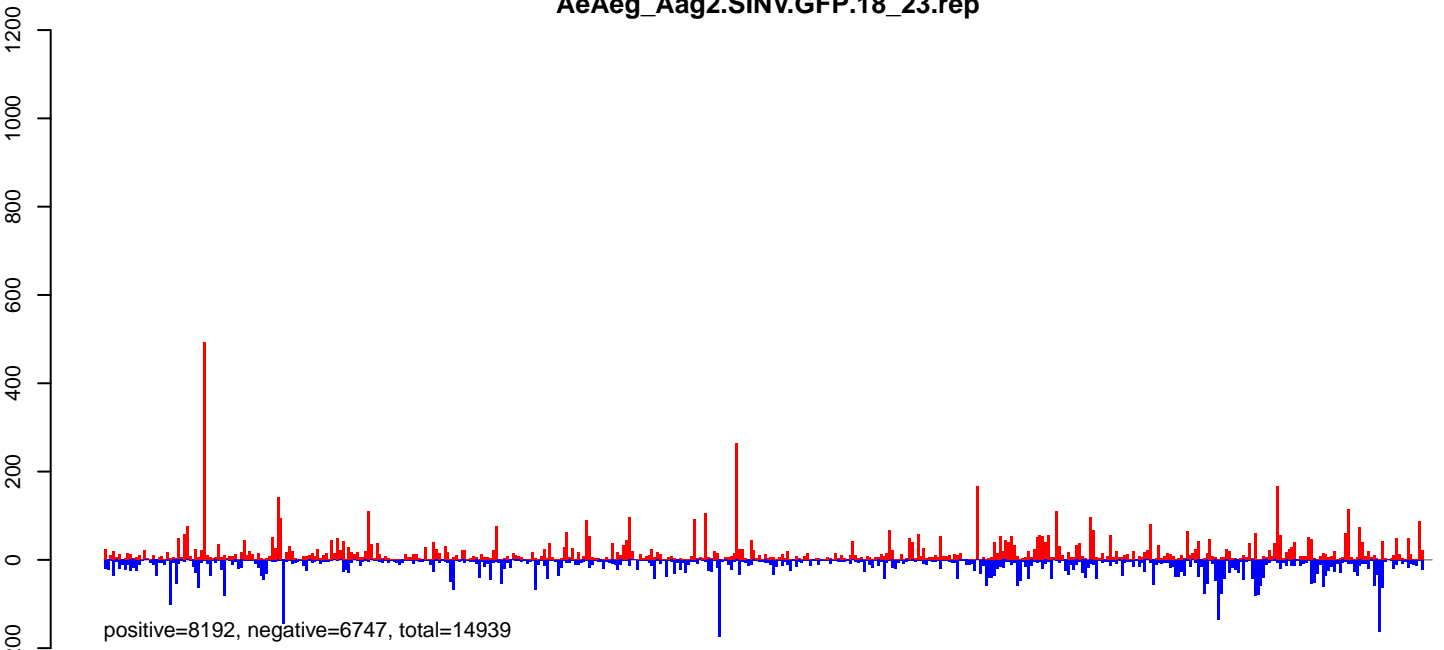
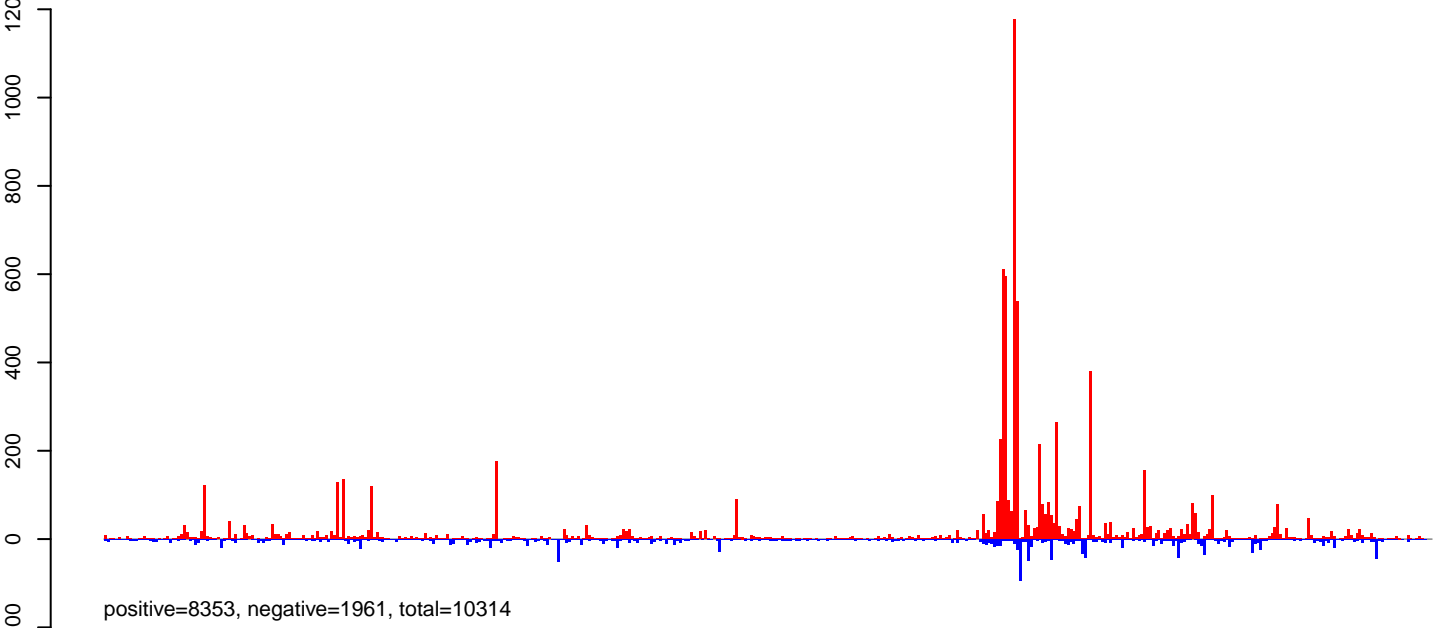


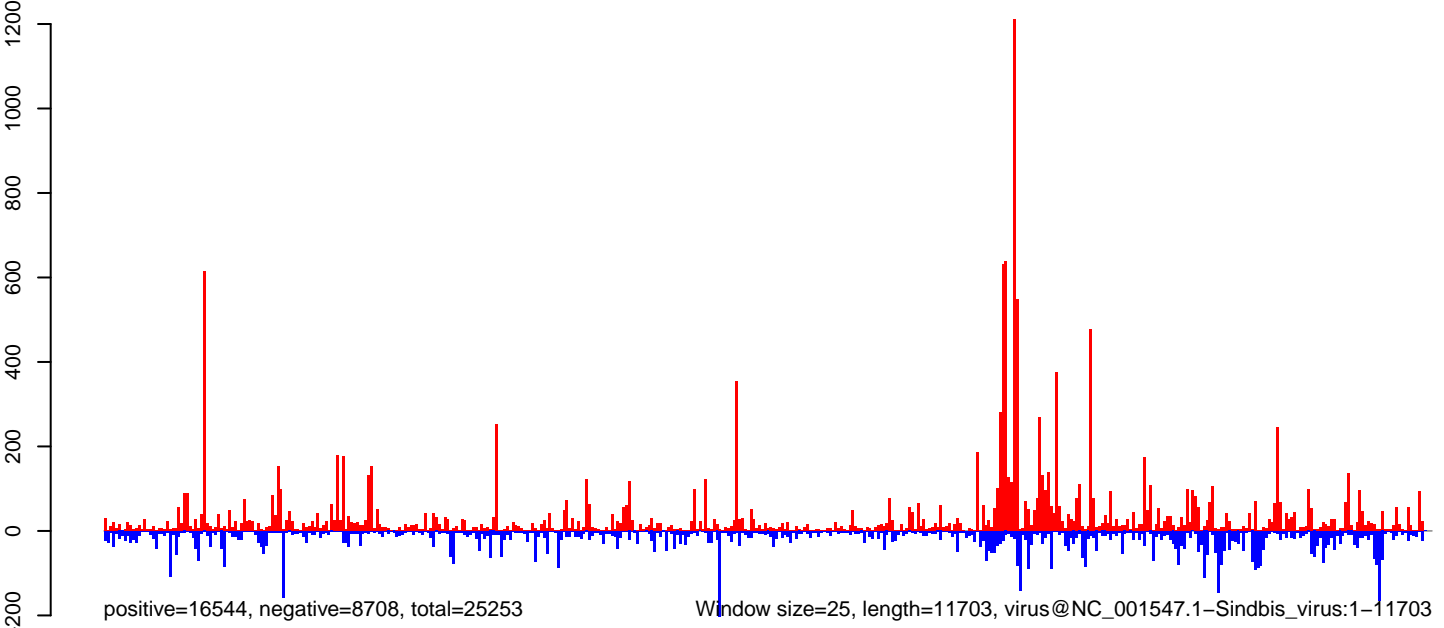
AeAeg_Aag2.SINV.GFP.18_23.rep



AeAeg_Aag2.SINV.GFP.24_35.rep



AeAeg_Aag2.SINV.GFP.rep



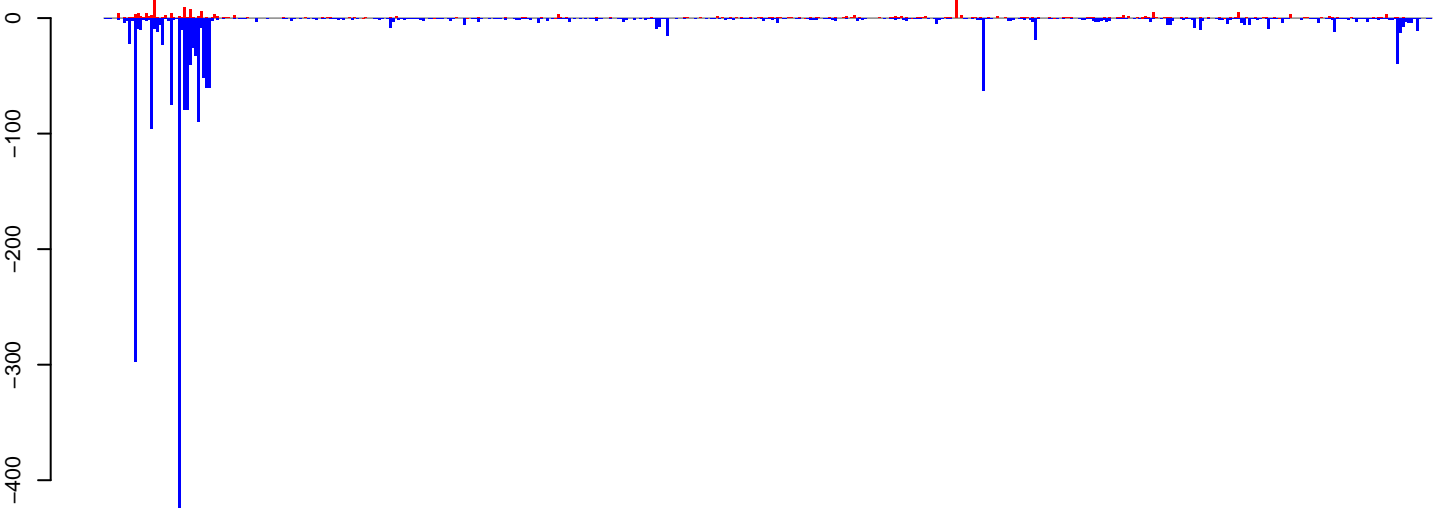
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AeAeg_Aag2.SINV.GFP.18_23.rep



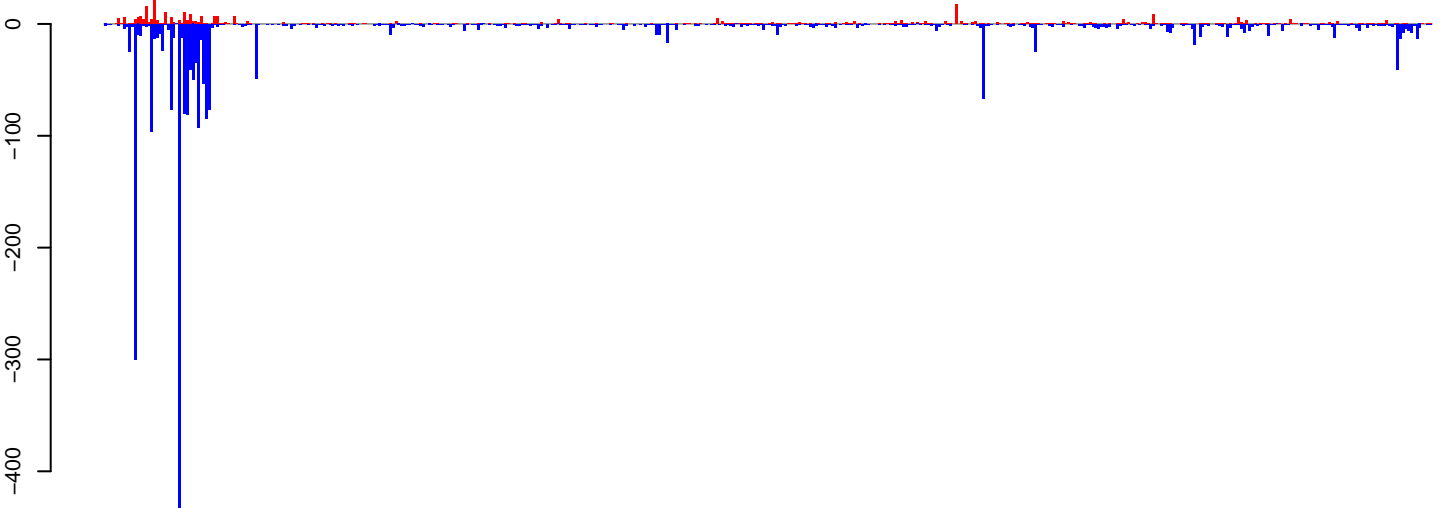
positive=143, negative=368, total=511

AeAeg_Aag2.SINV.GFP.24_35.rep



positive=214, negative=2067, total=2281

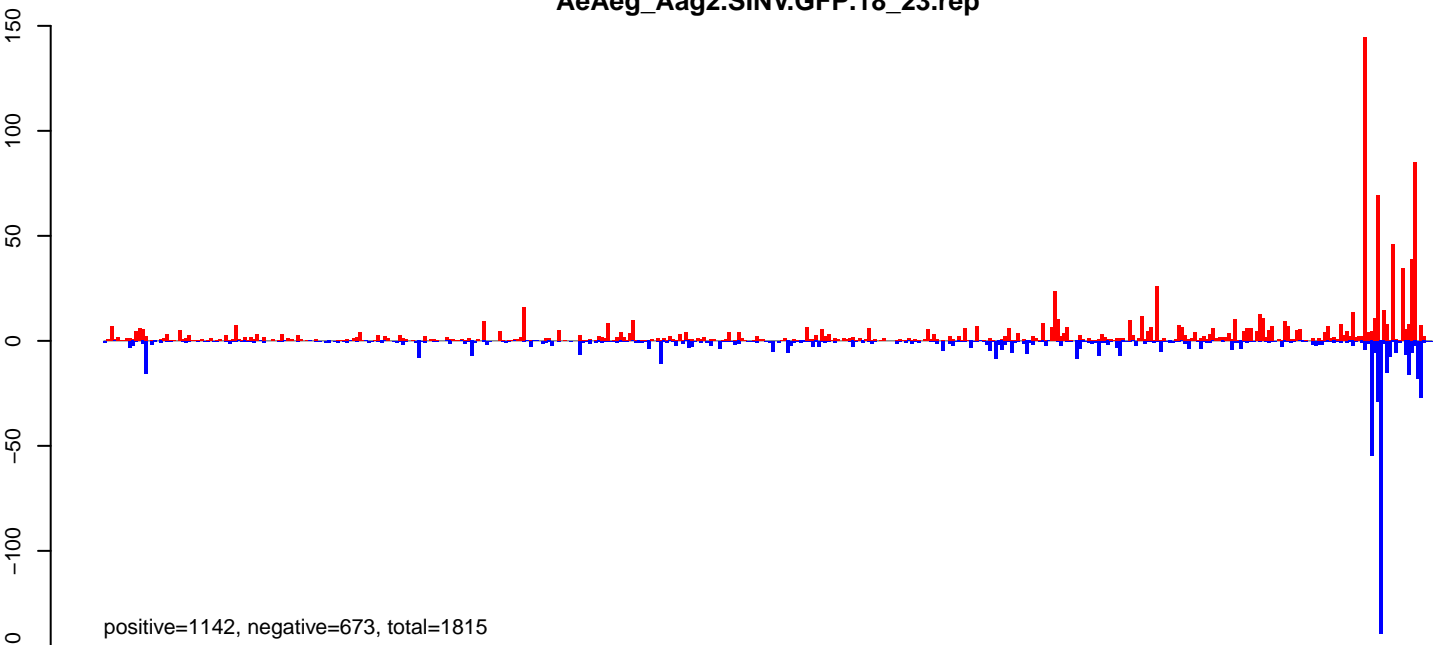
AeAeg_Aag2.SINV.GFP.rep



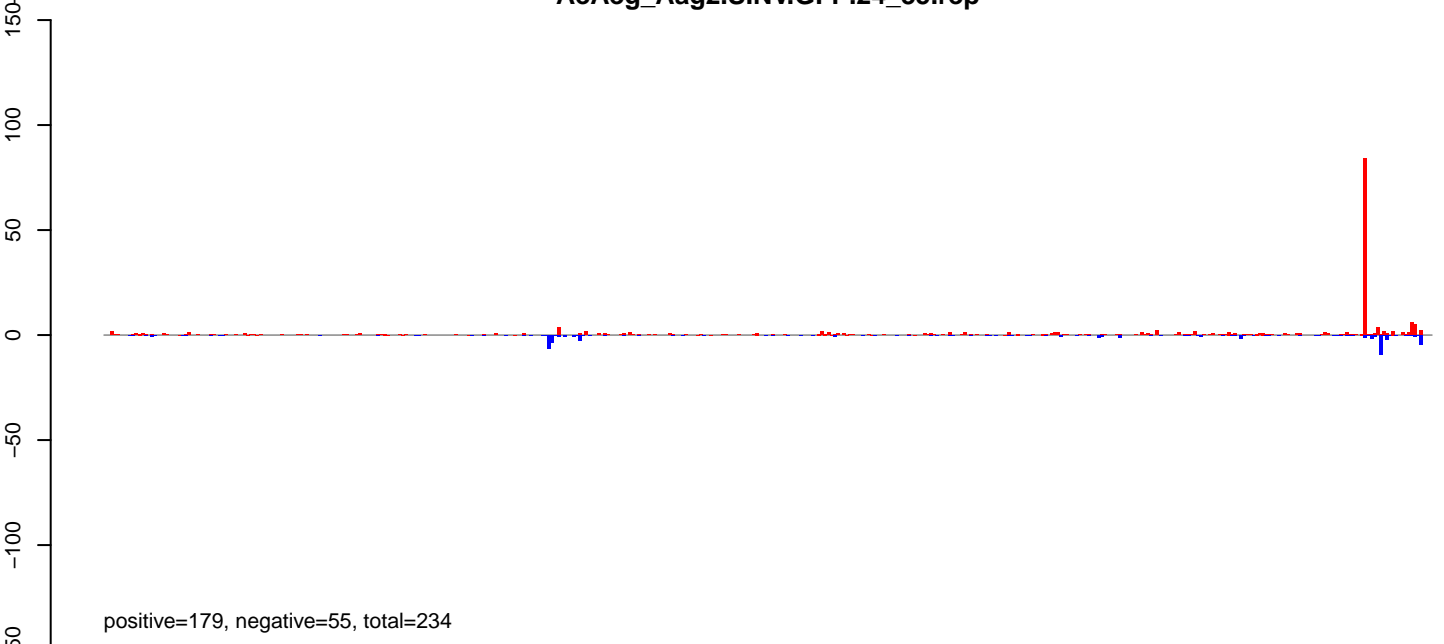
=25, positive=209, negative=2438, total=2762
@1624382661=2762
si_Charoen-like_virus_isolate_Rio_segment_S_plus_segment_M_plus_segment_L_Nucle:1-12099

0 2000 4000 6000 8000 10000 12000

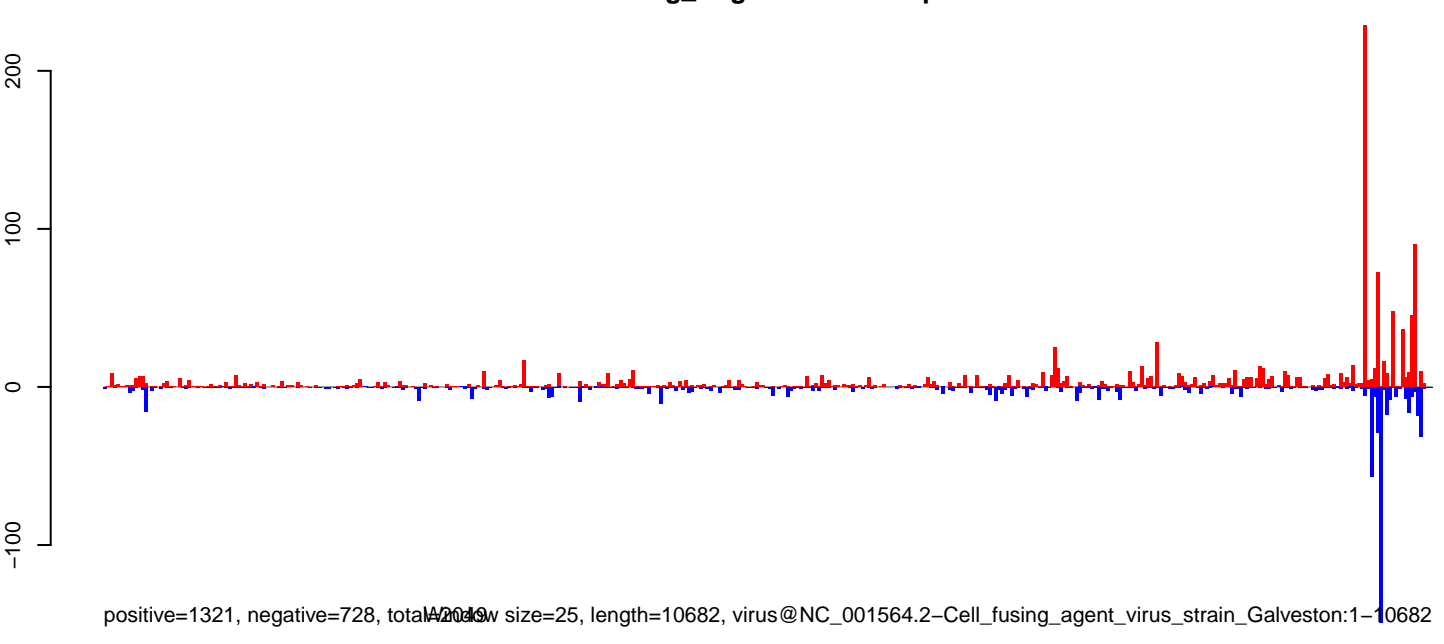
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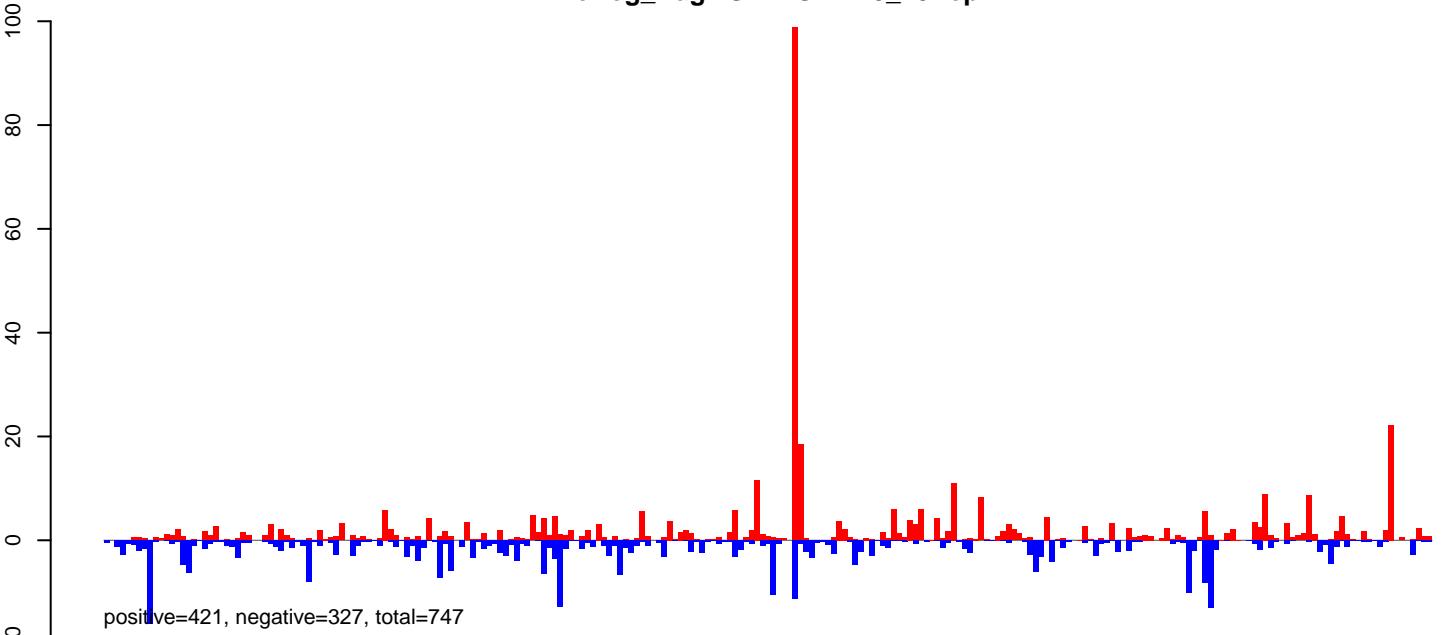
AeAeg_Aag2.SINV.GFP.24_35.rep



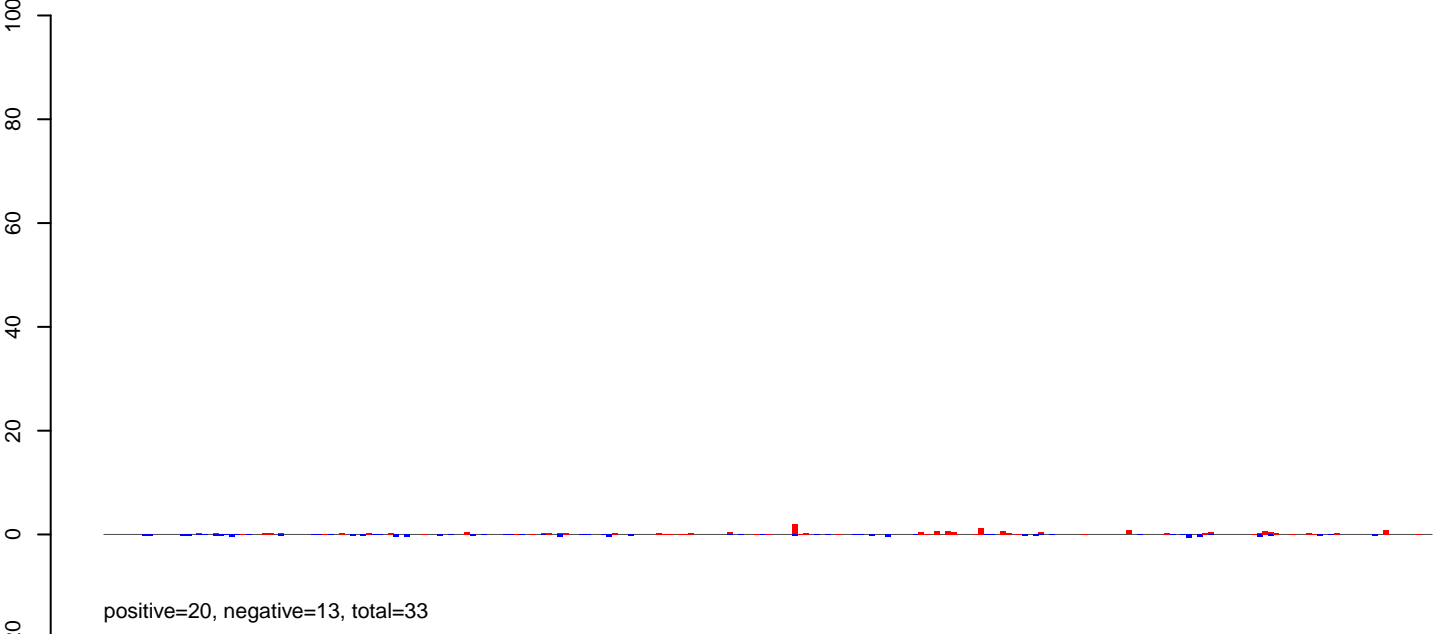
AeAeg_Aag2.SINV.GFP.rep



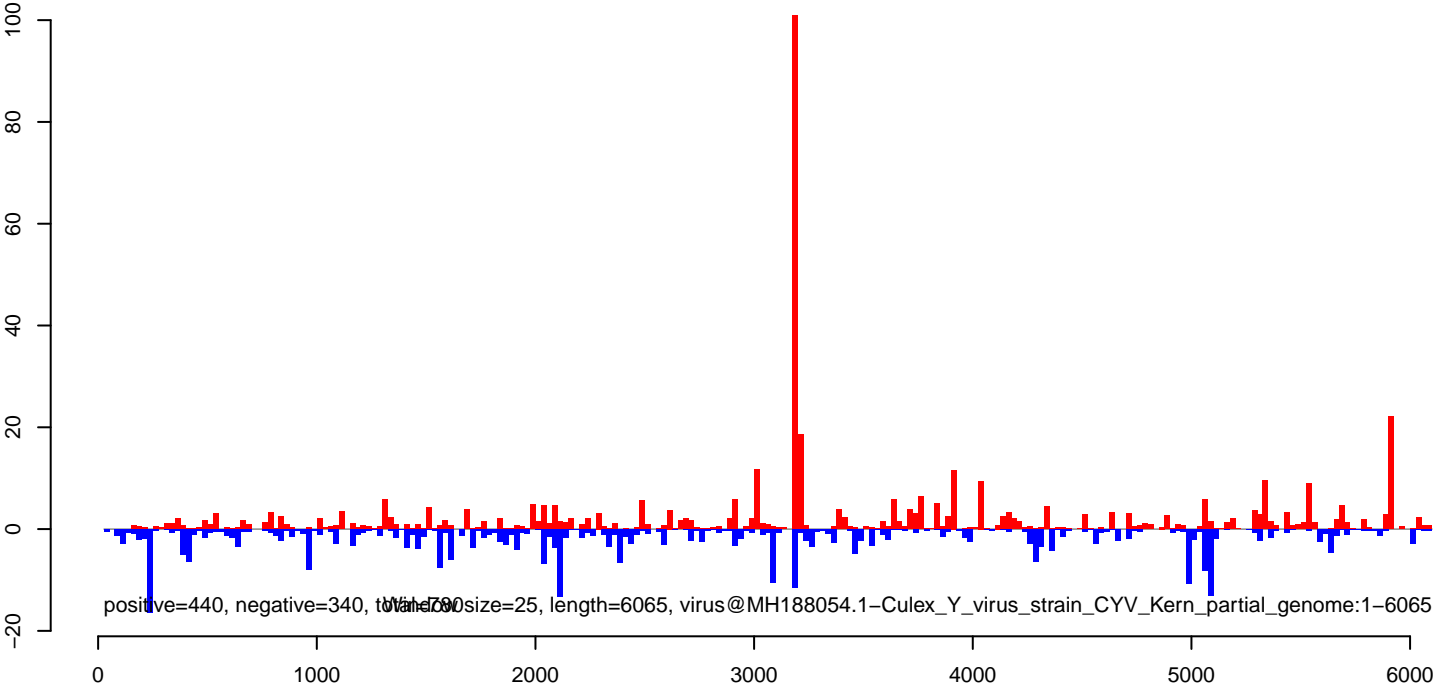
AeAeg_Aag2.SINV.GFP.18_23.rep



AeAeg_Aag2.SINV.GFP.24_35.rep

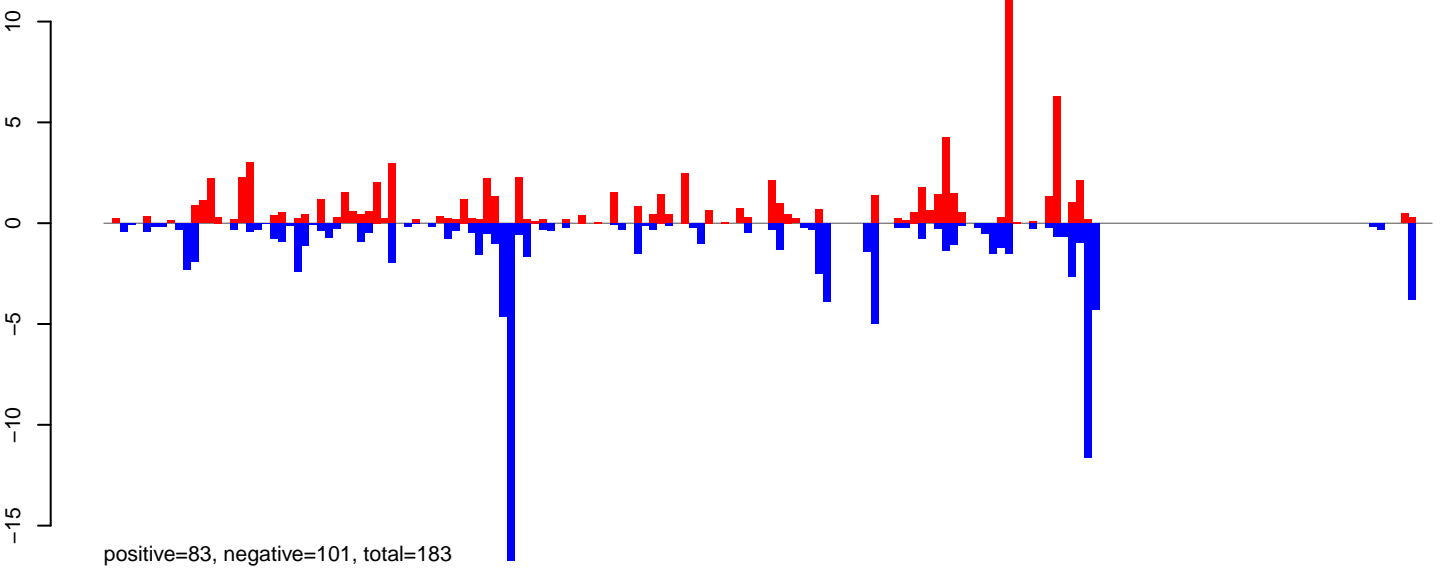


AeAeg_Aag2.SINV.GFP.rep

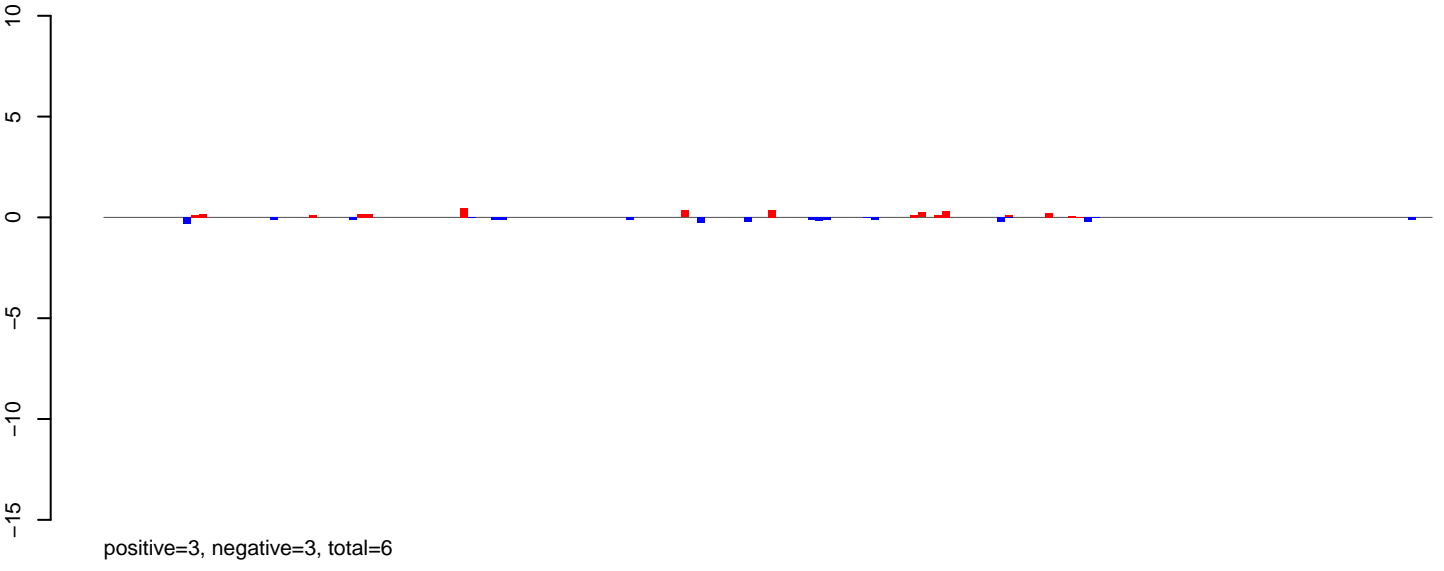


0 1000 2000 3000 4000 5000 6000
virus@MH188054.1-Culex_Y_virus_strain_CYV_Kern_partial_genome:1-6065

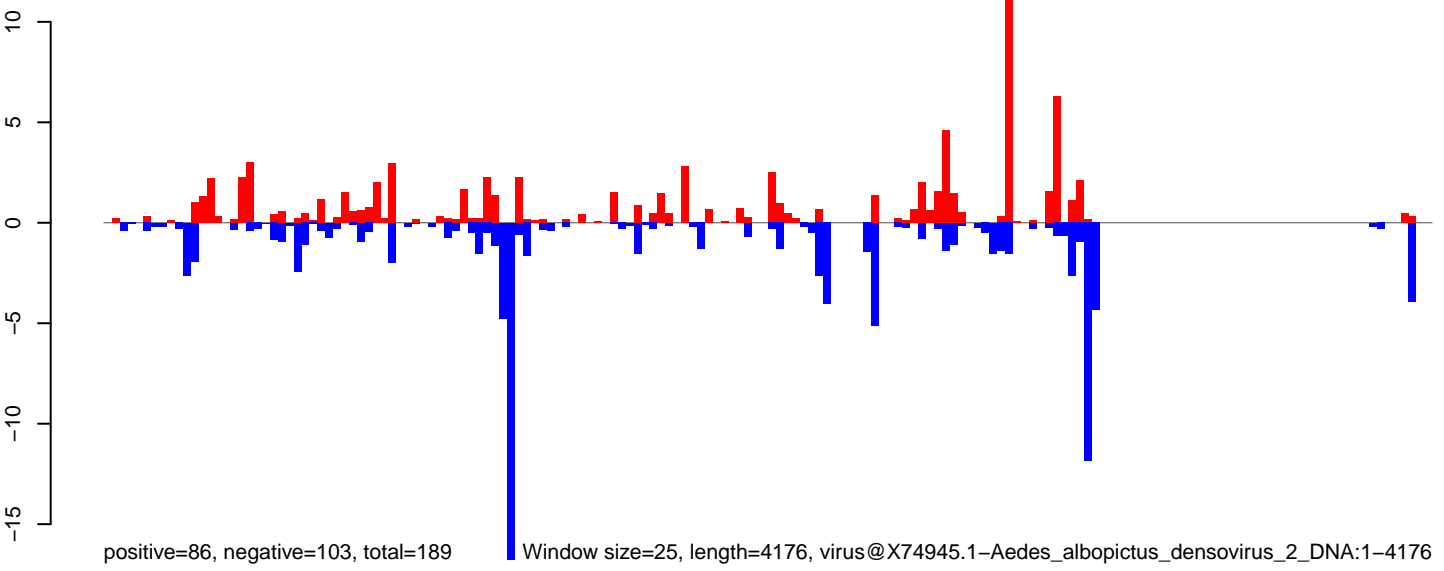
AeAeg_Aag2.SINV.GFP.18_23.rep



AeAeg_Aag2.SINV.GFP.24_35.rep



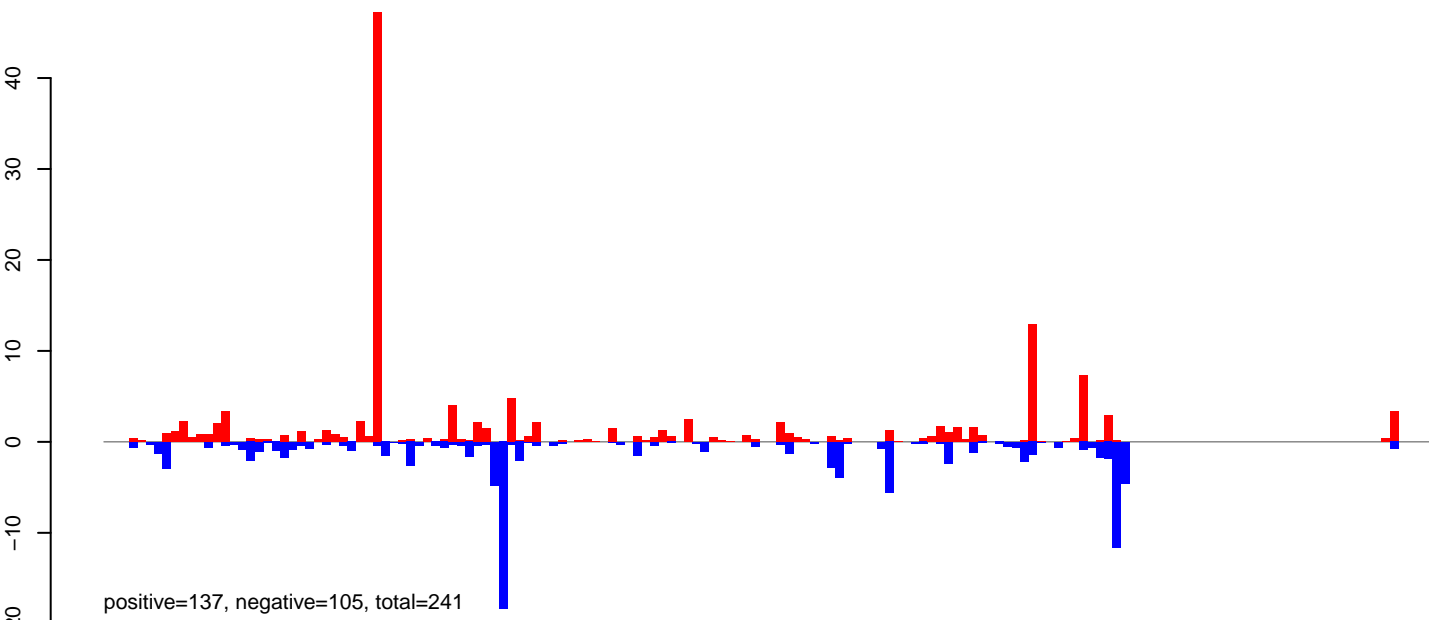
AeAeg_Aag2.SINV.GFP.rep



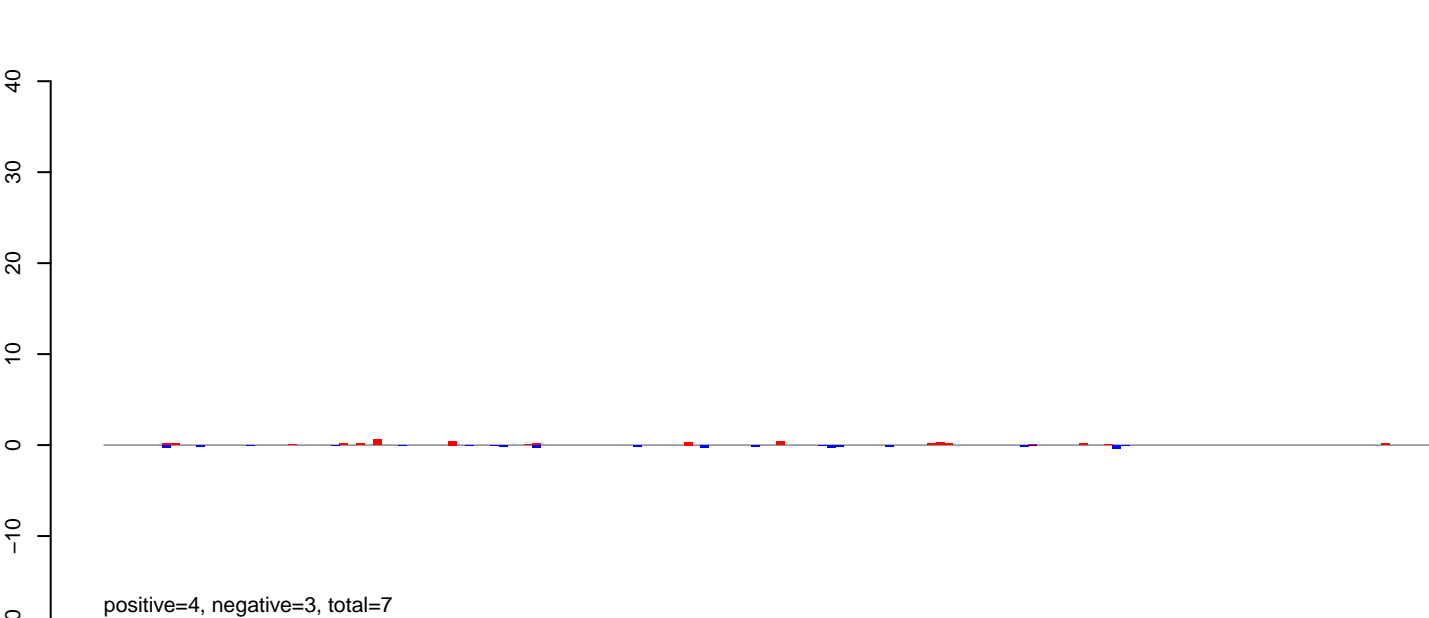
Window size=25, length=4176, virus@X74945.1-Aedes_albopictus_densovirus_2_DNA:1-4176

0 1000 2000 3000 4000

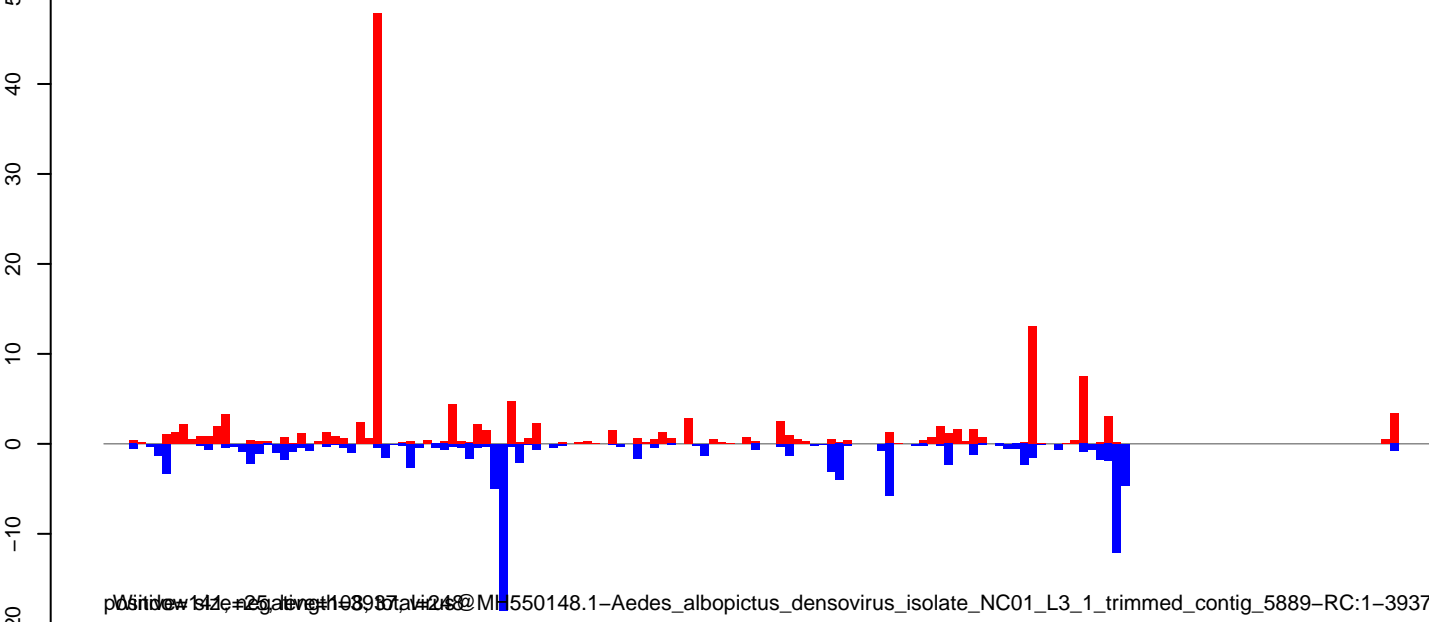
AeAeg_Aag2.SINV.GFP.18_23.rep



AeAeg_Aag2.SINV.GFP.24_35.rep

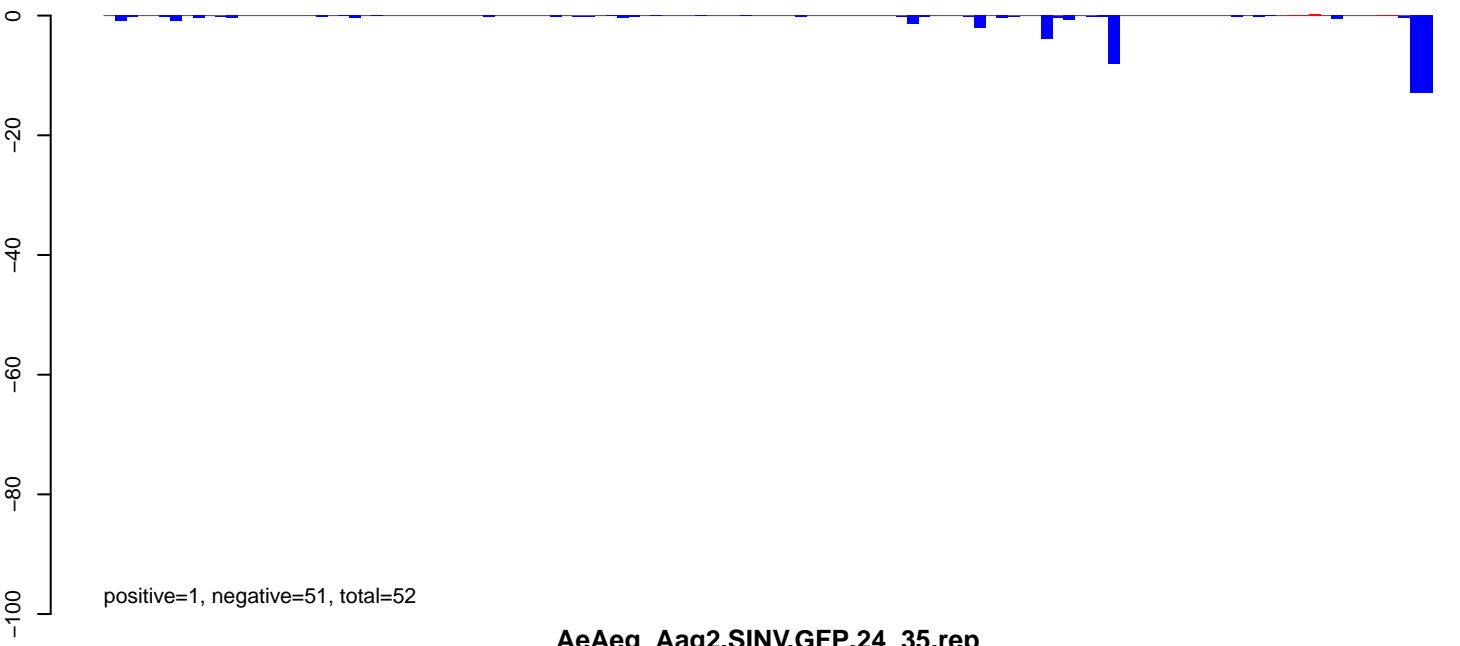


AeAeg_Aag2.SINV.GFP.rep

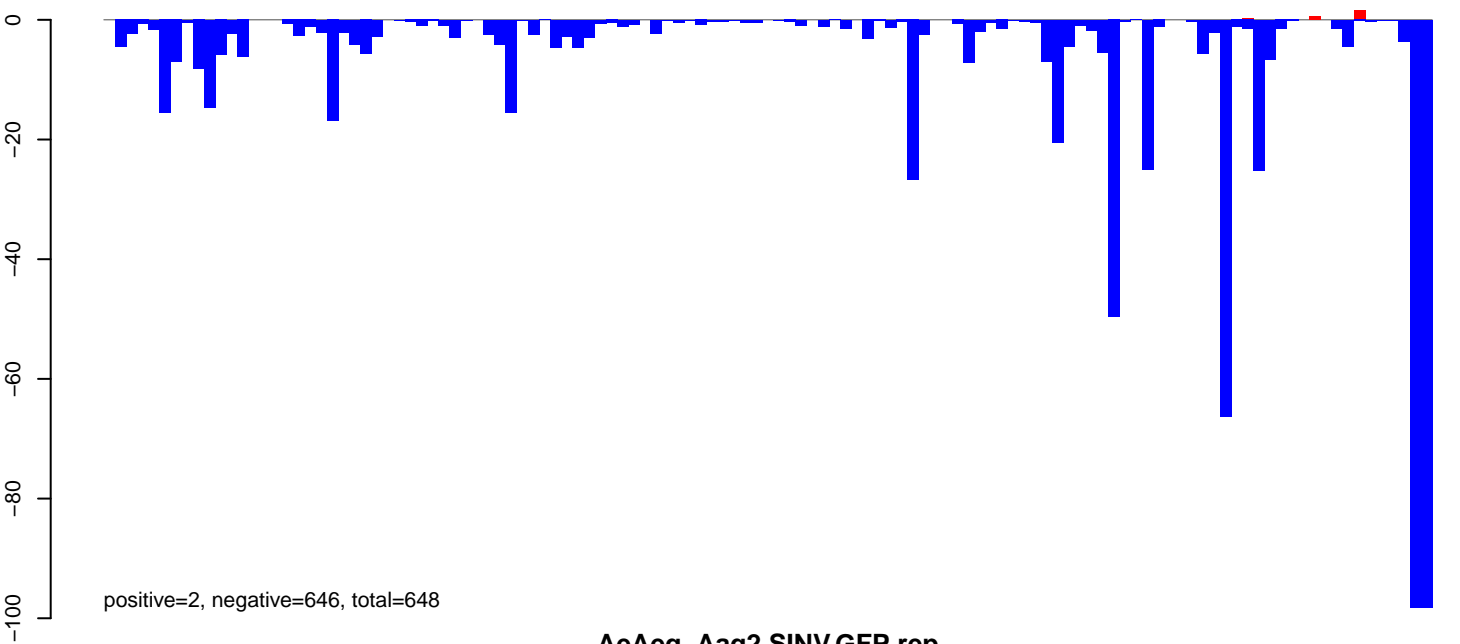


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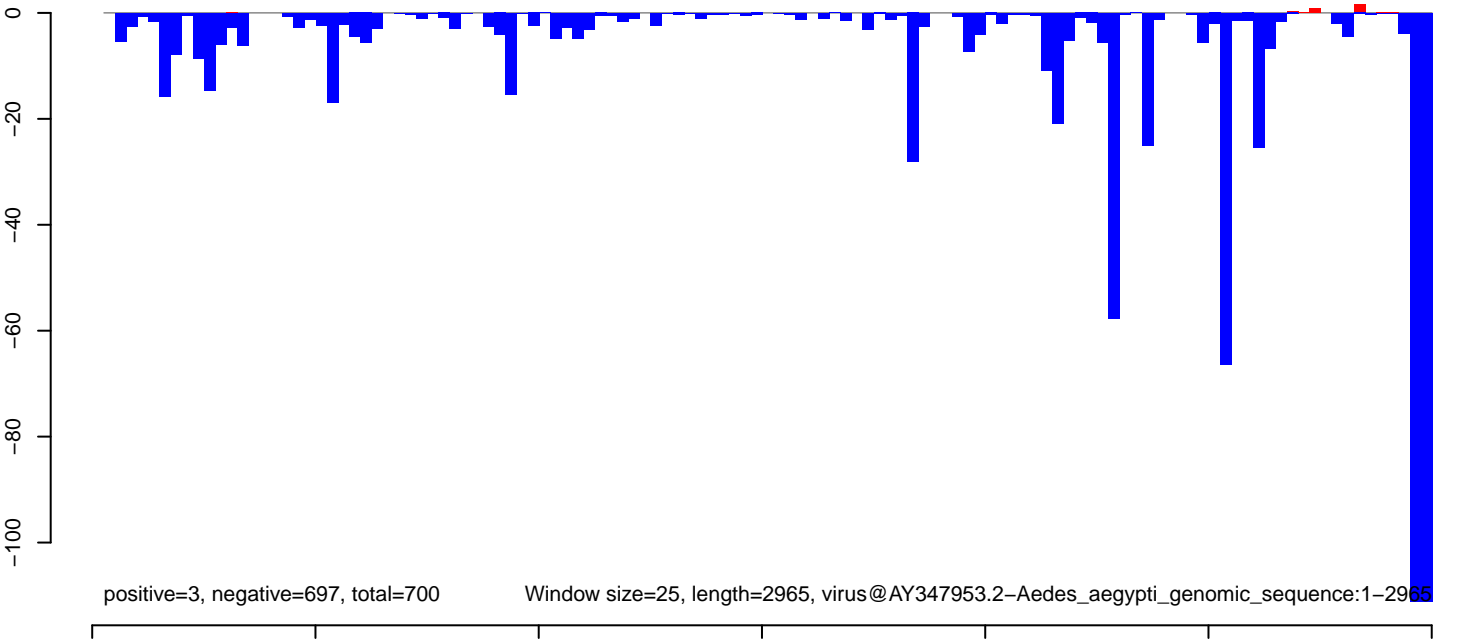
AeAeg_Aag2.SINV.GFP.18_23.rep



AeAeg_Aag2.SINV.GFP.24_35.rep

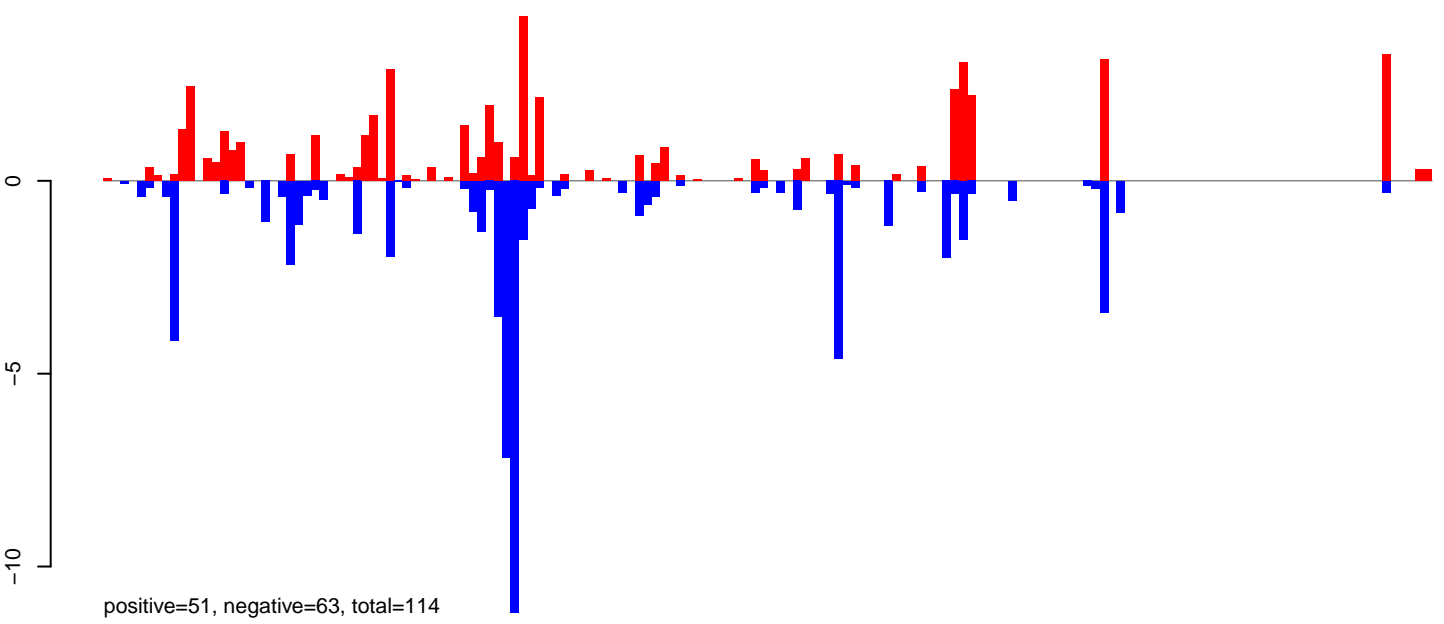


AeAeg_Aag2.SINV.GFP.rep

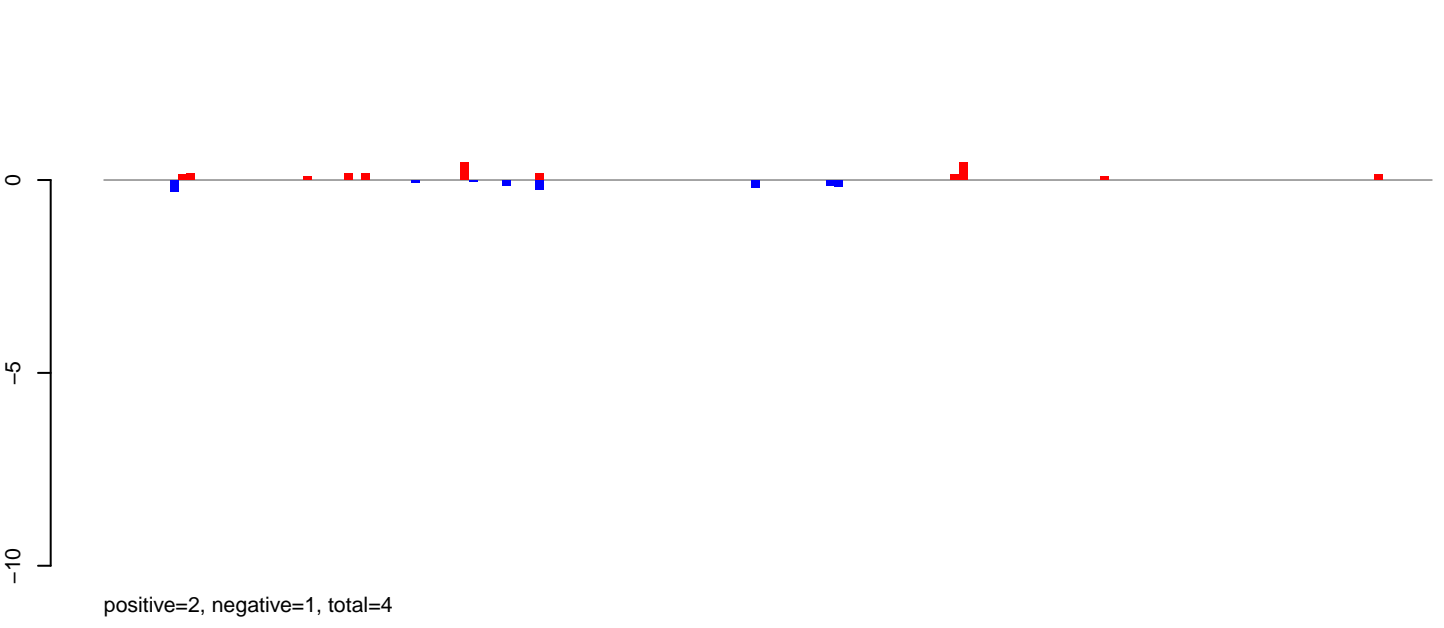


Window size=25, length=2965, virus@AY347953.2-Aedes_aegypti_genomic_sequence:1-2965

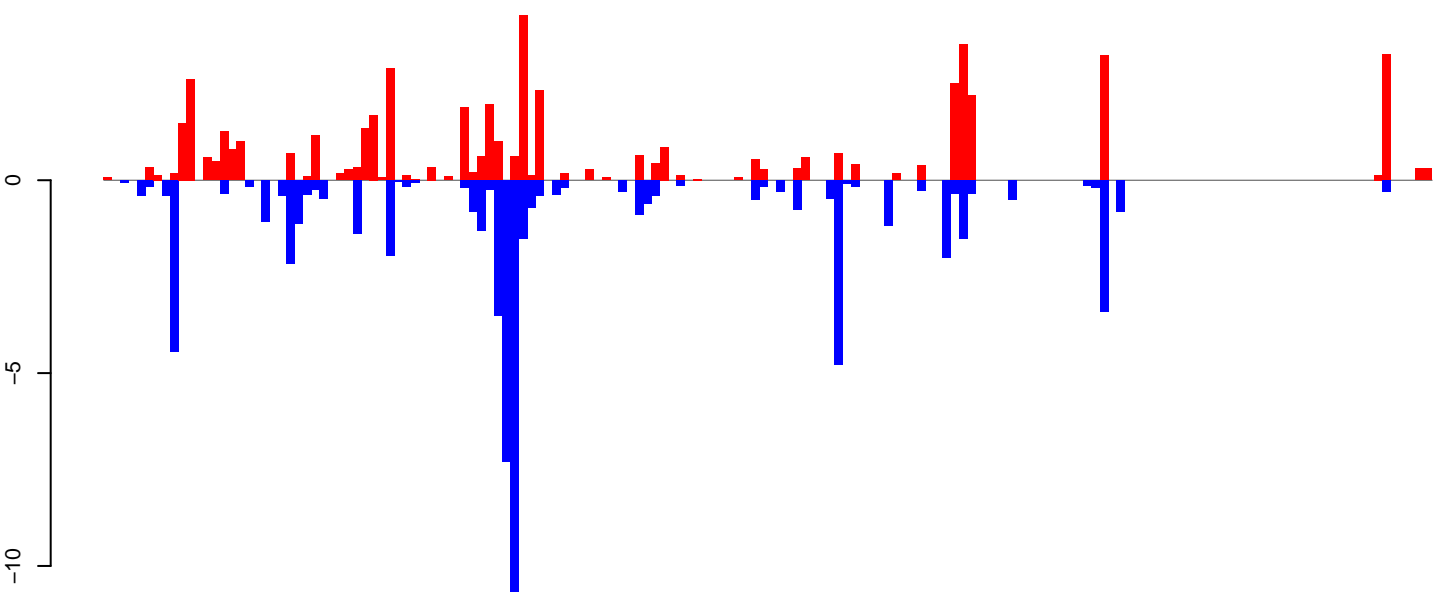
AeAeg_Aag2.SINV.GFP.18_23.rep



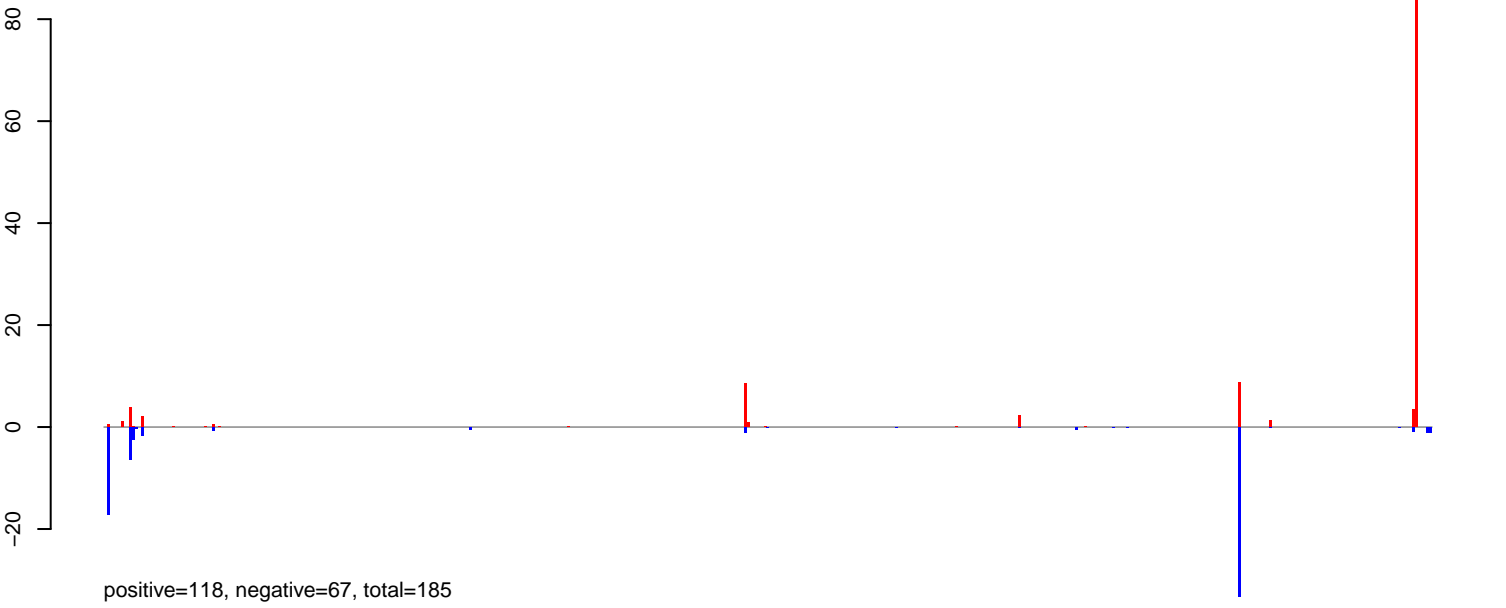
AeAeg_Aag2.SINV.GFP.24_35.rep



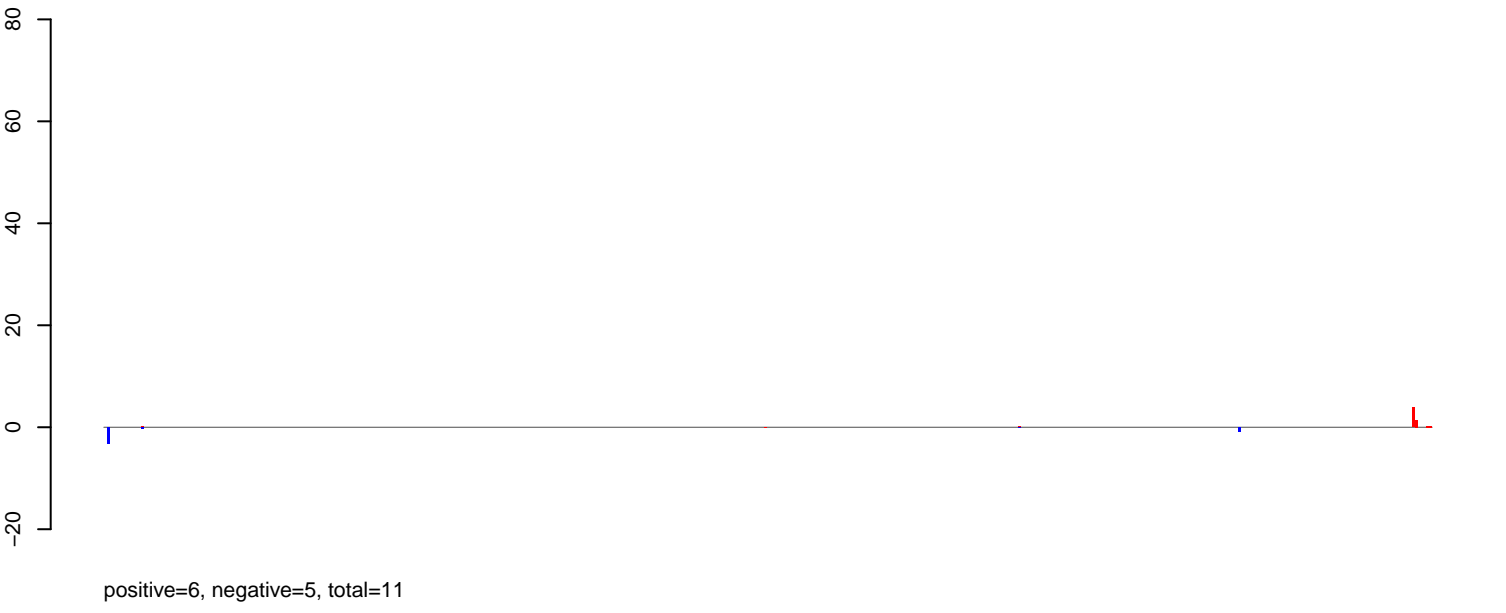
AeAeg_Aag2.SINV.GFP.rep



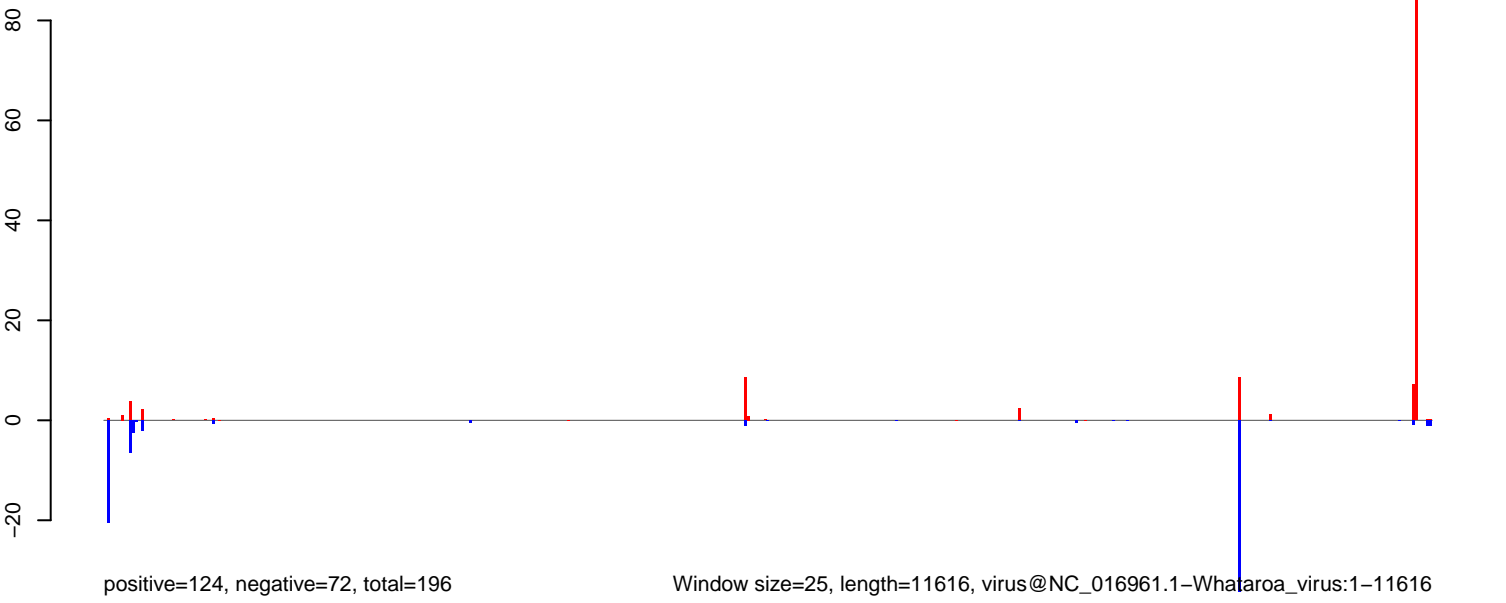
AeAeg_Aag2.SINV.GFP.18_23.rep



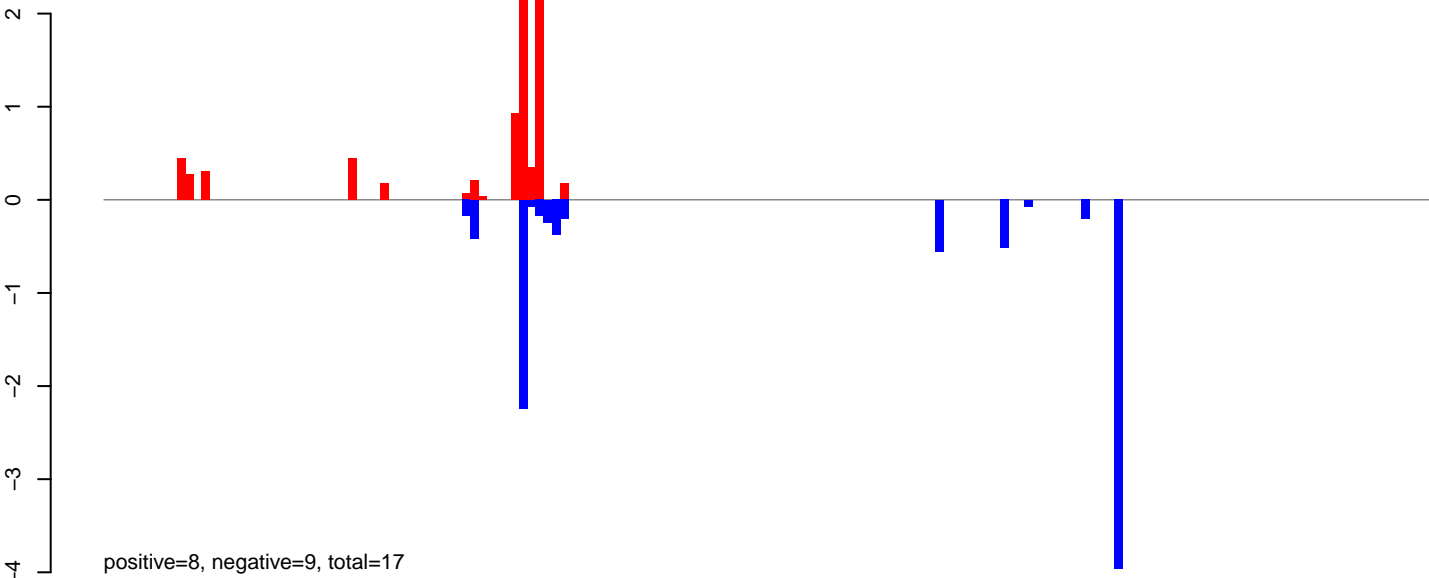
AeAeg_Aag2.SINV.GFP.24_35.rep



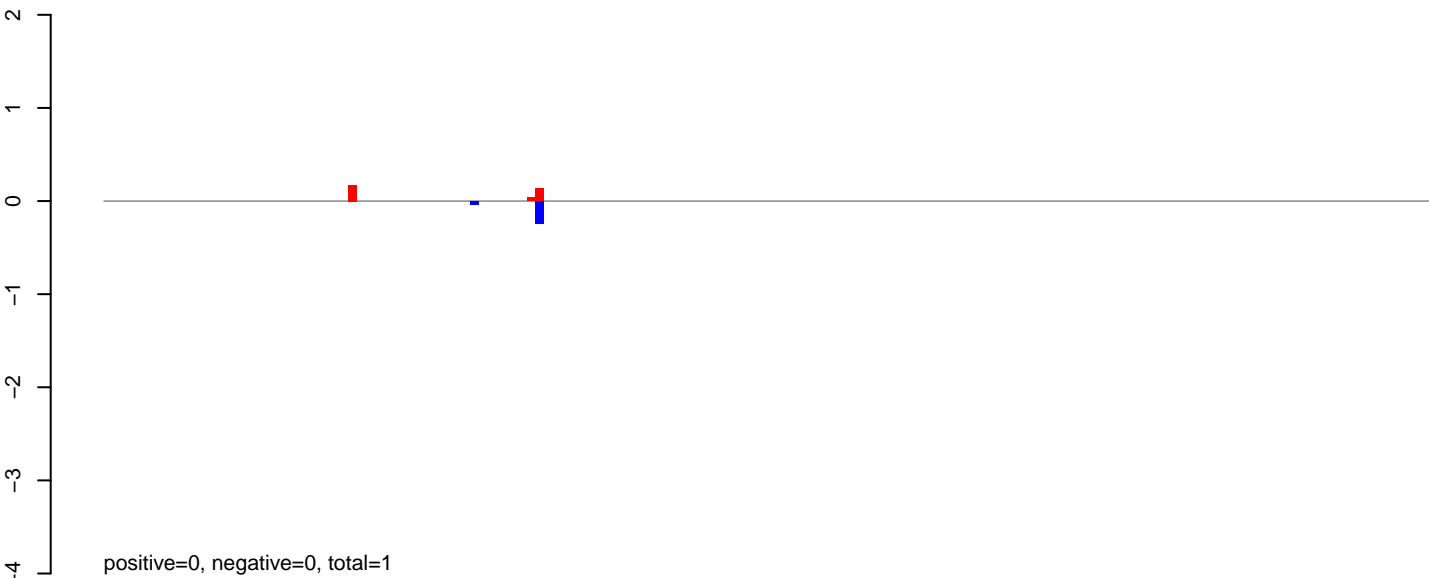
AeAeg_Aag2.SINV.GFP.rep



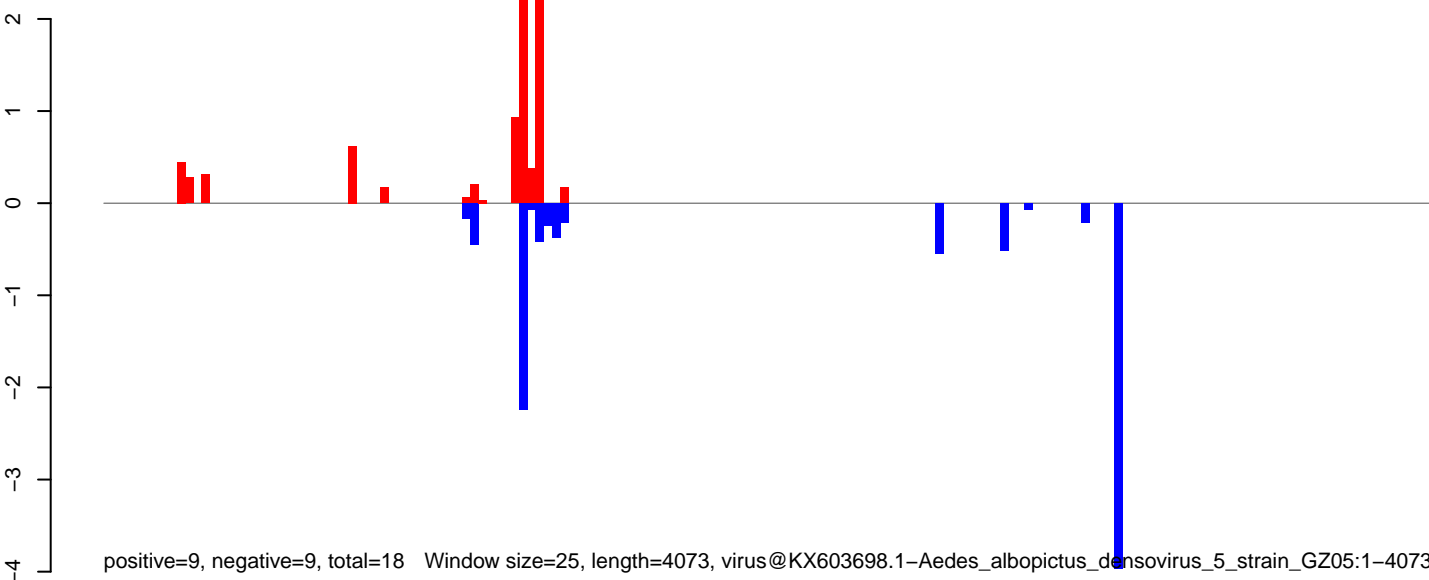
AeAeg_Aag2.SINV.GFP.18_23.rep



AeAeg_Aag2.SINV.GFP.24_35.rep

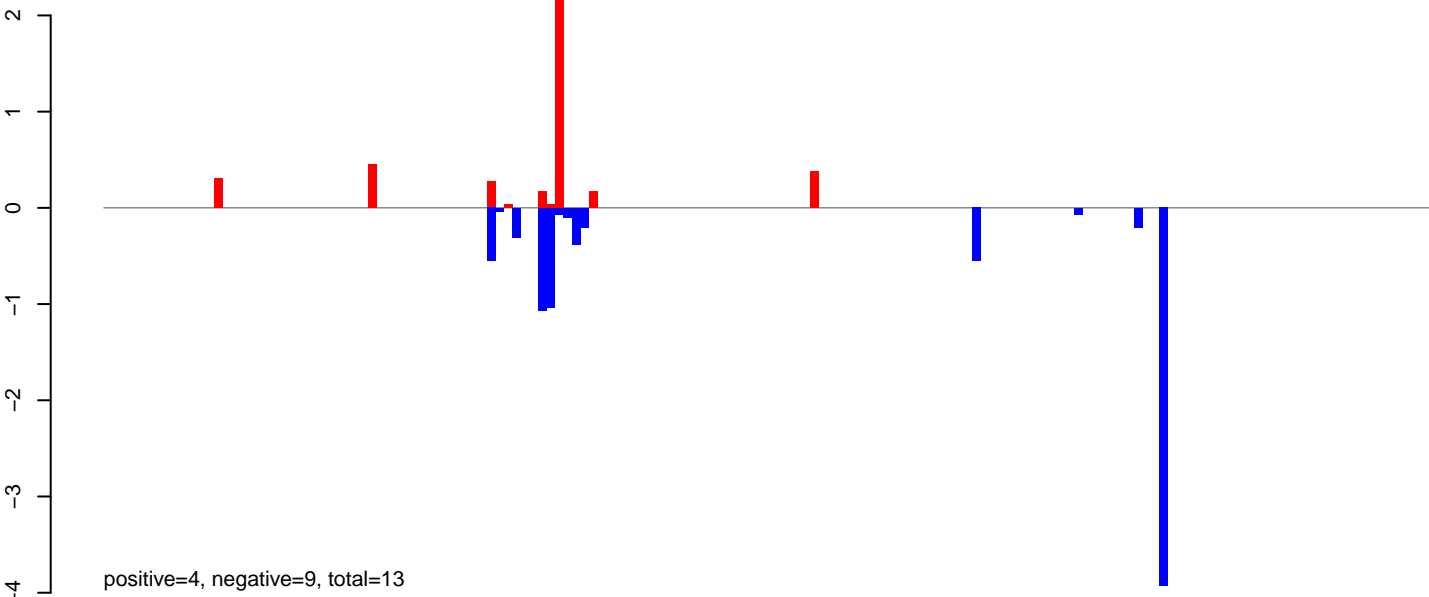


AeAeg_Aag2.SINV.GFP.rep

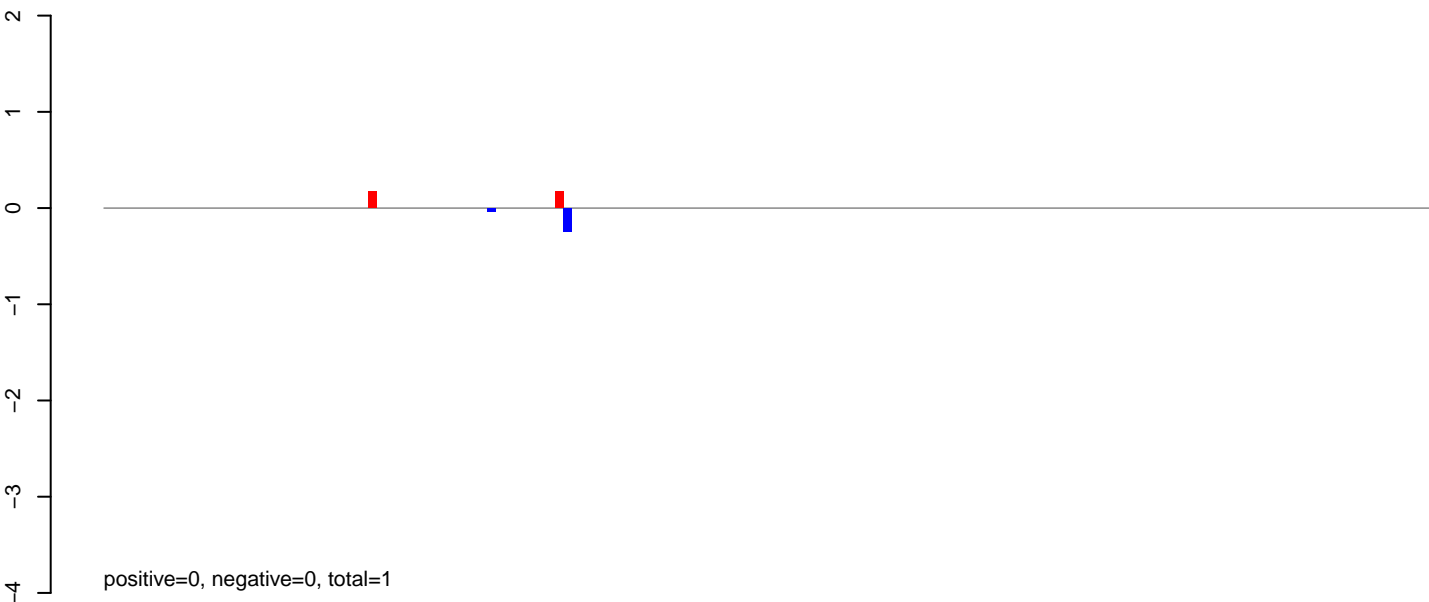


Window size=25, length=4073, virus@KX603698.1-Aedes albopictus_densovirus_5_strain_GZ05:1-4073

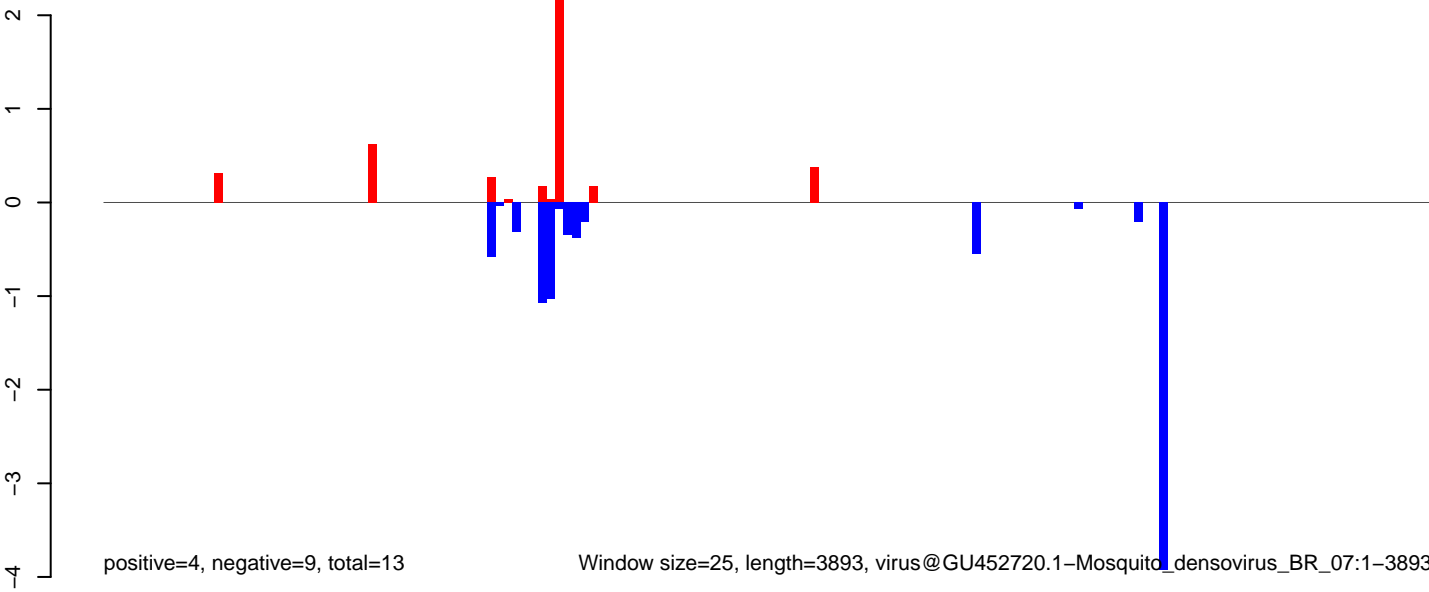
AeAeg_Aag2.SINV.GFP.18_23.rep



AeAeg_Aag2.SINV.GFP.24_35.rep



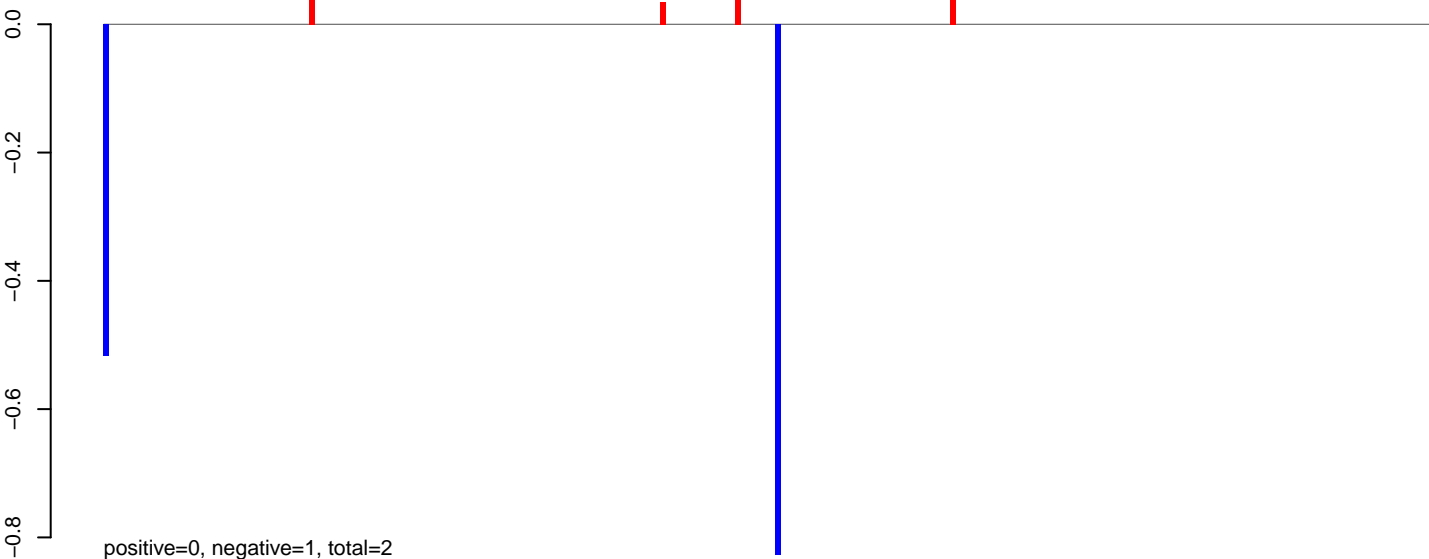
AeAeg_Aag2.SINV.GFP.rep



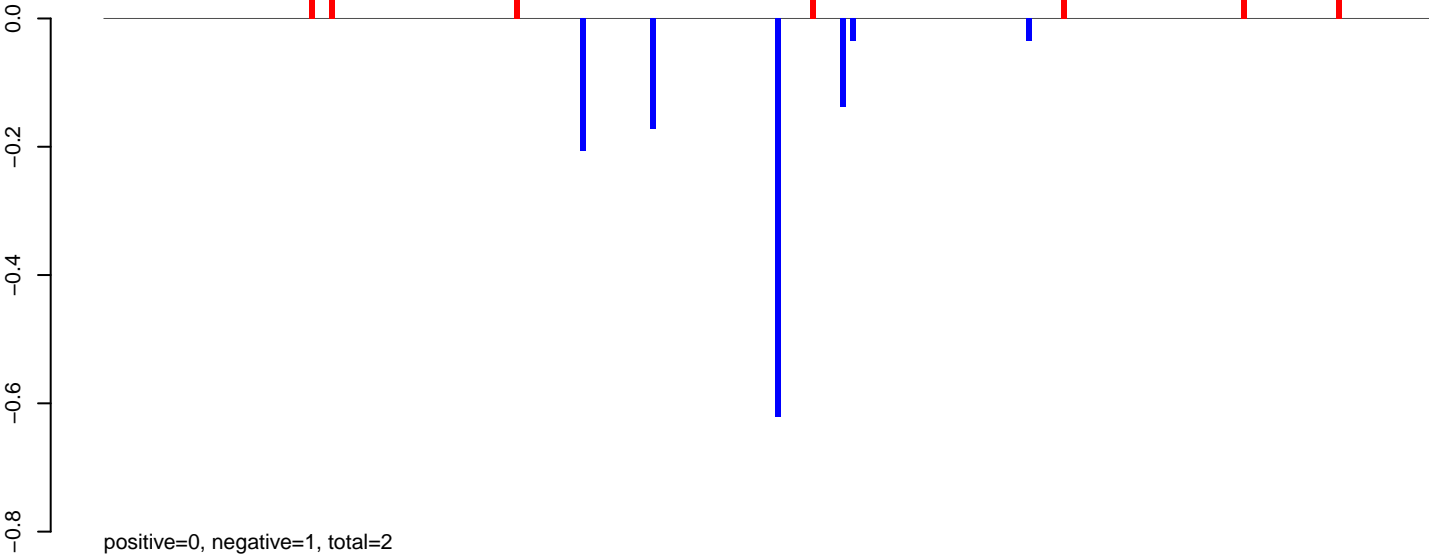
Window size=25, length=3893, virus@GU452720.1-Mosquito_densovirus_BR_07:1-3893

0 1000 2000 3000 4000

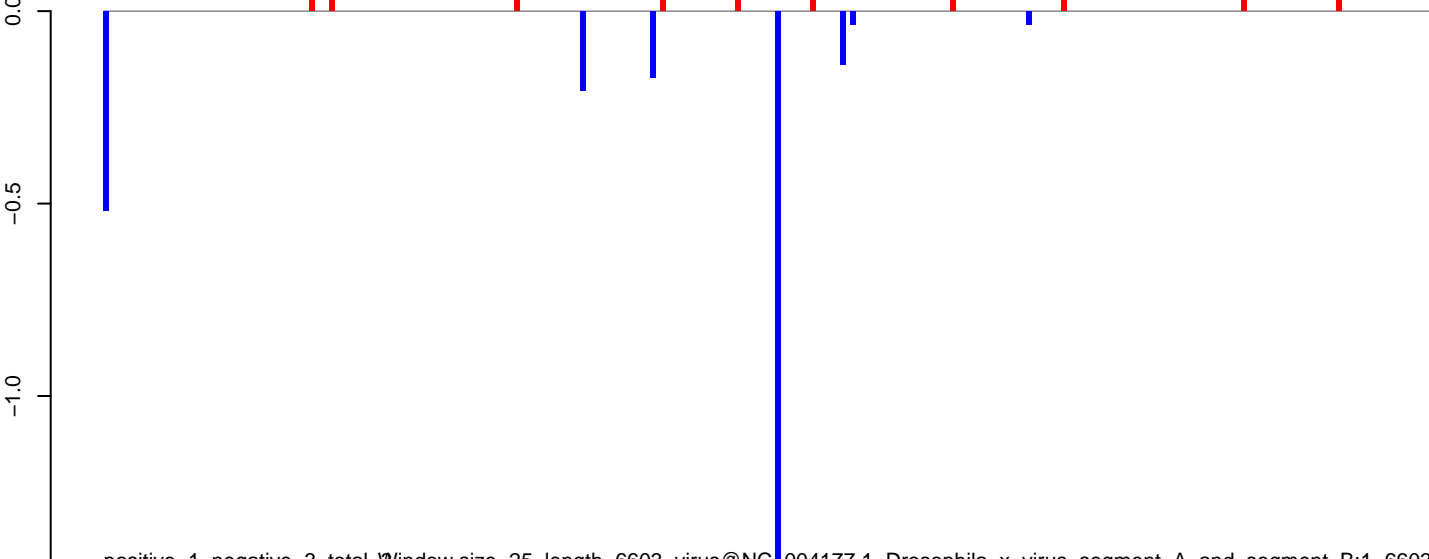
AeAeg_Aag2.SINV.GFP.18_23.rep



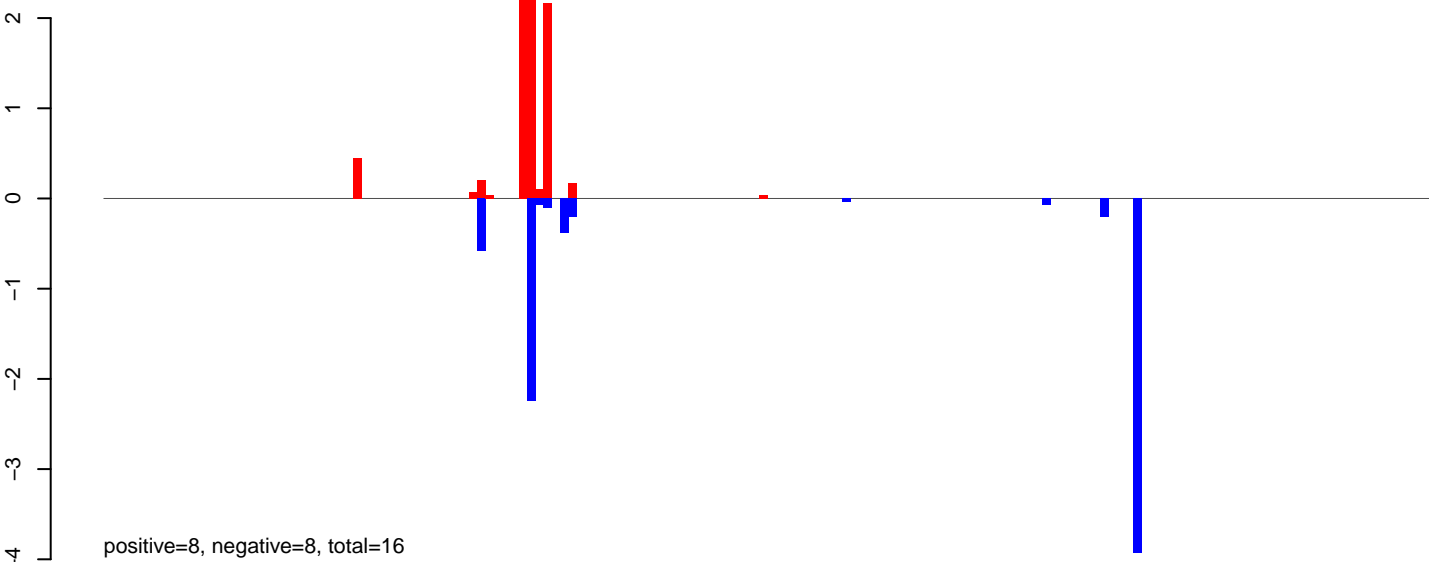
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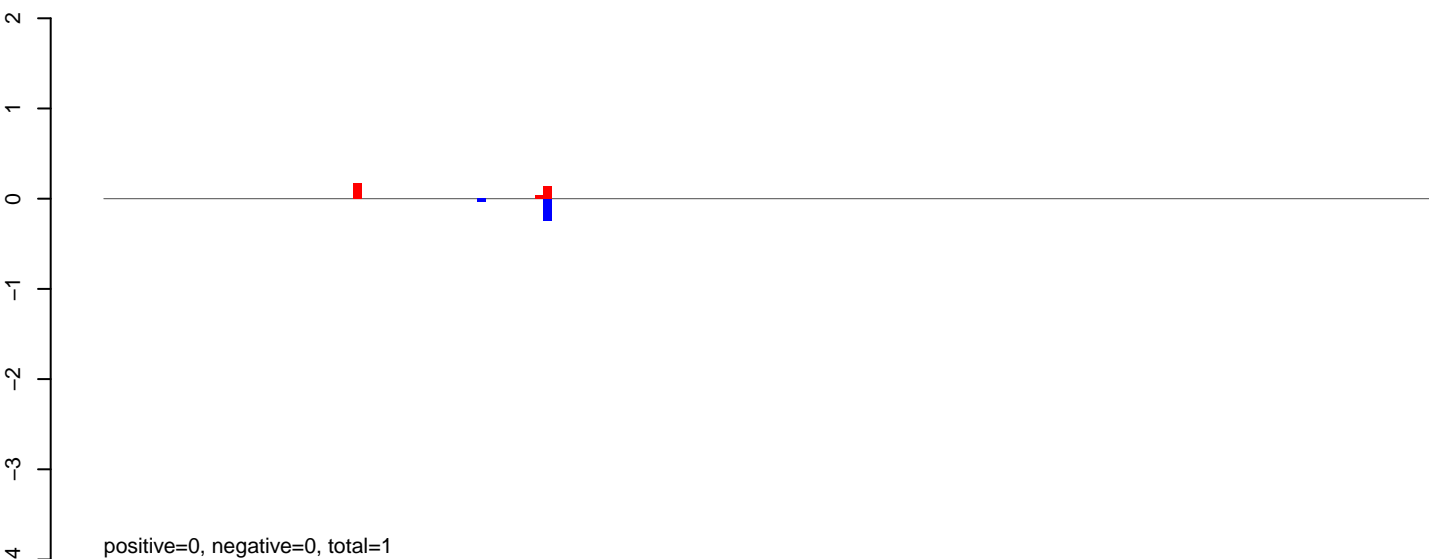
AeAeg_Aag2.SINV.GFP.rep



