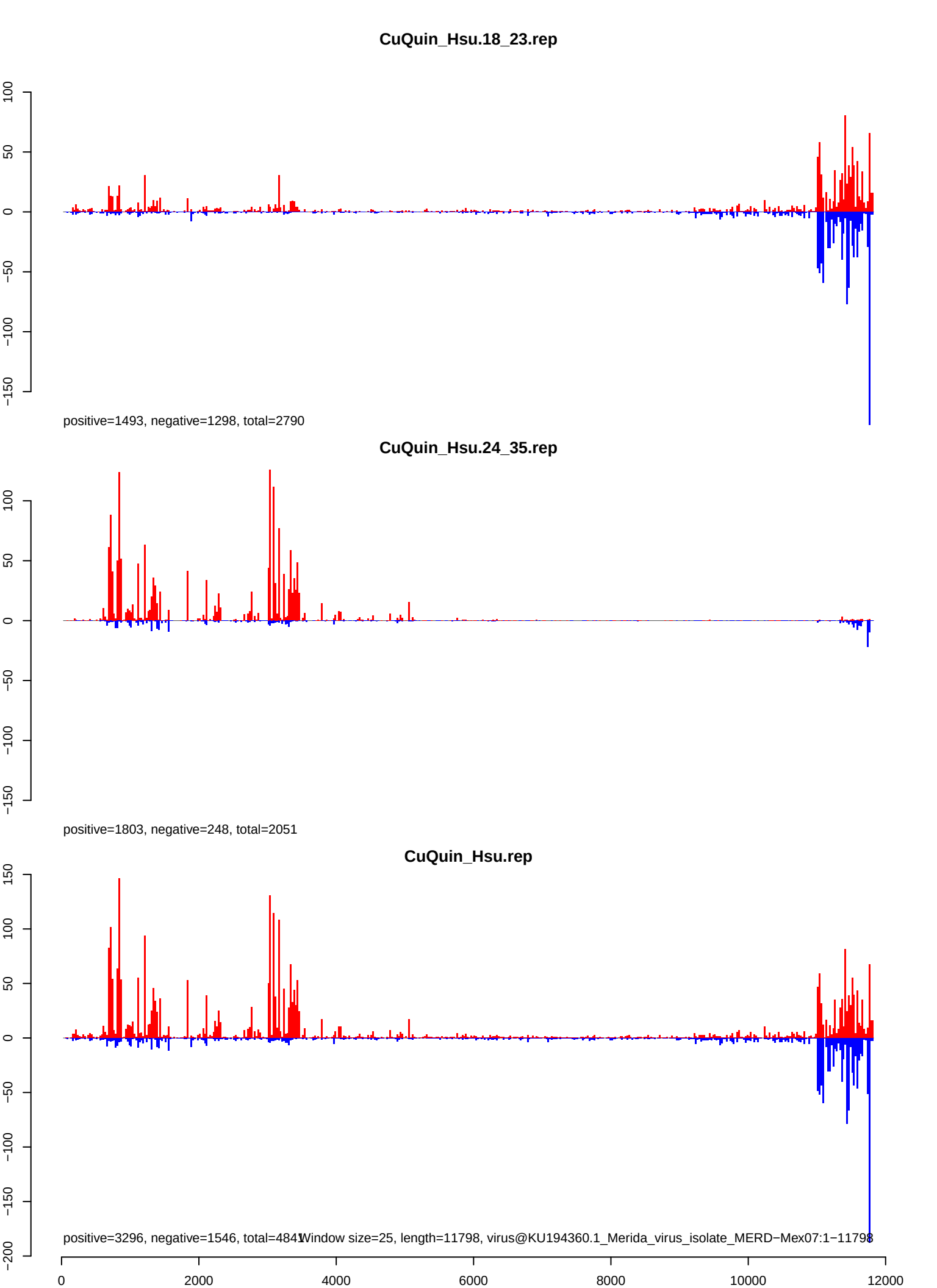
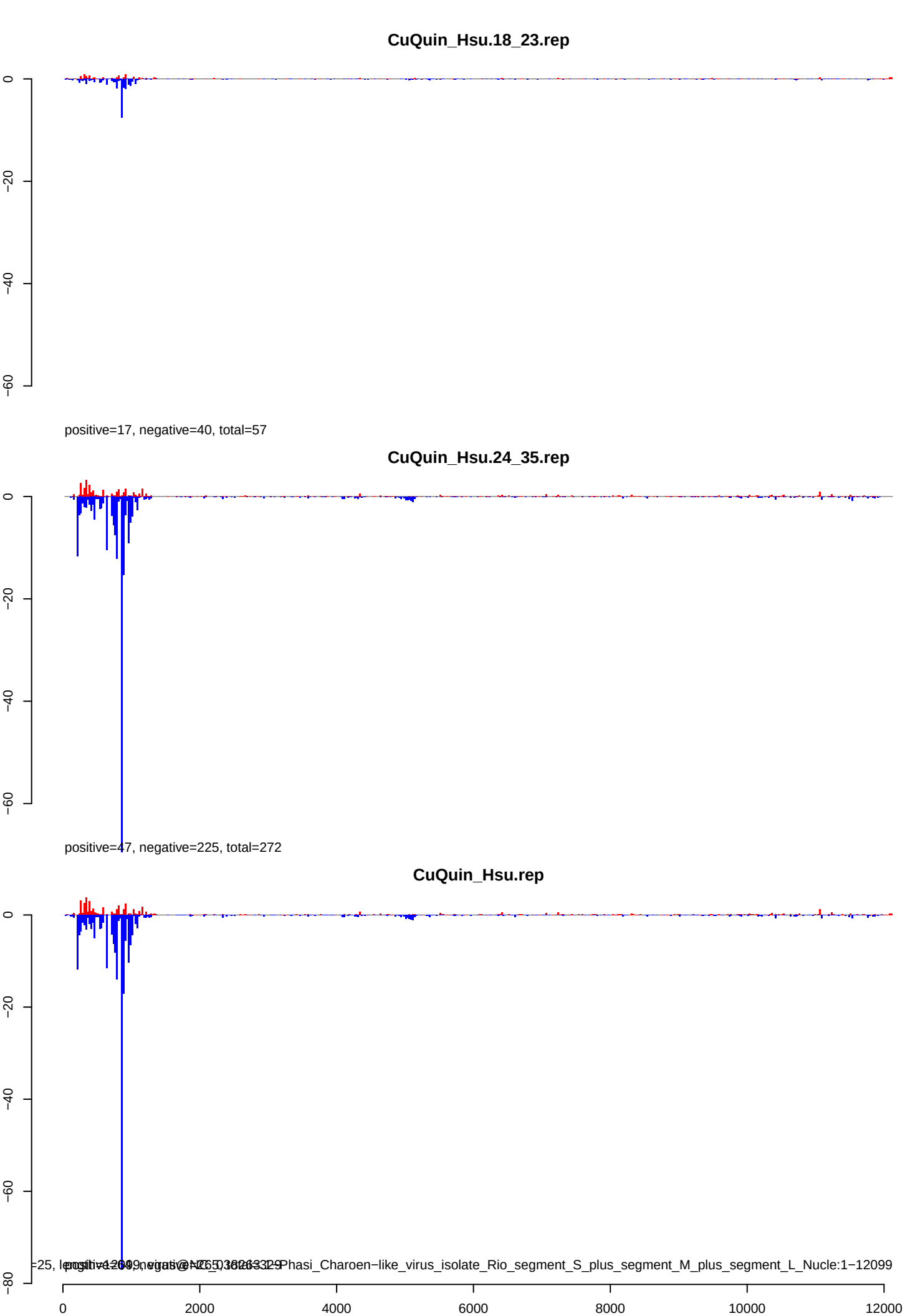
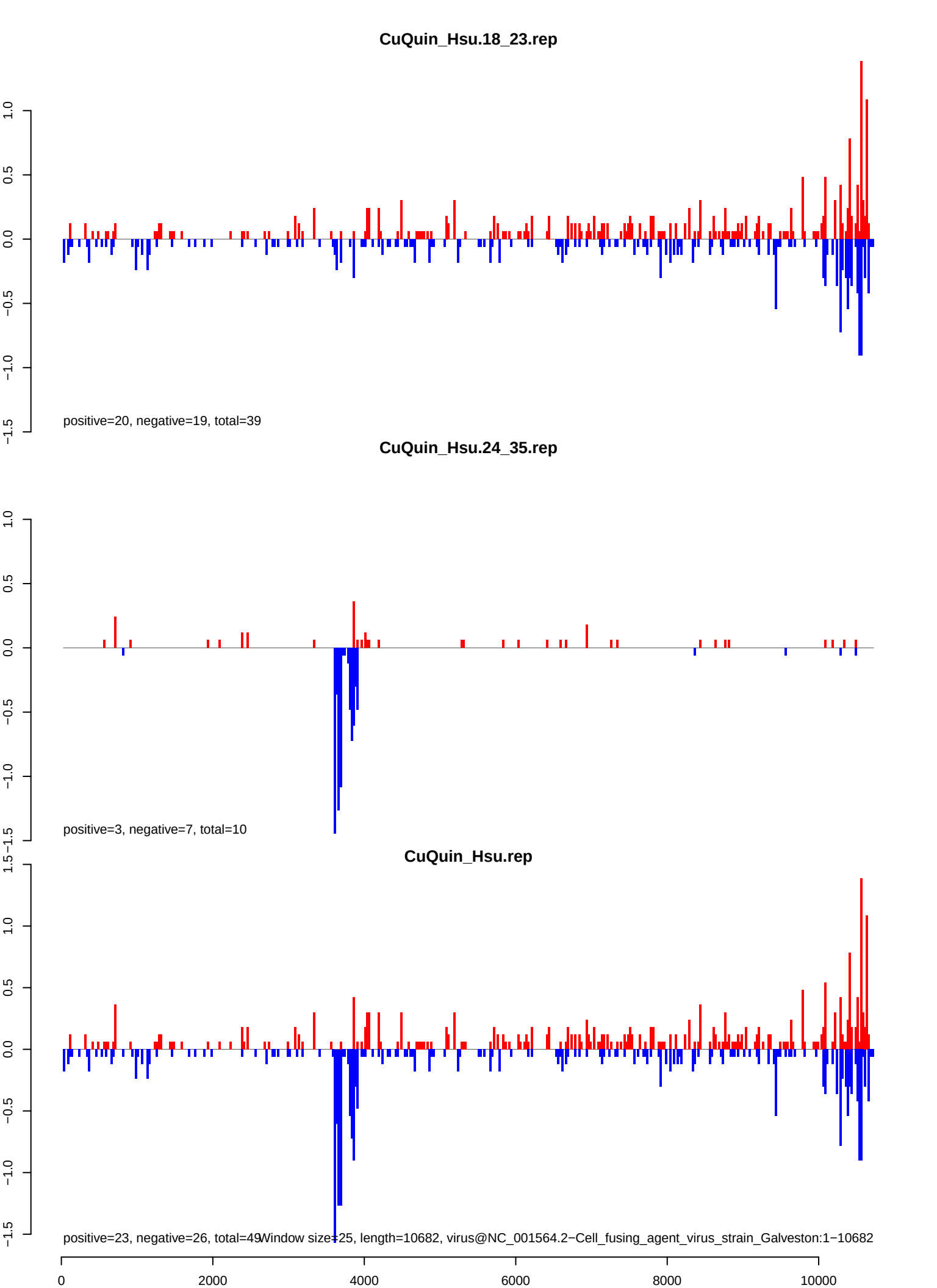
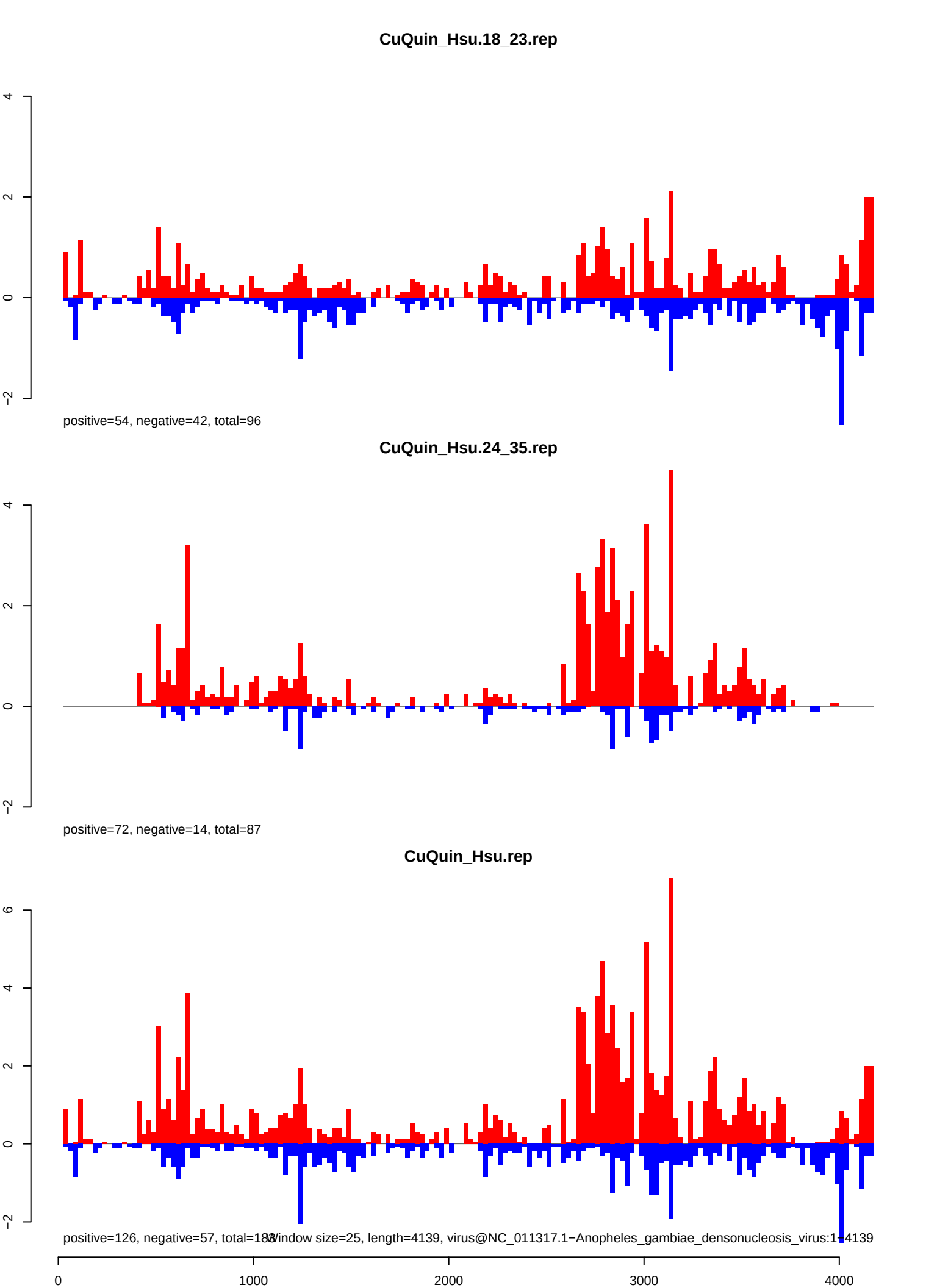
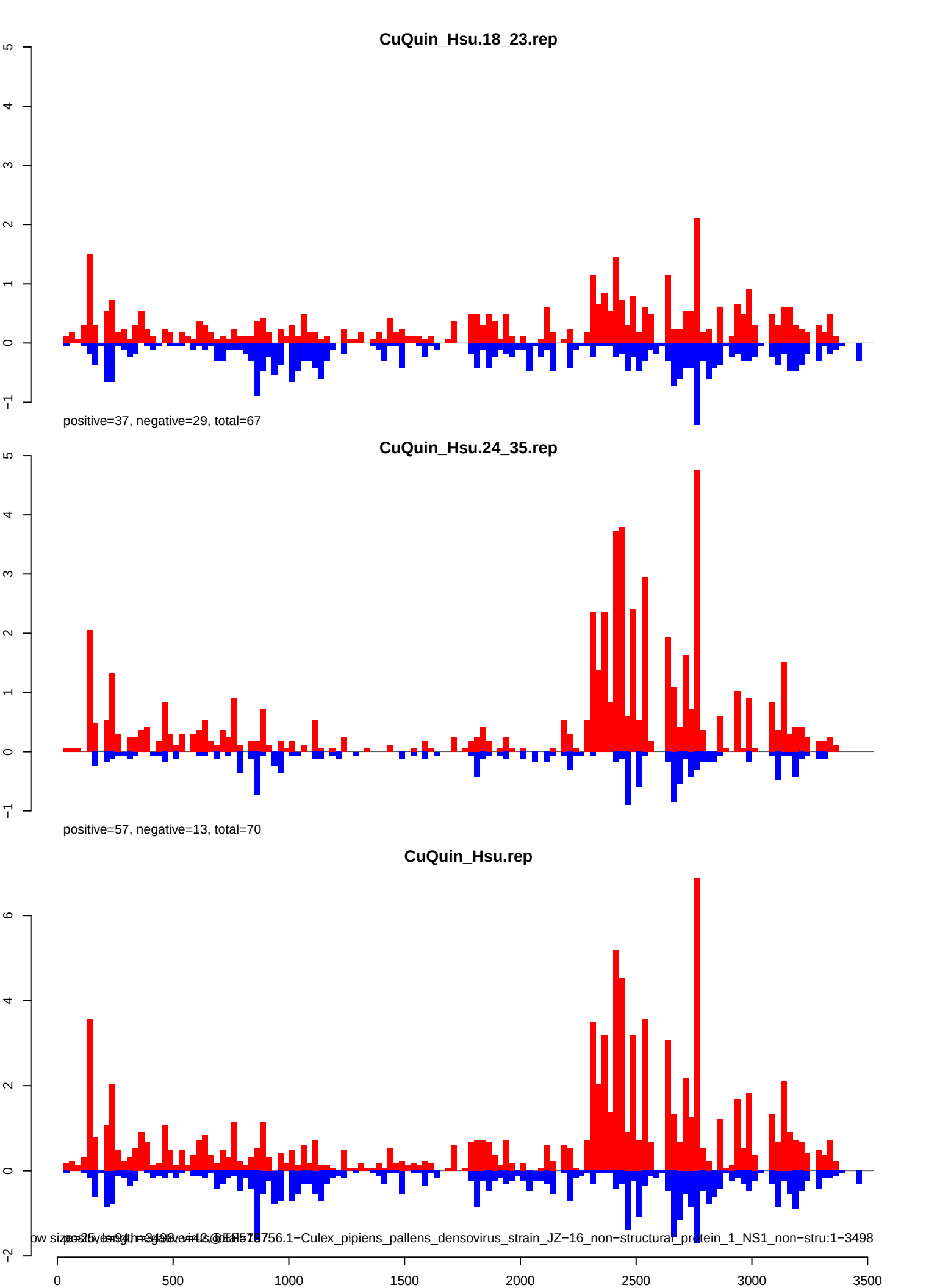
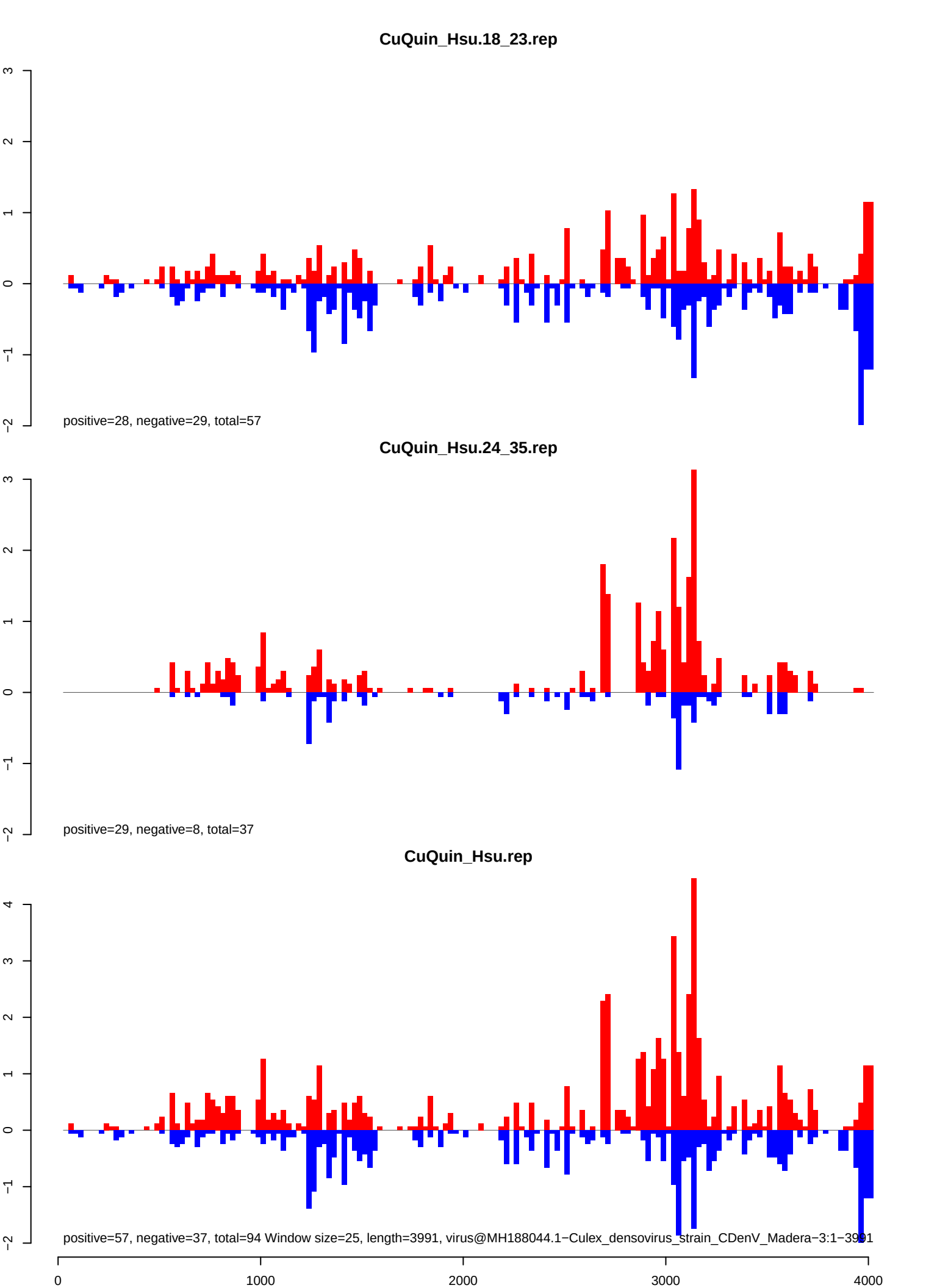

CuQuin_Hsu.18_23.rep
positive=1493, negative=1298, total=2790
CuQuin_Hsu.24_35.rep
positive=1803, negative=248, total=2051
CuQuin_Hsu.rep
positive=3296, negative=1546, total=4841
Window size=25, length=11798, virus@KU194360.1_Merida_virus_isolate_MERD−Mex07:1−11798
0
2000
4000
6000
8000
10000
12000

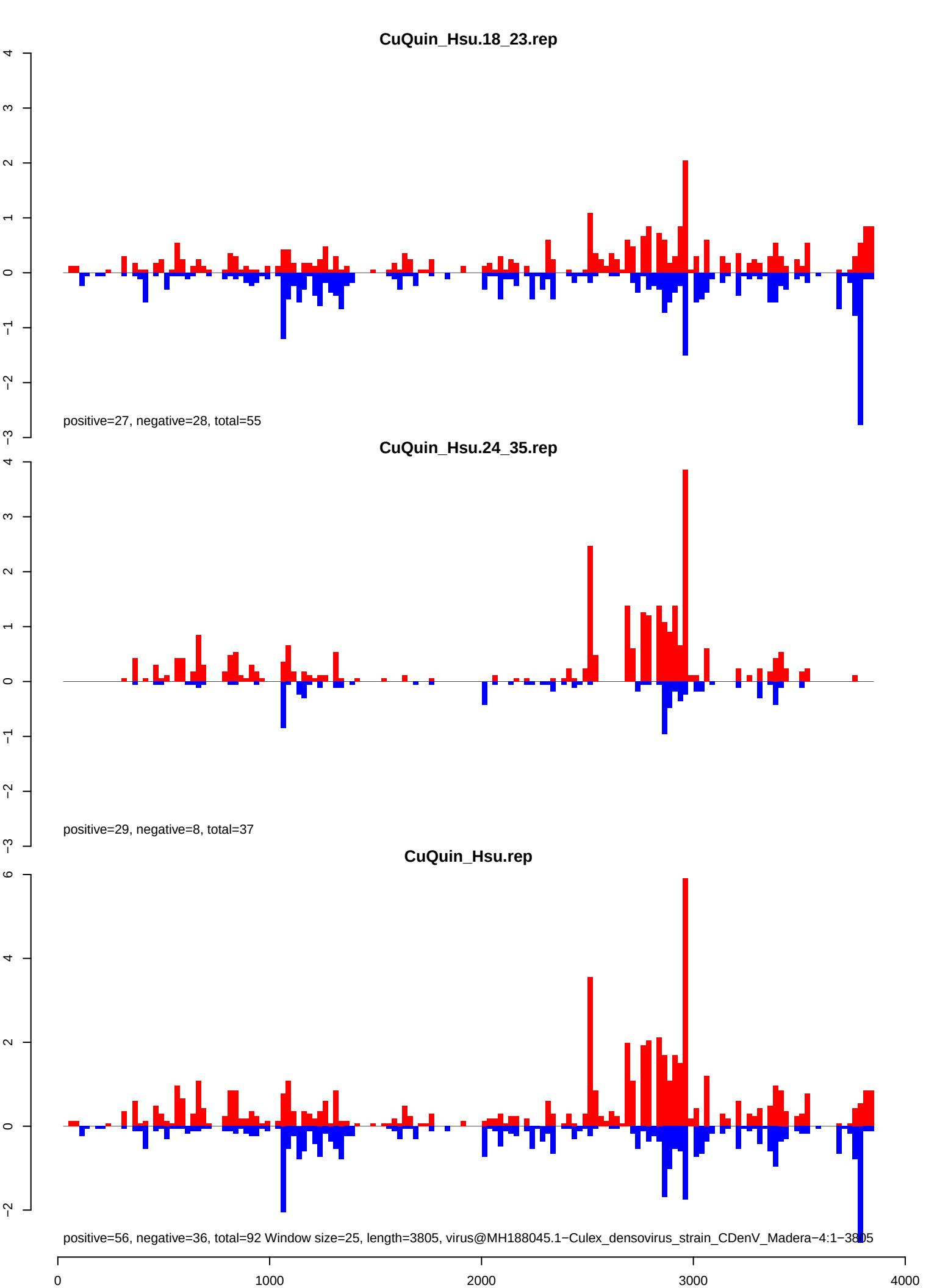

CuQuin_Hsu.18_23.rep
0
−20
−40
−60
positive=17, negative=40, total=57
CuQuin_Hsu.24_35.rep
0
−20
−40
−60
positive=47, negative=225, total=272
CuQuin_Hsu.rep
0
−20
−40
−60
−80
0
2000
4000
6000
8000
10000
12000

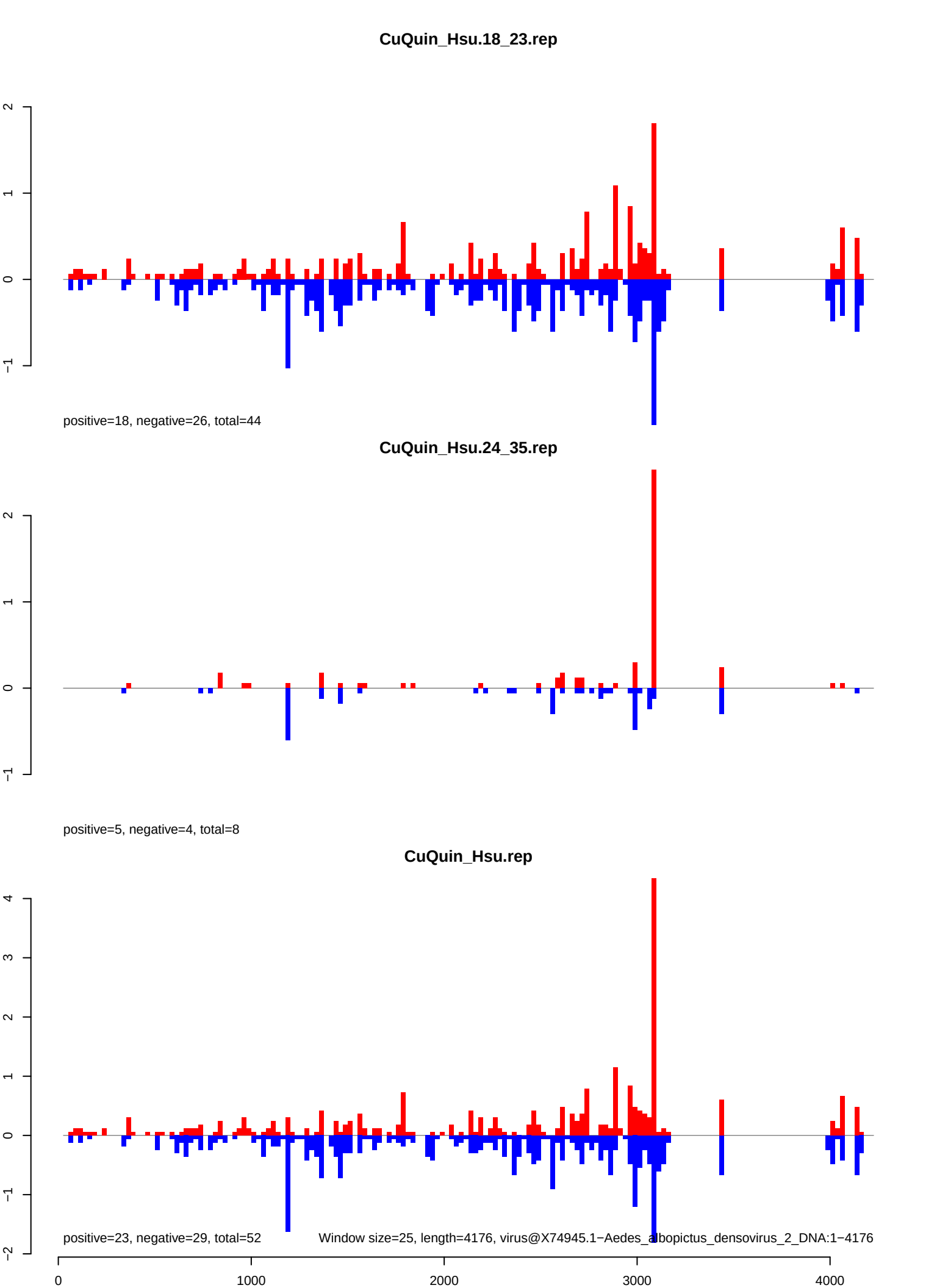

CuQuin_Hsu.18_23.rep
positive=20, negative=19, total=39
CuQuin_Hsu.24_35.rep
positive=3, negative=7, total=10
CuQuin_Hsu.rep
positive=23, negative=26, total=49
Window size=25, length=10682, virus@NC_001564.2−Cell_fusing_agent_virus_strain_Galveston:1−10682
1.5
1.0
0.5
0.0
−0.5
−1.0
−1.5
0
2000
4000
6000
8000
10000

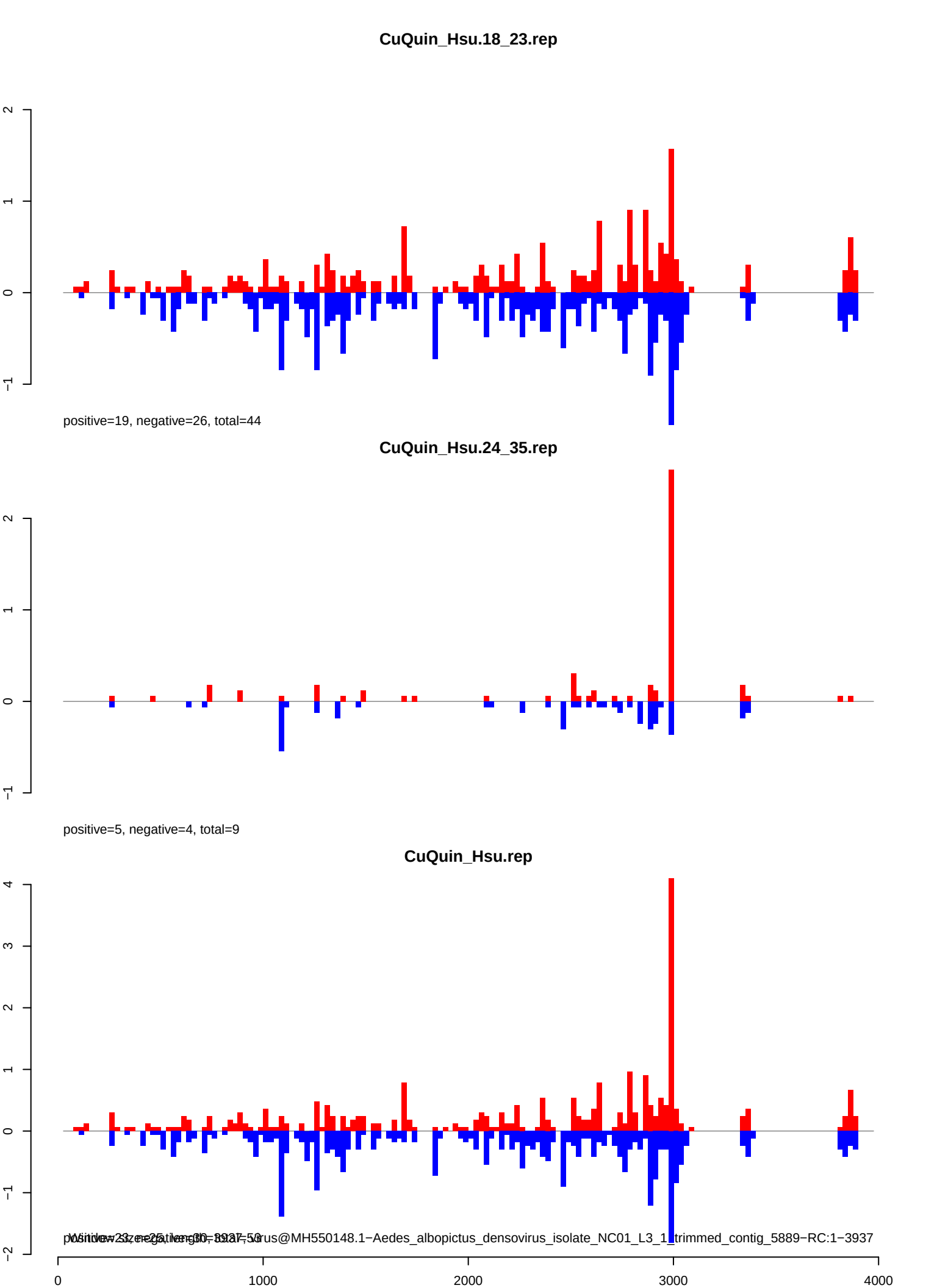

CuQuin_Hsu.18_23.rep
positive=54, negative=42, total=96
CuQuin_Hsu.24_35.rep
positive=72, negative=14, total=87
CuQuin_Hsu.rep
positive=126, negative=57, total=183
window size=25, length=4139, virus@NC_011317.1−Anopheles_gambiae_densonucleosis_virus:1−4139
0
1000
2000
3000
4000

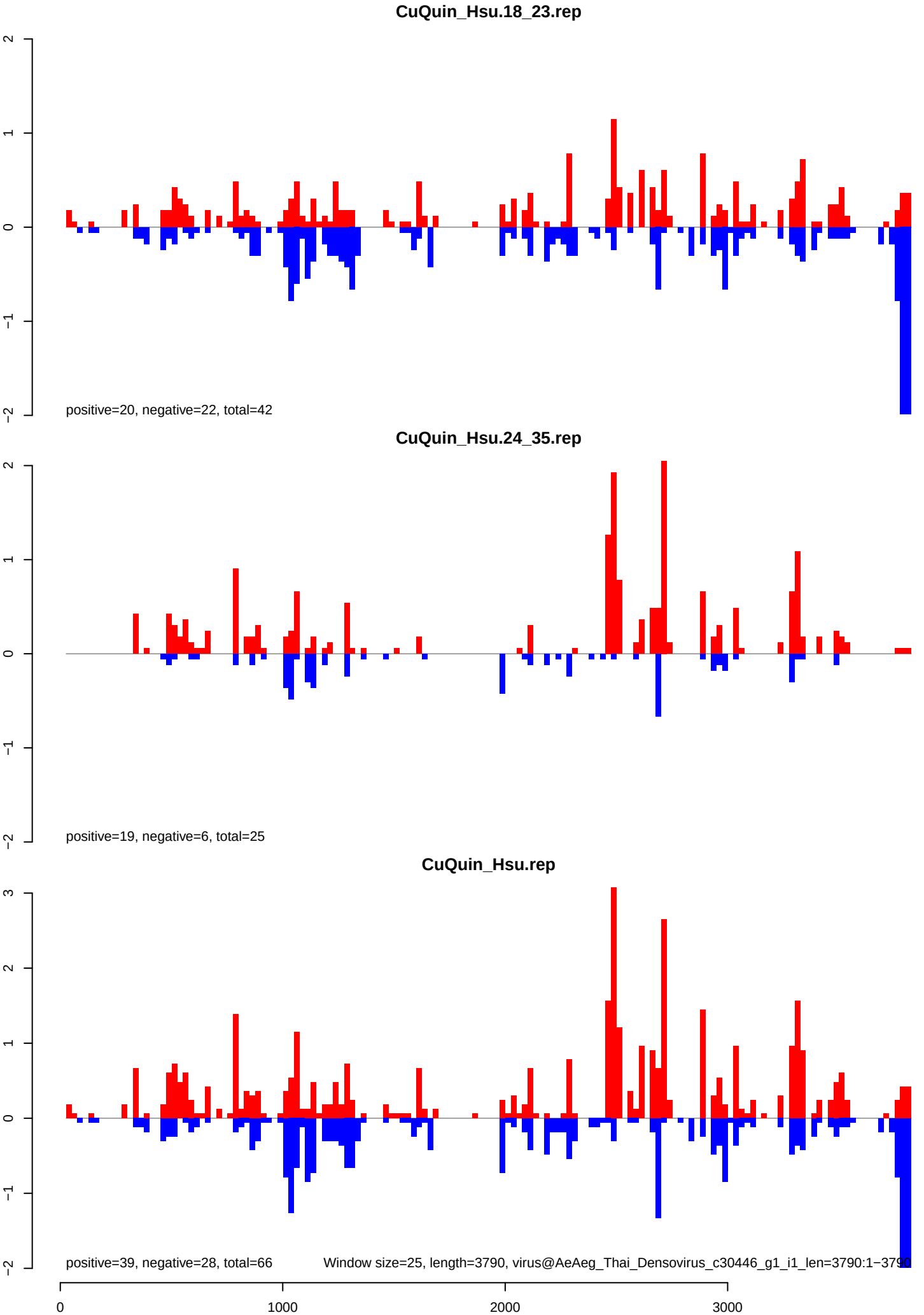

CuQuin_Hsu.18_23.rep
positive=37, negative=29, total=67
CuQuin_Hsu.24_35.rep
positive=57, negative=13, total=70
CuQuin_Hsu.rep
0
500
1000
1500
2000
2500
3000
3500

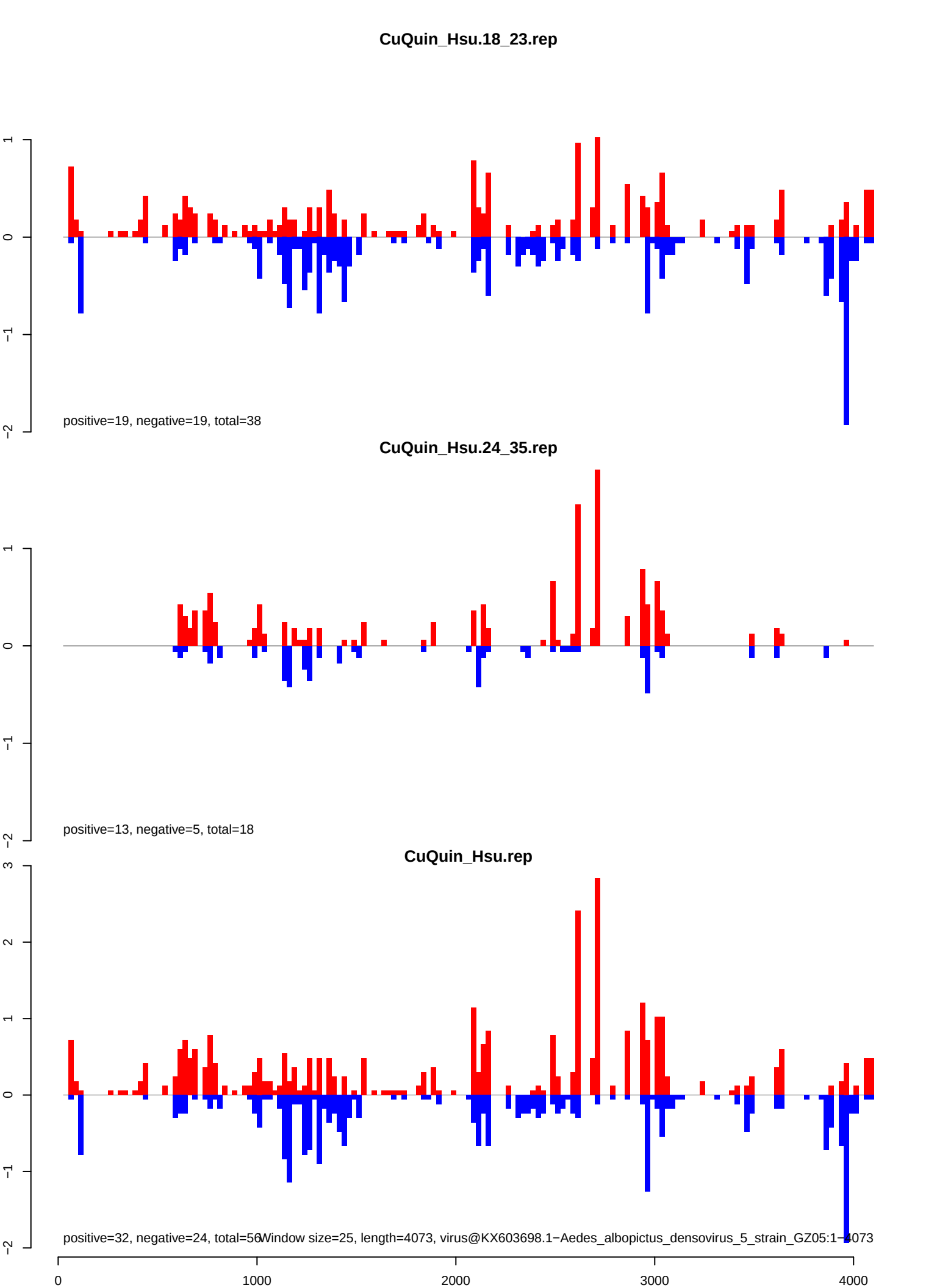

CuQuin_Hsu.18_23.rep
positive=28, negative=29, total=57
CuQuin_Hsu.24_35.rep
positive=29, negative=8, total=37
CuQuin_Hsu.rep
positive=57, negative=37, total=94 Window size=25, length=3991, virus@MH188044.1−Culex_densovirus_strain_CDenV_Madera−3:1−3991
0
1000
2000
3000
4000

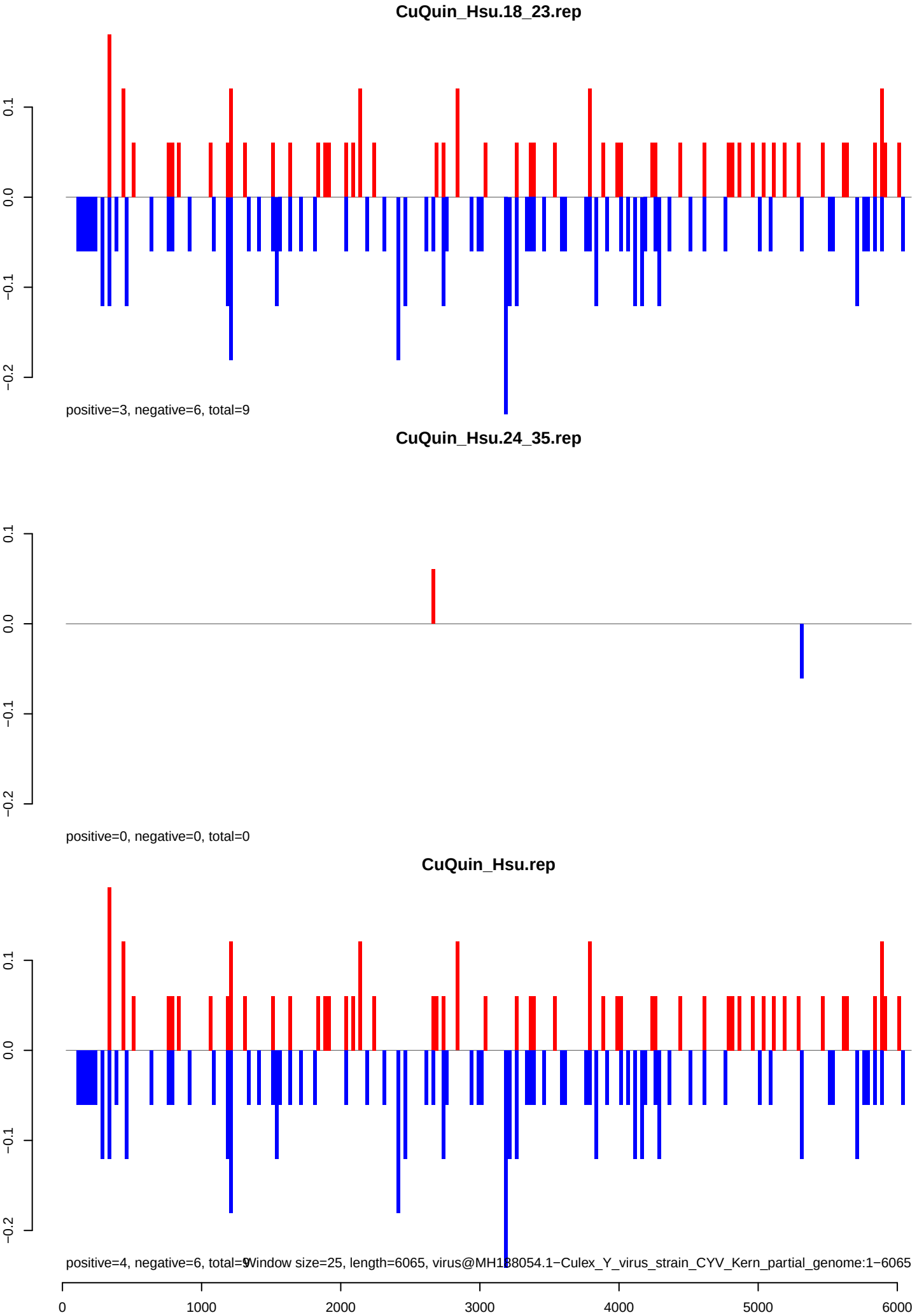

CuQuin_Hsu.18_23.rep
positive=27, negative=28, total=55
CuQuin_Hsu.24_35.rep
positive=29, negative=8, total=37
CuQuin_Hsu.rep
positive=56, negative=36, total=92 Window size=25, length=3805, virus@MH188045.1−Culex_densovirus_strain_CDenV_Madera−4:1−3805
0
1000
2000
3000
4000

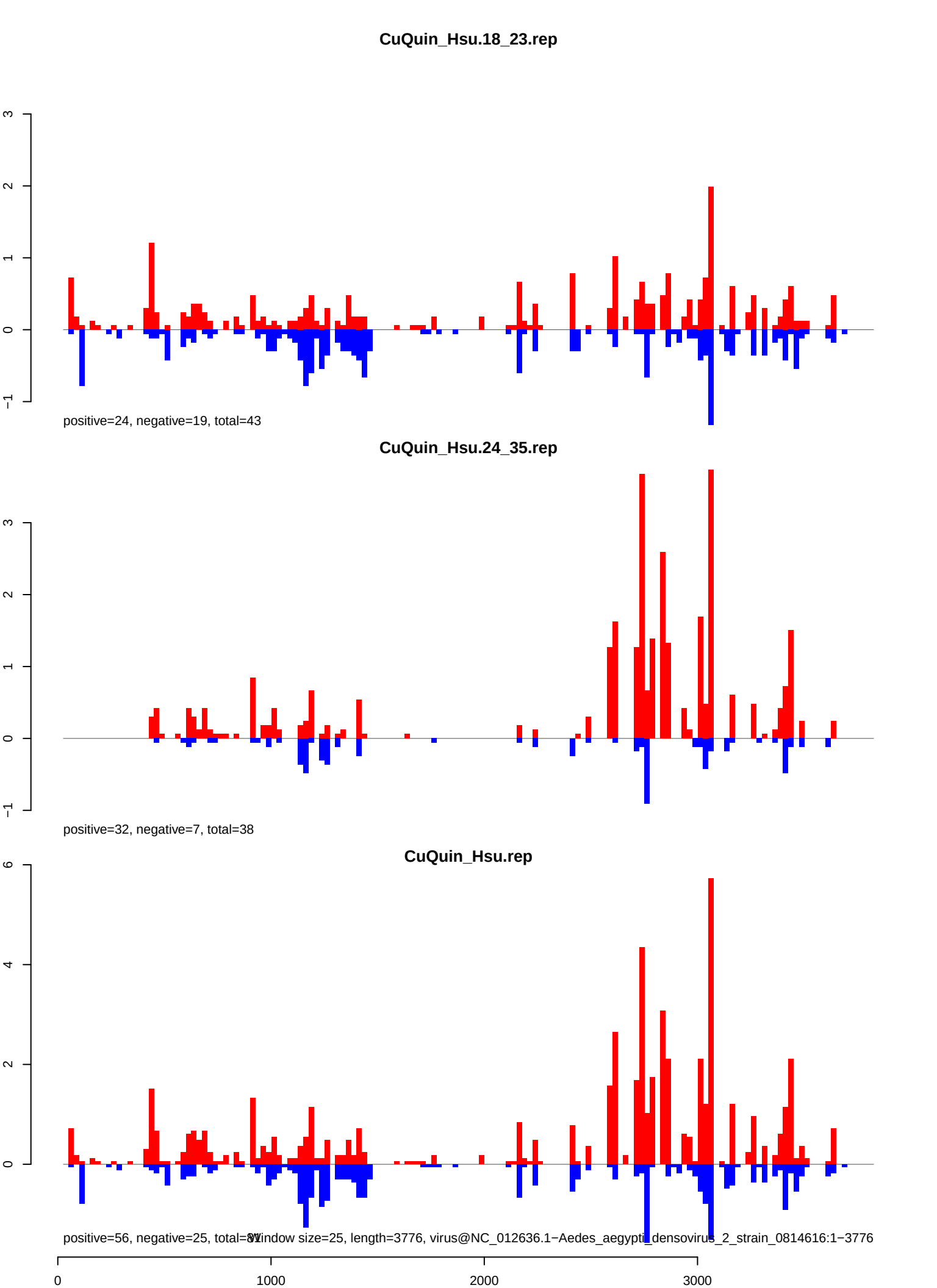

CuQuin_Hsu.18_23.rep
positive=18, negative=26, total=44
CuQuin_Hsu.24_35.rep
positive=5, negative=4, total=8
CuQuin_Hsu.rep
positive=23, negative=29, total=52
Window size=25, length=4176, virus@X74945.1−Aedes_albopictus_densovirus_2_DNA:1−4176
0
1000
2000
3000
4000

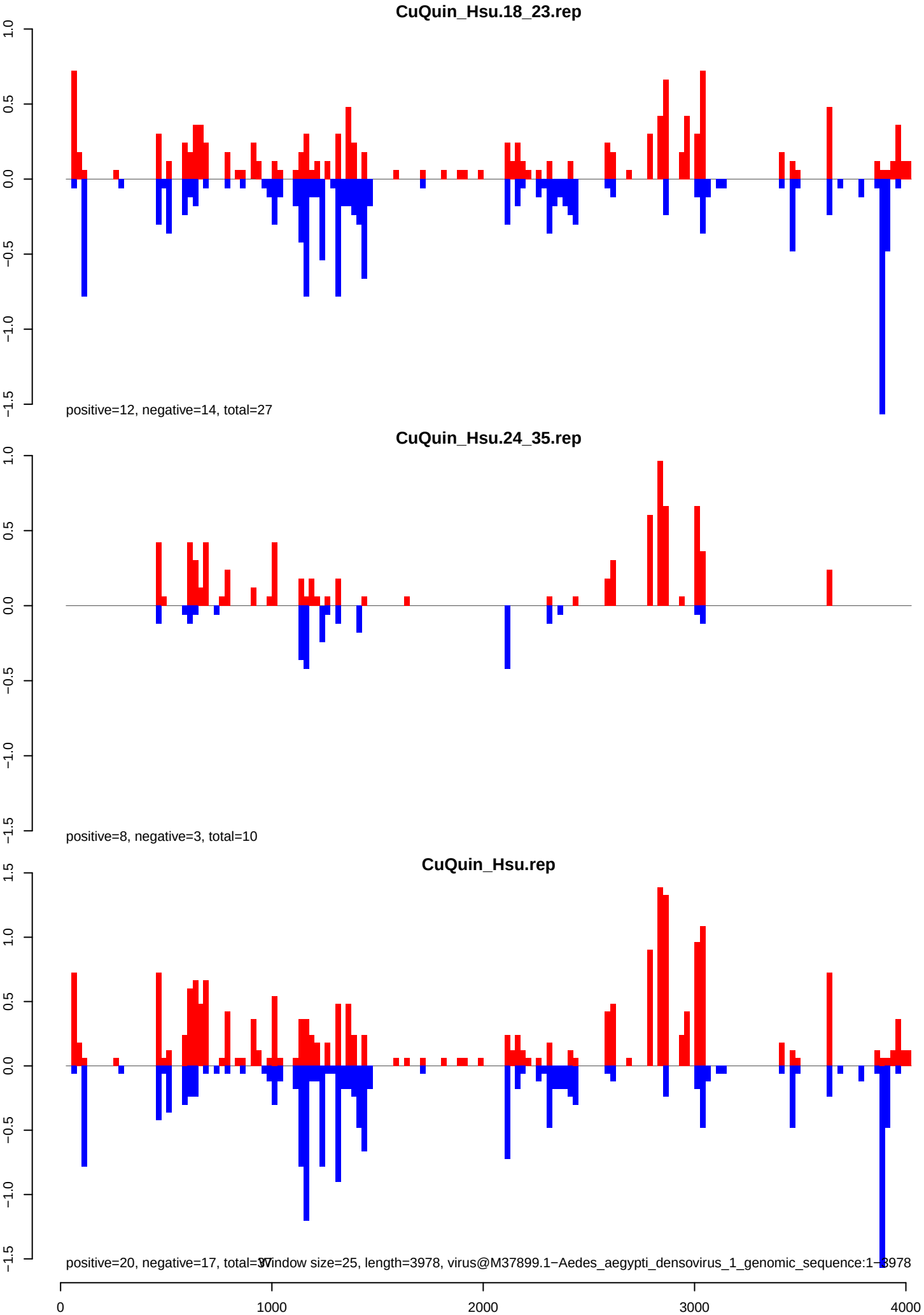

CuQuin_Hsu.18_23.rep
positive=19, negative=26, total=44
CuQuin_Hsu.24_35.rep
positive=5, negative=4, total=9
CuQuin_Hsu.rep
positive=23, negative=30, total=53
Window size=25, length=3937
virus@MH550148.1−Aedes_albopictus_densovirus_isolate_NC01_L3_1_trimmed_contig_5889−RC:1−3937
0
1000
2000
3000
4000

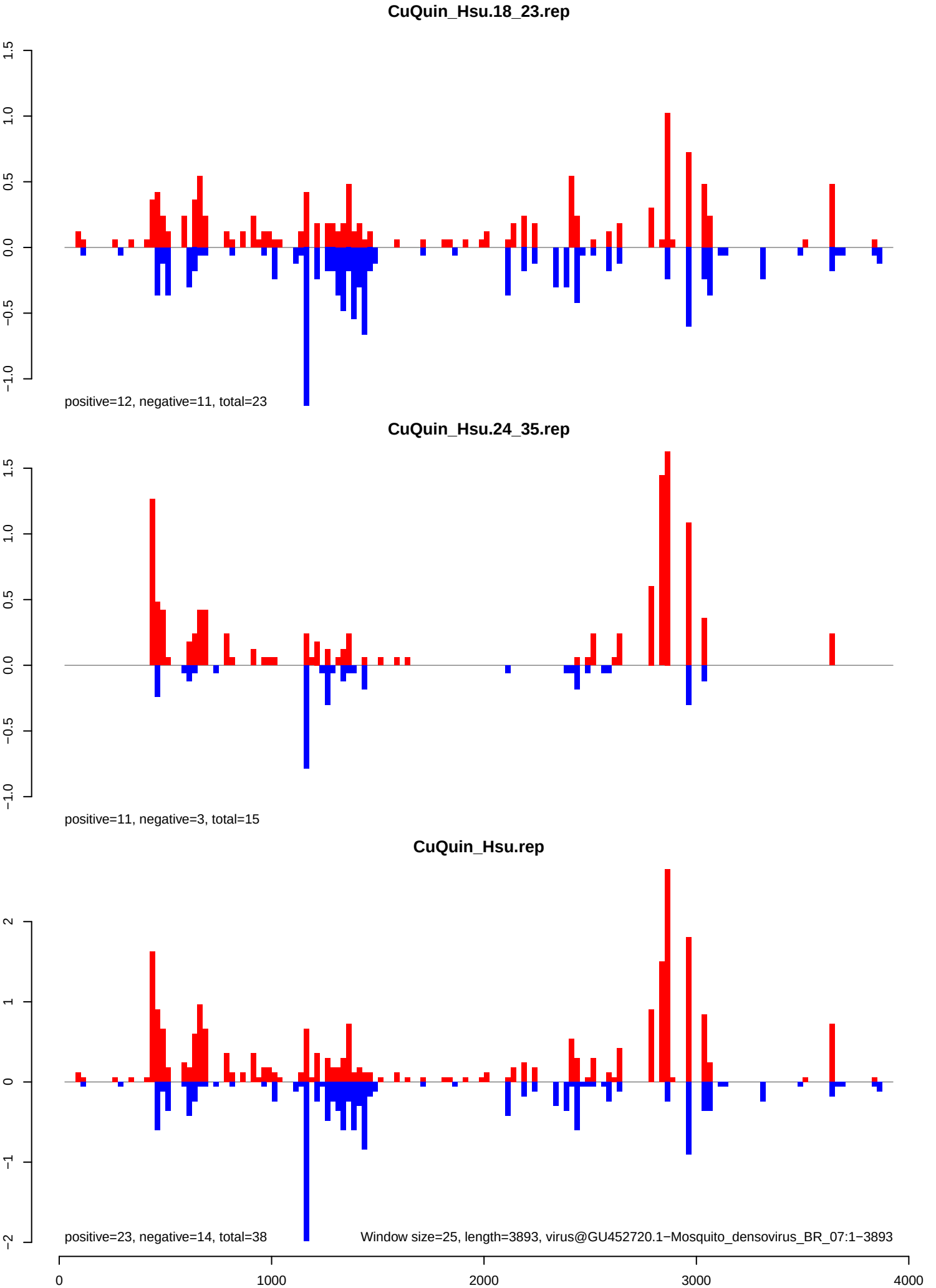

CuQuin_Hsu.18_23.rep
positive=20, negative=22, total=42
CuQuin_Hsu.24_35.rep
positive=19, negative=6, total=25
CuQuin_Hsu.rep
positive=39, negative=28, total=66
Window size=25, length=3790, virus@AeAeg_Thai_Densovirus_c30446_g1_i1_len=3790:1−3790
0
1000
2000
3000

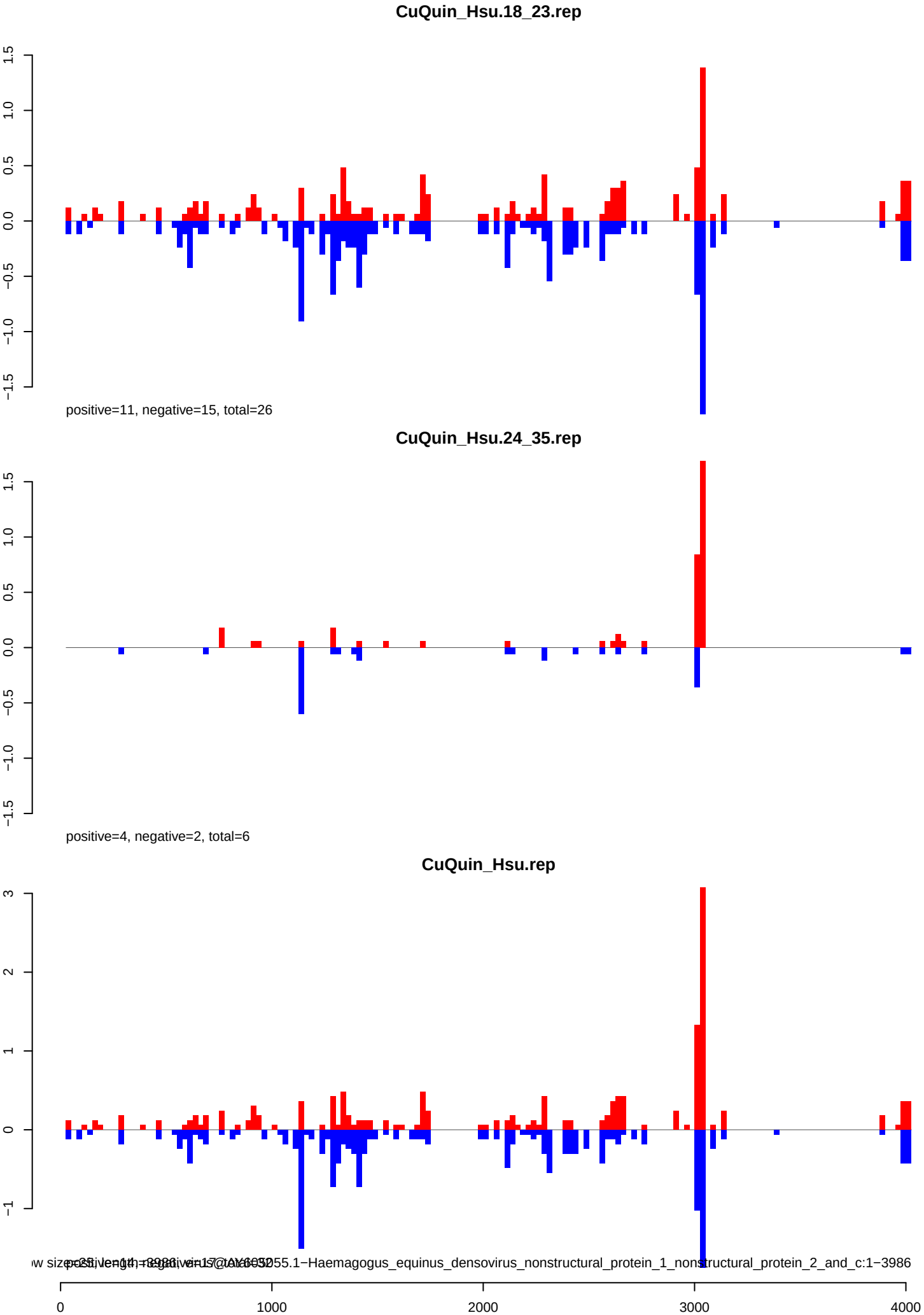

CuQuin_Hsu.18_23.rep
positive=19, negative=19, total=38
CuQuin_Hsu.24_35.rep
positive=13, negative=5, total=18
CuQuin_Hsu.rep
positive=32, negative=24, total=56
Window size=25, length=4073, virus@KX603698.1−Aedes_albopictus_densovirus_5_strain_GZ05:1−4073
0
1000
2000
3000
4000

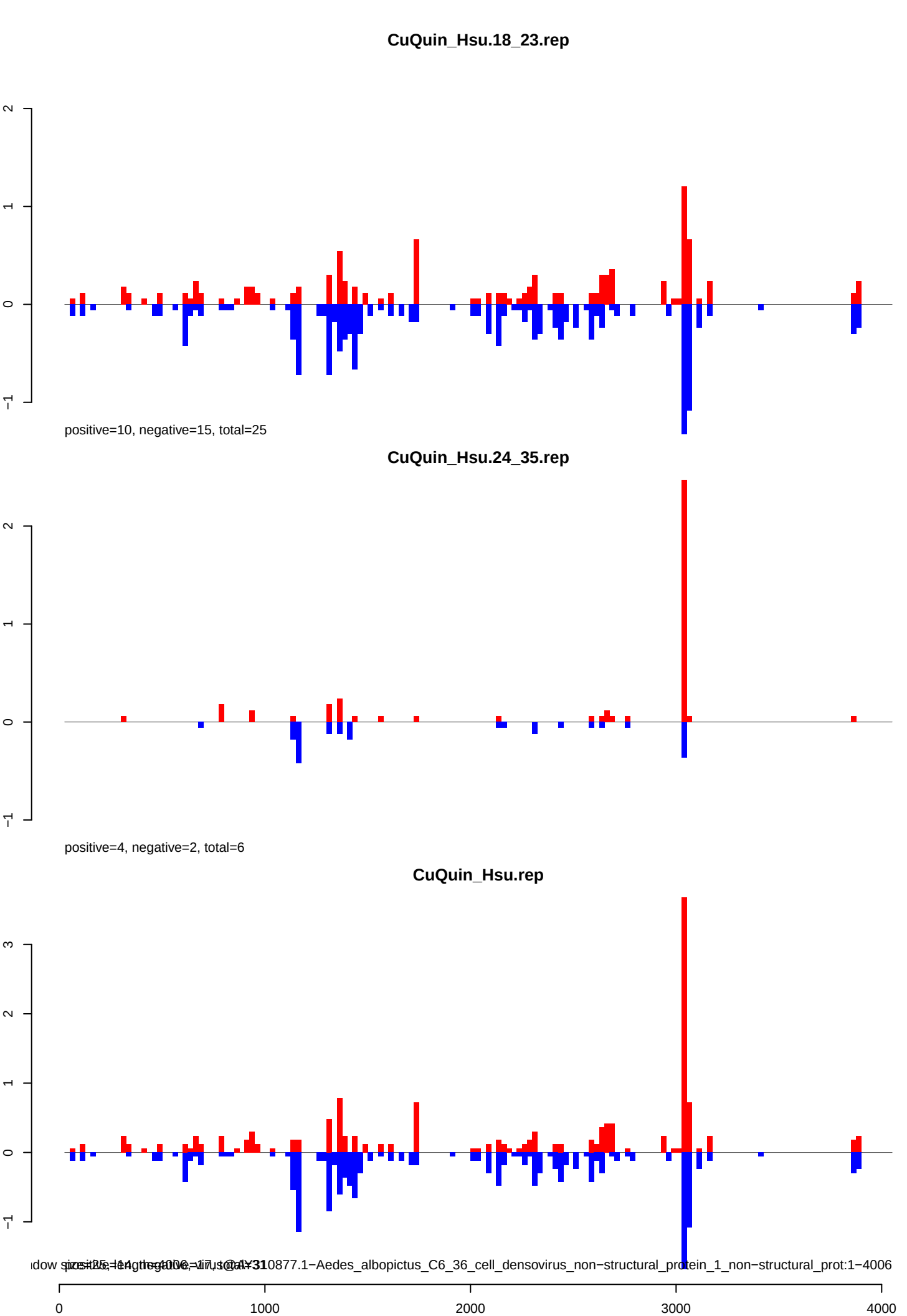

CuQuin_Hsu.18_23.rep
0.1
0.0
−0.1
−0.2
positive=3, negative=6, total=9
CuQuin_Hsu.24_35.rep
0.1
0.0
−0.1
−0.2
positive=0, negative=0, total=0
CuQuin_Hsu.rep
0.1
0.0
−0.1
−0.2
positive=4, negative=6, total=9
Window size=25, length=6065, virus@MH188054.1−Culex_Y_virus_strain_CYV_Kern_partial_genome:1−6065
0
1000
2000
3000
4000
5000
6000

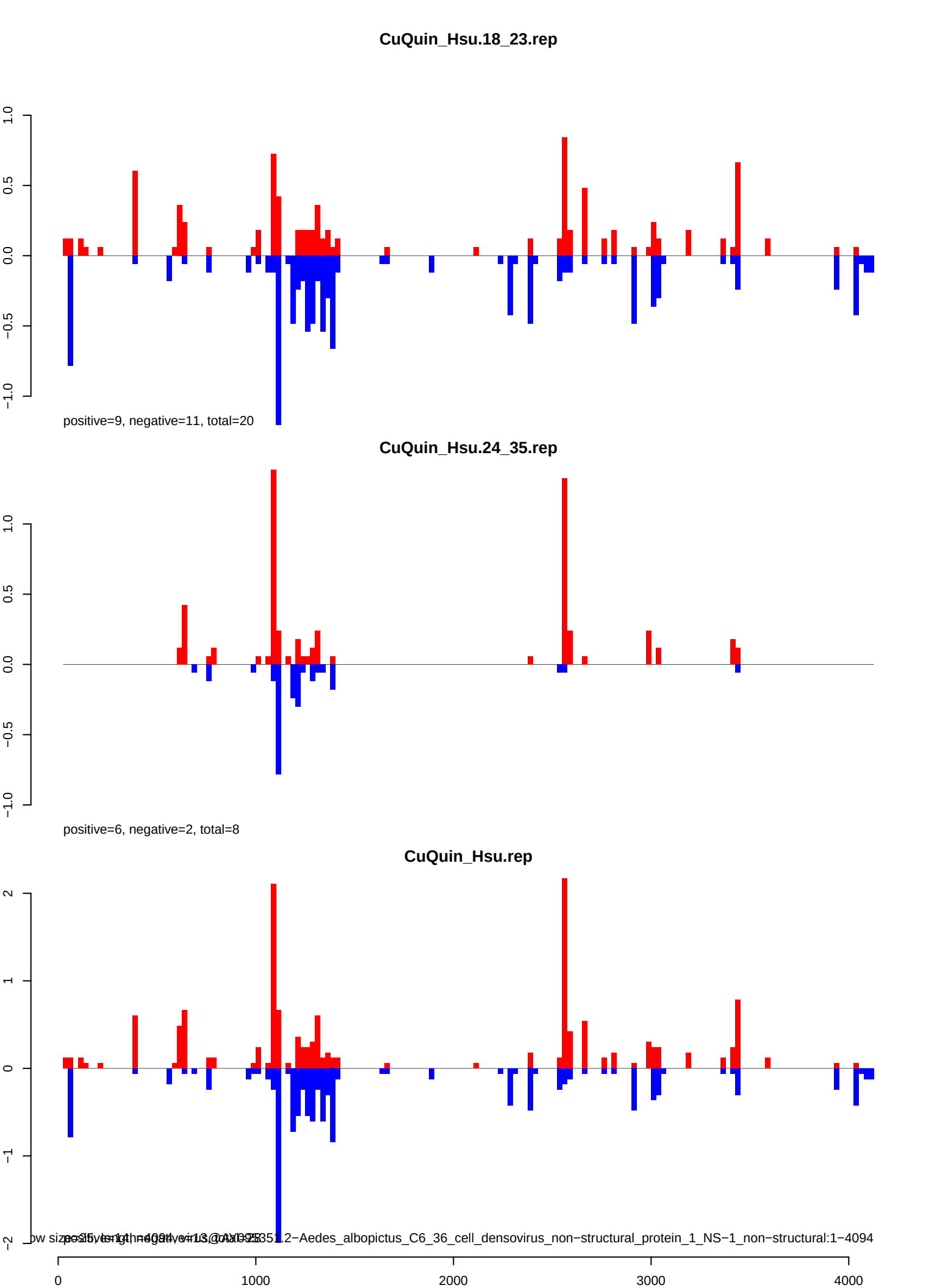

CuQuin_Hsu.18_23.rep
positive=24, negative=19, total=43
CuQuin_Hsu.24_35.rep
positive=32, negative=7, total=38
CuQuin_Hsu.rep
positive=56, negative=25, total=81
Window size=25, length=3776, virus@NC_012636.1−Aedes_aegypti_densovirus_2_strain_0814616:1−3776
0
1000
2000
3000

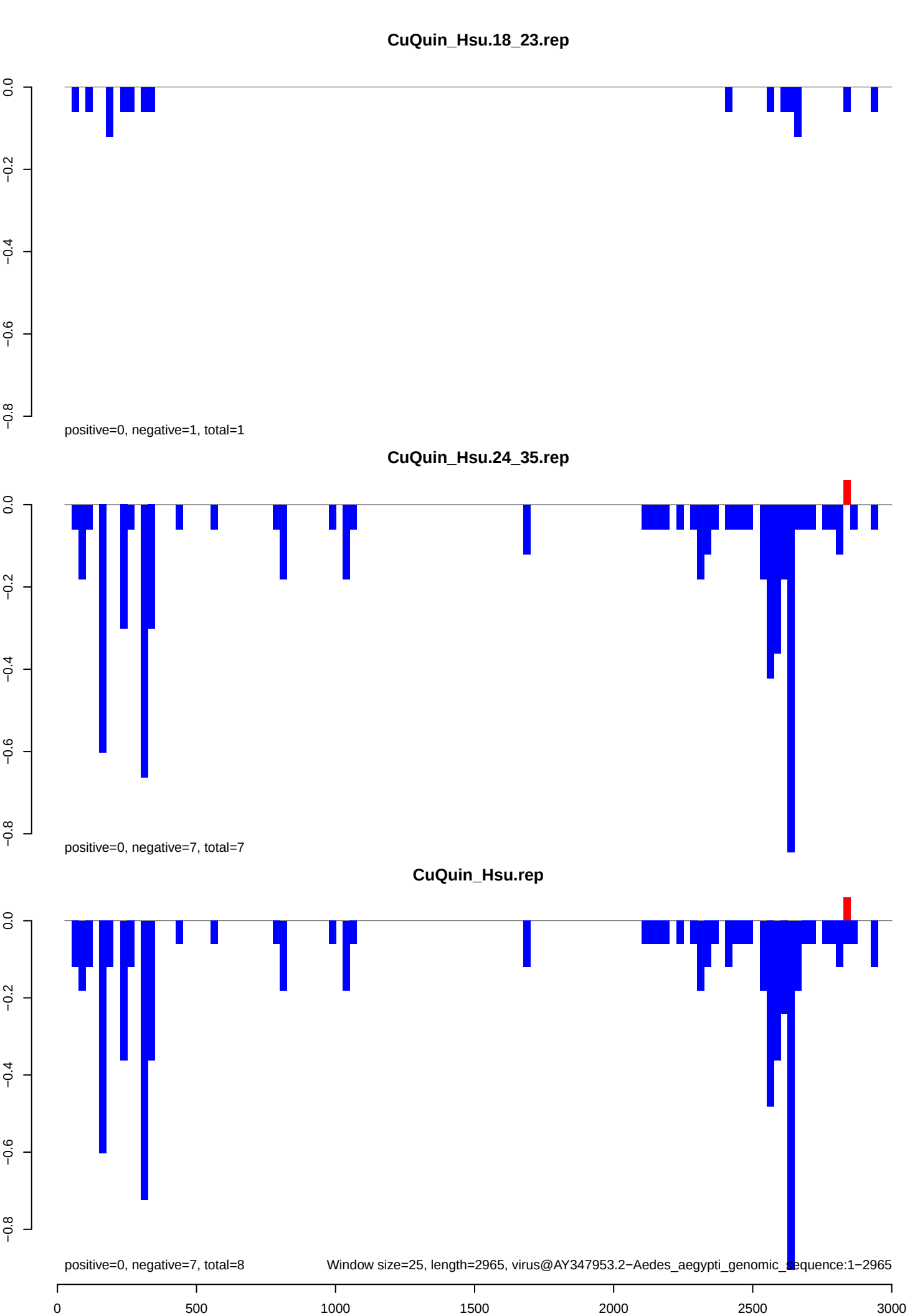

CuQuin_Hsu.18_23.rep
1.0
0.5
0.0
−0.5
−1.0
−1.5
positive=12, negative=14, total=27
CuQuin_Hsu.24_35.rep
1.0
0.5
0.0
−0.5
−1.0
−1.5
positive=8, negative=3, total=10
CuQuin_Hsu.rep
1.5
1.0
0.5
0.0
−0.5
−1.0
−1.5
positive=20, negative=17, total=37
Window size=25, length=3978, virus@M37899.1−Aedes_aegypti_densovirus_1_genomic_sequence:1−3978
0
1000
2000
3000
4000

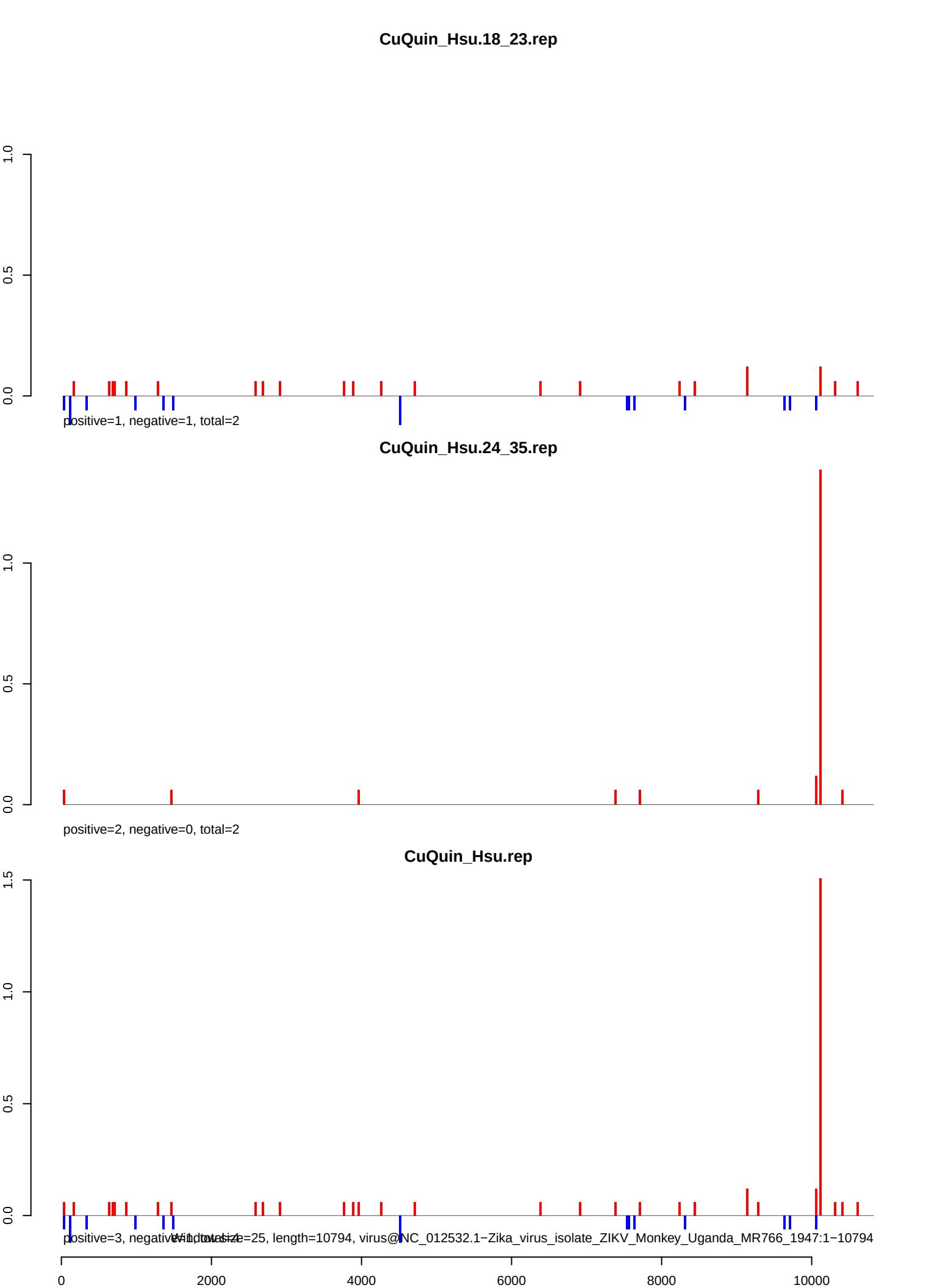

CuQuin_Hsu.18_23.rep
1.5
1.0
0.5
0.0
−0.5
−1.0
positive=12, negative=11, total=23
CuQuin_Hsu.24_35.rep
1.5
1.0
0.5
0.0
−0.5
−1.0
positive=11, negative=3, total=15
CuQuin_Hsu.rep
2
1
0
−1
−2
positive=23, negative=14, total=38
Window size=25, length=3893, virus@GU452720.1−Mosquito_densovirus_BR_07:1−3893
0
1000
2000
3000
4000

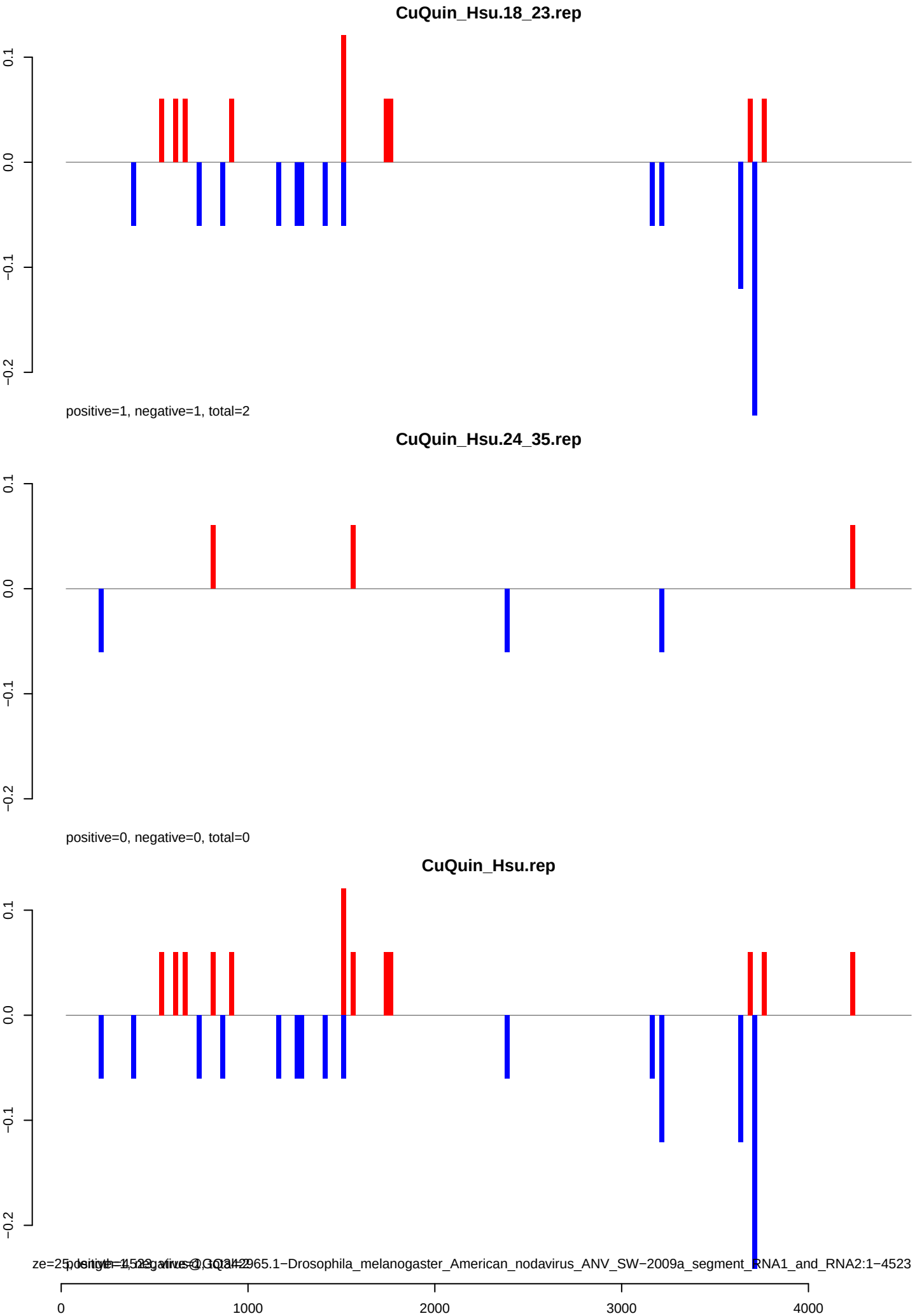

CuQuin_Hsu.18_23.rep
positive=11, negative=15, total=26
CuQuin_Hsu.24_35.rep
positive=4, negative=2, total=6
CuQuin_Hsu.rep
0
1000
2000
3000
4000

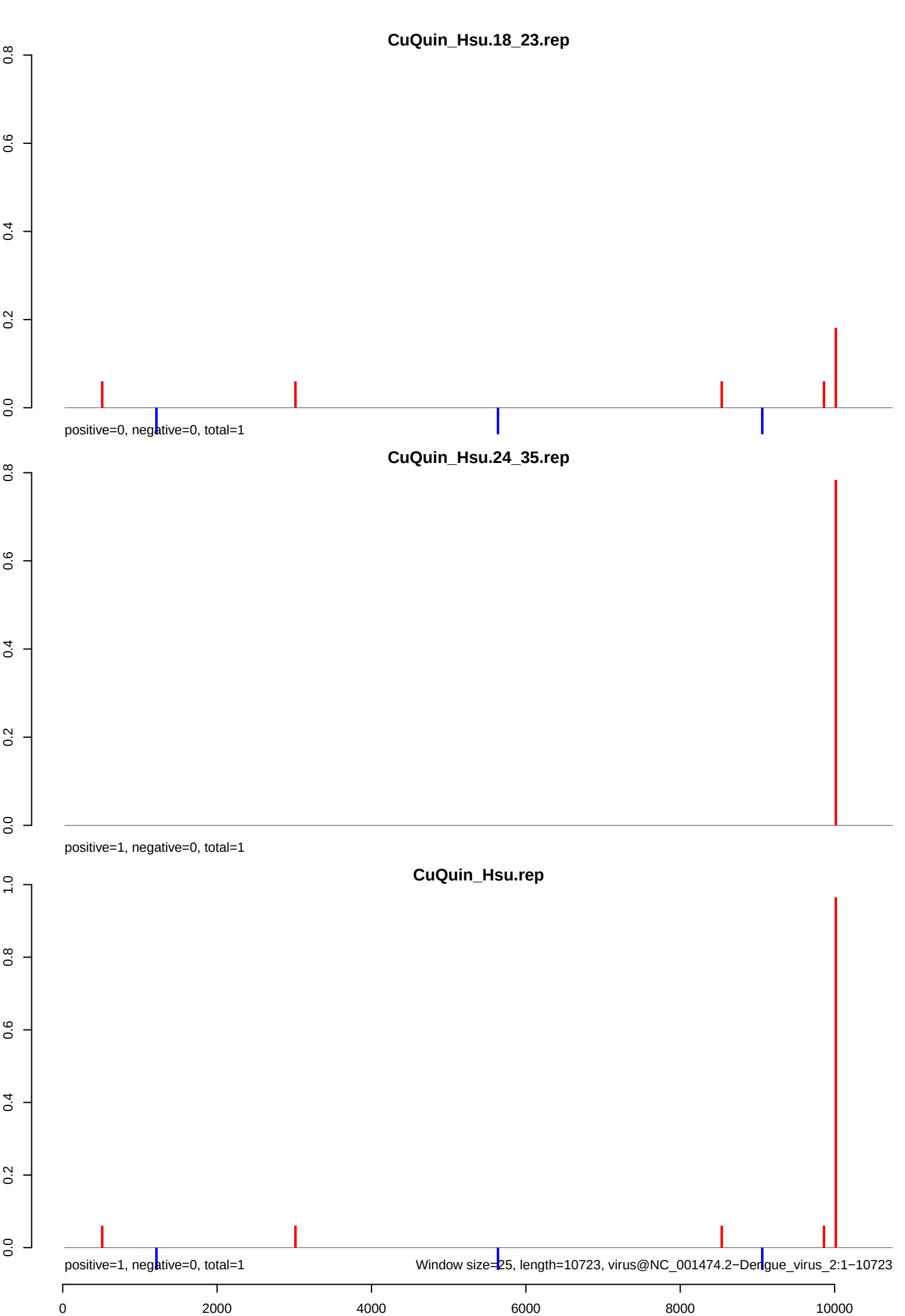

CuQuin_Hsu.18_23.rep
positive=10, negative=15, total=25
CuQuin_Hsu.24_35.rep
positive=4, negative=2, total=6
CuQuin_Hsu.rep
0
1000
2000
3000
4000

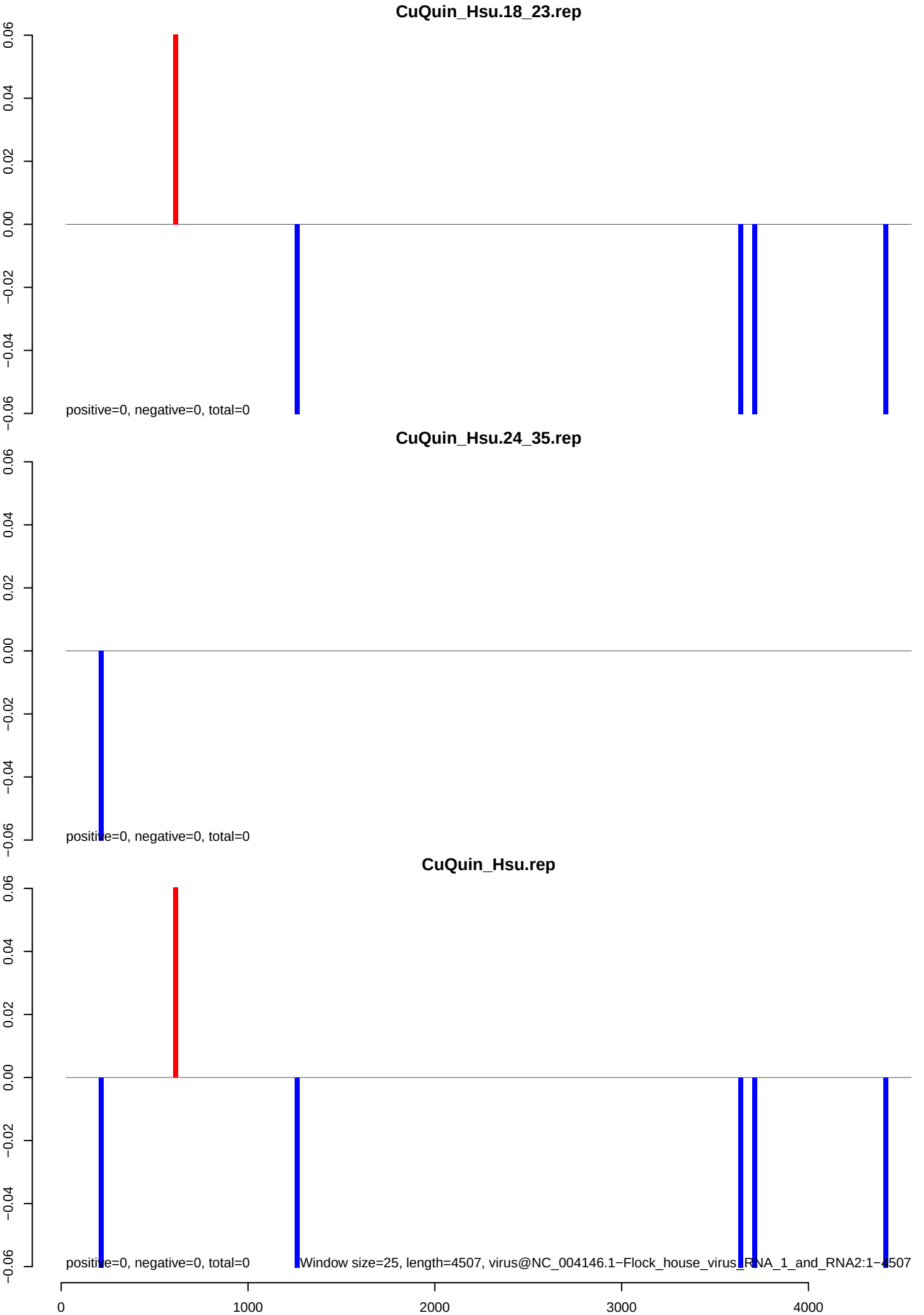

CuQuin_Hsu.18_23.rep
positive=9, negative=11, total=20
CuQuin_Hsu.24_35.rep
positive=6, negative=2, total=8
CuQuin_Hsu.rep
positive=15, length=4094, window size=13, MAX=2.351.2−Aedes_albopictus_C6_36_cell_densovirus_non−structural_protein_1_NS−1_non−structural:1−4094
0
1000
2000
3000
4000

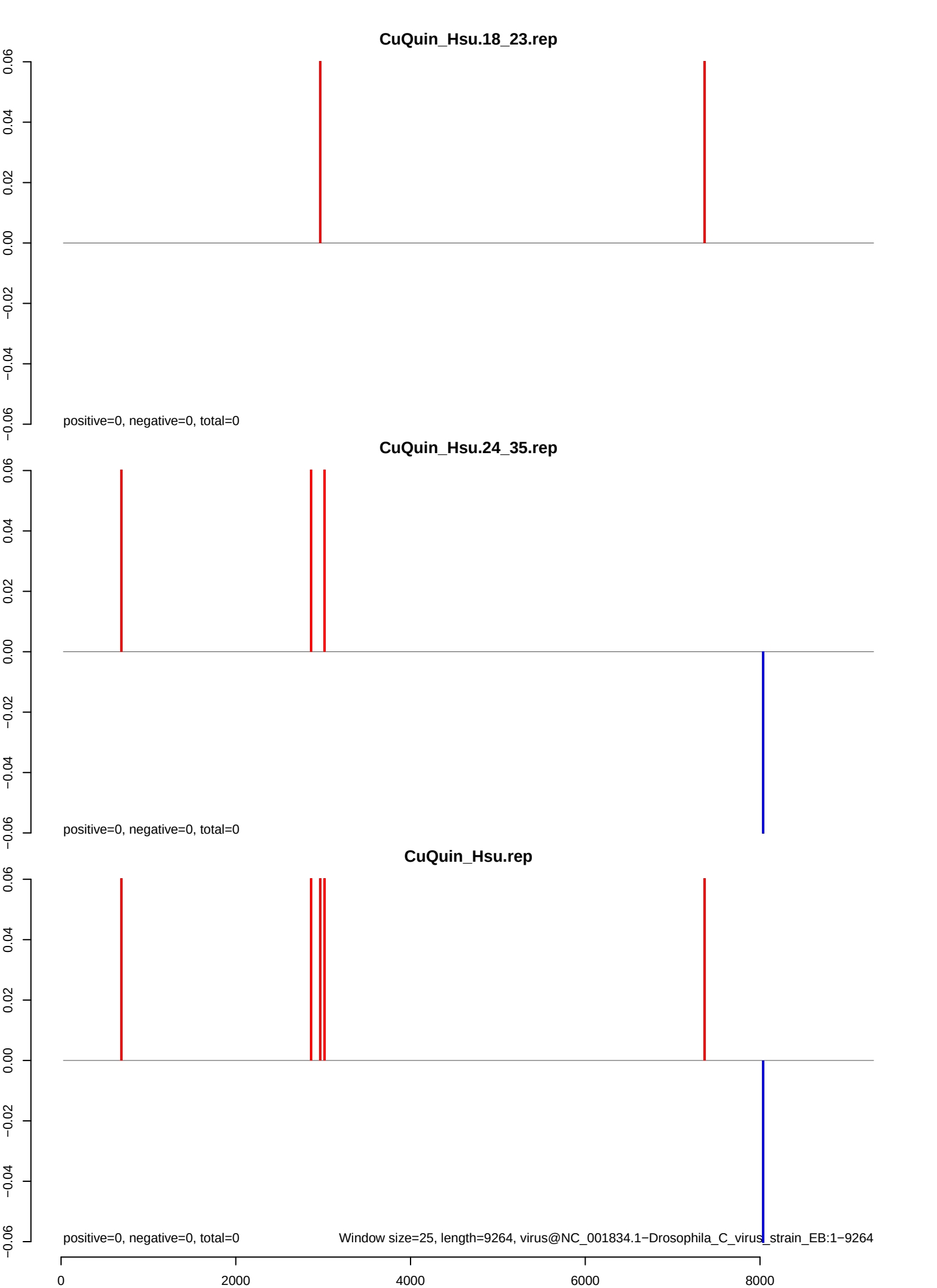

CuQuin_Hsu.18_23.rep
0.0
−0.2
−0.4
−0.6
−0.8
positive=0, negative=1, total=1
CuQuin_Hsu.24_35.rep
0.0
−0.2
−0.4
−0.6
−0.8
positive=0, negative=7, total=7
CuQuin_Hsu.rep
0.0
−0.2
−0.4
−0.6
−0.8
positive=0, negative=7, total=8
Window size=25, length=2965, virus@AY347953.2−Aedes_aegypti_genomic_sequence:1−2965
0
500
1000
1500
2000
2500
3000

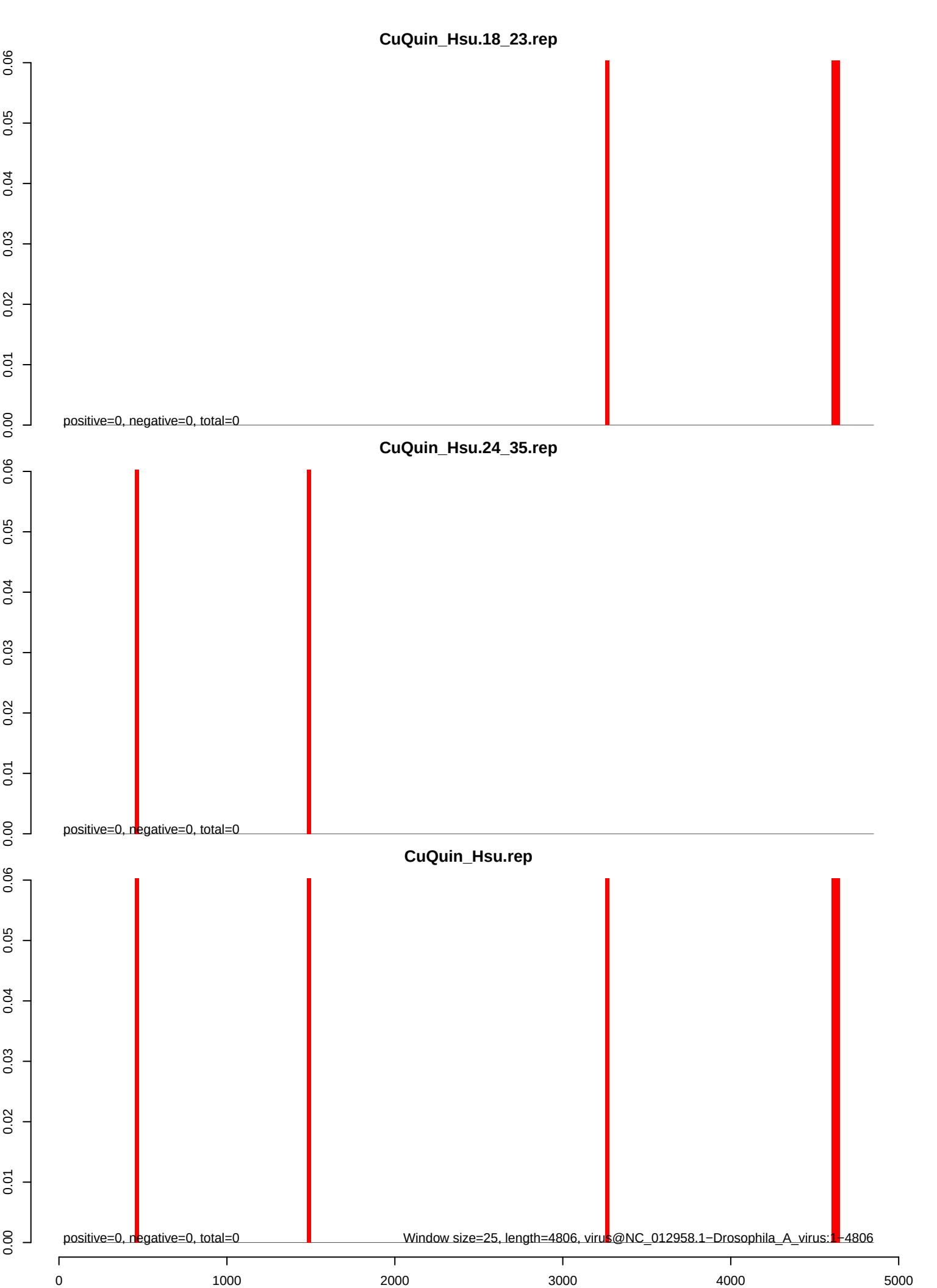

CuQuin_Hsu.18_23.rep
1.0
0.5
0.0
positive=1, negative=1, total=2
CuQuin_Hsu.24_35.rep
1.0
0.5
0.0
positive=2, negative=0, total=2
CuQuin_Hsu.rep
1.5
1.0
0.5
0.0
positive=3, negative=1, total=4
Window size=25, length=10794, virus@NC_012532.1−Zika_virus_isolate_ZIKV_Monkey_Uganda_MR766_1947:1−10794
0
2000
4000
6000
8000
10000

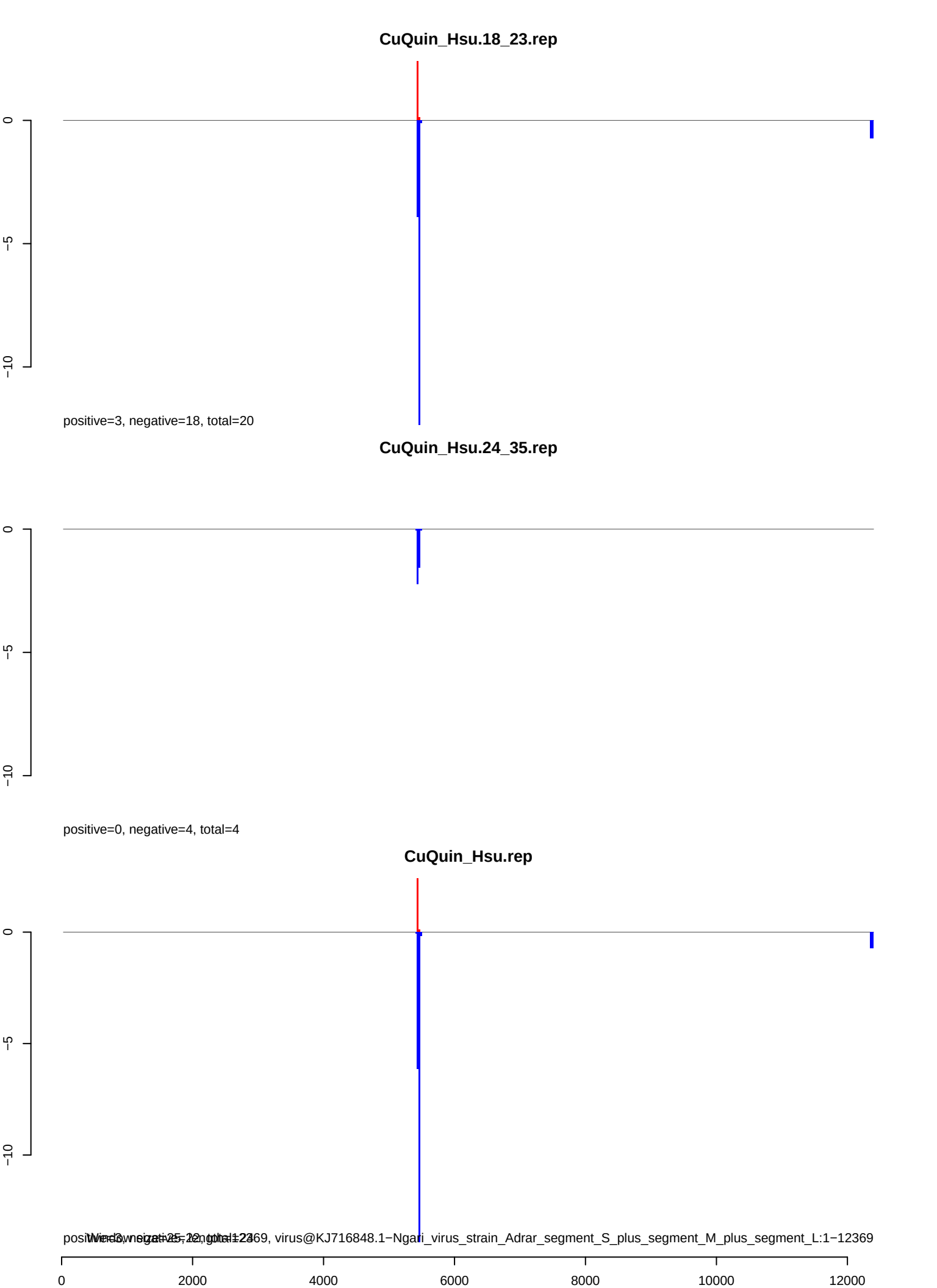

CuQuin_Hsu.18_23.rep
0.1
0.0
−0.1
−0.2
positive=1, negative=1, total=2
CuQuin_Hsu.24_35.rep
0.1
0.0
−0.1
−0.2
positive=0, negative=0, total=0
CuQuin_Hsu.rep
0.1
0.0
−0.1
−0.2
ze=25, length=4523, positive=2, negative=2, total=4 gi|9629965.1−Drosophila_melanogaster_American_nodavirus_ANV_SW−2009a_segment_RNA1_and_RNA2:1−4523
0
1000
2000
3000
4000

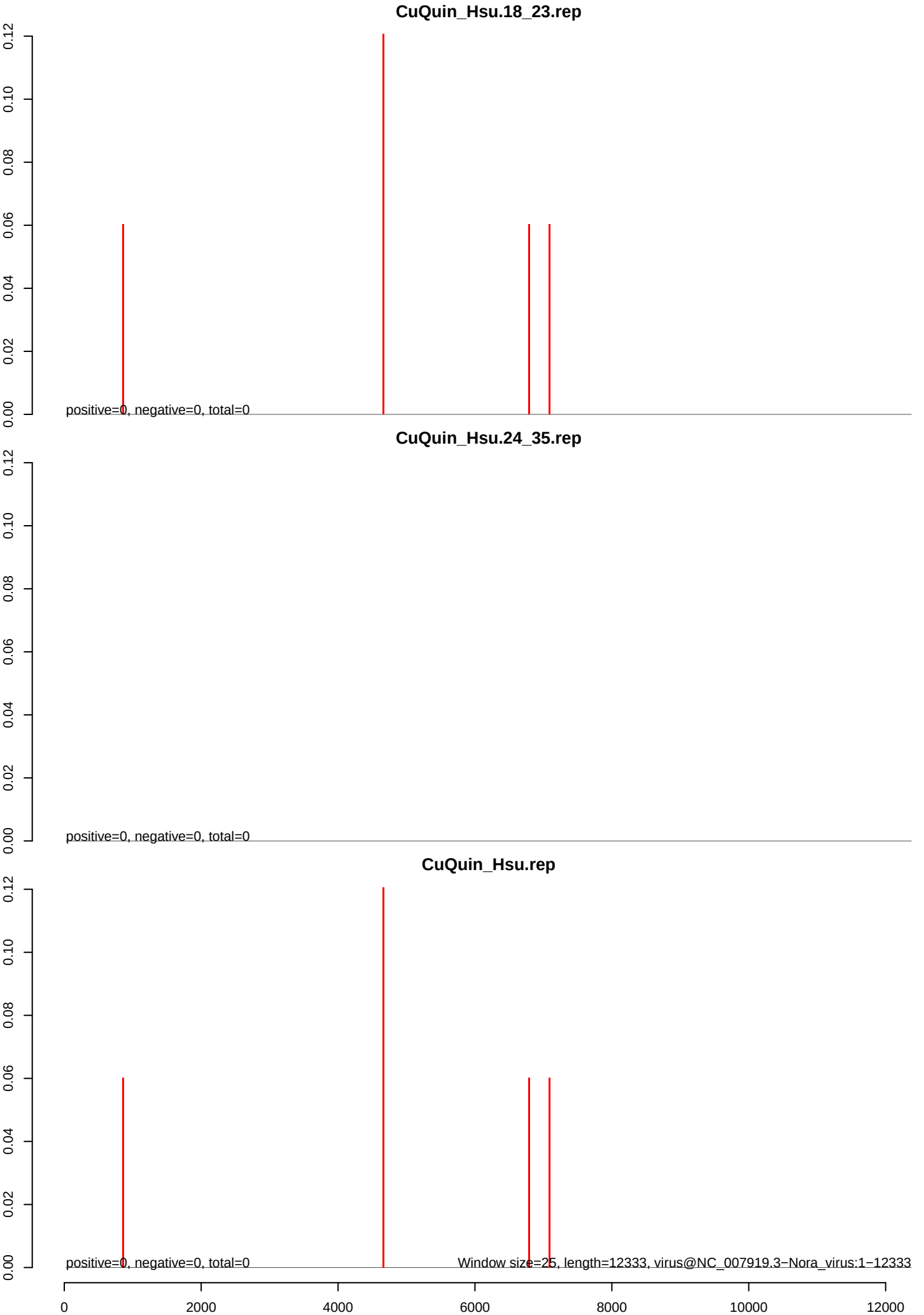

CuQuin_Hsu.18_23.rep
0.0
0.2
0.4
0.6
0.8
positive=0, negative=0, total=1
CuQuin_Hsu.24_35.rep
0.0
0.2
0.4
0.6
0.8
positive=1, negative=0, total=1
CuQuin_Hsu.rep
0.0
0.2
0.4
0.6
0.8
1.0
positive=1, negative=0, total=1
Window size=25, length=10723, virus@NC_001474.2−Dengue_virus_2:1−10723
0
2000
4000
6000
8000
10000

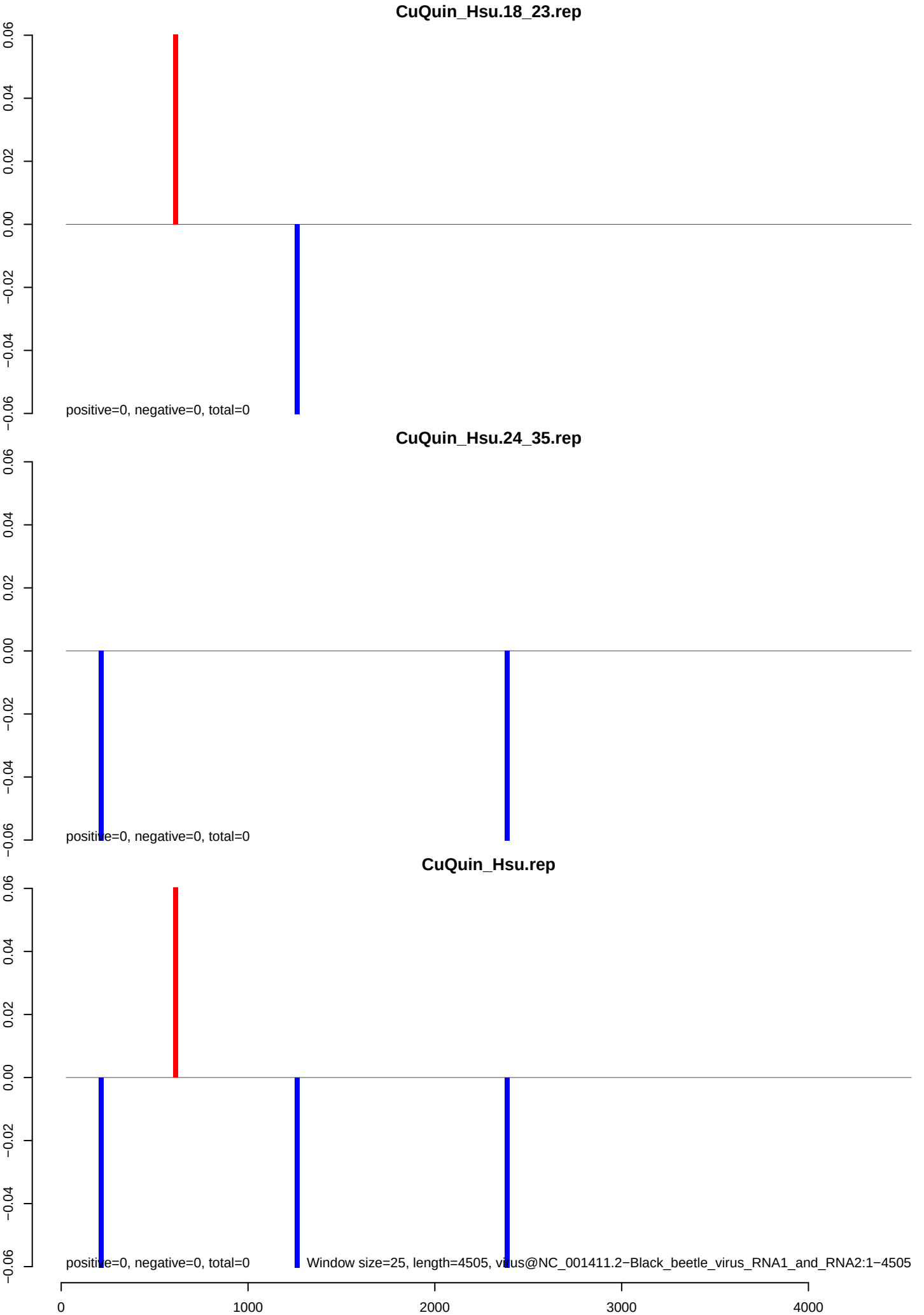

CuQuin_Hsu.18_23.rep
0.06
0.04
0.02
0.00
−0.02
−0.04
−0.06
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
0.06
0.04
0.02
0.00
−0.02
−0.04
−0.06
positive=0, negative=0, total=0
CuQuin_Hsu.rep
0.06
0.04
0.02
0.00
−0.02
−0.04
−0.06
positive=0, negative=0, total=0
Window size=25, length=4507, virus@NC_004146.1−Flock_house_virus_RNA_1_and_RNA2:1−4507
0
1000
2000
3000
4000

