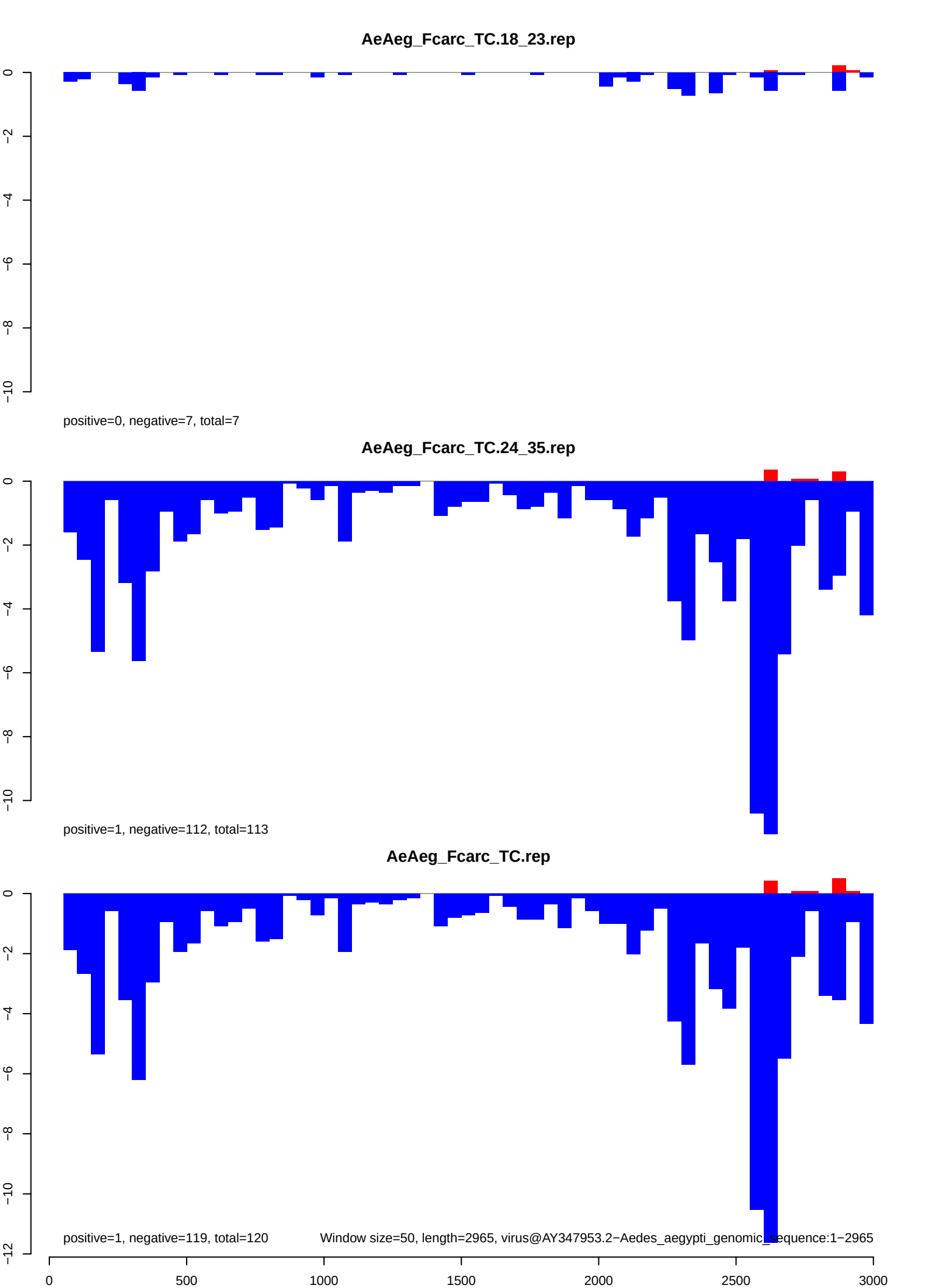
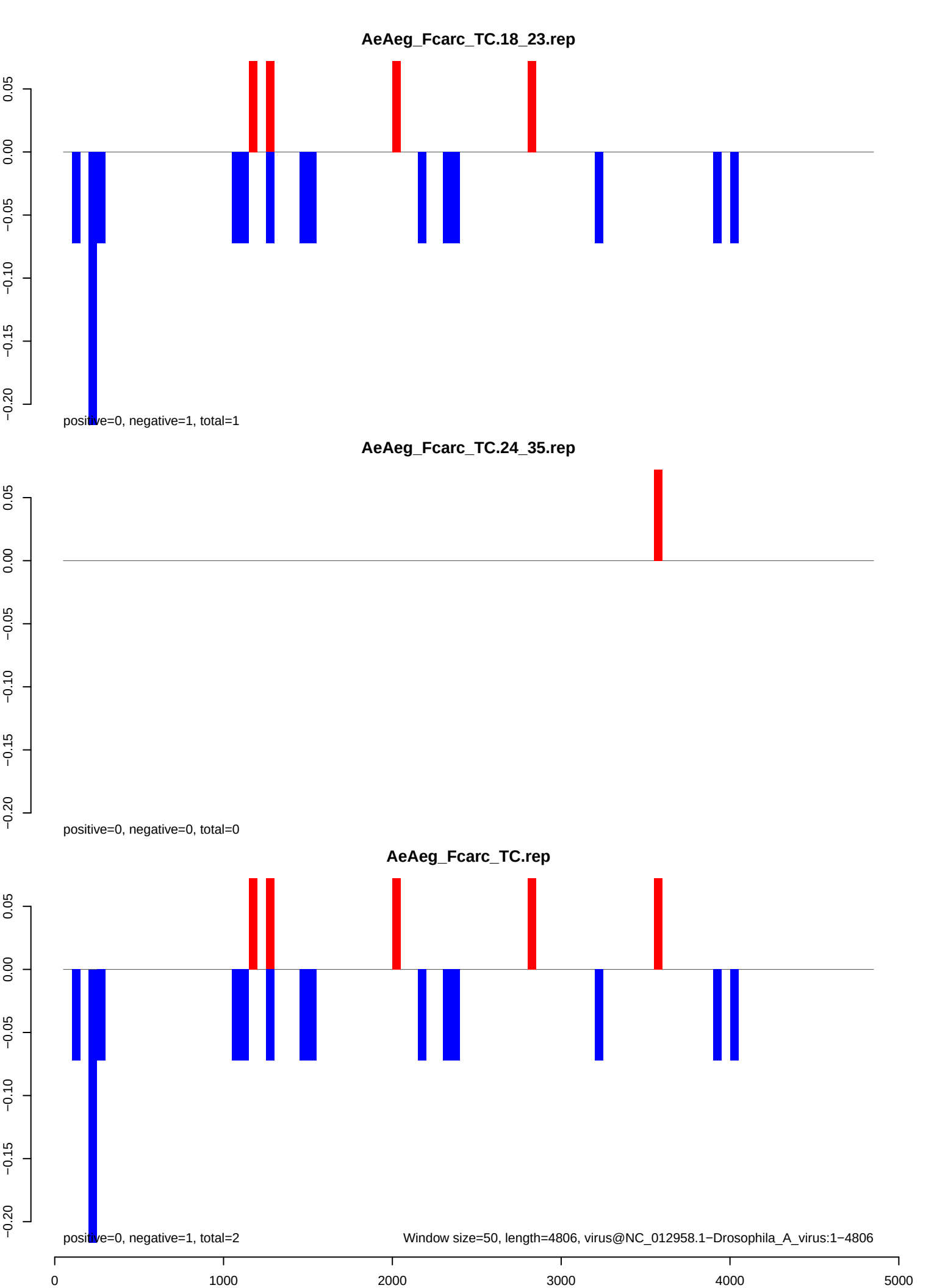
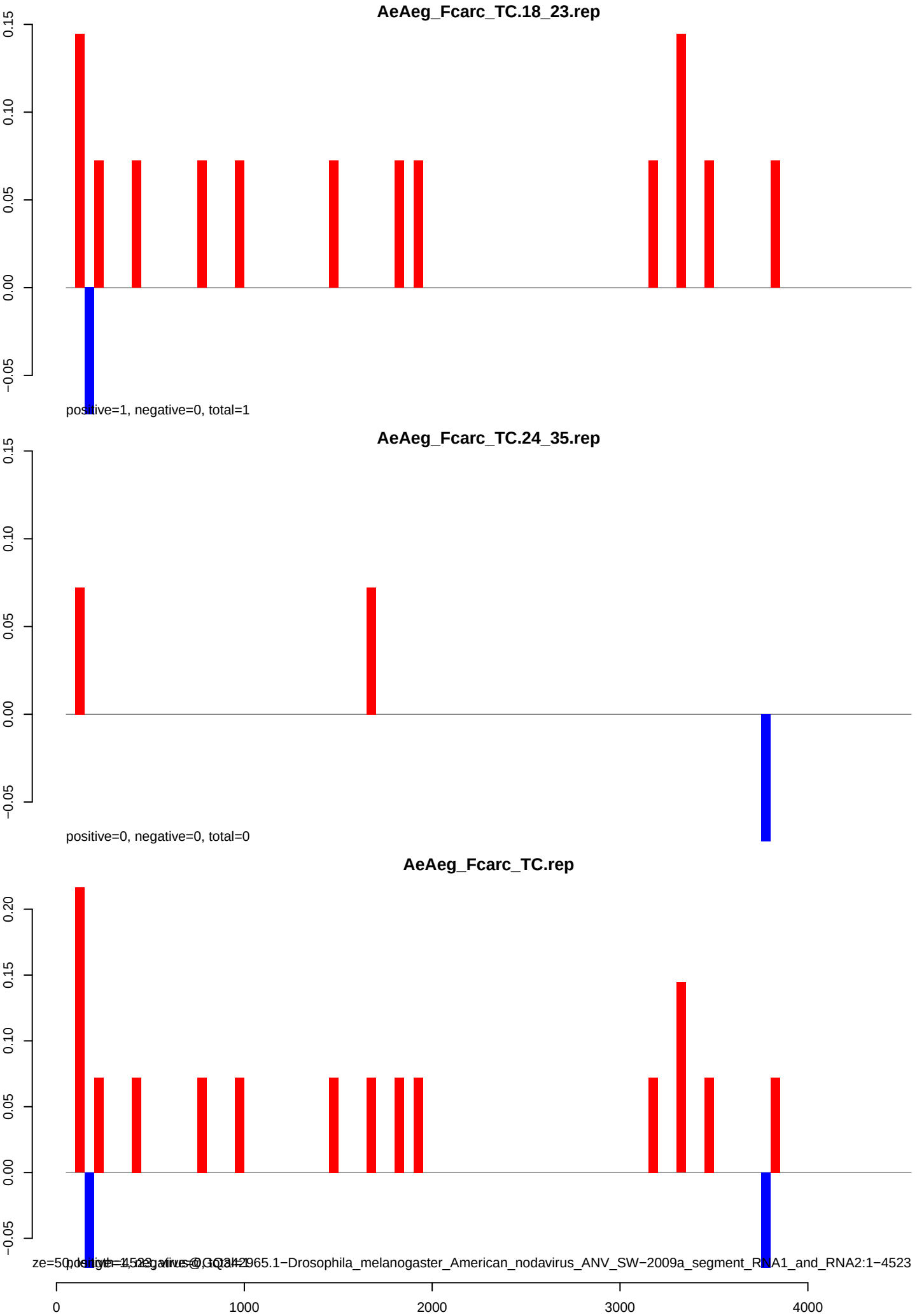
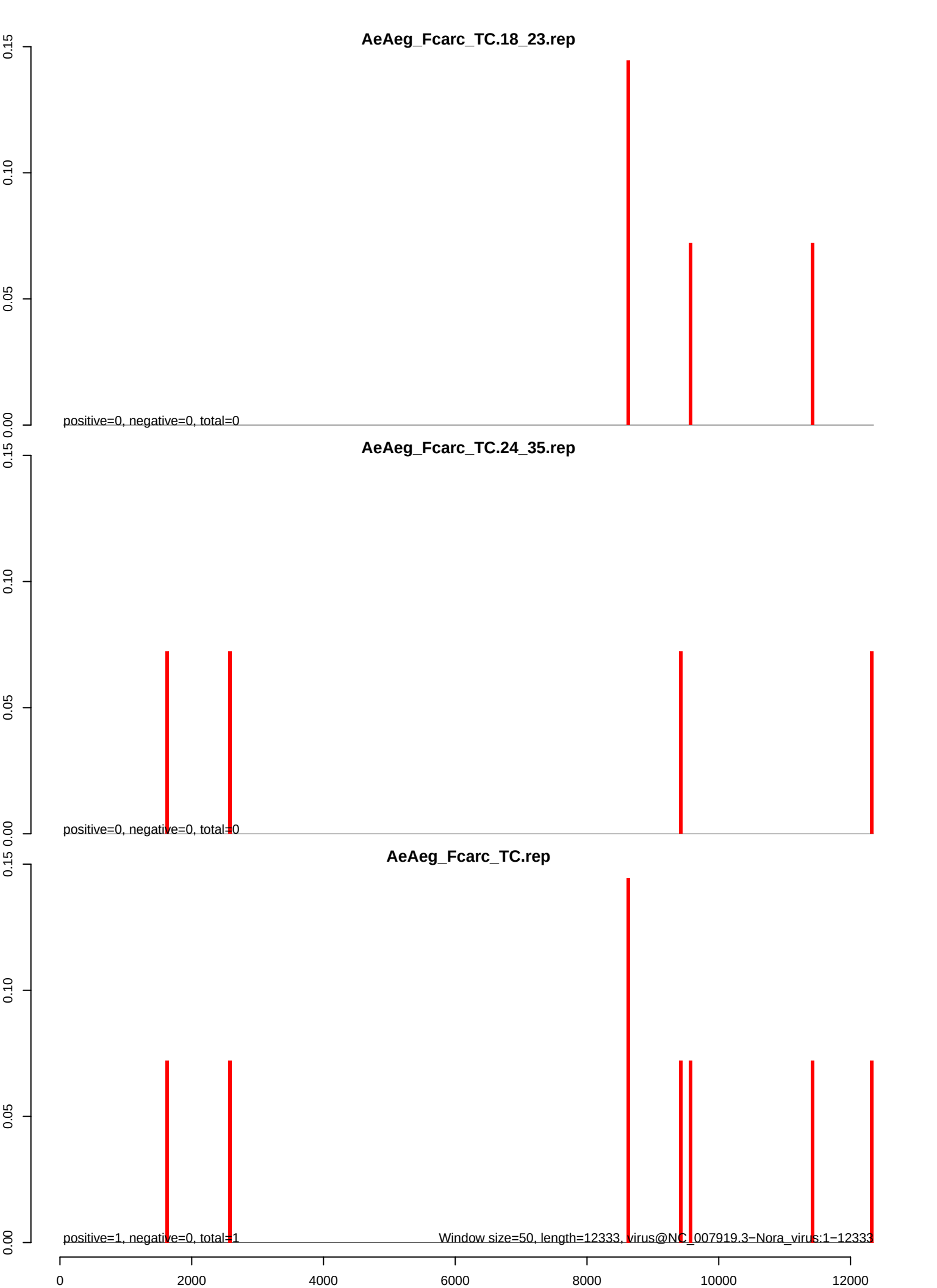
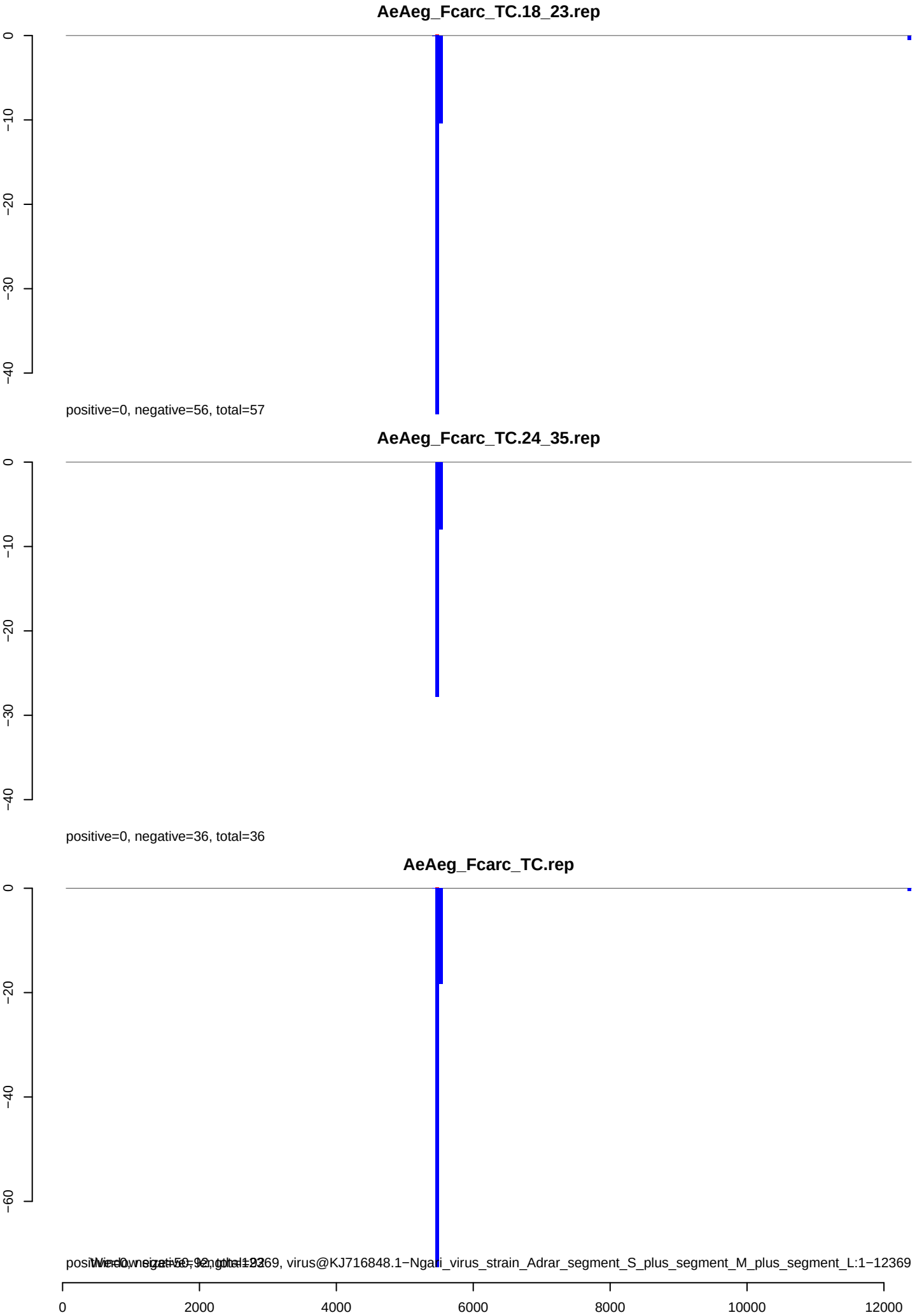
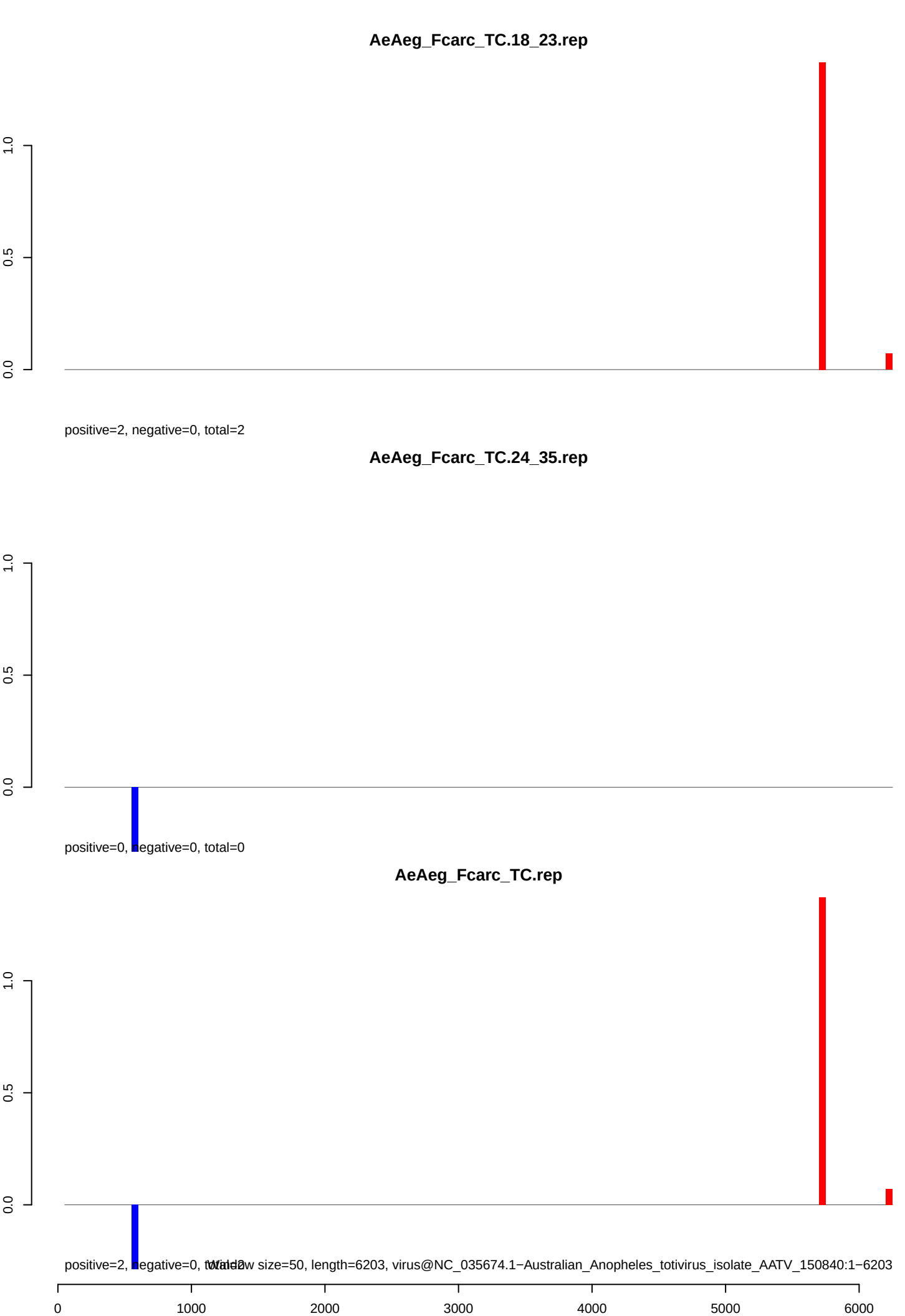

AeAeg_Fcarc_TC.18_23.rep
positive=0, negative=7, total=7
AeAeg_Fcarc_TC.24_35.rep
positive=1, negative=112, total=113
AeAeg_Fcarc_TC.rep
positive=1, negative=119, total=120
Window size=50, length=2965, virus@AY347953.2−Aedes_aegypti_genomic_sequence:1−2965
0
500
1000
1500
2000
2500
3000

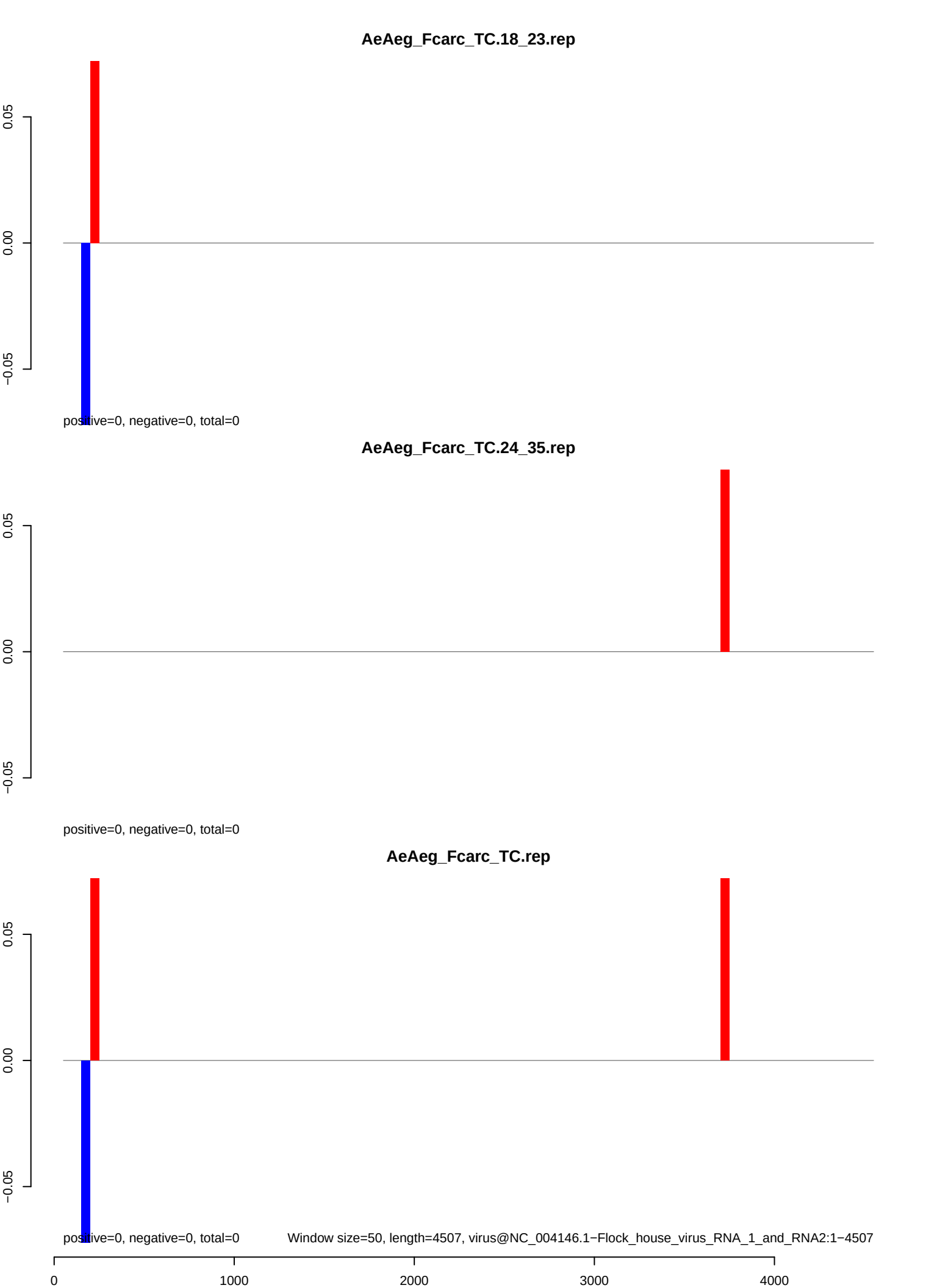

AeAeg_Fcarc_TC.18_23.rep
0.05
0.00
−0.05
−0.10
−0.15
−0.20
positive=0, negative=1, total=1
AeAeg_Fcarc_TC.24_35.rep
0.05
0.00
−0.05
−0.10
−0.15
−0.20
positive=0, negative=0, total=0
AeAeg_Fcarc_TC.rep
0.05
0.00
−0.05
−0.10
−0.15
−0.20
positive=0, negative=1, total=2
Window size=50, length=4806, virus@NC_012958.1−Drosophila_A_virus:1−4806
0
1000
2000
3000
4000
5000

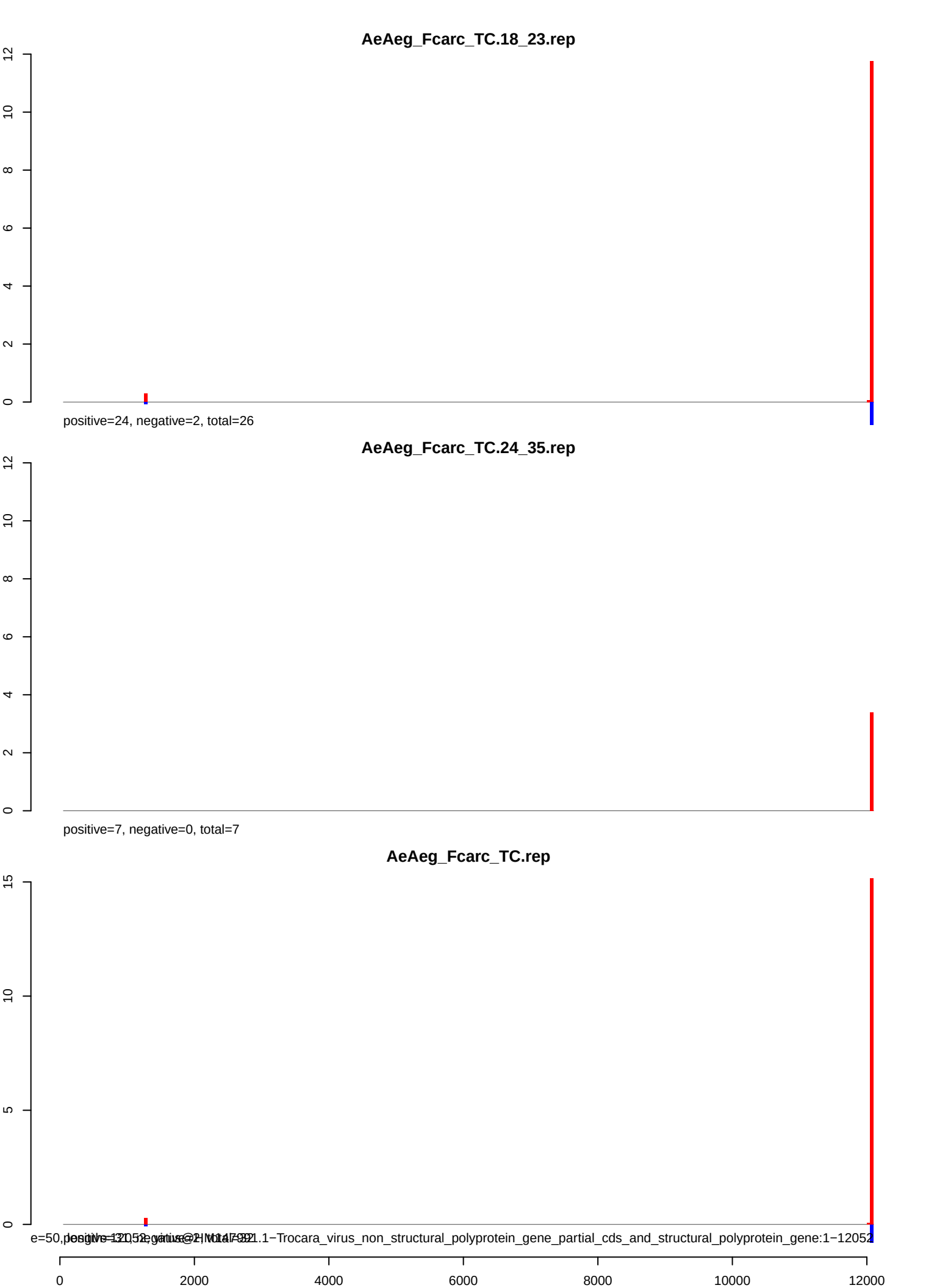

AeAeg_Fcarc_TC.18_23.rep
0.15
0.10
0.05
0.00
−0.05
positive=1, negative=0, total=1
AeAeg_Fcarc_TC.24_35.rep
0.15
0.10
0.05
0.00
−0.05
positive=0, negative=0, total=0
AeAeg_Fcarc_TC.rep
0.20
0.15
0.10
0.05
0.00
−0.05
0
1000
2000
3000
4000

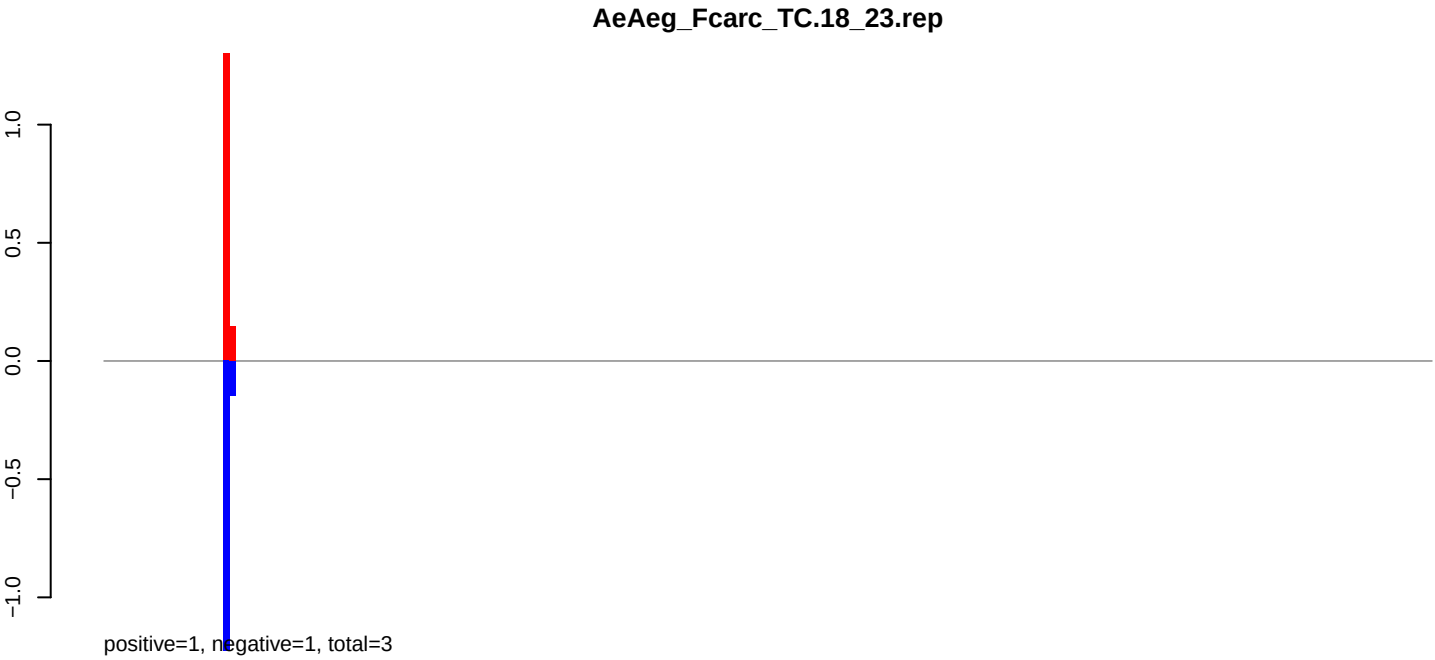

AeAeg_Fcarc_TC.18_23.rep
0.15
0.10
0.05
0.00
positive=0, negative=0, total=0
AeAeg_Fcarc_TC.24_35.rep
0.15
0.10
0.05
0.00
positive=0, negative=0, total=0
AeAeg_Fcarc_TC.rep
0.15
0.10
0.05
0.00
positive=1, negative=0, total=1
Window size=50, length=12333, virus@NC_007919.3−Nora_virus:1−12333
0
2000
4000
6000
8000
10000
12000

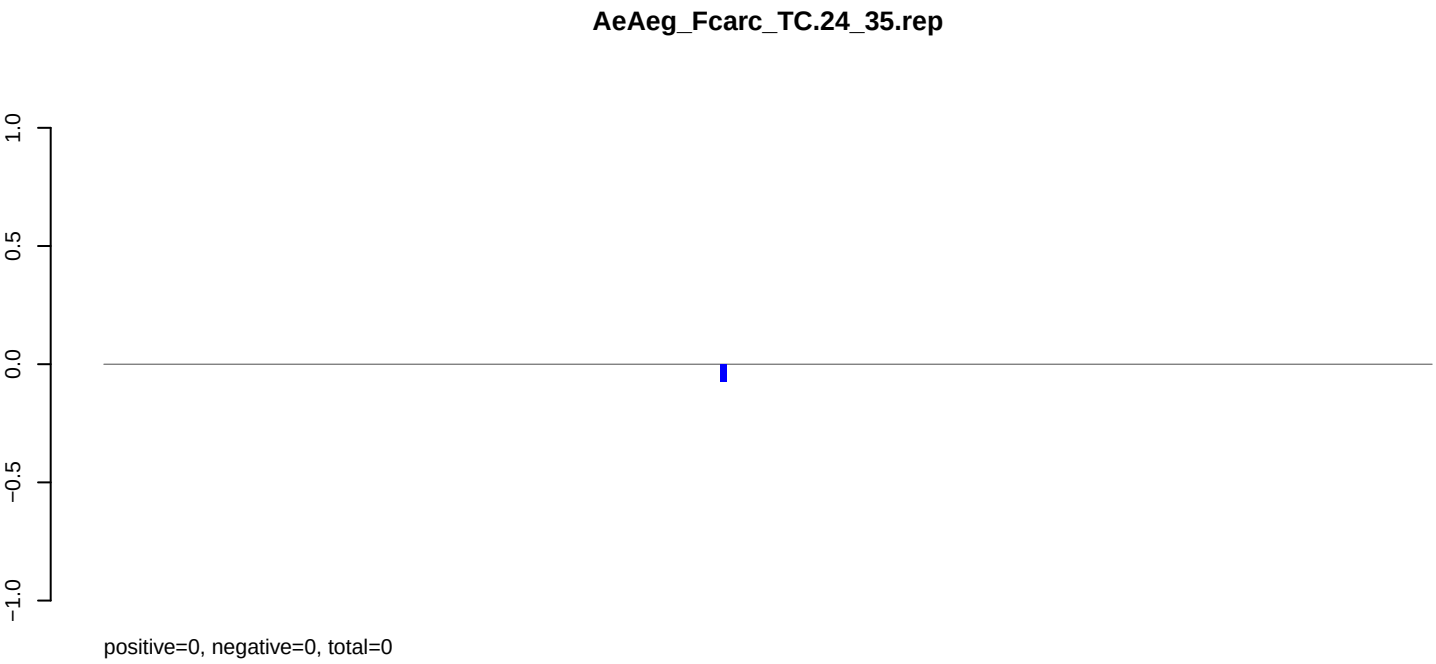

AeAeg_Fcarc_TC.18_23.rep
0
−10
−20
−30
−40
positive=0, negative=56, total=57
AeAeg_Fcarc_TC.24_35.rep
0
−10
−20
−30
−40
positive=0, negative=36, total=36
AeAeg_Fcarc_TC.rep
0
−20
−40
−60
virus@KJ716848.1−Ngaoundi_virus_strain_Adrar_segment_S_plus_segment_M_plus_segment_L:1−12369
0
2000
4000
6000
8000
10000
12000

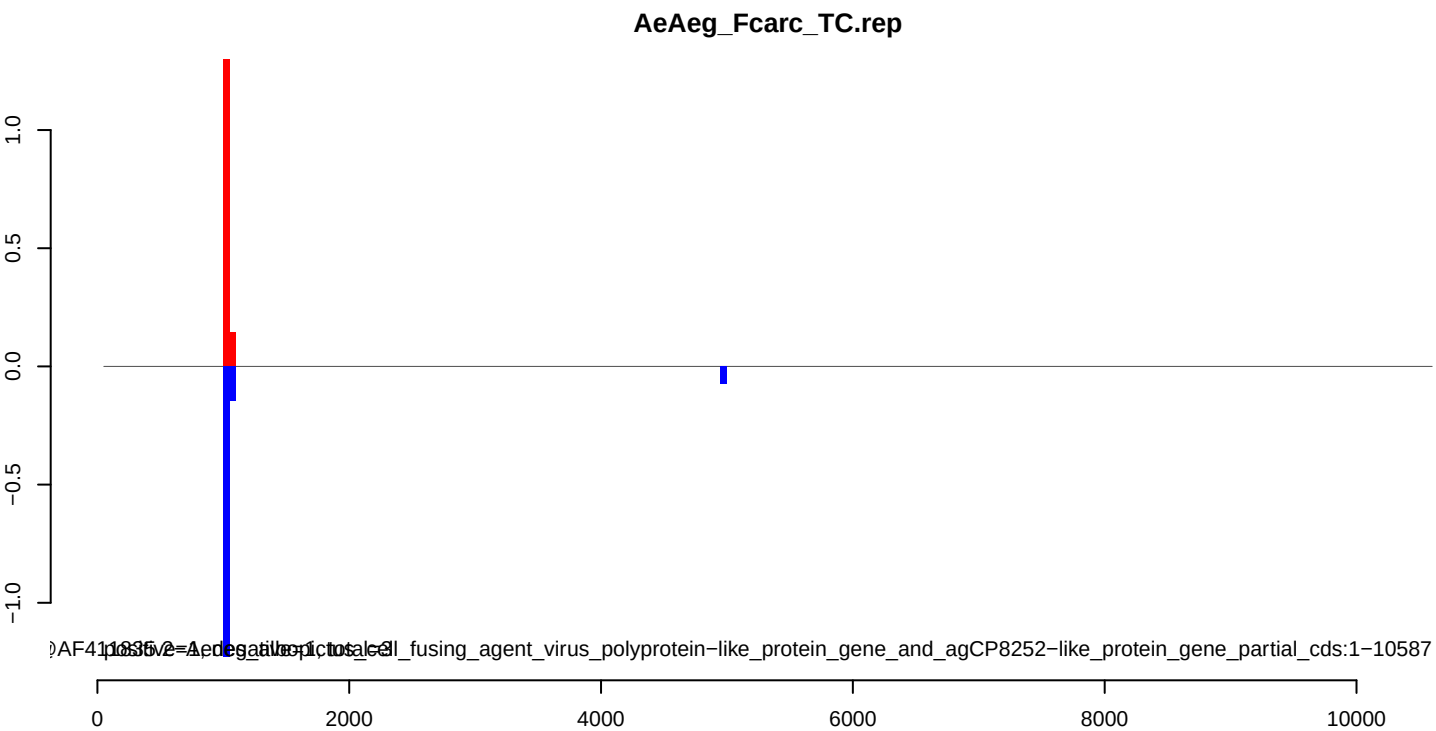

AeAeg_Fcarc_TC.18_23.rep
1.0
0.5
0.0
positive=2, negative=0, total=2
AeAeg_Fcarc_TC.24_35.rep
1.0
0.5
0.0
positive=0, negative=0, total=0
AeAeg_Fcarc_TC.rep
1.0
0.5
0.0
positive=2, negative=0, total=2
window size=50, length=6203, virus@NC_035674.1−Australian_Anopheles_totivirus_isolate_AATV_150840:1−6203
0
1000
2000
3000
4000
5000
6000

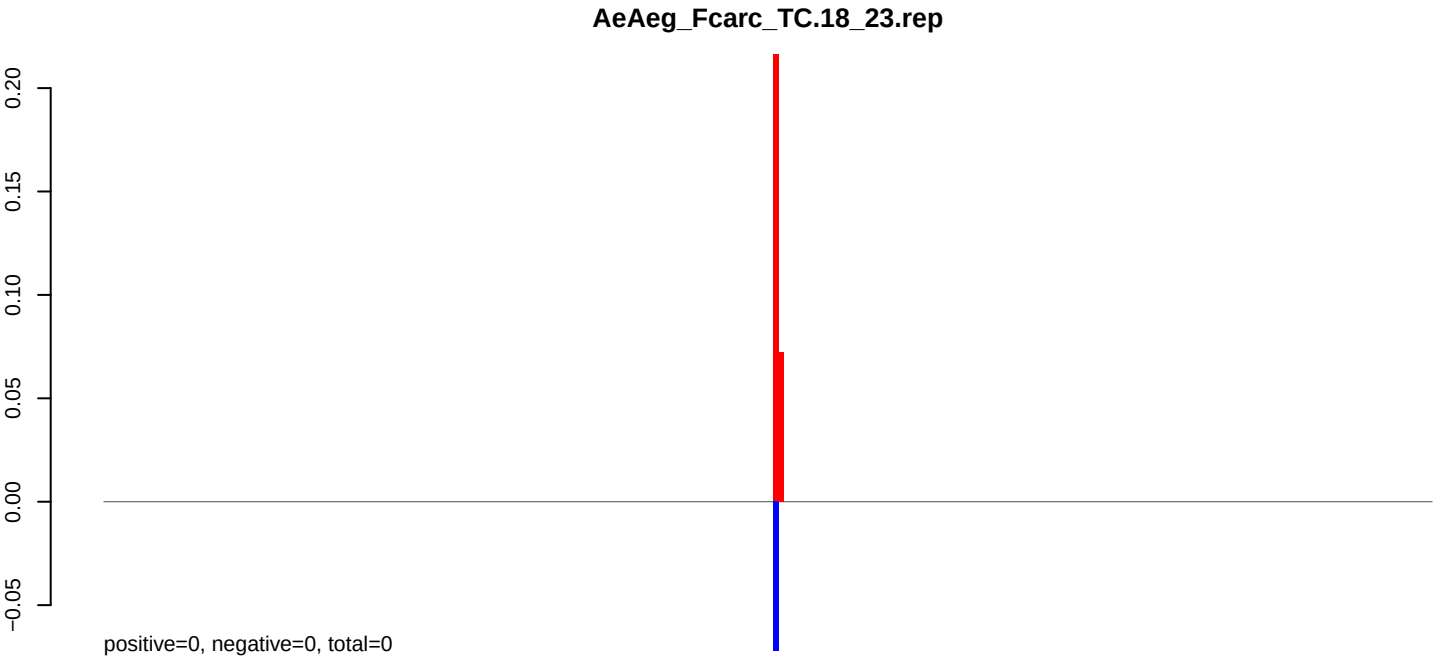

AeAeg_Fcarc_TC.18_23.rep
0.05
0.00
−0.05
positive=0, negative=0, total=0
AeAeg_Fcarc_TC.24_35.rep
0.05
0.00
−0.05
positive=0, negative=0, total=0
AeAeg_Fcarc_TC.rep
0.05
0.00
−0.05
positive=0, negative=0, total=0
Window size=50, length=4507, virus@NC_004146.1−Flock_house_virus_RNA_1_and_RNA2:1−4507
0
1000
2000
3000
4000

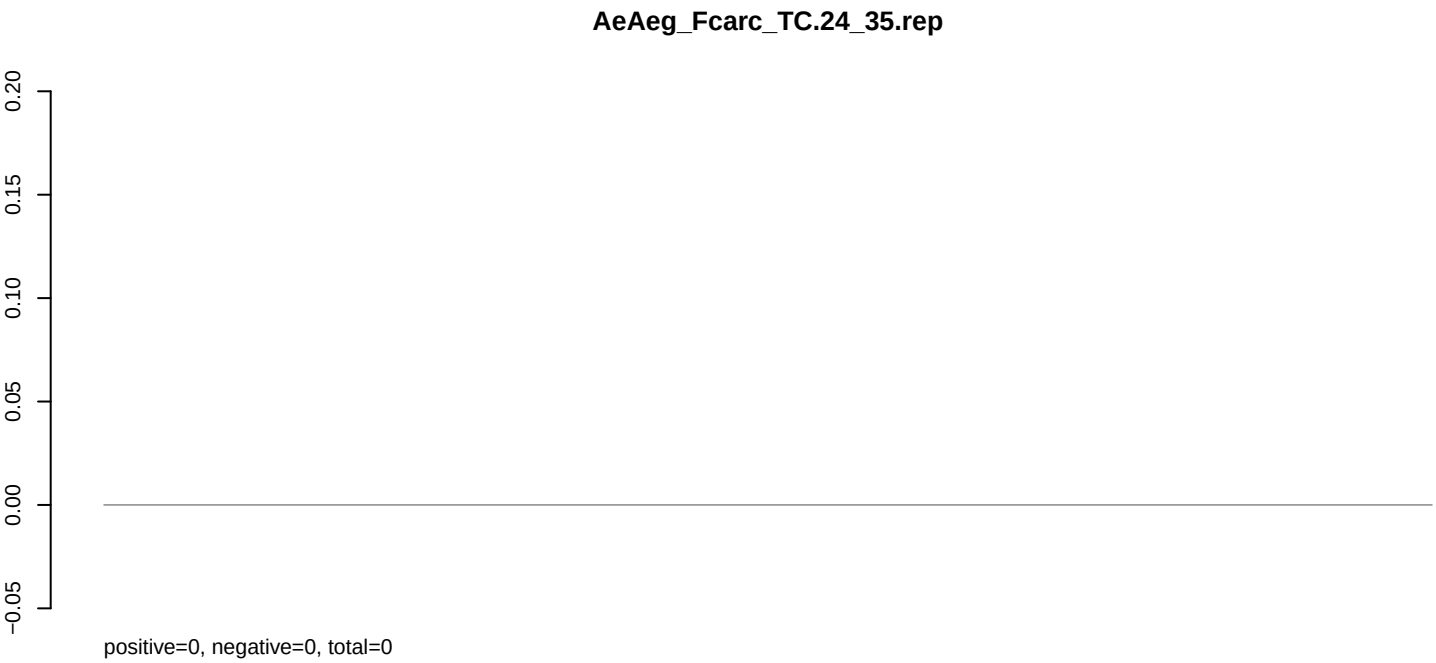

AeAeg_Fcarc_TC.18_23.rep
positive=24, negative=2, total=26
AeAeg_Fcarc_TC.24_35.rep
positive=7, negative=0, total=7
AeAeg_Fcarc_TC.rep
0
2000
4000
6000
8000
10000
12000

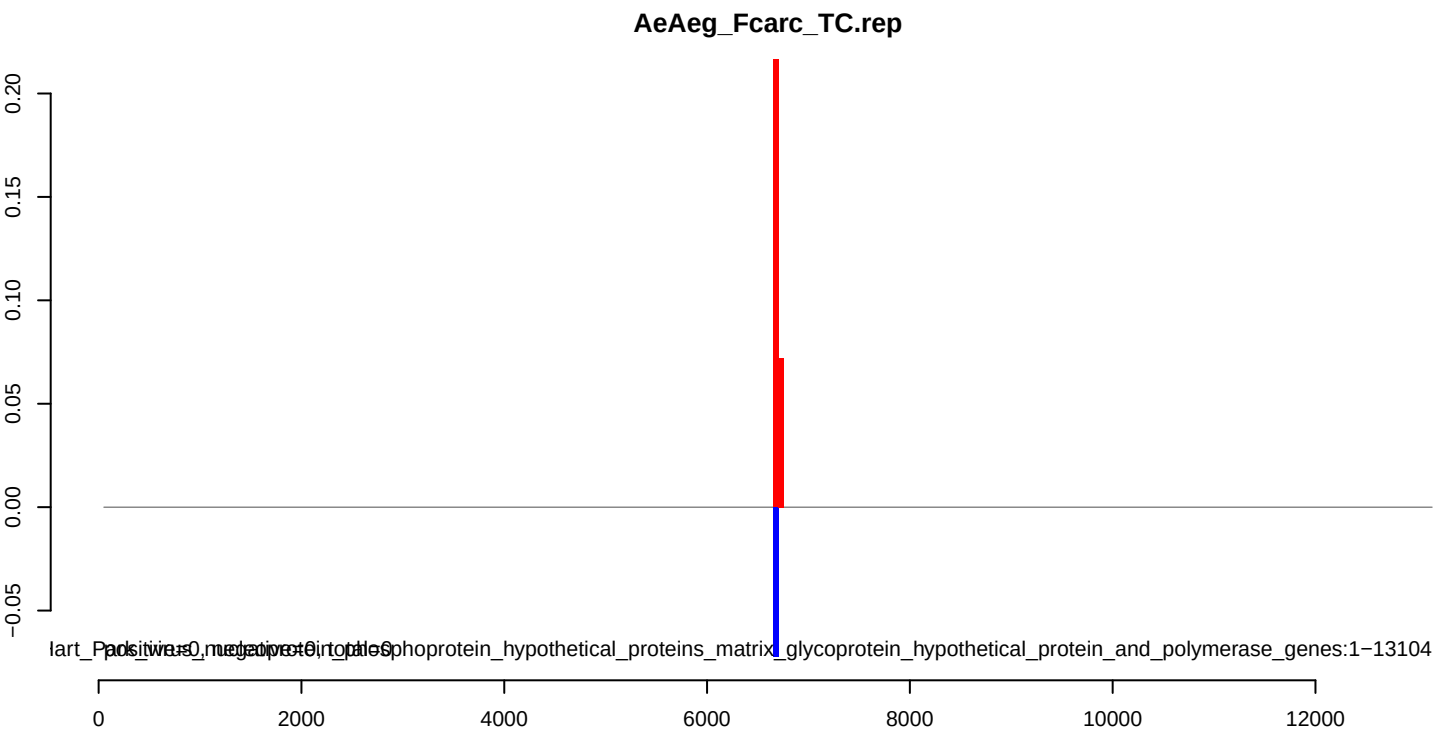

AeAeg_Fcarc_TC.18_23.rep
1.0
0.5
0.0
−0.5
−1.0
positive=1, negative=1, total=3

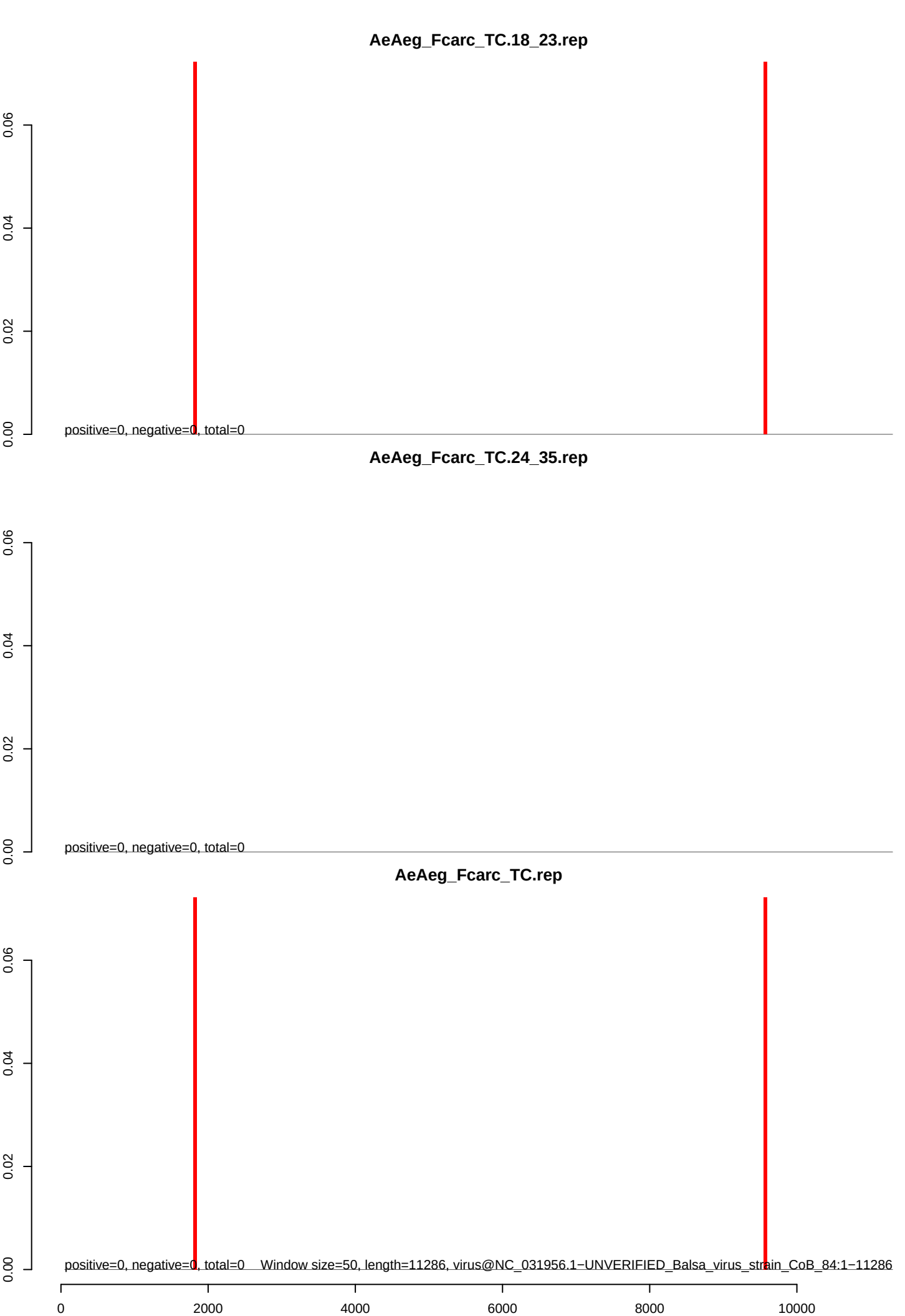

AeAeg_Fcarc_TC.24_35.rep
1.0
0.5
0.0
−0.5
−1.0
positive=0, negative=0, total=0

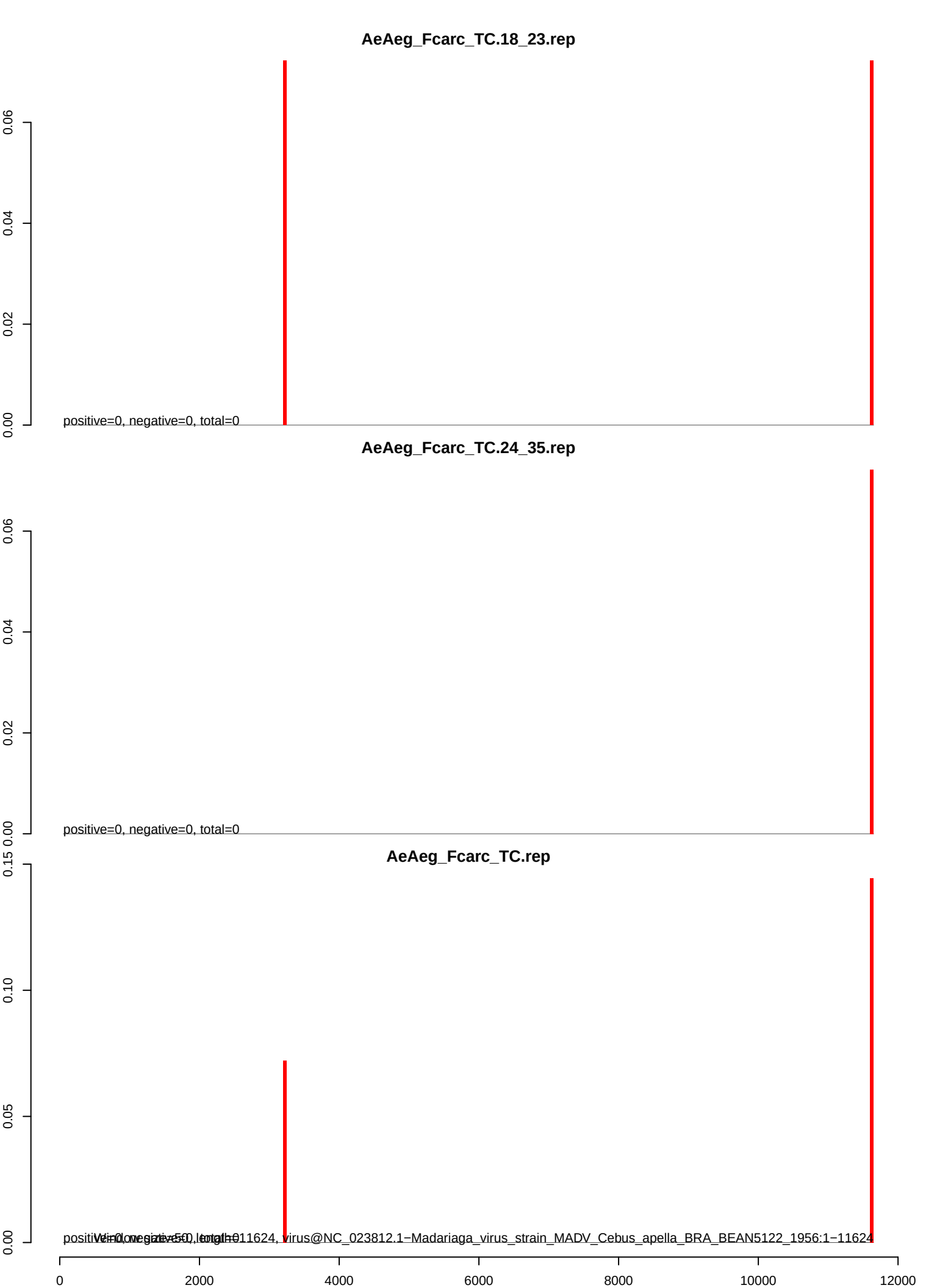

AeAeg_Fcarc_TC.rep
1.0
0.5
0.0
−0.5
−1.0
0
2000
4000
6000
8000
10000

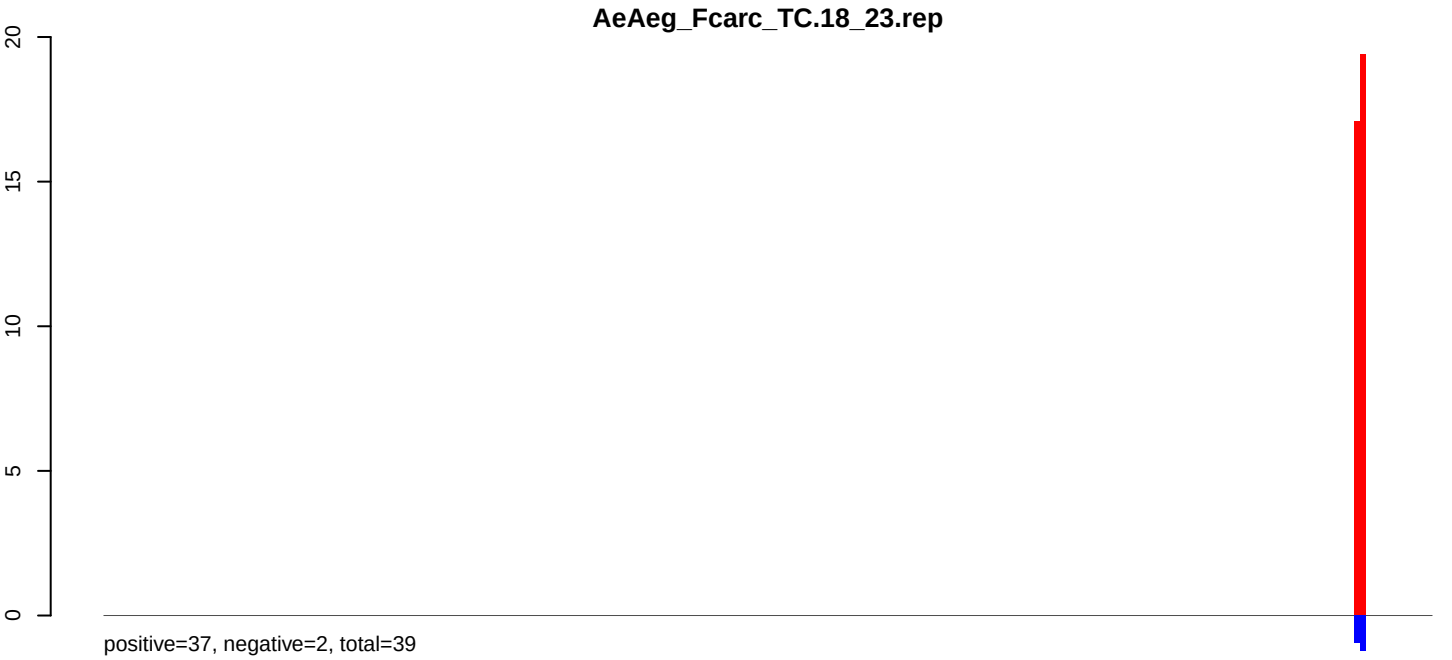

AeAeg_Fcarc_TC.18_23.rep
0.20
0.15
0.10
0.05
0.00
−0.05
positive=0, negative=0, total=0


AeAeg_Fcarc_TC.24_35.rep
0.20
0.15
0.10
0.05
0.00
−0.05
positive=0, negative=0, total=0

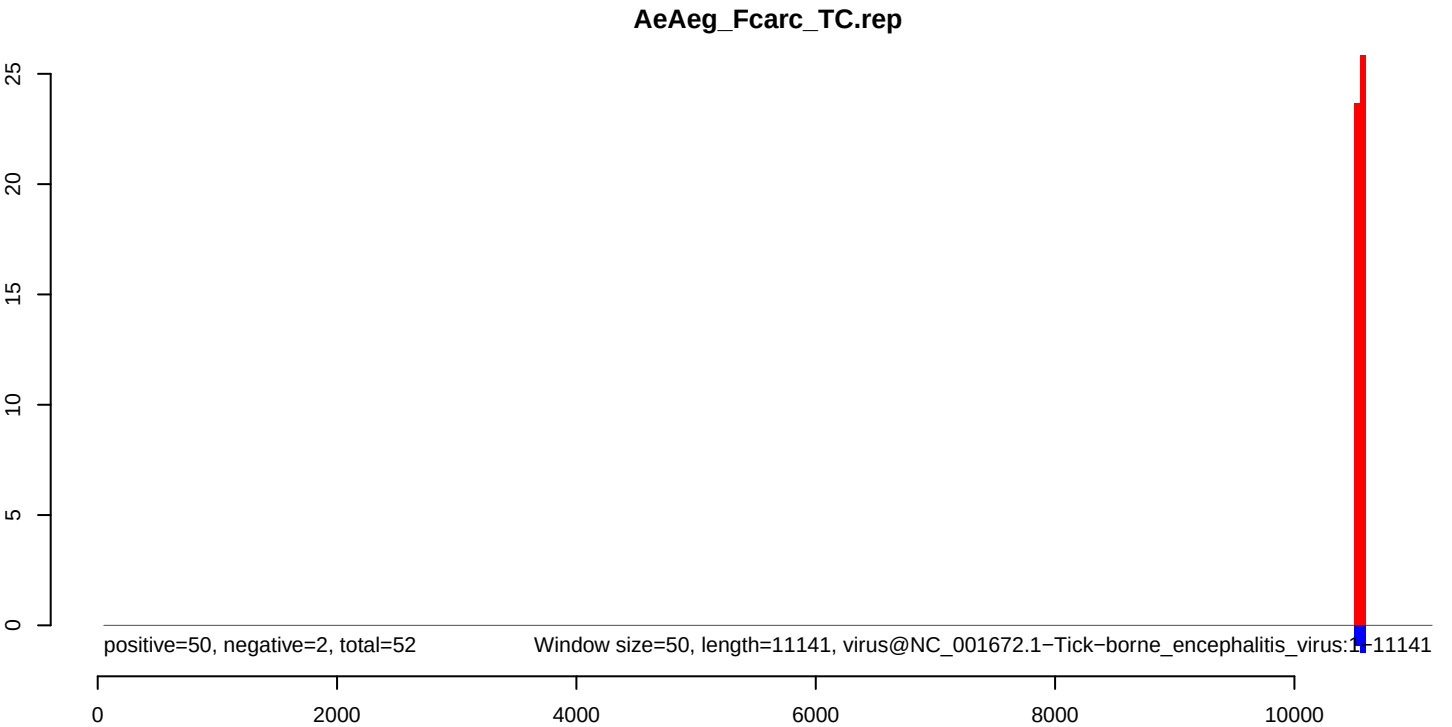

AeAeg_Fcarc_TC.rep
0.20
0.15
0.10
0.05
0.00
−0.05
0
2000
4000
6000
8000
10000
12000

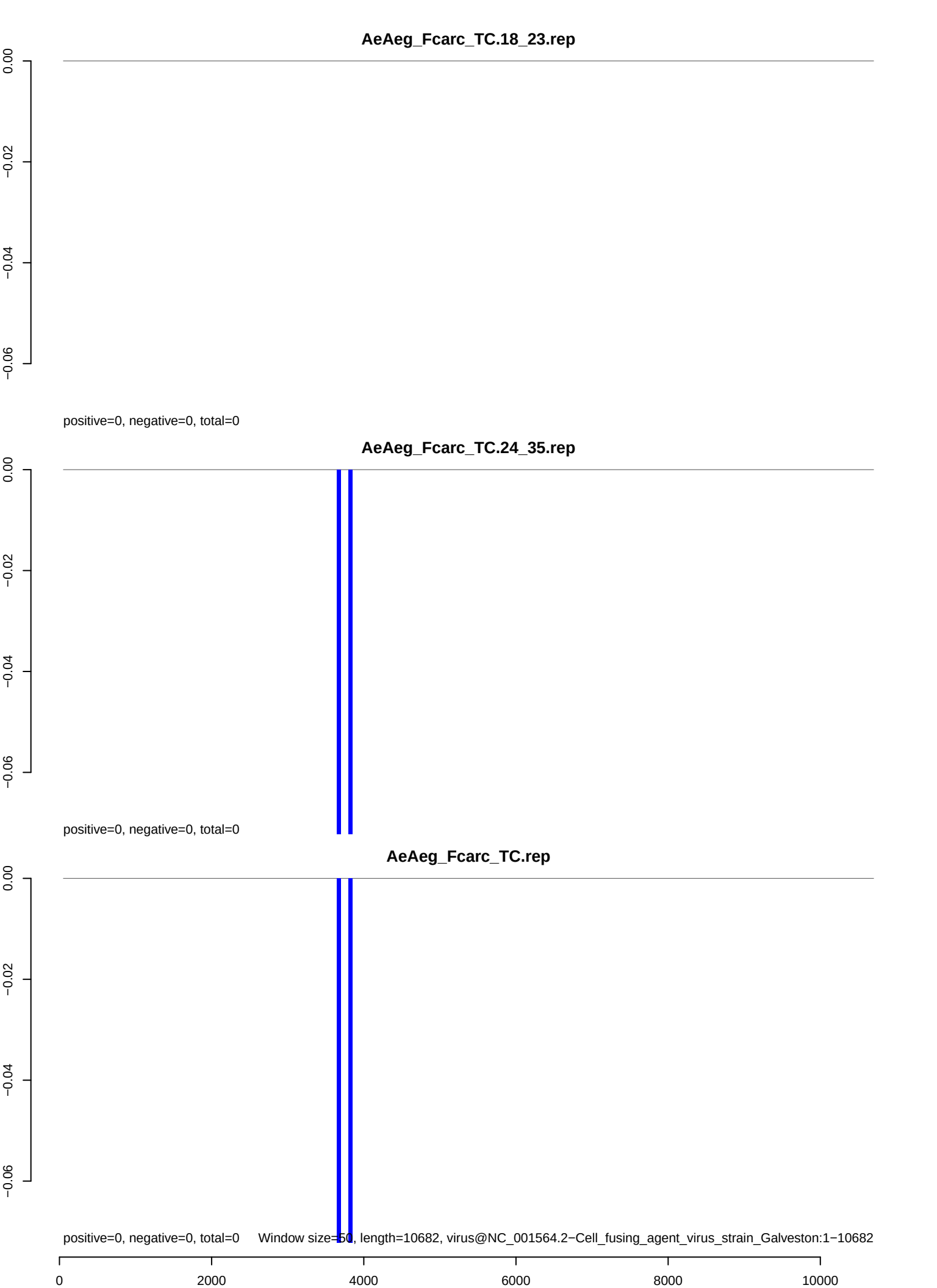

AeAeg_Fcarc_TC.18_23.rep
0.00
0.02
0.04
0.06
positive=0, negative=0, total=0
AeAeg_Fcarc_TC.24_35.rep
0.00
0.02
0.04
0.06
positive=0, negative=0, total=0
AeAeg_Fcarc_TC.rep
0.00
0.02
0.04
0.06
positive=0, negative=0, total=0
Window size=50, length=11286, virus@NC_031956.1−UNVERIFIED_Balsa_virus_strain_CoB_84:1−11286
0
2000
4000
6000
8000
10000

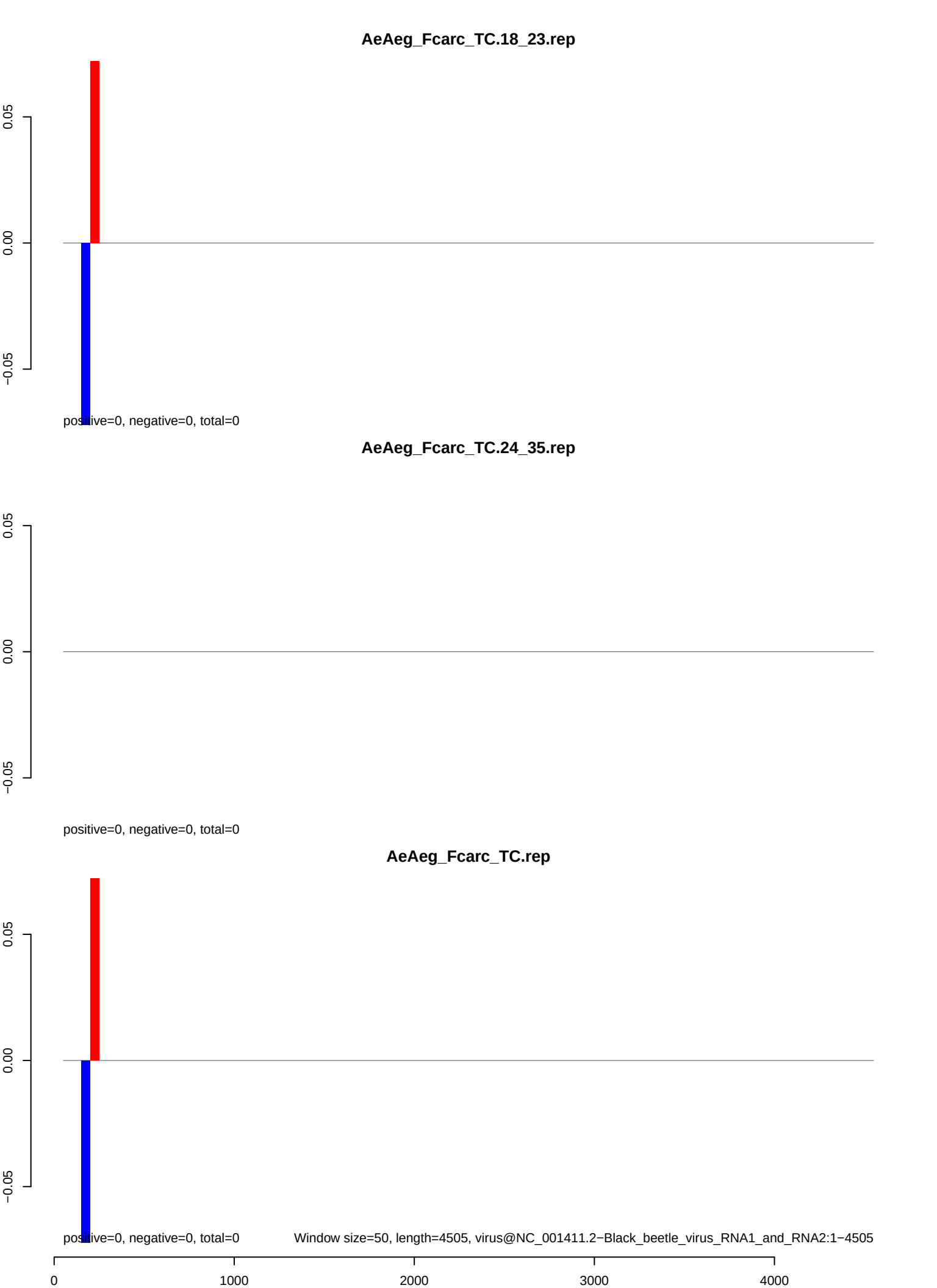

AeAeg_Fcarc_TC.18_23.rep
0.00
0.02
0.04
0.06
positive=0, negative=0, total=0
AeAeg_Fcarc_TC.24_35.rep
0.00
0.02
0.04
0.06
positive=0, negative=0, total=0
AeAeg_Fcarc_TC.rep
0.00
0.05
0.10
0.15
positive=0, negative=0, total=0
Window size=50, length=11624, virus@NC_023812.1−Madariaga_virus_strain_MADV_Cebus_apella_BRA_BEAN5122_1956:1−11624
0
2000
4000
6000
8000
10000
12000

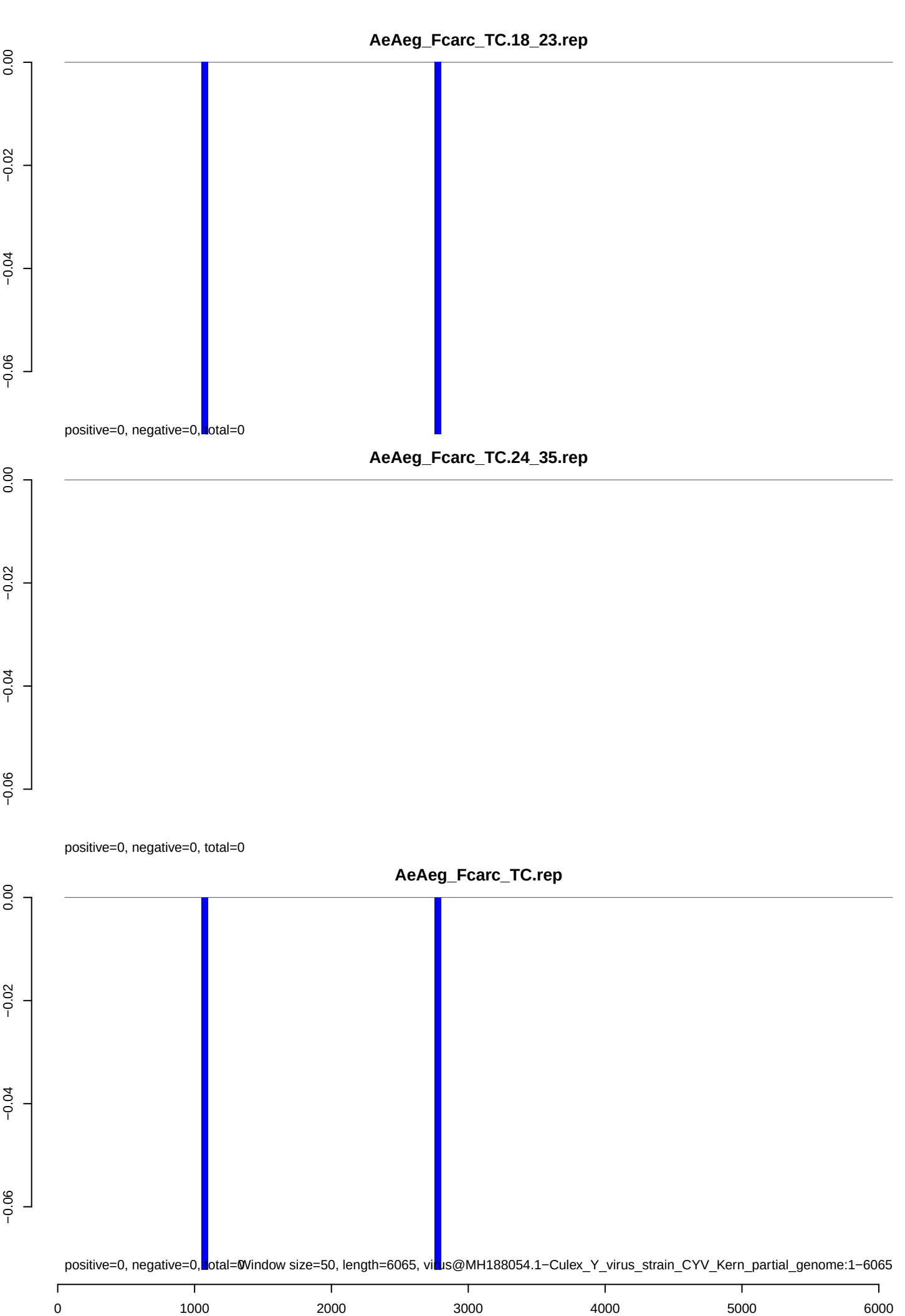

AeAeg_Fcarc_TC.18_23.rep
0
5
10
15
20
positive=37, negative=2, total=39

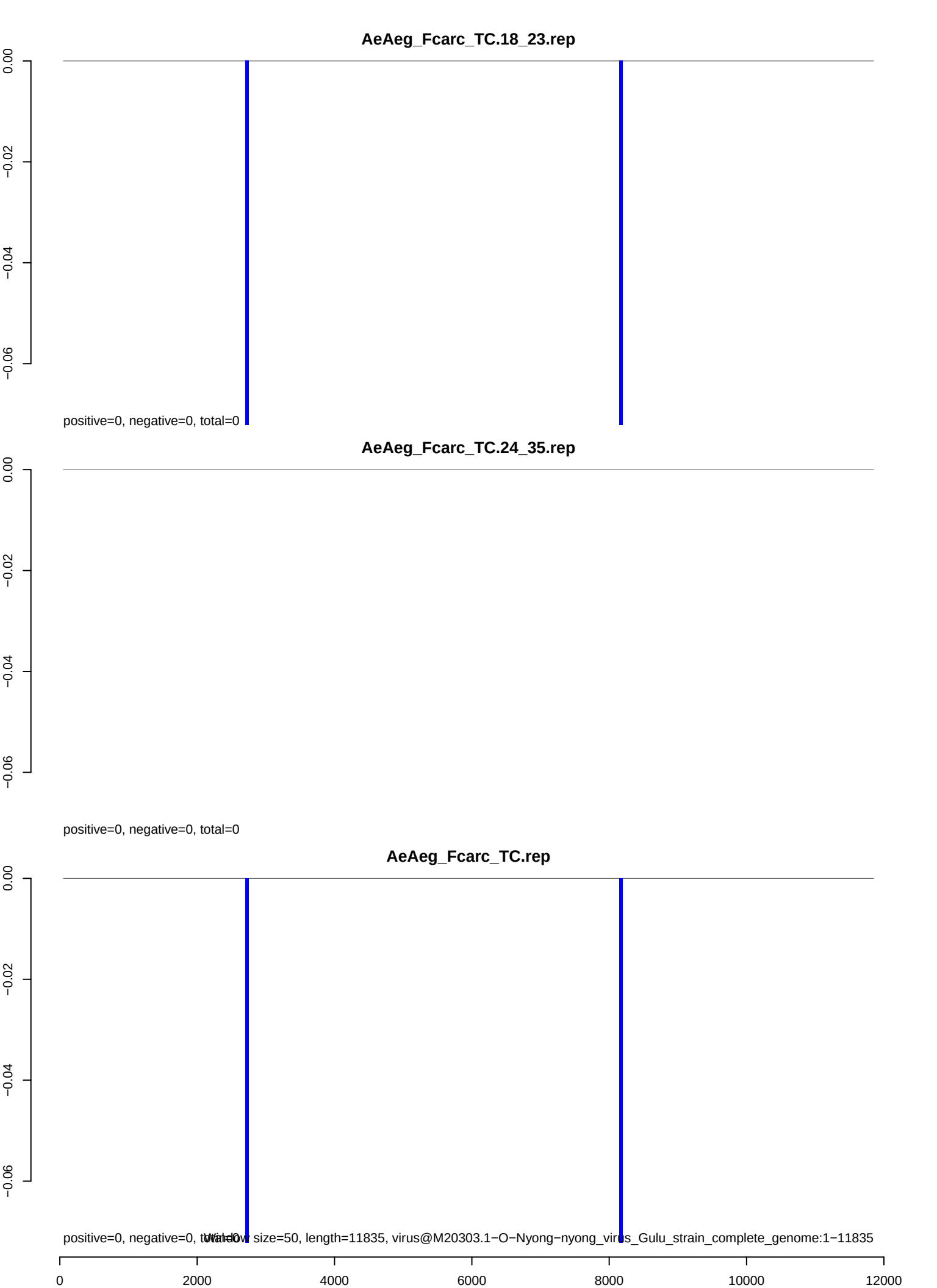
AeAeg_Fcarc_TC.24_35.rep
0
5
10
15
20
positive=13, negative=0, total=13

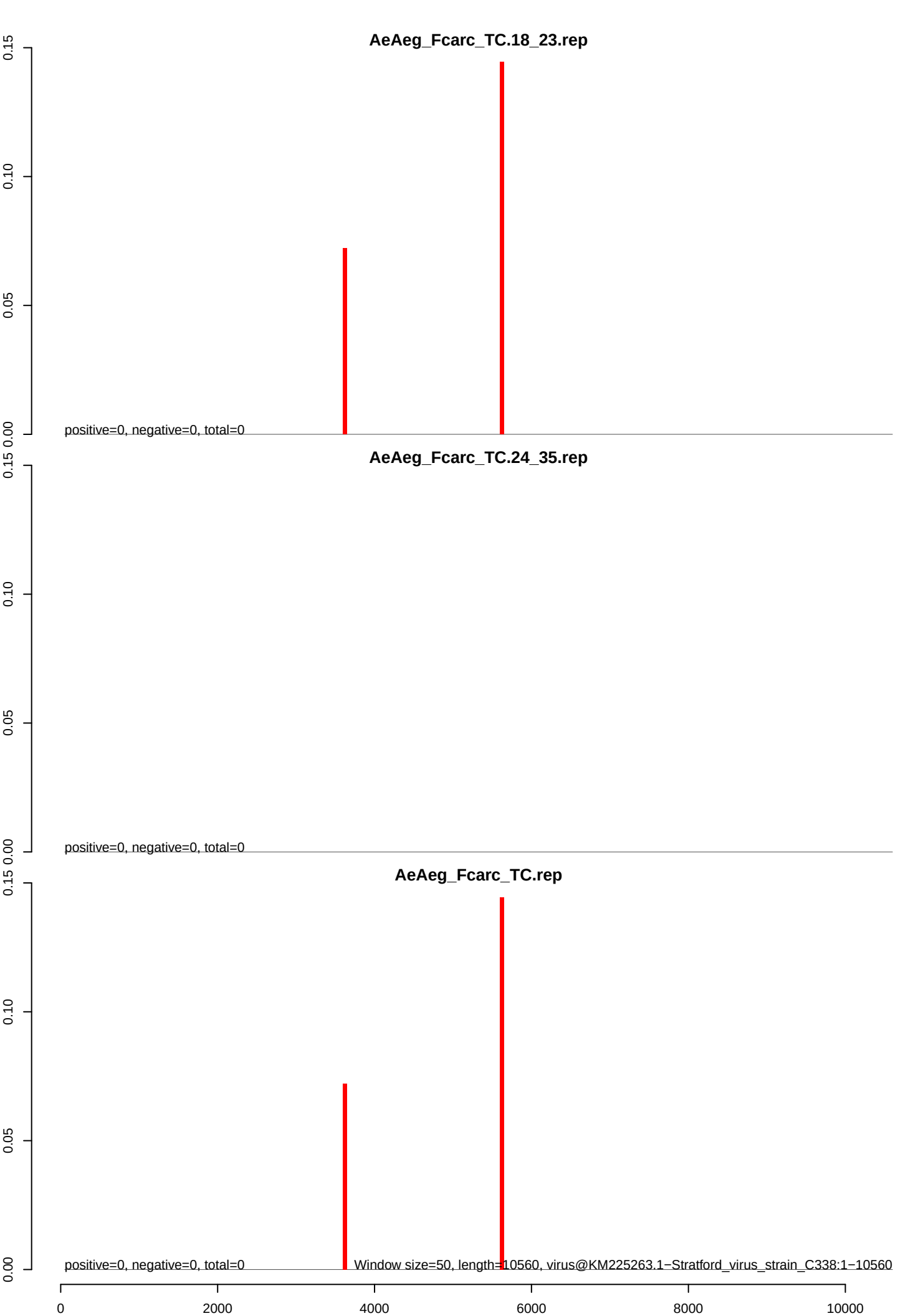

AeAeg_Fcarc_TC.rep
0
5
10
15
20
25
positive=50, negative=2, total=52
Window size=50, length=11141, virus@NC_001672.1−Tick−borne_encephalitis_virus:1−11141
0
2000
4000
6000
8000
10000


AeAeg_Fcarc_TC.18_23.rep
0.00
−0.02
−0.04
−0.06
positive=0, negative=0, total=0
AeAeg_Fcarc_TC.24_35.rep
0.00
−0.02
−0.04
−0.06
positive=0, negative=0, total=0
AeAeg_Fcarc_TC.rep
0.00
−0.02
−0.04
−0.06
positive=0, negative=0, total=0
Window size=50, length=10682, virus@NC_001564.2−Cell_fusing_agent_virus_strain_Galveston:1−10682
0
2000
4000
6000
8000
10000


AeAeg_Fcarc_TC.18_23.rep
0.05
0.00
−0.05
positive=0, negative=0, total=0
AeAeg_Fcarc_TC.24_35.rep
0.05
0.00
−0.05
positive=0, negative=0, total=0
AeAeg_Fcarc_TC.rep
0.05
0.00
−0.05
positive=0, negative=0, total=0
Window size=50, length=4505, virus@NC_001411.2−Black_beetle_virus_RNA1_and_RNA2:1−4505
0
1000
2000
3000
4000


AeAeg_Fcarc_TC.18_23.rep
0.00
−0.02
−0.04
−0.06
positive=0, negative=0, total=0
AeAeg_Fcarc_TC.24_35.rep
0.00
−0.02
−0.04
−0.06
positive=0, negative=0, total=0
AeAeg_Fcarc_TC.rep
0.00
−0.02
−0.04
−0.06
positive=0, negative=0, total=0
Window size=50, length=6065, virus@MH188054.1−Culex_Y_virus_strain_CYV_Kern_partial_genome:1−6065
0
1000
2000
3000
4000
5000
6000


AeAeg_Fcarc_TC.18_23.rep
0.00
−0.02
−0.04
−0.06
positive=0, negative=0, total=0
AeAeg_Fcarc_TC.24_35.rep
0.00
−0.02
−0.04
−0.06
positive=0, negative=0, total=0
AeAeg_Fcarc_TC.rep
0.00
−0.02
−0.04
−0.06
positive=0, negative=0, total=0
Window size=50, length=11835, virus@M20303.1−O−Nyong−nyong_virus_Gulu_strain_complete_genome:1−11835
0
2000
4000
6000
8000
10000
12000


AeAeg_Fcarc_TC.18_23.rep
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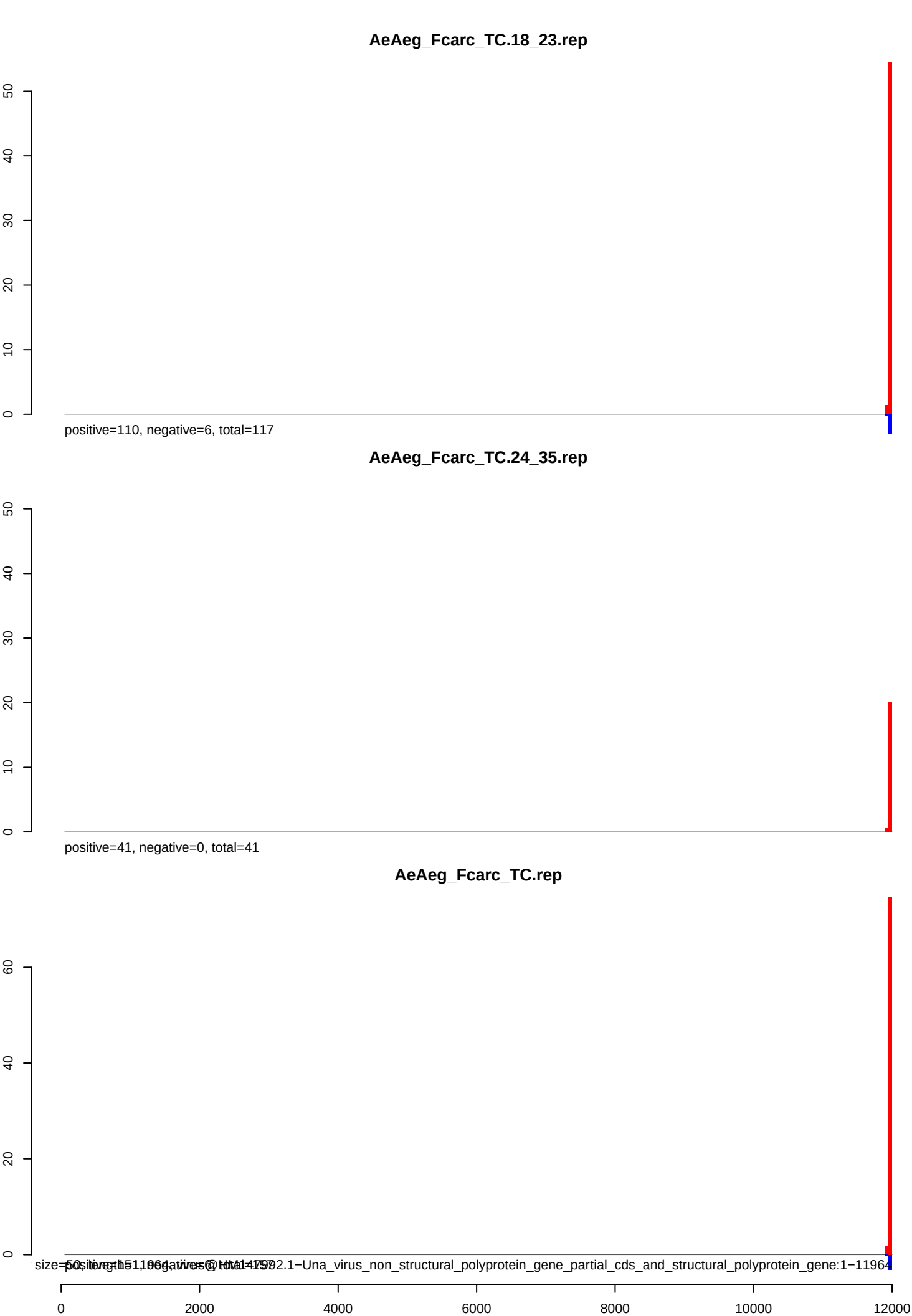
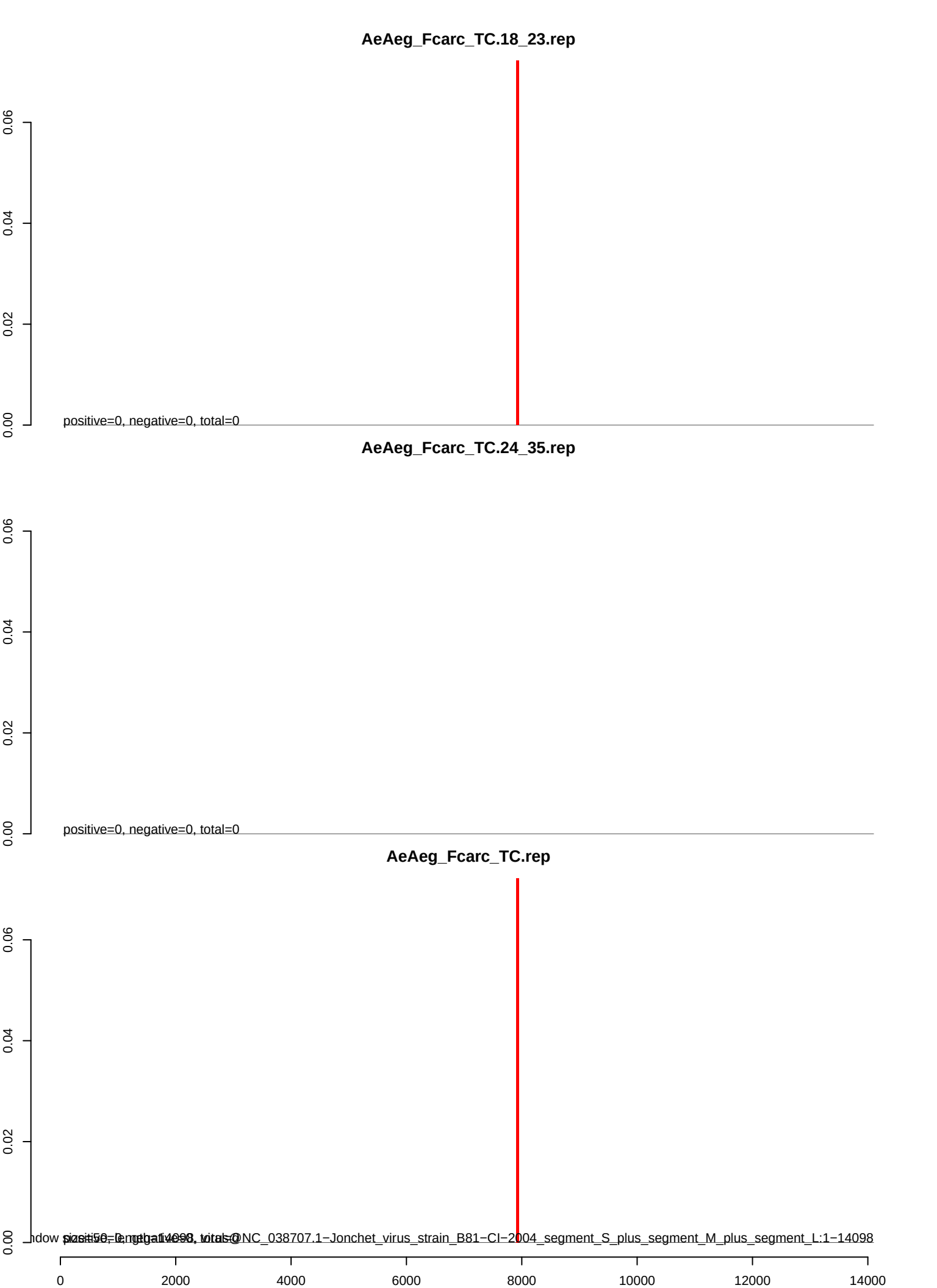
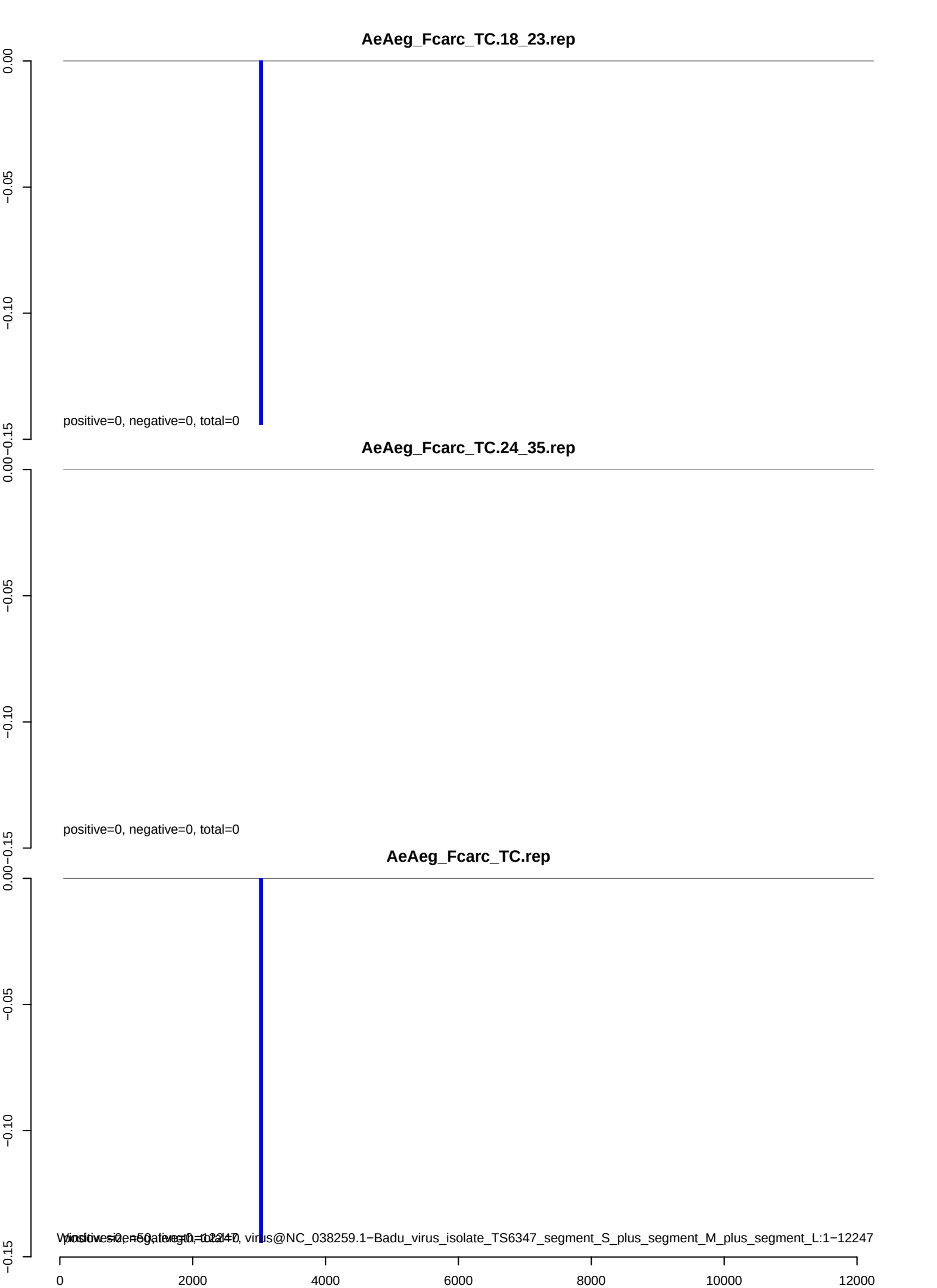
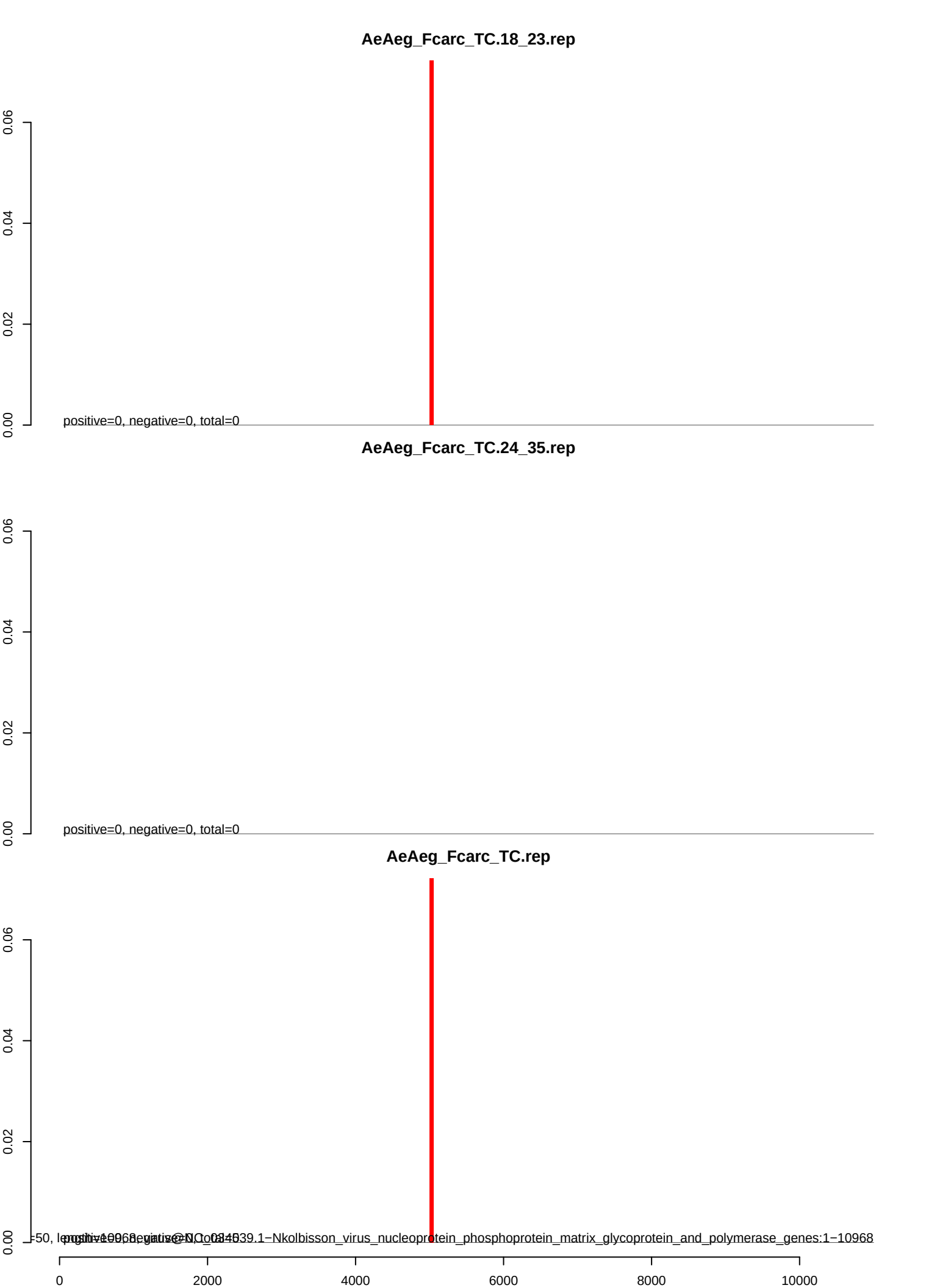
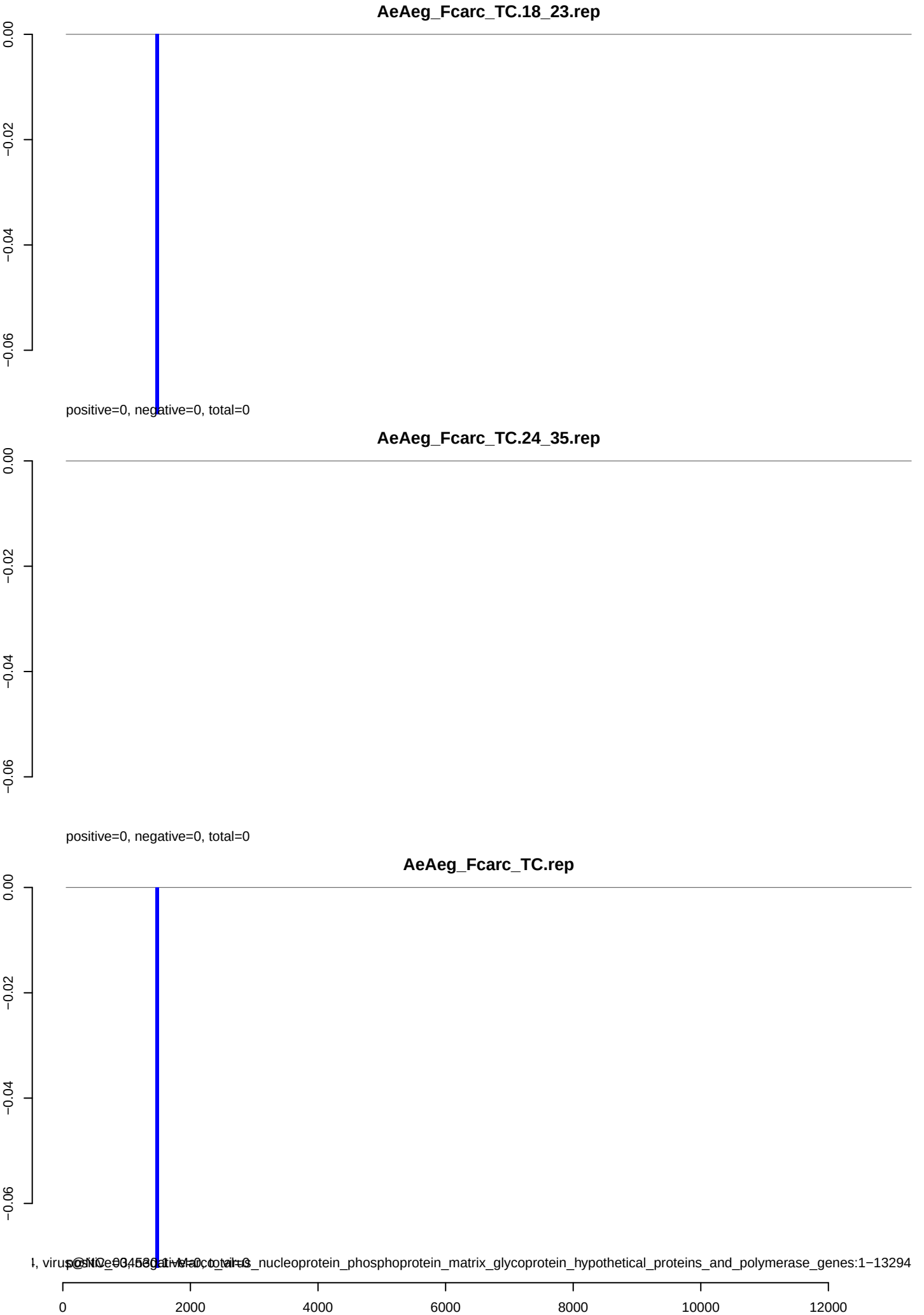
0.10
0.05
0.00
positive=0, negative=0, total=0
AeAeg_Fcarc_TC.24_35.rep
0.15
0.10
0.05
0.00
positive=0, negative=0, total=0
AeAeg_Fcarc_TC.rep
0.15
0.10
0.05
0.00
positive=0, negative=0, total=0
Window size=50, length=10560, virus@KM225263.1−Stratford_virus_strain_C338:1−10560
0
2000
4000
6000
8000
10000