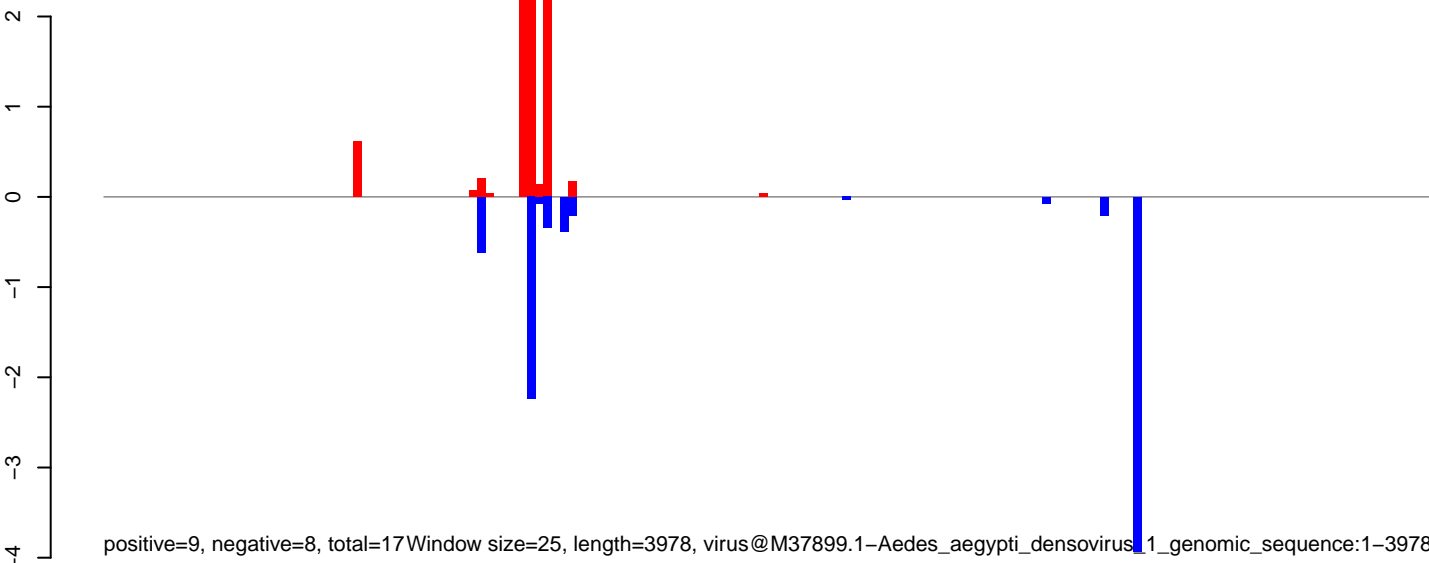
AeAeg_Aag2.SINV.GFP.18_23.rep



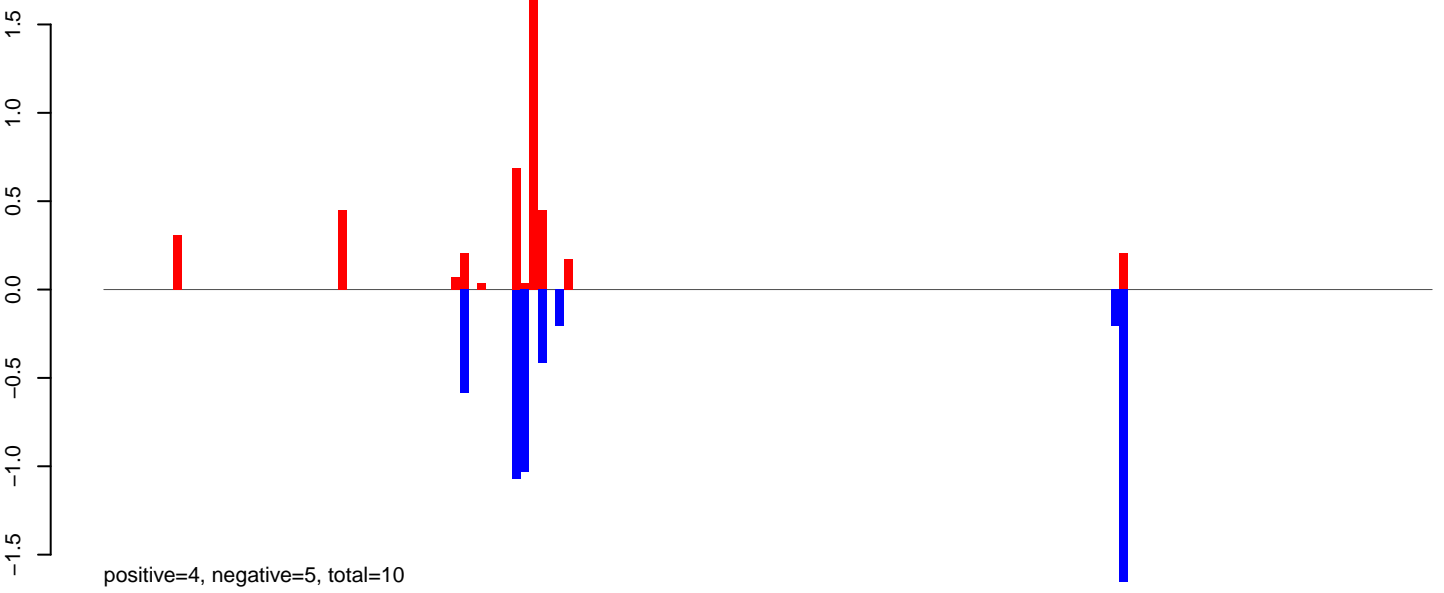
AeAeg_Aag2.SINV.GFP.24_35.rep



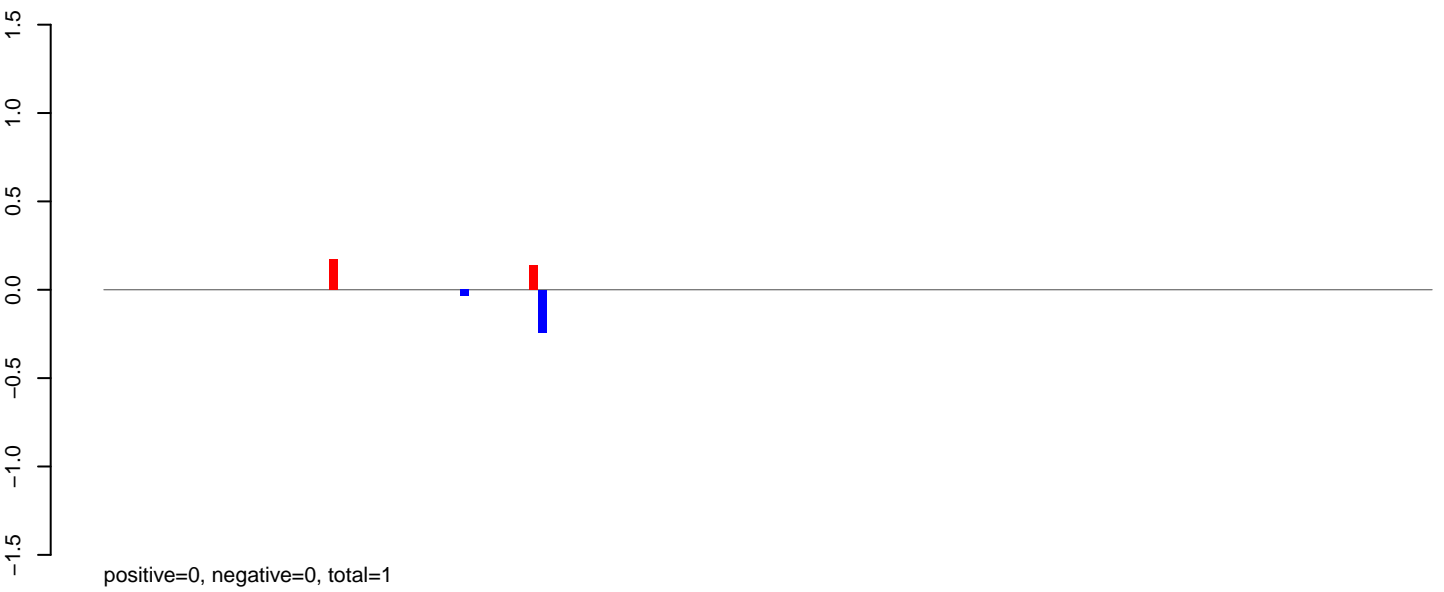
AeAeg_Aag2.SINV.GFP.rep



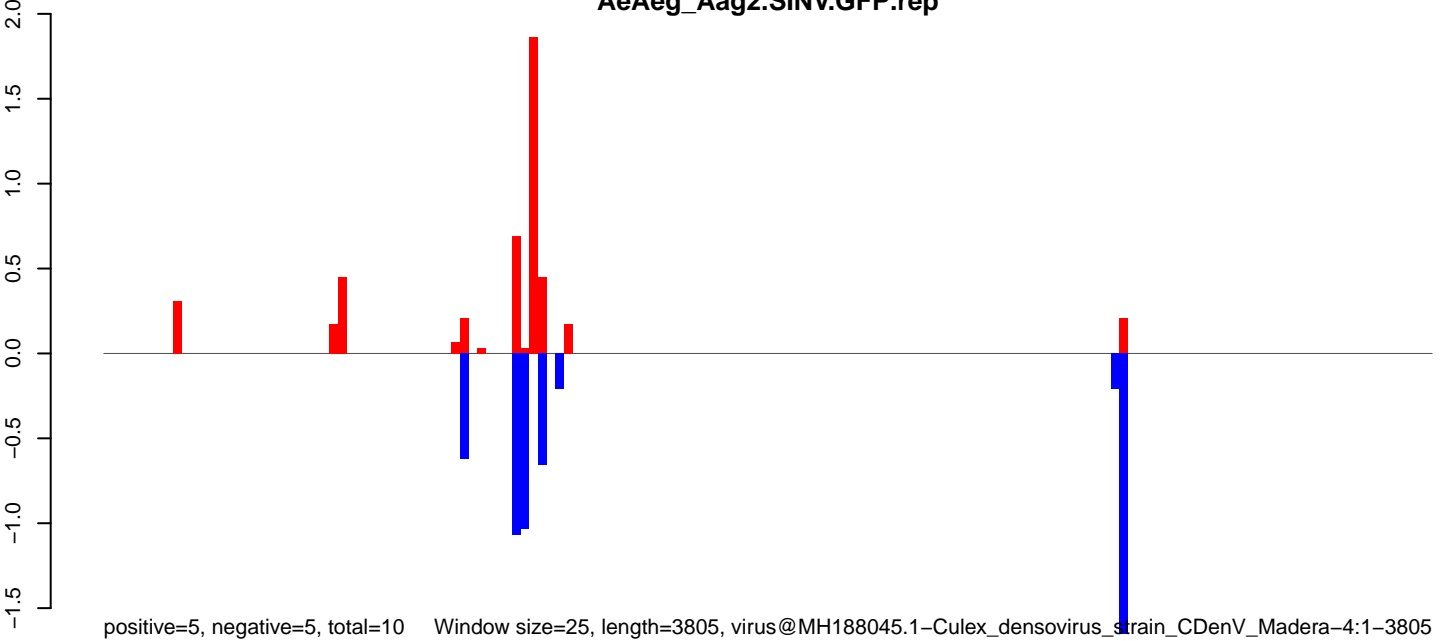
AeAeg_Aag2.SINV.GFP.18_23.rep



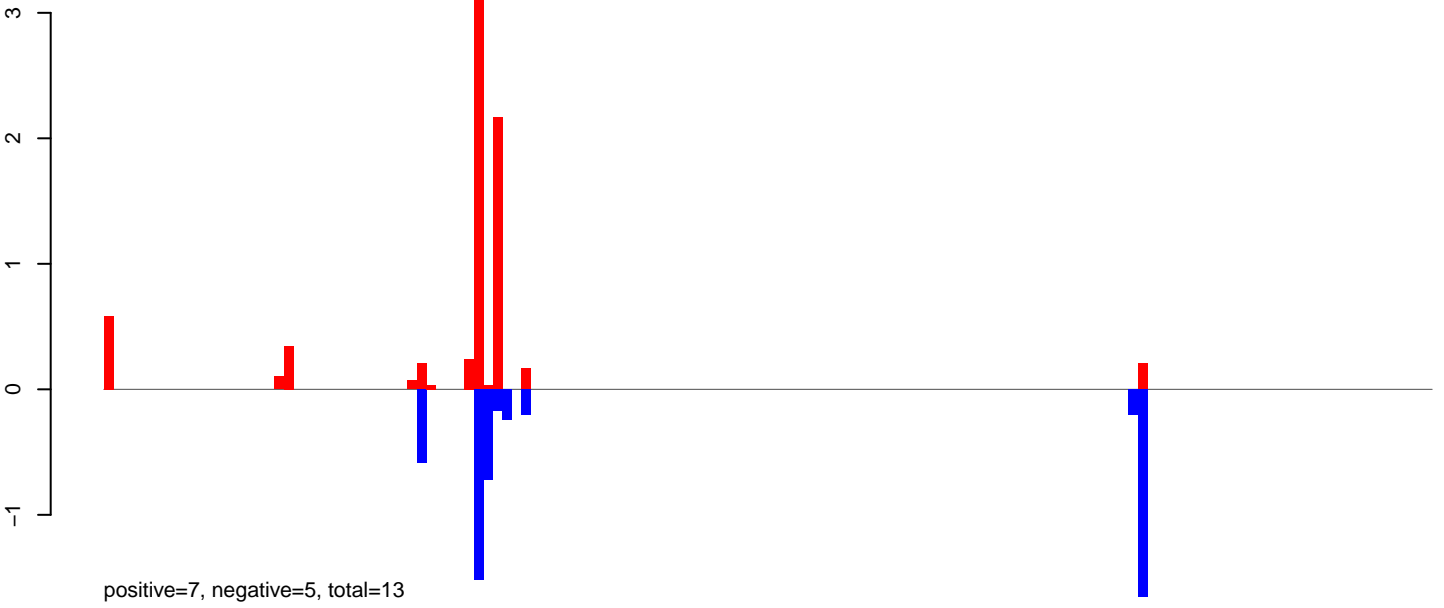
AeAeg_Aag2.SINV.GFP.24_35.rep



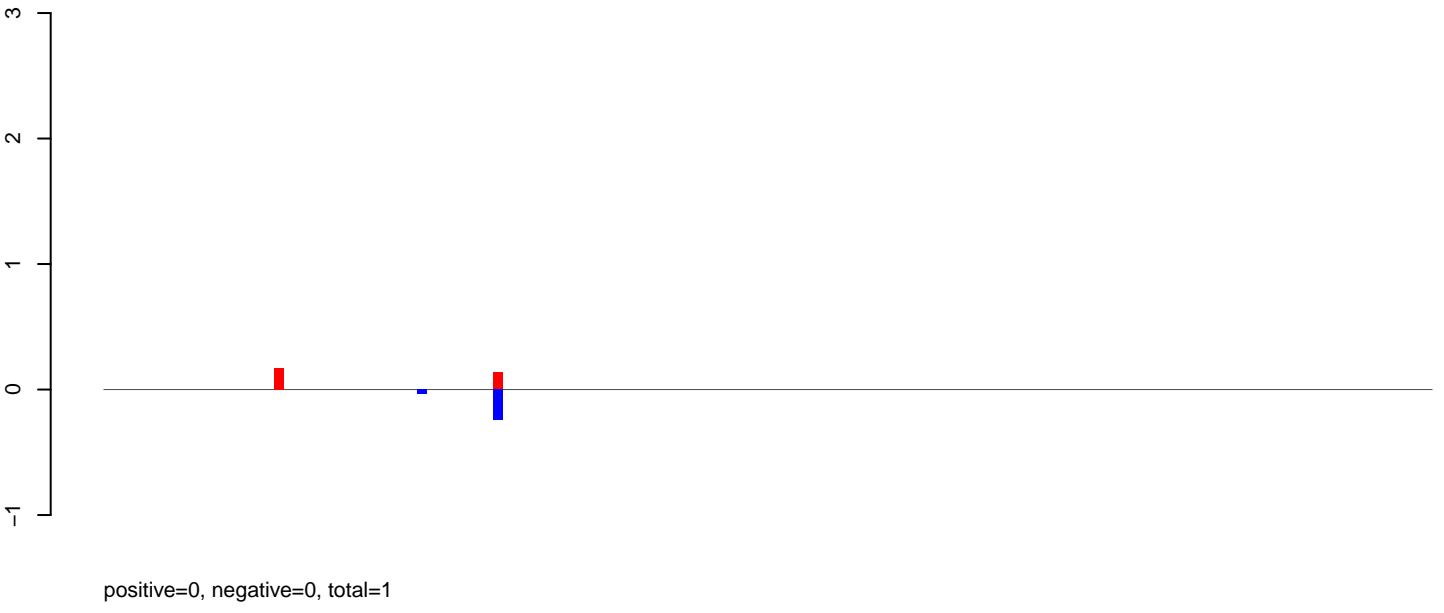
AeAeg_Aag2.SINV.GFP.rep



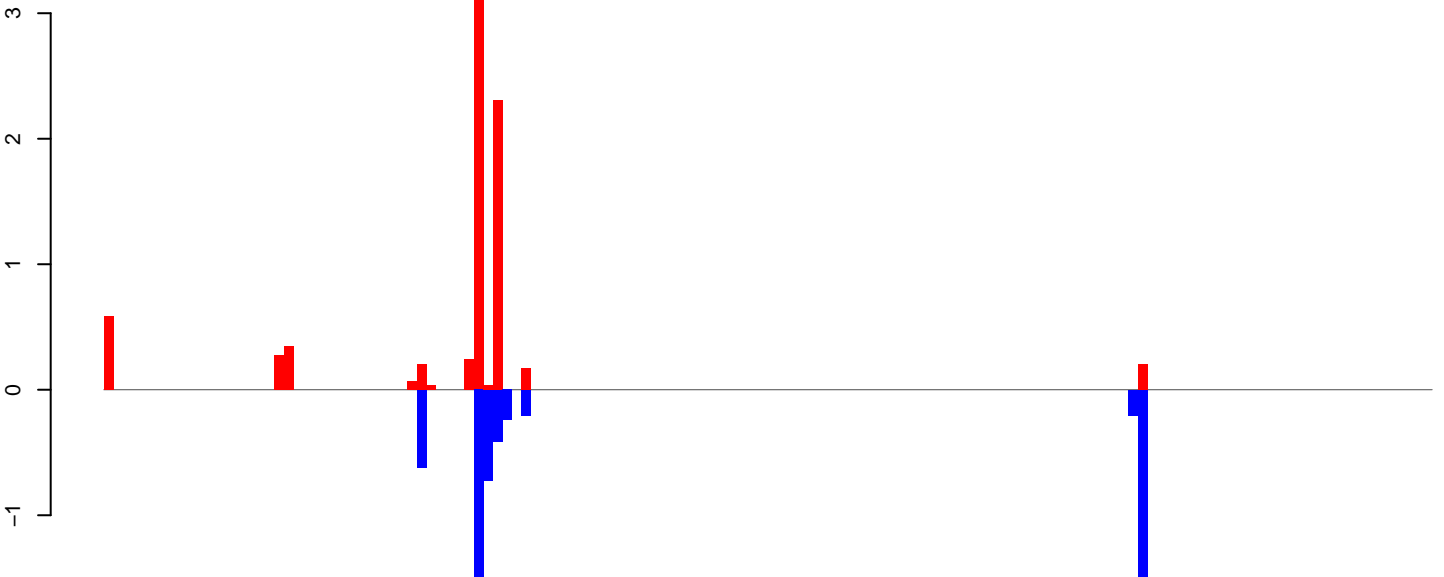
AeAeg_Aag2.SINV.GFP.18_23.rep



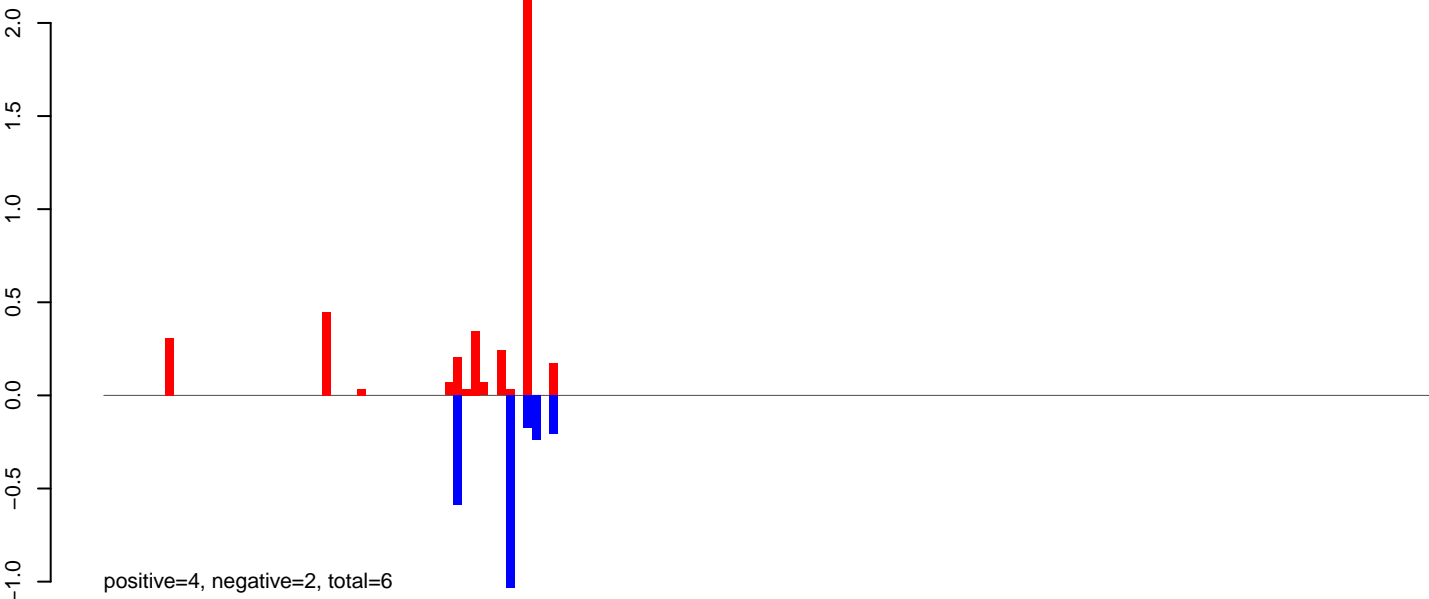
AeAeg_Aag2.SINV.GFP.24_35.rep



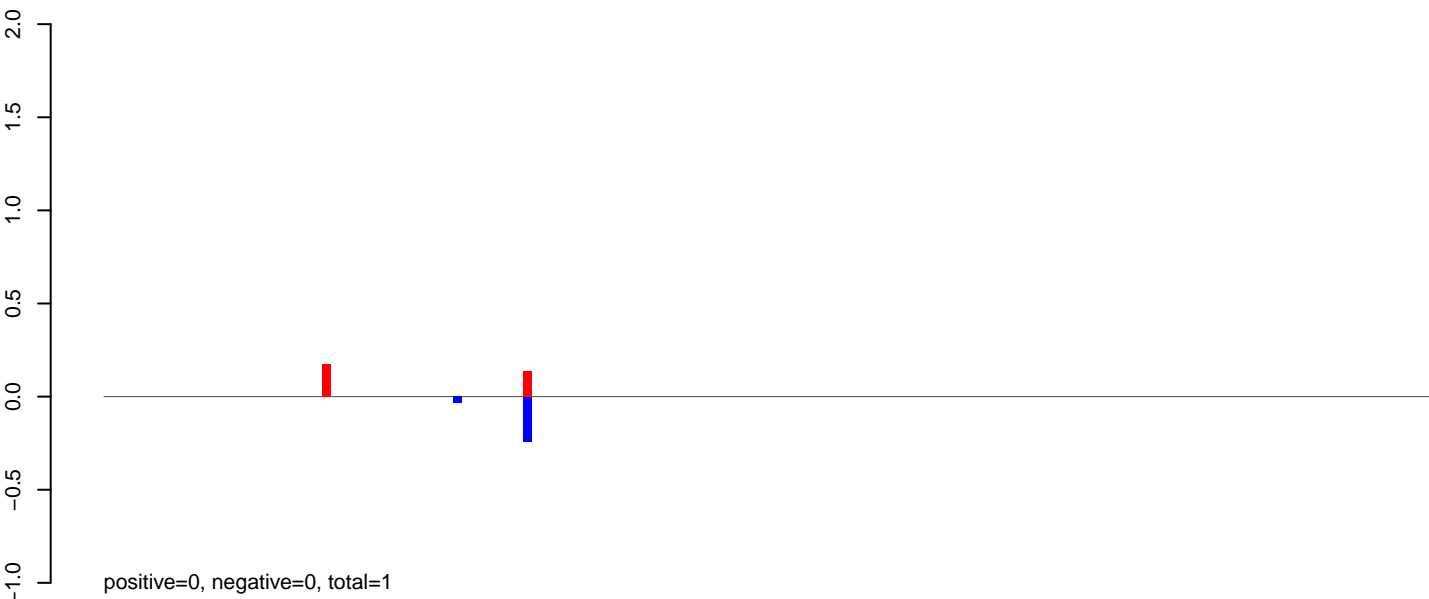
AeAeg_Aag2.SINV.GFP.rep



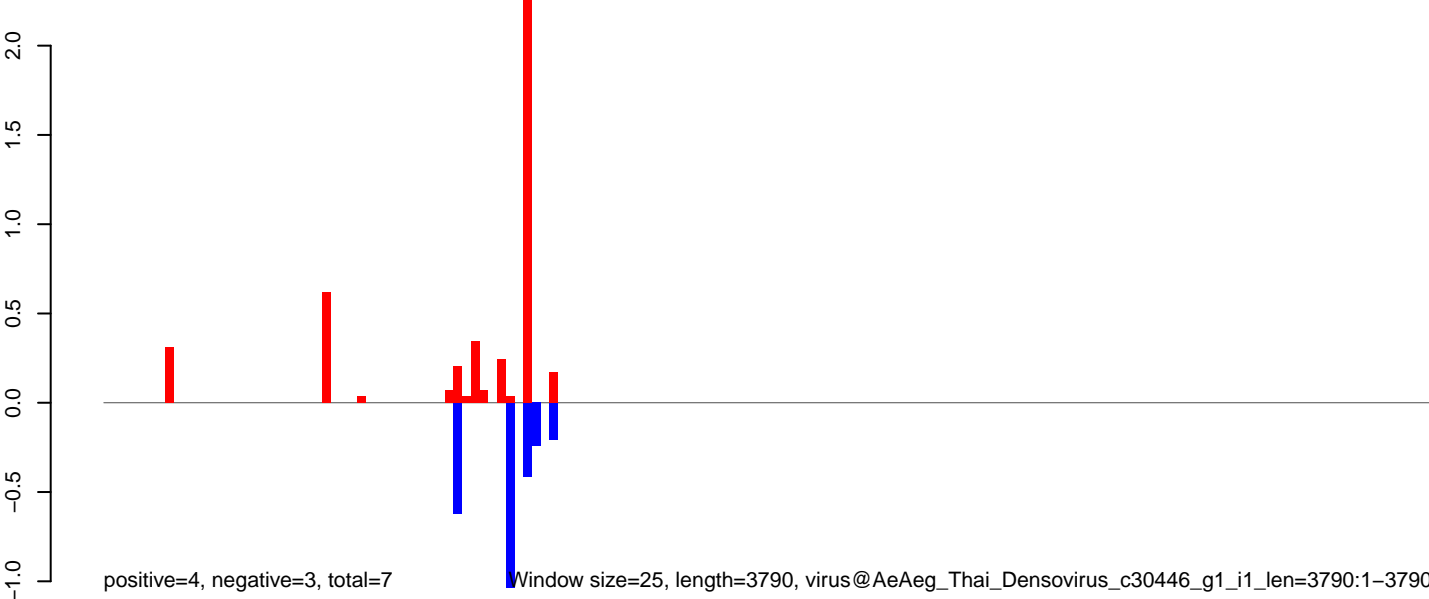
AeAeg_Aag2.SINV.GFP.18_23.rep



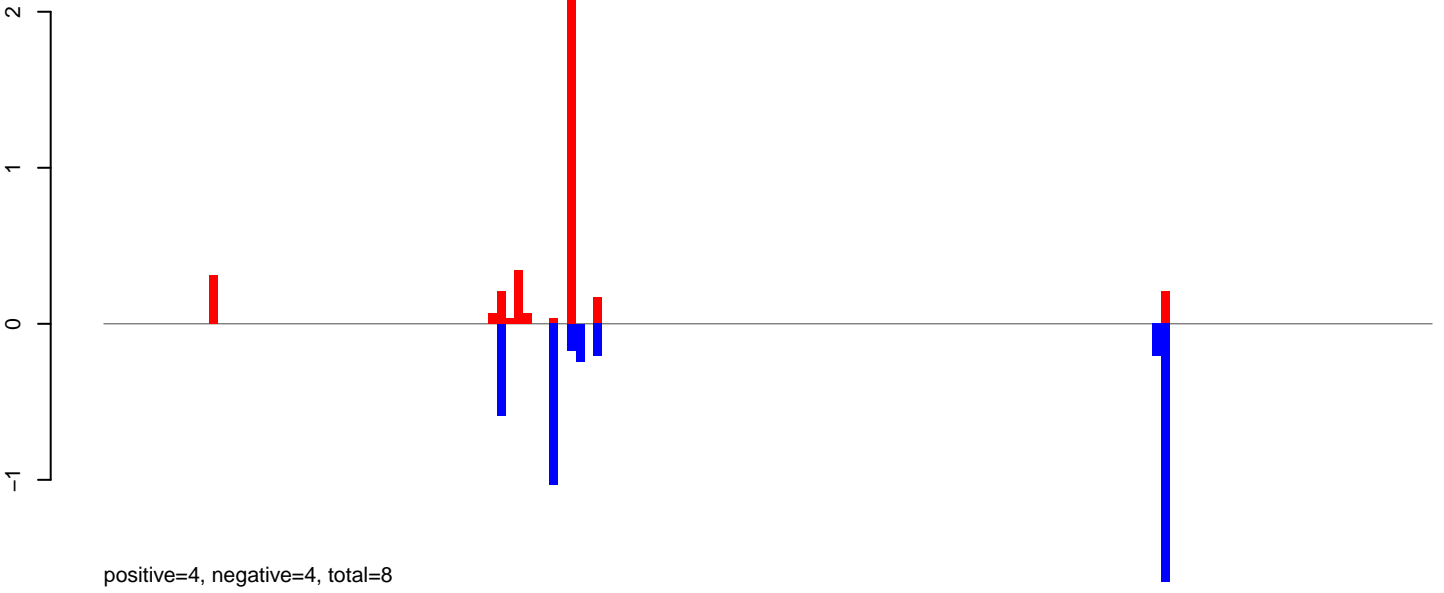
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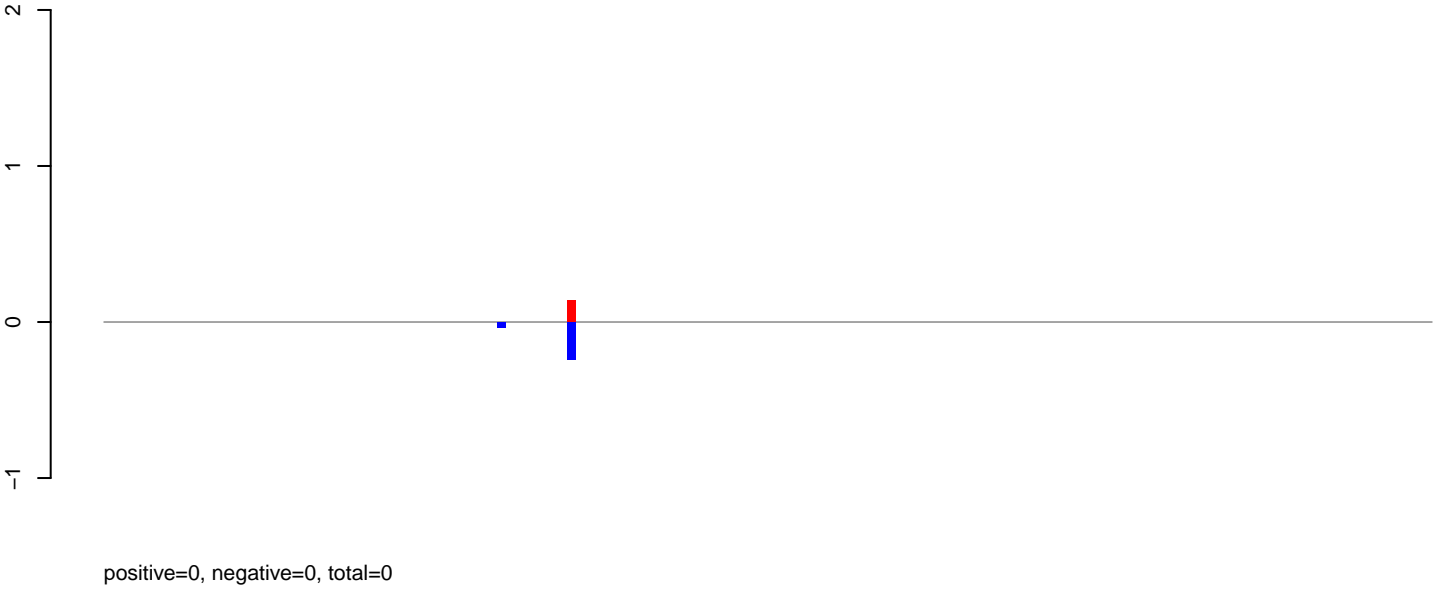
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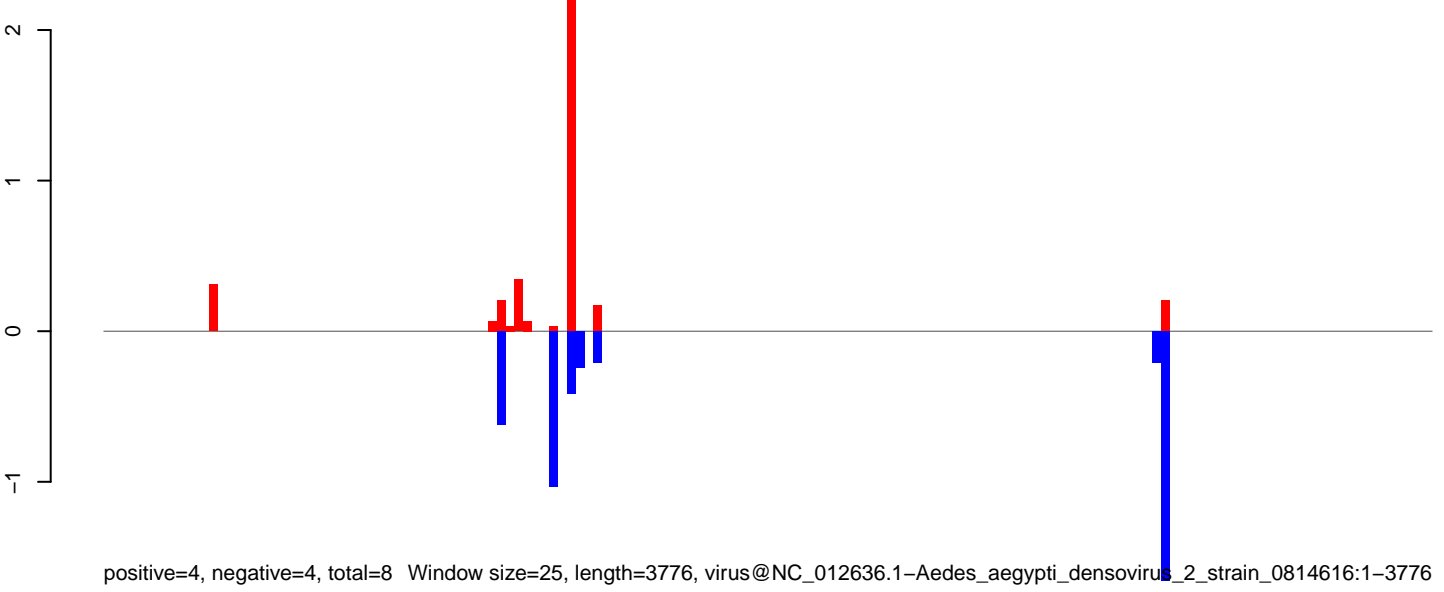
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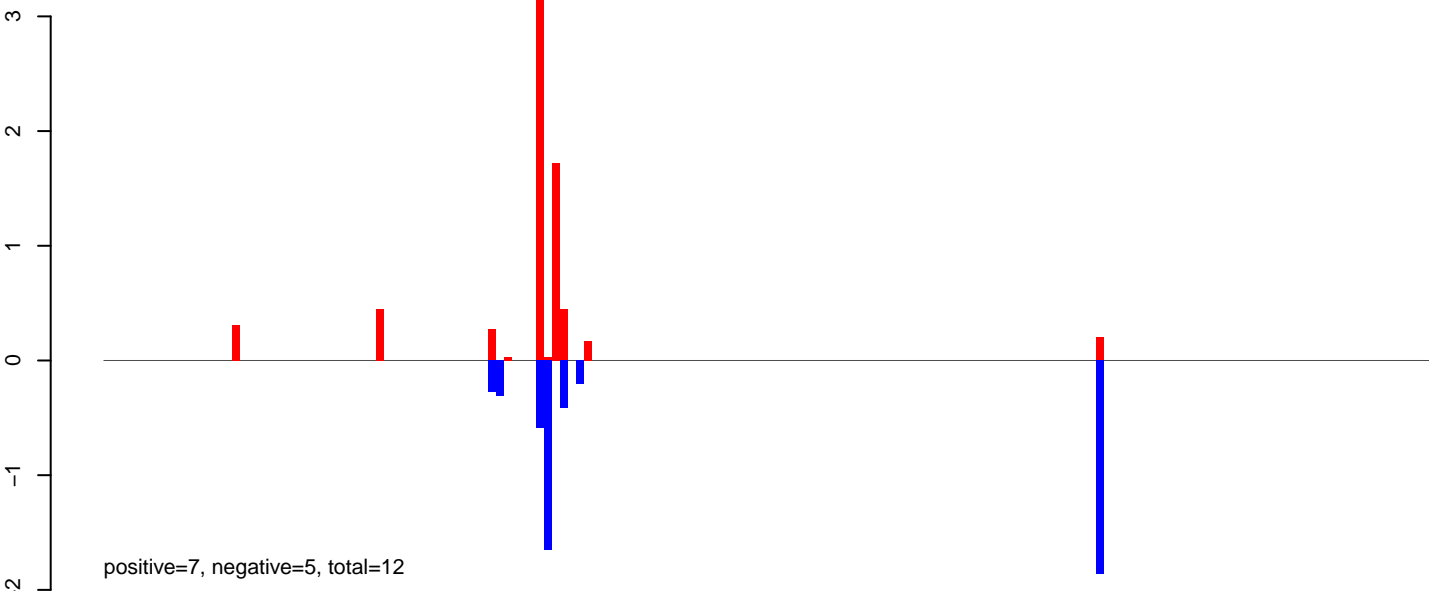
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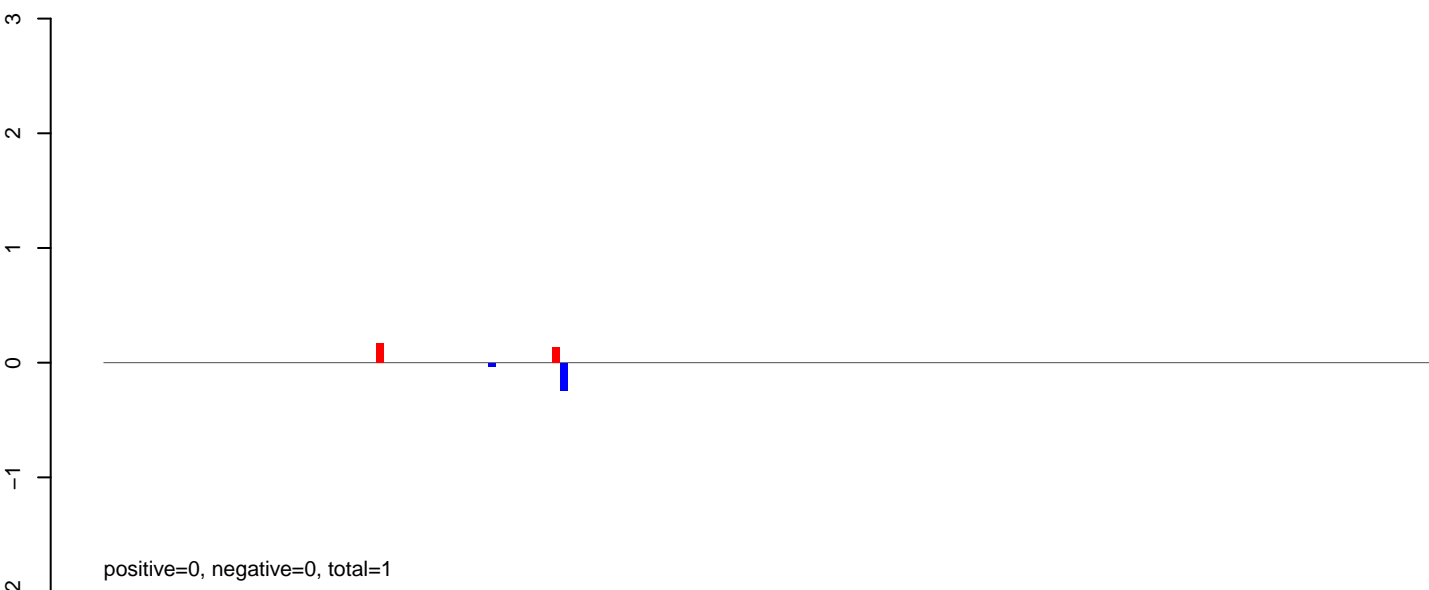
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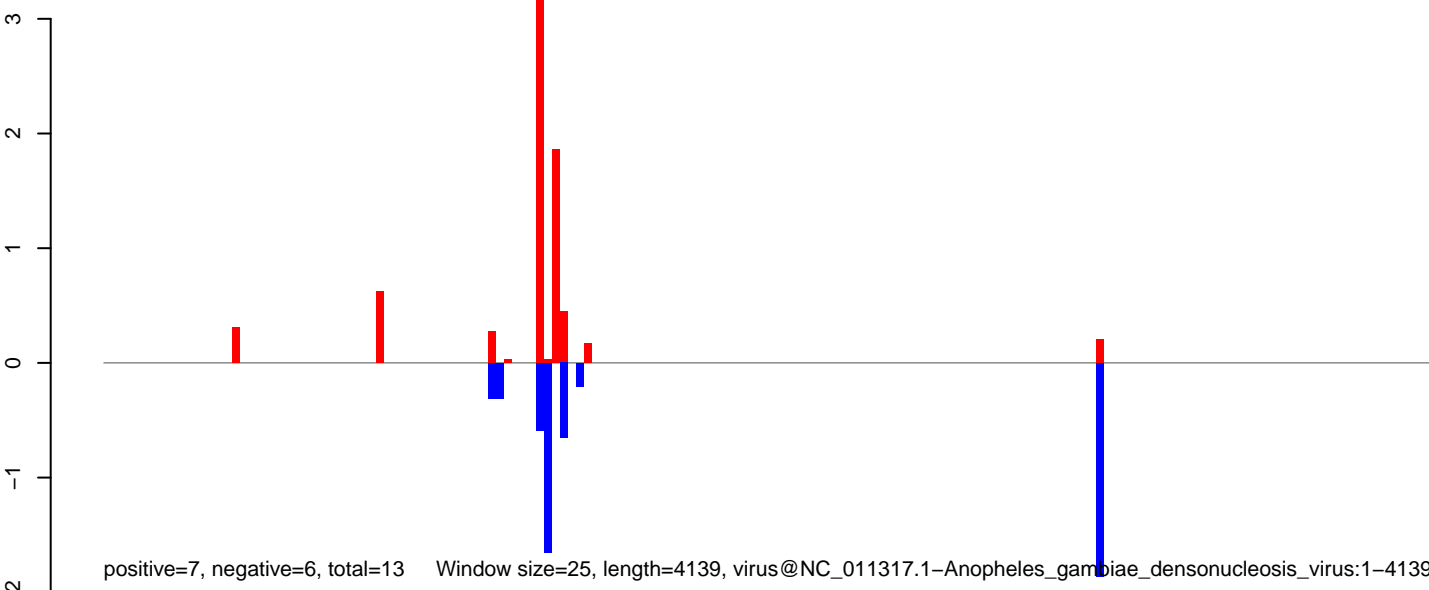
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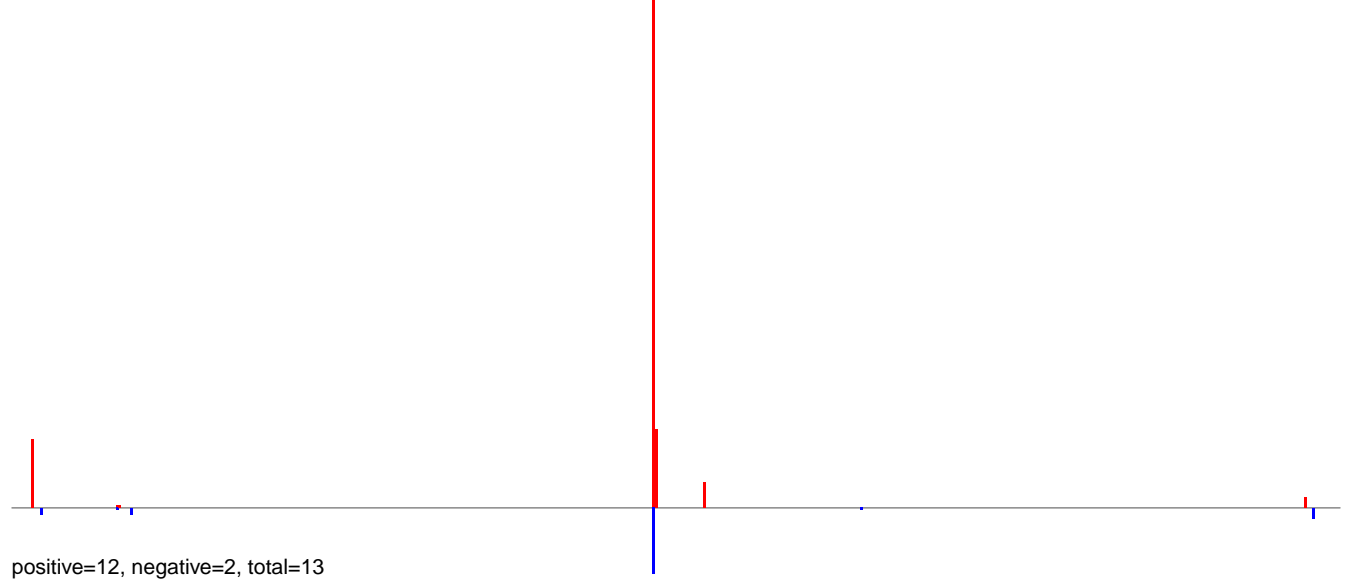
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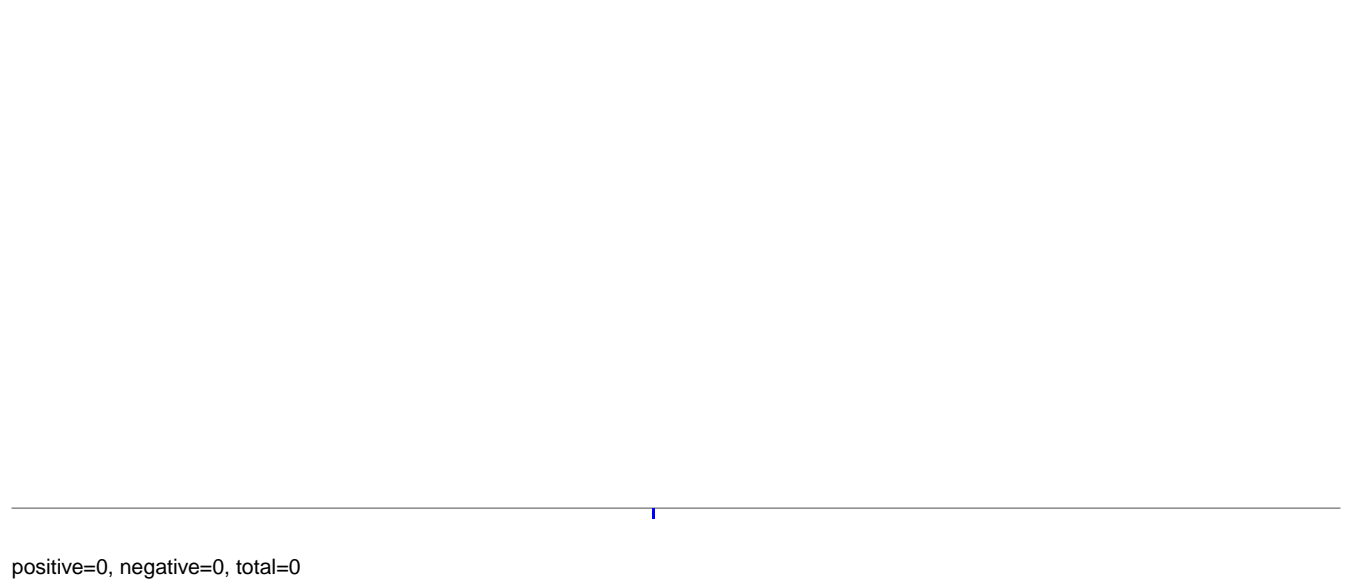
AeAeg_Aag2.SINV.GFP.rep



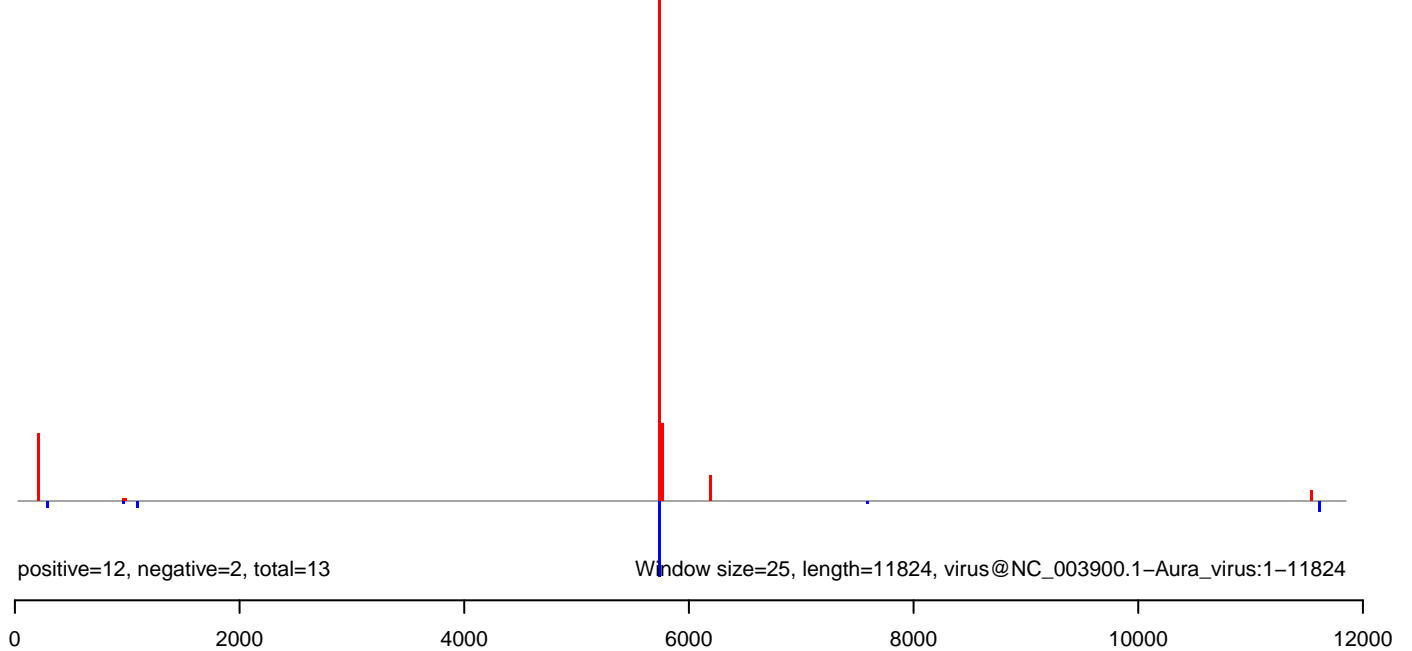
AeAeg_Aag2.SINV.GFP.18_23.rep



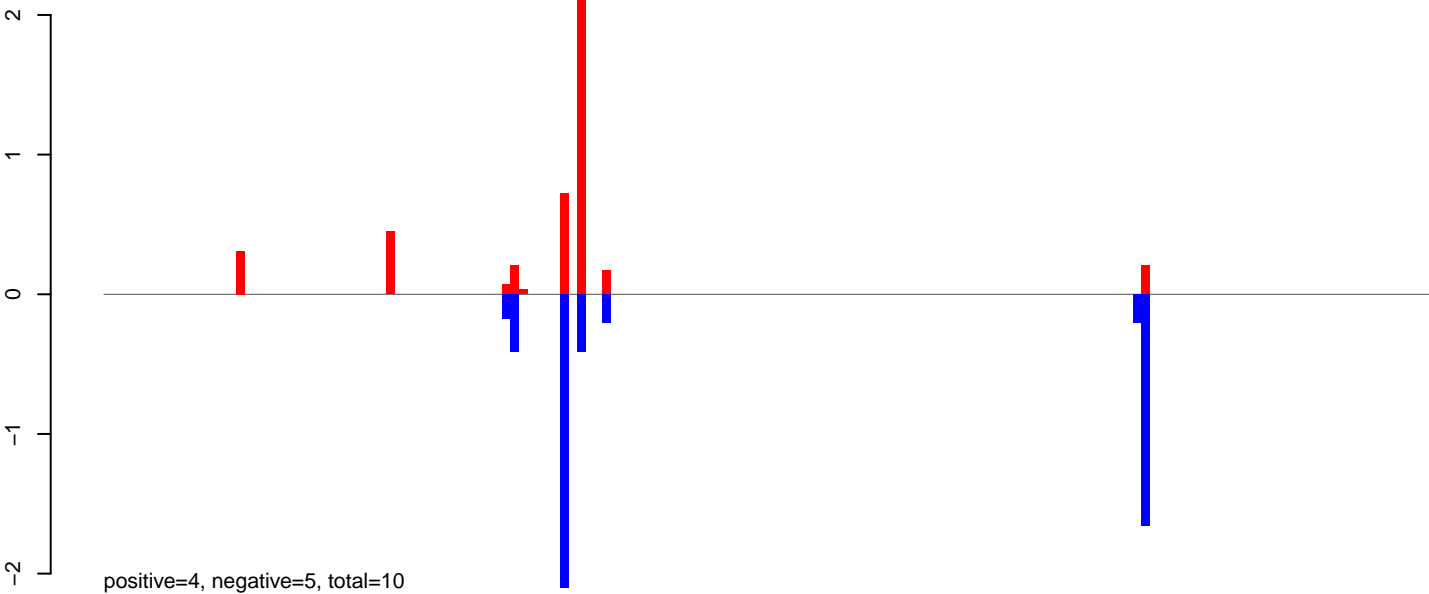
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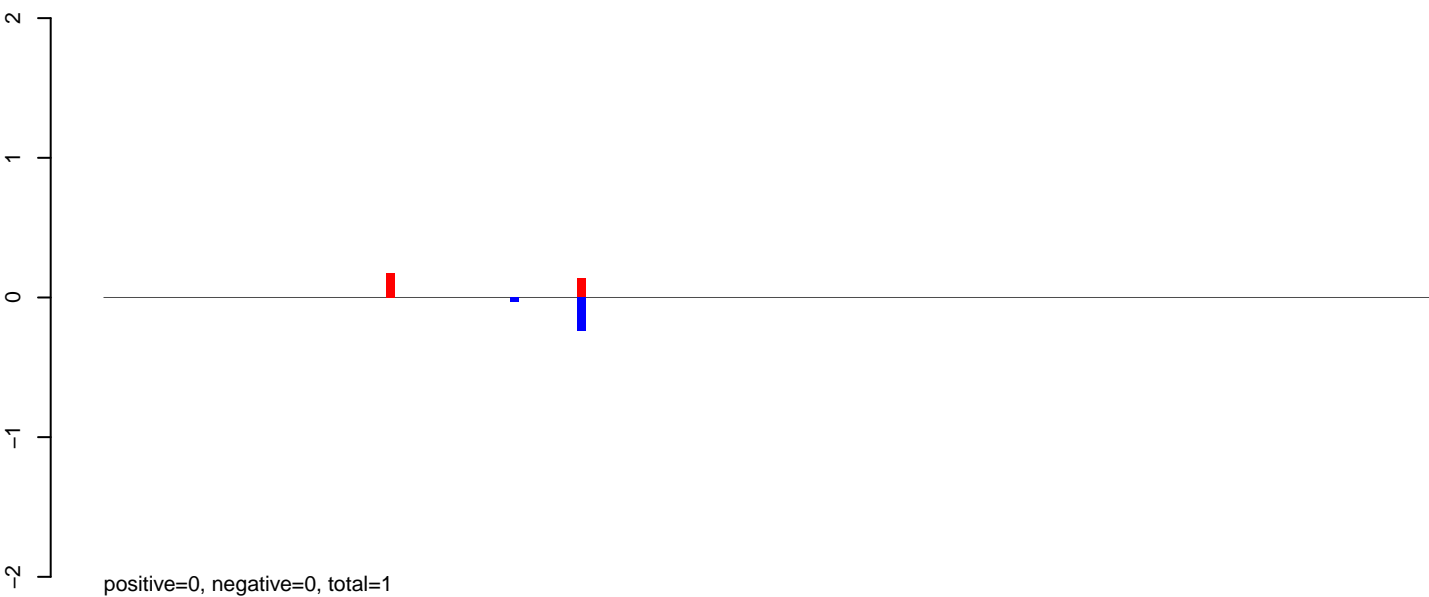
AeAeg_Aag2.SINV.GFP.rep



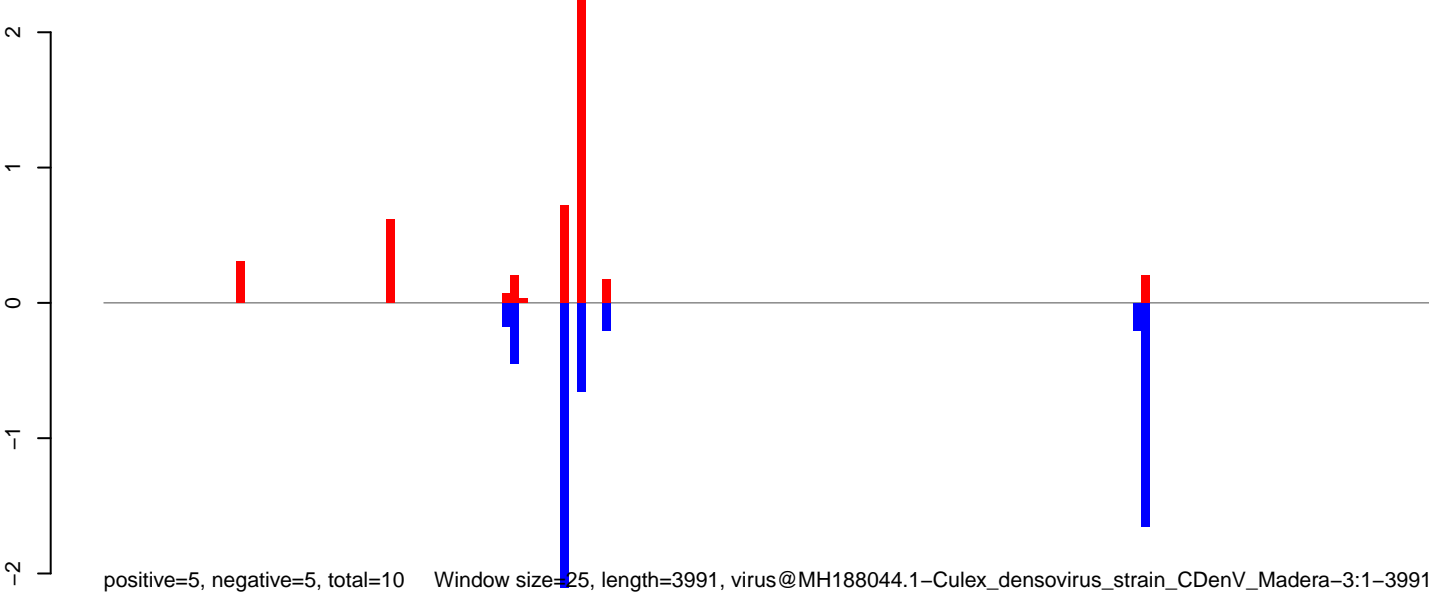
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AeAeg_Aag2.SINV.GFP.24_35.rep



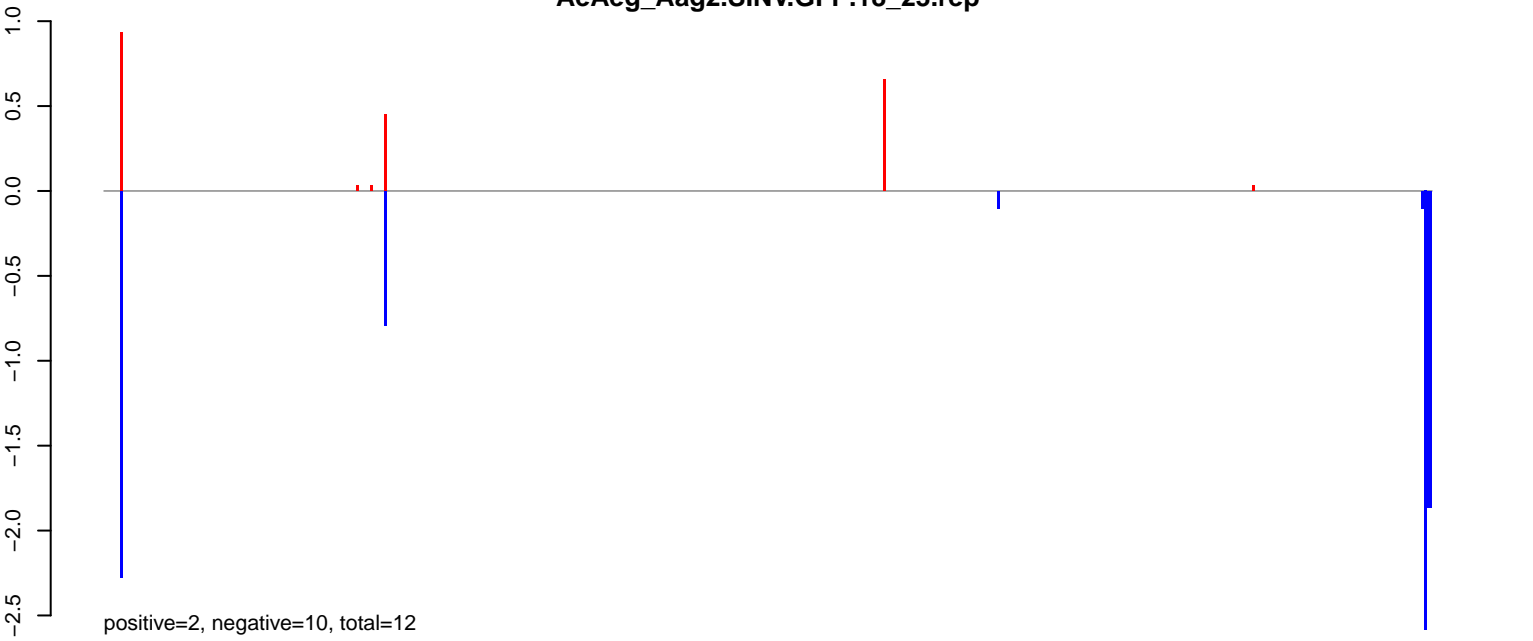
AeAeg_Aag2.SINV.GFP.rep



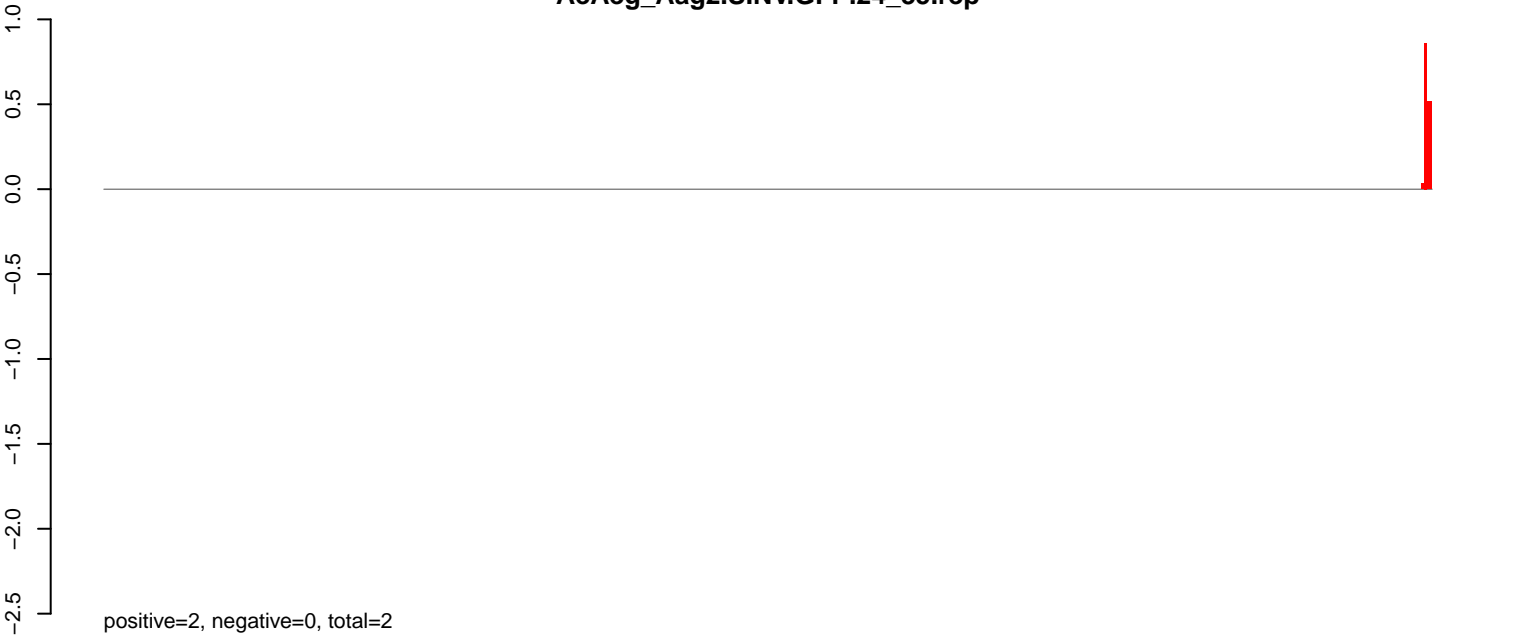
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0 1000 2000 3000 4000

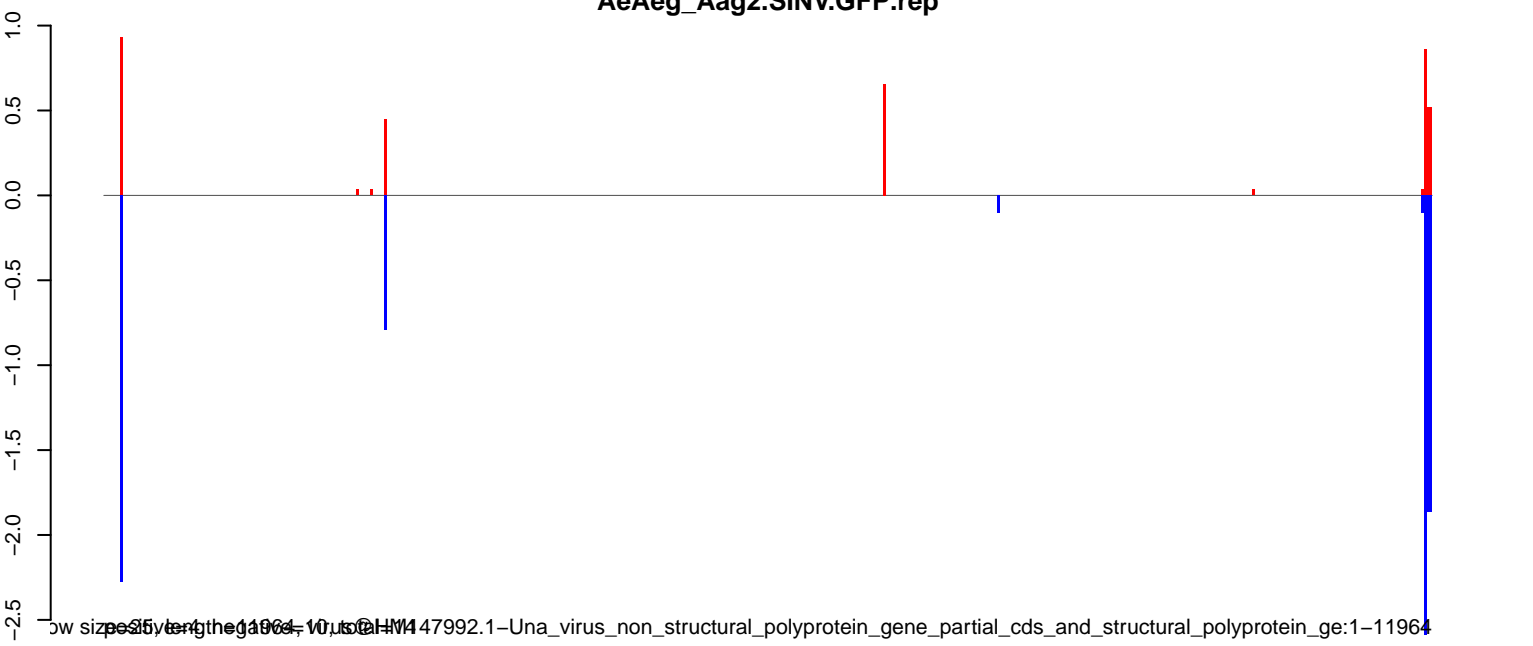
AeAeg_Aag2.SINV.GFP.18_23.rep



AeAeg_Aag2.SINV.GFP.24_35.rep

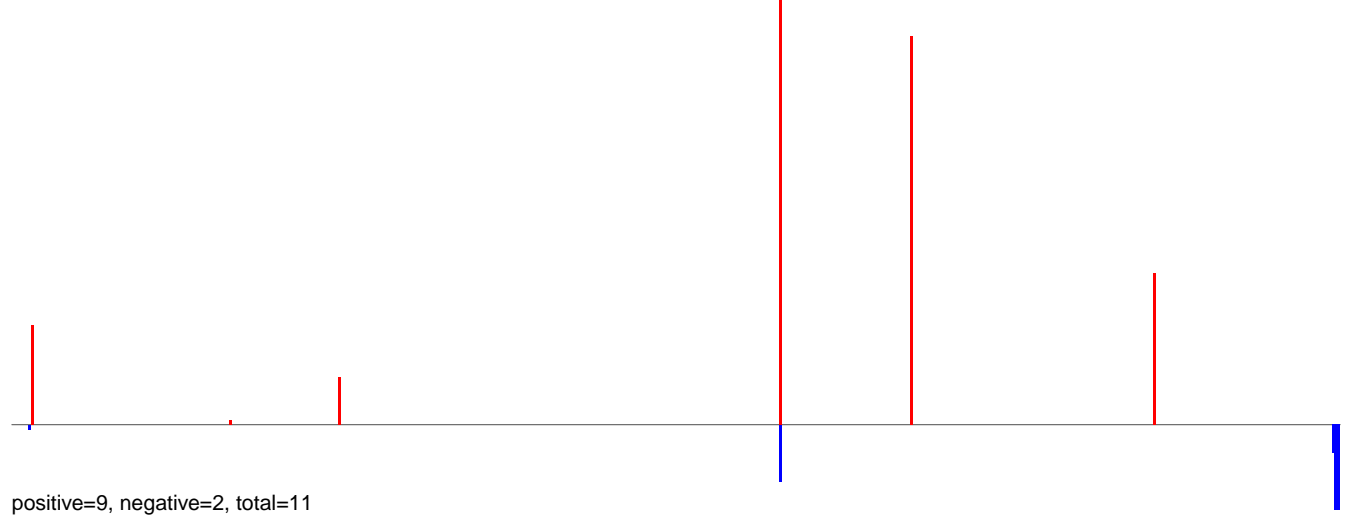


AeAeg_Aag2.SINV.GFP.rep

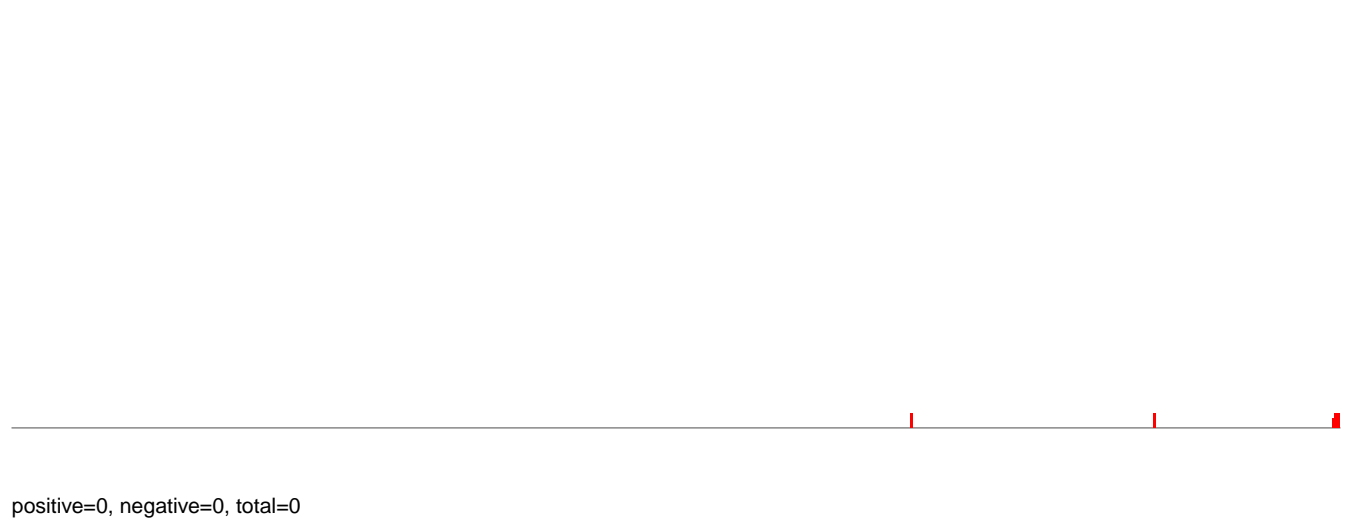


bow size=35, length=11964, k=10, GC=44.479921-Una_virus_non_structural_polyprotein_gene_partial_cds_and_structural_polyprotein_ge:1-11964

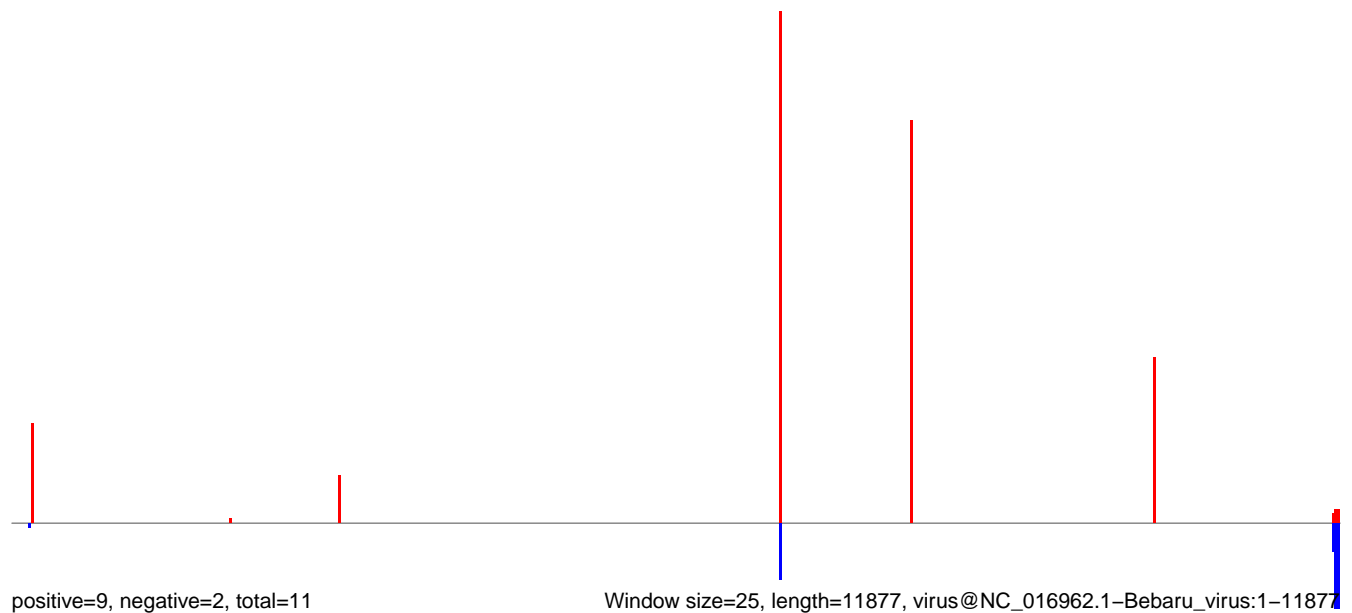
AeAeg_Aag2.SINV.GFP.18_23.rep



AeAeg_Aag2.SINV.GFP.24_35.rep



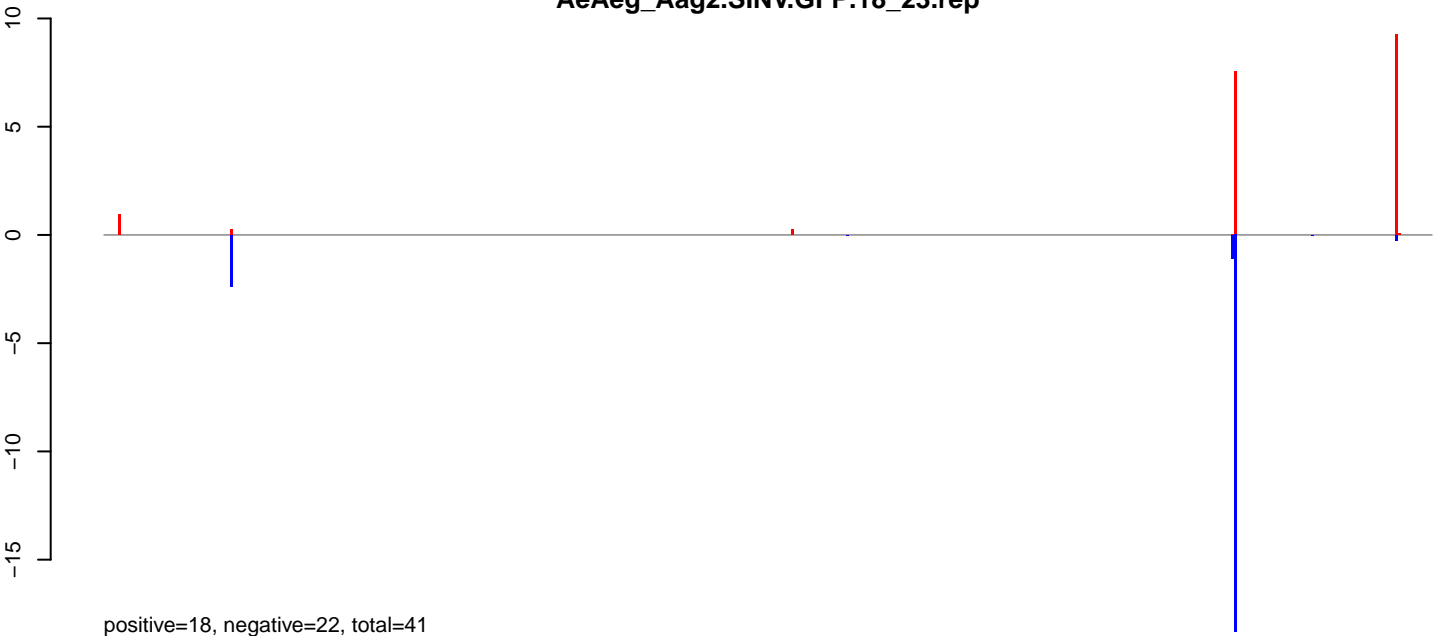
AeAeg_Aag2.SINV.GFP.rep



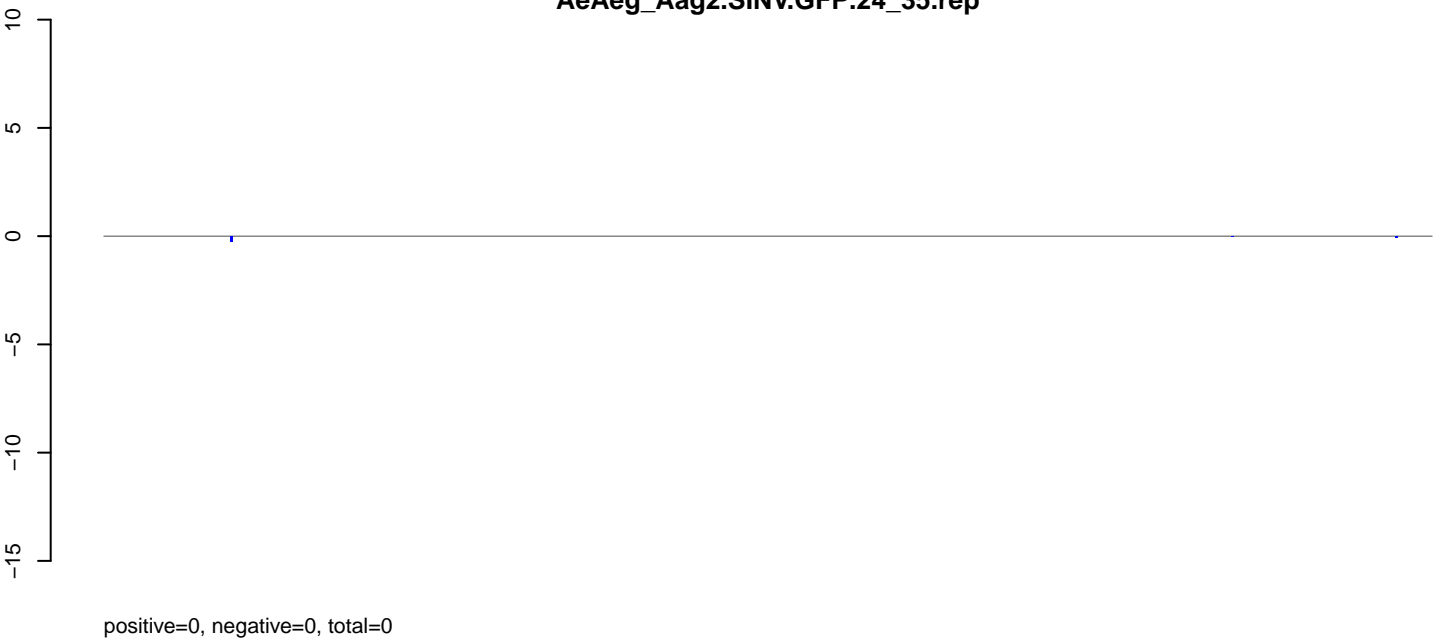
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0 2000 4000 6000 8000 10000 12000

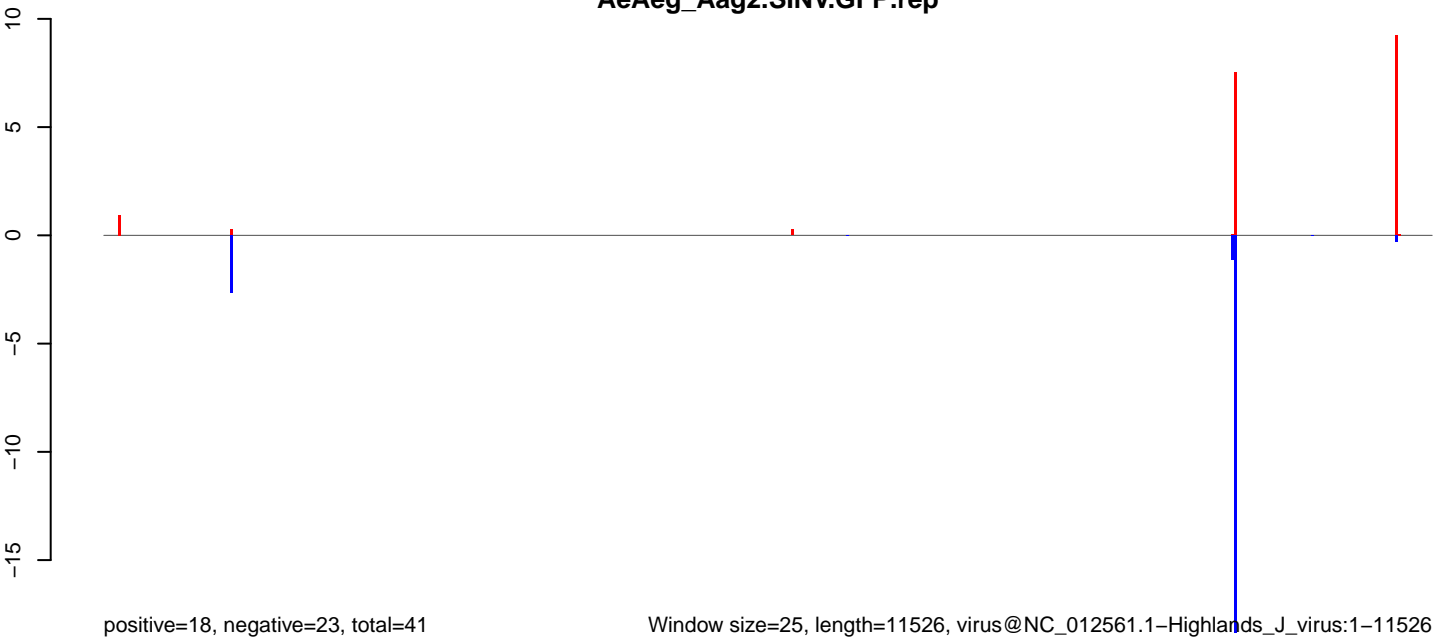
AeAeg_Aag2.SINV.GFP.18_23.rep



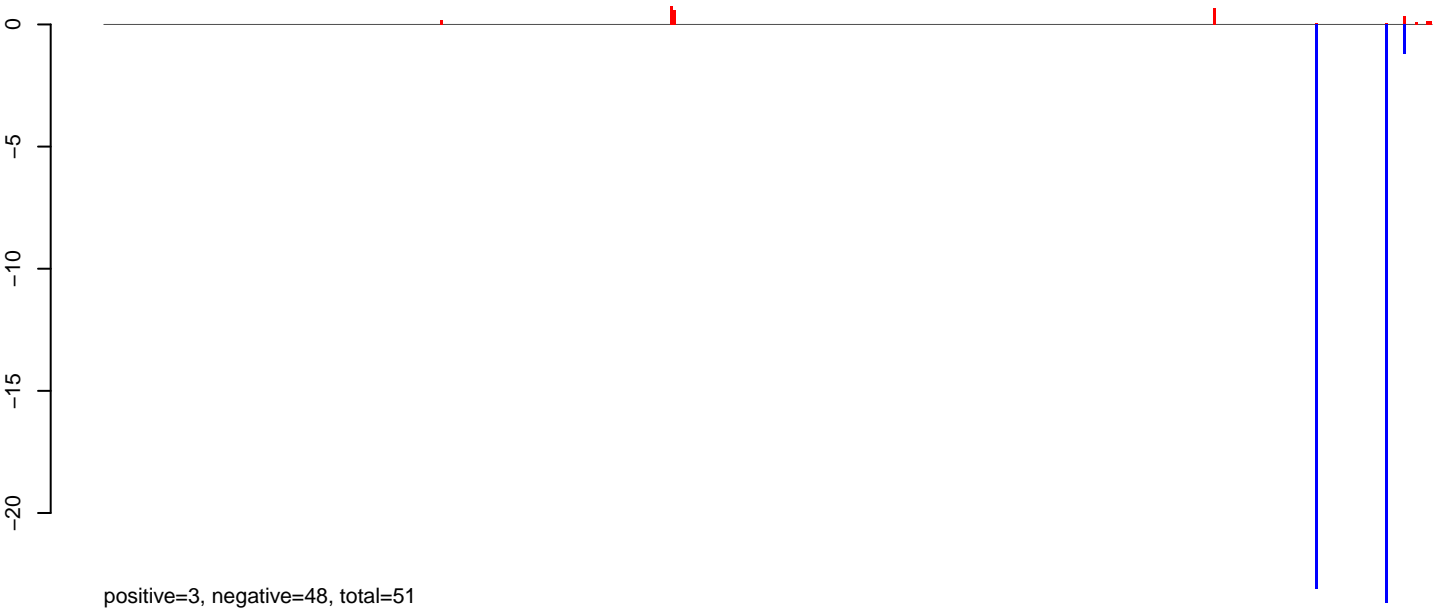
AeAeg_Aag2.SINV.GFP.24_35.rep



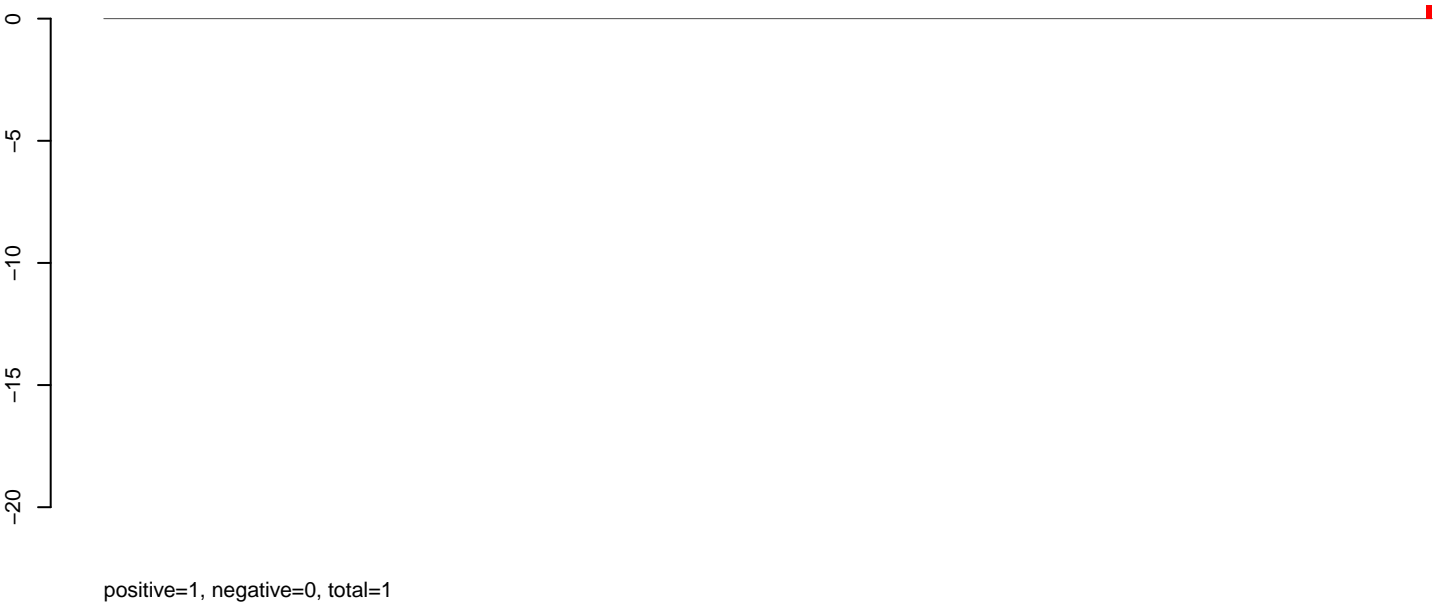
AeAeg_Aag2.SINV.GFP.rep



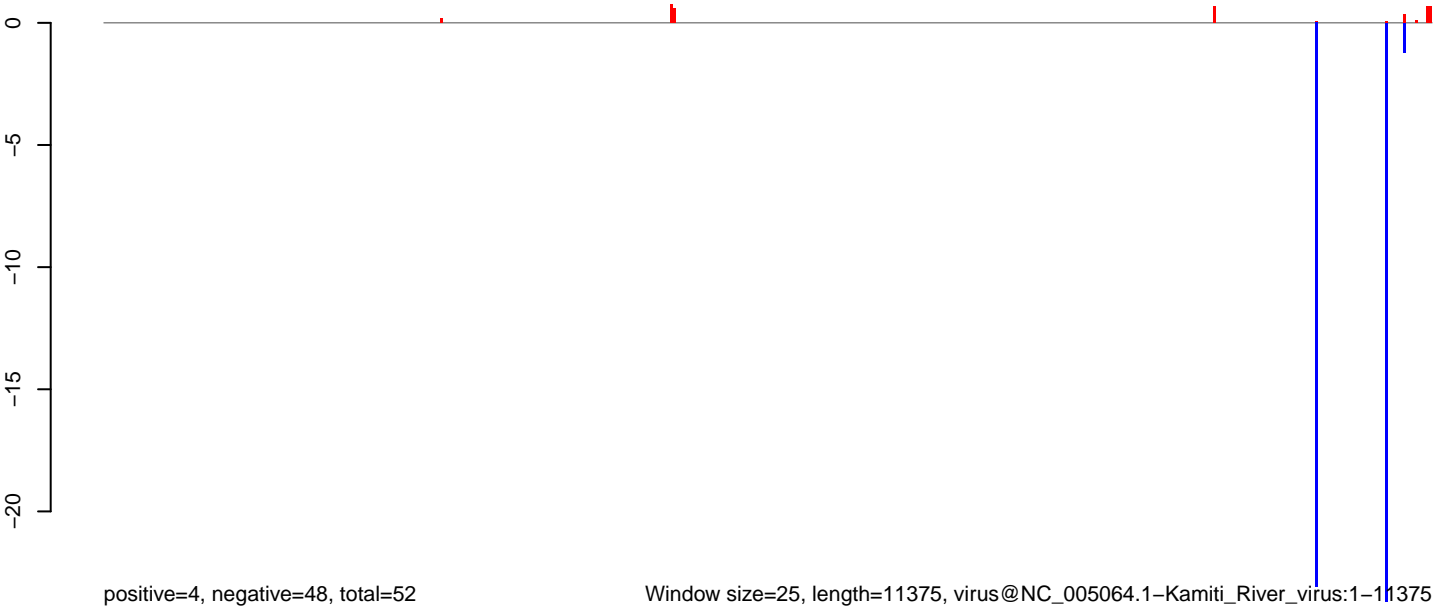
AeAeg_Aag2.SINV.GFP.18_23.rep



AeAeg_Aag2.SINV.GFP.24_35.rep



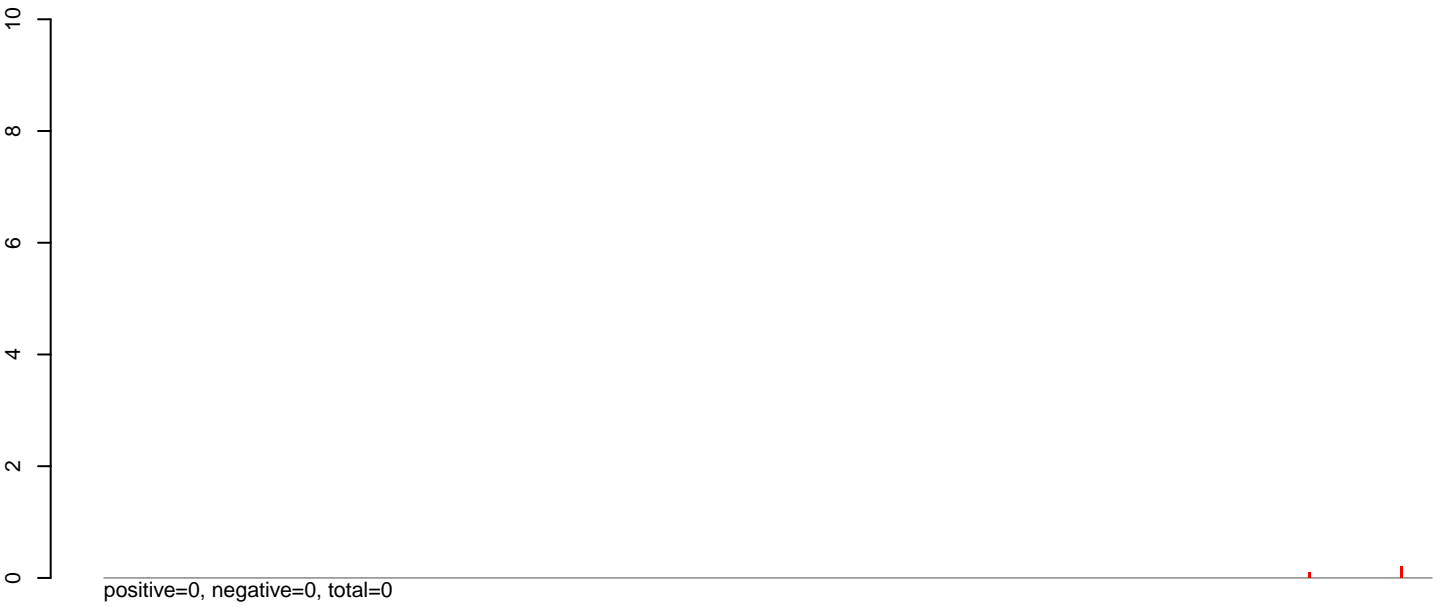
AeAeg_Aag2.SINV.GFP.rep



AeAeg_Aag2.SINV.GFP.18_23.rep



AeAeg_Aag2.SINV.GFP.24_35.rep

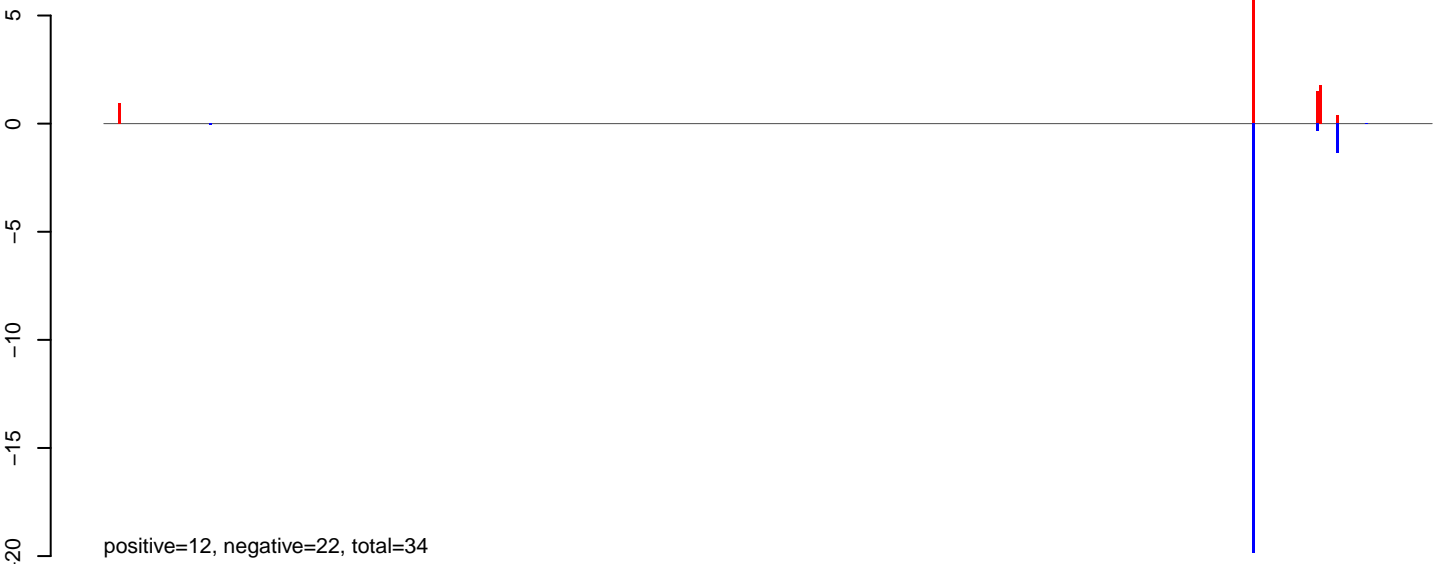


AeAeg_Aag2.SINV.GFP.rep

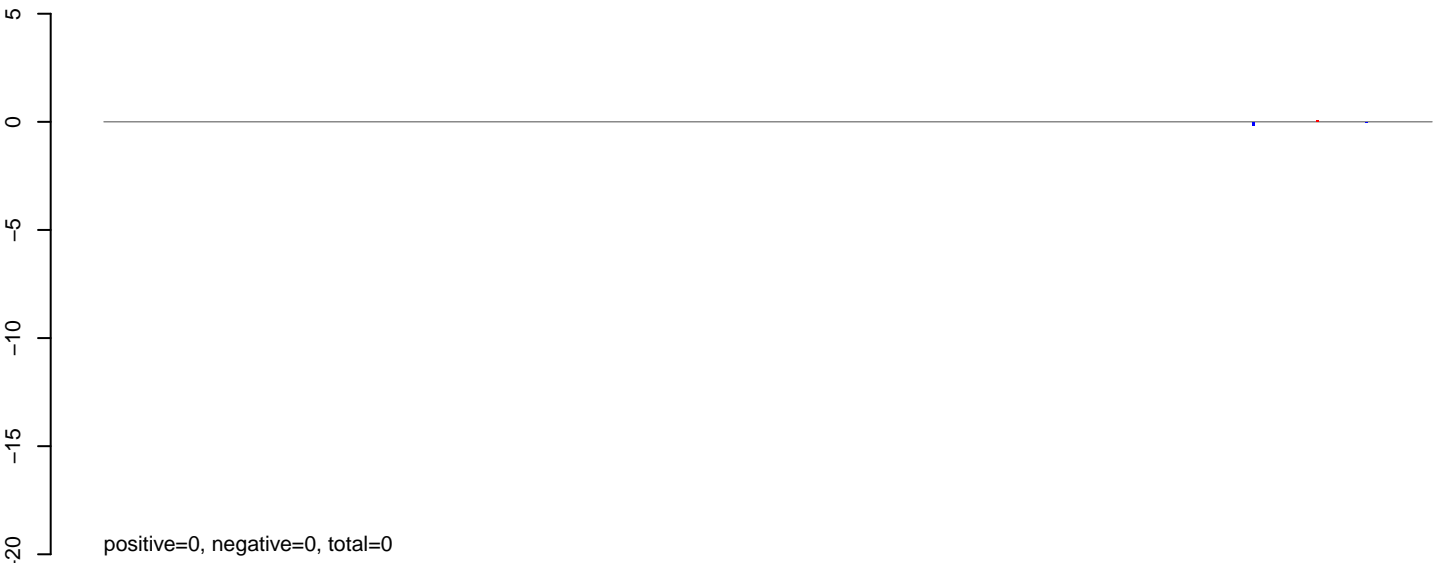


0 2000 4000 6000 8000 10000

AeAeg_Aag2.SINV.GFP.18_23.rep



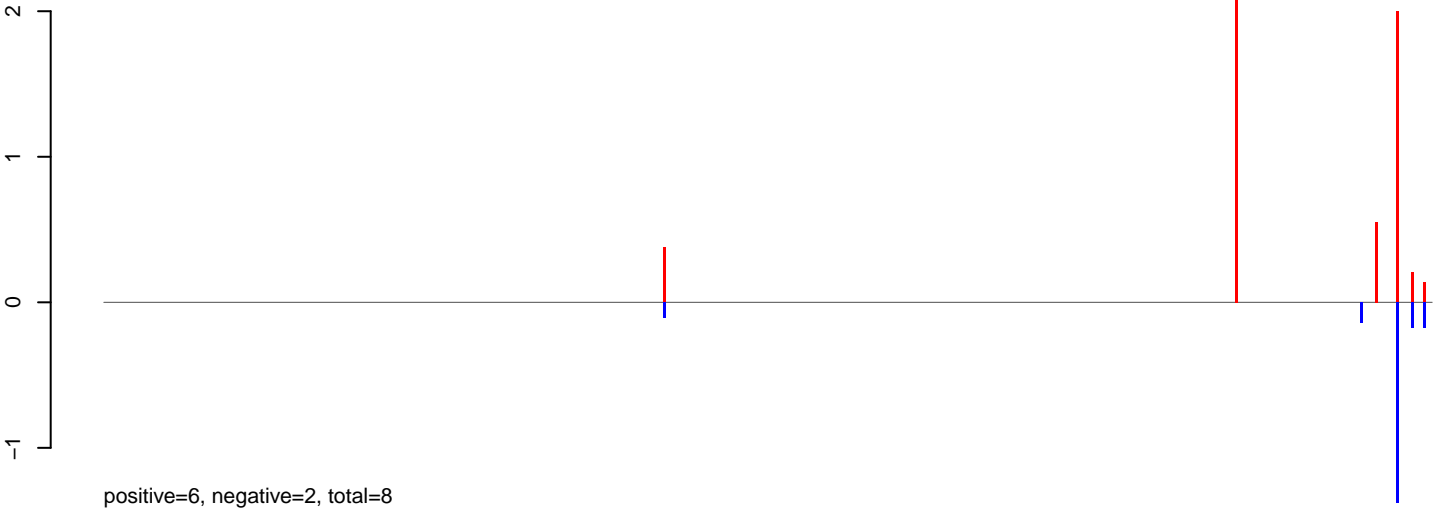
AeAeg_Aag2.SINV.GFP.24_35.rep



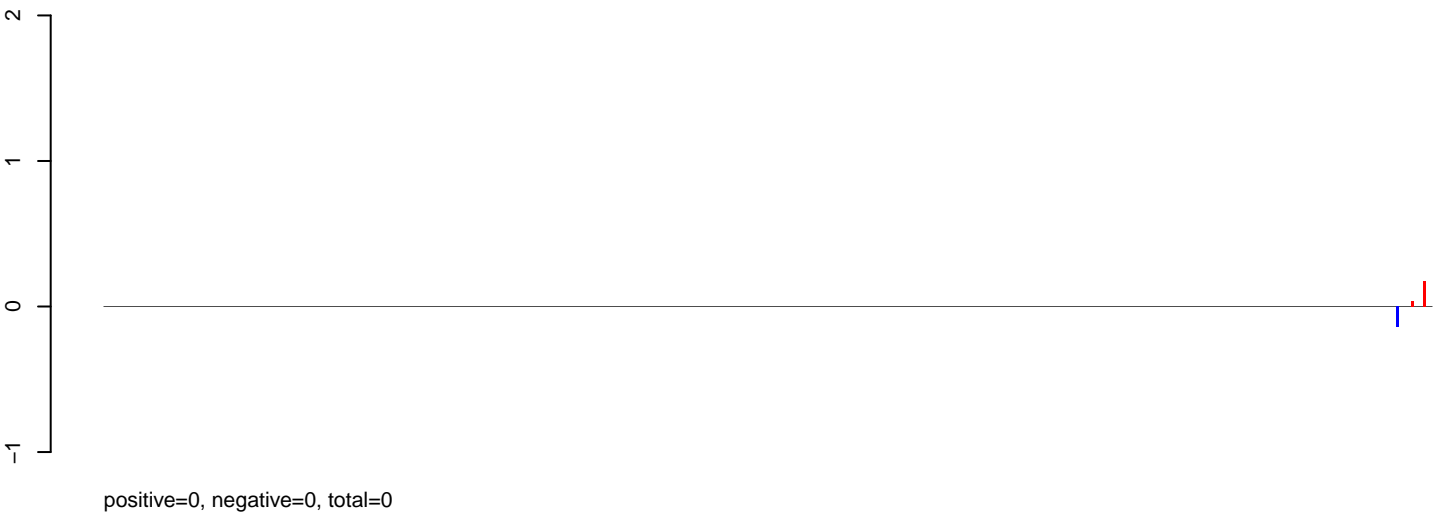
AeAeg_Aag2.SINV.GFP.rep



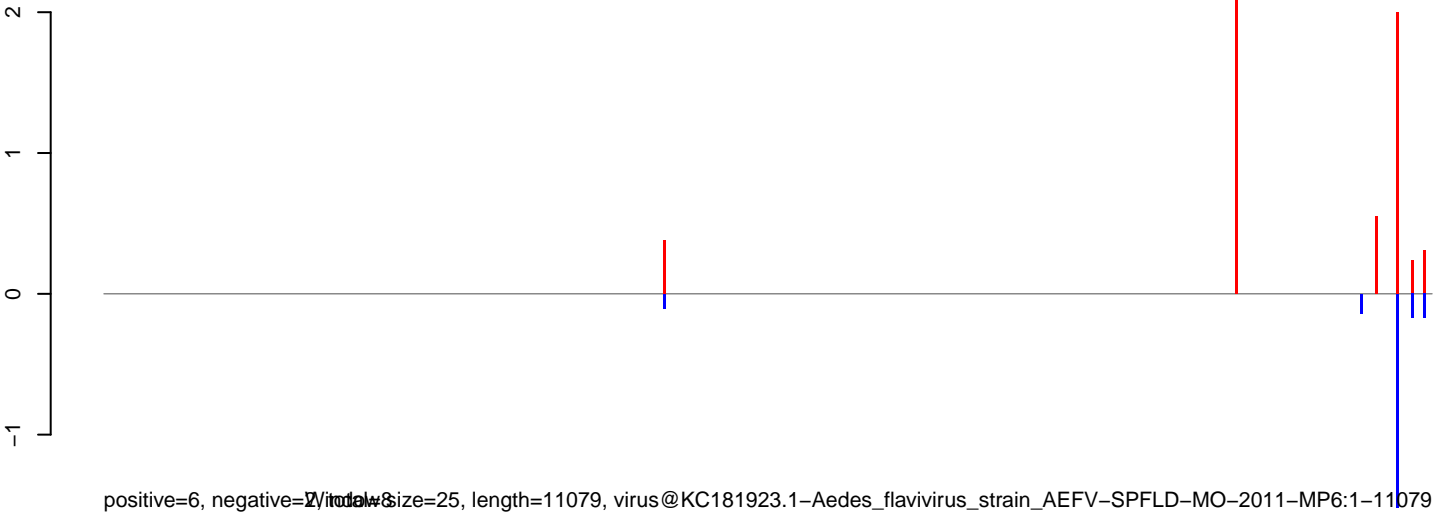
AeAeg_Aag2.SINV.GFP.18_23.rep



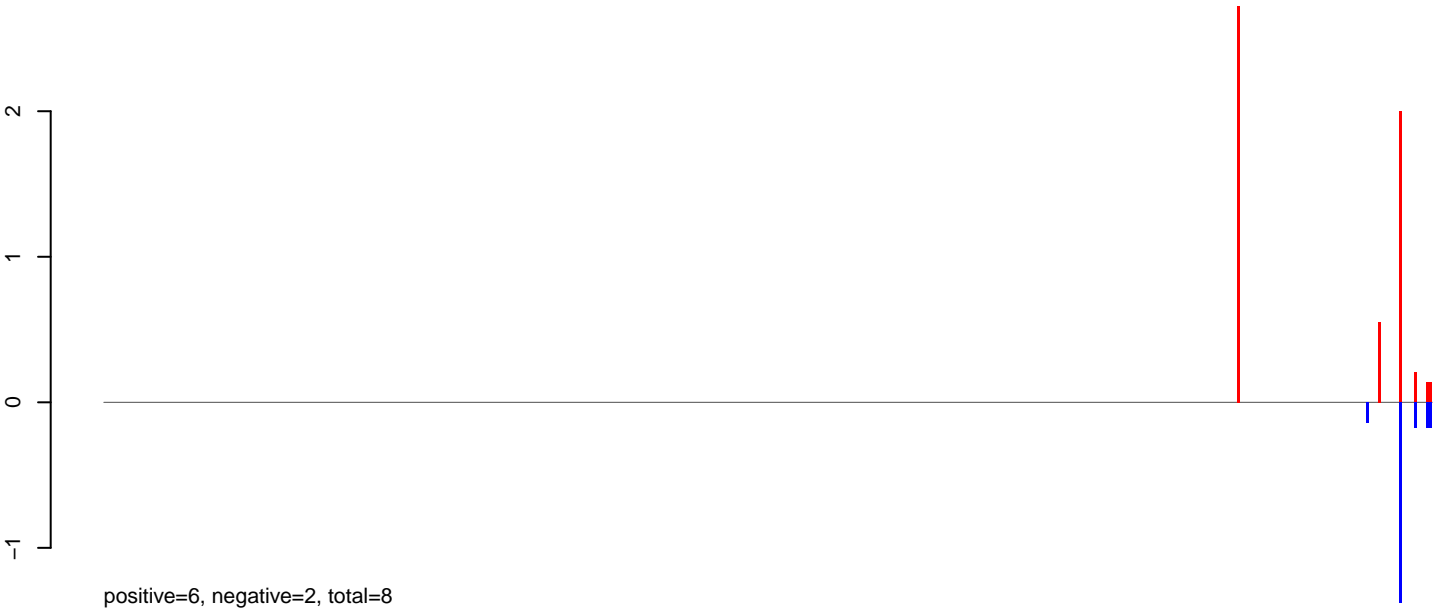
AeAeg_Aag2.SINV.GFP.24_35.rep



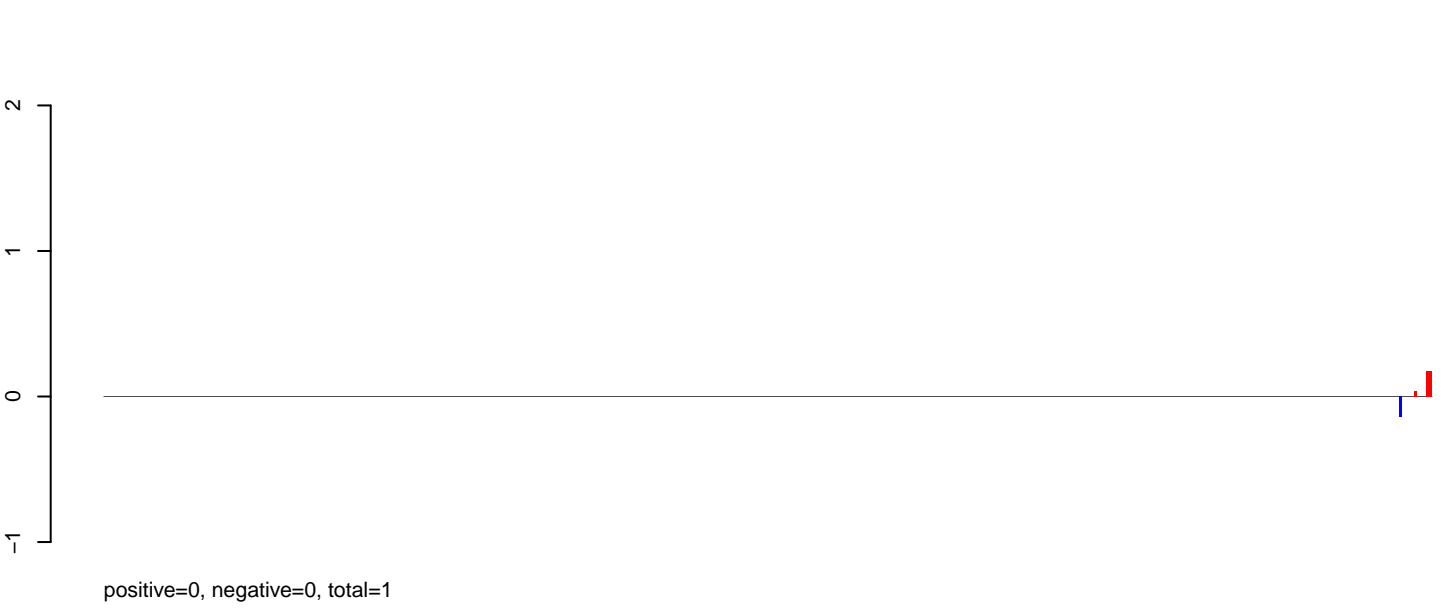
AeAeg_Aag2.SINV.GFP.rep



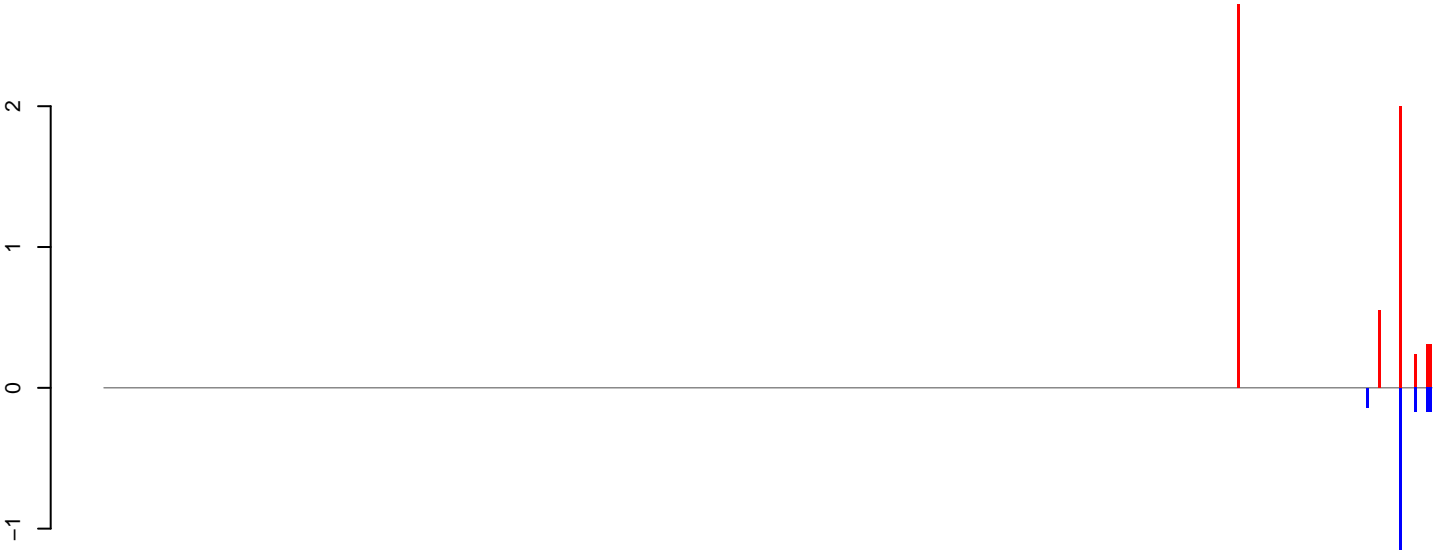
AeAeg_Aag2.SINV.GFP.18_23.rep



AeAeg_Aag2.SINV.GFP.24_35.rep



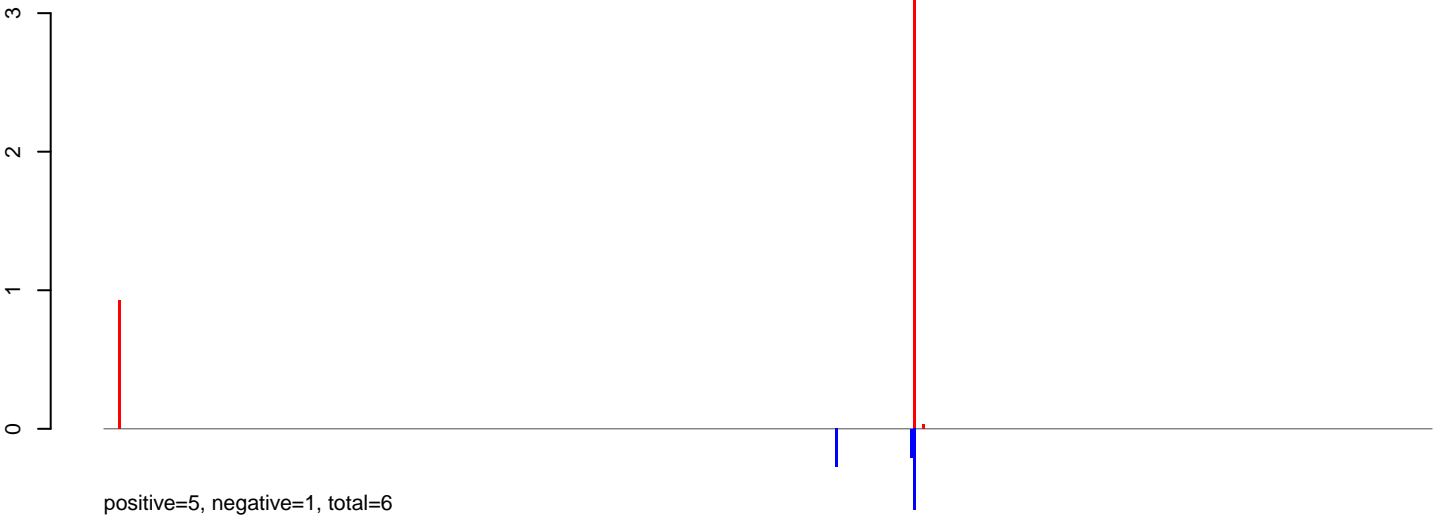
AeAeg_Aag2.SINV.GFP.rep



Window size=25, length=11064, virus@NC_012932.1-Aedes_flavivirus_genomic_RNA_strain_Narita-21:1-11064

0 2000 4000 6000 8000 10000

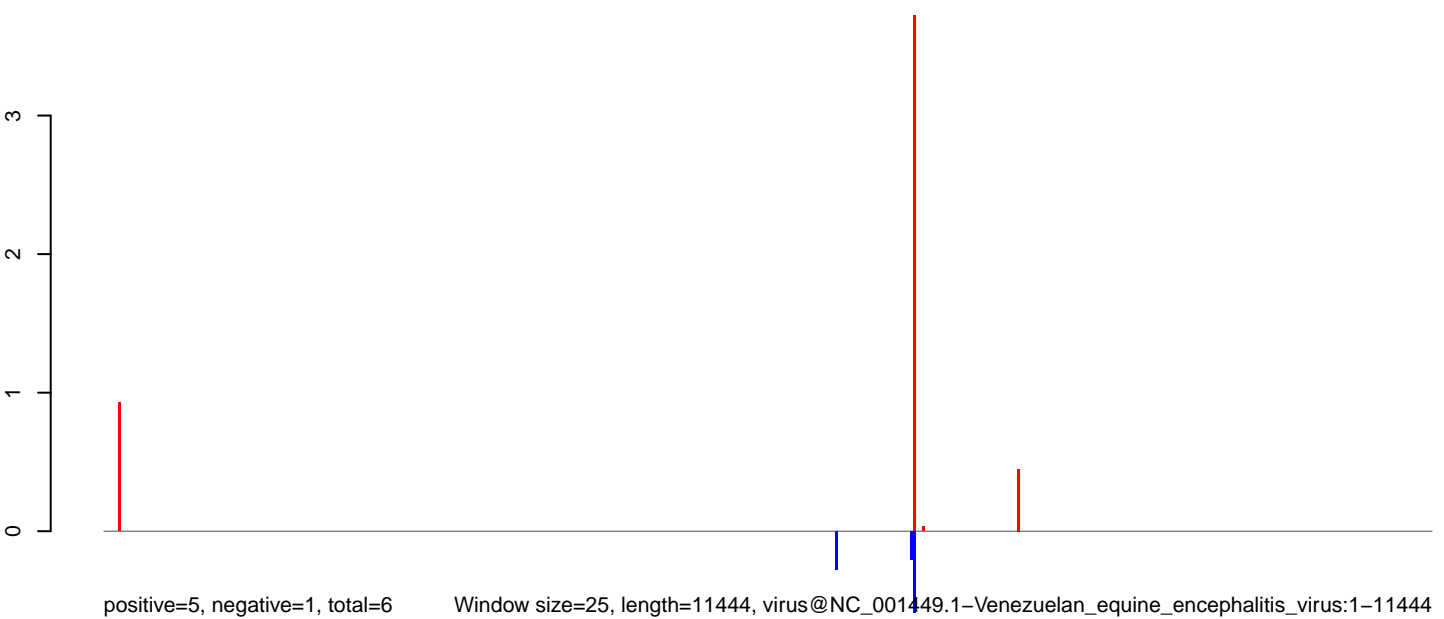
AeAeg_Aag2.SINV.GFP.18_23.rep



AeAeg_Aag2.SINV.GFP.24_35.rep



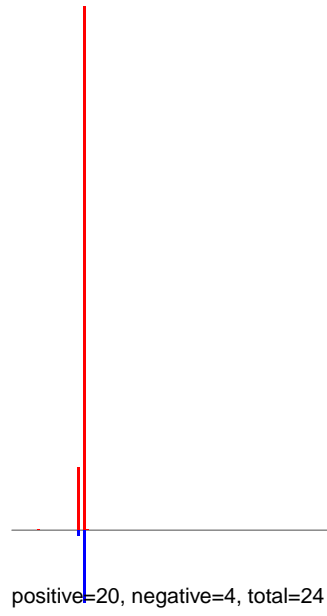
AeAeg_Aag2.SINV.GFP.rep



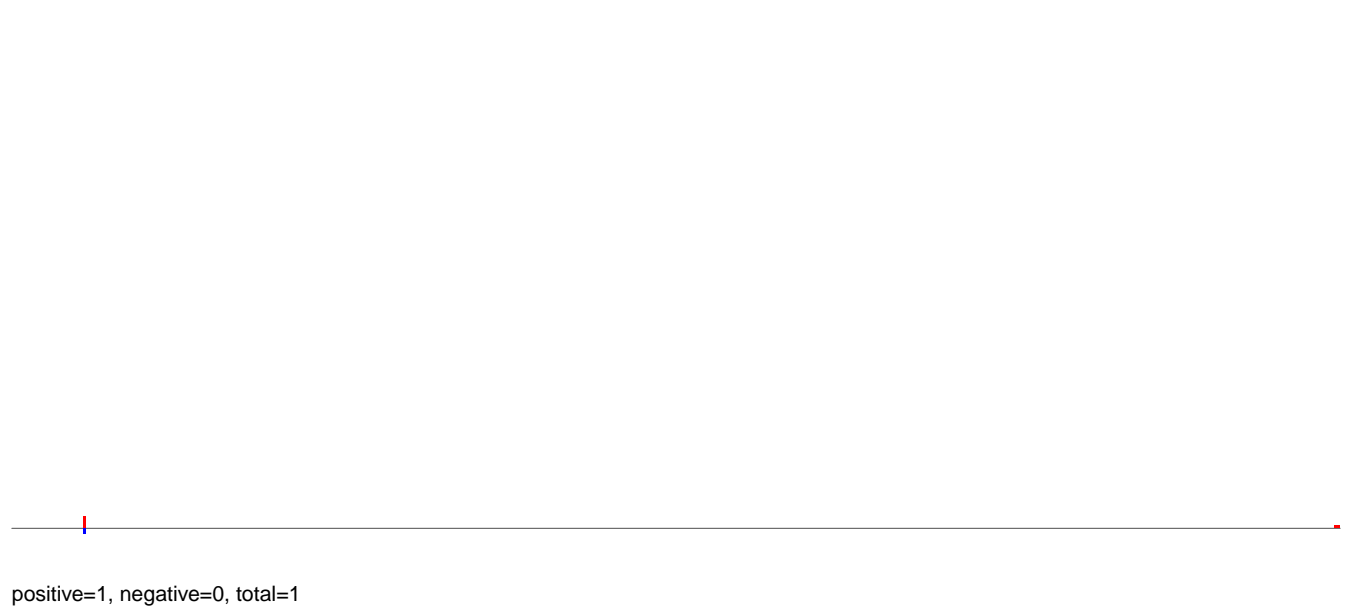
Window size=25, length=11444, virus@NC_001449.1-Venezuelan_equine_encephalitis_virus:1-11444

0 2000 4000 6000 8000 10000

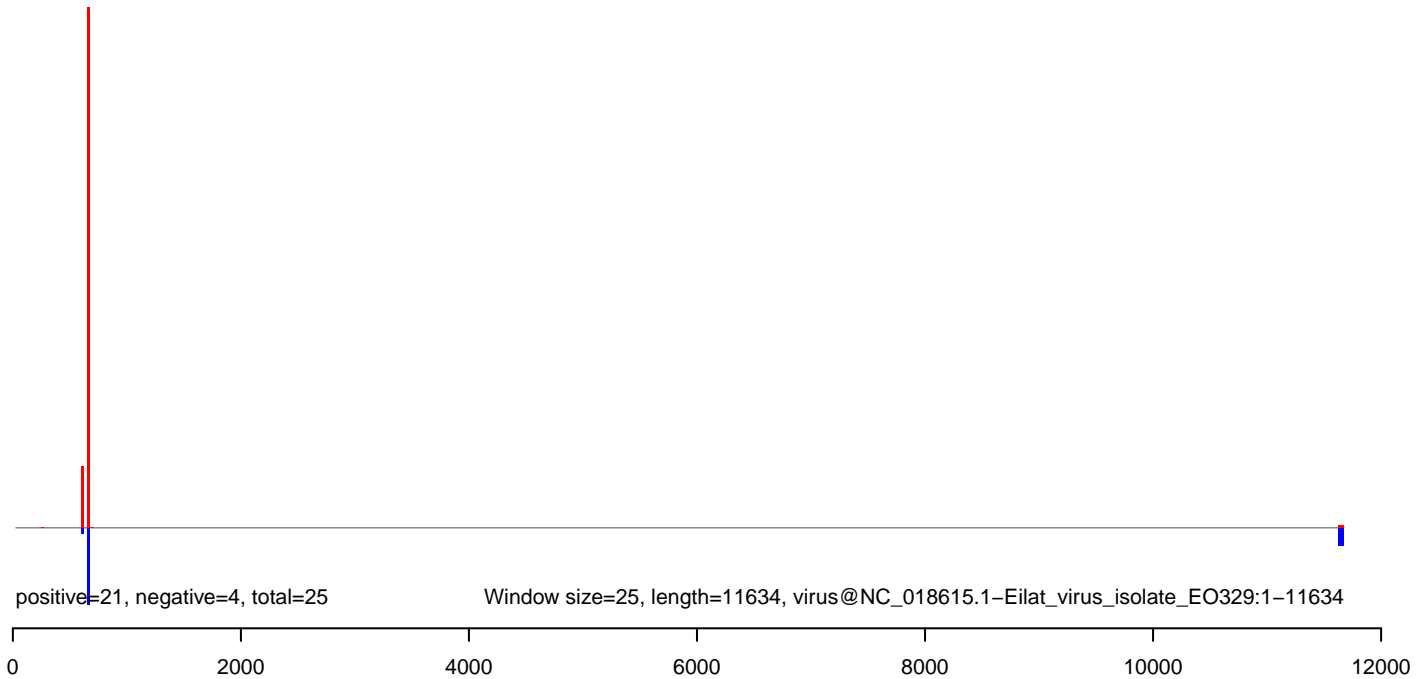
AeAeg_Aag2.SINV.GFP.18_23.rep



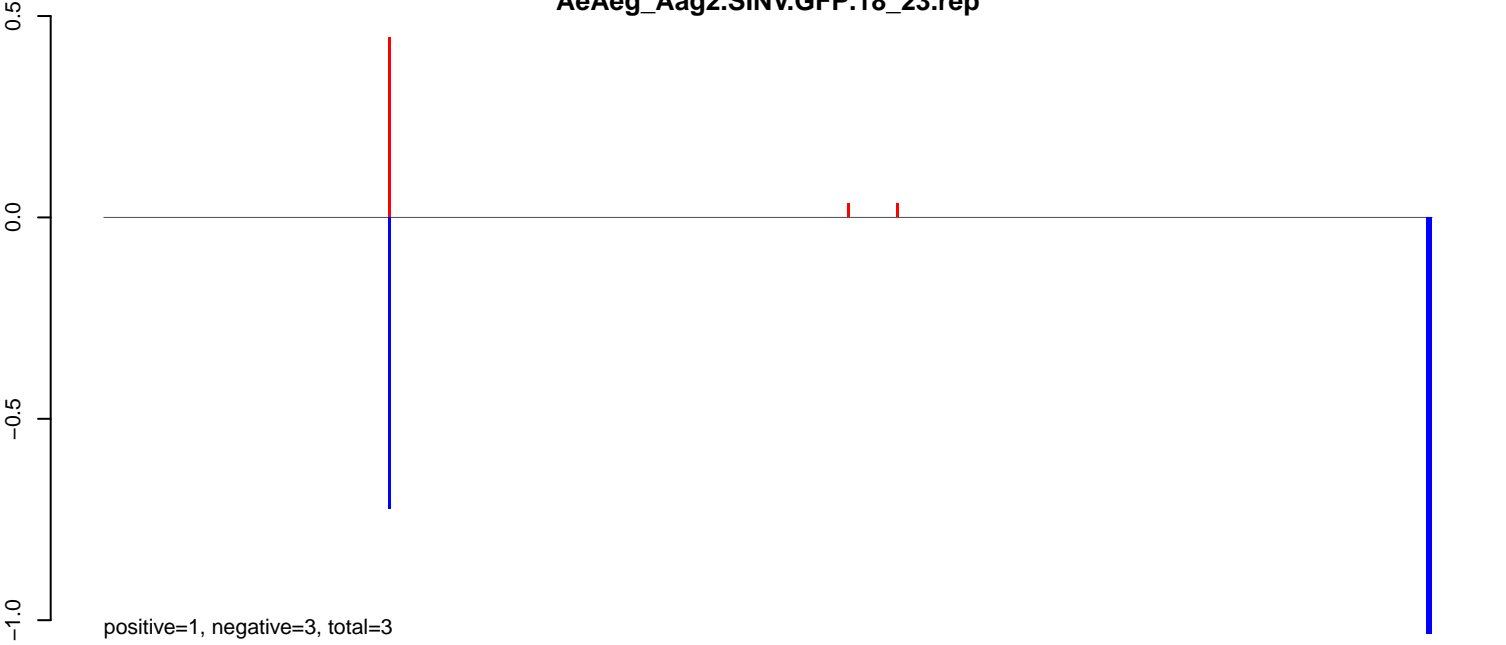
AeAeg_Aag2.SINV.GFP.24_35.rep



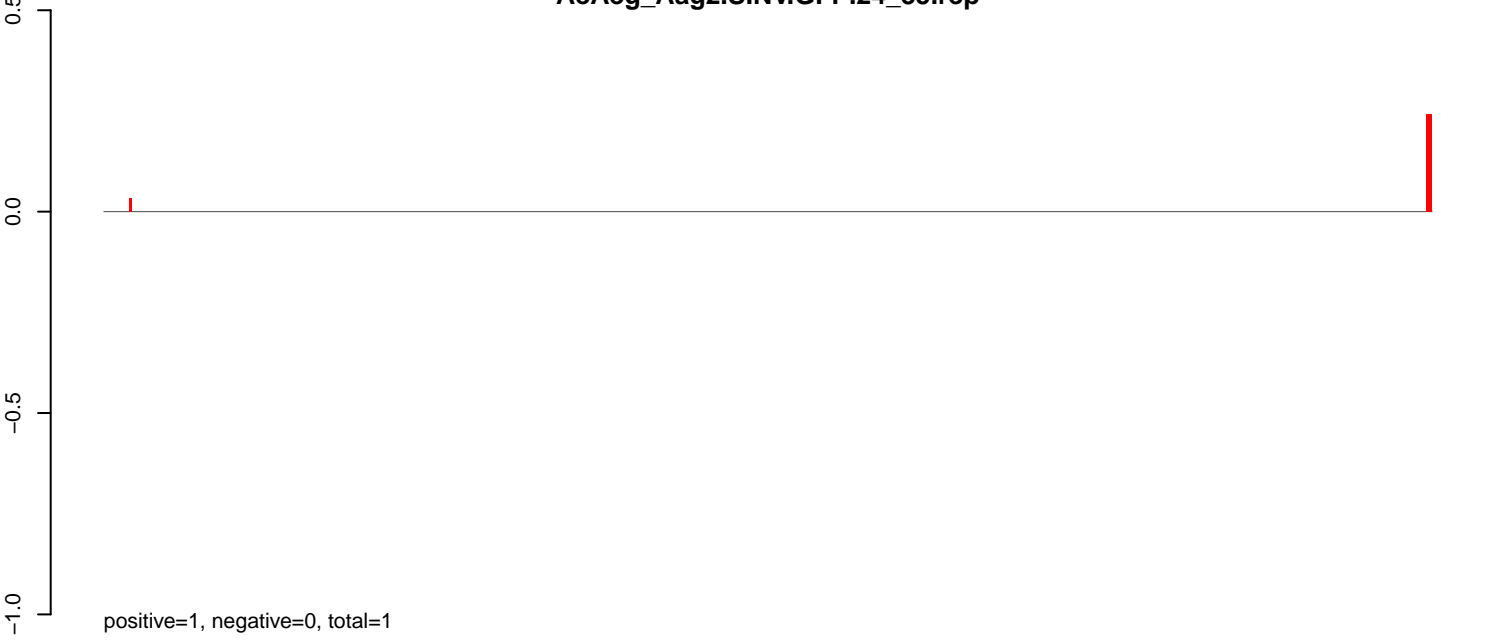
AeAeg_Aag2.SINV.GFP.rep



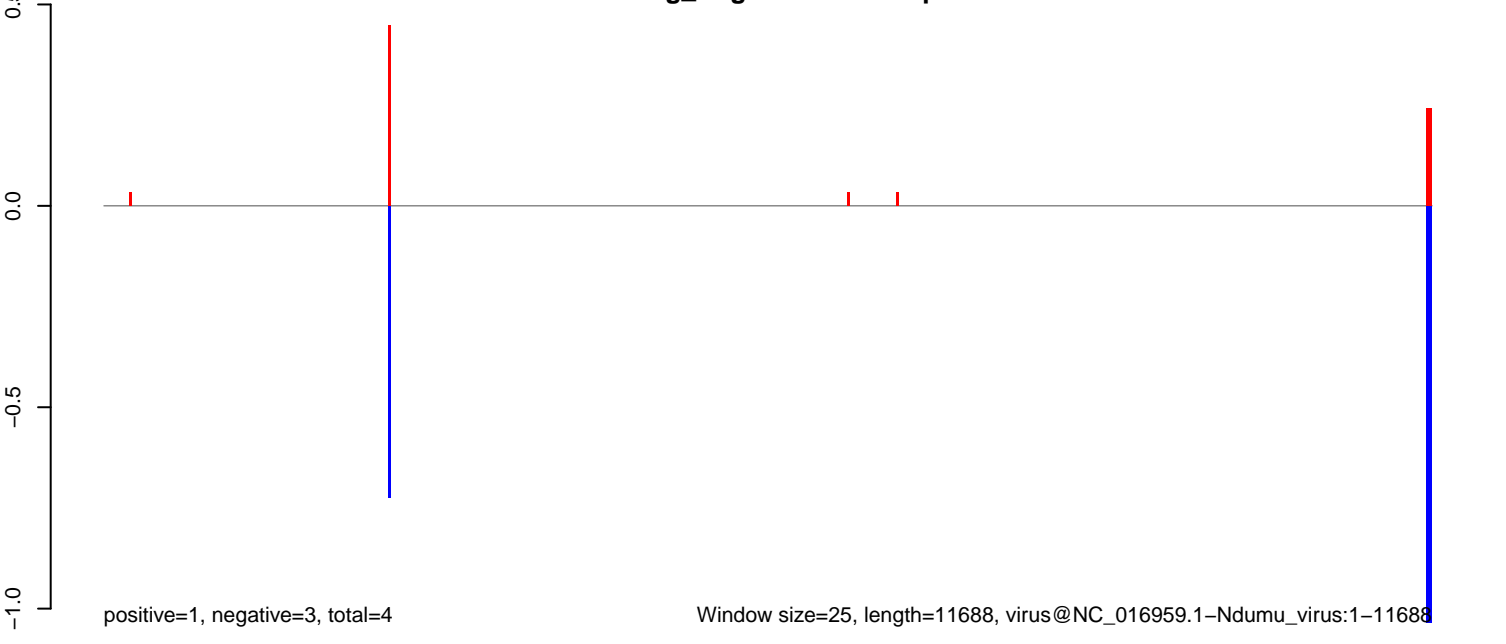
AeAeg_Aag2.SINV.GFP.18_23.rep



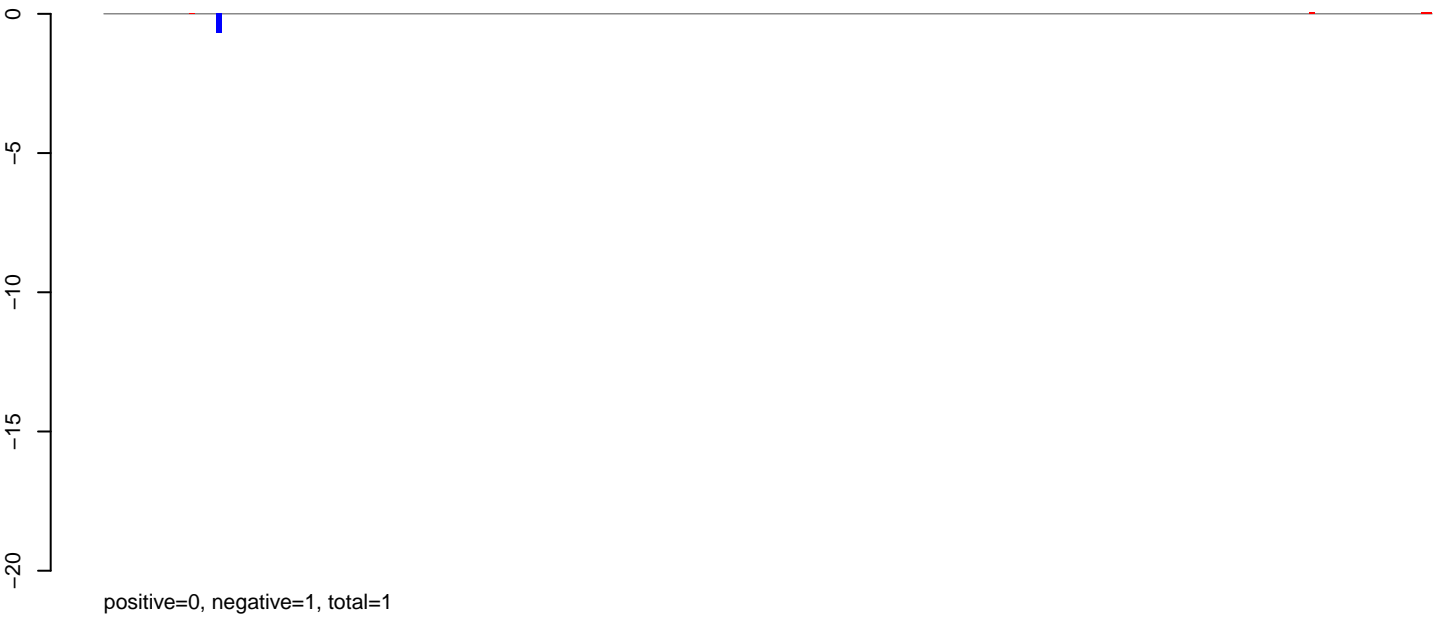
AeAeg_Aag2.SINV.GFP.24_35.rep



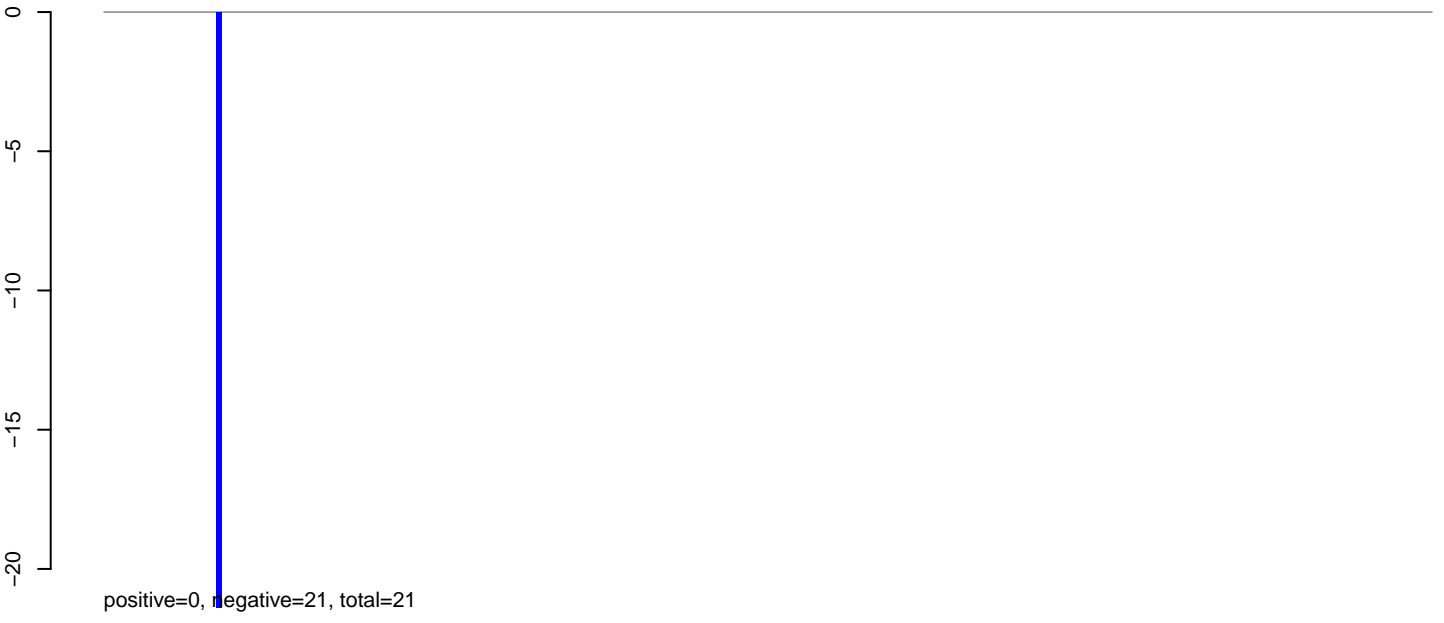
AeAeg_Aag2.SINV.GFP.rep



AeAeg_Aag2.SINV.GFP.18_23.rep



AeAeg_Aag2.SINV.GFP.24_35.rep



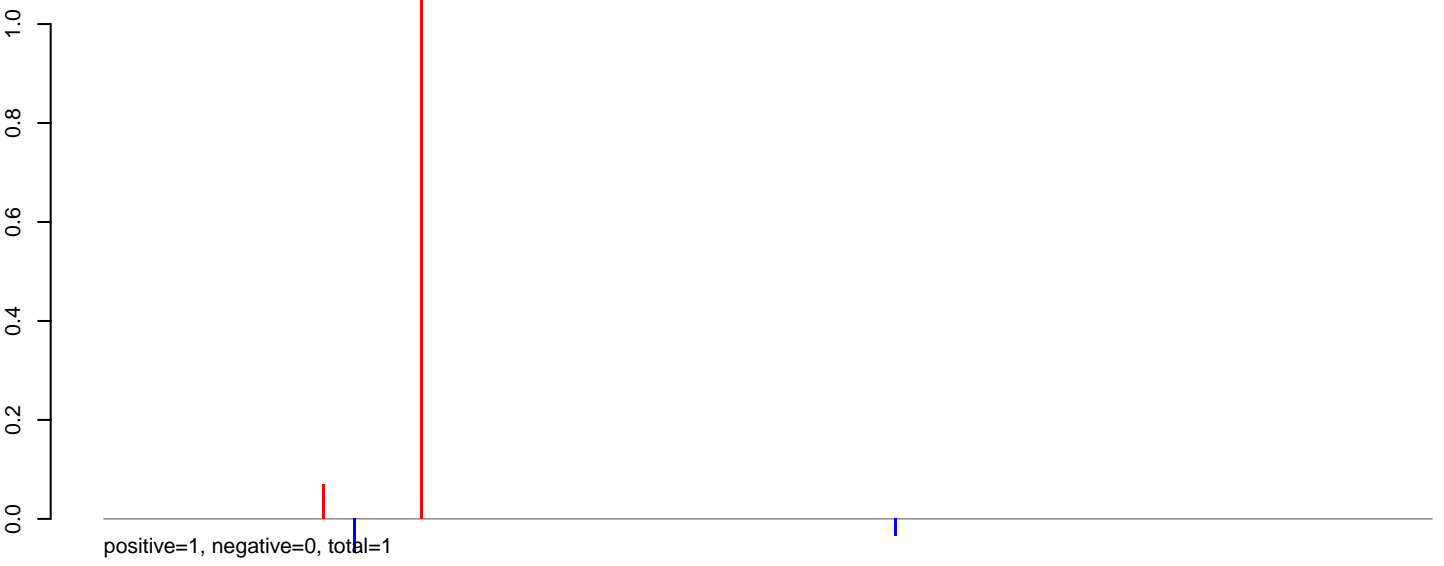
AeAeg_Aag2.SINV.GFP.rep



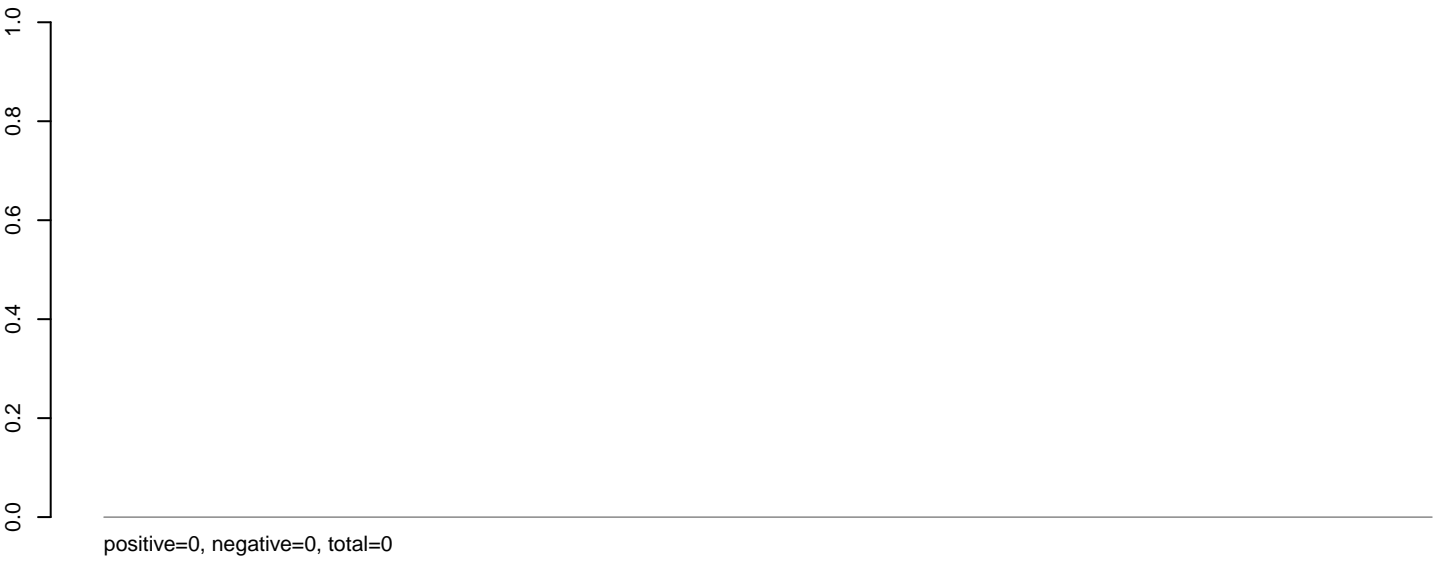
Winda 2022 size=25, length=6203, virus@NC_035674.1-Australian_Anopheles_totivirus_isolate_AATV_150840:1-6203