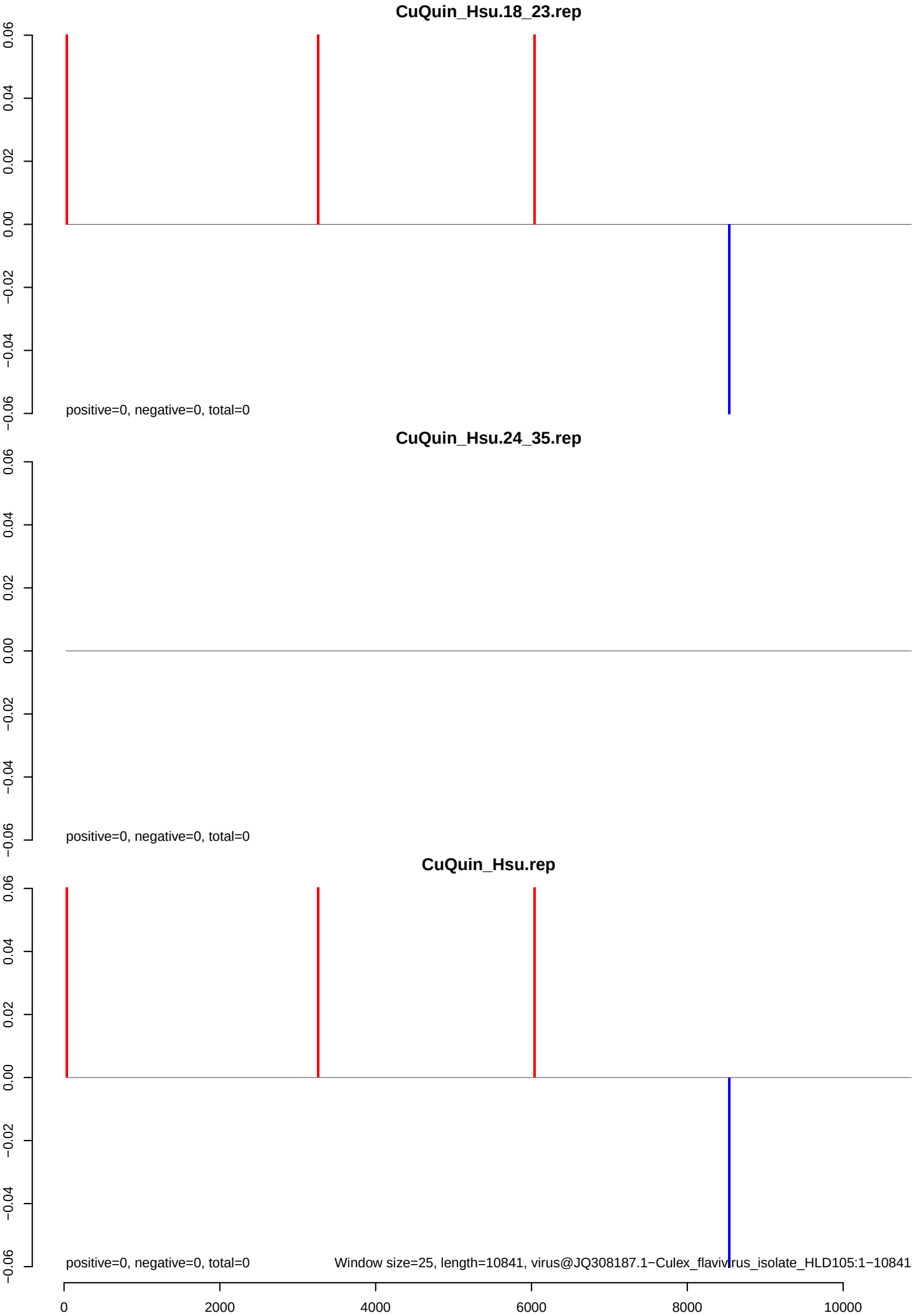

CuQuin_Hsu.18_23.rep
0.06
0.04
0.02
0.00
−0.02
−0.04
−0.06
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
0.06
0.04
0.02
0.00
−0.02
−0.04
−0.06
positive=0, negative=0, total=0
CuQuin_Hsu.rep
0.06
0.04
0.02
0.00
−0.02
−0.04
−0.06
positive=0, negative=0, total=0
Window size=25, length=9264, virus@NC_001834.1−Drosophila_C_virus_strain_EB:1−9264
0
2000
4000
6000
8000

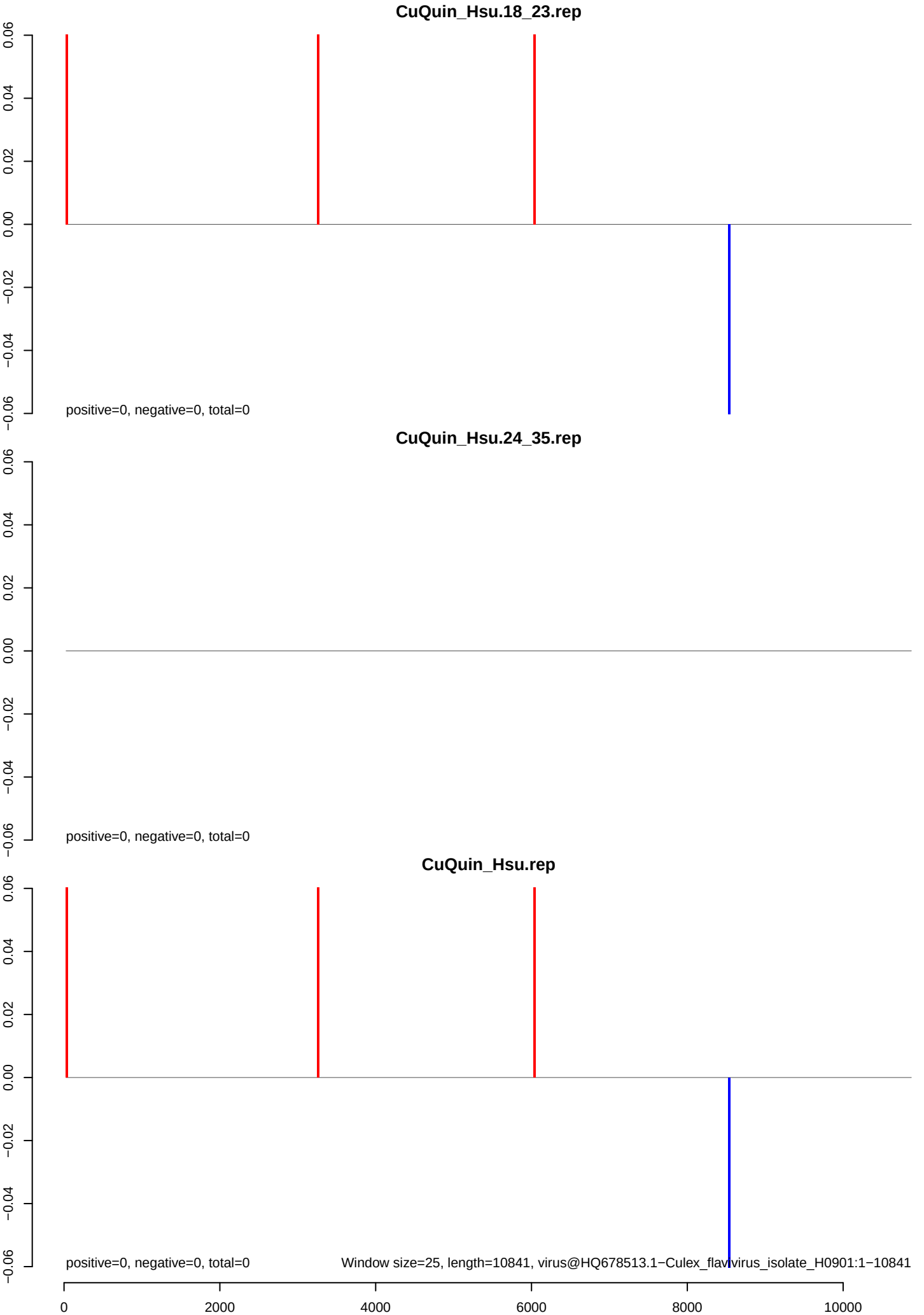

CuQuin_Hsu.18_23.rep
0.00
0.01
0.02
0.03
0.04
0.05
0.06
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
0.00
0.01
0.02
0.03
0.04
0.05
0.06
positive=0, negative=0, total=0
CuQuin_Hsu.rep
0.00
0.01
0.02
0.03
0.04
0.05
0.06
positive=0, negative=0, total=0
Window size=25, length=4806, virus@NC_012958.1−Drosophila_A_virus:1−4806
0
1000
2000
3000
4000
5000

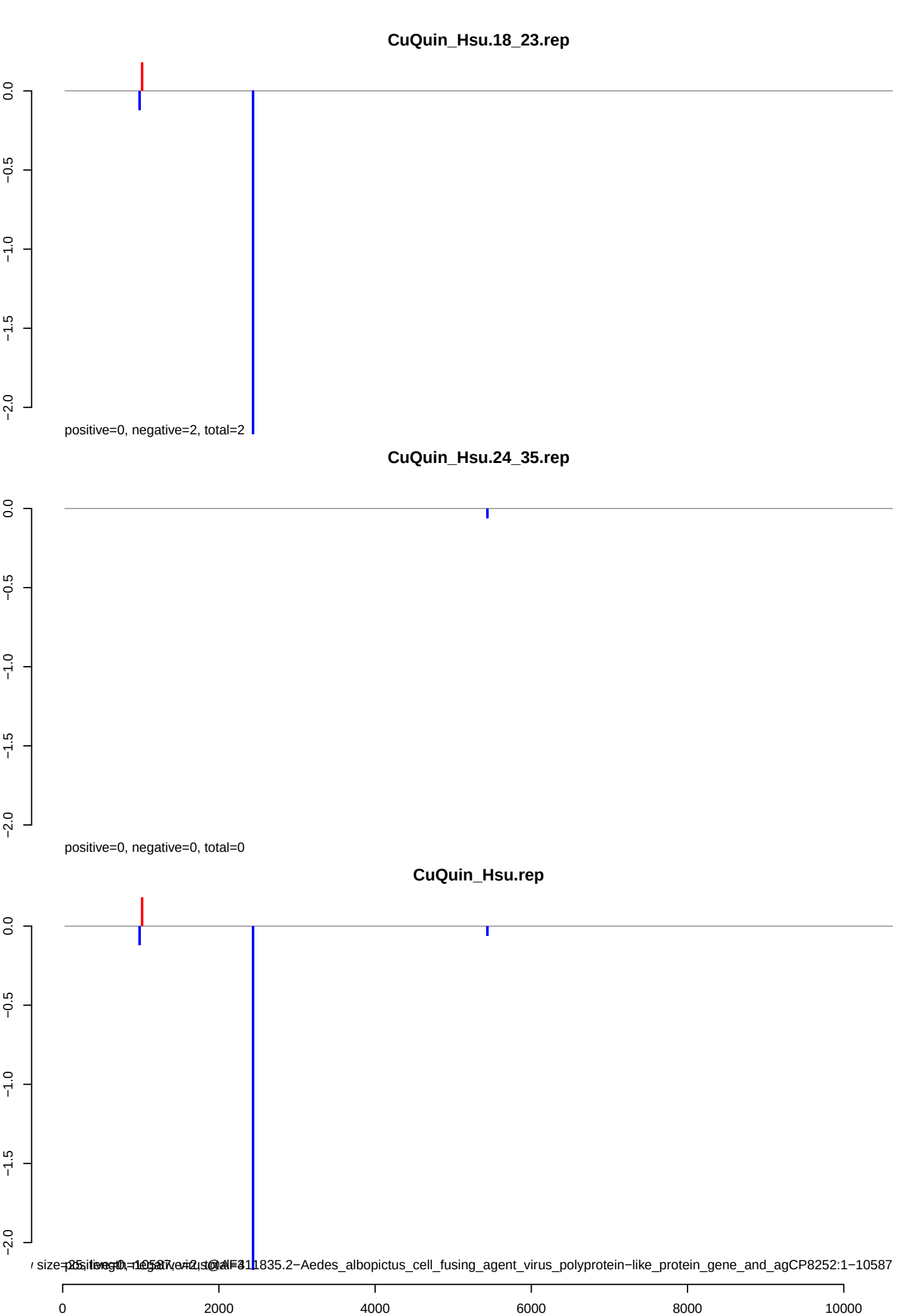

CuQuin_Hsu.18_23.rep
0
−5
−10
positive=3, negative=18, total=20
CuQuin_Hsu.24_35.rep
0
−5
−10
positive=0, negative=4, total=4
CuQuin_Hsu.rep
0
−5
−10
positive=3, negative=15, total=18
Wuhan_virus_strain_Adrar_segment_S_plus_segment_M_plus_segment_L:1−12469, virus@KJ716848.1−Ngaoui_virus_strain_Adrar_segment_S_plus_segment_M_plus_segment_L:1−12369
0
2000
4000
6000
8000
10000
12000

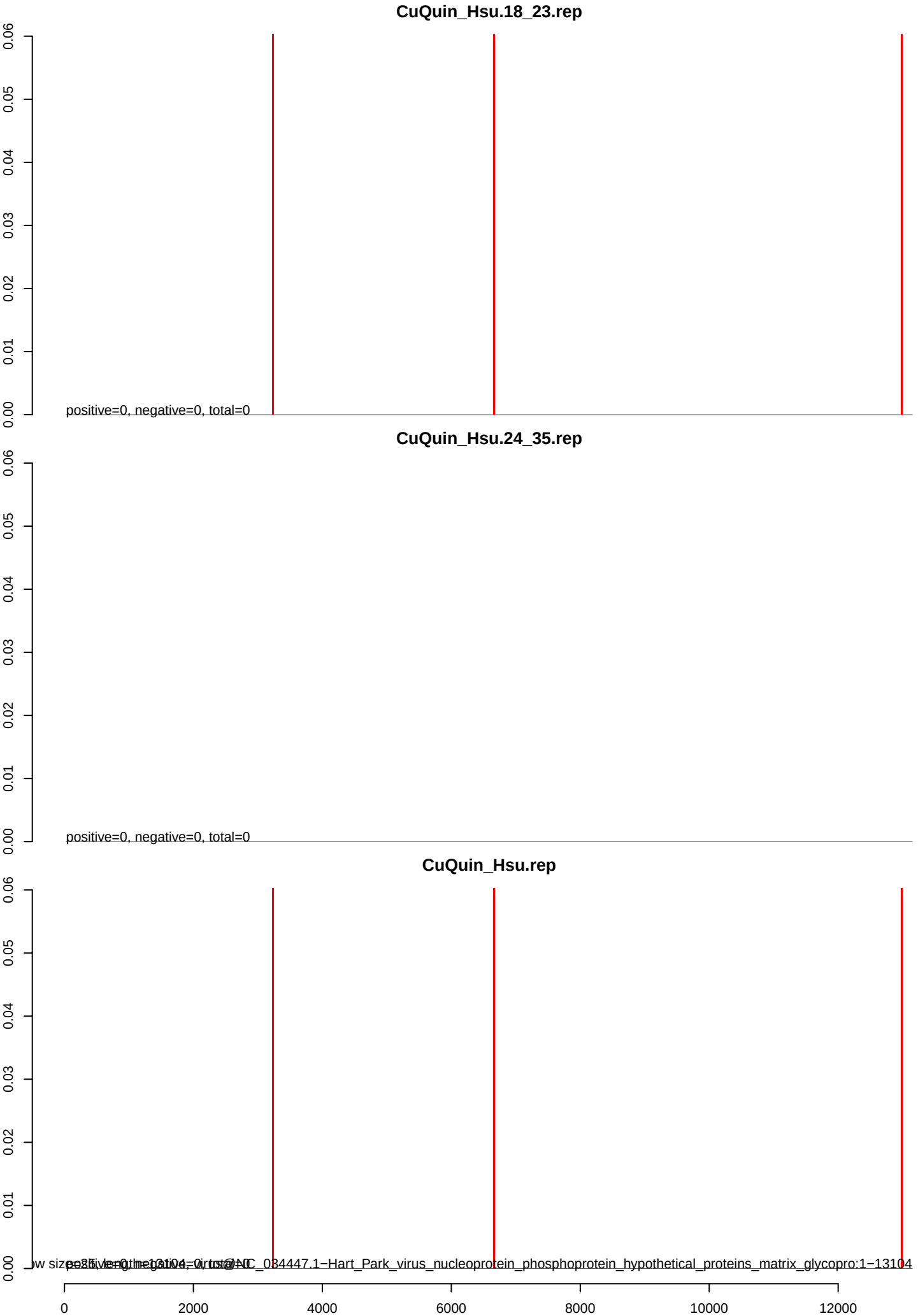

CuQuin_Hsu.18_23.rep
0.00
0.02
0.04
0.06
0.08
0.10
0.12
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
0.00
0.02
0.04
0.06
0.08
0.10
0.12
positive=0, negative=0, total=0
CuQuin_Hsu.rep
0.00
0.02
0.04
0.06
0.08
0.10
0.12
positive=0, negative=0, total=0
Window size=25, length=12333, virus@NC_007919.3−Nora_virus:1−12333
0
2000
4000
6000
8000
10000
12000

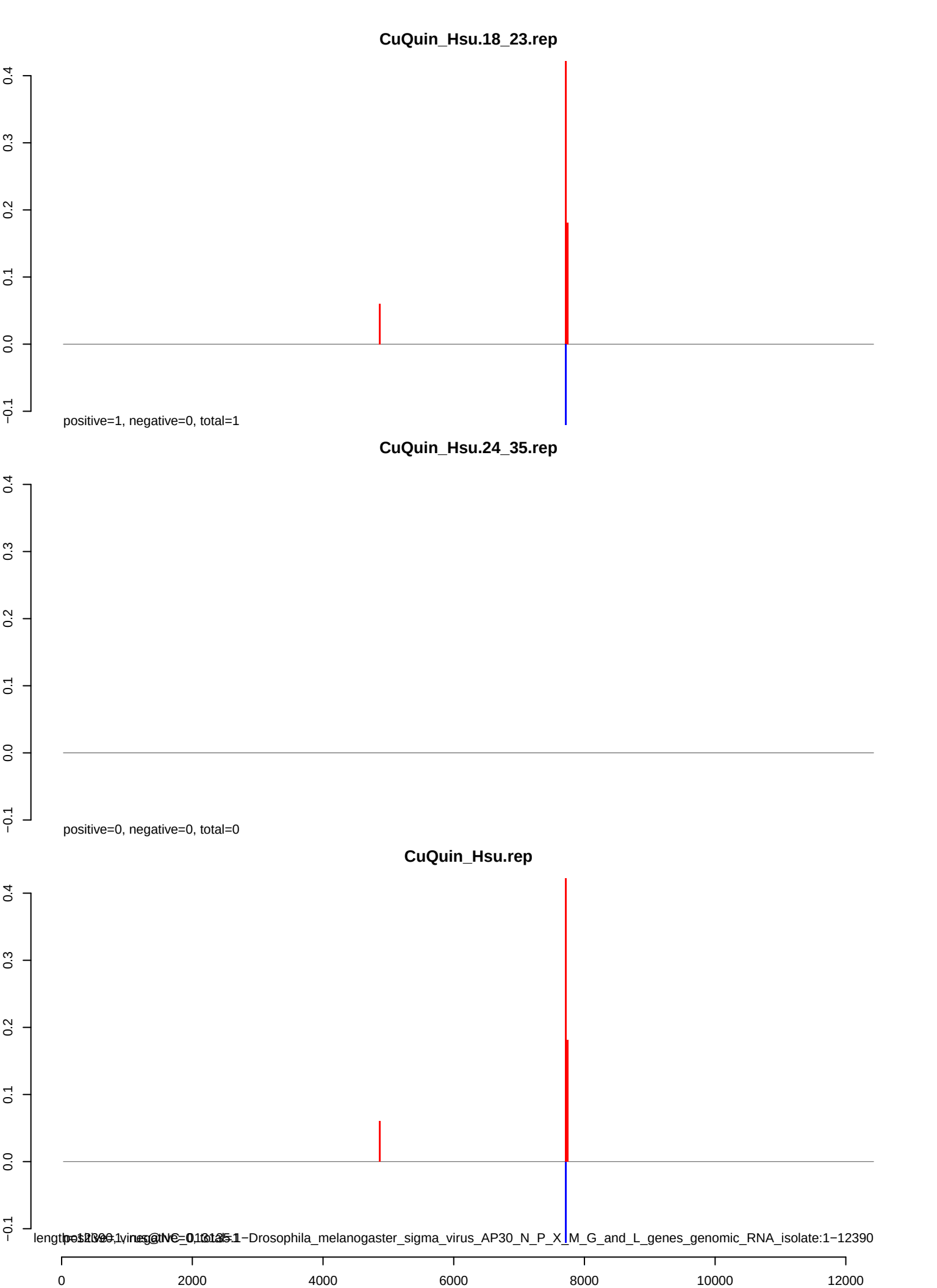

CuQuin_Hsu.18_23.rep
0.06
0.04
0.02
0.00
−0.02
−0.04
−0.06
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
0.06
0.04
0.02
0.00
−0.02
−0.04
−0.06
positive=0, negative=0, total=0
CuQuin_Hsu.rep
0.06
0.04
0.02
0.00
−0.02
−0.04
−0.06
positive=0, negative=0, total=0
Window size=25, length=4505, virus@NC_001411.2−Black_beetle_virus_RNA1_and_RNA2:1−4505
0
1000
2000
3000
4000

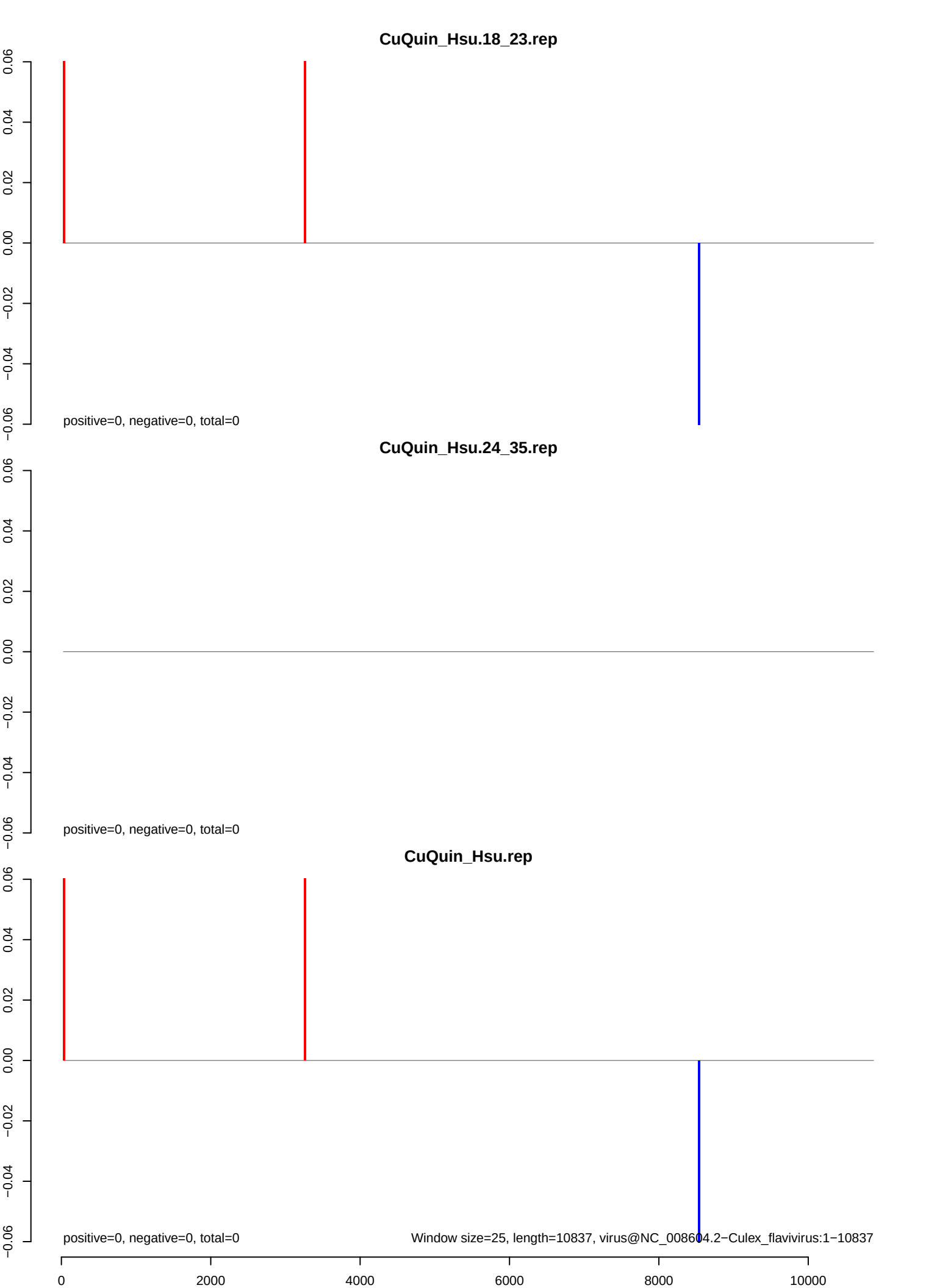

CuQuin_Hsu.18_23.rep
0.06
0.04
0.02
0.00
−0.02
−0.04
−0.06
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
0.06
0.04
0.02
0.00
−0.02
−0.04
−0.06
positive=0, negative=0, total=0
CuQuin_Hsu.rep
0.06
0.04
0.02
0.00
−0.02
−0.04
−0.06
positive=0, negative=0, total=0
Window size=25, length=10841, virus@JQ308187.1−Culex_flavivirus_isolate_HLD105:1−10841
0
2000
4000
6000
8000
10000

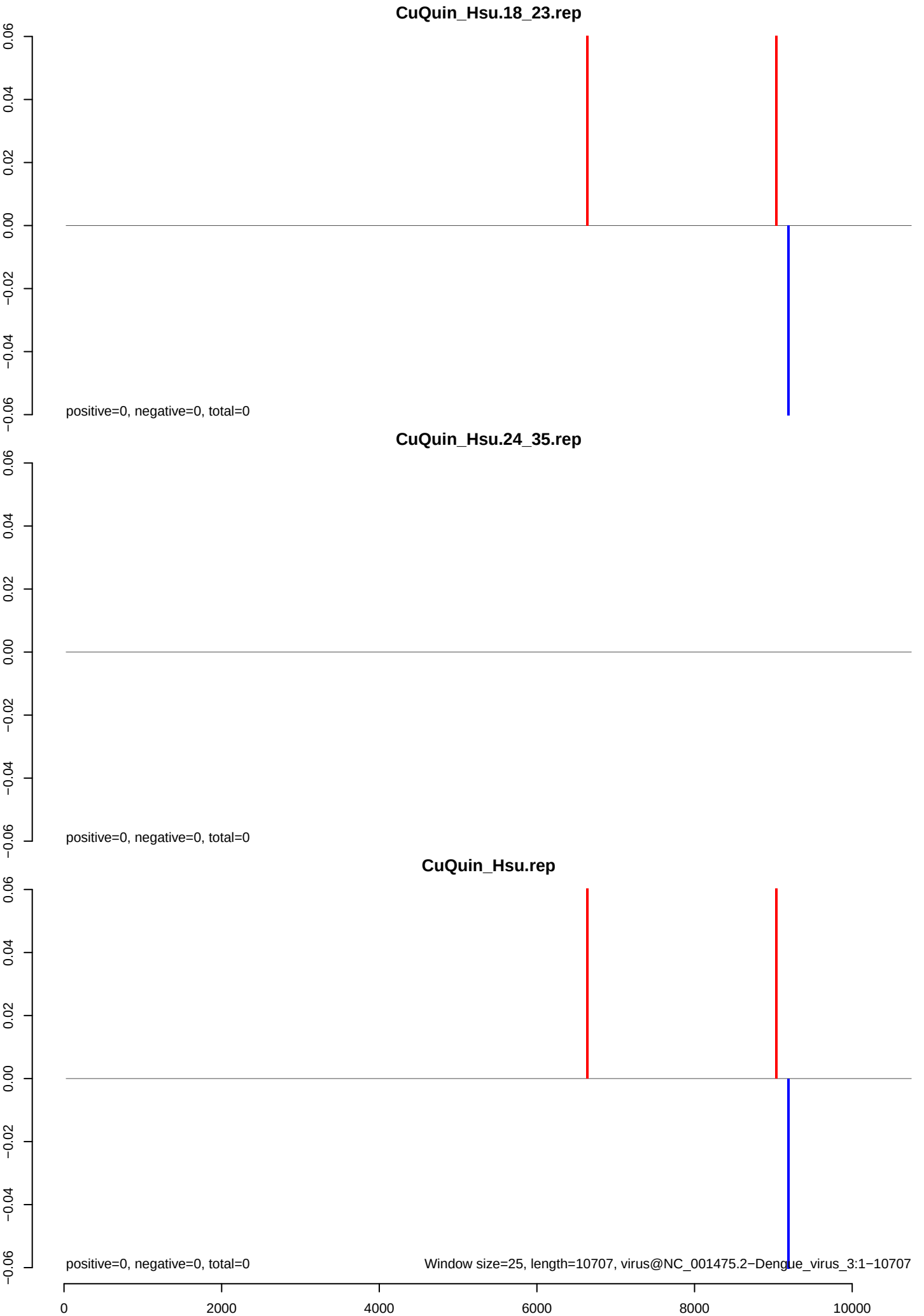

CuQuin_Hsu.18_23.rep
0.06
0.04
0.02
0.00
−0.02
−0.04
−0.06
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
0.06
0.04
0.02
0.00
−0.02
−0.04
−0.06
positive=0, negative=0, total=0
CuQuin_Hsu.rep
0.06
0.04
0.02
0.00
−0.02
−0.04
−0.06
positive=0, negative=0, total=0
Window size=25, length=10841, virus@HQ678513.1−Culex_flavivirus_isolate_H0901:1−10841
0
2000
4000
6000
8000
10000

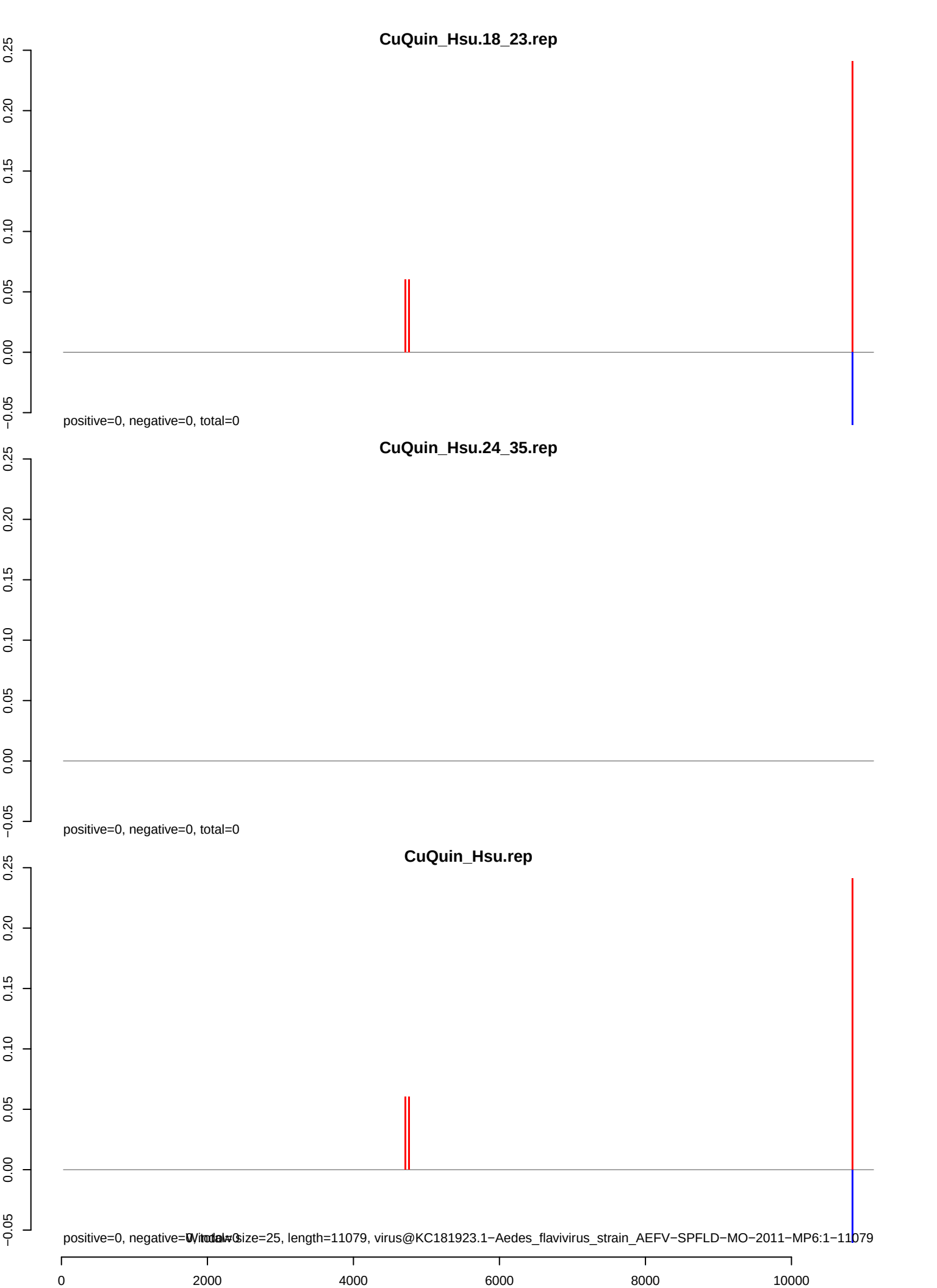

CuQuin_Hsu.18_23.rep
0.0
−0.5
−1.0
−1.5
−2.0
positive=0, negative=2, total=2
CuQuin_Hsu.24_35.rep
0.0
−0.5
−1.0
−1.5
−2.0
positive=0, negative=0, total=0
CuQuin_Hsu.rep
0.0
−0.5
−1.0
−1.5
−2.0
size=25,length=10587
positive=0, negative=2, total=311835.2−Aedes_albopictus_cell_fusing_agent_virus_polyprotein−like_protein_gene_and_agCP8252:1−10587
0
2000
4000
6000
8000
10000

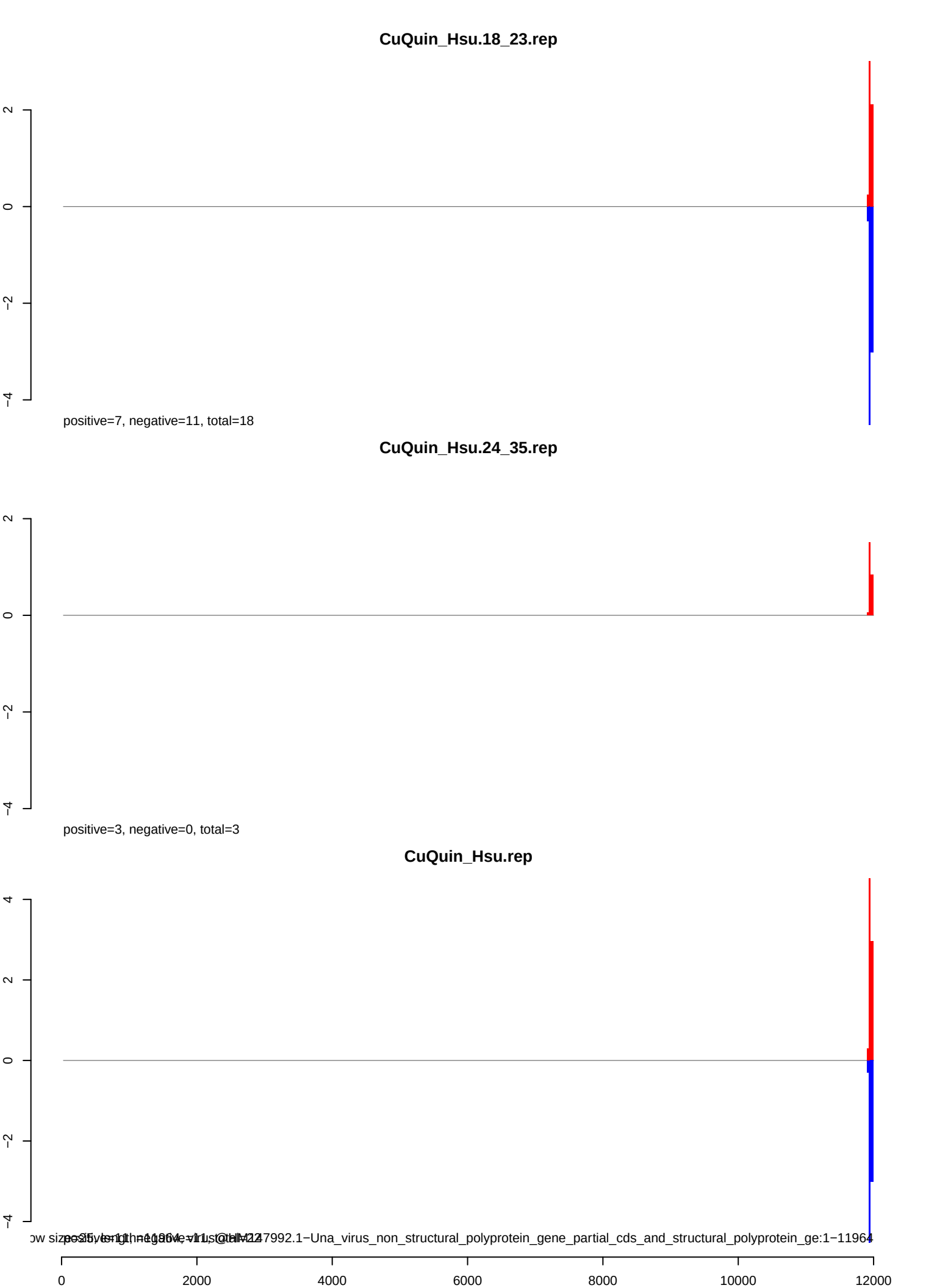

CuQuin_Hsu.18_23.rep
0.06
0.05
0.04
0.03
0.02
0.01
0.00
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
0.06
0.05
0.04
0.03
0.02
0.01
0.00
positive=0, negative=0, total=0
CuQuin_Hsu.rep
0.06
0.05
0.04
0.03
0.02
0.01
0.00
ow size=25 iv=0 he=13104 0 rna@NC_034447.1−Hart_Park_virus_nucleoprotein_phosphoprotein_hypothetical_proteins_matrix_glycopro:1−13104
0
2000
4000
6000
8000
10000
12000

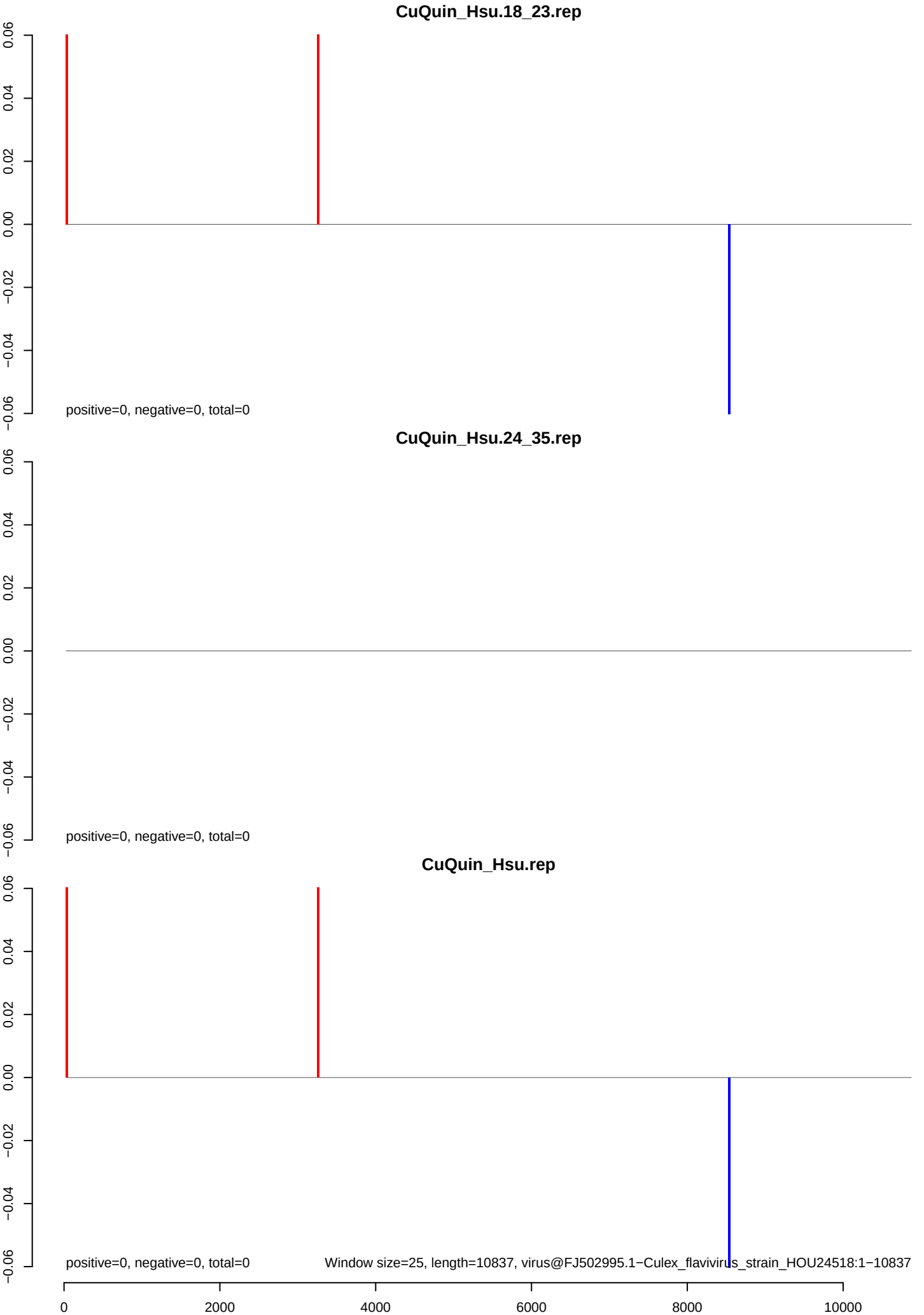

CuQuin_Hsu.18_23.rep
0.4
0.3
0.2
0.1
0.0
−0.1
positive=1, negative=0, total=1
CuQuin_Hsu.24_35.rep
0.4
0.3
0.2
0.1
0.0
−0.1
positive=0, negative=0, total=0
CuQuin_Hsu.rep
0.4
0.3
0.2
0.1
0.0
−0.1
length=12390 | positive=1, negative=0, total=1
NC_001345.1−Drosophila_melanogaster_sigma_virus_AP30_N_P_X_M_G_and_L_genes_genomic_RNA_isolate:1−12390
0
2000
4000
6000
8000
10000
12000

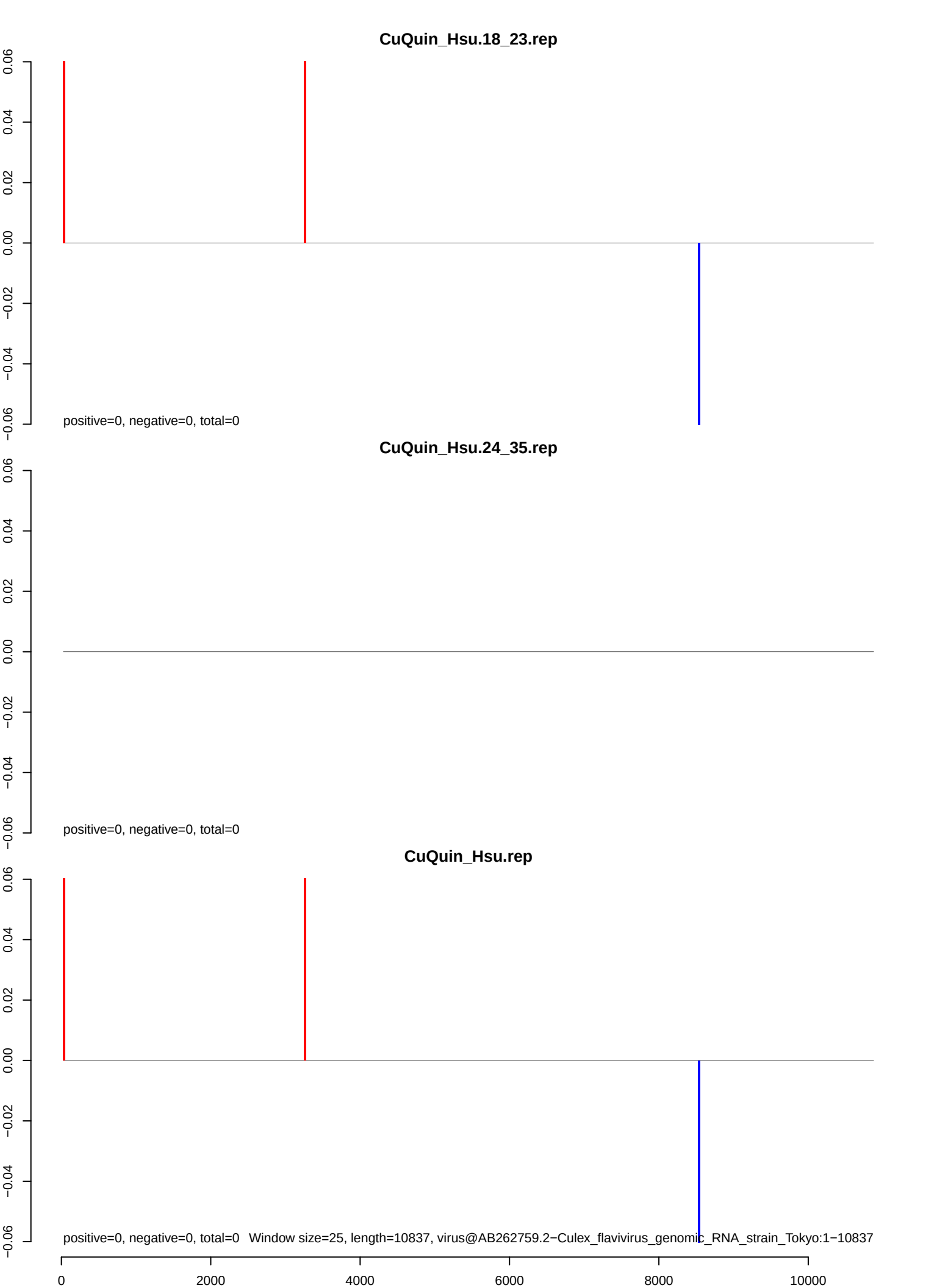

CuQuin_Hsu.18_23.rep
0.06
0.04
0.02
0.00
−0.02
−0.04
−0.06
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
0.06
0.04
0.02
0.00
−0.02
−0.04
−0.06
positive=0, negative=0, total=0
CuQuin_Hsu.rep
0.06
0.04
0.02
0.00
−0.02
−0.04
−0.06
positive=0, negative=0, total=0
Window size=25, length=10837, virus@NC_008604.2−Culex_flavivirus:1−10837
0
2000
4000
6000
8000
10000

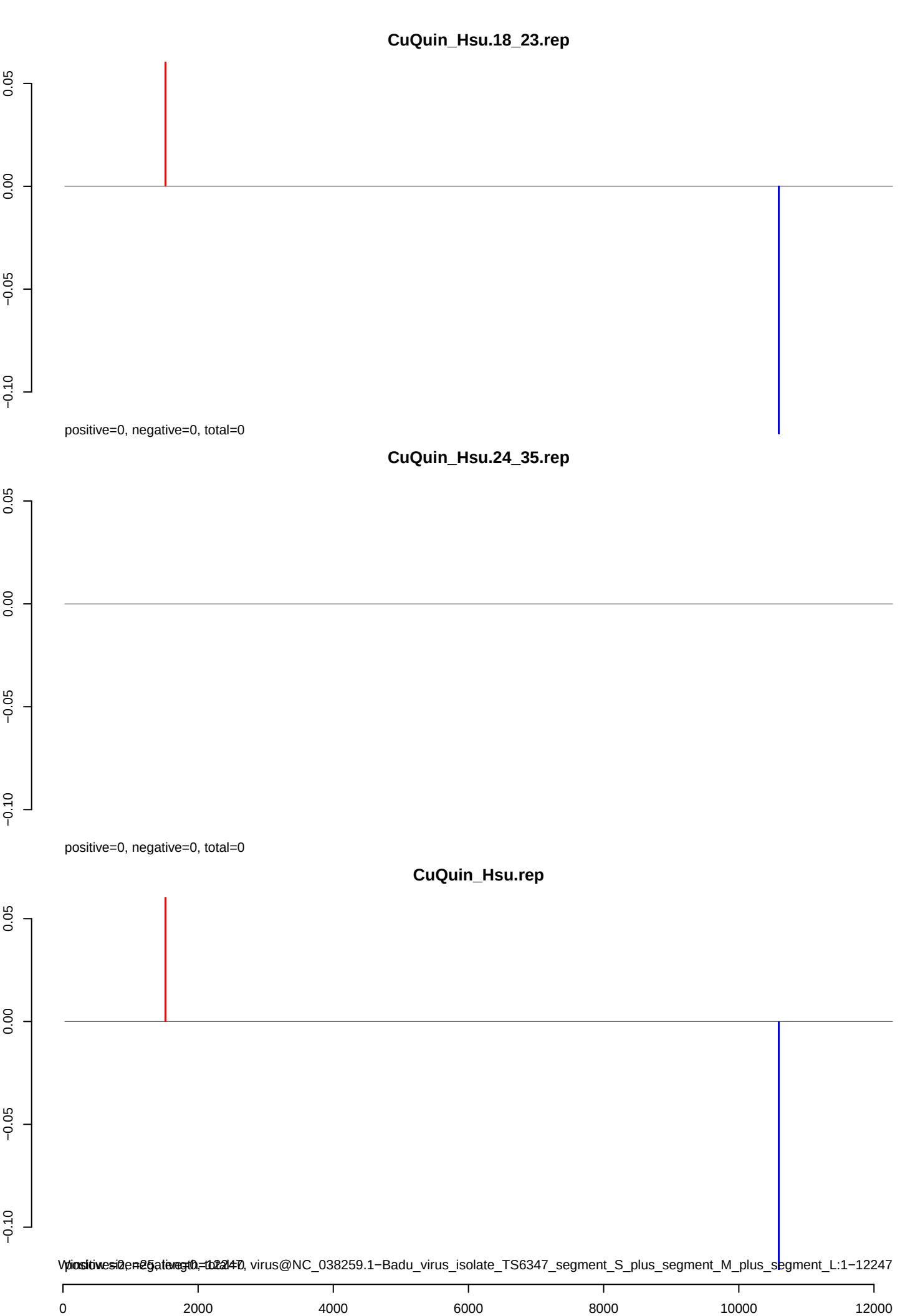

CuQuin_Hsu.18_23.rep
0.06
0.04
0.02
0.00
−0.02
−0.04
−0.06
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
0.06
0.04
0.02
0.00
−0.02
−0.04
−0.06
positive=0, negative=0, total=0
CuQuin_Hsu.rep
0.06
0.04
0.02
0.00
−0.02
−0.04
−0.06
positive=0, negative=0, total=0
Window size=25, length=10707, virus@NC_001475.2−Dengue_virus_3:1−10707
0
2000
4000
6000
8000
10000

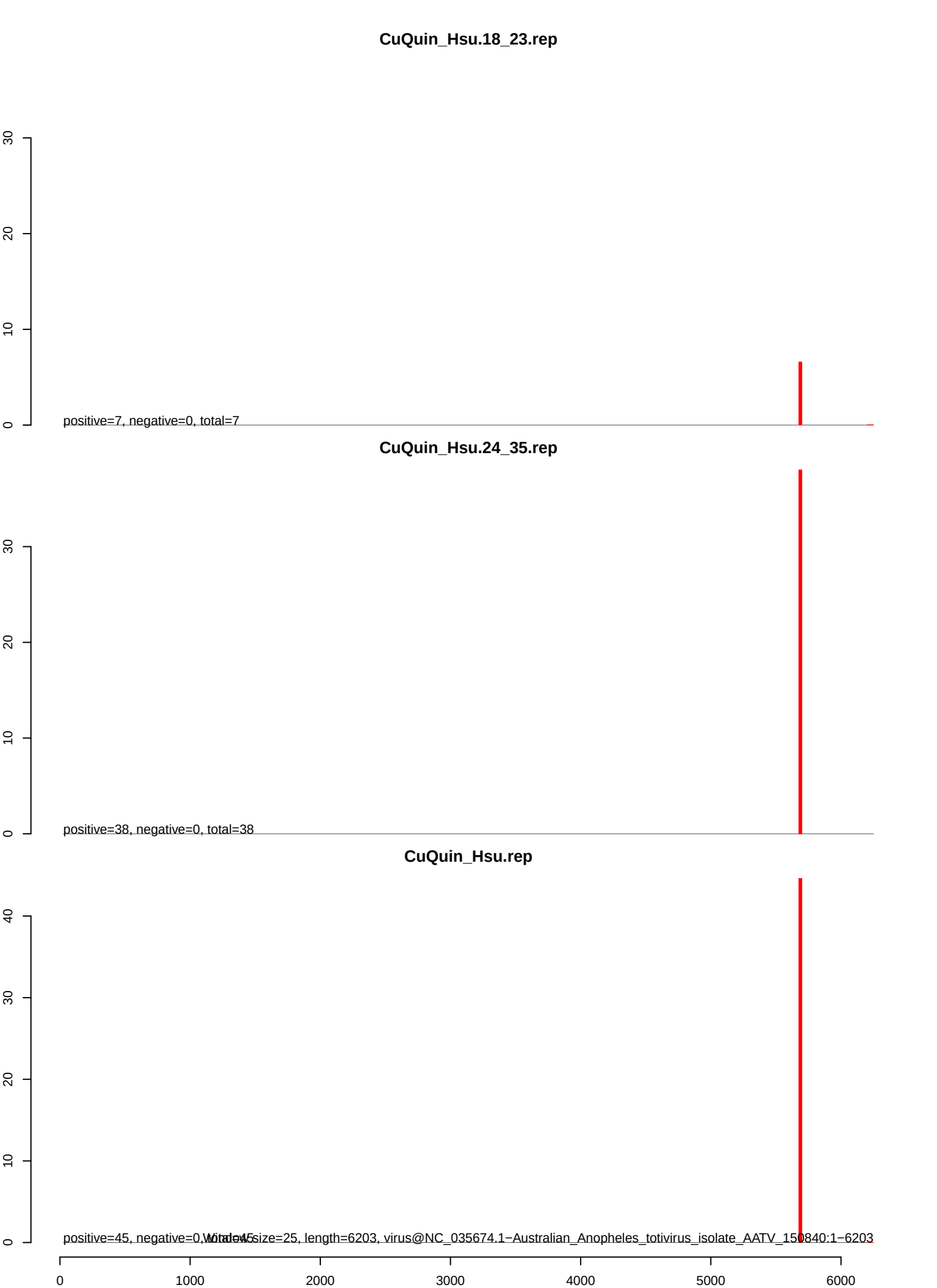

CuQuin_Hsu.18_23.rep
0.25
0.20
0.15
0.10
0.05
0.00
−0.05
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
0.25
0.20
0.15
0.10
0.05
0.00
−0.05
positive=0, negative=0, total=0
CuQuin_Hsu.rep
0.25
0.20
0.15
0.10
0.05
0.00
−0.05
positive=0, negative=0, total=0
Virtual size=25, length=11079, virus@KC181923.1−Aedes_flavivirus_strain_AEFV−SPFLD−MO−2011−MP6:1−11079
0
2000
4000
6000
8000
10000

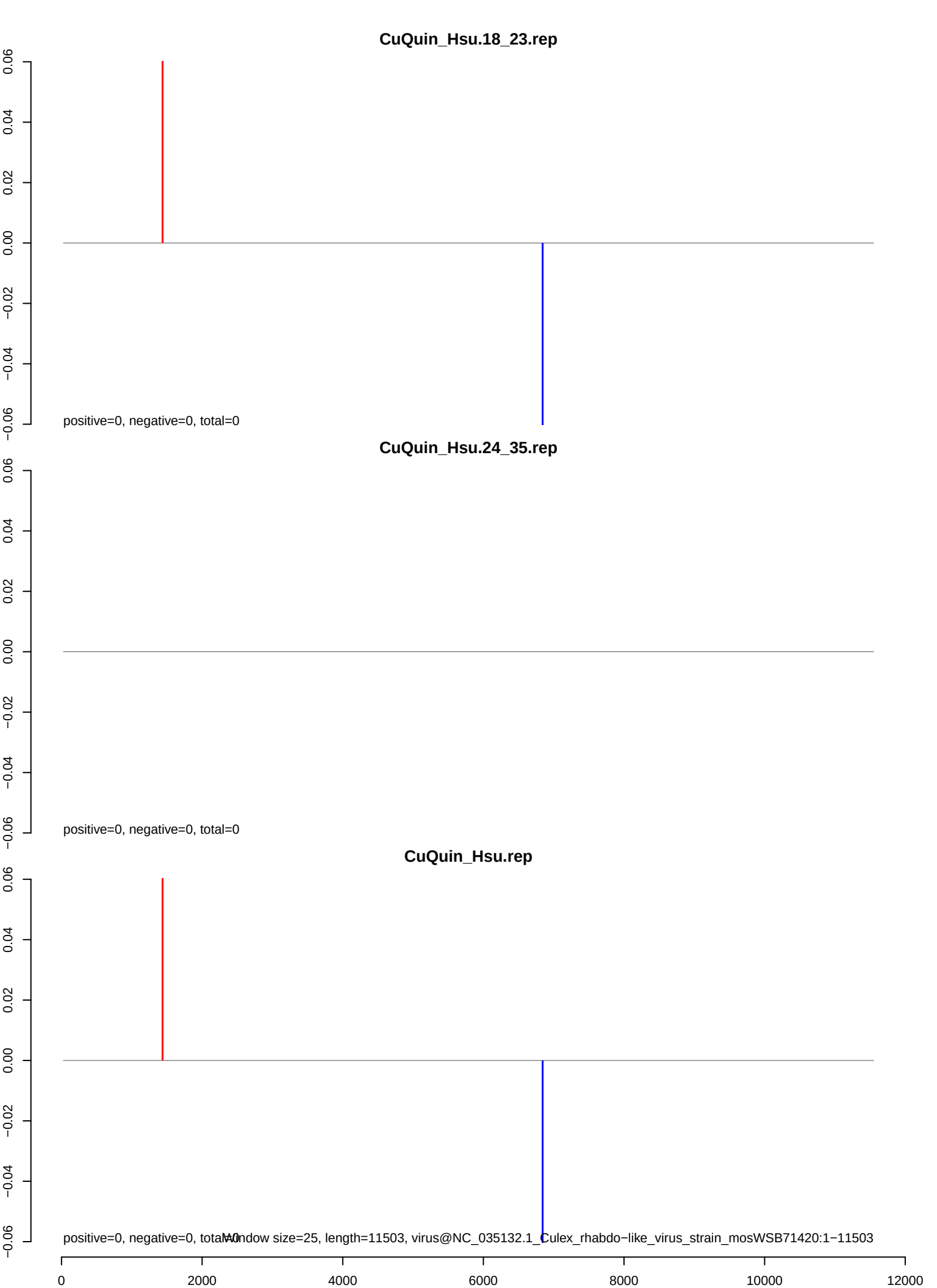

CuQuin_Hsu.18_23.rep
positive=7, negative=11, total=18
CuQuin_Hsu.24_35.rep
positive=3, negative=0, total=3
CuQuin_Hsu.rep
0
2000
4000
6000
8000
10000
12000

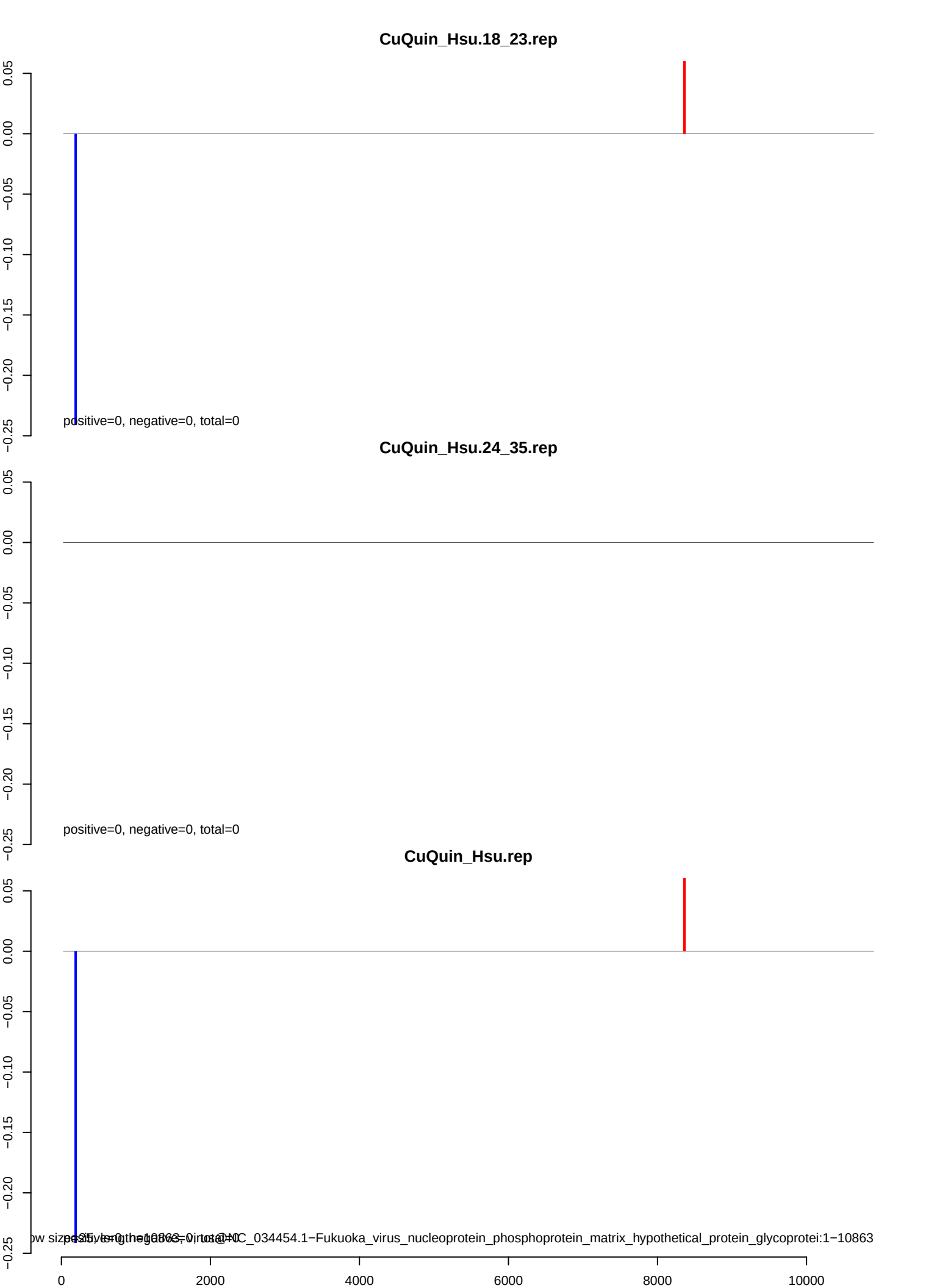

CuQuin_Hsu.18_23.rep
0.06
0.04
0.02
0.00
−0.02
−0.04
−0.06
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
0.06
0.04
0.02
0.00
−0.02
−0.04
−0.06
positive=0, negative=0, total=0
CuQuin_Hsu.rep
0.06
0.04
0.02
0.00
−0.02
−0.04
−0.06
positive=0, negative=0, total=0
Window size=25, length=10837, virus@FJ502995.1−Culex_flavivirus_strain_HOU24518:1−10837
0
2000
4000
6000
8000
10000

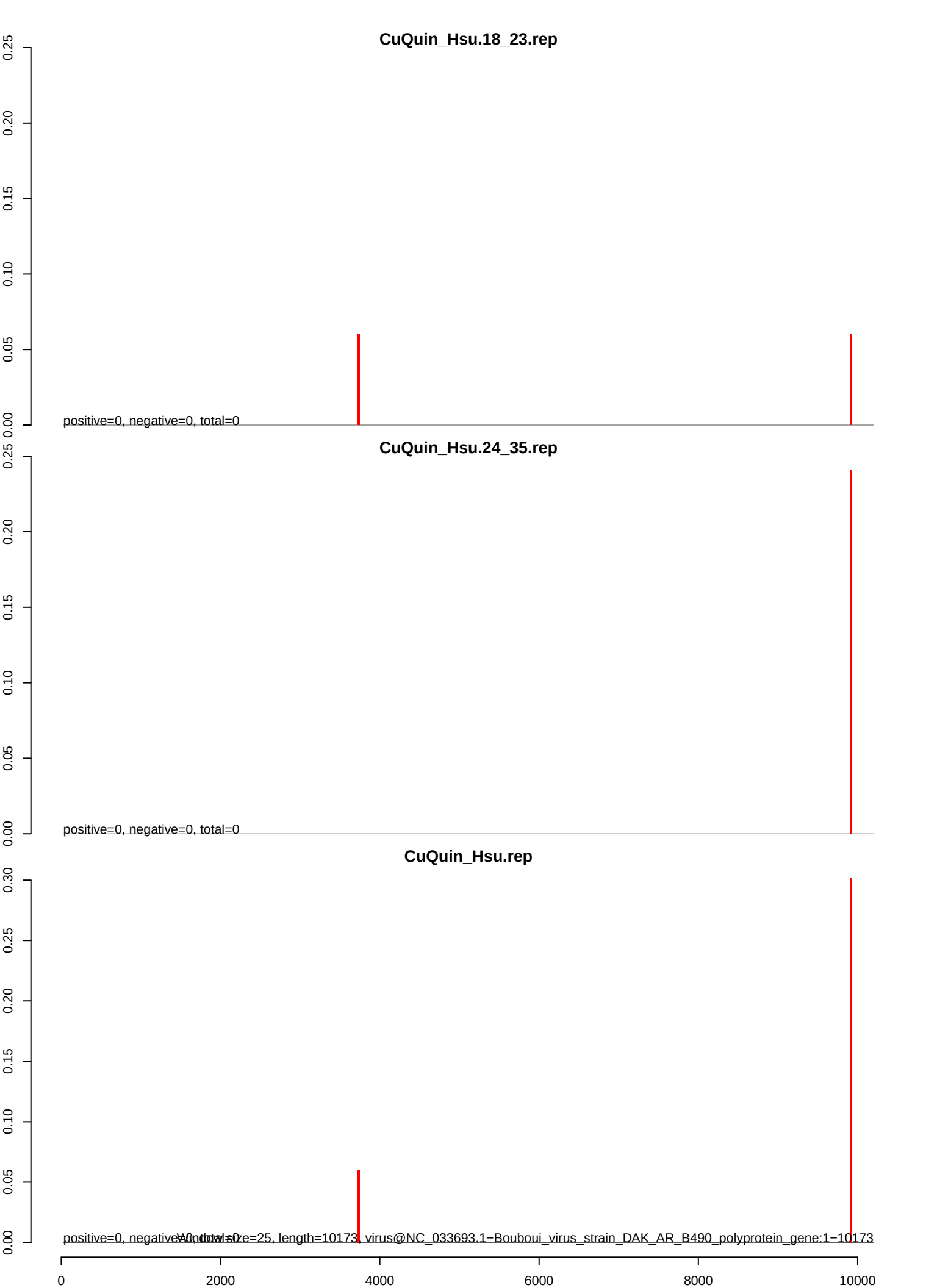

CuQuin_Hsu.18_23.rep
0.06
0.04
0.02
0.00
−0.02
−0.04
−0.06
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
0.06
0.04
0.02
0.00
−0.02
−0.04
−0.06
positive=0, negative=0, total=0
CuQuin_Hsu.rep
0.06
0.04
0.02
0.00
−0.02
−0.04
−0.06
positive=0, negative=0, total=0 Window size=25, length=10837, virus@AB262759.2−Culex_flavivirus_genomic_RNA_strain_Tokyo:1−10837
0
2000
4000
6000
8000
10000

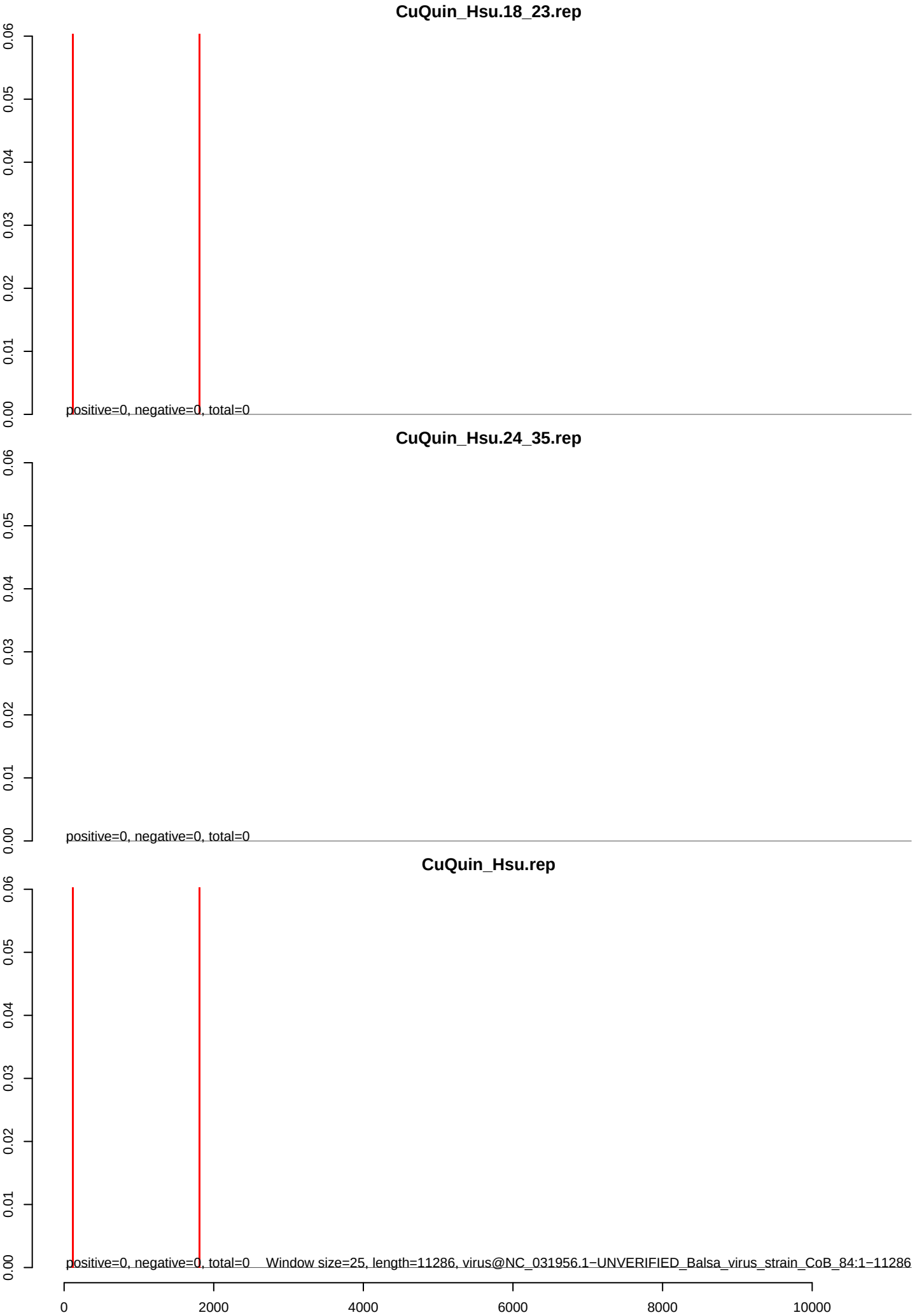

CuQuin_Hsu.18_23.rep
0.05
0.00
−0.05
−0.10
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
0.05
0.00
−0.05
−0.10
positive=0, negative=0, total=0
CuQuin_Hsu.rep
0.05
0.00
−0.05
−0.10
virus@NC_038259.1−Badu_virus_isolate_TS6347_segment_S_plus_segment_M_plus_segment_L:1−12247
0
2000
4000
6000
8000
10000
12000

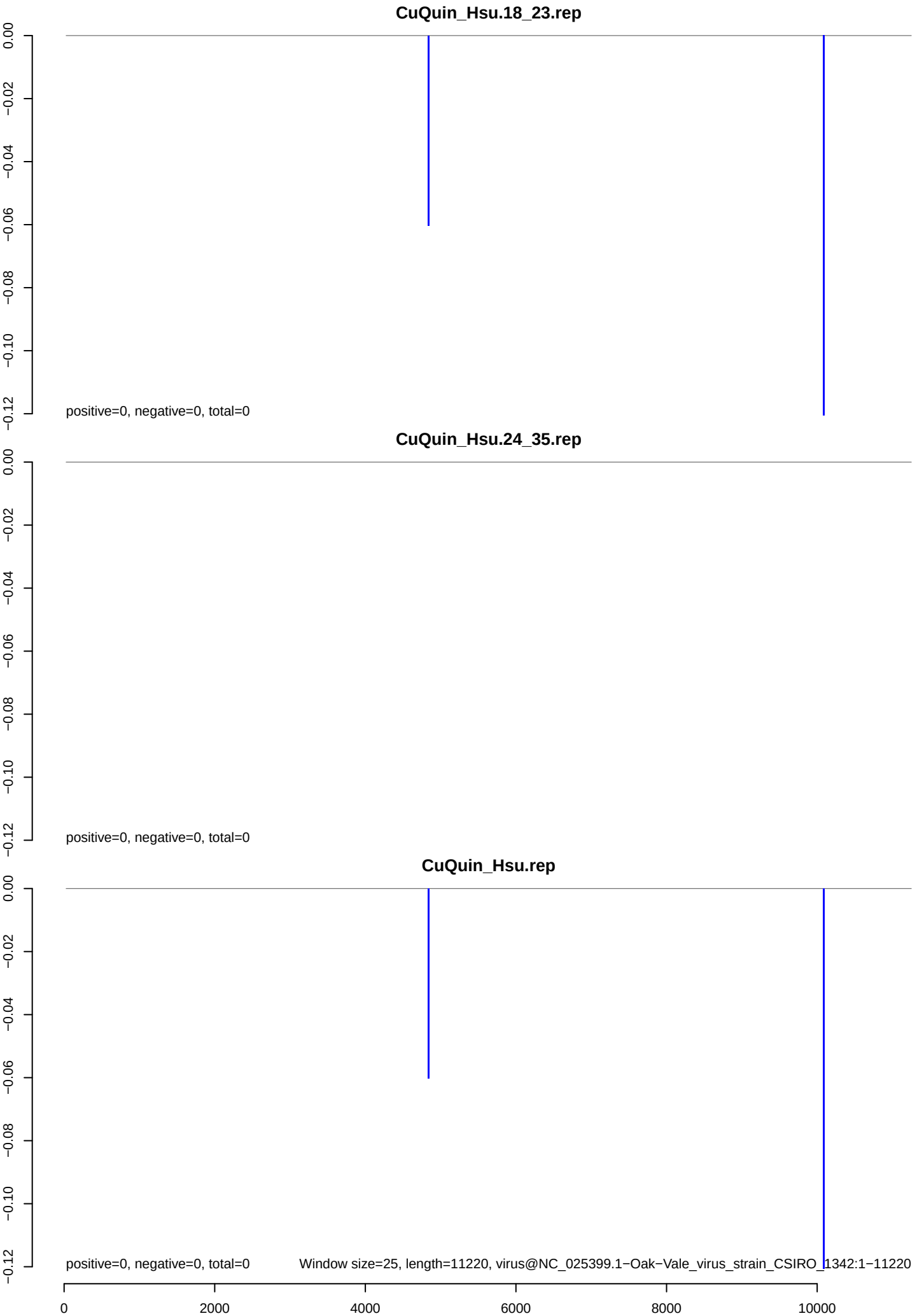

CuQuin_Hsu.18_23.rep
0
10
20
30
positive=7, negative=0, total=7
CuQuin_Hsu.24_35.rep
0
10
20
30
positive=38, negative=0, total=38
CuQuin_Hsu.rep
0
10
20
30
40
positive=45, negative=0, total=45
Window size=25, length=6203, virus@NC_035674.1−Australian_Anopheles_totivirus_isolate_AATV_150840:1−6203
0
1000
2000
3000
4000
5000
6000

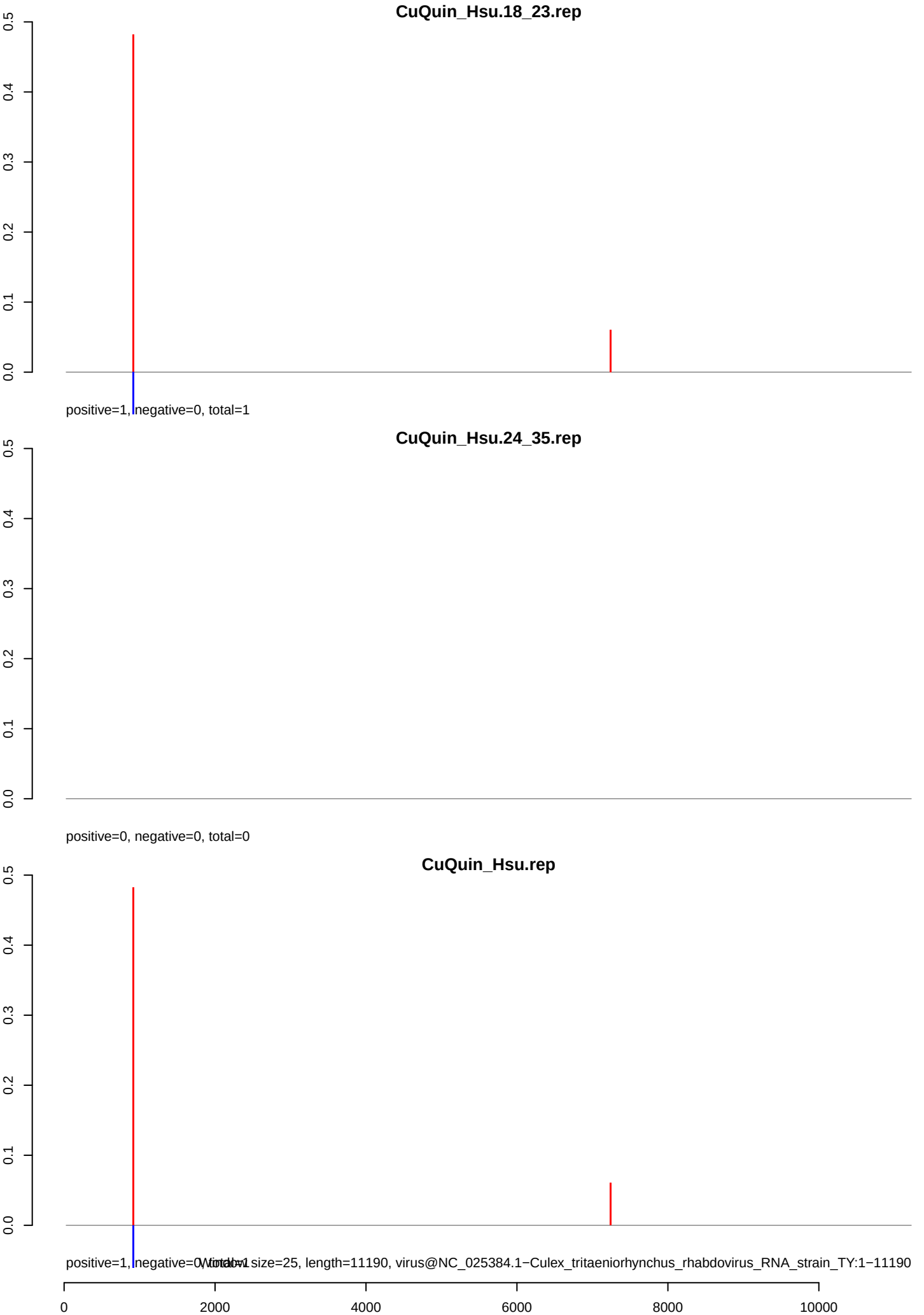

CuQuin_Hsu.18_23.rep
0.06
0.04
0.02
0.00
−0.02
−0.04
−0.06
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
0.06
0.04
0.02
0.00
−0.02
−0.04
−0.06
positive=0, negative=0, total=0
CuQuin_Hsu.rep
0.06
0.04
0.02
0.00
−0.02
−0.04
−0.06
positive=0, negative=0, total=0
Window size=25, length=11503, virus@NC_035132.1_Culex_rhabdo−like_virus_strain_mosWSB71420:1−1150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

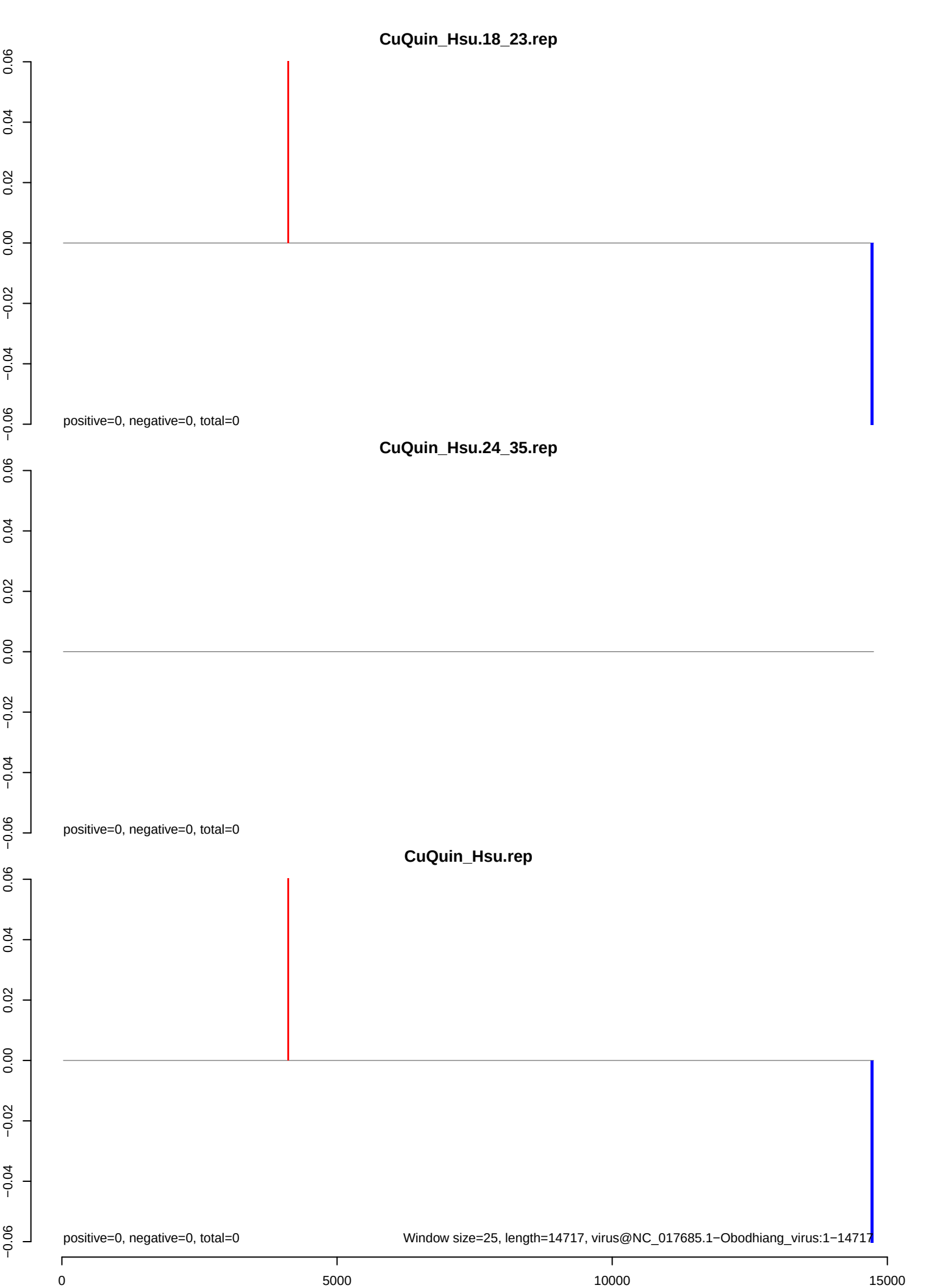

CuQuin_Hsu.18_23.rep
0.05
0.00
−0.05
−0.10
−0.15
−0.20
−0.25
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
0.05
0.00
−0.05
−0.10
−0.15
−0.20
−0.25
positive=0, negative=0, total=0
CuQuin_Hsu.rep
0.05
0.00
−0.05
−0.10
−0.15
−0.20
−0.25
0
2000
4000
6000
8000
10000

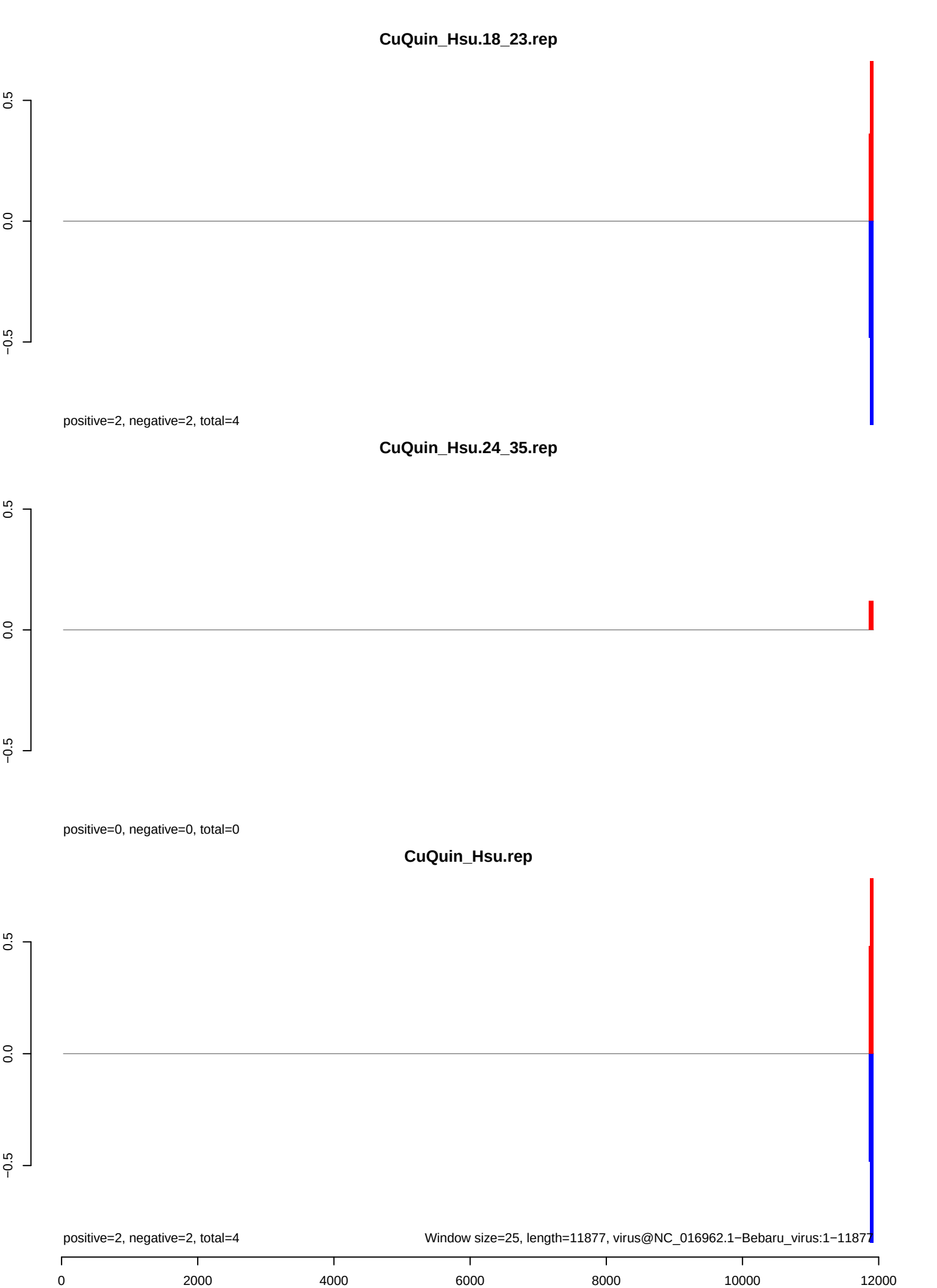

CuQuin_Hsu.18_23.rep
0.25
0.20
0.15
0.10
0.05
0.00
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
0.25
0.20
0.15
0.10
0.05
0.00
positive=0, negative=0, total=0
CuQuin_Hsu.rep
0.30
0.25
0.20
0.15
0.10
0.05
0.00
positive=0, negative=0, total=0
Window size=25, length=10173, virus@NC_033693.1−Bouboui_virus_strain_DAK_AR_B490_polyprotein_gene:1−10173
0
2000
4000
6000
8000
10000

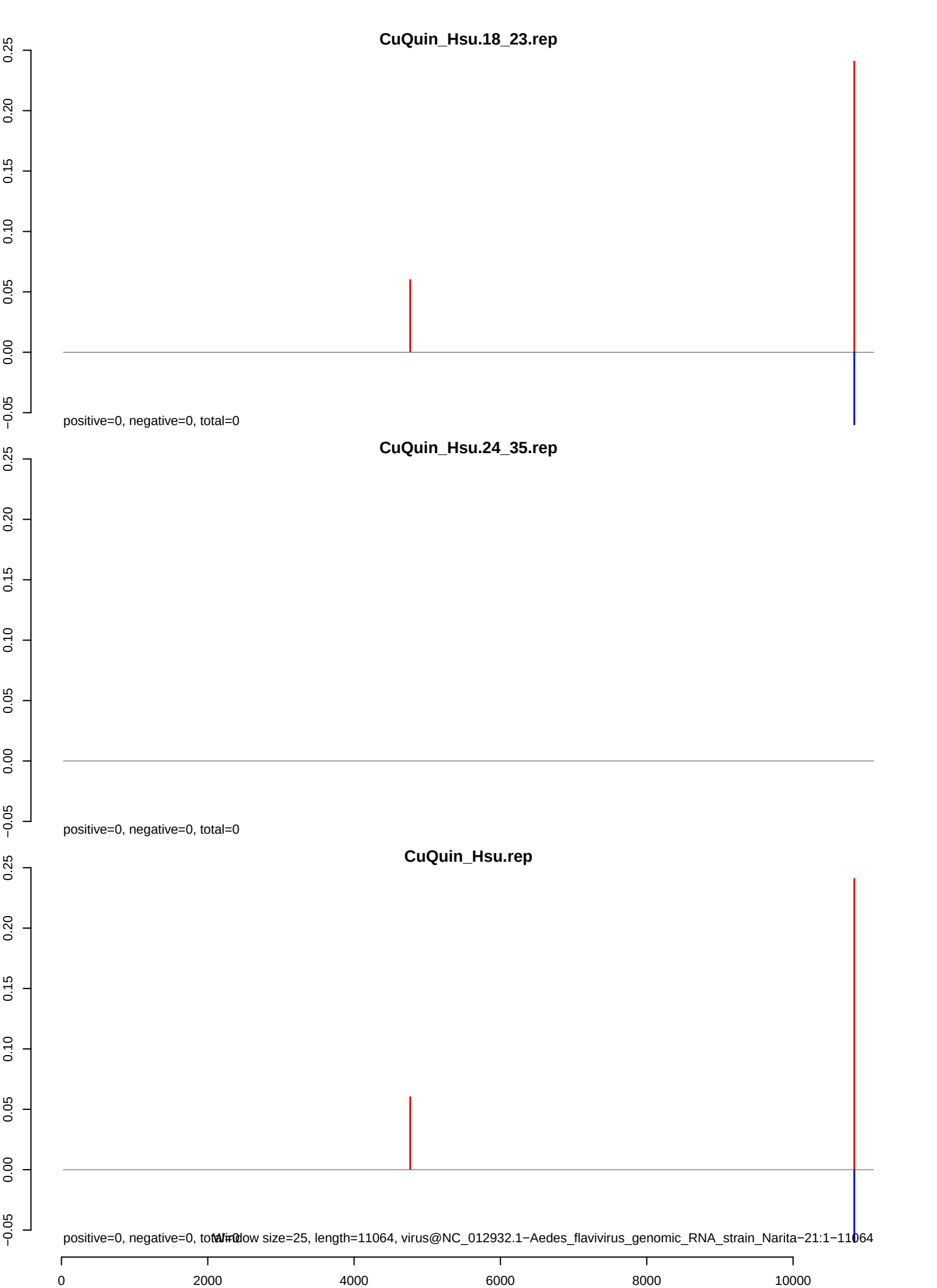

CuQuin_Hsu.18_23.rep
0.00
0.01
0.02
0.03
0.04
0.05
0.06
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
0.00
0.01
0.02
0.03
0.04
0.05
0.06
positive=0, negative=0, total=0
CuQuin_Hsu.rep
0.00
0.01
0.02
0.03
0.04
0.05
0.06
positive=0, negative=0, total=0 Window size=25, length=11286, virus@NC_031956.1−UNVERIFIED_Balsa_virus_strain_CoB_84:1−11286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

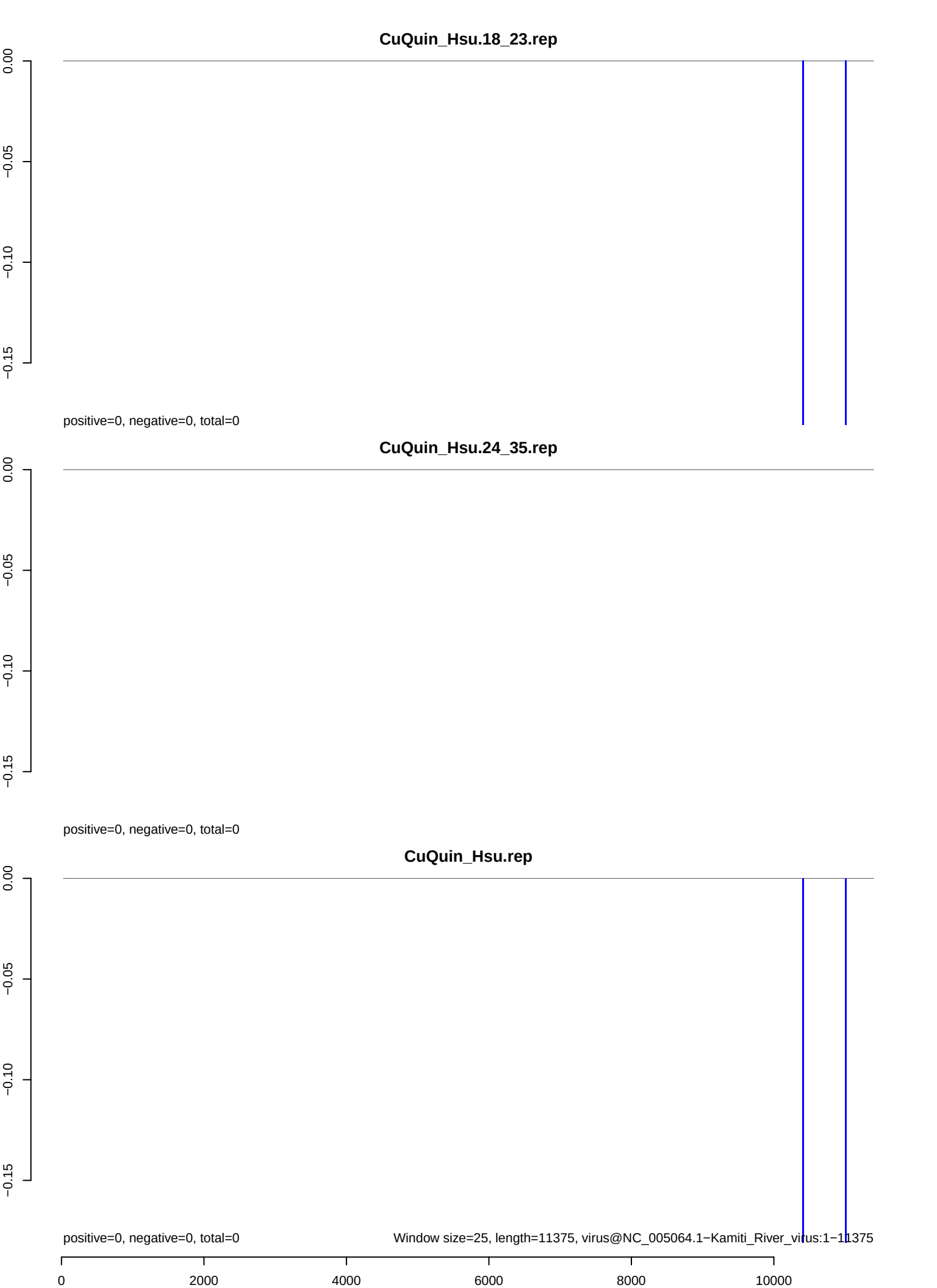

CuQuin_Hsu.18_23.rep
0.00
−0.02
−0.04
−0.06
−0.08
−0.10
−0.12
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
0.00
−0.02
−0.04
−0.06
−0.08
−0.10
−0.12
positive=0, negative=0, total=0
CuQuin_Hsu.rep
0.00
−0.02
−0.04
−0.06
−0.08
−0.10
−0.12
positive=0, negative=0, total=0
Window size=25, length=11220, virus@NC_025399.1−Oak−Vale_virus_strain_CSIRO_1342:1−11220
0
2000
4000
6000
8000
10000

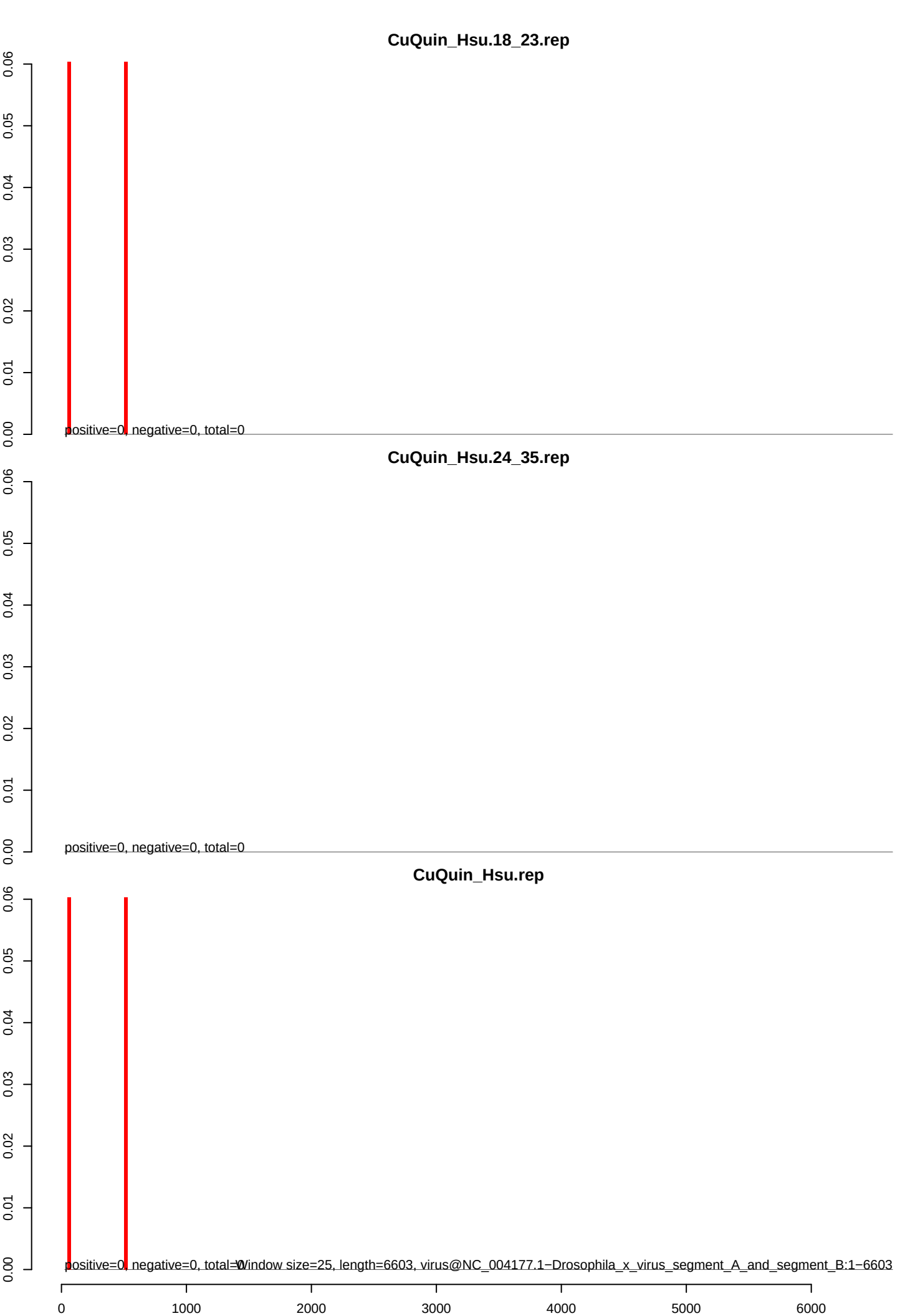

CuQuin_Hsu.18_23.rep
0.0
0.1
0.2
0.3
0.4
0.5
positive=1, negative=0, total=1
CuQuin_Hsu.24_35.rep
0.0
0.1
0.2
0.3
0.4
0.5
positive=0, negative=0, total=0
CuQuin_Hsu.rep
0.0
0.1
0.2
0.3
0.4
0.5
positive=1, negative=0, total=1
size=25, length=11190, virus@NC_025384.1−Culex_tritaeniorhynchus_rhabdovirus_RNA_strain_TY:1−11190
0
2000
4000
6000
8000
10000

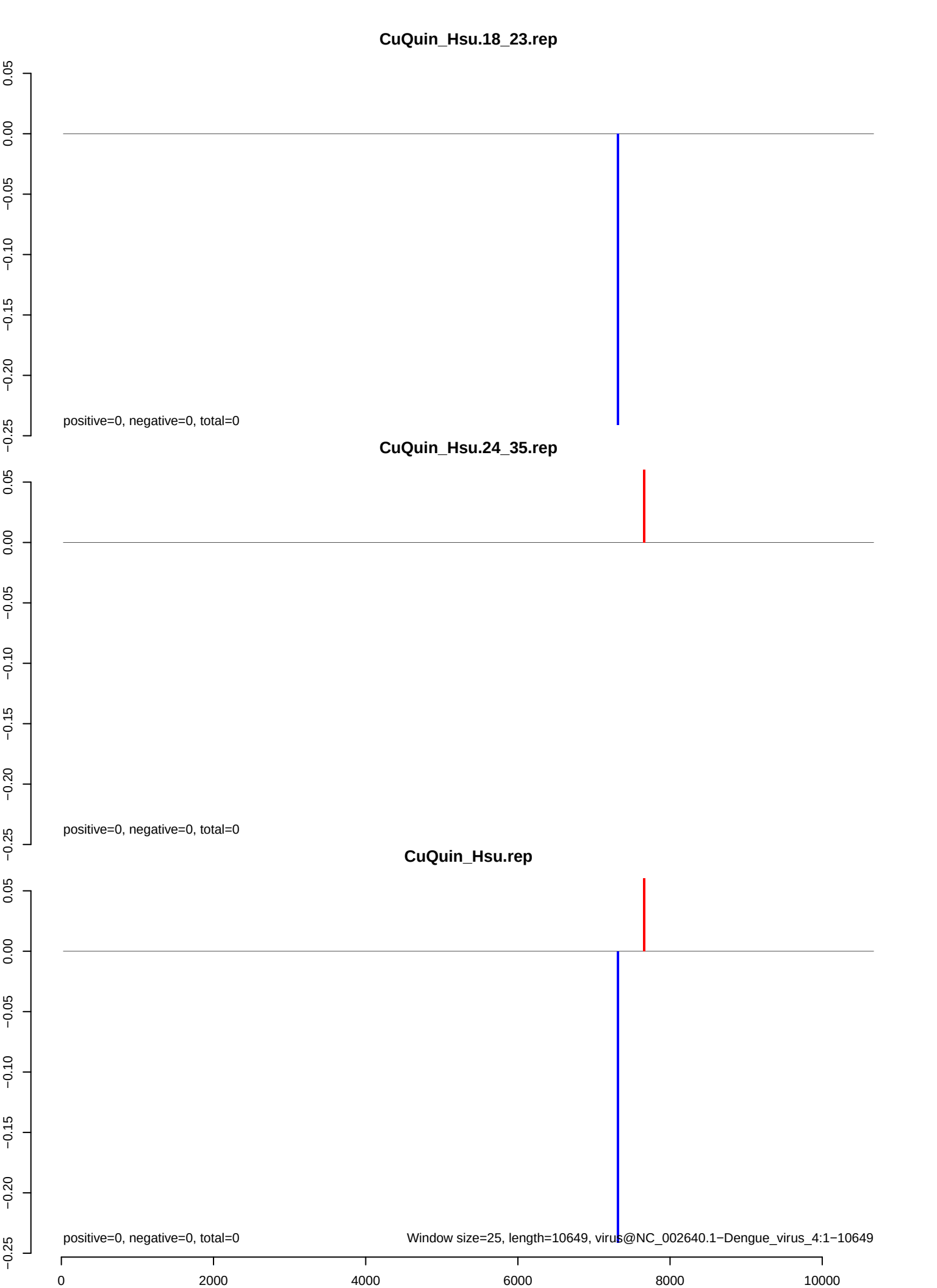

CuQuin_Hsu.18_23.rep
0.06
0.04
0.02
0.00
−0.02
−0.04
−0.06
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
0.06
0.04
0.02
0.00
−0.02
−0.04
−0.06
positive=0, negative=0, total=0
CuQuin_Hsu.rep
0.06
0.04
0.02
0.00
−0.02
−0.04
−0.06
positive=0, negative=0, total=0
Window size=25, length=14717, virus@NC_017685.1−Obodhiang_virus:1−14717
0
5000
10000
15000

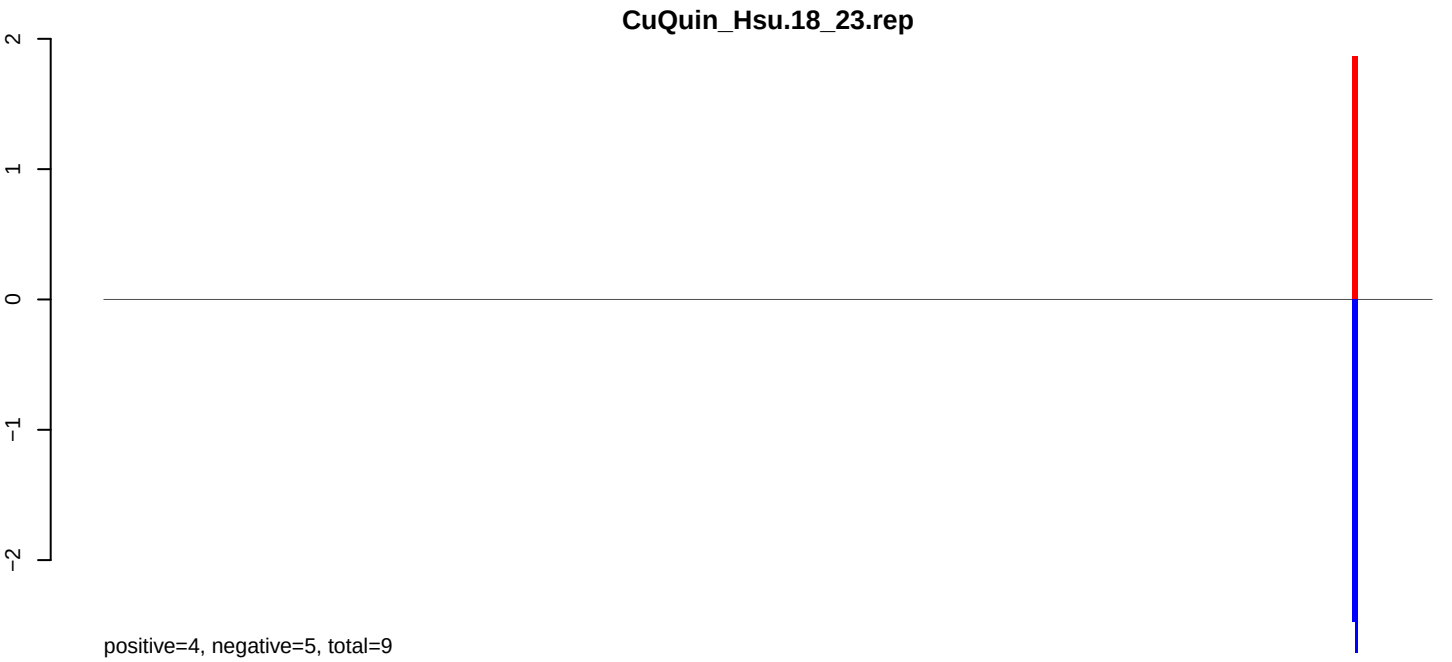

CuQuin_Hsu.18_23.rep
0.5
0.0
−0.5
positive=2, negative=2, total=4
CuQuin_Hsu.24_35.rep
0.5
0.0
−0.5
positive=0, negative=0, total=0
CuQuin_Hsu.rep
0.5
0.0
−0.5
positive=2, negative=2, total=4
Window size=25, length=11877, virus@NC_016962.1−Bebaru_virus:1−11877
0
2000
4000
6000
8000
10000
12000


CuQuin_Hsu.18_23.rep
0.25
0.20
0.15
0.10
0.05
0.00
−0.05
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
0.25
0.20
0.15
0.10
0.05
0.00
−0.05
positive=0, negative=0, total=0
CuQuin_Hsu.rep
0.25
0.20
0.15
0.10
0.05
0.00
−0.05
positive=0, negative=0, total=0
Window size=25, length=11064, virus@NC_012932.1−Aedes_flavivirus_genomic_RNA_strain_Narita−21:1−11064
0
2000
4000
6000
8000
10000

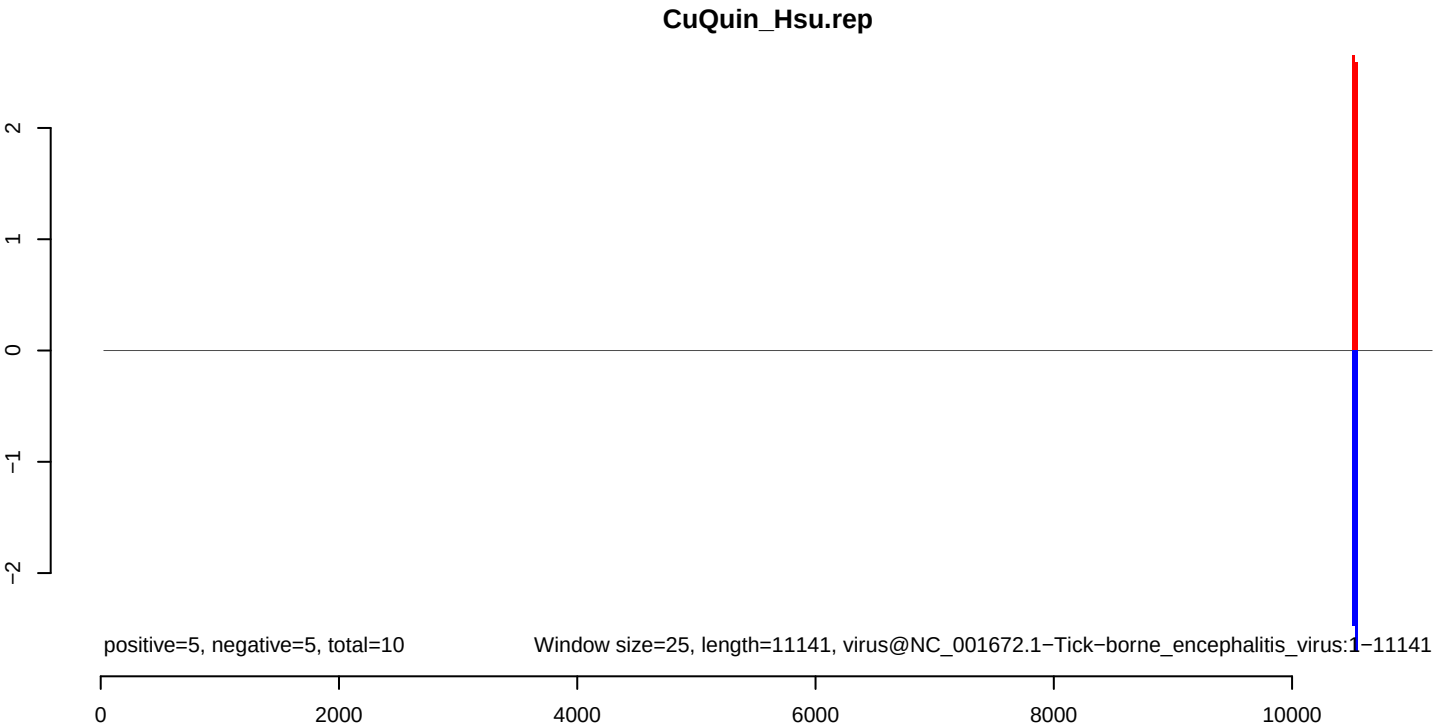

CuQuin_Hsu.18_23.rep
0.00
−0.05
−0.10
−0.15
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
0.00
−0.05
−0.10
−0.15
positive=0, negative=0, total=0
CuQuin_Hsu.rep
0.00
−0.05
−0.10
−0.15
positive=0, negative=0, total=0
Window size=25, length=11375, virus@NC_005064.1−Kamiti_River_virus:1−11375
0
2000
4000
6000
8000
10000

