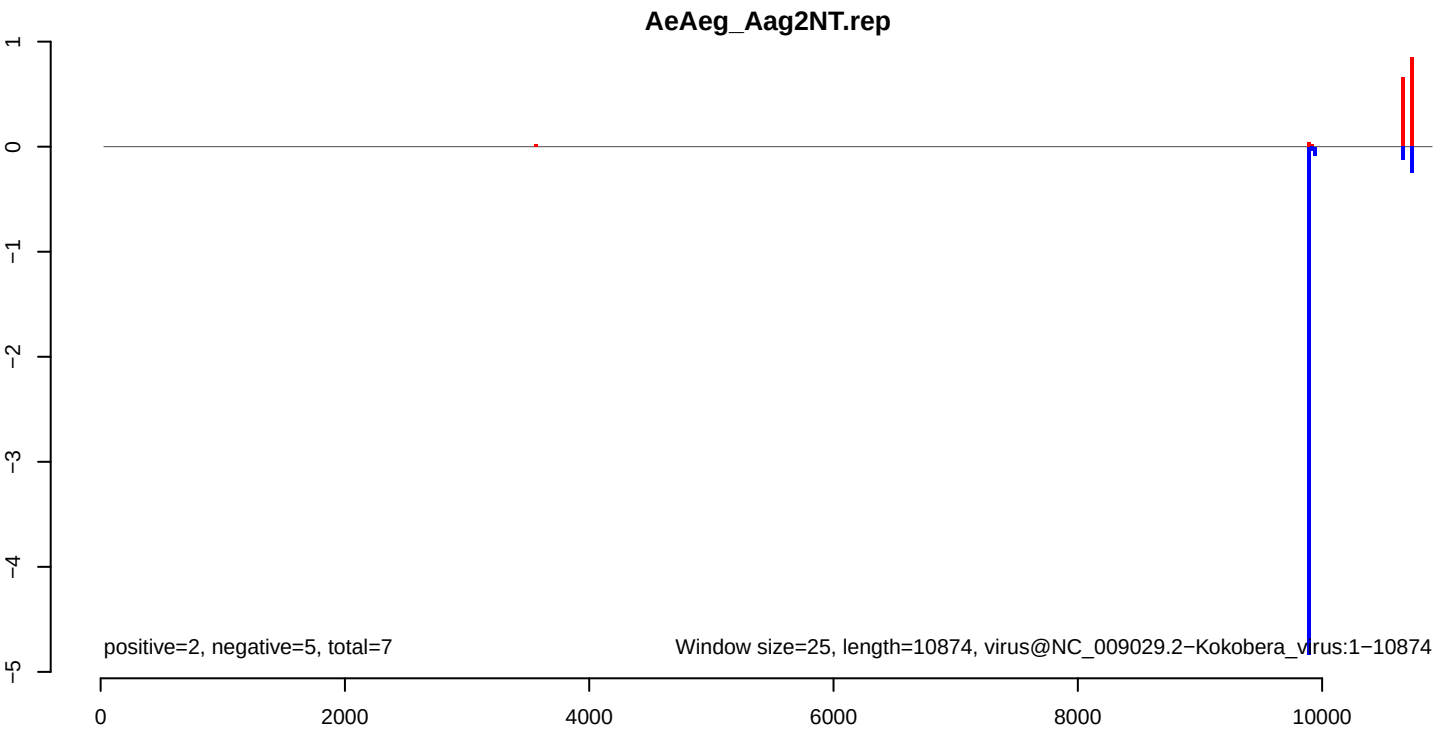

AeAeg_Aag2NT.18_23.rep
0.10
0.05
0.00
−0.05
−0.10
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
0.10
0.05
0.00
−0.05
−0.10
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.10
0.05
0.00
−0.05
−0.10
positive=0, negative=0, total=0
Window size=25, length=10878, virus@NC_024299.2−Nienokoue_virus_isolate_B51_CI_2004:1−10878
0
2000
4000
6000
8000
10000

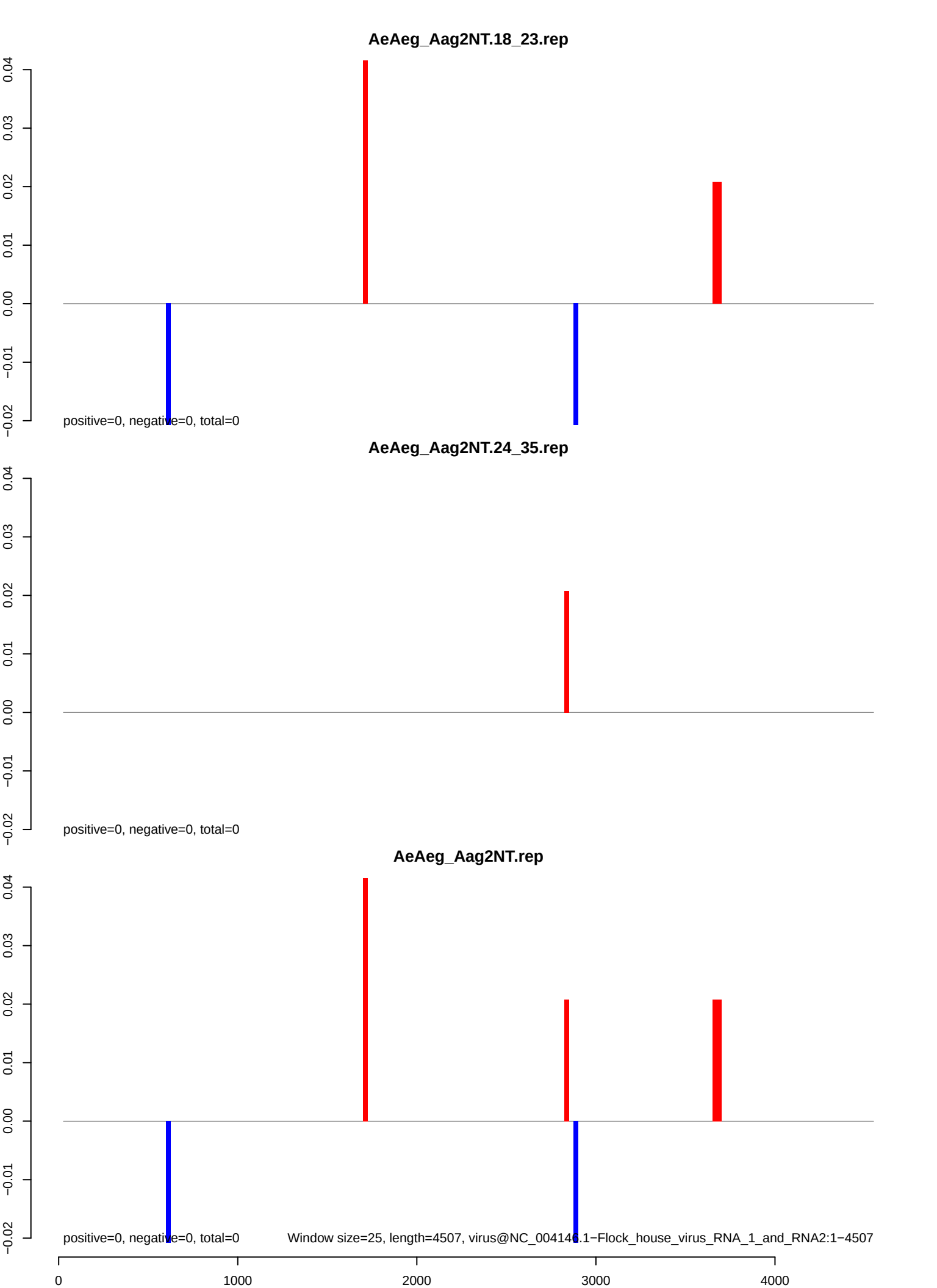

AeAeg_Aag2NT.18_23.rep
0.8
0.6
0.4
0.2
0.0
−0.2
positive=1, negative=0, total=2
AeAeg_Aag2NT.24_35.rep
0.8
0.6
0.4
0.2
0.0
−0.2
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.8
0.6
0.4
0.2
0.0
−0.2
positive=1, negative=0, total=2
Window size=25, length=10990, virus@NC_015843.2−Tembusu_virus_flavivirus_polyprotein_flavivirus_polyprotein_gene_gene:1−10990
0
2000
4000
6000
8000
10000

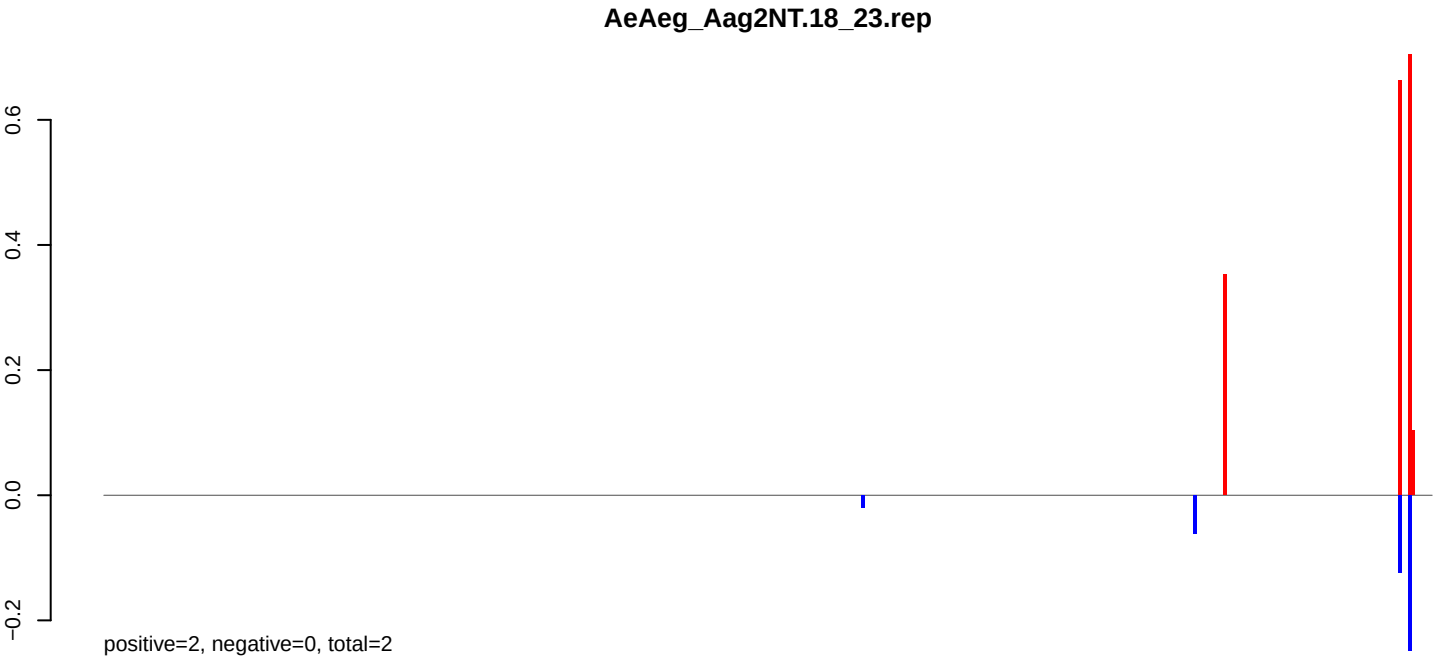

AeAeg_Aag2NT.18_23.rep
0.0
0.2
0.4
0.6
positive=1, negative=0, total=1
AeAeg_Aag2NT.24_35.rep
0.0
0.2
0.4
0.6
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.0
0.2
0.4
0.6
positive=1, negative=0, total=1
positive=25, length=10794, virus@NC_012532.1−Zika_virus_isolate_ZIKV_Monkey_Uganda_MR766_1947:1−10794
0
2000
4000
6000
8000
10000

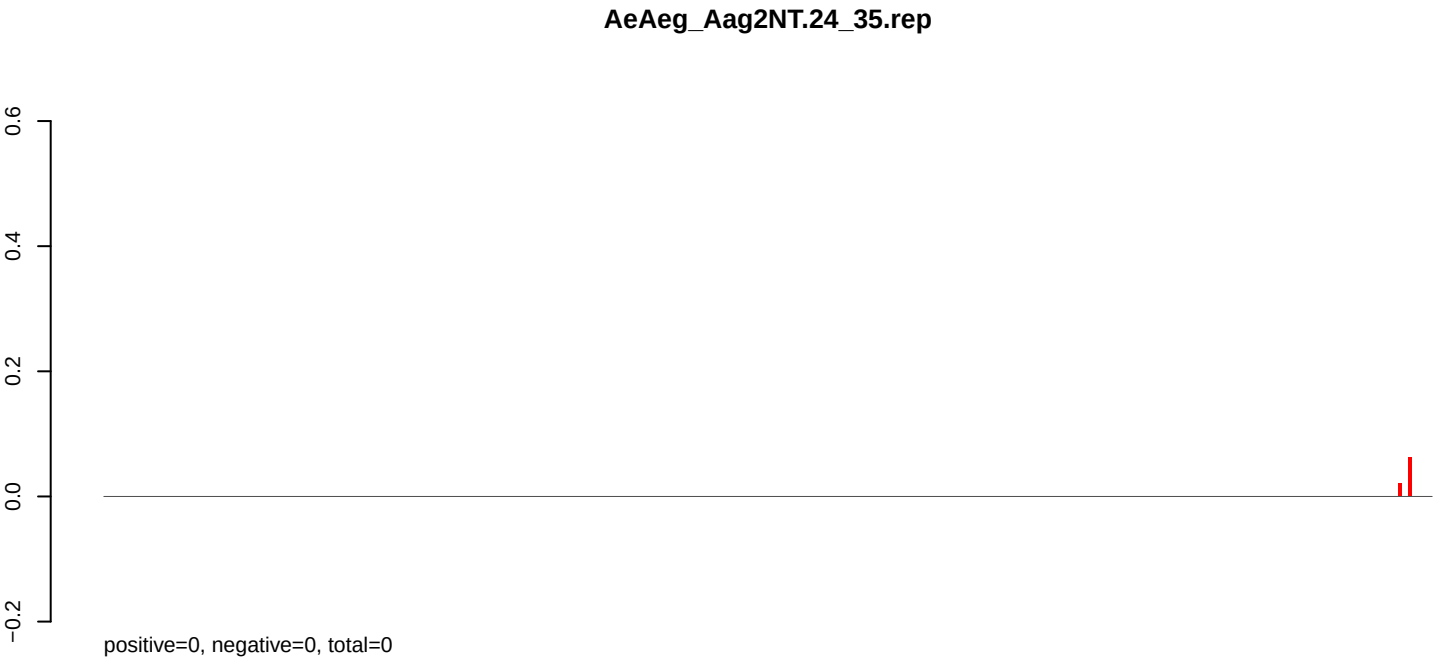

AeAeg_Aag2NT.18_23.rep
1
0
−1
−2
−3
−4
positive=2, negative=5, total=7

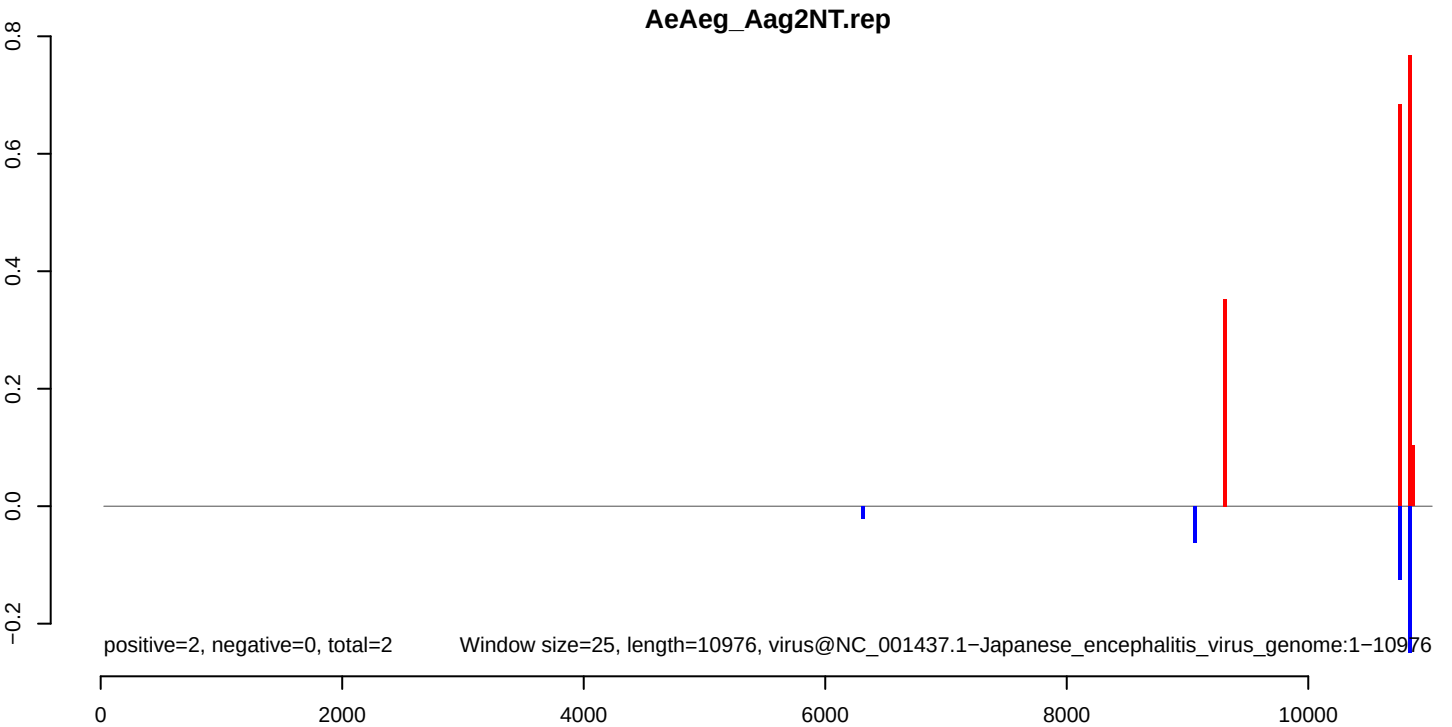
AeAeg_Aag2NT.24_35.rep
1
0
−1
−2
−3
−4
positive=0, negative=0, total=0

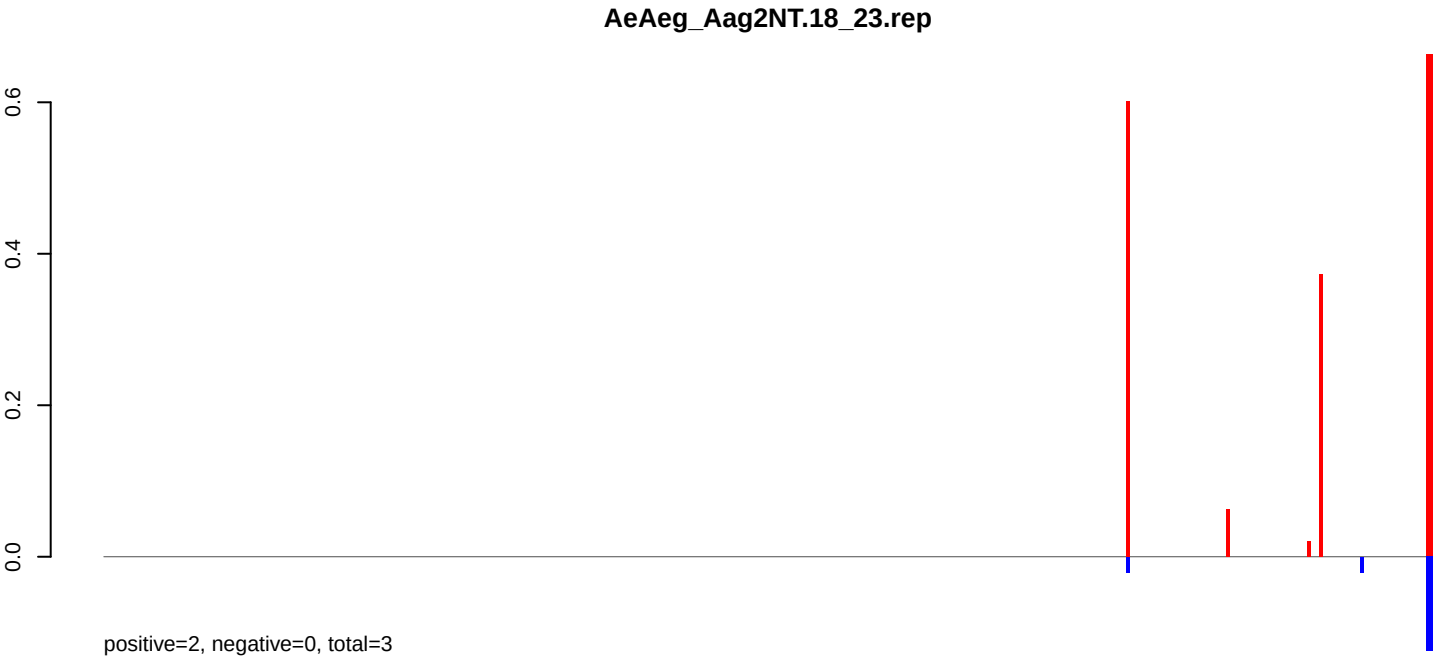

AeAeg_Aag2NT.rep
1
0
−1
−2
−3
−4
−5
positive=2, negative=5, total=7
Window size=25, length=10874, virus@NC_009029.2−Kokobera_virus:1−10874
0
2000
4000
6000
8000
10000

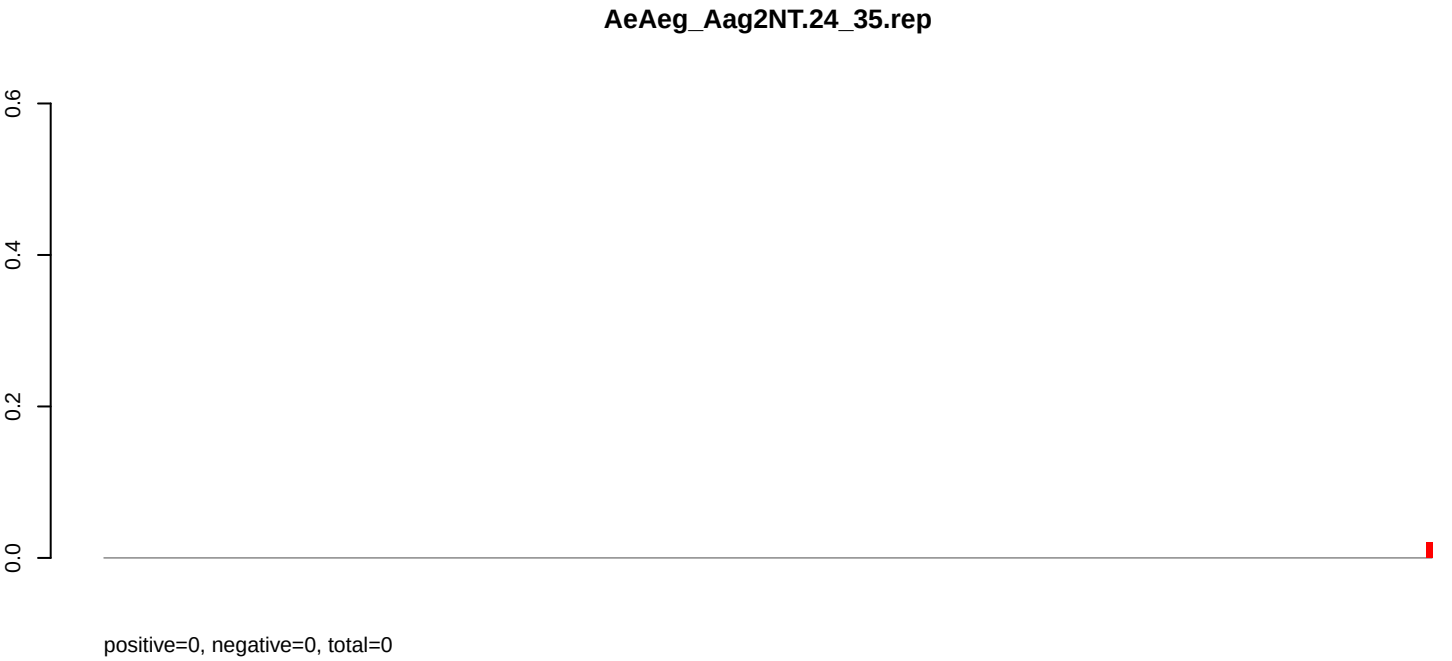

AeAeg_Aag2NT.18_23.rep
0.04
0.03
0.02
0.01
0.00
−0.01
−0.02
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
0.04
0.03
0.02
0.01
0.00
−0.01
−0.02
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.04
0.03
0.02
0.01
0.00
−0.01
−0.02
positive=0, negative=0, total=0
Window size=25, length=4507, virus@NC_004146.1−Flock_house_virus_RNA_1_and_RNA2:1−4507
0
1000
2000
3000
4000

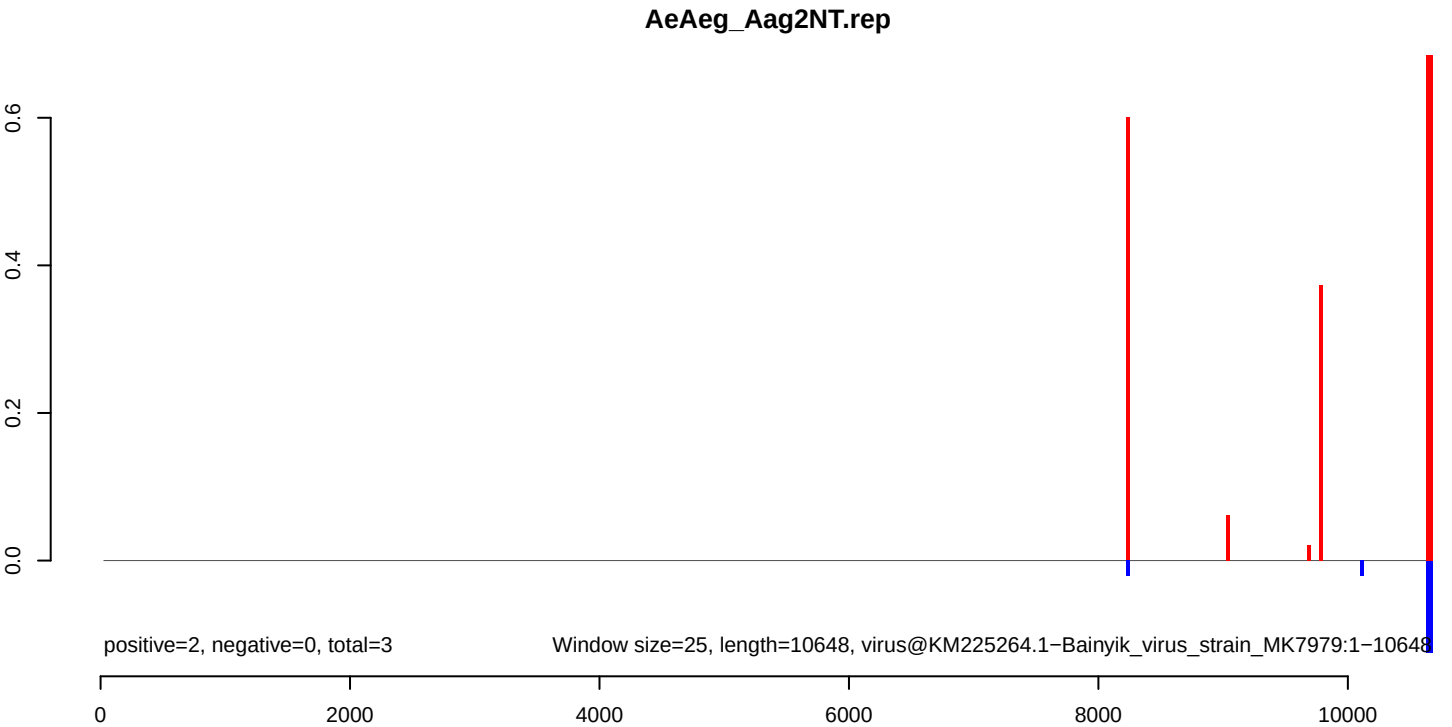

AeAeg_Aag2NT.18_23.rep
0.6
0.4
0.2
0.0
−0.2
positive=2, negative=0, total=2

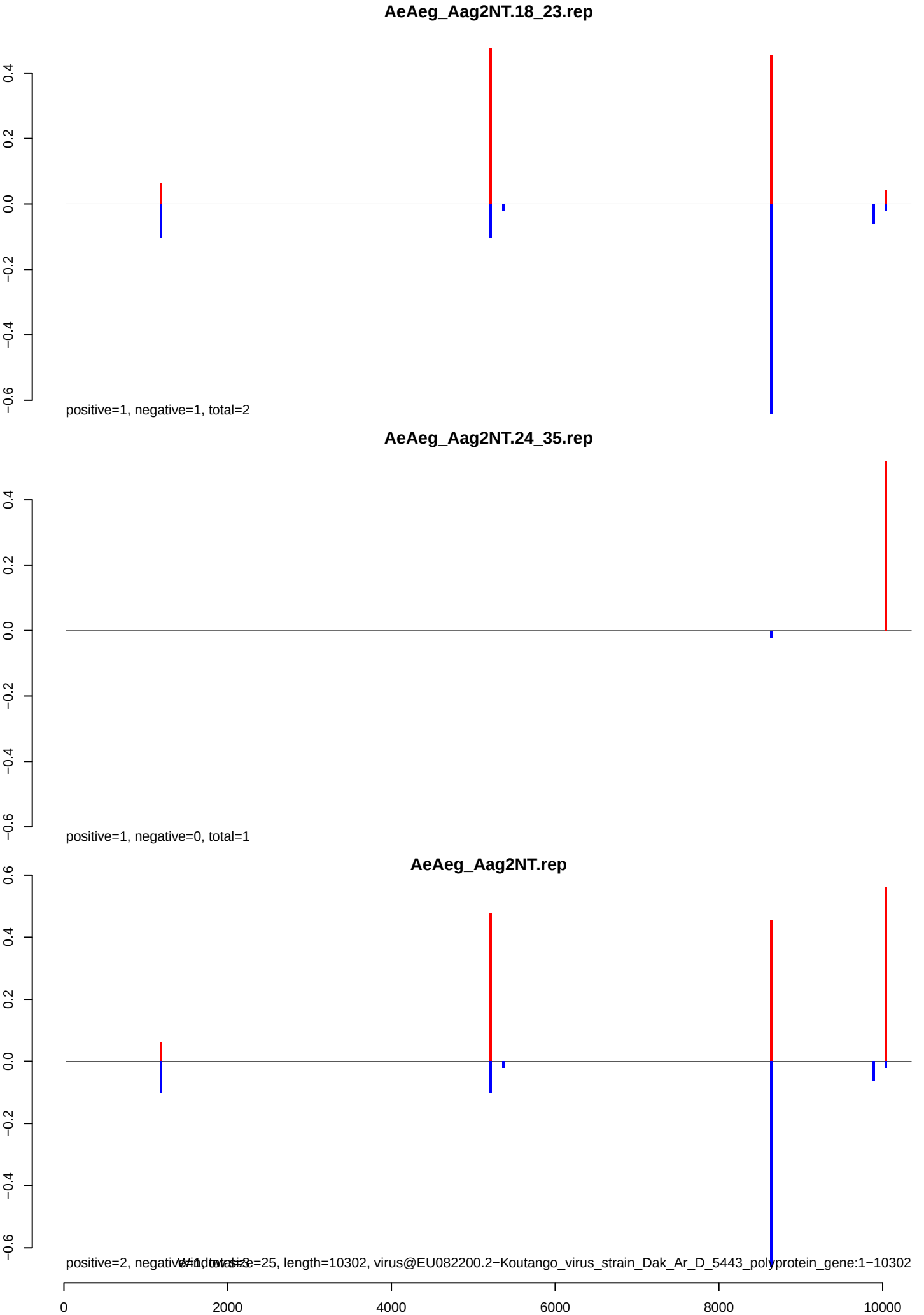

AeAeg_Aag2NT.24_35.rep
0.6
0.4
0.2
0.0
−0.2
positive=0, negative=0, total=0

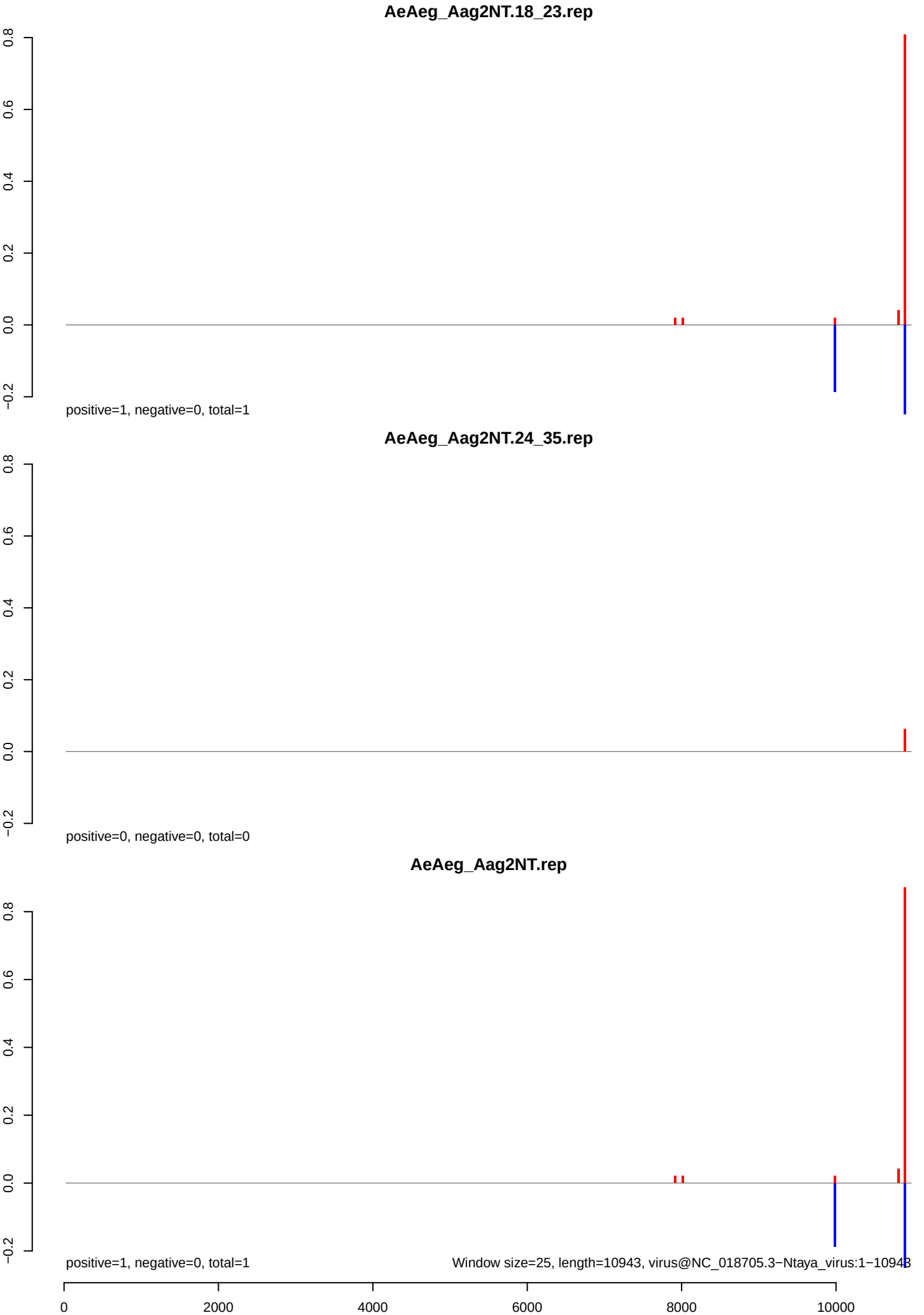

AeAeg_Aag2NT.rep
0.8
0.6
0.4
0.2
0.0
−0.2
positive=2, negative=0, total=2
Window size=25, length=10976, virus@NC_001437.1−Japanese_encephalitis_virus_genome:1−10976
0
2000
4000
6000
8000
10000

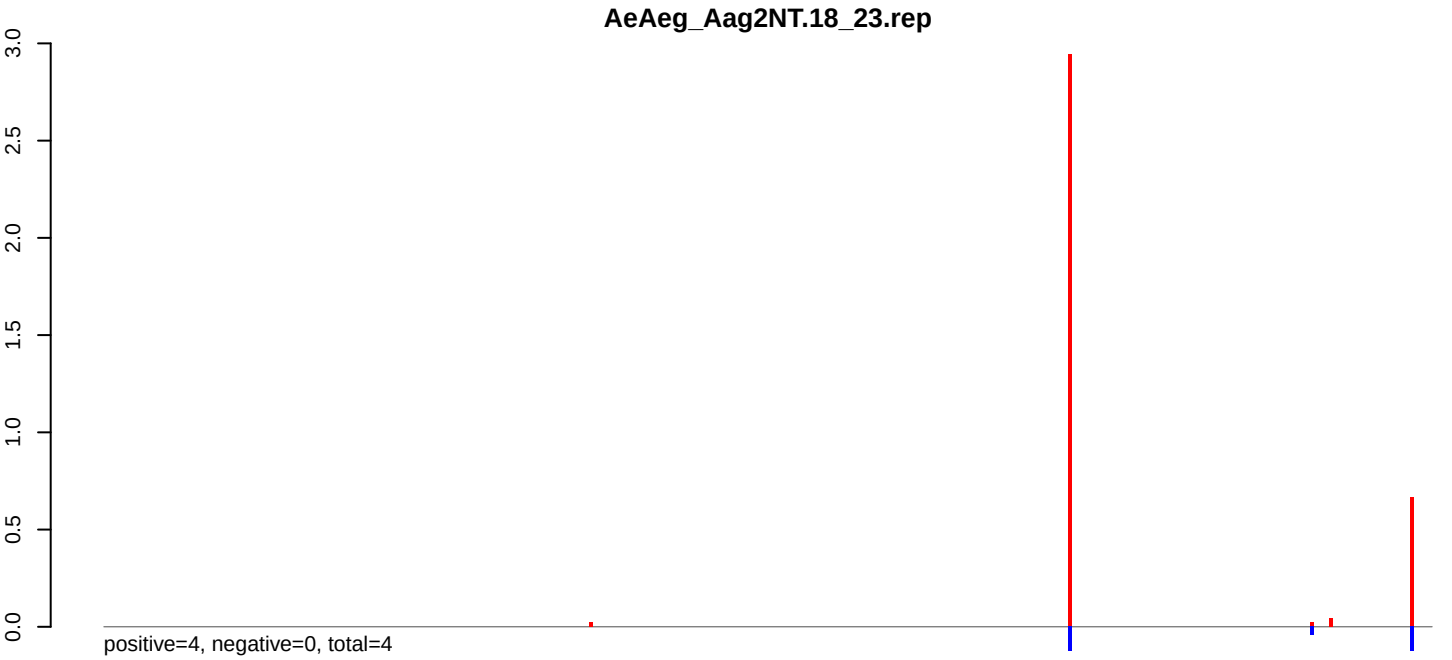

AeAeg_Aag2NT.18_23.rep
0.0
0.2
0.4
0.6
positive=2, negative=0, total=3

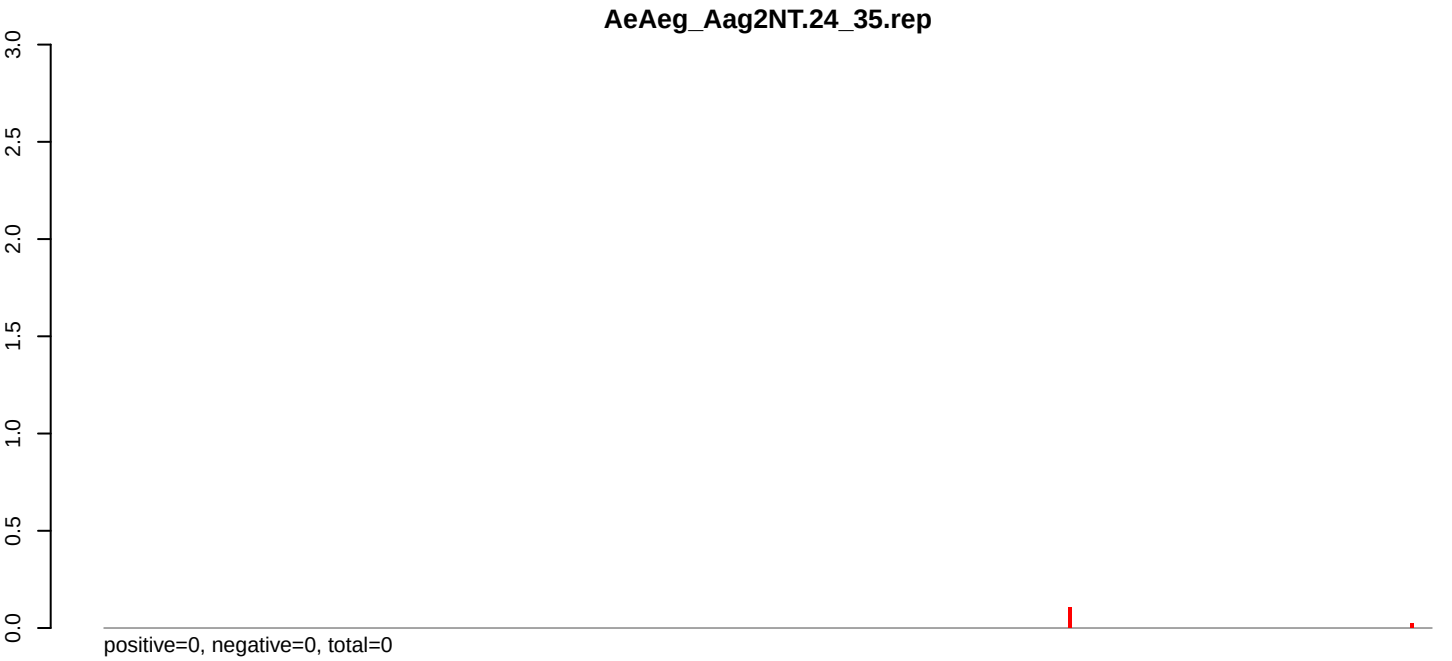

AeAeg_Aag2NT.24_35.rep
0.0
0.2
0.4
0.6
positive=0, negative=0, total=0

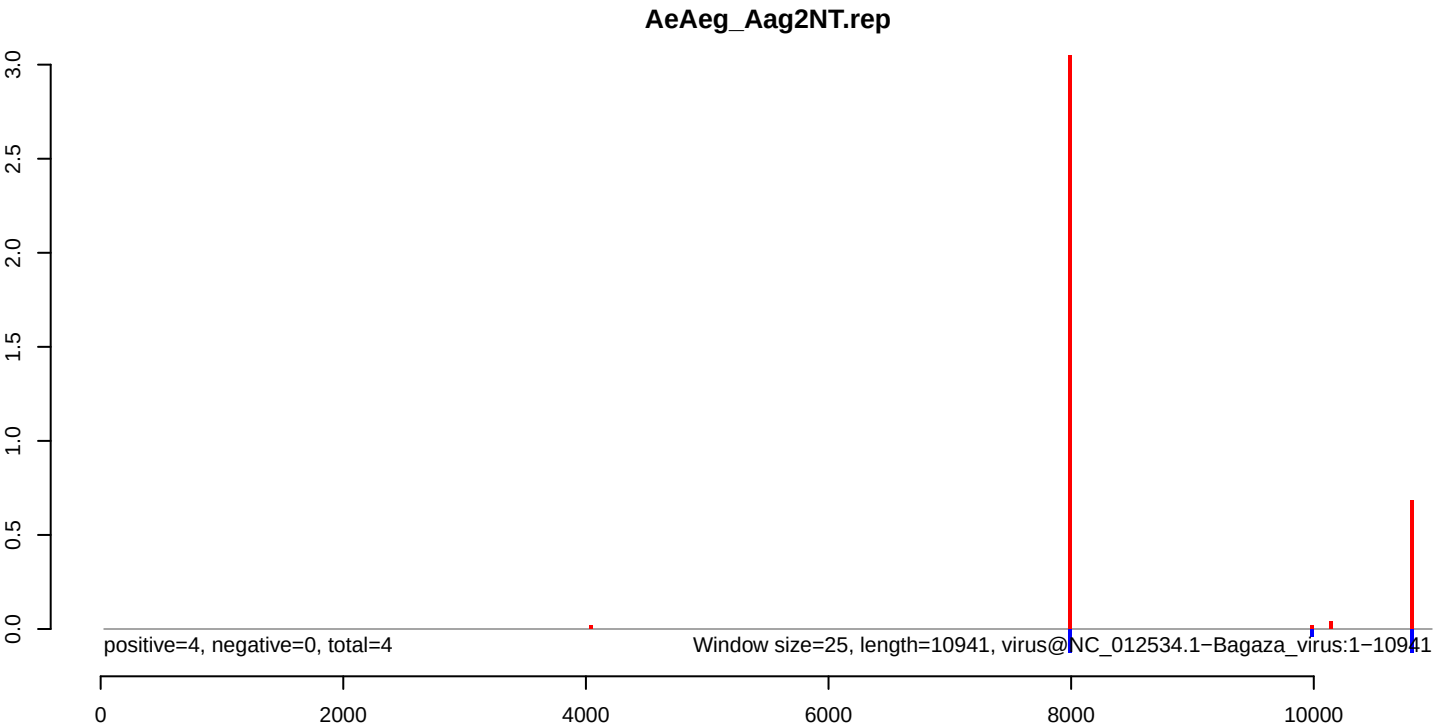

AeAeg_Aag2NT.rep
0.0
0.2
0.4
0.6
positive=2, negative=0, total=3
Window size=25, length=10648, virus@KM225264.1−Bainyik_virus_strain_MK7979:1−10648
0
2000
4000
6000
8000
10000

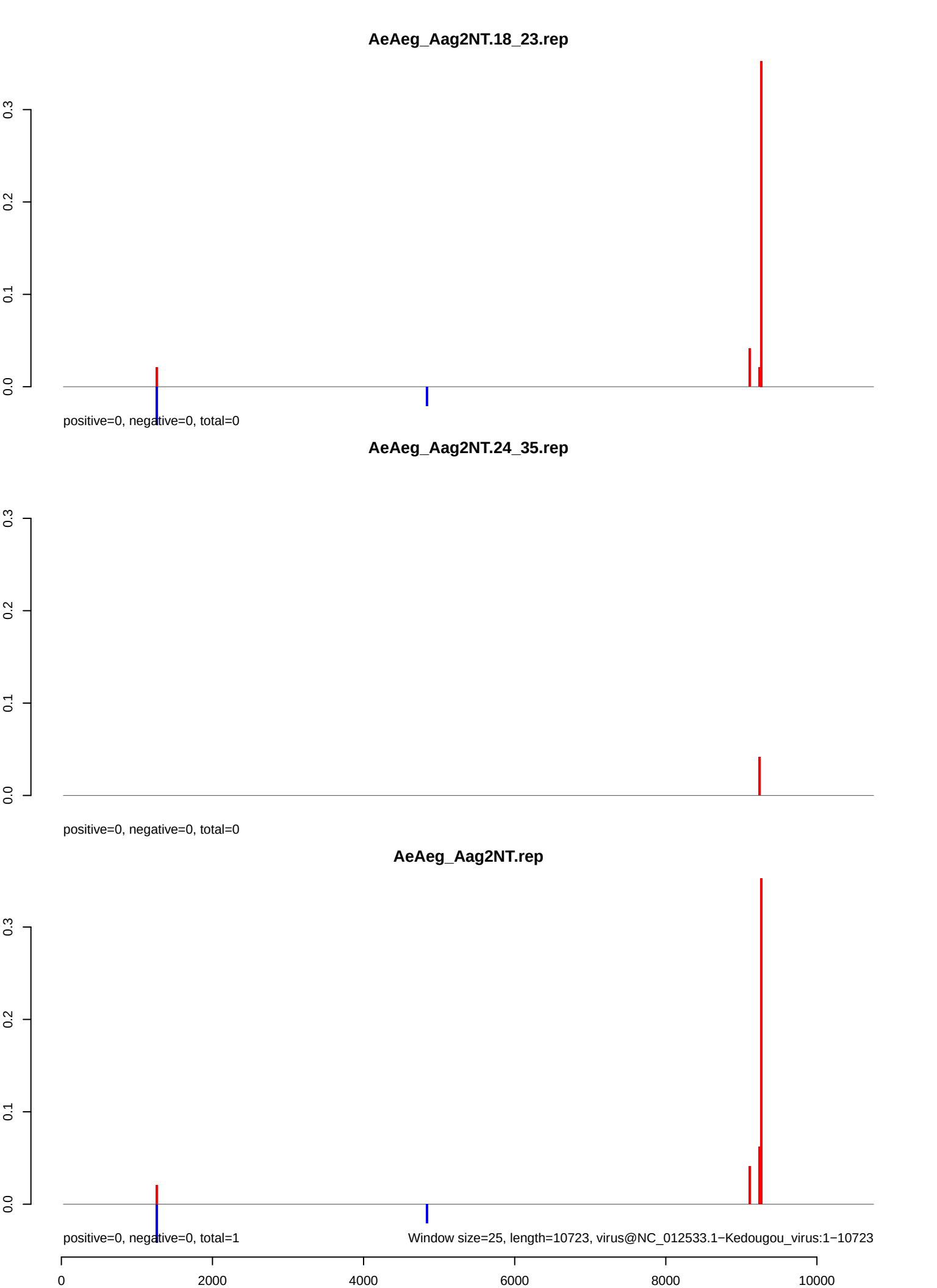

AeAeg_Aag2NT.18_23.rep
0.4
0.2
0.0
−0.2
−0.4
−0.6
positive=1, negative=1, total=2
AeAeg_Aag2NT.24_35.rep
0.4
0.2
0.0
−0.2
−0.4
−0.6
positive=1, negative=0, total=1
AeAeg_Aag2NT.rep
0.6
0.4
0.2
0.0
−0.2
−0.4
−0.6
positive=2, negative=1, total=3
Window size=25, length=10302, virus@EU082200.2−Koutango_virus_strain_Dak_Ar_D_5443_polyprotein_gene:1−10302
0
2000
4000
6000
8000
10000

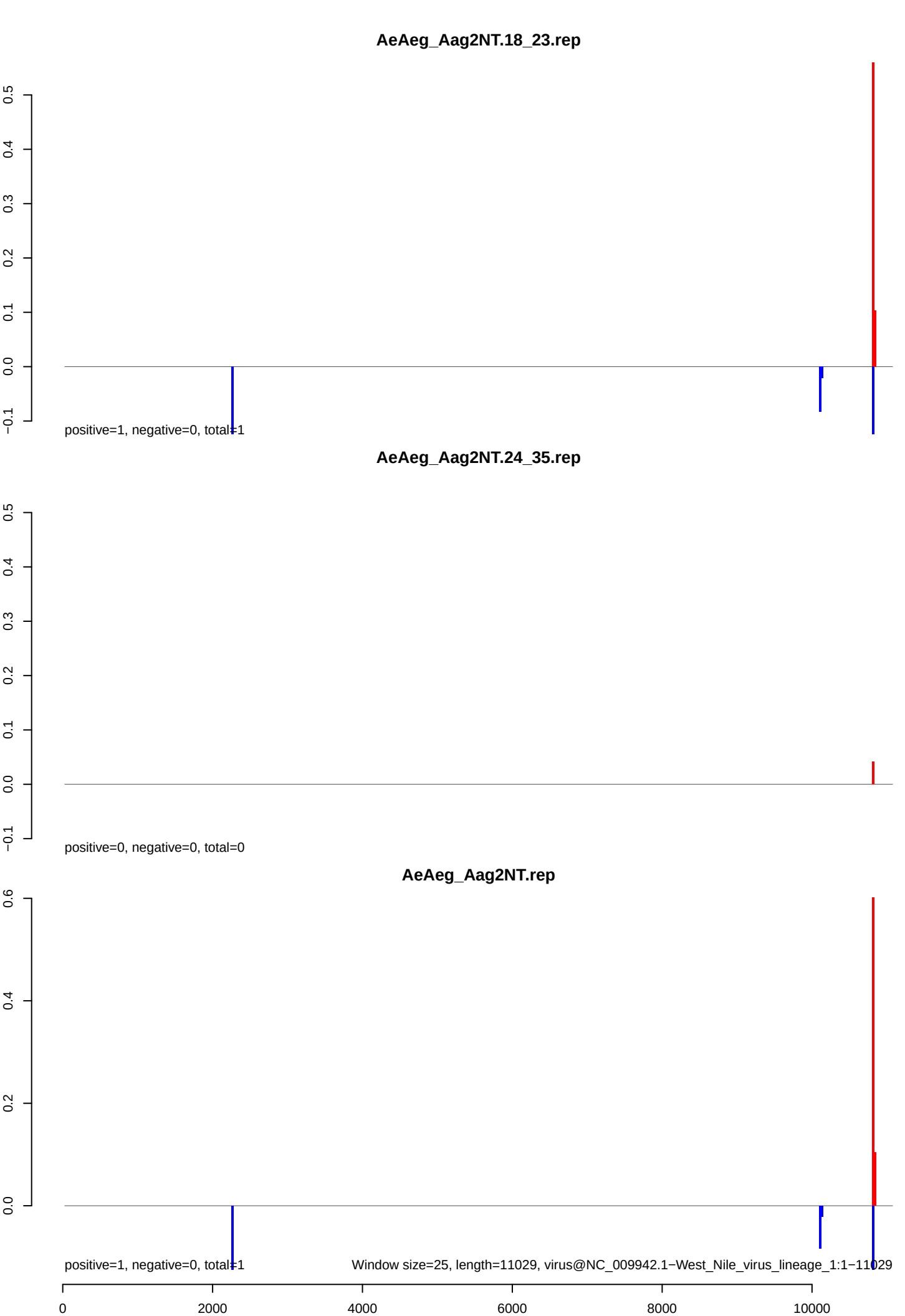

AeAeg_Aag2NT.18_23.rep
0.8
0.6
0.4
0.2
0.0
−0.2
positive=1, negative=0, total=1
AeAeg_Aag2NT.24_35.rep
0.8
0.6
0.4
0.2
0.0
−0.2
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.8
0.6
0.4
0.2
0.0
−0.2
positive=1, negative=0, total=1
Window size=25, length=10943, virus@NC_018705.3−Ntaya_virus:1−10943
0
2000
4000
6000
8000
10000

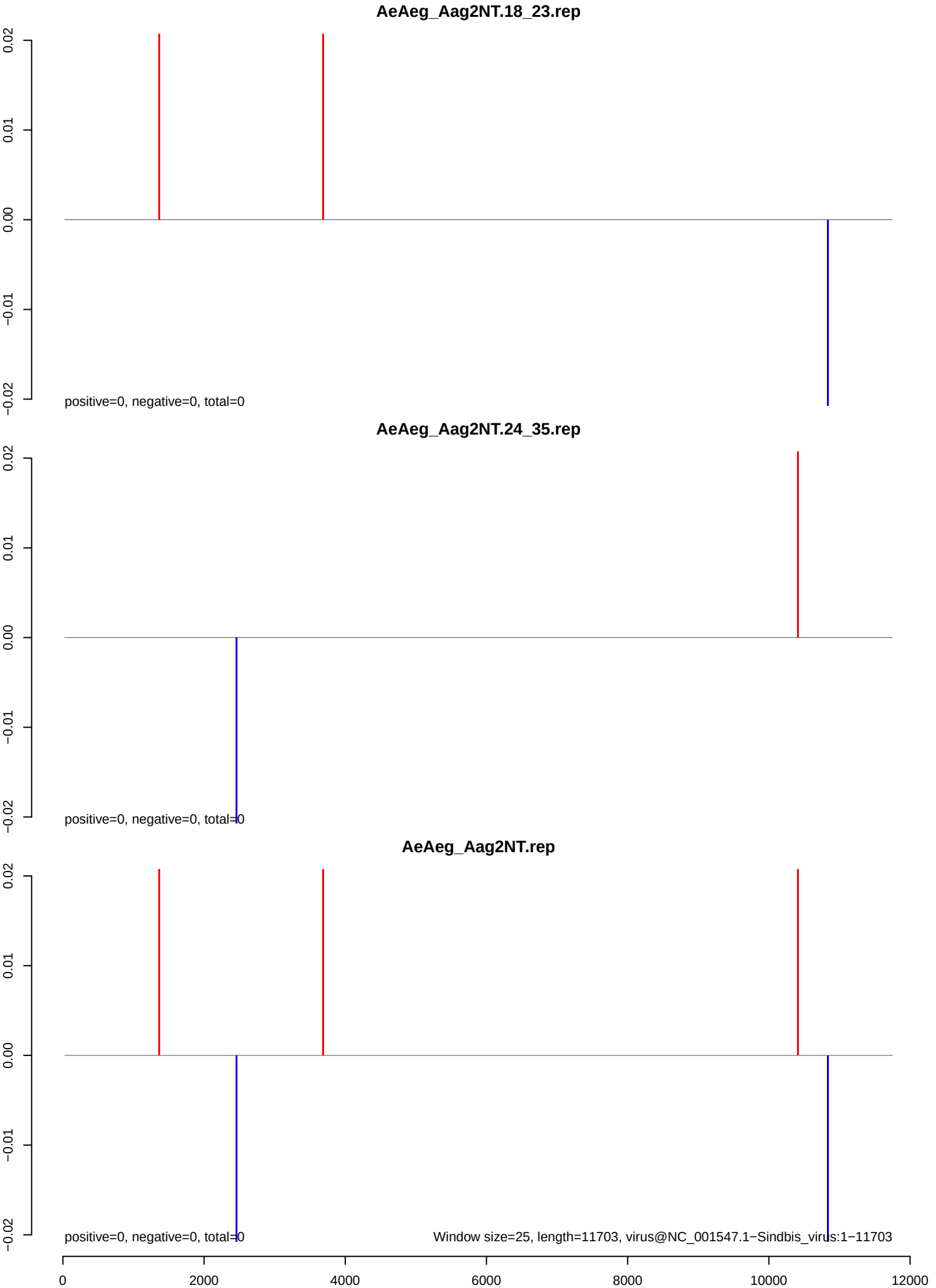

AeAeg_Aag2NT.18_23.rep
3.0
2.5
2.0
1.5
1.0
0.5
0.0
positive=4, negative=0, total=4

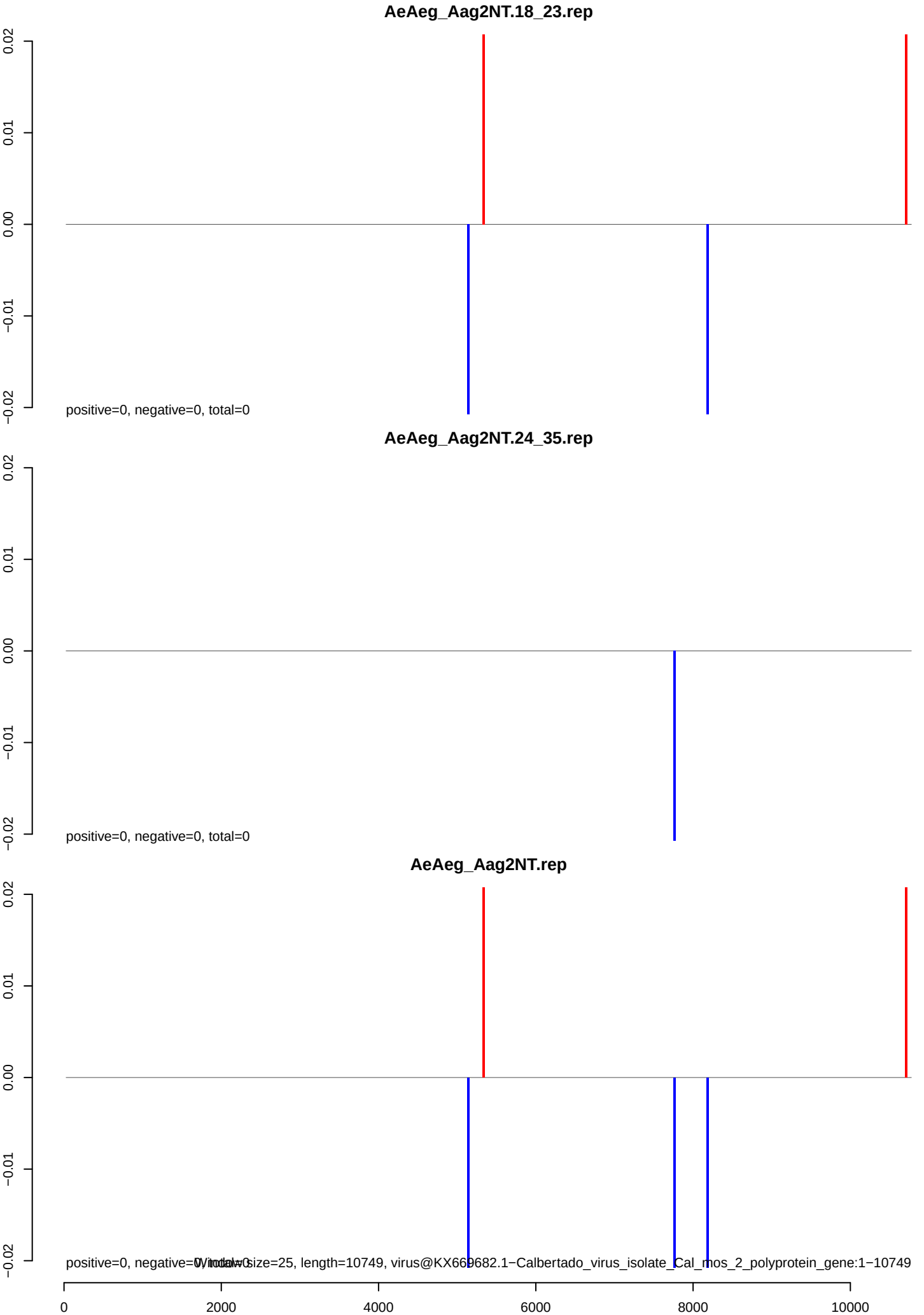

AeAeg_Aag2NT.24_35.rep
3.0
2.5
2.0
1.5
1.0
0.5
0.0
positive=0, negative=0, total=0

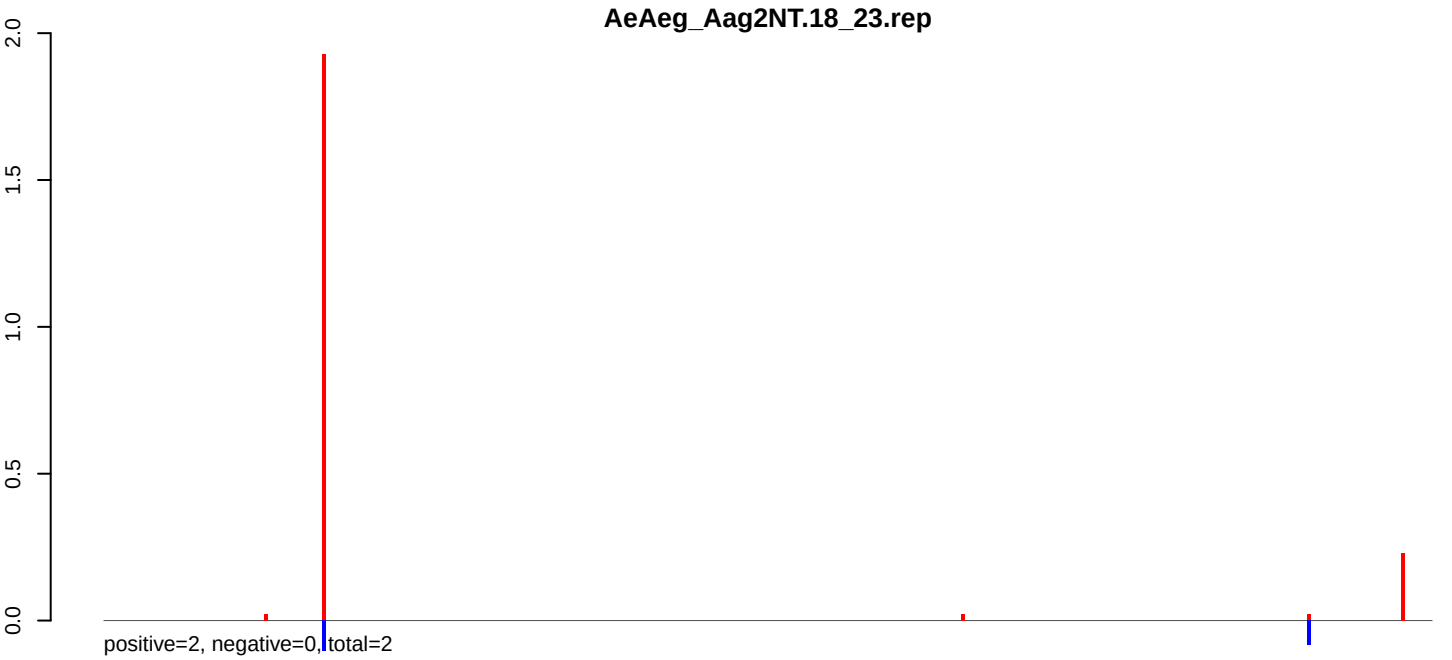

AeAeg_Aag2NT.rep
3.0
2.5
2.0
1.5
1.0
0.5
0.0
positive=4, negative=0, total=4
Window size=25, length=10941, virus@NC_012534.1−Bagaza_virus:1−10941
0
2000
4000
6000
8000
10000

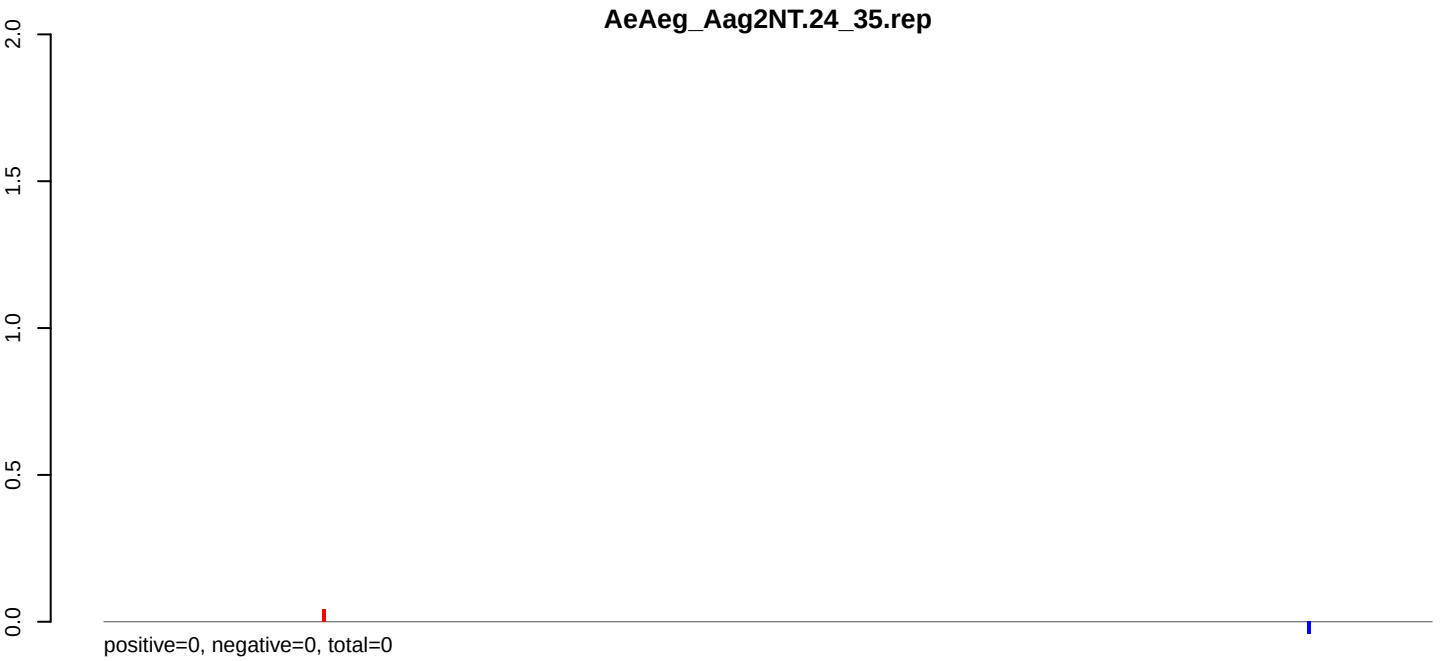

AeAeg_Aag2NT.18_23.rep
0.0
0.1
0.2
0.3
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
0.0
0.1
0.2
0.3
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.0
0.1
0.2
0.3
positive=0, negative=0, total=1
Window size=25, length=10723, virus@NC_012533.1−Kedougou_virus:1−10723
0
2000
4000
6000
8000
10000

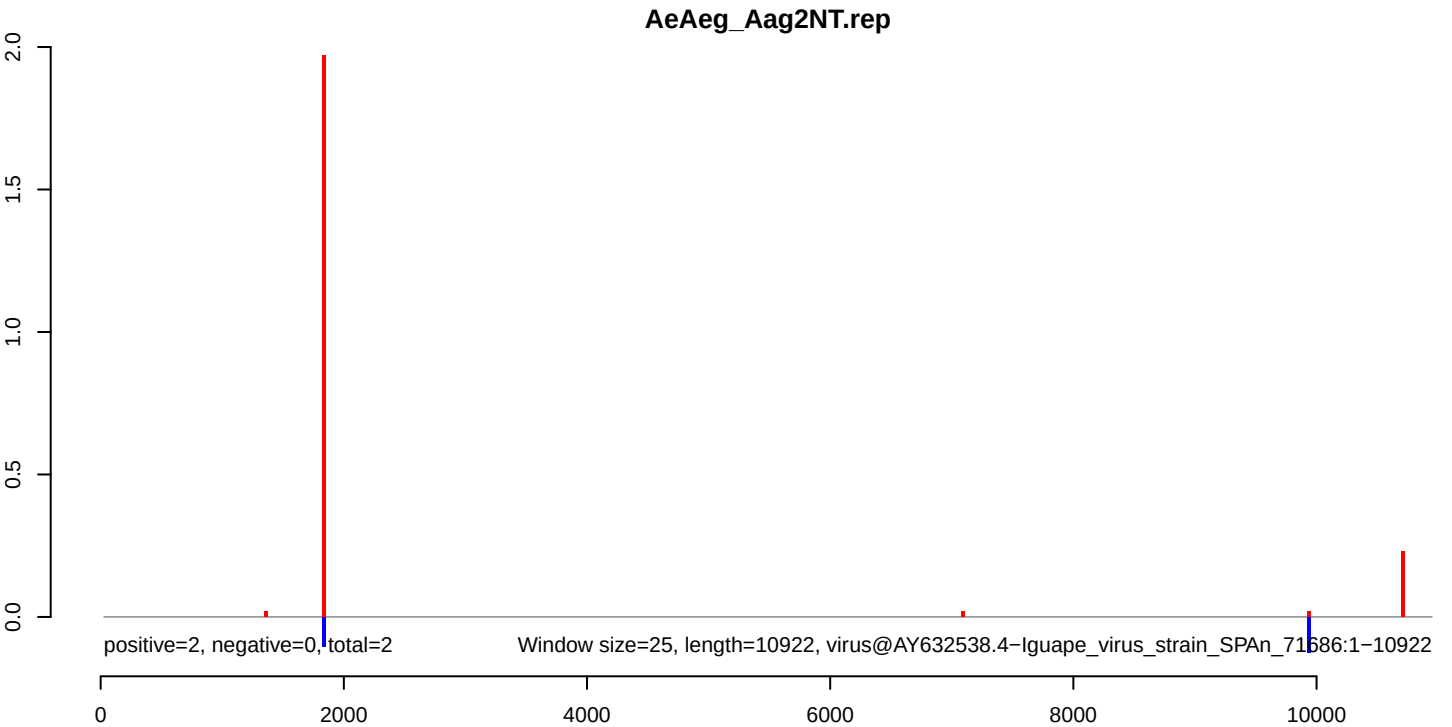

AeAeg_Aag2NT.18_23.rep
0.5
0.4
0.3
0.2
0.1
0.0
−0.1
positive=1, negative=0, total=1
AeAeg_Aag2NT.24_35.rep
0.5
0.4
0.3
0.2
0.1
0.0
−0.1
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.6
0.4
0.2
0.0
positive=1, negative=0, total=1
Window size=25, length=11029, virus@NC_009942.1−West_Nile_virus_lineage_1:1−11029
0
2000
4000
6000
8000
10000


AeAeg_Aag2NT.18_23.rep
0.02
0.01
0.00
−0.01
−0.02
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
0.02
0.01
0.00
−0.01
−0.02
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.02
0.01
0.00
−0.01
−0.02
positive=0, negative=0, total=0
Window size=25, length=11703, virus@NC_001547.1−Sindbis_virus:1−11703
0
2000
4000
6000
8000
10000
12000


AeAeg_Aag2NT.18_23.rep
0.02
0.01
0.00
−0.01
−0.02
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
0.02
0.01
0.00
−0.01
−0.02
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.02
0.01
0.00
−0.01
−0.02
positive=0, negative=0, total=0
Window size=25, length=10749, virus@KX669682.1−Calbertado_virus_isolate_Cal_mos_2_polyprotein_gene:1−10749
0
2000
4000
6000
8000
10000

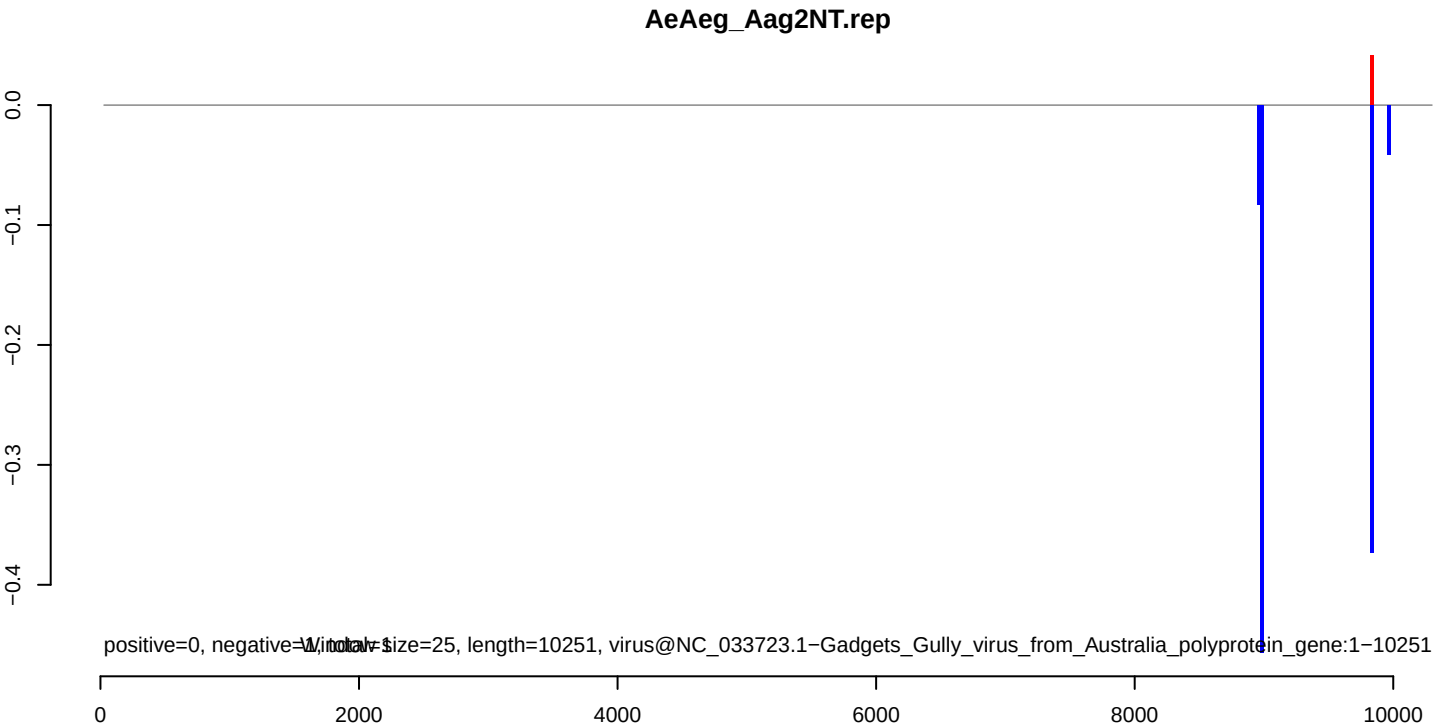

AeAeg_Aag2NT.18_23.rep
2.0
1.5
1.0
0.5
0.0
positive=2, negative=0, total=2

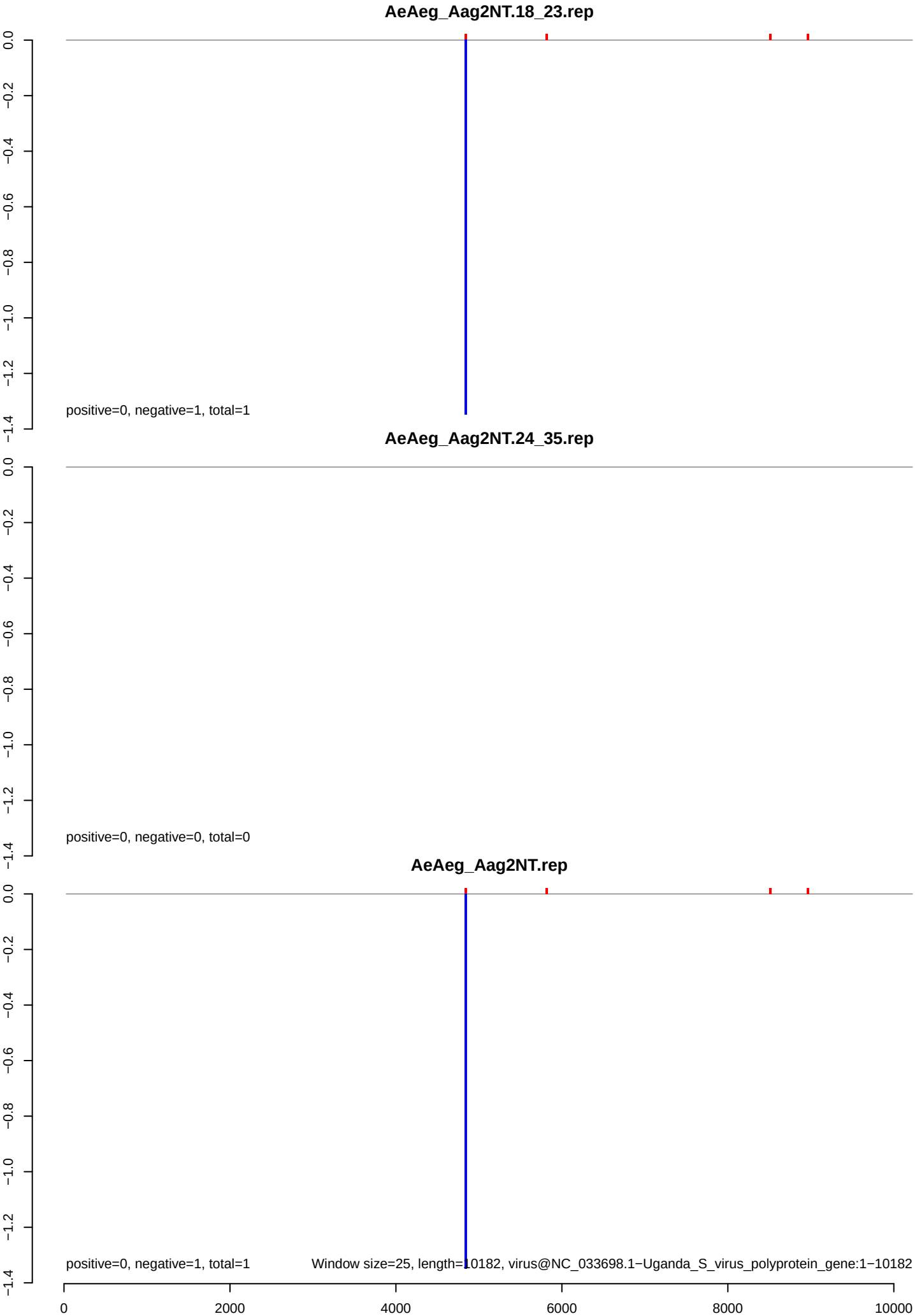

AeAeg_Aag2NT.24_35.rep
2.0
1.5
1.0
0.5
0.0
positive=0, negative=0, total=0

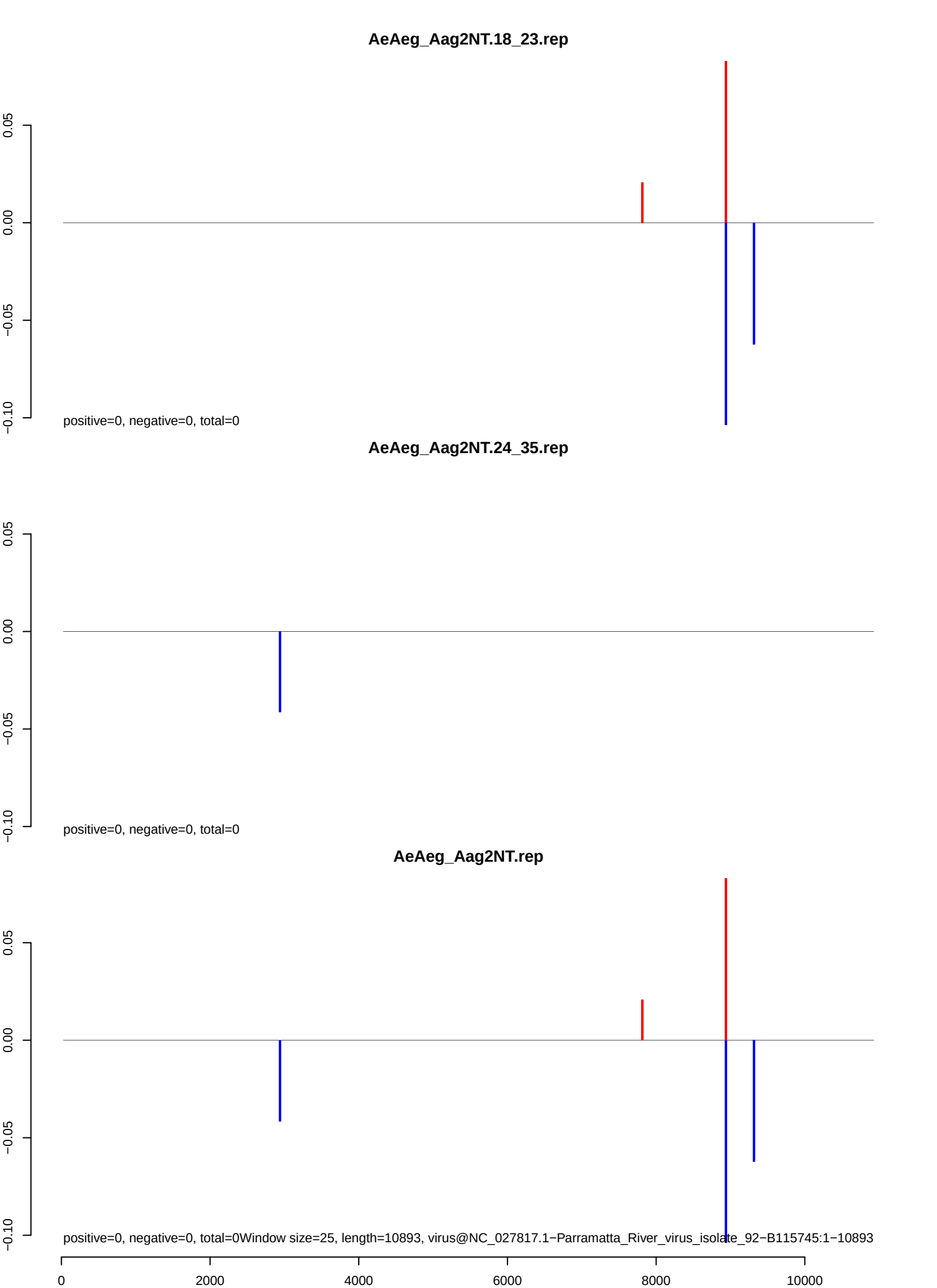

AeAeg_Aag2NT.rep
2.0
1.5
1.0
0.5
0.0
positive=2, negative=0, total=2
Window size=25, length=10922, virus@AY632538.4−Iguape_virus_strain_SPAn_71686:1−10922
0
2000
4000
6000
8000
10000

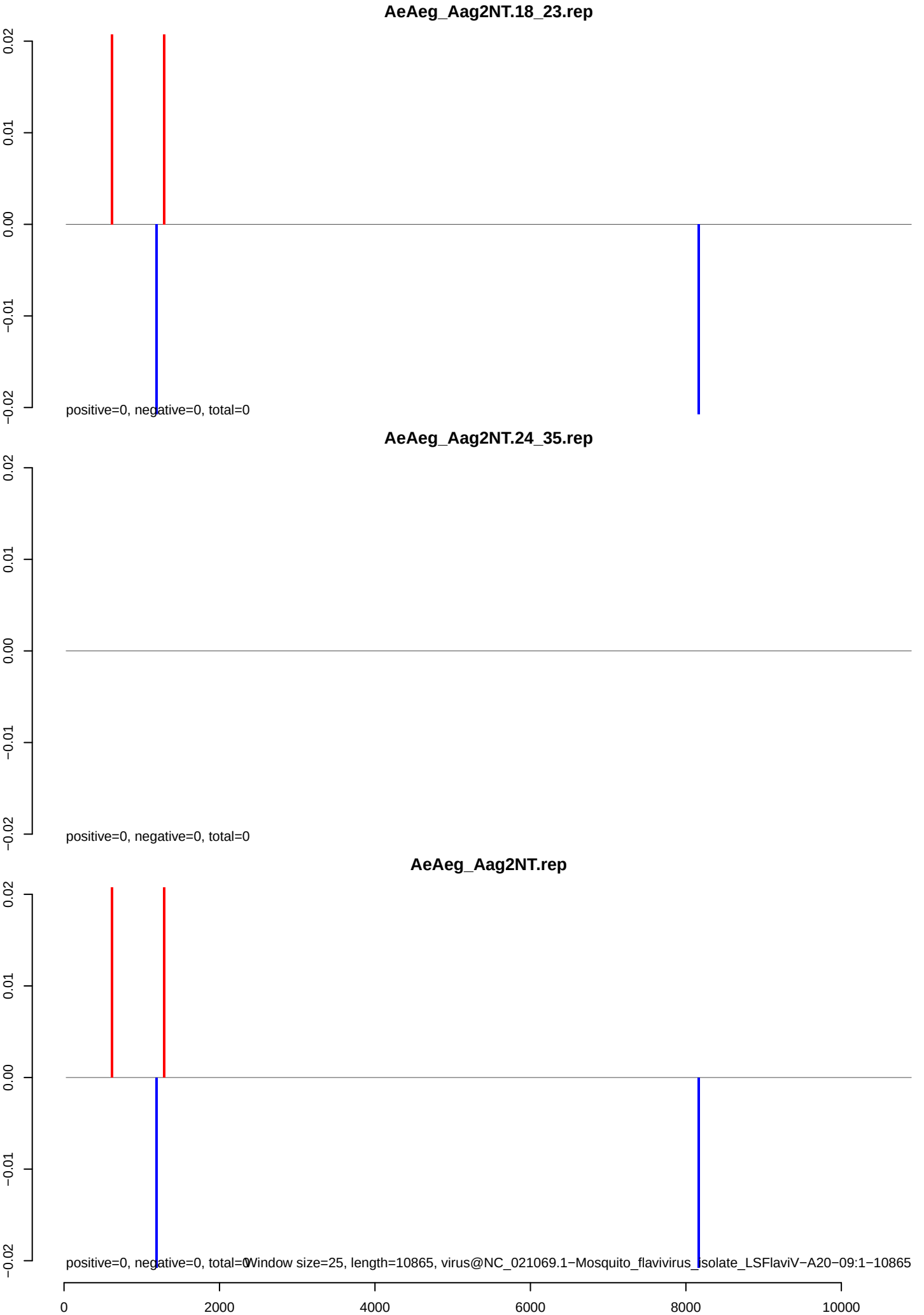
AeAeg_Aag2NT.18_23.rep
0.0
−0.1
−0.2
−0.3
−0.4
positive=0, negative=1, total=1

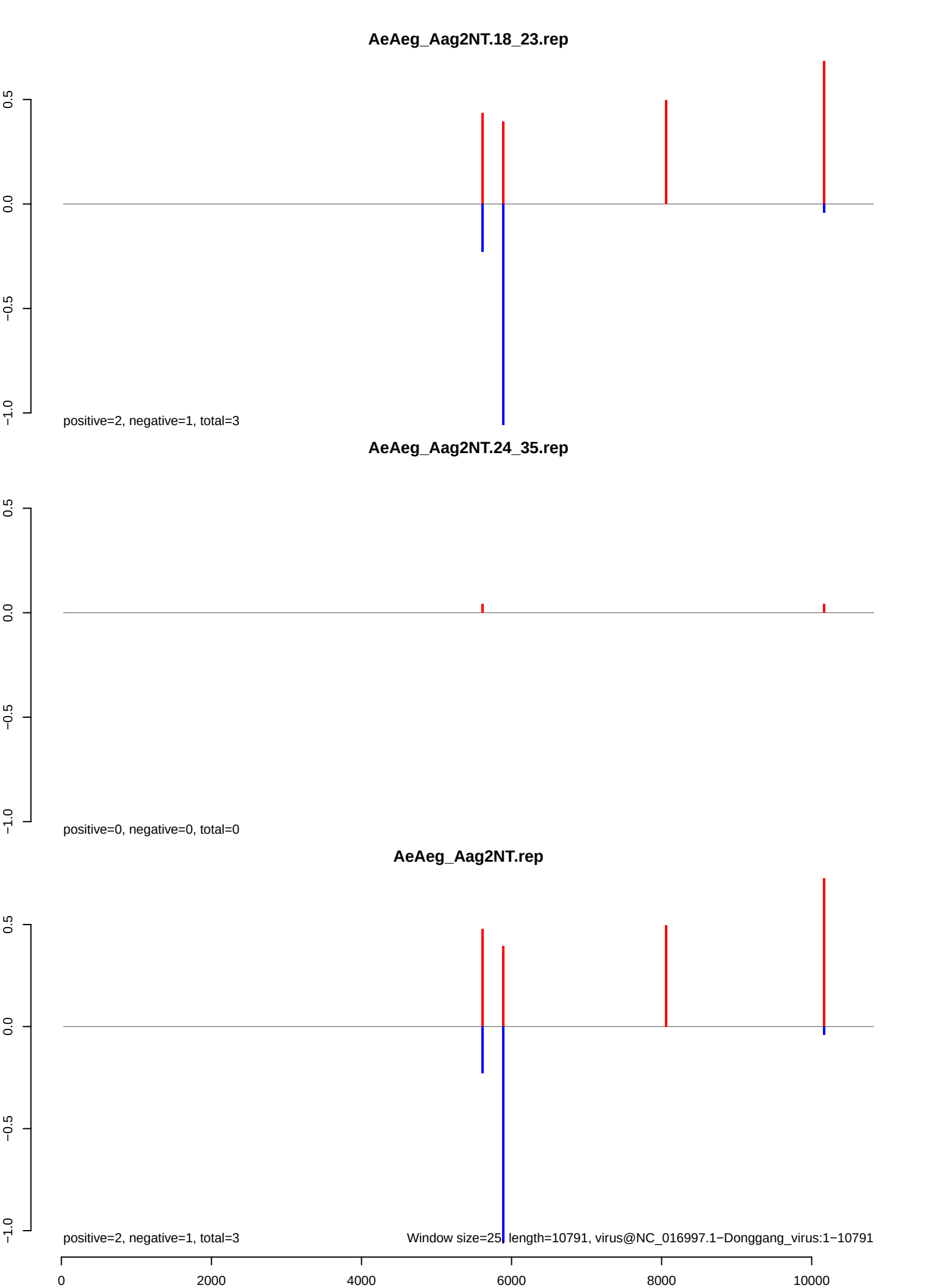
AeAeg_Aag2NT.24_35.rep
0.0
−0.1
−0.2
−0.3
−0.4
positive=0, negative=0, total=0

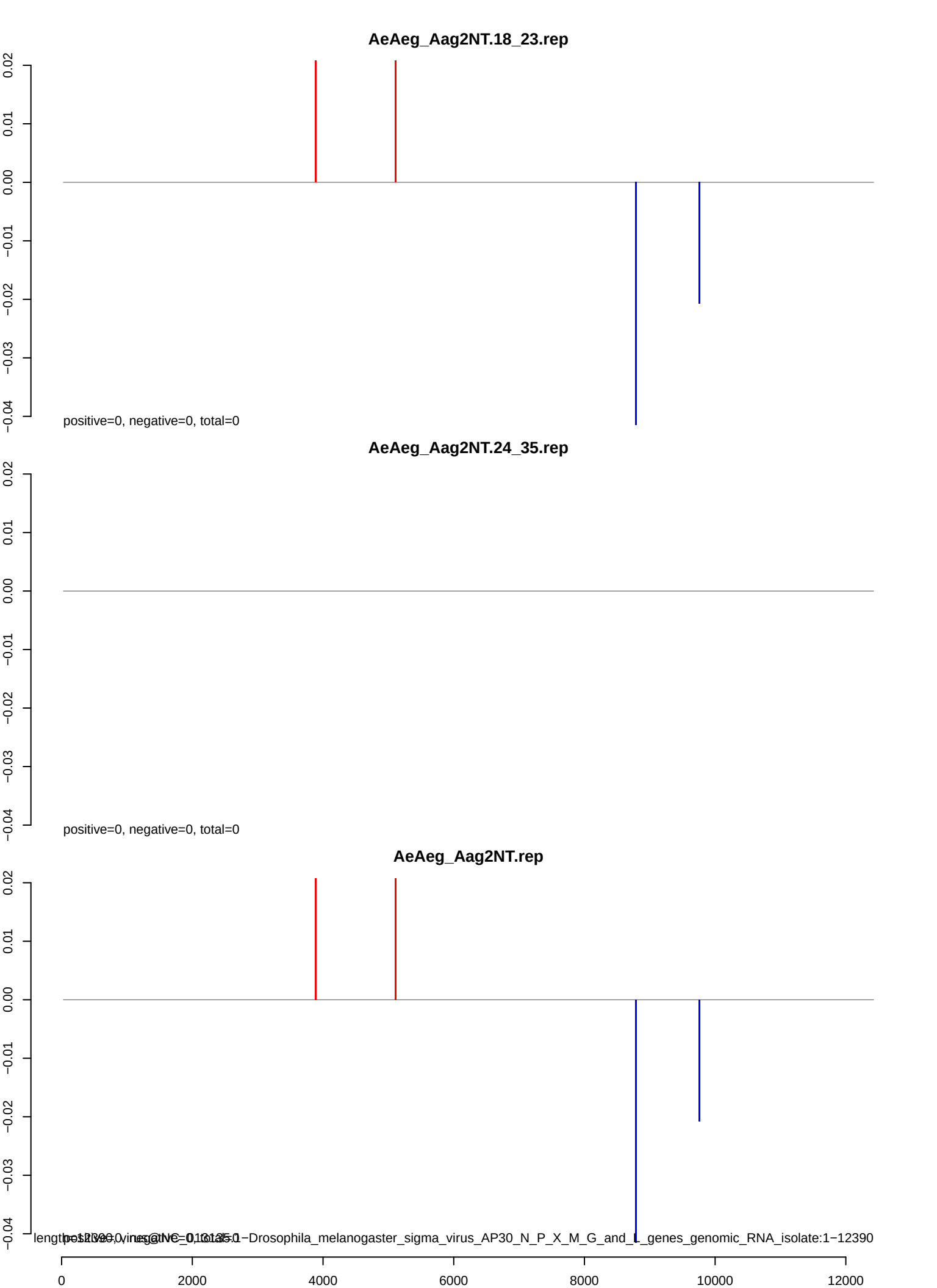

AeAeg_Aag2NT.rep
0.0
−0.1
−0.2
−0.3
−0.4
positive=0, negative=1, total=1
window size=25, length=10251, virus@NC_033723.1−Gadgets_Gully_virus_from_Australia_polyprotein_gene:1−10251
0
2000
4000
6000
8000
10000

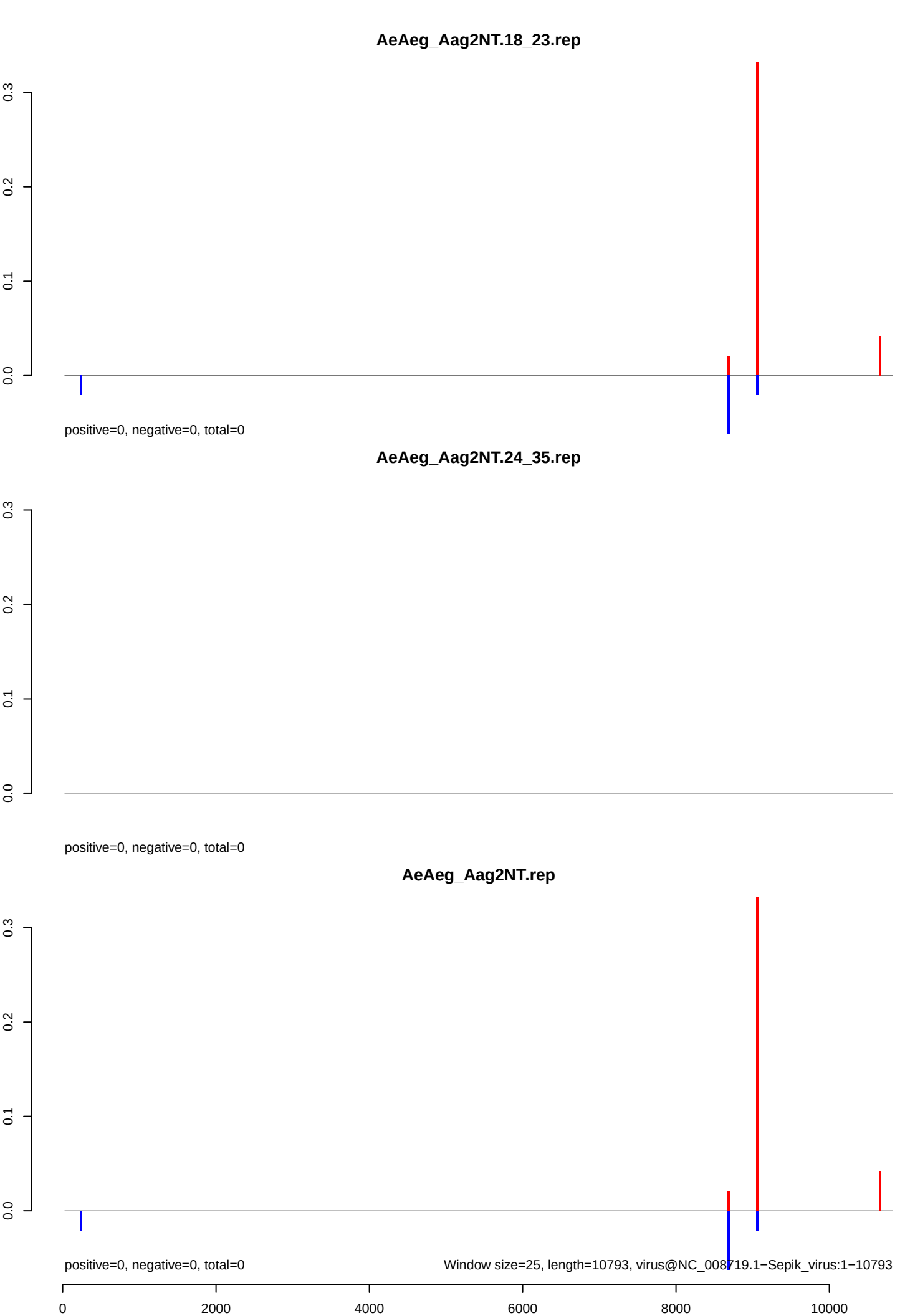

AeAeg_Aag2NT.18_23.rep
0.0
−0.2
−0.4
−0.6
−0.8
−1.0
−1.2
−1.4
positive=0, negative=1, total=1
AeAeg_Aag2NT.24_35.rep
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
positive=0, negative=1, total=1
Window size=25, length=10182, virus@NC_033698.1−Uganda_S_virus_polyprotein_gene:1−10182
0
2000
4000
6000
8000
10000

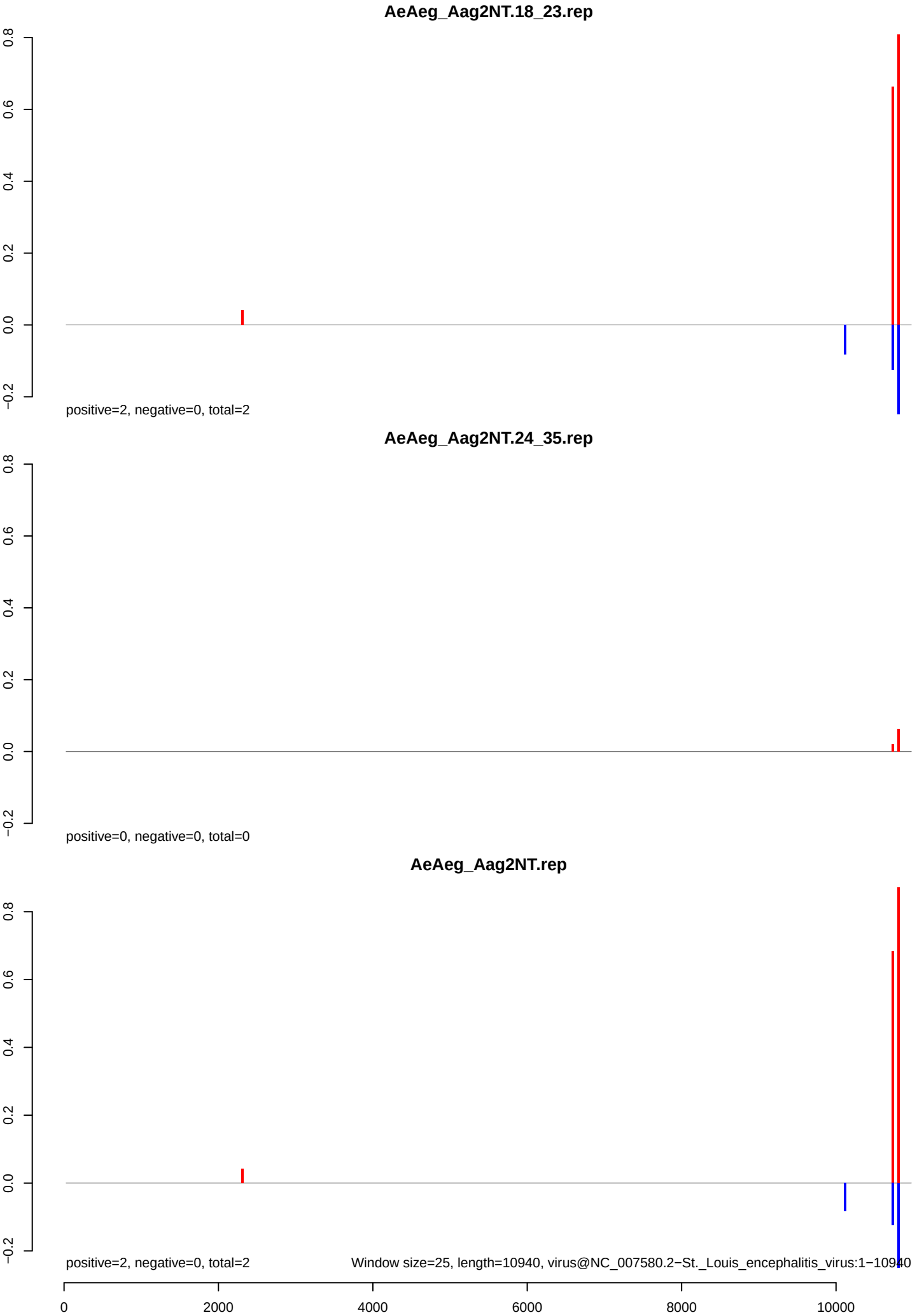

AeAeg_Aag2NT.18_23.rep
0.05
0.00
−0.05
−0.10
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
0.05
0.00
−0.05
−0.10
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.05
0.00
−0.05
−0.10
positive=0, negative=0, total=0Window size=25, length=10893, virus@NC_027817.1−Parramatta_River_virus_isolate_92−B115745:1−10893
0
2000
4000
6000
8000
10000