AeAeg_Fcarc_TC.18_23.rep
0
10
20
30
40
50
positive=110, negative=6, total=117
AeAeg_Fcarc_TC.24_35.rep
0
10
20
30
40
50
positive=41, negative=0, total=41
AeAeg_Fcarc_TC.rep
0
20
40
60
size=positive=151, negative=6, total=157
0
2000
4000
6000
8000
10000
12000


AeAeg_Fcarc_TC.18_23.rep
0.00
0.02
0.04
0.06
positive=0, negative=0, total=0
AeAeg_Fcarc_TC.24_35.rep
0.00
0.02
0.04
0.06
positive=0, negative=0, total=0
AeAeg_Fcarc_TC.rep
0.00
0.02
0.04
0.06
0
2000
4000
6000
8000
10000
12000
14000


AeAeg_Fcarc_TC.18_23.rep
positive=0, negative=0, total=0
AeAeg_Fcarc_TC.24_35.rep
positive=0, negative=0, total=0
AeAeg_Fcarc_TC.rep
positive=0, negative=0, total=0
virus@NC_038259.1−Badu_virus_isolate_TS6347_segment_S_plus_segment_M_plus_segment_L:1−12247
0.00
−0.05
−0.10
−0.15
0
2000
4000
6000
8000
10000
12000


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


AeAeg_Fcarc_TC.18_23.rep
0.00
−0.02
−0.04
−0.06
positive=0, negative=0, total=0
AeAeg_Fcarc_TC.24_35.rep
0.00
−0.02
−0.04
−0.06
positive=0, negative=0, total=0
AeAeg_Fcarc_TC.rep
0.00
−0.02
−0.04
−0.06
0
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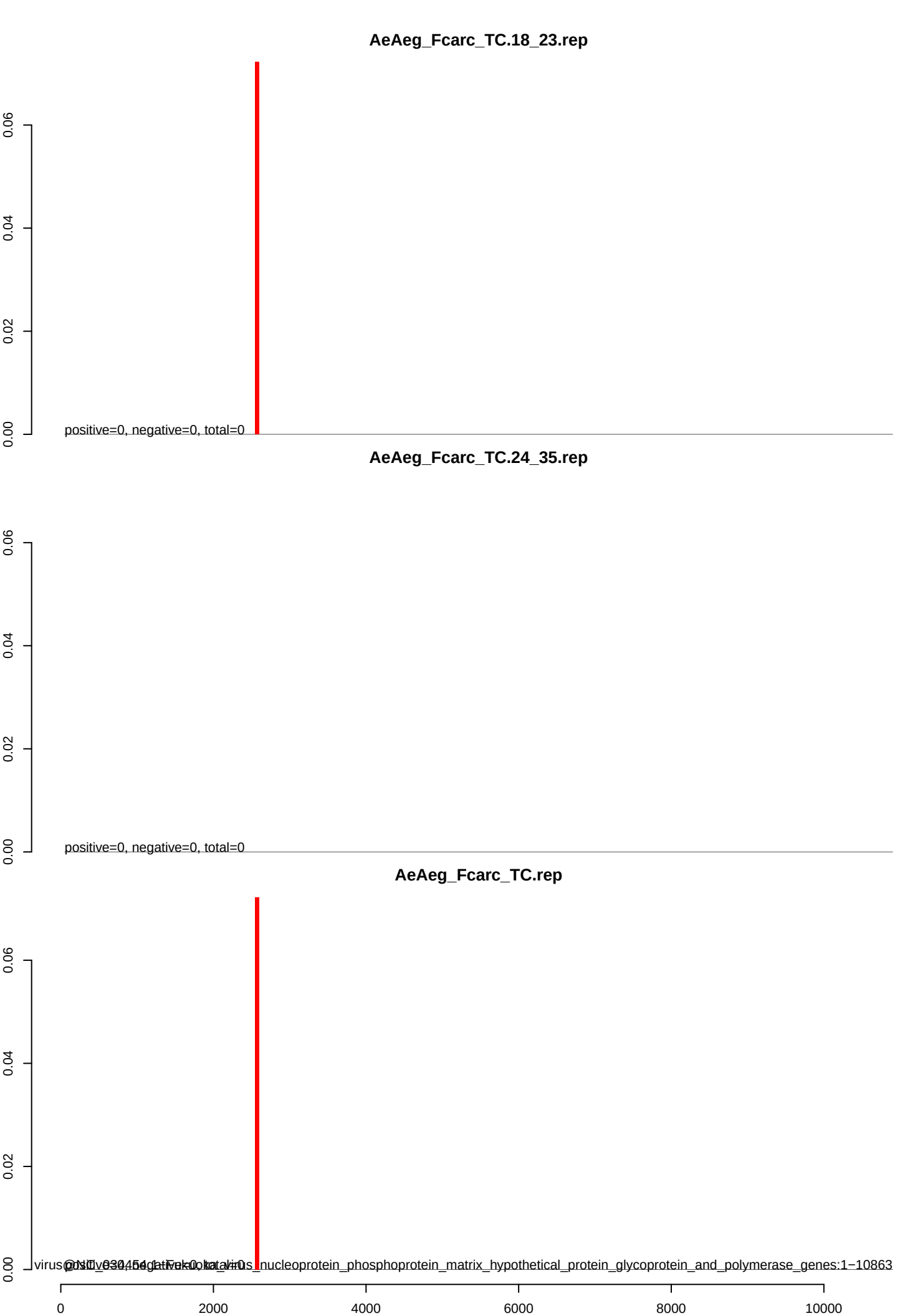
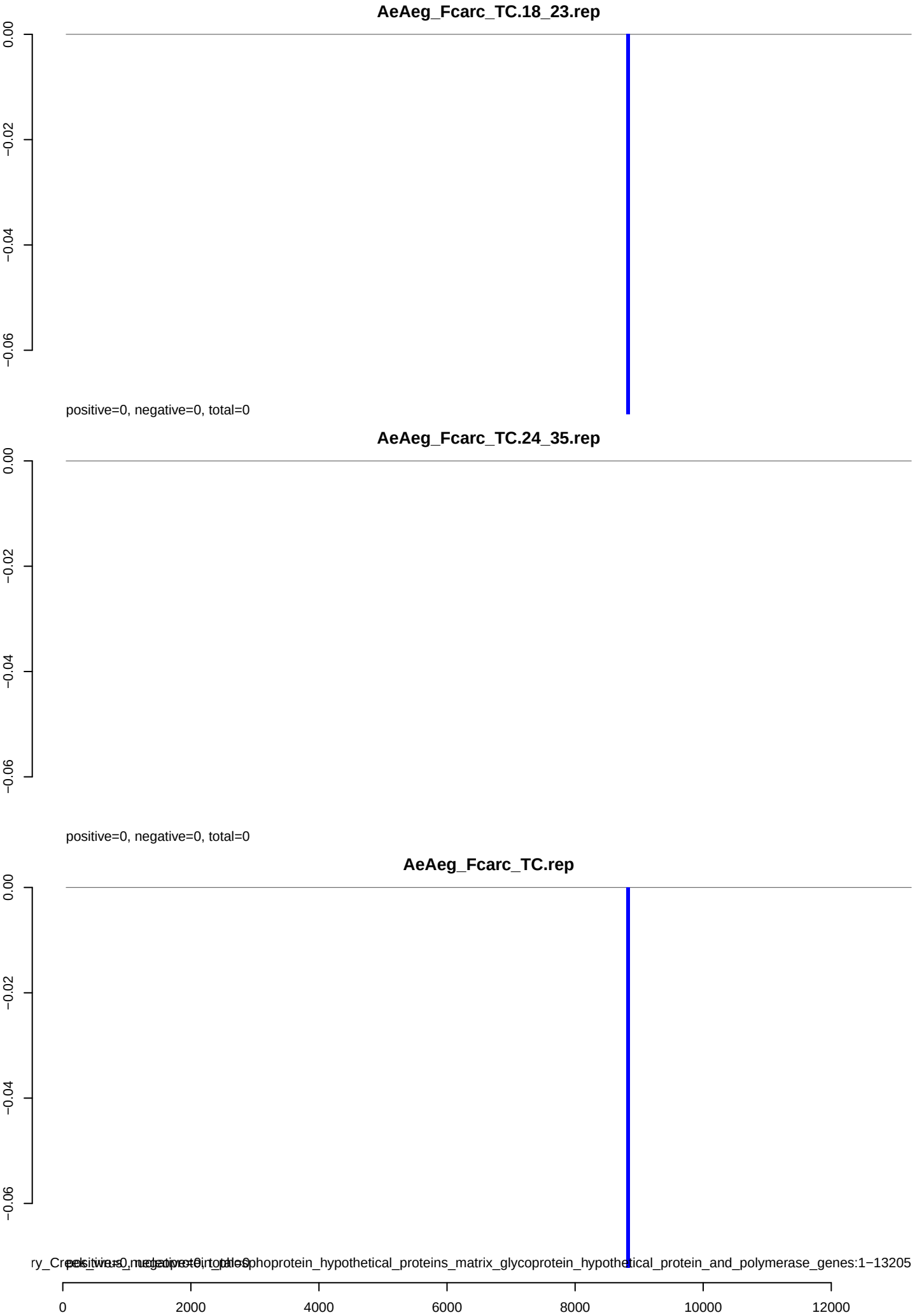
4000
6000
8000
10000
12000


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


AeAeg_Fcarc_TC.18_23.rep
0.00
−0.02
−0.04
−0.06
positive=0, negative=0, total=0
AeAeg_Fcarc_TC.24_35.rep
0.00
−0.02
−0.04
−0.06
positive=0, negative=0, total=0
AeAeg_Fcarc_TC.rep
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−0.04
−0.06
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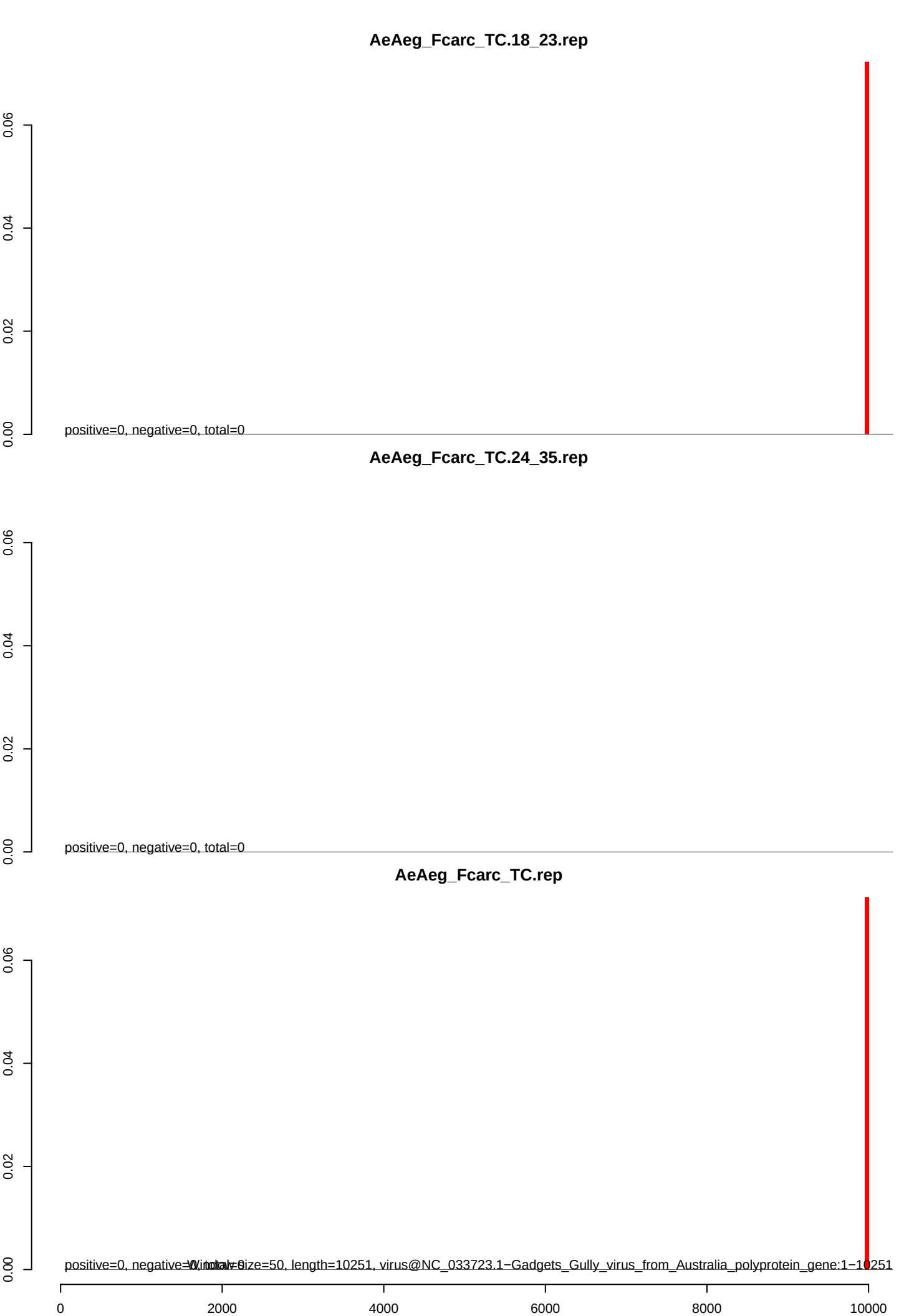
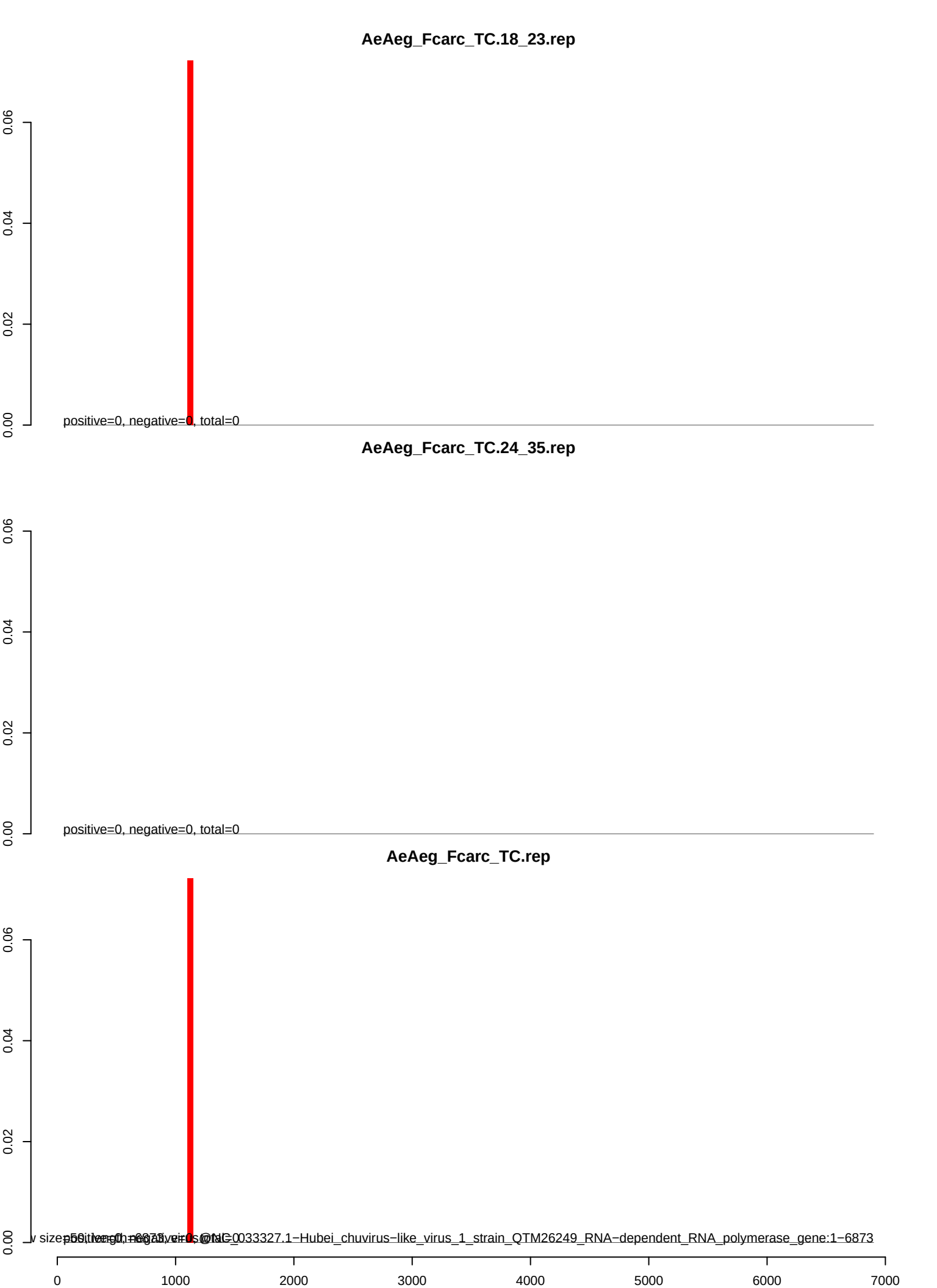
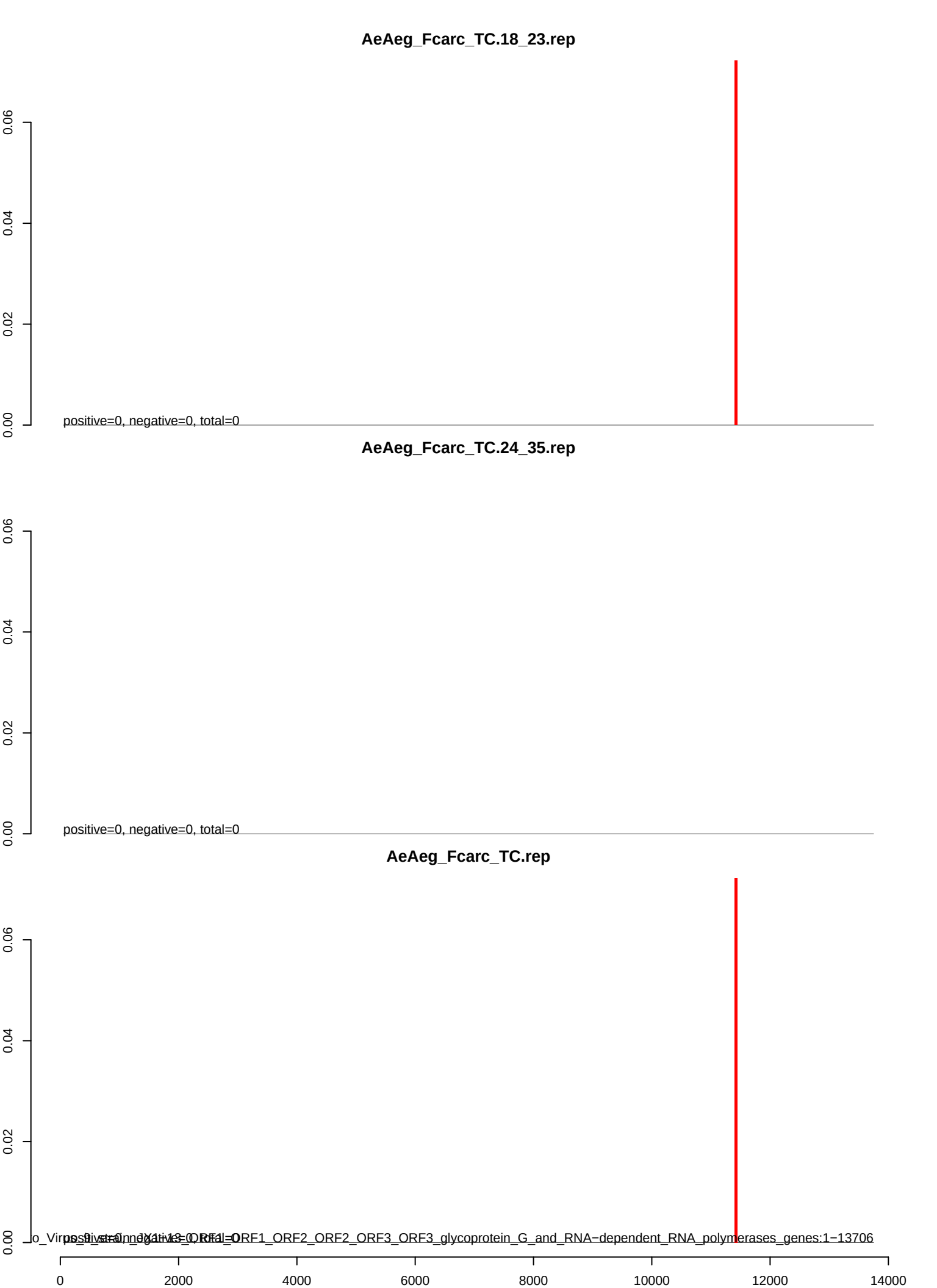
6000
8000
10000
12000


AeAeg_Fcarc_TC.18_23.rep
0.00
0.02
0.04
0.06
positive=0, negative=0, total=0
AeAeg_Fcarc_TC.24_35.rep
0.00
0.02
0.04
0.06
positive=0, negative=0, total=0
AeAeg_Fcarc_TC.rep
0.00
0.02
0.04
0.06
positive=0, negative=0, total=0
window size=50, length=10251, virus@NC_033723.1−Gadgets_Gully_virus_from_Australia_polyprotein_gene:1−10251
0
2000
4000
6000
8000
10000


AeAeg_Fcarc_TC.18_23.rep
0.00
0.02
0.04
0.06
positive=0, negative=0, total=0
AeAeg_Fcarc_TC.24_35.rep
0.00
0.02
0.04
0.06
positive=0, negative=0, total=0
AeAeg_Fcarc_TC.rep
0.00
0.02
0.04
0.06
0
1000
2000
3000
4000
5000
6000
7000


AeAeg_Fcarc_TC.18_23.rep
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0.02
0.04
0.06
positive=0, negative=0, total=0
AeAeg_Fcarc_TC.24_35.rep
0.00
0.02
0.04
0.06
positive=0, negative=0, total=0
AeAeg_Fcarc_TC.rep
0.00
0.02
0.04
0.06
0
2000
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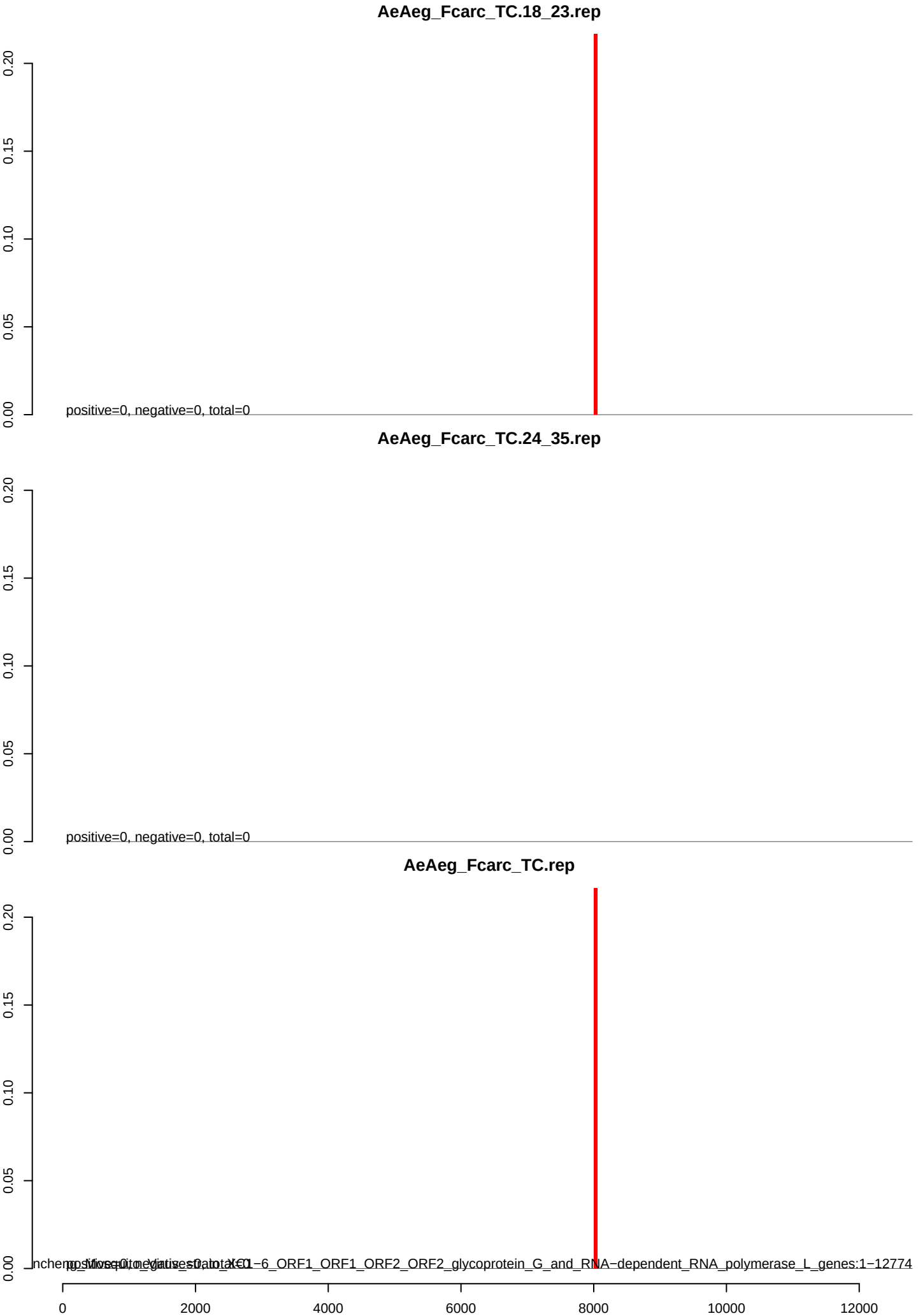
6000
8000
10000
12000
14000


AeAeg_Fcarc_TC.18_23.rep
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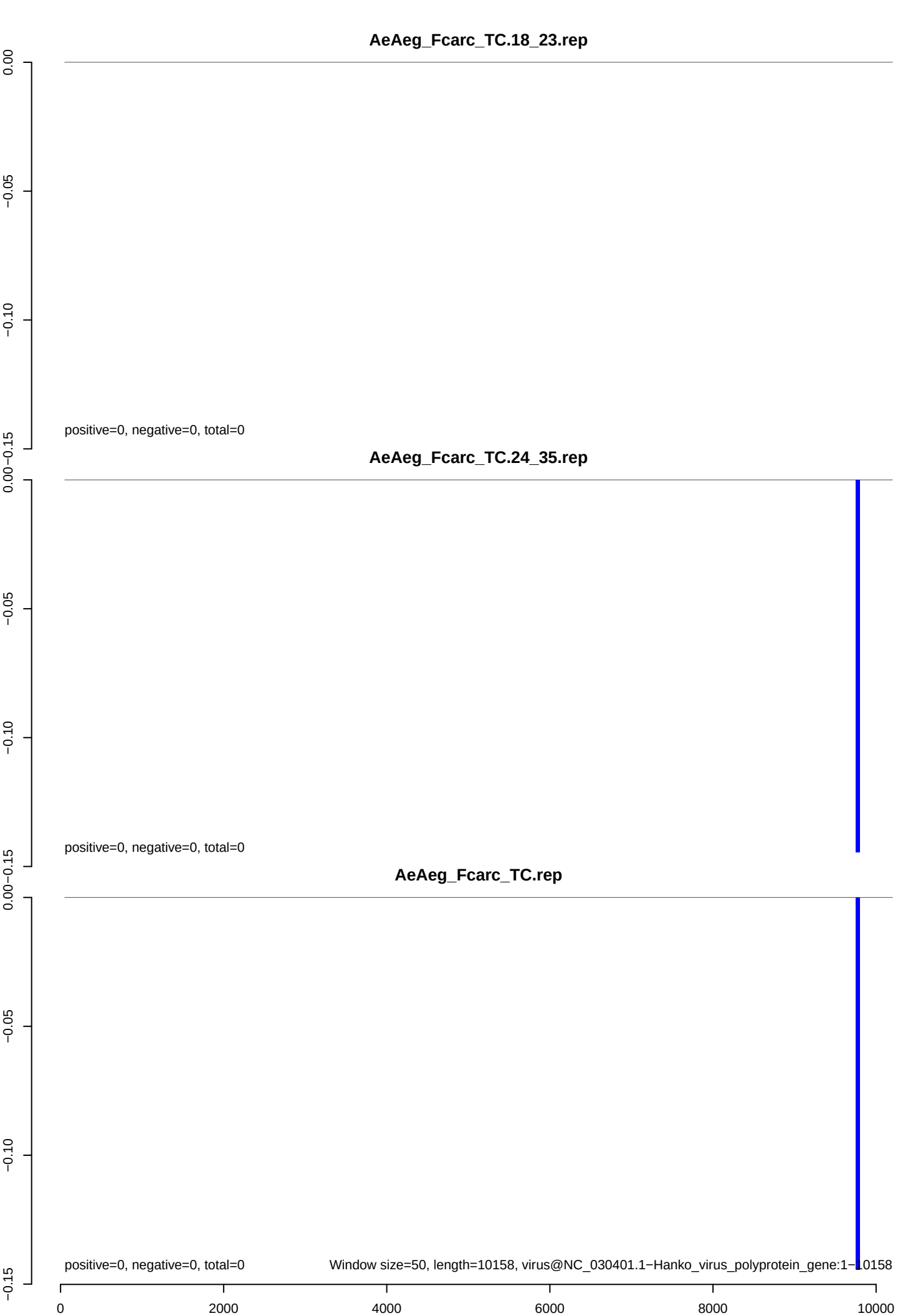
0.05
0.10
0.15
0.20
positive=0, negative=0, total=0
AeAeg_Fcarc_TC.24_35.rep
0.00
0.05
0.10
0.15
0.20
positive=0, negative=0, total=0
AeAeg_Fcarc_TC.rep
0.00
0.05
0.10
0.15
0.20
0
2000
4000
6000
8000
10000
12000


AeAeg_Fcarc_TC.18_23.rep
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−0.05
−0.10
−0.15
positive=0, negative=0, total=0
AeAeg_Fcarc_TC.24_35.rep
0.00
−0.05
−0.10
−0.15
positive=0, negative=0, total=0
AeAeg_Fcarc_TC.rep
0.00
−0.05
−0.10
−0.15
positive=0, negative=0, total=0
Window size=50, length=10158, virus@NC_030401.1−Hanko_virus_polyprotein_gene:1−10158
0
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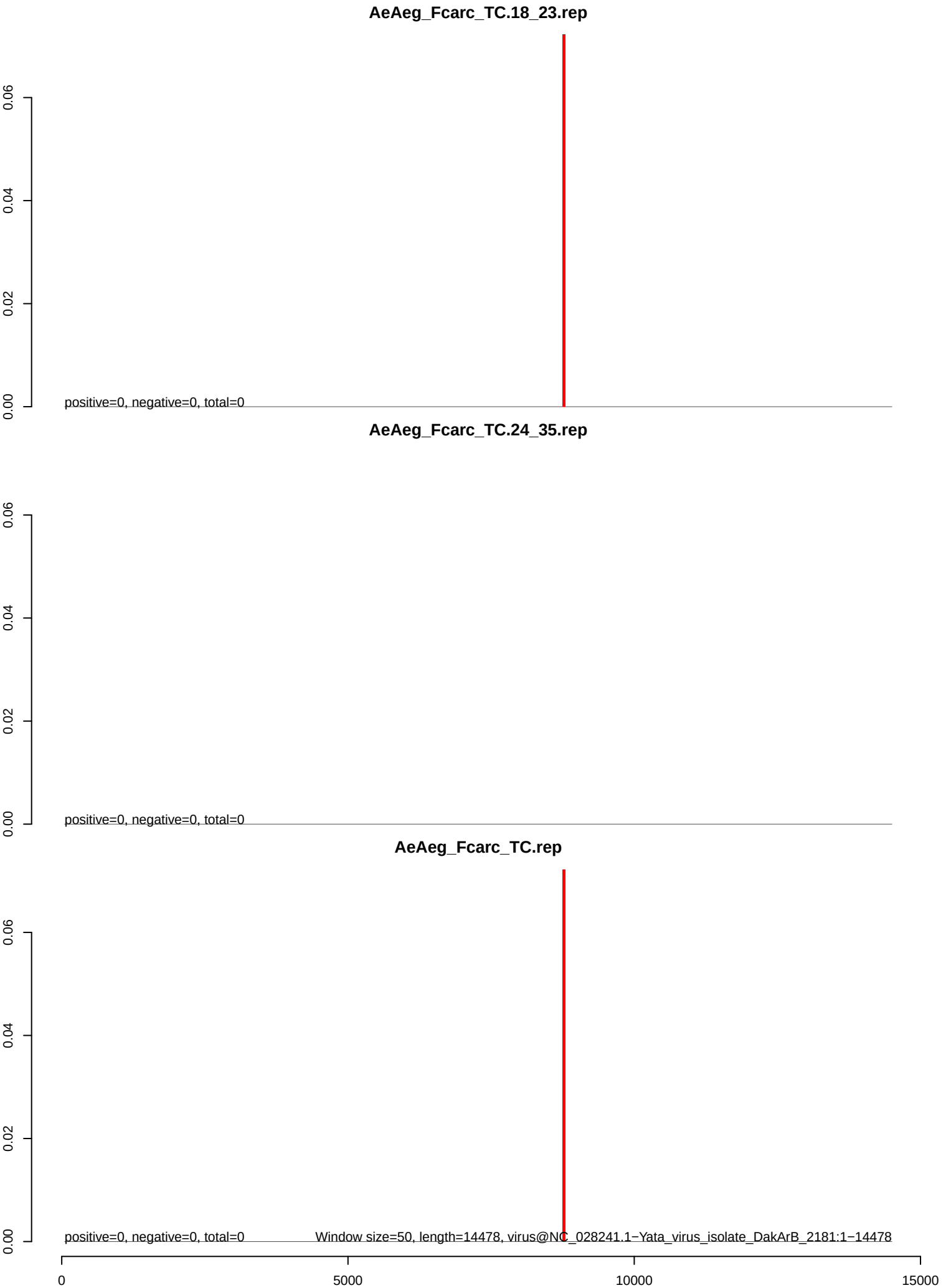
4000
6000
8000
10000


AeAeg_Fcarc_TC.18_23.rep
0.00
0.02
0.04
0.06
positive=0, negative=0, total=0
AeAeg_Fcarc_TC.24_35.rep
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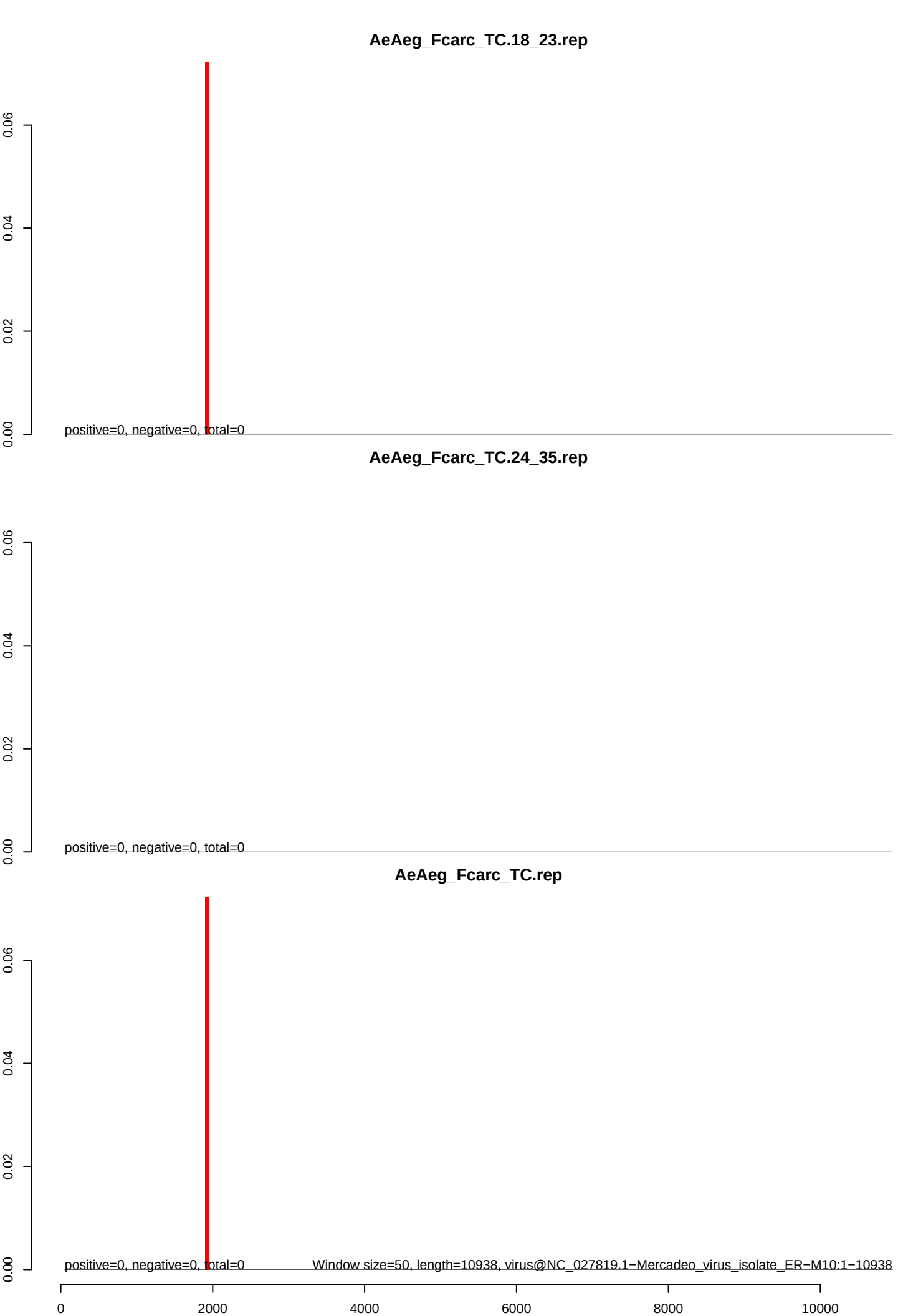
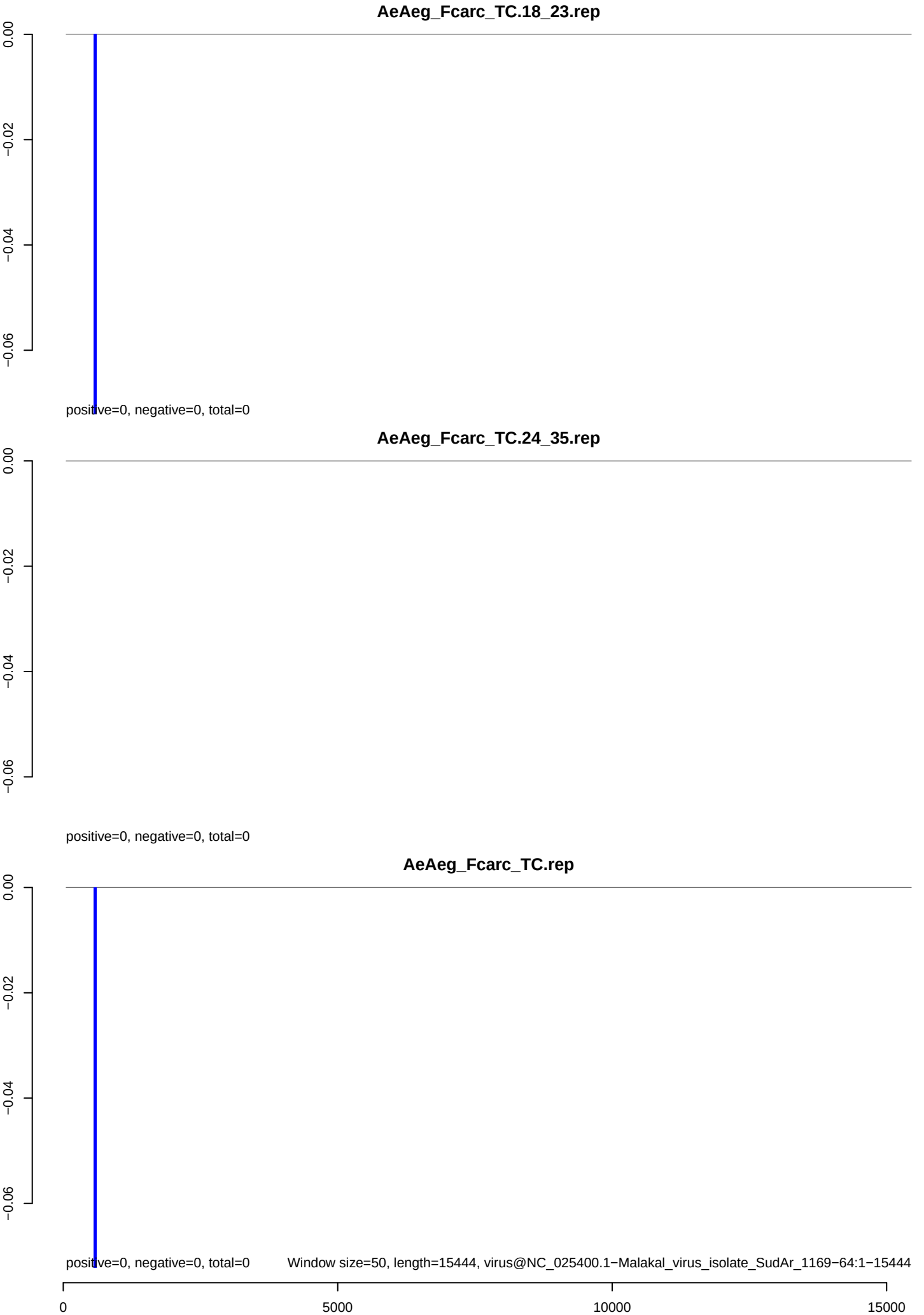
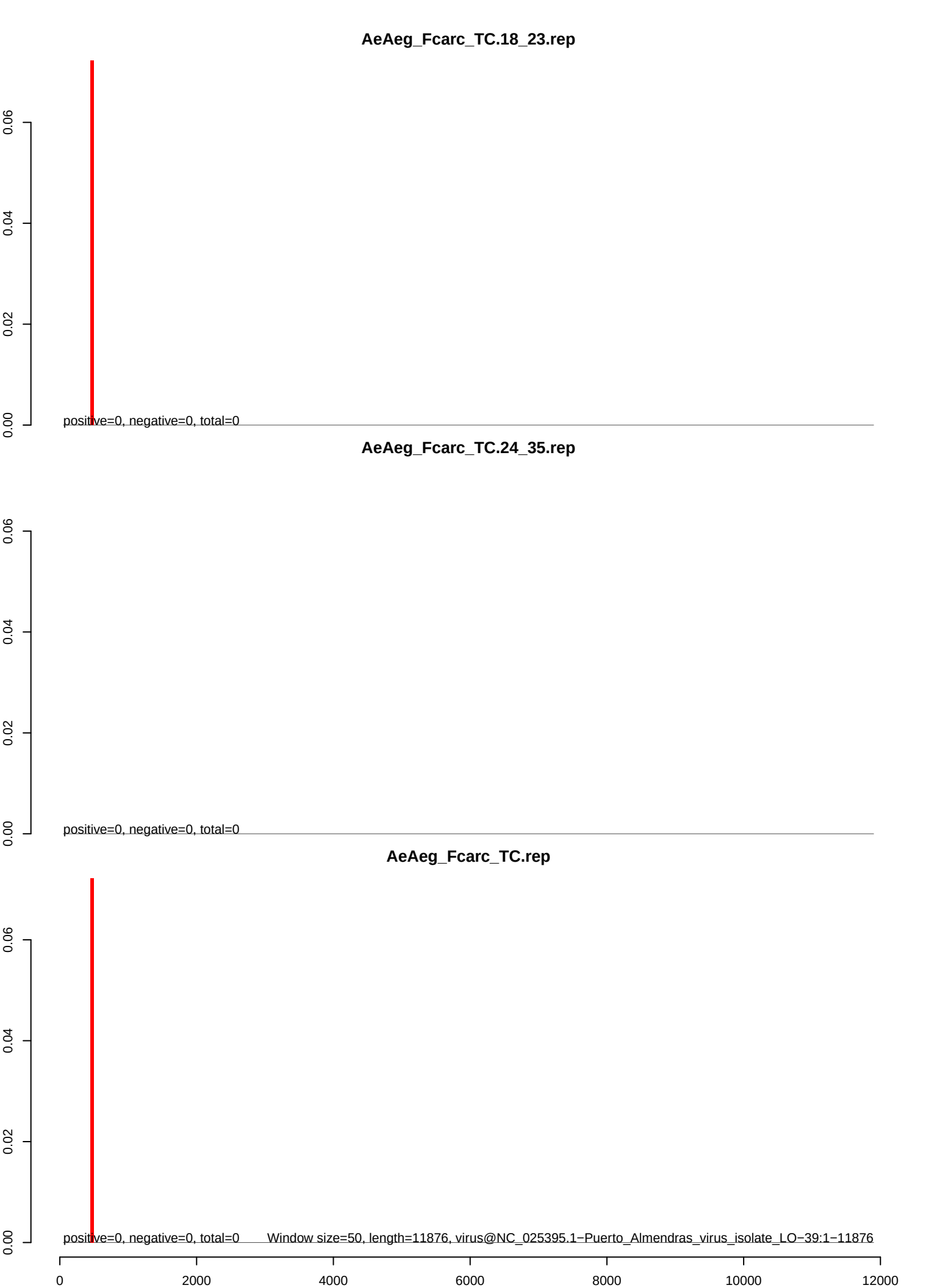
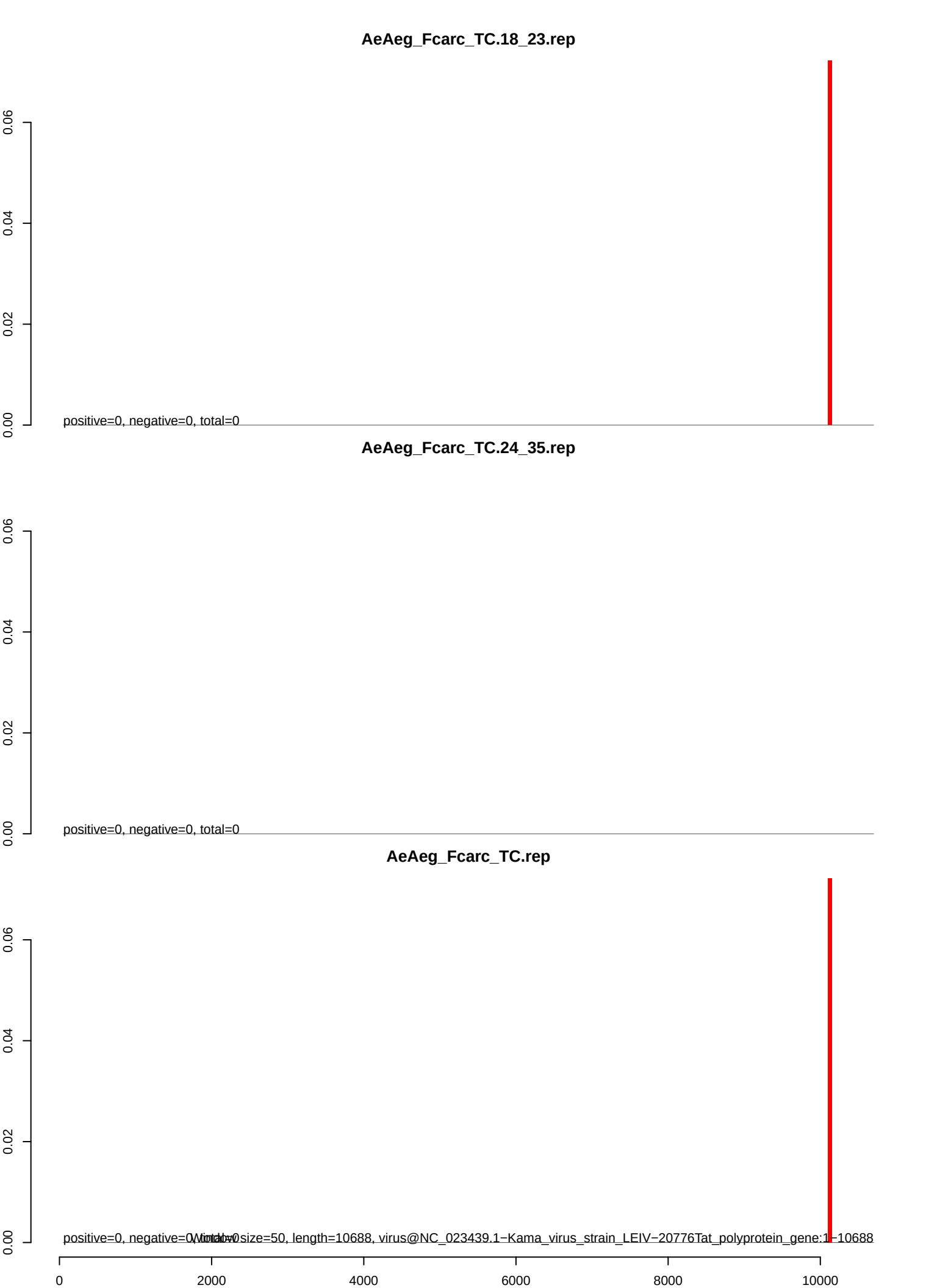
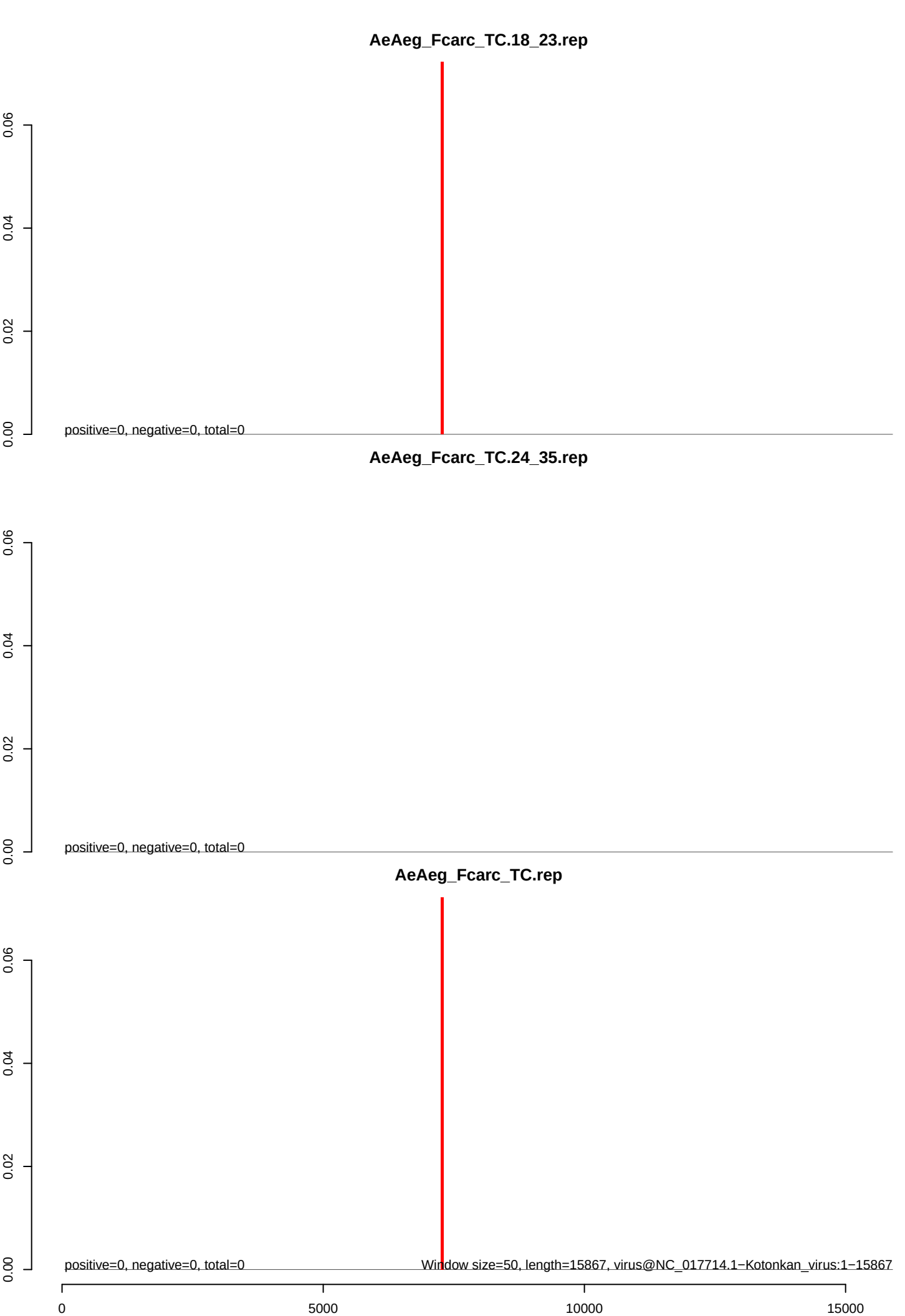
0.02
0.04
0.06
positive=0, negative=0, total=0
AeAeg_Fcarc_TC.rep
0.00
0.02
0.04
0.06
positive=0, negative=0, total=0
Window size=50, length=14478, virus@NC_028241.1−Yata_virus_isolate_DakArB_2181:1−14478
0
5000
10000
15000

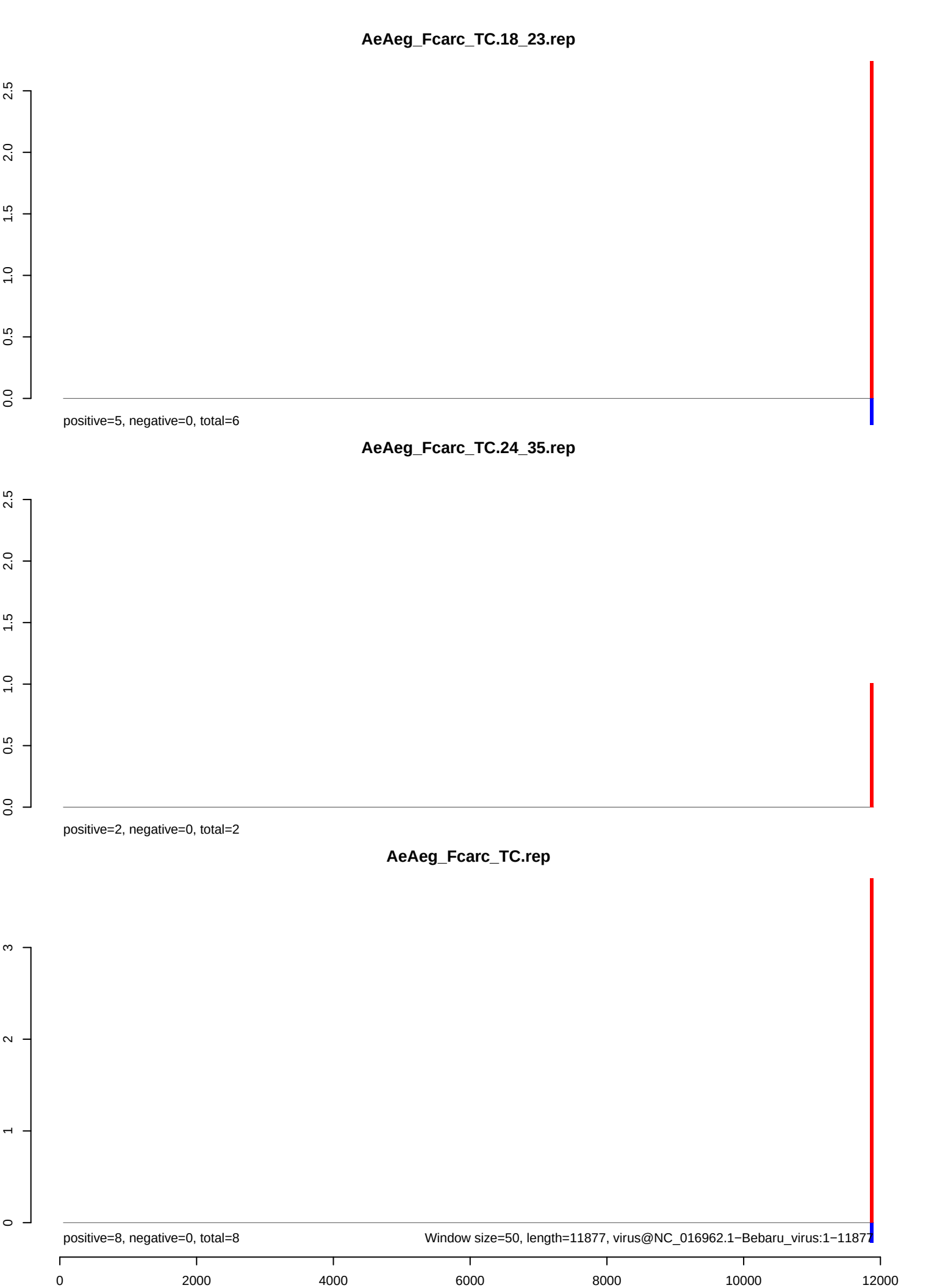

AeAeg_Fcarc_TC.18_23.rep
0.00
0.02
0.04
0.06
positive=0, negative=0, total=0
AeAeg_Fcarc_TC.24_35.rep
0.00
0.02
0.04
0.06
positive=0, negative=0, total=0
AeAeg_Fcarc_TC.rep
0.00
0.02
0.04
0.06
positive=0, negative=0, total=0
Window size=50, length=10938, virus@NC_027819.1−Mercadeo_virus_isolate_ER−M10:1−10938
0
2000
4000
6000
8000
10000

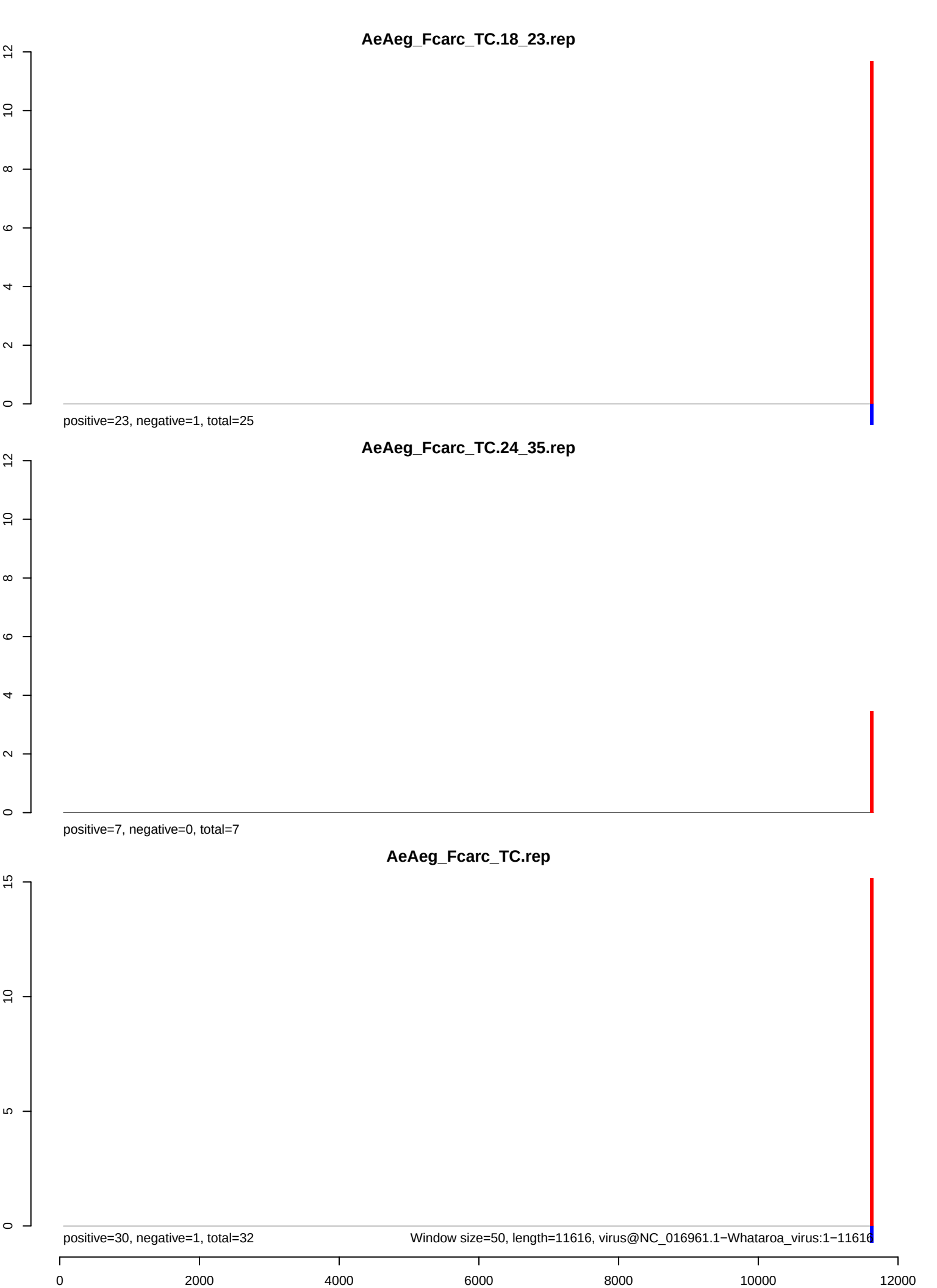

AeAeg_Fcarc_TC.18_23.rep
0.00
−0.02
−0.04
−0.06
positive=0, negative=0, total=0
AeAeg_Fcarc_TC.24_35.rep
0.00
−0.02
−0.04
−0.06
positive=0, negative=0, total=0
AeAeg_Fcarc_TC.rep
0.00
−0.02
−0.04
−0.06
positive=0, negative=0, total=0
Window size=50, length=15444, virus@NC_025400.1−Malakal_virus_isolate_SudAr_1169−64:1−15444
0
5000
10000
15000

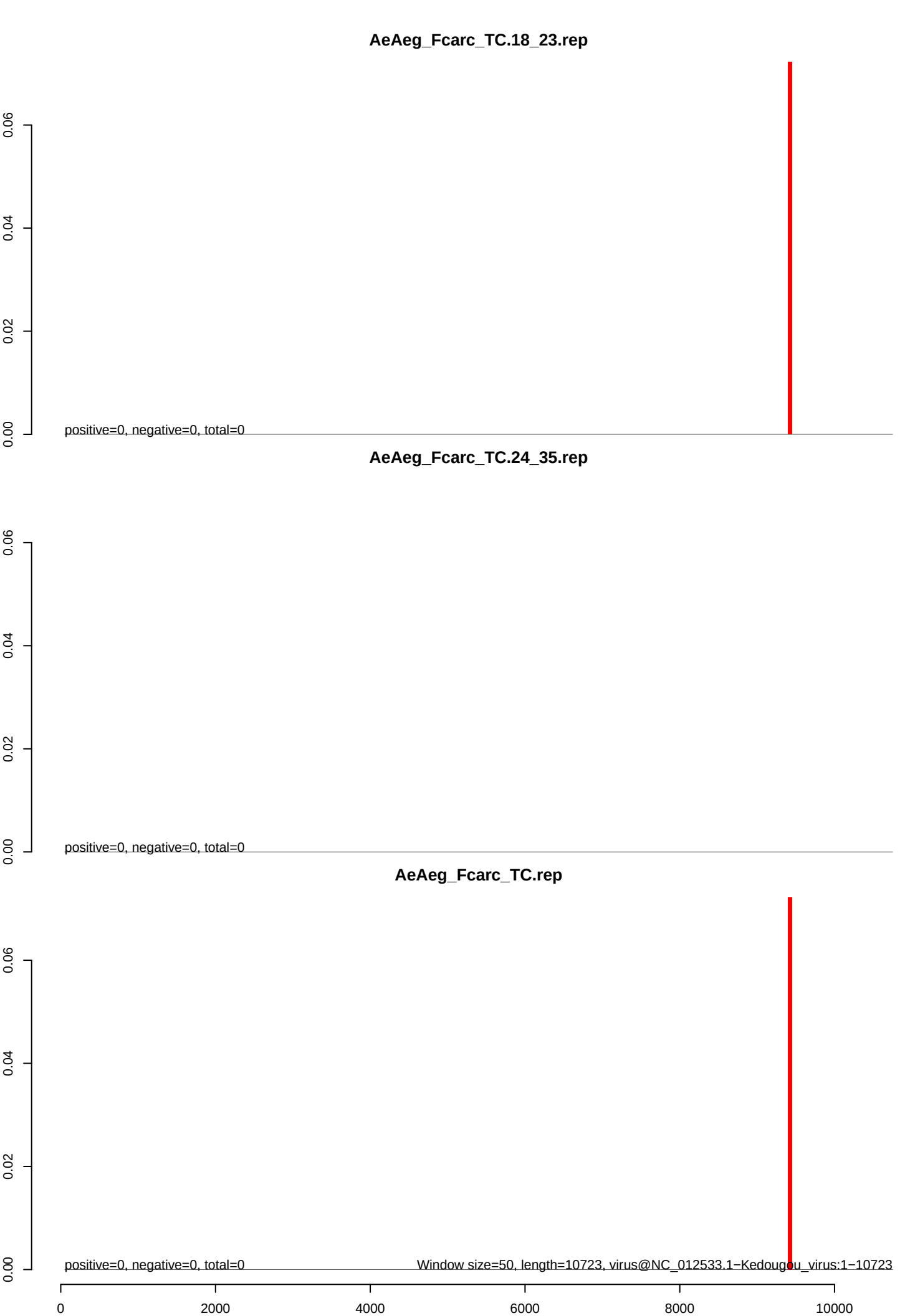

AeAeg_Fcarc_TC.18_23.rep
0.00
0.02
0.04
0.06
positive=0, negative=0, total=0
AeAeg_Fcarc_TC.24_35.rep
0.00
0.02
0.04
0.06
positive=0, negative=0, total=0
AeAeg_Fcarc_TC.rep
0.00
0.02
0.04
0.06
positive=0, negative=0, total=0
Window size=50, length=11876, virus@NC_025395.1−Puerto_Almendras_virus_isolate_LO−39:1−11876
0
2000
4000
6000
8000
10000
12000

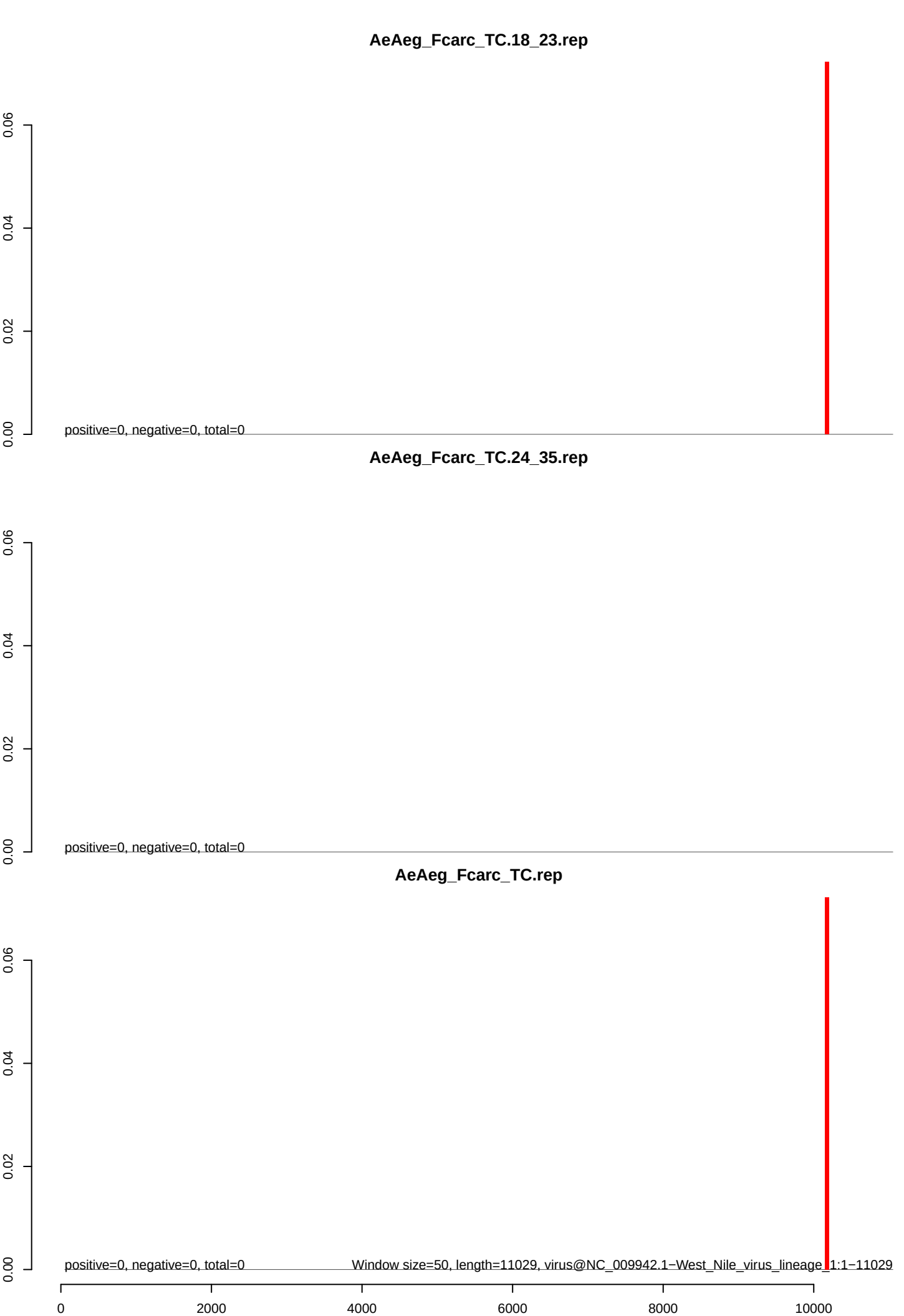

AeAeg_Fcarc_TC.18_23.rep
0.00
0.02
0.04
0.06
positive=0, negative=0, total=0
AeAeg_Fcarc_TC.24_35.rep
0.00
0.02
0.04
0.06
positive=0, negative=0, total=0
AeAeg_Fcarc_TC.rep
0.00
0.02
0.04
0.06
positive=0, negative=0, total=0
size=50, length=10688, virus@NC_023439.1−Kama_virus_strain_LEIV−20776Tat_polyprotein_gene:1−10688
0
2000
4000
6000
8000
10000

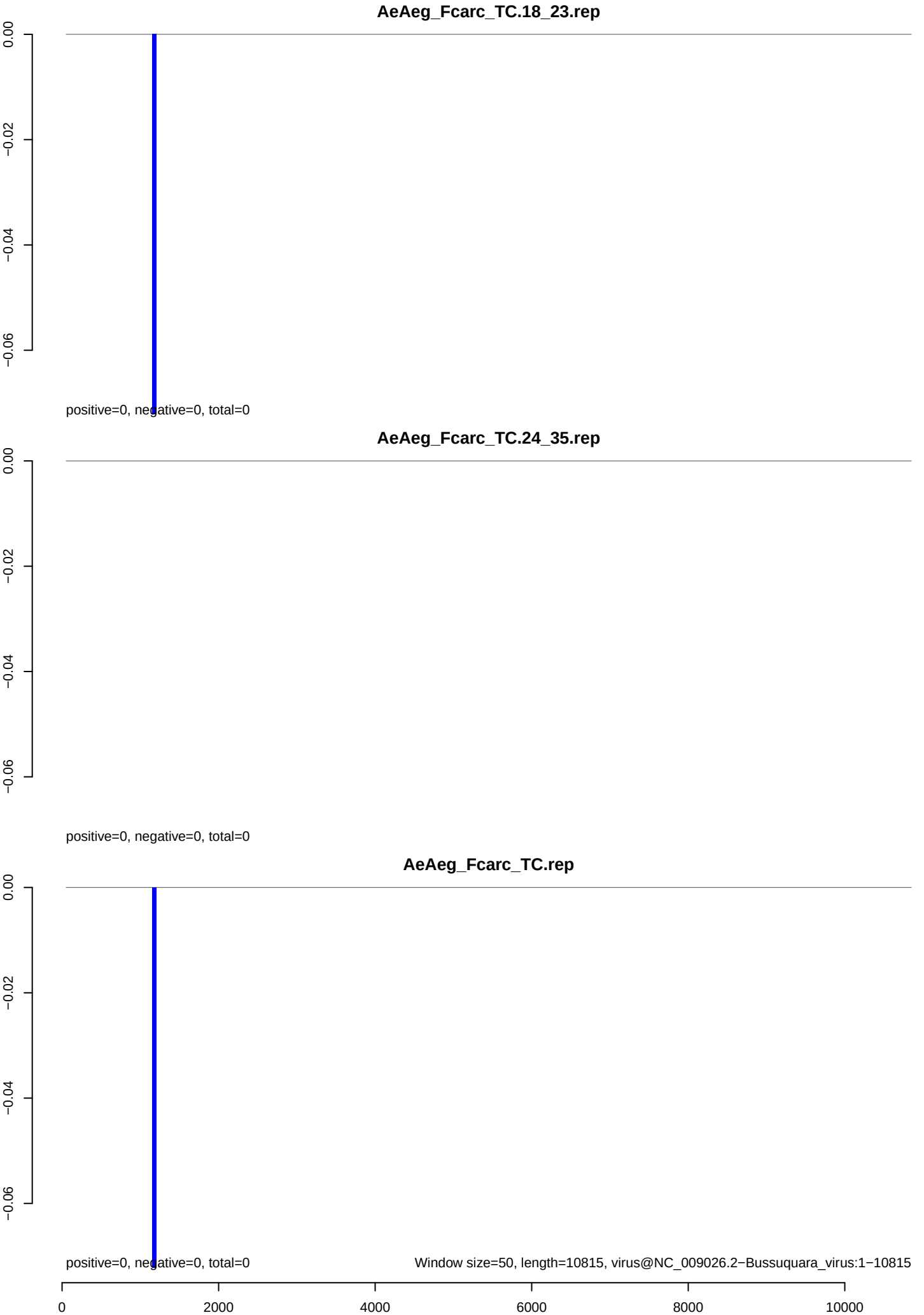

AeAeg_Fcarc_TC.18_23.rep
0.06
0.04
0.02
0.00
positive=0, negative=0, total=0
AeAeg_Fcarc_TC.24_35.rep
0.06
0.04
0.02
0.00
positive=0, negative=0, total=0
AeAeg_Fcarc_TC.rep
0.06
0.04
0.02
0.00
positive=0, negative=0, total=0
Window size=50, length=15867, virus@NC_017714.1−Kotonkan_virus:1−15867
0
5000
10000
15000


AeAeg_Fcarc_TC.18_23.rep
0.0
0.5
1.0
1.5
2.0
2.5
positive=5, negative=0, total=6
AeAeg_Fcarc_TC.24_35.rep
0.0
0.5
1.0
1.5
2.0
2.5
positive=2, negative=0, total=2
AeAeg_Fcarc_TC.rep
0
1
2
3
positive=8, negative=0, total=8
Window size=50, length=11877, virus@NC_016962.1−Bebaru_virus:1−11877
0
2000
4000
6000
8000
10000
12000


AeAeg_Fcarc_TC.18_23.rep
0
2
4
6
8
10
12
positive=23, negative=1, total=25
AeAeg_Fcarc_TC.24_35.rep
0
2
4
6
8
10
12
positive=7, negative=0, total=7
AeAeg_Fcarc_TC.rep
0
5
10
15
positive=30, negative=1, total=32
Window size=50, length=11616, virus@NC_016961.1−Whataroa_virus:1−11616
0
2000
4000
6000
8000
10000
12000


AeAeg_Fcarc_TC.18_23.rep
0.00
0.02
0.04
0.06
positive=0, negative=0, total=0
AeAeg_Fcarc_TC.24_35.rep
0.00
0.02
0.04
0.06
positive=0, negative=0, total=0
AeAeg_Fcarc_TC.rep
0.00
0.02
0.04
0.06
positive=0, negative=0, total=0
Window size=50, length=10723, virus@NC_012533.1−Kedougou_virus:1−10723
0
2000
4000
6000
8000
10000


AeAeg_Fcarc_TC.18_23.rep
0.00
0.02
0.04
0.06
positive=0, negative=0, total=0
AeAeg_Fcarc_TC.24_35.rep
0.00
0.02
0.04
0.06
positive=0, negative=0, total=0
AeAeg_Fcarc_TC.rep
0.00
0.02
0.04
0.06
positive=0, negative=0, total=0
Window size=50, length=11029, virus@NC_009942.1−West_Nile_virus_lineage_1:1−11029
0
2000
4000
6000
8000
10000


AeAeg_Fcarc_TC.18_23.rep
0.00
−0.02
−0.04
−0.06
positive=0, negative=0, total=0
AeAeg_Fcarc_TC.24_35.rep
0.00
−0.02
−0.04
−0.06
positive=0, negative=0, total=0
AeAeg_Fcarc_TC.rep
0.00
−0.02
−0.04
−0.06
positive=0, negative=0, total=0
Window size=50, length=10815, virus@NC_009026.2−Bussuquara_virus:1−10815
0
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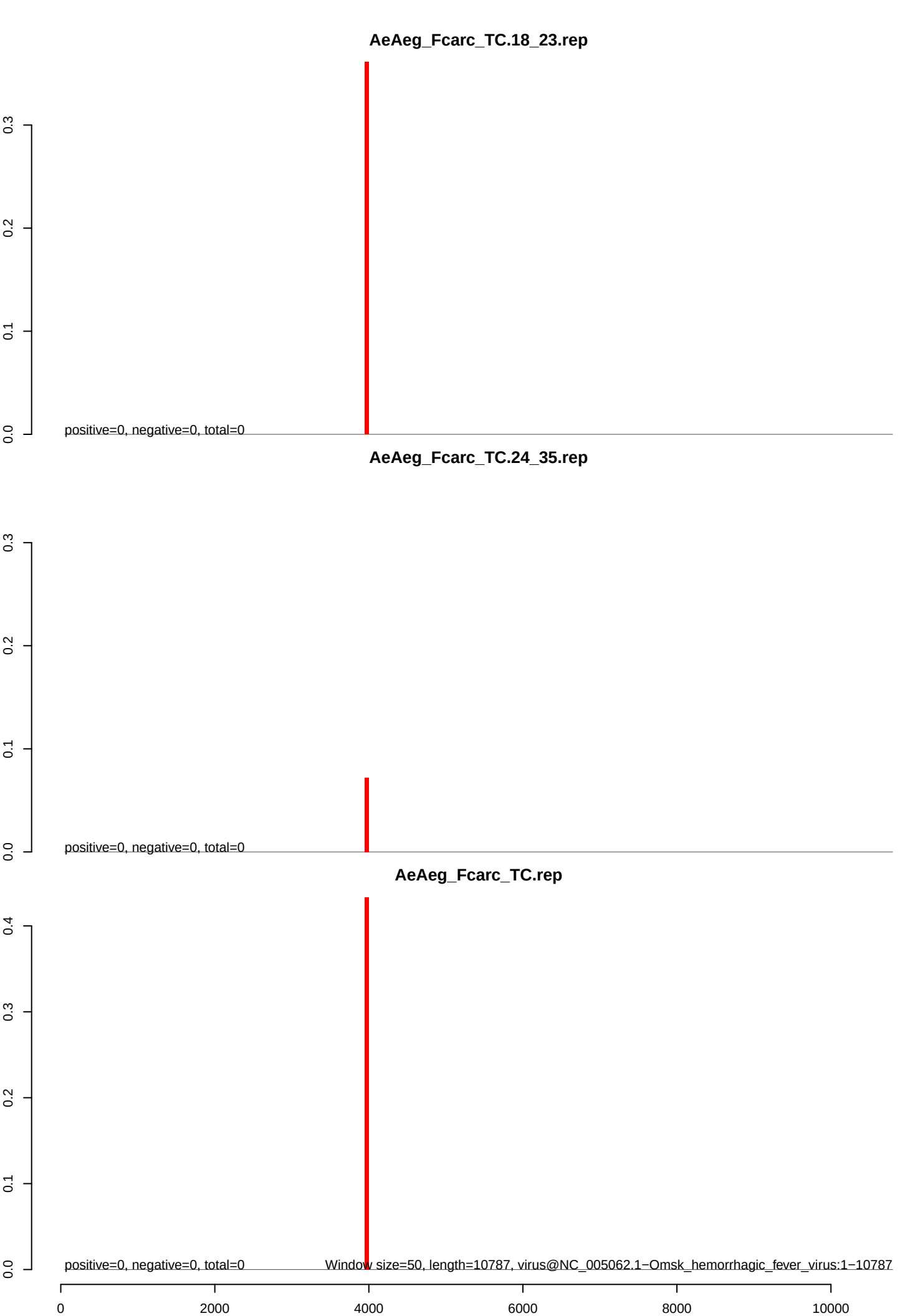
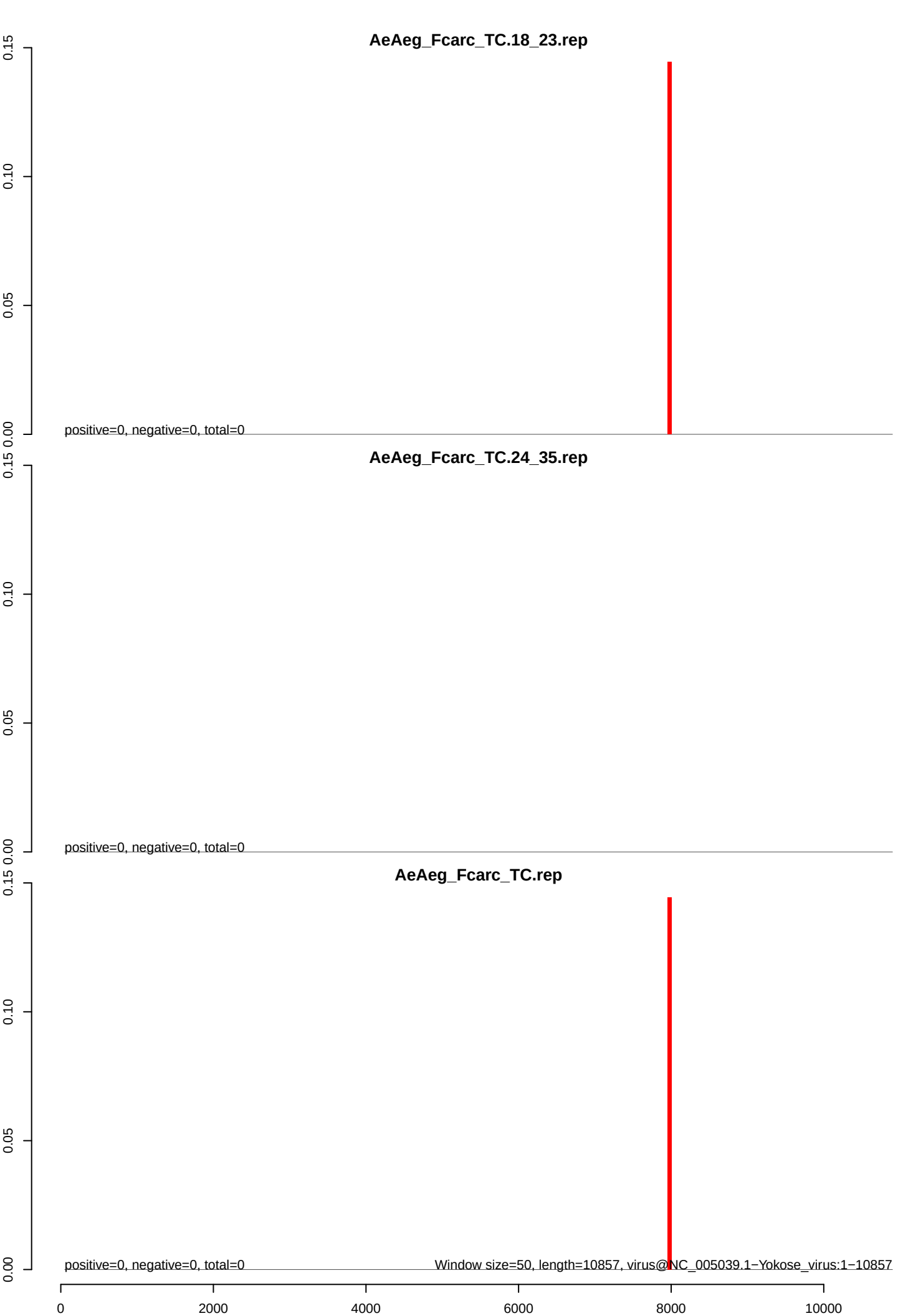
4000
6000
8000
10000


AeAeg_Fcarc_TC.18_23.rep
0.0
0.1
0.2
0.3
positive=0, negative=0, total=0
AeAeg_Fcarc_TC.24_35.rep
0.0
0.1
0.2
0.3
positive=0, negative=0, total=0
AeAeg_Fcarc_TC.rep
0.0
0.1
0.2
0.3
0.4
positive=0, negative=0, total=0
Window size=50, length=10787, virus@NC_005062.1−Omsk_hemorrhagic_fever_virus:1−10787
0
2000
4000
6000
8000
10000


AeAeg_Fcarc_TC.18_23.rep
0.15
0.10
0.05
0.00
positive=0, negative=0, total=0
AeAeg_Fcarc_TC.24_35.rep
0.15
0.10
0.05
0.00
positive=0, negative=0, total=0
AeAeg_Fcarc_TC.rep
0.15
0.10
0.05
0.00
positive=0, negative=0, total=0
Window size=50, length=10857, virus@NC_005039.1−Yokose_virus:1−10857
0
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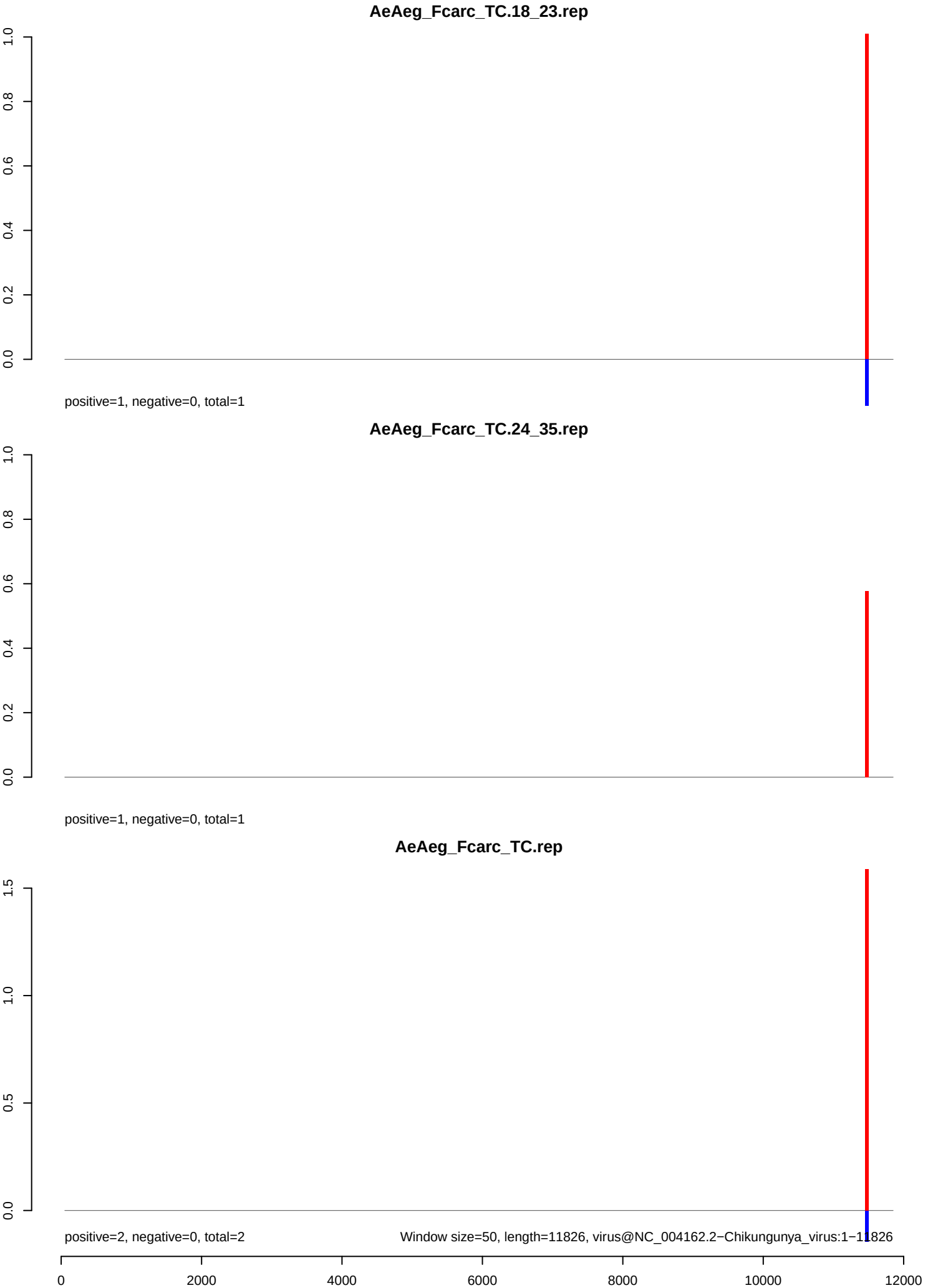
4000
6000
8000
10000