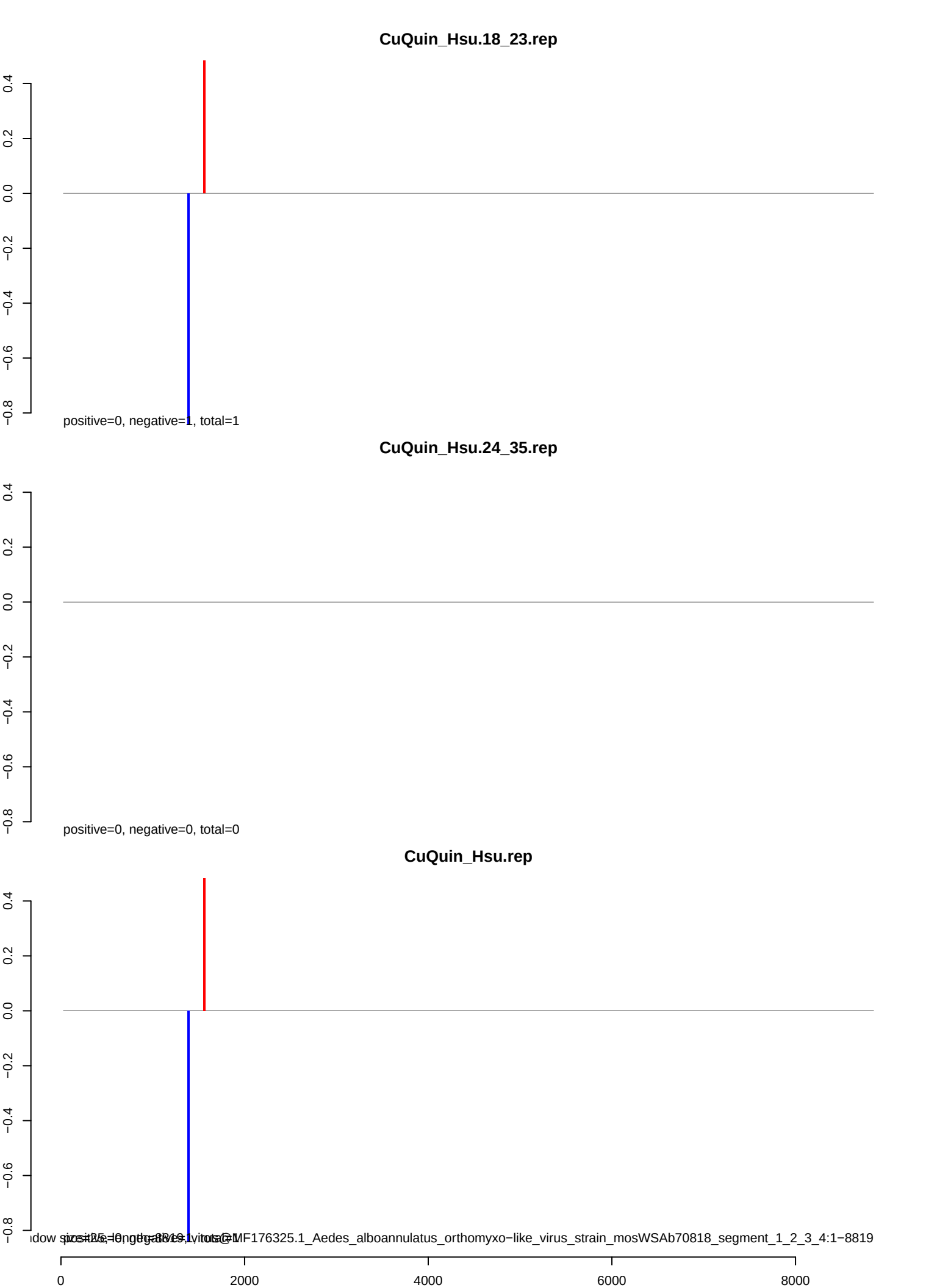

CuQuin_Hsu.18_23.rep
0.00
0.01
0.02
0.03
0.04
0.05
0.06
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
0.00
0.01
0.02
0.03
0.04
0.05
0.06
positive=0, negative=0, total=0
CuQuin_Hsu.rep
0.00
0.01
0.02
0.03
0.04
0.05
0.06
positive=0, negative=0, total=0
Window size=25, length=6603, virus@NC_004177.1−Drosophila_x_virus_segment_A_and_segment_B:1−6603
0
1000
2000
3000
4000
5000
6000

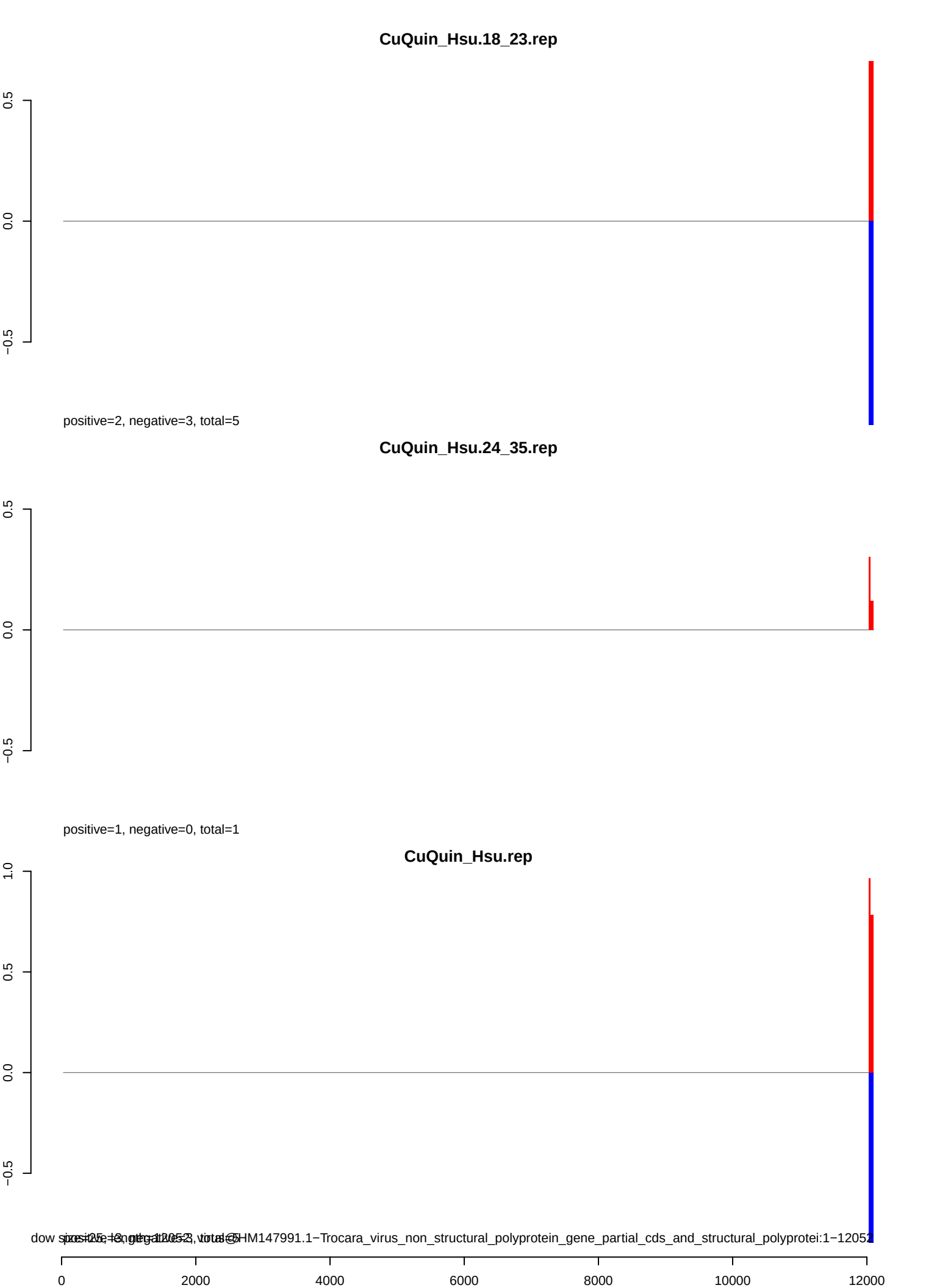

CuQuin_Hsu.18_23.rep
0.05
0.00
−0.05
−0.10
−0.15
−0.20
−0.25
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
0.05
0.00
−0.05
−0.10
−0.15
−0.20
−0.25
positive=0, negative=0, total=0
CuQuin_Hsu.rep
0.05
0.00
−0.05
−0.10
−0.15
−0.20
−0.25
positive=0, negative=0, total=0
Window size=25, length=10649, virus@NC_002640.1−Dengue_virus_4:1−10649
0
2000
4000
6000
8000
10000

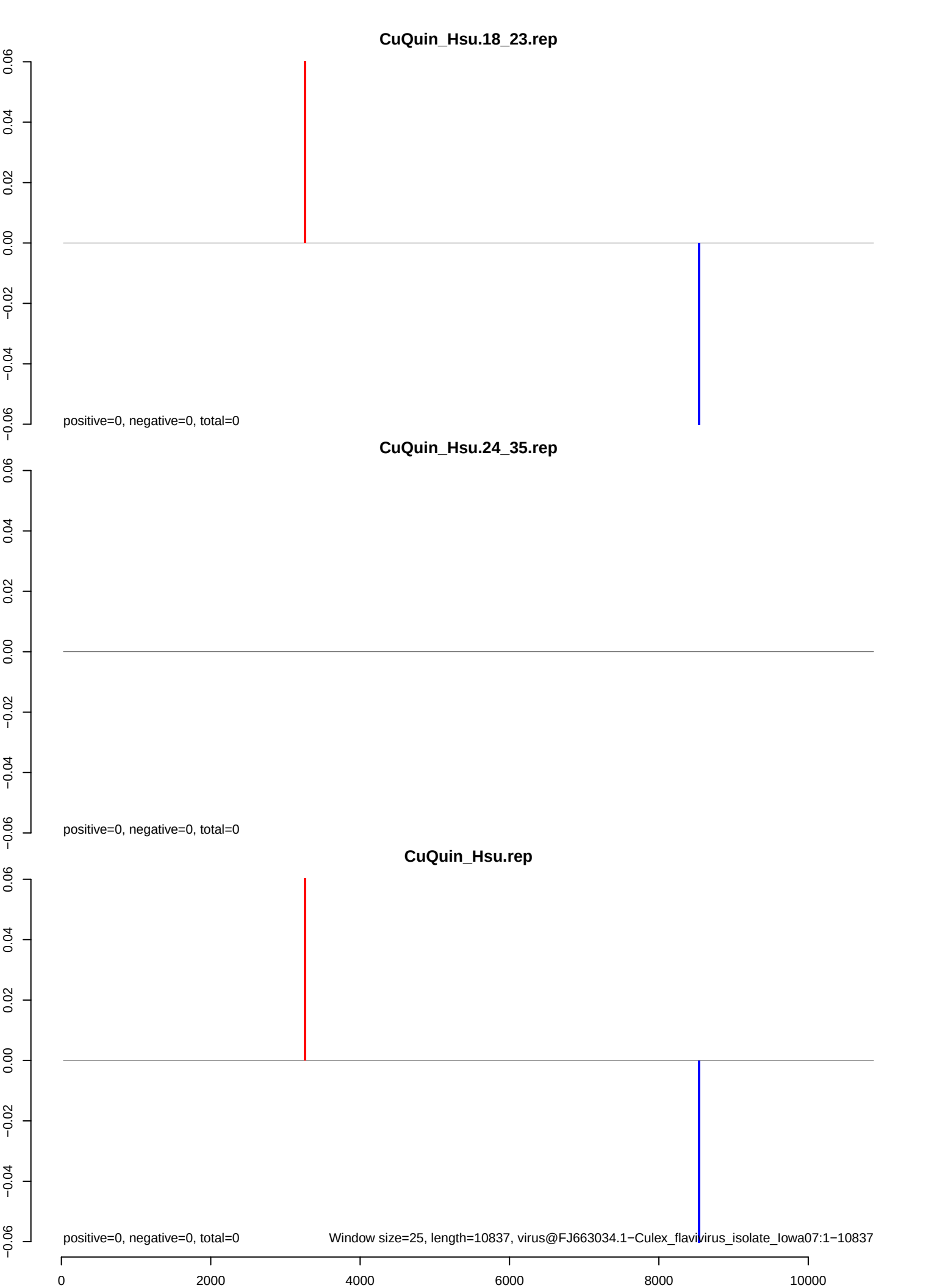

CuQuin_Hsu.18_23.rep
2
1
0
−1
−2
positive=4, negative=5, total=9

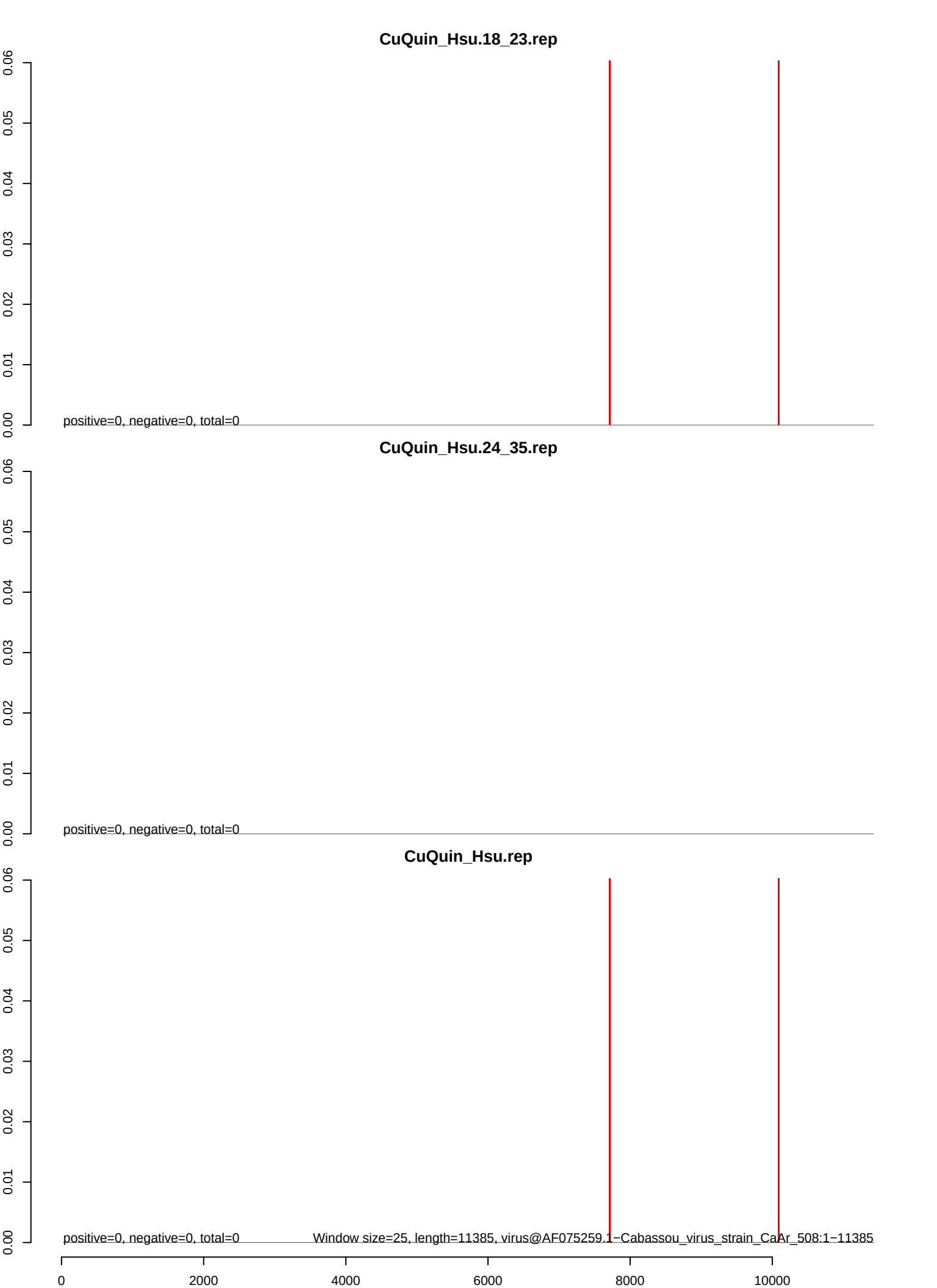
CuQuin_Hsu.24_35.rep
2
1
0
−1
−2
positive=2, negative=0, total=2

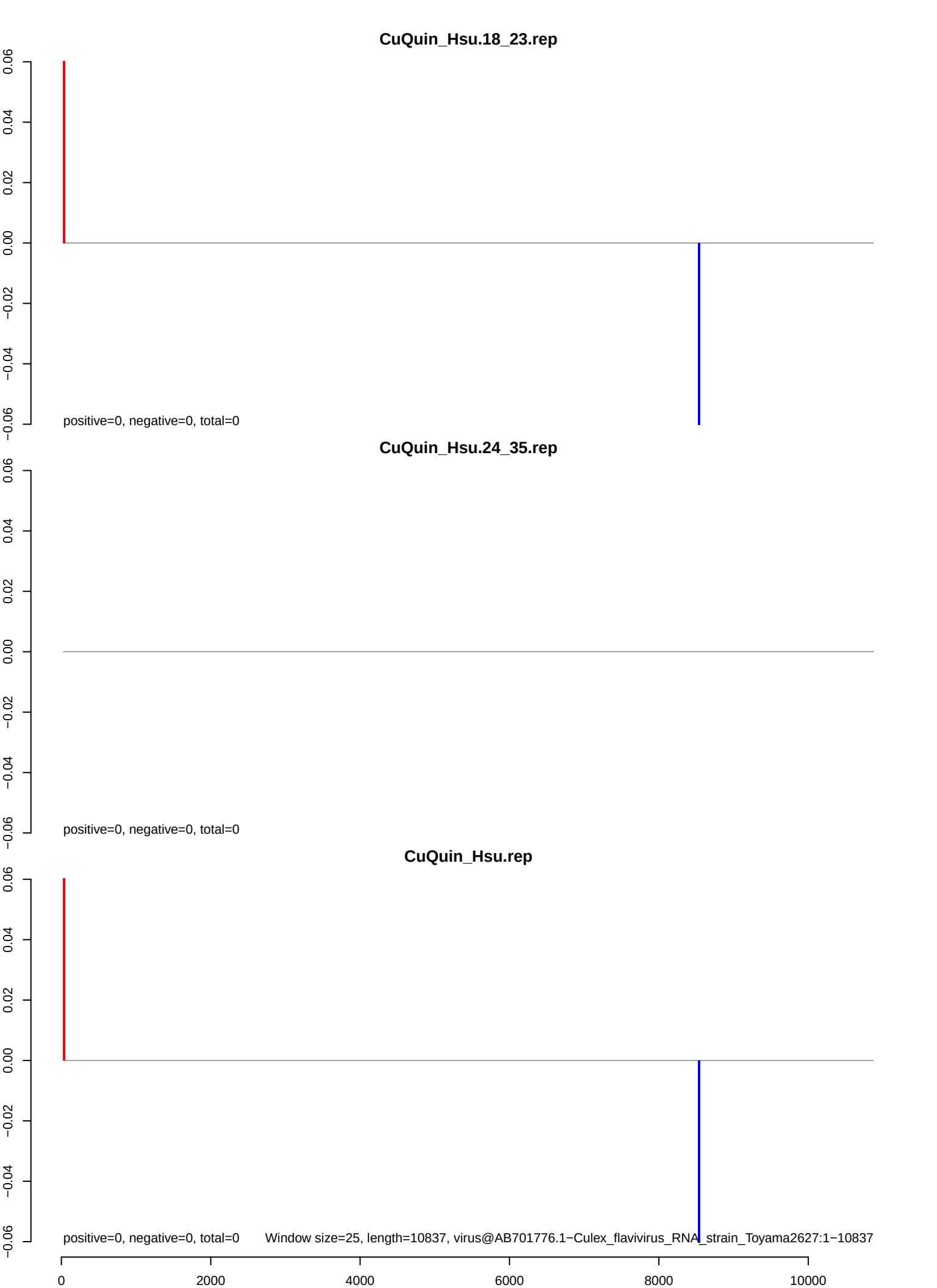

CuQuin_Hsu.rep
2
1
0
−1
−2
positive=5, negative=5, total=10
Window size=25, length=11141, virus@NC_001672.1−Tick−borne_encephalitis_virus:1−11141
0
2000
4000
6000
8000
10000

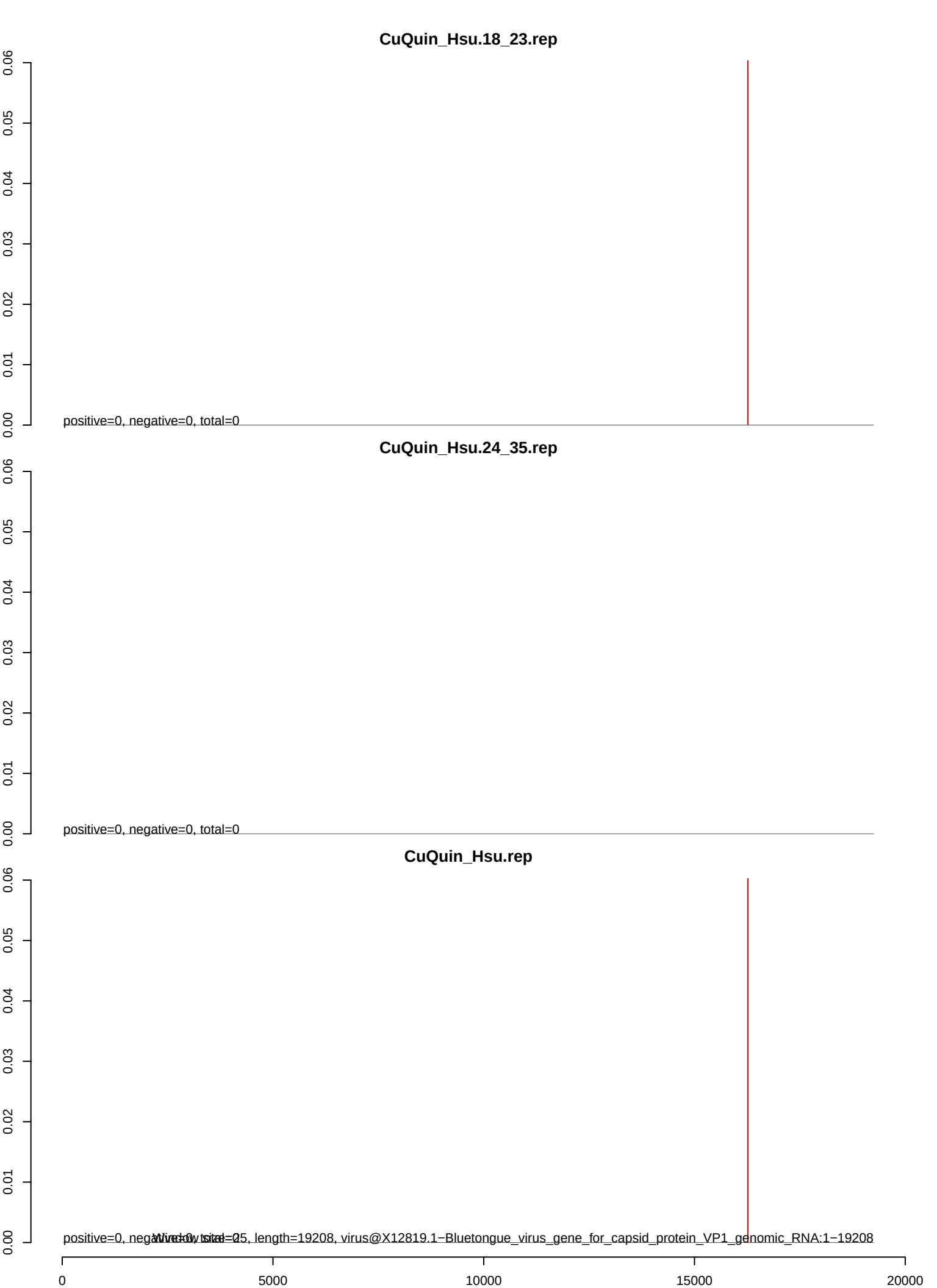

CuQuin_Hsu.18_23.rep
0.4
0.2
0.0
−0.2
−0.4
−0.6
−0.8
positive=0, negative=1, total=1
CuQuin_Hsu.24_35.rep
0.4
0.2
0.0
−0.2
−0.4
−0.6
−0.8
positive=0, negative=0, total=0
CuQuin_Hsu.rep
0.4
0.2
0.0
−0.2
−0.4
−0.6
−0.8
0
2000
4000
6000
8000

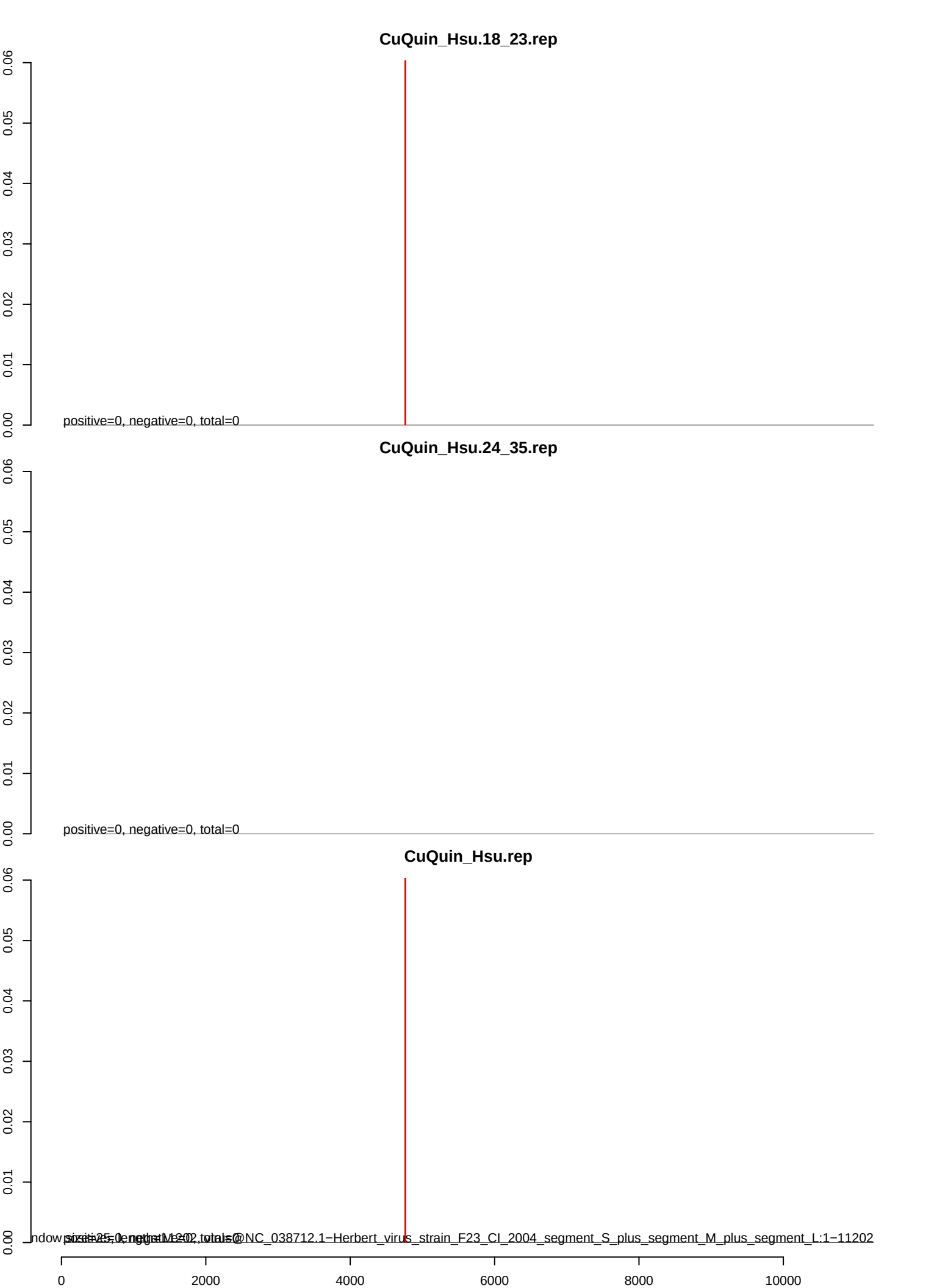

CuQuin_Hsu.18_23.rep
0.5
0.0
−0.5
positive=2, negative=3, total=5
CuQuin_Hsu.24_35.rep
0.5
0.0
−0.5
positive=1, negative=0, total=1
CuQuin_Hsu.rep
1.0
0.5
0.0
−0.5
dow
HM147991.1−Trocara_virus_non_structural_polyprotein_gene_partial_cds_and_structural_polyprotei:1−12052
0
2000
4000
6000
8000
10000
12000

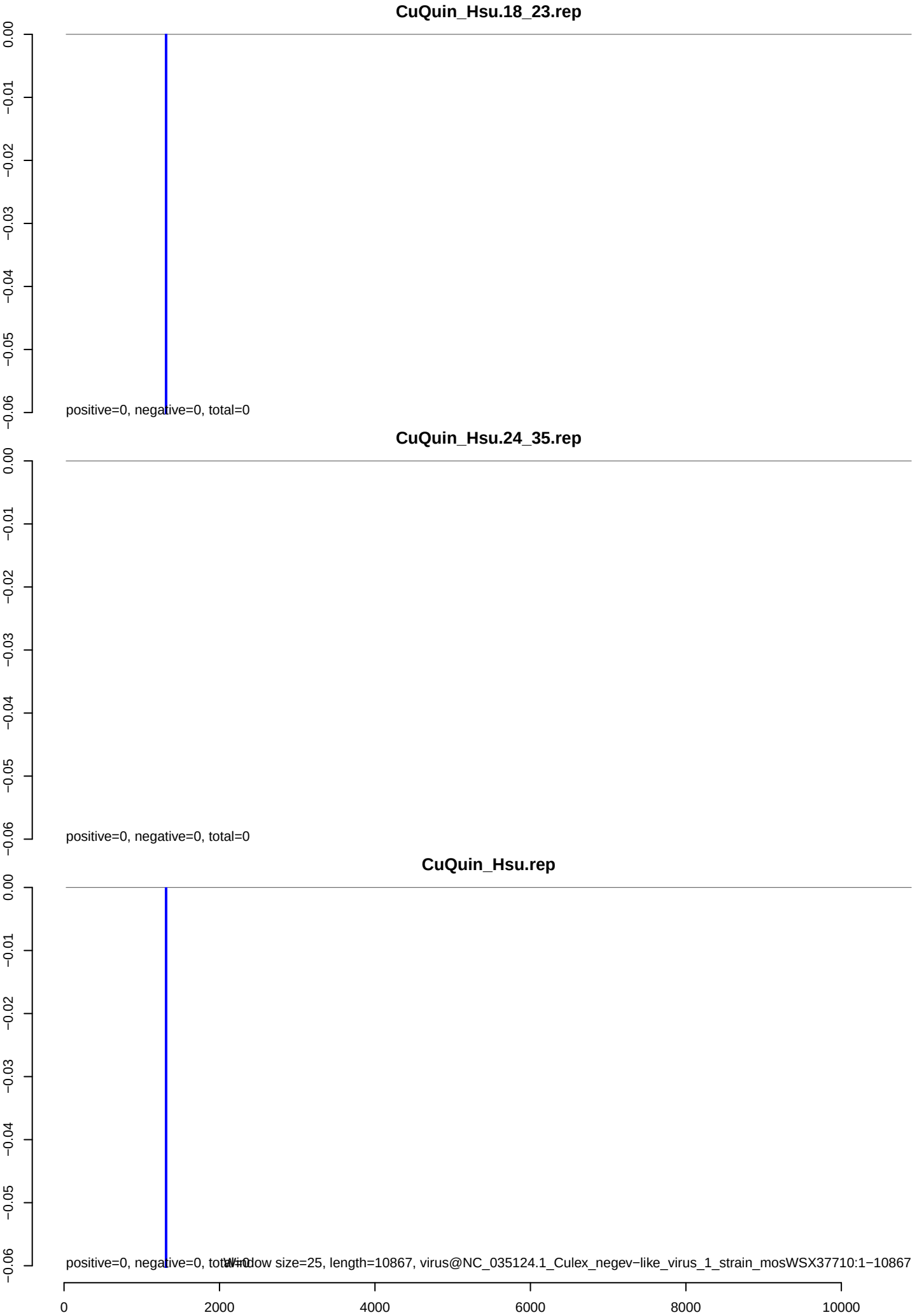

CuQuin_Hsu.18_23.rep
0.06
0.04
0.02
0.00
−0.02
−0.04
−0.06
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
0.06
0.04
0.02
0.00
−0.02
−0.04
−0.06
positive=0, negative=0, total=0
CuQuin_Hsu.rep
0.06
0.04
0.02
0.00
−0.02
−0.04
−0.06
positive=0, negative=0, total=0
Window size=25, length=10837, virus@FJ663034.1−Culex_flavivirus_isolate_Iowa07:1−10837
0
2000
4000
6000
8000
10000

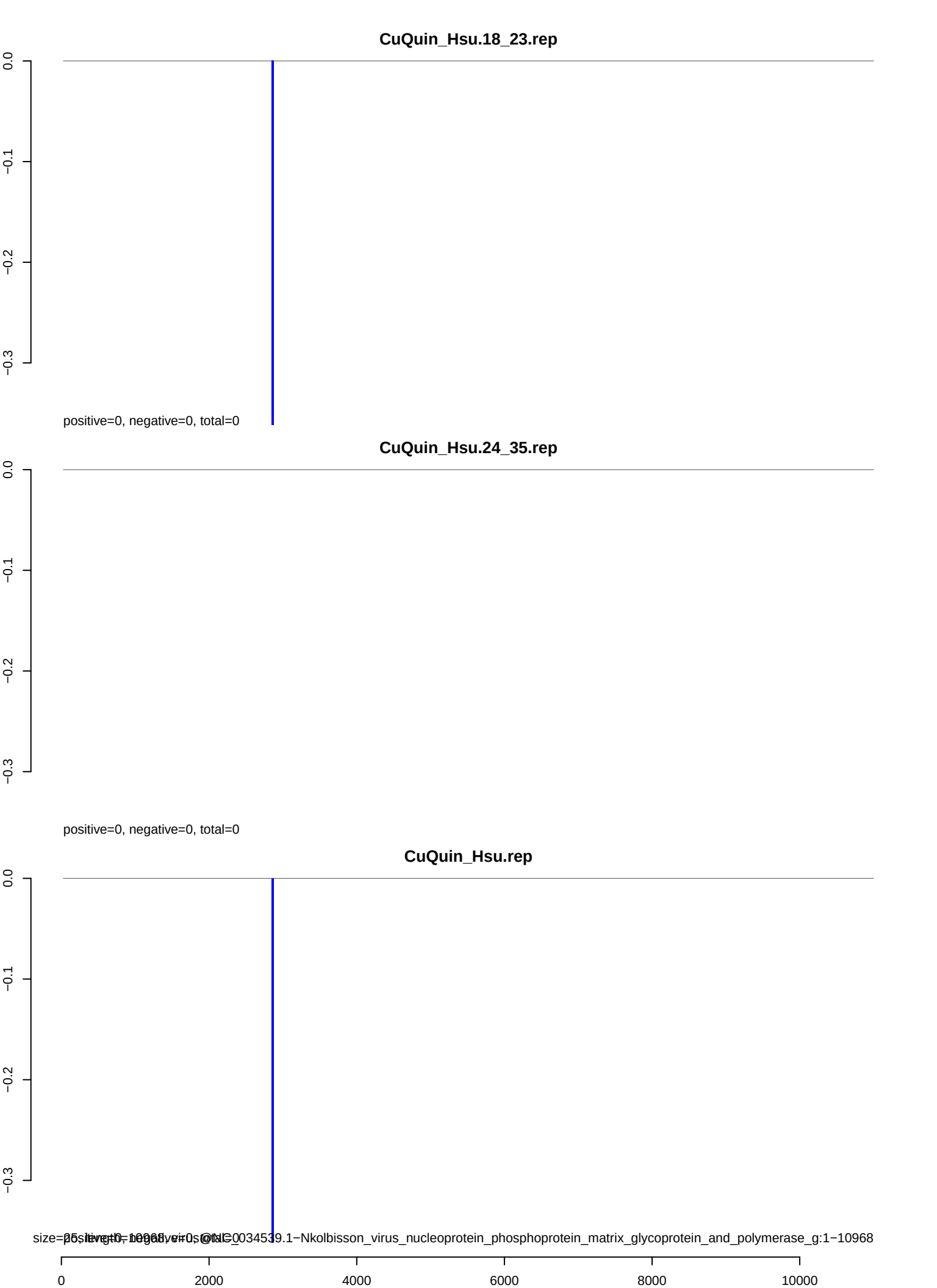

CuQuin_Hsu.18_23.rep
0.00
0.01
0.02
0.03
0.04
0.05
0.06
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
0.00
0.01
0.02
0.03
0.04
0.05
0.06
positive=0, negative=0, total=0
CuQuin_Hsu.rep
0.00
0.01
0.02
0.03
0.04
0.05
0.06
positive=0, negative=0, total=0
Window size=25, length=11385, virus@AF075259.1−Cabassou_virus_strain_CaAr_508:1−11385
0
2000
4000
6000
8000
10000

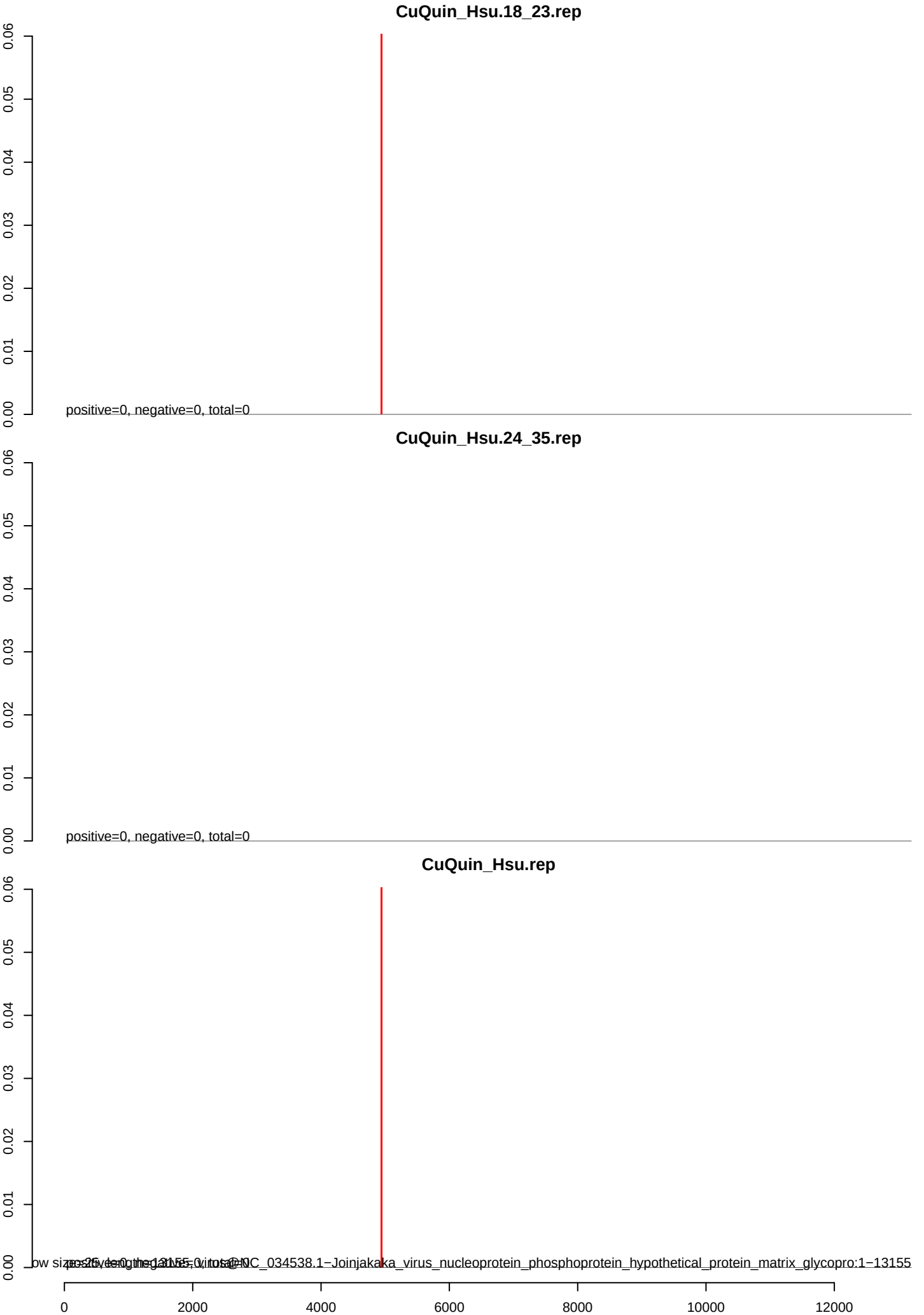

CuQuin_Hsu.18_23.rep
0.06
0.04
0.02
0.00
−0.02
−0.04
−0.06
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
0.06
0.04
0.02
0.00
−0.02
−0.04
−0.06
positive=0, negative=0, total=0
CuQuin_Hsu.rep
0.06
0.04
0.02
0.00
−0.02
−0.04
−0.06
positive=0, negative=0, total=0
Window size=25, length=10837, virus@AB701776.1−Culex_flavivirus_RNA_strain_Toyama2627:1−10837
0
2000
4000
6000
8000
10000

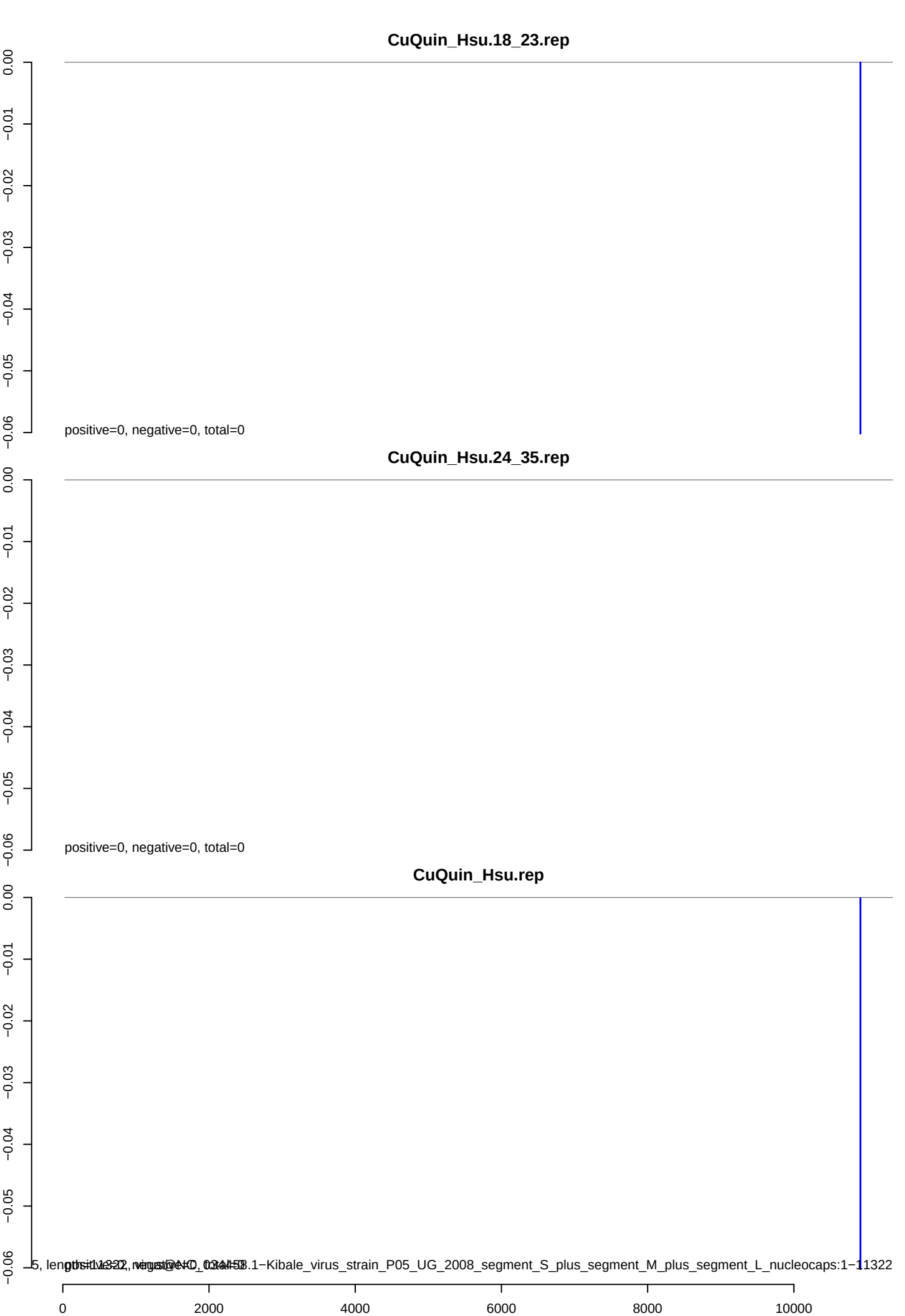

CuQuin_Hsu.18_23.rep
0.06
0.05
0.04
0.03
0.02
0.01
0.00
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
0.06
0.05
0.04
0.03
0.02
0.01
0.00
positive=0, negative=0, total=0
CuQuin_Hsu.rep
0.06
0.05
0.04
0.03
0.02
0.01
0.00
positive=0, negative=0, total=25, length=19208, virus@X12819.1−Bluetongue_virus_gene_for_capsid_protein_VP1_genomic_RNA:1−19208
0
5000
10000
15000
20000

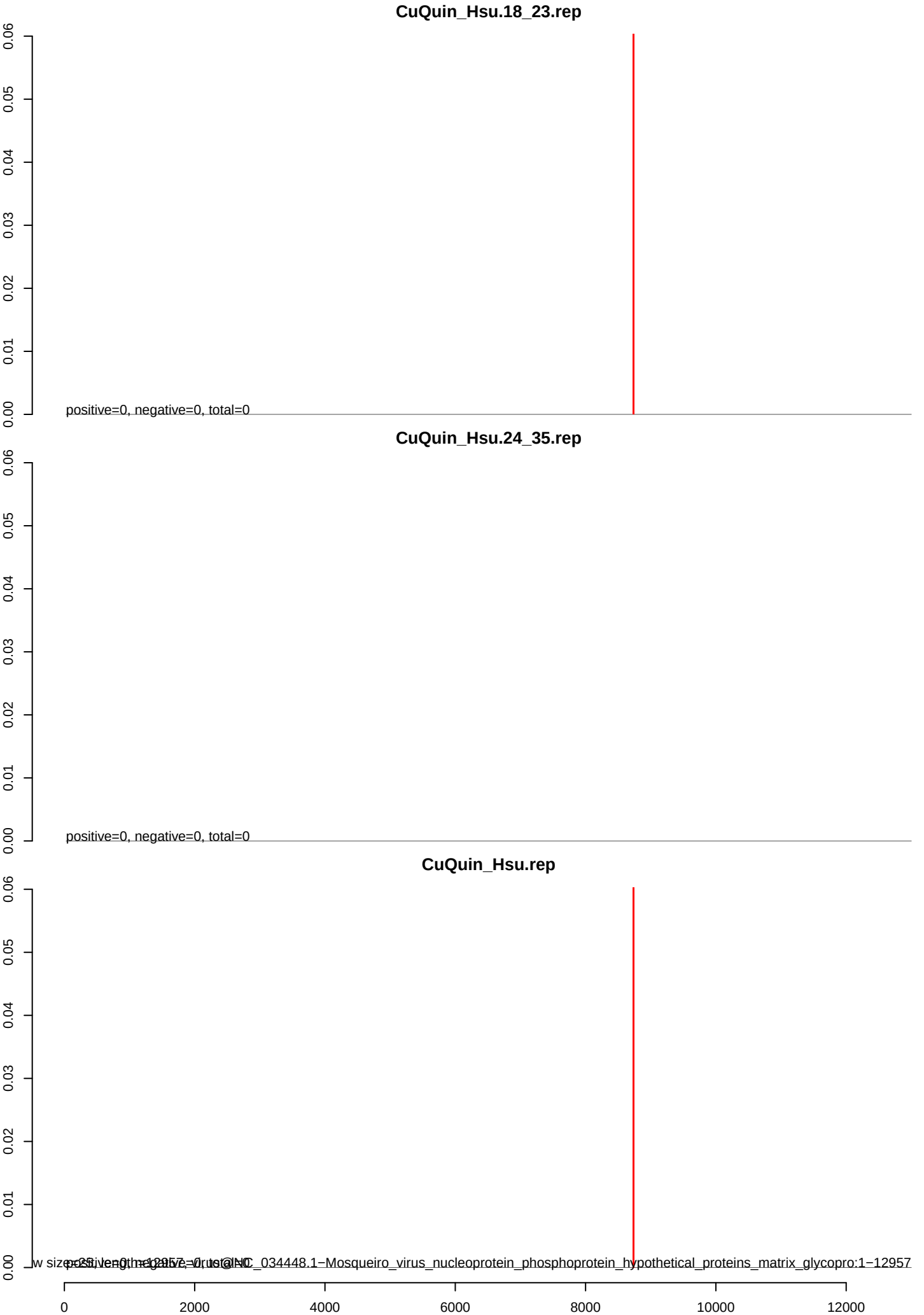

CuQuin_Hsu.18_23.rep
0.00
0.01
0.02
0.03
0.04
0.05
0.06
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
0.00
0.01
0.02
0.03
0.04
0.05
0.06
positive=0, negative=0, total=0
CuQuin_Hsu.rep
0.00
0.01
0.02
0.03
0.04
0.05
0.06
ndow
NC_038712.1−Herbert_virus_strain_F23_CI_2004_segment_S_plus_segment_M_plus_segment_L:1−11202
0
2000
4000
6000
8000
10000

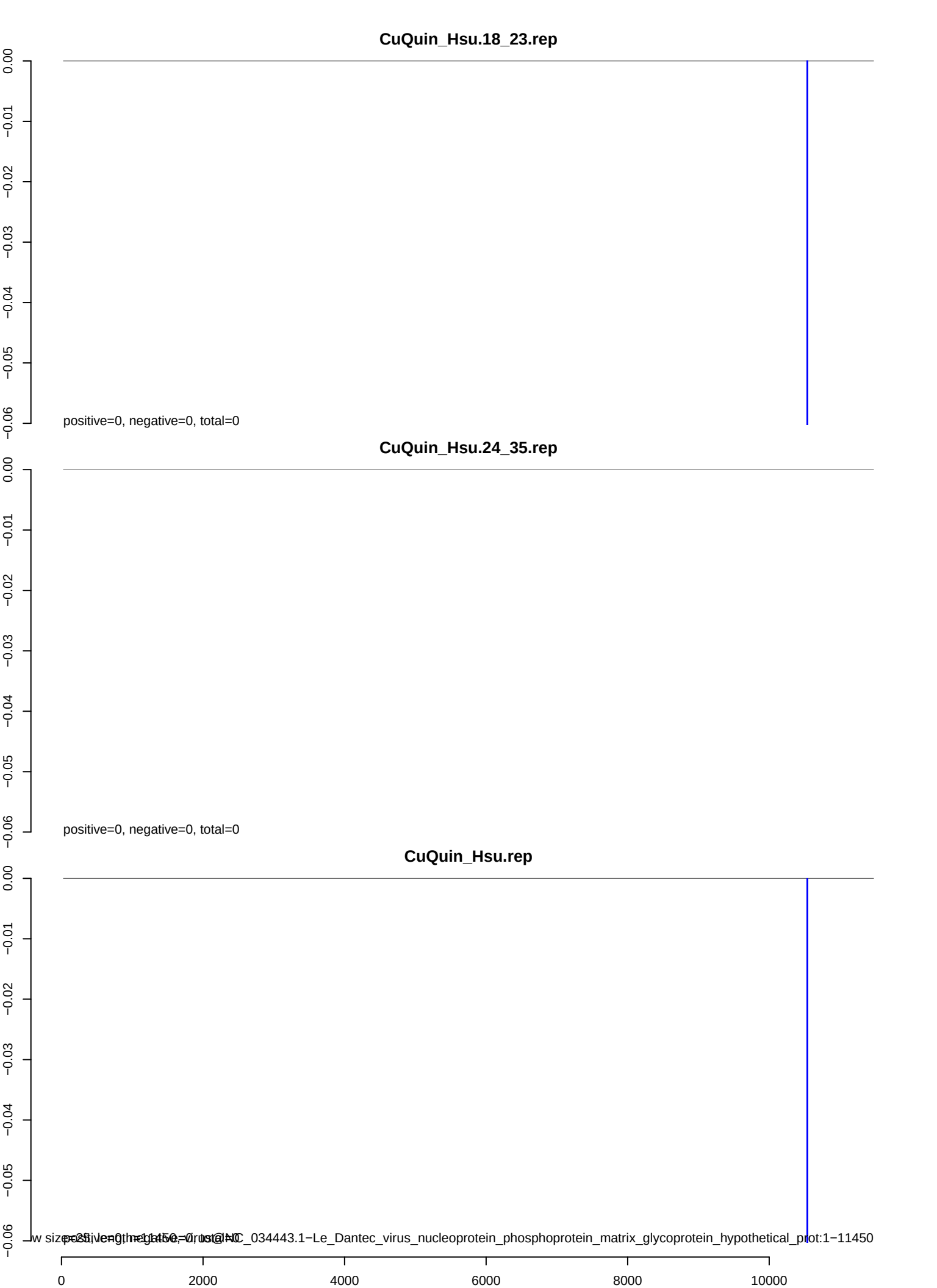

CuQuin_Hsu.18_23.rep
0.00
−0.01
−0.02
−0.03
−0.04
−0.05
−0.06
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
0.00
−0.01
−0.02
−0.03
−0.04
−0.05
−0.06
positive=0, negative=0, total=0
CuQuin_Hsu.rep
0.00
−0.01
−0.02
−0.03
−0.04
−0.05
−0.06
positive=0, negative=0, total=0
Window size=25, length=10867, virus@NC_035124.1_Culex_negev−like_virus_1_strain_mosWSX37710:1−10867
0
2000
4000
6000
8000
10000

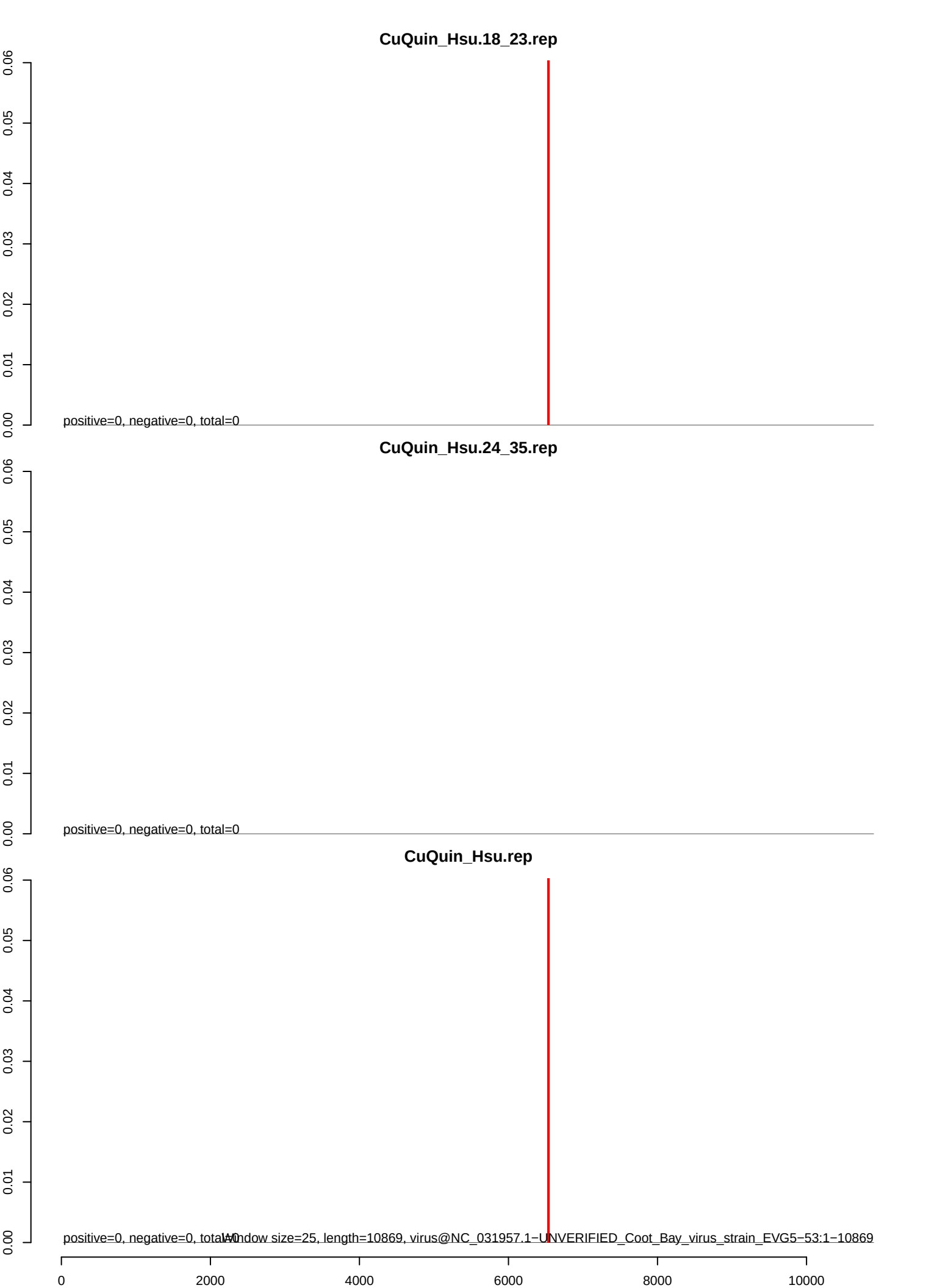

CuQuin_Hsu.18_23.rep
0.0
−0.1
−0.2
−0.3
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
0.0
−0.1
−0.2
−0.3
positive=0, negative=0, total=0
CuQuin_Hsu.rep
0.0
−0.1
−0.2
−0.3
size=25, length=10968, positive=0, negative=0, total=0
NC_034539.1−Nkolbisson_virus_nucleoprotein_phosphoprotein_matrix_glycoprotein_and_polymerase_g:1−10968
0
2000
4000
6000
8000
10000

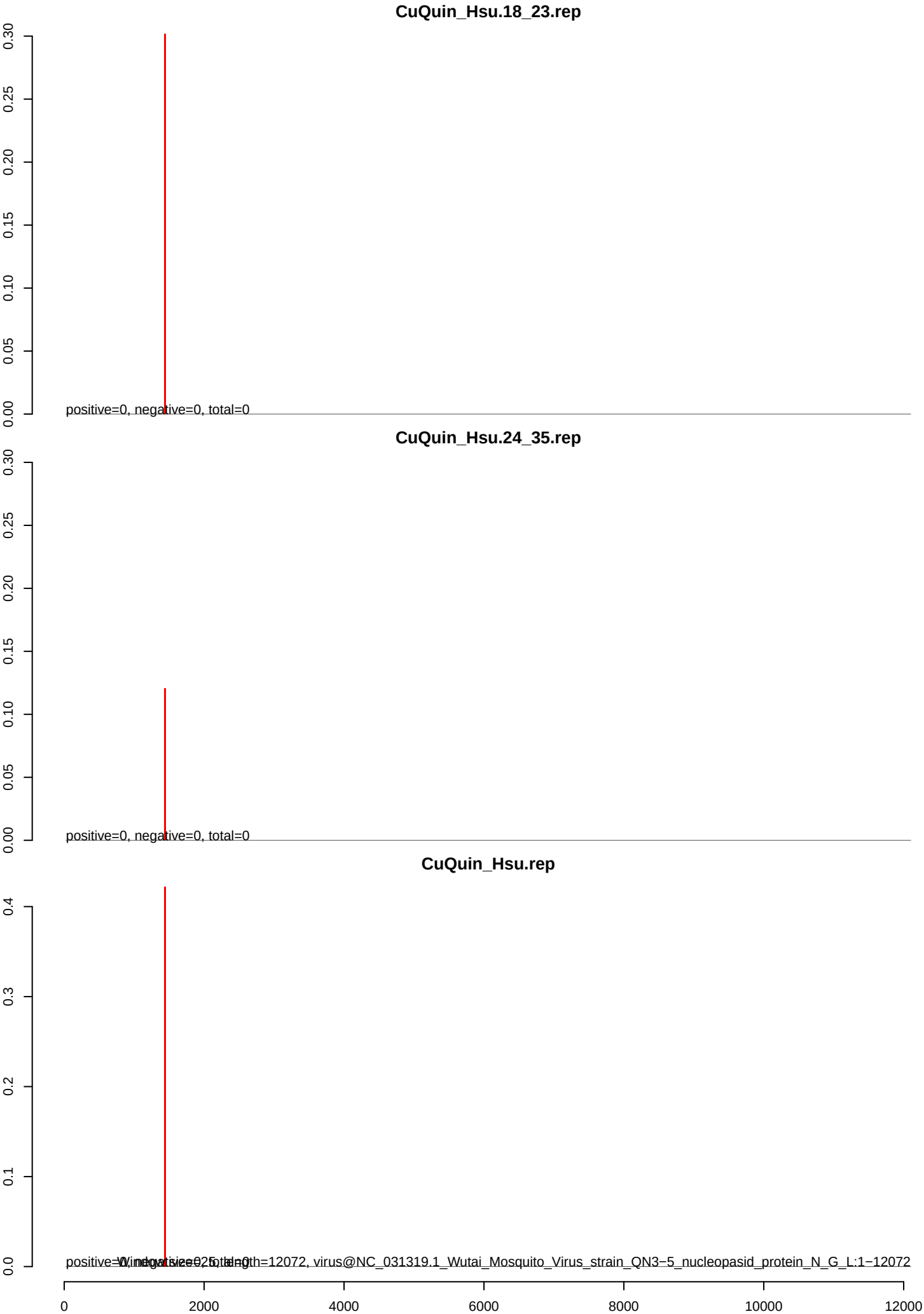

CuQuin_Hsu.18_23.rep
0.06
0.05
0.04
0.03
0.02
0.01
0.00
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
0.06
0.05
0.04
0.03
0.02
0.01
0.00
positive=0, negative=0, total=0
CuQuin_Hsu.rep
0.06
0.05
0.04
0.03
0.02
0.01
0.00
ow size=26, length=13155, total=1
NC_034538.1−Joinjakaka_virus_nucleoprotein_phosphoprotein_hypothetical_protein_matrix_glycopro:1−13155
0
2000
4000
6000
8000
10000
12000

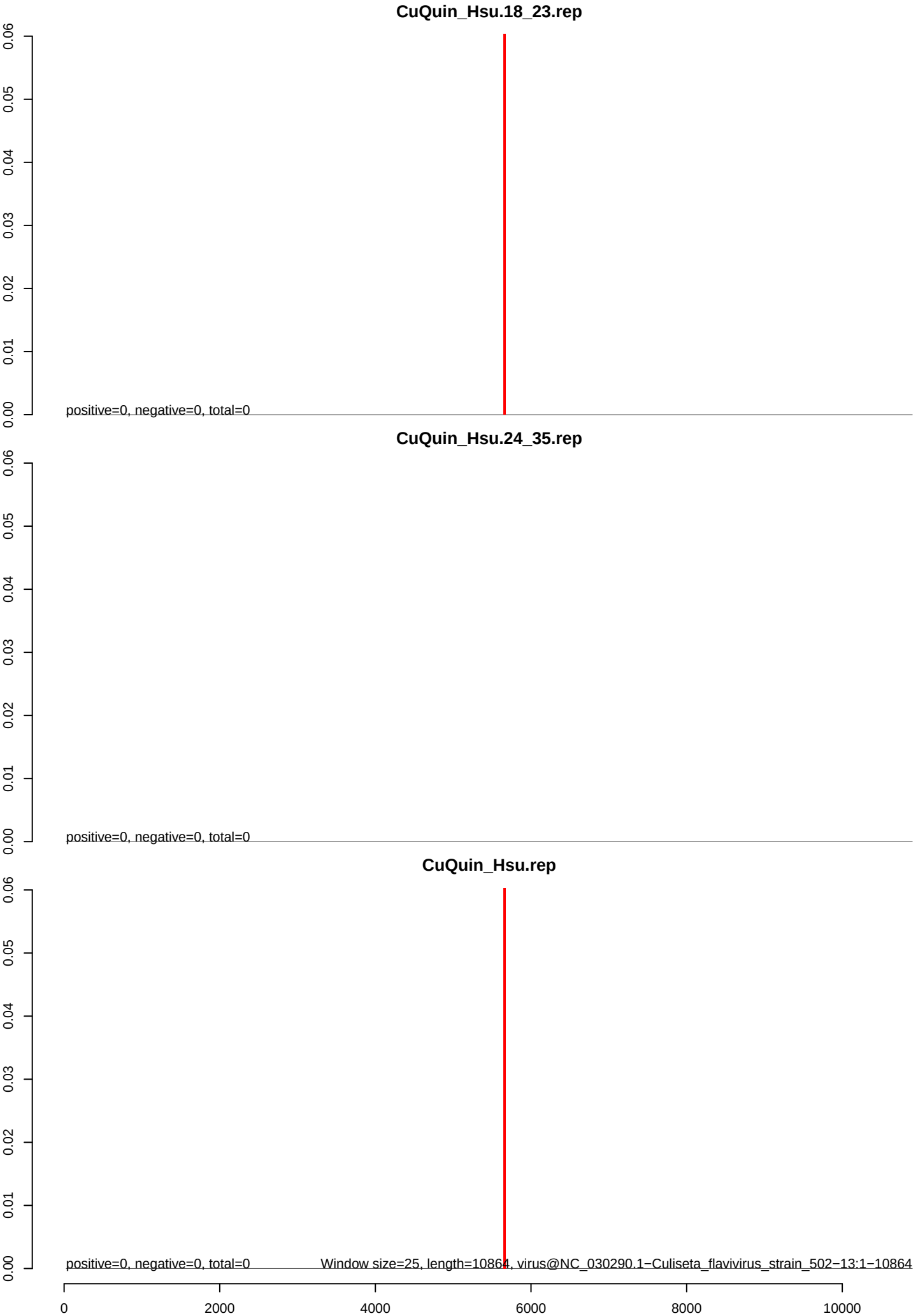

CuQuin_Hsu.18_23.rep
0.00
−0.01
−0.02
−0.03
−0.04
−0.05
−0.06
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
0.00
−0.01
−0.02
−0.03
−0.04
−0.05
−0.06
positive=0, negative=0, total=0
CuQuin_Hsu.rep
0.00
−0.01
−0.02
−0.03
−0.04
−0.05
−0.06
5, length=11322, negative=0, total=5
gb|MH044058.1−Kibale_virus_strain_P05_UG_2008_segment_S_plus_segment_M_plus_segment_L_nucleocaps:1−11322
0
2000
4000
6000
8000
10000

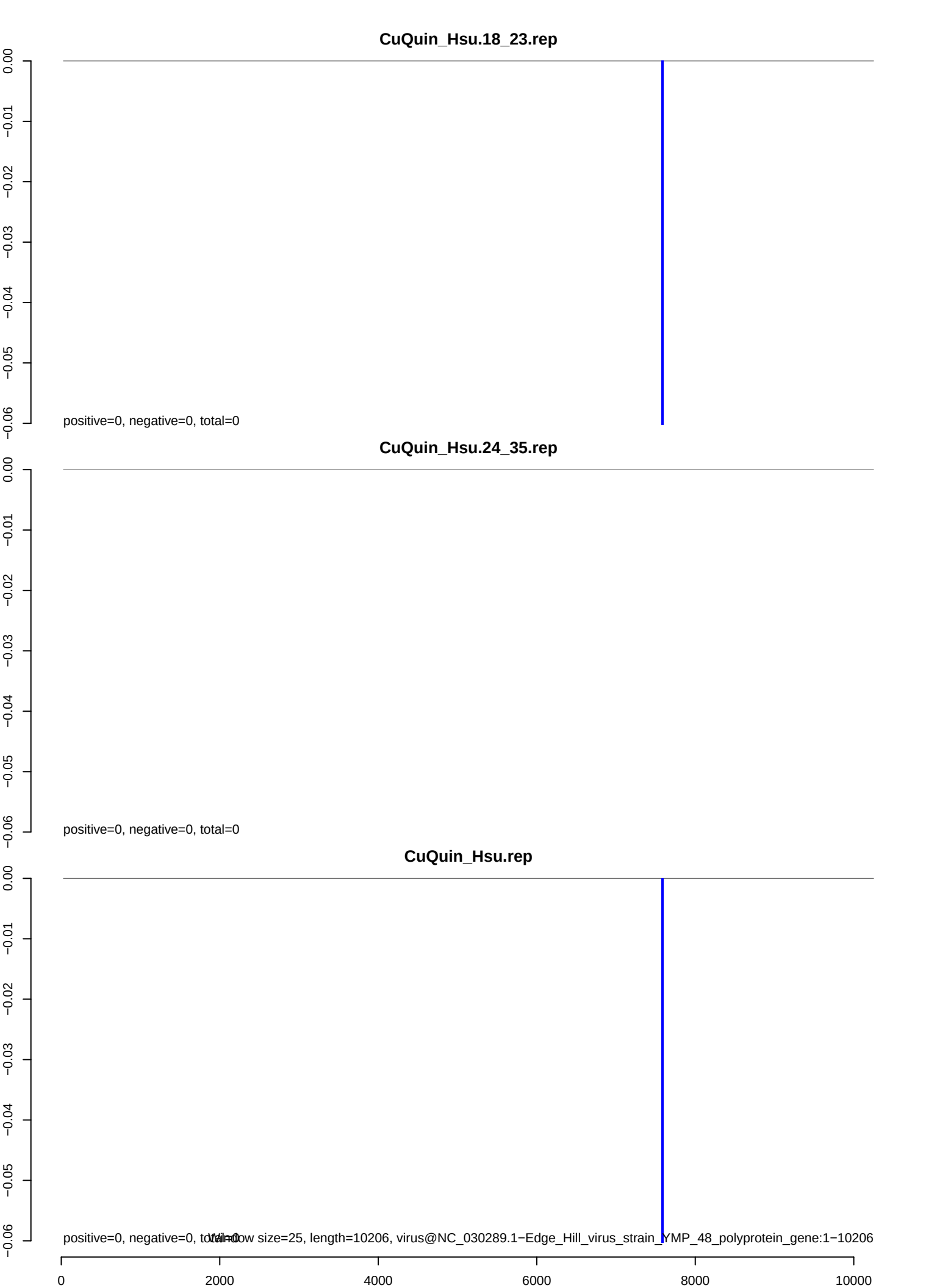

CuQuin_Hsu.18_23.rep
0.06
0.05
0.04
0.03
0.02
0.01
0.00
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
0.06
0.05
0.04
0.03
0.02
0.01
0.00
positive=0, negative=0, total=0
CuQuin_Hsu.rep
0.06
0.05
0.04
0.03
0.02
0.01
0.00
w size=25, length=12957, strand=NC_034448.1−Mosqueiro_virus_nucleoprotein_phosphoprotein_hypothetical_proteins_matrix_glycopro:1−12957
0
2000
4000
6000
8000
10000
12000

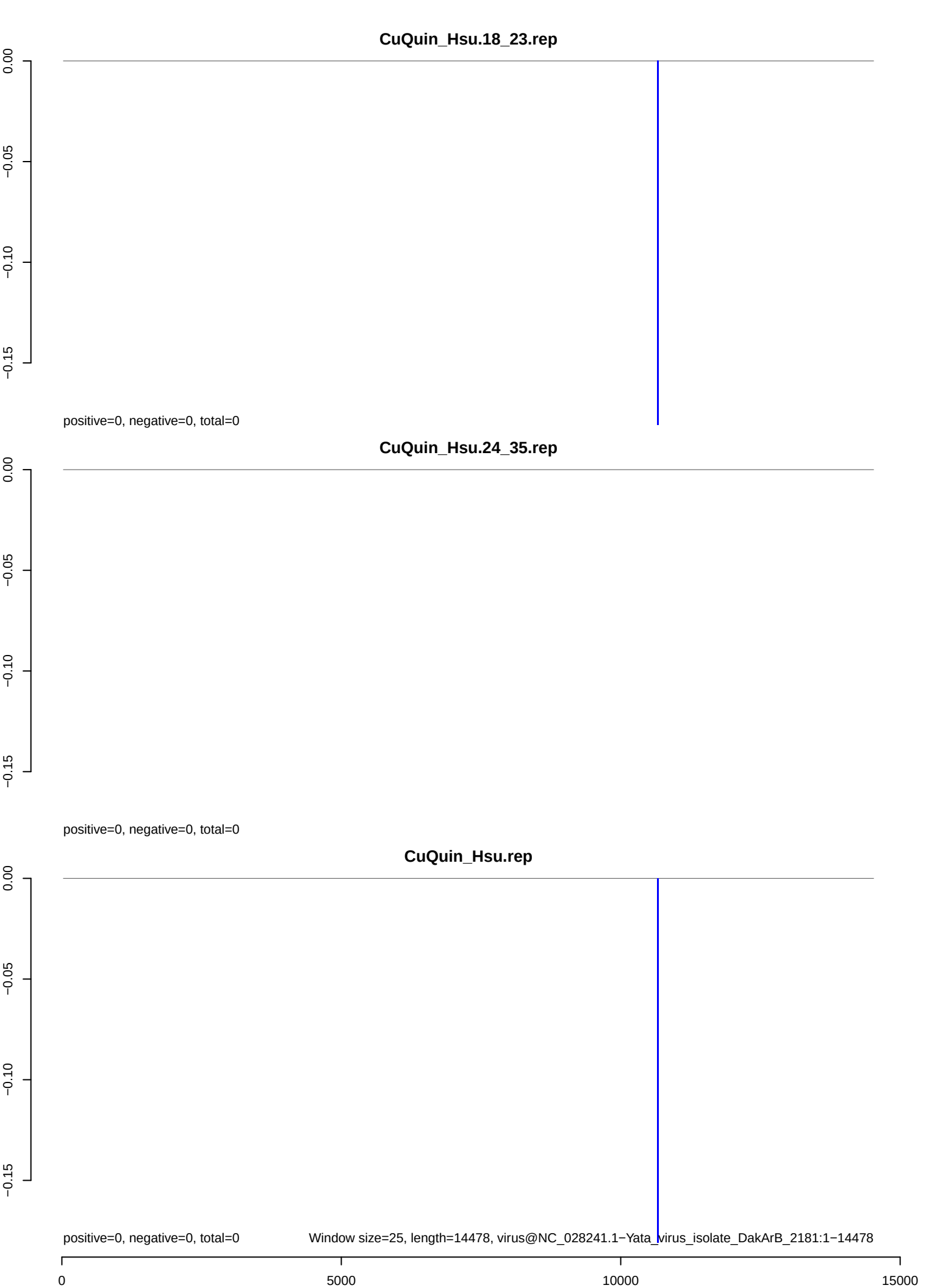

CuQuin_Hsu.18_23.rep
0.00
−0.01
−0.02
−0.03
−0.04
−0.05
−0.06
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
0.00
−0.01
−0.02
−0.03
−0.04
−0.05
−0.06
positive=0, negative=0, total=0
CuQuin_Hsu.rep
0.00
−0.01
−0.02
−0.03
−0.04
−0.05
−0.06
w size=25, length=11450, offset=0
NC_034443.1−Le_Dantec_virus_nucleoprotein_phosphoprotein_matrix_glycoprotein_hypothetical_prot:1−11450
0
2000
4000
6000
8000
10000

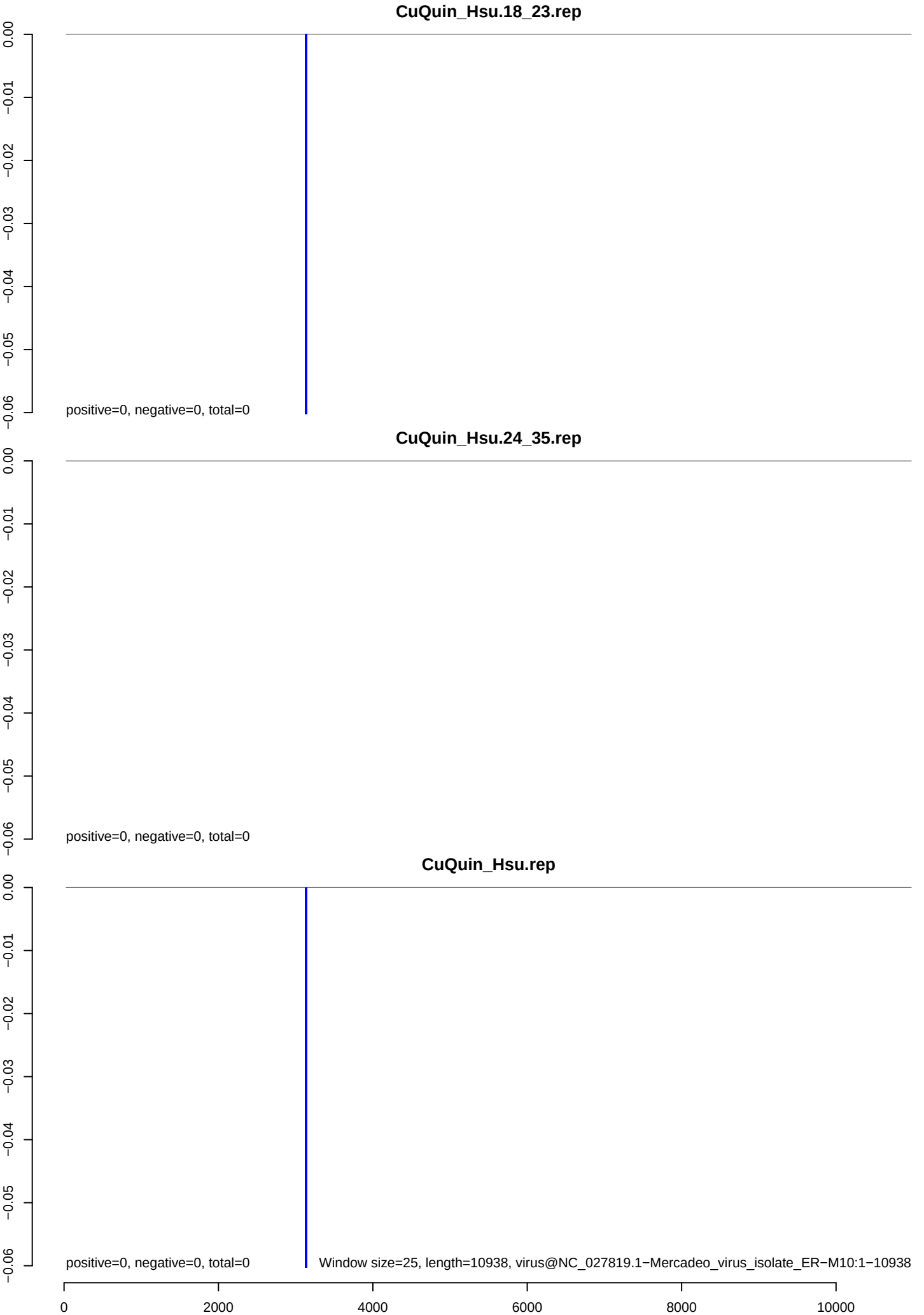

CuQuin_Hsu.18_23.rep
0.00
0.01
0.02
0.03
0.04
0.05
0.06
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
0.00
0.01
0.02
0.03
0.04
0.05
0.06
positive=0, negative=0, total=0
CuQuin_Hsu.rep
0.00
0.01
0.02
0.03
0.04
0.05
0.06
positive=0, negative=0, total=0
Window size=25, length=10869, virus@NC_031957.1−UNVERIFIED_Coot_Bay_virus_strain_EVG5−53:1−10869
0
2000
4000
6000
8000
10000

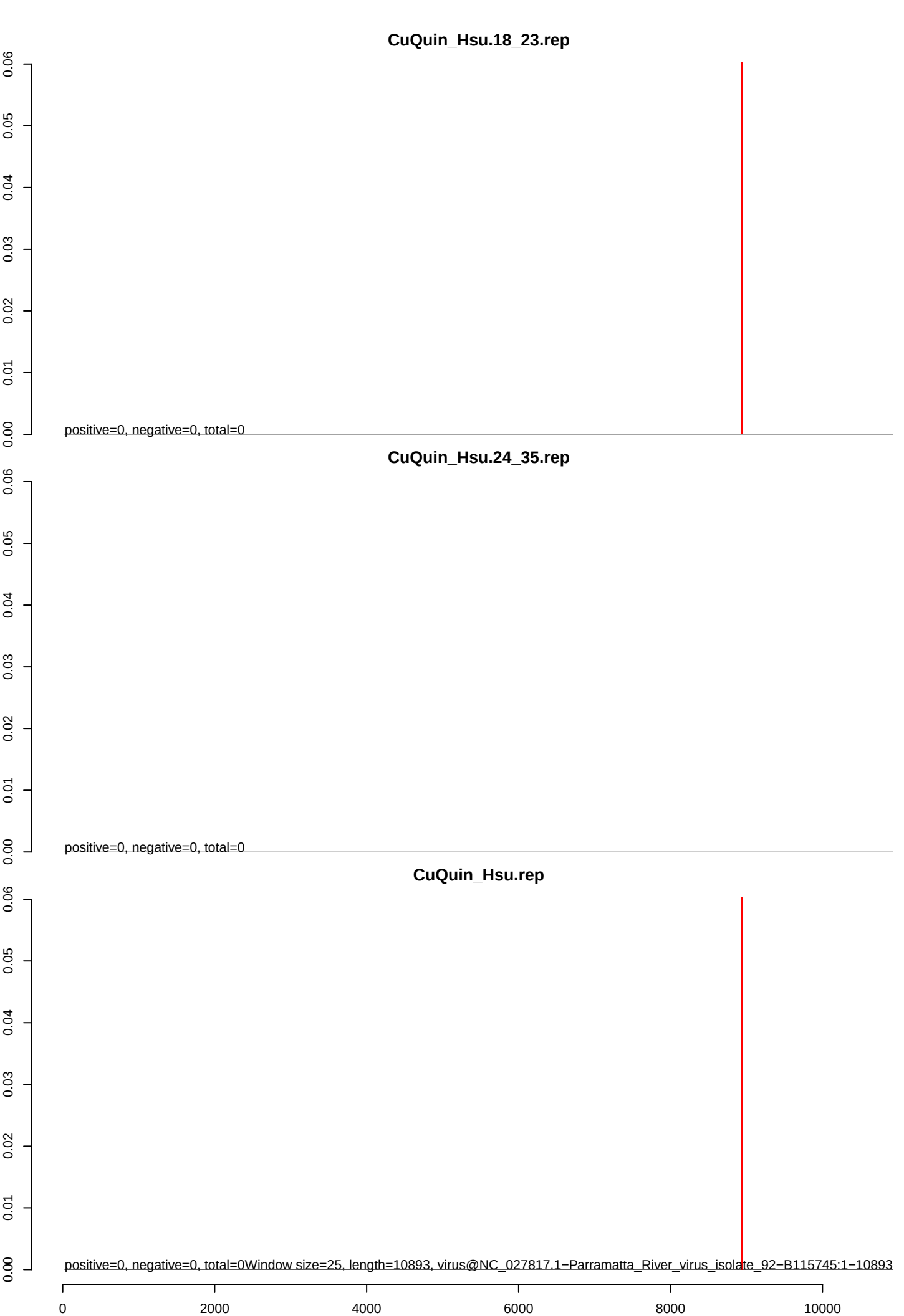

CuQuin_Hsu.18_23.rep
0.30
0.25
0.20
0.15
0.10
0.05
0.00
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
0.30
0.25
0.20
0.15
0.10
0.05
0.00
positive=0, negative=0, total=0
CuQuin_Hsu.rep
0.4
0.3
0.2
0.1
0.0
positive=0, negative=25, total=0
length=12072, virus@NC_031319.1_Wutai_Mosquito_Virus_strain_QN3−5_nucleopasid_protein_N_G_L:1−12072
0
2000
4000
6000
8000
10000
12000

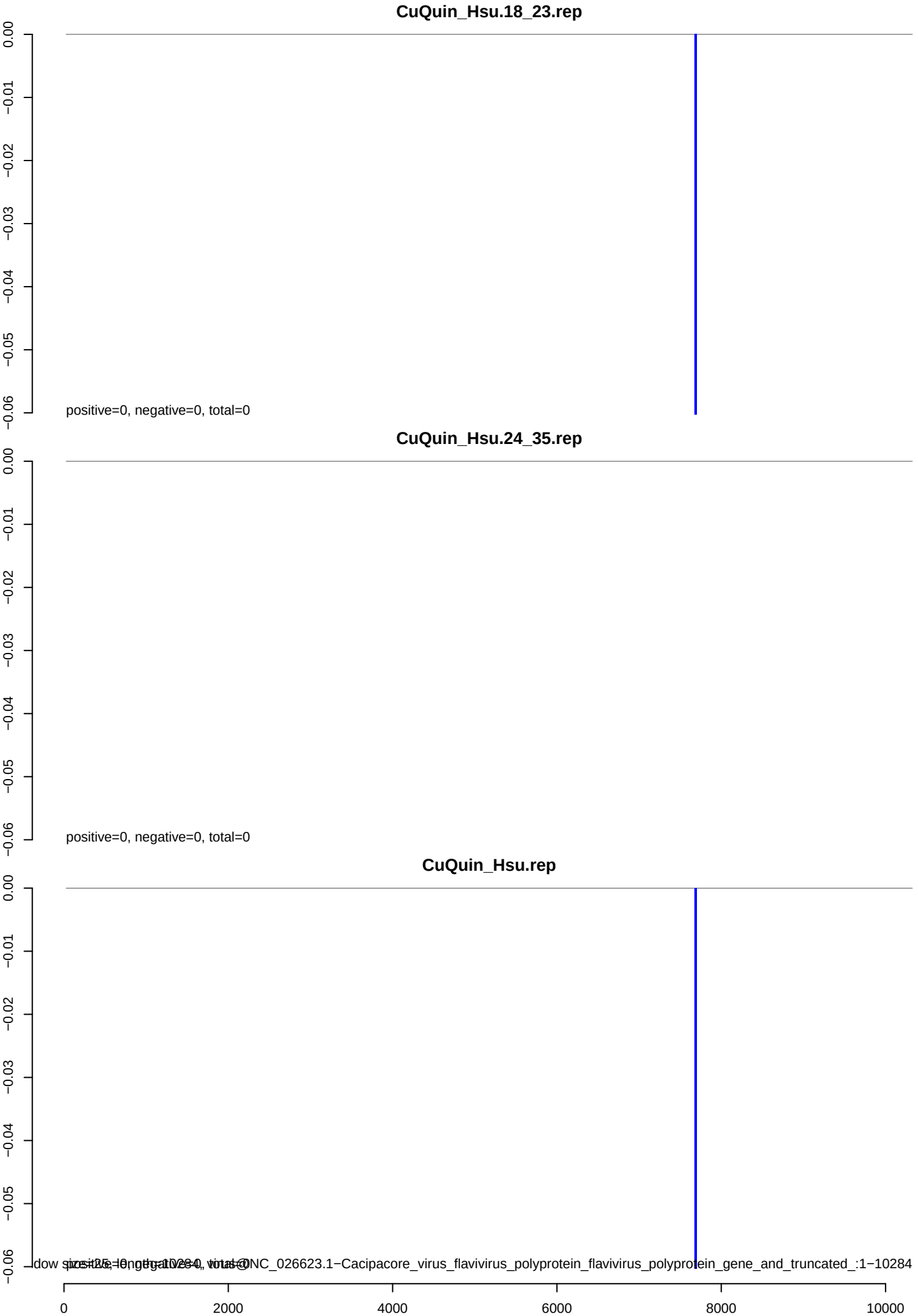

CuQuin_Hsu.18_23.rep
0.06
0.05
0.04
0.03
0.02
0.01
0.00
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
0.06
0.05
0.04
0.03
0.02
0.01
0.00
positive=0, negative=0, total=0
CuQuin_Hsu.rep
0.06
0.05
0.04
0.03
0.02
0.01
0.00
positive=0, negative=0, total=0
Window size=25, length=10864, virus@NC_030290.1−Culiseta_flavivirus_strain_502−13:1−10864
0
2000
4000
6000
8000
10000

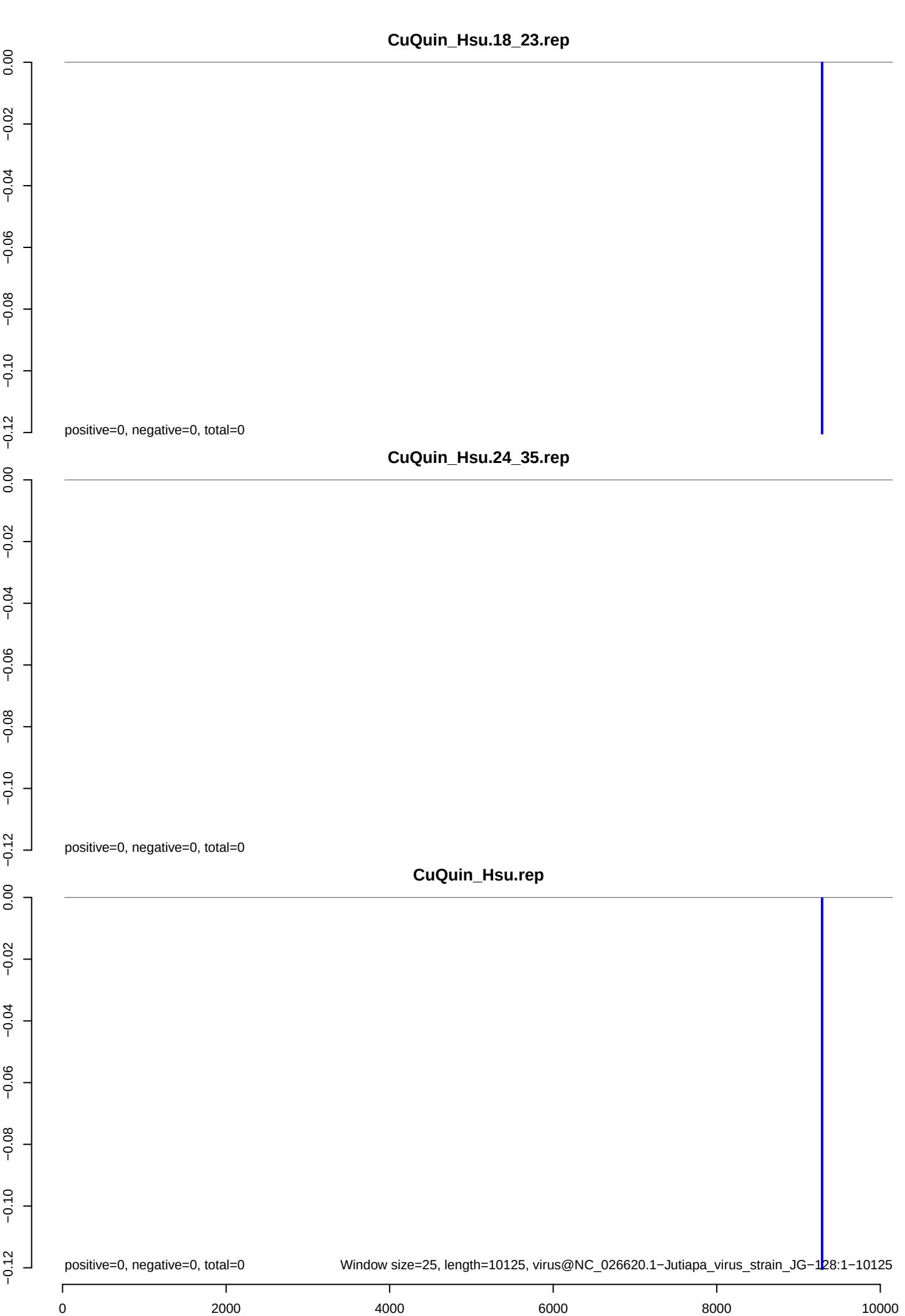

CuQuin_Hsu.18_23.rep
0.00
−0.01
−0.02
−0.03
−0.04
−0.05
−0.06
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
0.00
−0.01
−0.02
−0.03
−0.04
−0.05
−0.06
positive=0, negative=0, total=0
CuQuin_Hsu.rep
0.00
−0.01
−0.02
−0.03
−0.04
−0.05
−0.06
positive=0, negative=0, total=0
window size=25, length=10206, virus@NC_030289.1−Edge_Hill_virus_strain_YMP_48_polyprotein_gene:1−10206
0
2000
4000
6000
8000
10000

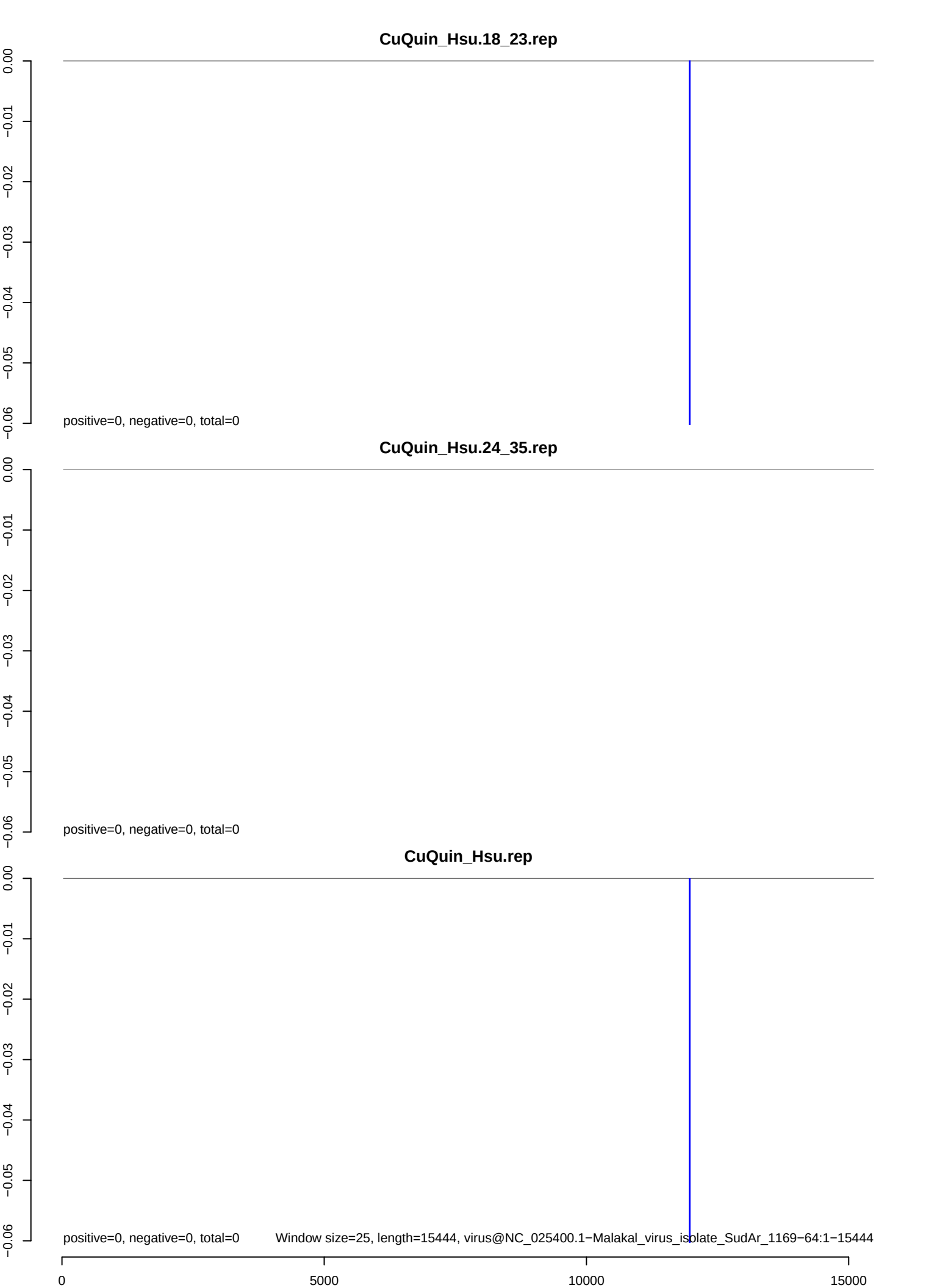

CuQuin_Hsu.18_23.rep
0.00
−0.05
−0.10
−0.15
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
0.00
−0.05
−0.10
−0.15
positive=0, negative=0, total=0
CuQuin_Hsu.rep
0.00
−0.05
−0.10
−0.15
positive=0, negative=0, total=0
Window size=25, length=14478, virus@NC_028241.1−Yata_virus_isolate_DakArB_2181:1−14478
0
5000
10000
15000

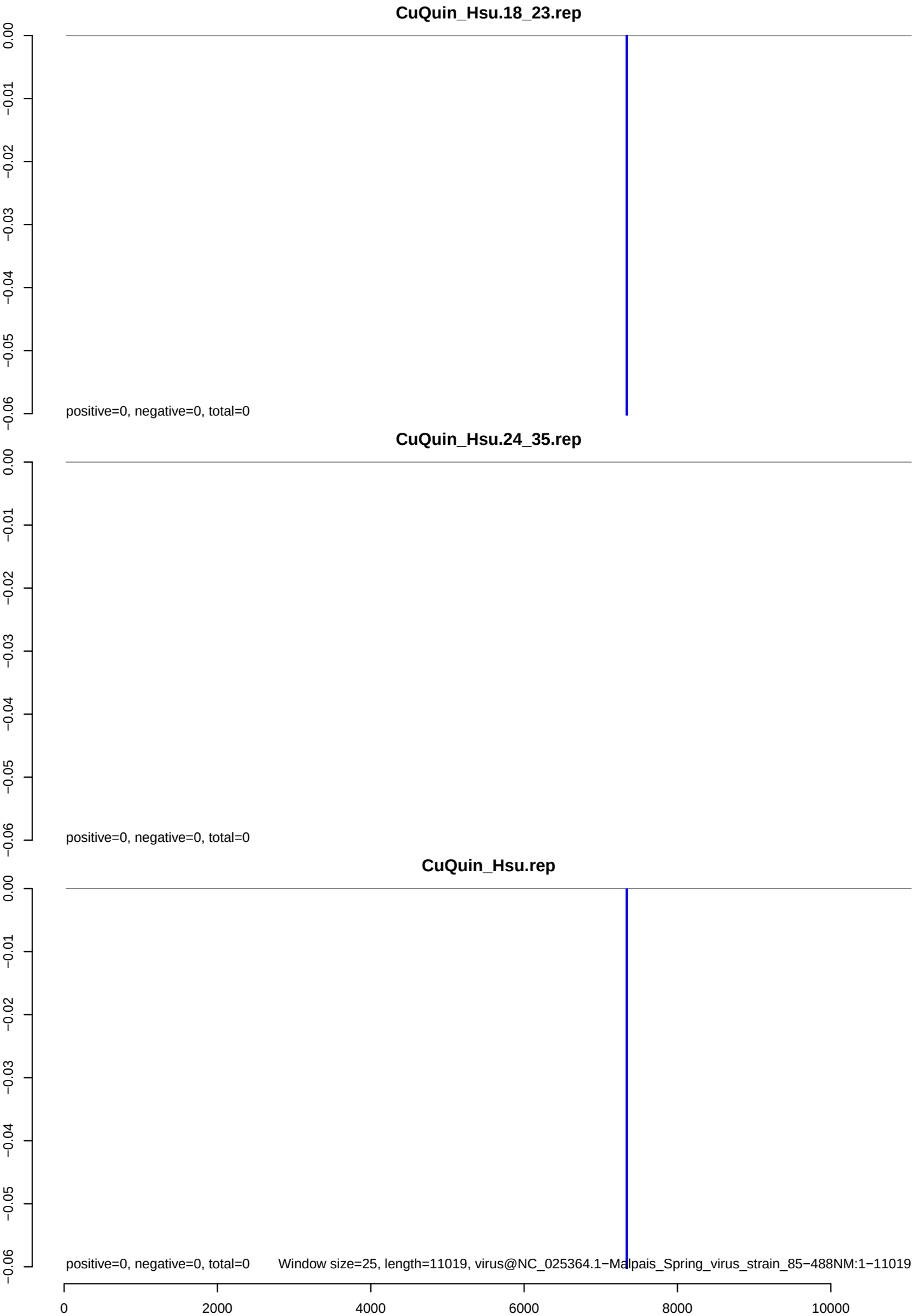

CuQuin_Hsu.18_23.rep
0.00
−0.01
−0.02
−0.03
−0.04
−0.05
−0.06
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
0.00
−0.01
−0.02
−0.03
−0.04
−0.05
−0.06
positive=0, negative=0, total=0
CuQuin_Hsu.rep
0.00
−0.01
−0.02
−0.03
−0.04
−0.05
−0.06
positive=0, negative=0, total=0
Window size=25, length=10938, virus@NC_027819.1−Mercadeo_virus_isolate_ER−M10:1−10938
0
2000
4000
6000
8000
10000

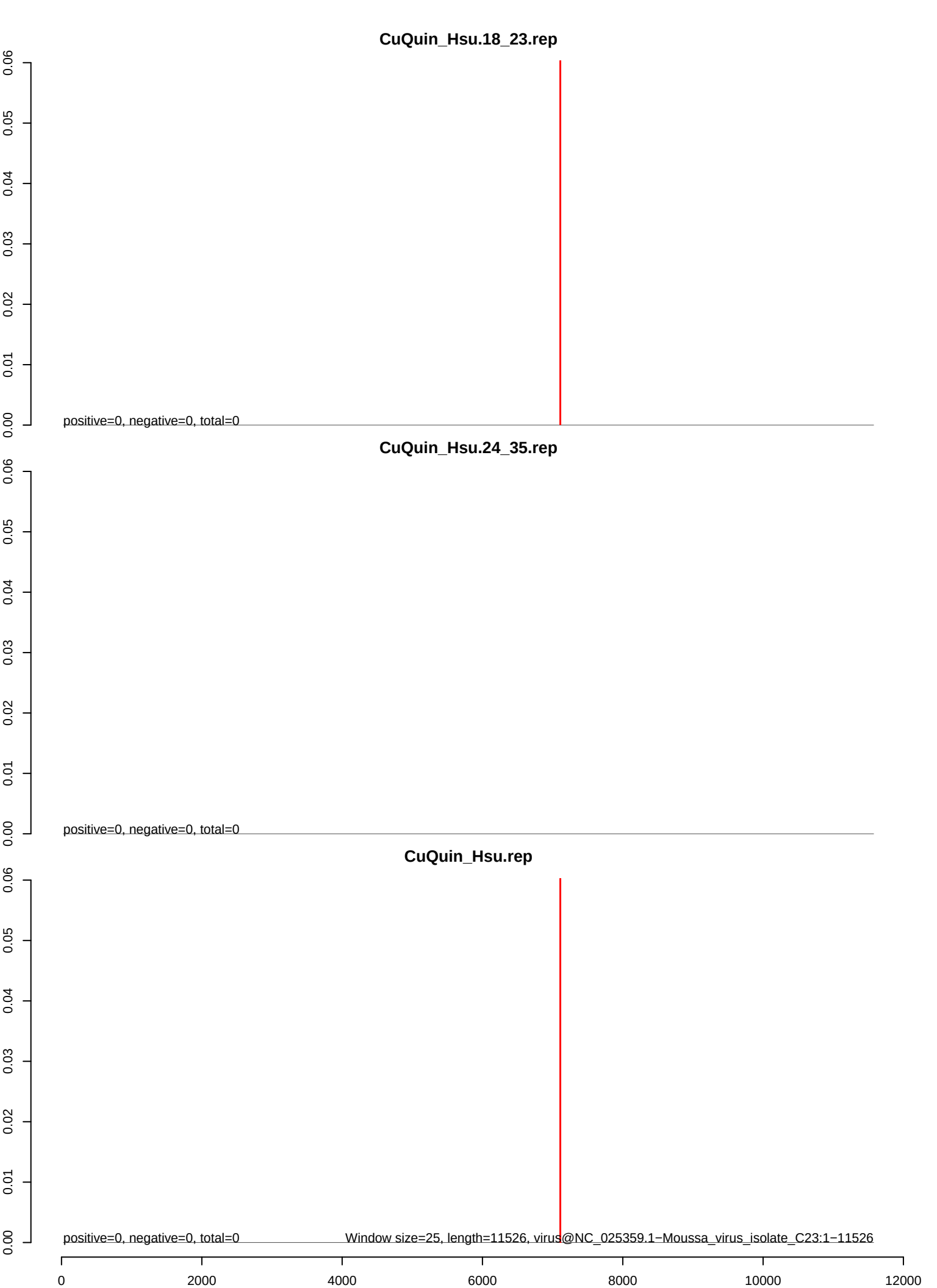

CuQuin_Hsu.18_23.rep
0.00
0.01
0.02
0.03
0.04
0.05
0.06
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
0.00
0.01
0.02
0.03
0.04
0.05
0.06
positive=0, negative=0, total=0
CuQuin_Hsu.rep
0.00
0.01
0.02
0.03
0.04
0.05
0.06
positive=0, negative=0, total=0Window size=25, length=10893, virus@NC_027817.1−Parramatta_River_virus_isolate_92−B115745:1−10893
0
2000
4000
6000
8000
10000

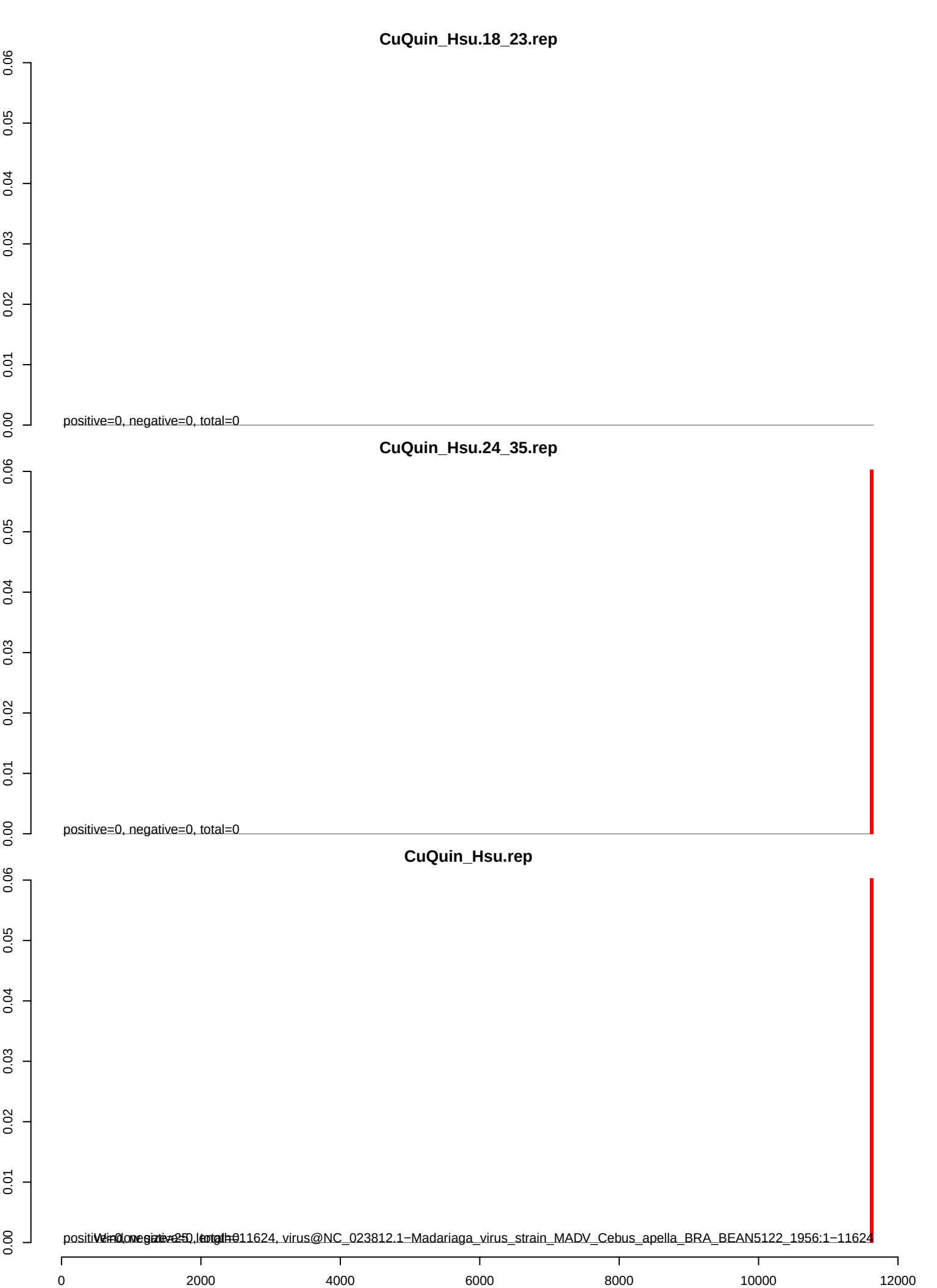

CuQuin_Hsu.18_23.rep
0.00
−0.01
−0.02
−0.03
−0.04
−0.05
−0.06
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
0.00
−0.01
−0.02
−0.03
−0.04
−0.05
−0.06
positive=0, negative=0, total=0
CuQuin_Hsu.rep
0.00
−0.01
−0.02
−0.03
−0.04
−0.05
−0.06
dow size=25, length=10284, total=
NC_026623.1−Cacipacore_virus_flavivirus_polyprotein_flavivirus_polyprotein_gene_and_truncated_:1−10284
0
2000
4000
6000
8000
10000

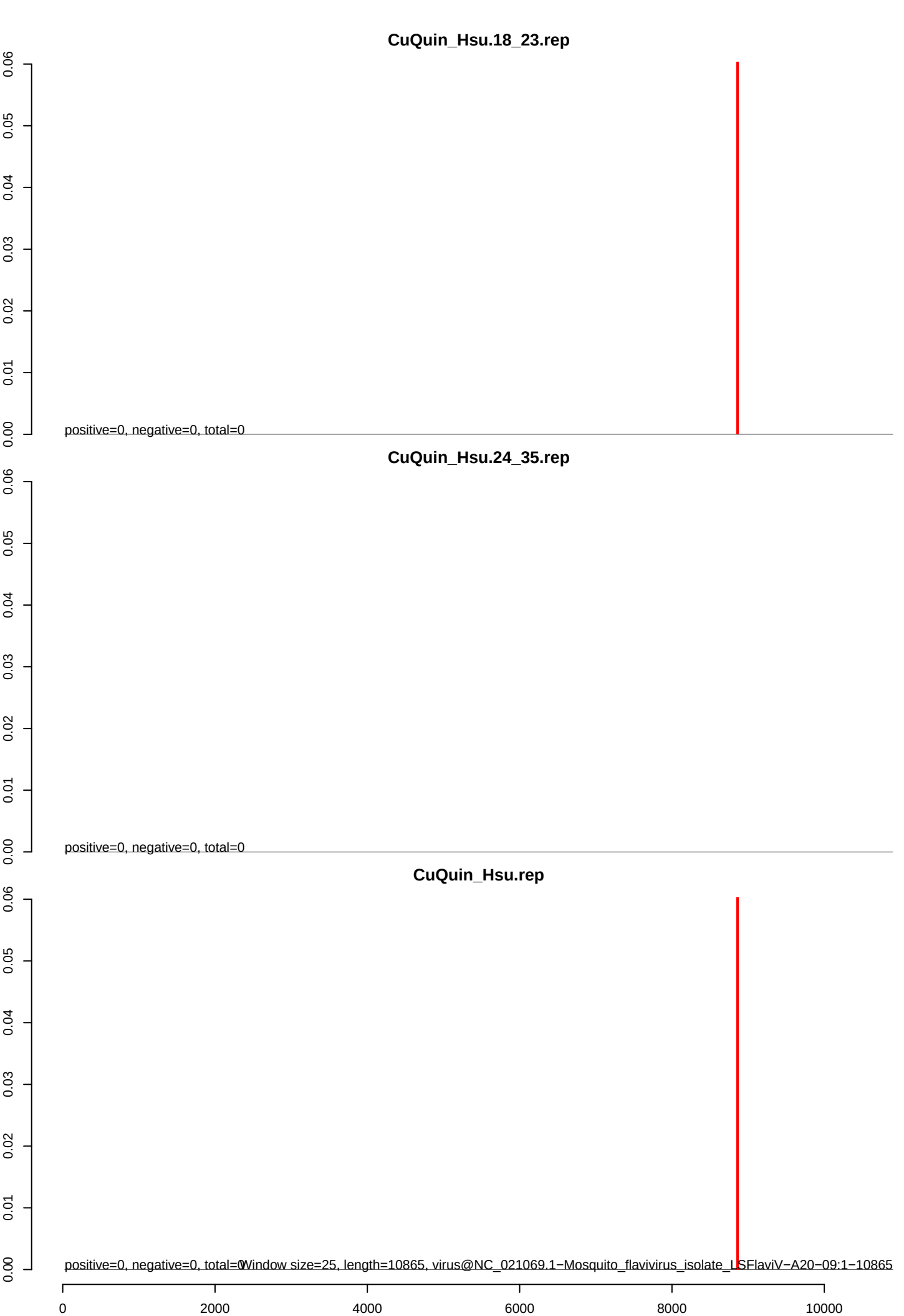

CuQuin_Hsu.18_23.rep
0.00
−0.02
−0.04
−0.06
−0.08
−0.10
−0.12
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
0.00
−0.02
−0.04
−0.06
−0.08
−0.10
−0.12
positive=0, negative=0, total=0
CuQuin_Hsu.rep
0.00
−0.02
−0.04
−0.06
−0.08
−0.10
−0.12
positive=0, negative=0, total=0
Window size=25, length=10125, virus@NC_026620.1−Jutiapa_virus_strain_JG−128:1−10125
0
2000
4000
6000
8000
10000

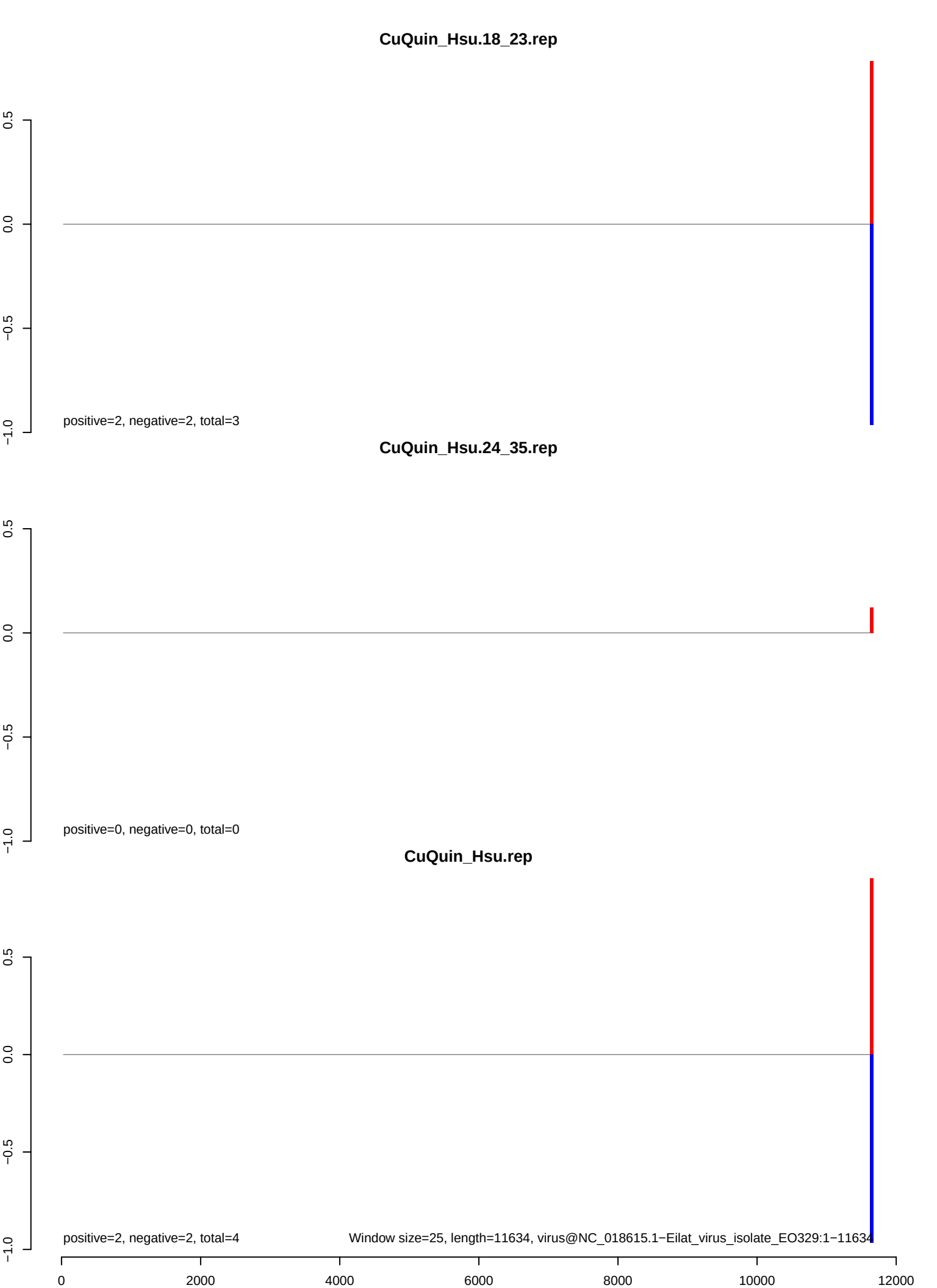

CuQuin_Hsu.18_23.rep
0.00
−0.01
−0.02
−0.03
−0.04
−0.05
−0.06
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
0.00
−0.01
−0.02
−0.03
−0.04
−0.05
−0.06
positive=0, negative=0, total=0
CuQuin_Hsu.rep
0.00
−0.01
−0.02
−0.03
−0.04
−0.05
−0.06
positive=0, negative=0, total=0
Window size=25, length=15444, virus@NC_025400.1−Malakal_virus_isolate_SudAr_1169−64:1−15444
0
5000
10000
15000