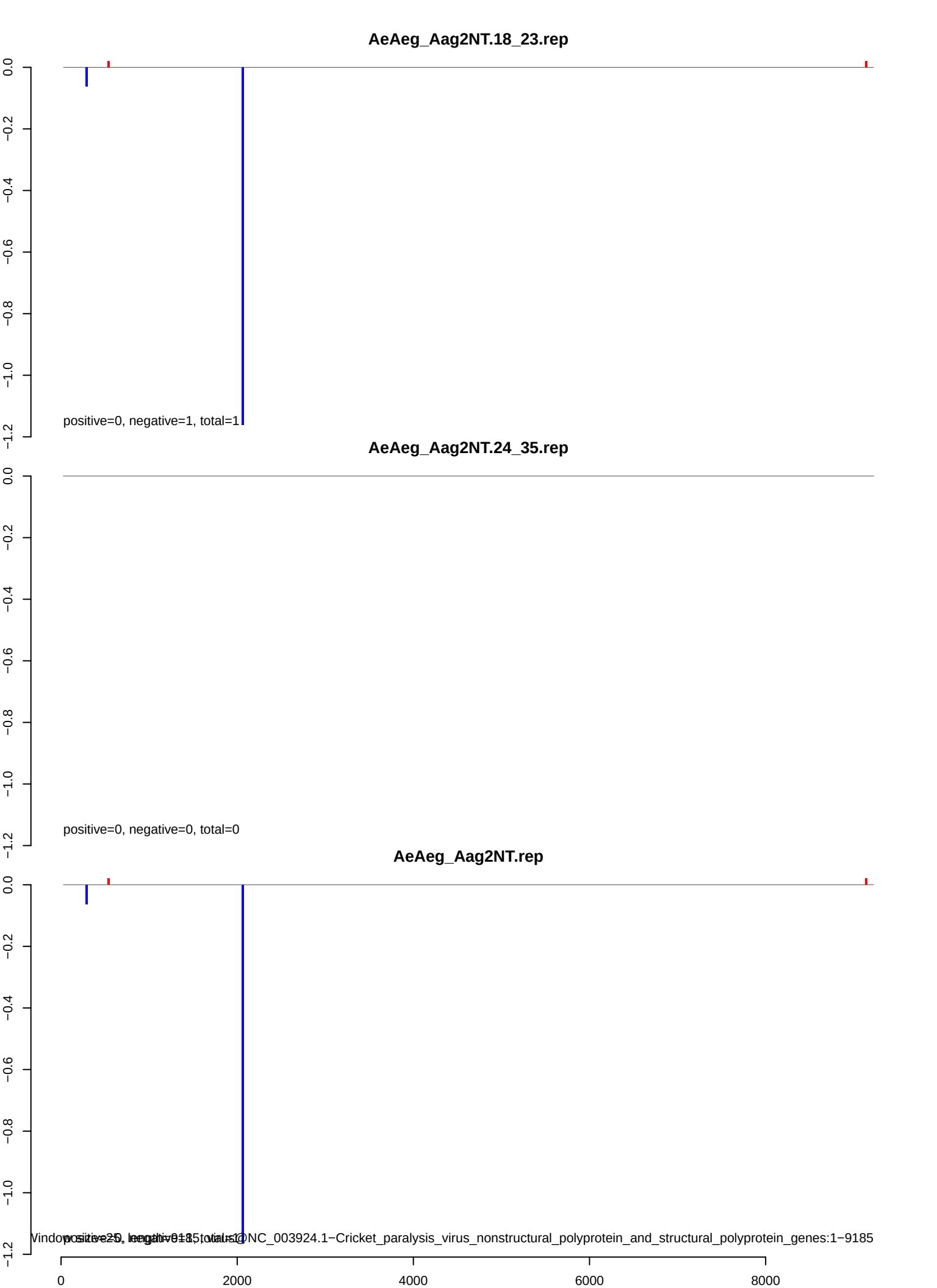

AeAeg_Aag2NT.18_23.rep
0.02
0.01
0.00
−0.01
−0.02
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
0.02
0.01
0.00
−0.01
−0.02
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.02
0.01
0.00
−0.01
−0.02
positive=0, negative=0, total=0
Window size=25, length=10865, virus@NC_021069.1−Mosquito_flavivirus_isolate_LSFlaviV−A20−09:1−10865
0
2000
4000
6000
8000
10000

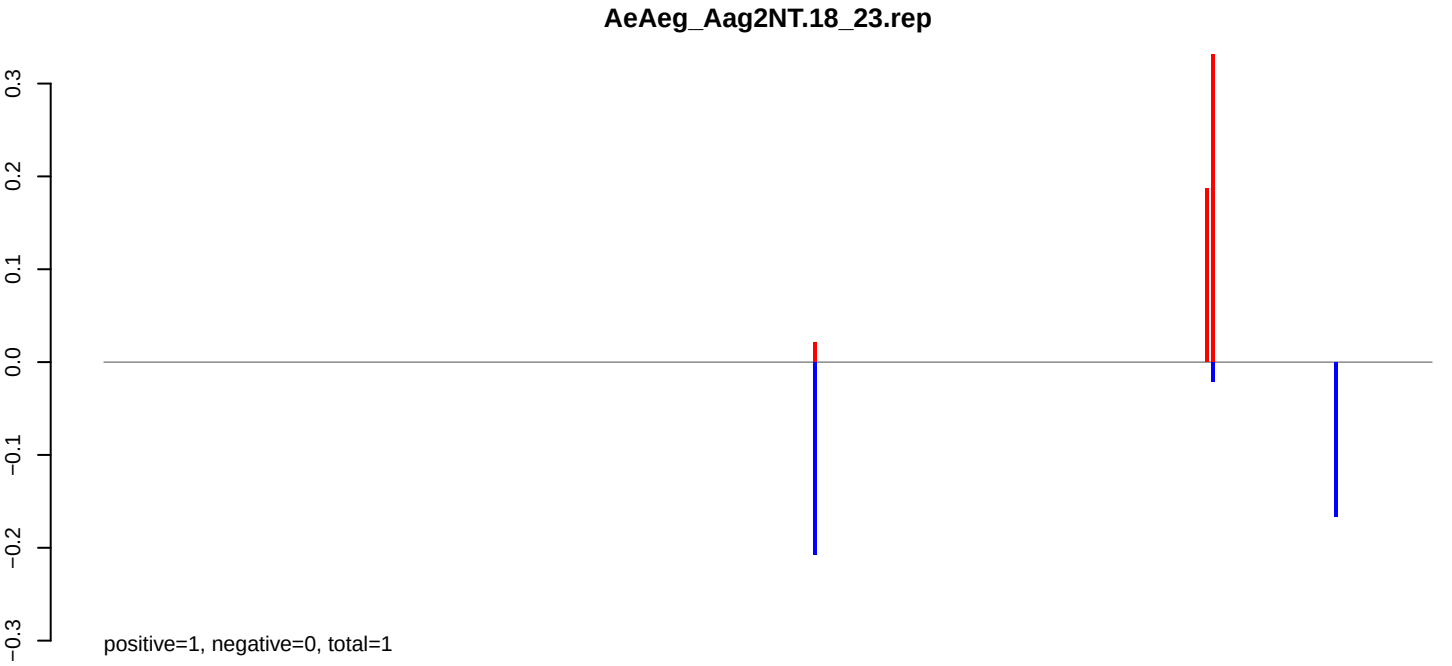

AeAeg_Aag2NT.18_23.rep
0.5
0.0
−0.5
−1.0
positive=2, negative=1, total=3
AeAeg_Aag2NT.24_35.rep
0.5
0.0
−0.5
−1.0
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.5
0.0
−0.5
−1.0
positive=2, negative=1, total=3
Window size=25, length=10791, virus@NC_016997.1−Donggang_virus:1−10791
0
2000
4000
6000
8000
10000


AeAeg_Aag2NT.18_23.rep
0.02
0.01
0.00
−0.01
−0.02
−0.03
−0.04
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
0.02
0.01
0.00
−0.01
−0.02
−0.03
−0.04
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.02
0.01
0.00
−0.01
−0.02
−0.03
−0.04
length=12390 | positive=0, negative=0, total=0
NC_001654.1−Drosophila_melanogaster_sigma_virus_AP30_N_P_X_M_G_and_L_genes_genomic_RNA_isolate:1−12390
0
2000
4000
6000
8000
10000
12000

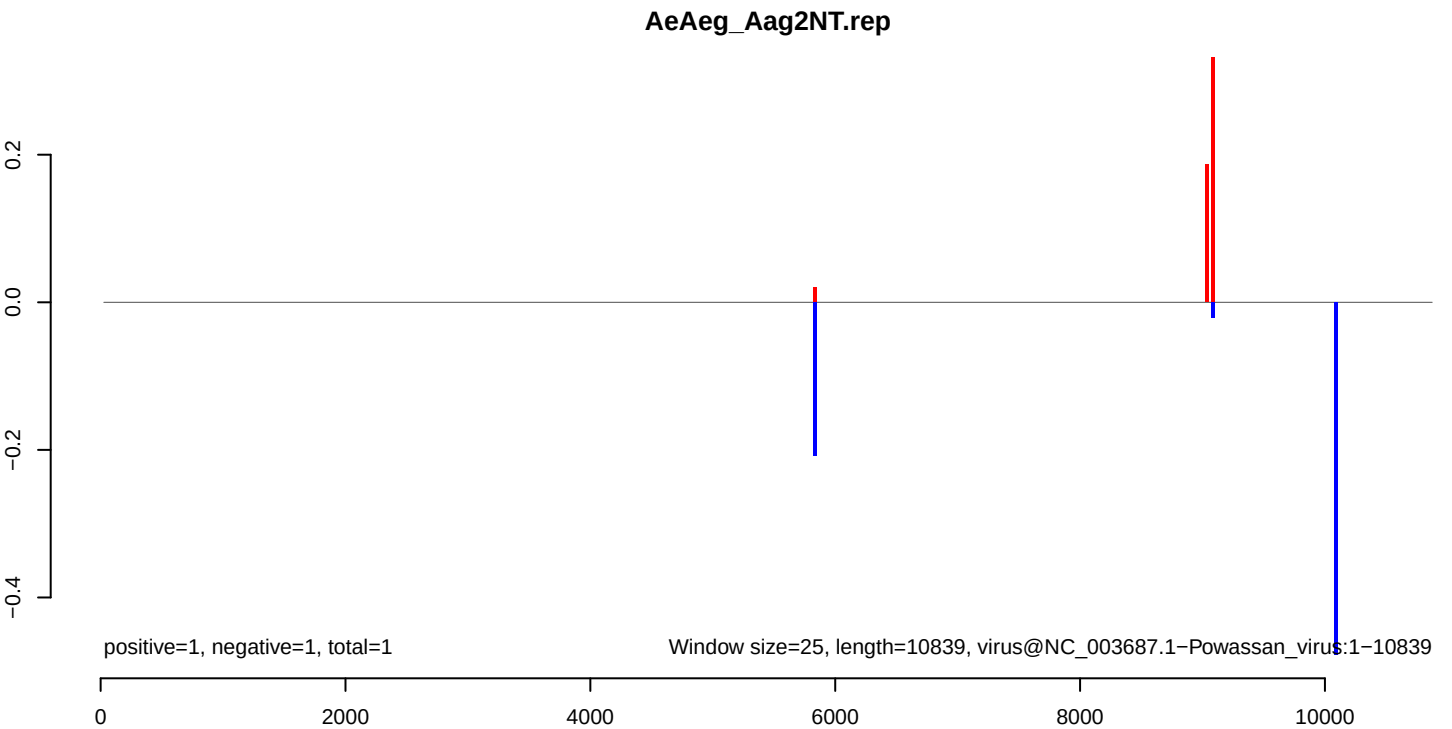

AeAeg_Aag2NT.18_23.rep
0.0
0.1
0.2
0.3
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
0.0
0.1
0.2
0.3
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.0
0.1
0.2
0.3
positive=0, negative=0, total=0
Window size=25, length=10793, virus@NC_008719.1−Sepik_virus:1−10793
0
2000
4000
6000
8000
10000

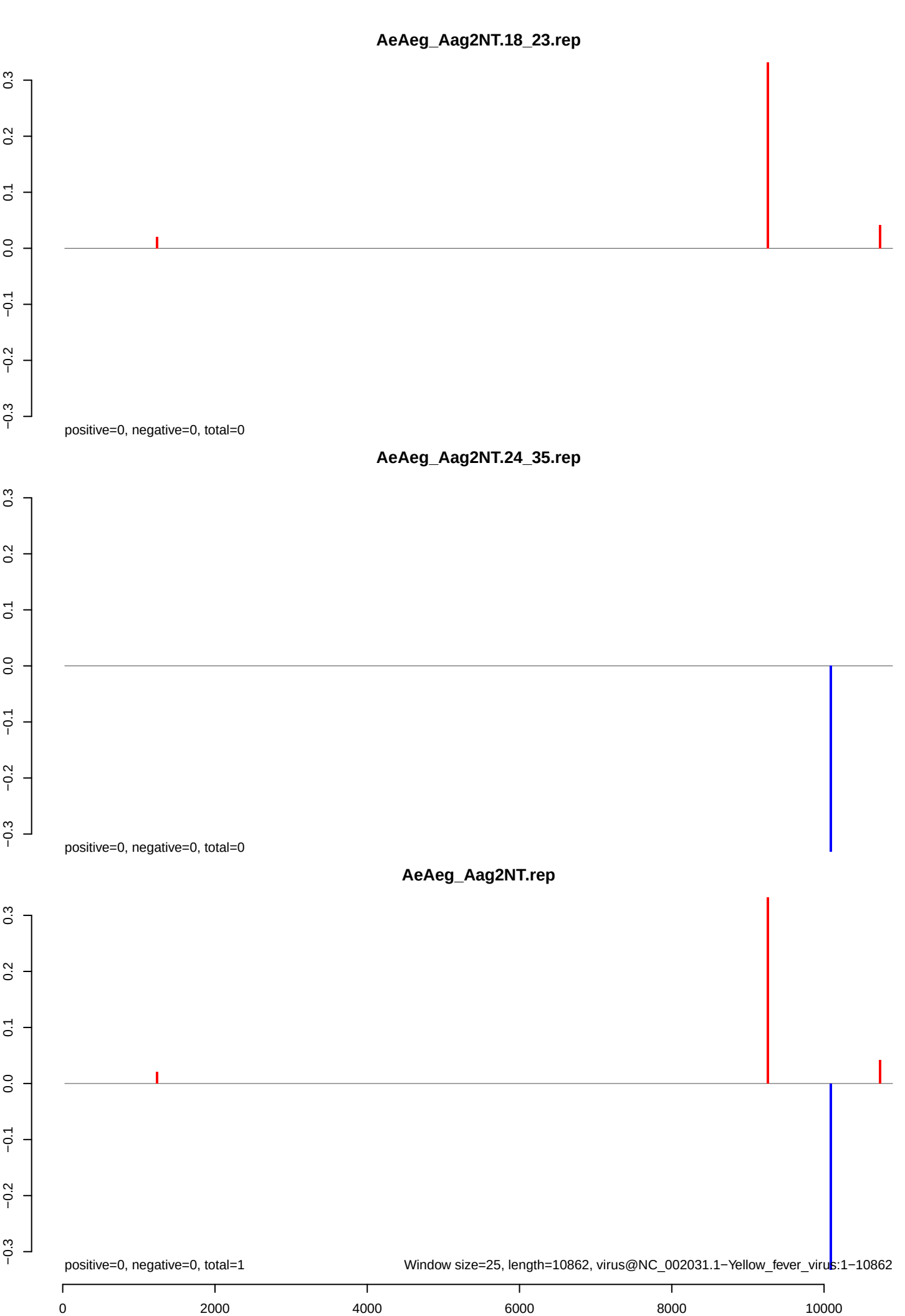

AeAeg_Aag2NT.18_23.rep
0.8
0.6
0.4
0.2
0.0
−0.2
positive=2, negative=0, total=2
AeAeg_Aag2NT.24_35.rep
0.8
0.6
0.4
0.2
0.0
−0.2
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.8
0.6
0.4
0.2
0.0
−0.2
positive=2, negative=0, total=2
Window size=25, length=10940, virus@NC_007580.2−St._Louis_encephalitis_virus:1−10940
0
2000
4000
6000
8000
10000

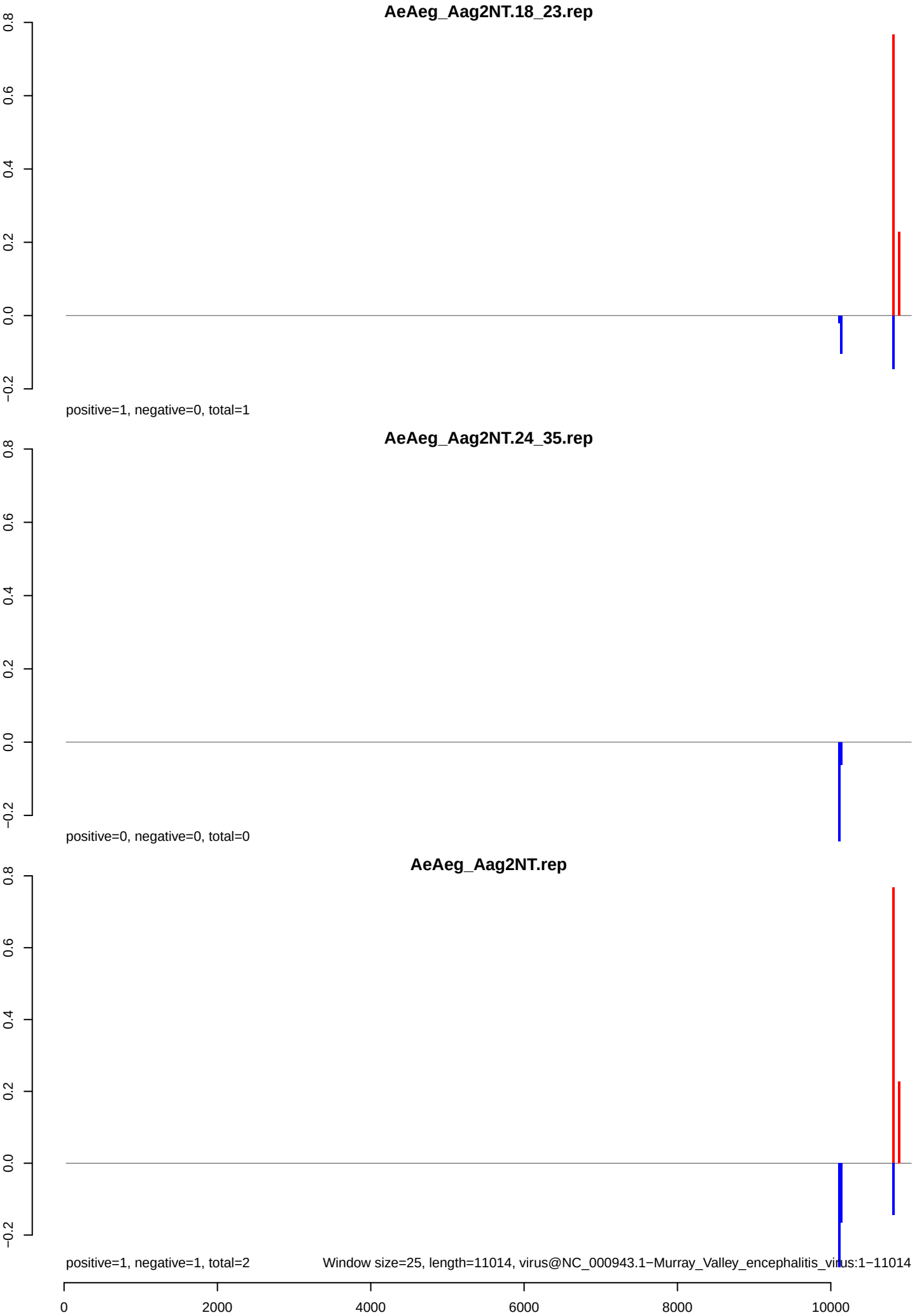

AeAeg_Aag2NT.18_23.rep
0.0
−0.2
−0.4
−0.6
−0.8
−1.0
−1.2
positive=0, negative=1, total=1
AeAeg_Aag2NT.24_35.rep
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
positive=0, negative=1, total=1
Vindow
NC_003924.1−Cricket_paralysis_virus_nonstructural_polyprotein_and_structural_polyprotein_genes:1−9185
0
2000
4000
6000
8000

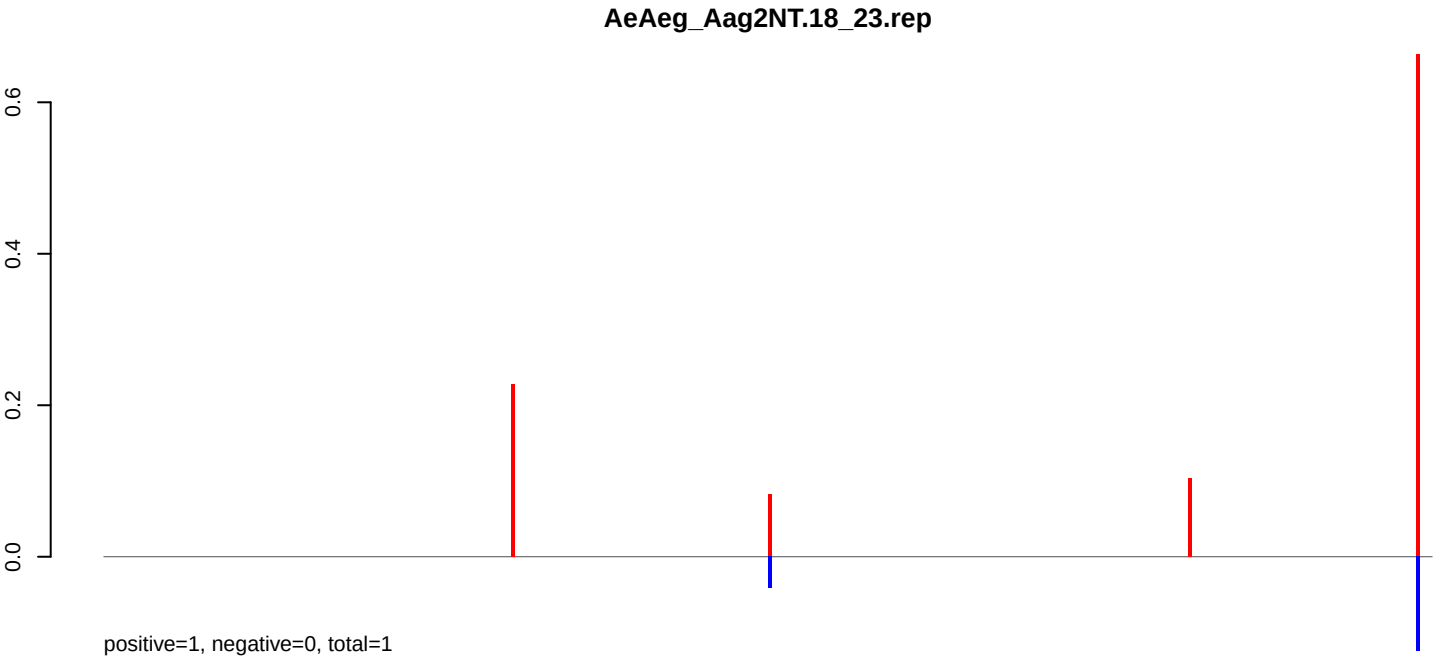

AeAeg_Aag2NT.18_23.rep
0.3
0.2
0.1
0.0
−0.1
−0.2
−0.3
positive=1, negative=0, total=1

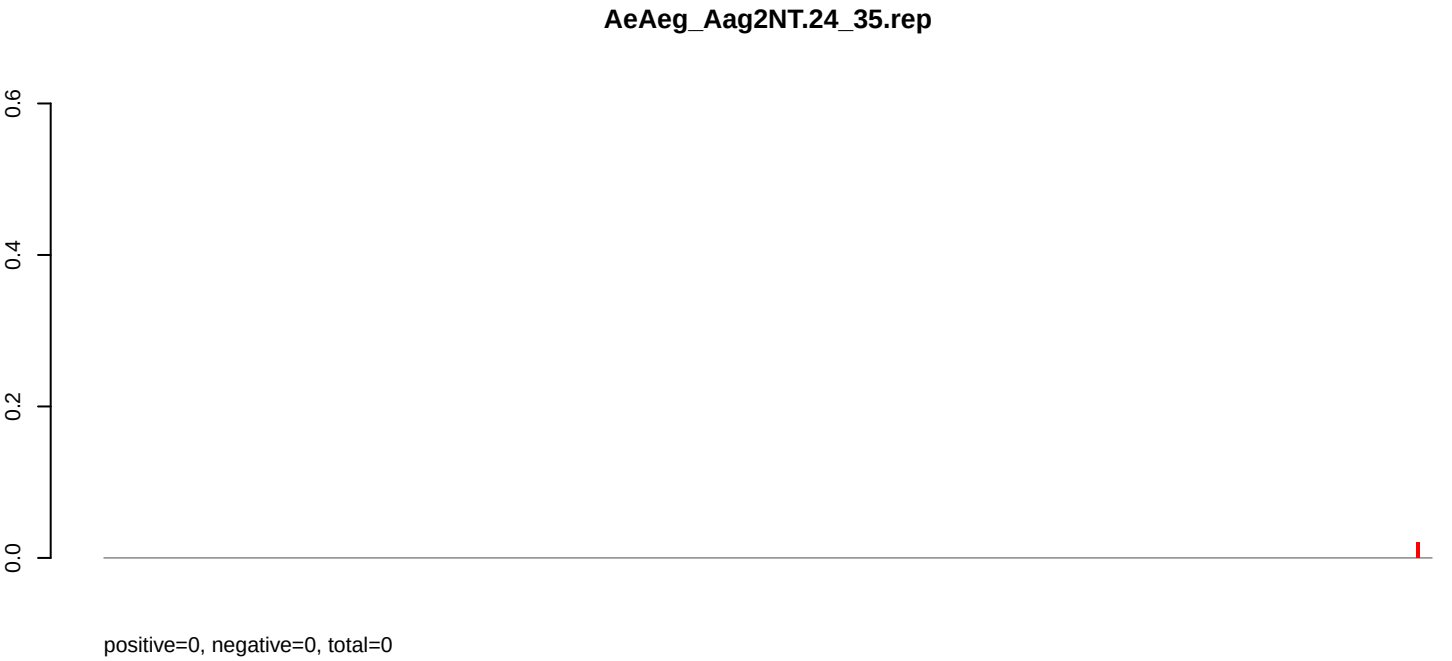
AeAeg_Aag2NT.24_35.rep
0.3
0.2
0.1
0.0
−0.1
−0.2
−0.3
positive=0, negative=0, total=0

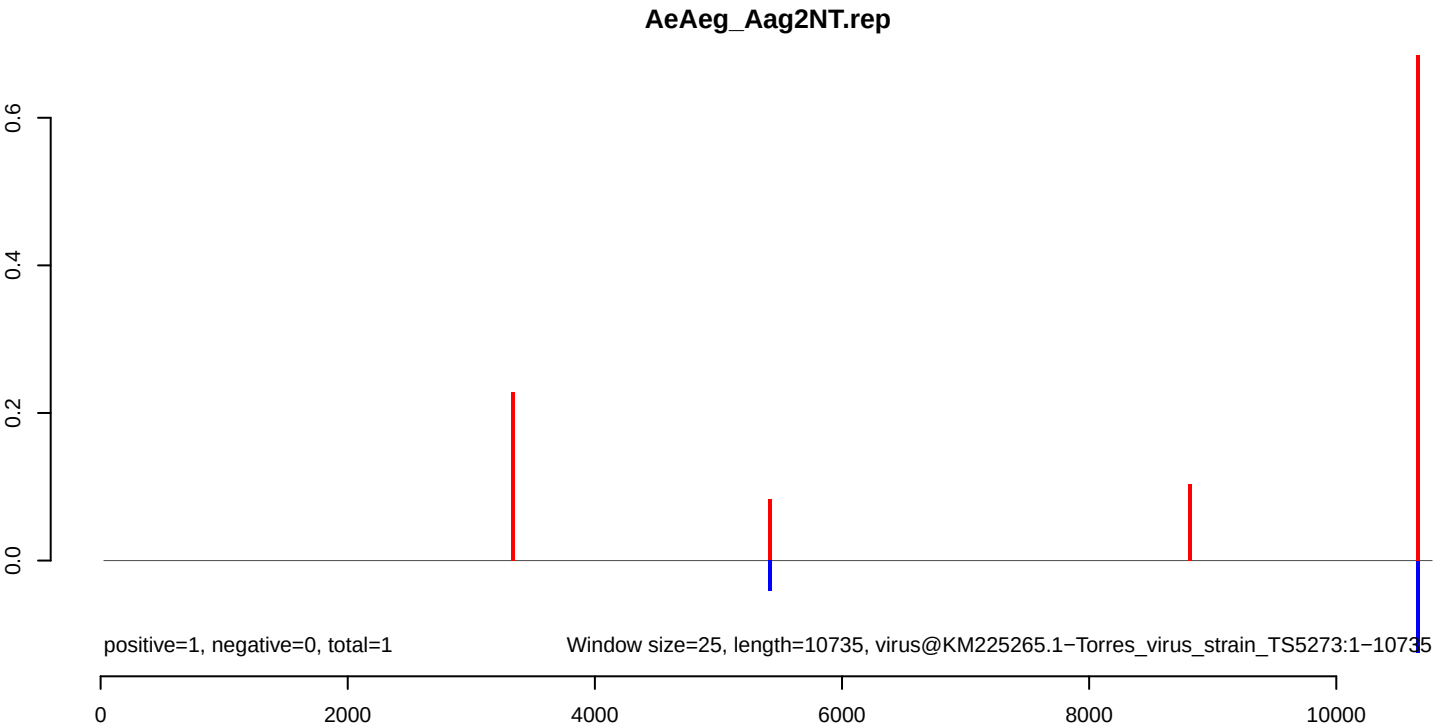

AeAeg_Aag2NT.rep
0.2
0.0
−0.2
−0.4
positive=1, negative=1, total=1
Window size=25, length=10839, virus@NC_003687.1−Powassan_virus:1−10839
0
2000
4000
6000
8000
10000


AeAeg_Aag2NT.18_23.rep
0.3
0.2
0.1
0.0
−0.1
−0.2
−0.3
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
0.3
0.2
0.1
0.0
−0.1
−0.2
−0.3
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.3
0.2
0.1
0.0
−0.1
−0.2
−0.3
positive=0, negative=0, total=1
Window size=25, length=10862, virus@NC_002031.1−Yellow_fever_virus:1−10862
0
2000
4000
6000
8000
10000


AeAeg_Aag2NT.18_23.rep
0.8
0.6
0.4
0.2
0.0
−0.2
positive=1, negative=0, total=1
AeAeg_Aag2NT.24_35.rep
0.8
0.6
0.4
0.2
0.0
−0.2
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.8
0.6
0.4
0.2
0.0
−0.2
positive=1, negative=1, total=2
Window size=25, length=11014, virus@NC_000943.1−Murray_Valley_encephalitis_virus:1−11014
0
2000
4000
6000
8000
10000


AeAeg_Aag2NT.18_23.rep
0.0
0.2
0.4
0.6
positive=1, negative=0, total=1


AeAeg_Aag2NT.24_35.rep
0.0
0.2
0.4
0.6
positive=0, negative=0, total=0


AeAeg_Aag2NT.rep
0.0
0.2
0.4
0.6
positive=1, negative=0, total=1
Window size=25, length=10735, virus@KM225265.1−Torres_virus_strain_TS5273:1−10735
0
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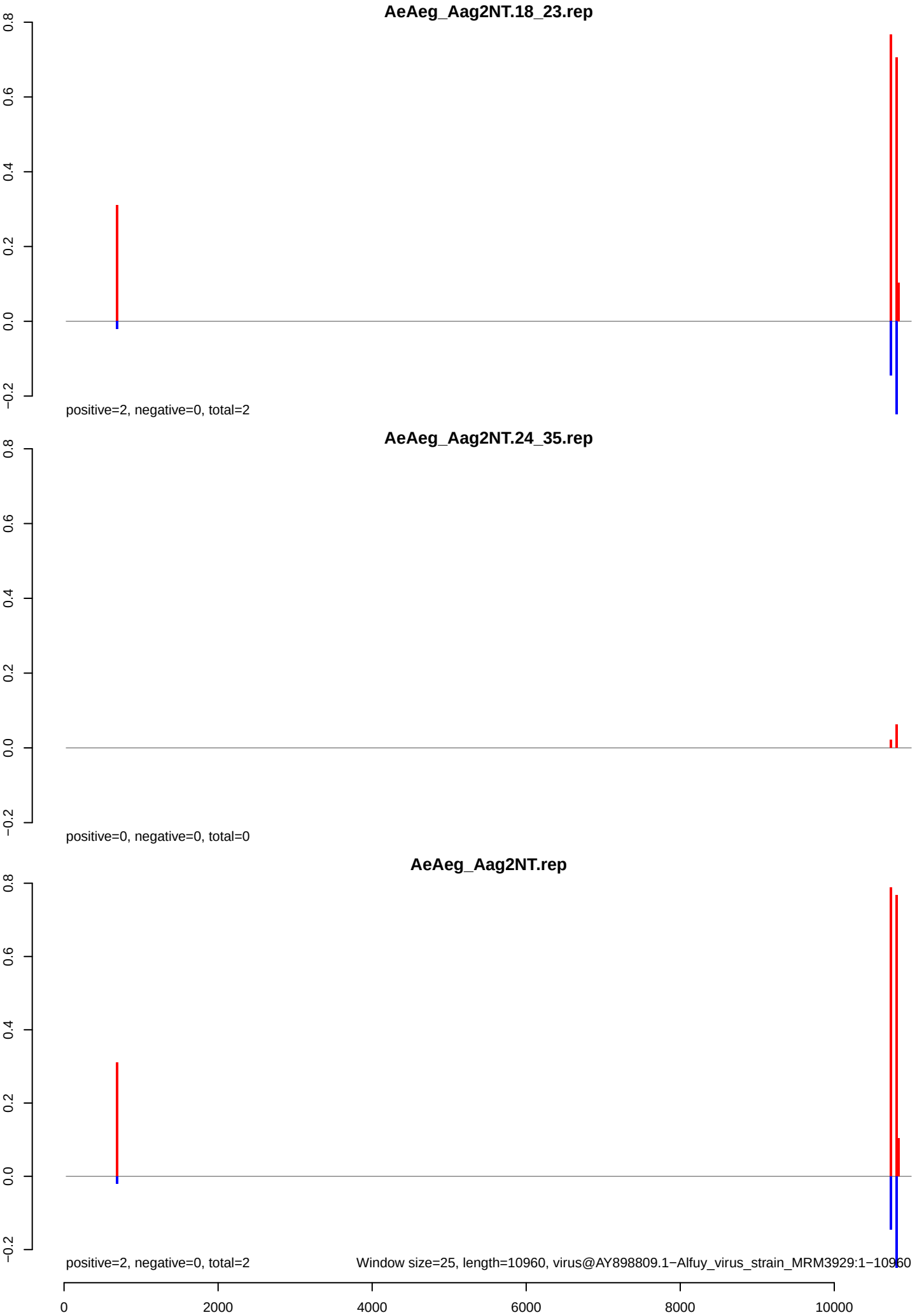
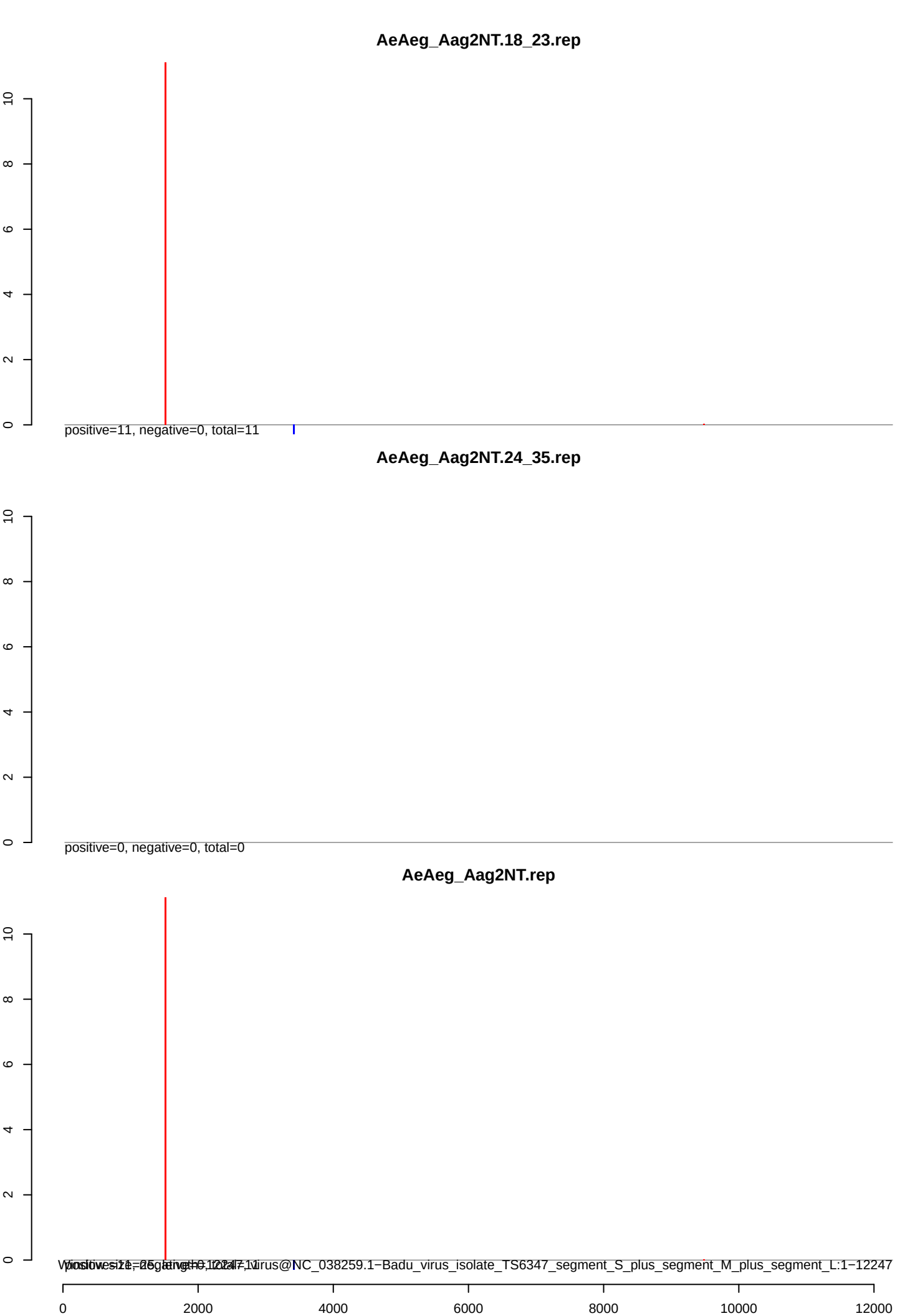
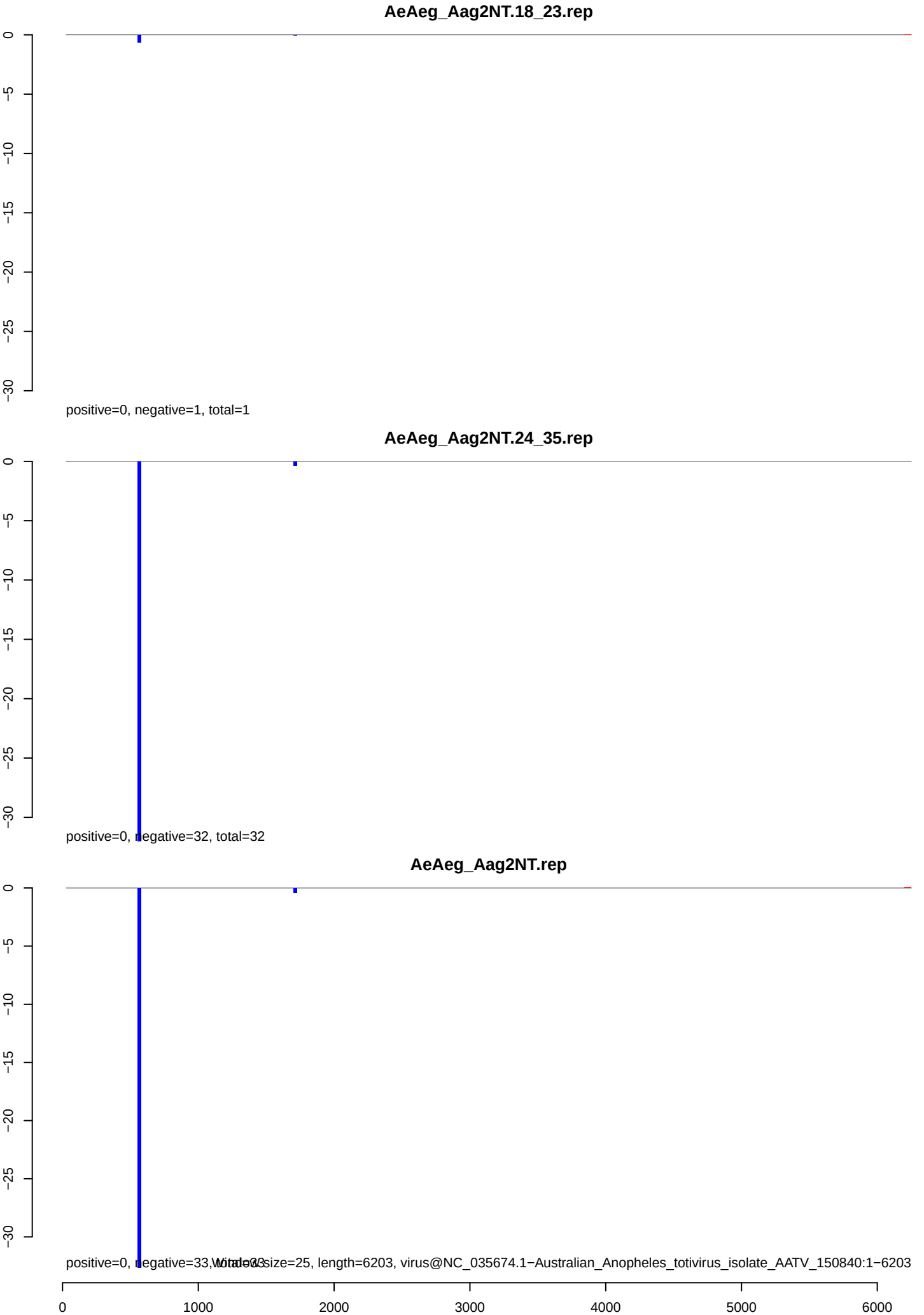
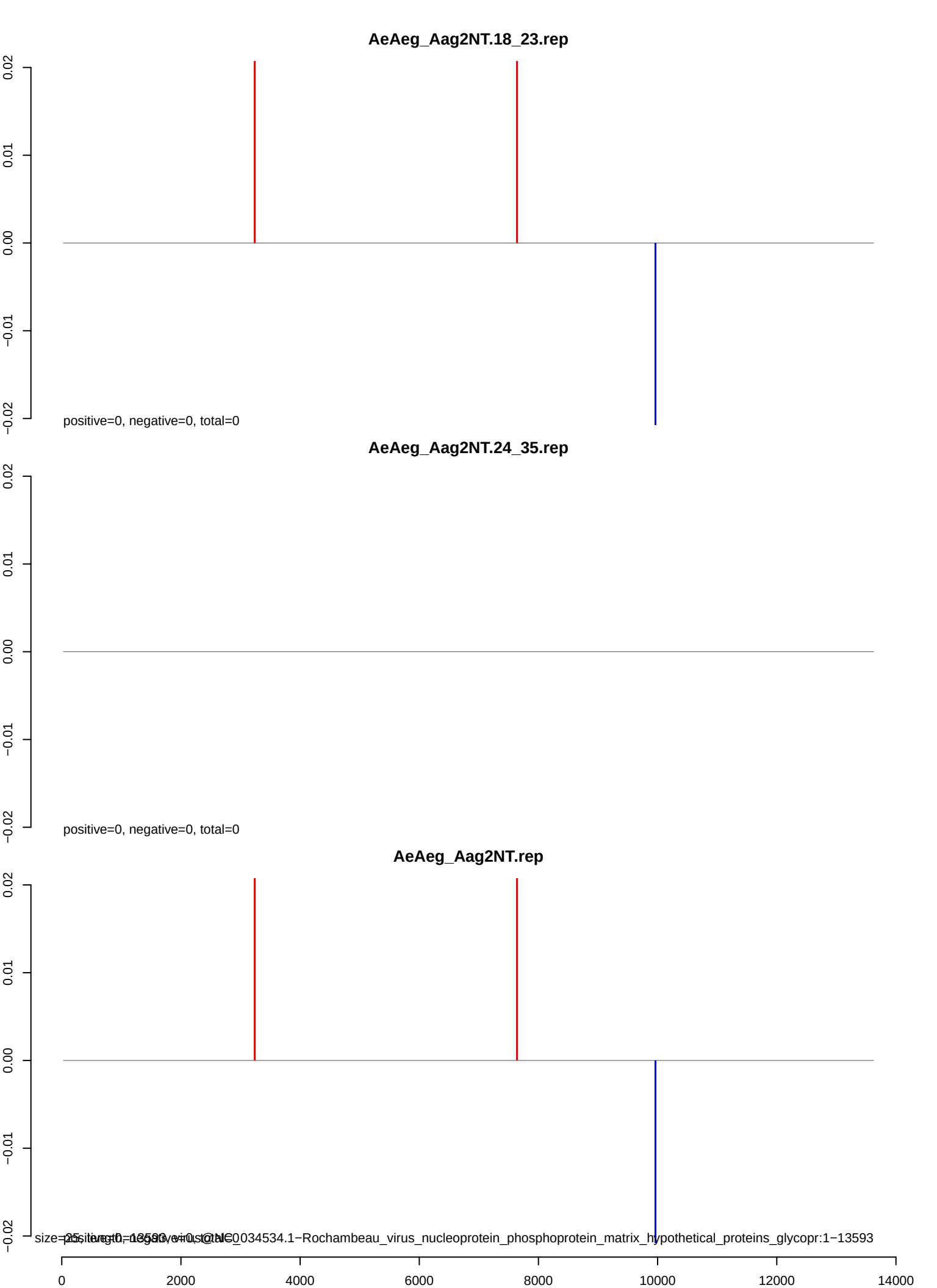
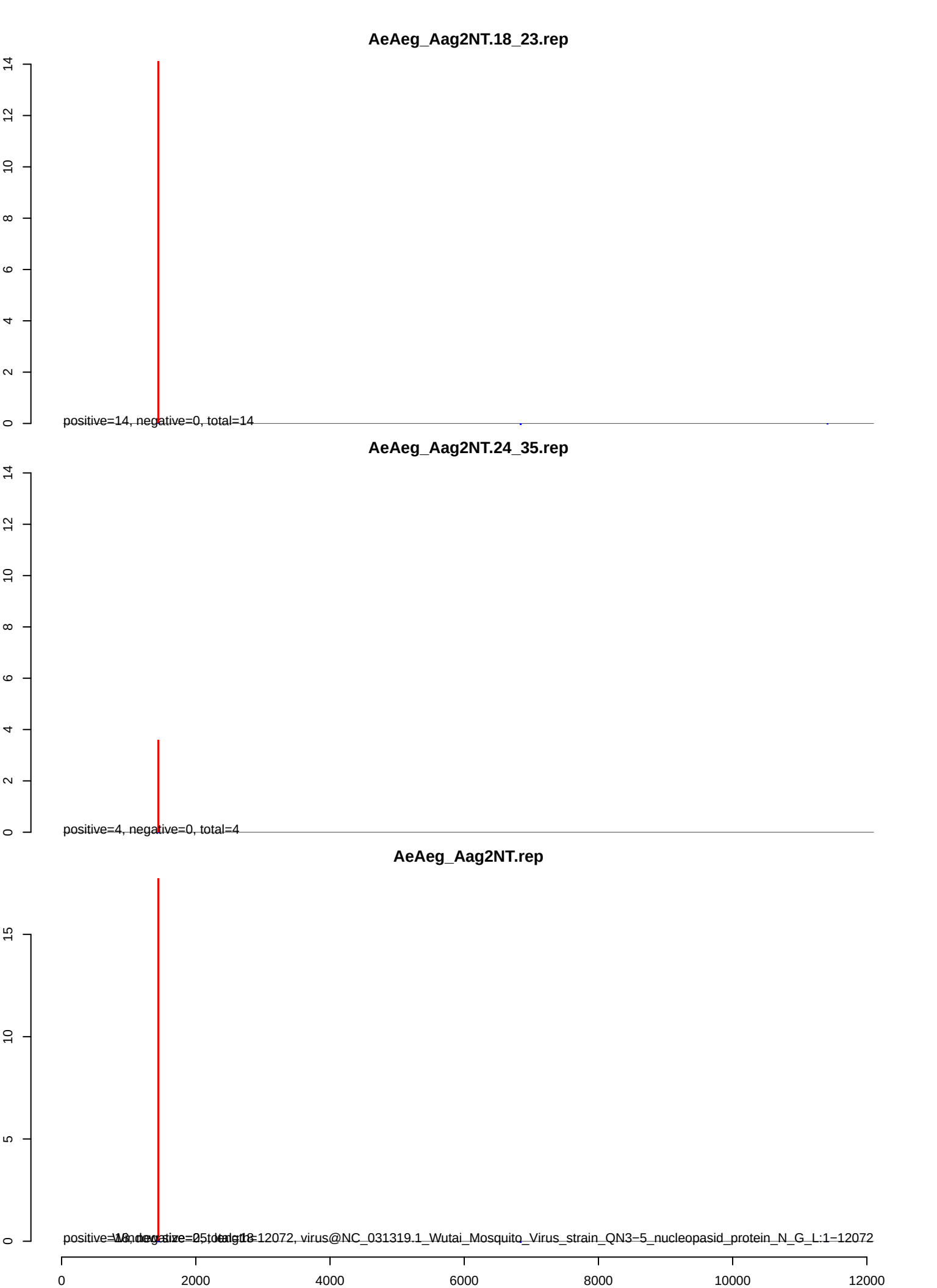
4000
6000
8000
10000

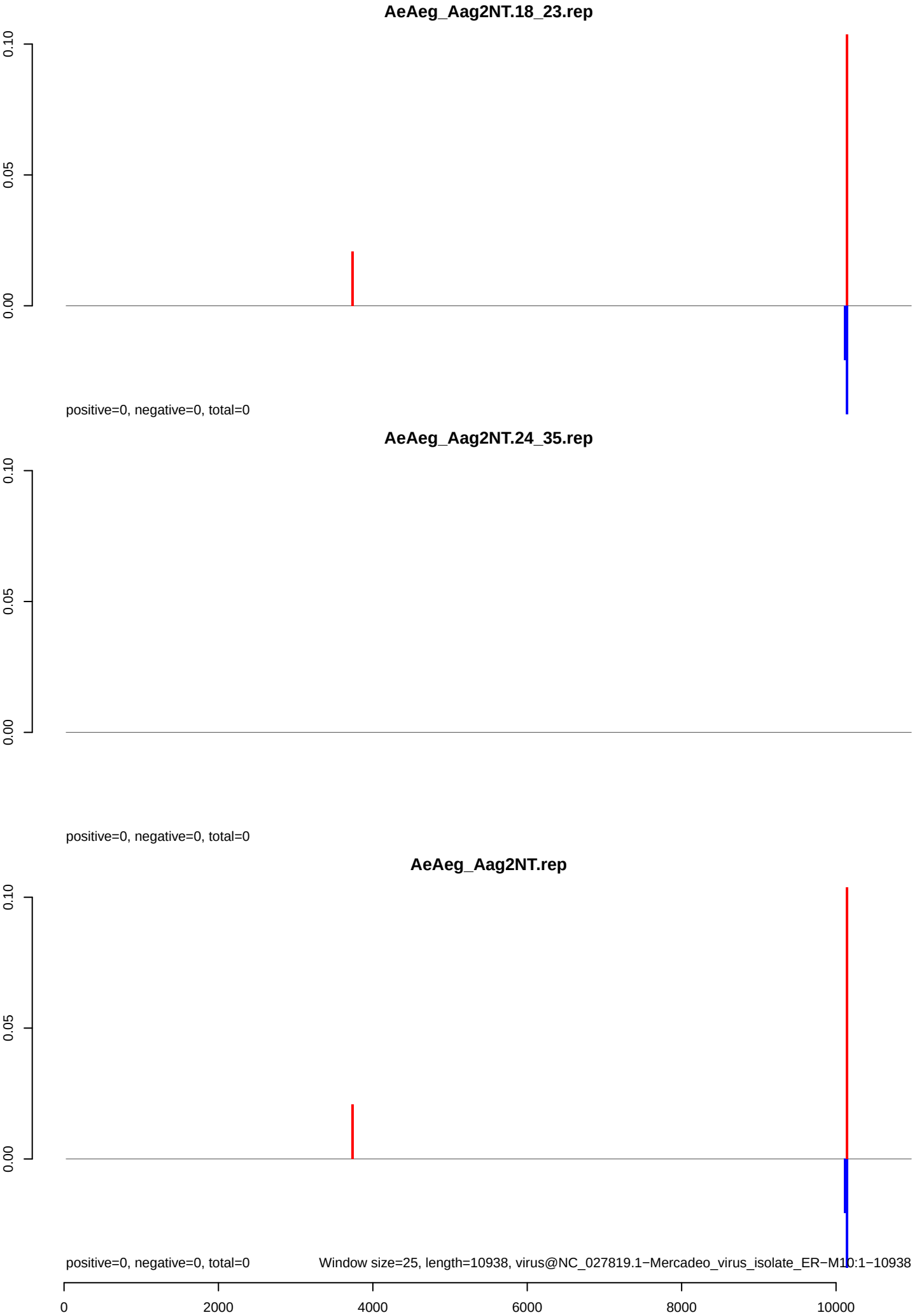

AeAeg_Aag2NT.18_23.rep
0.8
0.6
0.4
0.2
0.0
−0.2
positive=2, negative=0, total=2
AeAeg_Aag2NT.24_35.rep
0.8
0.6
0.4
0.2
0.0
−0.2
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.8
0.6
0.4
0.2
0.0
−0.2
positive=2, negative=0, total=2
Window size=25, length=10960, virus@AY898809.1−Alfuy_virus_strain_MRM3929:1−10960
0
2000
4000
6000
8000
10000

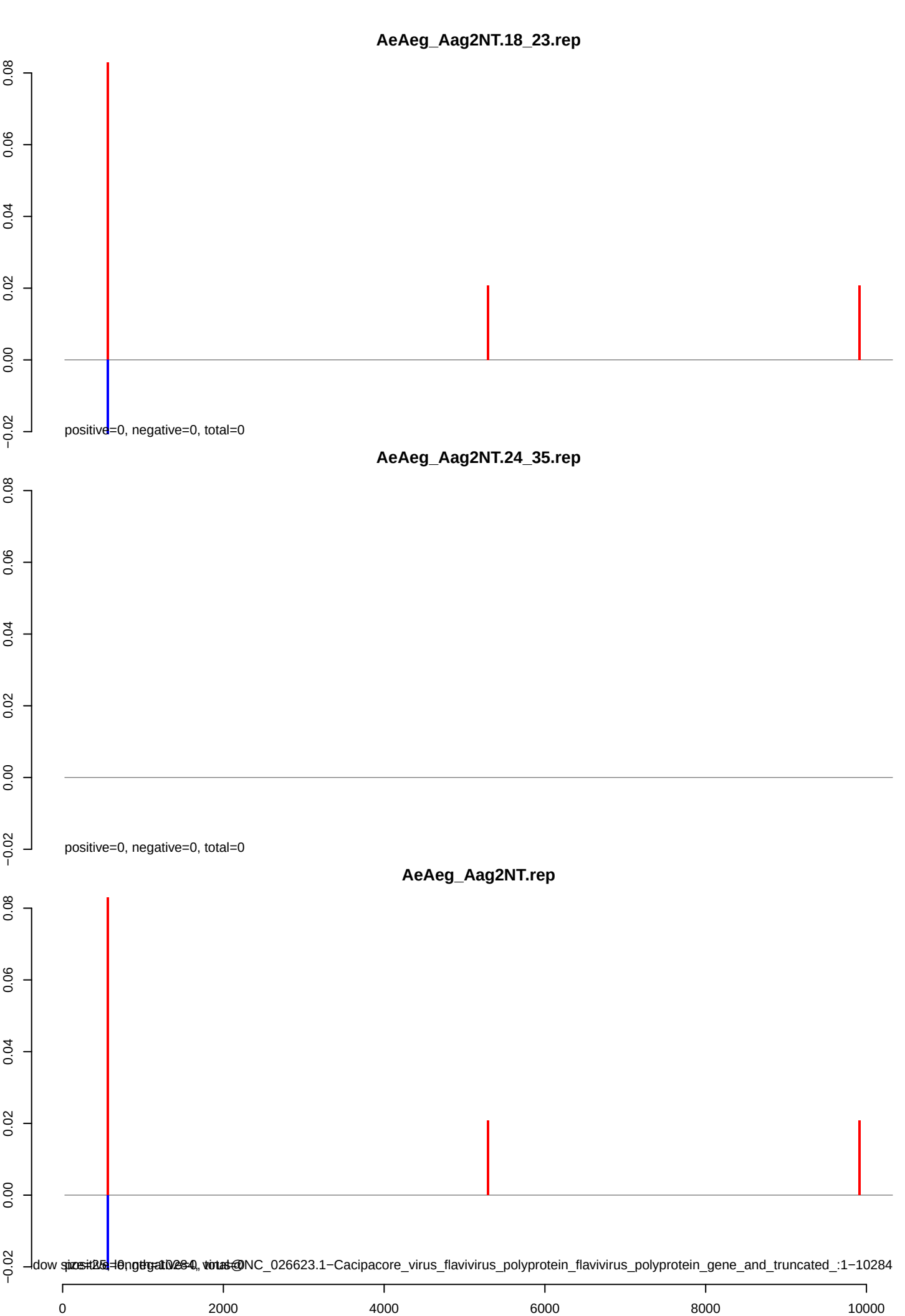

AeAeg_Aag2NT.18_23.rep
0
2
4
6
8
10
positive=11, negative=0, total=11
AeAeg_Aag2NT.24_35.rep
0
2
4
6
8
10
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0
2
4
6
8
10
0
2000
4000
6000
8000
10000
12000

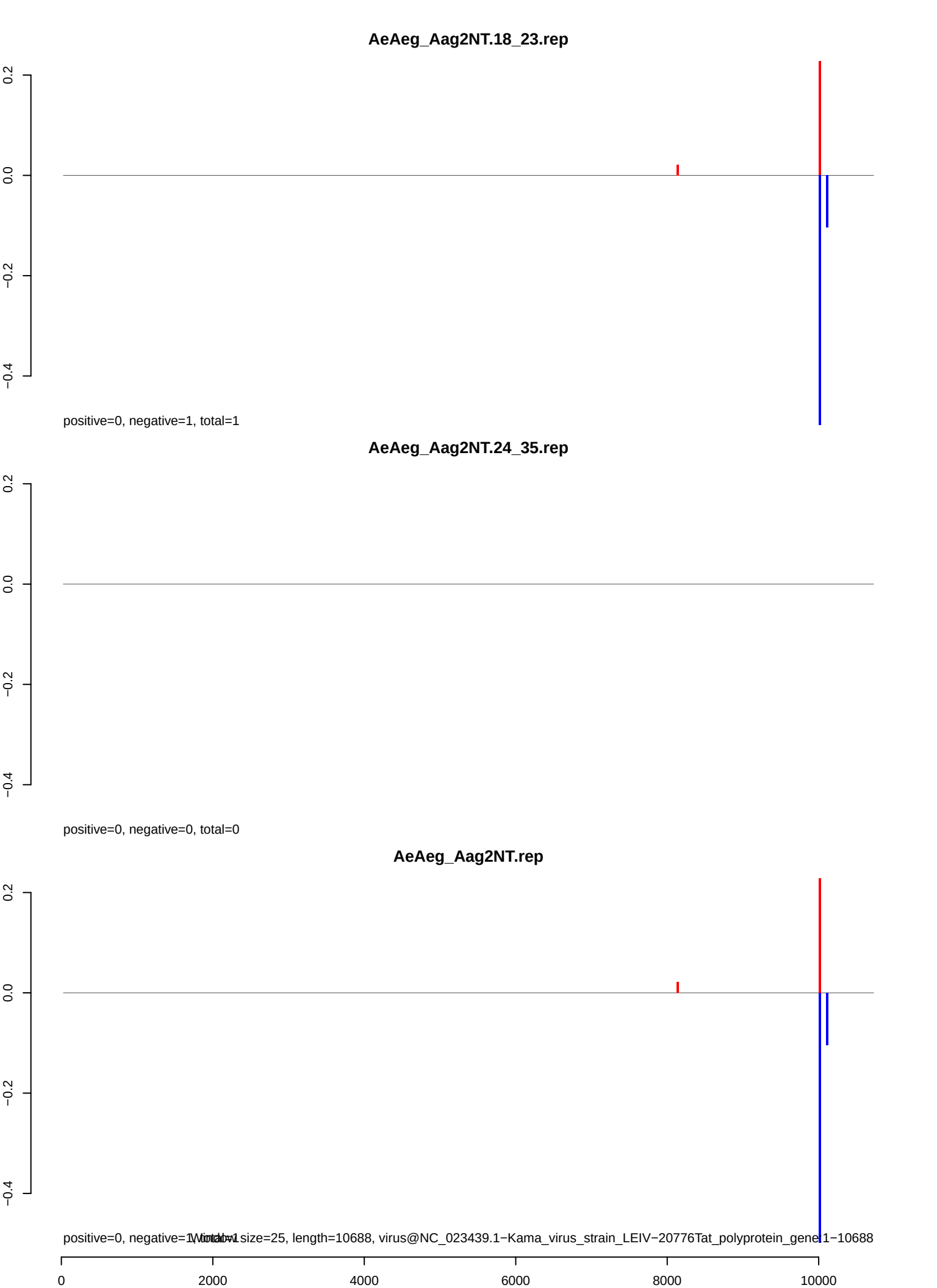

AeAeg_Aag2NT.18_23.rep
0
−5
−10
−15
−20
−25
−30
positive=0, negative=1, total=1
AeAeg_Aag2NT.24_35.rep
0
−5
−10
−15
−20
−25
−30
positive=0, negative=32, total=32
AeAeg_Aag2NT.rep
0
−5
−10
−15
−20
−25
−30
positive=0, negative=33, total=33
window size=25, length=6203, virus@NC_035674.1−Australian_Anopheles_totivirus_isolate_AATV_150840:1−6203
0
1000
2000
3000
4000
5000
6000

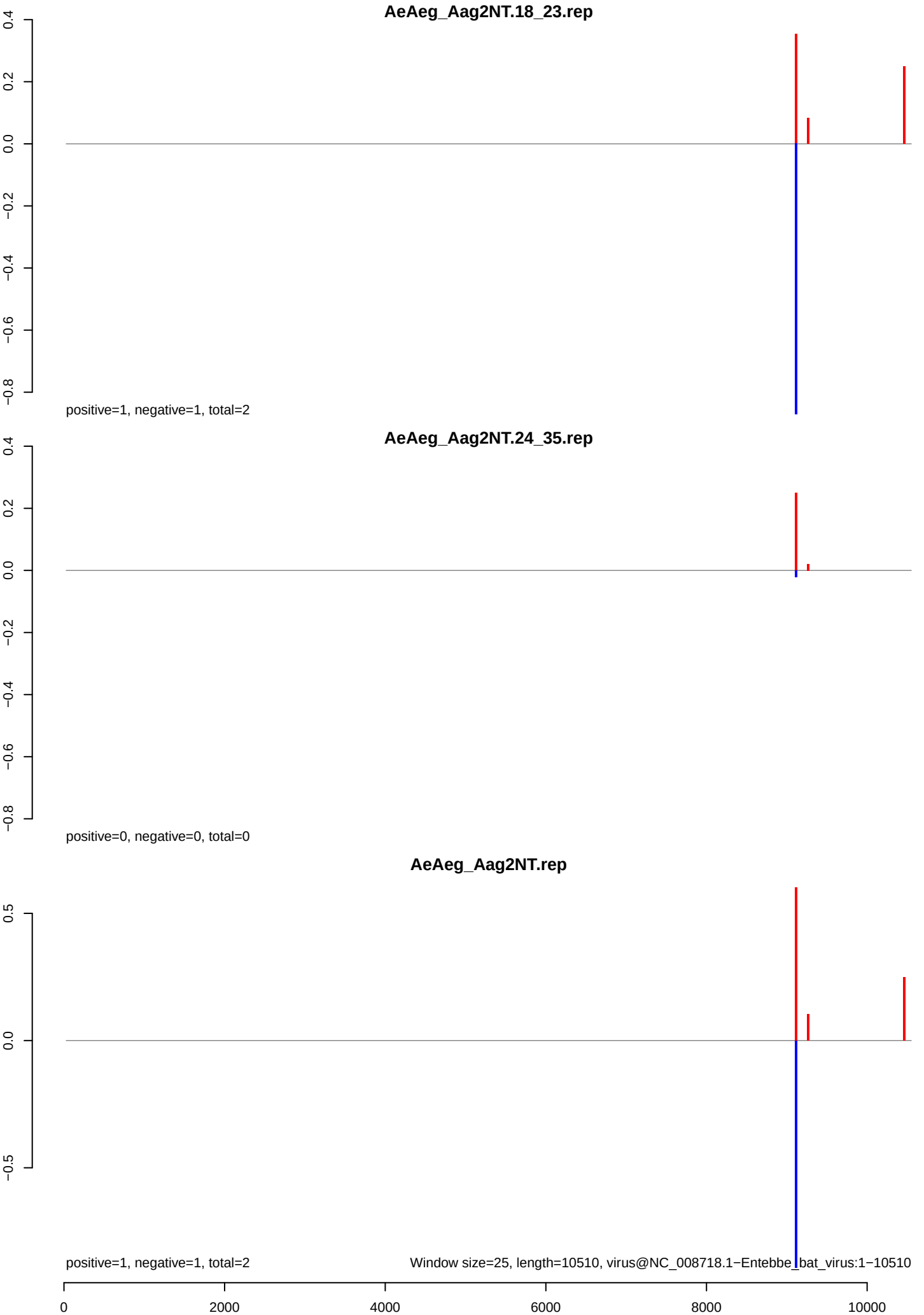

AeAeg_Aag2NT.18_23.rep
0.02
0.01
0.00
−0.01
−0.02
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
0.02
0.01
0.00
−0.01
−0.02
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.02
0.01
0.00
−0.01
−0.02
size=25, length=13593, positive=0, negative=0, total=0
gi|1034534.1−Rochambeau_virus_nucleoprotein_phosphoprotein_matrix_hypothetical_proteins_glycopr:1−13593
0
2000
4000
6000
8000
10000
12000
14000

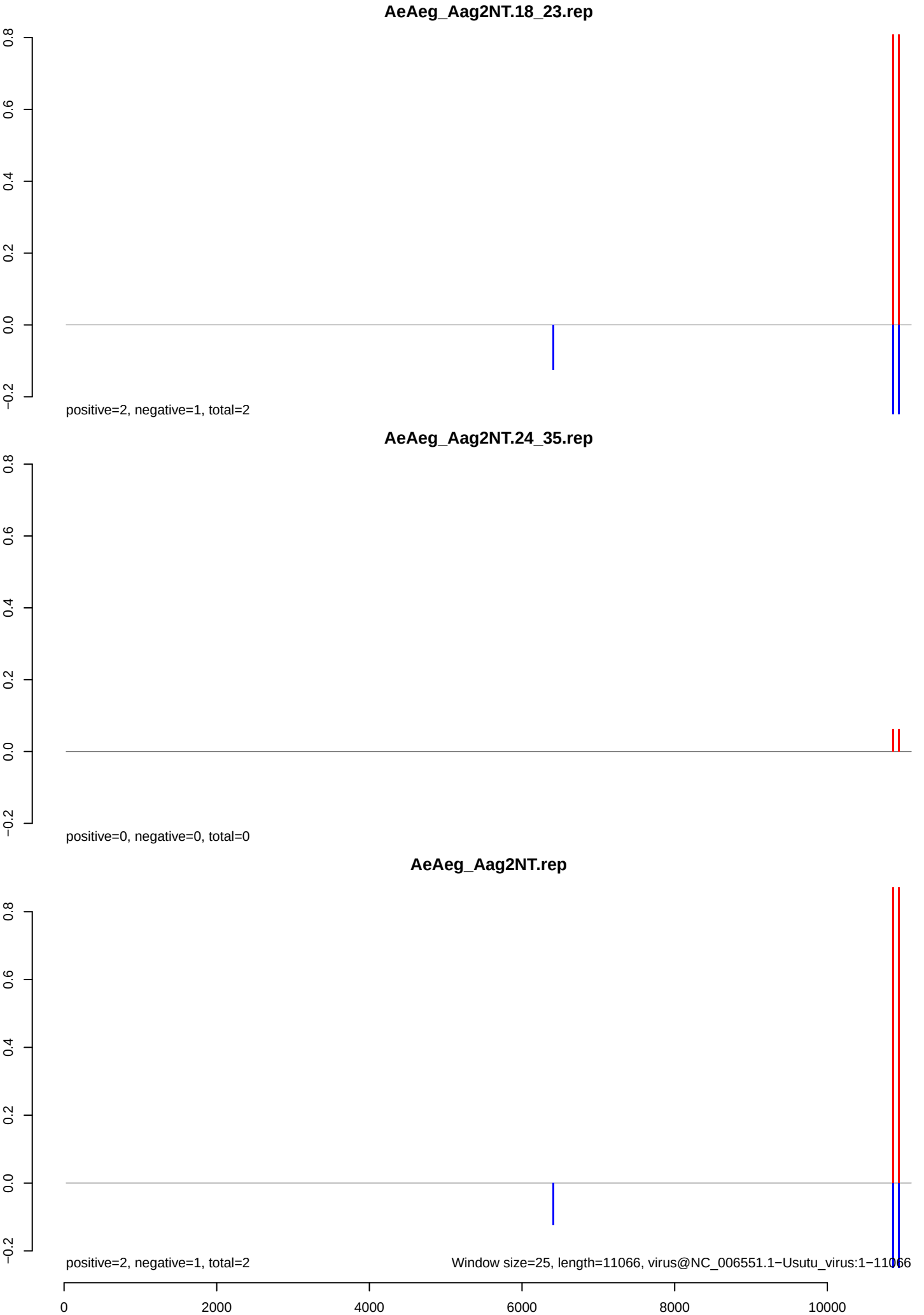

AeAeg_Aag2NT.18_23.rep
positive=14, negative=0, total=14
AeAeg_Aag2NT.24_35.rep
positive=4, negative=0, total=4
AeAeg_Aag2NT.rep
positive=18, negative=0, total=18
virus@NC_031319.1_Wutai_Mosquito_Virus_strain_QN3−5_nucleopasid_protein_N_G_L:1−12072
0
2000
4000
6000
8000
10000
12000

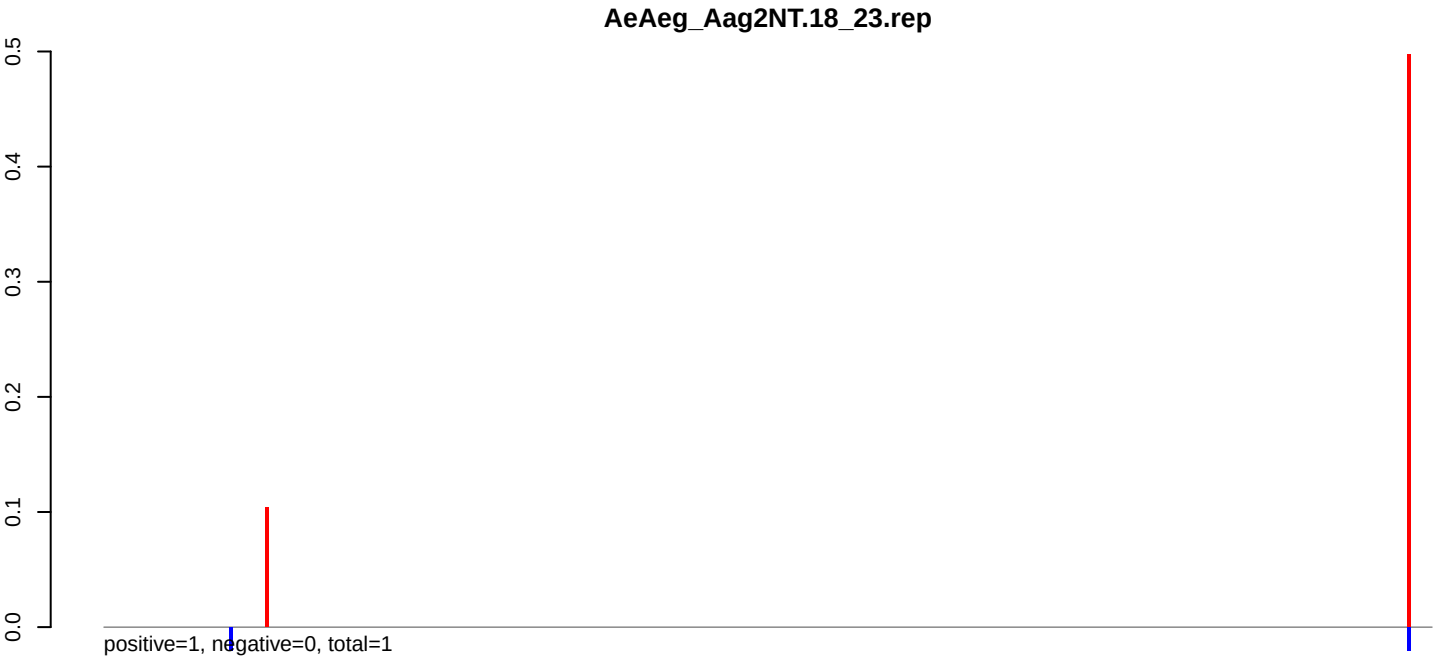

AeAeg_Aag2NT.18_23.rep
0.10
0.05
0.00
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
0.10
0.05
0.00
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.10
0.05
0.00
positive=0, negative=0, total=0
Window size=25, length=10938, virus@NC_027819.1−Mercadeo_virus_isolate_ER−M10:1−10938
0
2000
4000
6000
8000
10000

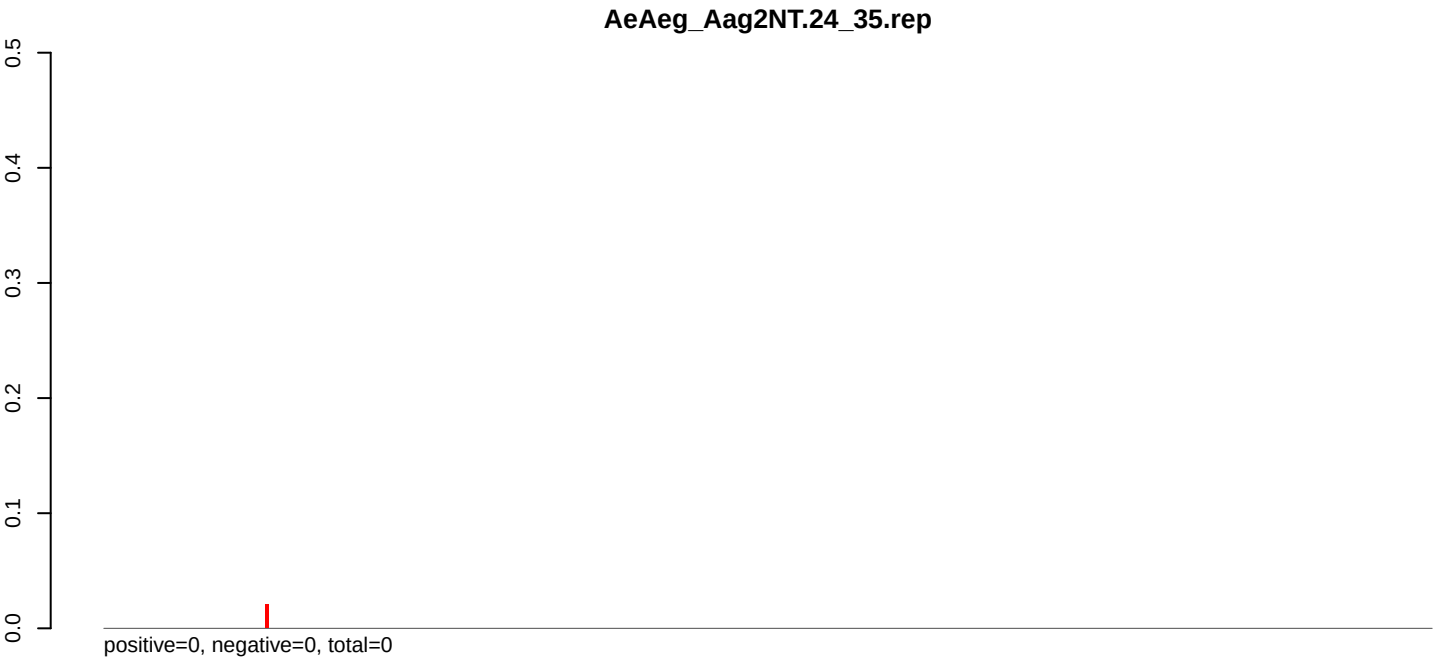

AeAeg_Aag2NT.18_23.rep
0.08
0.06
0.04
0.02
0.00
−0.02
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
0.08
0.06
0.04
0.02
0.00
−0.02
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.08
0.06
0.04
0.02
0.00
−0.02
0
2000
4000
6000
8000
10000

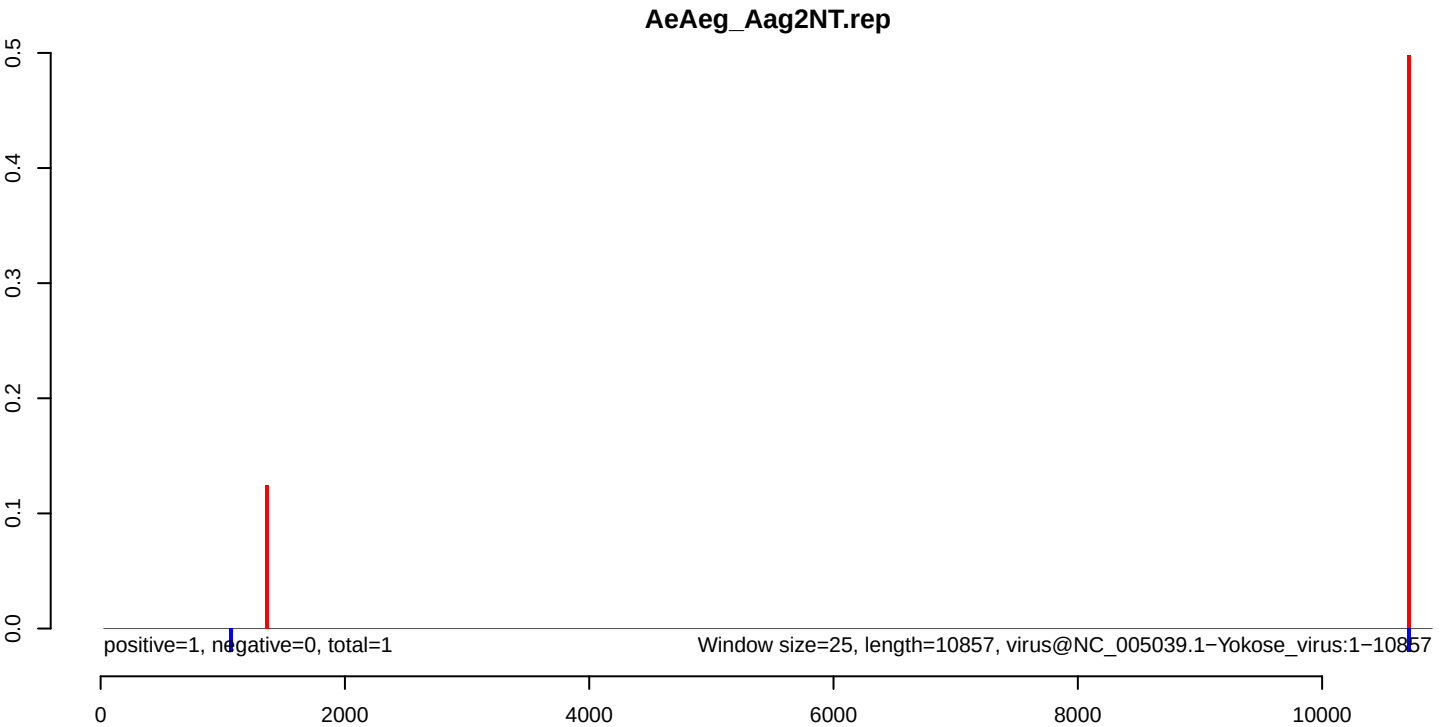

AeAeg_Aag2NT.18_23.rep
0.2
0.0
−0.2
−0.4
positive=0, negative=1, total=1
AeAeg_Aag2NT.24_35.rep
0.2
0.0
−0.2
−0.4
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.2
0.0
−0.2
−0.4
positive=0, negative=1, total=1
window size=25, length=10688, virus@NC_023439.1−Kama_virus_strain_LEIV−20776Tat_polyprotein_gene1−10688
0
2000
4000
6000
8000
10000

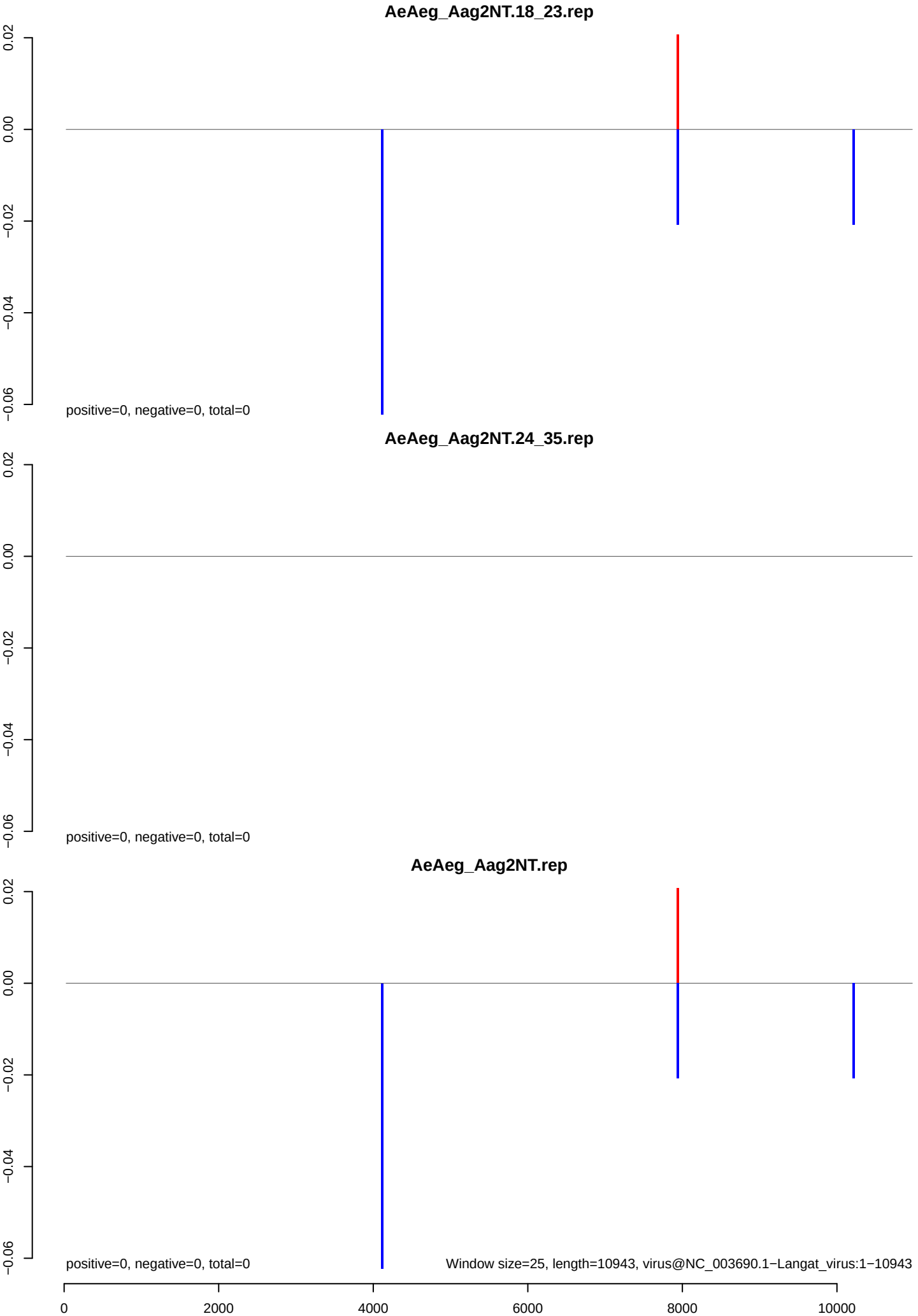

AeAeg_Aag2NT.18_23.rep
0.4
0.2
0.0
−0.2
−0.4
−0.6
−0.8
positive=1, negative=1, total=2
AeAeg_Aag2NT.24_35.rep
0.4
0.2
0.0
−0.2
−0.4
−0.6
−0.8
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.5
0.0
−0.5
positive=1, negative=1, total=2
Window size=25, length=10510, virus@NC_008718.1−Entebbe_bat_virus:1−10510
0
2000
4000
6000
8000
10000

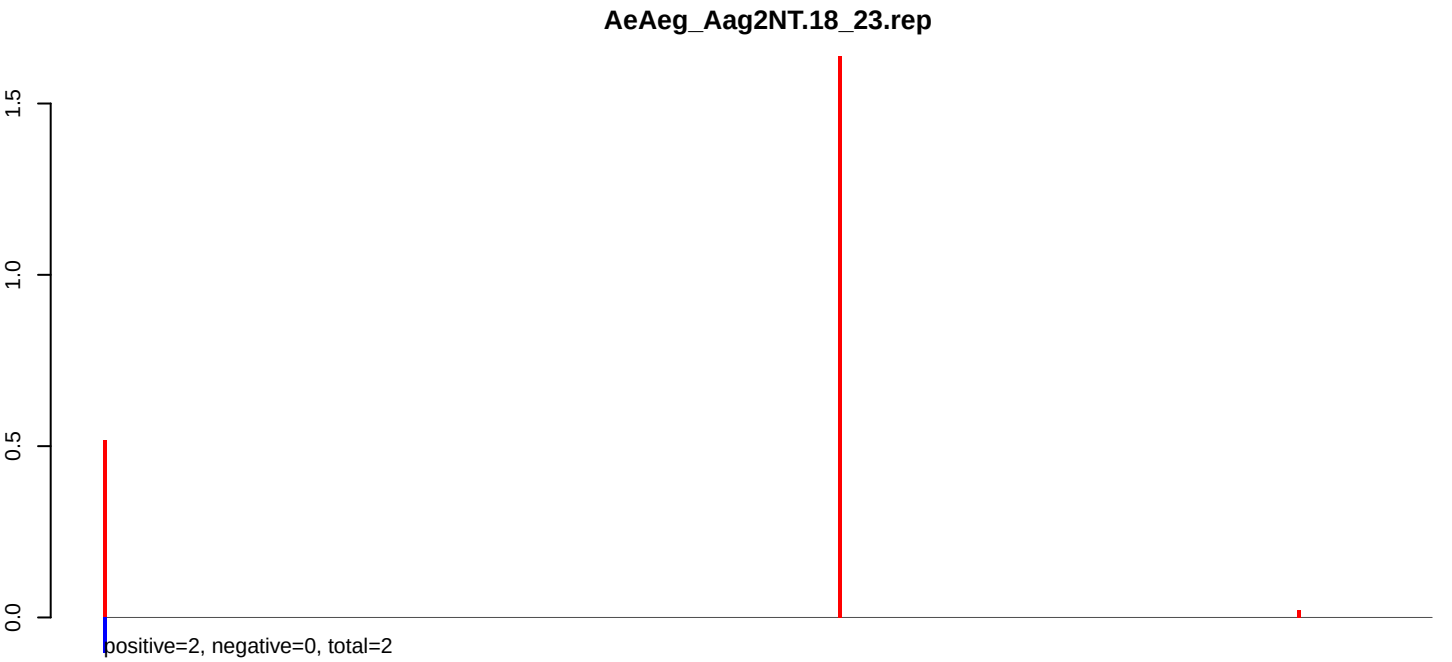

AeAeg_Aag2NT.18_23.rep
0.8
0.6
0.4
0.2
0.0
−0.2
positive=2, negative=1, total=2
AeAeg_Aag2NT.24_35.rep
0.8
0.6
0.4
0.2
0.0
−0.2
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.8
0.6
0.4
0.2
0.0
−0.2
positive=2, negative=1, total=2
Window size=25, length=11066, virus@NC_006551.1−Usutu_virus:1−11066
0
2000
4000
6000
8000
10000

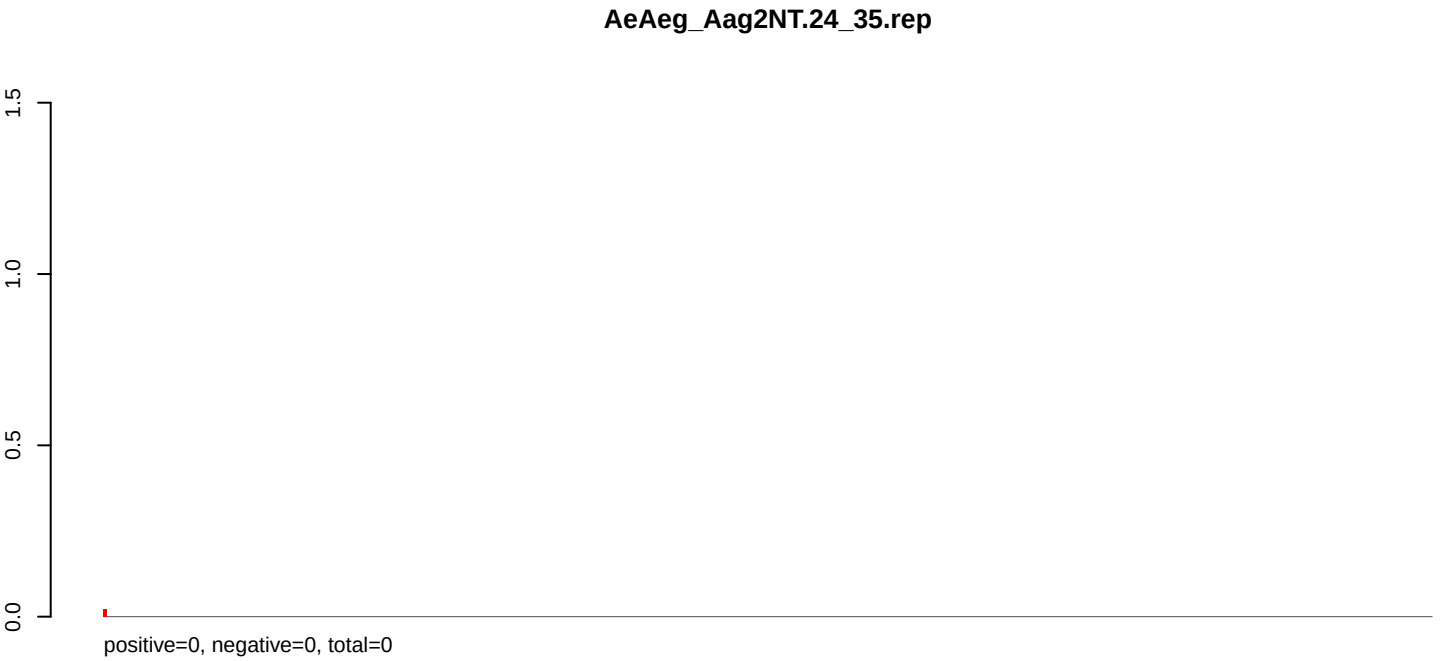

AeAeg_Aag2NT.18_23.rep
0.0
0.1
0.2
0.3
0.4
0.5
positive=1, negative=0, total=1

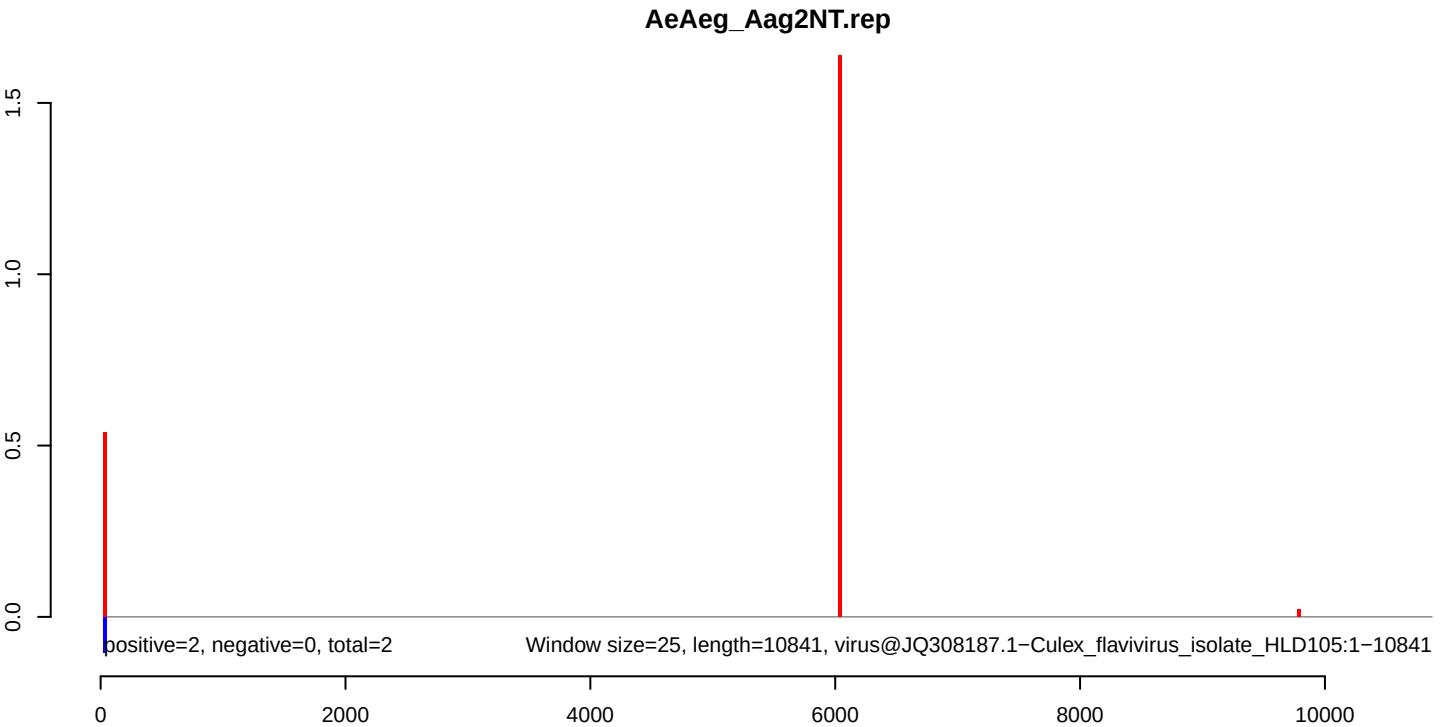

AeAeg_Aag2NT.24_35.rep
0.0
0.1
0.2
0.3
0.4
0.5
positive=0, negative=0, total=0


AeAeg_Aag2NT.rep
0.0
0.1
0.2
0.3
0.4
0.5
positive=1, negative=0, total=1
Window size=25, length=10857, virus@NC_005039.1−Yokose_virus:1−10857
0
2000
4000
6000
8000
10000


AeAeg_Aag2NT.18_23.rep
0.02
0.00
−0.02
−0.04
−0.06
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
0.02
0.00
−0.02
−0.04
−0.06
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.02
0.00
−0.02
−0.04
−0.06
positive=0, negative=0, total=0
Window size=25, length=10943, virus@NC_003690.1−Langat_virus:1−10943
0
2000
4000
6000
8000
10000