AeAeg_Fcarc_TC.18_23.rep
1.0
0.8
0.6
0.4
0.2
0.0
positive=1, negative=0, total=1
AeAeg_Fcarc_TC.24_35.rep
1.0
0.8
0.6
0.4
0.2
0.0
positive=1, negative=0, total=1
AeAeg_Fcarc_TC.rep
1.5
1.0
0.5
0.0
positive=2, negative=0, total=2
Window size=50, length=11826, virus@NC_004162.2−Chikungunya_virus:1−11826
0
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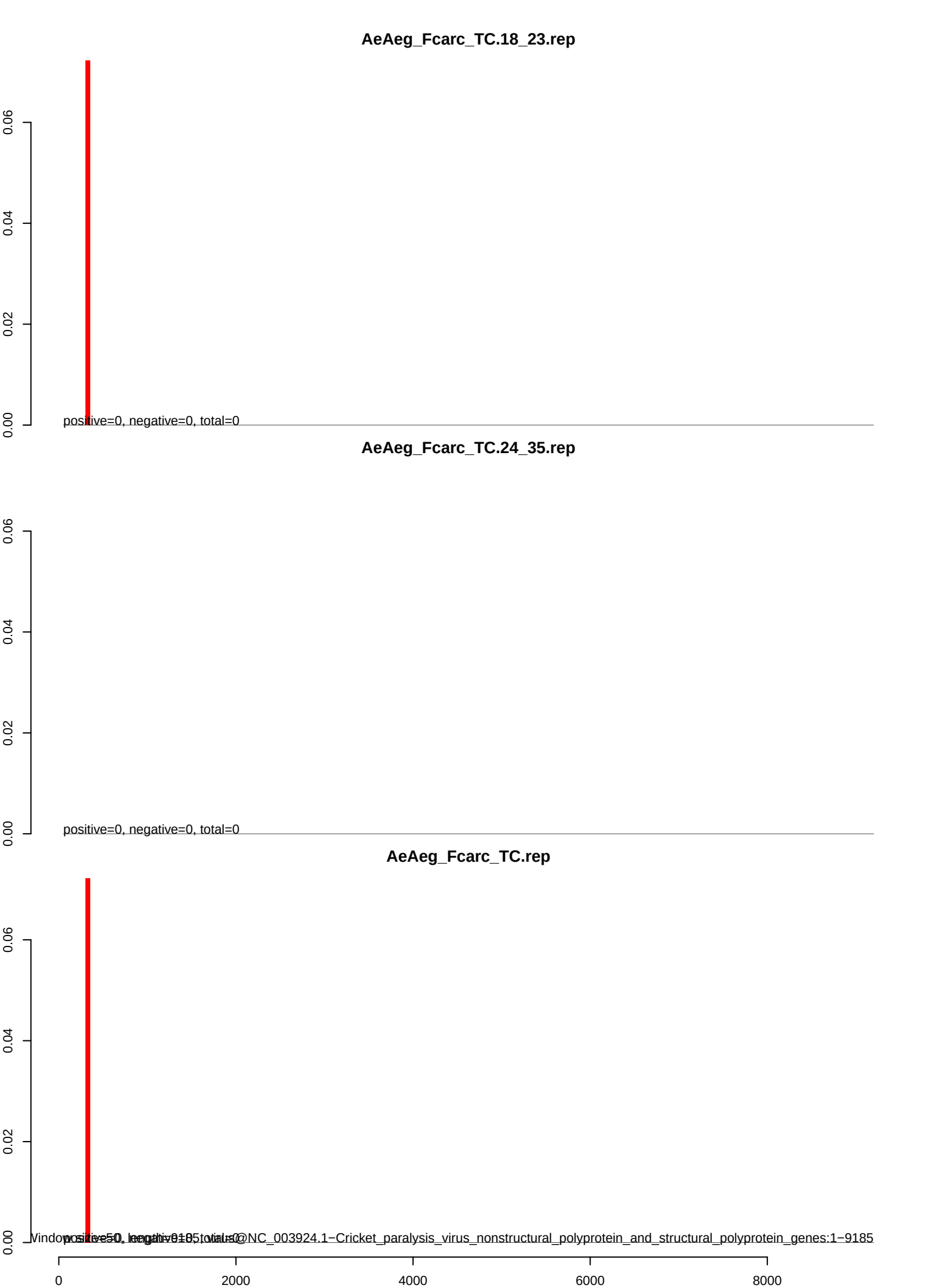
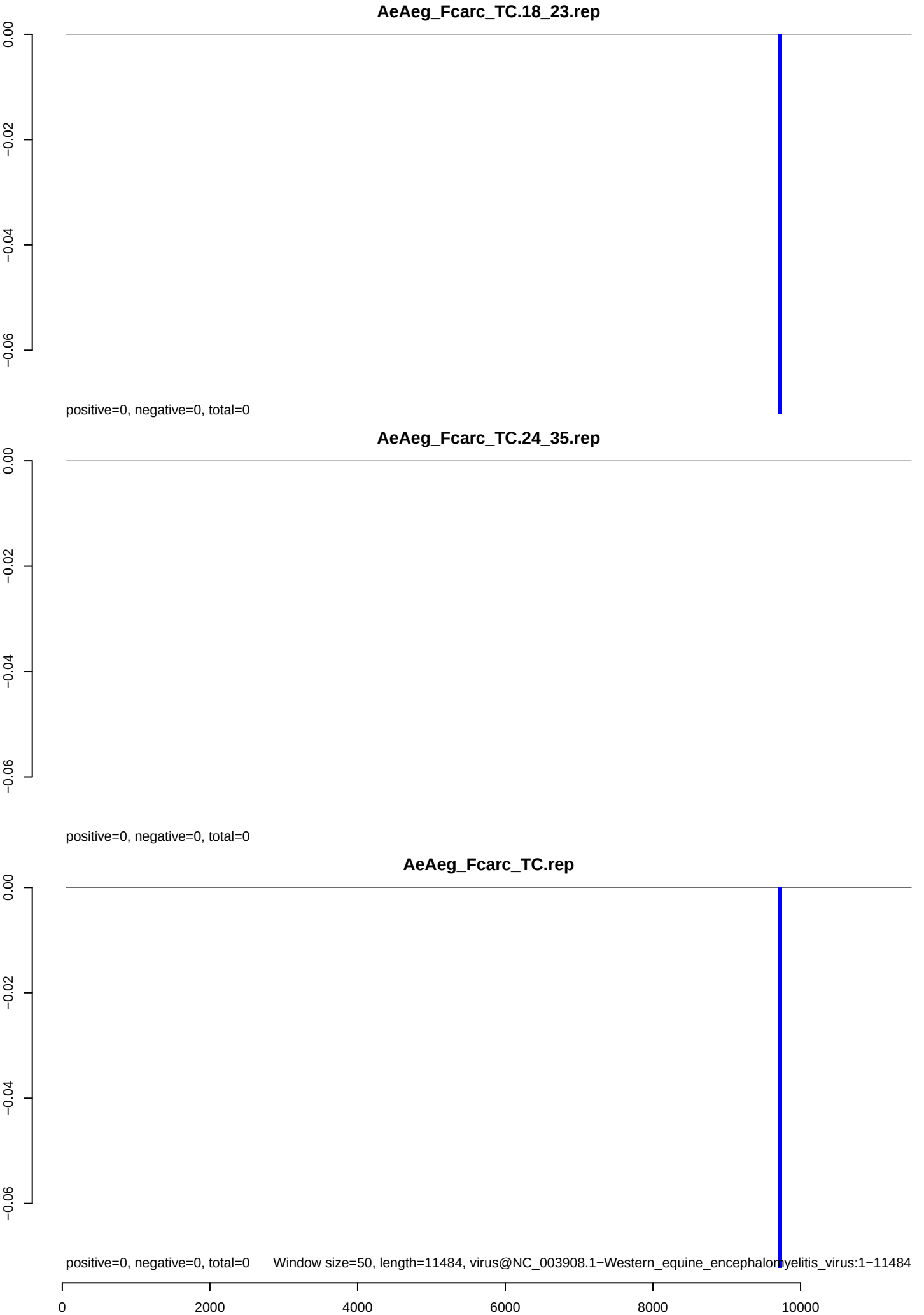
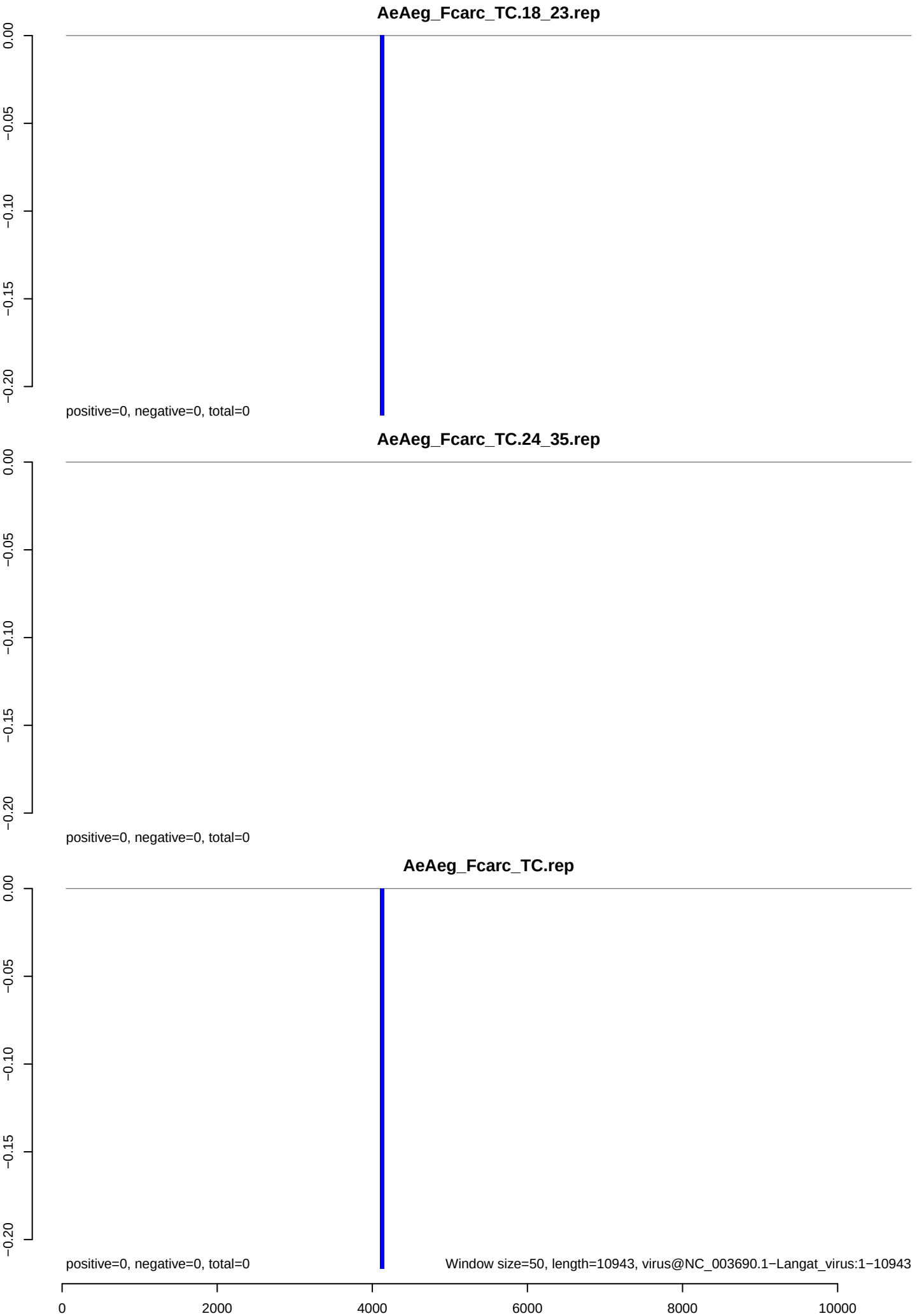
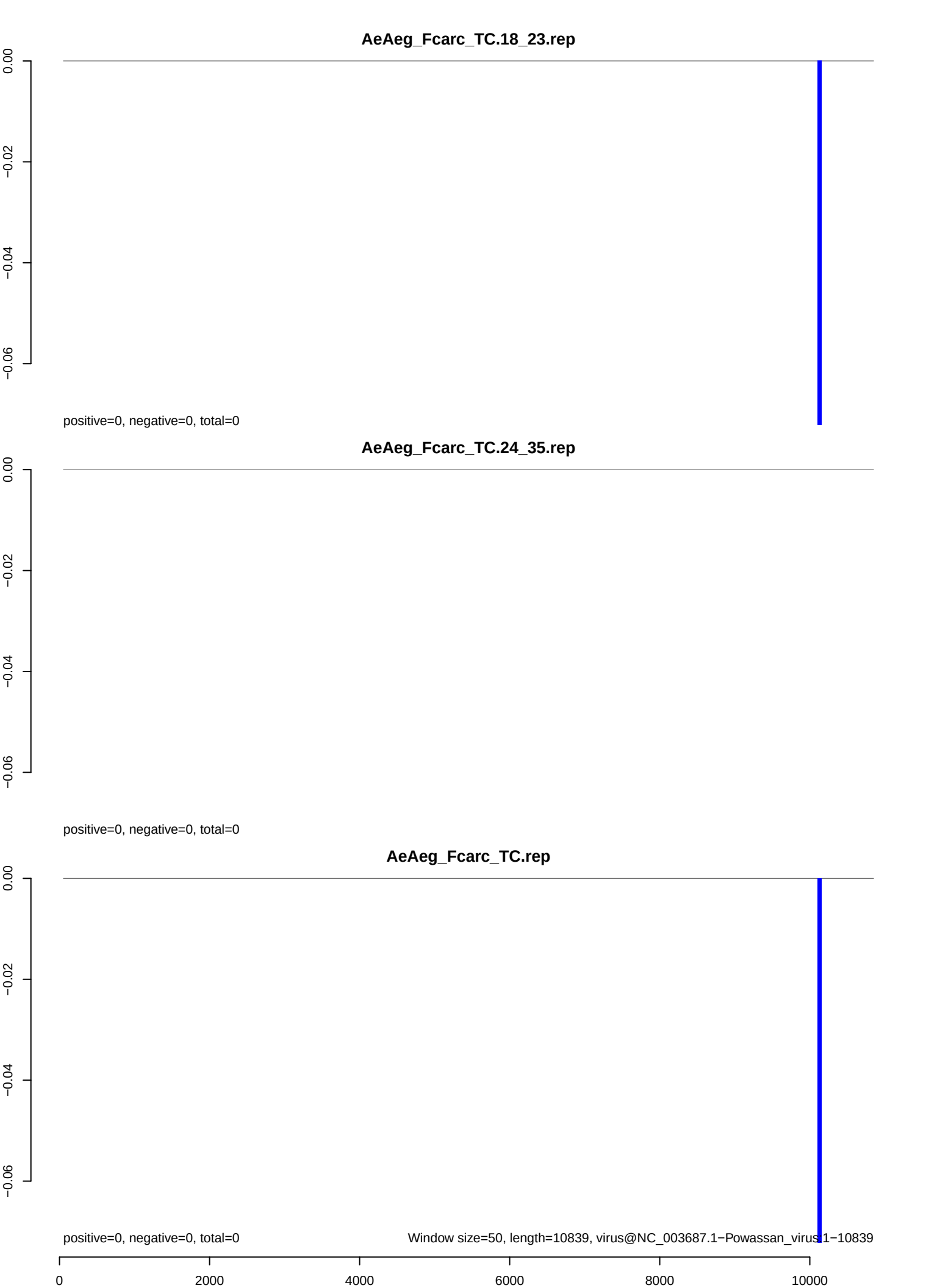
4000
6000
8000
10000
12000


AeAeg_Fcarc_TC.18_23.rep
0.00
0.02
0.04
0.06
positive=0, negative=0, total=0
AeAeg_Fcarc_TC.24_35.rep
0.00
0.02
0.04
0.06
positive=0, negative=0, total=0
AeAeg_Fcarc_TC.rep
0.00
0.02
0.04
0.06
Vindow positive=50, length=9185, total=0@NC_003924.1−Cricket_paralysis_virus_nonstructural_polyprotein_and_structural_polyprotein_genes:1−9185
0
2000
4000
6000
8000


AeAeg_Fcarc_TC.18_23.rep
0.00
−0.02
−0.04
−0.06
positive=0, negative=0, total=0
AeAeg_Fcarc_TC.24_35.rep
0.00
−0.02
−0.04
−0.06
positive=0, negative=0, total=0
AeAeg_Fcarc_TC.rep
0.00
−0.02
−0.04
−0.06
positive=0, negative=0, total=0
Window size=50, length=11484, virus@NC_003908.1−Western_equine_encephalomyelitis_virus:1−11484
0
2000
4000
6000
8000
10000


AeAeg_Fcarc_TC.18_23.rep
0.00
−0.05
−0.10
−0.15
−0.20
positive=0, negative=0, total=0
AeAeg_Fcarc_TC.24_35.rep
0.00
−0.05
−0.10
−0.15
−0.20
positive=0, negative=0, total=0
AeAeg_Fcarc_TC.rep
0.00
−0.05
−0.10
−0.15
−0.20
positive=0, negative=0, total=0
Window size=50, length=10943, virus@NC_003690.1−Langat_virus:1−10943
0
2000
4000
6000
8000
10000