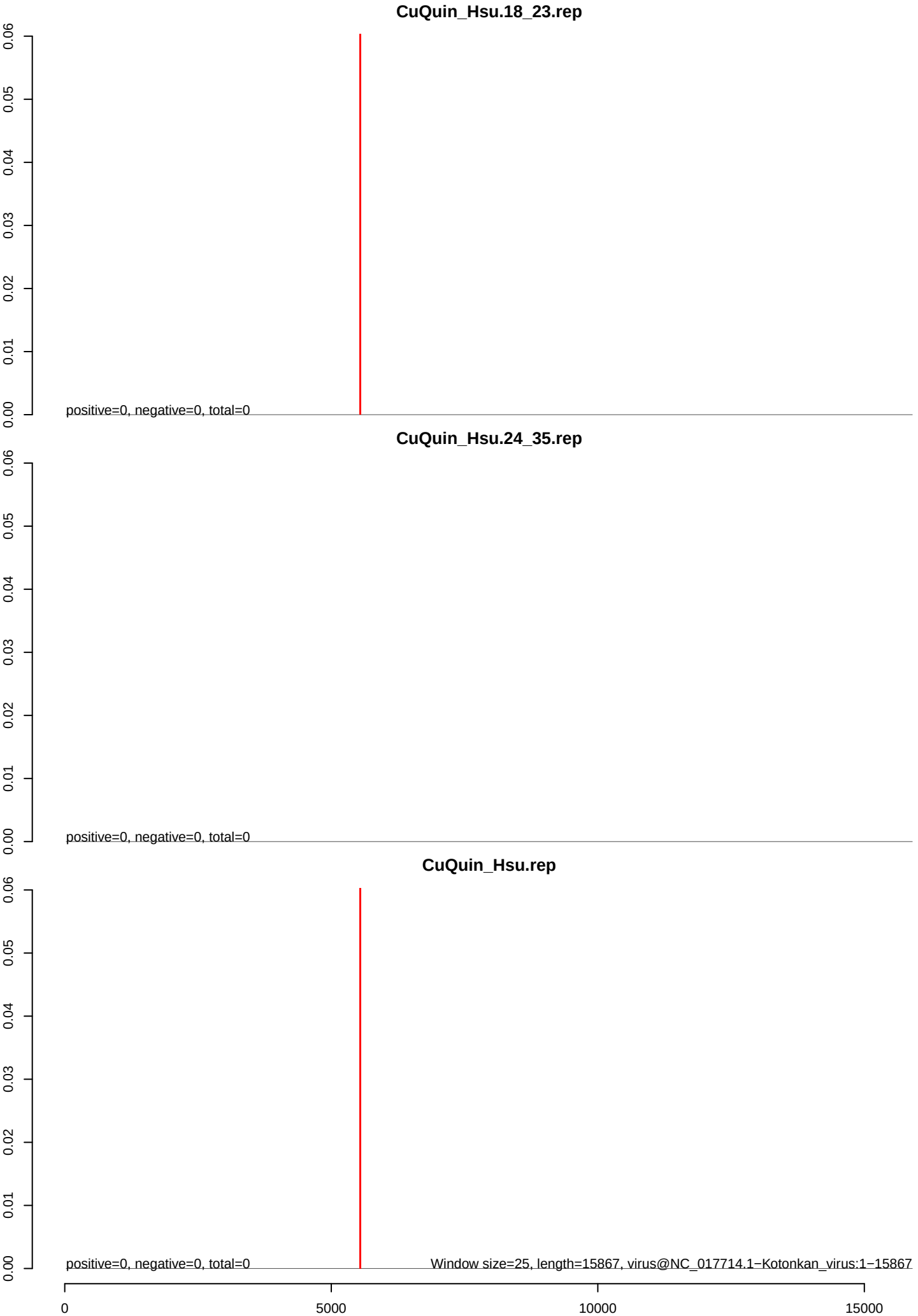

CuQuin_Hsu.18_23.rep
0.00
−0.01
−0.02
−0.03
−0.04
−0.05
−0.06
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
0.00
−0.01
−0.02
−0.03
−0.04
−0.05
−0.06
positive=0, negative=0, total=0
CuQuin_Hsu.rep
0.00
−0.01
−0.02
−0.03
−0.04
−0.05
−0.06
positive=0, negative=0, total=0
Window size=25, length=11019, virus@NC_025364.1−Malpais_Spring_virus_strain_85−488NM:1−11019
0
2000
4000
6000
8000
10000

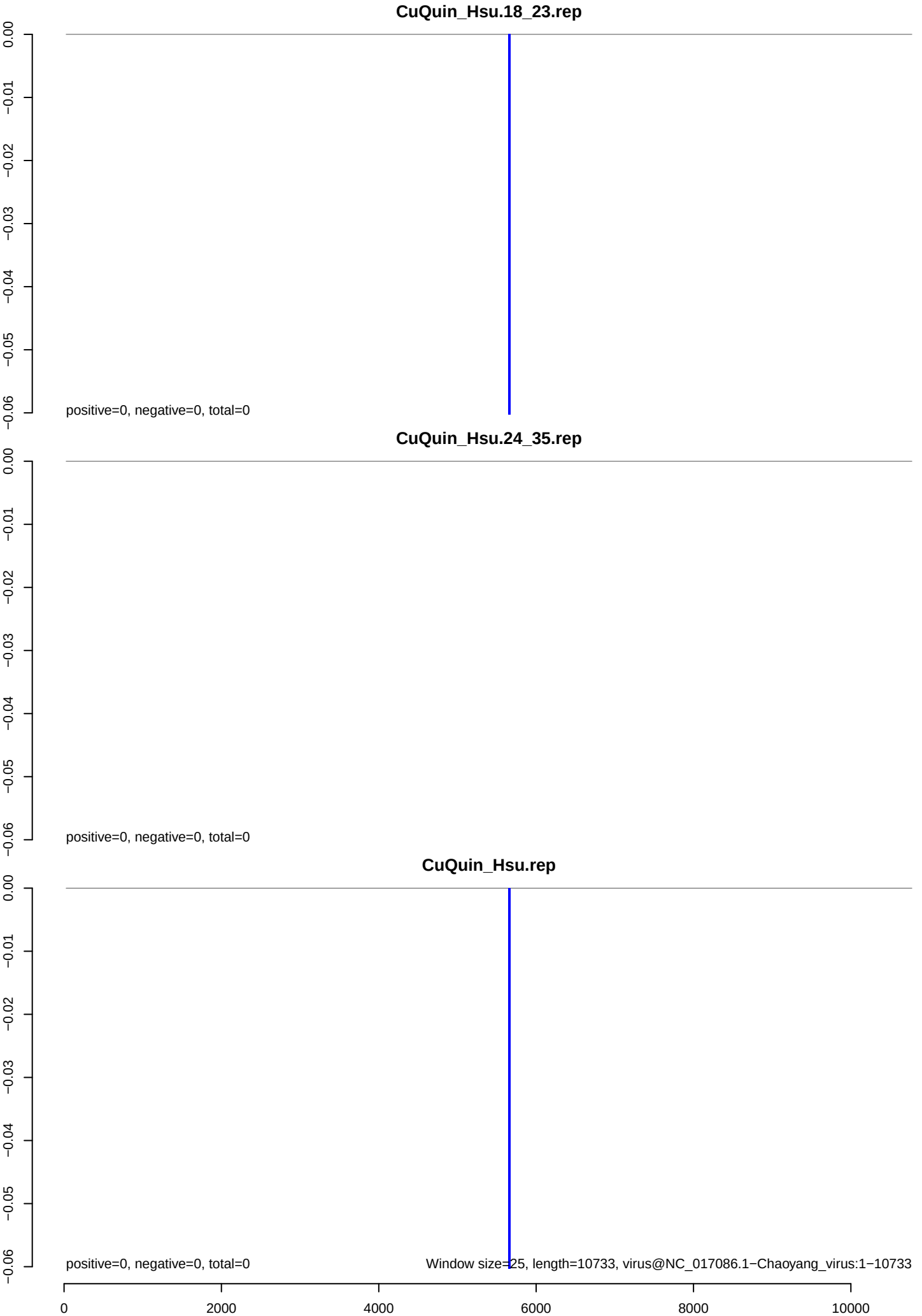

CuQuin_Hsu.18_23.rep
0.00
0.01
0.02
0.03
0.04
0.05
0.06
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
0.00
0.01
0.02
0.03
0.04
0.05
0.06
positive=0, negative=0, total=0
CuQuin_Hsu.rep
0.00
0.01
0.02
0.03
0.04
0.05
0.06
positive=0, negative=0, total=0
Window size=25, length=11526, virus@NC_025359.1−Moussa_virus_isolate_C23:1−11526
0
2000
4000
6000
8000
10000
12000

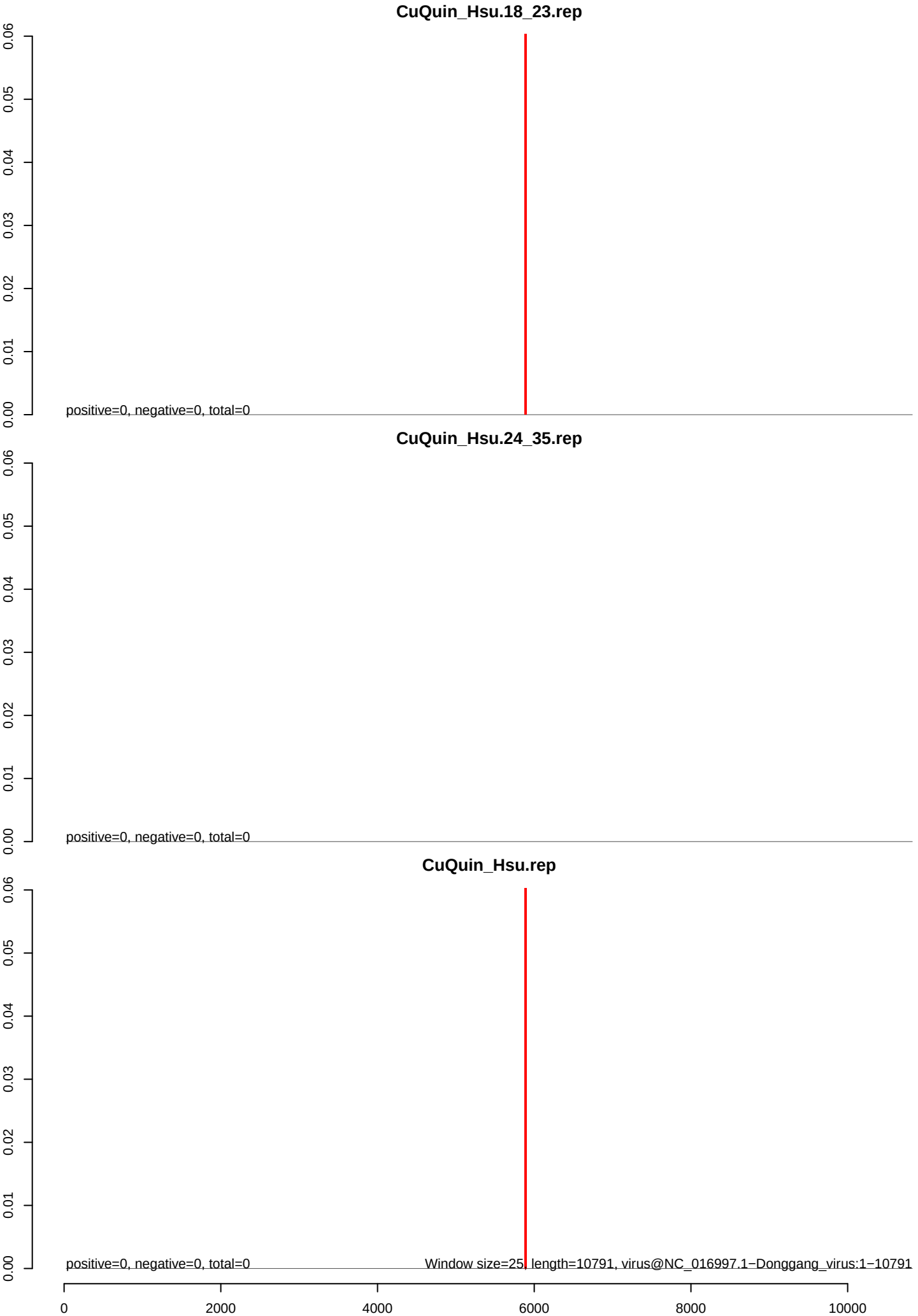

CuQuin_Hsu.18_23.rep
0.00
0.01
0.02
0.03
0.04
0.05
0.06
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
0.00
0.01
0.02
0.03
0.04
0.05
0.06
positive=0, negative=0, total=0
CuQuin_Hsu.rep
0.00
0.01
0.02
0.03
0.04
0.05
0.06
positive=0, negative=0, total=0
Virus:1-11624, virus@NC_023812.1−Madariaga_virus_strain_MADV_Cebus_apella_BRA_BEAN5122_1956:1−11624
0
2000
4000
6000
8000
10000
12000

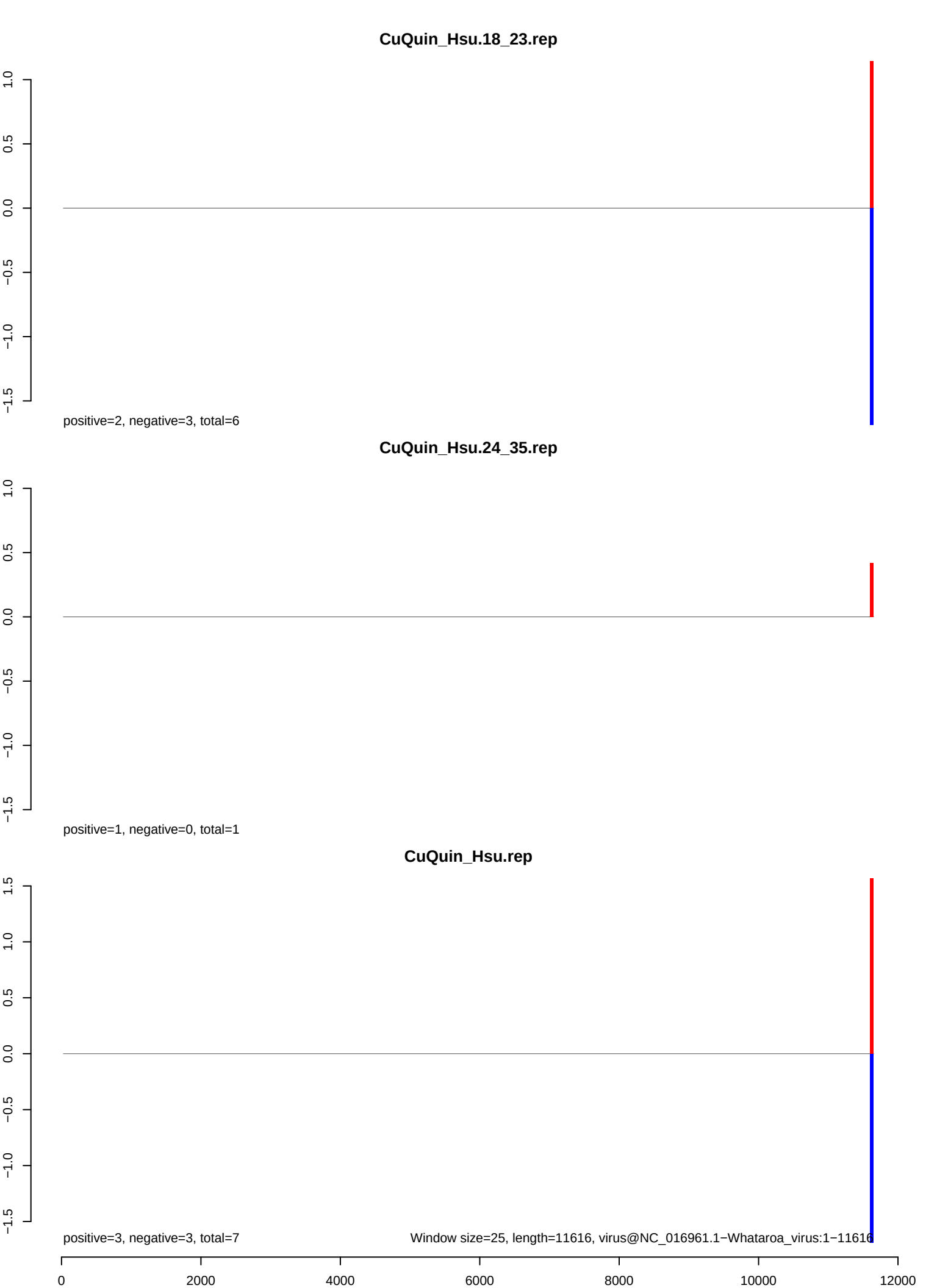

CuQuin_Hsu.18_23.rep
0.00
0.01
0.02
0.03
0.04
0.05
0.06
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
0.00
0.01
0.02
0.03
0.04
0.05
0.06
positive=0, negative=0, total=0
CuQuin_Hsu.rep
0.00
0.01
0.02
0.03
0.04
0.05
0.06
positive=0, negative=0, total=0
Window size=25, length=10865, virus@NC_021069.1−Mosquito_flavivirus_isolate_USFlaviV−A20−09:1−10865
0
2000
4000
6000
8000
10000

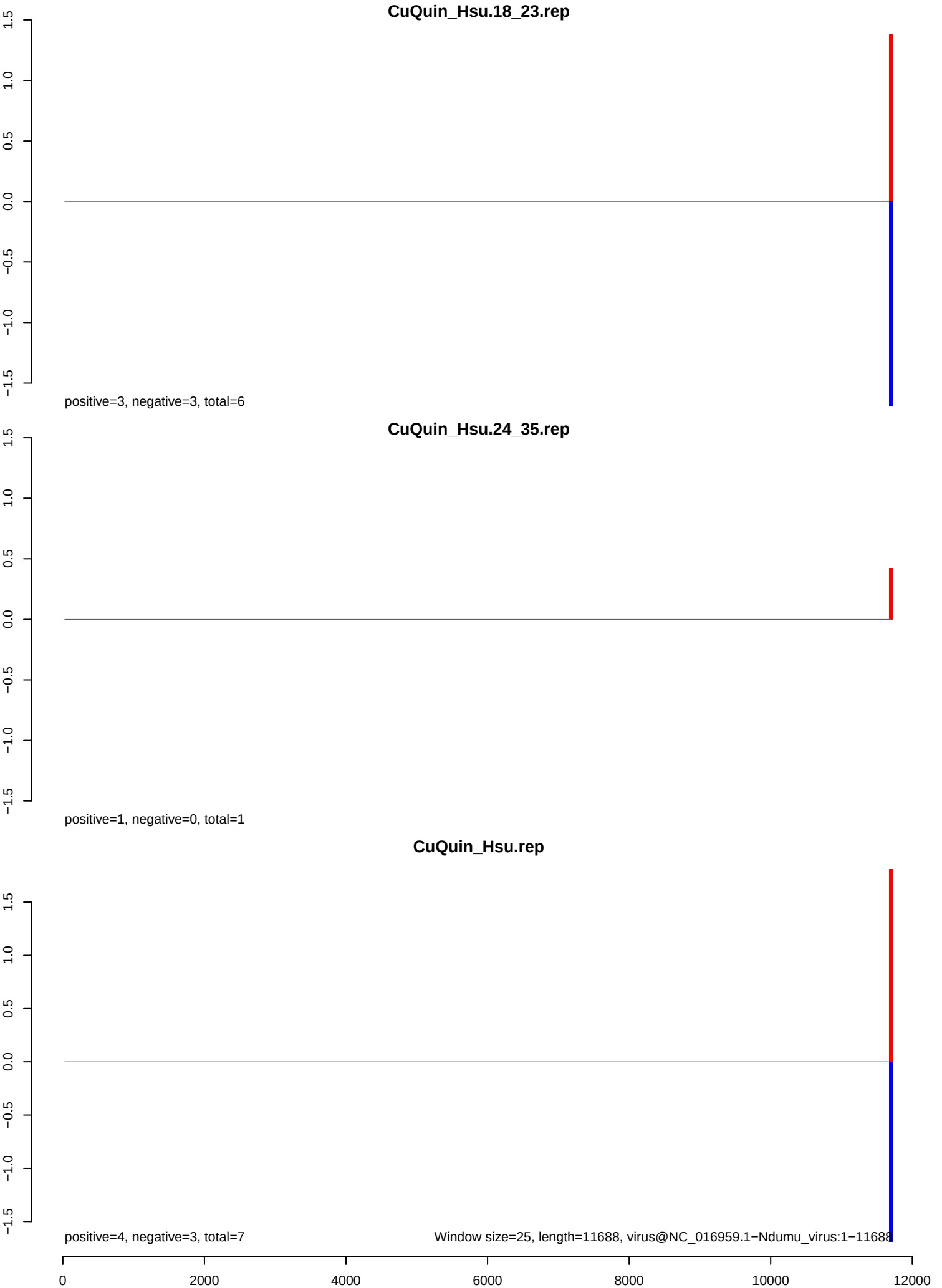

CuQuin_Hsu.18_23.rep
0.5
0.0
−0.5
−1.0
positive=2, negative=2, total=3
CuQuin_Hsu.24_35.rep
0.5
0.0
−0.5
−1.0
positive=0, negative=0, total=0
CuQuin_Hsu.rep
0.5
0.0
−0.5
−1.0
positive=2, negative=2, total=4
Window size=25, length=11634, virus@NC_018615.1−Eilat_virus_isolate_EO329:1−11634
0
2000
4000
6000
8000
10000
12000

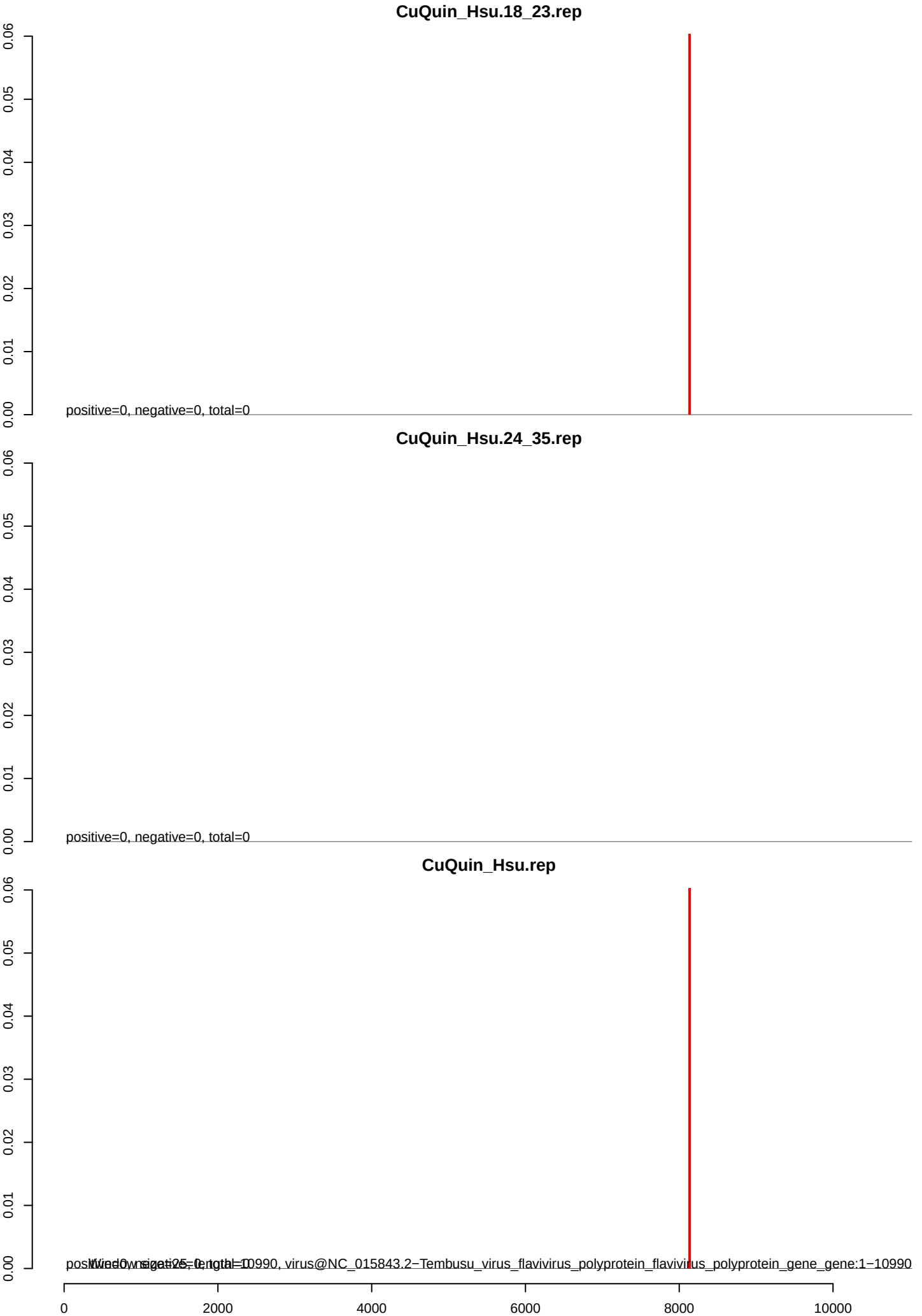

CuQuin_Hsu.18_23.rep
0.06
0.05
0.04
0.03
0.02
0.01
0.00
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
0.06
0.05
0.04
0.03
0.02
0.01
0.00
positive=0, negative=0, total=0
CuQuin_Hsu.rep
0.06
0.05
0.04
0.03
0.02
0.01
0.00
positive=0, negative=0, total=0
Window size=25, length=15867, virus@NC_017714.1−Kotonkan_virus:1−15867
0
5000
10000
15000

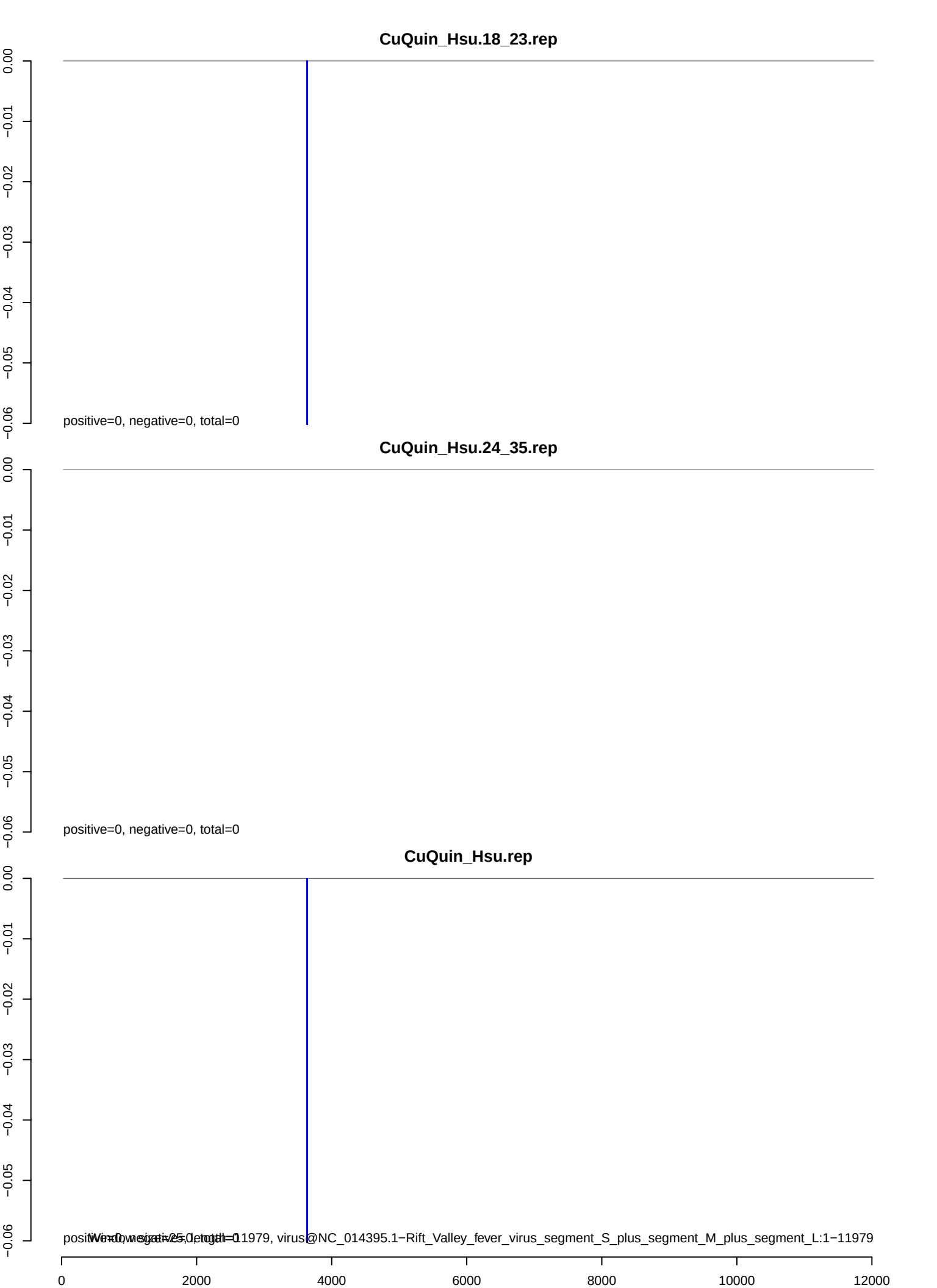

CuQuin_Hsu.18_23.rep
0.00
−0.01
−0.02
−0.03
−0.04
−0.05
−0.06
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
0.00
−0.01
−0.02
−0.03
−0.04
−0.05
−0.06
positive=0, negative=0, total=0
CuQuin_Hsu.rep
0.00
−0.01
−0.02
−0.03
−0.04
−0.05
−0.06
positive=0, negative=0, total=0
Window size=25, length=10733, virus@NC_017086.1−Chaoyang_virus:1−10733
0
2000
4000
6000
8000
10000

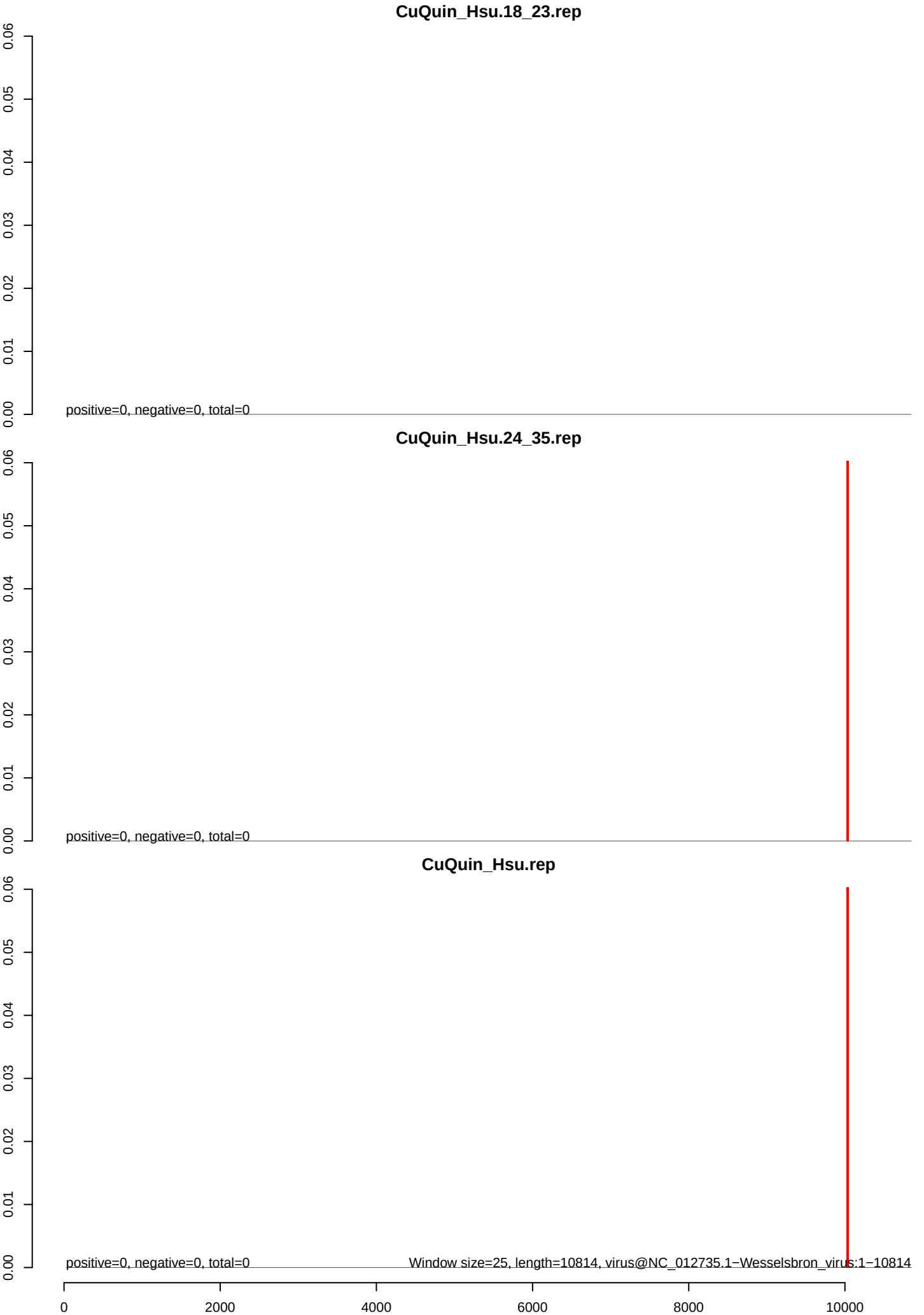

CuQuin_Hsu.18_23.rep
0.00
0.01
0.02
0.03
0.04
0.05
0.06
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
0.00
0.01
0.02
0.03
0.04
0.05
0.06
positive=0, negative=0, total=0
CuQuin_Hsu.rep
0.00
0.01
0.02
0.03
0.04
0.05
0.06
positive=0, negative=0, total=0
Window size=25, length=10791, virus@NC_016997.1−Donggang_virus:1−10791
0
2000
4000
6000
8000
10000

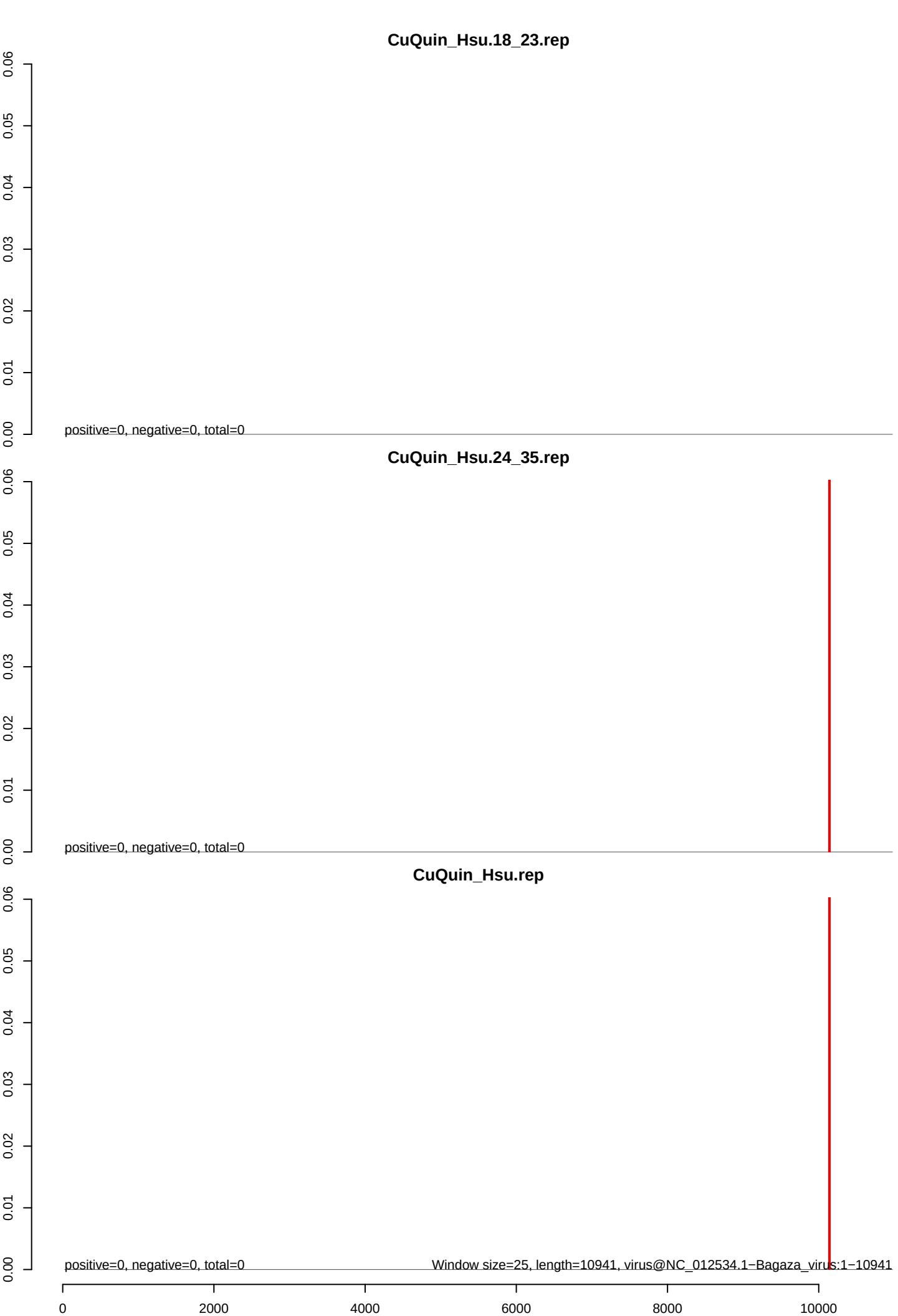

CuQuin_Hsu.18_23.rep
1.0
0.5
0.0
−0.5
−1.0
−1.5
positive=2, negative=3, total=6
CuQuin_Hsu.24_35.rep
1.0
0.5
0.0
−0.5
−1.0
−1.5
positive=1, negative=0, total=1
CuQuin_Hsu.rep
1.5
1.0
0.5
0.0
−0.5
−1.0
−1.5
positive=3, negative=3, total=7
Window size=25, length=11616, virus@NC_016961.1−Whataroa_virus:1−11616
0
2000
4000
6000
8000
10000
12000

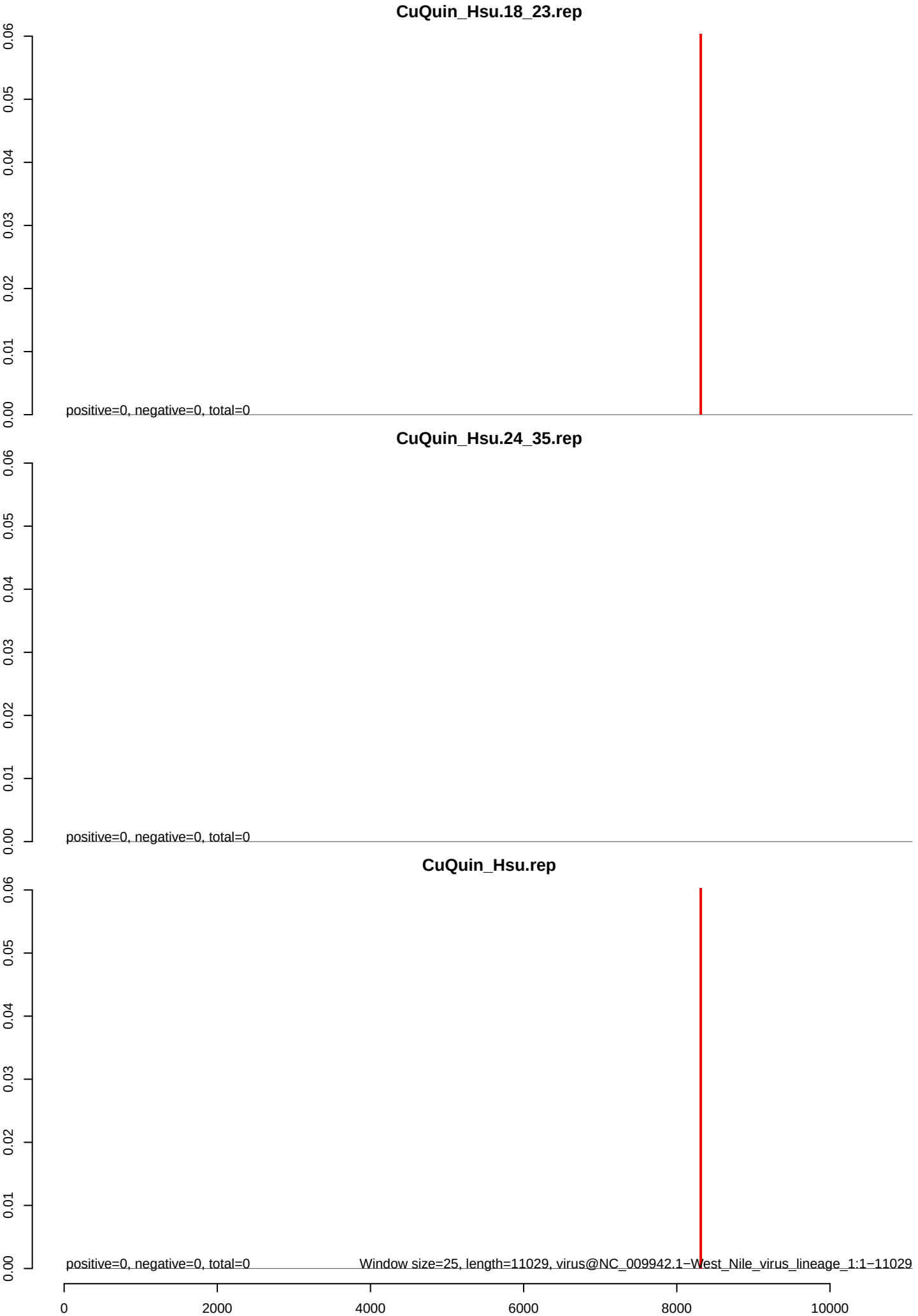

CuQuin_Hsu.18_23.rep
1.5
1.0
0.5
0.0
−0.5
−1.0
−1.5
positive=3, negative=3, total=6
CuQuin_Hsu.24_35.rep
1.5
1.0
0.5
0.0
−0.5
−1.0
−1.5
positive=1, negative=0, total=1
CuQuin_Hsu.rep
1.5
1.0
0.5
0.0
−0.5
−1.0
−1.5
positive=4, negative=3, total=7
Window size=25, length=11688, virus@NC_016959.1−Ndumu_virus:1−11688
0
2000
4000
6000
8000
10000
12000


CuQuin_Hsu.18_23.rep
0.06
0.05
0.04
0.03
0.02
0.01
0.00
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
0.06
0.05
0.04
0.03
0.02
0.01
0.00
positive=0, negative=0, total=0
CuQuin_Hsu.rep
0.06
0.05
0.04
0.03
0.02
0.01
0.00
positive=0, negative=25, total=10990, virus@NC_015843.2−Tembusu_virus_flavivirus_polyprotein_flavivirus_polyprotein_gene_gene:1−10990
Window size=25, total=10990, virus@NC_015843.2−Tembusu_virus_flavivirus_polyprotein_flavivirus_polyprotein_gene_gene:1−10990
0
2000
4000
6000
8000
10000


CuQuin_Hsu.18_23.rep
0.00
−0.01
−0.02
−0.03
−0.04
−0.05
−0.06
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
0.00
−0.01
−0.02
−0.03
−0.04
−0.05
−0.06
positive=0, negative=0, total=0
CuQuin_Hsu.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=11979, virus@NC_014395.1−Rift_Valley_fever_virus_segment_S_plus_segment_M_plus_segment_L:1−11979
0
2000
4000
6000
8000
10000
12000


CuQuin_Hsu.18_23.rep
0.06
0.05
0.04
0.03
0.02
0.01
0.00
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
0.06
0.05
0.04
0.03
0.02
0.01
0.00
positive=0, negative=0, total=0
CuQuin_Hsu.rep
0.06
0.05
0.04
0.03
0.02
0.01
0.00
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


CuQuin_Hsu.18_23.rep
0.00
0.01
0.02
0.03
0.04
0.05
0.06
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
0.00
0.01
0.02
0.03
0.04
0.05
0.06
positive=0, negative=0, total=0
CuQuin_Hsu.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=10941, virus@NC_012534.1−Bagaza_virus:1−10941
0
2000
4000
6000
8000
10000


CuQuin_Hsu.18_23.rep
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0.02
0.03
0.04
0.05
0.06
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
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0.01
0.02
0.03
0.04
0.05
0.06
positive=0, negative=0, total=0
CuQuin_Hsu.rep
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0.03
0.04
0.05
0.06
positive=0, negative=0, total=0
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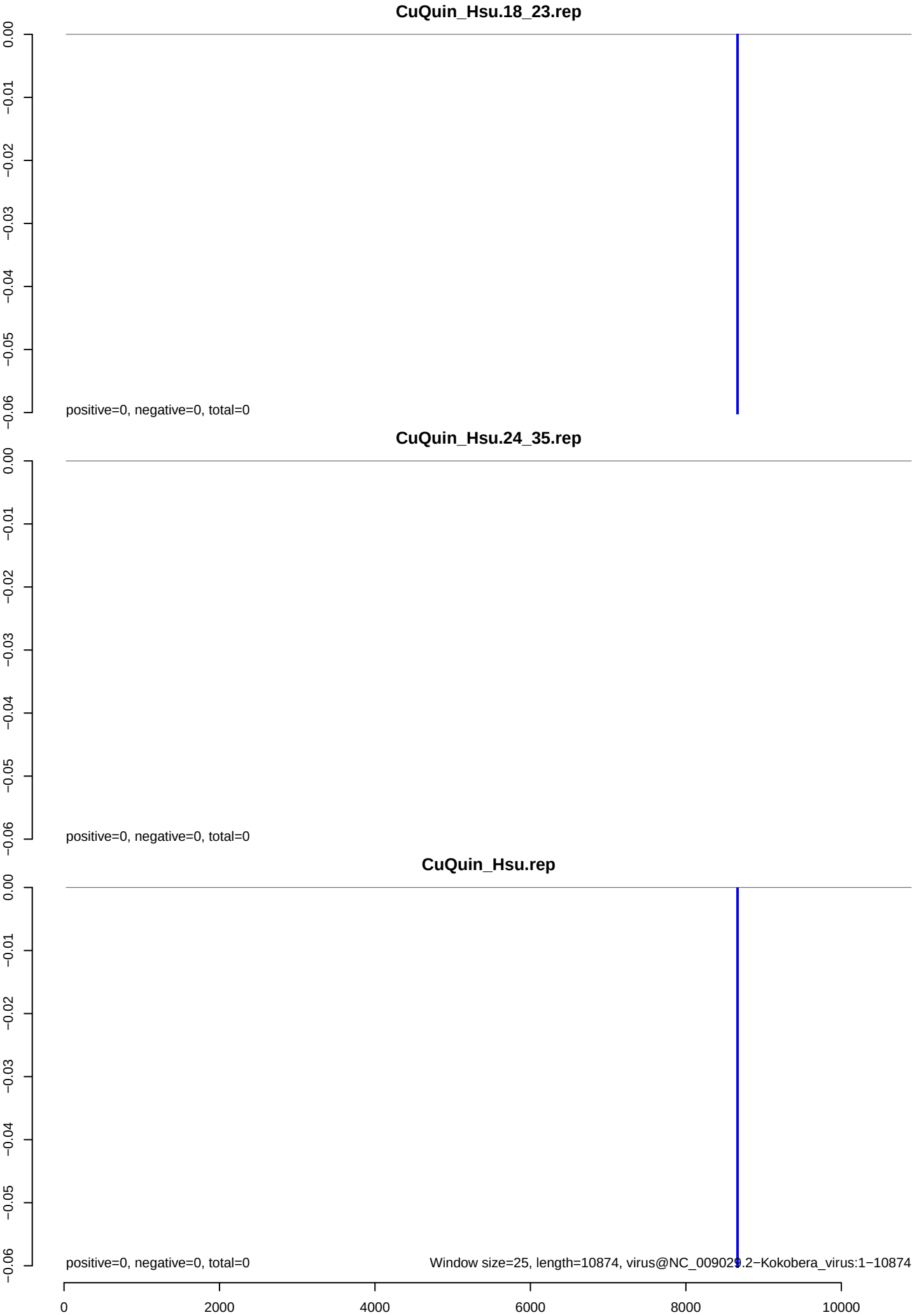
6000
8000
10000


CuQuin_Hsu.18_23.rep
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−0.06
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
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−0.01
−0.02
−0.03
−0.04
−0.05
−0.06
positive=0, negative=0, total=0
CuQuin_Hsu.rep
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−0.03
−0.04
−0.05
−0.06
positive=0, negative=0, total=0
Window size=25, length=10874, virus@NC_009029.2−Kokobera_virus:1−10874
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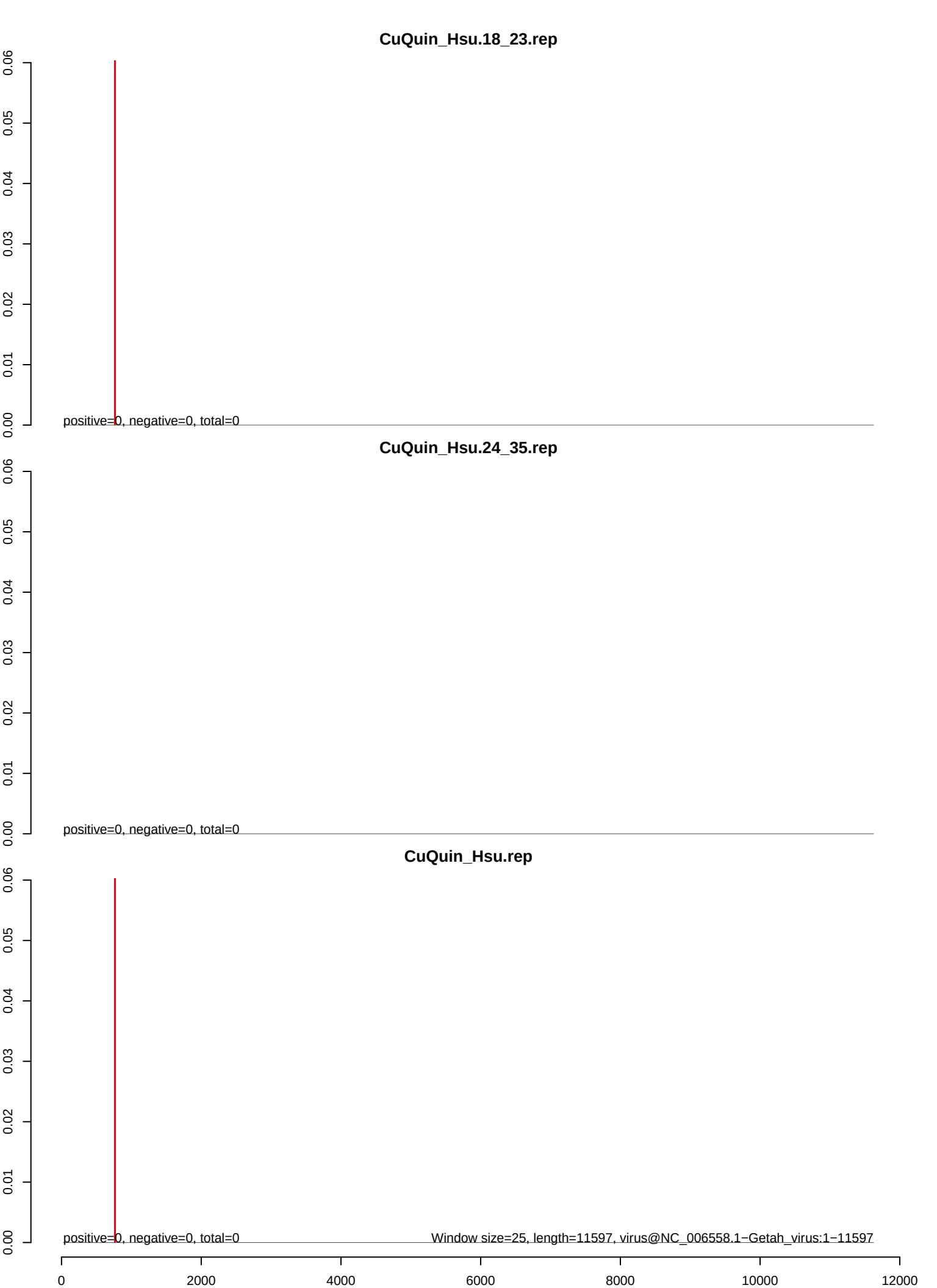
8000
10000


CuQuin_Hsu.18_23.rep
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0.06
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
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0.01
0.02
0.03
0.04
0.05
0.06
positive=0, negative=0, total=0
CuQuin_Hsu.rep
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0.01
0.02
0.03
0.04
0.05
0.06
positive=0, negative=0, total=0
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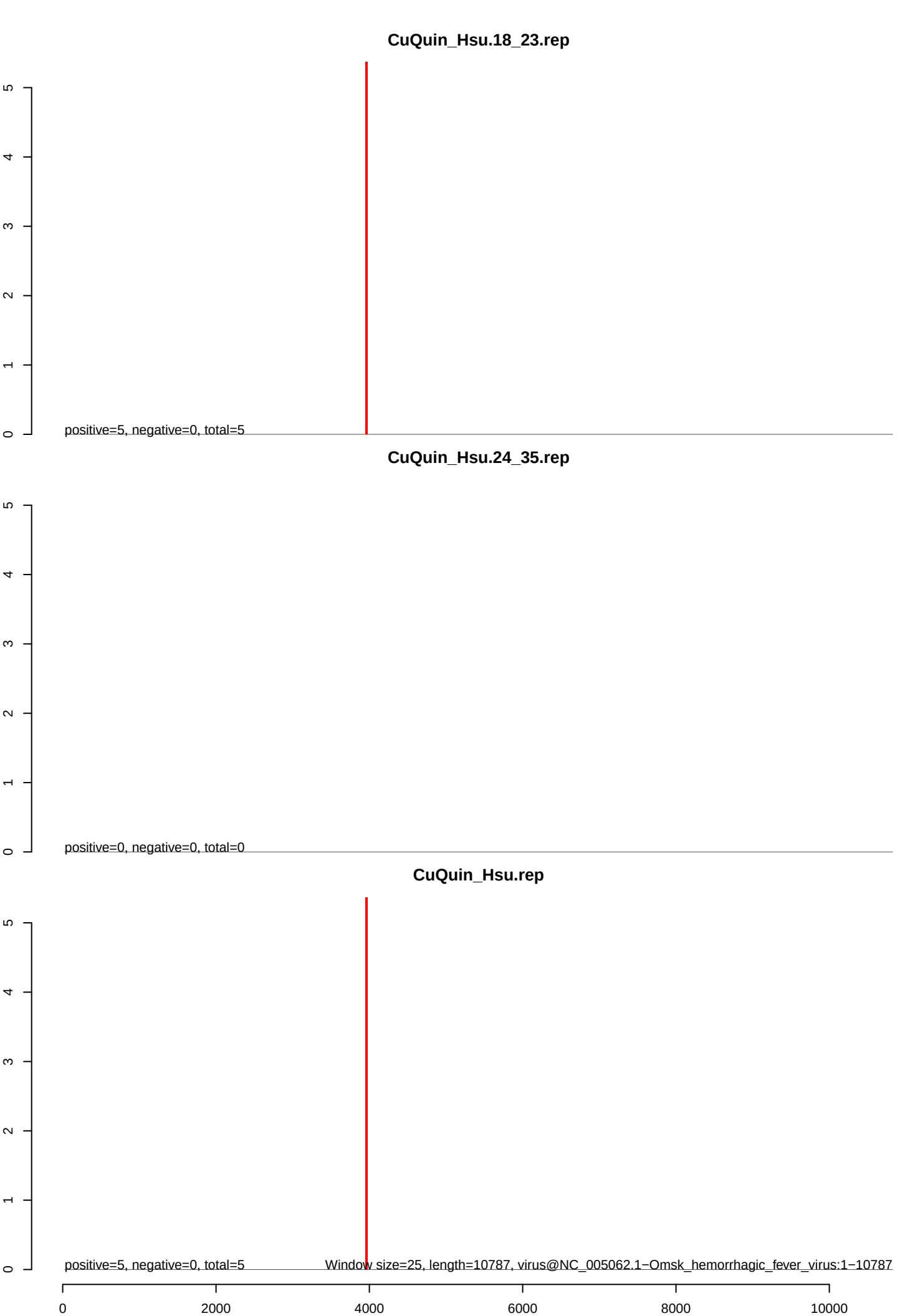
6000
8000
10000
12000


CuQuin_Hsu.18_23.rep
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1
2
3
4
5
positive=5, negative=0, total=5
CuQuin_Hsu.24_35.rep
0
1
2
3
4
5
positive=0, negative=0, total=0
CuQuin_Hsu.rep
0
1
2
3
4
5
positive=5, negative=0, total=5
Window size=25, length=10787, virus@NC_005062.1−Omsk_hemorrhagic_fever_virus:1−10787
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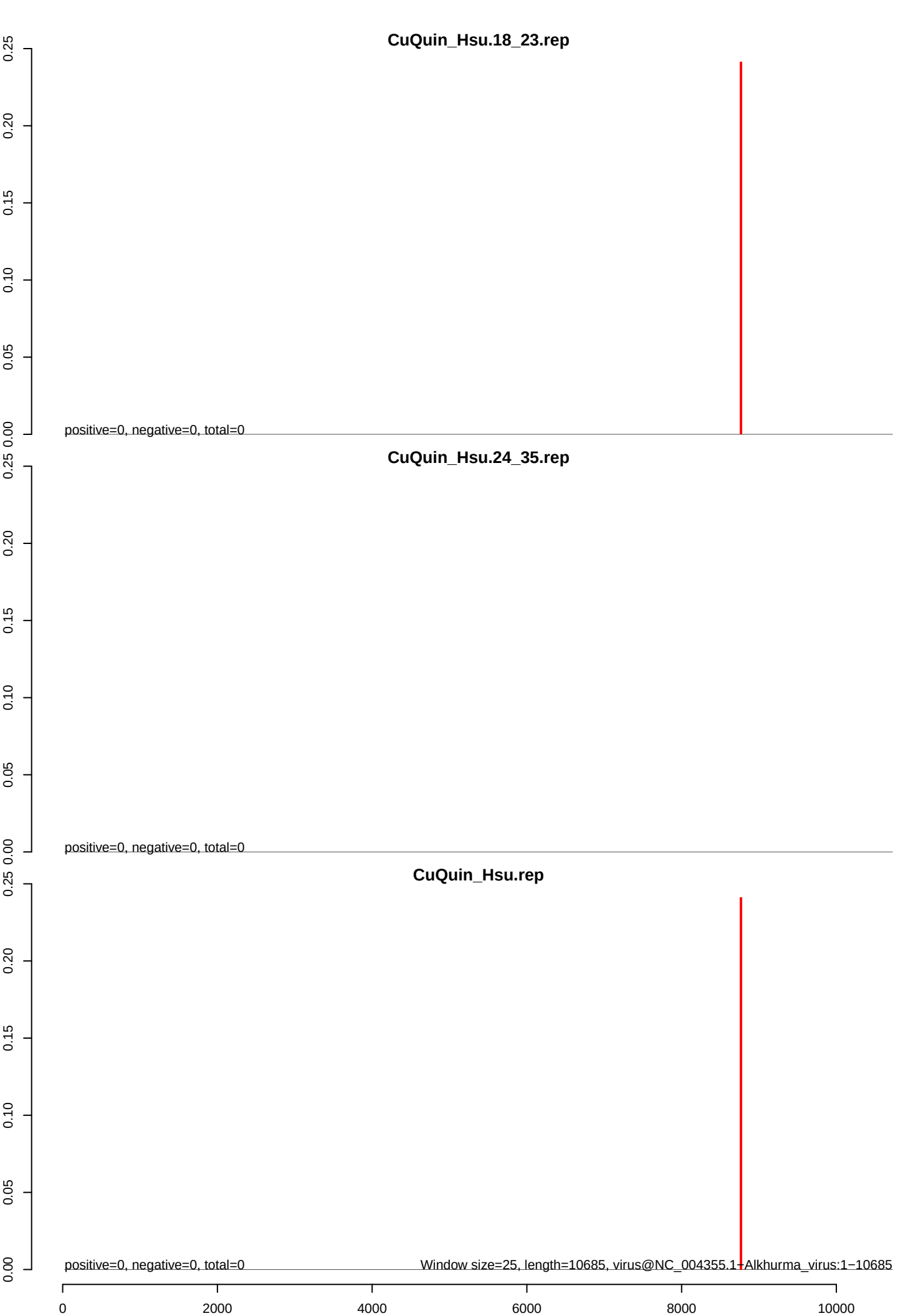
4000
6000
8000
10000


CuQuin_Hsu.18_23.rep
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0.15
0.10
0.05
0.00
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
0.25
0.20
0.15
0.10
0.05
0.00
positive=0, negative=0, total=0
CuQuin_Hsu.rep
0.25
0.20
0.15
0.10
0.05
0.00
positive=0, negative=0, total=0
Window size=25, length=10685, virus@NC_004355.1+Alkhurma_virus:1−10685
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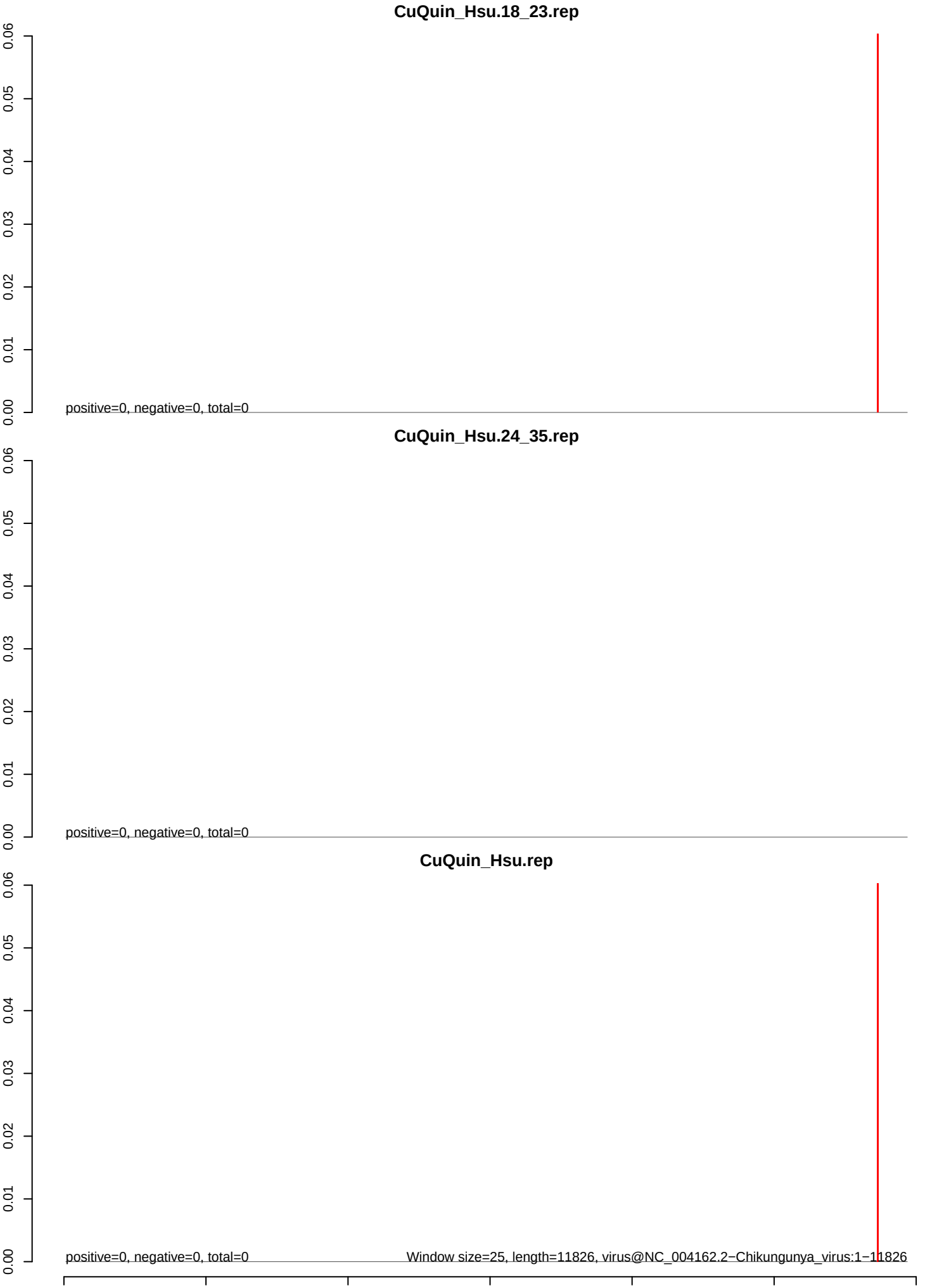
4000
6000
8000
10000


CuQuin_Hsu.18_23.rep
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0.01
0.02
0.03
0.04
0.05
0.06
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
0.00
0.01
0.02
0.03
0.04
0.05
0.06
positive=0, negative=0, total=0
CuQuin_Hsu.rep
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0.01
0.02
0.03
0.04
0.05
0.06
positive=0, negative=0, total=0
Window size=25, length=11826, virus@NC_004162.2−Chikungunya_virus:1−11826
0
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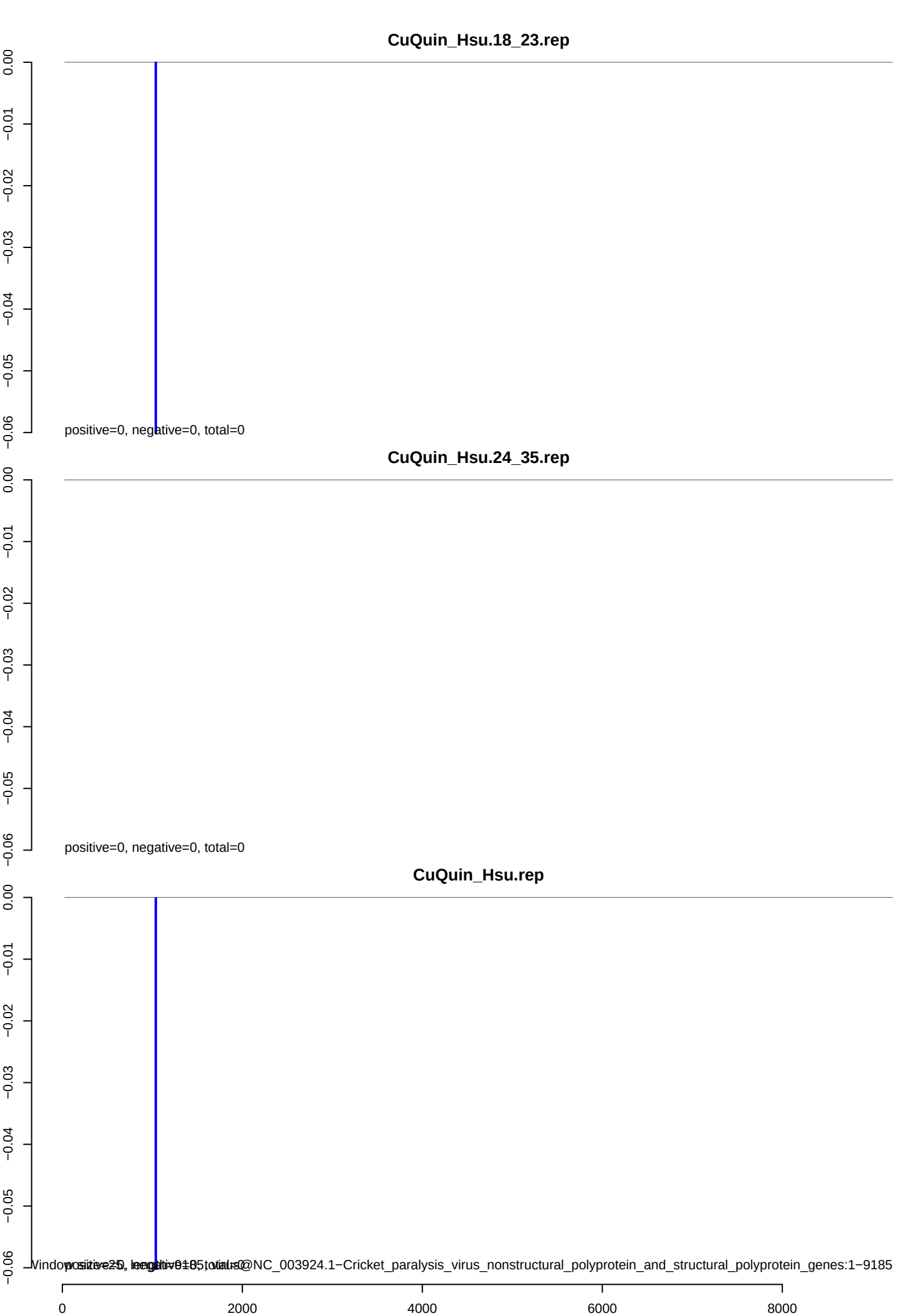
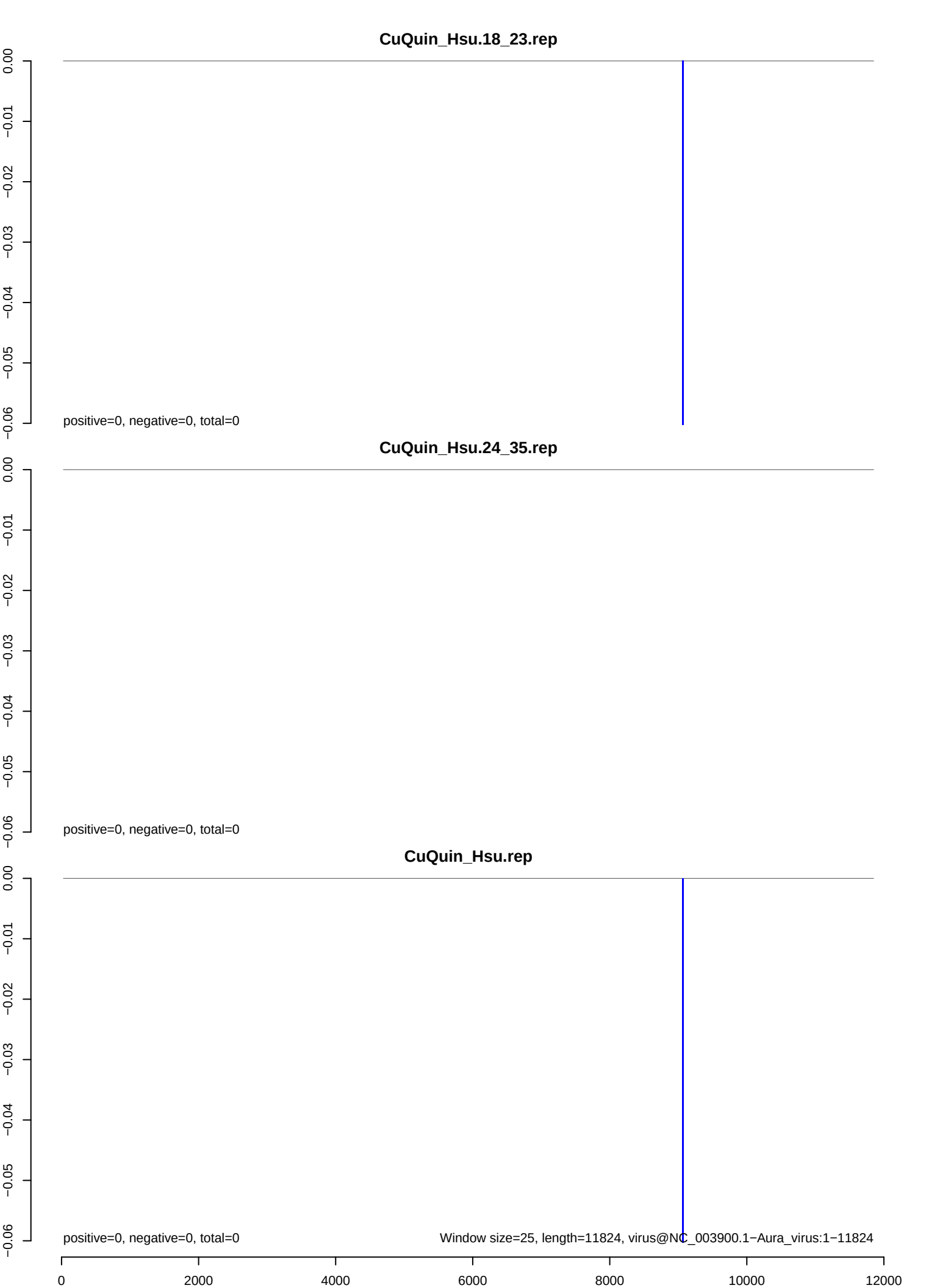
4000
6000
8000
10000
12000


CuQuin_Hsu.18_23.rep
0.00
−0.01
−0.02
−0.03
−0.04
−0.05
−0.06
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
0.00
−0.01
−0.02
−0.03
−0.04
−0.05
−0.06
positive=0, negative=0, total=0
CuQuin_Hsu.rep
0.00
−0.01
−0.02
−0.03
−0.04
−0.05
−0.06
Vindow
positive=0, negative=0, total=0@NC_003924.1−Cricket_paralysis_virus_nonstructural_polyprotein_and_structural_polyprotein_genes:1−9185
0
2000
4000
6000
8000


CuQuin_Hsu.18_23.rep
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−0.01
−0.02
−0.03
−0.04
−0.05
−0.06
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
0.00
−0.01
−0.02
−0.03
−0.04
−0.05
−0.06
positive=0, negative=0, total=0
CuQuin_Hsu.rep
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−0.01
−0.02
−0.03
−0.04
−0.05
−0.06
positive=0, negative=0, total=0
Window size=25, length=11824, virus@NC_003900.1−Aura_virus:1−11824
0
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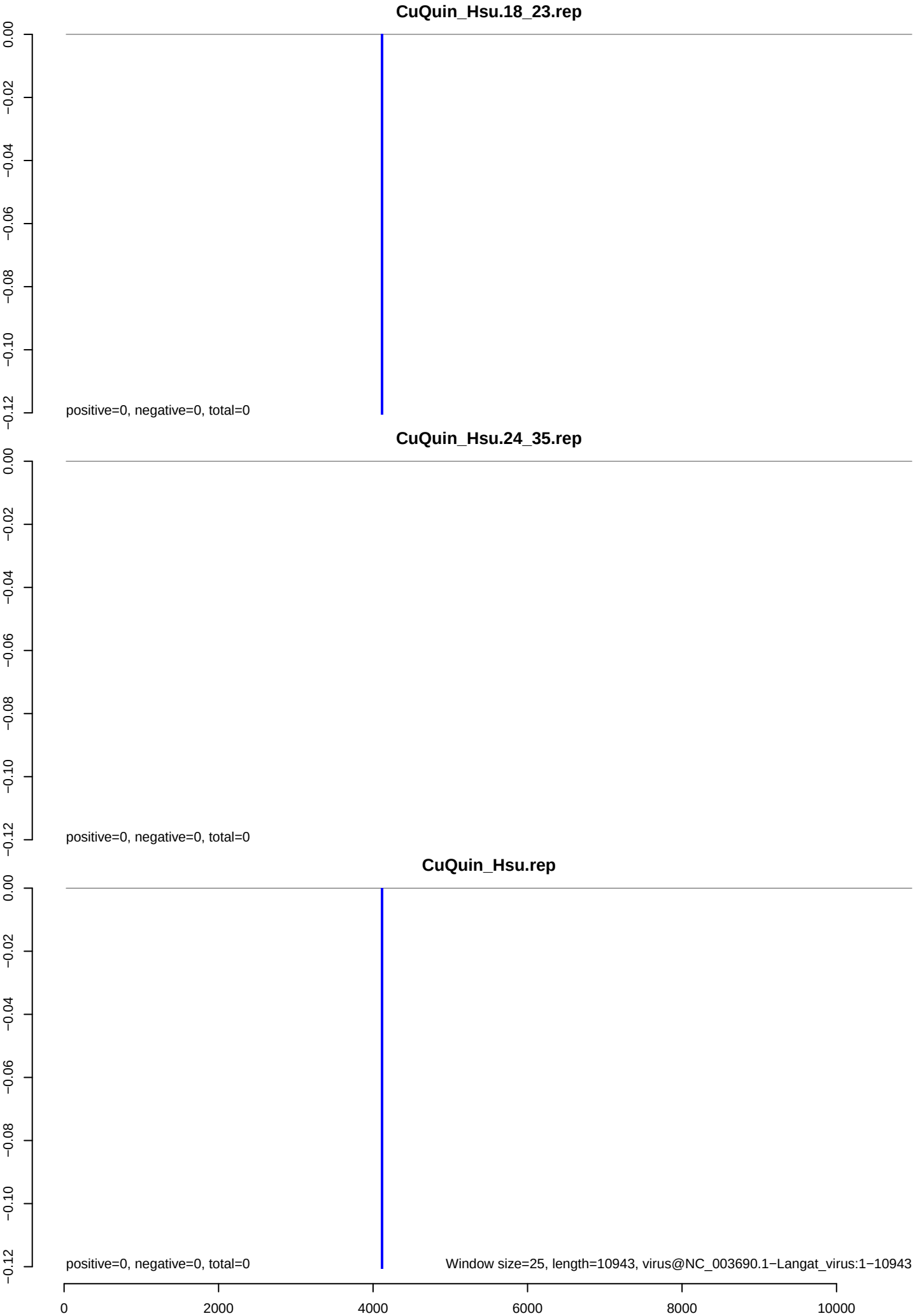
4000
6000
8000
10000
12000


CuQuin_Hsu.18_23.rep
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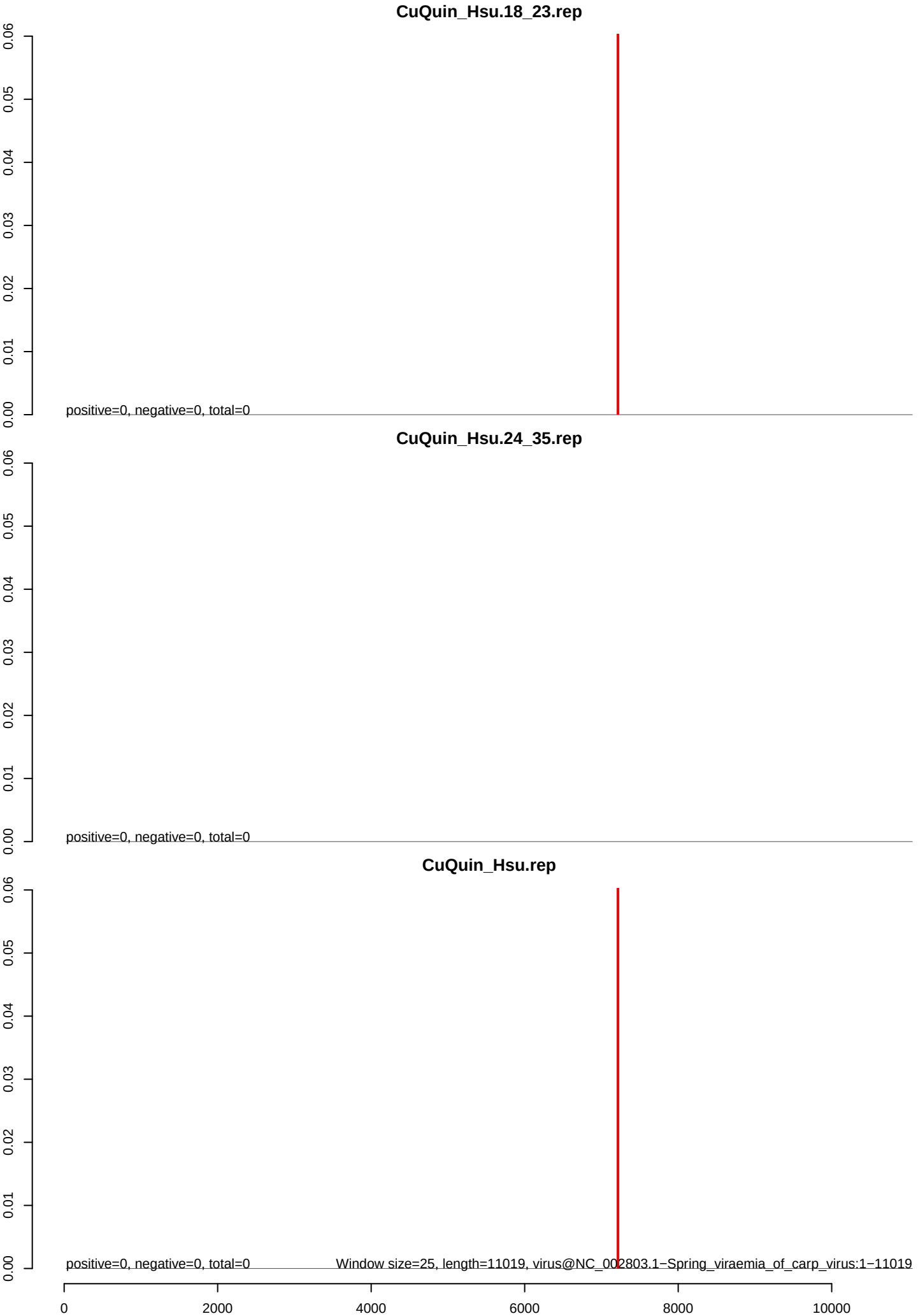
−0.06
−0.08
−0.10
−0.12
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
0.00
−0.02
−0.04
−0.06
−0.08
−0.10
−0.12
positive=0, negative=0, total=0
CuQuin_Hsu.rep
0.00
−0.02
−0.04
−0.06
−0.08
−0.10
−0.12
positive=0, negative=0, total=0
Window size=25, length=10943, virus@NC_003690.1−Langat_virus:1−10943
0
2000
4000
6000
8000
10000


CuQuin_Hsu.18_23.rep
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0.02
0.03
0.04
0.05
0.06
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
0.00
0.01
0.02
0.03
0.04
0.05
0.06
positive=0, negative=0, total=0
CuQuin_Hsu.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=11019, virus@NC_002803.1−Spring_viraemia_of_carp_virus:1−11019
0
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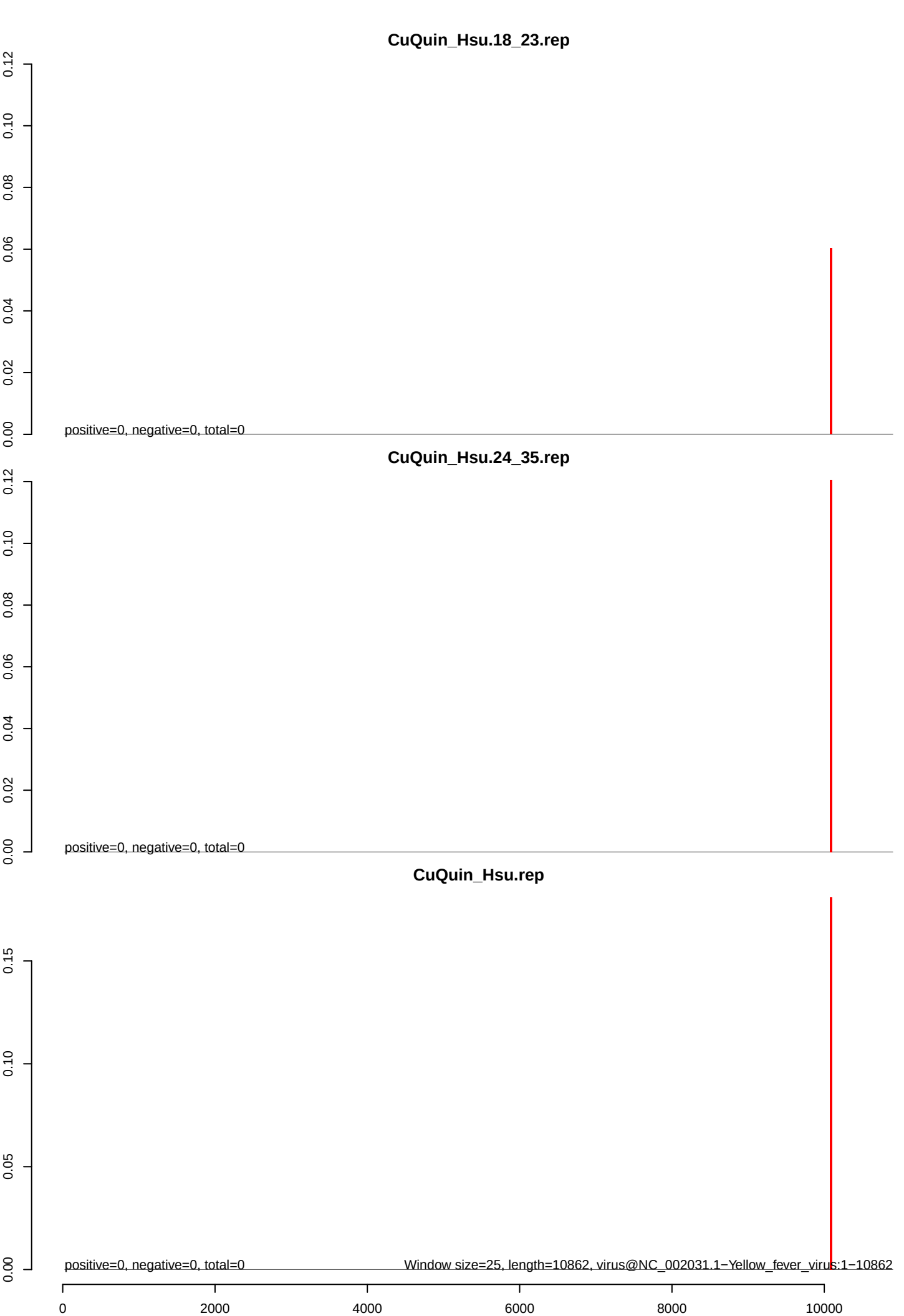
4000
6000
8000
10000


CuQuin_Hsu.18_23.rep
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0.00
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
0.12
0.10
0.08
0.06
0.04
0.02
0.00
positive=0, negative=0, total=0
CuQuin_Hsu.rep
0.15
0.10
0.05
0.00
positive=0, negative=0, total=0
Window size=25, length=10862, virus@NC_002031.1−Yellow_fever_virus:1−10862
0
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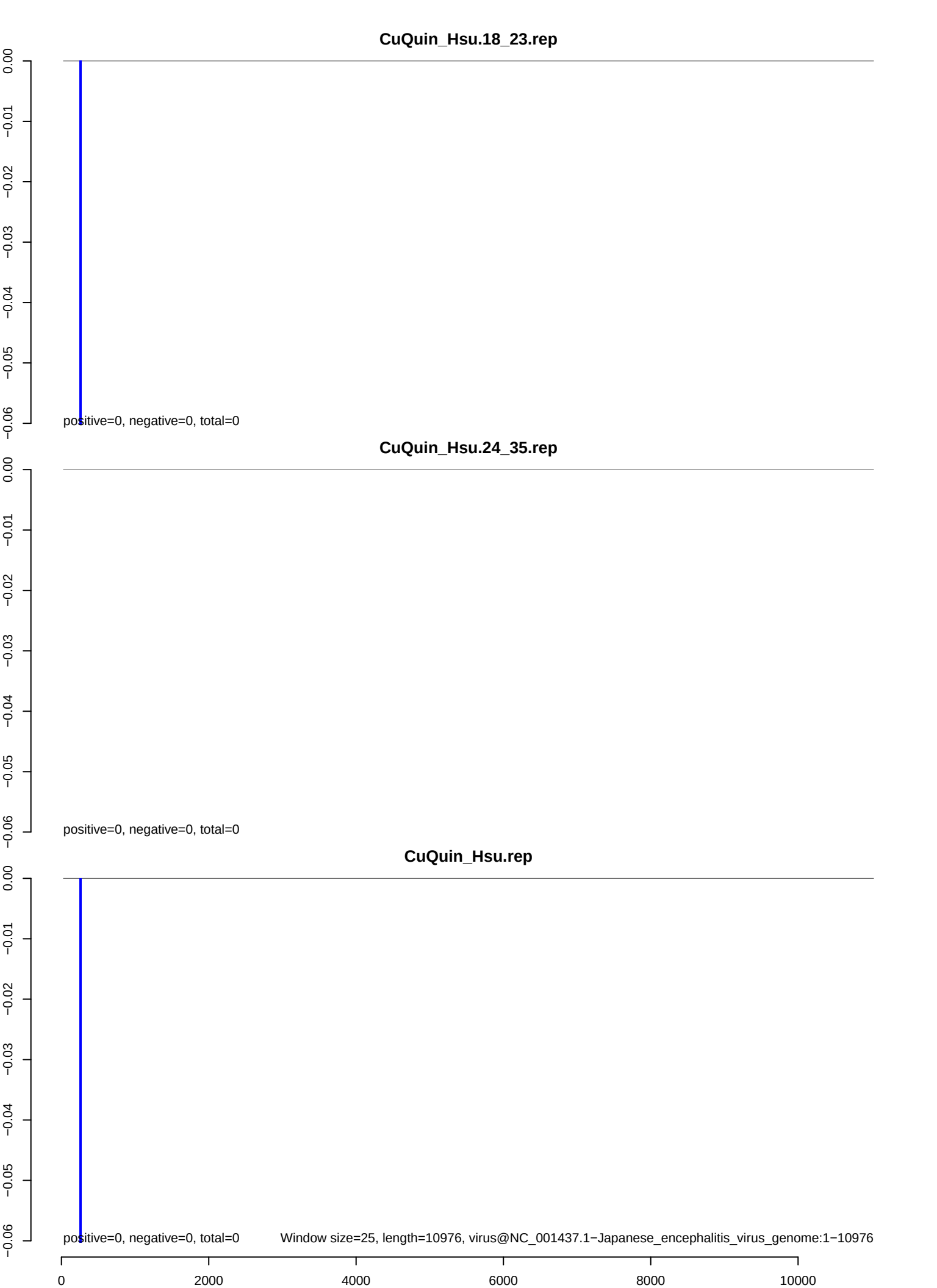
4000
6000
8000
10000


CuQuin_Hsu.18_23.rep
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−0.01
−0.02
−0.03
−0.04
−0.05
−0.06
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
0.00
−0.01
−0.02
−0.03
−0.04
−0.05
−0.06
positive=0, negative=0, total=0
CuQuin_Hsu.rep
0.00
−0.01
−0.02
−0.03
−0.04
−0.05
−0.06
positive=0, negative=0, total=0
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0
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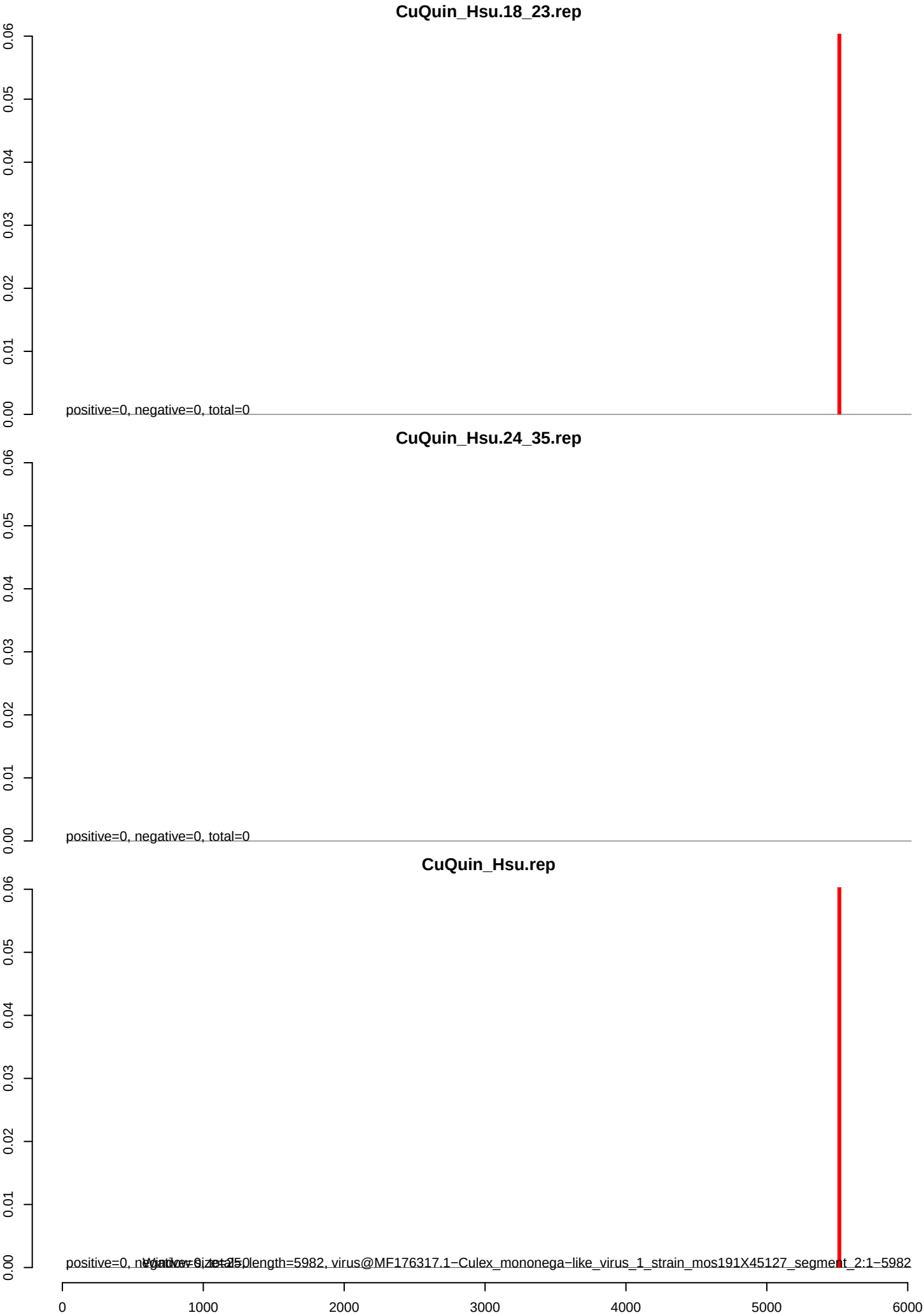
4000
6000
8000
10000


CuQuin_Hsu.18_23.rep
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0.02
0.03
0.04
0.05
0.06
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
0.00
0.01
0.02
0.03
0.04
0.05
0.06
positive=0, negative=0, total=0
CuQuin_Hsu.rep
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0.01
0.02
0.03
0.04
0.05
0.06
positive=0, negative=0, total=0
length=5982, virus@MF176317.1−Culex_mononega−like_virus_1_strain_mos191X45127_segment_2:1−5982
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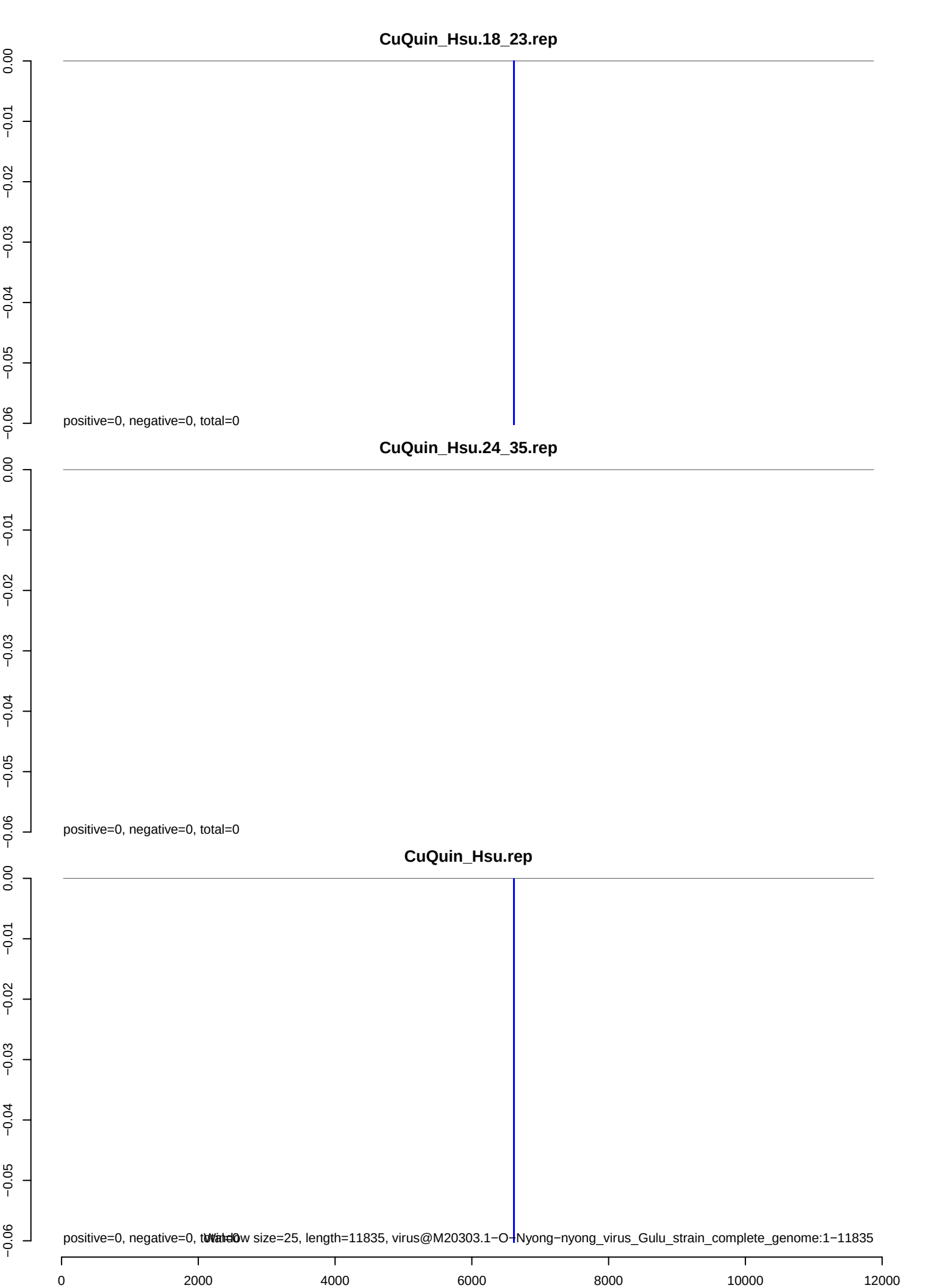
3000
4000
5000
6000


CuQuin_Hsu.18_23.rep
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−0.01
−0.02
−0.03
−0.04
−0.05
−0.06
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
0.00
−0.01
−0.02
−0.03
−0.04
−0.05
−0.06
positive=0, negative=0, total=0
CuQuin_Hsu.rep
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−0.01
−0.02
−0.03
−0.04
−0.05
−0.06
positive=0, negative=0, total=0
Window size=25, length=11835, virus@M20303.1−O−Nyong−nyong_virus_Gulu_strain_complete_genome:1−11835
0
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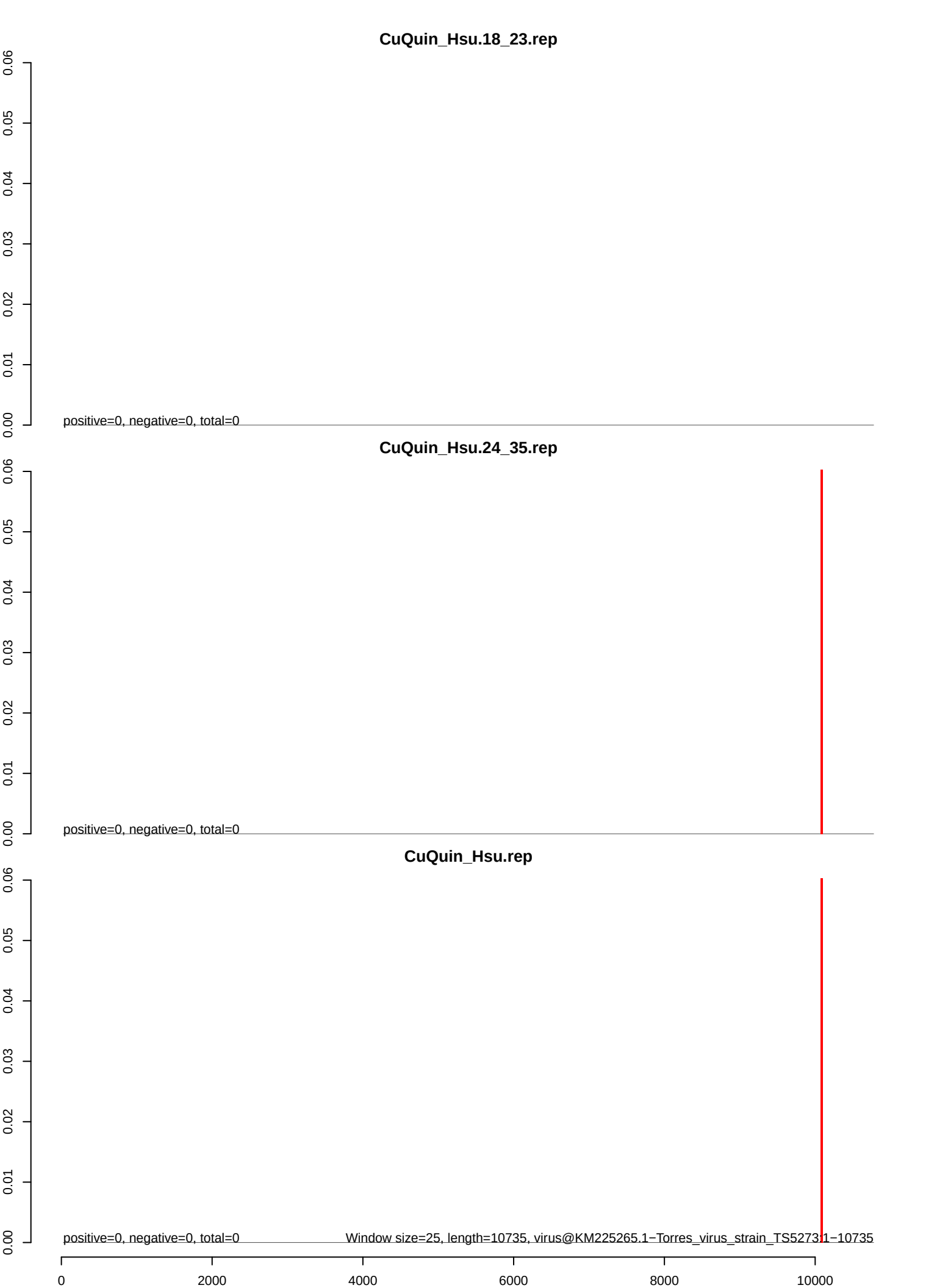
4000
6000
8000
10000
12000


CuQuin_Hsu.18_23.rep
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0.02
0.03
0.04
0.05
0.06
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
0.00
0.01
0.02
0.03
0.04
0.05
0.06
positive=0, negative=0, total=0
CuQuin_Hsu.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=10735, virus@KM225265.1−Torres_virus_strain_TS5273.1−10735
0
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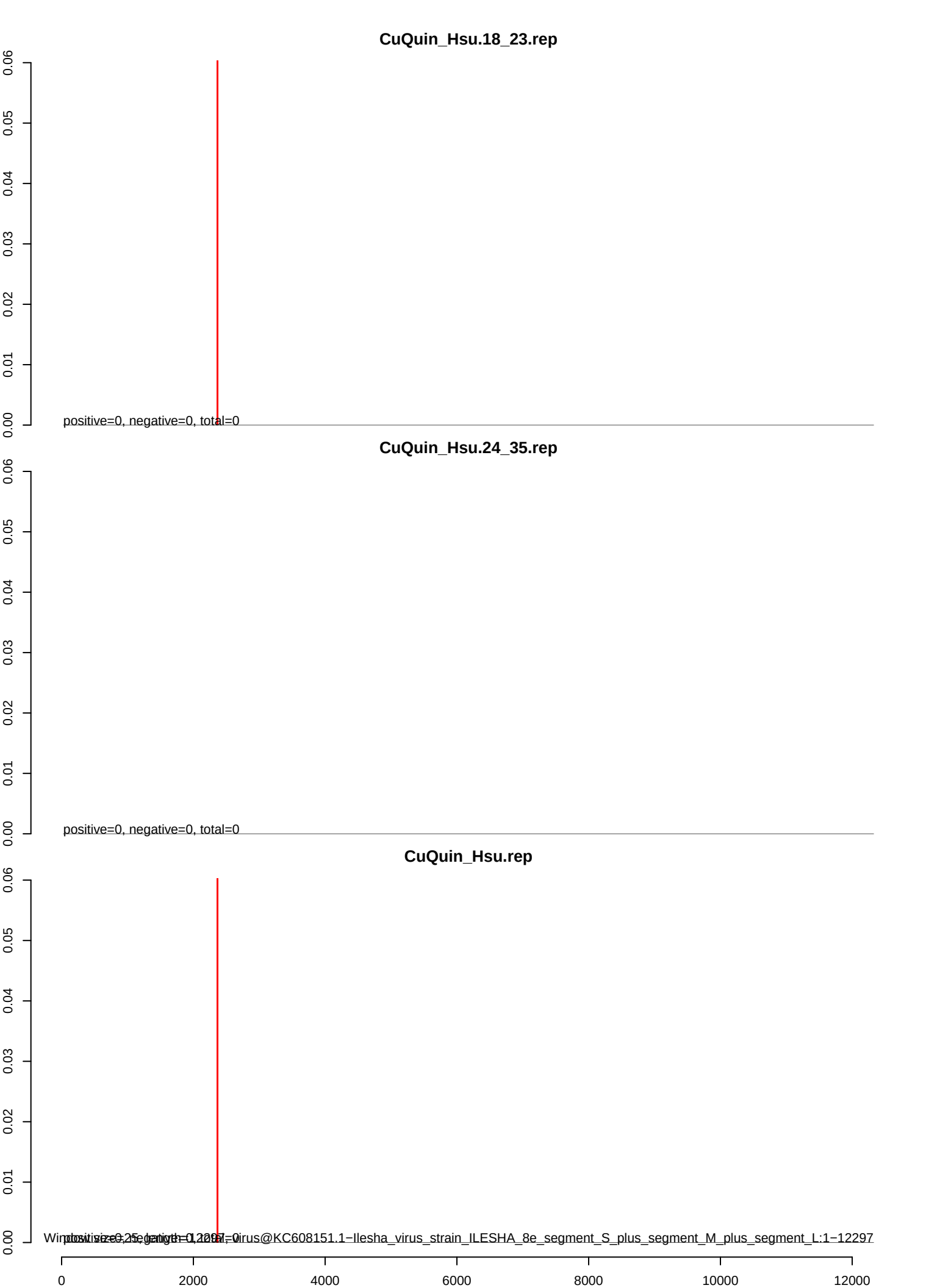
4000
6000
8000
10000


CuQuin_Hsu.18_23.rep
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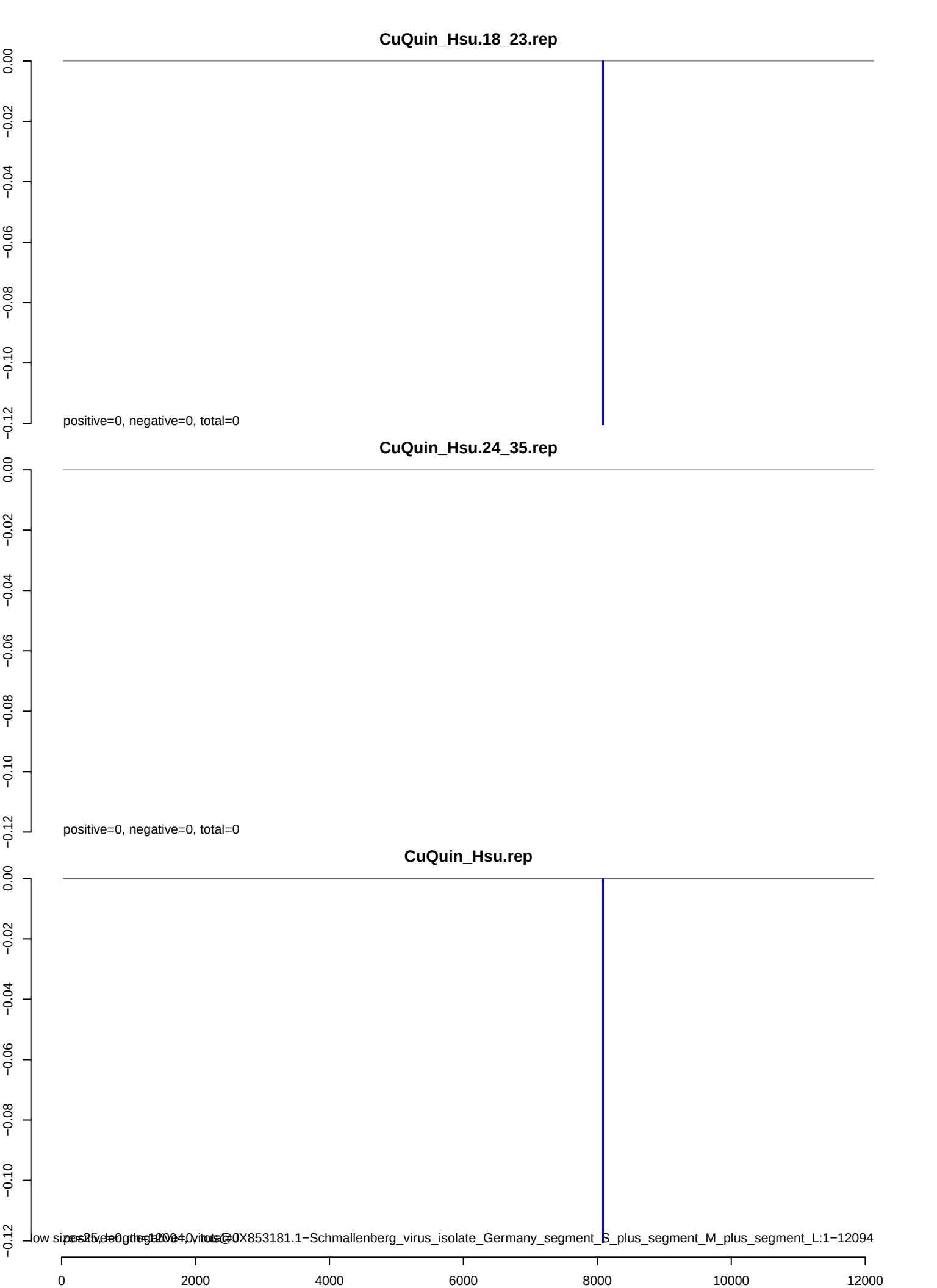
0.01
0.02
0.03
0.04
0.05
0.06
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
0.00
0.01
0.02
0.03
0.04
0.05
0.06
positive=0, negative=0, total=0
CuQuin_Hsu.rep
0.00
0.01
0.02
0.03
0.04
0.05
0.06
positive=0, negative=0, total=0
0
2000
4000
6000
8000
10000
12000


CuQuin_Hsu.18_23.rep
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−0.02
−0.04
−0.06
−0.08
−0.10
−0.12
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
0.00
−0.02
−0.04
−0.06
−0.08
−0.10
−0.12
positive=0, negative=0, total=0
CuQuin_Hsu.rep
0.00
−0.02
−0.04
−0.06
−0.08
−0.10
−0.12
positive=0, negative=0, total=0
low sizes: 1:12094 | total: 1
LR853181.1−Schmallenberg_virus_isolate_Germany_segment_S_plus_segment_M_plus_segment_L:1−12094
0
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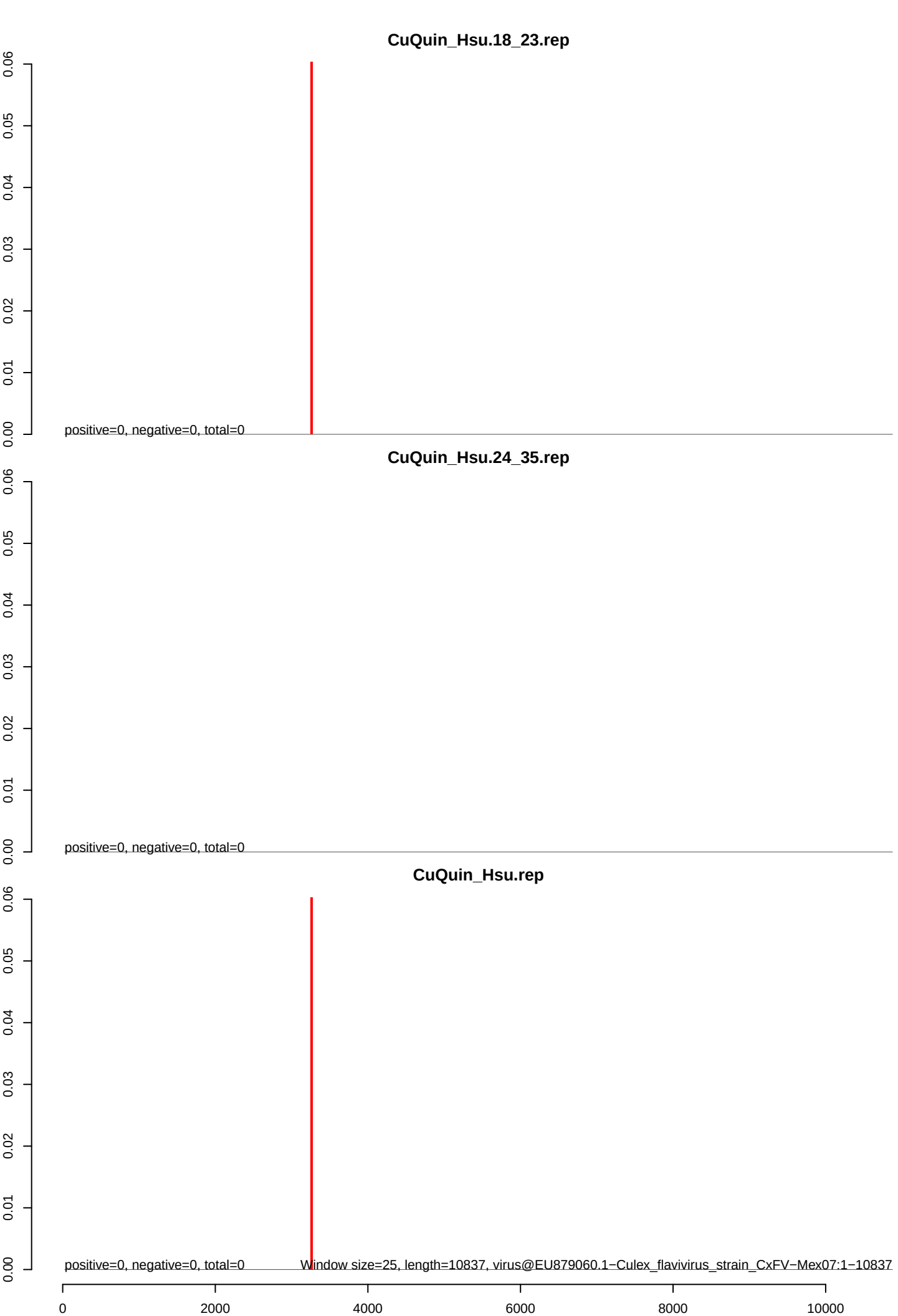
4000
6000
8000
10000
12000