AeAeg_Aag2NT.18_23.rep
1.5
1.0
0.5
0.0
positive=2, negative=0, total=2


AeAeg_Aag2NT.24_35.rep
1.5
1.0
0.5
0.0
positive=0, negative=0, total=0


AeAeg_Aag2NT.rep
1.5
1.0
0.5
0.0
positive=2, negative=0, total=2
Window size=25, length=10841, virus@JQ308187.1−Culex_flavivirus_isolate_HLD105:1−10841
0
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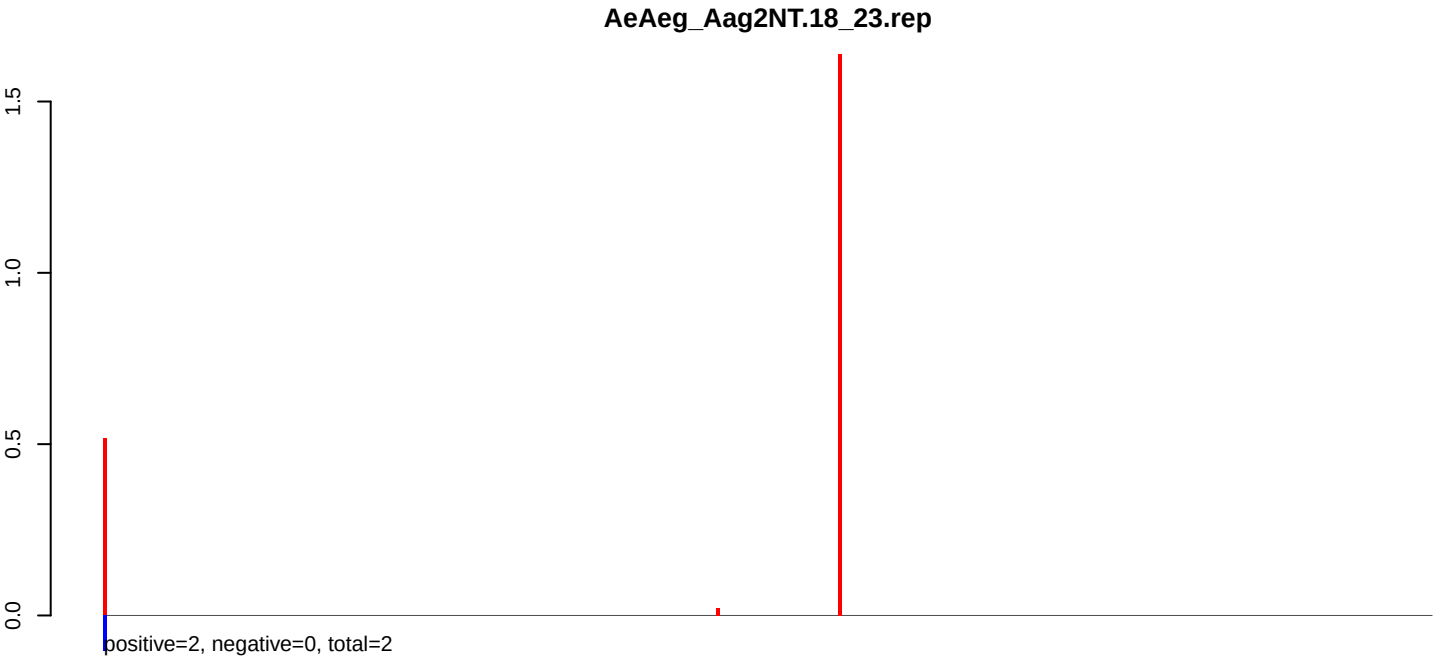
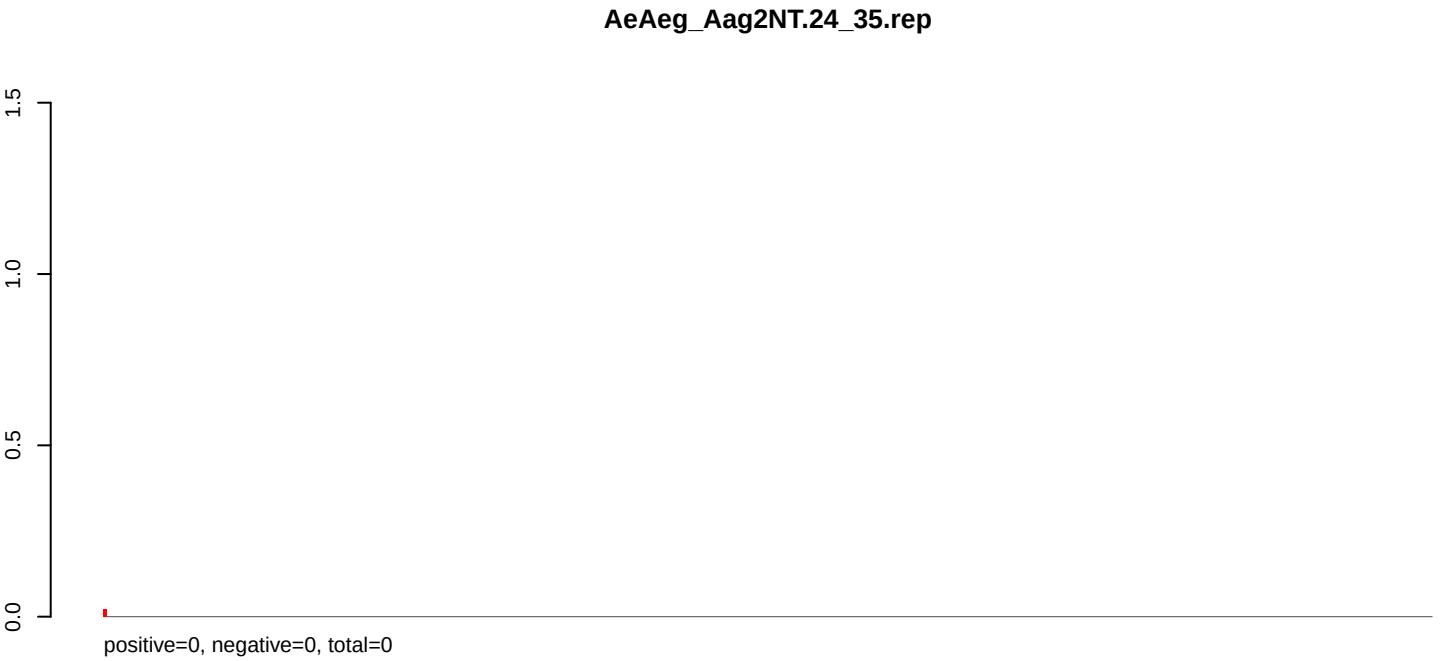
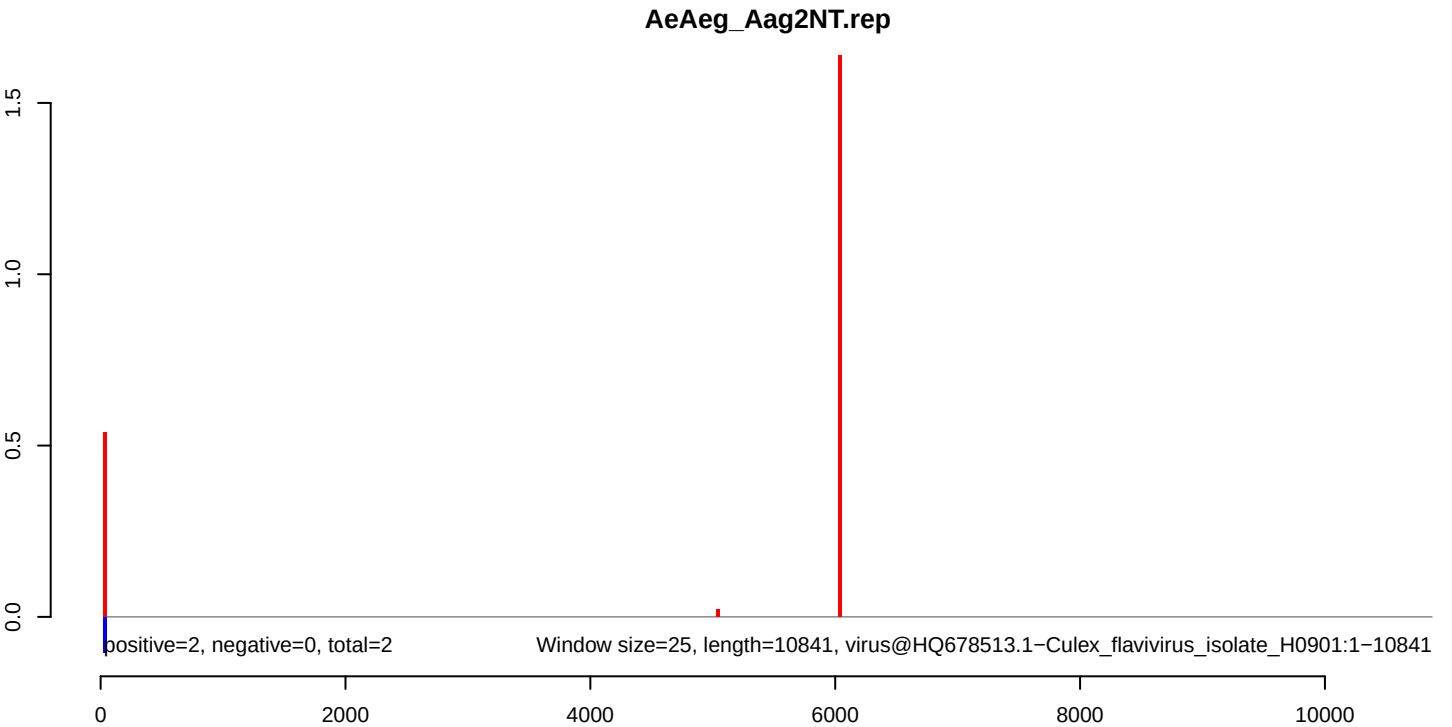
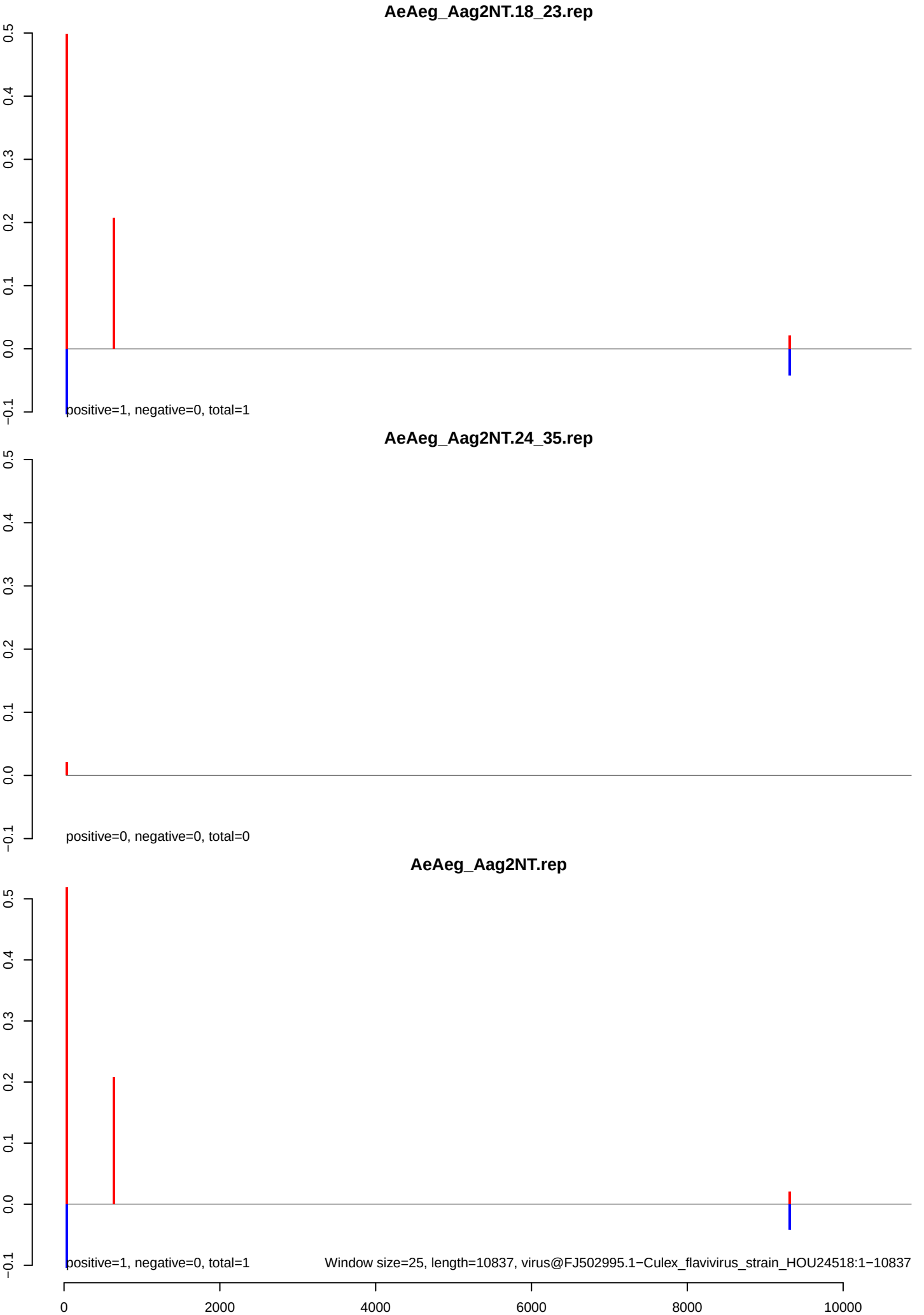
4000
6000
8000
10000


AeAeg_Aag2NT.18_23.rep
1.5
1.0
0.5
0.0
positive=2, negative=0, total=2


AeAeg_Aag2NT.24_35.rep
1.5
1.0
0.5
0.0
positive=0, negative=0, total=0


AeAeg_Aag2NT.rep
1.5
1.0
0.5
0.0
positive=2, negative=0, total=2
Window size=25, length=10841, virus@HQ678513.1−Culex_flavivirus_isolate_H0901:1−10841
0
2000
4000
6000
8000
10000


AeAeg_Aag2NT.18_23.rep
0.5
0.4
0.3
0.2
0.1
0.0
−0.1
positive=1, negative=0, total=1
AeAeg_Aag2NT.24_35.rep
0.5
0.4
0.3
0.2
0.1
0.0
−0.1
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.5
0.4
0.3
0.2
0.1
0.0
−0.1
positive=1, negative=0, total=1
Window size=25, length=10837, virus@FJ502995.1−Culex_flavivirus_strain_HOU24518:1−10837
0
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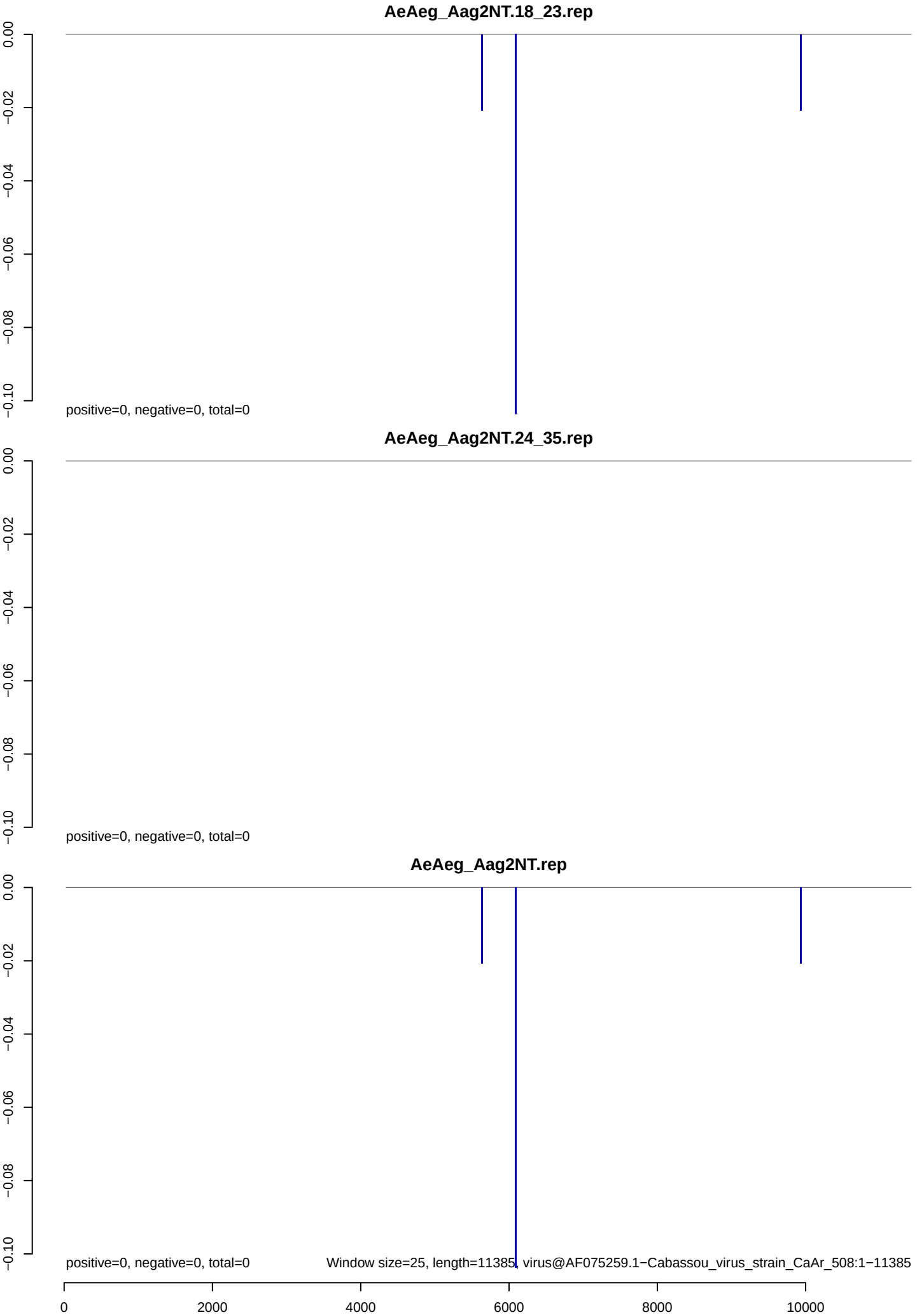
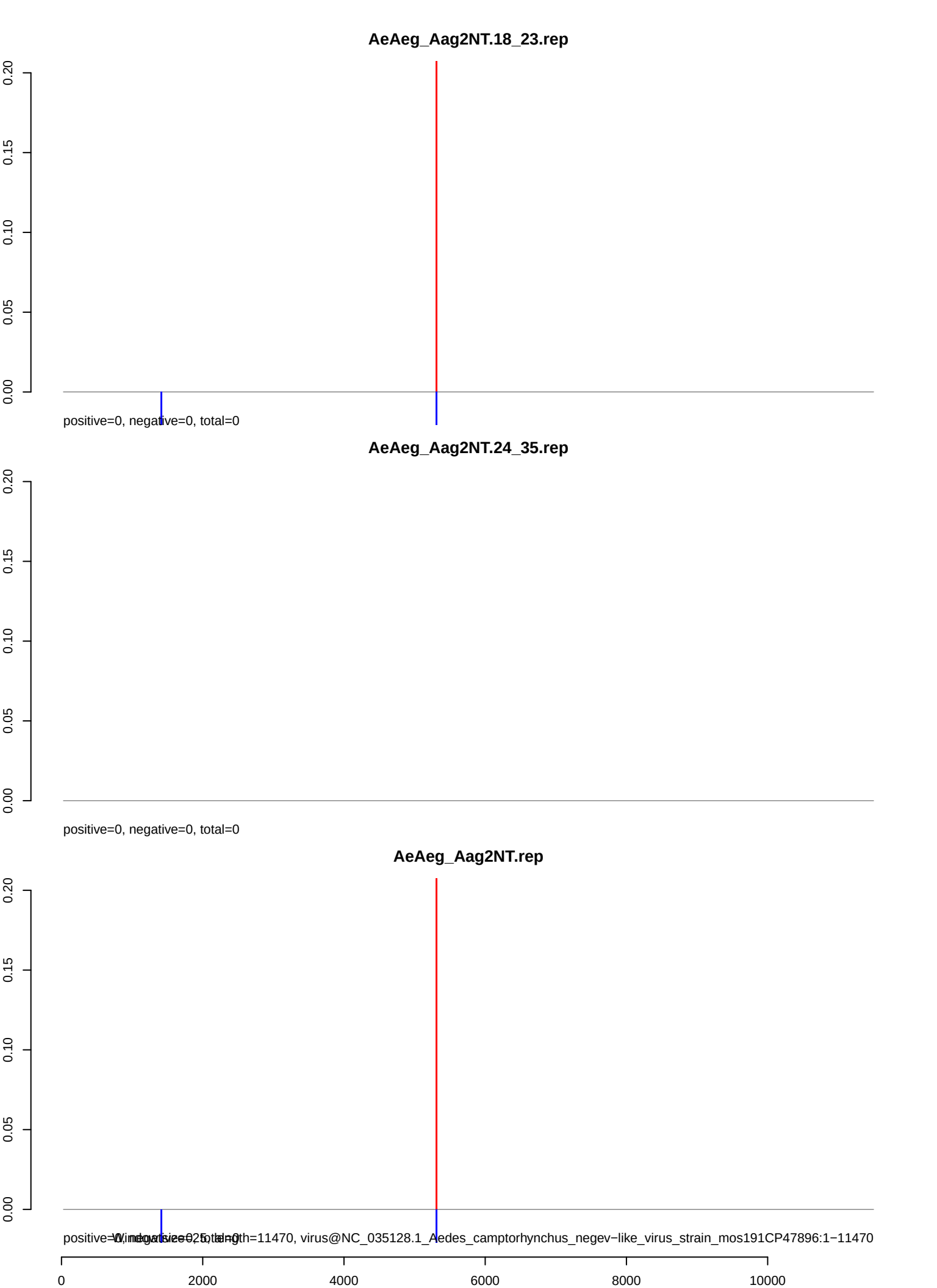
4000
6000
8000
10000


AeAeg_Aag2NT.18_23.rep
0.00
−0.02
−0.04
−0.06
−0.08
−0.10
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
0.00
−0.02
−0.04
−0.06
−0.08
−0.10
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.00
−0.02
−0.04
−0.06
−0.08
−0.10
positive=0, negative=0, total=0
Window size=25, length=11385, virus@AF075259.1−Cabassou_virus_strain_CaAr_508:1−11385
0
2000
4000
6000
8000
10000


AeAeg_Aag2NT.18_23.rep
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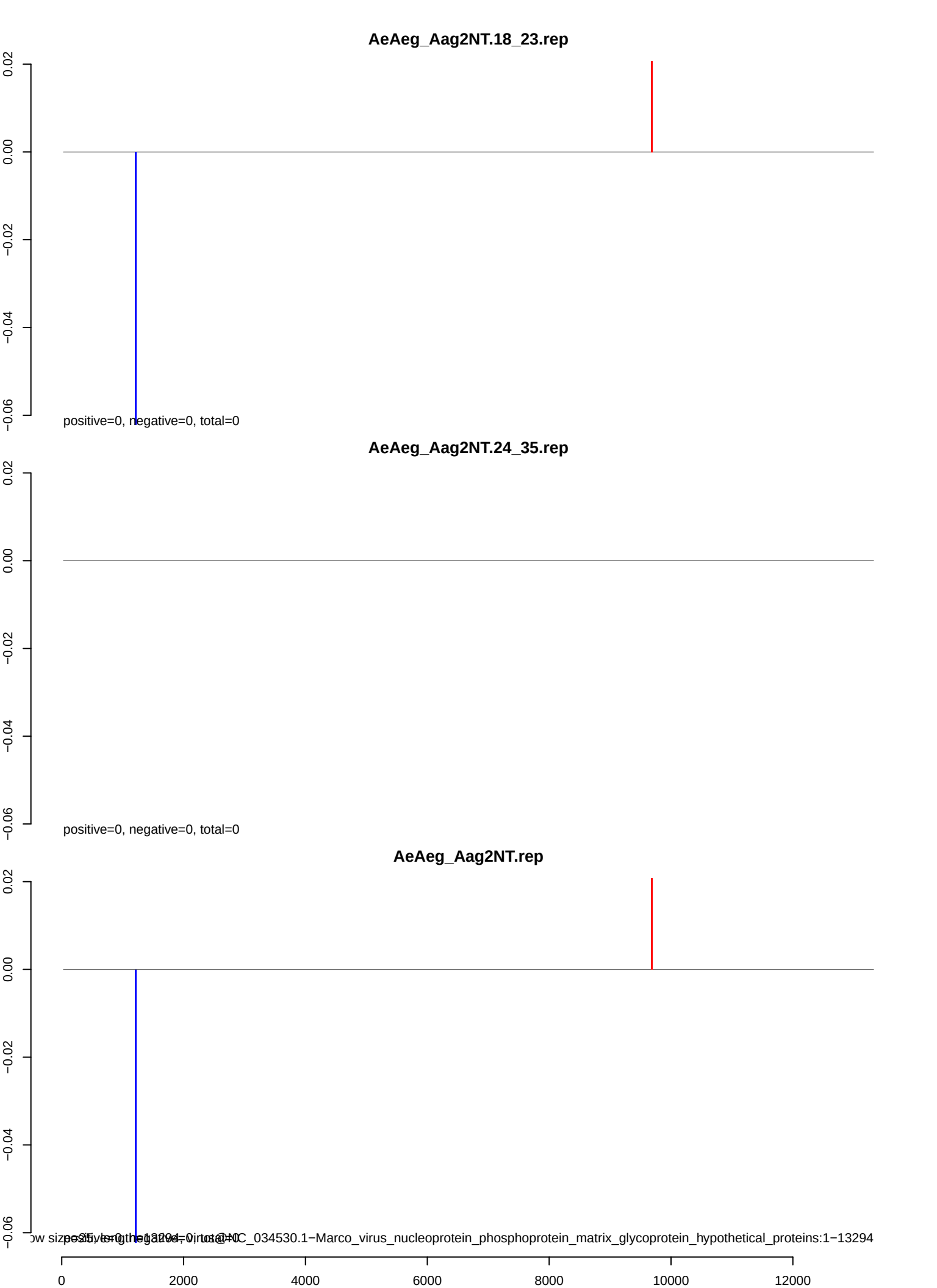
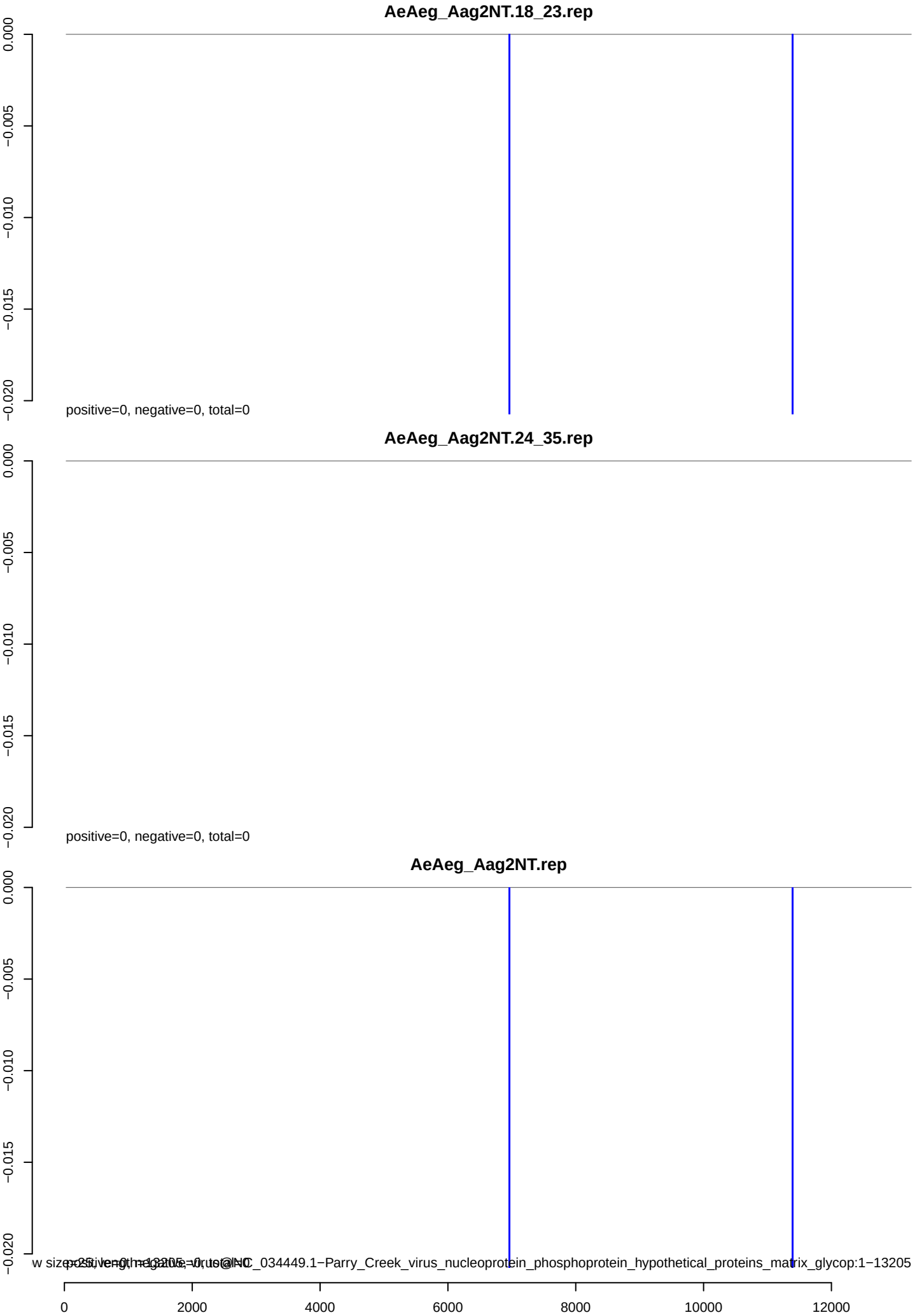
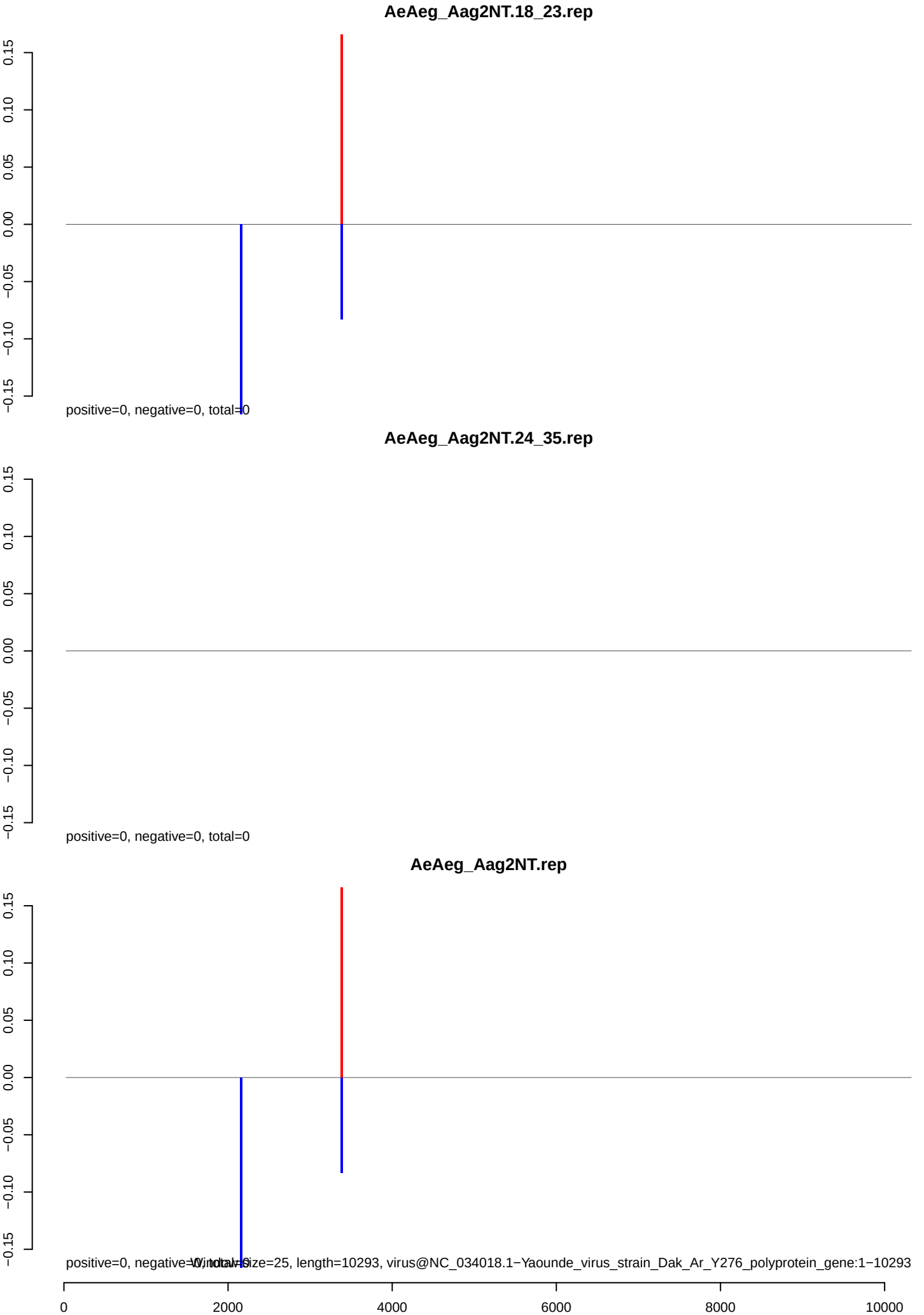
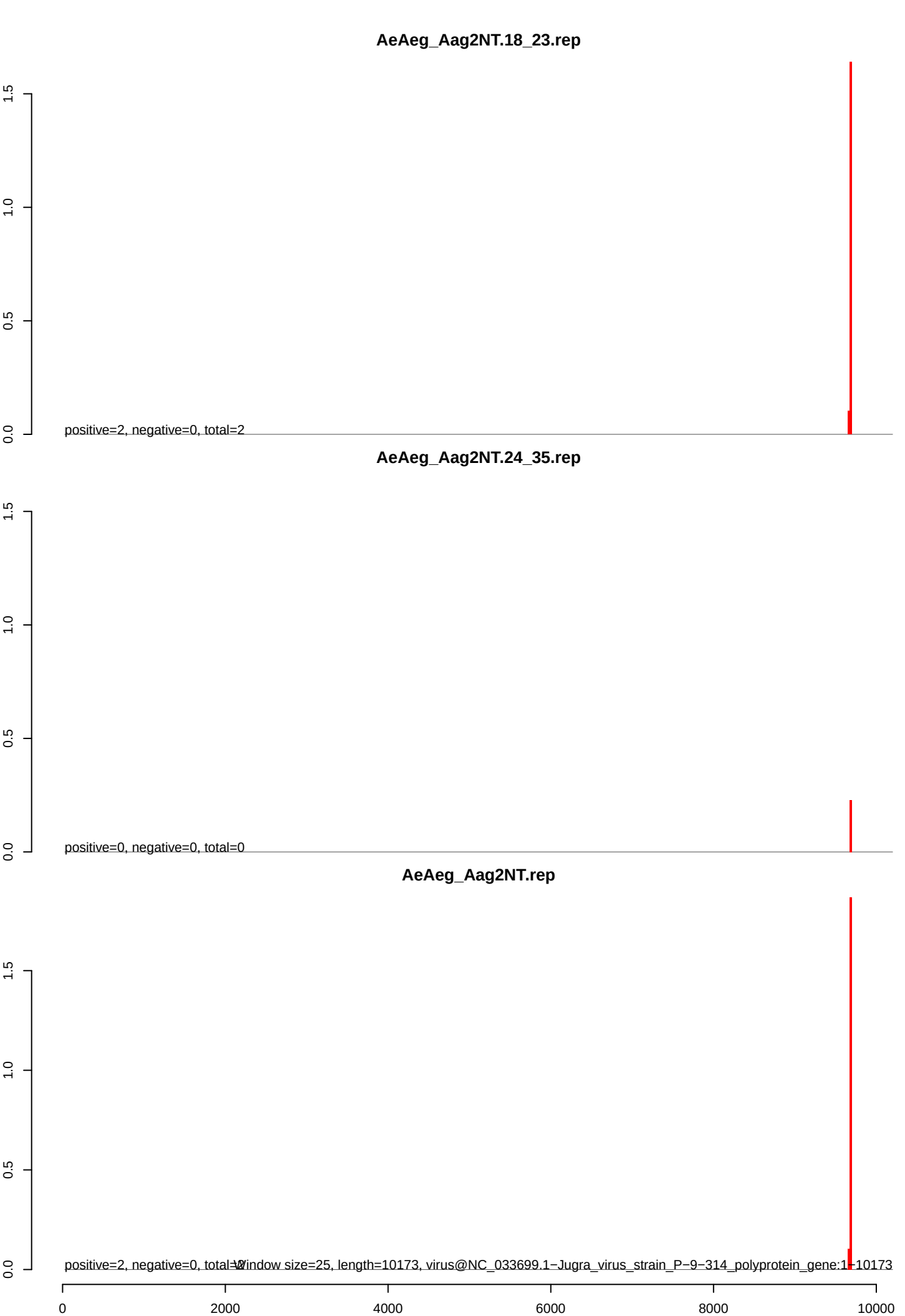
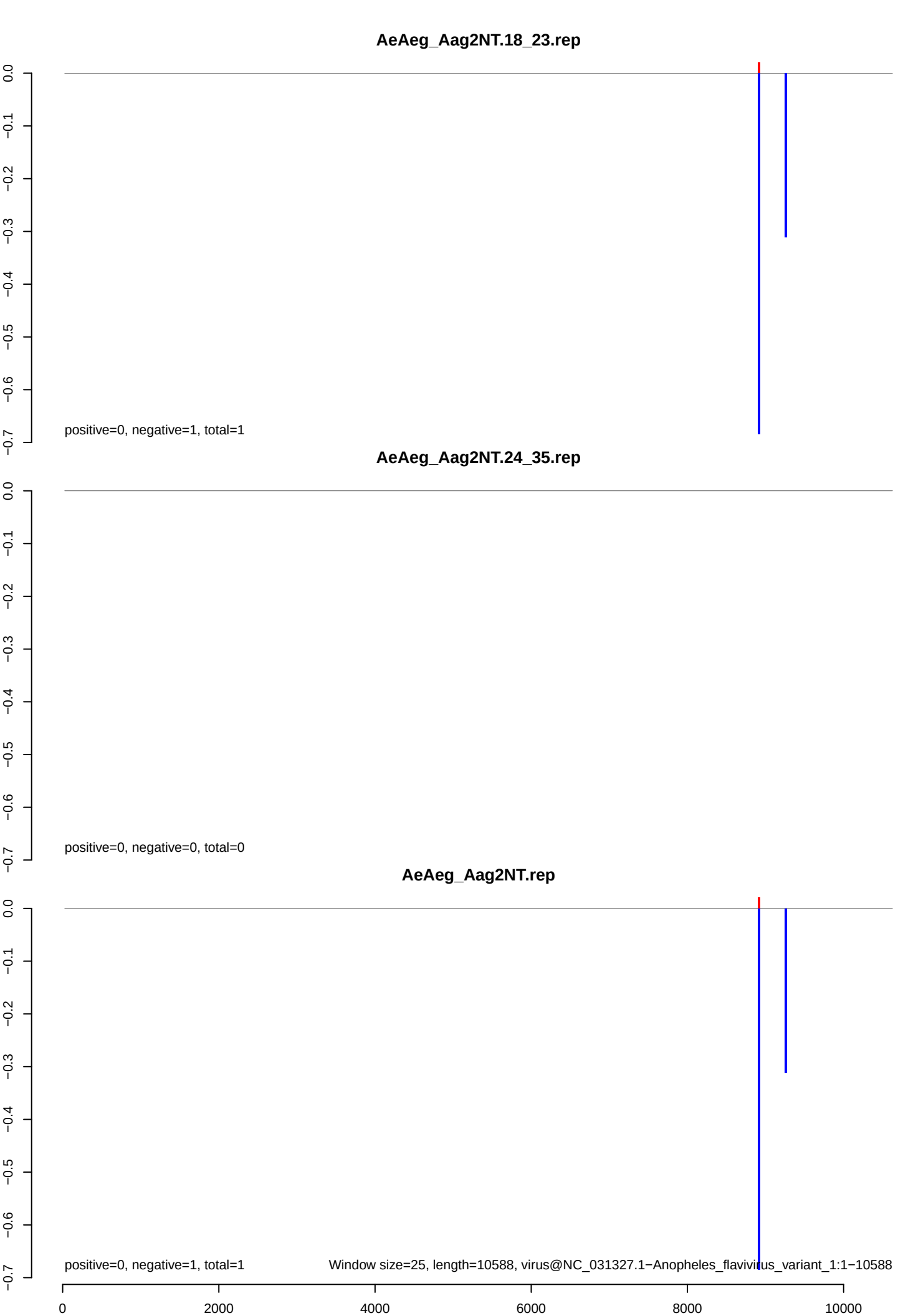
0.05
0.10
0.15
0.20
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
0.00
0.05
0.10
0.15
0.20
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.00
0.05
0.10
0.15
0.20
positive=0, negative=0, total=0
0
2000
4000
6000
8000
10000

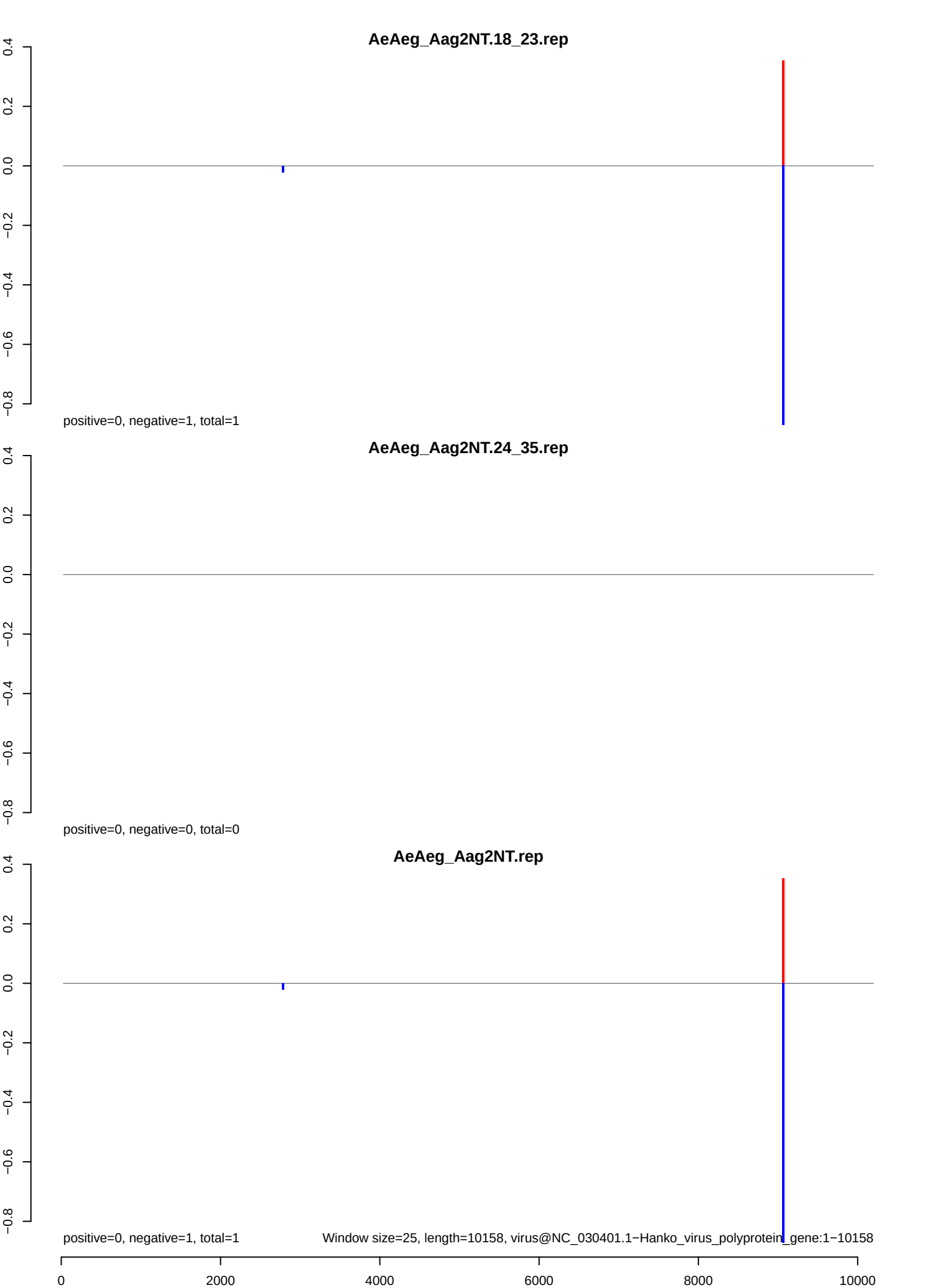

AeAeg_Aag2NT.18_23.rep
0.02
0.00
−0.02
−0.04
−0.06
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
0.02
0.00
−0.02
−0.04
−0.06
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.02
0.00
−0.02
−0.04
−0.06
ow size=25, length=13294, virus@NC_034530.1−Marco_virus_nucleoprotein_phosphoprotein_matrix_glycoprotein_hypothetical_proteins:1−13294
0
2000
4000
6000
8000
10000
12000

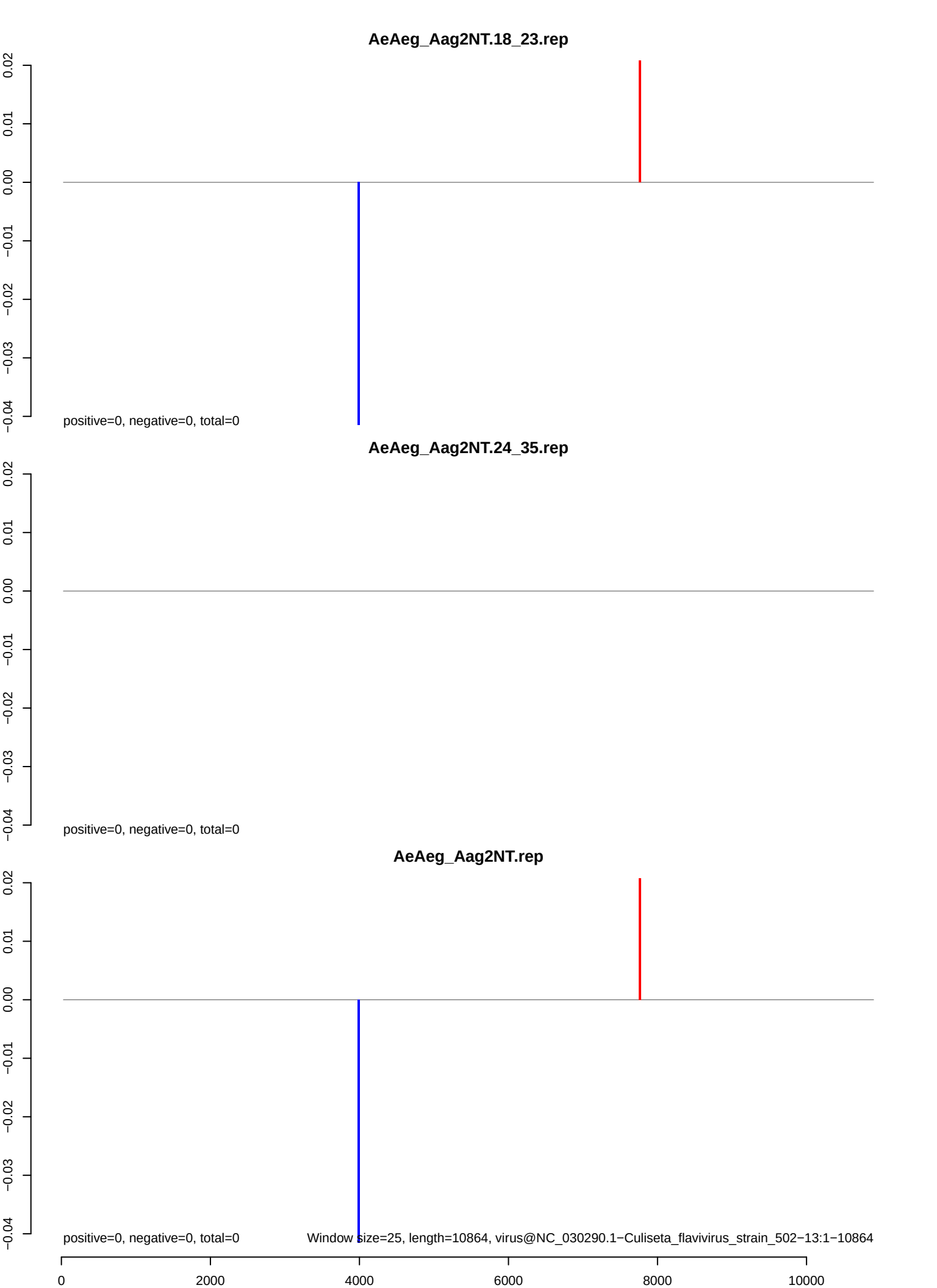

AeAeg_Aag2NT.18_23.rep
0.000
−0.005
−0.010
−0.015
−0.020
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
0.000
−0.005
−0.010
−0.015
−0.020
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.000
−0.005
−0.010
−0.015
−0.020
w size=25, length=13205, 0, ust@NC_034449.1−Parry_Creek_virus_nucleoprotein_phosphoprotein_hypothetical_proteins_matrix_glycop:1−13205
0
2000
4000
6000
8000
10000
12000

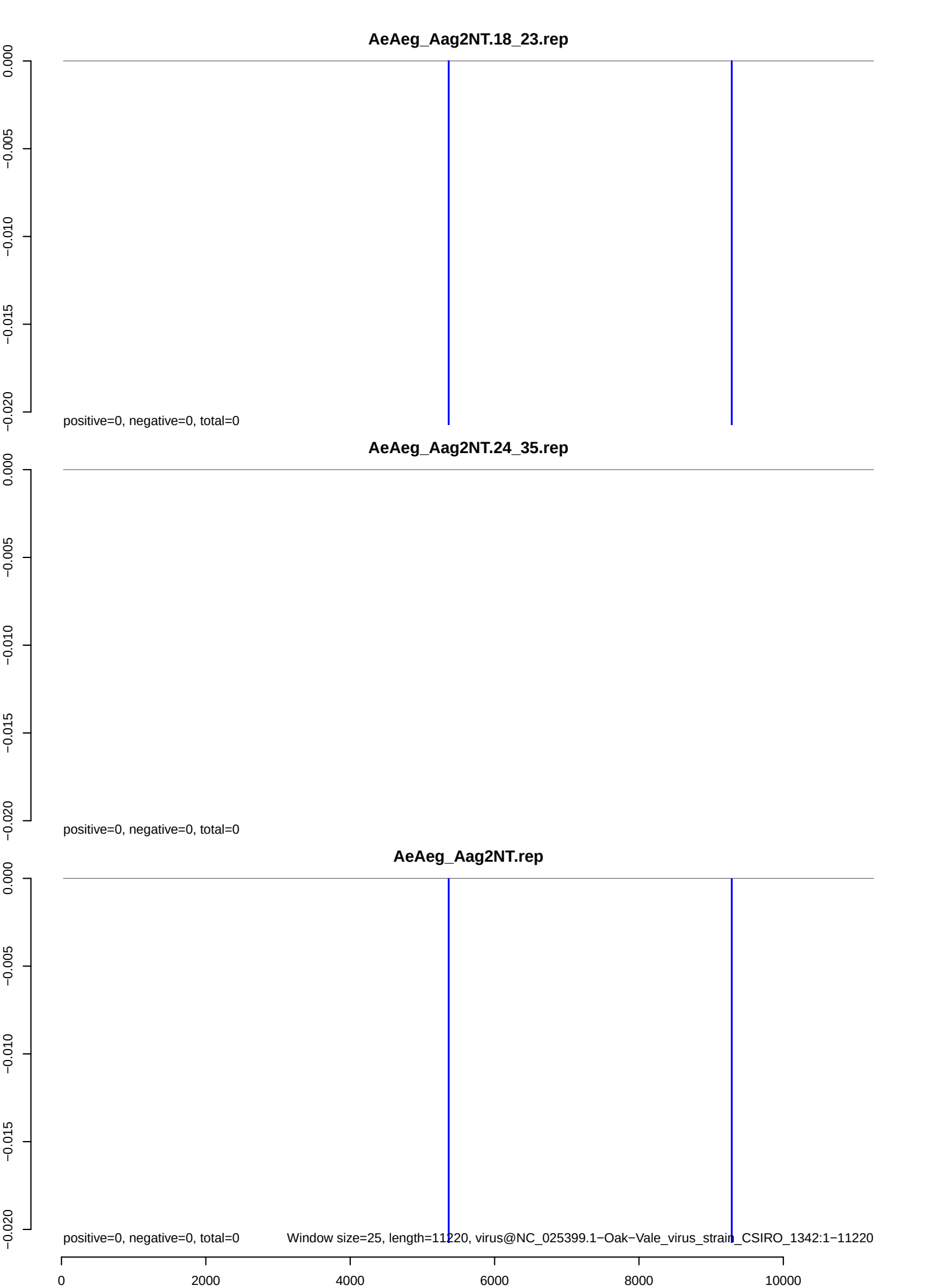

AeAeg_Aag2NT.18_23.rep
0.15
0.10
0.05
0.00
−0.05
−0.10
−0.15
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
0.15
0.10
0.05
0.00
−0.05
−0.10
−0.15
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.15
0.10
0.05
0.00
−0.05
−0.10
−0.15
positive=0, negative=0, total=0
Window Size=25, length=10293, virus@NC_034018.1−Yaounde_virus_strain_Dak_Ar_Y276_polyprotein_gene:1−10293
0
2000
4000
6000
8000
10000

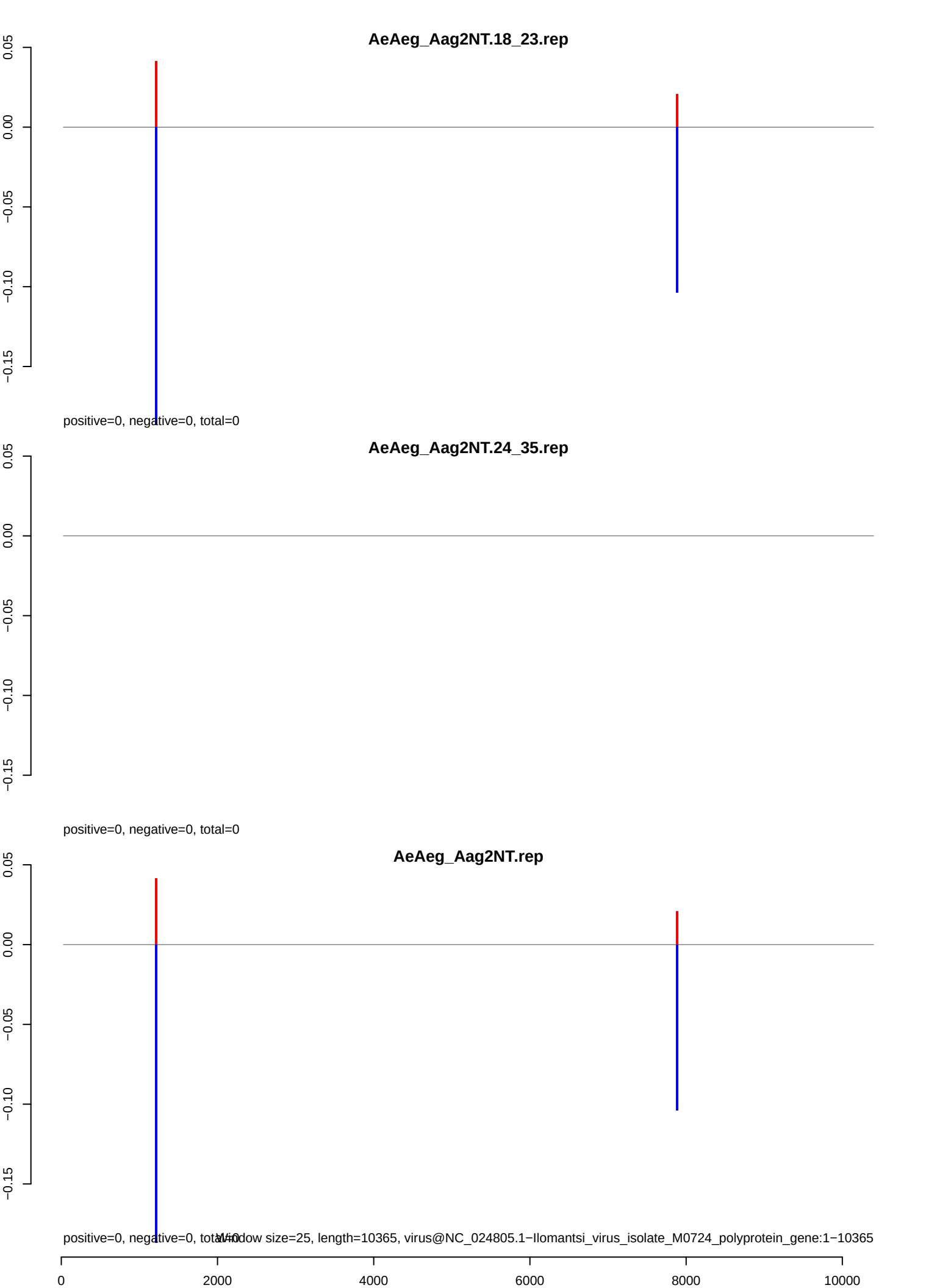

AeAeg_Aag2NT.18_23.rep
1.5
1.0
0.5
0.0
positive=2, negative=0, total=2
AeAeg_Aag2NT.24_35.rep
1.5
1.0
0.5
0.0
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
1.5
1.0
0.5
0.0
positive=2, negative=0, total=2
Window size=25, length=10173, virus@NC_033699.1−Jugra_virus_strain_P−9−314_polyprotein_gene:1−10173
0
2000
4000
6000
8000
10000

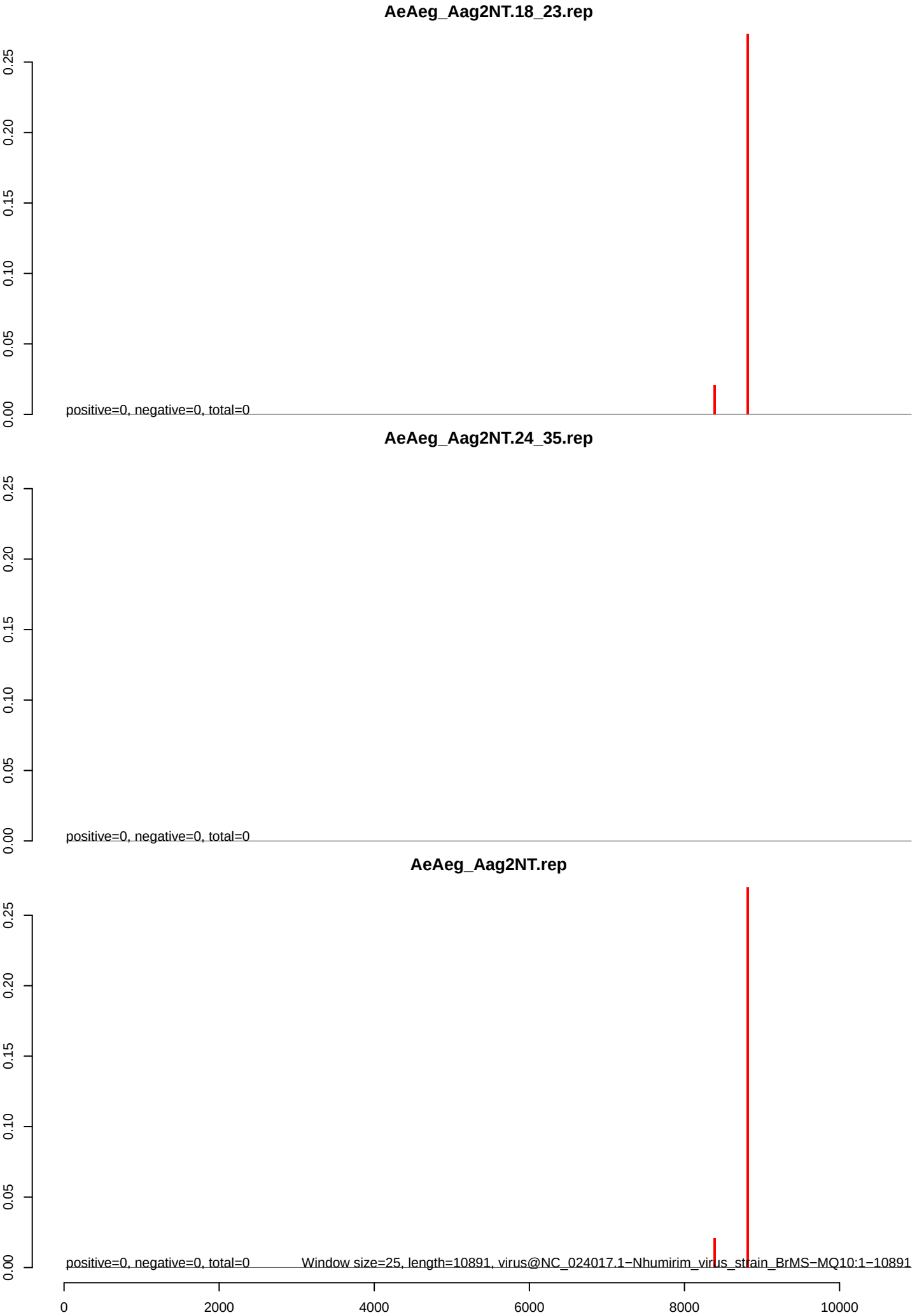

AeAeg_Aag2NT.18_23.rep
0.0
−0.1
−0.2
−0.3
−0.4
−0.5
−0.6
−0.7
positive=0, negative=1, total=1
AeAeg_Aag2NT.24_35.rep
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
positive=0, negative=1, total=1
Window size=25, length=10588, virus@NC_031327.1−Anopheles_flavivirus_variant_1:1−10588
0
2000
4000
6000
8000
10000

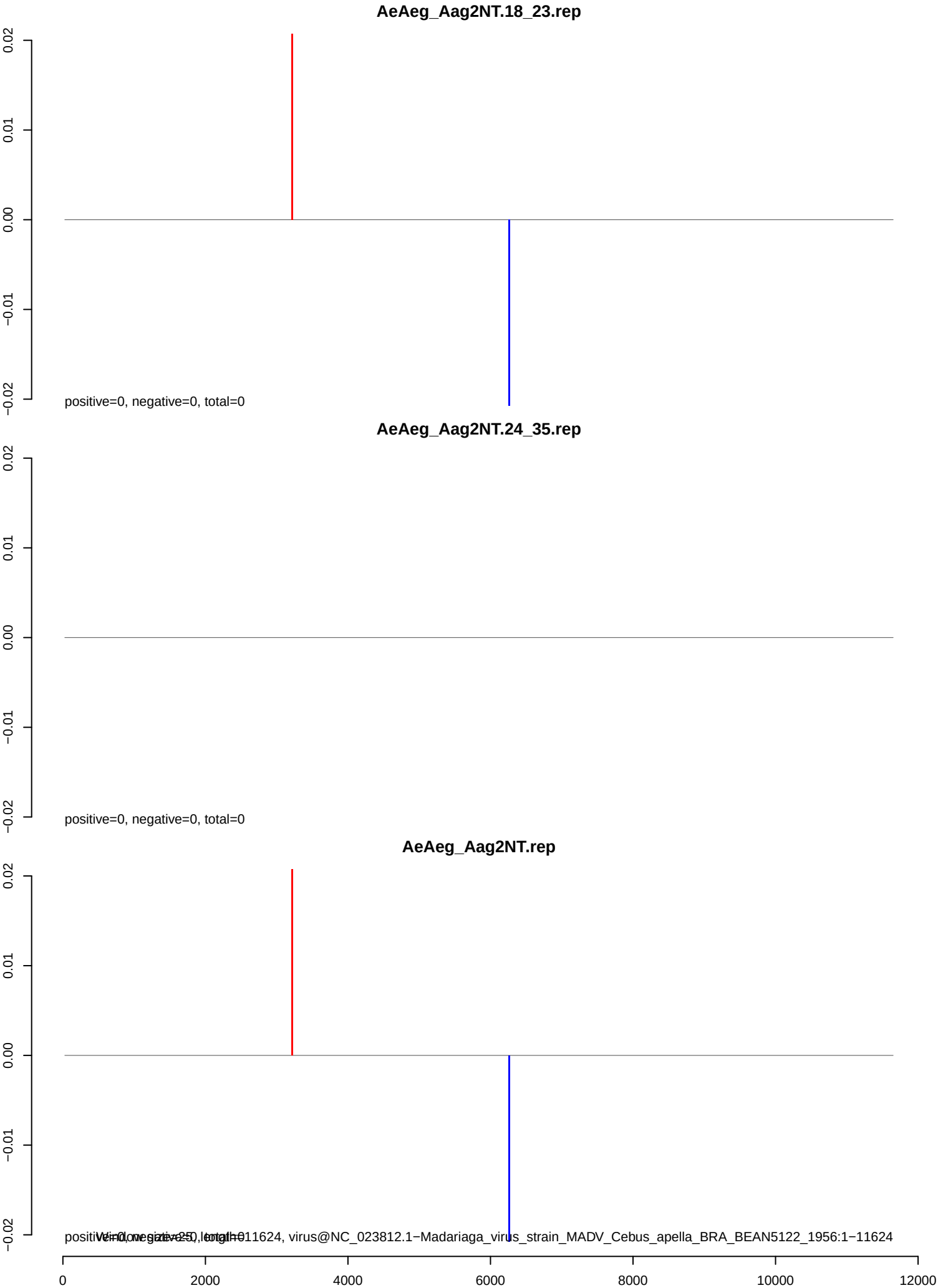

AeAeg_Aag2NT.18_23.rep
0.4
0.2
0.0
−0.2
−0.4
−0.6
−0.8
positive=0, negative=1, total=1
AeAeg_Aag2NT.24_35.rep
0.4
0.2
0.0
−0.2
−0.4
−0.6
−0.8
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.4
0.2
0.0
−0.2
−0.4
−0.6
−0.8
positive=0, negative=1, total=1
Window size=25, length=10158, virus@NC_030401.1−Hanko_virus_polyprotein_gene:1−10158
0
2000
4000
6000
8000
10000

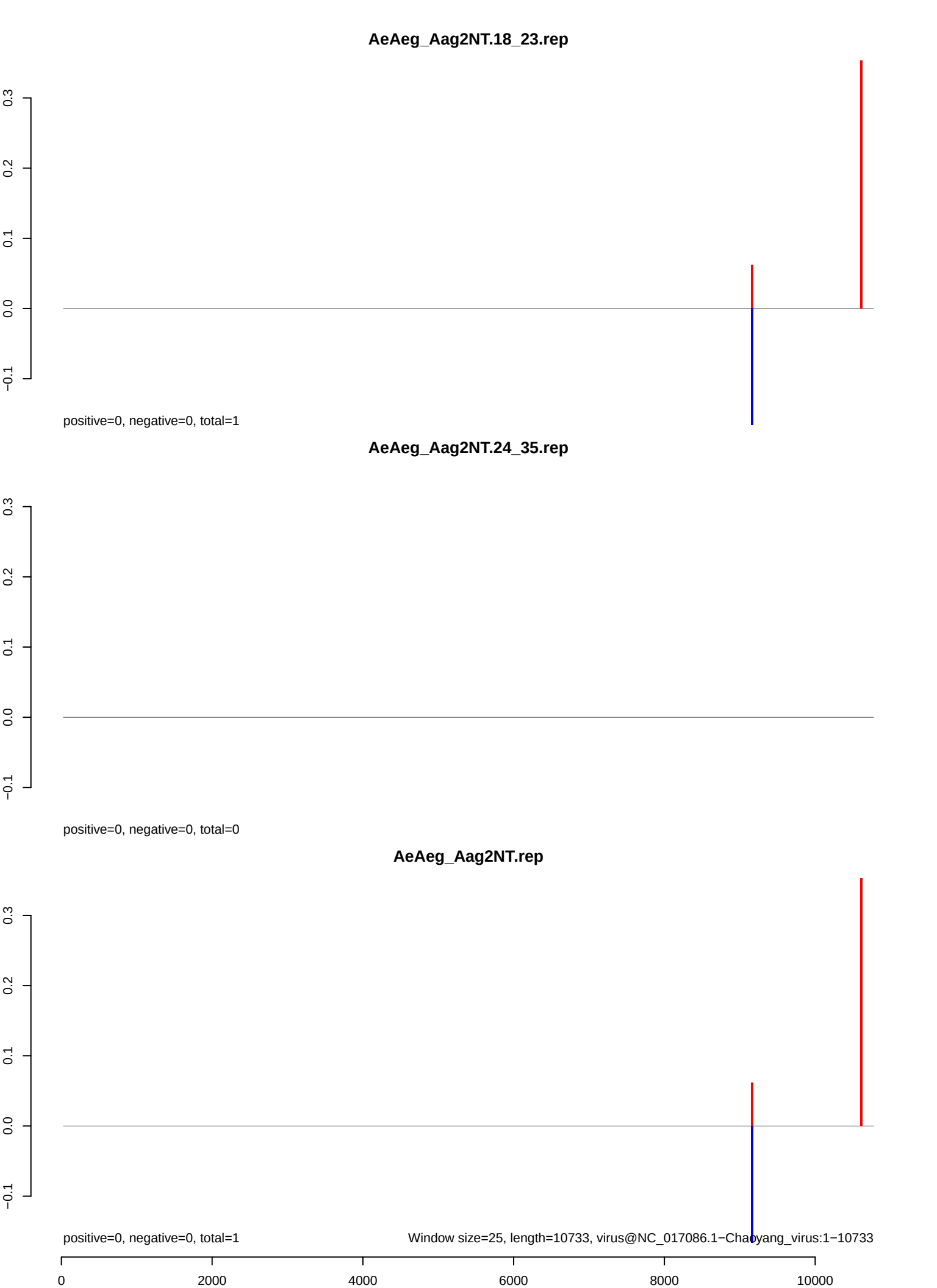

AeAeg_Aag2NT.18_23.rep
0.02
0.01
0.00
−0.01
−0.02
−0.03
−0.04
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
0.02
0.01
0.00
−0.01
−0.02
−0.03
−0.04
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.02
0.01
0.00
−0.01
−0.02
−0.03
−0.04
positive=0, negative=0, total=0
Window size=25, length=10864, virus@NC_030290.1−Culiseta_flavivirus_strain_502−13:1−10864
0
2000
4000
6000
8000
10000

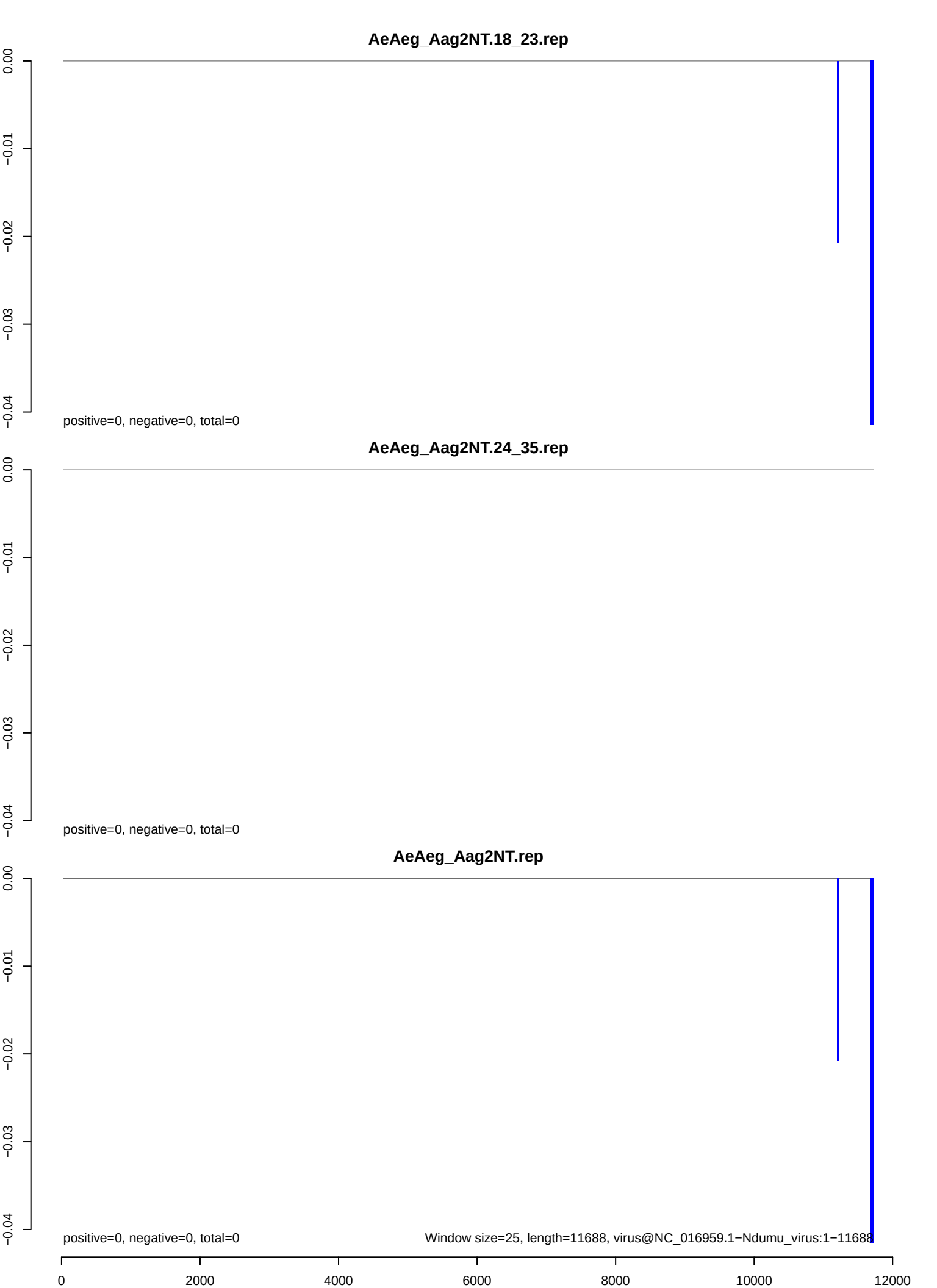

AeAeg_Aag2NT.18_23.rep
0.000
−0.005
−0.010
−0.015
−0.020
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
0.000
−0.005
−0.010
−0.015
−0.020
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.000
−0.005
−0.010
−0.015
−0.020
positive=0, negative=0, total=0
Window size=25, length=11220, virus@NC_025399.1−Oak−Vale_virus_strain_CSIRO_1342:1−11220
0
2000
4000
6000
8000
10000

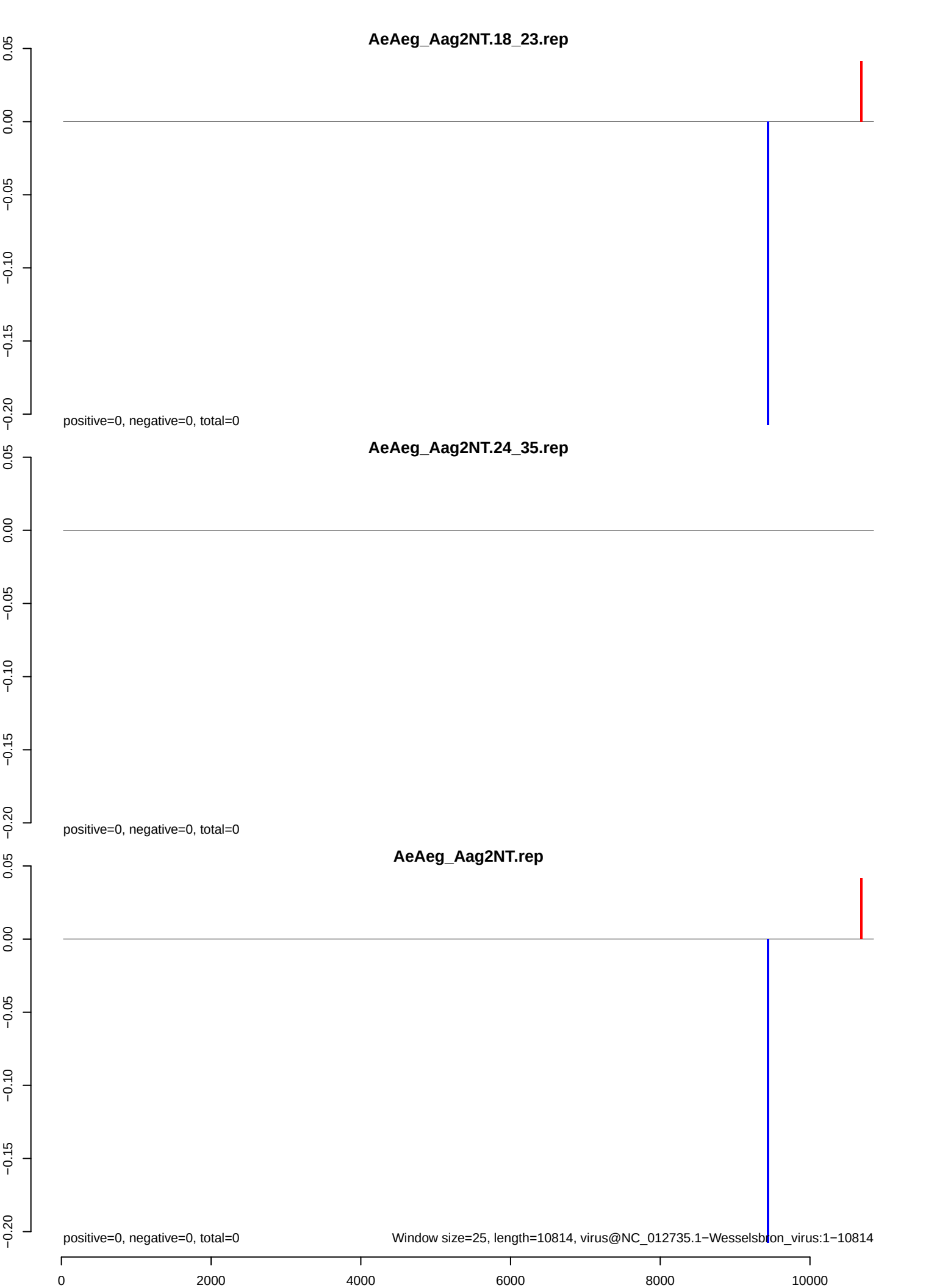

AeAeg_Aag2NT.18_23.rep
0.05
0.00
−0.05
−0.10
−0.15
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
0.05
0.00
−0.05
−0.10
−0.15
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.05
0.00
−0.05
−0.10
−0.15
positive=0, negative=0, total=0
Window size=25, length=10365, virus@NC_024805.1−Ilomantsi_virus_isolate_M0724_polyprotein_gene:1−10365
0
2000
4000
6000
8000
10000

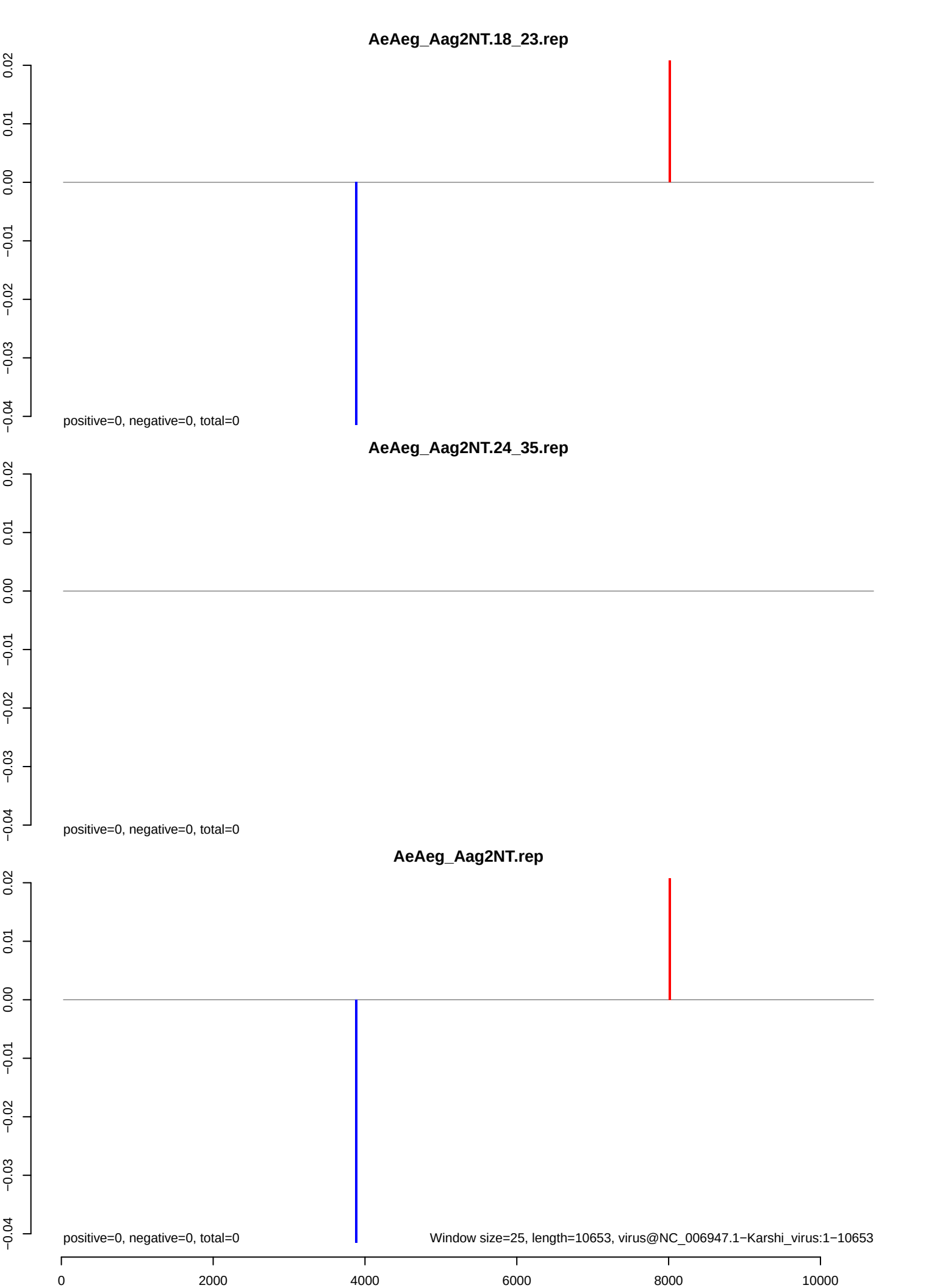

AeAeg_Aag2NT.18_23.rep
0.25
0.20
0.15
0.10
0.05
0.00
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
0.25
0.20
0.15
0.10
0.05
0.00
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.25
0.20
0.15
0.10
0.05
0.00
positive=0, negative=0, total=0
Window size=25, length=10891, virus@NC_024017.1−Nhumirim_virus_strain_BrMS−MQ10:1−10891
0
2000
4000
6000
8000
10000

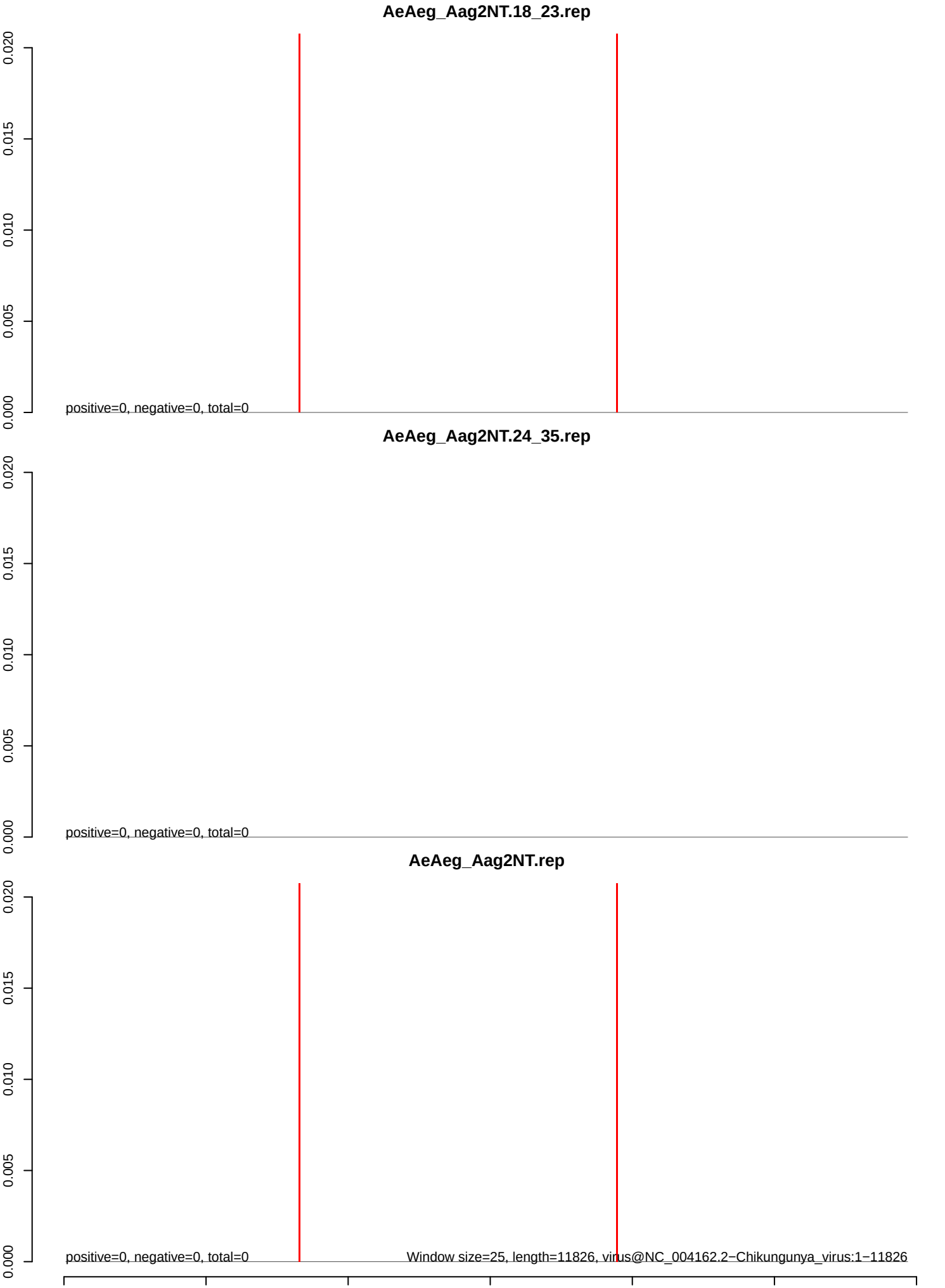

AeAeg_Aag2NT.18_23.rep
0.02
0.01
0.00
−0.01
−0.02
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
0.02
0.01
0.00
−0.01
−0.02
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.02
0.01
0.00
−0.01
−0.02
positive=0, negative=0, total=0
Virus@NC_023812.1−Madariaga_virus_strain_MADV_Cebus_apella_BRA_BEAN5122_1956:1−11624
0
2000
4000
6000
8000
10000
12000

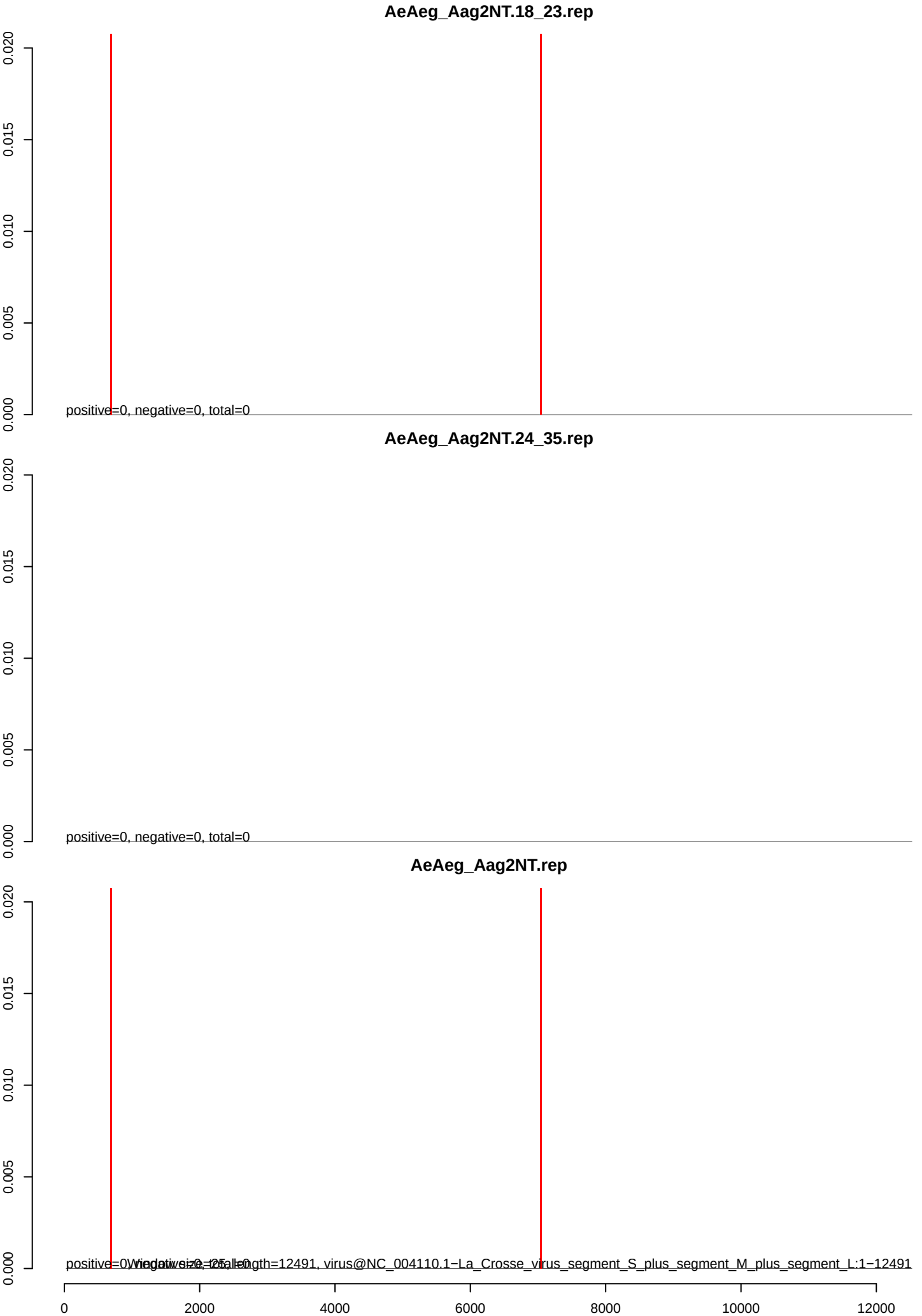

AeAeg_Aag2NT.18_23.rep
0.3
0.2
0.1
0.0
−0.1
positive=0, negative=0, total=1
AeAeg_Aag2NT.24_35.rep
0.3
0.2
0.1
0.0
−0.1
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.3
0.2
0.1
0.0
−0.1
positive=0, negative=0, total=1
Window size=25, length=10733, virus@NC_017086.1−Chaoyang_virus:1−10733
0
2000
4000
6000
8000
10000

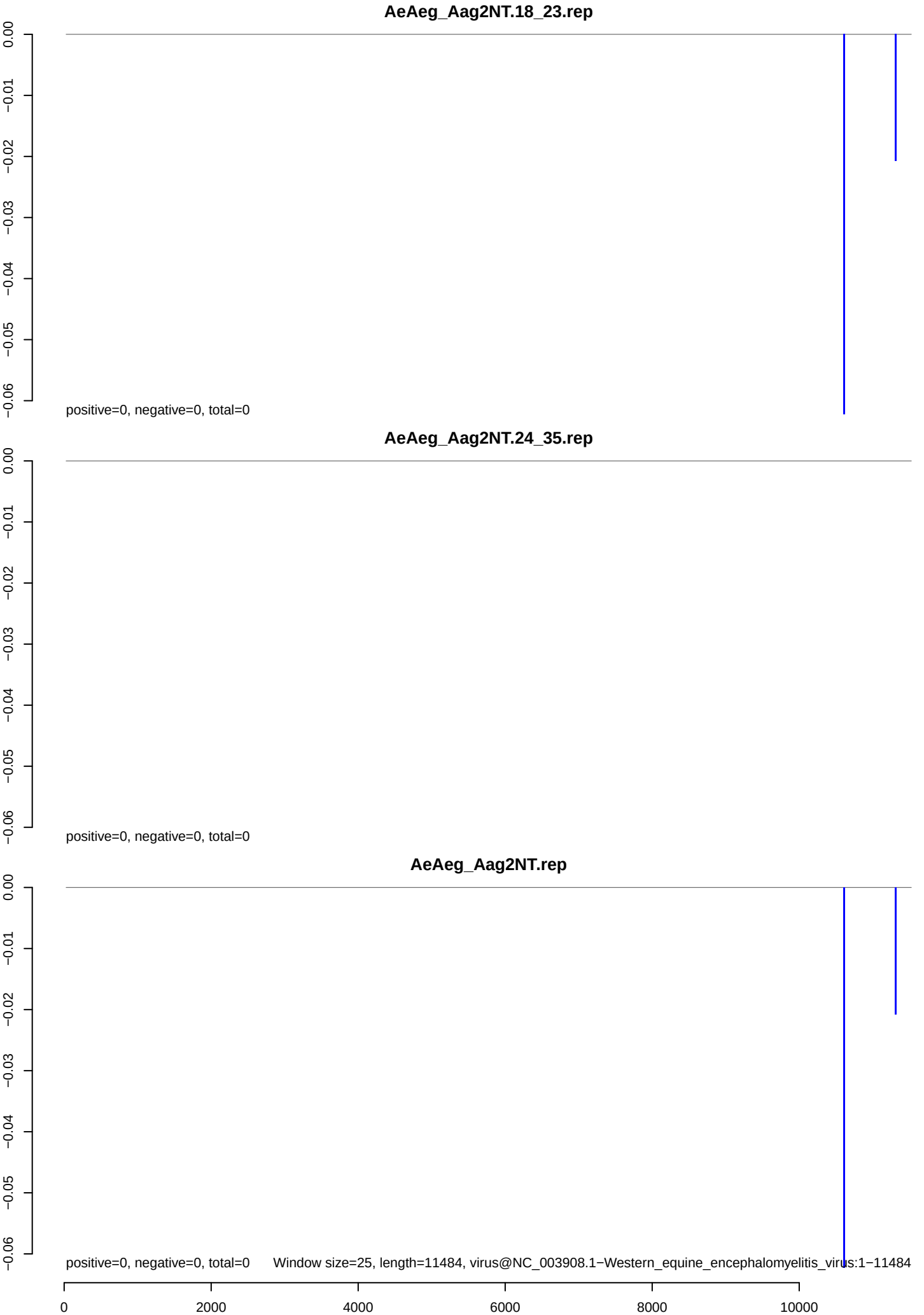

AeAeg_Aag2NT.18_23.rep
0.00
−0.01
−0.02
−0.03
−0.04
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
0.00
−0.01
−0.02
−0.03
−0.04
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.00
−0.01
−0.02
−0.03
−0.04
positive=0, negative=0, total=0
Window size=25, length=11688, virus@NC_016959.1−Ndumu_virus:1−11688
0
2000
4000
6000
8000
10000
12000

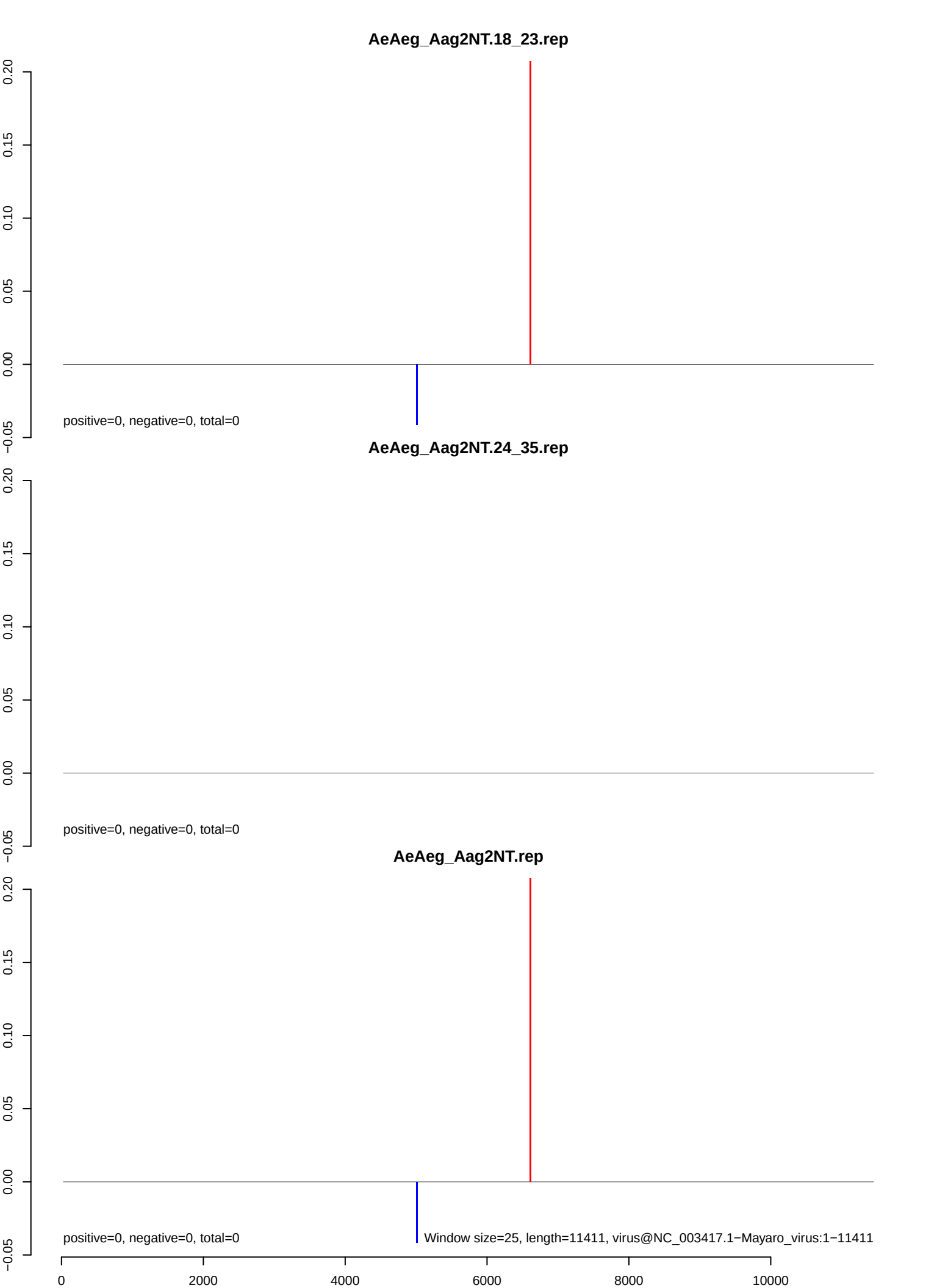

AeAeg_Aag2NT.18_23.rep
0.05
0.00
−0.05
−0.10
−0.15
−0.20
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
0.05
0.00
−0.05
−0.10
−0.15
−0.20
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.05
0.00
−0.05
−0.10
−0.15
−0.20
positive=0, negative=0, total=0
Window size=25, length=10814, virus@NC_012735.1−Wesselsbron_virus:1−10814
0
2000
4000
6000
8000
10000

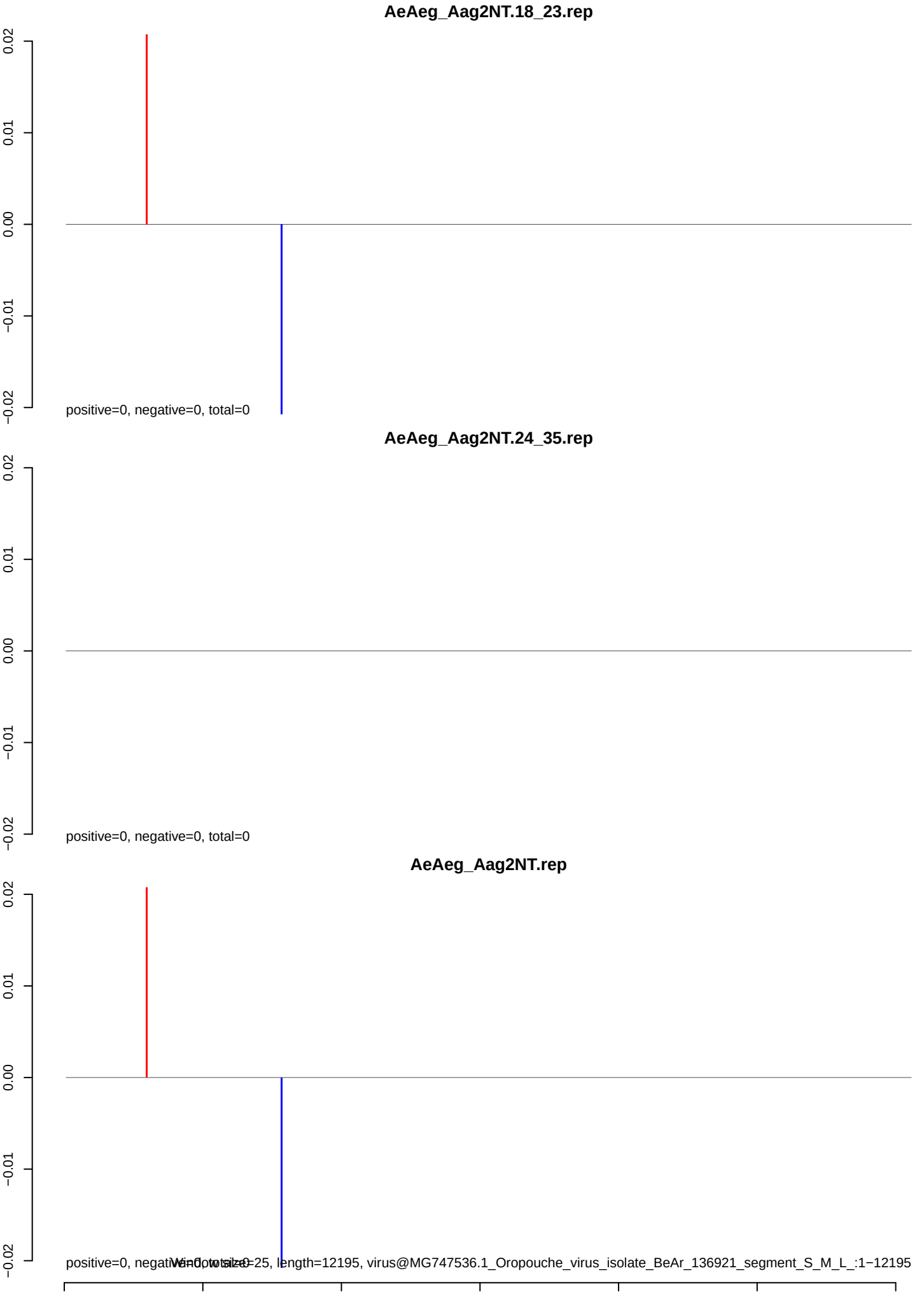

AeAeg_Aag2NT.18_23.rep
0.02
0.01
0.00
−0.01
−0.02
−0.03
−0.04
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
0.02
0.01
0.00
−0.01
−0.02
−0.03
−0.04
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.02
0.01
0.00
−0.01
−0.02
−0.03
−0.04
positive=0, negative=0, total=0
Window size=25, length=10653, virus@NC_006947.1−Karshi_virus:1−10653
0
2000
4000
6000
8000
10000

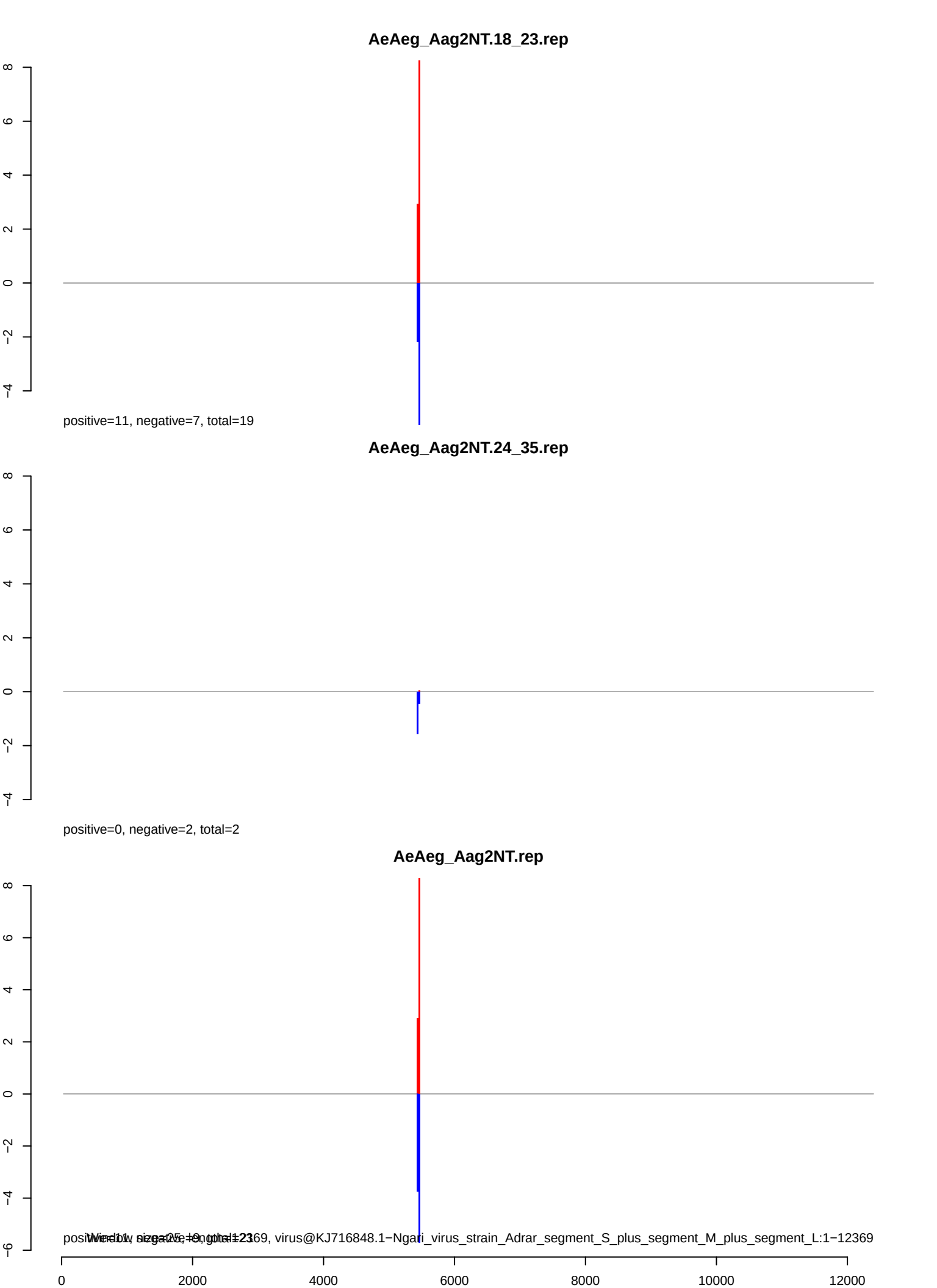

AeAeg_Aag2NT.18_23.rep
0.020
0.015
0.010
0.005
0.000
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
0.020
0.015
0.010
0.005
0.000
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.020
0.015
0.010
0.005
0.000
positive=0, negative=0, total=0
Window size=25, length=11826, virus@NC_004162.2−Chikungunya_virus:1−11826
0
2000
4000
6000
8000
10000
12000