0 1000 2000 3000 4000 5000 6000

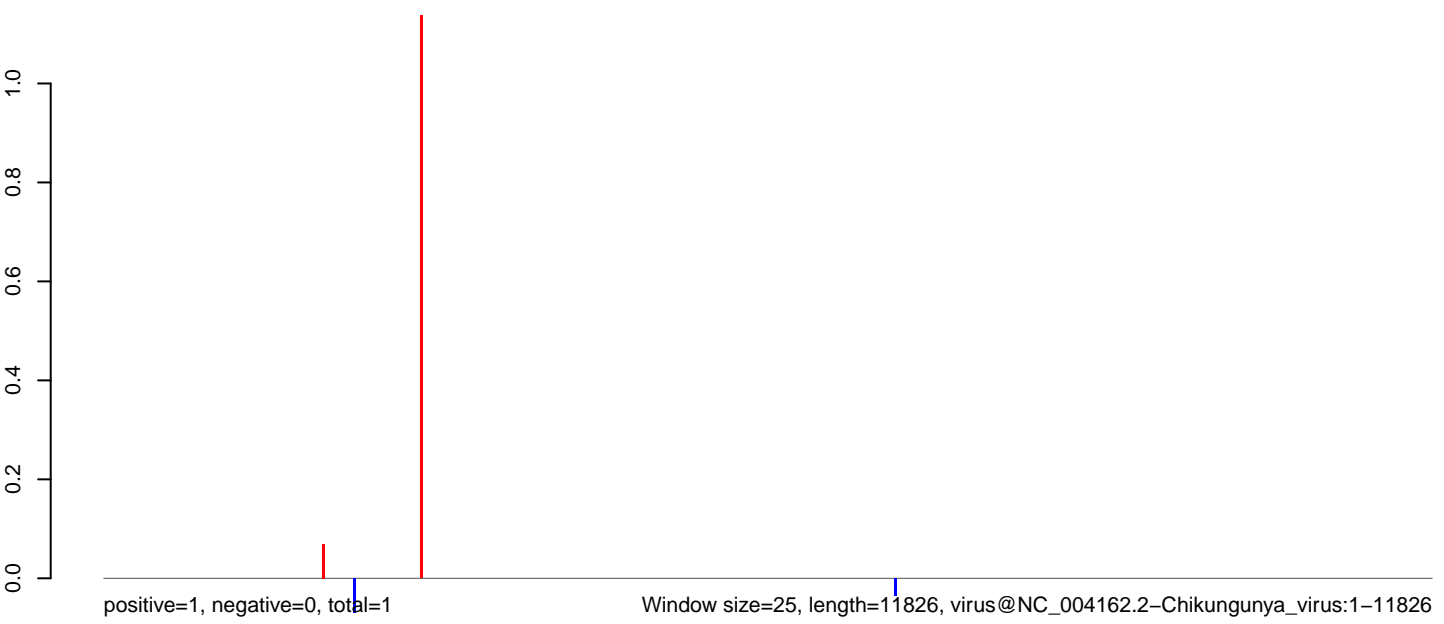
AeAeg_Aag2.SINV.GFP.18_23.rep



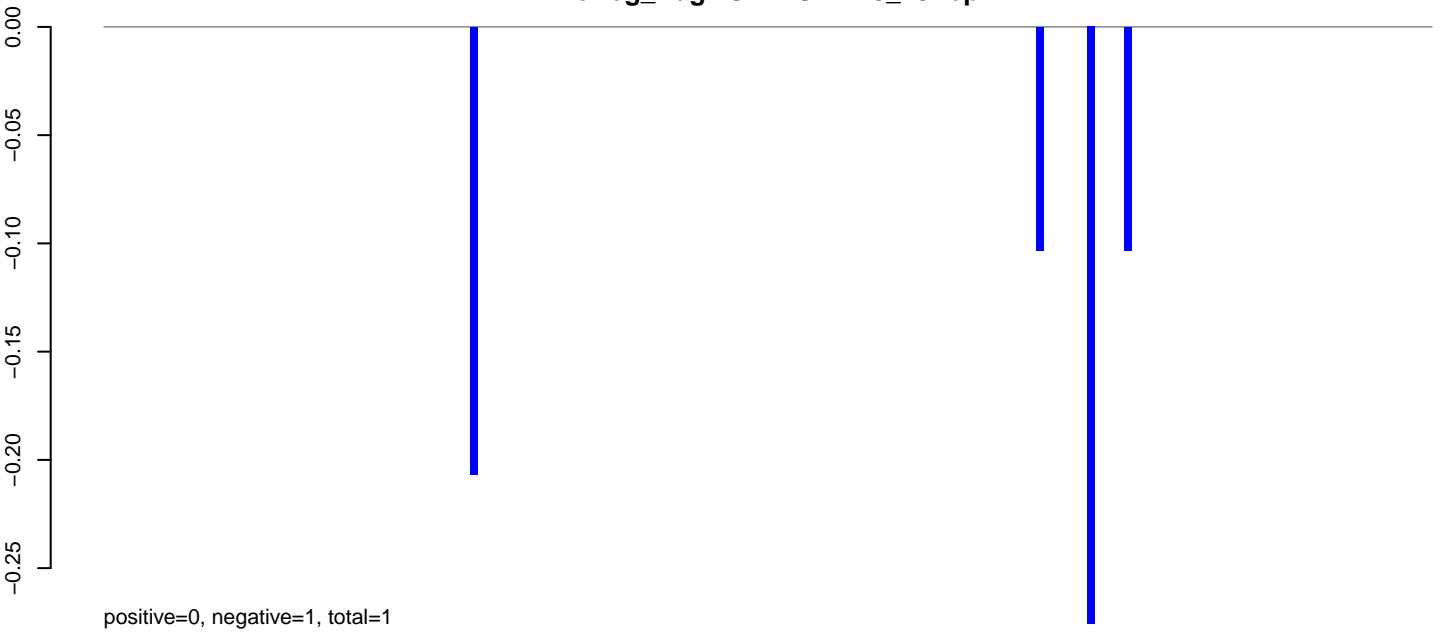
AeAeg_Aag2.SINV.GFP.24_35.rep



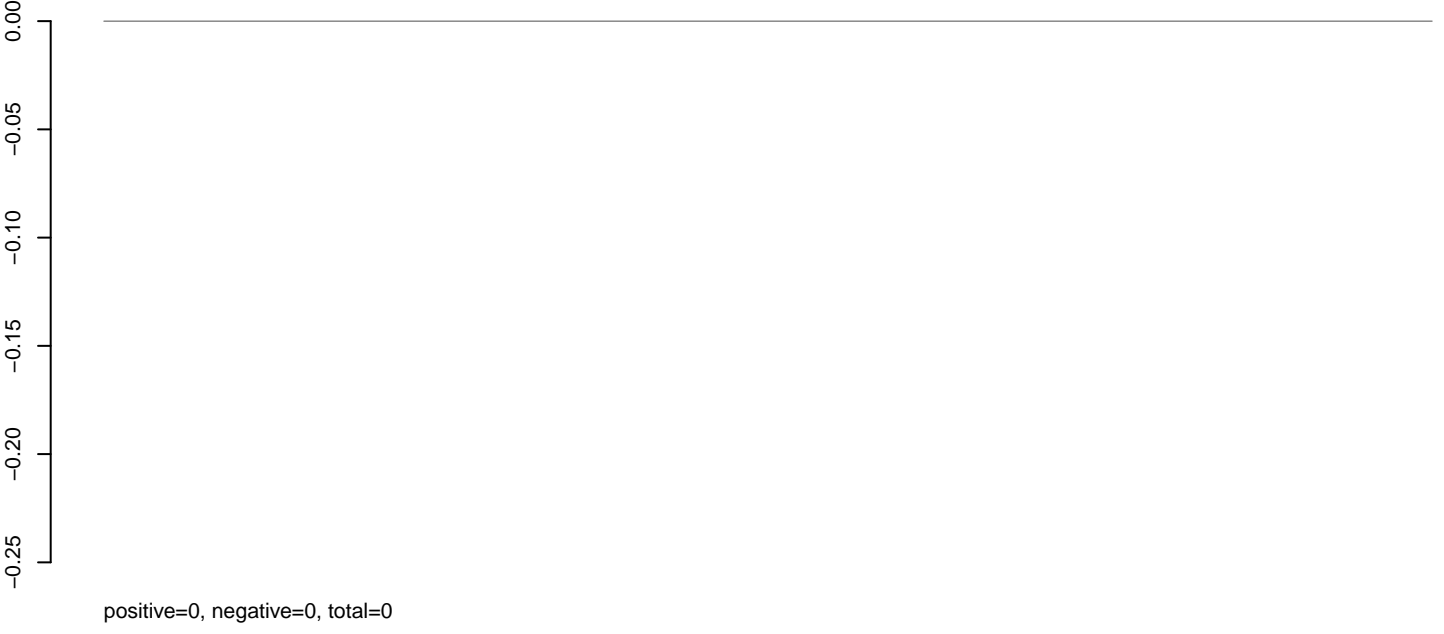
AeAeg_Aag2.SINV.GFP.rep



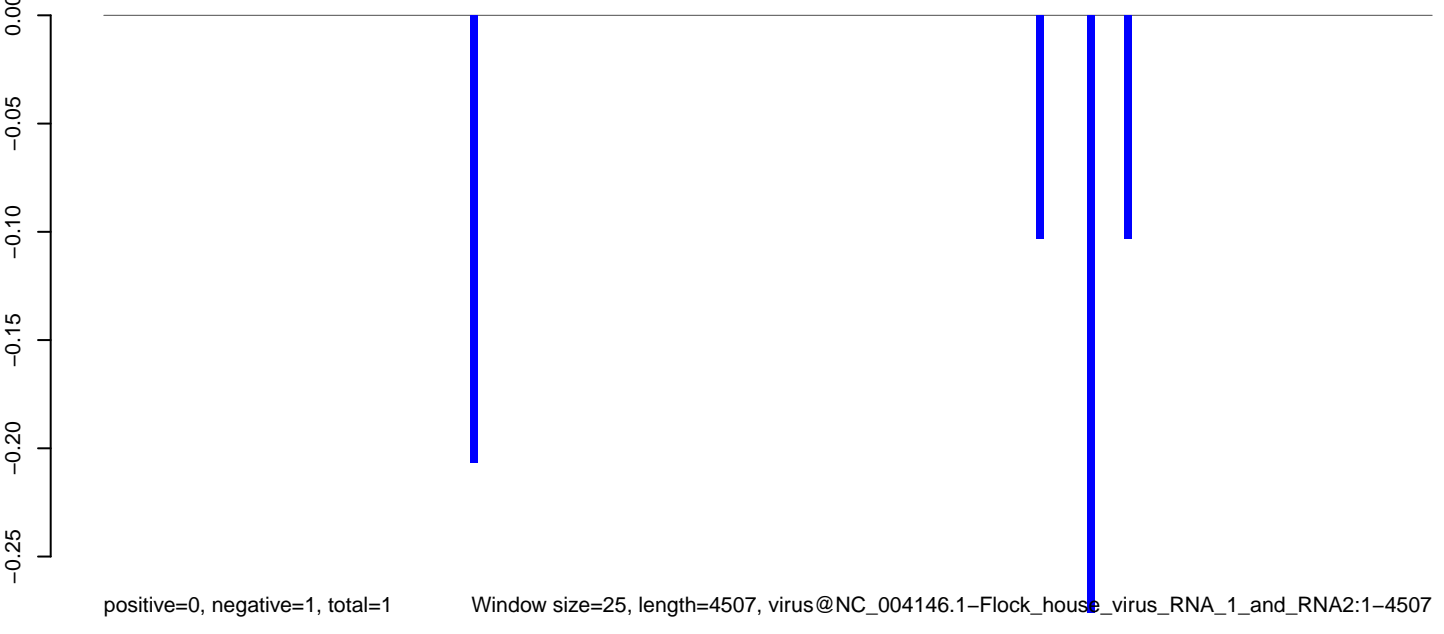
AeAeg_Aag2.SINV.GFP.18_23.rep



AeAeg_Aag2.SINV.GFP.24_35.rep



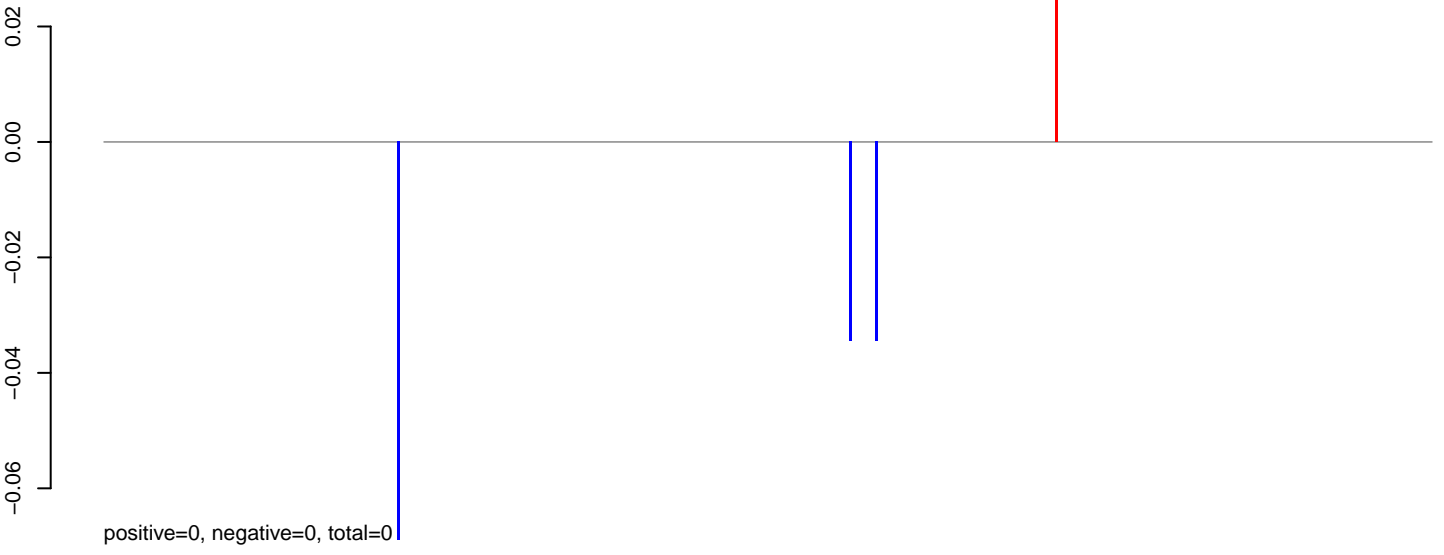
AeAeg_Aag2.SINV.GFP.rep



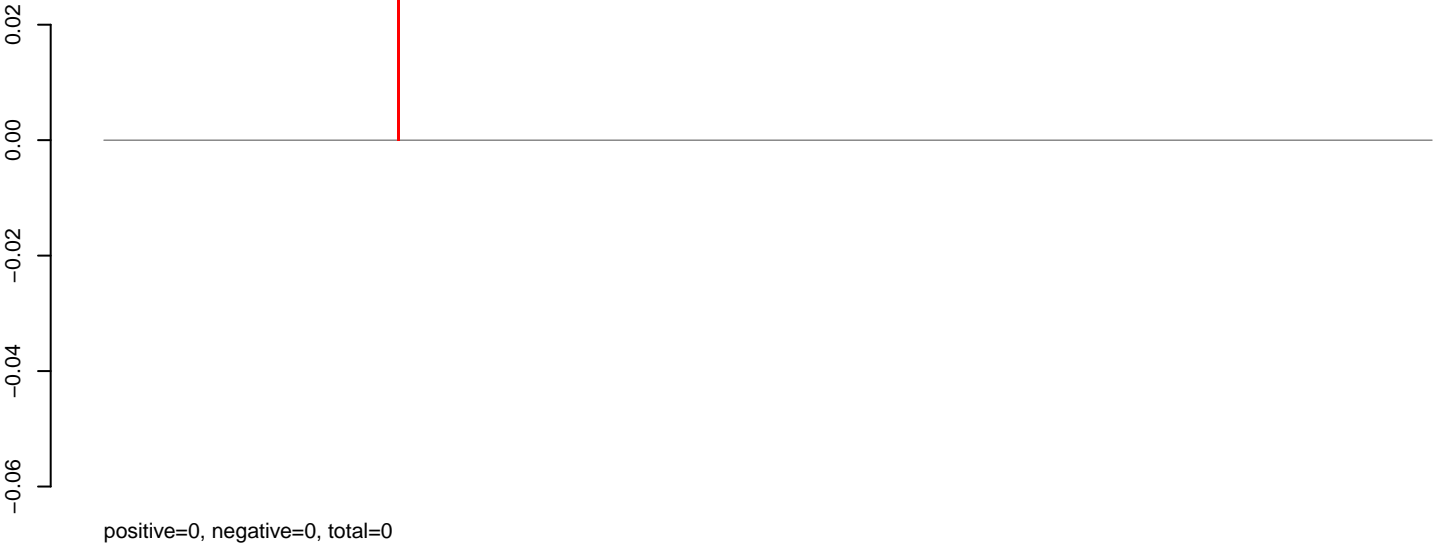
Window size=25, length=4507, virus@NC_004146.1-Flock_house_virus_RNA_1_and_RNA2:1-4507

0 1000 2000 3000 4000

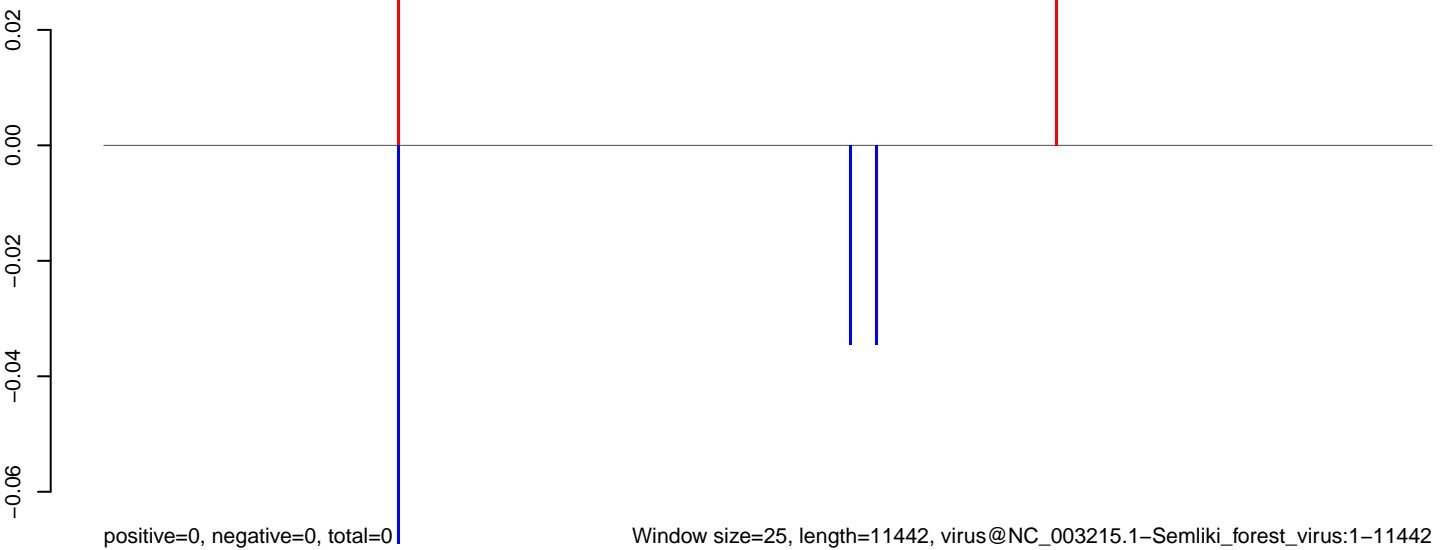
AeAeg_Aag2.SINV.GFP.18_23.rep



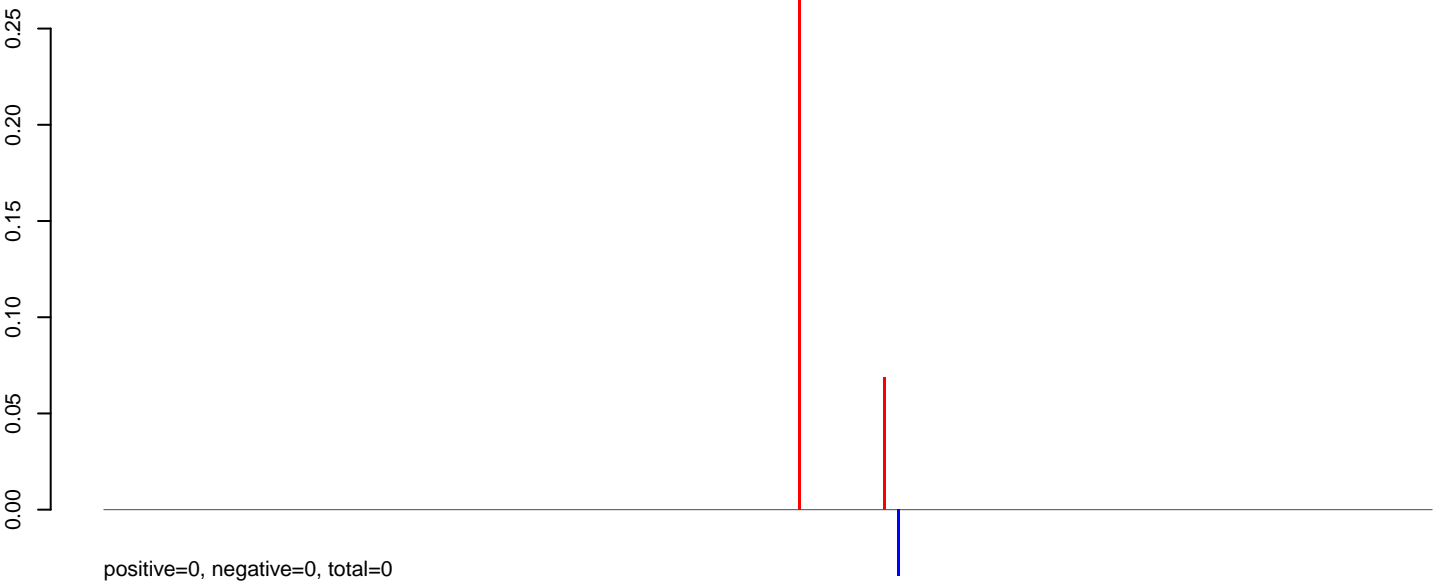
AeAeg_Aag2.SINV.GFP.24_35.rep



AeAeg_Aag2.SINV.GFP.rep



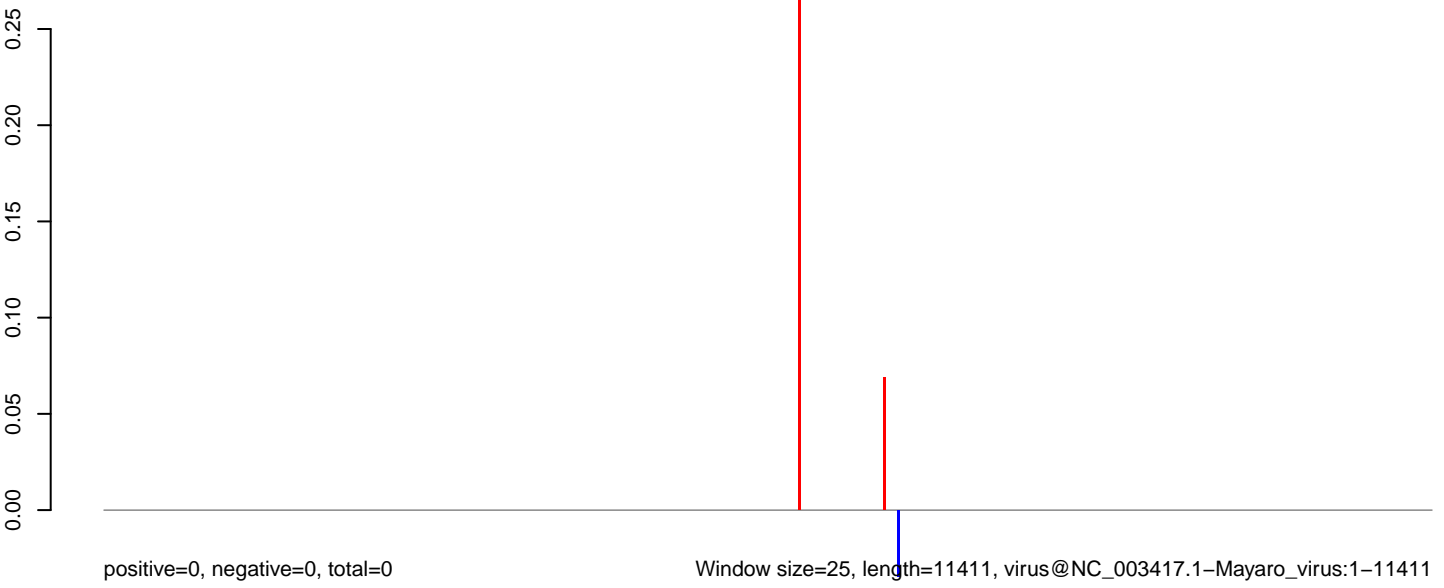
AeAeg_Aag2.SINV.GFP.18_23.rep



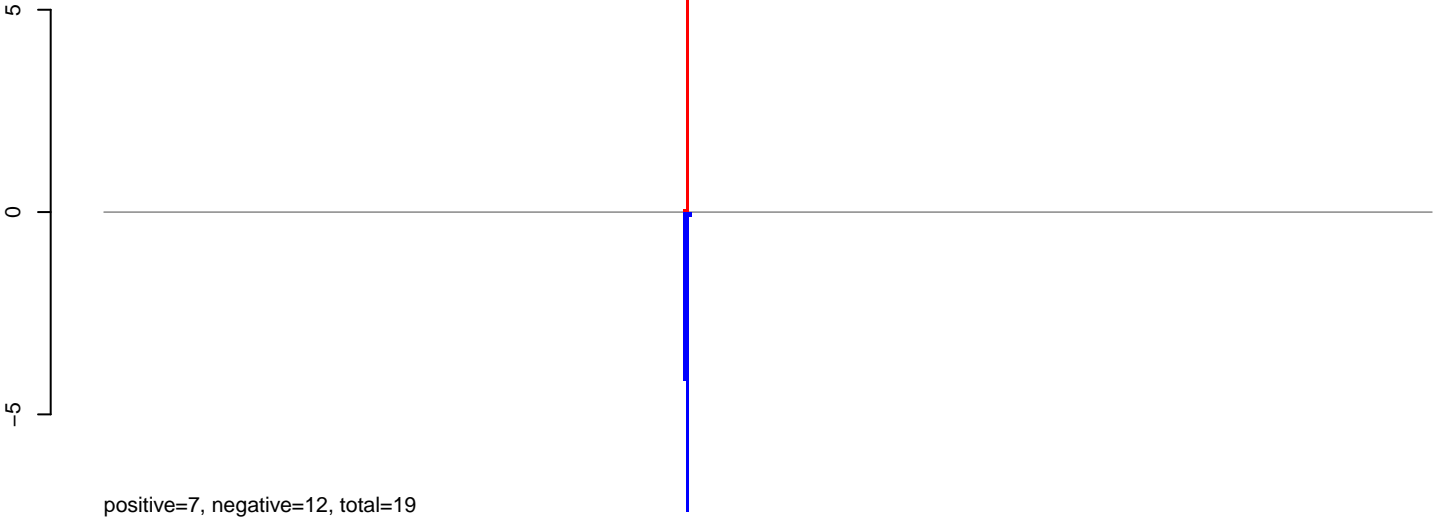
AeAeg_Aag2.SINV.GFP.24_35.rep



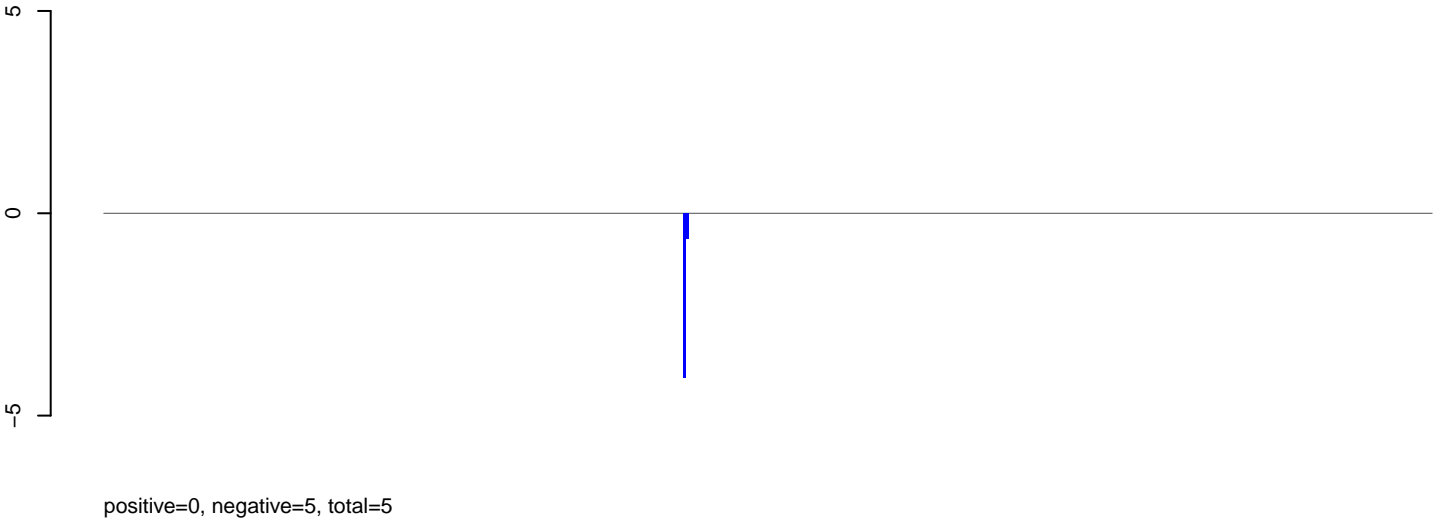
AeAeg_Aag2.SINV.GFP.rep



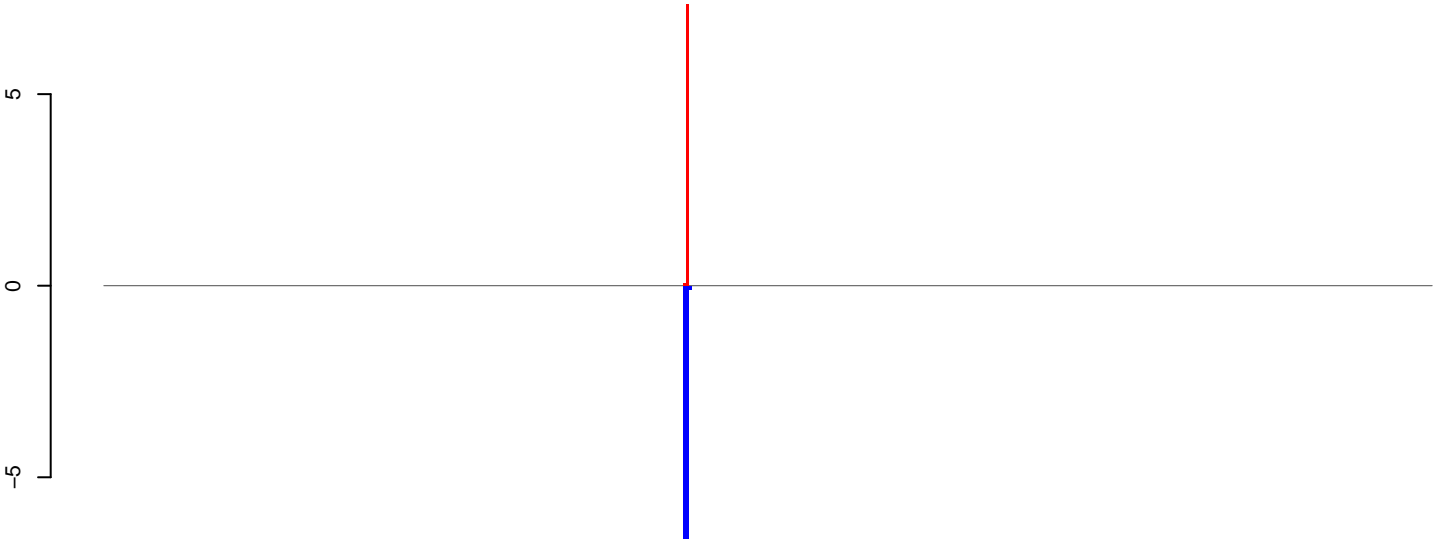
AeAeg_Aag2.SINV.GFP.18_23.rep



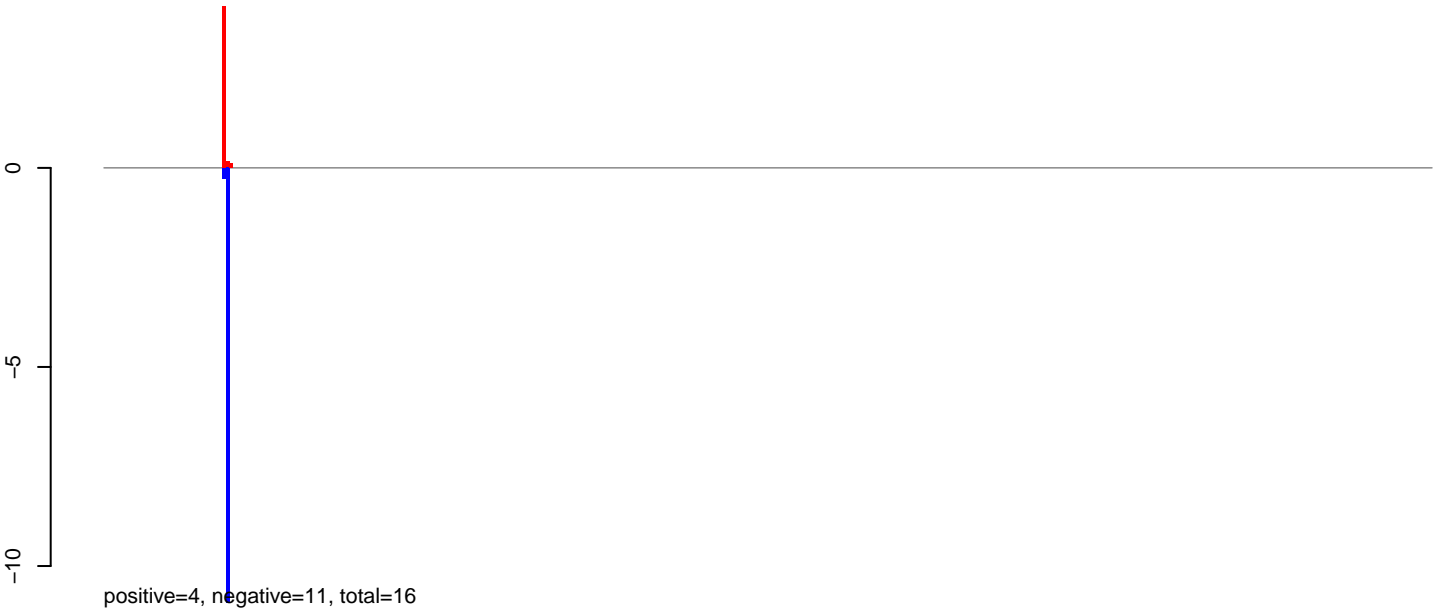
AeAeg_Aag2.SINV.GFP.24_35.rep



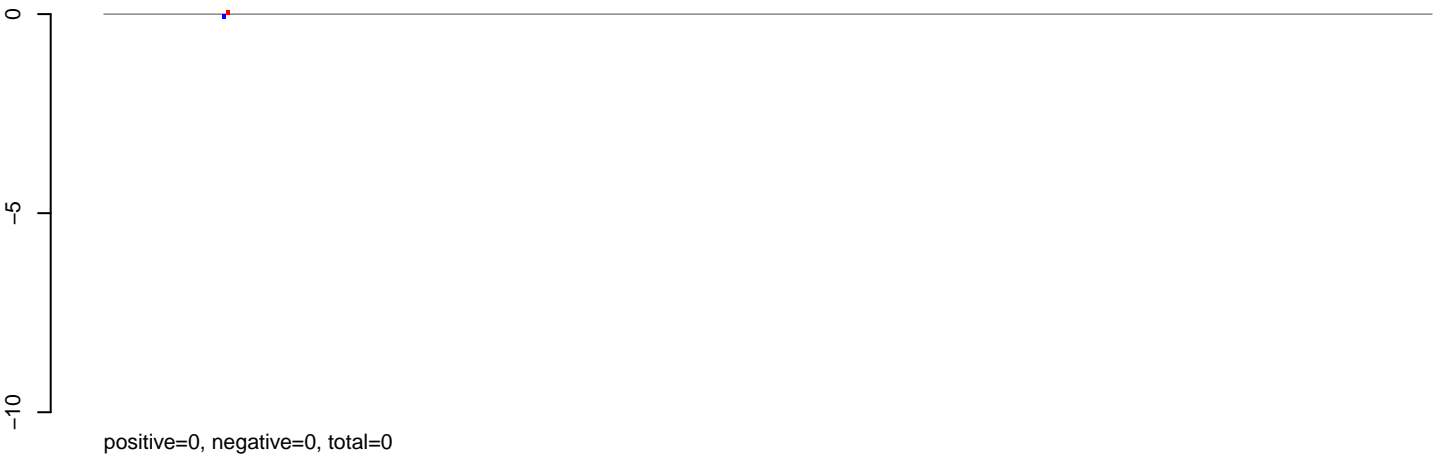
AeAeg_Aag2.SINV.GFP.rep



AeAeg_Aag2.SINV.GFP.18_23.rep



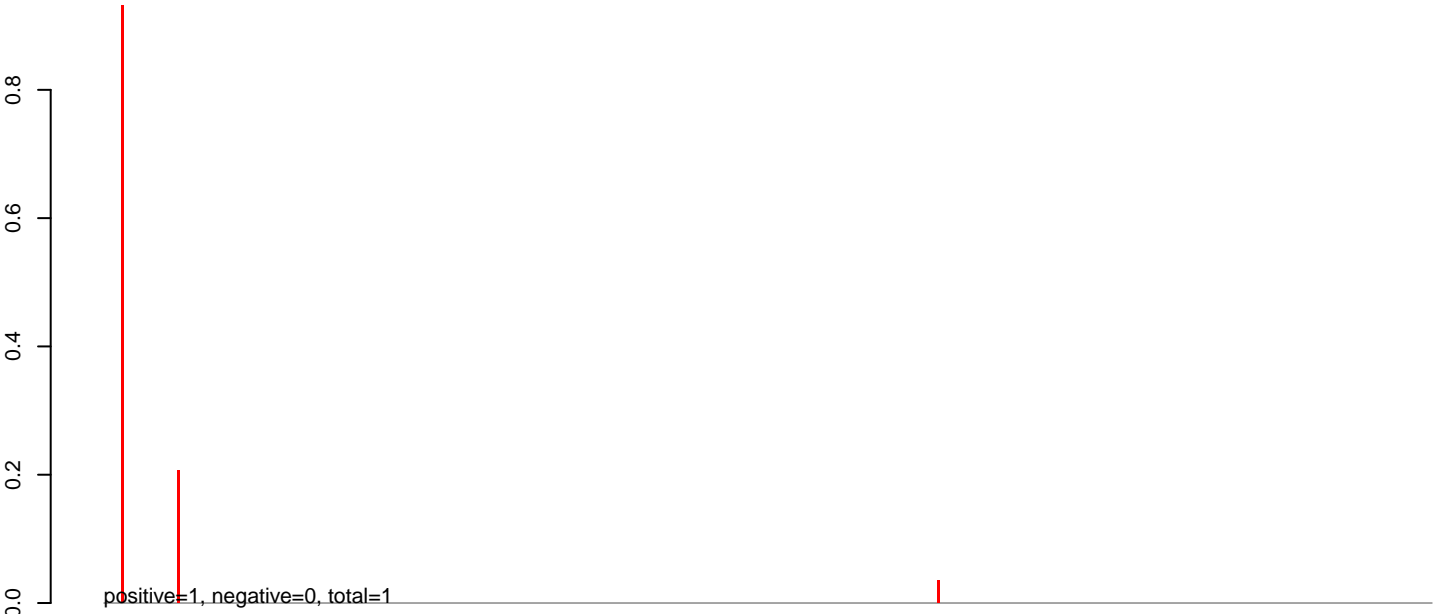
AeAeg_Aag2.SINV.GFP.24_35.rep



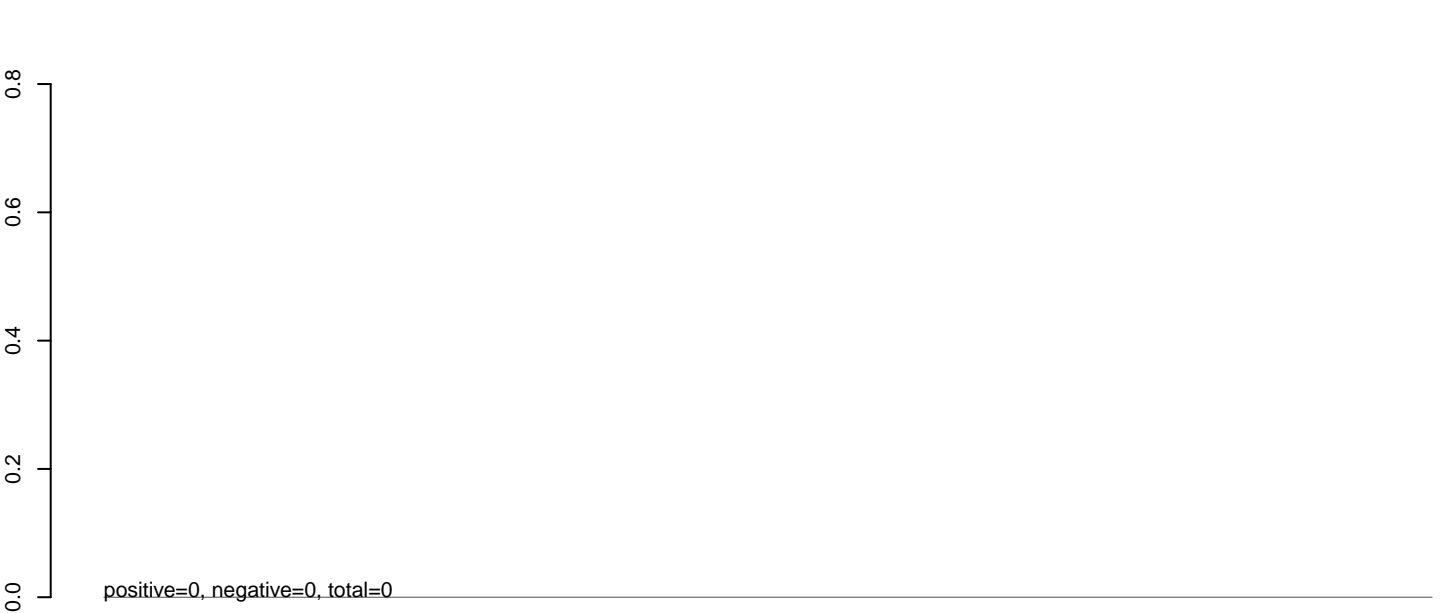
AeAeg_Aag2.SINV.GFP.rep



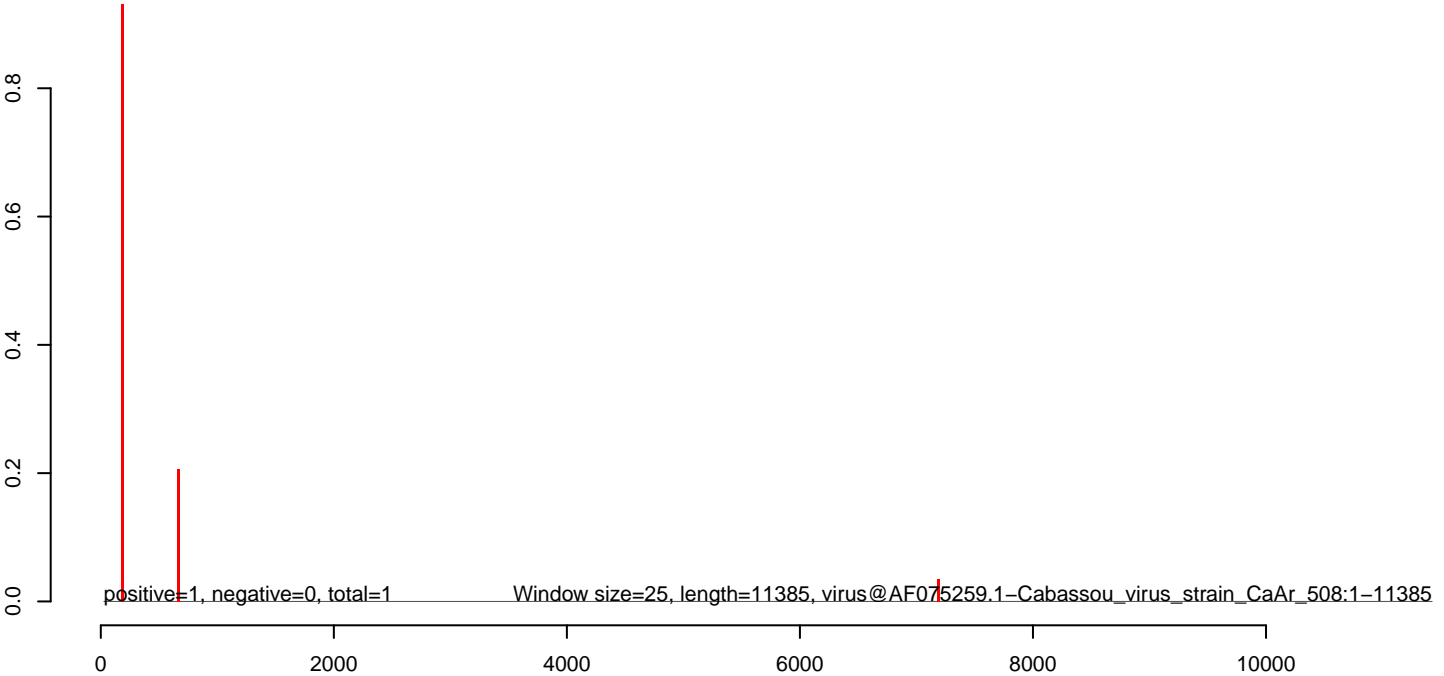
AeAeg_Aag2.SINV.GFP.18_23.rep



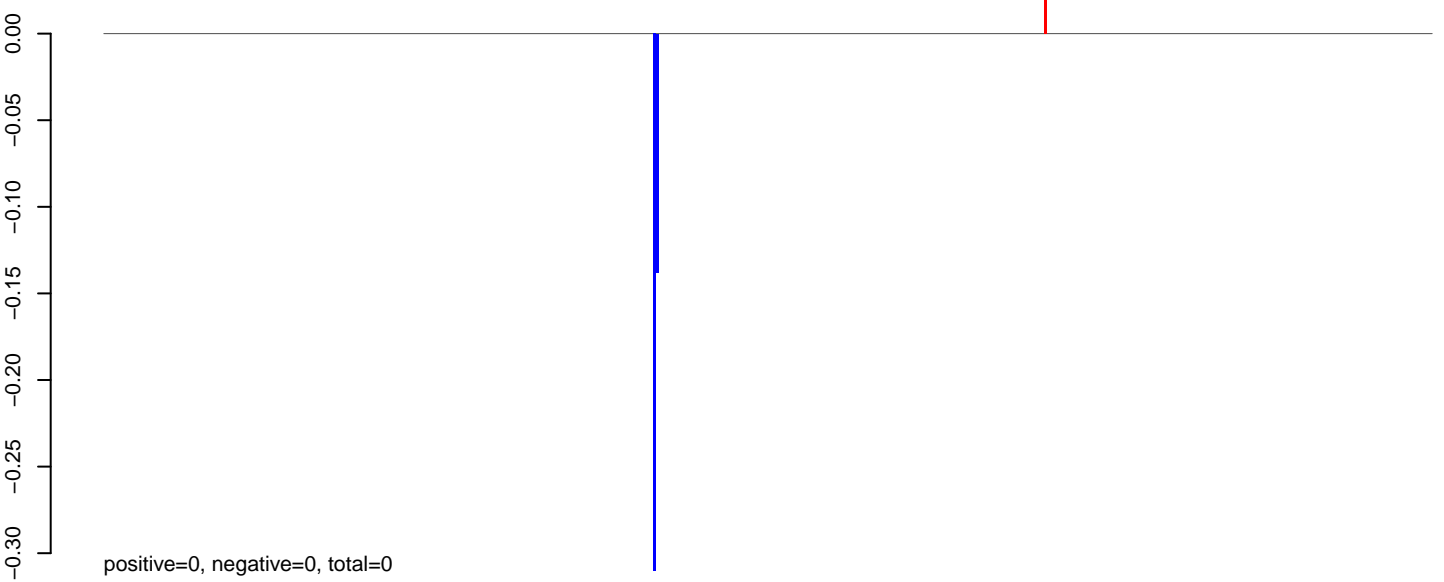
AeAeg_Aag2.SINV.GFP.24_35.rep



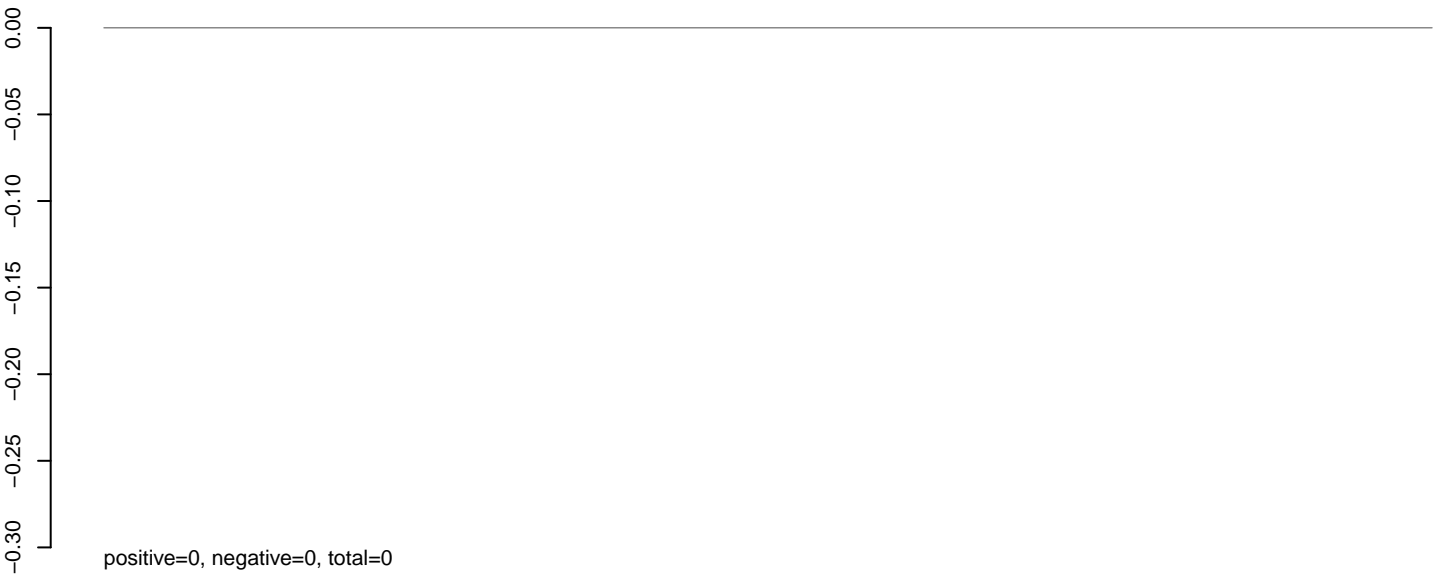
AeAeg_Aag2.SINV.GFP.rep



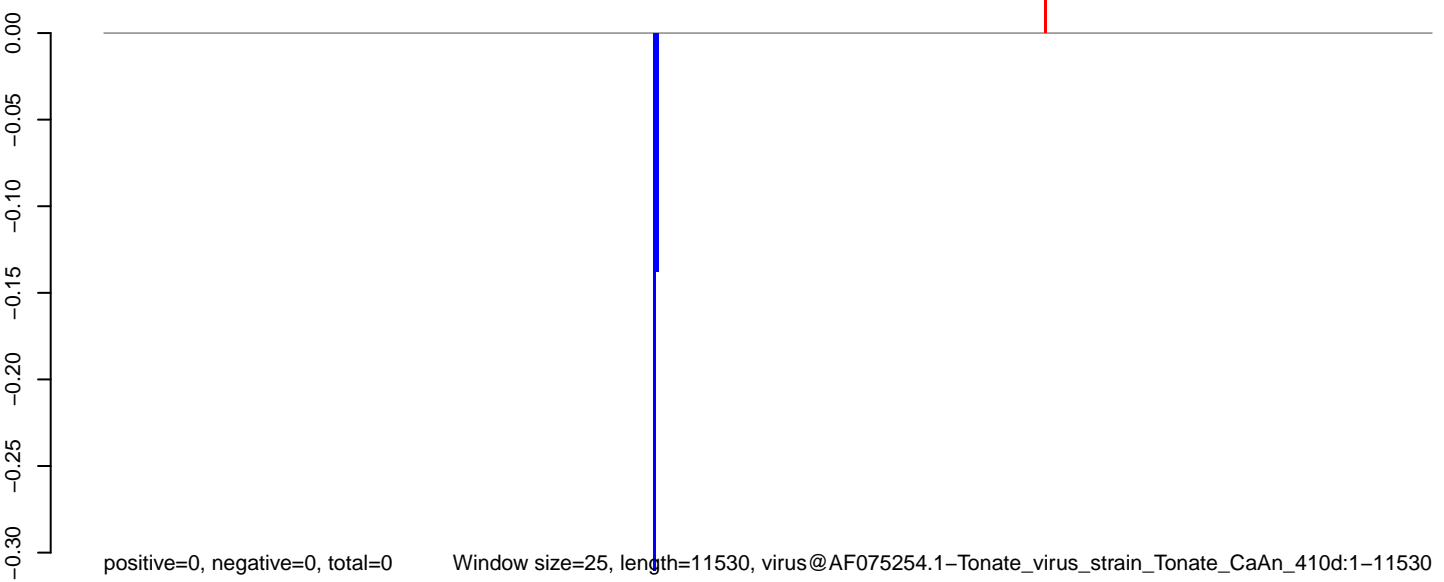
AeAeg_Aag2.SINV.GFP.18_23.rep



AeAeg_Aag2.SINV.GFP.24_35.rep



AeAeg_Aag2.SINV.GFP.rep

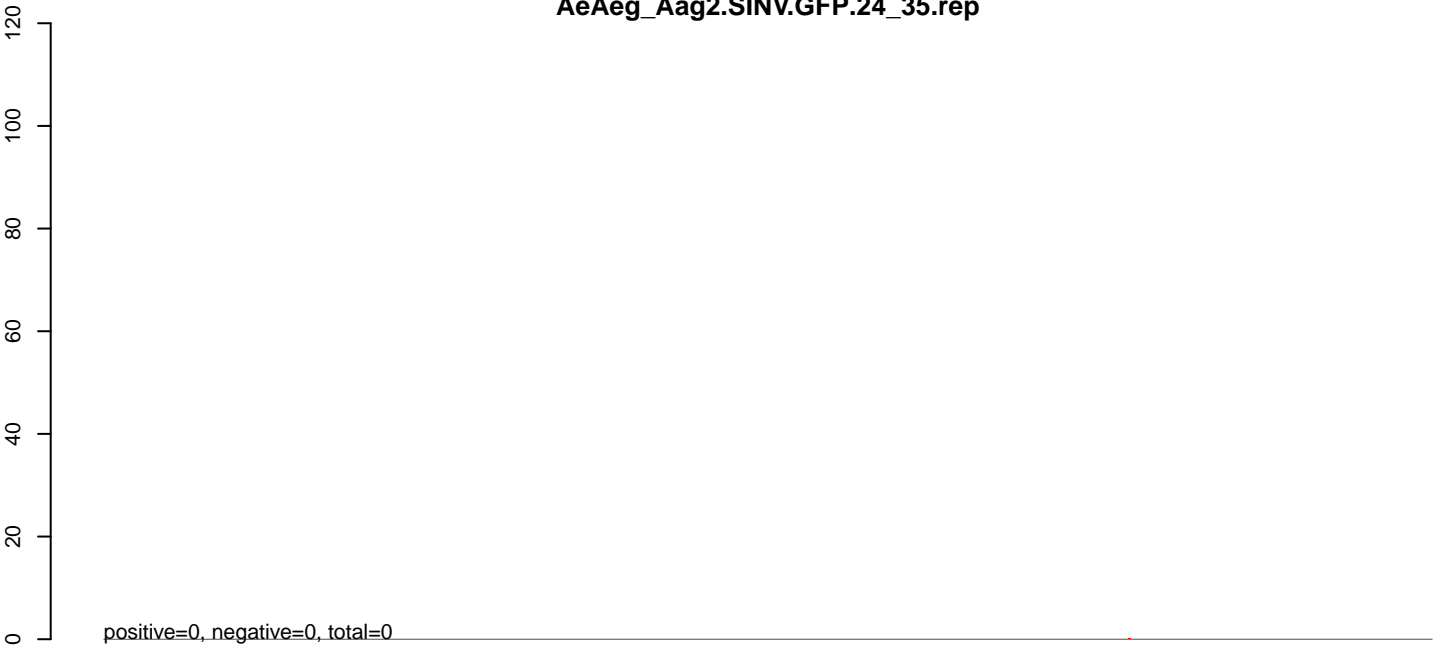


0 2000 4000 6000 8000 10000 12000

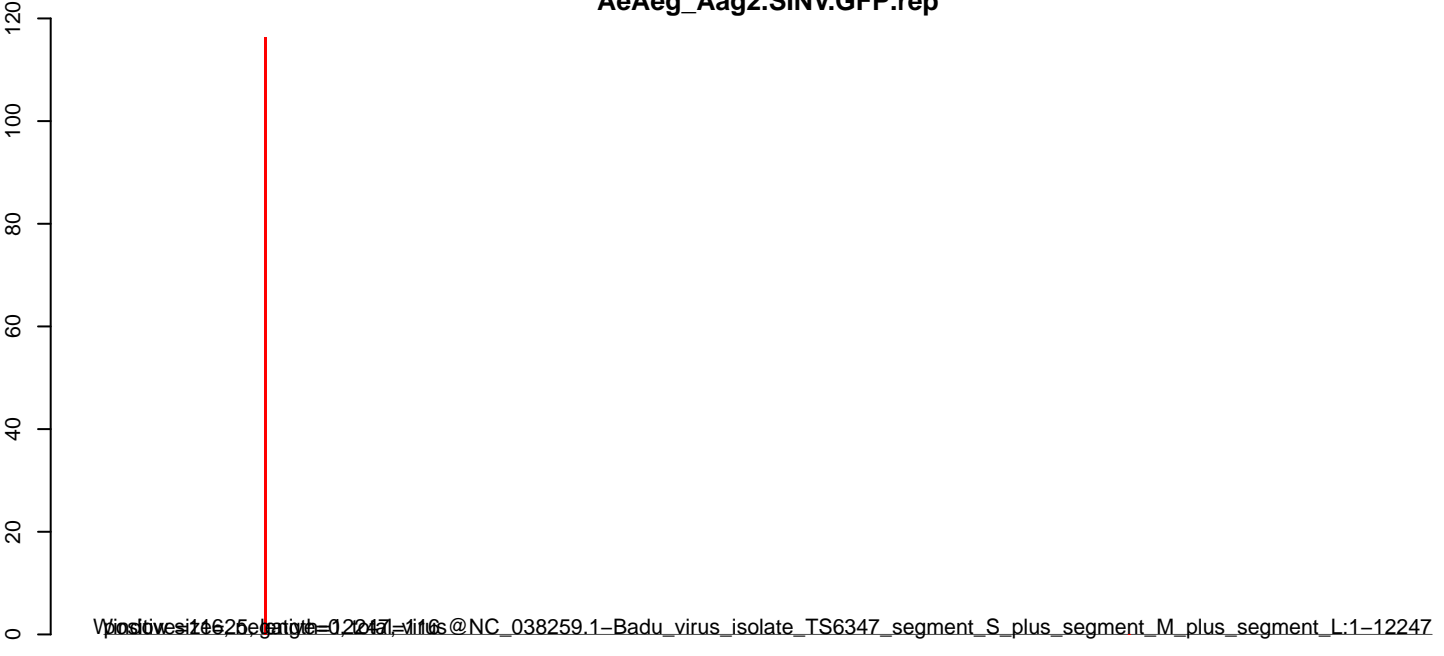
AeAeg_Aag2.SINV.GFP.18_23.rep



AeAeg_Aag2.SINV.GFP.24_35.rep



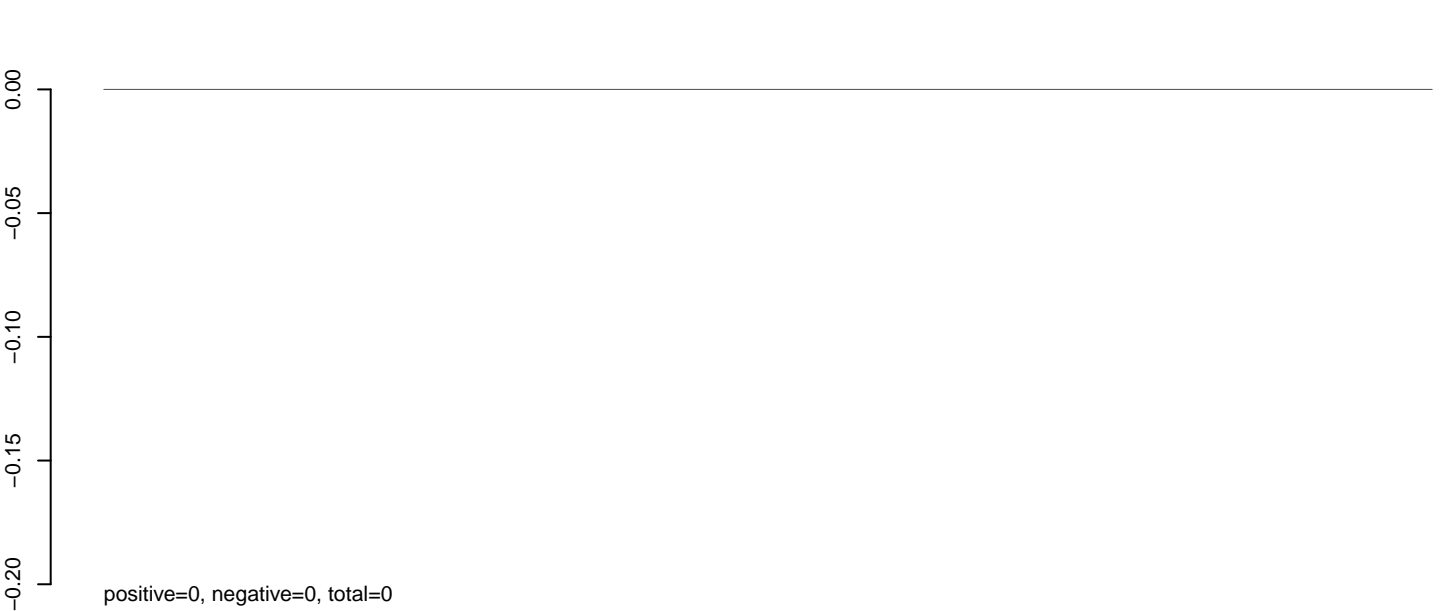
AeAeg_Aag2.SINV.GFP.rep



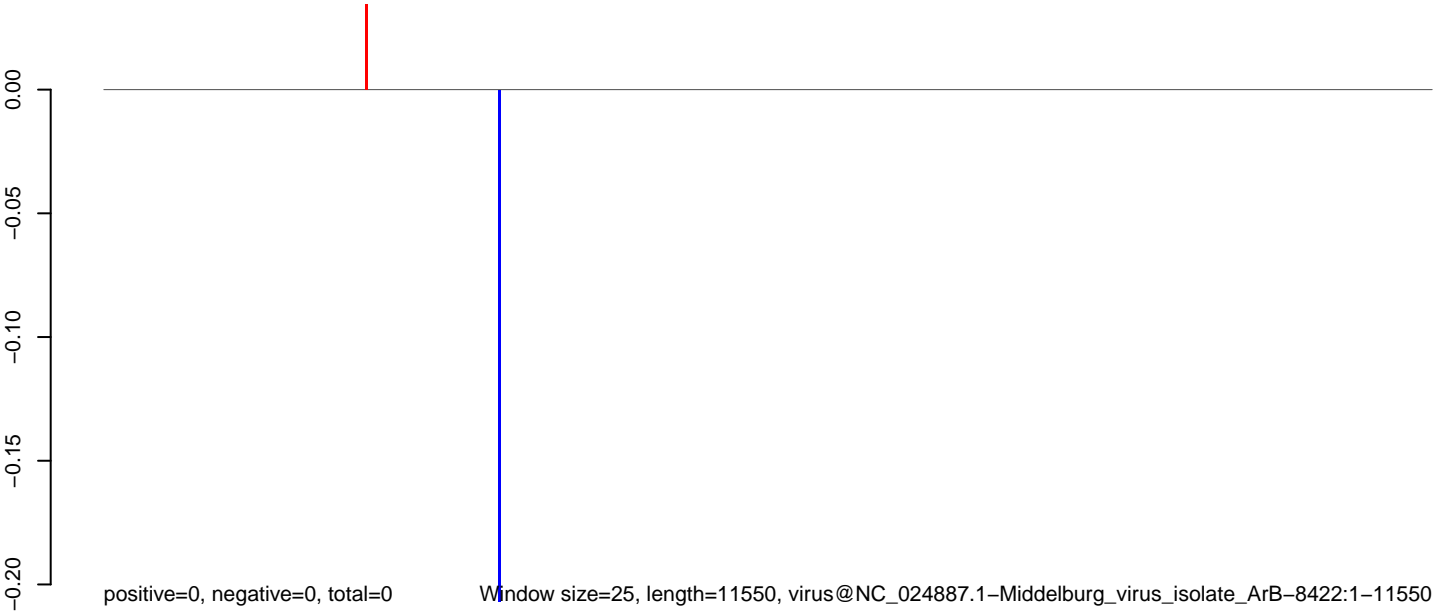
AeAeg_Aag2.SINV.GFP.18_23.rep



AeAeg_Aag2.SINV.GFP.24_35.rep



AeAeg_Aag2.SINV.GFP.rep



AeAeg_Aag2.SINV.GFP.18_23.rep

positive=1, negative=0, total=1

AeAeg_Aag2.SINV.GFP.24_35.rep

positive=0, negative=0, total=0

AeAeg_Aag2.SINV.GFP.rep

positive=1, negative=0, total=1

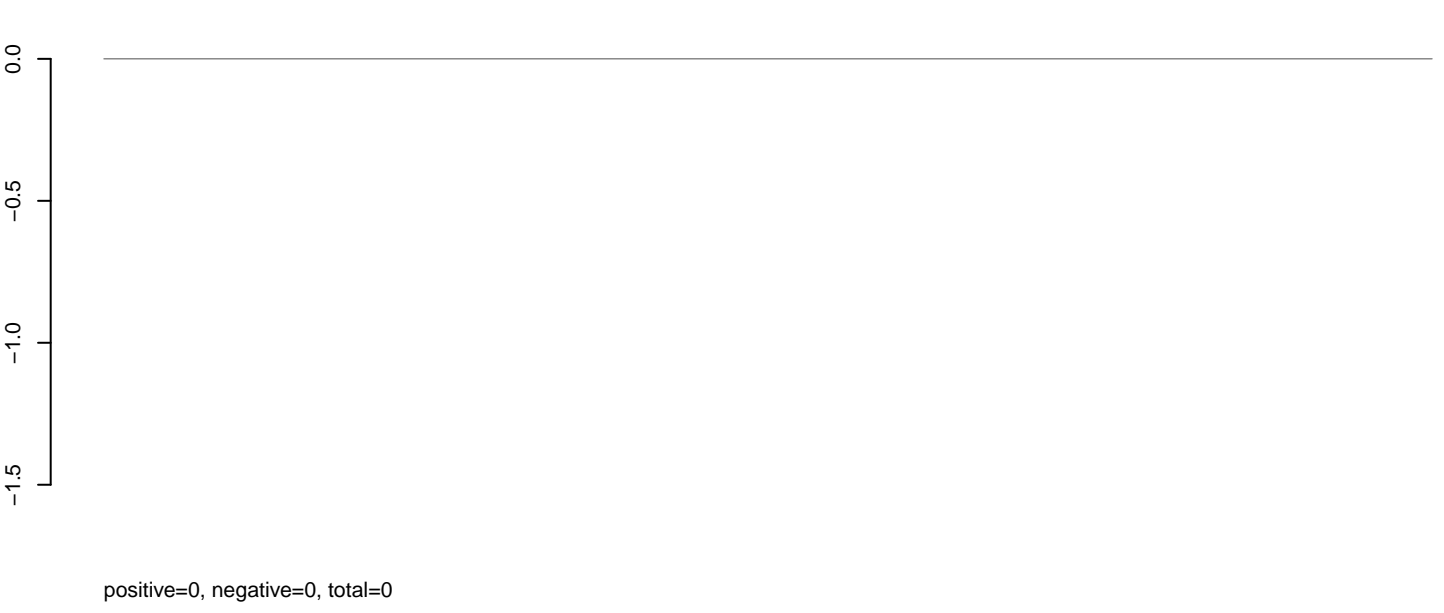
Window size=25, length=10815, virus@NC_009026.2-Bussuquara_virus1-10815

0 2000 4000 6000 8000 10000

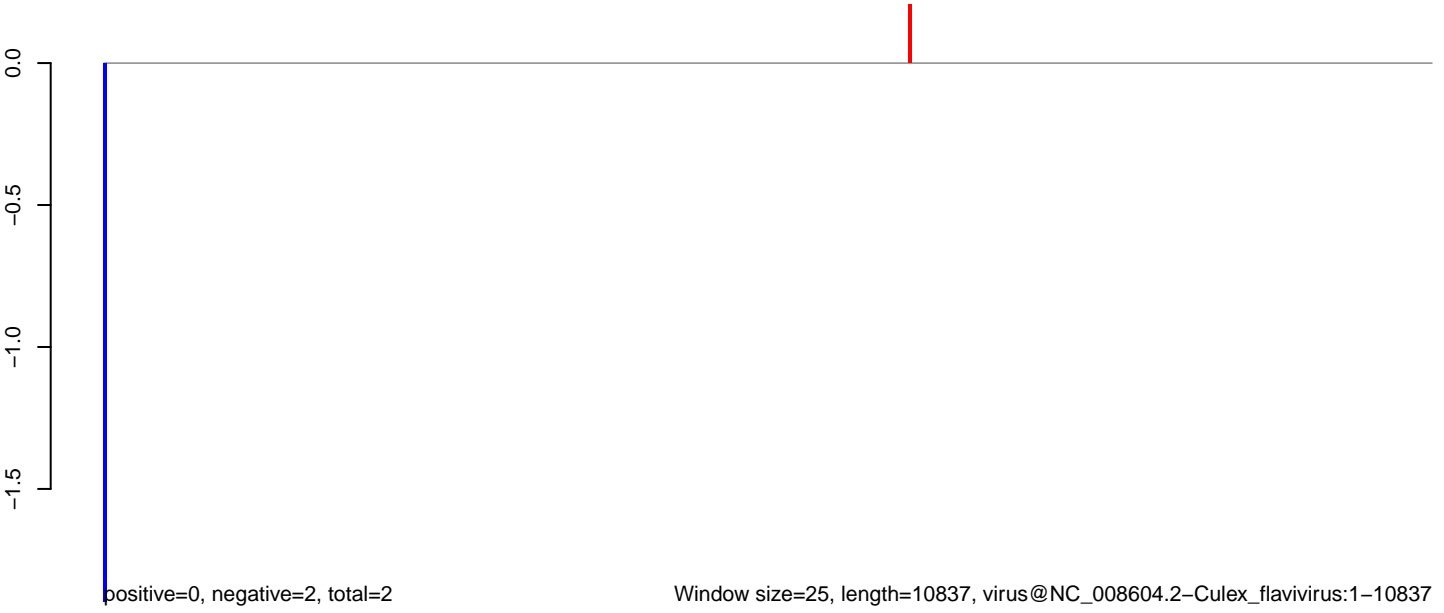
AeAeg_Aag2.SINV.GFP.18_23.rep



AeAeg_Aag2.SINV.GFP.24_35.rep



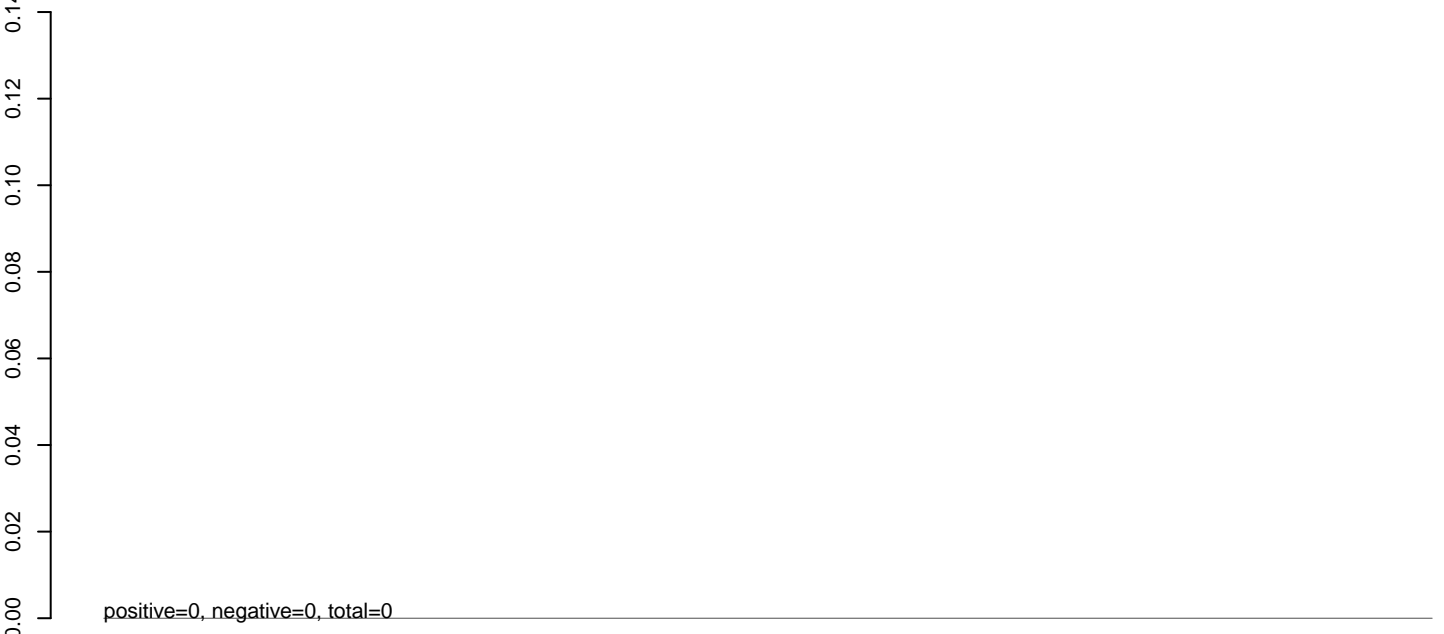
AeAeg_Aag2.SINV.GFP.rep



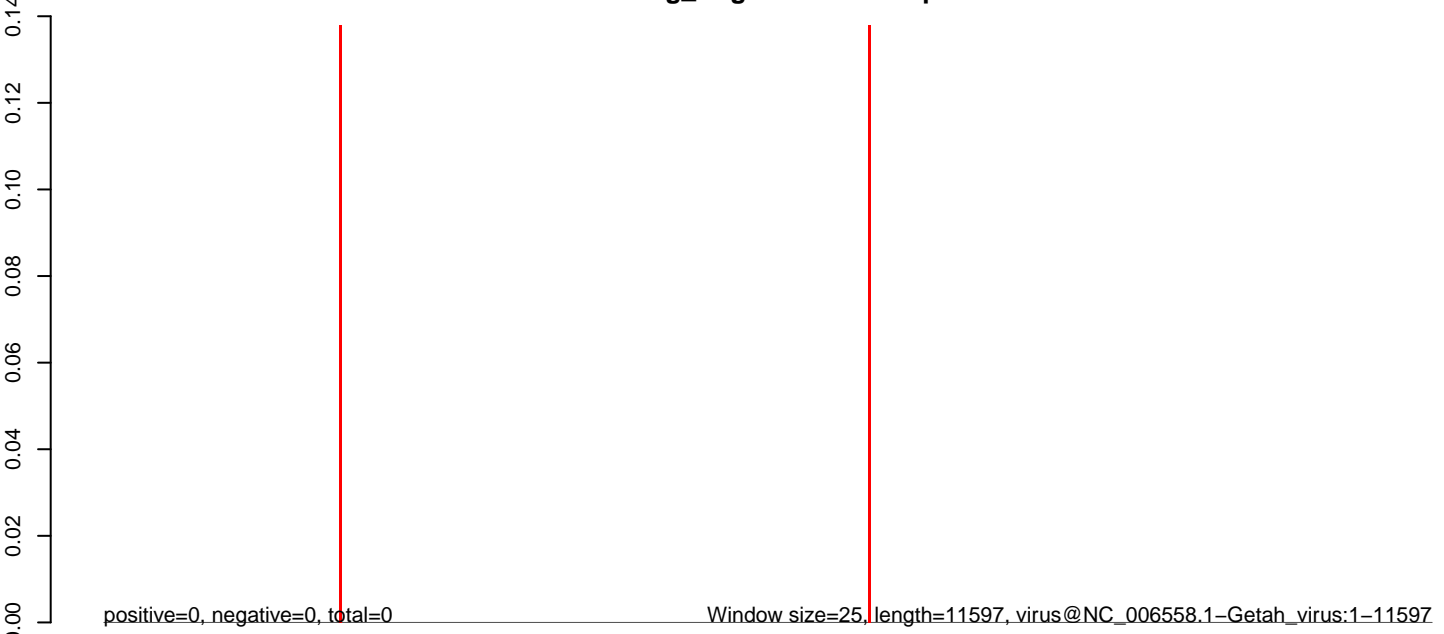
AeAeg_Aag2.SINV.GFP.18_23.rep



AeAeg_Aag2.SINV.GFP.24_35.rep



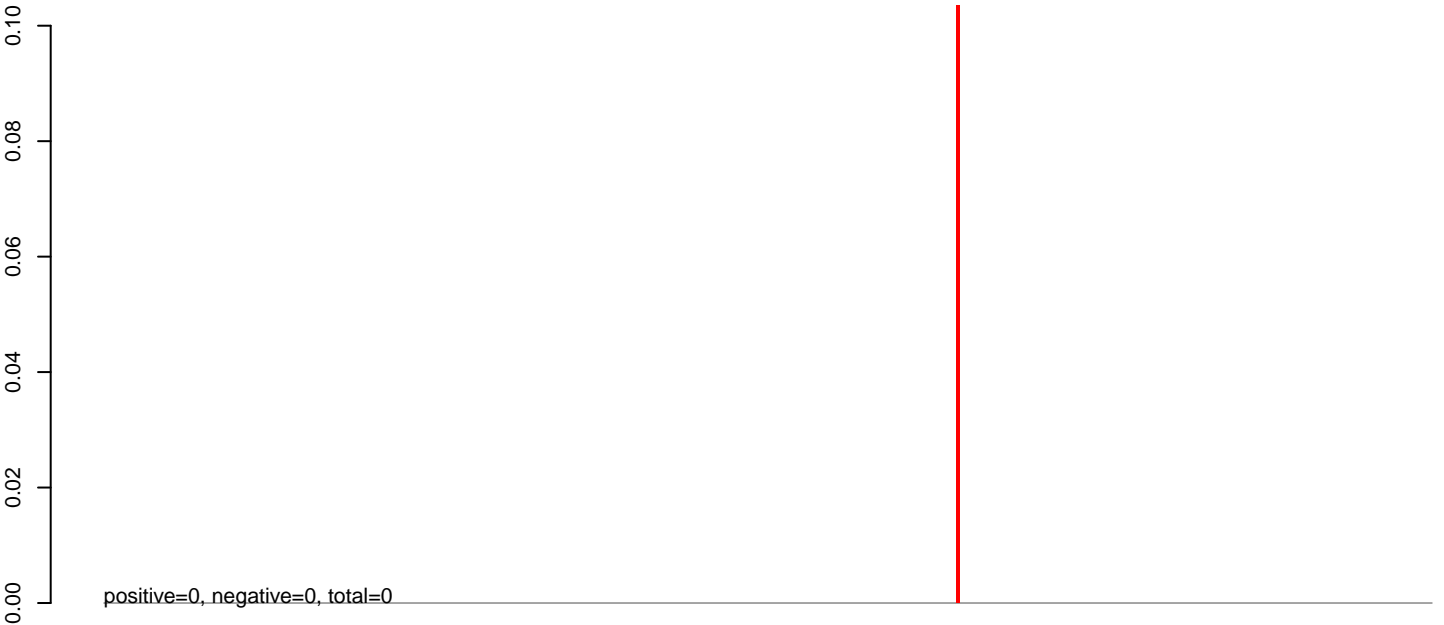
AeAeg_Aag2.SINV.GFP.rep



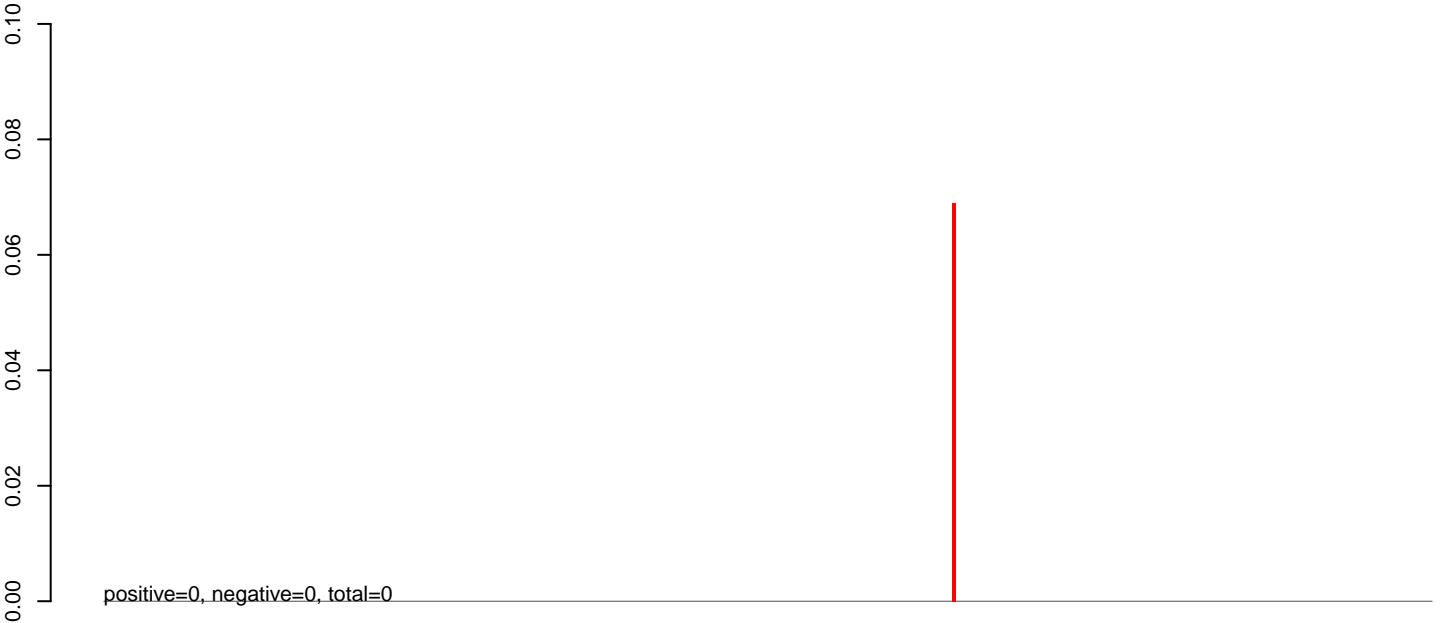
Window size=25, length=11597, virus@NC_006558.1-Getah_virus:1-11597

0 2000 4000 6000 8000 10000 12000

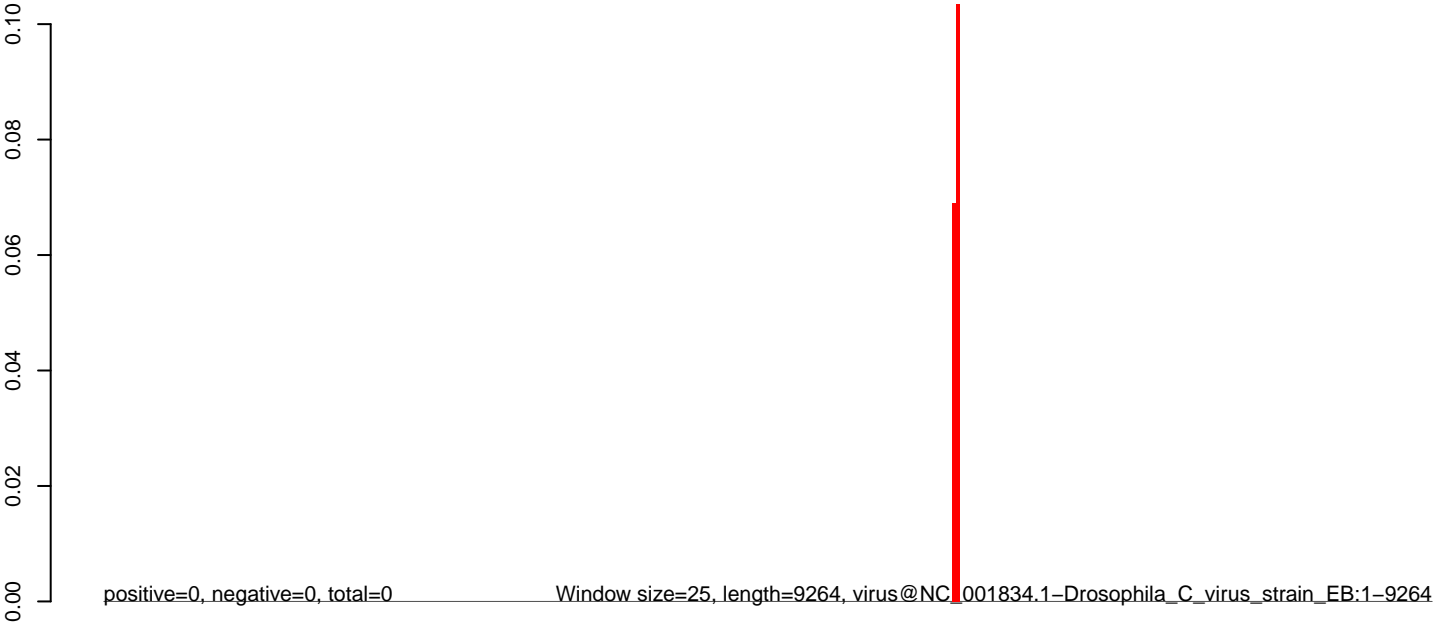
AeAeg_Aag2.SINV.GFP.18_23.rep



AeAeg_Aag2.SINV.GFP.24_35.rep



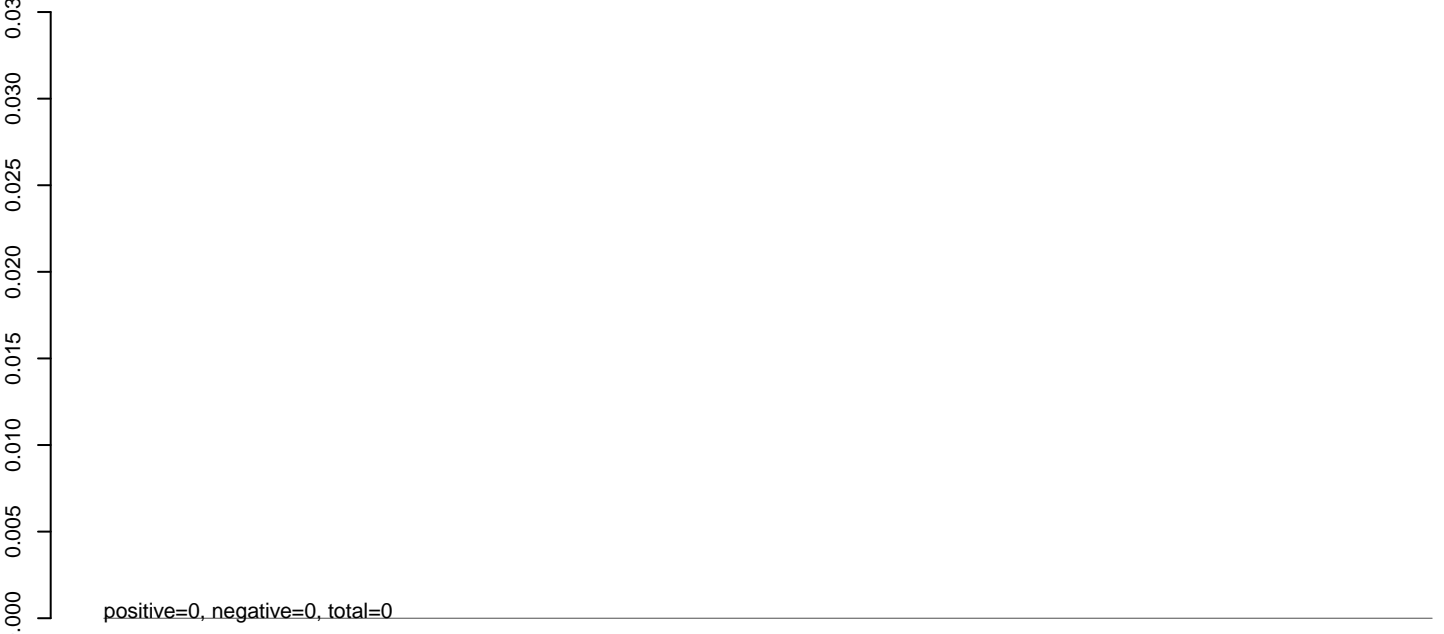
AeAeg_Aag2.SINV.GFP.rep



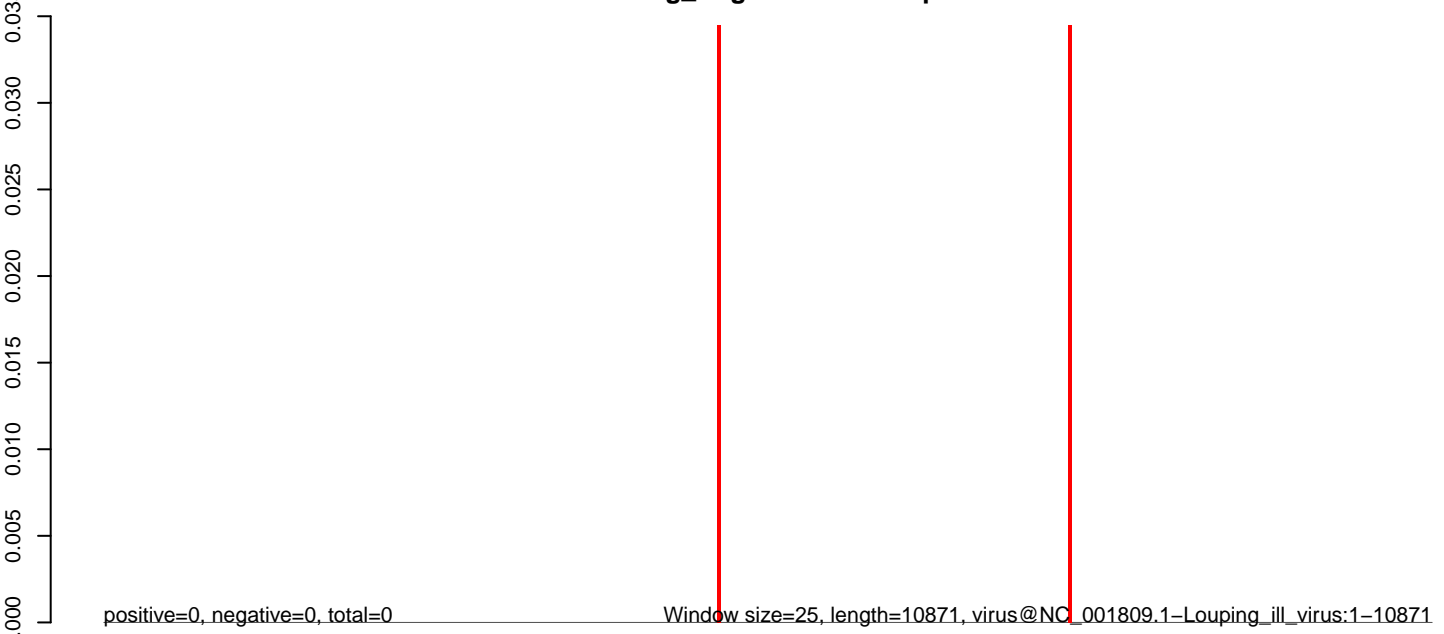
AeAeg_Aag2.SINV.GFP.18_23.rep



AeAeg_Aag2.SINV.GFP.24_35.rep

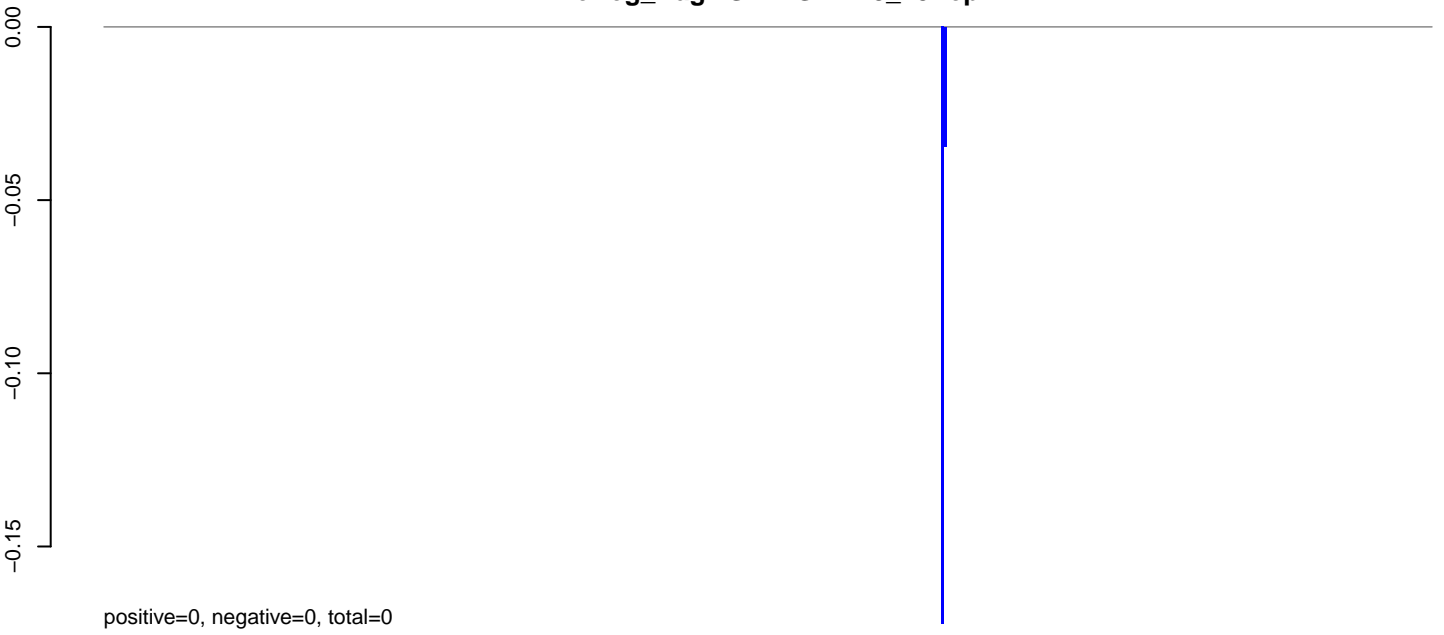


AeAeg_Aag2.SINV.GFP.rep

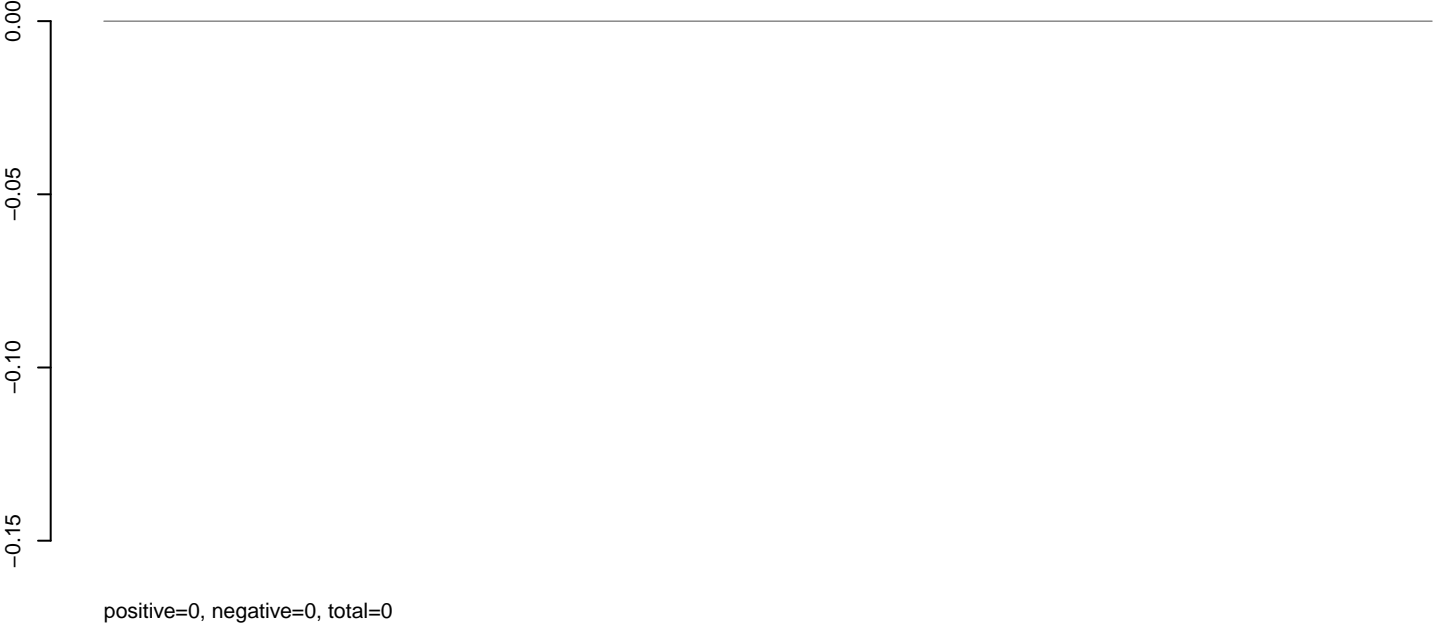


0 2000 4000 6000 8000 10000

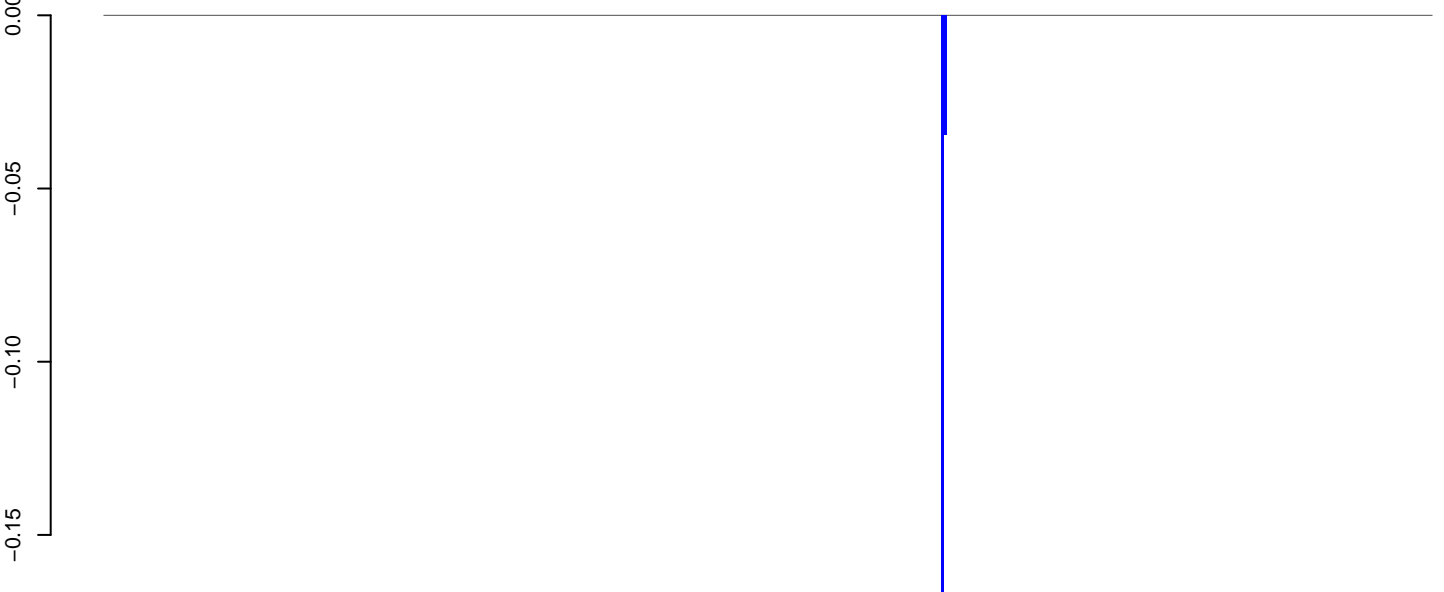
AeAeg_Aag2.SINV.GFP.18_23.rep



AeAeg_Aag2.SINV.GFP.24_35.rep



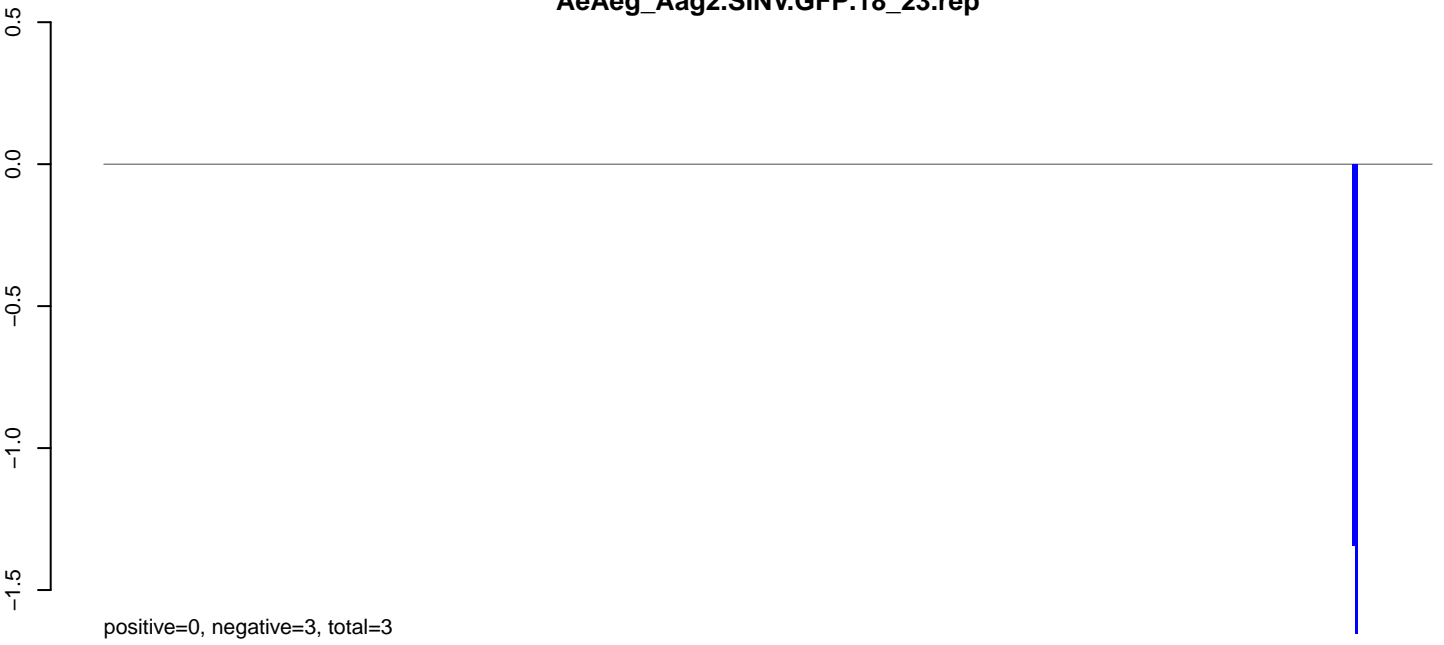
AeAeg_Aag2.SINV.GFP.rep



Window size=25, length=11488, virus@NC_001786.1-Barmah_Forest_virus:1-11488

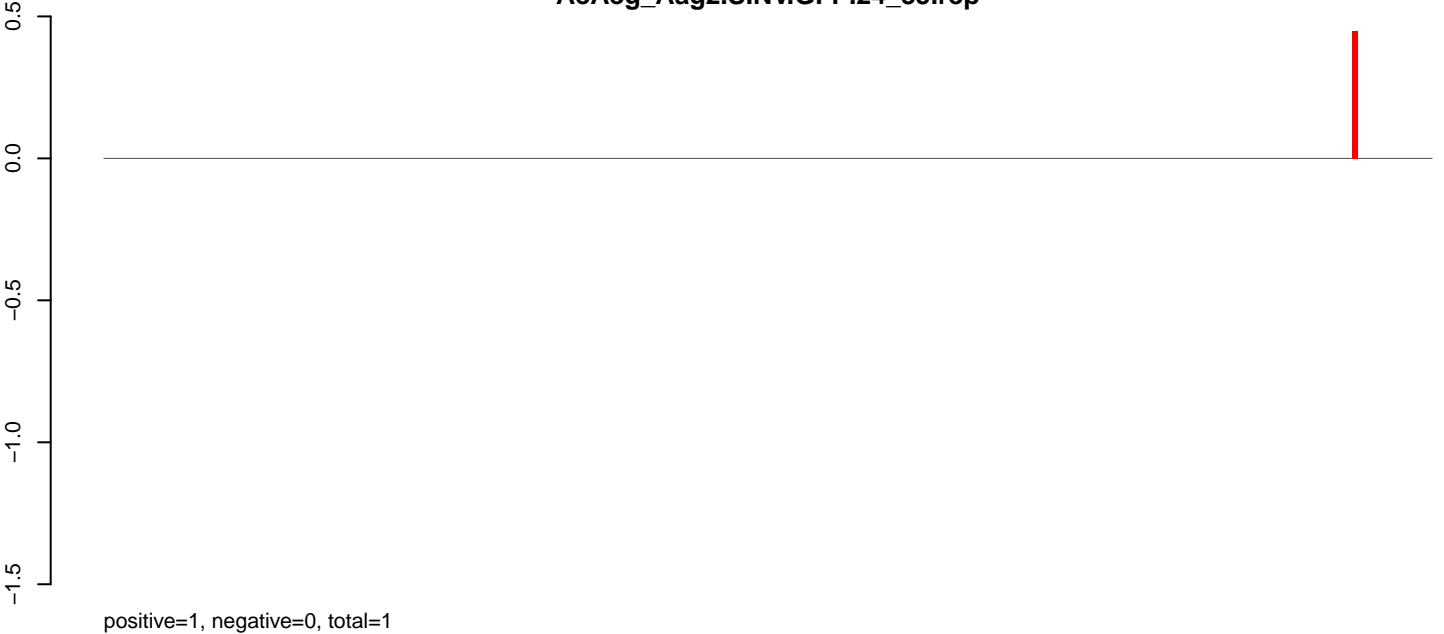
0 2000 4000 6000 8000 10000

AeAeg_Aag2.SINV.GFP.18_23.rep



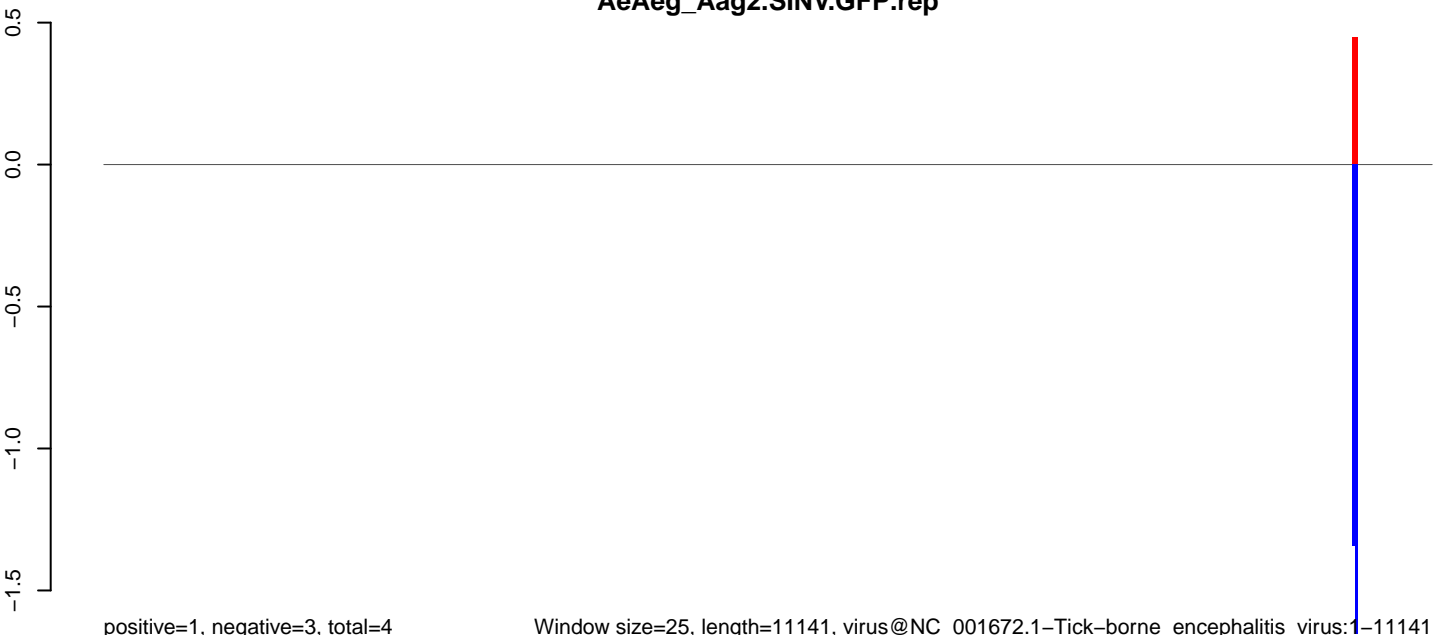
positive=0, negative=3, total=3

AeAeg_Aag2.SINV.GFP.24_35.rep



positive=1, negative=0, total=1

AeAeg_Aag2.SINV.GFP.rep

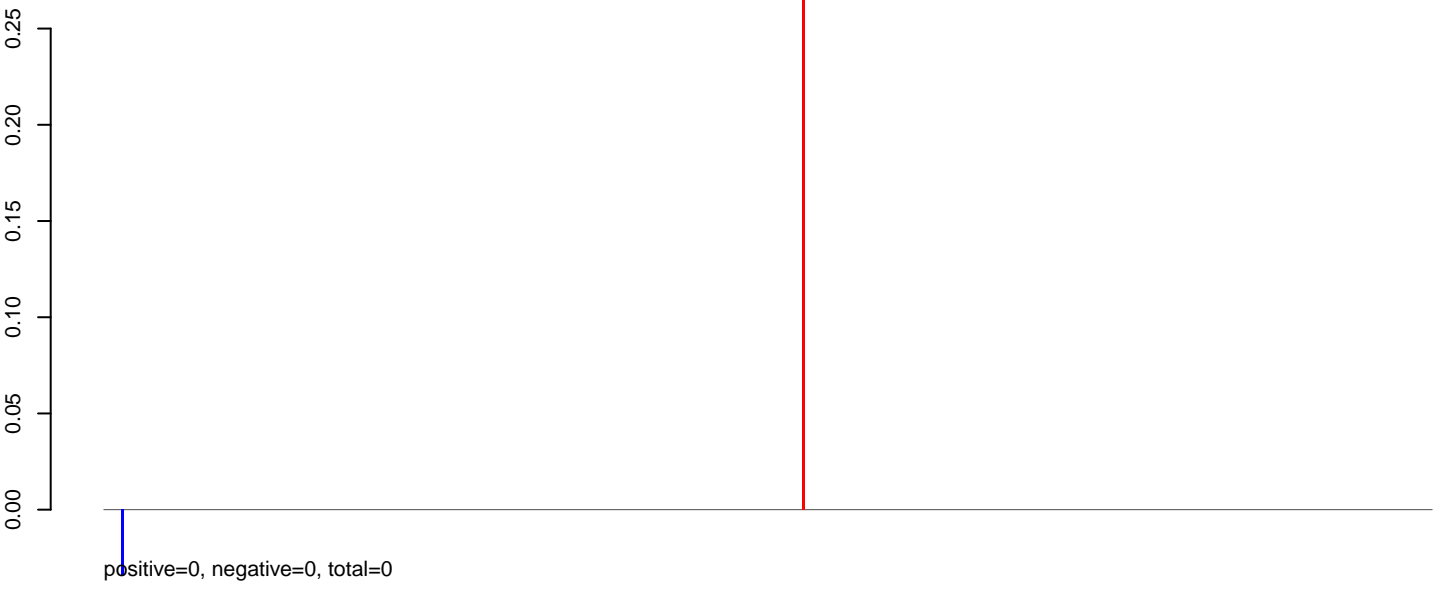


positive=1, negative=3, total=4

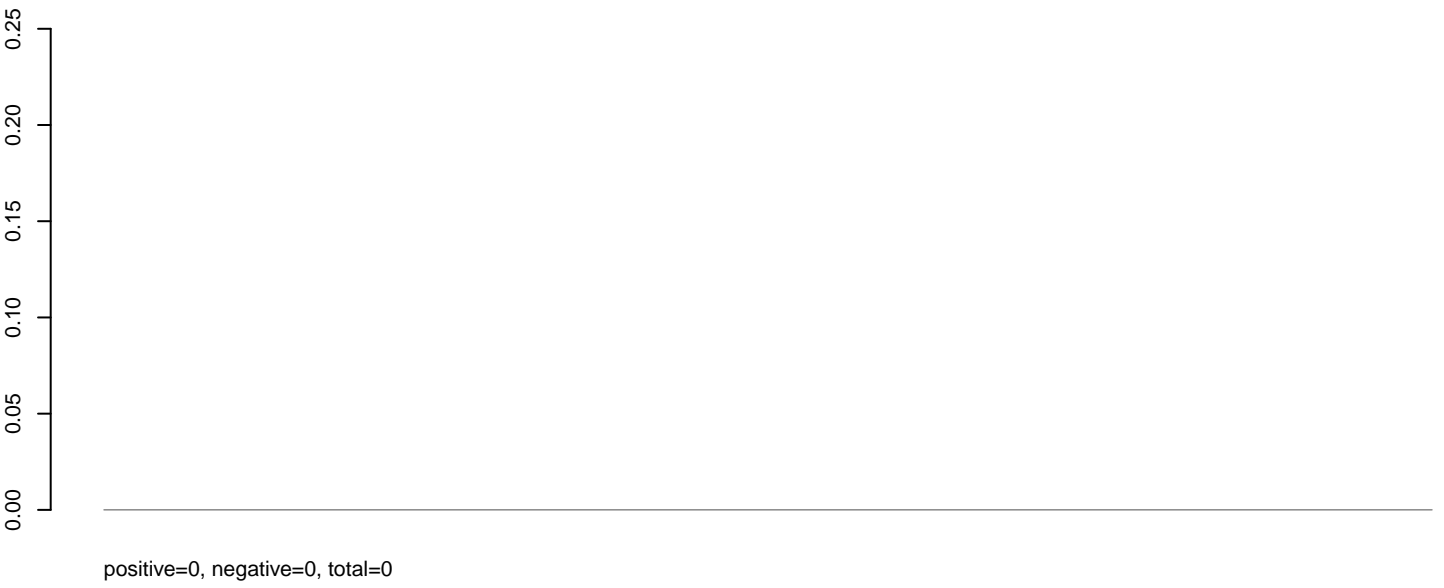
Window size=25, length=11141, virus@NC_001672.1-Tick-borne-encephalitis_virus:1-11141

0 2000 4000 6000 8000 10000

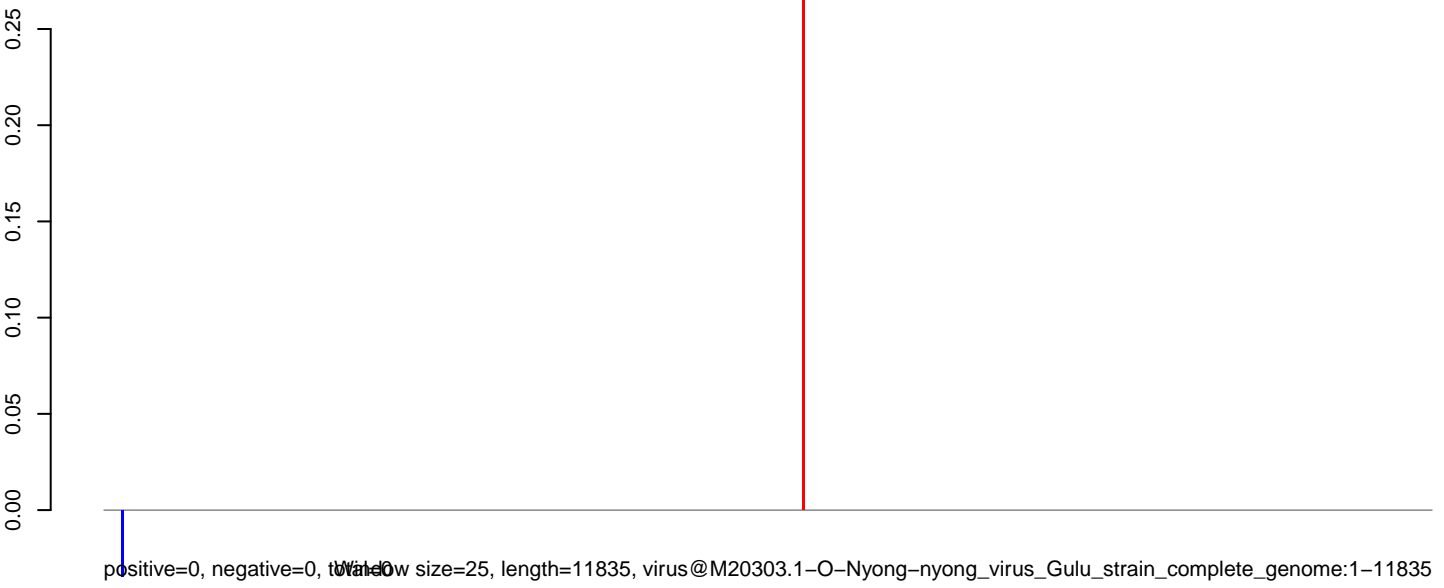
AeAeg_Aag2.SINV.GFP.18_23.rep



AeAeg_Aag2.SINV.GFP.24_35.rep



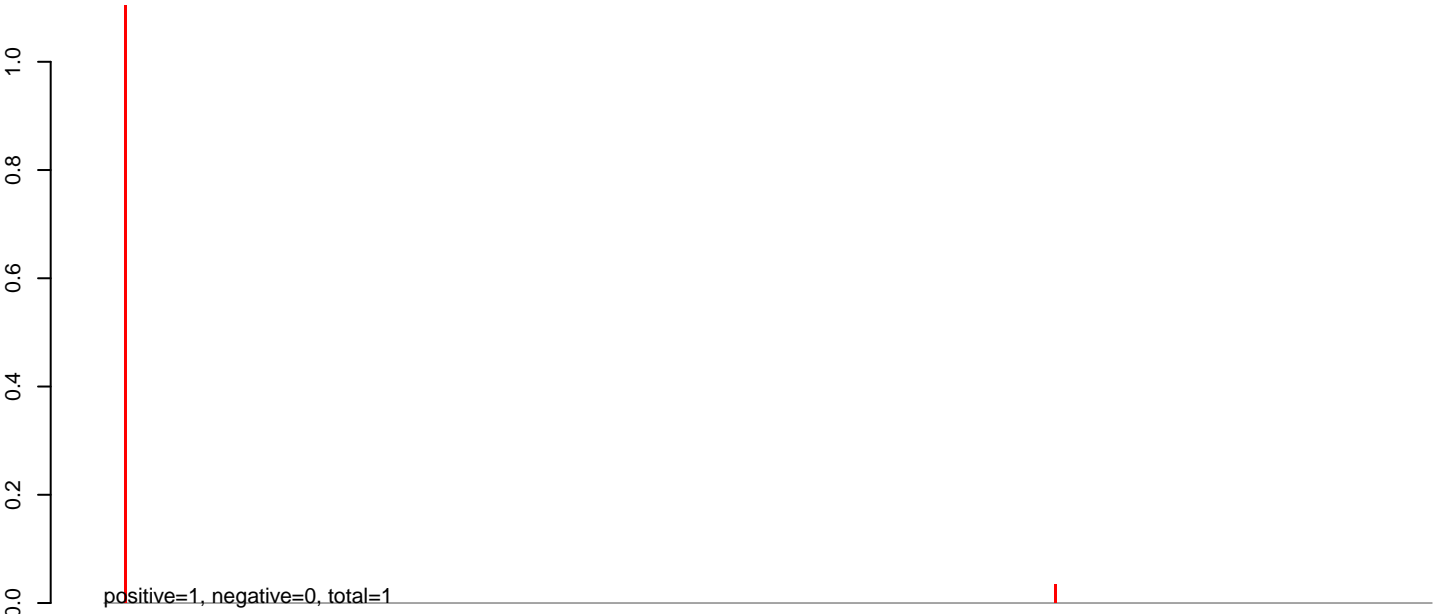
AeAeg_Aag2.SINV.GFP.rep



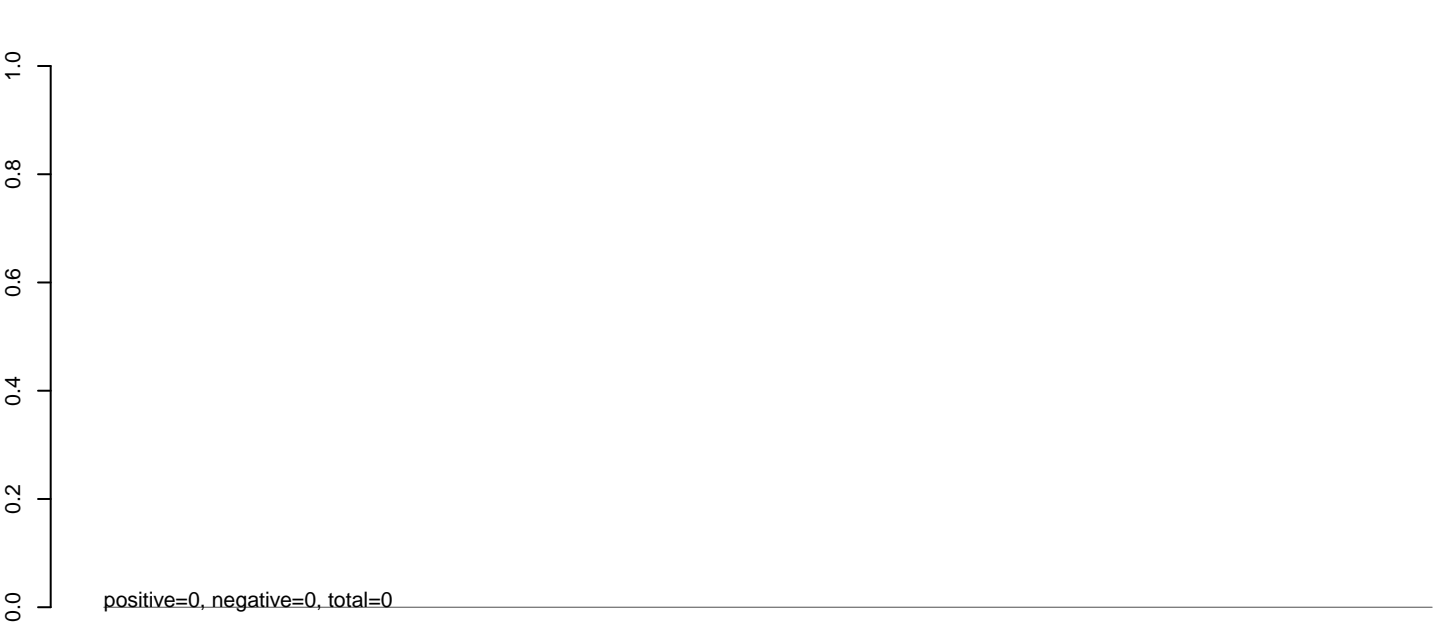
Window size=25, length=11835, virus@M20303.1-O-Nyong-nyong_virus_Gulu_strain_complete_genome:1-11835