CuQuin_Hsu.18_23.rep
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0.01
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0.03
0.04
0.05
0.06
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
0.00
0.01
0.02
0.03
0.04
0.05
0.06
positive=0, negative=0, total=0
CuQuin_Hsu.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=10837, virus@EU879060.1−Culex_flavivirus_strain_CxFV−Mex07:1−10837
0
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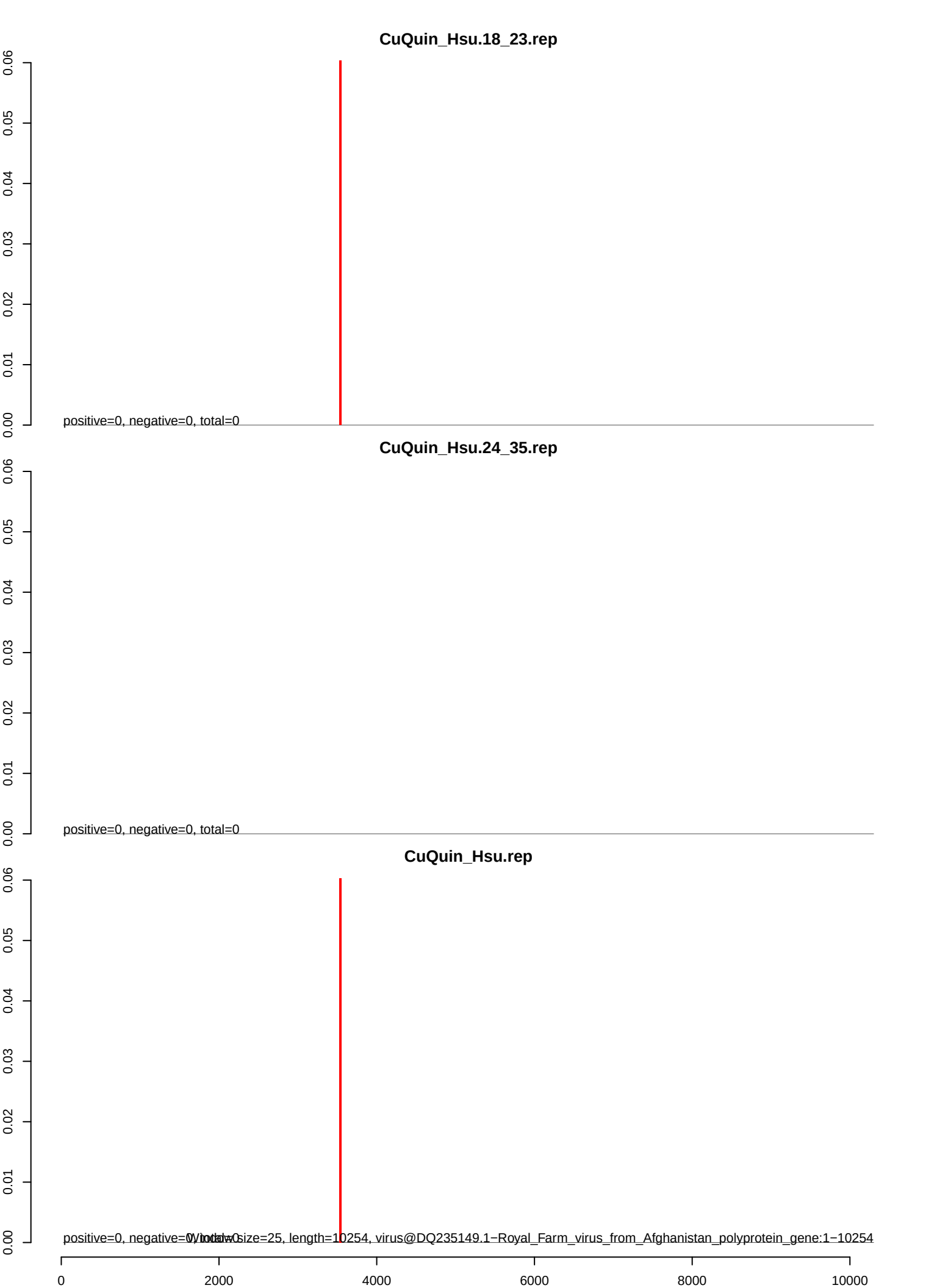
4000
6000
8000
10000


CuQuin_Hsu.18_23.rep
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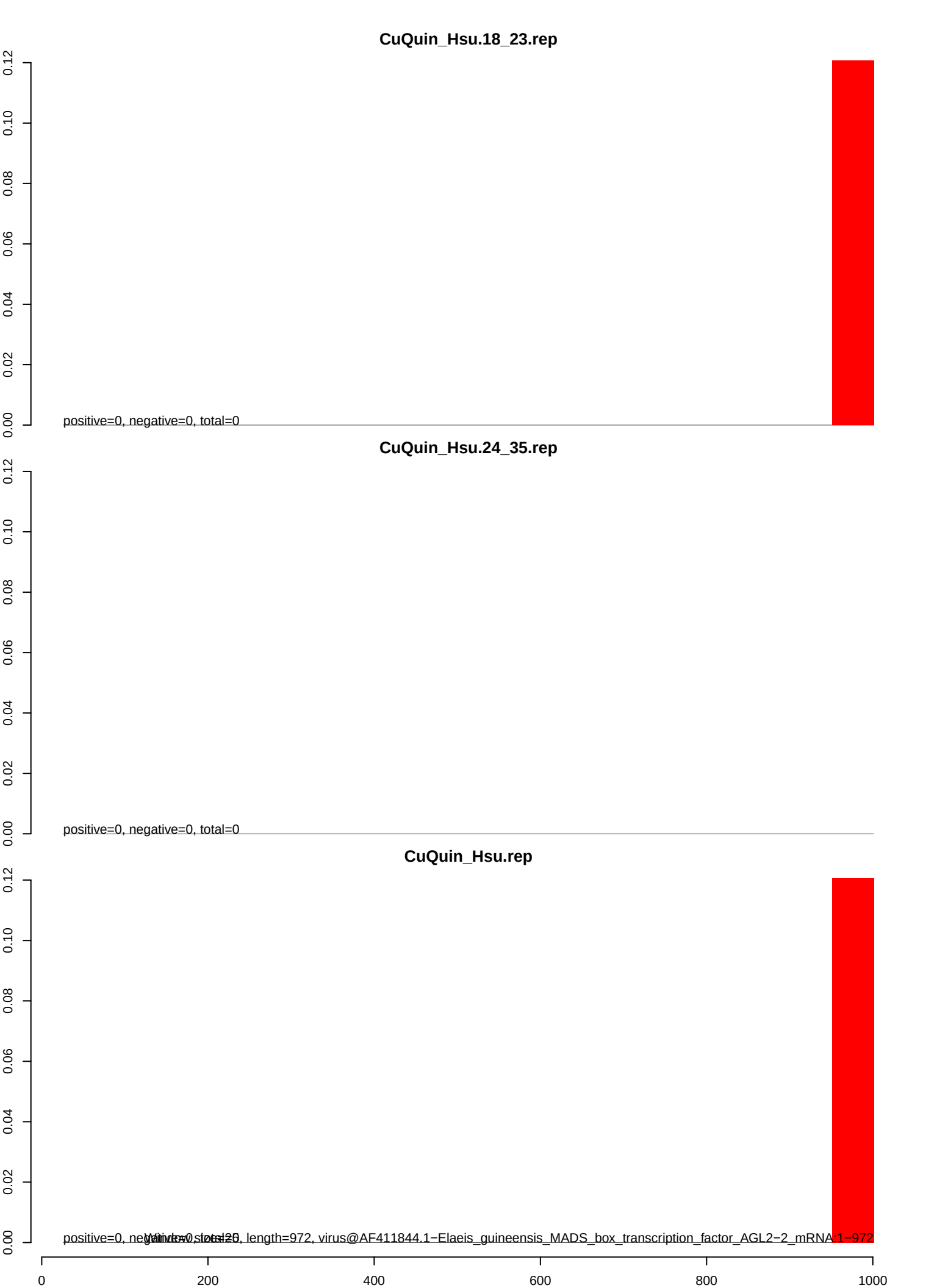
0.05
0.04
0.03
0.02
0.01
0.00
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
0.06
0.05
0.04
0.03
0.02
0.01
0.00
positive=0, negative=0, total=0
CuQuin_Hsu.rep
0.06
0.05
0.04
0.03
0.02
0.01
0.00
positive=0, negative=0, total=0
Window size=25, length=10254, virus@DQ235149.1−Royal_Farm_virus_from_Afghanistan_polyprotein_gene:1−10254
0
2000
4000
6000
8000
10000


CuQuin_Hsu.18_23.rep
0.00
0.02
0.04
0.06
0.08
0.10
0.12
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
0.00
0.02
0.04
0.06
0.08
0.10
0.12
positive=0, negative=0, total=0
CuQuin_Hsu.rep
0.00
0.02
0.04
0.06
0.08
0.10
0.12
positive=0, negative=0, total=0, length=972, virus@AF411844.1−Elaeis_guineensis_MADS_box_transcription_factor_AGL2−2_mRNA:1−972
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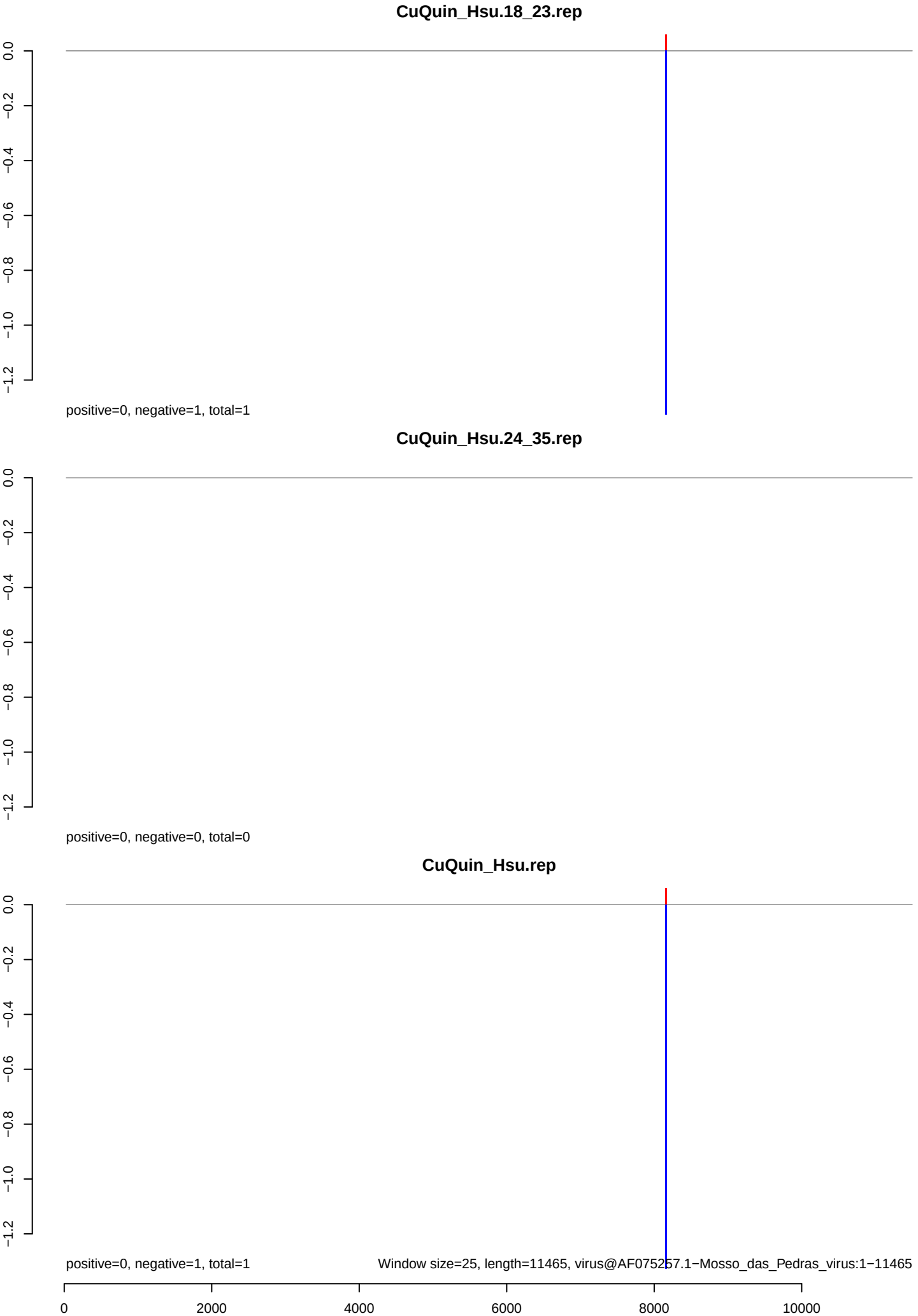
400
600
800
1000


CuQuin_Hsu.18_23.rep
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−0.2
−0.4
−0.6
−0.8
−1.0
−1.2
positive=0, negative=1, total=1
CuQuin_Hsu.24_35.rep
0.0
−0.2
−0.4
−0.6
−0.8
−1.0
−1.2
positive=0, negative=0, total=0
CuQuin_Hsu.rep
0.0
−0.2
−0.4
−0.6
−0.8
−1.0
−1.2
positive=0, negative=1, total=1
Window size=25, length=11465, virus@AF075257.1−Mosso_das_Pedras_virus:1−11465
0
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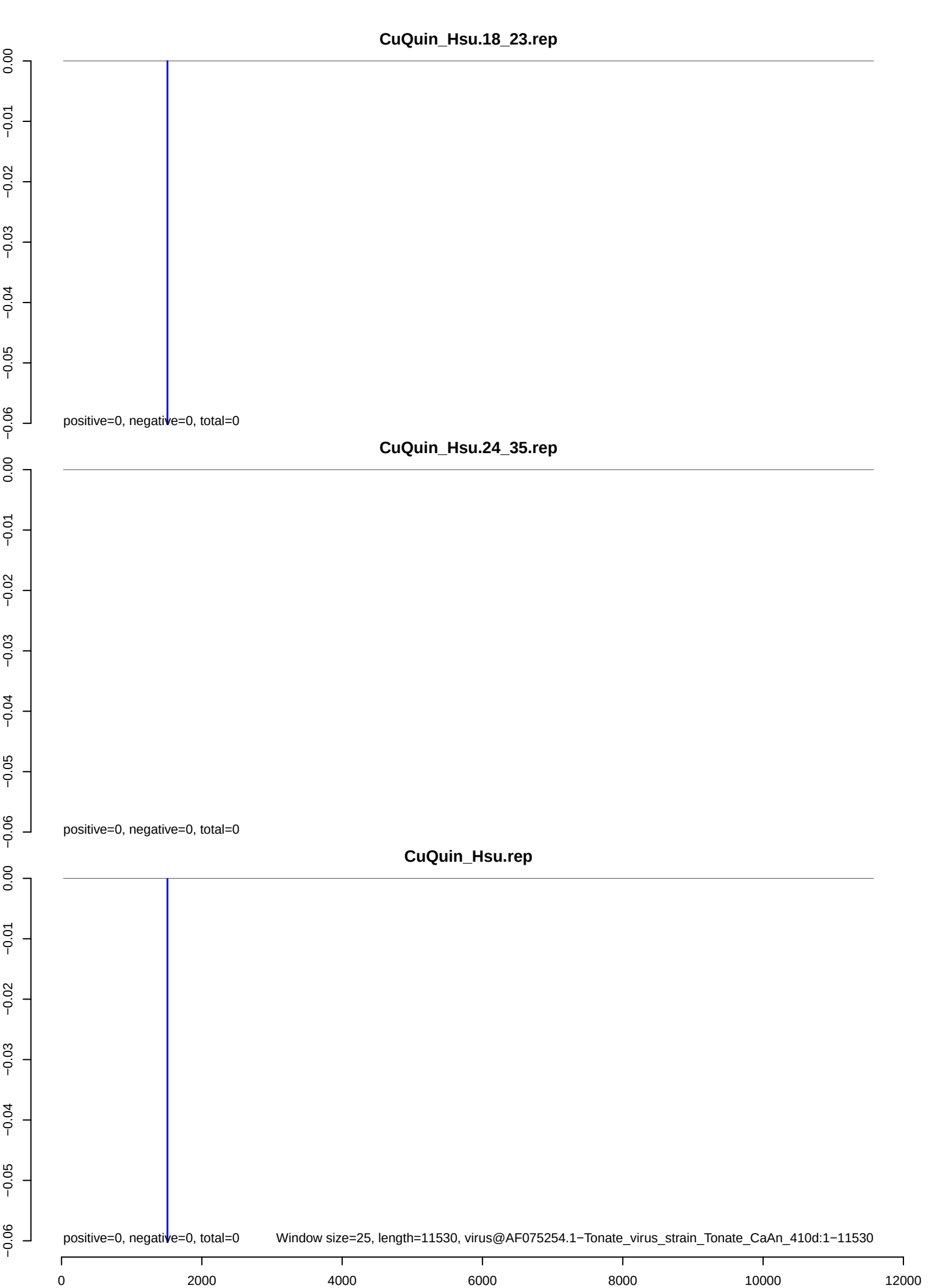
4000
6000
8000
10000


CuQuin_Hsu.18_23.rep
0.00
−0.01
−0.02
−0.03
−0.04
−0.05
−0.06
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
0.00
−0.01
−0.02
−0.03
−0.04
−0.05
−0.06
positive=0, negative=0, total=0
CuQuin_Hsu.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=11530, virus@AF075254.1−Tonate_virus_strain_Tonate_CaAn_410d:1−11530
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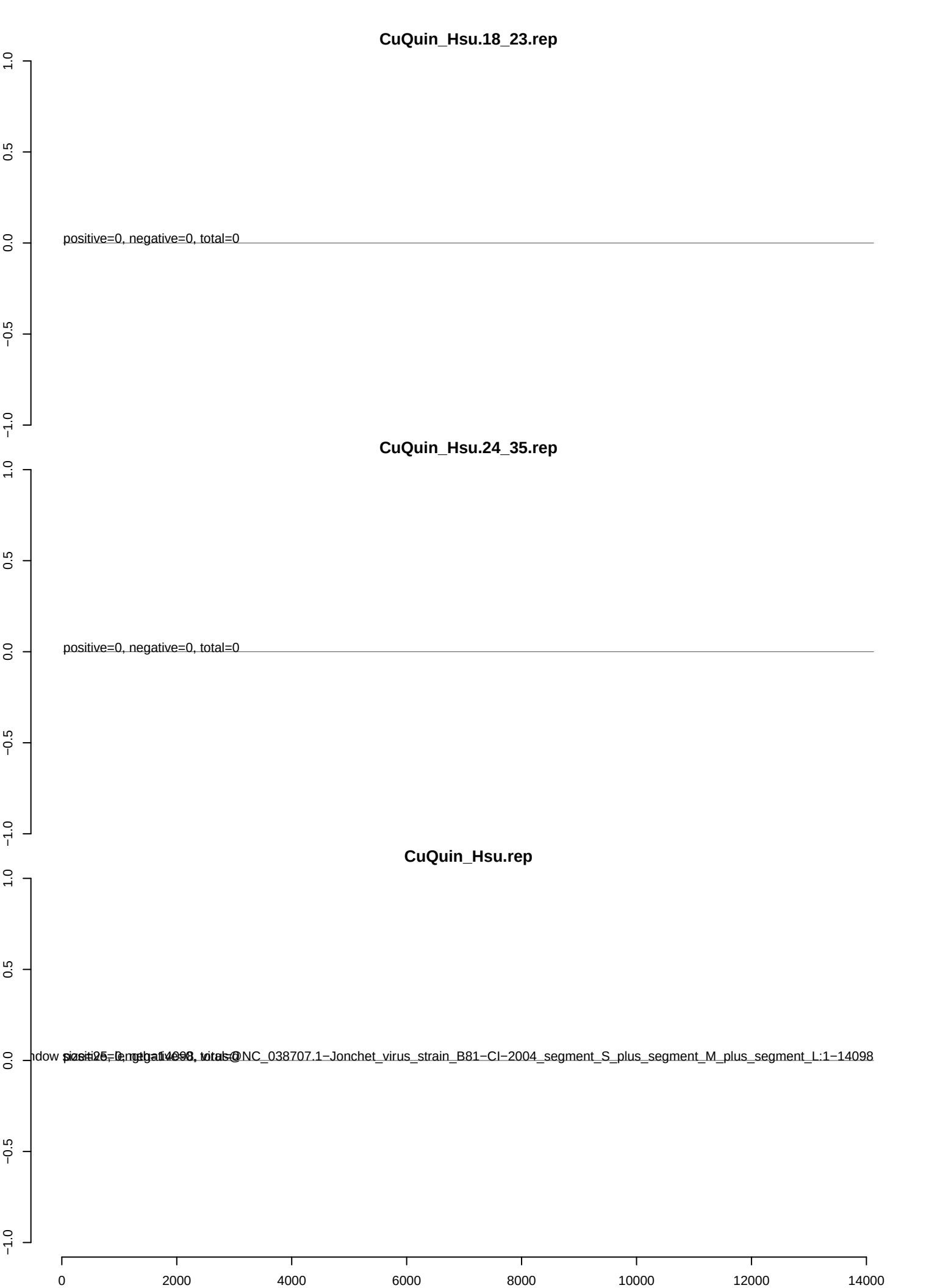
6000
8000
10000
12000


CuQuin_Hsu.18_23.rep
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
positive=0, negative=0, total=0
CuQuin_Hsu.rep
positive=0, negative=0, total=0
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0.5
0.0
−0.5
−1.0
0
2000
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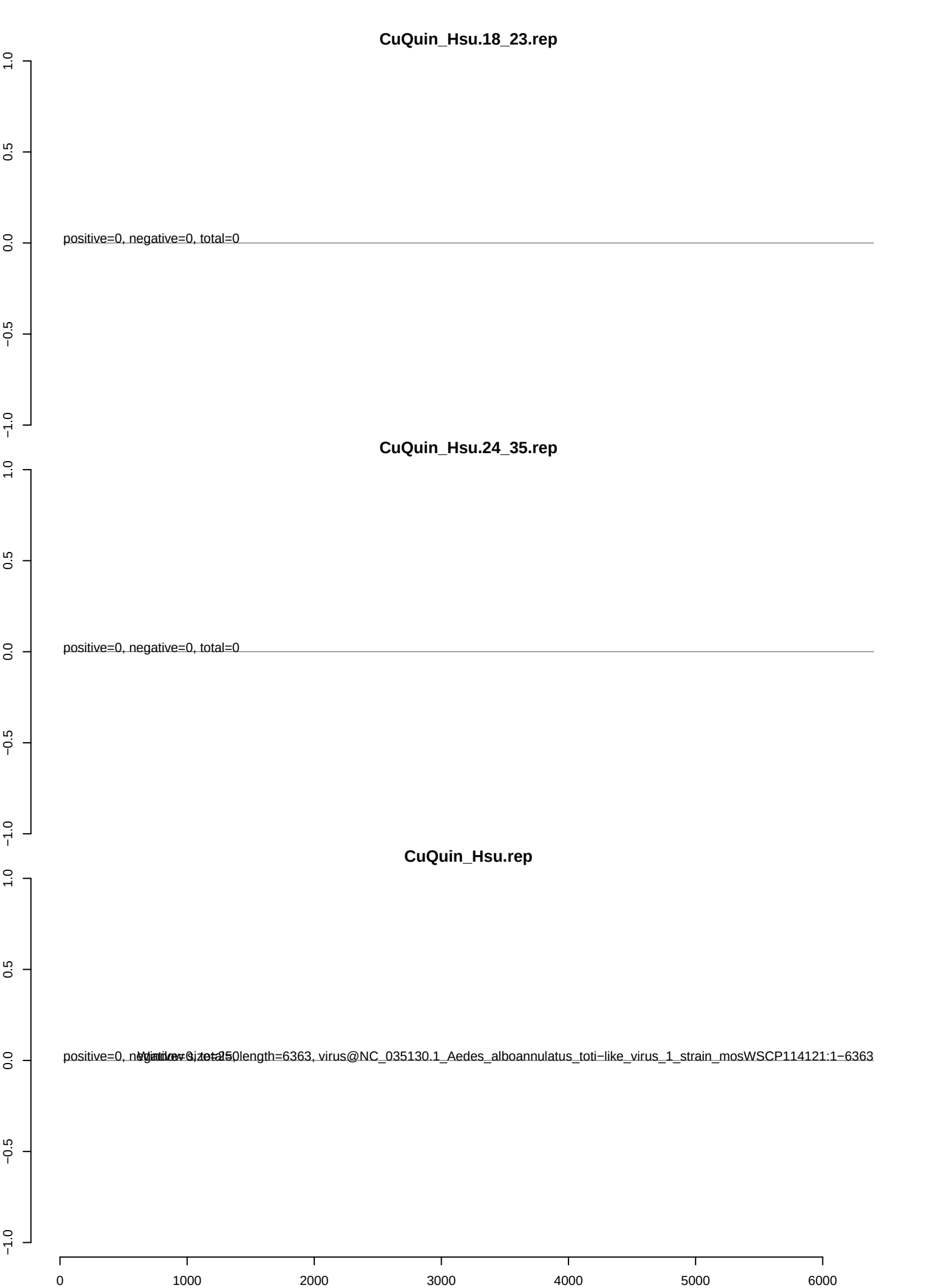
6000
8000
10000
12000
14000


CuQuin_Hsu.18_23.rep
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
positive=0, negative=0, total=0
CuQuin_Hsu.rep
positive=0, negative=0, total=0
Window size=250
length=6363, virus@NC_035130.1_Aedes_alboannulatus_toti−like_virus_1_strain_mosWSCP114121:1−6363
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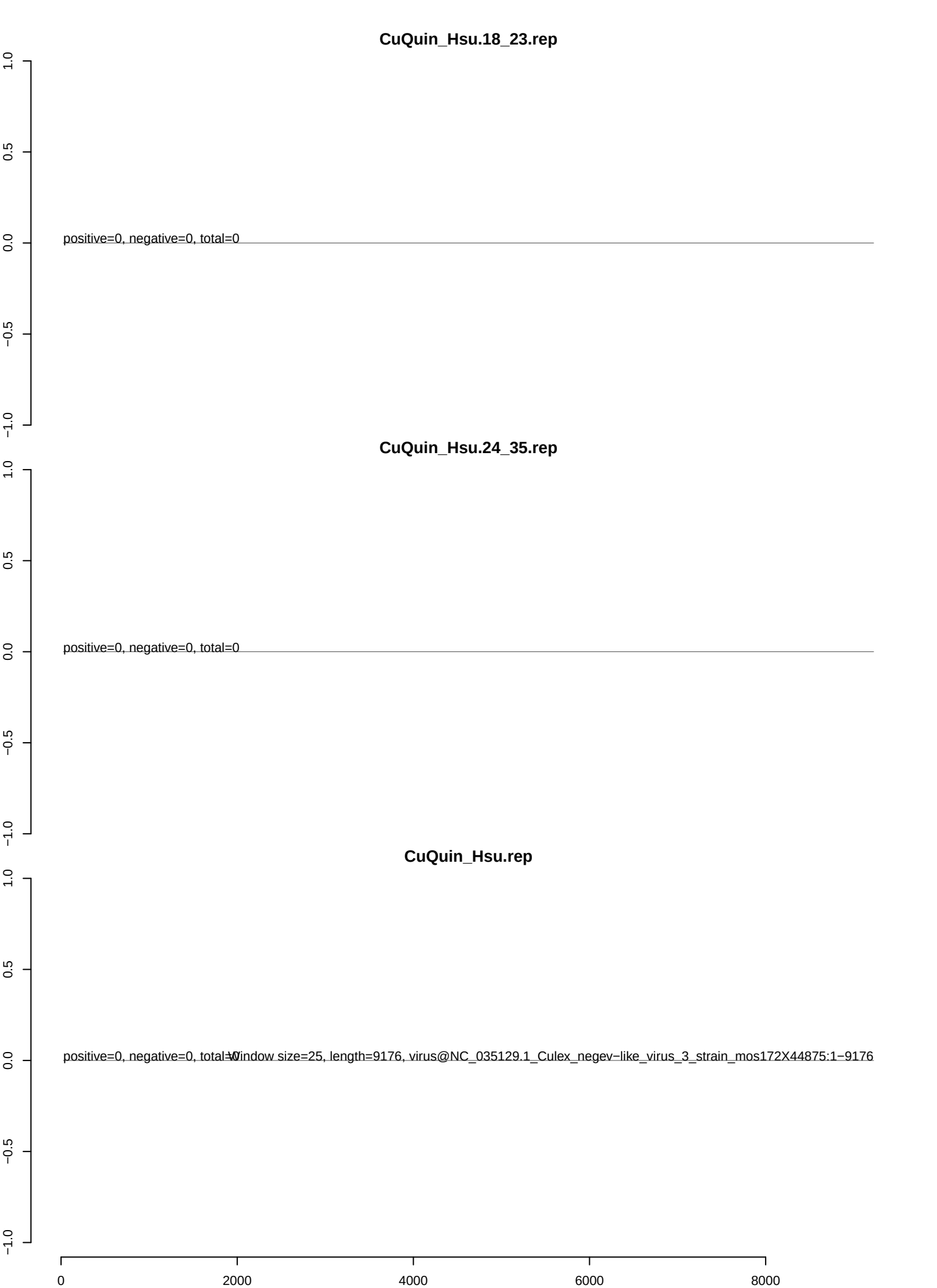
3000
4000
5000
6000


CuQuin_Hsu.18_23.rep
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
positive=0, negative=0, total=0
CuQuin_Hsu.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
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0.0
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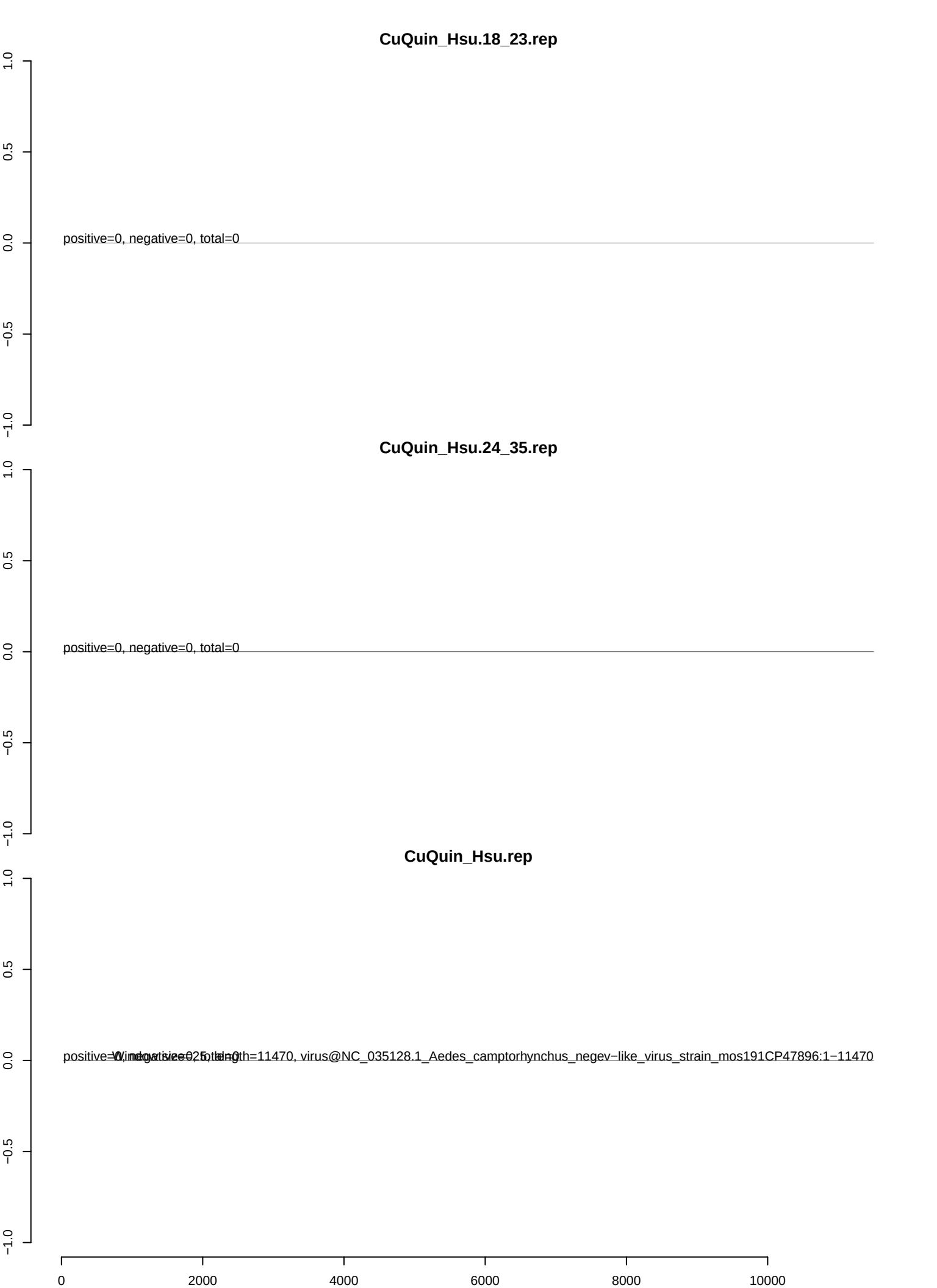
6000
8000


CuQuin_Hsu.18_23.rep
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
positive=0, negative=0, total=0
CuQuin_Hsu.rep
positive=0, negative=0, total=0, length=11470, virus@NC_035128.1_Aedes_camptorhynchus_negev−like_virus_strain_mos191CP47896:1−11470
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0.0
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−1.0
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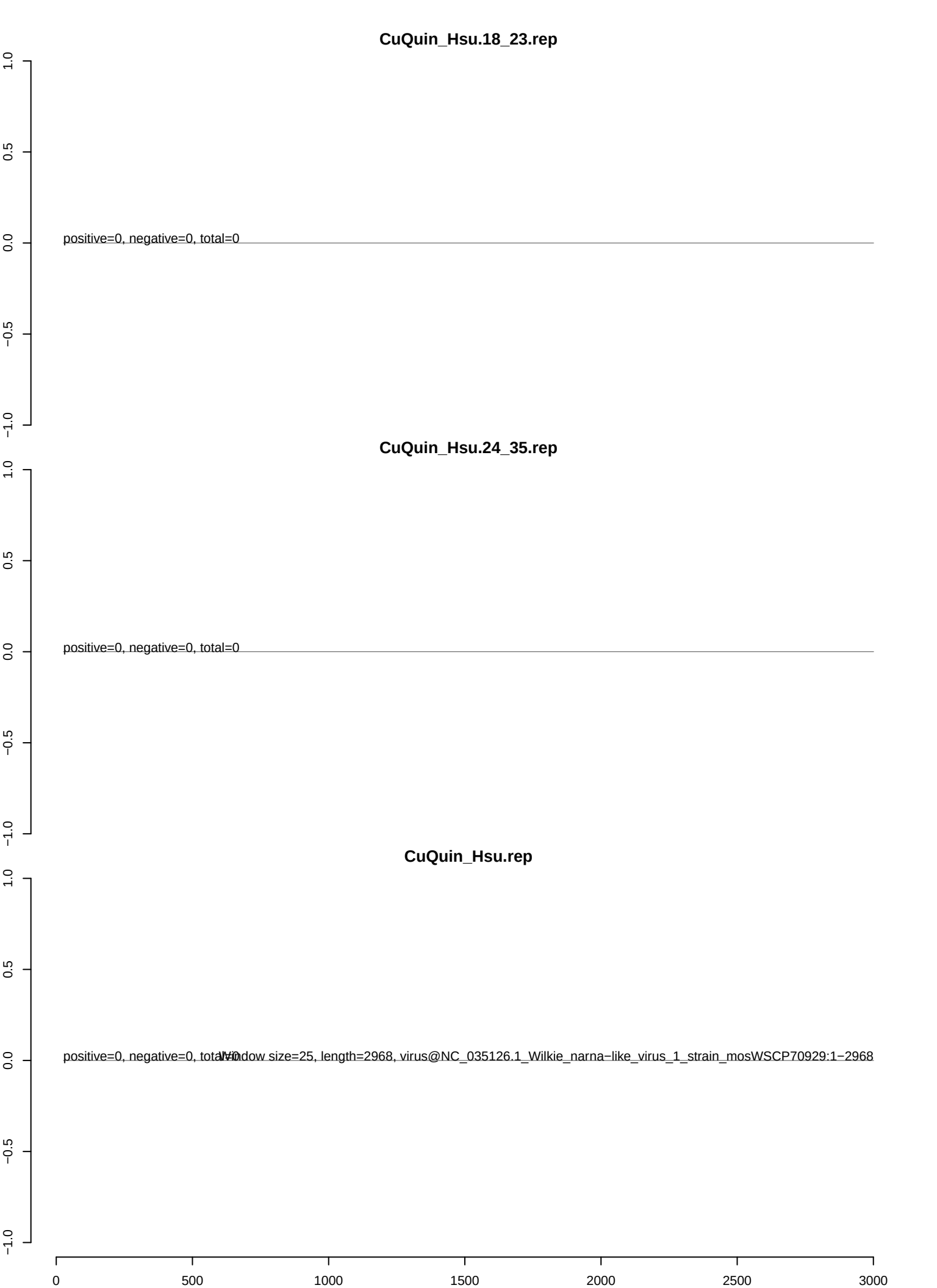
8000
10000


CuQuin_Hsu.18_23.rep
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
positive=0, negative=0, total=0
CuQuin_Hsu.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
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0.0
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−1.0
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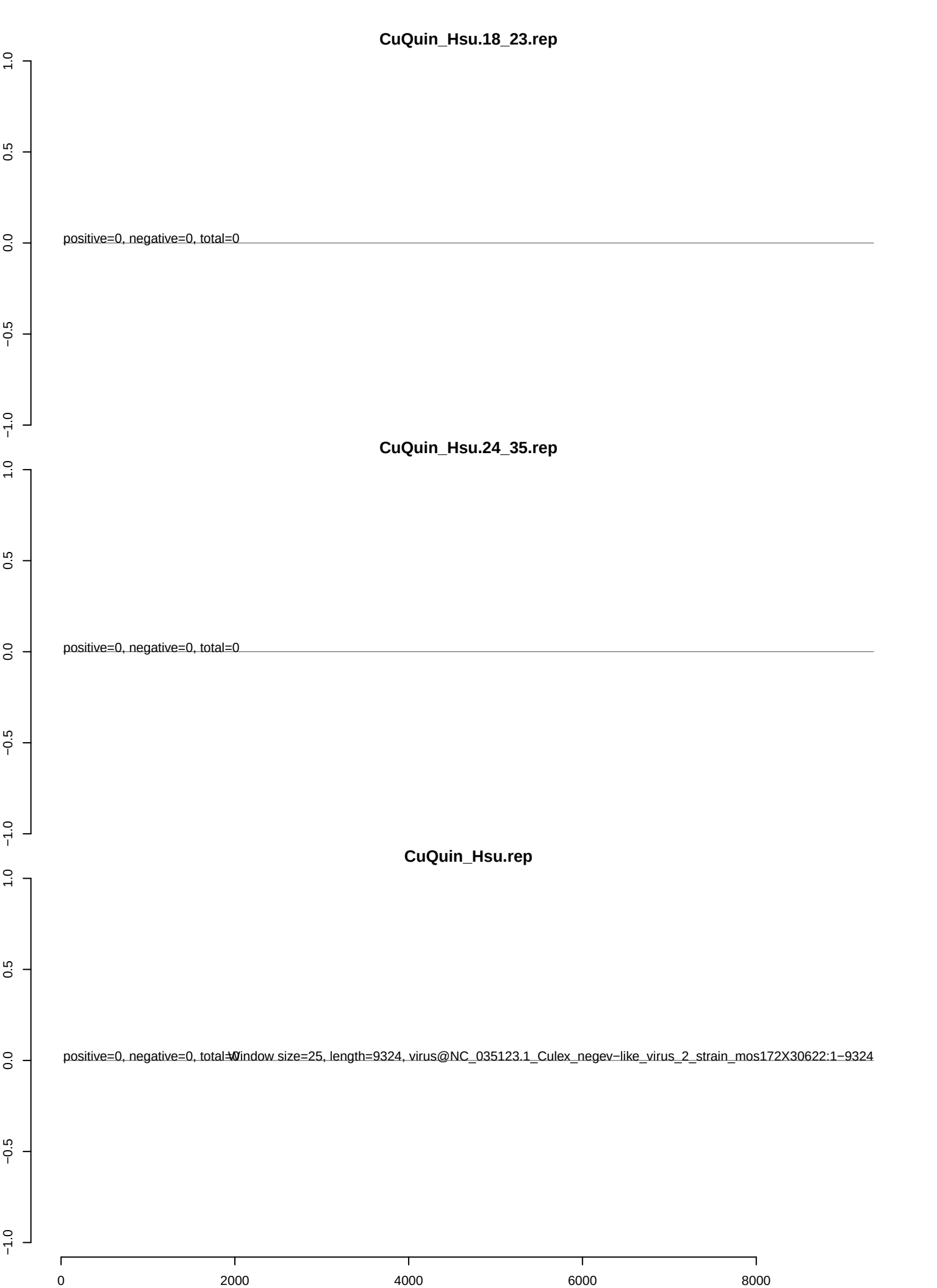
1500
2000
2500
3000


CuQuin_Hsu.18_23.rep
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
positive=0, negative=0, total=0
CuQuin_Hsu.rep
positive=0, negative=0, total=0
Window size=25, length=9324, virus@NC_035123.1_Culex_negev−like_virus_2_strain_mos172X30622:1−9324
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0.5
0.0
−0.5
−1.0
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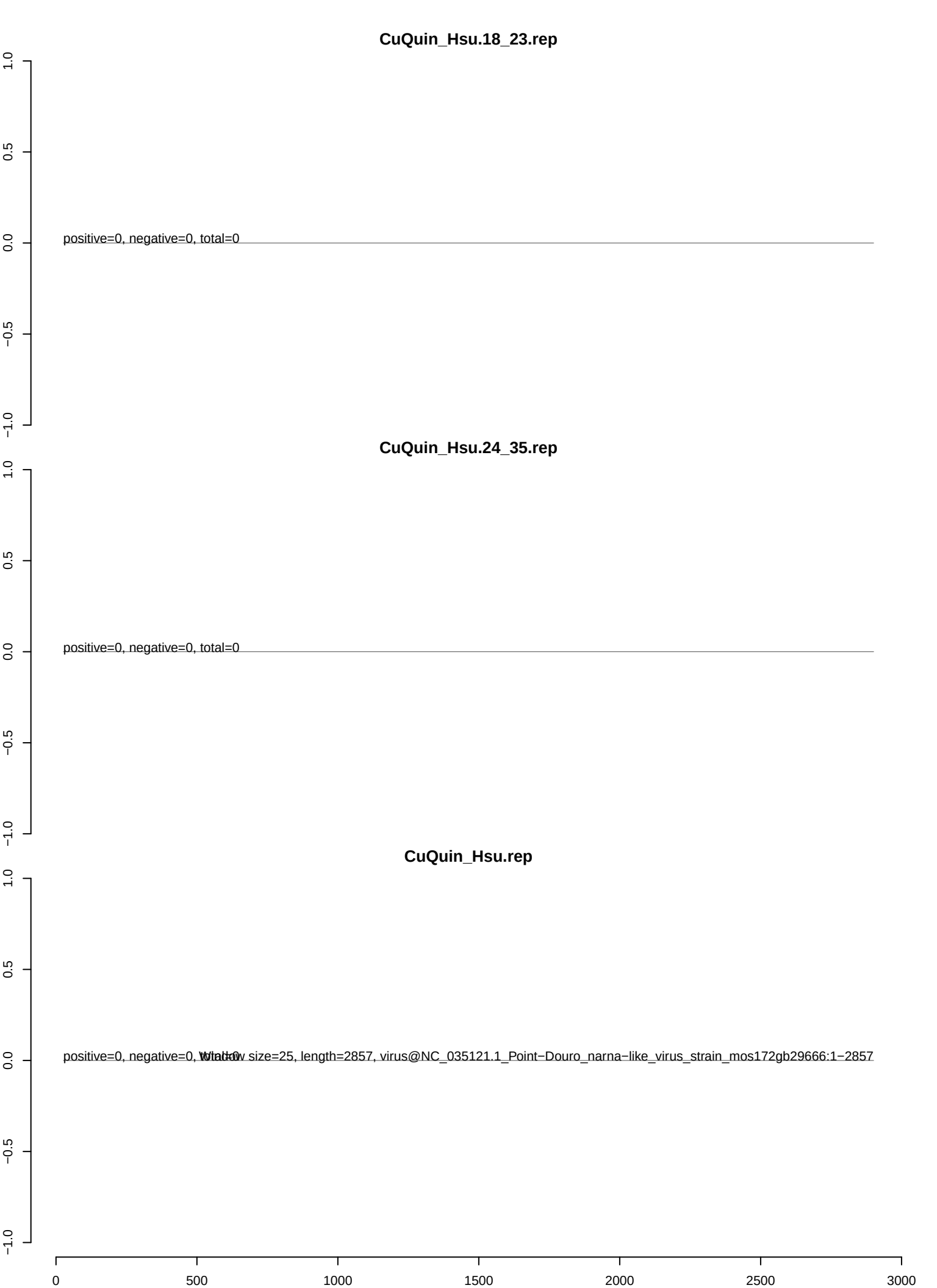
4000
6000
8000


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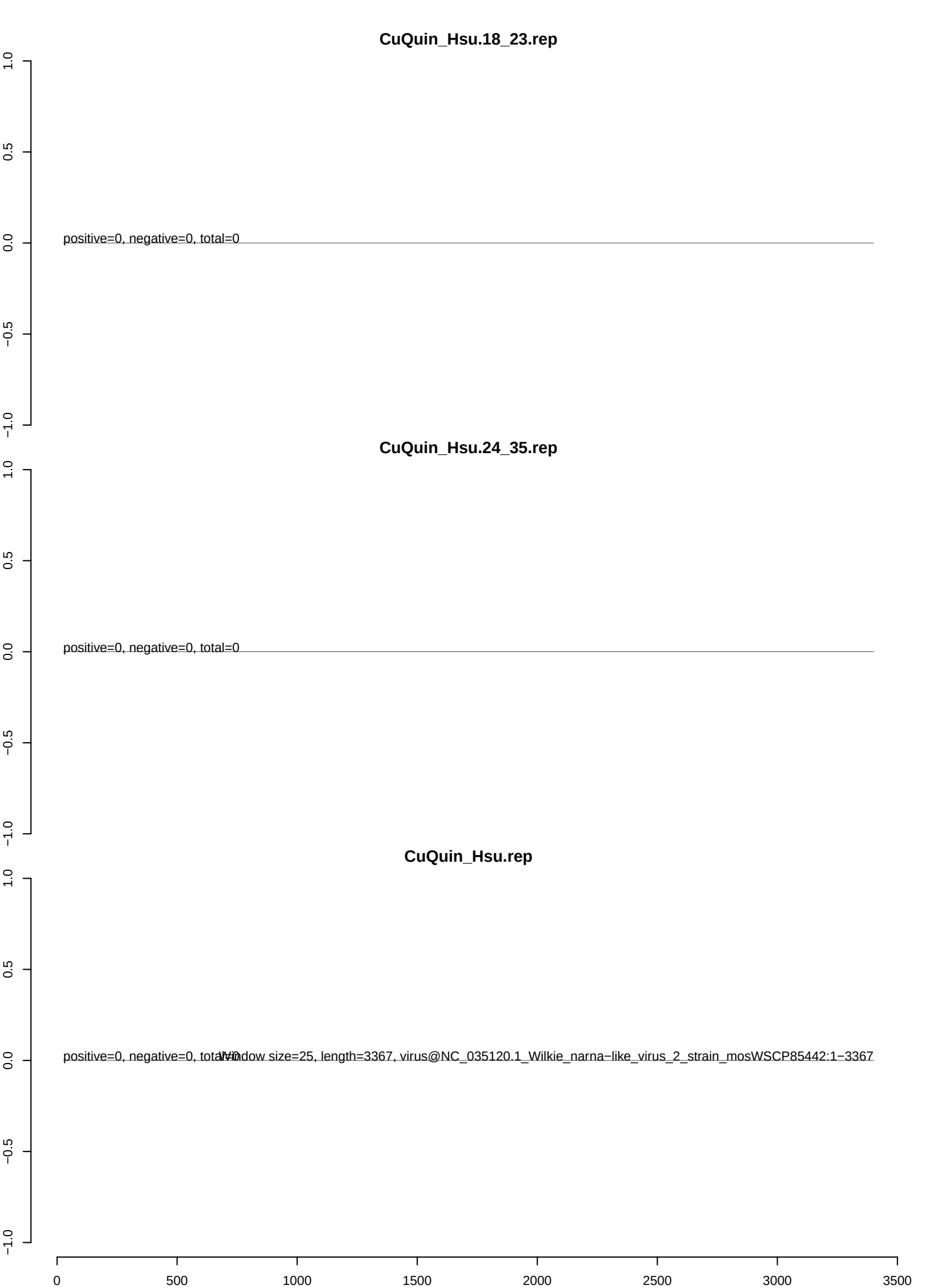
1500
2000
2500
3000


CuQuin_Hsu.18_23.rep
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
positive=0, negative=0, total=0
CuQuin_Hsu.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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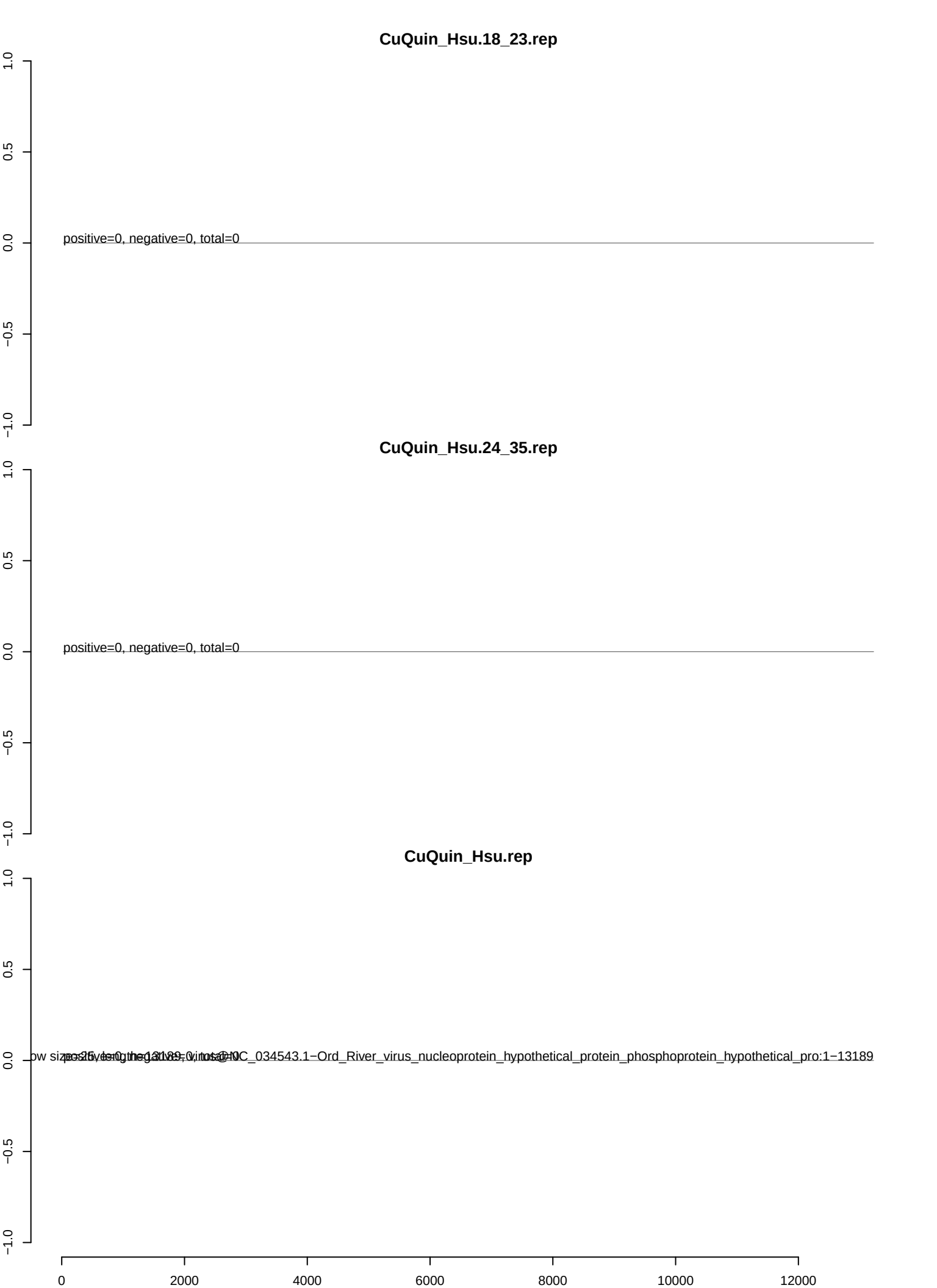
0.5
0.0
−0.5
−1.0
0
500
1000
1500
2000
2500
3000
3500


CuQuin_Hsu.18_23.rep
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
positive=0, negative=0, total=0
CuQuin_Hsu.rep
positive=0, negative=0, total=0
NC_034543.1−Ord_River_virus_nucleoprotein_hypothetical_protein_phosphoprotein_hypothetical_pro:1−13189
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0.5
0.0
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−1.0
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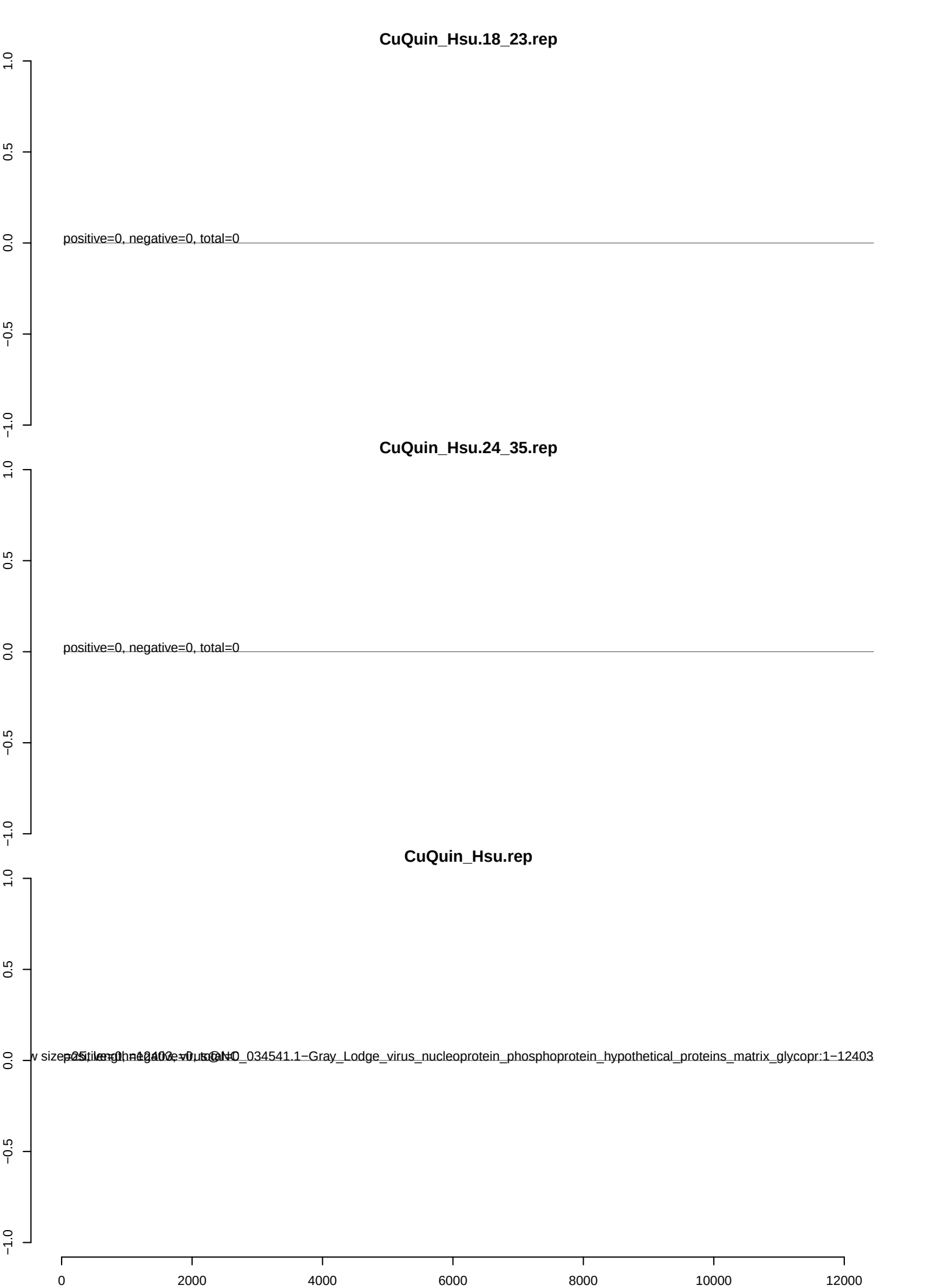
6000
8000
10000
12000


CuQuin_Hsu.18_23.rep
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
positive=0, negative=0, total=0
CuQuin_Hsu.rep
positive=0, negative=0, total=0
w size=25, length=12403, value=0, isGN=0_034541.1−Gray_Lodge_virus_nucleoprotein_phosphoprotein_hypothetical_proteins_matrix_glycopr:1−12403
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0.5
0.0
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−1.0
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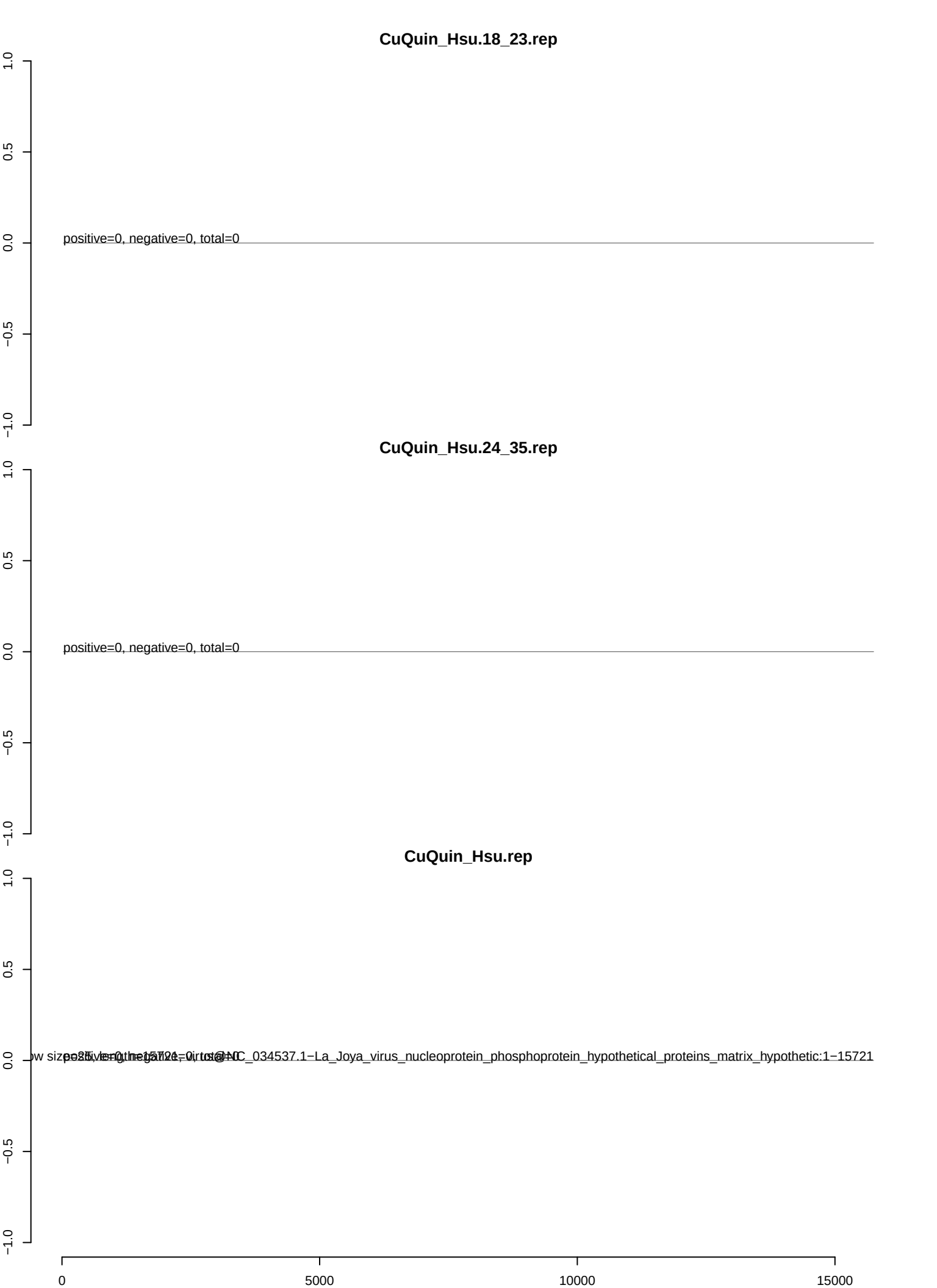
2000
4000
6000
8000
10000
12000


CuQuin_Hsu.18_23.rep
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
positive=0, negative=0, total=0
CuQuin_Hsu.rep
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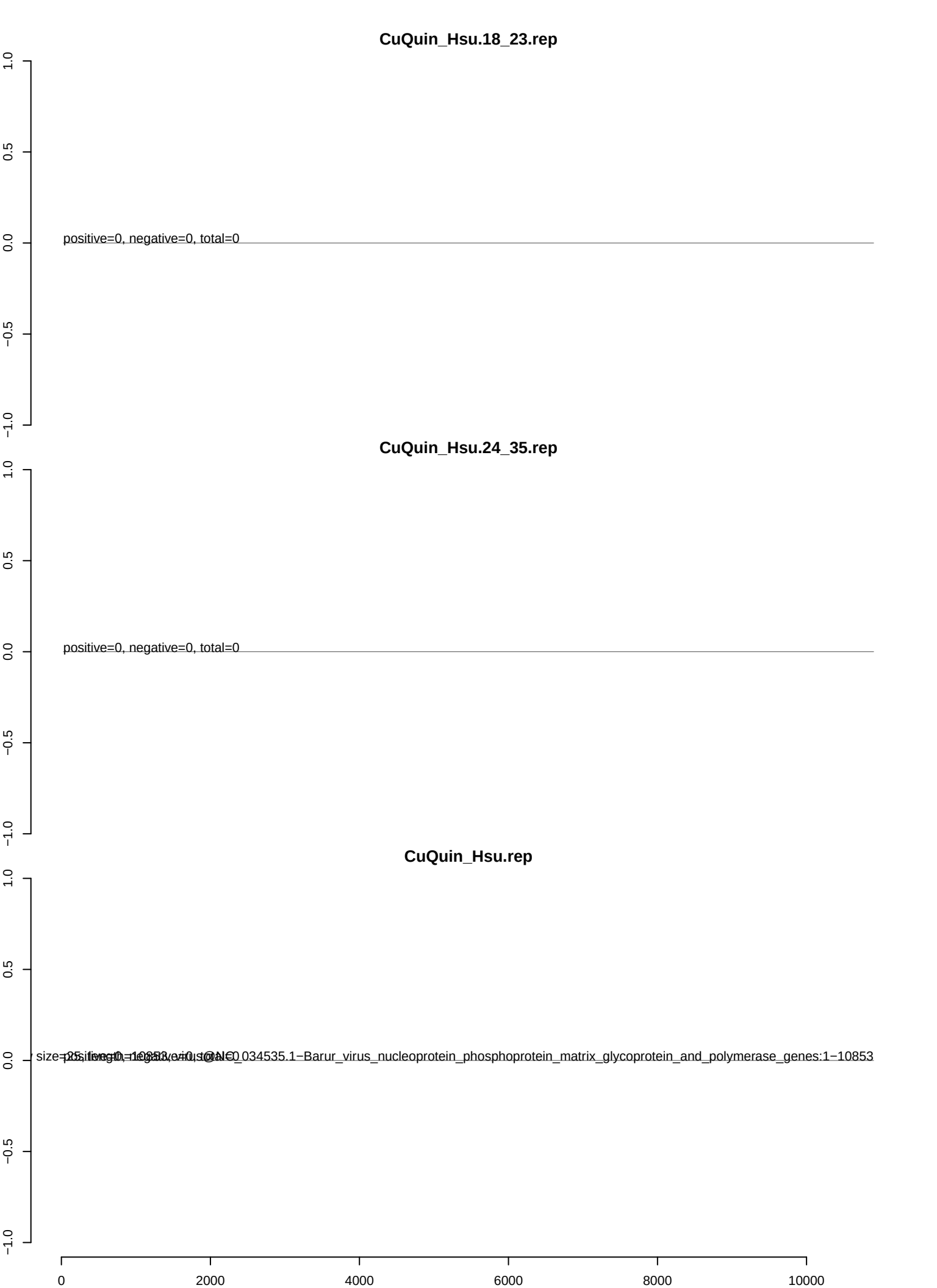
0.5
0.0
−0.5
−1.0
0
5000
10000
15000


CuQuin_Hsu.18_23.rep
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
positive=0, negative=0, total=0
CuQuin_Hsu.rep
size=25, length=10853, strand=0, GNL|Genbank|gb|NC_034535.1−Barur_virus_nucleoprotein_phosphoprotein_matrix_glycoprotein_and_polymerase_genes:1−10853
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0.0
−0.5
−1.0
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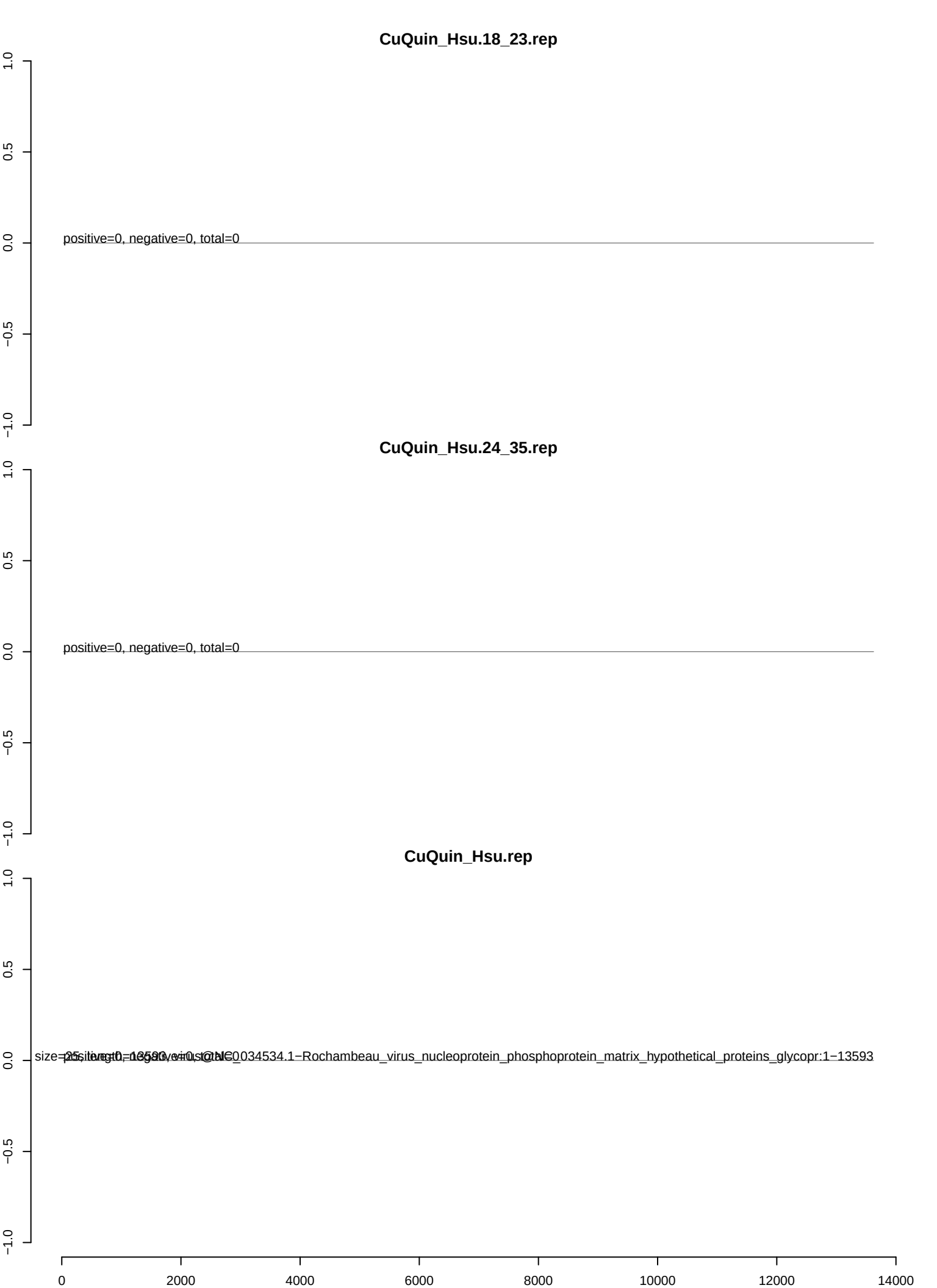
4000
6000
8000
10000


CuQuin_Hsu.18_23.rep
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
positive=0, negative=0, total=0
CuQuin_Hsu.rep
size=25; length=13593; positive=0; negative=0; total=0
25; length=13593; positive=0; negative=0; total=0
NC_034534.1−Rochambeau_virus_nucleoprotein_phosphoprotein_matrix_hypothetical_proteins_glycopr:1−13593
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0.5
0.0
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−1.0
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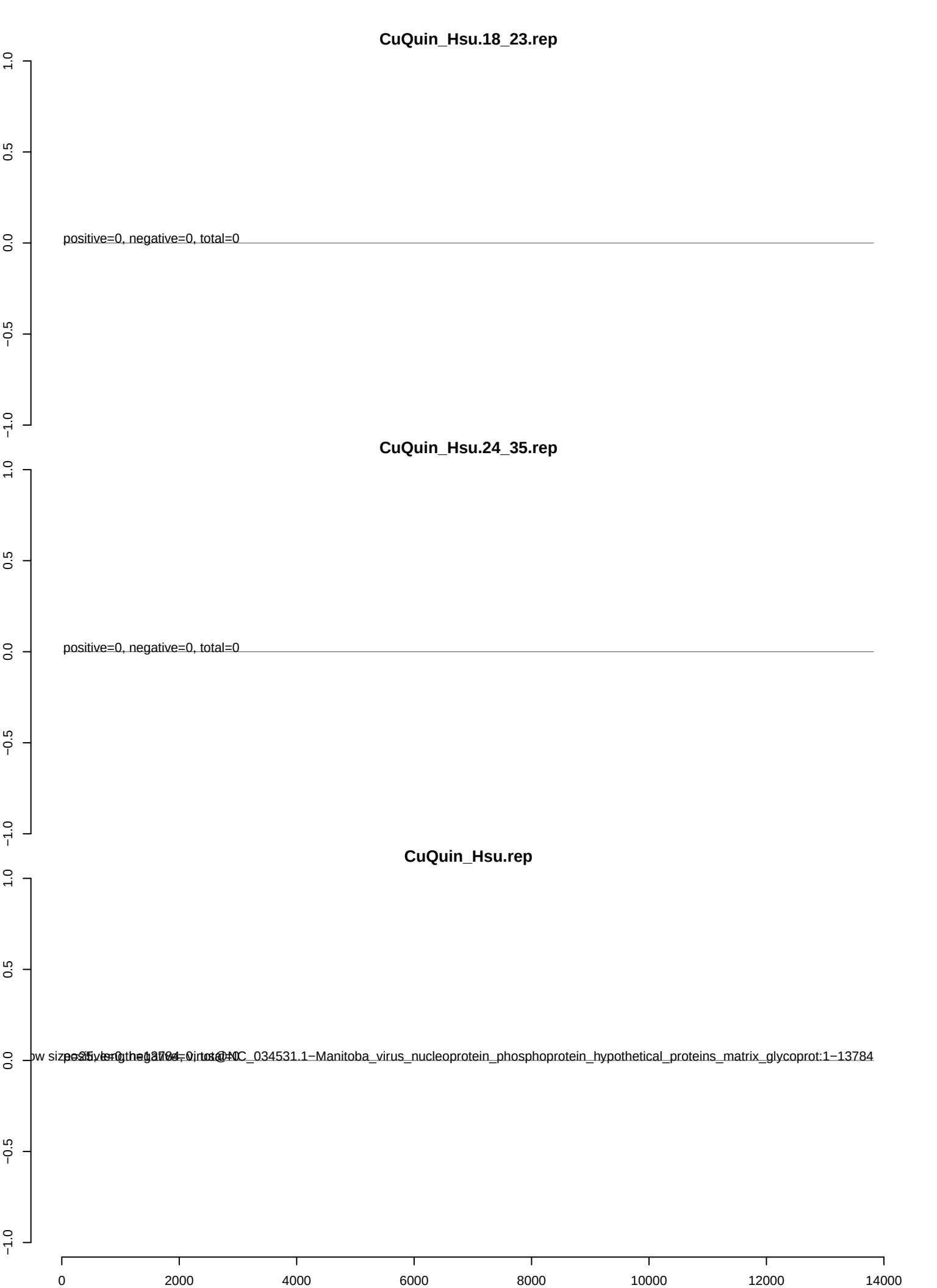
6000
8000
10000
12000
14000


CuQuin_Hsu.18_23.rep
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
positive=0, negative=0, total=0
CuQuin_Hsu.rep
positive=0, negative=0, total=0
low size=95, length=13794, total=1
NC_034531.1−Manitoba_virus_nucleoprotein_phosphoprotein_hypothetical_proteins_matrix_glycoprot:1−13784
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0.5
0.0
−0.5
−1.0
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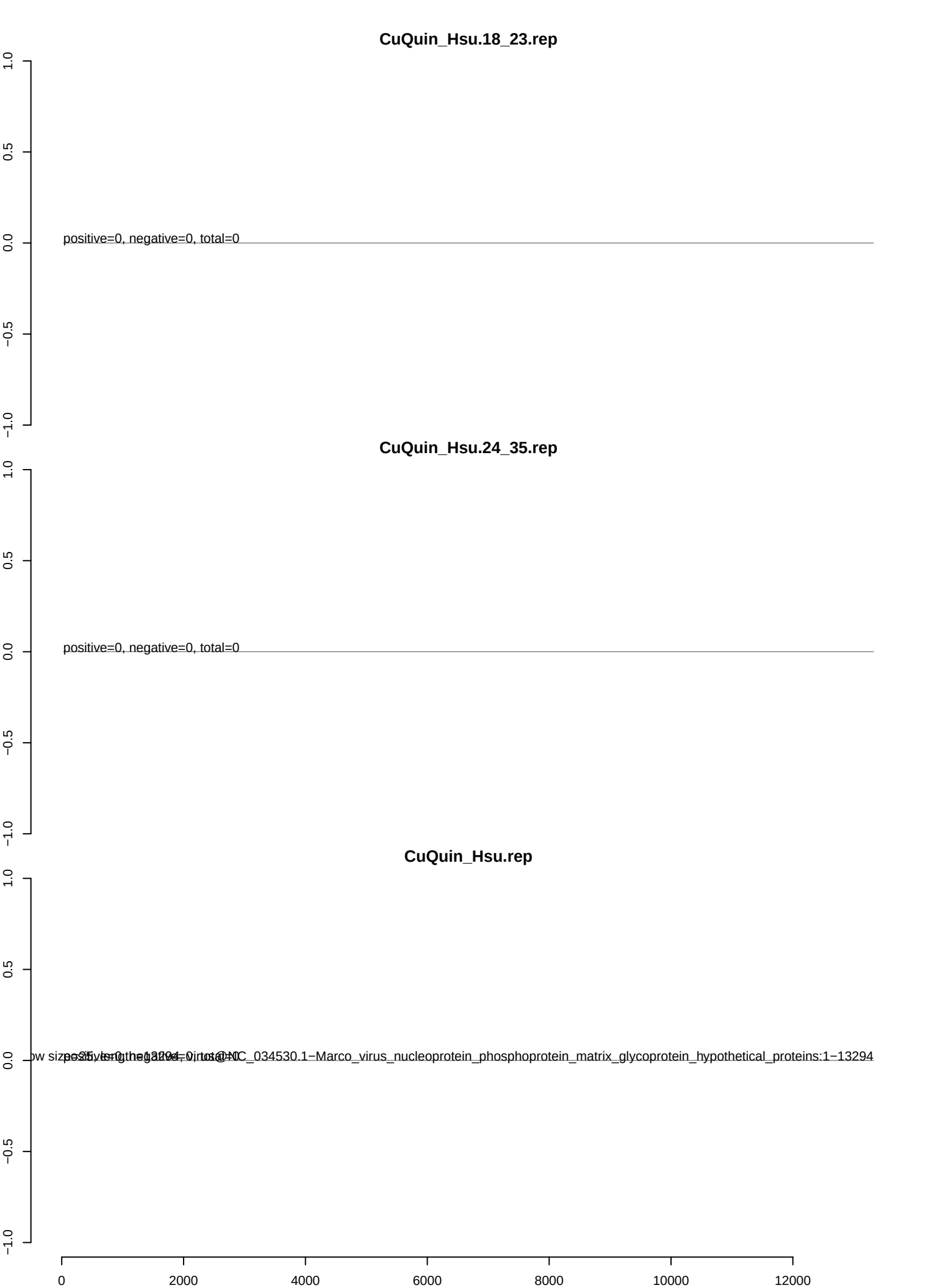
8000
10000
12000
14000


CuQuin_Hsu.18_23.rep
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
positive=0, negative=0, total=0
CuQuin_Hsu.rep
positive=0, negative=0, total=0
low size: NC_034530.1−Marco_virus_nucleoprotein_phosphoprotein_matrix_glycoprotein_hypothetical_proteins:1−13294
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0.5
0.0
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−1.0
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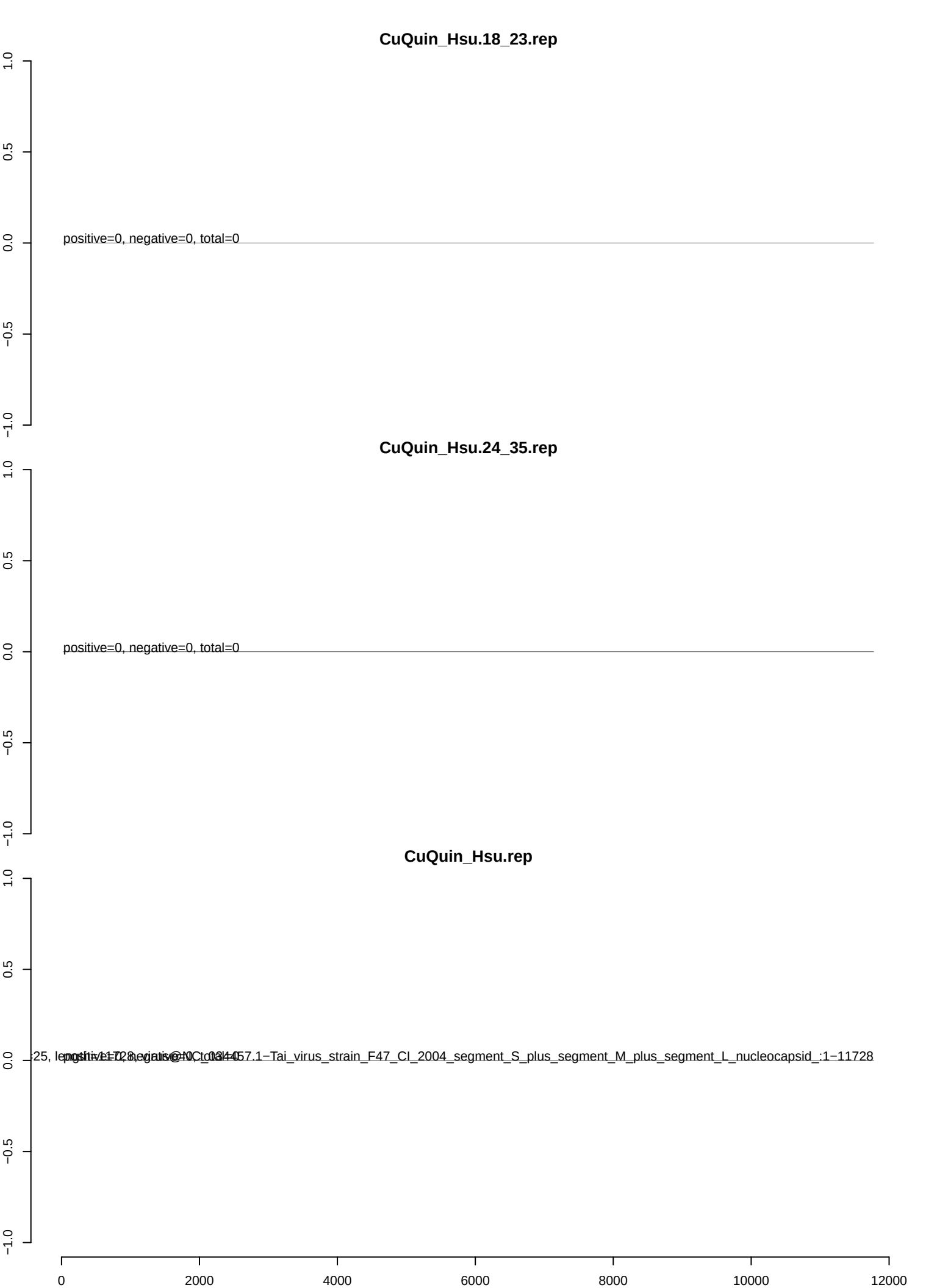
6000
8000
10000
12000


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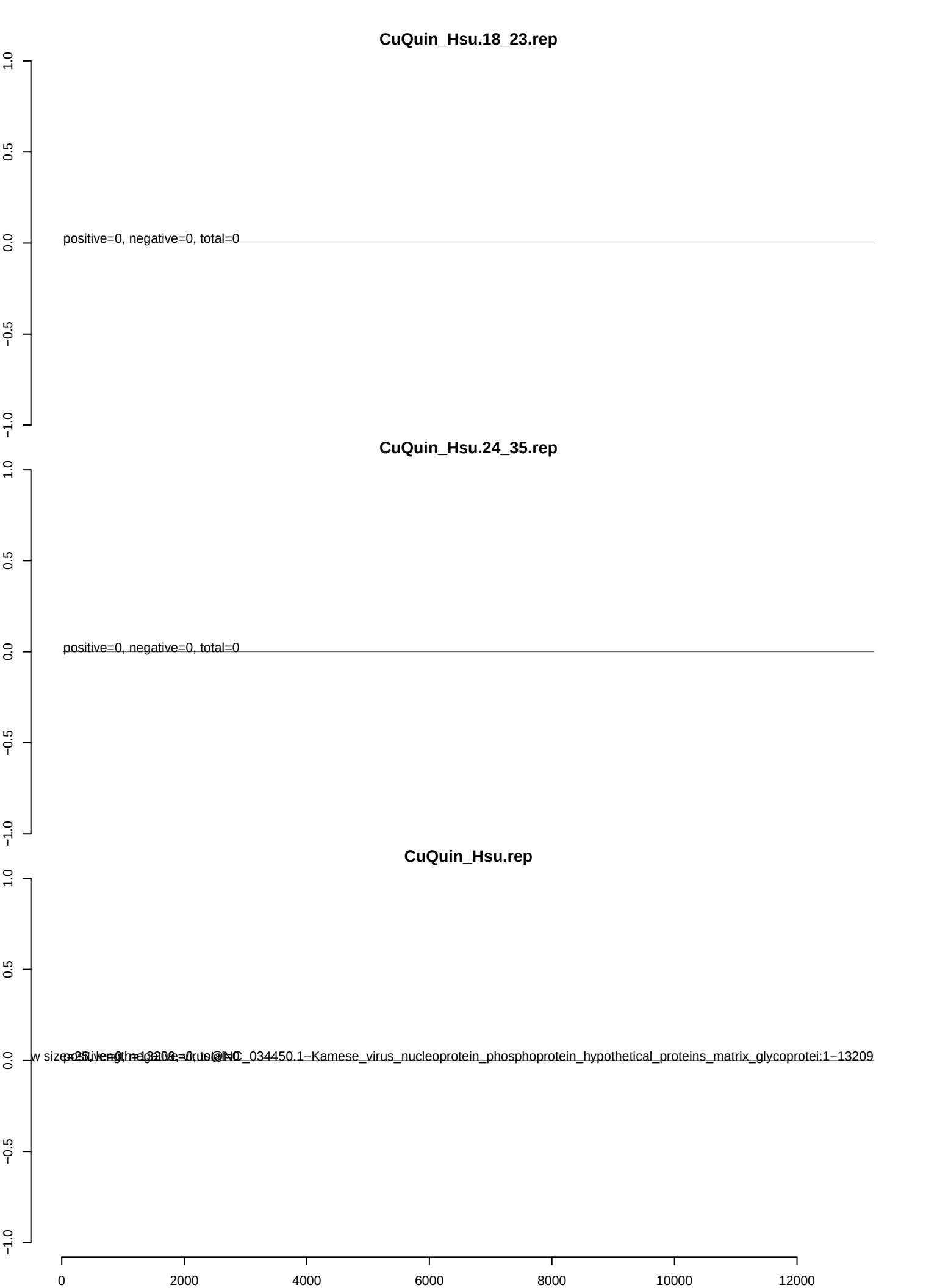
4000
6000
8000
10000
12000


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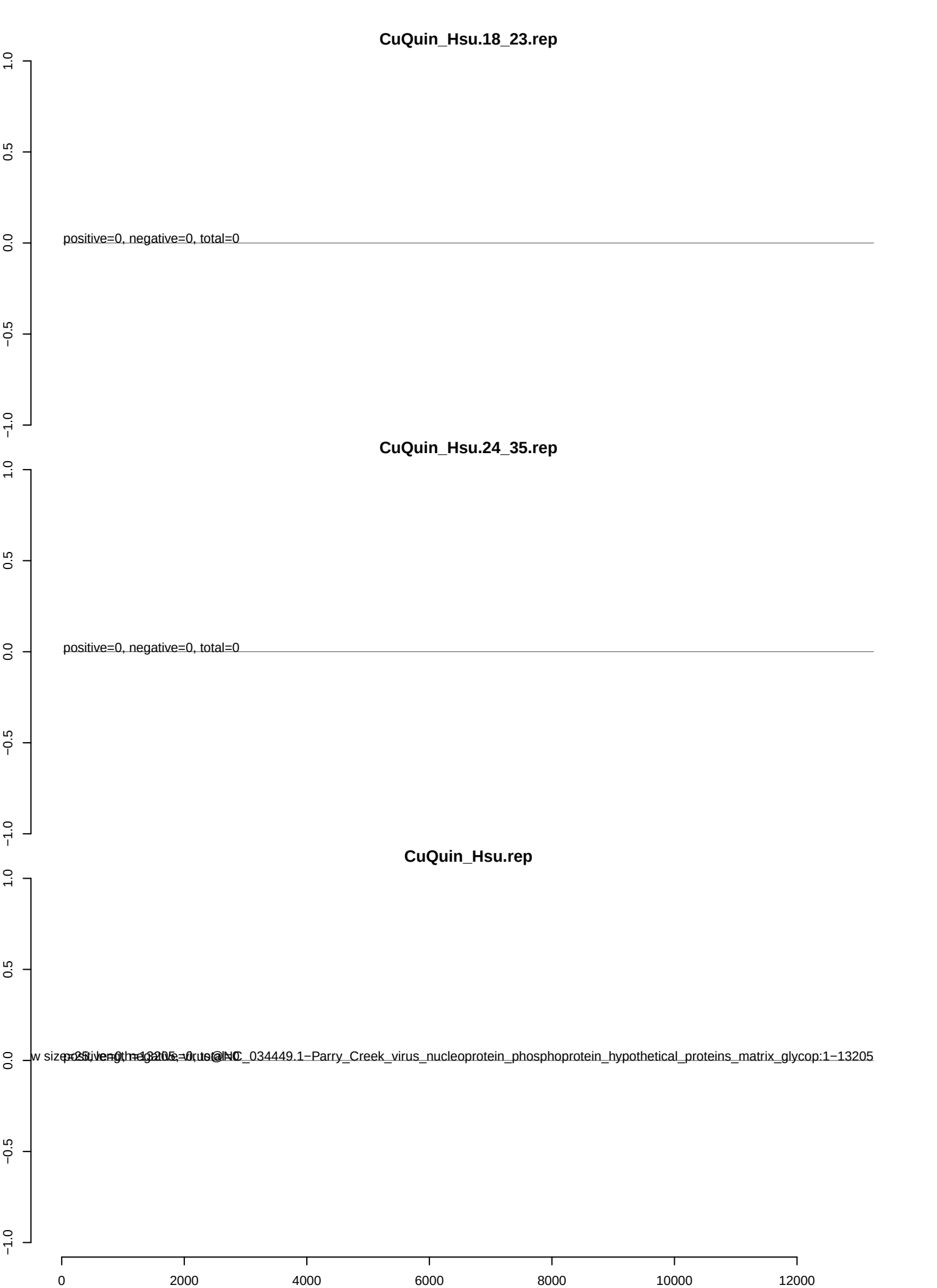
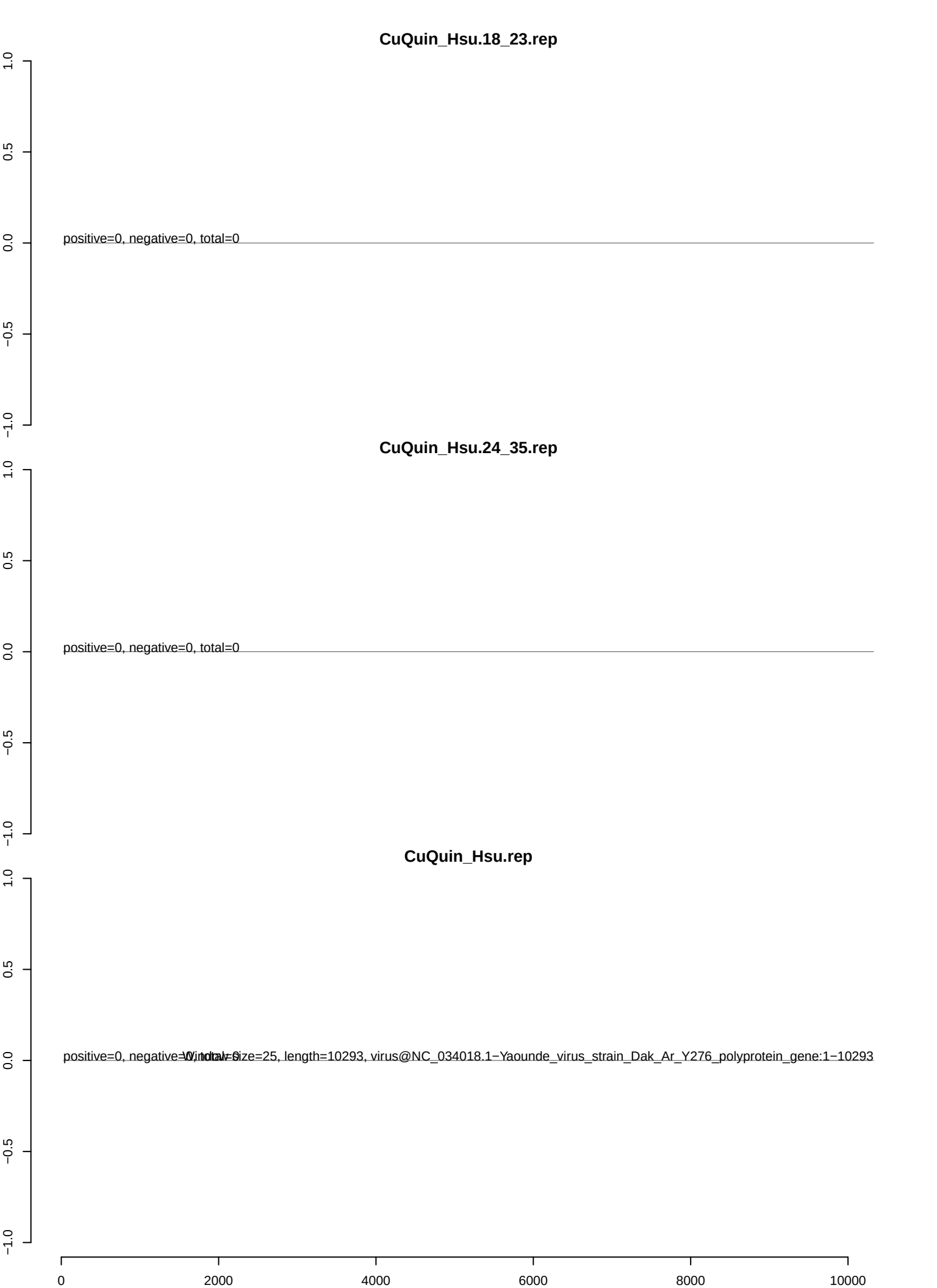
6000
8000
10000
12000


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


CuQuin_Hsu.18_23.rep
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
positive=0, negative=0, total=0
CuQuin_Hsu.rep
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
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0.0
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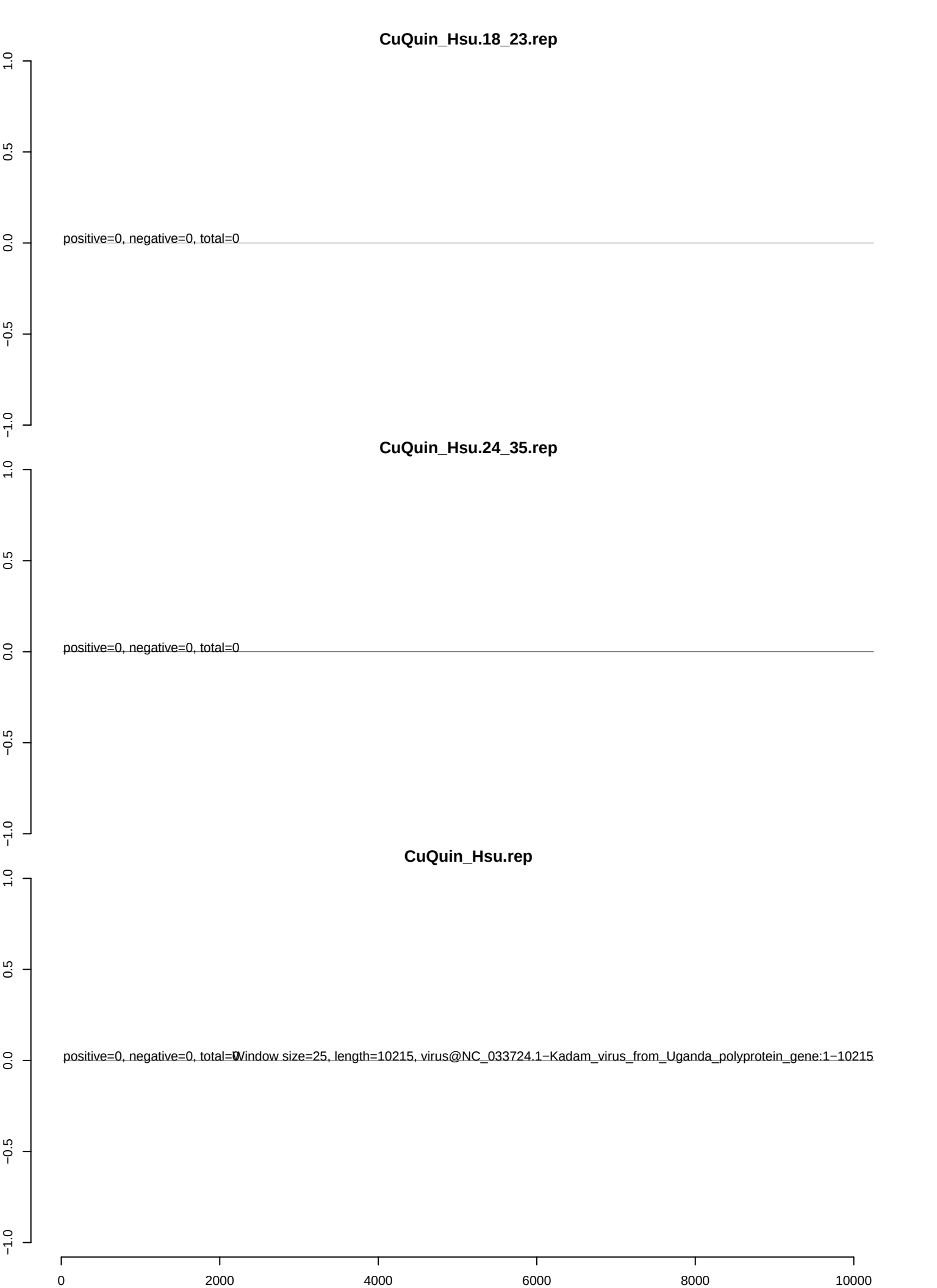
4000
6000
8000
10000


CuQuin_Hsu.18_23.rep
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
positive=0, negative=0, total=0
CuQuin_Hsu.rep
positive=0, negative=0, total=0
Window size=25, length=10215, virus@NC_033724.1−Kadam_virus_from_Uganda_polyprotein_gene:1−10215
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0.0
−0.5
−1.0
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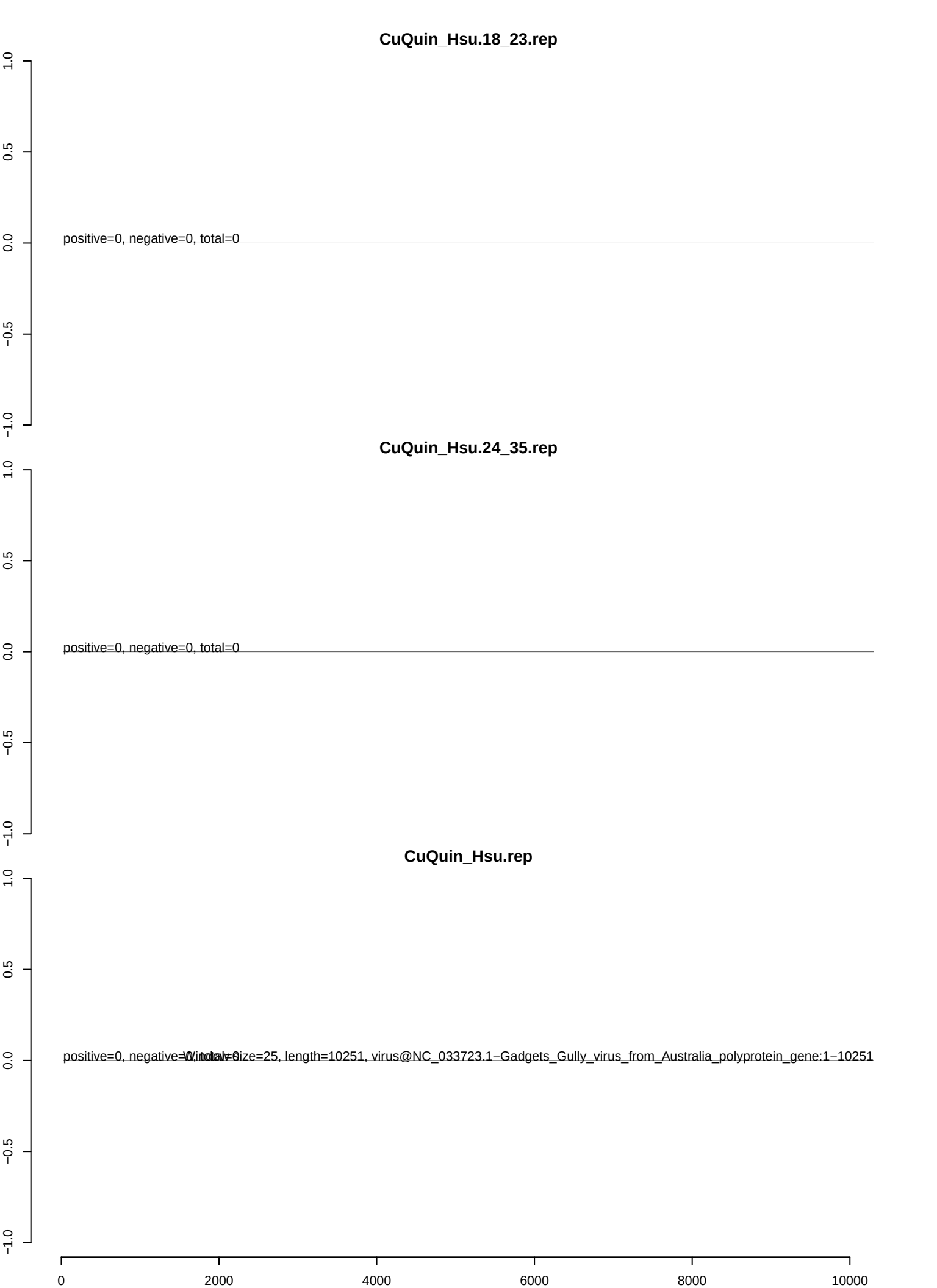
2000
4000
6000
8000
10000


CuQuin_Hsu.18_23.rep
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
positive=0, negative=0, total=0
CuQuin_Hsu.rep
positive=0, negative=0, total=0
Window size=25, length=10251, virus@NC_033723.1−Gadgets_Gully_virus_from_Australia_polyprotein_gene:1−10251
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−1.0
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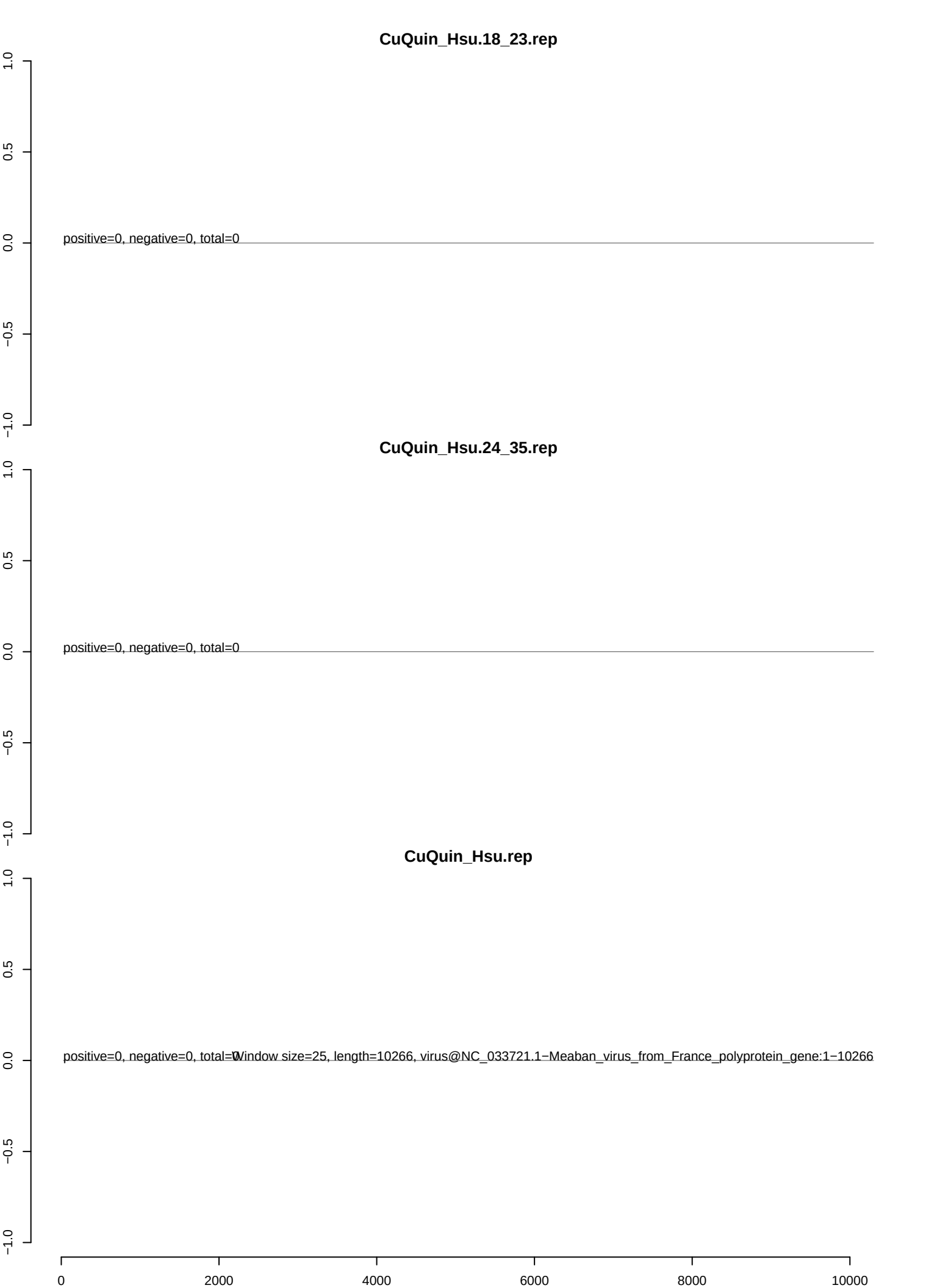
2000
4000
6000
8000
10000


CuQuin_Hsu.18_23.rep
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
positive=0, negative=0, total=0
CuQuin_Hsu.rep
positive=0, negative=0, total=0
Window size=25, length=10266, virus@NC_033721.1−Meaban_virus_from_France_polyprotein_gene:1−10266
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0.0
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−1.0
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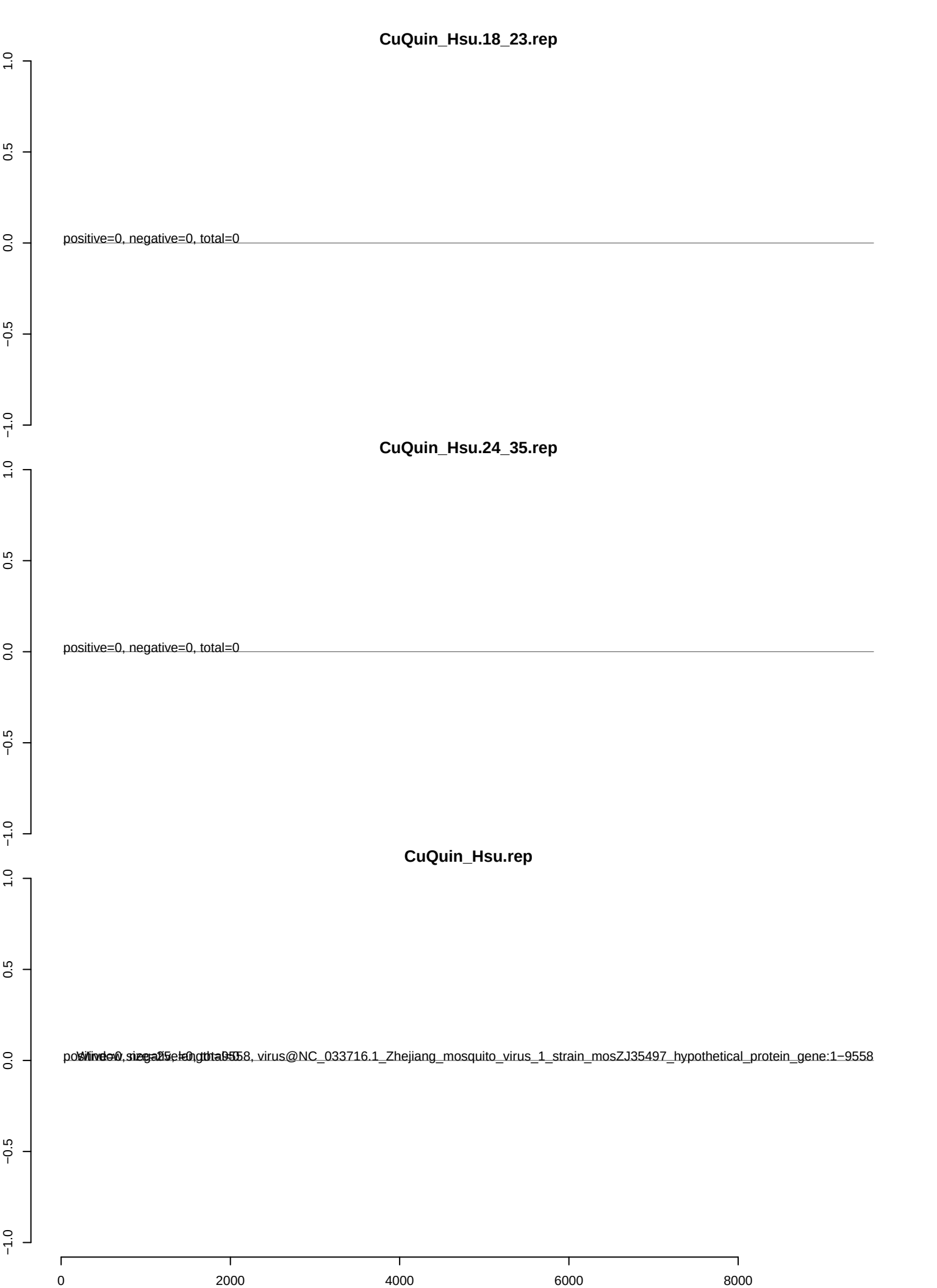
4000
6000
8000
10000


CuQuin_Hsu.18_23.rep
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
positive=0, negative=0, total=0
CuQuin_Hsu.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
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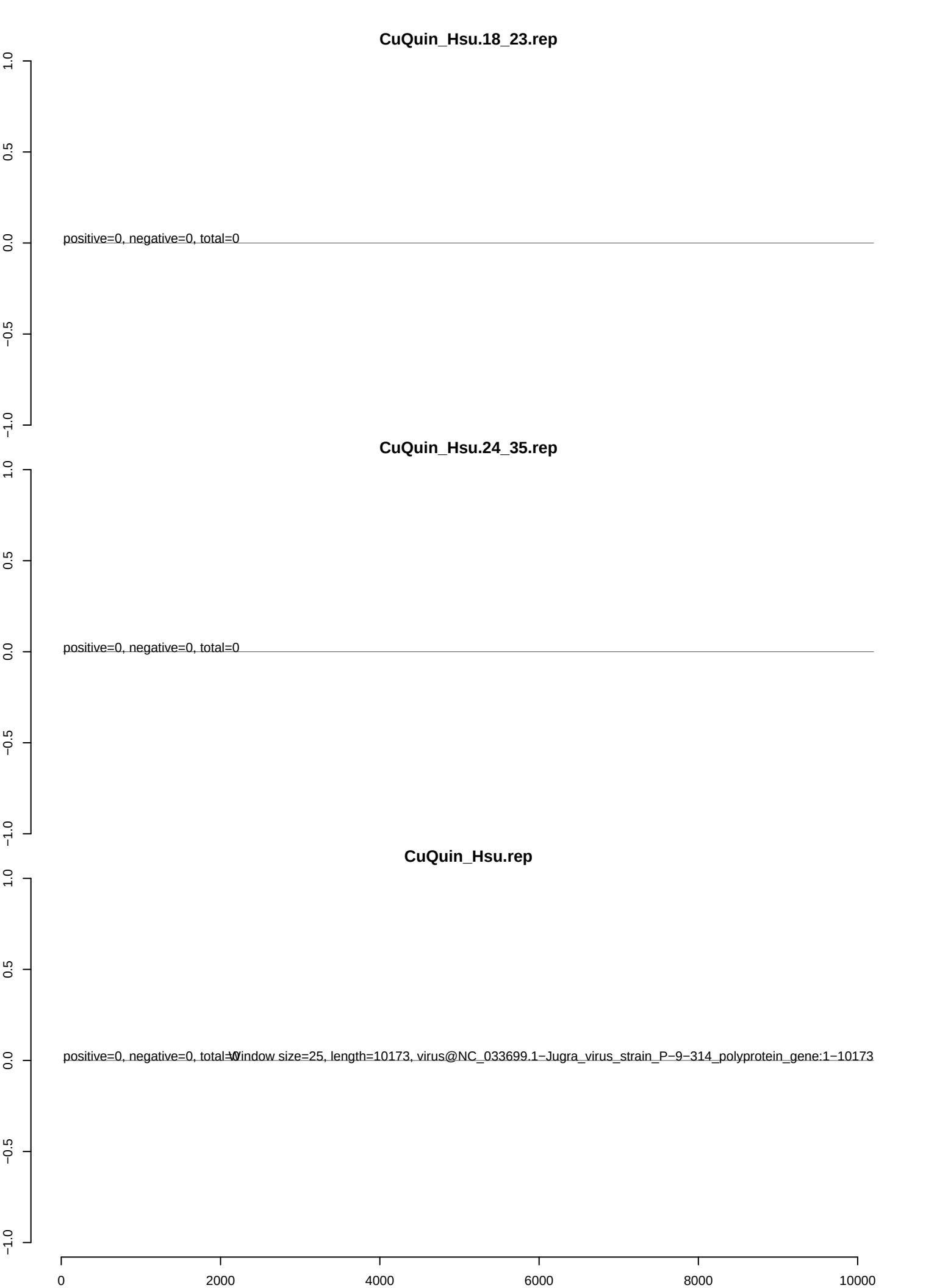
−1.0
0
2000
4000
6000
8000