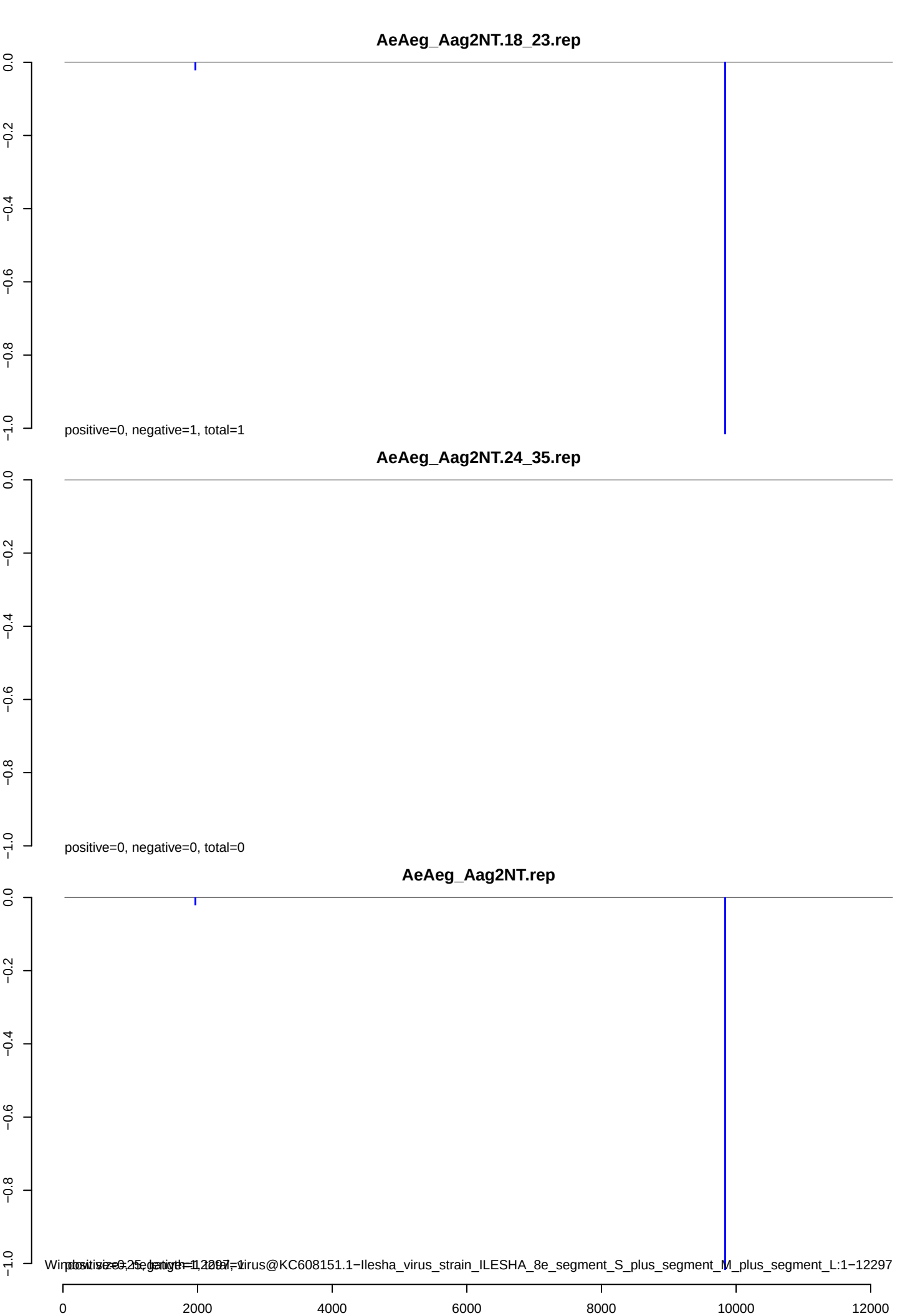

AeAeg_Aag2NT.18_23.rep
0.020
0.015
0.010
0.005
0.000
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
0.020
0.015
0.010
0.005
0.000
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.020
0.015
0.010
0.005
0.000
positive=0, negative=0, total=0
length=12491, virus@NC_004110.1−La_Crosse_virus_segment_S_plus_segment_M_plus_segment_L:1−12491
0
2000
4000
6000
8000
10000
12000

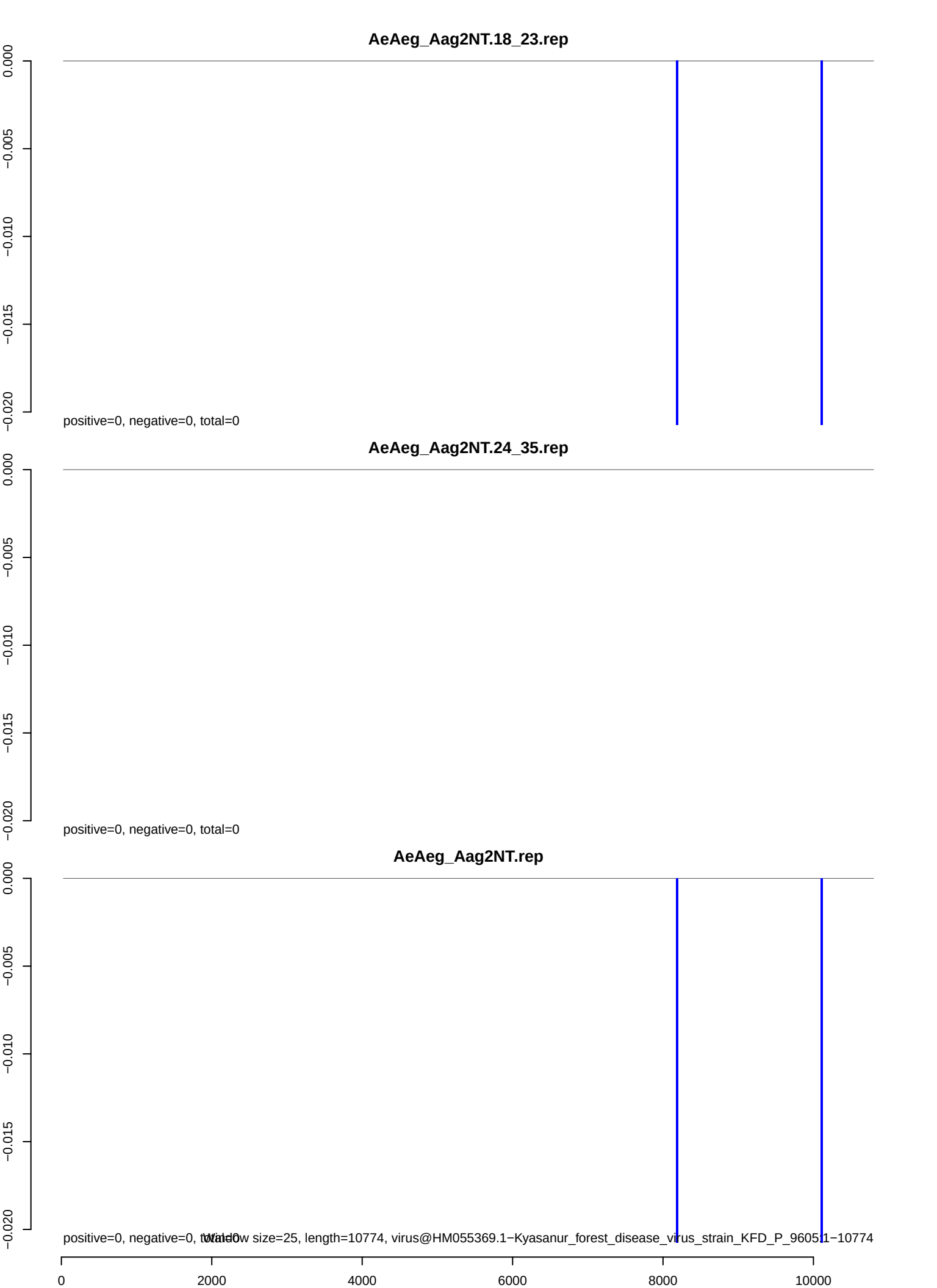

AeAeg_Aag2NT.18_23.rep
0.00
−0.01
−0.02
−0.03
−0.04
−0.05
−0.06
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
0.00
−0.01
−0.02
−0.03
−0.04
−0.05
−0.06
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.00
−0.01
−0.02
−0.03
−0.04
−0.05
−0.06
positive=0, negative=0, total=0
Window size=25, length=11484, virus@NC_003908.1−Western_equine_encephalomyelitis_virus:1−11484
0
2000
4000
6000
8000
10000

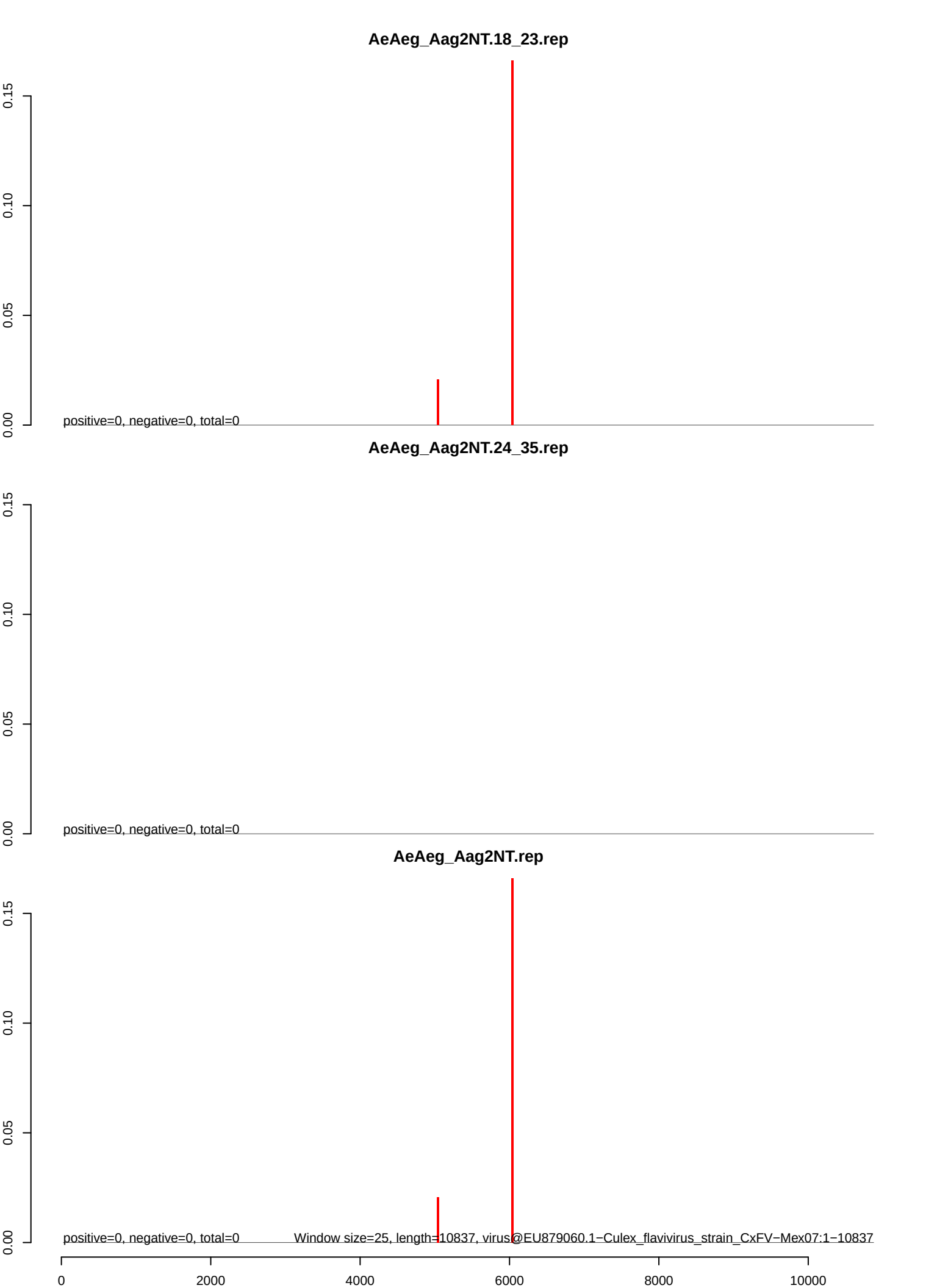

AeAeg_Aag2NT.18_23.rep
0.20
0.15
0.10
0.05
0.00
−0.05
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
0.20
0.15
0.10
0.05
0.00
−0.05
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.20
0.15
0.10
0.05
0.00
−0.05
positive=0, negative=0, total=0
Window size=25, length=11411, virus@NC_003417.1−Mayaro_virus:1−11411
0
2000
4000
6000
8000
10000

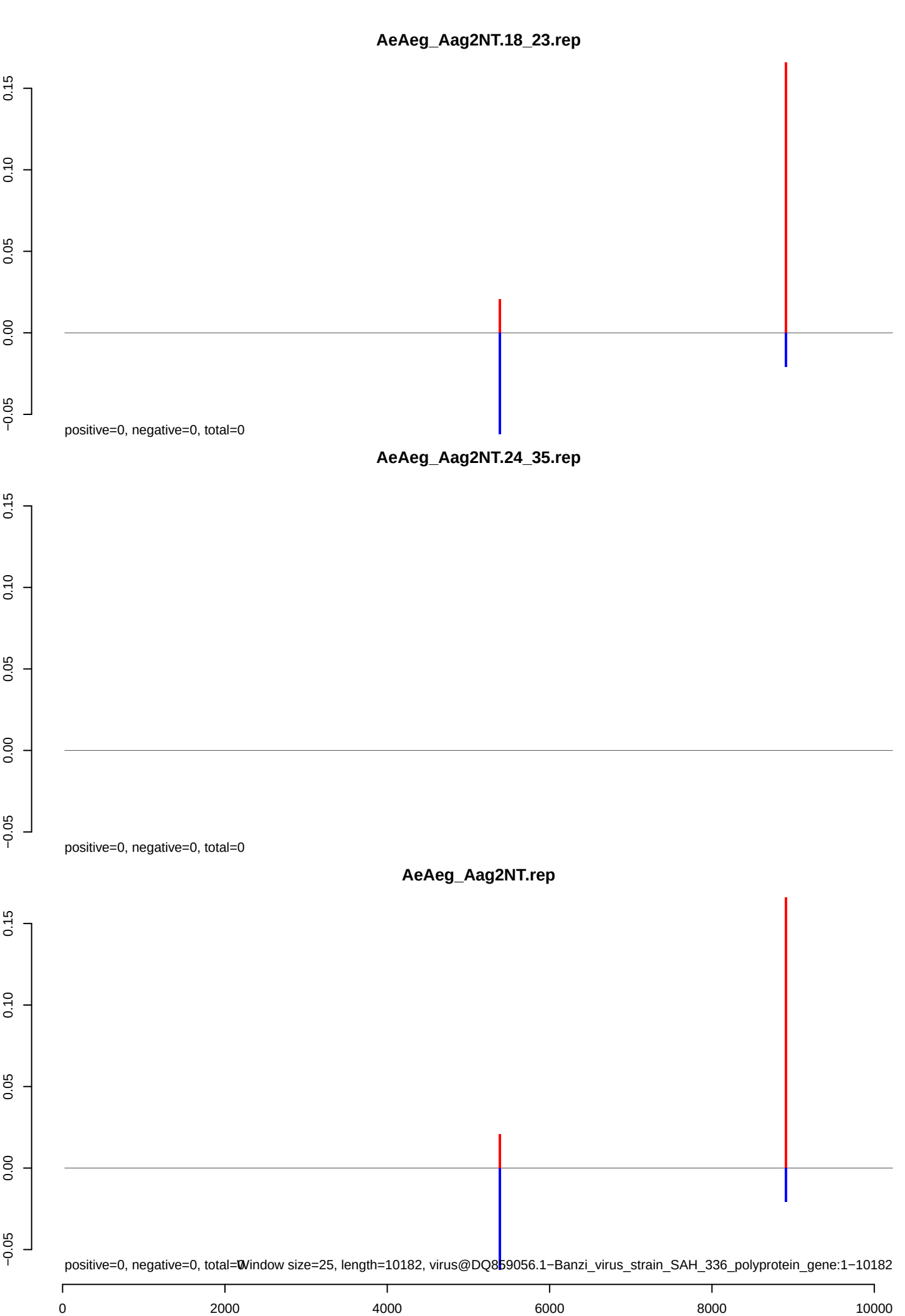

AeAeg_Aag2NT.18_23.rep
0.02
0.01
0.00
−0.01
−0.02
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
0.02
0.01
0.00
−0.01
−0.02
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.02
0.01
0.00
−0.01
−0.02
positive=0, negative=0, total=0
Window size=25, length=12195, virus@MG747536.1_Oropouche_virus_isolate_BeAr_136921_segment_S_M_L_:1−12195
0
2000
4000
6000
8000
10000
12000

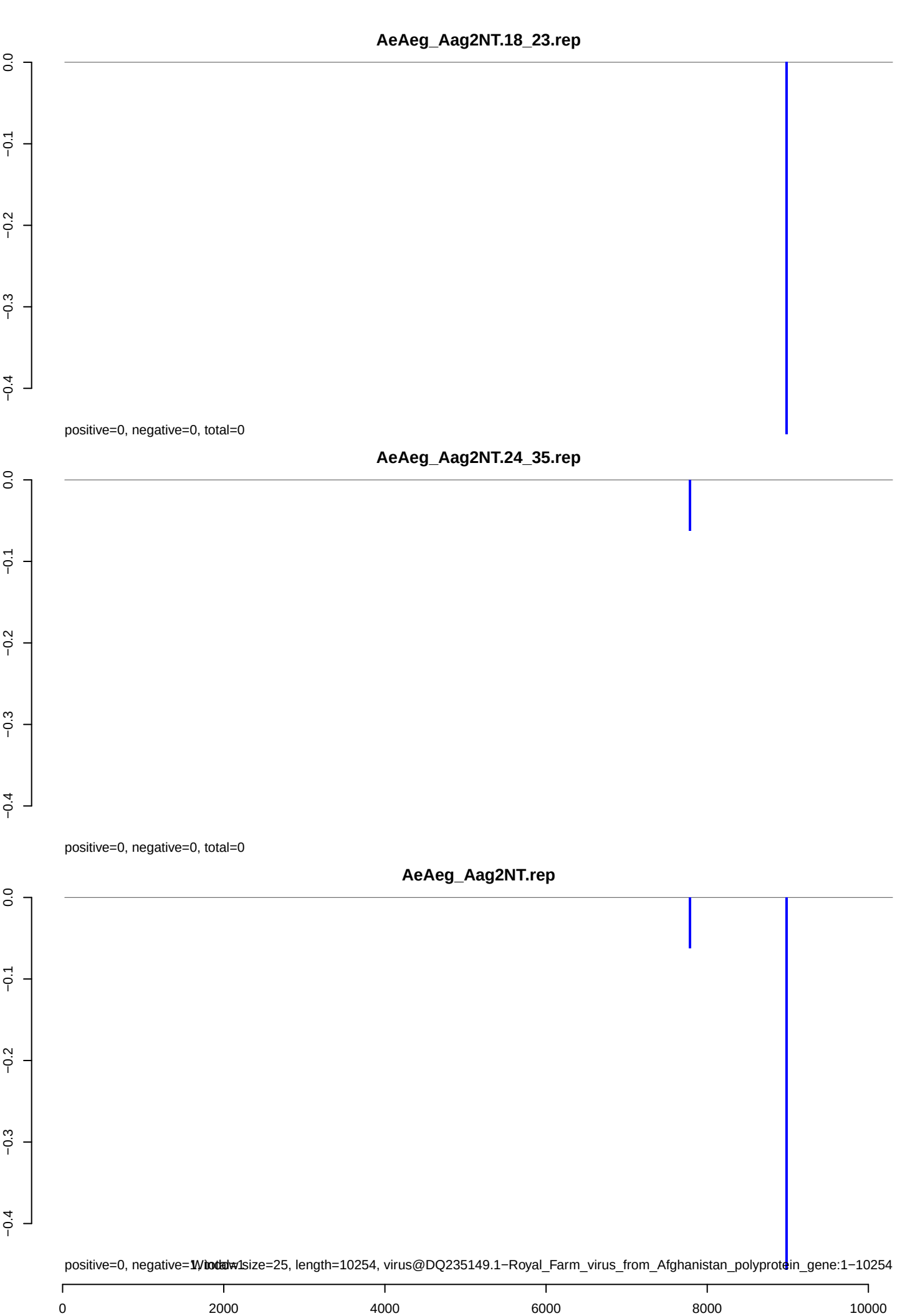

AeAeg_Aag2NT.18_23.rep
positive=11, negative=7, total=19
AeAeg_Aag2NT.24_35.rep
positive=0, negative=2, total=2
AeAeg_Aag2NT.rep
positive=11, negative=7, total=23
virus@KJ716848.1−Ngari_virus_strain_Adrar_segment_S_plus_segment_M_plus_segment_L:1−12369
0
2000
4000
6000
8000
10000
12000

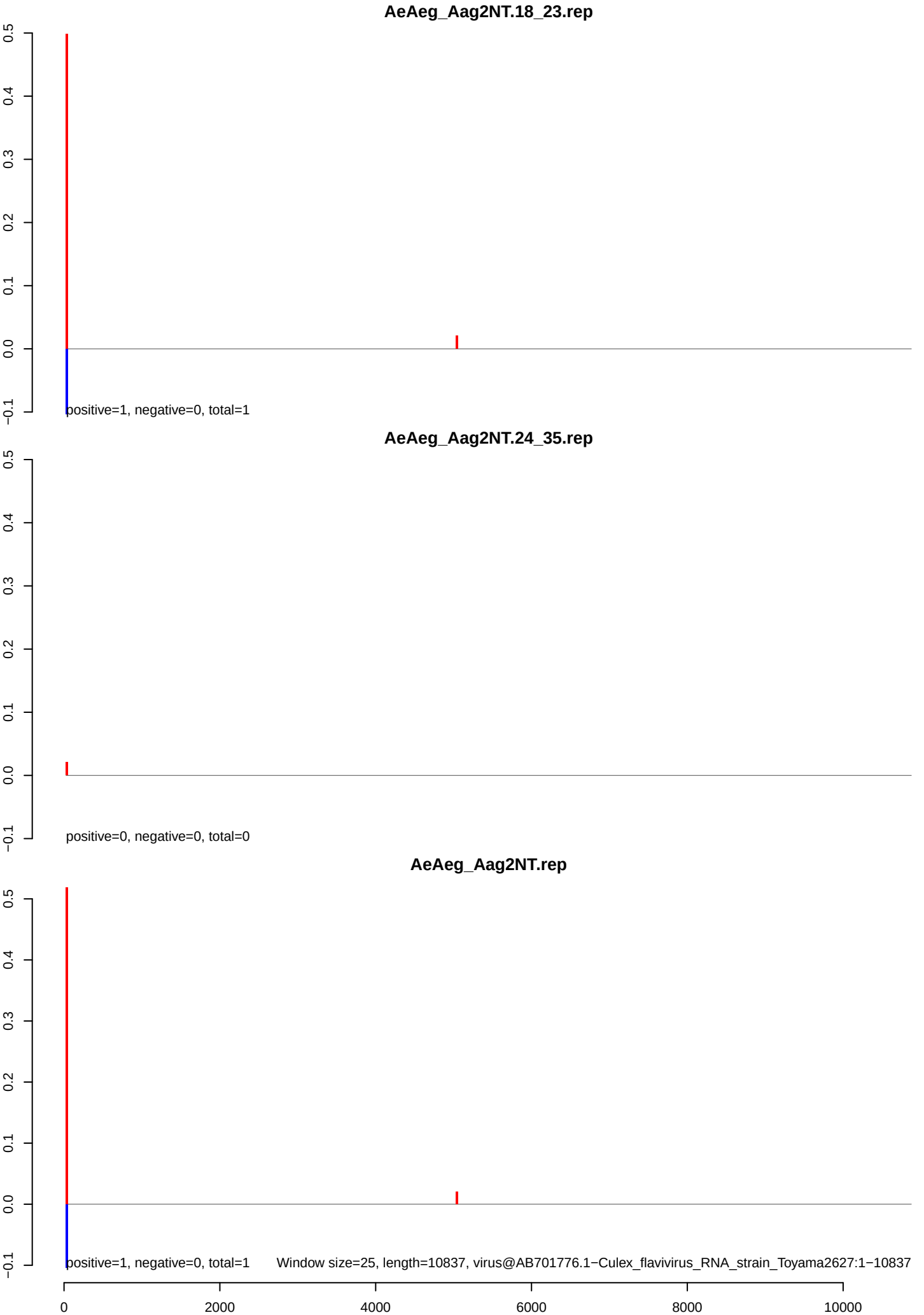

AeAeg_Aag2NT.18_23.rep
0.0
−0.2
−0.4
−0.6
−0.8
−1.0
positive=0, negative=1, total=1
AeAeg_Aag2NT.24_35.rep
0.0
−0.2
−0.4
−0.6
−0.8
−1.0
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.0
−0.2
−0.4
−0.6
−0.8
−1.0
positive=0, negative=1, total=1
Window size=0.25, length=12297−1
positive=0,25,length=12297−virus@KC608151.1−Ilesha_virus_strain_ILESHA_8e_segment_S_plus_segment_M_plus_segment_L:1−12297
0
2000
4000
6000
8000
10000
12000

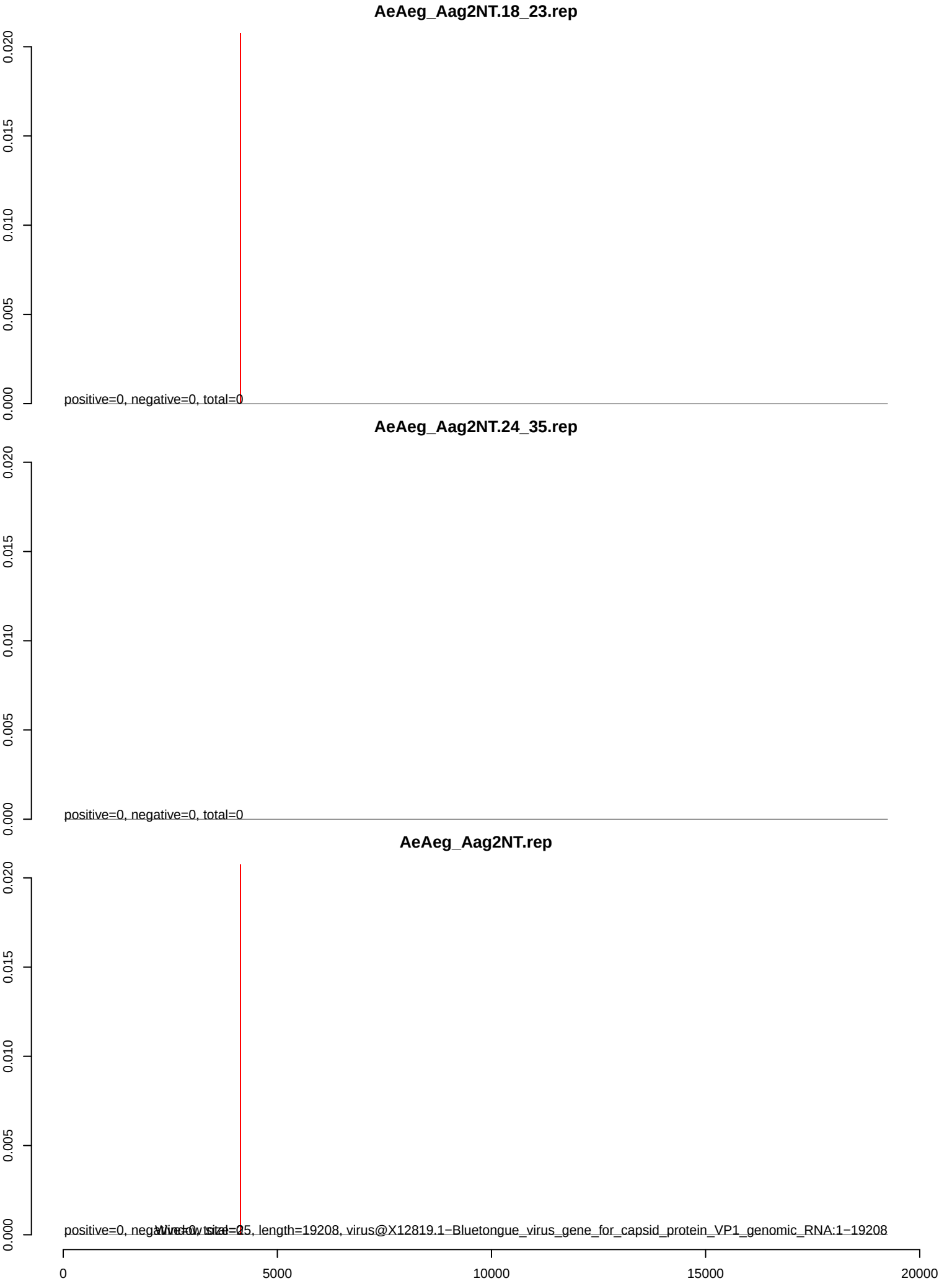

AeAeg_Aag2NT.18_23.rep
0.000
−0.005
−0.010
−0.015
−0.020
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
0.000
−0.005
−0.010
−0.015
−0.020
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.000
−0.005
−0.010
−0.015
−0.020
positive=0, negative=0, total=0
Window size=25, length=10774, virus@HM055369.1−Kyasanur_forest_disease_virus_strain_KFD_P_9605.1−10774
0
2000
4000
6000
8000
10000

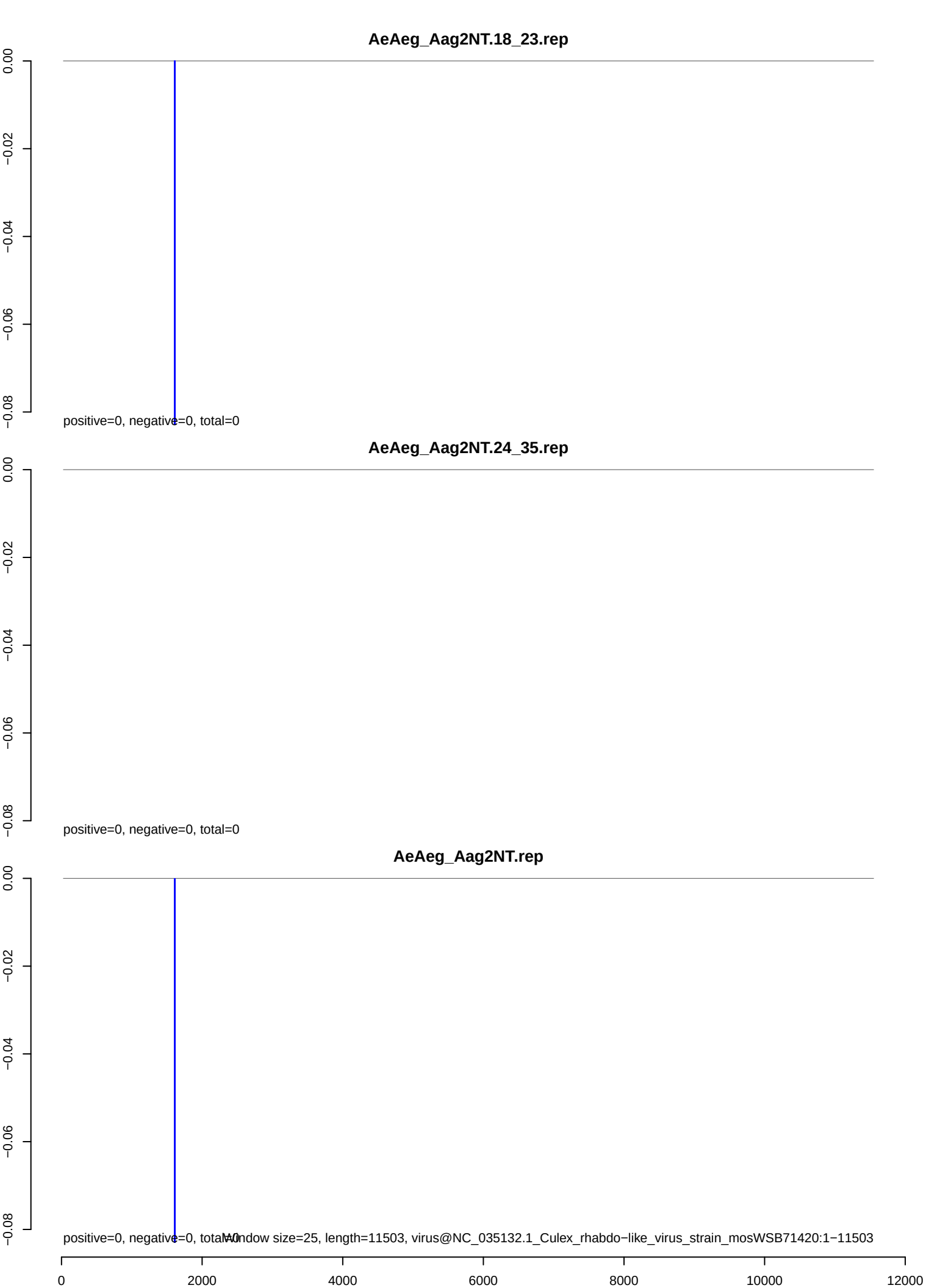

AeAeg_Aag2NT.18_23.rep
0.15
0.10
0.05
0.00
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
0.15
0.10
0.05
0.00
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.15
0.10
0.05
0.00
positive=0, negative=0, total=0
Window size=25, length=10837, virus@EU879060.1−Culex_flavivirus_strain_CxFV−Mex07:1−10837
0
2000
4000
6000
8000
10000

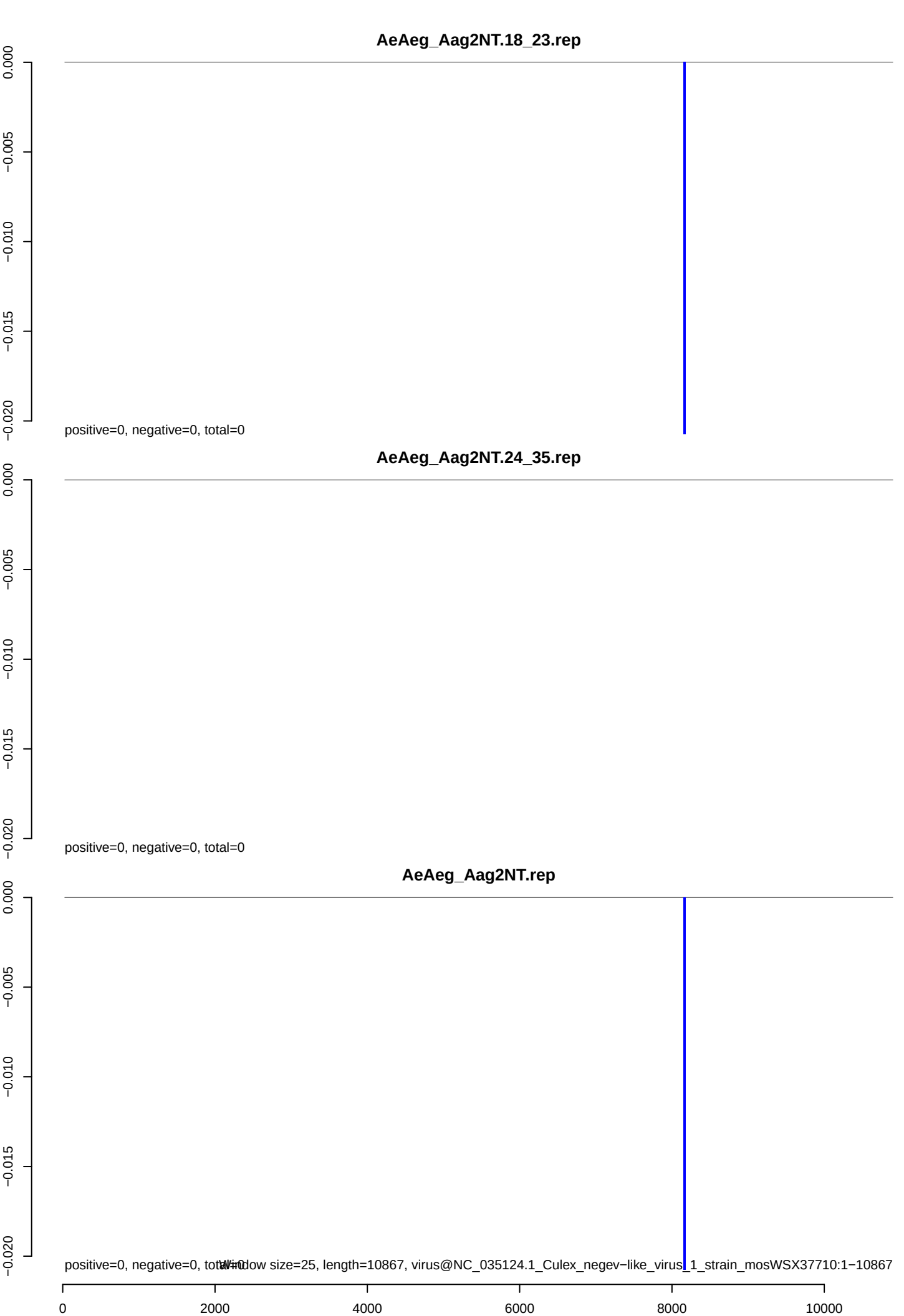

AeAeg_Aag2NT.18_23.rep
0.15
0.10
0.05
0.00
−0.05
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
0.15
0.10
0.05
0.00
−0.05
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.15
0.10
0.05
0.00
−0.05
positive=0, negative=0, total=0
Window size=25, length=10182, virus@DQ859056.1−Banzi_virus_strain_SAH_336_polyprotein_gene:1−10182
0
2000
4000
6000
8000
10000

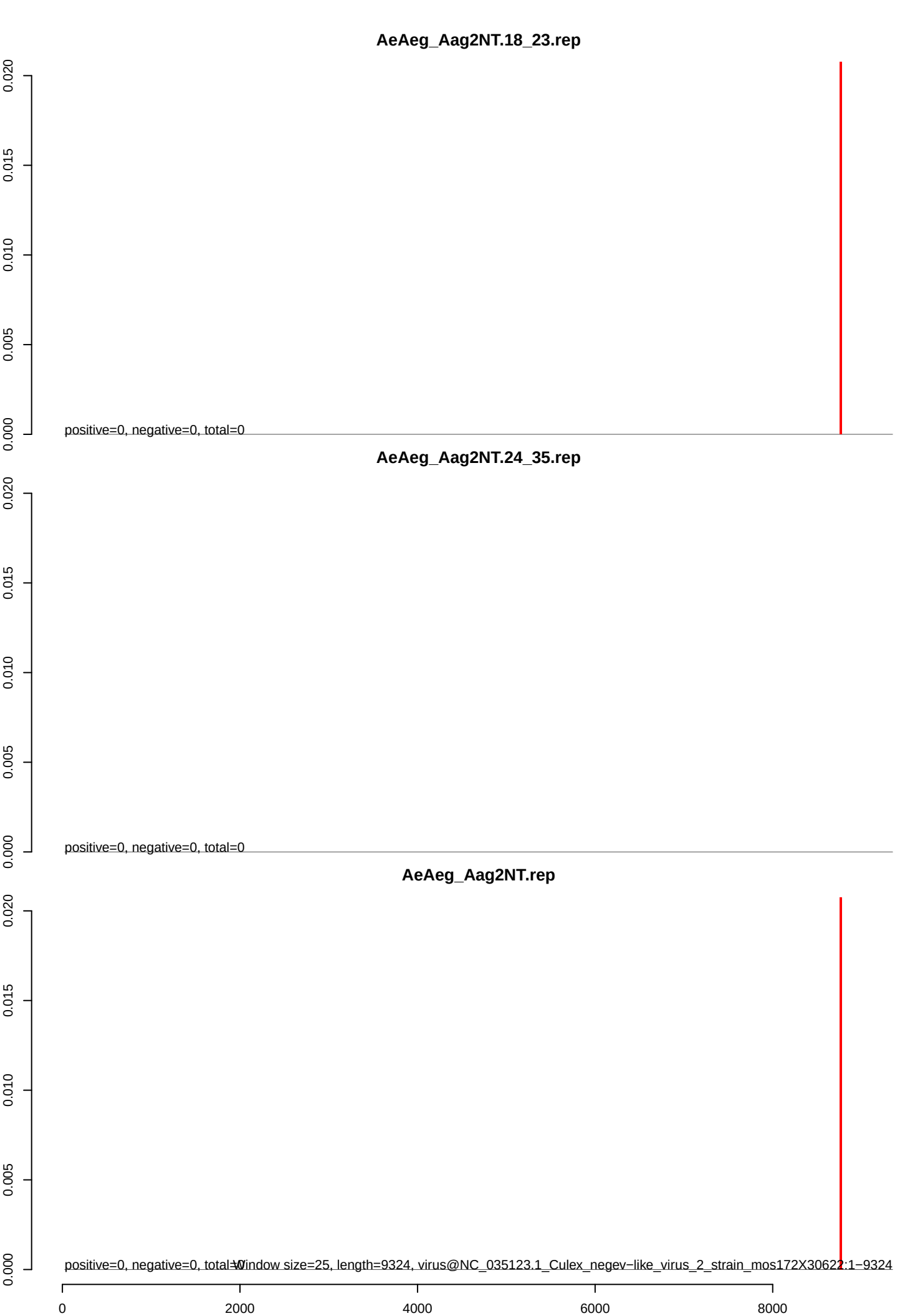

AeAeg_Aag2NT.18_23.rep
0.0
−0.1
−0.2
−0.3
−0.4
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
0.0
−0.1
−0.2
−0.3
−0.4
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.0
−0.1
−0.2
−0.3
−0.4
positive=0, negative=1, total=1
Window size=25, length=10254, virus@DQ235149.1−Royal_Farm_virus_from_Afghanistan_polyprotein_gene:1−10254
0
2000
4000
6000
8000
10000

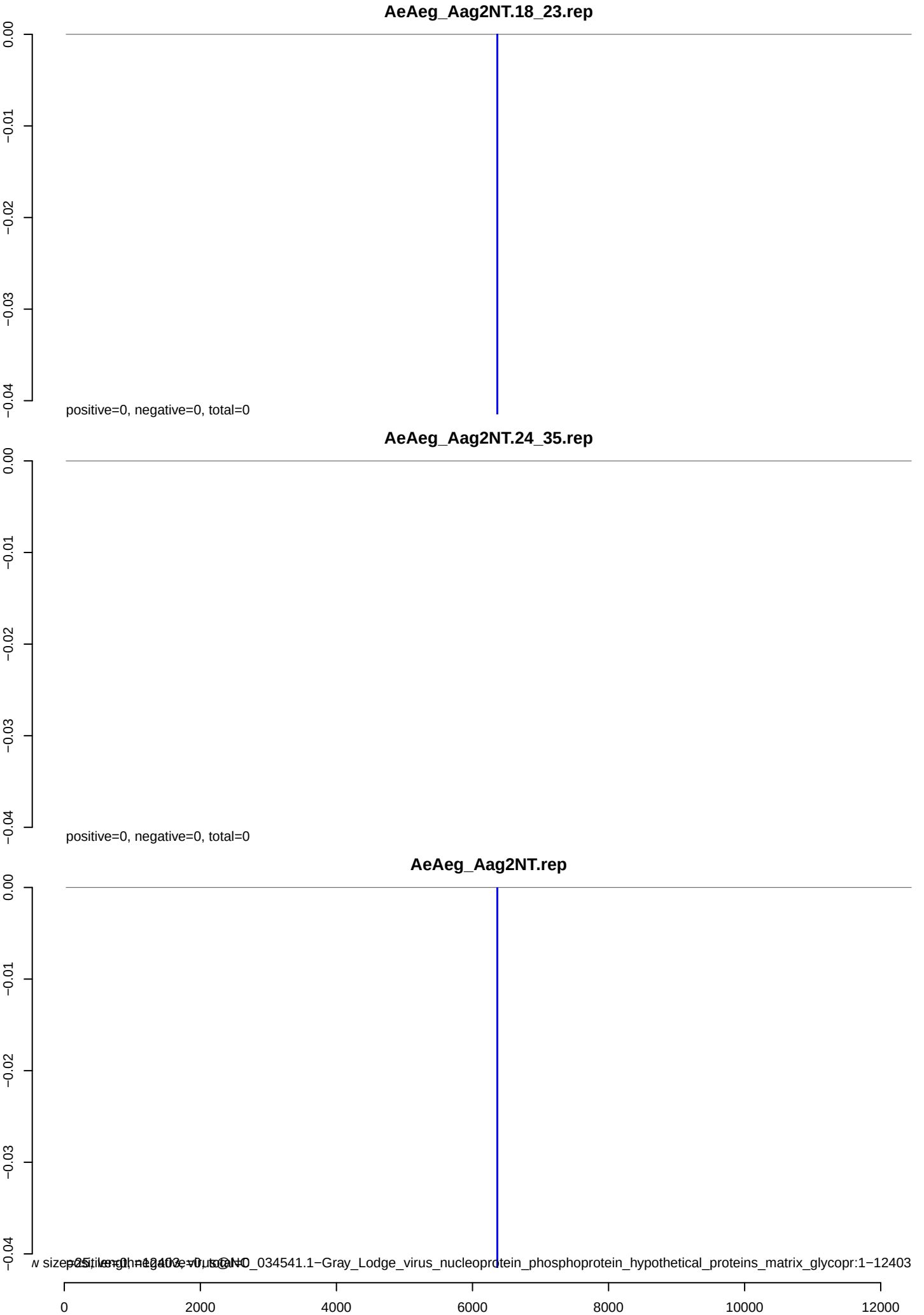

AeAeg_Aag2NT.18_23.rep
0.5
0.4
0.3
0.2
0.1
0.0
−0.1
positive=1, negative=0, total=1
AeAeg_Aag2NT.24_35.rep
0.5
0.4
0.3
0.2
0.1
0.0
−0.1
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.5
0.4
0.3
0.2
0.1
0.0
−0.1
positive=1, negative=0, total=1
Window size=25, length=10837, virus@AB701776.1−Culex_flavivirus_RNA_strain_Toyama2627:1−10837
0
2000
4000
6000
8000
10000

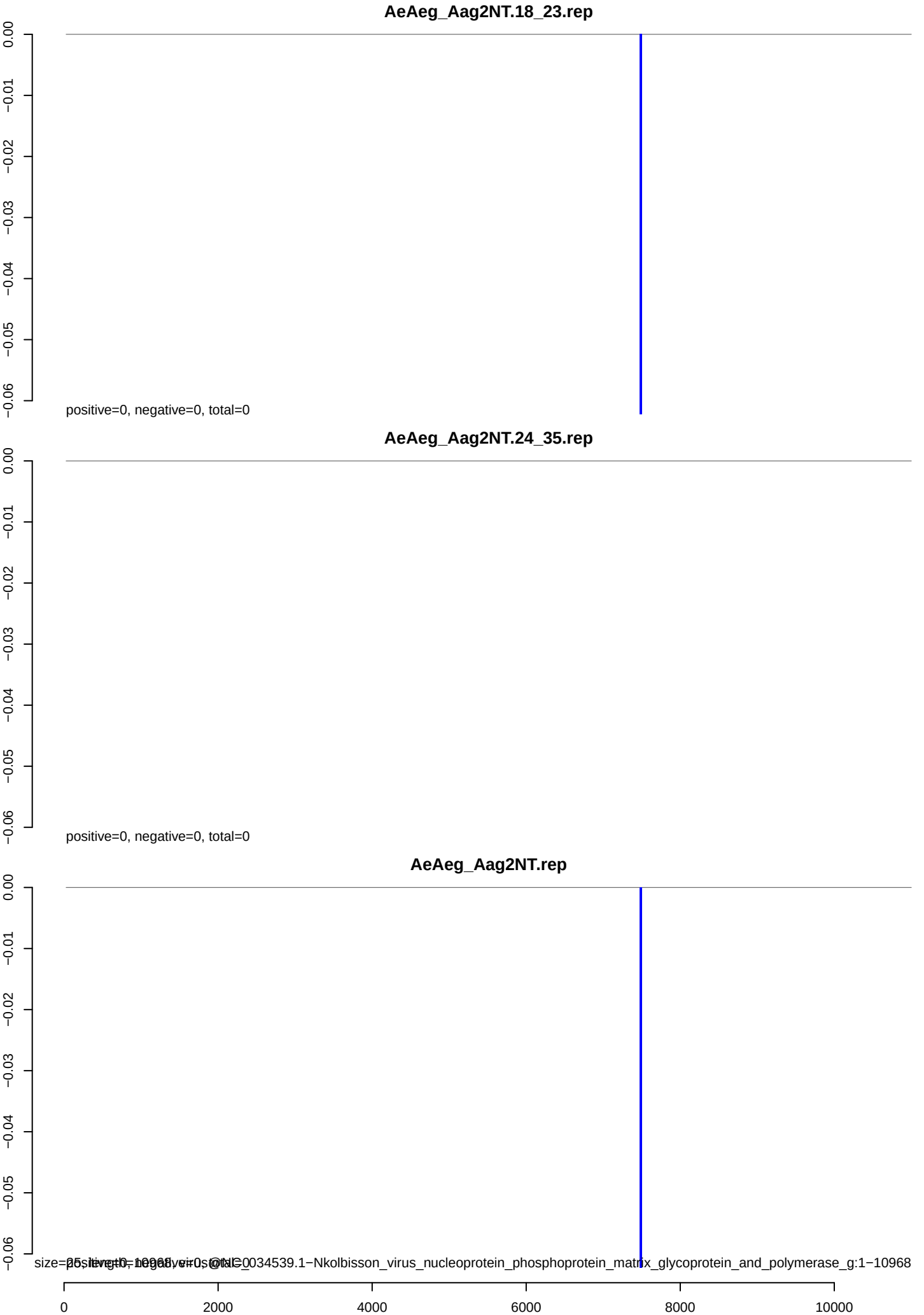

AeAeg_Aag2NT.18_23.rep
0.020
0.015
0.010
0.005
0.000
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
0.020
0.015
0.010
0.005
0.000
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.020
0.015
0.010
0.005
0.000
positive=0, negative=0, total=0, length=19208, virus@X12819.1−Bluetongue_virus_gene_for_capsid_protein_VP1_genomic_RNA:1−19208
0
5000
10000
15000
20000

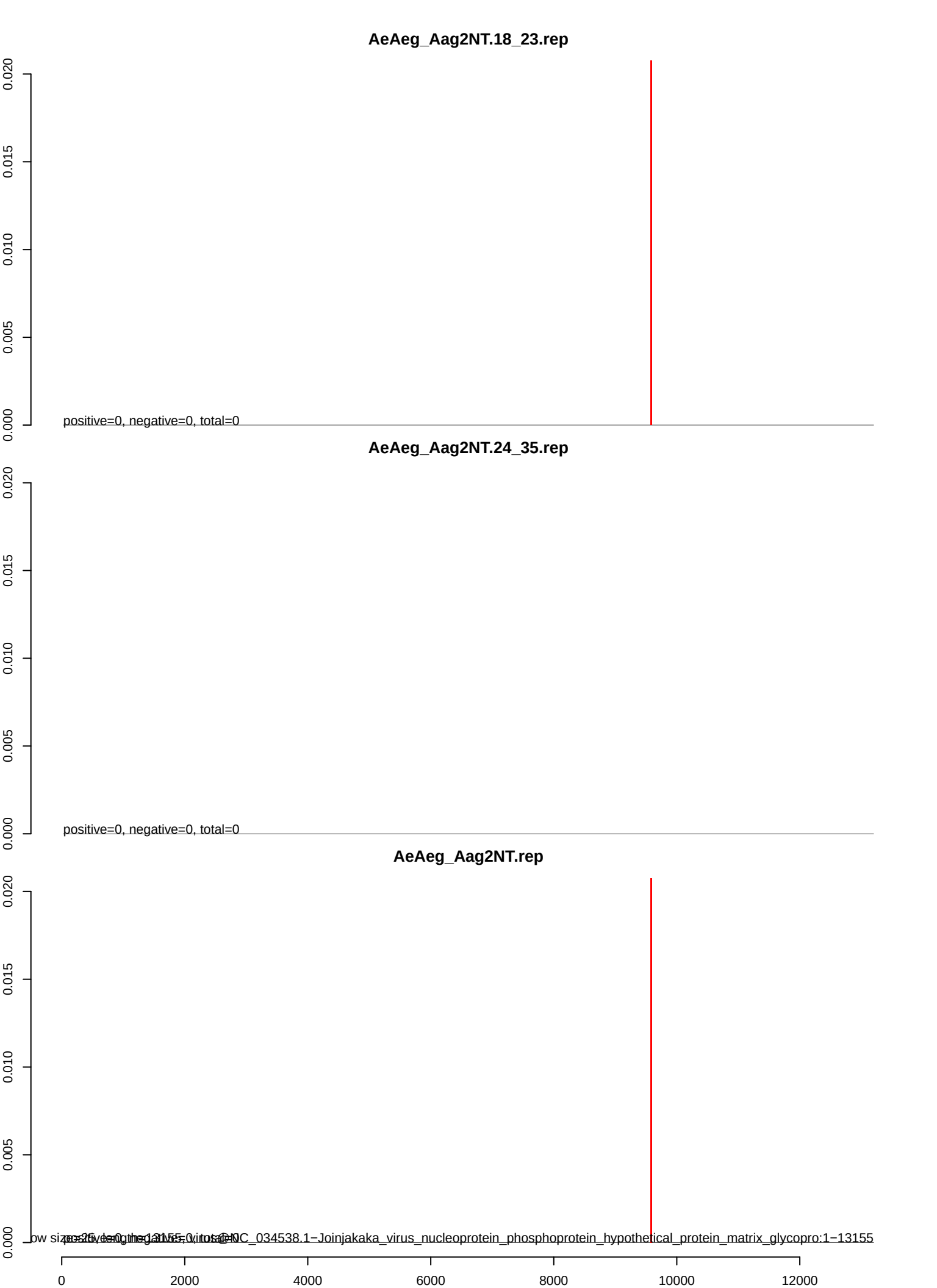

AeAeg_Aag2NT.18_23.rep
0.00
−0.02
−0.04
−0.06
−0.08
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
0.00
−0.02
−0.04
−0.06
−0.08
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.00
−0.02
−0.04
−0.06
−0.08
positive=0, negative=0, total=0
window size=25, length=11503, virus@NC_035132.1_Culex_rhabdo−like_virus_strain_mosWSB71420:1−11503
0
2000
4000
6000
8000
10000
12000

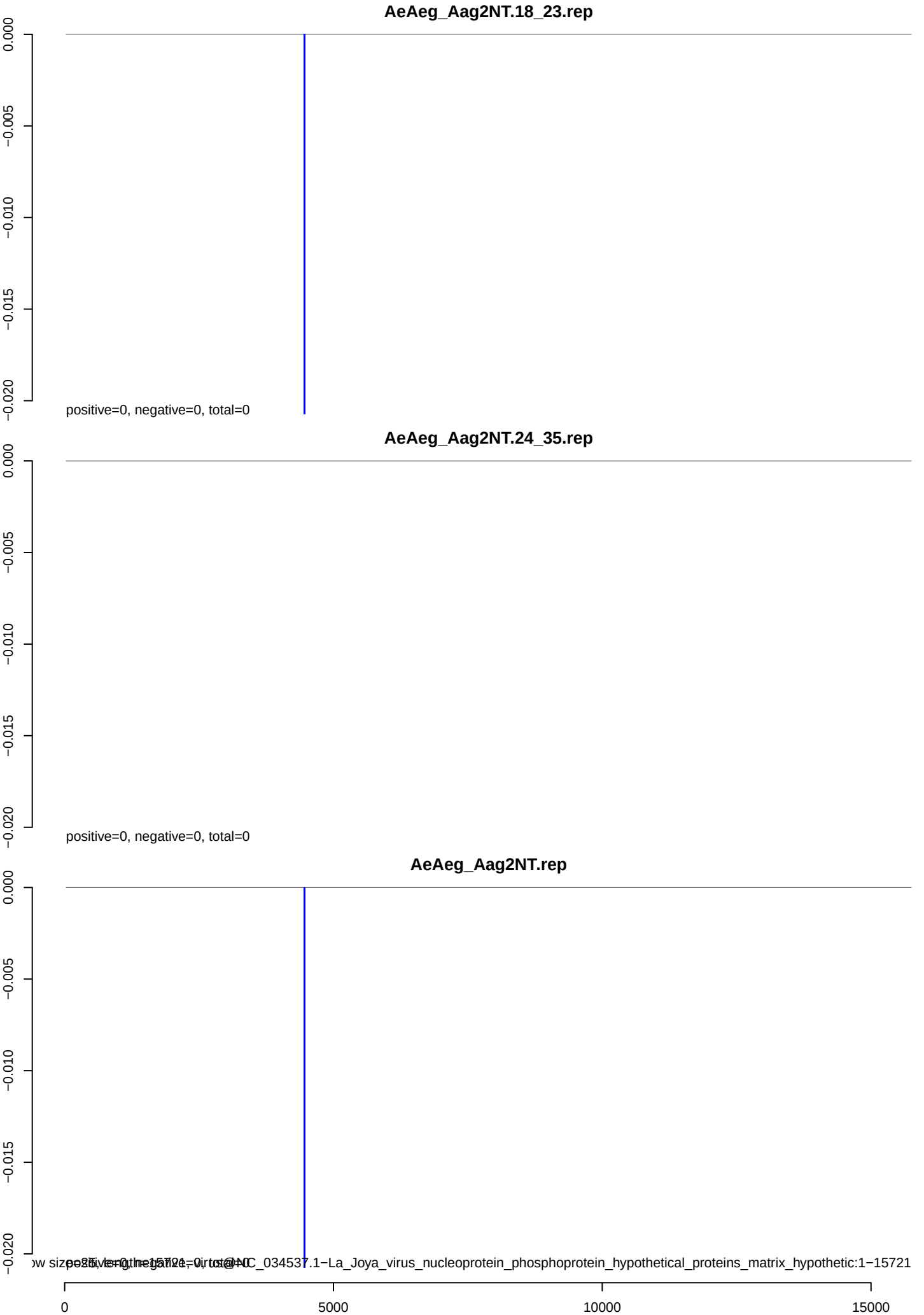

AeAeg_Aag2NT.18_23.rep
0.000
−0.005
−0.010
−0.015
−0.020
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
0.000
−0.005
−0.010
−0.015
−0.020
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.000
−0.005
−0.010
−0.015
−0.020
positive=0, negative=0, total=0
Window size=25, length=10867, virus@NC_035124.1_Culex_negev−like_virus_1_strain_mosWSX37710:1−10867
0
2000
4000
6000
8000
10000

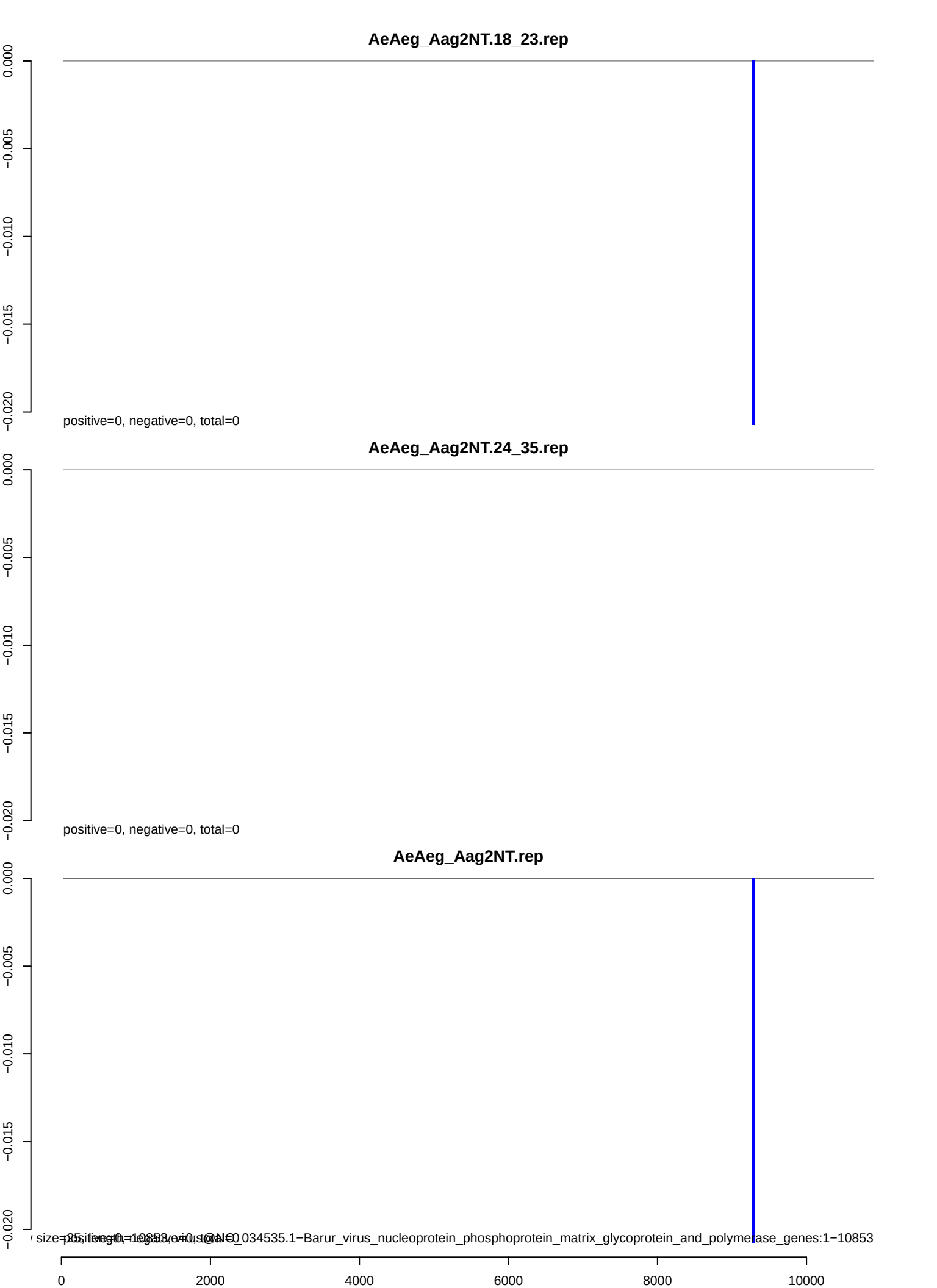

AeAeg_Aag2NT.18_23.rep
0.020
0.015
0.010
0.005
0.000
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
0.020
0.015
0.010
0.005
0.000
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.020
0.015
0.010
0.005
0.000
positive=0, negative=0, total=0
Window size=25, length=9324, virus@NC_035123.1_Culex_negev−like_virus_2_strain_mos172X30622:1−9324
0
2000
4000
6000
8000

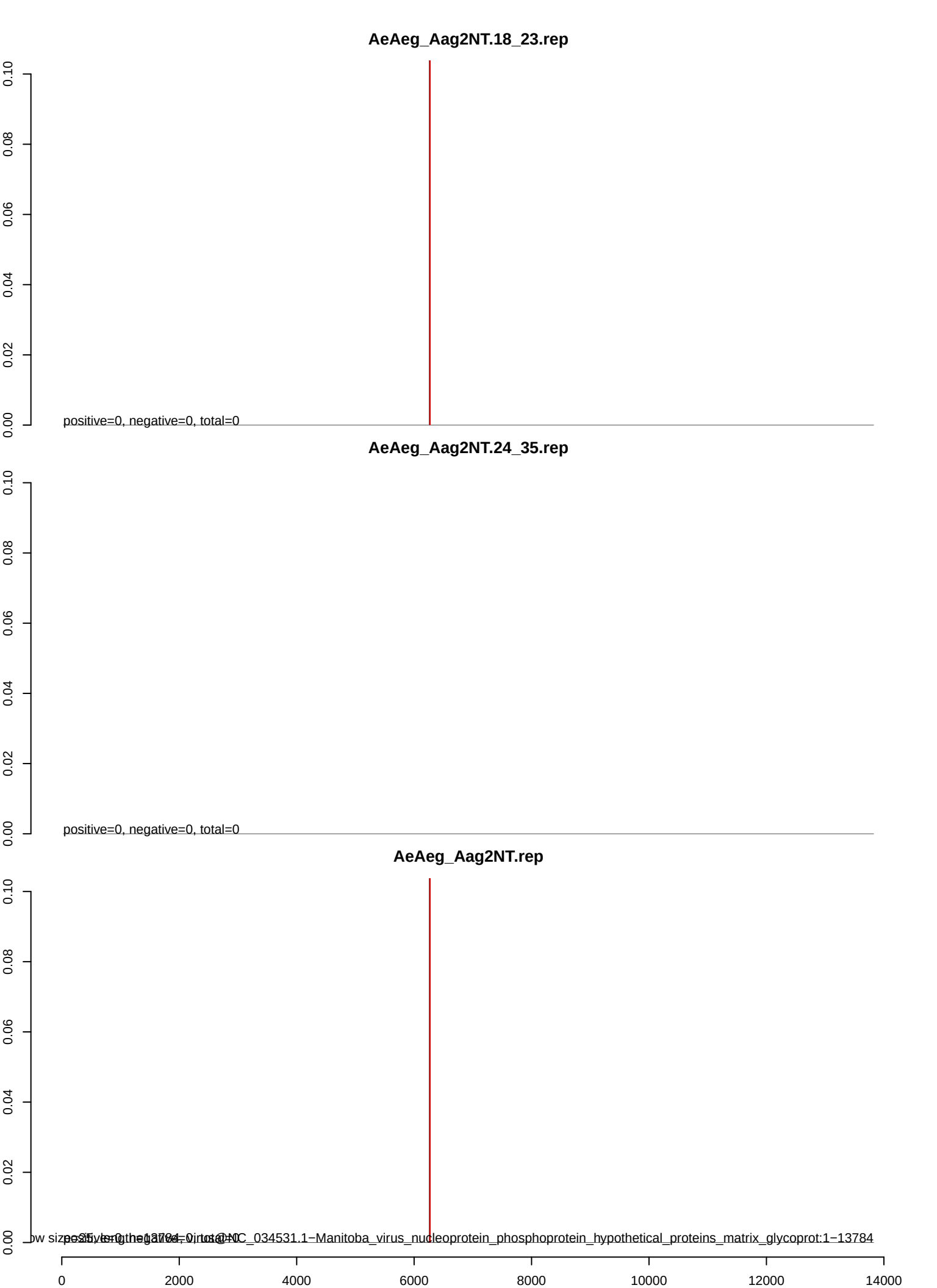

AeAeg_Aag2NT.18_23.rep
0.00
−0.01
−0.02
−0.03
−0.04
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
0.00
−0.01
−0.02
−0.03
−0.04
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.00
−0.01
−0.02
−0.03
−0.04
positive=0, negative=0, total=0
NC_034541.1−Gray_Lodge_virus_nucleoprotein_phosphoprotein_hypothetical_proteins_matrix_glycopr:1−12403
0
2000
4000
6000
8000
10000
12000

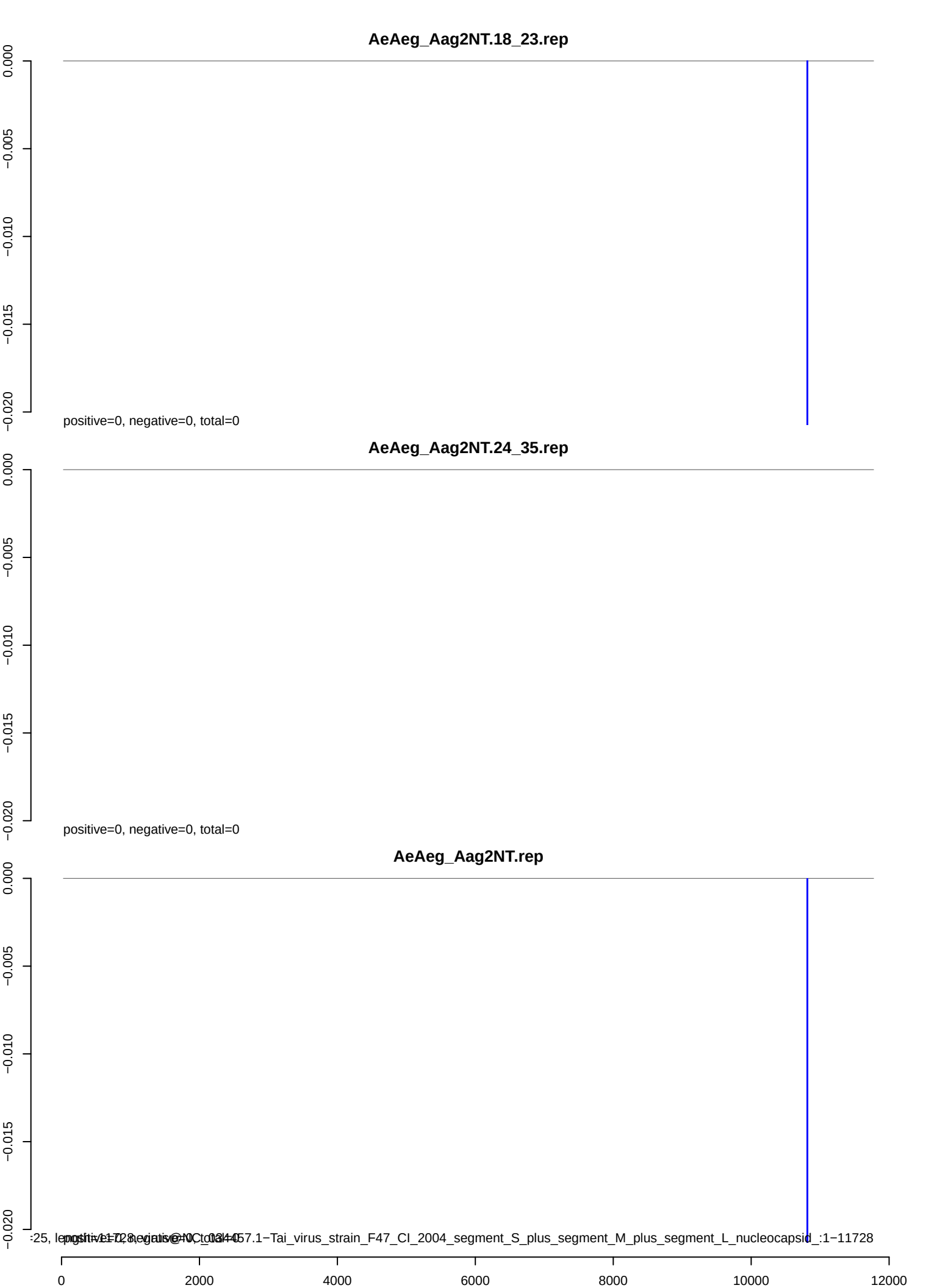

AeAeg_Aag2NT.18_23.rep
0.00
−0.01
−0.02
−0.03
−0.04
−0.05
−0.06
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
0.00
−0.01
−0.02
−0.03
−0.04
−0.05
−0.06
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.00
−0.01
−0.02
−0.03
−0.04
−0.05
−0.06
positive=0, negative=0, total=0
size=25, length=10968, virus=NC_0034539.1−Nkolbisson_virus_nucleoprotein_phosphoprotein_matrix_glycoprotein_and_polymerase_g:1−10968
0
2000
4000
6000
8000
10000

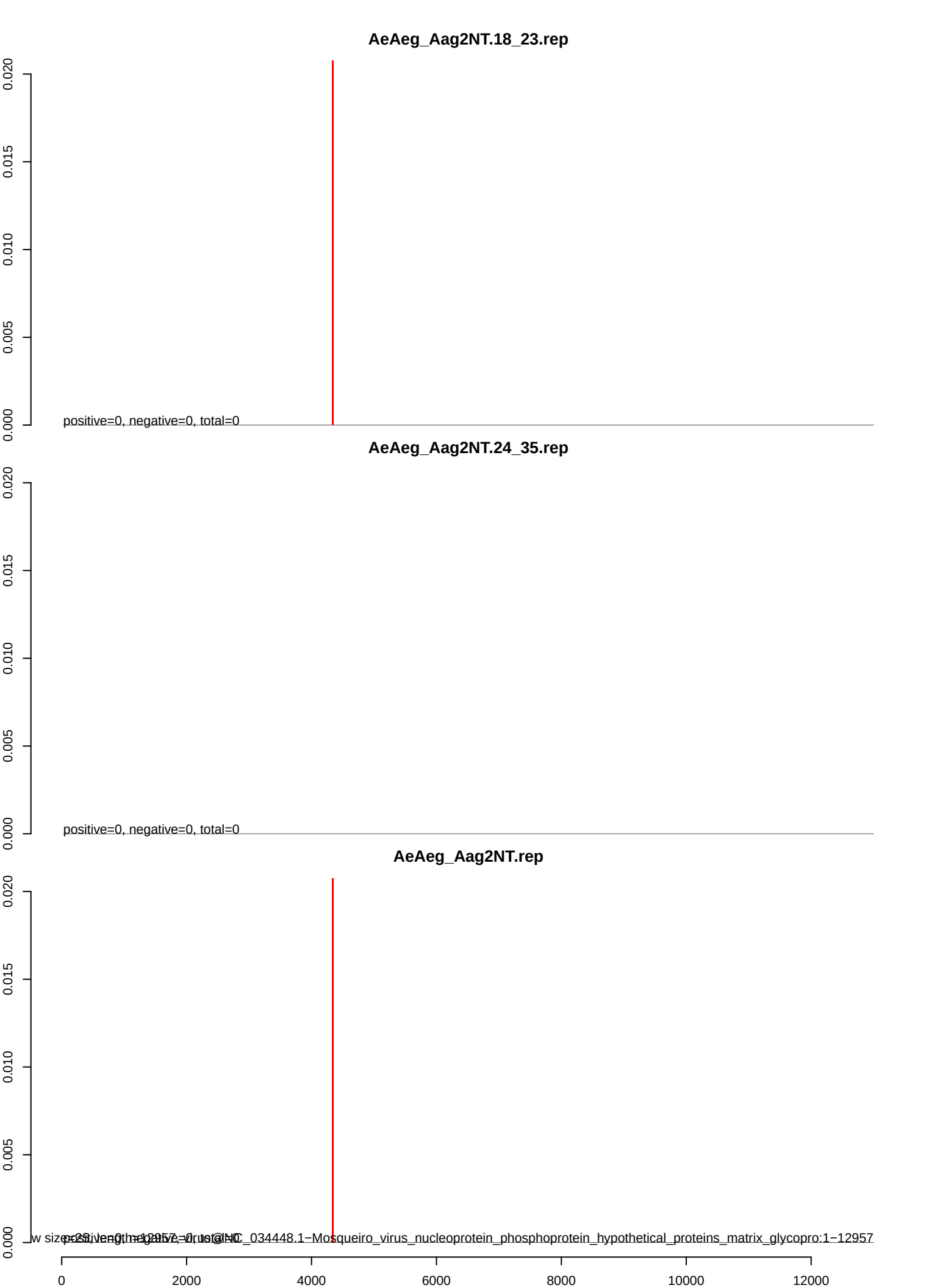

AeAeg_Aag2NT.18_23.rep
0.020
0.015
0.010
0.005
0.000
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
0.020
0.015
0.010
0.005
0.000
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.020
0.015
0.010
0.005
0.000
ow size=25, length=13155, total=NC_034538.1−Joinjakaka_virus_nucleoprotein_phosphoprotein_hypothetical_protein_matrix_glycopro:1−13155
0
2000
4000
6000
8000
10000
12000

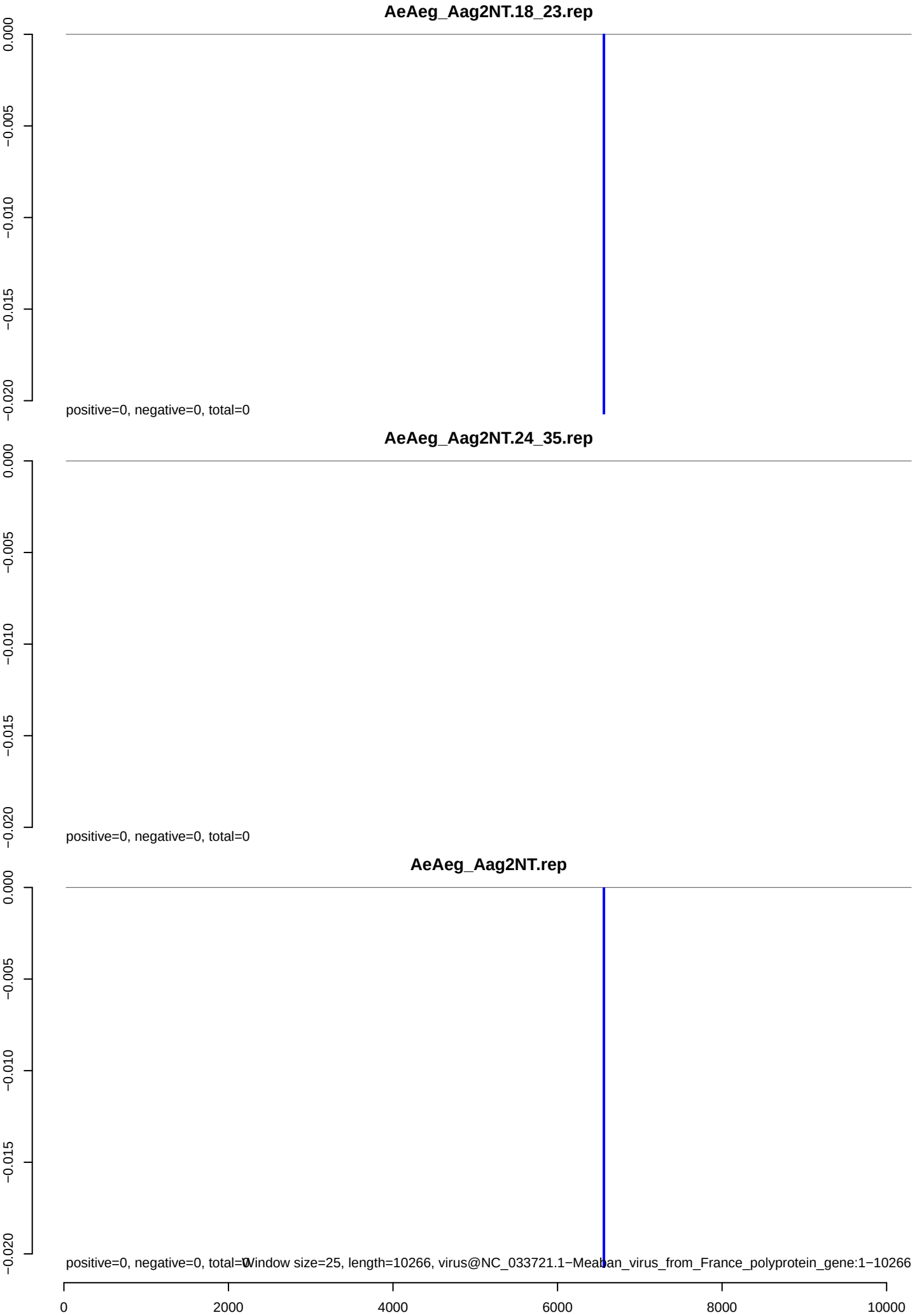

AeAeg_Aag2NT.18_23.rep
0.000
−0.005
−0.010
−0.015
−0.020
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
0.000
−0.005
−0.010
−0.015
−0.020
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.000
−0.005
−0.010
−0.015
−0.020
ow size=25, interval=1, virus@NC_034537.1−La_Joya_virus_nucleoprotein_phosphoprotein_hypothetical_proteins_matrix_hypothetic:1−15721
0
5000
10000
15000

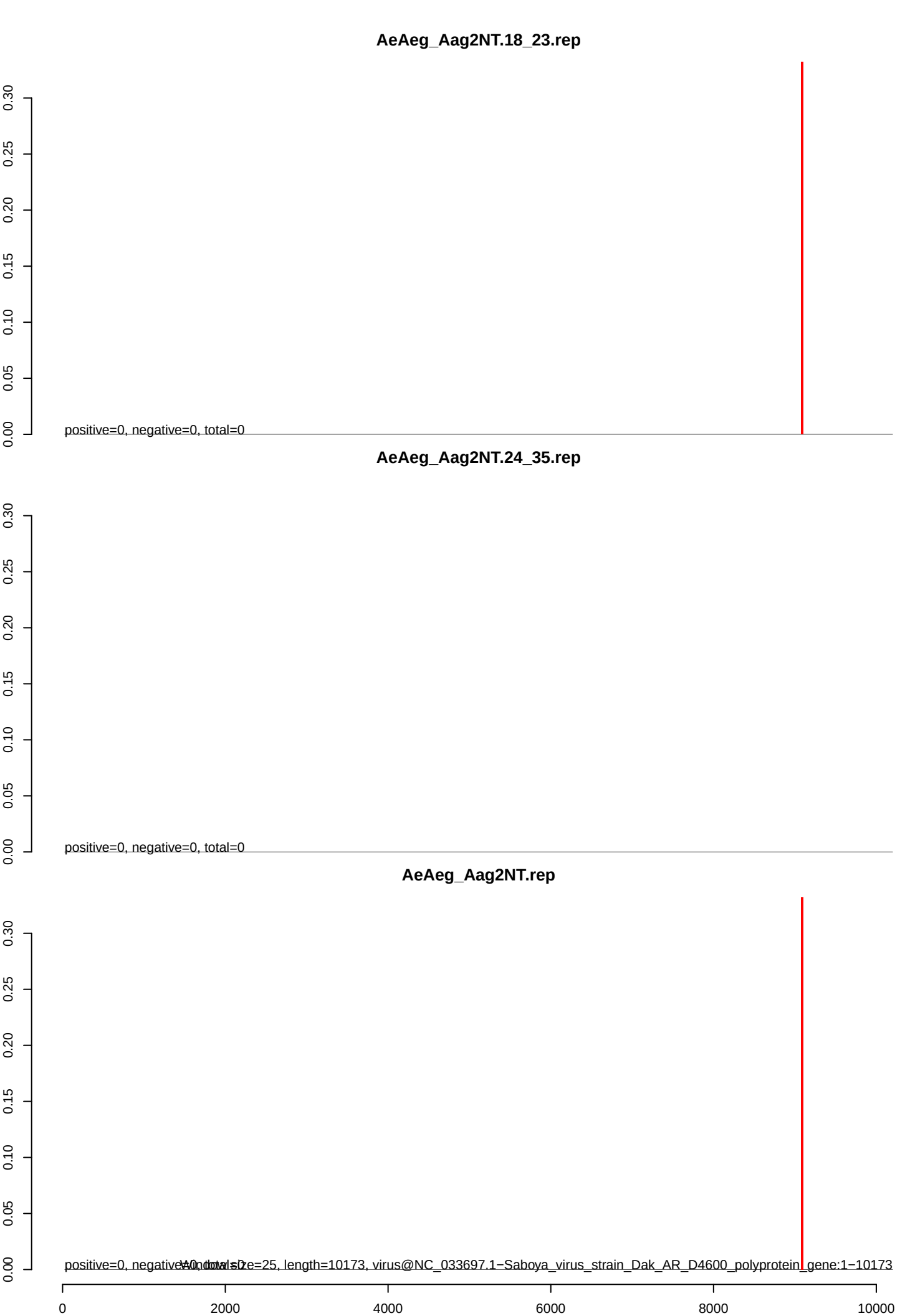

AeAeg_Aag2NT.18_23.rep
0.000
−0.005
−0.010
−0.015
−0.020
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
0.000
−0.005
−0.010
−0.015
−0.020
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.000
−0.005
−0.010
−0.015
−0.020
size=25, length=10853, positive=0, negative=0, total=0
NC_034535.1−Barur_virus_nucleoprotein_phosphoprotein_matrix_glycoprotein_and_polymerase_genes:1−10853
0
2000
4000
6000
8000
10000

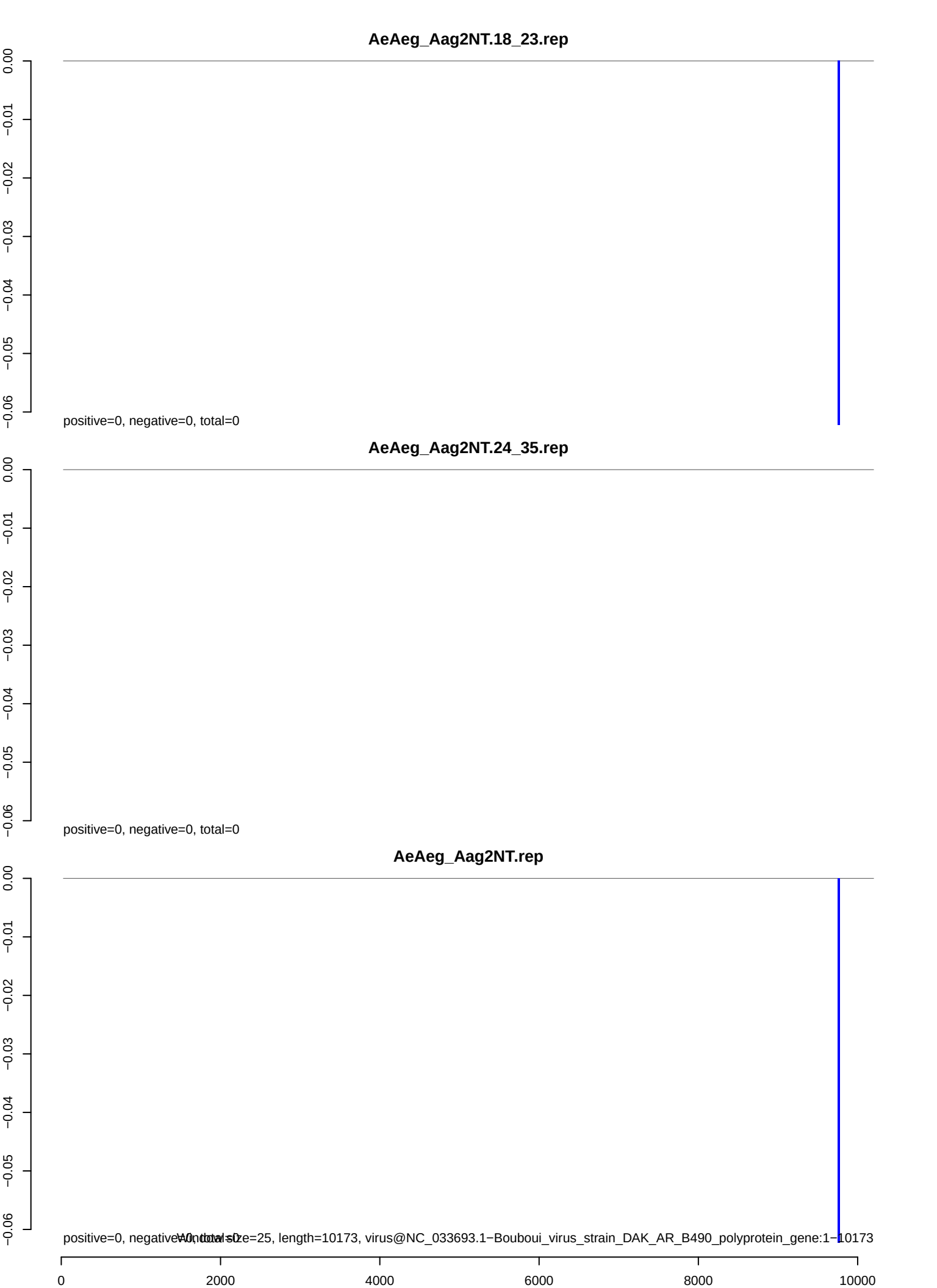

AeAeg_Aag2NT.18_23.rep
0.00
0.02
0.04
0.06
0.08
0.10
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
0.00
0.02
0.04
0.06
0.08
0.10
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.00
0.02
0.04
0.06
0.08
0.10
ow size=25, length=13784, total=0
NC_034531.1−Manitoba_virus_nucleoprotein_phosphoprotein_hypothetical_proteins_matrix_glycoprot:1−13784
0
2000
4000
6000
8000
10000
12000
14000

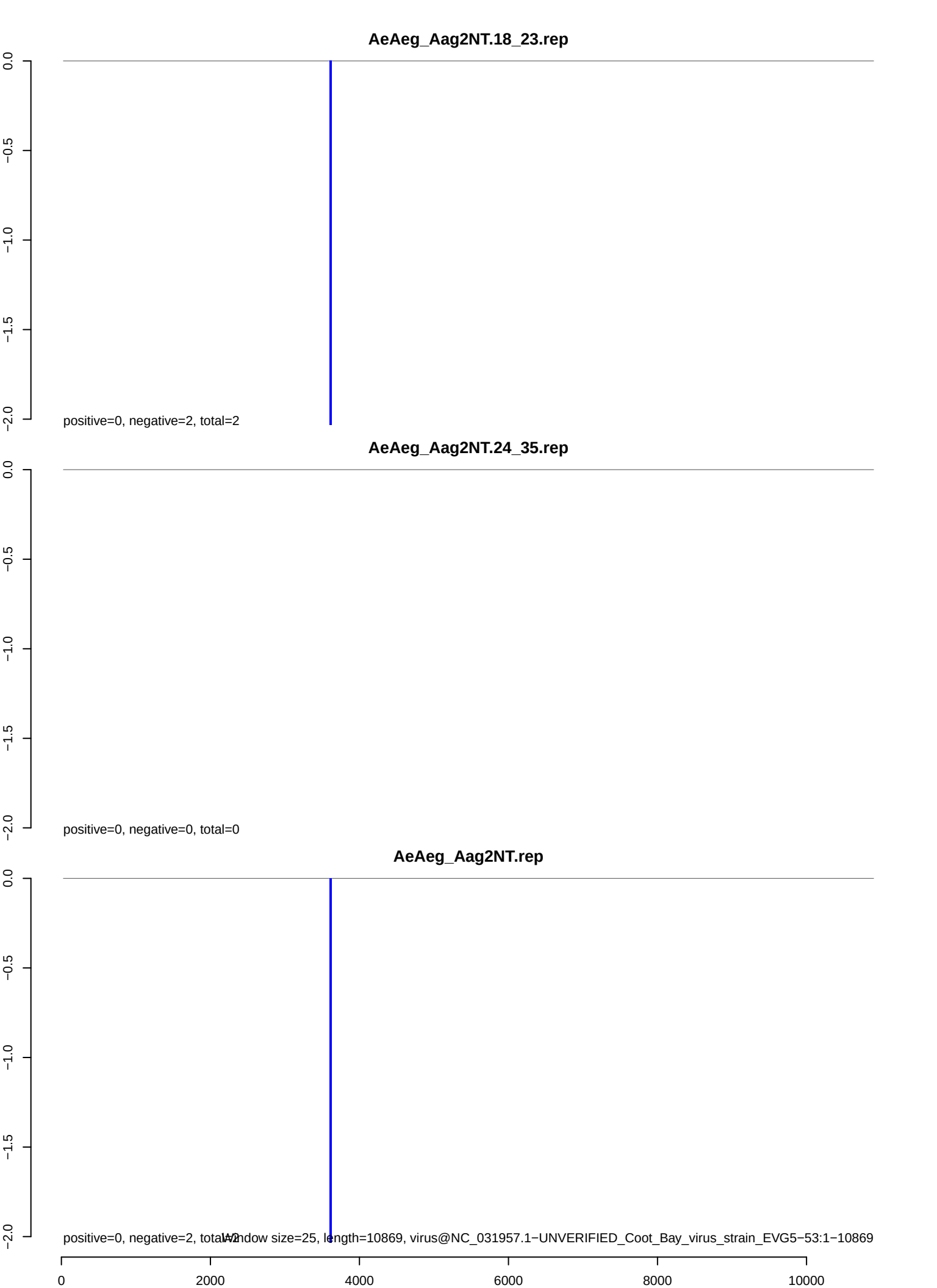

AeAeg_Aag2NT.18_23.rep
0.000
−0.005
−0.010
−0.015
−0.020
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
0.000
−0.005
−0.010
−0.015
−0.020
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.000
−0.005
−0.010
−0.015
−0.020
0
2000
4000
6000
8000
10000
12000

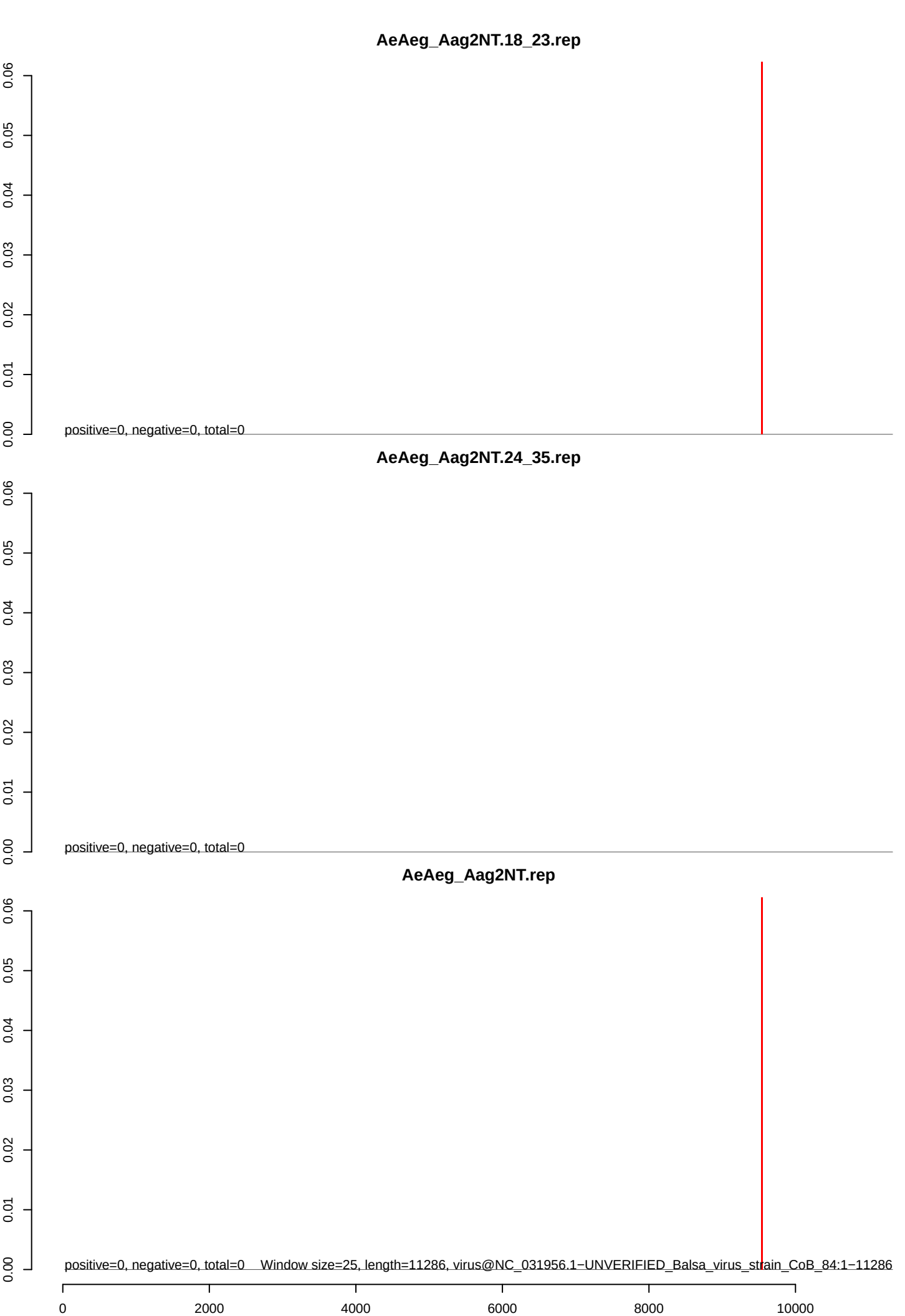

AeAeg_Aag2NT.18_23.rep
0.020
0.015
0.010
0.005
0.000
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
0.020
0.015
0.010
0.005
0.000
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.020
0.015
0.010
0.005
0.000
w size=25, length=12957, url=NC_034448.1−Mosqueiro_virus_nucleoprotein_phosphoprotein_hypothetical_proteins_matrix_glycopro:1−12957
0
2000
4000
6000
8000
10000
12000

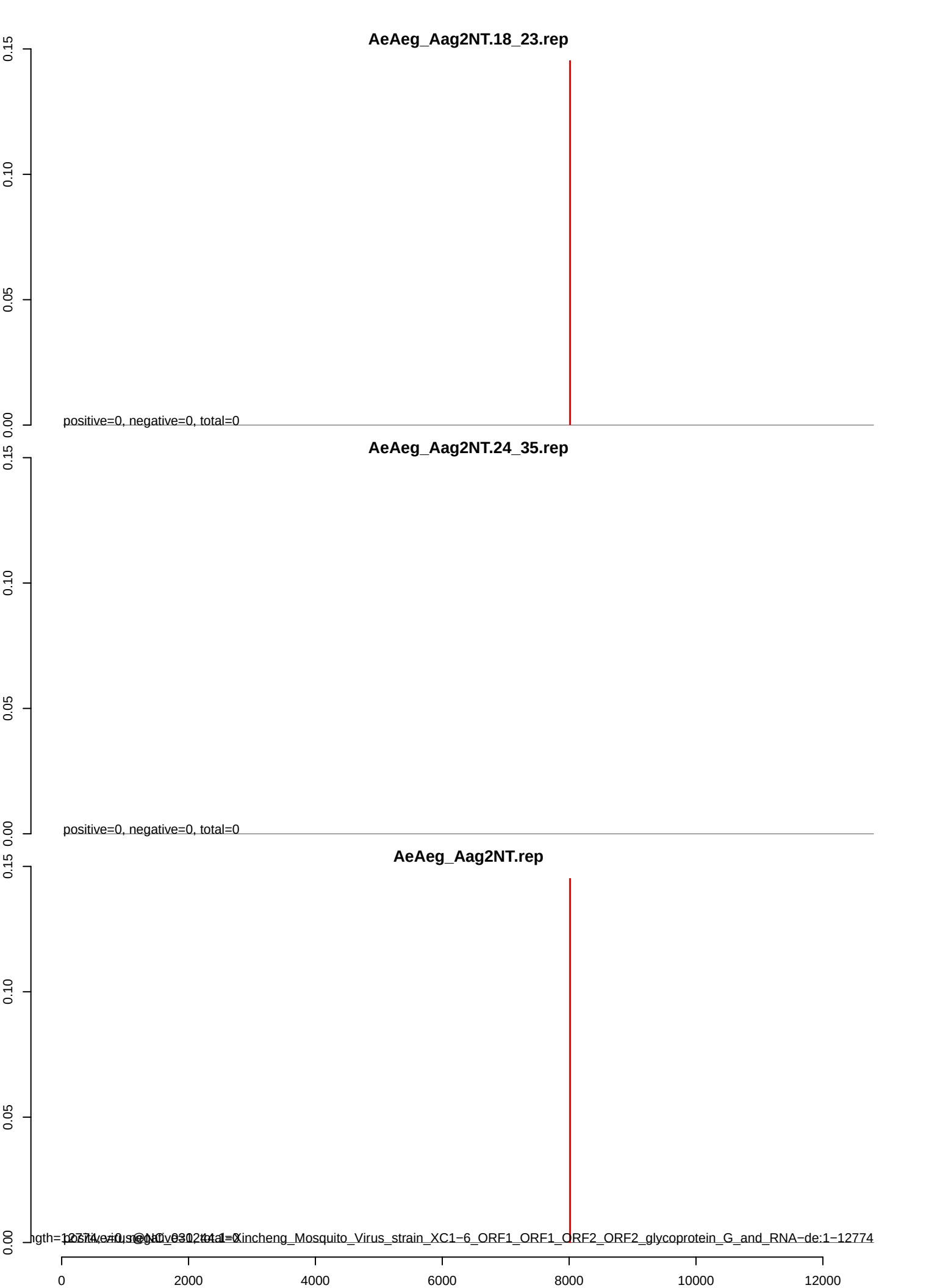

AeAeg_Aag2NT.18_23.rep
0.000
−0.005
−0.010
−0.015
−0.020
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
0.000
−0.005
−0.010
−0.015
−0.020
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.000
−0.005
−0.010
−0.015
−0.020
positive=0, negative=0, total=0
Window size=25, length=10266, virus@NC_033721.1−Meaban_virus_from_France_polyprotein_gene:1−10266
0
2000
4000
6000
8000
10000