0 2000 4000 6000 8000 10000 12000

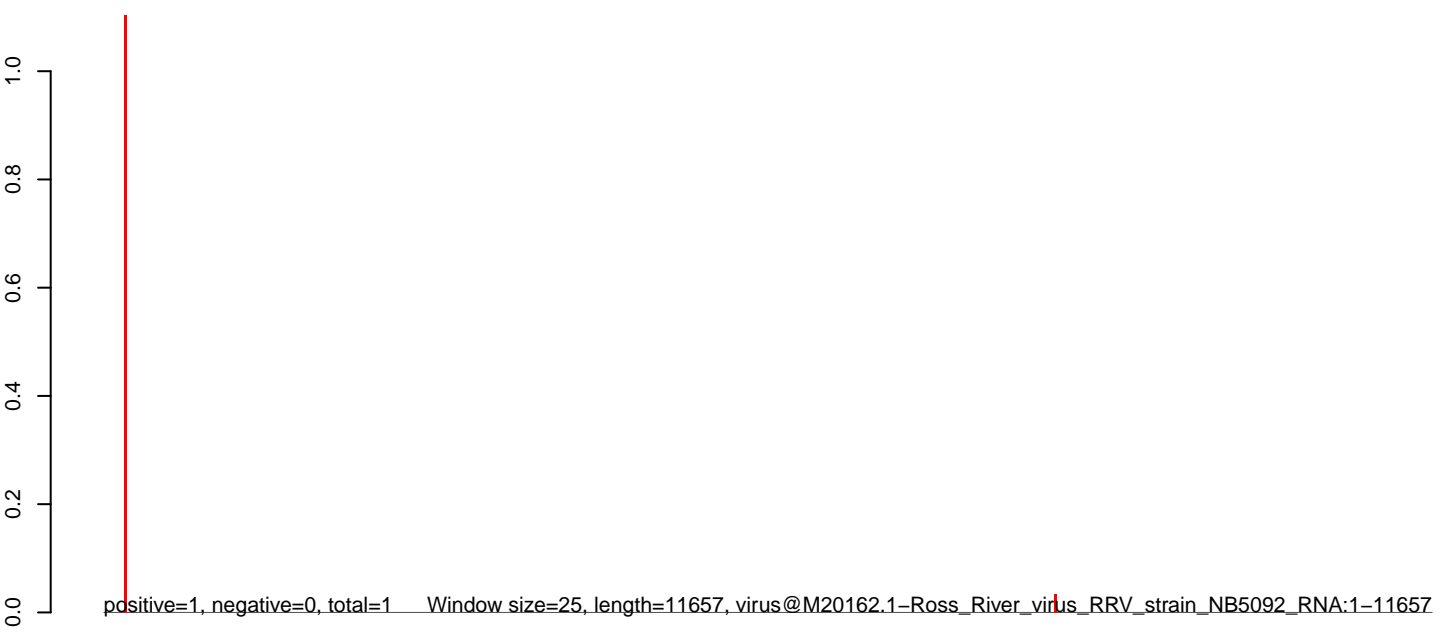
AeAeg_Aag2.SINV.GFP.18_23.rep



AeAeg_Aag2.SINV.GFP.24_35.rep



AeAeg_Aag2.SINV.GFP.rep

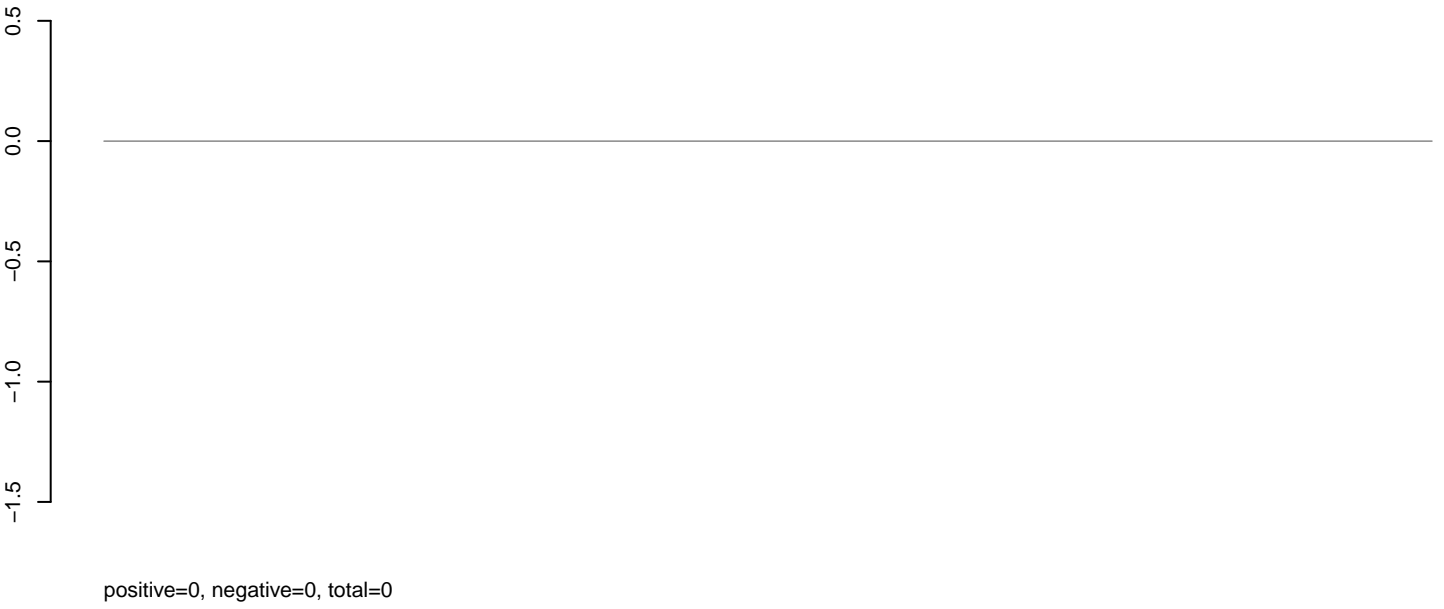


Window size=25, length=11657, virus@M20162.1-Ross_River_virus_RRV_strain_NB5092_RNA:1-11657

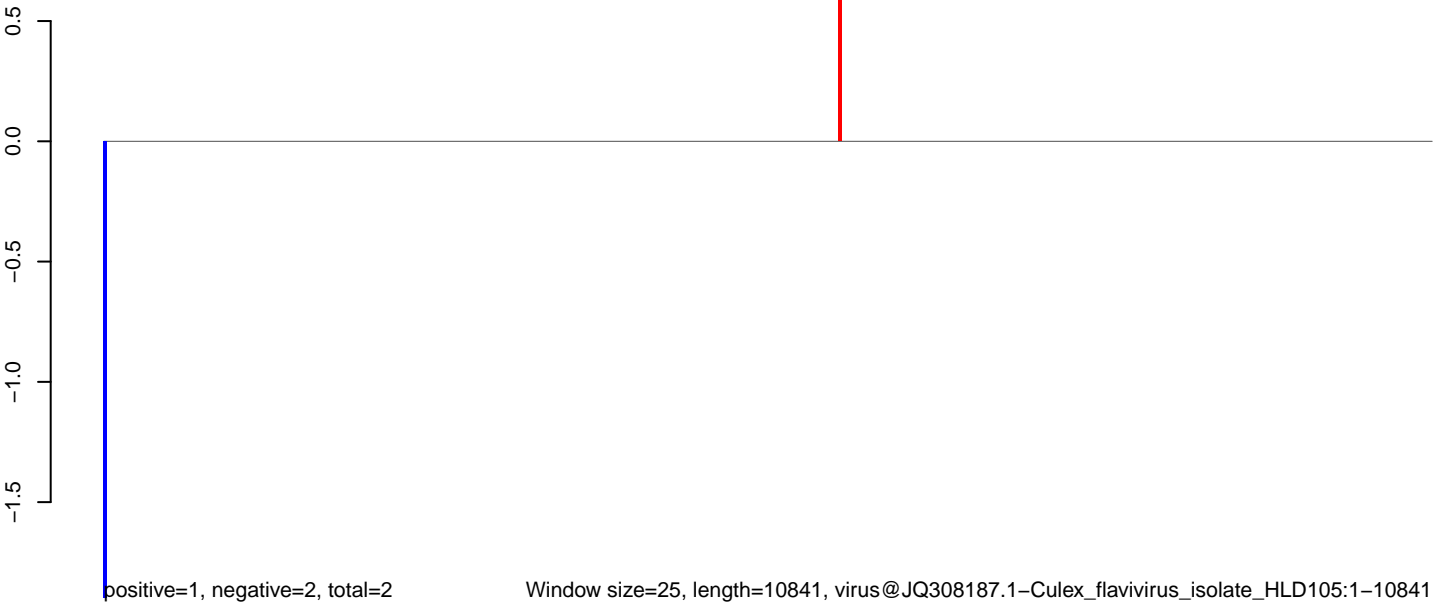
AeAeg_Aag2.SINV.GFP.18_23.rep



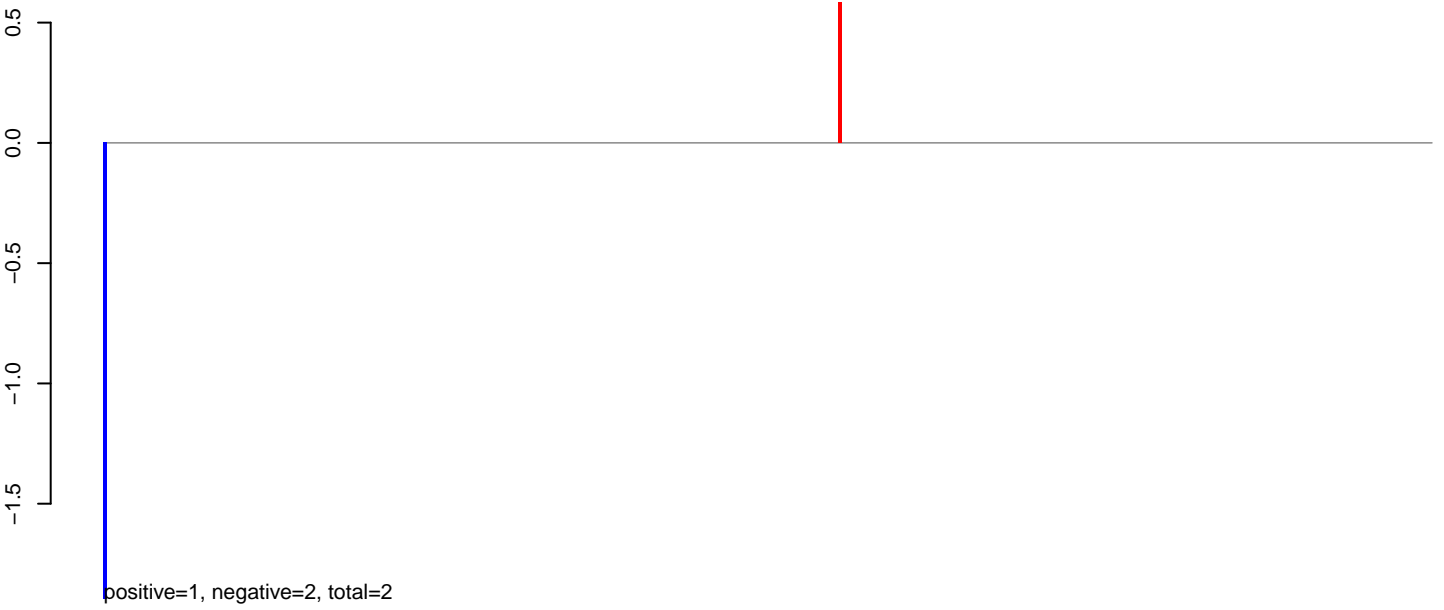
AeAeg_Aag2.SINV.GFP.24_35.rep



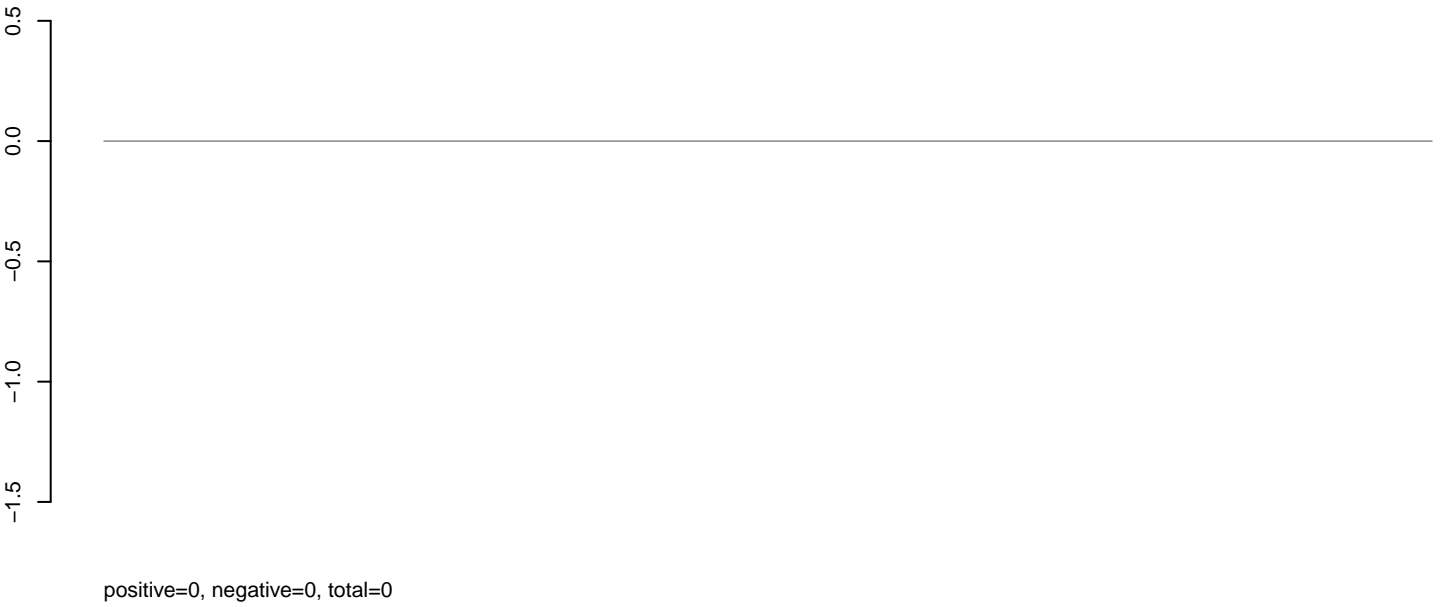
AeAeg_Aag2.SINV.GFP.rep



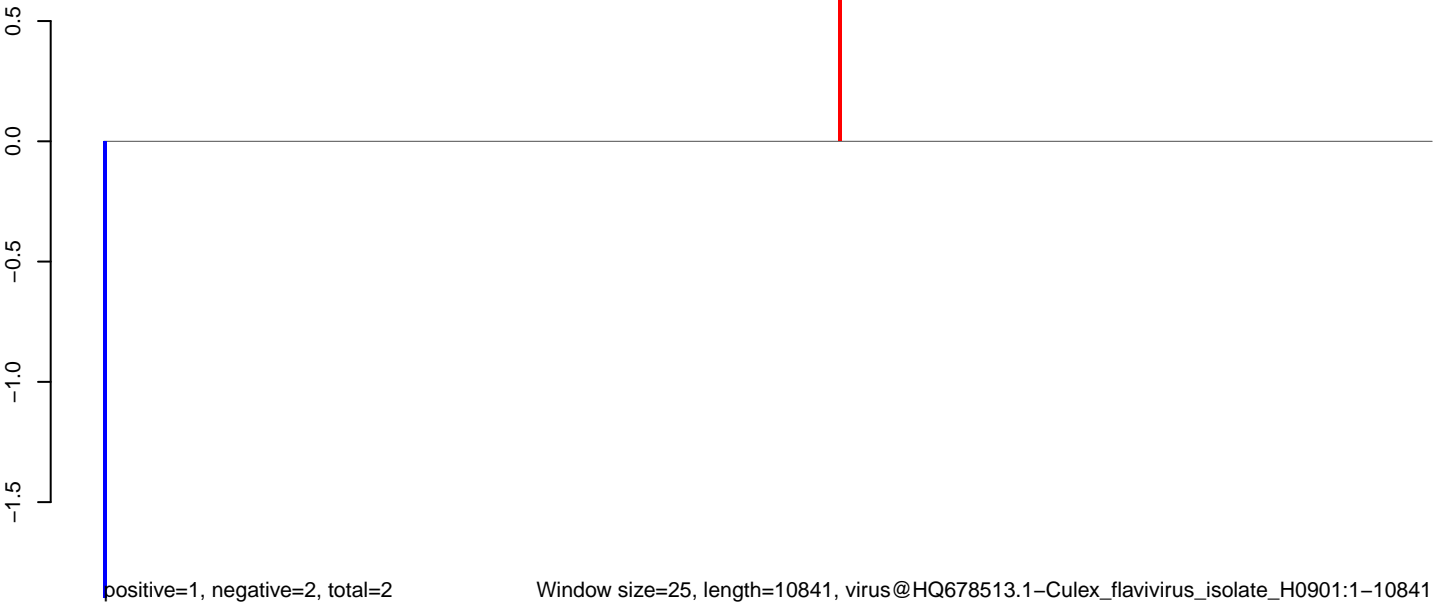
AeAeg_Aag2.SINV.GFP.18_23.rep



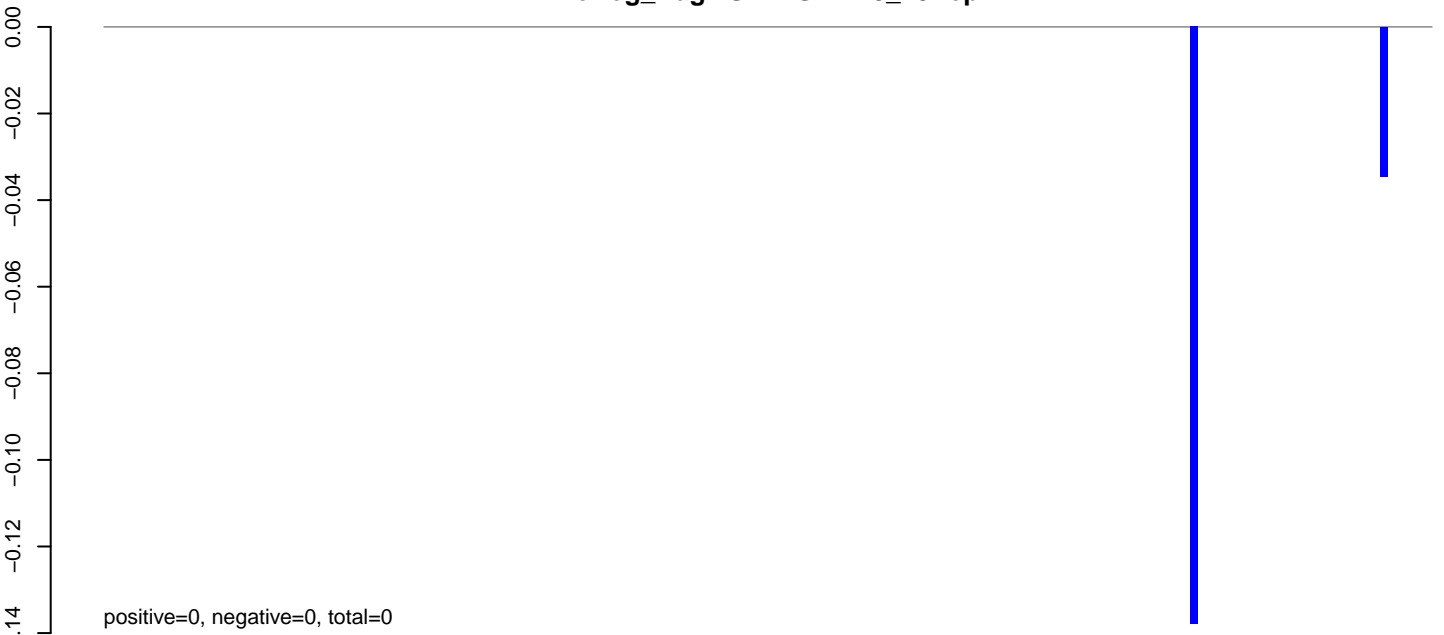
AeAeg_Aag2.SINV.GFP.24_35.rep



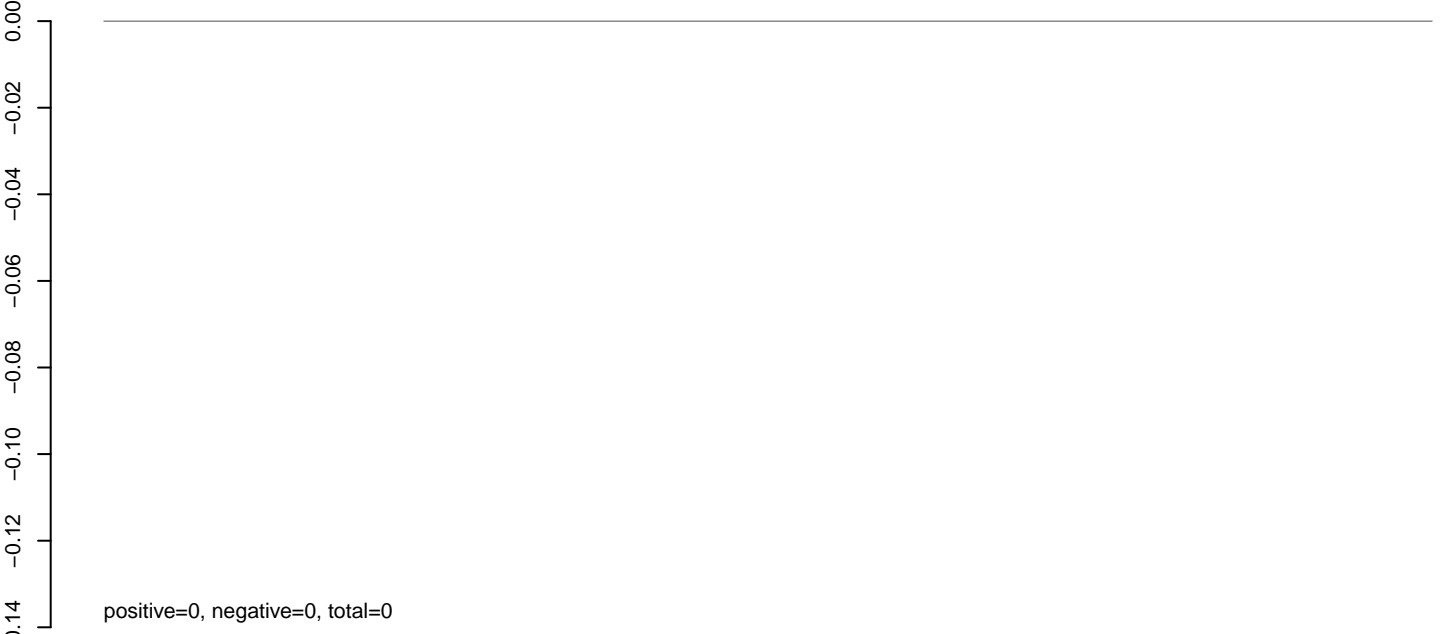
AeAeg_Aag2.SINV.GFP.rep



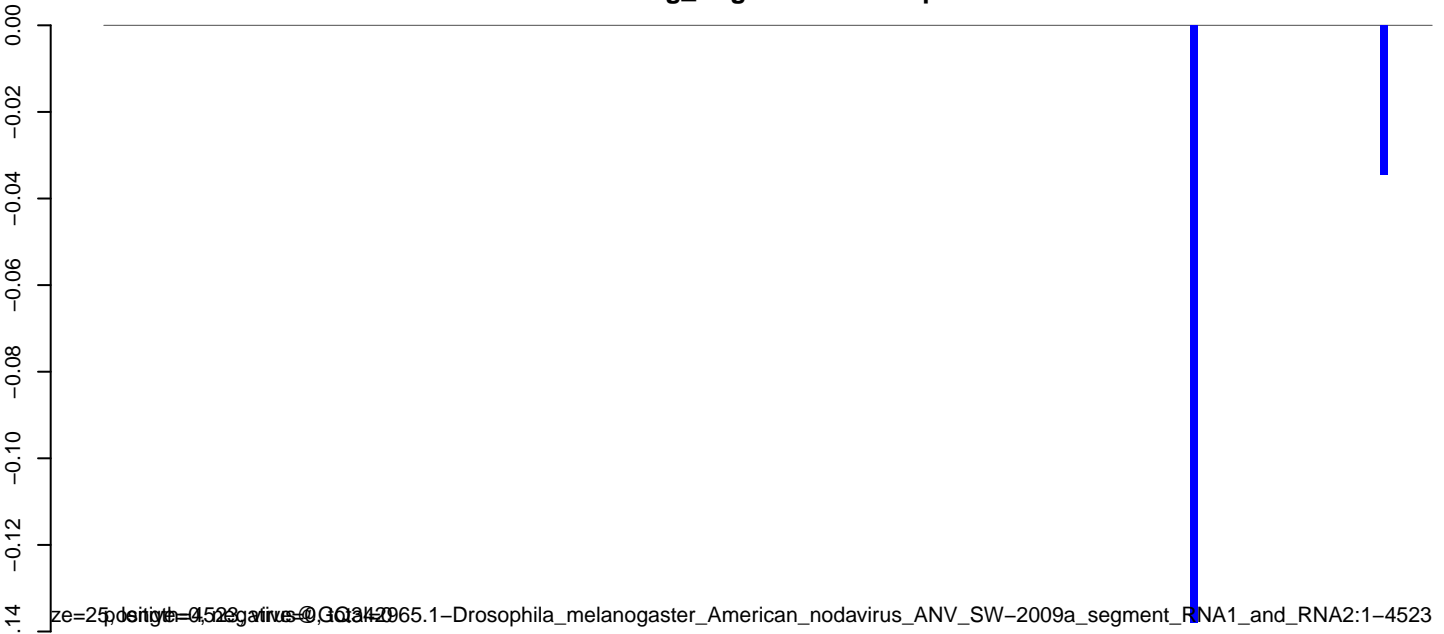
AeAeg_Aag2.SINV.GFP.18_23.rep



AeAeg_Aag2.SINV.GFP.24_35.rep



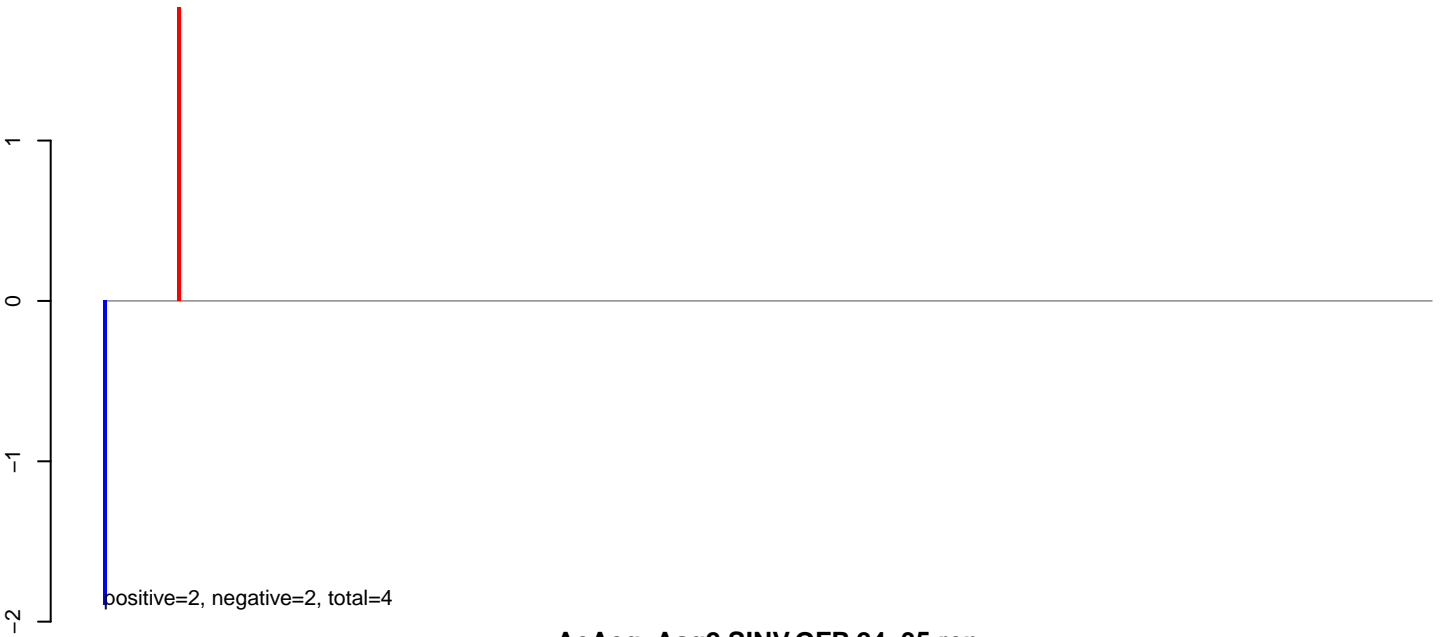
AeAeg_Aag2.SINV.GFP.rep



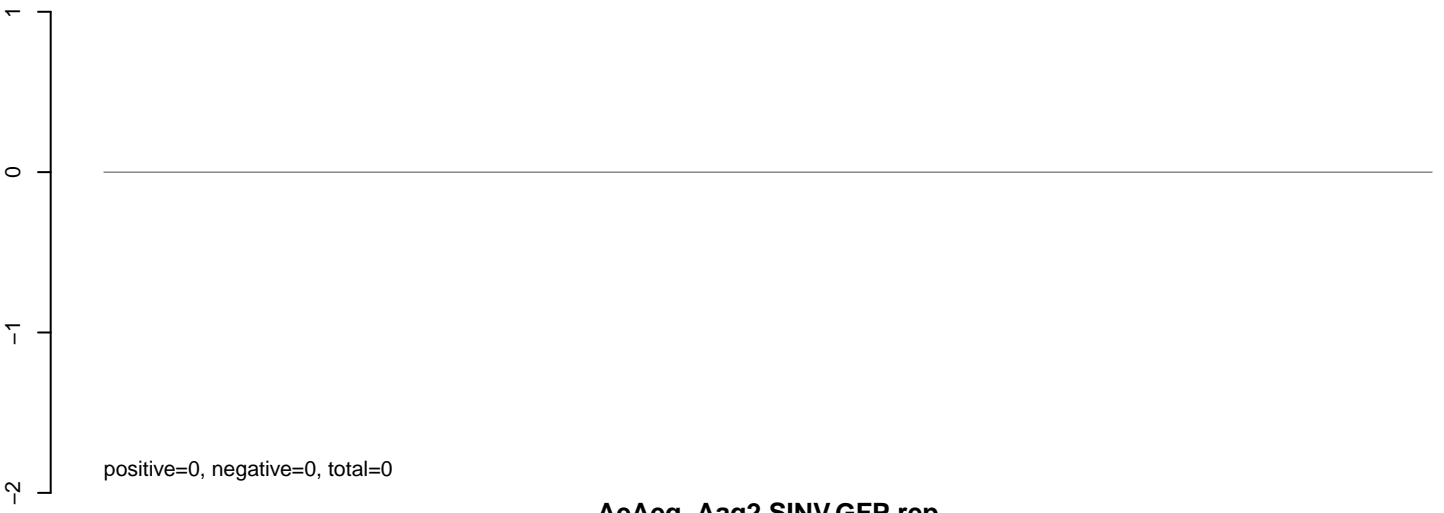
ze=25 positive=4522 negative=0 total=4522 65.1-Drosophila_melanogaster_American_nodavirus_ANV_SW-2009a_segment_RNA1_and_RNA2:1-4523

0 1000 2000 3000 4000

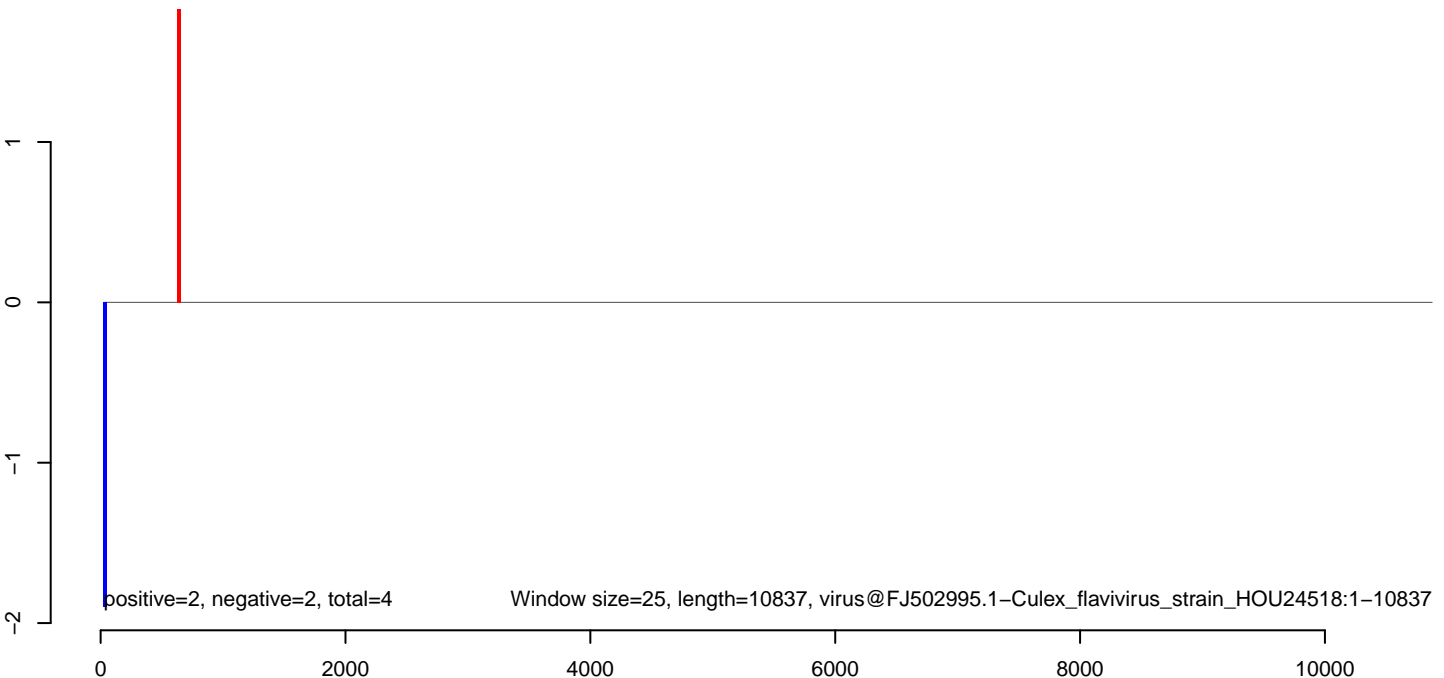
AeAeg_Aag2.SINV.GFP.18_23.rep

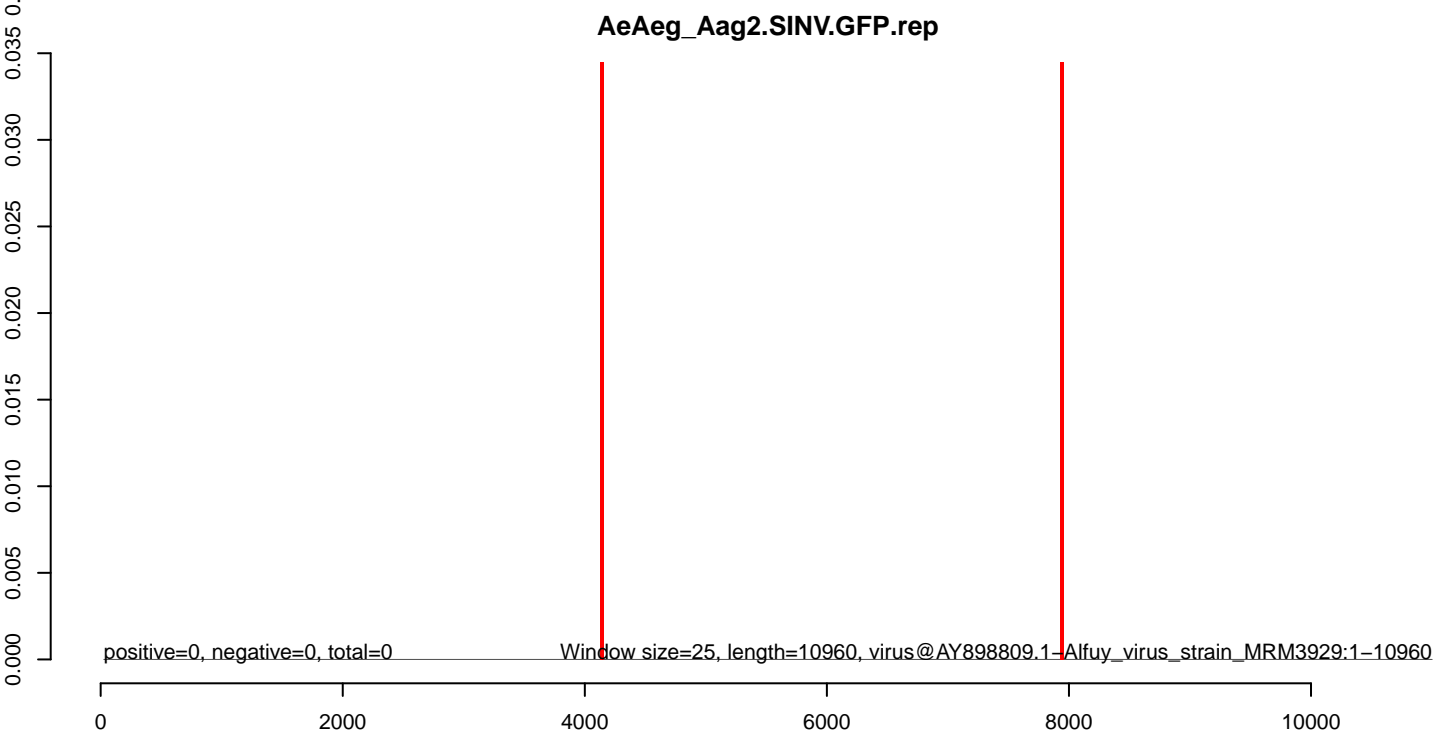
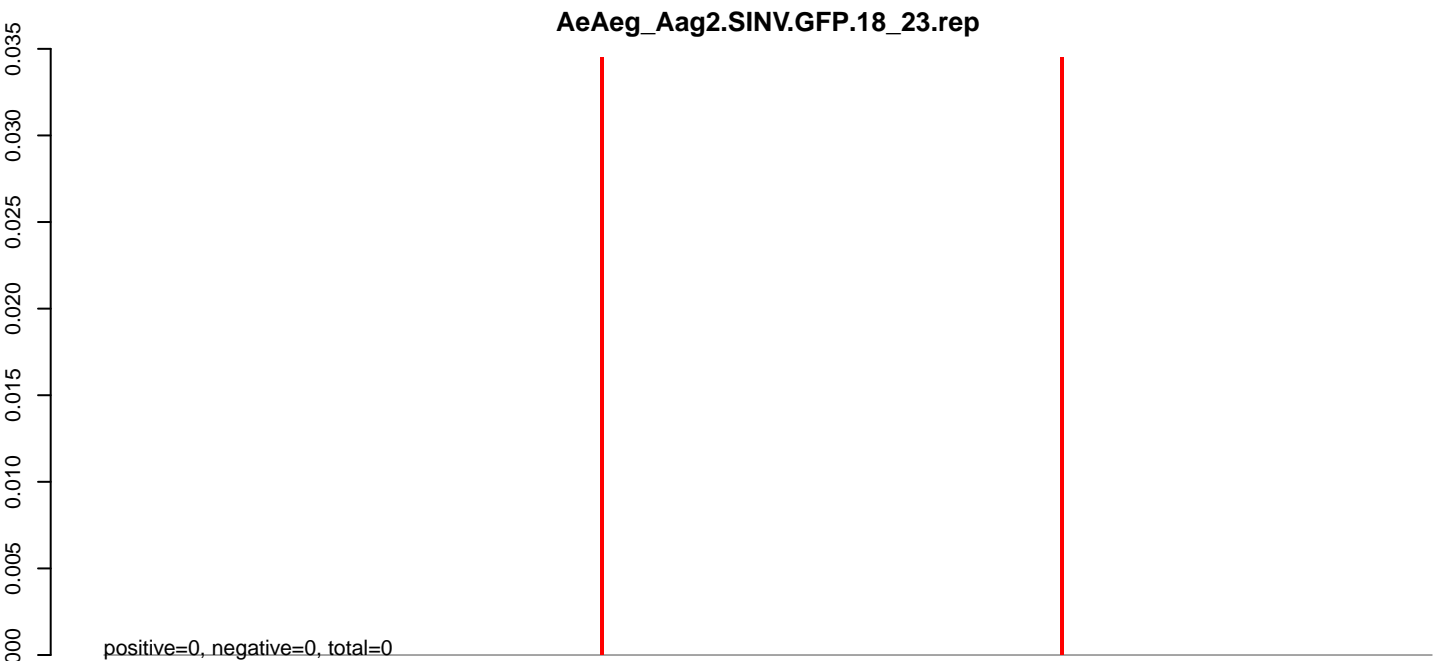


AeAeg_Aag2.SINV.GFP.24_35.rep

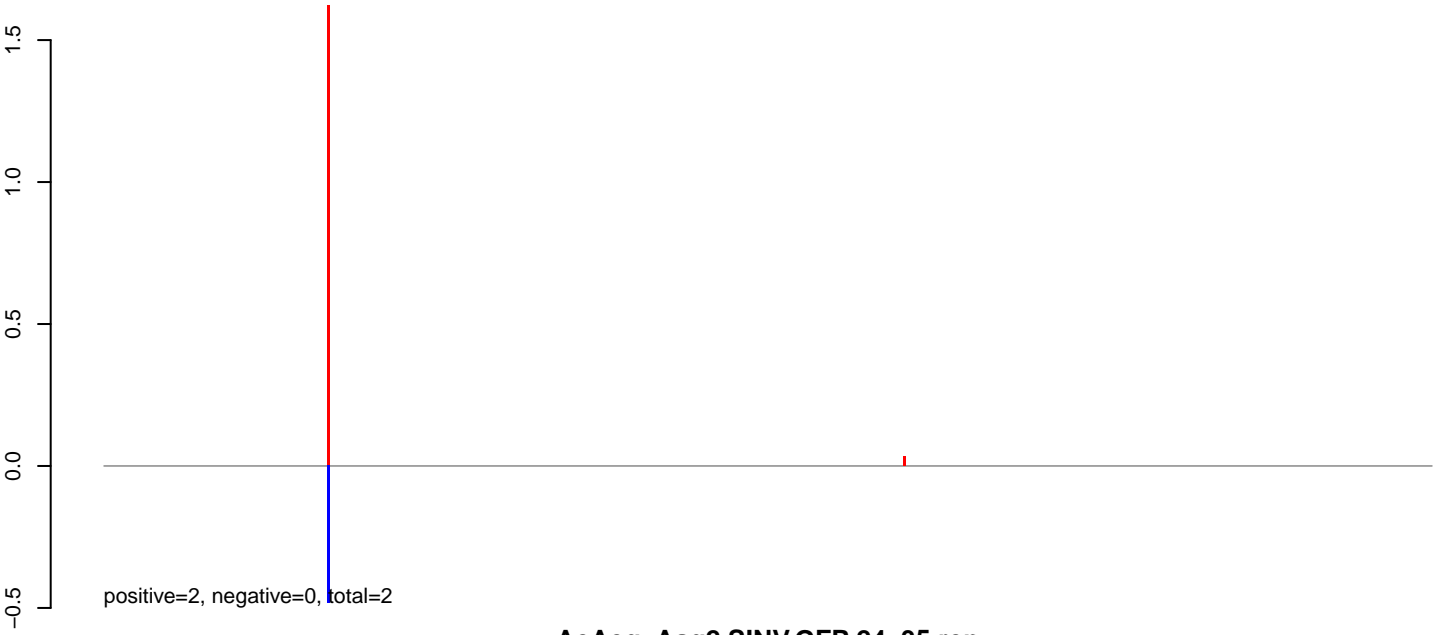


AeAeg_Aag2.SINV.GFP.rep

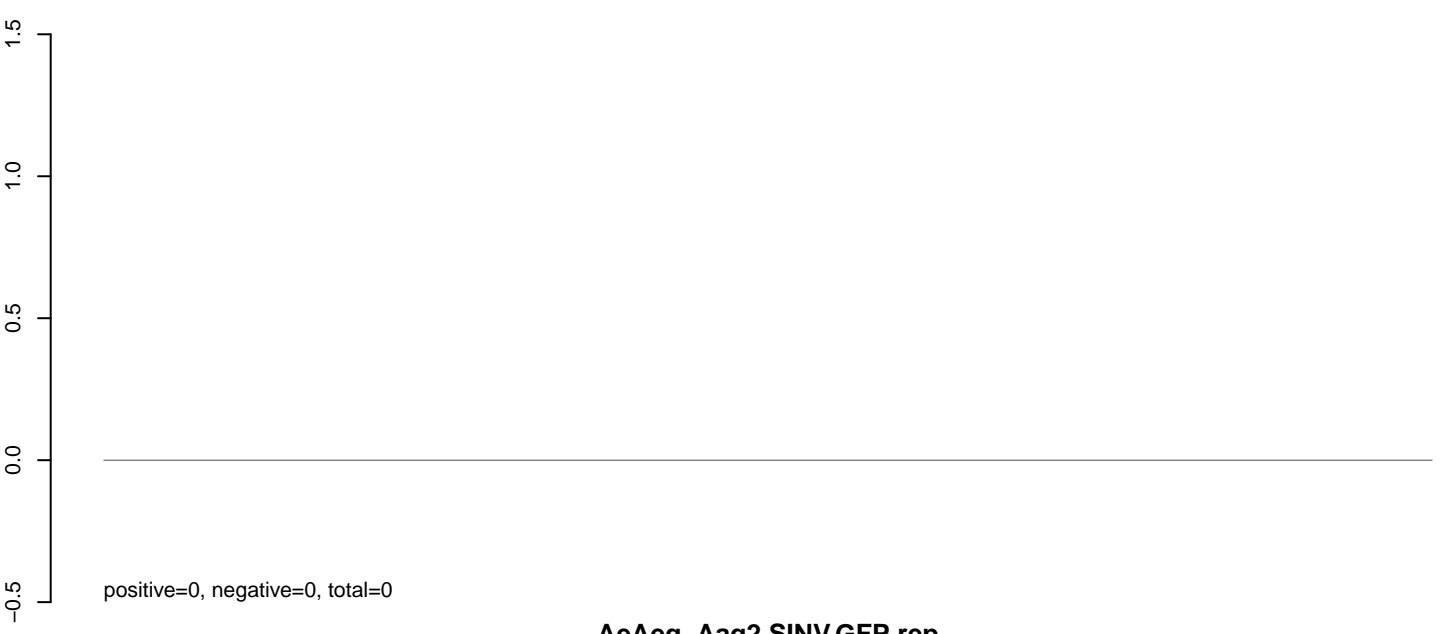




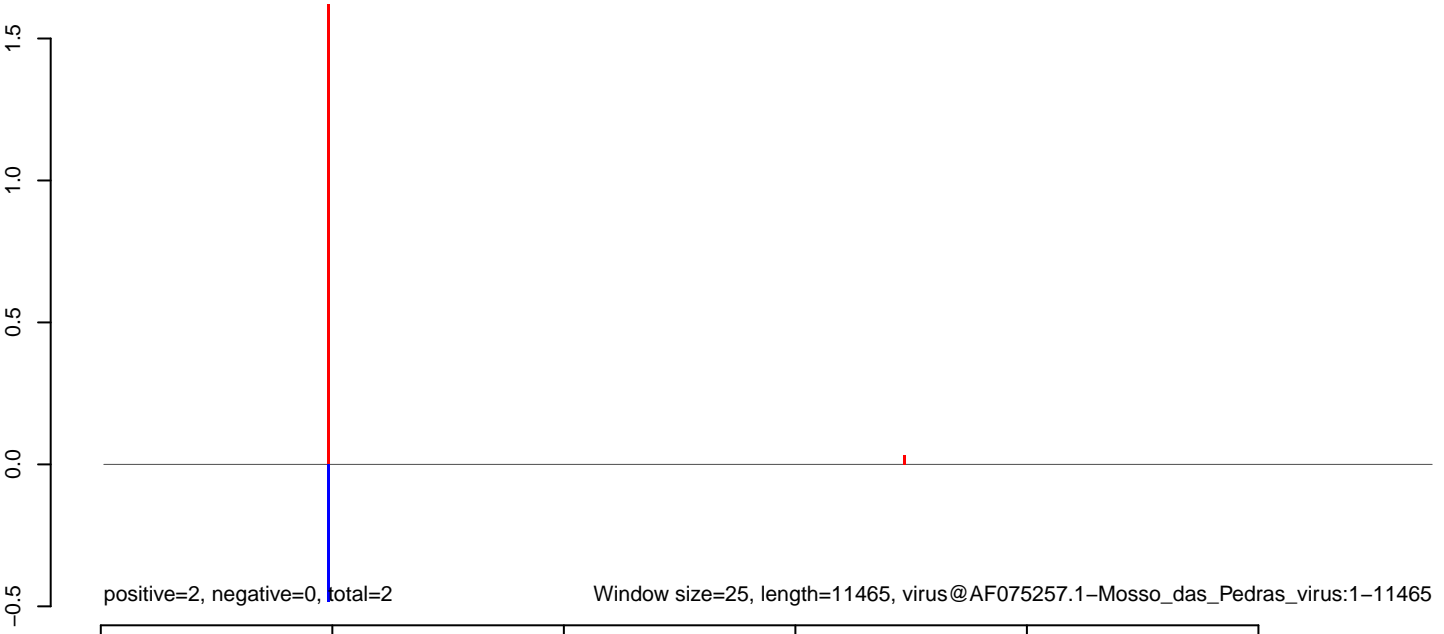
AeAeg_Aag2.SINV.GFP.18_23.rep



AeAeg_Aag2.SINV.GFP.24_35.rep

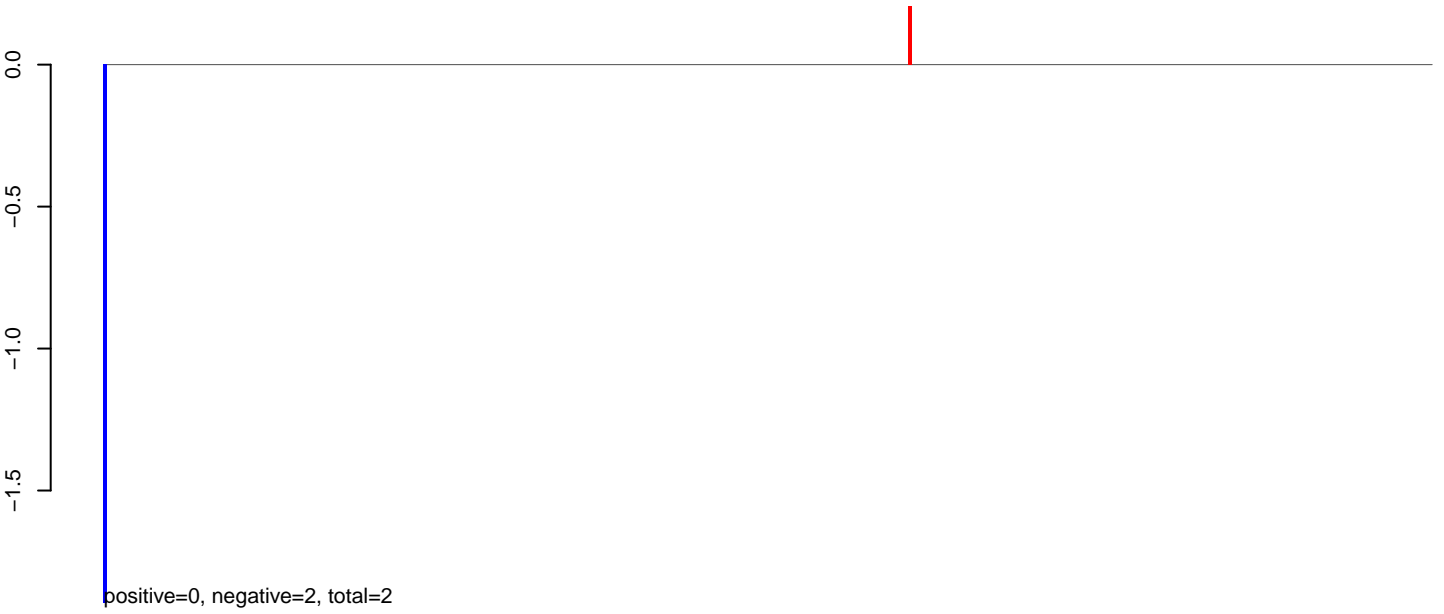


AeAeg_Aag2.SINV.GFP.rep

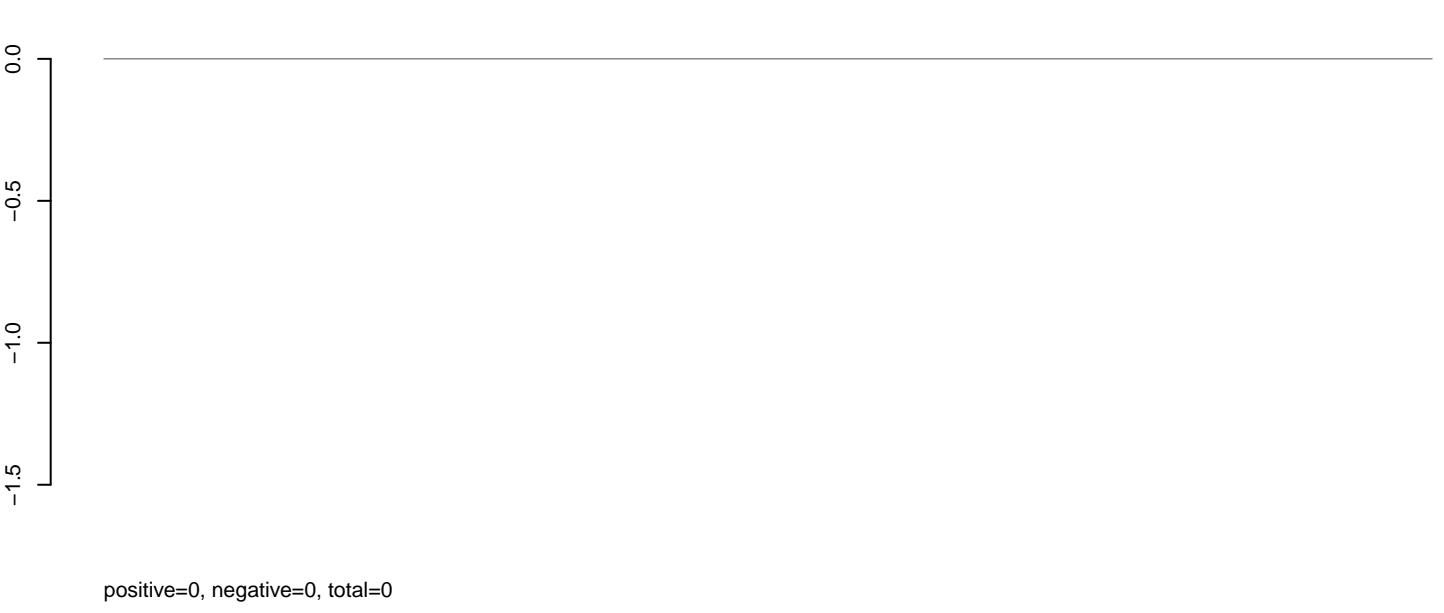


Window size=25, length=11465, virus@AF075257.1-Mosso_das_Pedras_virus:1-11465

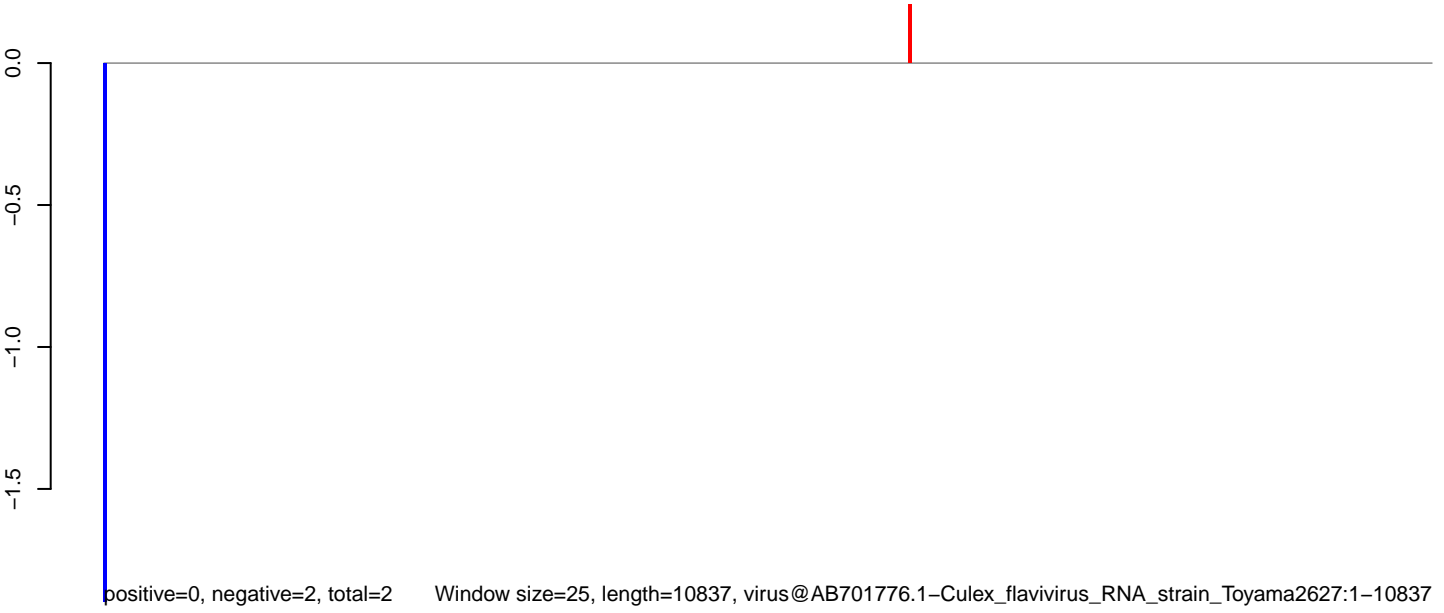
AeAeg_Aag2.SINV.GFP.18_23.rep



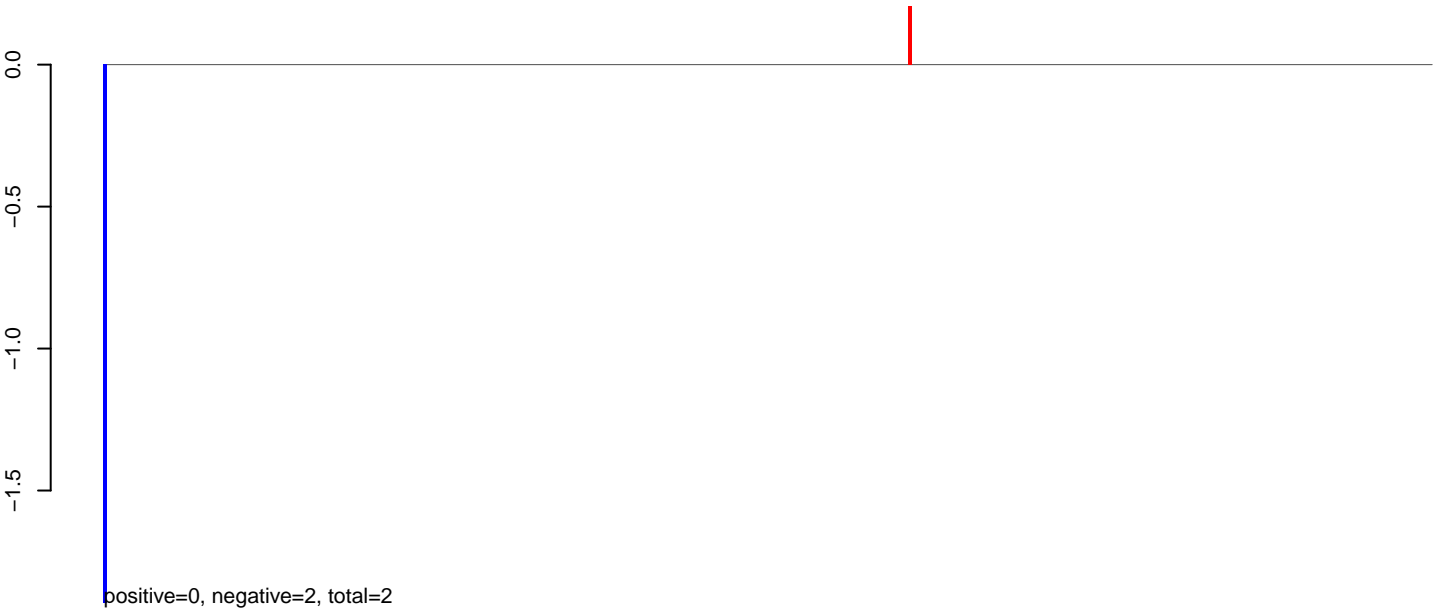
AeAeg_Aag2.SINV.GFP.24_35.rep



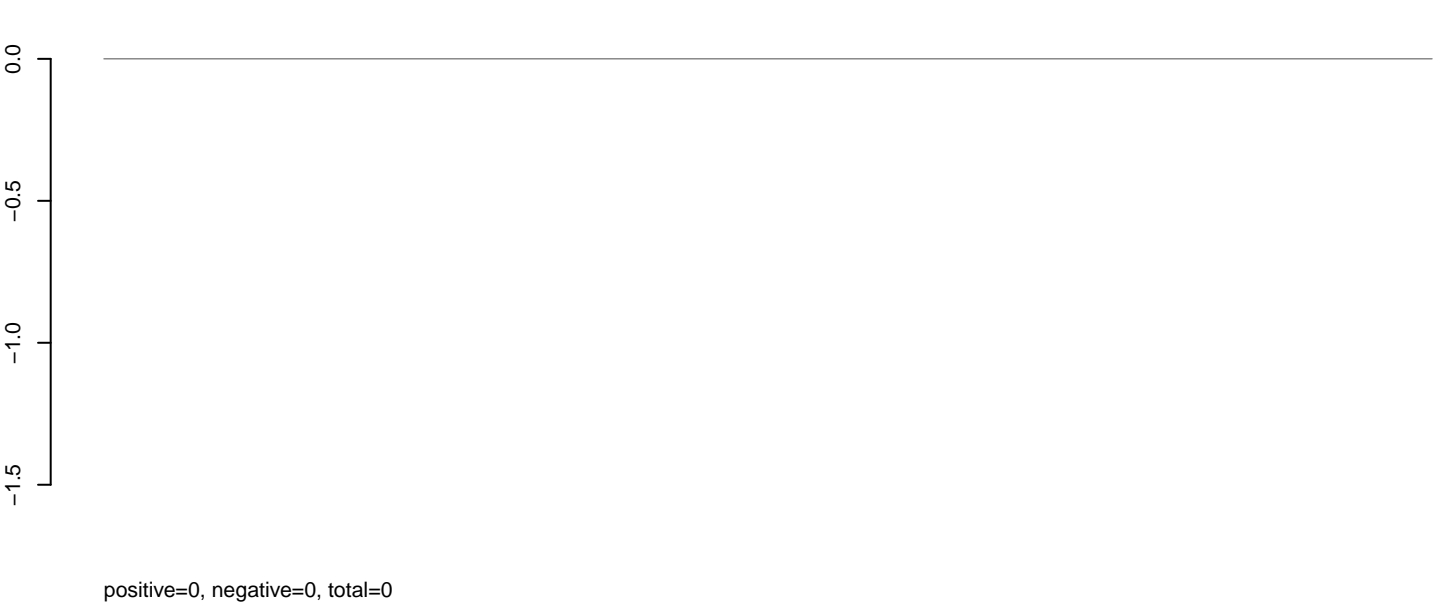
AeAeg_Aag2.SINV.GFP.rep



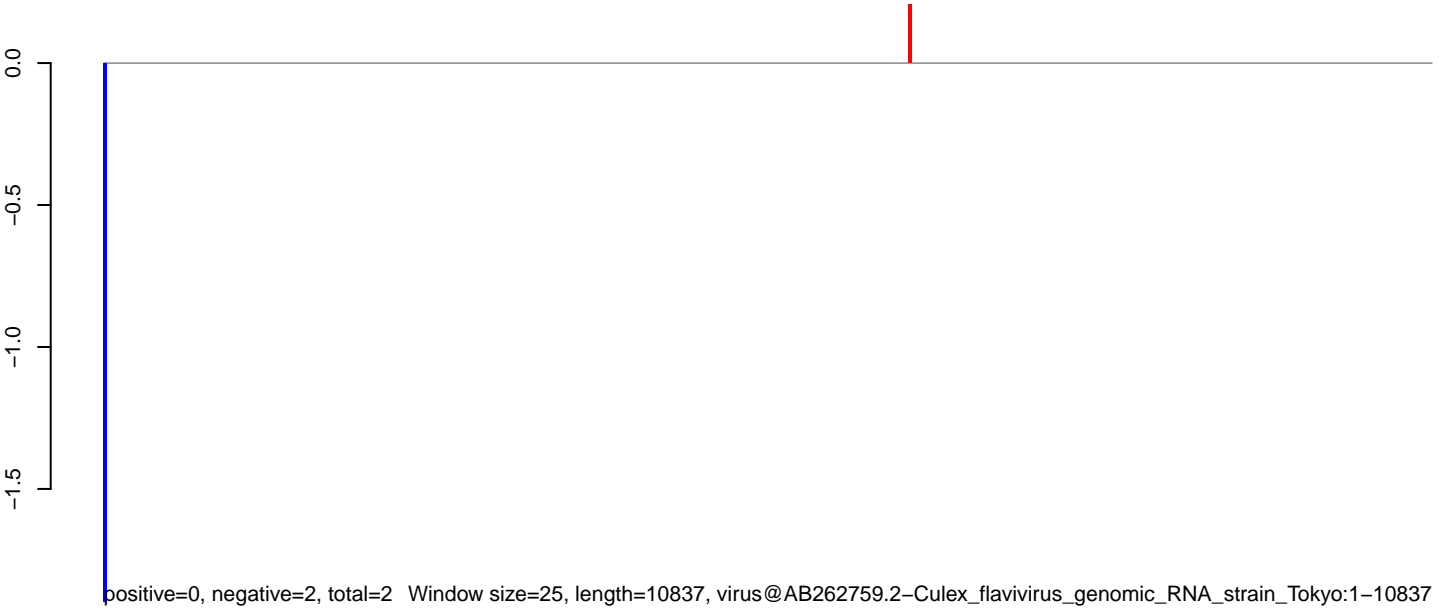
AeAeg_Aag2.SINV.GFP.18_23.rep



AeAeg_Aag2.SINV.GFP.24_35.rep



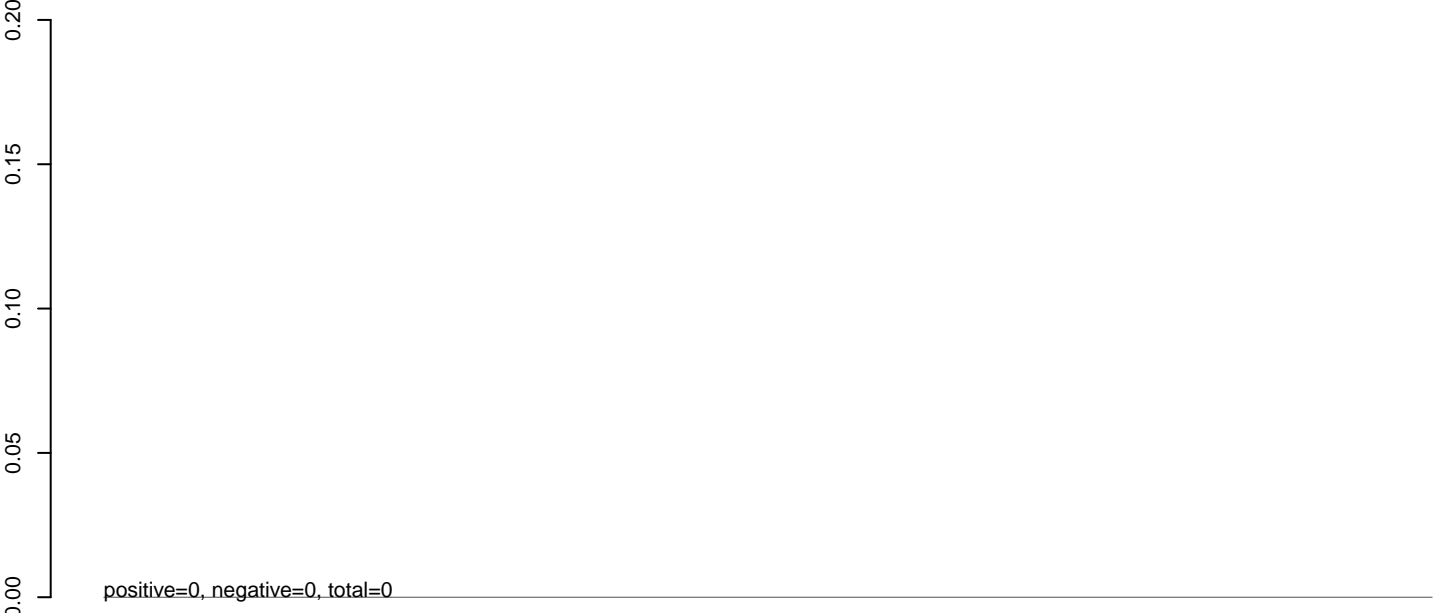
AeAeg_Aag2.SINV.GFP.rep



AeAeg_Aag2.SINV.GFP.18_23.rep

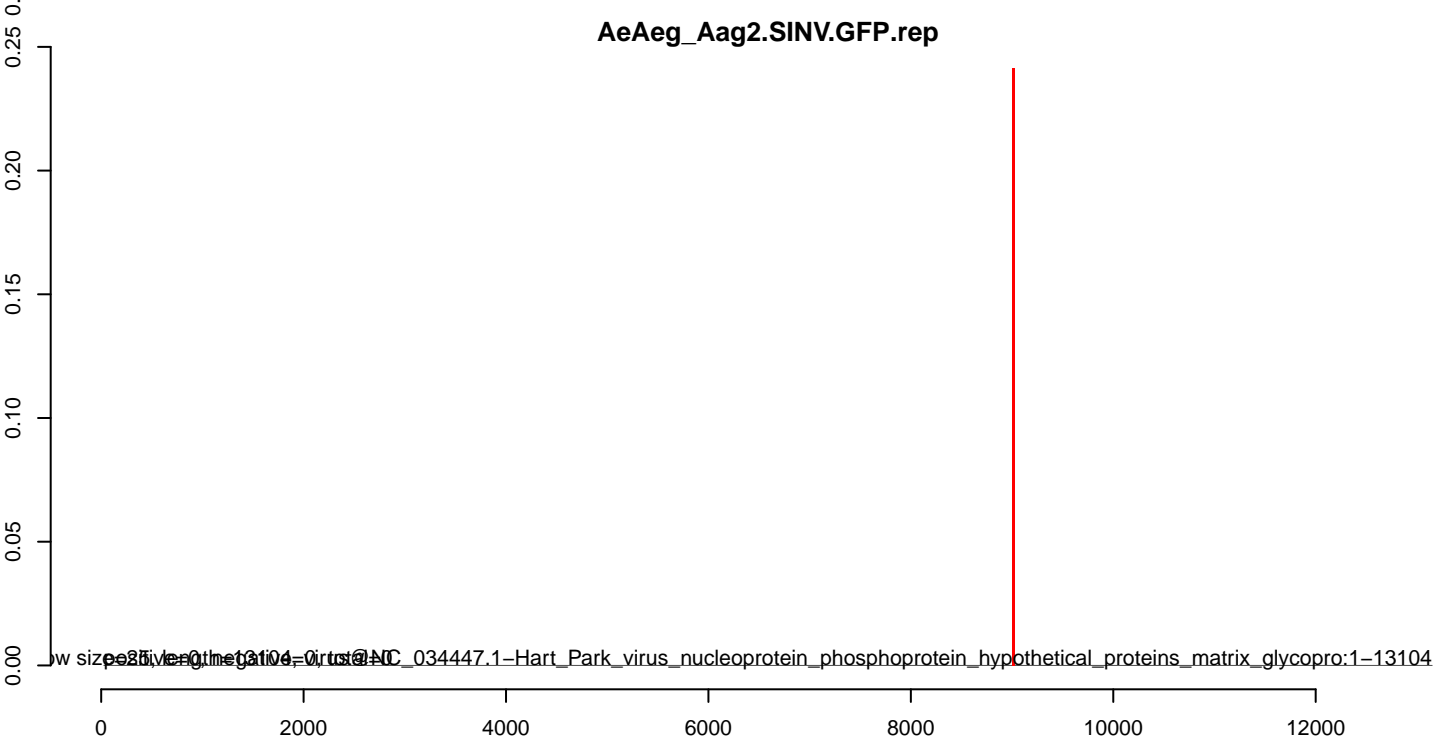
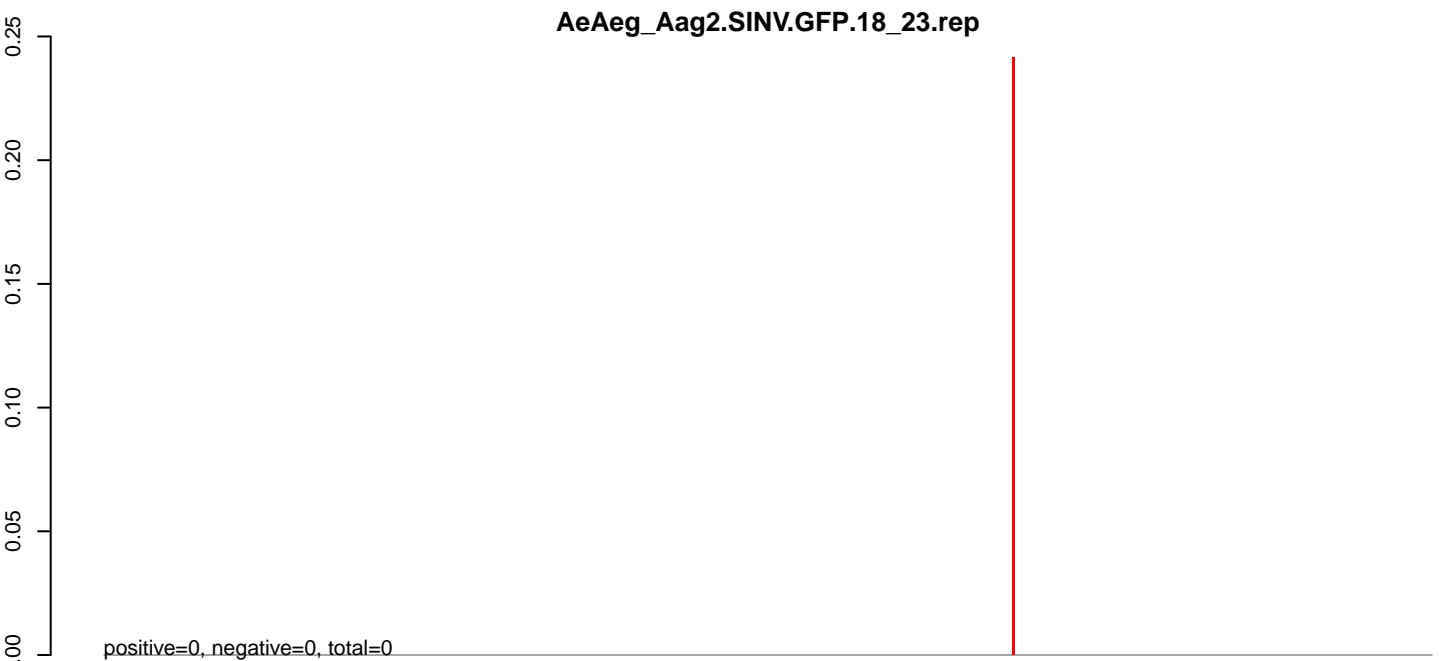


AeAeg_Aag2.SINV.GFP.24_35.rep

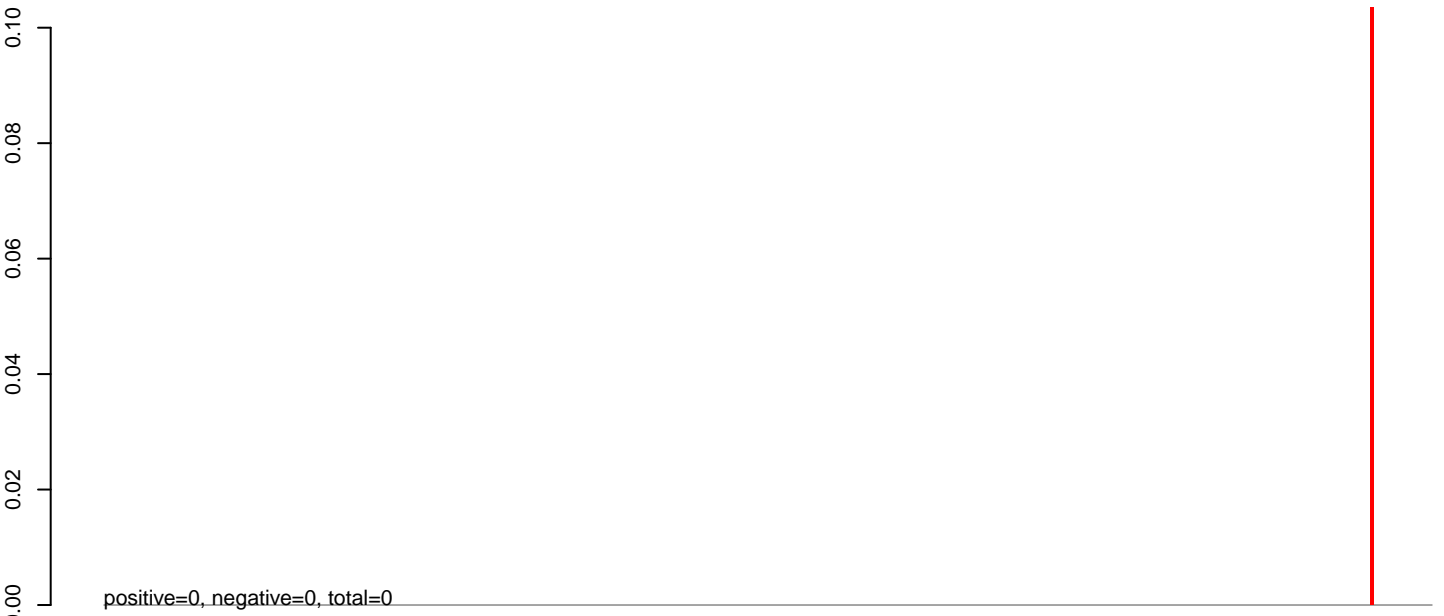


AeAeg_Aag2.SINV.GFP.rep

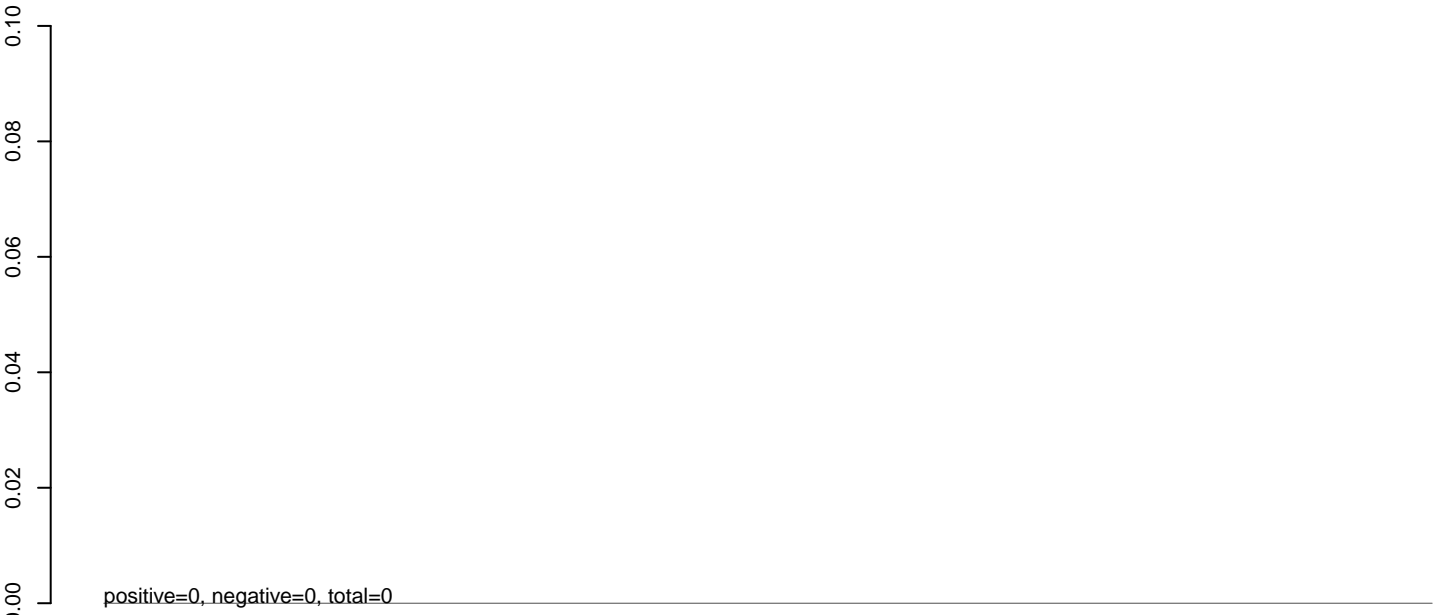




AeAeg_Aag2.SINV.GFP.18_23.rep



AeAeg_Aag2.SINV.GFP.24_35.rep



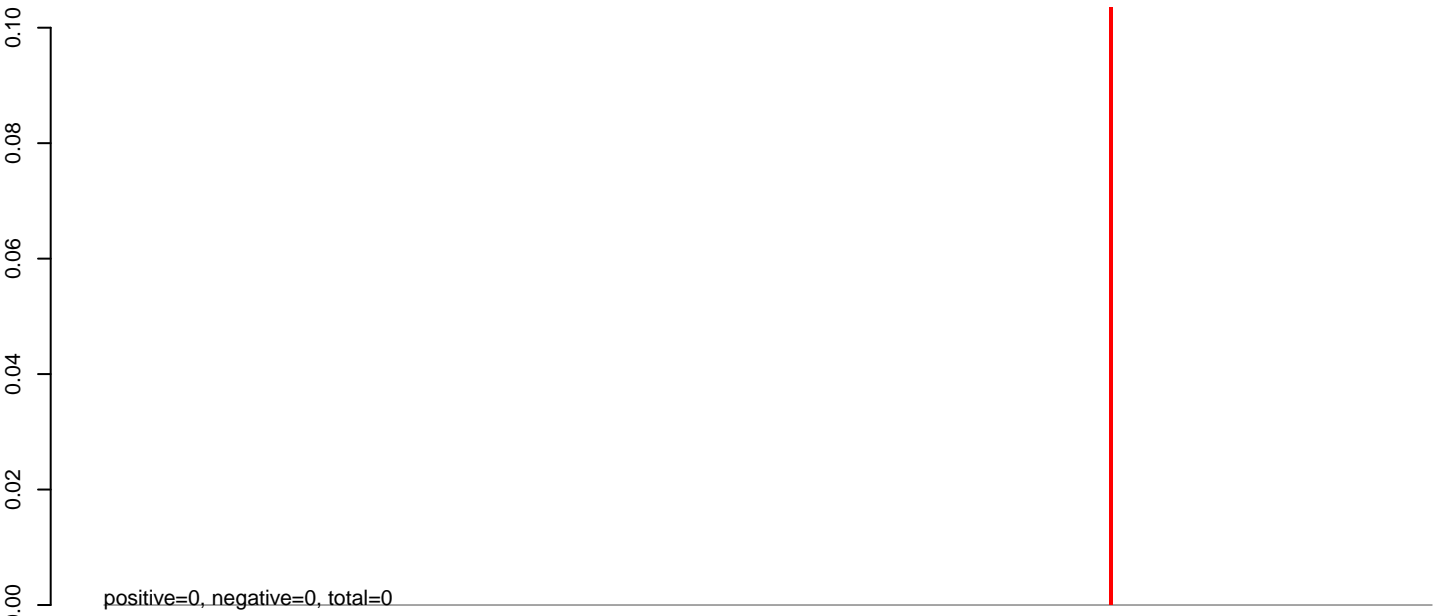
AeAeg_Aag2.SINV.GFP.rep



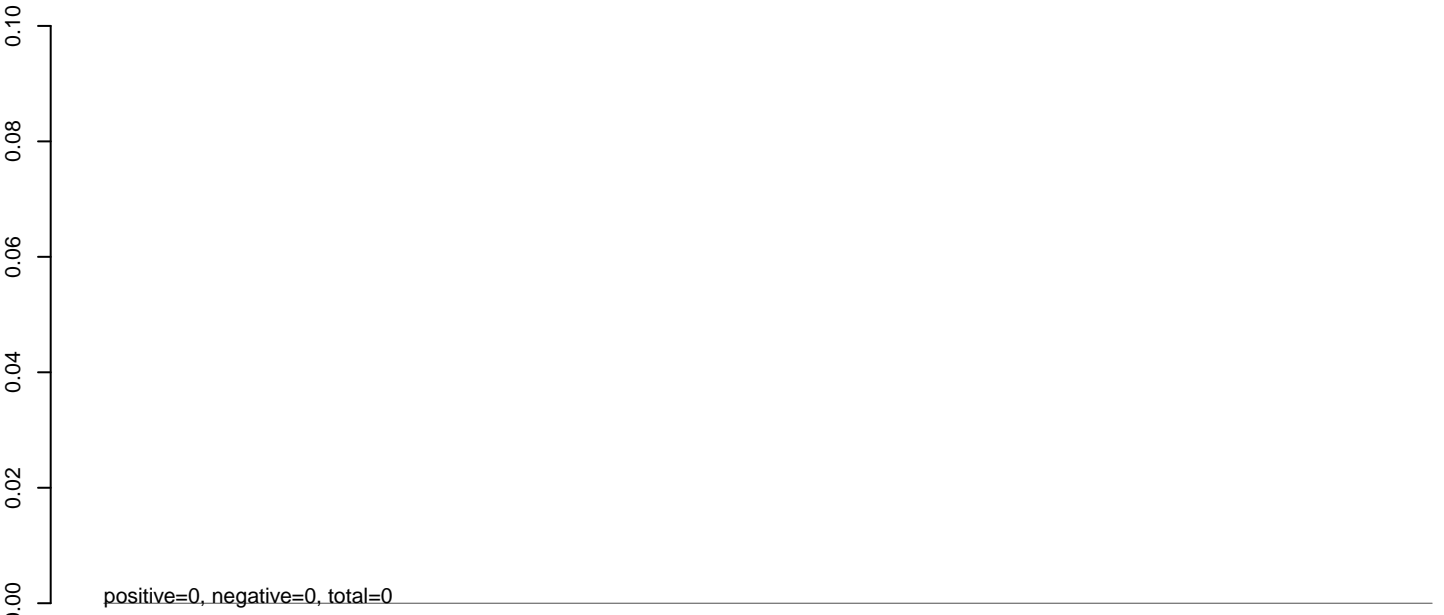
positive=0, negative=0, total=6, size=25, length=10251, virus@NC_033723.1-Gadgets_Gully_virus_from_Australia_polyprotein_gene:1-10251

0 2000 4000 6000 8000 10000

AeAeg_Aag2.SINV.GFP.18_23.rep



AeAeg_Aag2.SINV.GFP.24_35.rep

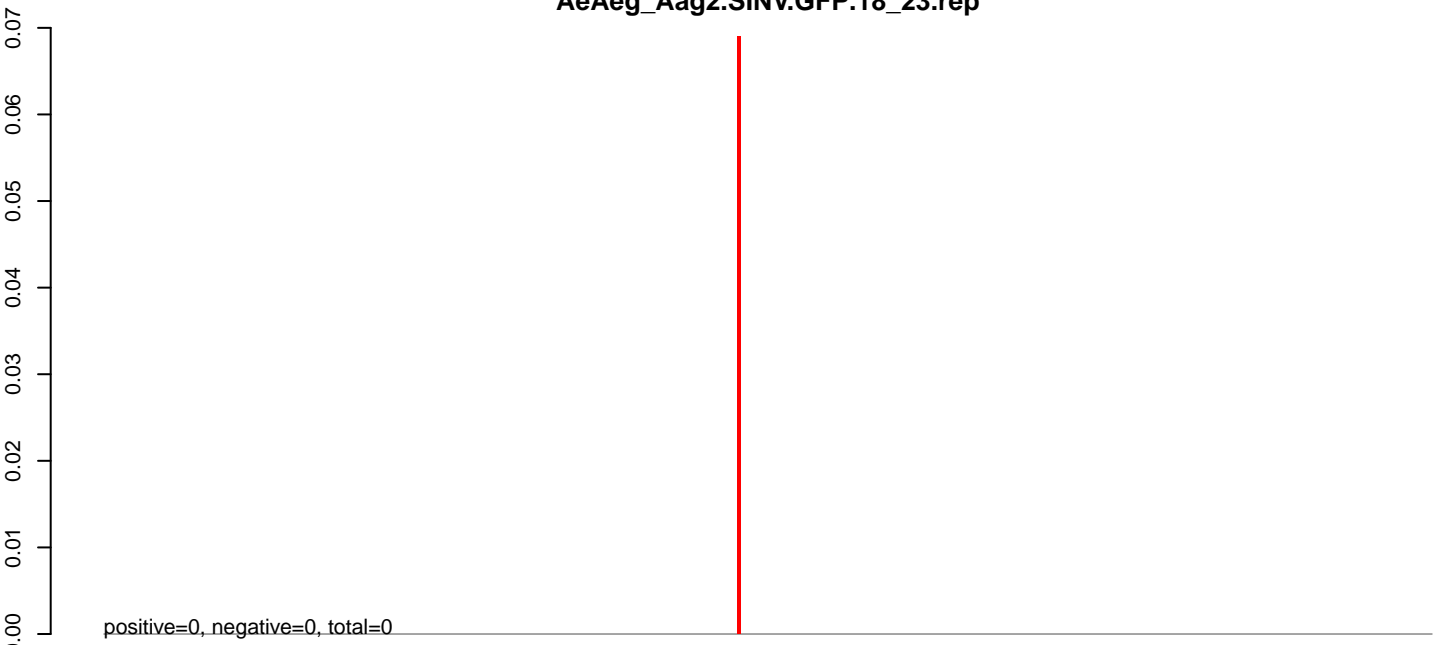


AeAeg_Aag2.SINV.GFP.rep

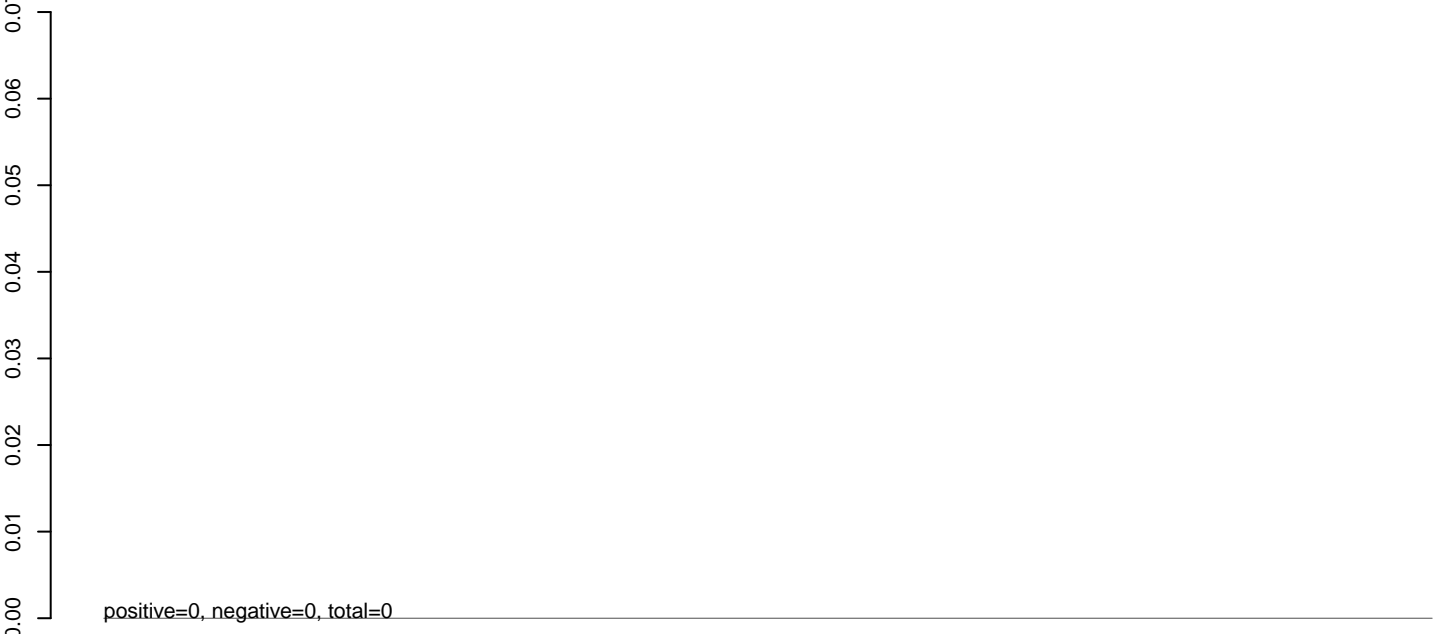


Window size=25, length=10266, virus@NC_033721.1-Meaban_virus_from_France_polyprotein_gene:1-10266

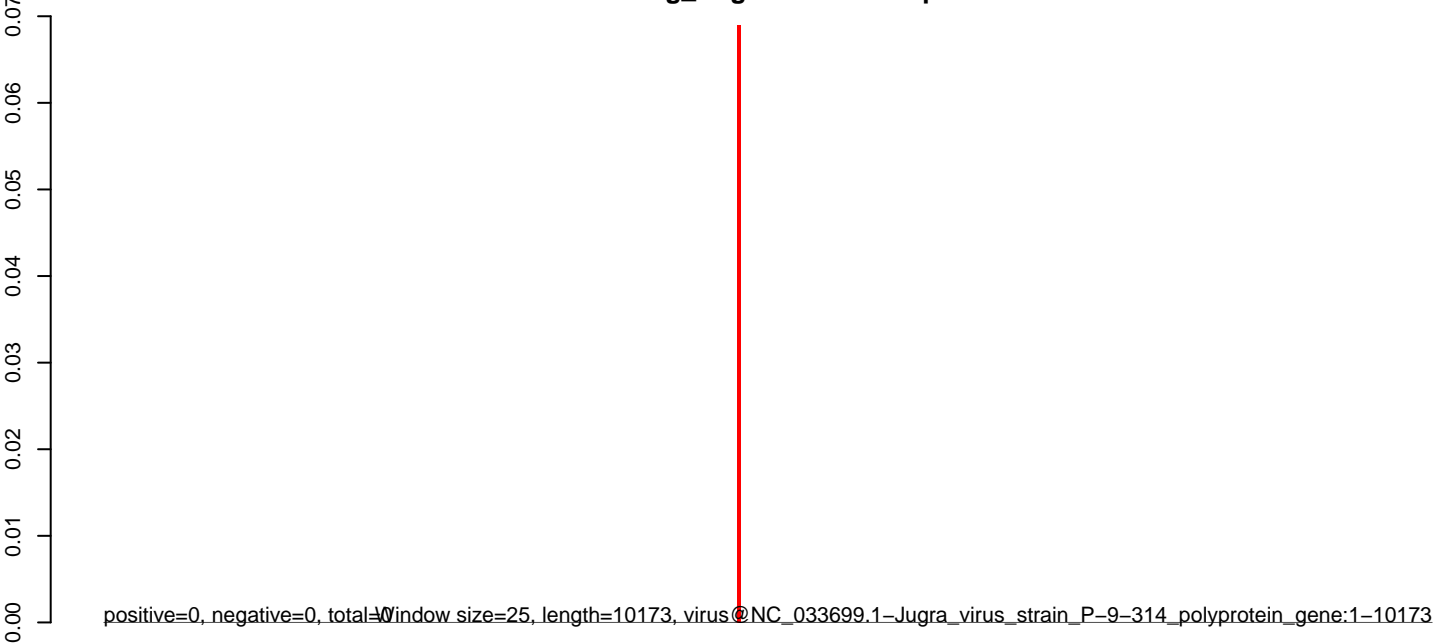
AeAeg_Aag2.SINV.GFP.18_23.rep



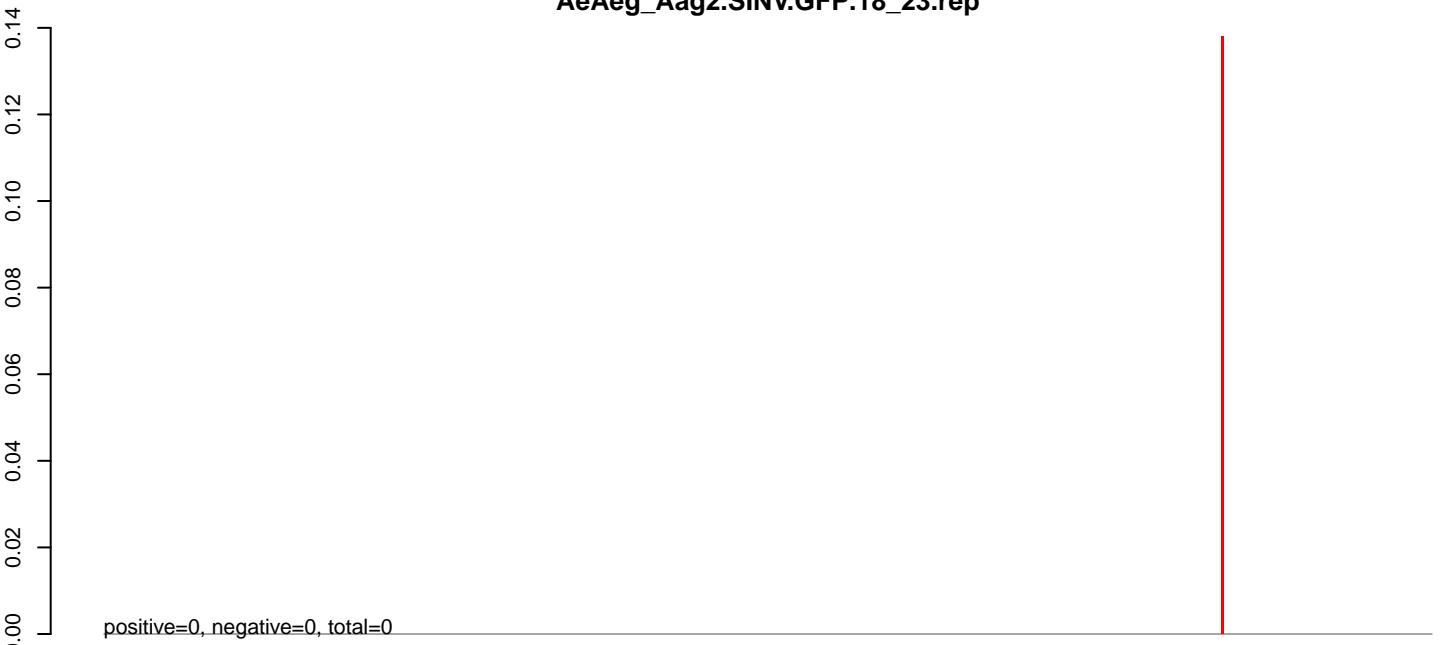
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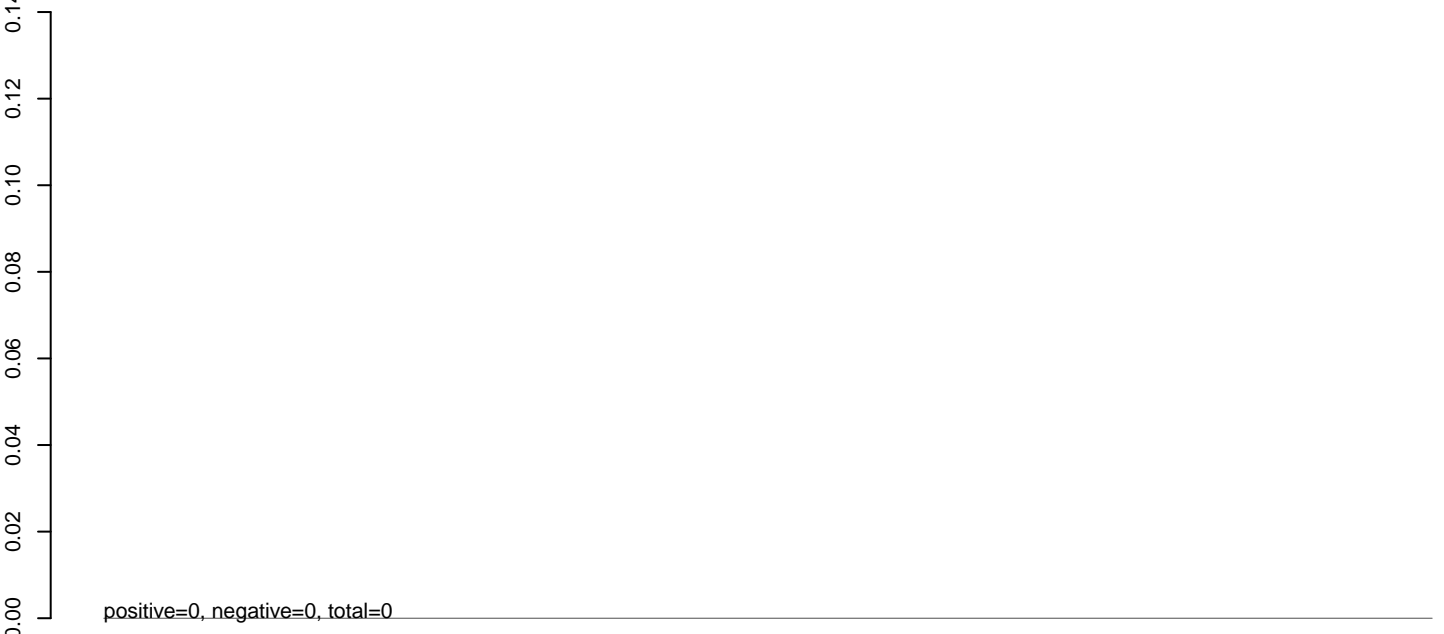
AeAeg_Aag2.SINV.GFP.rep



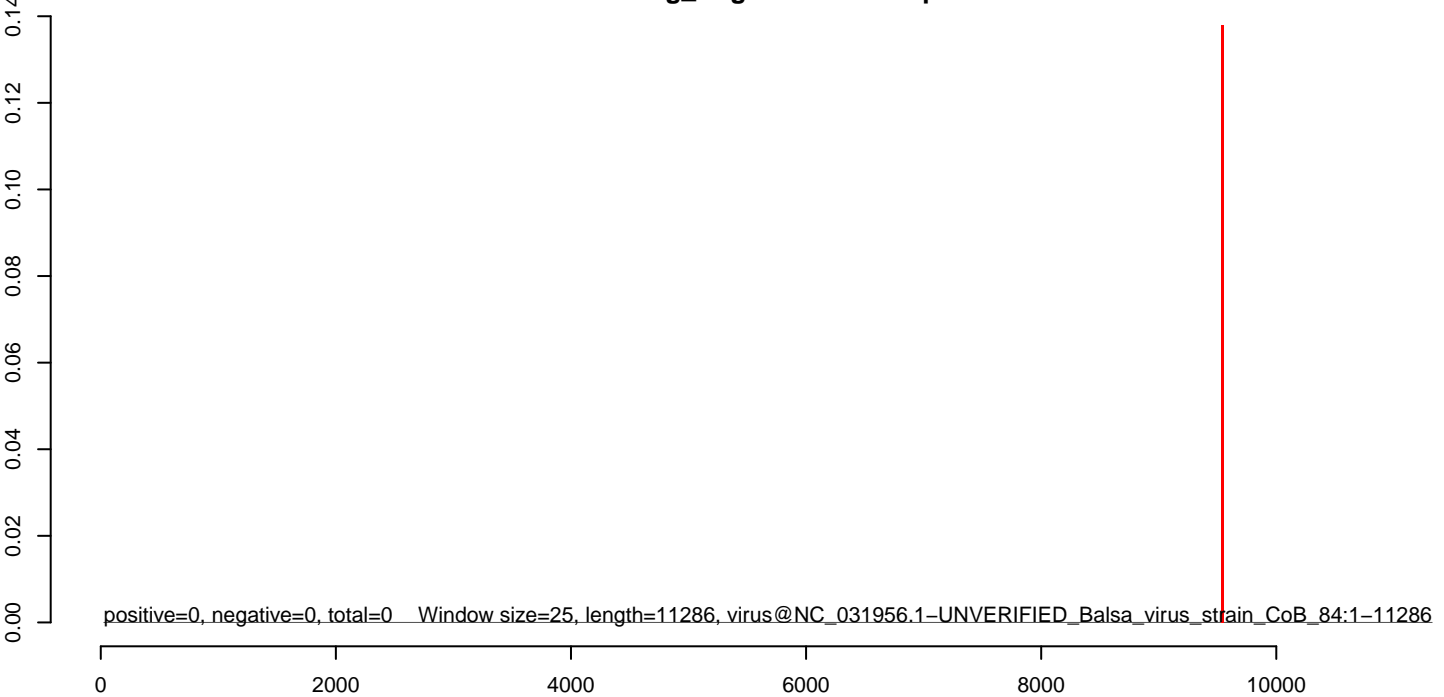
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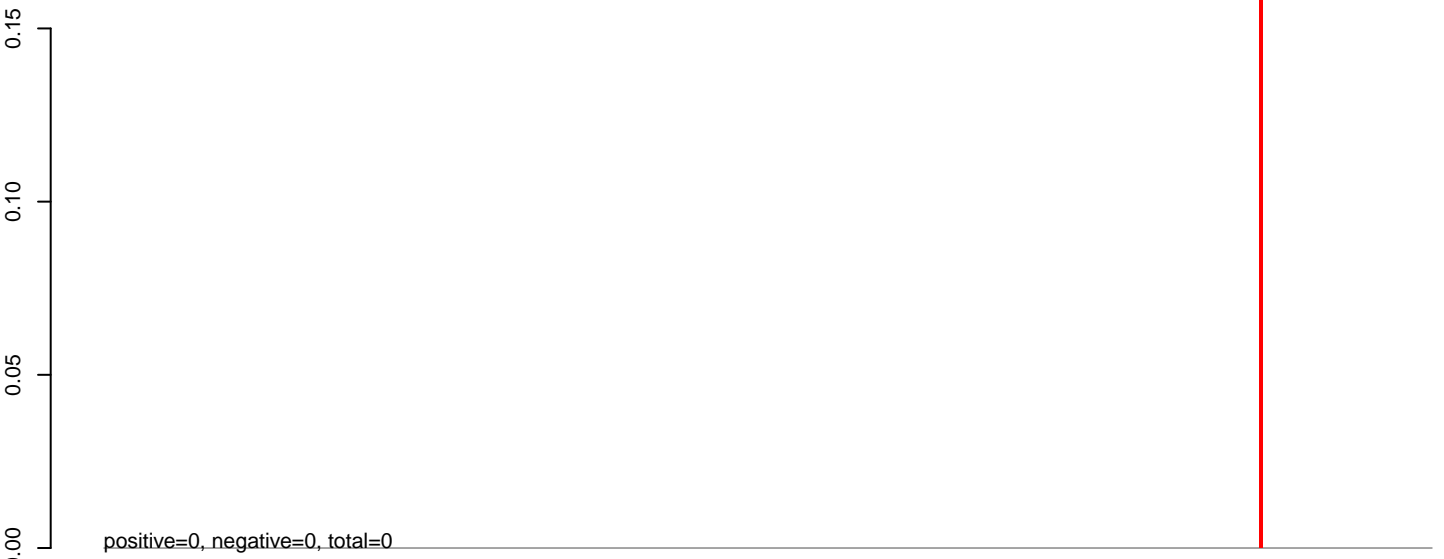
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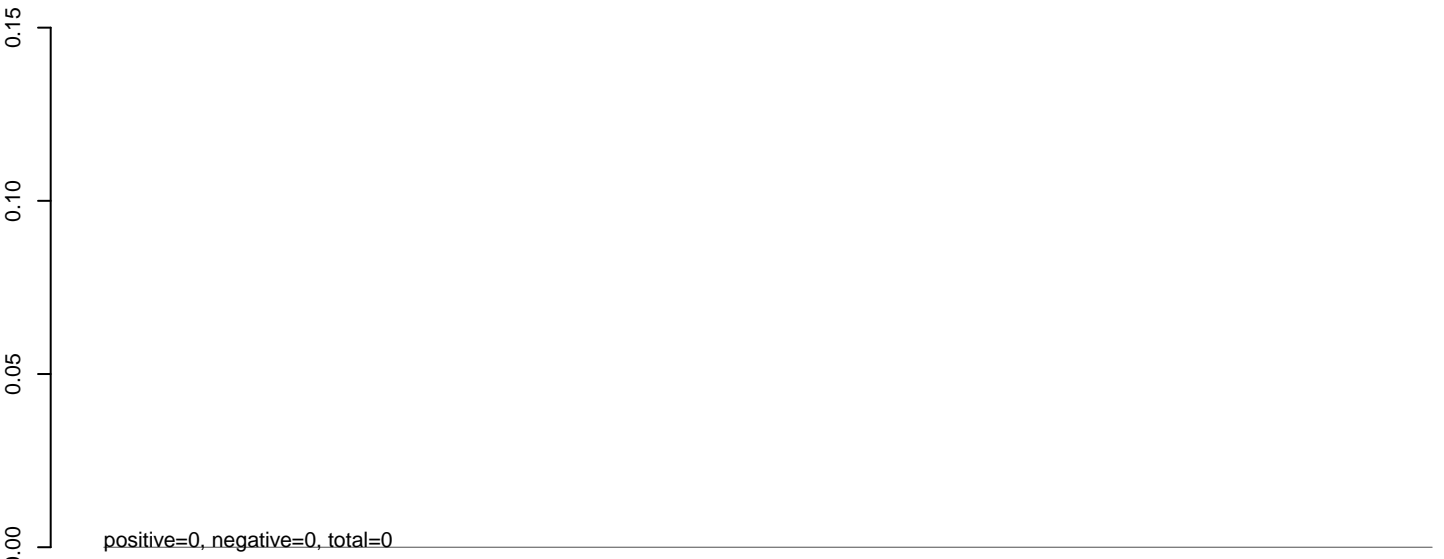
AeAeg_Aag2.SINV.GFP.rep



AeAeg_Aag2.SINV.GFP.18_23.rep



AeAeg_Aag2.SINV.GFP.24_35.rep



AeAeg_Aag2.SINV.GFP.rep



AeAeg_Aag2.SINV.GFP.18_23.rep



AeAeg_Aag2.SINV.GFP.24_35.rep

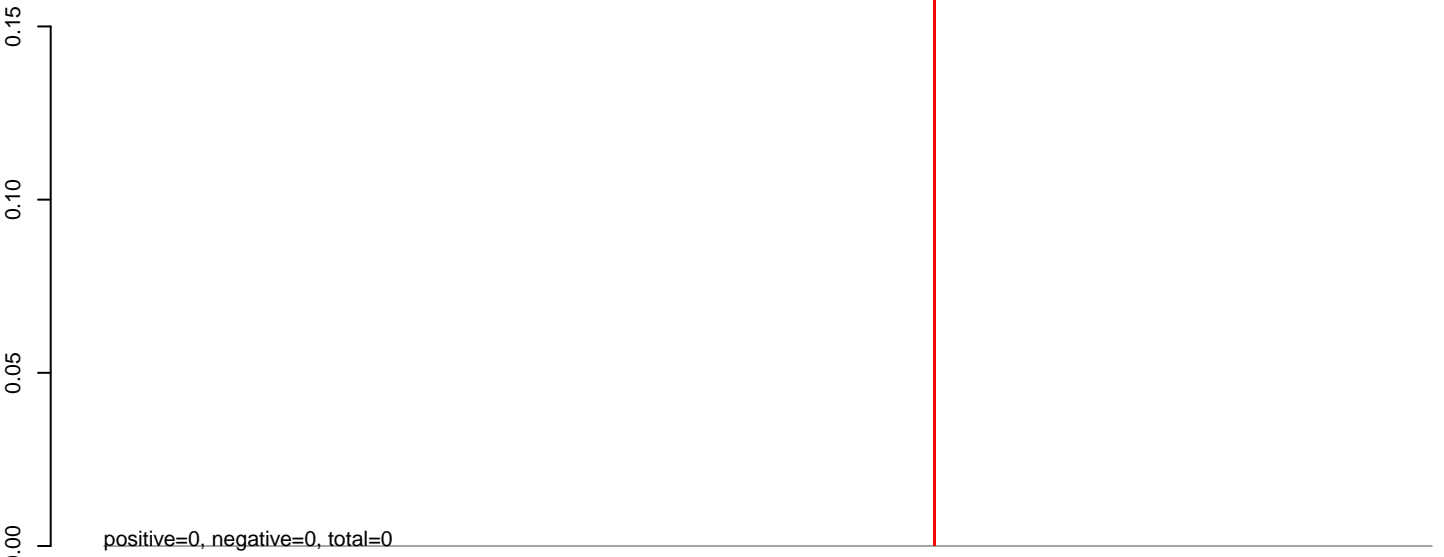


AeAeg_Aag2.SINV.GFP.rep

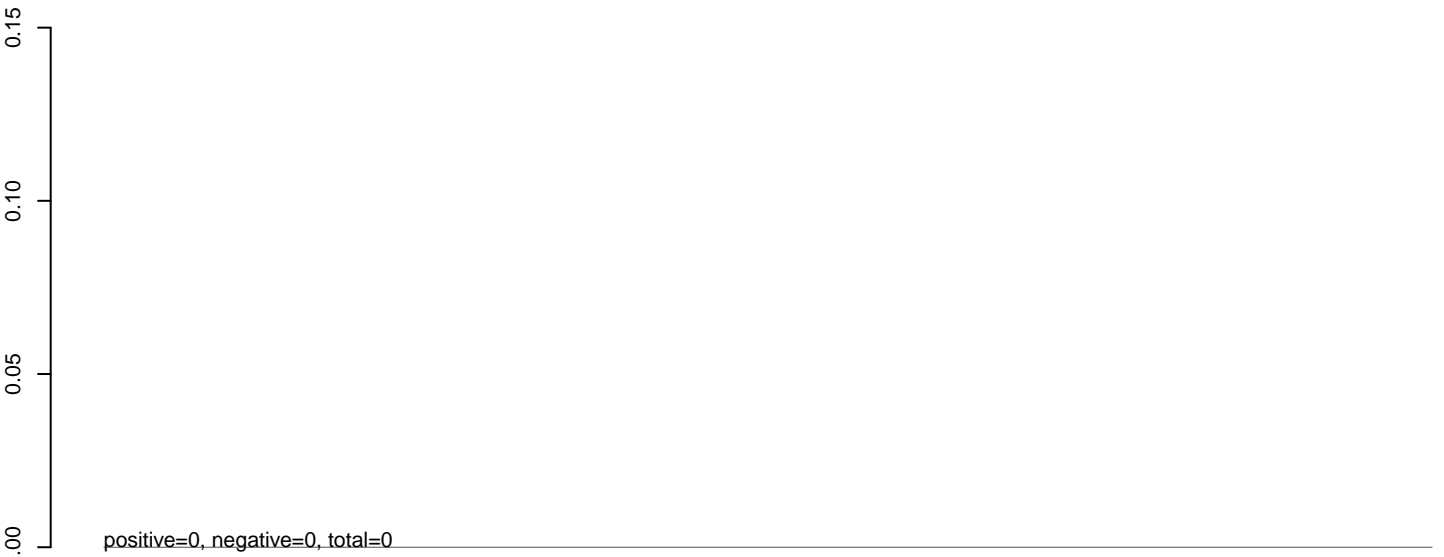


W7200012072, virus@NC_031319.1_Wutai_Mosquito_Virus_strain_QN3-5_nucleopasid_protein_N_G_L:1-12072

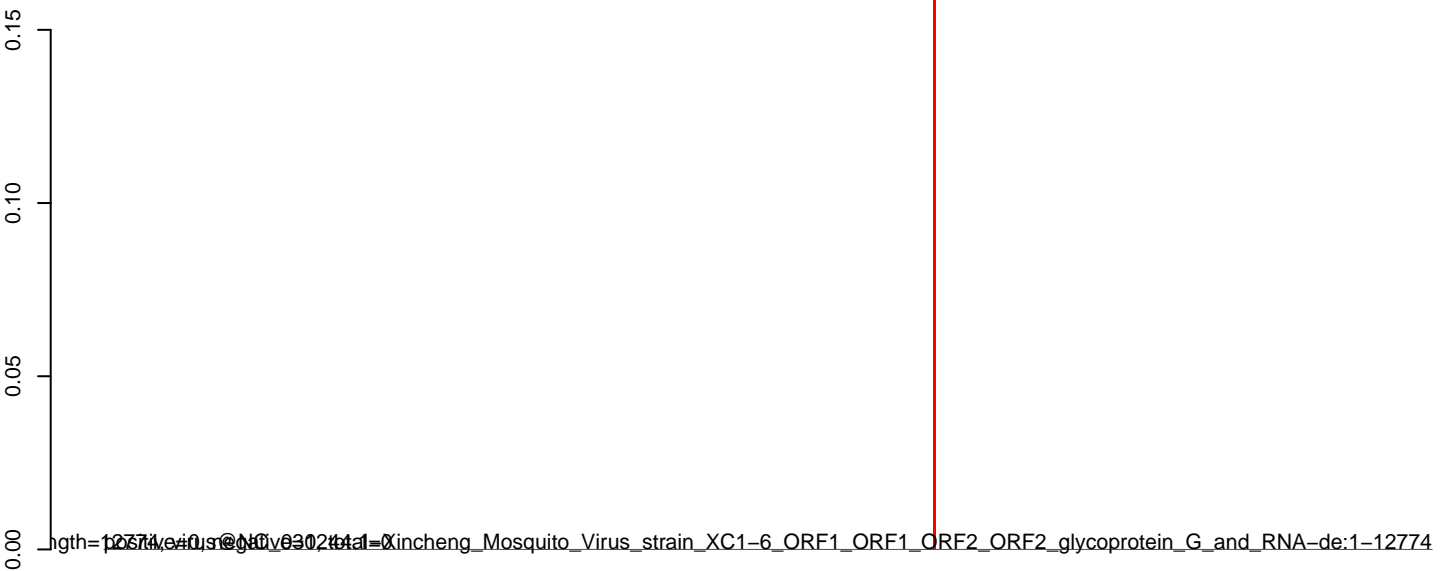
AeAeg_Aag2.SINV.GFP.18_23.rep



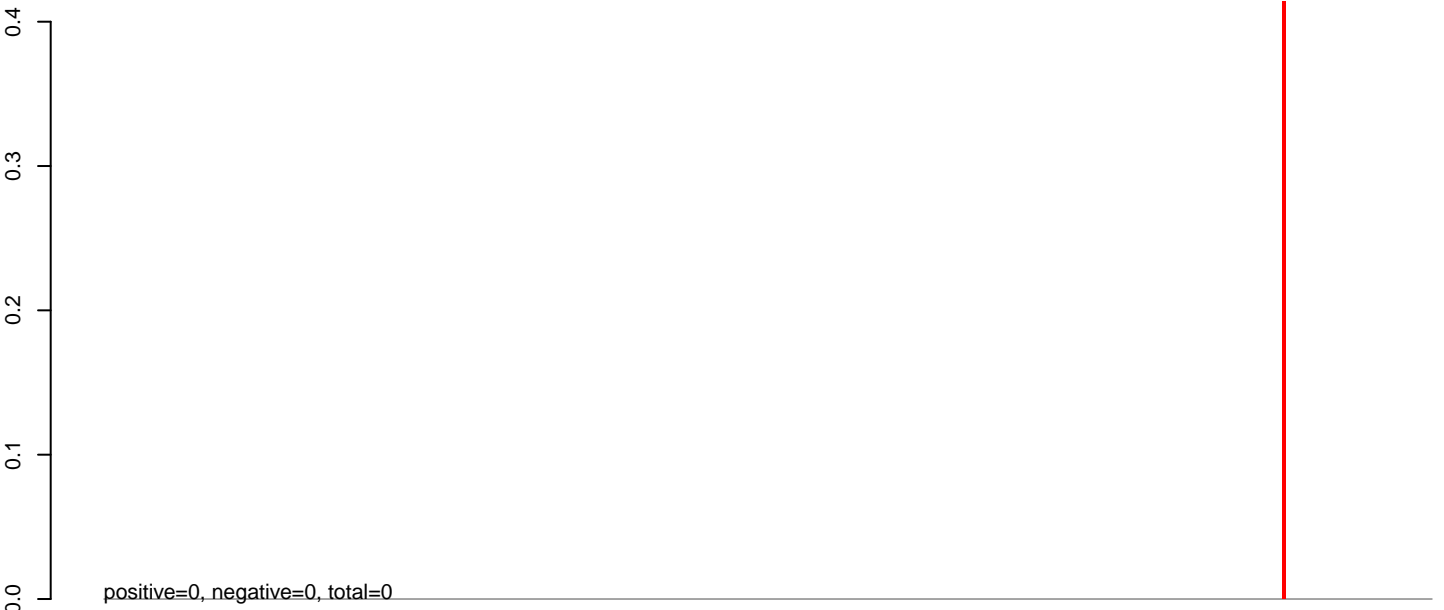
AeAeg_Aag2.SINV.GFP.24_35.rep



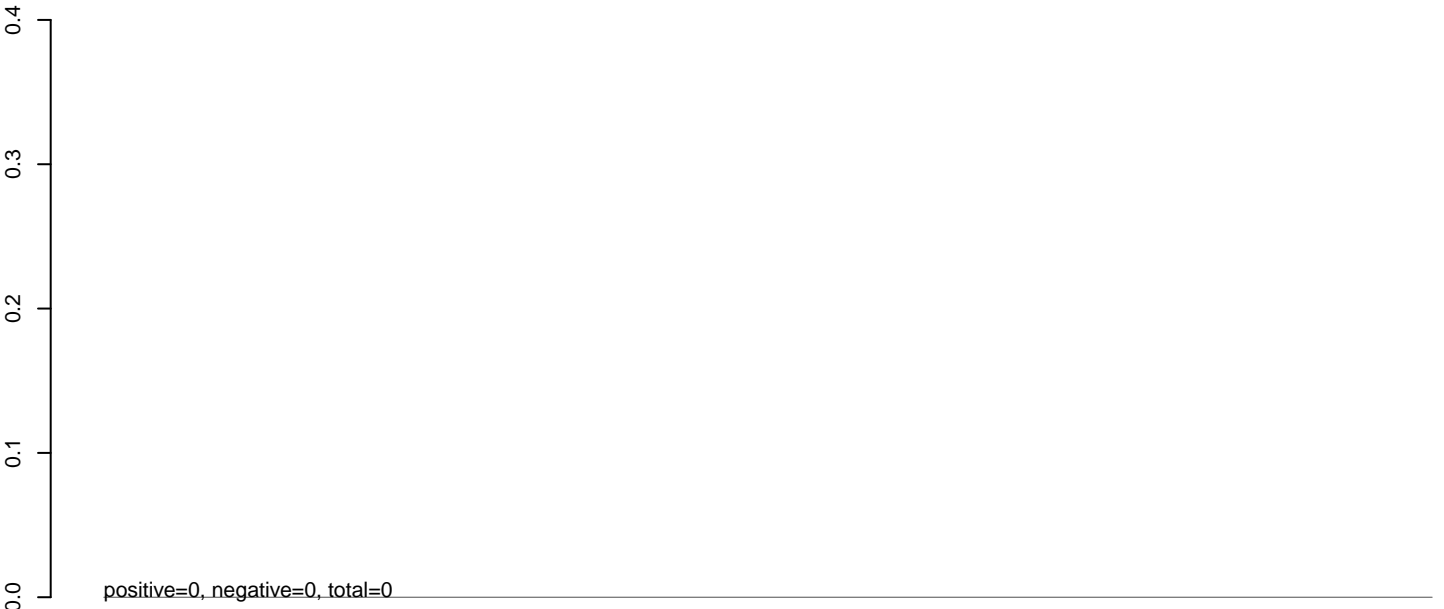
AeAeg_Aag2.SINV.GFP.rep



AeAeg_Aag2.SINV.GFP.18_23.rep



AeAeg_Aag2.SINV.GFP.24_35.rep

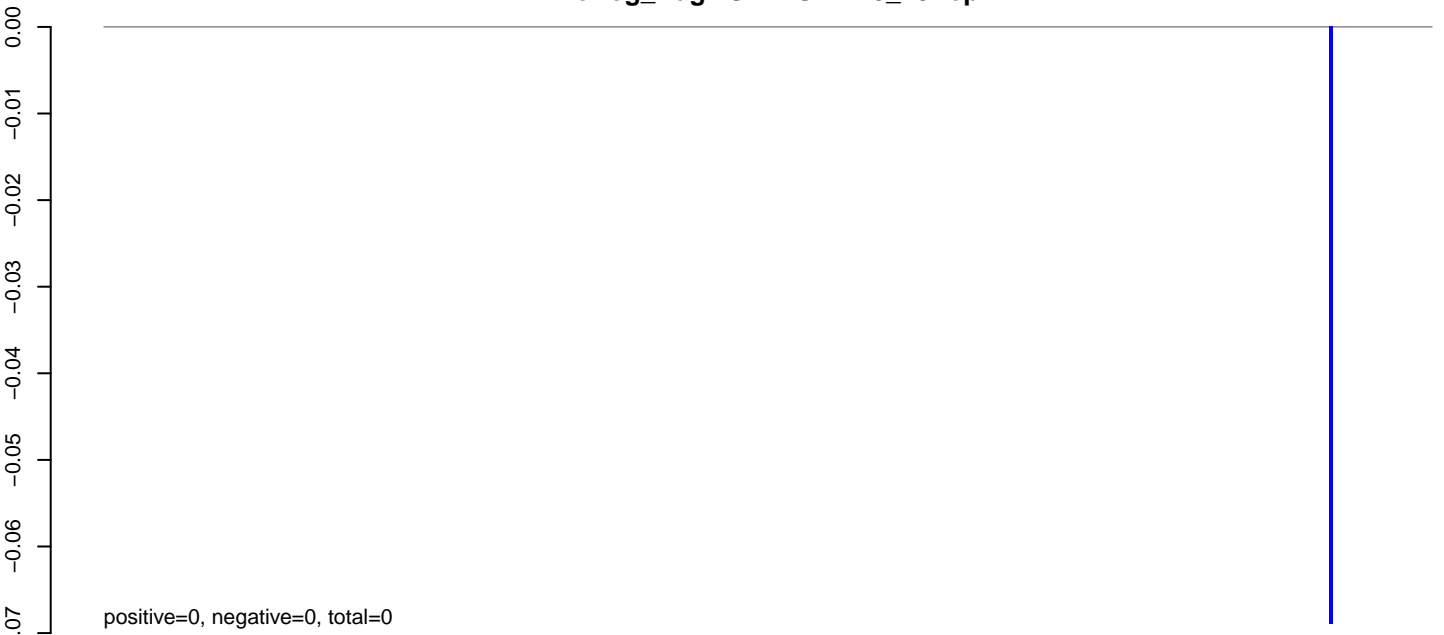


AeAeg_Aag2.SINV.GFP.rep

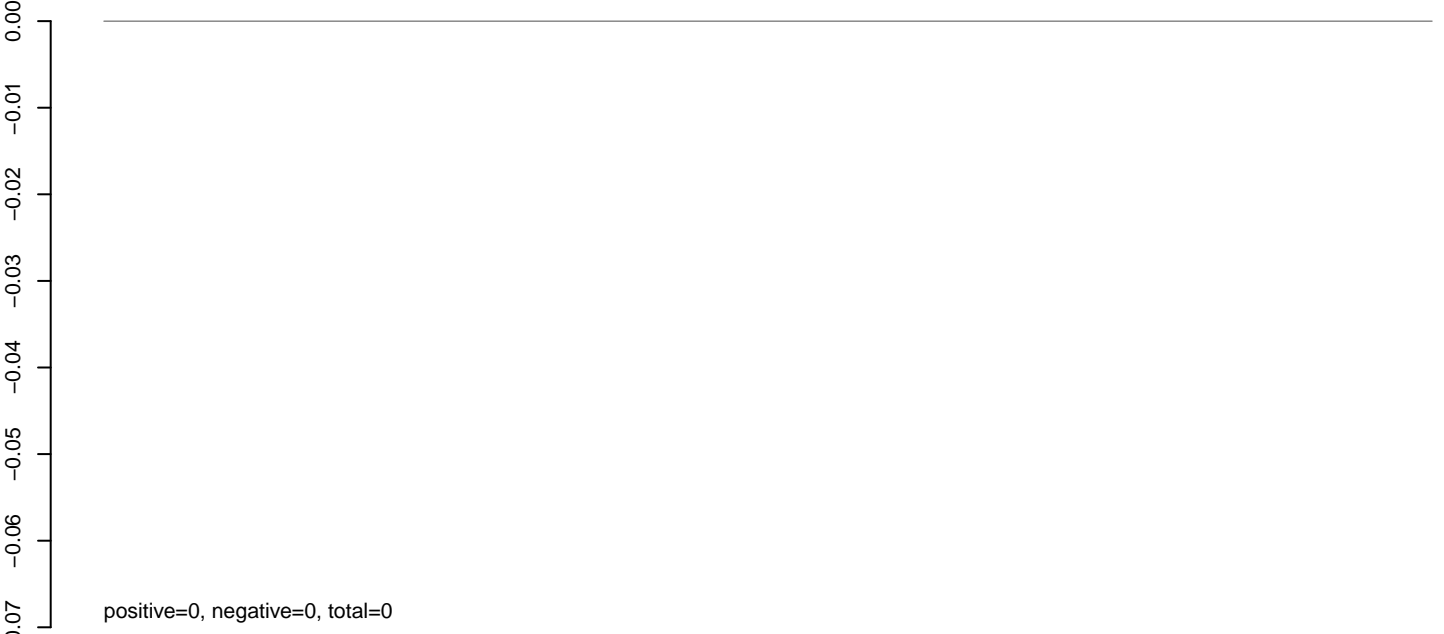


0 2000 4000 6000 8000 10000

AeAeg_Aag2.SINV.GFP.18_23.rep



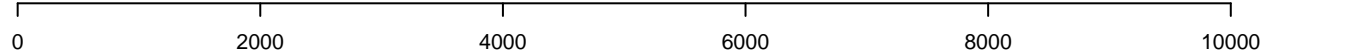
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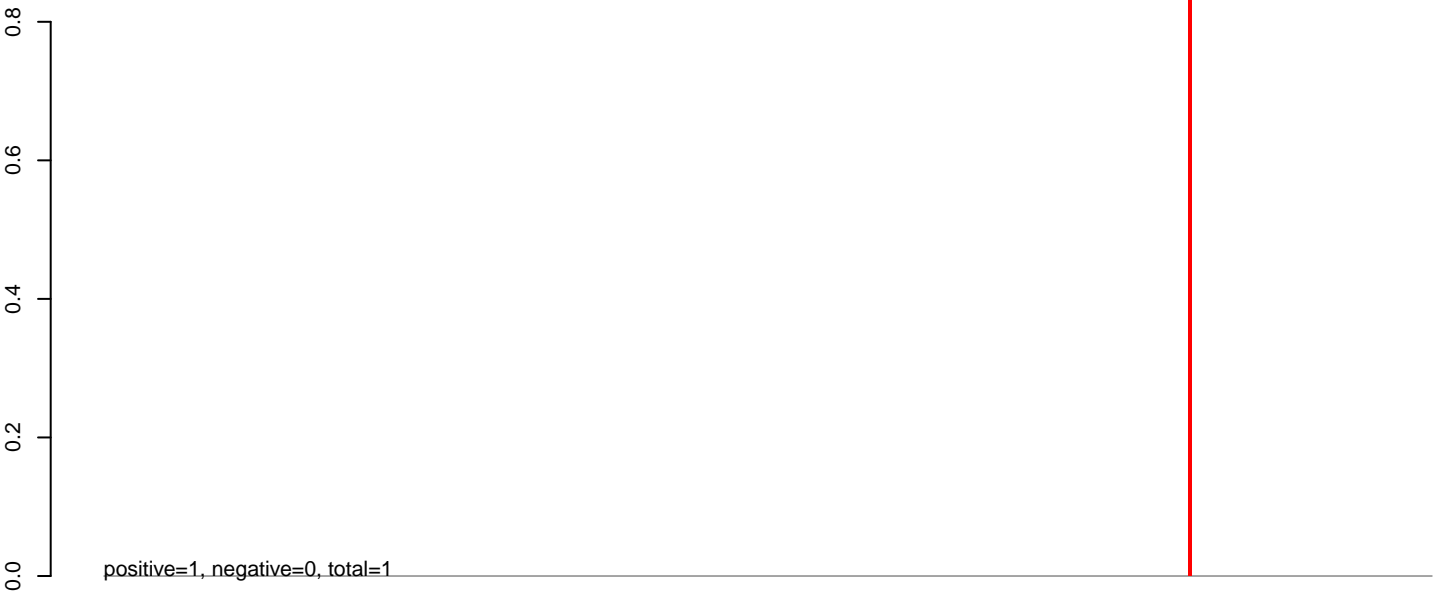
AeAeg_Aag2.SINV.GFP.rep