AeAeg_Fcarc_TC.18_23.rep
0.00
−0.02
−0.04
−0.06
positive=0, negative=0, total=0
AeAeg_Fcarc_TC.24_35.rep
0.00
−0.02
−0.04
−0.06
positive=0, negative=0, total=0
AeAeg_Fcarc_TC.rep
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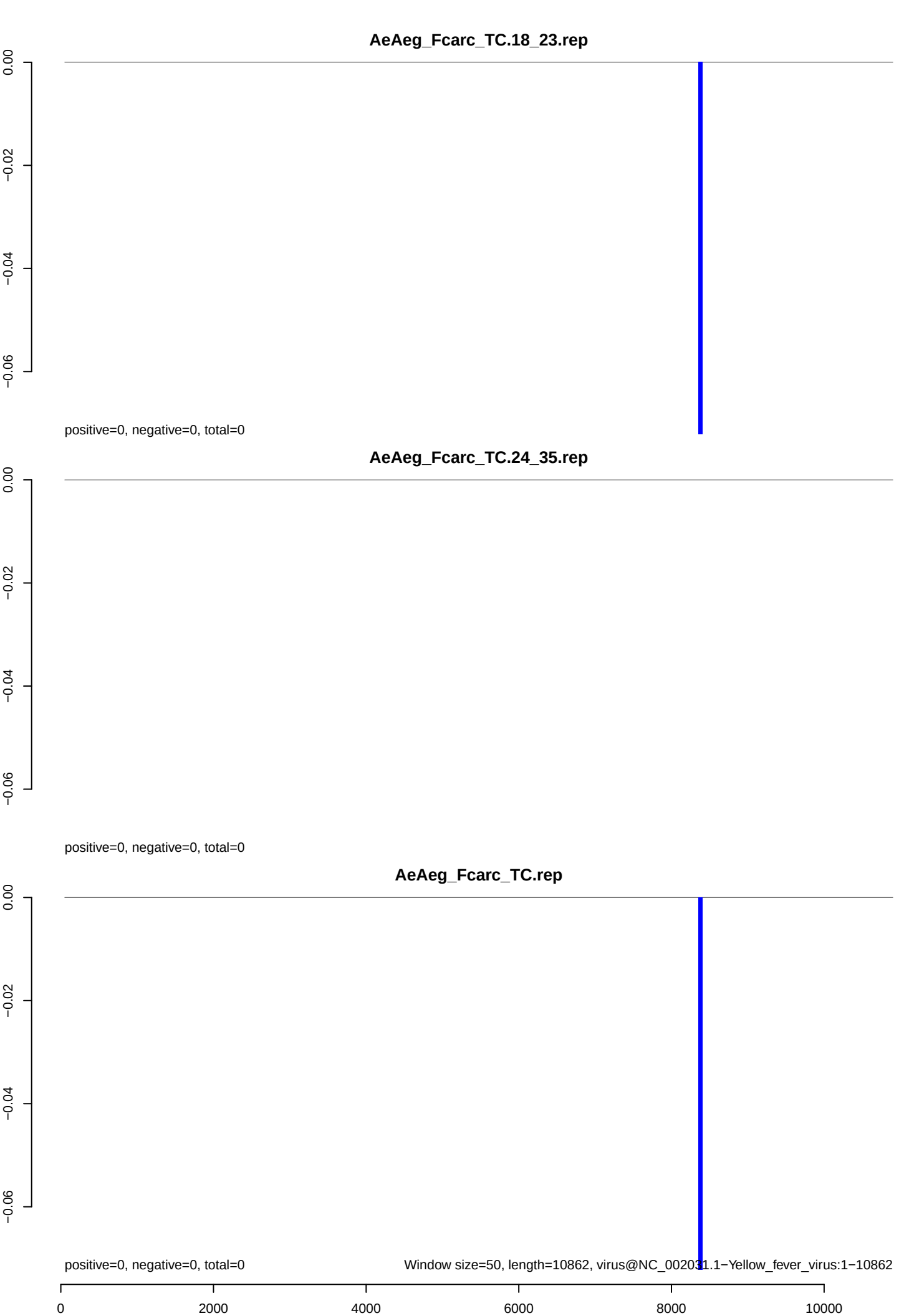
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positive=0, negative=0, total=0
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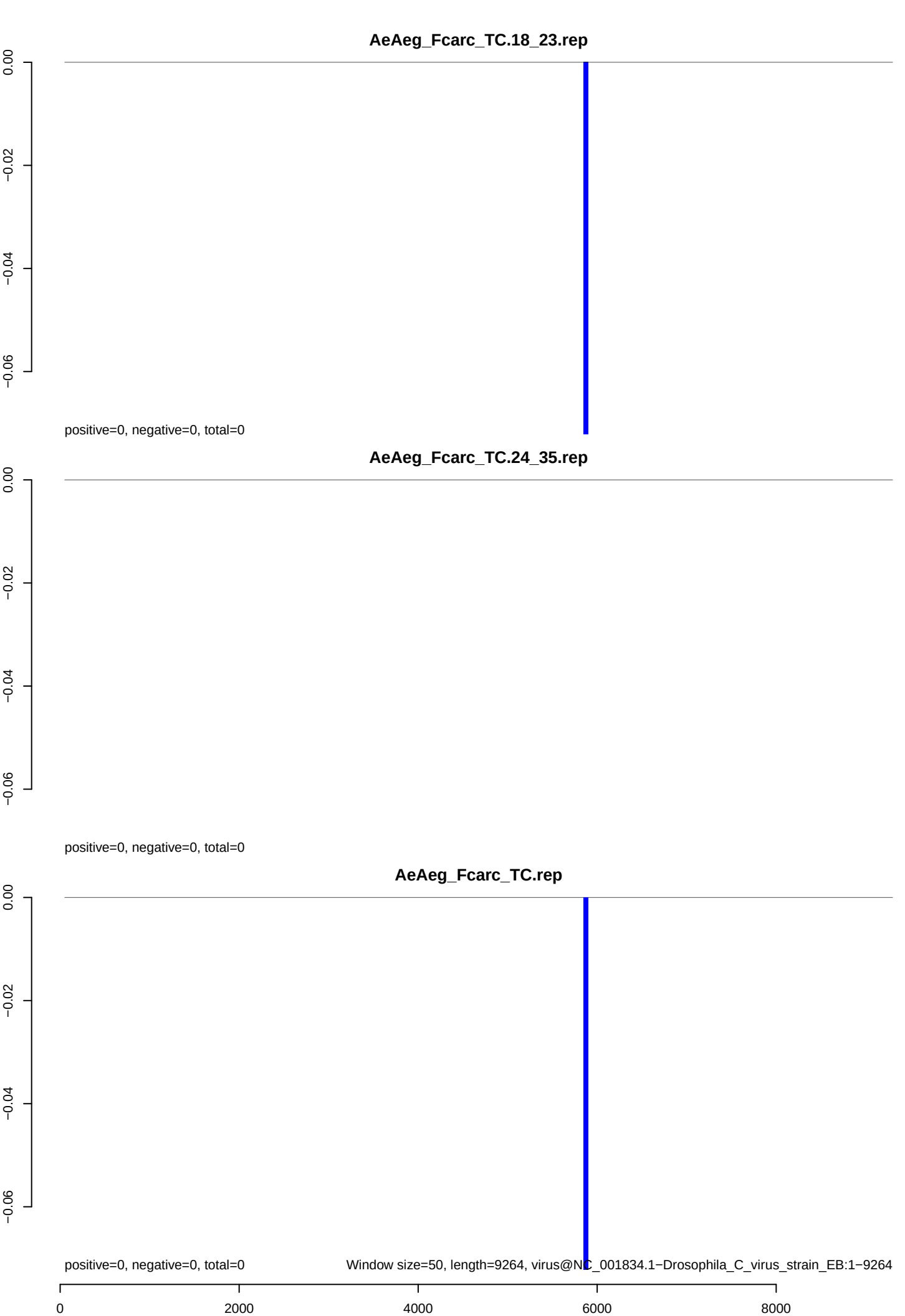
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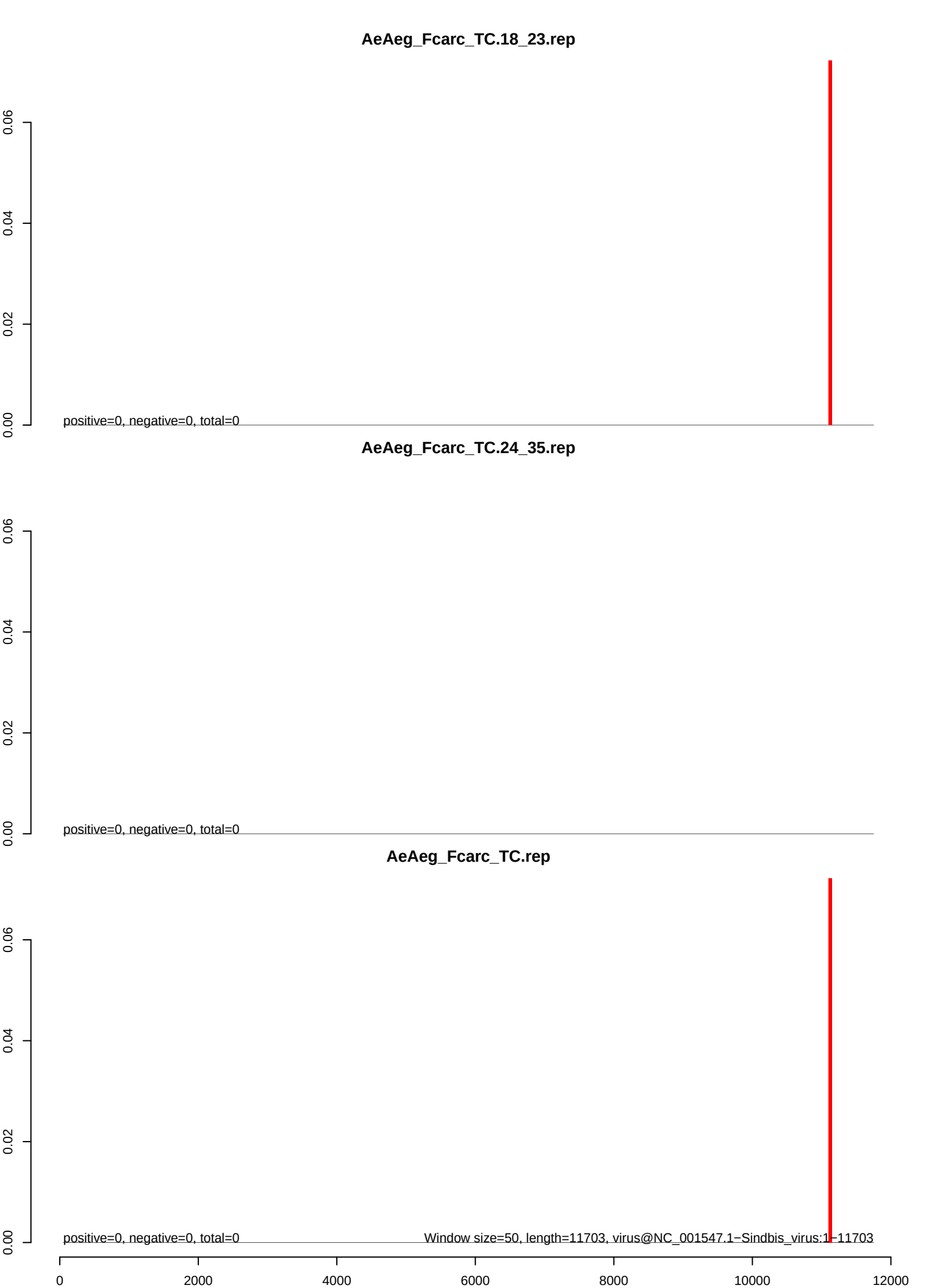
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positive=0, negative=0, total=0
AeAeg_Fcarc_TC.24_35.rep
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positive=0, negative=0, total=0
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positive=0, negative=0, total=0
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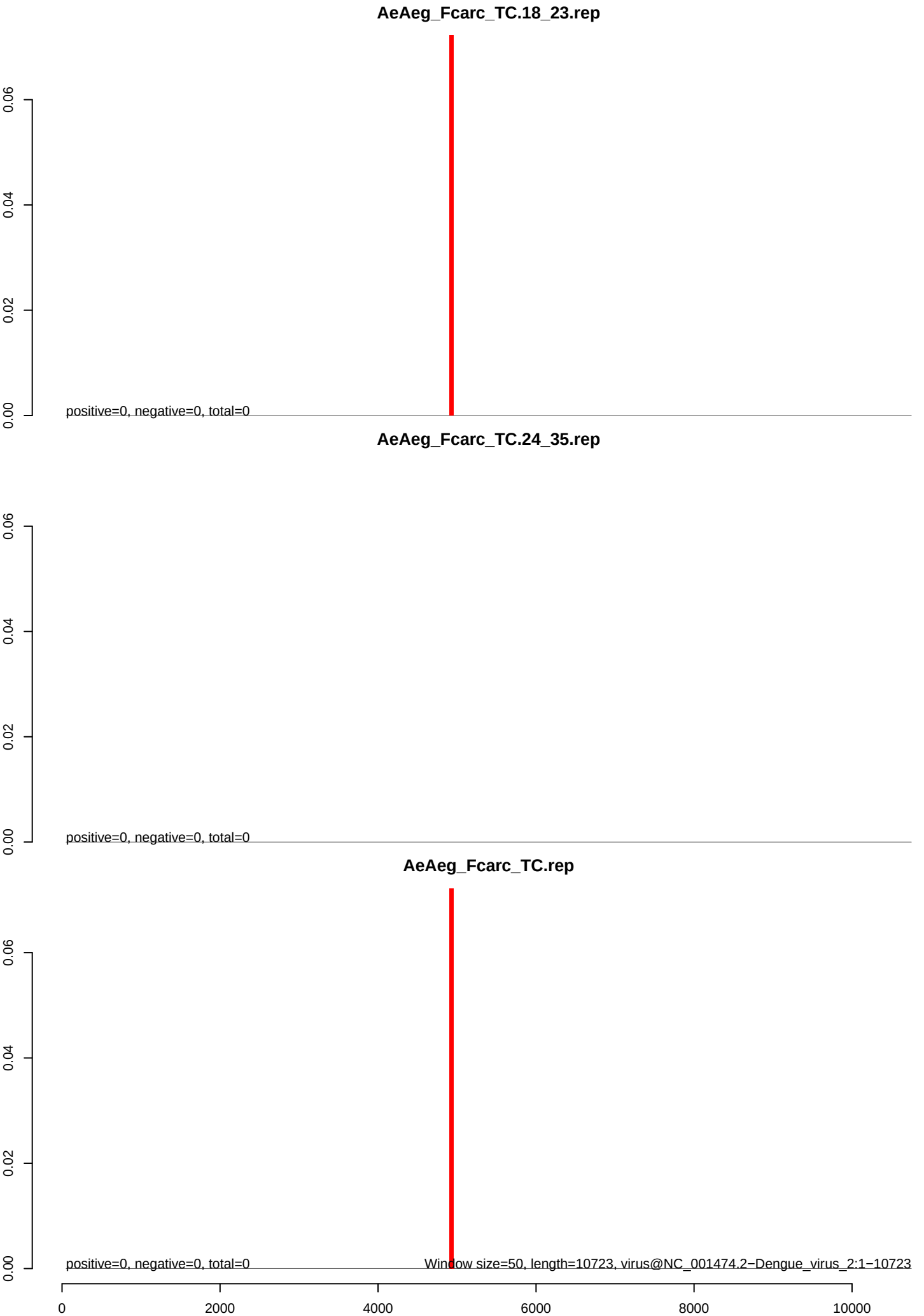
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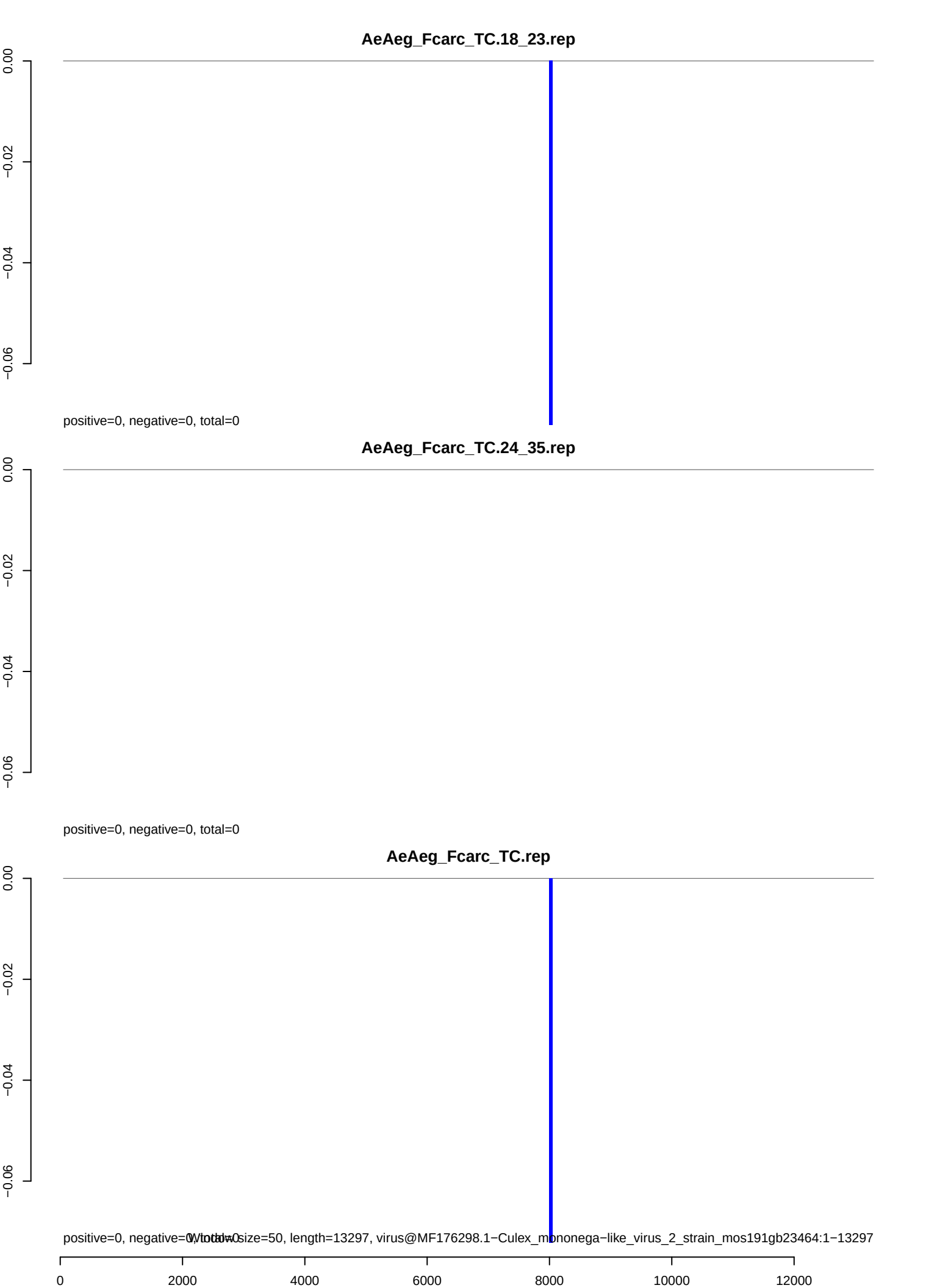
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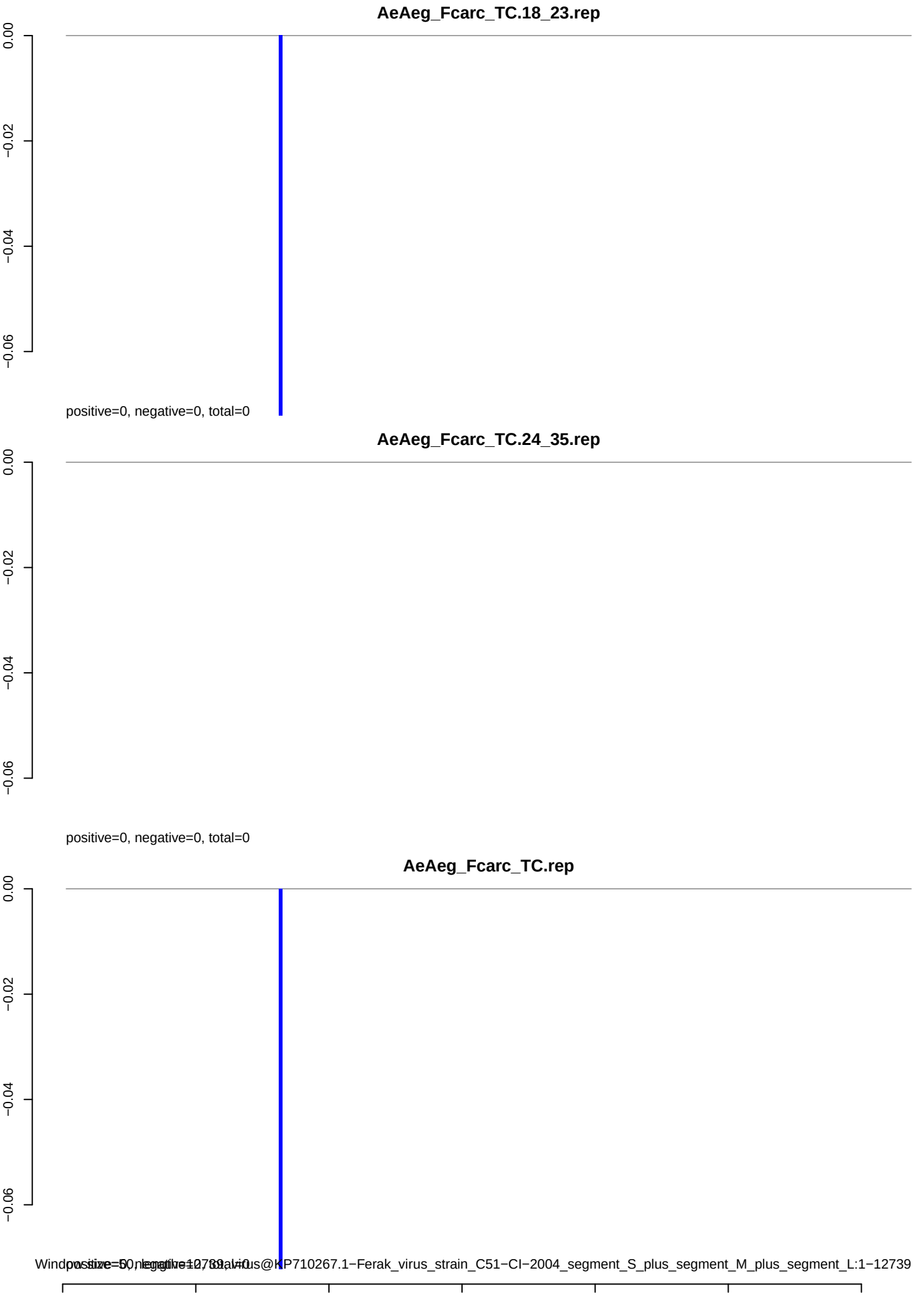
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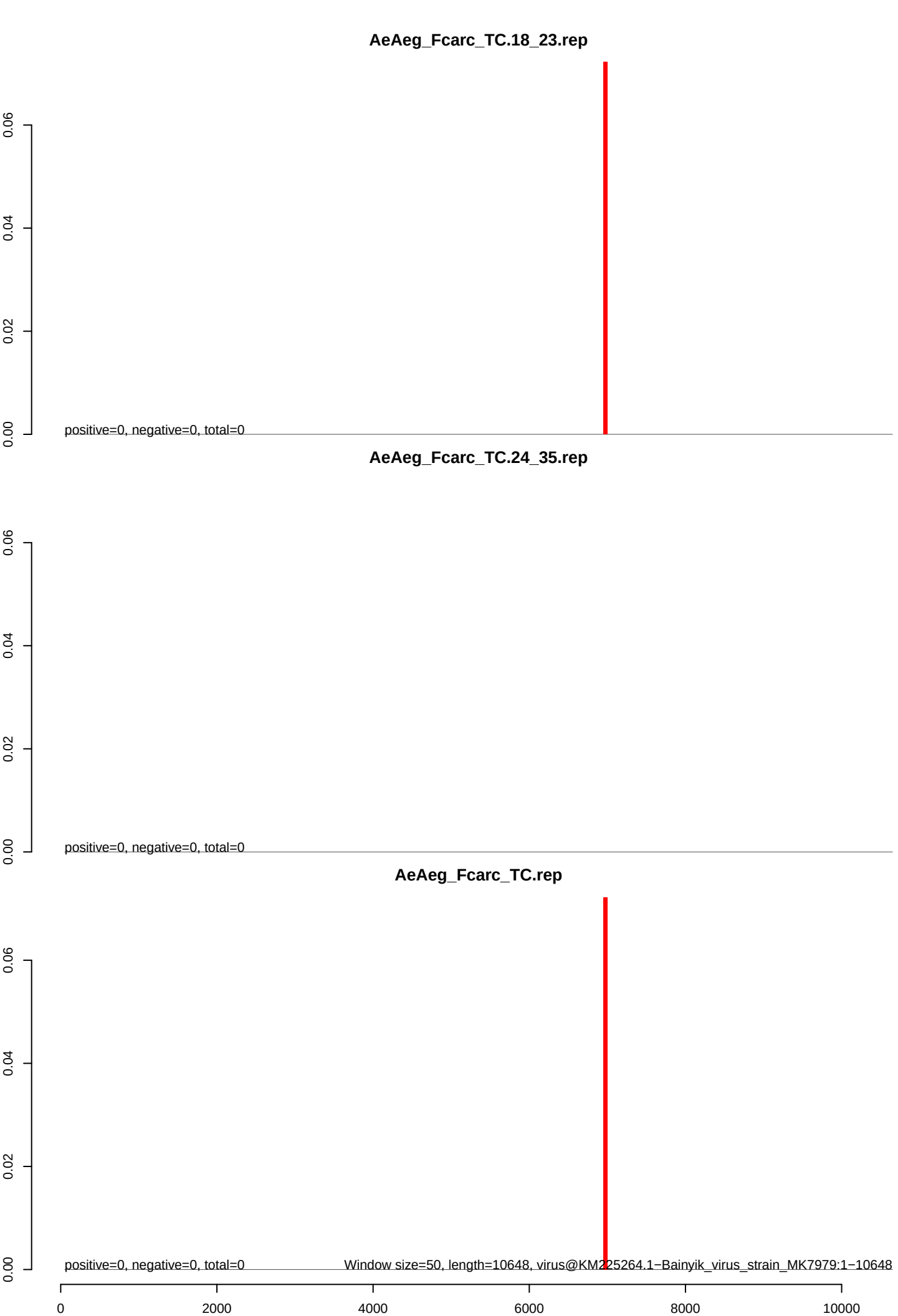
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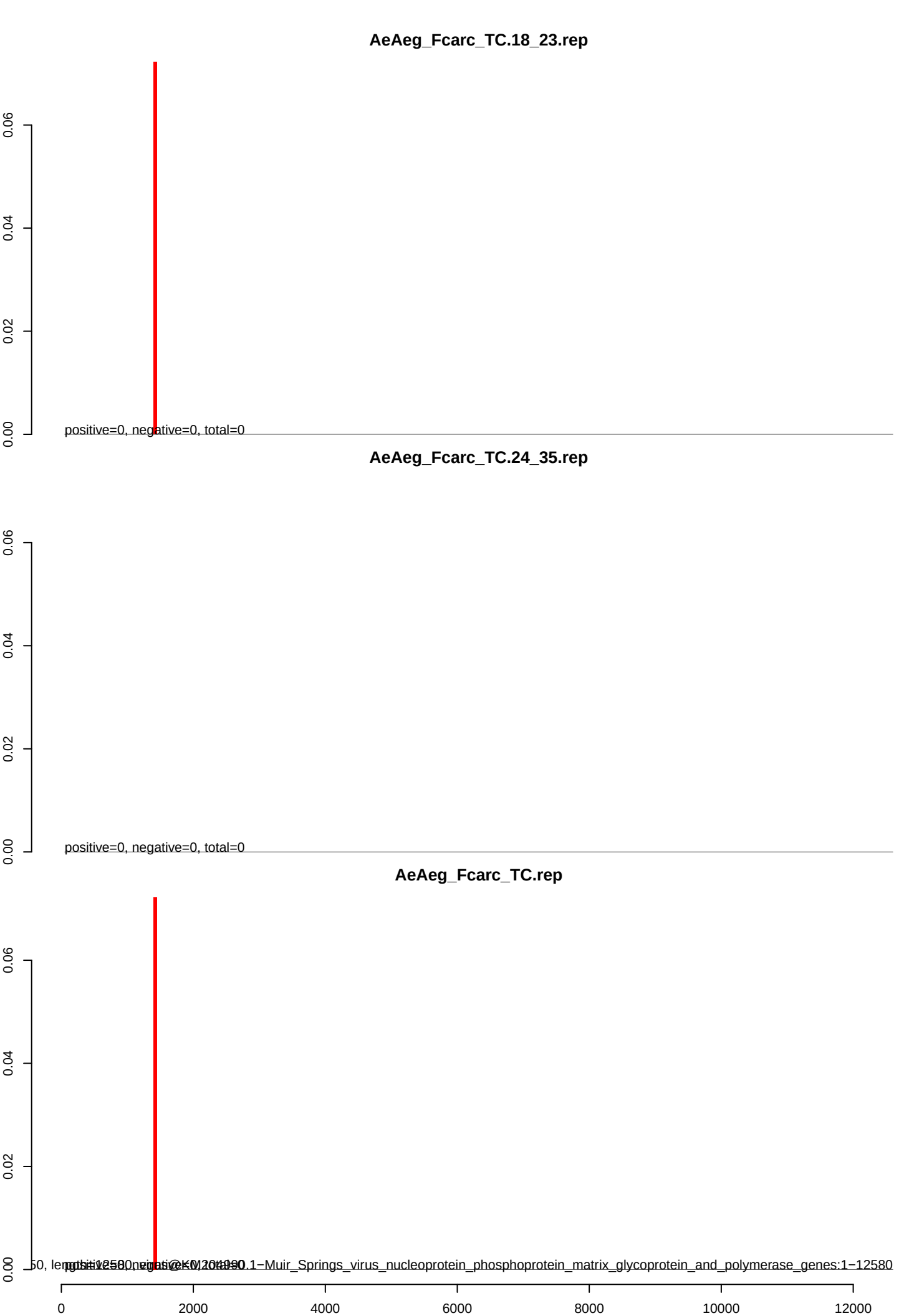
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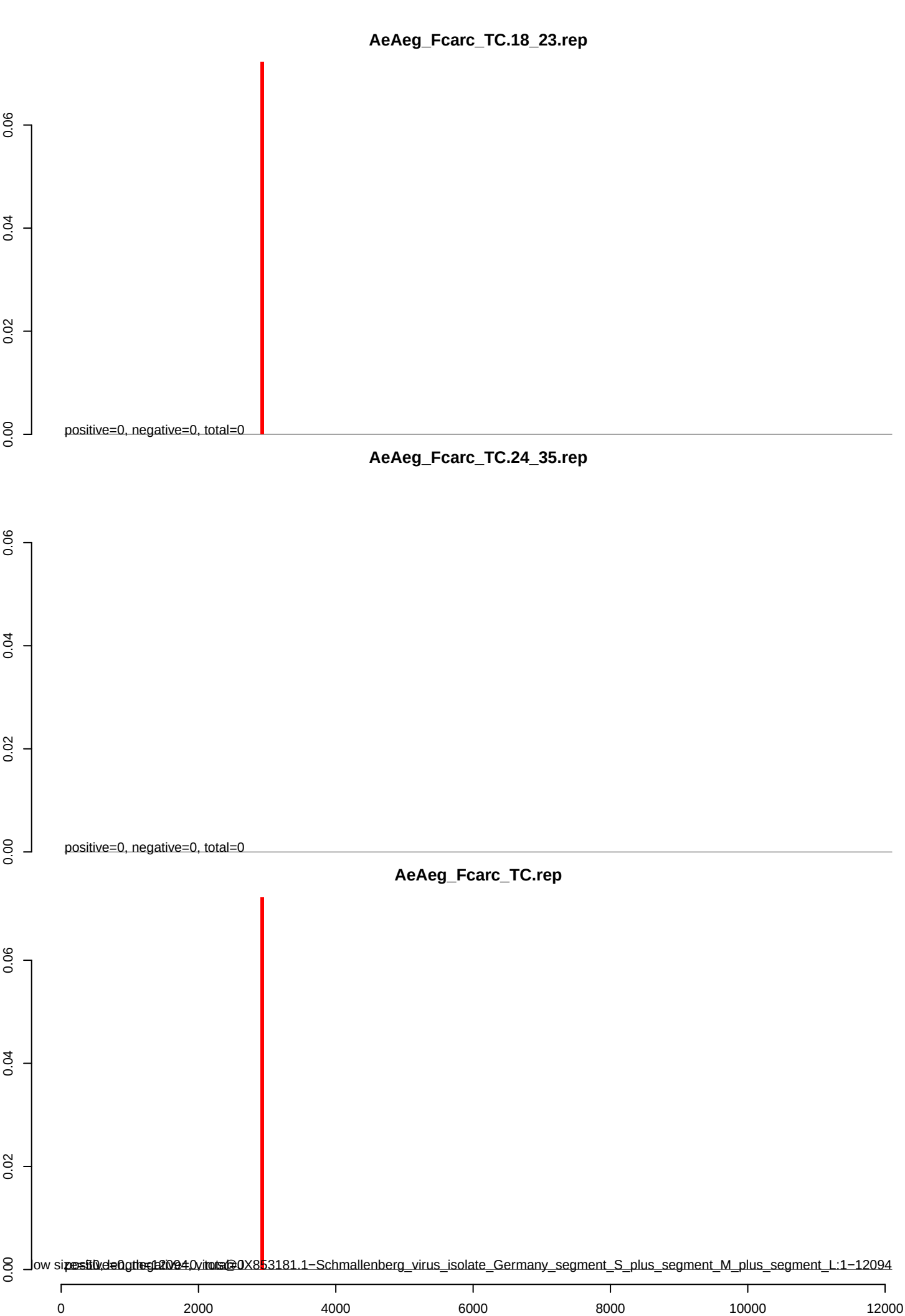
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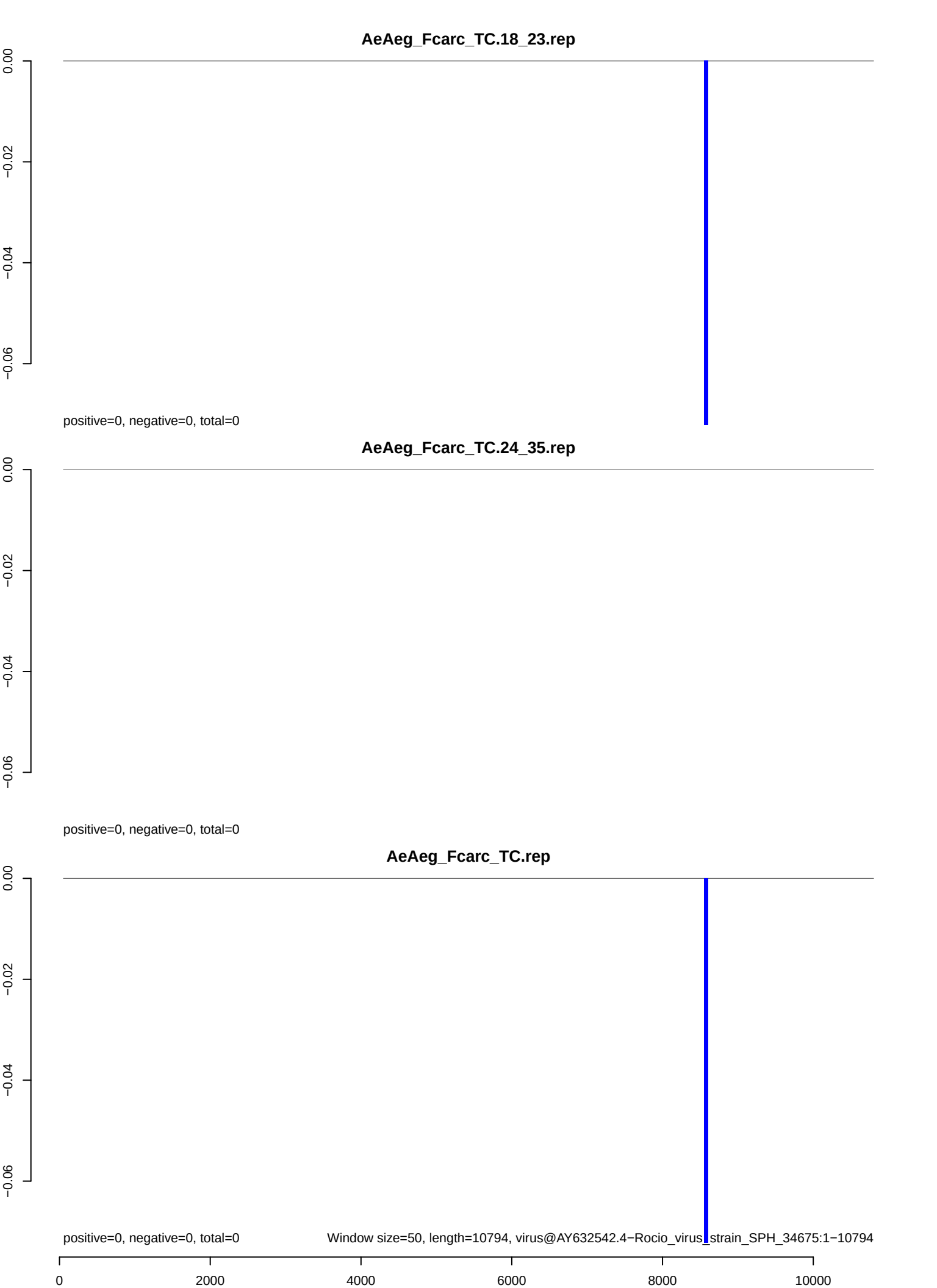
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positive=0, negative=0, total=0
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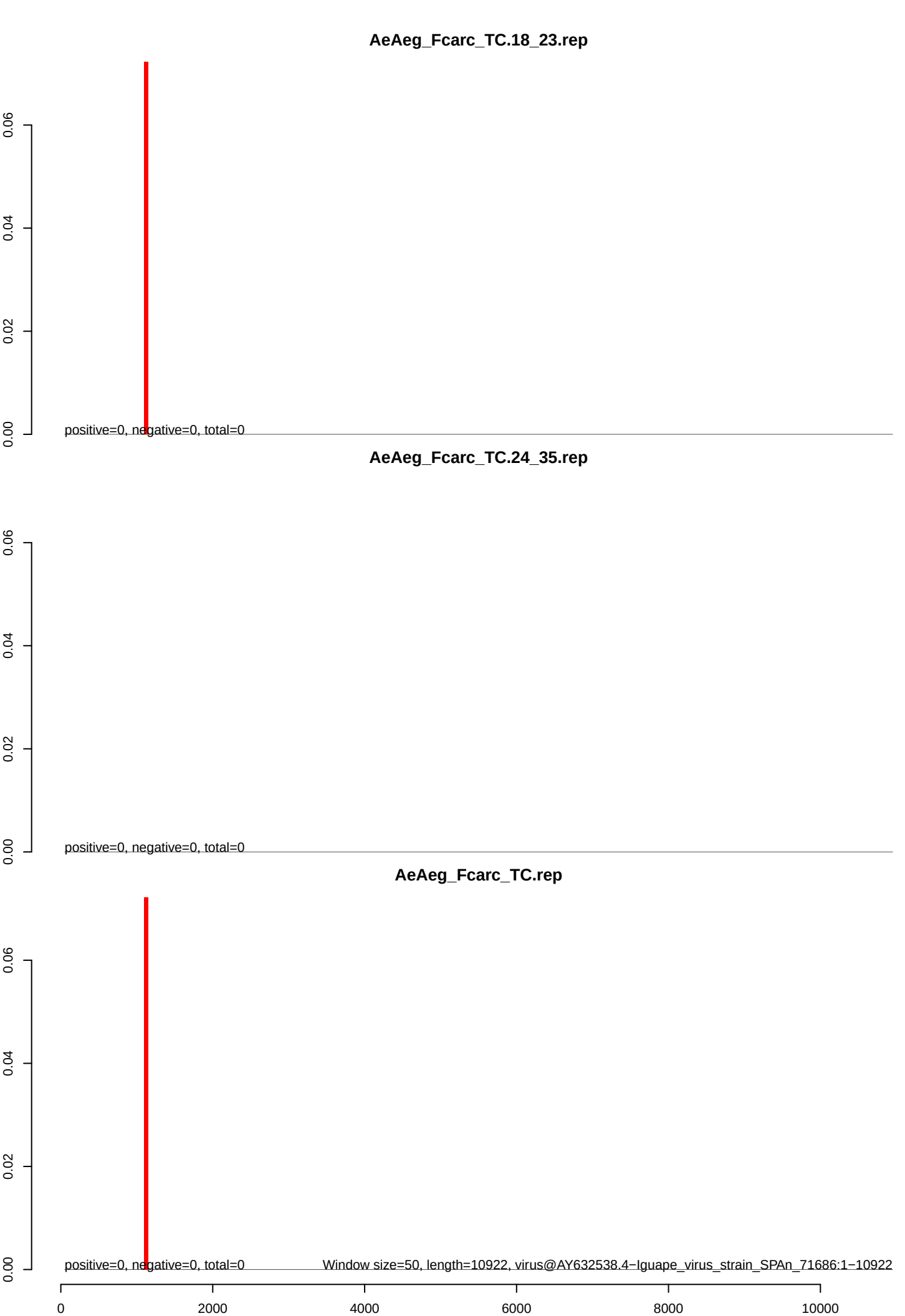
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positive=0, negative=0, total=0
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0.04
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positive=0, negative=0, total=0
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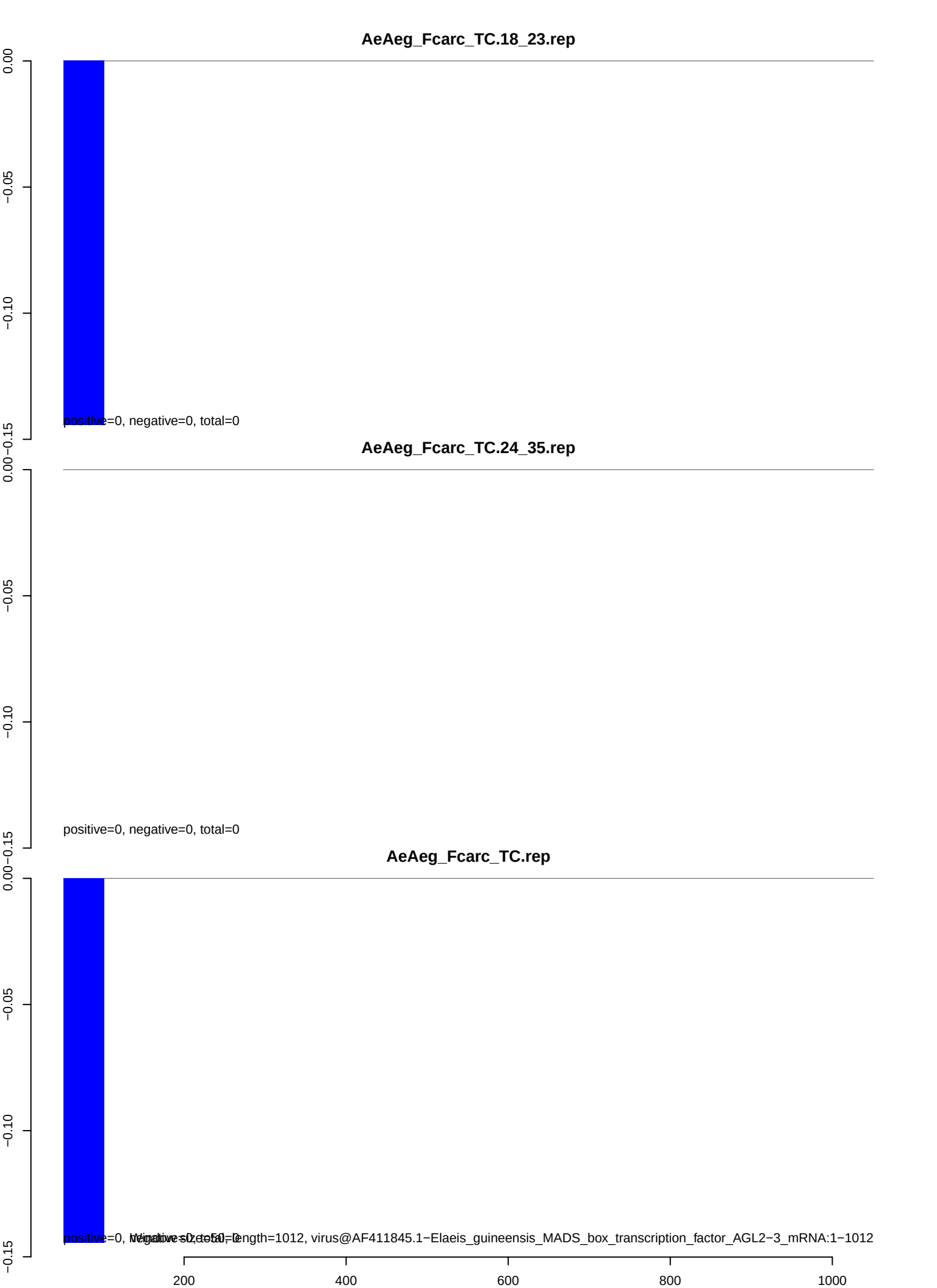
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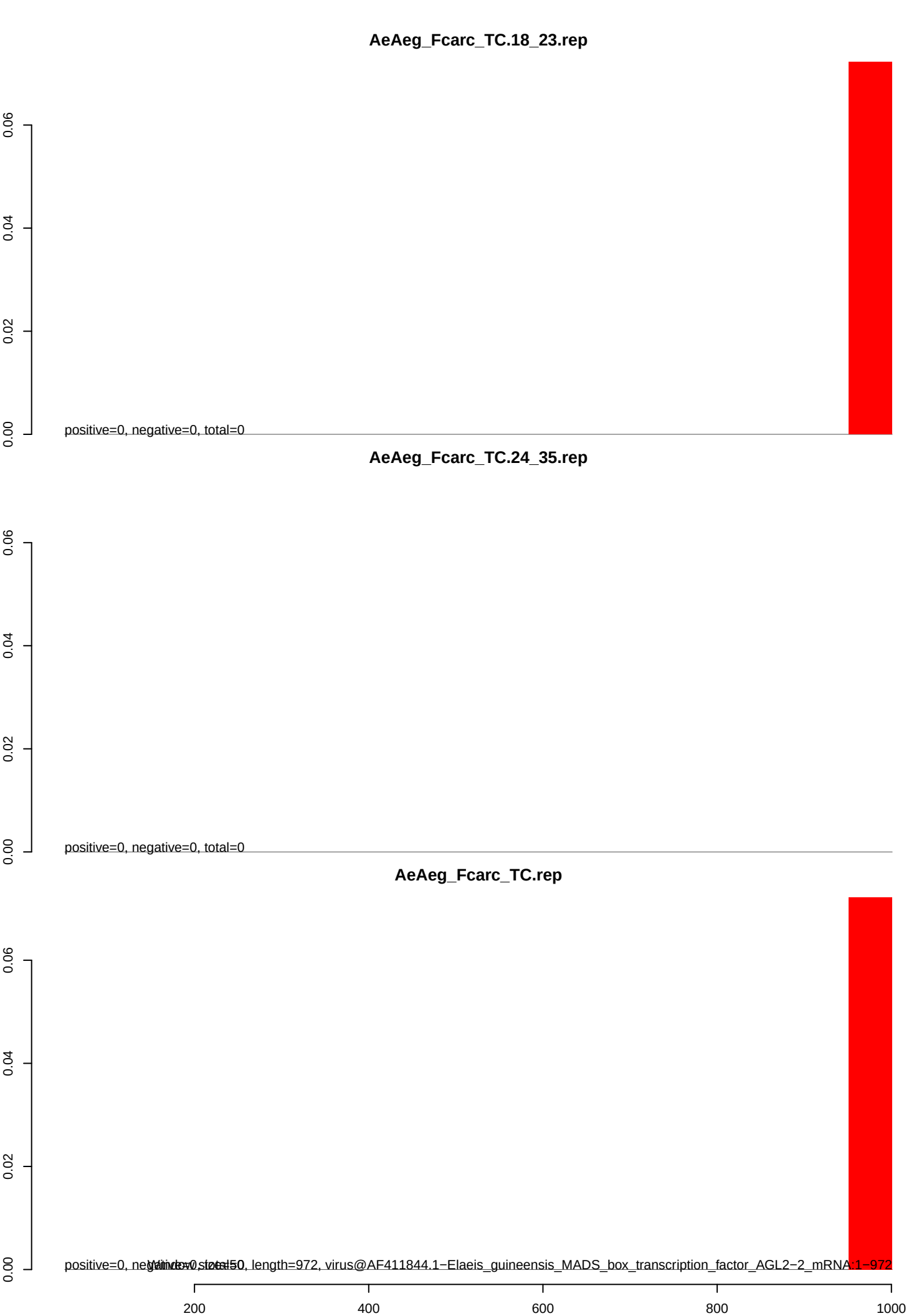
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0.04
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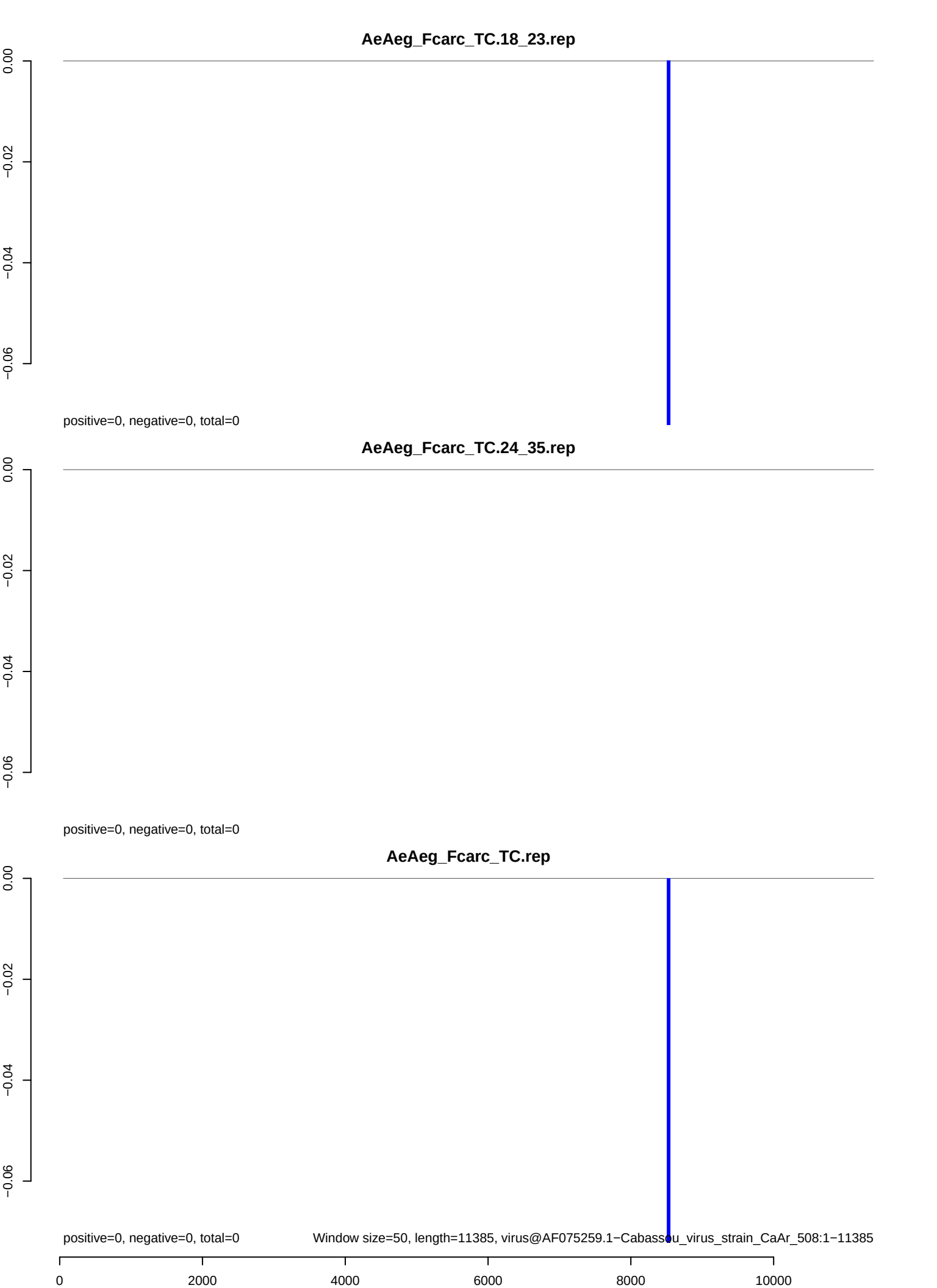
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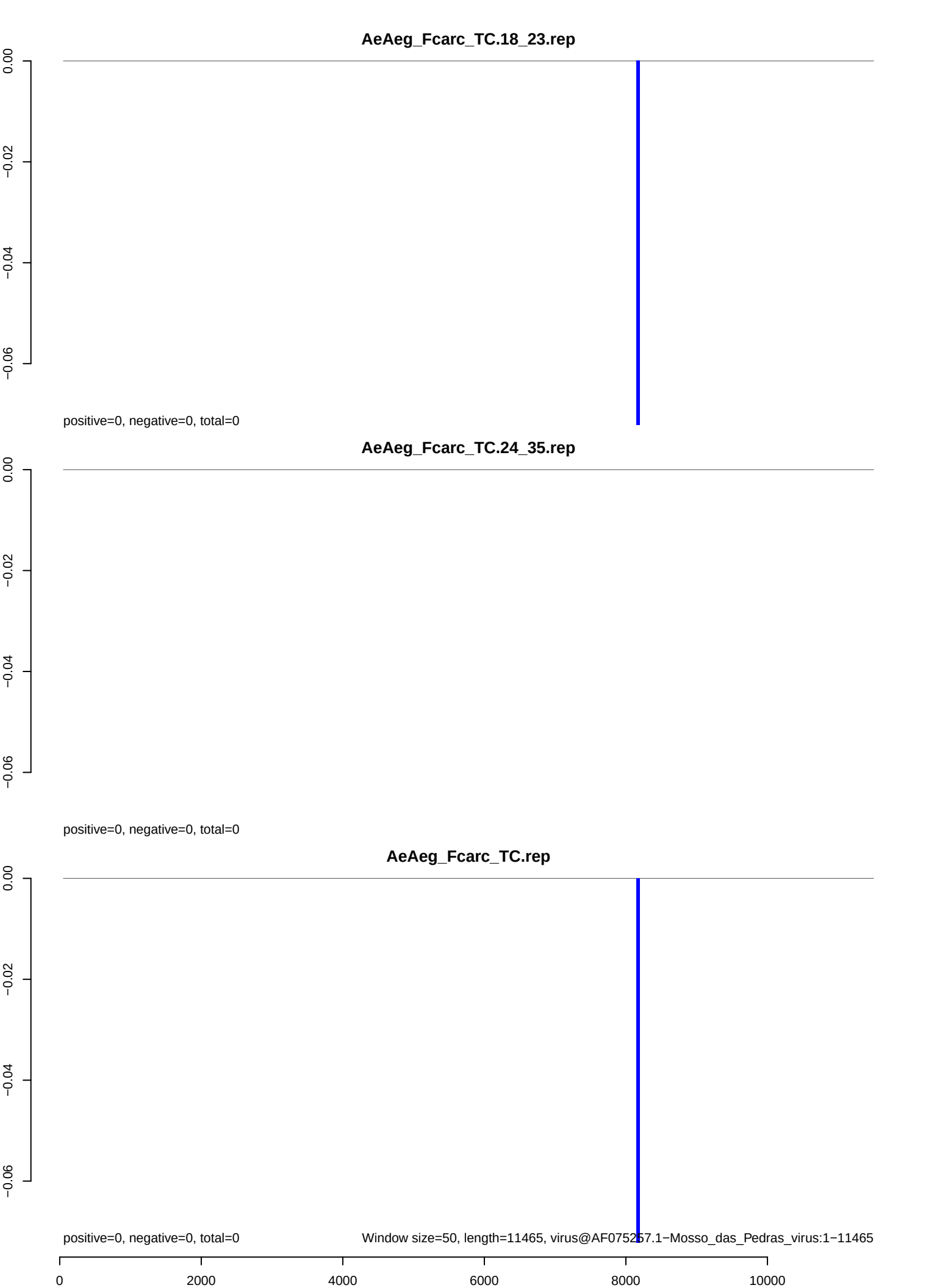
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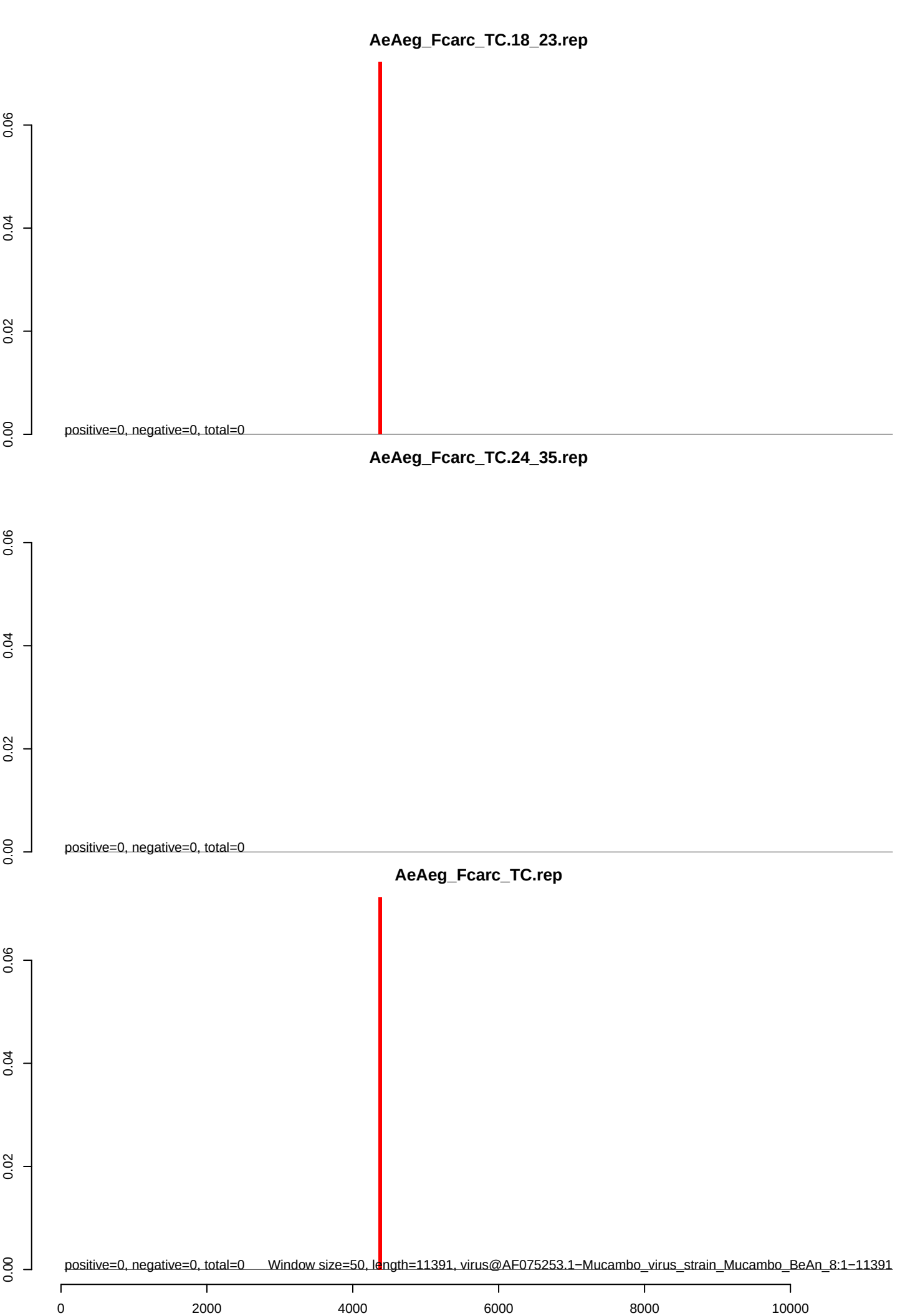
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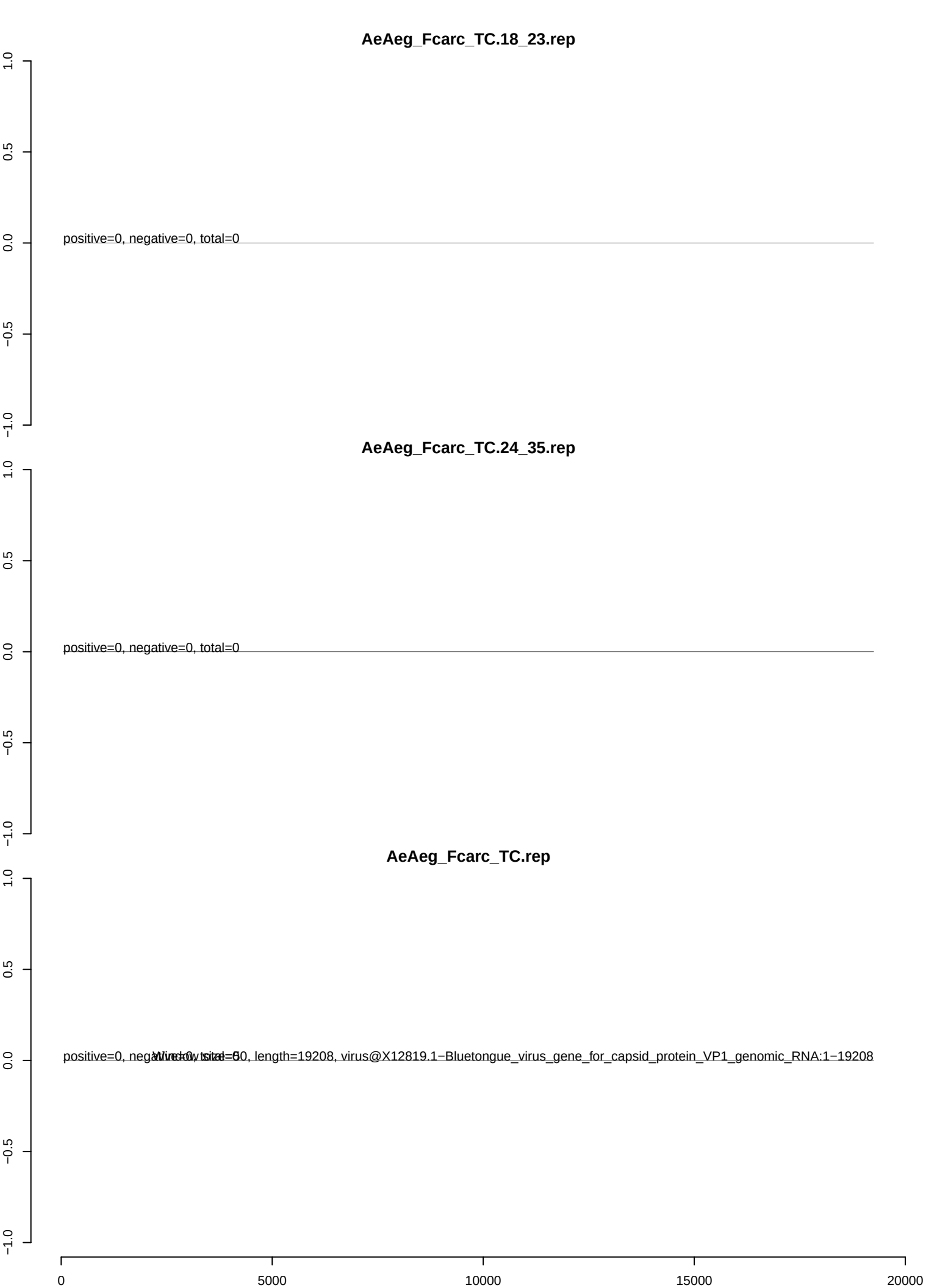
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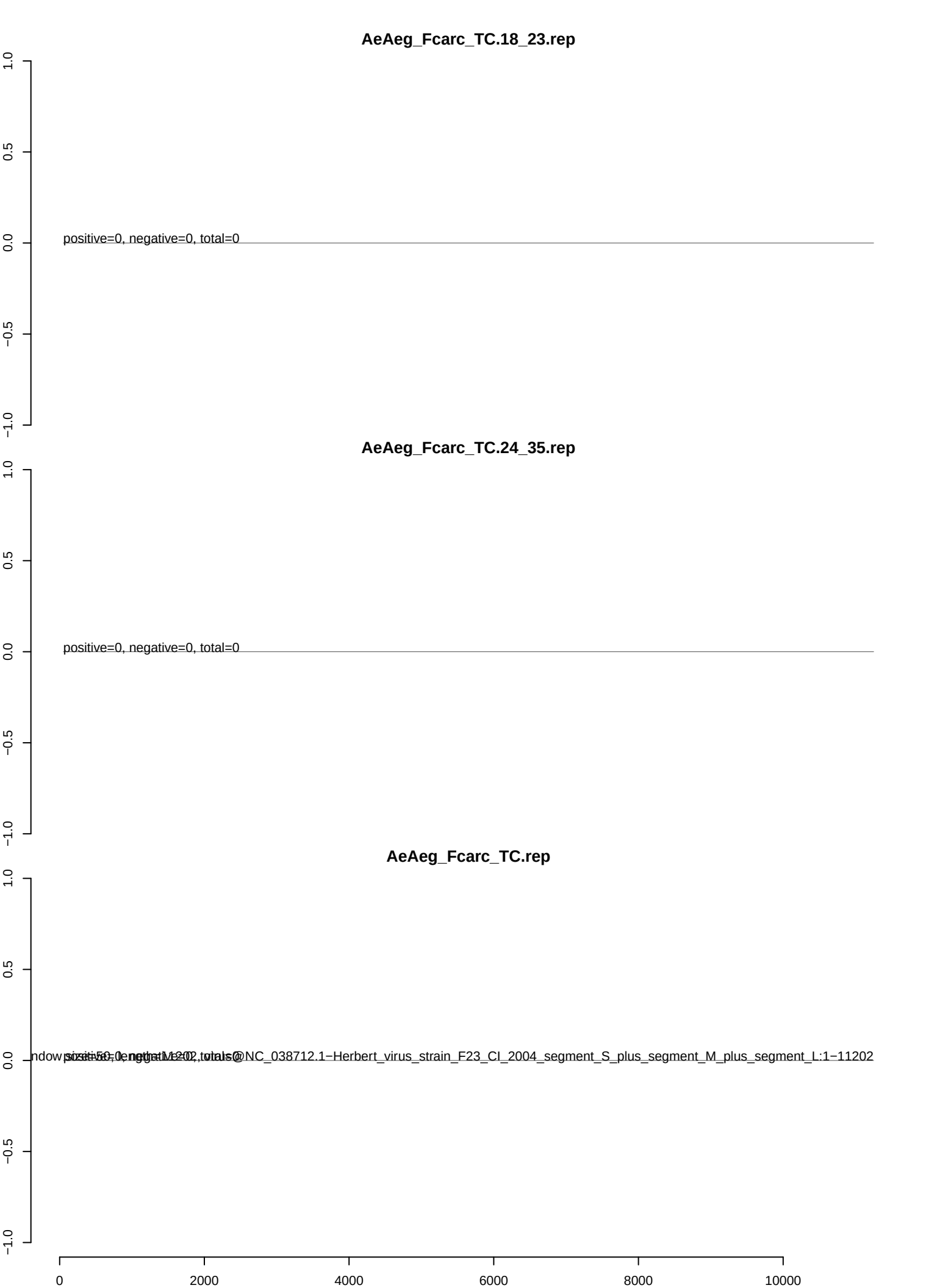
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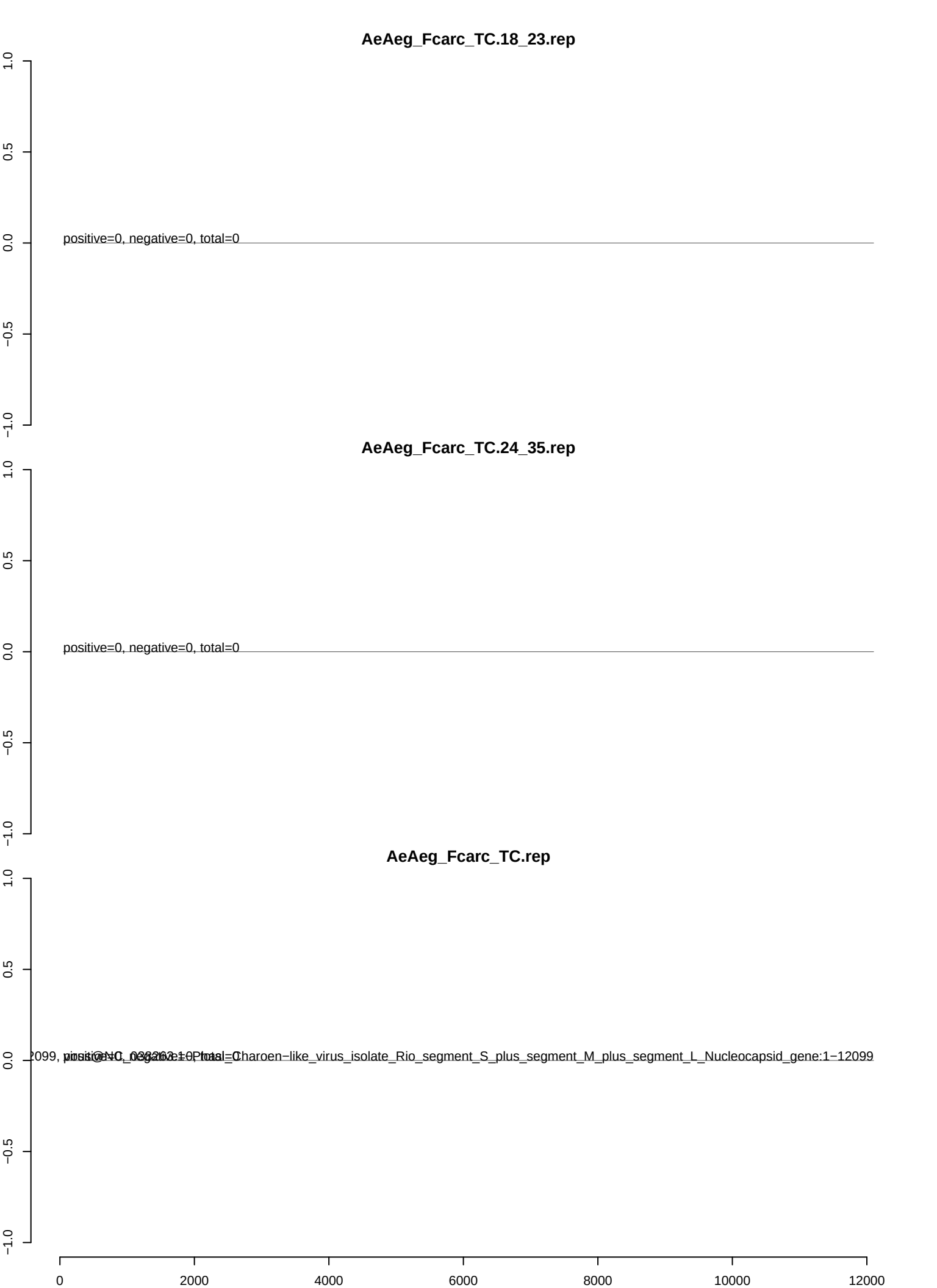
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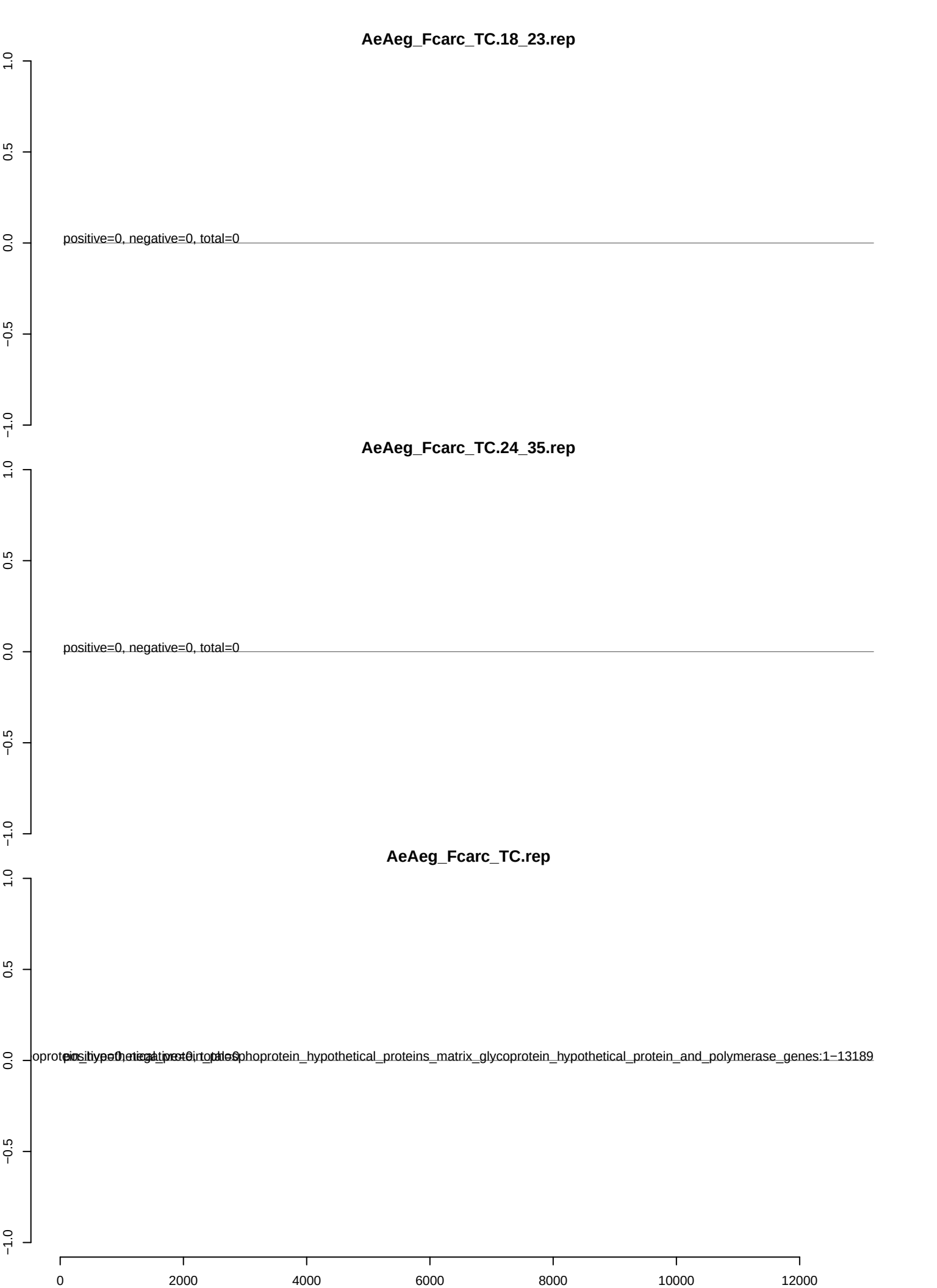
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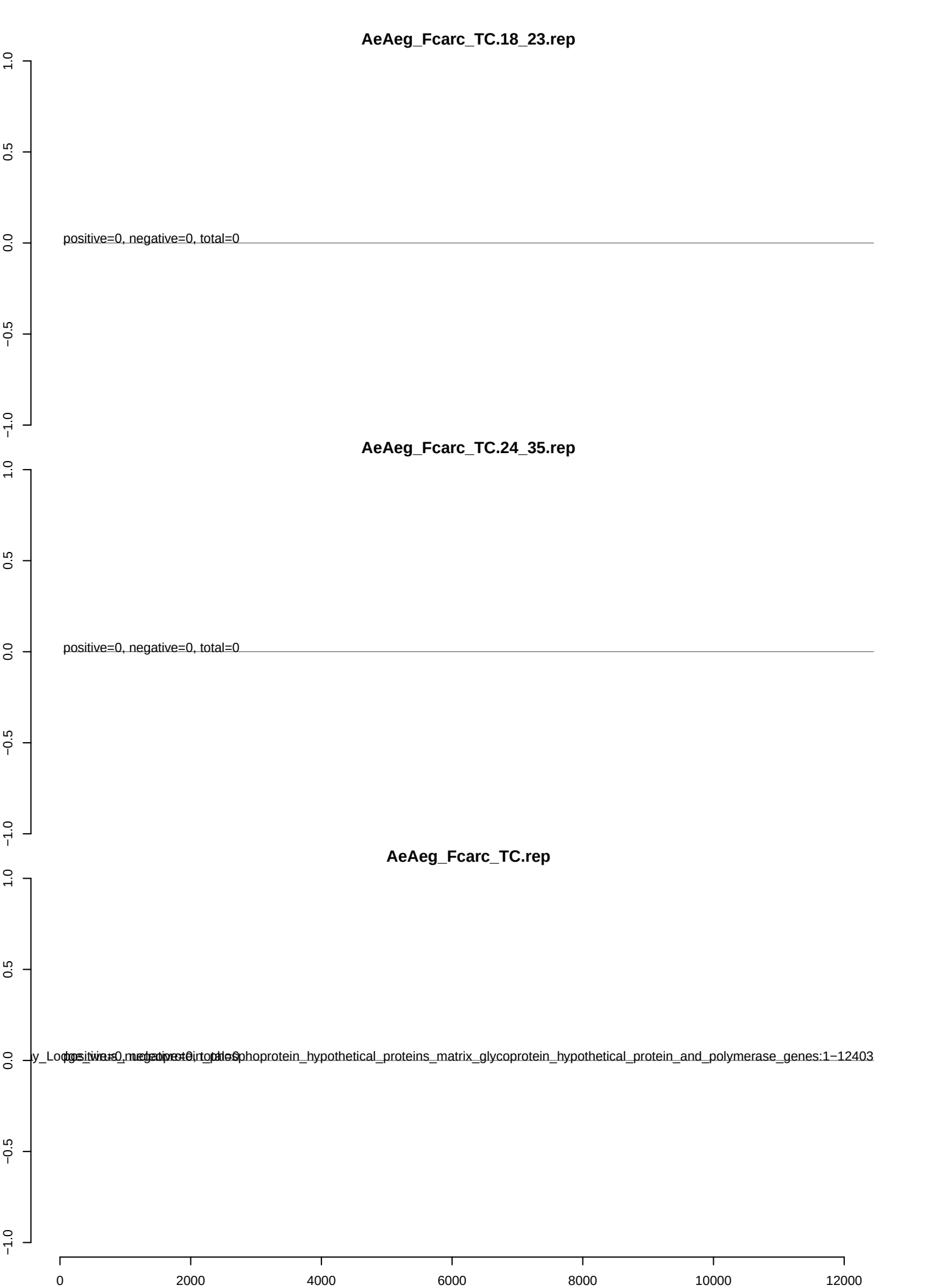
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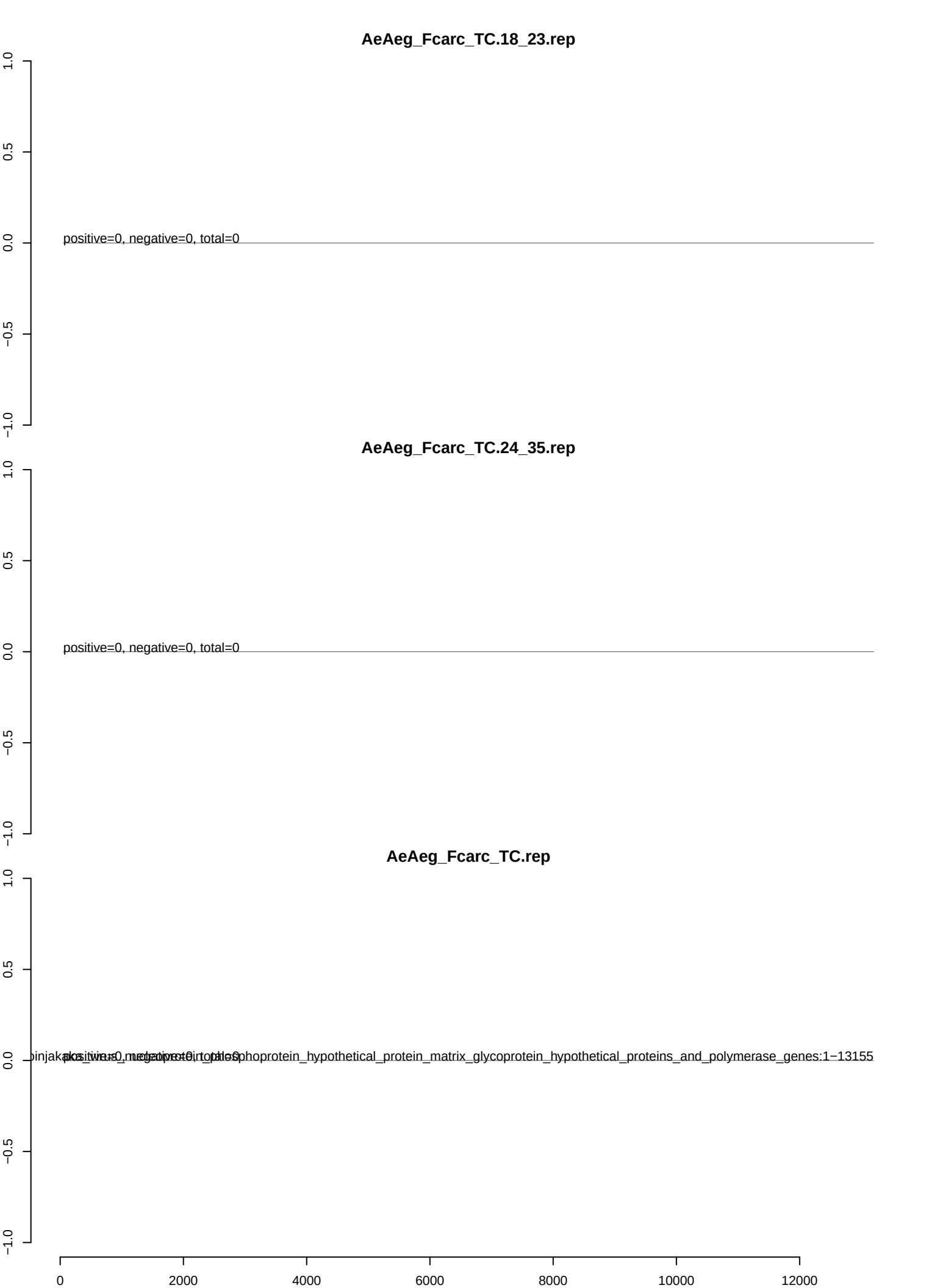
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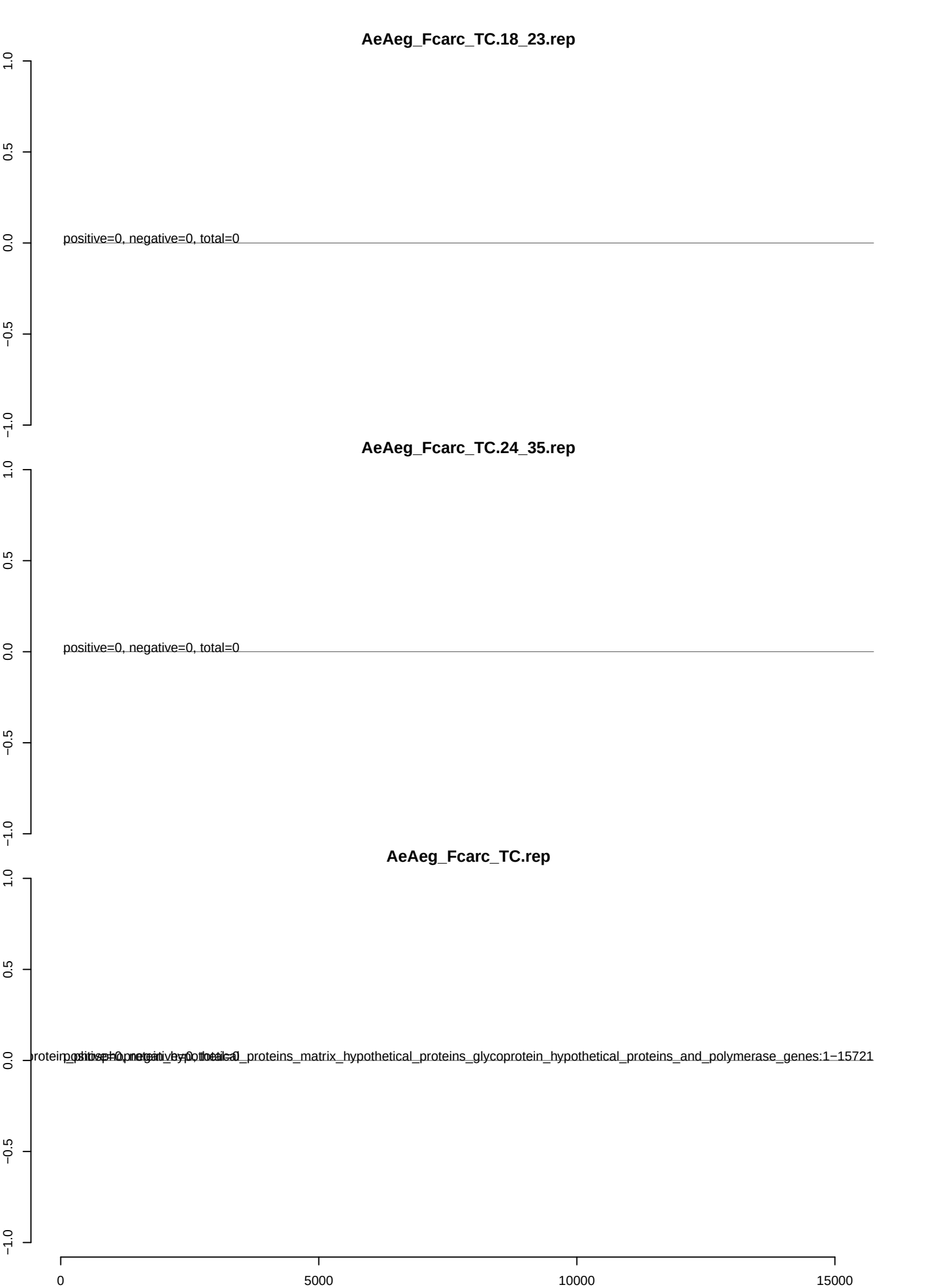
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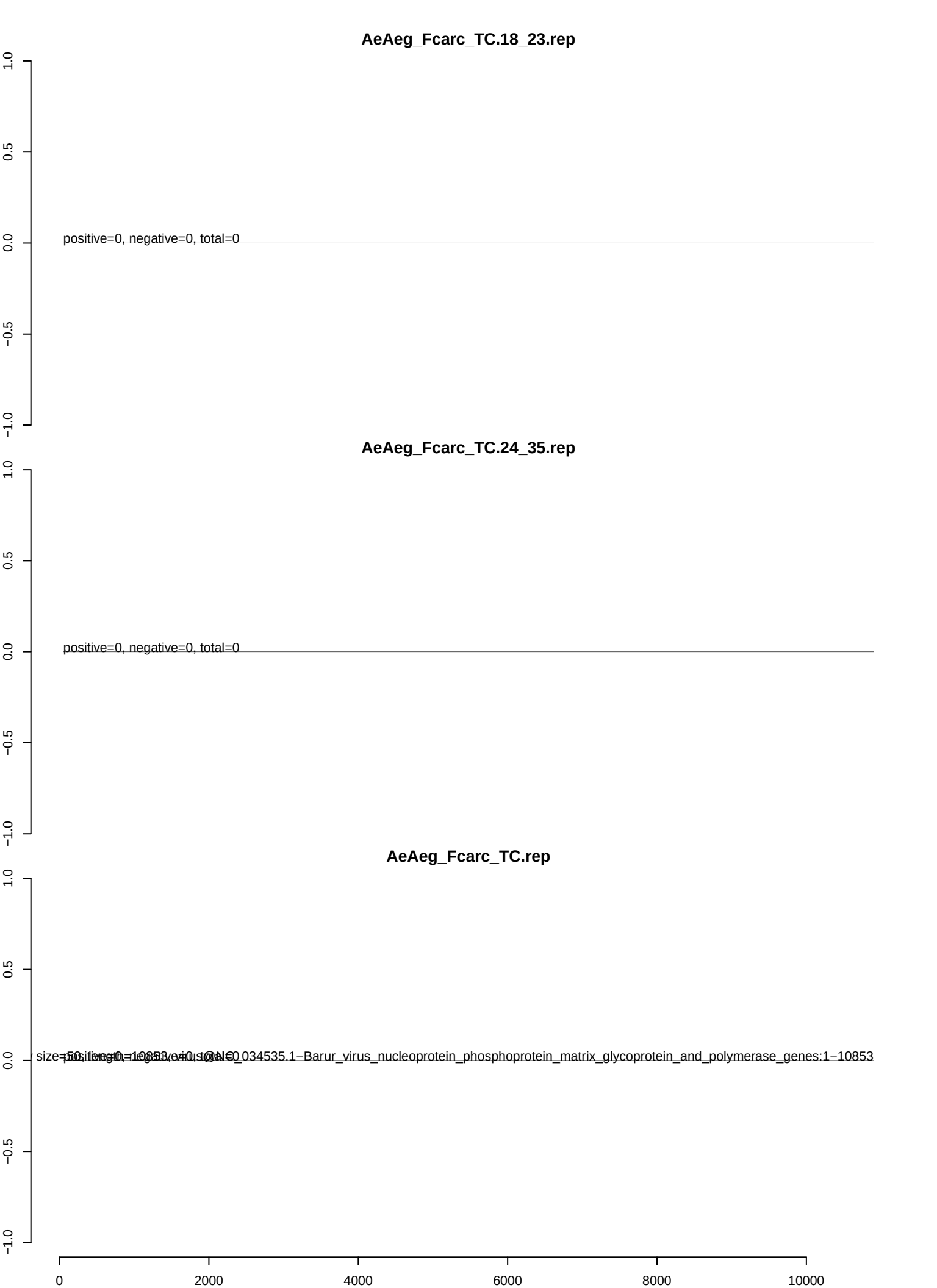
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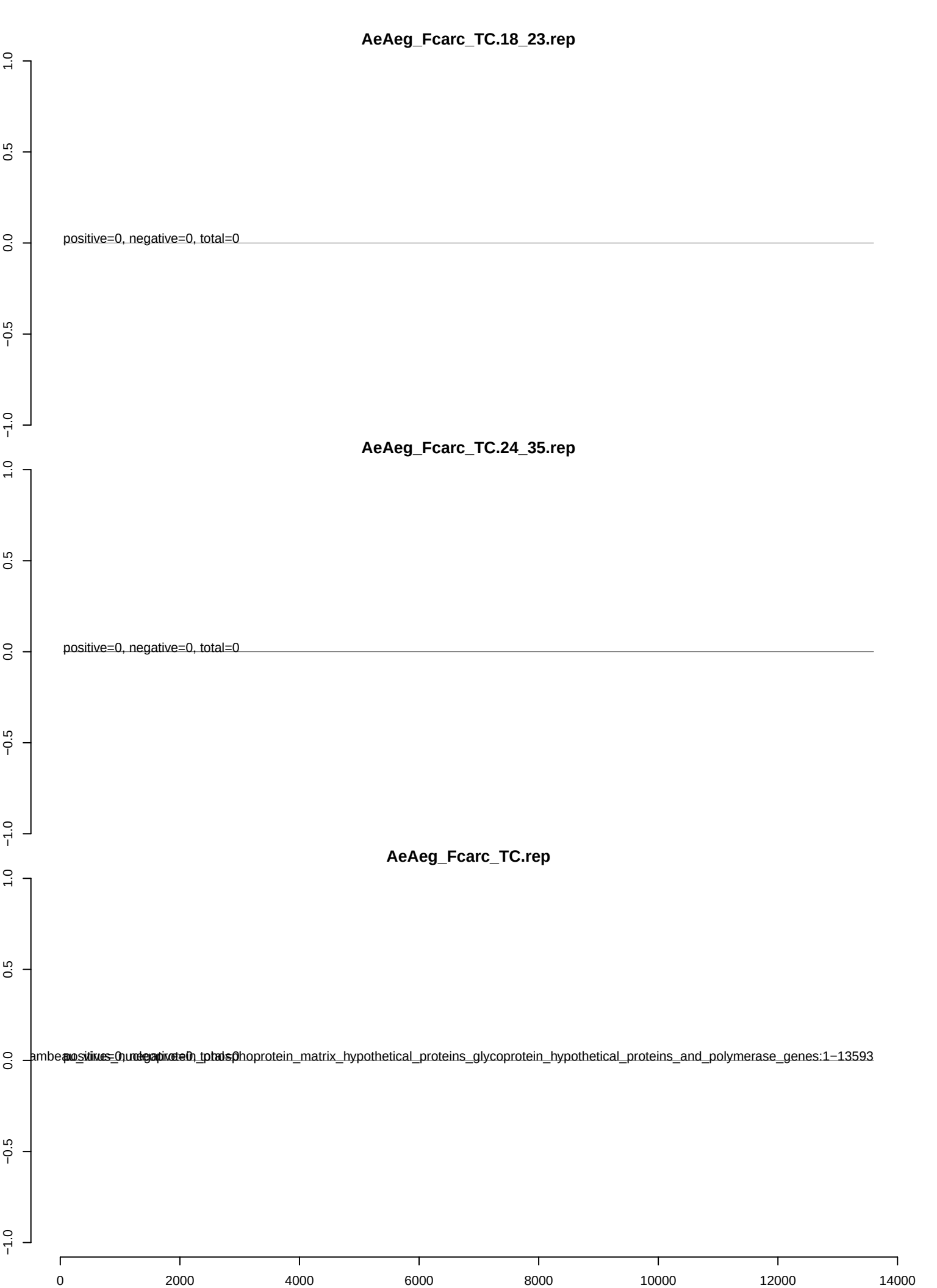
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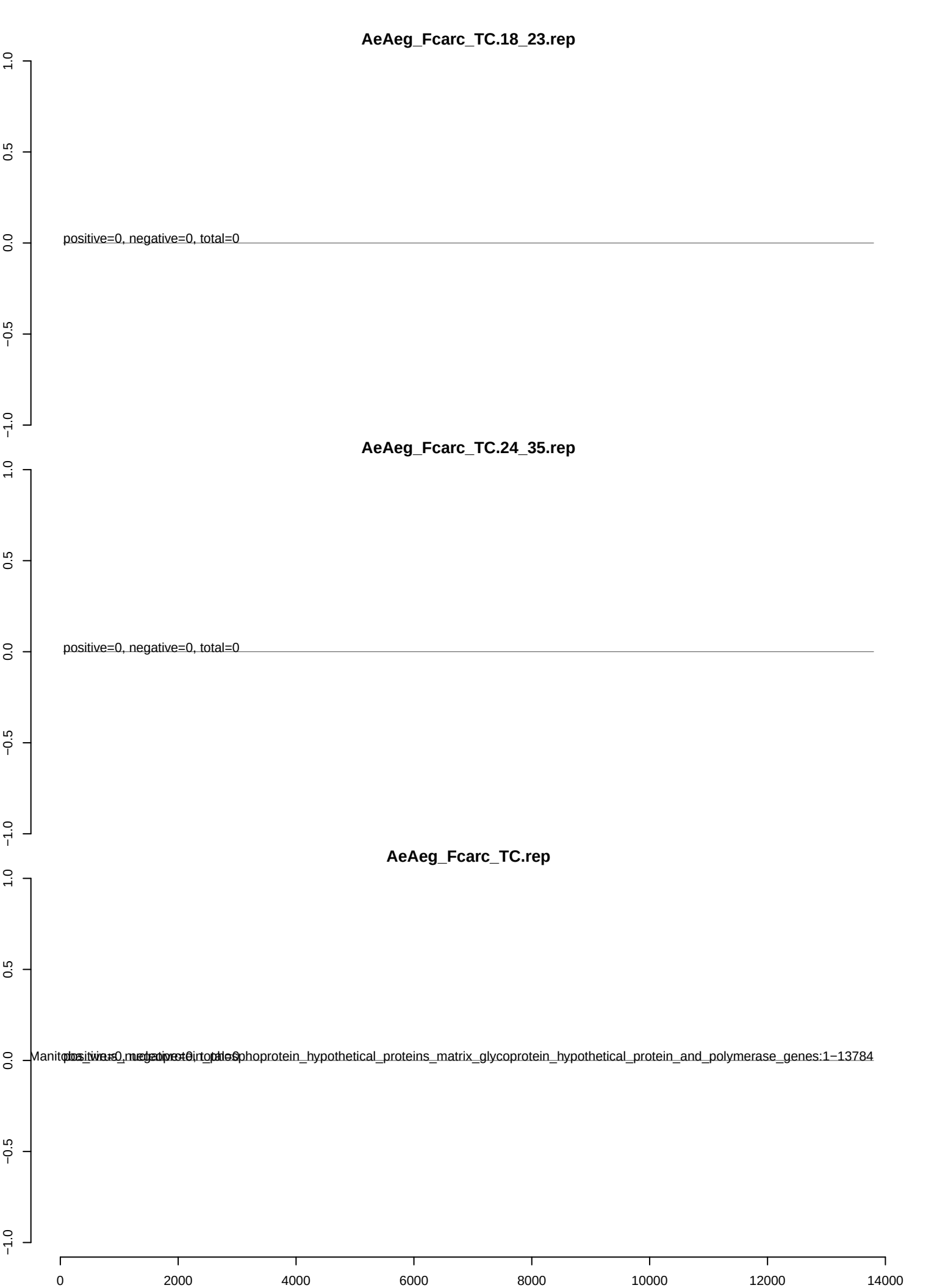
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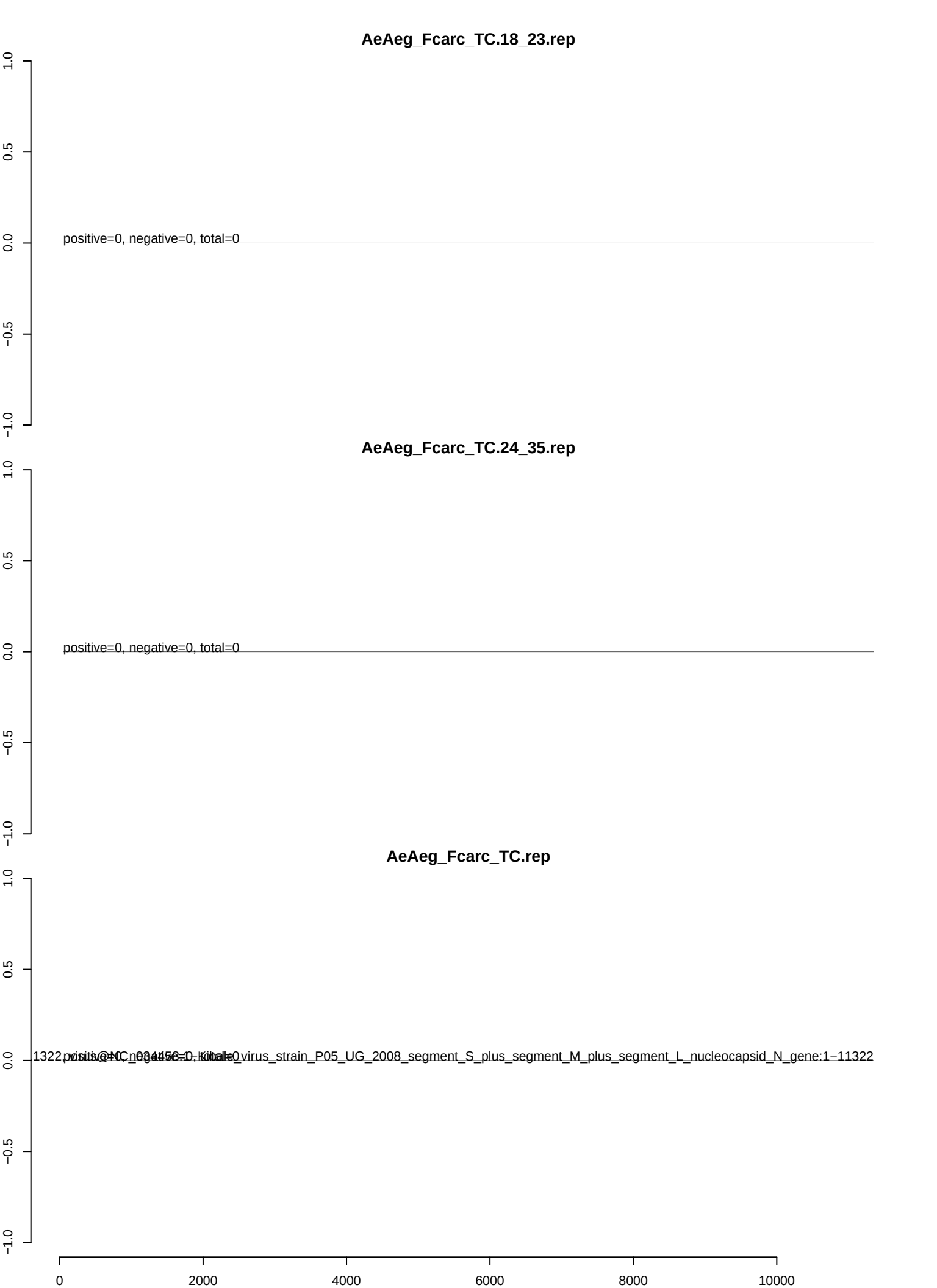
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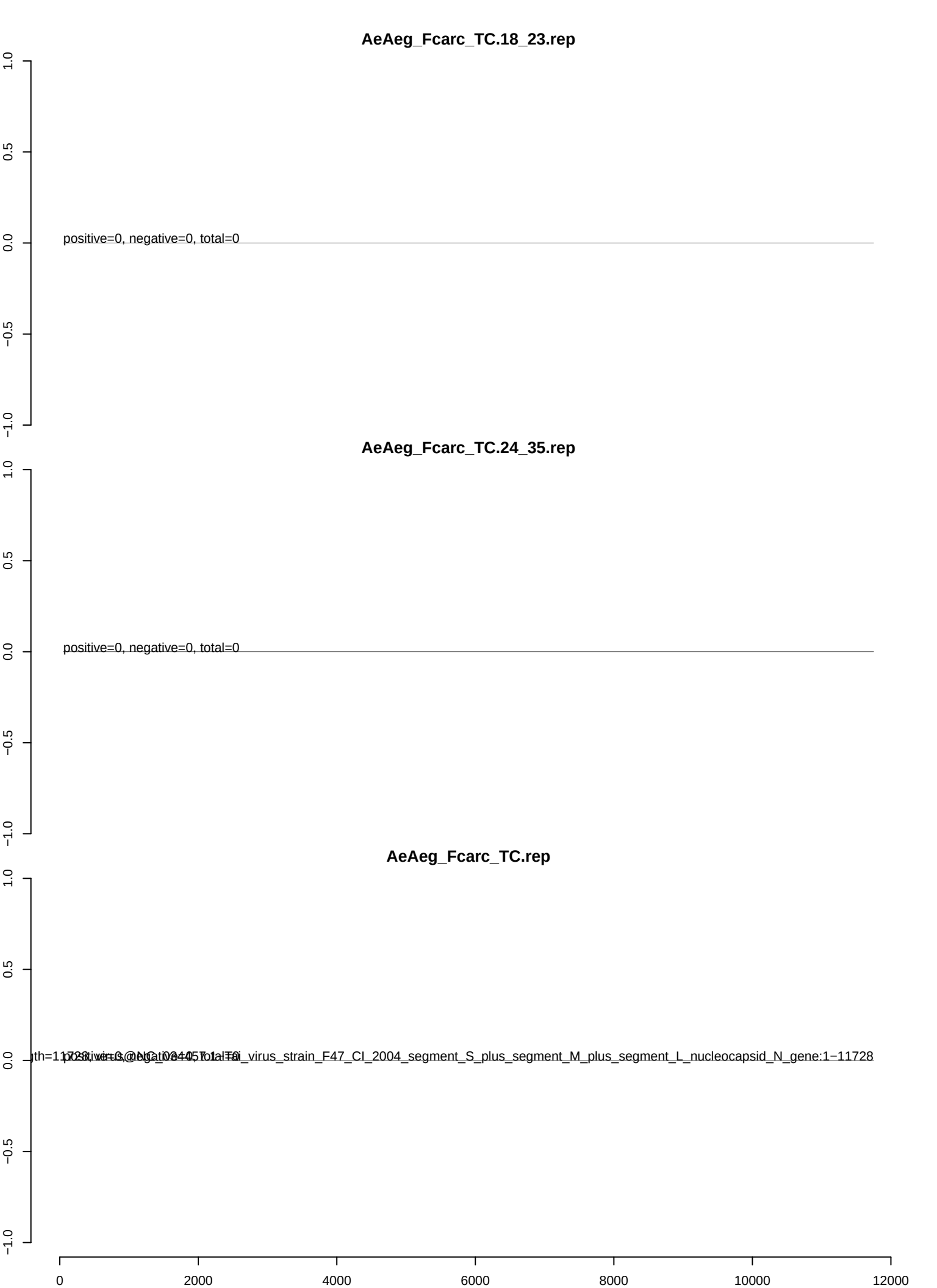
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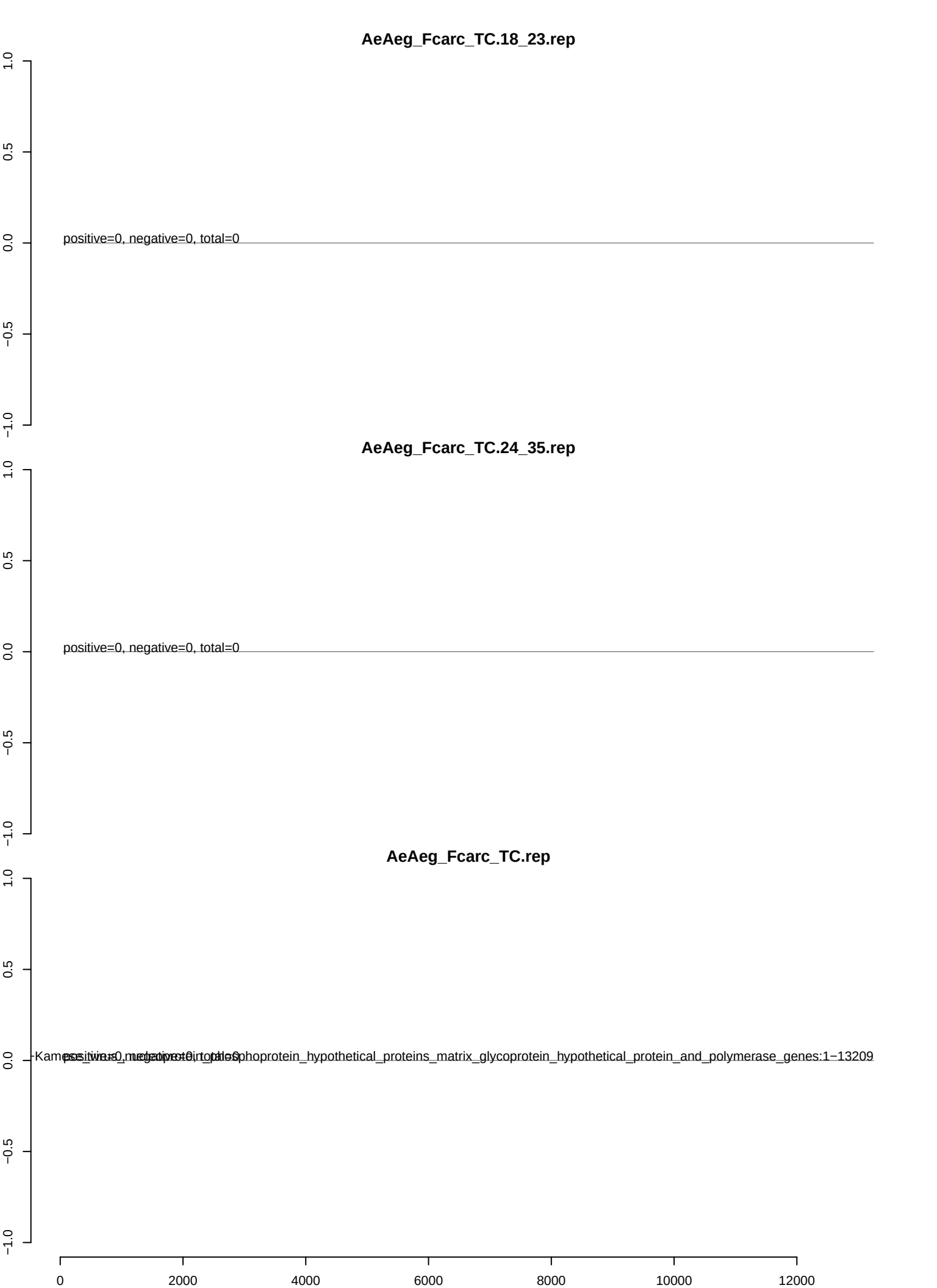
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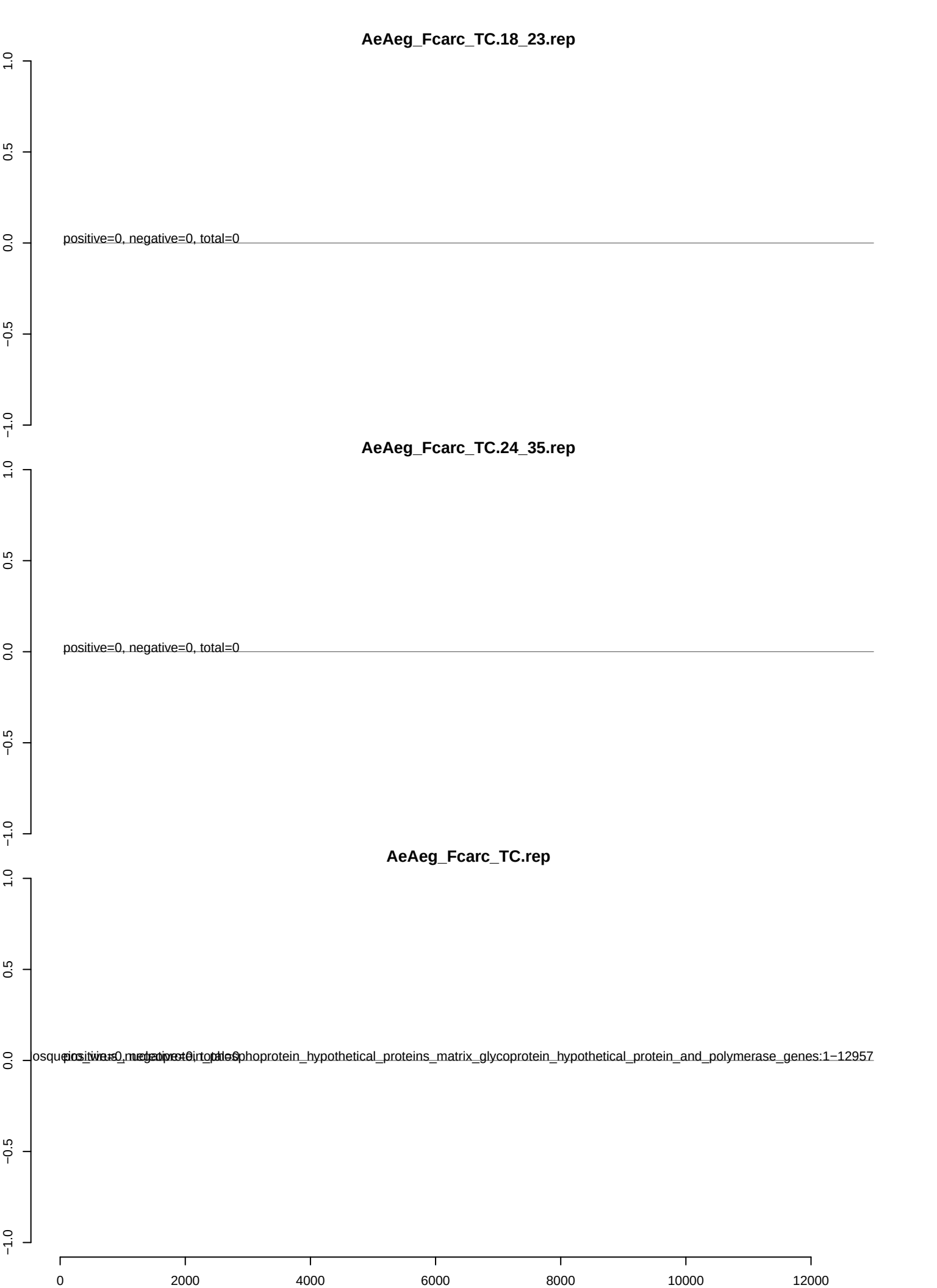
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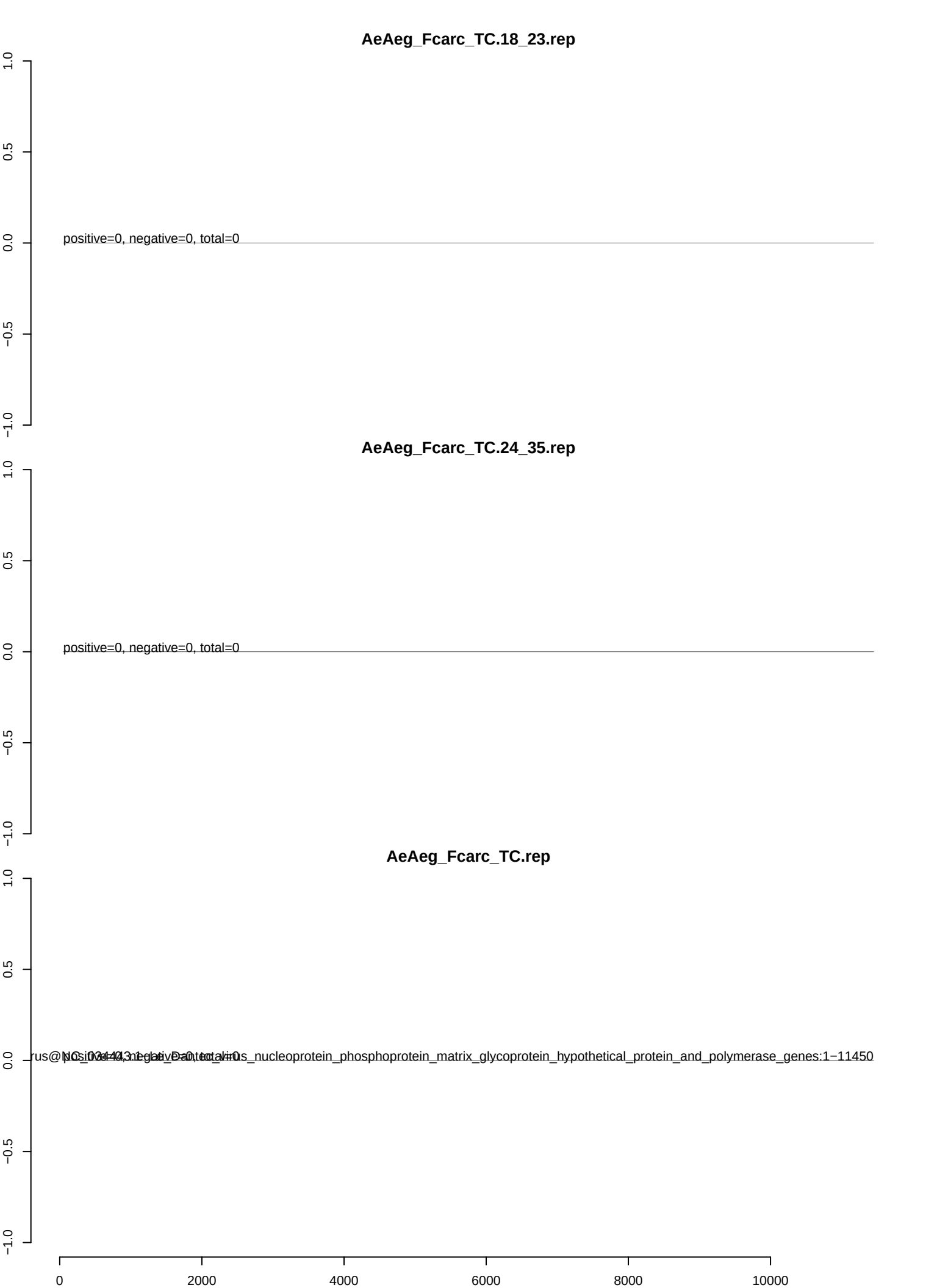
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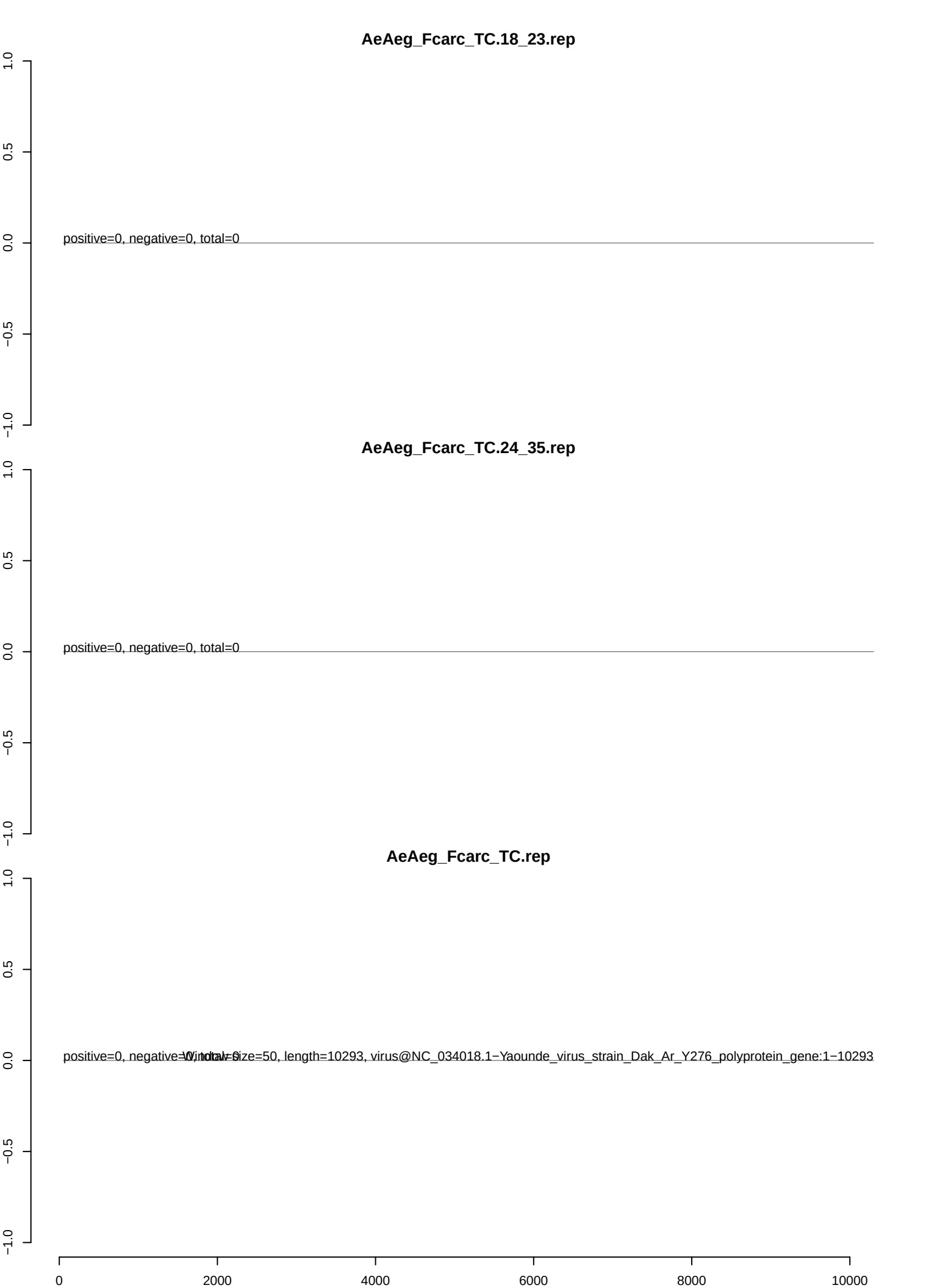
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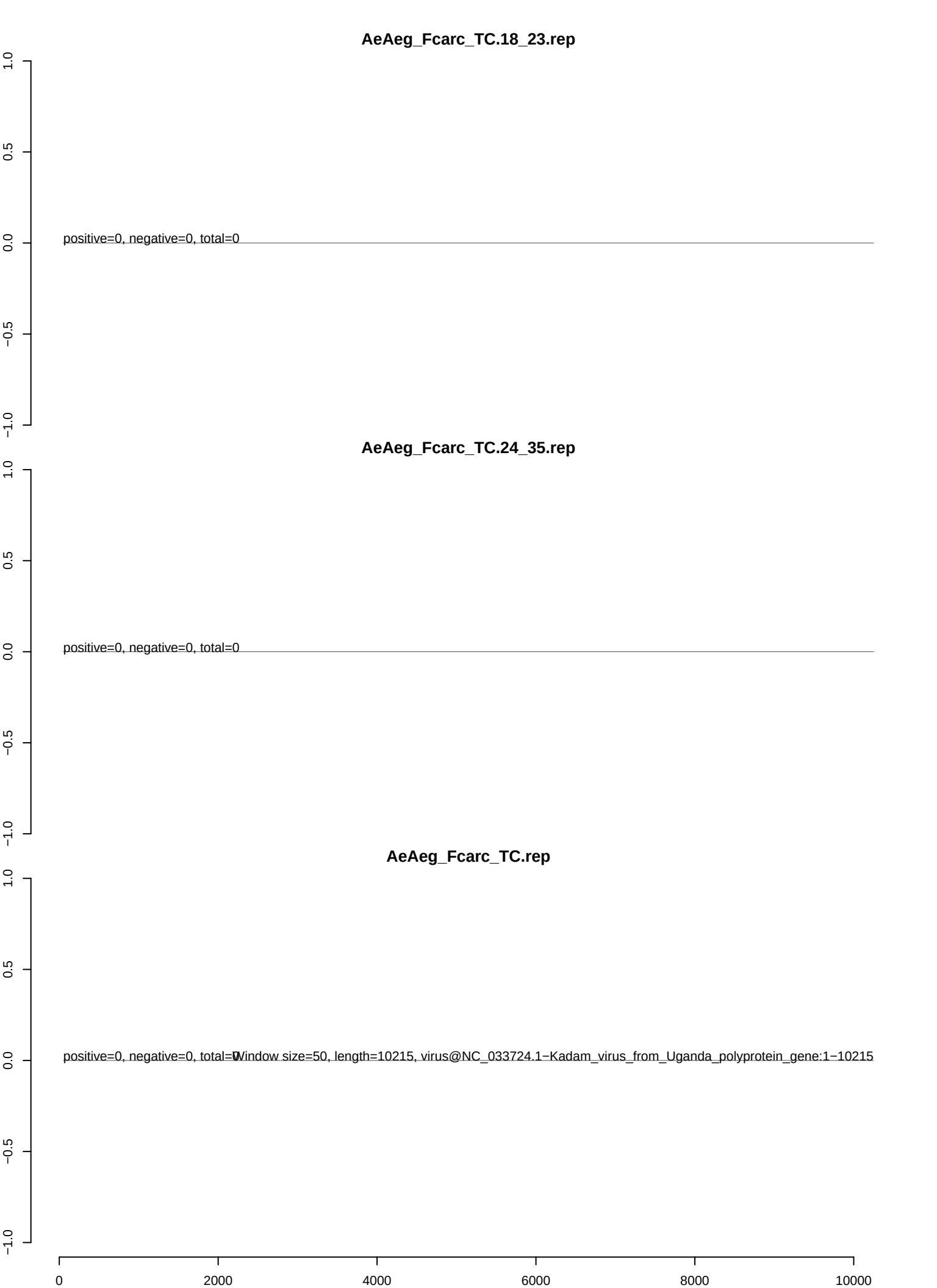
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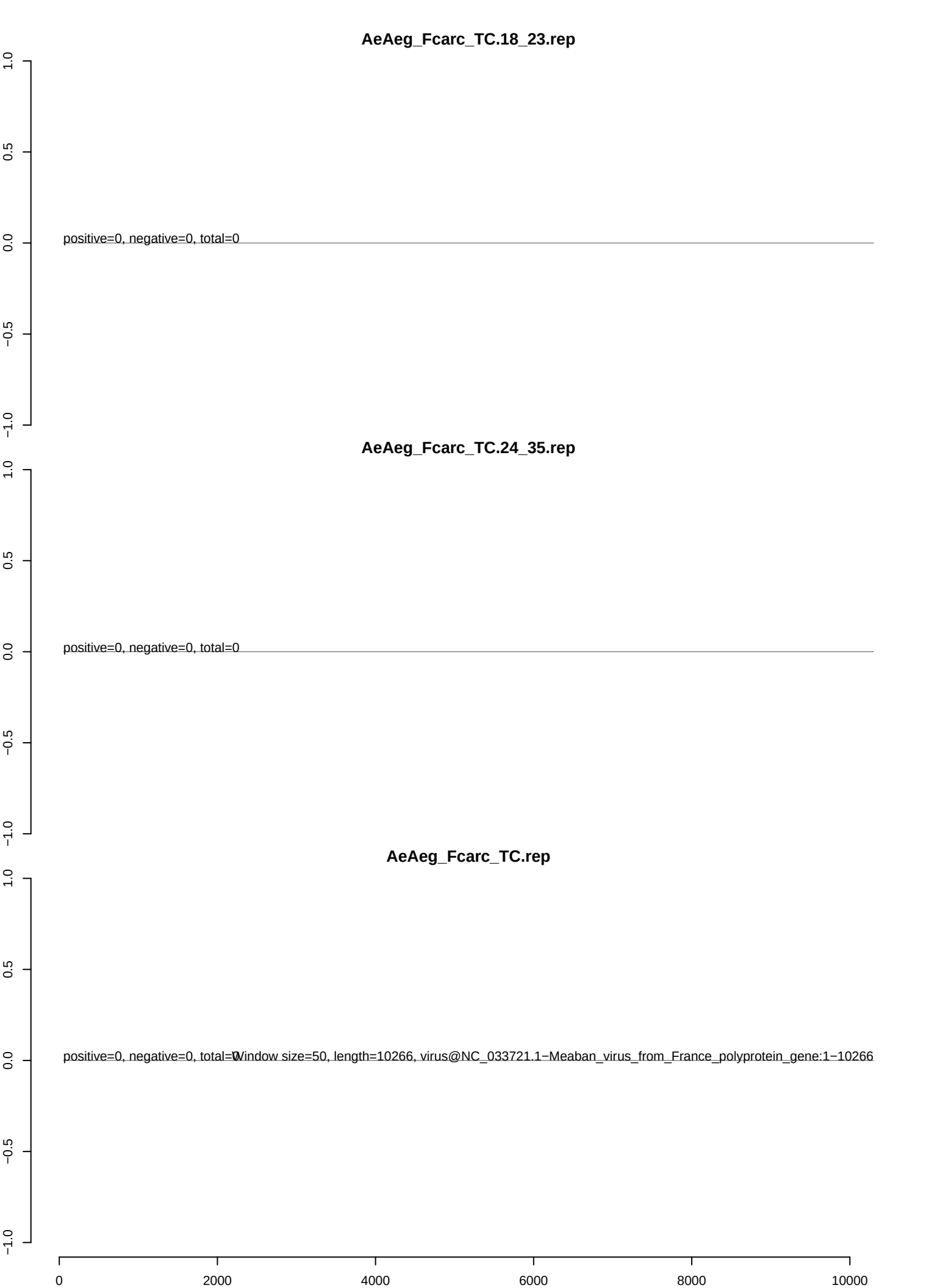
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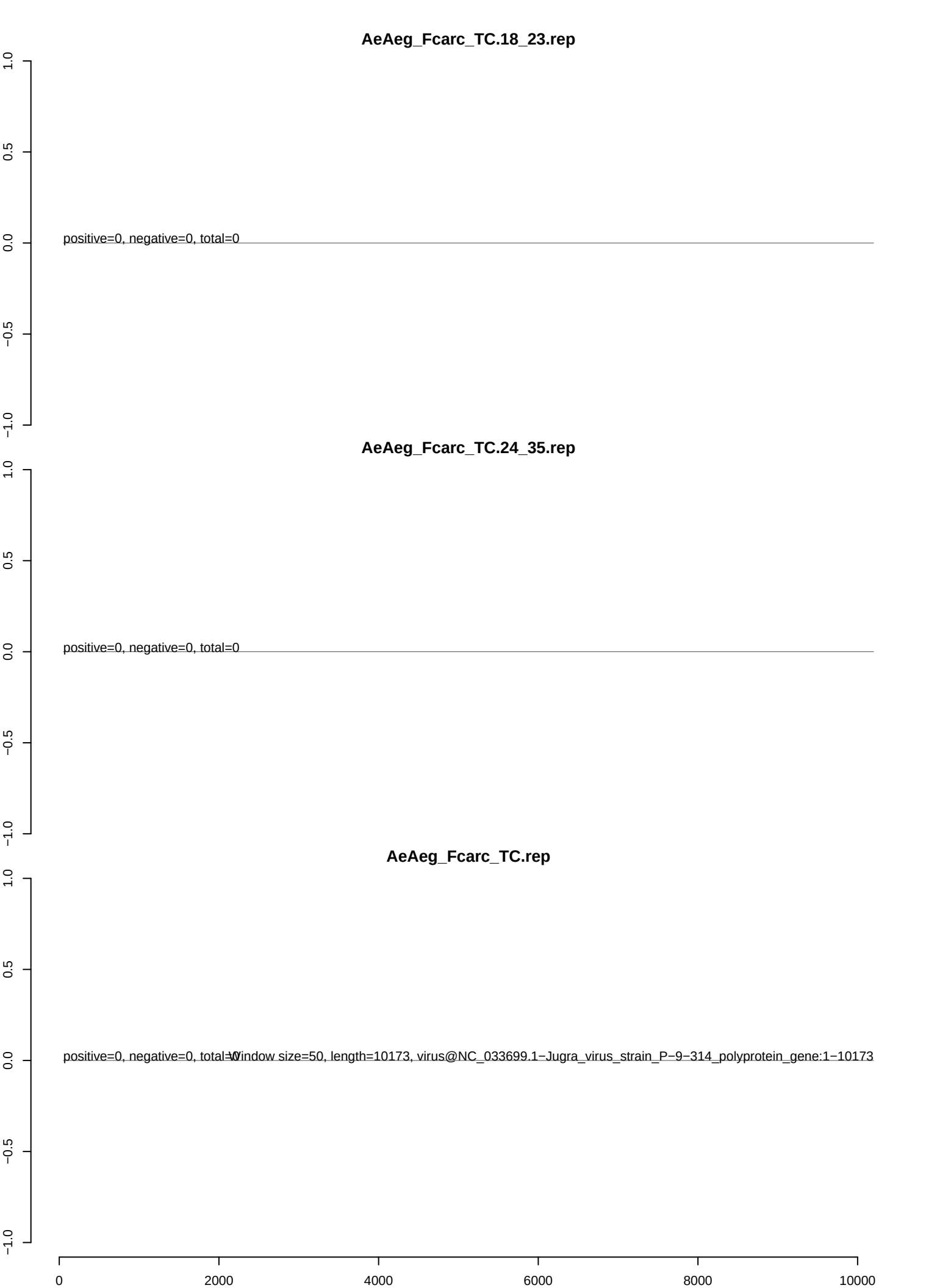
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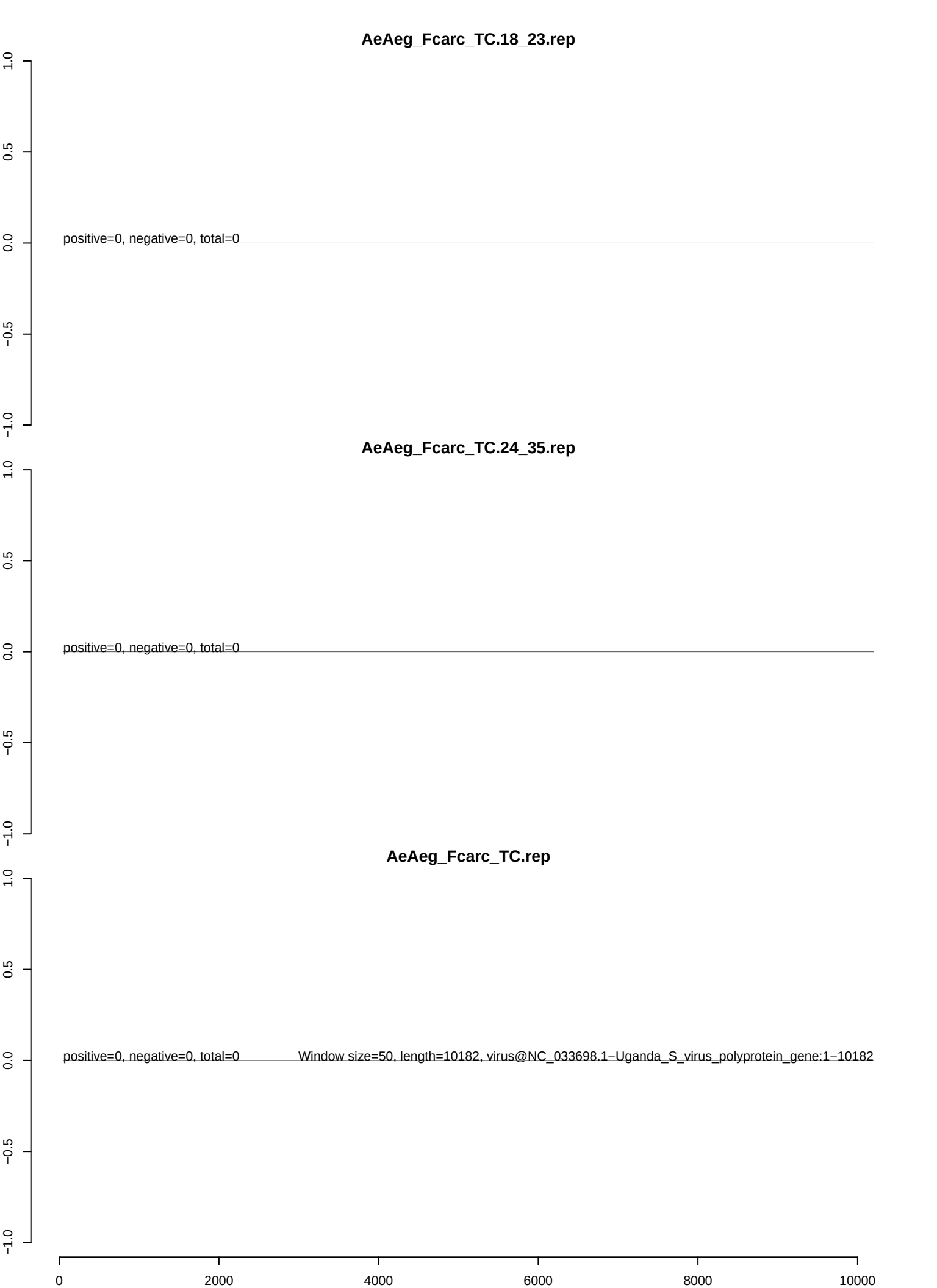
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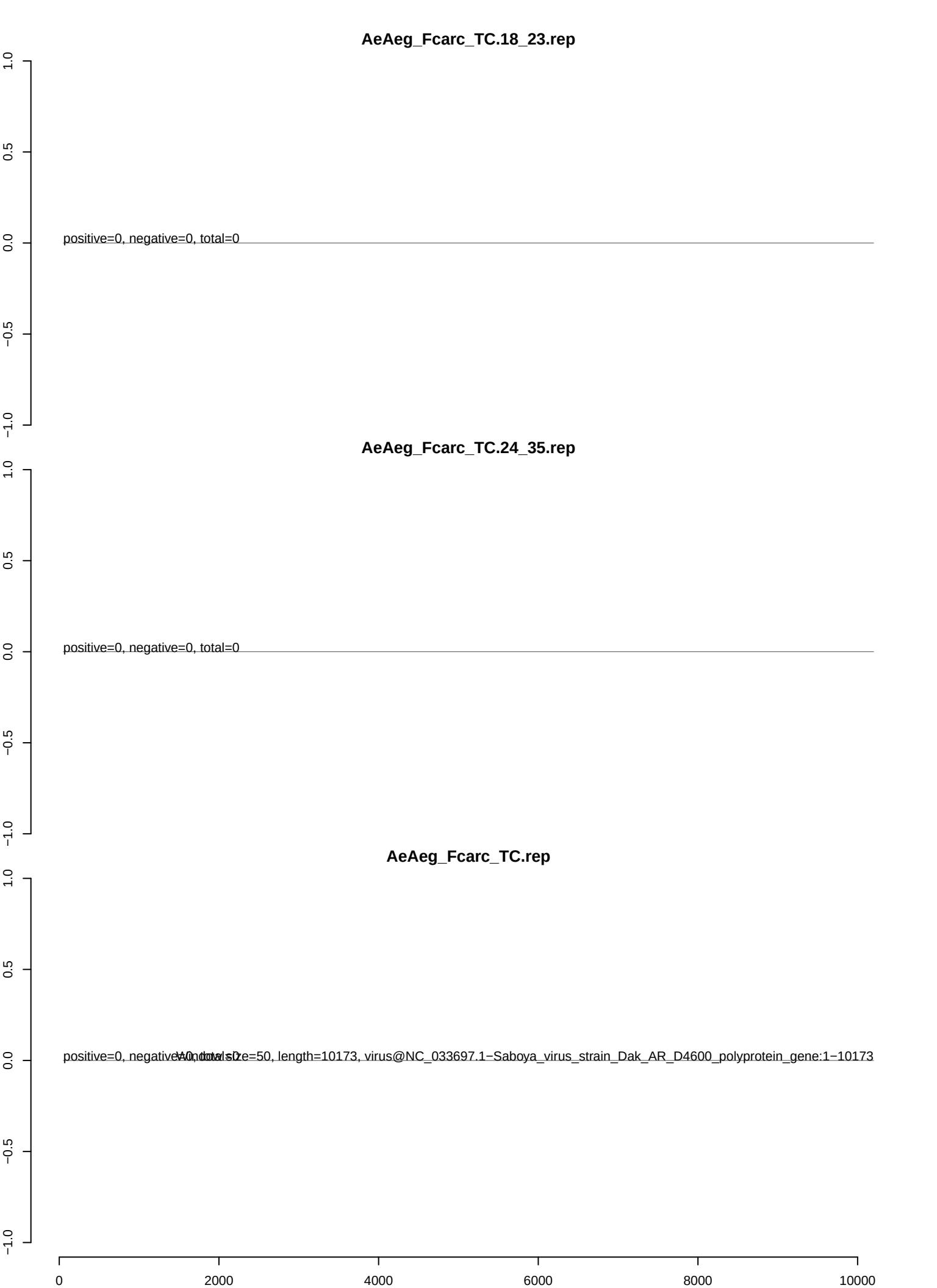
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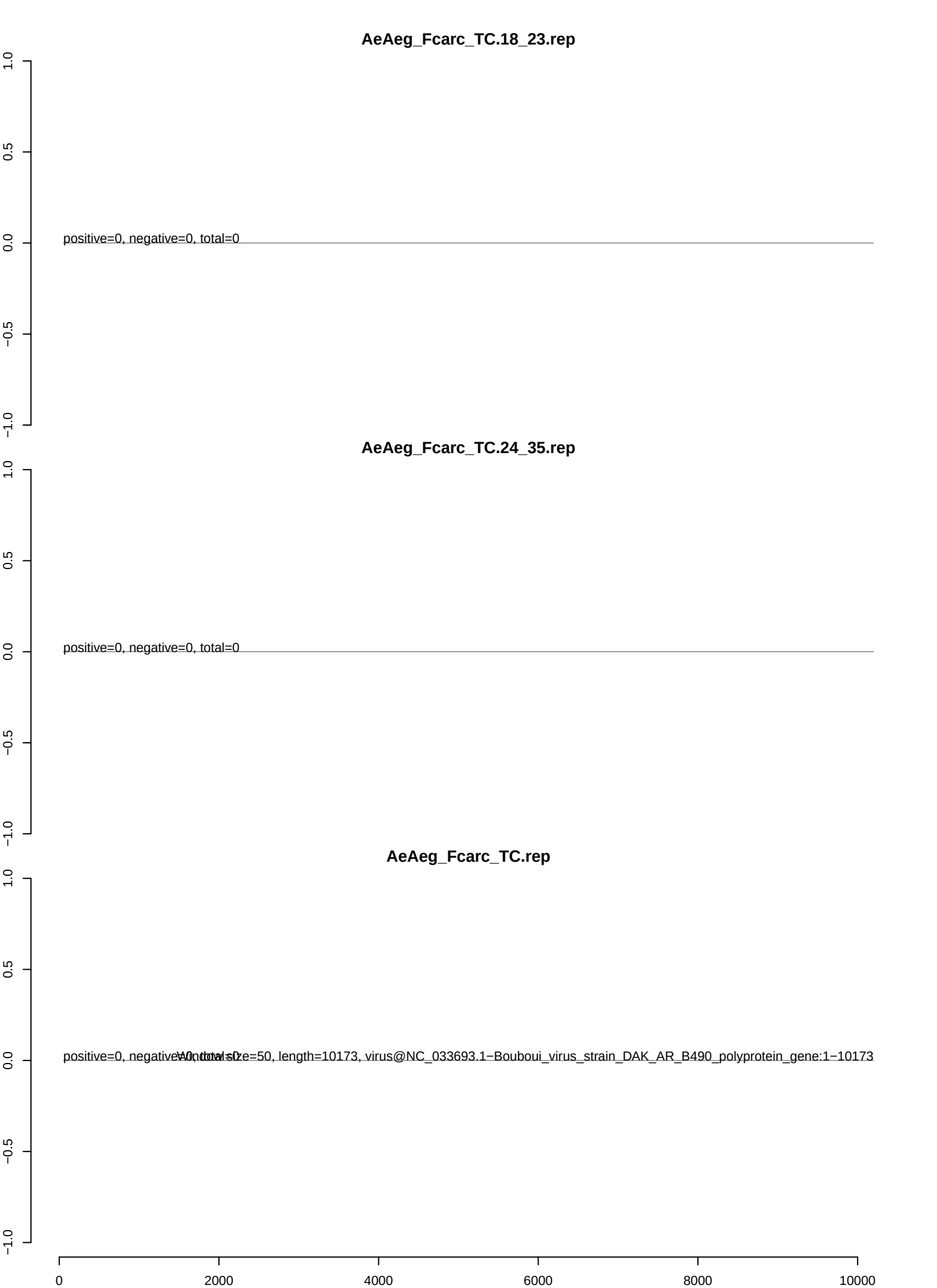
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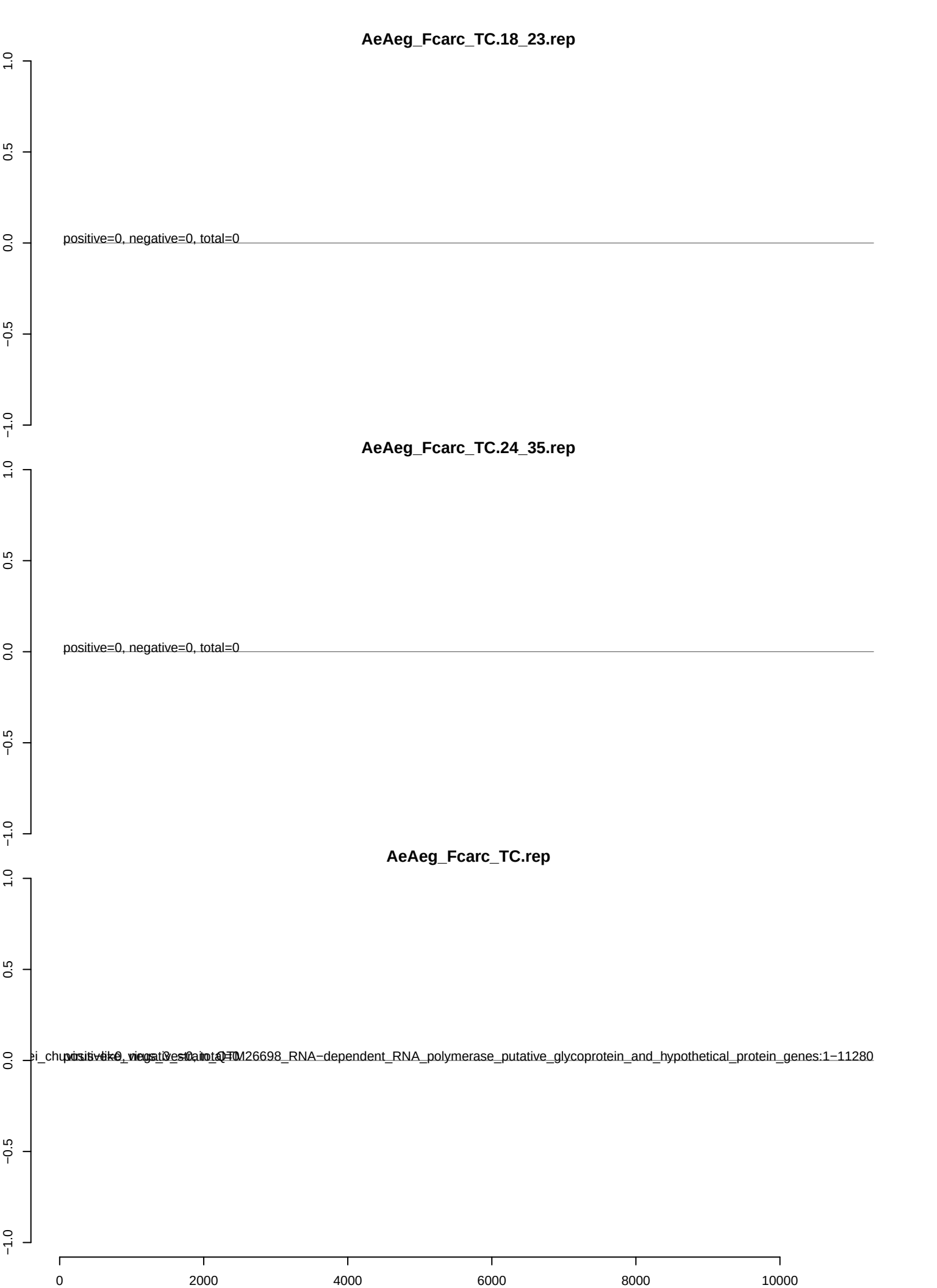
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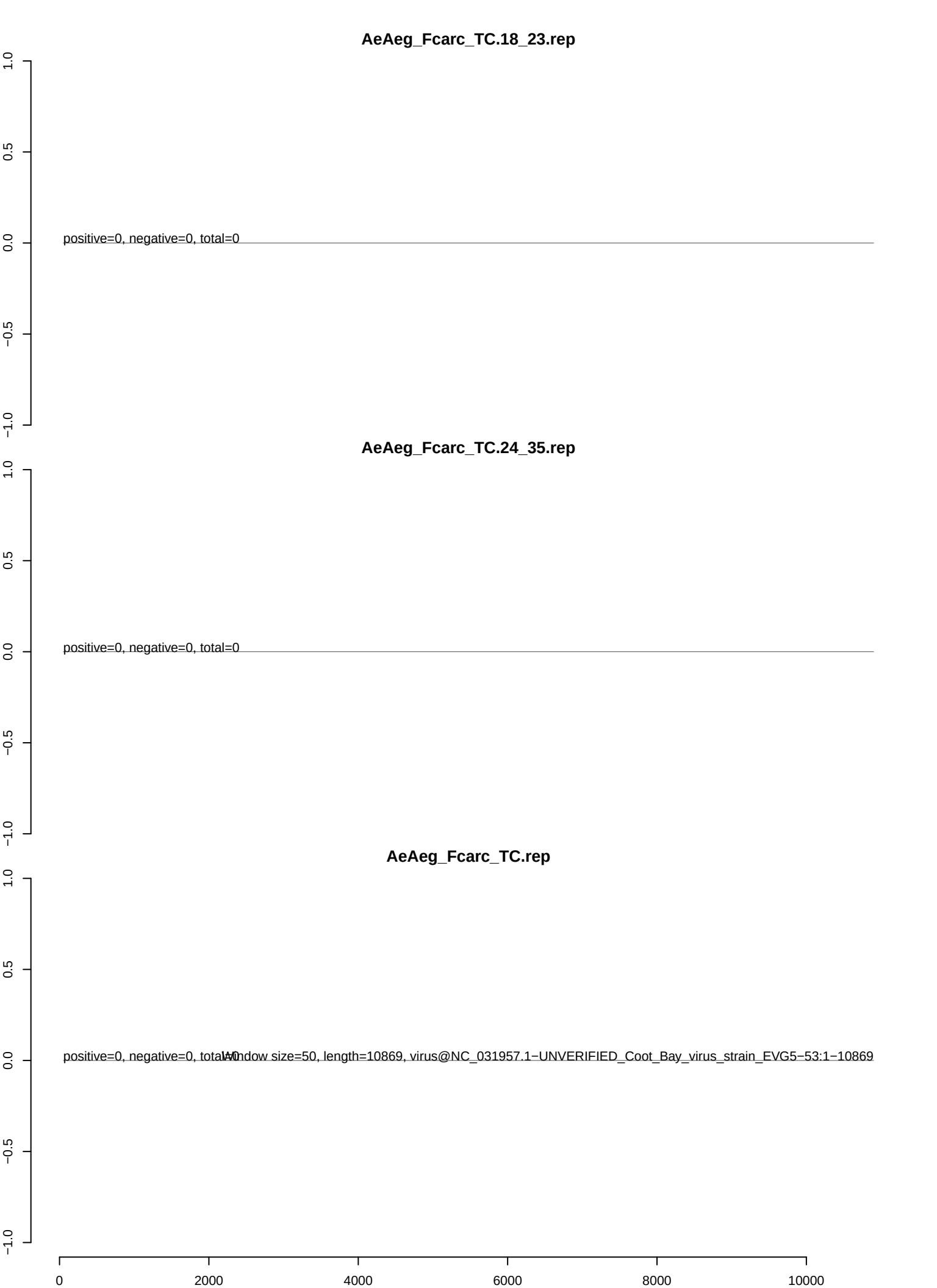