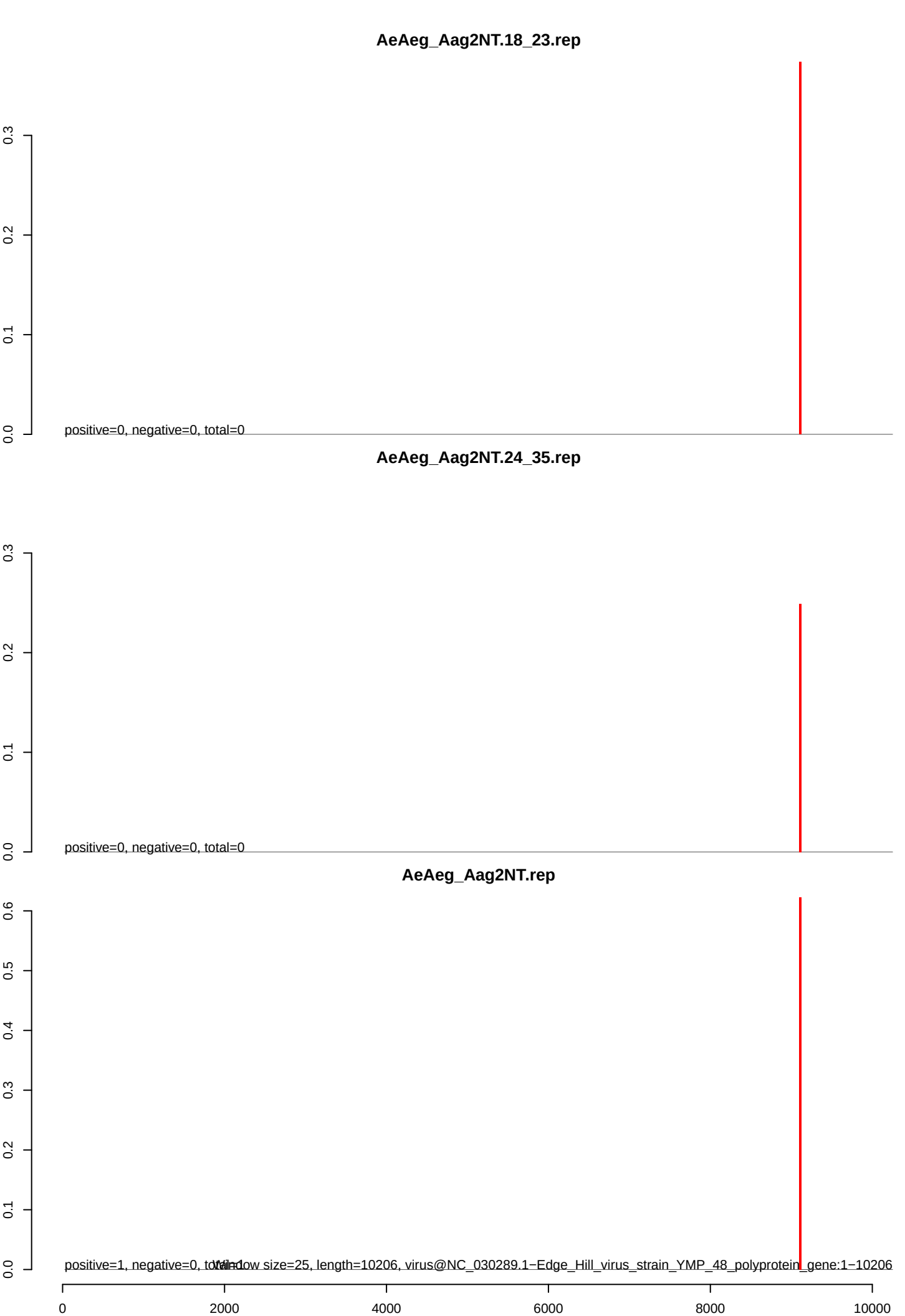

AeAeg_Aag2NT.18_23.rep
0.00
0.05
0.10
0.15
0.20
0.25
0.30
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
0.00
0.05
0.10
0.15
0.20
0.25
0.30
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.00
0.05
0.10
0.15
0.20
0.25
0.30
positive=0, negative=0, total=0
window size=25, length=10173, virus@NC_033697.1−Saboya_virus_strain_Dak_AR_D4600_polyprotein_gene:1−10173
0
2000
4000
6000
8000
10000

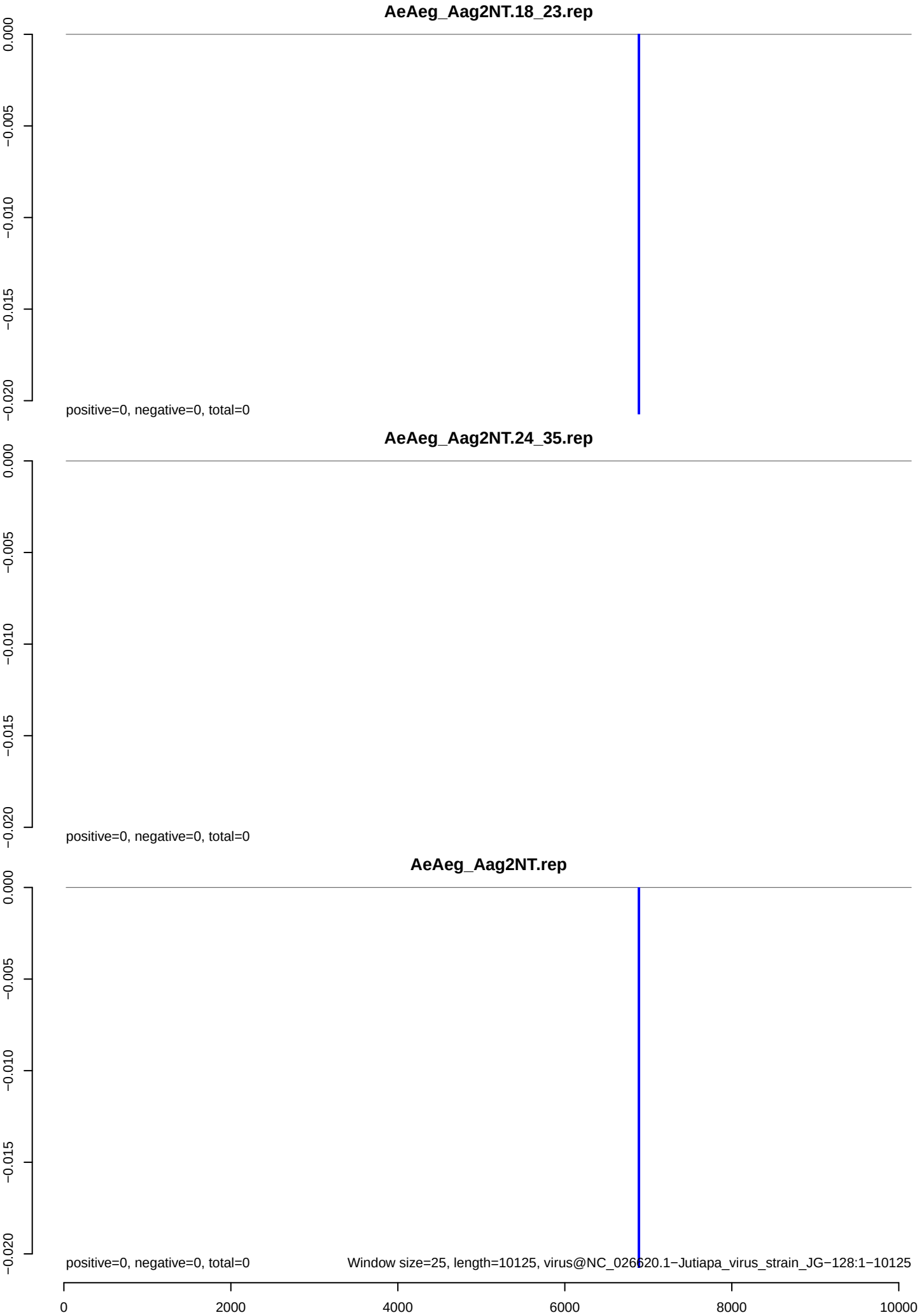

AeAeg_Aag2NT.18_23.rep
0.00
−0.01
−0.02
−0.03
−0.04
−0.05
−0.06
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
0.00
−0.01
−0.02
−0.03
−0.04
−0.05
−0.06
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.00
−0.01
−0.02
−0.03
−0.04
−0.05
−0.06
positive=0, negative=0, total=0
window size=25, length=10173, virus@NC_033693.1−Bouboui_virus_strain_DAK_AR_B490_polyprotein_gene:1−10173
0
2000
4000
6000
8000
10000

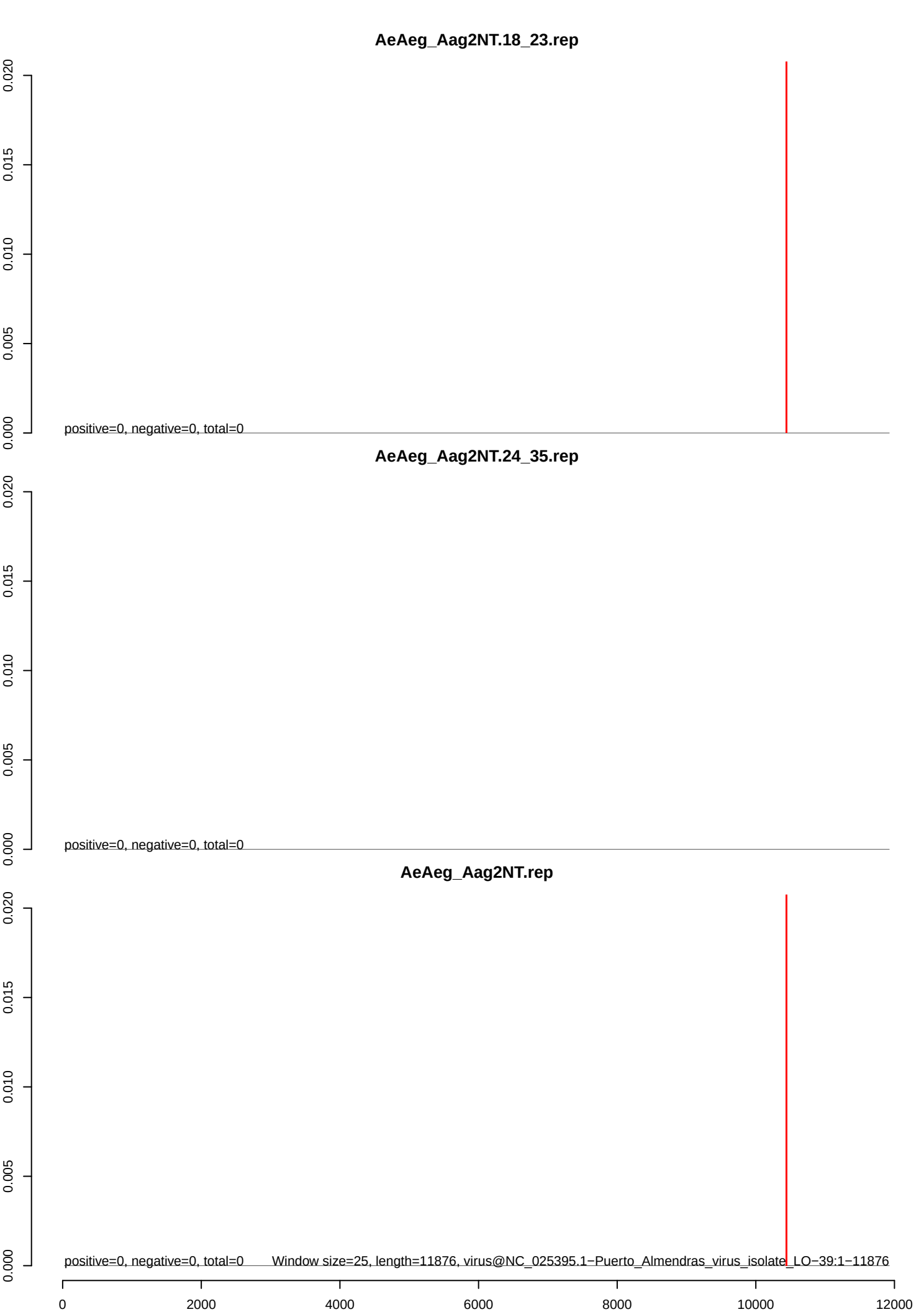

AeAeg_Aag2NT.18_23.rep
0.0
−0.5
−1.0
−1.5
−2.0
positive=0, negative=2, total=2
AeAeg_Aag2NT.24_35.rep
0.0
−0.5
−1.0
−1.5
−2.0
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.0
−0.5
−1.0
−1.5
−2.0
positive=0, negative=2, total=2
window size=25, length=10869, virus@NC_031957.1−UNVERIFIED_Coot_Bay_virus_strain_EVG5−53:1−10869
0
2000
4000
6000
8000
10000

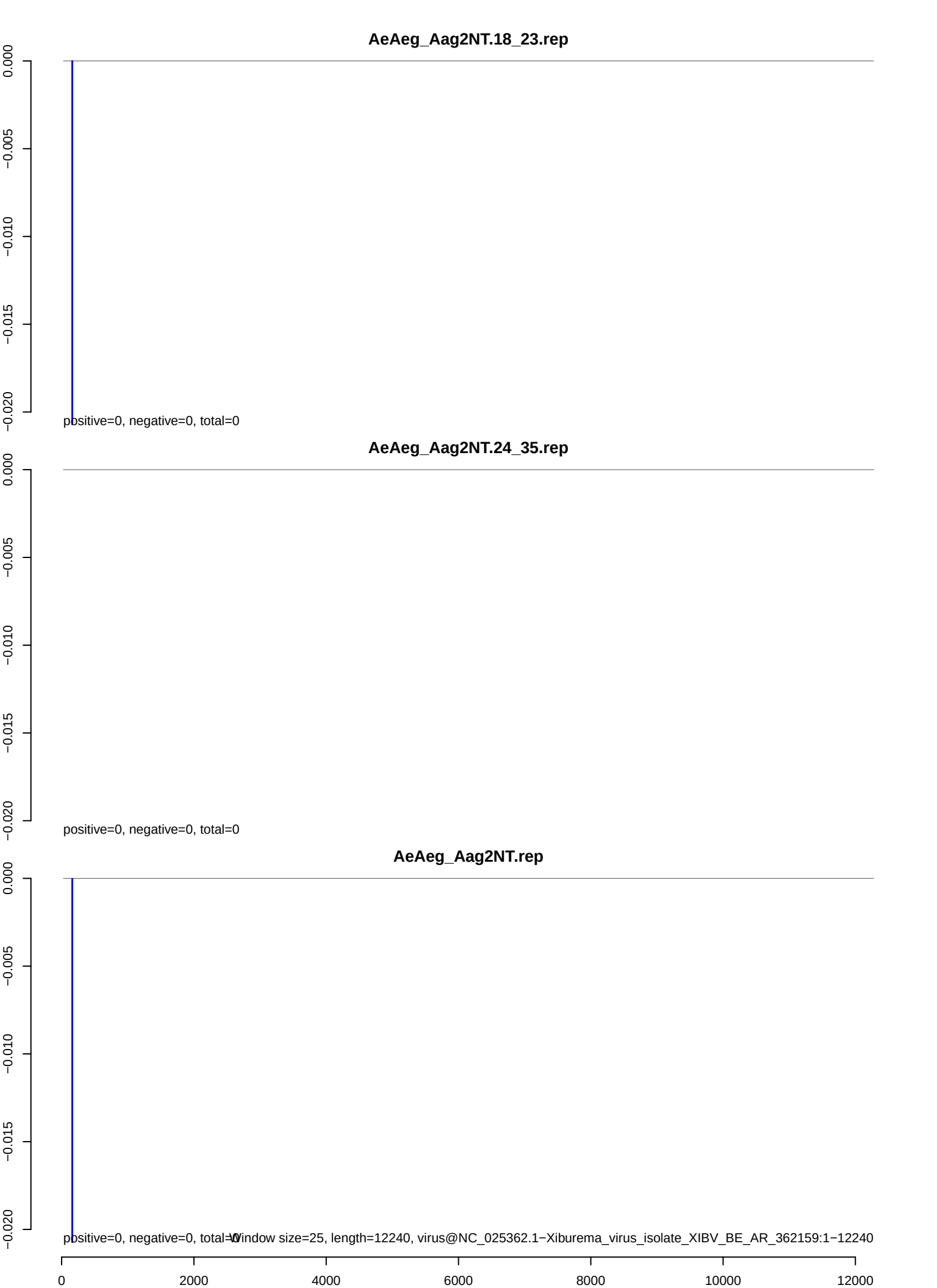

AeAeg_Aag2NT.18_23.rep
0.00
0.01
0.02
0.03
0.04
0.05
0.06
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
0.00
0.01
0.02
0.03
0.04
0.05
0.06
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.00
0.01
0.02
0.03
0.04
0.05
0.06
positive=0, negative=0, total=0 Window size=25, length=11286, virus@NC_031956.1−UNVERIFIED_Balsa_virus_strain_CoB_84:1−11286
0
2000
4000
6000
8000
10000

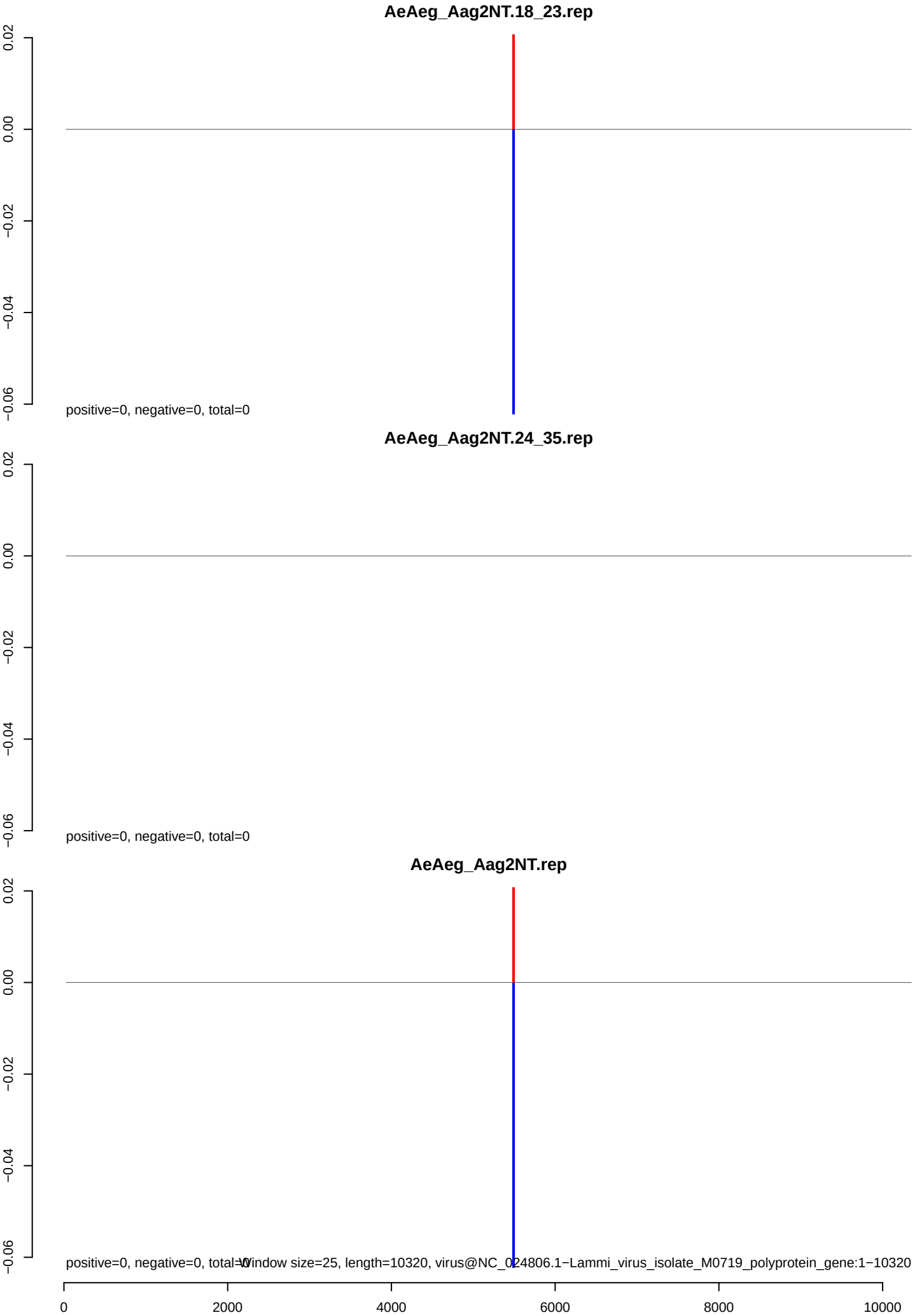

AeAeg_Aag2NT.18_23.rep
0.15
0.10
0.05
0.00
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
0.15
0.10
0.05
0.00
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.15
0.10
0.05
0.00
ngth=12774 virus@NC_030274.1=Xincheng_Mosquito_Virus_strain_XC1−6_ORF1_ORF1_ORF2_ORF2_glycoprotein_G_and_RNA−de:1−12774
0
2000
4000
6000
8000
10000
12000

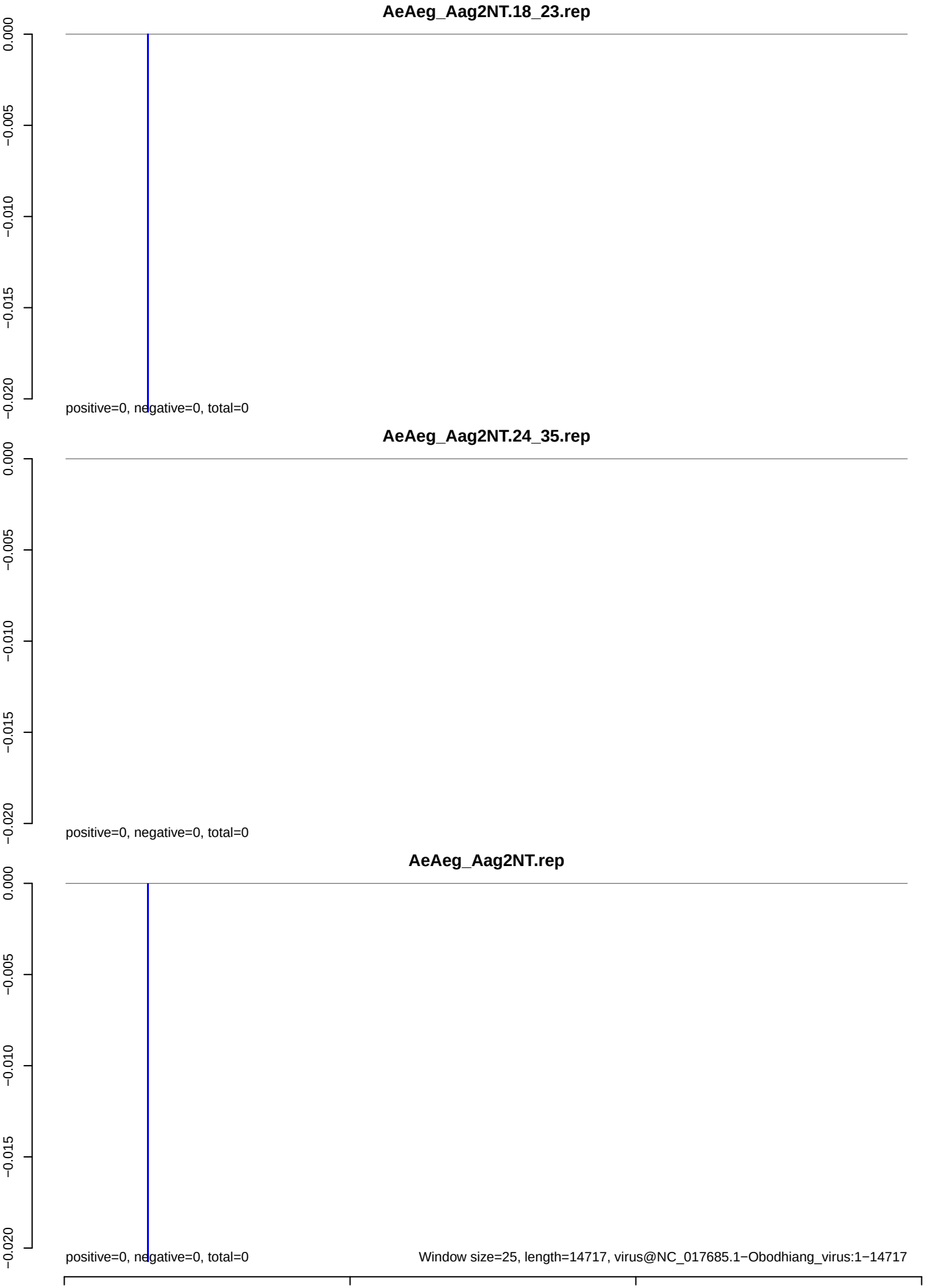

AeAeg_Aag2NT.18_23.rep
0.0
0.1
0.2
0.3
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
0.0
0.1
0.2
0.3
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.0
0.1
0.2
0.3
0.4
0.5
0.6
positive=1, negative=0, total=1
window size=25, length=10206, virus@NC_030289.1−Edge_Hill_virus_strain_YMP_48_polyprotein_gene:1−10206
0
2000
4000
6000
8000
10000

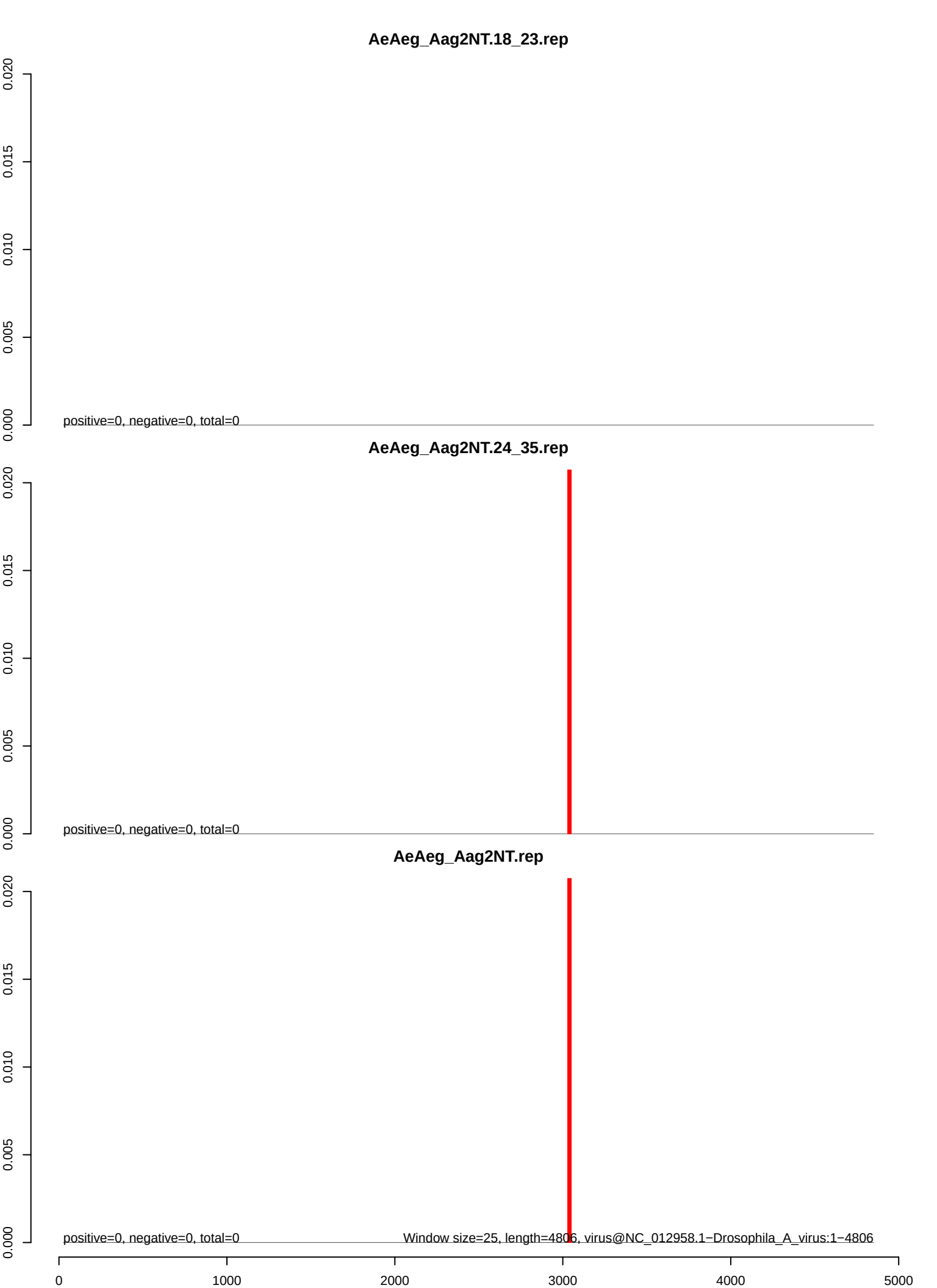

AeAeg_Aag2NT.18_23.rep
0.000
−0.005
−0.010
−0.015
−0.020
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
0.000
−0.005
−0.010
−0.015
−0.020
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.000
−0.005
−0.010
−0.015
−0.020
positive=0, negative=0, total=0
Window size=25, length=10125, virus@NC_026620.1−Jutiapa_virus_strain_JG−128:1−10125
0
2000
4000
6000
8000
10000

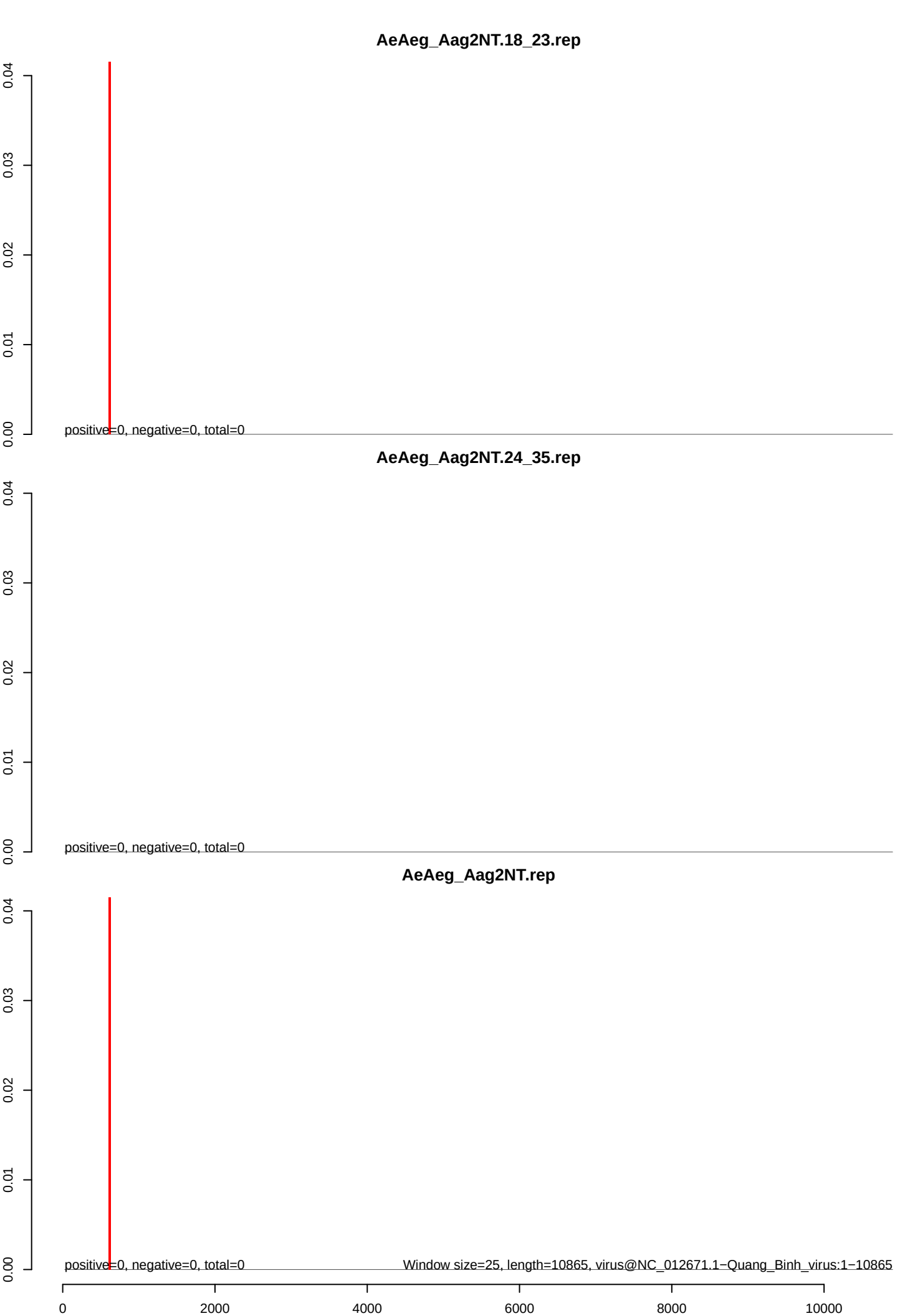

AeAeg_Aag2NT.18_23.rep
0.020
0.015
0.010
0.005
0.000
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
0.020
0.015
0.010
0.005
0.000
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.020
0.015
0.010
0.005
0.000
positive=0, negative=0, total=0
Window size=25, length=11876, virus@NC_025395.1−Puerto_Almendras_virus_isolate_LO−39:1−11876
0
2000
4000
6000
8000
10000
12000

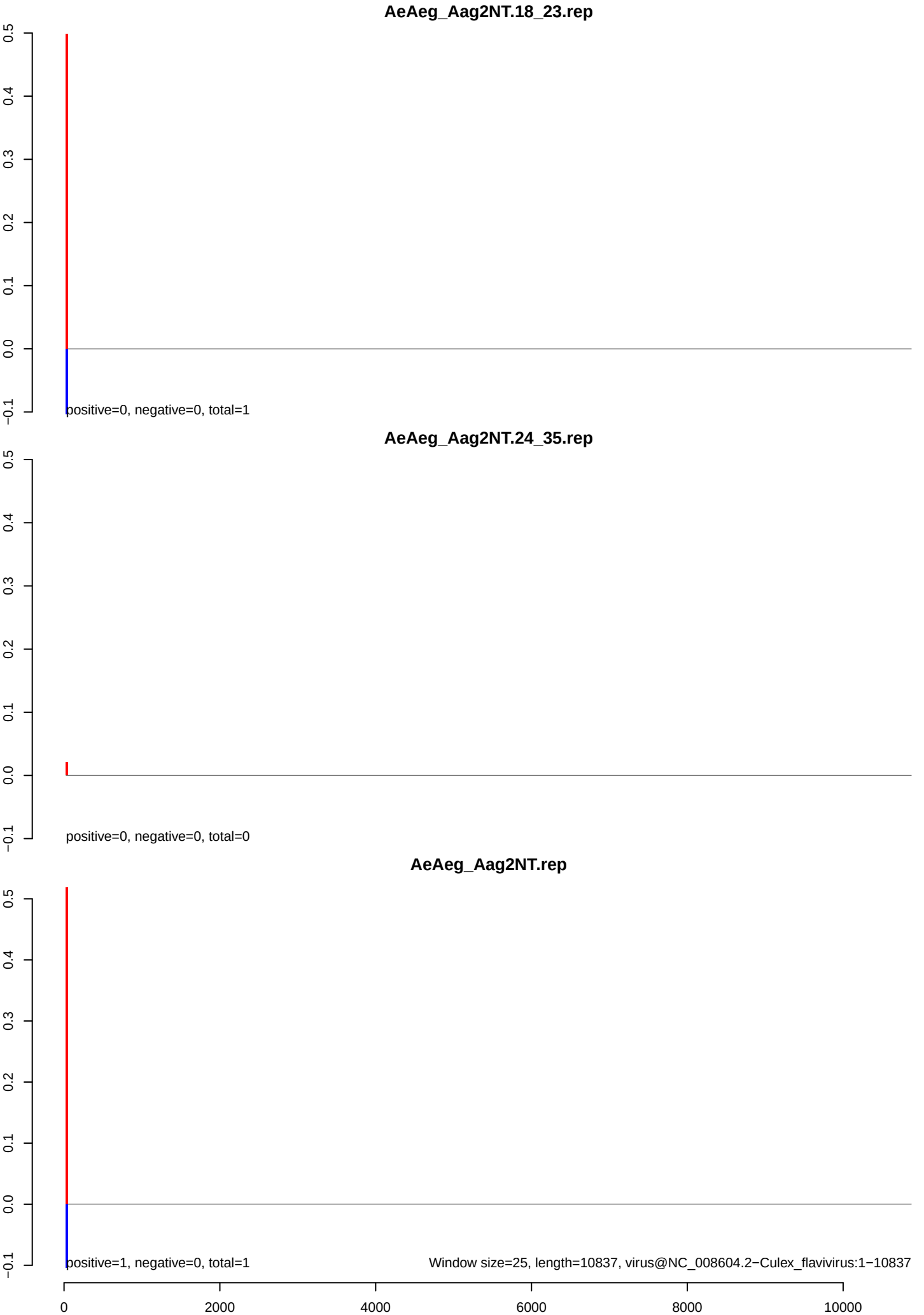

AeAeg_Aag2NT.18_23.rep
0.000
−0.005
−0.010
−0.015
−0.020
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
0.000
−0.005
−0.010
−0.015
−0.020
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.000
−0.005
−0.010
−0.015
−0.020
positive=0, negative=0, total=0
Window size=25, length=12240, virus@NC_025362.1−Xiburema_virus_isolate_XIBV_BE_AR_362159:1−12240
0
2000
4000
6000
8000
10000
12000

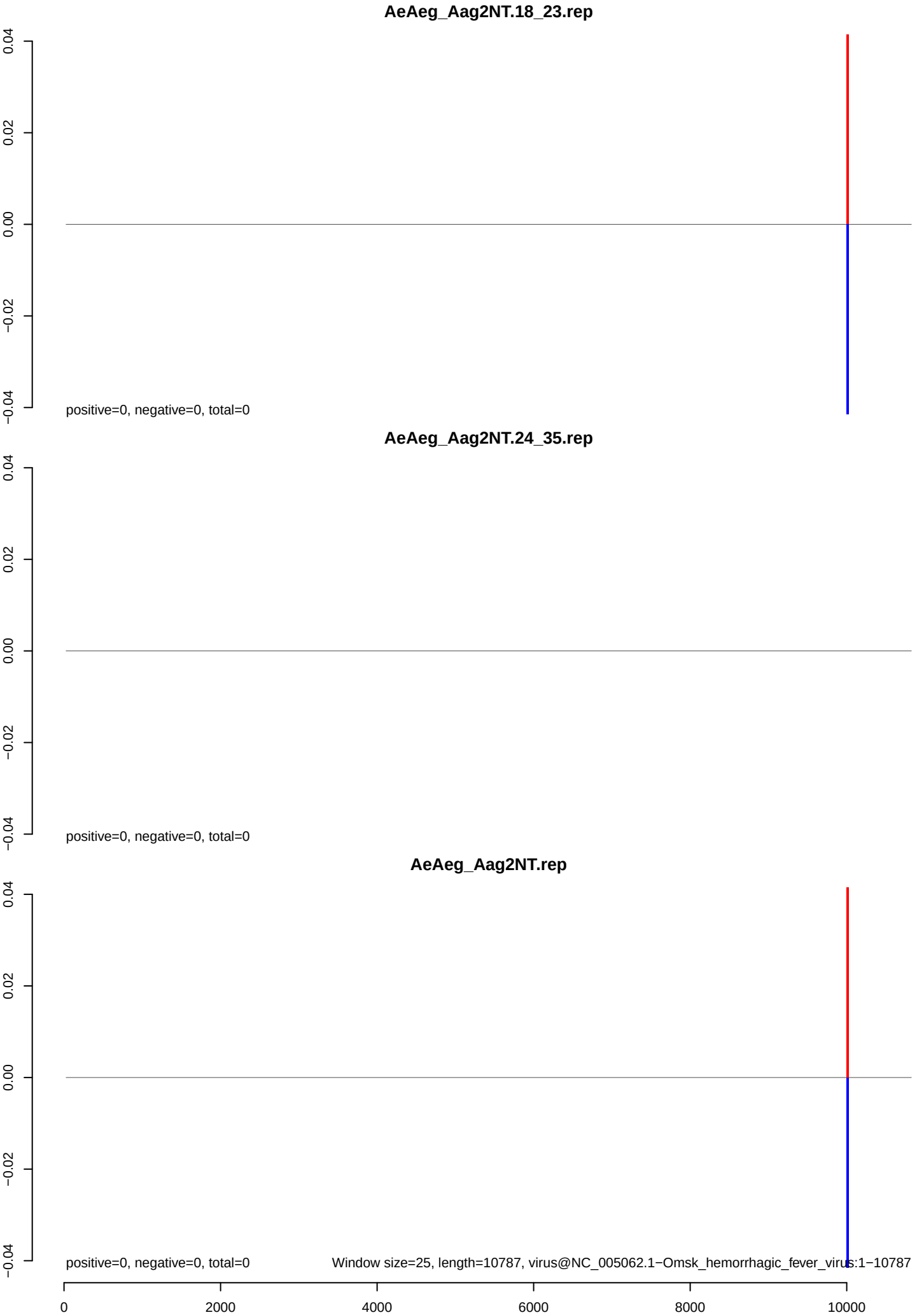

AeAeg_Aag2NT.18_23.rep
0.02
0.00
−0.02
−0.04
−0.06
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
0.02
0.00
−0.02
−0.04
−0.06
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.02
0.00
−0.02
−0.04
−0.06
positive=0, negative=0, total=0
Window size=25, length=10320, virus@NC_024806.1−Lammi_virus_isolate_M0719_polyprotein_gene:1−10320
0
2000
4000
6000
8000
10000

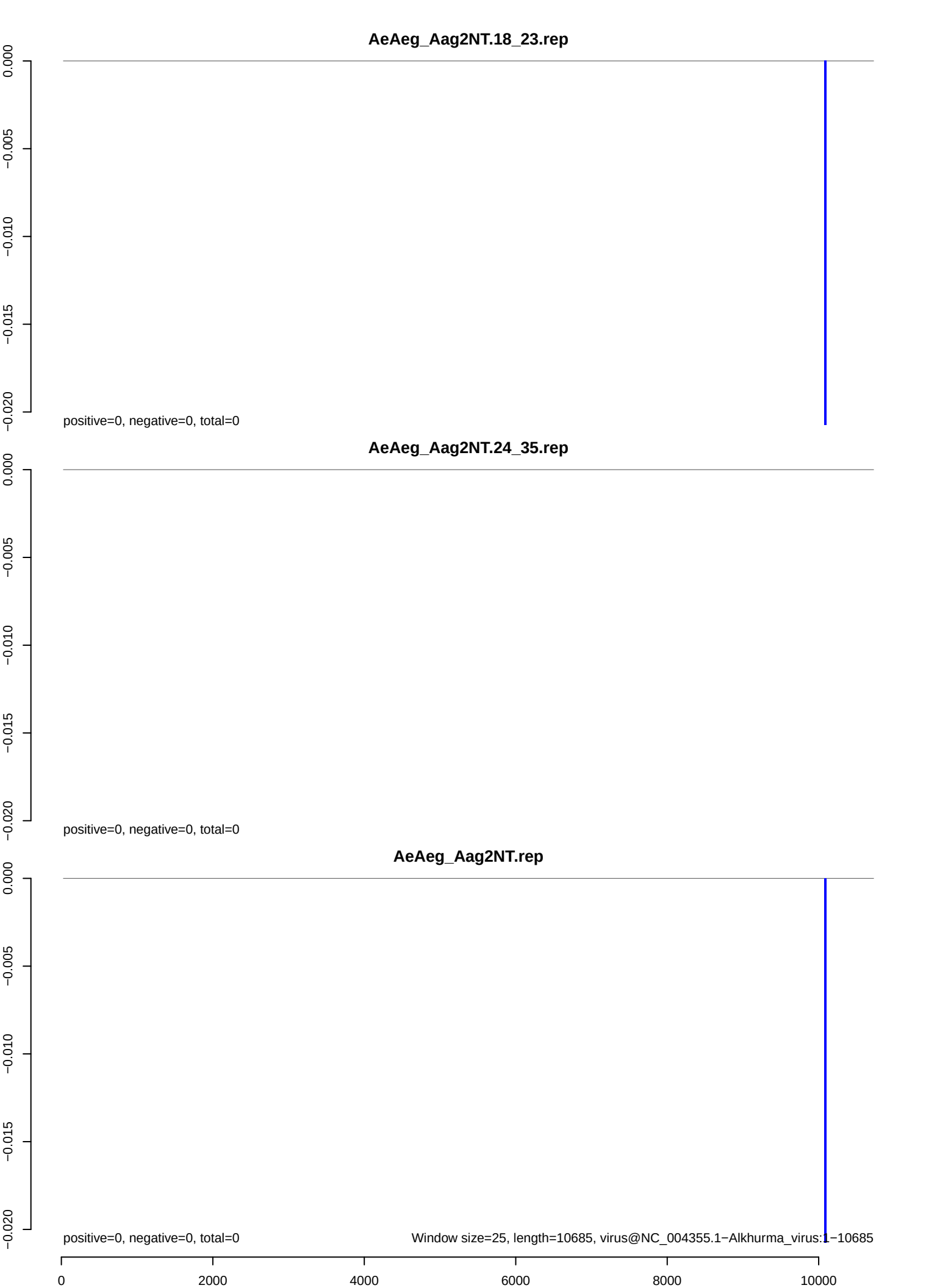

AeAeg_Aag2NT.18_23.rep
0.000
−0.005
−0.010
−0.015
−0.020
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
0.000
−0.005
−0.010
−0.015
−0.020
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.000
−0.005
−0.010
−0.015
−0.020
positive=0, negative=0, total=0
Window size=25, length=14717, virus@NC_017685.1−Obodhiang_virus:1−14717
0
5000
10000
15000

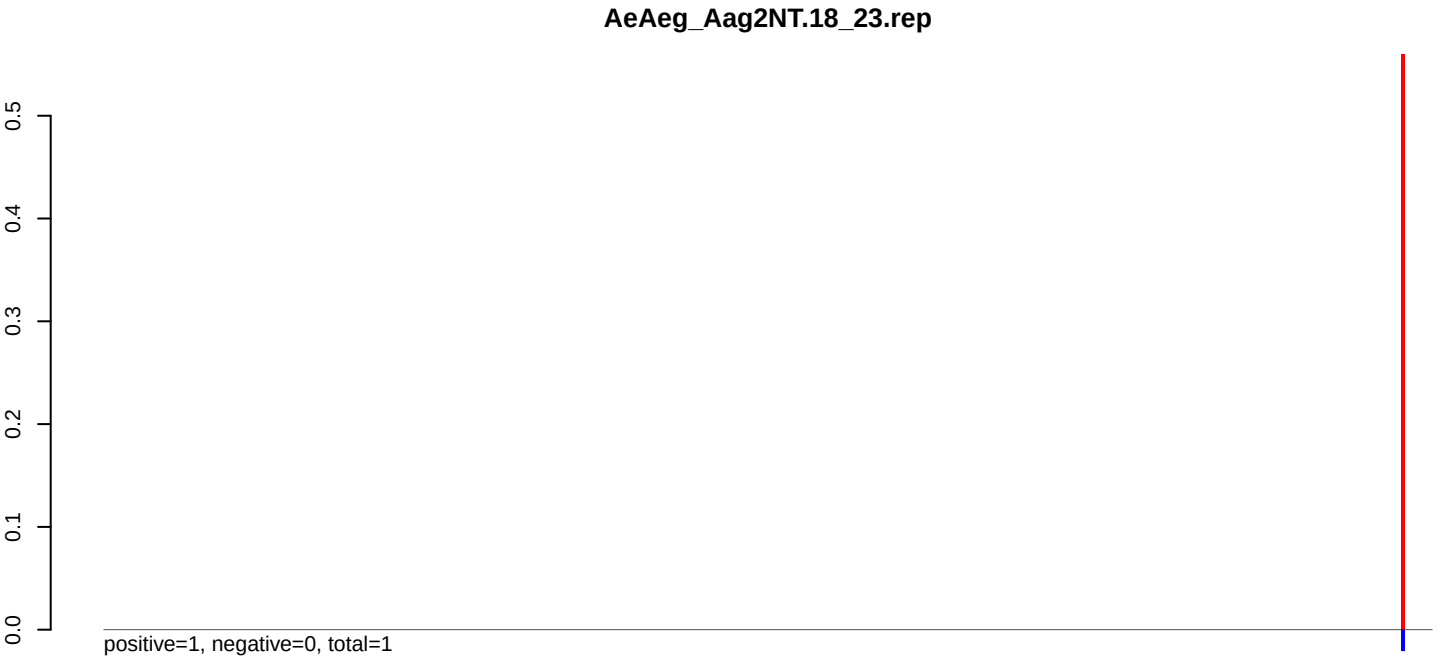

AeAeg_Aag2NT.18_23.rep
0.020
0.015
0.010
0.005
0.000
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
0.020
0.015
0.010
0.005
0.000
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.020
0.015
0.010
0.005
0.000
positive=0, negative=0, total=0
Window size=25, length=4806, virus@NC_012958.1−Drosophila_A_virus:1−4806
0
1000
2000
3000
4000
5000

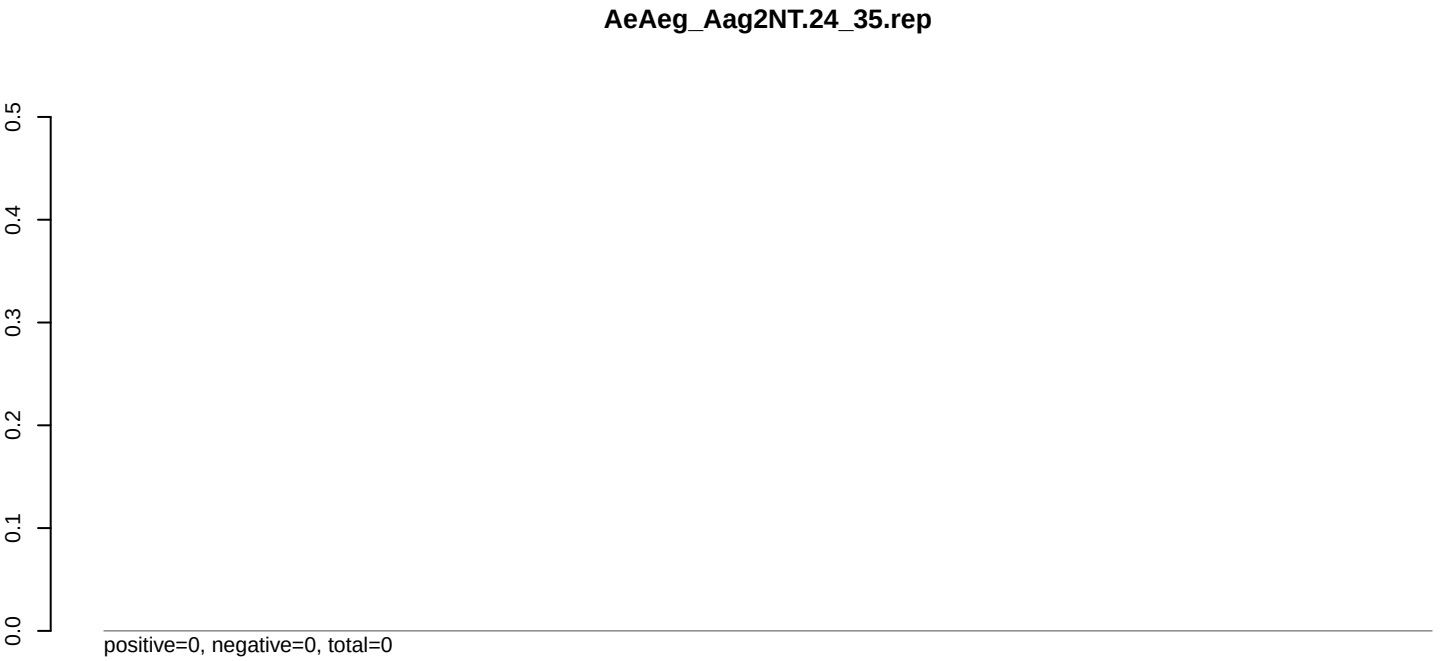

AeAeg_Aag2NT.18_23.rep
0.04
0.03
0.02
0.01
0.00
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
0.04
0.03
0.02
0.01
0.00
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.04
0.03
0.02
0.01
0.00
positive=0, negative=0, total=0
Window size=25, length=10865, virus@NC_012671.1−Quang_Binh_virus:1−10865
0
2000
4000
6000
8000
10000

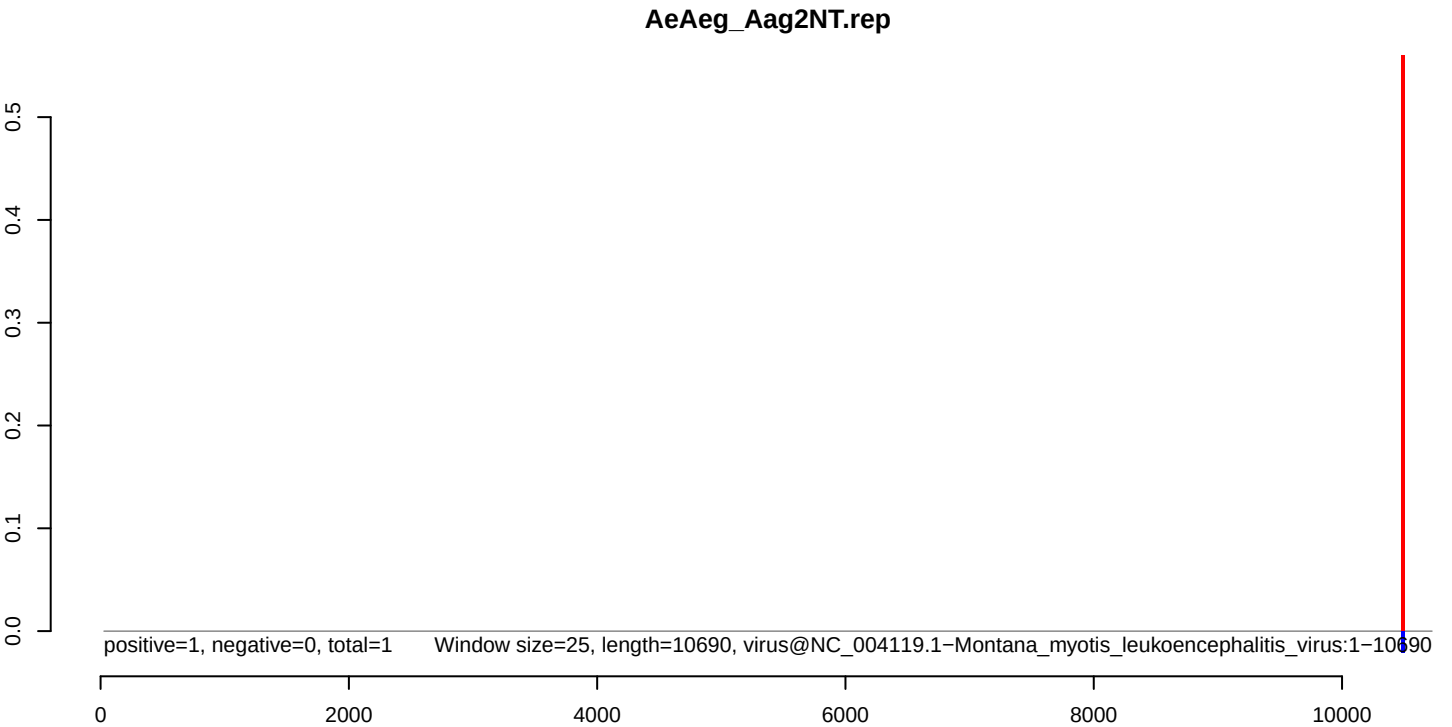

AeAeg_Aag2NT.18_23.rep
0.5
0.4
0.3
0.2
0.1
0.0
−0.1
positive=0, negative=0, total=1
AeAeg_Aag2NT.24_35.rep
0.5
0.4
0.3
0.2
0.1
0.0
−0.1
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.5
0.4
0.3
0.2
0.1
0.0
−0.1
positive=1, negative=0, total=1
Window size=25, length=10837, virus@NC_008604.2−Culex_flavivirus:1−10837
0
2000
4000
6000
8000
10000

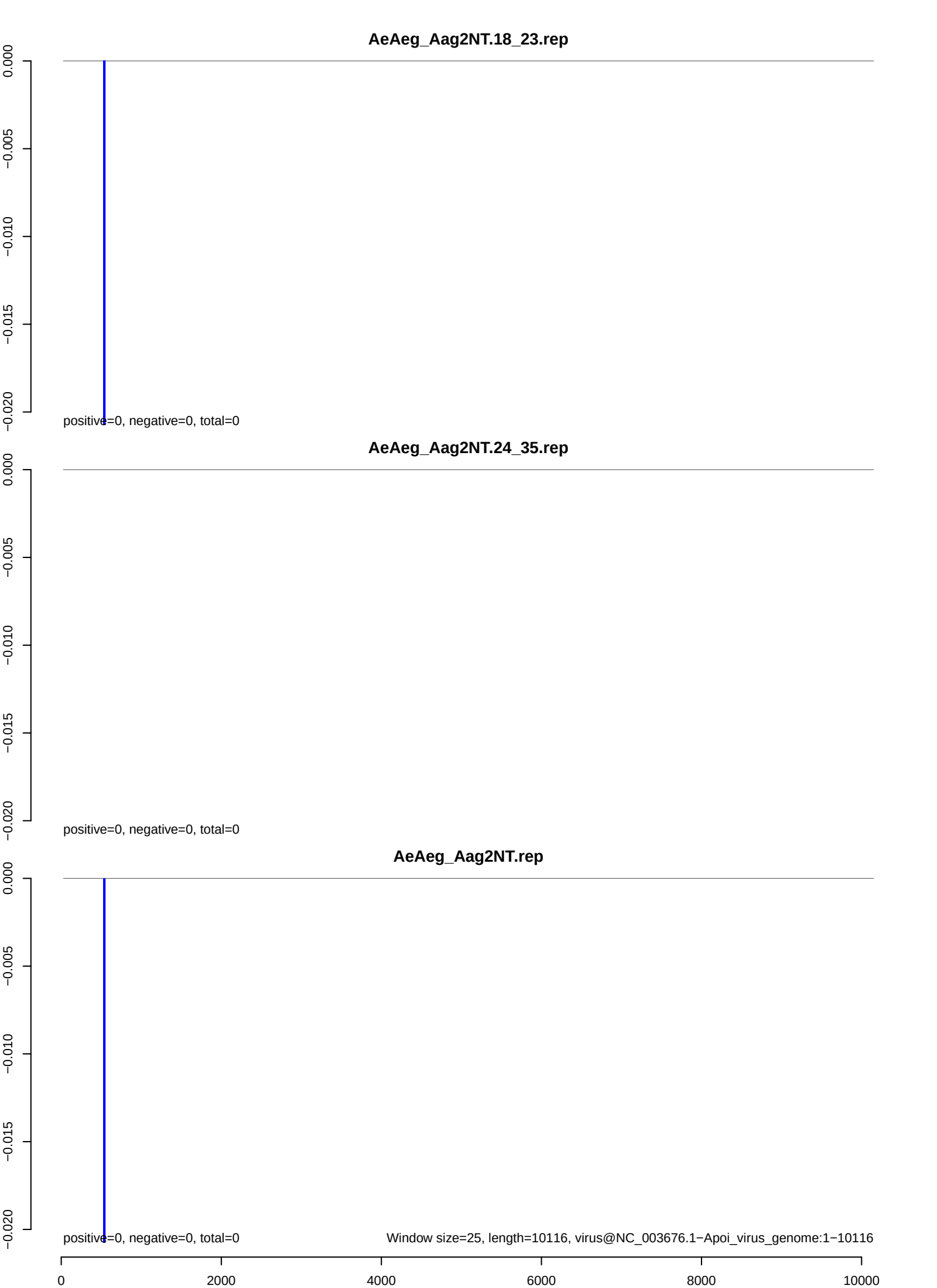

AeAeg_Aag2NT.18_23.rep
0.04
0.02
0.00
−0.02
−0.04
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
0.04
0.02
0.00
−0.02
−0.04
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.04
0.02
0.00
−0.02
−0.04
positive=0, negative=0, total=0
Window size=25, length=10787, virus@NC_005062.1−Omsk_hemorrhagic_fever_virus:1−10787
0
2000
4000
6000
8000
10000

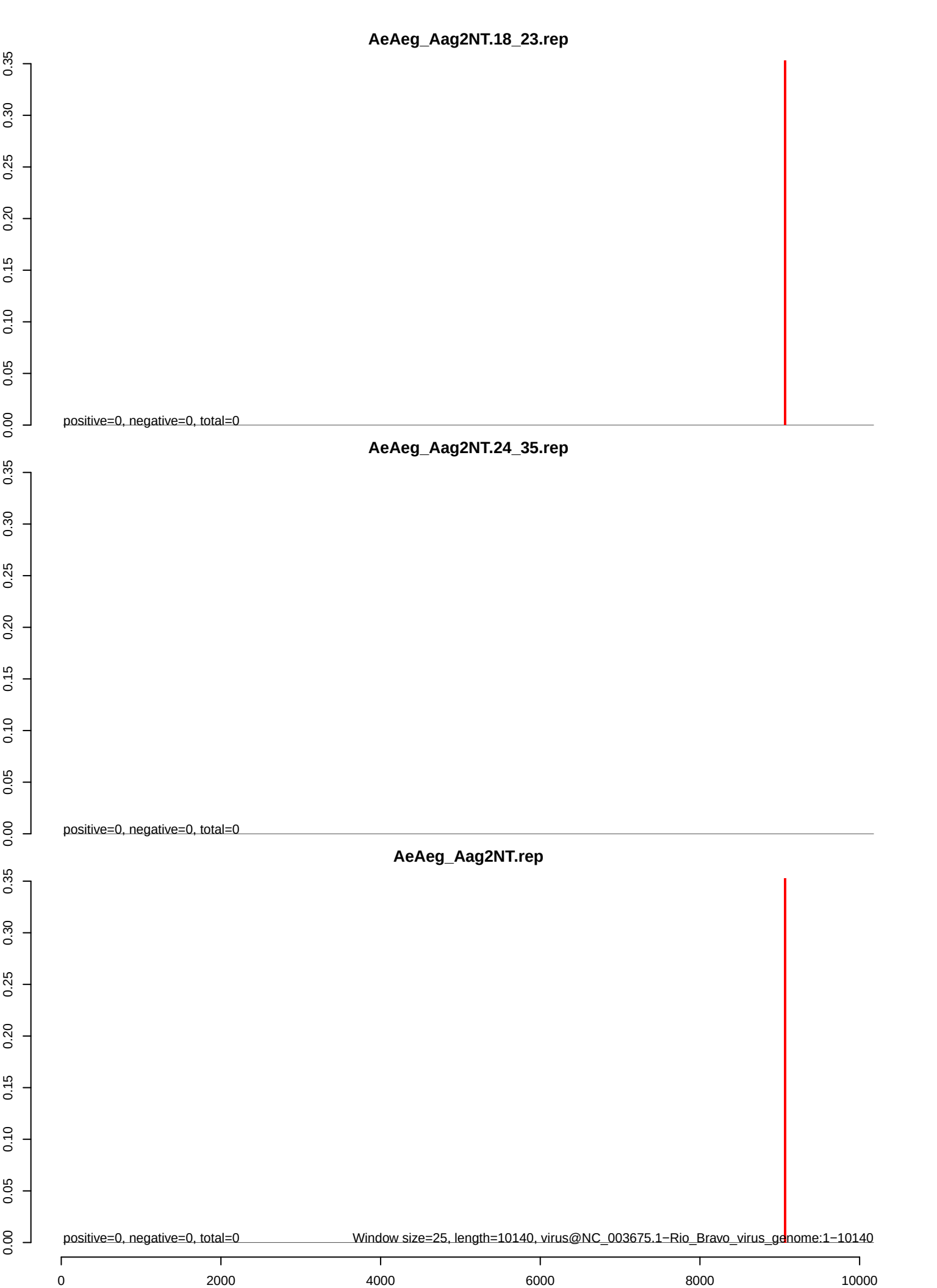

AeAeg_Aag2NT.18_23.rep
0.000
−0.005
−0.010
−0.015
−0.020
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
0.000
−0.005
−0.010
−0.015
−0.020
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.000
−0.005
−0.010
−0.015
−0.020
positive=0, negative=0, total=0
Window size=25, length=10685, virus@NC_004355.1−Alkhurma_virus:1−10685
0
2000
4000
6000
8000
10000

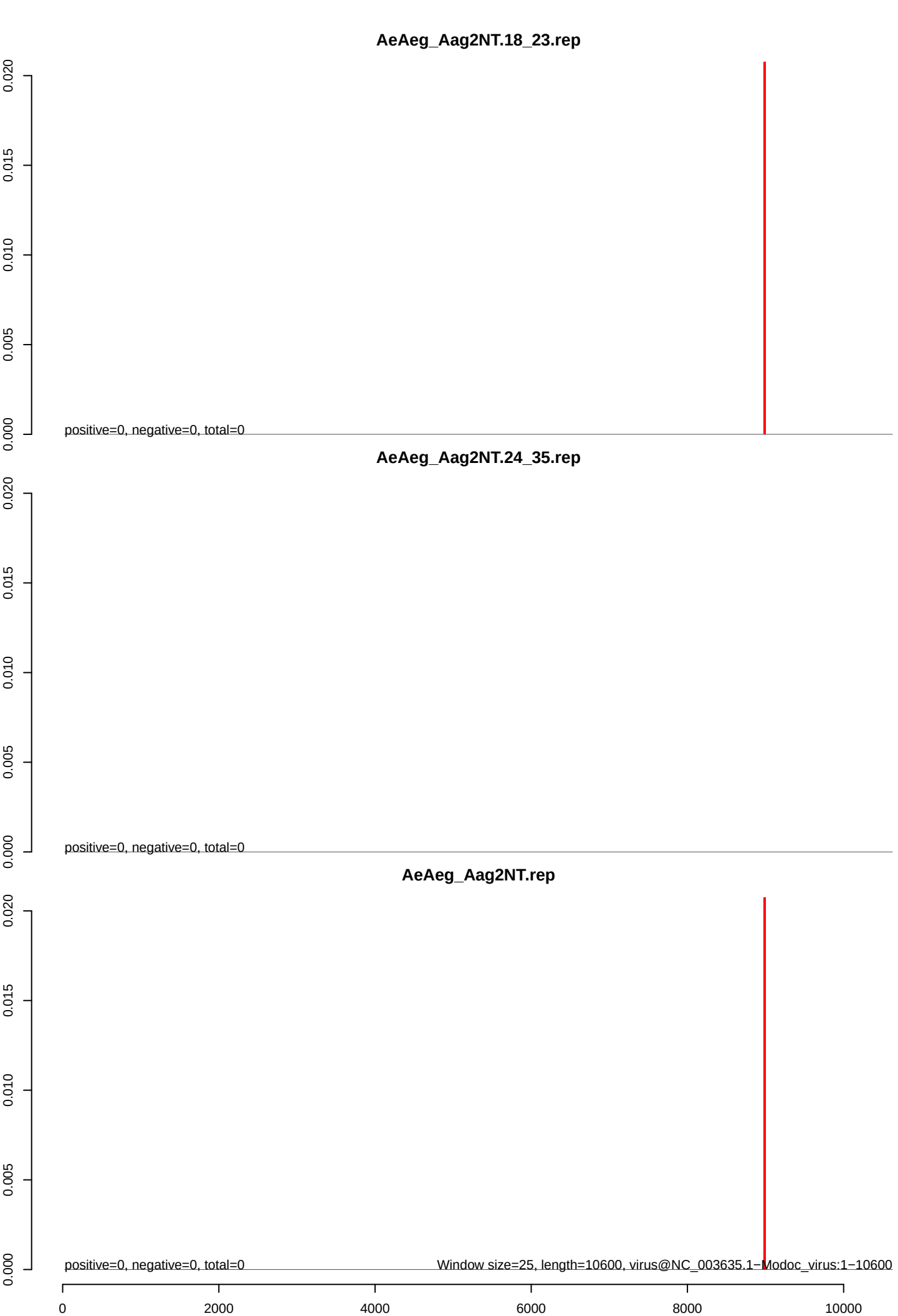

AeAeg_Aag2NT.18_23.rep
0.0
0.1
0.2
0.3
0.4
0.5
positive=1, negative=0, total=1

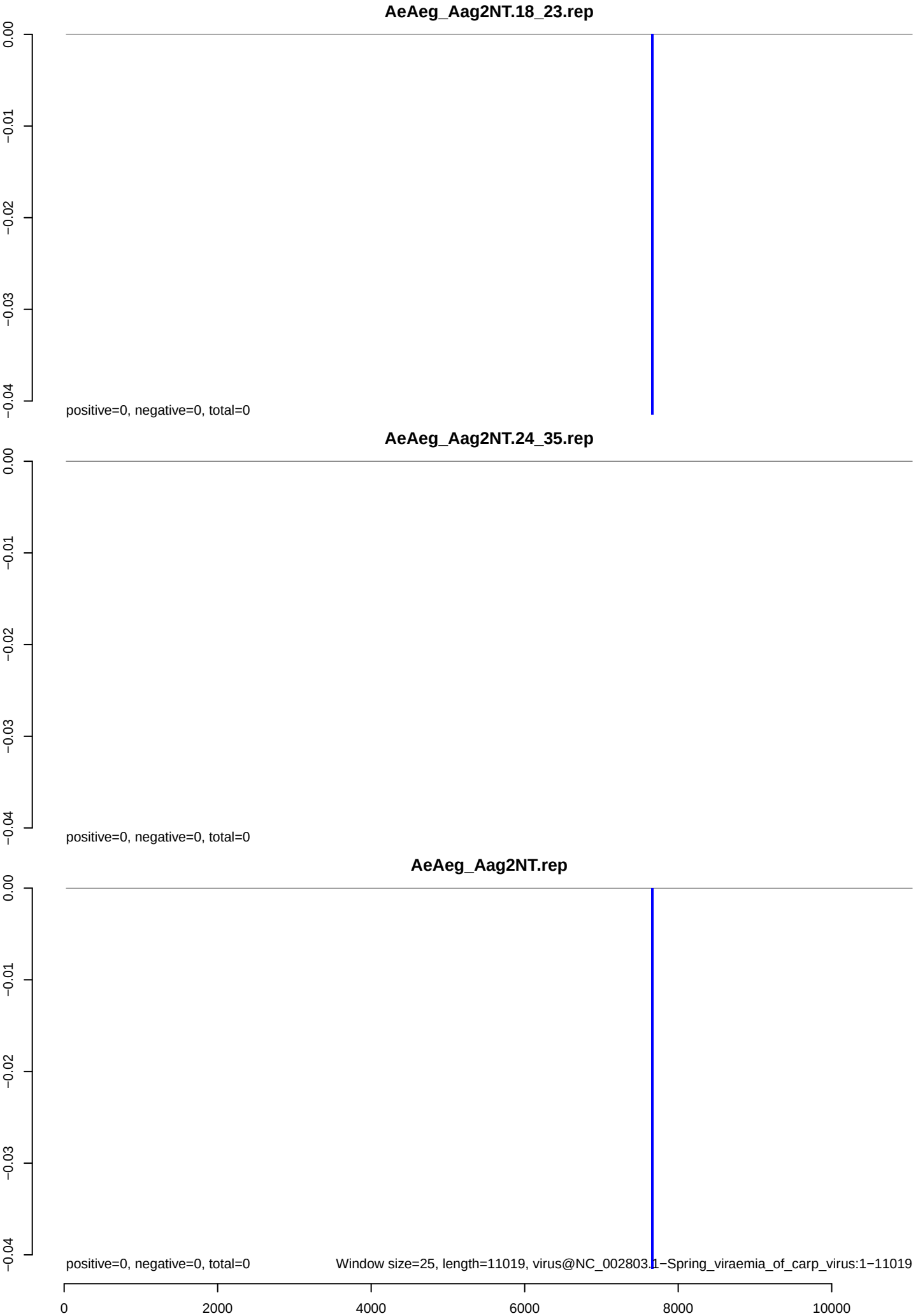

AeAeg_Aag2NT.24_35.rep
0.0
0.1
0.2
0.3
0.4
0.5
positive=0, negative=0, total=0

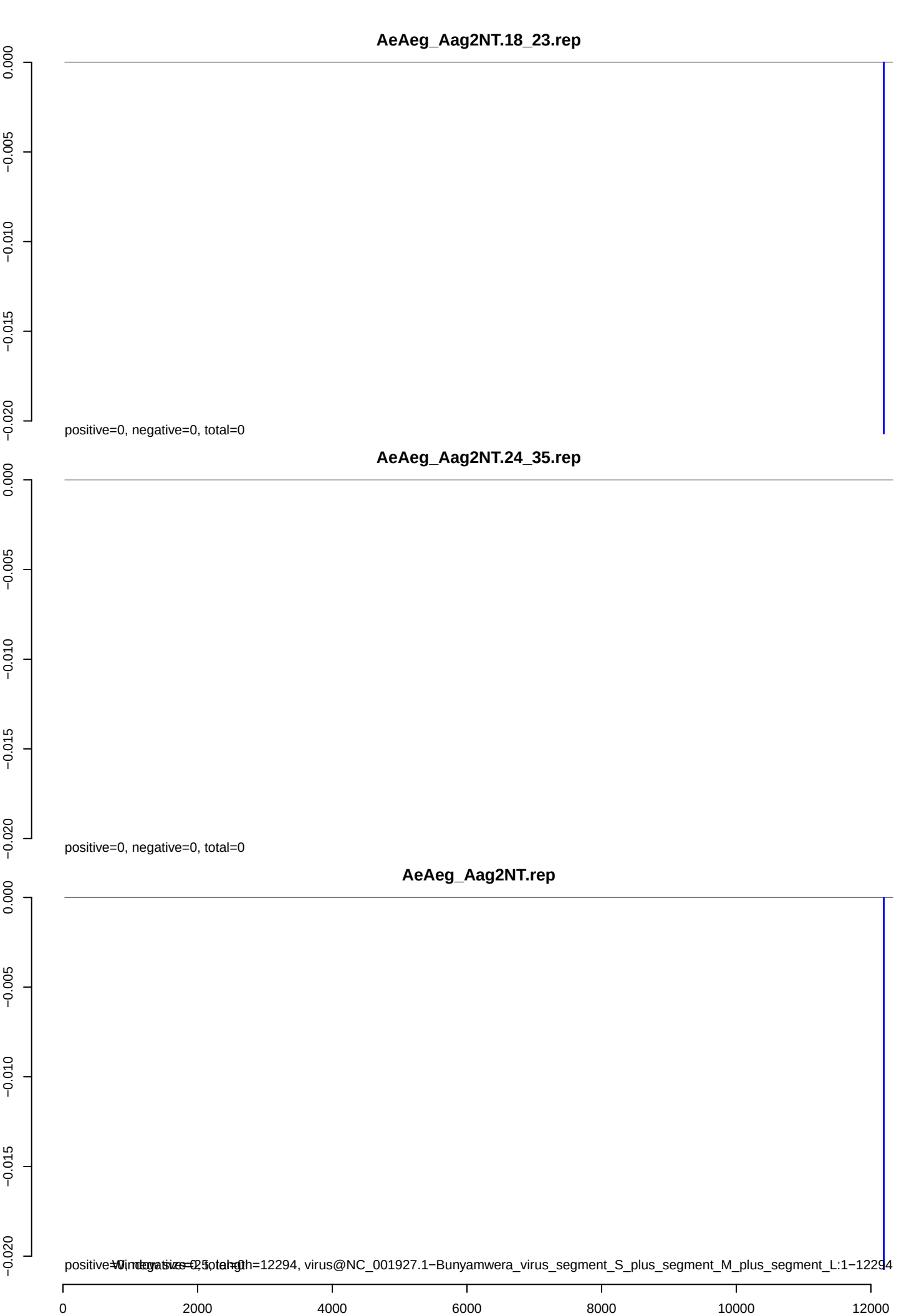

AeAeg_Aag2NT.rep
0.0
0.1
0.2
0.3
0.4
0.5
positive=1, negative=0, total=1
Window size=25, length=10690, virus@NC_004119.1−Montana_myotis_leukoencephalitis_virus:1−10690
0
2000
4000
6000
8000
10000

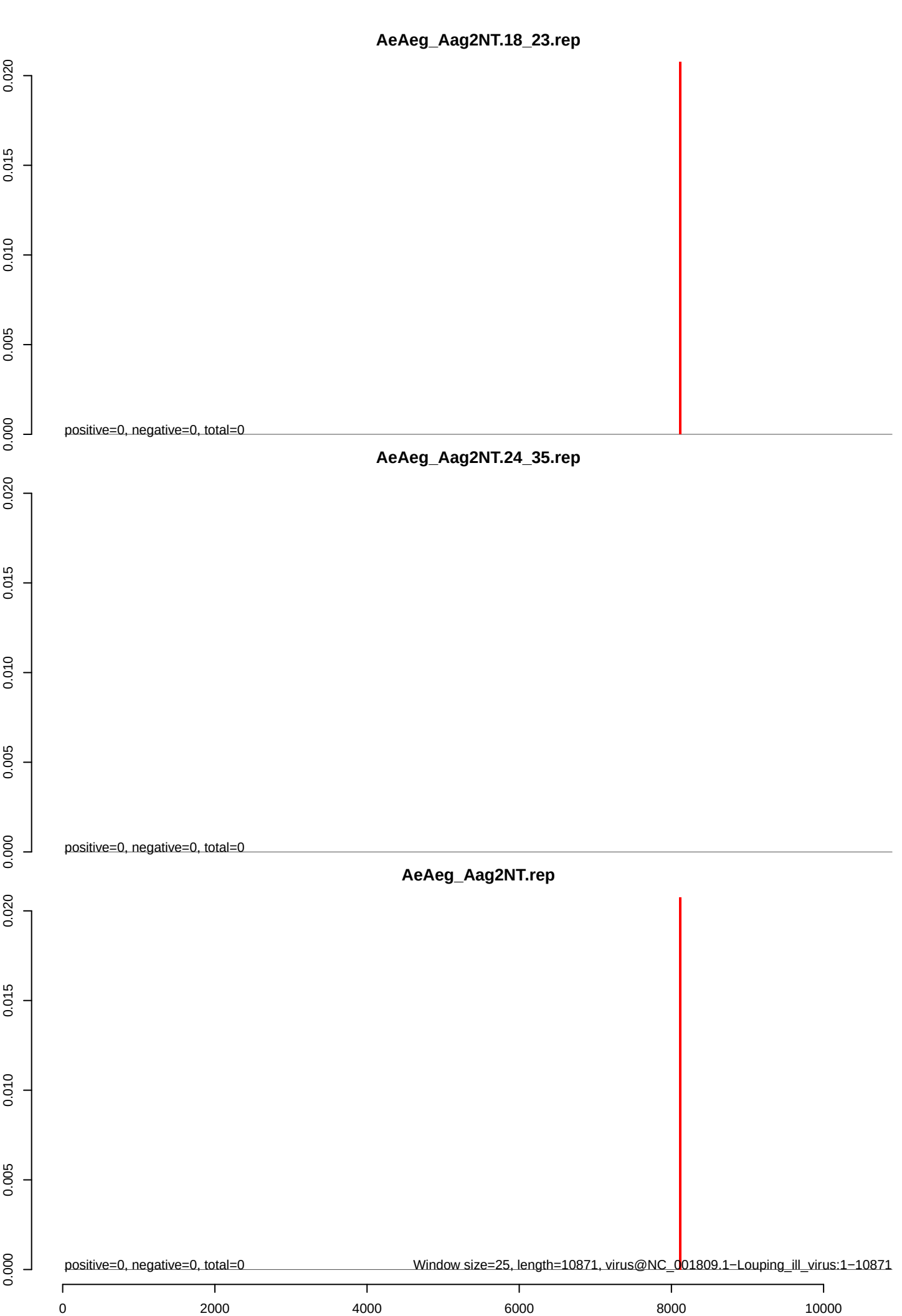

AeAeg_Aag2NT.18_23.rep
0.000
−0.005
−0.010
−0.015
−0.020
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
0.000
−0.005
−0.010
−0.015
−0.020
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.000
−0.005
−0.010
−0.015
−0.020
positive=0, negative=0, total=0
Window size=25, length=10116, virus@NC_003676.1−Apoi_virus_genome:1−10116
0
2000
4000
6000
8000
10000

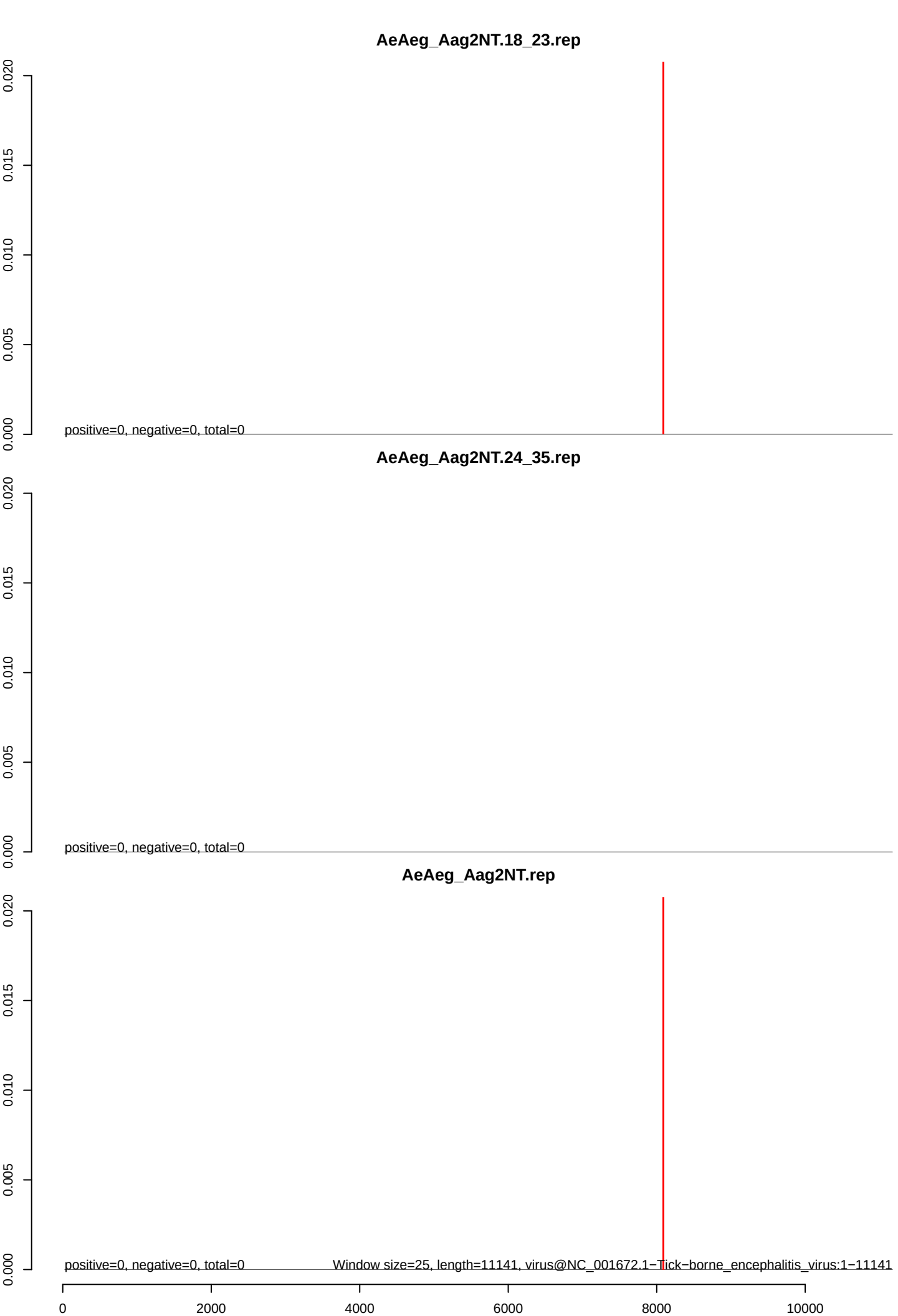

AeAeg_Aag2NT.18_23.rep
0.00
0.05
0.10
0.15
0.20
0.25
0.30
0.35
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
0.00
0.05
0.10
0.15
0.20
0.25
0.30
0.35
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.00
0.05
0.10
0.15
0.20
0.25
0.30
0.35
positive=0, negative=0, total=0
Window size=25, length=10140, virus@NC_003675.1−Rio_Bravo_virus_genome:1−10140
0
2000
4000
6000
8000
10000

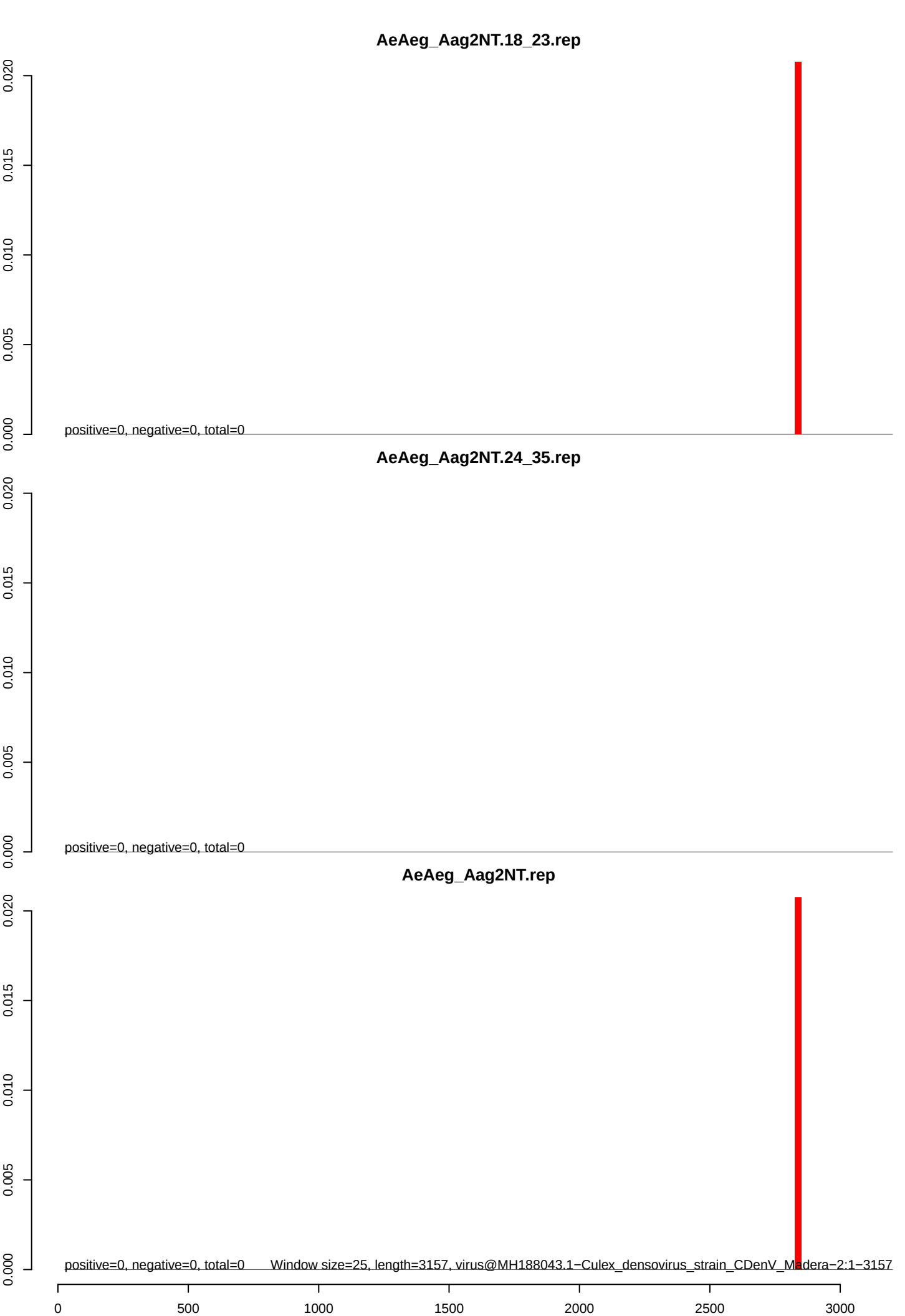

AeAeg_Aag2NT.18_23.rep
0.020
0.015
0.010
0.005
0.000
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
0.020
0.015
0.010
0.005
0.000
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.020
0.015
0.010
0.005
0.000
positive=0, negative=0, total=0
Window size=25, length=10600, virus@NC_003635.1−Modoc_virus:1−10600
0
2000
4000
6000
8000
10000

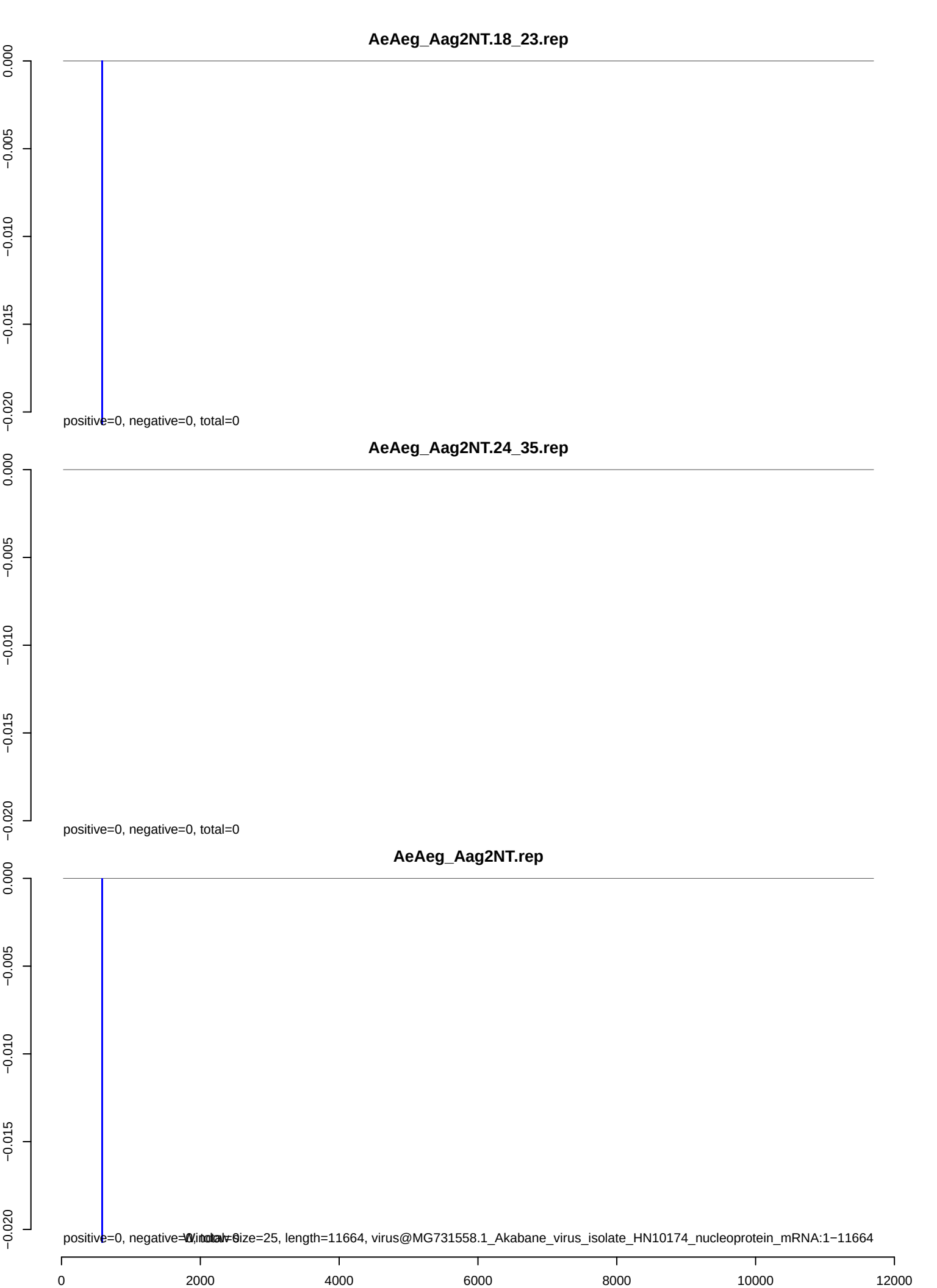

AeAeg_Aag2NT.18_23.rep
0.00
−0.01
−0.02
−0.03
−0.04
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
0.00
−0.01
−0.02
−0.03
−0.04
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.00
−0.01
−0.02
−0.03
−0.04
positive=0, negative=0, total=0
Window size=25, length=11019, virus@NC_002803.1−Spring_viraemia_of_carp_virus:1−11019
0
2000
4000
6000
8000
10000

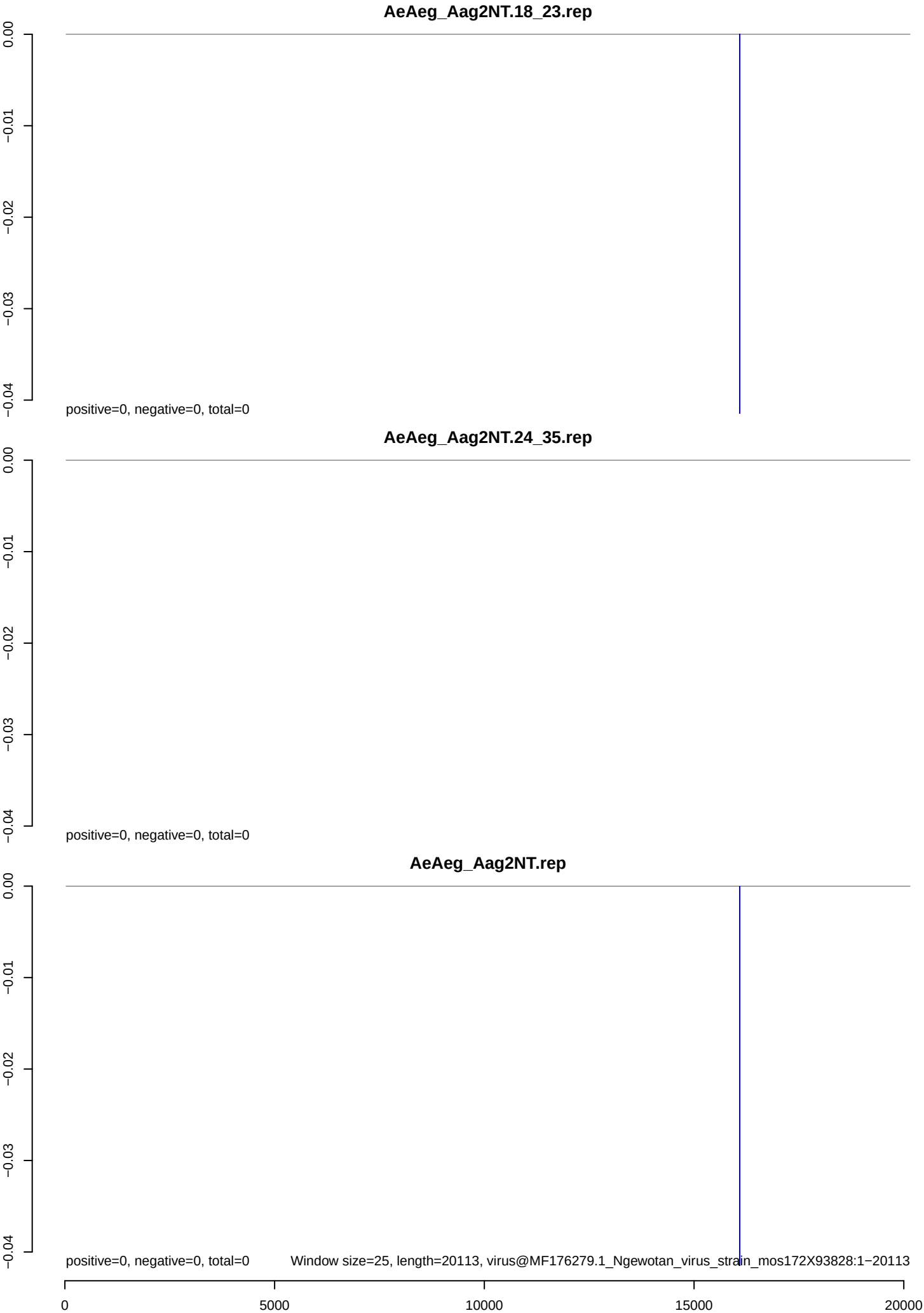

AeAeg_Aag2NT.18_23.rep
0.000
−0.005
−0.010
−0.015
−0.020
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
0.000
−0.005
−0.010
−0.015
−0.020
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.000
−0.005
−0.010
−0.015
−0.020
positive=0, negative=0, total=0
0
2000
4000
6000
8000
10000
12000

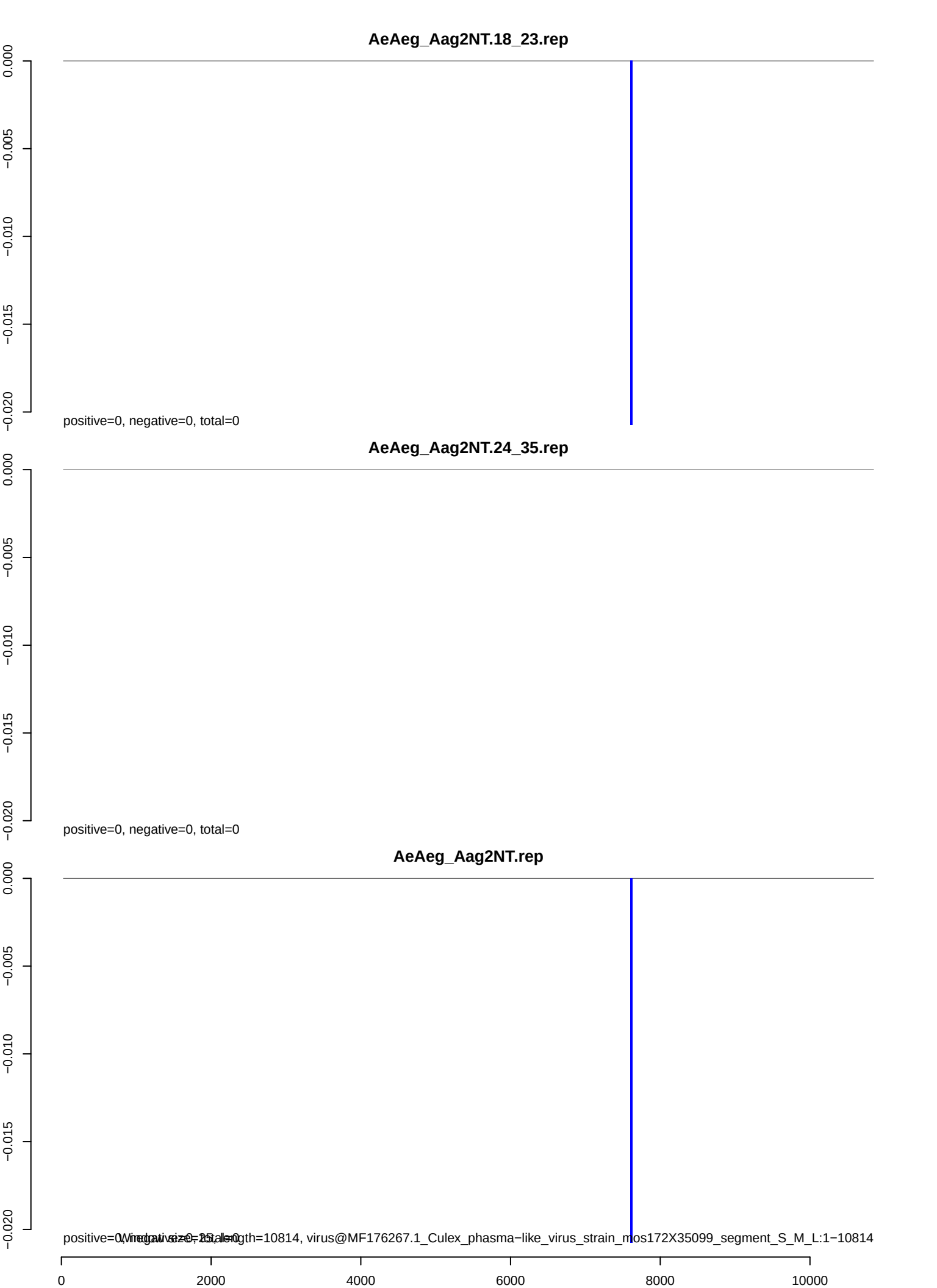

AeAeg_Aag2NT.18_23.rep
0.020
0.015
0.010
0.005
0.000
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
0.020
0.015
0.010
0.005
0.000
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.020
0.015
0.010
0.005
0.000
positive=0, negative=0, total=0
Window size=25, length=10871, virus@NC_001809.1−Louping_ill_virus:1−10871
0
2000
4000
6000
8000
10000

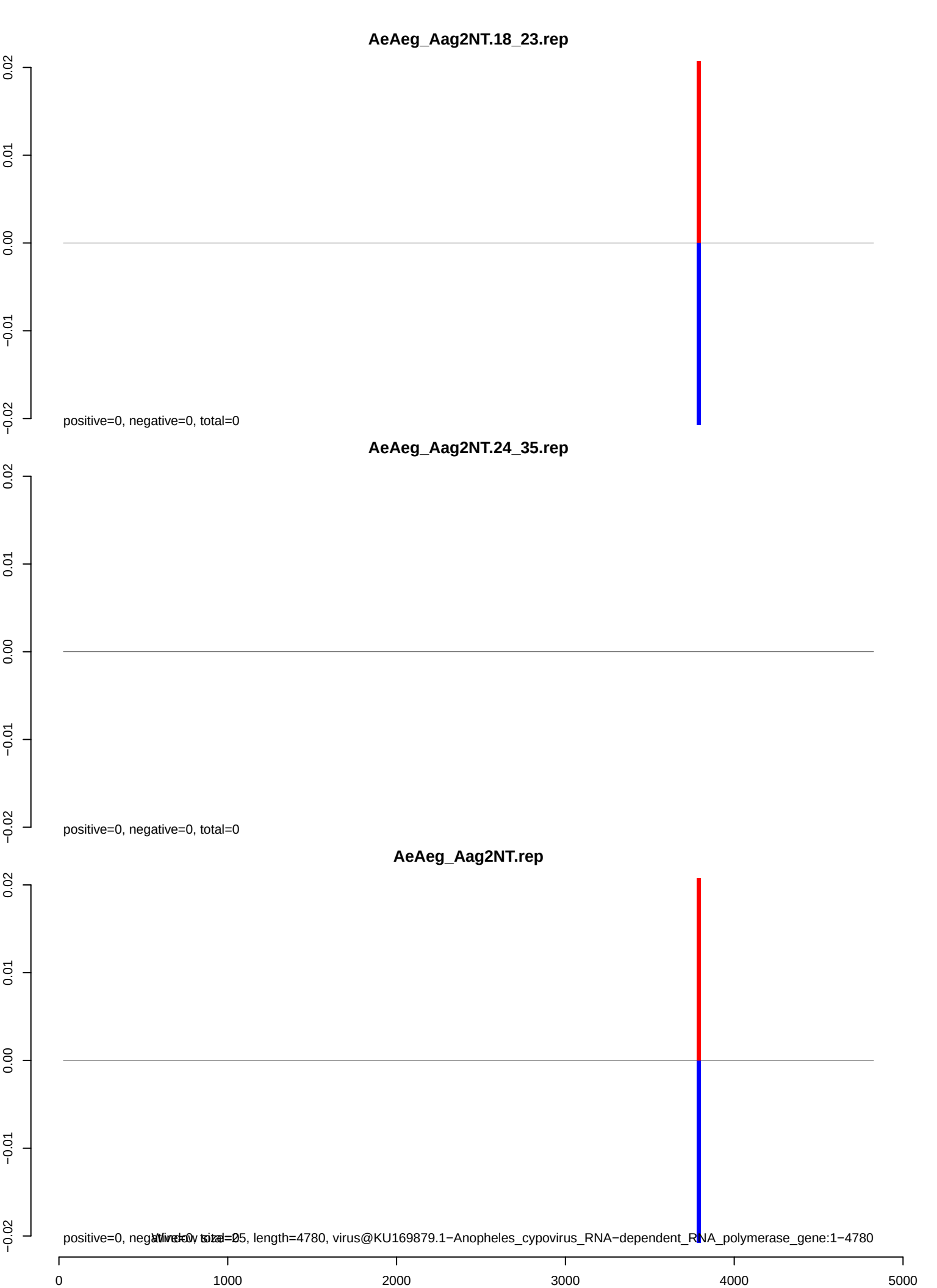

AeAeg_Aag2NT.18_23.rep
0.020
0.015
0.010
0.005
0.000
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
0.020
0.015
0.010
0.005
0.000
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.020
0.015
0.010
0.005
0.000
positive=0, negative=0, total=0
Window size=25, length=11141, virus@NC_001672.1−Tick−borne_encephalitis_virus:1−11141
0
2000
4000
6000
8000
10000