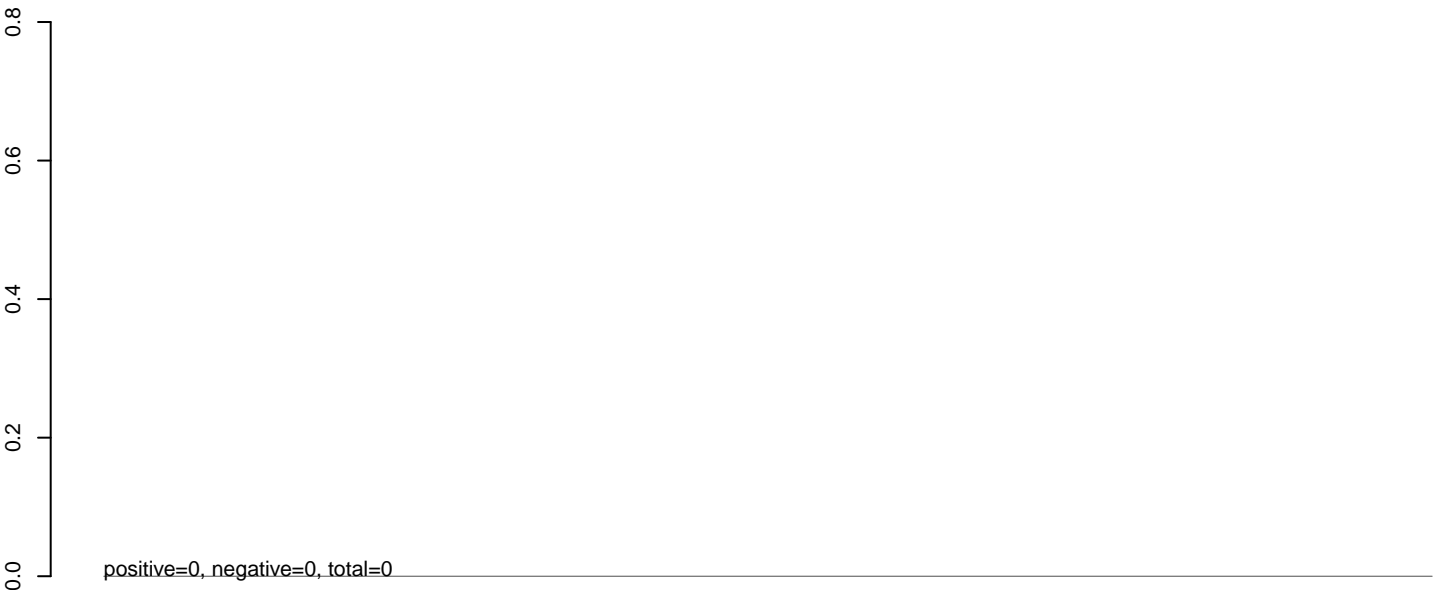
Window size=25, length=10938, virus@NC_027819.1-Mercadeo_virus_isolate_ER-M10:1-10938



AeAeg_Aag2.SINV.GFP.18_23.rep



AeAeg_Aag2.SINV.GFP.24_35.rep

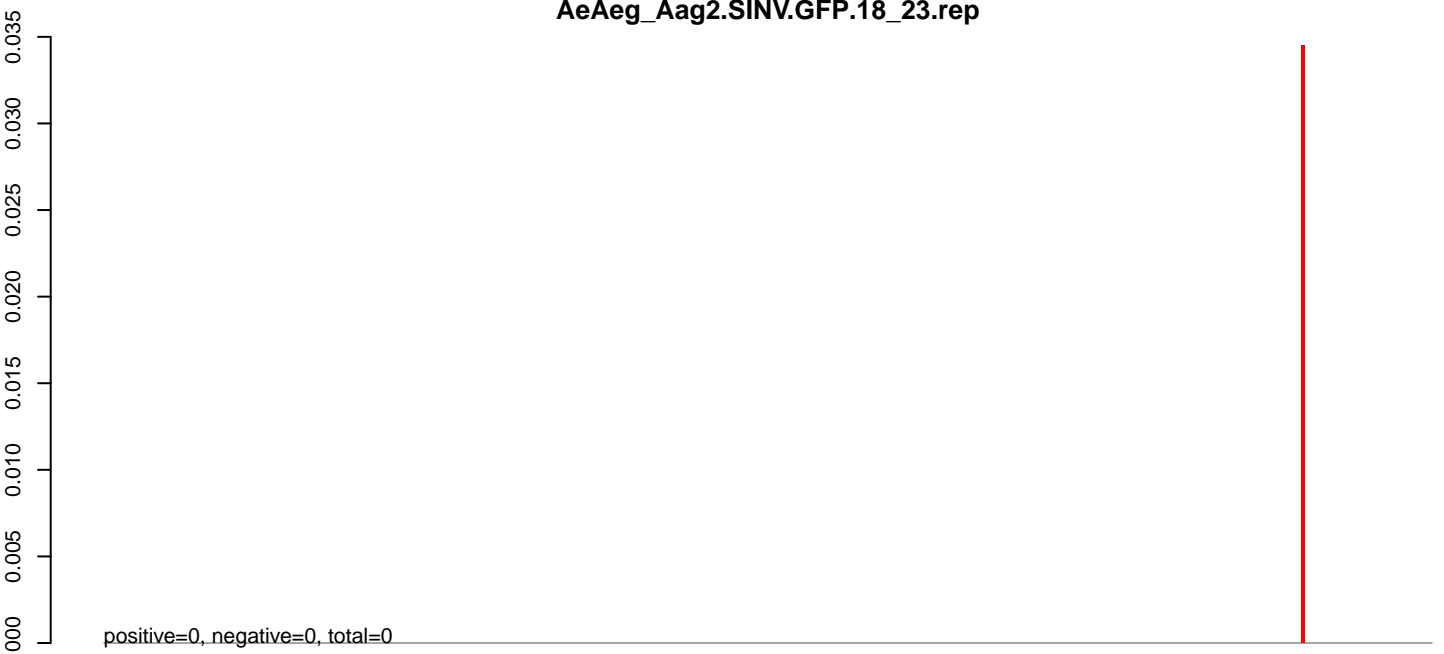


AeAeg_Aag2.SINV.GFP.rep

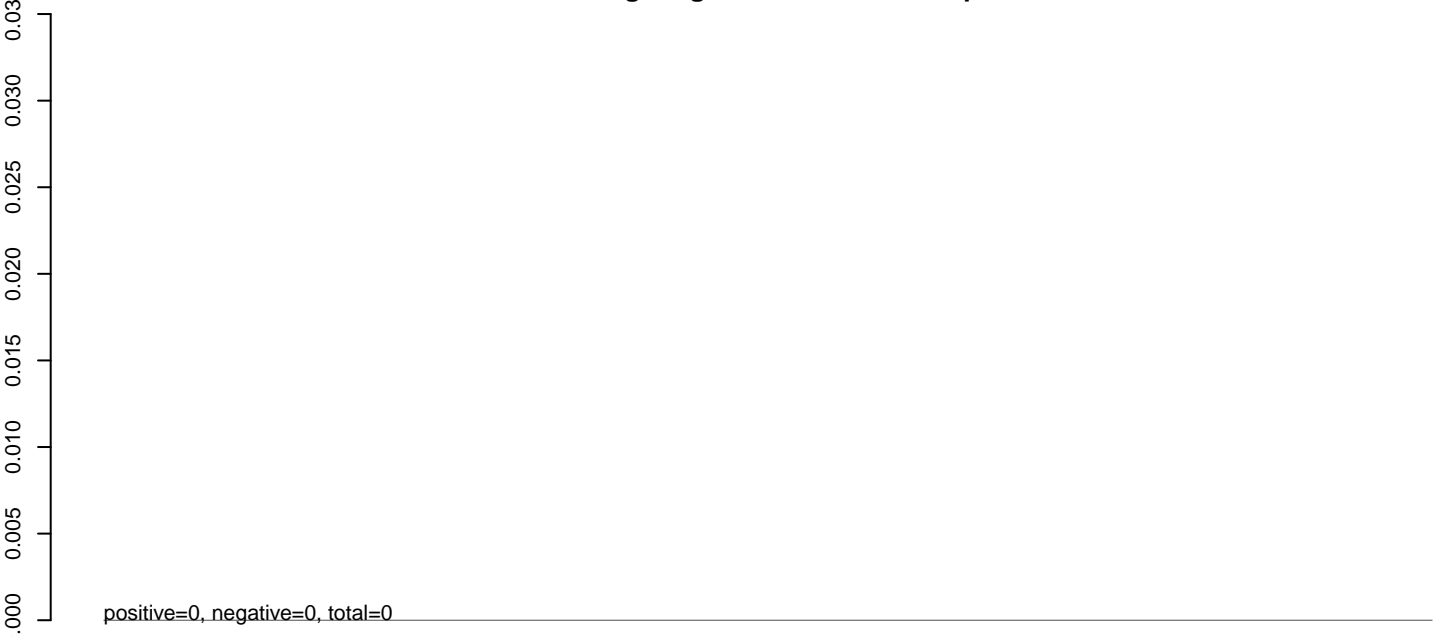


0 2000 4000 6000 8000 10000

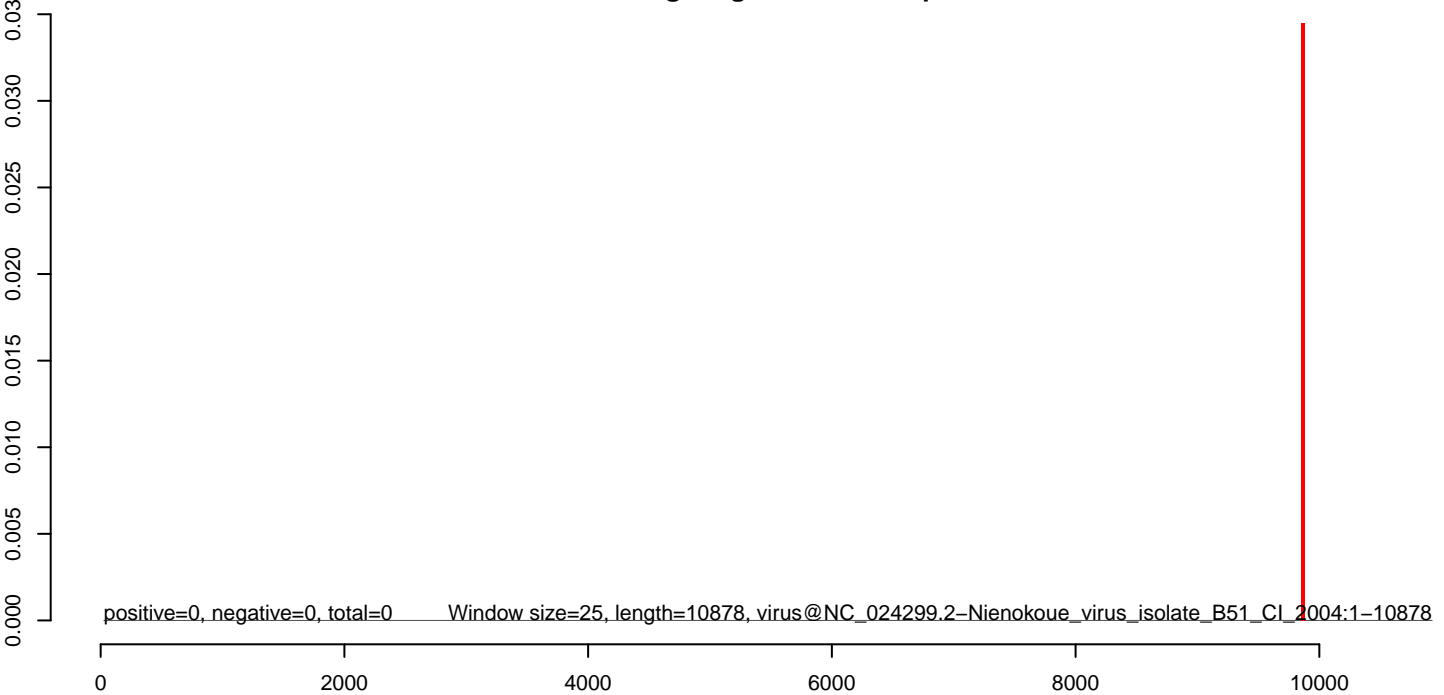
AeAeg_Aag2.SINV.GFP.18_23.rep



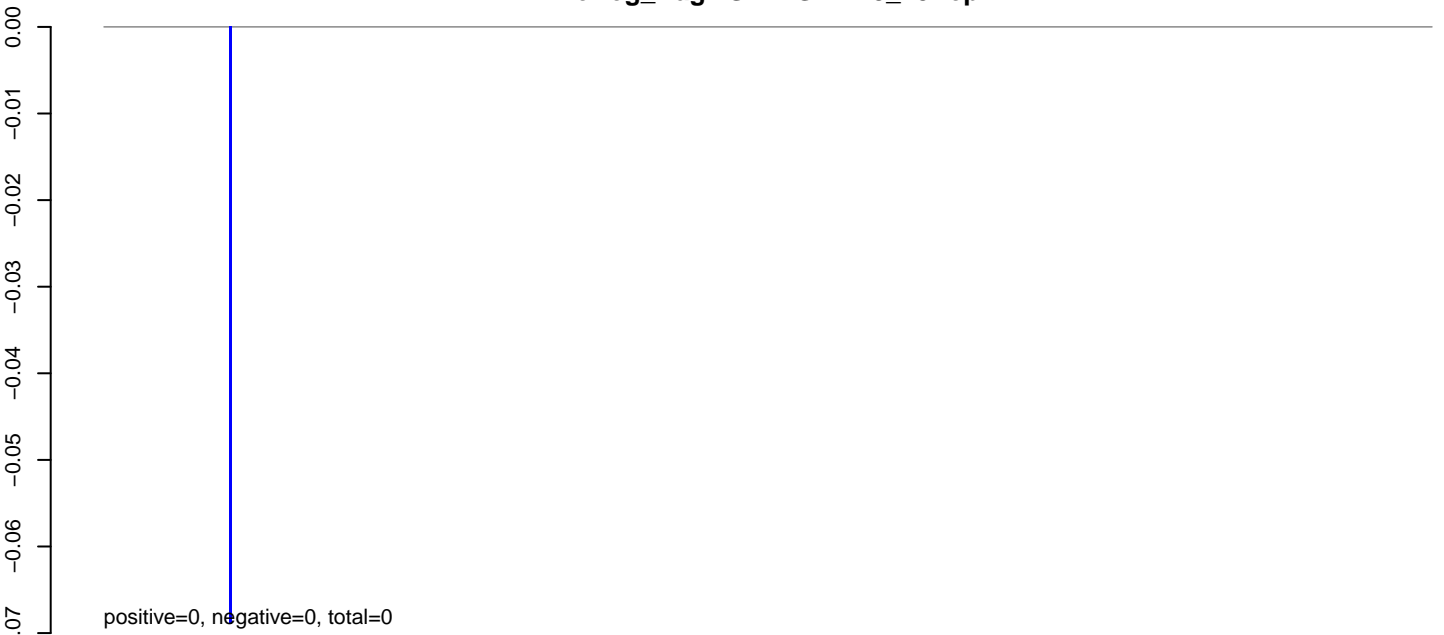
AeAeg_Aag2.SINV.GFP.24_35.rep



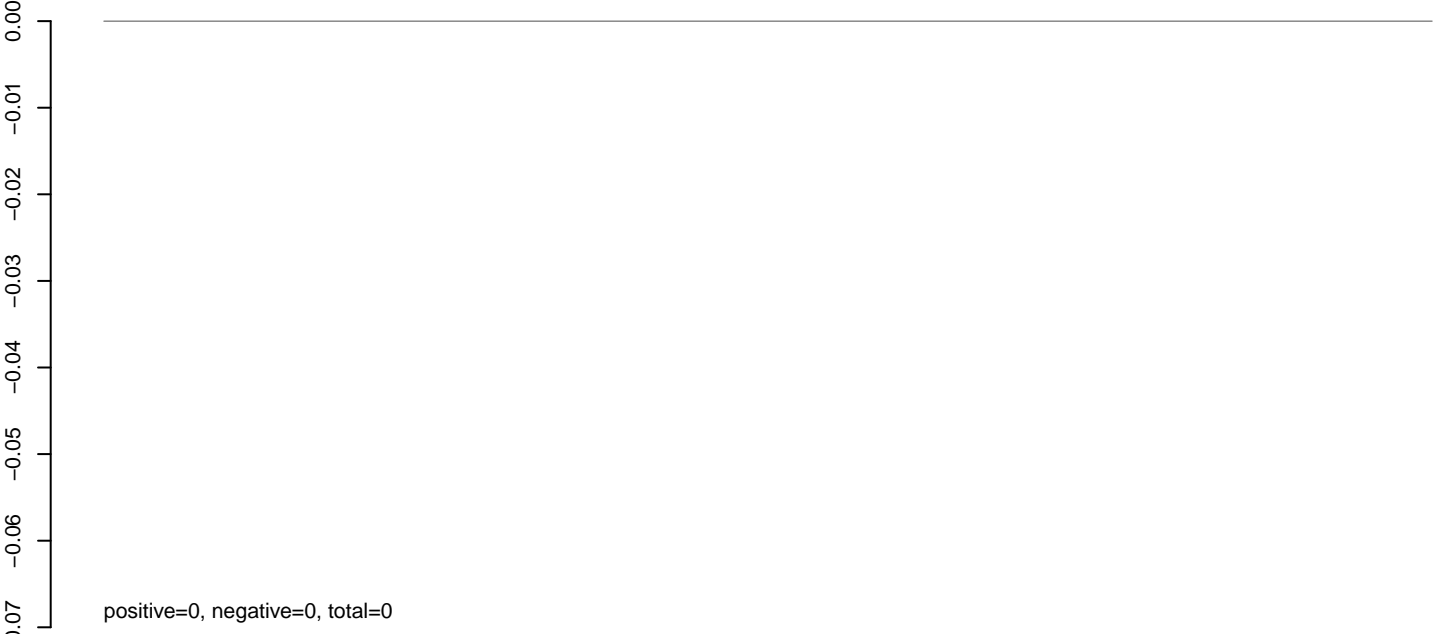
AeAeg_Aag2.SINV.GFP.rep



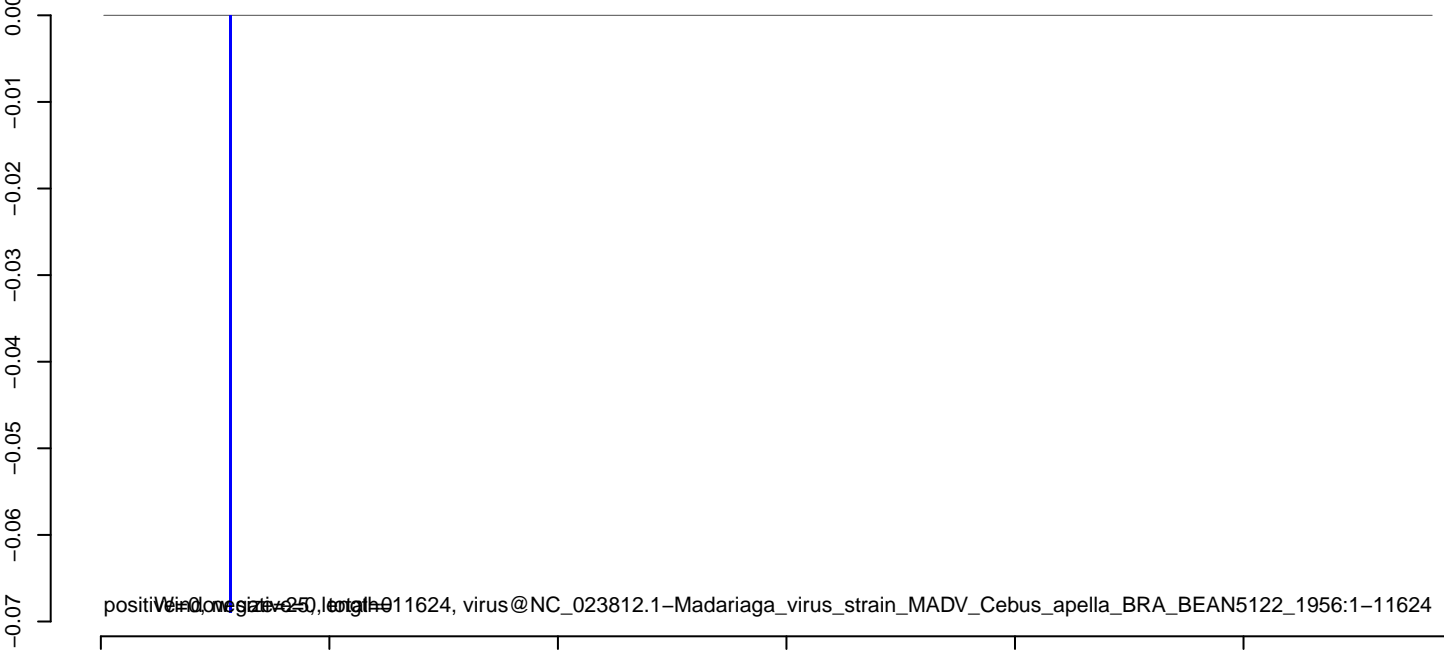
AeAeg_Aag2.SINV.GFP.18_23.rep



AeAeg_Aag2.SINV.GFP.24_35.rep

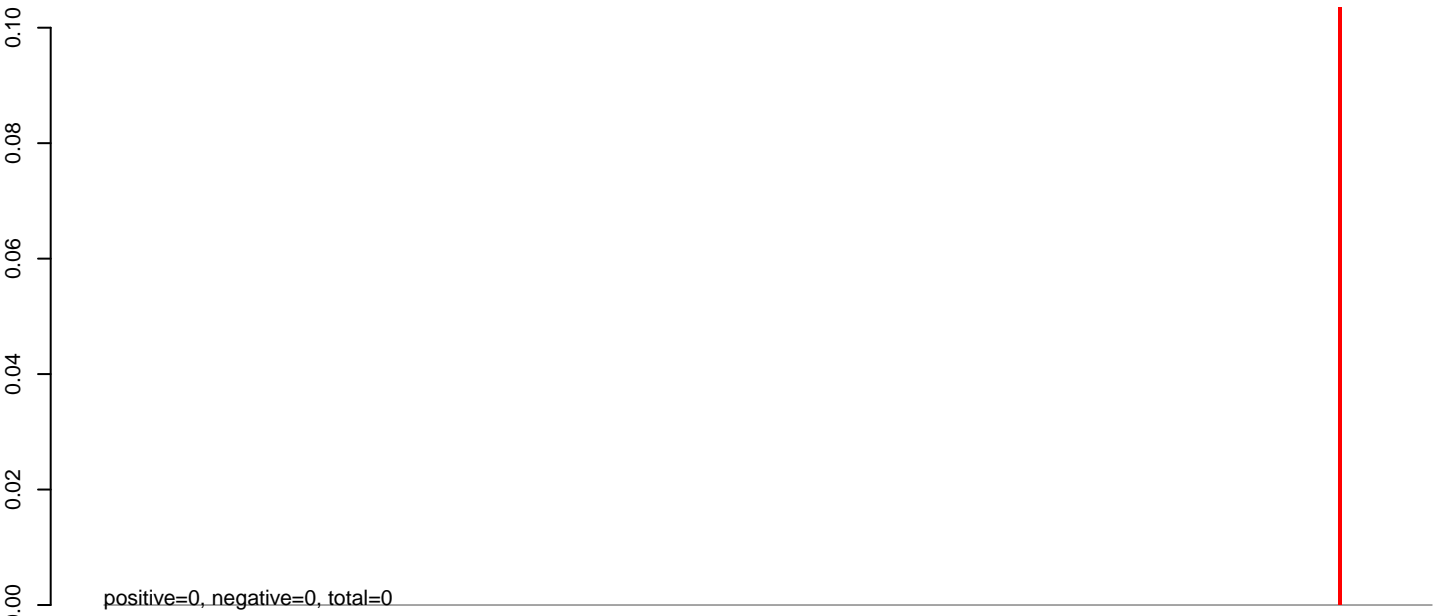


AeAeg_Aag2.SINV.GFP.rep

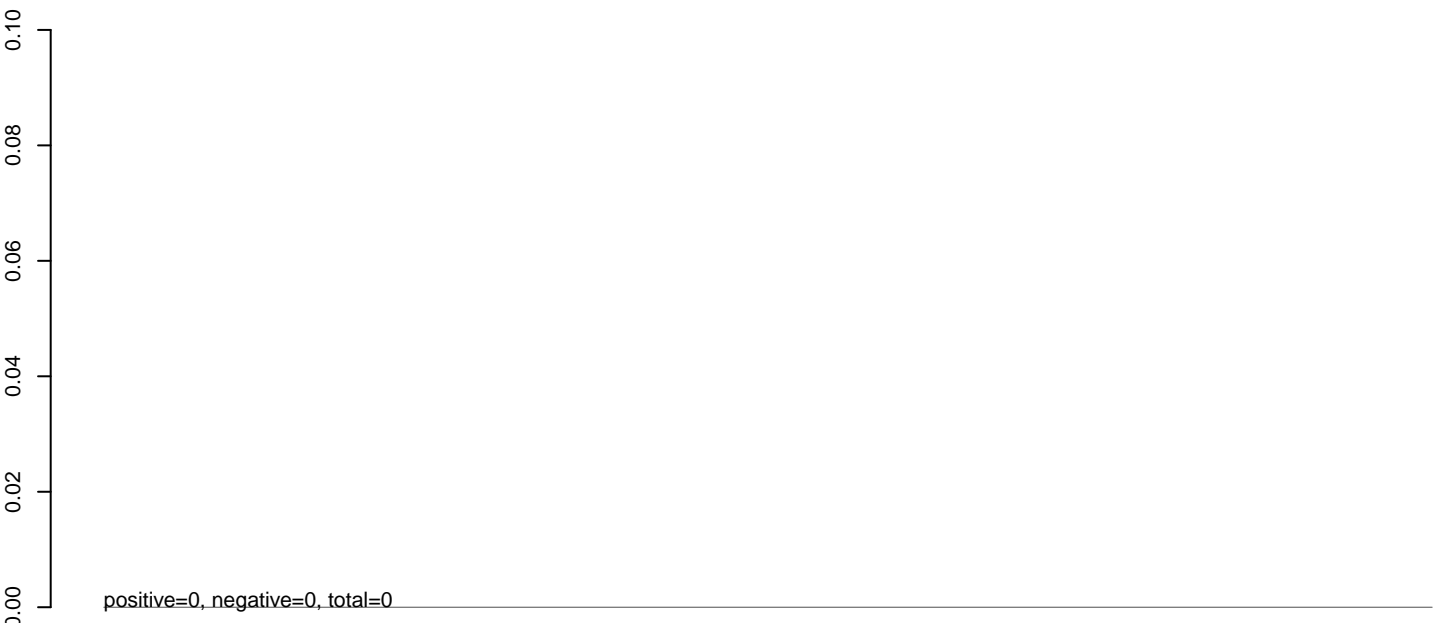


0 2000 4000 6000 8000 10000 12000

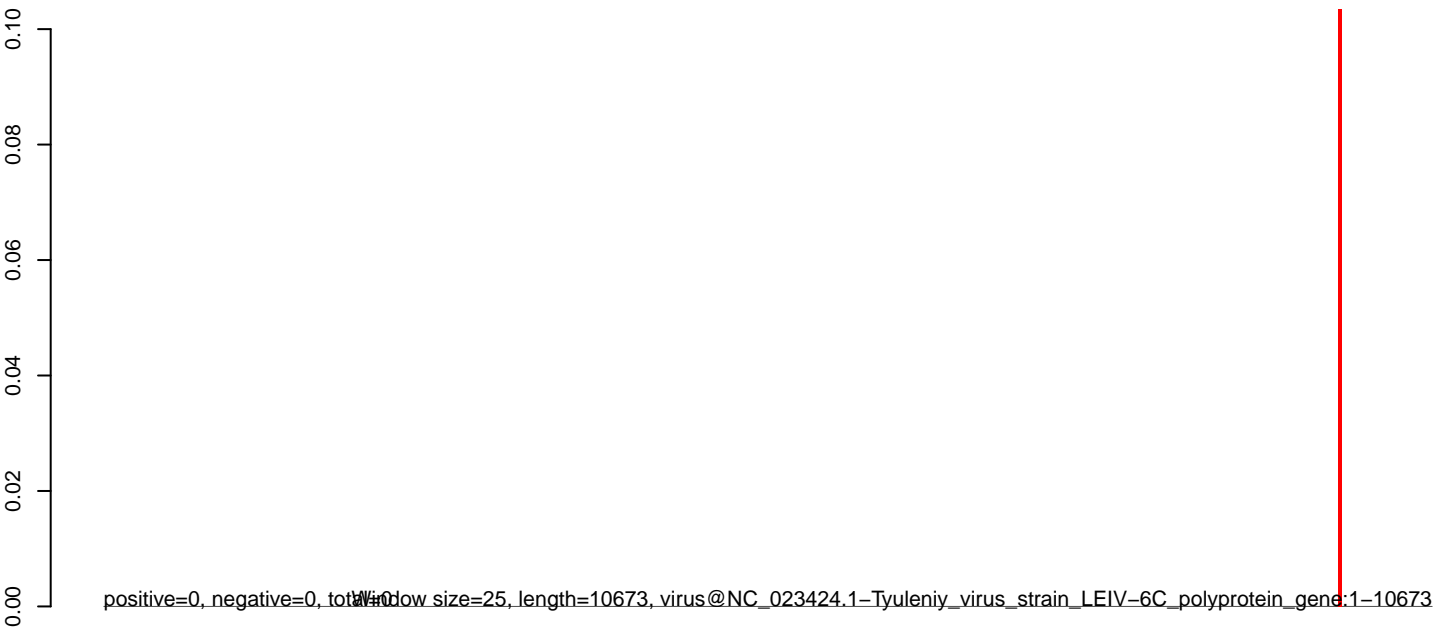
AeAeg_Aag2.SINV.GFP.18_23.rep



AeAeg_Aag2.SINV.GFP.24_35.rep



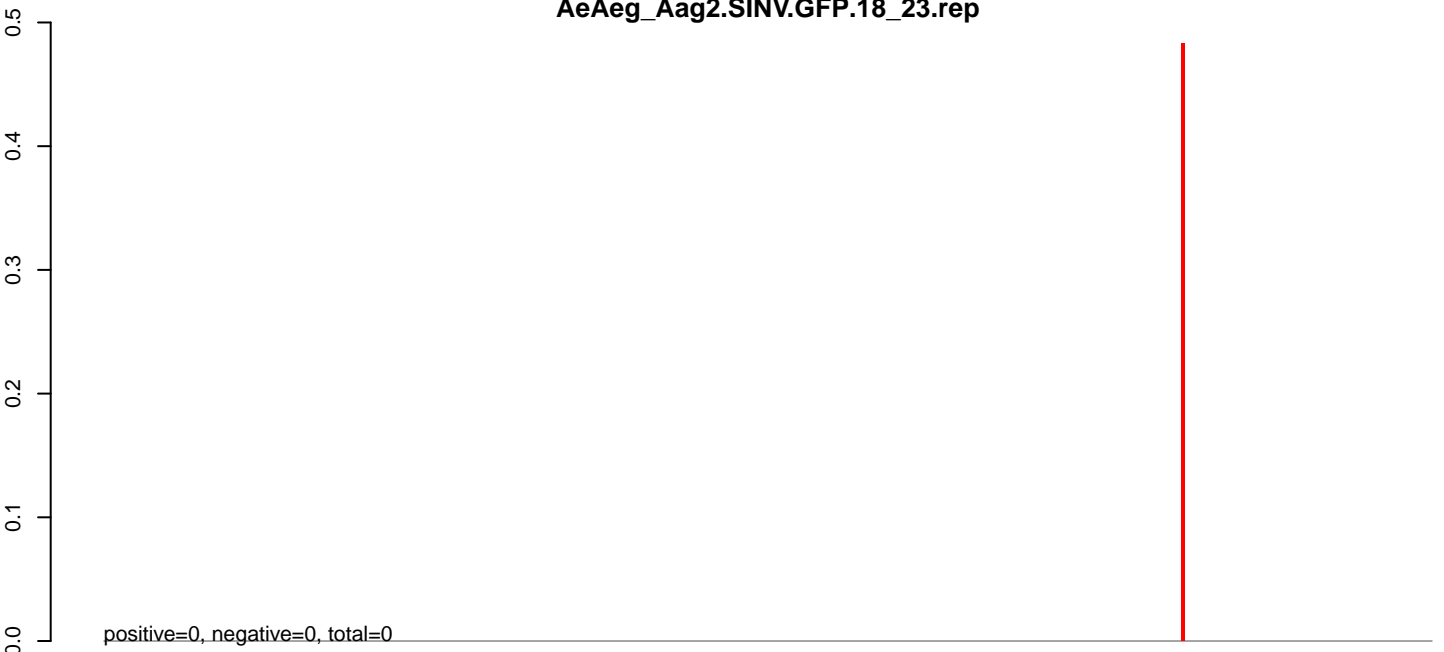
AeAeg_Aag2.SINV.GFP.rep



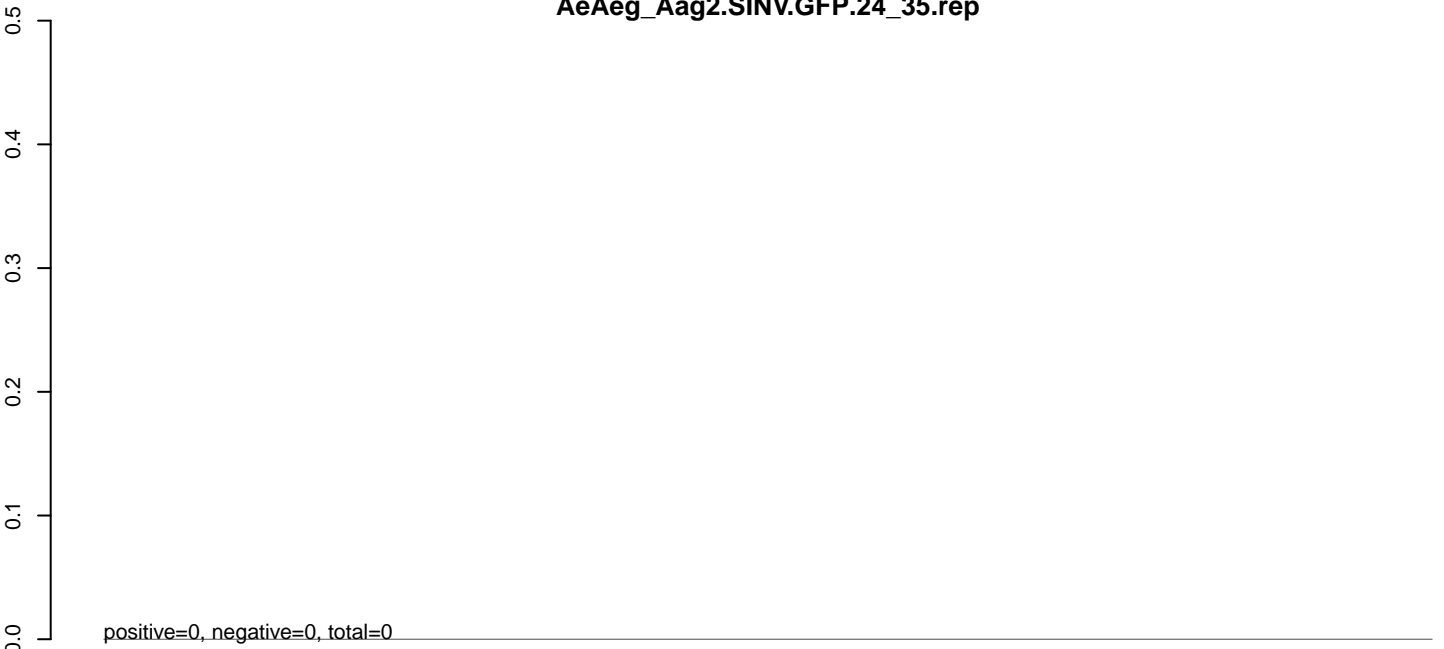
Window size=25, length=10673, virus@NC_023424.1-Tyuleniy_virus_strain_LEIV-6C_polyprotein_gene:1-10673

0 2000 4000 6000 8000 10000

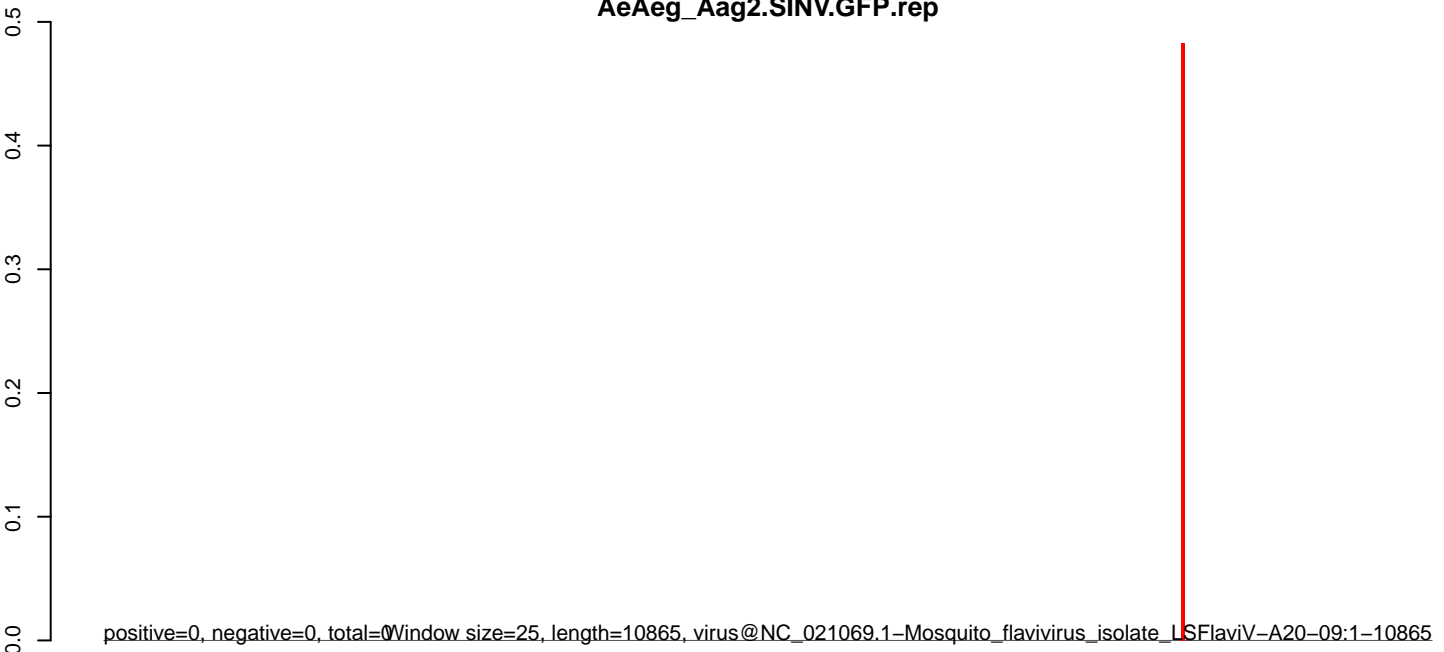
AeAeg_Aag2.SINV.GFP.18_23.rep



AeAeg_Aag2.SINV.GFP.24_35.rep

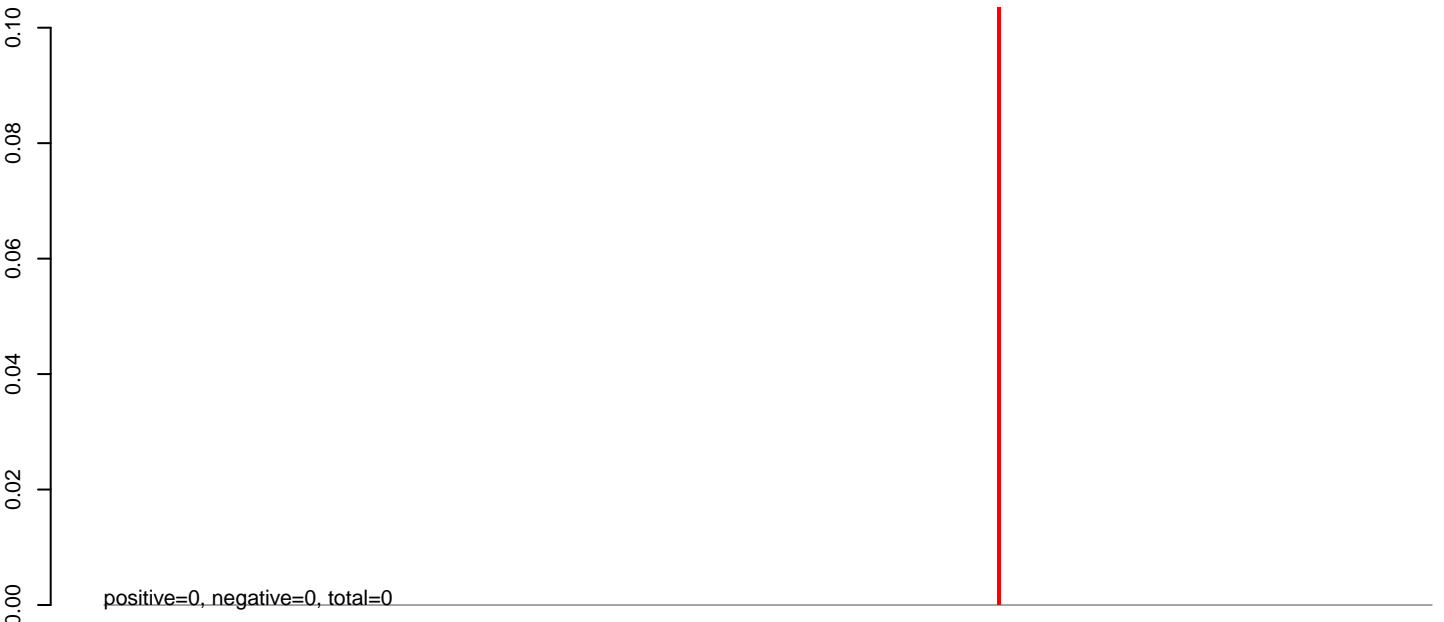


AeAeg_Aag2.SINV.GFP.rep

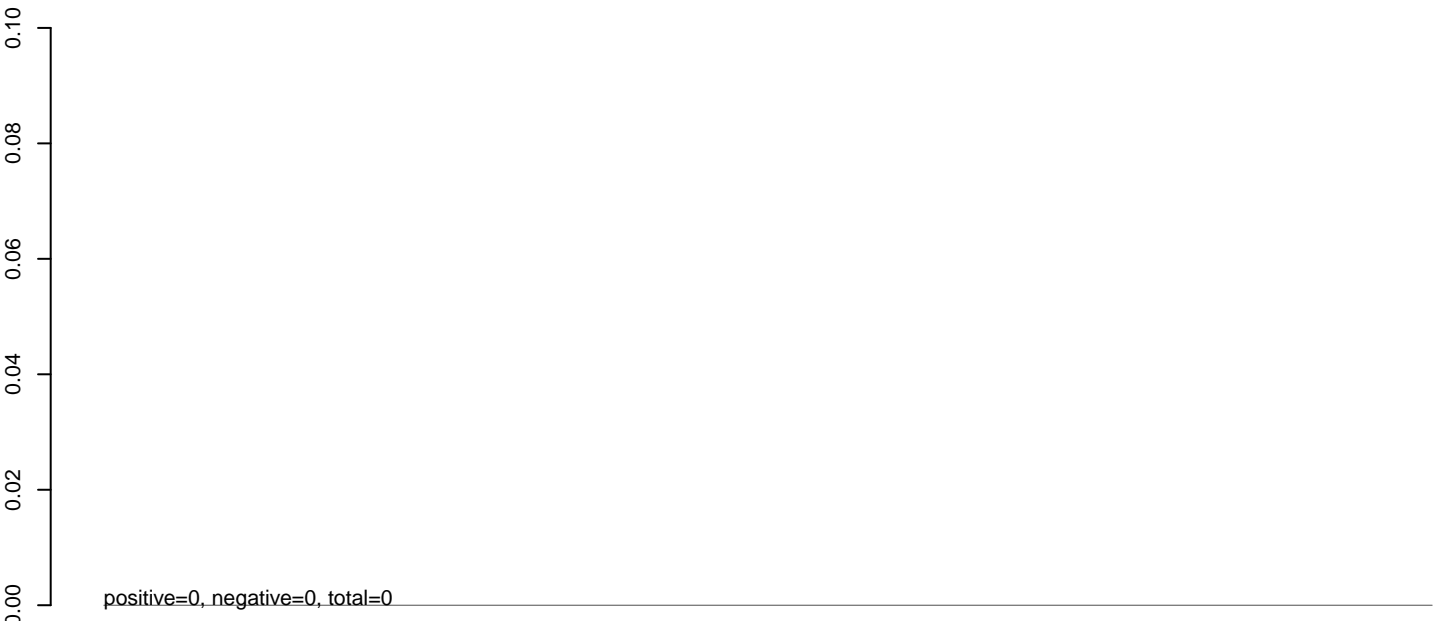


Window size=25, length=10865, virus@NC_021069.1-Mosquito_flavivirus_isolate_LSFlaviV-A20-09:1-10865

AeAeg_Aag2.SINV.GFP.18_23.rep



AeAeg_Aag2.SINV.GFP.24_35.rep

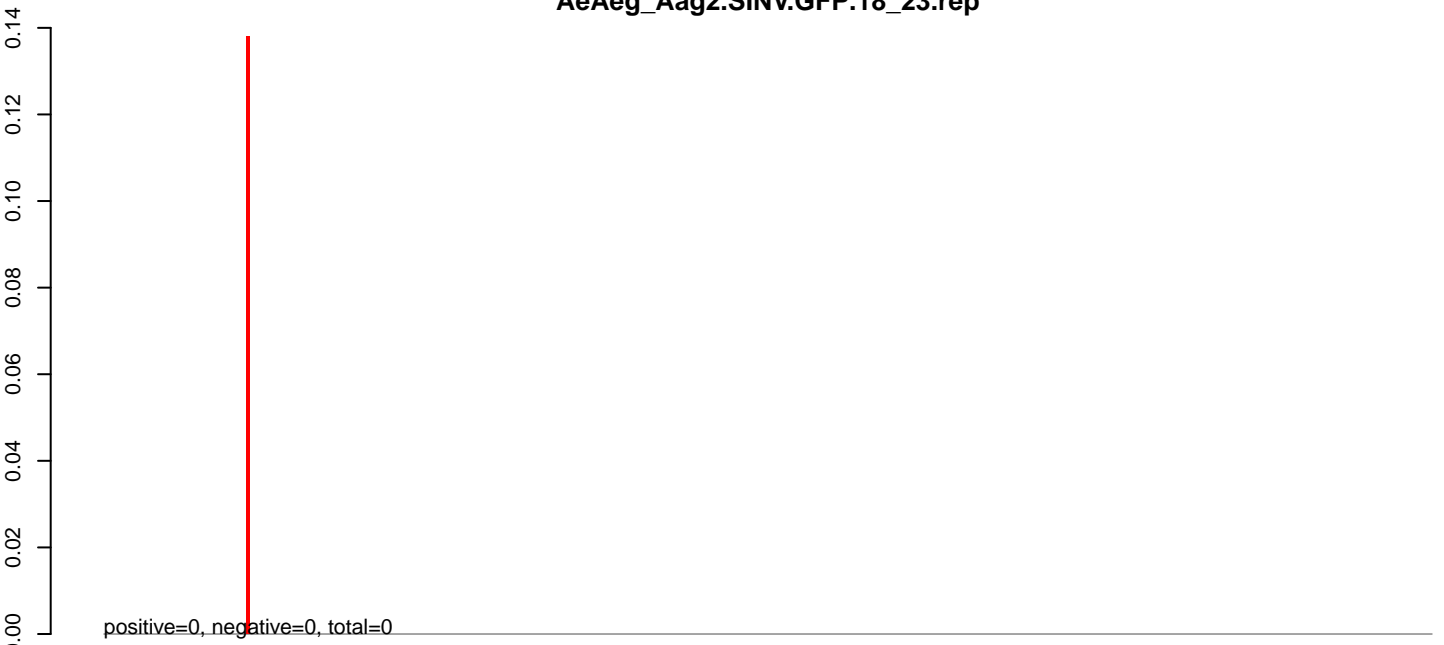


AeAeg_Aag2.SINV.GFP.rep

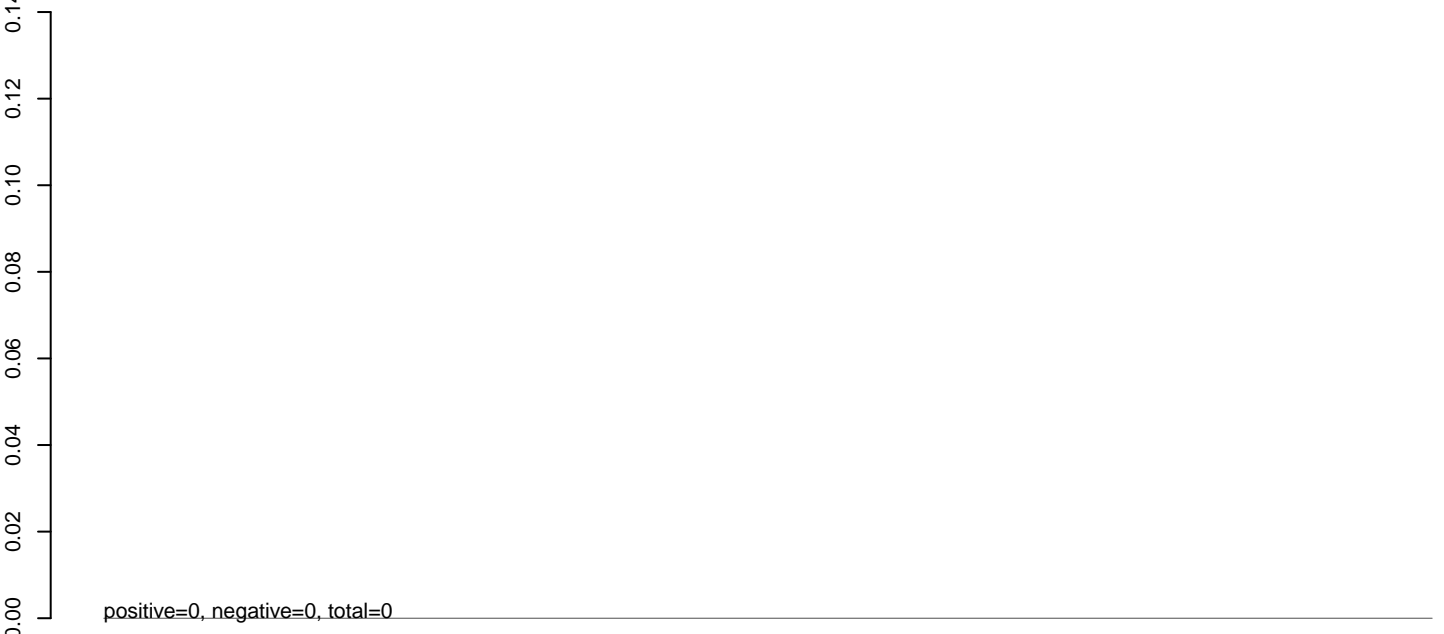


0 2000 4000 6000 8000 10000

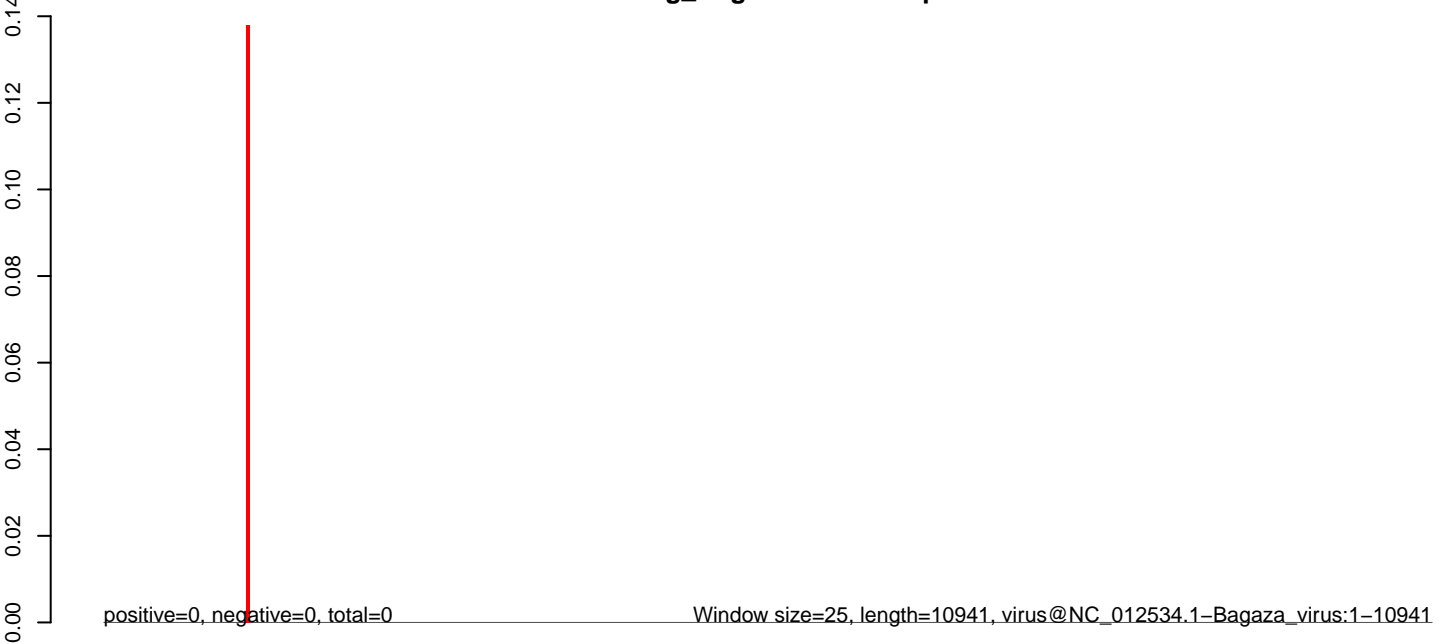
AeAeg_Aag2.SINV.GFP.18_23.rep



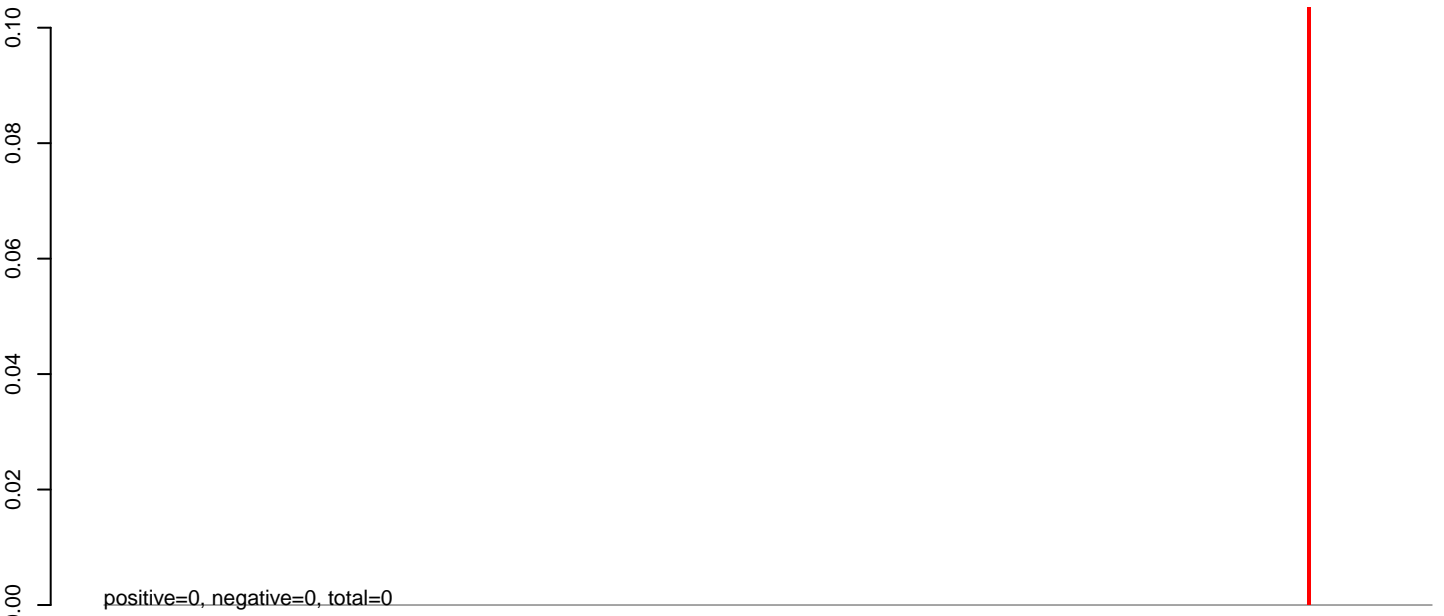
AeAeg_Aag2.SINV.GFP.24_35.rep



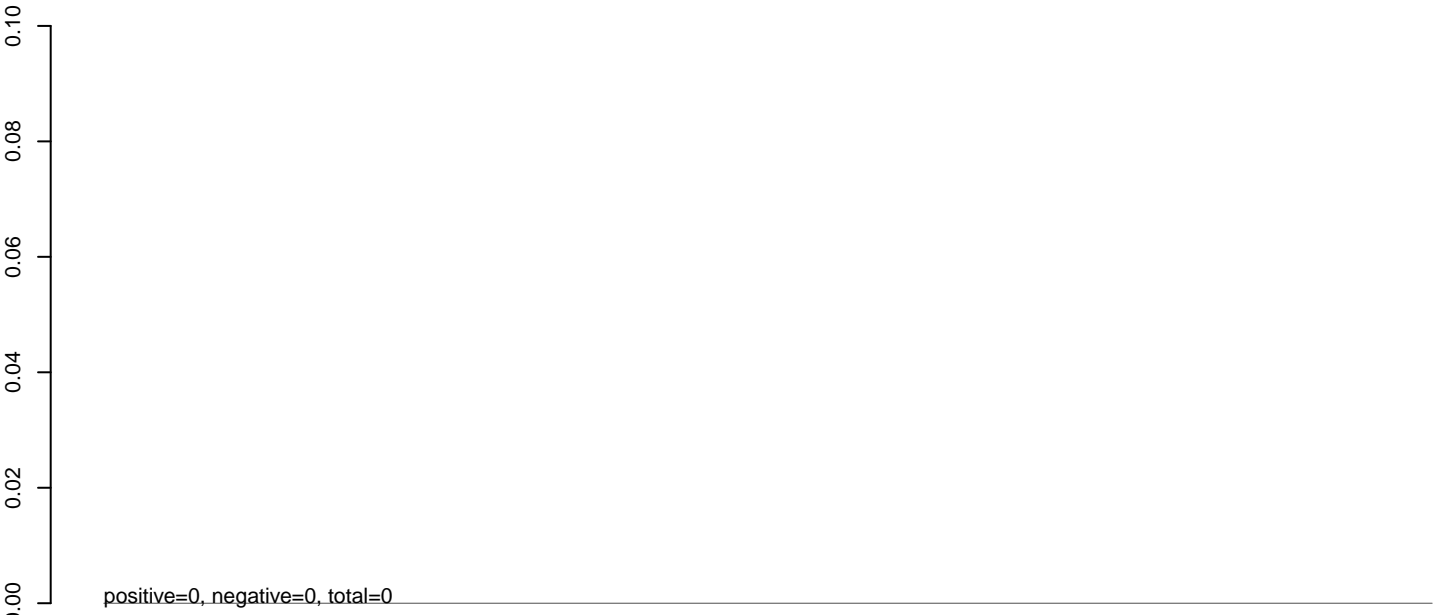
AeAeg_Aag2.SINV.GFP.rep



AeAeg_Aag2.SINV.GFP.18_23.rep



AeAeg_Aag2.SINV.GFP.24_35.rep

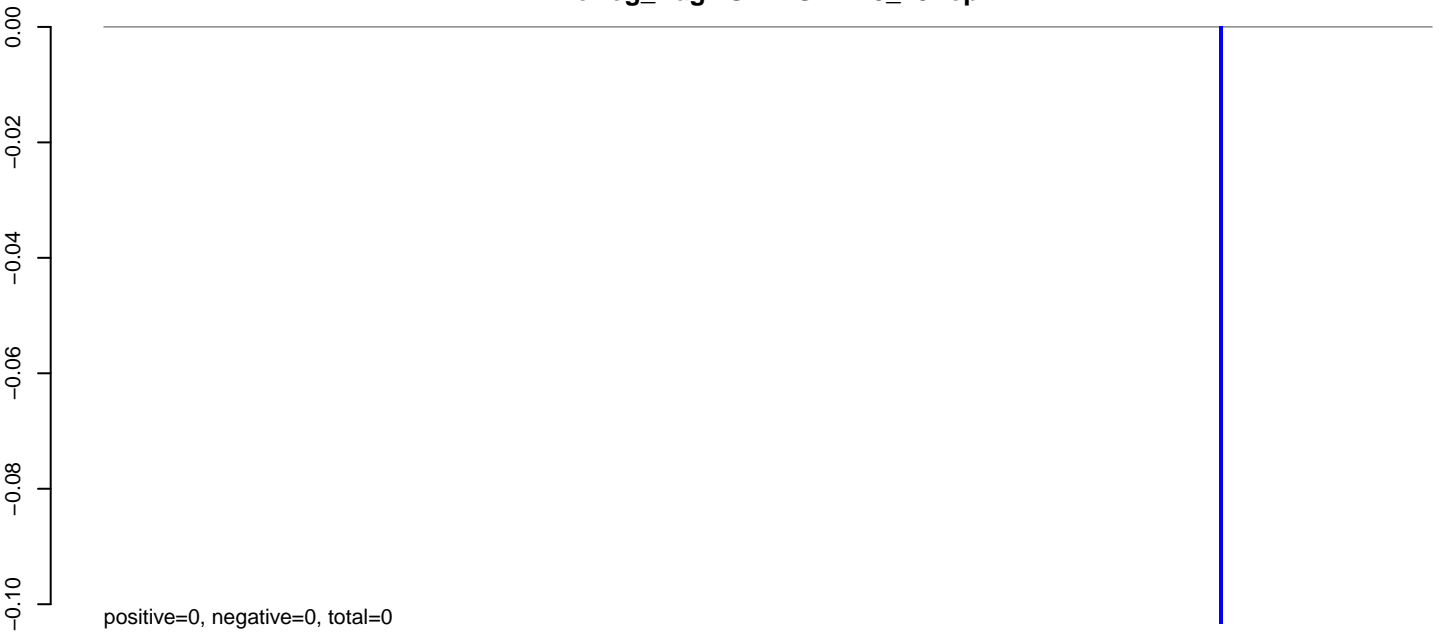


AeAeg_Aag2.SINV.GFP.rep

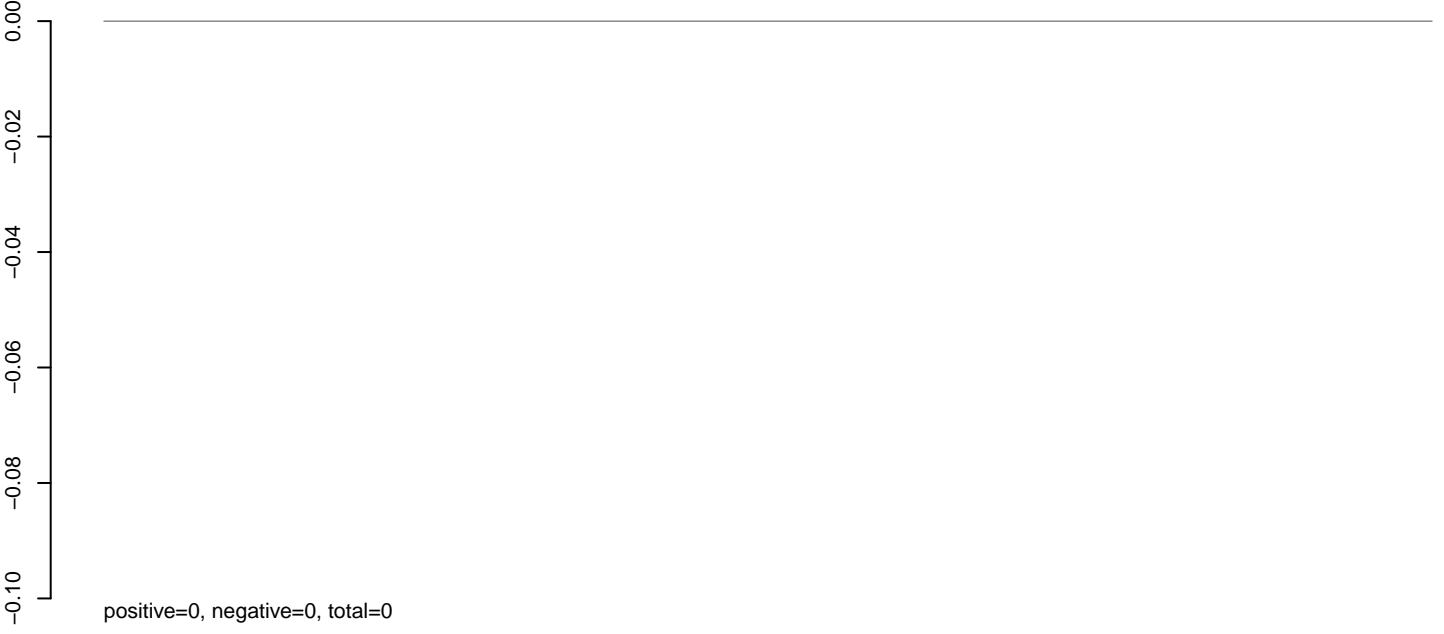


0 2000 4000 6000 8000 10000

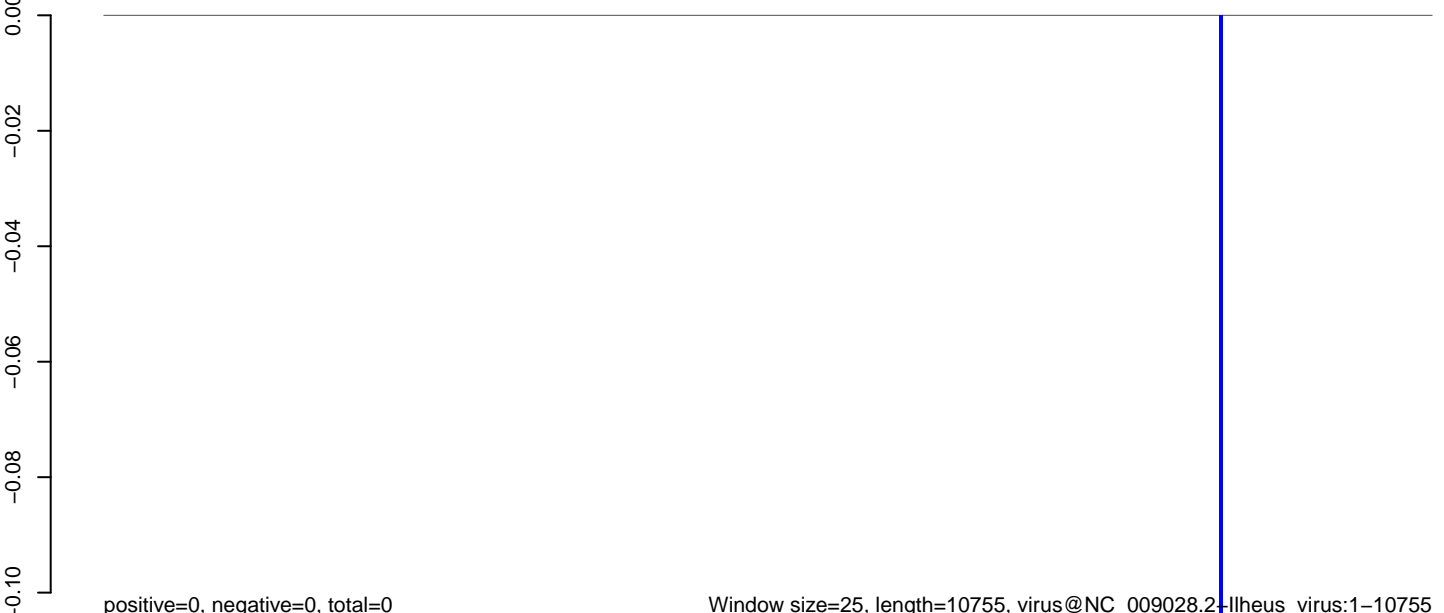
AeAeg_Aag2.SINV.GFP.18_23.rep



AeAeg_Aag2.SINV.GFP.24_35.rep

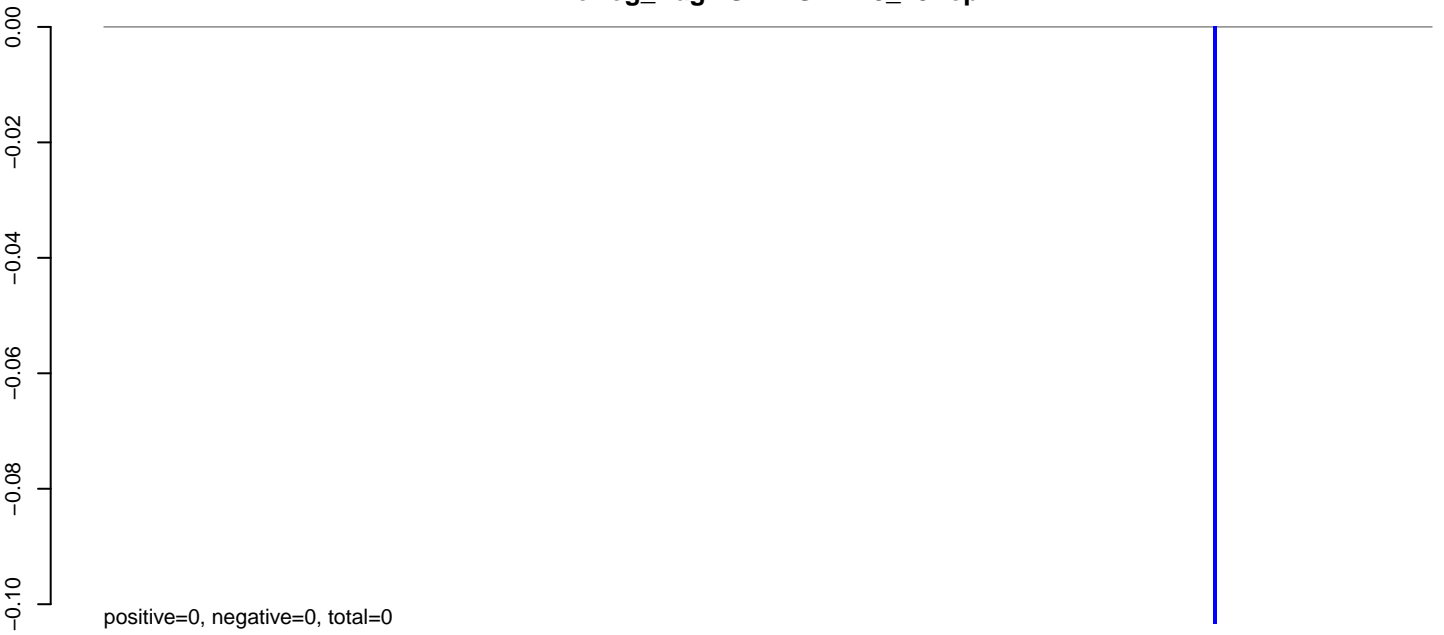


AeAeg_Aag2.SINV.GFP.rep

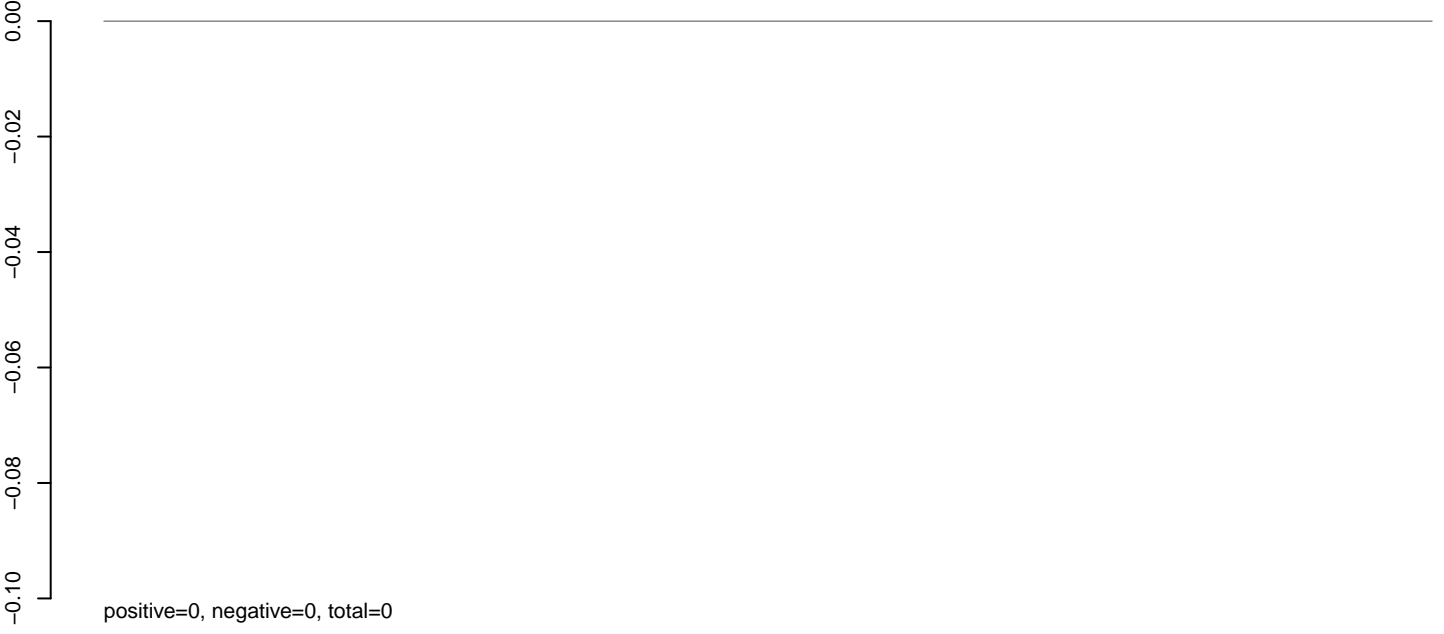


0 2000 4000 6000 8000 10000

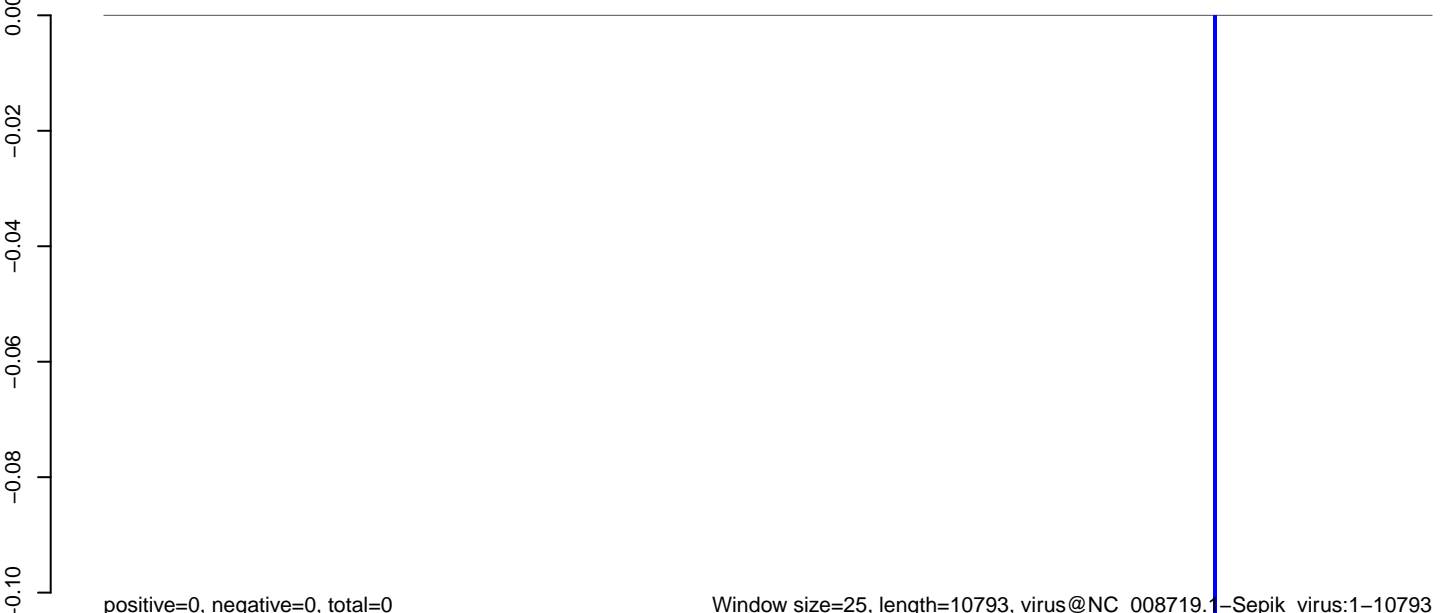
AeAeg_Aag2.SINV.GFP.18_23.rep



AeAeg_Aag2.SINV.GFP.24_35.rep



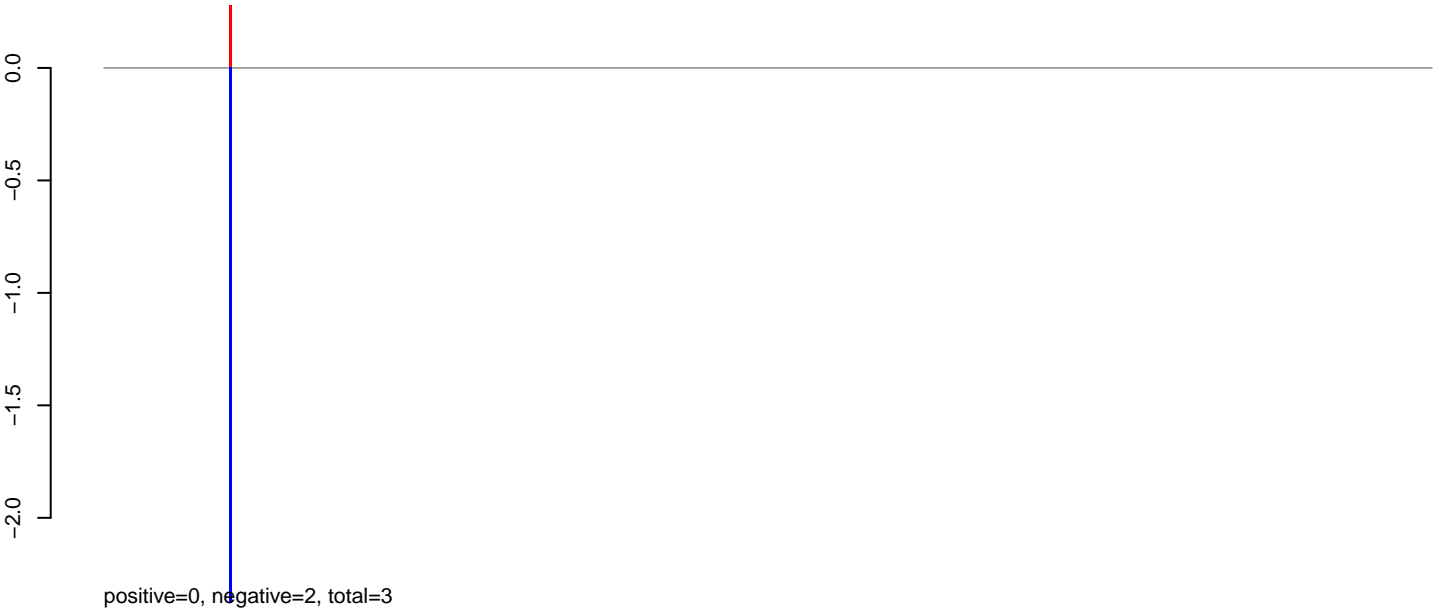
AeAeg_Aag2.SINV.GFP.rep



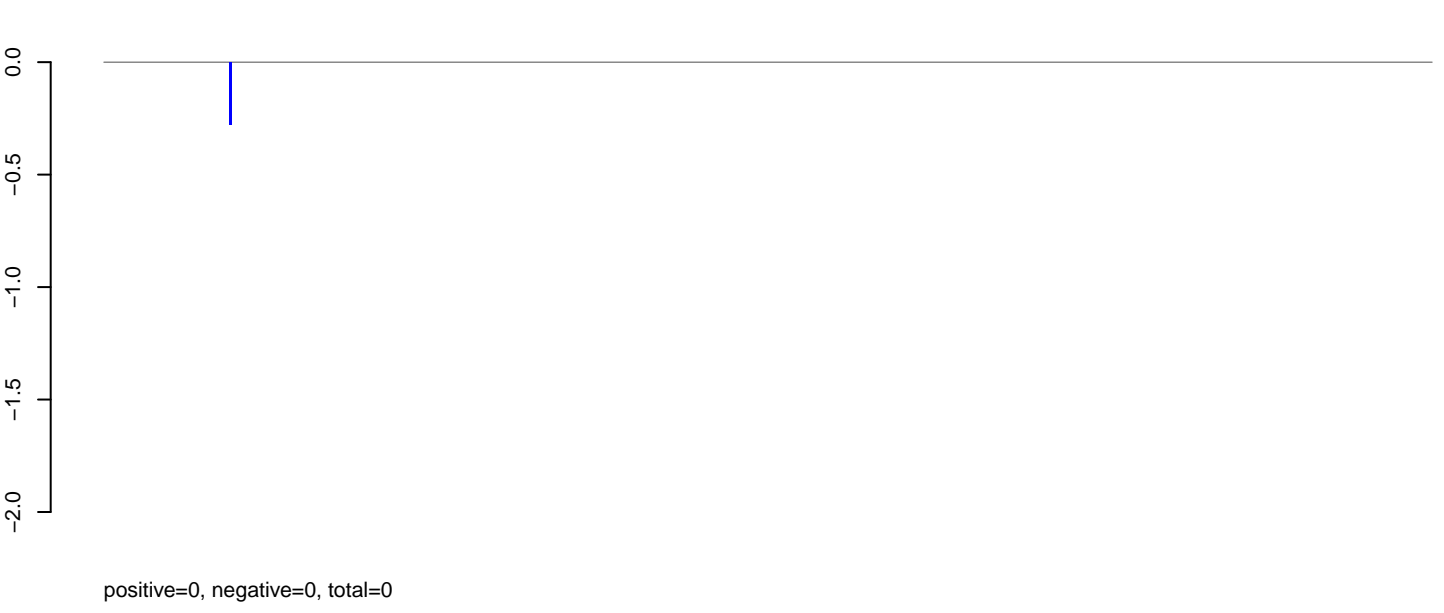
Window size=25, length=10793, virus@NC_008719.1-Sepik_virus:1-10793

0 2000 4000 6000 8000 10000

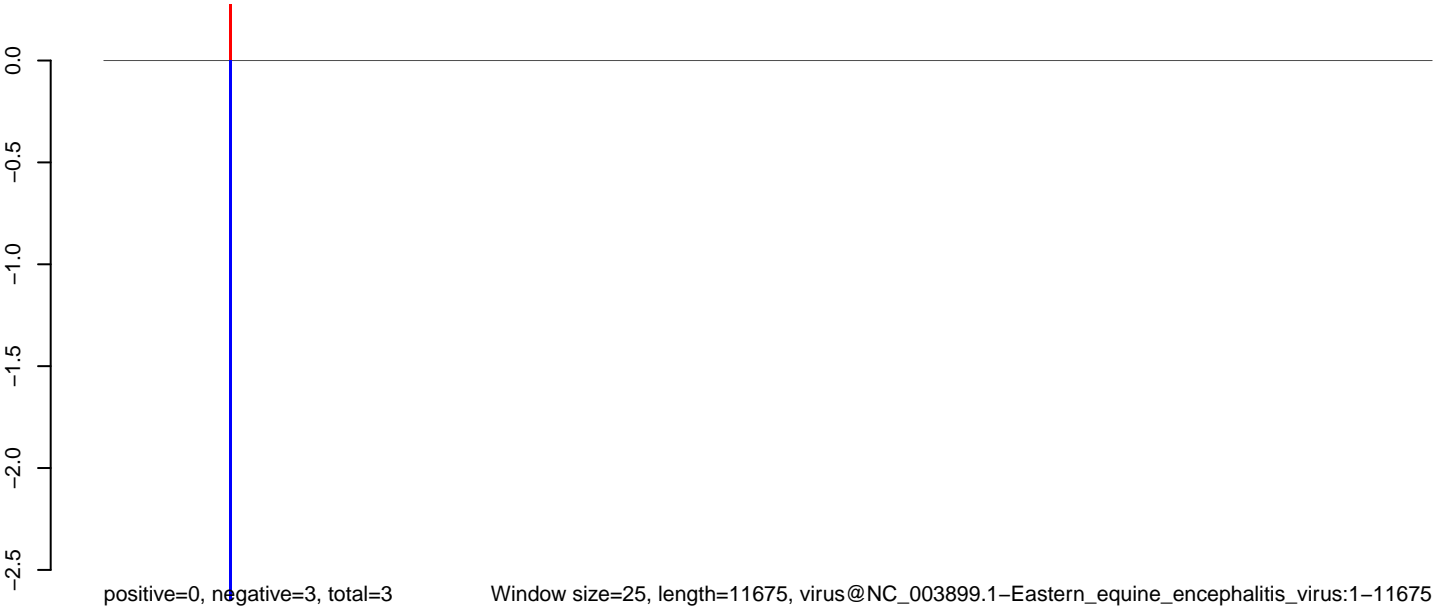
AeAeg_Aag2.SINV.GFP.18_23.rep



AeAeg_Aag2.SINV.GFP.24_35.rep



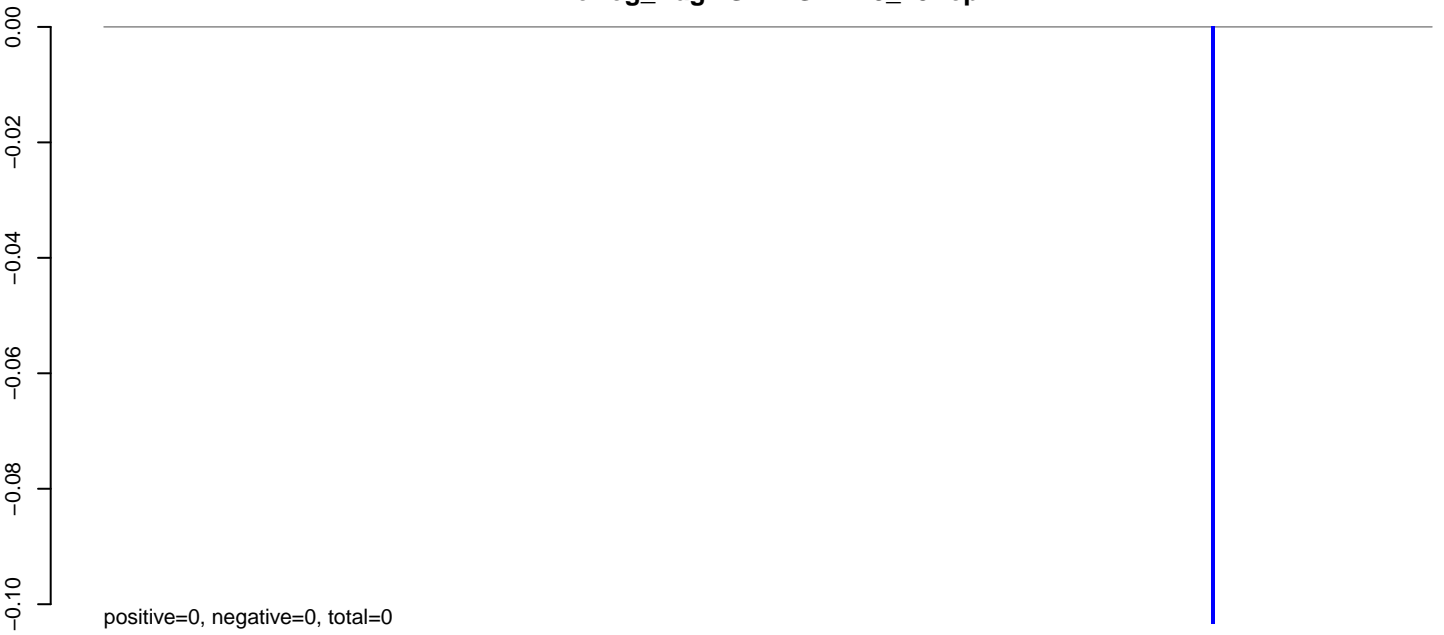
AeAeg_Aag2.SINV.GFP.rep



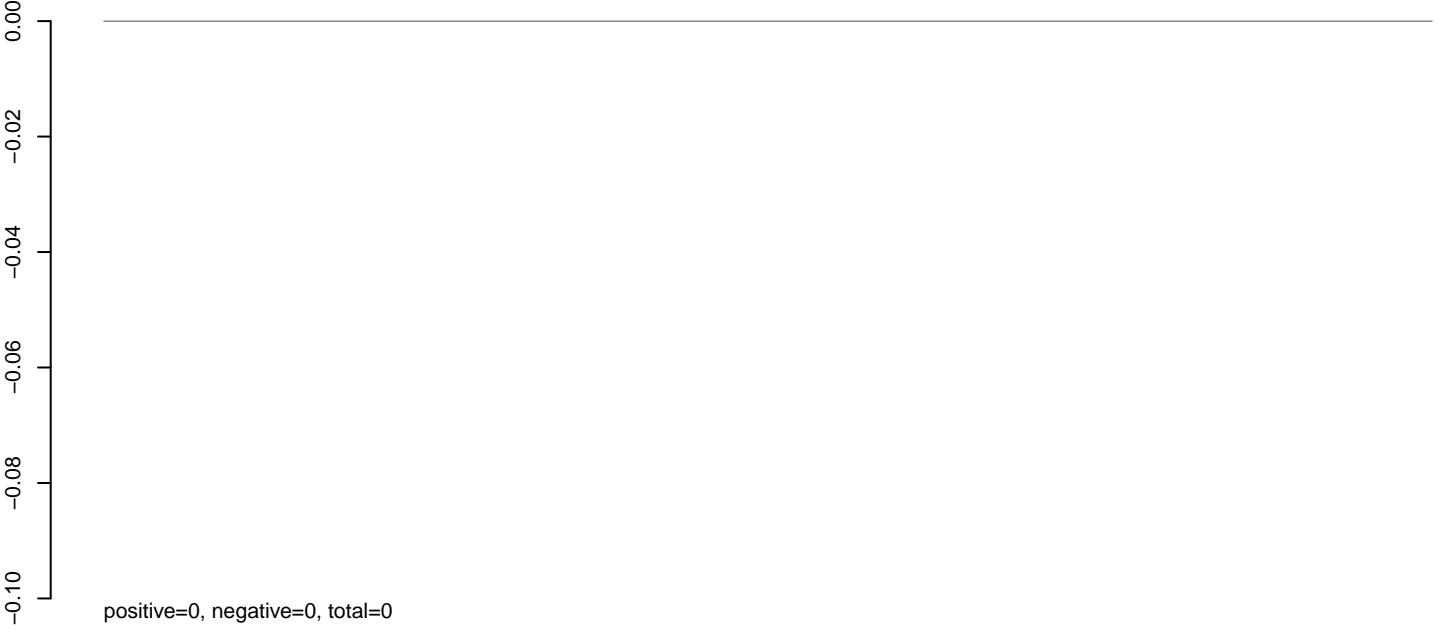
Window size=25, length=11675, virus@NC_003899.1-Eastern_equine_encephalitis_virus:1-11675

0 2000 4000 6000 8000 10000 12000

AeAeg_Aag2.SINV.GFP.18_23.rep



AeAeg_Aag2.SINV.GFP.24_35.rep

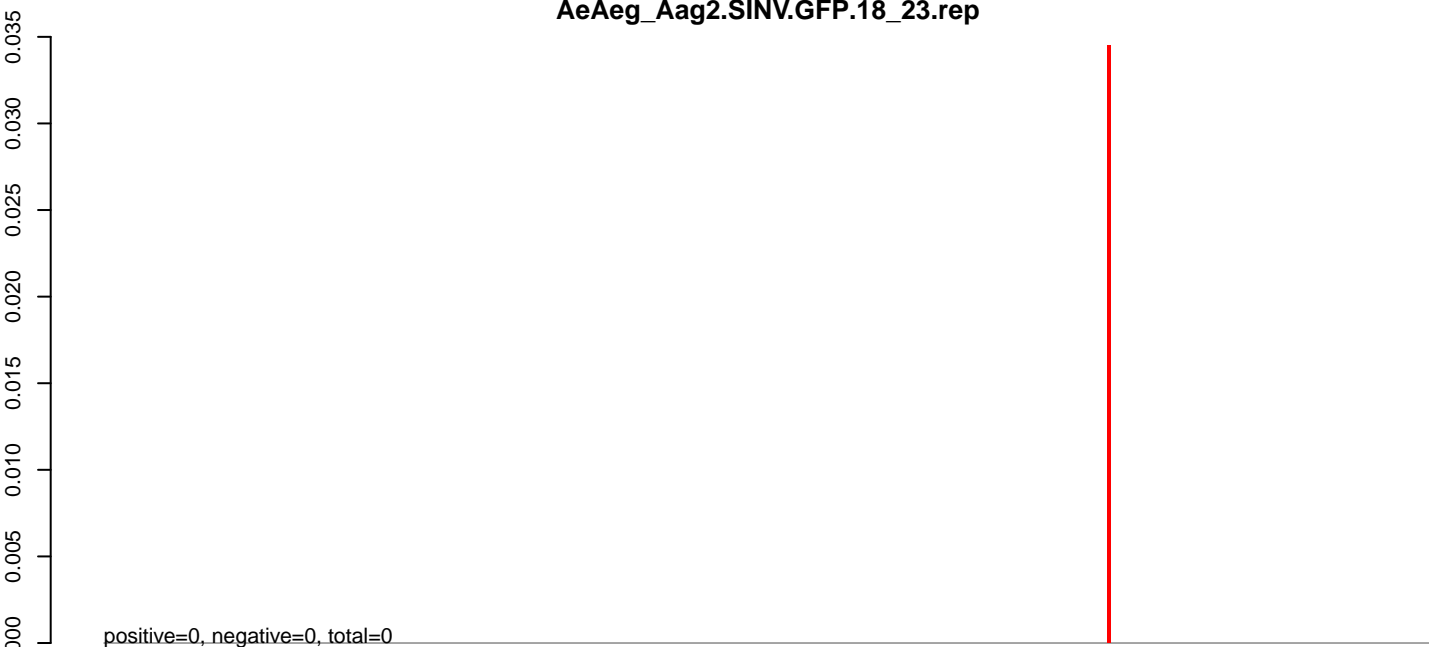


AeAeg_Aag2.SINV.GFP.rep

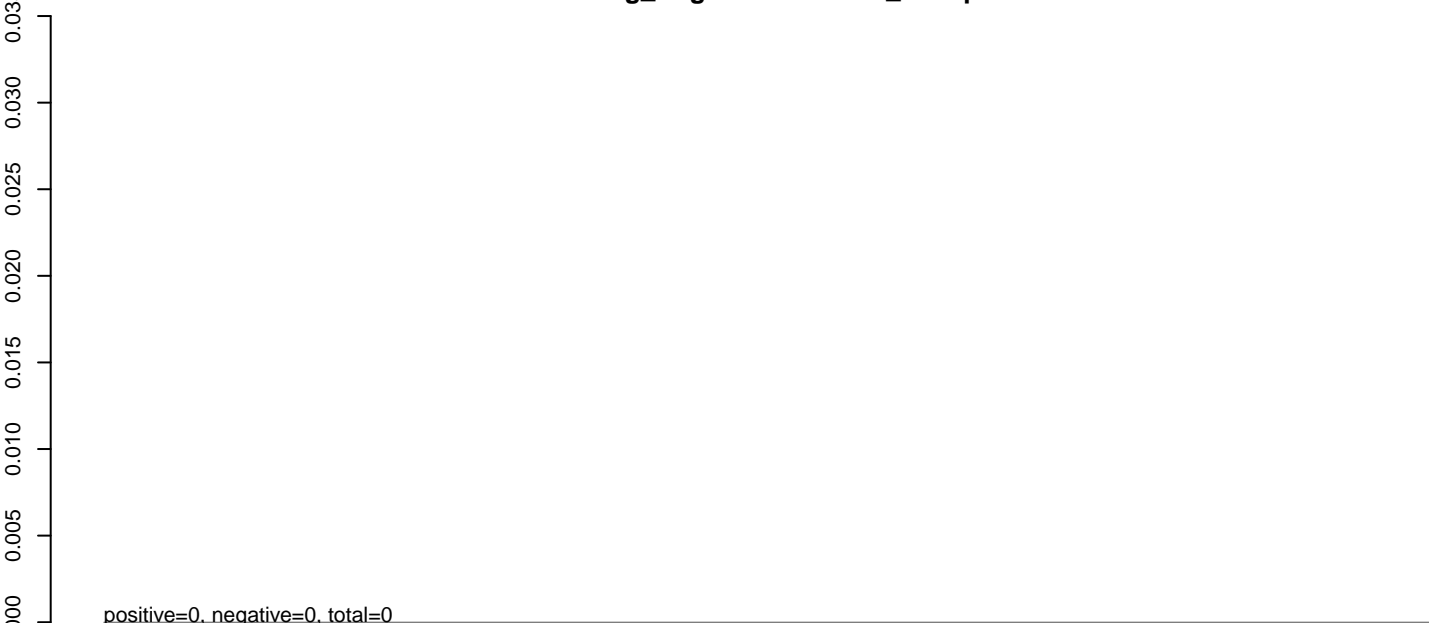


0 2000 4000 6000 8000 10000

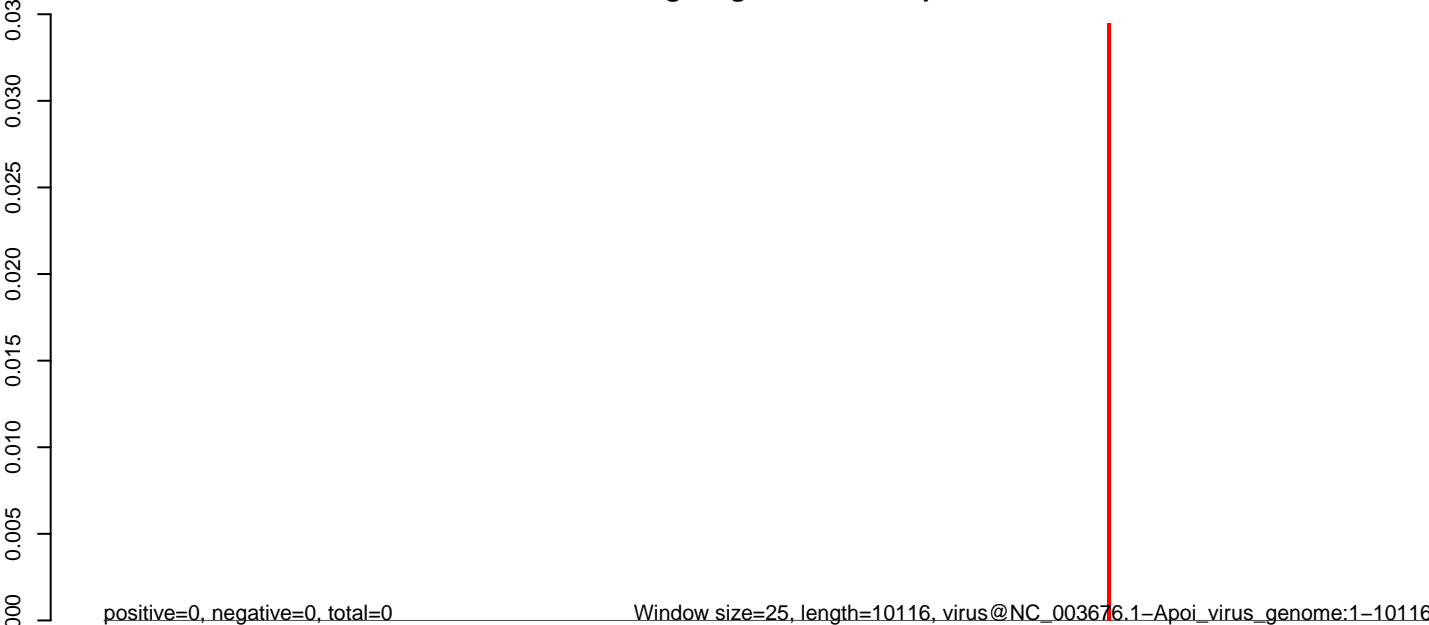
AeAeg_Aag2.SINV.GFP.18_23.rep



AeAeg_Aag2.SINV.GFP.24_35.rep

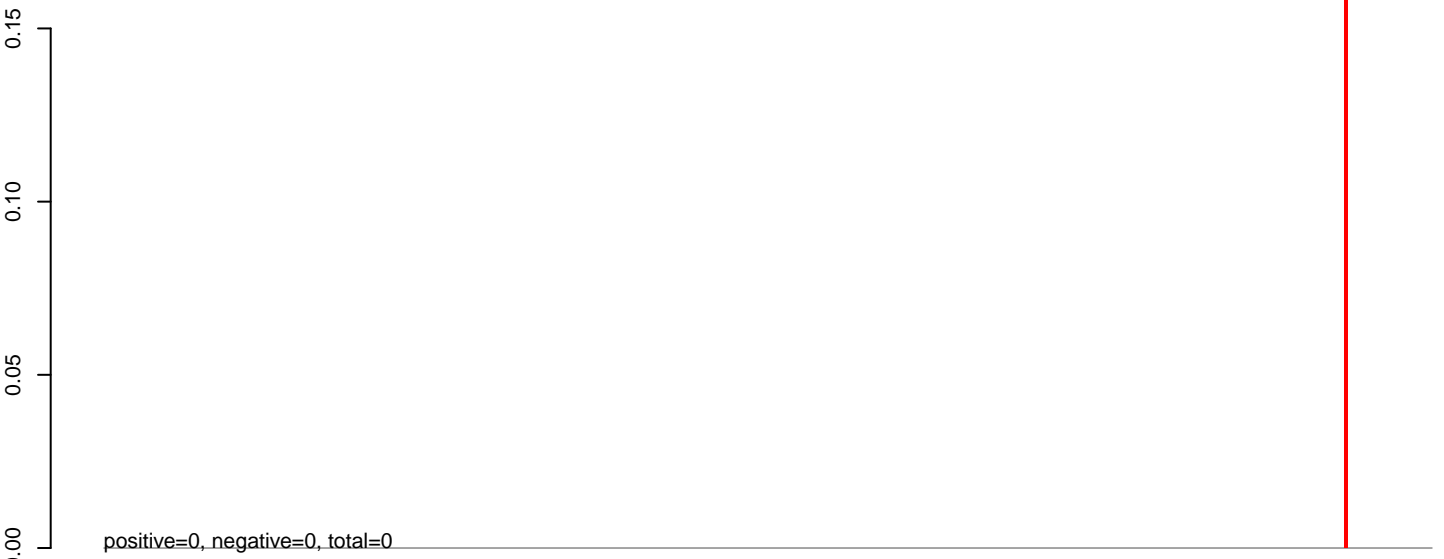


AeAeg_Aag2.SINV.GFP.rep

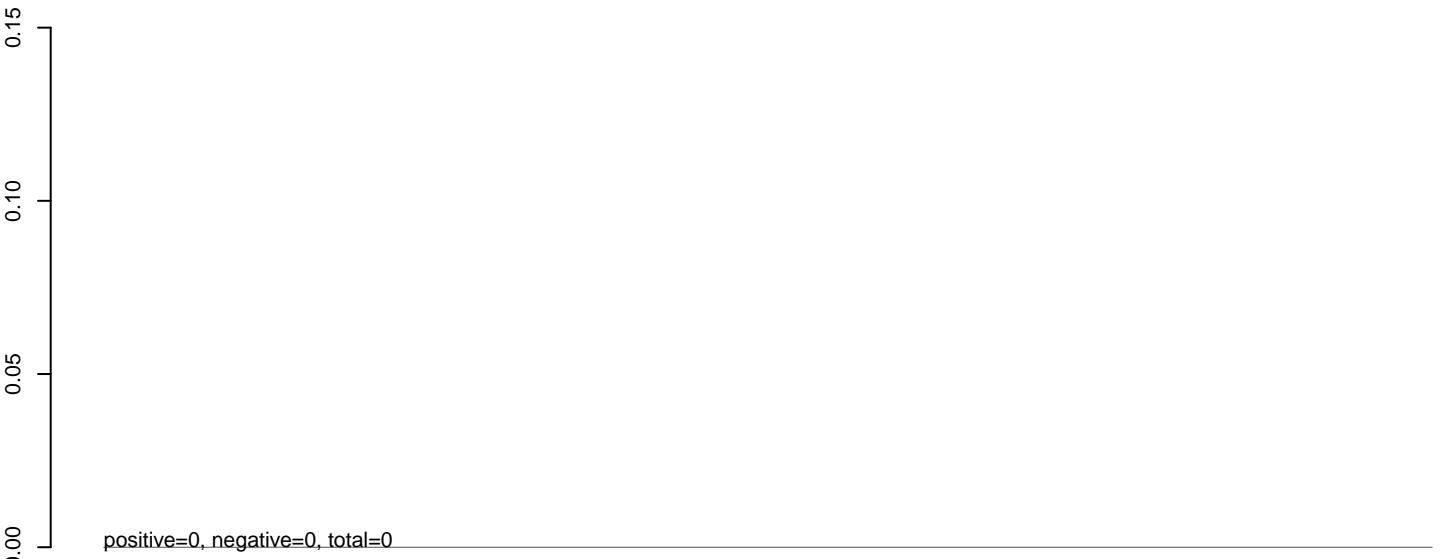


0 2000 4000 6000 8000 10000

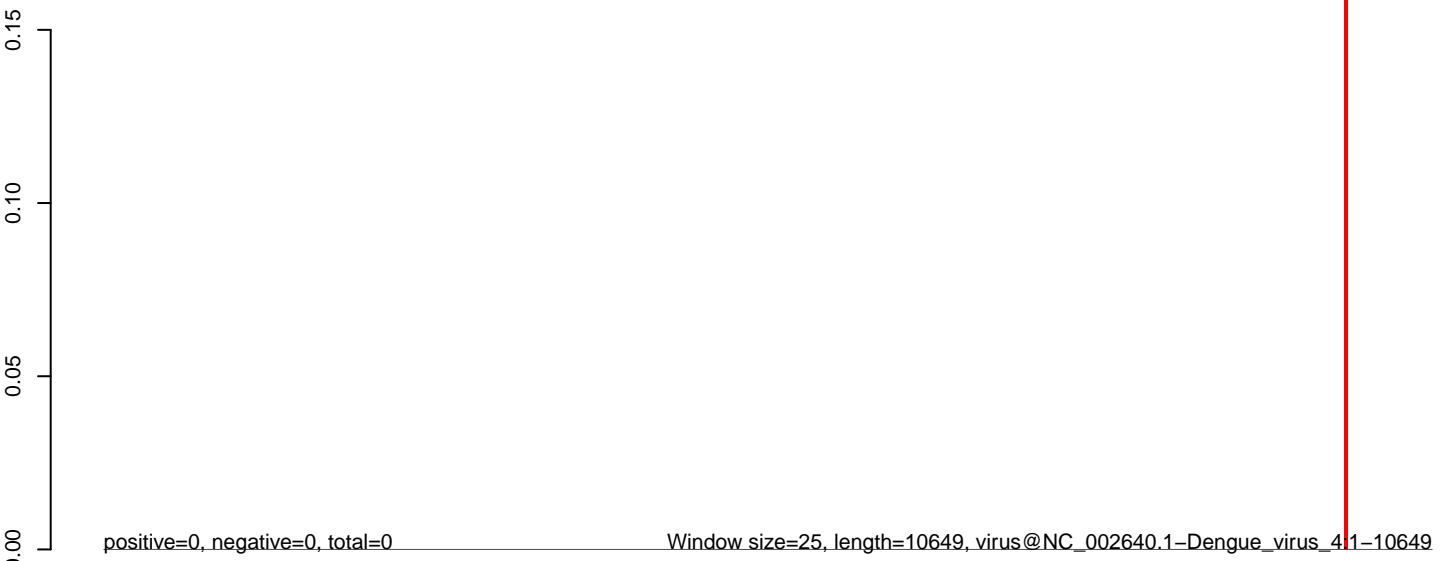
AeAeg_Aag2.SINV.GFP.18_23.rep



AeAeg_Aag2.SINV.GFP.24_35.rep

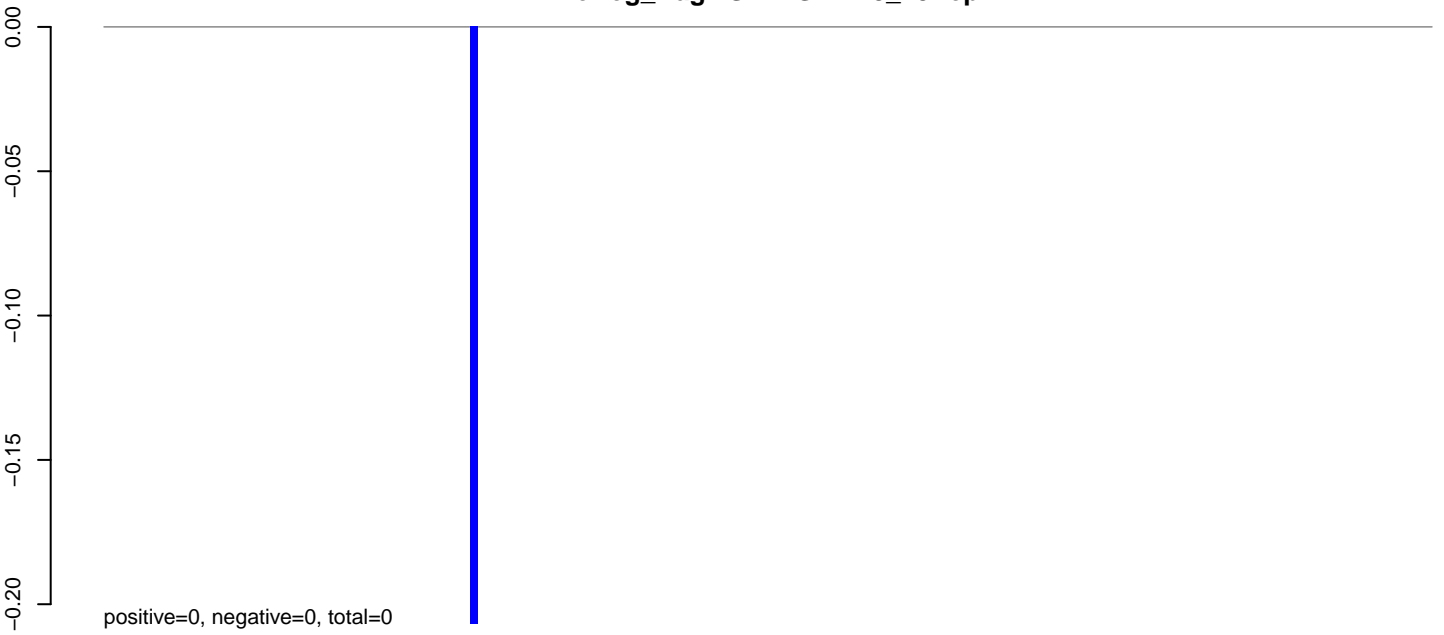


AeAeg_Aag2.SINV.GFP.rep

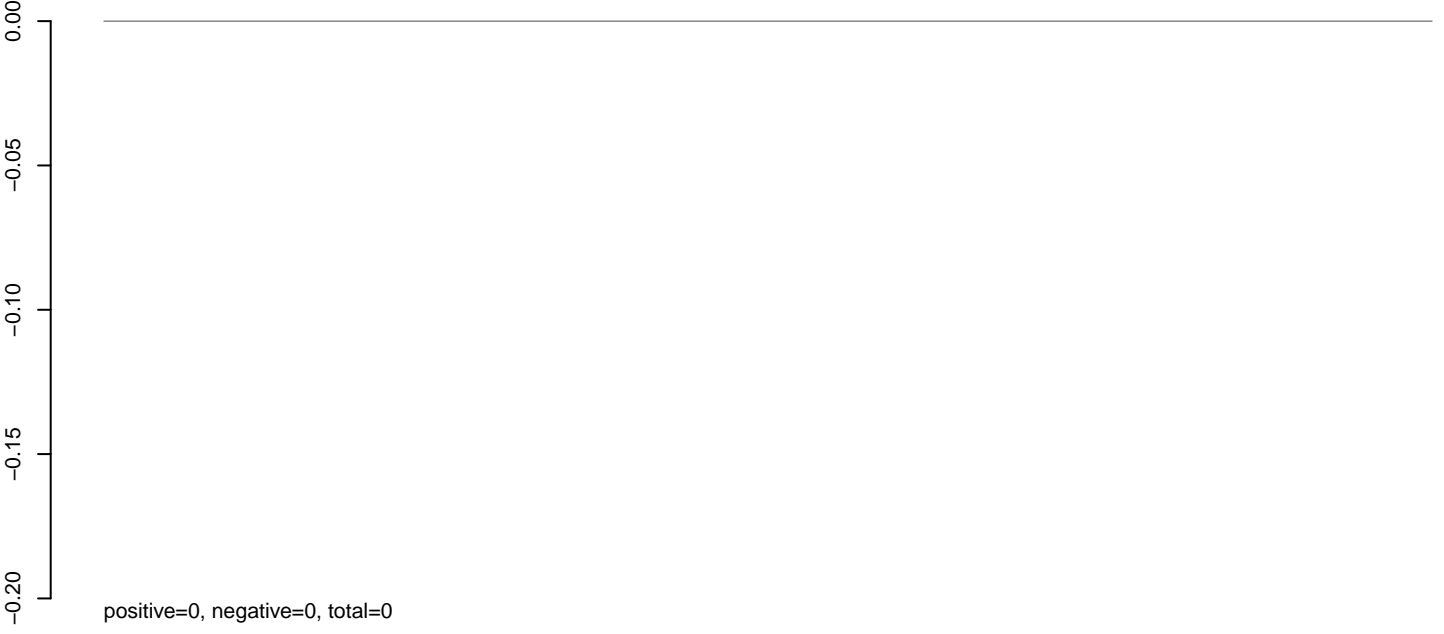


0 2000 4000 6000 8000 10000

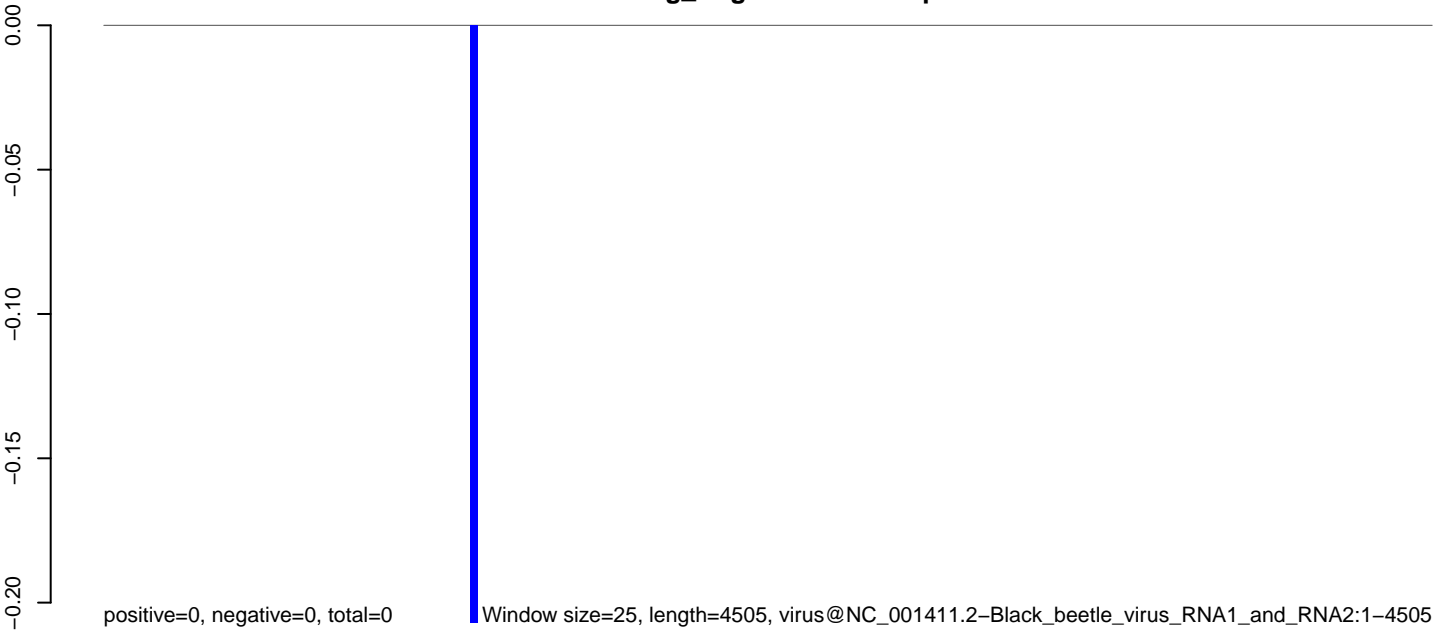
AeAeg_Aag2.SINV.GFP.18_23.rep



AeAeg_Aag2.SINV.GFP.24_35.rep

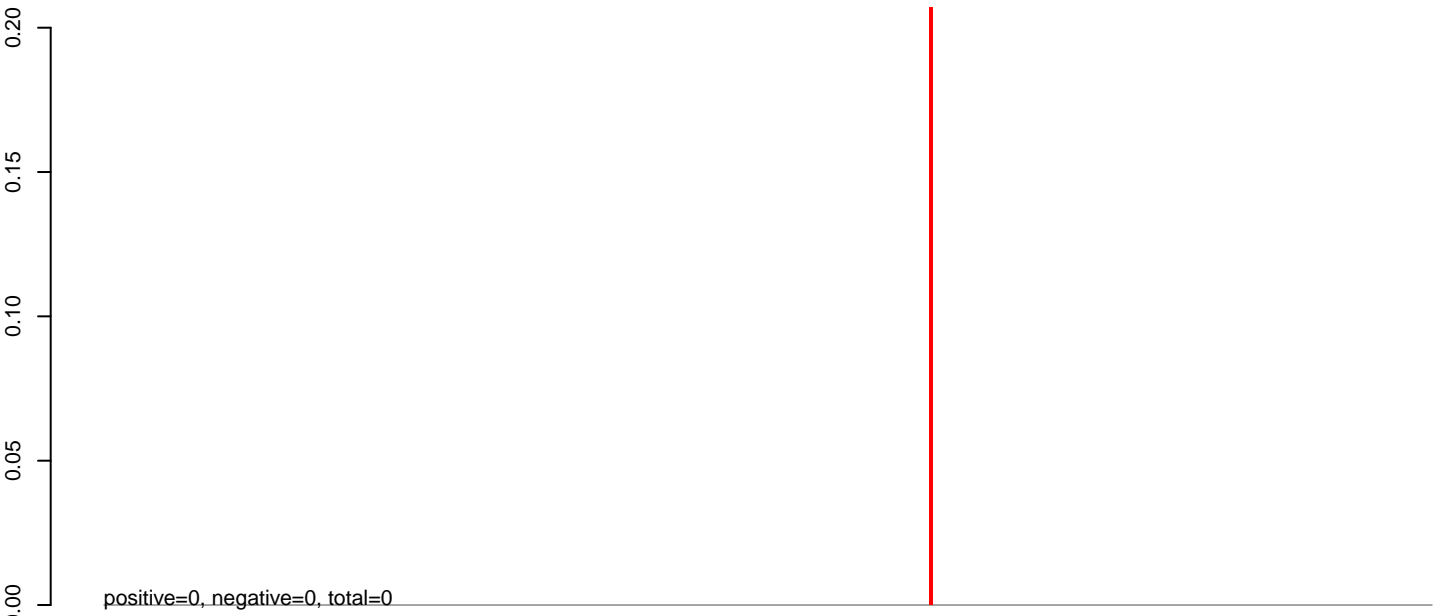


AeAeg_Aag2.SINV.GFP.rep

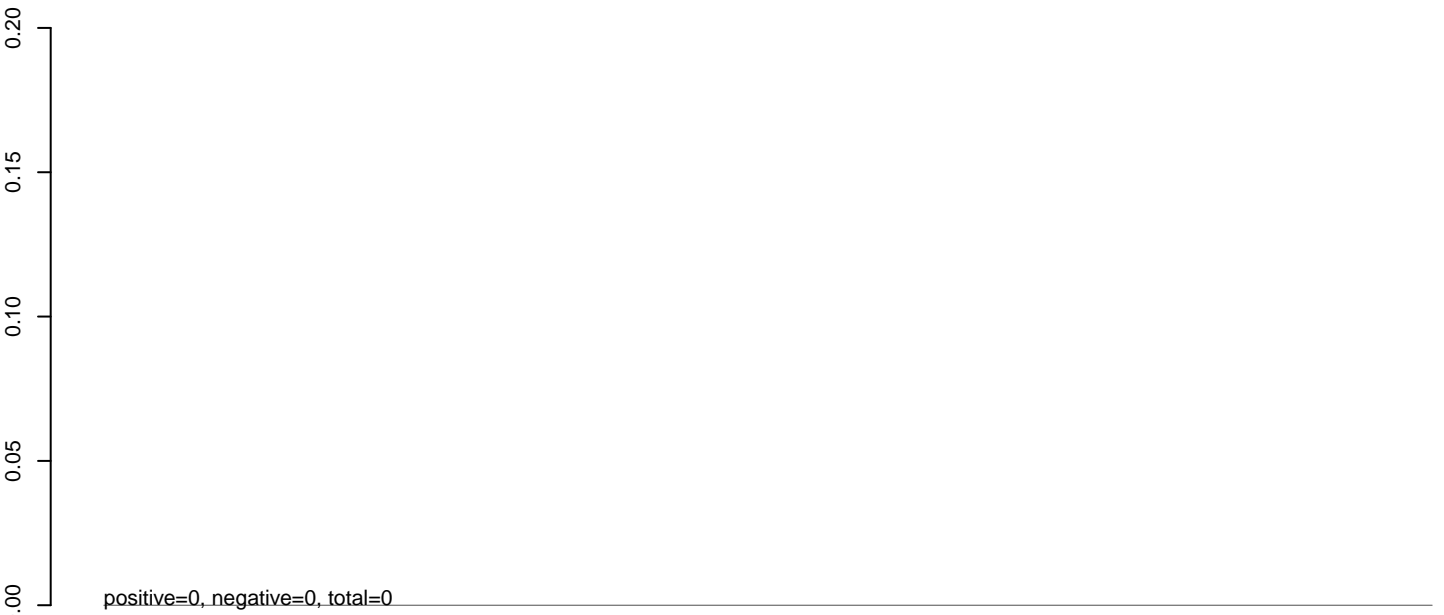


0 1000 2000 3000 4000
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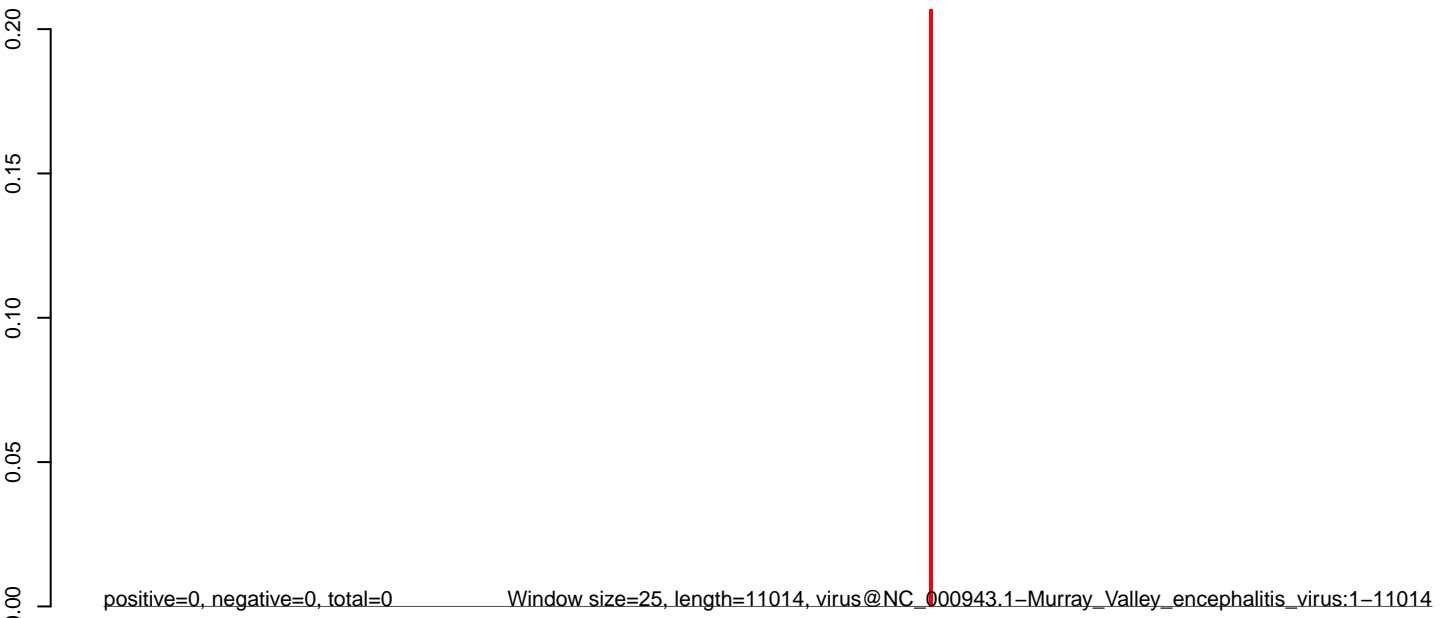
AeAeg_Aag2.SINV.GFP.18_23.rep