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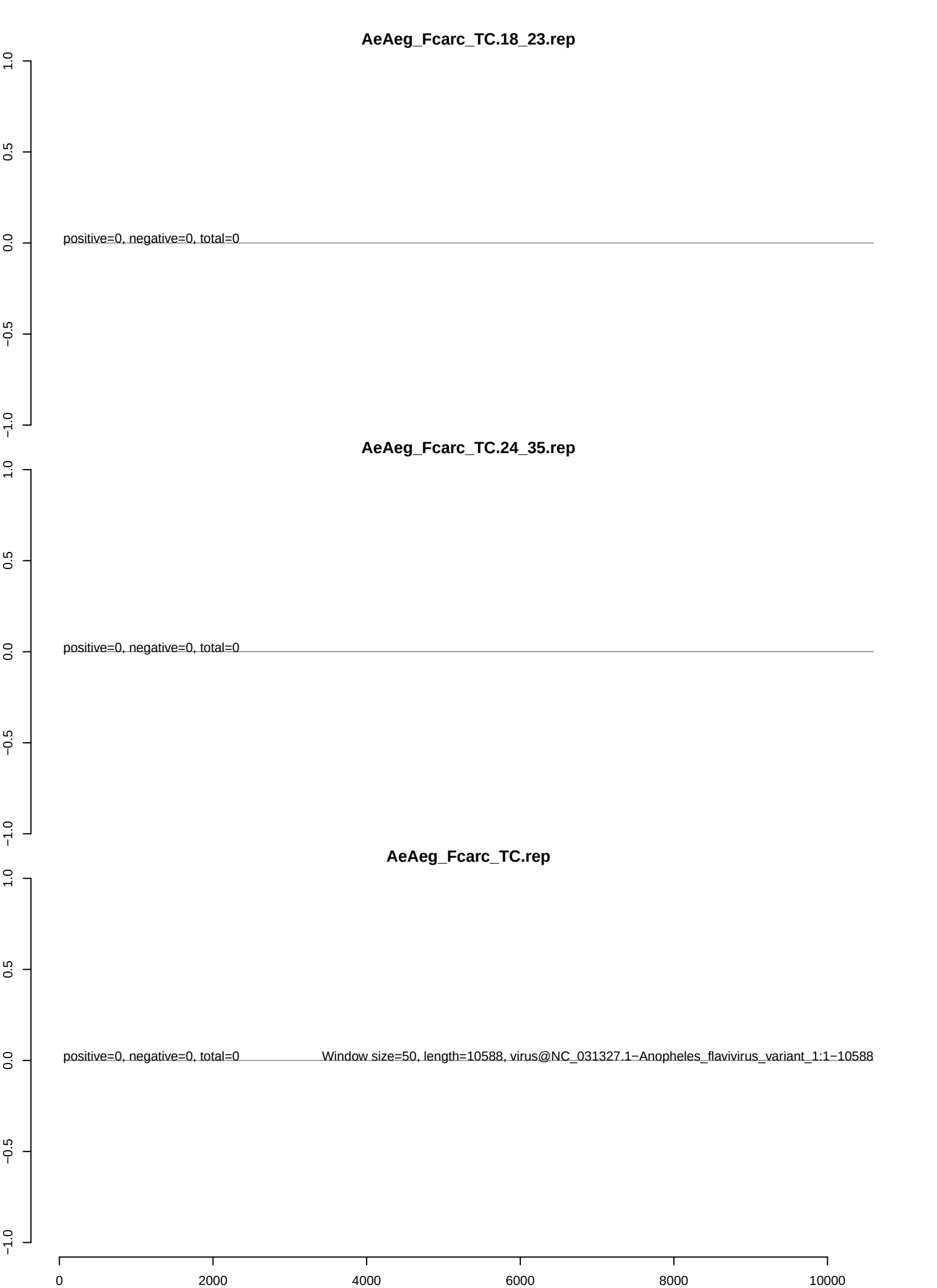
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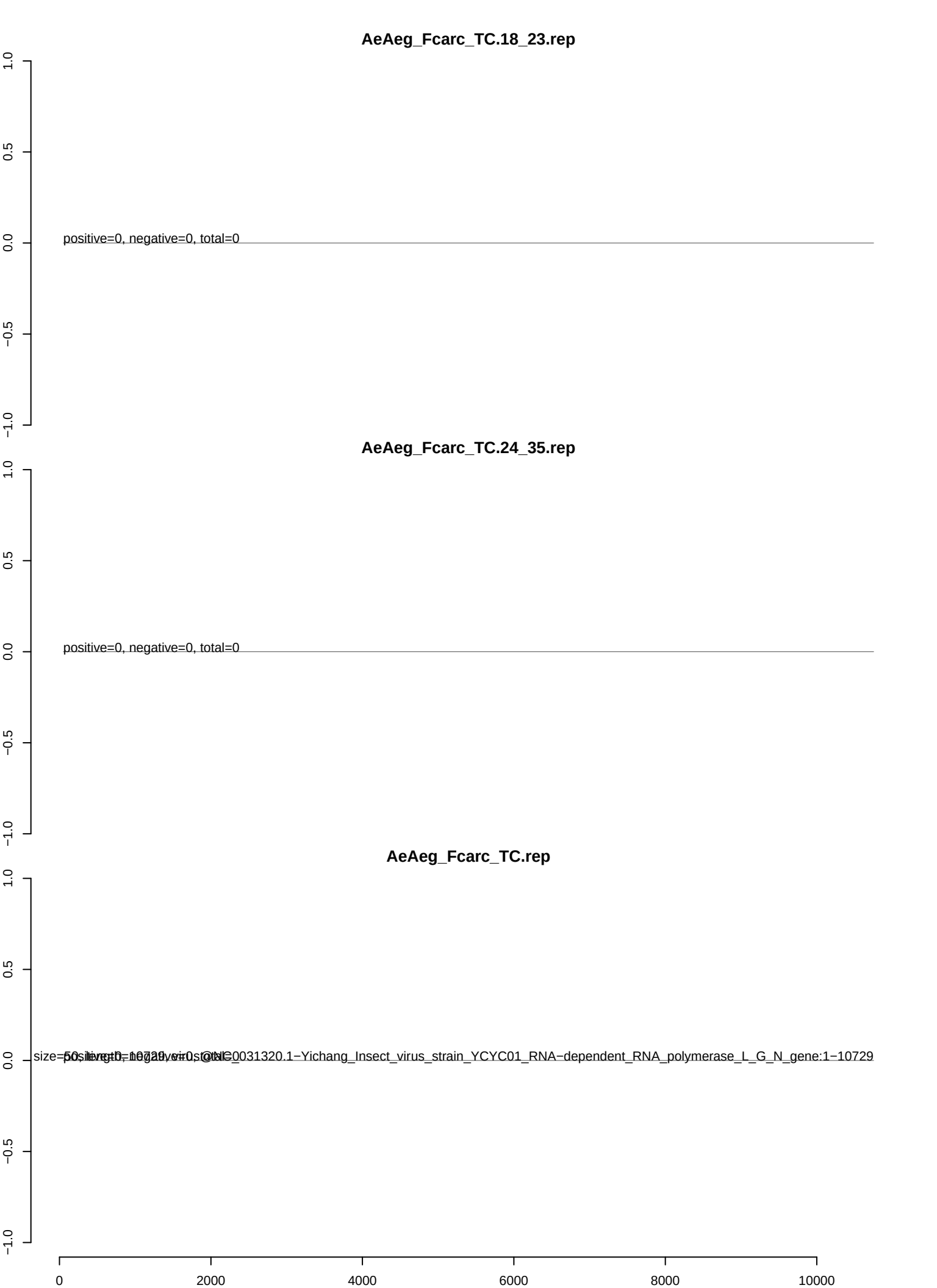
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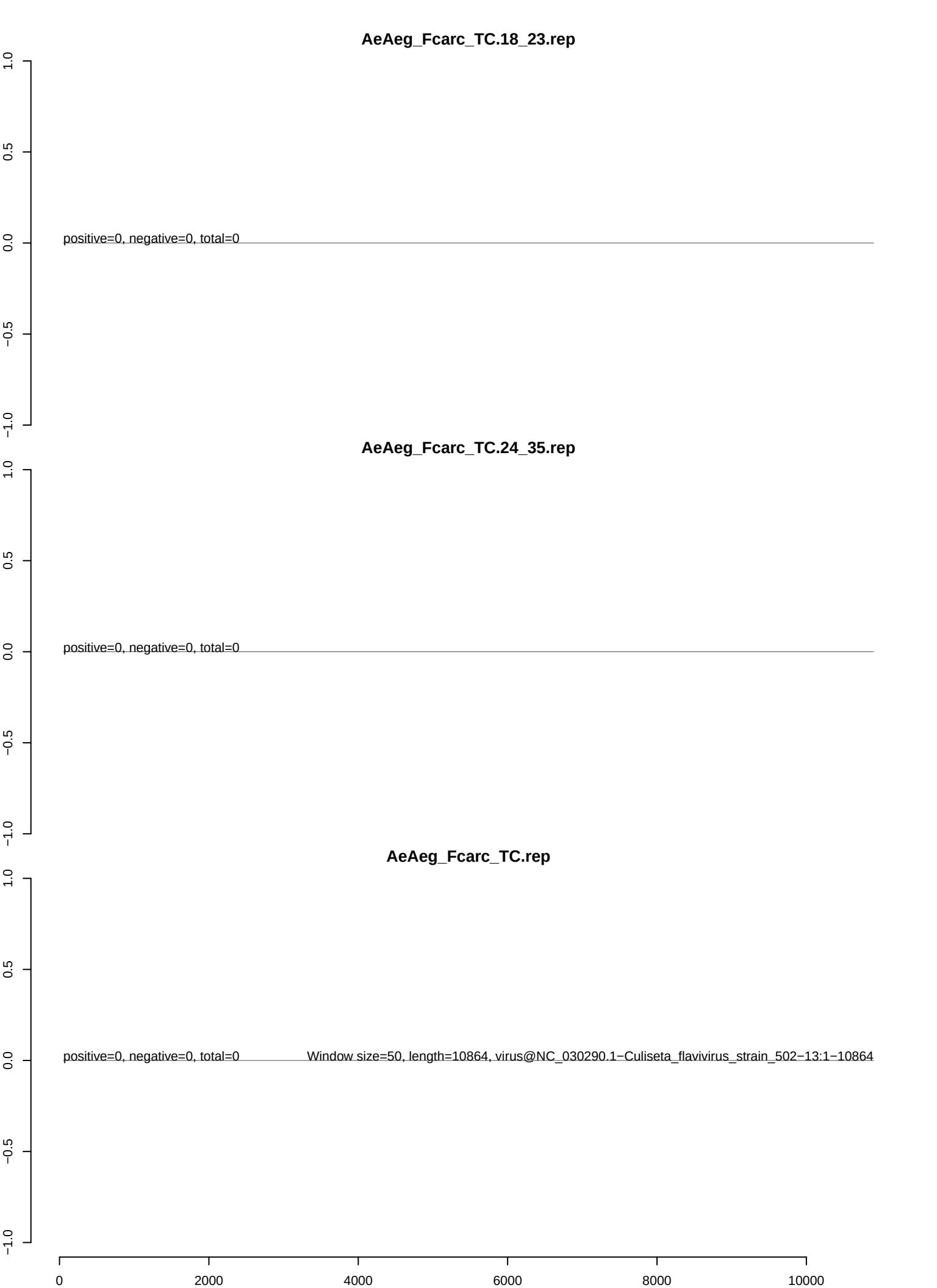
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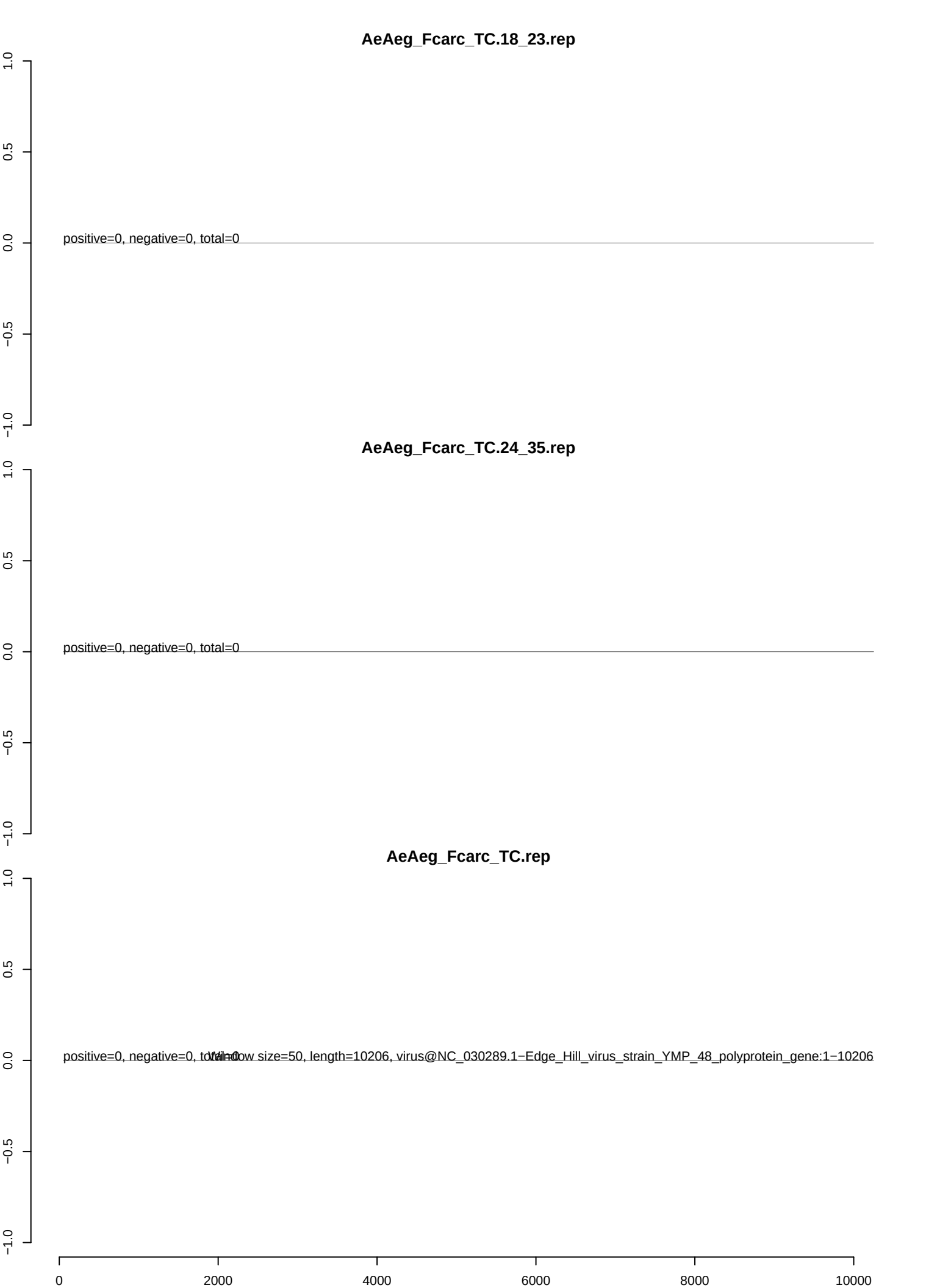
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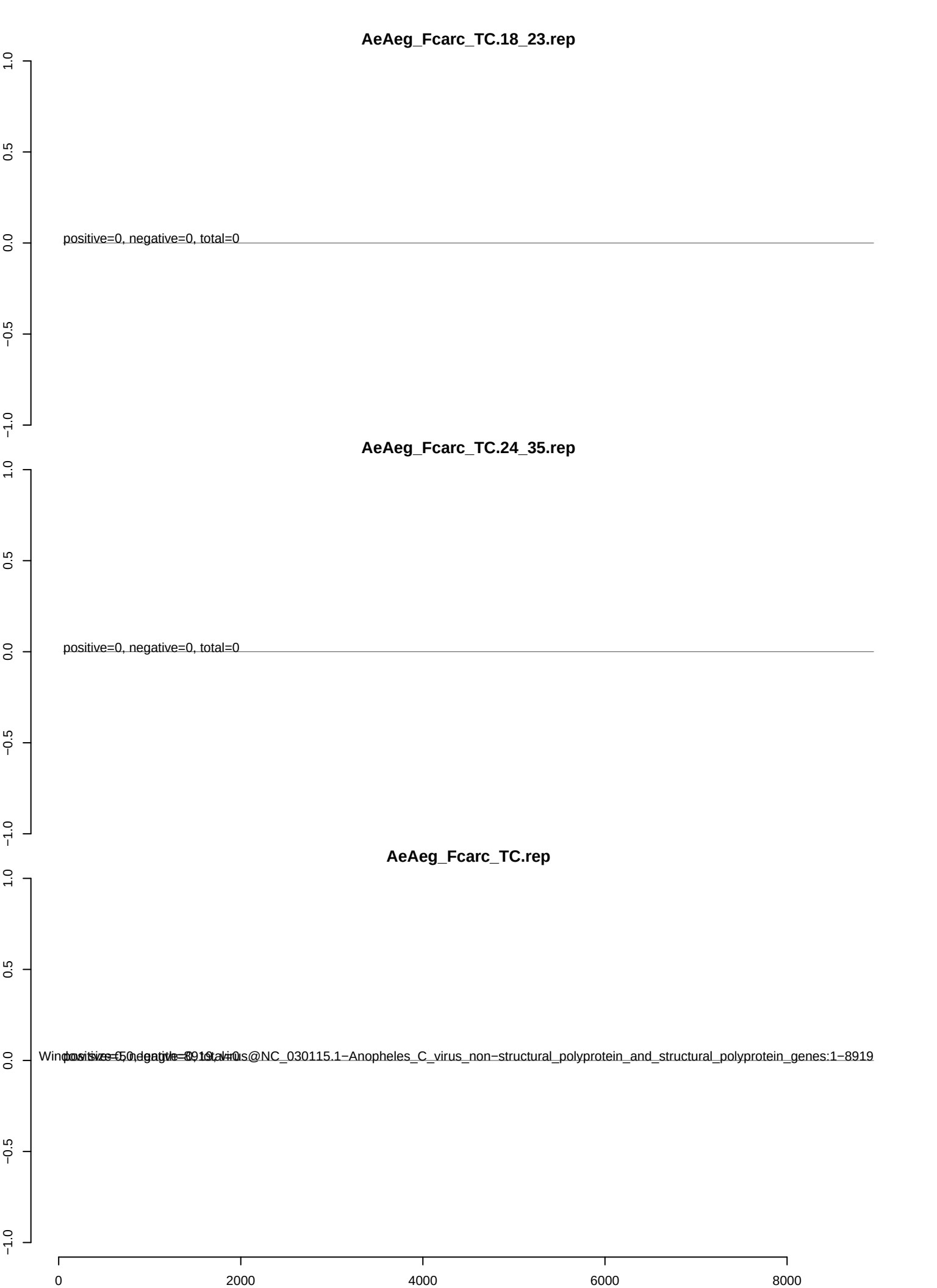
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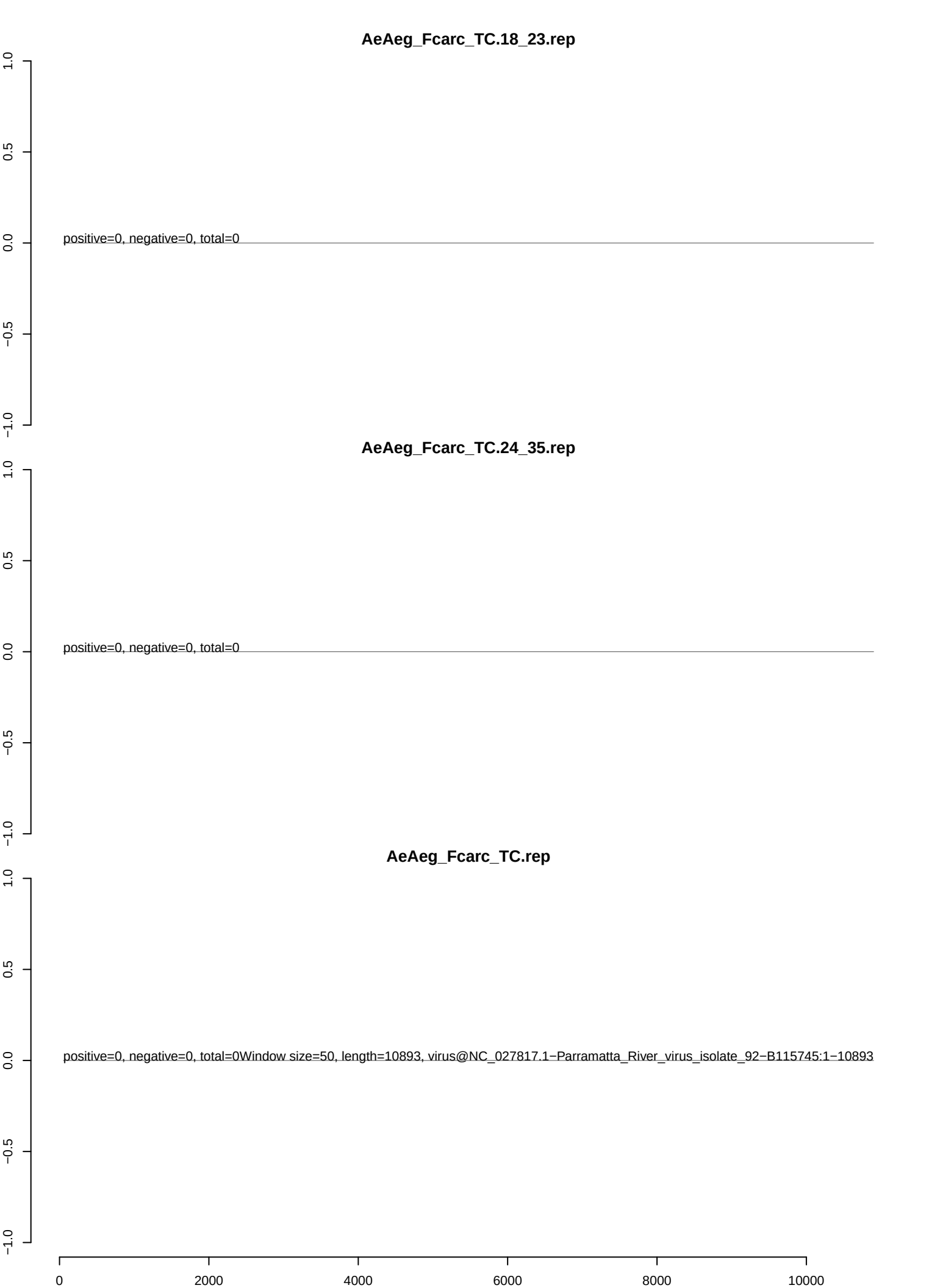
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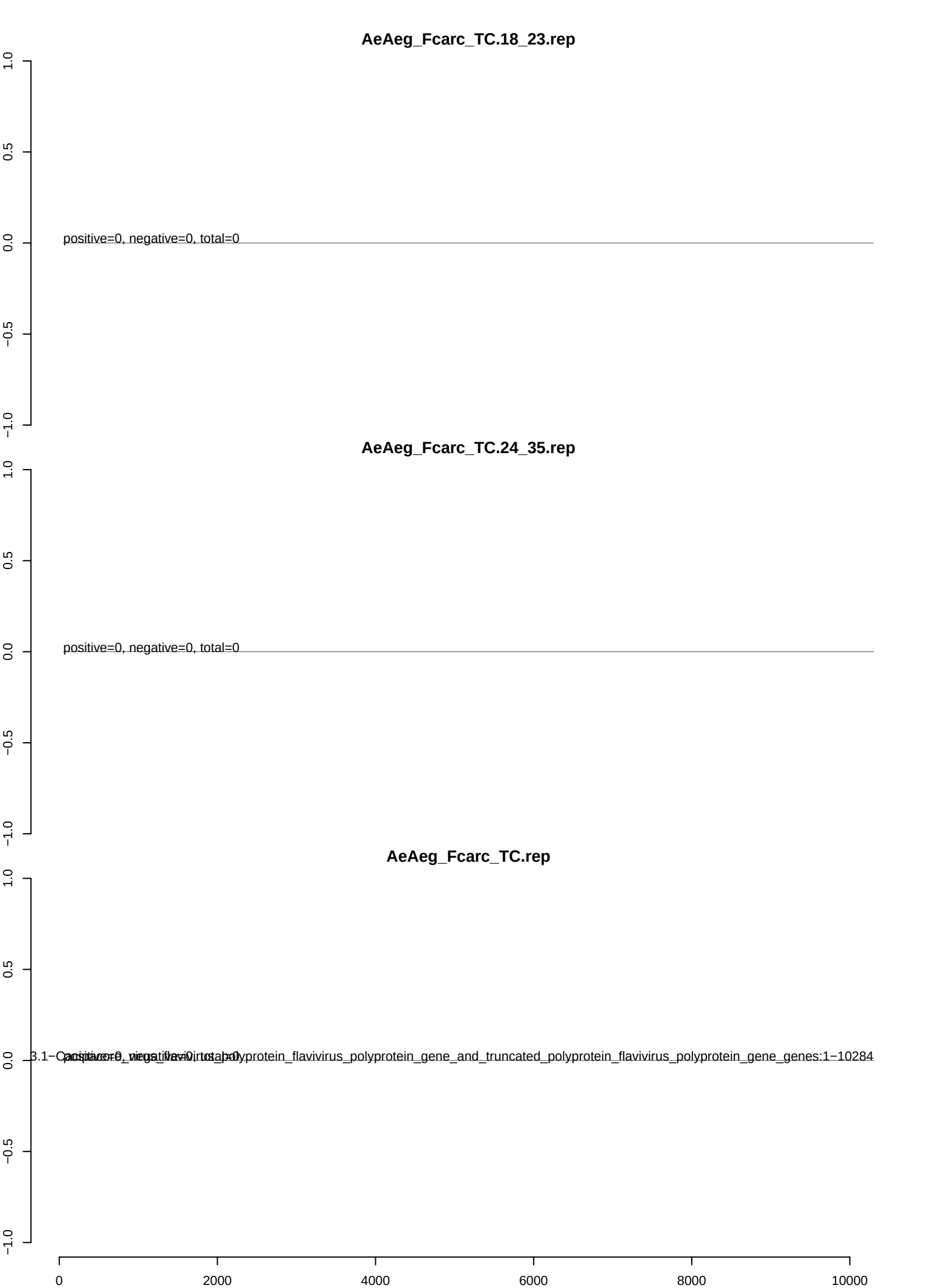
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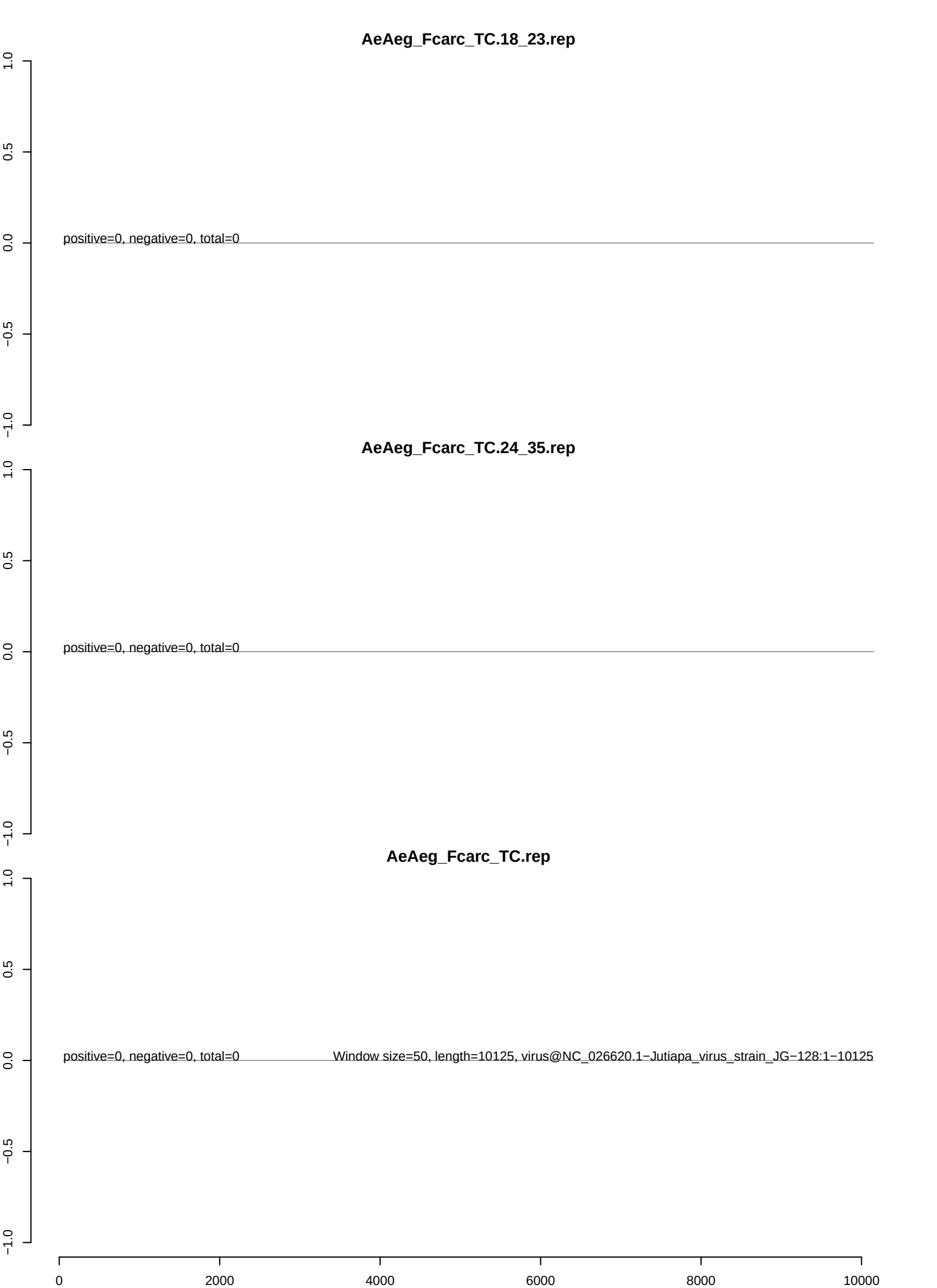
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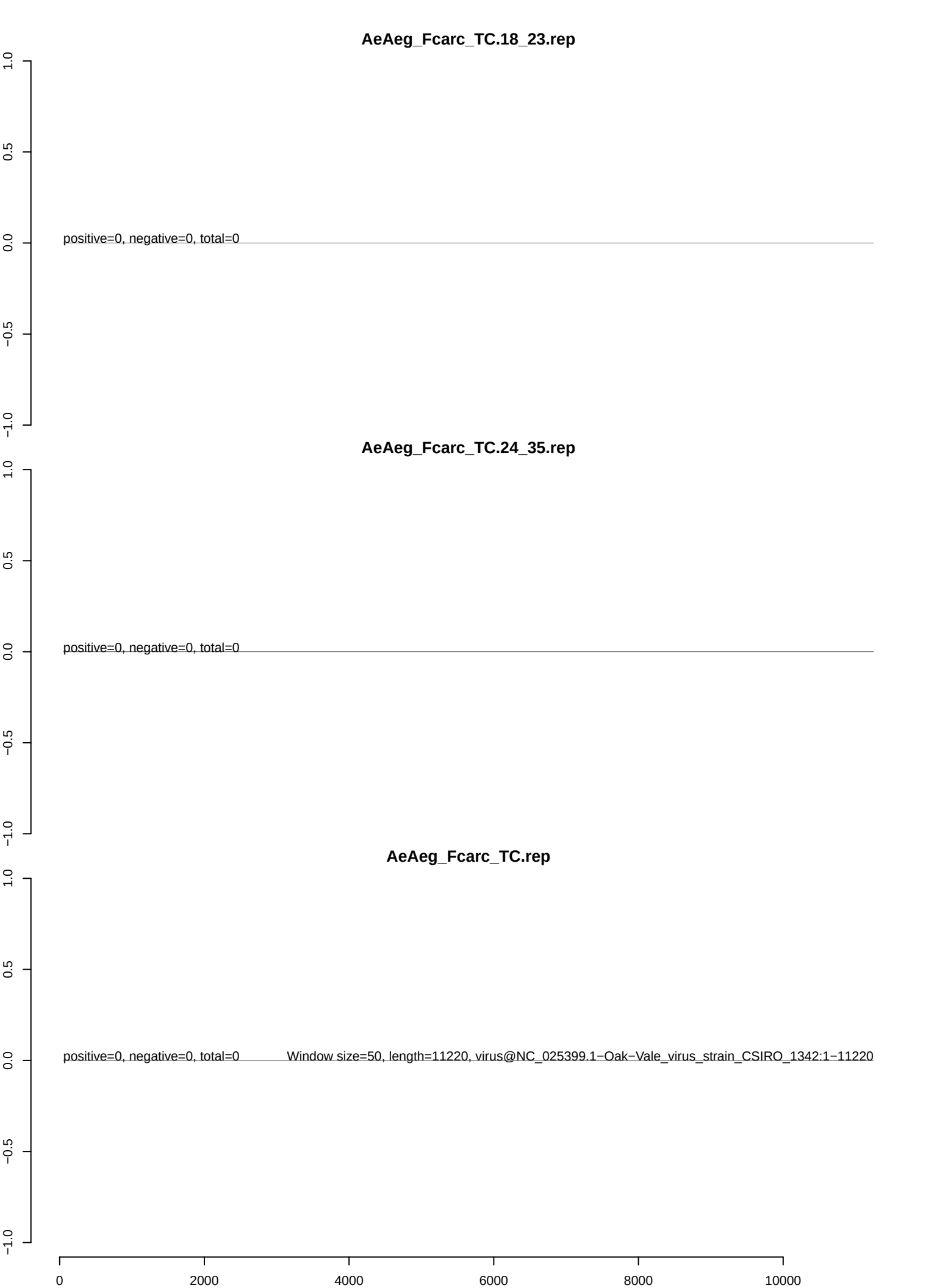
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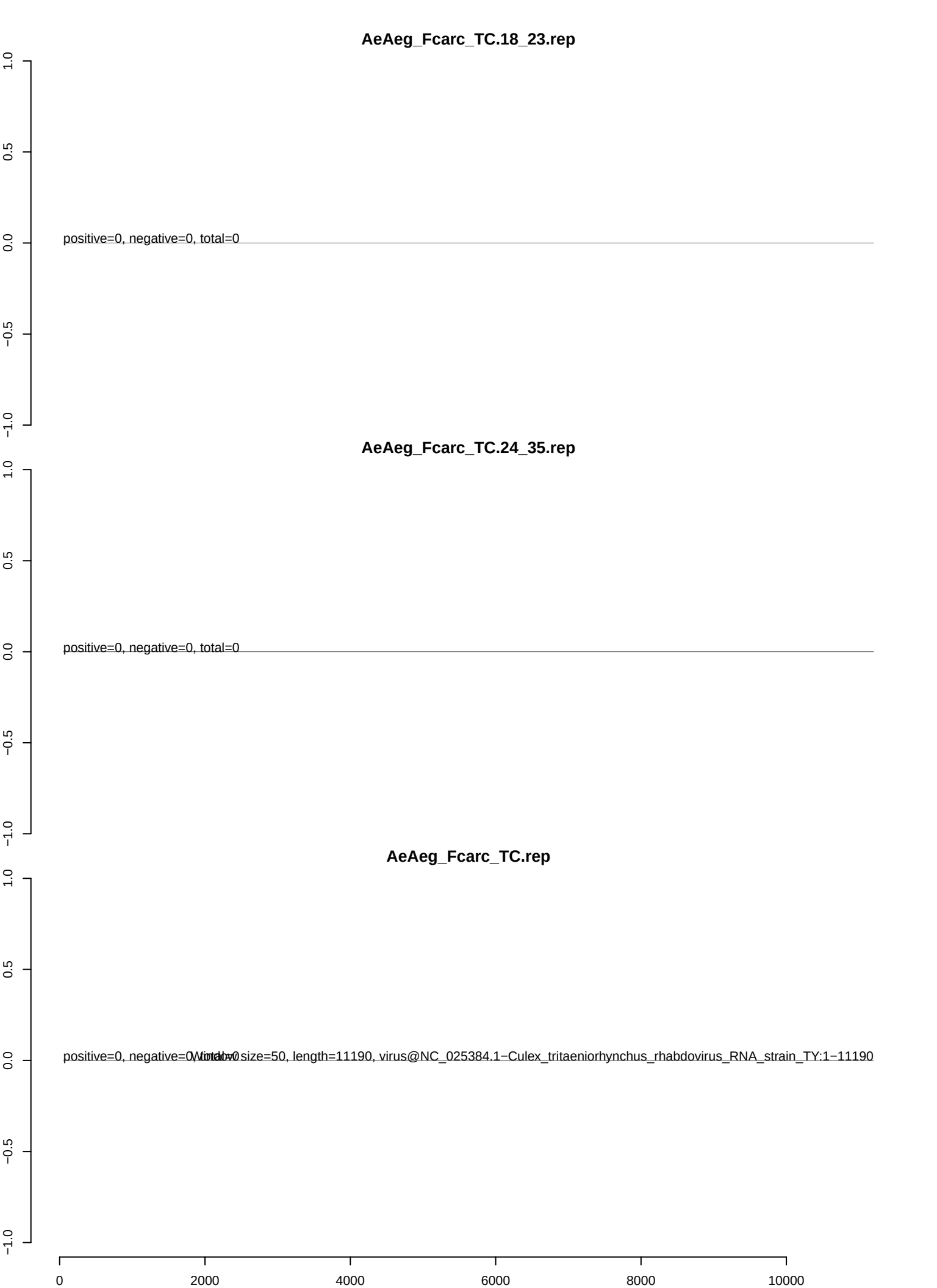
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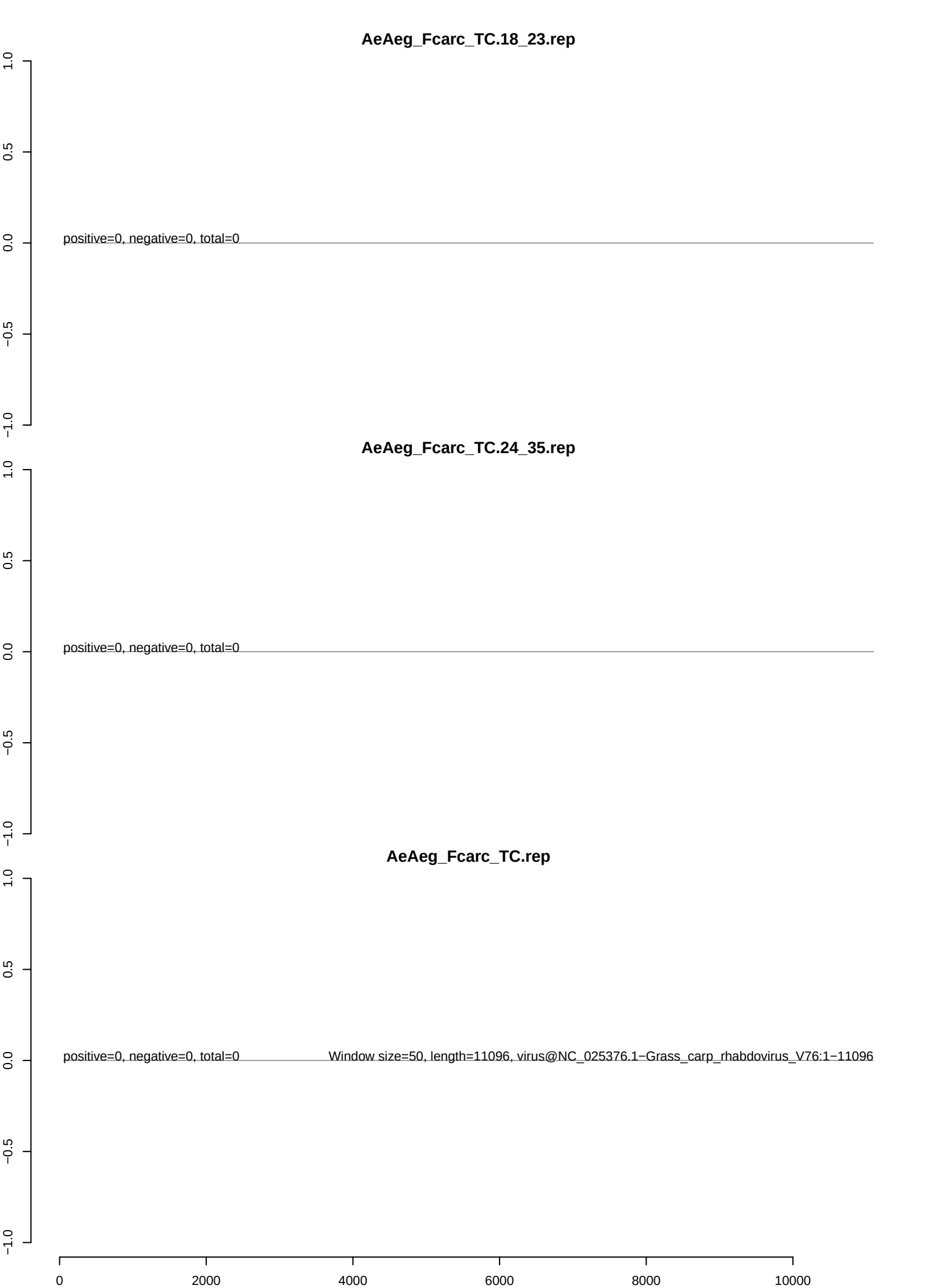
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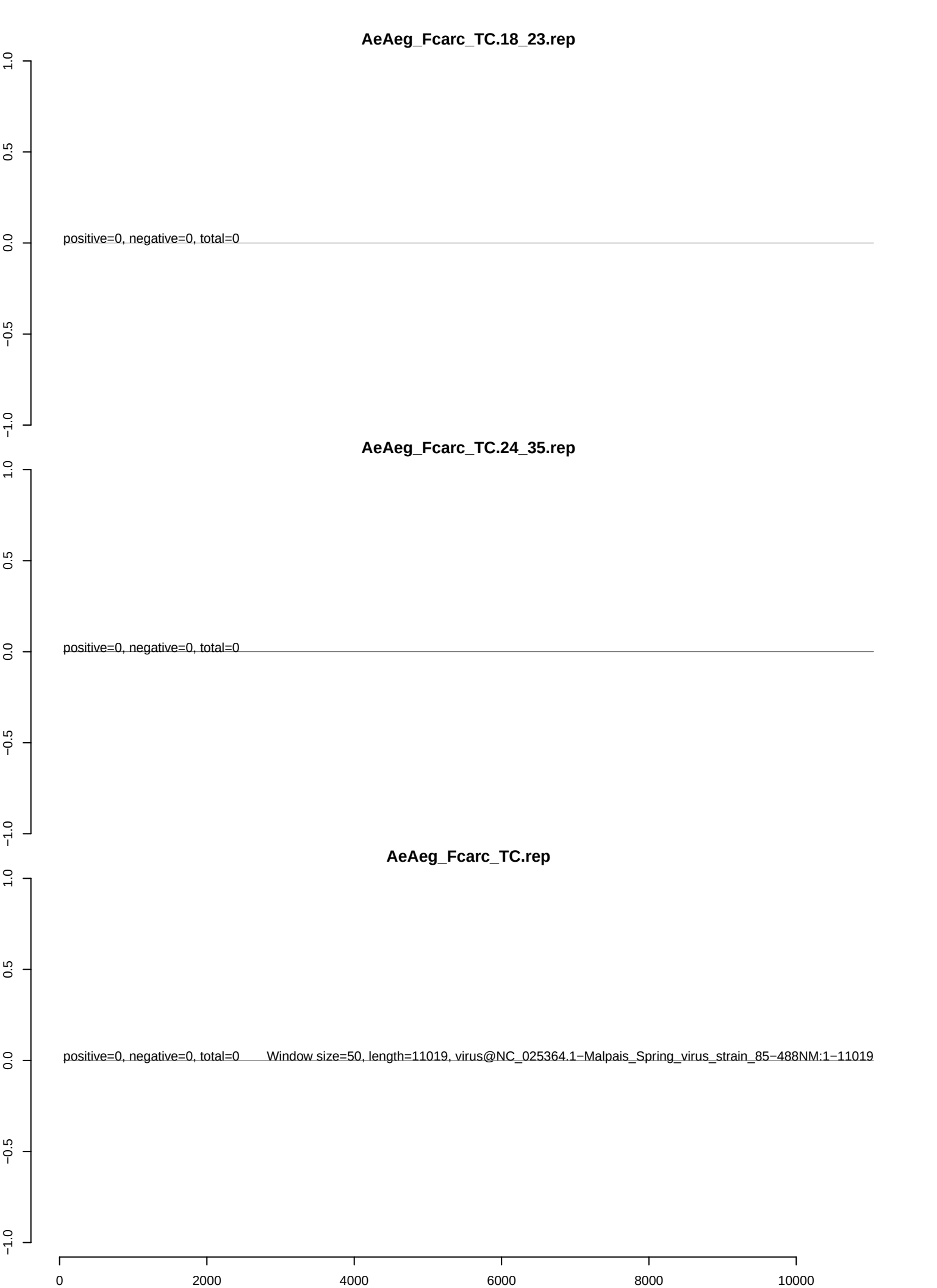
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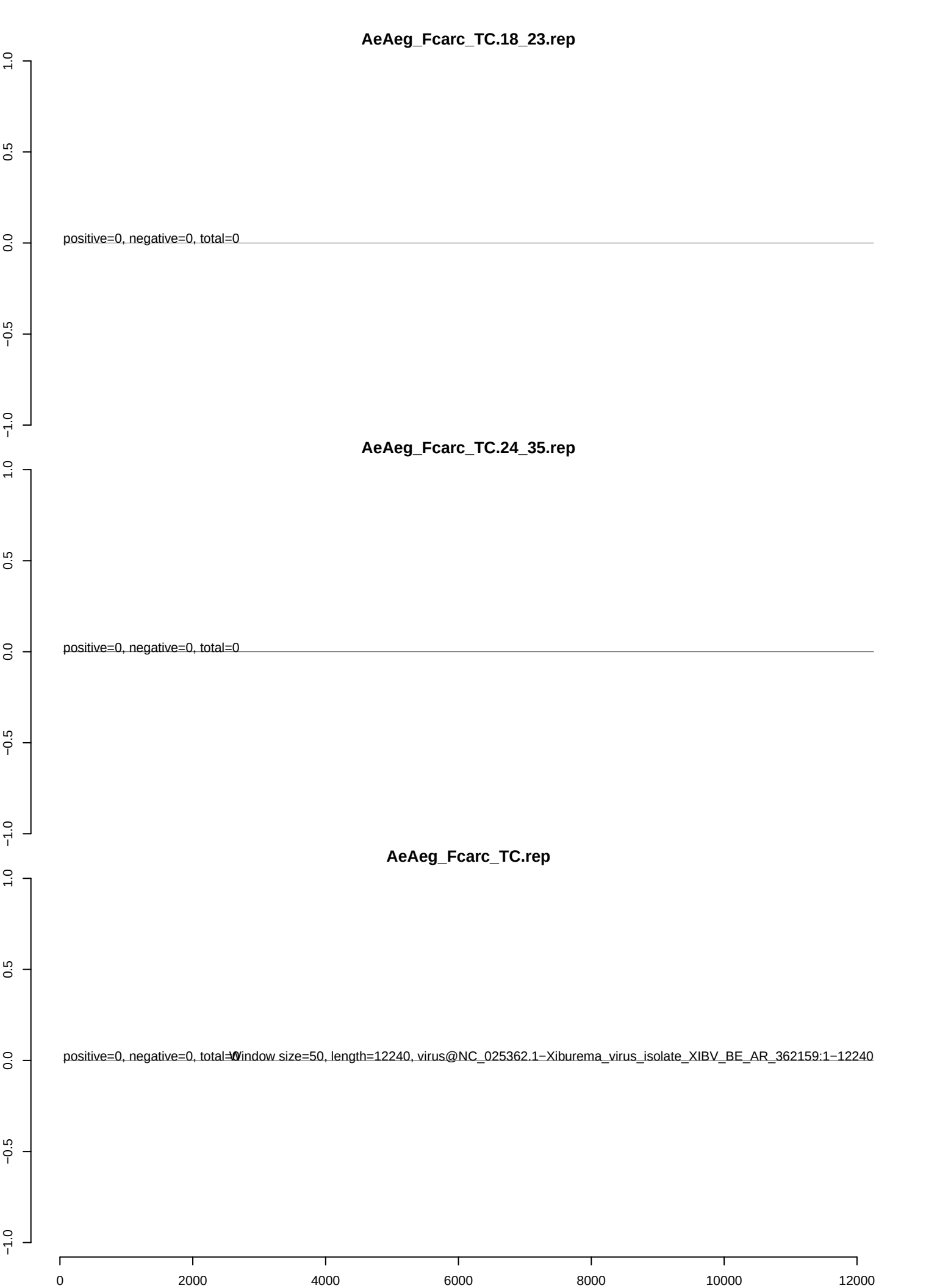
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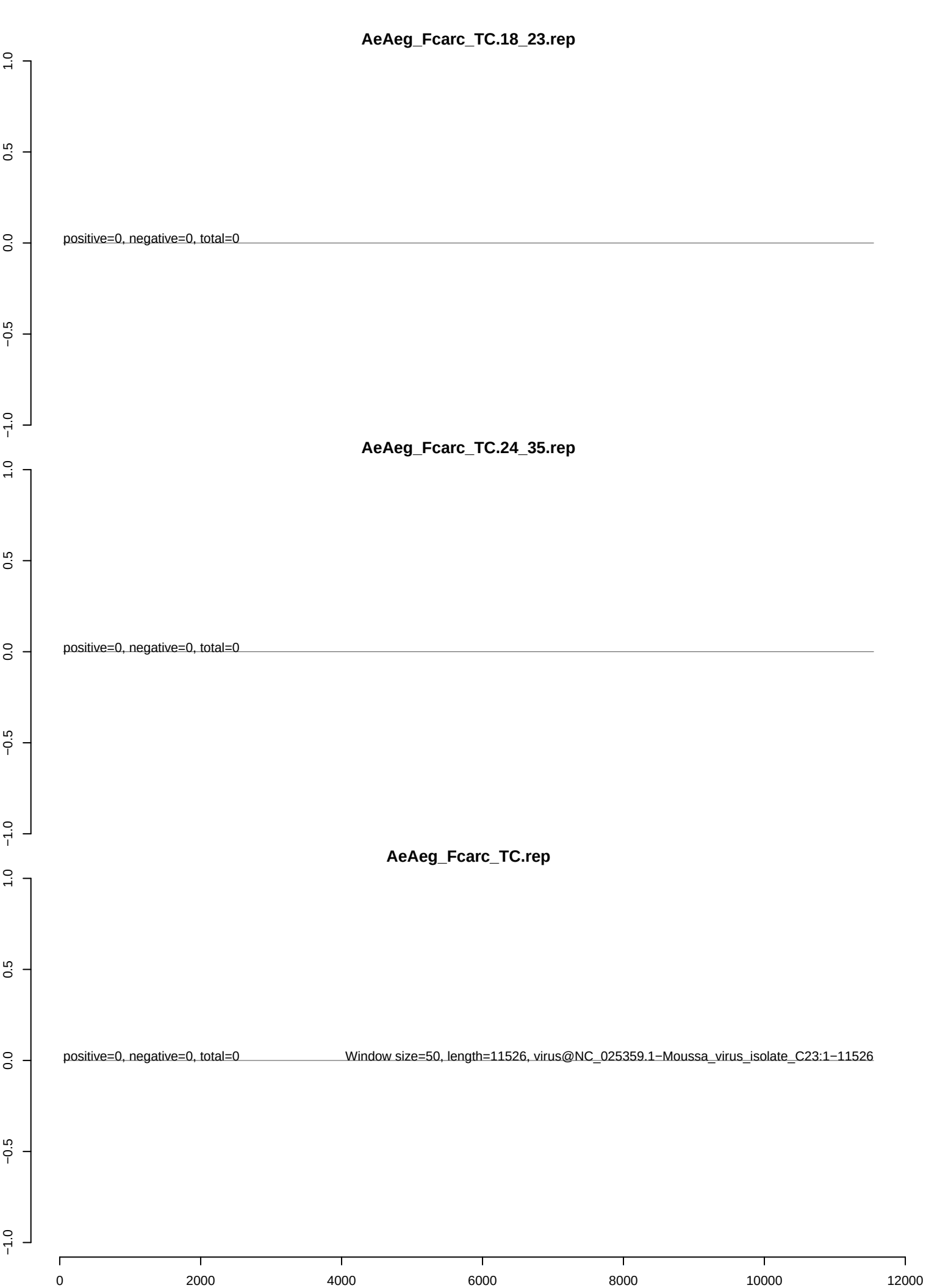
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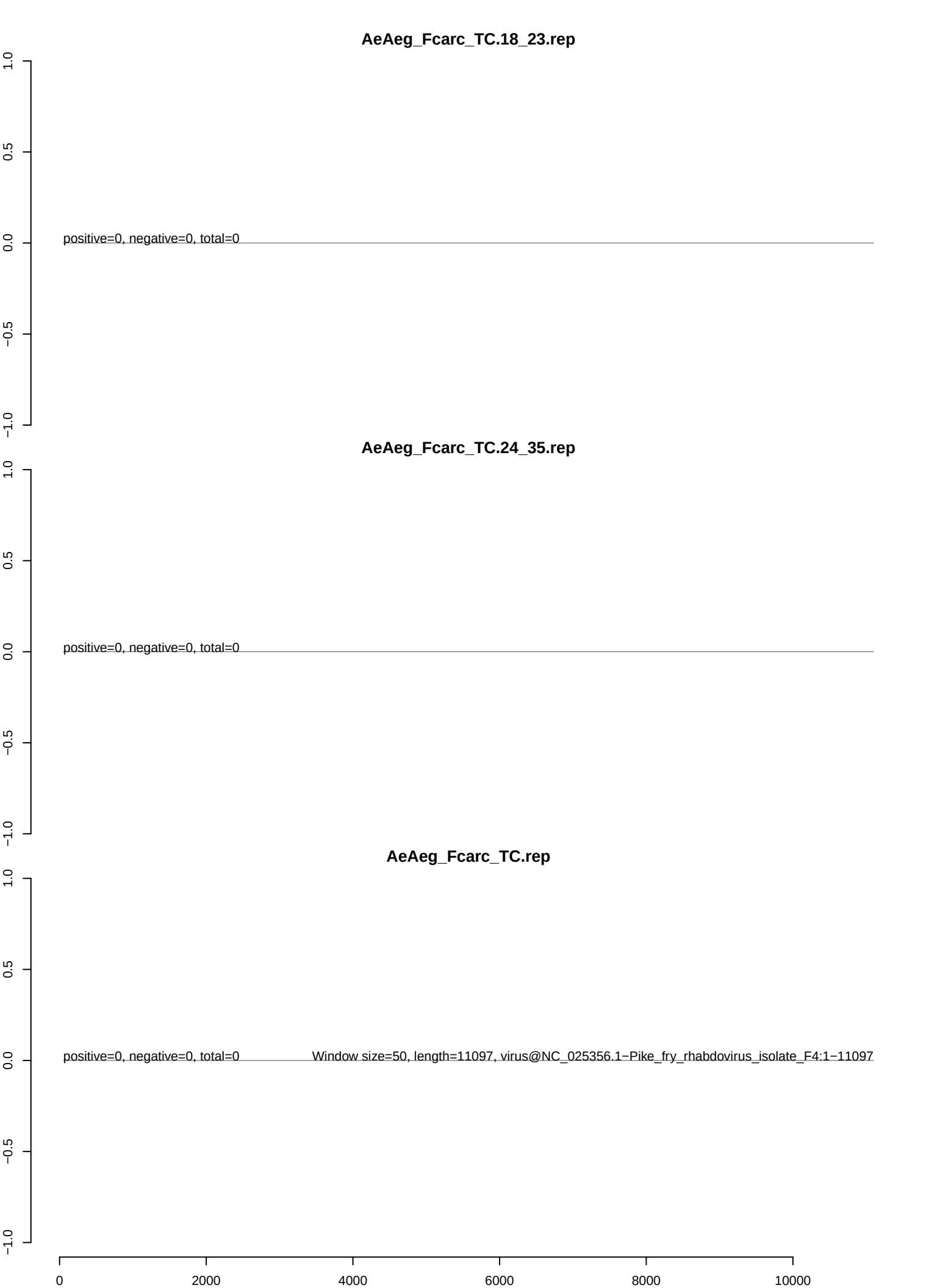
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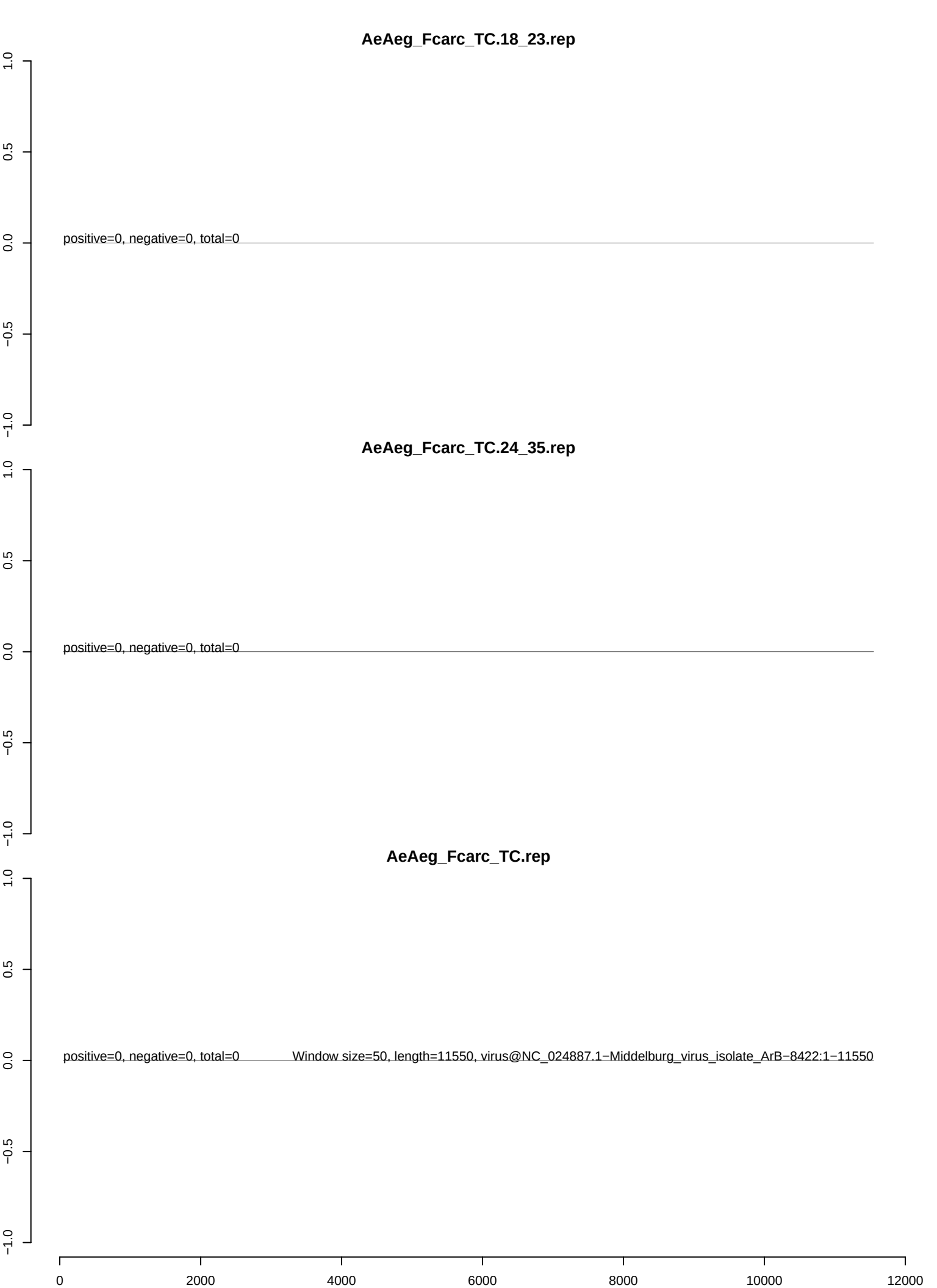
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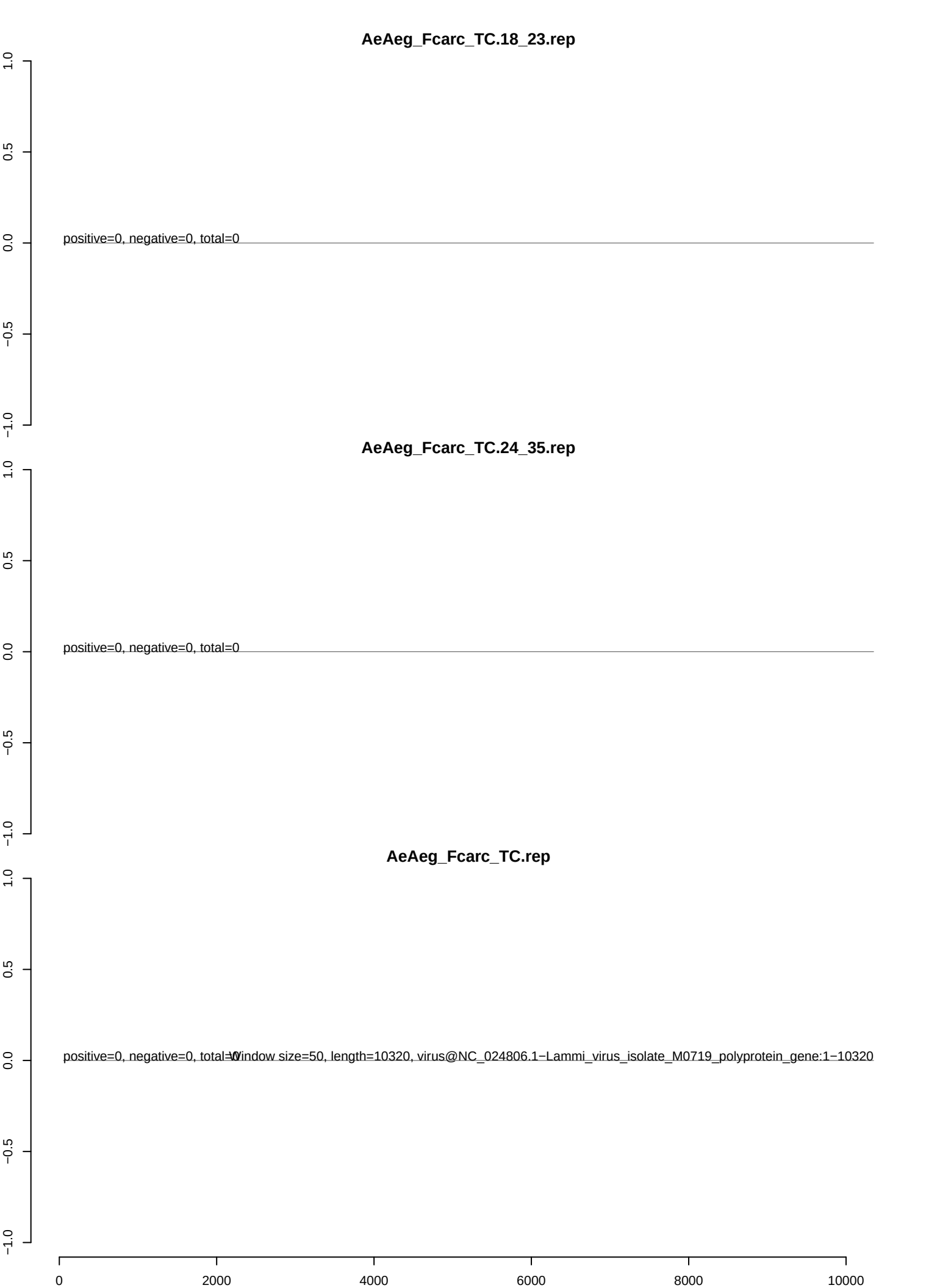
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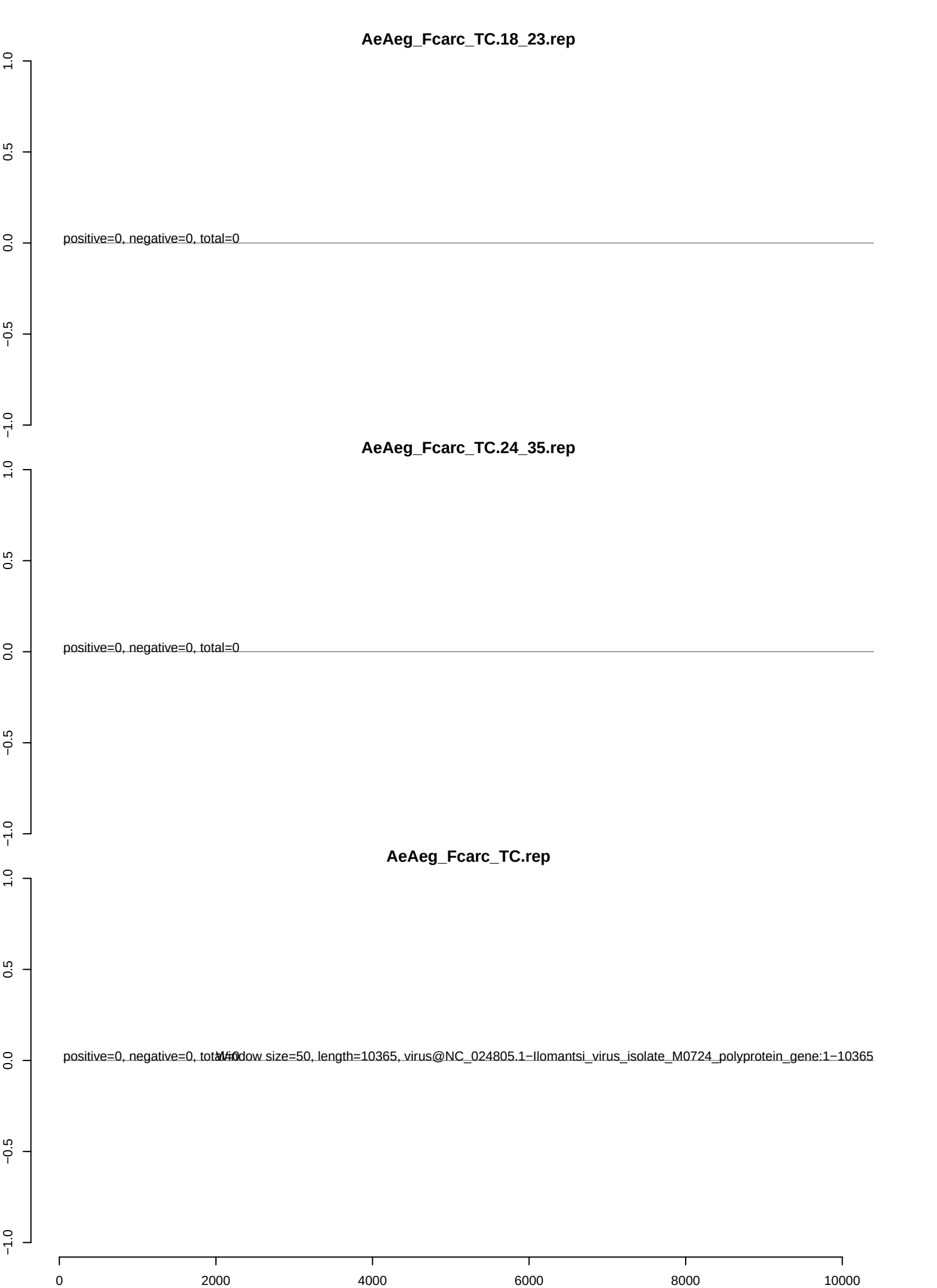
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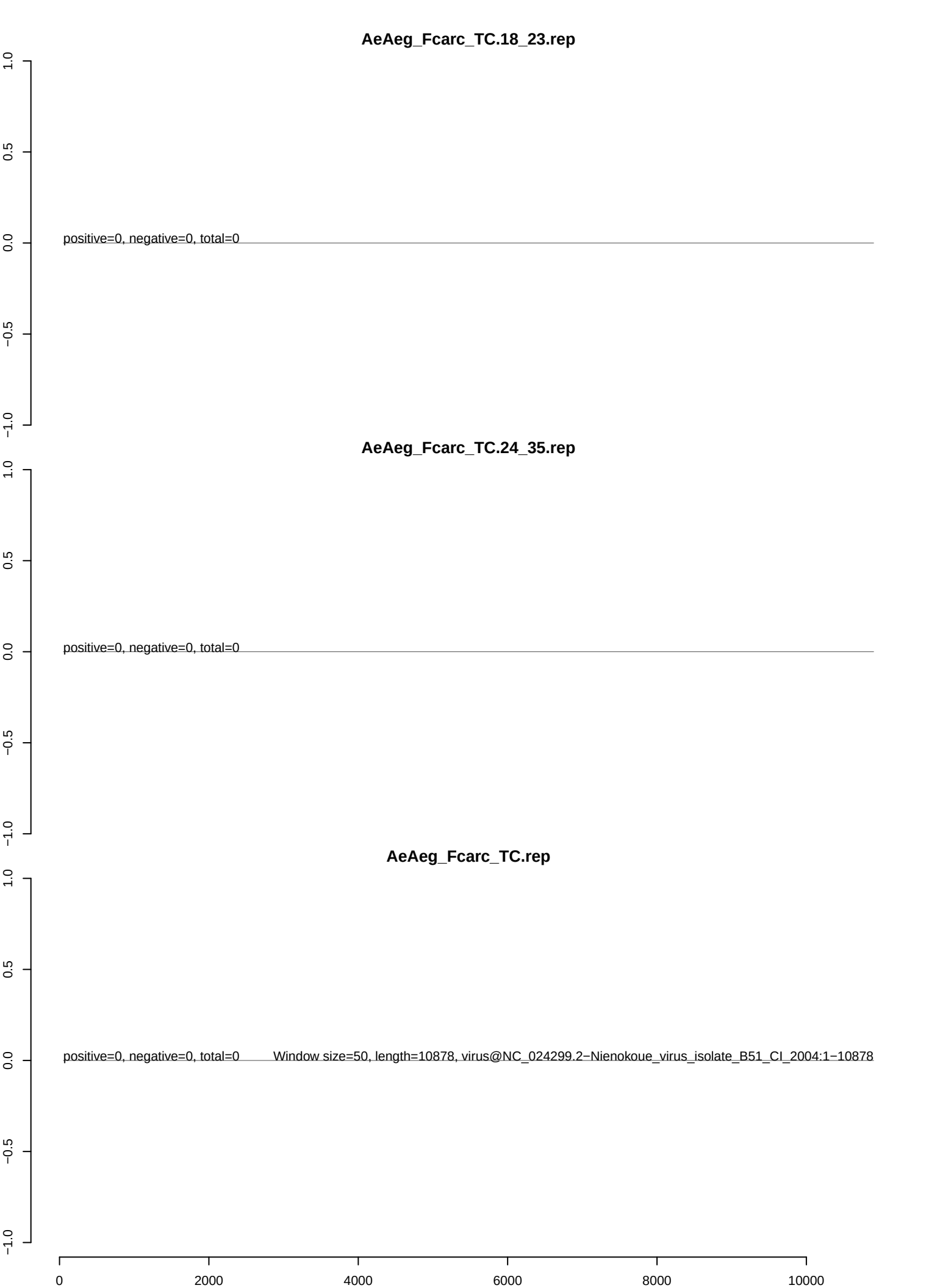
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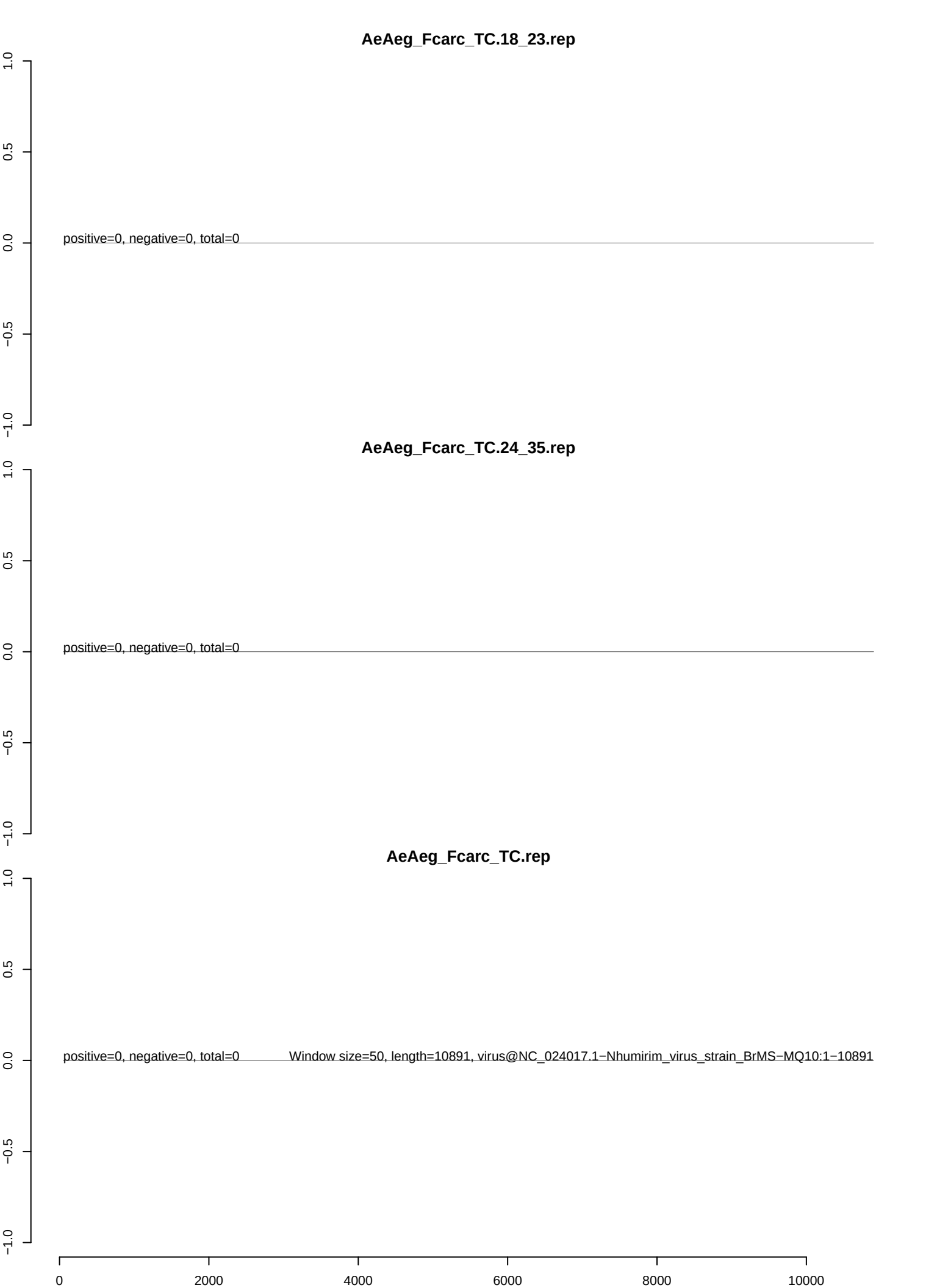
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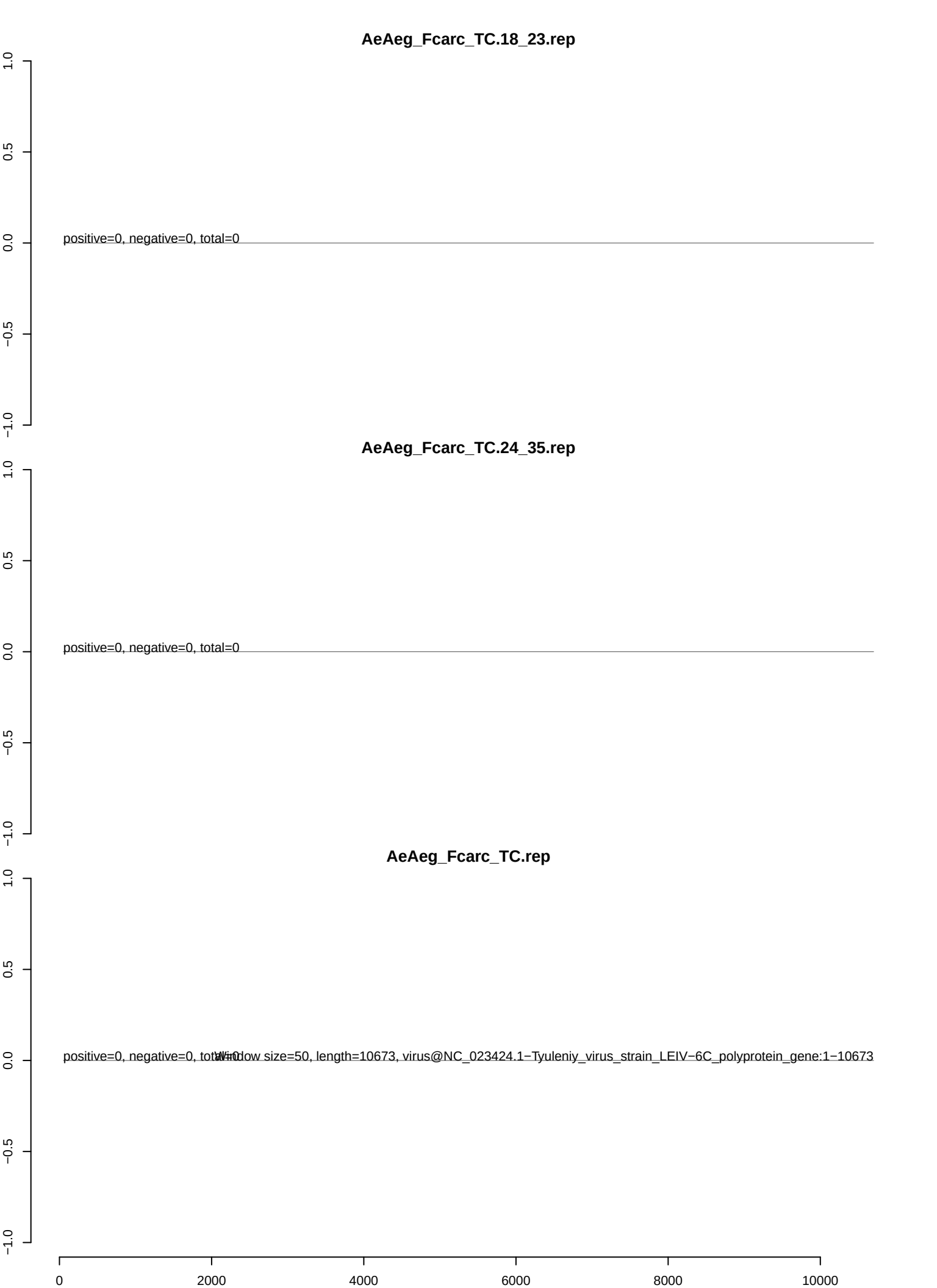
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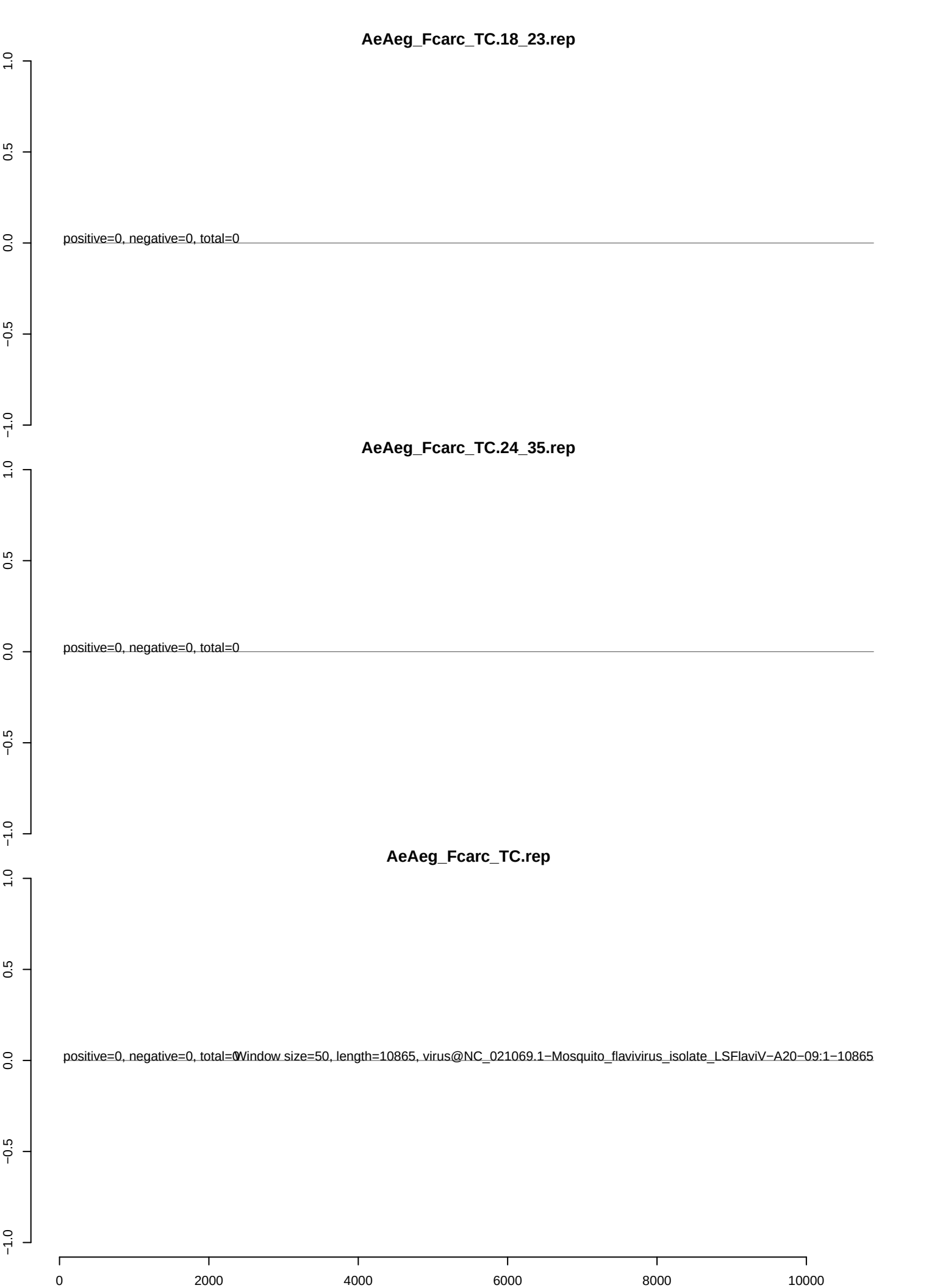
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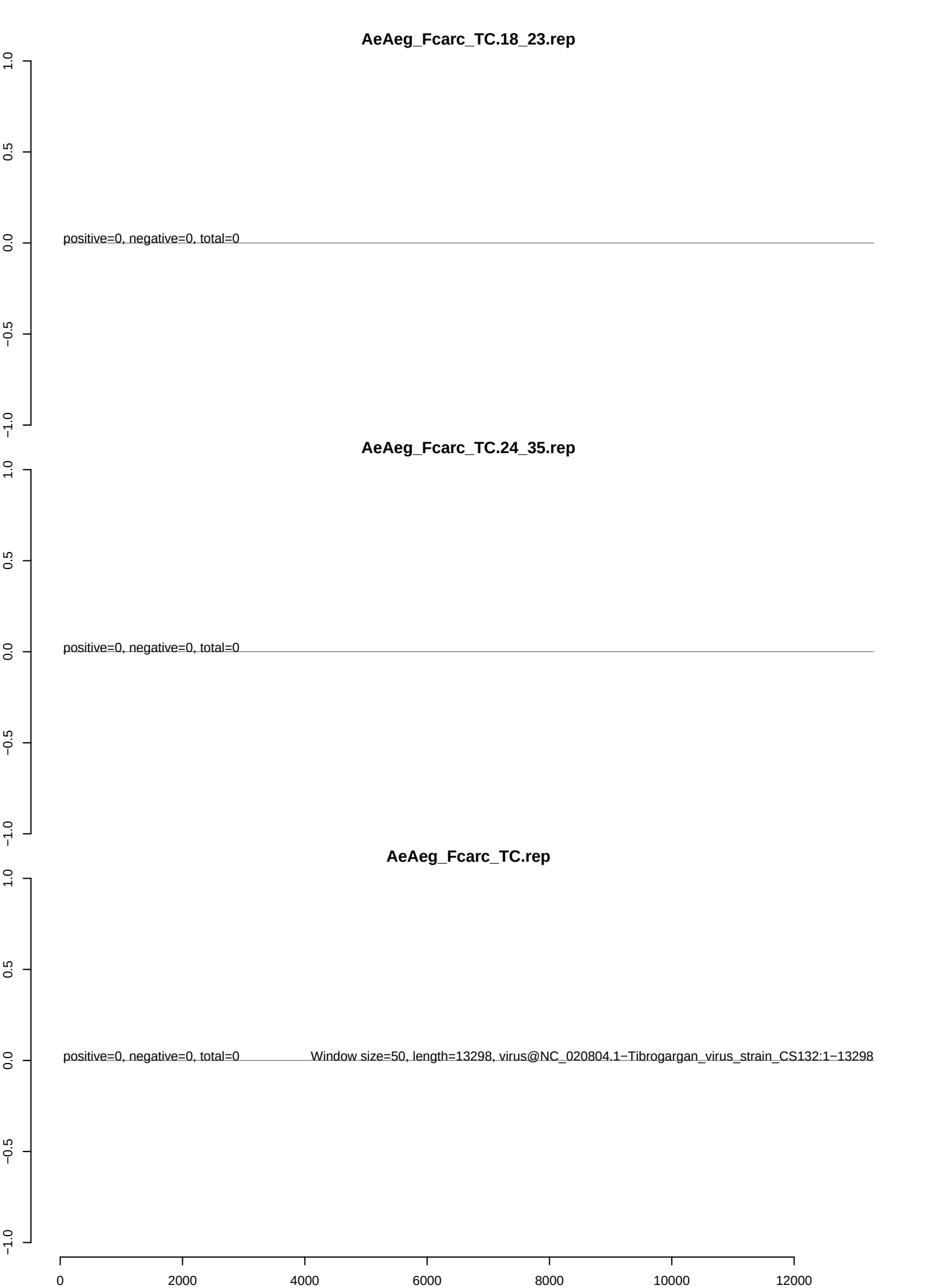
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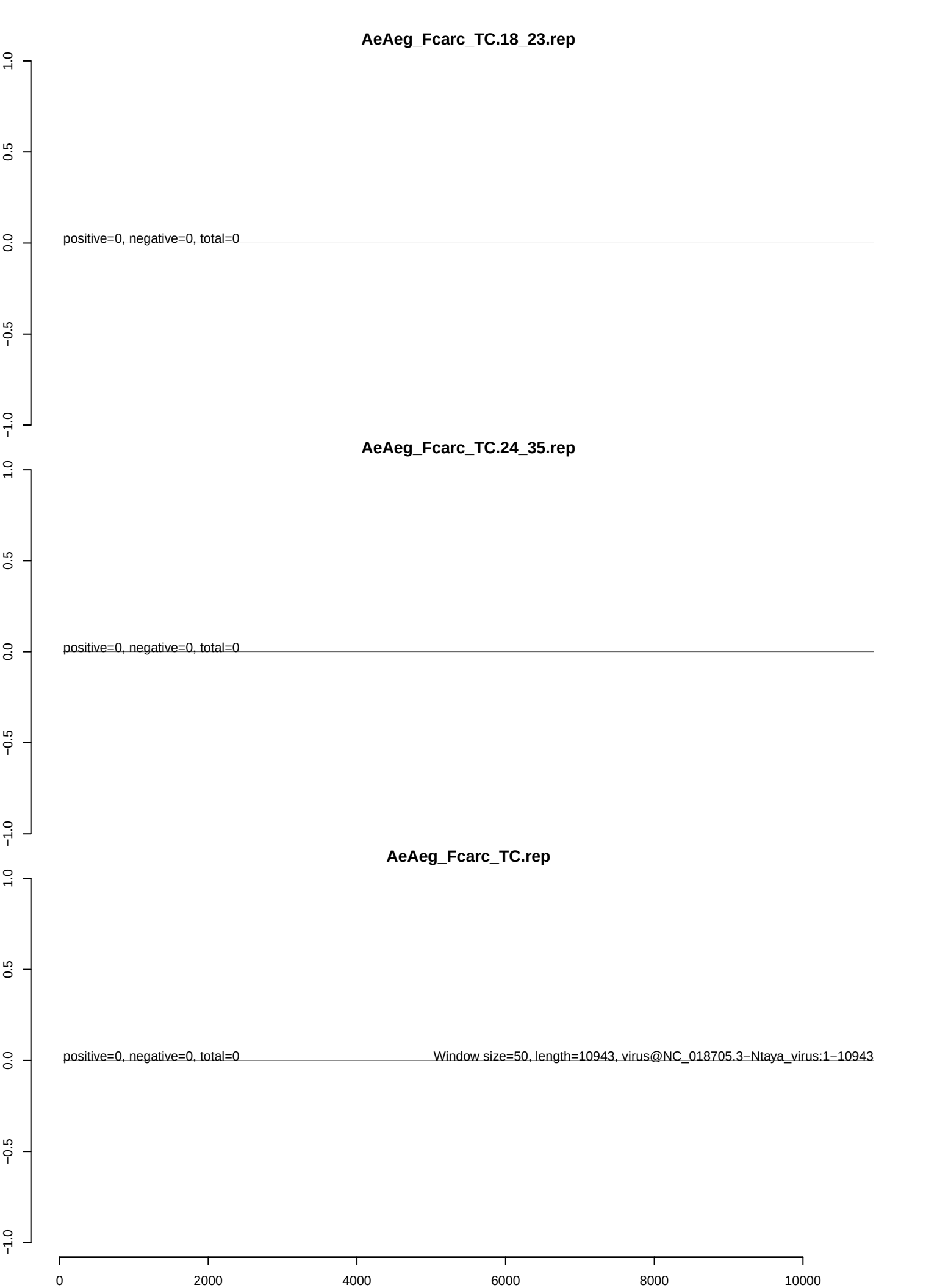
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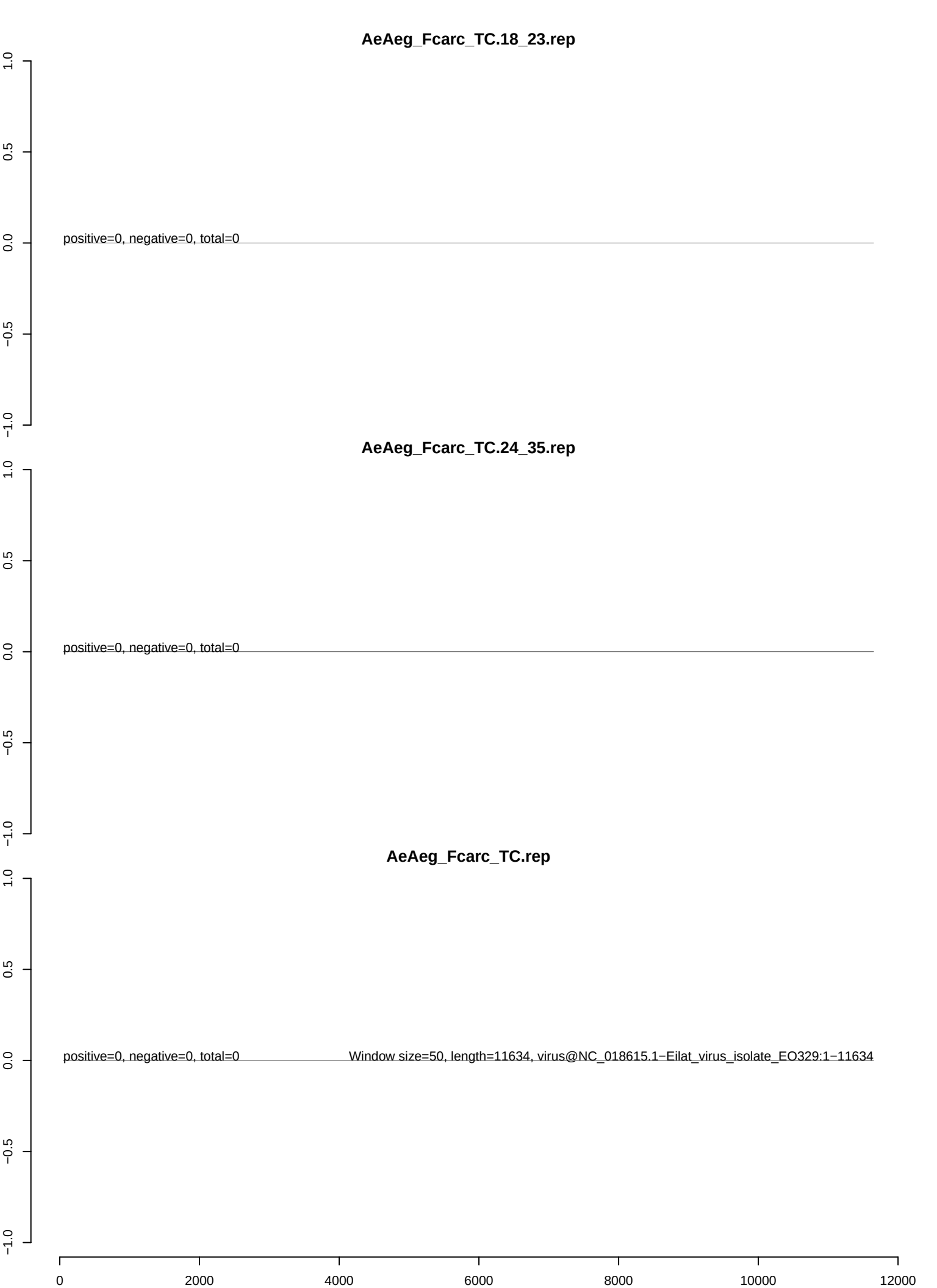
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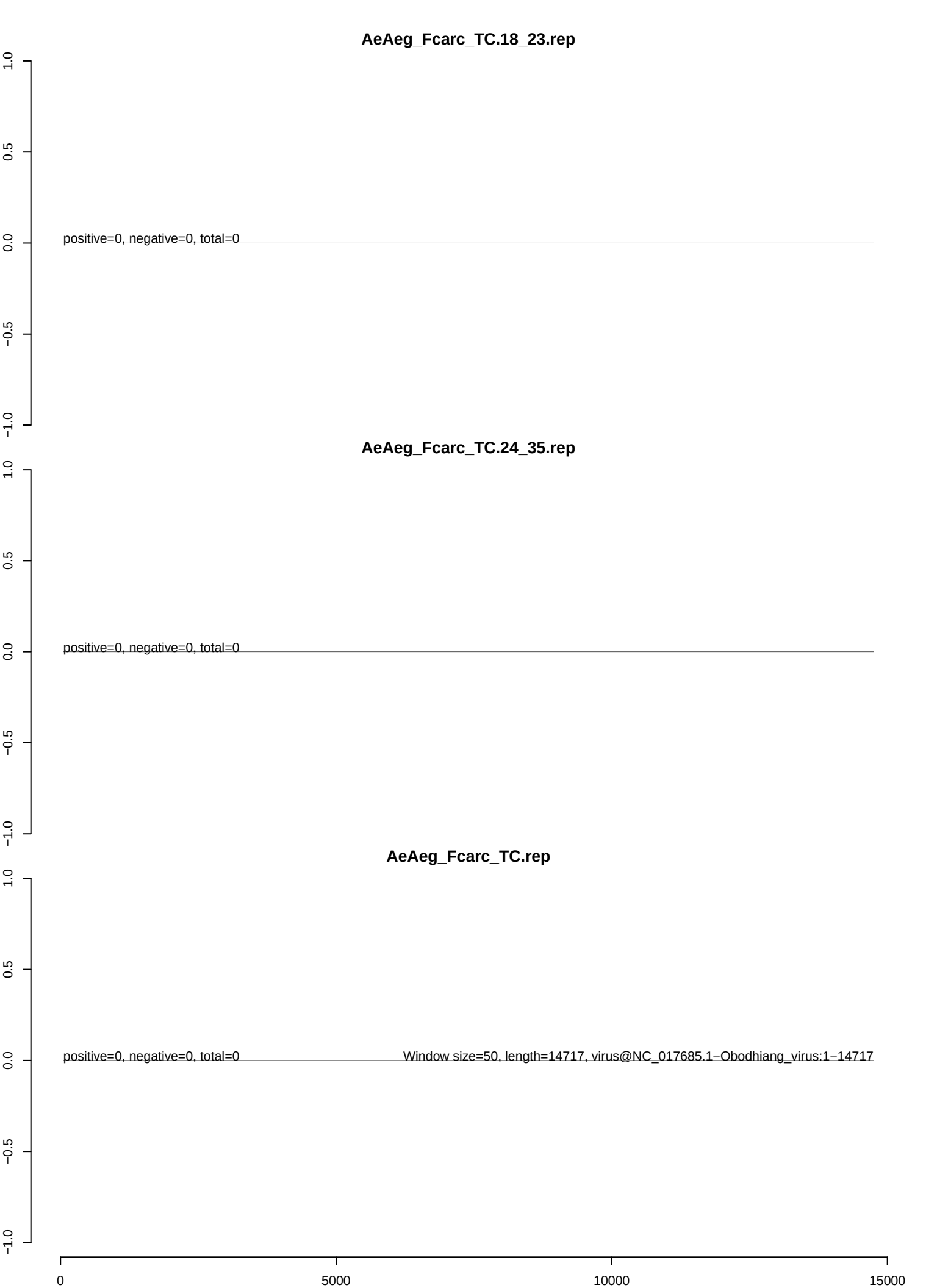
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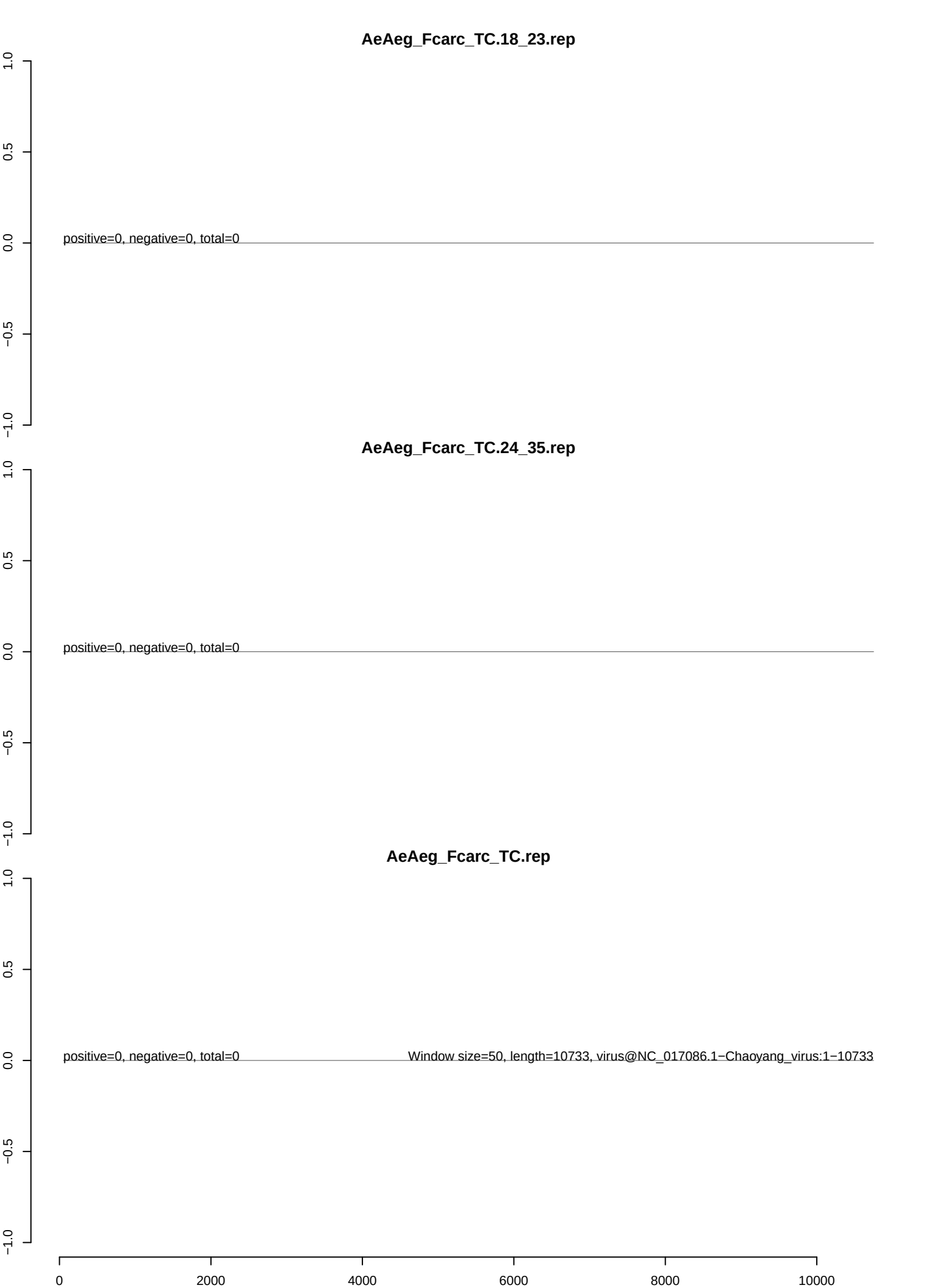
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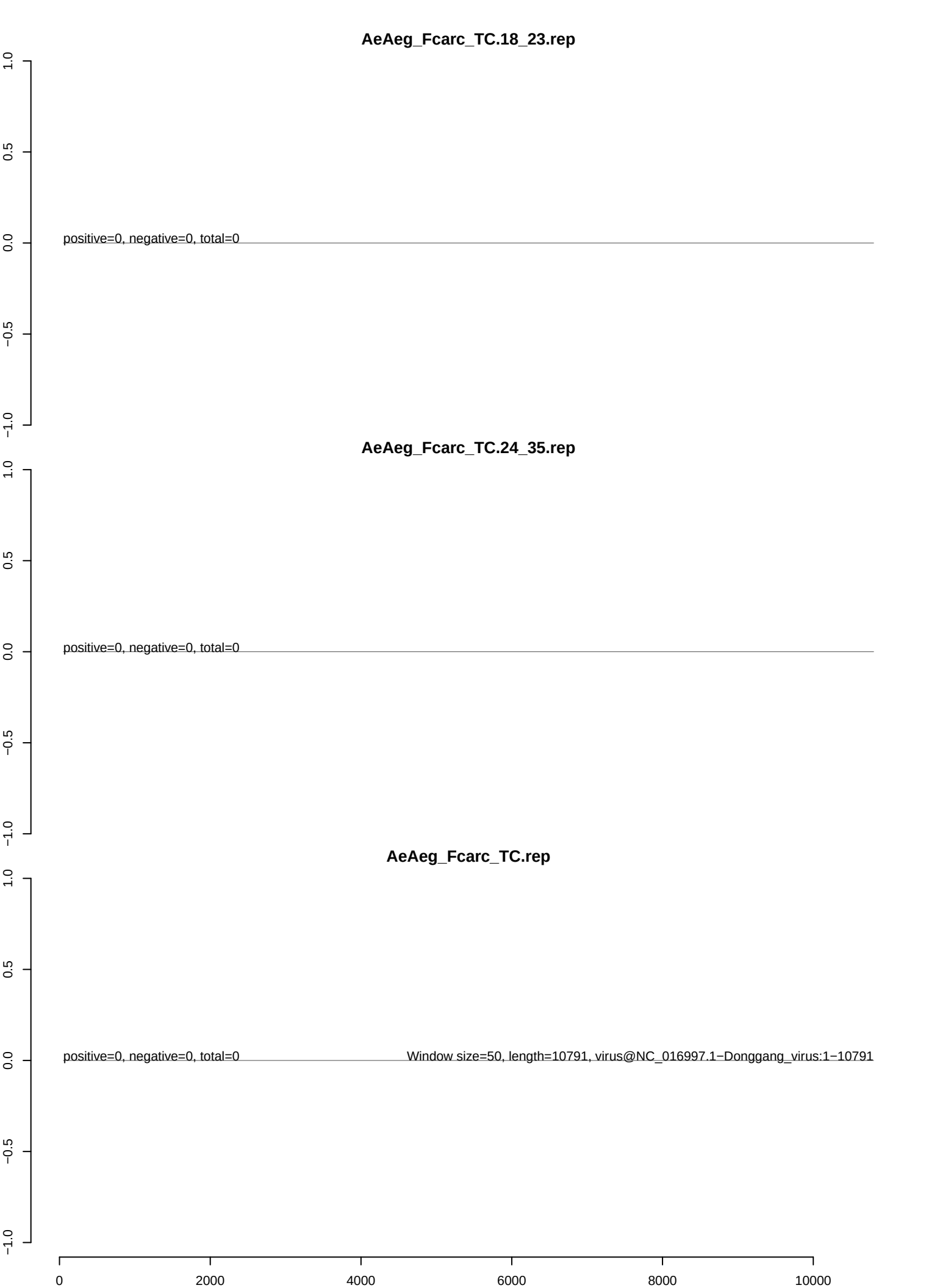
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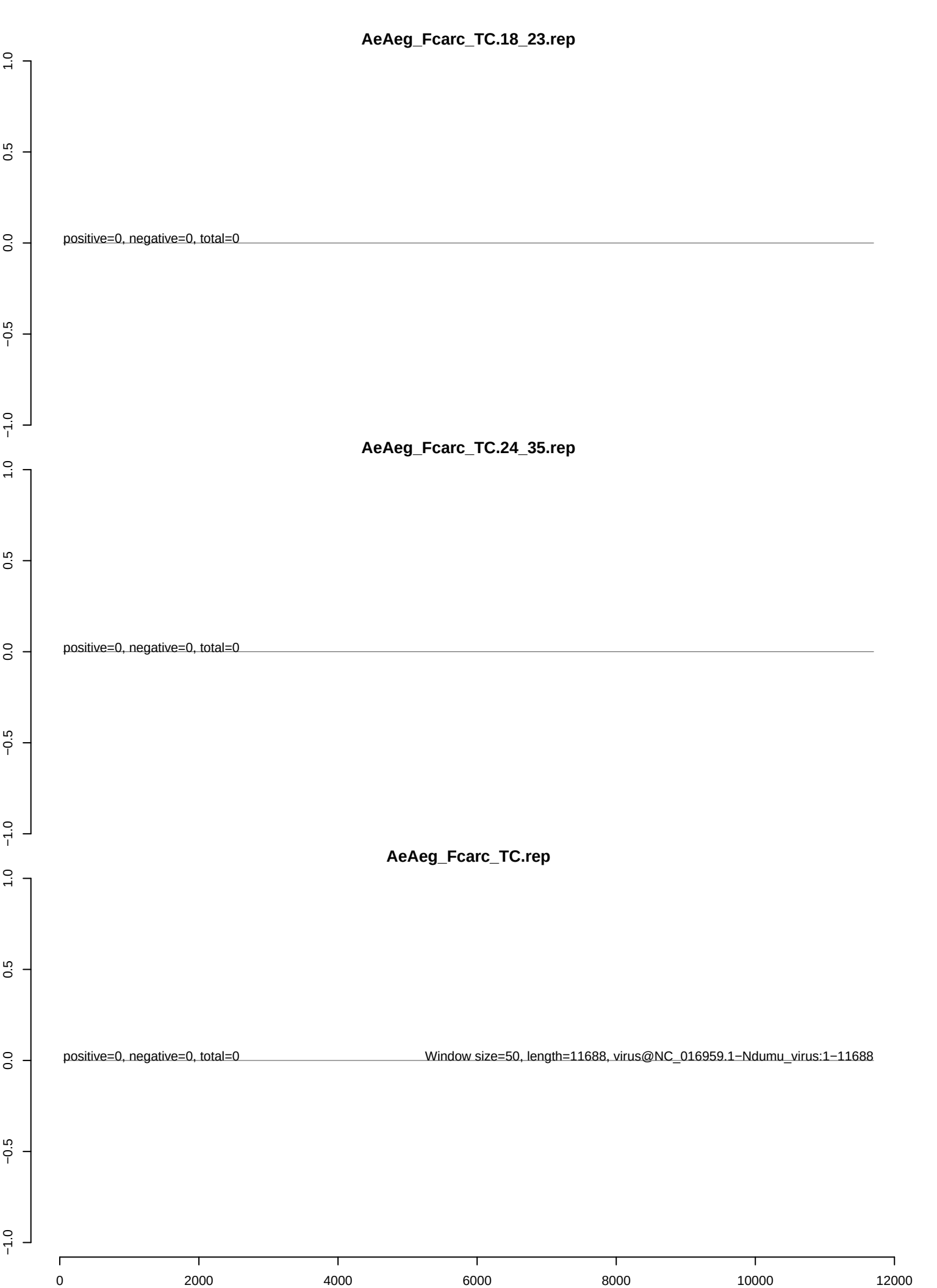
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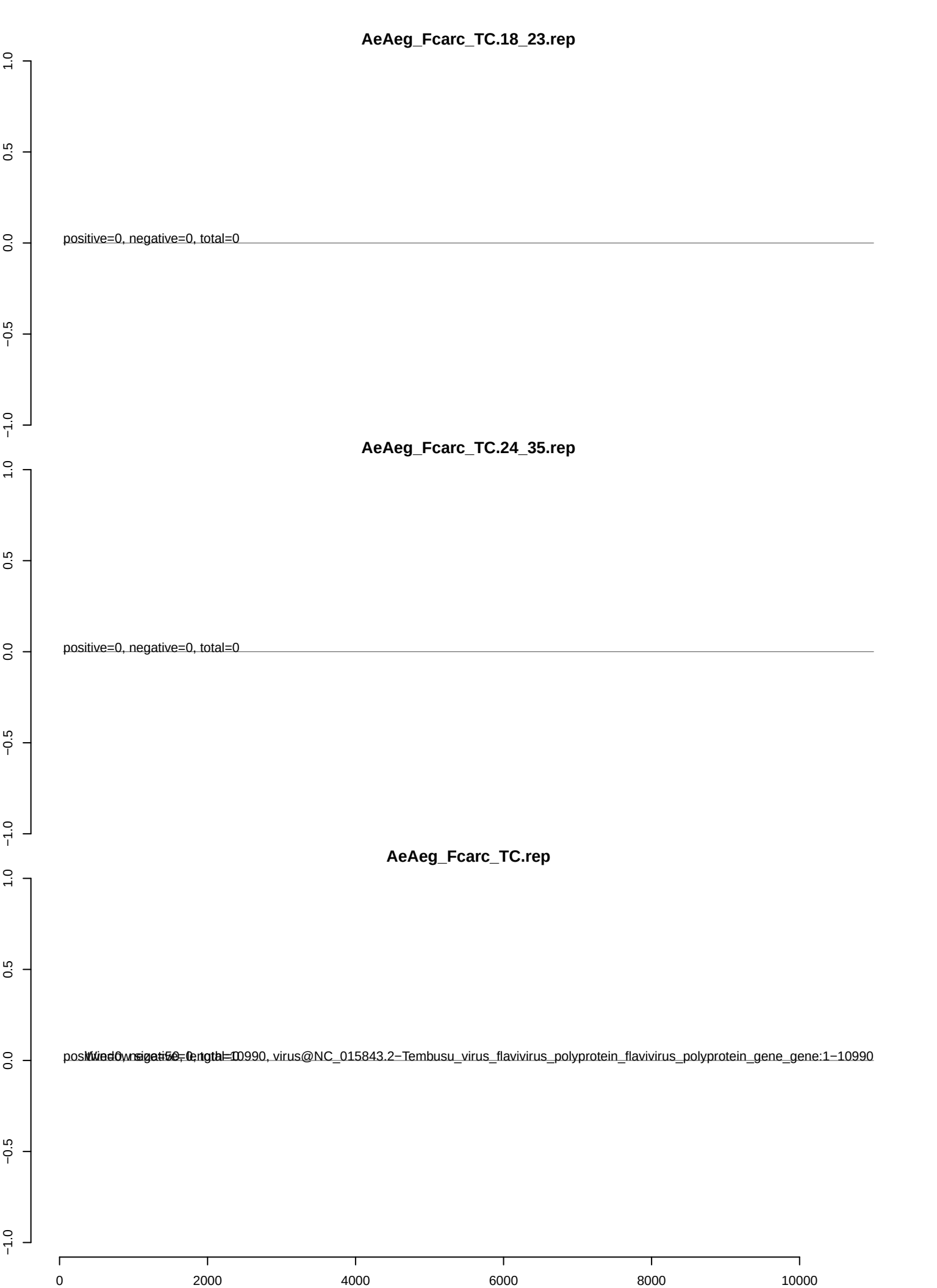
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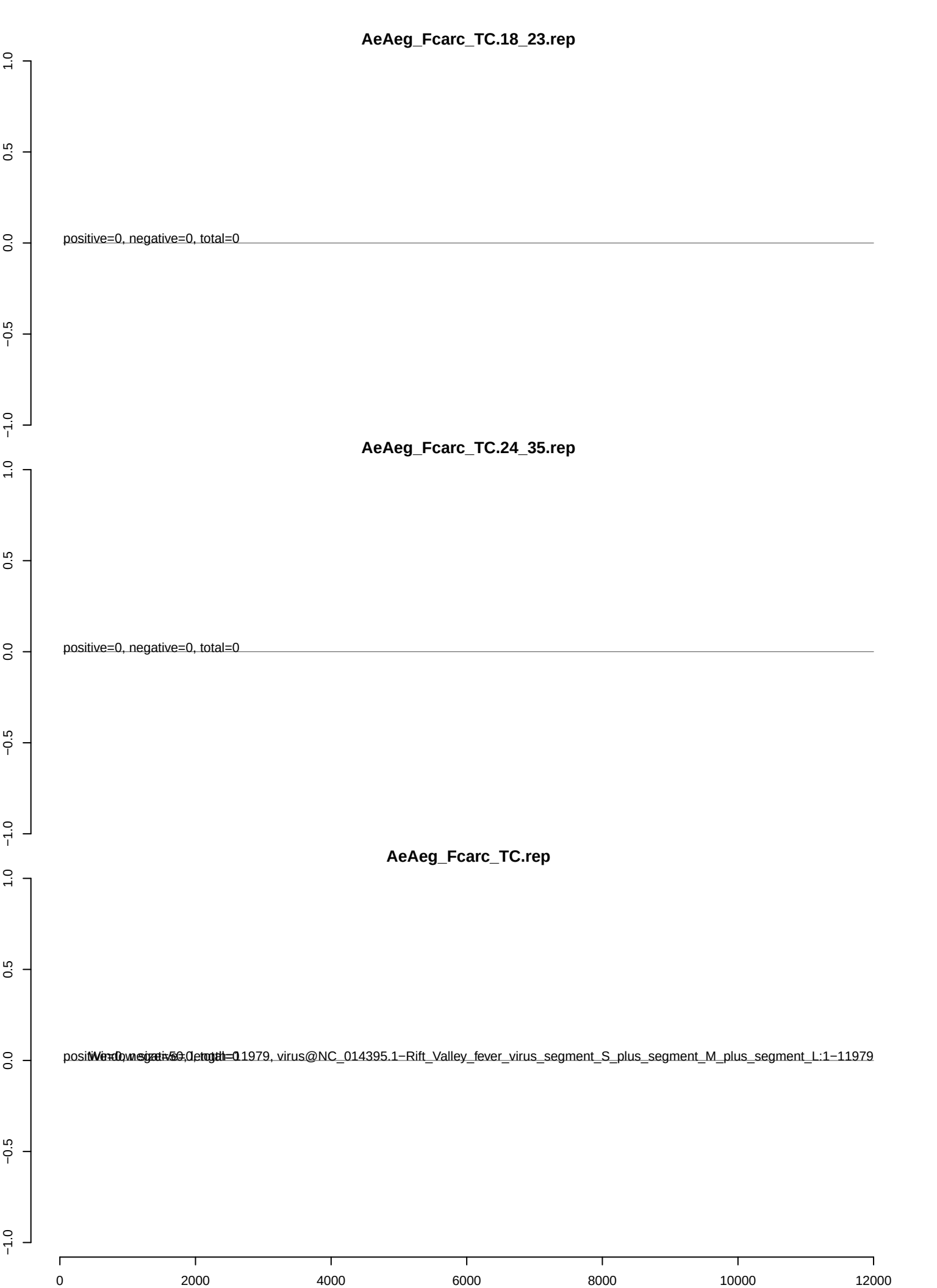
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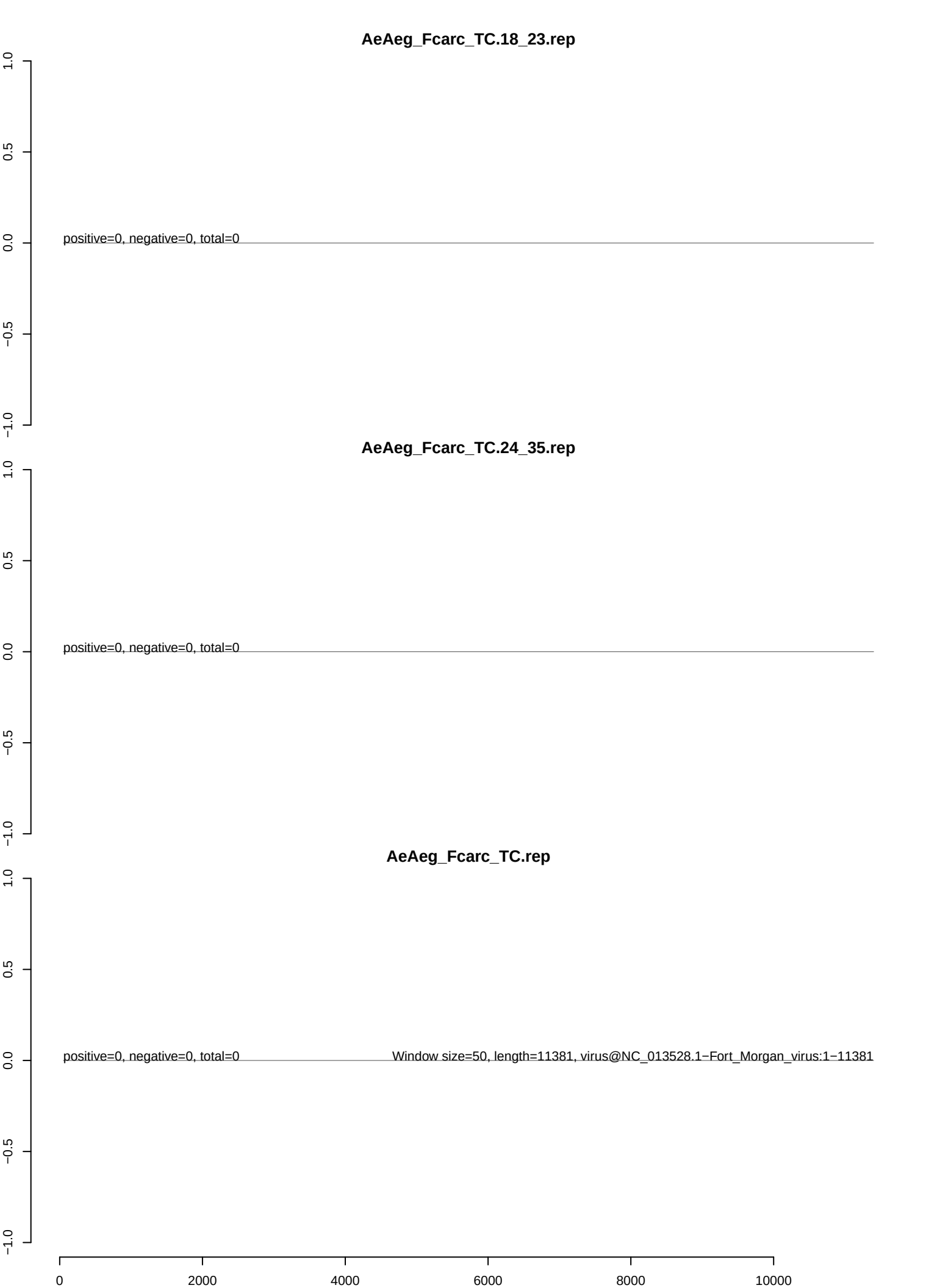
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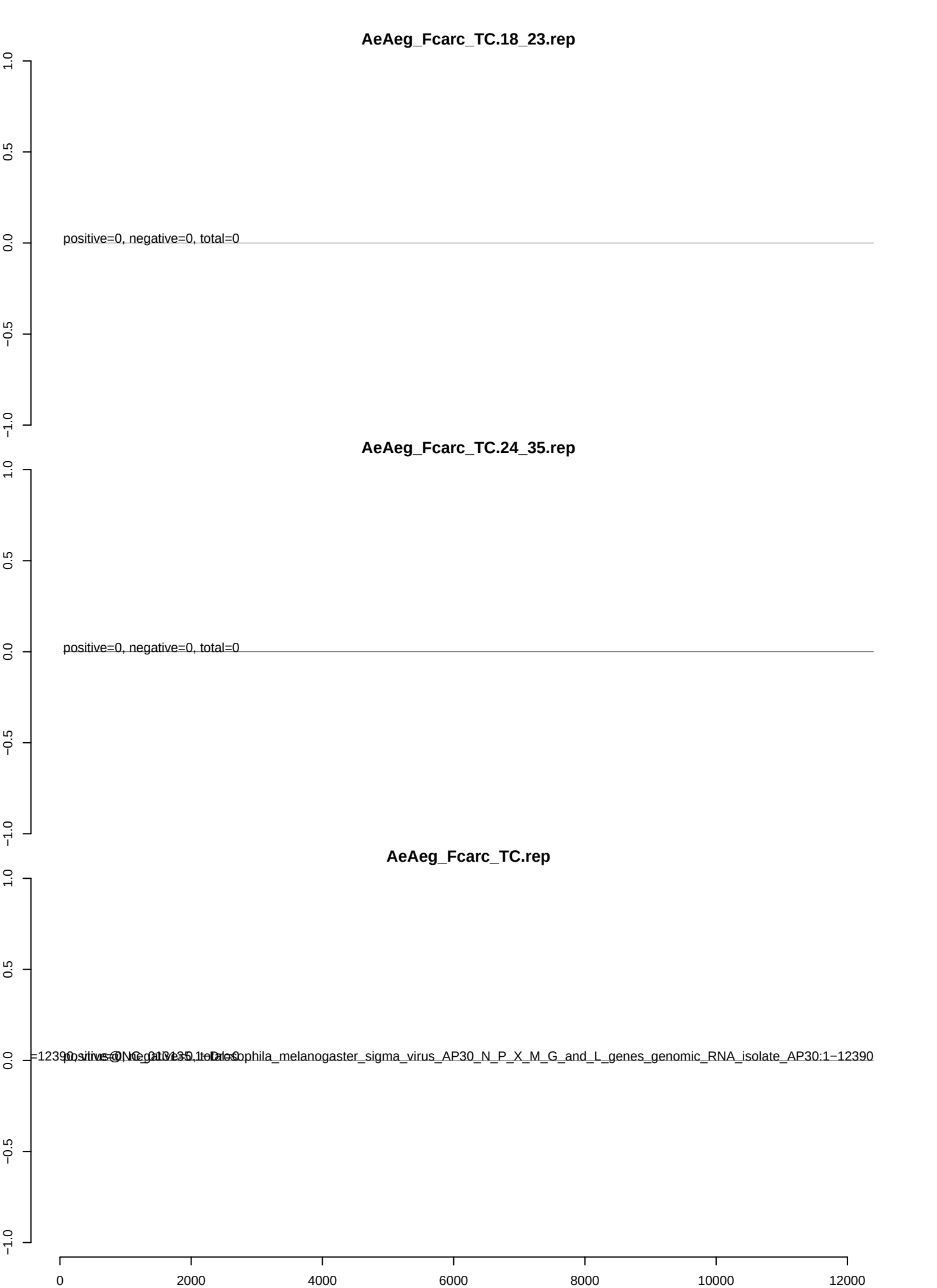
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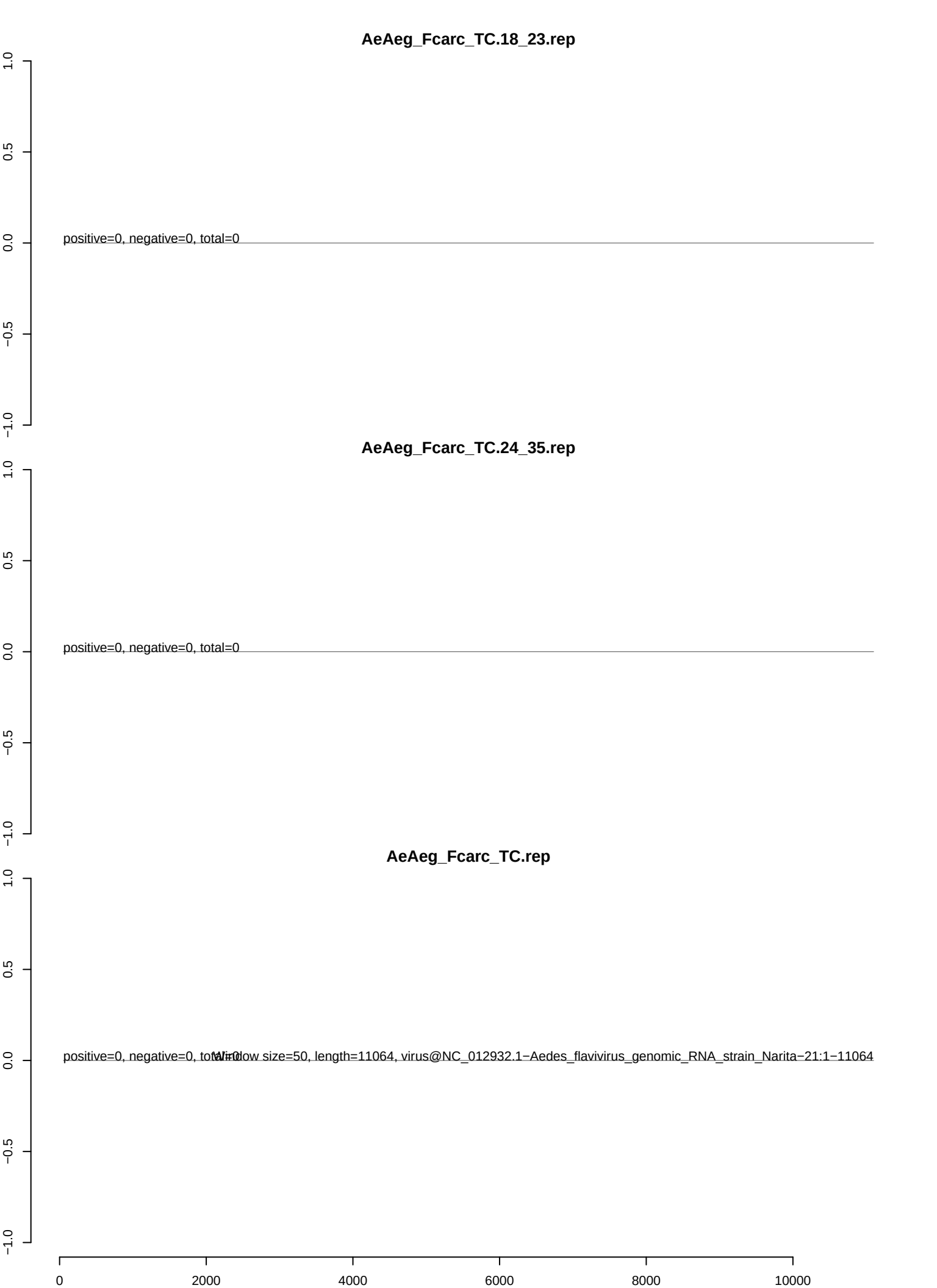
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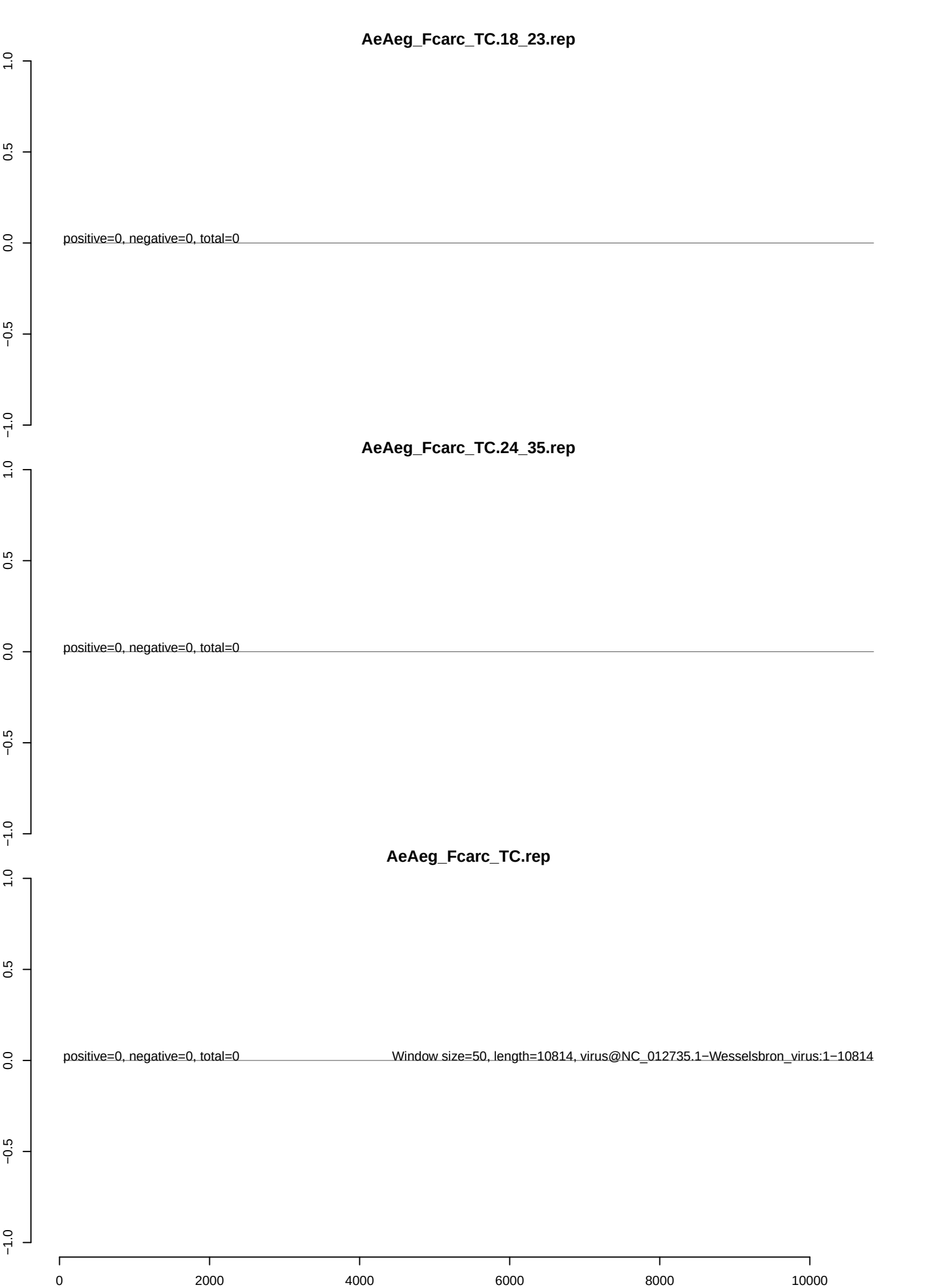
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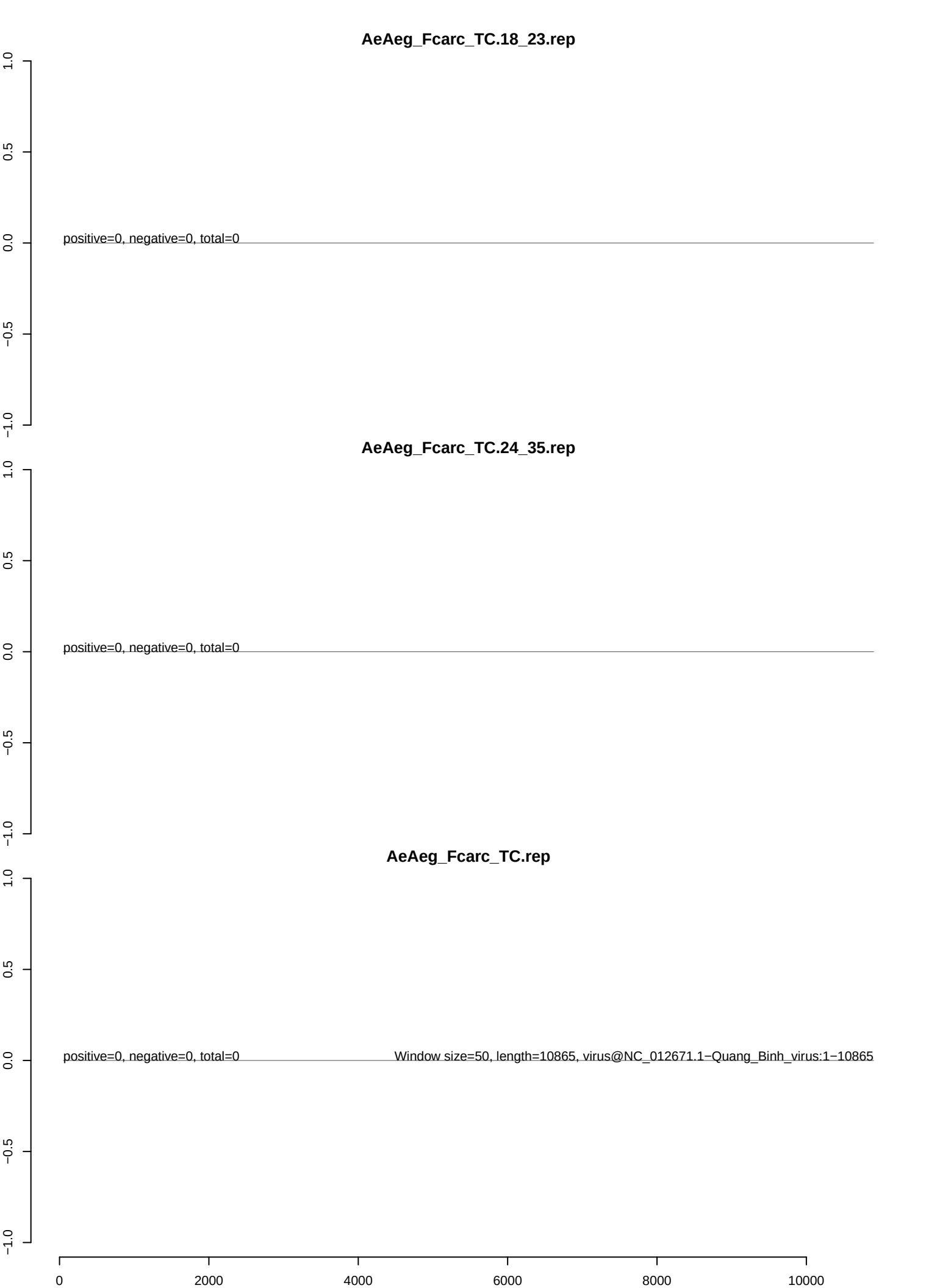
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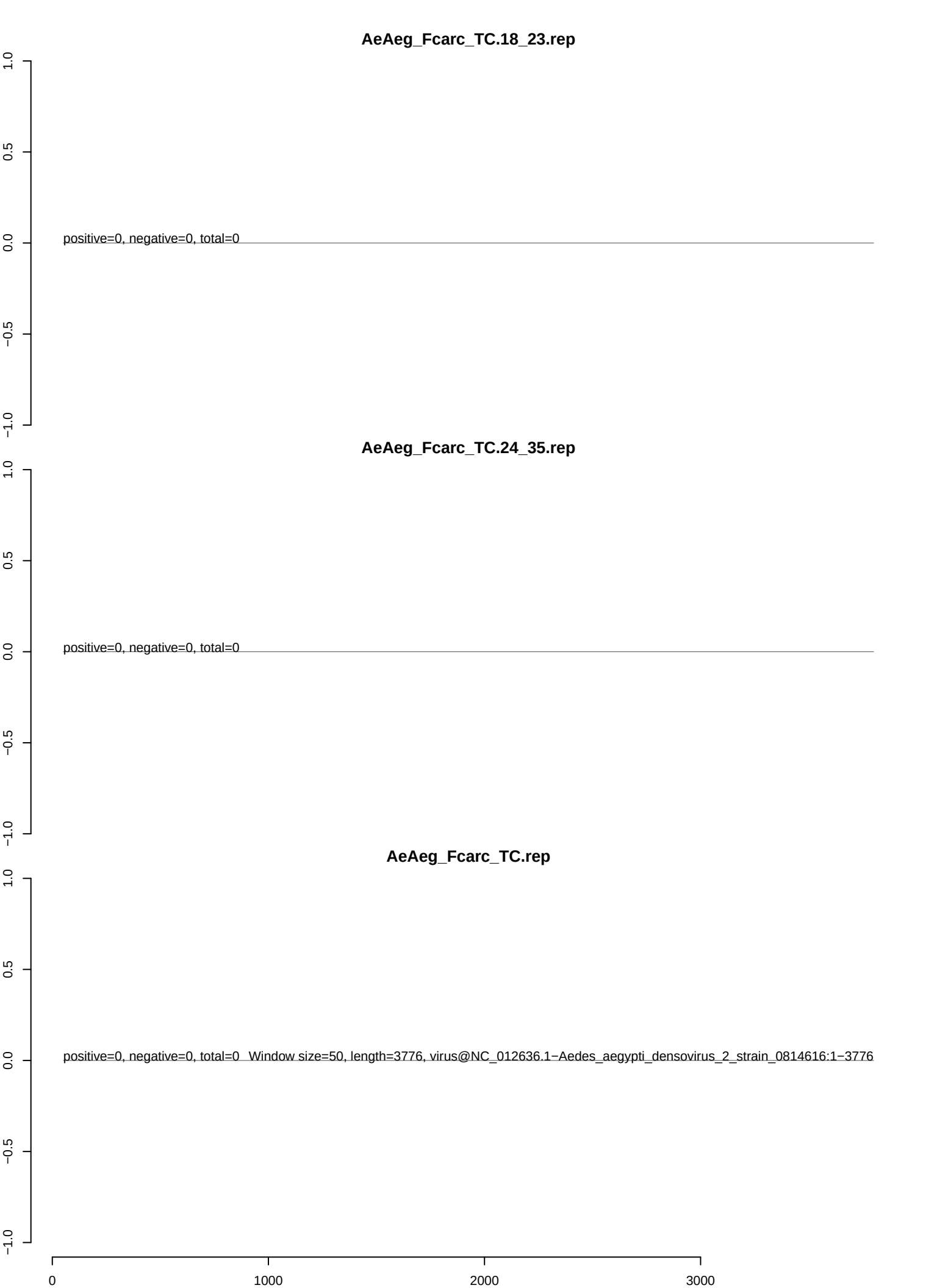
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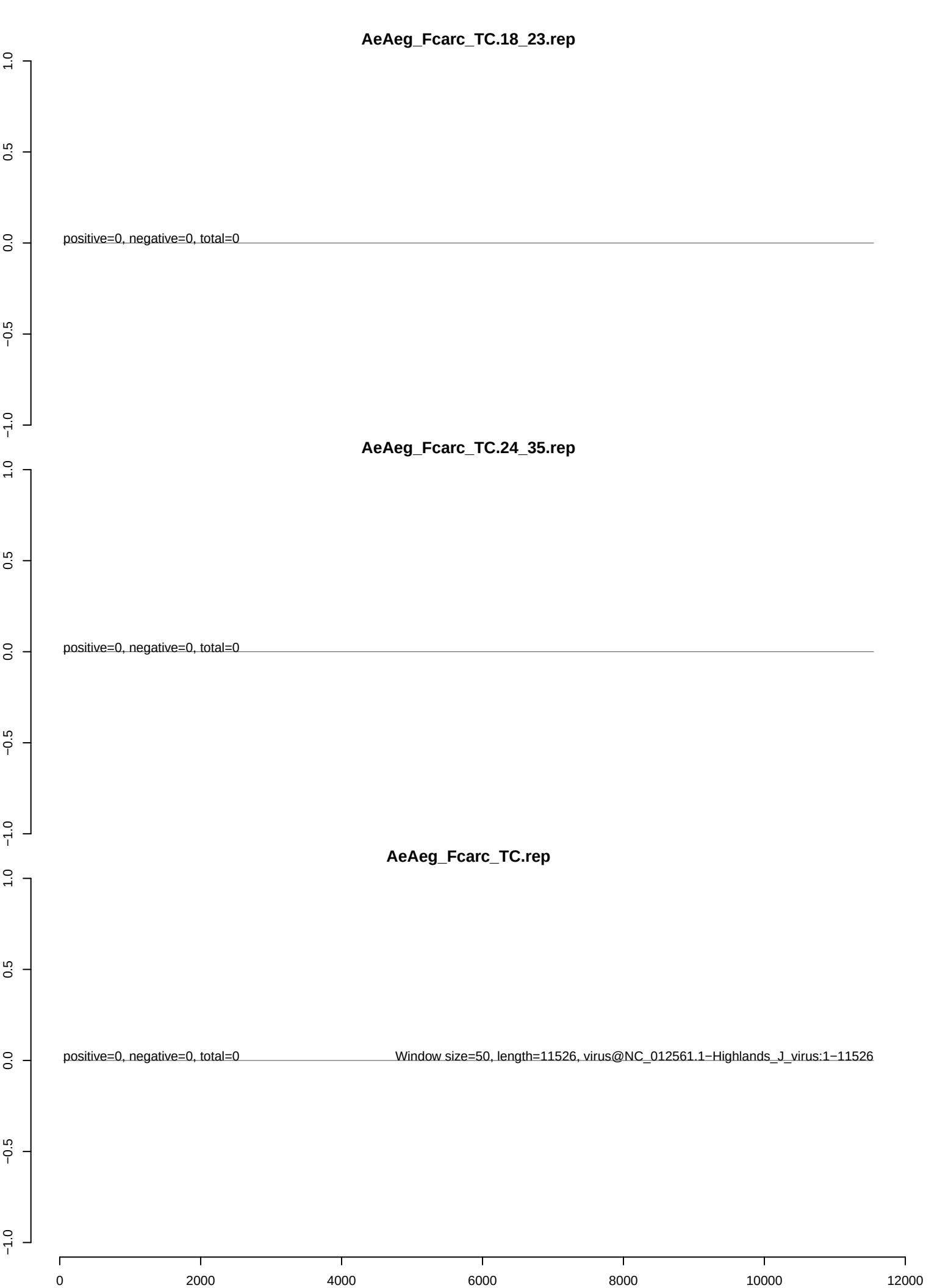
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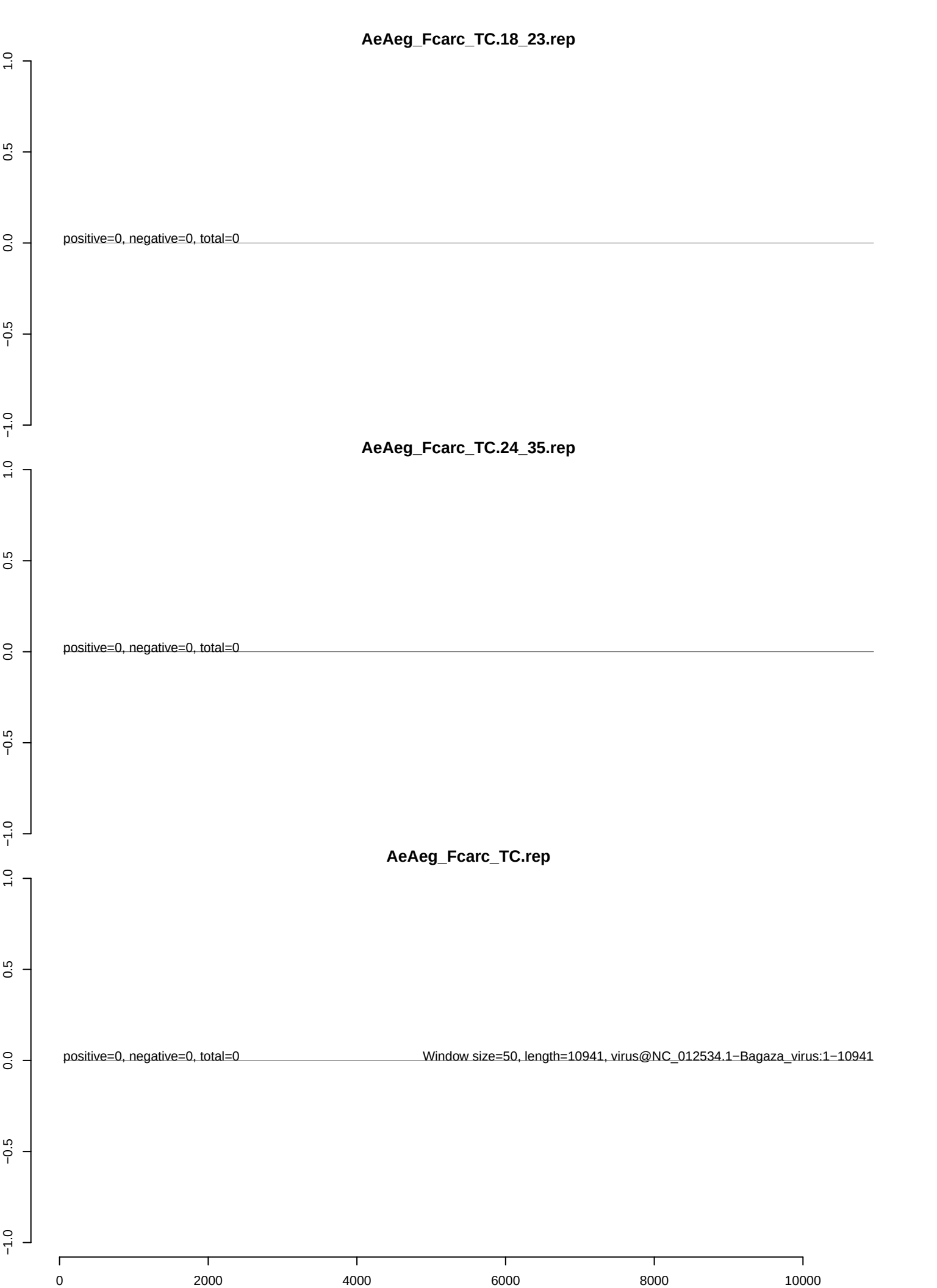
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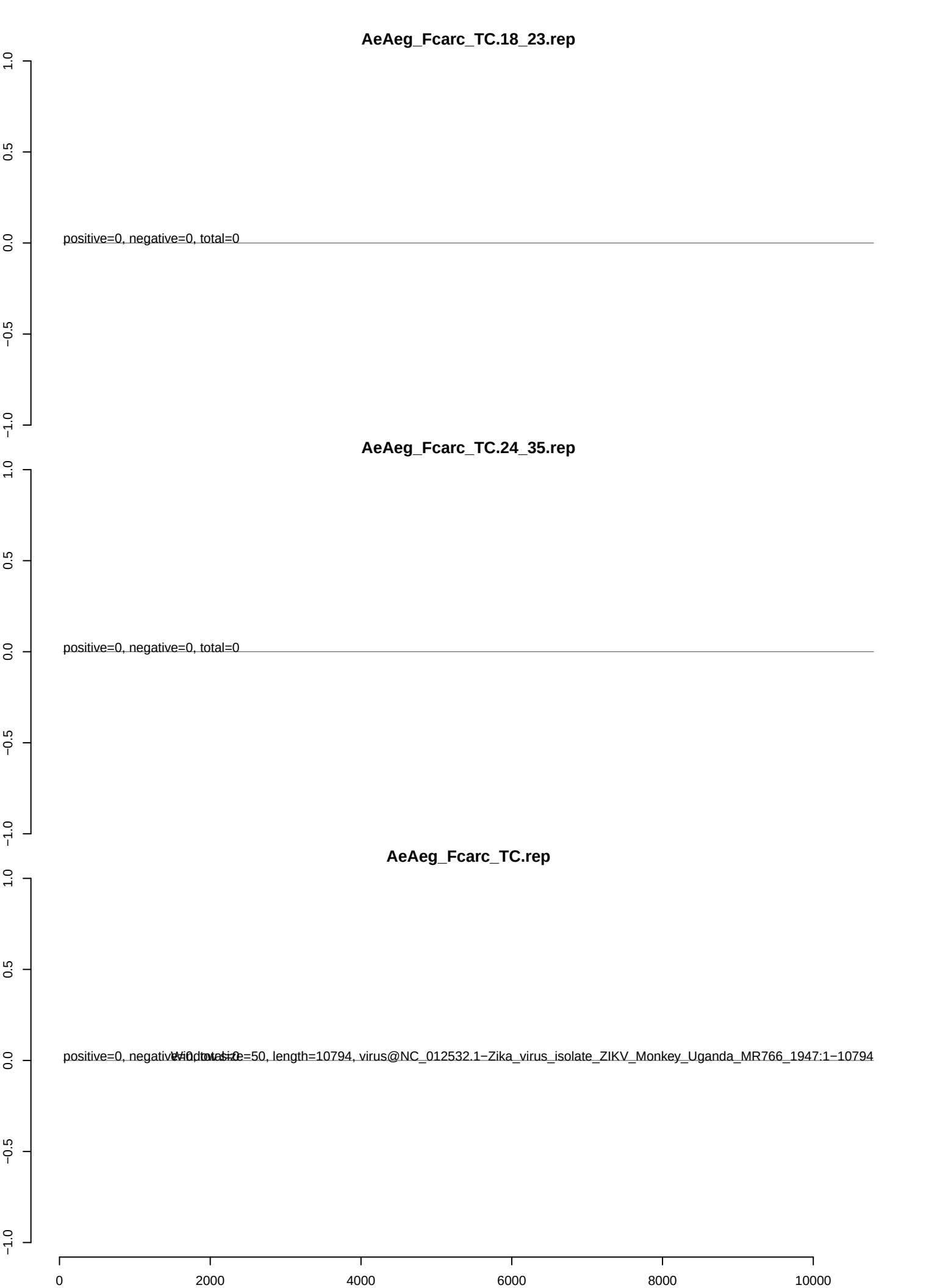
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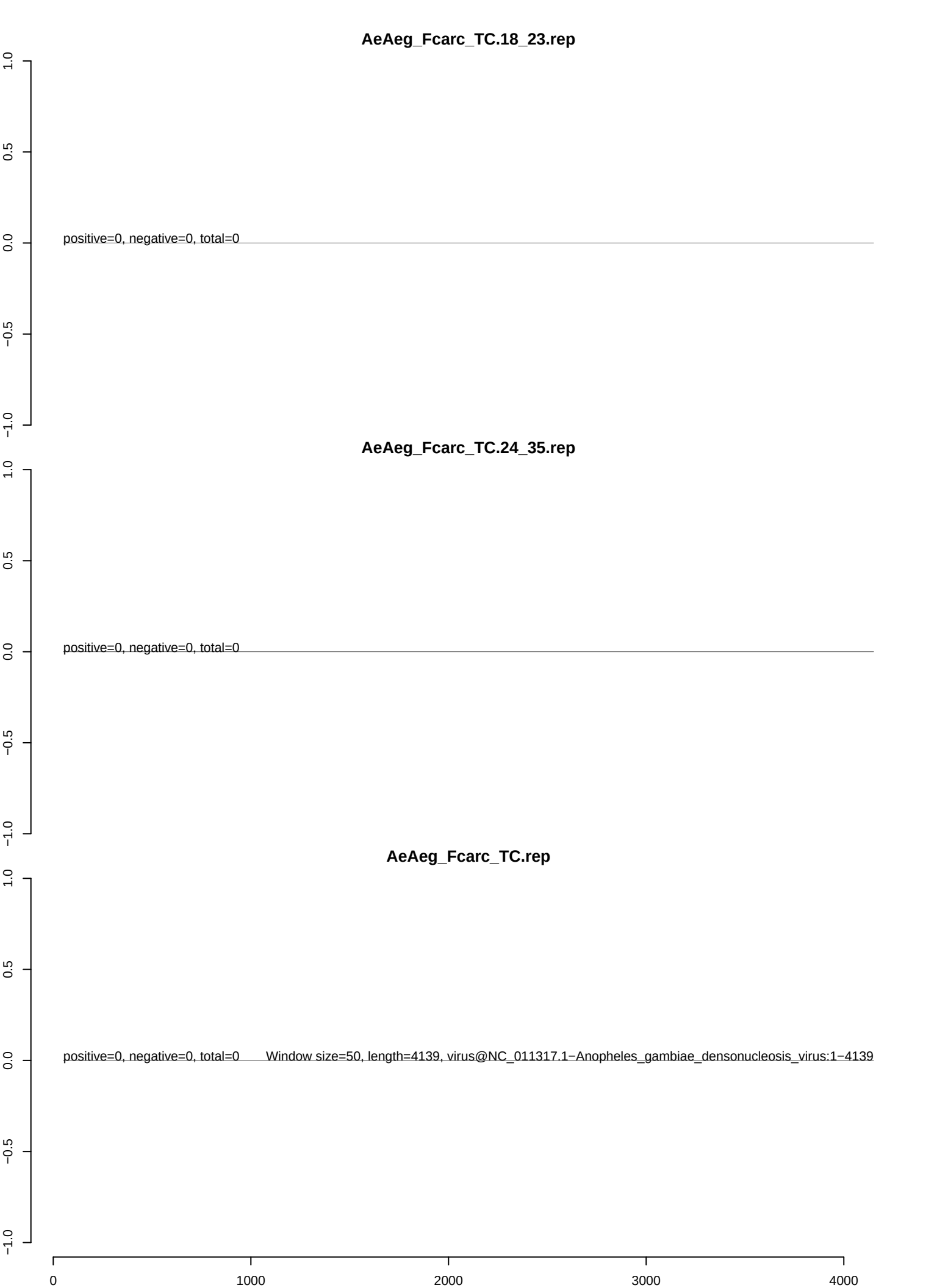
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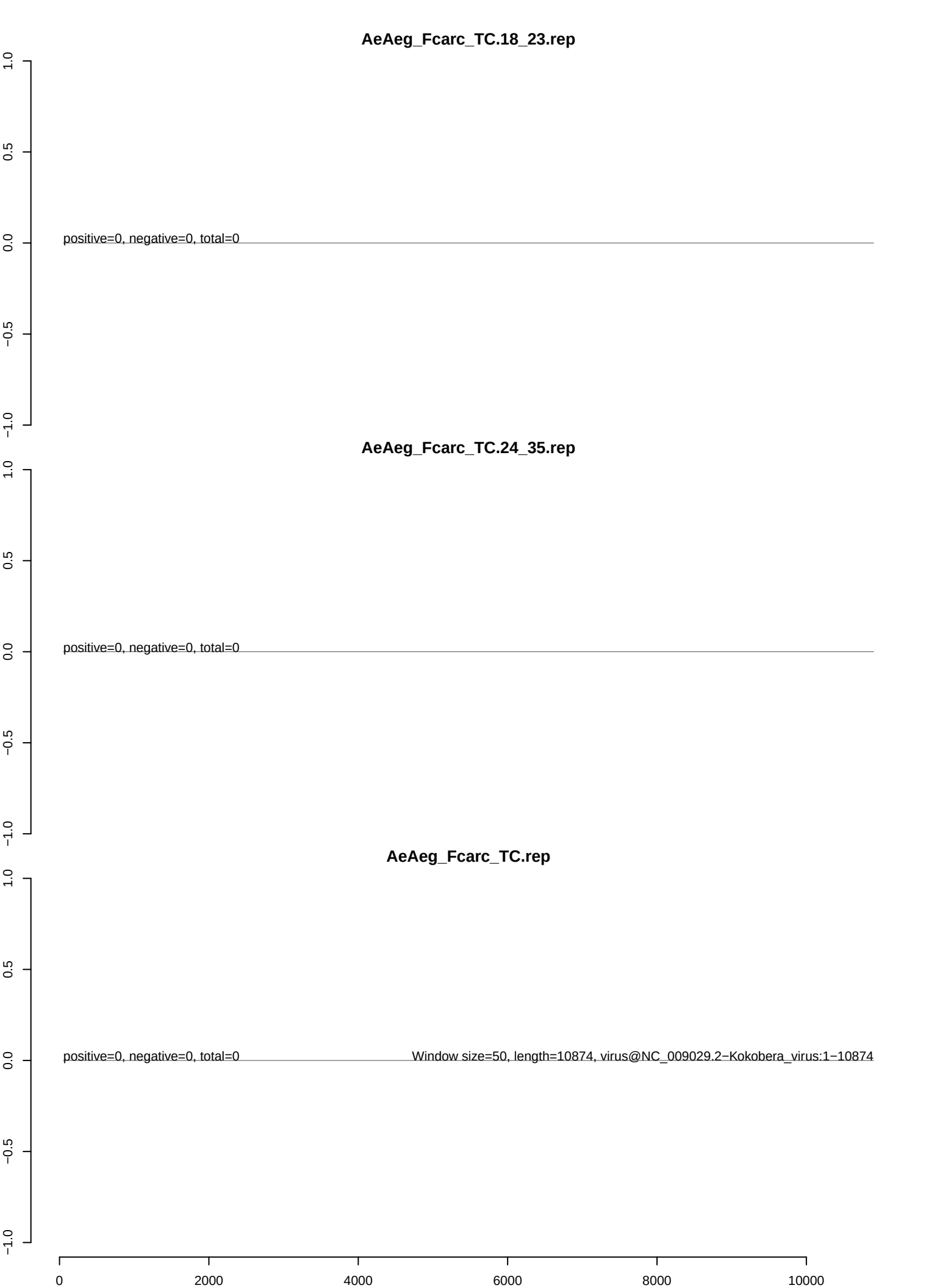
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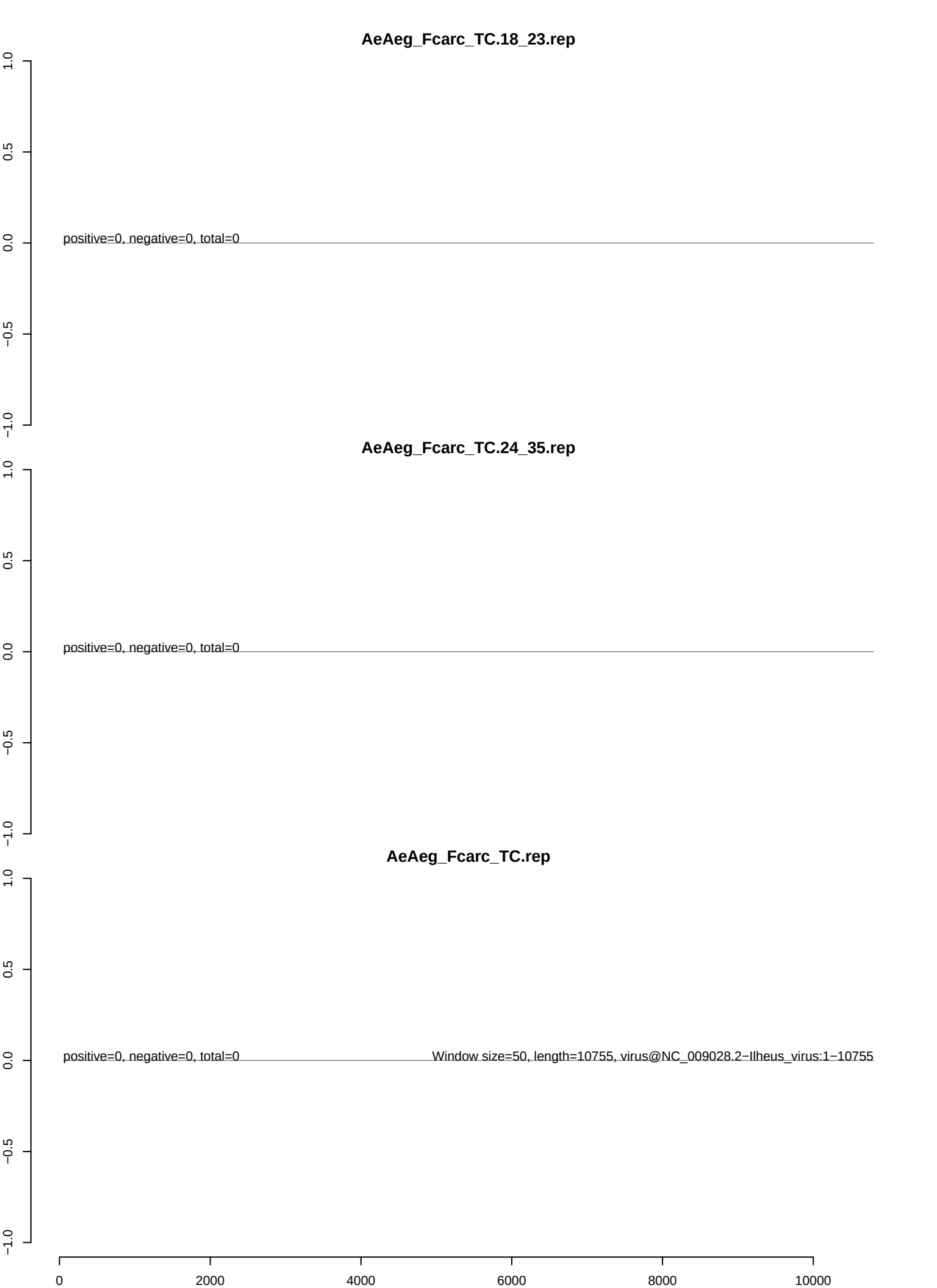
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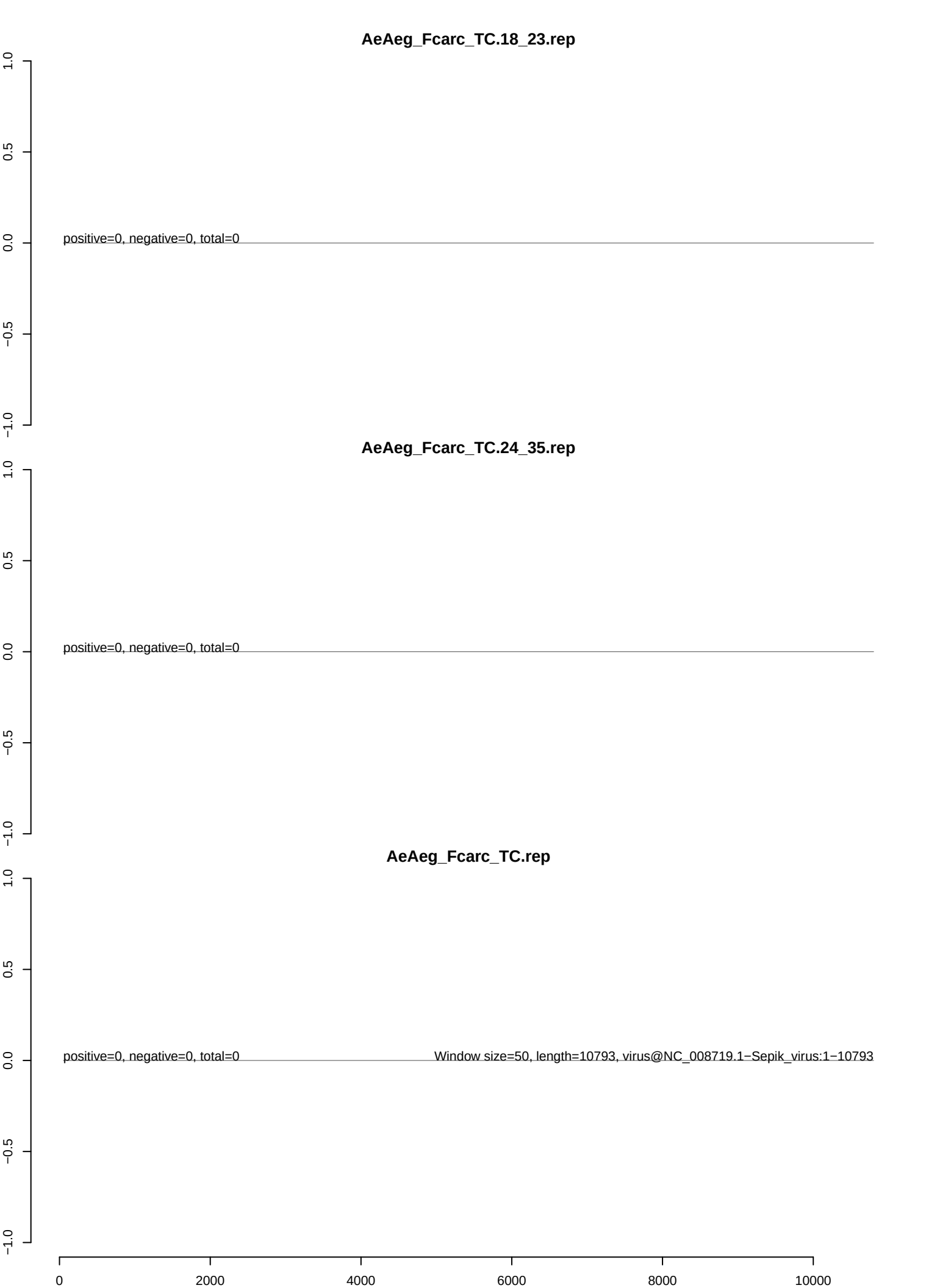
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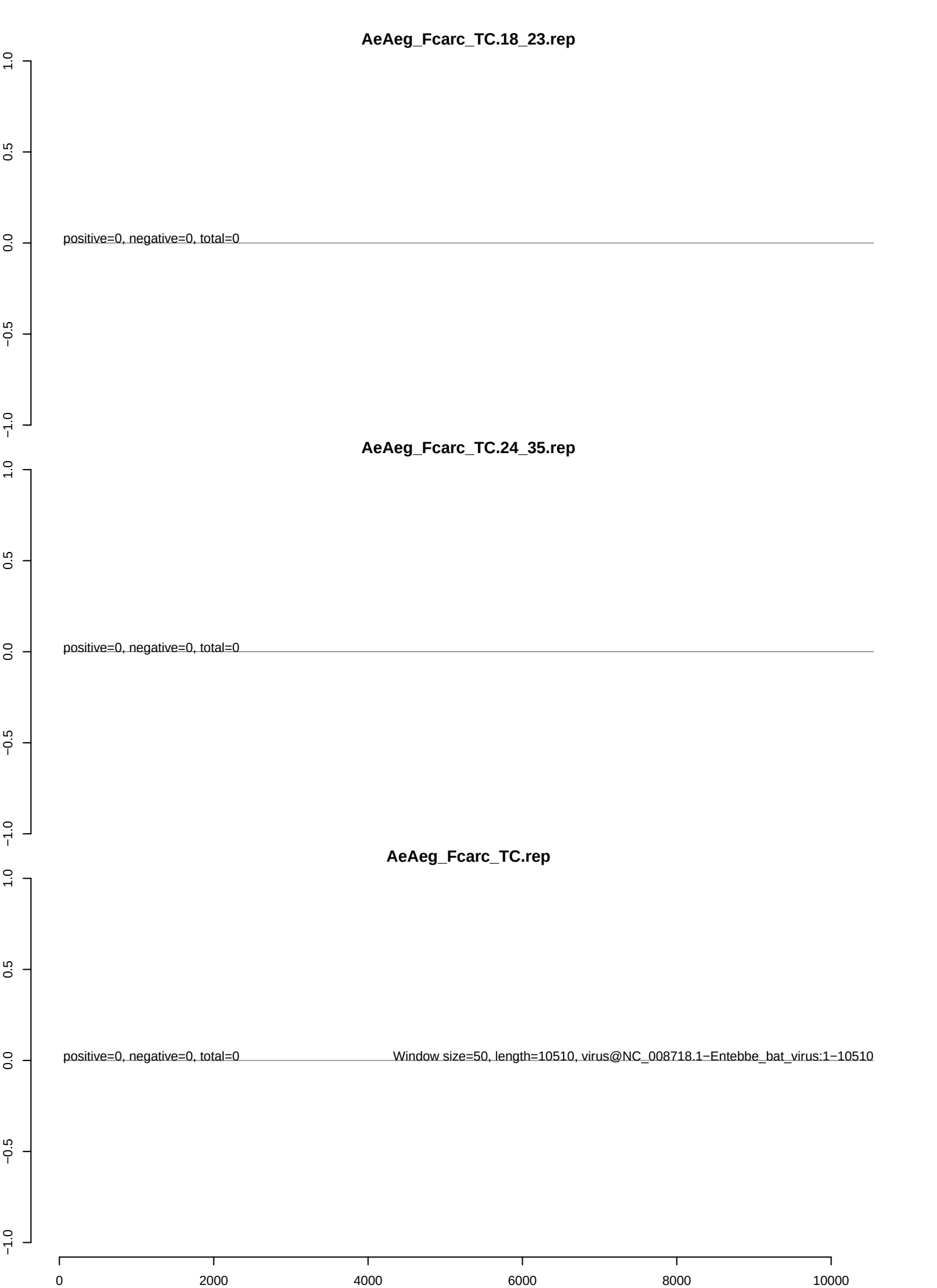
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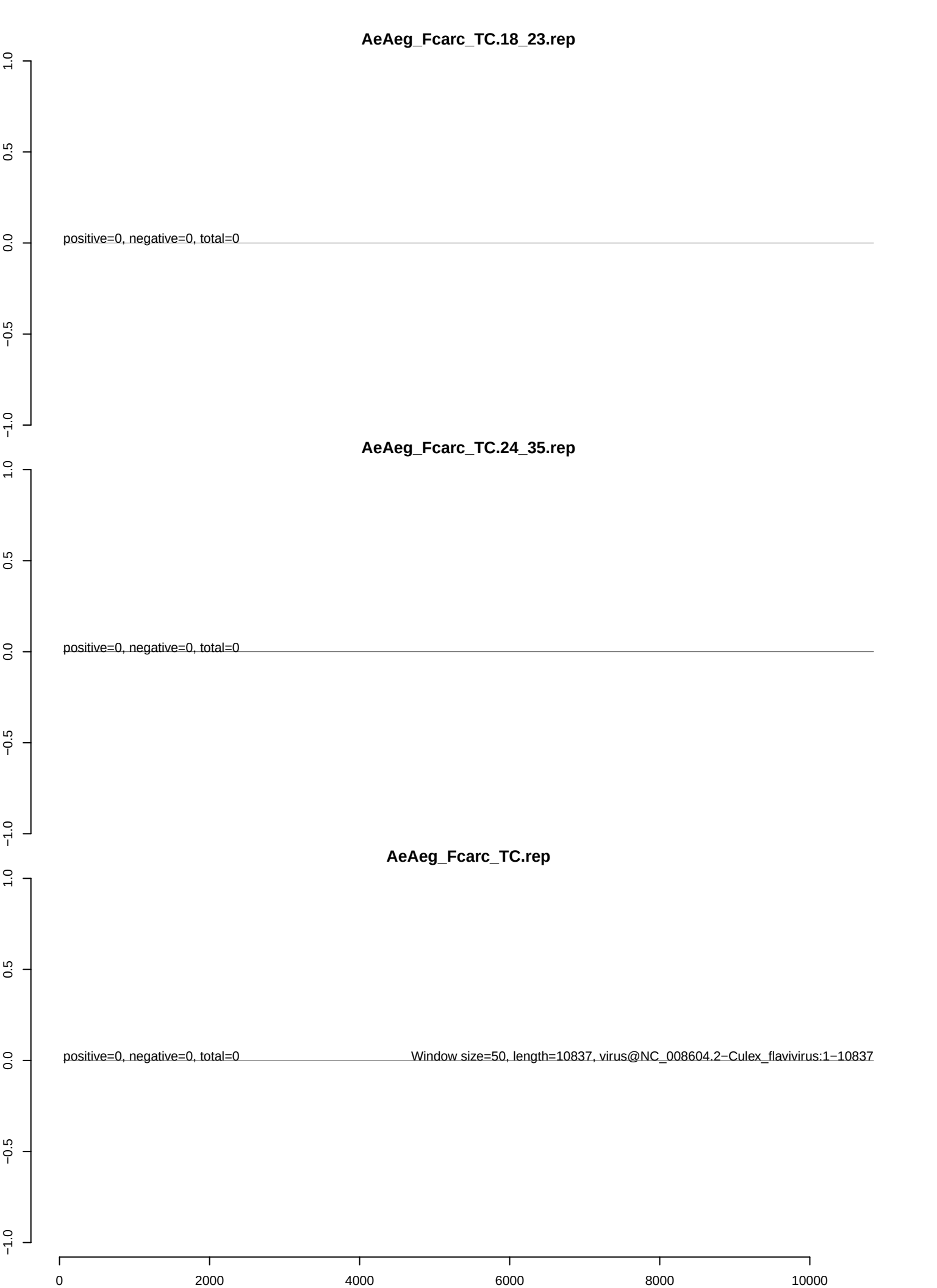
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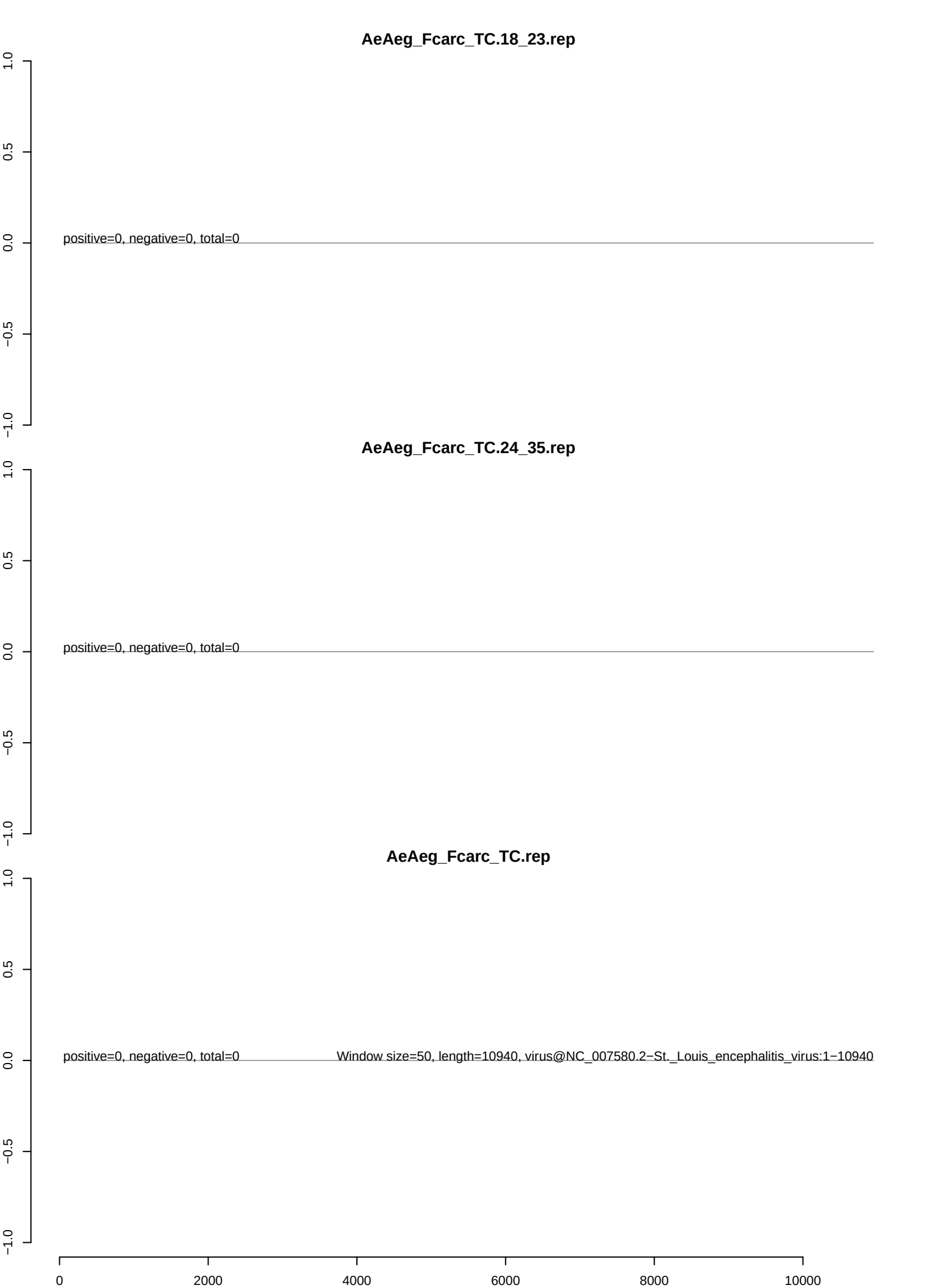
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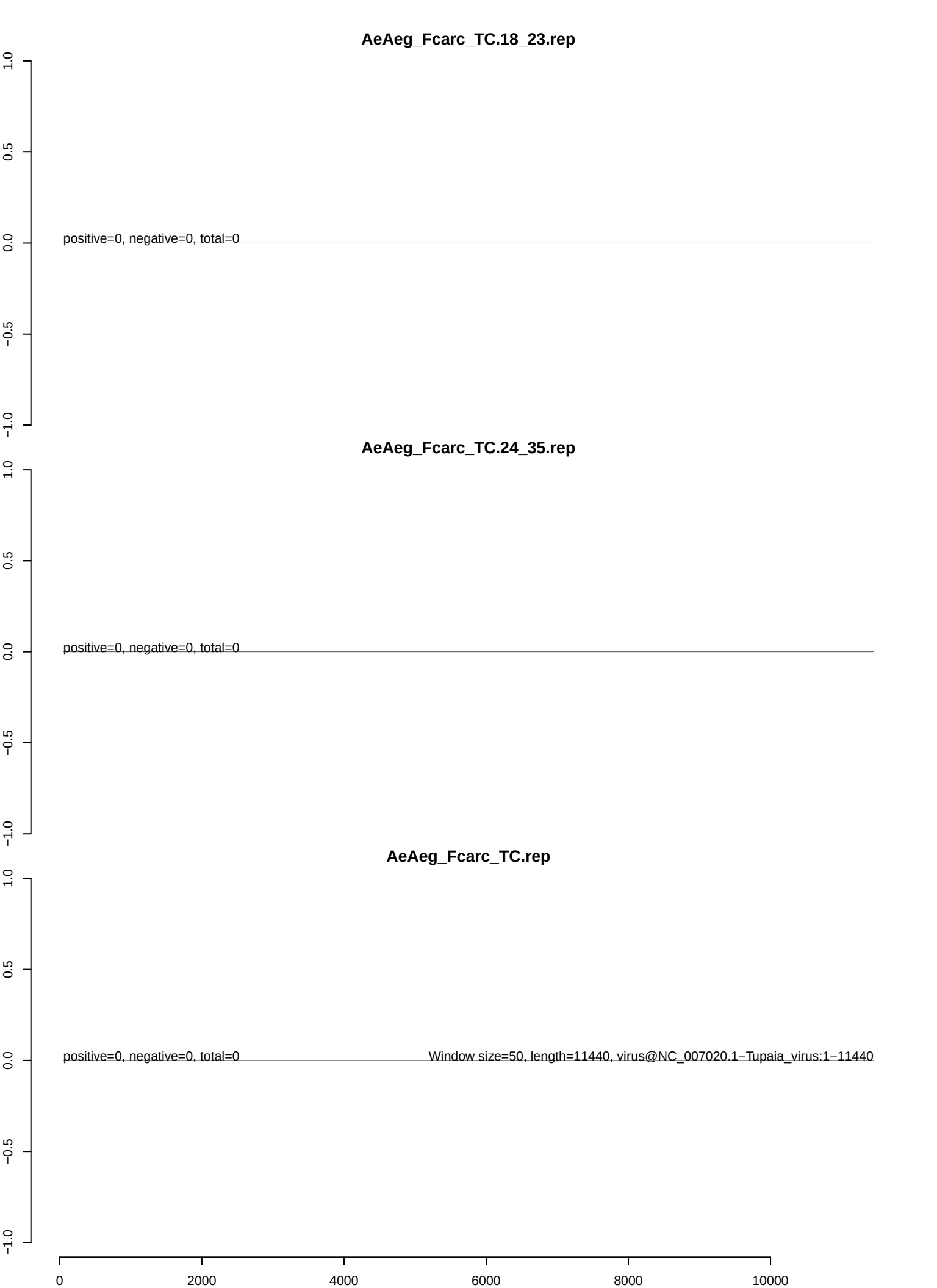
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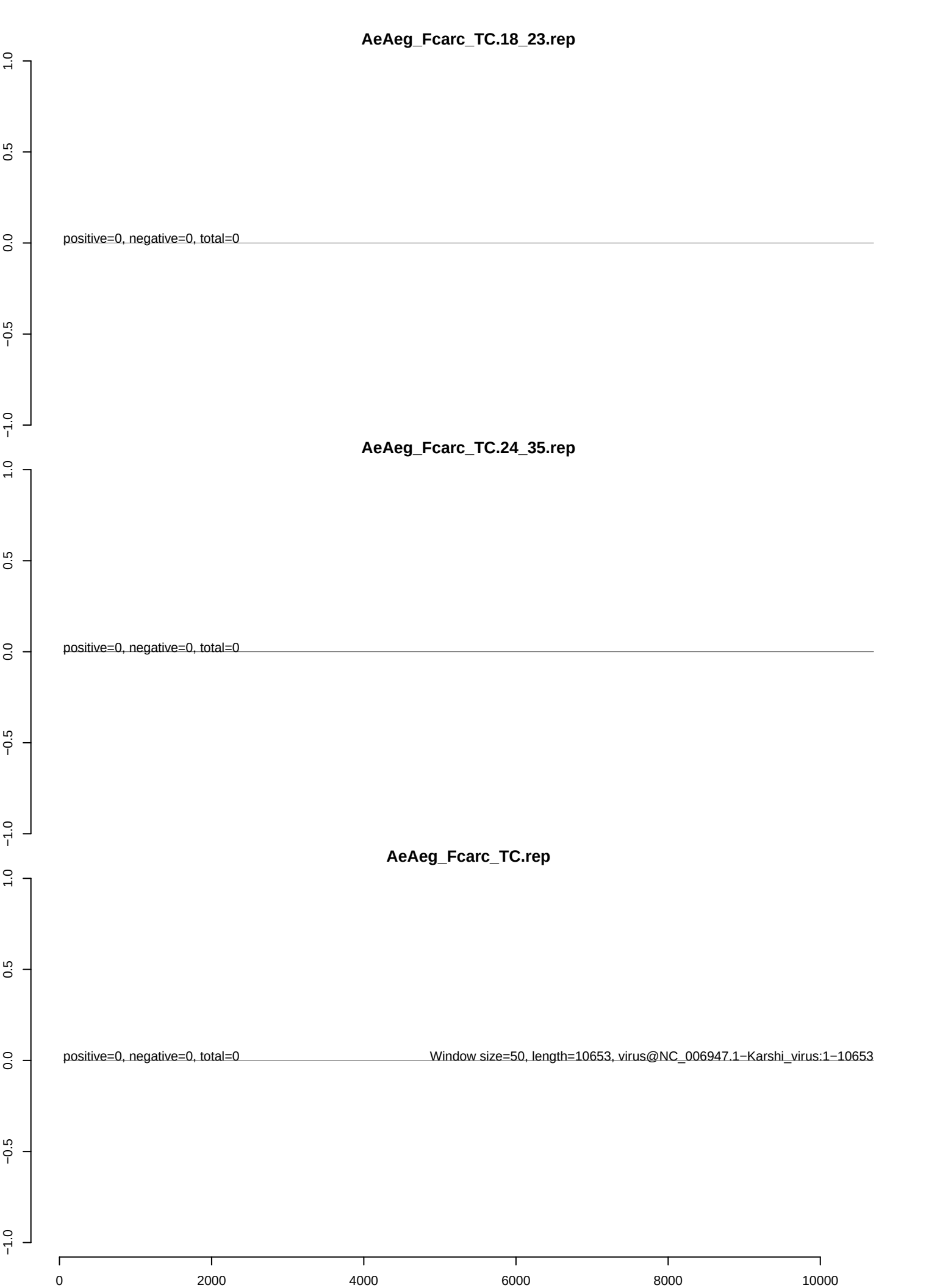
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positive=0, negative=0, total=0