AeAeg_Aag2NT.18_23.rep
0.020
0.015
0.010
0.005
0.000
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
0.020
0.015
0.010
0.005
0.000
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.020
0.015
0.010
0.005
0.000
positive=0, negative=0, total=0
Window size=25, length=3157, virus@MH188043.1−Culex_densovirus_strain_CDenV_Madera−2:1−3157
0
500
1000
1500
2000
2500
3000


AeAeg_Aag2NT.18_23.rep
0.000
−0.005
−0.010
−0.015
−0.020
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
0.000
−0.005
−0.010
−0.015
−0.020
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.000
−0.005
−0.010
−0.015
−0.020
positive=0, negative=0, total=0
window size=25, length=11664, virus@MG731558.1_Akabane_virus_isolate_HN10174_nucleoprotein_mRNA:1−11664
0
2000
4000
6000
8000
10000
12000


AeAeg_Aag2NT.18_23.rep
0.00
−0.01
−0.02
−0.03
−0.04
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
0.00
−0.01
−0.02
−0.03
−0.04
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.00
−0.01
−0.02
−0.03
−0.04
positive=0, negative=0, total=0
Window size=25, length=20113, virus@MF176279.1_Ngewotan_virus_strain_mos172X93828:1−20113
0
5000
10000
15000
20000


AeAeg_Aag2NT.18_23.rep
0.000
−0.005
−0.010
−0.015
−0.020
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
0.000
−0.005
−0.010
−0.015
−0.020
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.000
−0.005
−0.010
−0.015
−0.020
positive=0, negative=0, total=0
virus@MF176267.1_Culex_phasma−like_virus_strain_mos172X35099_segment_S_M_L:1−10814
0
2000
4000
6000
8000
10000


AeAeg_Aag2NT.18_23.rep
0.02
0.01
0.00
−0.01
−0.02
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
0.02
0.01
0.00
−0.01
−0.02
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.02
0.01
0.00
−0.01
−0.02
positive=0, negative=0, total=0, length=4780, virus@KU169879.1−Anopheles_cypovirus_RNA−dependent_RNA_polymerase_gene:1−4780
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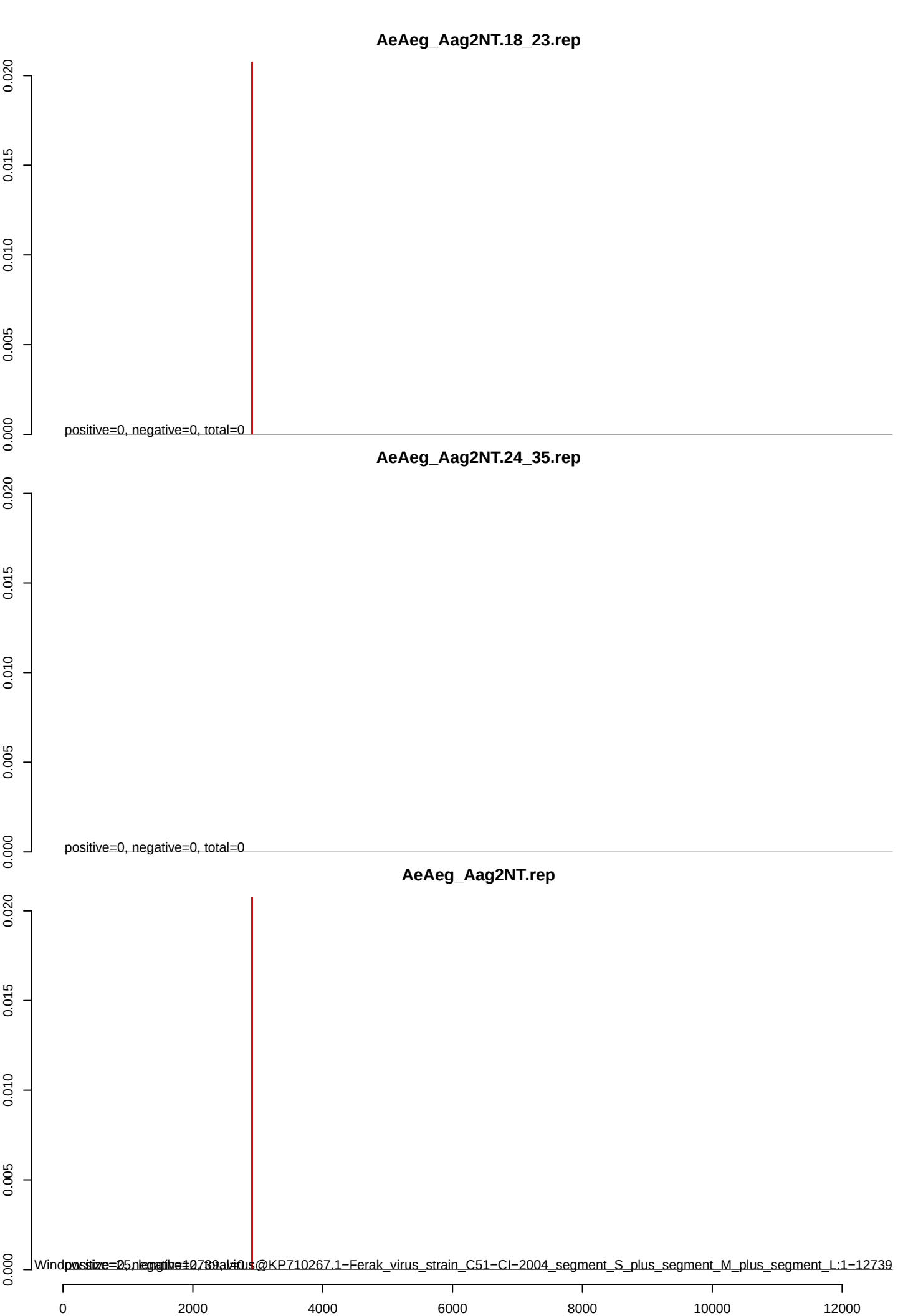
2000
3000
4000
5000


AeAeg_Aag2NT.18_23.rep
0.020
0.015
0.010
0.005
0.000
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
0.020
0.015
0.010
0.005
0.000
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.020
0.015
0.010
0.005
0.000
Window size=25, length=12739
virus@KP710267.1−Ferak_virus_strain_C51−CI−2004_segment_S_plus_segment_M_plus_segment_L:1−12739
0
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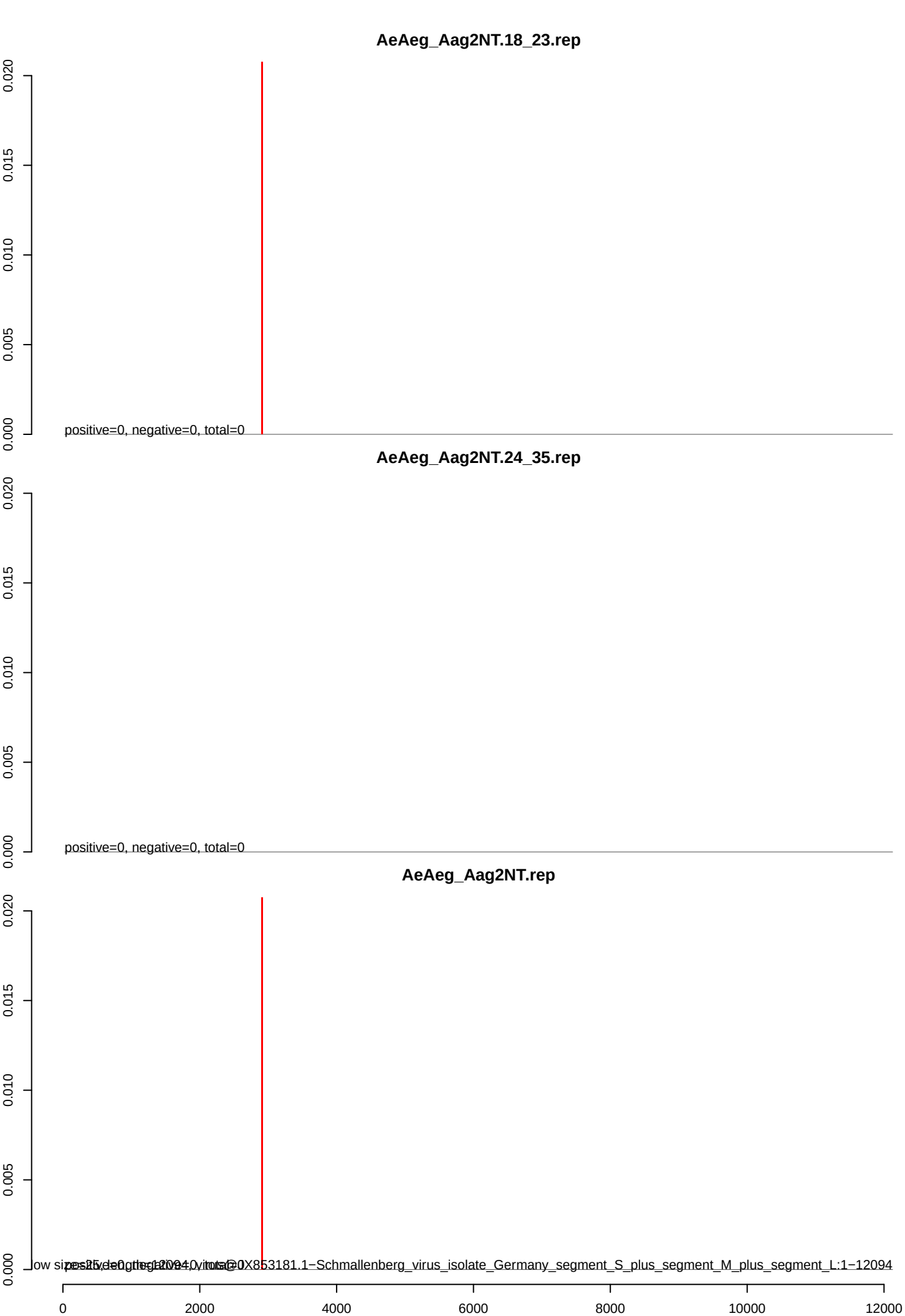
4000
6000
8000
10000
12000


AeAeg_Aag2NT.18_23.rep
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0.015
0.010
0.005
0.000
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
0.020
0.015
0.010
0.005
0.000
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.020
0.015
0.010
0.005
0.000
positive=0, negative=0, total=0
low size=25, deg=1, seg=2094, virus=OX853181.1−Schmallenberg_virus_isolate_Germany_segment_S_plus_segment_M_plus_segment_L:1−12094
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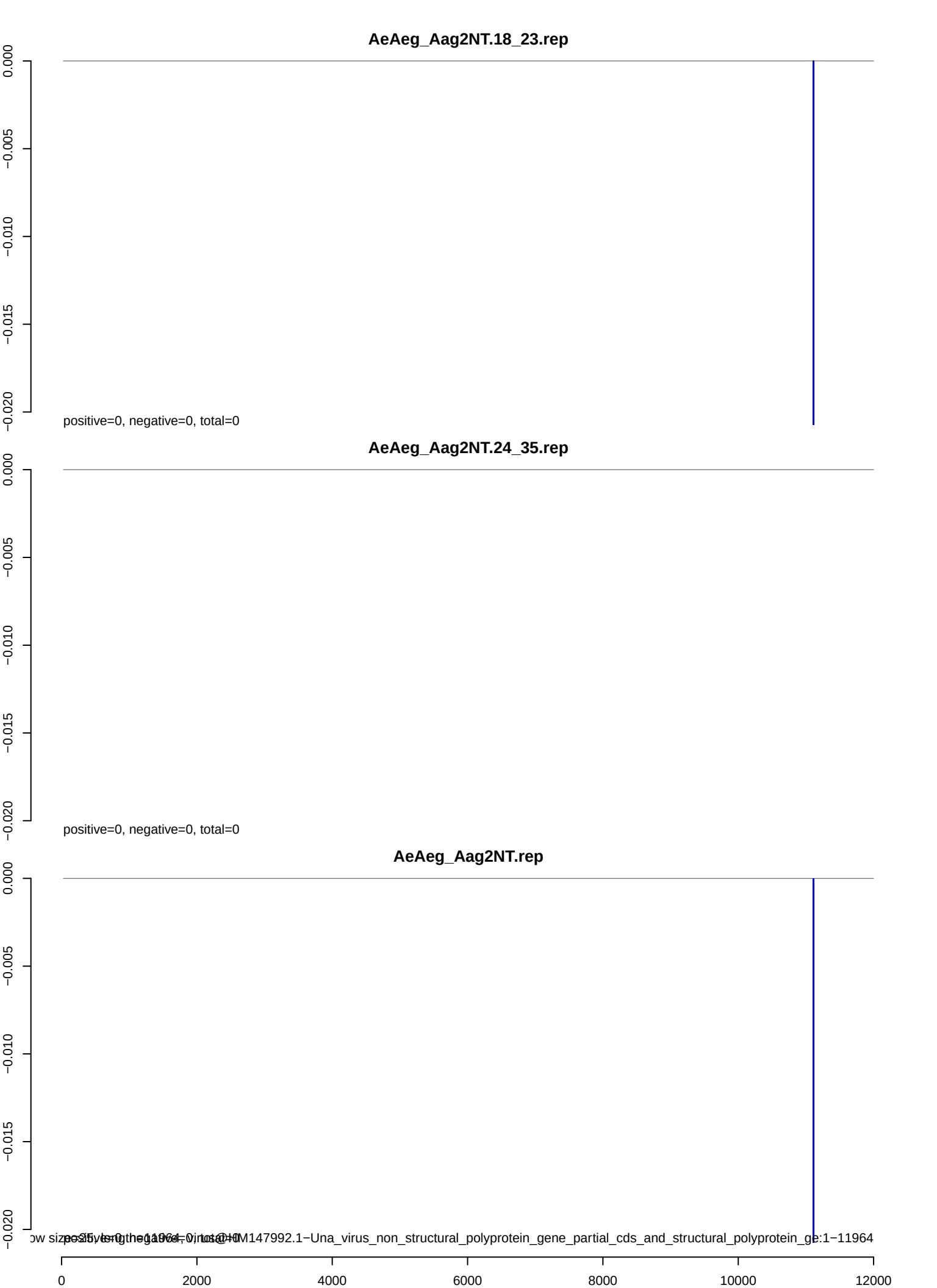
6000
8000
10000
12000


AeAeg_Aag2NT.18_23.rep
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−0.005
−0.010
−0.015
−0.020
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
0.000
−0.005
−0.010
−0.015
−0.020
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.000
−0.005
−0.010
−0.015
−0.020
ow size=35, length=11964, total=0
NC_035889.1−Una_virus_non_structural_polyprotein_gene_partial_cds_and_structural_polyprotein_ge:1−11964
0
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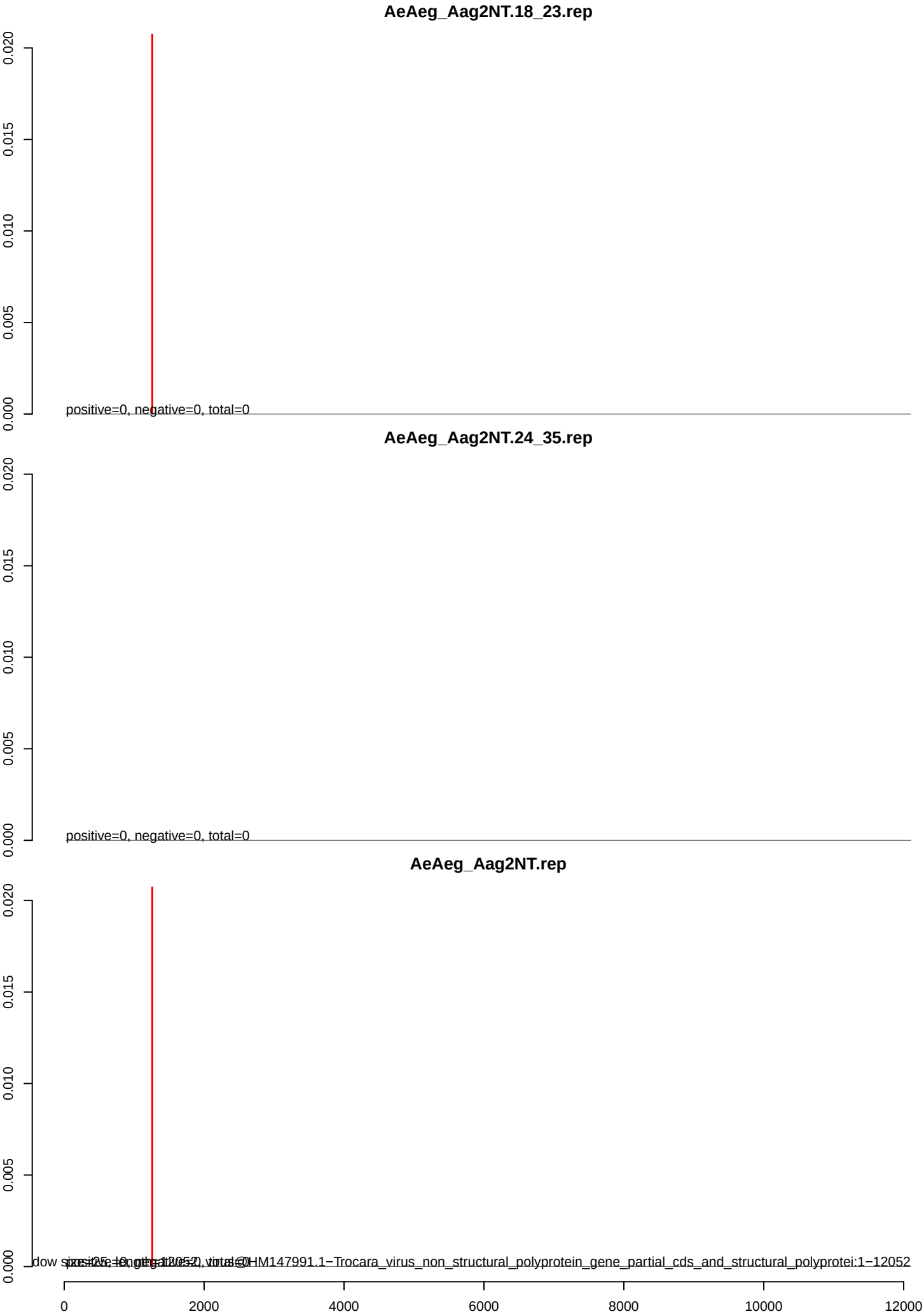
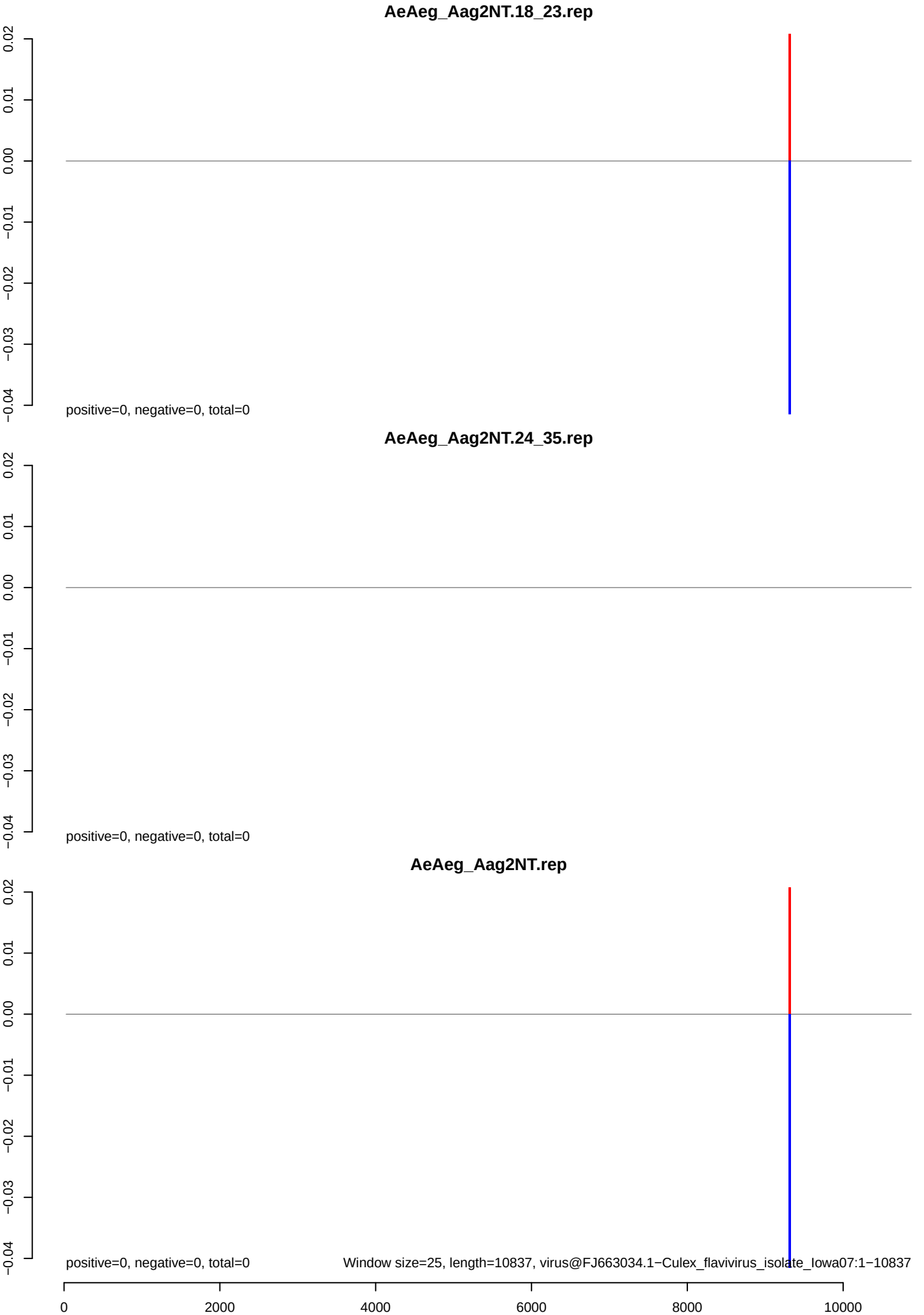
4000
6000
8000
10000
12000


AeAeg_Aag2NT.18_23.rep
0.020
0.015
0.010
0.005
0.000
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
0.020
0.015
0.010
0.005
0.000
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.020
0.015
0.010
0.005
0.000
dow size=25, length=12052, total=1
HM147991.1−Trocara_virus_non_structural_polyprotein_gene_partial_cds_and_structural_polyprotei:1−12052
0
2000
4000
6000
8000
10000
12000


AeAeg_Aag2NT.18_23.rep
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0.01
0.00
−0.01
−0.02
−0.03
−0.04
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
0.02
0.01
0.00
−0.01
−0.02
−0.03
−0.04
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.02
0.01
0.00
−0.01
−0.02
−0.03
−0.04
positive=0, negative=0, total=0
Window size=25, length=10837, virus@FJ663034.1−Culex_flavivirus_isolate_Iowa07:1−10837
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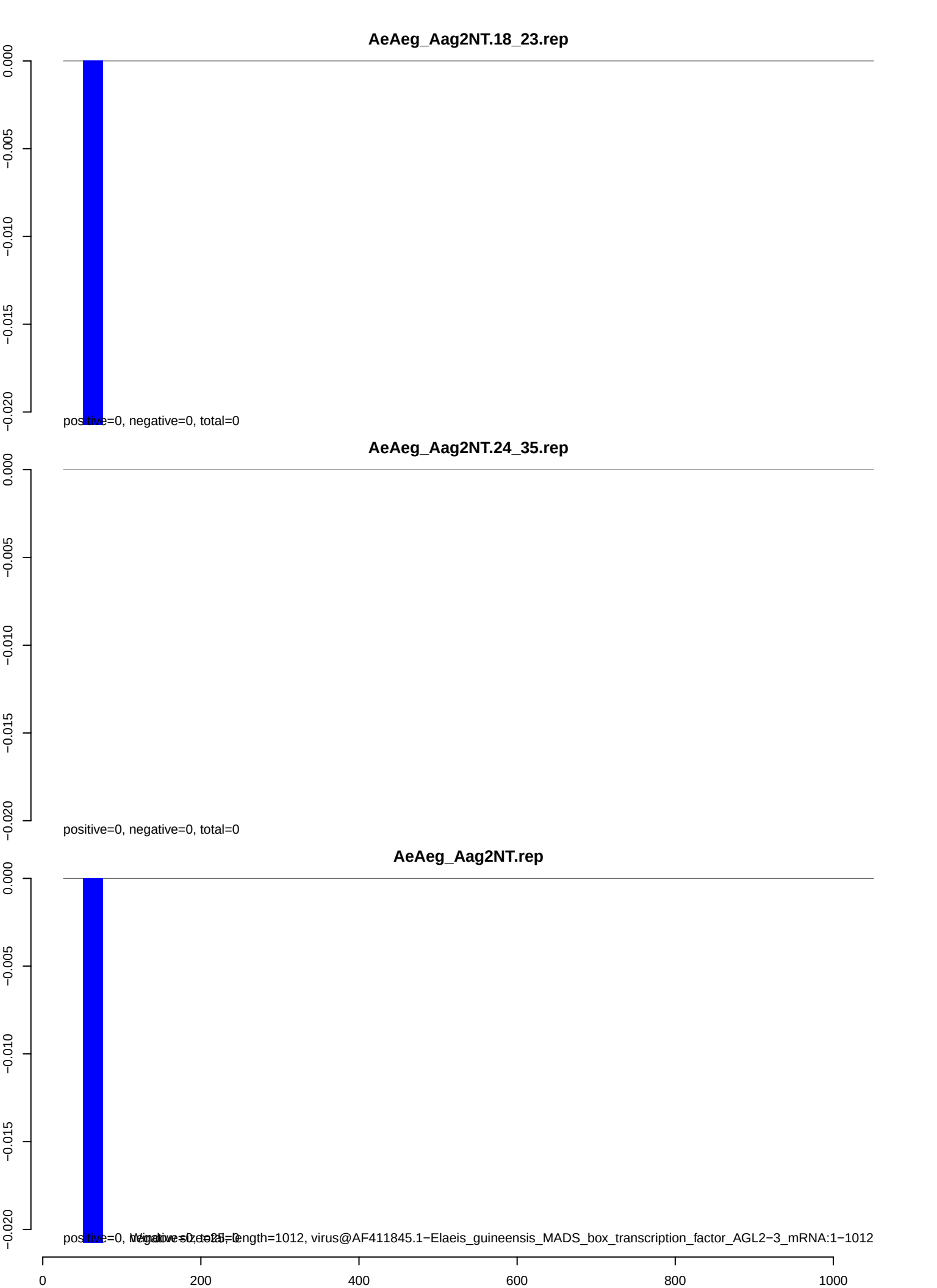
4000
6000
8000
10000


AeAeg_Aag2NT.18_23.rep
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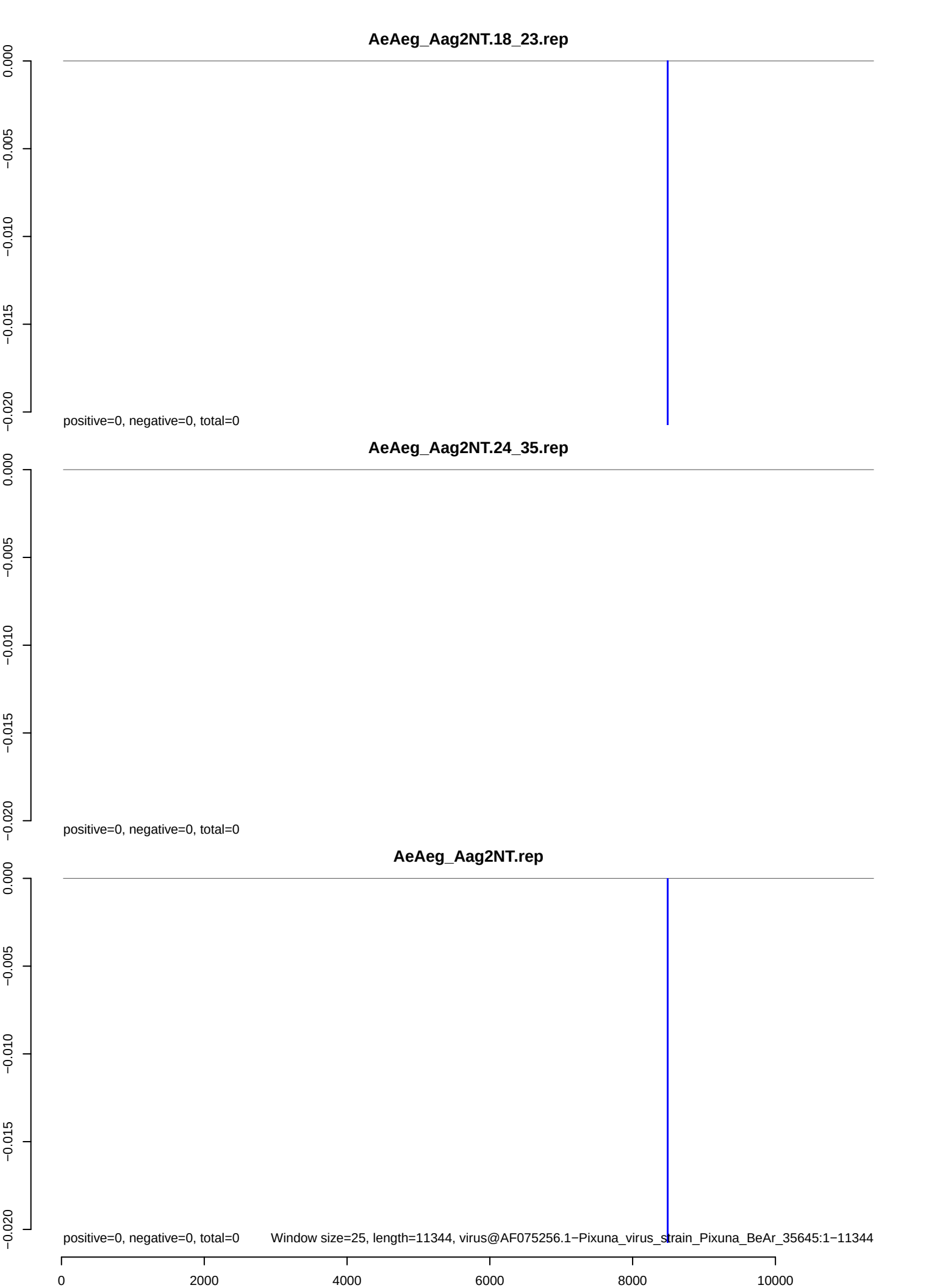
−0.005
−0.010
−0.015
−0.020
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
0.000
−0.005
−0.010
−0.015
−0.020
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.000
−0.005
−0.010
−0.015
−0.020
positive=0, negative=0, total=0
0
200
400
600
800
1000


AeAeg_Aag2NT.18_23.rep
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−0.005
−0.010
−0.015
−0.020
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
0.000
−0.005
−0.010
−0.015
−0.020
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.000
−0.005
−0.010
−0.015
−0.020
positive=0, negative=0, total=0
Window size=25, length=11344, virus@AF075256.1−Pixuna_virus_strain_Pixuna_BeAr_35645:1−11344
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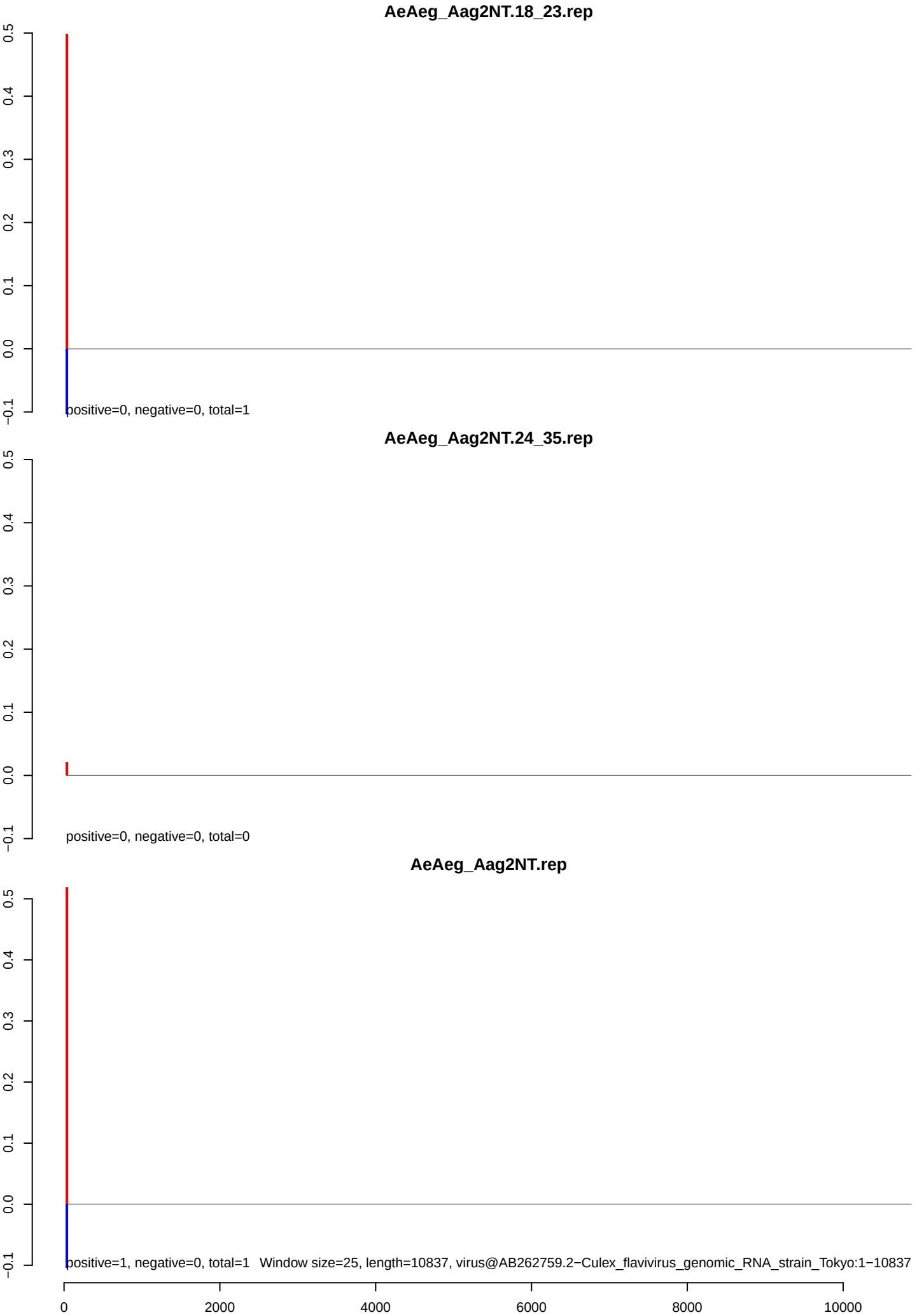
4000
6000
8000
10000


AeAeg_Aag2NT.18_23.rep
0.5
0.4
0.3
0.2
0.1
0.0
−0.1
positive=0, negative=0, total=1
AeAeg_Aag2NT.24_35.rep
0.5
0.4
0.3
0.2
0.1
0.0
−0.1
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
0.5
0.4
0.3
0.2
0.1
0.0
−0.1
positive=1, negative=0, total=1 Window size=25, length=10837, virus@AB262759.2−Culex_flavivirus_genomic_RNA_strain_Tokyo:1−10837
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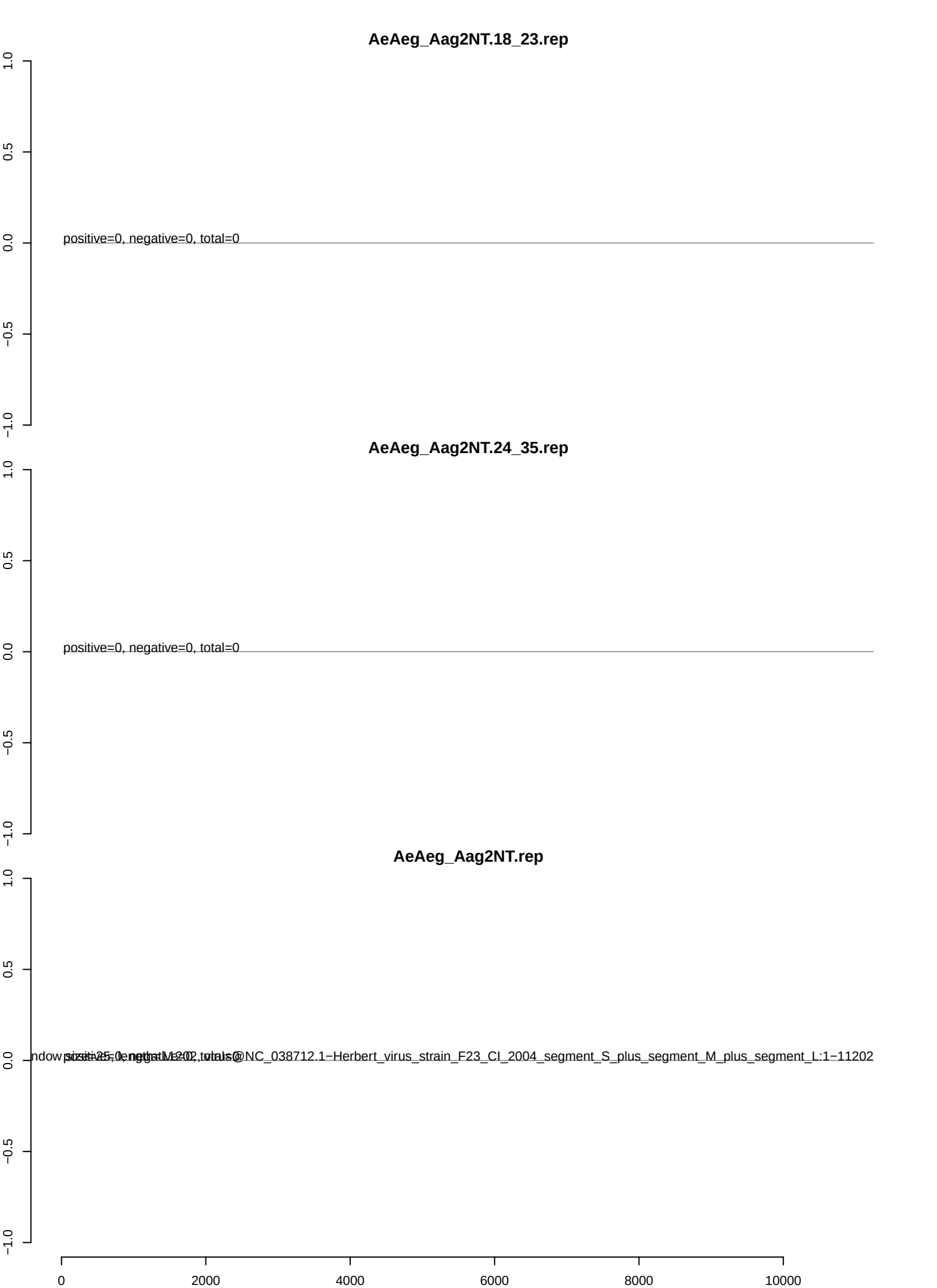
4000
6000
8000
10000


AeAeg_Aag2NT.18_23.rep
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
positive=25, negative=202, total=0@NC_038712.1−Herbert_virus_strain_F23_CI_2004_segment_S_plus_segment_M_plus_segment_L:1−11202
1.0
0.5
0.0
−0.5
−1.0
0
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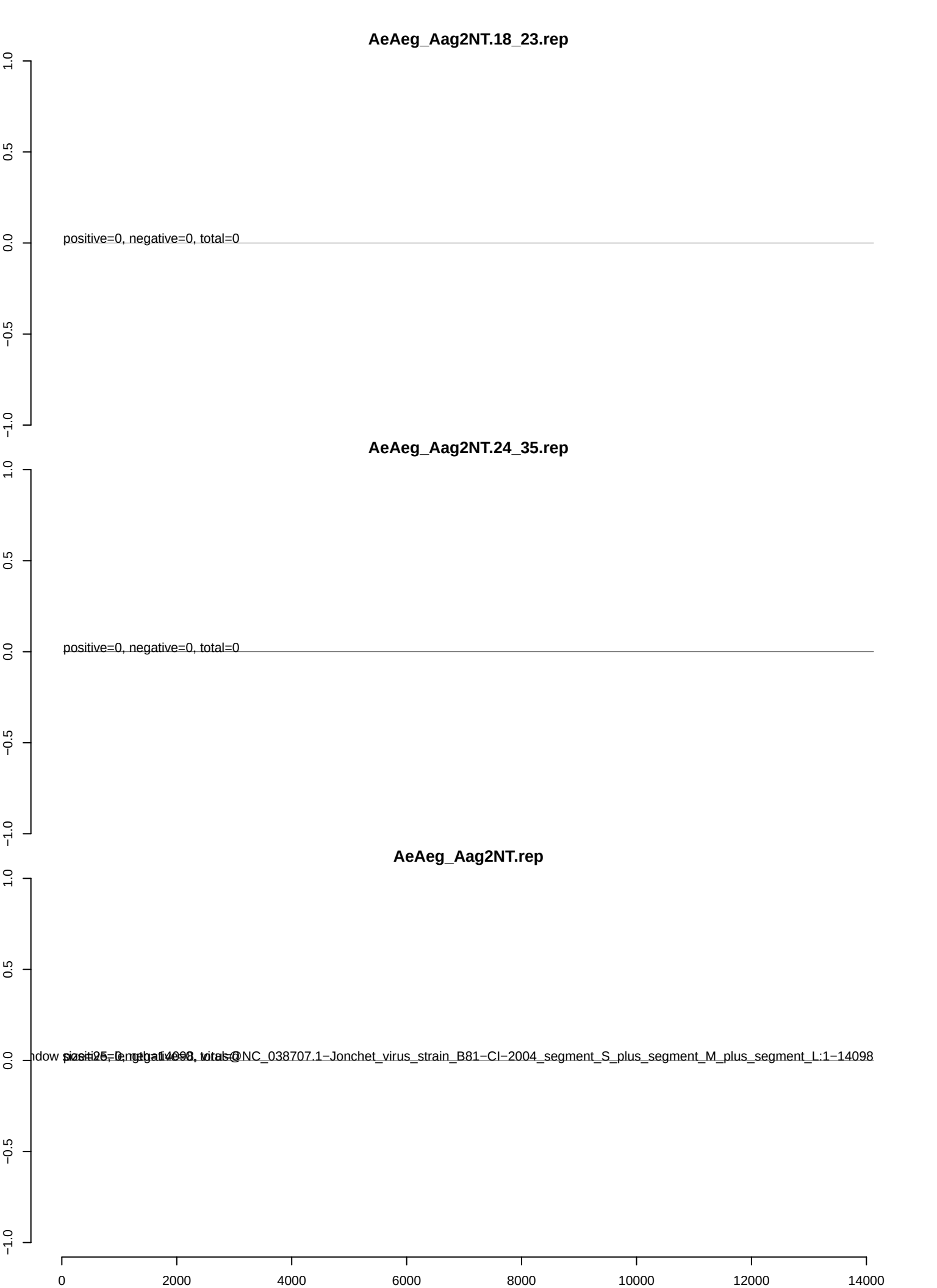
4000
6000
8000
10000


AeAeg_Aag2NT.18_23.rep
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
positive=0, negative=0, total=0
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0.5
0.0
−0.5
−1.0
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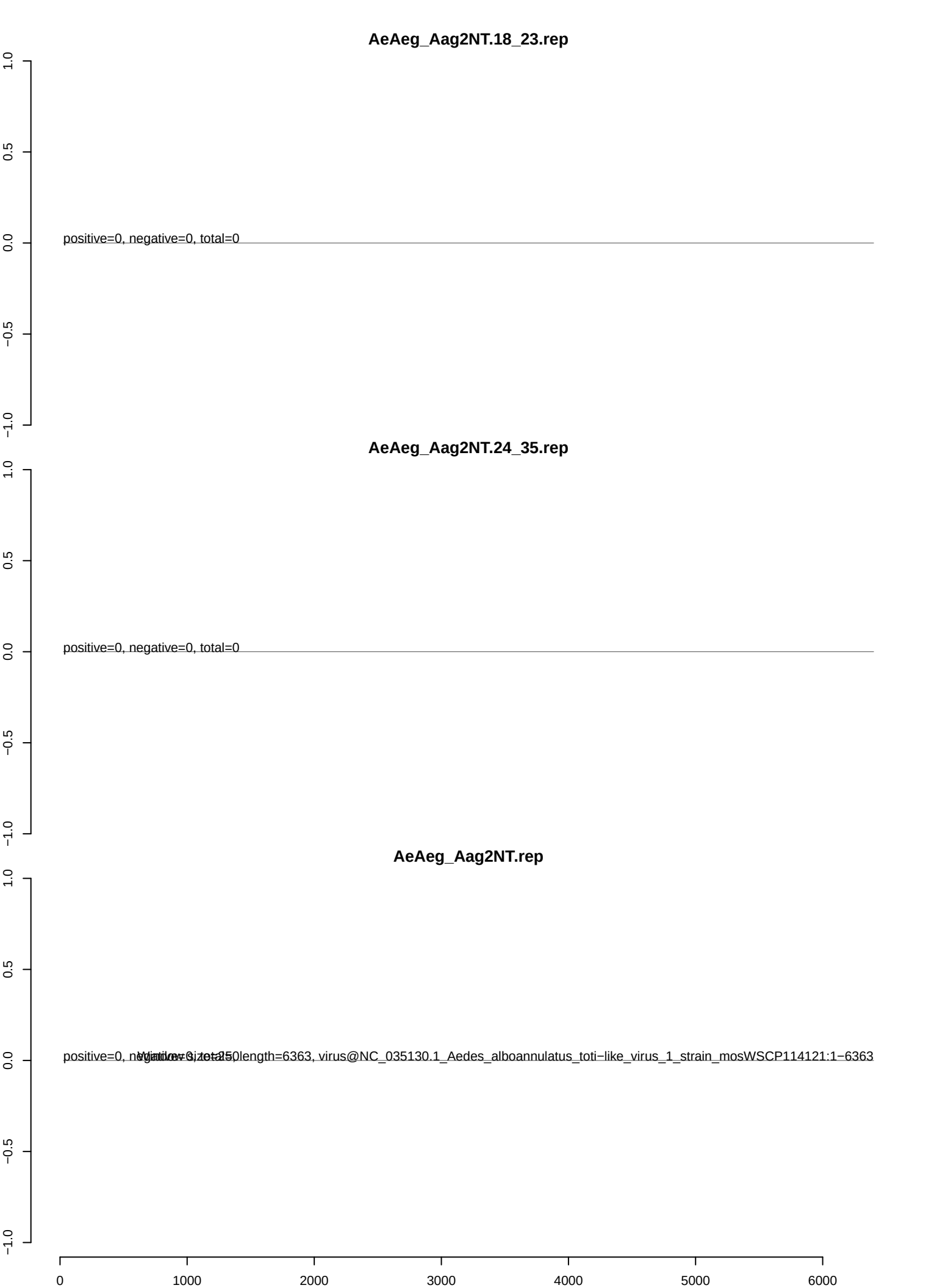
6000
8000
10000
12000
14000


AeAeg_Aag2NT.18_23.rep
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
positive=0, negative=0, total=0
length=6363, virus@NC_035130.1_Aedes_alboannulatus_toti−like_virus_1_strain_mosWSCP114121:1−6363
1.0
0.5
0.0
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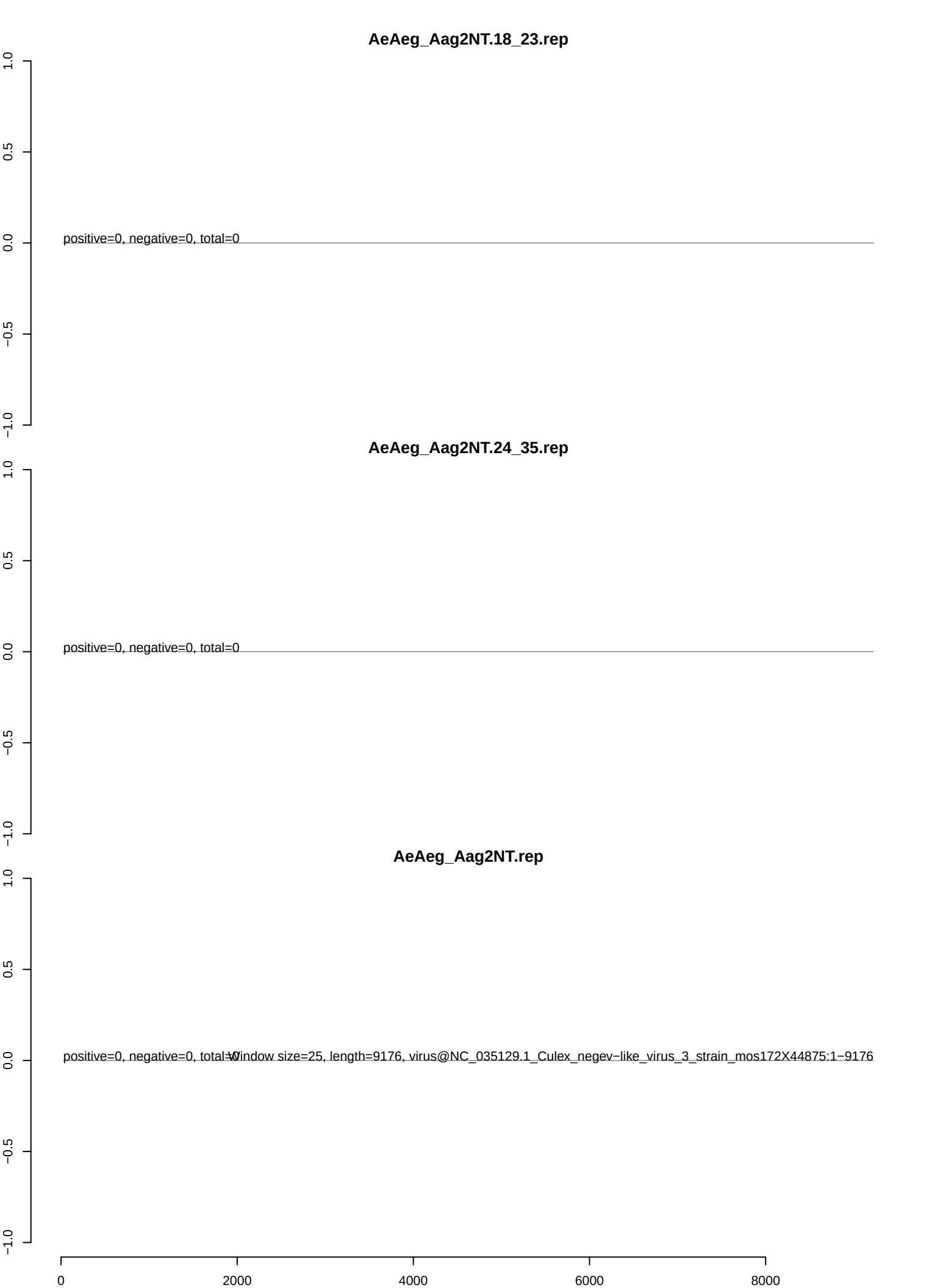
3000
4000
5000
6000


AeAeg_Aag2NT.18_23.rep
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
positive=0, negative=0, total=0
Window size=25, length=9176, virus@NC_035129.1_Culex_negev−like_virus_3_strain_mos172X44875:1−9176
1.0
0.5
0.0
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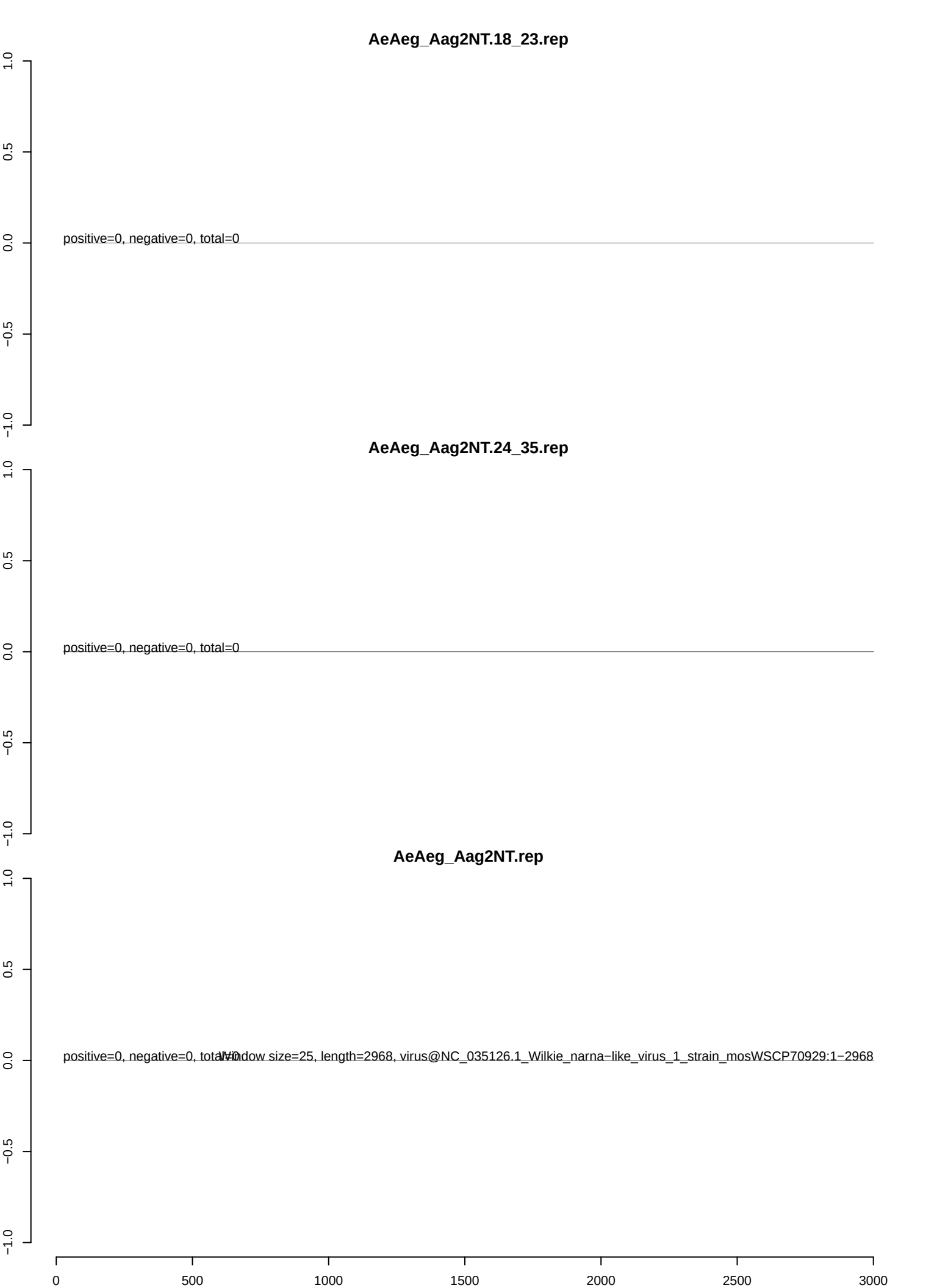
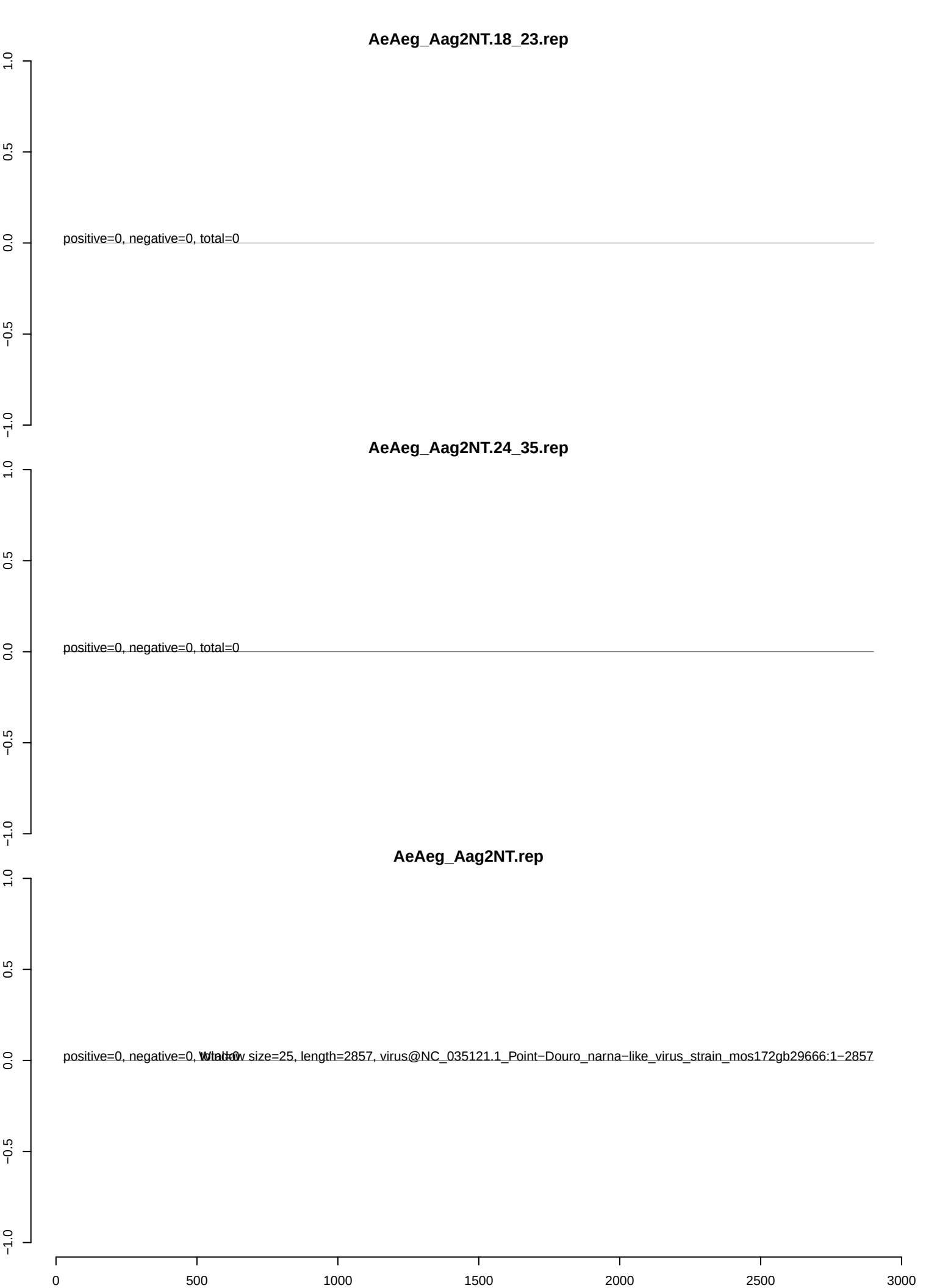
−1.0
0
2000
4000
6000
8000


AeAeg_Aag2NT.18_23.rep
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
positive=0, negative=0, total=0
Window size=25, length=2968, virus@NC_035126.1_Wilkie_narna−like_virus_1_strain_mosWSCP70929:1−2968
1.0
0.5
0.0
−0.5
−1.0
0
500
1000
1500
2000
2500
3000


AeAeg_Aag2NT.18_23.rep
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
positive=0, negative=0, total=0
window size=25, length=2857, virus@NC_035121.1_Point−Douro_narna−like_virus_strain_mos172gb29666:1−2857
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0.5
0.0
−0.5
−1.0
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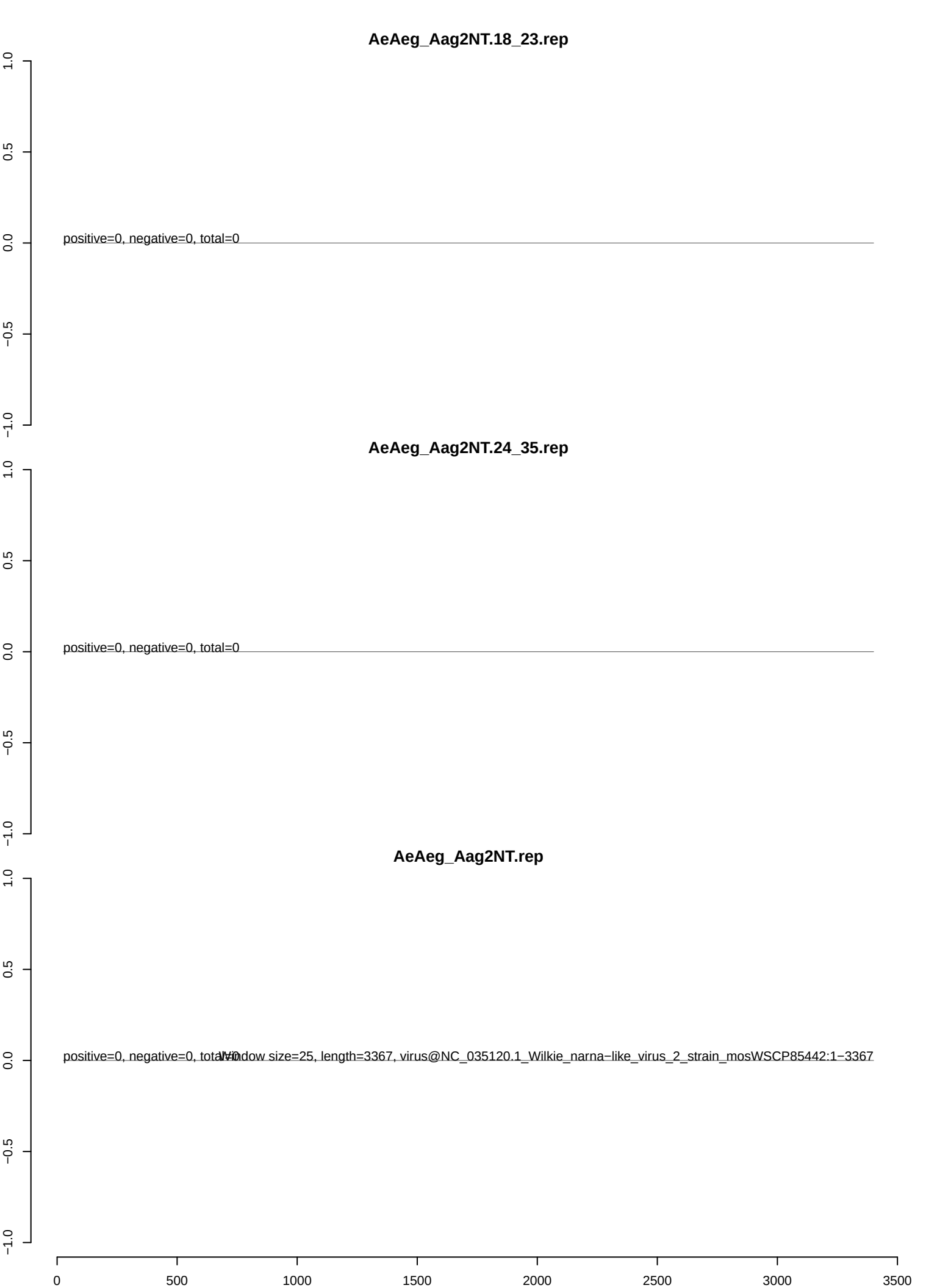
500
1000
1500
2000
2500
3000


AeAeg_Aag2NT.18_23.rep
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
positive=0, negative=0, total=0
Window size=25, length=3367, virus@NC_035120.1_Wilkie_narna−like_virus_2_strain_mosWSCP85442:1−3367
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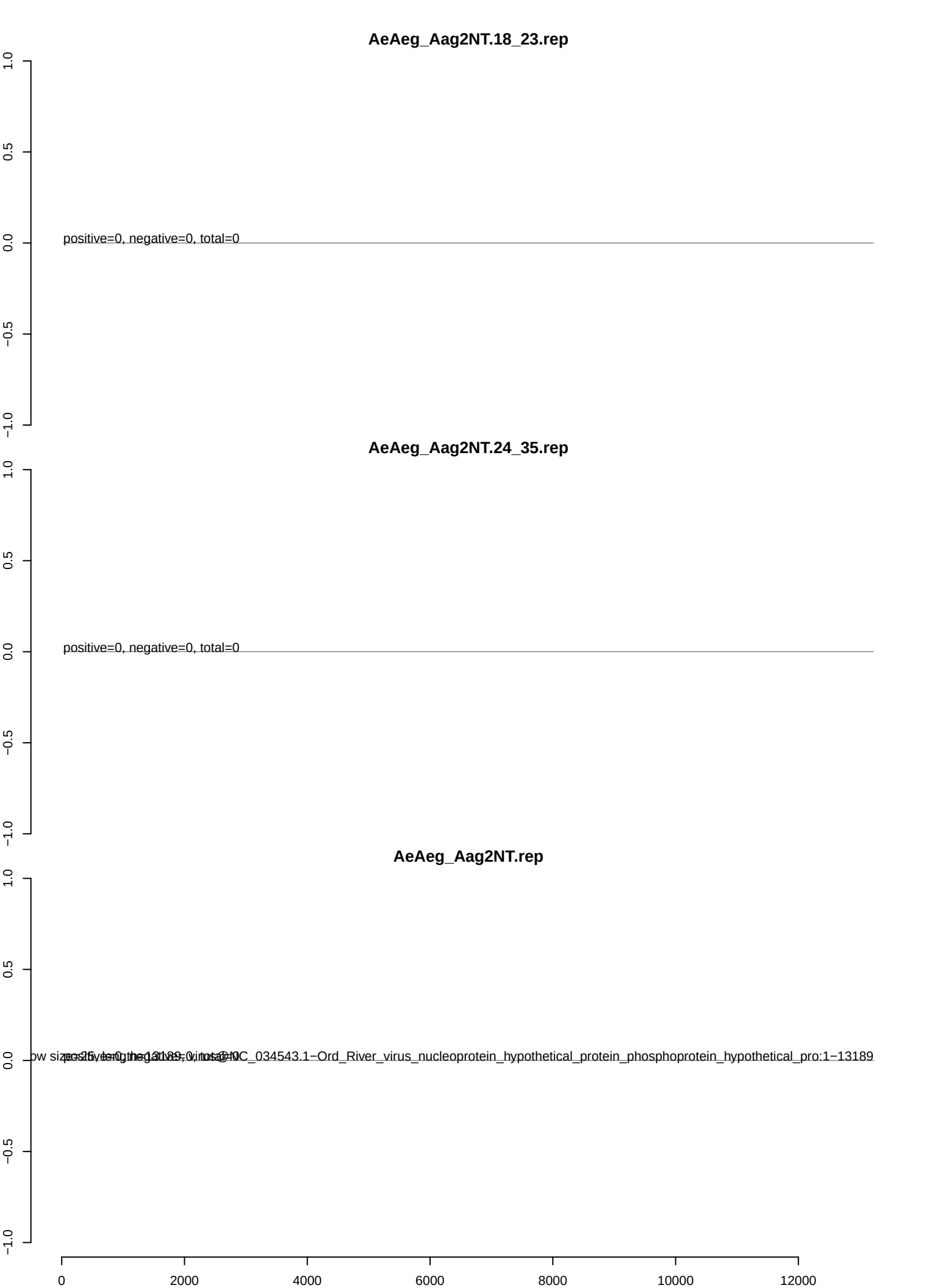
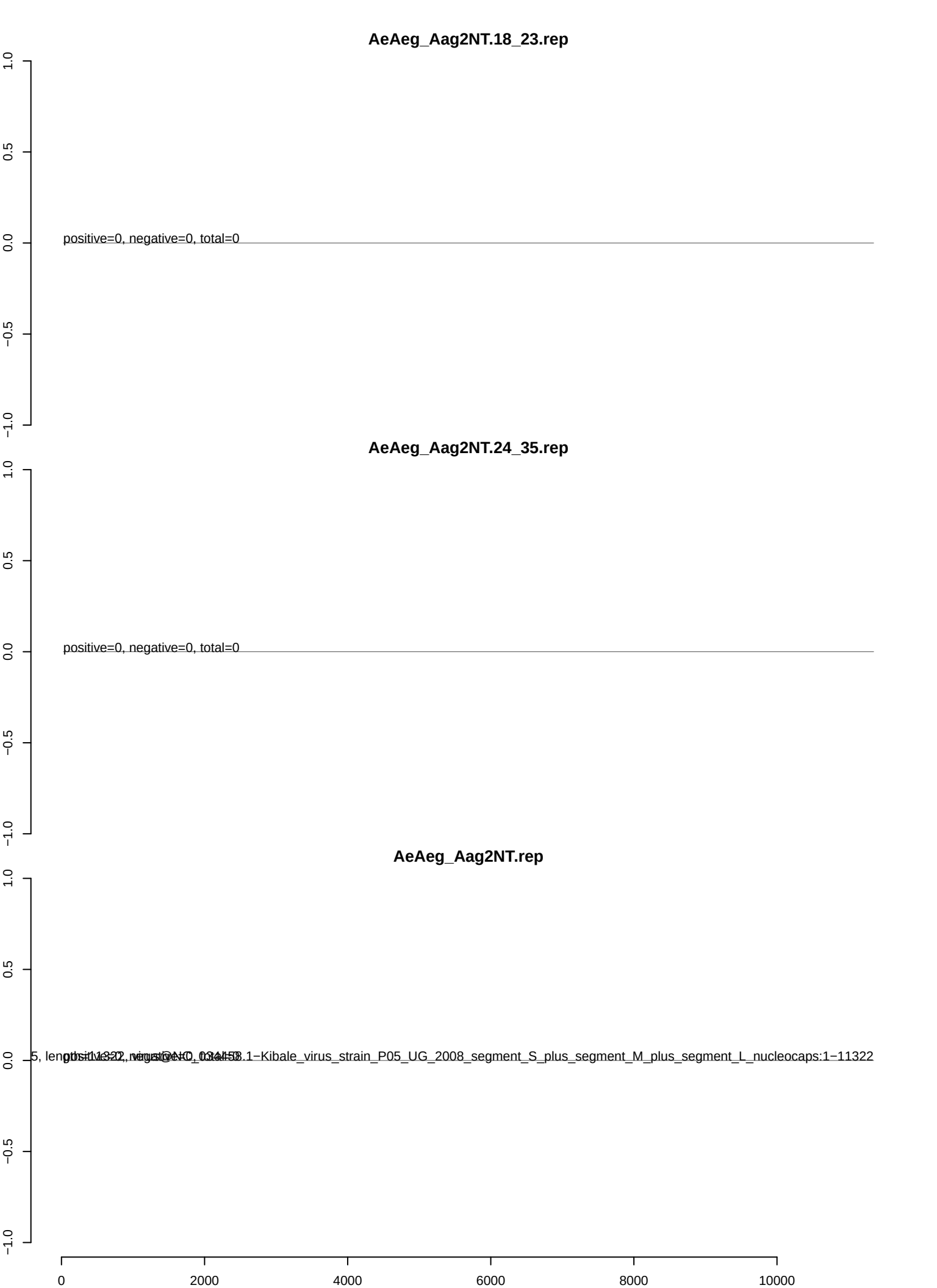
0.5
0.0
−0.5
−1.0
0
500
1000
1500
2000
2500
3000
3500


AeAeg_Aag2NT.18_23.rep
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
1.0
0.5
0.0
−0.5
−1.0
0
2000
4000
6000
8000
10000
12000


AeAeg_Aag2NT.18_23.rep
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
positive=1, negative=0, total=1
gb|KC834158.1|Kibale_virus_strain_P05_UG_2008_segment_S_plus_segment_M_plus_segment_L_nucleocaps:1-11322
1.0
0.5
0.0
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−1.0
0
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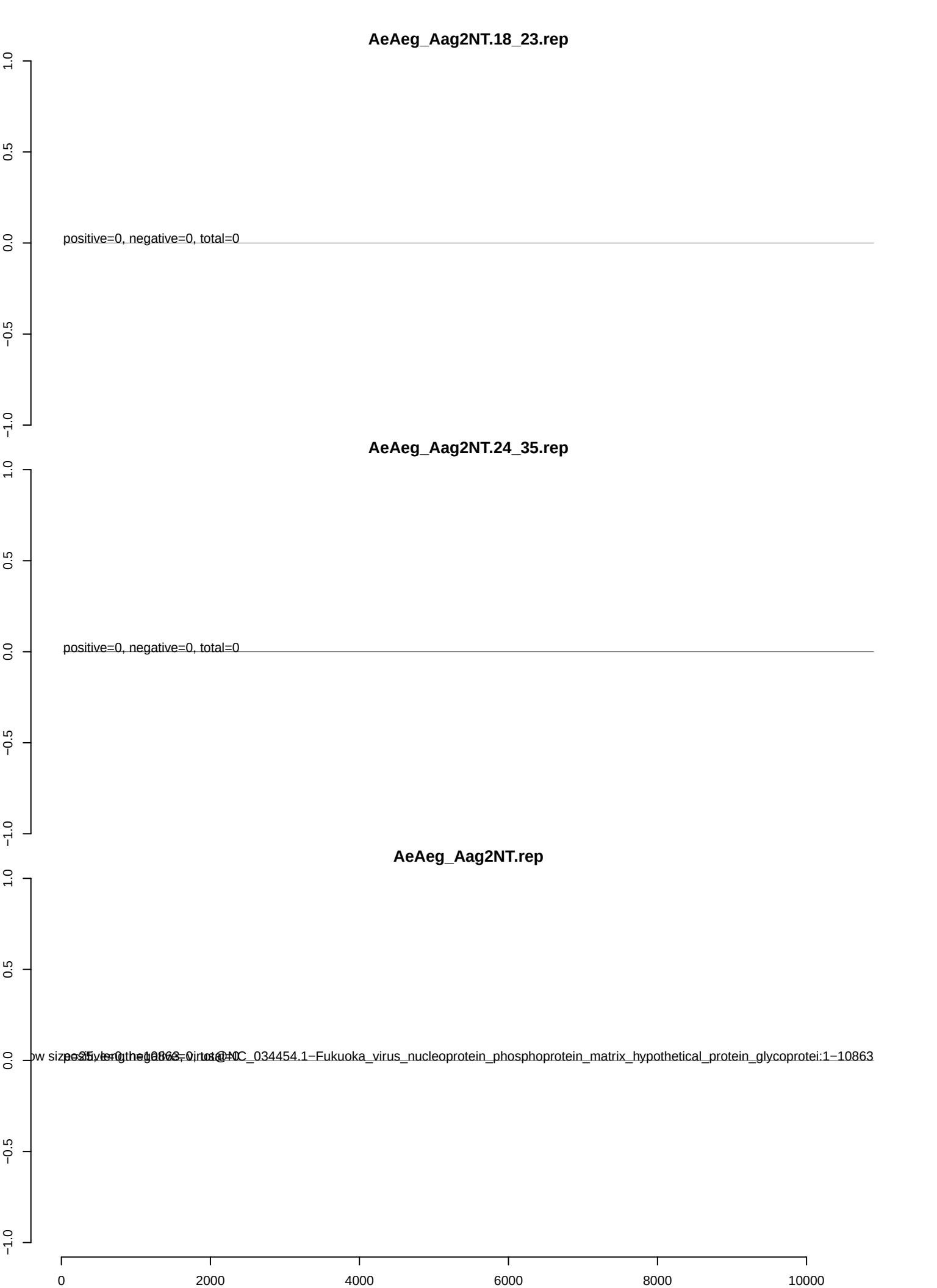
4000
6000
8000
10000


AeAeg_Aag2NT.18_23.rep
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
positive=0, negative=0, total=0
low size=25 type=gtheta863=0, total=0
NC_034454.1−Fukuoka_virus_nucleoprotein_phosphoprotein_matrix_hypothetical_protein_glycoprotei:1−10863
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−1.0
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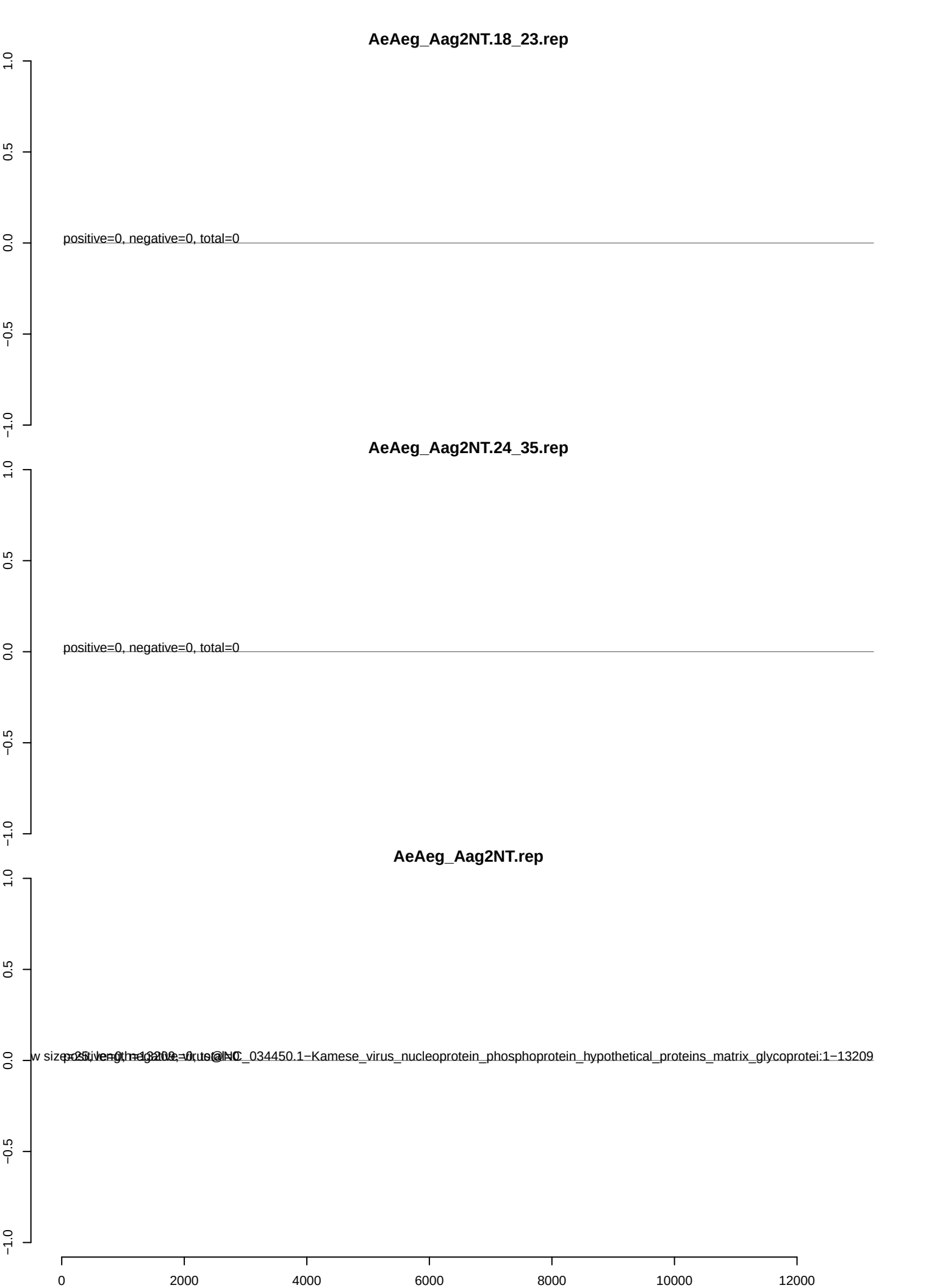
4000
6000
8000
10000


AeAeg_Aag2NT.18_23.rep
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
positive=0, negative=0, total=0
NC_034450.1−Kamese_virus_nucleoprotein_phosphoprotein_hypothetical_proteins_matrix_glycoprotei:1−13209
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0.0
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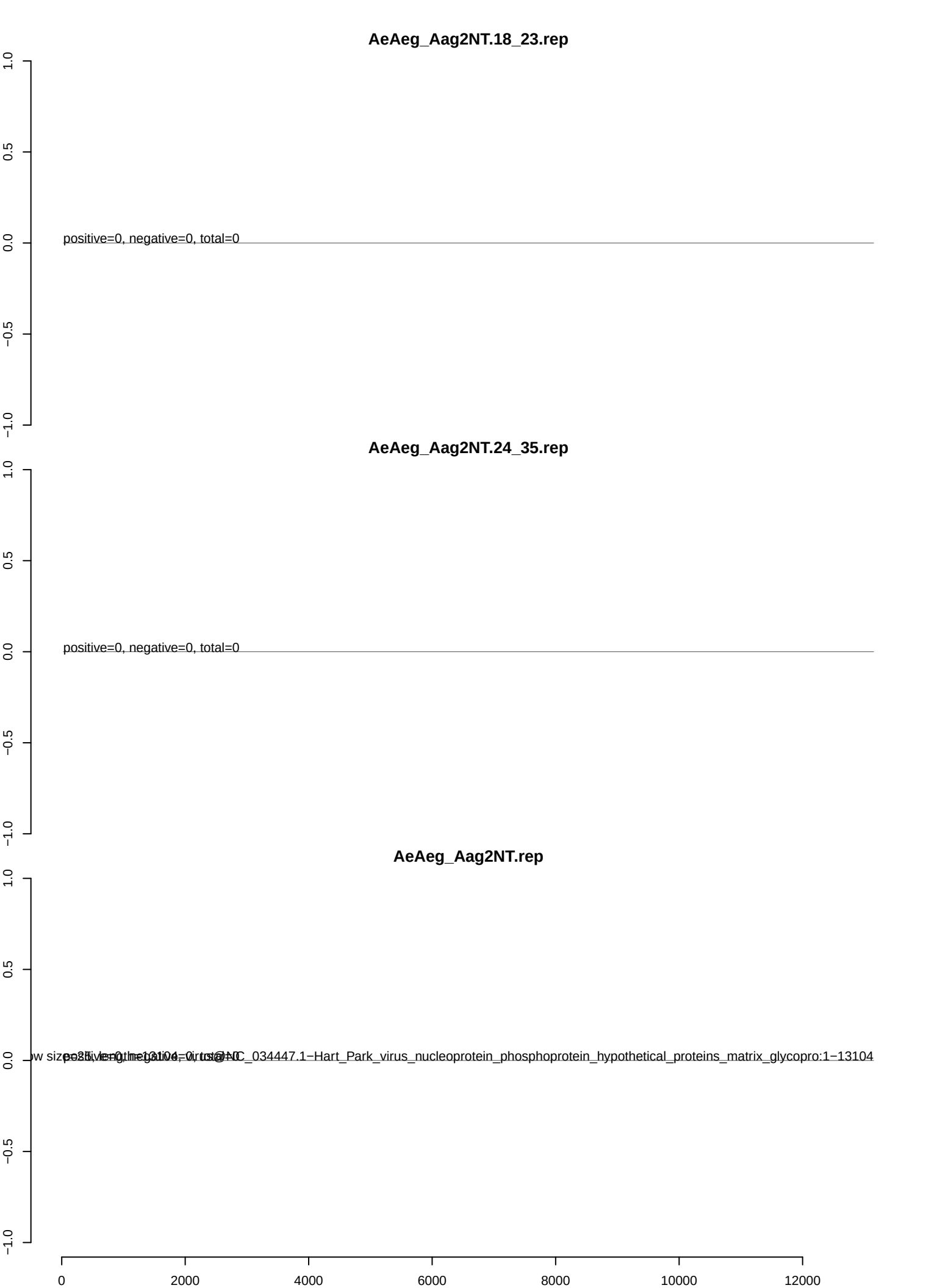
4000
6000
8000
10000
12000


AeAeg_Aag2NT.18_23.rep
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
positive=0, negative=0, total=0
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positive=0, negative=0, total=0
1.0
0.5
0.0
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−1.0
0
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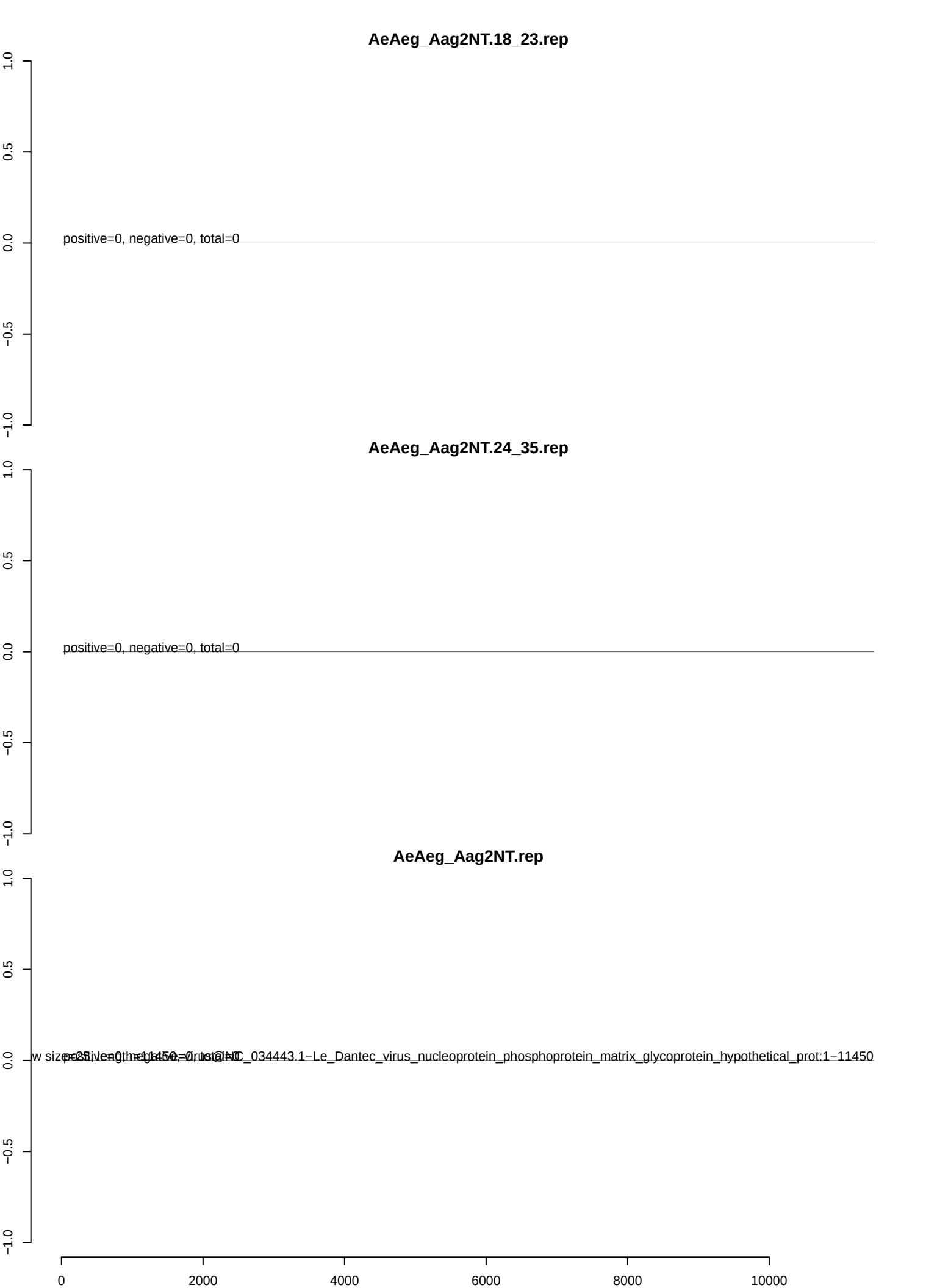
6000
8000
10000
12000


AeAeg_Aag2NT.18_23.rep
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
positive=0, negative=0, total=0
w size=25, overlap=0, min=1450, max=11450
gi|1034443.1−Le_Dantec_virus_nucleoprotein_phosphoprotein_matrix_glycoprotein_hypothetical_prot:1−11450
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4000
6000
8000
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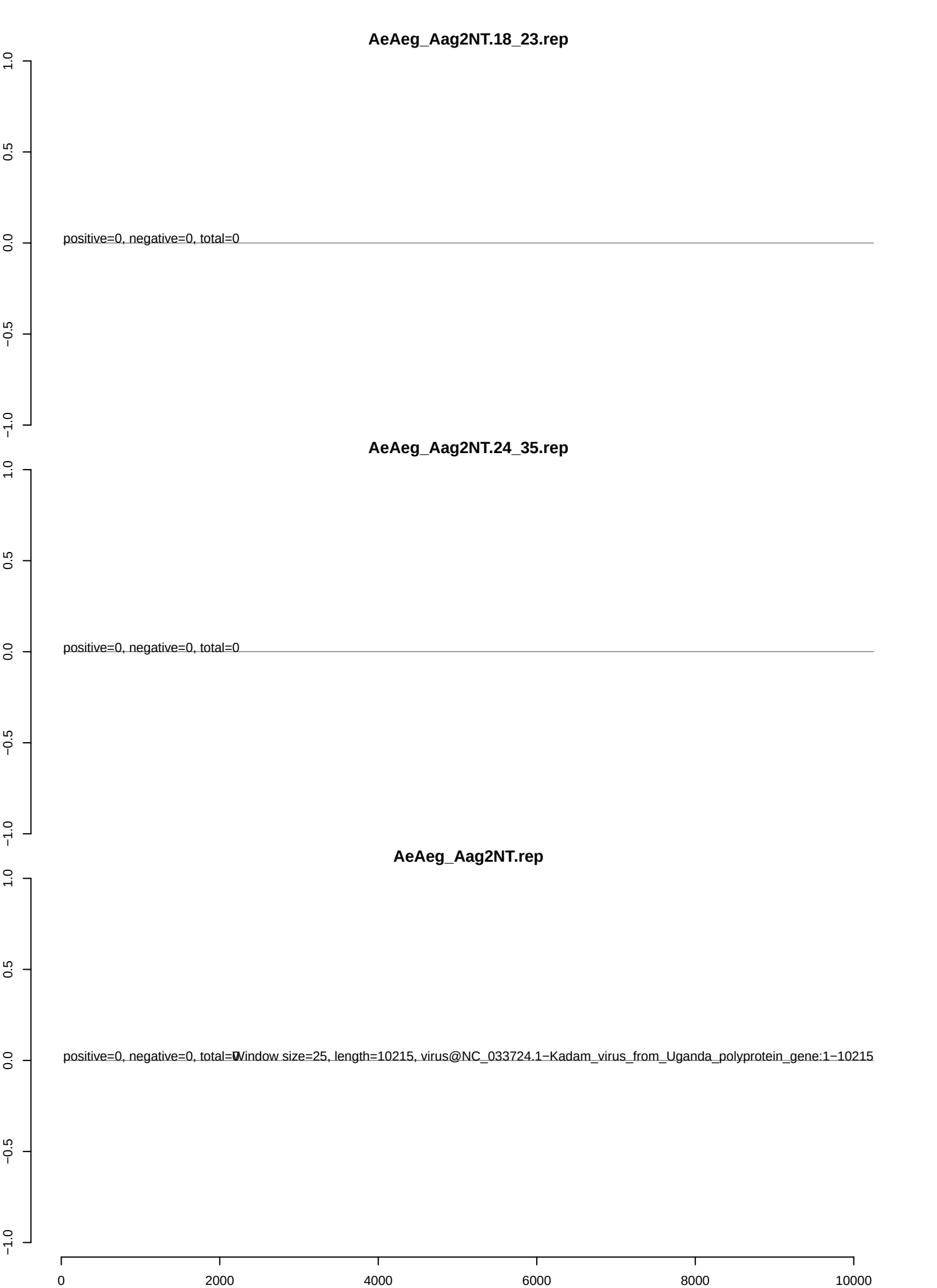
AeAeg_Aag2NT.18_23.rep
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
positive=0, negative=0, total=0
Window size=25, length=10215, virus@NC_033724.1−Kadam_virus_from_Uganda_polyprotein_gene:1−10215
1.0
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−1.0
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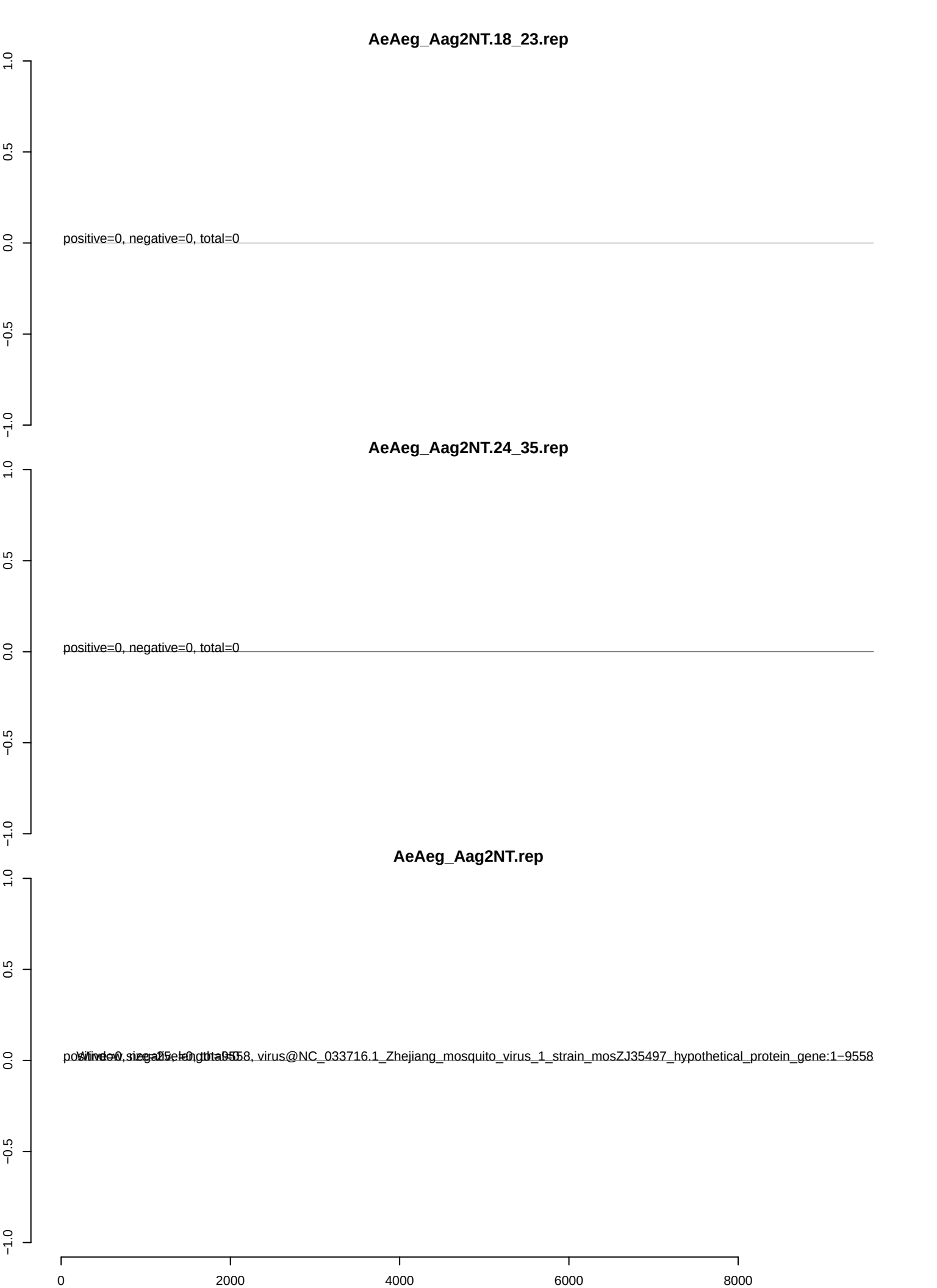
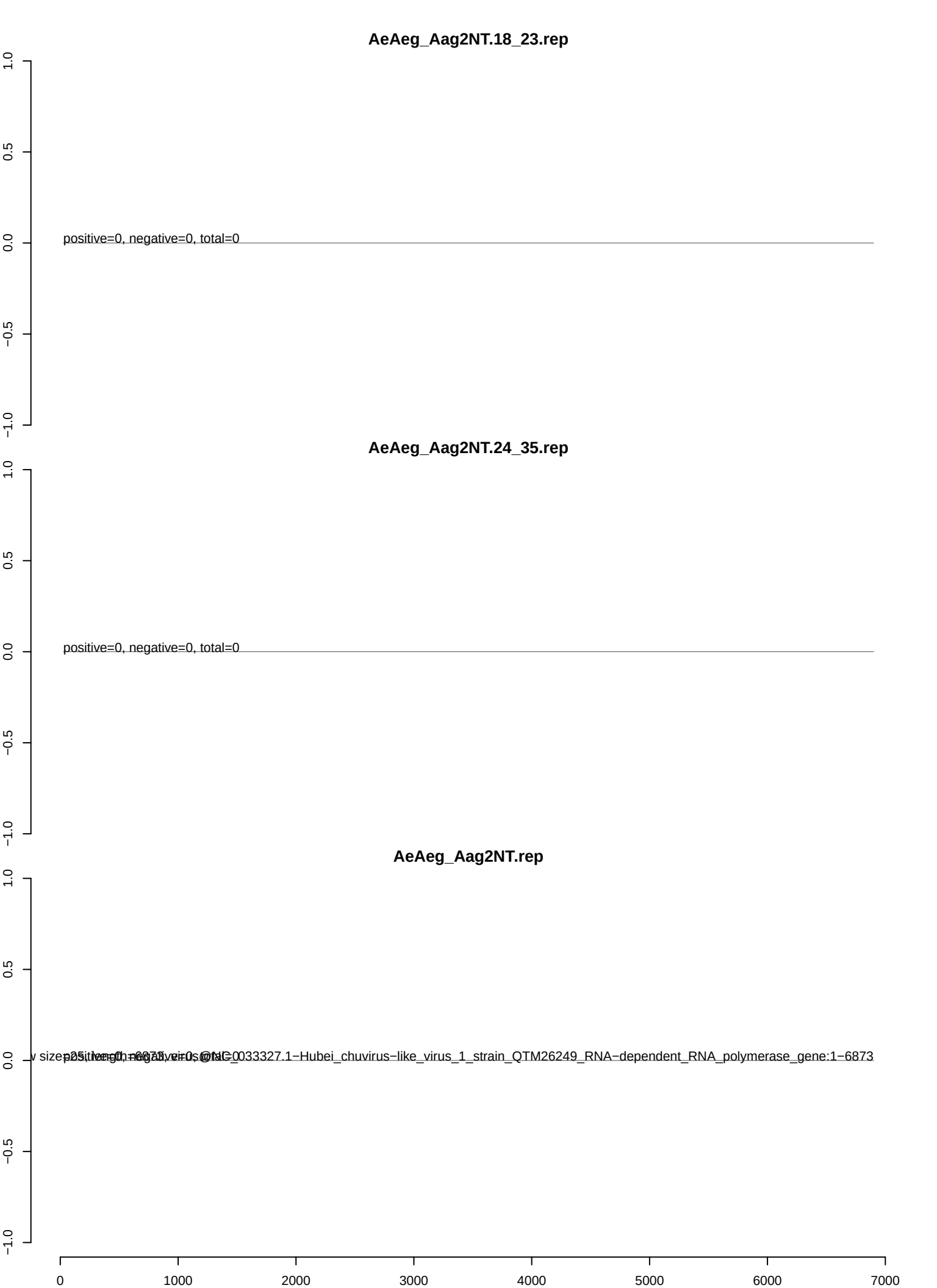
4000
6000
8000
10000


AeAeg_Aag2NT.18_23.rep
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
positive=0, negative=0, total=0
Window size=25, length=9558, virus@NC_033716.1_Zhejiang_mosquito_virus_1_strain_mosZJ35497_hypothetical_protein_gene:1−9558
1.0
0.5
0.0
−0.5
−1.0
0
2000
4000
6000
8000