AeAeg_Aag2.SINV.GFP.24_35.rep

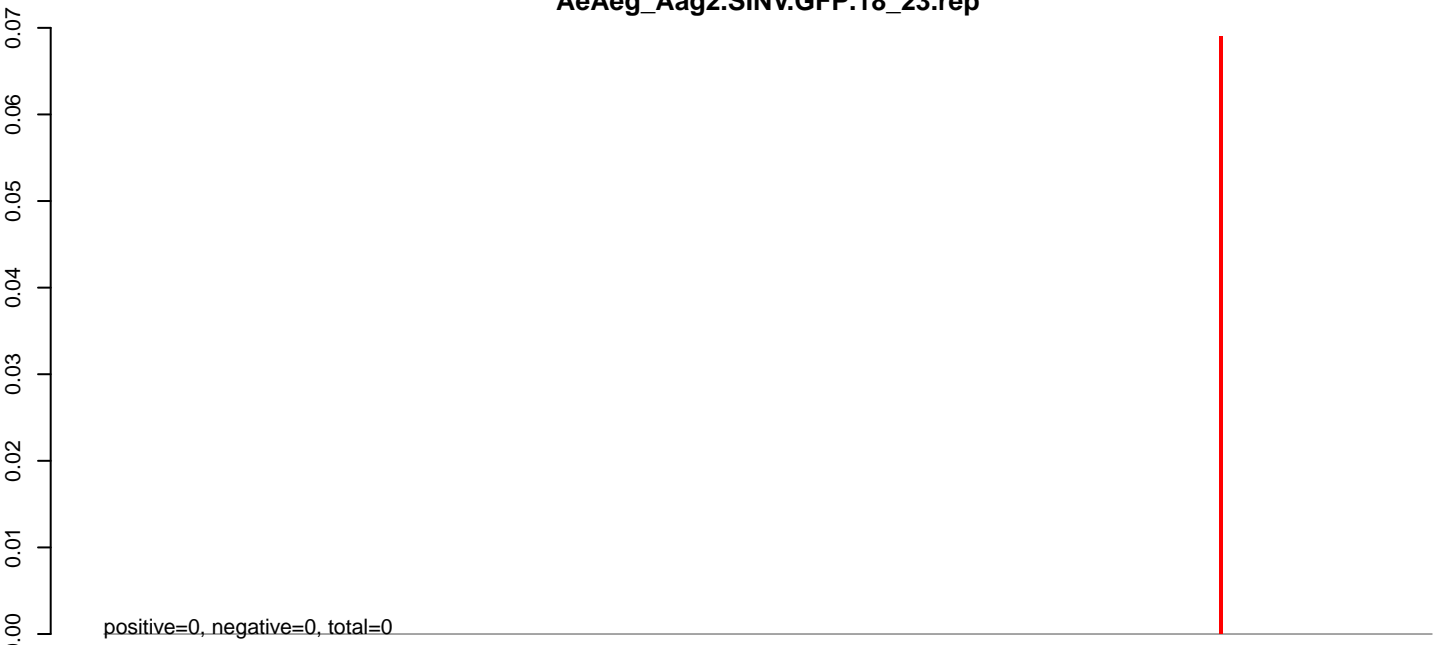


AeAeg_Aag2.SINV.GFP.rep

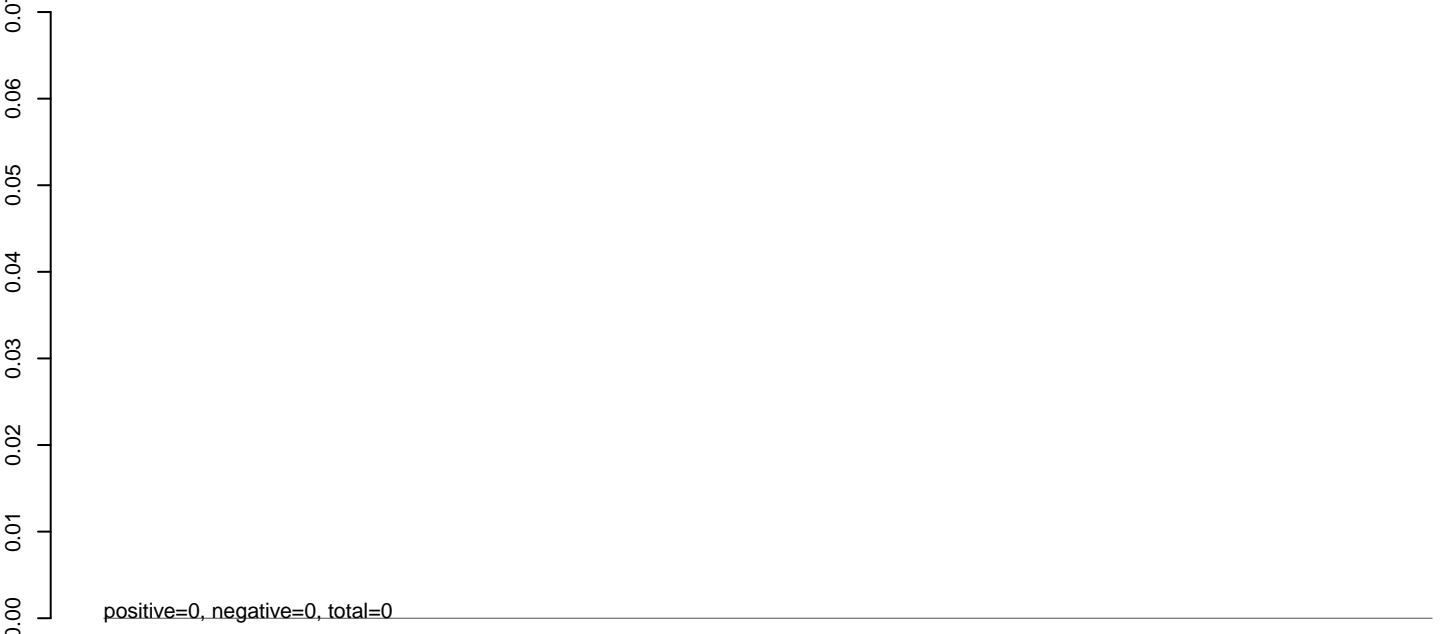


0 2000 4000 6000 8000 10000

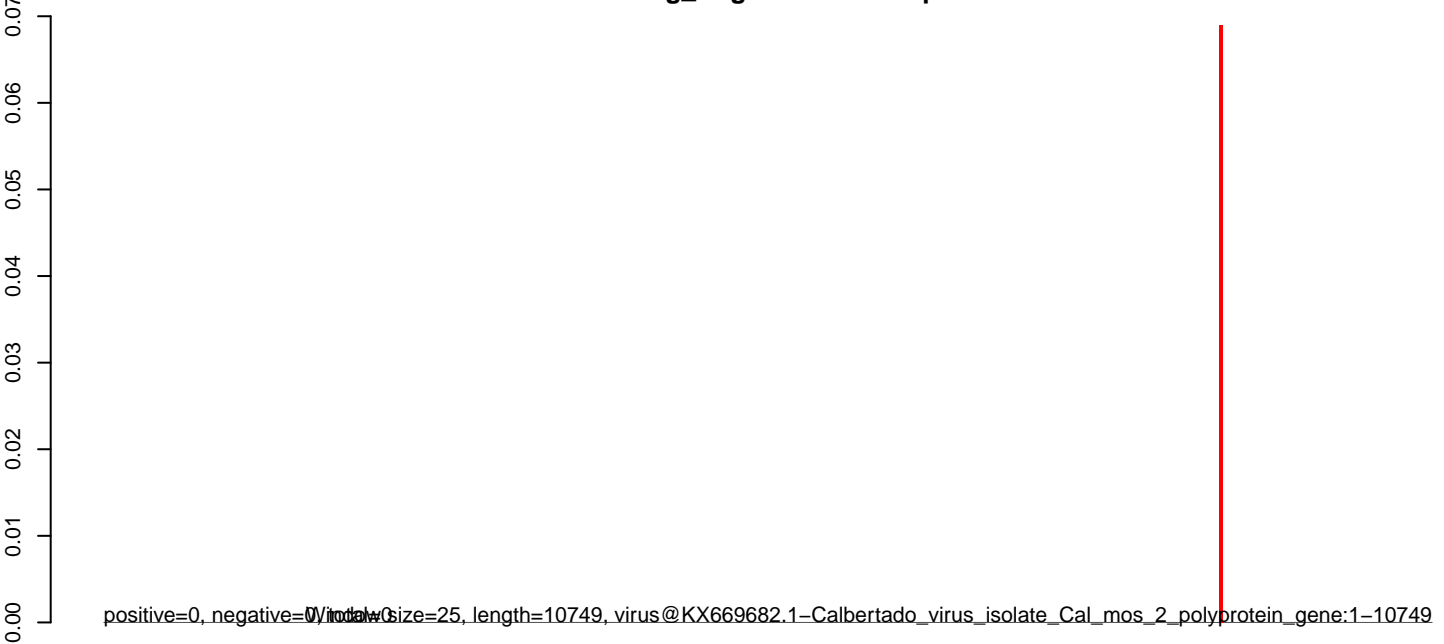
AeAeg_Aag2.SINV.GFP.18_23.rep



AeAeg_Aag2.SINV.GFP.24_35.rep

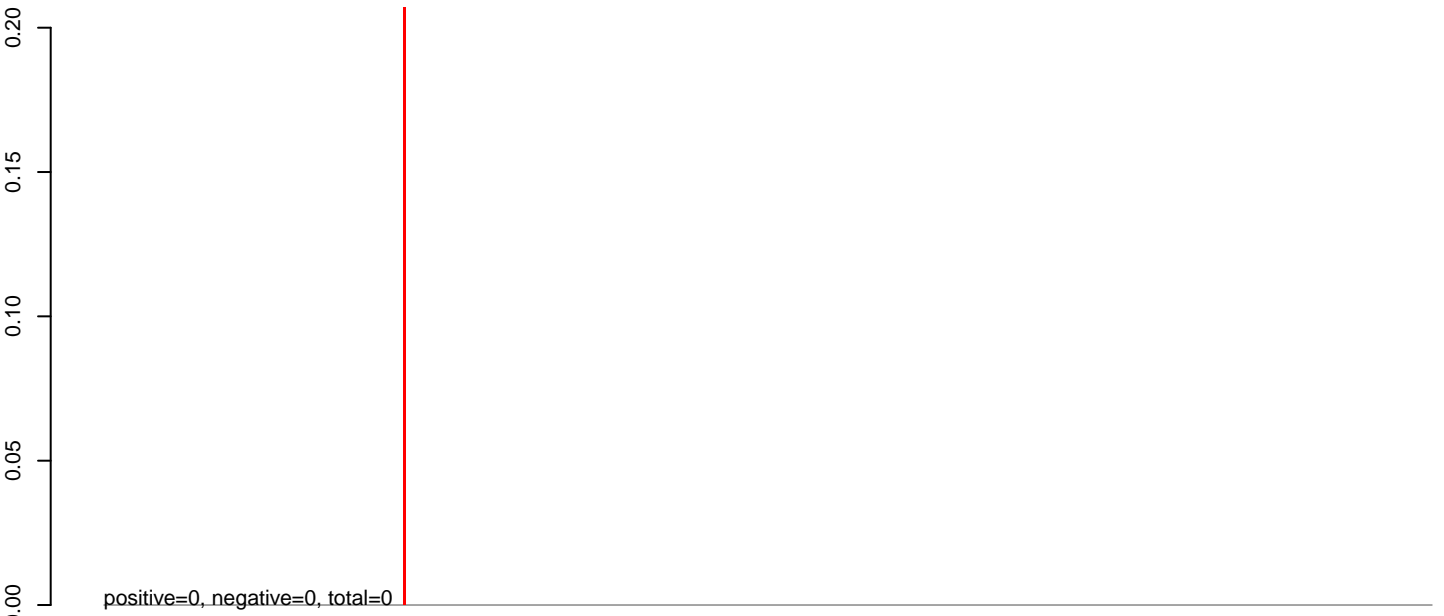


AeAeg_Aag2.SINV.GFP.rep

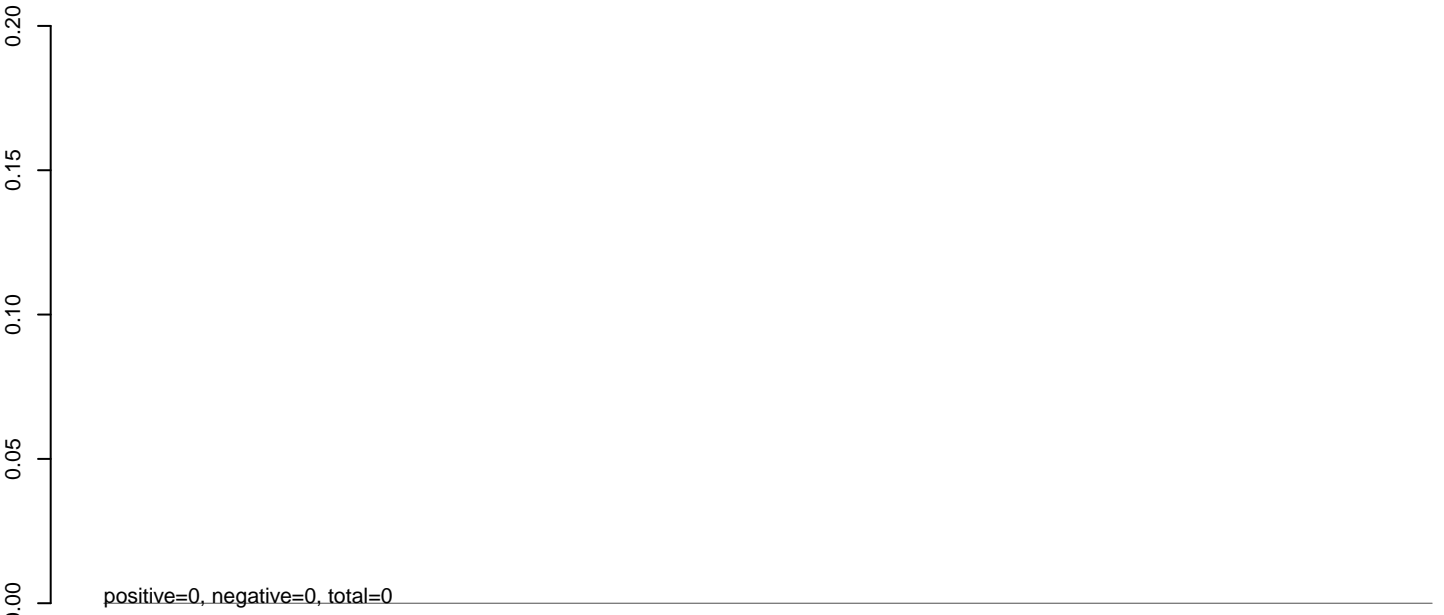


Window size=25, length=10749, virus@KX669682.1-Calbertado_virus_isolate_Cal_mos_2_polyprotein_gene:1-10749

AeAeg_Aag2.SINV.GFP.18_23.rep



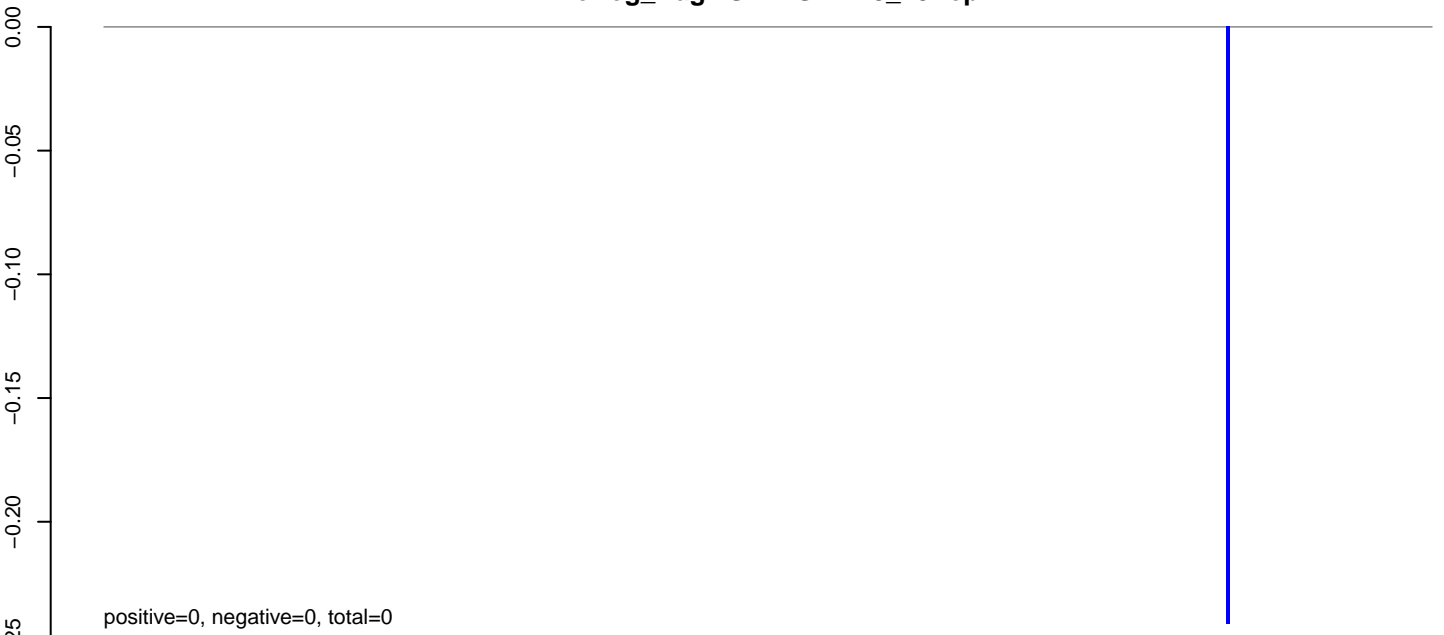
AeAeg_Aag2.SINV.GFP.24_35.rep



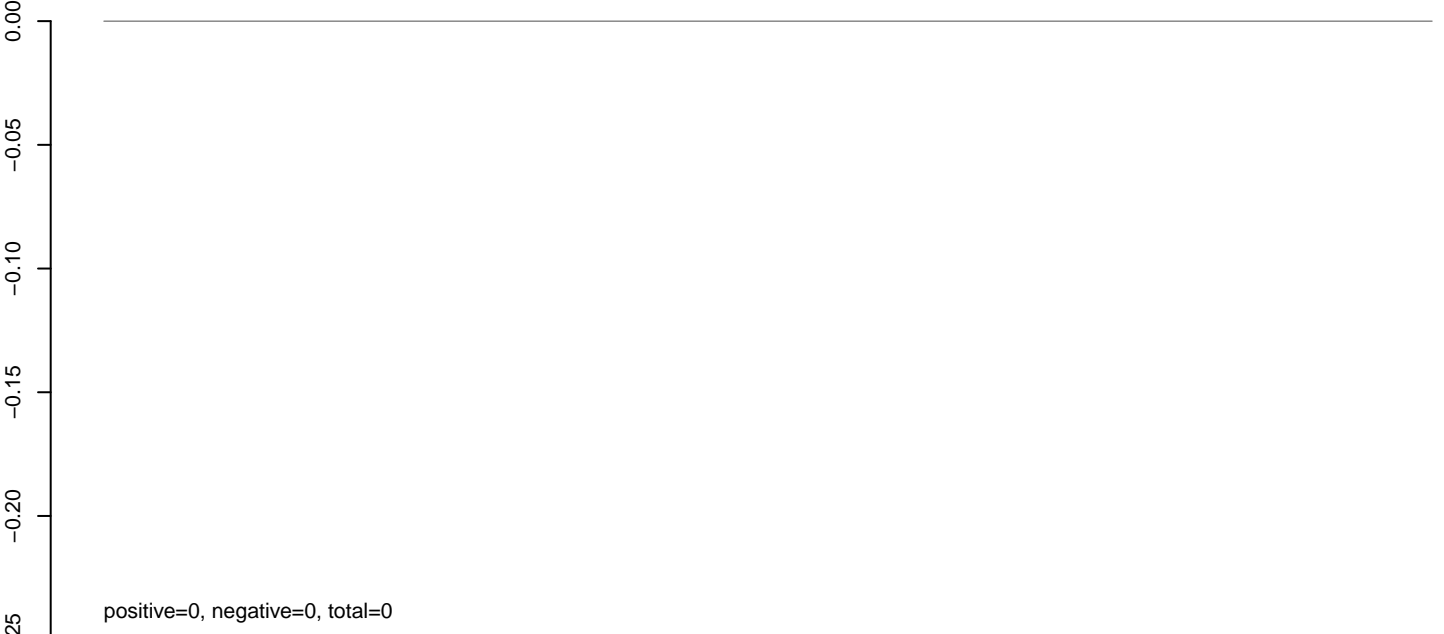
AeAeg_Aag2.SINV.GFP.rep



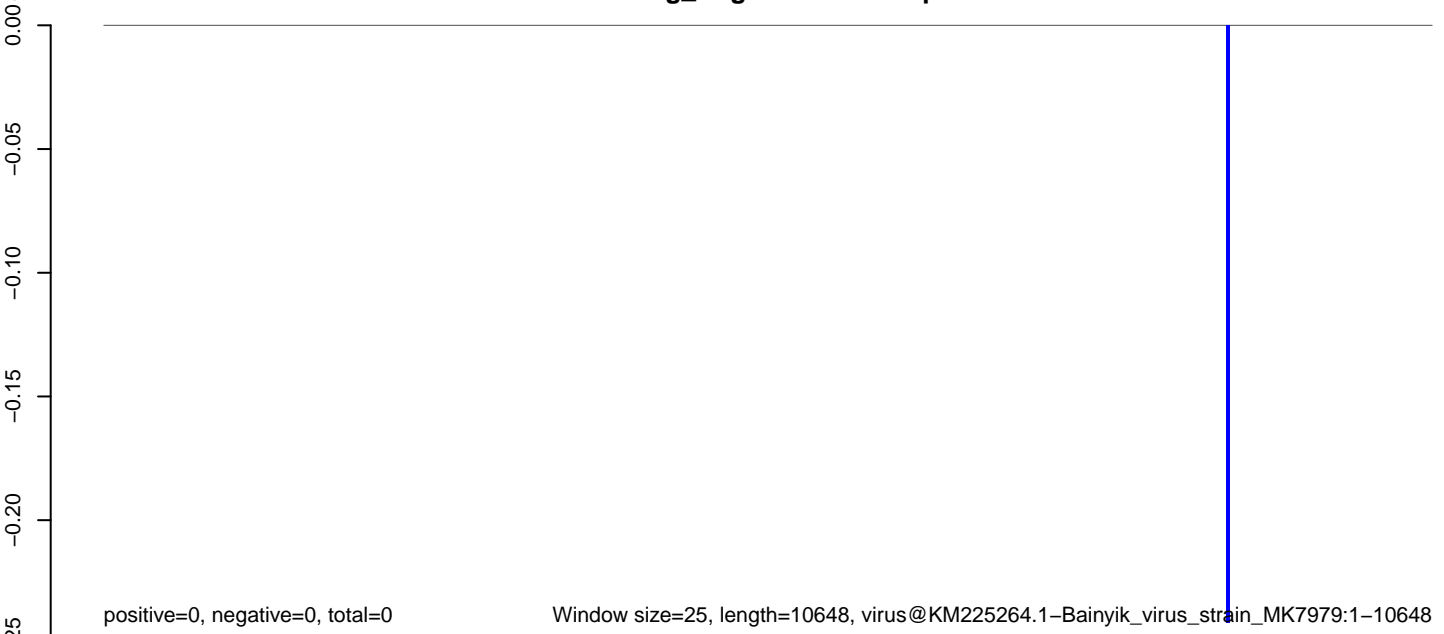
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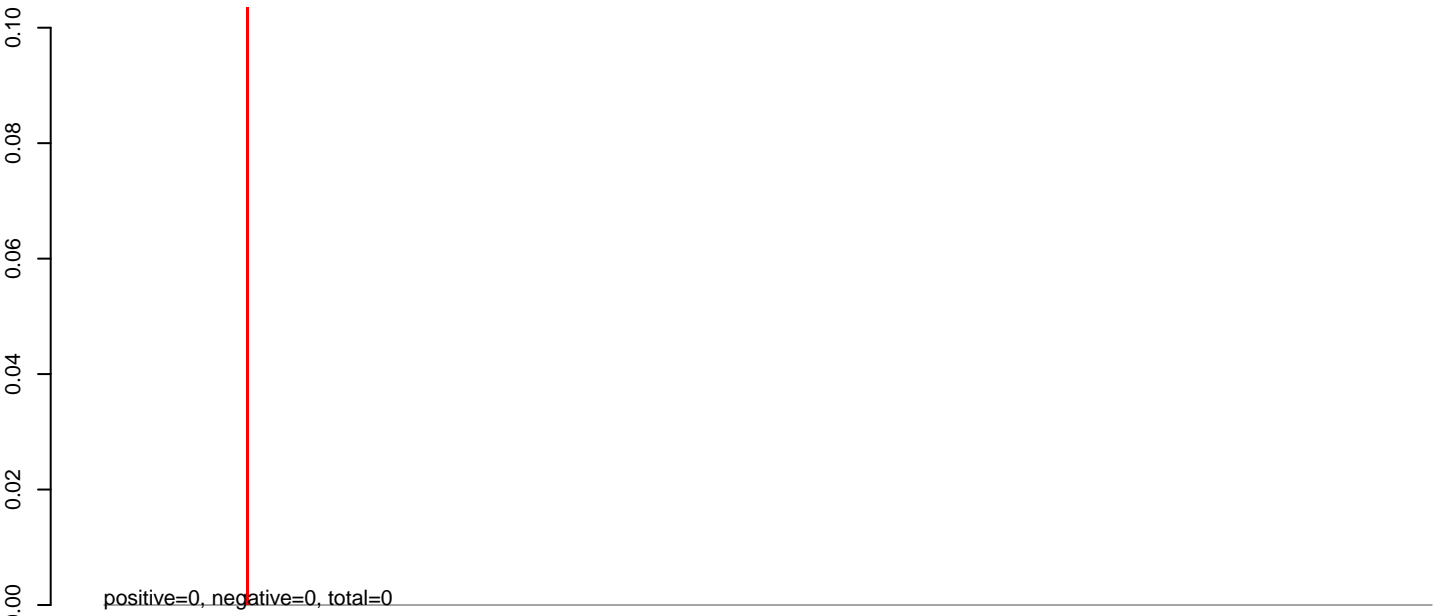
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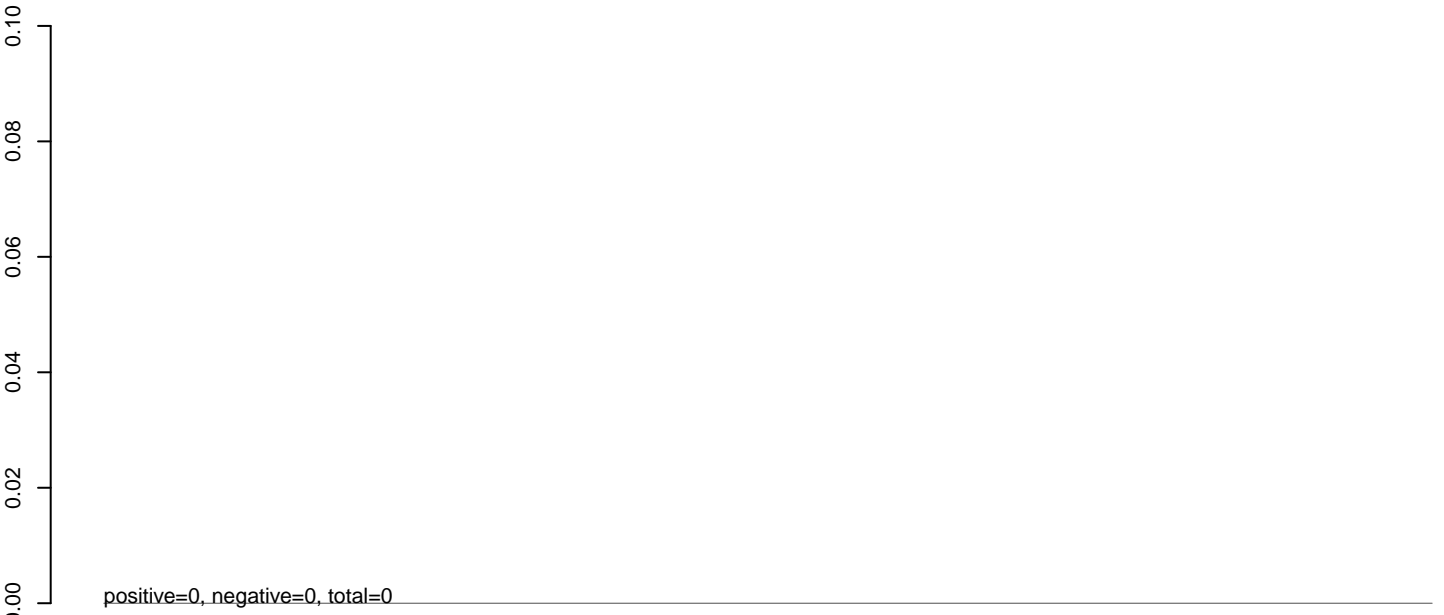
AeAeg_Aag2.SINV.GFP.rep



AeAeg_Aag2.SINV.GFP.18_23.rep



AeAeg_Aag2.SINV.GFP.24_35.rep



AeAeg_Aag2.SINV.GFP.rep

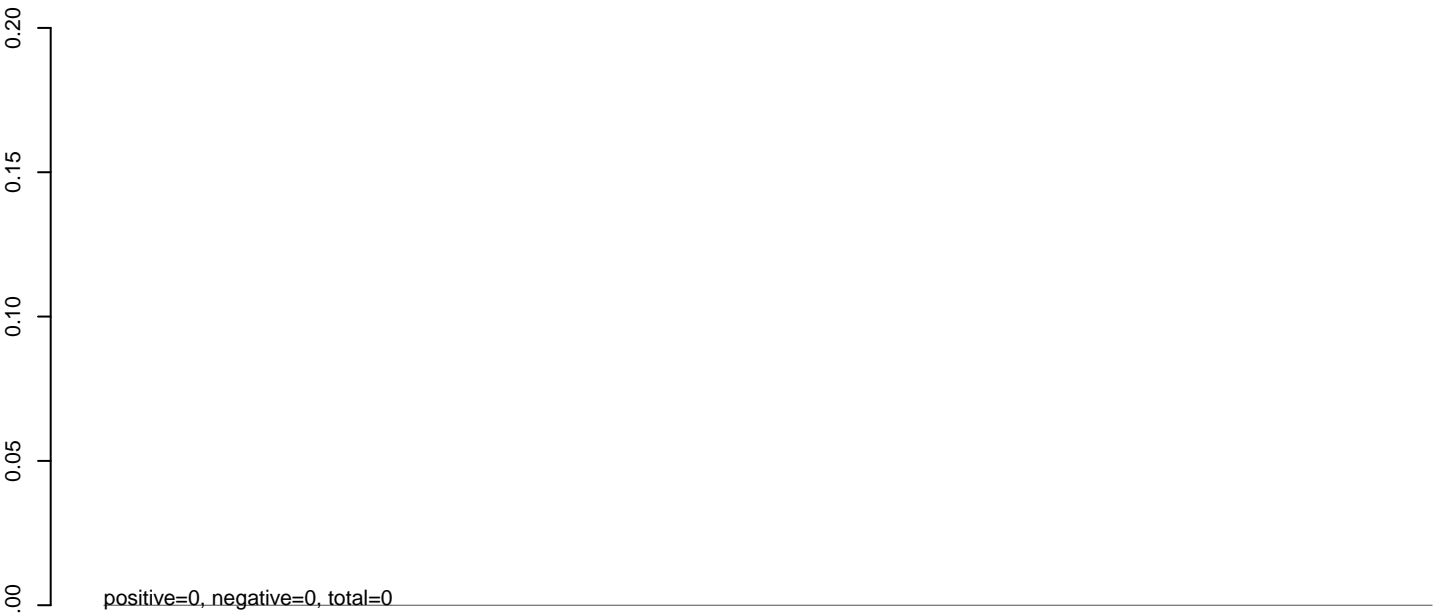


0 2000 4000 6000 8000 10000 12000

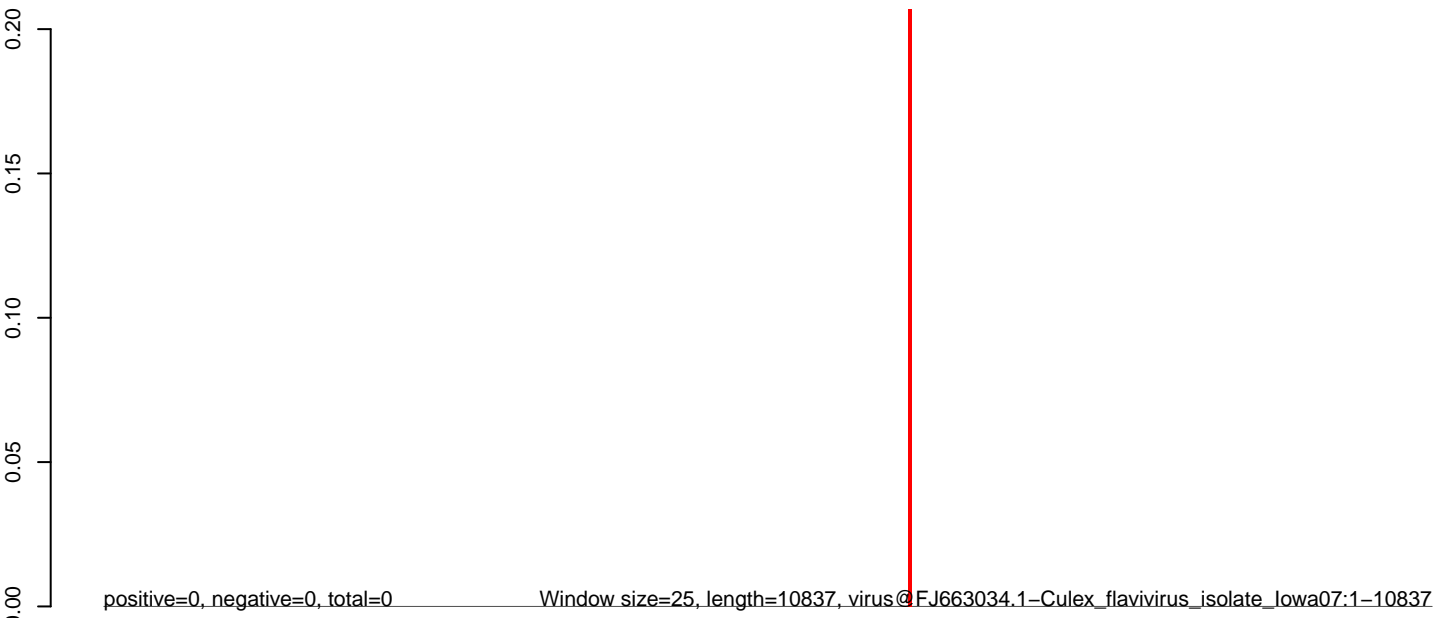
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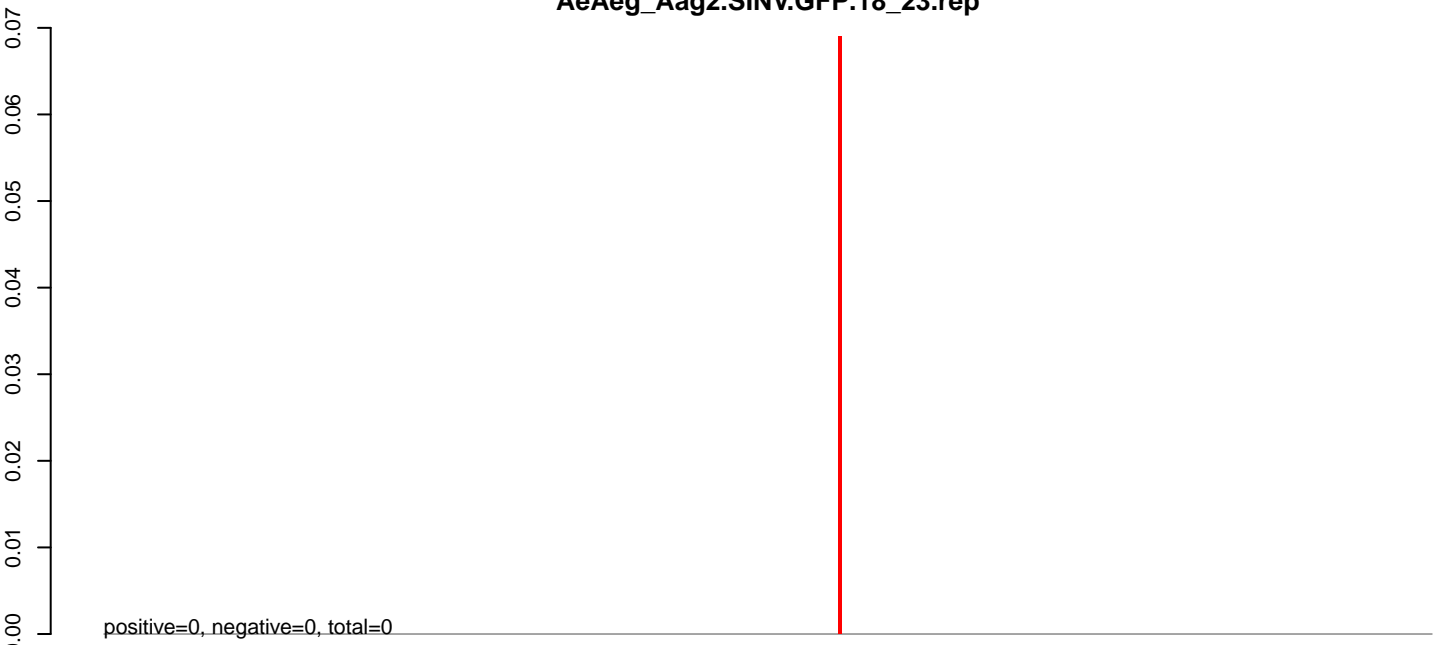
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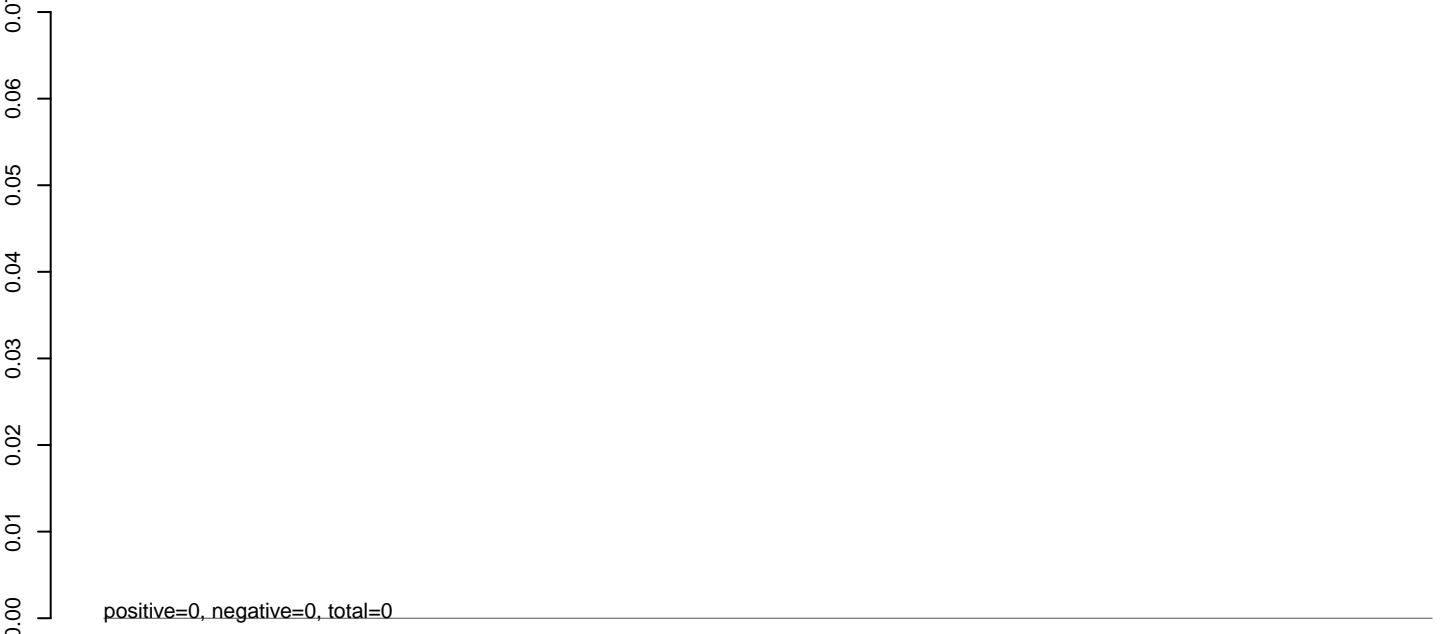
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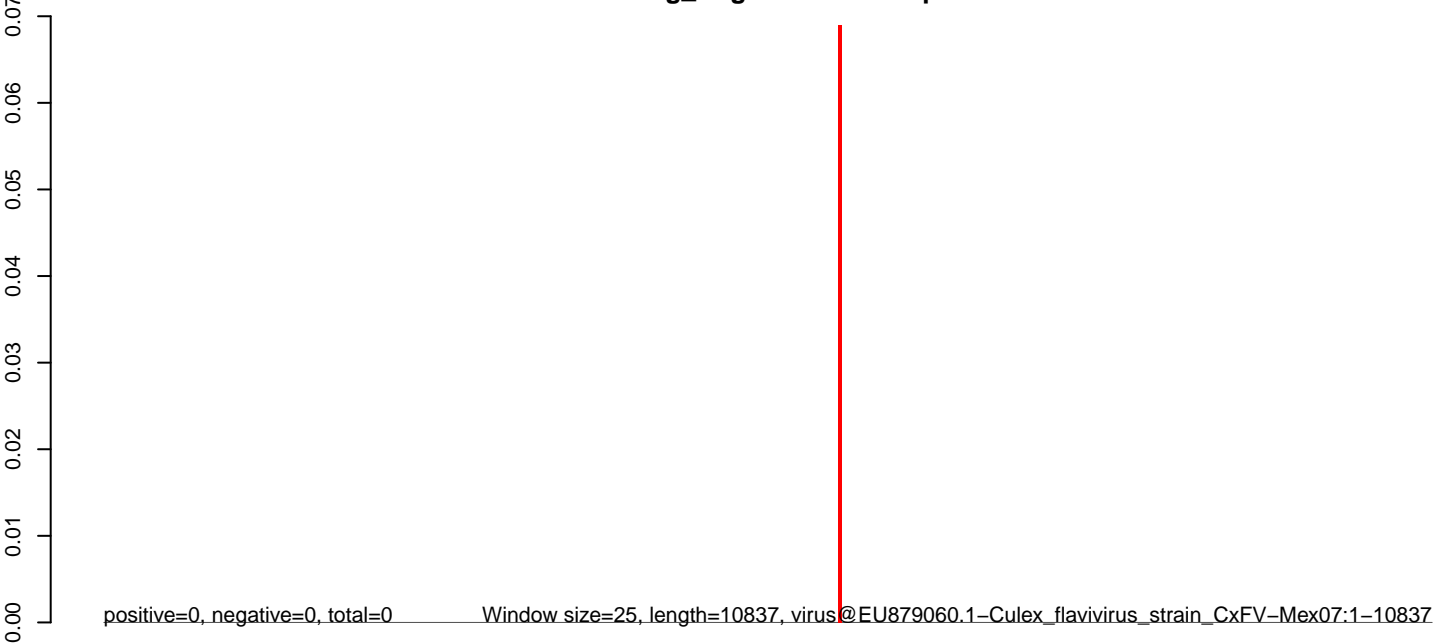
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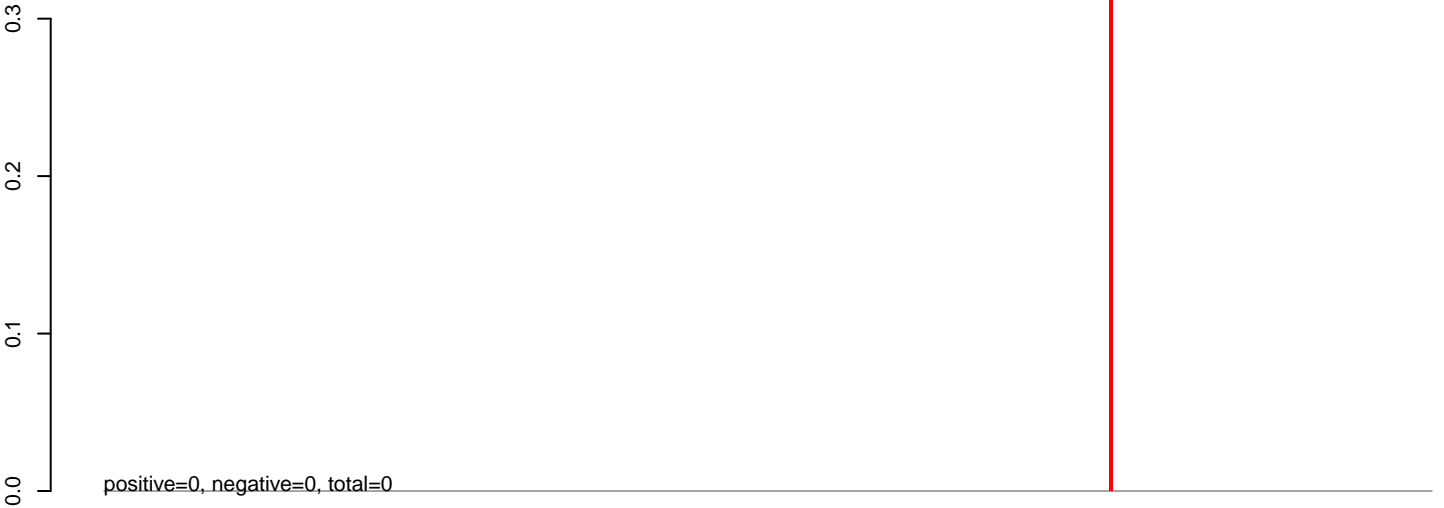
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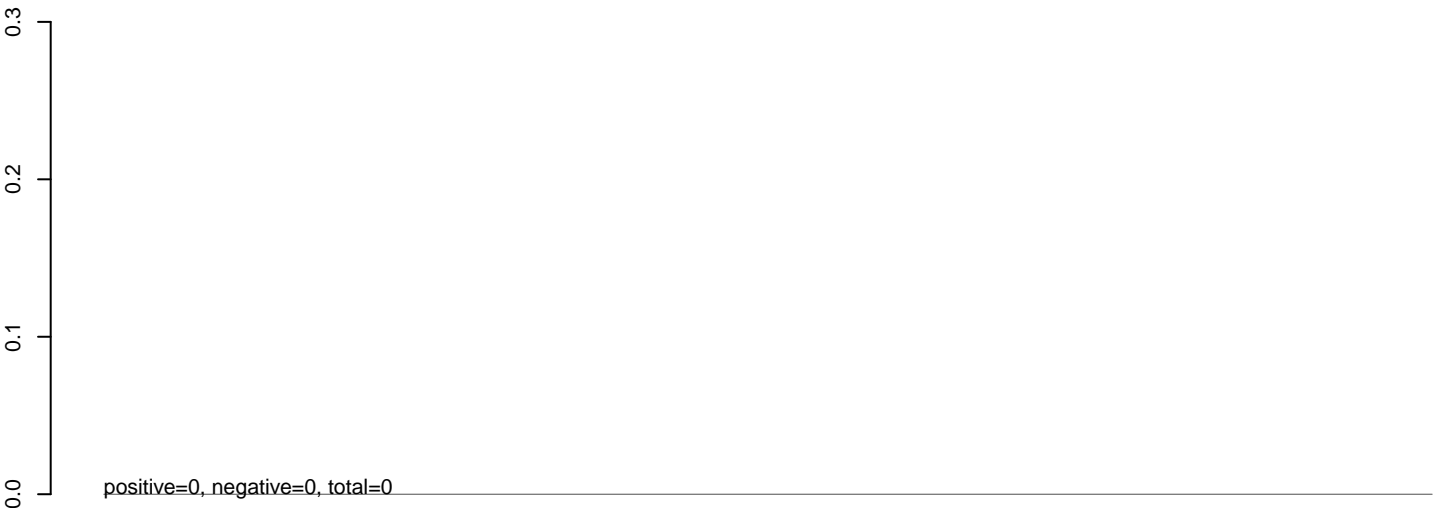
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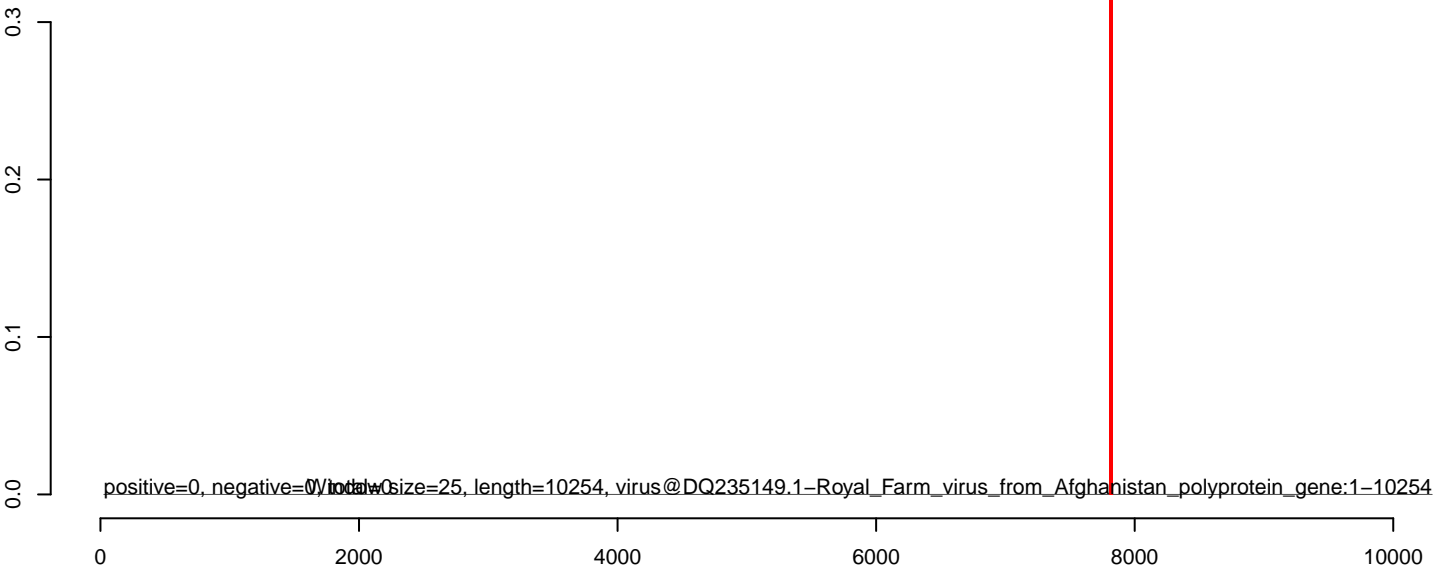
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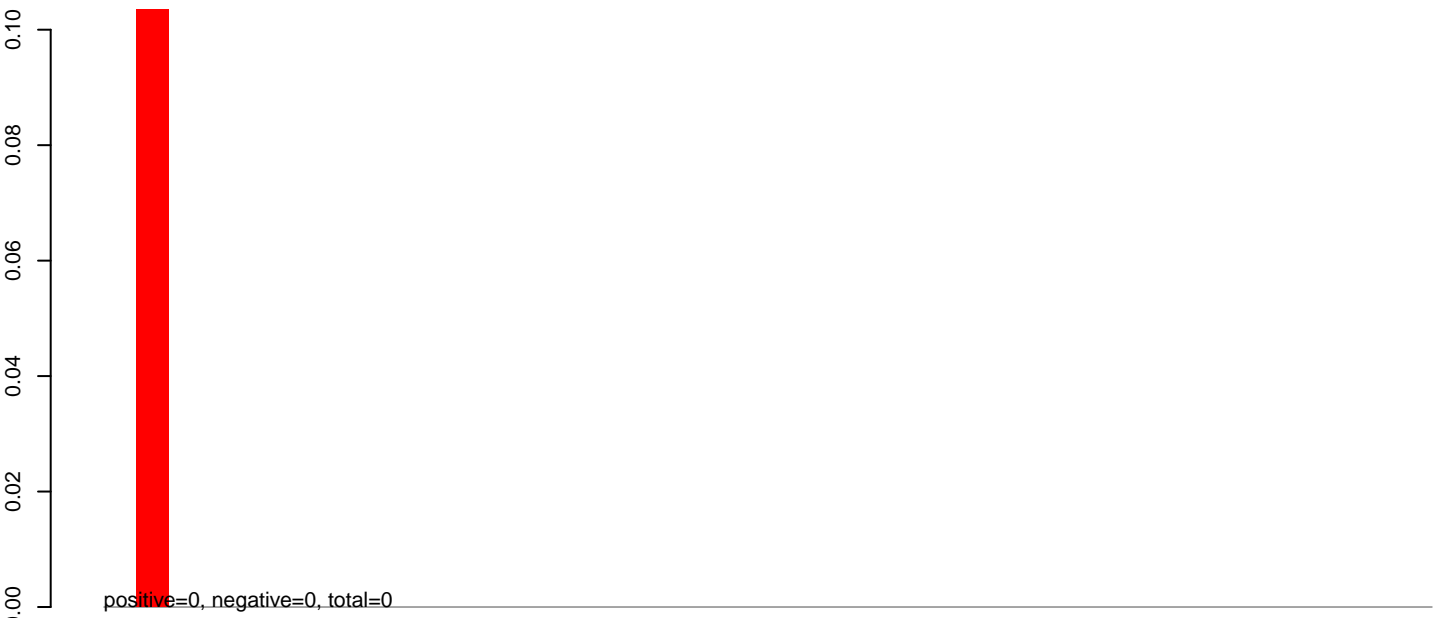
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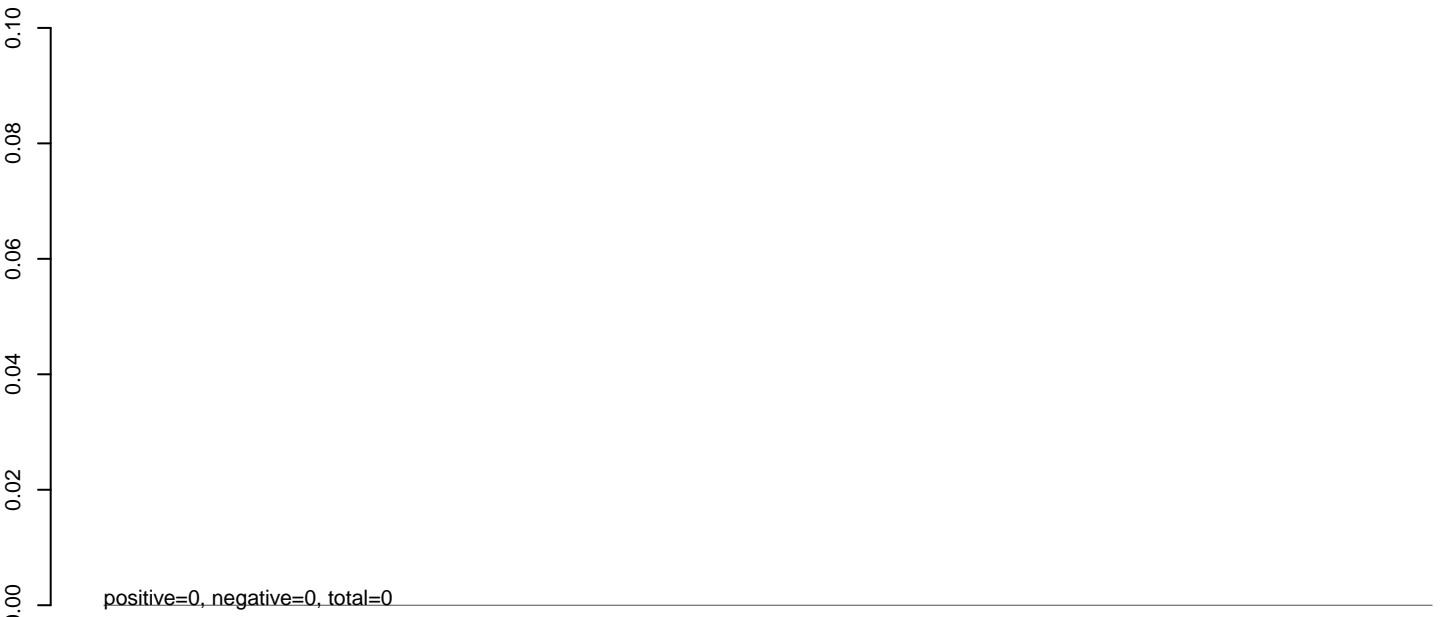
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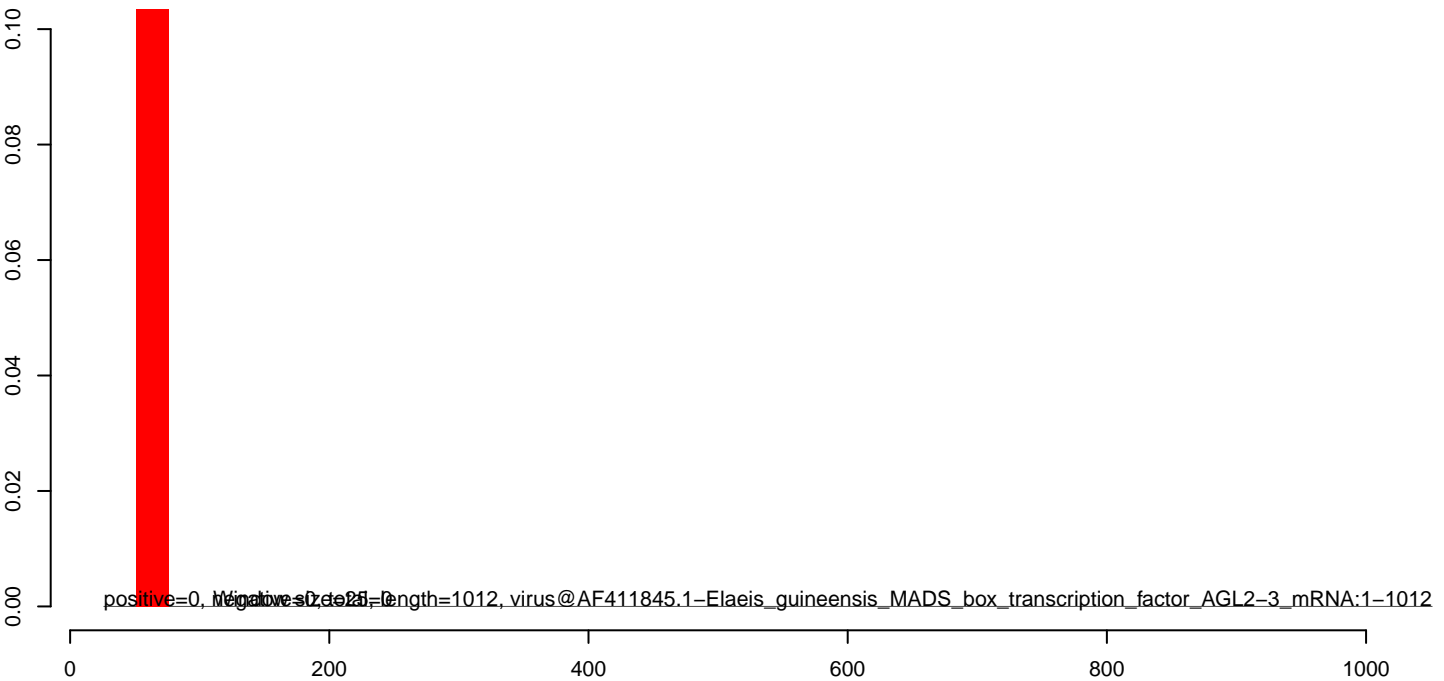
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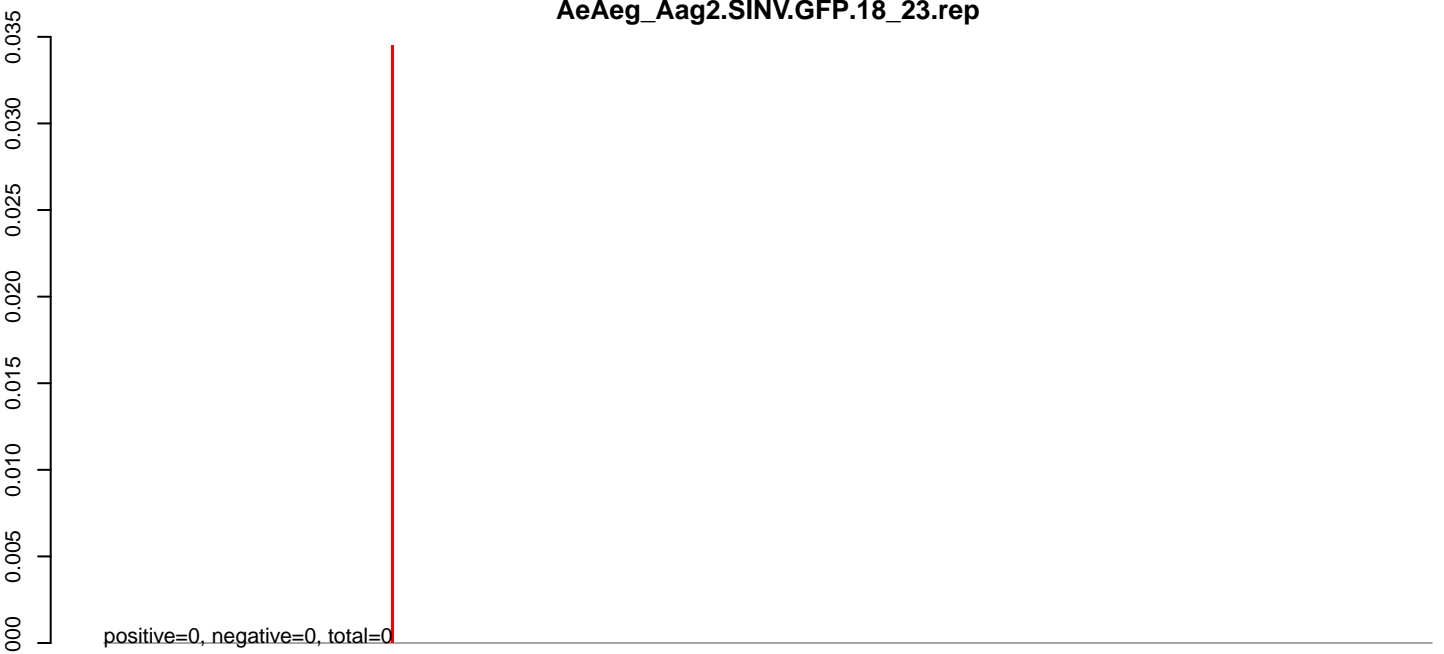
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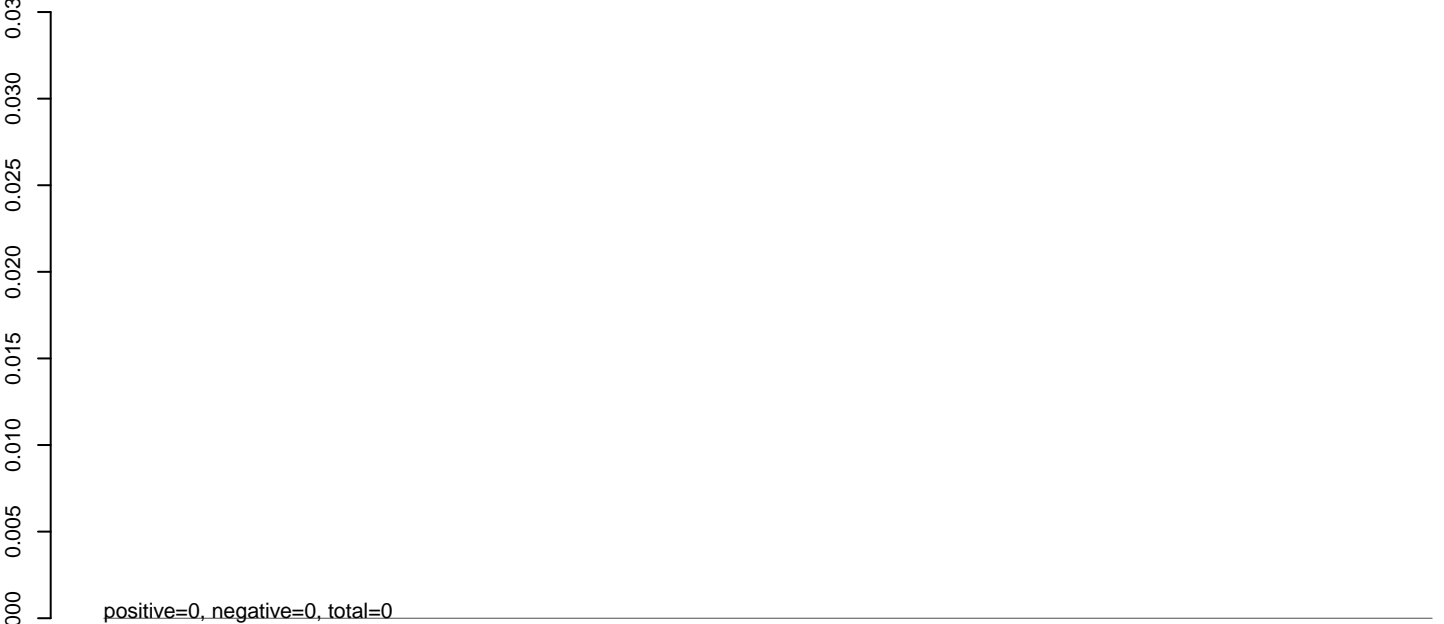
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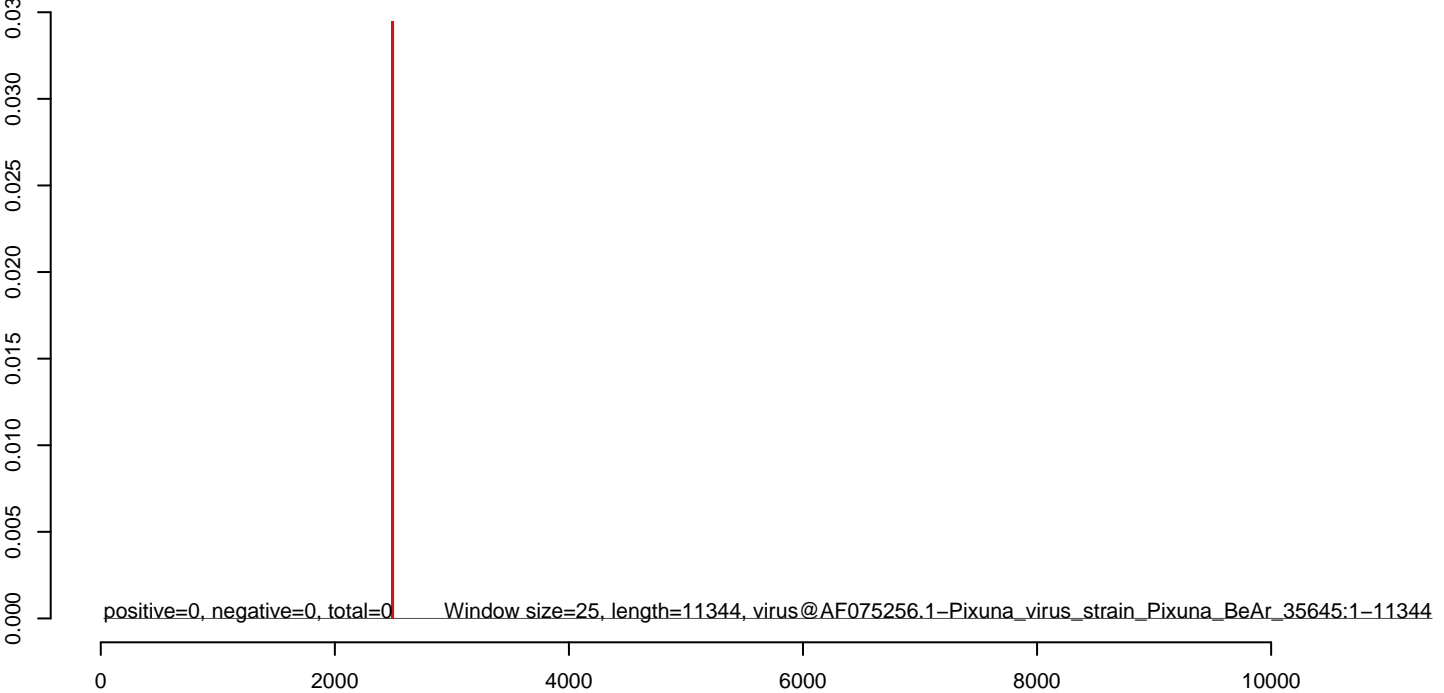
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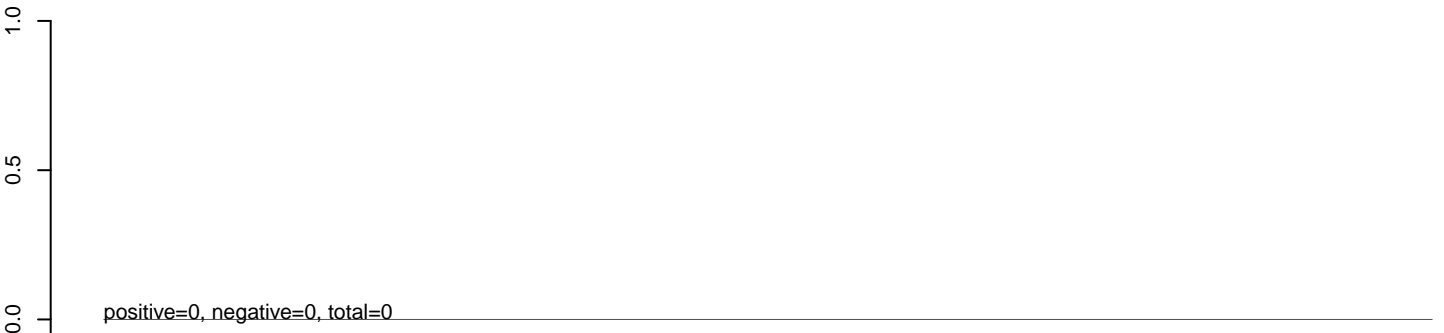
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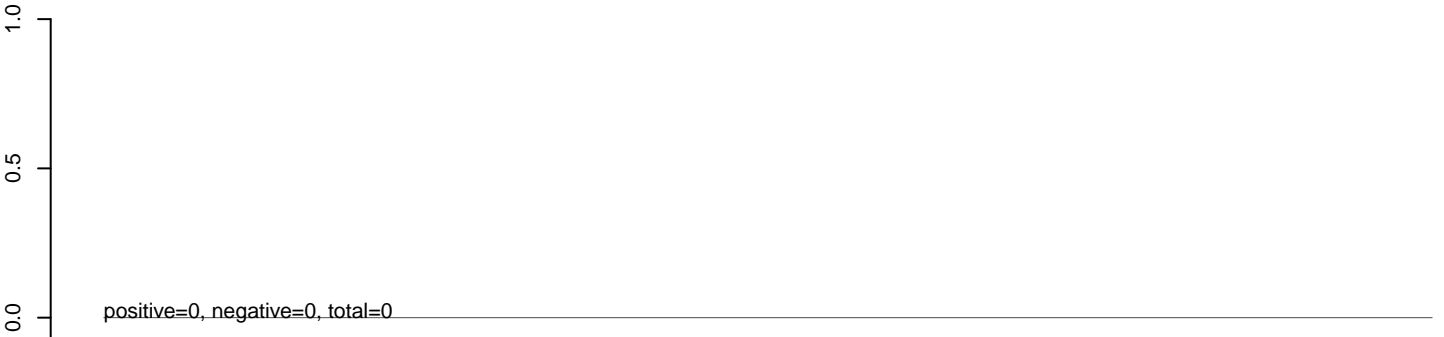
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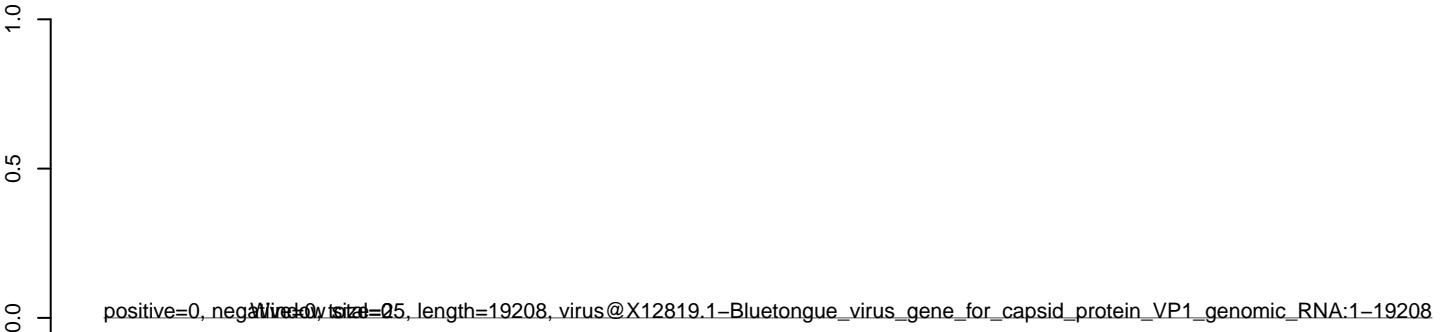
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AeAeg_Aag2.SINV.GFP.24_35.rep



AeAeg_Aag2.SINV.GFP.rep



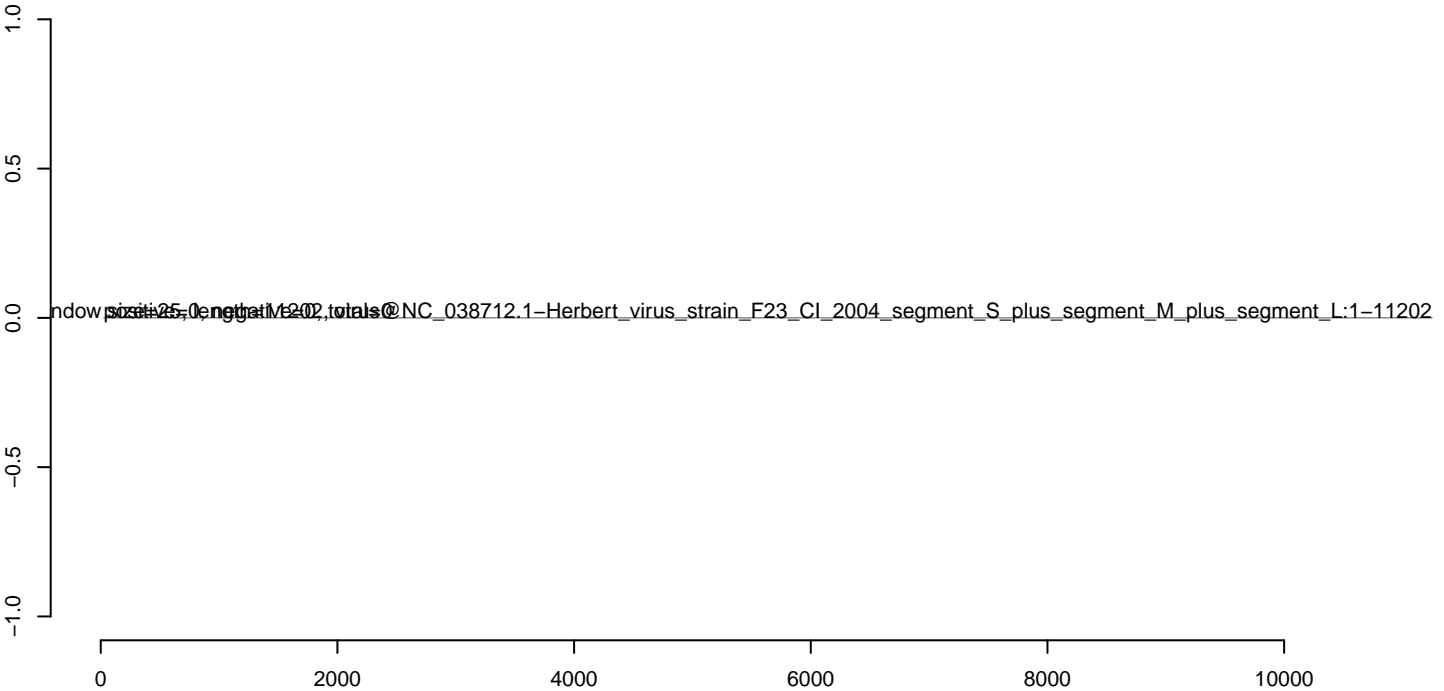
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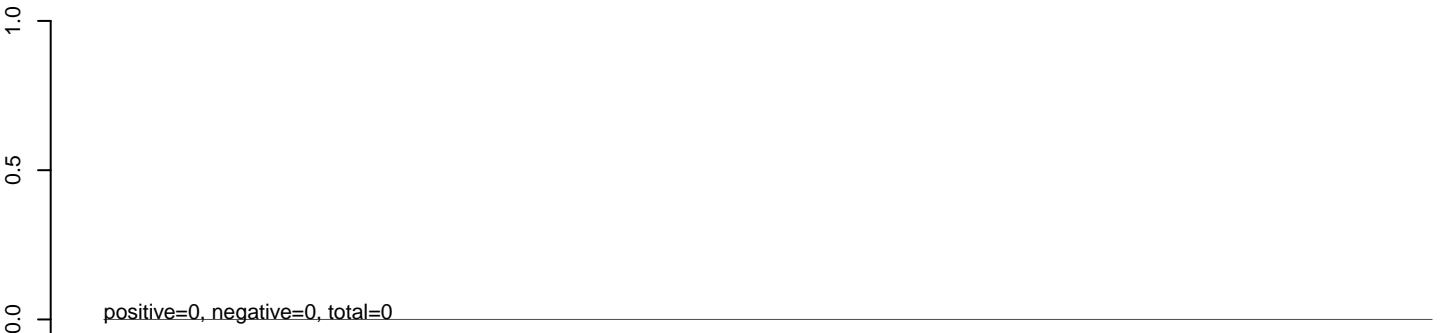
AeAeg_Aag2.SINV.GFP.24_35.rep



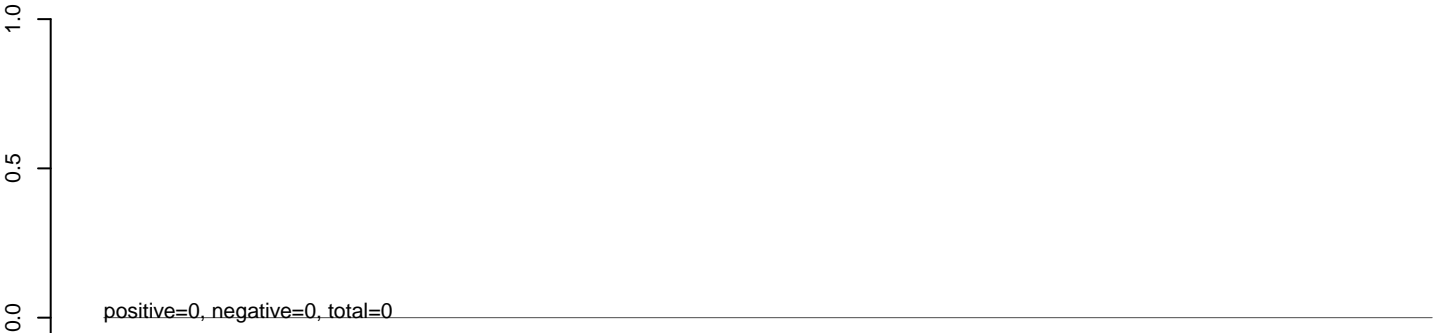
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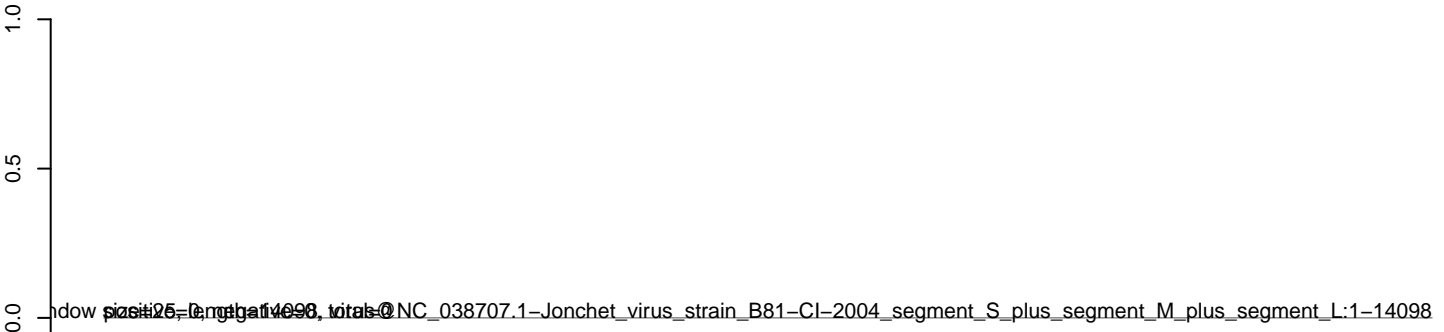
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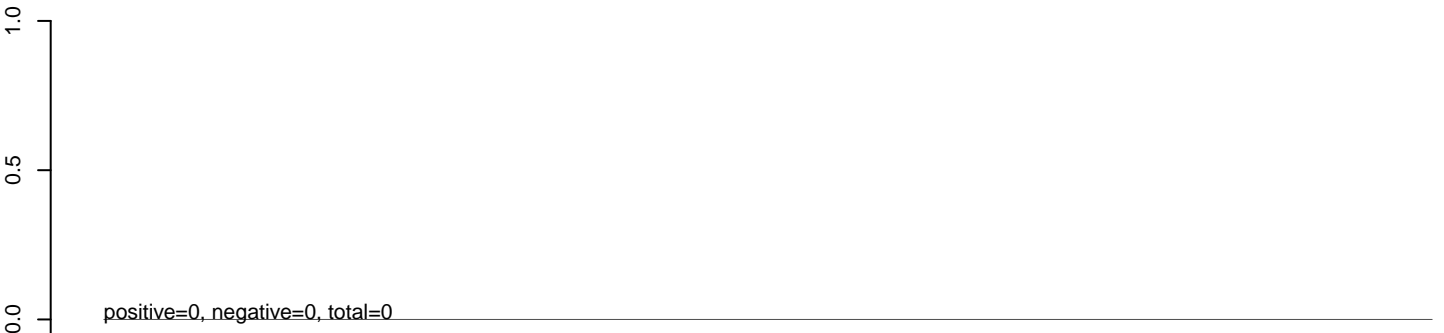
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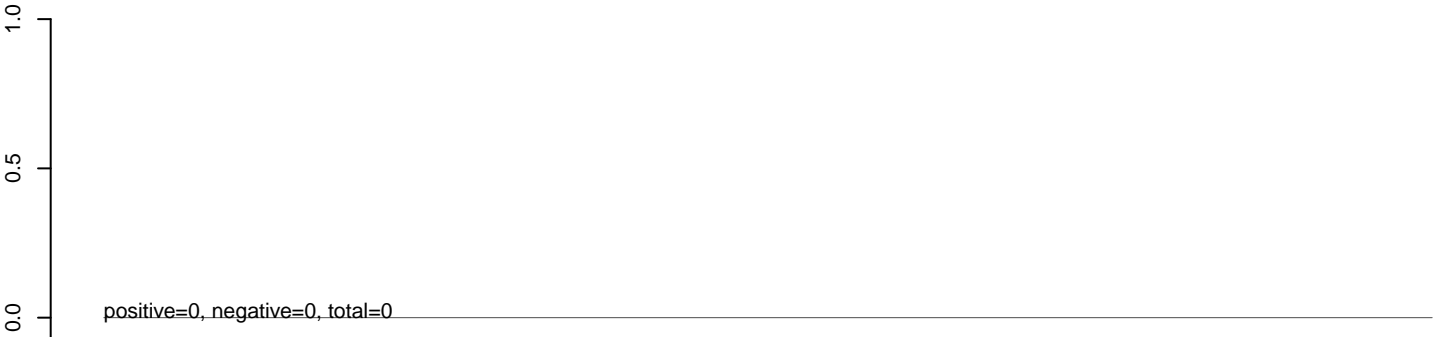
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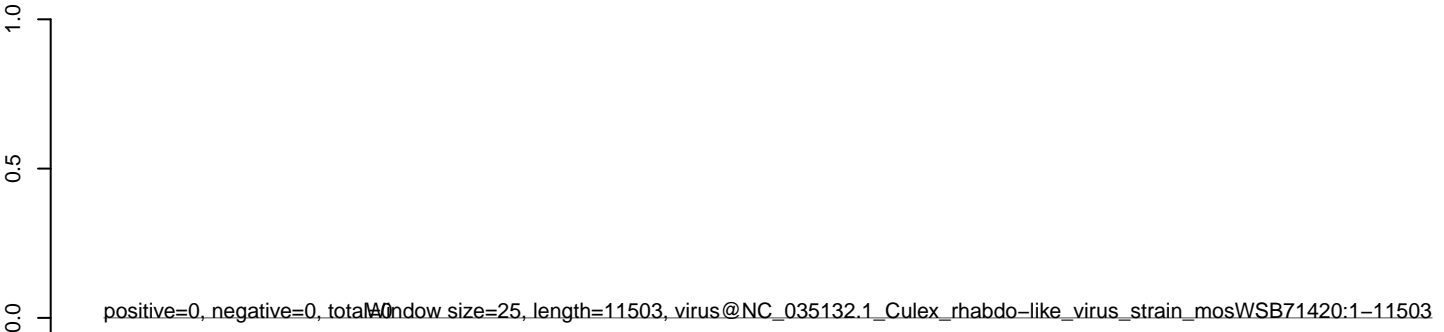
AeAeg_Aag2.SINV.GFP.18_23.rep



AeAeg_Aag2.SINV.GFP.24_35.rep



AeAeg_Aag2.SINV.GFP.rep



0 2000 4000 6000 8000 10000 12000

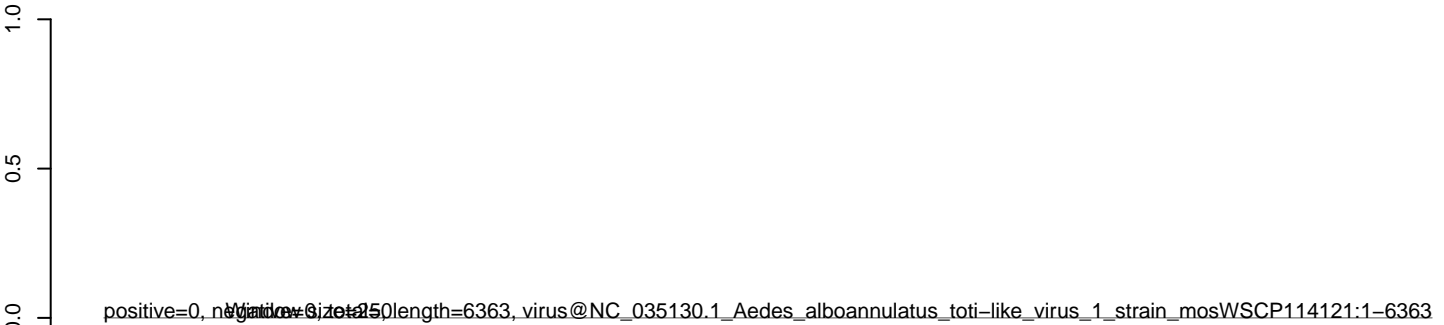
AeAeg_Aag2.SINV.GFP.18_23.rep



AeAeg_Aag2.SINV.GFP.24_35.rep



AeAeg_Aag2.SINV.GFP.rep



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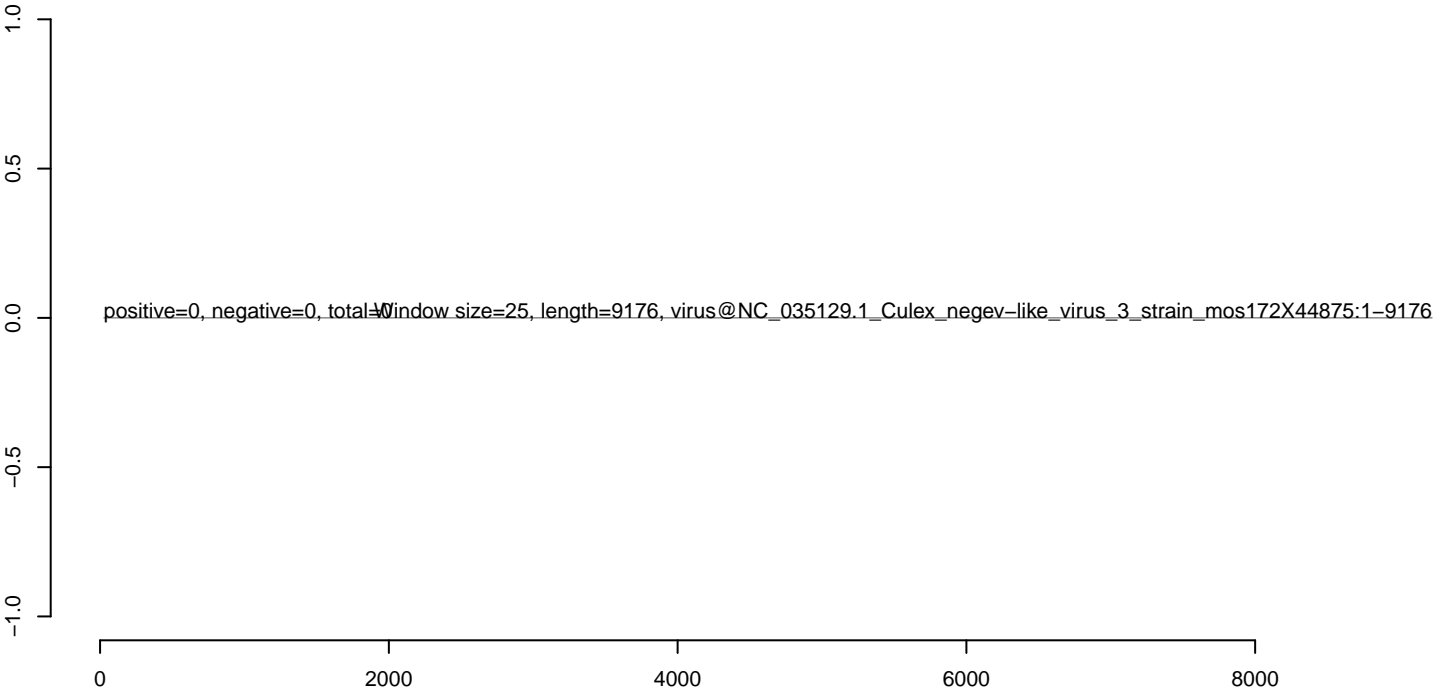
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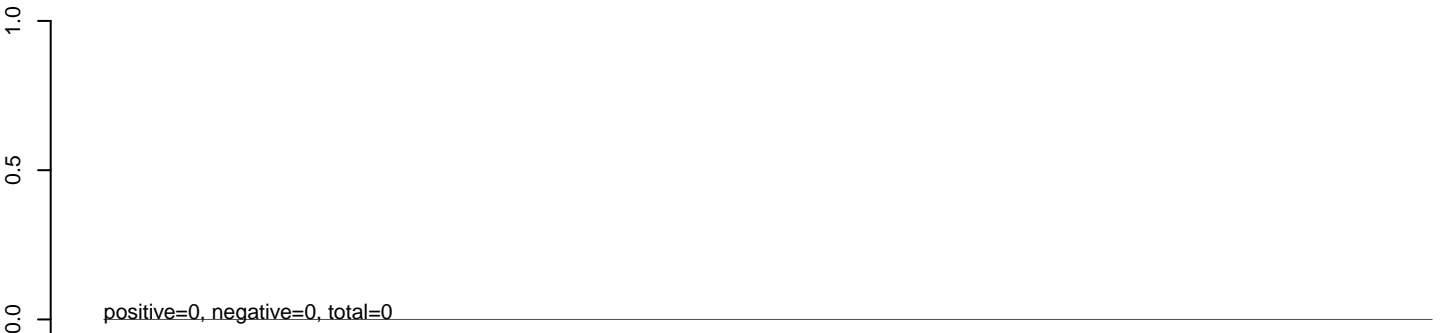
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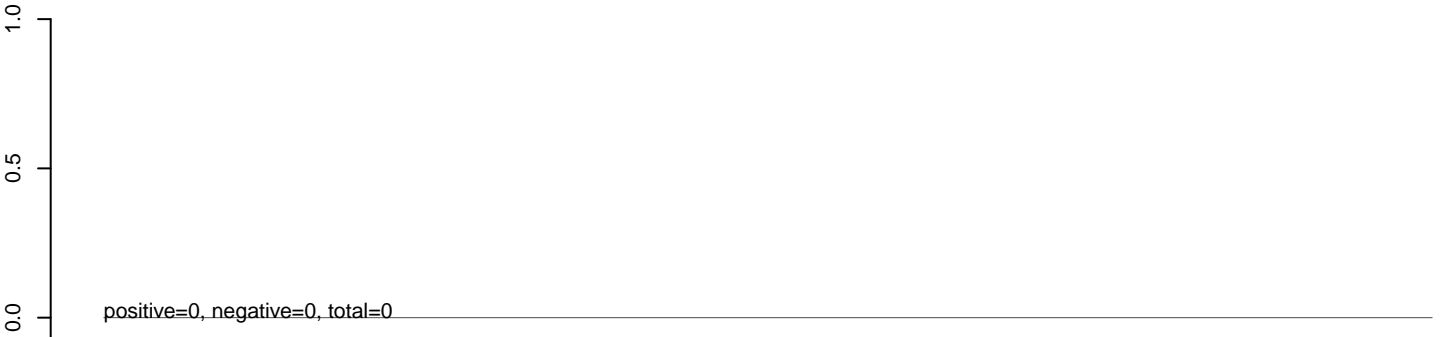
AeAeg_Aag2.SINV.GFP.rep



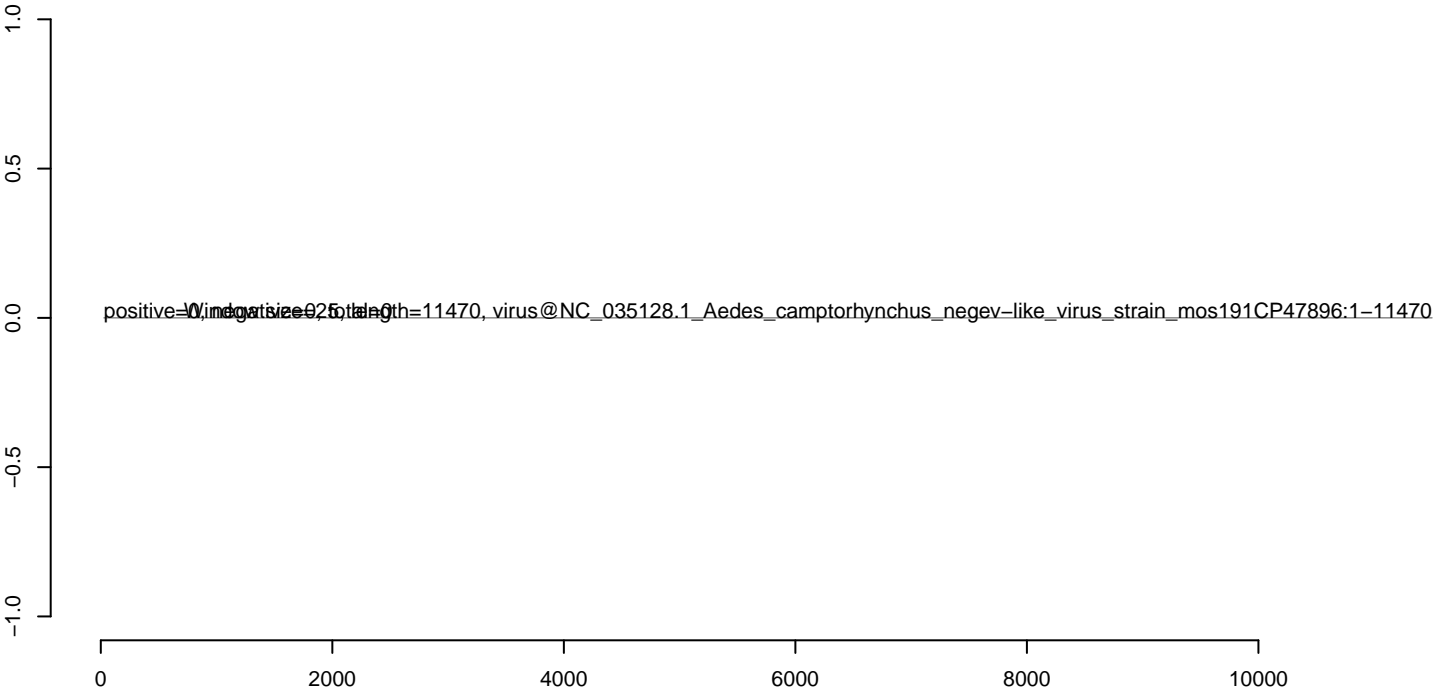
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AeAeg_Aag2.SINV.GFP.24_35.rep



AeAeg_Aag2.SINV.GFP.rep



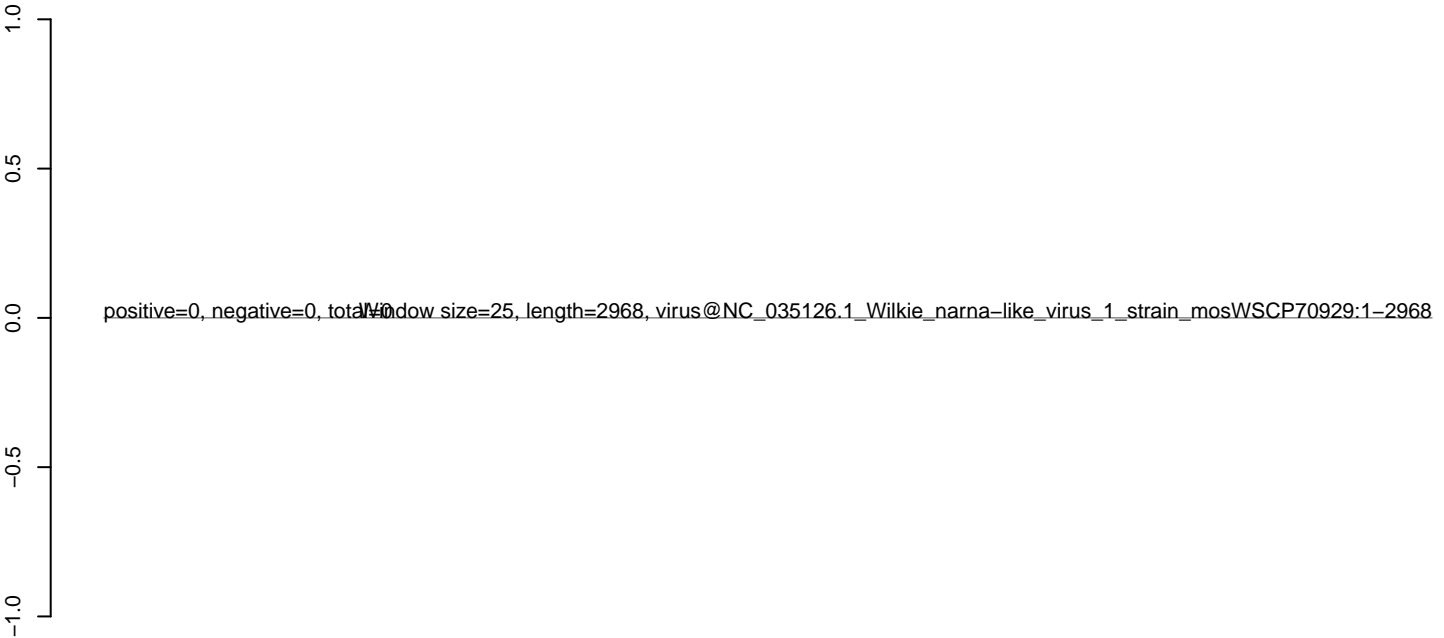
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AeAeg_Aag2.SINV.GFP.24_35.rep



AeAeg_Aag2.SINV.GFP.rep



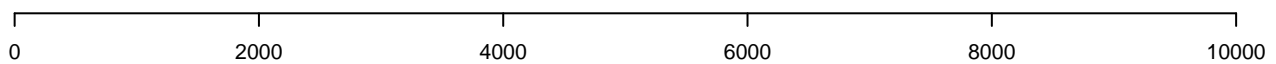
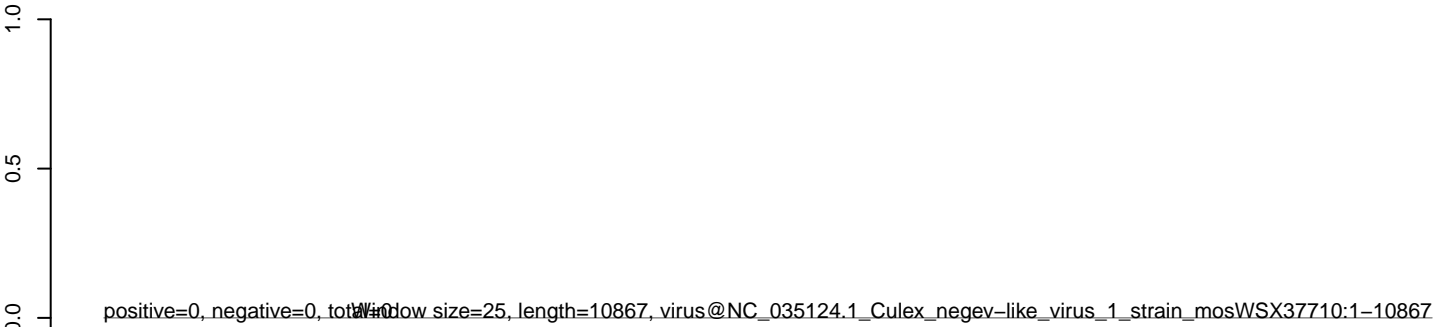
AeAeg_Aag2.SINV.GFP.18_23.rep



AeAeg_Aag2.SINV.GFP.24_35.rep



AeAeg_Aag2.SINV.GFP.rep



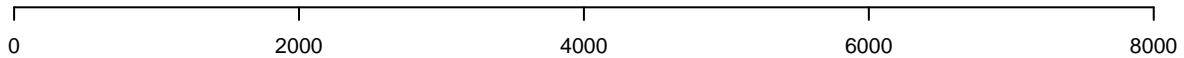
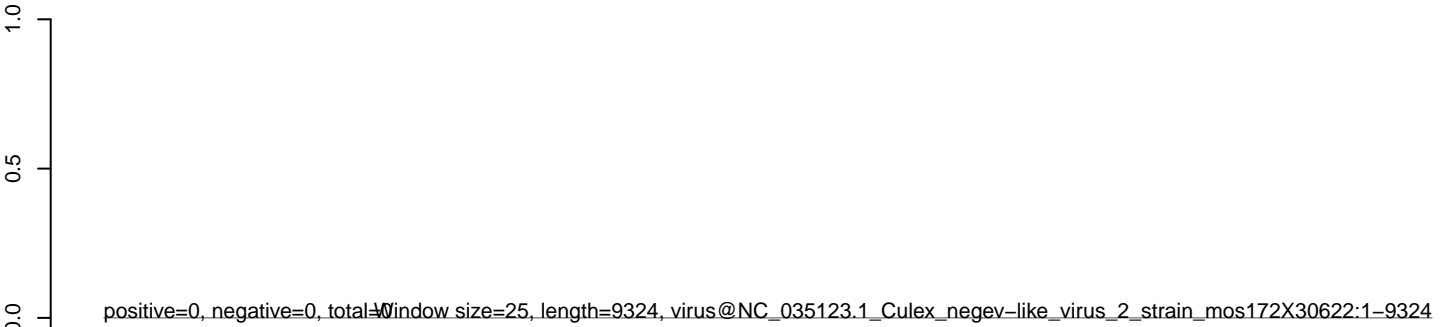
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AeAeg_Aag2.SINV.GFP.24_35.rep



AeAeg_Aag2.SINV.GFP.rep



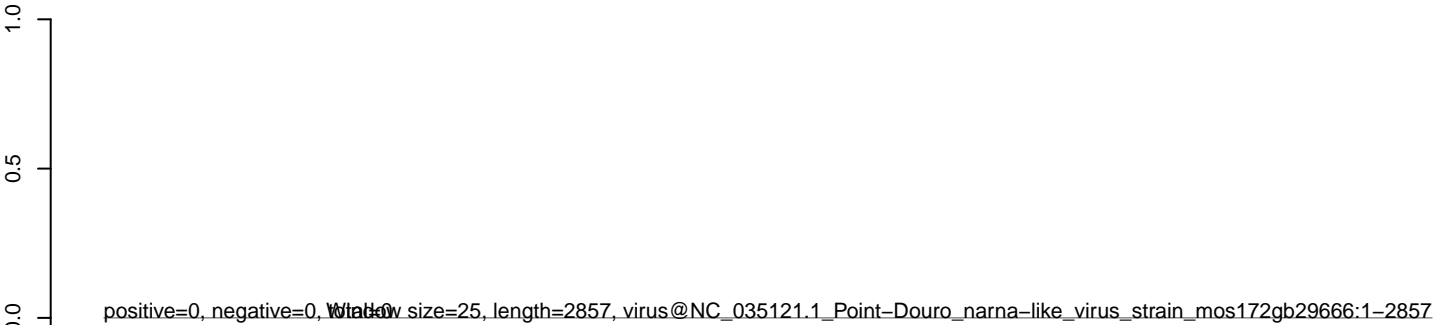
AeAeg_Aag2.SINV.GFP.18_23.rep



AeAeg_Aag2.SINV.GFP.24_35.rep



AeAeg_Aag2.SINV.GFP.rep

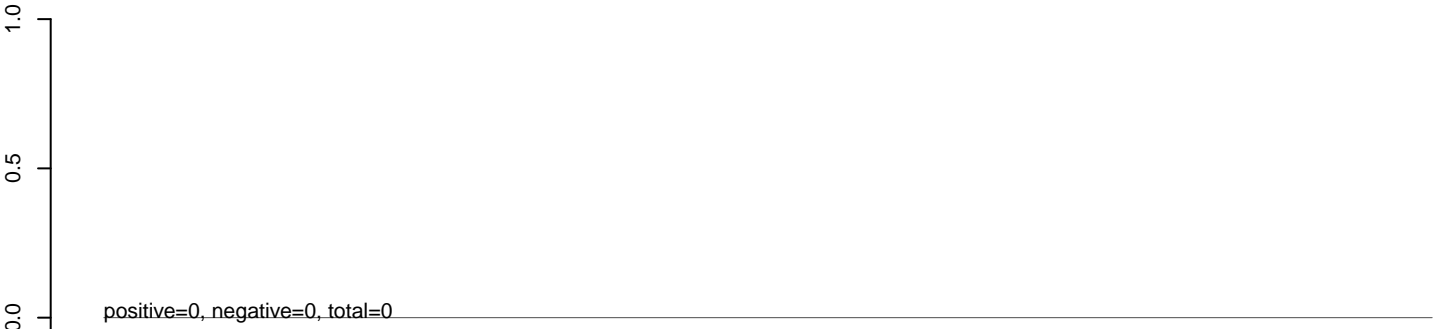


0 500 1000 1500 2000 2500 3000

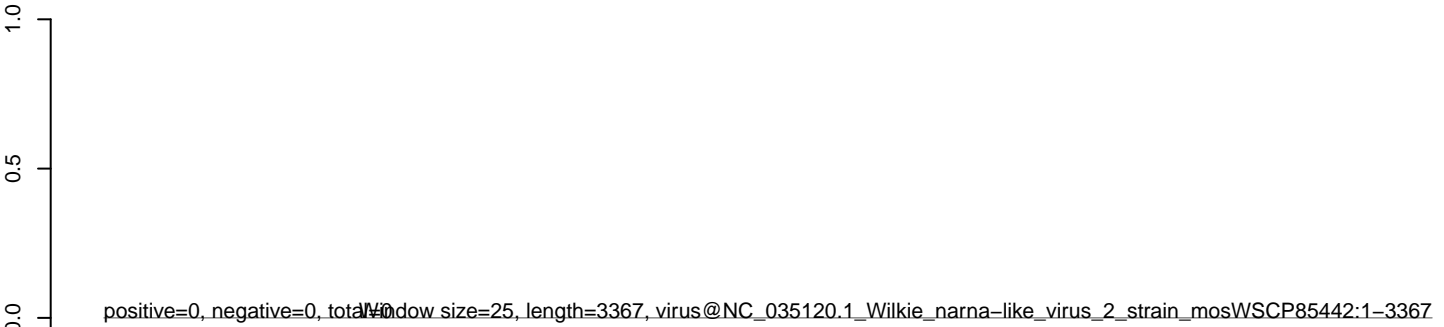
AeAeg_Aag2.SINV.GFP.18_23.rep



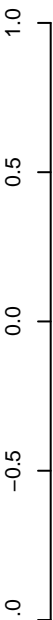
AeAeg_Aag2.SINV.GFP.24_35.rep



AeAeg_Aag2.SINV.GFP.rep

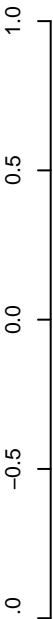


AeAeg_Aag2.SINV.GFP.18_23.rep



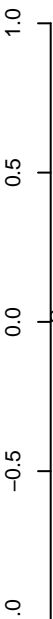
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AeAeg_Aag2.SINV.GFP.24_35.rep

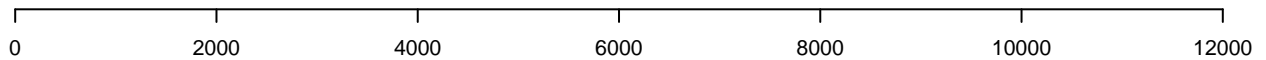


positive=0, negative=0, total=0

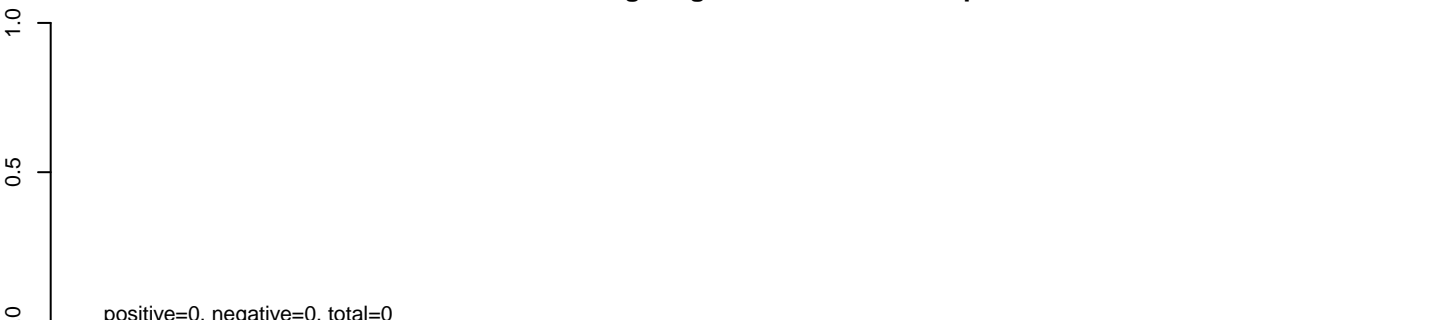
AeAeg_Aag2.SINV.GFP.rep



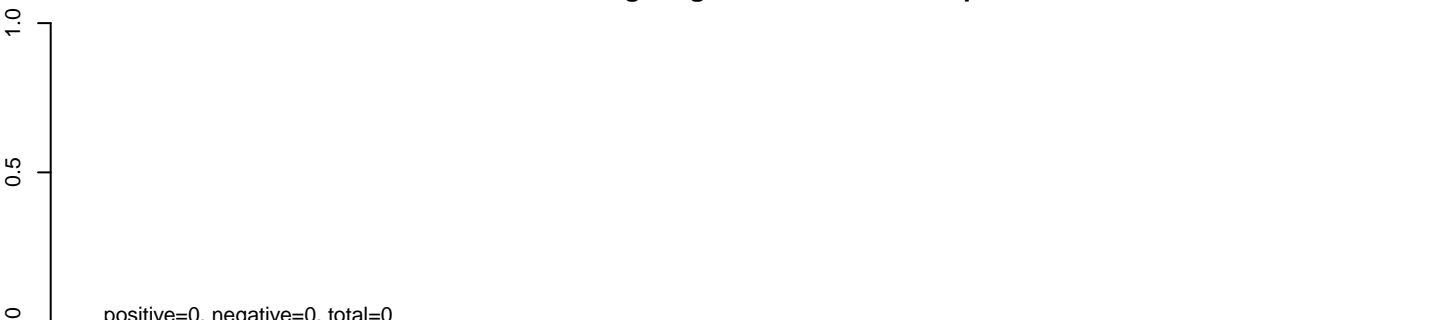
low sizes 25 kb, the 13189 nt, NC_034543.1-Ord_River_virus_nucleoprotein_hypothetical_protein_phosphoprotein_hypothetical_pro:1-13189