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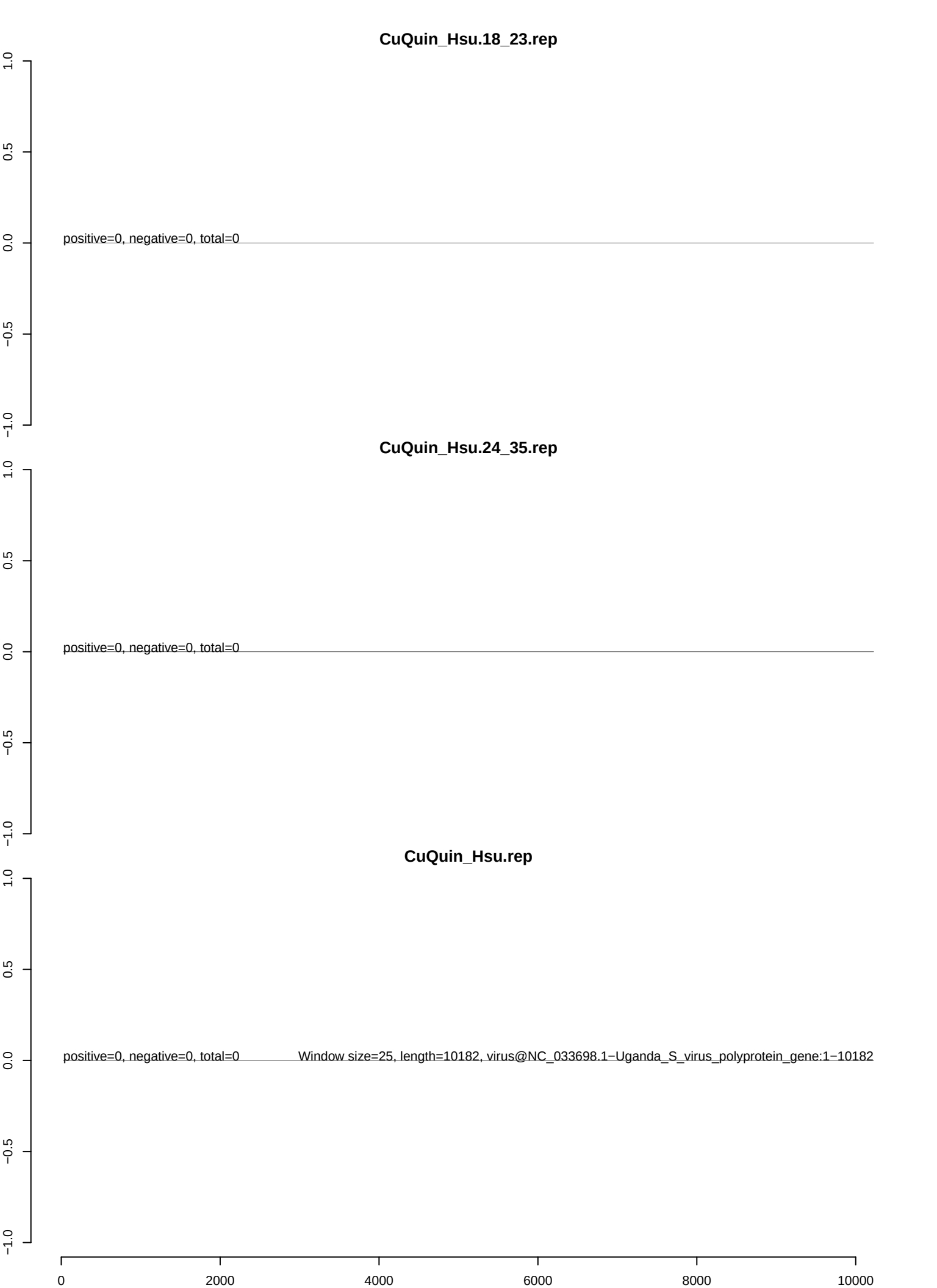
0.0
−0.5
−1.0
0
2000
4000
6000
8000
10000


CuQuin_Hsu.18_23.rep
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0.5
0.0
−0.5
−1.0
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
1.0
0.5
0.0
−0.5
−1.0
positive=0, negative=0, total=0
CuQuin_Hsu.rep
1.0
0.5
0.0
−0.5
−1.0
positive=0, negative=0, total=0
Window size=25, length=10182, virus@NC_033698.1−Uganda_S_virus_polyprotein_gene:1−10182
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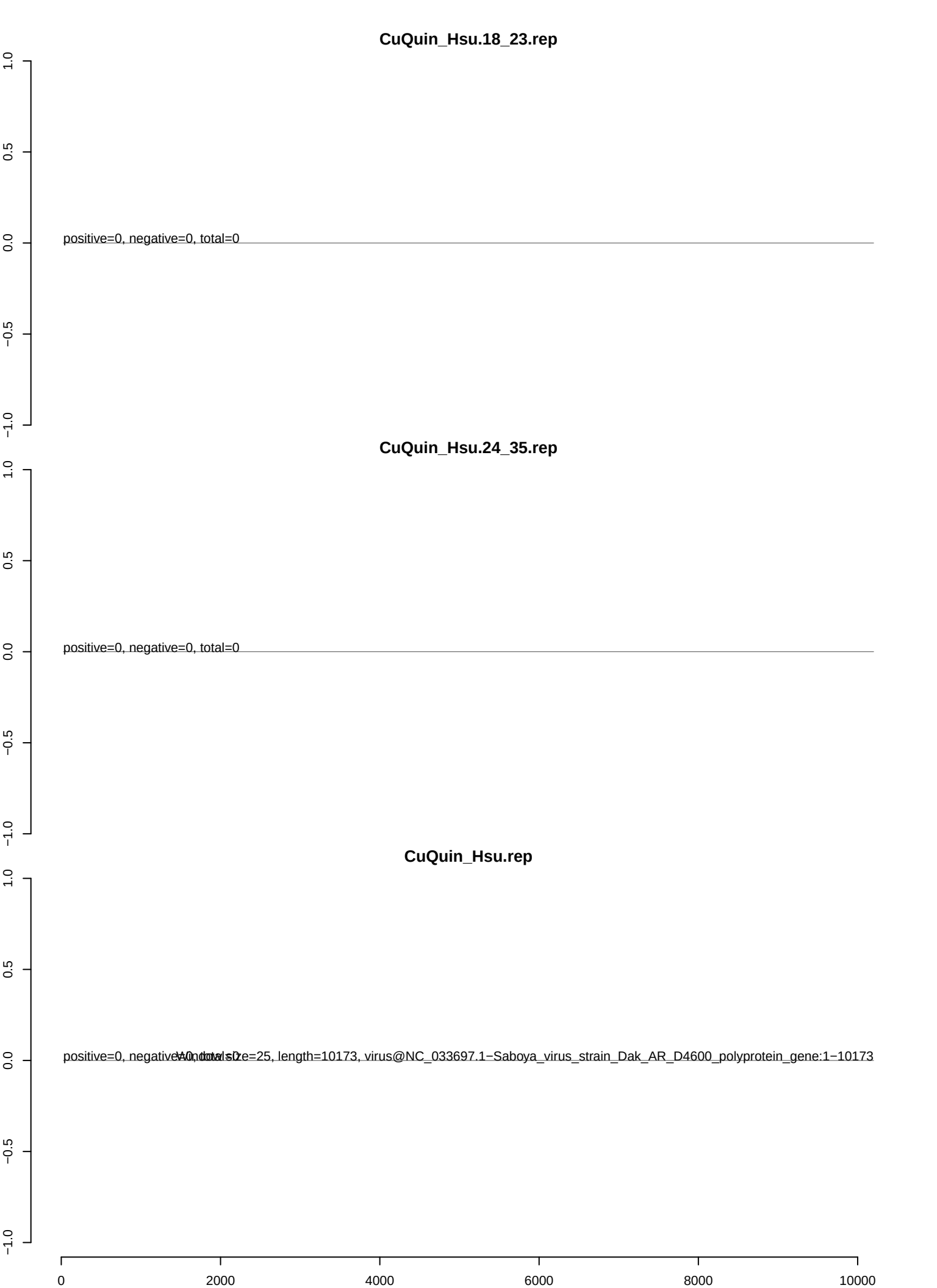
4000
6000
8000
10000


CuQuin_Hsu.18_23.rep
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
positive=0, negative=0, total=0
CuQuin_Hsu.rep
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1.0
0.5
0.0
−0.5
−1.0
0
2000
4000
6000
8000
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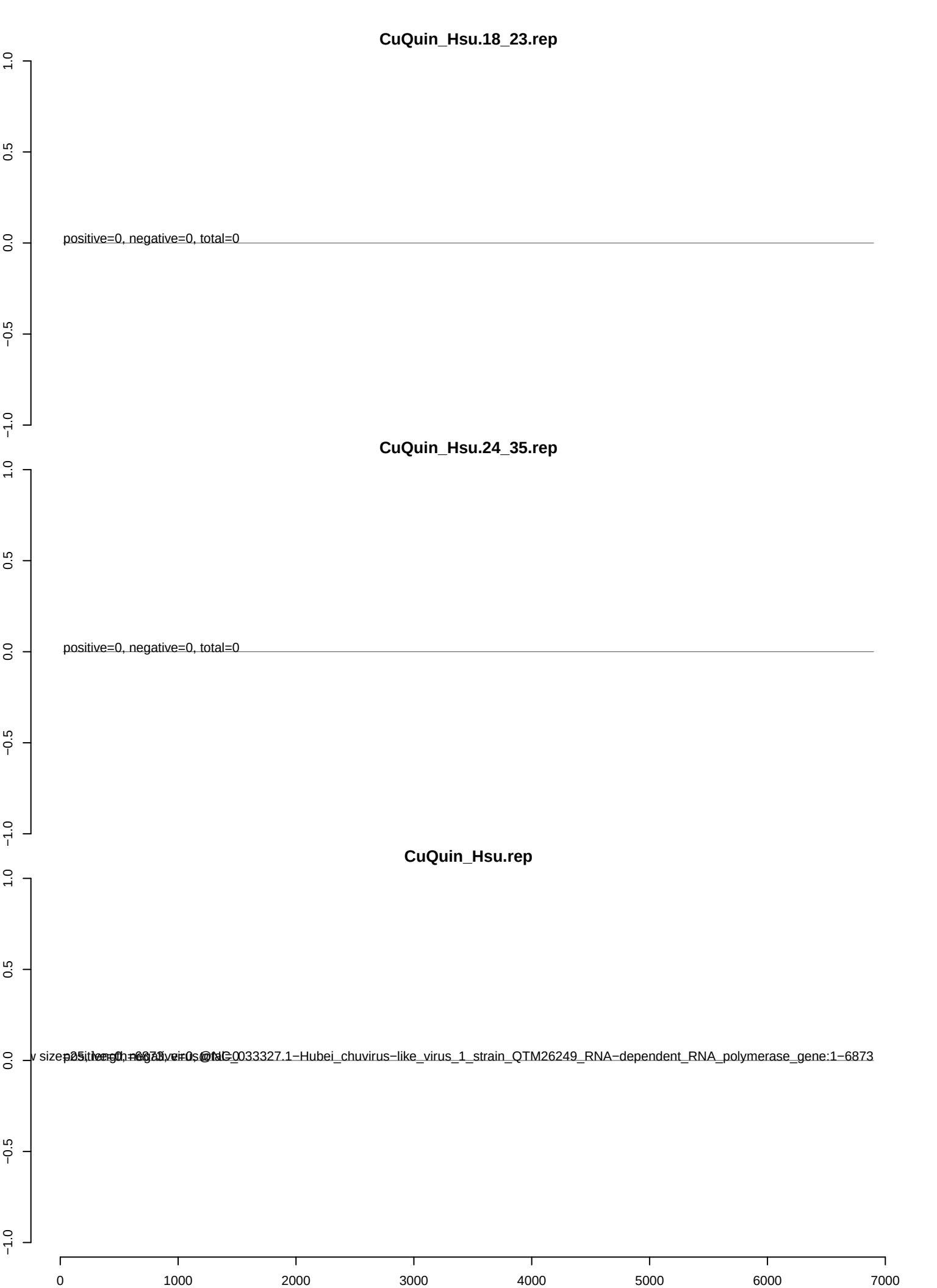
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CuQuin_Hsu.24_35.rep
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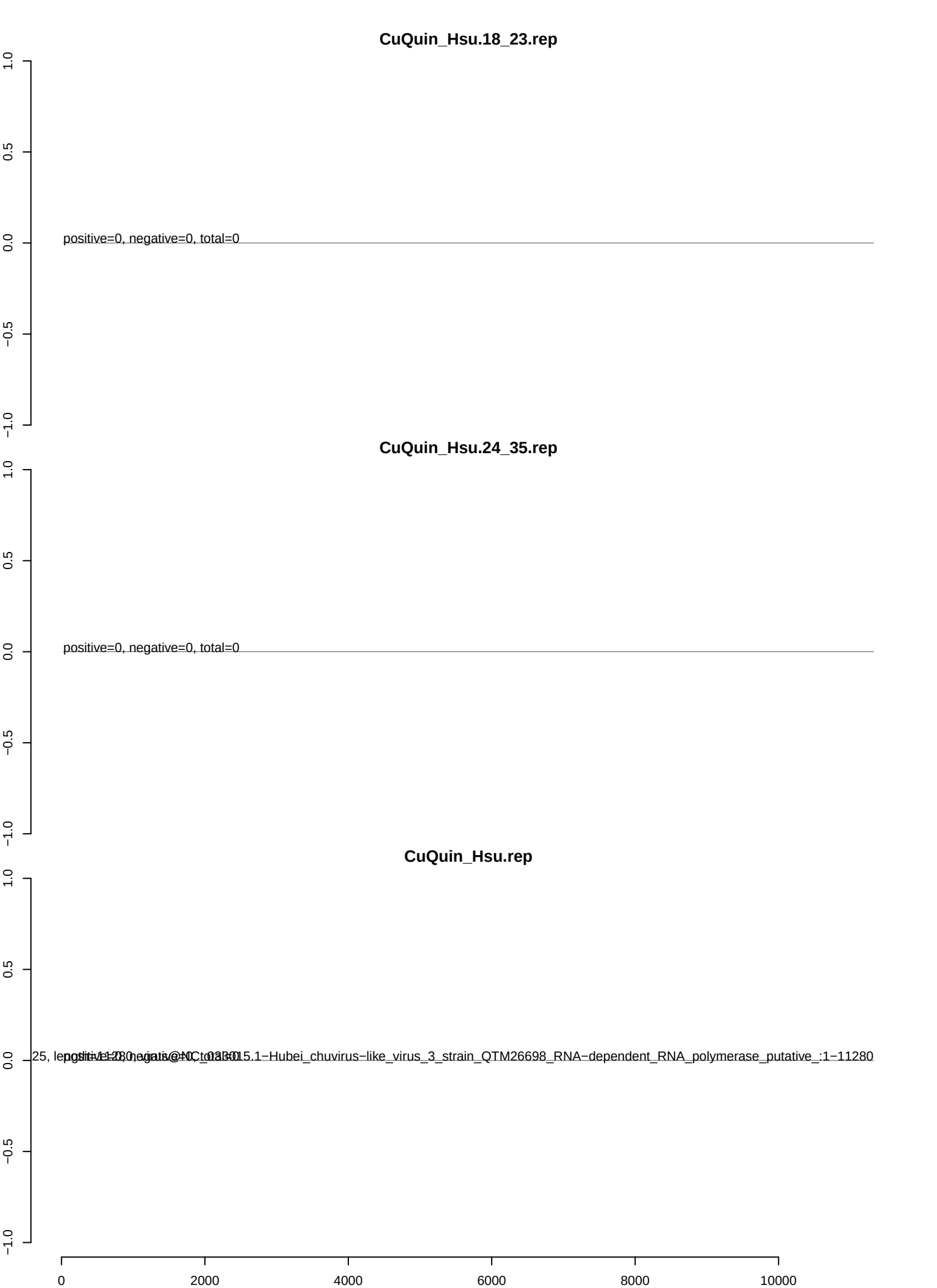
CuQuin_Hsu.18_23.rep
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CuQuin_Hsu.24_35.rep
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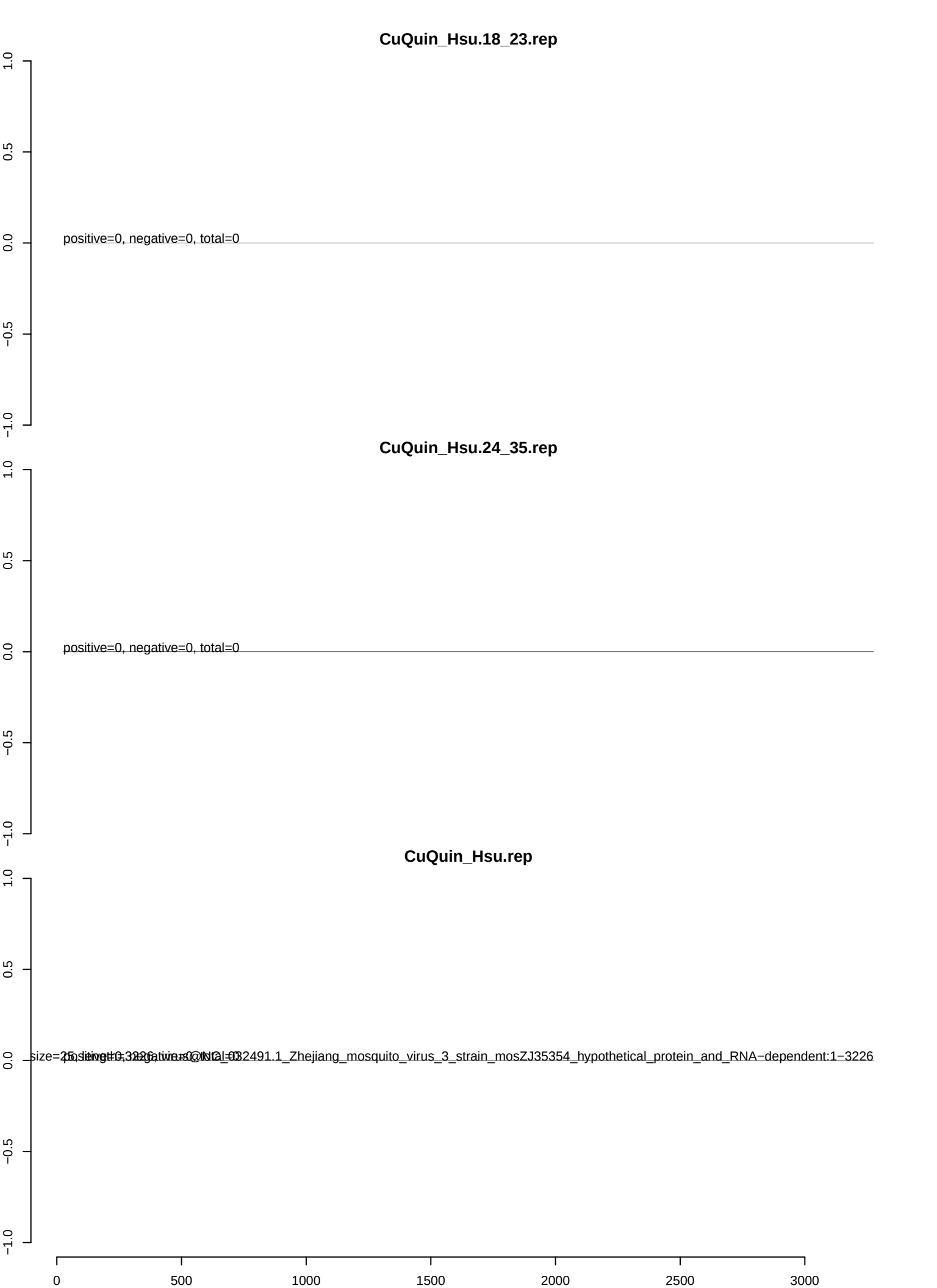
CuQuin_Hsu.18_23.rep
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CuQuin_Hsu.24_35.rep
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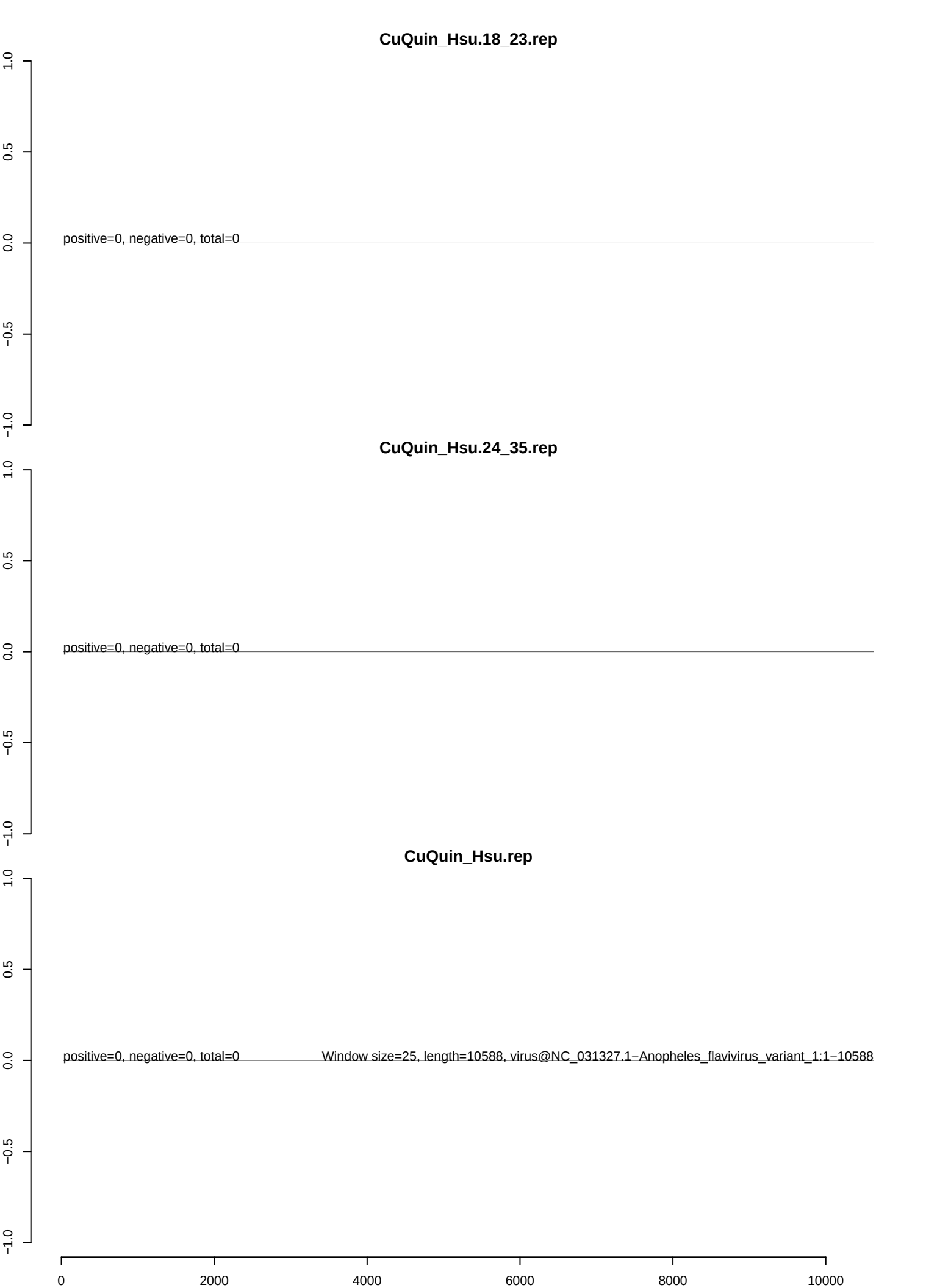
CuQuin_Hsu.18_23.rep
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positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
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0.5
0.0
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−1.0
positive=0, negative=0, total=0
CuQuin_Hsu.rep
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0.5
0.0
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−1.0
positive=0, negative=0, total=0
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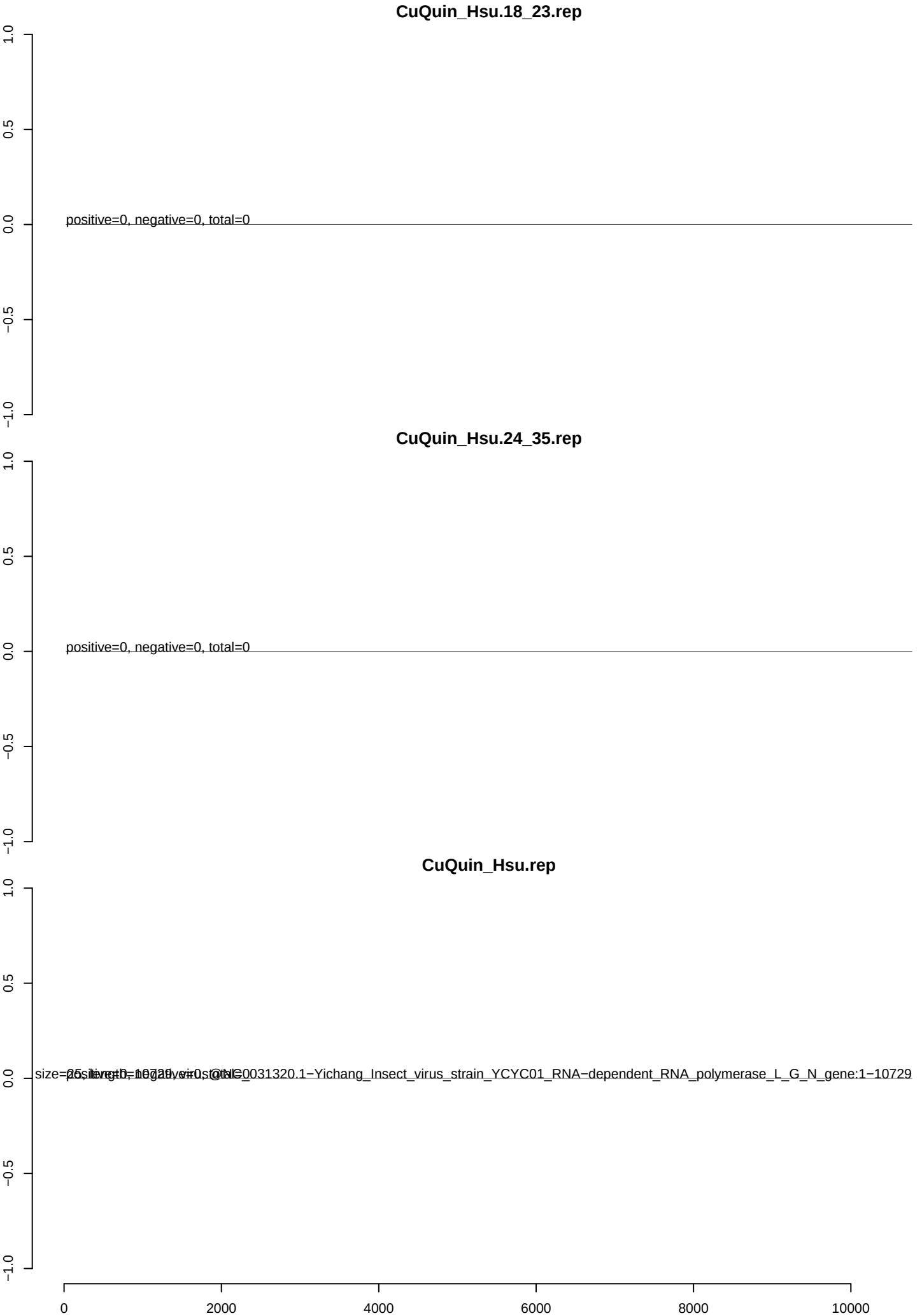
CuQuin_Hsu.18_23.rep
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CuQuin_Hsu.24_35.rep
positive=0, negative=0, total=0
CuQuin_Hsu.rep
size=25, length=10729, positive=0, negative=0, total=0
QNL31320.1−Yichang_Insect_virus_strain_YCYC01_RNA−dependent_RNA_polymerase_L_G_N_gene:1−10729
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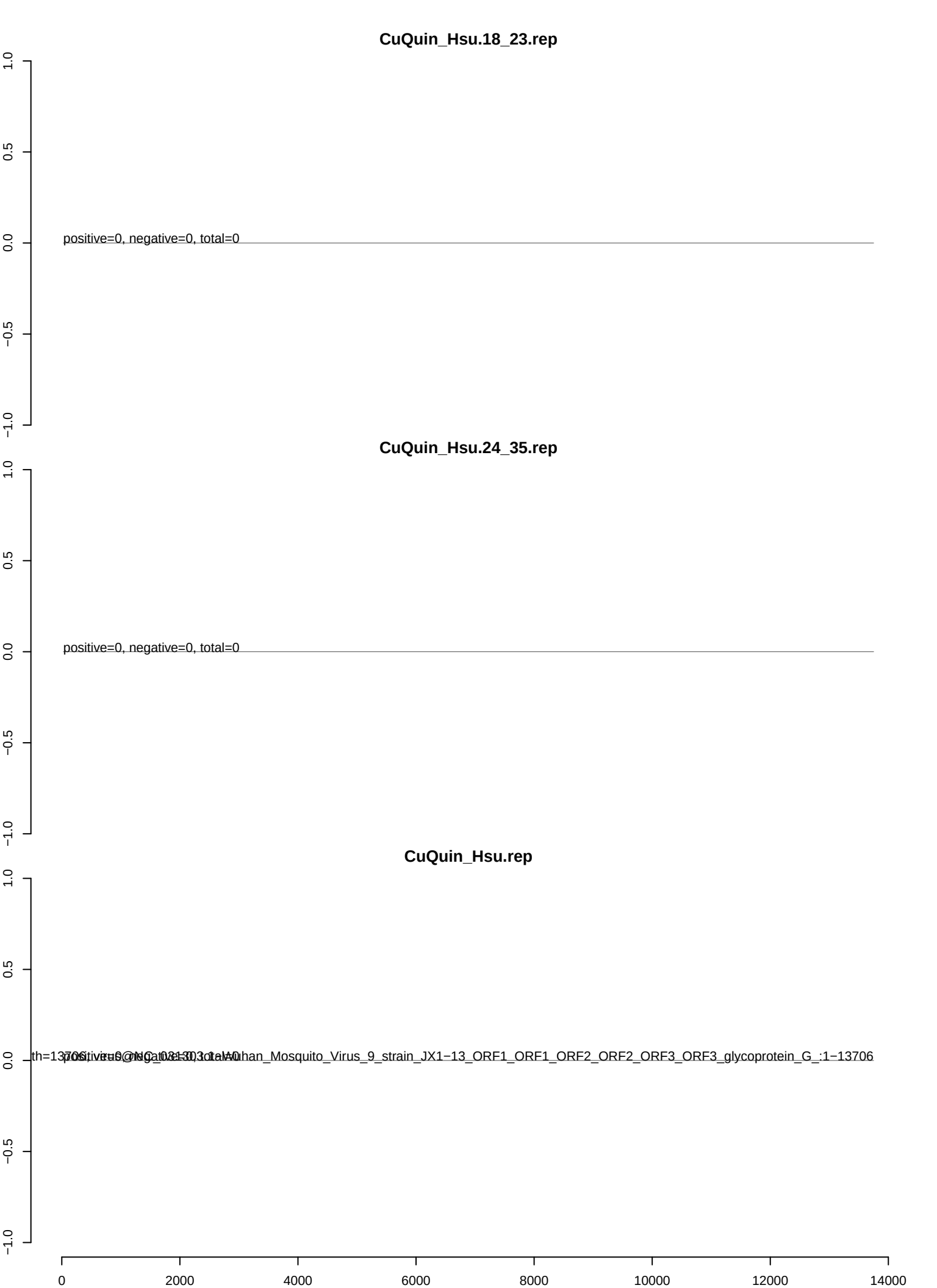
CuQuin_Hsu.18_23.rep
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CuQuin_Hsu.24_35.rep
positive=0, negative=0, total=0
CuQuin_Hsu.rep
positive=0, negative=0, total=0
Wuhan_Mosquito_Virus_9_strain_JX1−13_ORF1_ORF1_ORF2_ORF2_ORF3_ORF3_glycoprotein_G_:1−13706
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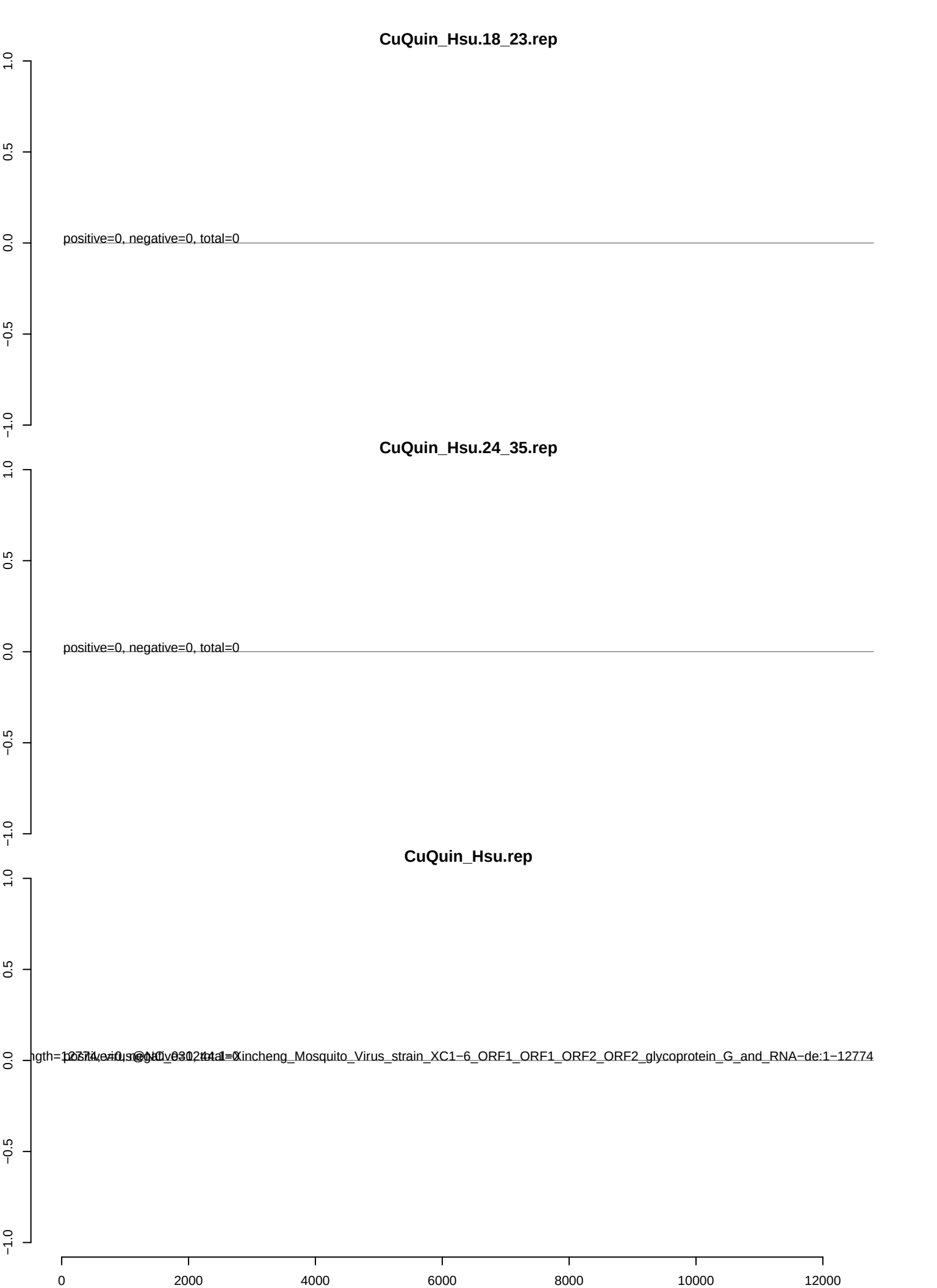
CuQuin_Hsu.18_23.rep
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CuQuin_Hsu.24_35.rep
positive=0, negative=0, total=0
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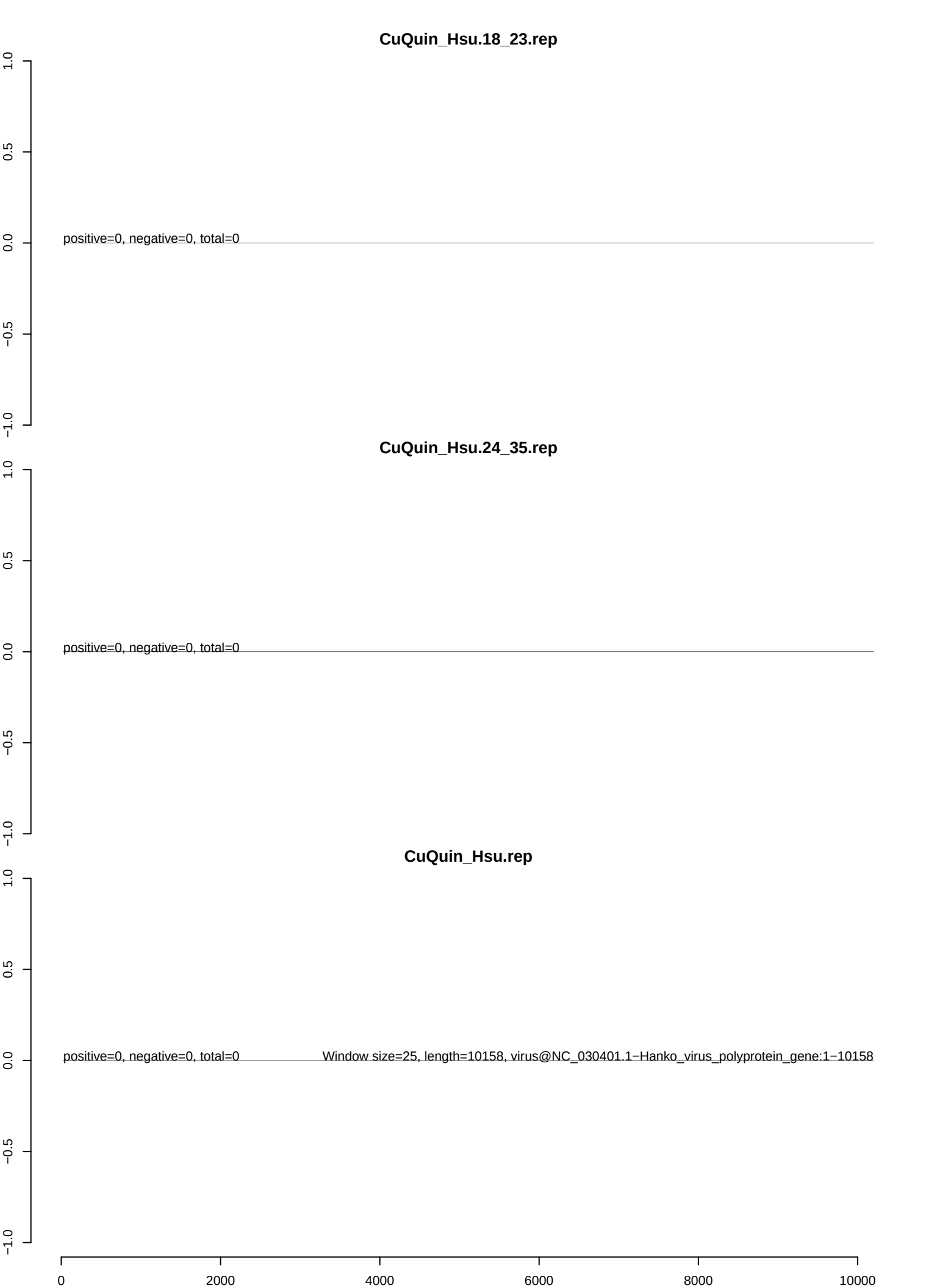
CuQuin_Hsu.18_23.rep
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positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
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0.5
0.0
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−1.0
positive=0, negative=0, total=0
CuQuin_Hsu.rep
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0.0
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positive=0, negative=0, total=0
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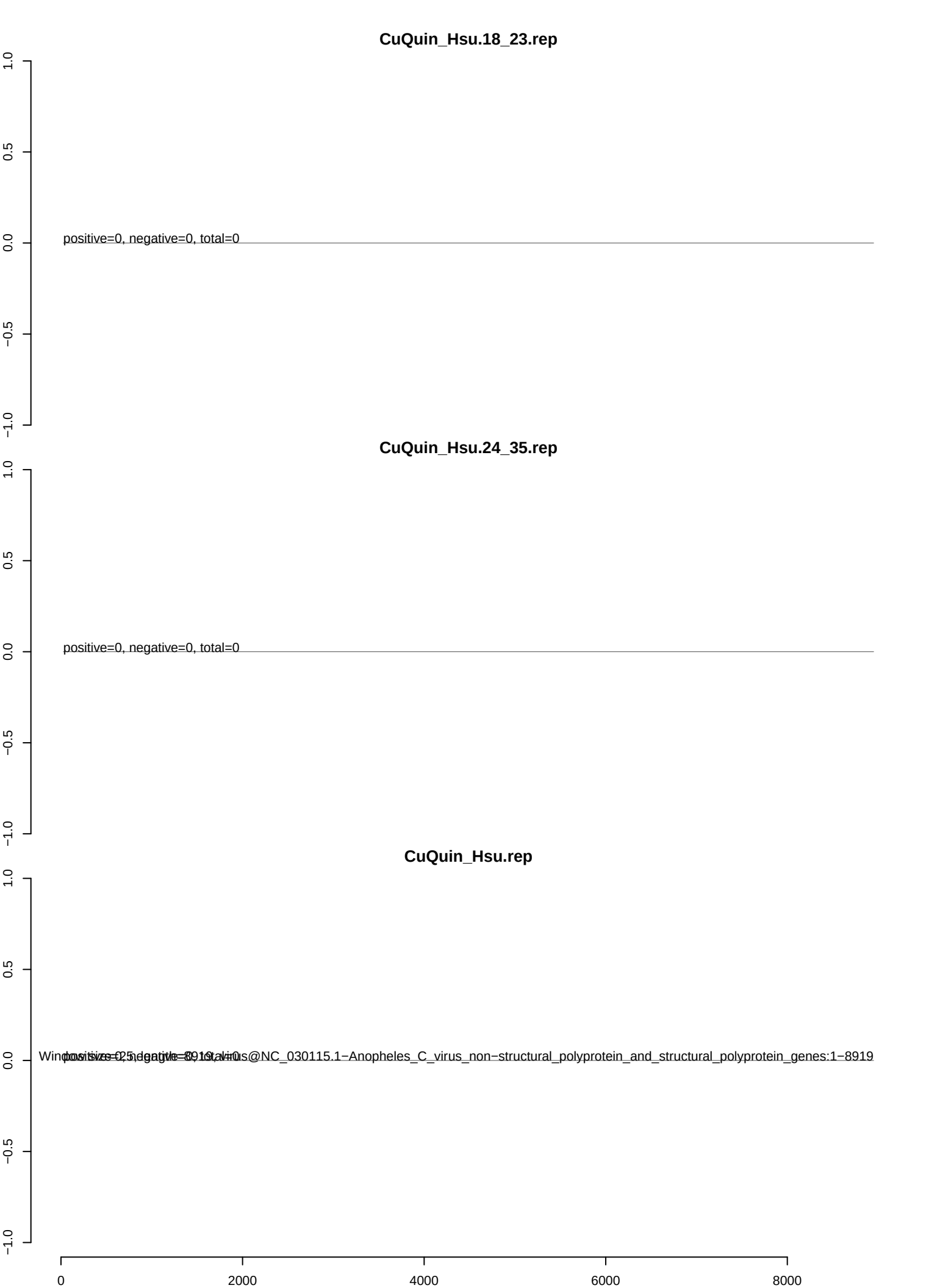
CuQuin_Hsu.18_23.rep
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
positive=0, negative=0, total=0
CuQuin_Hsu.rep
positive=25, negative=8919, total=0
Window size=5, gap=0, step=1
Anopheles_C_virus@NC_030115.1−Anopheles_C_virus_non−structural_polyprotein_and_structural_polyprotein_genes:1−8919
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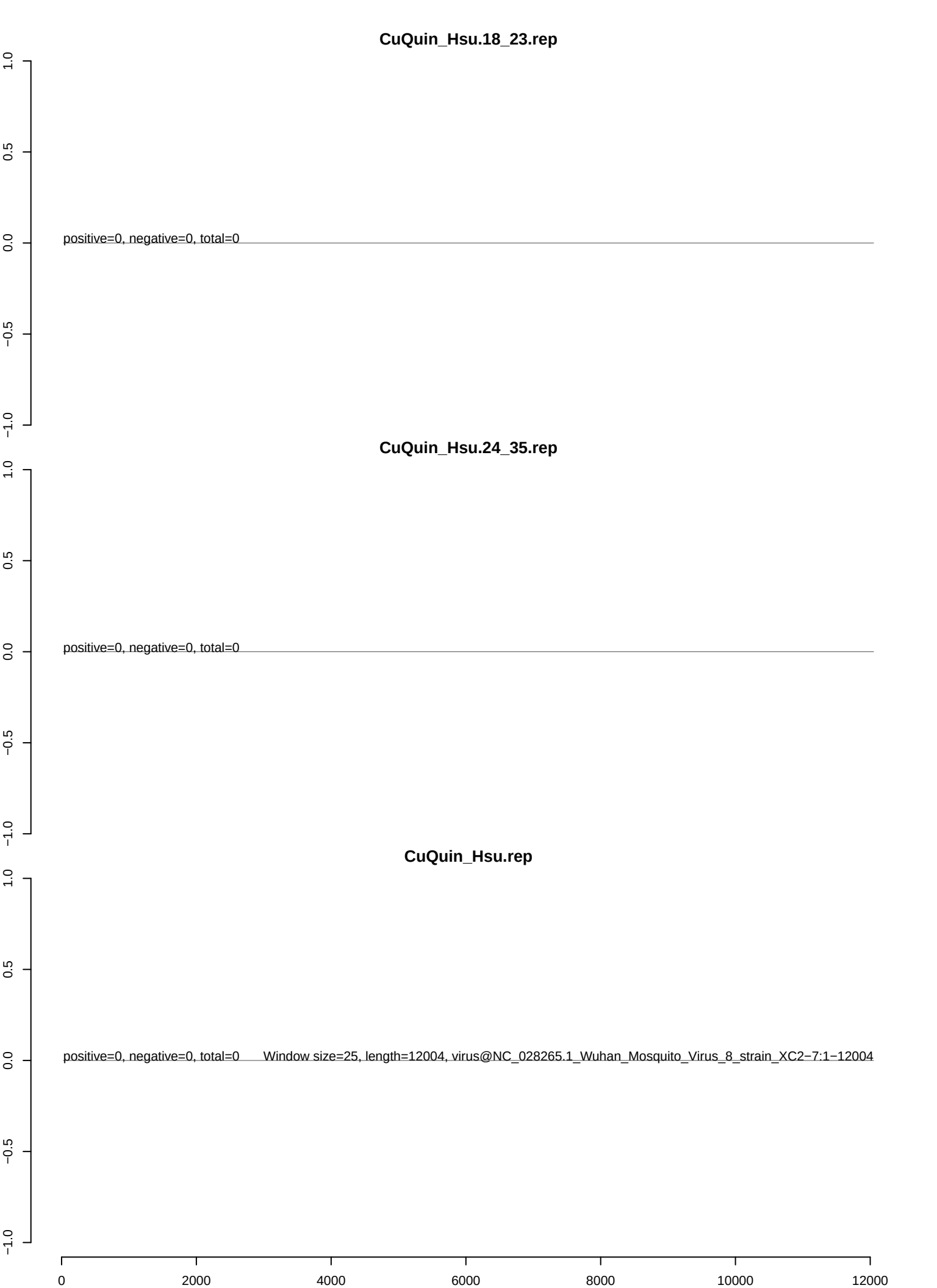
CuQuin_Hsu.18_23.rep
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CuQuin_Hsu.24_35.rep
positive=0, negative=0, total=0
CuQuin_Hsu.rep
positive=0, negative=0, total=0
Window size=25, length=12004, virus@NC_028265.1_Wuhan_Mosquito_Virus_8_strain_XC2−7:1−12004
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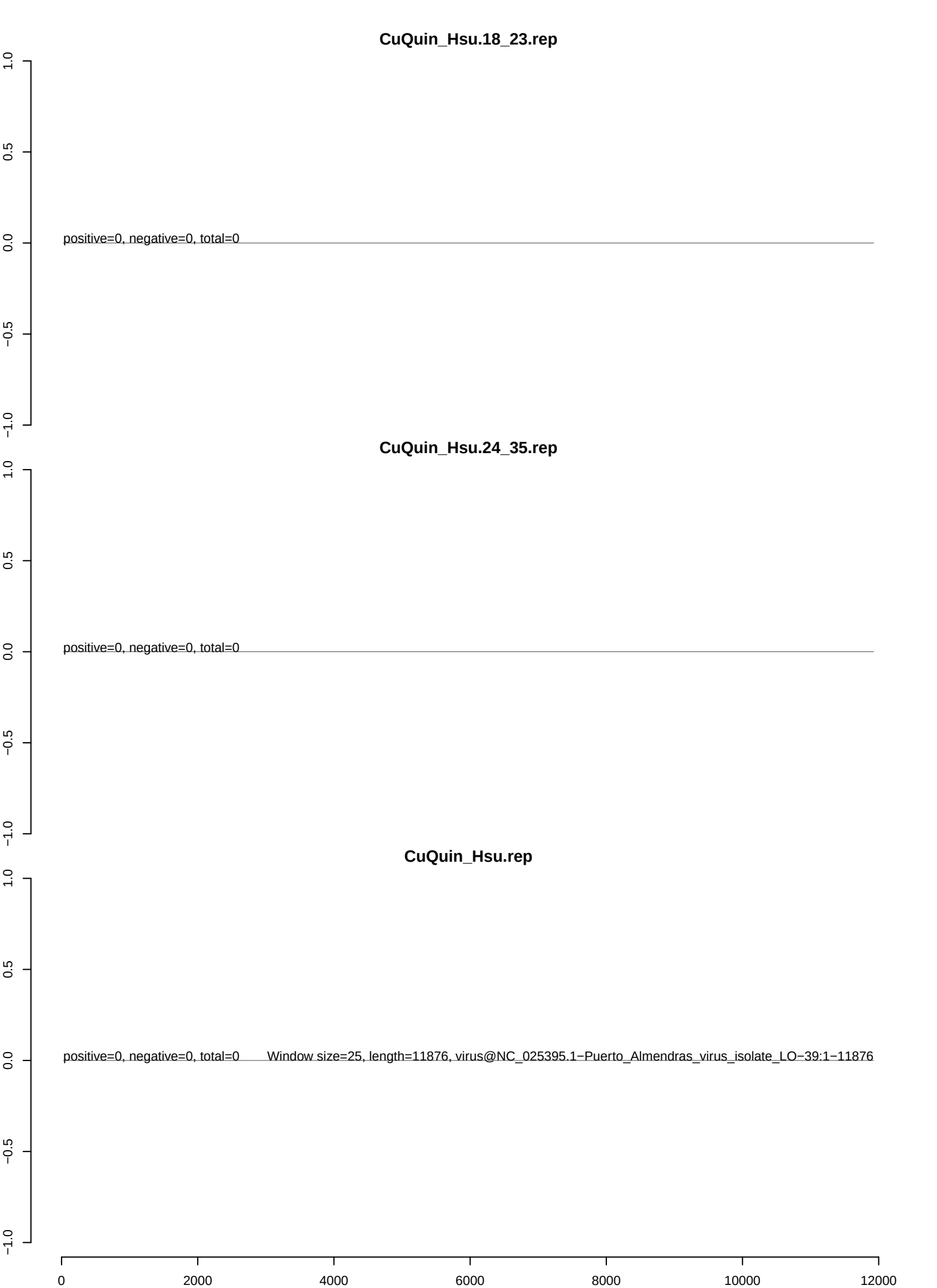
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CuQuin_Hsu.24_35.rep
positive=0, negative=0, total=0
CuQuin_Hsu.rep
positive=0, negative=0, total=0
Window size=25, length=11876, virus@NC_025395.1−Puerto_Almendras_virus_isolate_LO−39:1−11876
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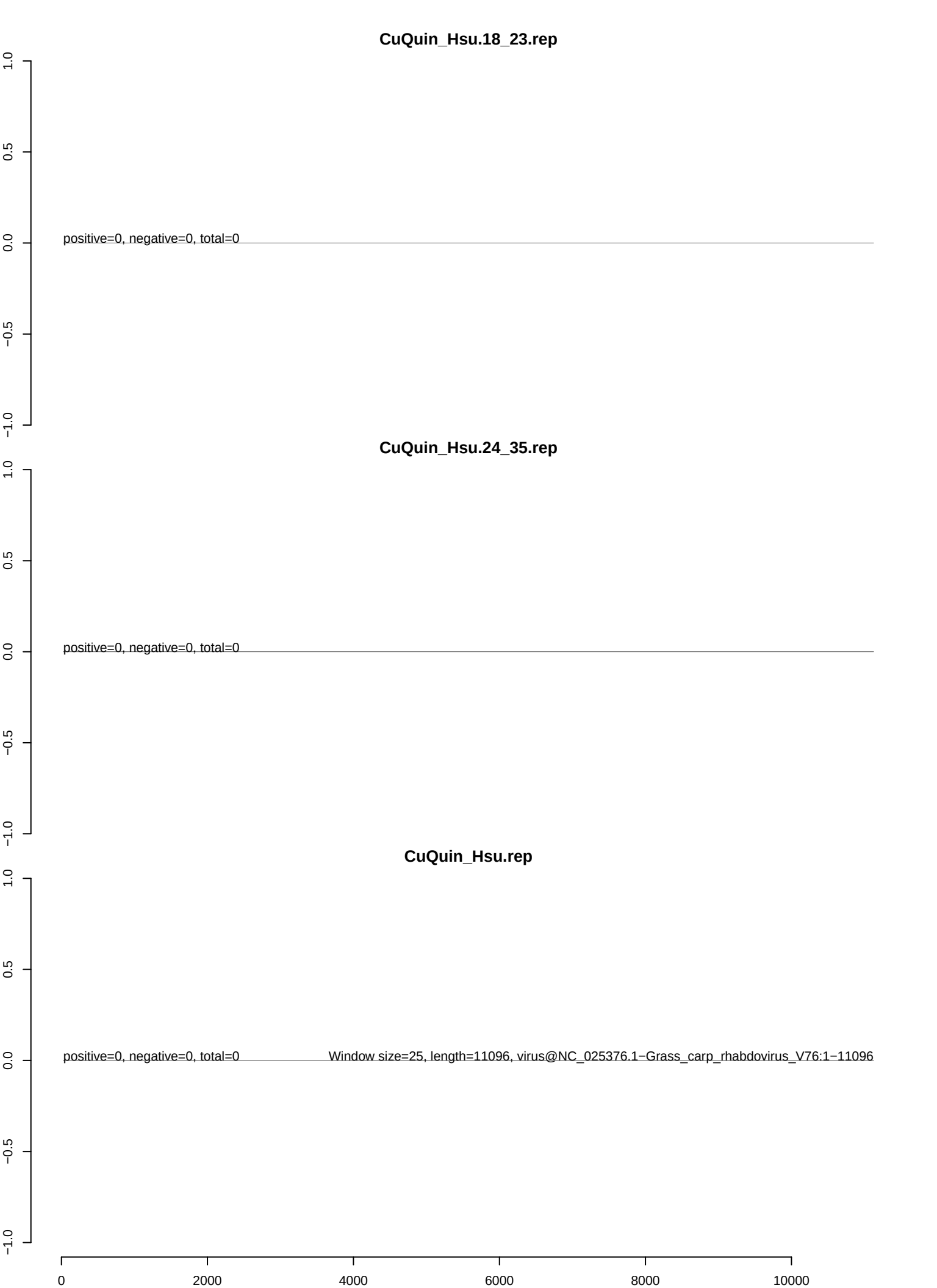
CuQuin_Hsu.18_23.rep
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positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
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positive=0, negative=0, total=0
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0.0
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−1.0
positive=0, negative=0, total=0
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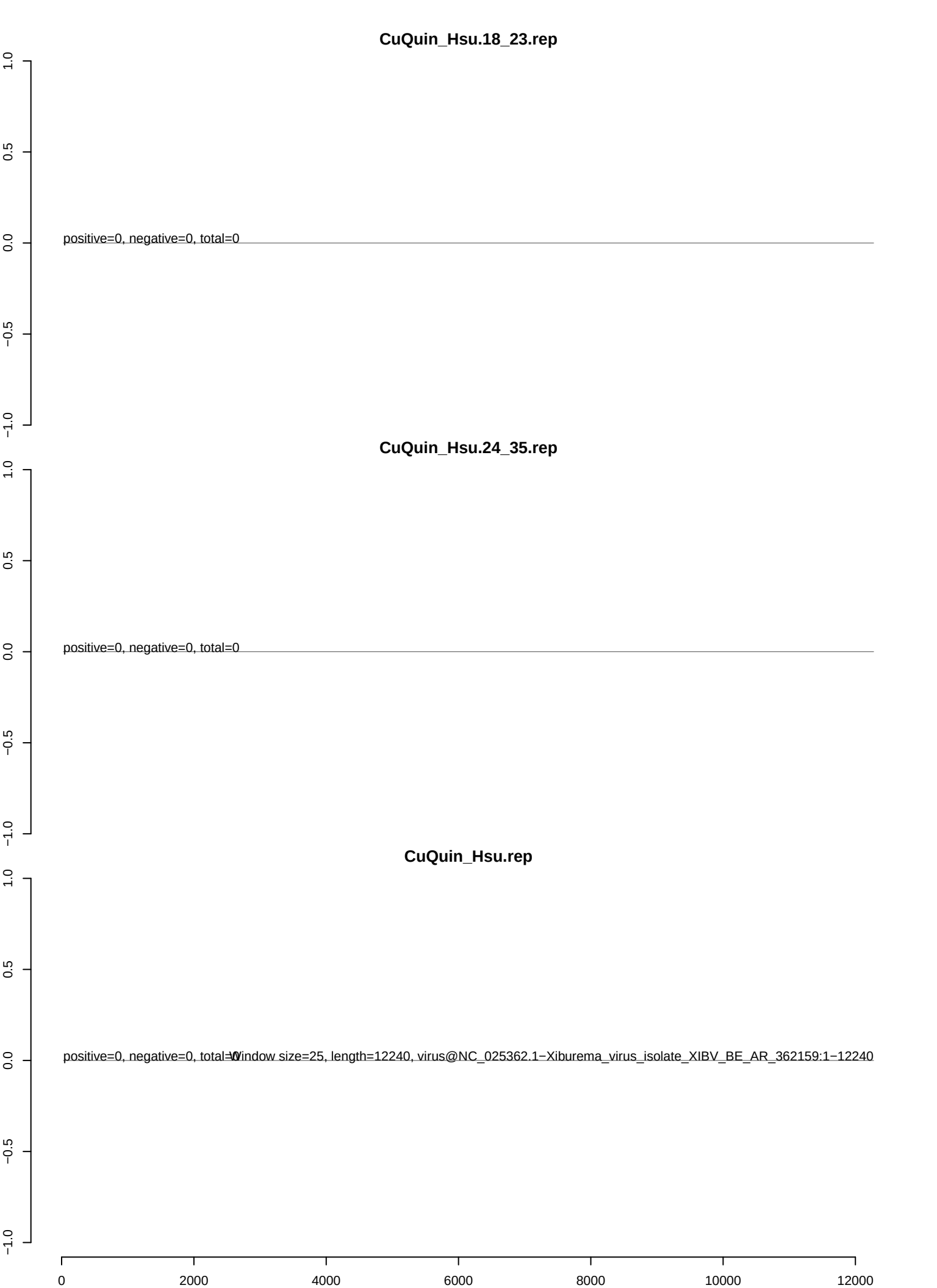
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positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
positive=0, negative=0, total=0
CuQuin_Hsu.rep
positive=0, negative=0, total=0
Window size=25, length=12240, virus@NC_025362.1−Xiburema_virus_isolate_XIBV_BE_AR_362159:1−12240
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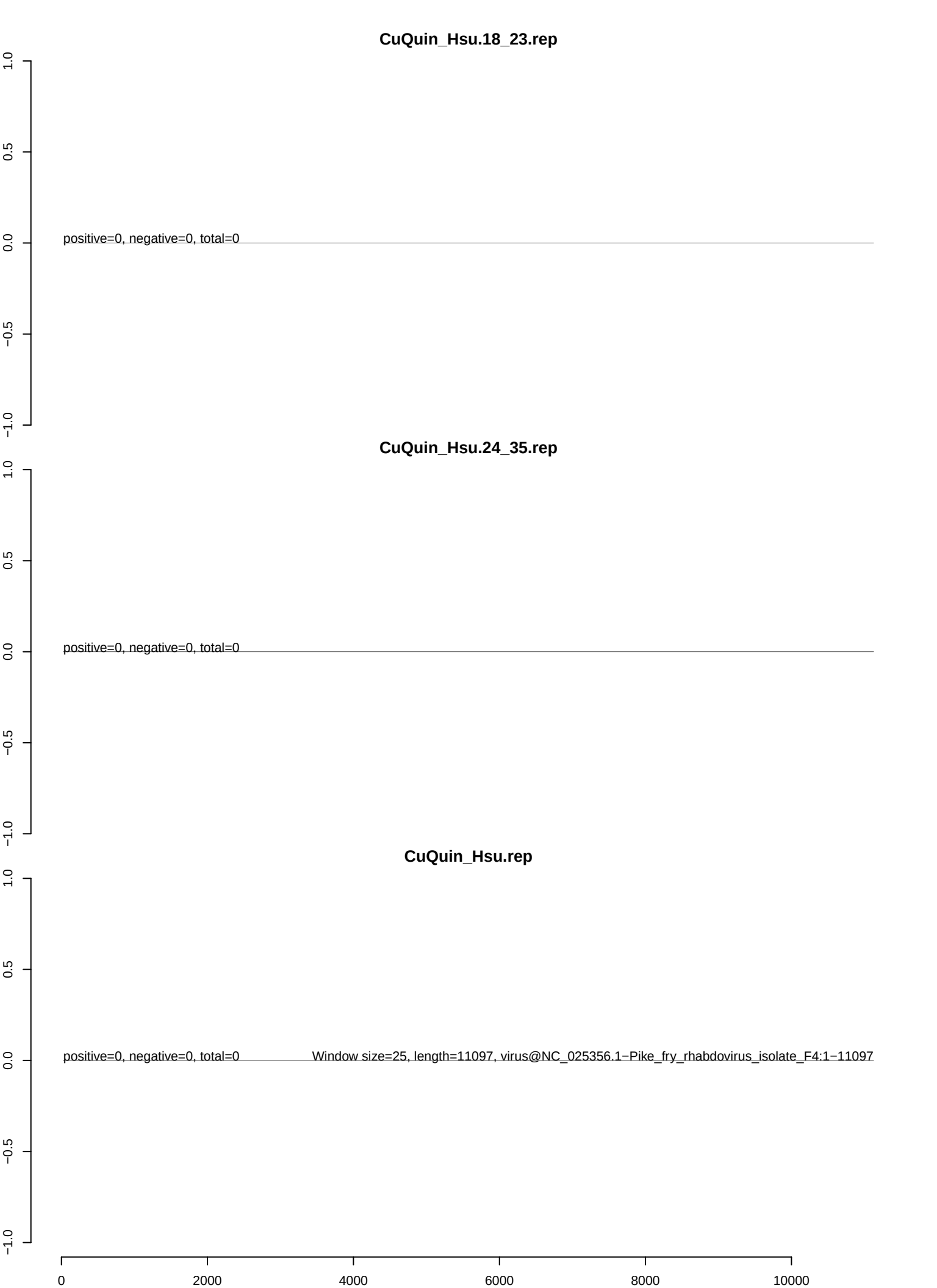
CuQuin_Hsu.18_23.rep
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positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
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positive=0, negative=0, total=0
CuQuin_Hsu.rep
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positive=0, negative=0, total=0
Window size=25, length=11097, virus@NC_025356.1−Pike_fry_rhabdovirus_isolate_F4:1−11097
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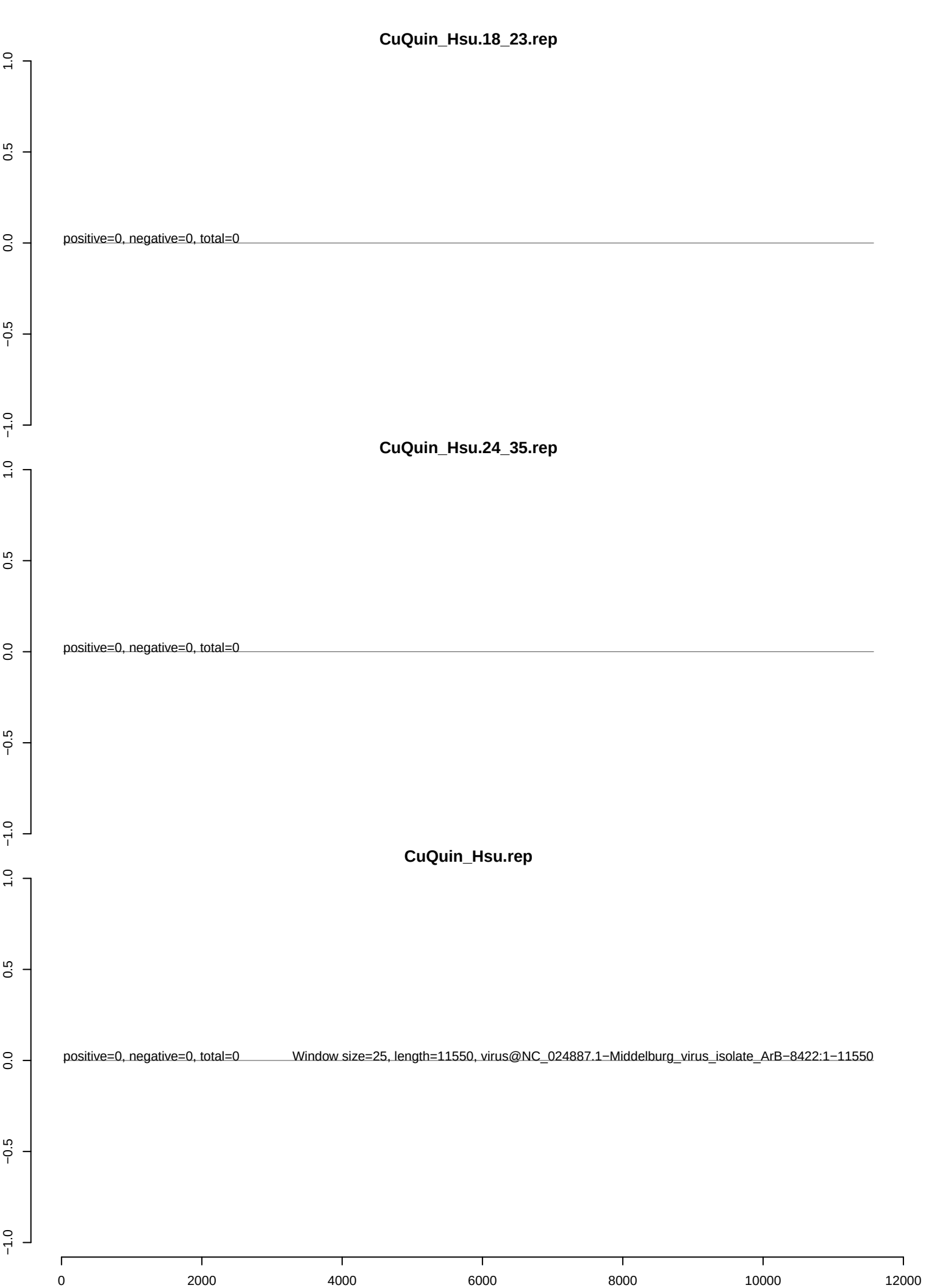
CuQuin_Hsu.18_23.rep
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
positive=0, negative=0, total=0
CuQuin_Hsu.rep
positive=0, negative=0, total=0
Window size=25, length=11550, virus@NC_024887.1−Middelburg_virus_isolate_ArB−8422:1−11550
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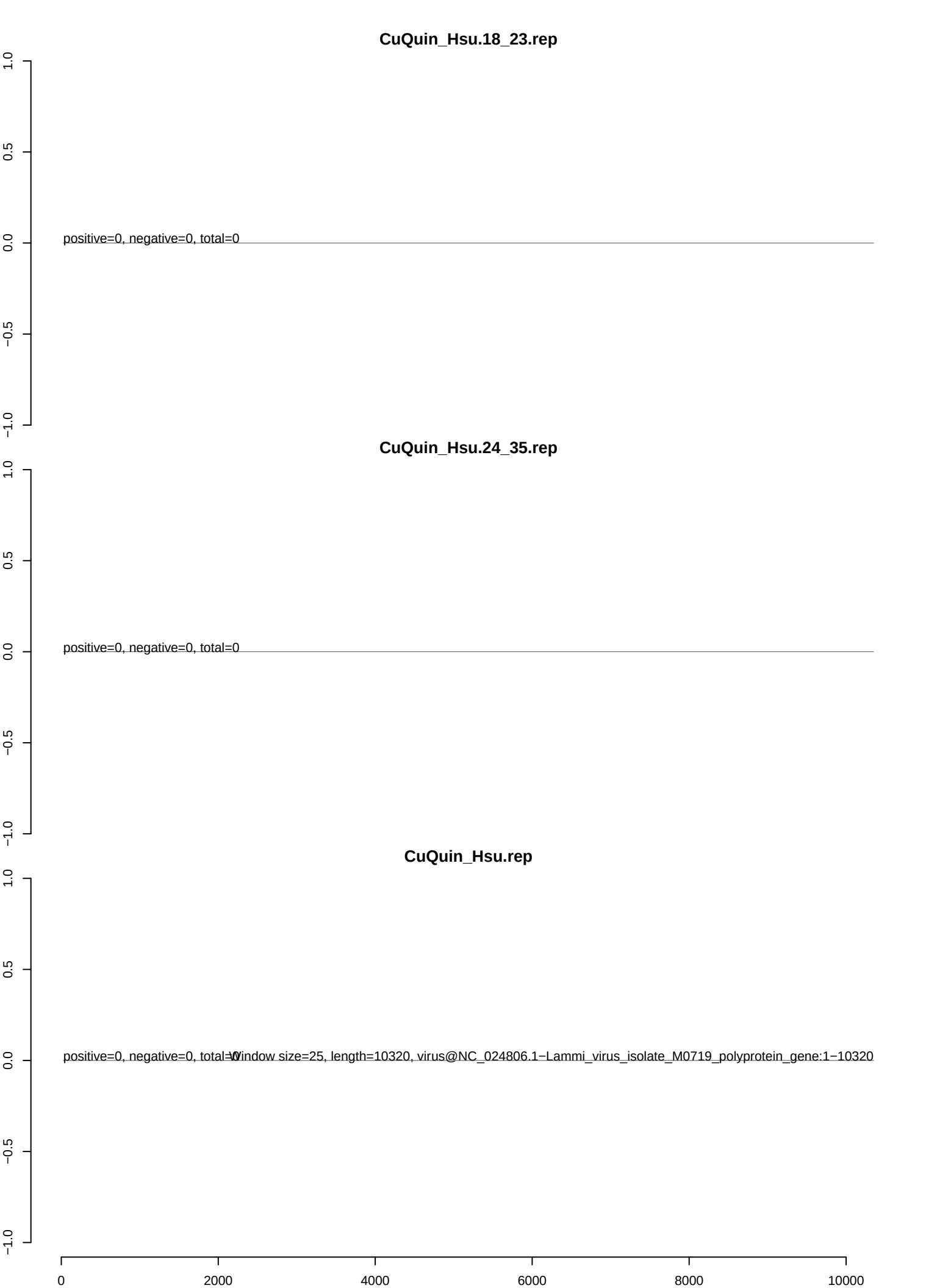
CuQuin_Hsu.18_23.rep
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CuQuin_Hsu.24_35.rep
positive=0, negative=0, total=0
CuQuin_Hsu.rep
positive=0, negative=0, total=0
Window size=25, length=10320, virus@NC_024806.1−Lammi_virus_isolate_M0719_polyprotein_gene:1−10320
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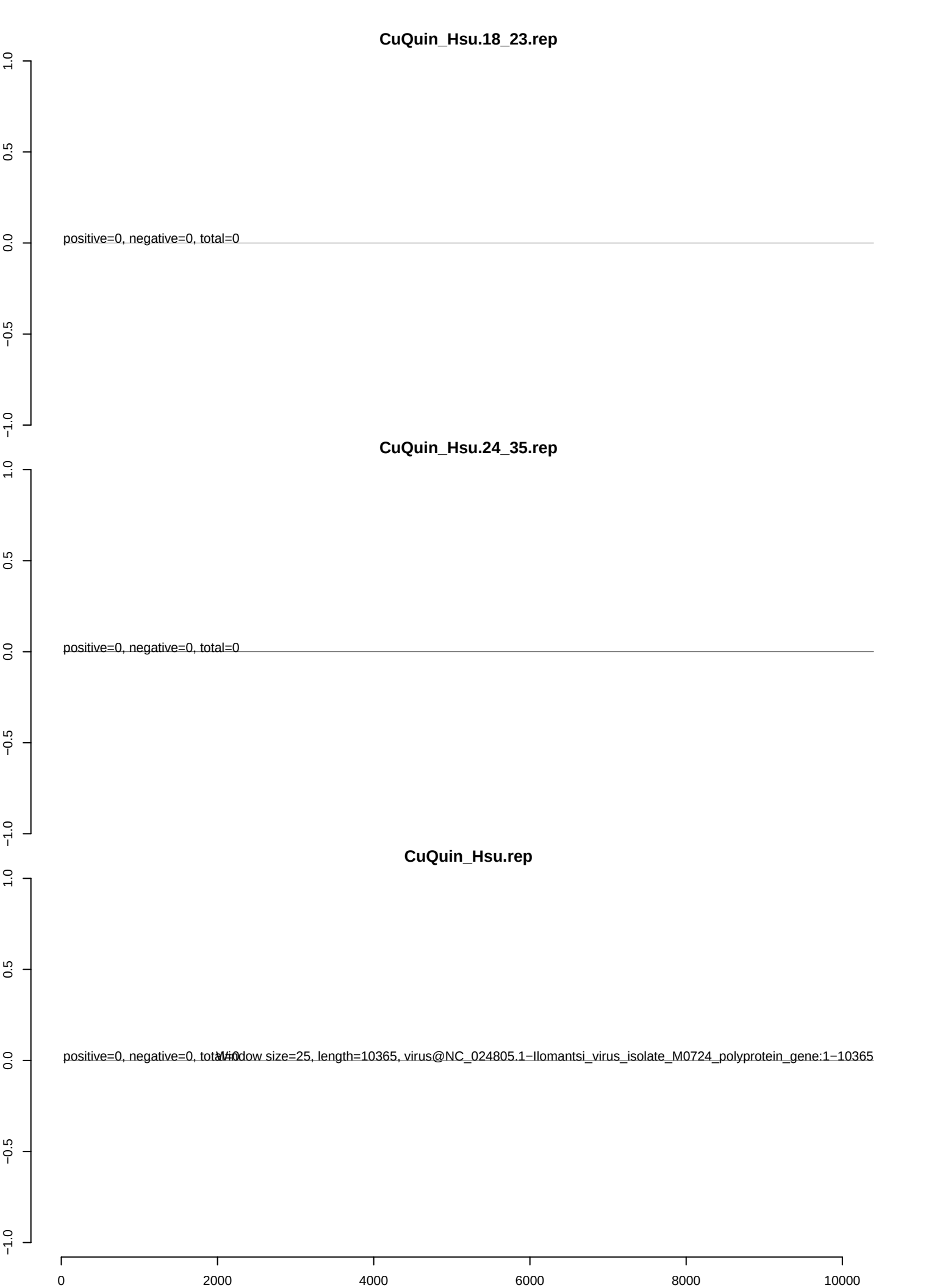
CuQuin_Hsu.18_23.rep
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CuQuin_Hsu.24_35.rep
positive=0, negative=0, total=0
CuQuin_Hsu.rep
positive=0, negative=0, total=0
Window size=25, length=10365, virus@NC_024805.1−Ilomantsi_virus_isolate_M0724_polyprotein_gene:1−10365
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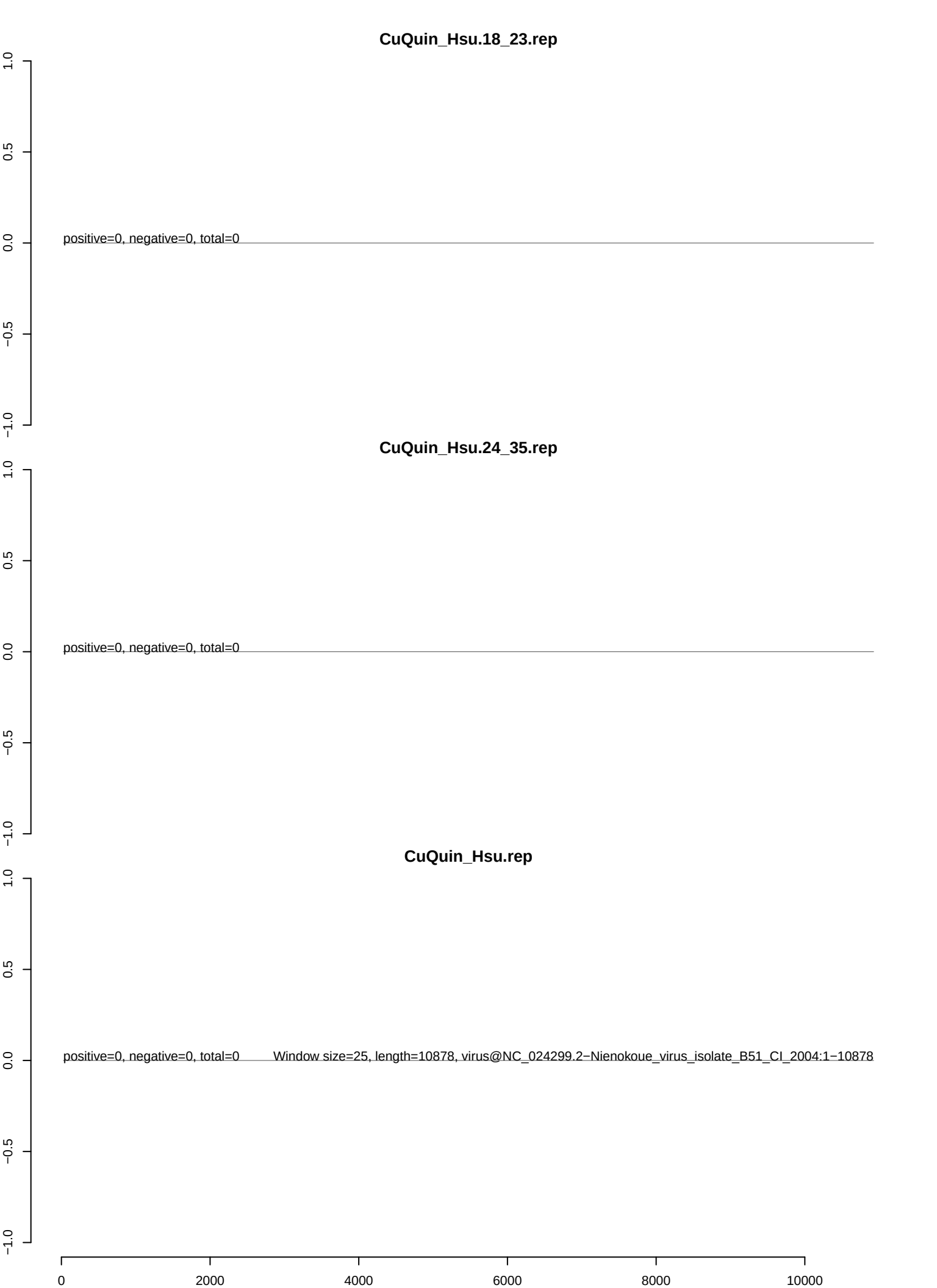
CuQuin_Hsu.18_23.rep
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CuQuin_Hsu.24_35.rep
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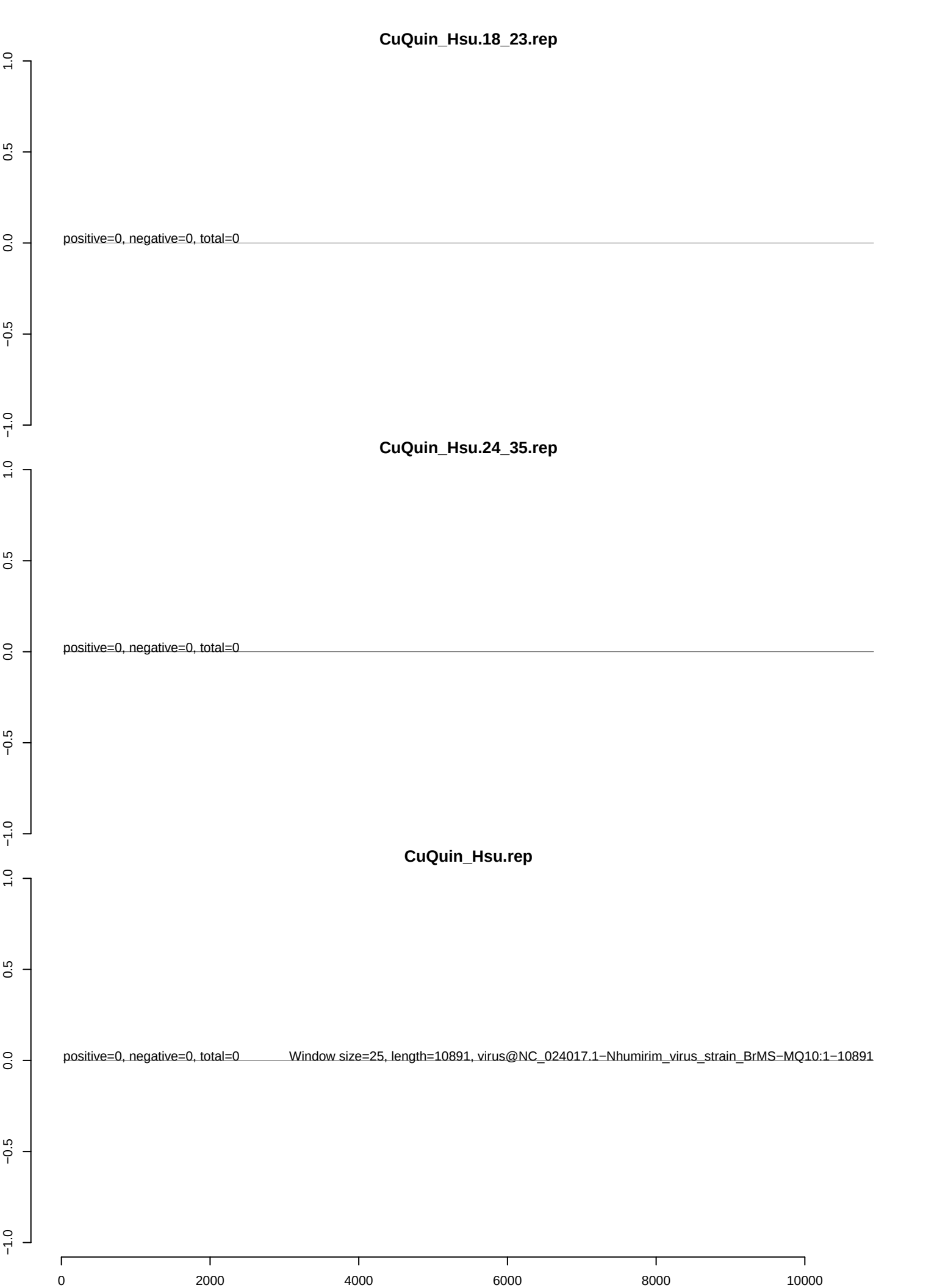
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CuQuin_Hsu.24_35.rep
positive=0, negative=0, total=0
CuQuin_Hsu.rep
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Window size=25, length=10891, virus@NC_024017.1−Nhumirim_virus_strain_BrMS−MQ10:1−10891
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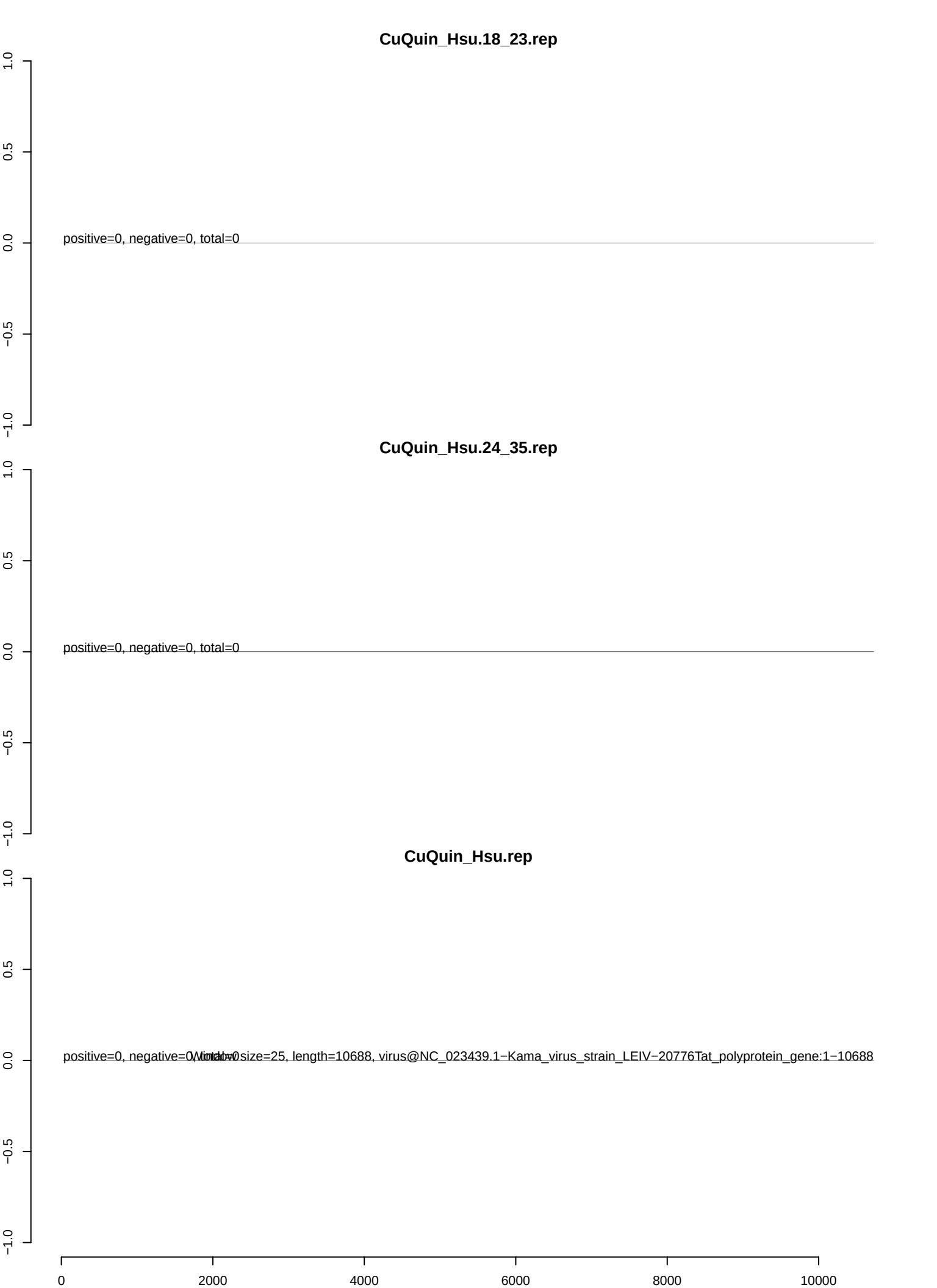
CuQuin_Hsu.18_23.rep
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
positive=0, negative=0, total=0
CuQuin_Hsu.rep
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Window size=25, length=10688, virus@NC_023439.1−Kama_virus_strain_LEIV−20776Tat_polyprotein_gene:1−10688
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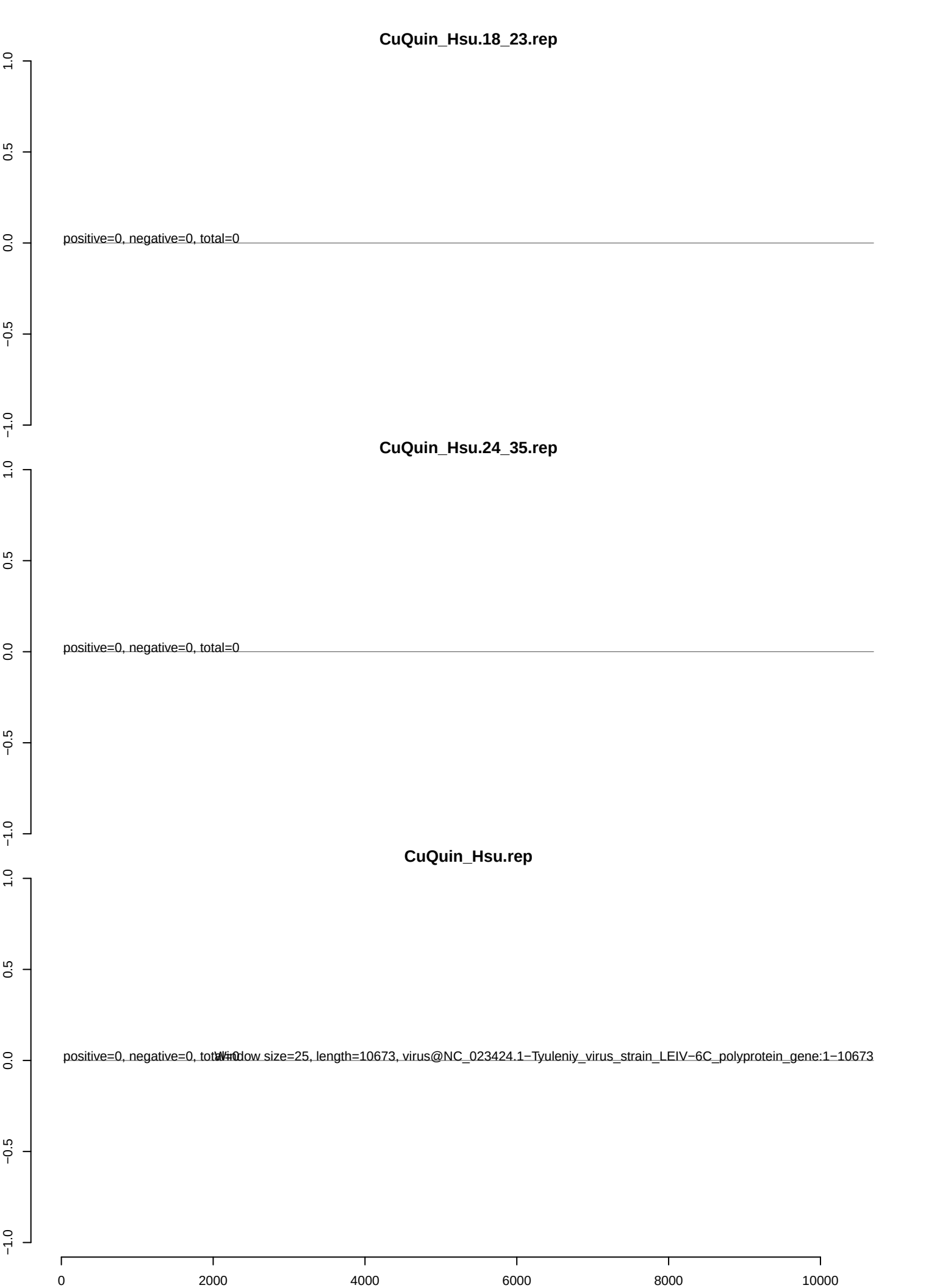
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CuQuin_Hsu.24_35.rep
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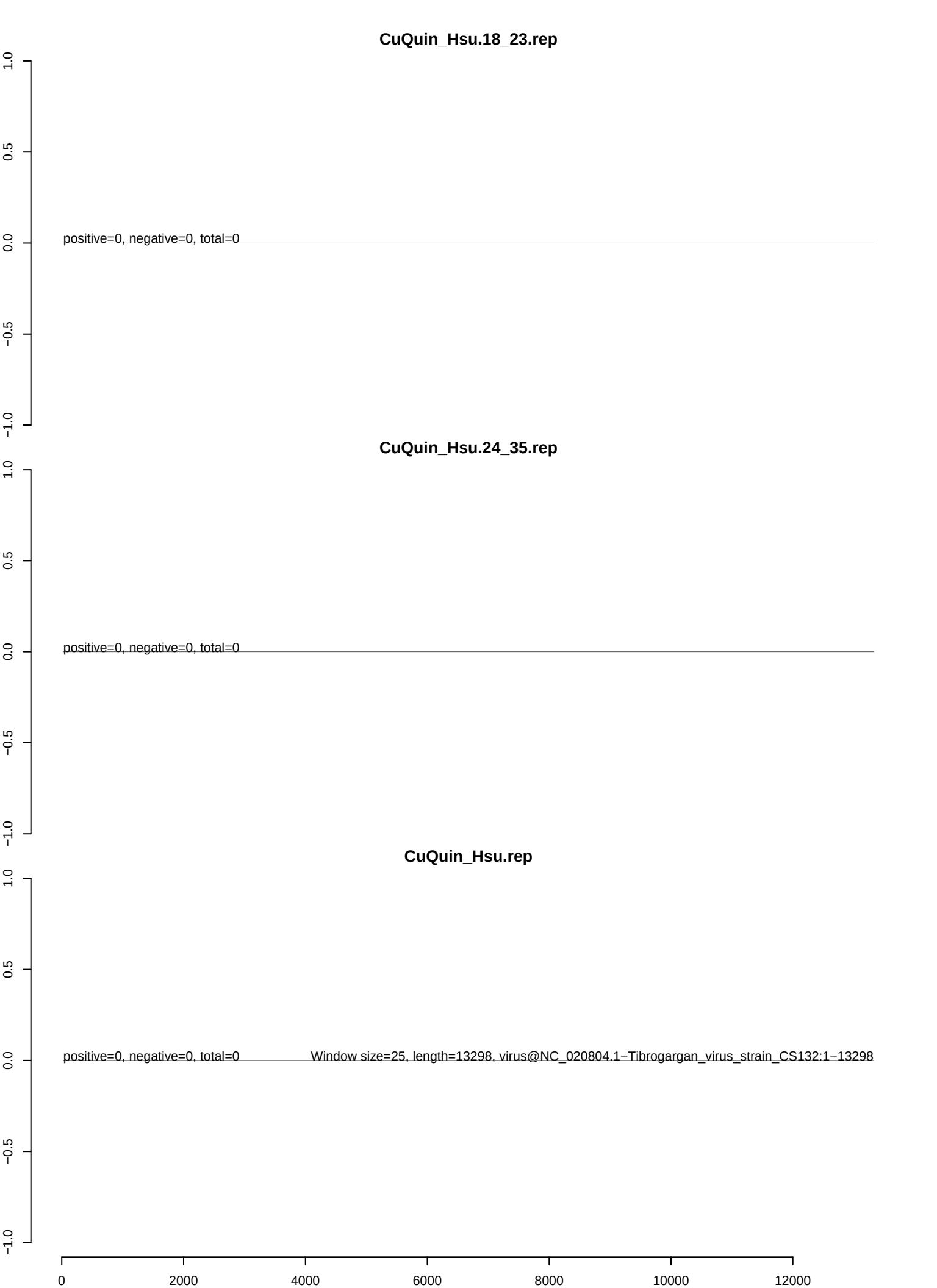
CuQuin_Hsu.18_23.rep
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CuQuin_Hsu.24_35.rep
positive=0, negative=0, total=0
CuQuin_Hsu.rep
positive=0, negative=0, total=0
Window size=25, length=13298, virus@NC_020804.1−Tibrogargan_virus_strain_CS132:1−13298
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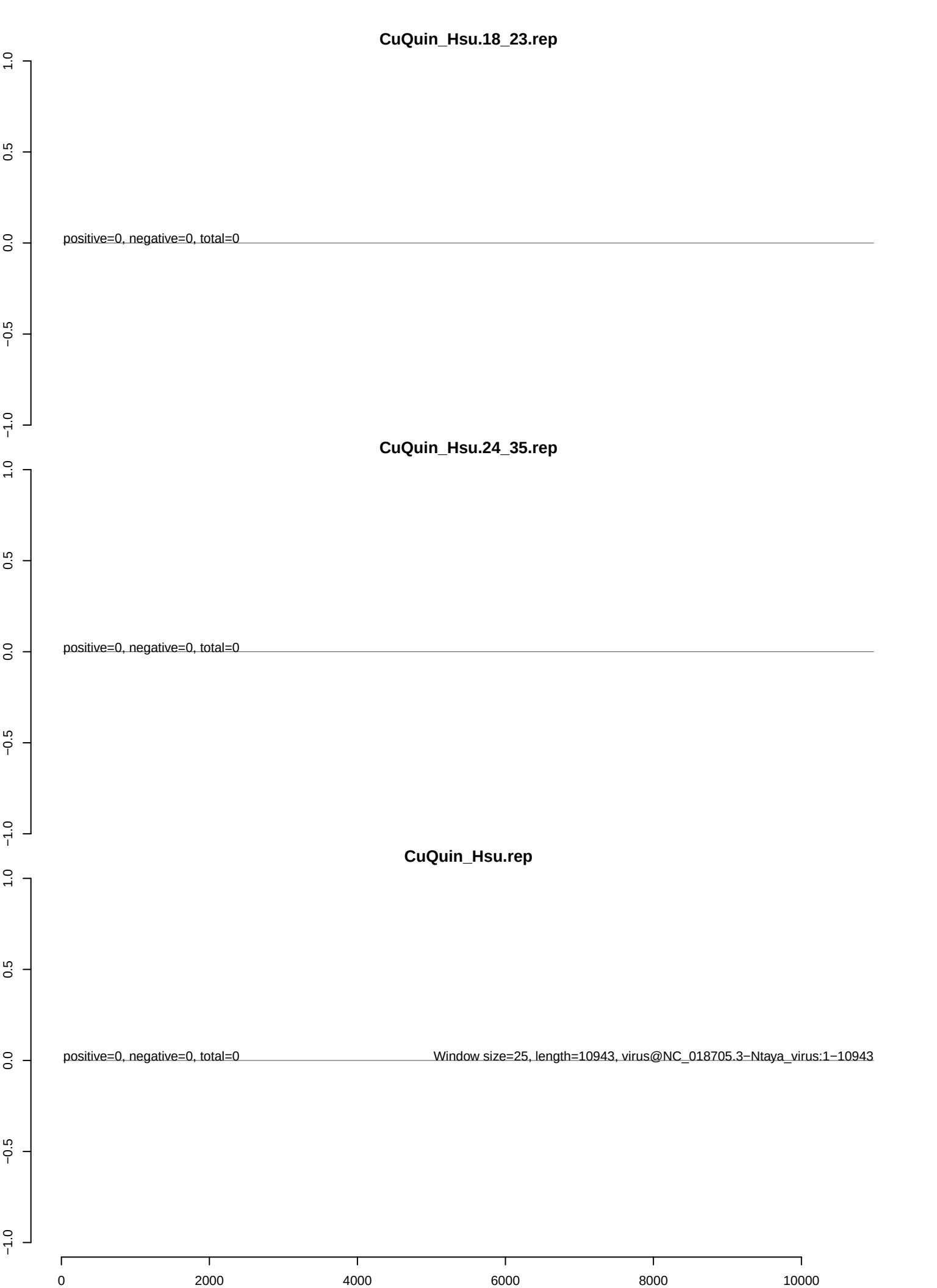
CuQuin_Hsu.18_23.rep
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CuQuin_Hsu.24_35.rep
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CuQuin_Hsu.rep
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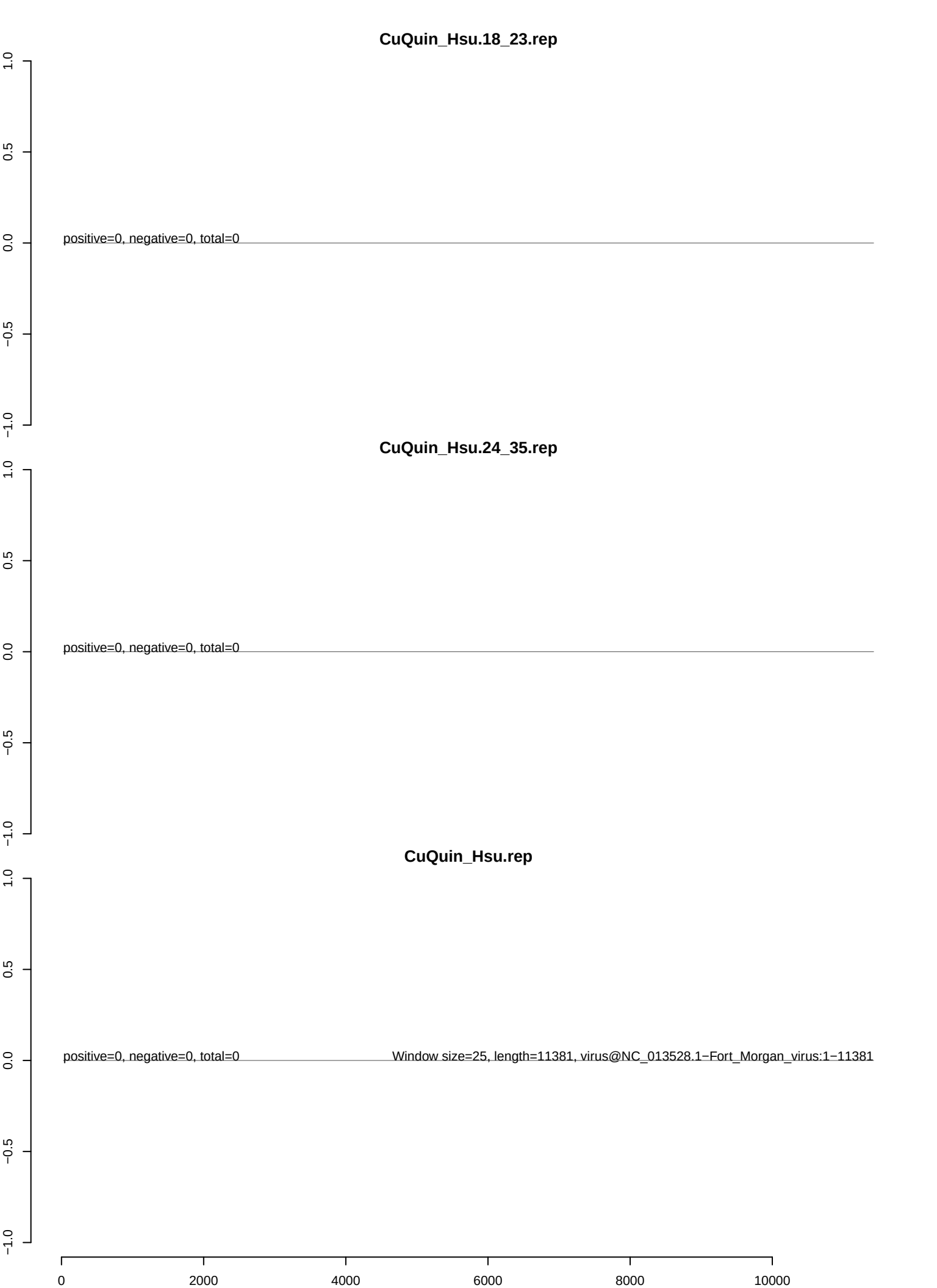
CuQuin_Hsu.18_23.rep
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CuQuin_Hsu.24_35.rep
positive=0, negative=0, total=0
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Window size=25, length=11381, virus@NC_013528.1−Fort_Morgan_virus:1−11381
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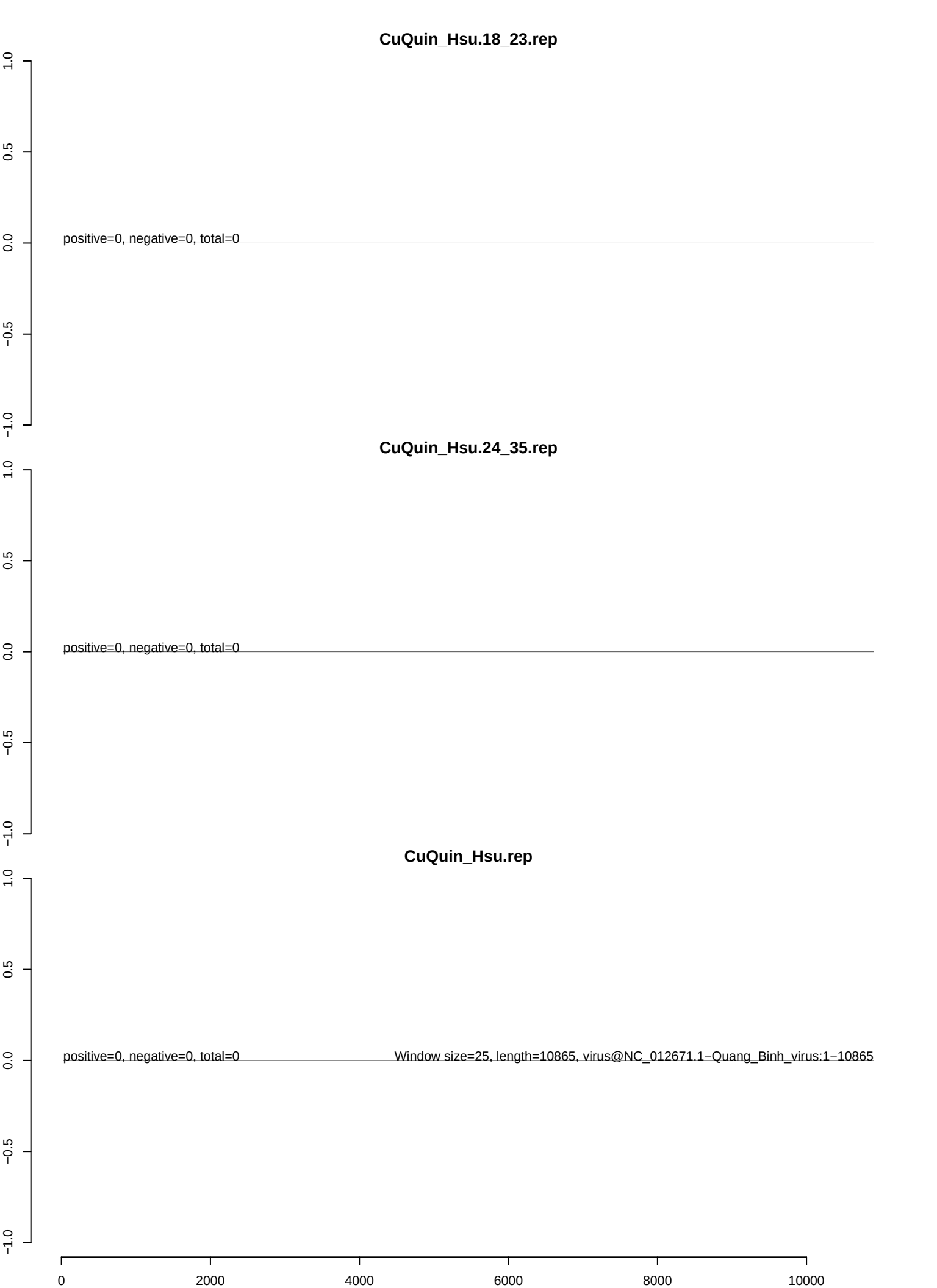
CuQuin_Hsu.18_23.rep
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
positive=0, negative=0, total=0
CuQuin_Hsu.rep
positive=0, negative=0, total=0
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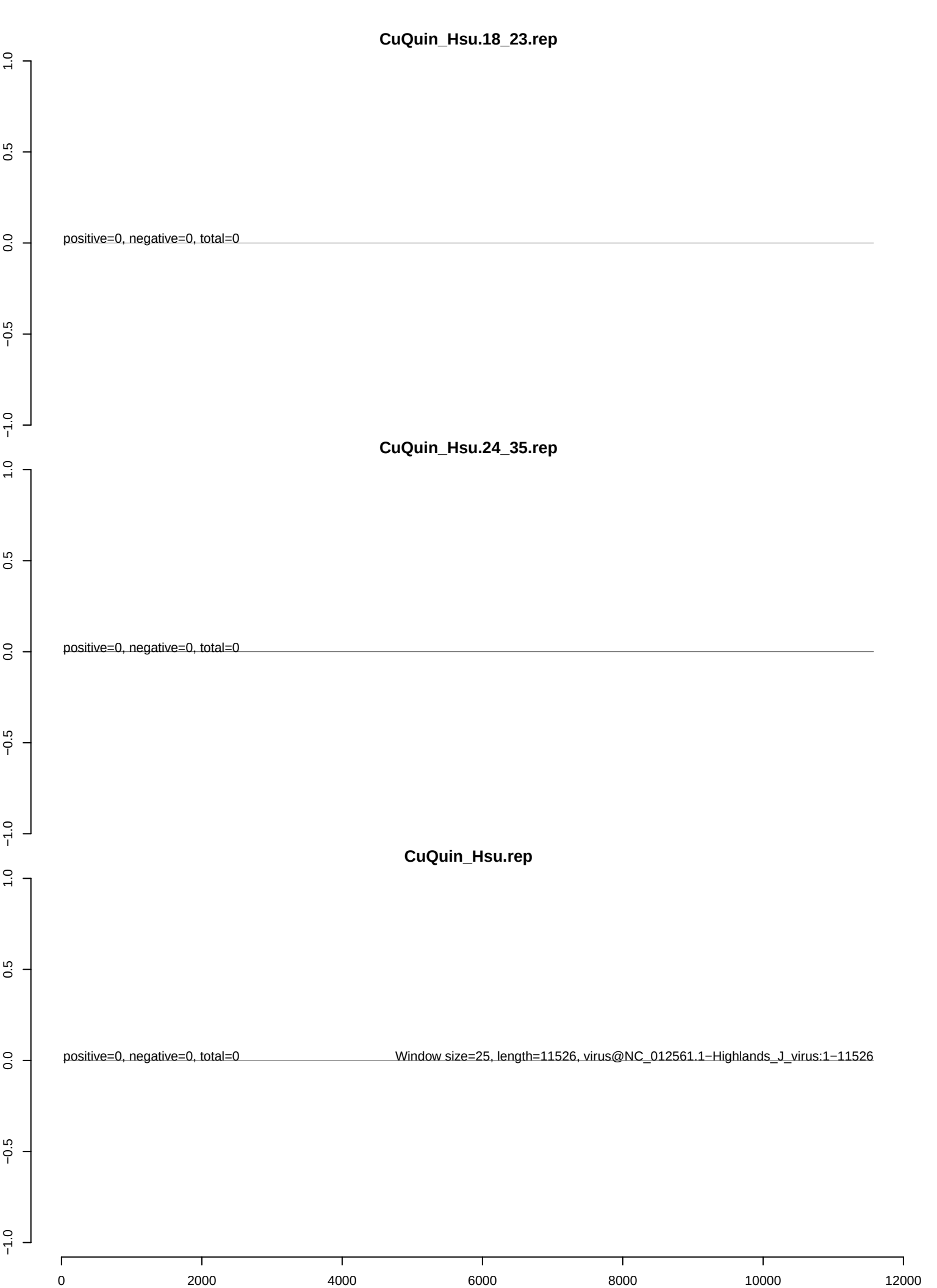
CuQuin_Hsu.18_23.rep
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
positive=0, negative=0, total=0
CuQuin_Hsu.rep
positive=0, negative=0, total=0
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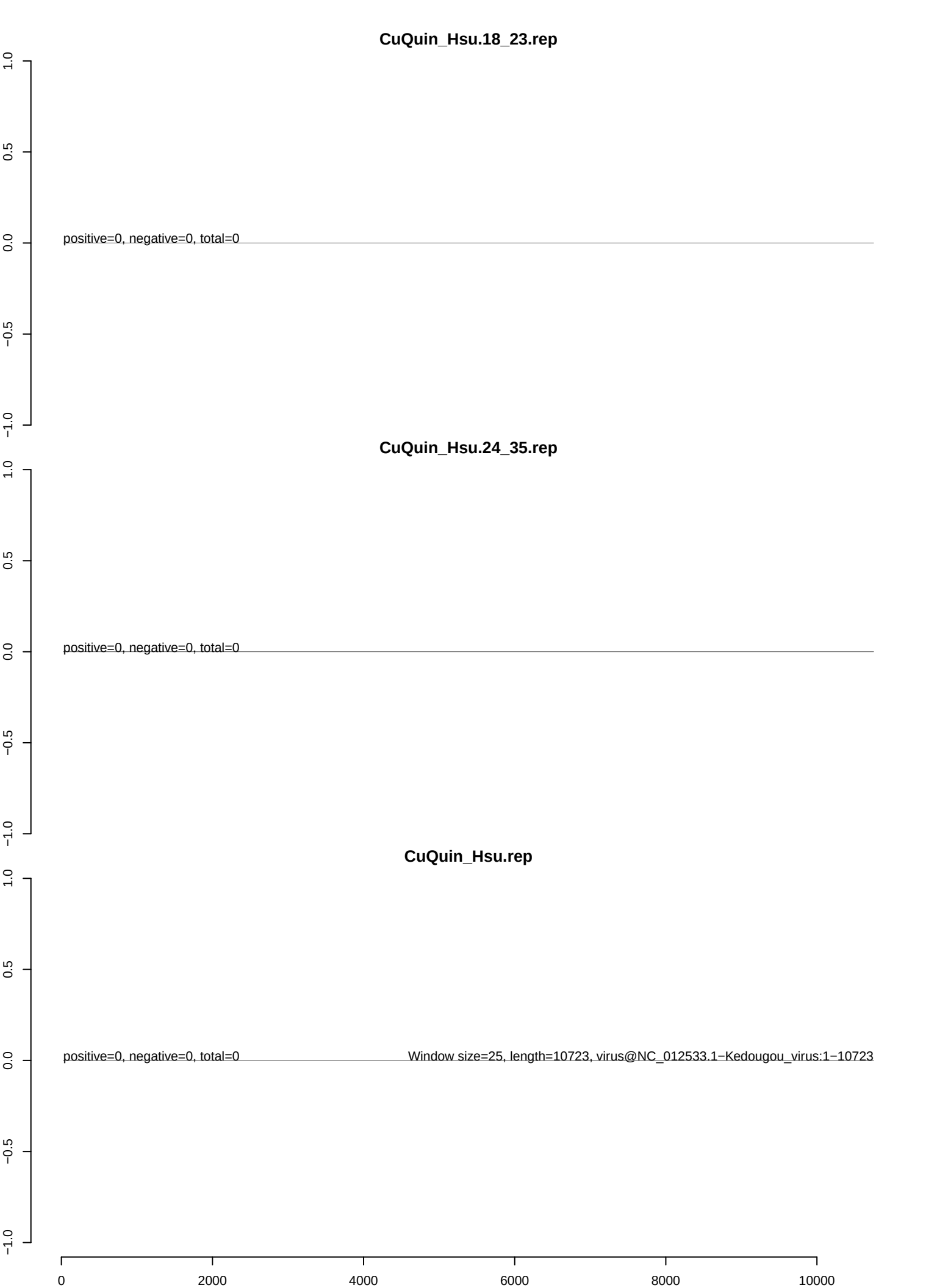
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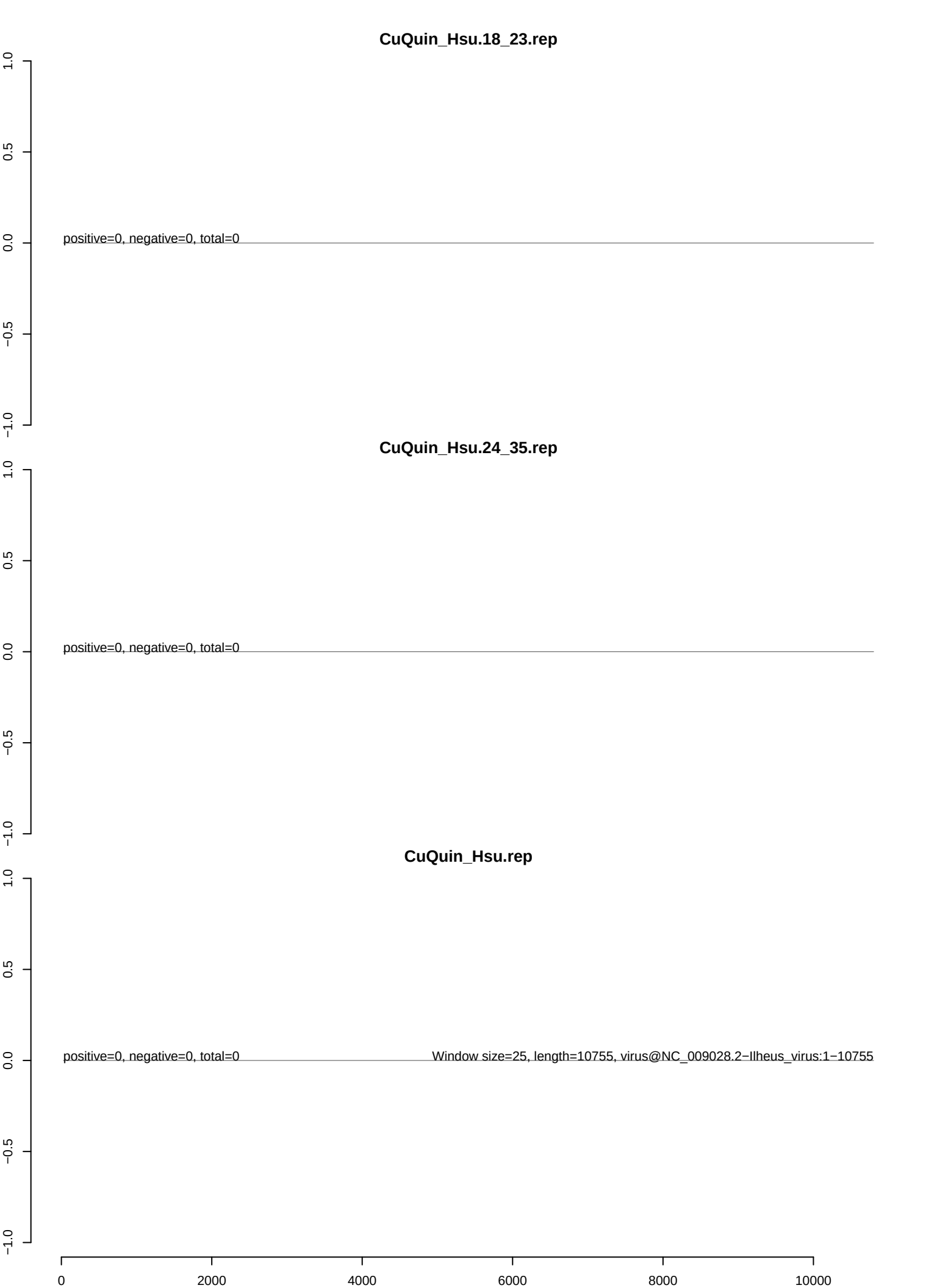
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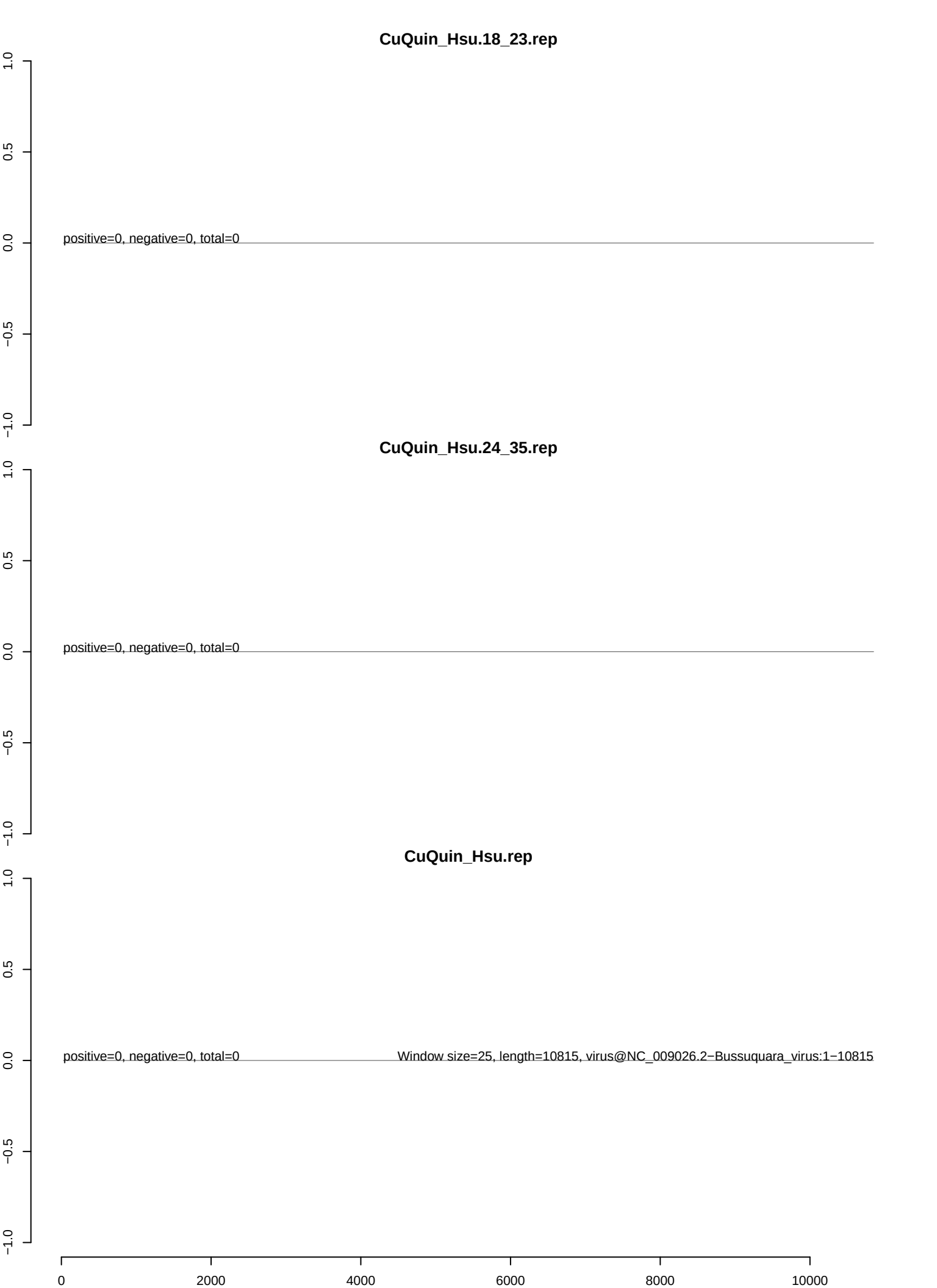
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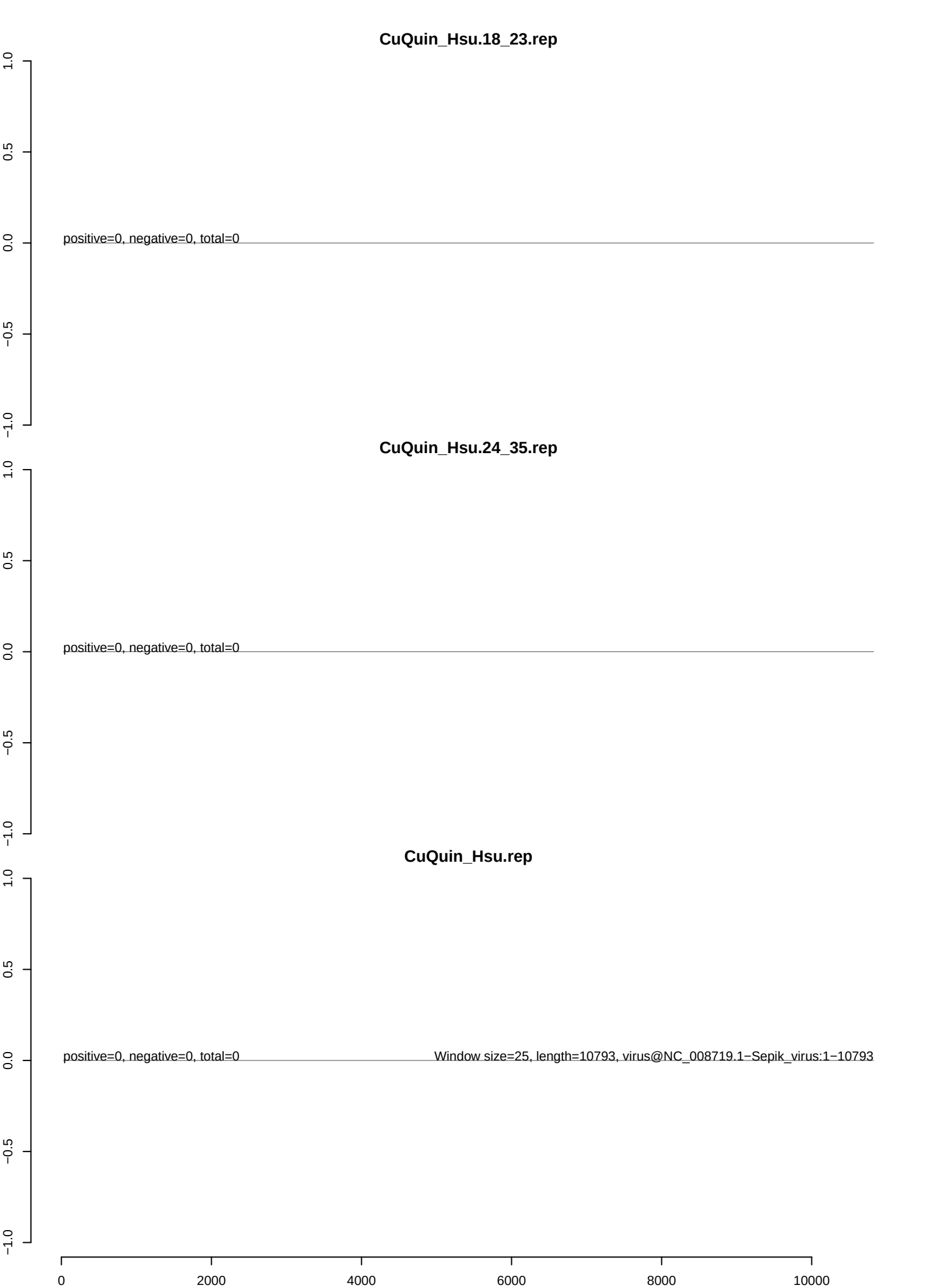
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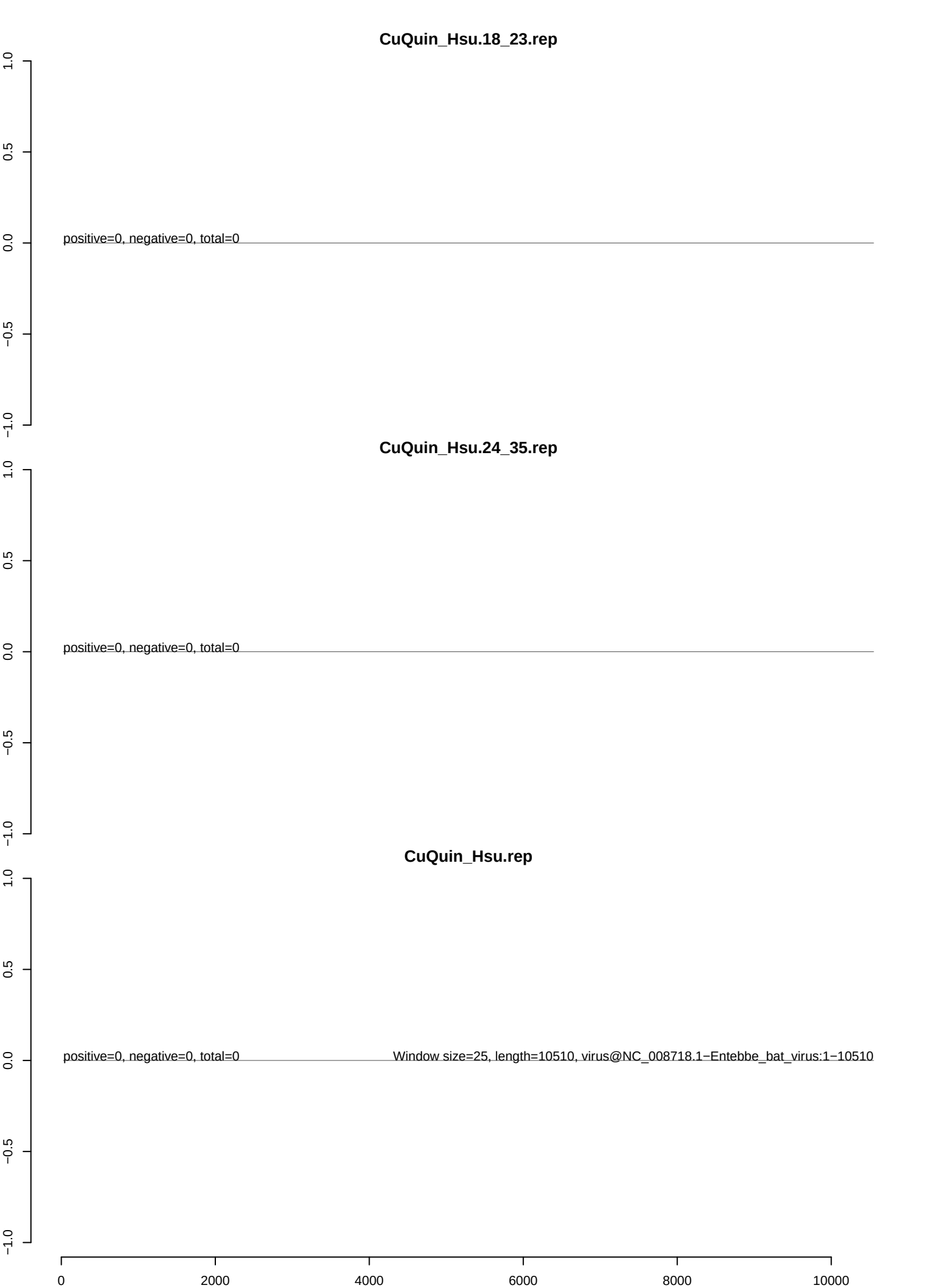
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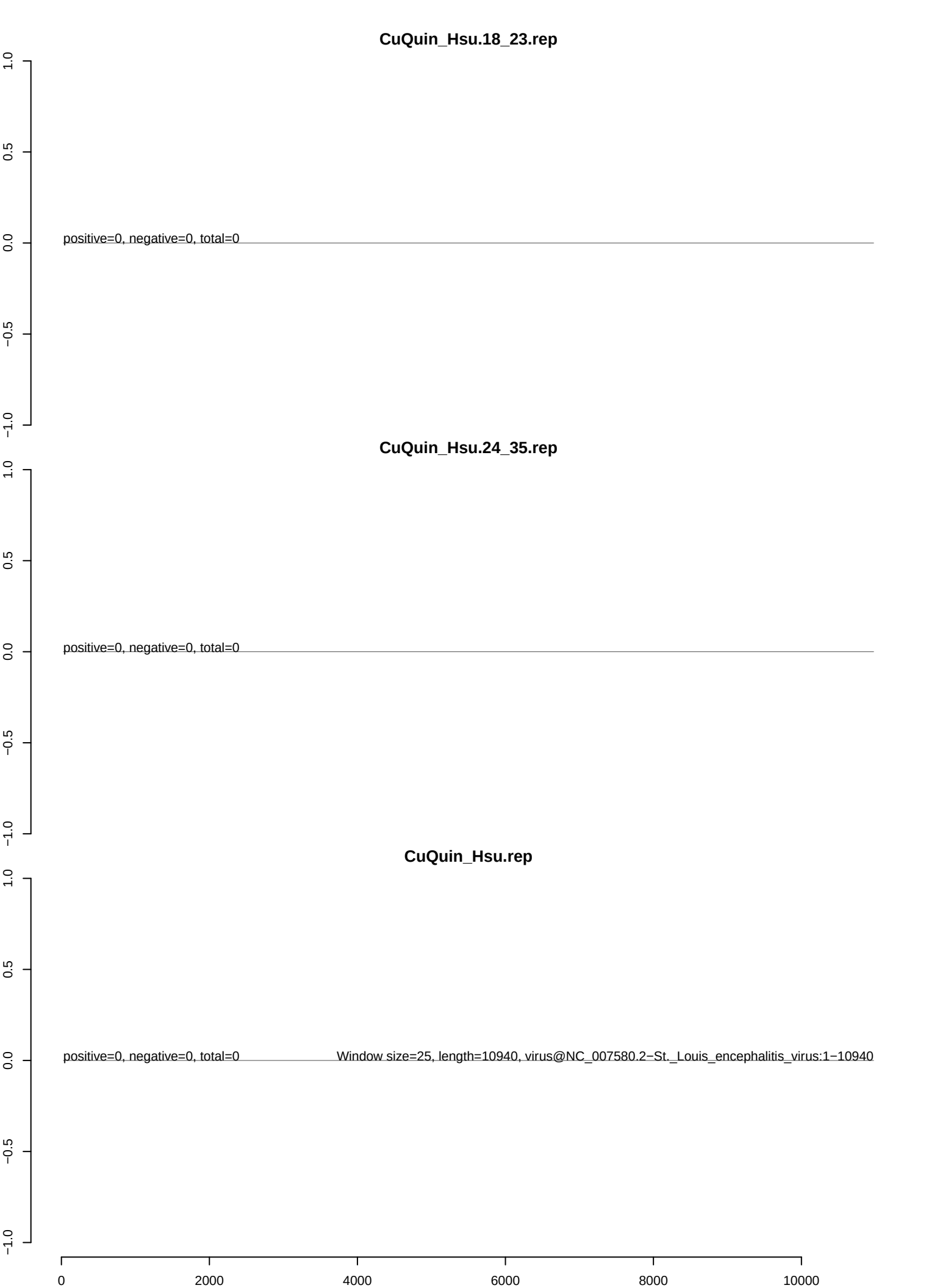
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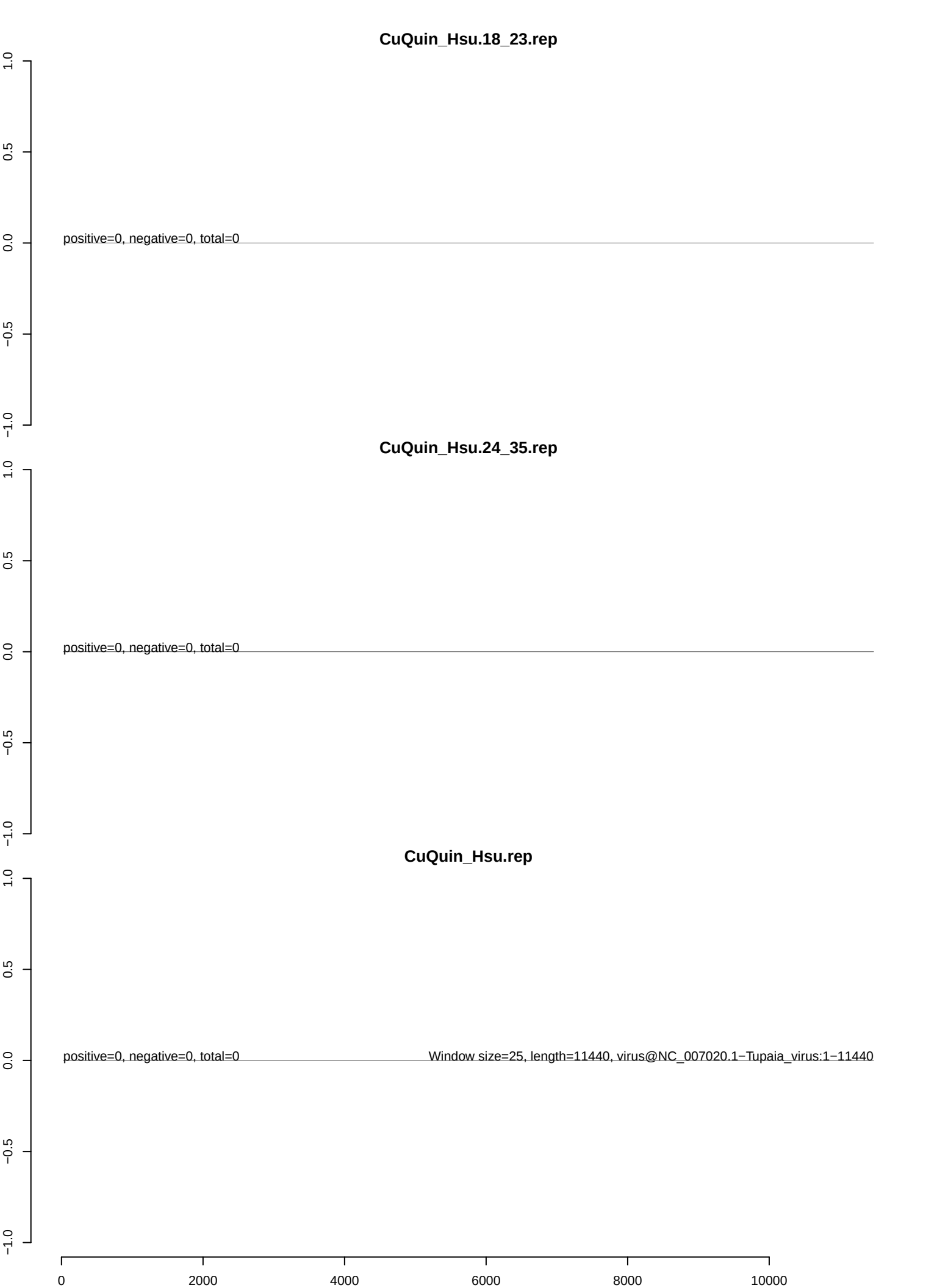
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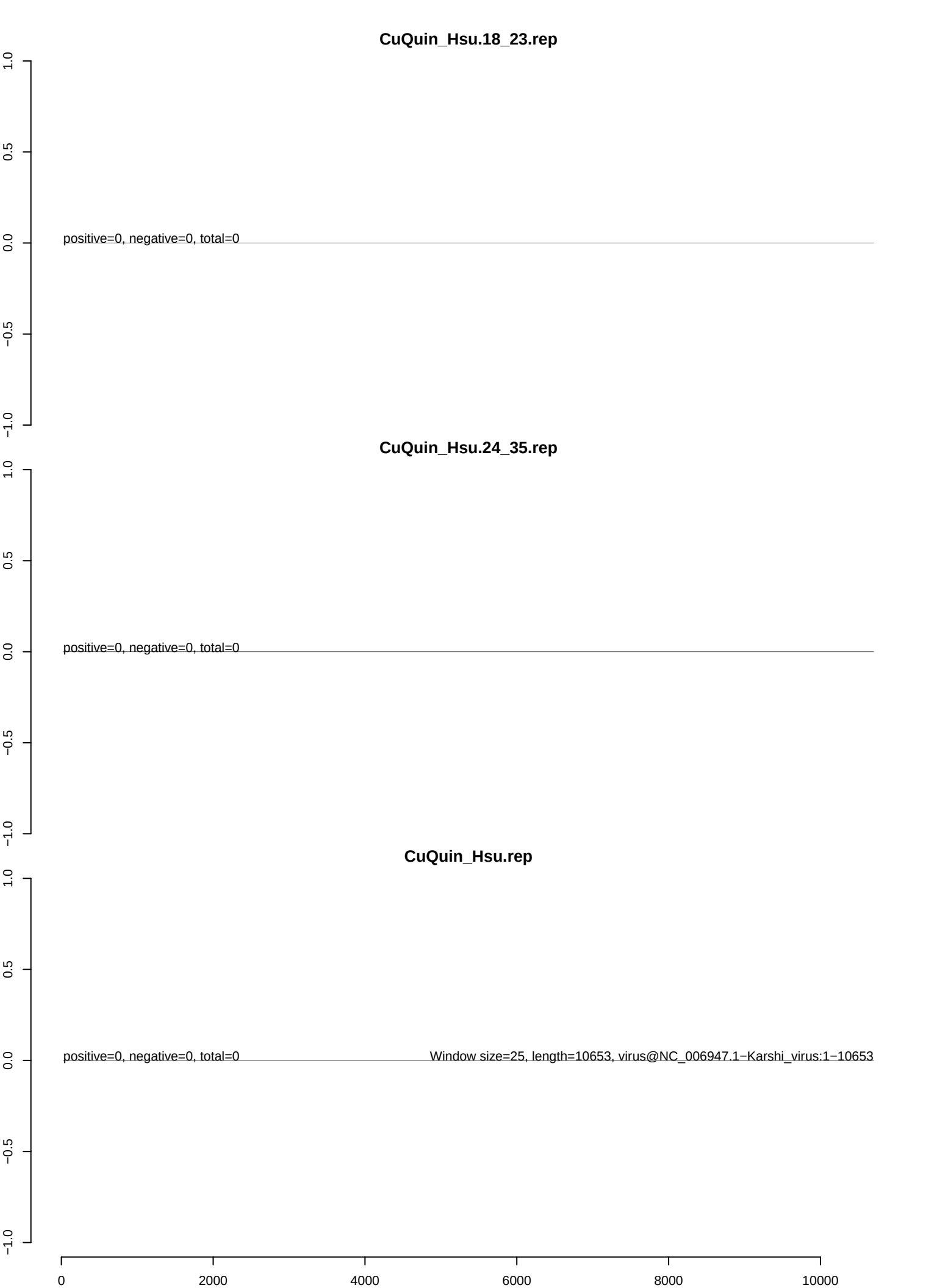
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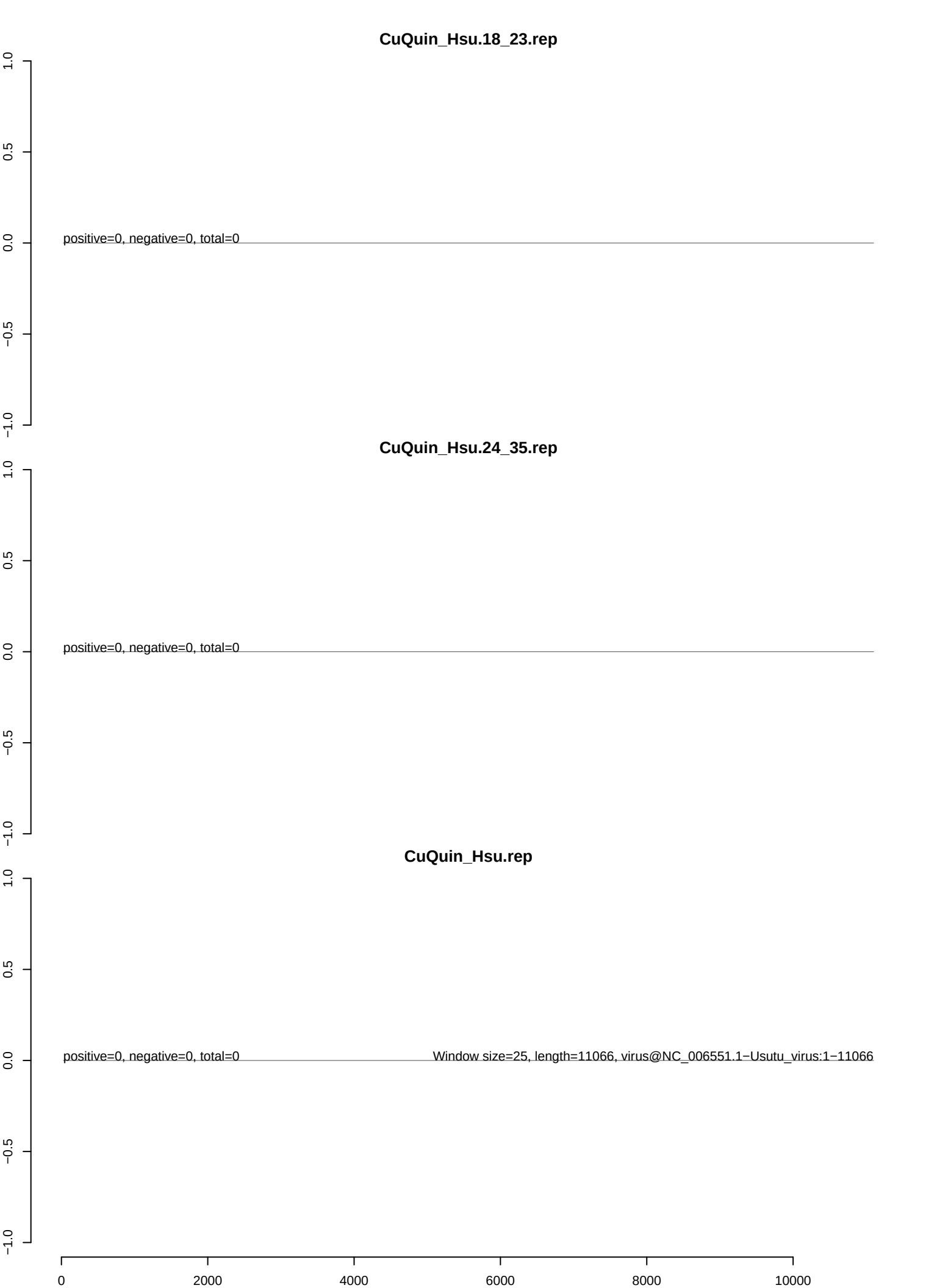
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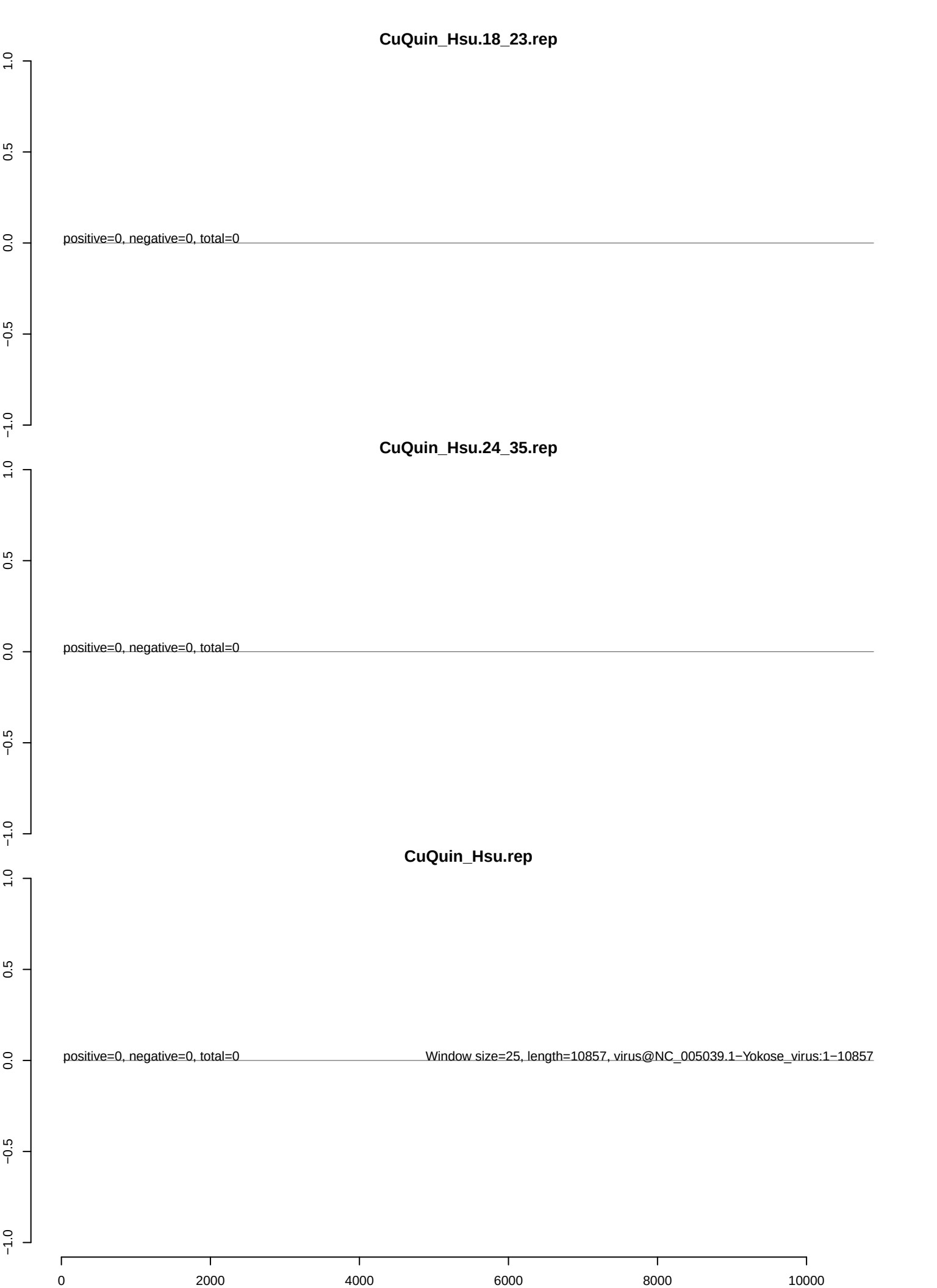
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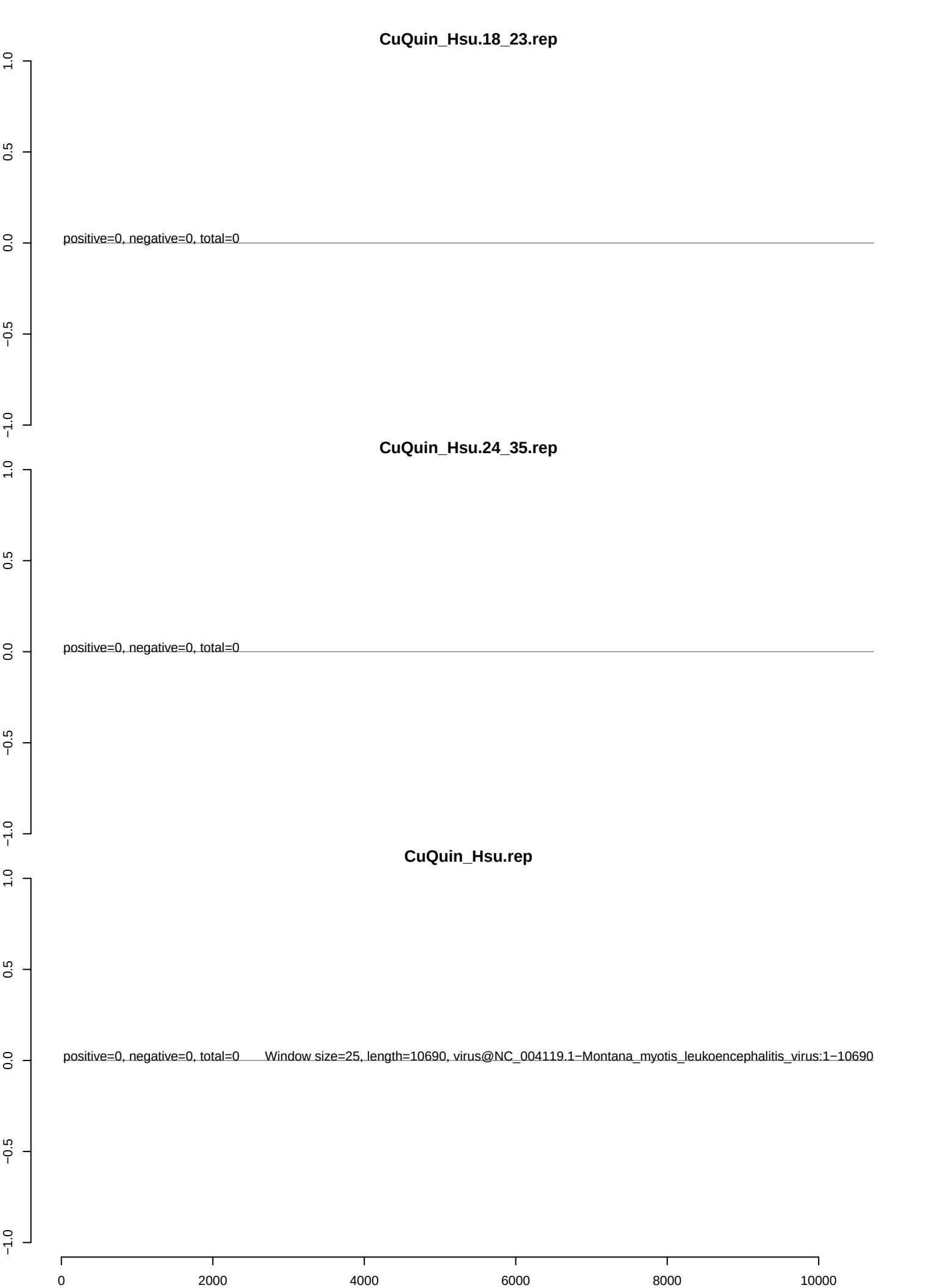
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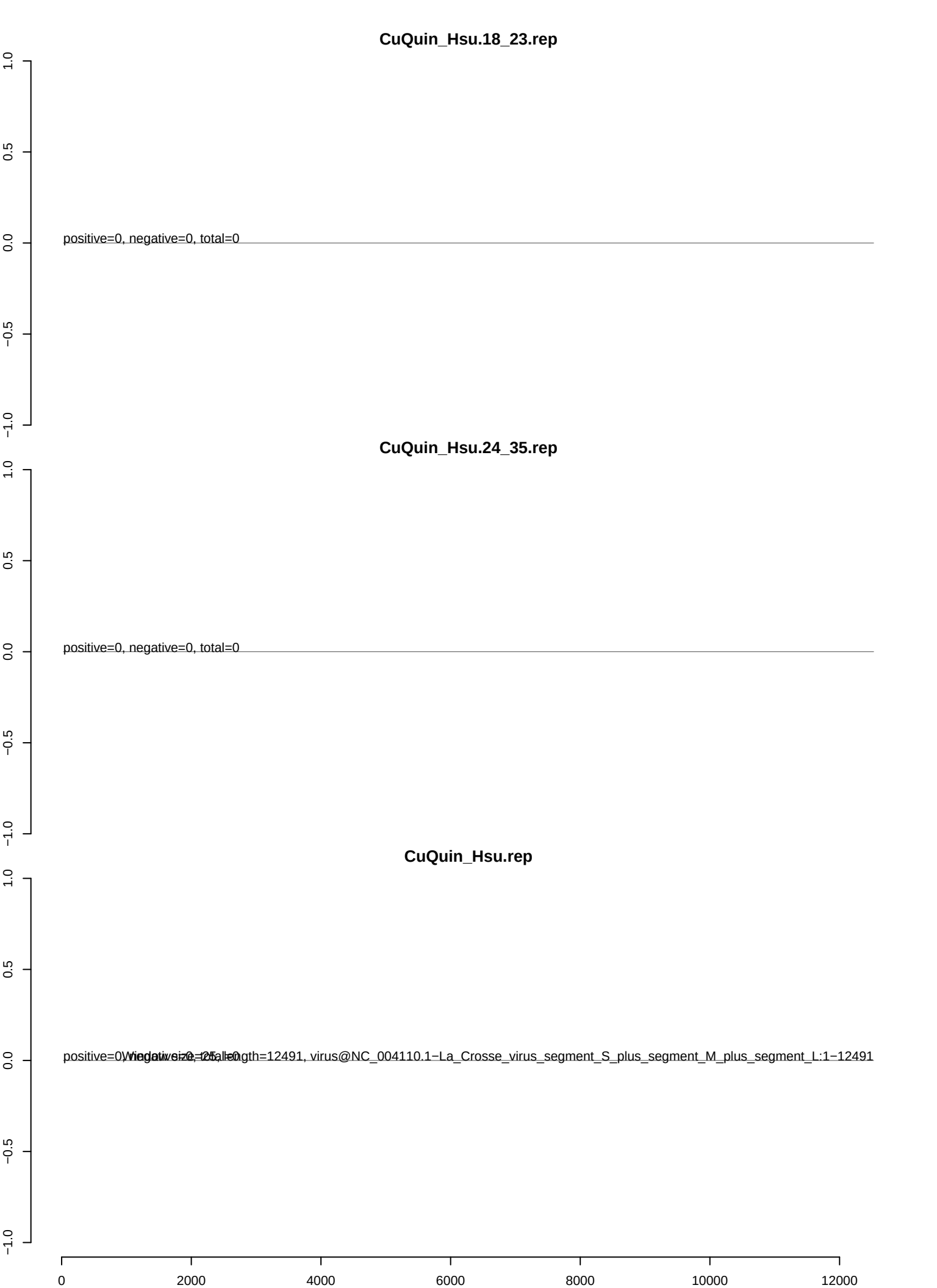
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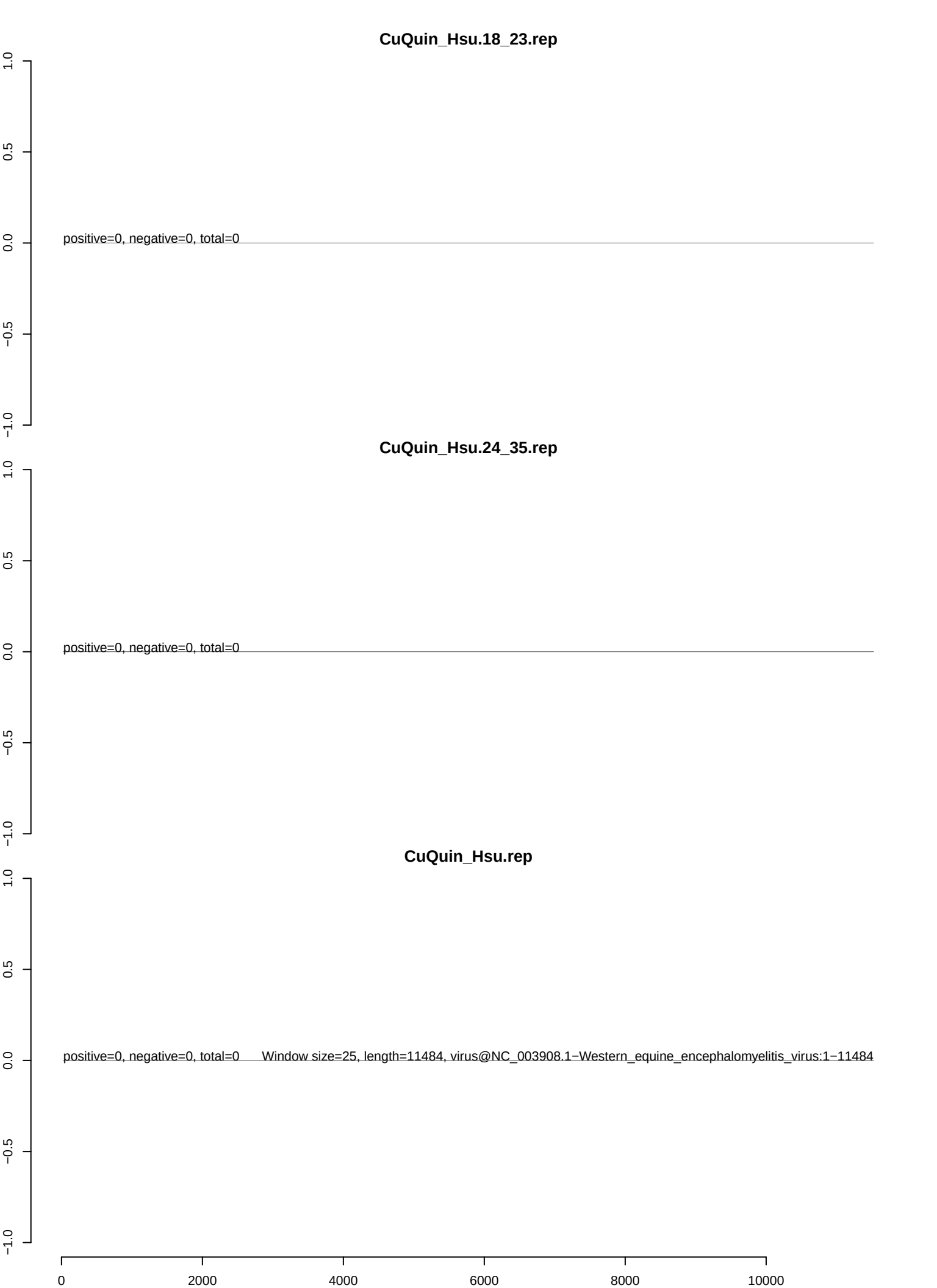
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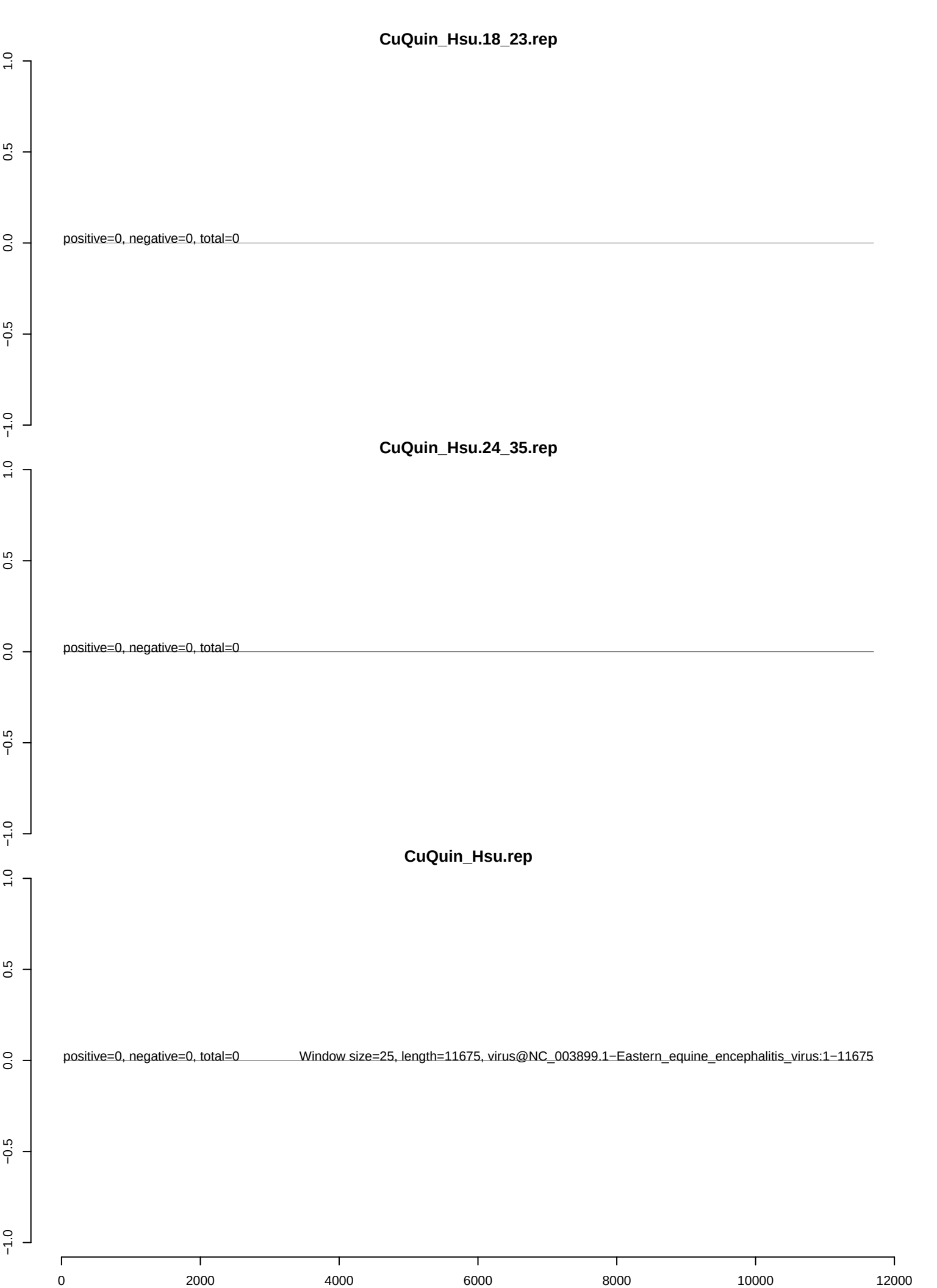
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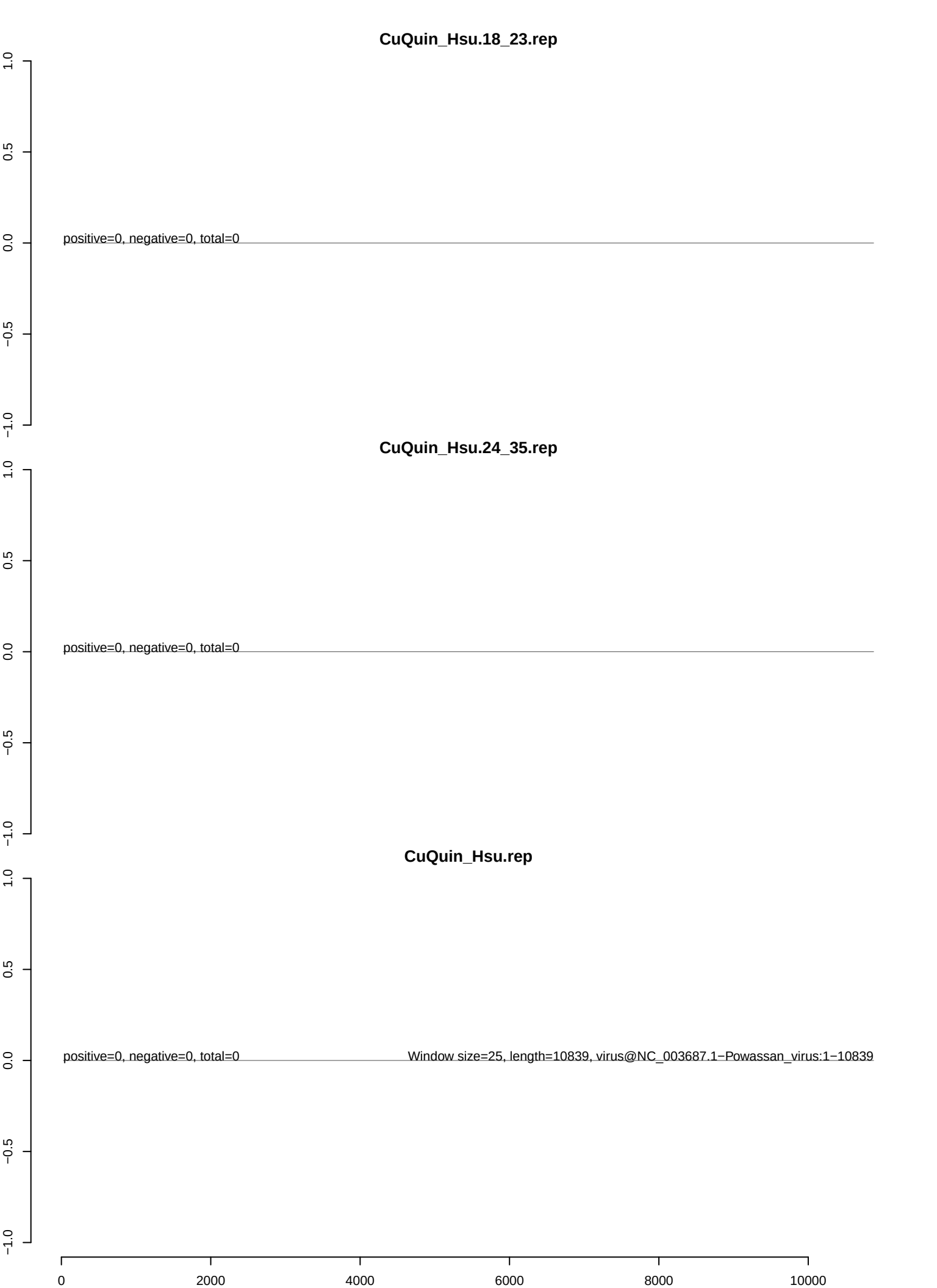
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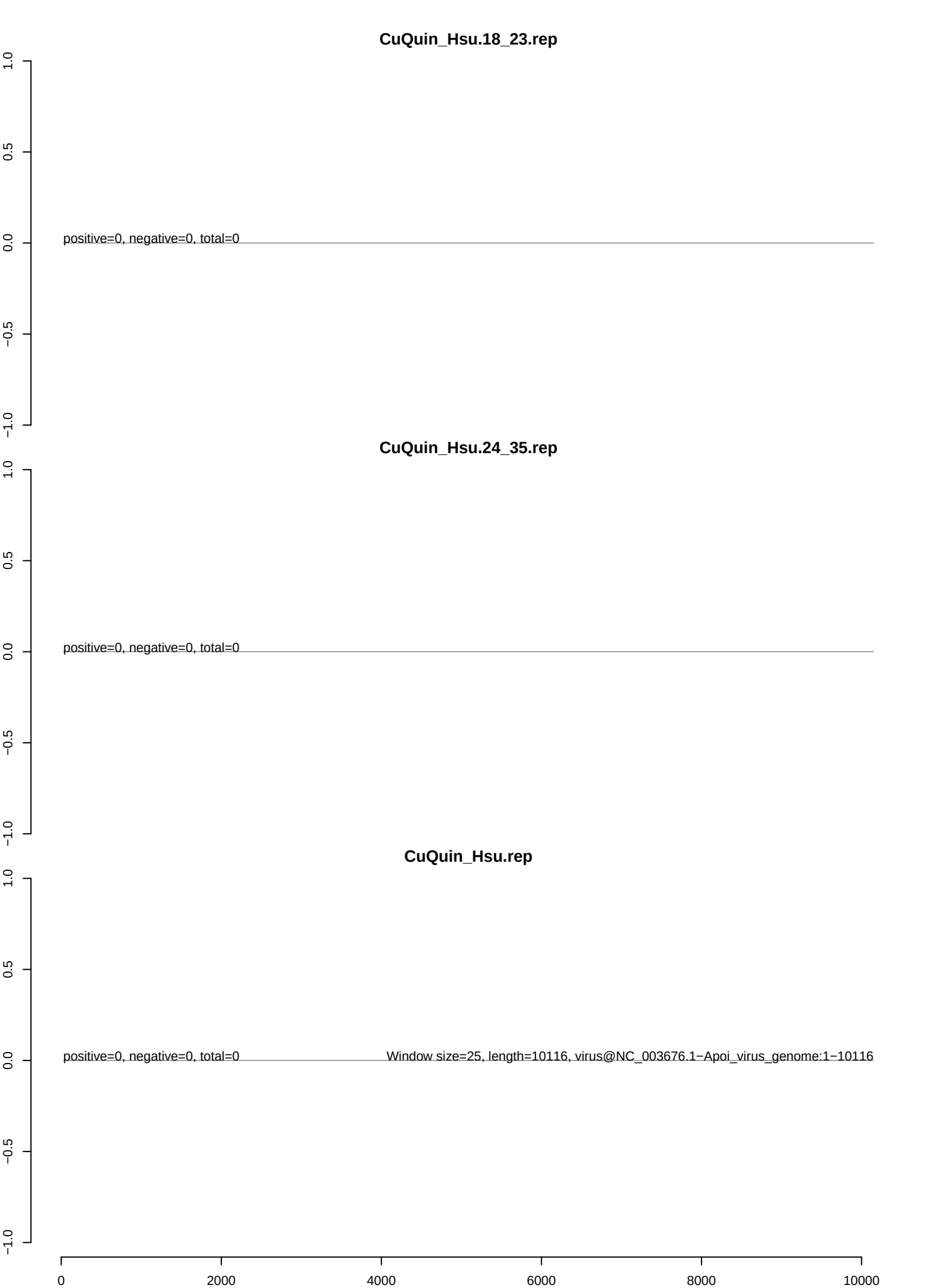
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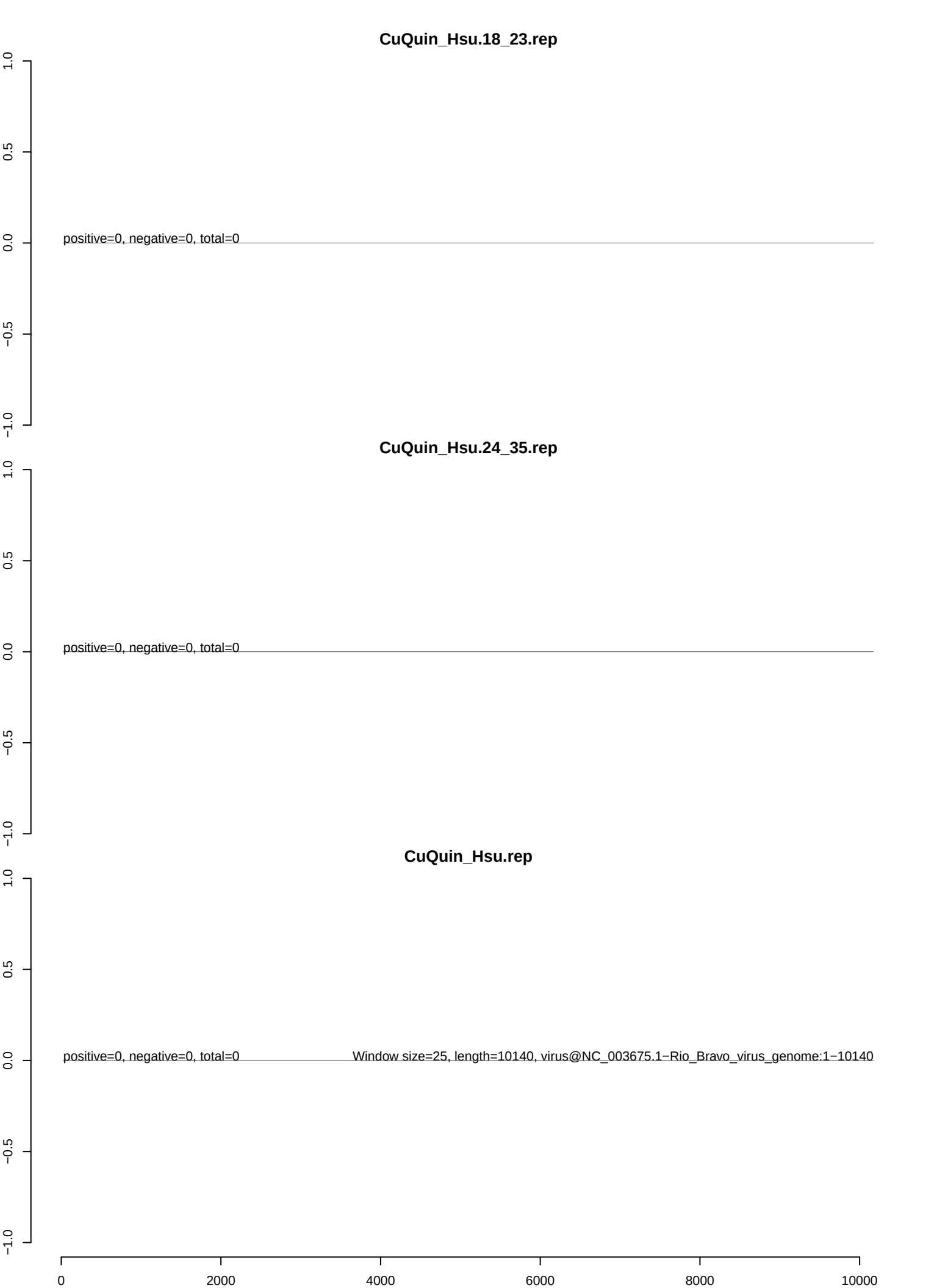
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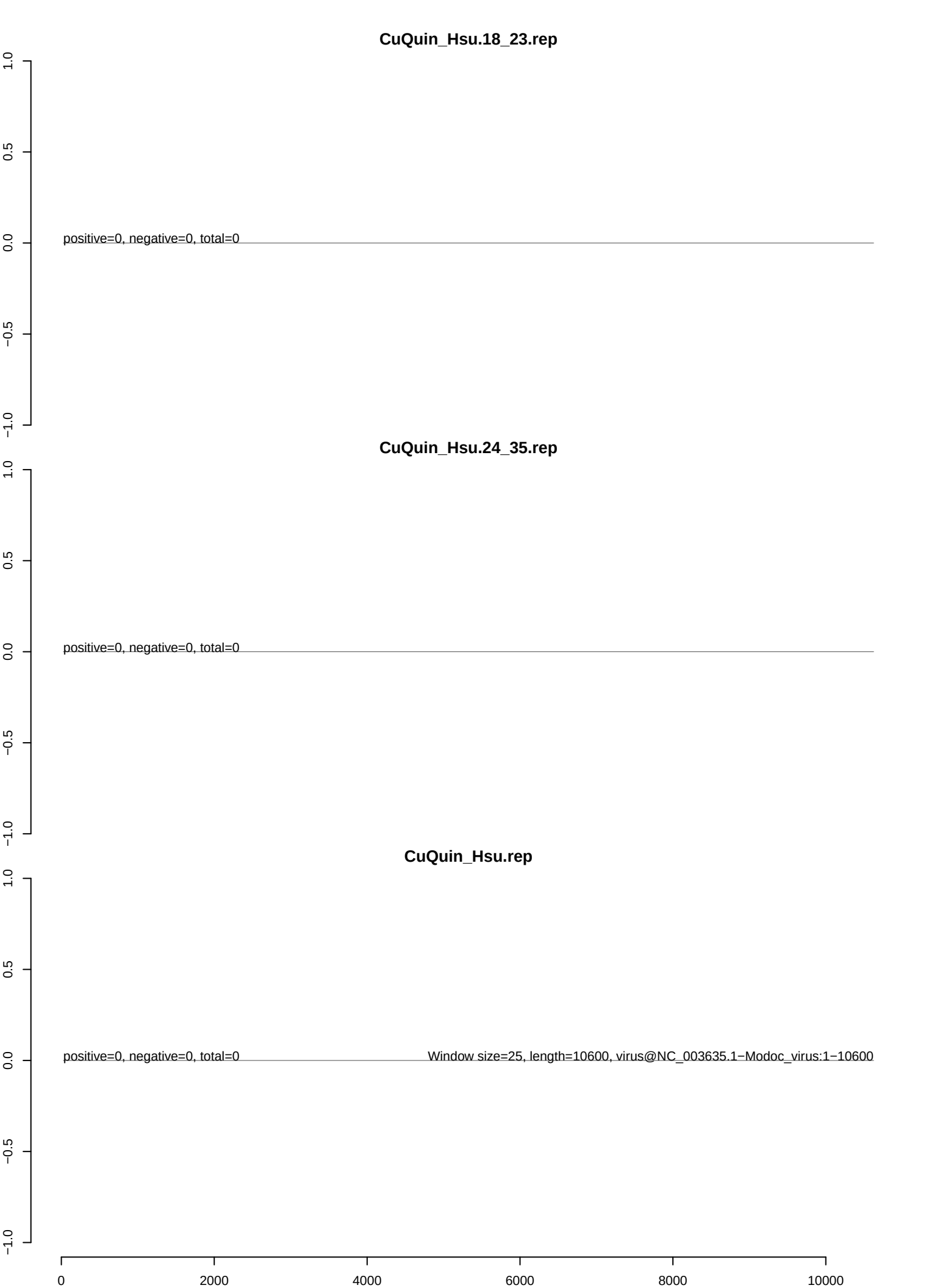
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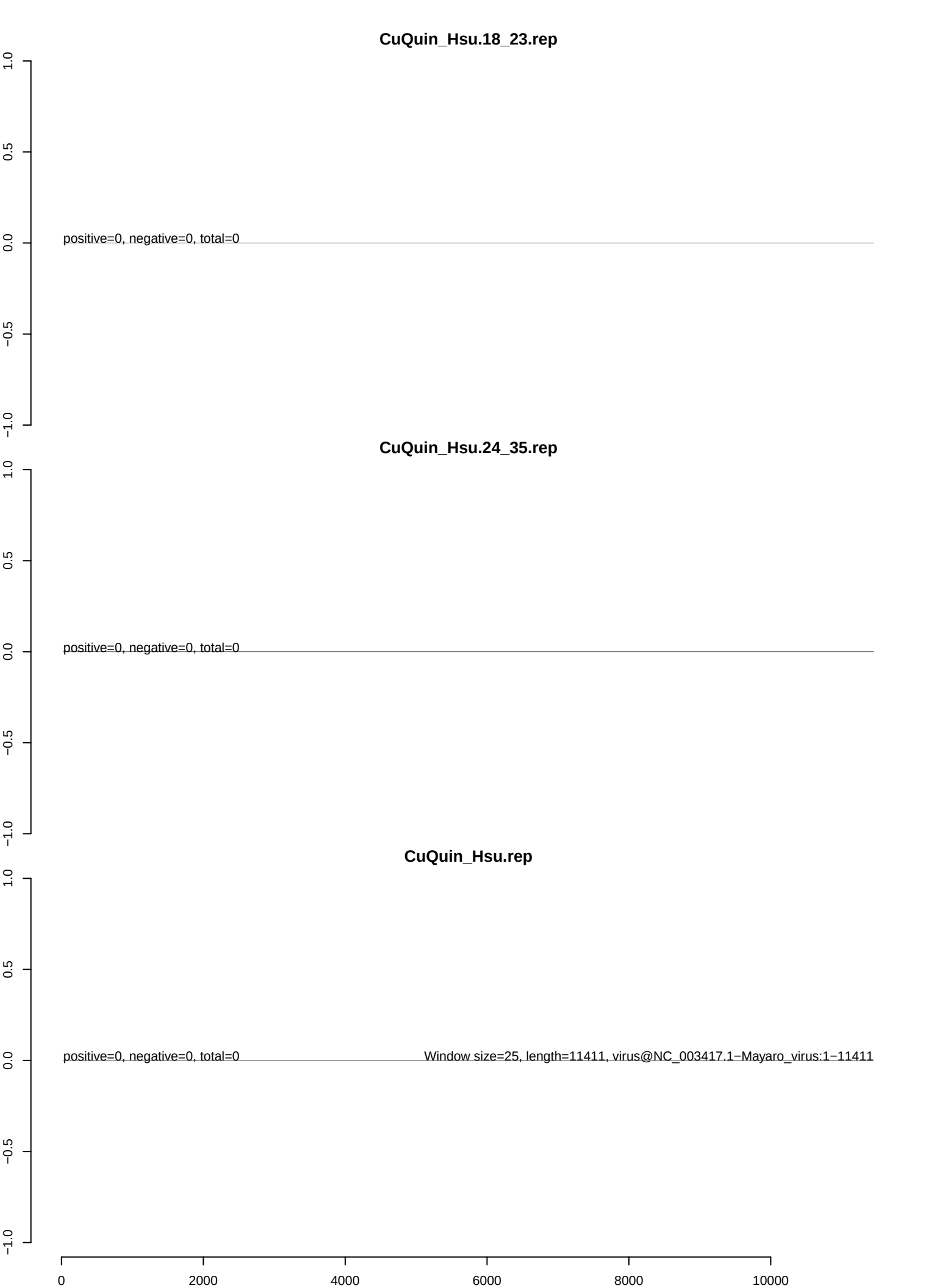
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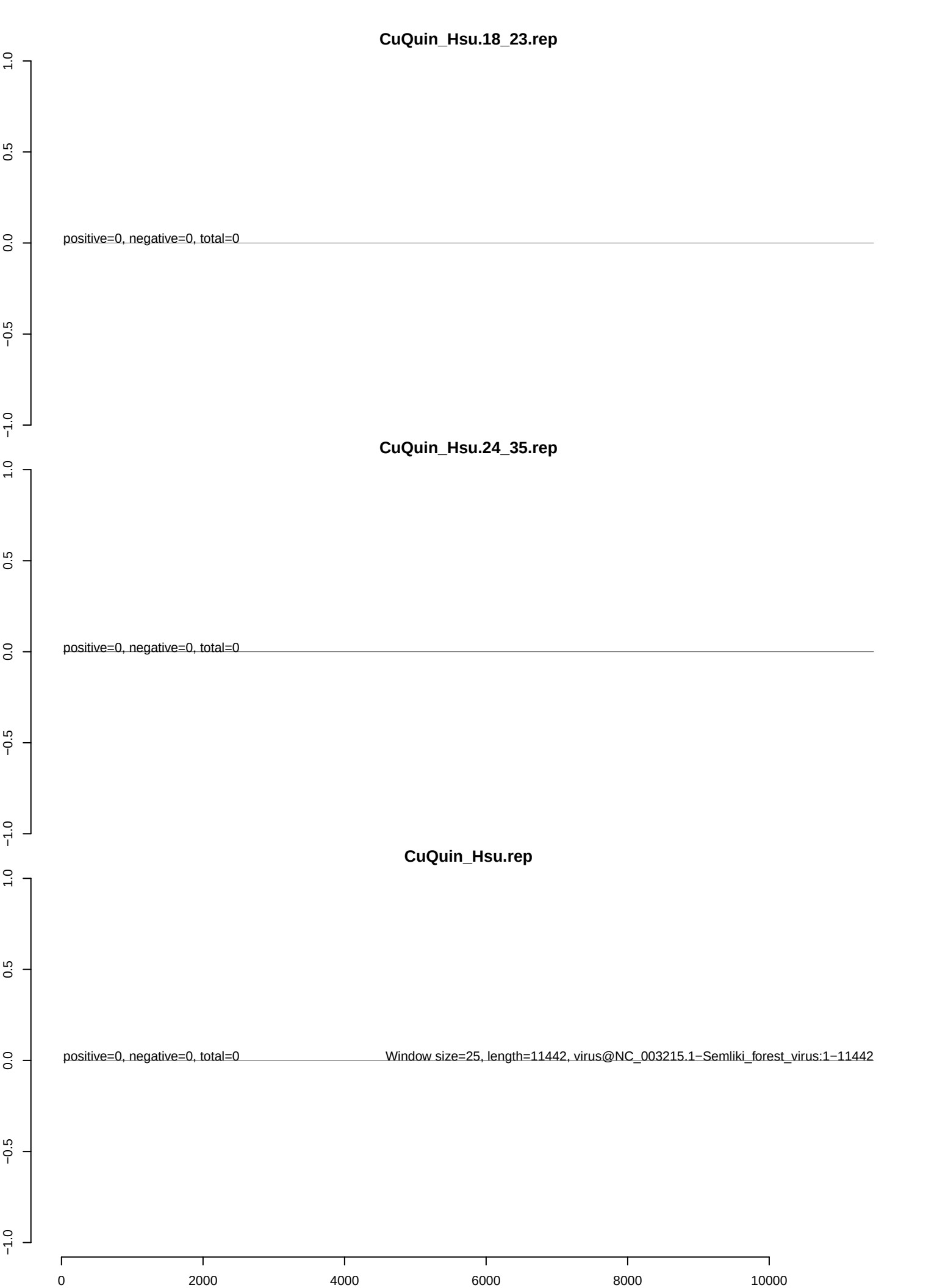
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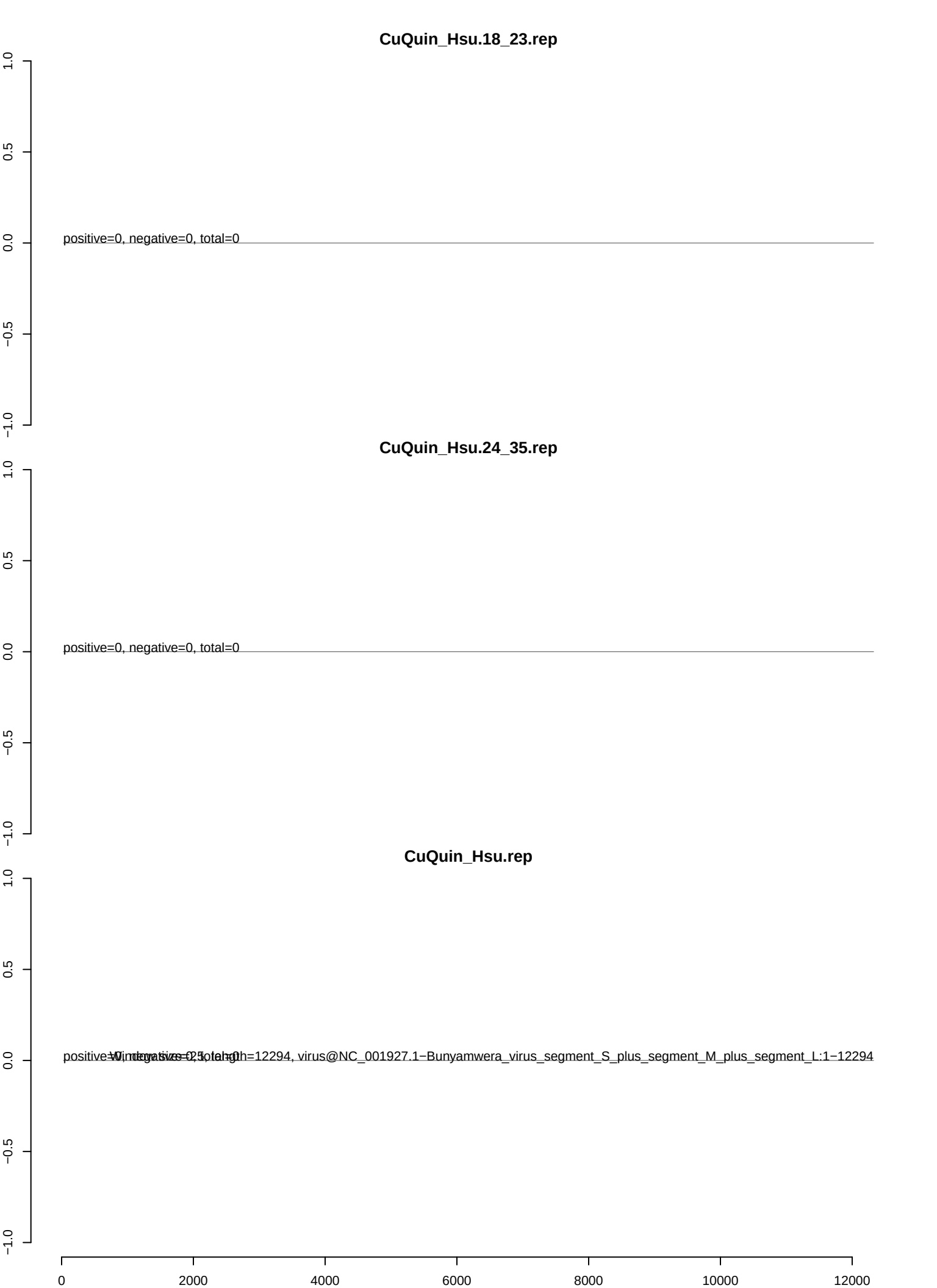
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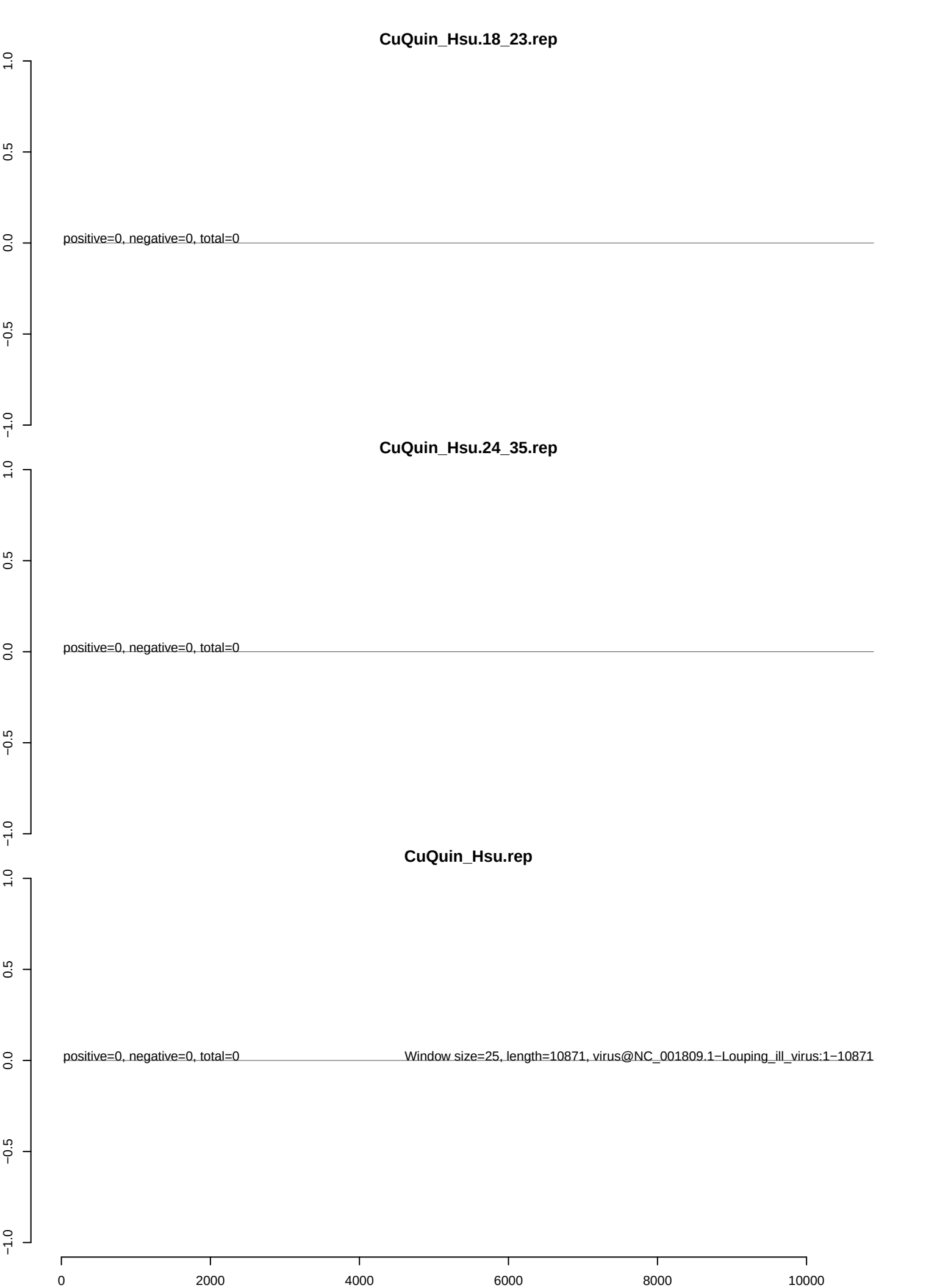
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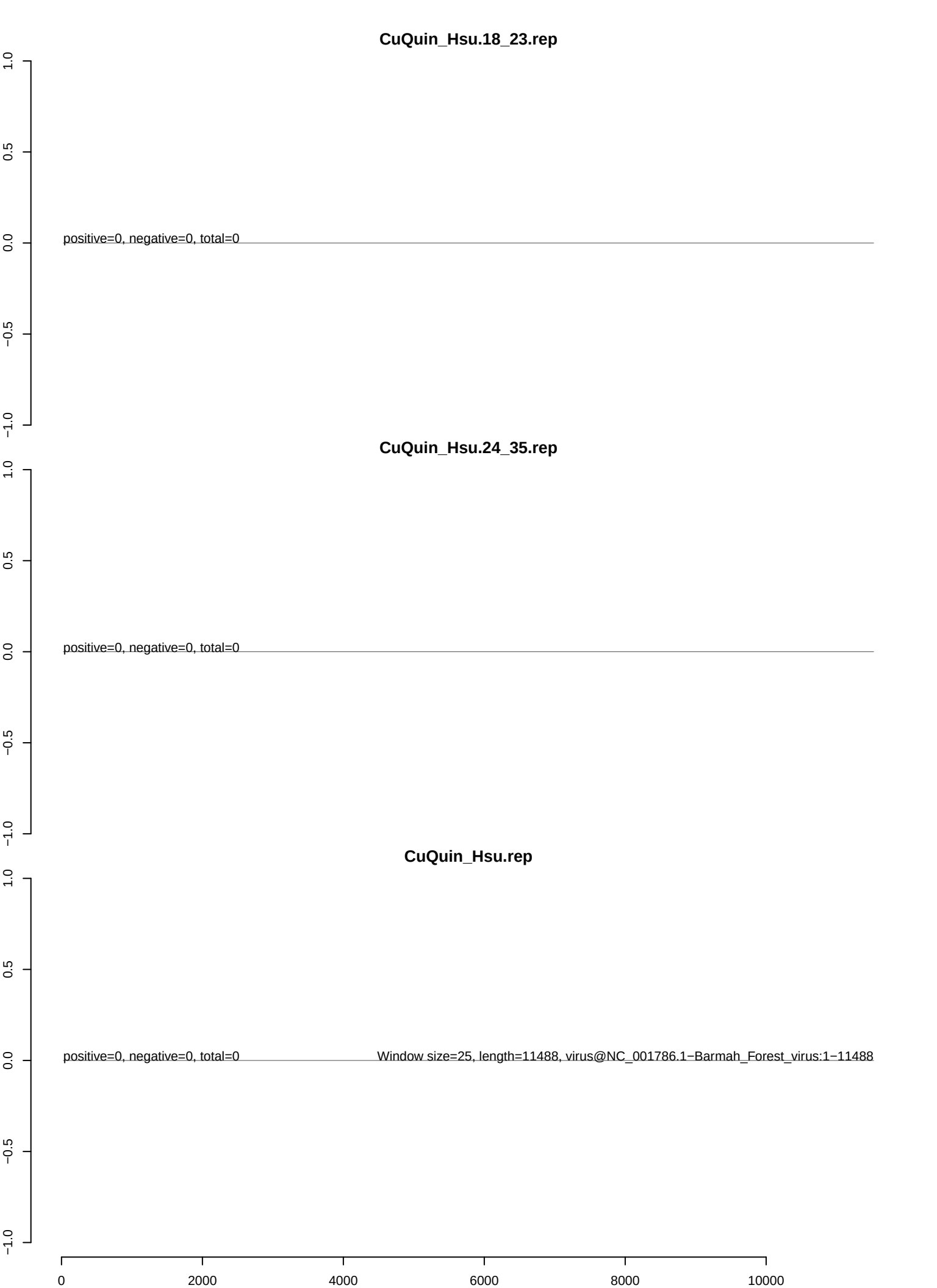
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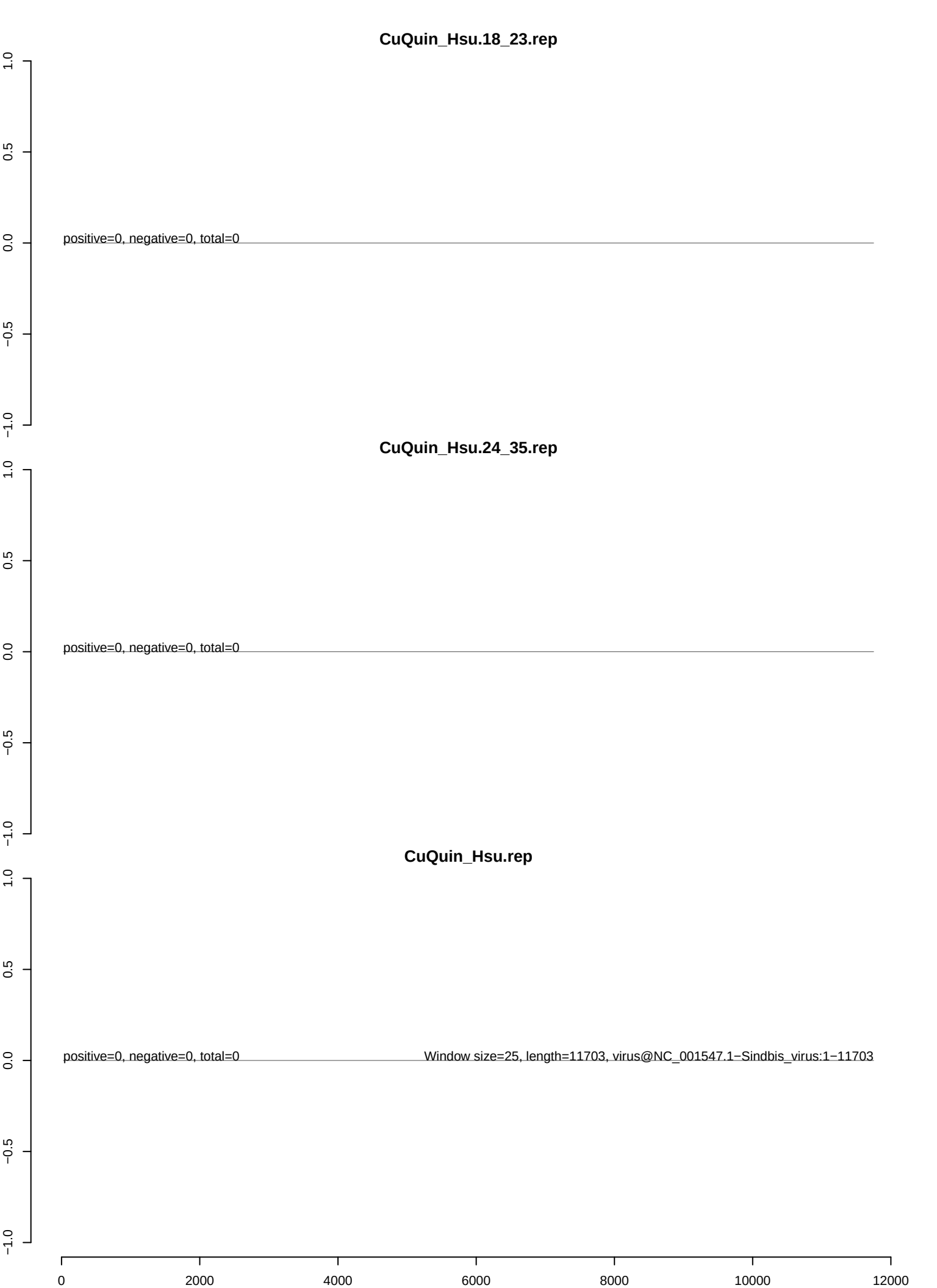
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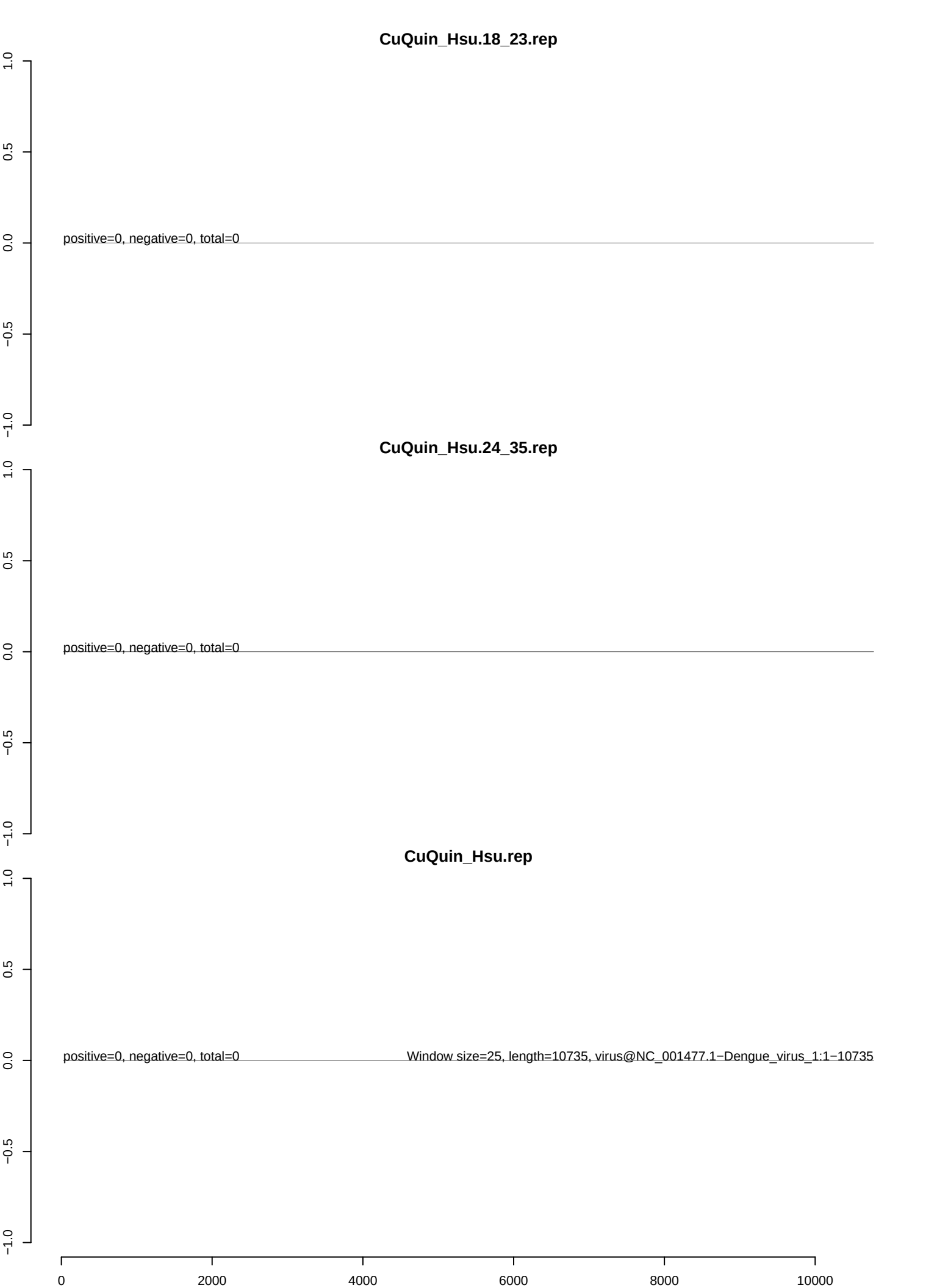
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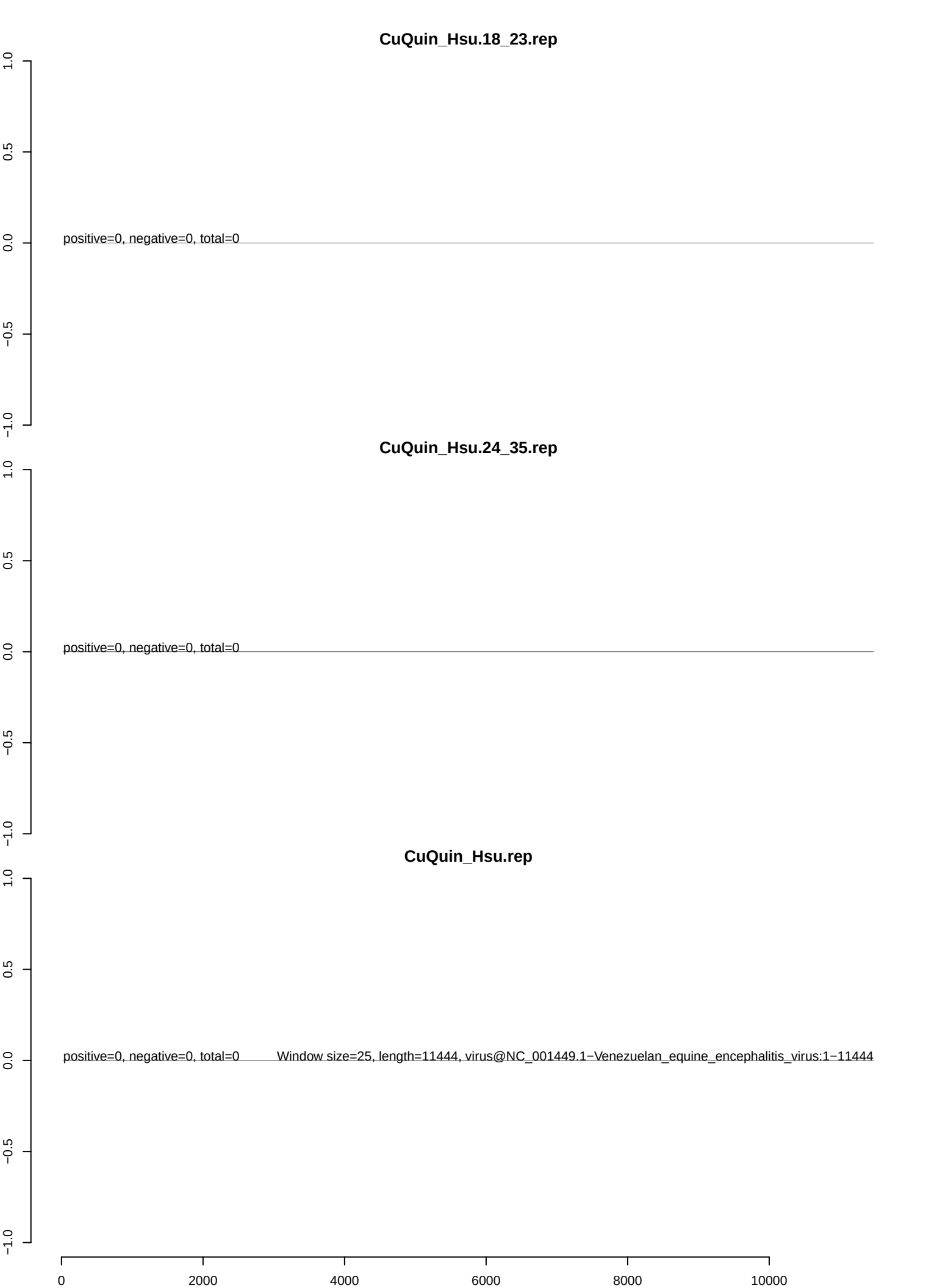
CuQuin_Hsu.18_23.rep
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
positive=0, negative=0, total=0
CuQuin_Hsu.rep
positive=0, negative=0, total=0
Window size=25, length=11444, virus@NC_001449.1−Venezuelan_equine_encephalitis_virus:1−11444
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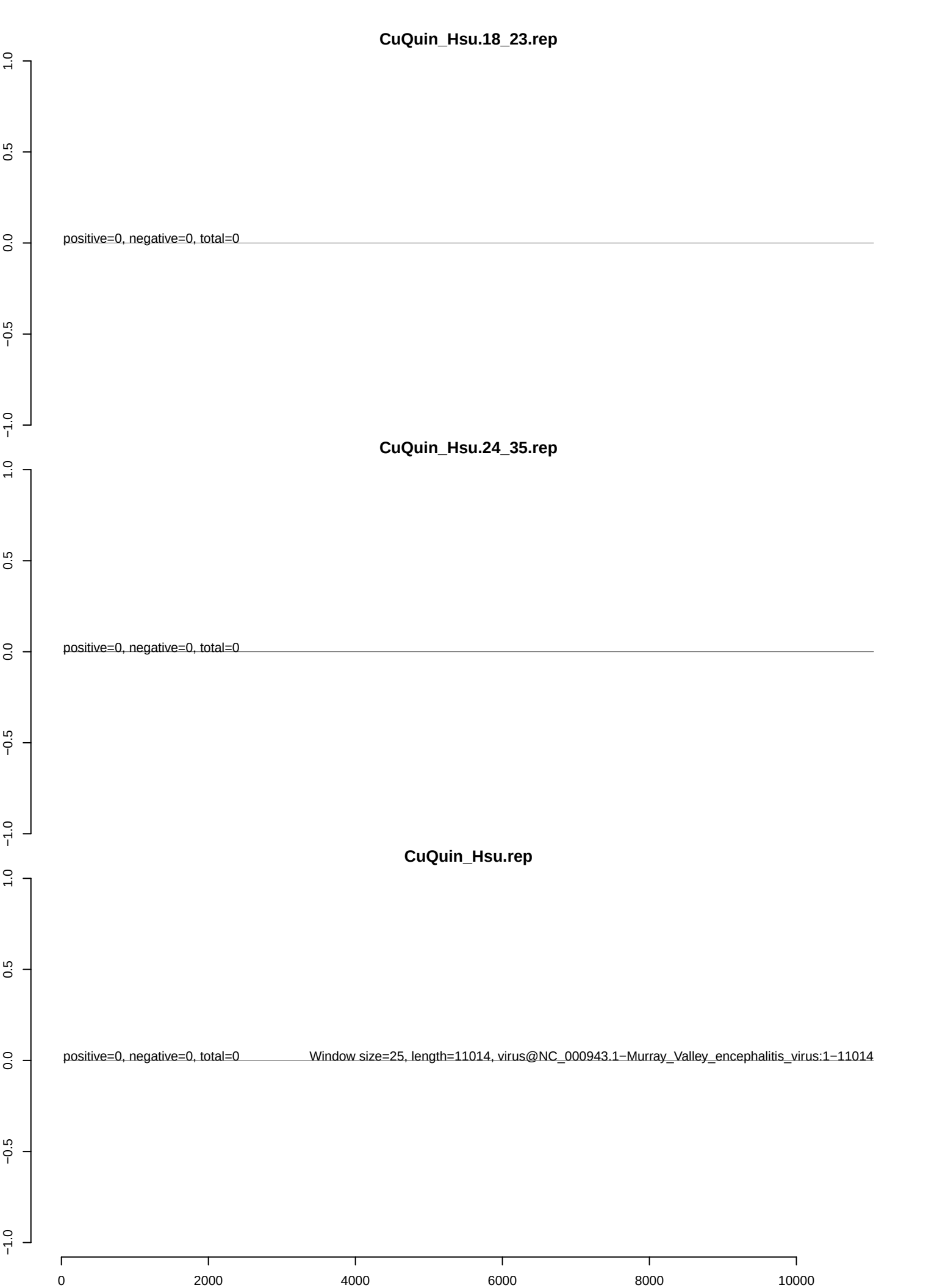
8000
10000