AeAeg_Aag2NT.18_23.rep
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positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
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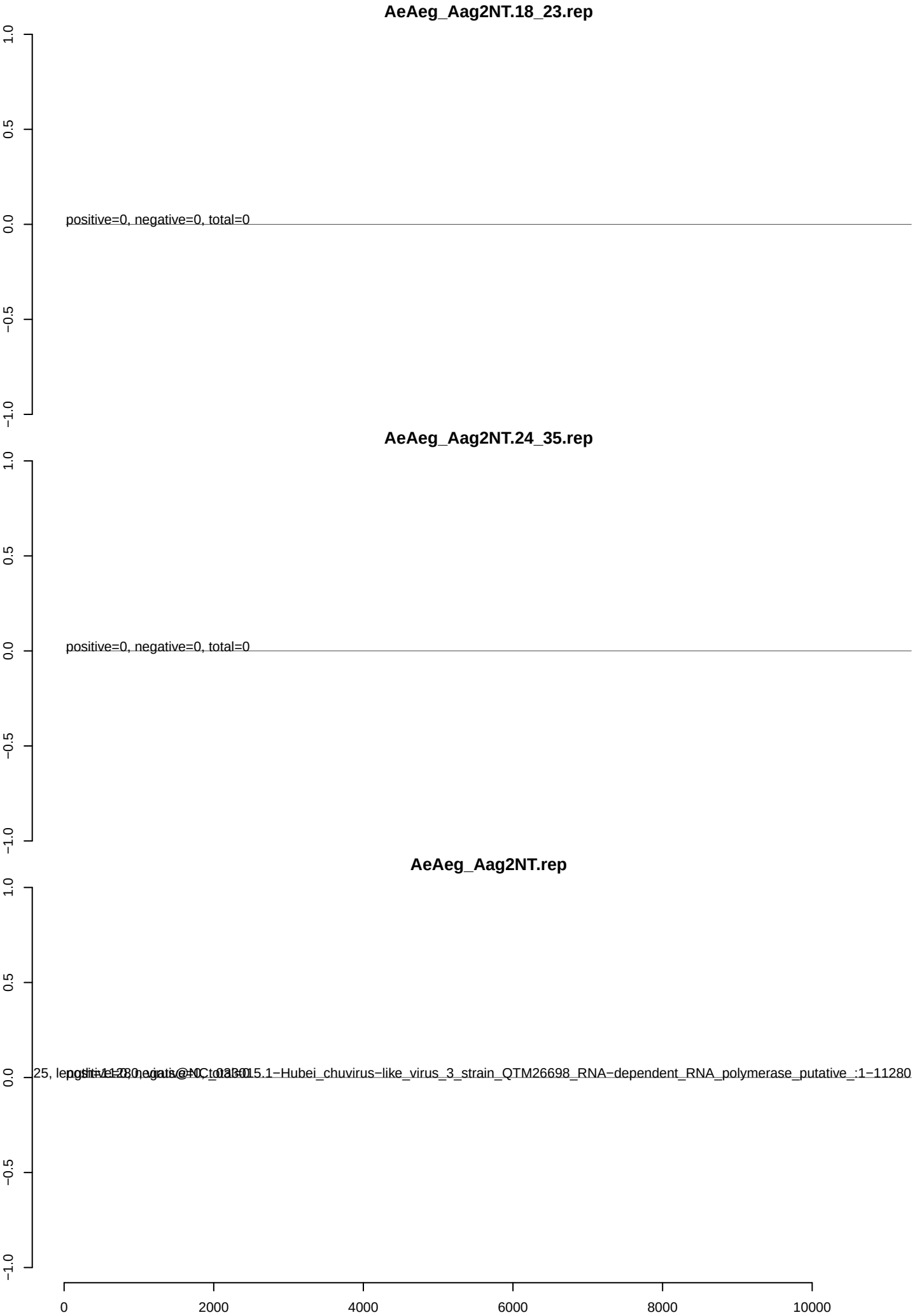
6000
7000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AeAeg_Aag2NT.24_35.rep
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
positive=1, negative=0, total=1
25, length=11280
gi|1234567|ref|NC_012345.1|Hubei_chuvirus-like_virus_3_strain_QTM26698_RNA-dependent_RNA_polymerase_putative_:1-11280
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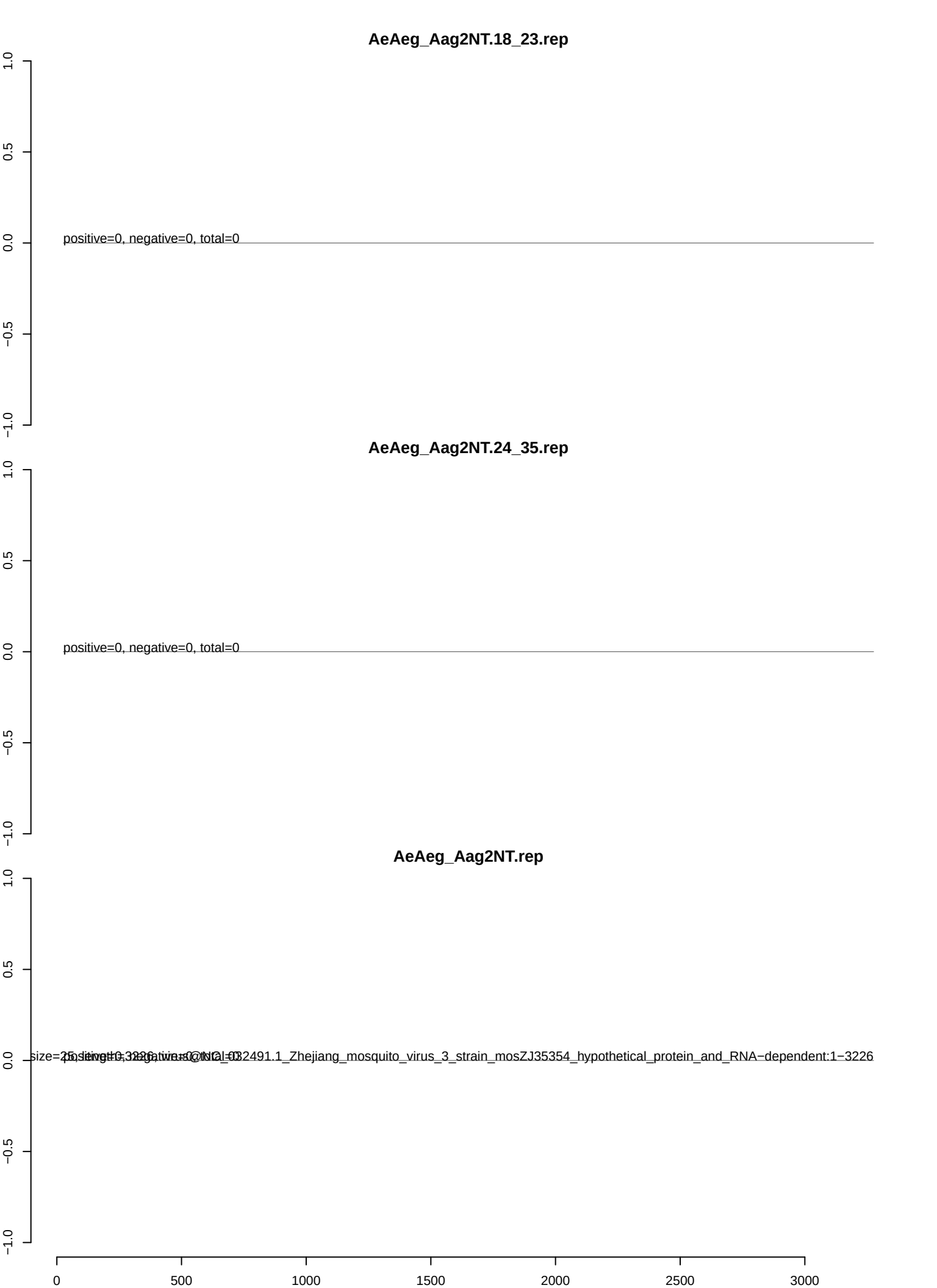
AeAeg_Aag2NT.18_23.rep
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
positive=0, negative=0, total=0
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size=25, length=3226, positive=0, negative=0, total=0
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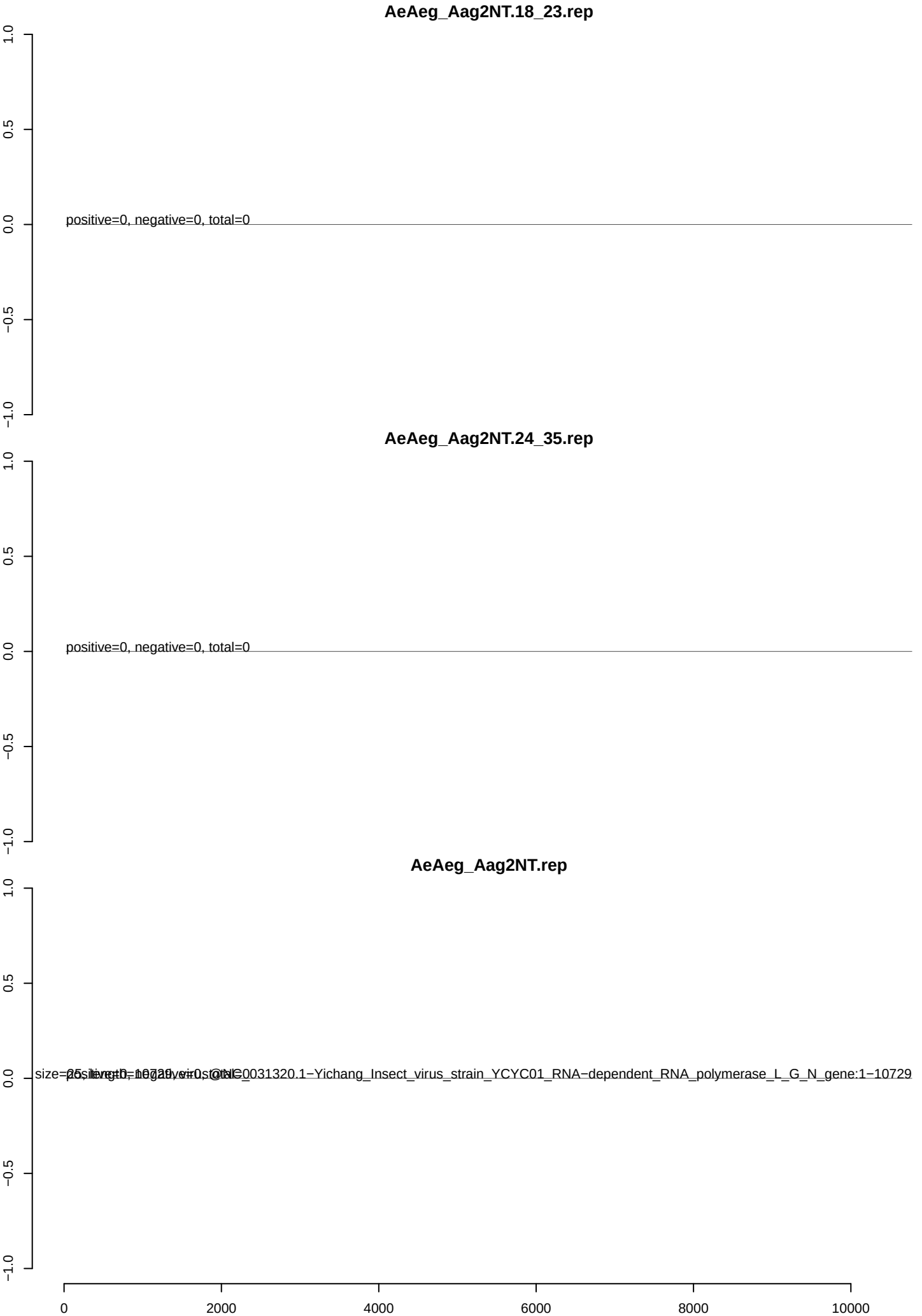
2500
3000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AeAeg_Aag2NT.24_35.rep
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
size=25, length=10729, positive=0, negative=0, total=0
gi|1873031320.1|GNL|Yichang_Insect_virus_strain_YCYC01_RNA-dependent_RNA_polymerase_L_G_N_gene:1-10729
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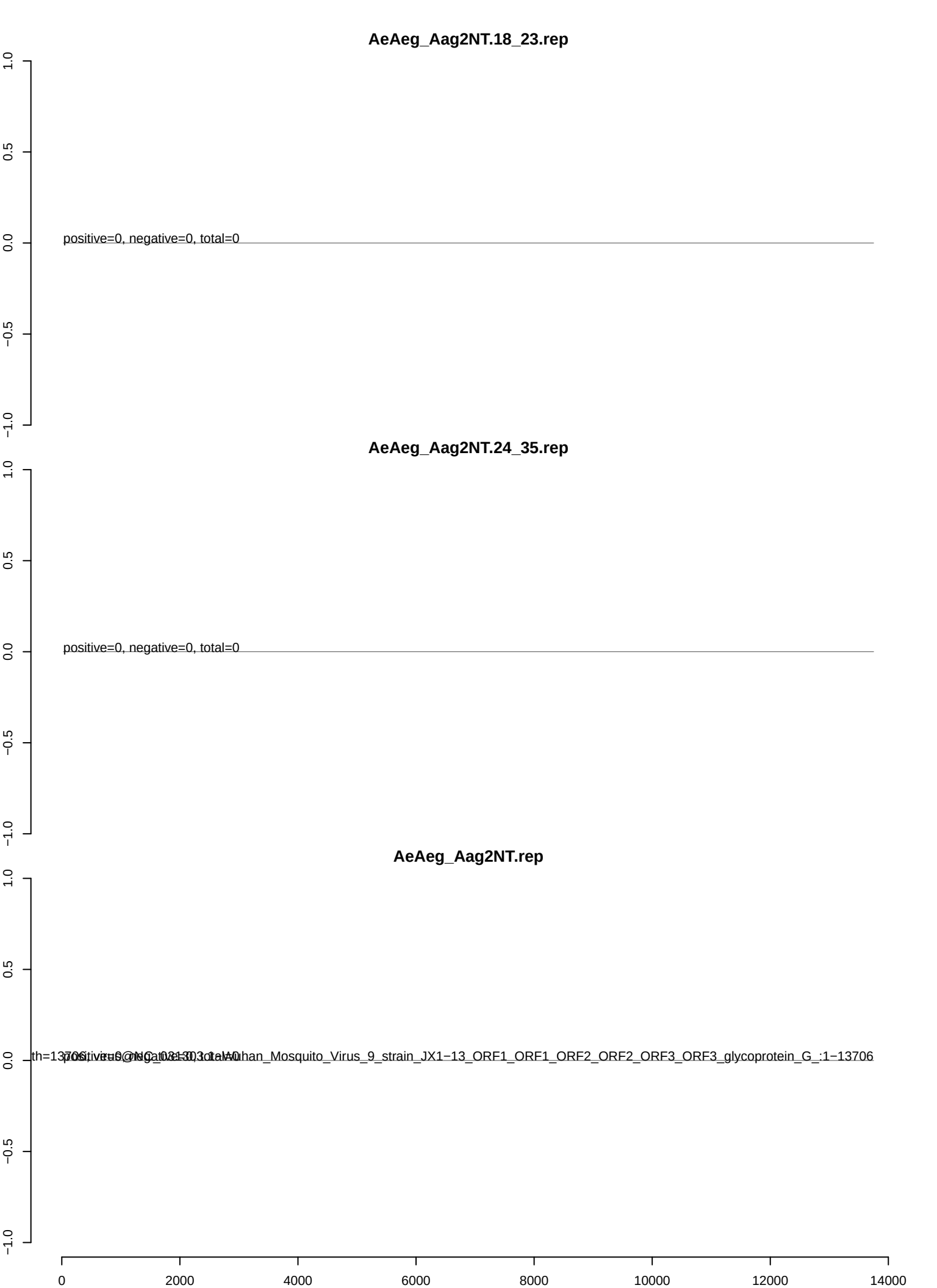
AeAeg_Aag2NT.18_23.rep
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
positive=0, negative=0, total=0
Wuhan_Mosquito_Virus_9_strain_JX1−13_ORF1_ORF1_ORF2_ORF2_ORF3_ORF3_glycoprotein_G_:1−13706
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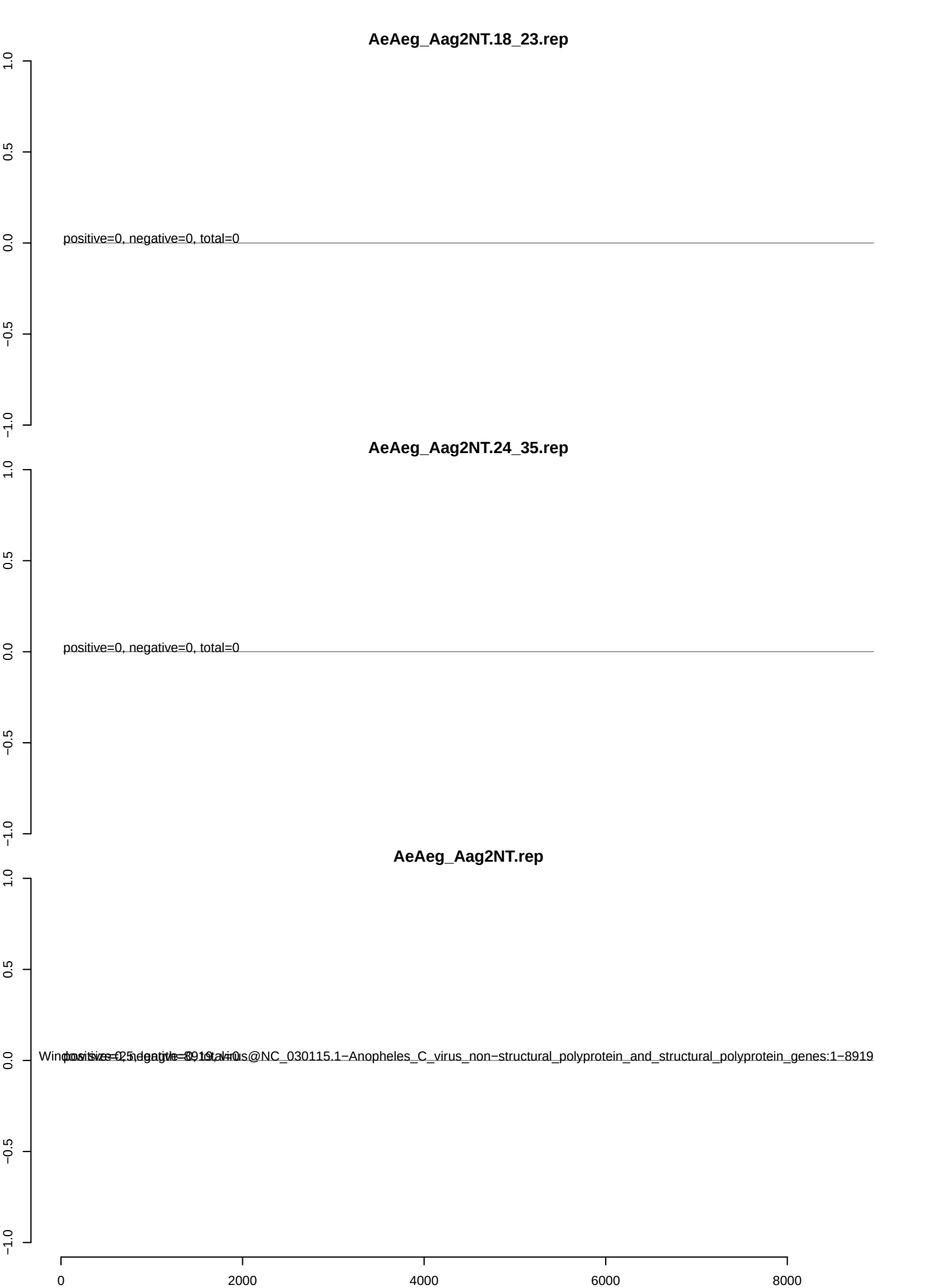
14000