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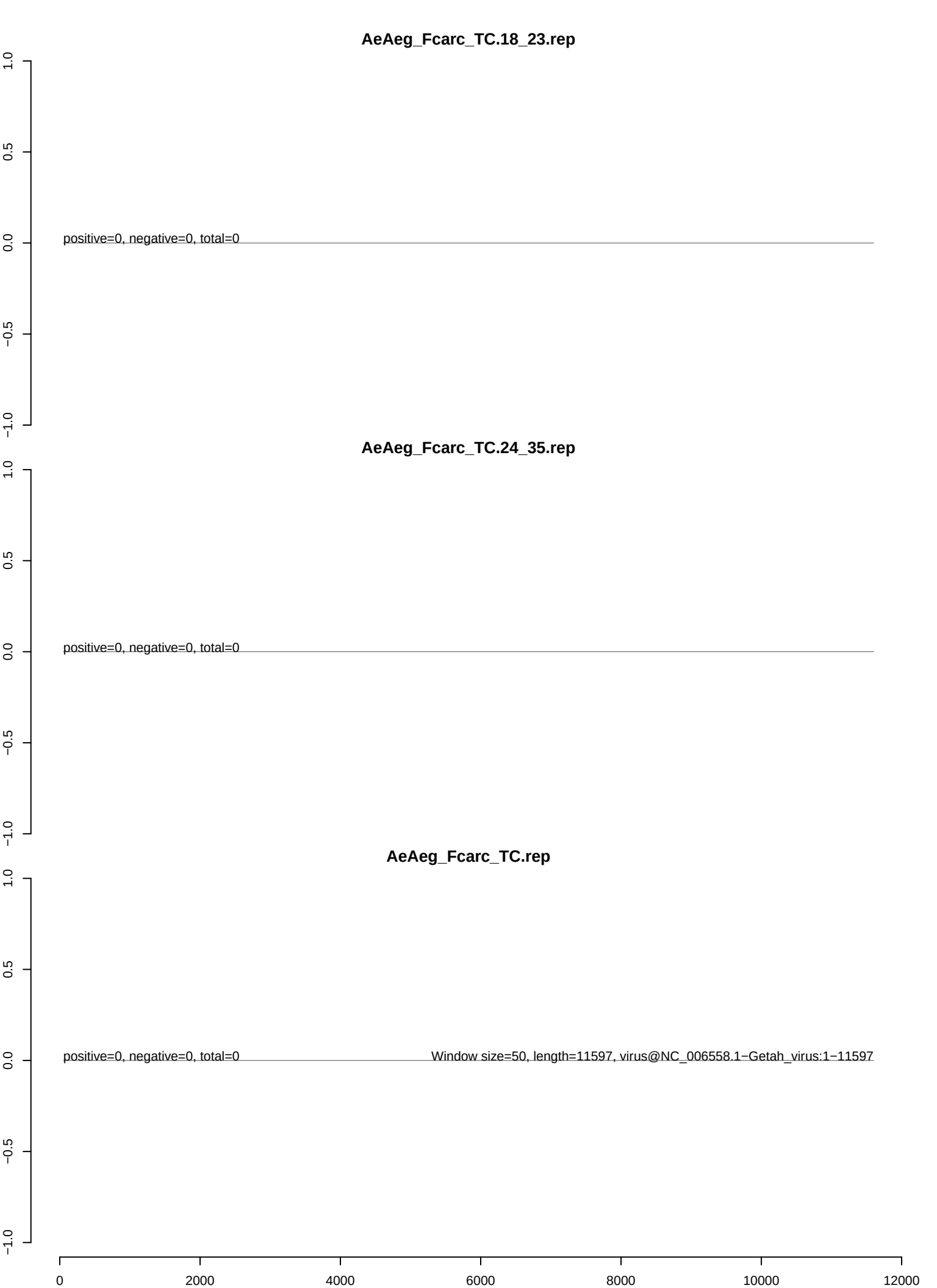
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positive=0, negative=0, total=0
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−1.0
positive=0, negative=0, total=0
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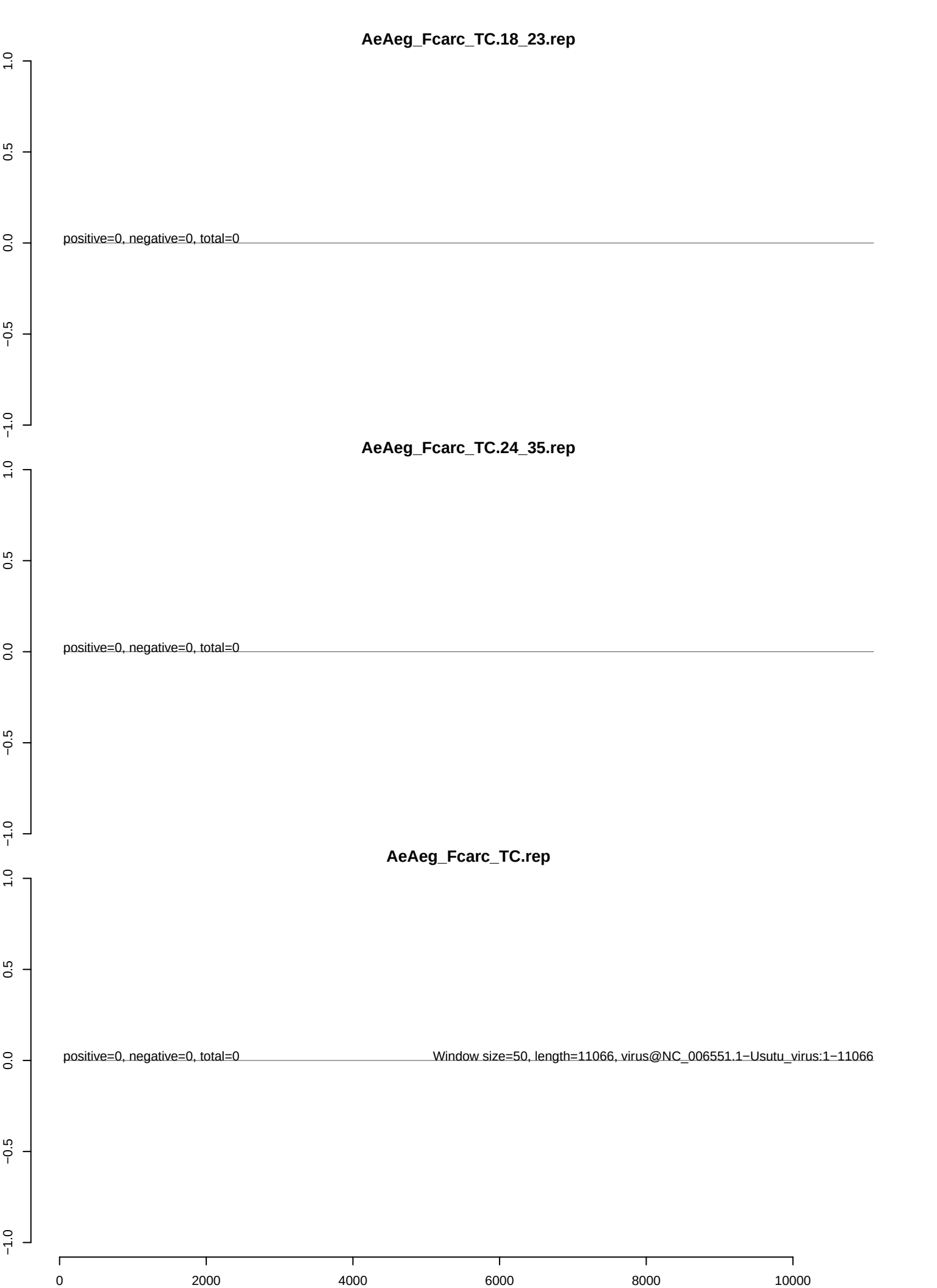
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Window size=50, length=11066, virus@NC_006551.1−Usutu_virus:1−11066
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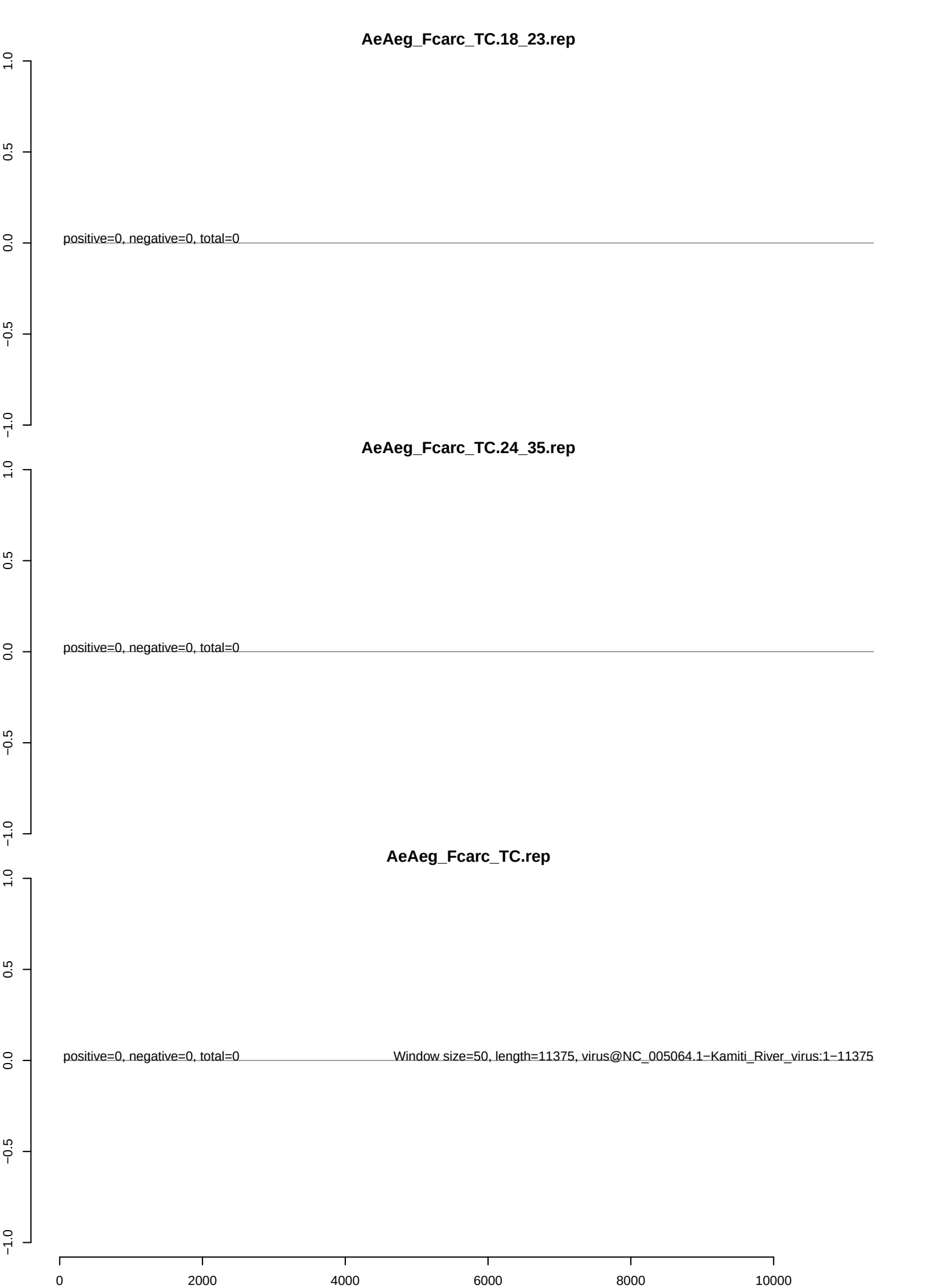
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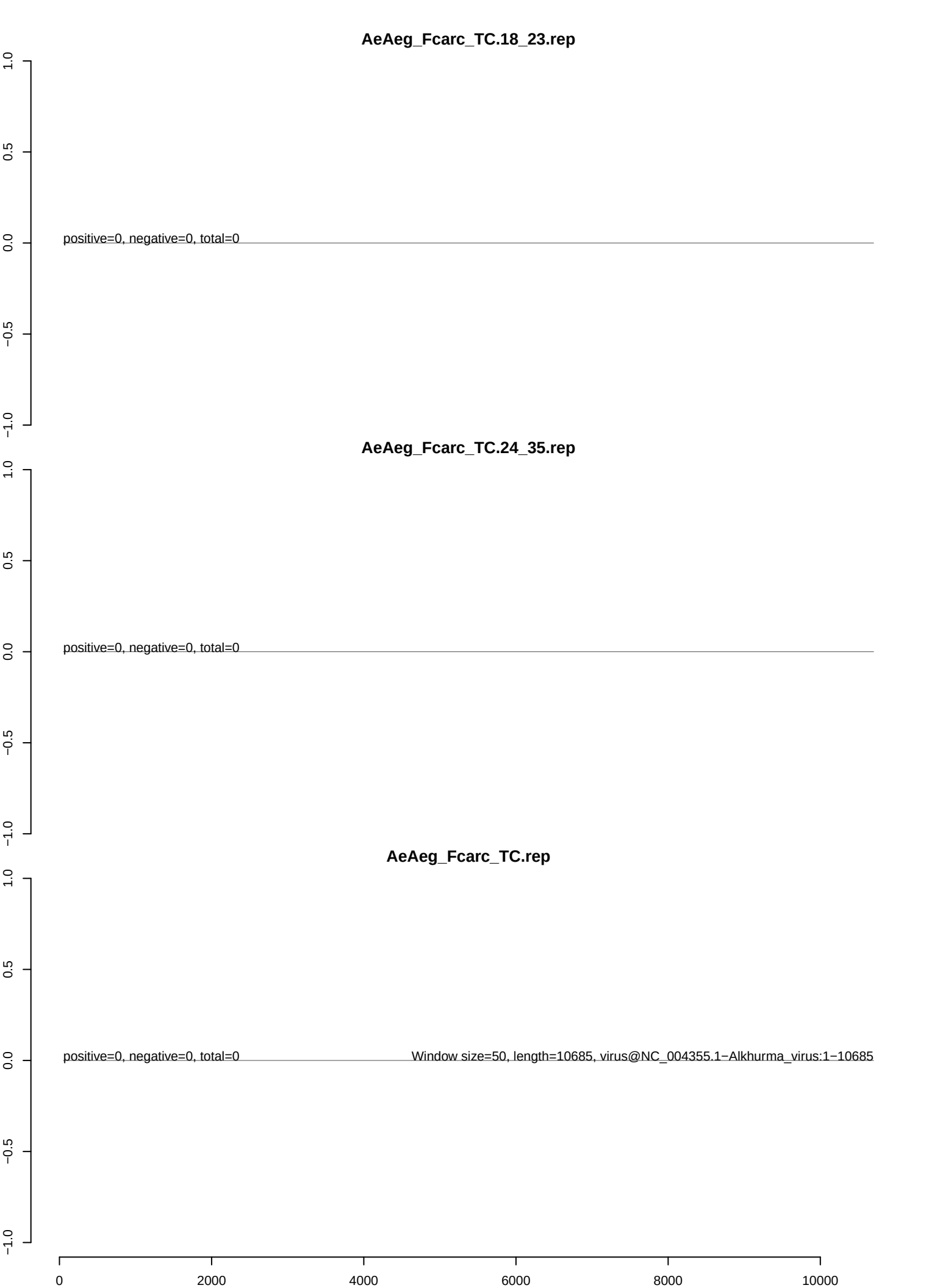
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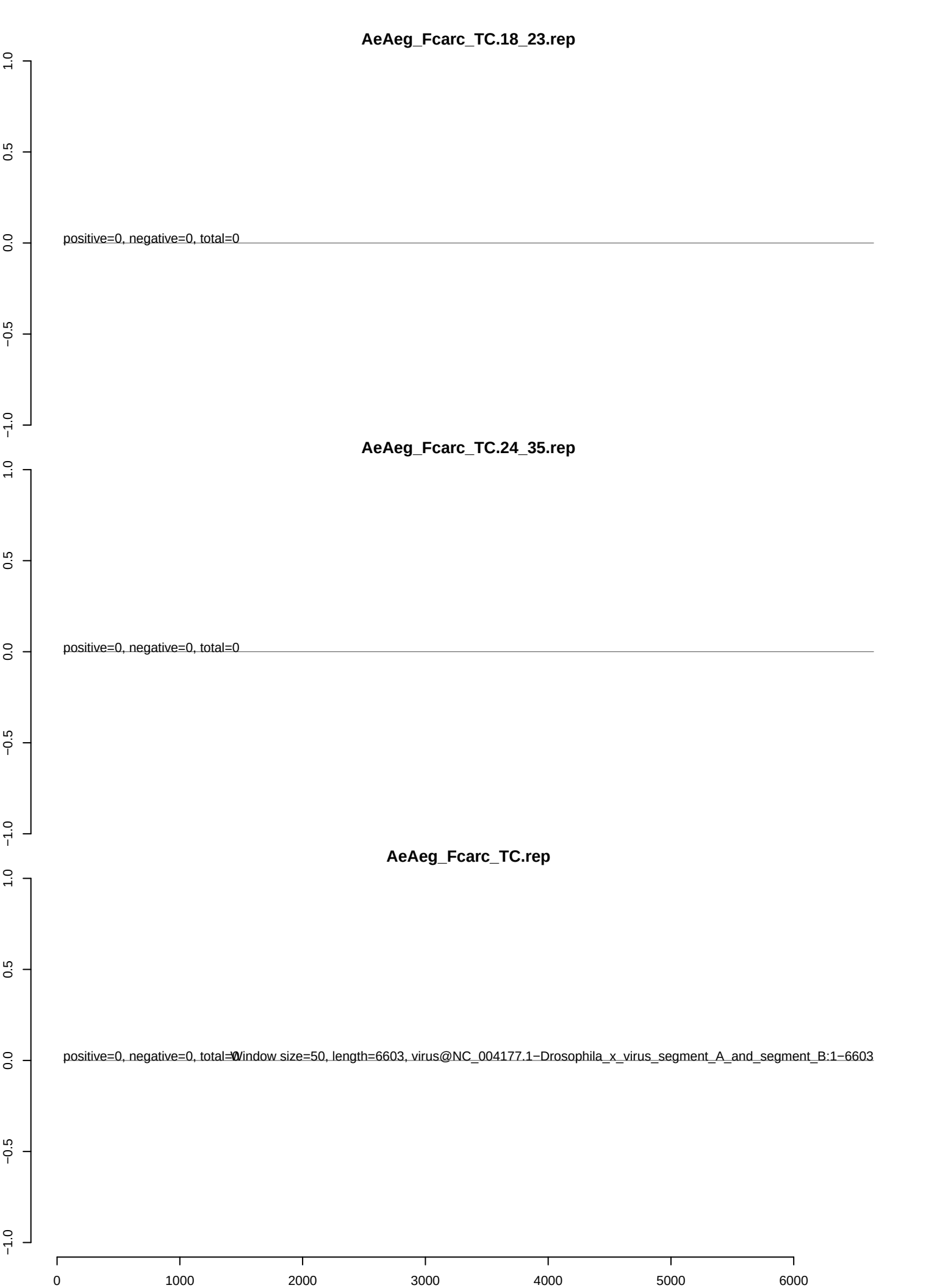
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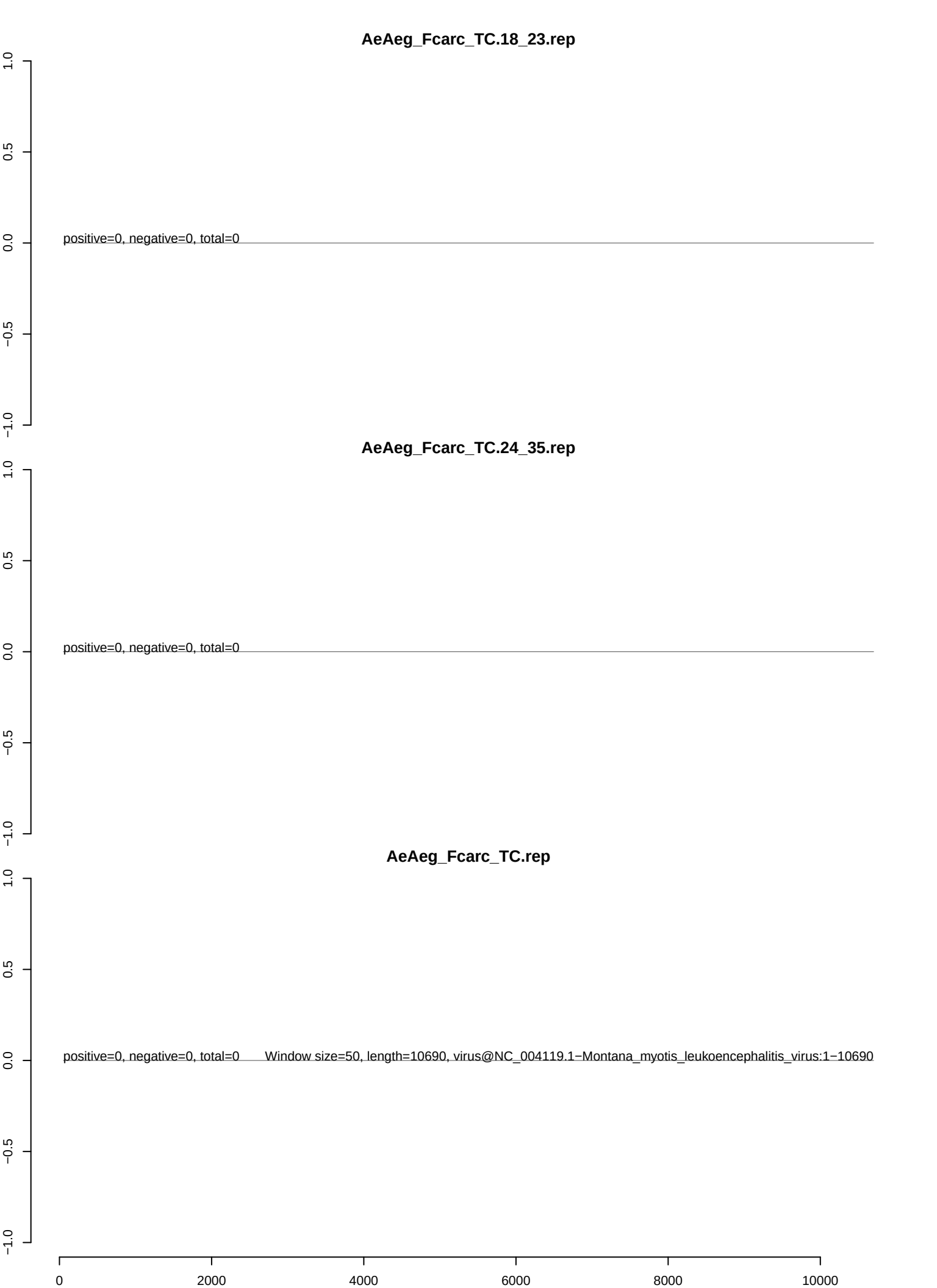
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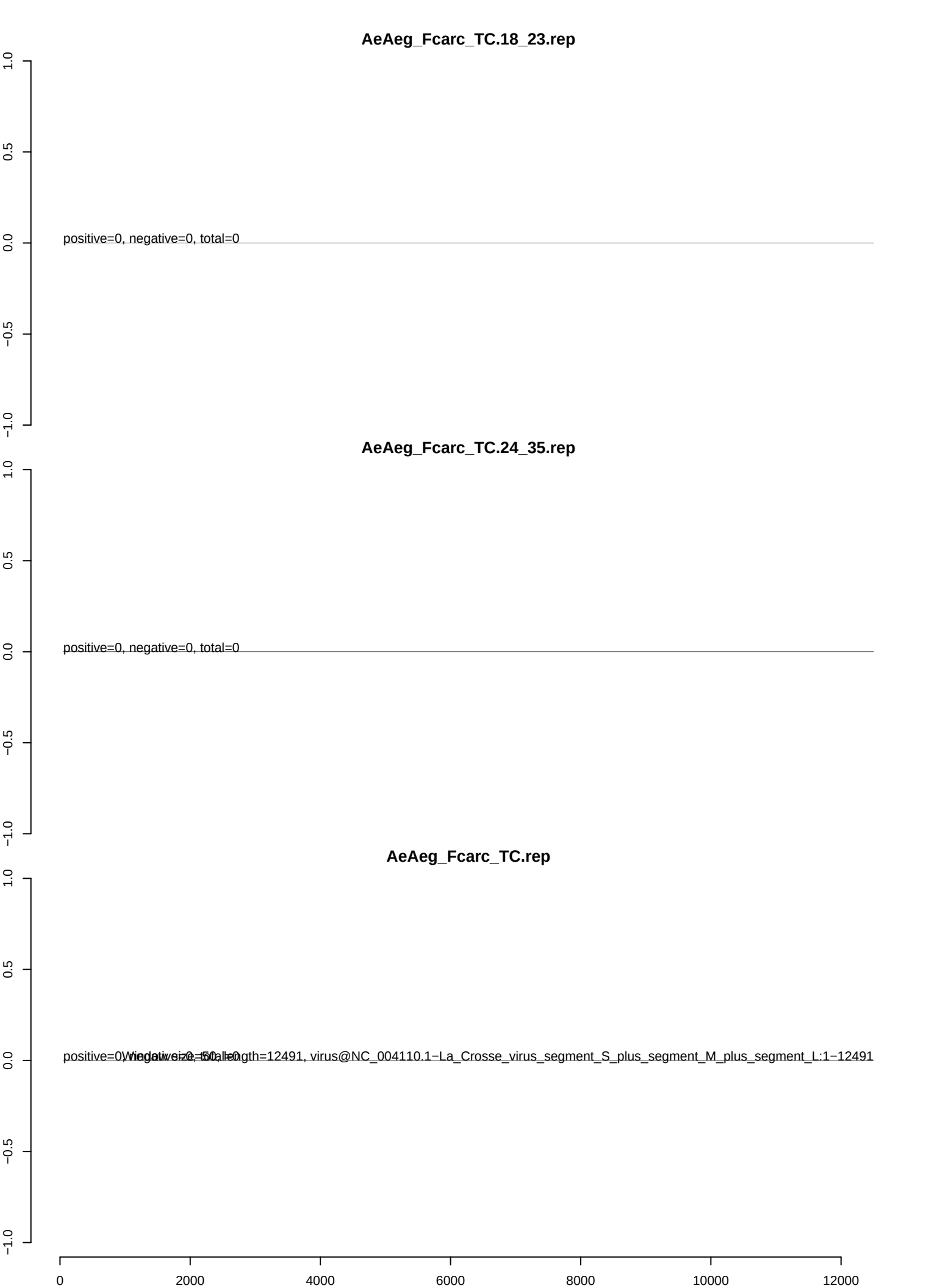
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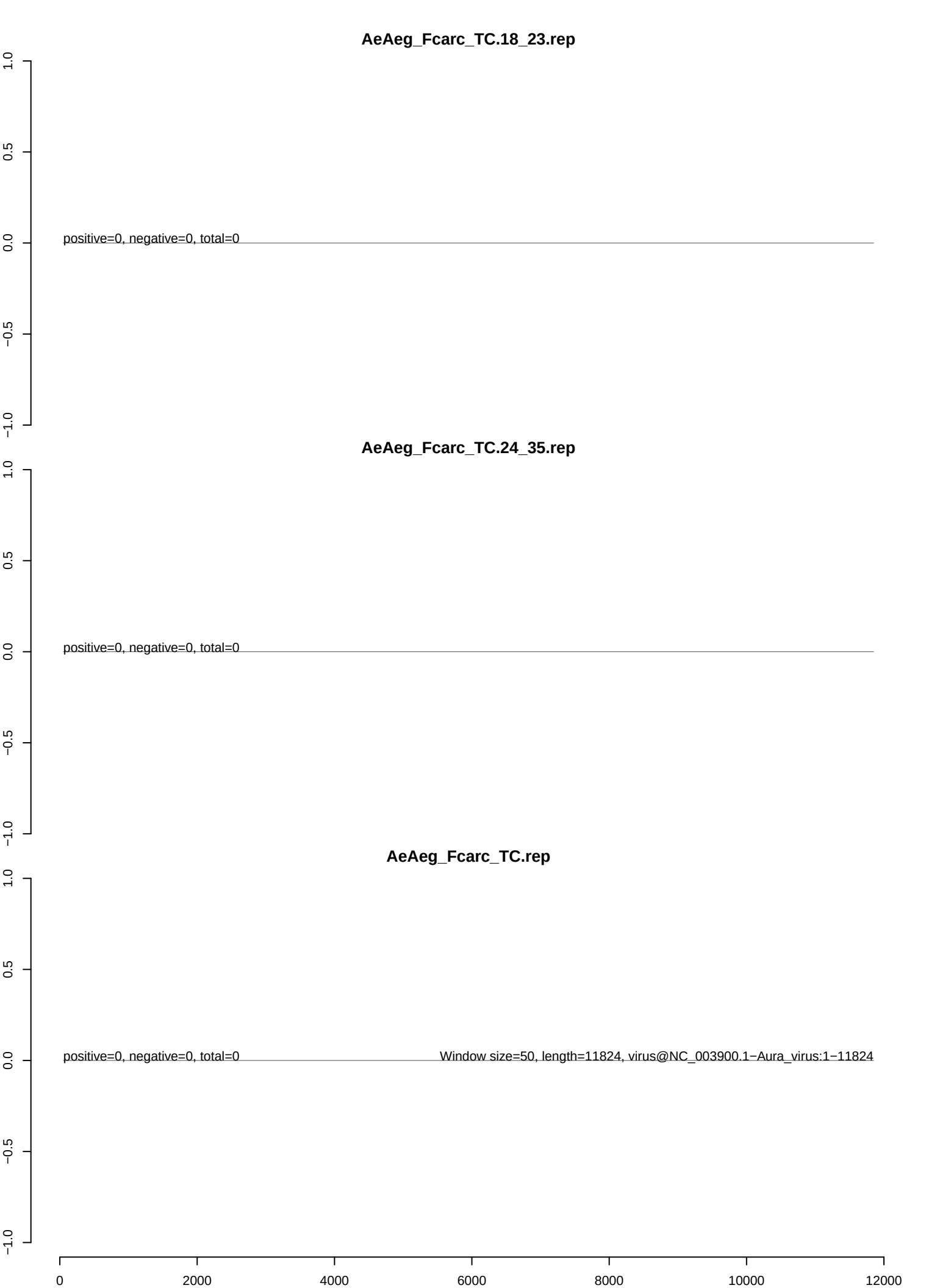
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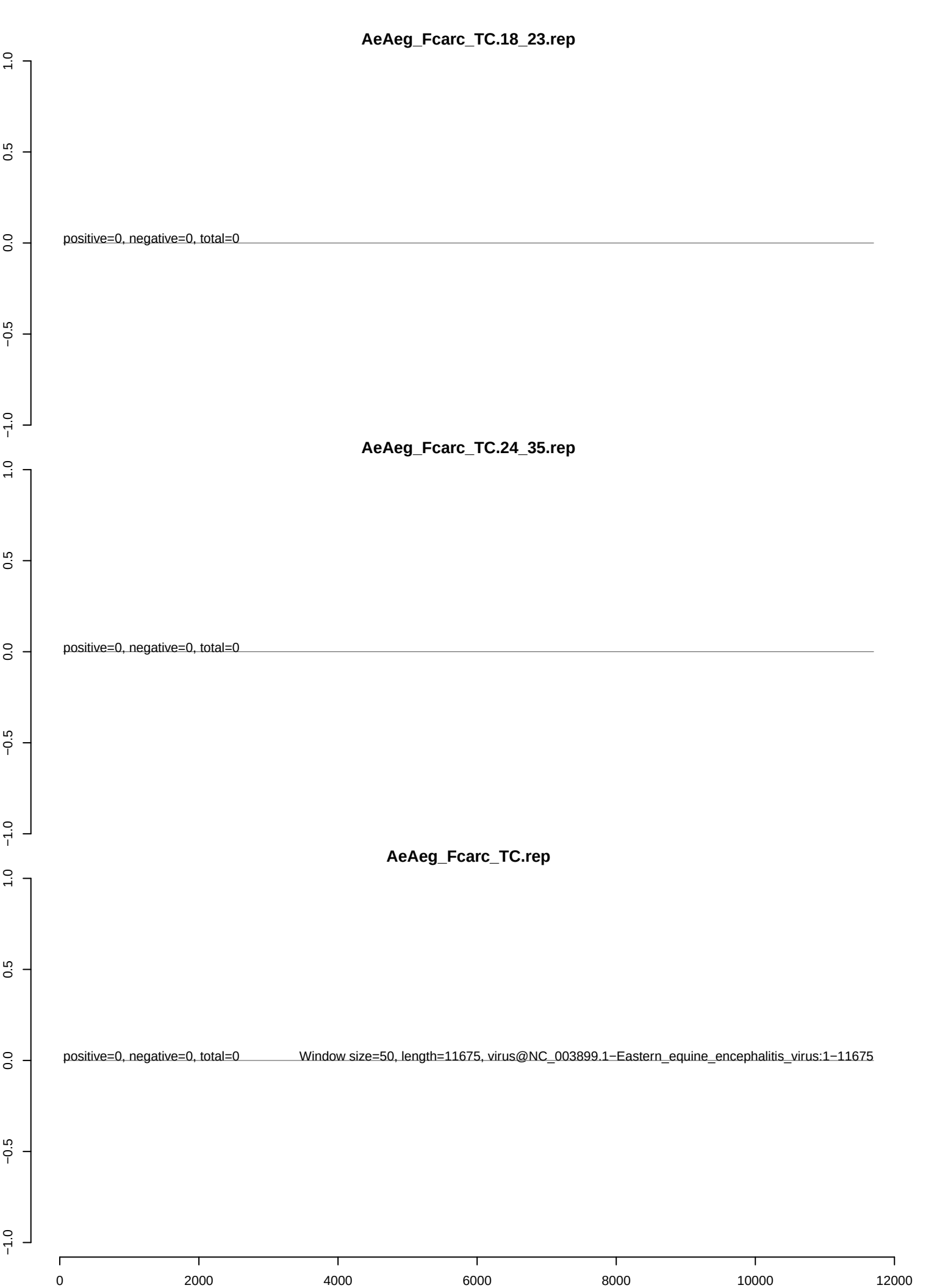
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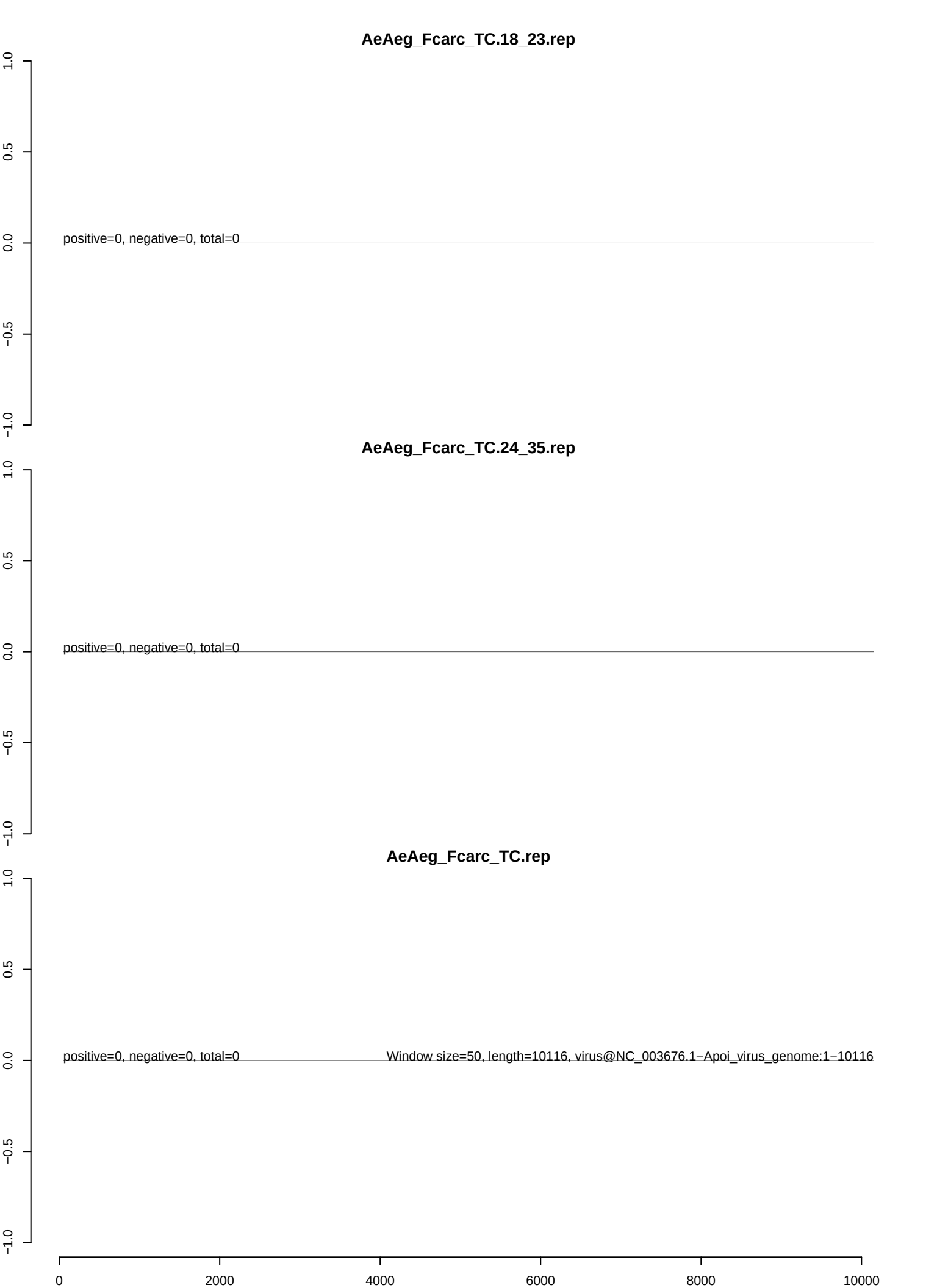
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Window size=50, length=10116, virus@NC_003676.1−Apoi_virus_genome:1−10116
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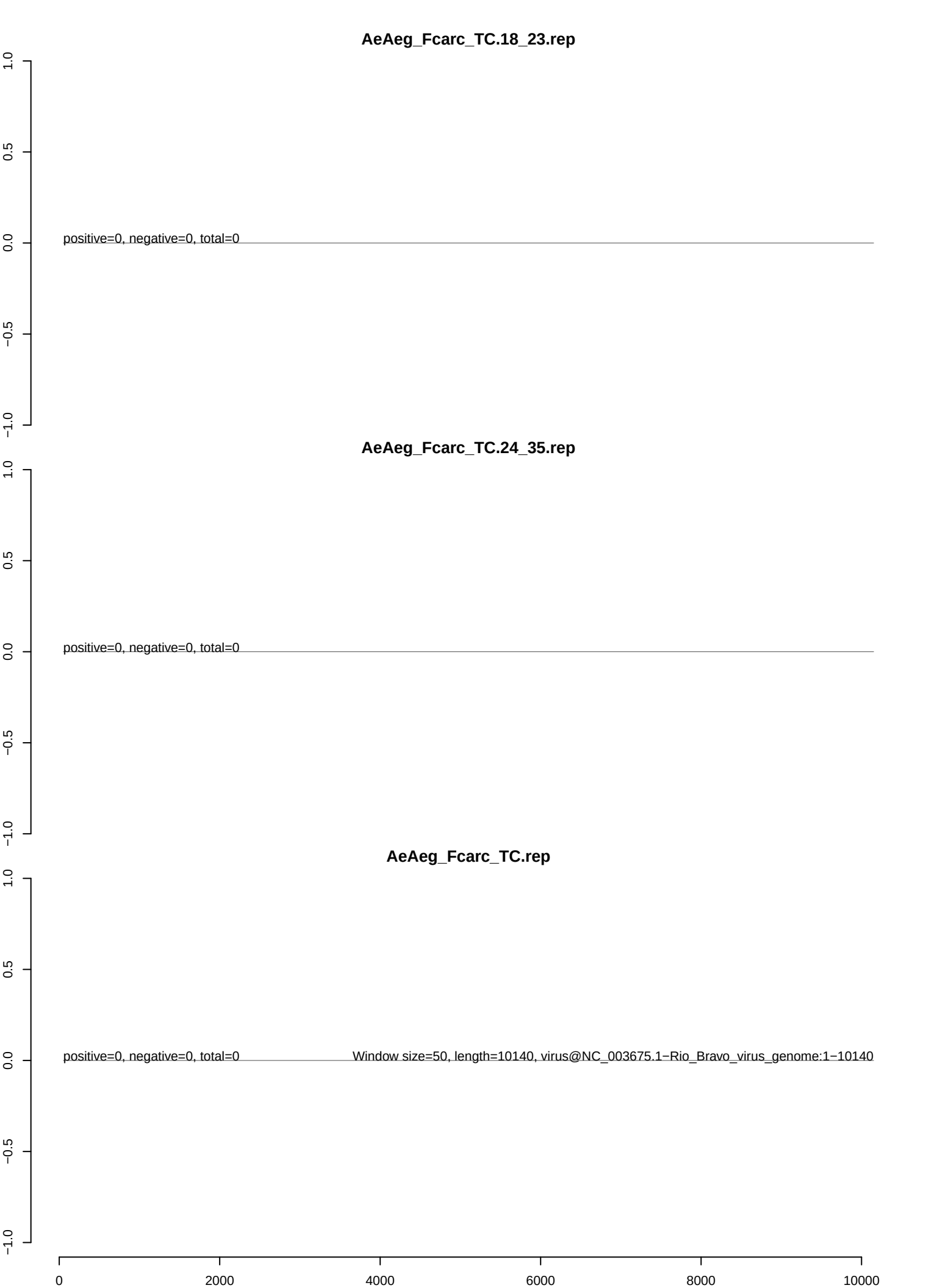
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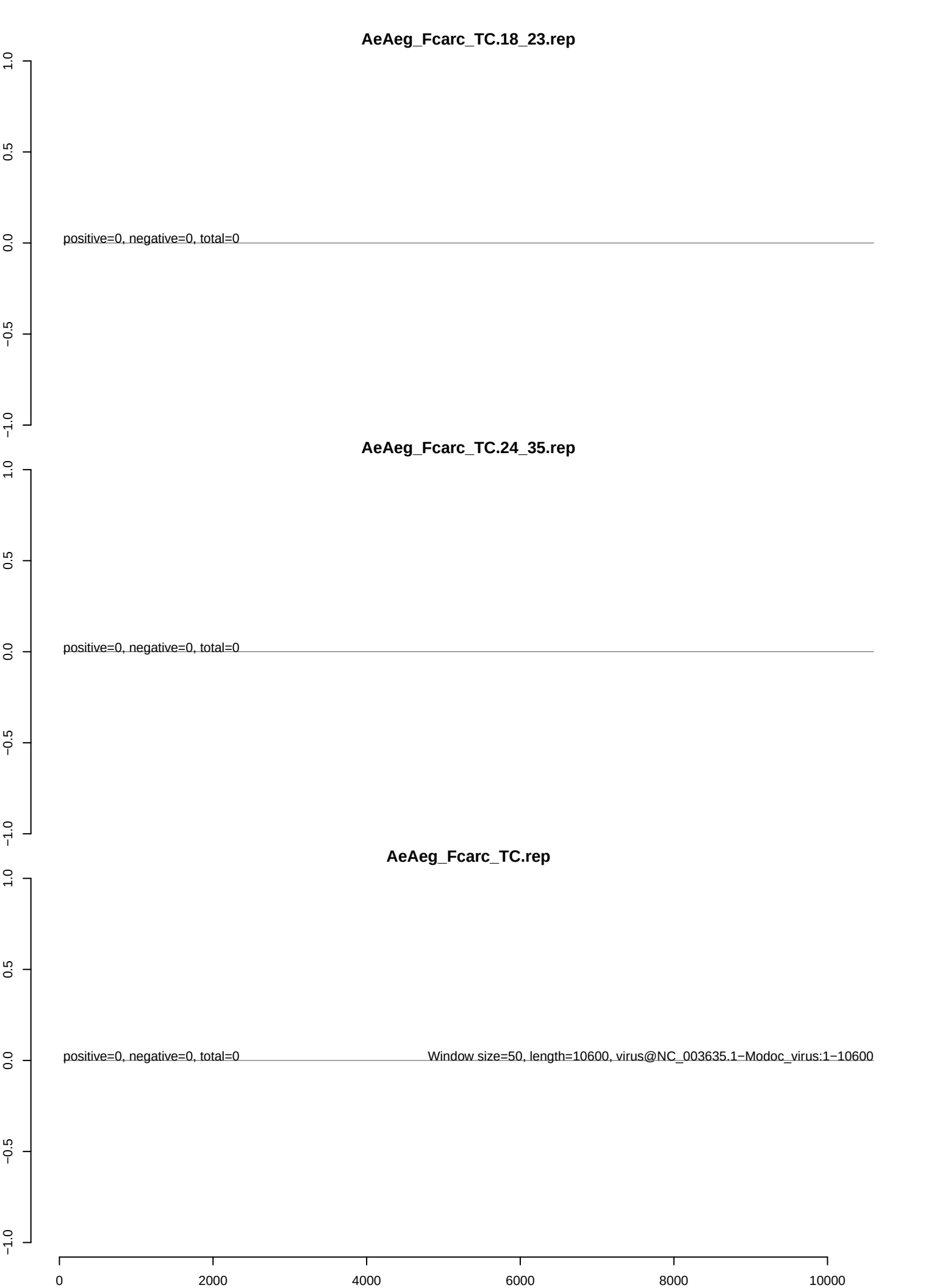
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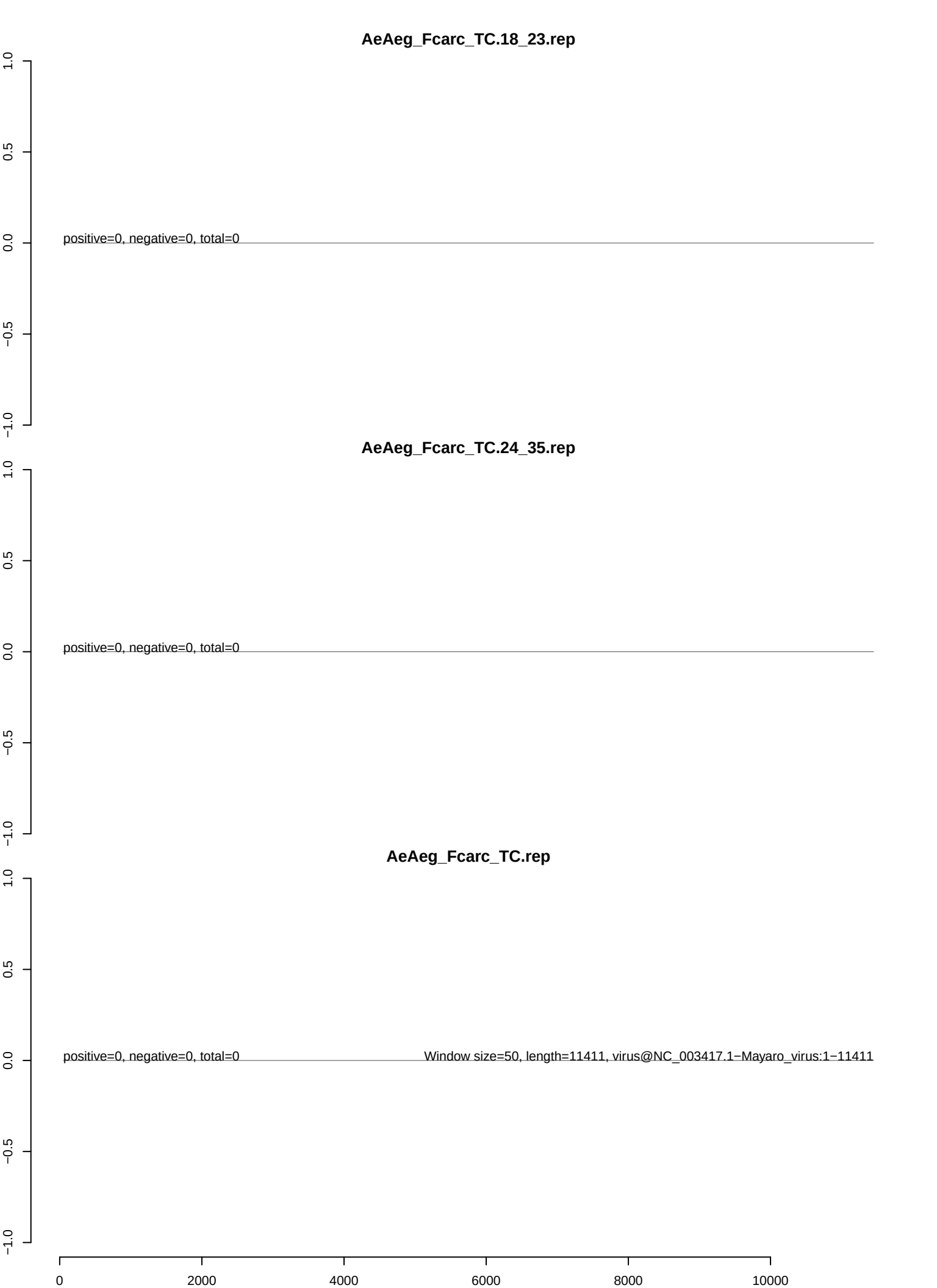
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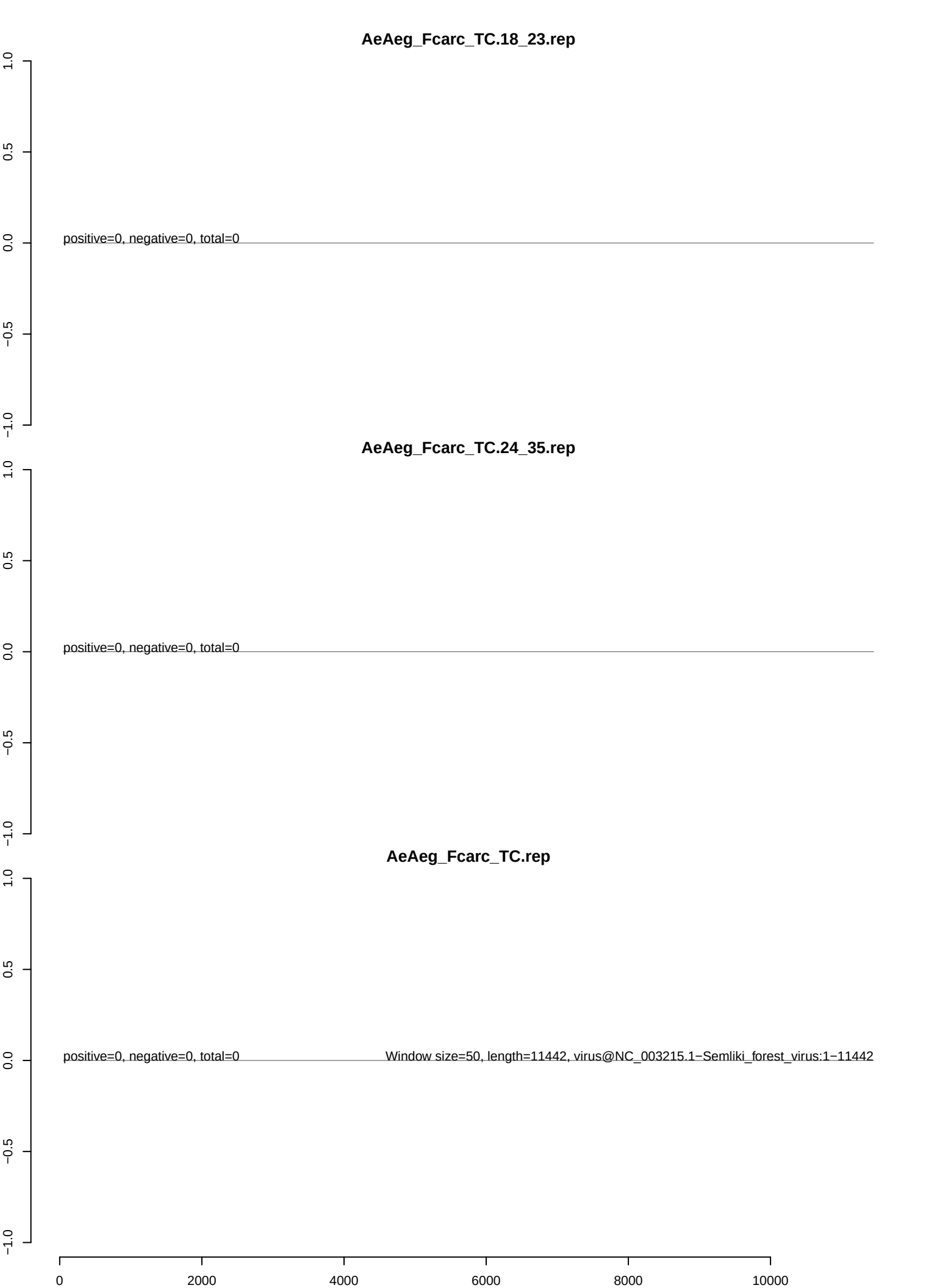
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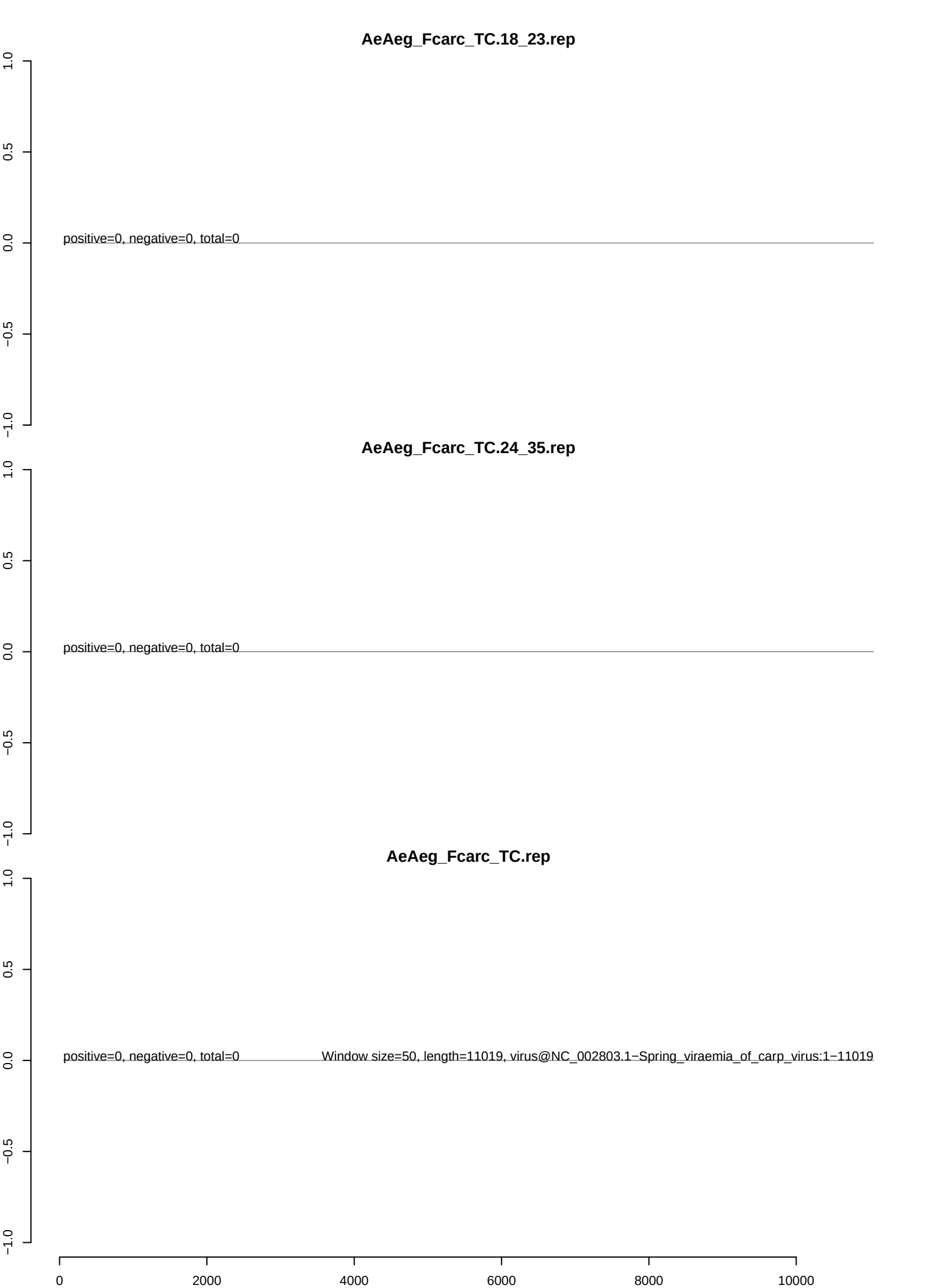
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positive=0, negative=0, total=0
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positive=0, negative=0, total=0
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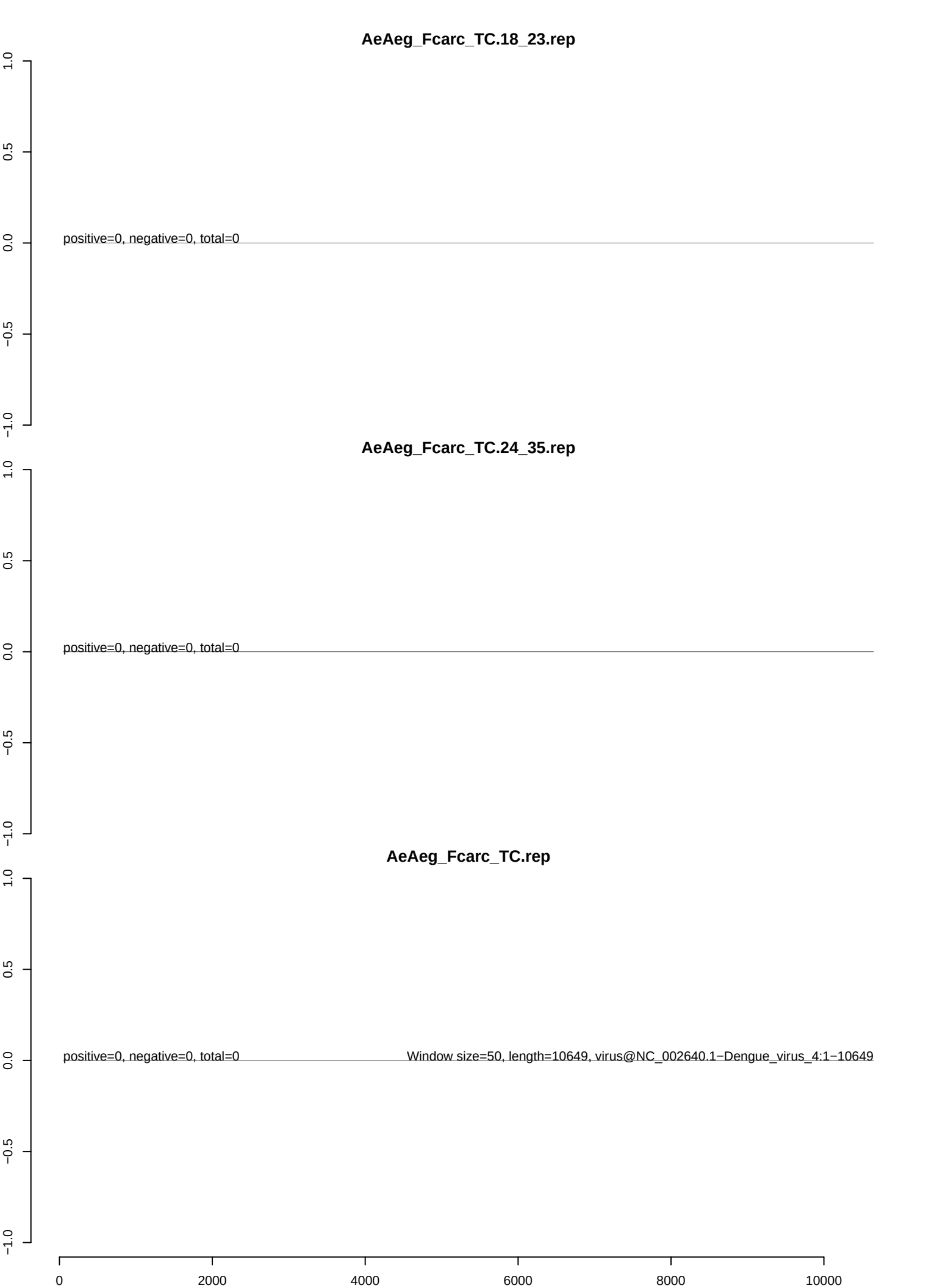
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positive=0, negative=0, total=0
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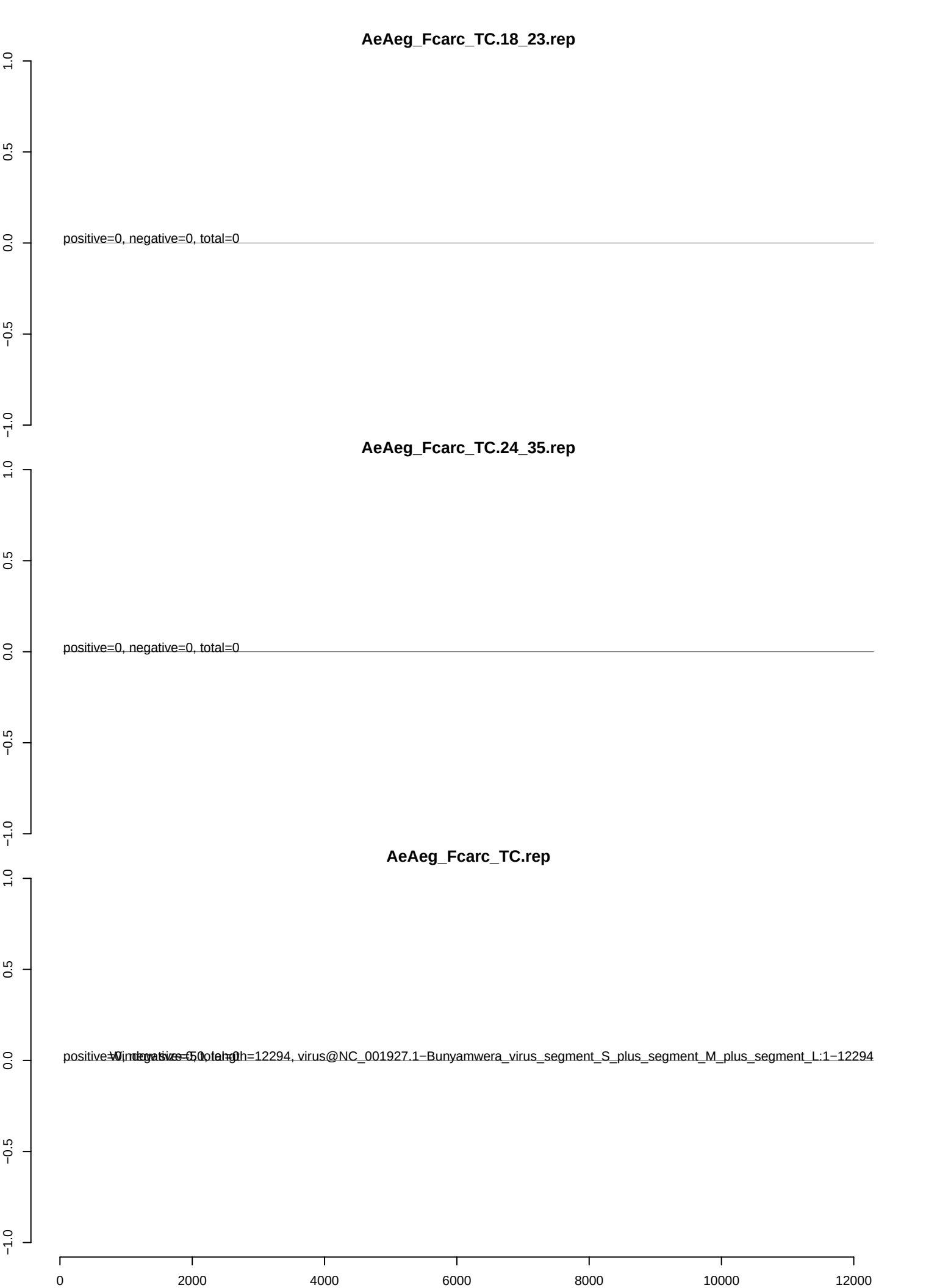
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positive=0, negative=0, total=0
virus@NC_001927.1−Bunyamwera_virus_segment_S_plus_segment_M_plus_segment_L:1−12294
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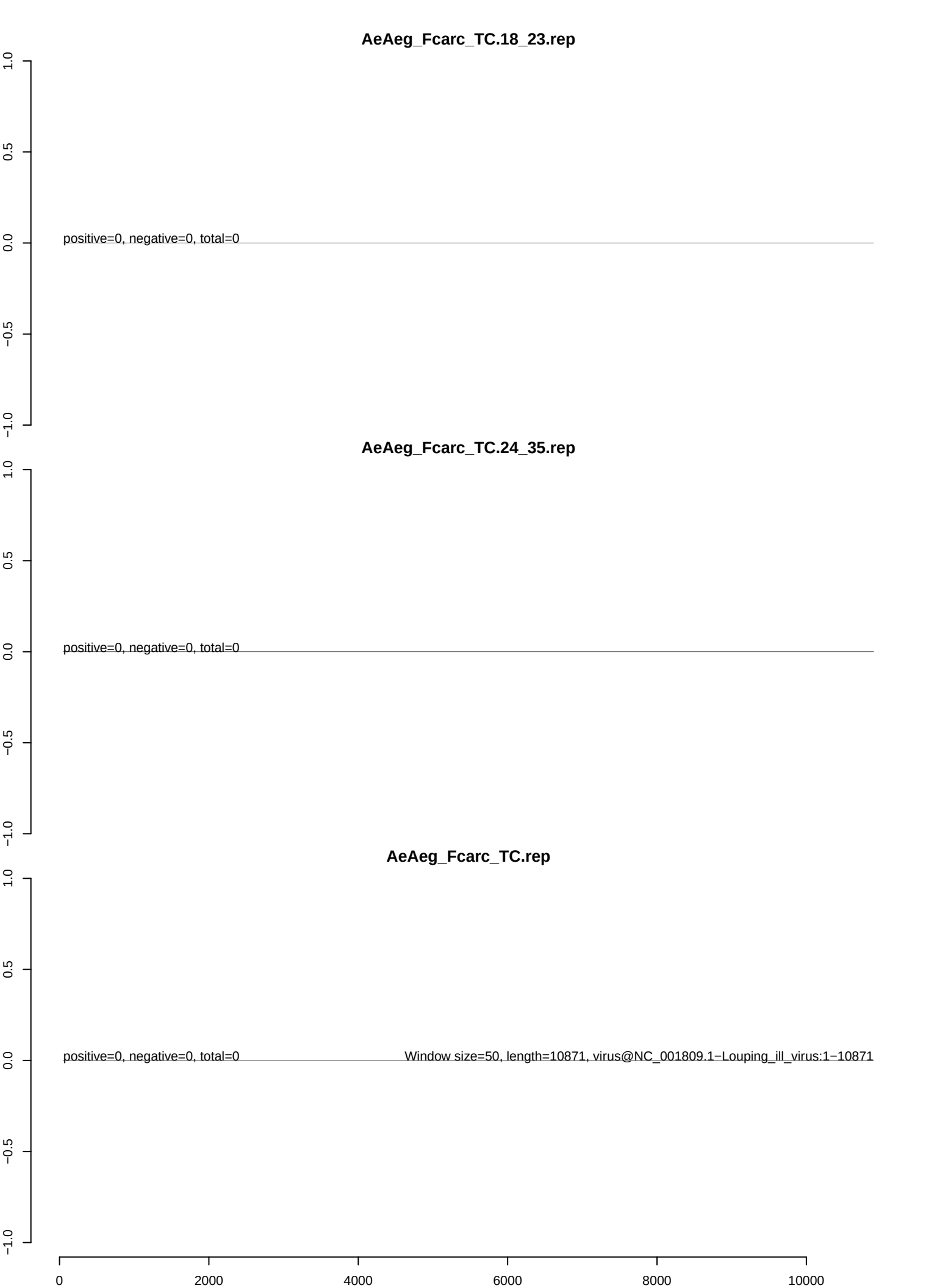
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positive=0, negative=0, total=0
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positive=0, negative=0, total=0
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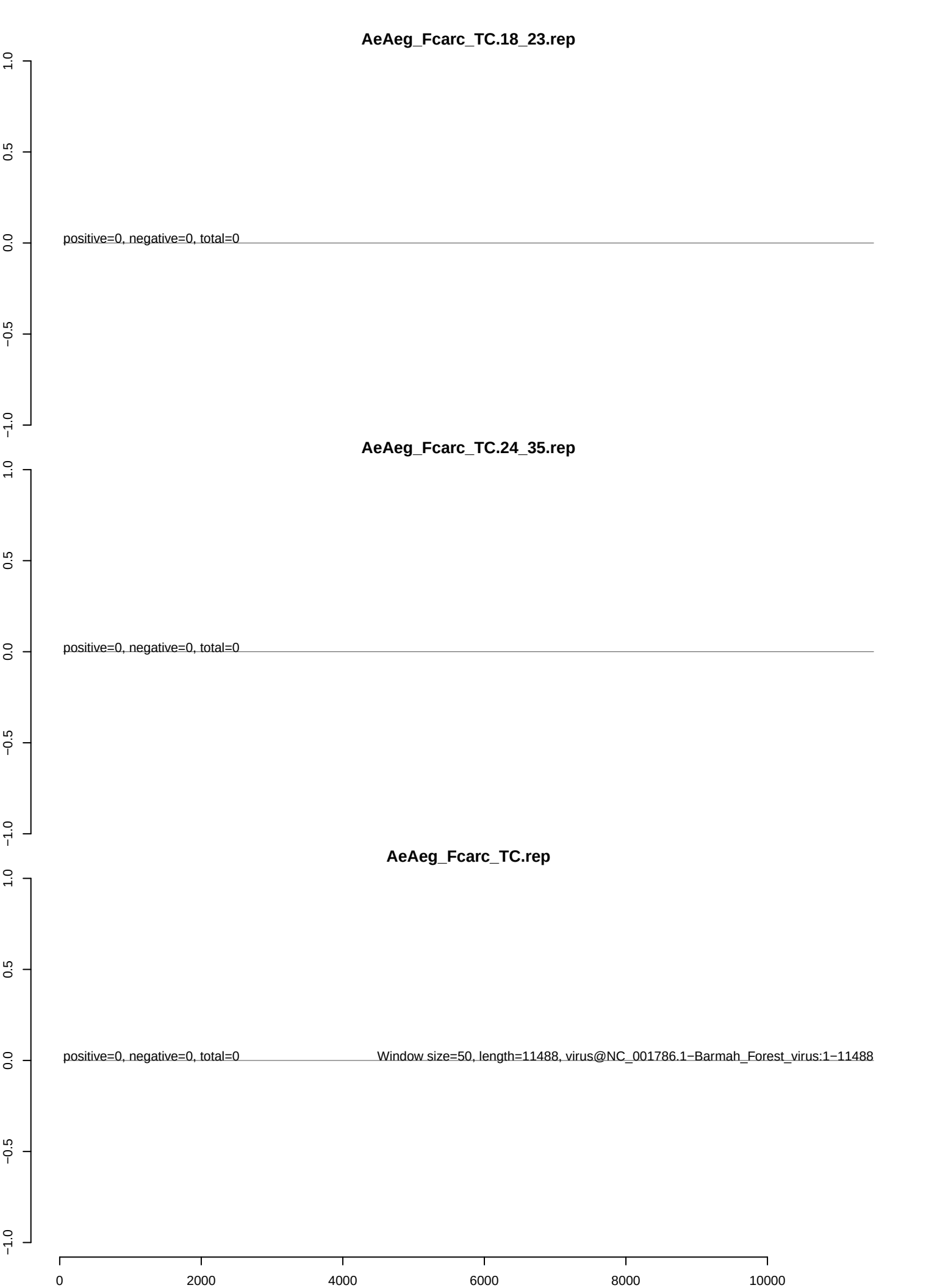
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positive=0, negative=0, total=0
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positive=0, negative=0, total=0
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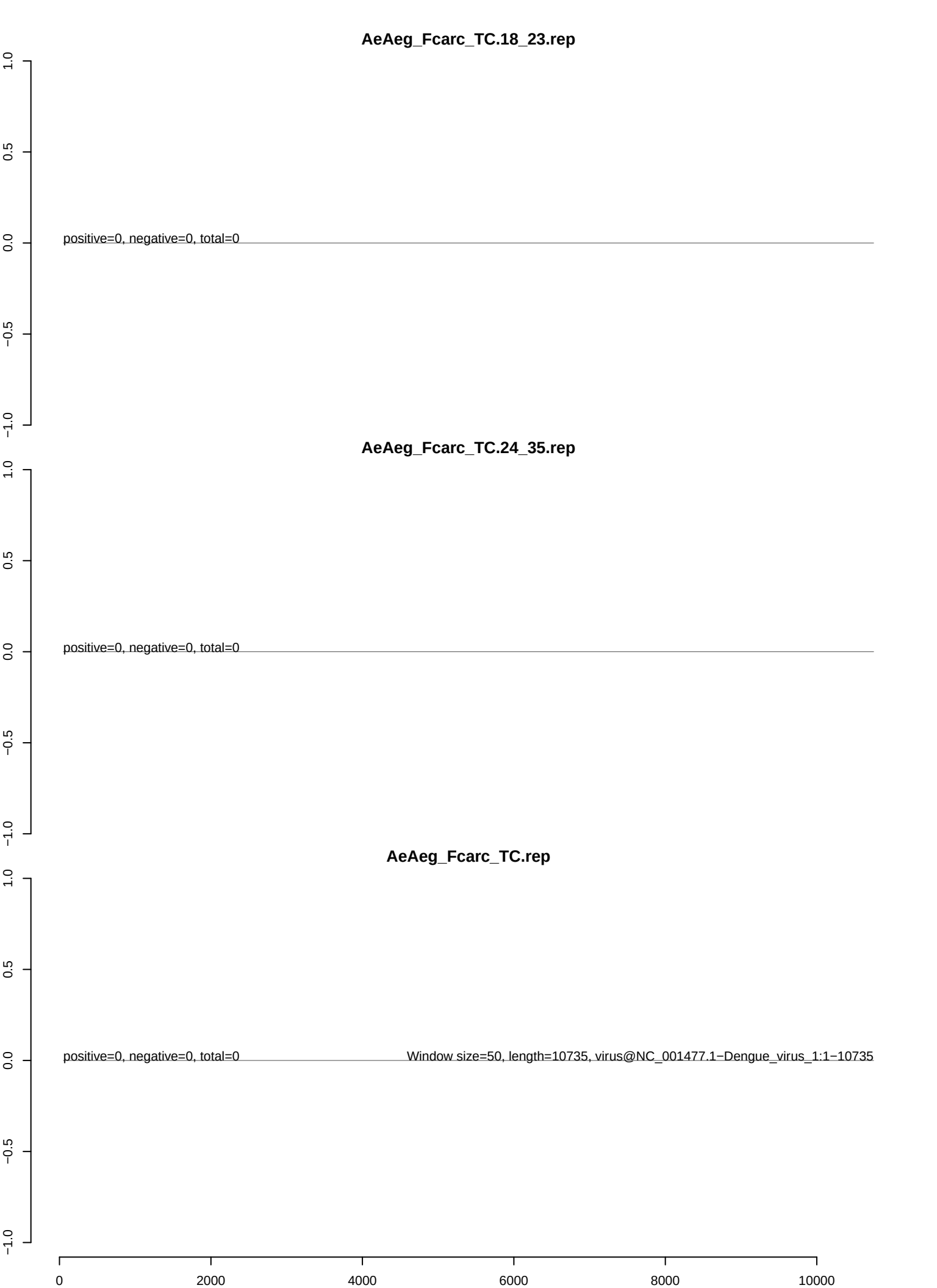
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positive=0, negative=0, total=0
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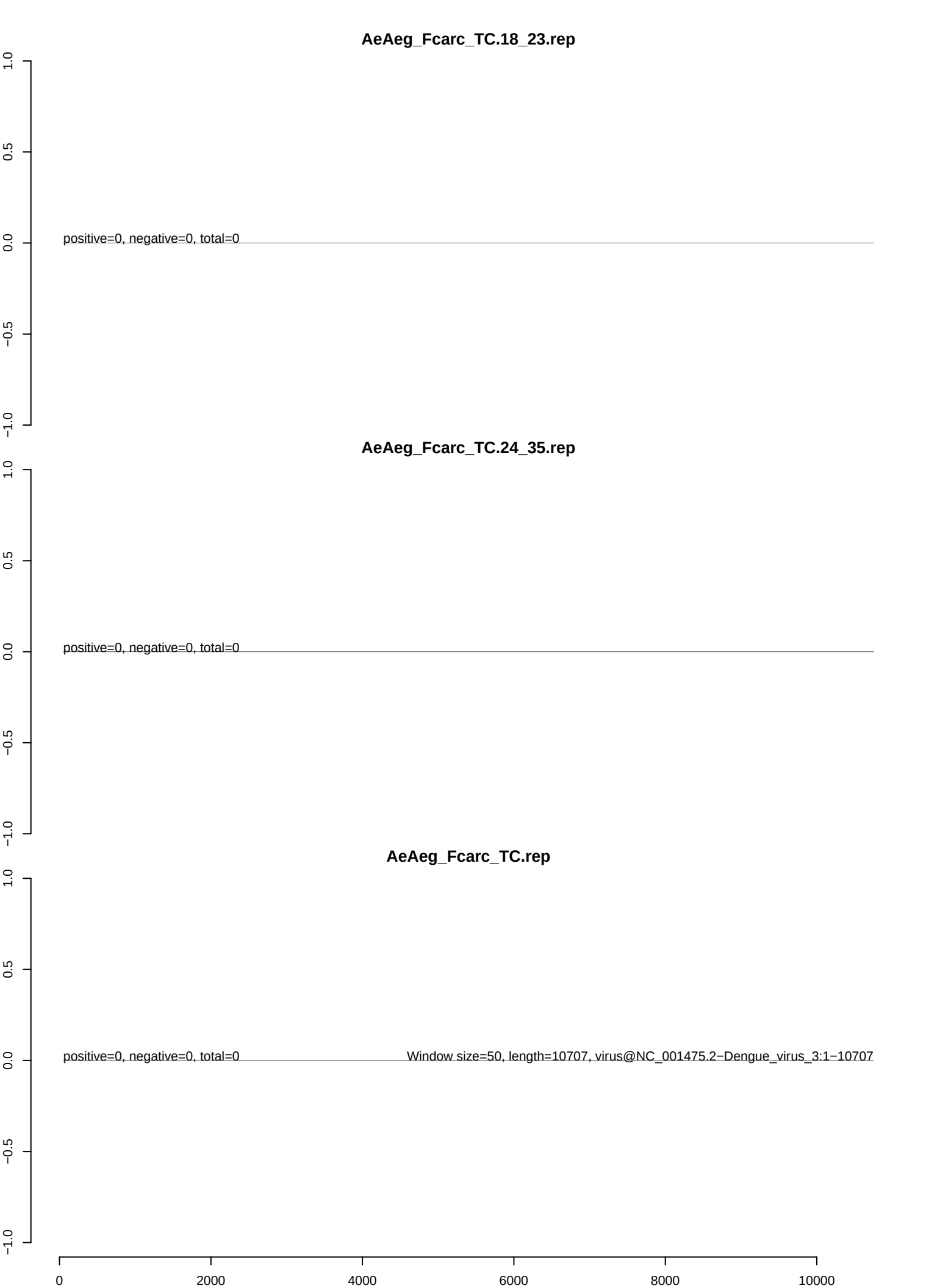
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positive=0, negative=0, total=0
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positive=0, negative=0, total=0
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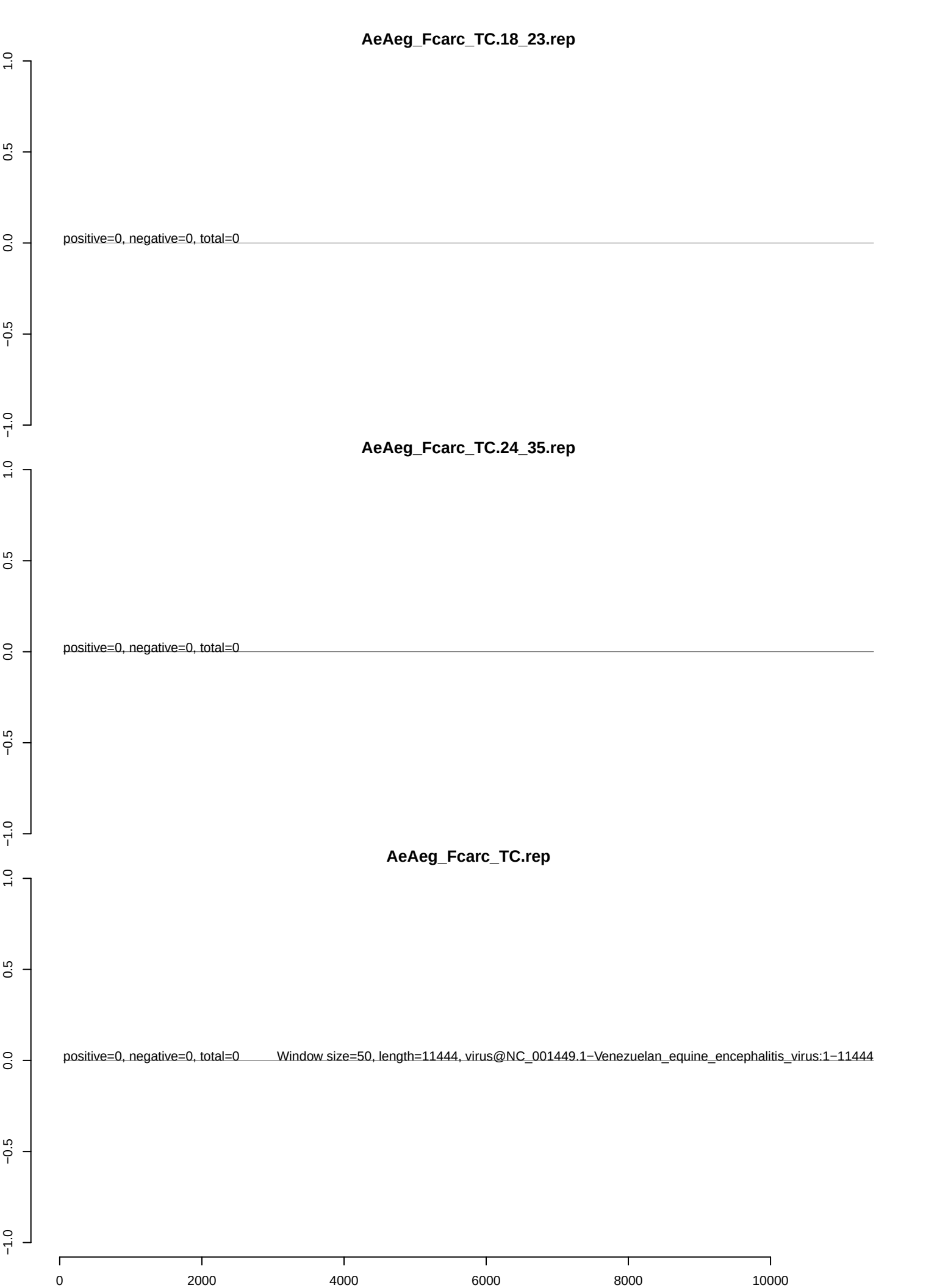
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positive=0, negative=0, total=0
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positive=0, negative=0, total=0
Window size=50, length=11444, virus@NC_001449.1−Venezuelan_equine_encephalitis_virus:1−11444
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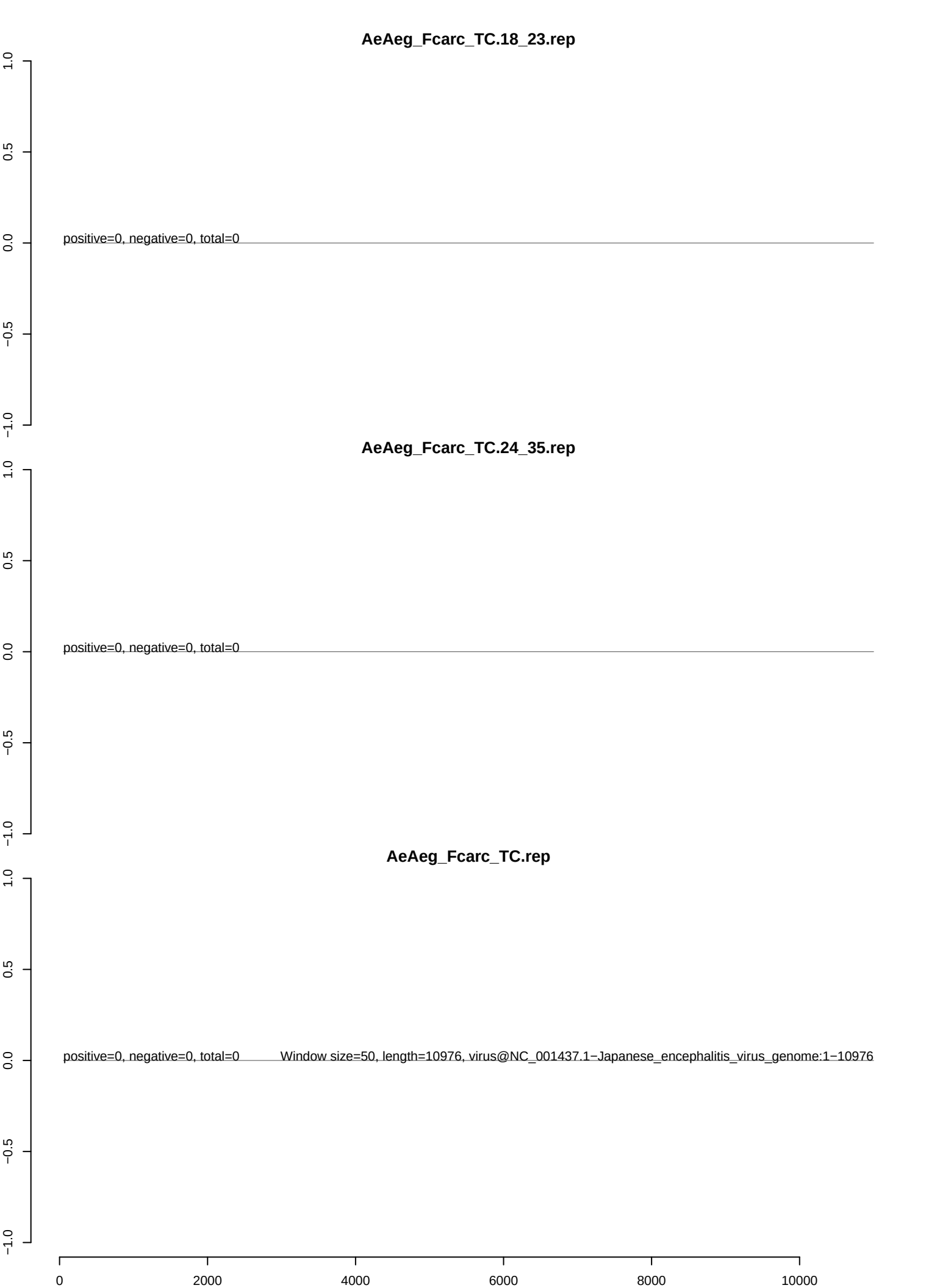
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positive=0, negative=0, total=0
Window size=50, length=10976, virus@NC_001437.1−Japanese_encephalitis_virus_genome:1−10976
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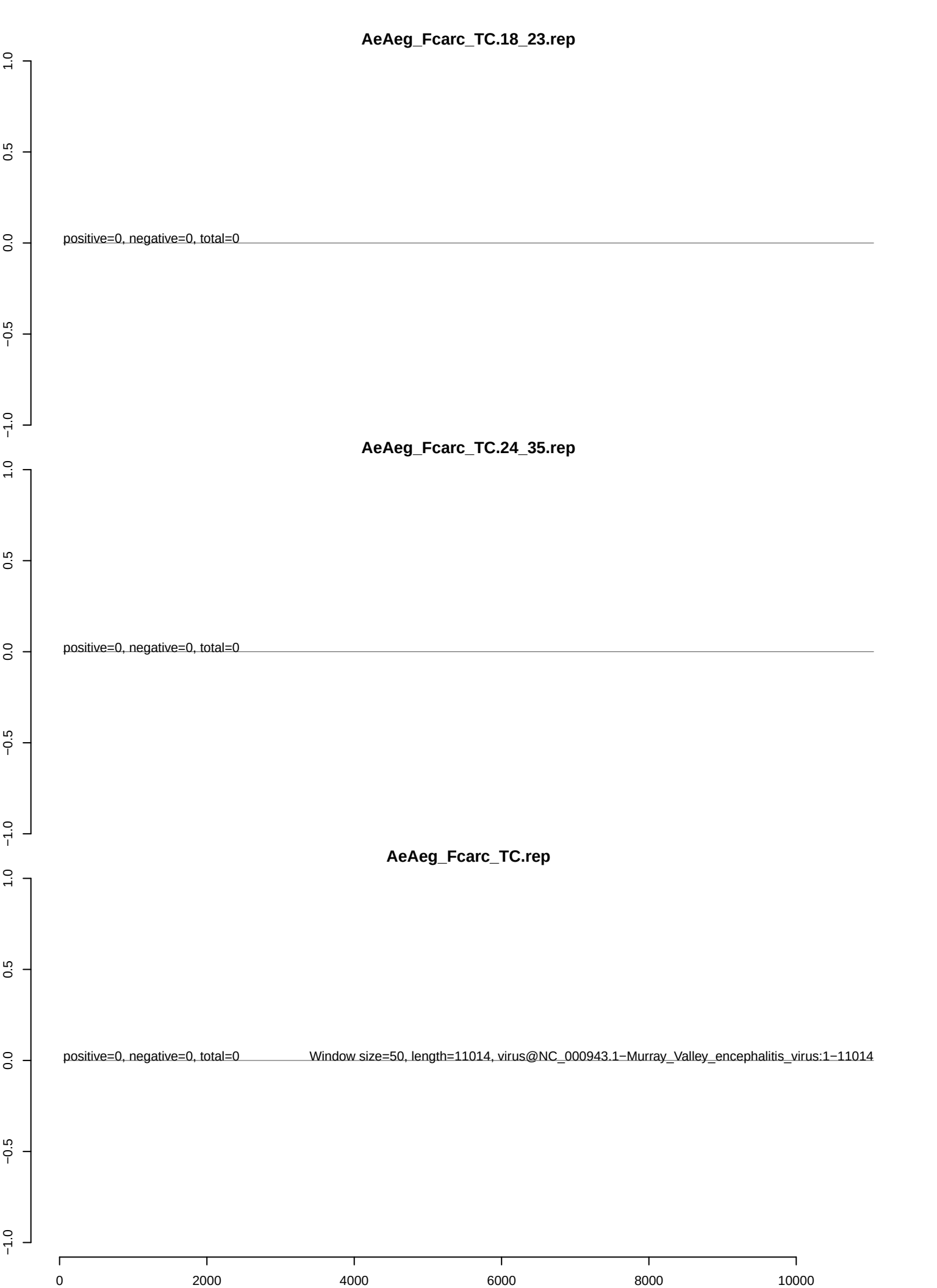
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positive=0, negative=0, total=0
Window size=50, length=11014, virus@NC_000943.1−Murray_Valley_encephalitis_virus:1−11014
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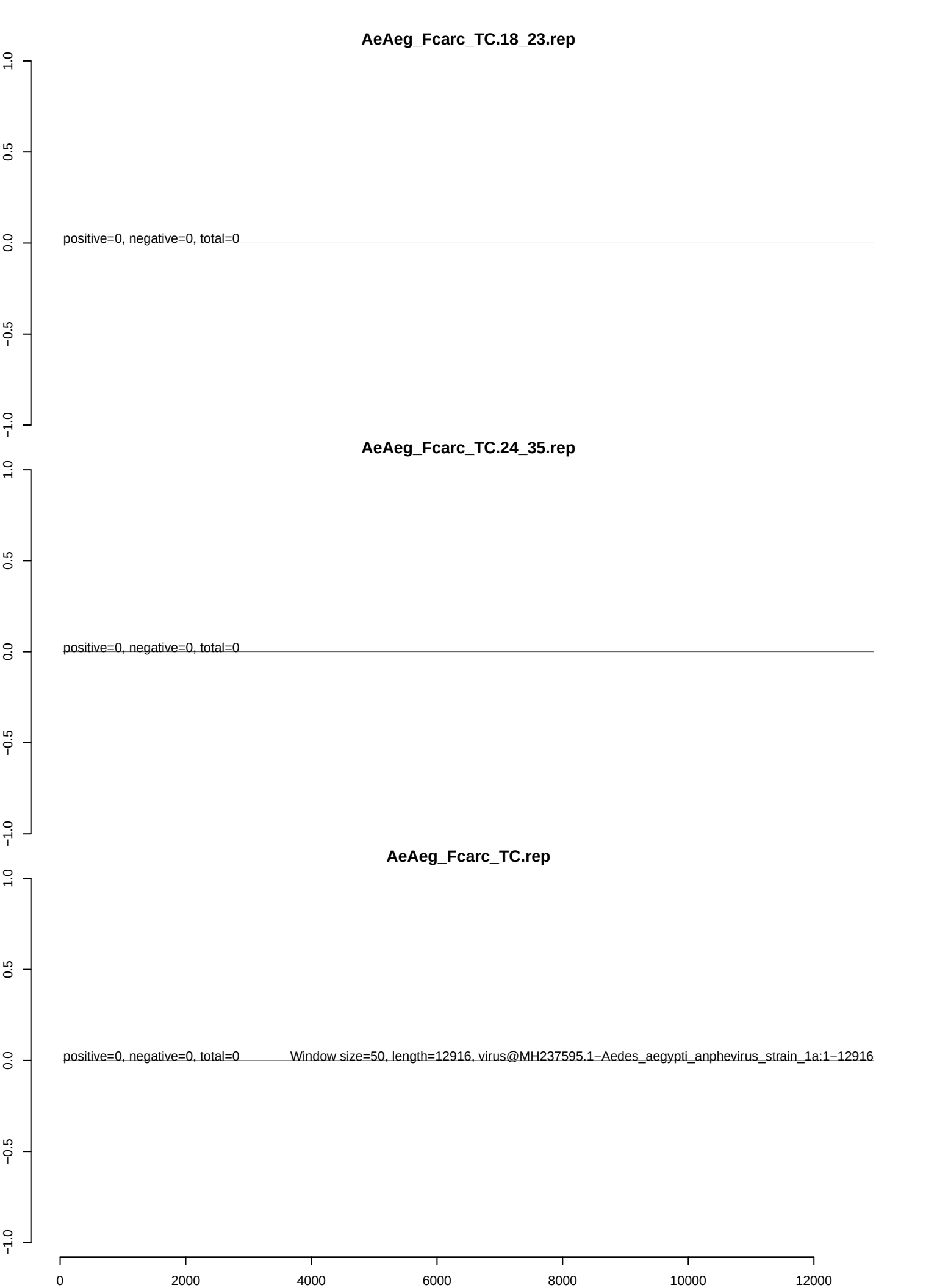
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positive=0, negative=0, total=0
Window size=50, length=12916, virus@MH237595.1−Aedes_aegypti_anphevirus_strain_1a:1−12916
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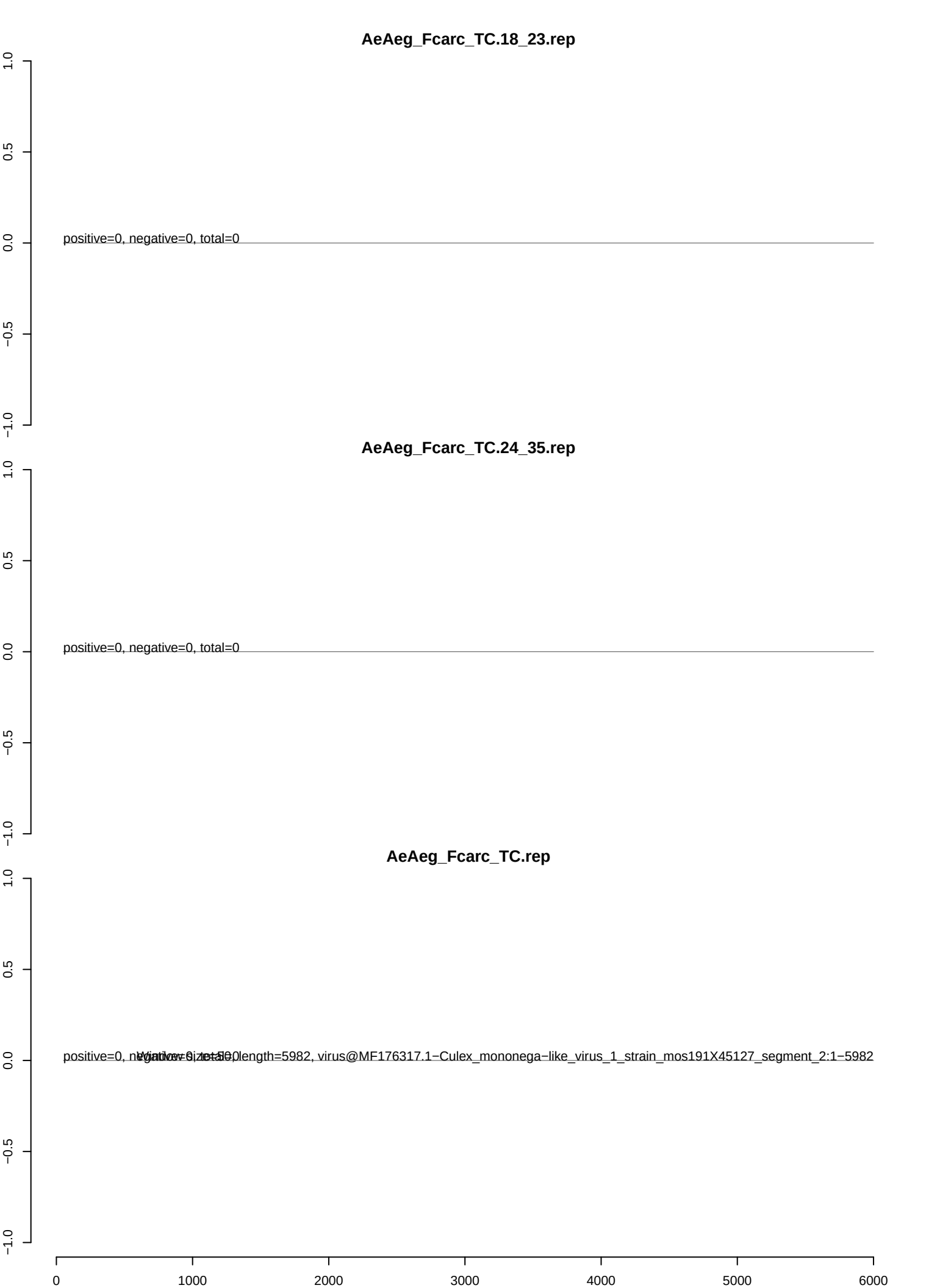
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positive=0, negative=0, total=0