CuQuin_Hsu.18_23.rep
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
positive=0, negative=0, total=0
CuQuin_Hsu.rep
positive=0, negative=0, total=0
Window size=25, length=11014, virus@NC_000943.1−Murray_Valley_encephalitis_virus:1−11014
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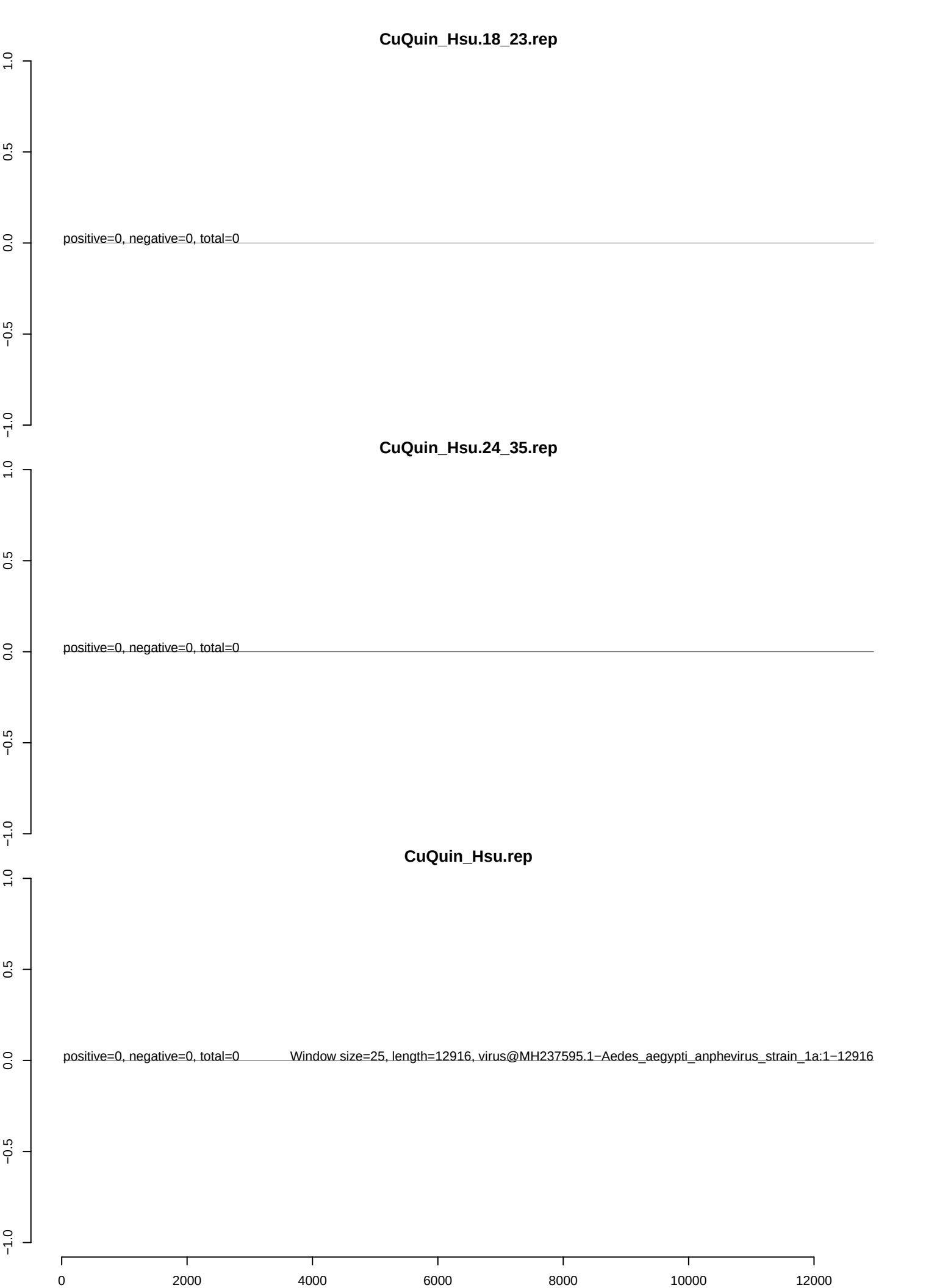
CuQuin_Hsu.18_23.rep
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
positive=0, negative=0, total=0
CuQuin_Hsu.rep
positive=0, negative=0, total=0
Window size=25, length=12916, virus@MH237595.1−Aedes_aegypti_anphevirus_strain_1a:1−12916
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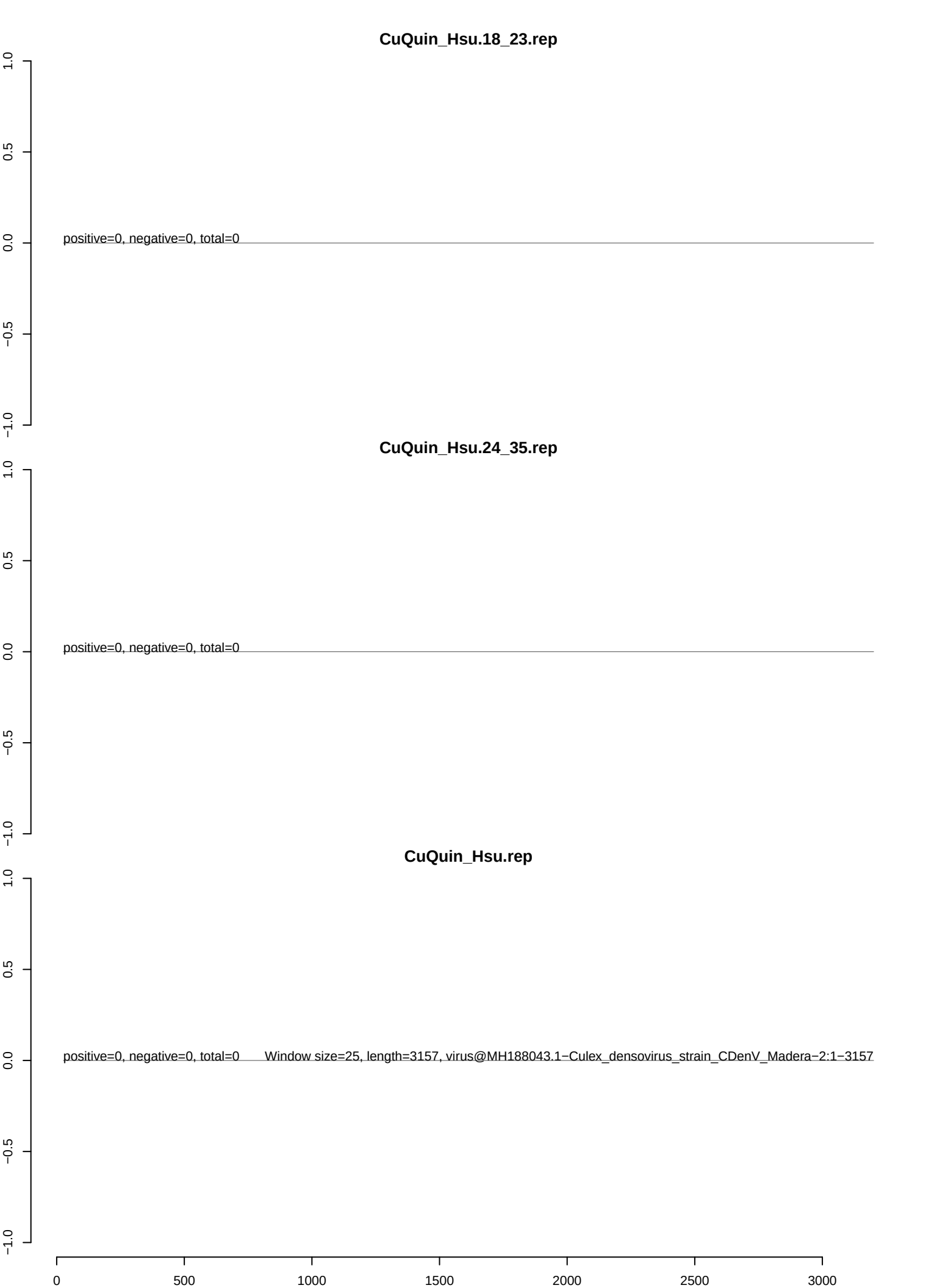
CuQuin_Hsu.18_23.rep
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CuQuin_Hsu.24_35.rep
positive=0, negative=0, total=0
CuQuin_Hsu.rep
positive=0, negative=0, total=0
Window size=25, length=3157, virus@MH188043.1−Culex_densovirus_strain_CDenV_Madera−2:1−3157
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1500
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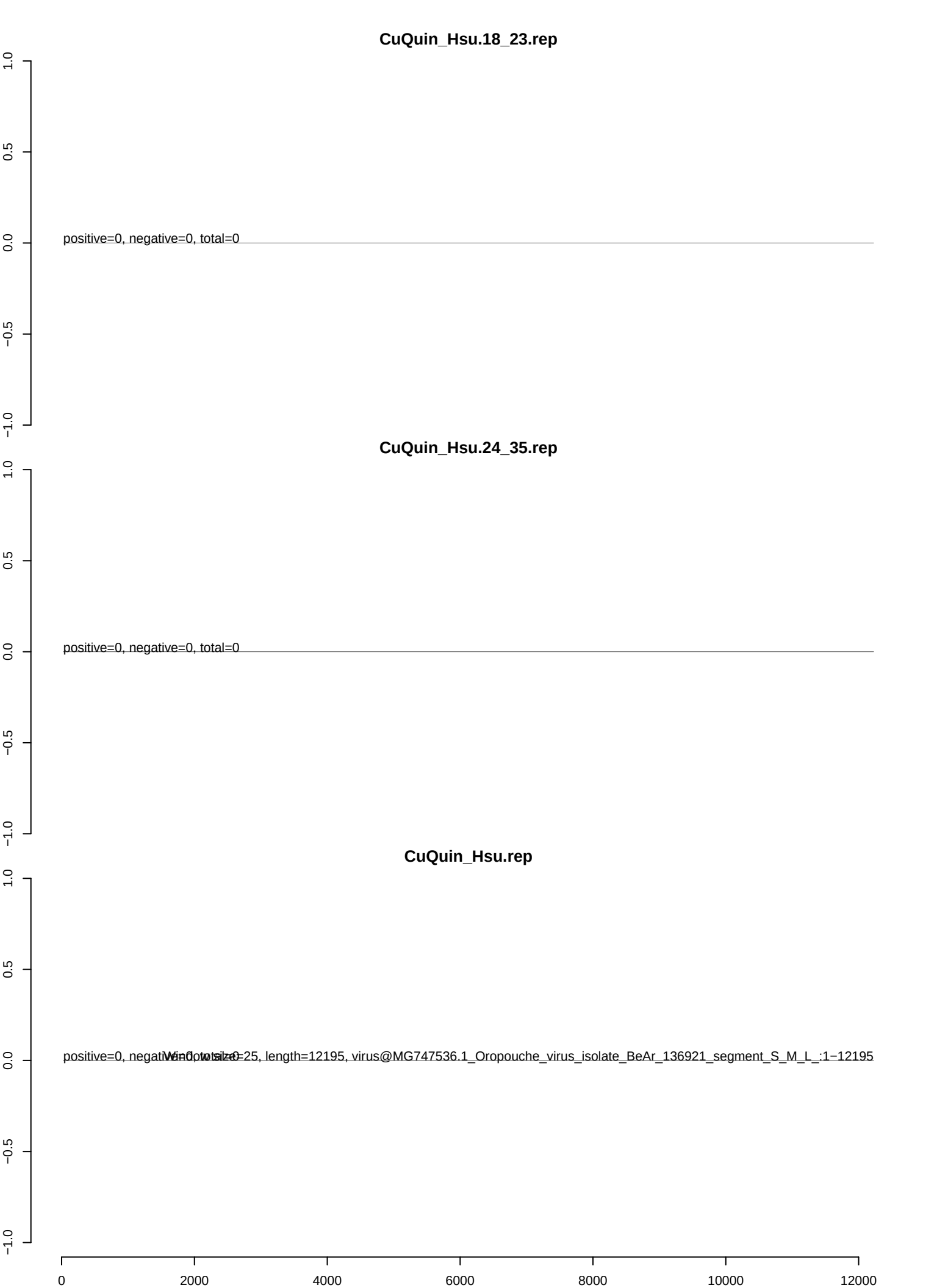
2500
3000


CuQuin_Hsu.18_23.rep
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CuQuin_Hsu.24_35.rep
positive=0, negative=0, total=0
CuQuin_Hsu.rep
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
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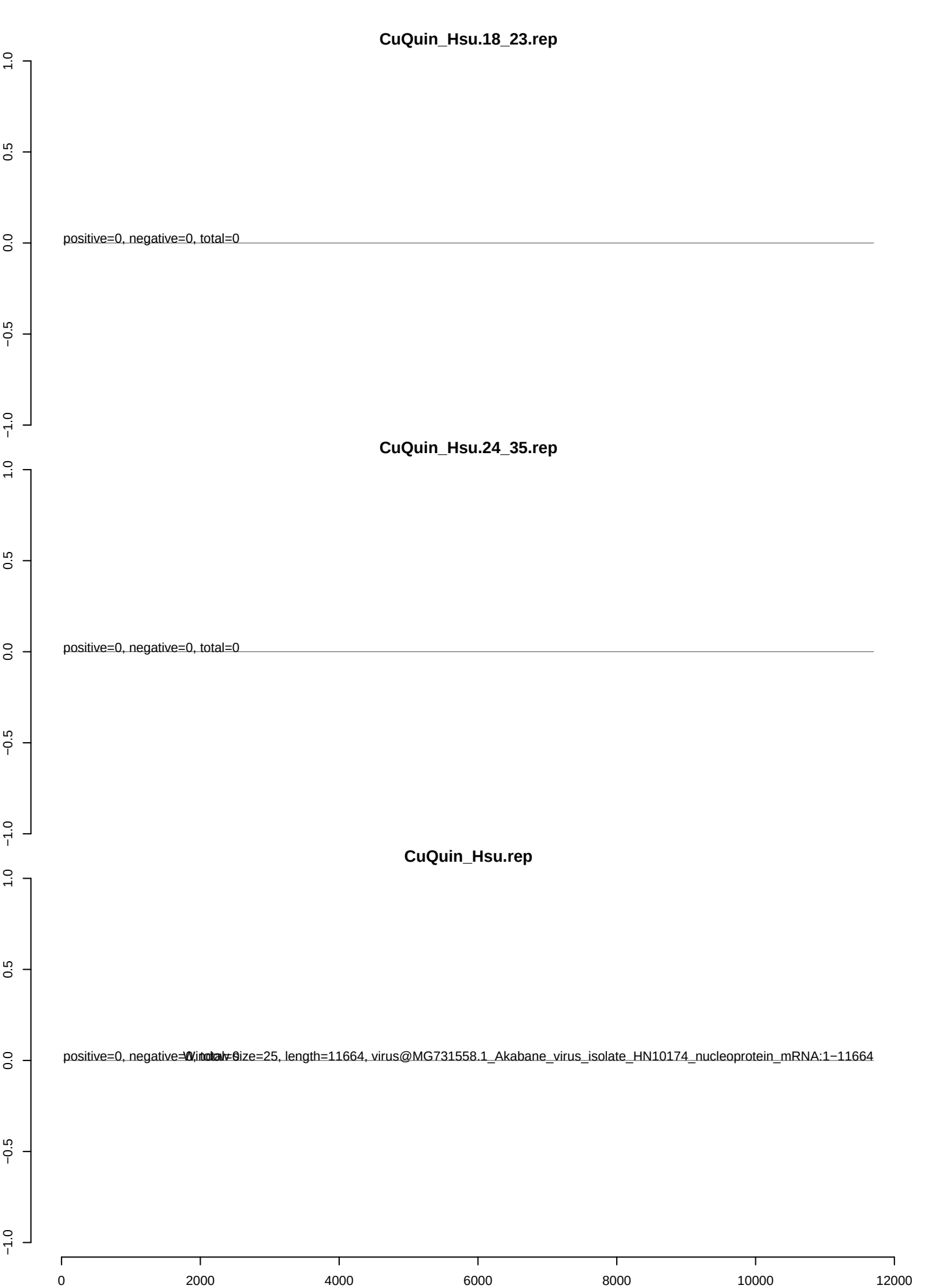
12000