AeAeg_Aag2NT.18_23.rep
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AeAeg_Aag2NT.24_35.rep
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
positive=25, negative=8919, total=0
Windows@Anopheles_C_virus@NC_030115.1−Anopheles_C_virus_non−structural_polyprotein_and_structural_polyprotein_genes:1−8919
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6000
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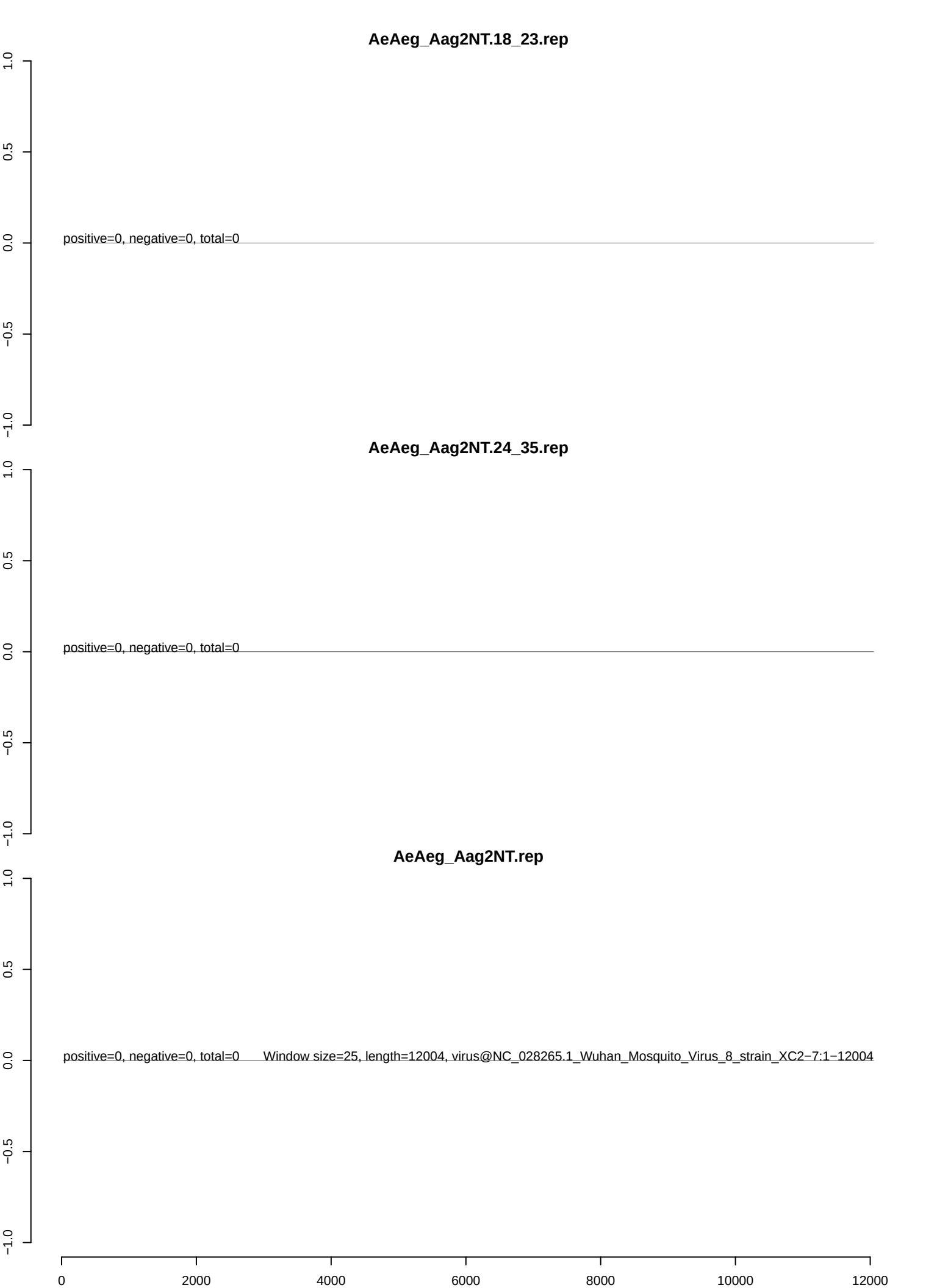
AeAeg_Aag2NT.18_23.rep
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
positive=0, negative=0, total=0
Window size=25, length=12004, virus@NC_028265.1_Wuhan_Mosquito_Virus_8_strain_XC2−7:1−12004
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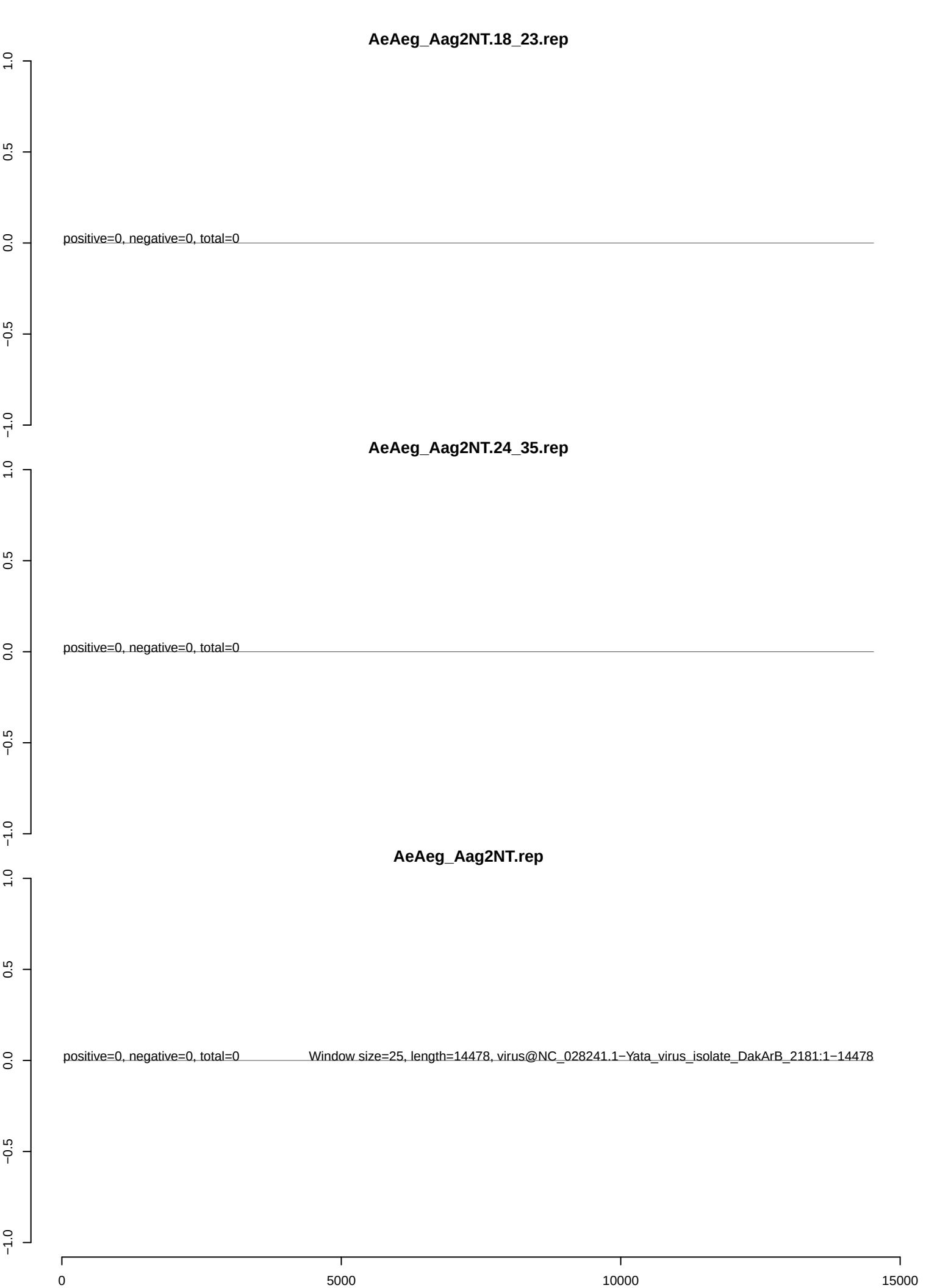
AeAeg_Aag2NT.18_23.rep
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
positive=0, negative=0, total=0
Window size=25, length=14478, virus@NC_028241.1−Yata_virus_isolate_DakArB_2181:1−14478
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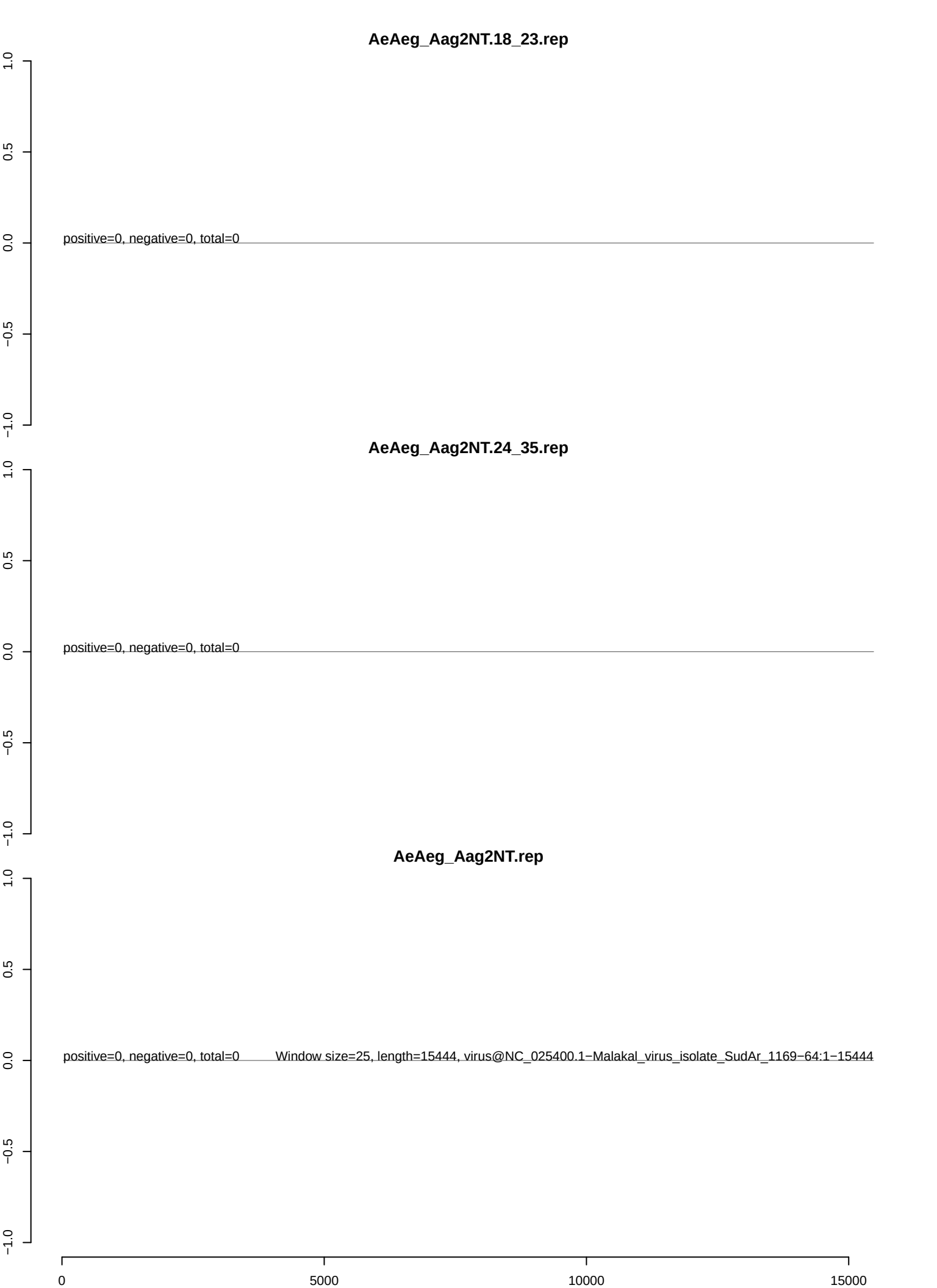
AeAeg_Aag2NT.18_23.rep
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
positive=0, negative=0, total=0
Window size=25, length=15444, virus@NC_025400.1−Malakal_virus_isolate_SudAr_1169−64:1−15444
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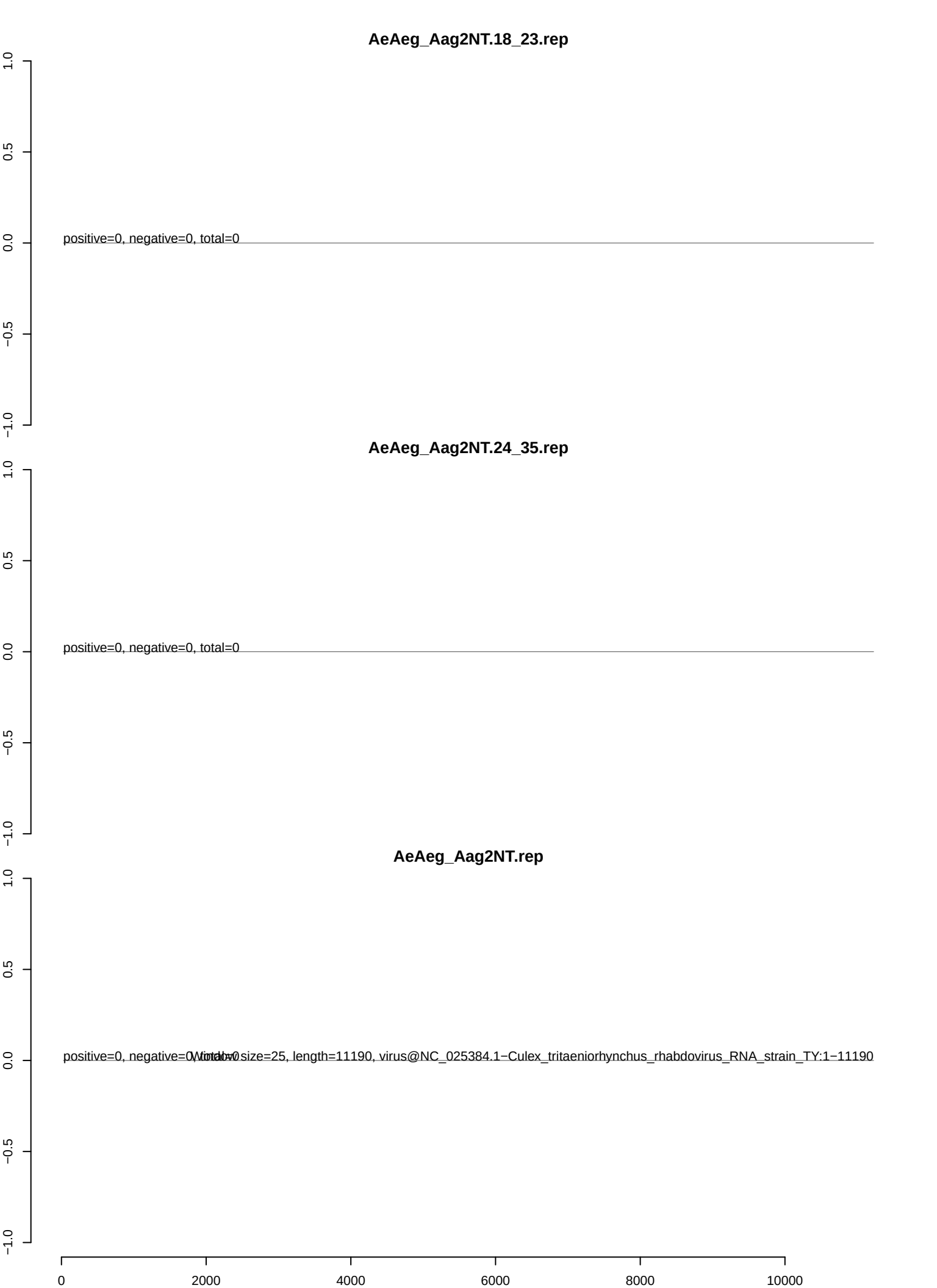
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AeAeg_Aag2NT.24_35.rep
positive=0, negative=0, total=0
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positive=0, negative=0, total=0
window size=25, length=11190, virus@NC_025384.1−Culex_tritaeniorhynchus_rhabdovirus_RNA_strain_TY:1−11190
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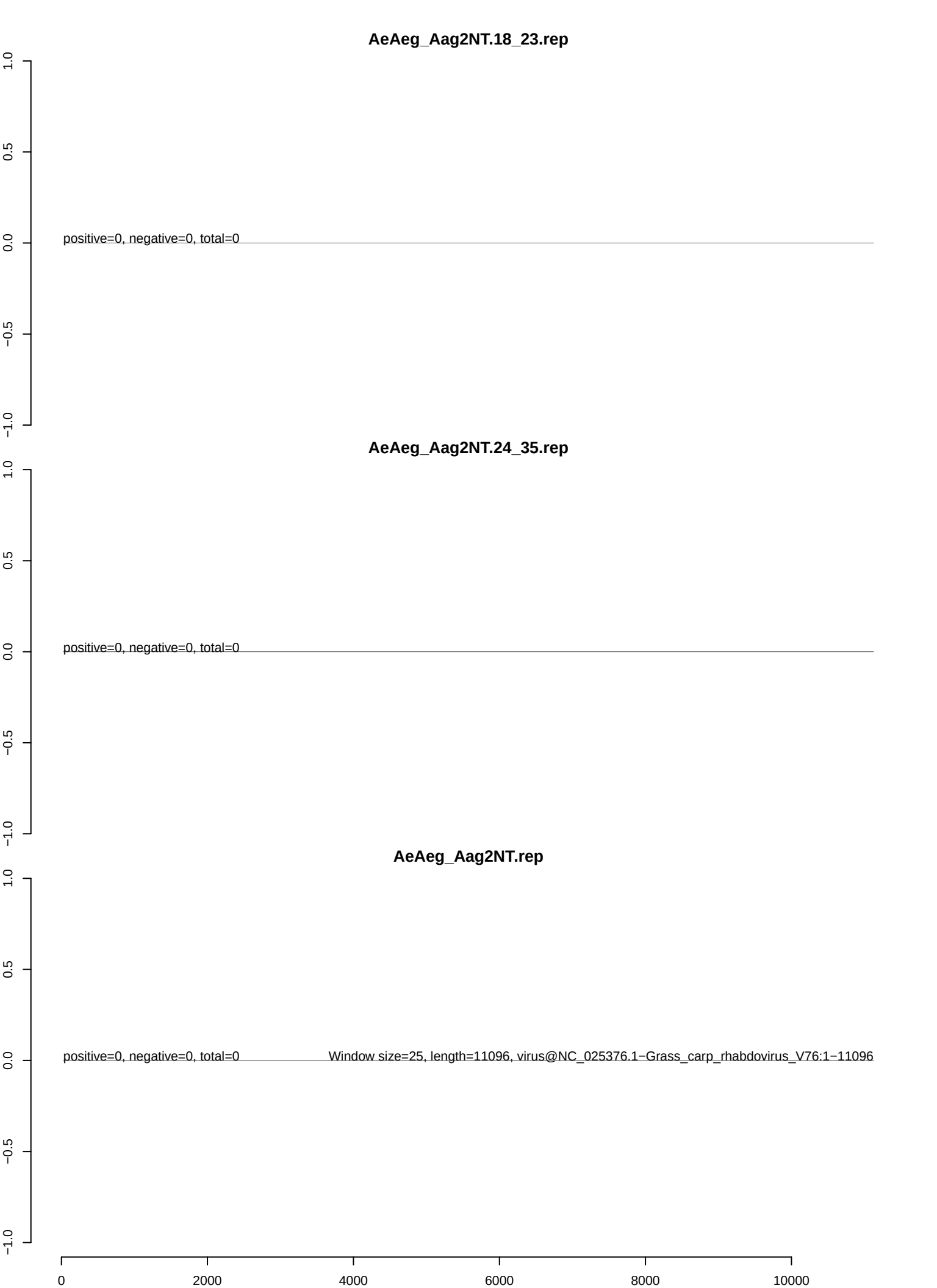
AeAeg_Aag2NT.18_23.rep
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
positive=0, negative=0, total=0
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positive=0, negative=0, total=0
Window size=25, length=11096, virus@NC_025376.1−Grass_carp_rhabdovirus_V76:1−11096
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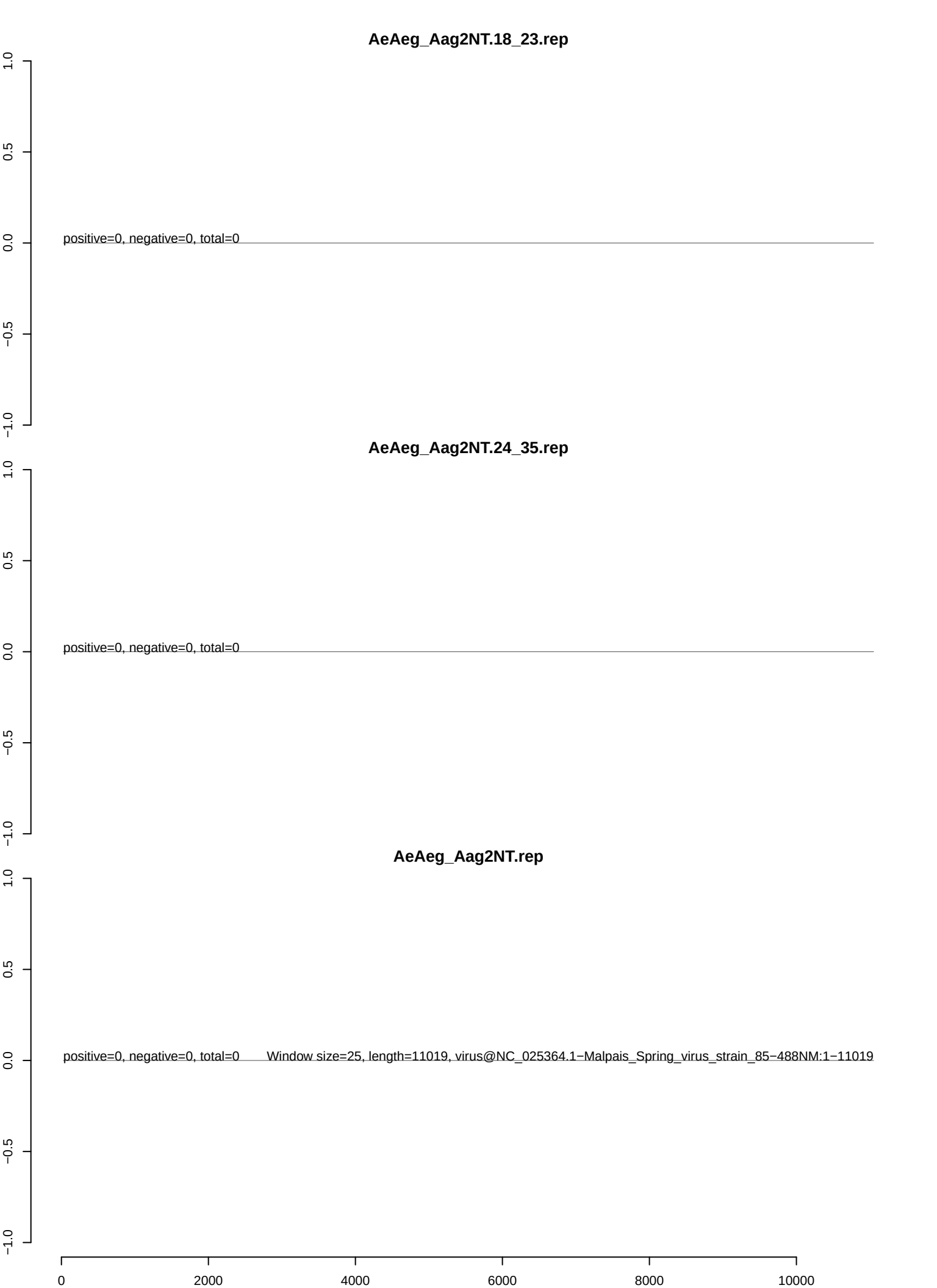
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positive=0, negative=0, total=0
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positive=0, negative=0, total=0
Window size=25, length=11019, virus@NC_025364.1−Malpais_Spring_virus_strain_85−488NM:1−11019
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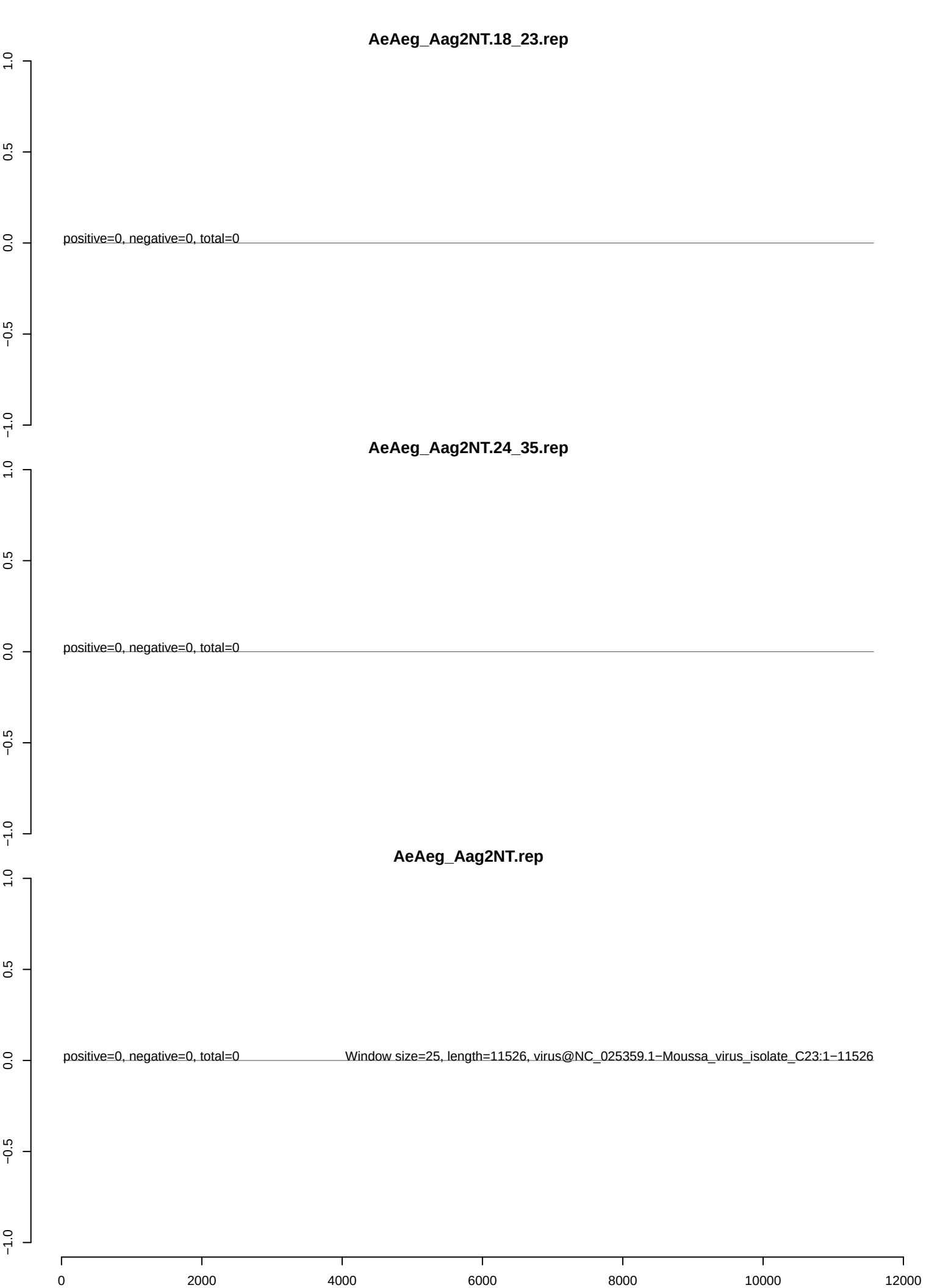
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positive=0, negative=0, total=0
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positive=0, negative=0, total=0
Window size=25, length=11526, virus@NC_025359.1−Moussa_virus_isolate_C23:1−11526
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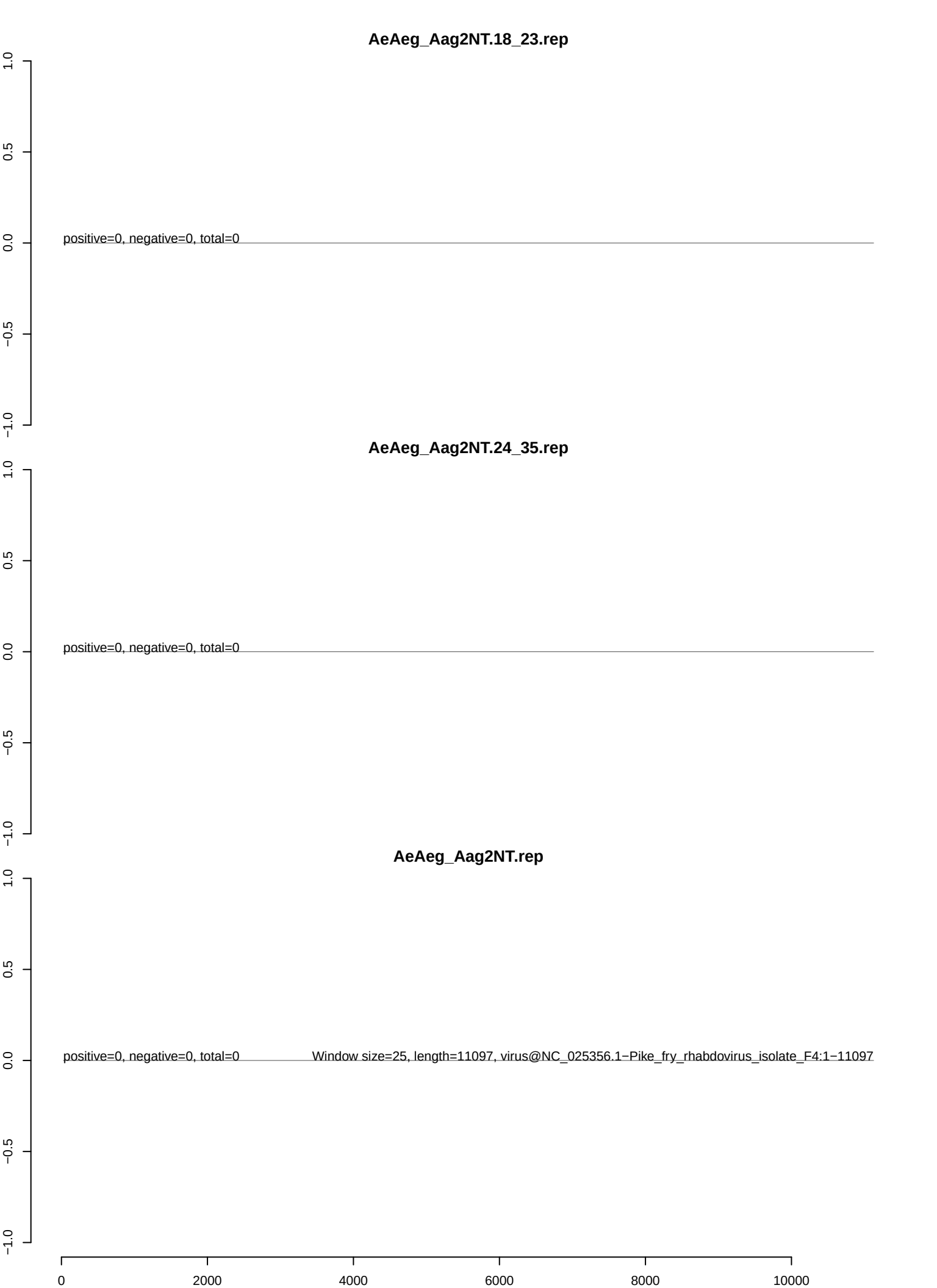
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positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
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0.0
−0.5
−1.0
positive=0, negative=0, total=0
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0.0
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−1.0
positive=0, negative=0, total=0
Window size=25, length=11097, virus@NC_025356.1−Pike_fry_rhabdovirus_isolate_F4:1−11097
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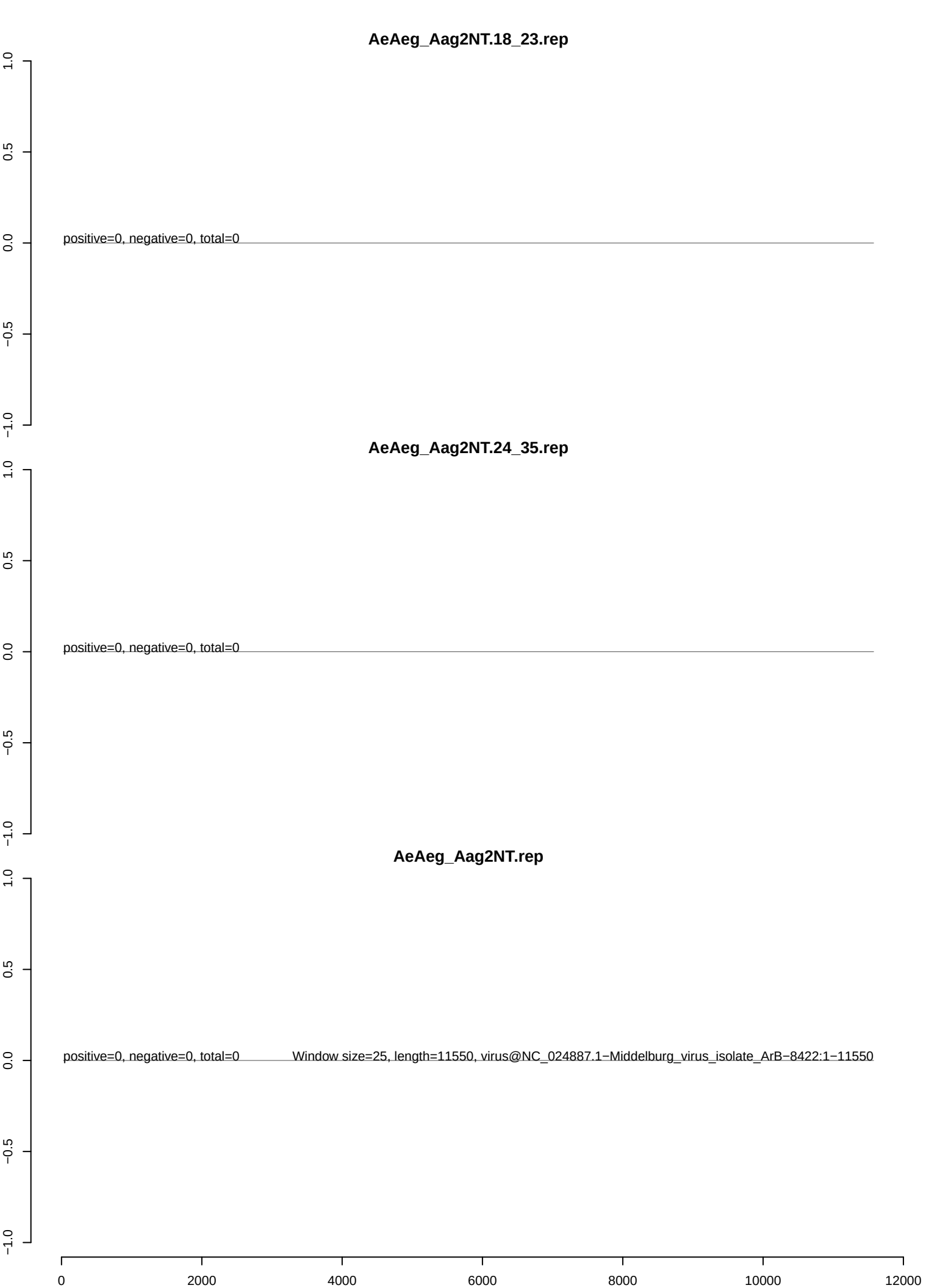
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AeAeg_Aag2NT.24_35.rep
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
positive=0, negative=0, total=0
Window size=25, length=11550, virus@NC_024887.1−Middelburg_virus_isolate_ArB−8422:1−11550
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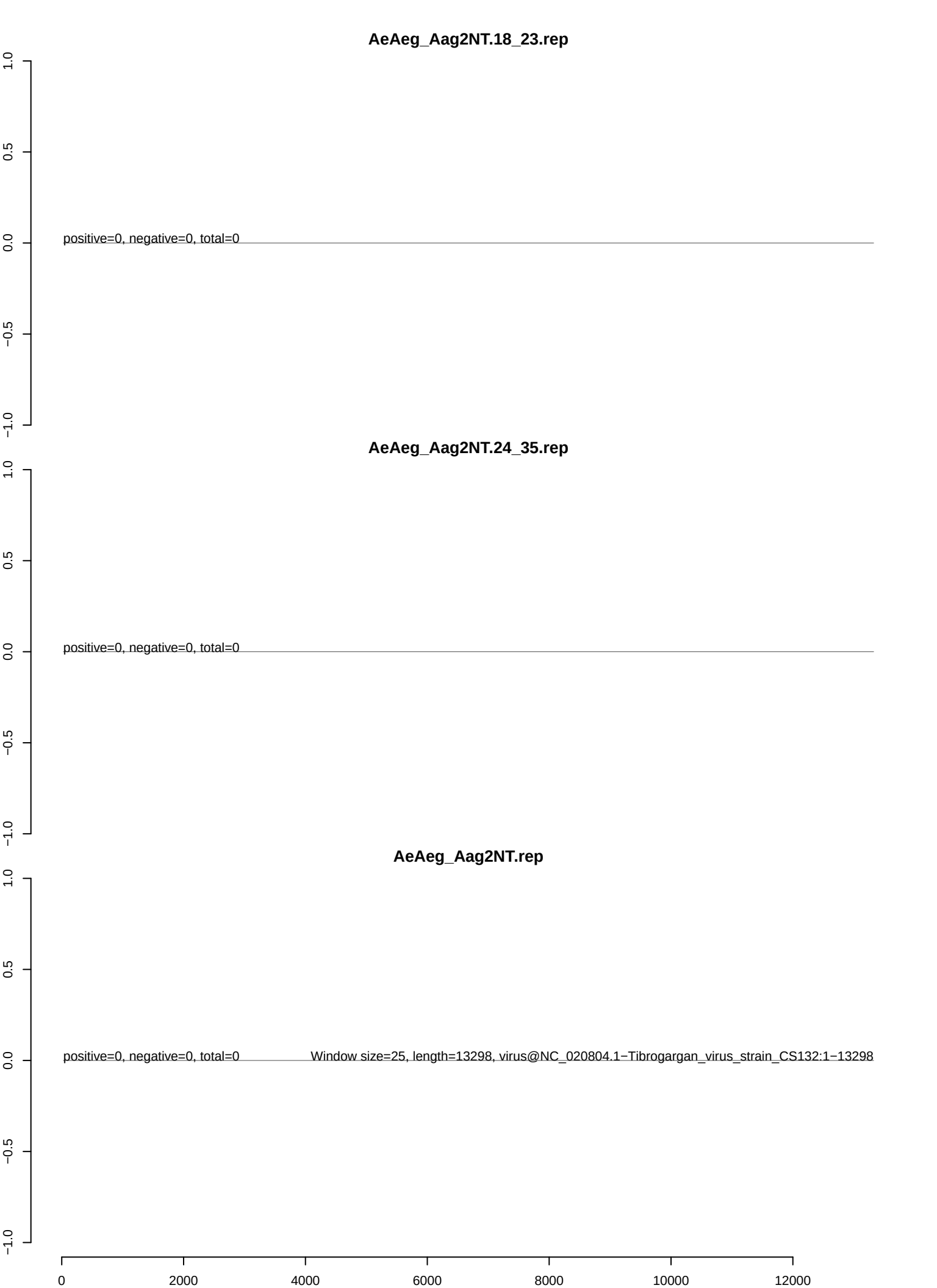
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AeAeg_Aag2NT.24_35.rep
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
positive=0, negative=0, total=0
Window size=25, length=13298, virus@NC_020804.1−Tibrogargan_virus_strain_CS132:1−13298
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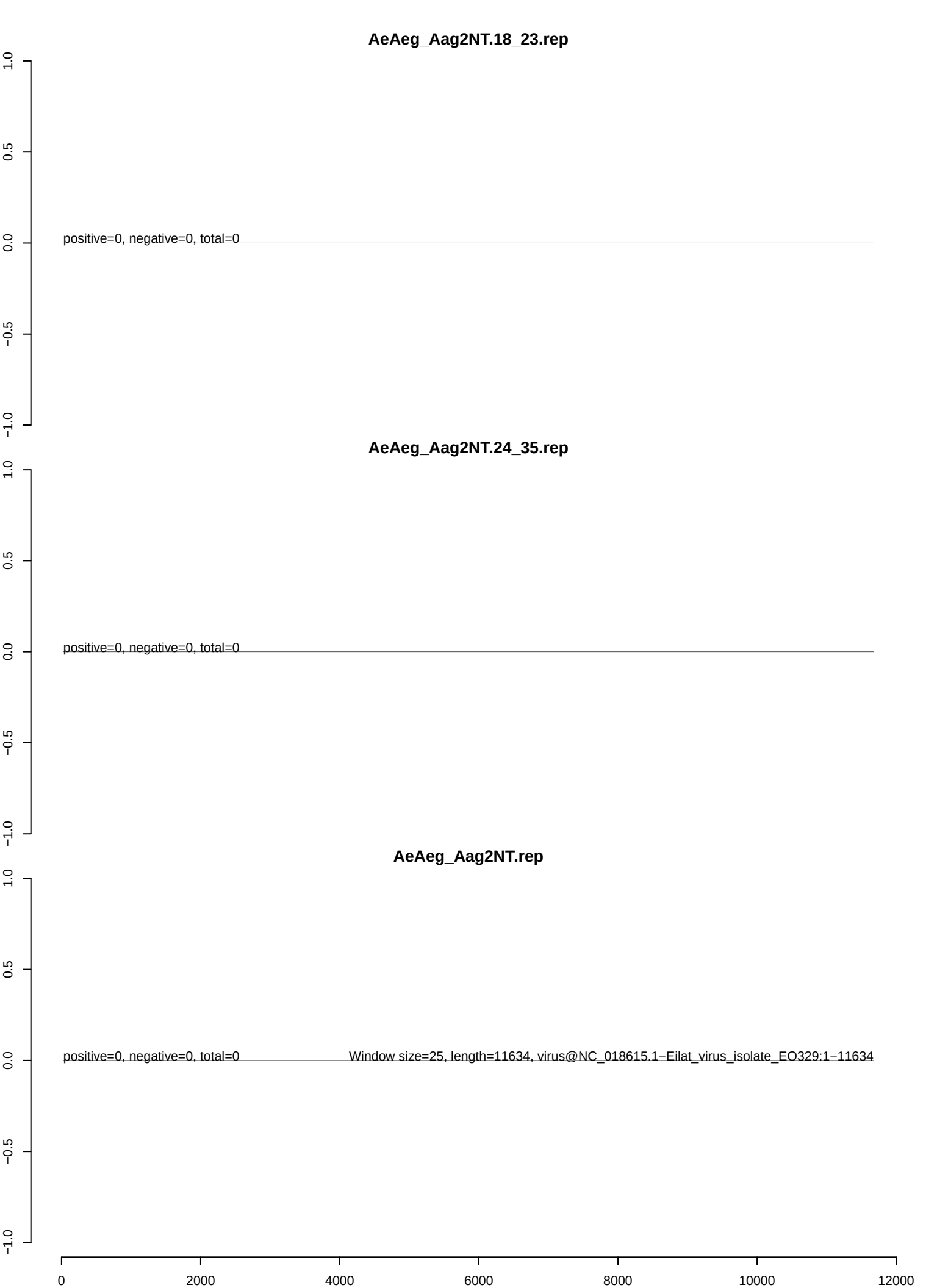
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positive=0, negative=0, total=0
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positive=0, negative=0, total=0
Window size=25, length=11634, virus@NC_018615.1−Eilat_virus_isolate_EO329:1−11634
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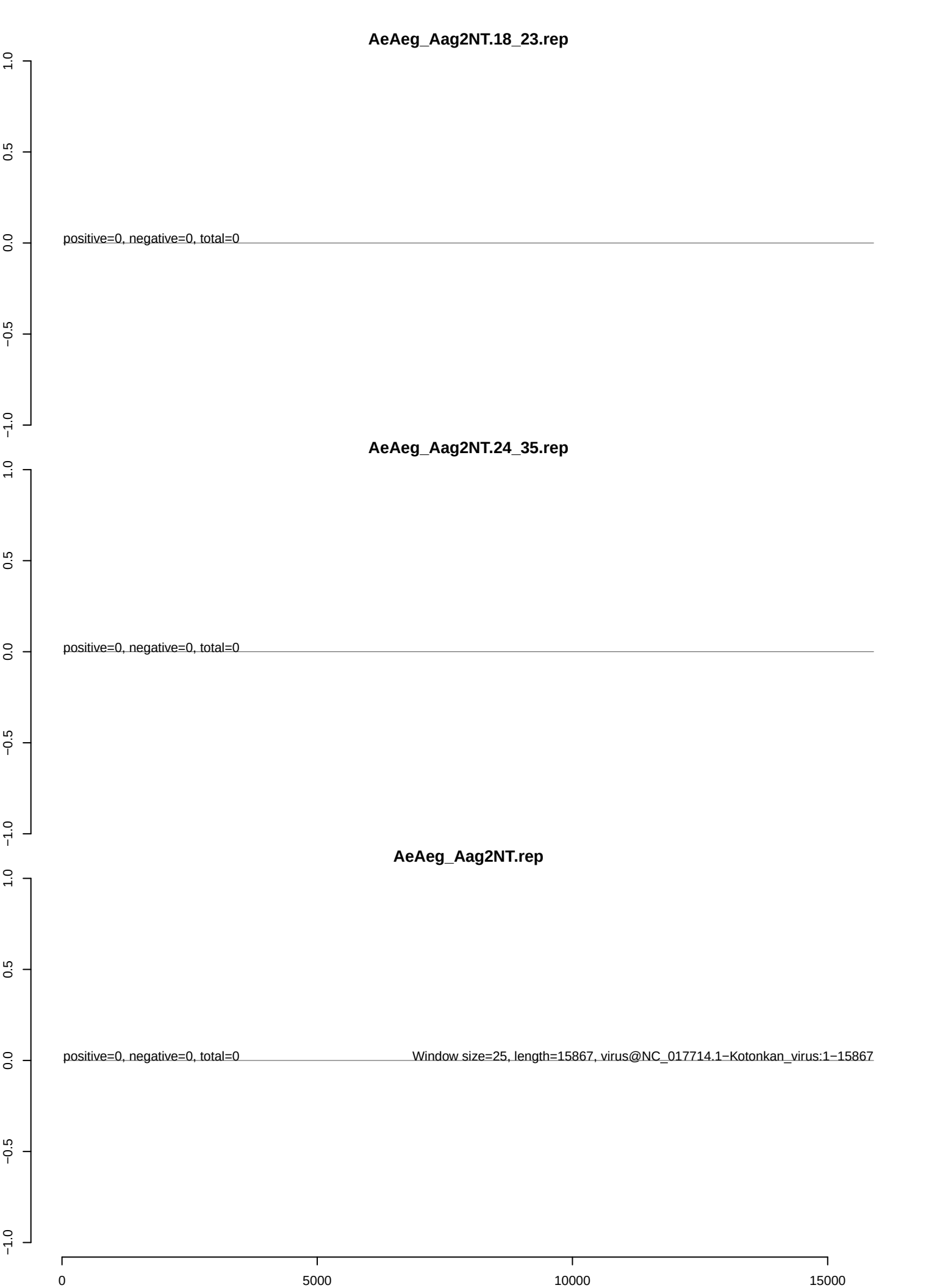
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AeAeg_Aag2NT.24_35.rep
positive=0, negative=0, total=0
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positive=0, negative=0, total=0
Window size=25, length=15867, virus@NC_017714.1−Kotonkan_virus:1−15867
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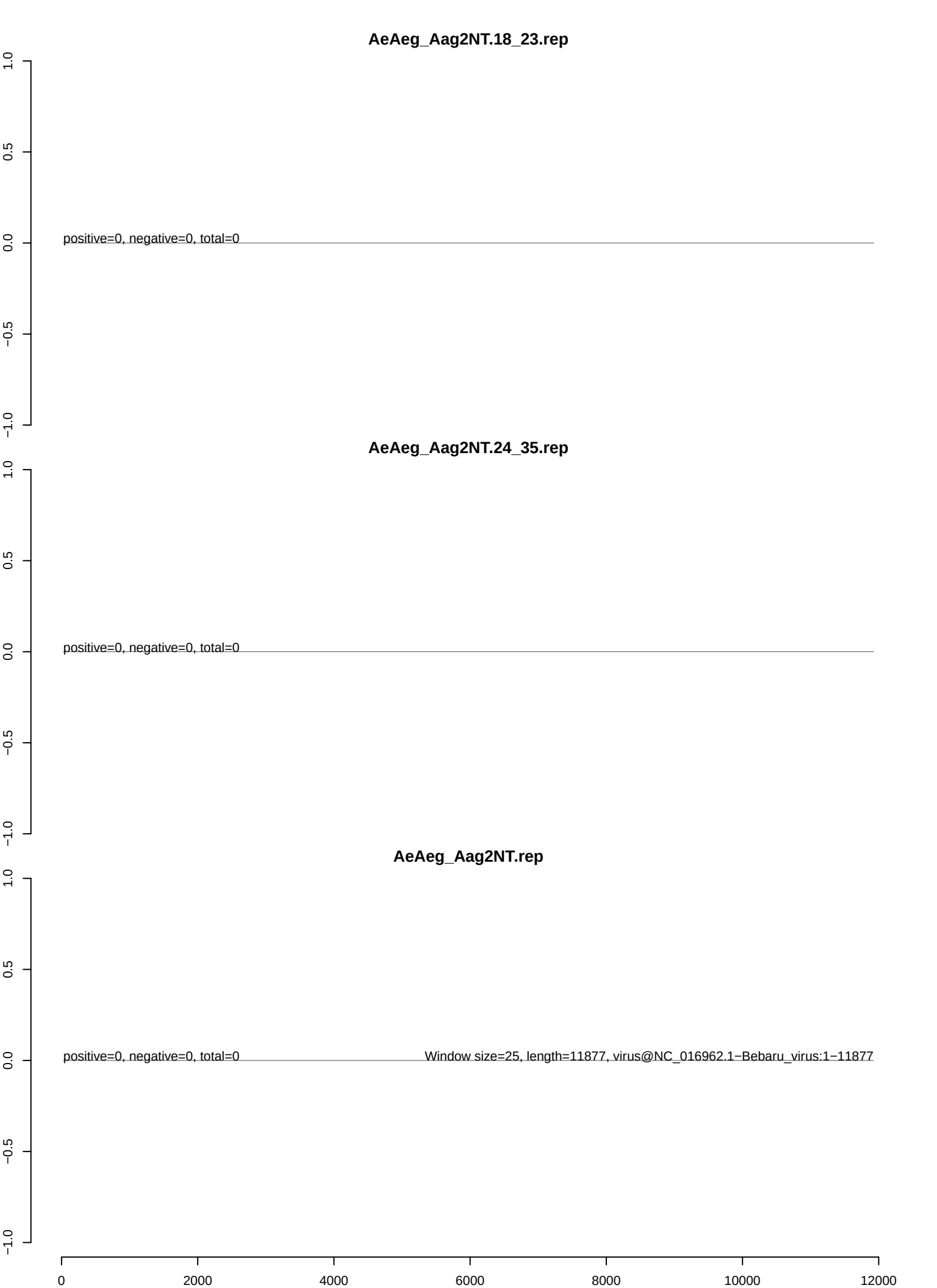
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positive=0, negative=0, total=0
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positive=0, negative=0, total=0
Window size=25, length=11877, virus@NC_016962.1−Bebaru_virus:1−11877
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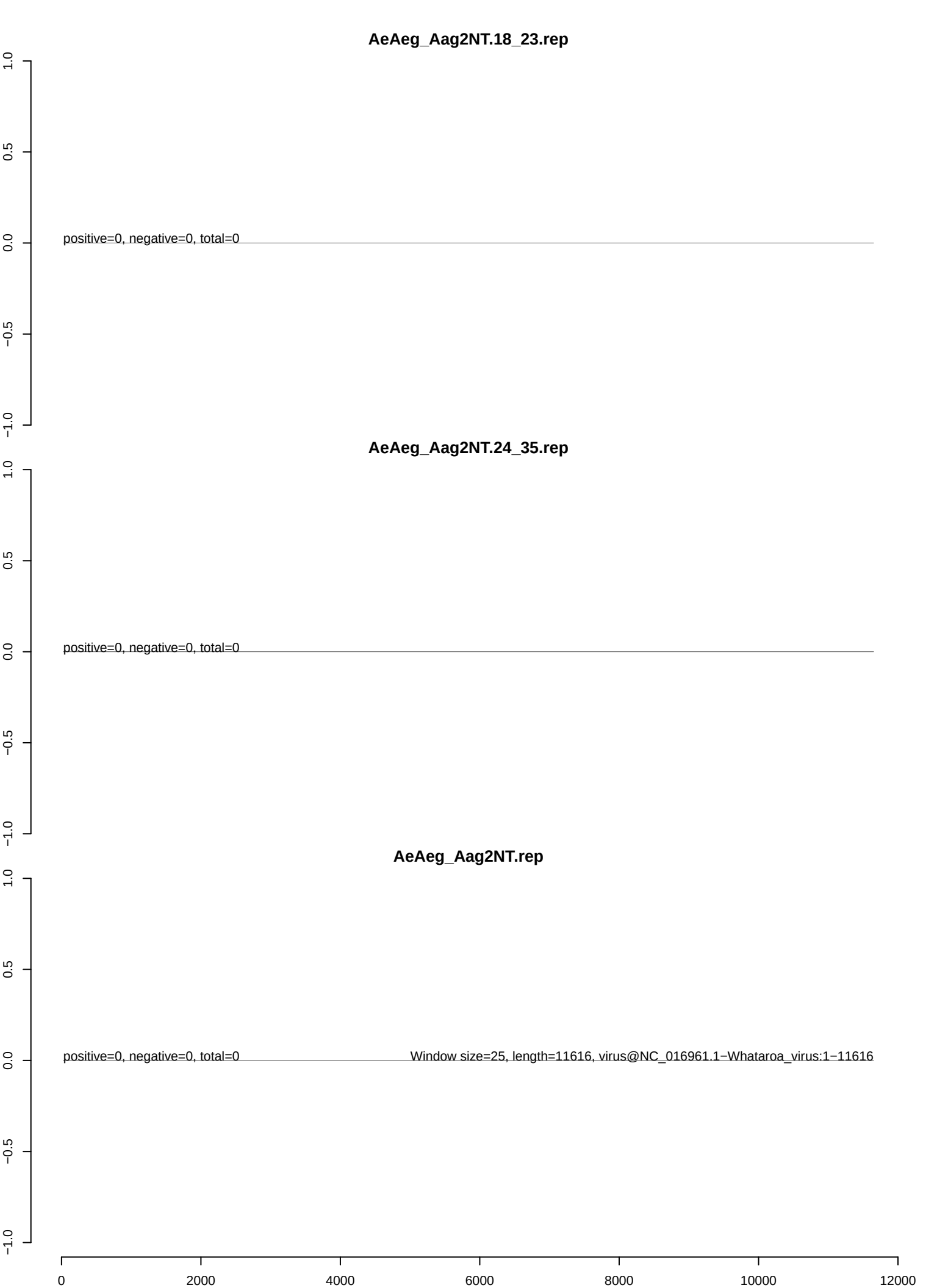
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positive=0, negative=0, total=0
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positive=0, negative=0, total=0
Window size=25, length=11616, virus@NC_016961.1−Whataroa_virus:1−11616
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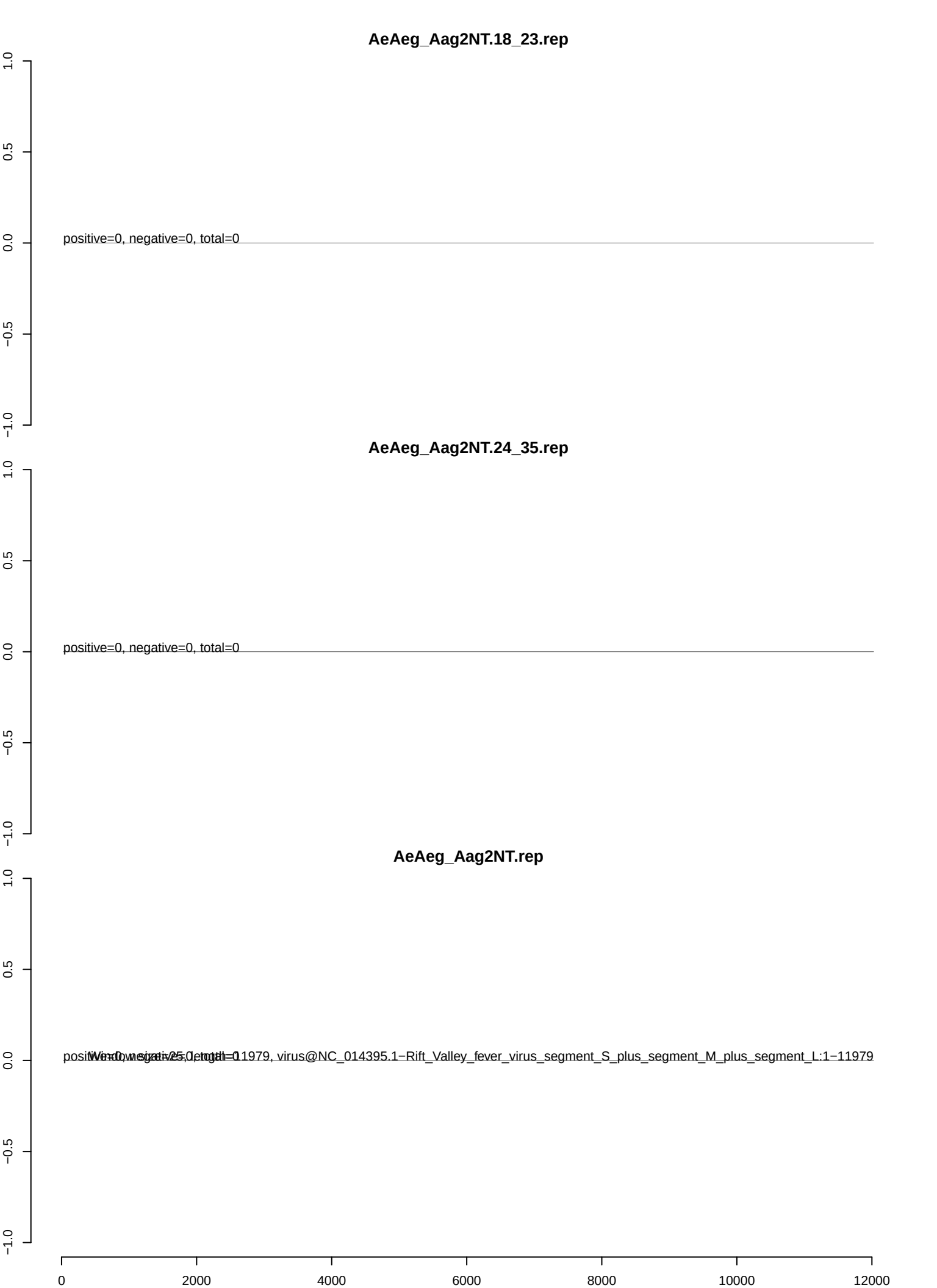
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Window size=25, length=11979, virus@NC_014395.1−Rift_Valley_fever_virus_segment_S_plus_segment_M_plus_segment_L:1−11979
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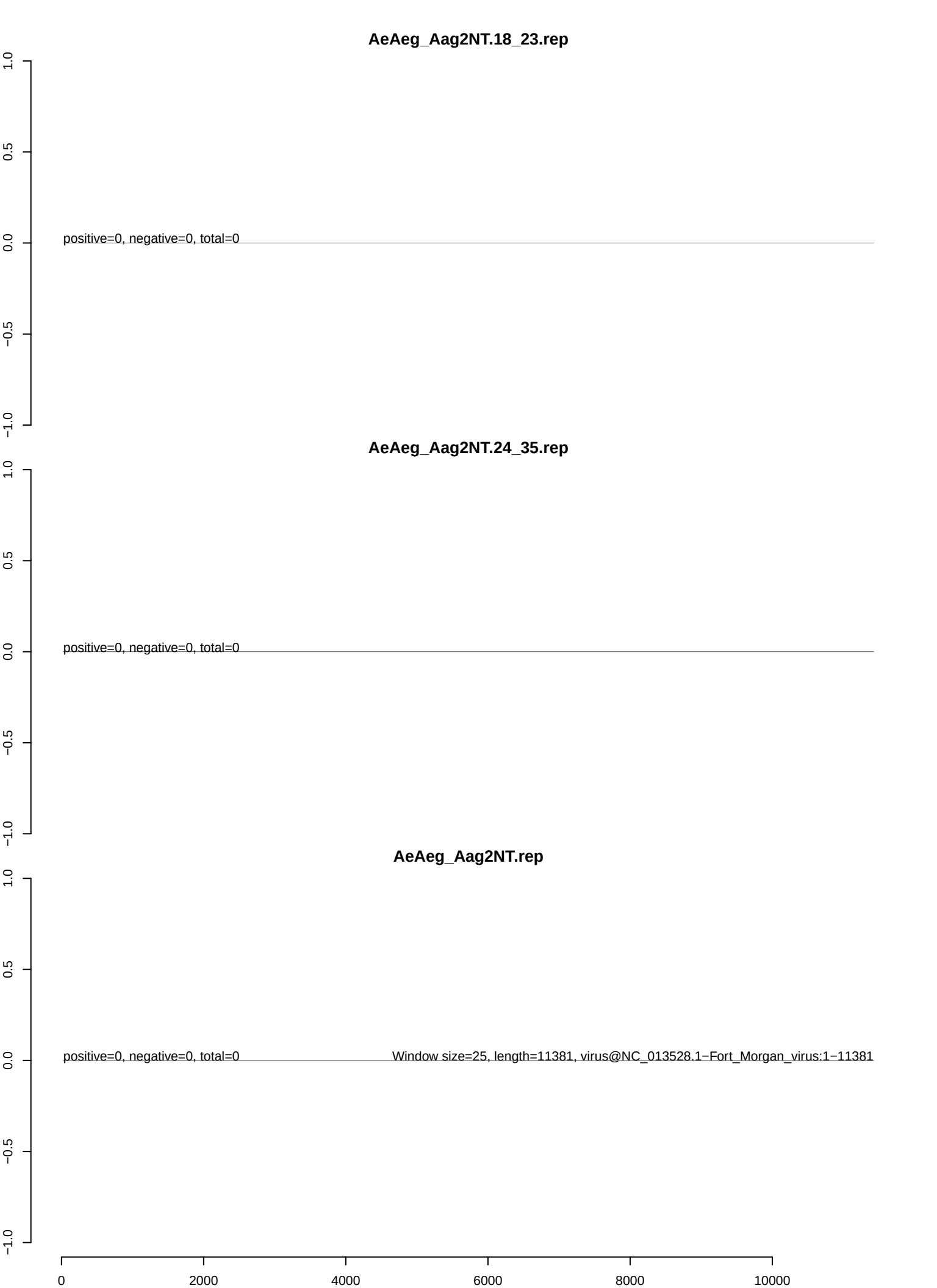
AeAeg_Aag2NT.18_23.rep
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AeAeg_Aag2NT.24_35.rep
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positive=0, negative=0, total=0
Window size=25, length=11381, virus@NC_013528.1−Fort_Morgan_virus:1−11381
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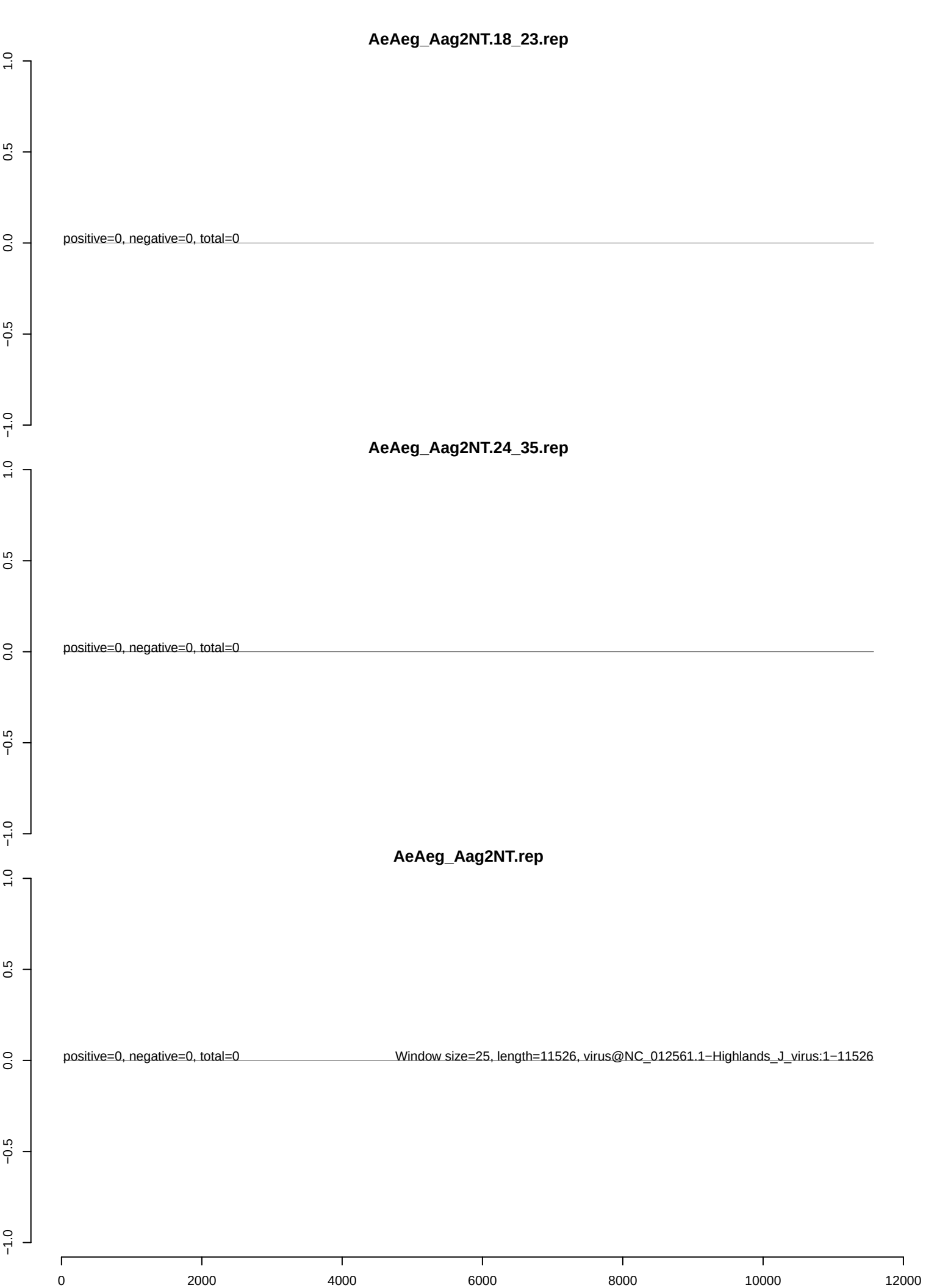
AeAeg_Aag2NT.18_23.rep
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
positive=0, negative=0, total=0
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positive=0, negative=0, total=0
Window size=25, length=11526, virus@NC_012561.1−Highlands_J_virus:1−11526
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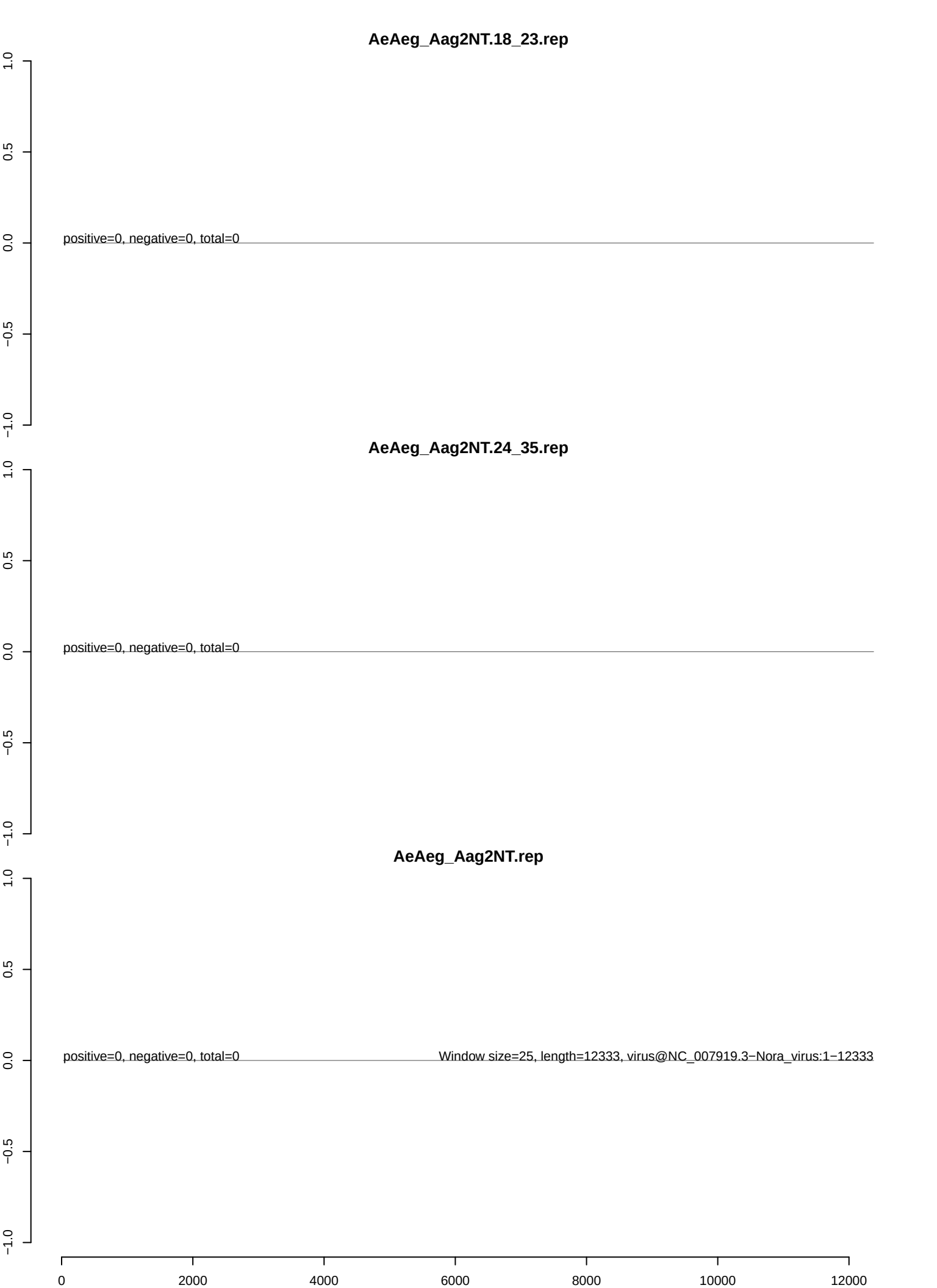
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positive=0, negative=0, total=0
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positive=0, negative=0, total=0
Window size=25, length=12333, virus@NC_007919.3−Nora_virus:1−12333
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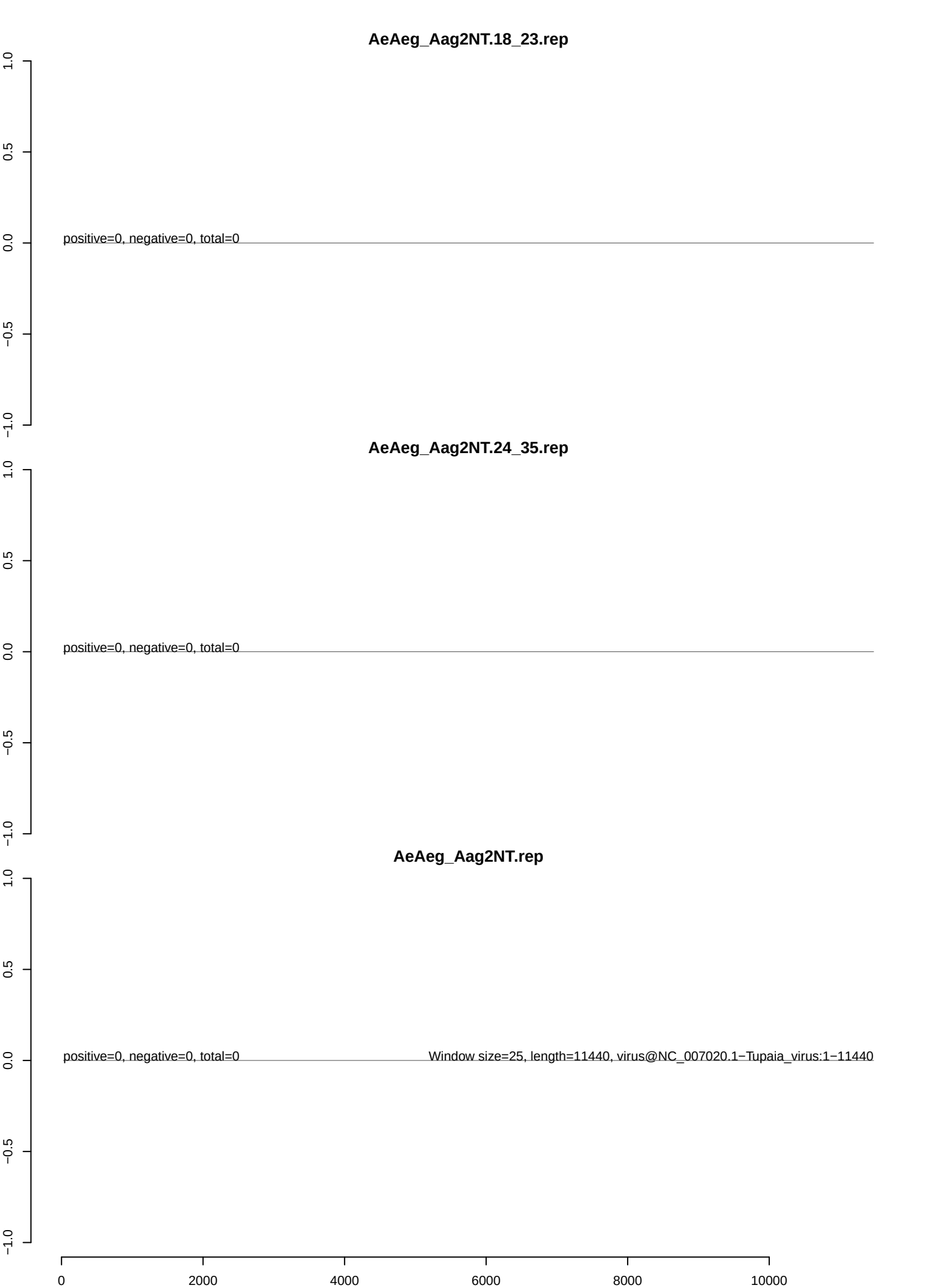
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AeAeg_Aag2NT.24_35.rep
positive=0, negative=0, total=0
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Window size=25, length=11440, virus@NC_007020.1−Tupaia_virus:1−11440
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8000
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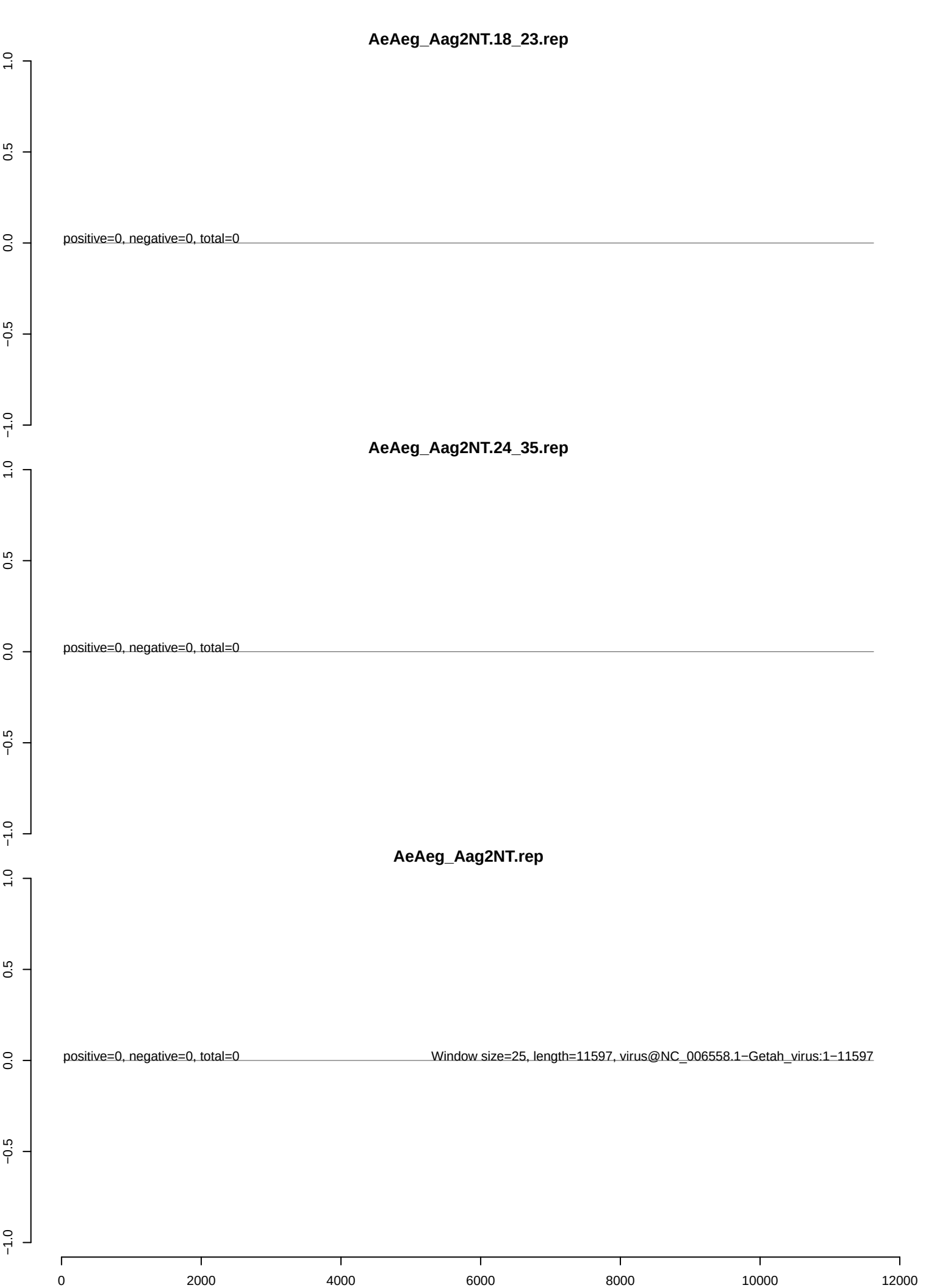
AeAeg_Aag2NT.18_23.rep
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
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Window size=25, length=11597, virus@NC_006558.1−Getah_virus:1−11597
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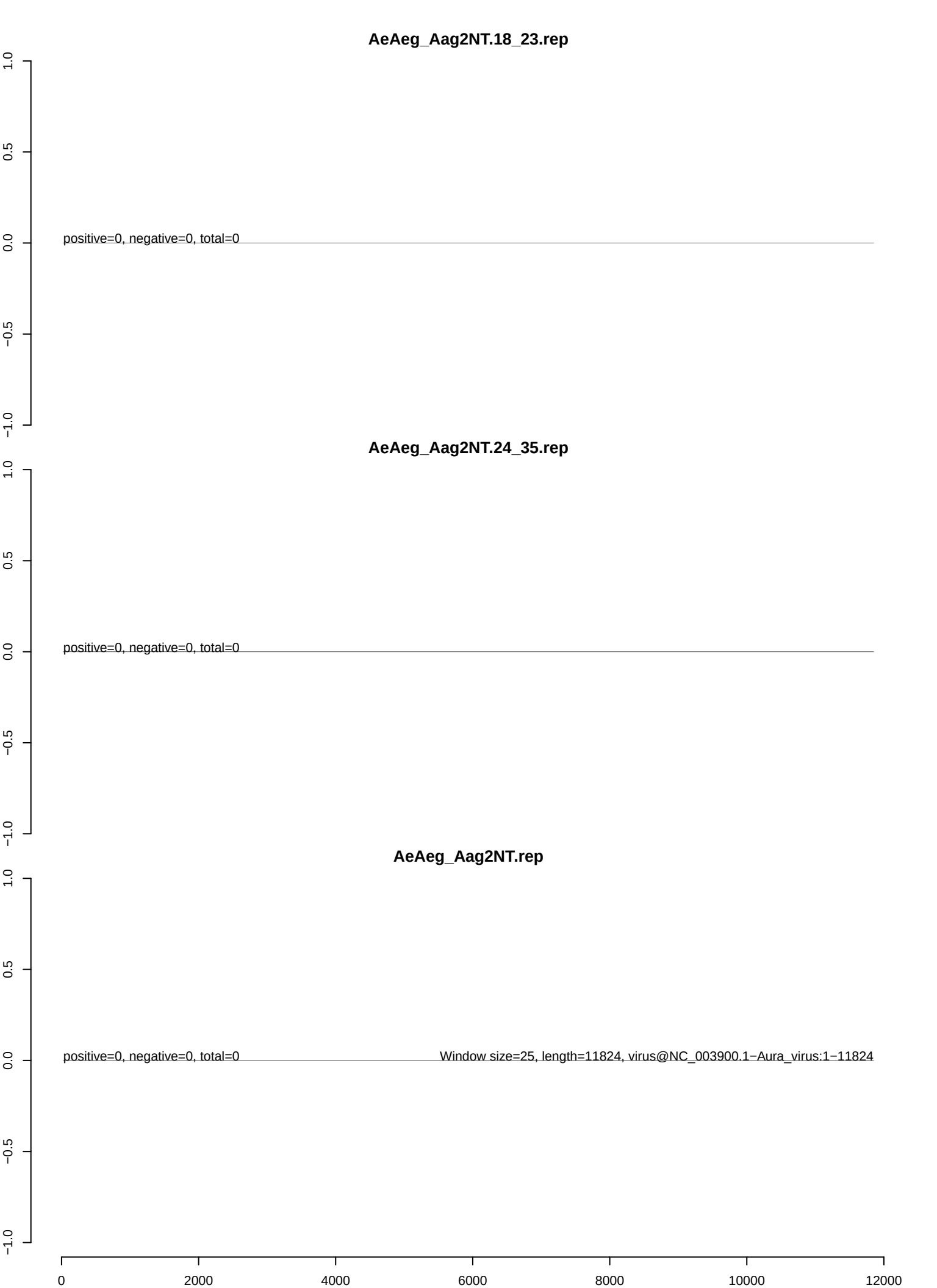
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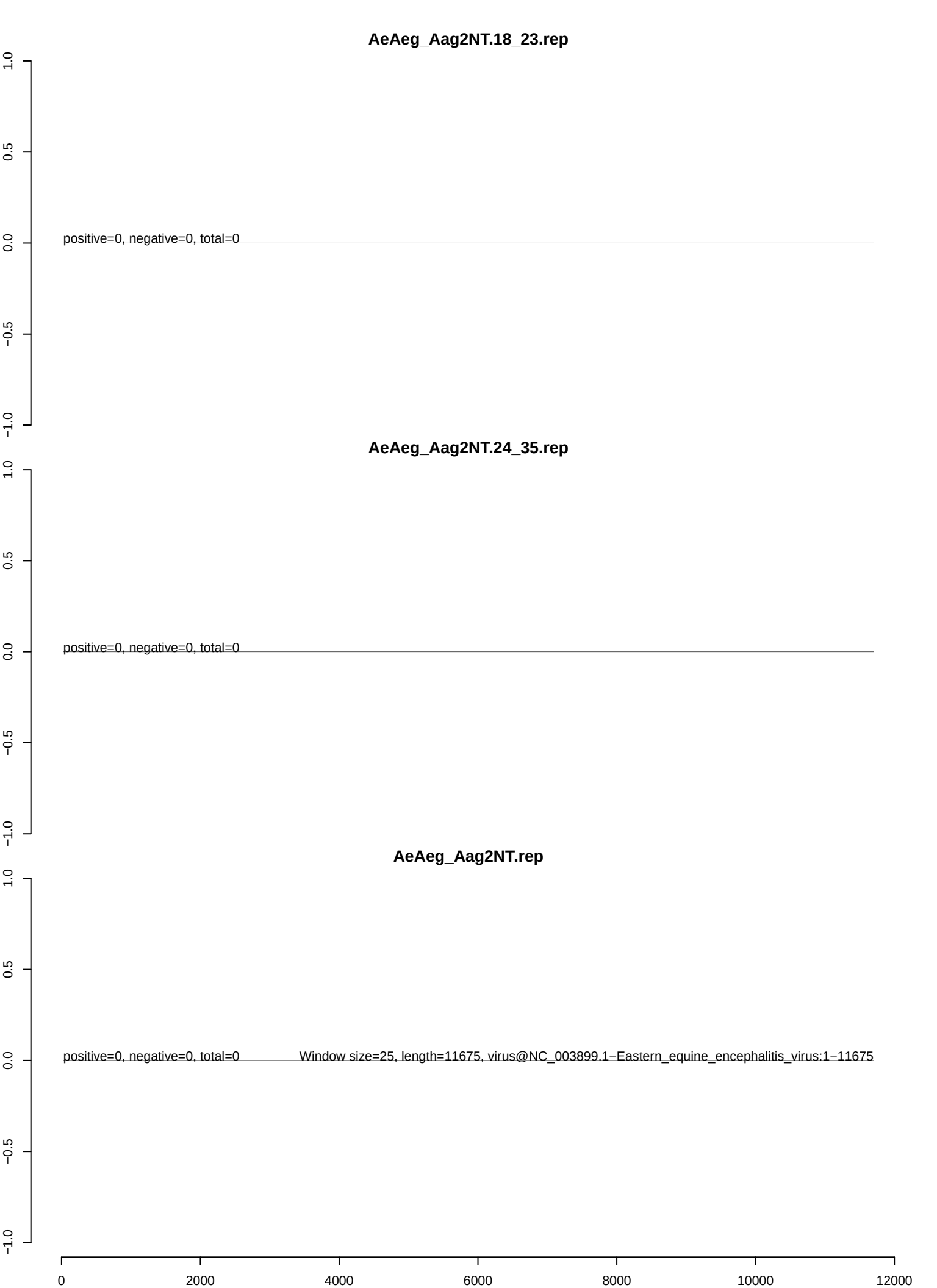
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positive=0, negative=0, total=0
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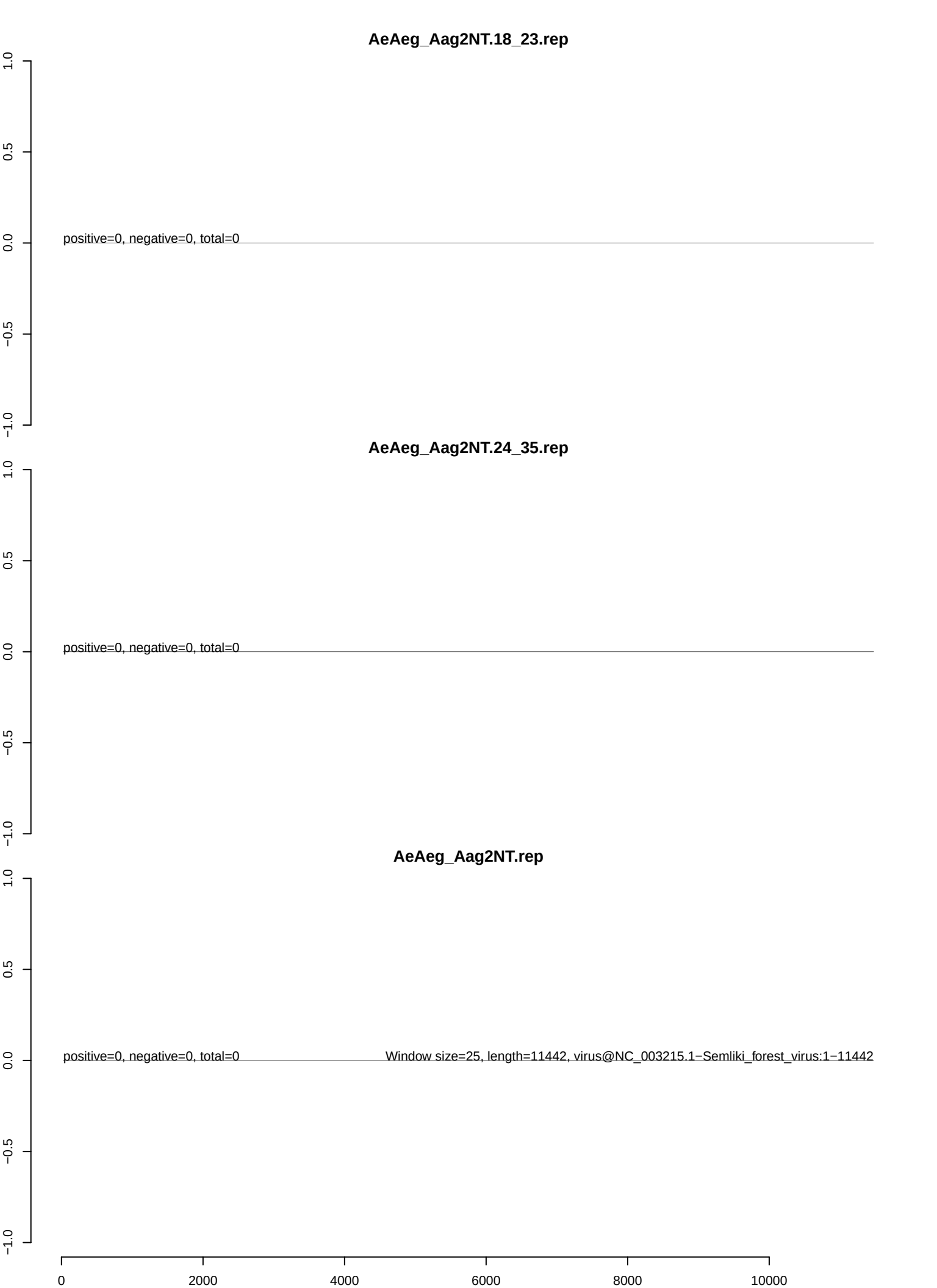
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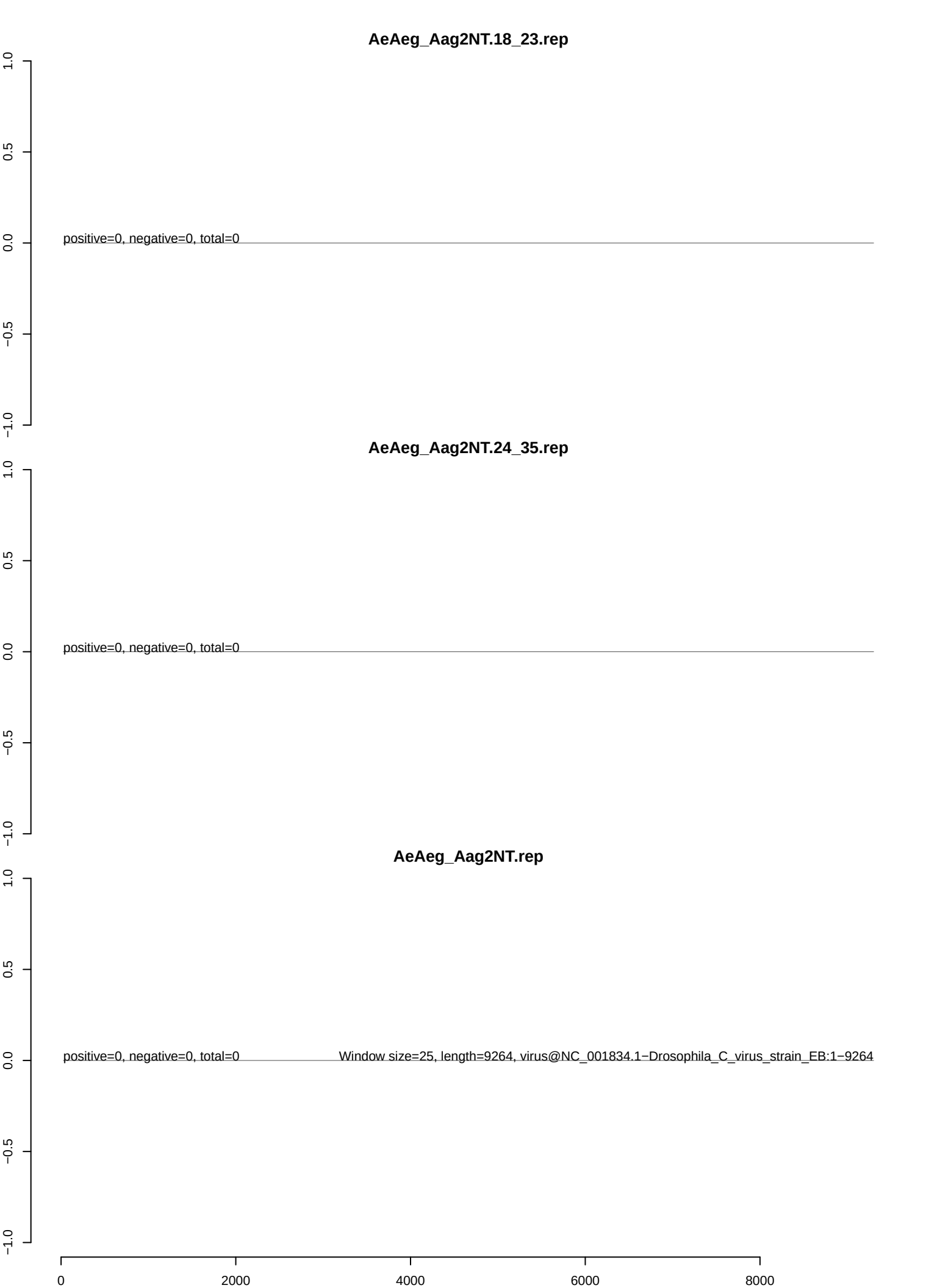
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positive=0, negative=0, total=0
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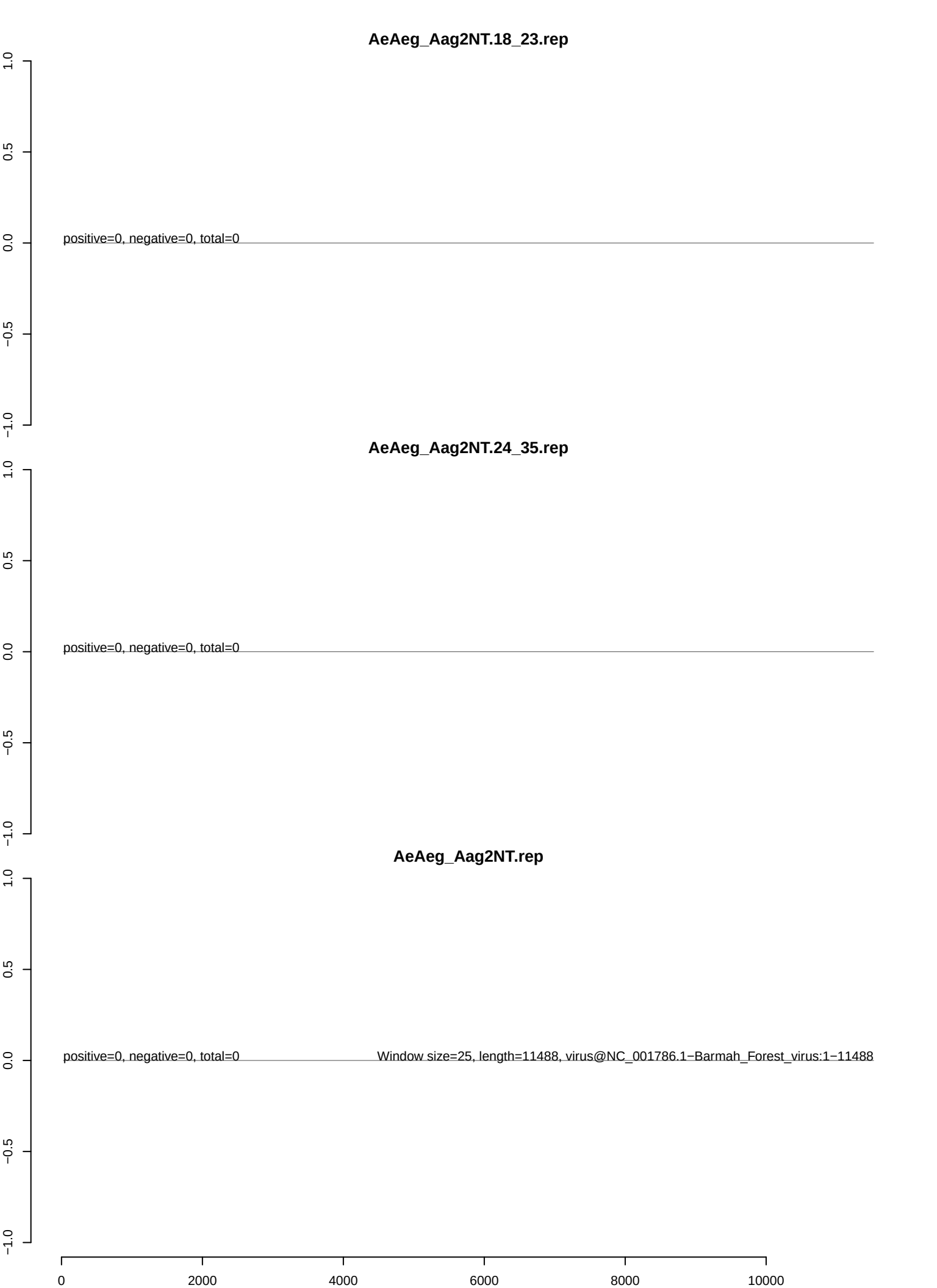
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positive=0, negative=0, total=0
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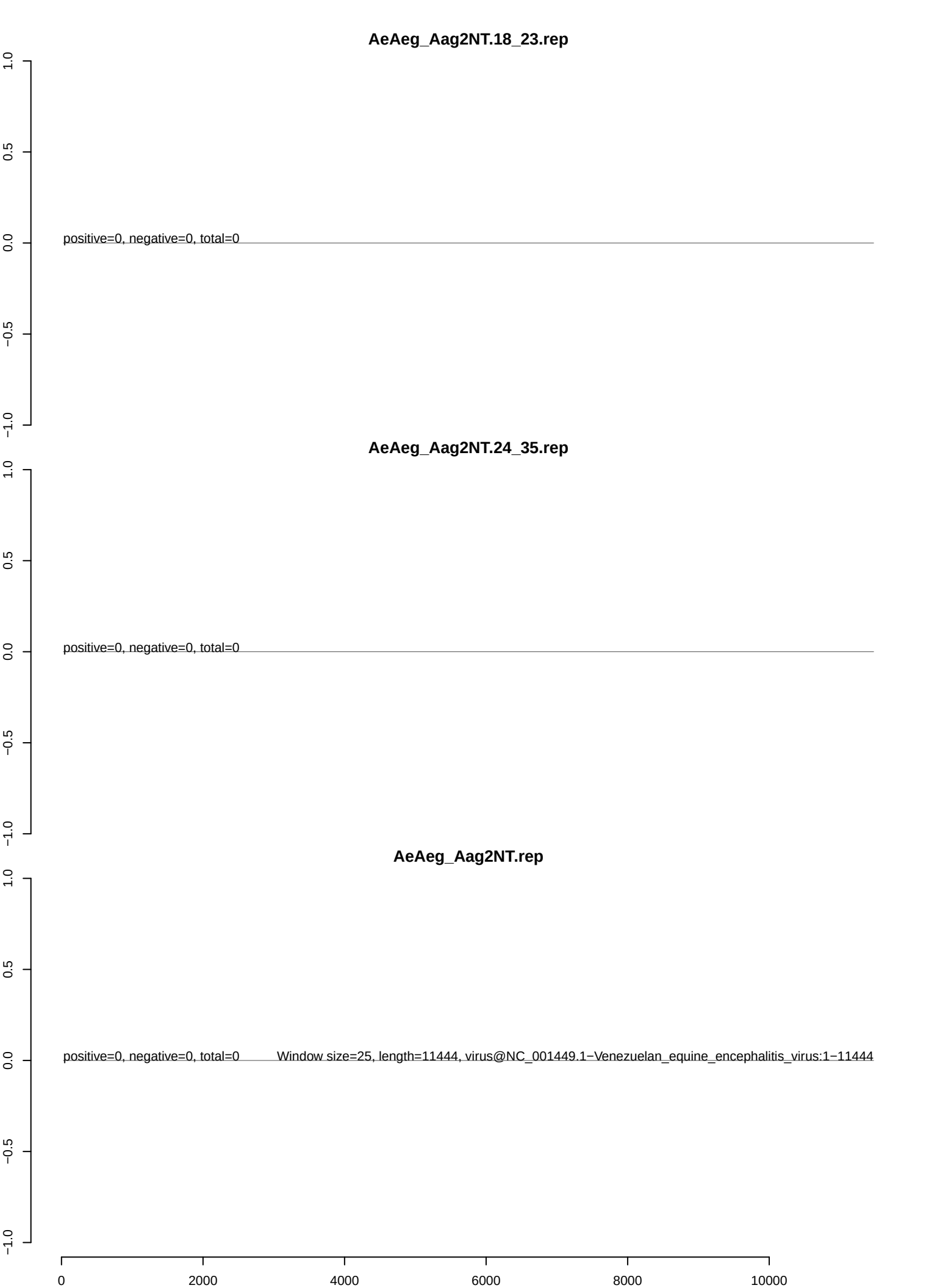
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Window size=25, length=11444, virus@NC_001449.1−Venezuelan_equine_encephalitis_virus:1−11444
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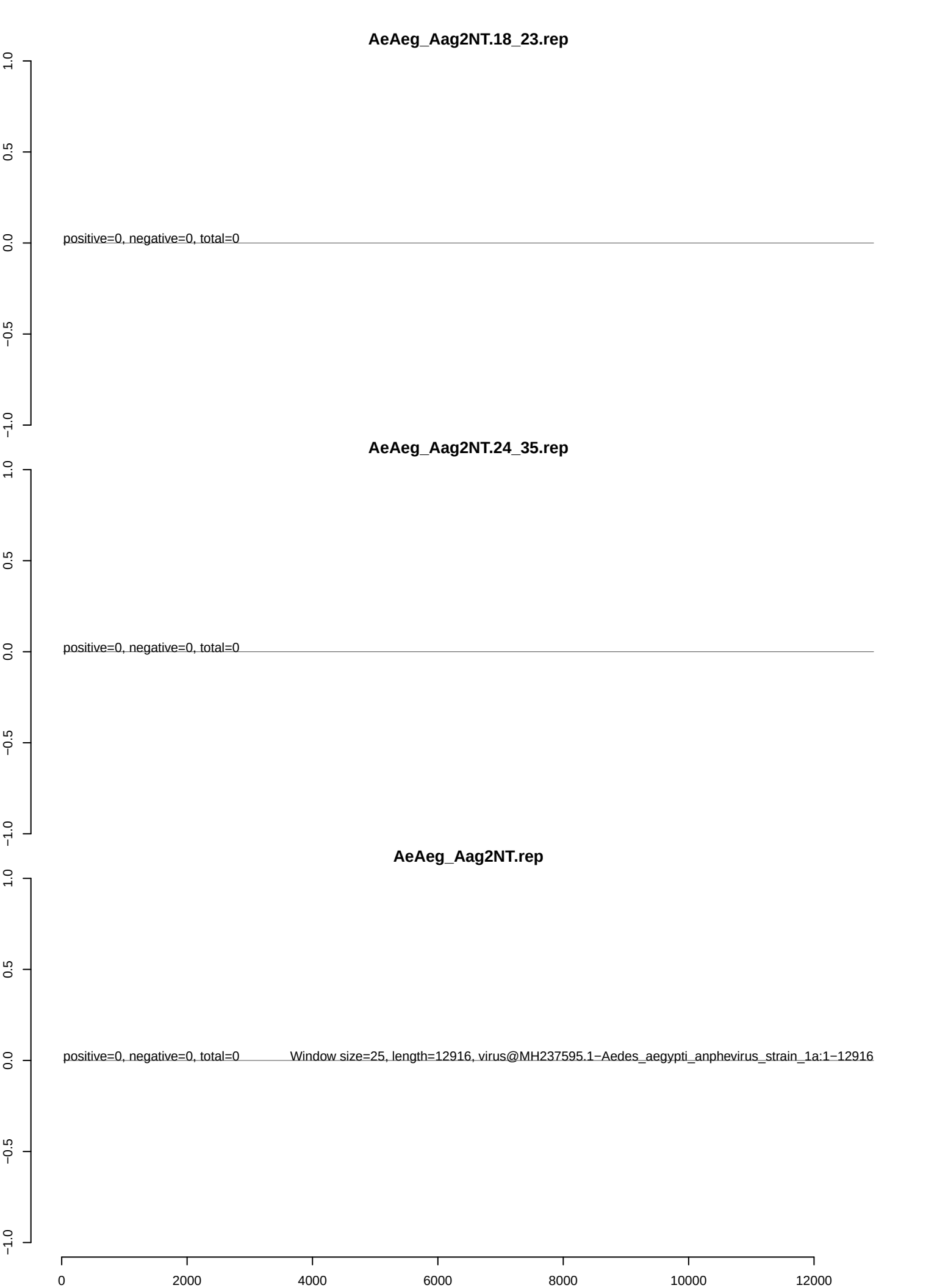
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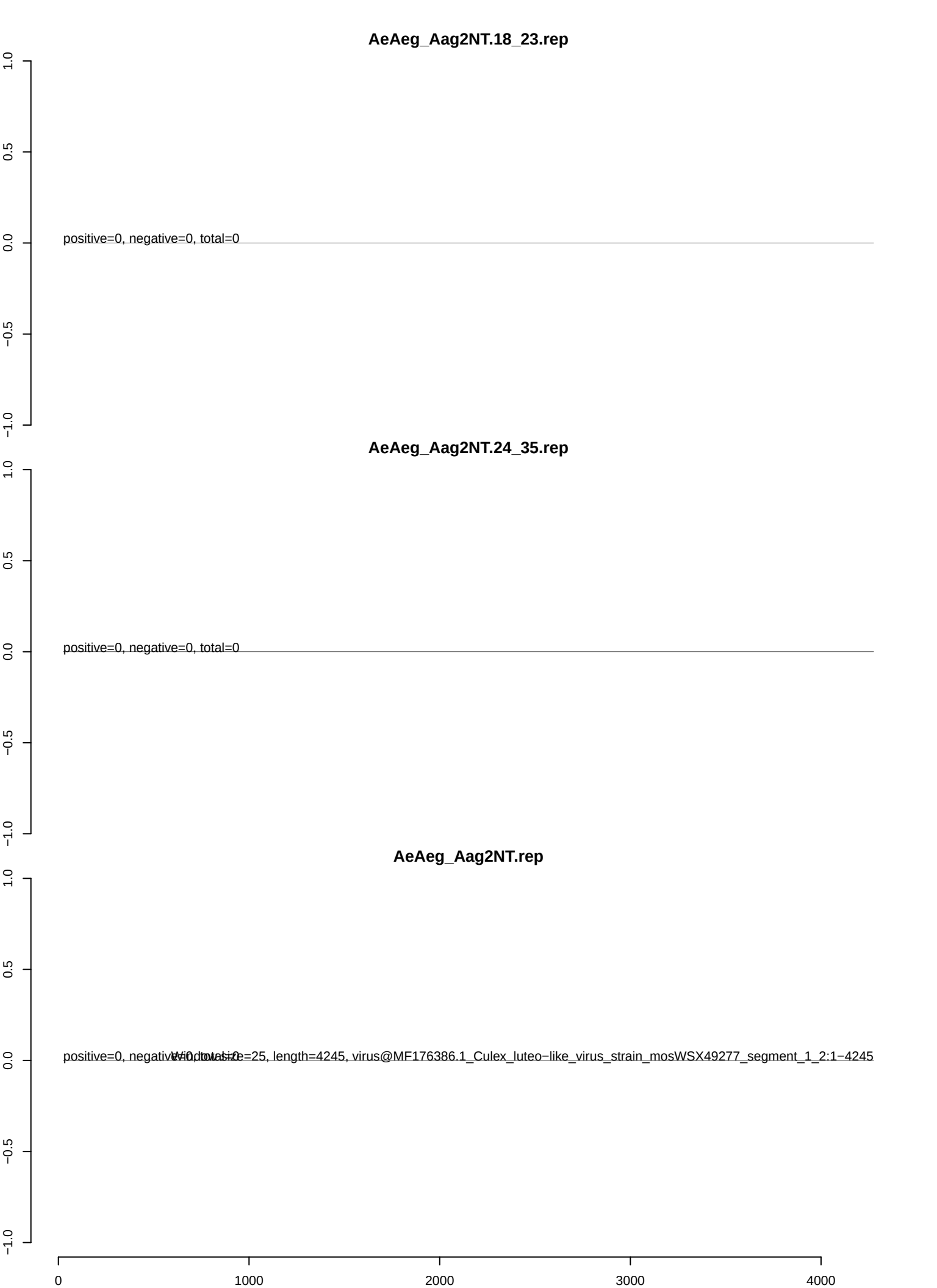
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AeAeg_Aag2NT.24_35.rep
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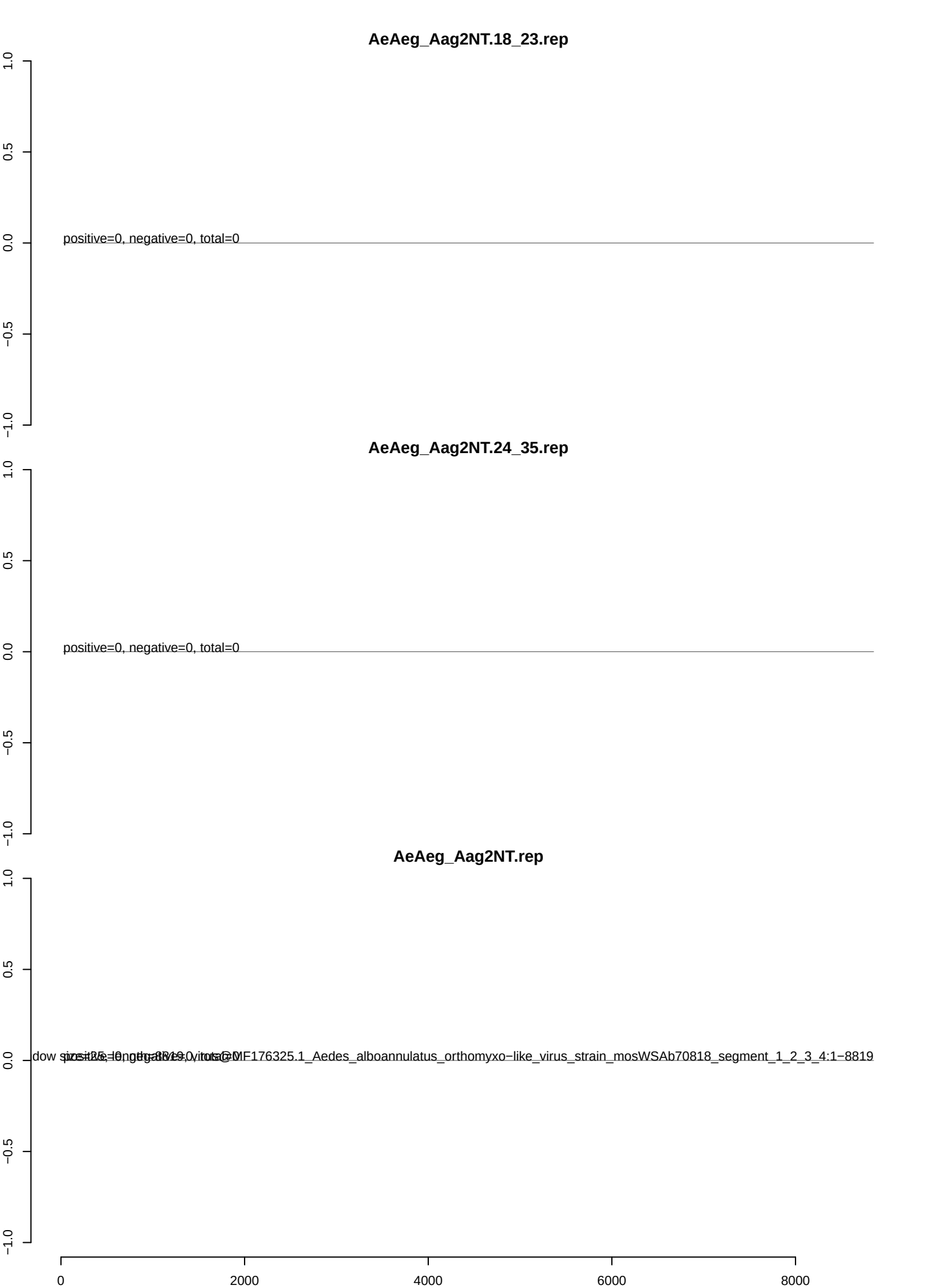
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positive=0, negative=0, total=0
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dow size=25, longest=8819, total=MF176325.1_Aedes_alboannulatus_orthomyxo−like_virus_strain_mosWSAb70818_segment_1_2_3_4:1−8819
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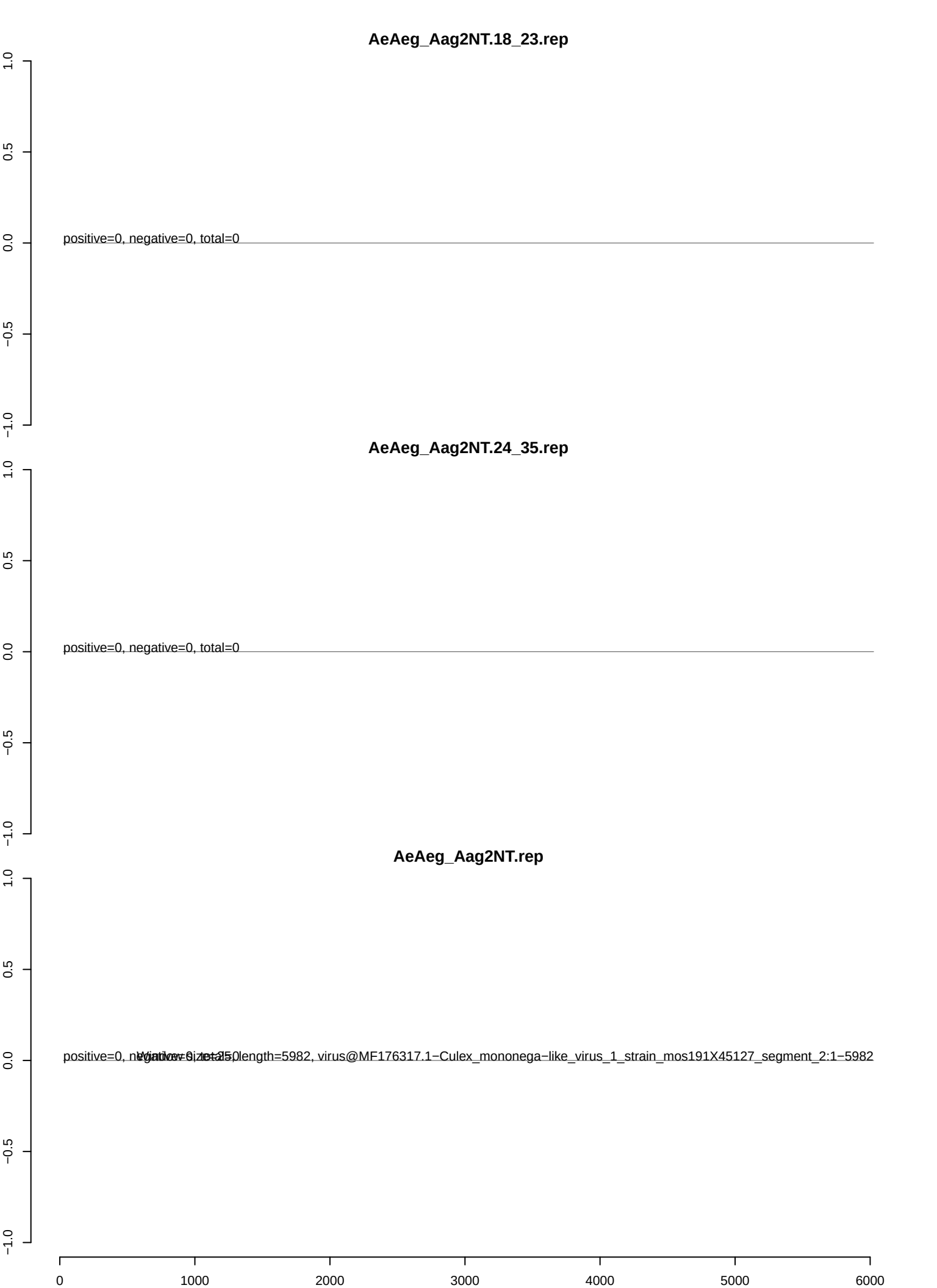
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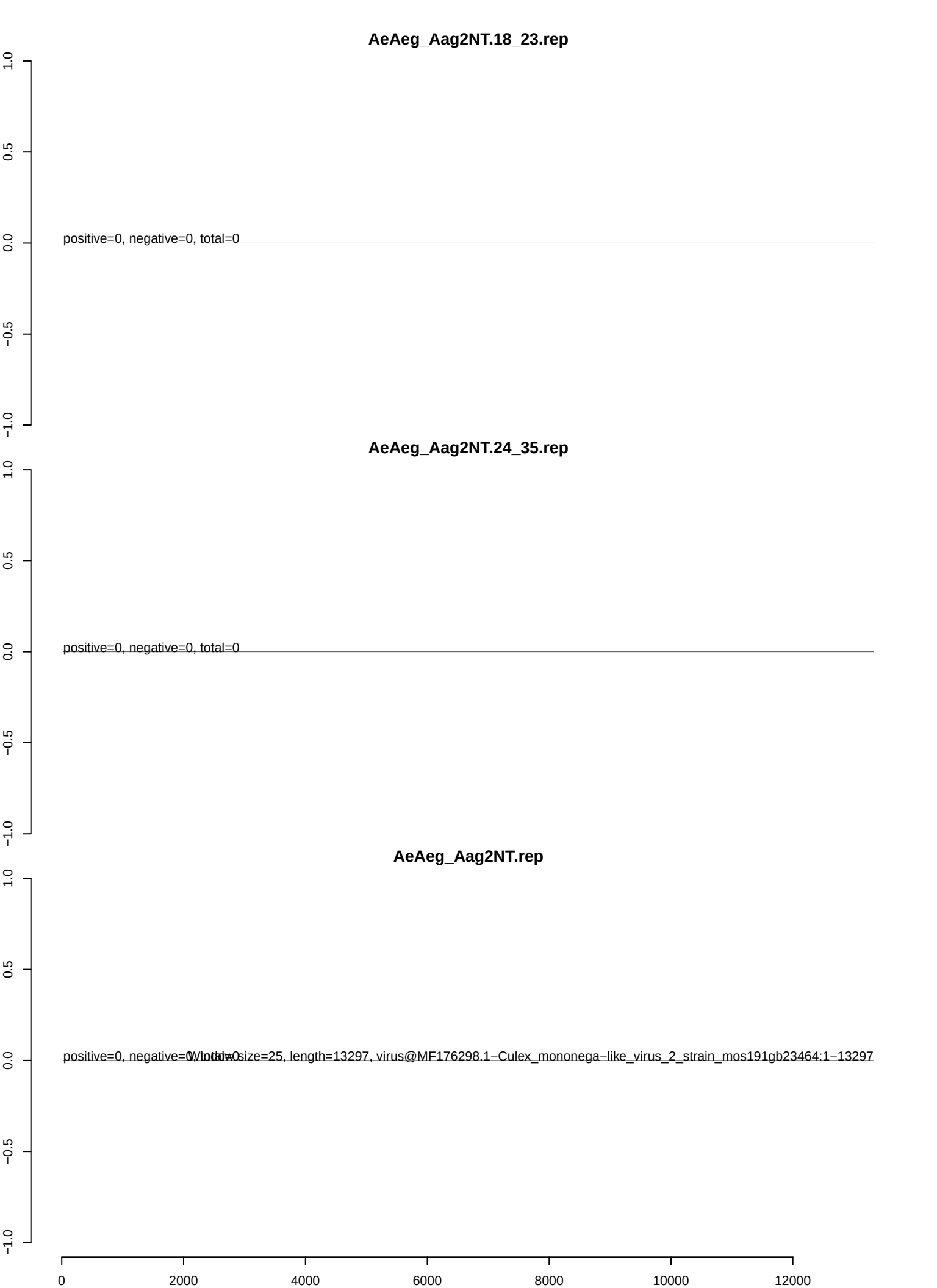
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positive=0, negative=0, total=0
window size=25, length=13297, virus@MF176298.1−Culex_mononega−like_virus_2_strain_mos191gb23464:1−13297
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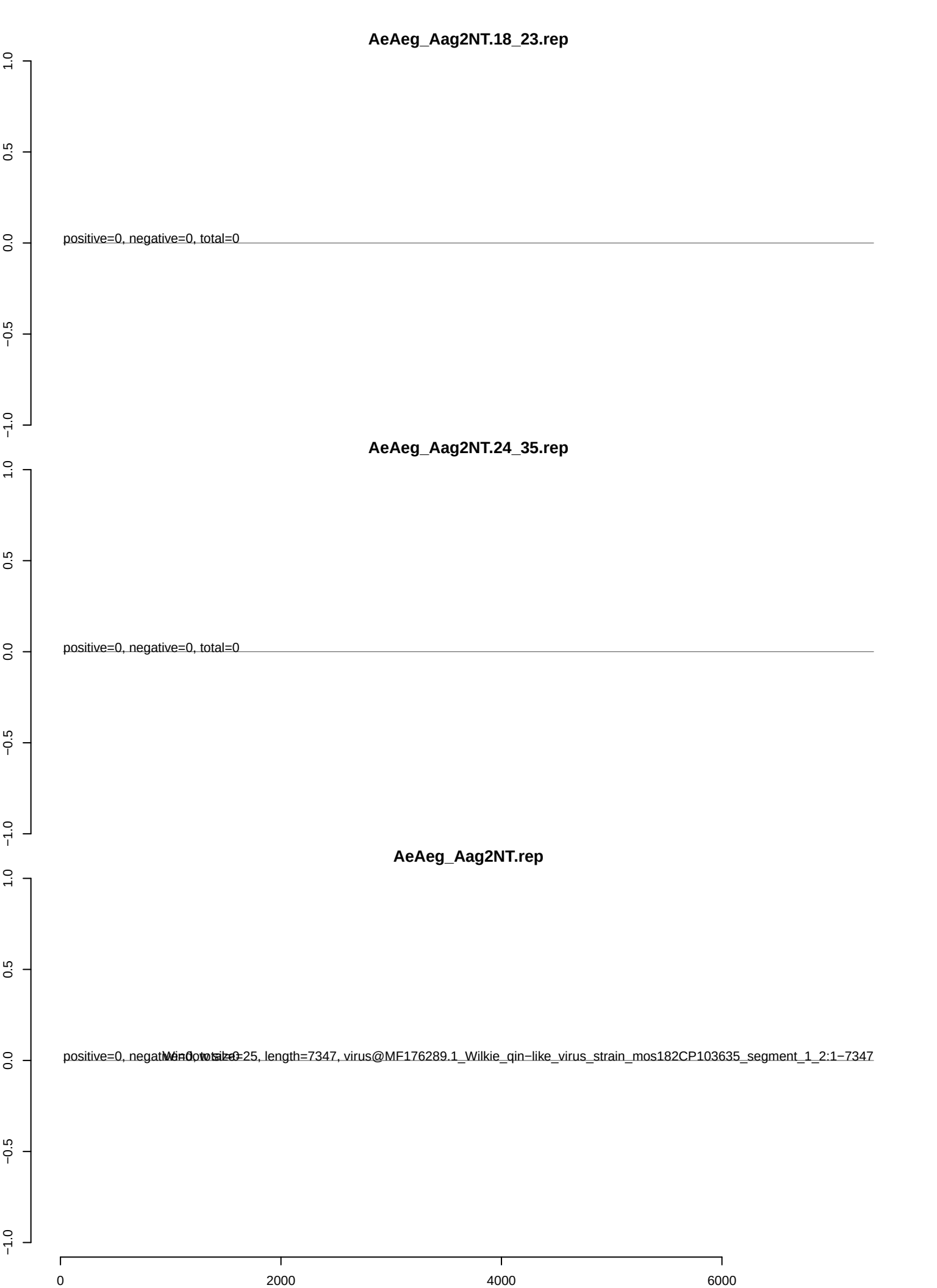
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Window size=25, length=7347, virus@MF176289.1_Wilkie_qin−like_virus_strain_mos182CP103635_segment_1_2:1−7347
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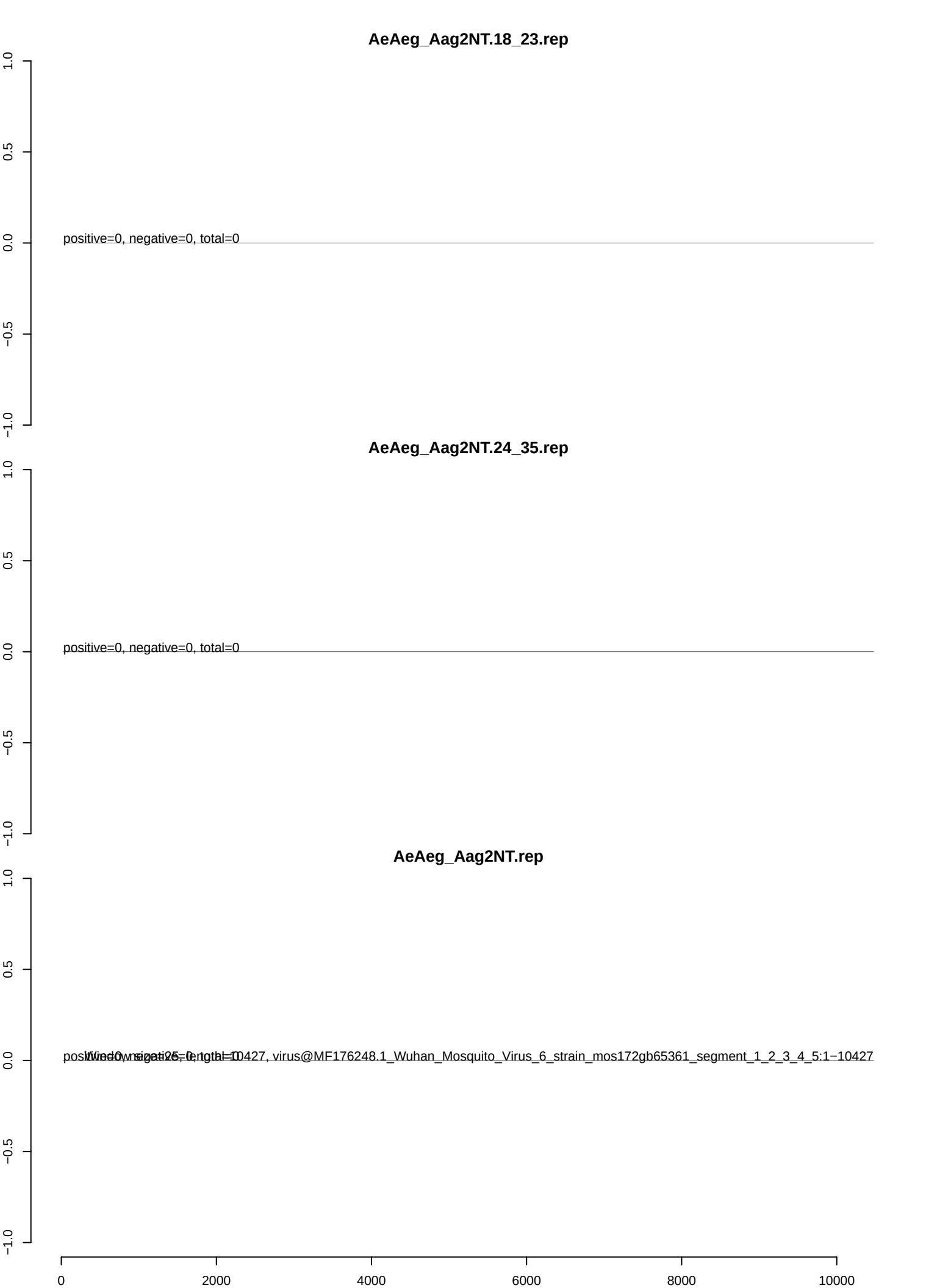
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positive=25, negative=0, total=10427, virus@MF176248.1_Wuhan_Mosquito_Virus_6_strain_mos172gb65361_segment_1_2_3_4_5:1−10427
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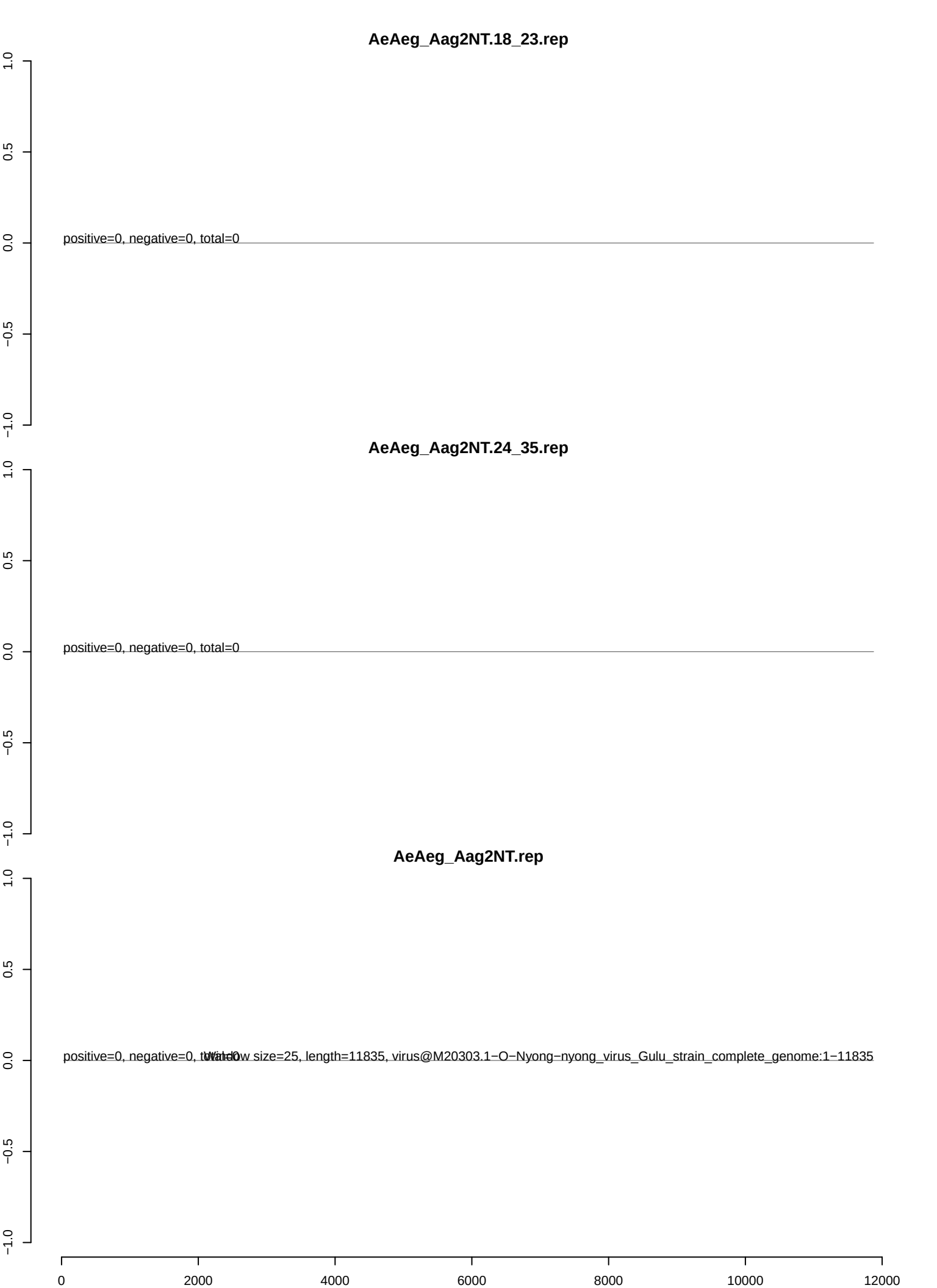
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positive=0, negative=0, total=0
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positive=0, negative=0, total=0
Window size=25, length=11835, virus@M20303.1−O−Nyong−nyong_virus_Gulu_strain_complete_genome:1−11835
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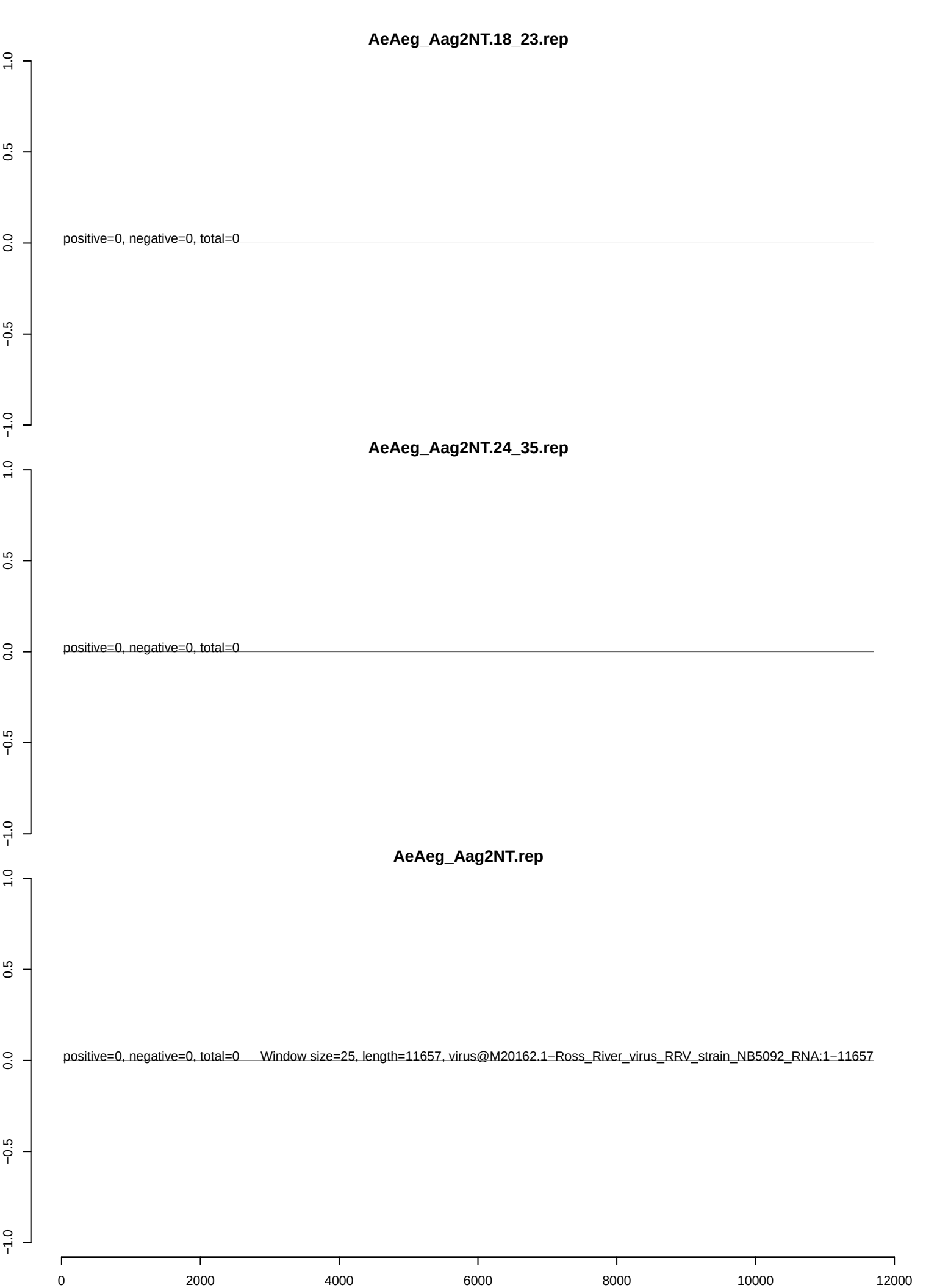
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AeAeg_Aag2NT.24_35.rep
positive=0, negative=0, total=0
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positive=0, negative=0, total=0
Window size=25, length=11657, virus@M20162.1−Ross_River_virus_RRV_strain_NB5092_RNA:1−11657
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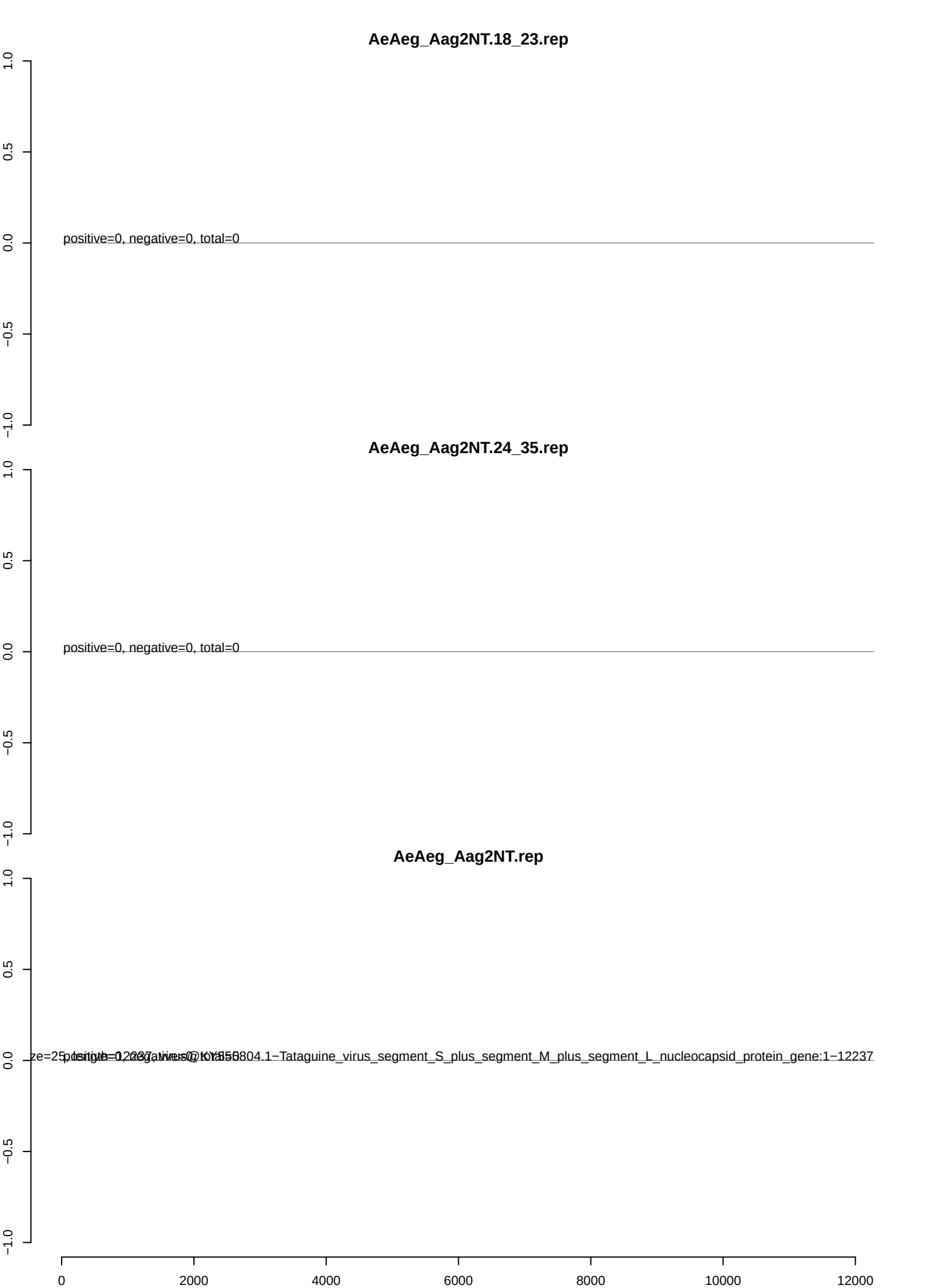
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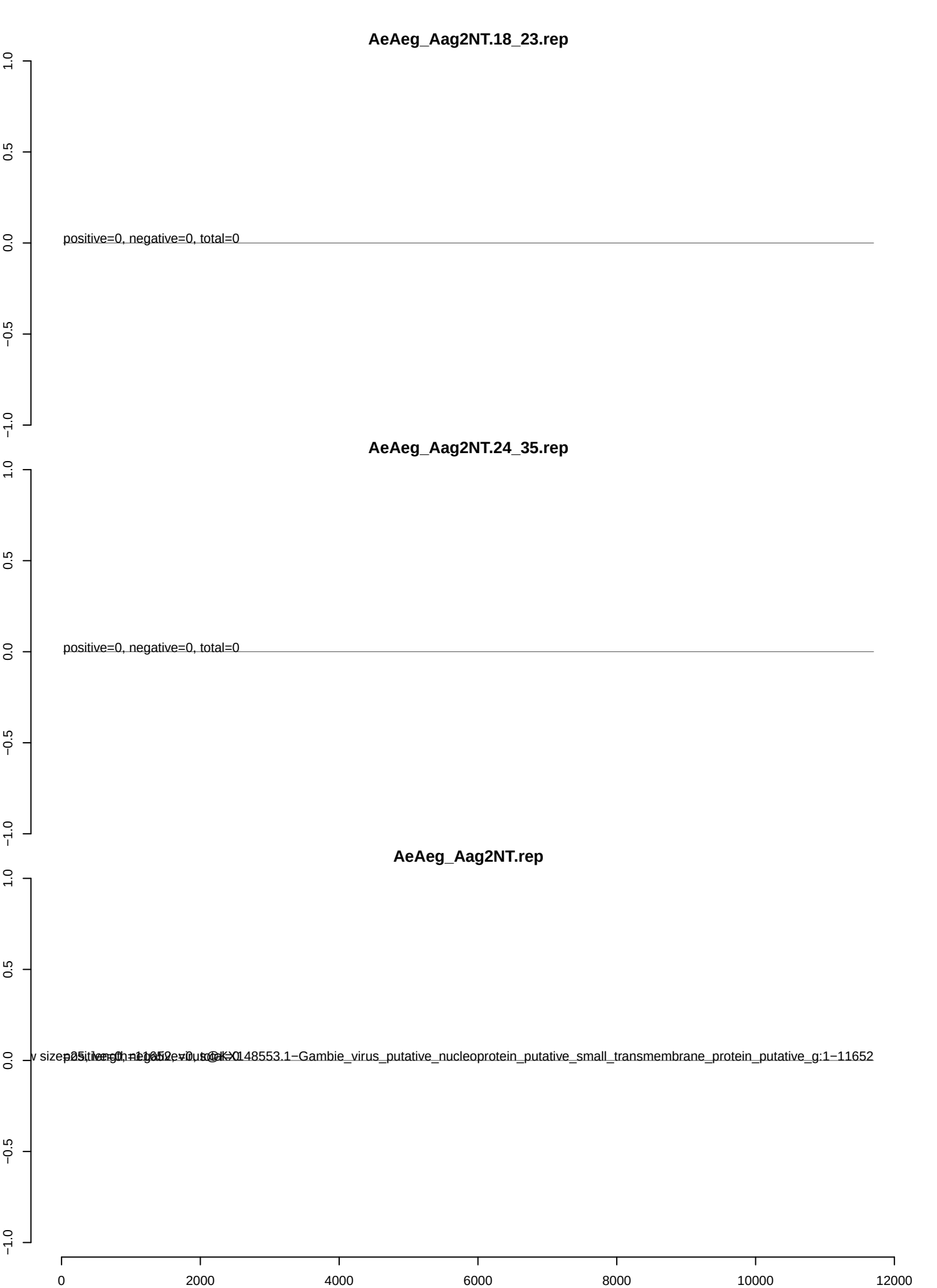
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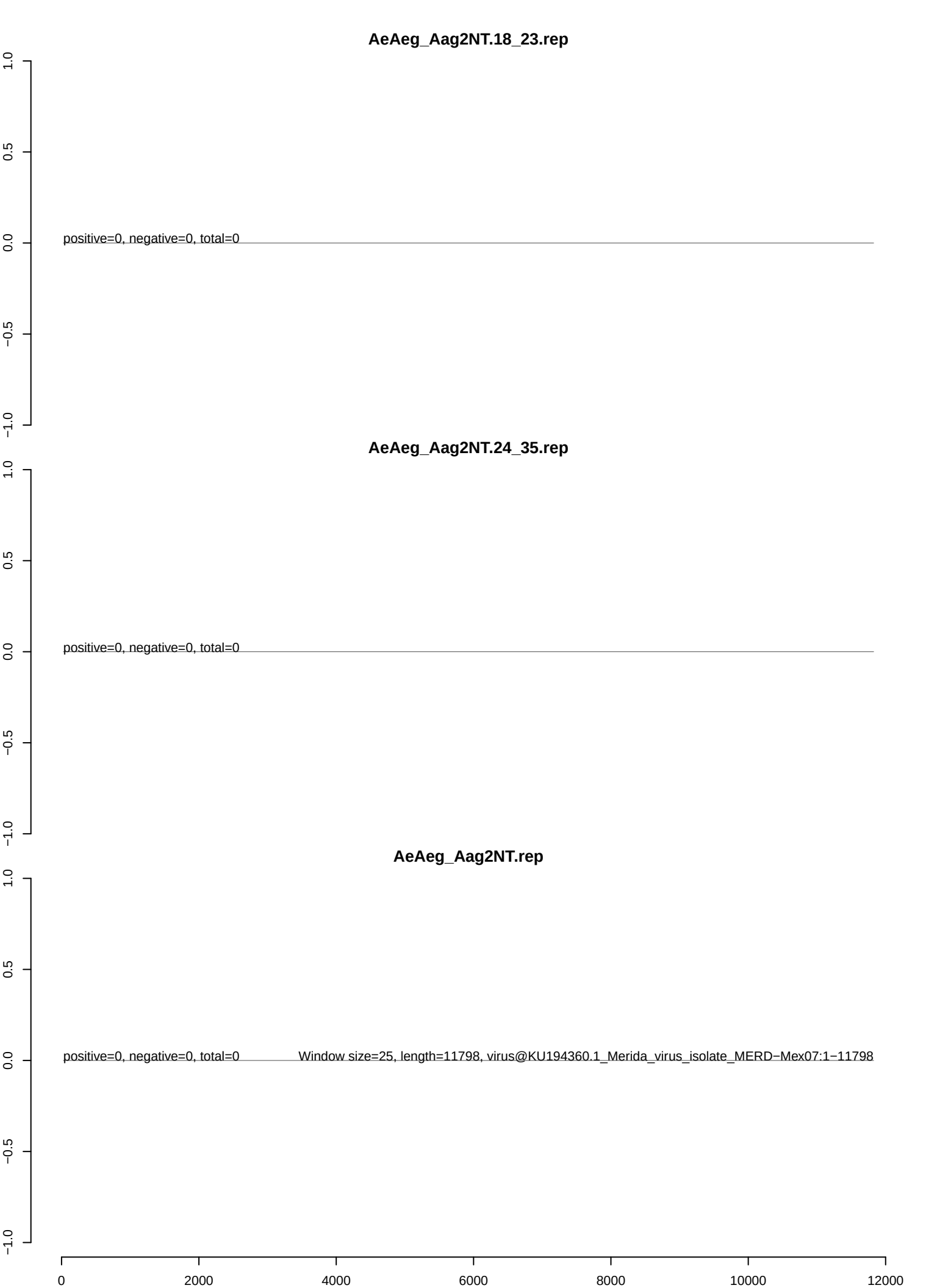
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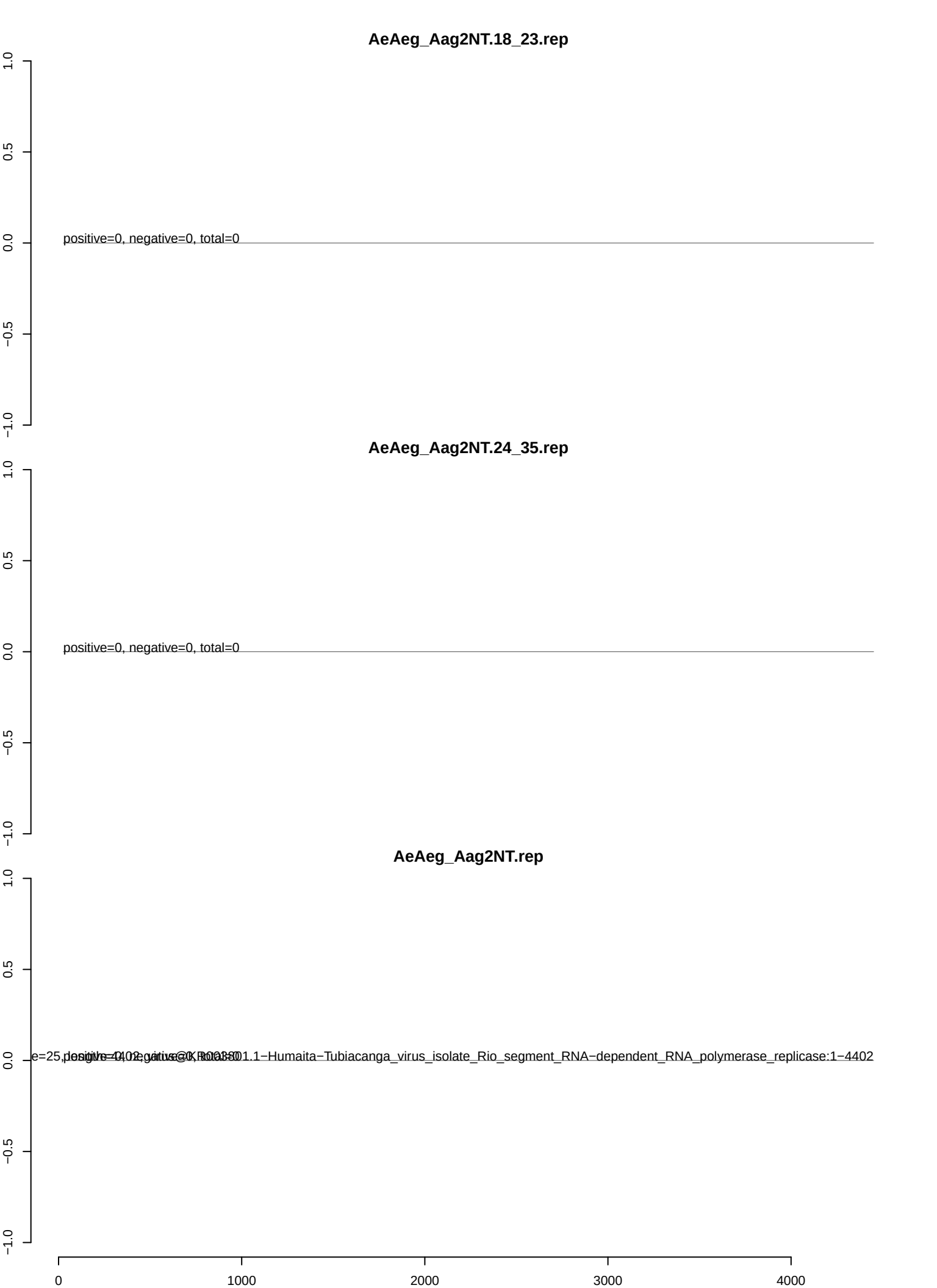
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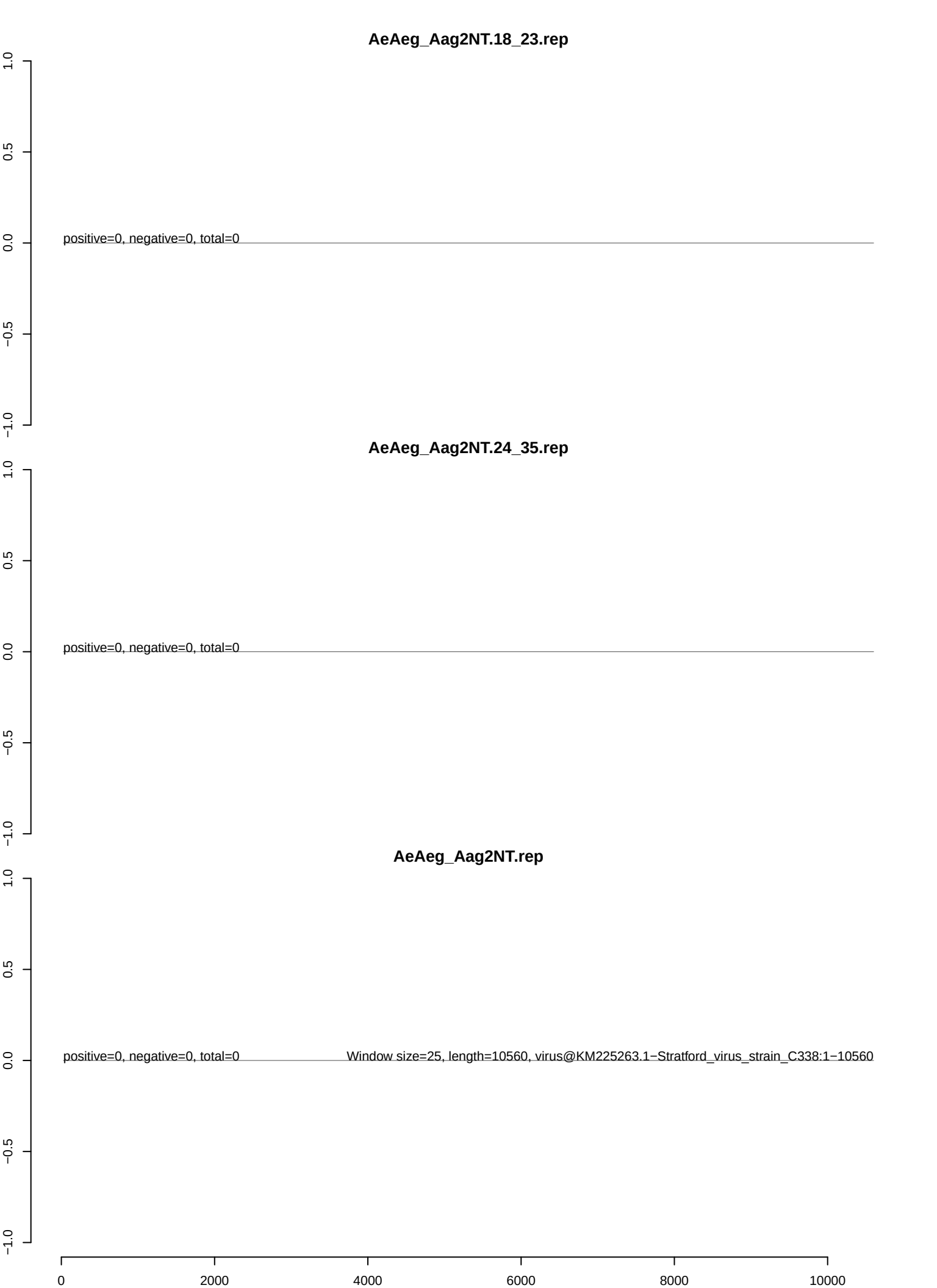
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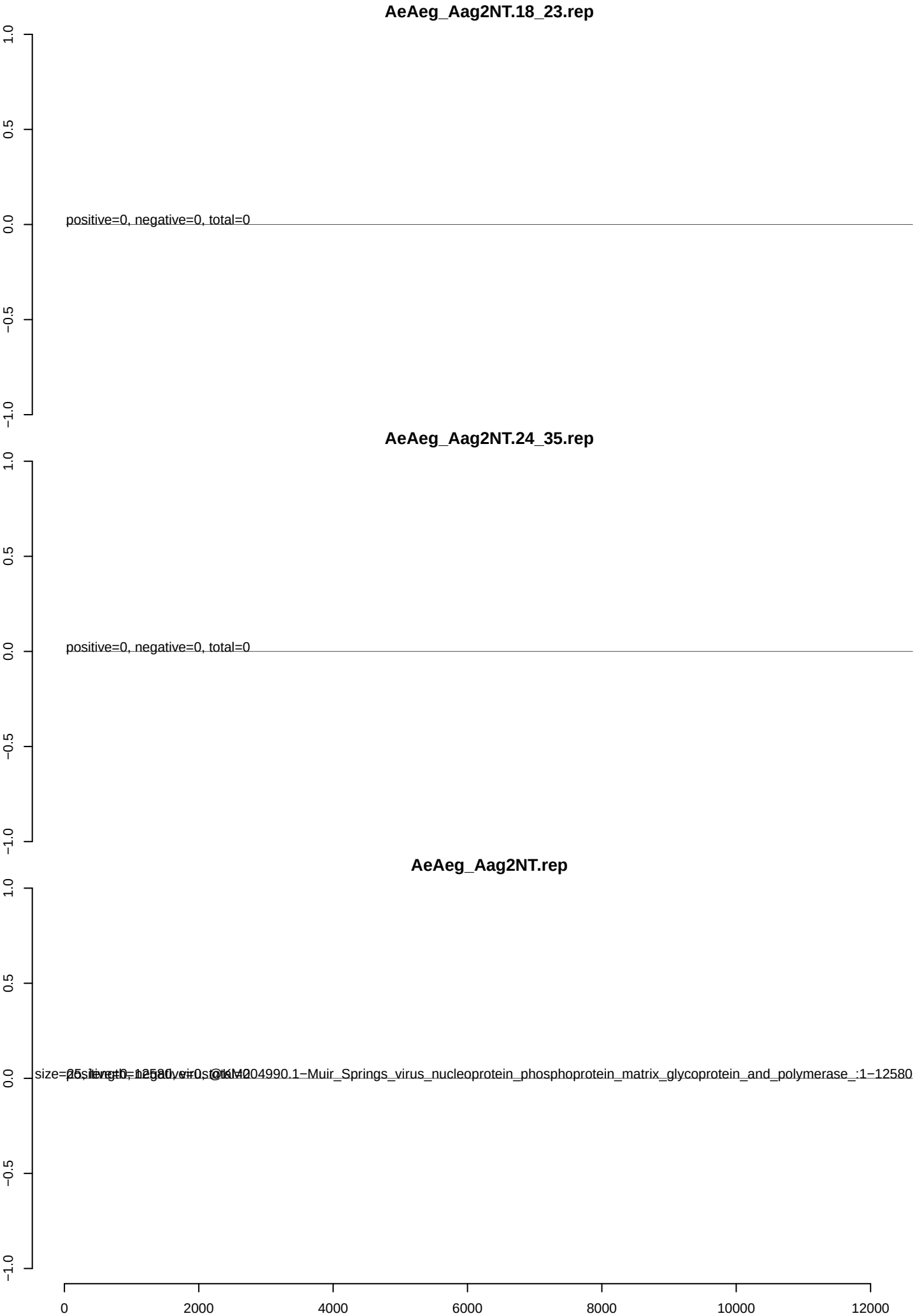
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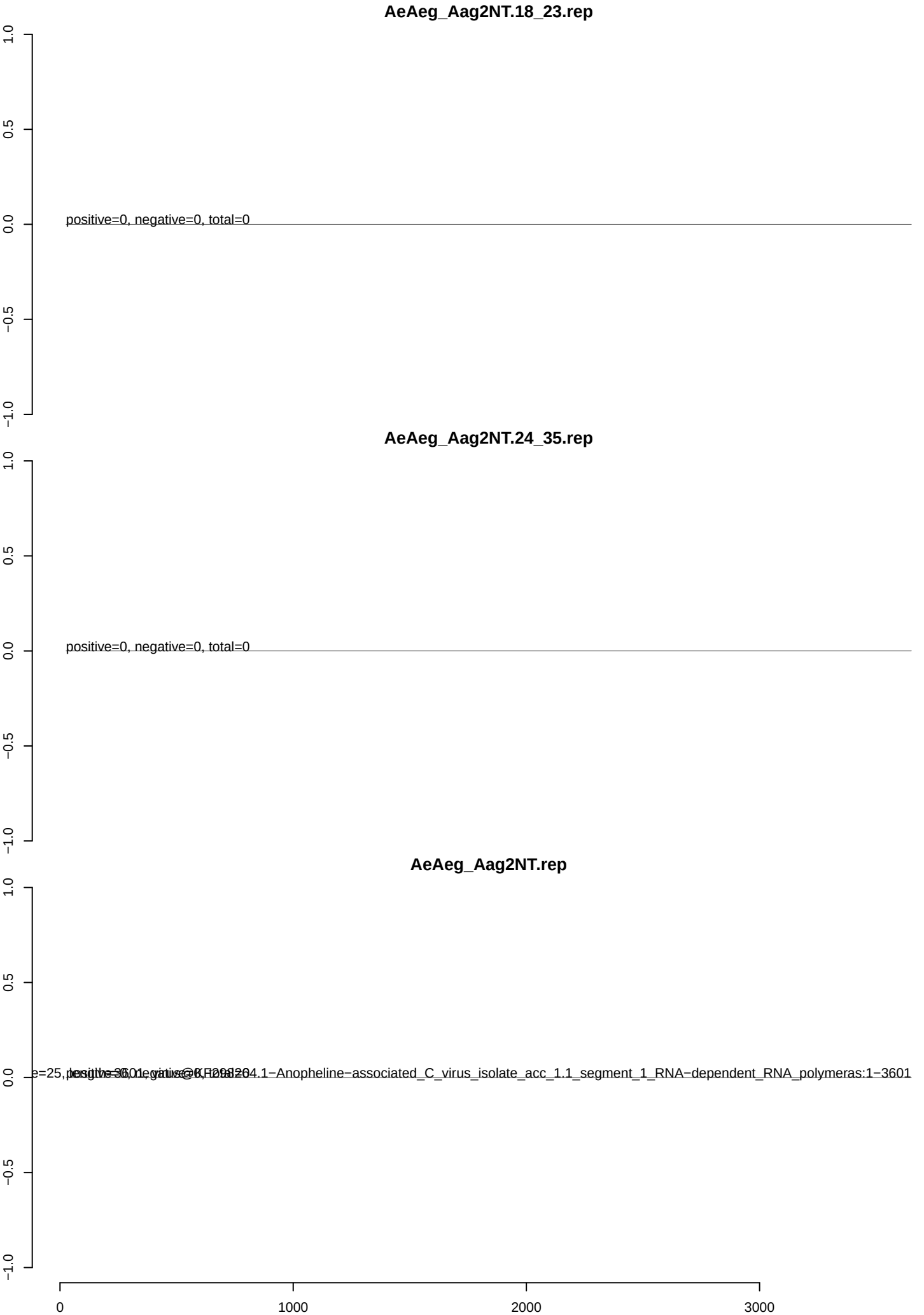
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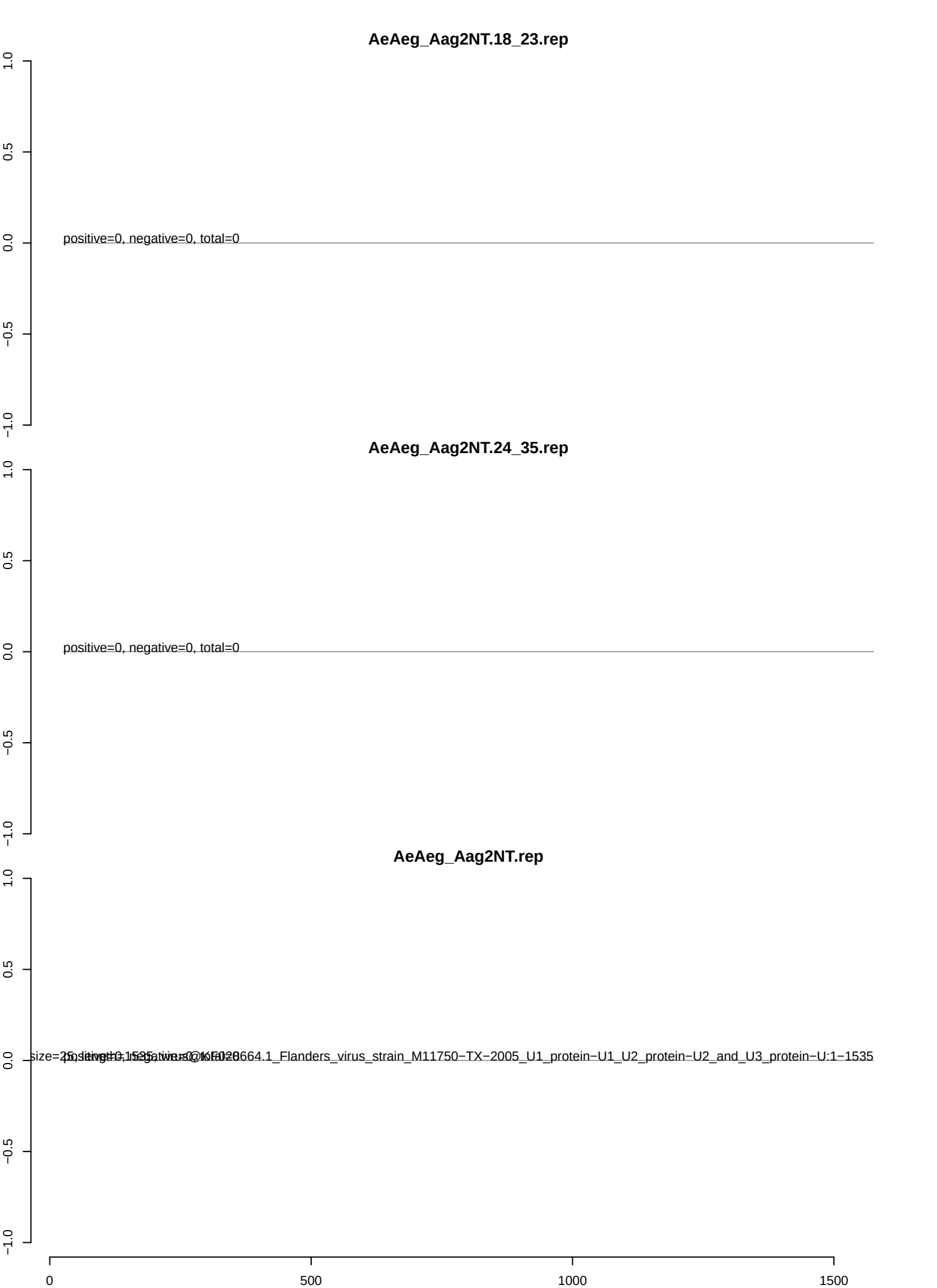
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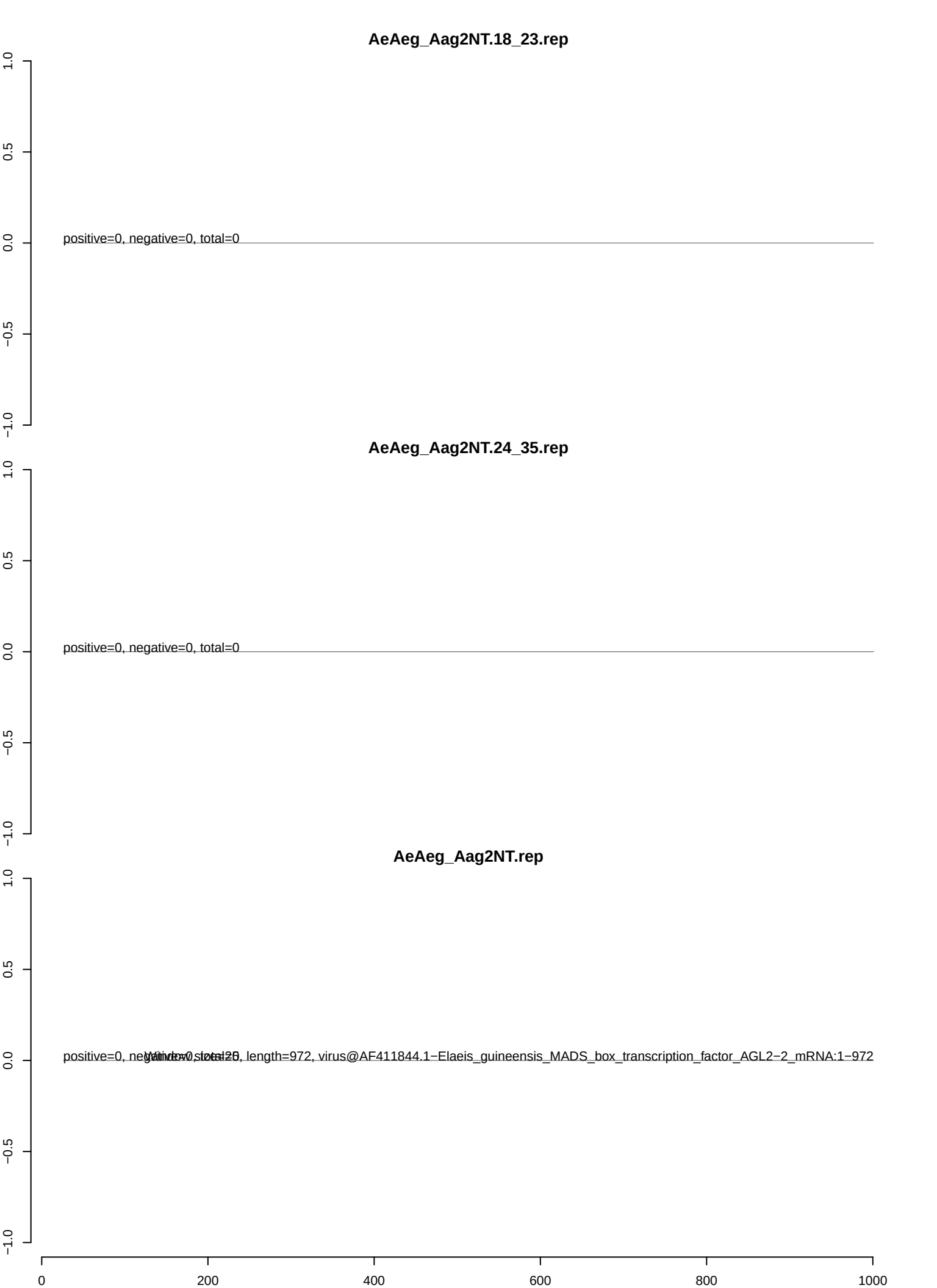
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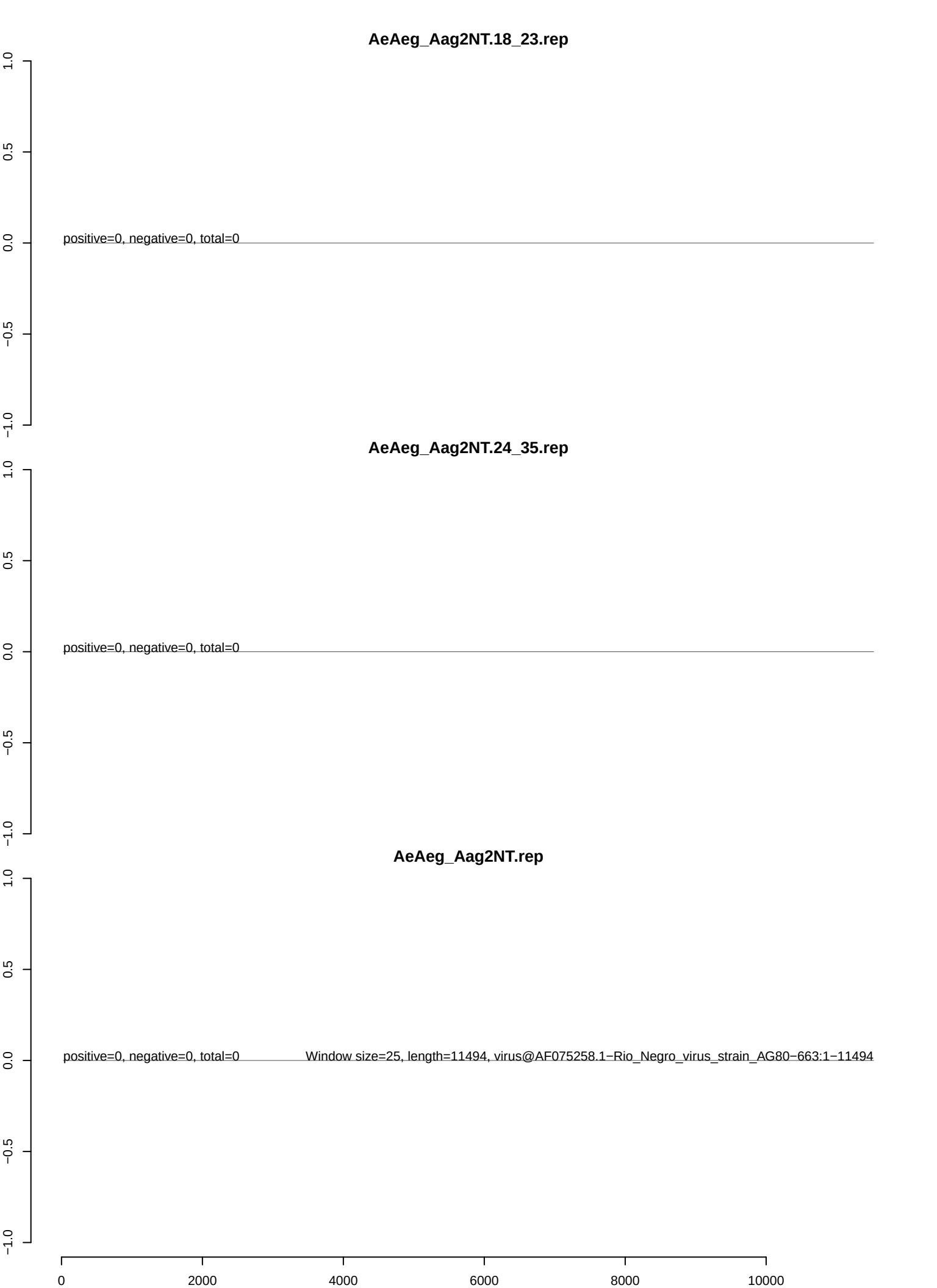
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positive=0, negative=0, total=0
Window size=25, length=11494, virus@AF075258.1−Rio_Negro_virus_strain_AG80−663:1−11494
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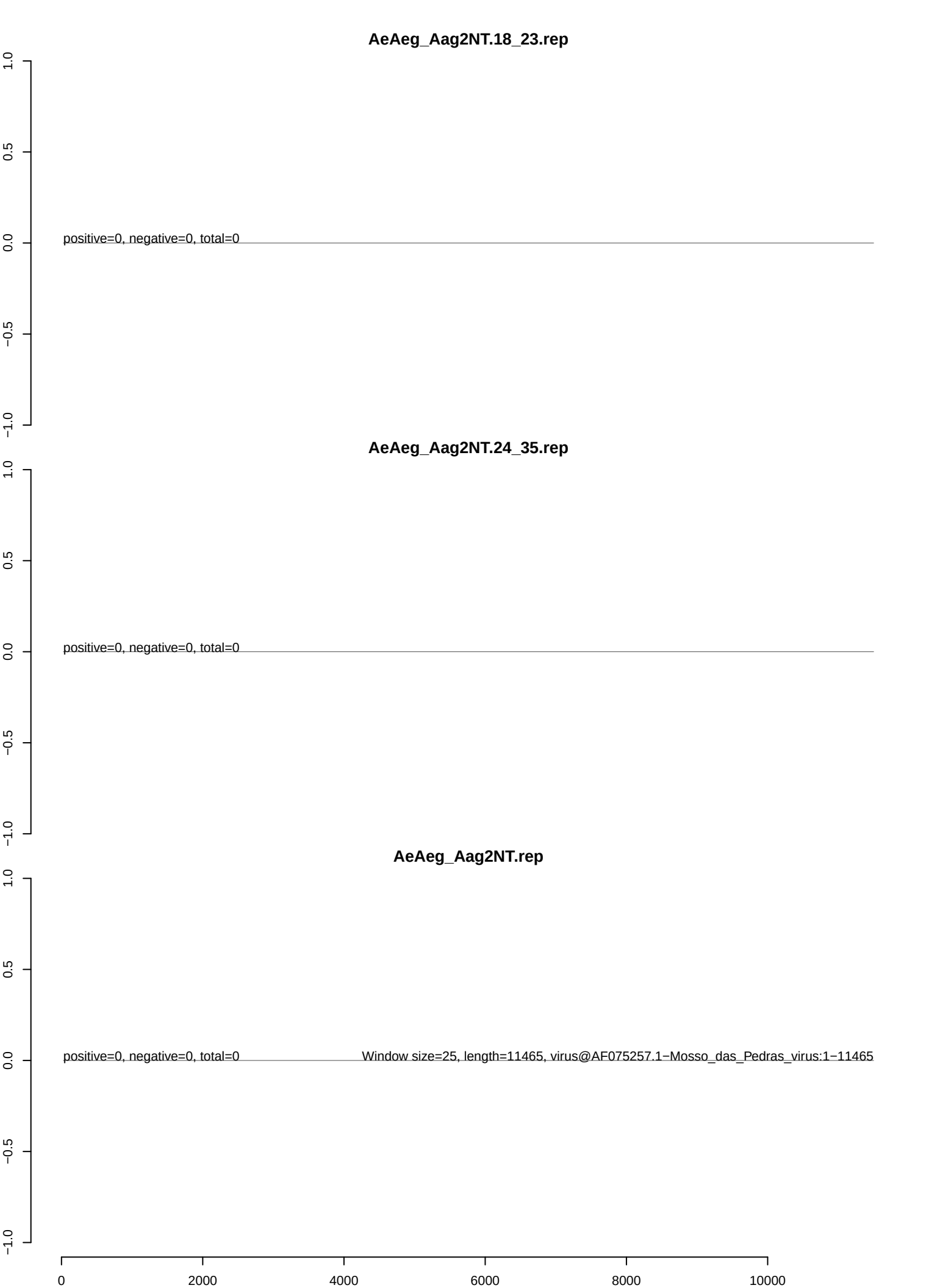
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positive=0, negative=0, total=0
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Window size=25, length=11465, virus@AF075257.1−Mosso_das_Pedras_virus:1−11465
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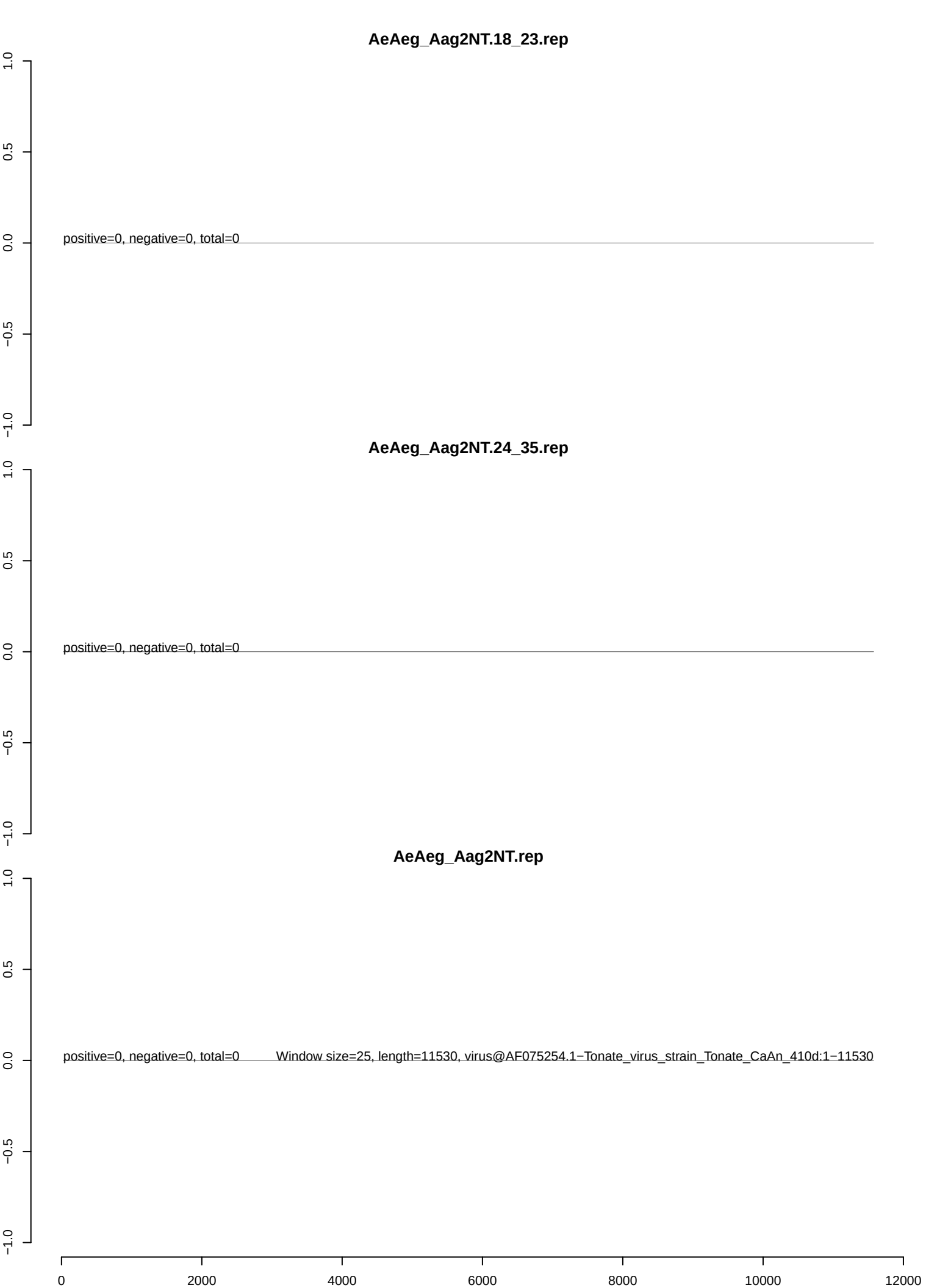
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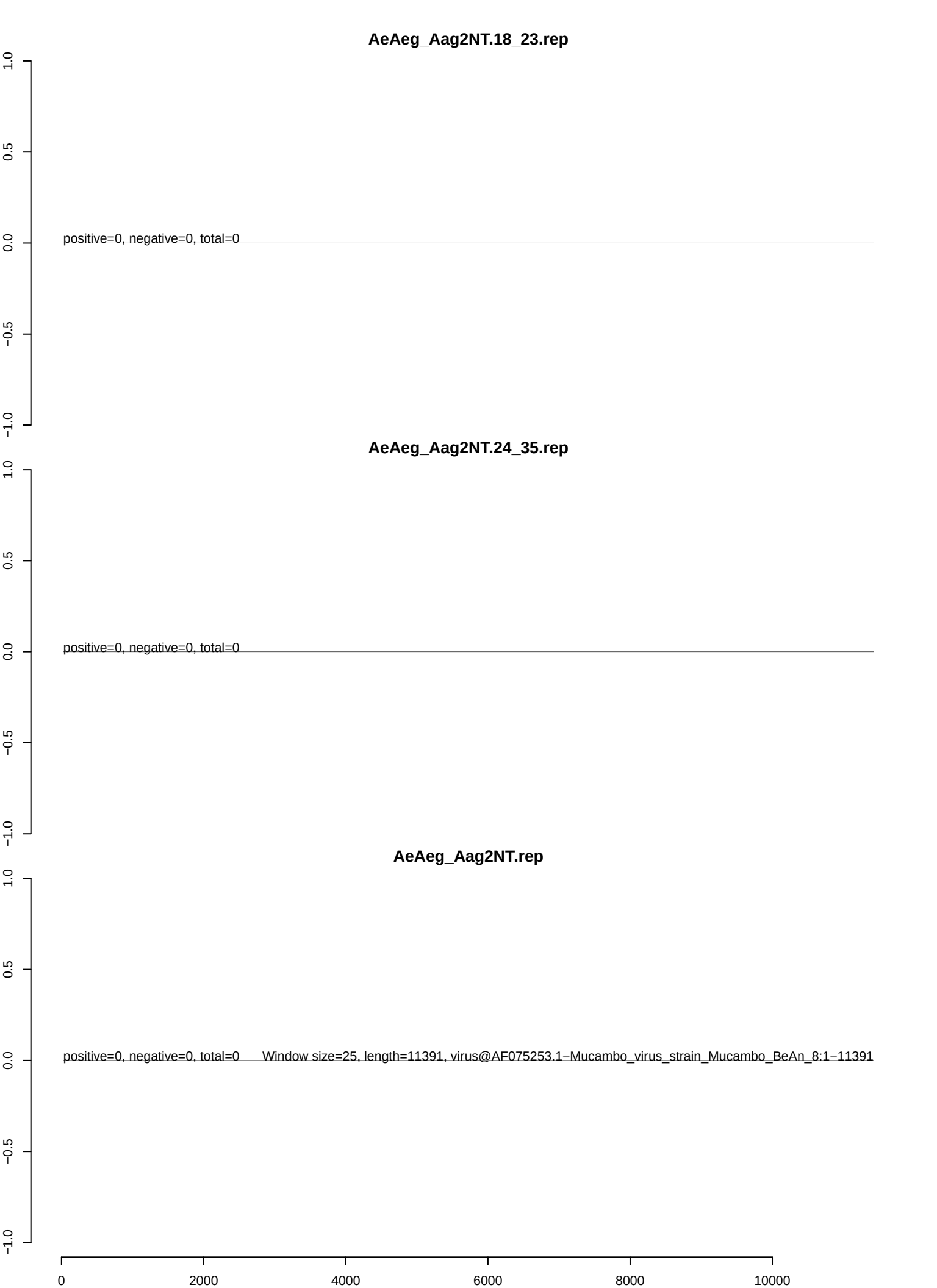
AeAeg_Aag2NT.24_35.rep
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
positive=0, negative=0, total=0
Window size=25, length=11530, virus@AF075254.1−Tonate_virus_strain_Tonate_CaAn_410d:1−11530
1.0
0.5
0.0
−0.5
−1.0
0
2000
4000
6000
8000
10000
12000


AeAeg_Aag2NT.18_23.rep
positive=0, negative=0, total=0
AeAeg_Aag2NT.24_35.rep
positive=0, negative=0, total=0
AeAeg_Aag2NT.rep
positive=0, negative=0, total=0
Window size=25, length=11391, virus@AF075253.1−Mucambo_virus_strain_Mucambo_BeAn_8:1−11391
1.0
0.5
0.0
−0.5
−1.0
0
2000
4000
6000
8000
10000