length=5982, virus@MF176317.1−Culex_mononega−like_virus_1_strain_mos191X45127_segment_2:1−5982
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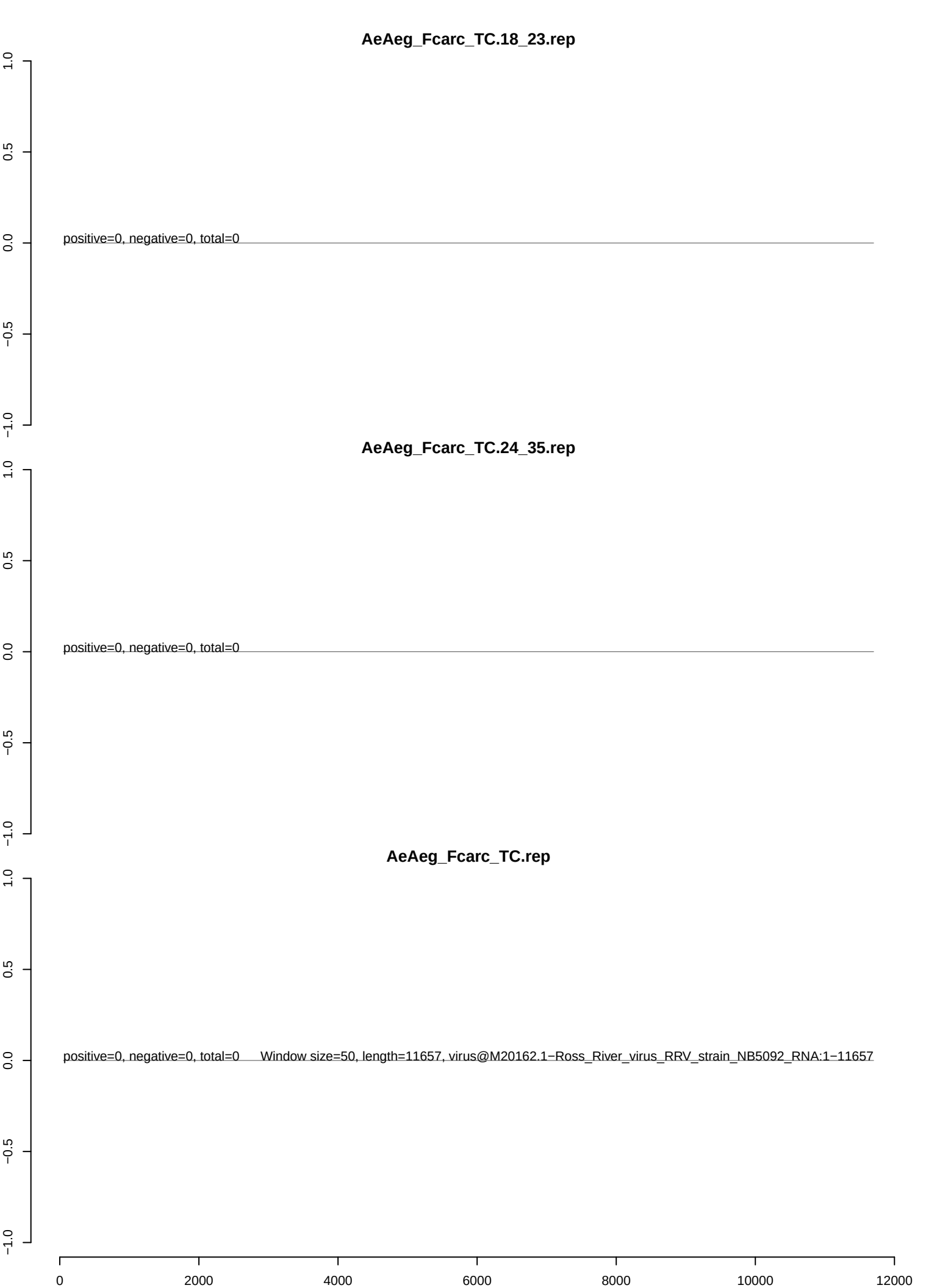
3000
4000
5000
6000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positive=0, negative=0, total=0
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positive=0, negative=0, total=0
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positive=0, negative=0, total=0
Window size=50, length=11657, virus@M20162.1−Ross_River_virus_RRV_strain_NB5092_RNA:1−11657
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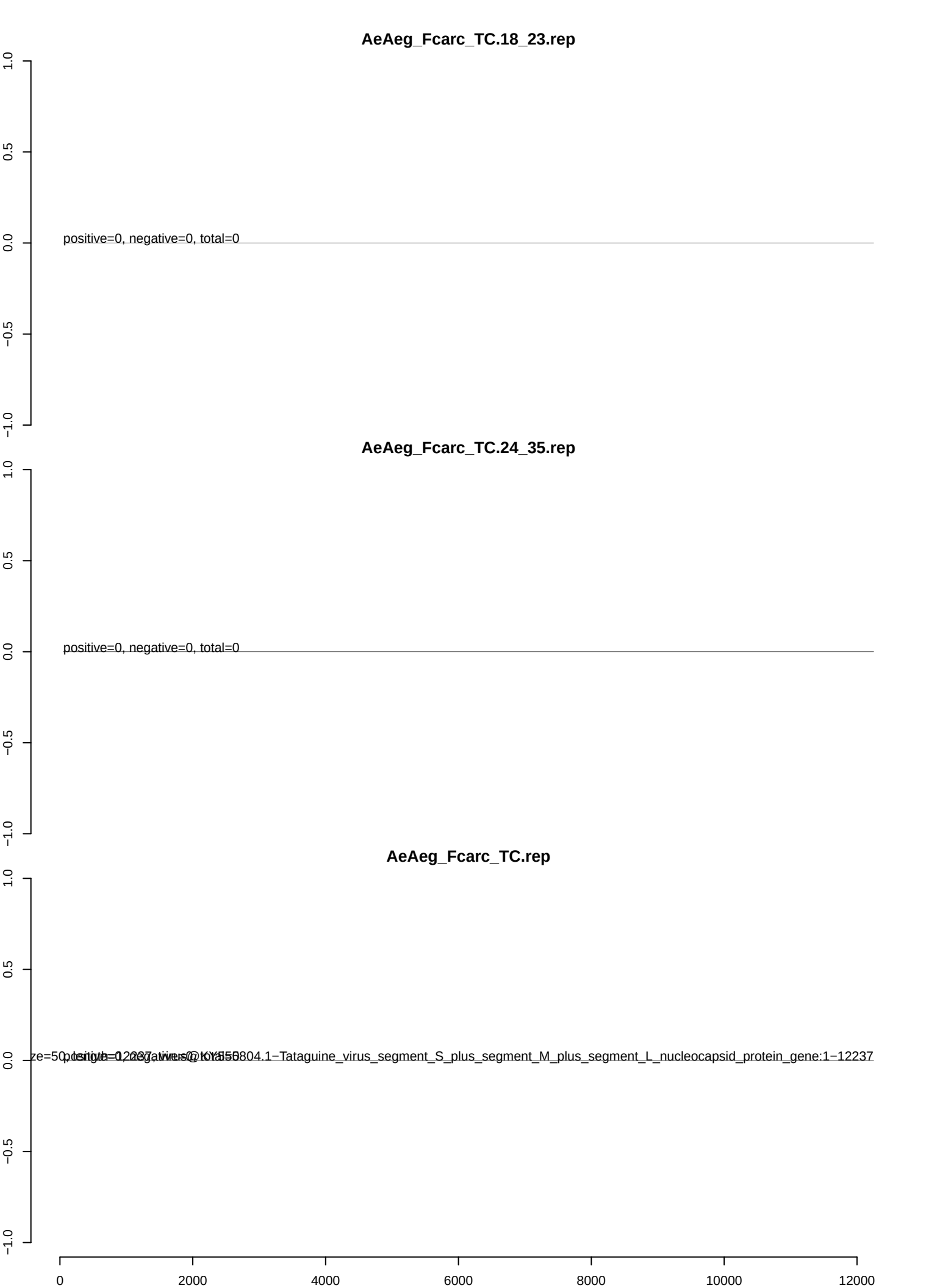
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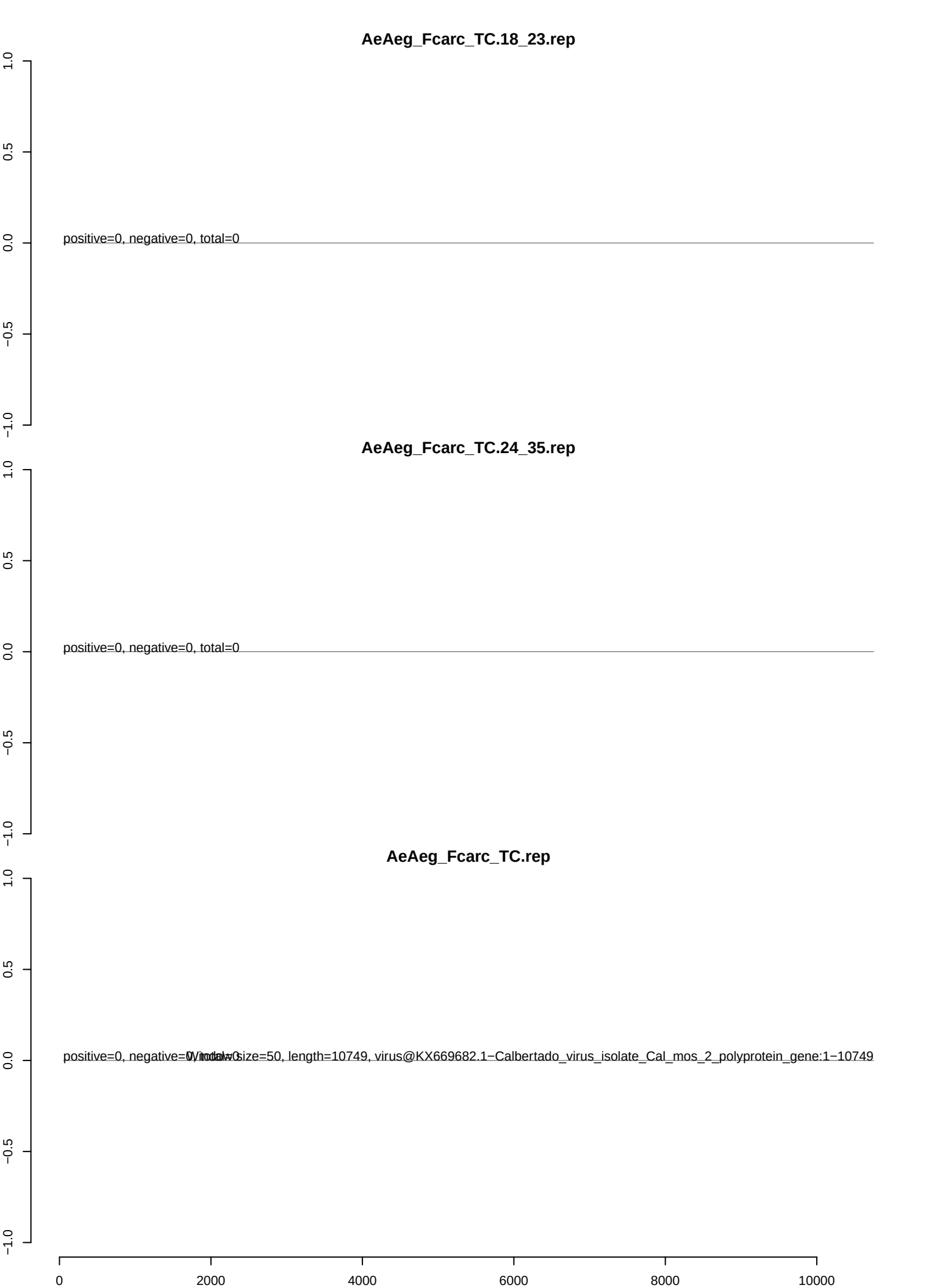
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window size=50, length=10749, virus@KX669682.1−Calbertado_virus_isolate_Cal_mos_2_polyprotein_gene:1−10749
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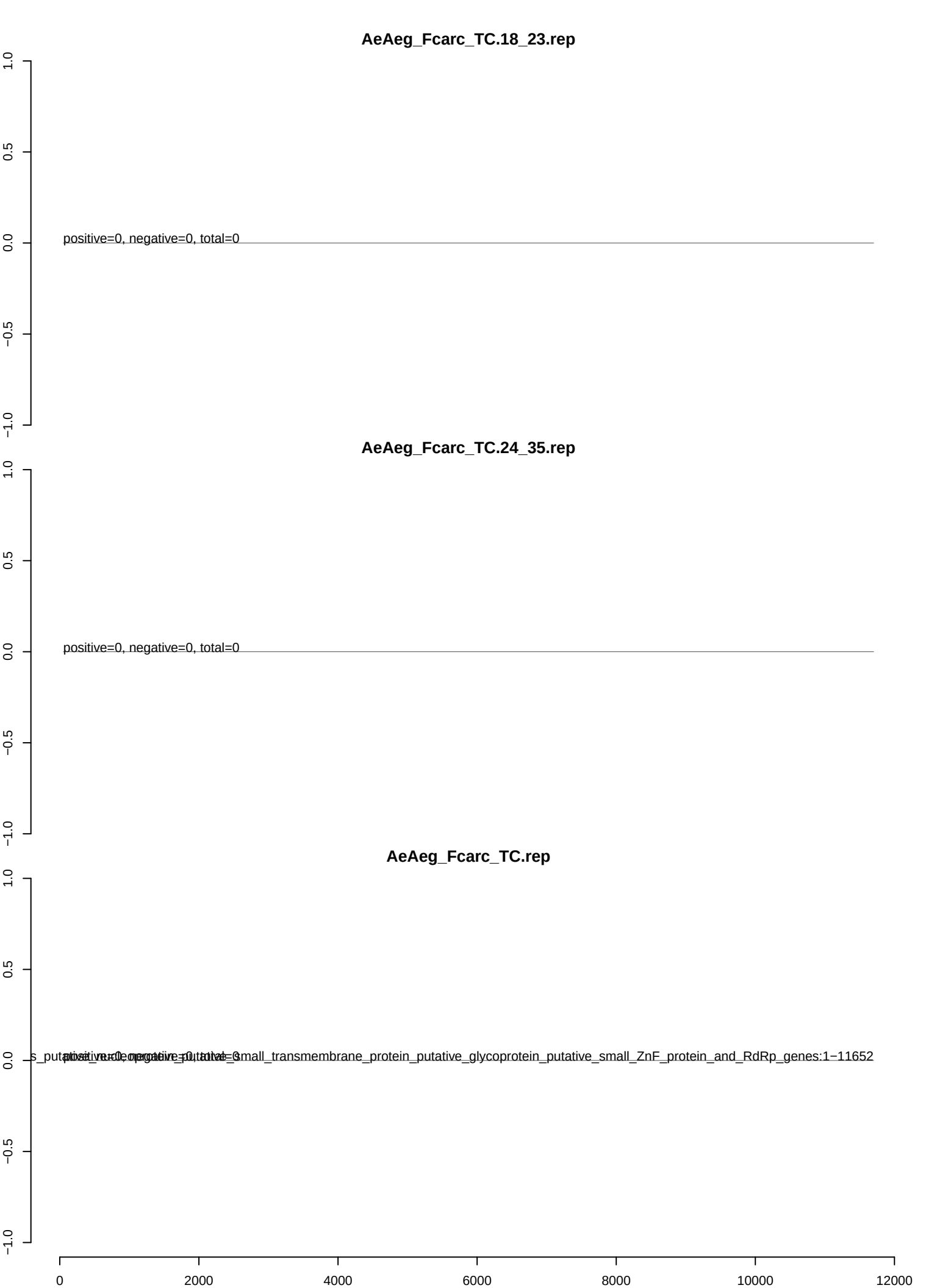
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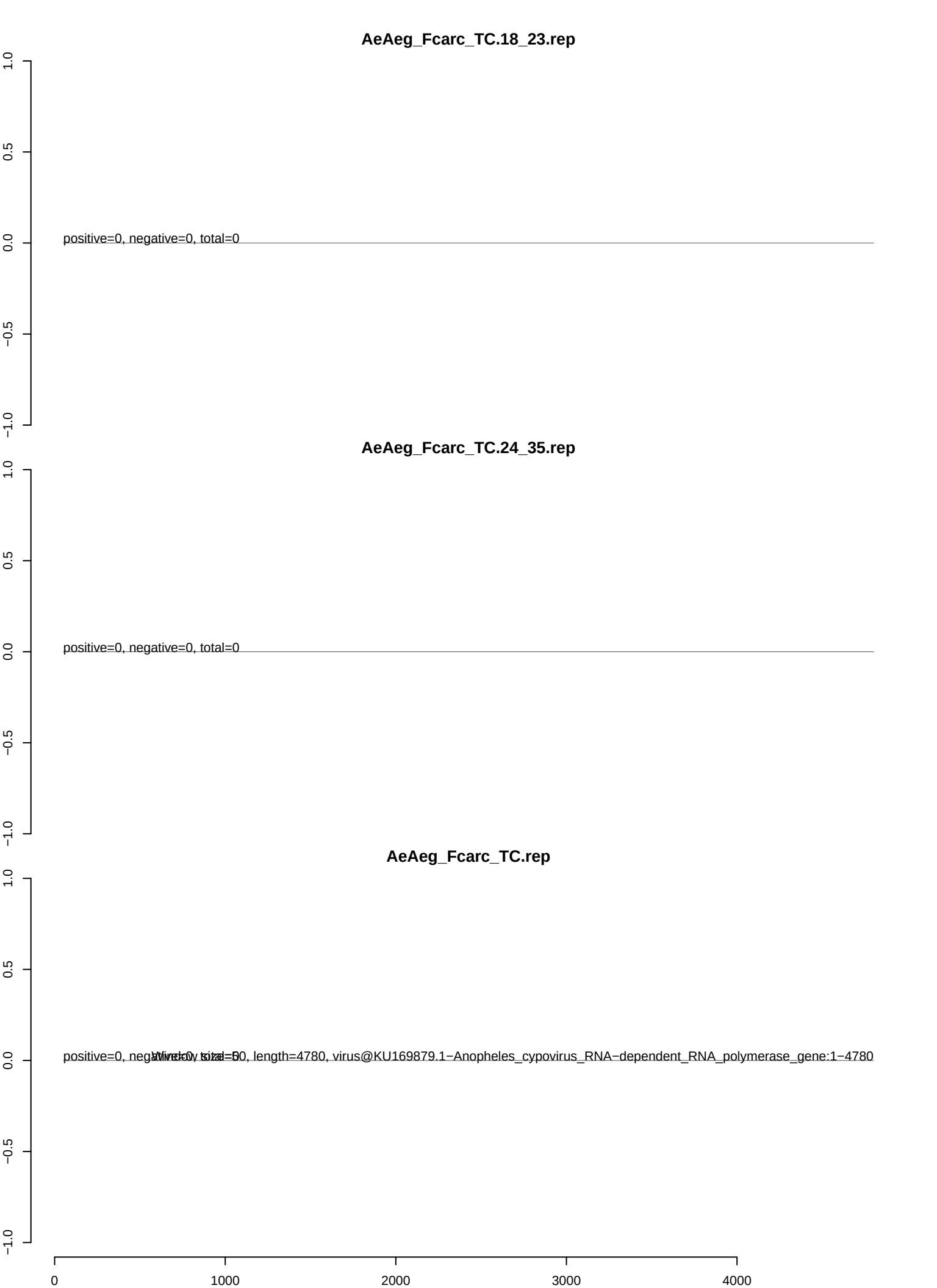
12000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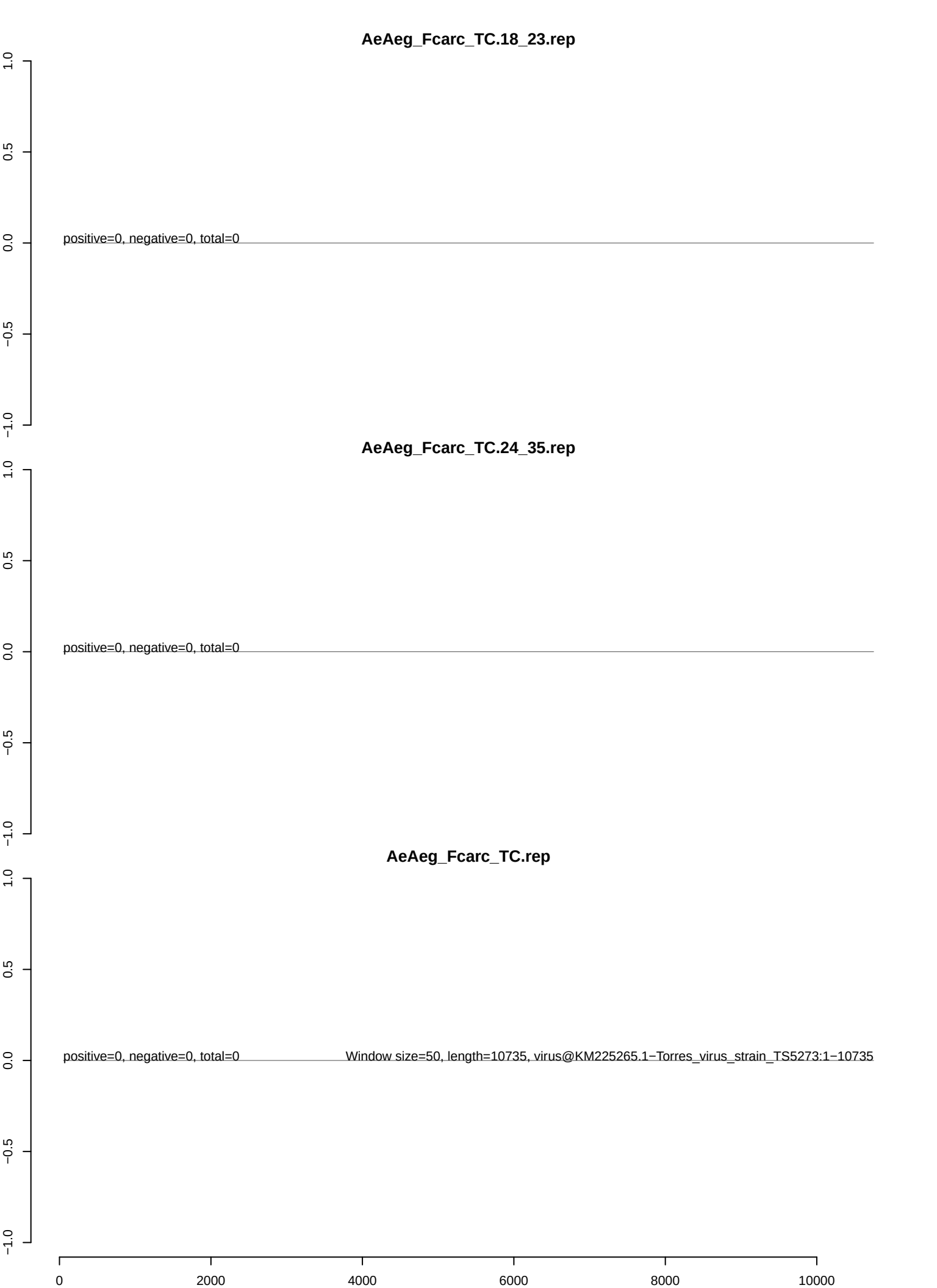
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Window size=50, length=10735, virus@KM225265.1−Torres_virus_strain_TS5273:1−10735
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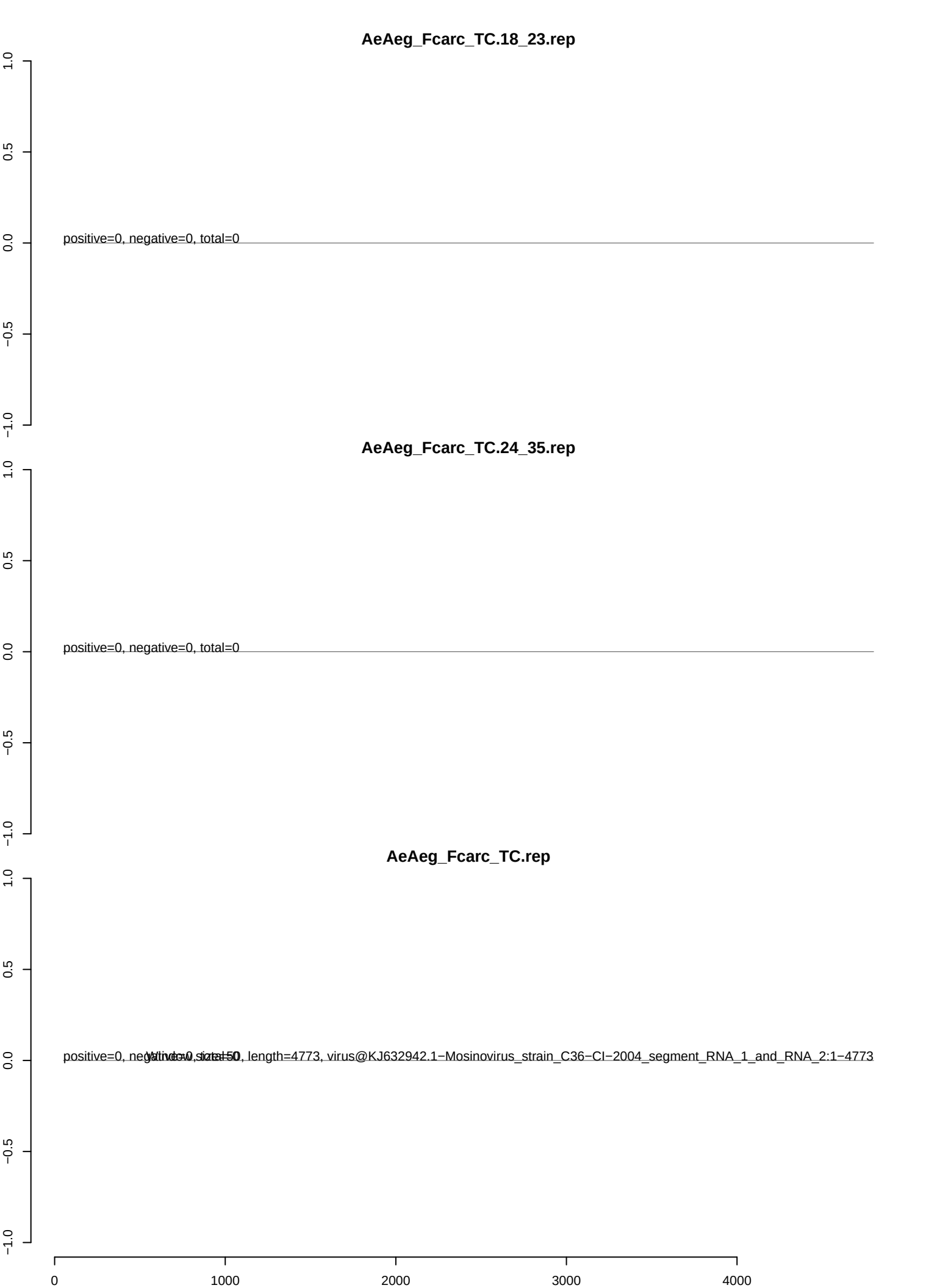
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Window size=50, length=4773, virus@KJ632942.1−Mosinovirus_strain_C36−CI−2004_segment_RNA_1_and_RNA_2:1−4773
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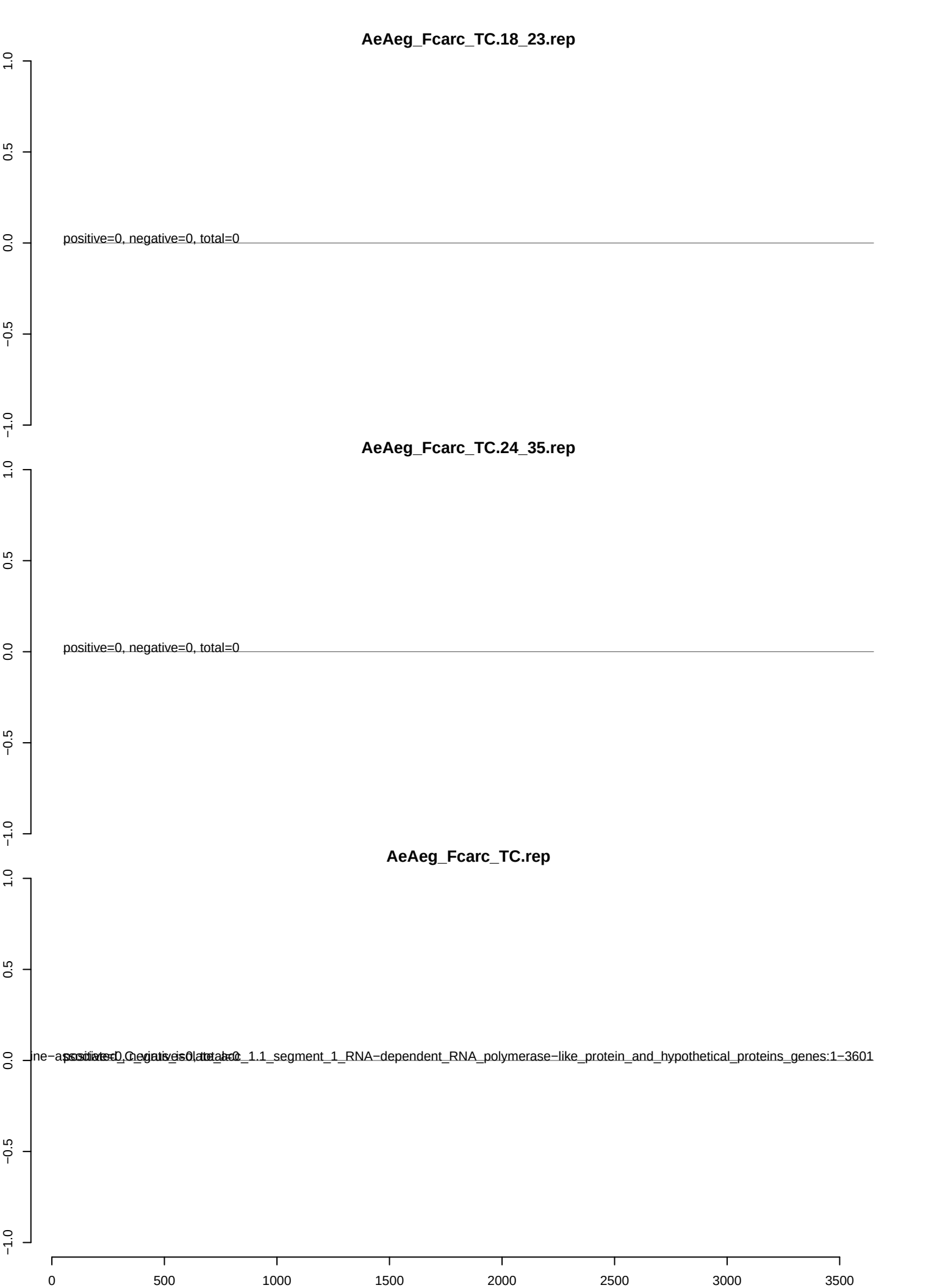
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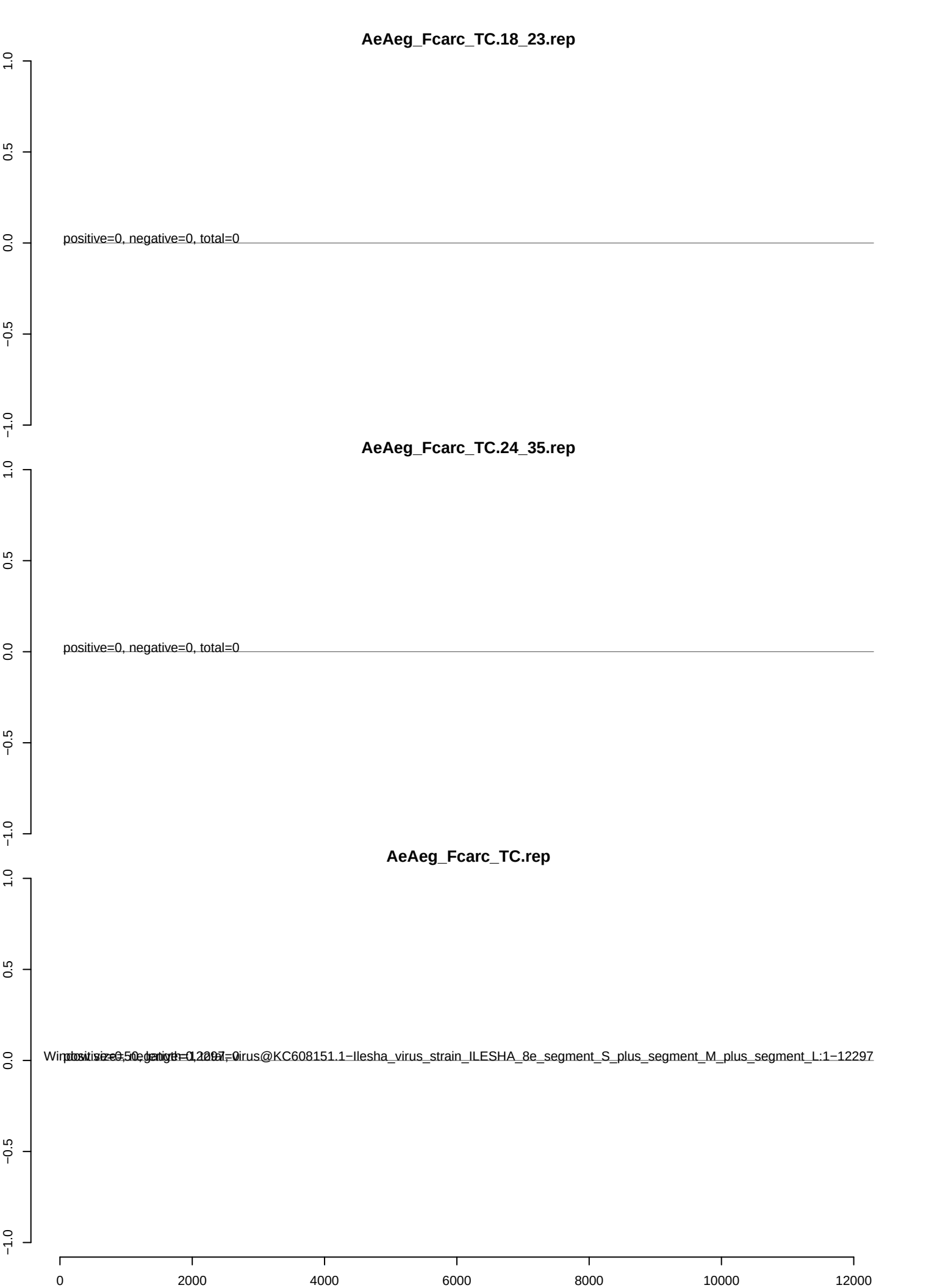
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Window size=50, length=12297, virus@KC608151.1−Ilesha_virus_strain_ILESHA_8e_segment_S_plus_segment_M_plus_segment_L:1−12297
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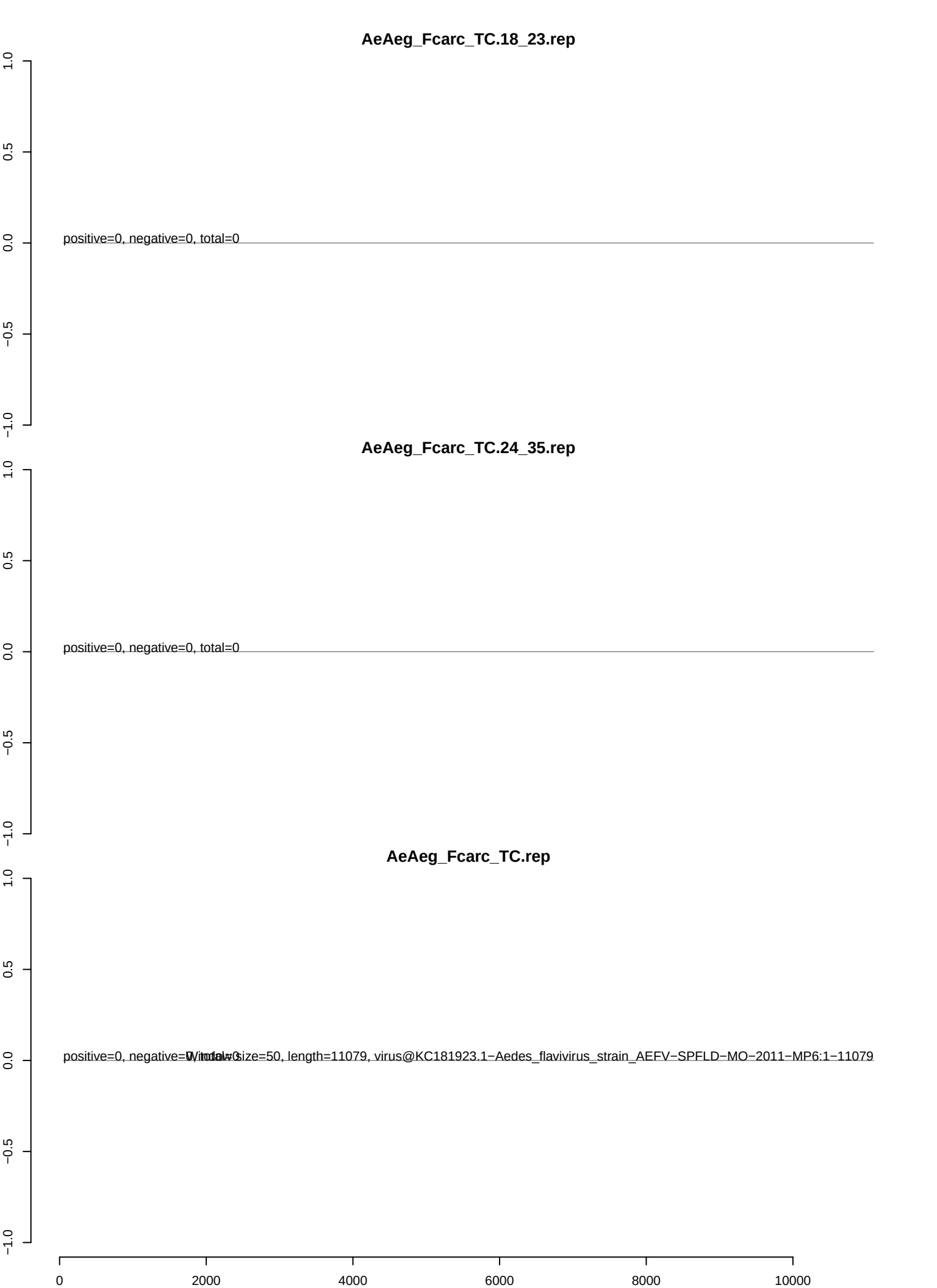
12000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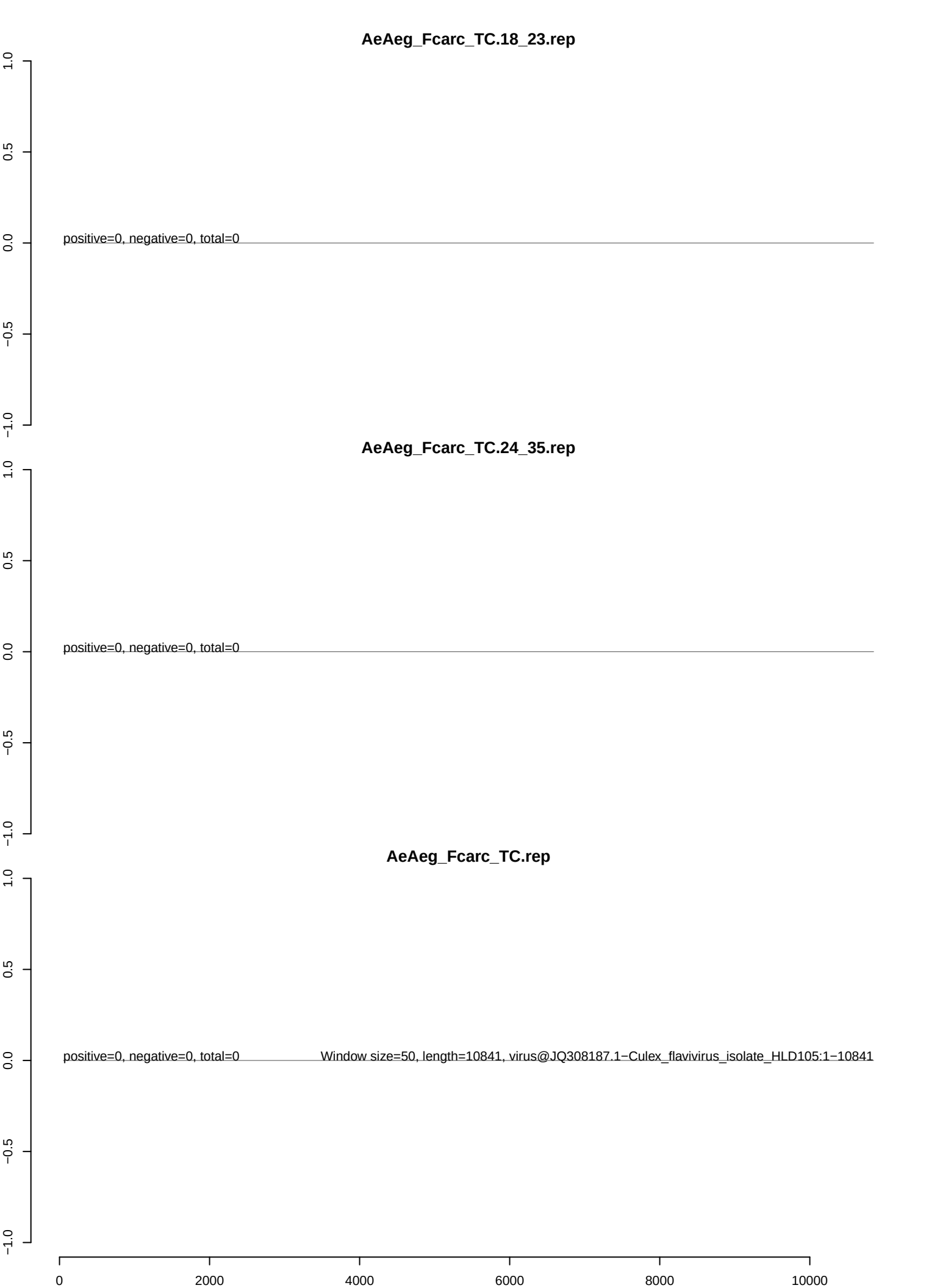
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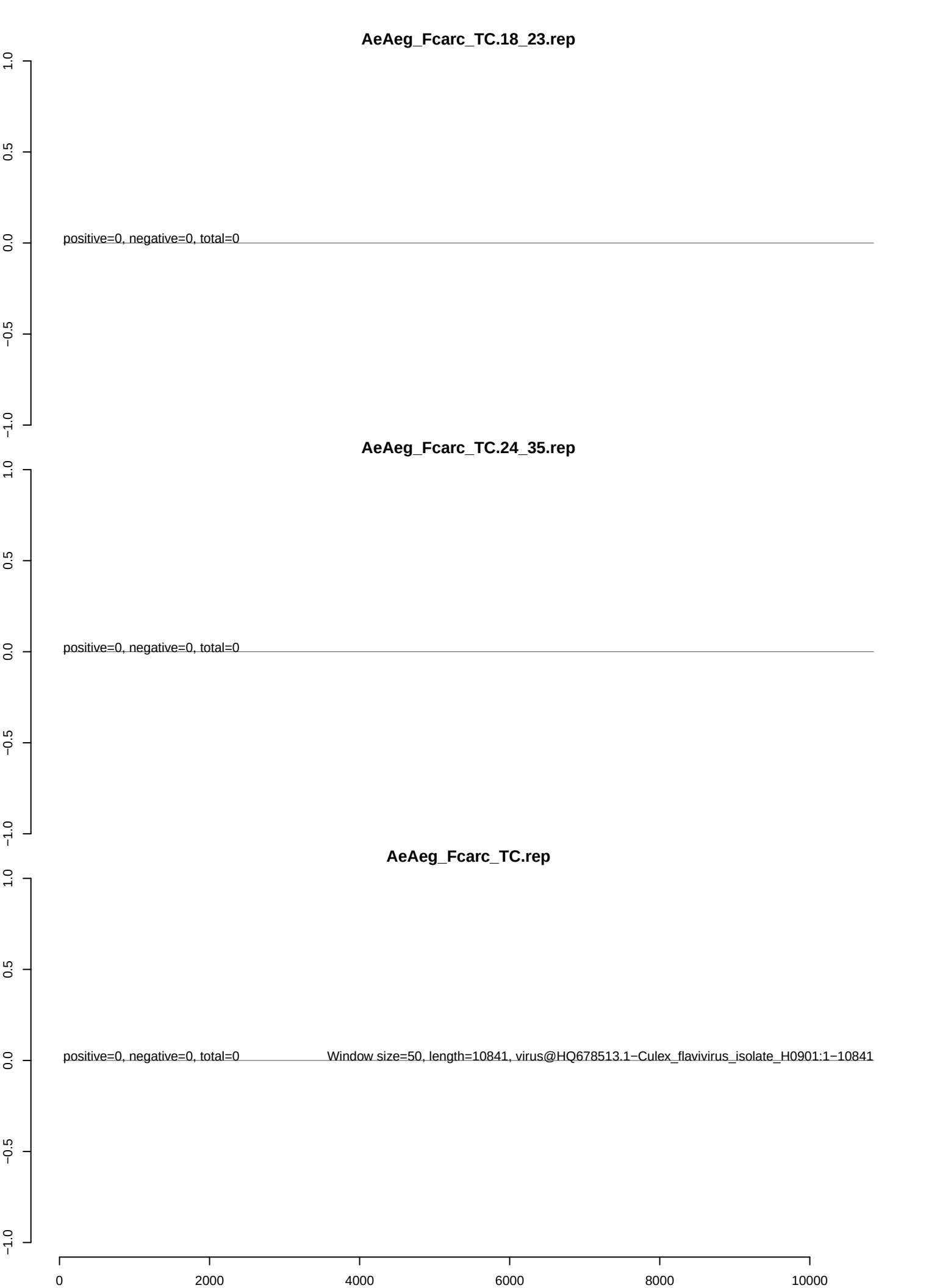
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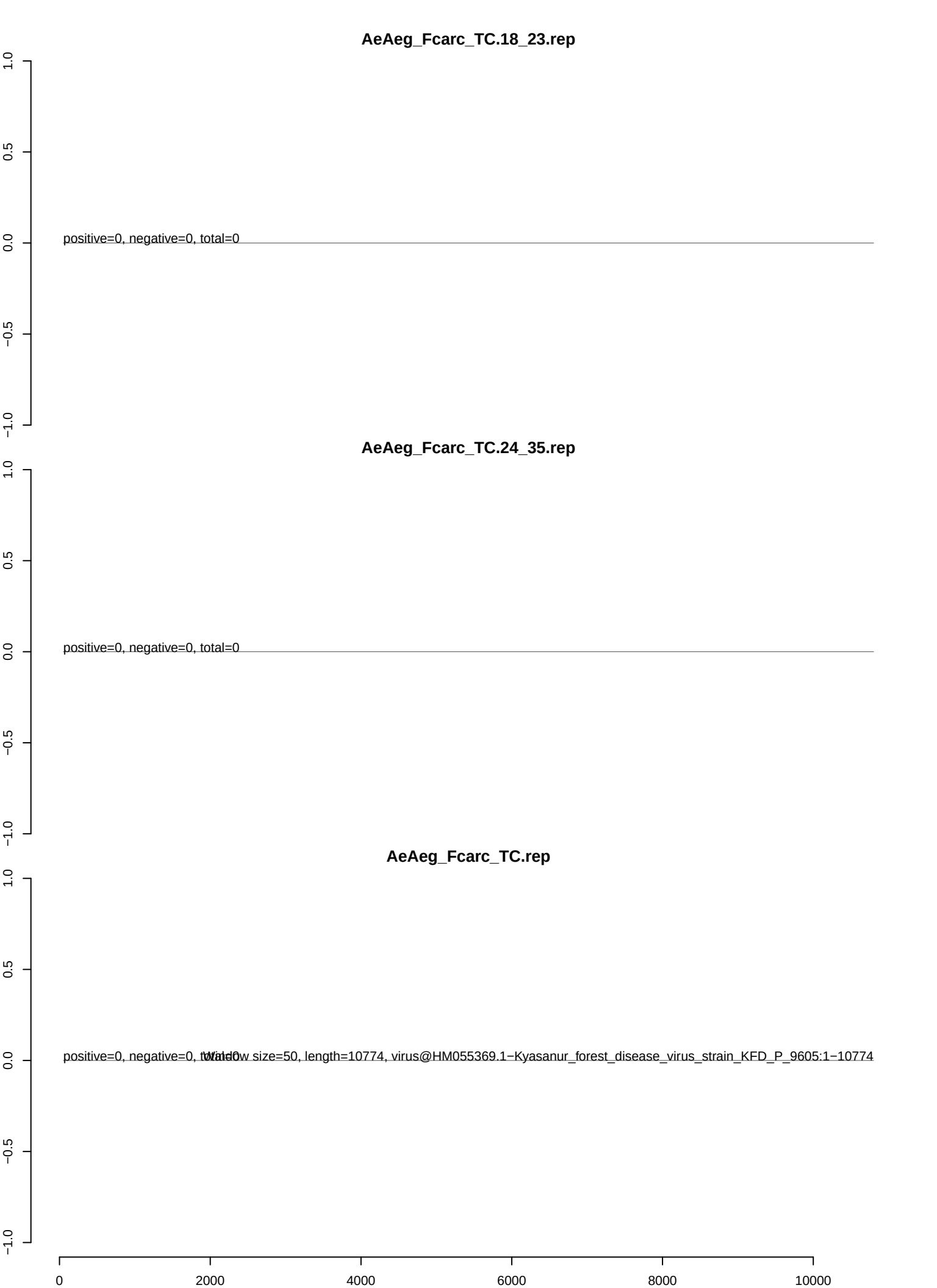
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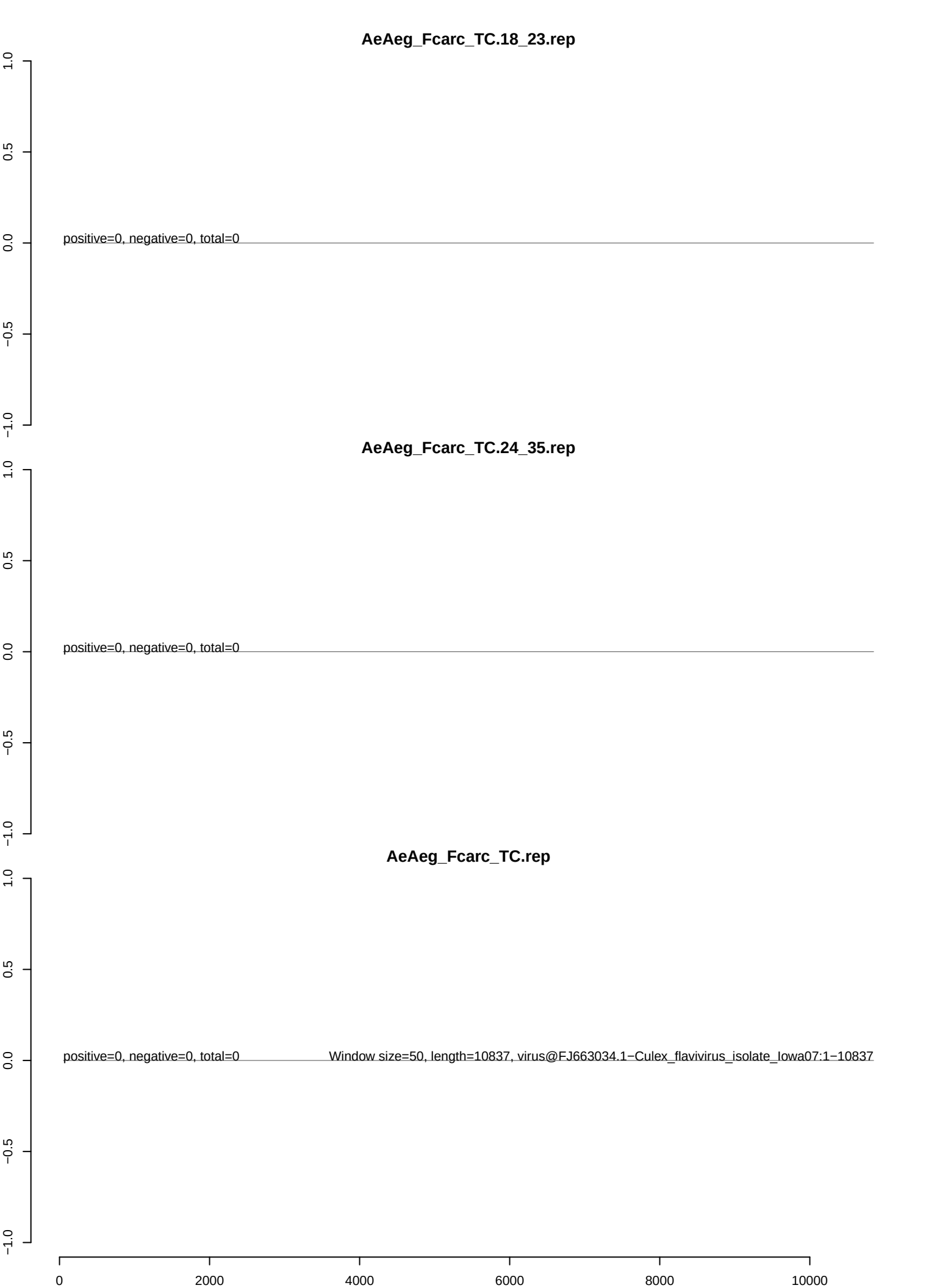
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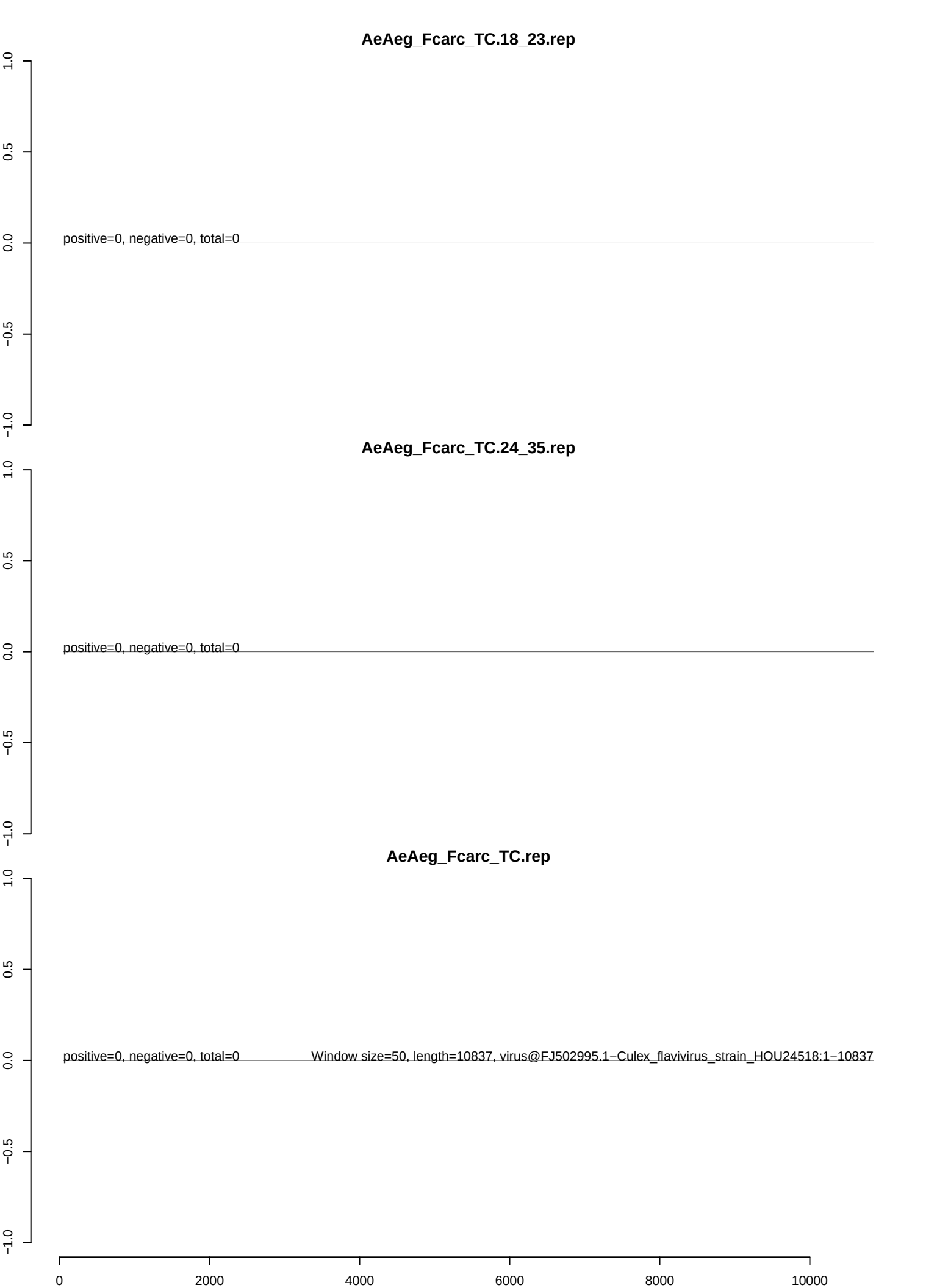
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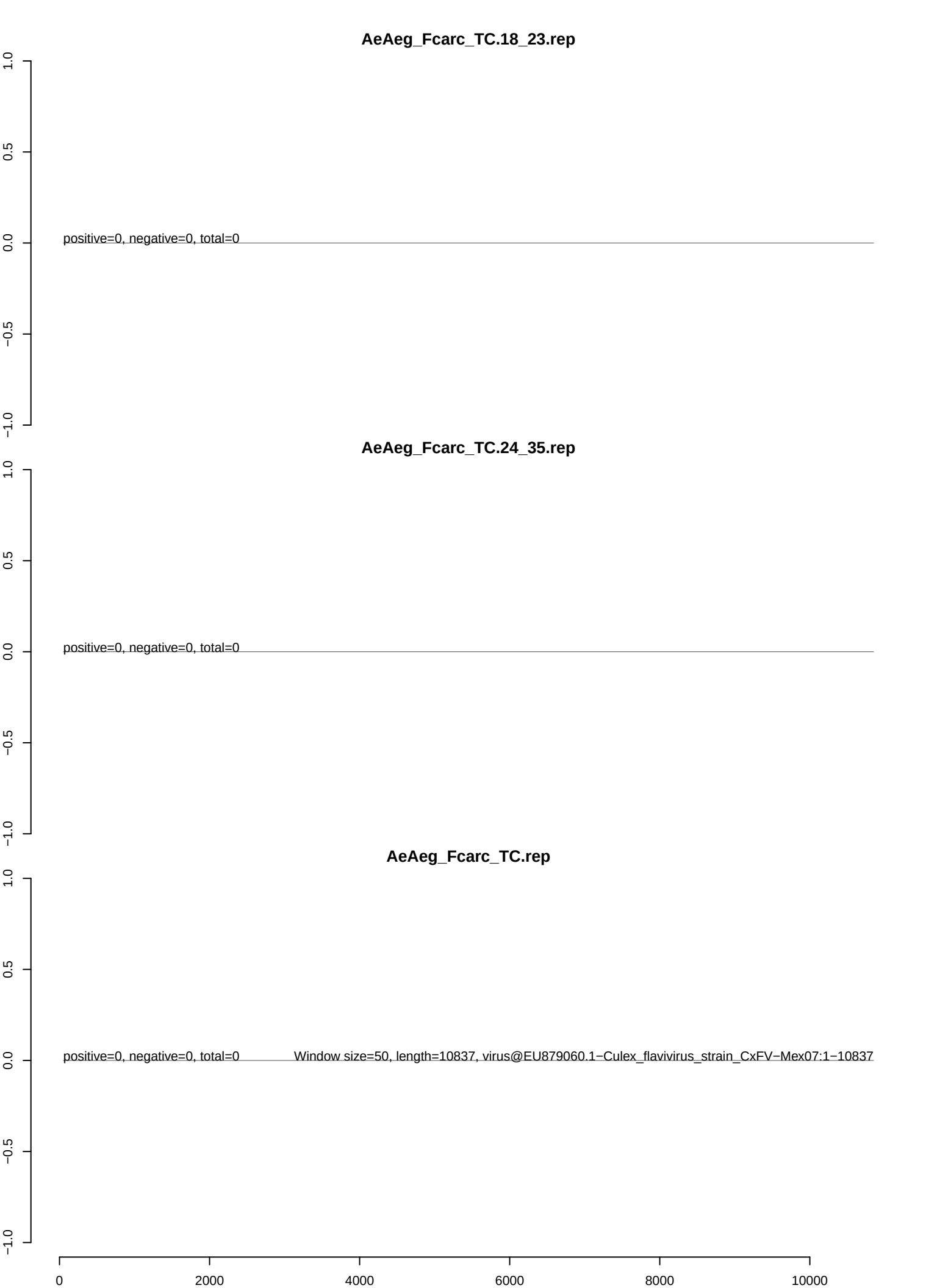
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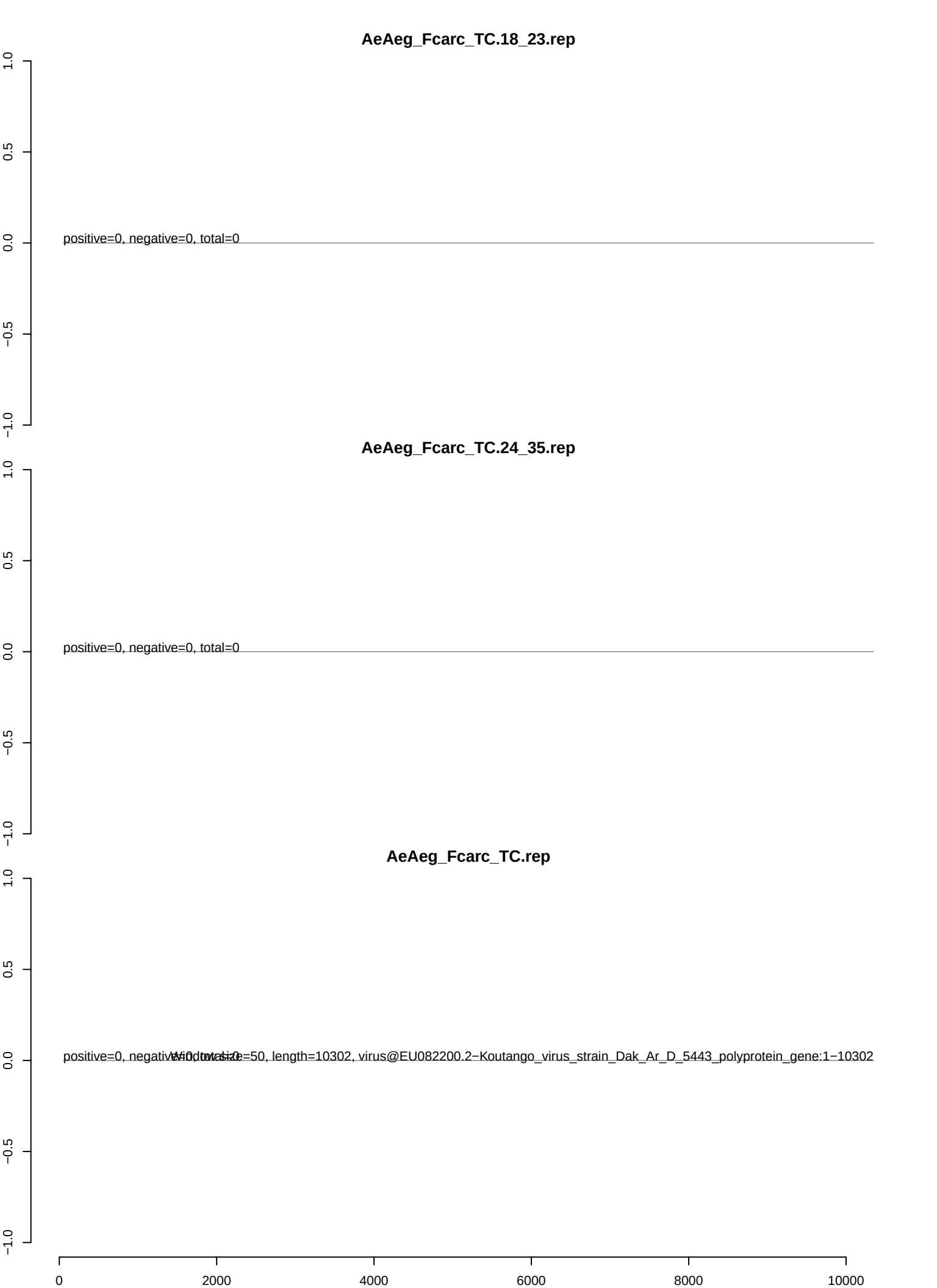
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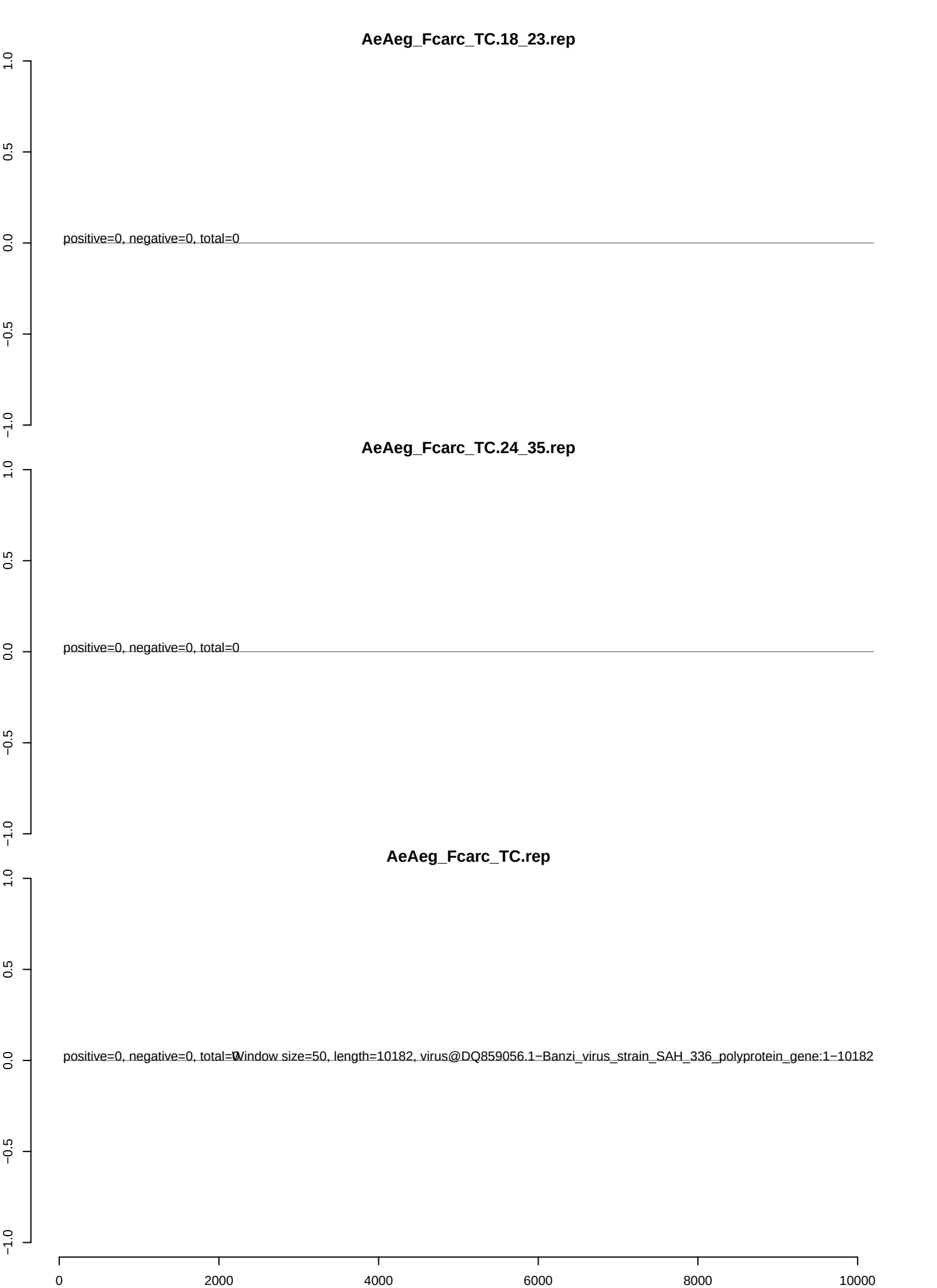
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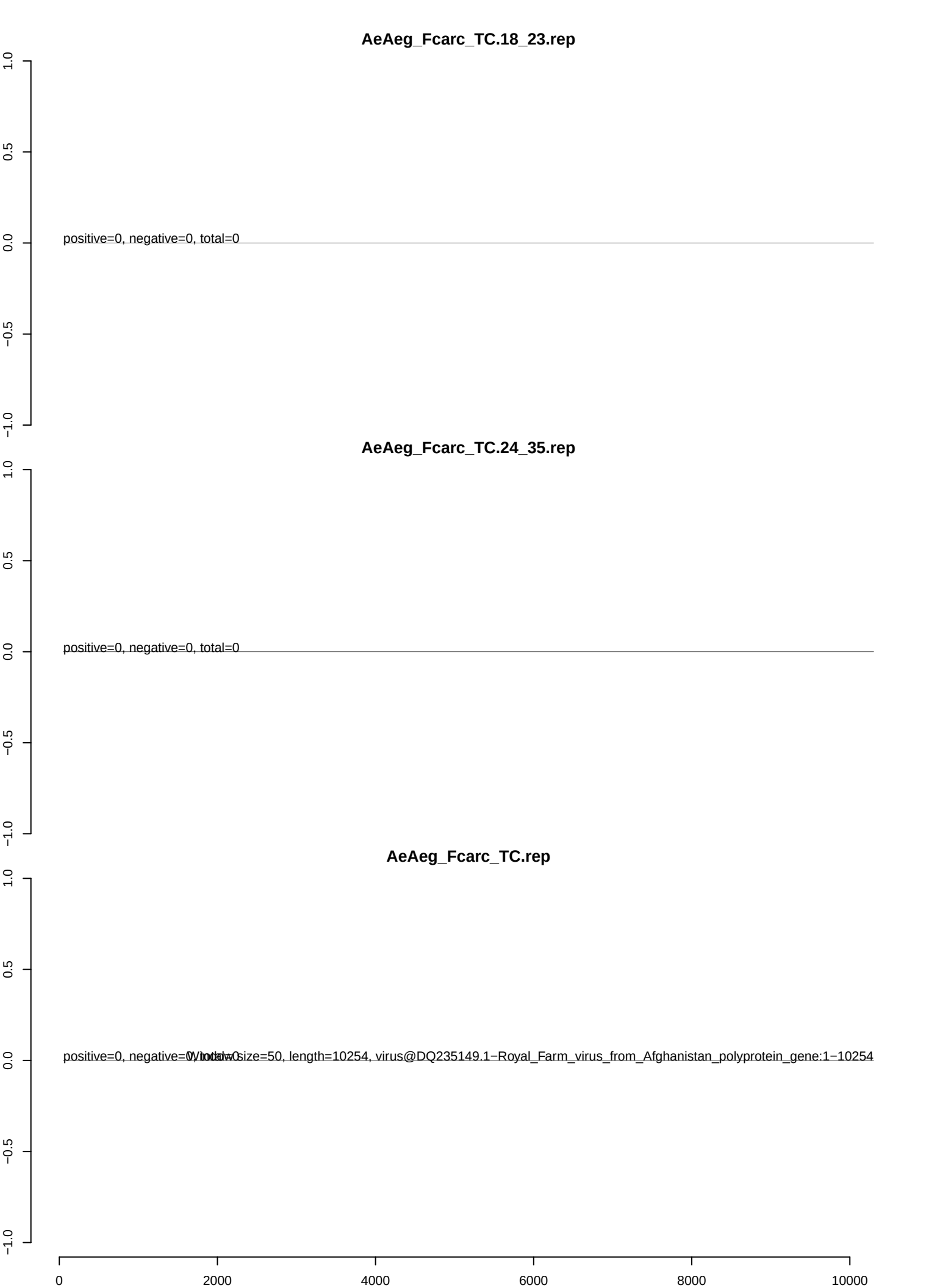
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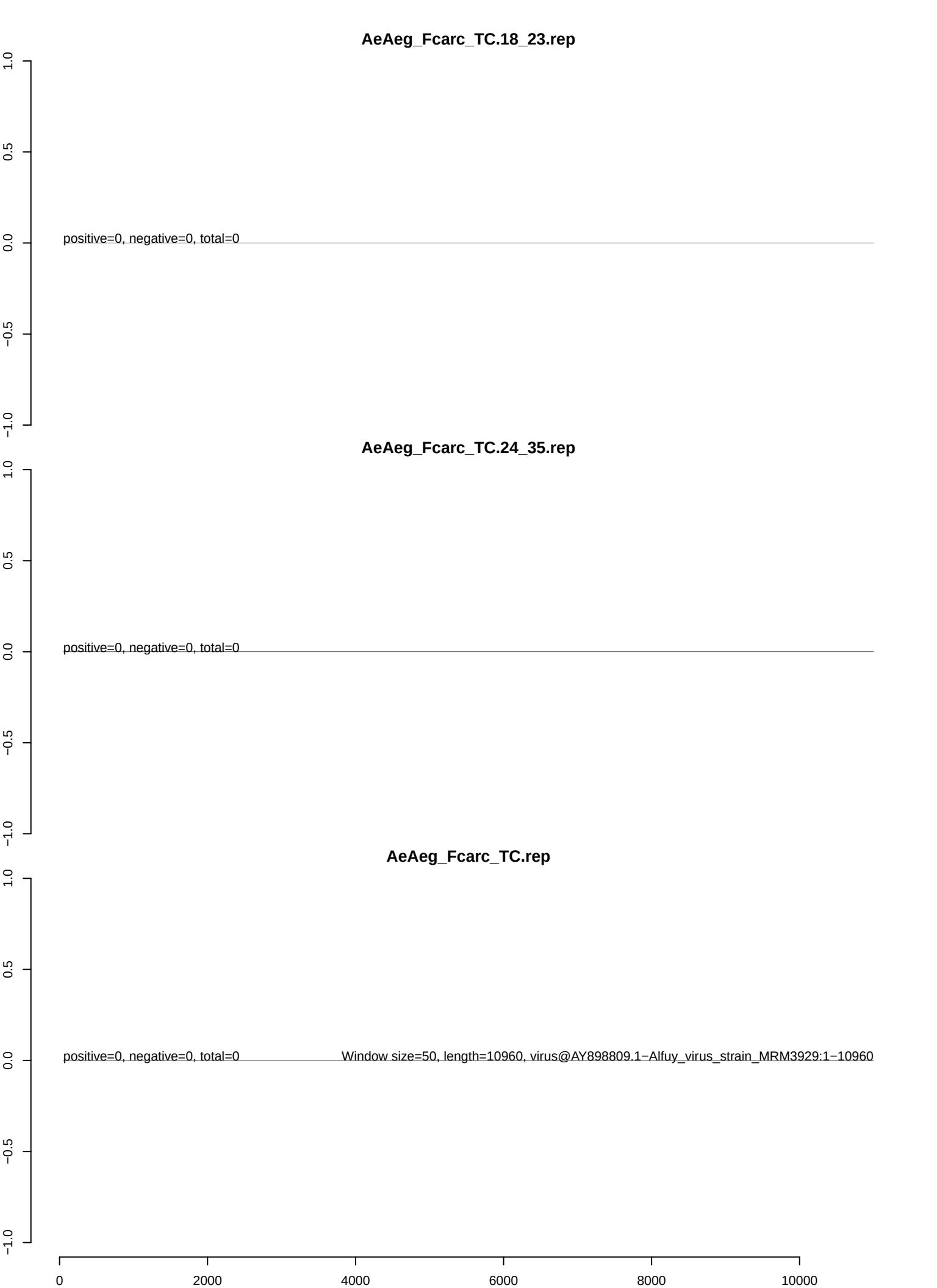
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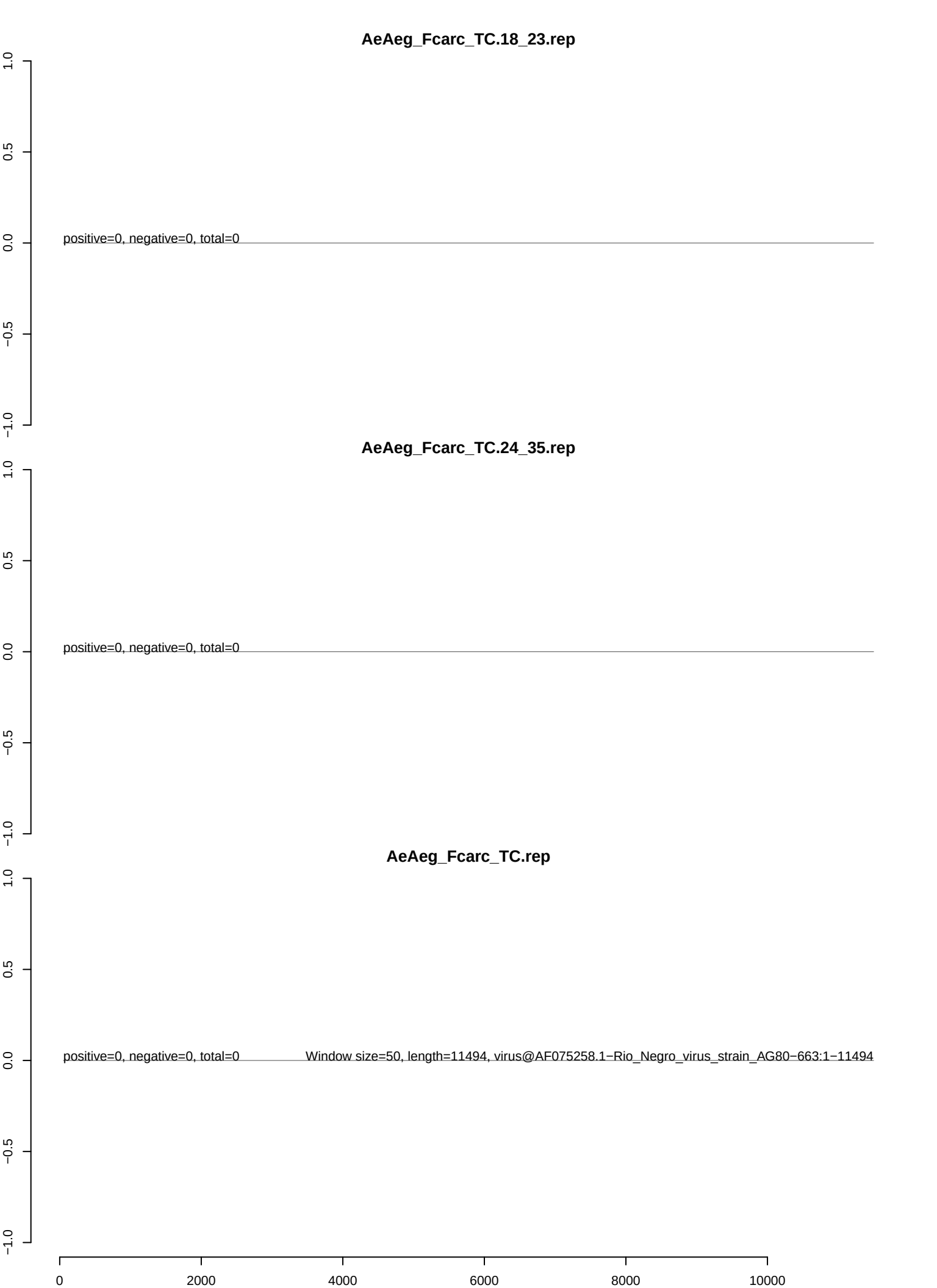
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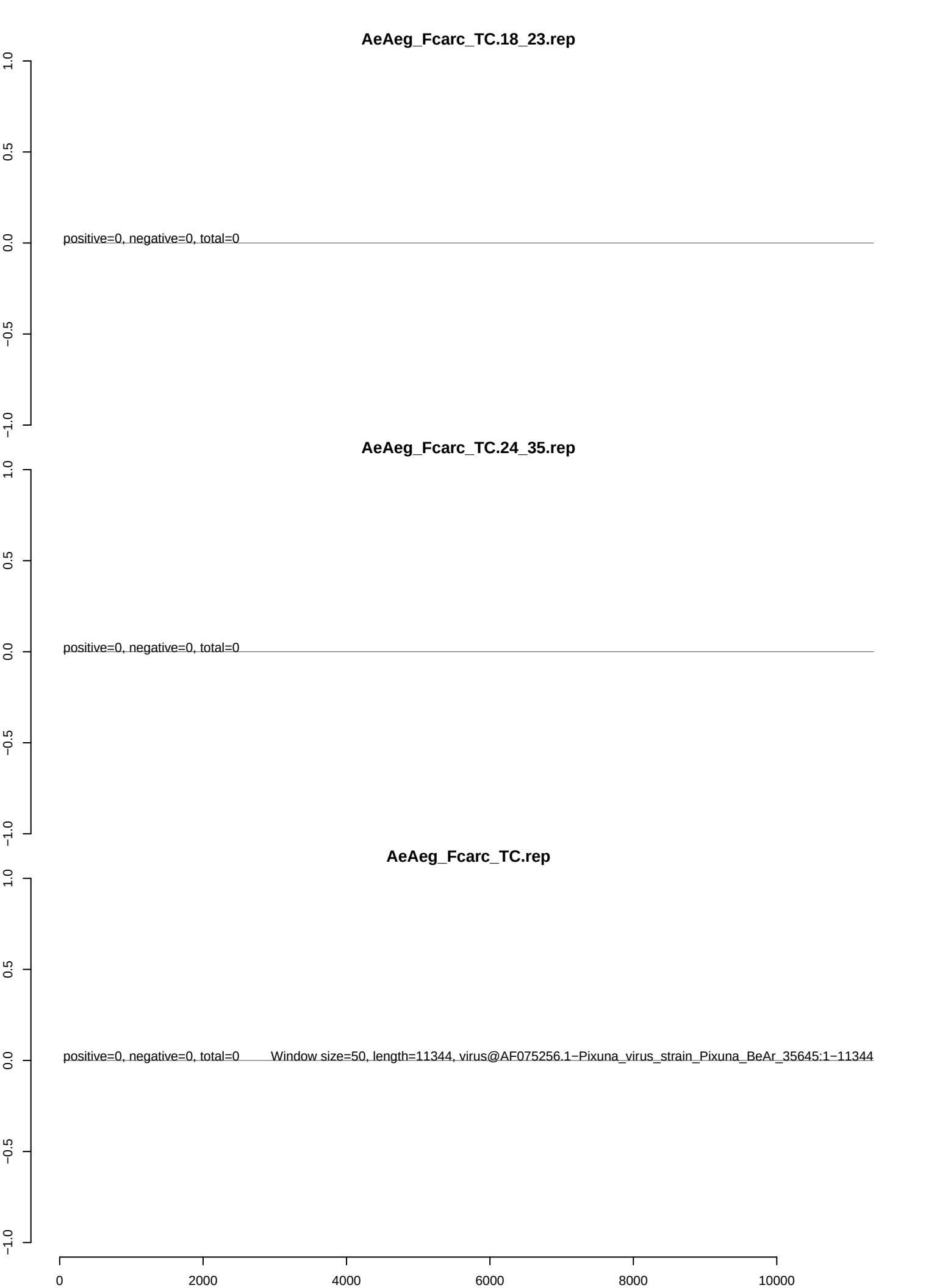
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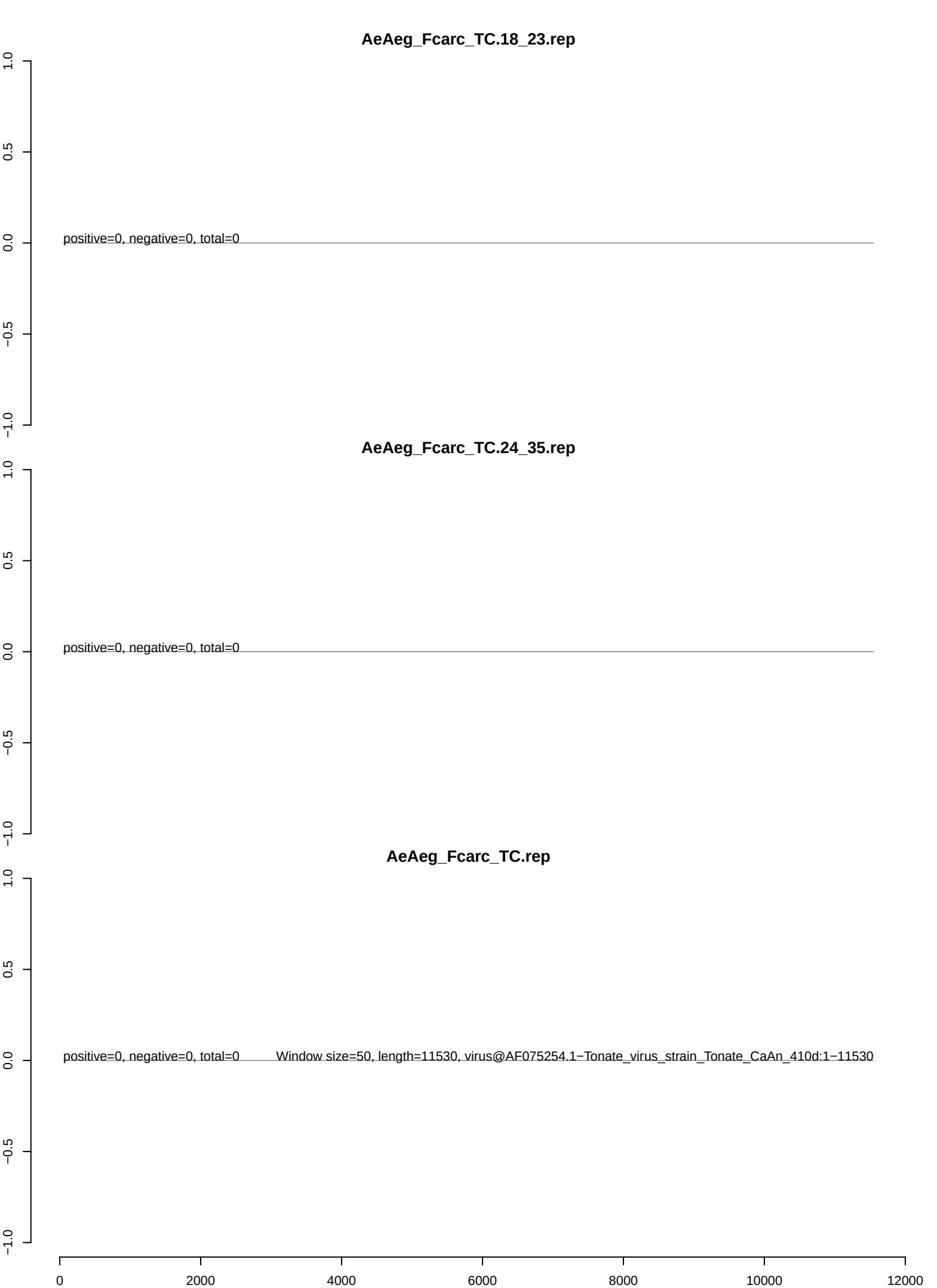
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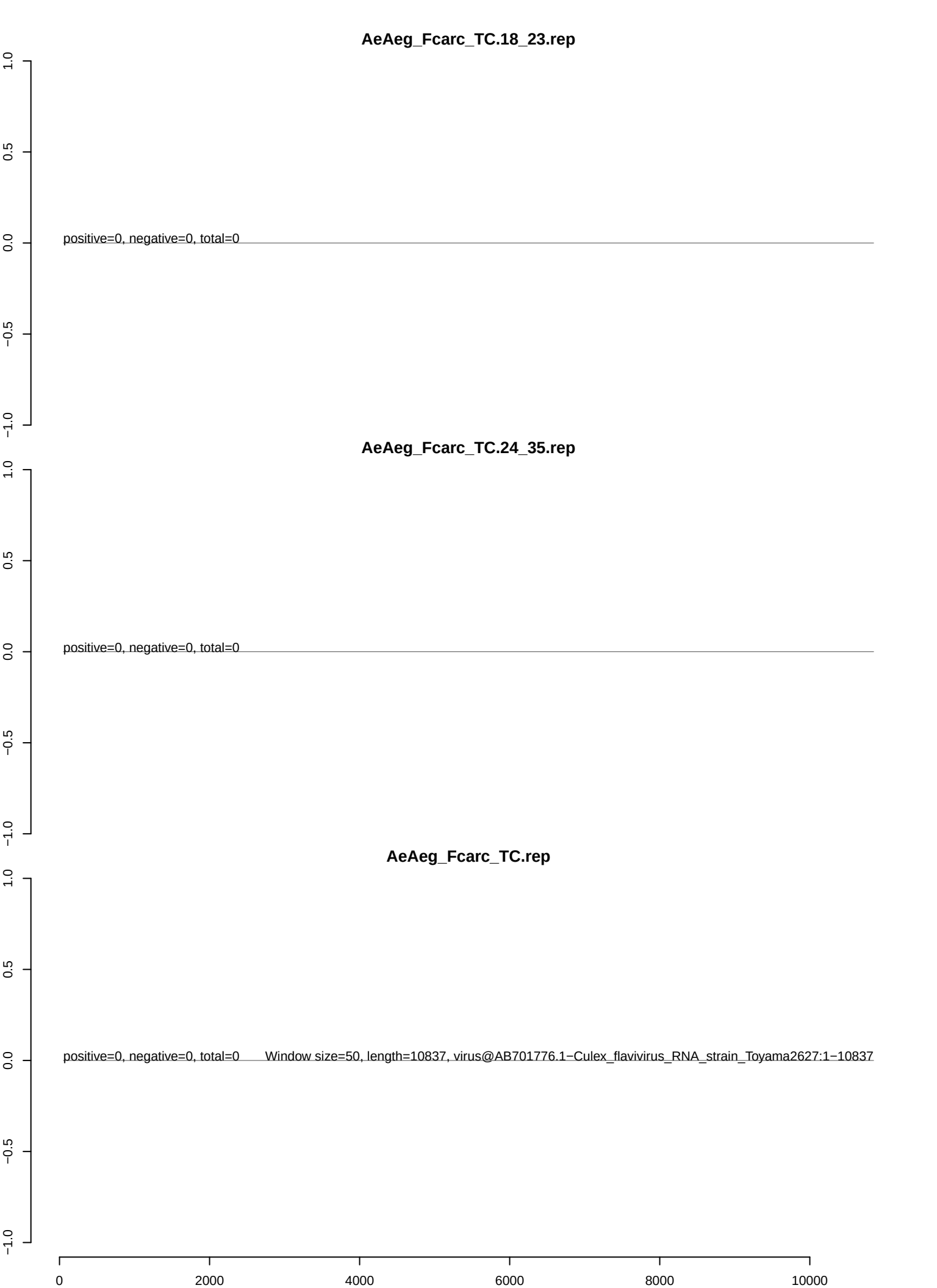
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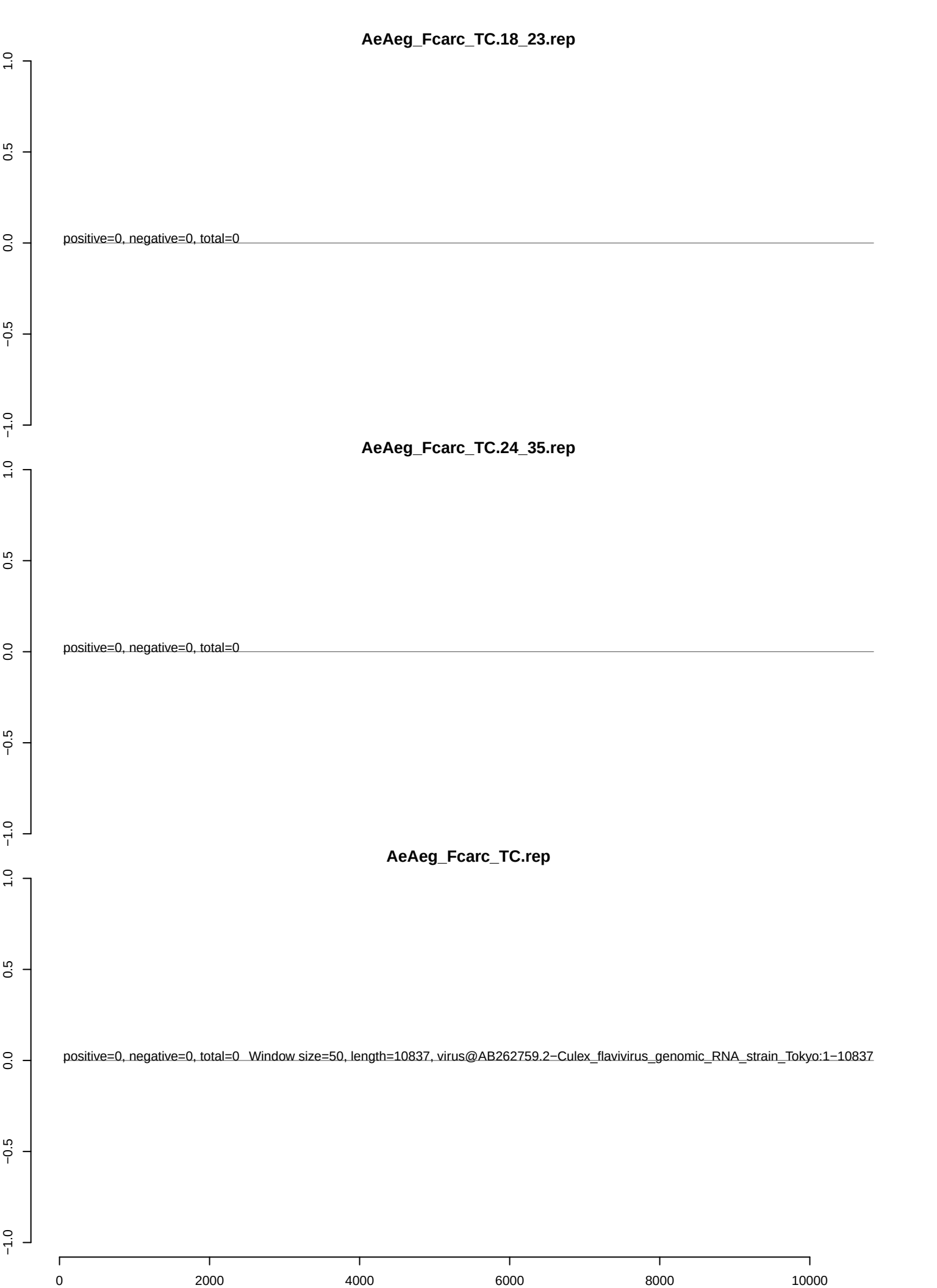
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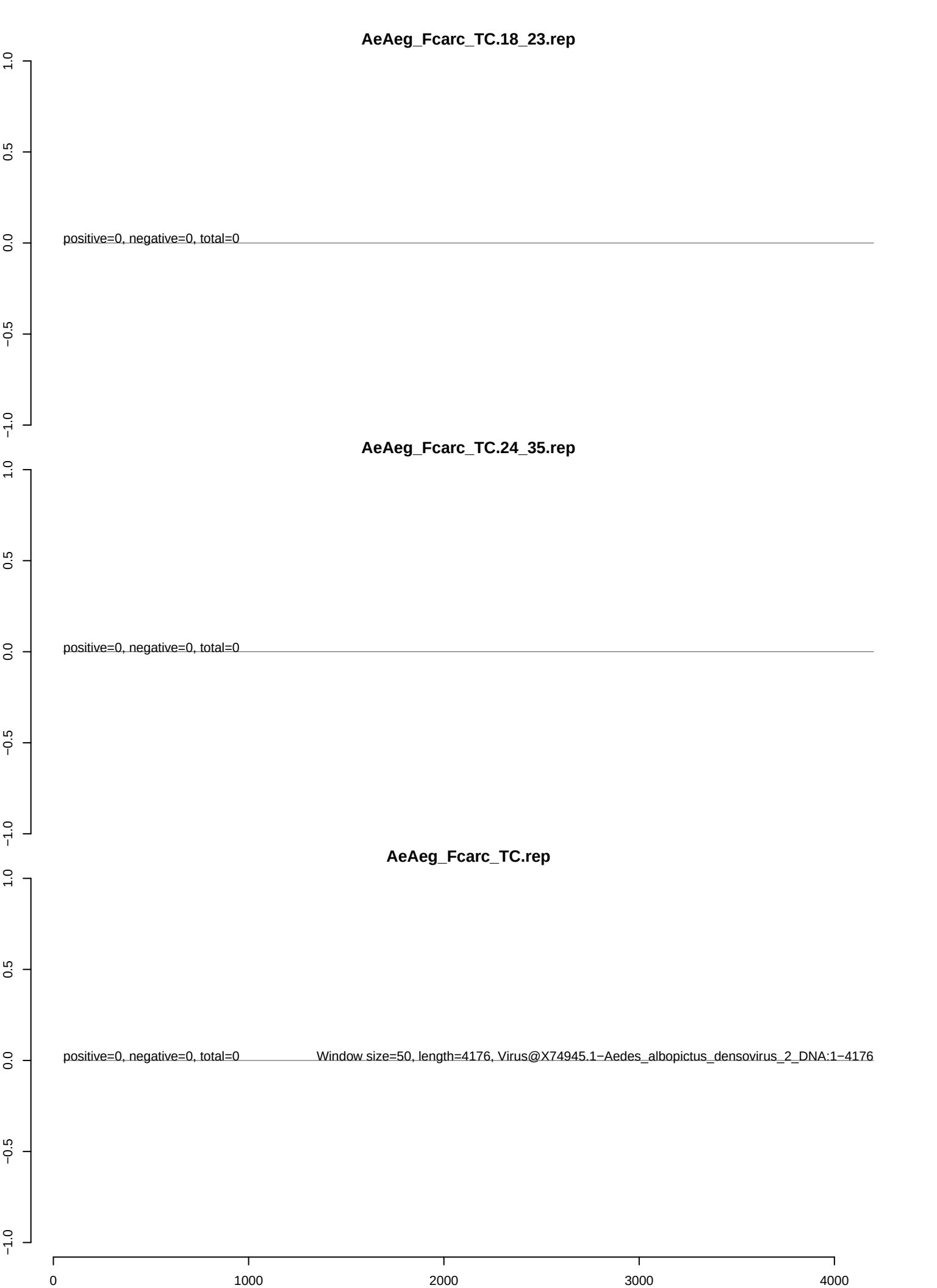
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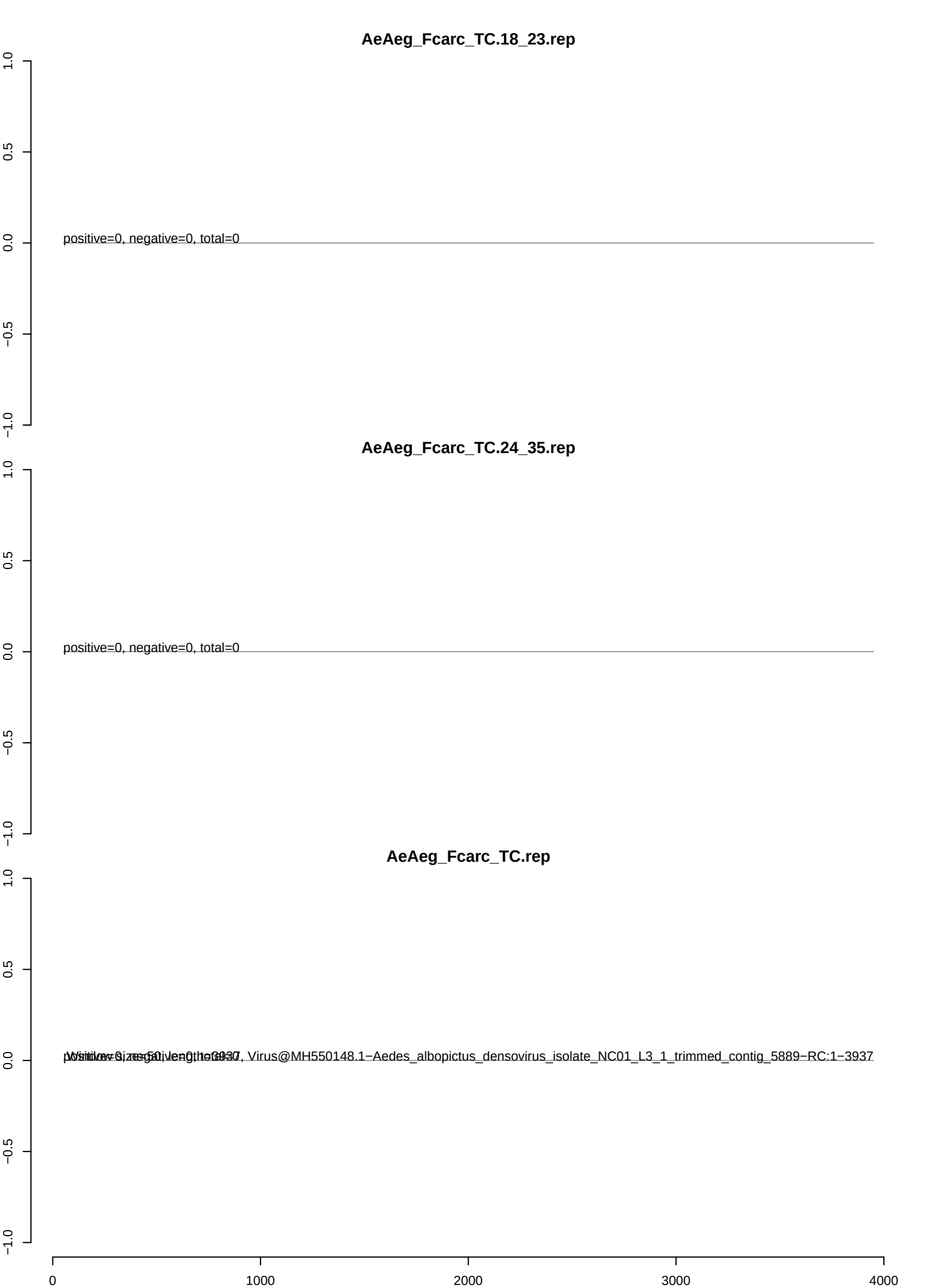
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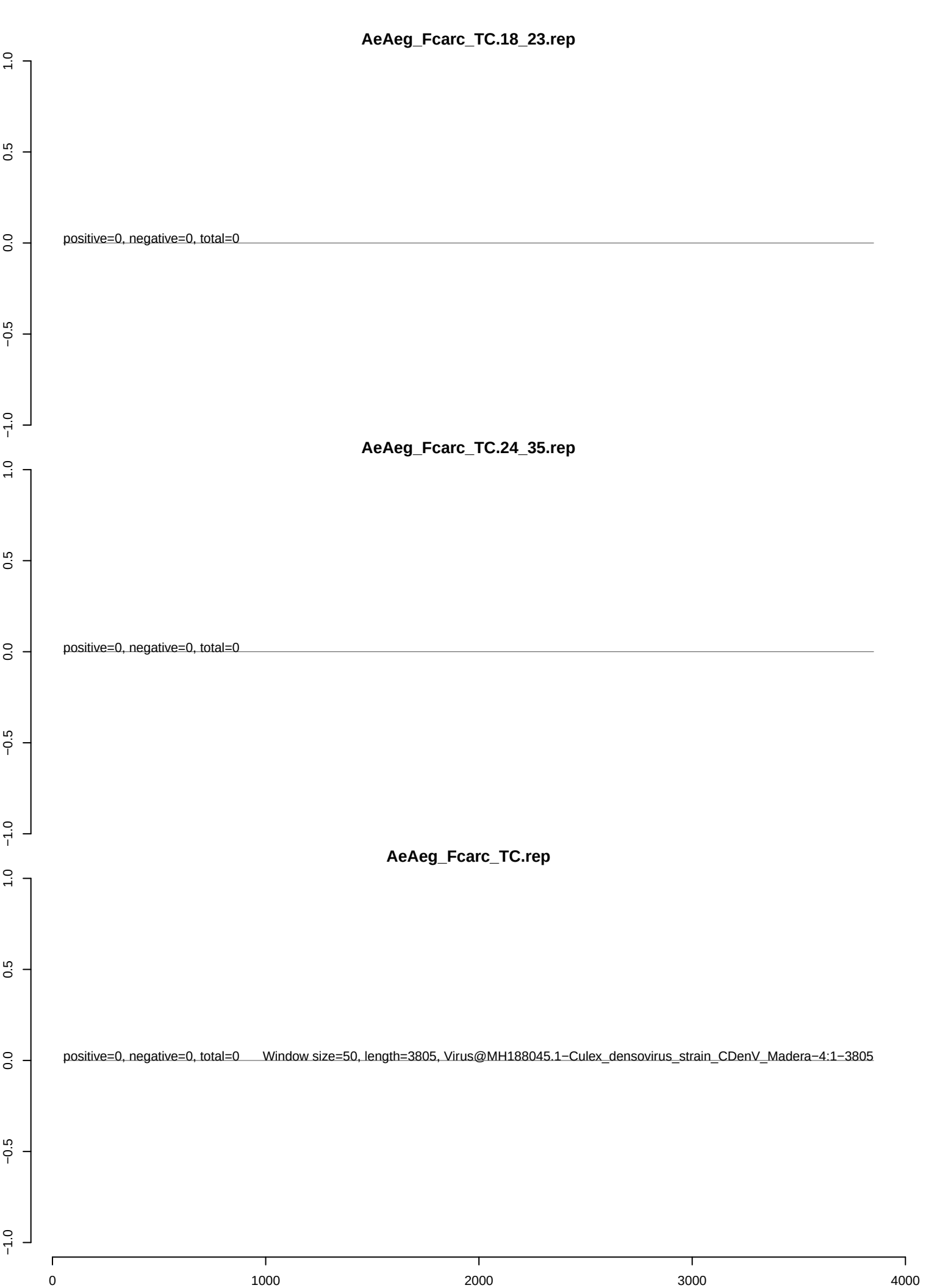
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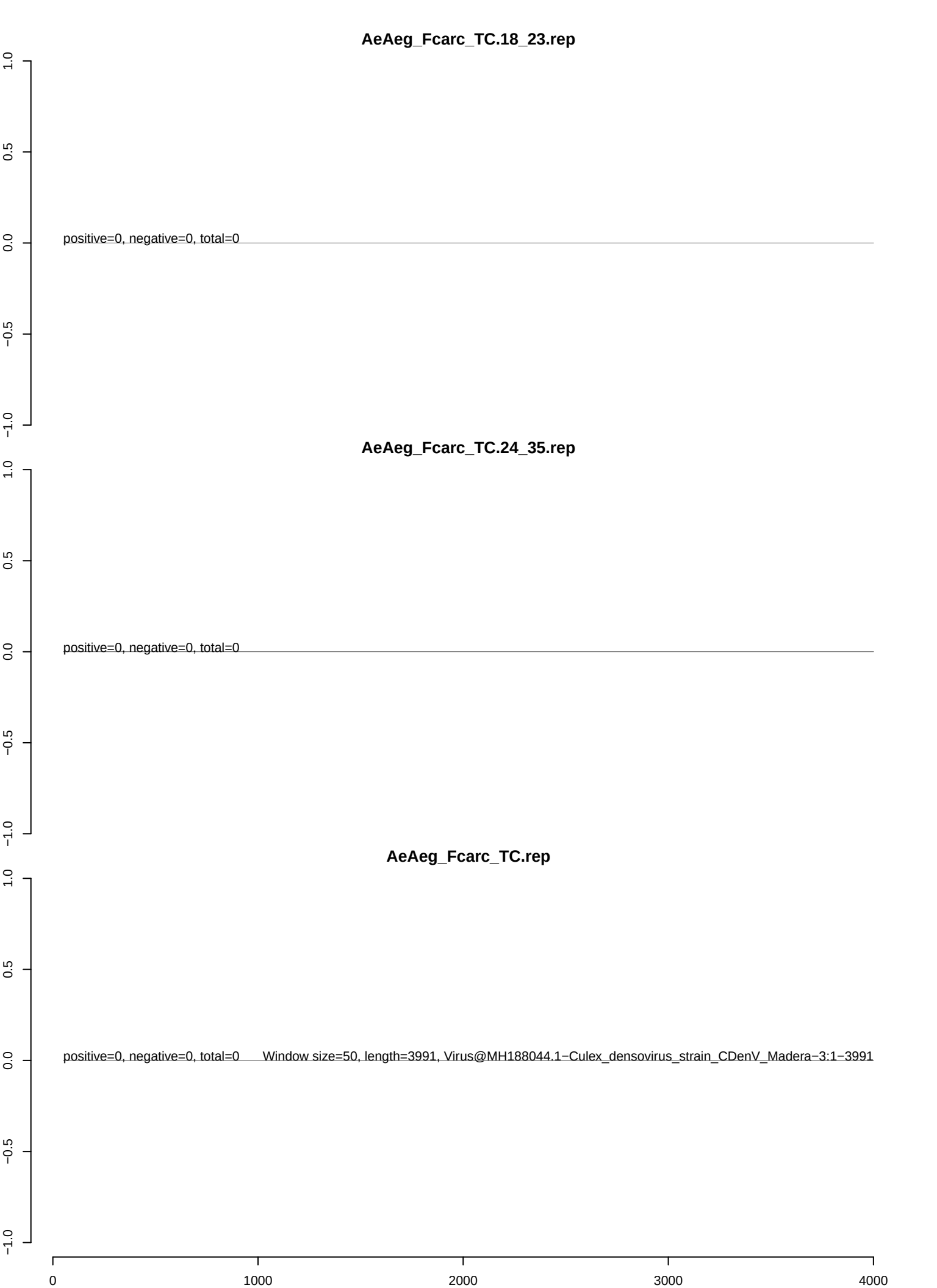
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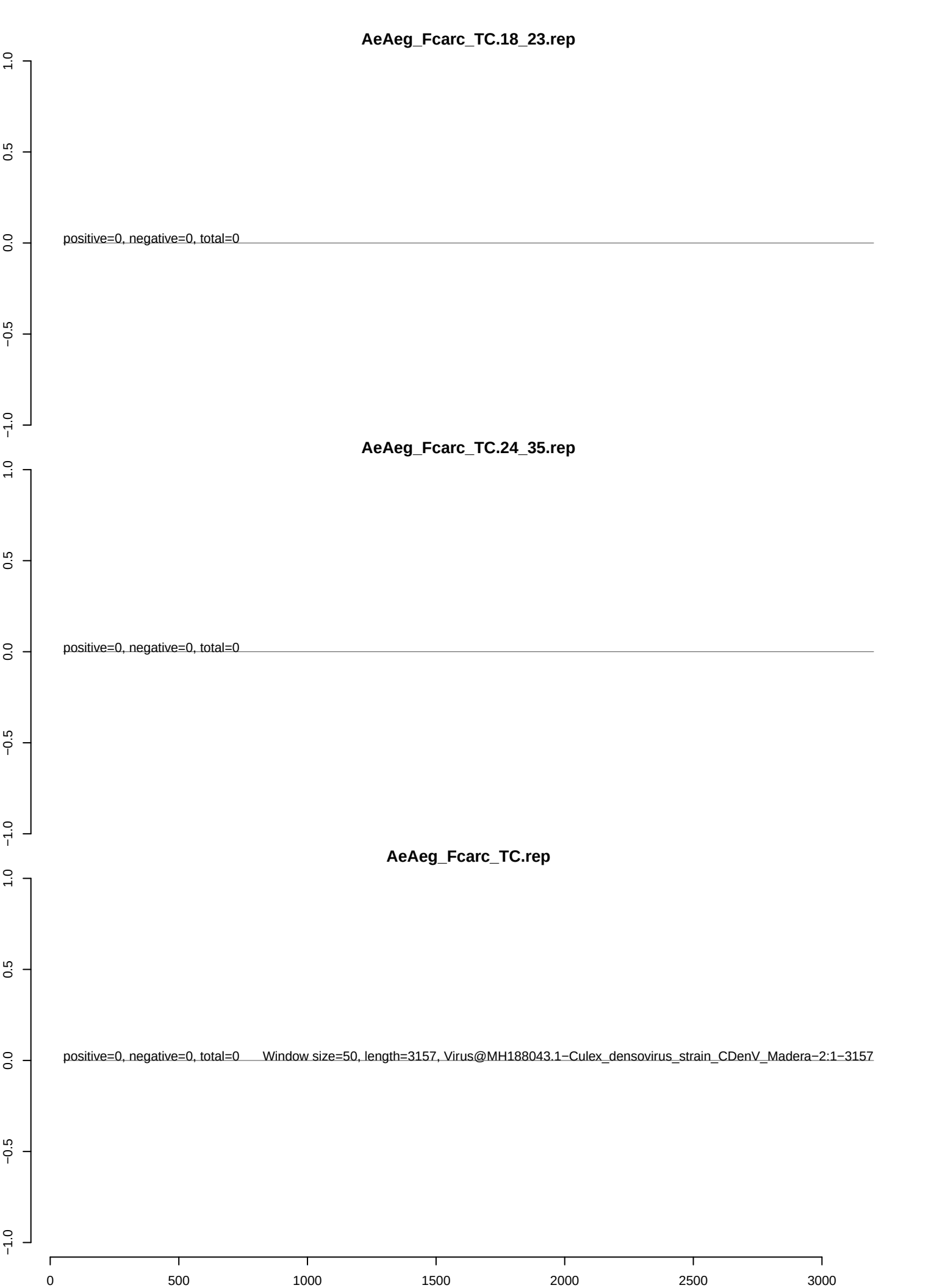
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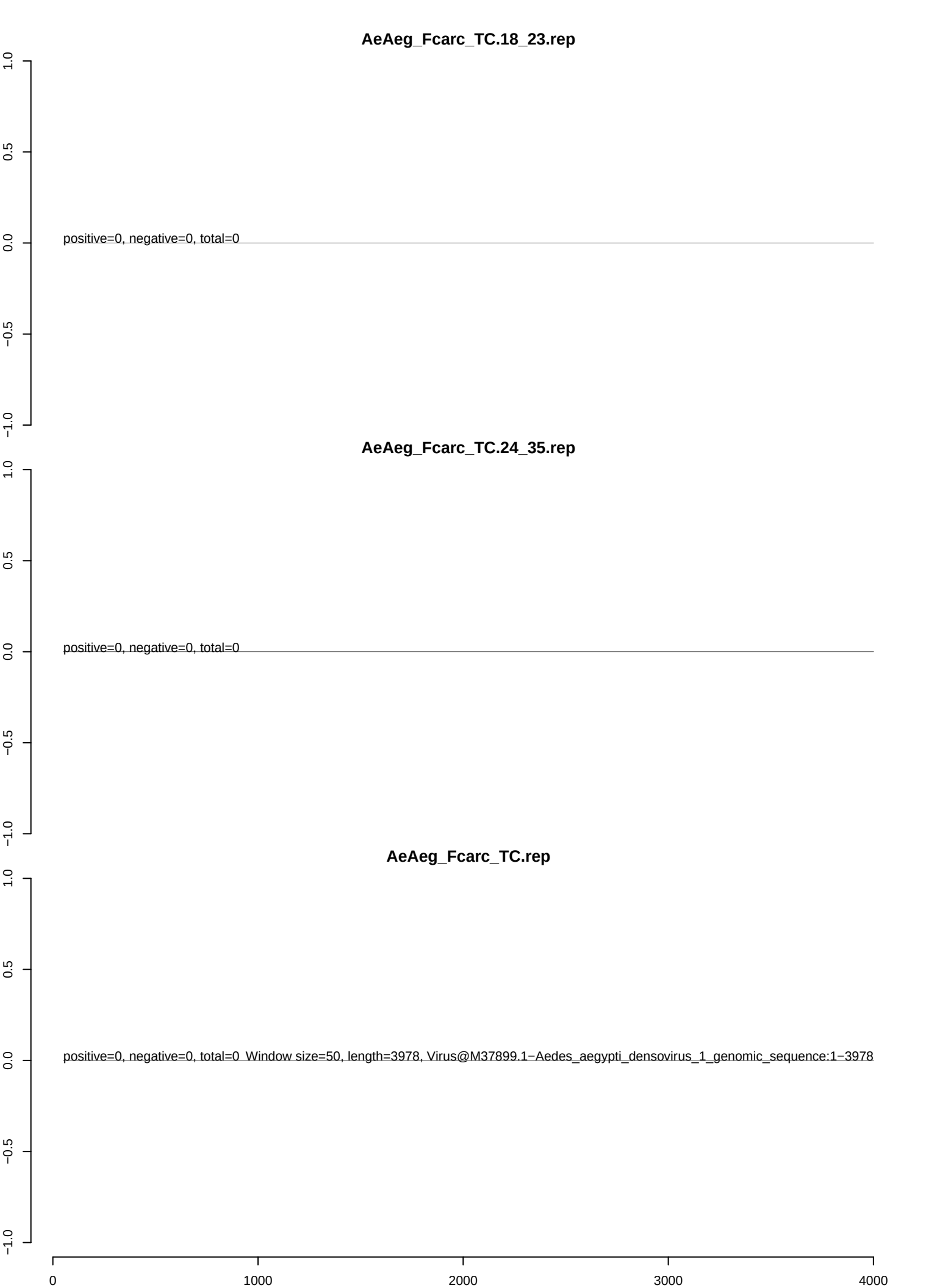
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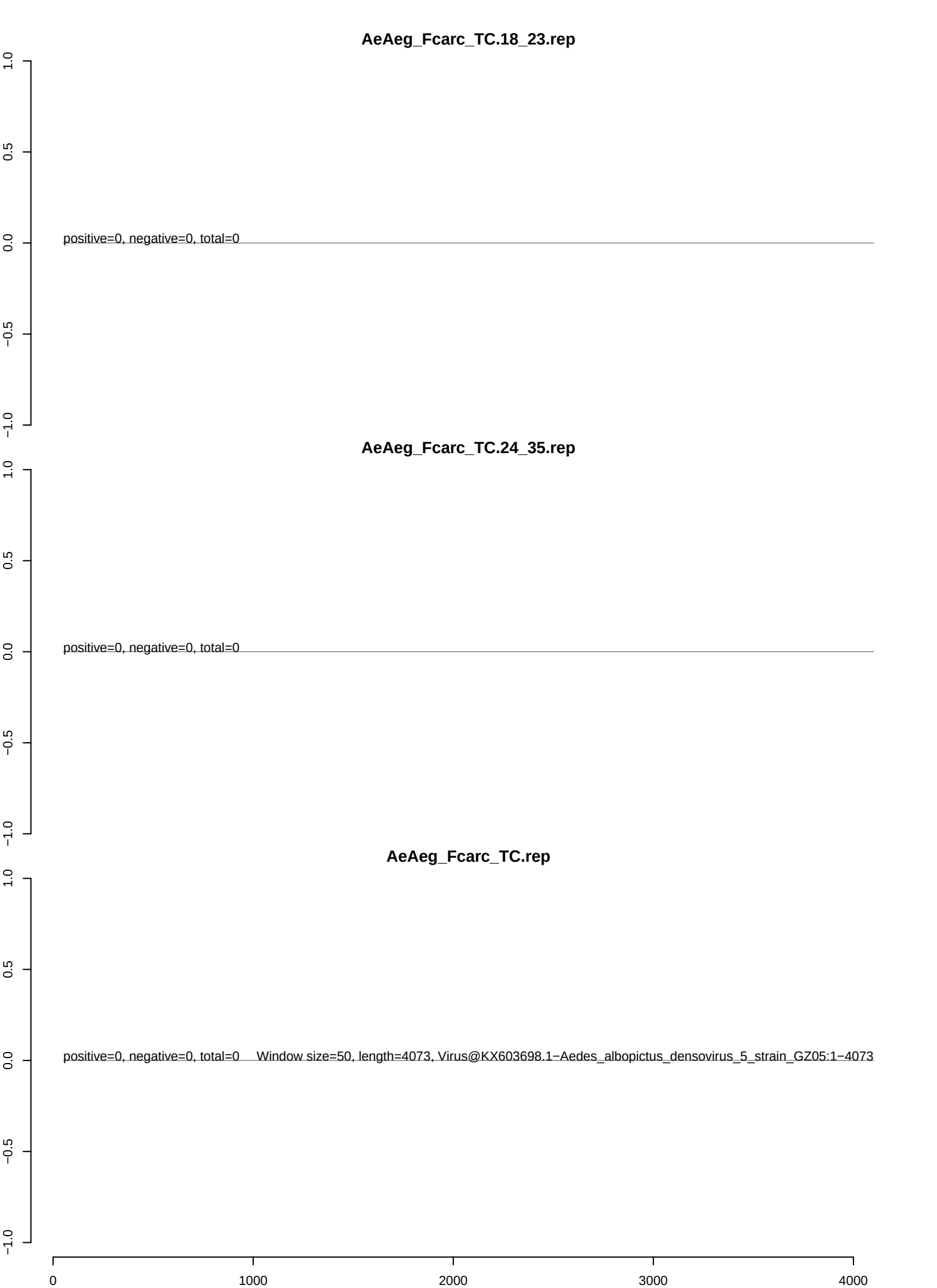
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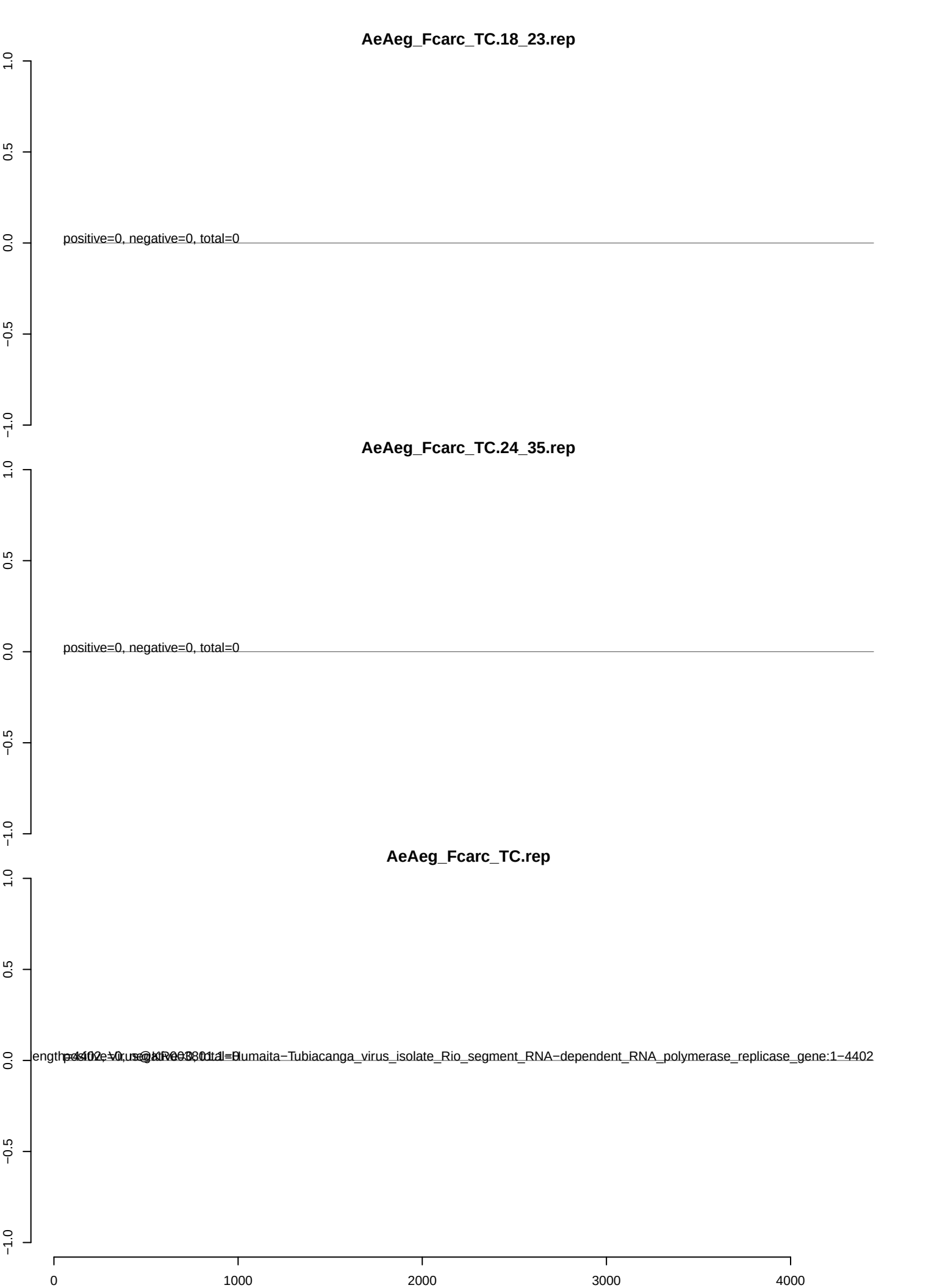
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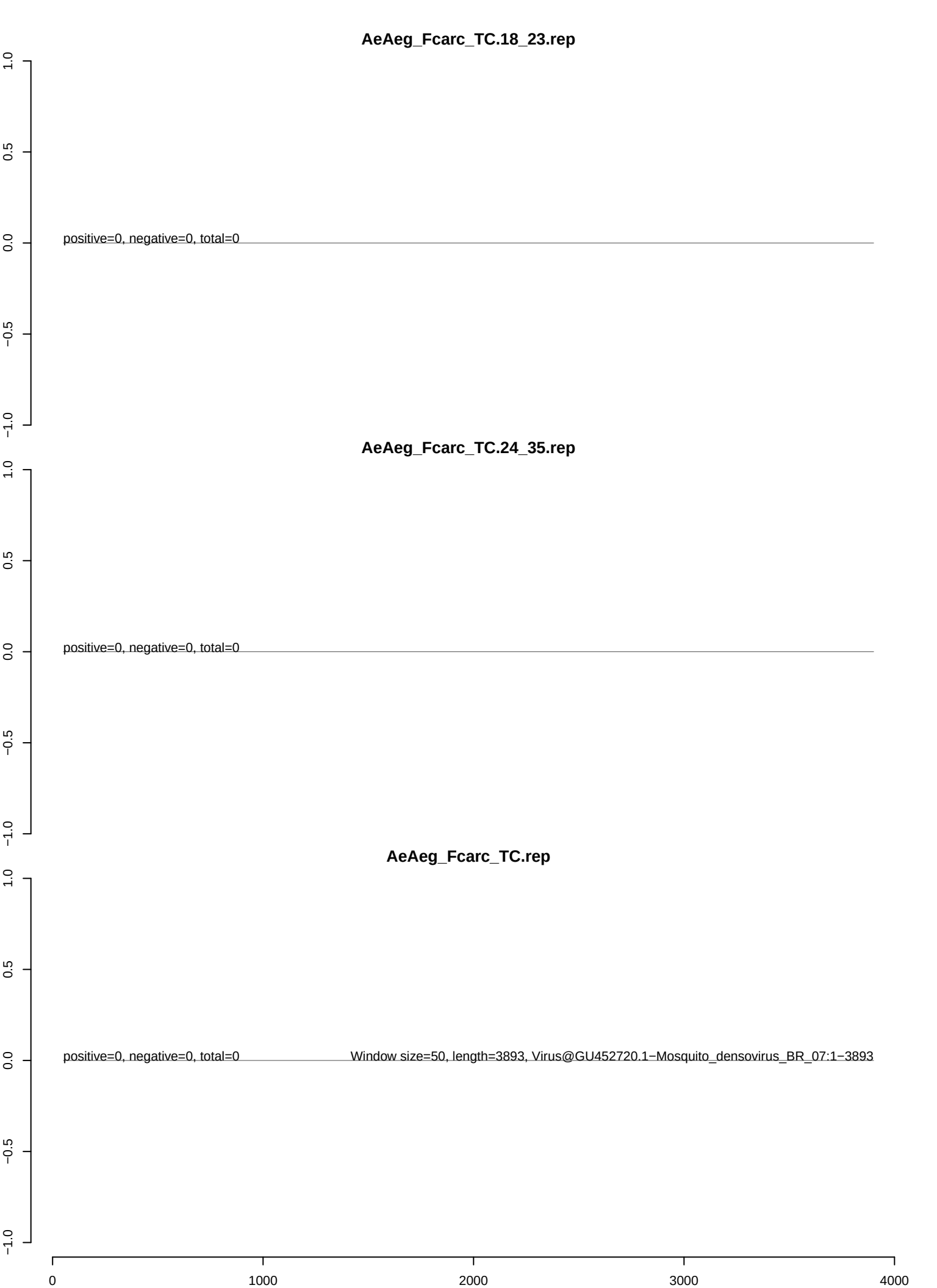
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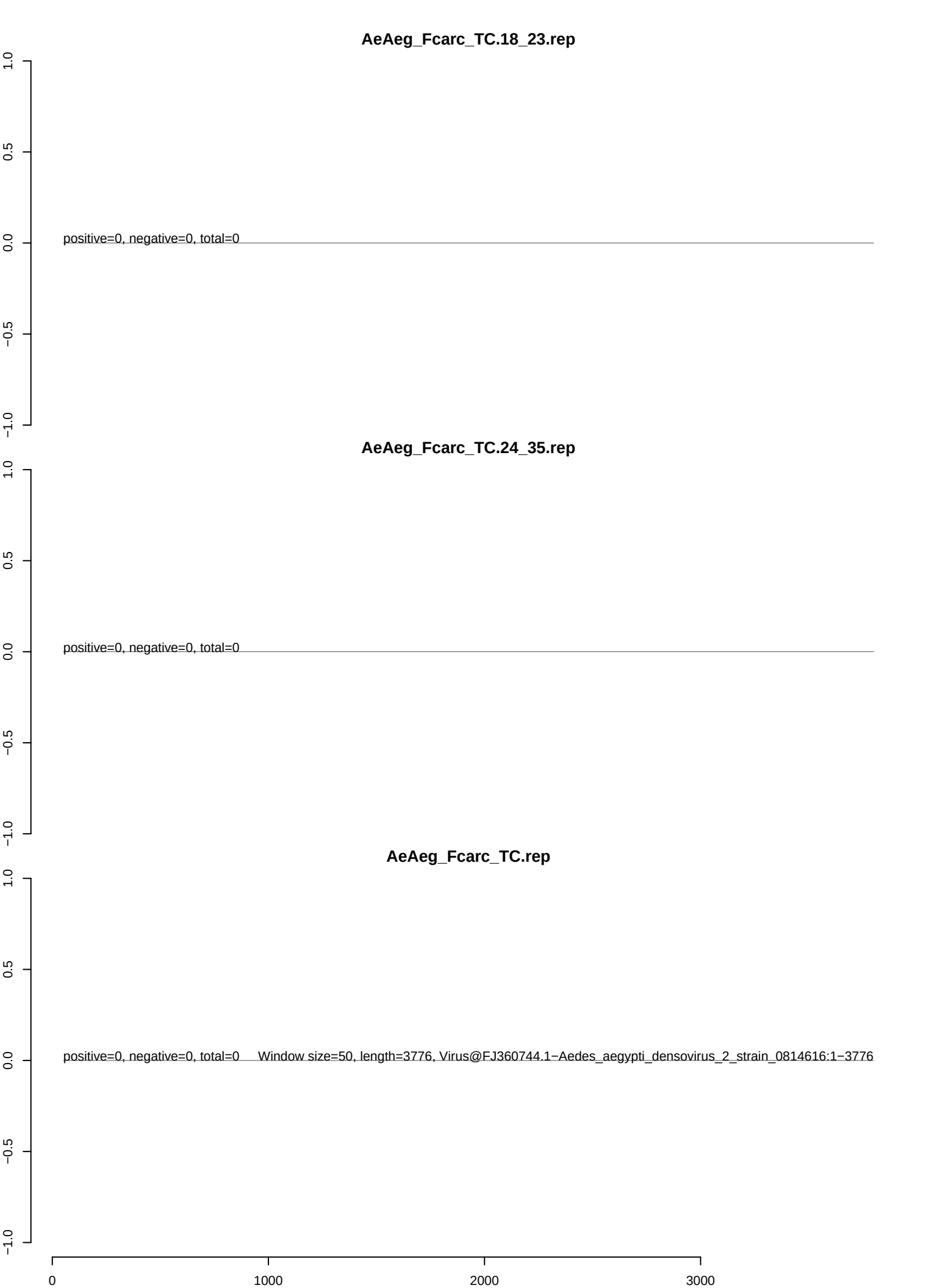
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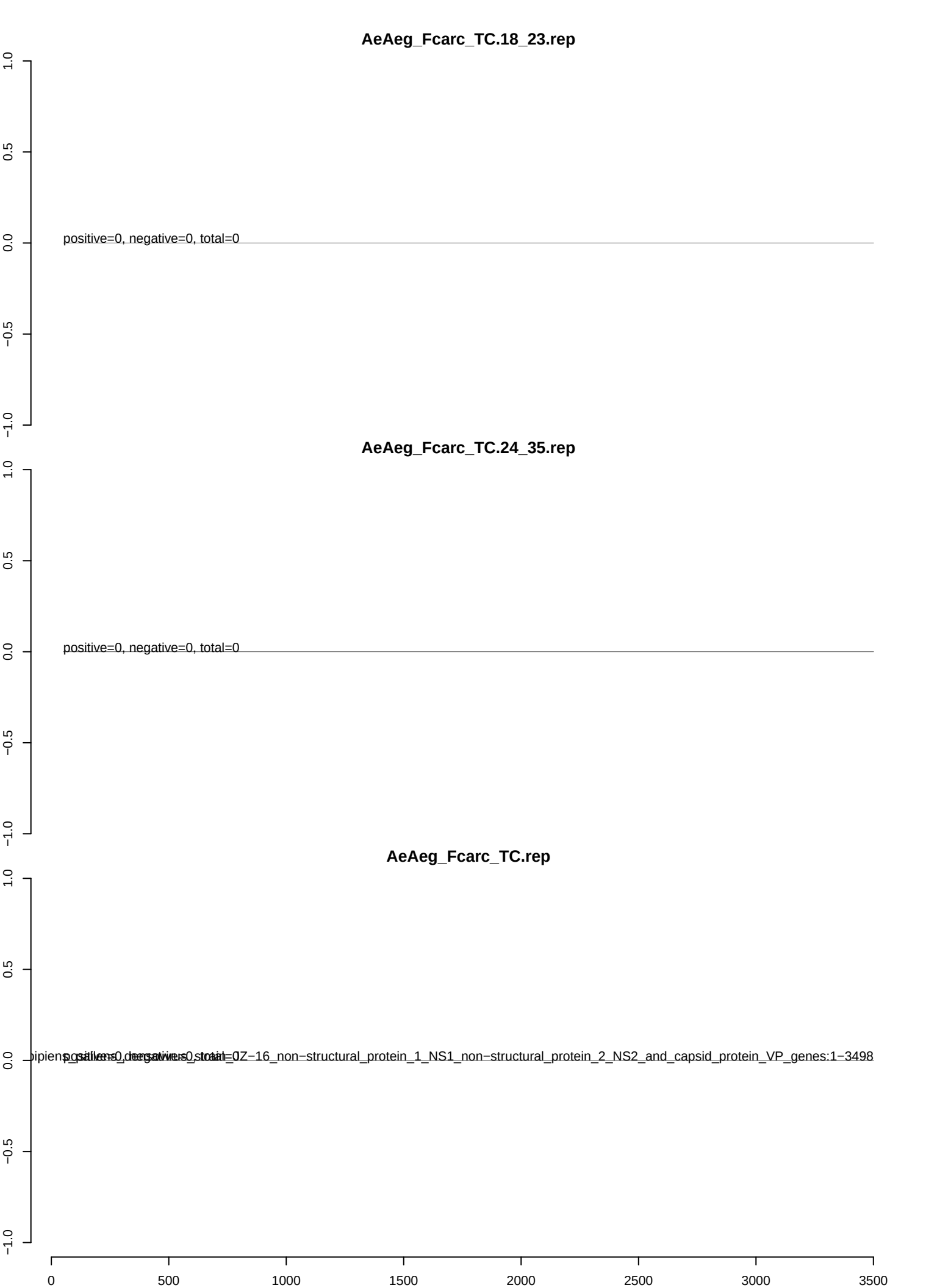
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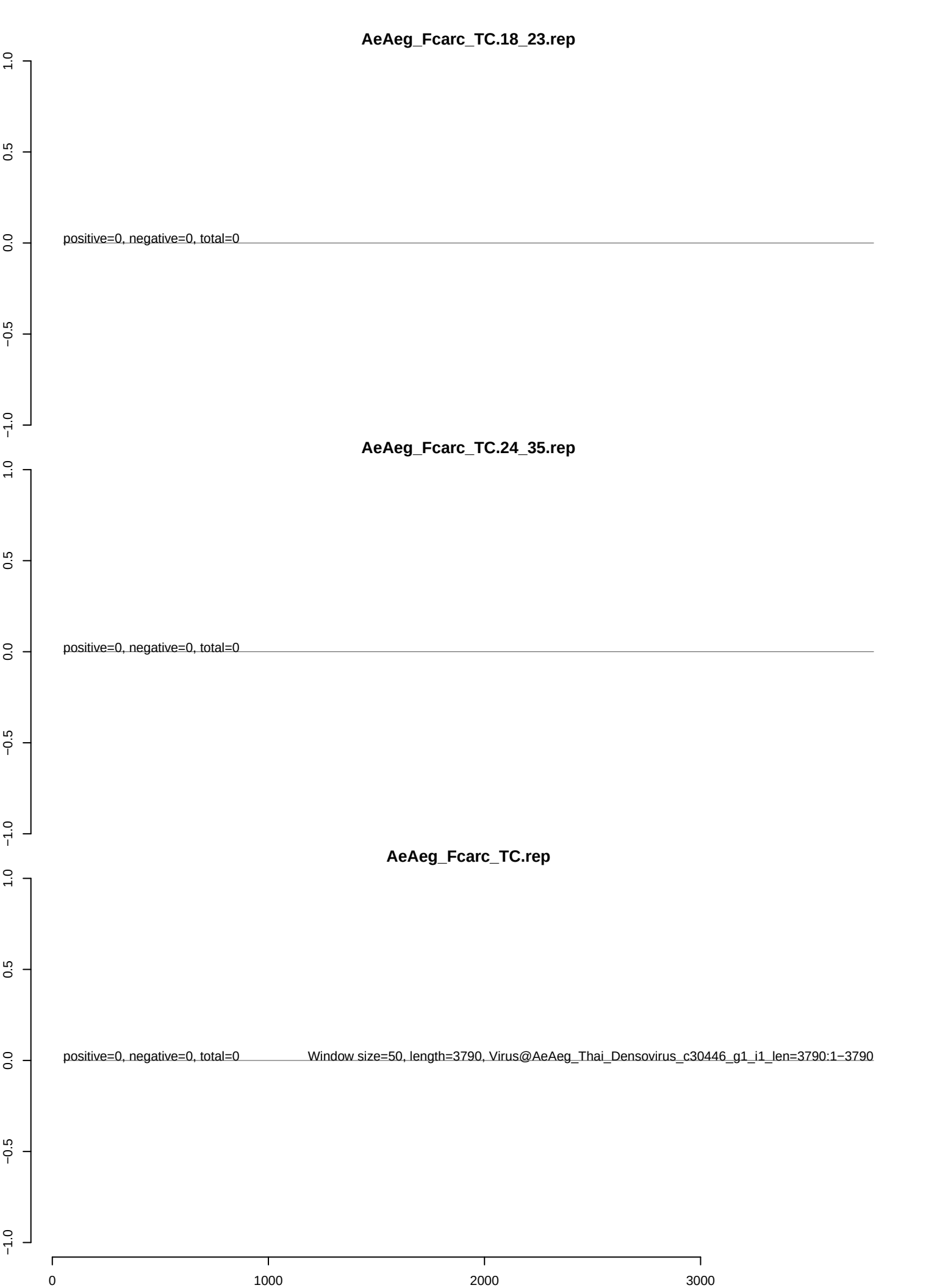
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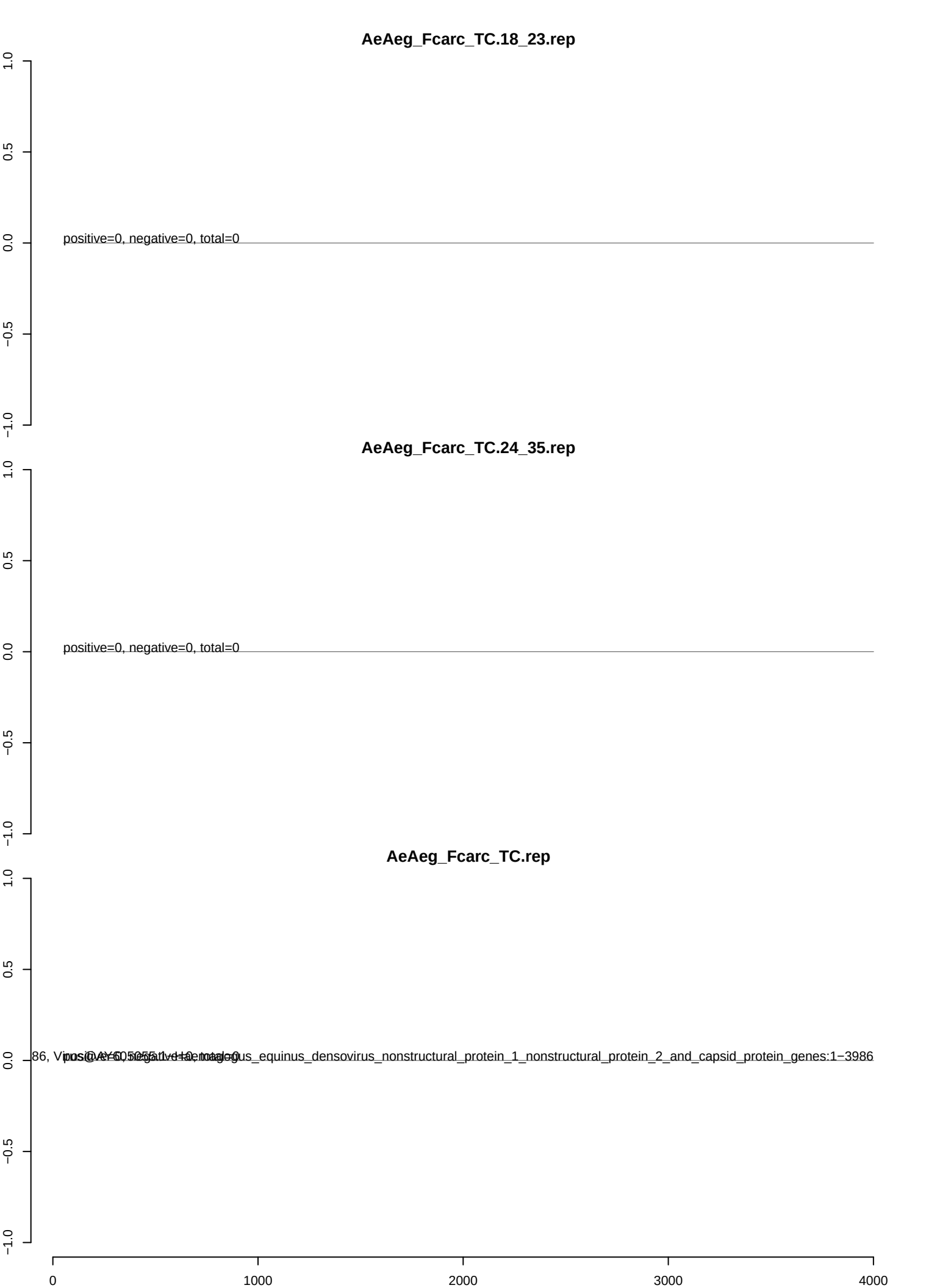
−1.0
0
1000
2000
3000