CuQuin_Hsu.18_23.rep
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CuQuin_Hsu.24_35.rep
positive=0, negative=0, total=0
CuQuin_Hsu.rep
positive=0, negative=0, total=0
Window size=25, length=11664, virus@MG731558.1_Akabane_virus_isolate_HN10174_nucleoprotein_mRNA:1−11664
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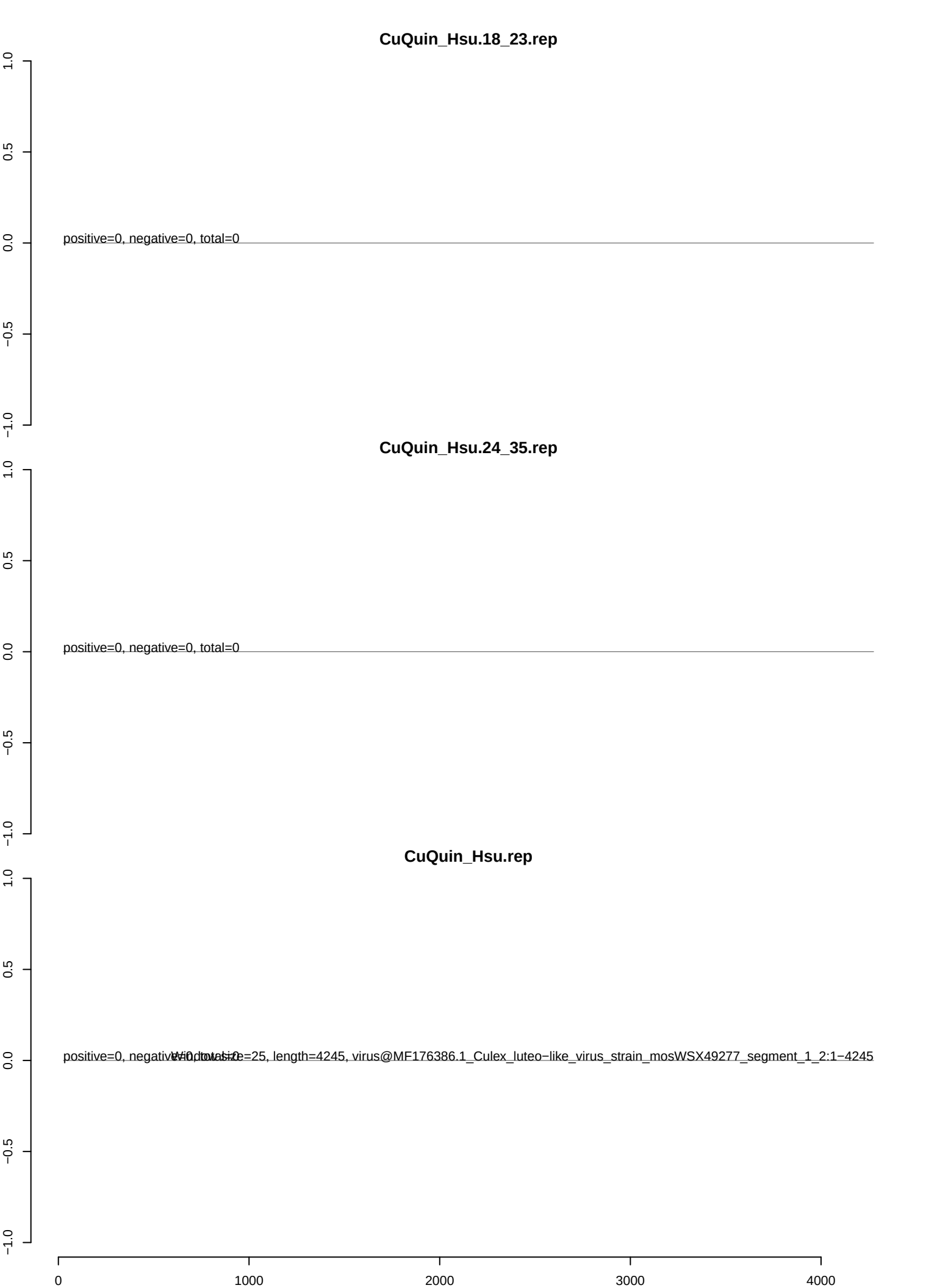
8000
10000
12000


CuQuin_Hsu.18_23.rep
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CuQuin_Hsu.24_35.rep
positive=0, negative=0, total=0
CuQuin_Hsu.rep
positive=0, negative=0, total=25, length=4245, virus@MF176386.1_Culex_luteo−like_virus_strain_mosWSX49277_segment_1_2:1−4245
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2000
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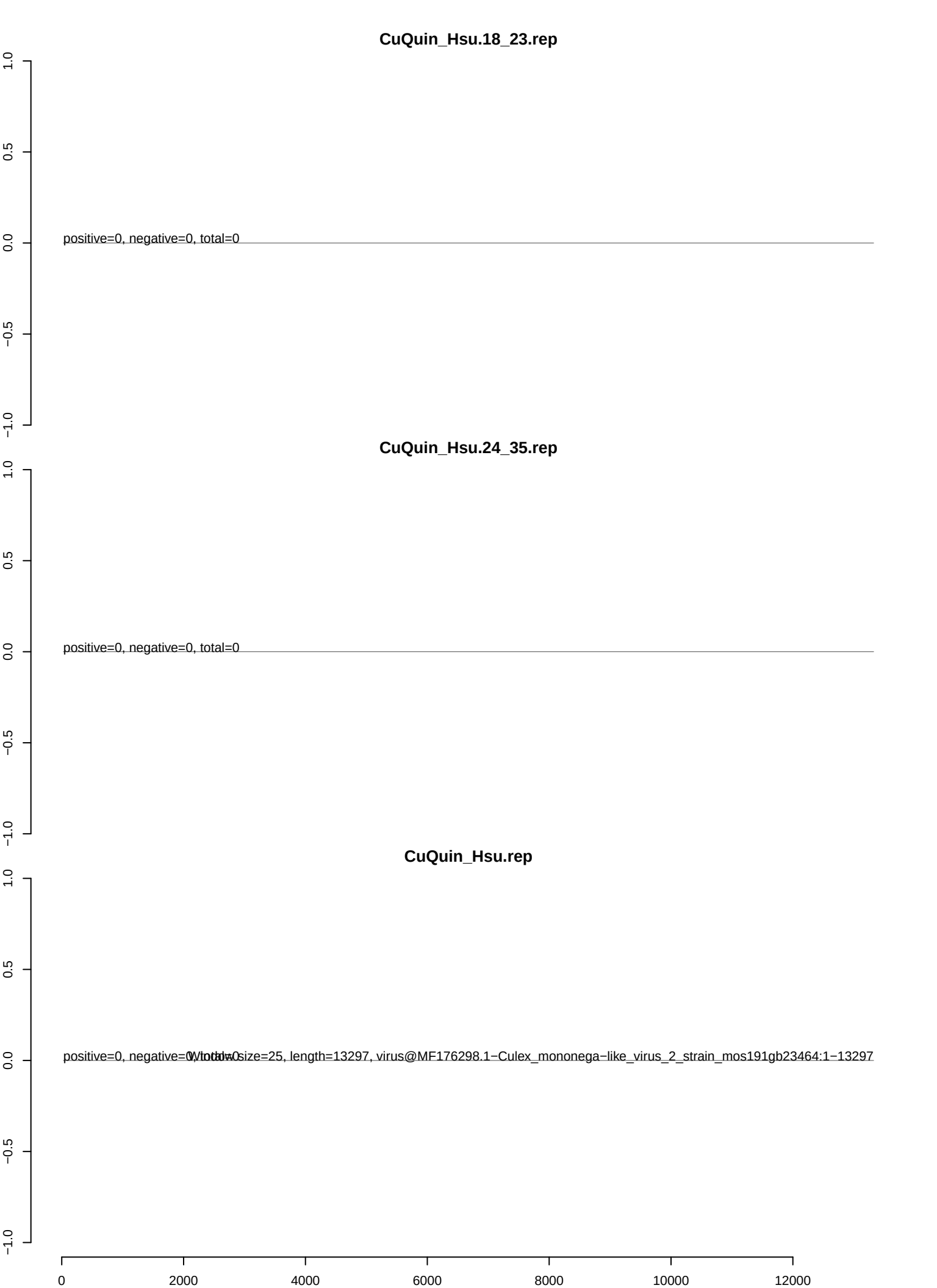
4000


CuQuin_Hsu.18_23.rep
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
positive=0, negative=0, total=0
CuQuin_Hsu.rep
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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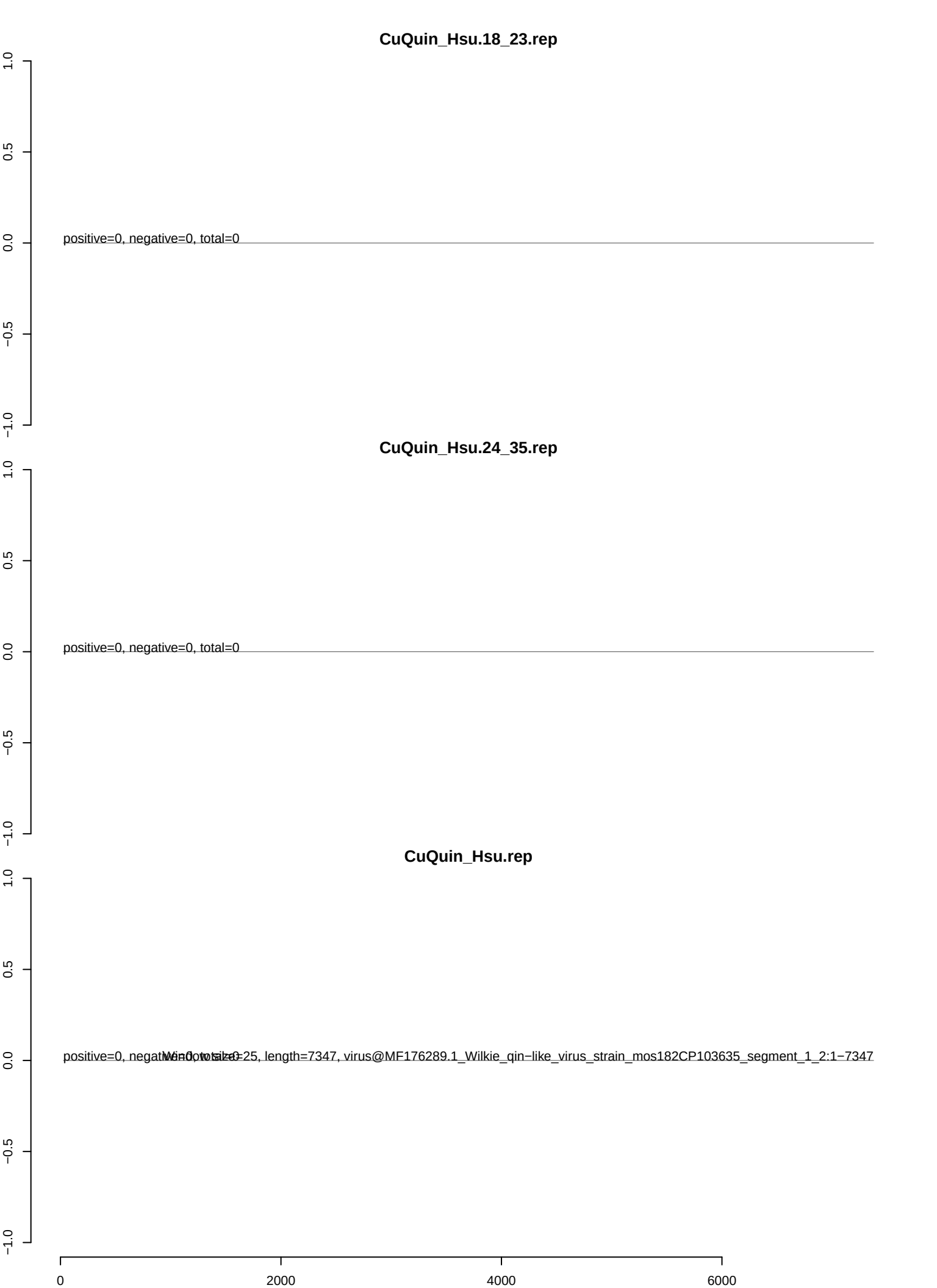
6000
8000
10000
12000


CuQuin_Hsu.18_23.rep
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
positive=0, negative=0, total=0
CuQuin_Hsu.rep
positive=0, negative=0, total=0
Window size=25, length=7347, virus@MF176289.1_Wilkie_qin−like_virus_strain_mos182CP103635_segment_1_2:1−7347
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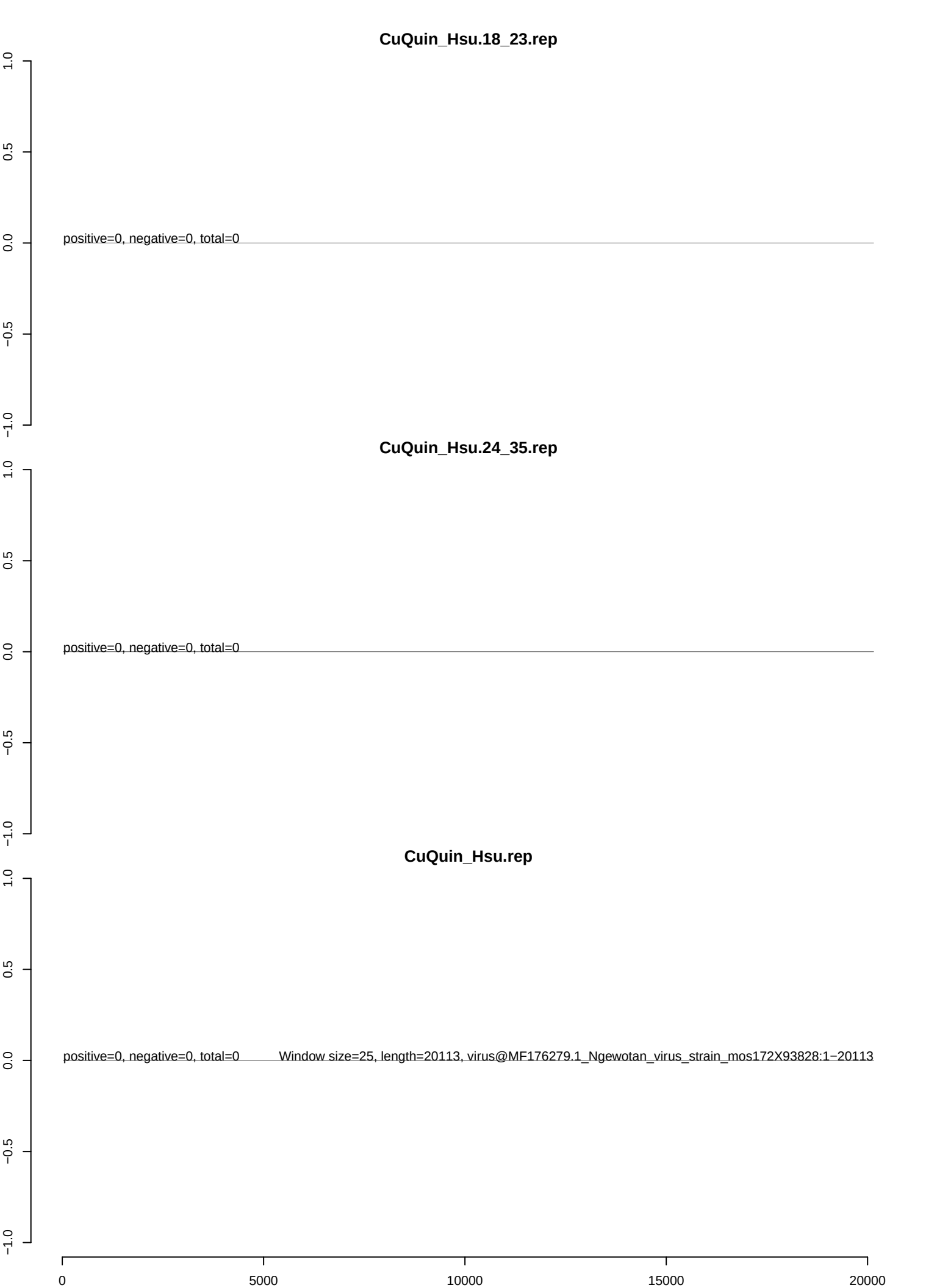
4000
6000


CuQuin_Hsu.18_23.rep
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
positive=0, negative=0, total=0
CuQuin_Hsu.rep
positive=0, negative=0, total=0
Window size=25, length=20113, virus@MF176279.1_Ngewotan_virus_strain_mos172X93828:1−20113
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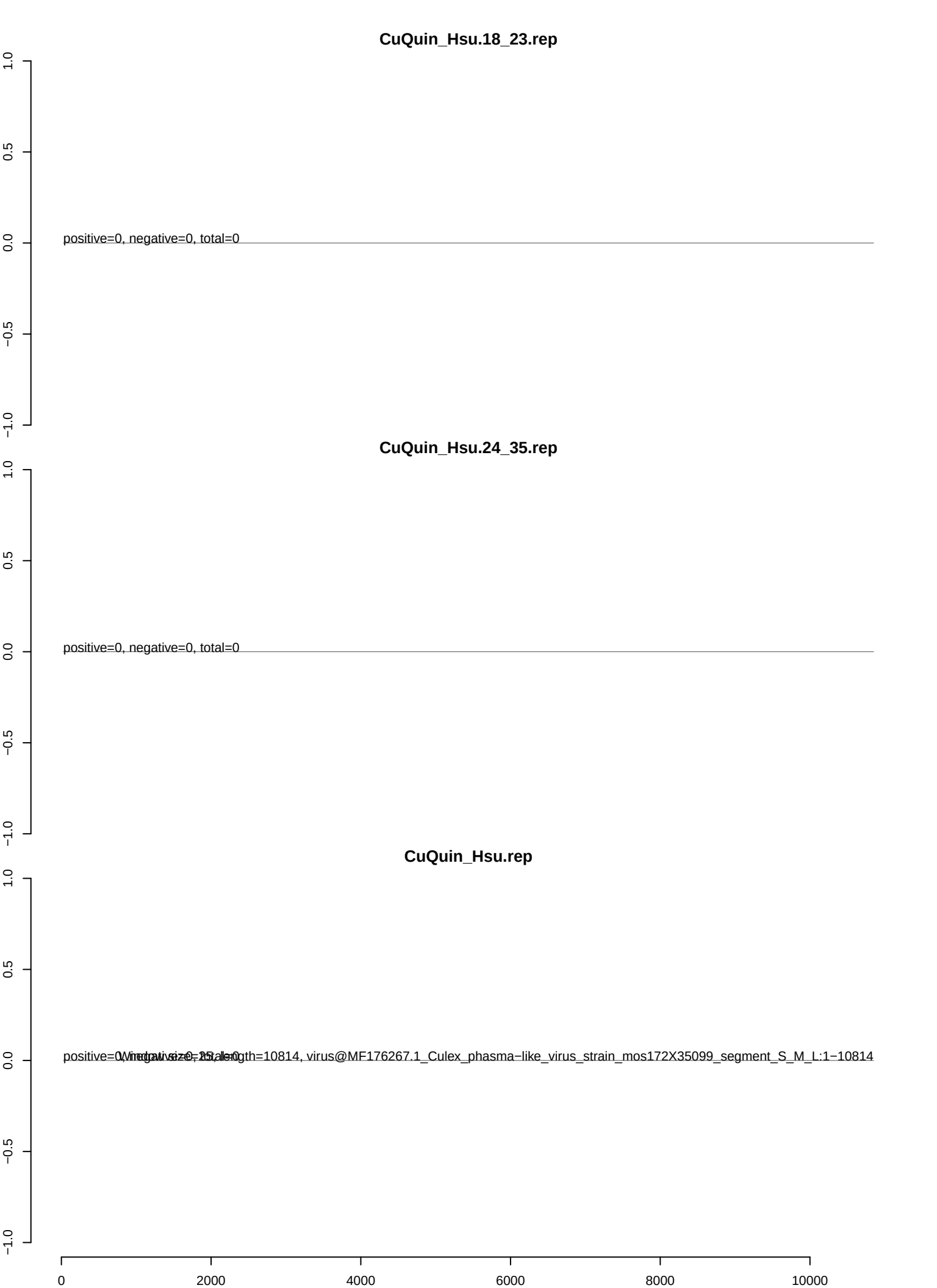
15000
20000


CuQuin_Hsu.18_23.rep
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CuQuin_Hsu.24_35.rep
positive=0, negative=0, total=0
CuQuin_Hsu.rep
positive=0, negative=0, total=0
virus@MF176267.1_Culex_phasma−like_virus_strain_mos172X35099_segment_S_M_L:1−10814
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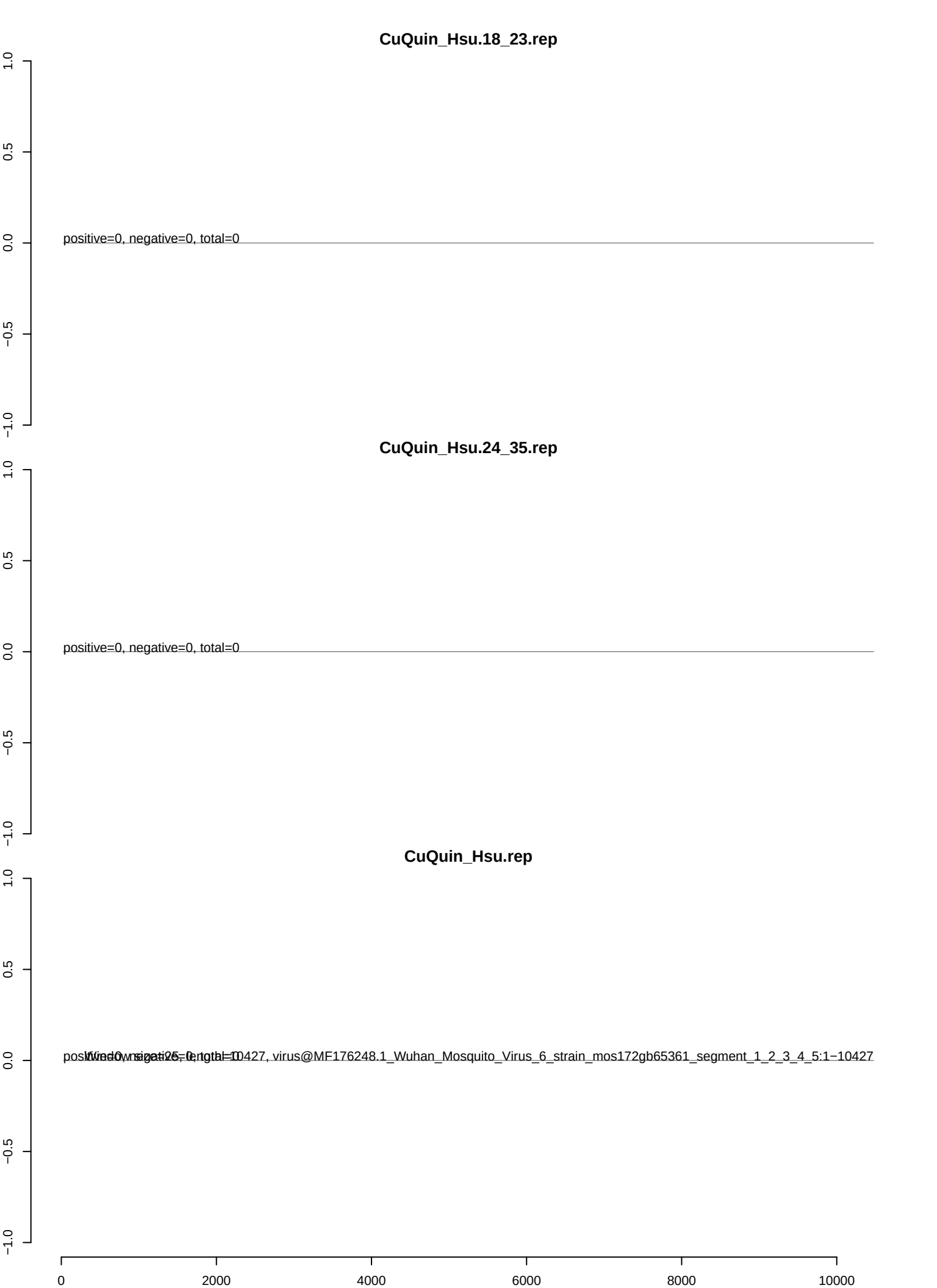
8000
10000


CuQuin_Hsu.18_23.rep
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
positive=0, negative=0, total=0
CuQuin_Hsu.rep
positive=0, negative=0, total=0
Window size=25, length=10427, virus@MF176248.1_Wuhan_Mosquito_Virus_6_strain_mos172gb65361_segment_1_2_3_4_5:1−10427
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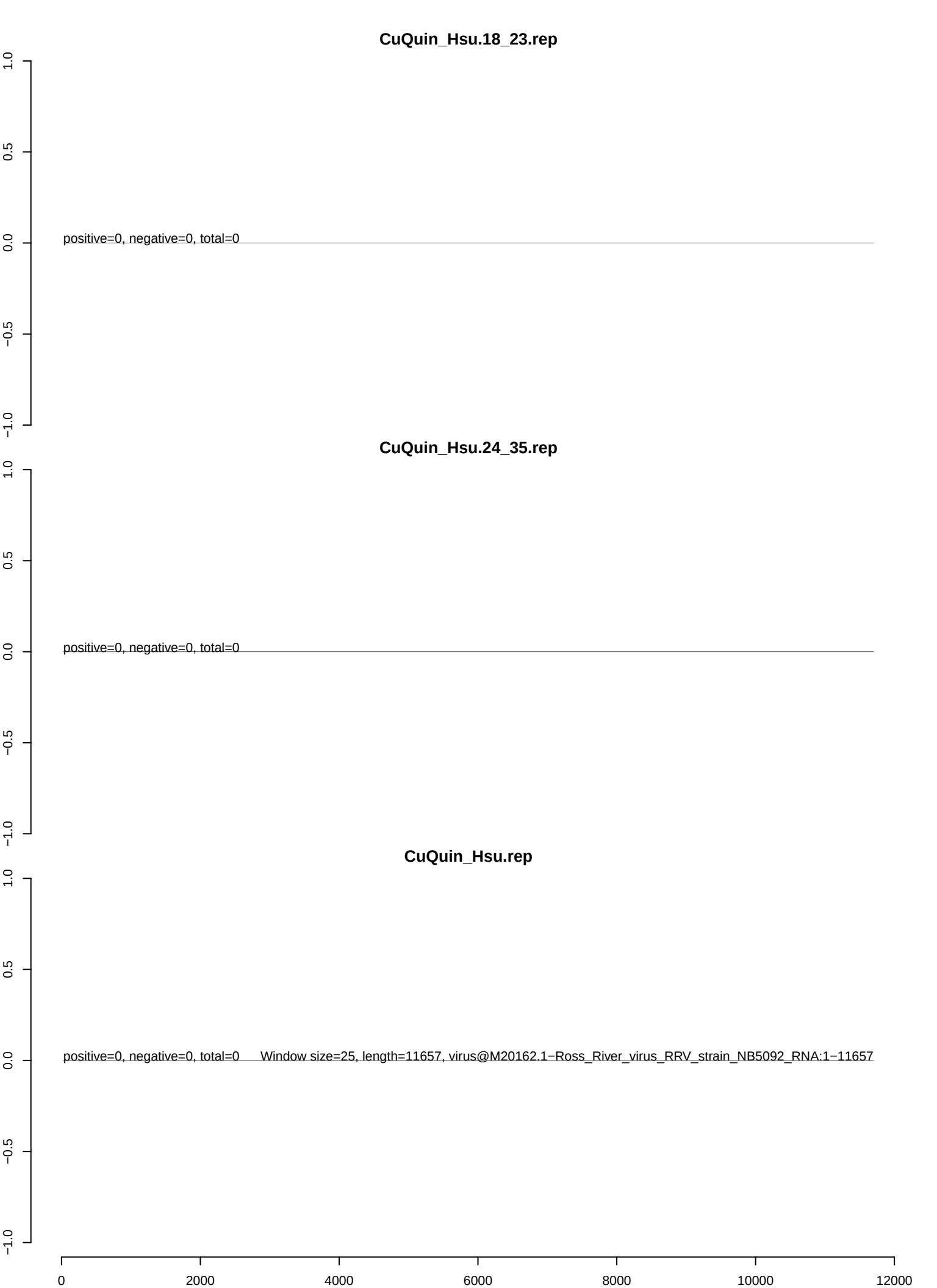
10000


CuQuin_Hsu.18_23.rep
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
positive=0, negative=0, total=0
CuQuin_Hsu.rep
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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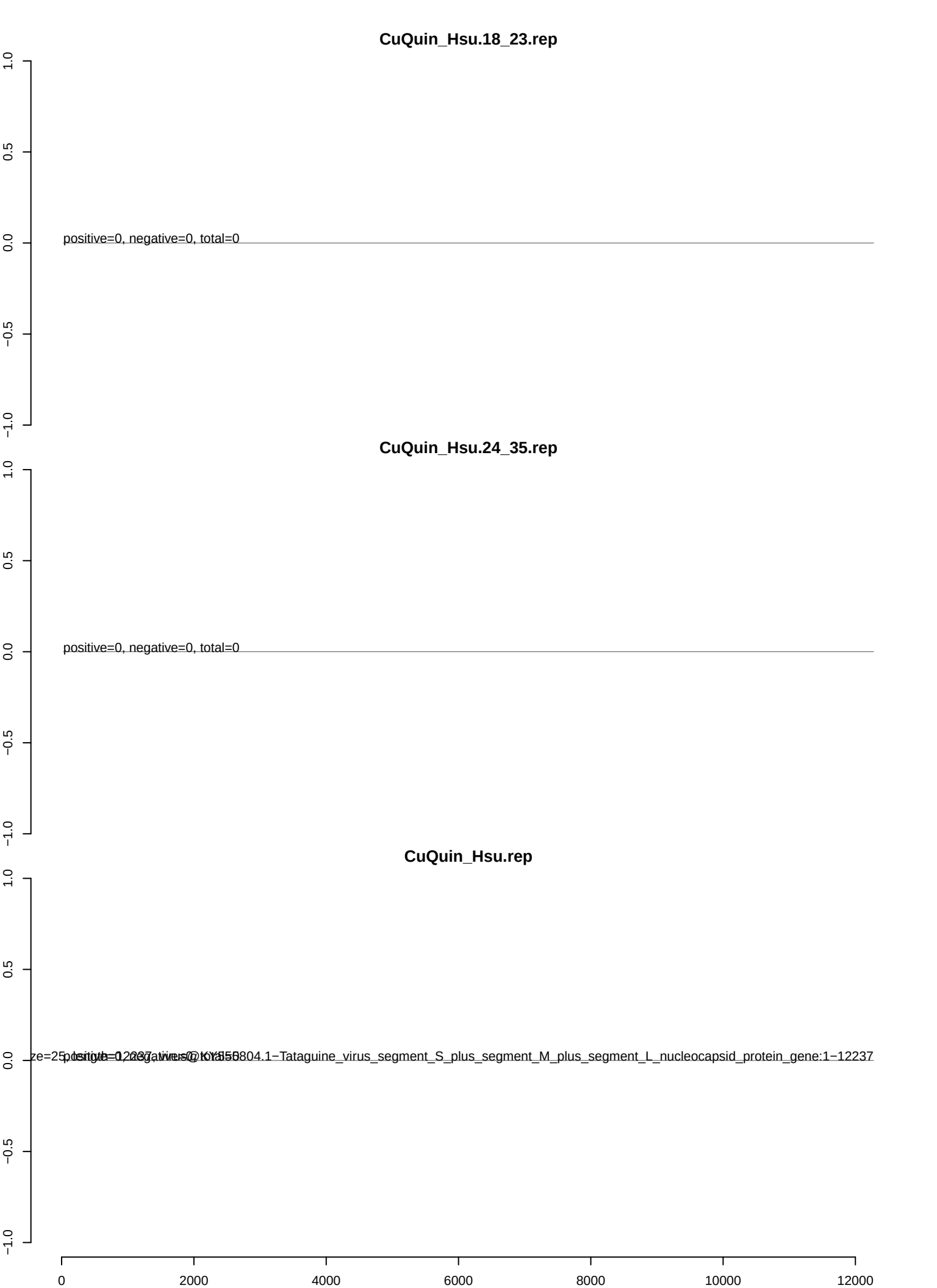
8000
10000
12000


CuQuin_Hsu.18_23.rep
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
positive=0, negative=0, total=0
CuQuin_Hsu.rep
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0.0
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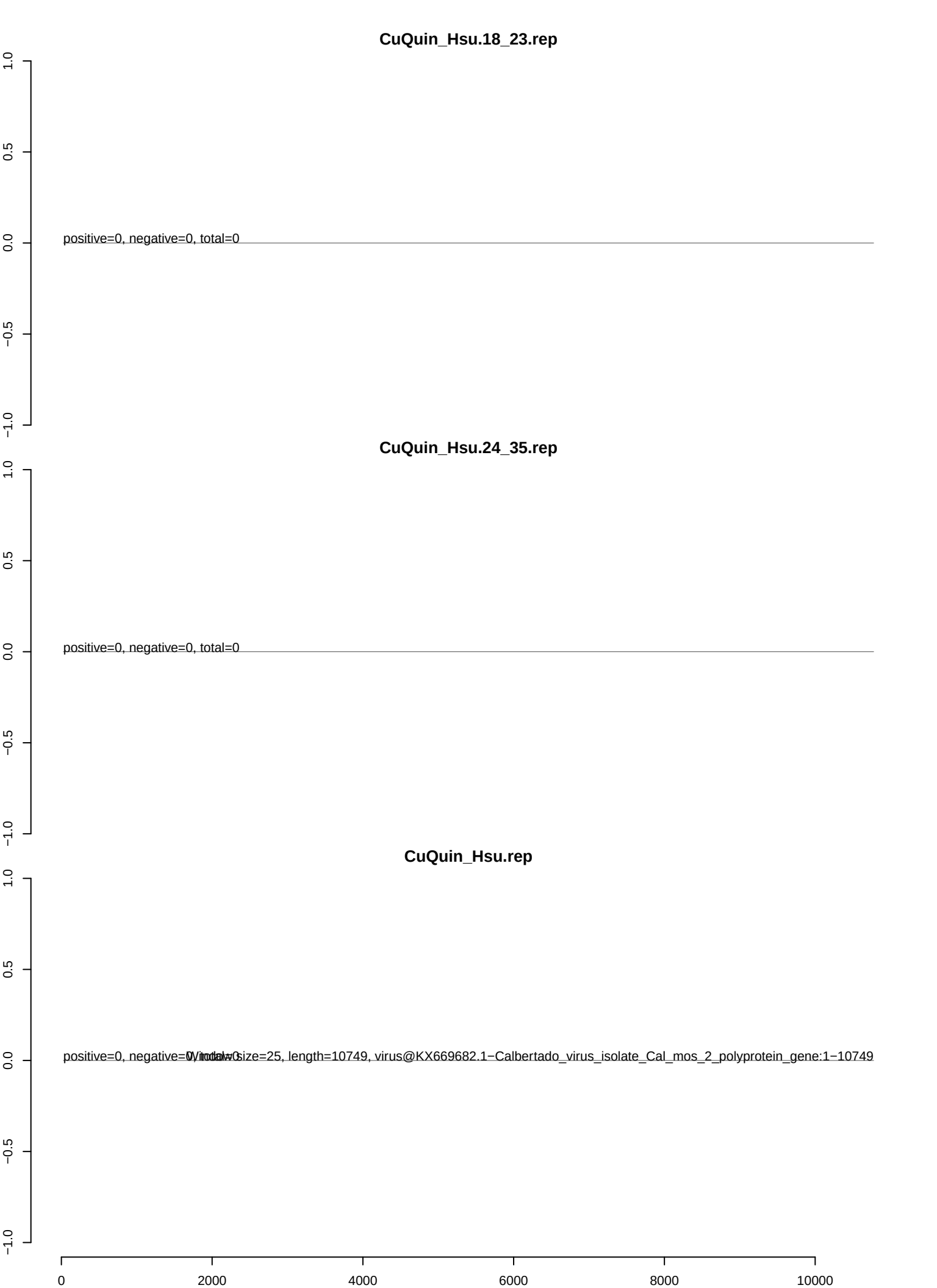
10000
12000


CuQuin_Hsu.18_23.rep
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
positive=0, negative=0, total=0
CuQuin_Hsu.rep
positive=0, negative=0, total=0
window size=25, length=10749, virus@KX669682.1−Calbertado_virus_isolate_Cal_mos_2_polyprotein_gene:1−10749
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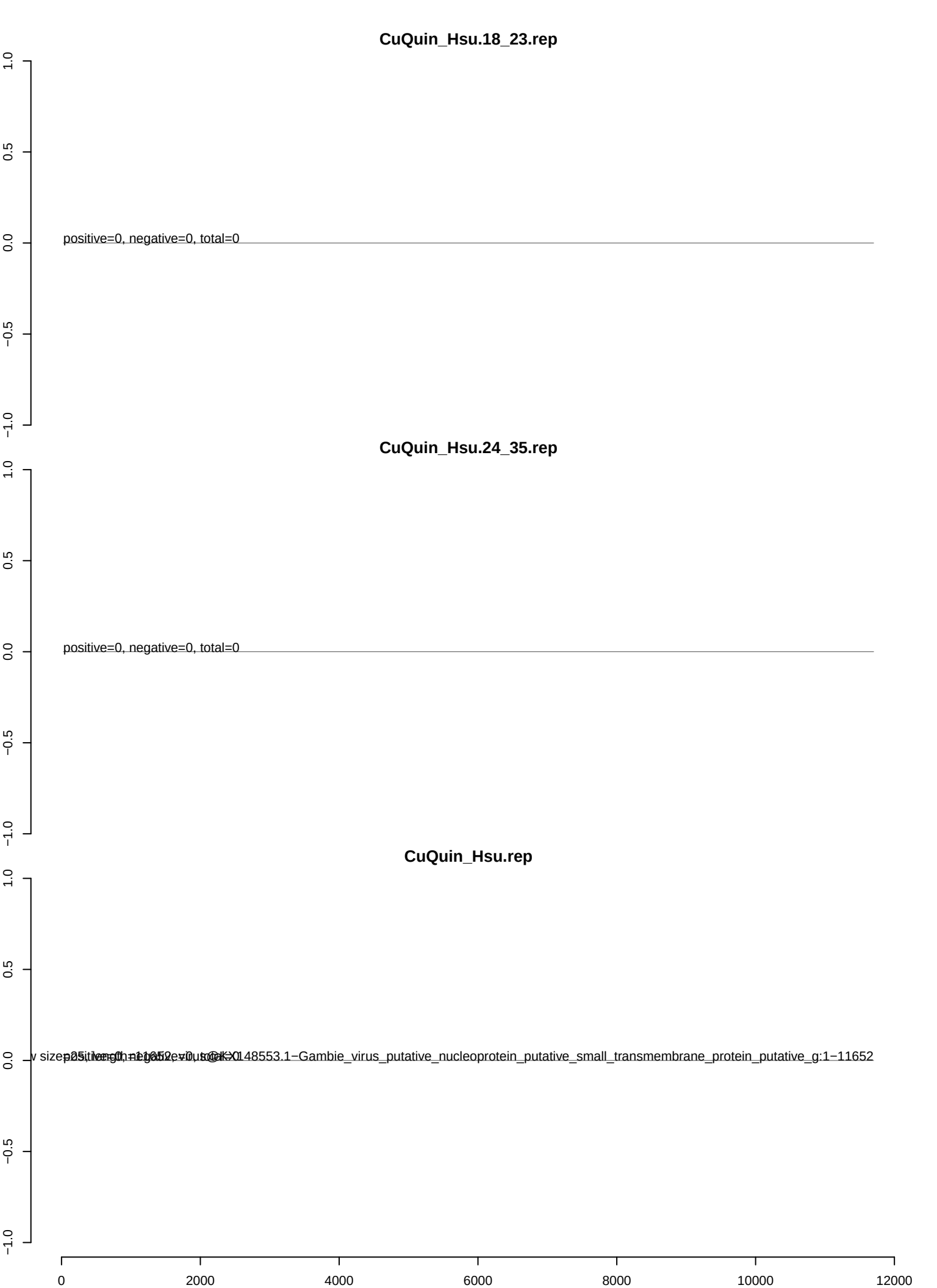
CuQuin_Hsu.18_23.rep
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
positive=0, negative=0, total=0
CuQuin_Hsu.rep
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0.0
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−1.0
0
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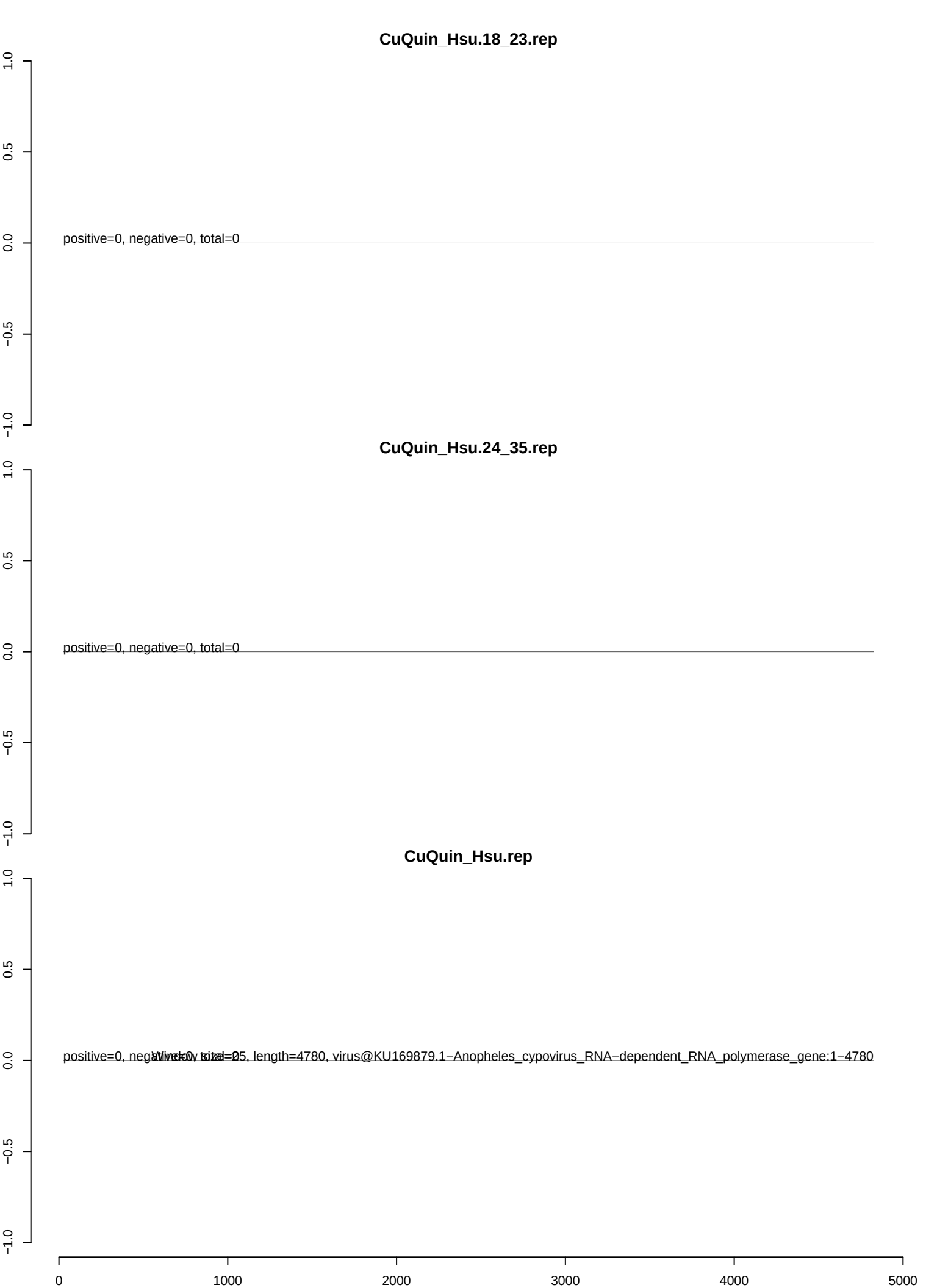
6000
8000
10000
12000


CuQuin_Hsu.18_23.rep
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
positive=0, negative=0, total=0
CuQuin_Hsu.rep
positive=0, negative=0, total=25, length=4780, virus@KU169879.1−Anopheles_cypovirus_RNA−dependent_RNA_polymerase_gene:1−4780
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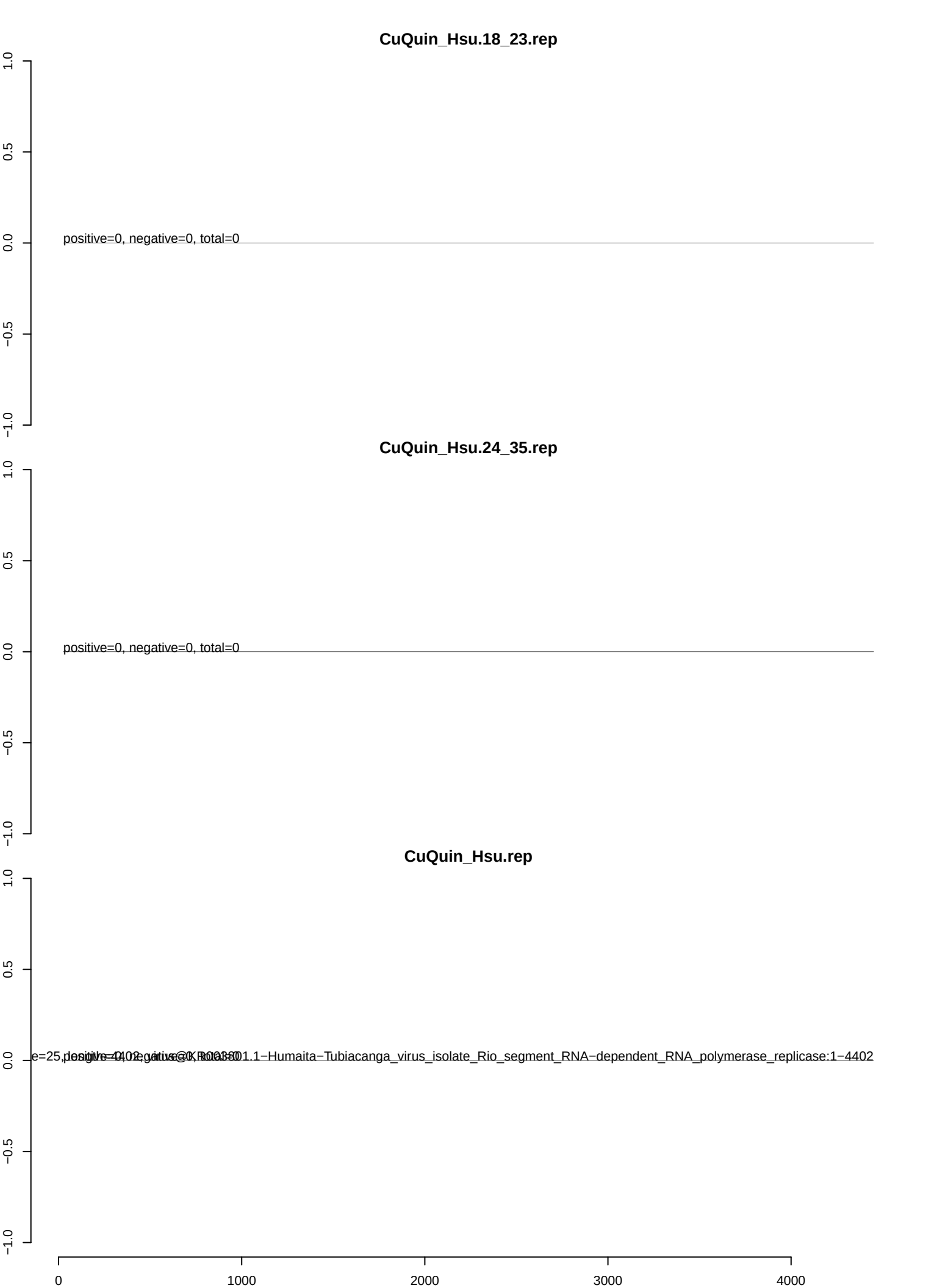
4000
5000


CuQuin_Hsu.18_23.rep
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
positive=0, negative=0, total=0
CuQuin_Hsu.rep
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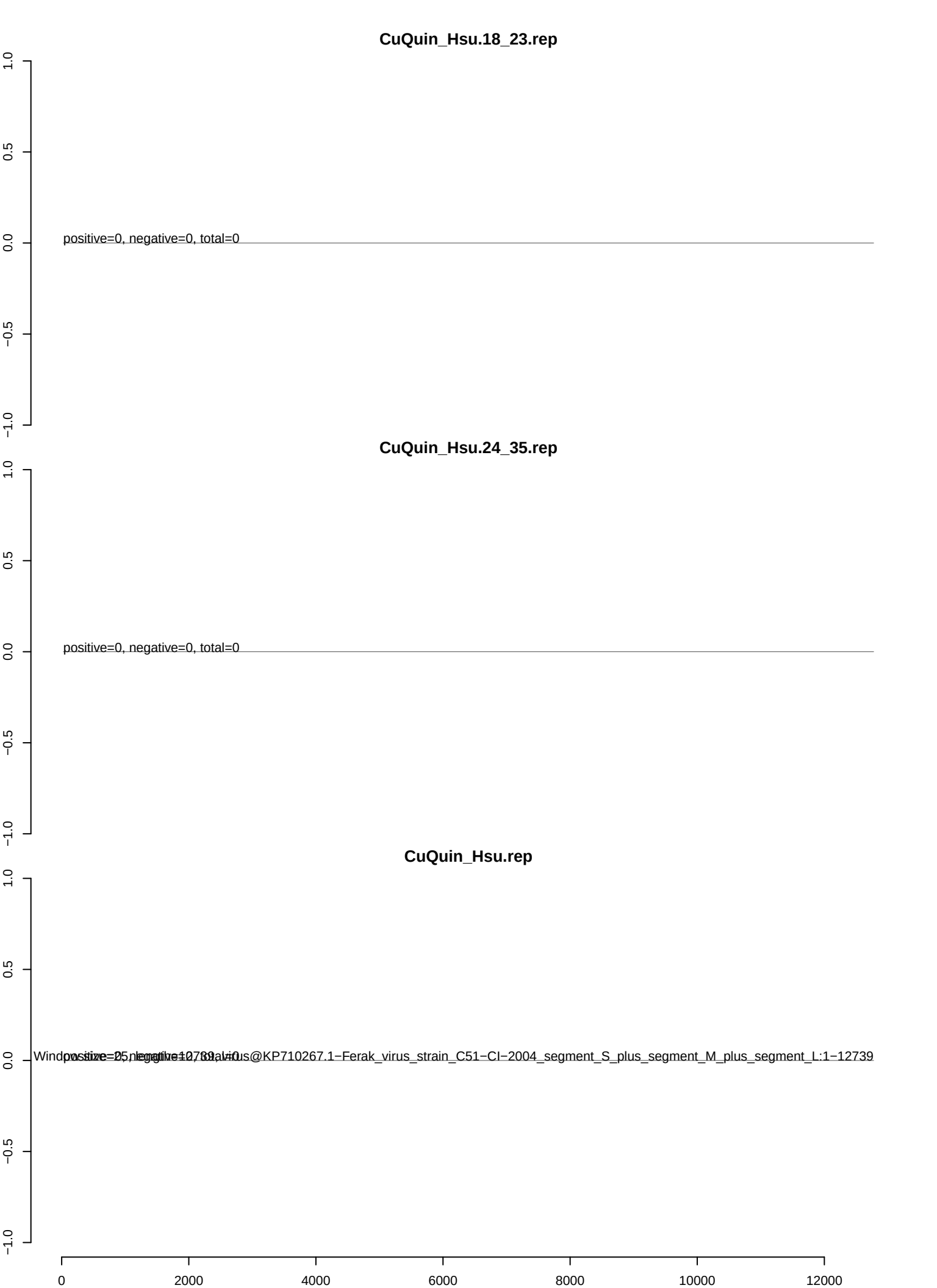
0
1000
2000
3000
4000


CuQuin_Hsu.18_23.rep
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CuQuin_Hsu.24_35.rep
positive=0, negative=0, total=0
CuQuin_Hsu.rep
positive=25, negative=17, total=0
Window size=25
Segment=Ferak_virus@KP710267.1−Ferak_virus_strain_C51−CI−2004_segment_S_plus_segment_M_plus_segment_L:1−12739
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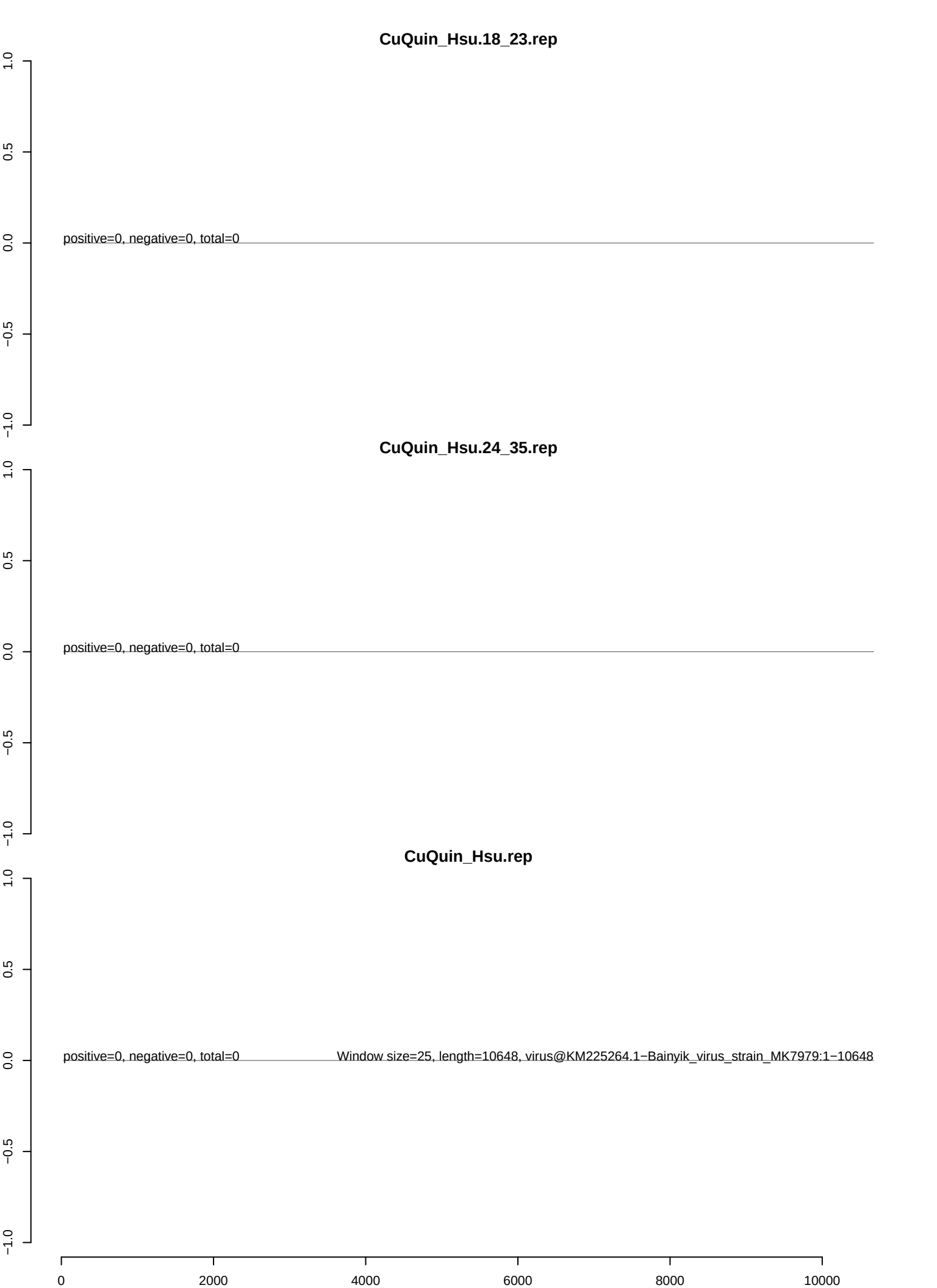
4000
6000
8000
10000
12000


CuQuin_Hsu.18_23.rep
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0.0
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−1.0
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
1.0
0.5
0.0
−0.5
−1.0
positive=0, negative=0, total=0
CuQuin_Hsu.rep
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0.5
0.0
−0.5
−1.0
positive=0, negative=0, total=0
Window size=25, length=10648, virus@KM225264.1−Bainyik_virus_strain_MK7979:1−10648
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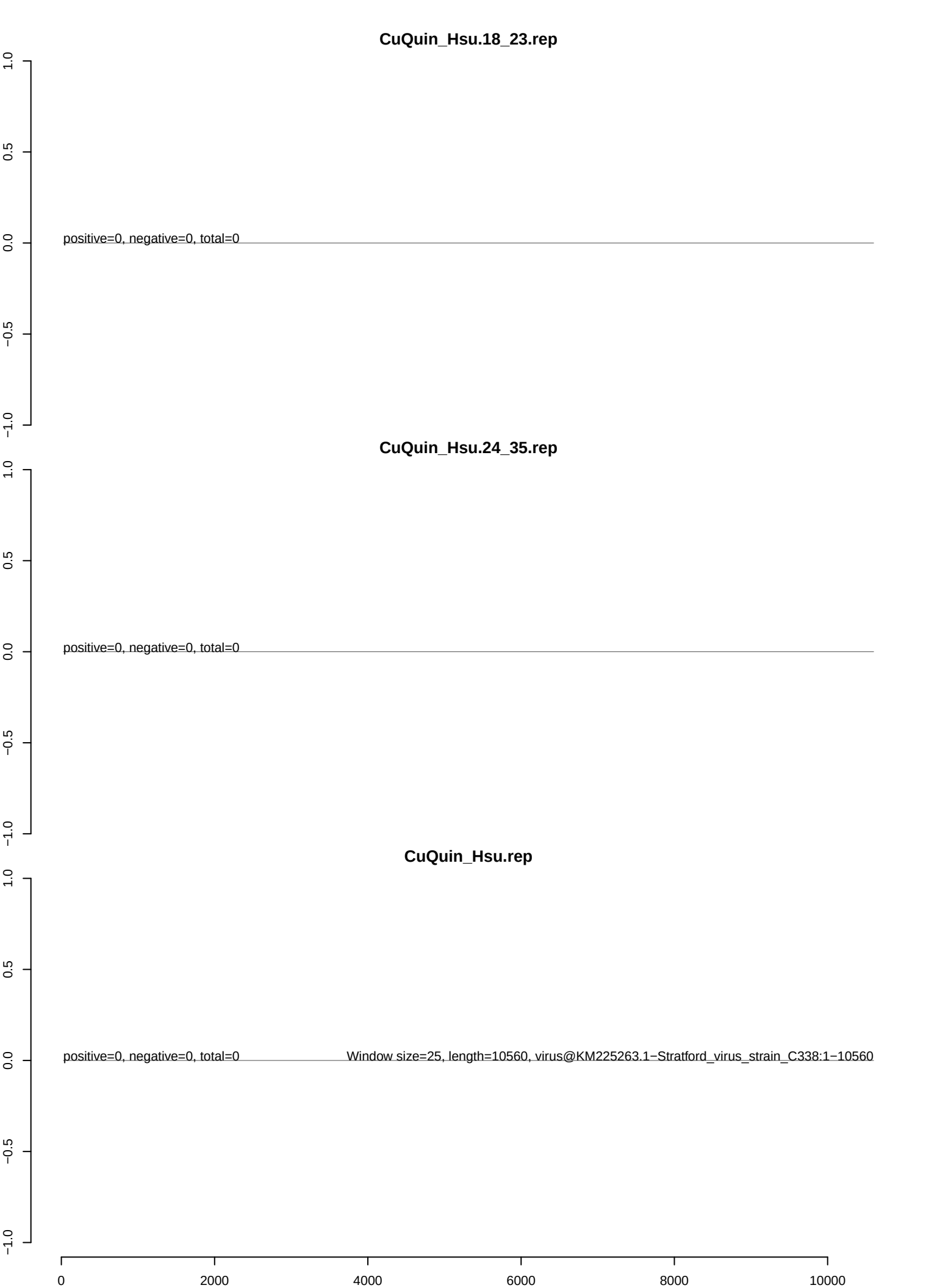
CuQuin_Hsu.18_23.rep
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0.0
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−1.0
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
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0.0
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−1.0
positive=0, negative=0, total=0
CuQuin_Hsu.rep
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0.5
0.0
−0.5
−1.0
positive=0, negative=0, total=0
Window size=25, length=10560, virus@KM225263.1−Stratford_virus_strain_C338:1−10560
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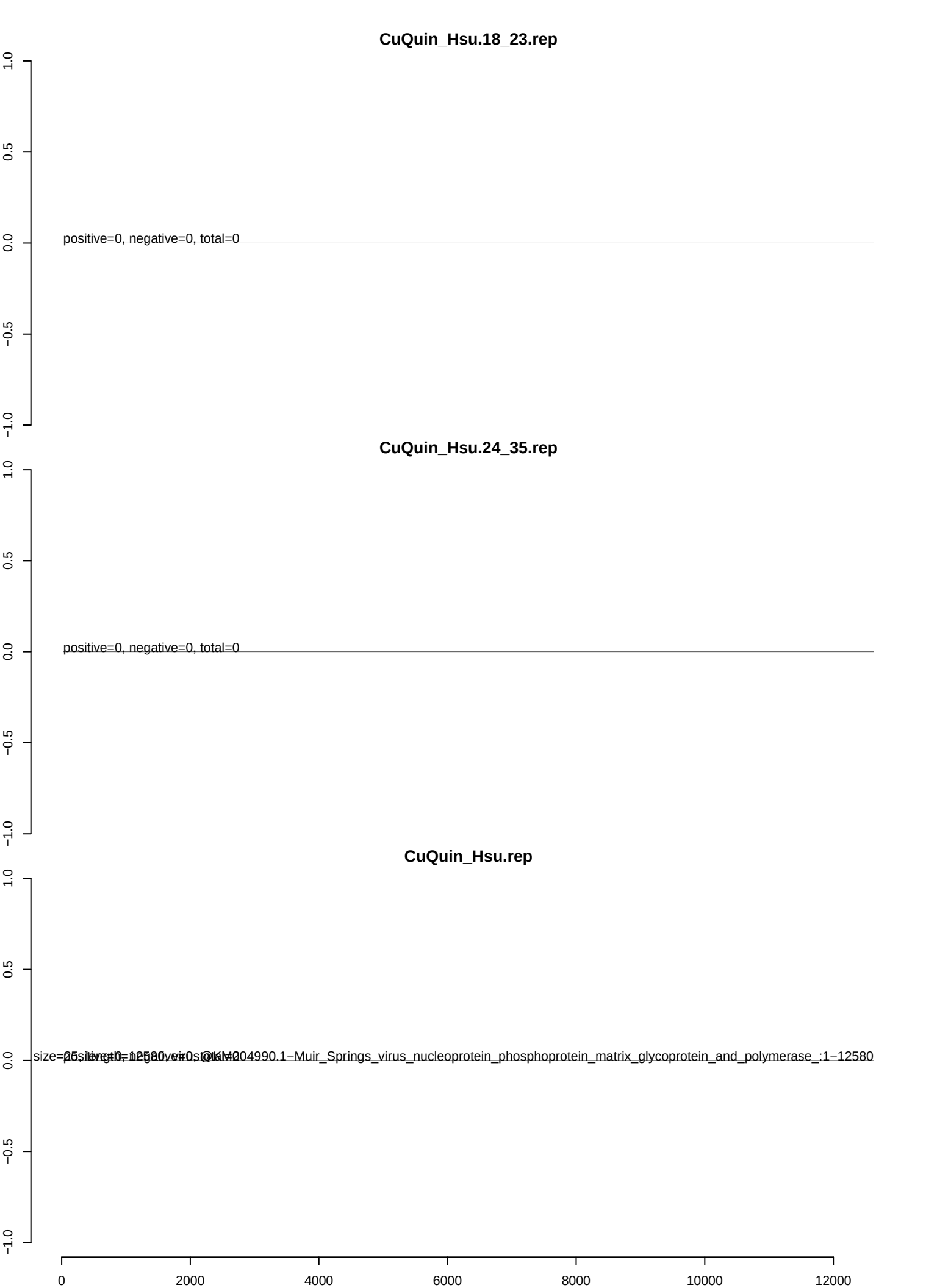
CuQuin_Hsu.18_23.rep
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
positive=0, negative=0, total=0
CuQuin_Hsu.rep
size=25, length=12580, virus=GenBank:YP_004990.1−Muir_Springs_virus_nucleoprotein_phosphoprotein_matrix_glycoprotein_and_polymerase_:1−12580
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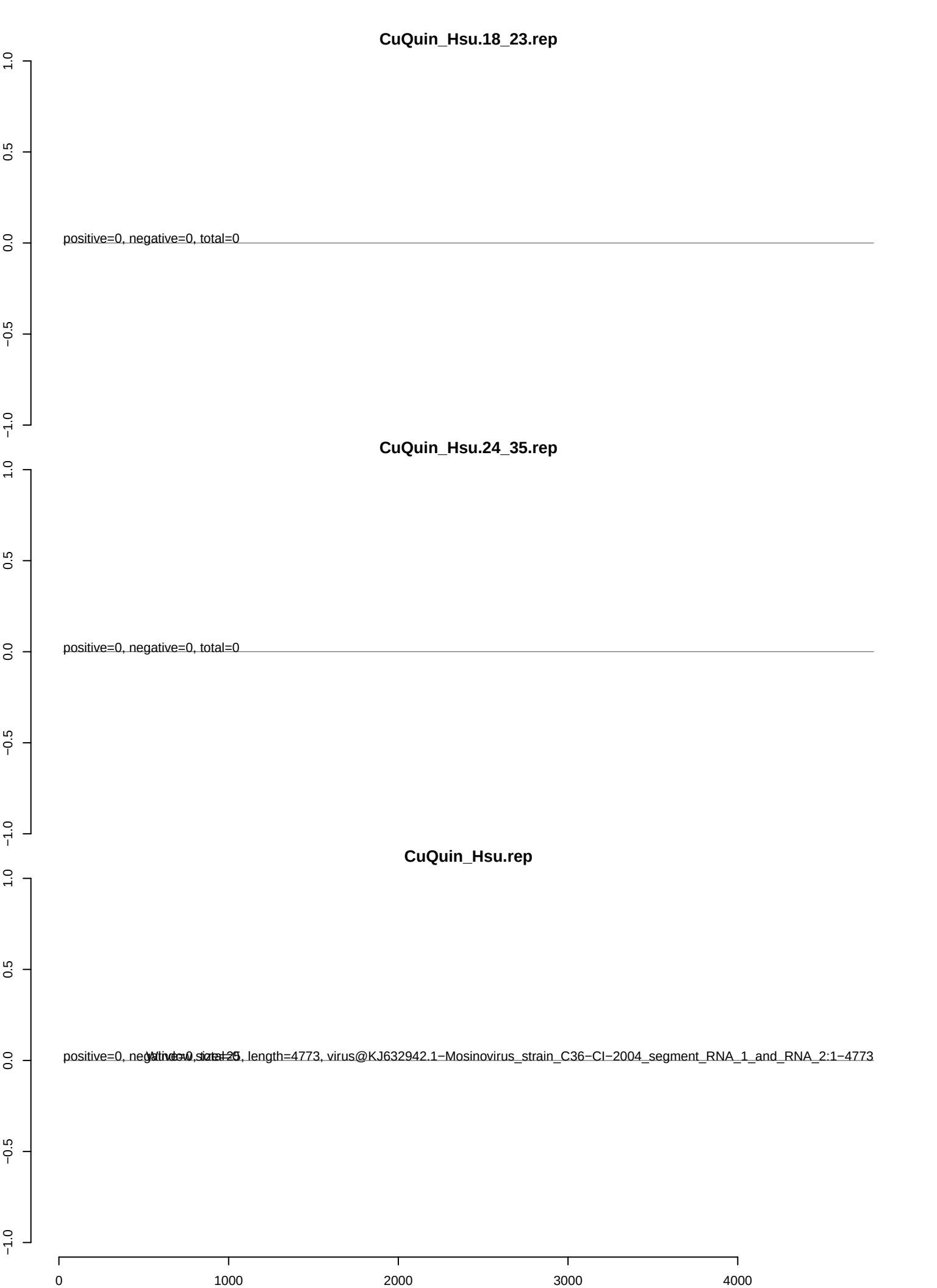
12000


CuQuin_Hsu.18_23.rep
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
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CuQuin_Hsu.rep
positive=0, negative=0, total=0, length=4773, virus@KJ632942.1−Mosinovirus_strain_C36−CI−2004_segment_RNA_1_and_RNA_2:1−4773
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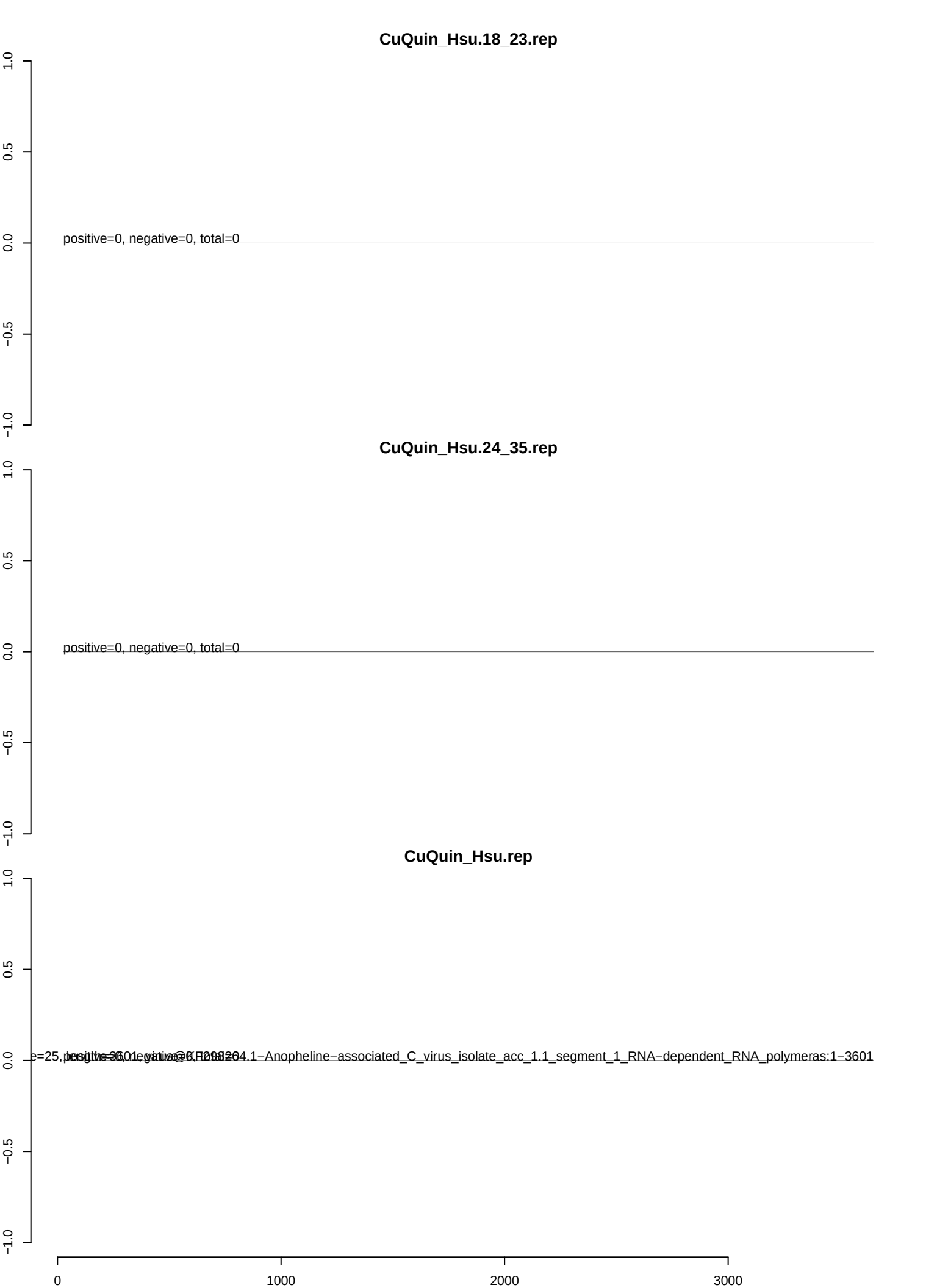
4000


CuQuin_Hsu.18_23.rep
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
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CuQuin_Hsu.rep
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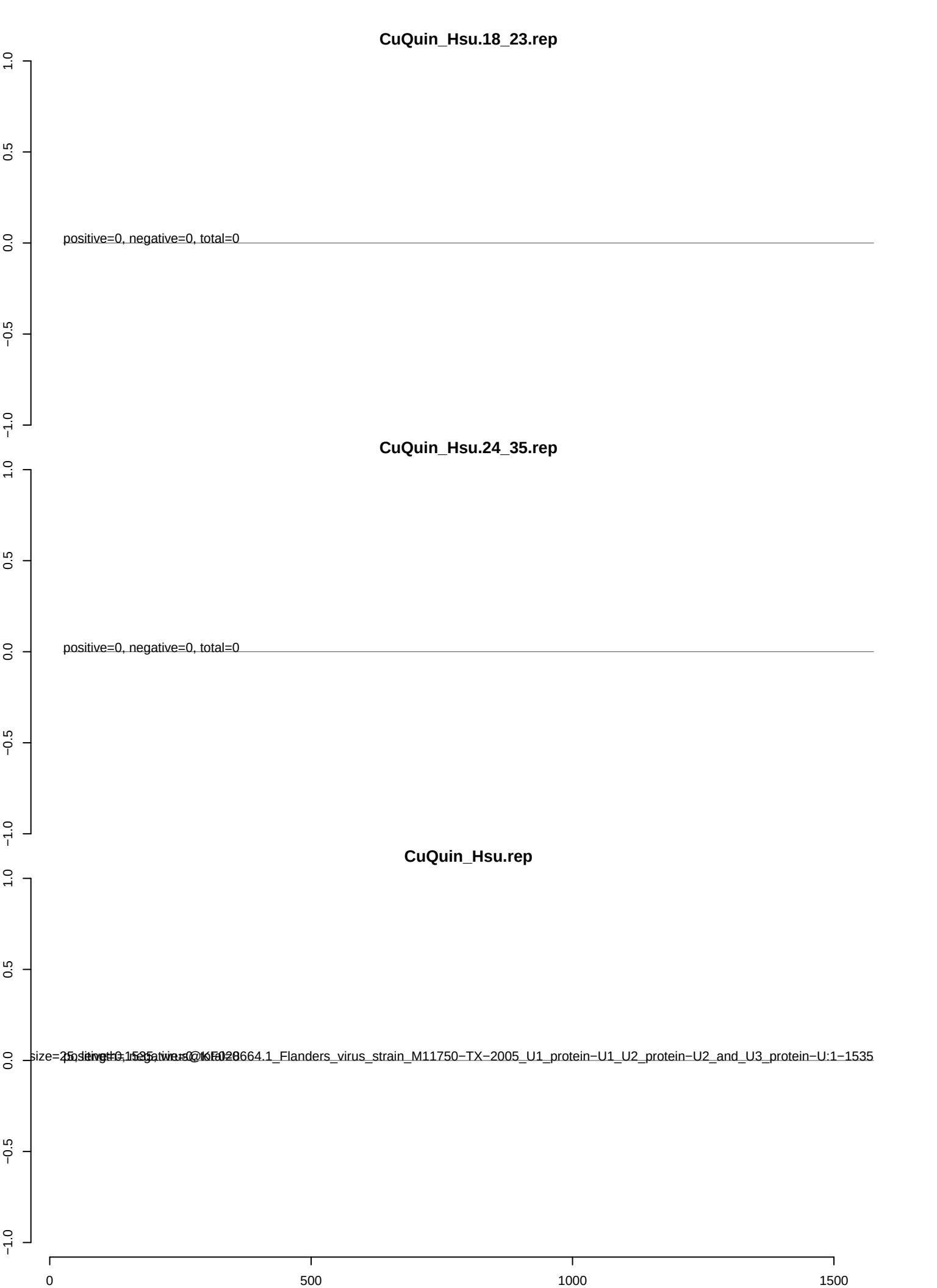
1000
2000
3000


CuQuin_Hsu.18_23.rep
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
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CuQuin_Hsu.rep
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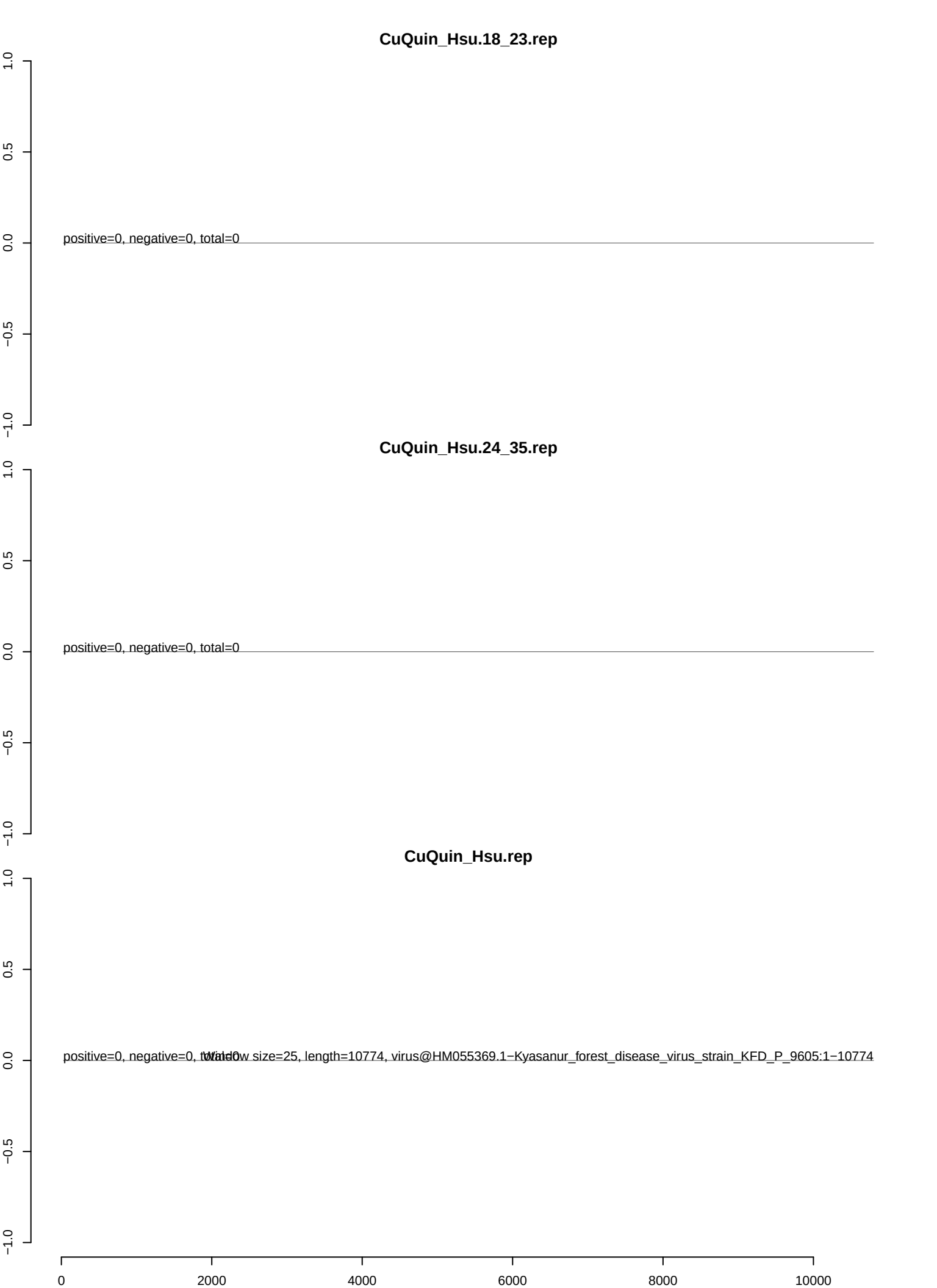
1000
1500


CuQuin_Hsu.18_23.rep
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
positive=0, negative=0, total=0
CuQuin_Hsu.rep
positive=0, negative=0, total=0
Window size=25, length=10774, virus@HM055369.1−Kyasanur_forest_disease_virus_strain_KFD_P_9605:1−10774
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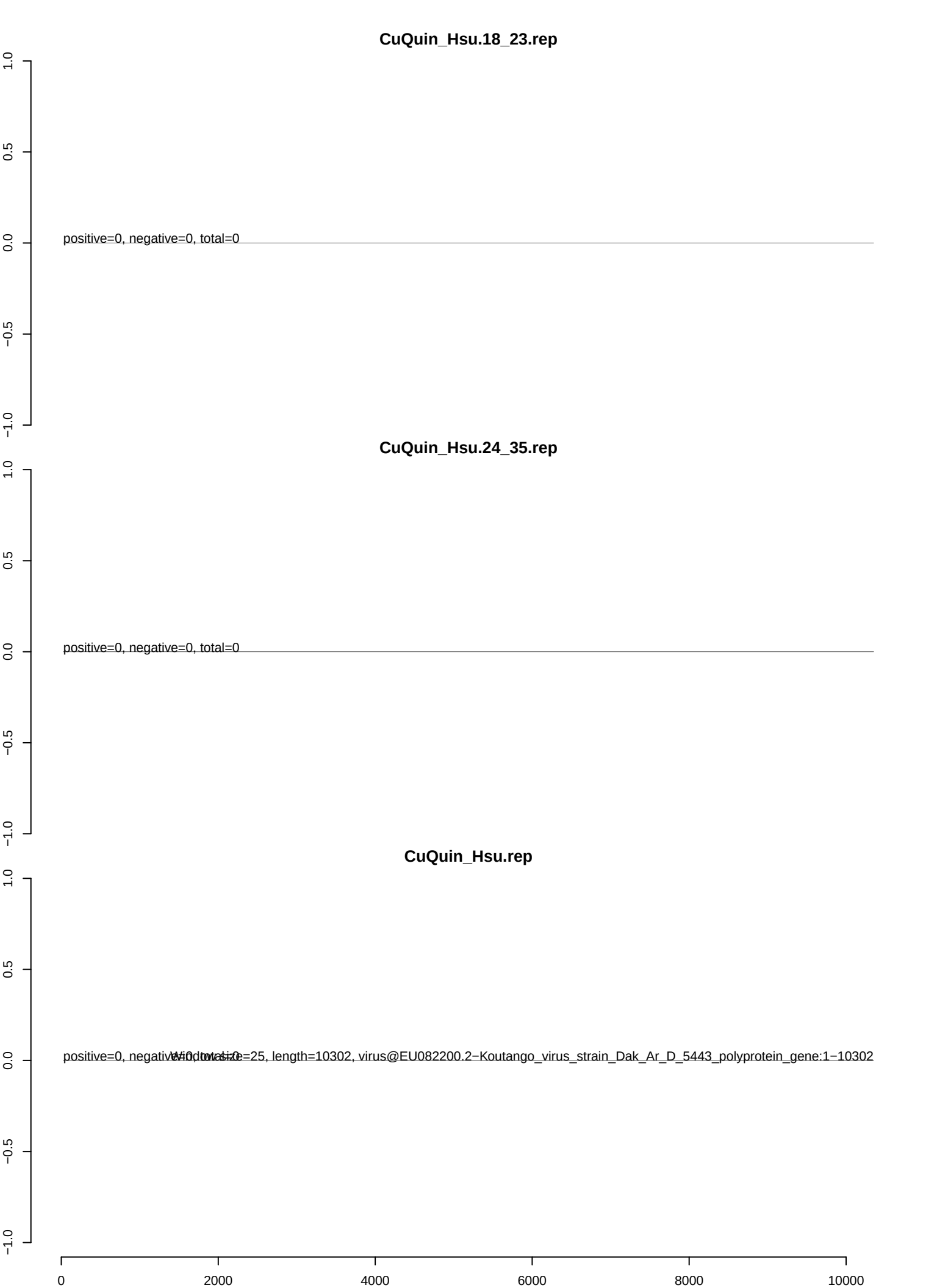
CuQuin_Hsu.18_23.rep
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
positive=0, negative=0, total=0
CuQuin_Hsu.rep
positive=0, negative=0, total=0
Window size=25, length=10302, virus@EU082200.2−Koutango_virus_strain_Dak_Ar_D_5443_polyprotein_gene:1−10302
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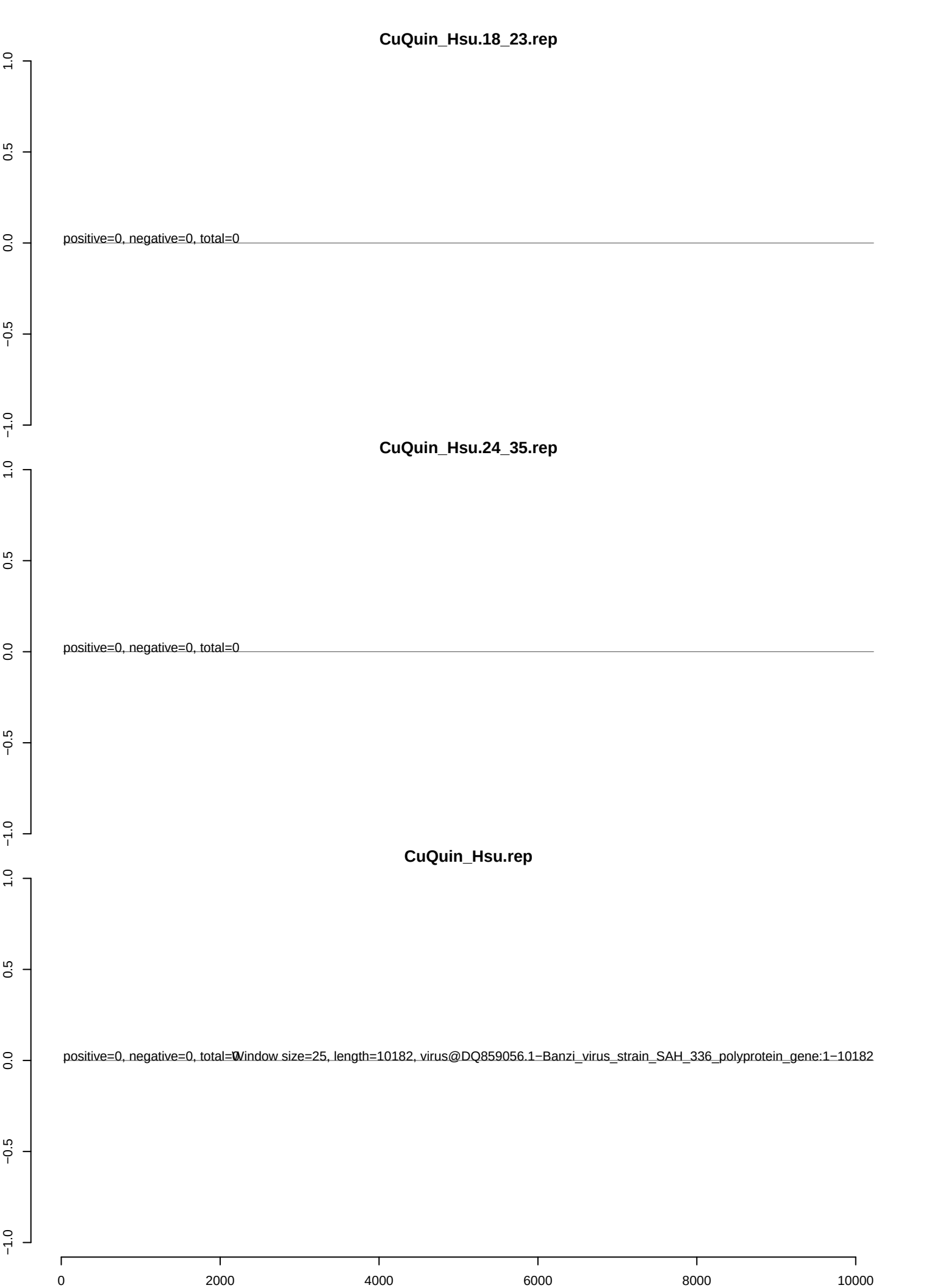
4000
6000
8000
10000


CuQuin_Hsu.18_23.rep
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
positive=0, negative=0, total=0
CuQuin_Hsu.rep
positive=0, negative=0, total=0
Window size=25, length=10182, virus@DQ859056.1−Banzi_virus_strain_SAH_336_polyprotein_gene:1−10182
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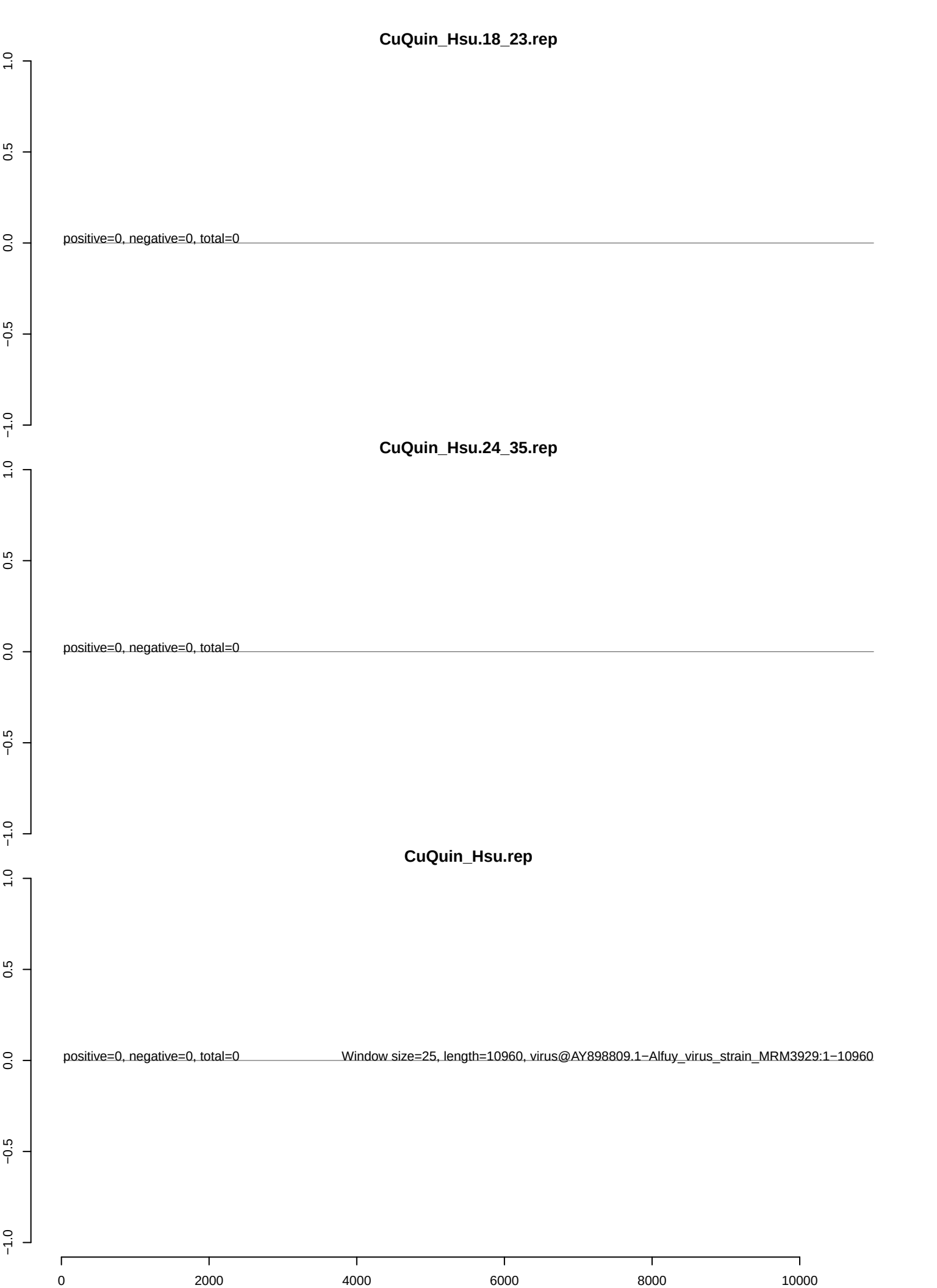
CuQuin_Hsu.18_23.rep
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
positive=0, negative=0, total=0
CuQuin_Hsu.rep
positive=0, negative=0, total=0
Window size=25, length=10960, virus@AY898809.1−Alfuy_virus_strain_MRM3929:1−10960
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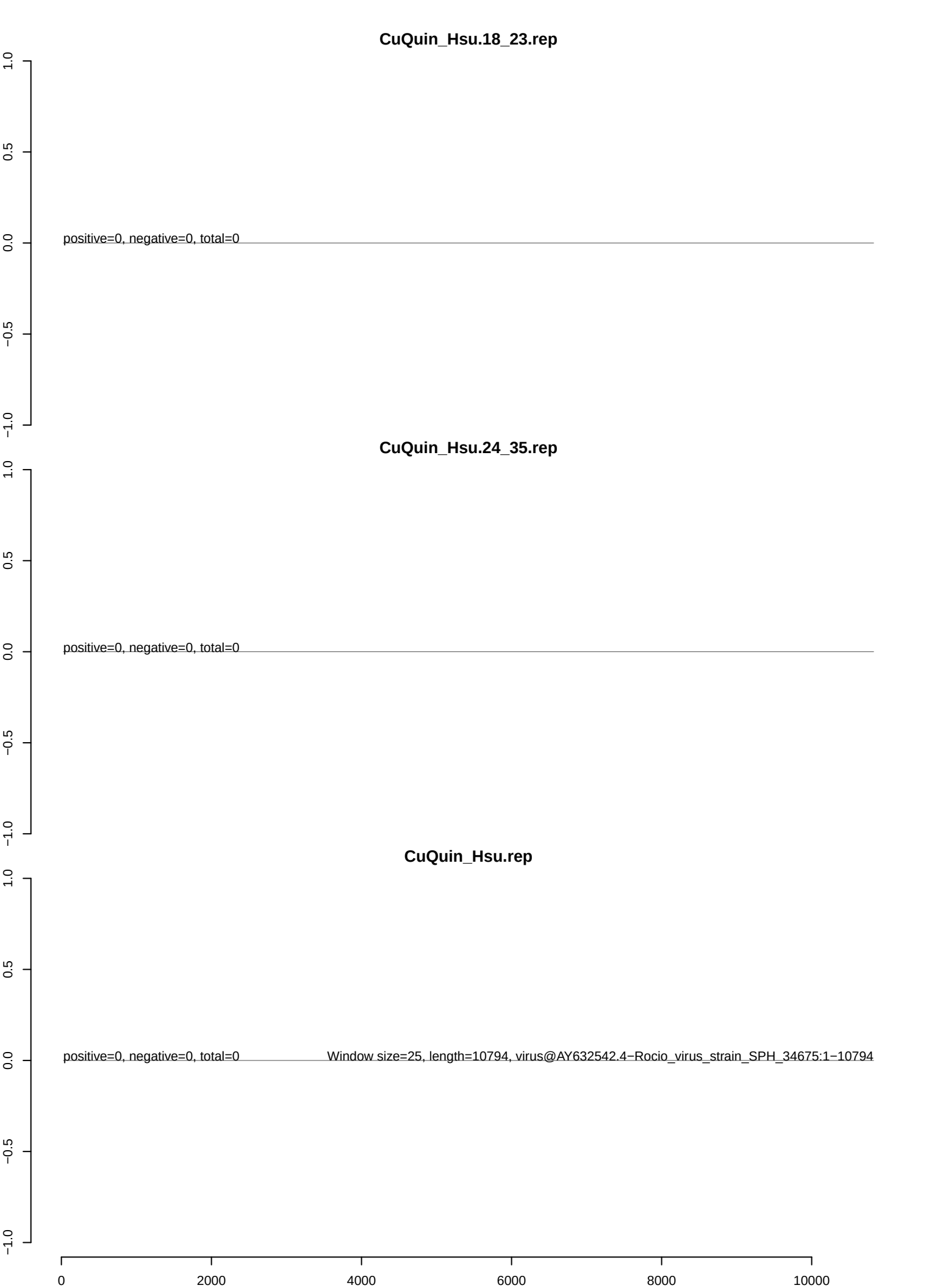
CuQuin_Hsu.18_23.rep
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0.0
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−1.0
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
1.0
0.5
0.0
−0.5
−1.0
positive=0, negative=0, total=0
CuQuin_Hsu.rep
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0.5
0.0
−0.5
−1.0
positive=0, negative=0, total=0
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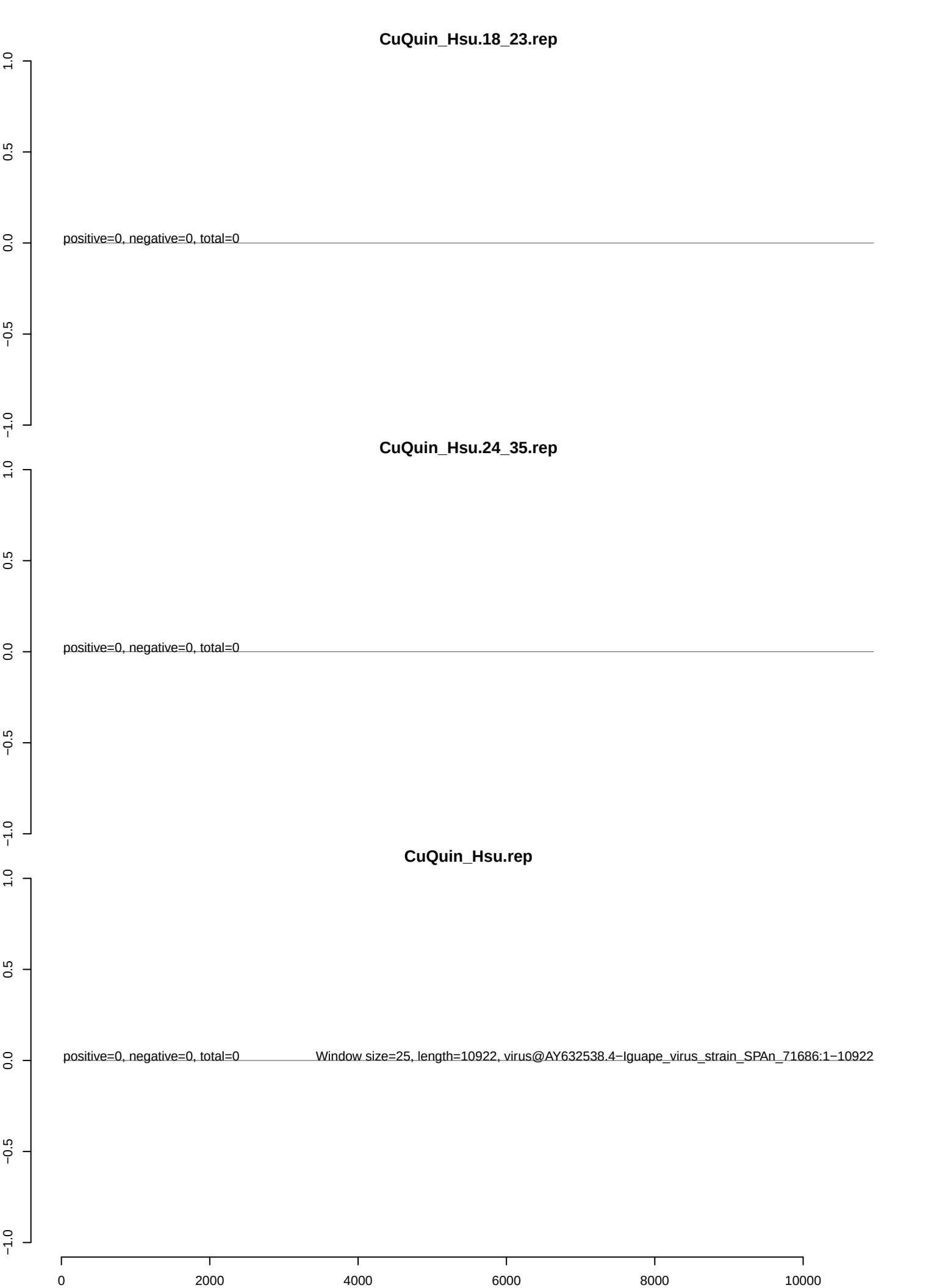
8000
10000


CuQuin_Hsu.18_23.rep
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CuQuin_Hsu.24_35.rep
positive=0, negative=0, total=0
CuQuin_Hsu.rep
positive=0, negative=0, total=0
Window size=25, length=10922, virus@AY632538.4−Iguape_virus_strain_SPAn_71686:1−10922
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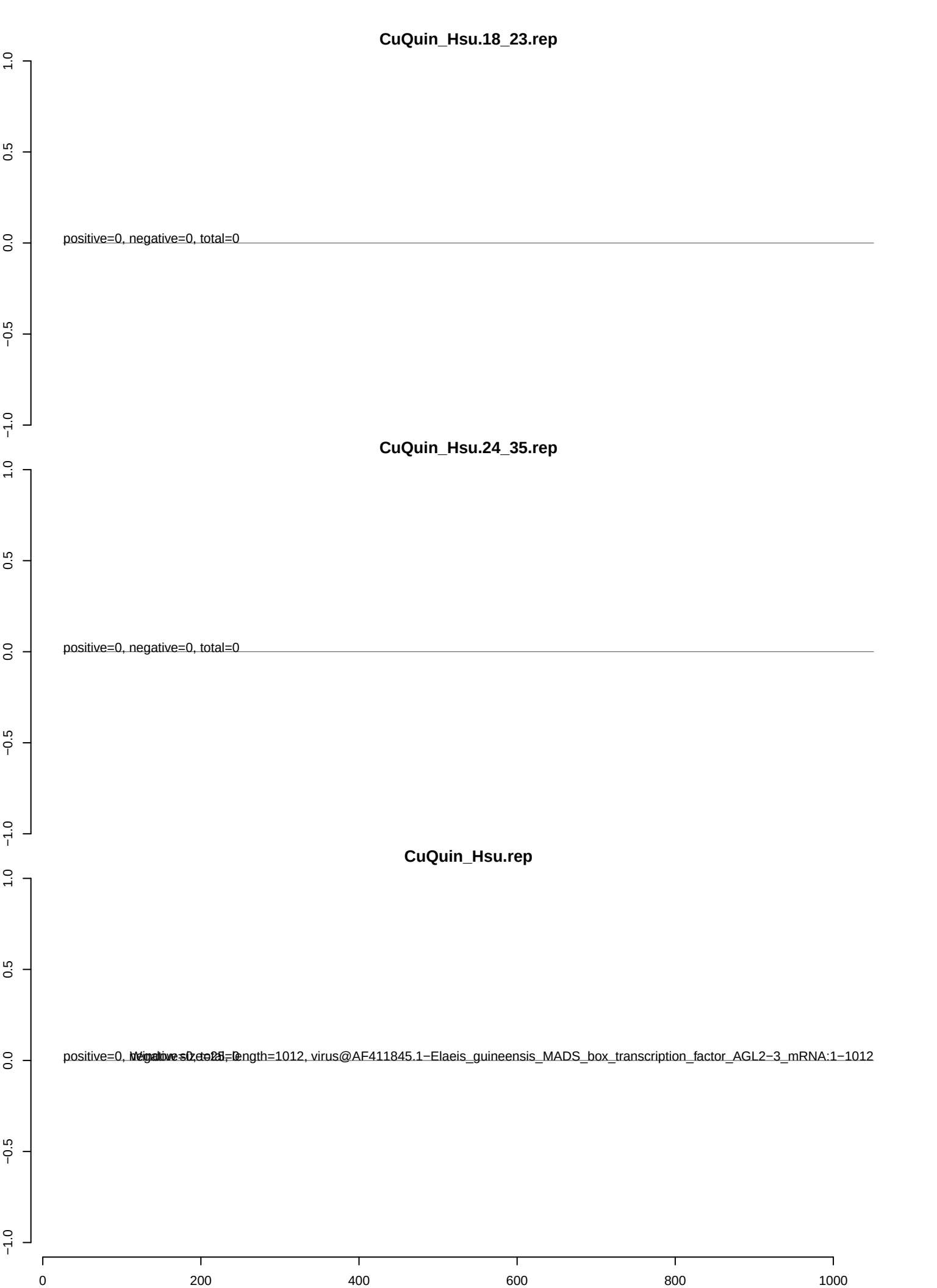
CuQuin_Hsu.18_23.rep
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
positive=0, negative=0, total=0
CuQuin_Hsu.rep
positive=0, negative=0, total=0
virus@AF411845.1−Elaeis_guineensis_MADS_box_transcription_factor_AGL2−3_mRNA:1−1012
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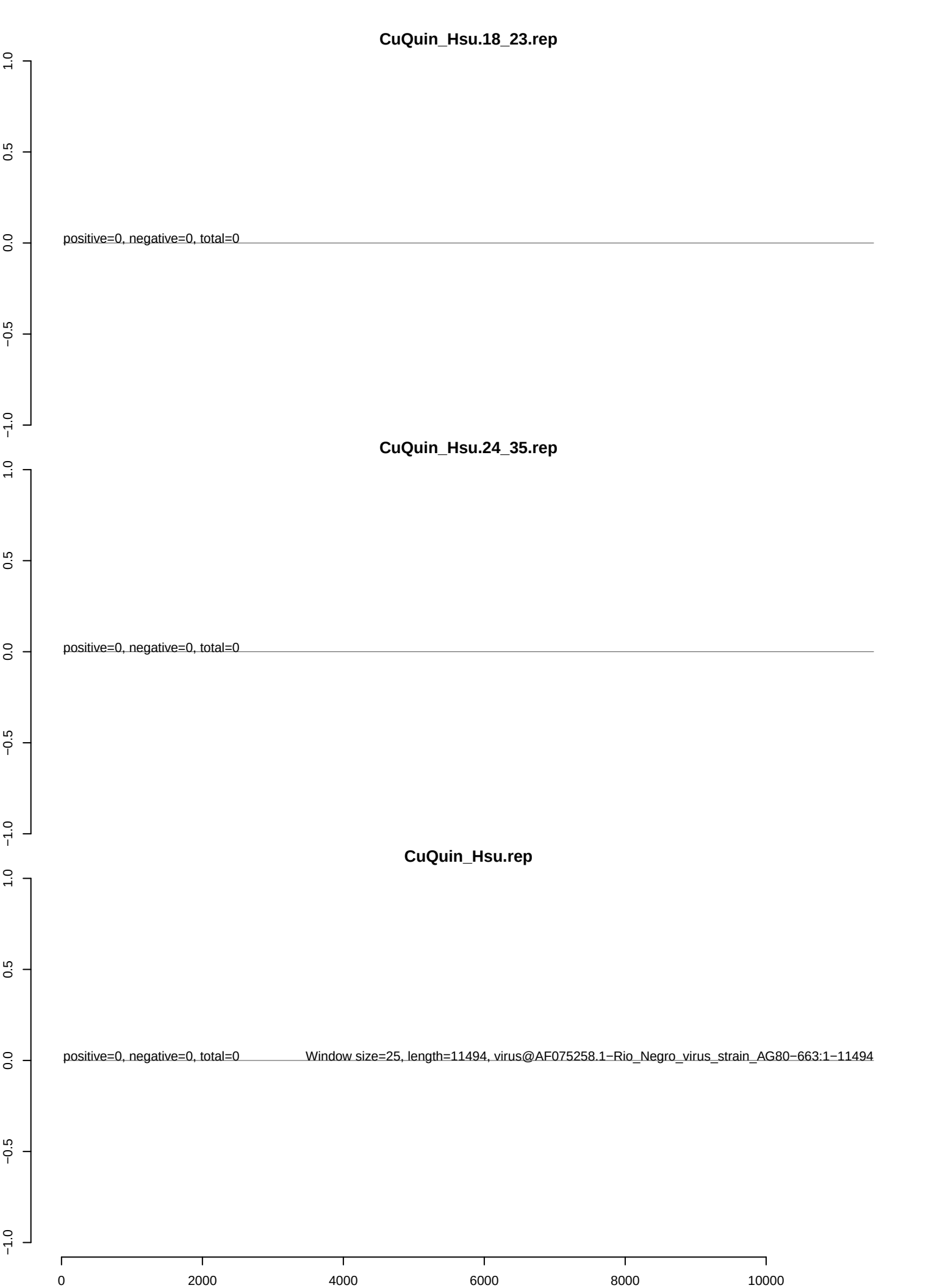
1000


CuQuin_Hsu.18_23.rep
positive=0, negative=0, total=0
CuQuin_Hsu.24_35.rep
positive=0, negative=0, total=0
CuQuin_Hsu.rep
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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−1.0
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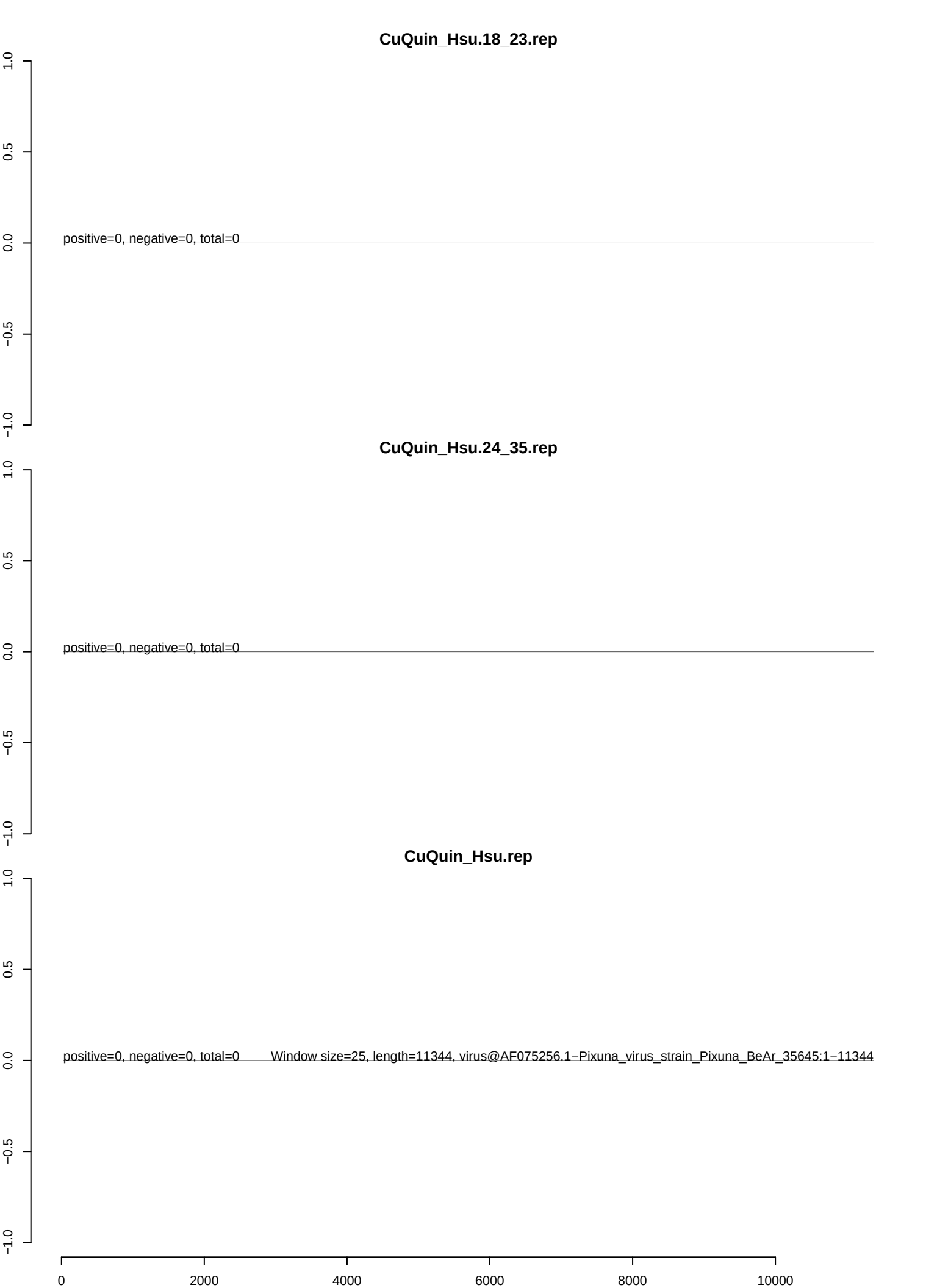
8000
10000


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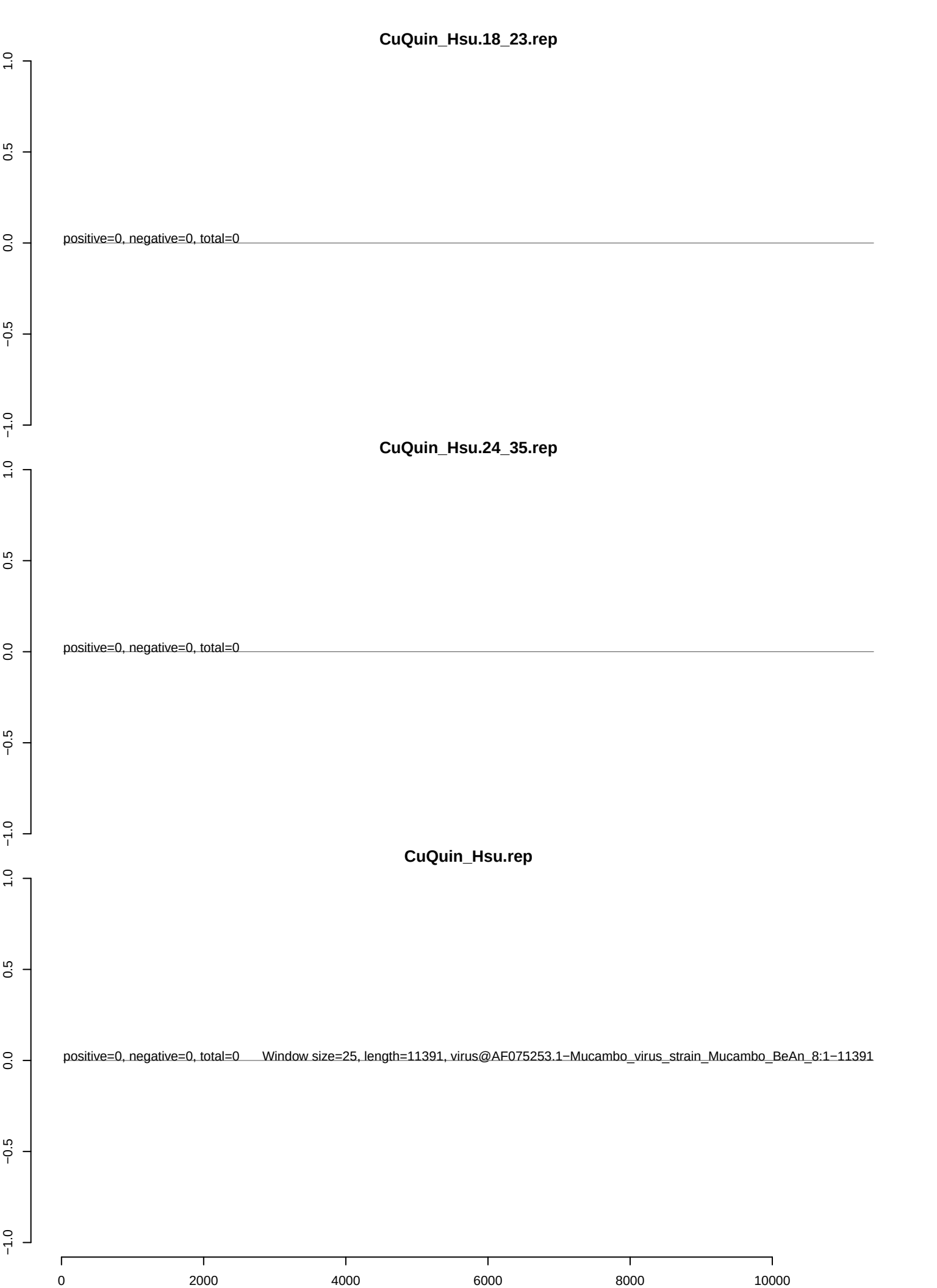
4000
6000
8000
10000


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