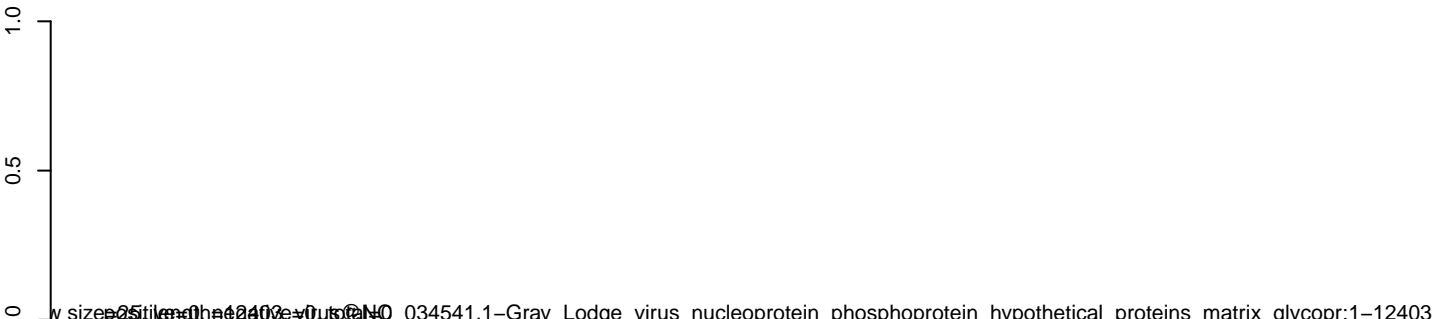
AeAeg_Aag2.SINV.GFP.18_23.rep



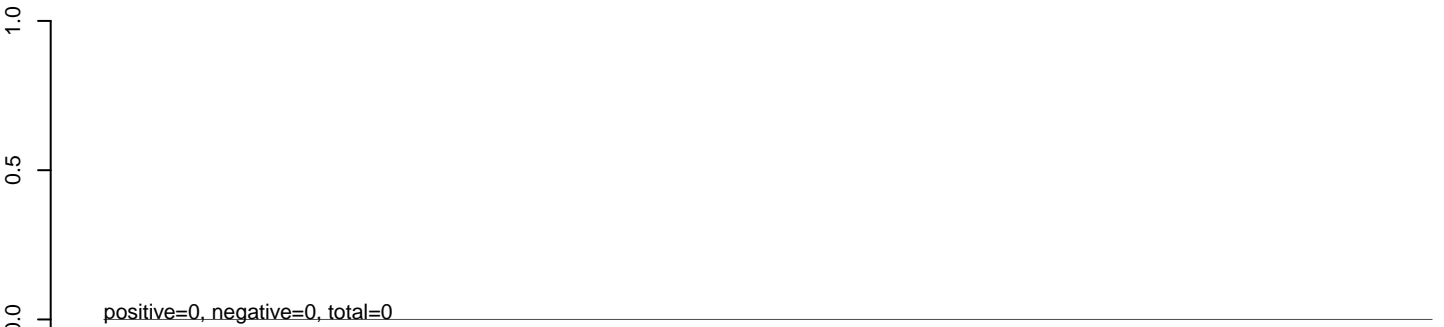
AeAeg_Aag2.SINV.GFP.24_35.rep



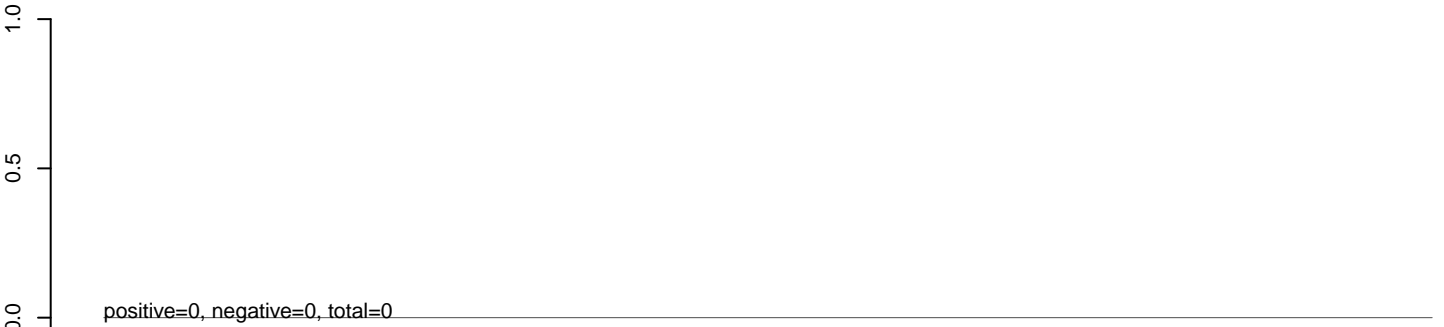
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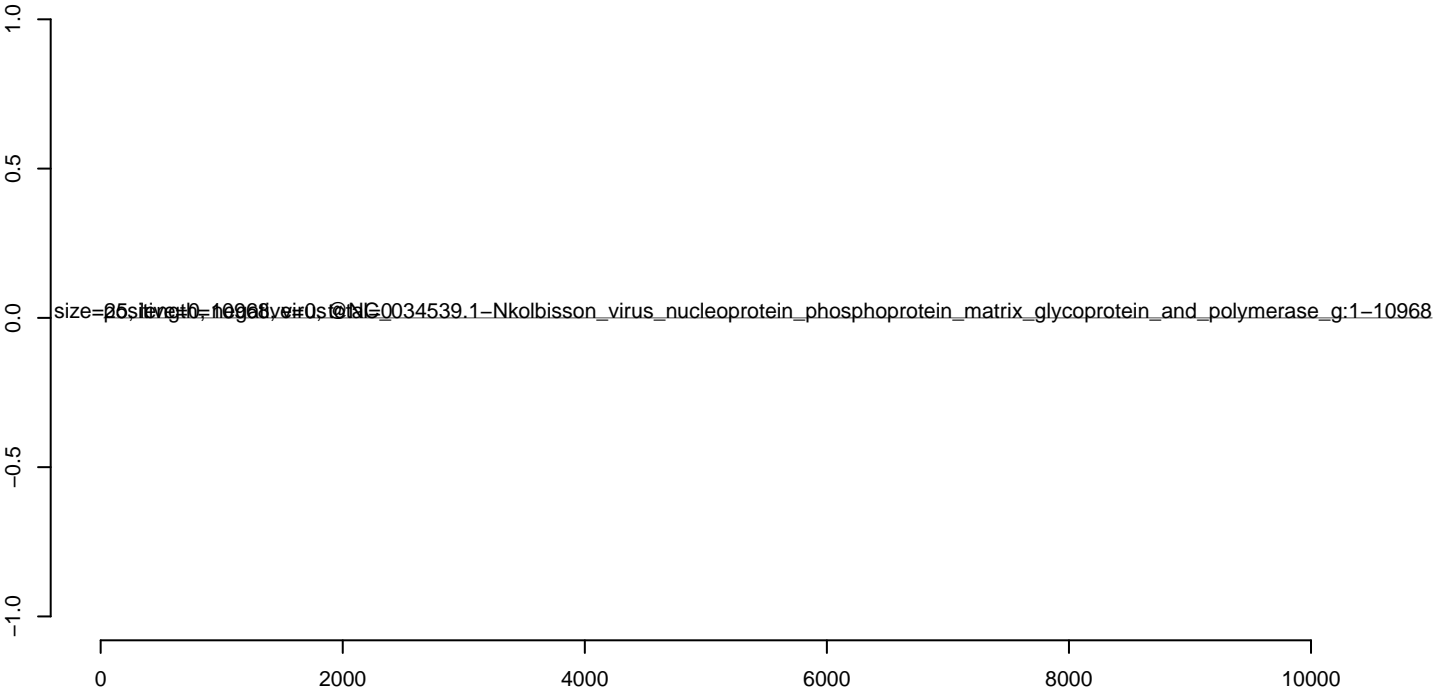
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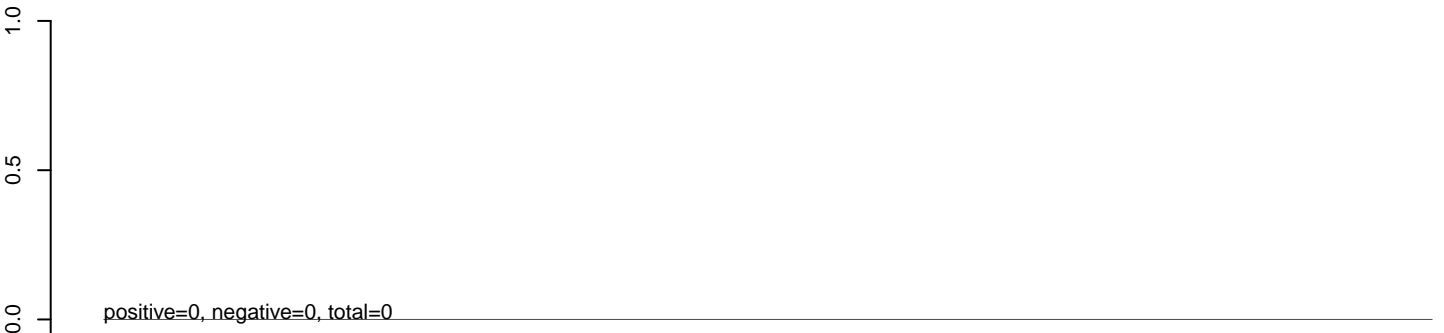
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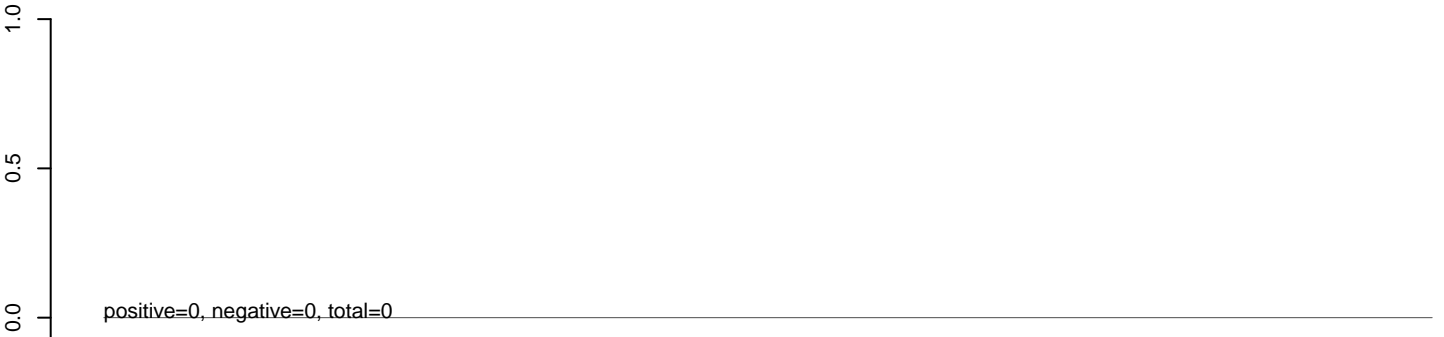
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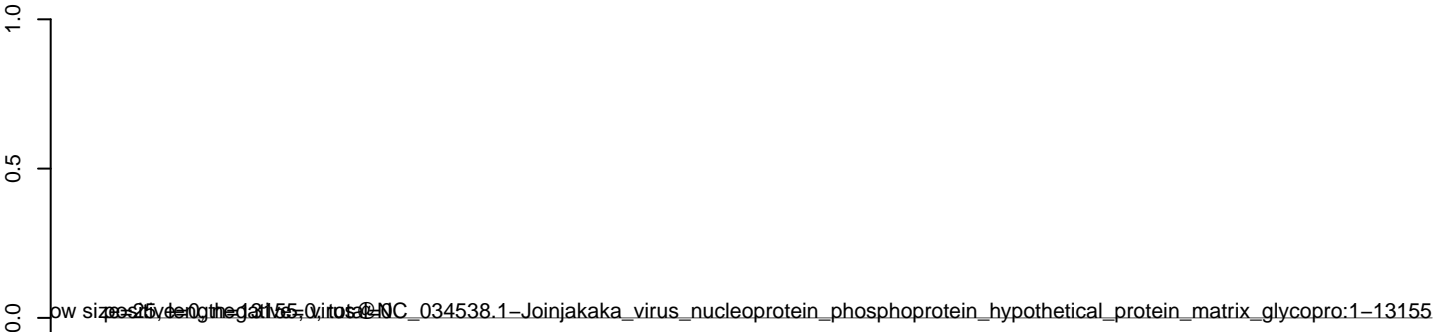
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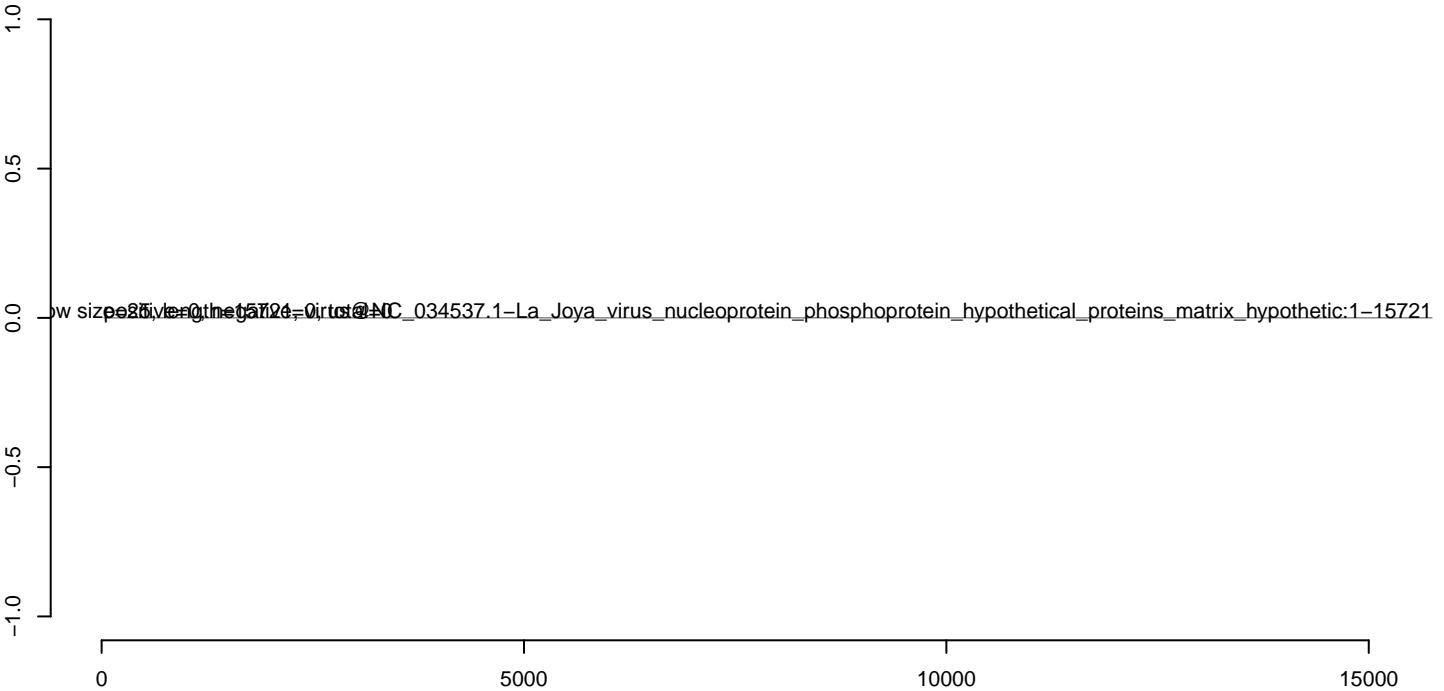
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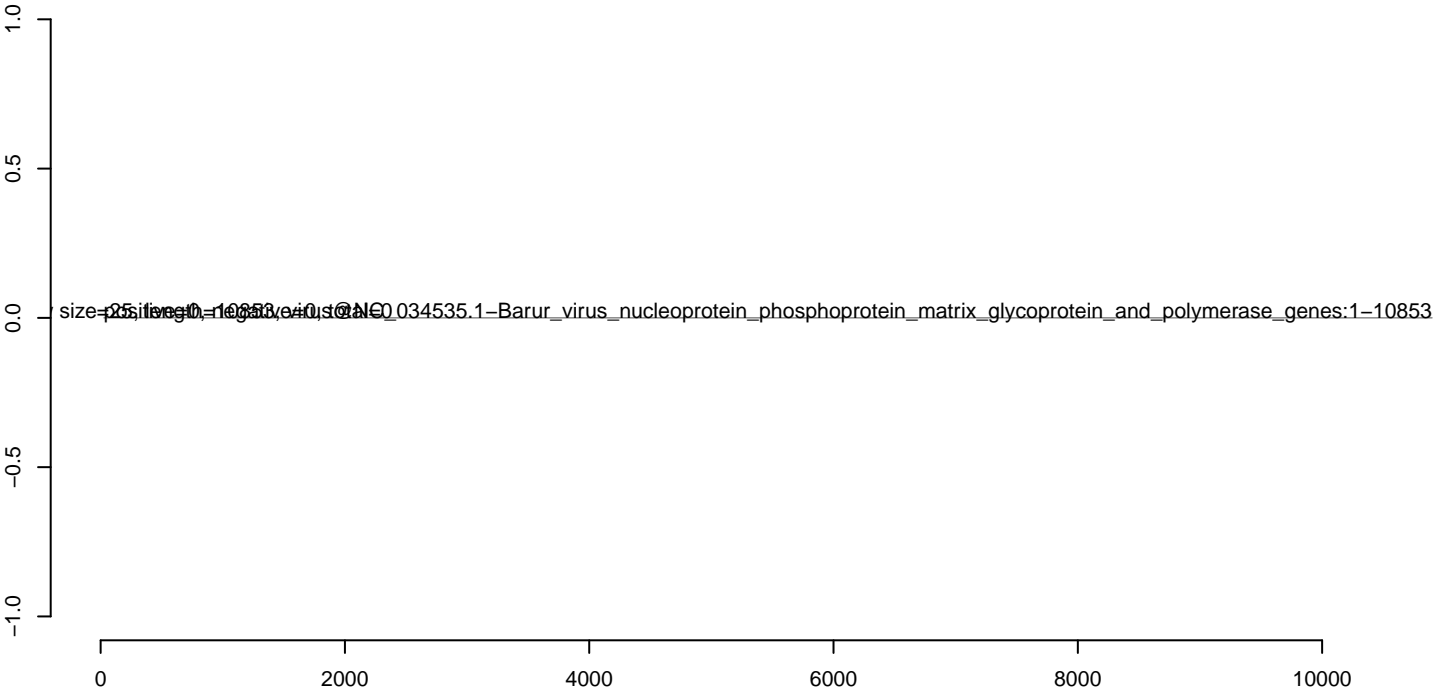
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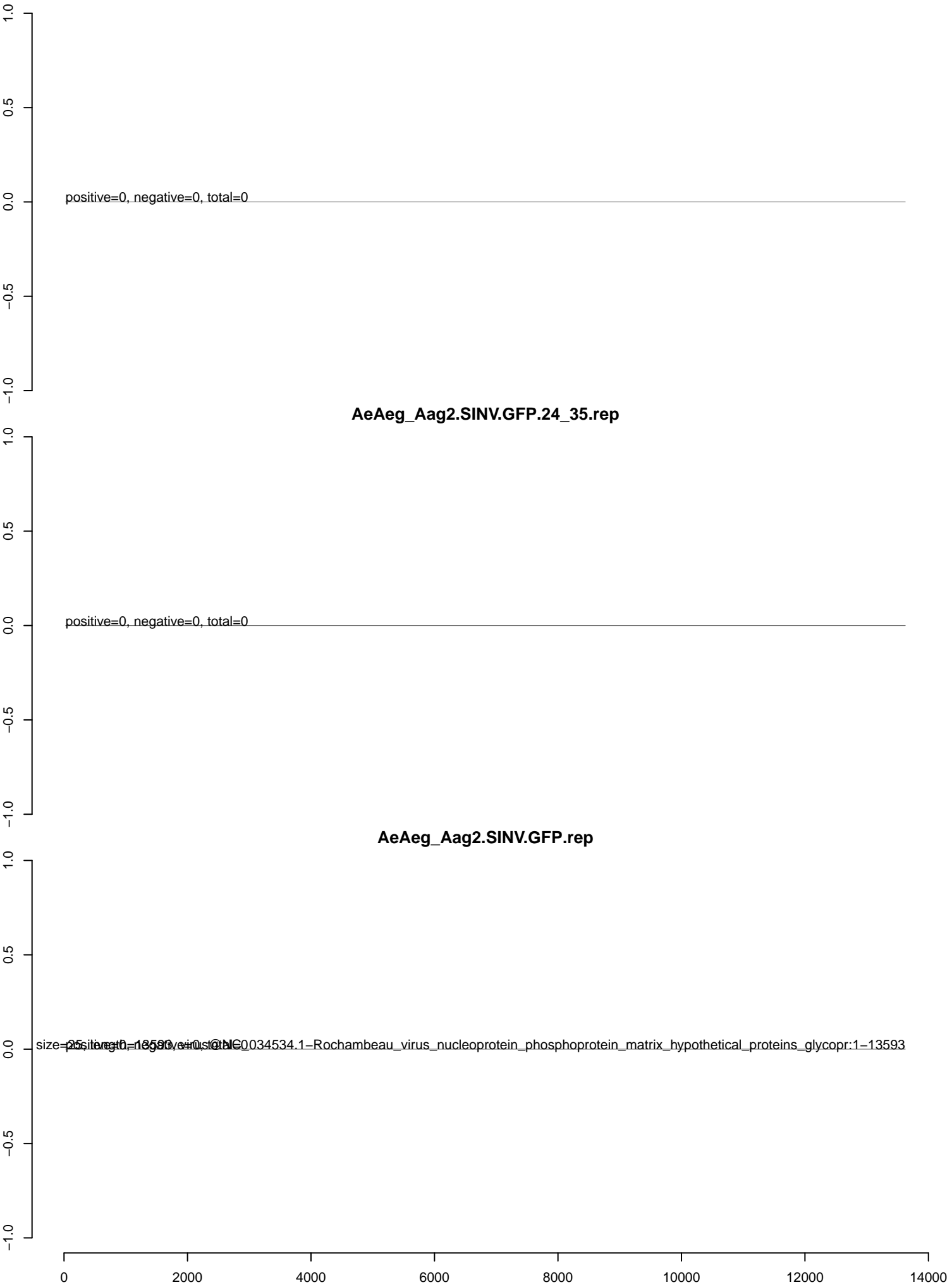
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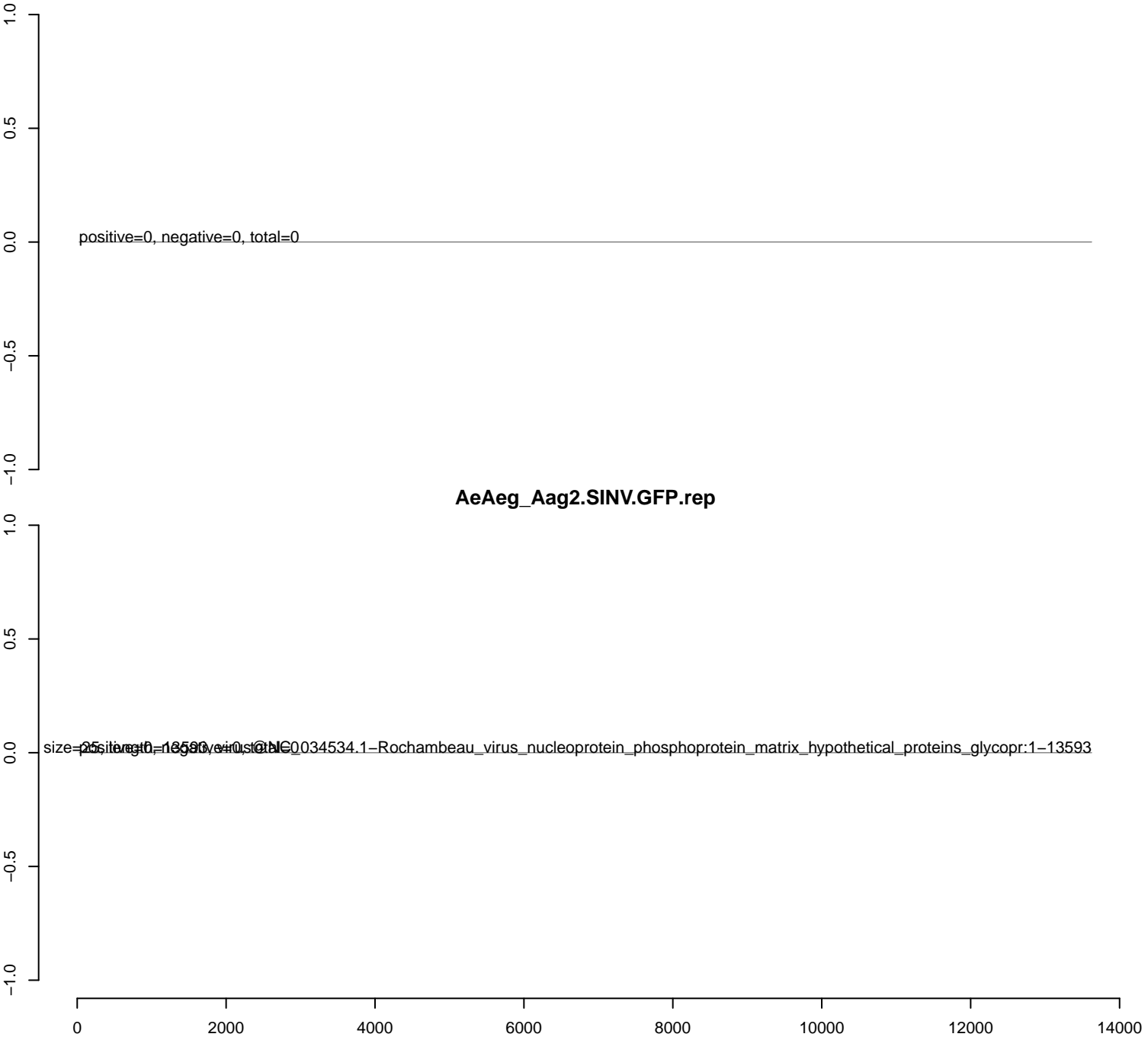
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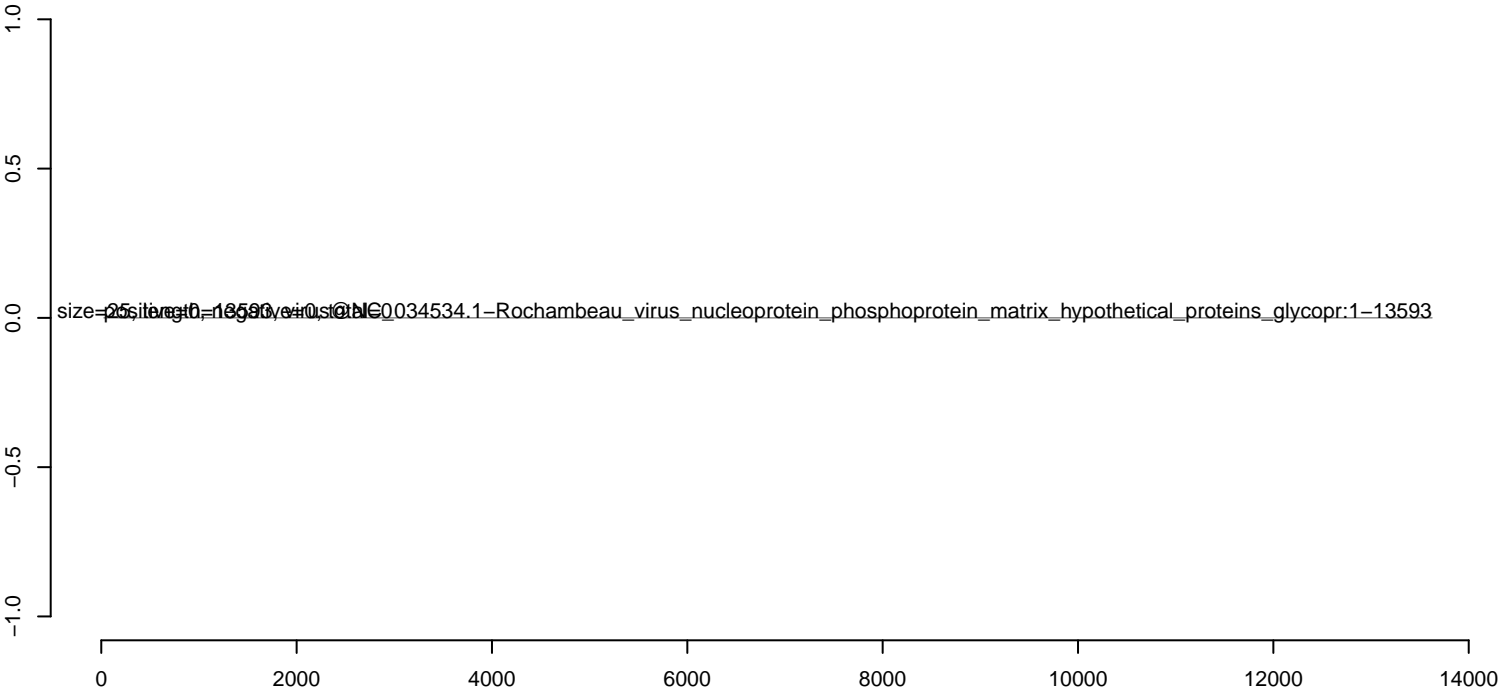
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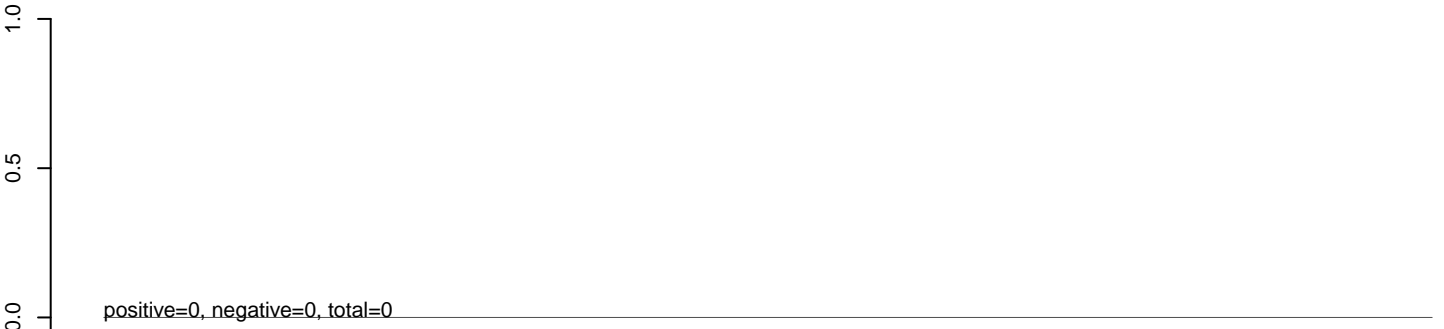
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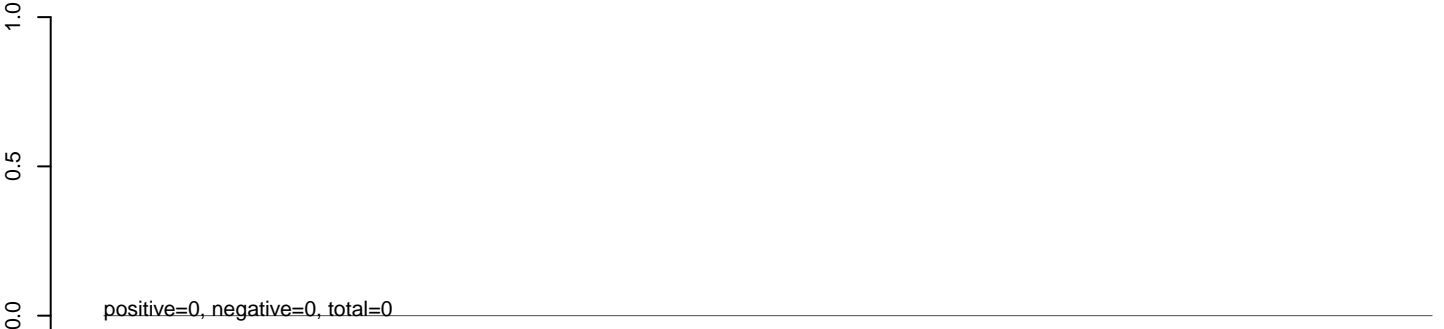
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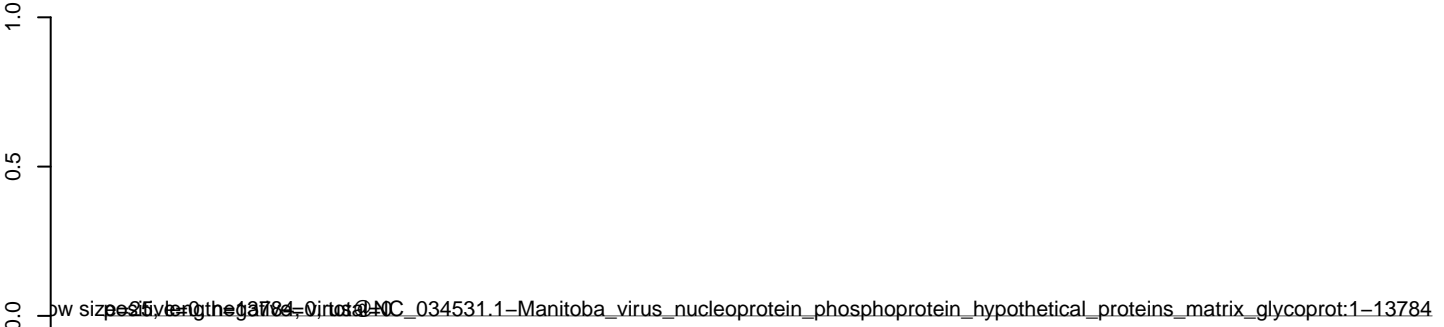
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AeAeg_Aag2.SINV.GFP.rep



low size of the genome (1784 nt) and the presence of a unique long (UL) segment (3453 nt) are characteristic of the genus *Aegyptius*. The genome organization is similar to that of other members of the genus, including the presence of a unique long (UL) segment (3453 nt) and a unique short (US) segment (1784 nt). The genome organization is similar to that of other members of the genus, including the presence of a unique long (UL) segment (3453 nt) and a unique short (US) segment (1784 nt).

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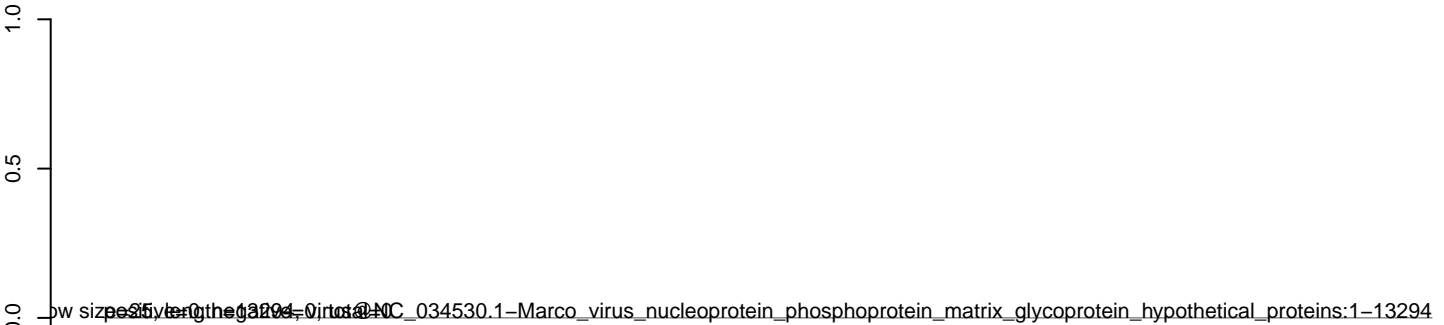
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AeAeg_Aag2.SINV.GFP.rep



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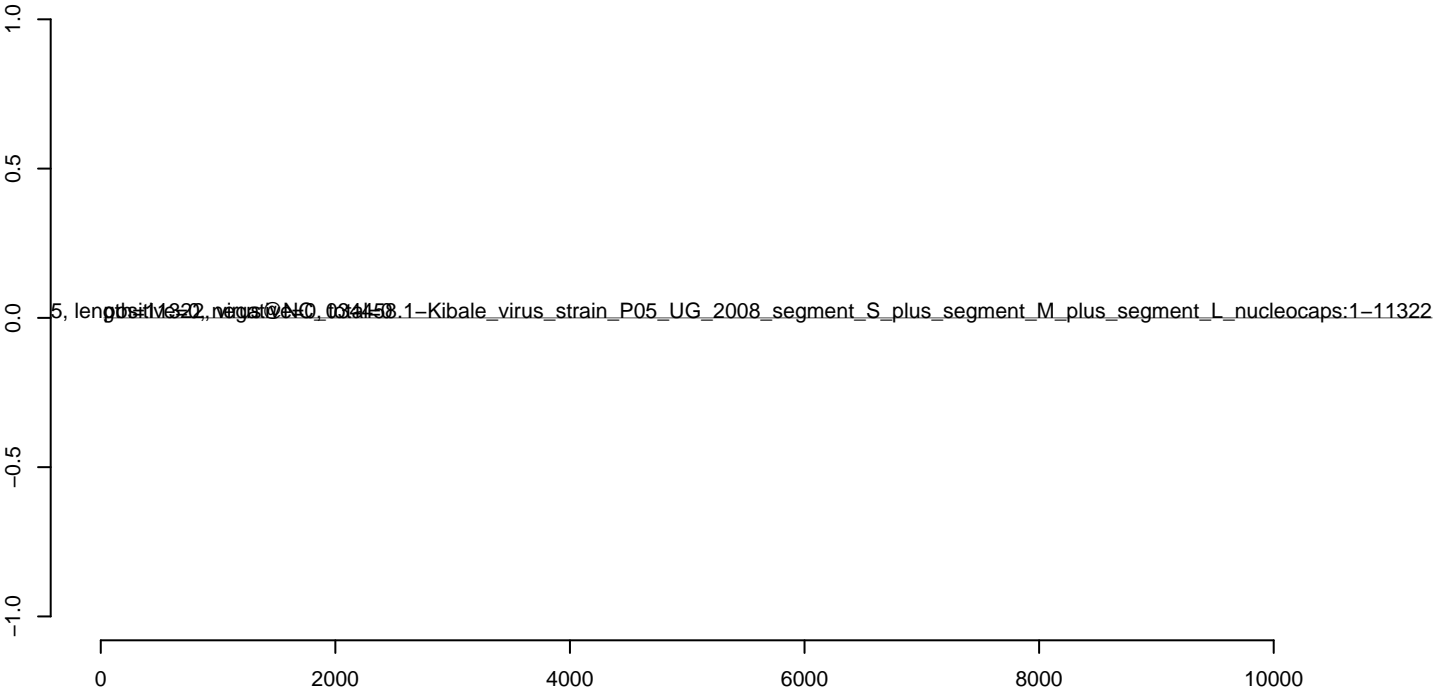
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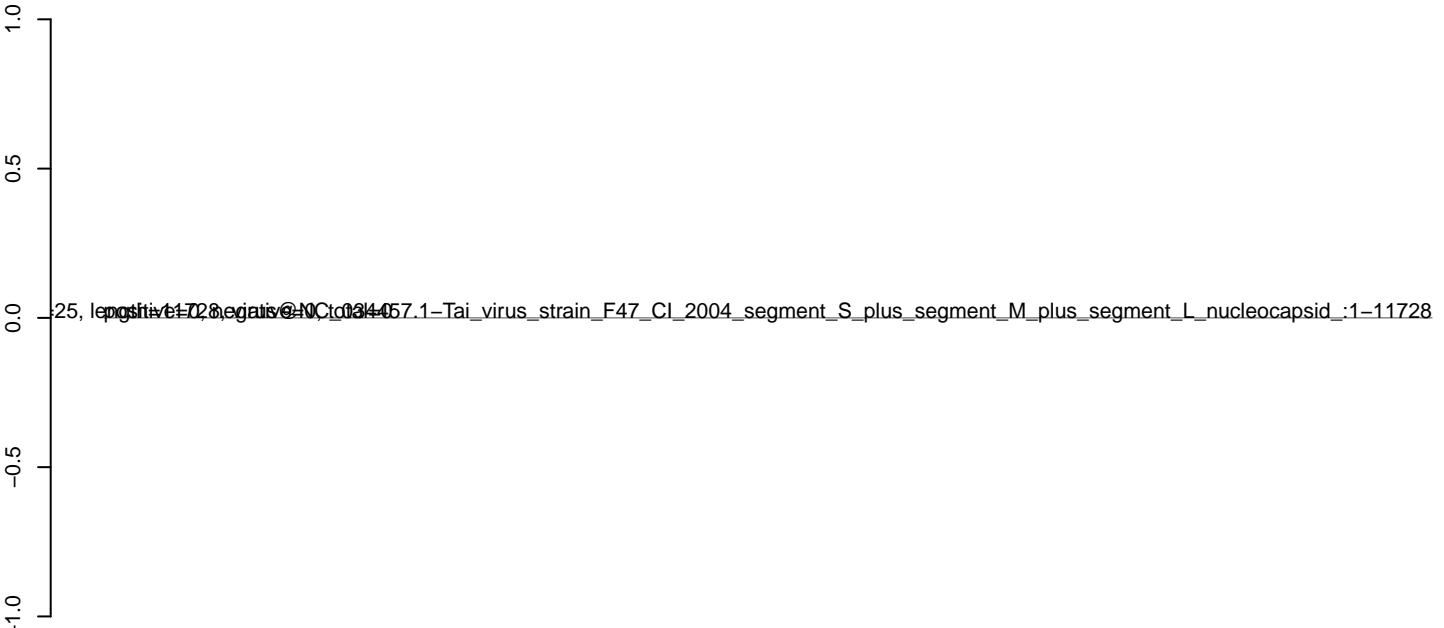
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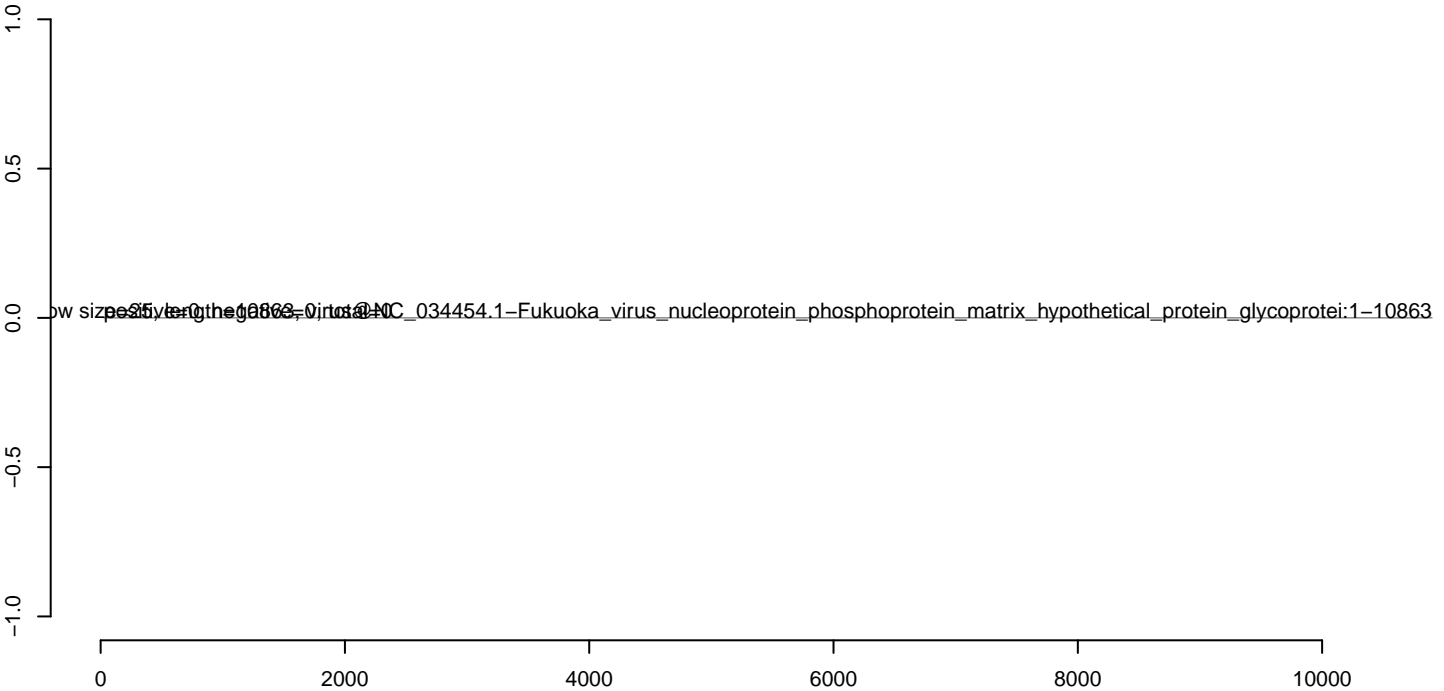
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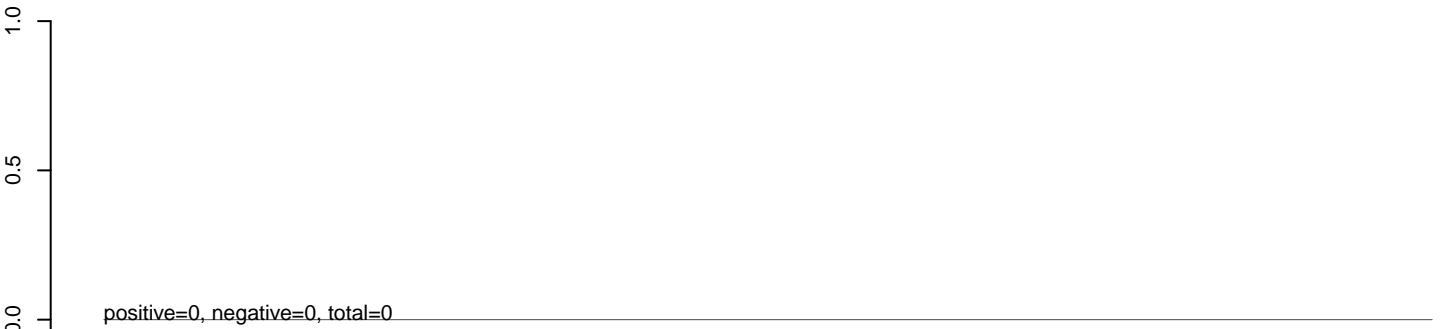
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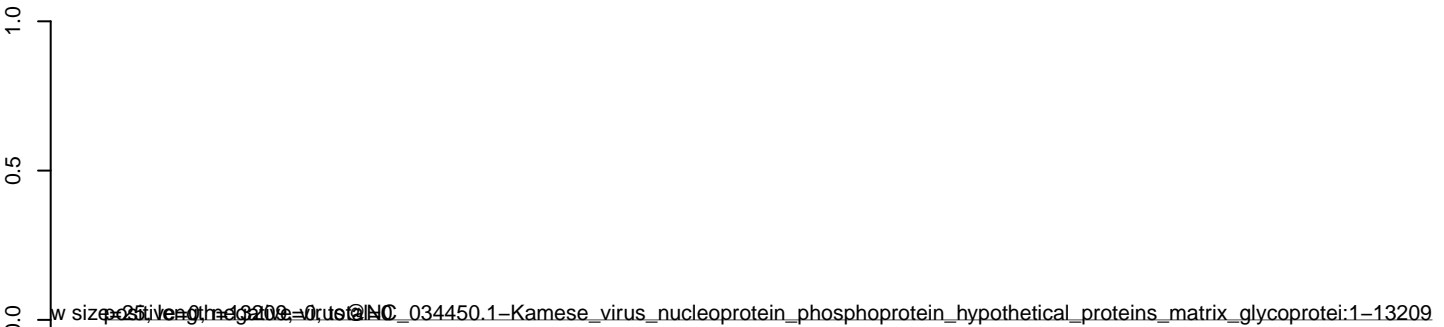
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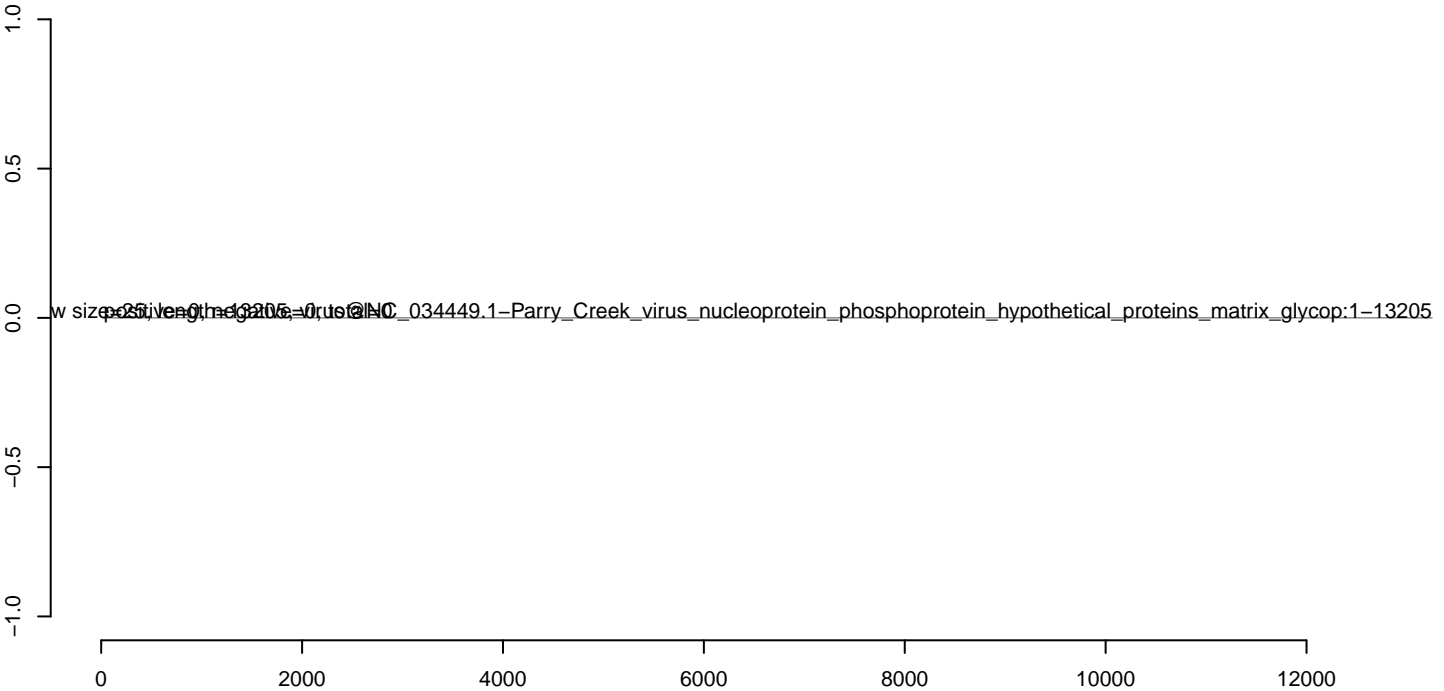
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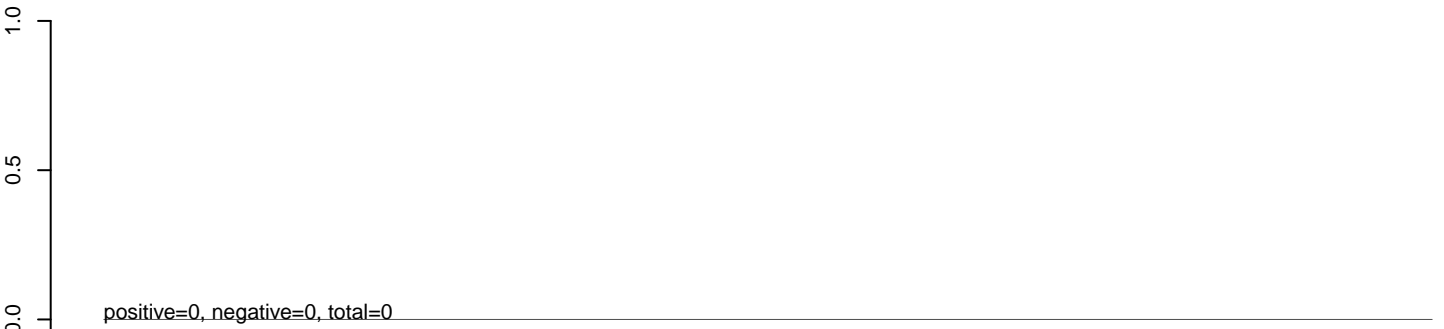
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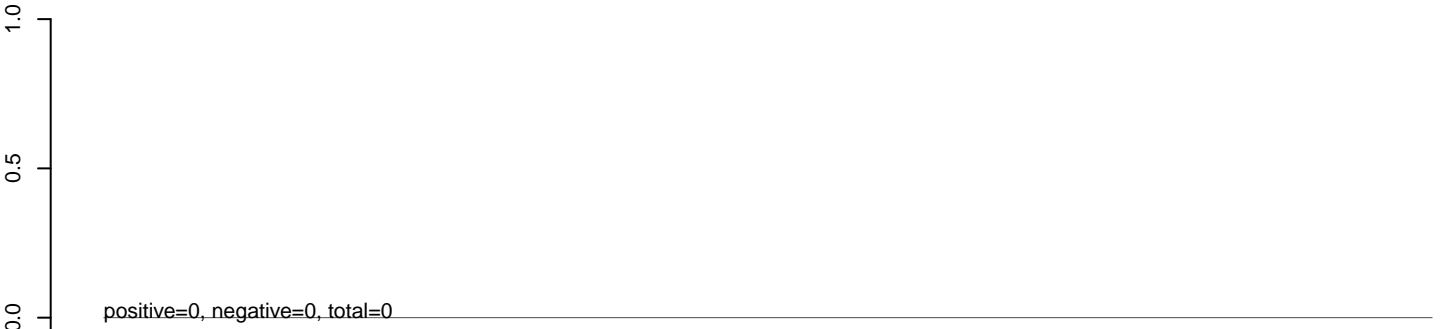
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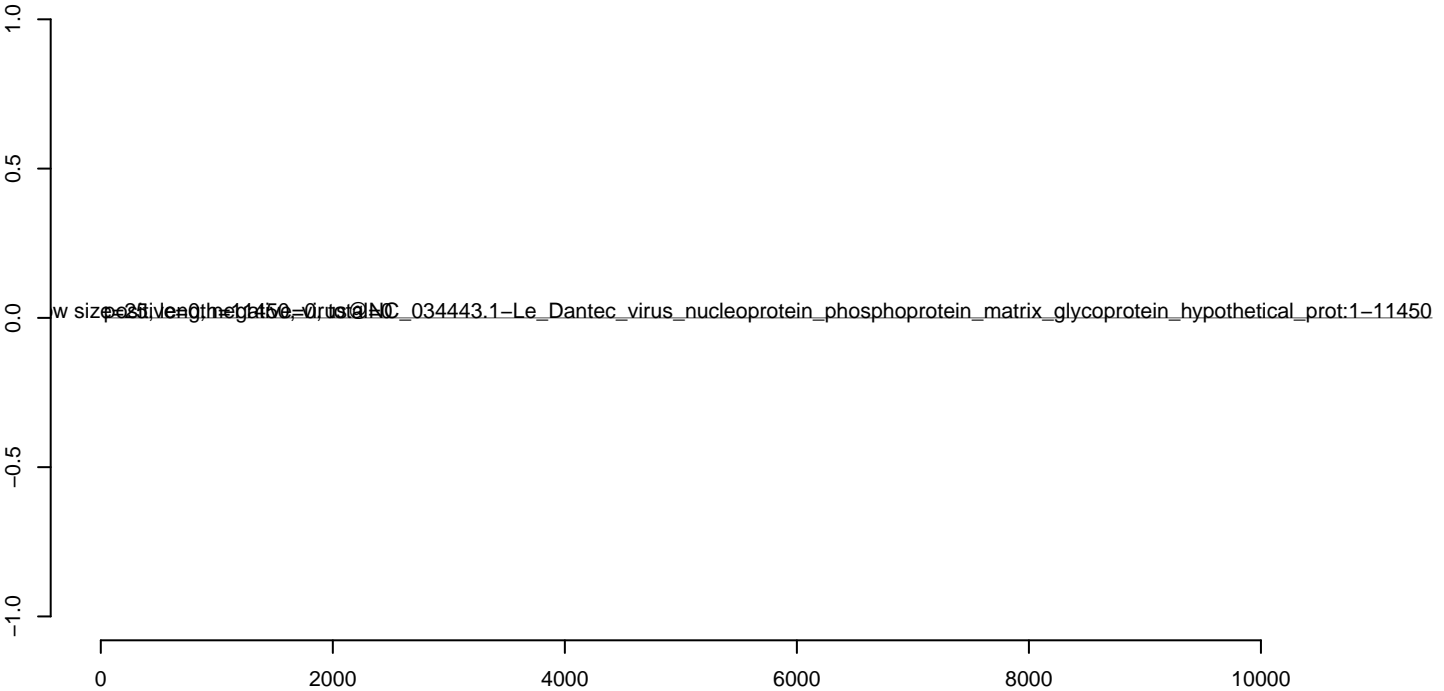
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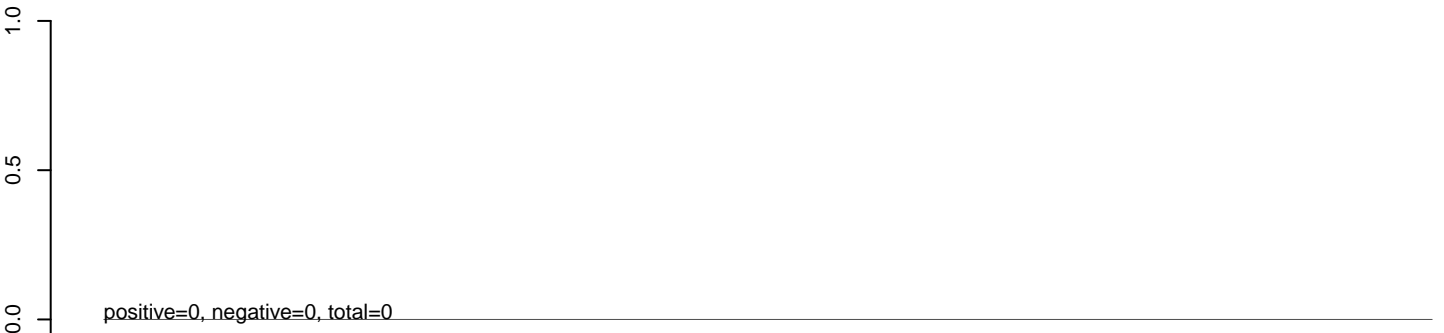
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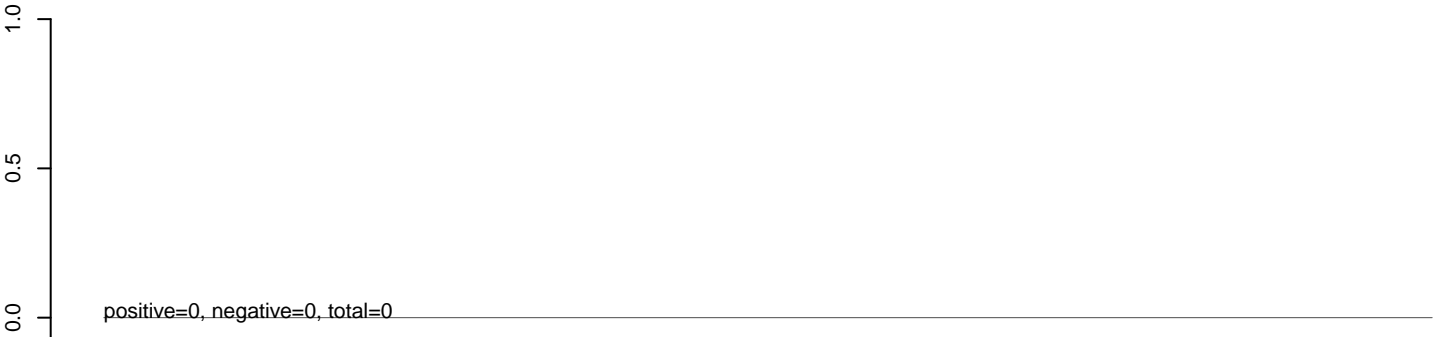
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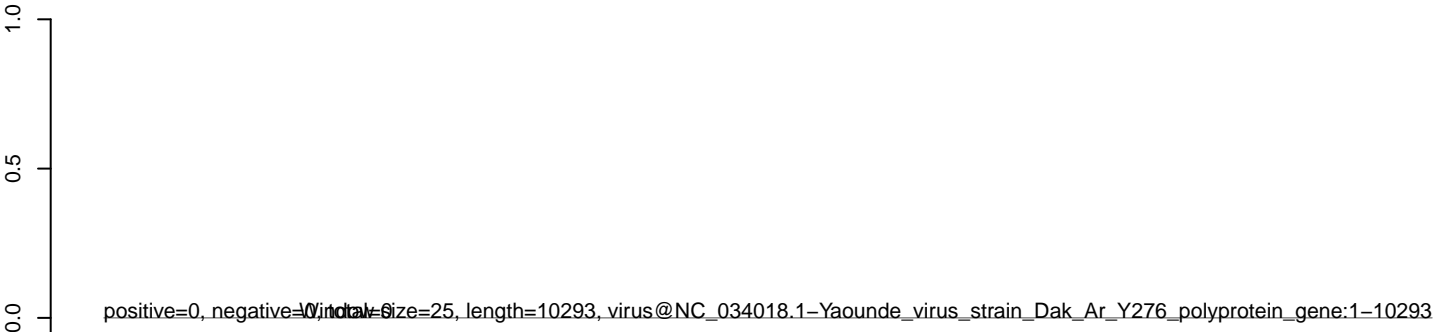
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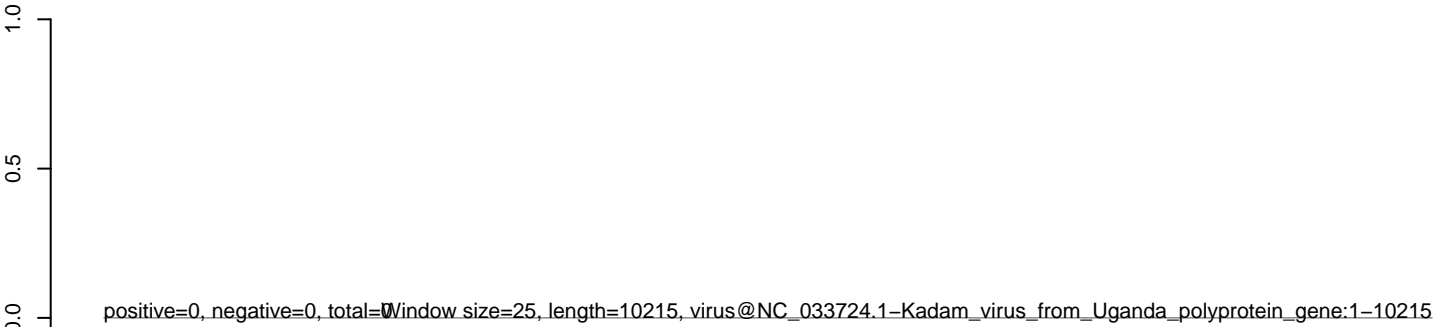
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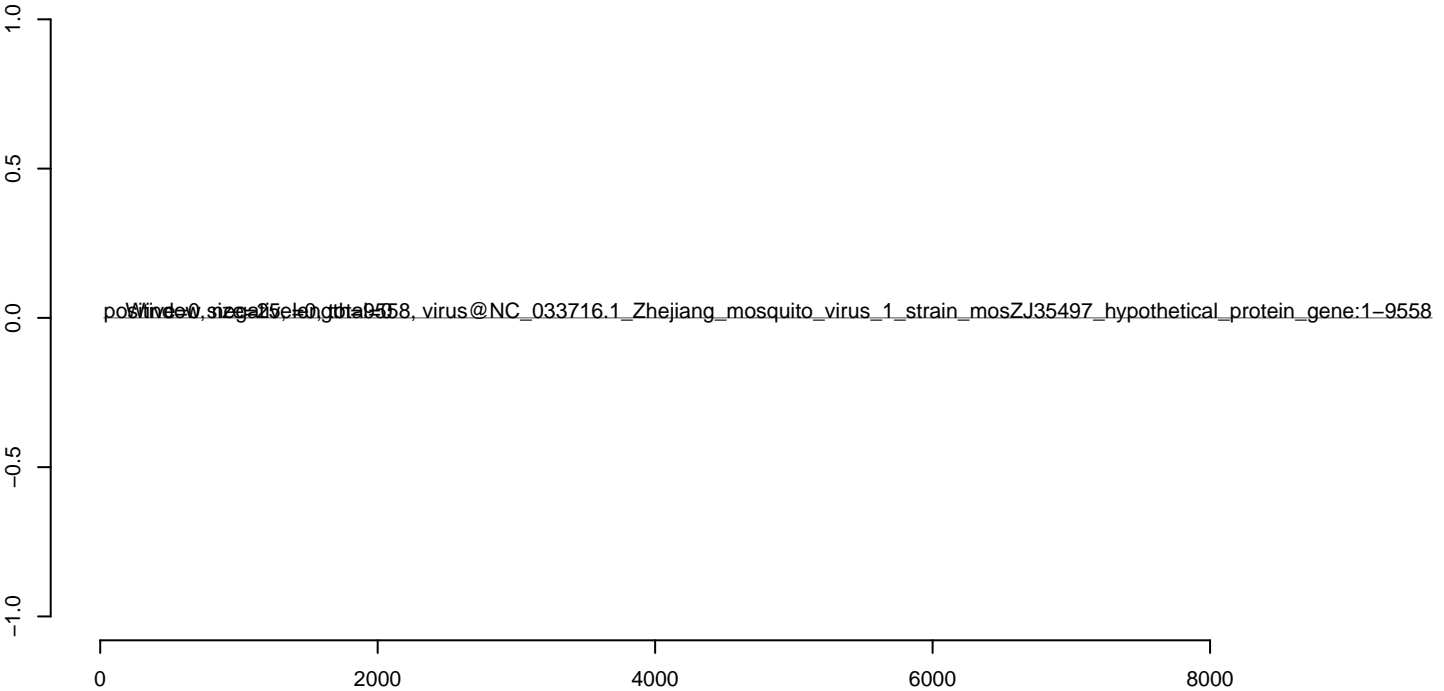
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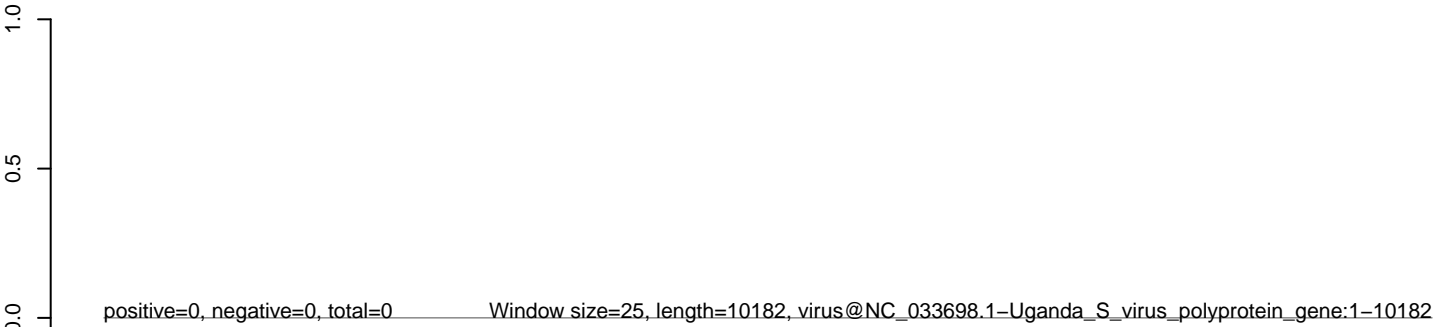
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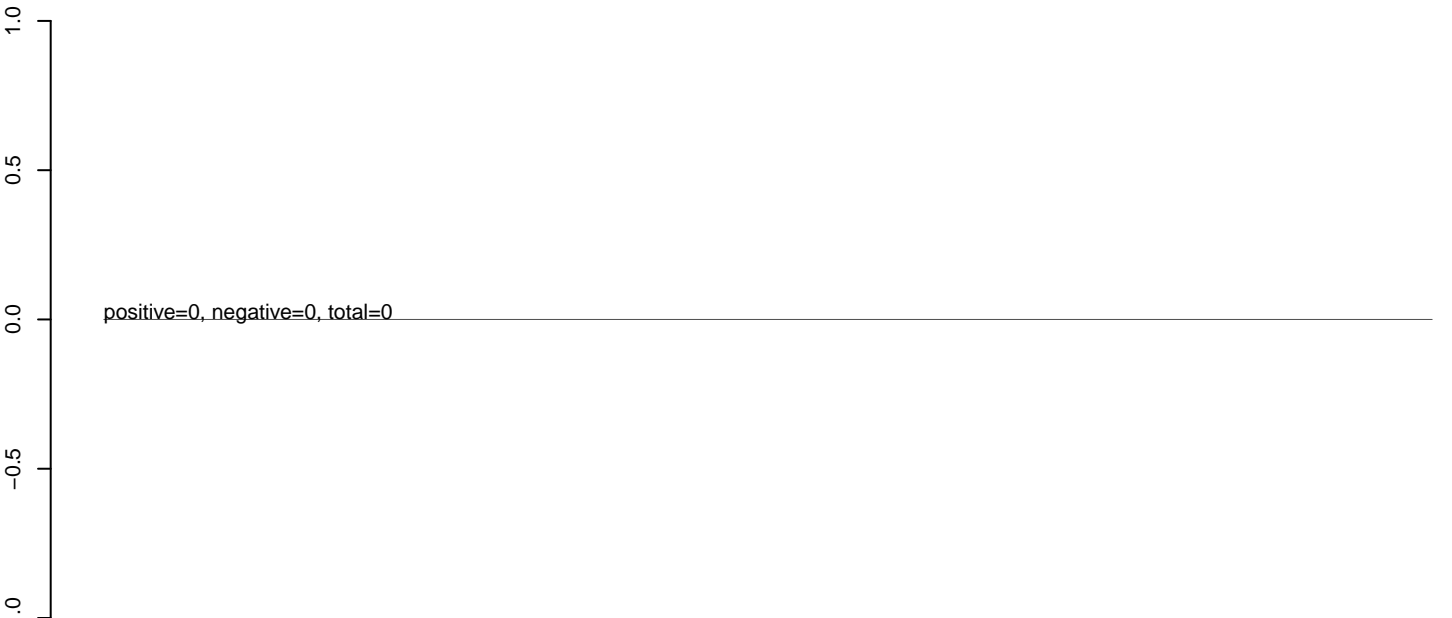


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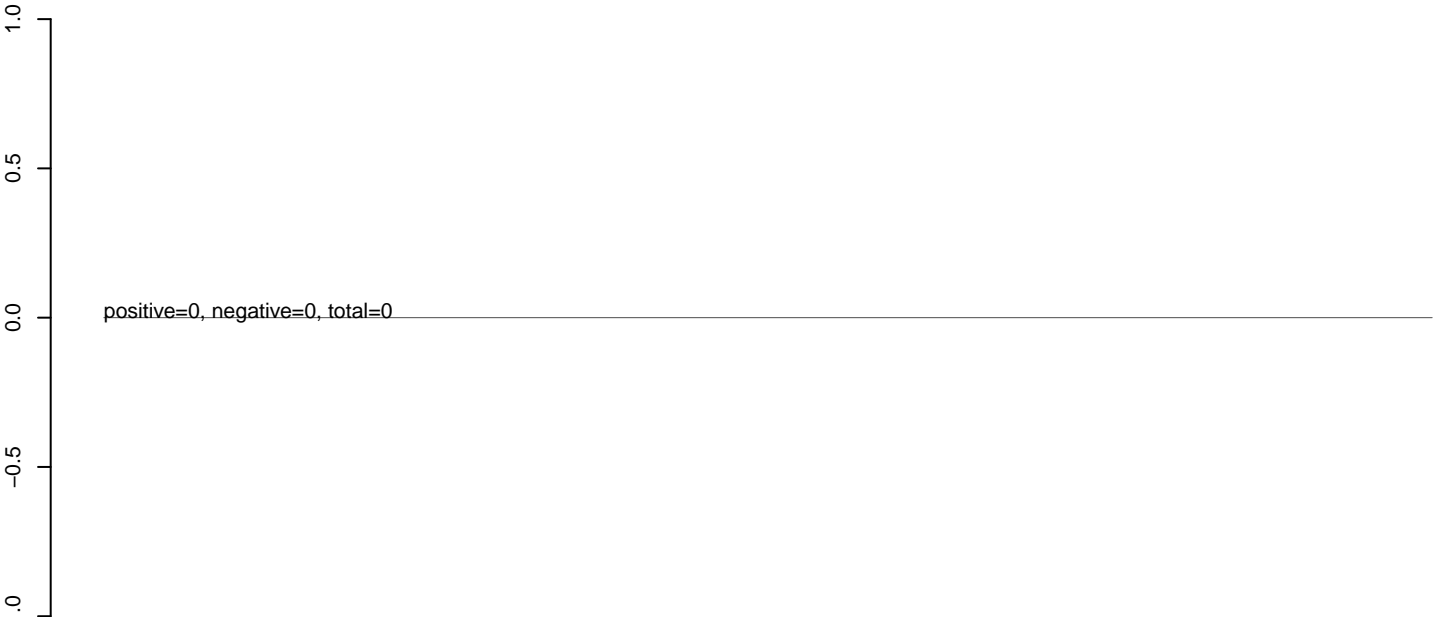


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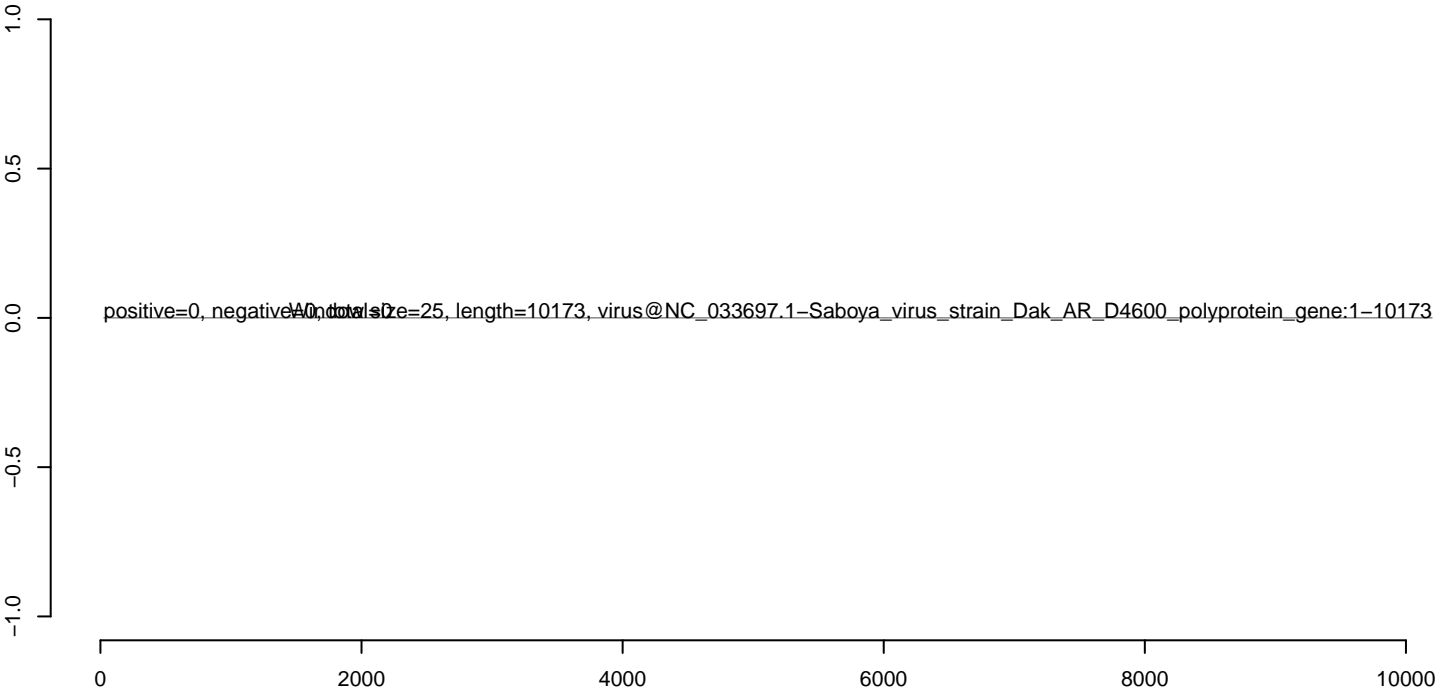
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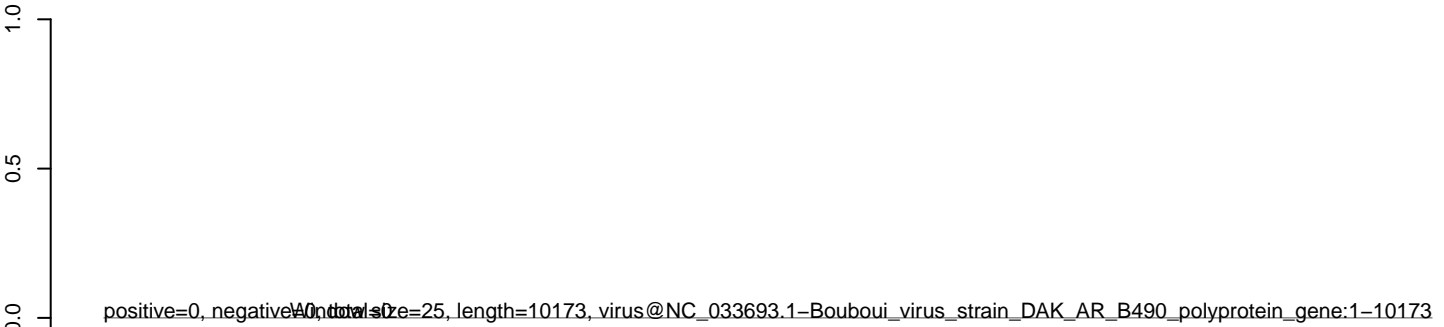
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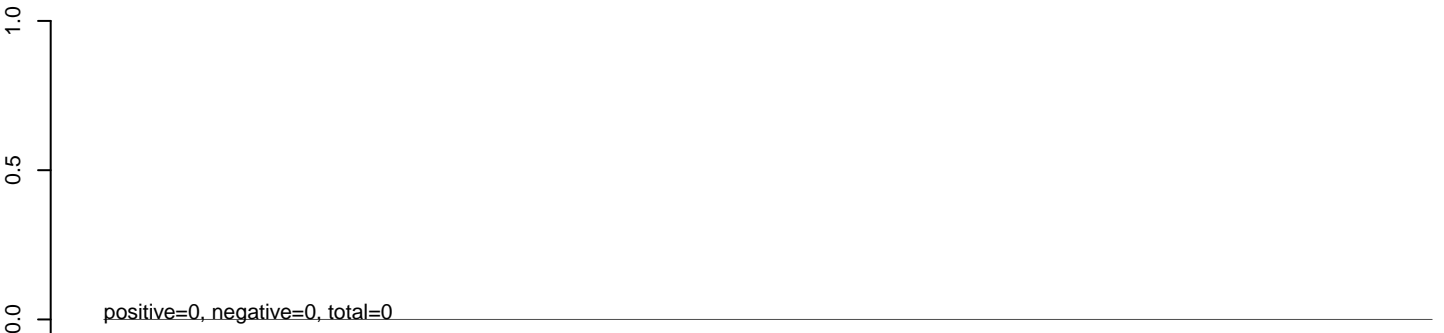
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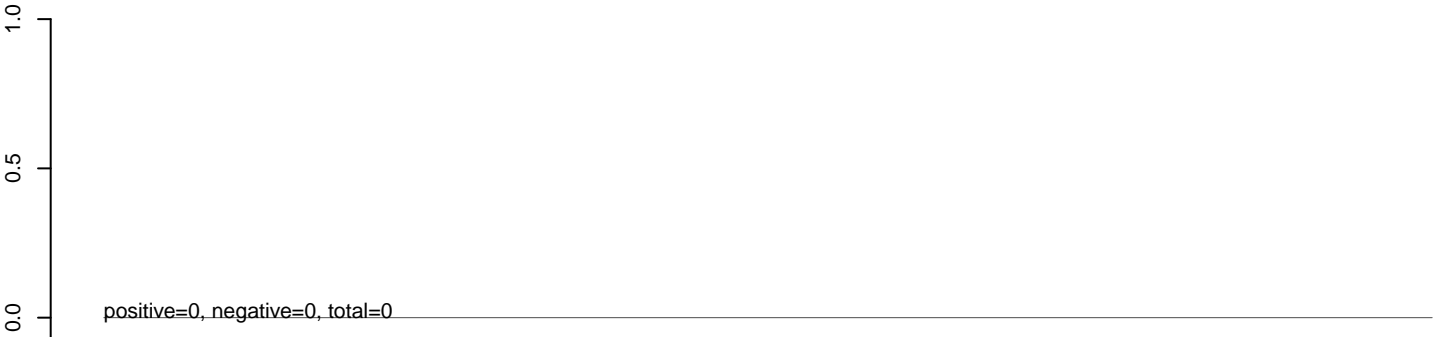
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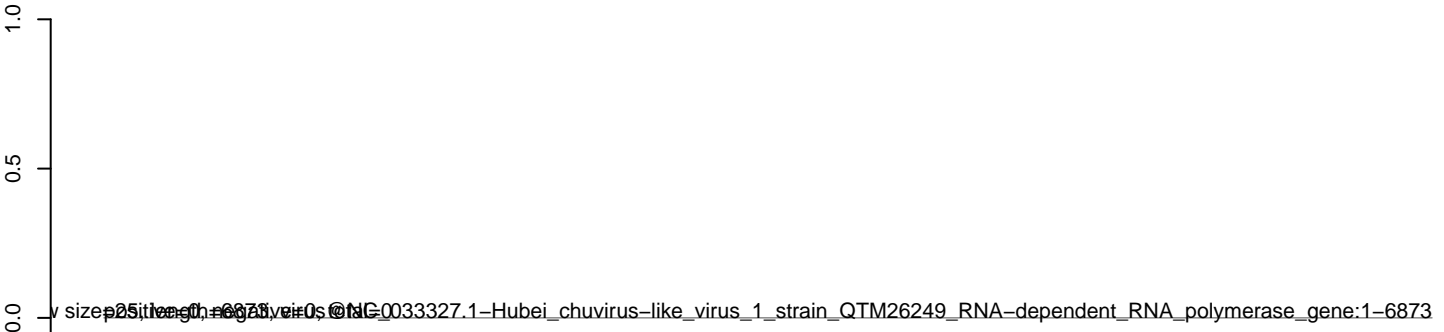
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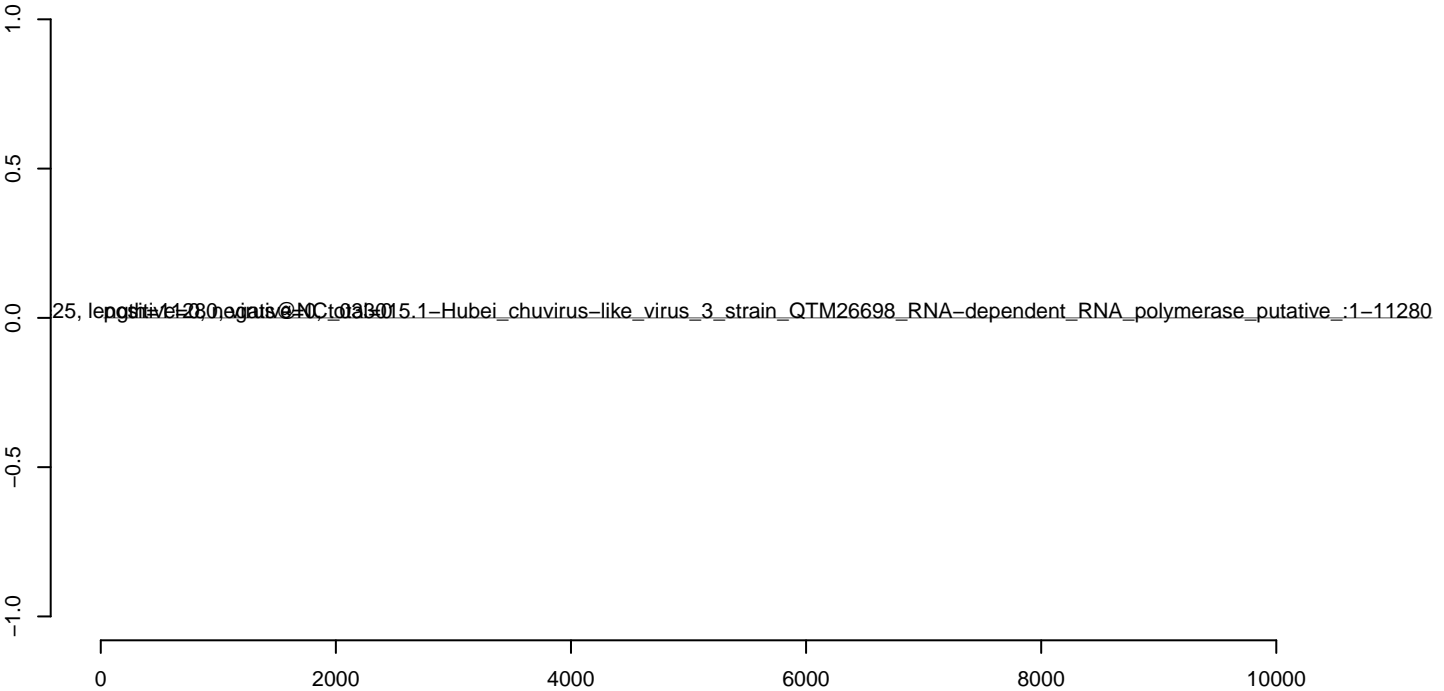
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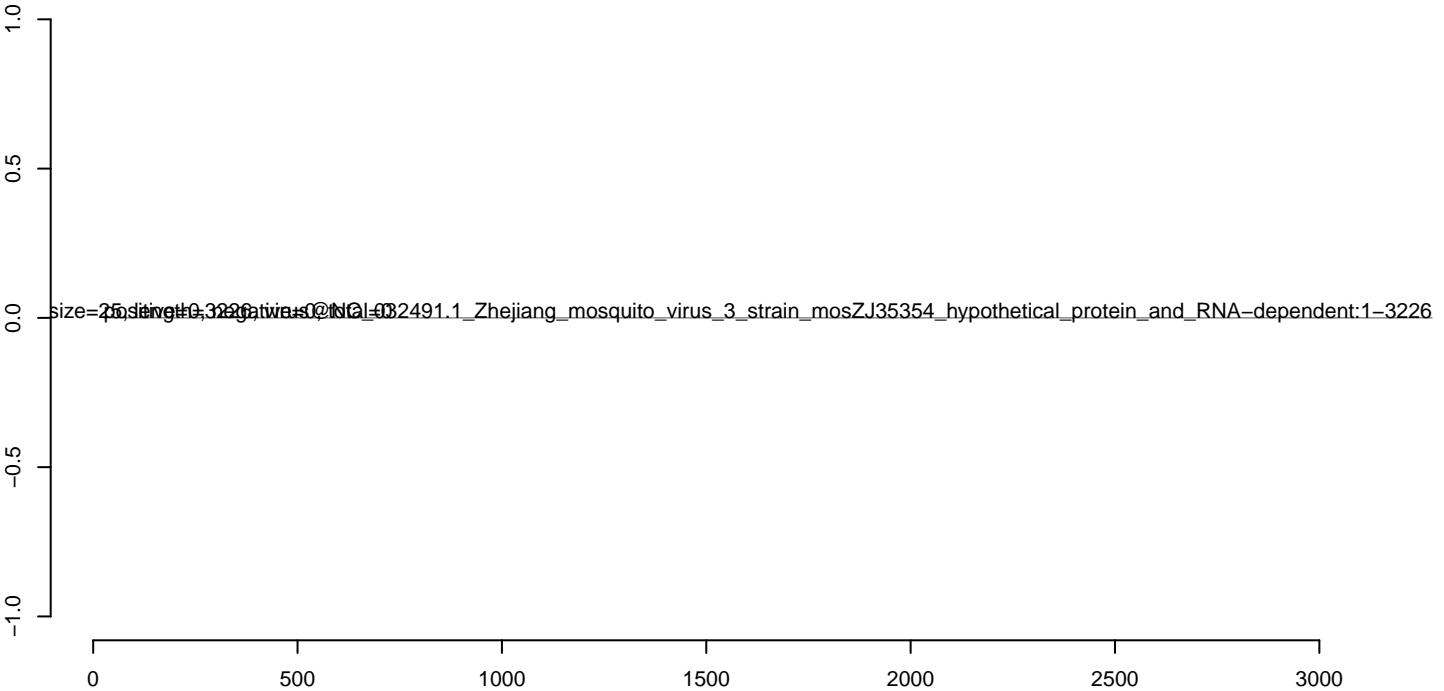
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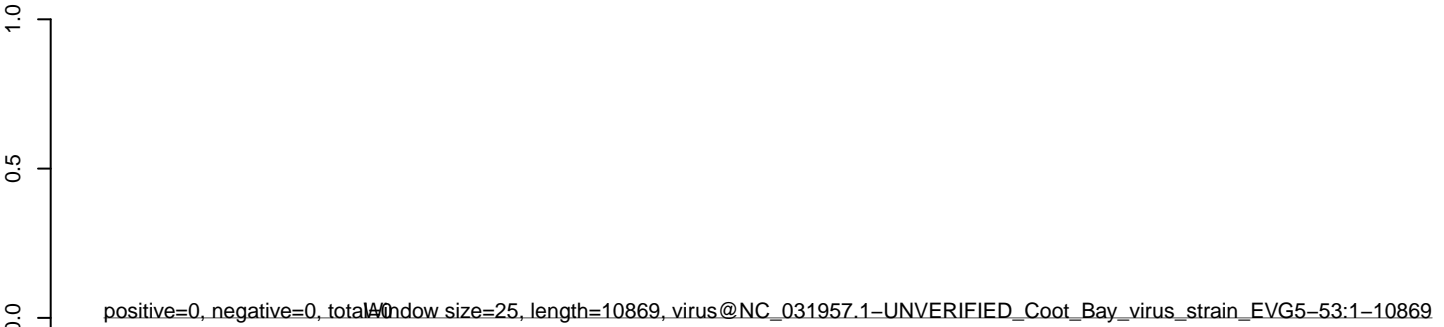
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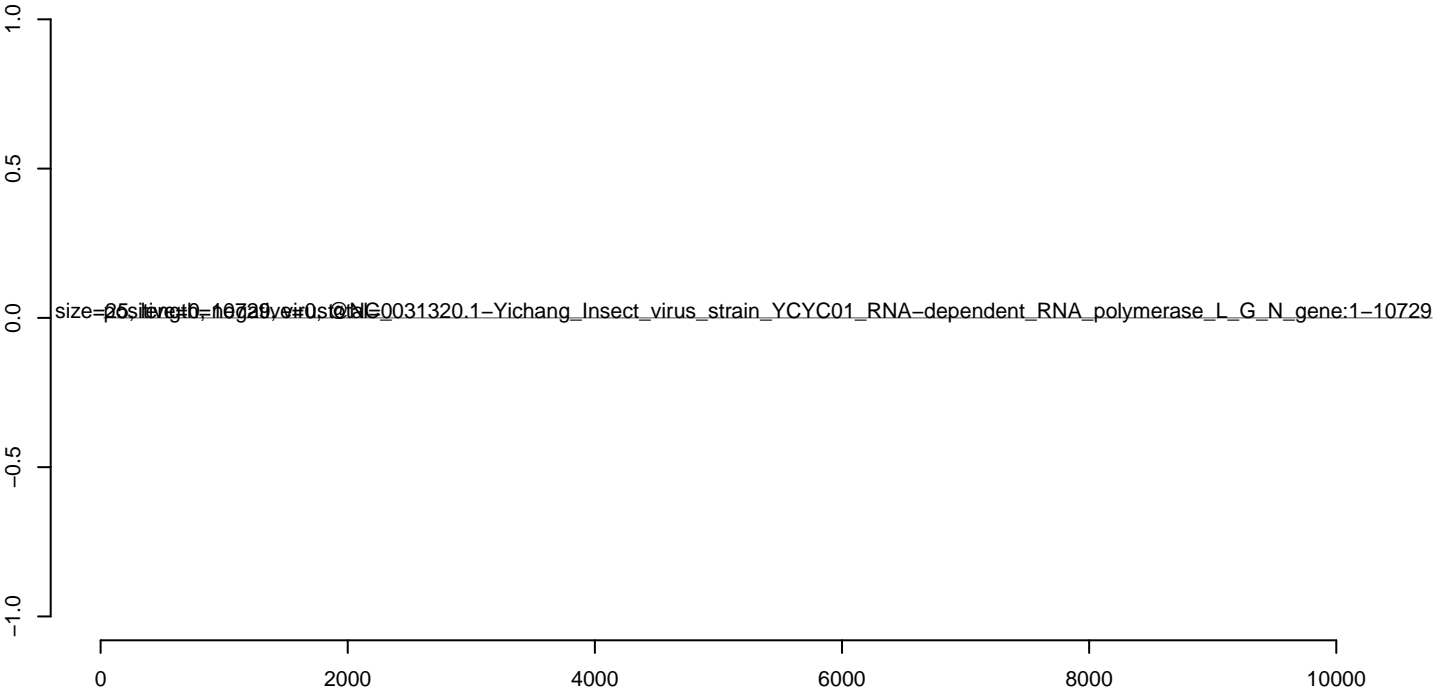
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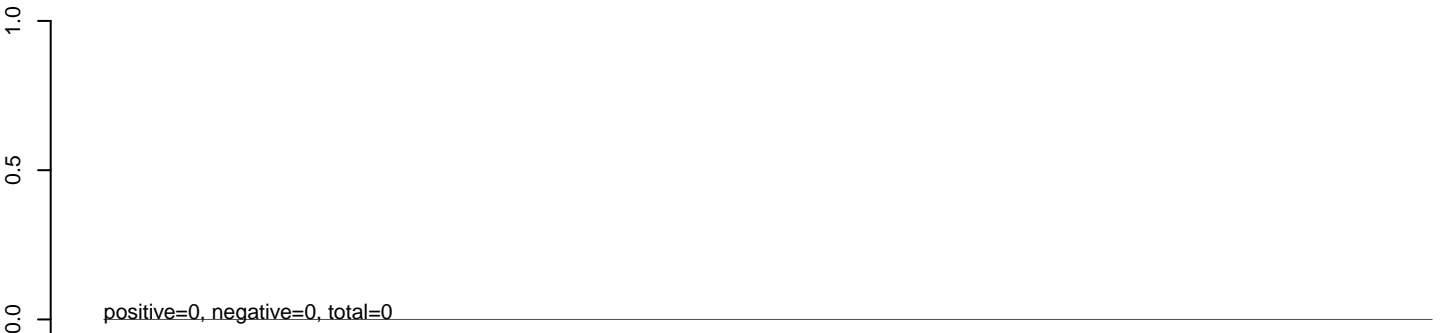
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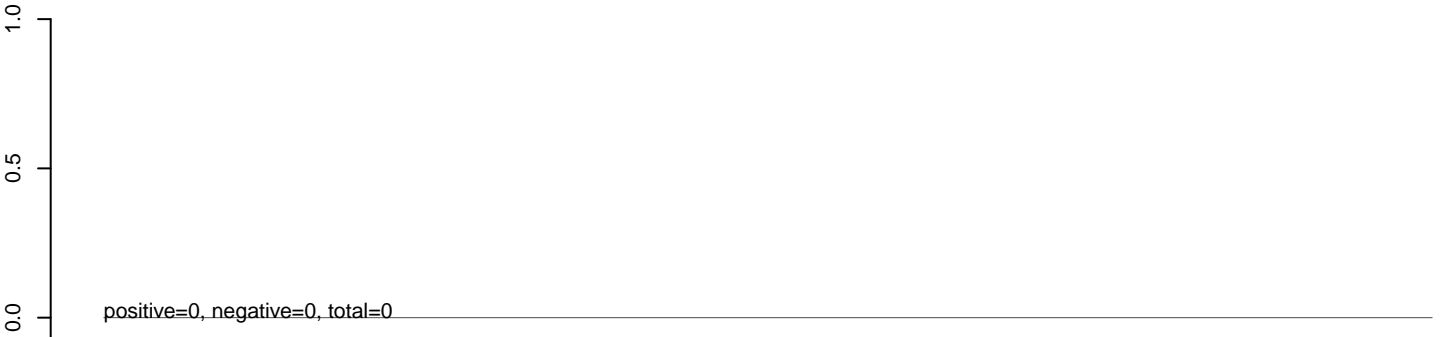
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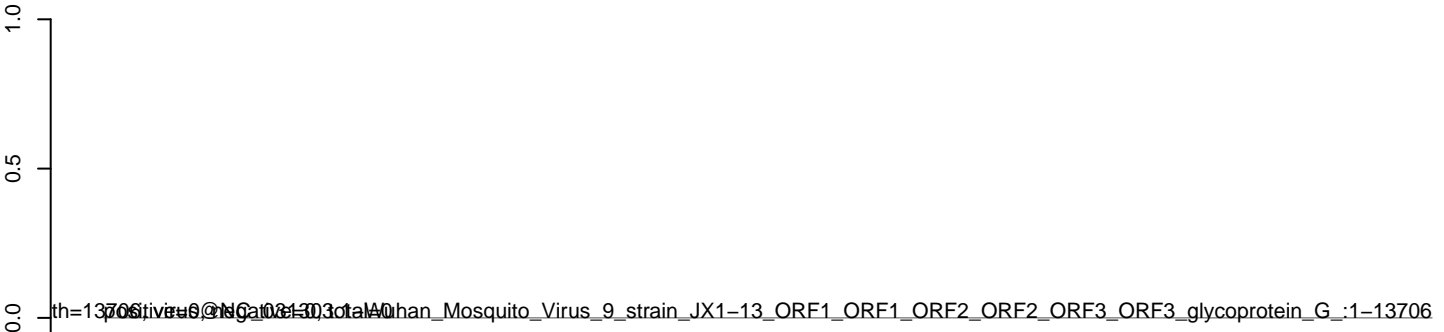
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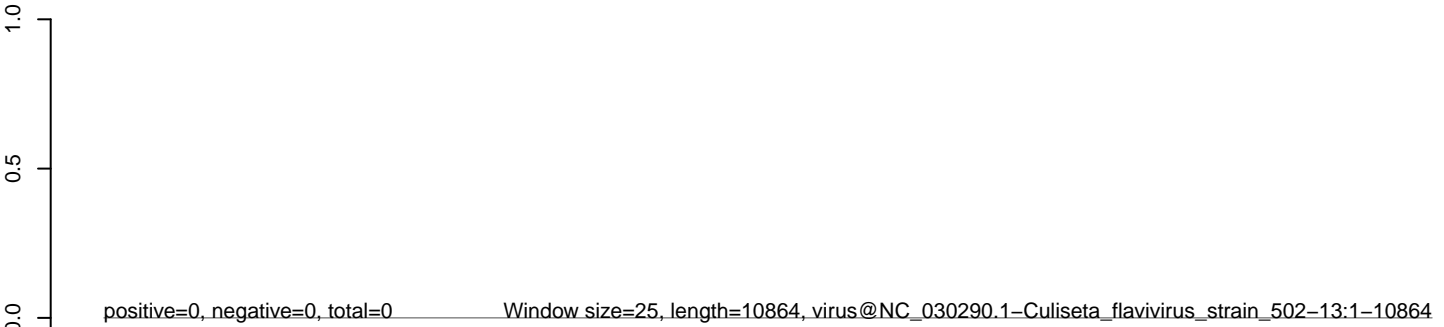
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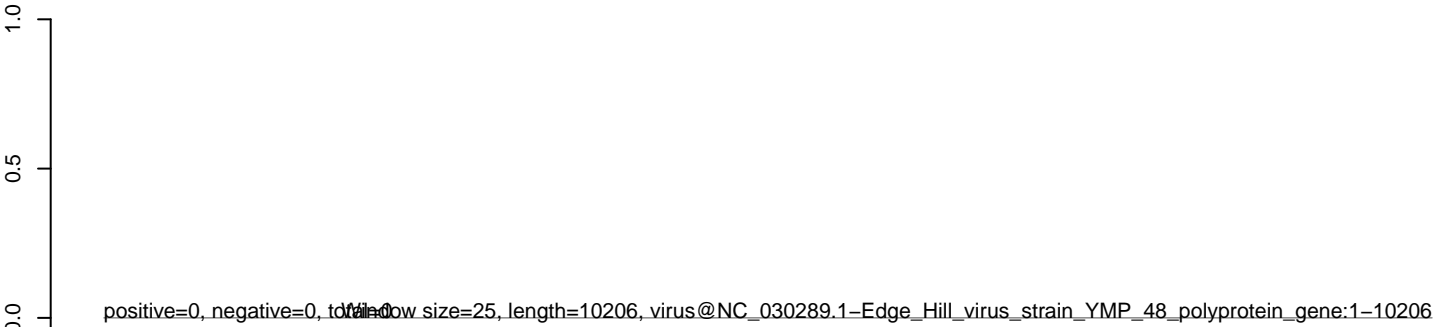
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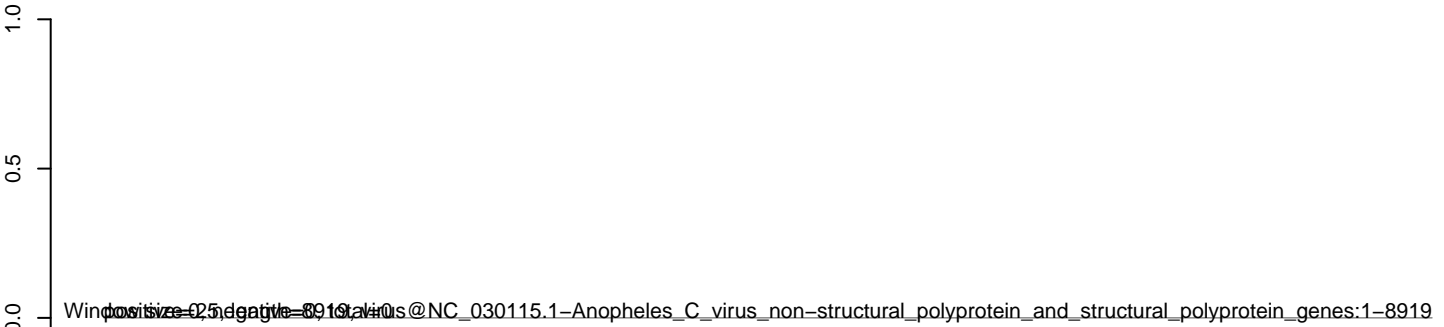
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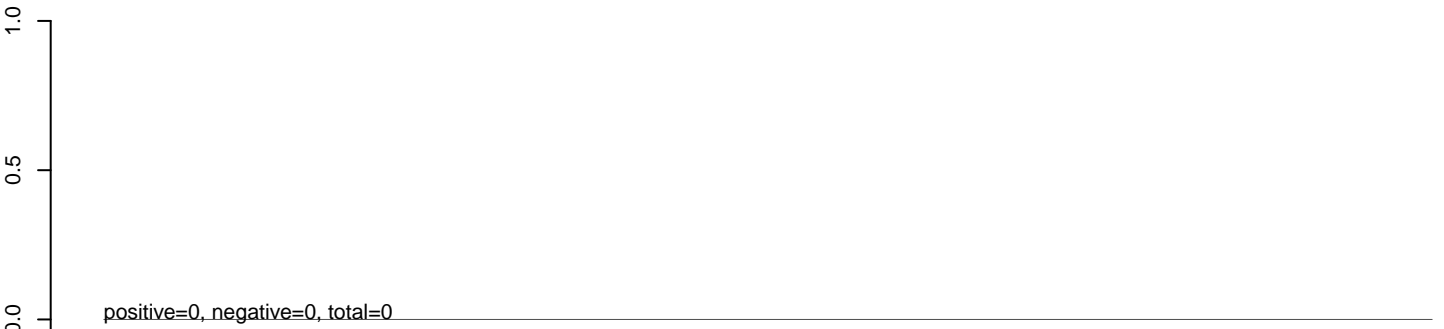


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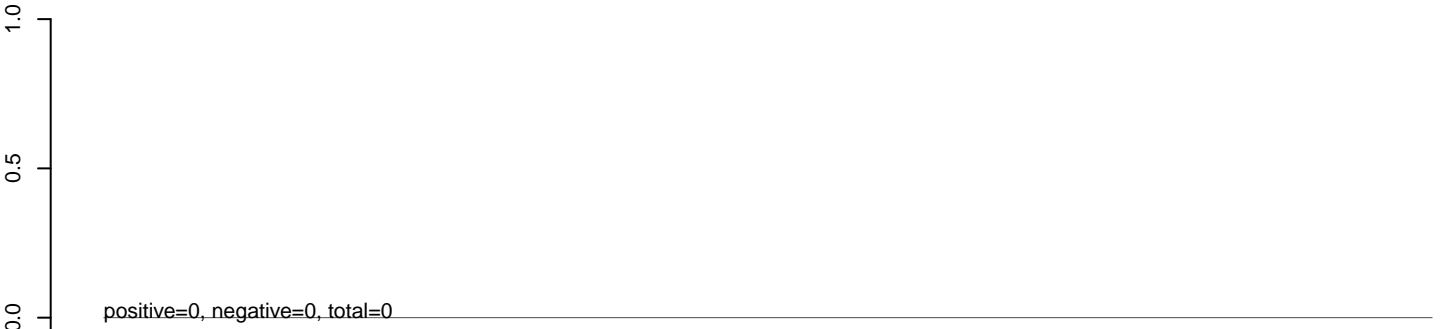


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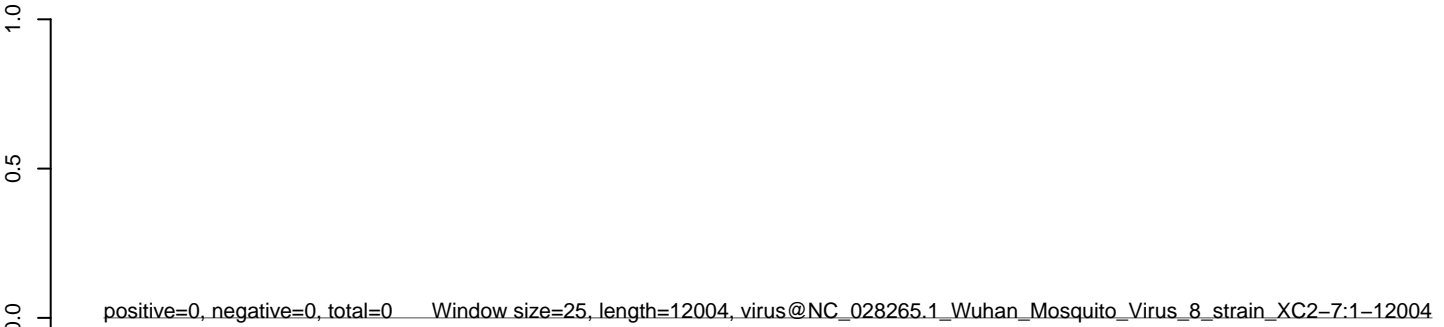
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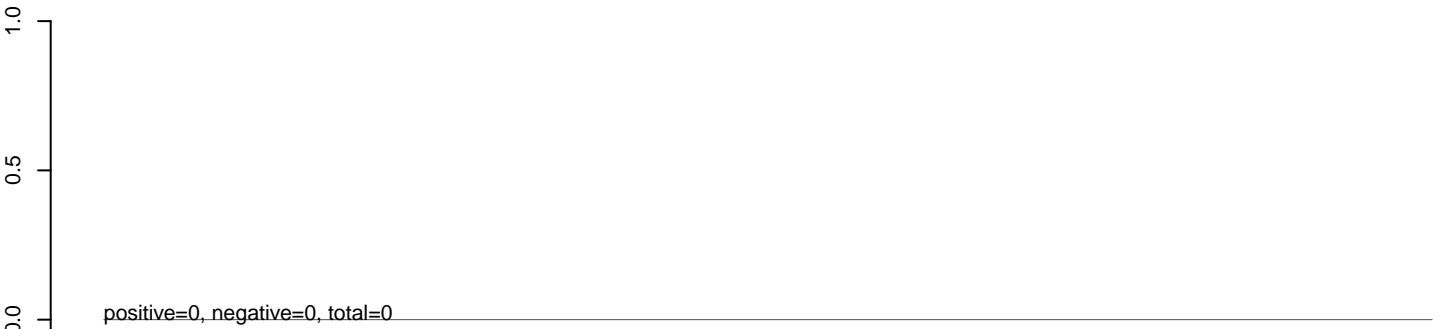


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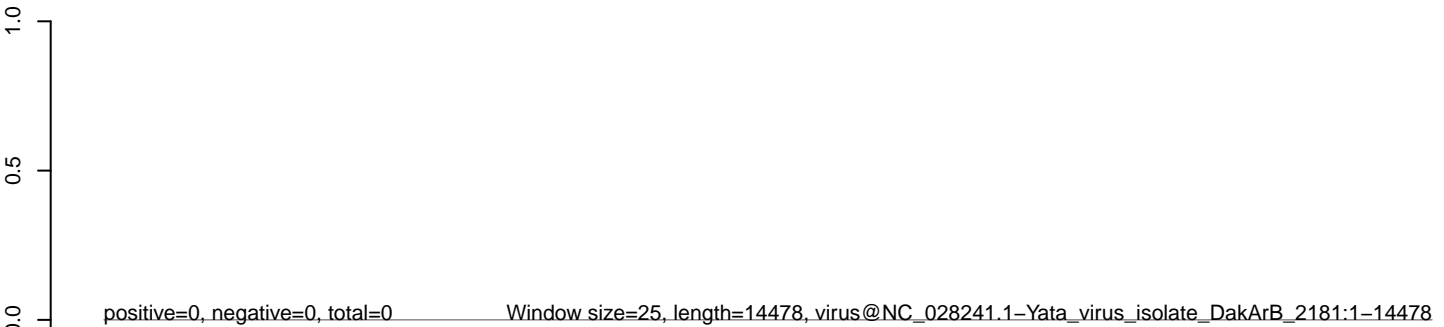
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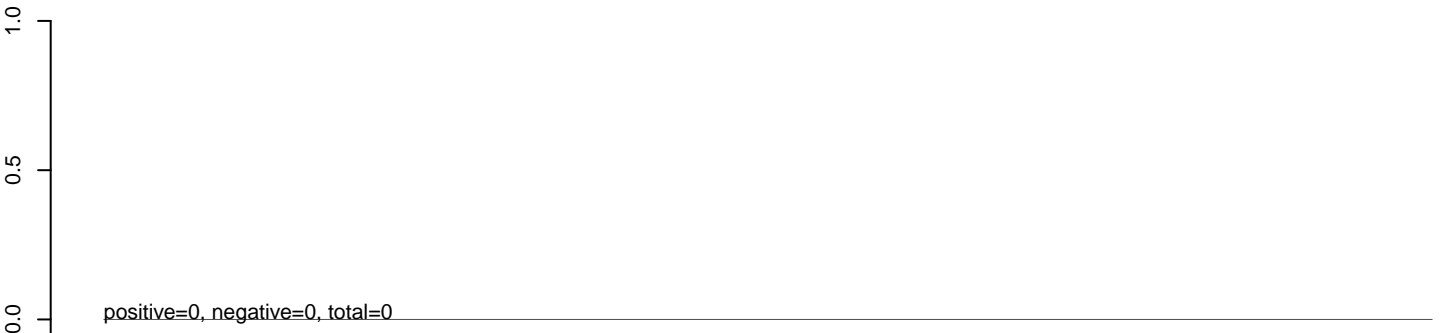
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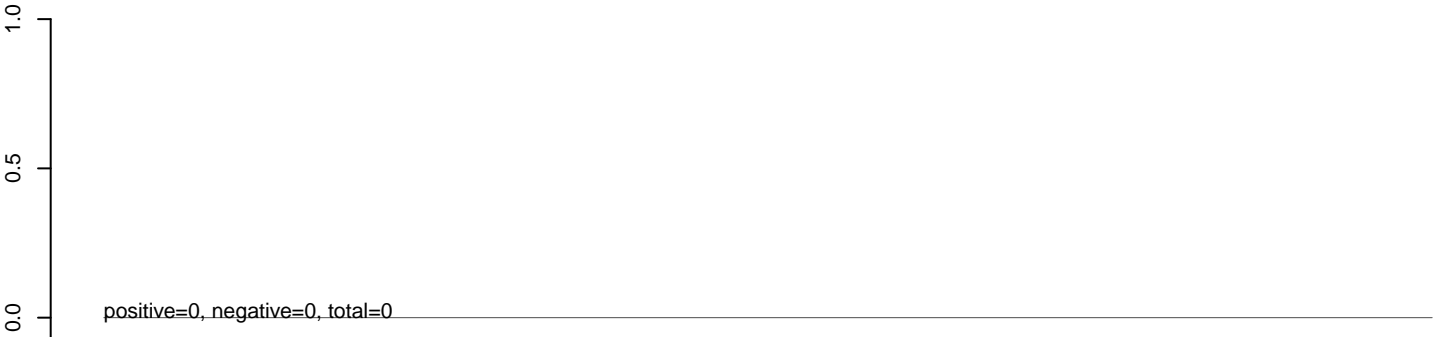
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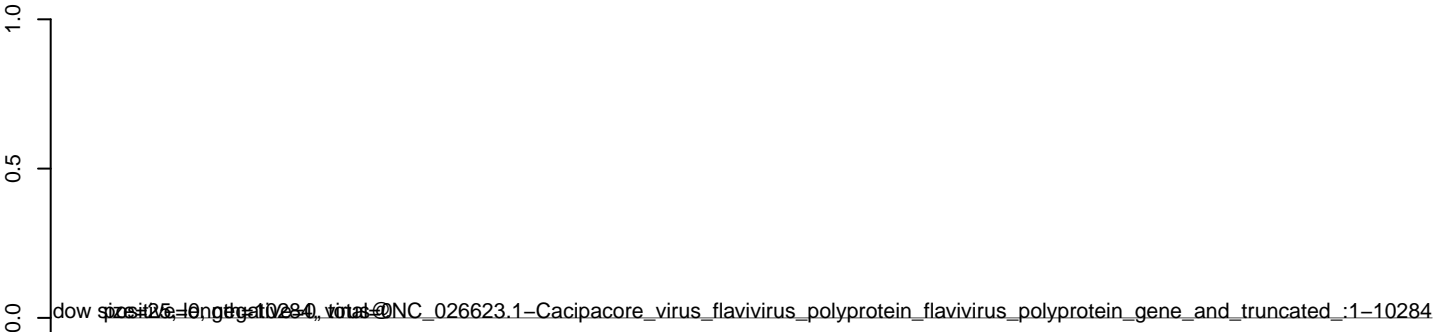
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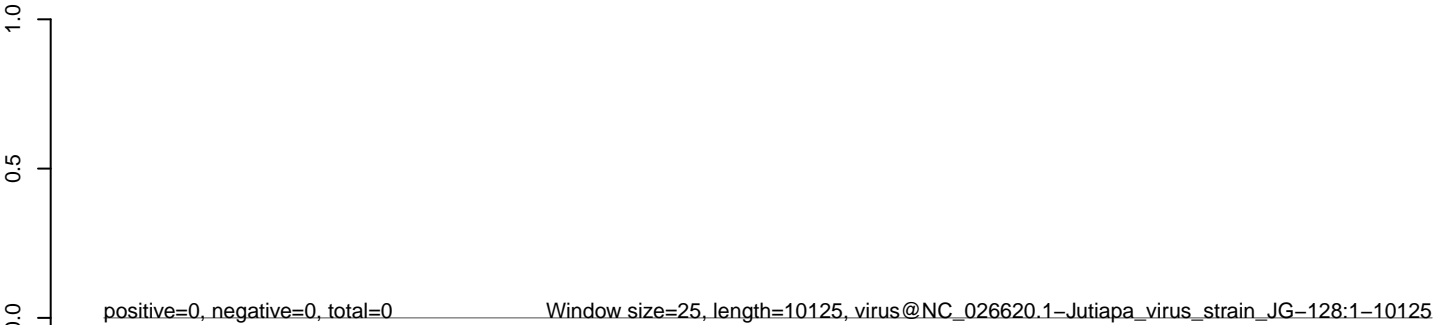
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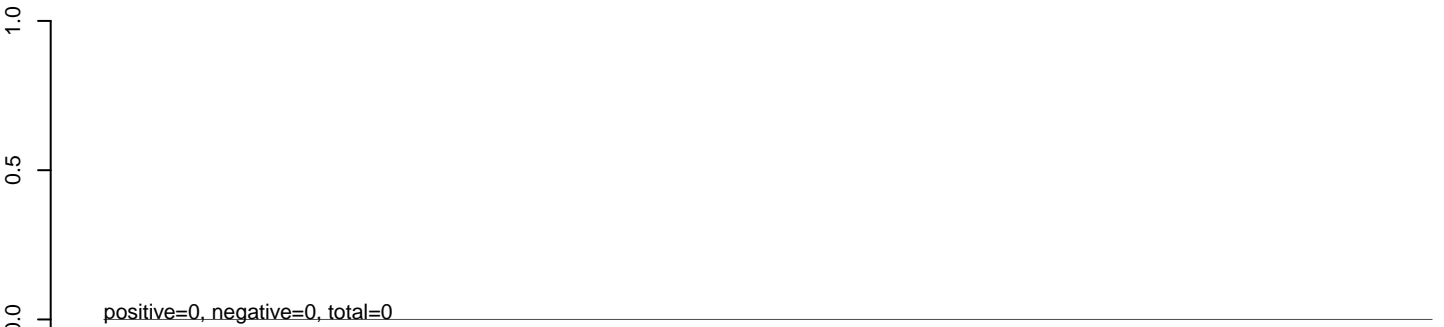
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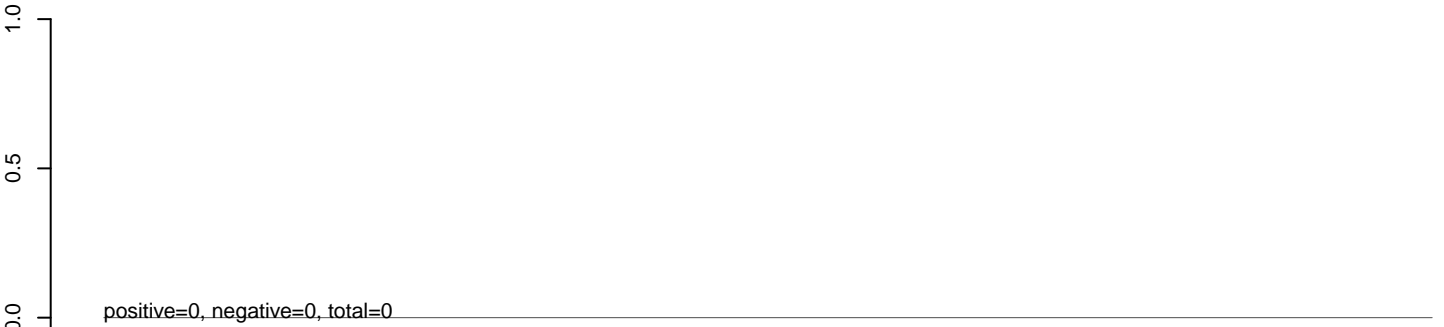
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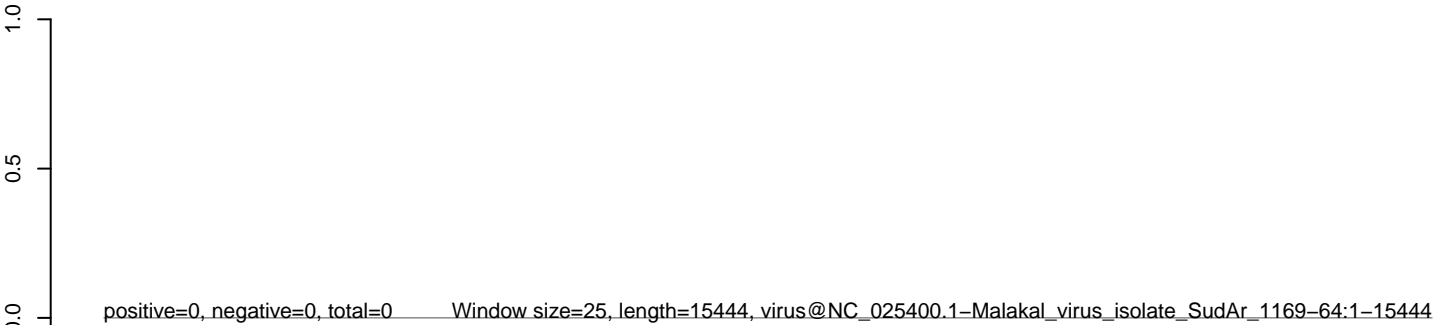
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AeAeg_Aag2.SINV.GFP.rep



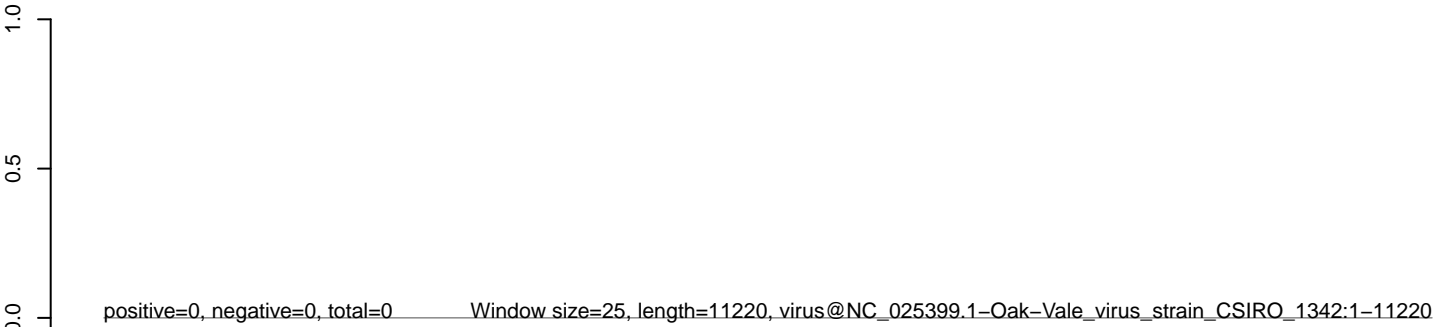
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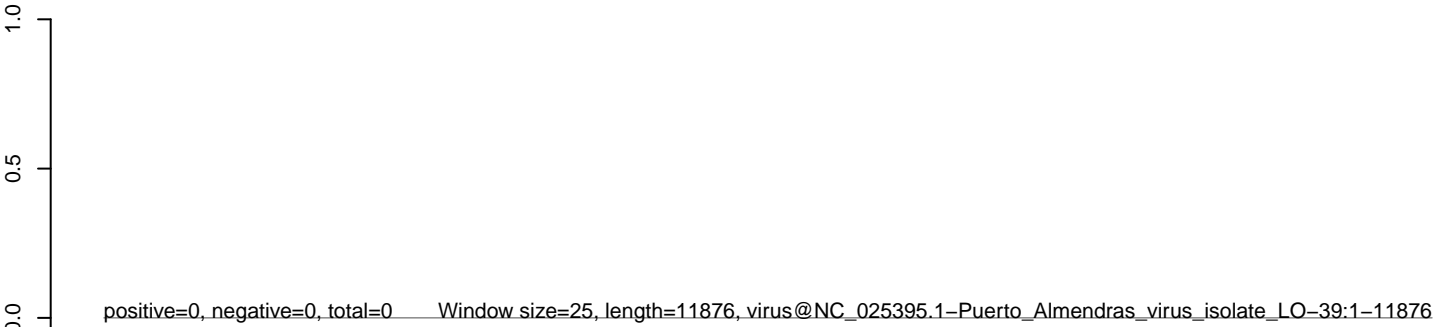
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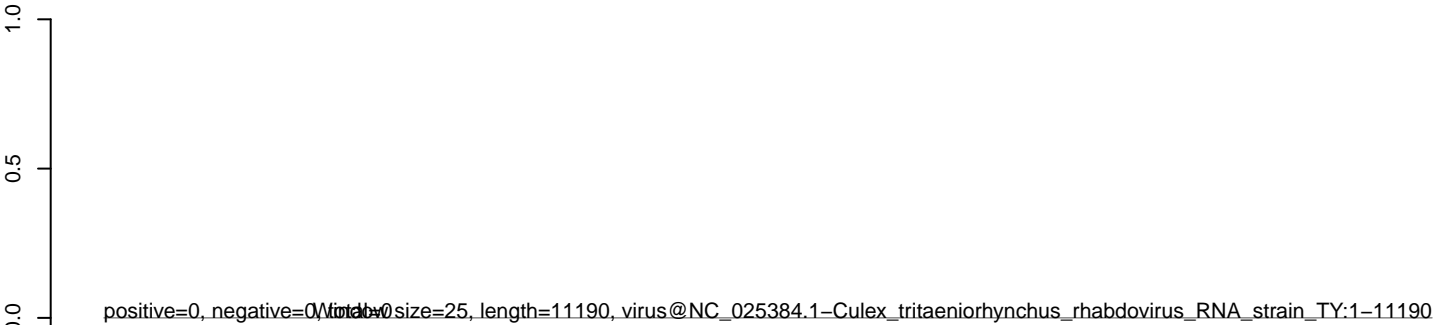
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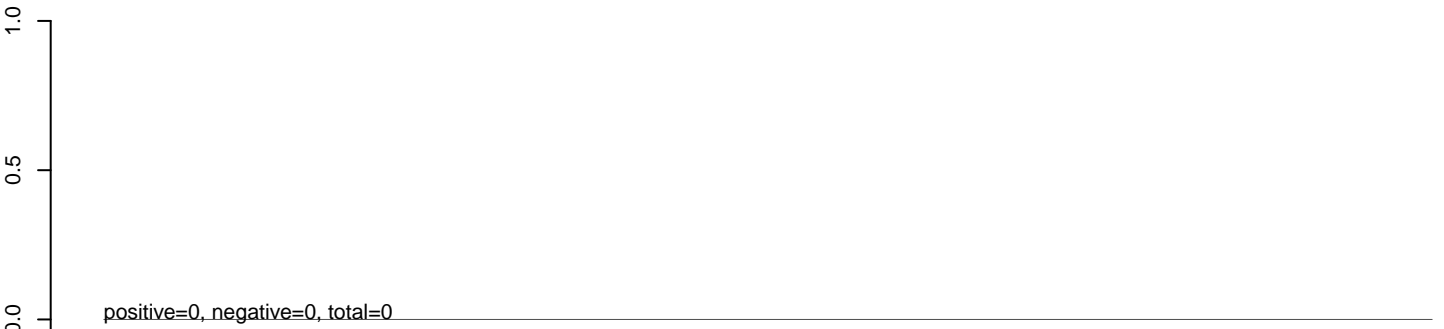


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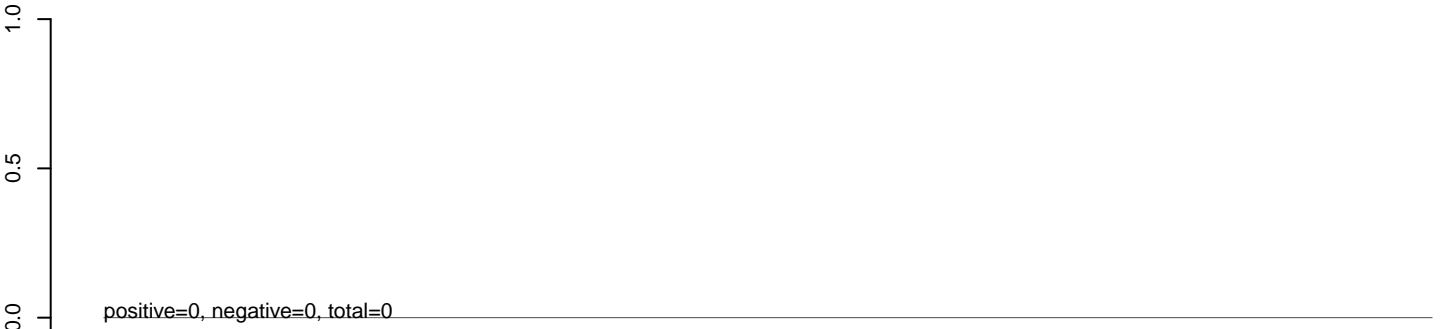


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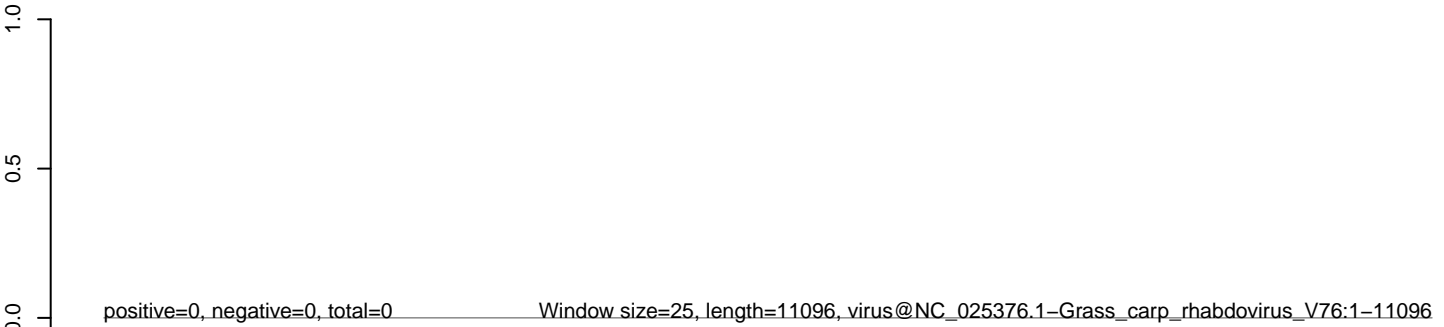
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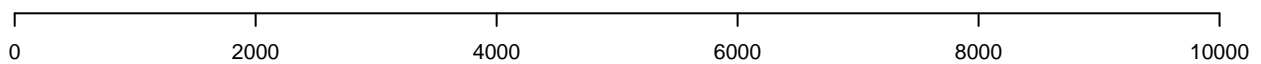
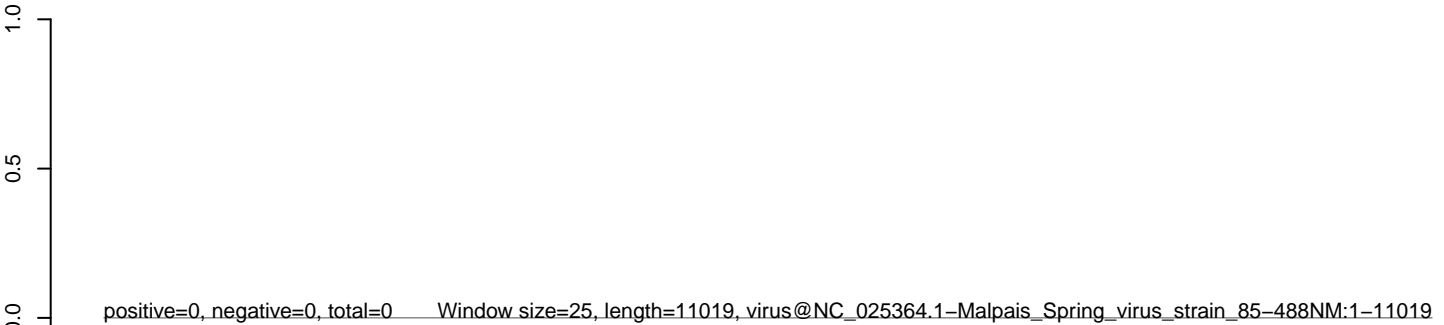
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AeAeg_Aag2.SINV.GFP.24_35.rep



AeAeg_Aag2.SINV.GFP.rep



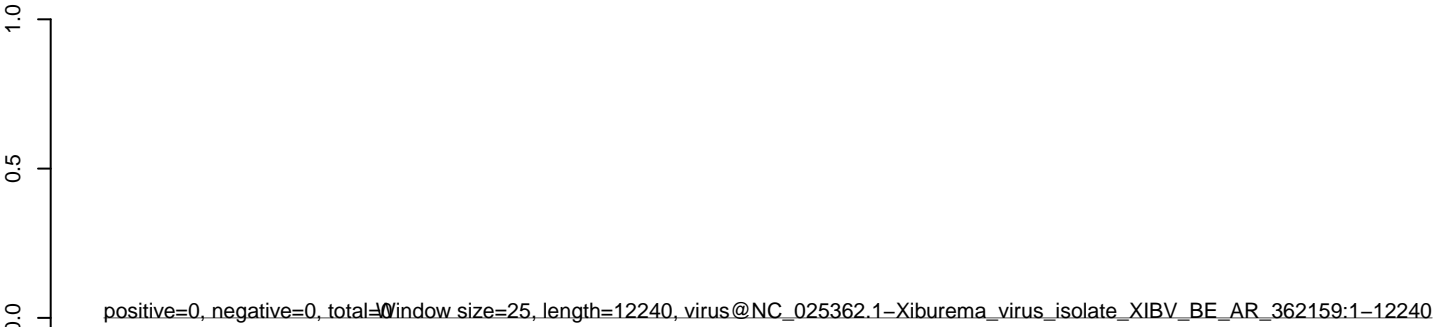
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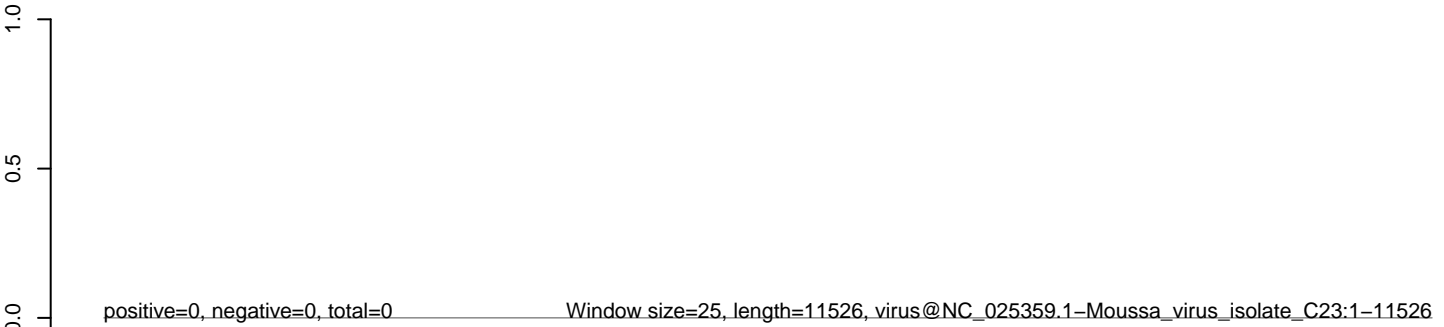
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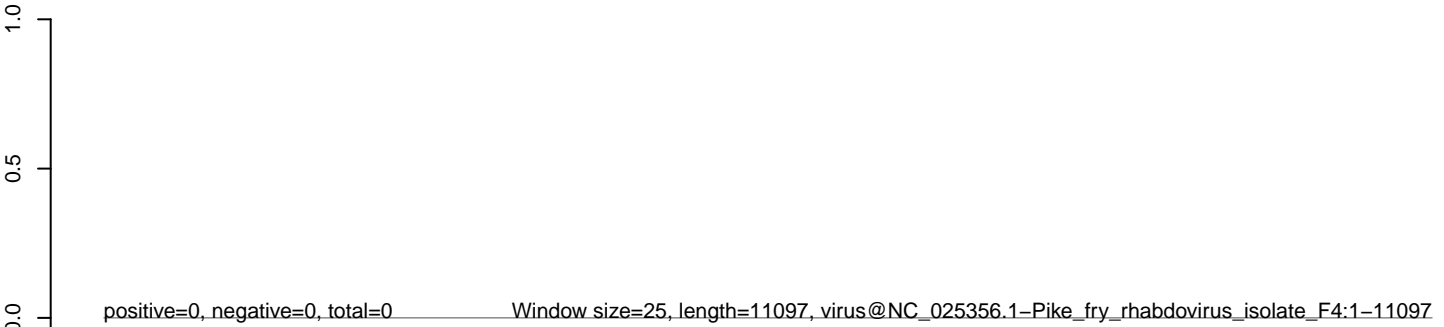
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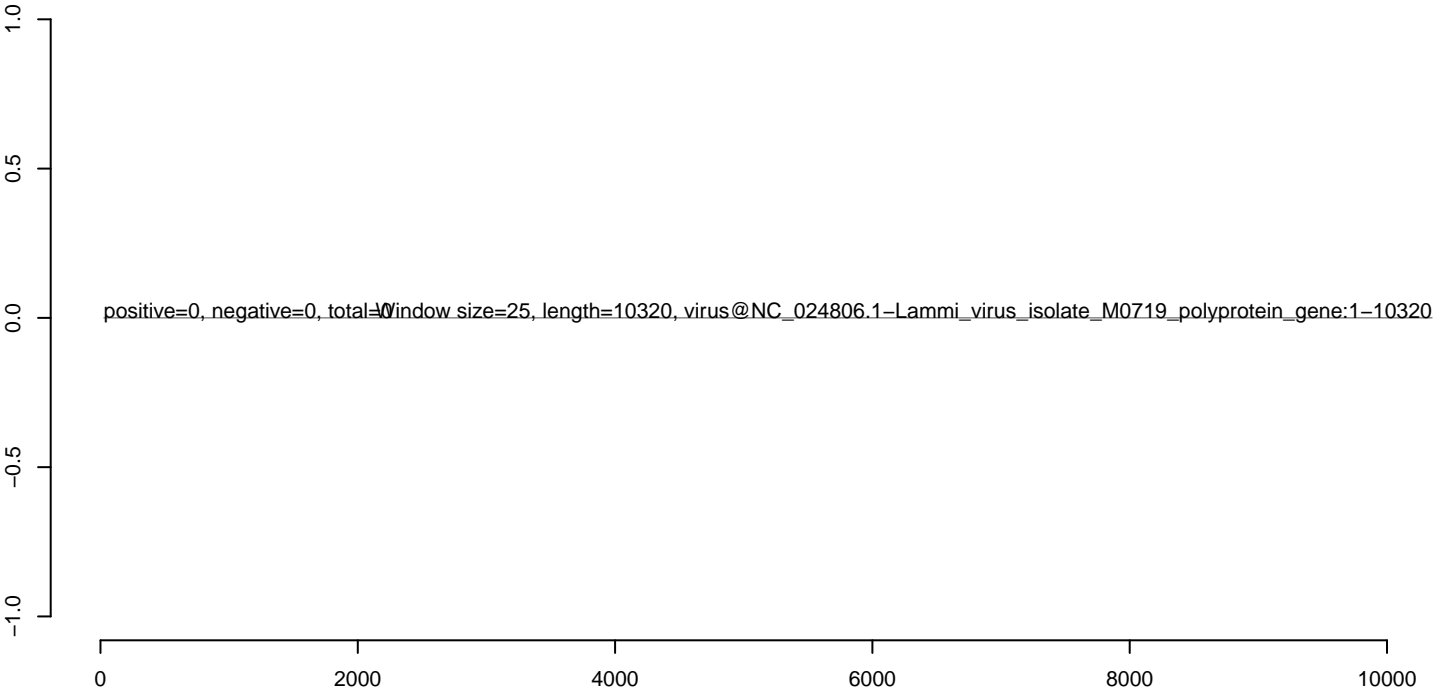
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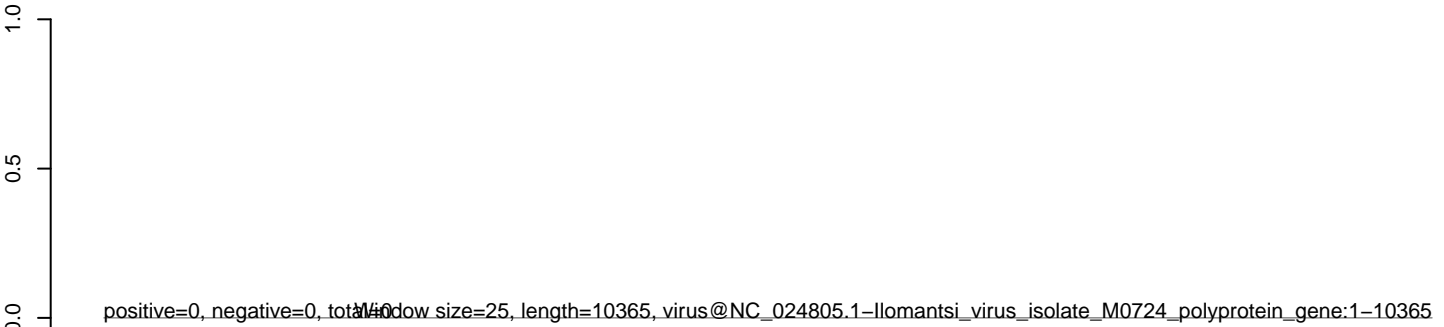
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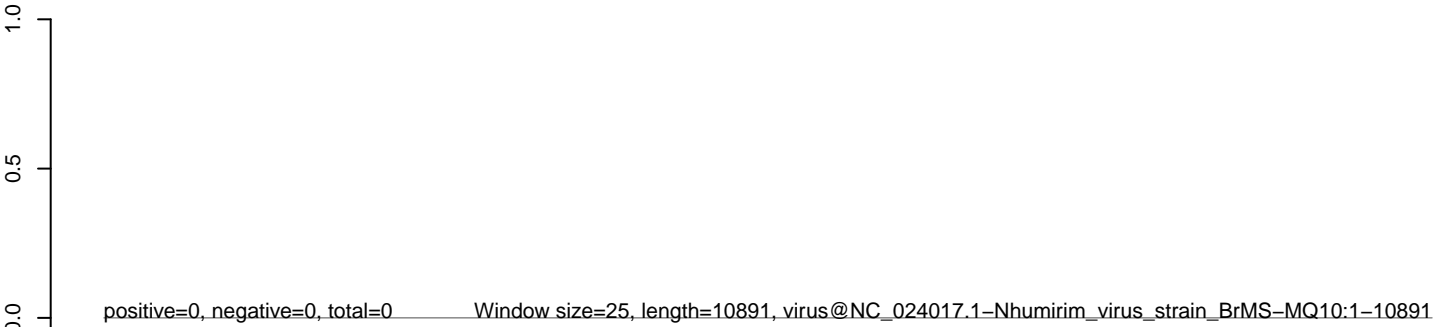
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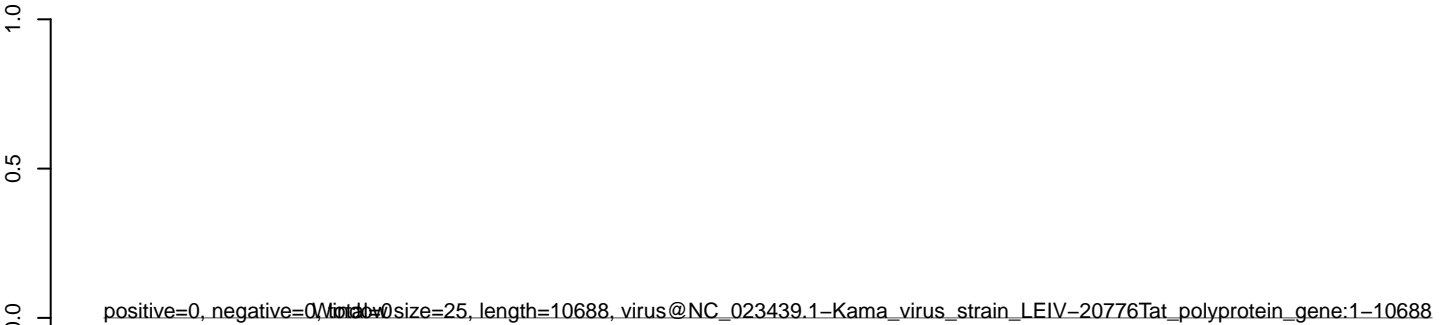
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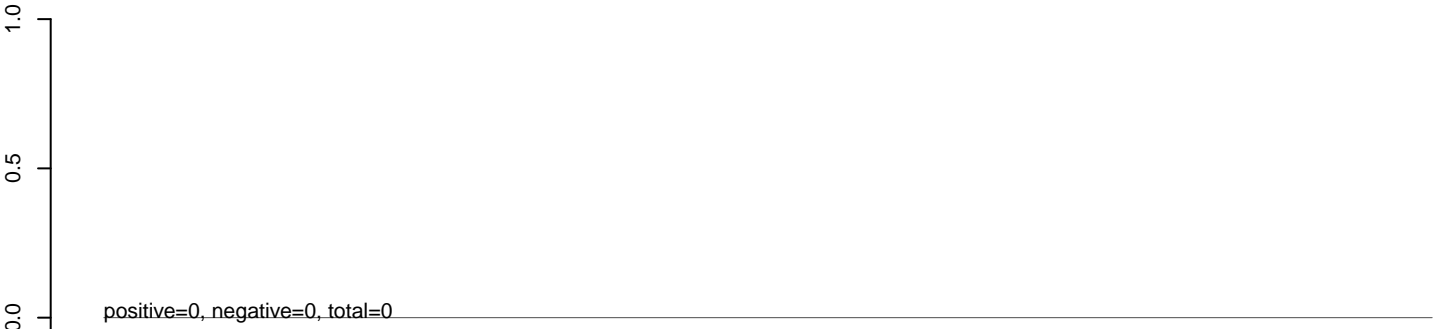
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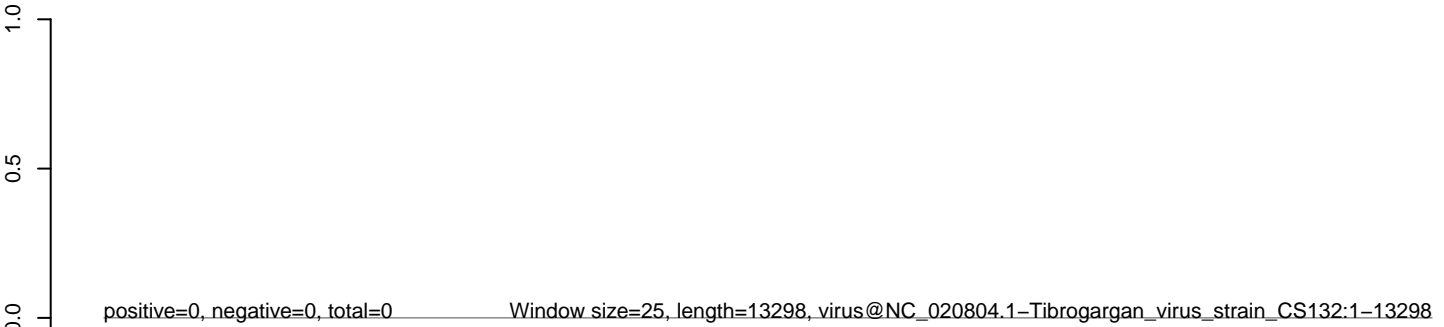
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0 2000 4000 6000 8000 10000 12000