AeAeg_Fcarc_TC.18_23.rep
positive=0, negative=0, total=0
AeAeg_Fcarc_TC.24_35.rep
positive=0, negative=0, total=0
AeAeg_Fcarc_TC.rep
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0.5
0.0
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−1.0
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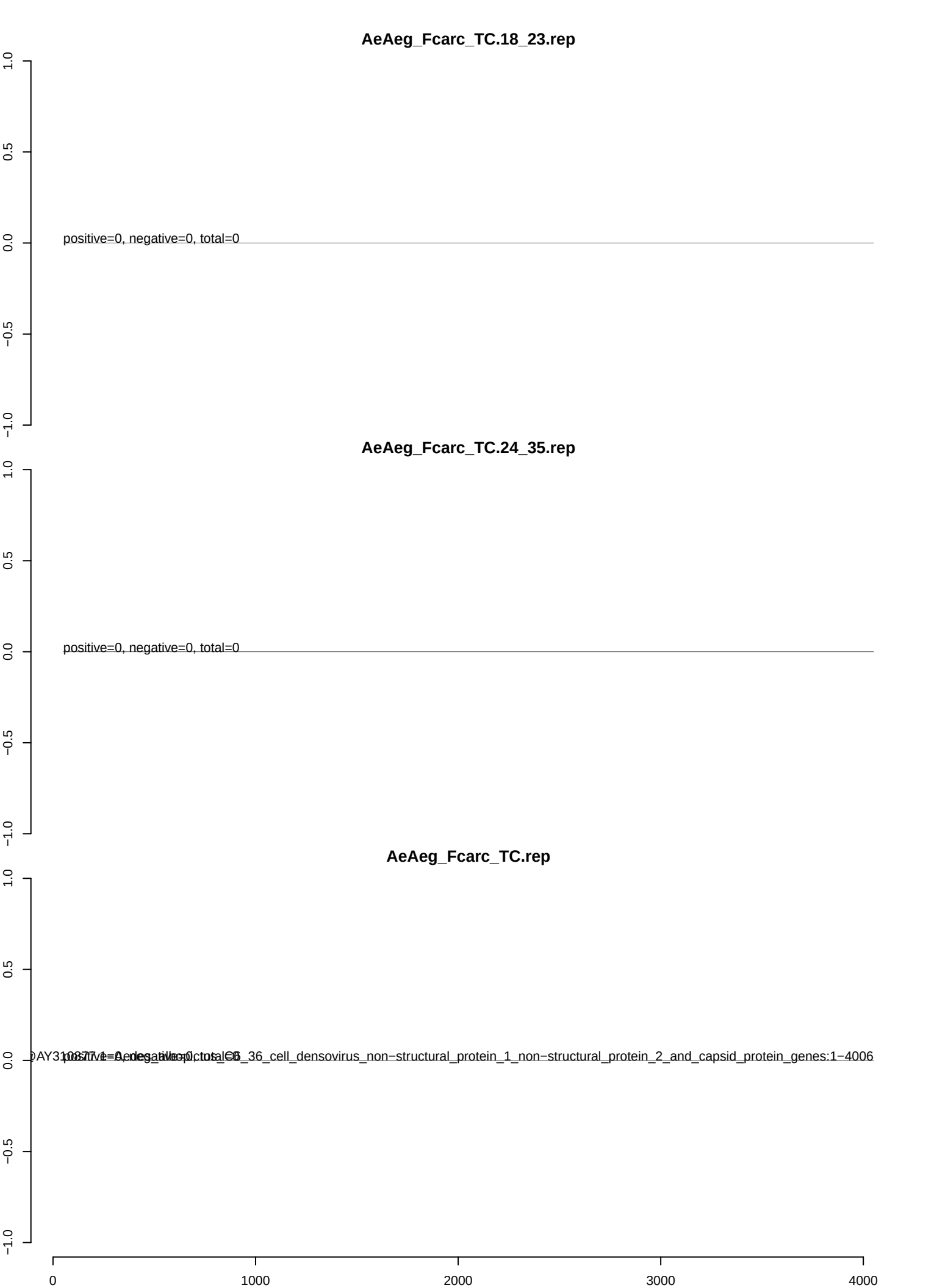
1000
2000
3000
4000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AeAeg_Fcarc_TC.24_35.rep
positive=0, negative=0, total=0
AeAeg_Fcarc_TC.rep
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0.5
0.0
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−1.0
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1000
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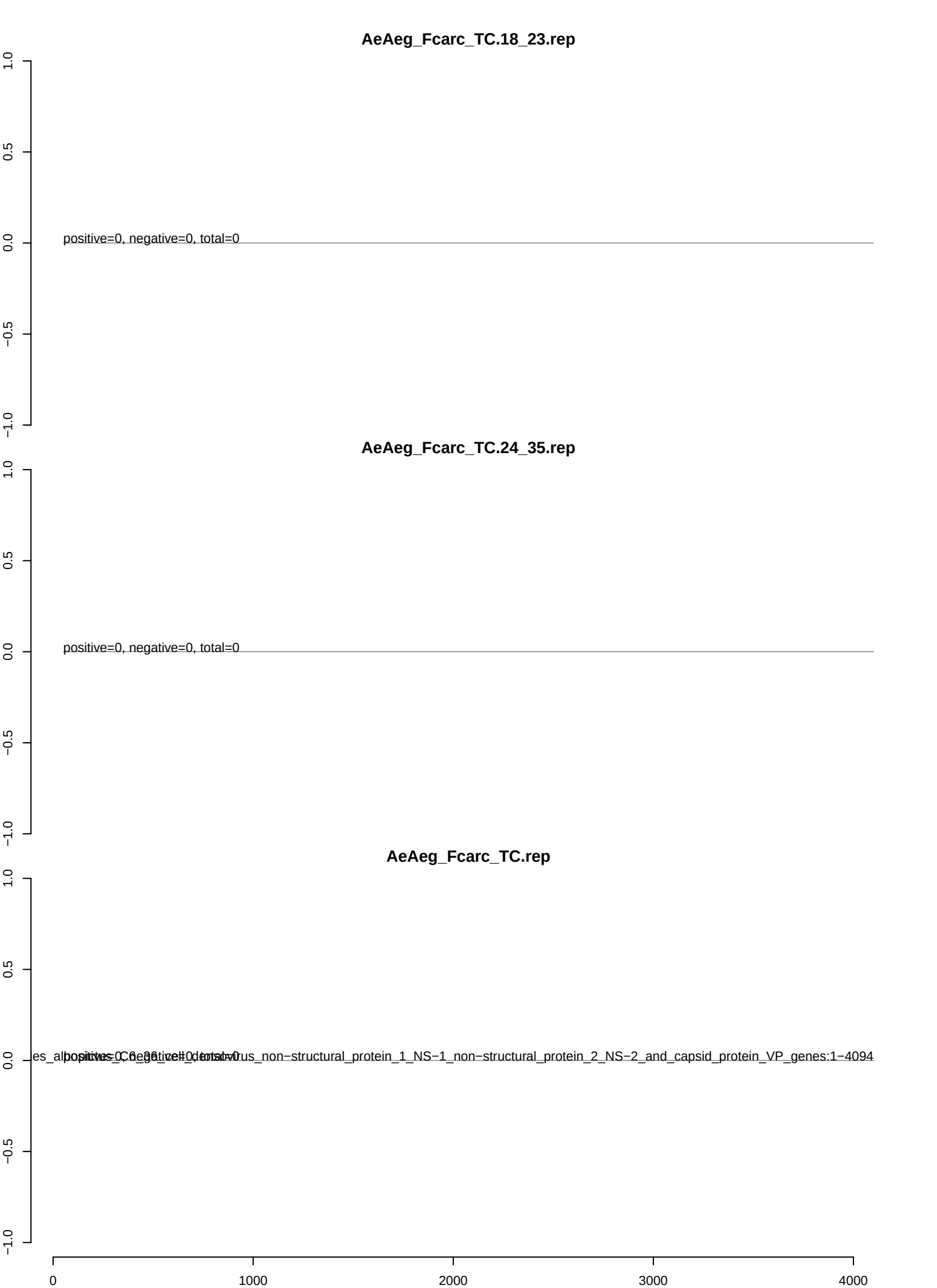
3000
4000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AeAeg_Fcarc_TC.24_35.rep
positive=0, negative=0, total=0
AeAeg_Fcarc_TC.rep
positive=0, negative=0, total=0
1.0
0.5
0.0
−0.5
−1.0
0
1000
2000
3000
4000