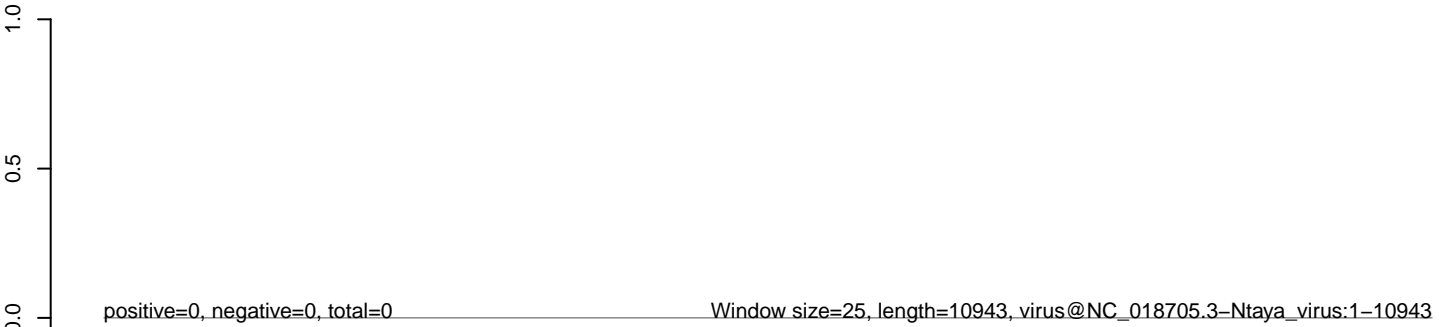
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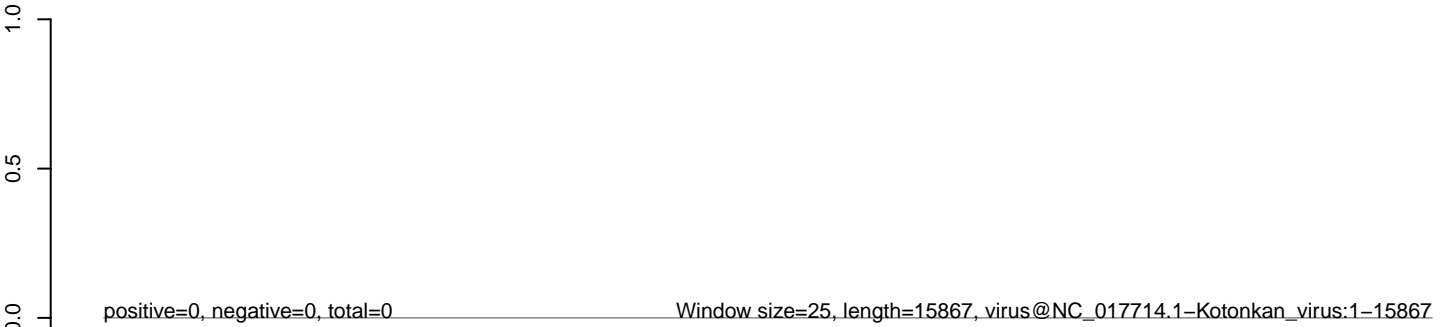
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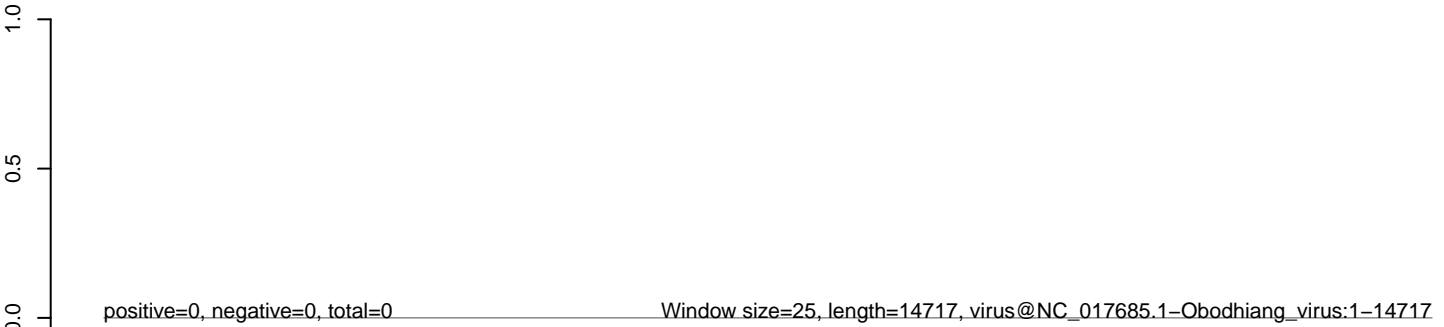
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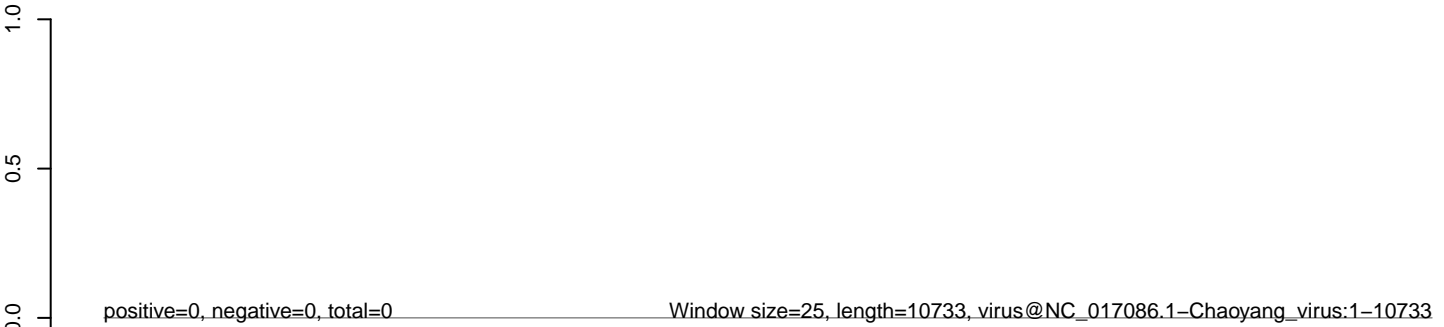
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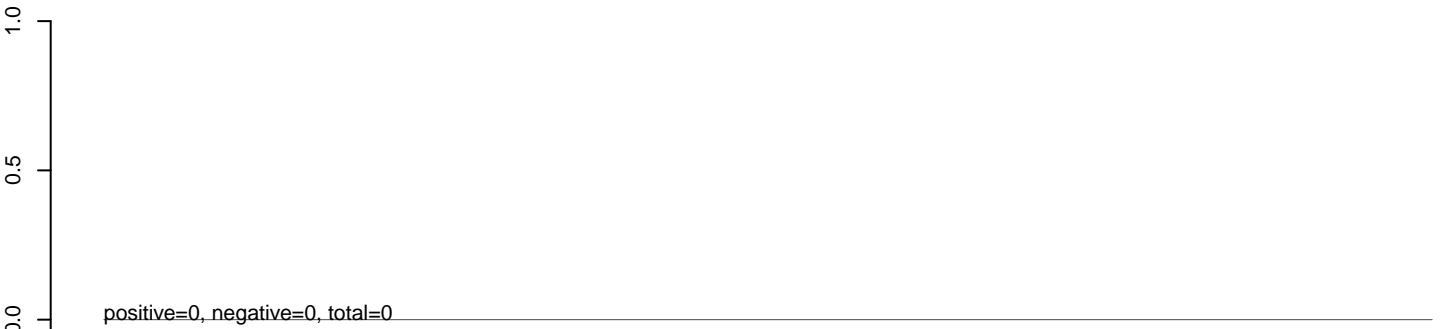


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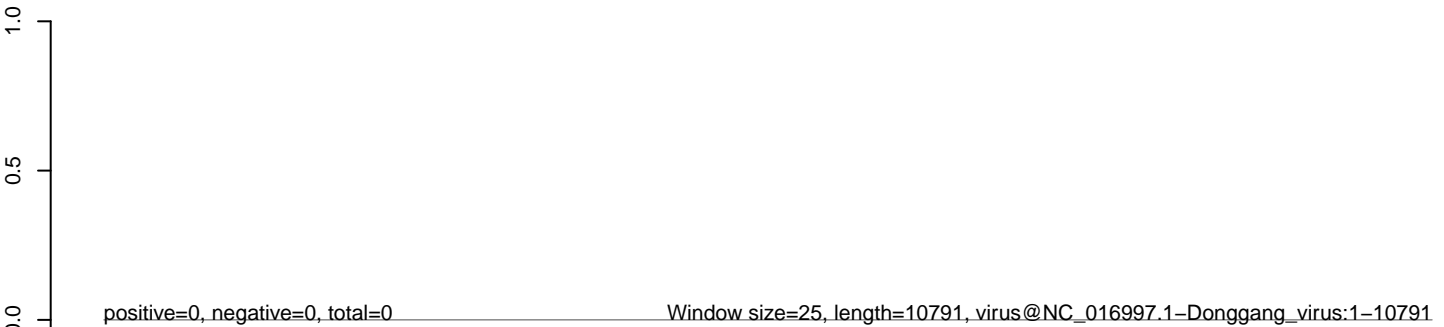
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AeAeg_Aag2.SINV.GFP.rep



0 2000 4000 6000 8000 10000

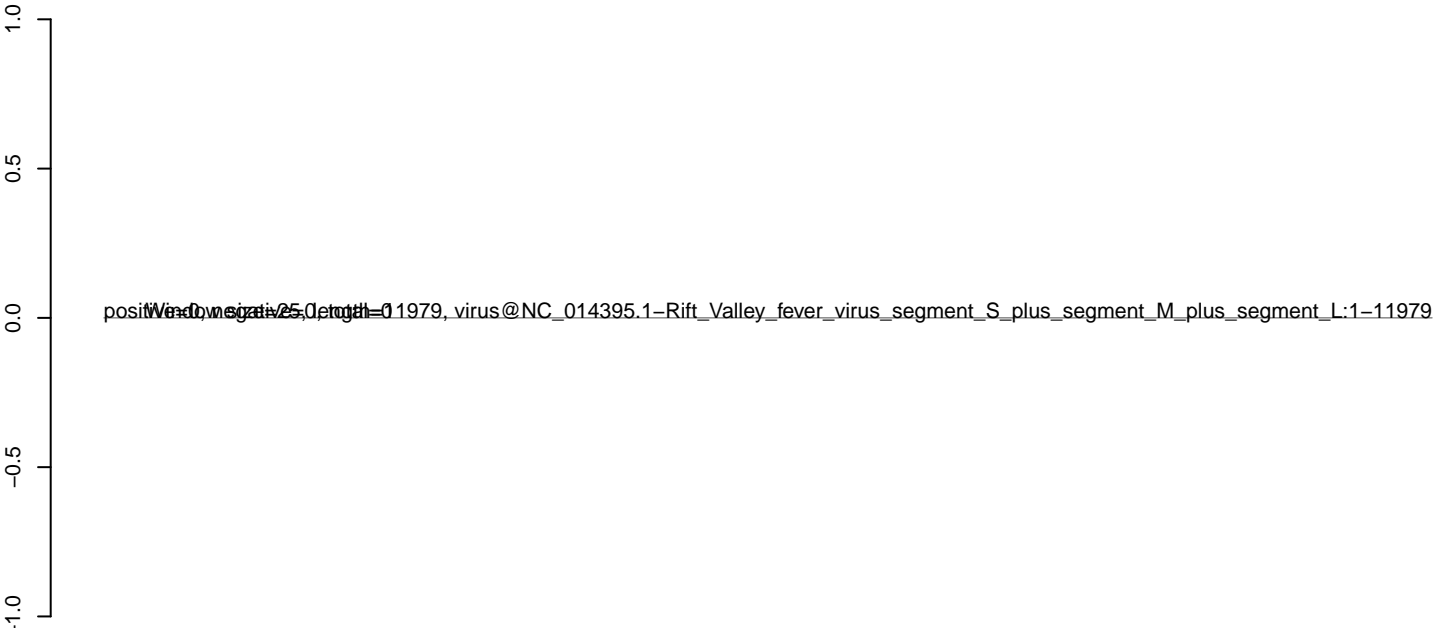
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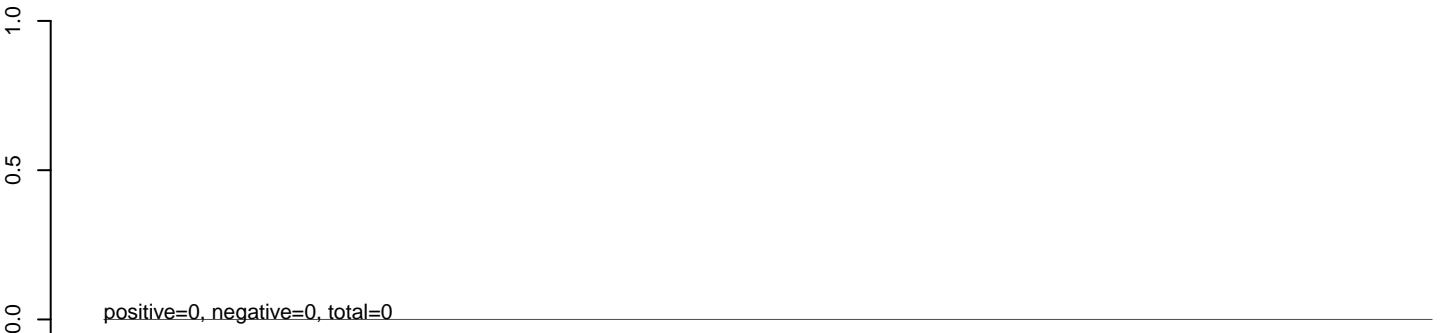
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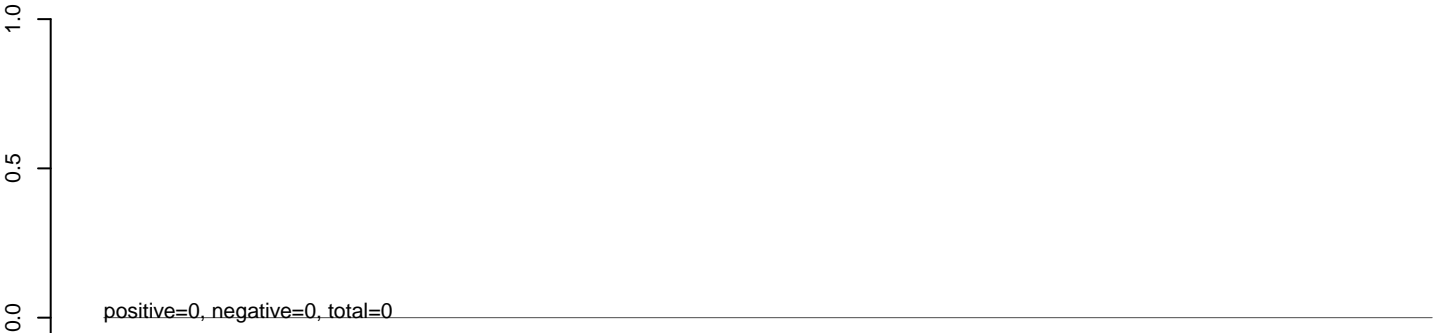
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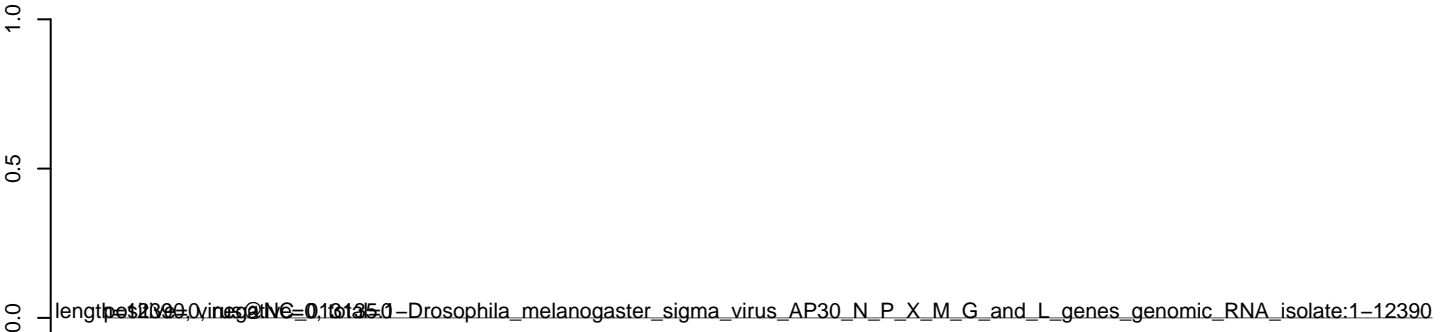
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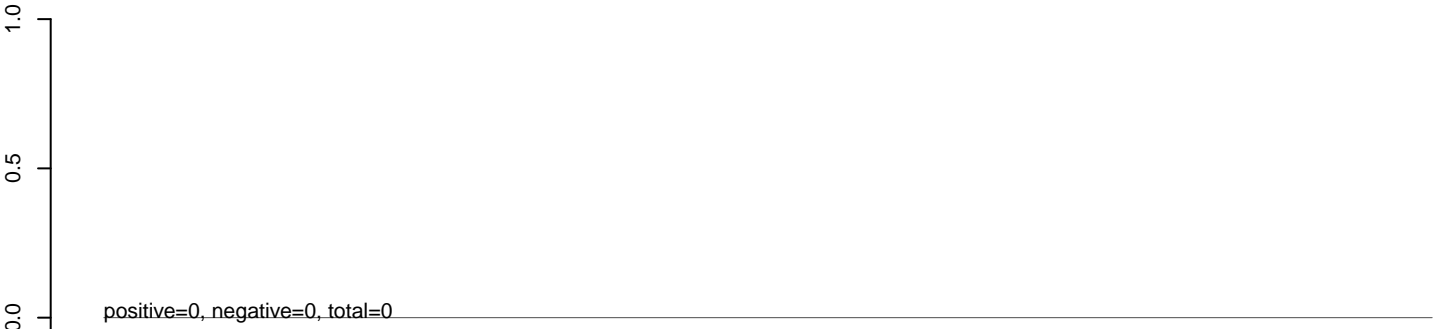
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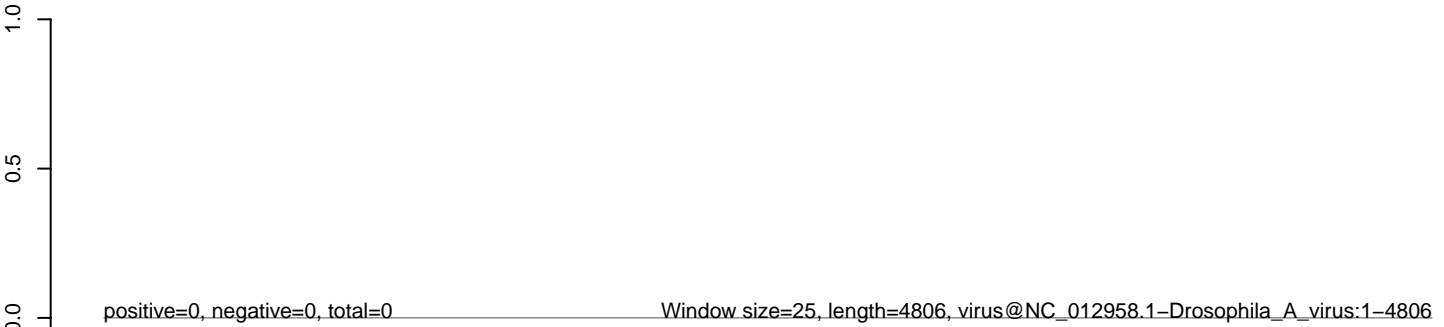
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AeAeg_Aag2.SINV.GFP.rep



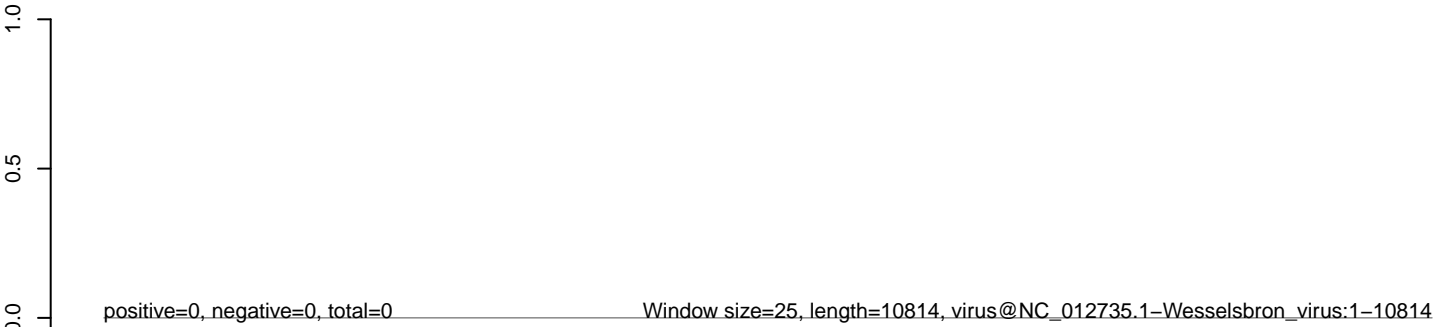
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0 2000 4000 6000 8000 10000

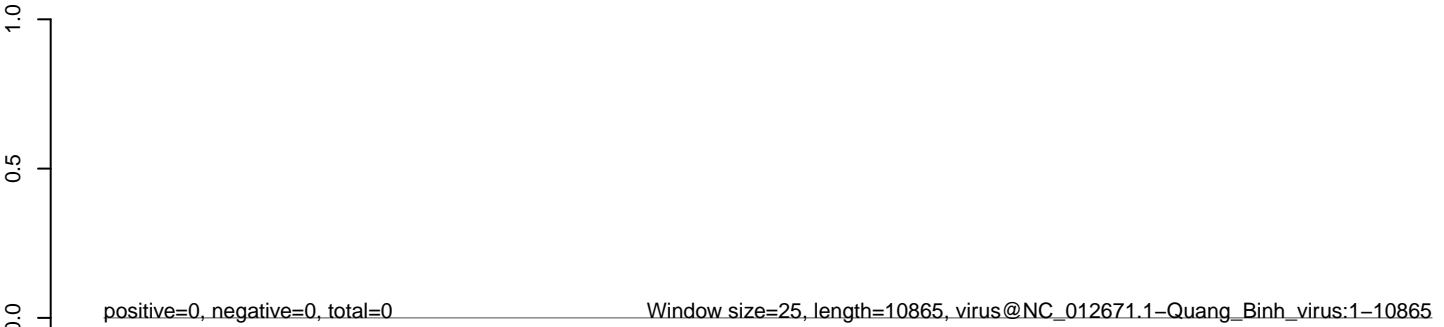
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AeAeg_Aag2.SINV.GFP.rep



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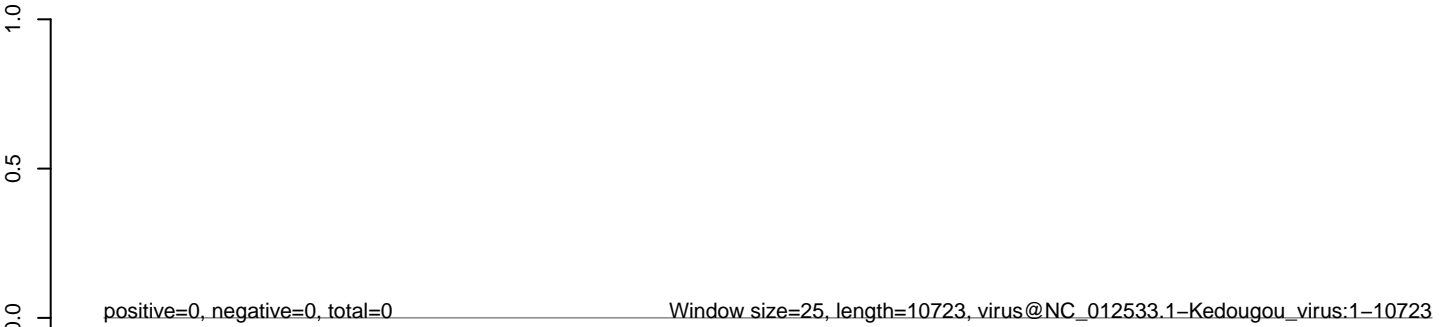
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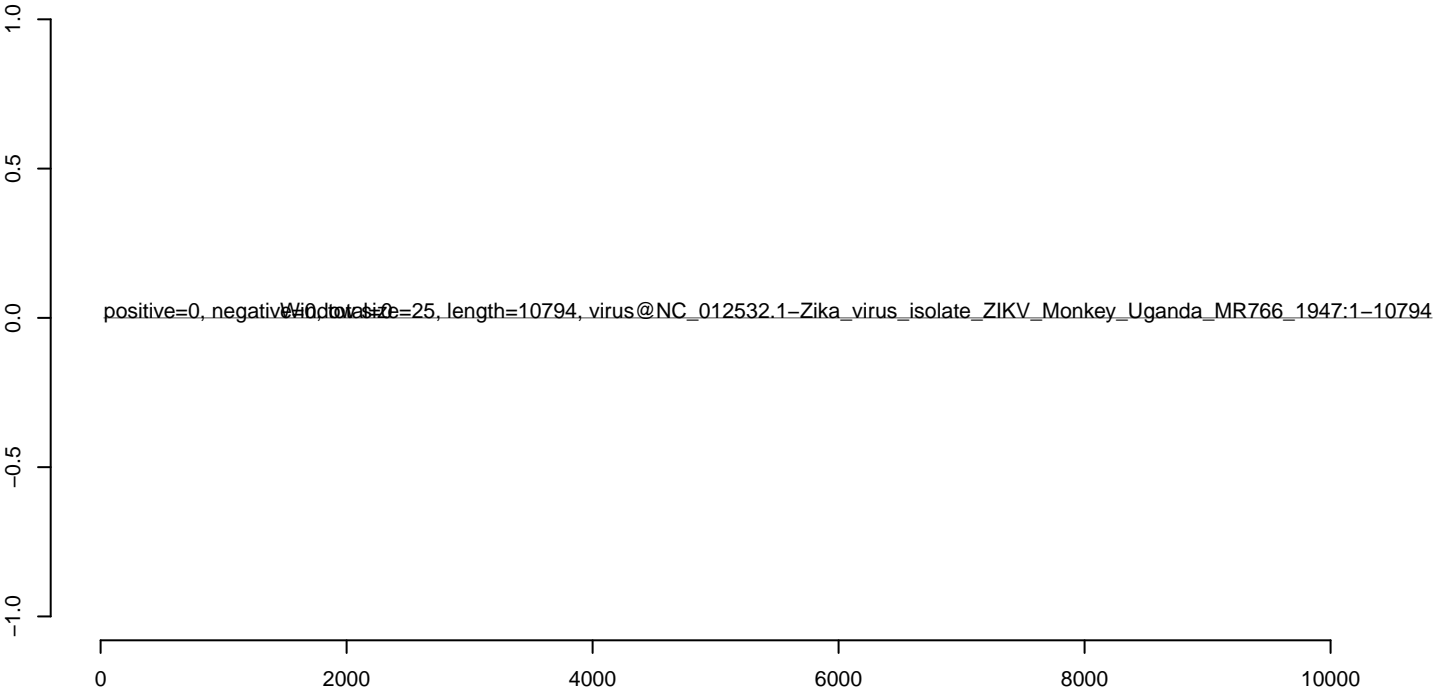
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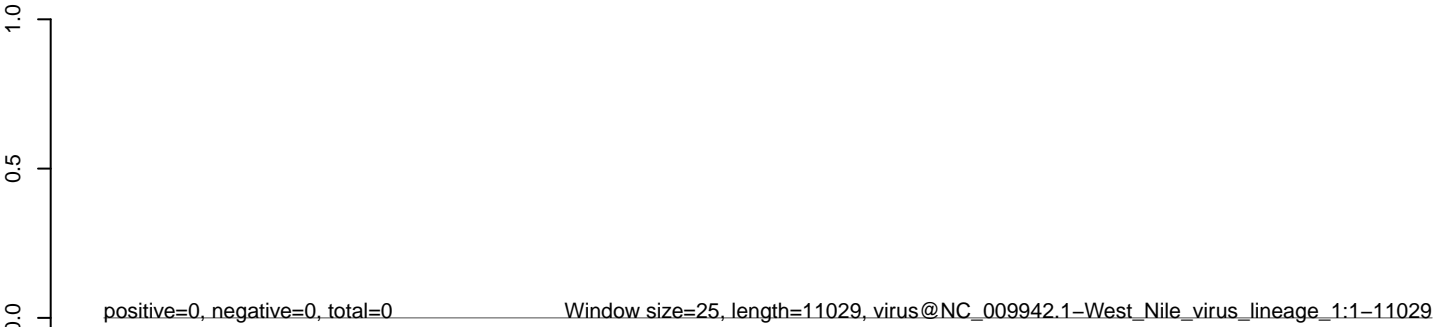
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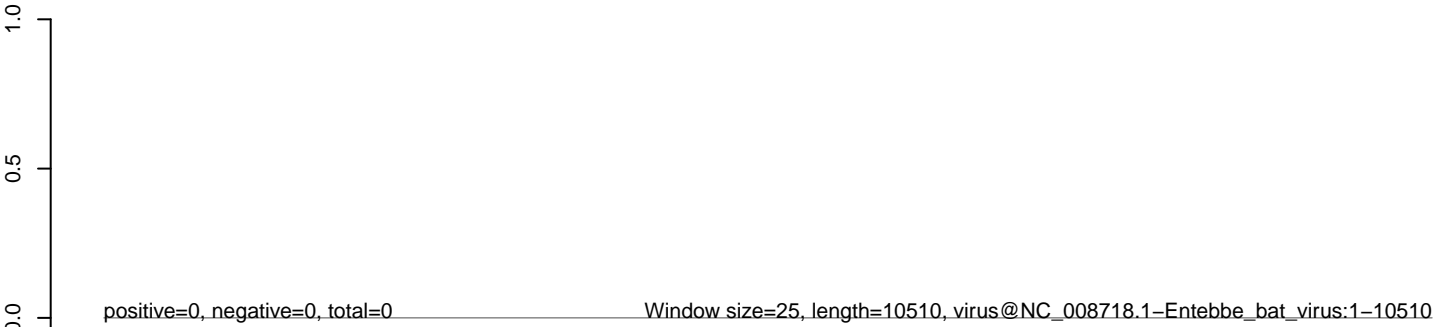
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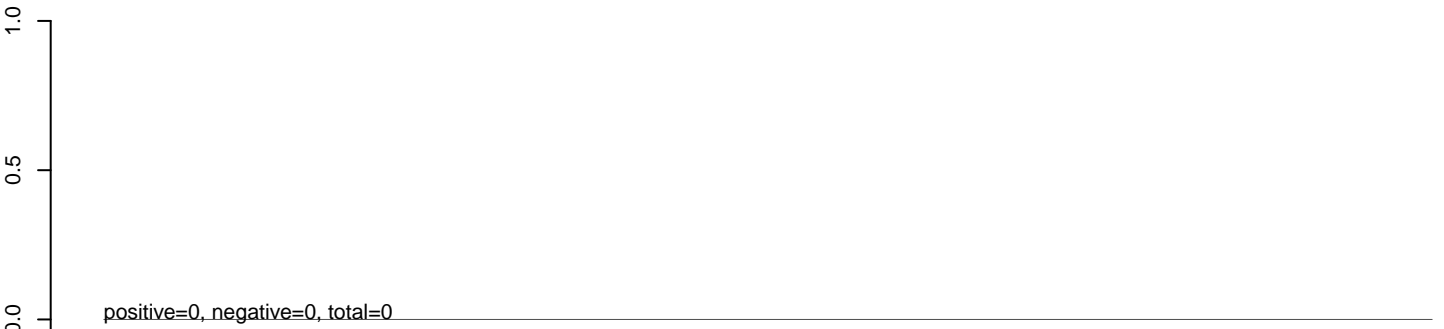


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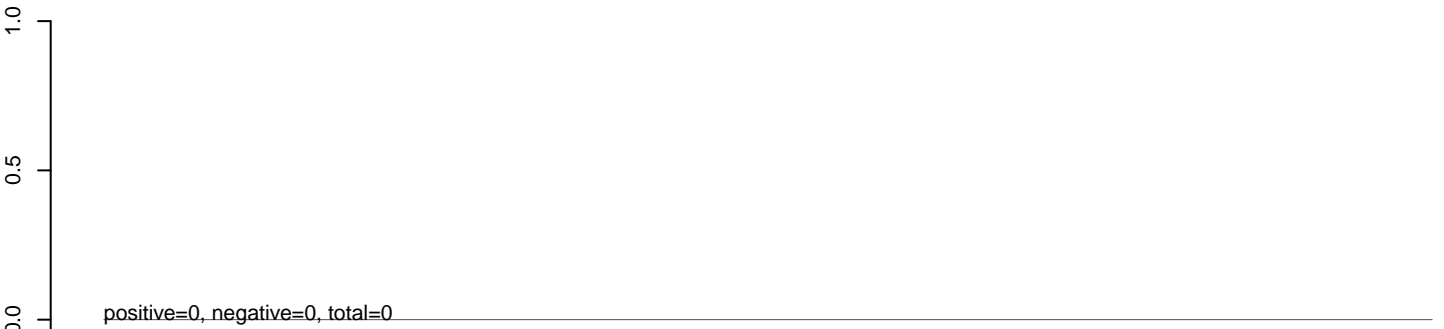


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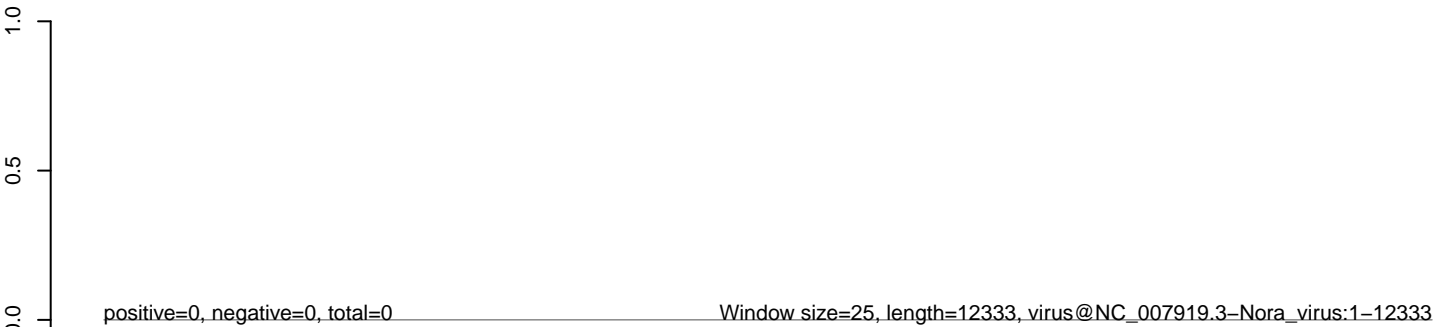
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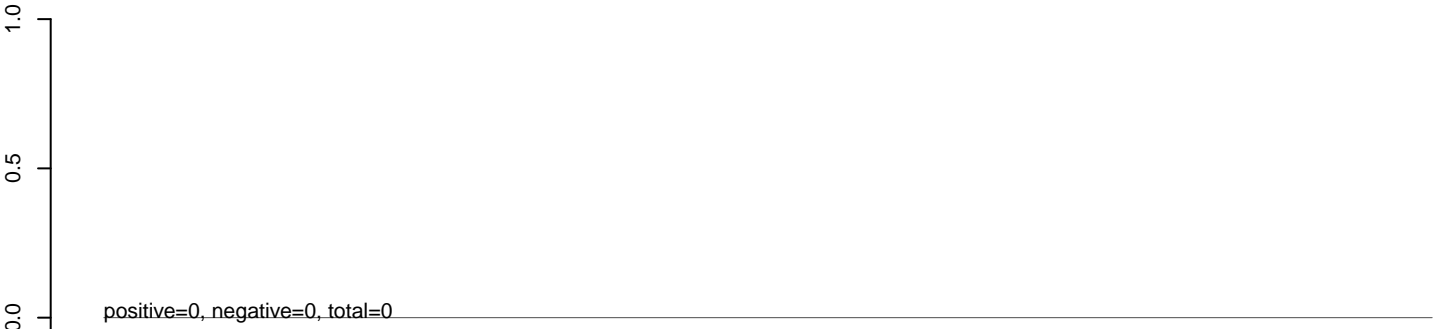


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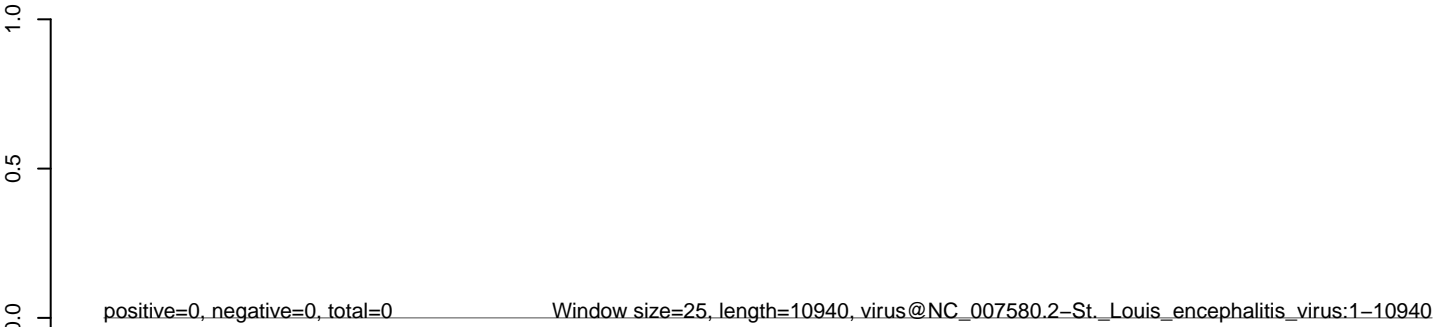
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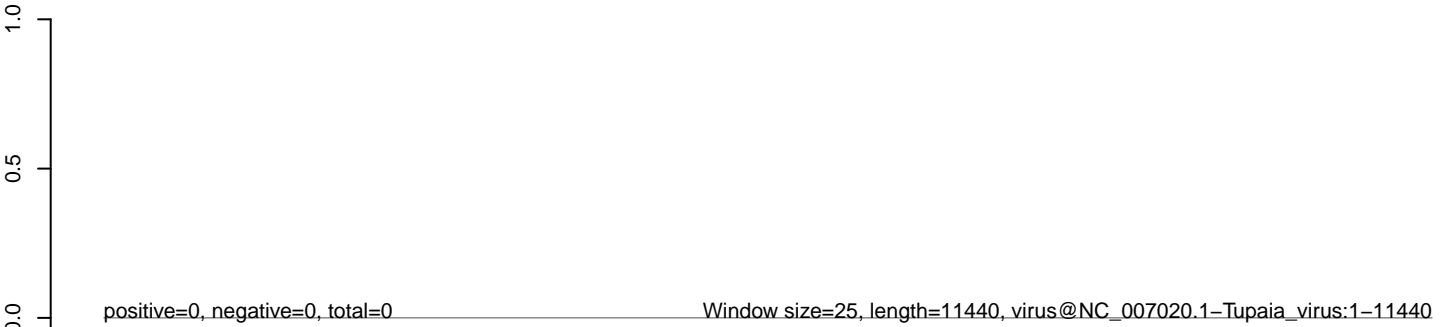
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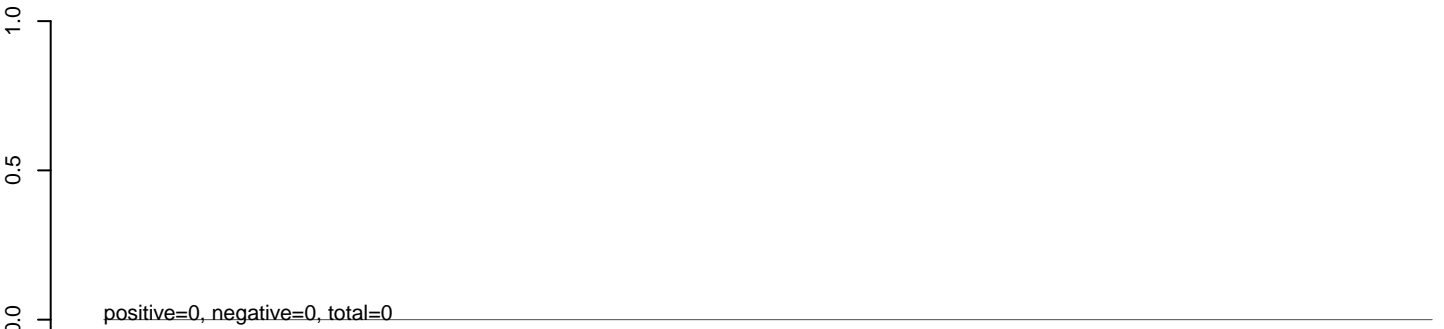


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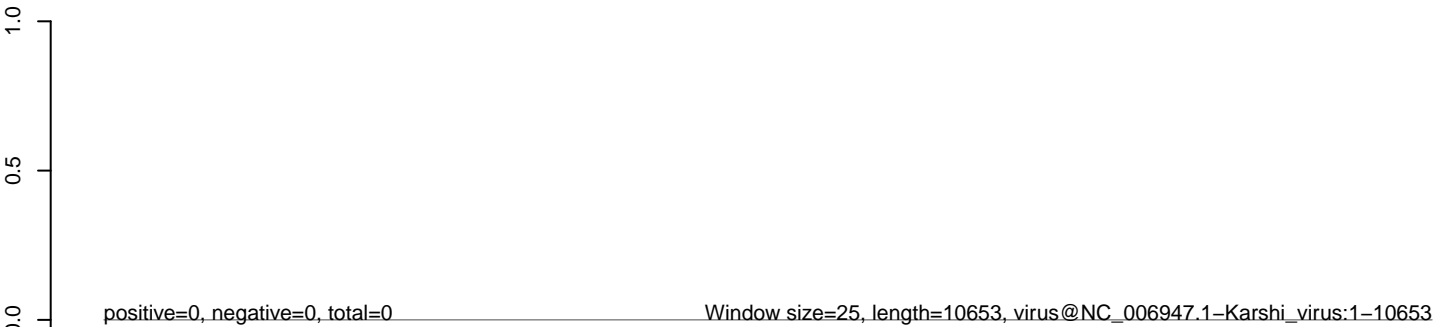
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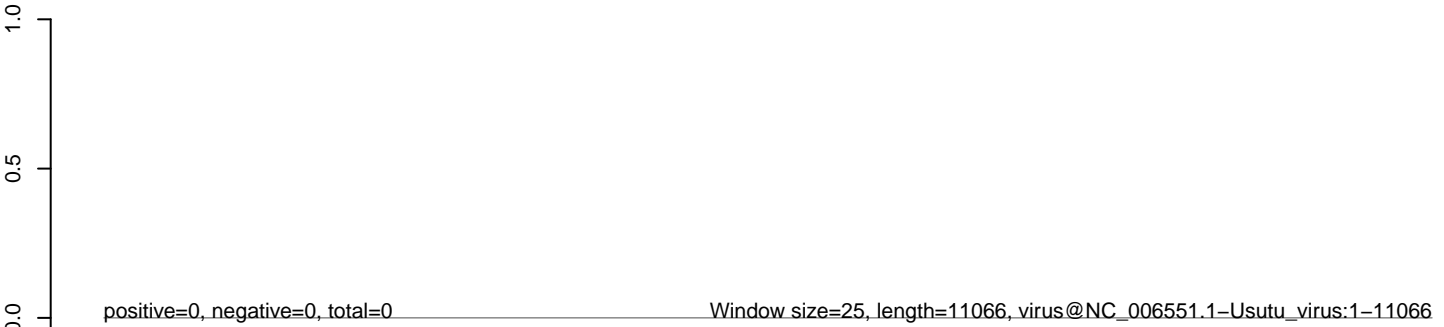
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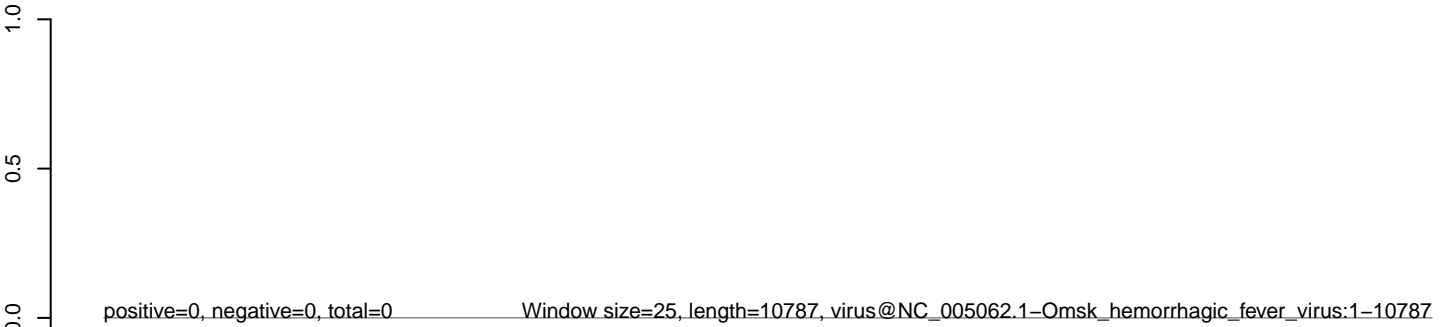
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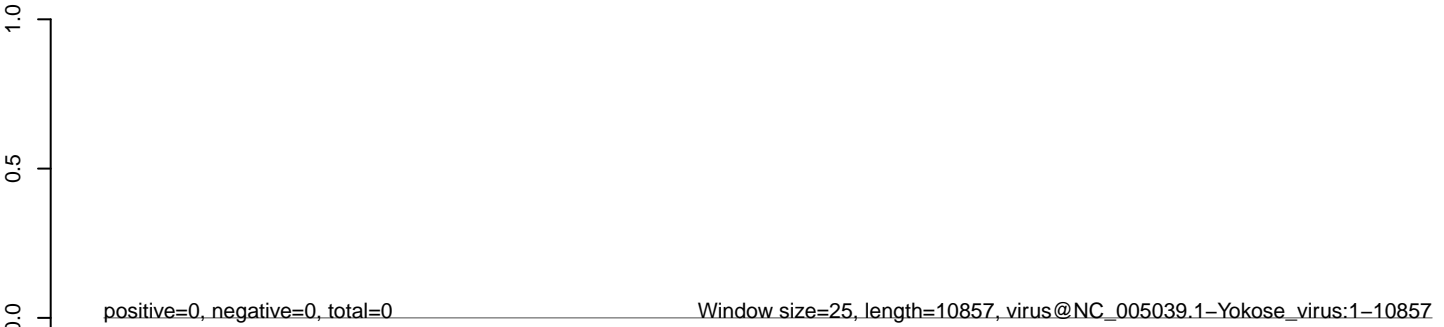
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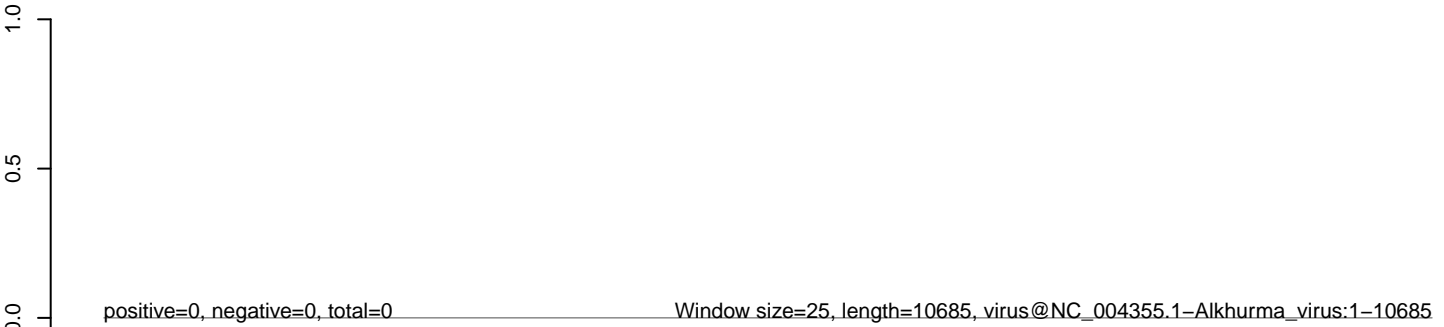
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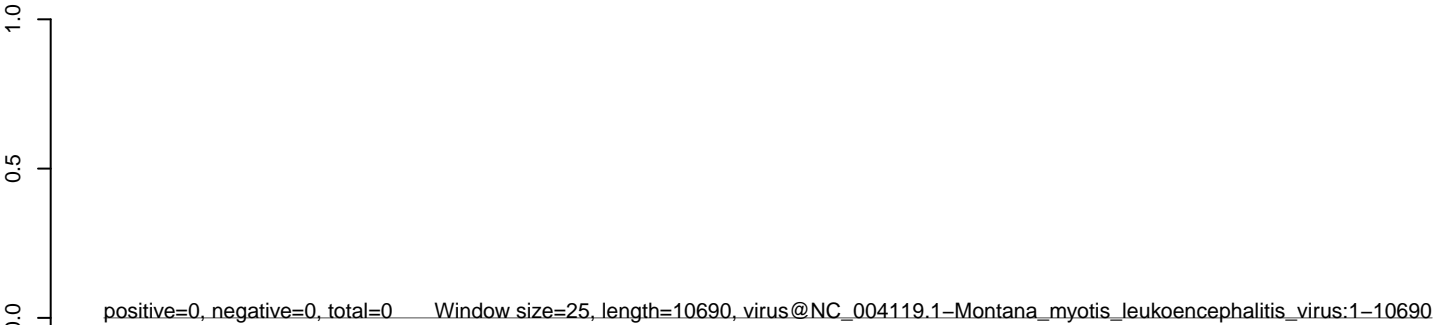
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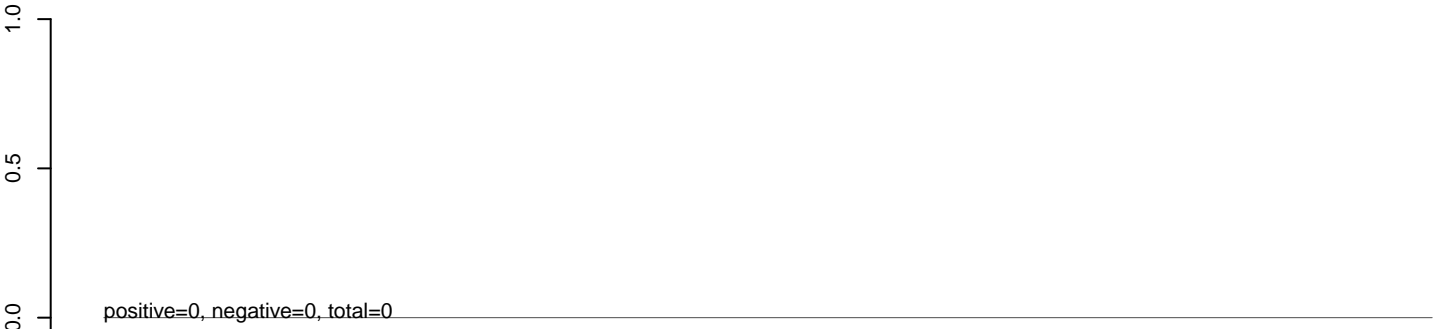
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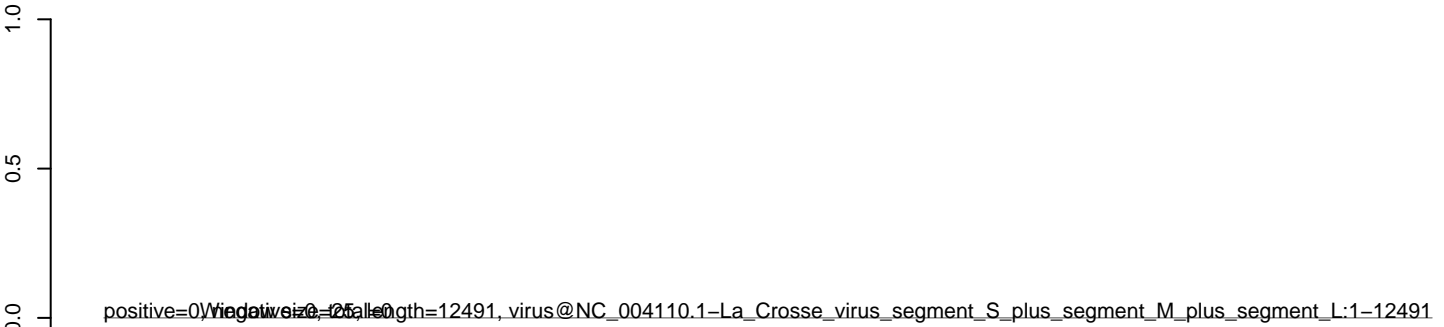
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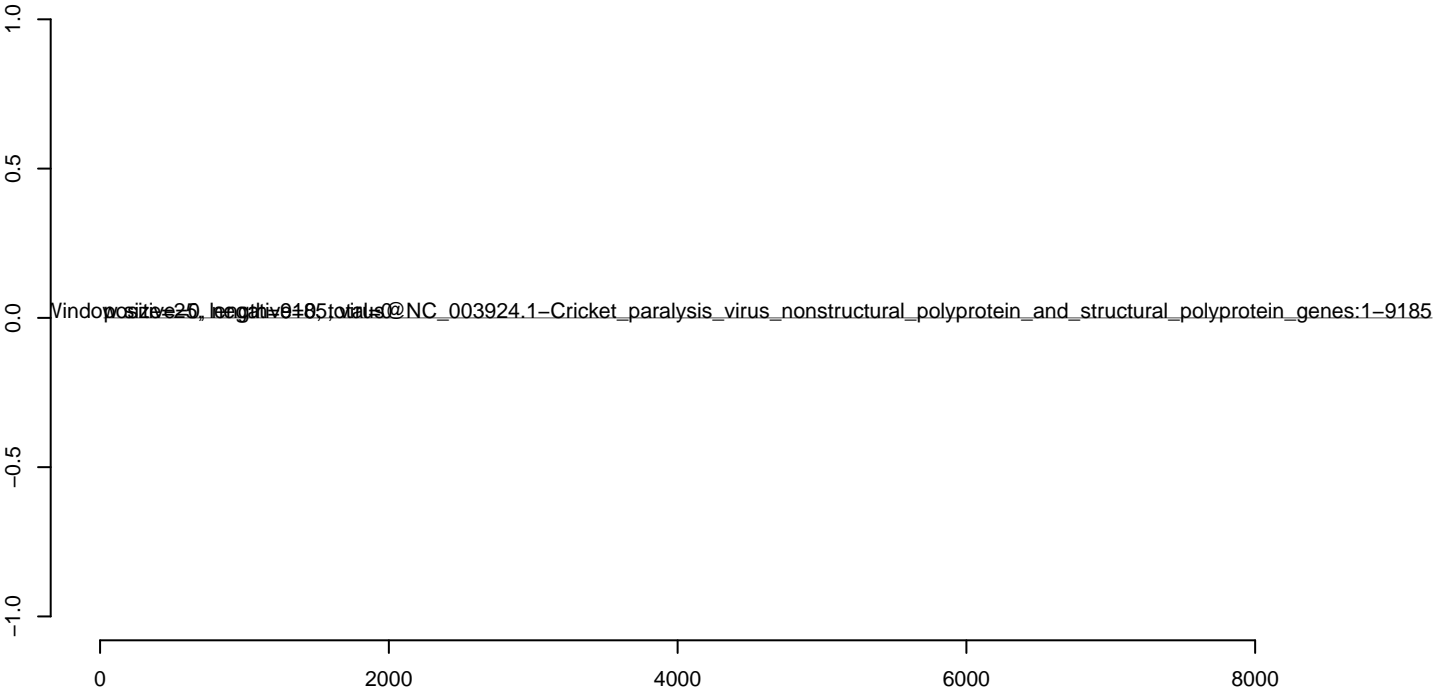
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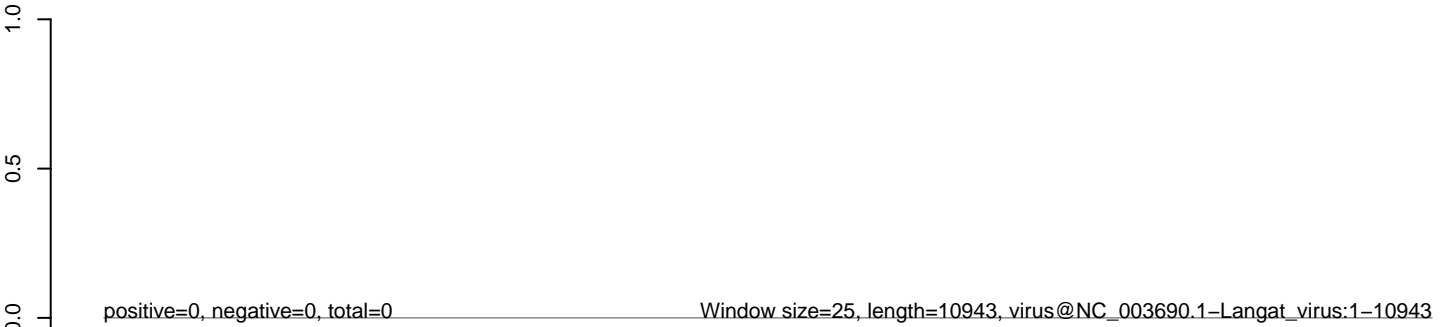
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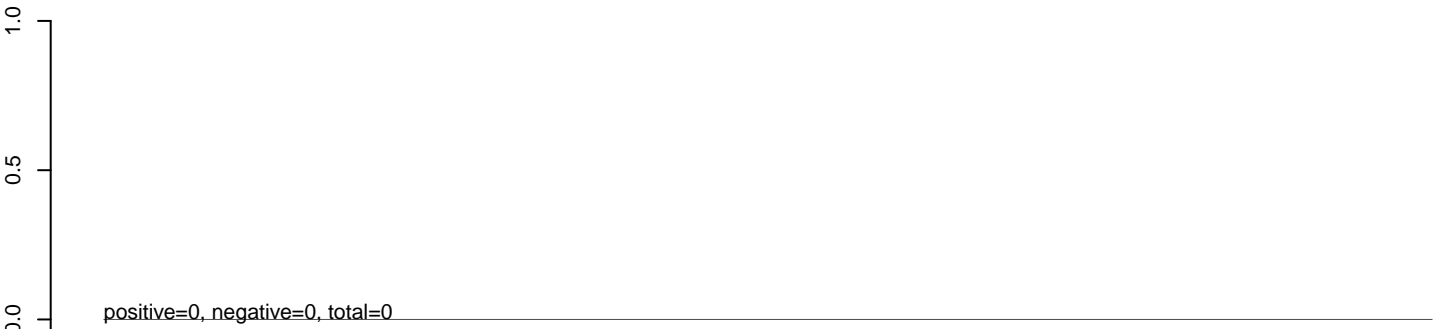


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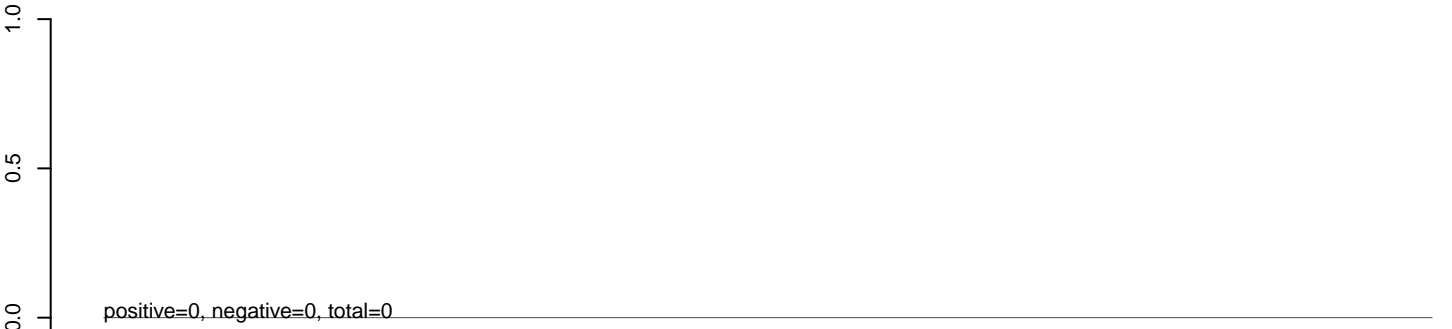


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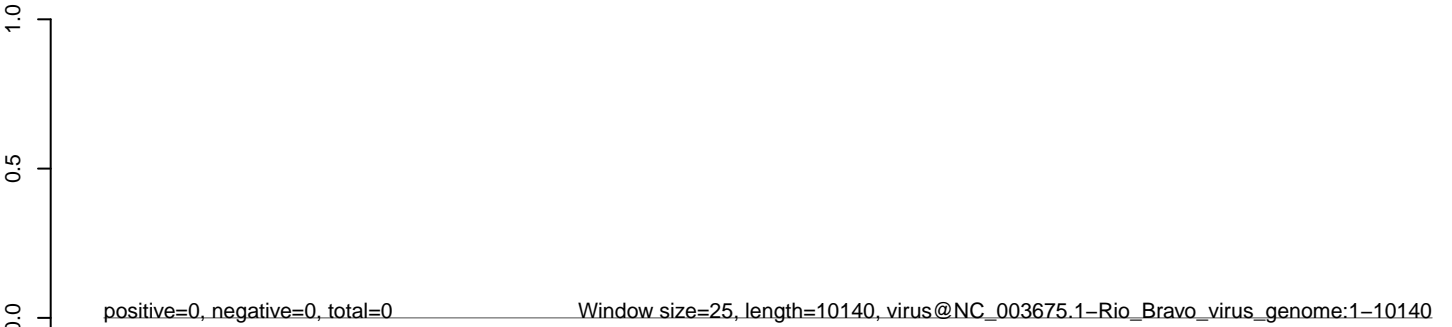
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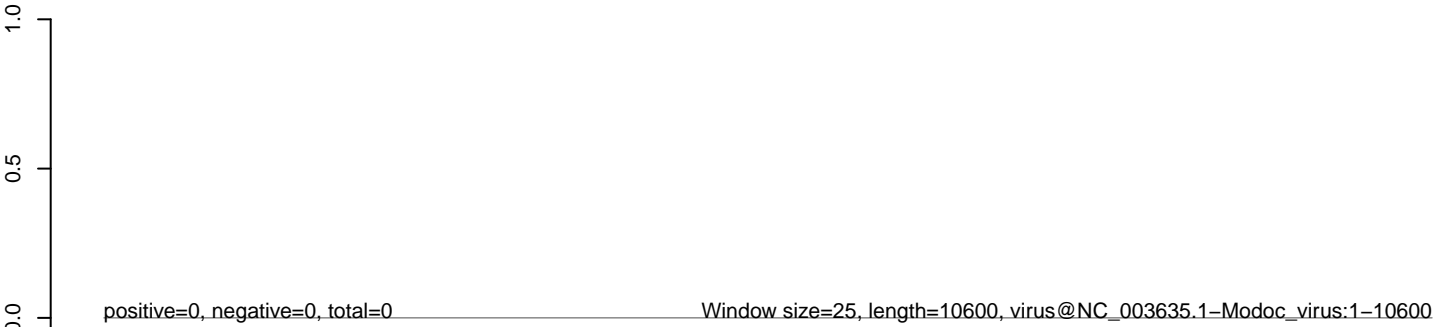
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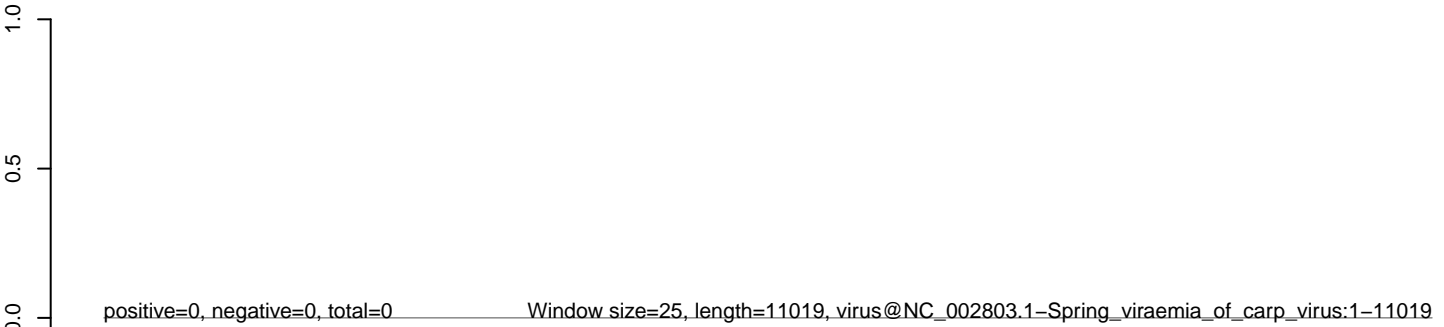
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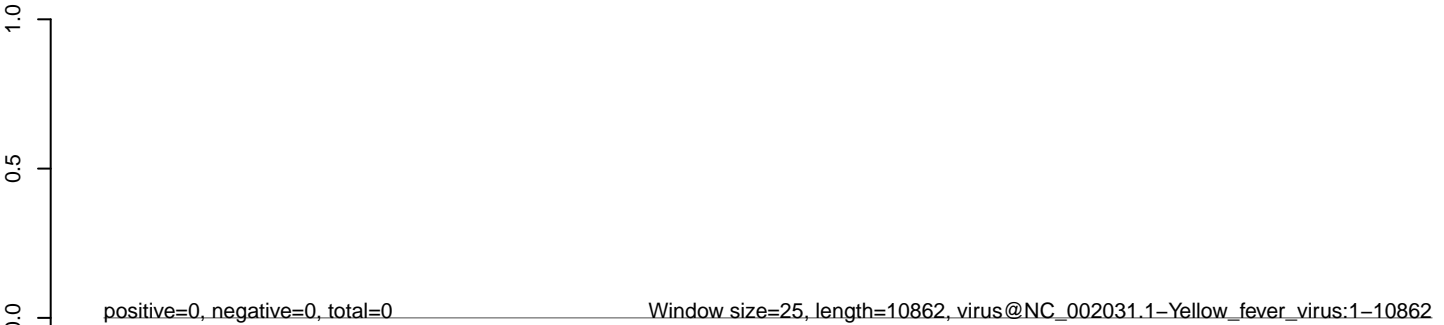
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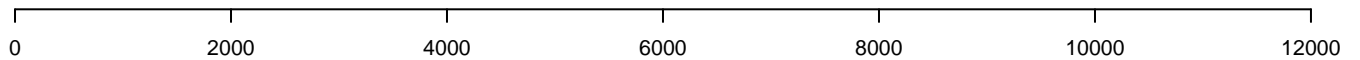
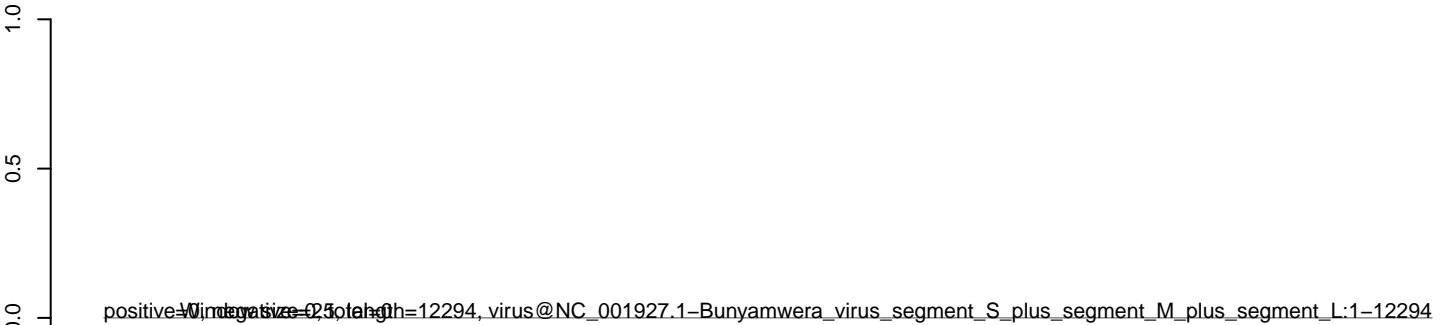
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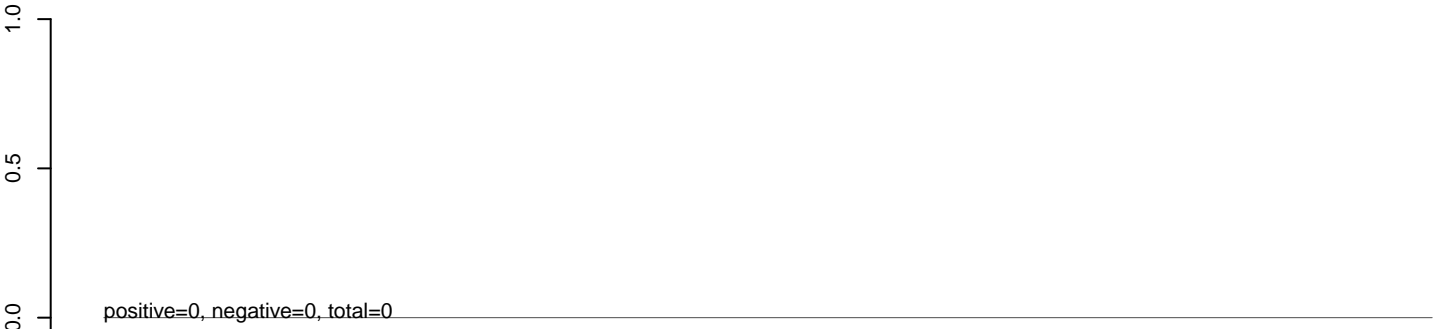
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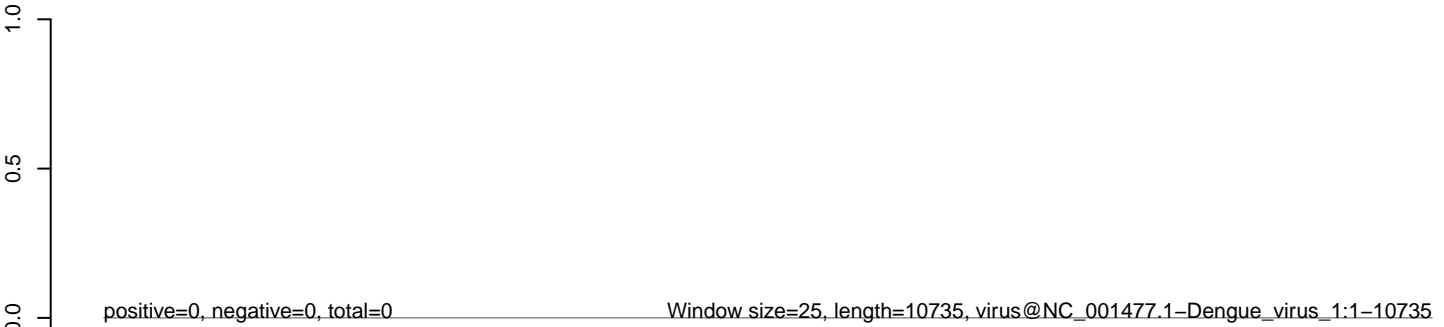
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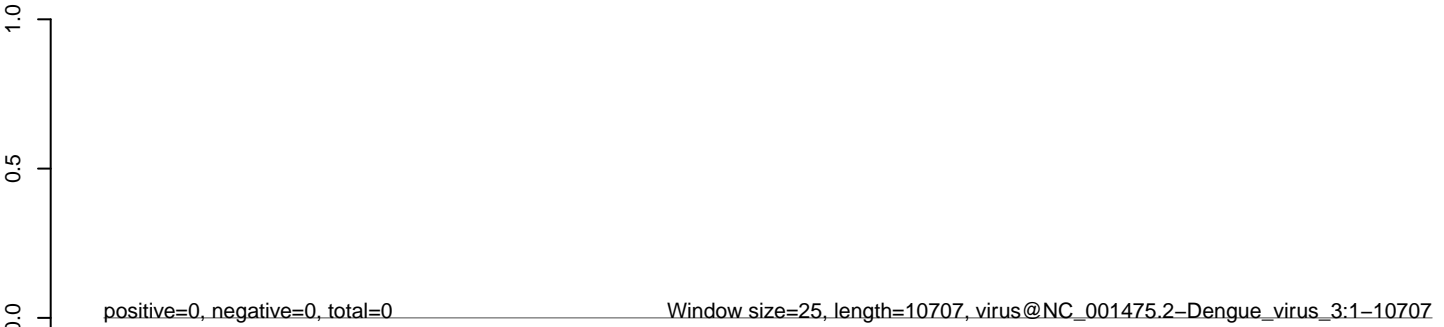
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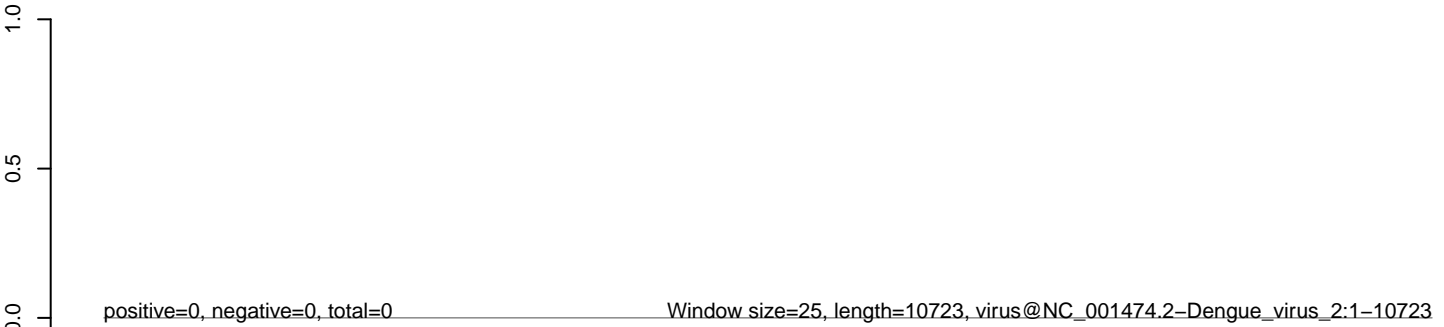
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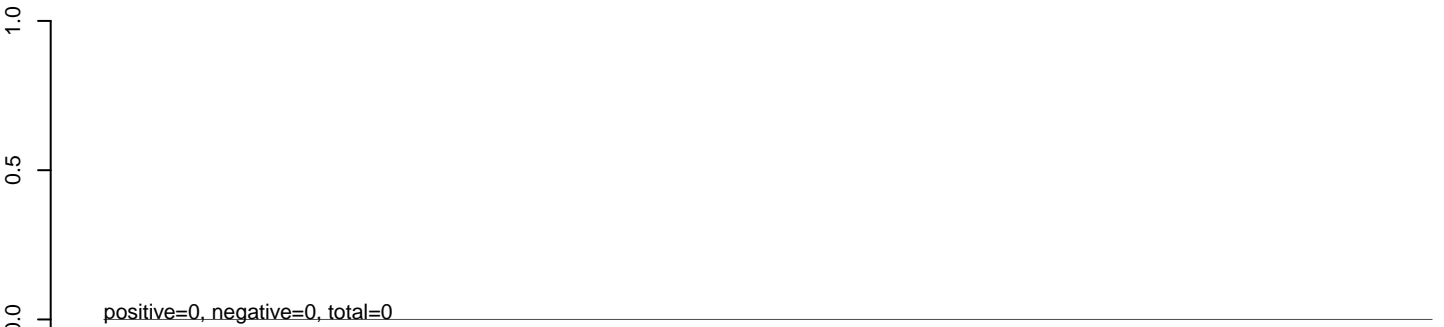


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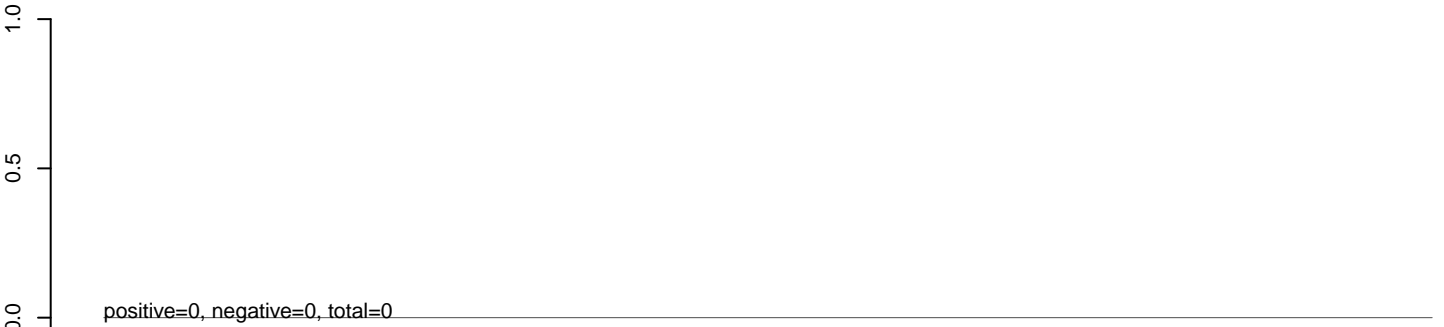


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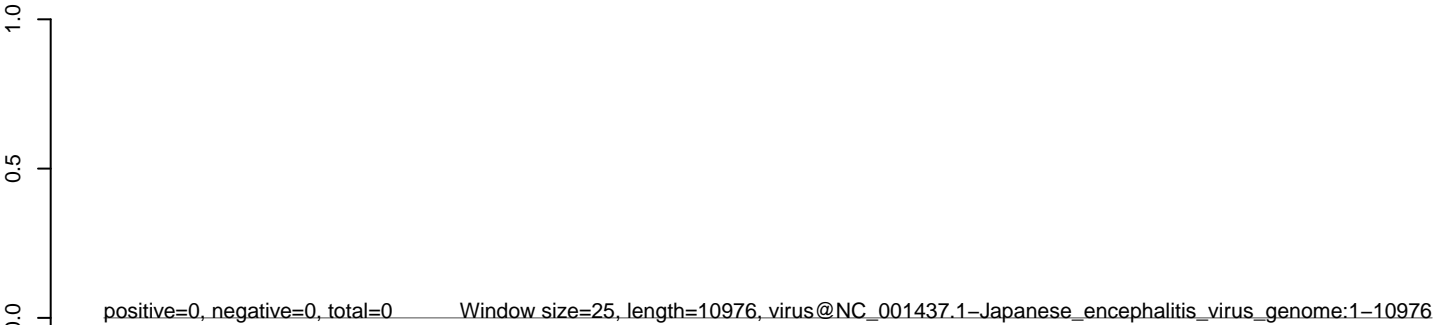
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AeAeg_Aag2.SINV.GFP.rep



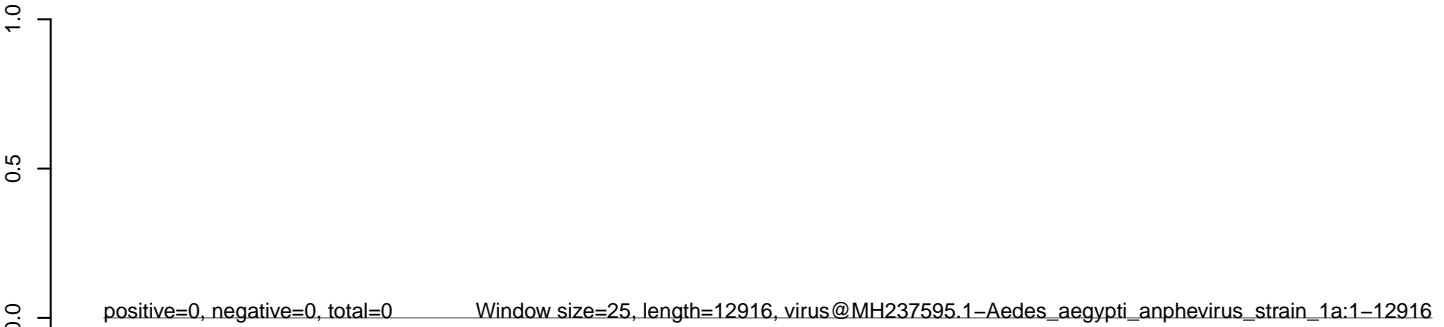
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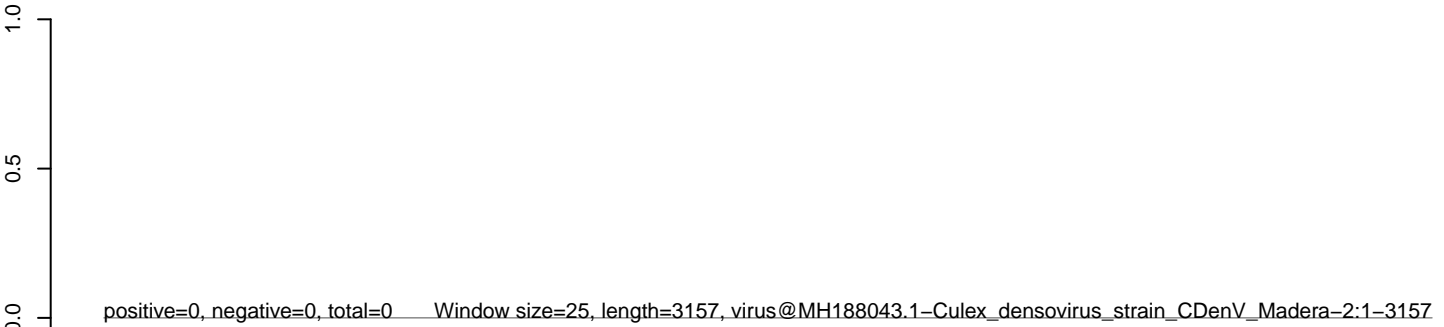
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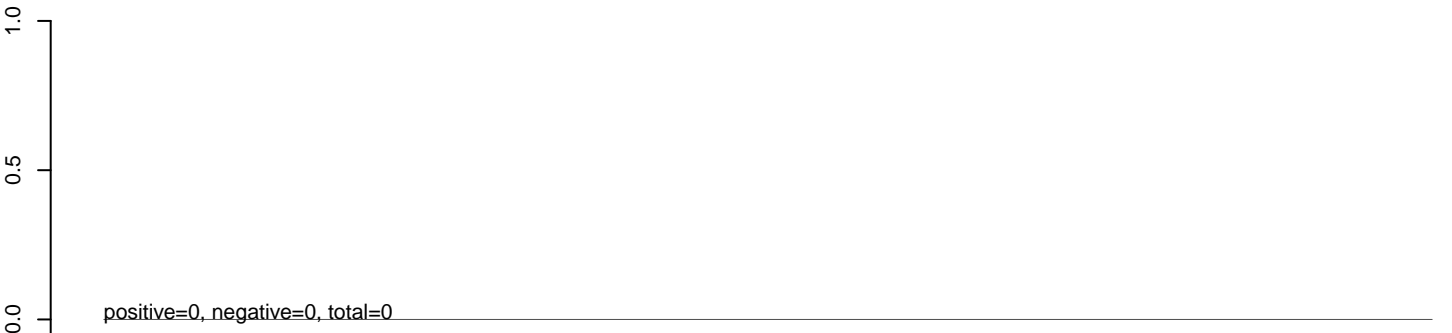
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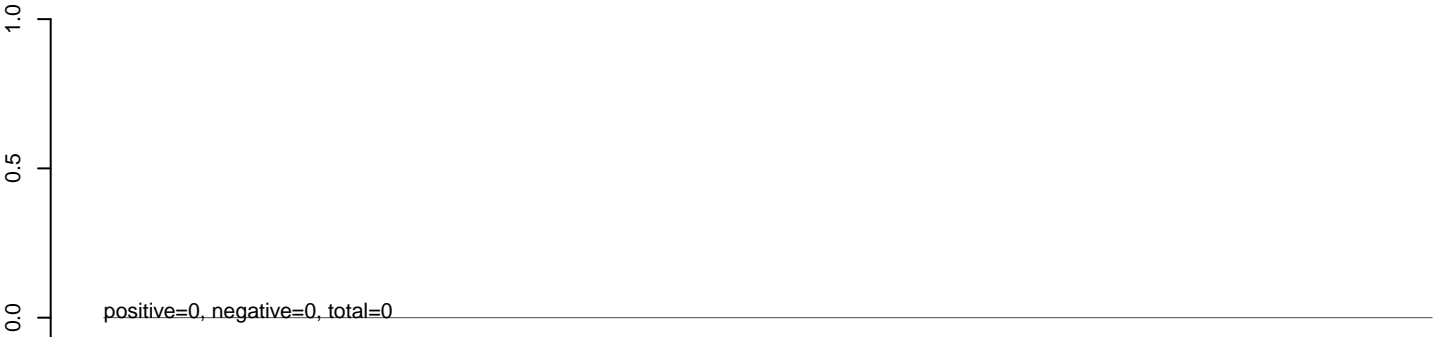
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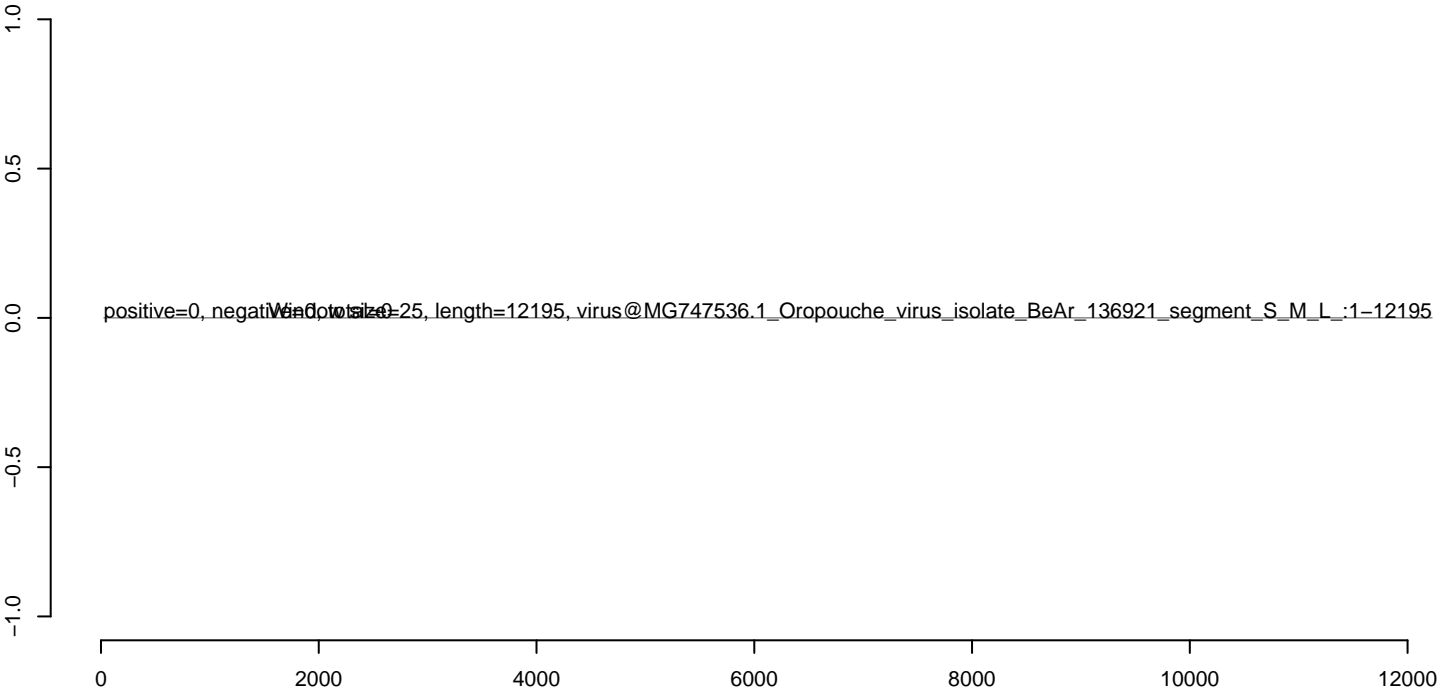
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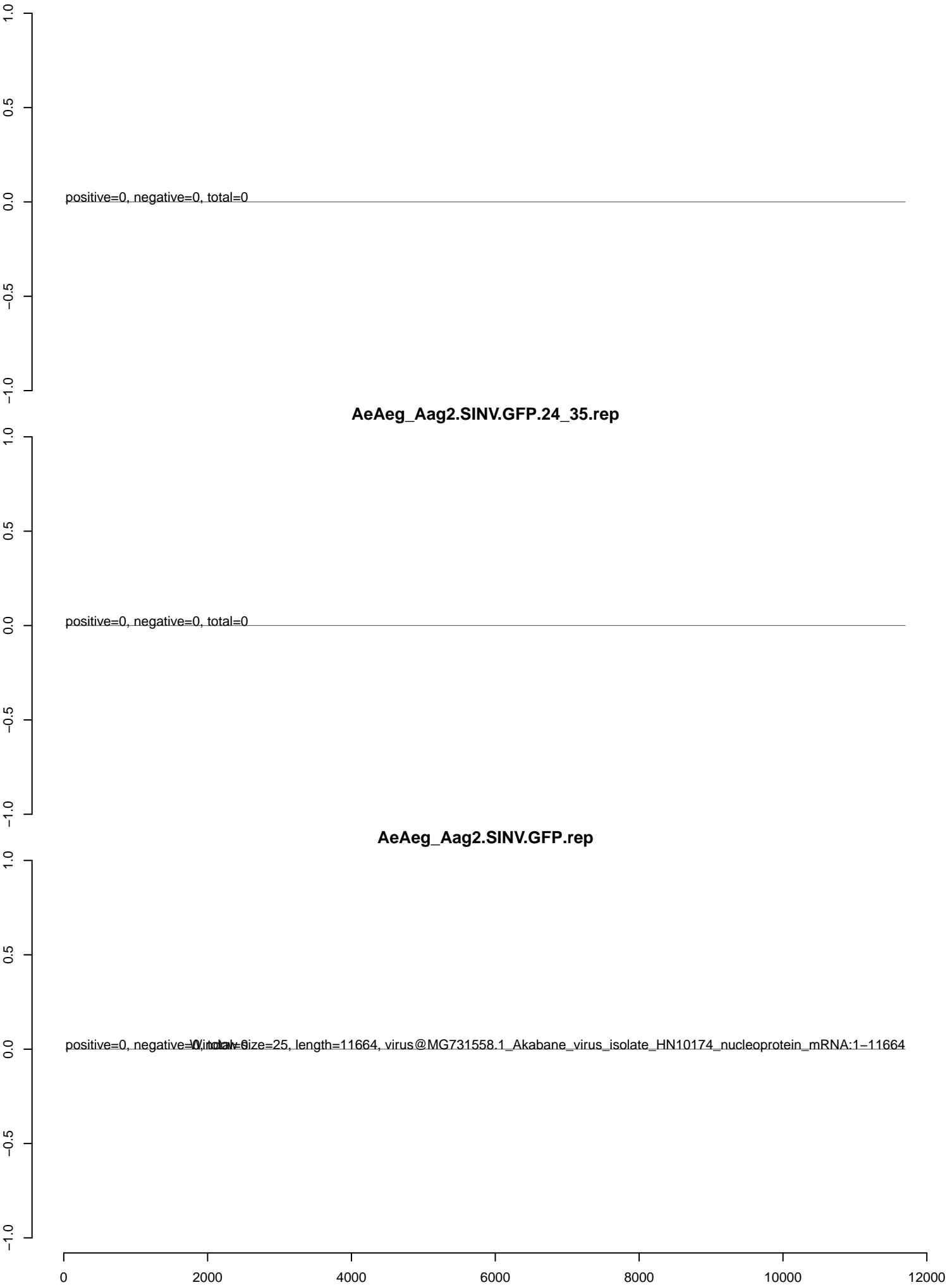
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AeAeg_Aag2.SINV.GFP.rep



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AeAeg_Aag2.SINV.GFP.18_23.rep



AeAeg_Aag2.SINV.GFP.24_35.rep



AeAeg_Aag2.SINV.GFP.rep



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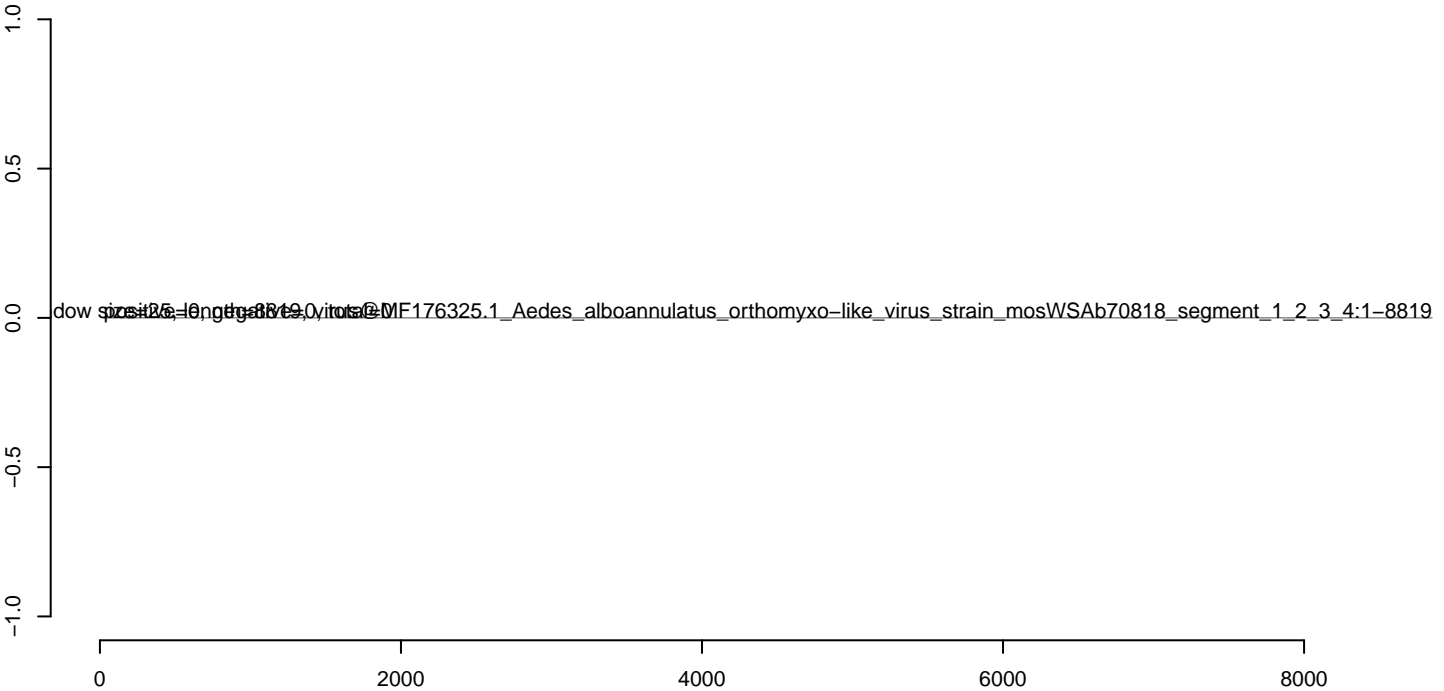
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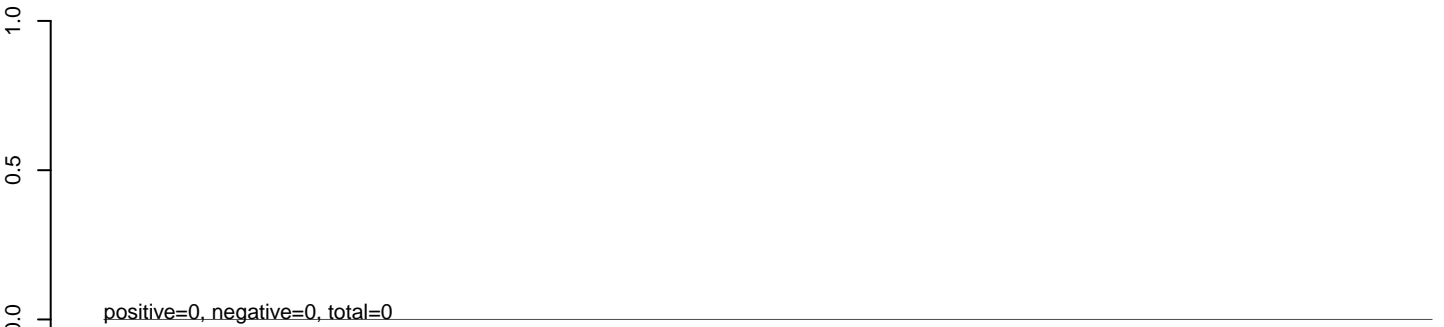


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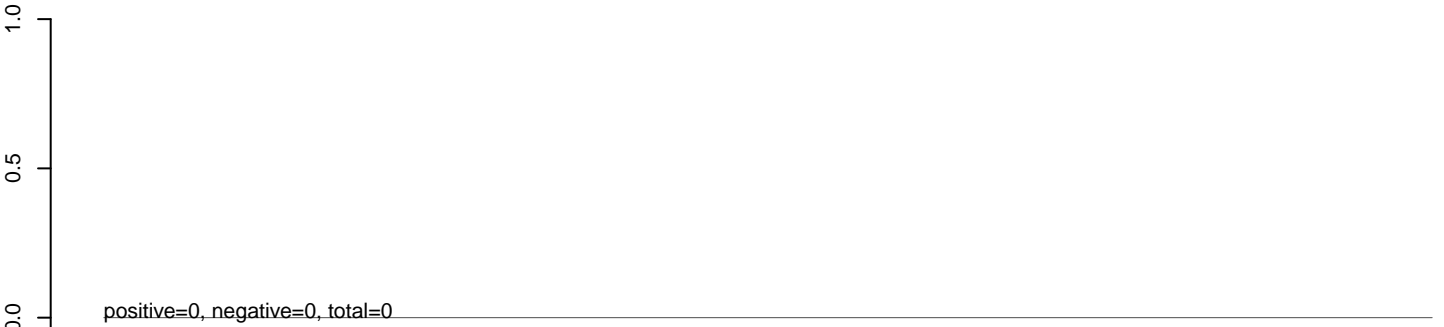


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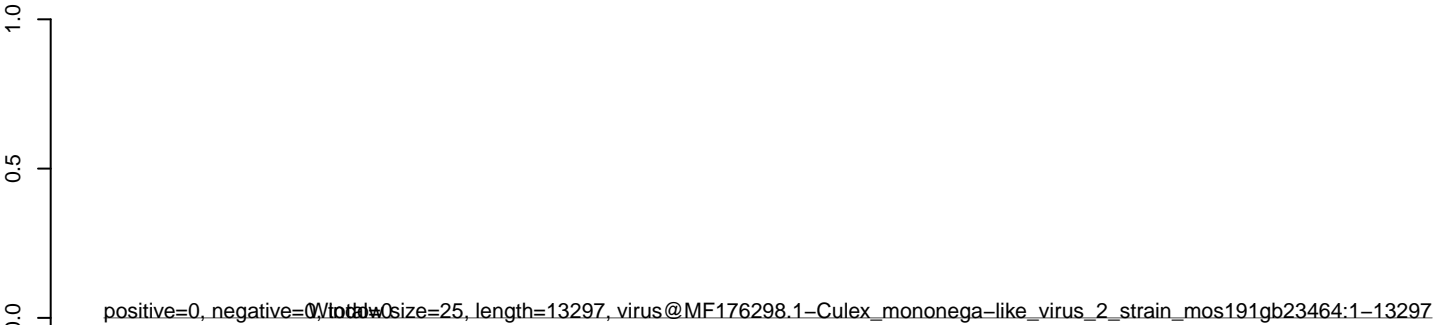
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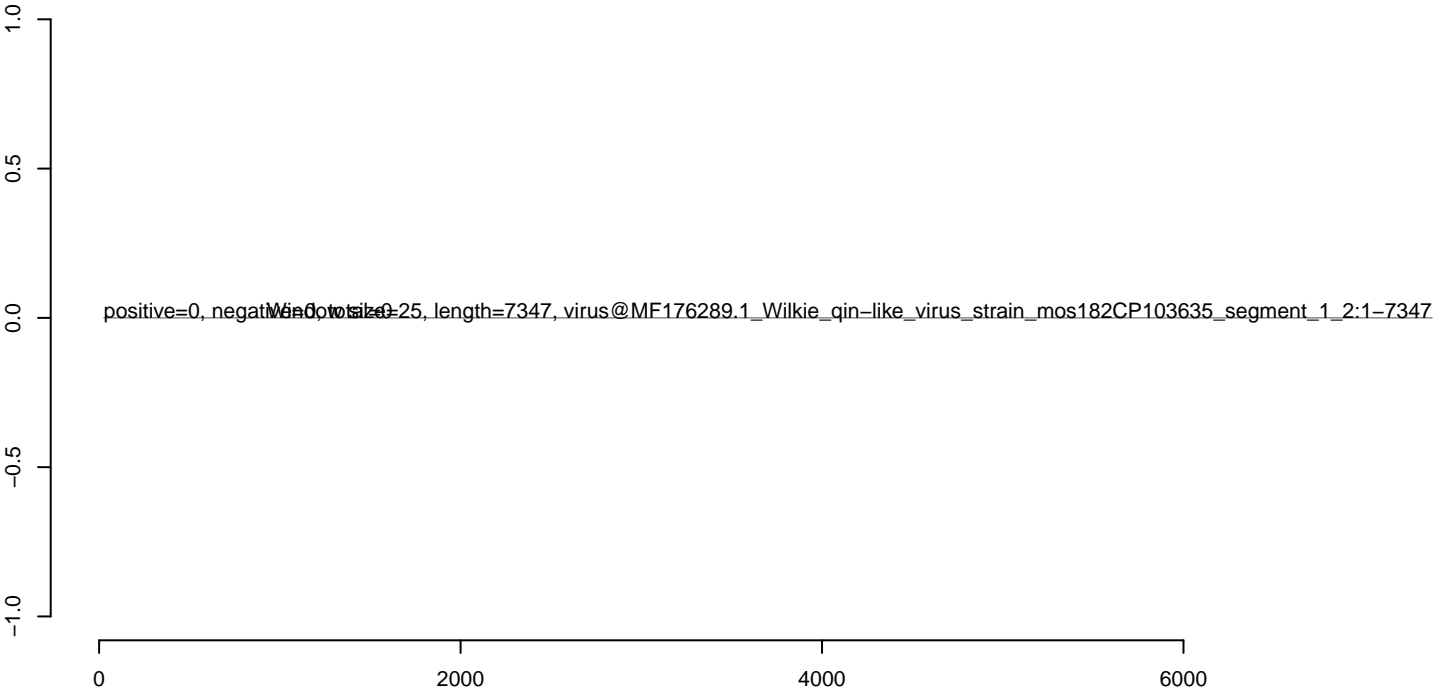
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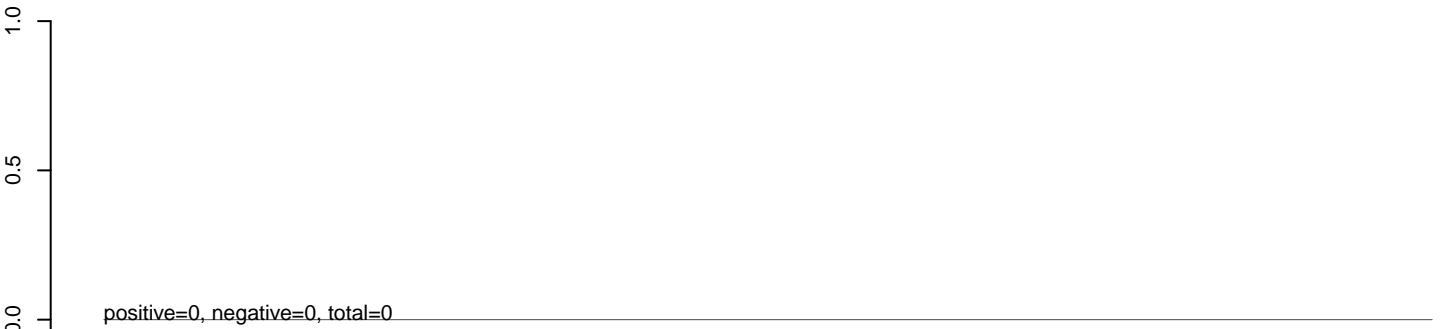
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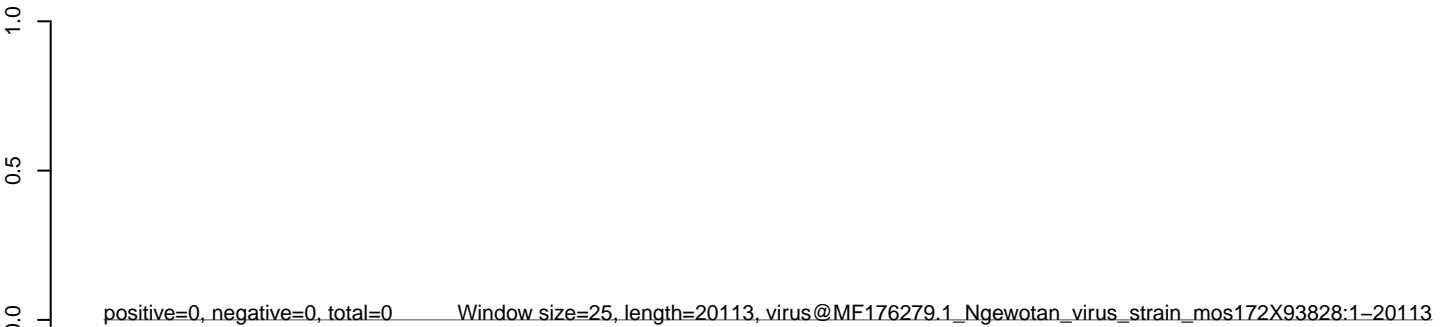
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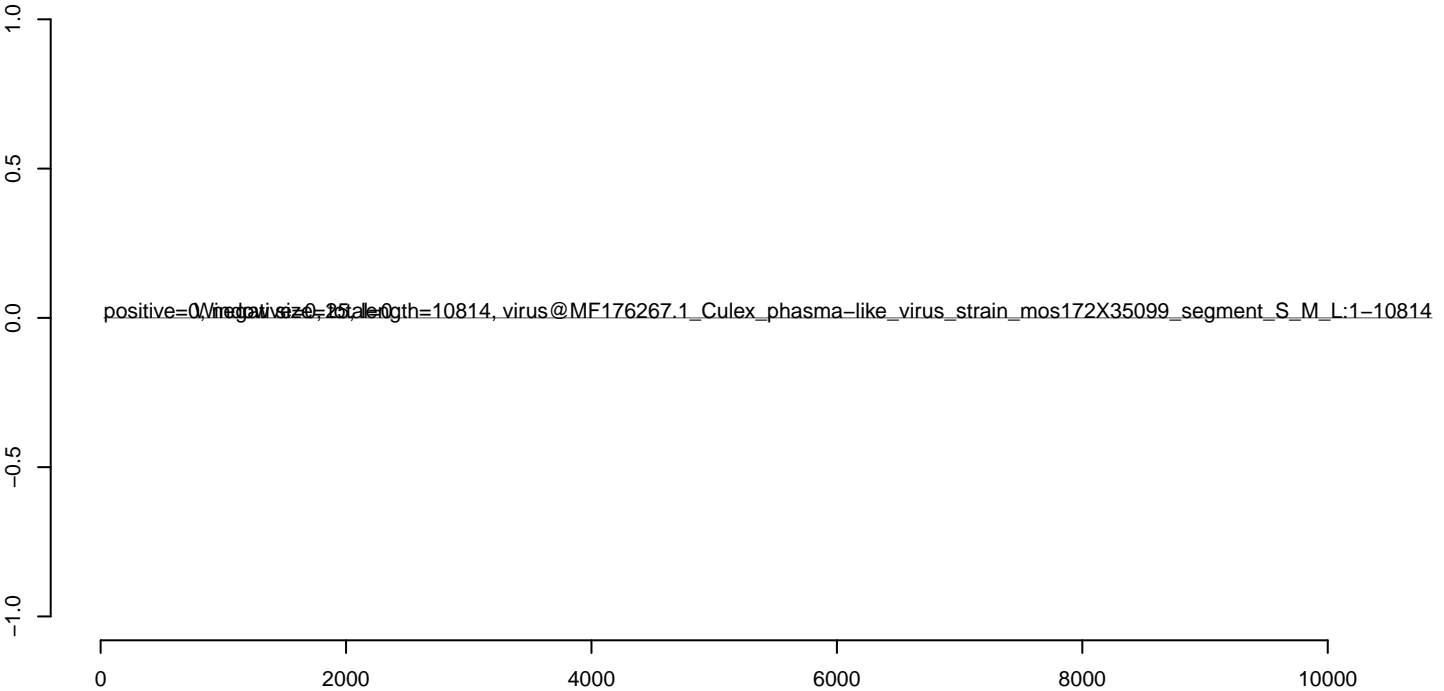
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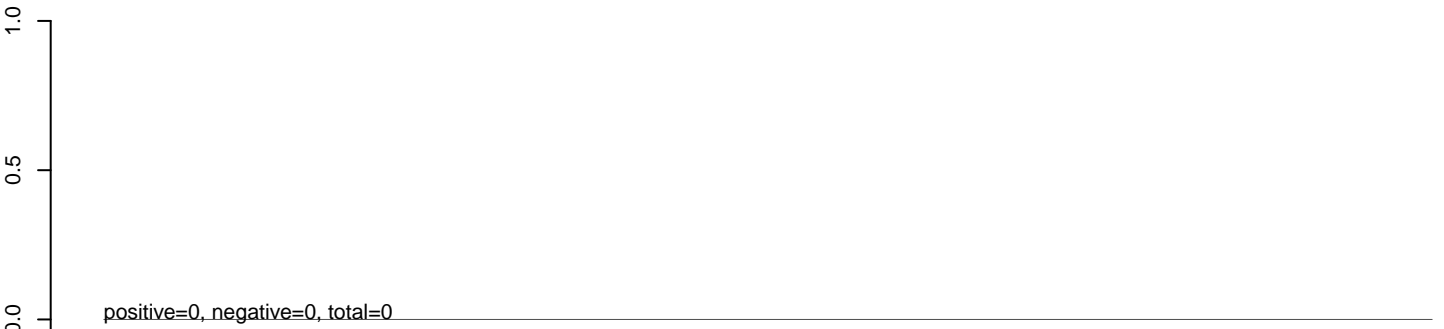
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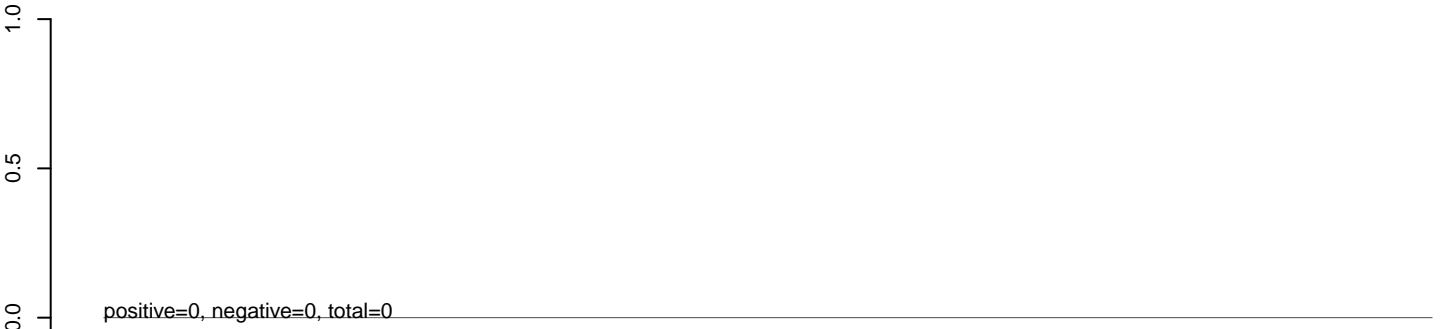
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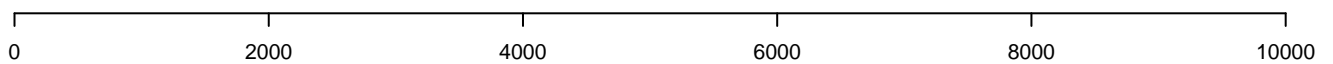
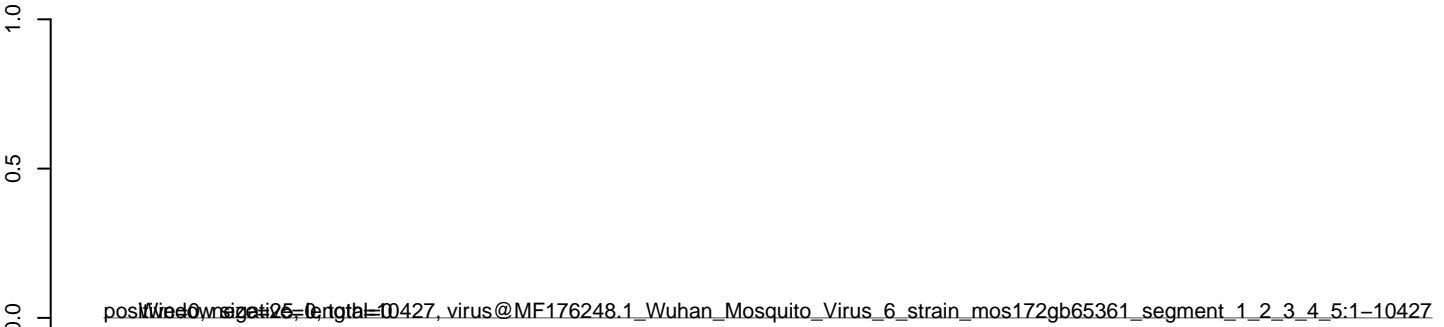
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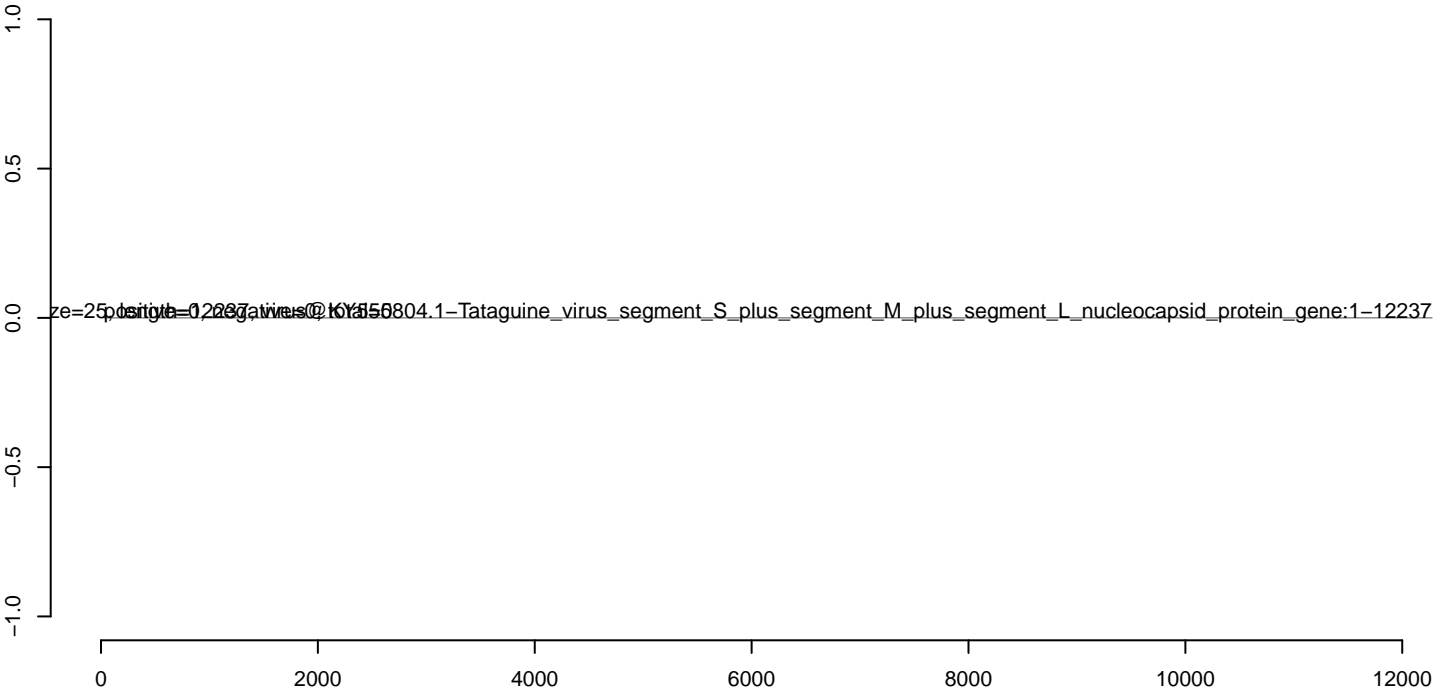
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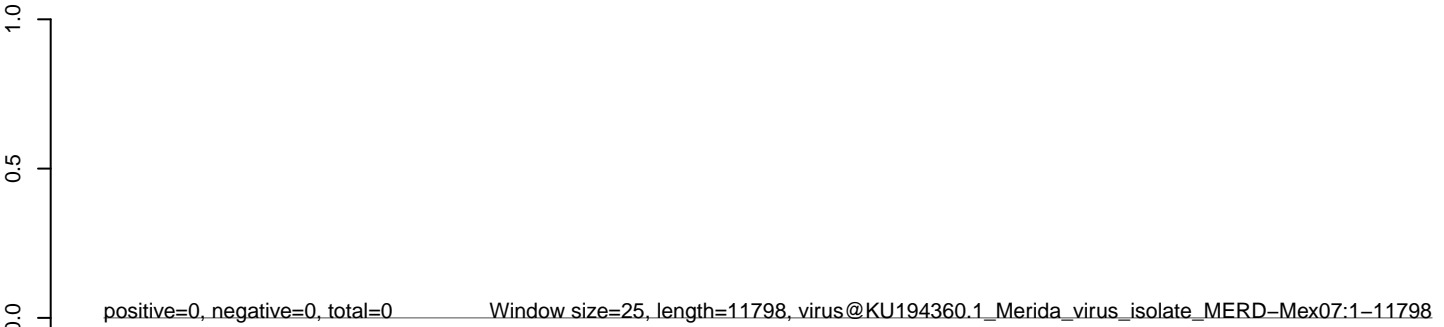
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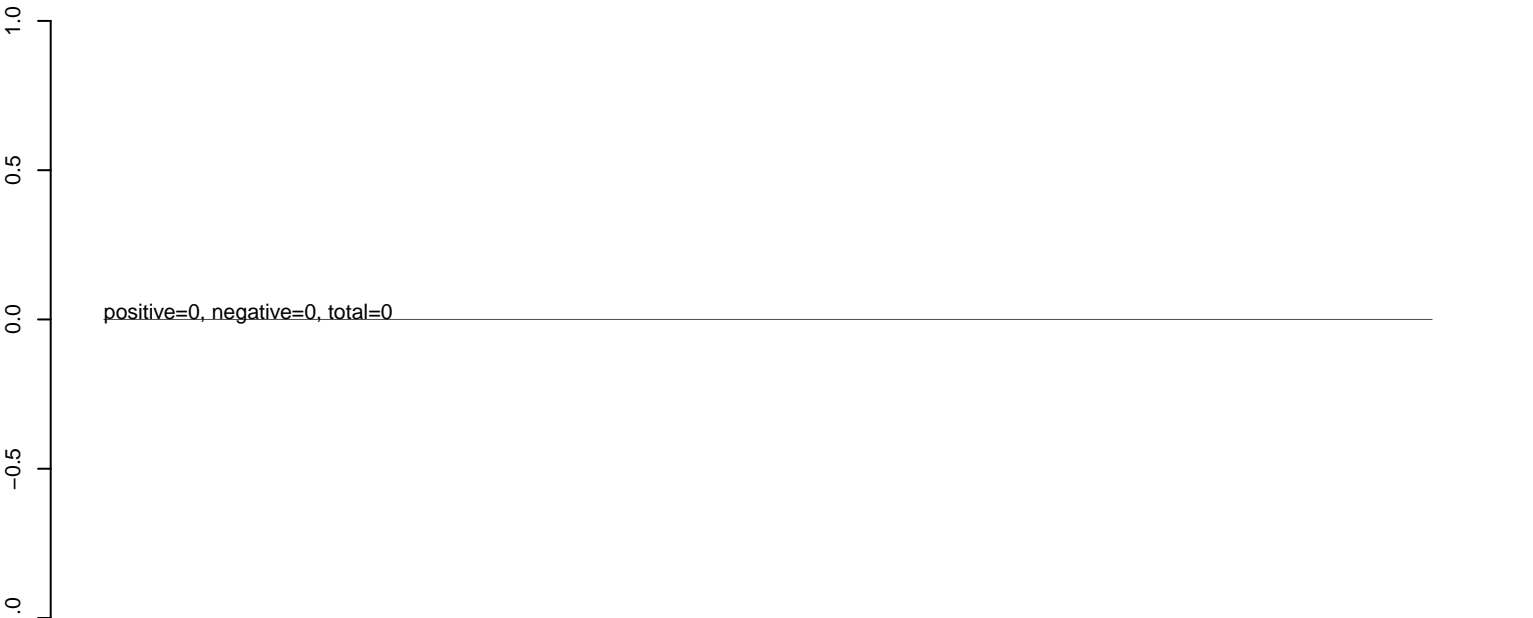


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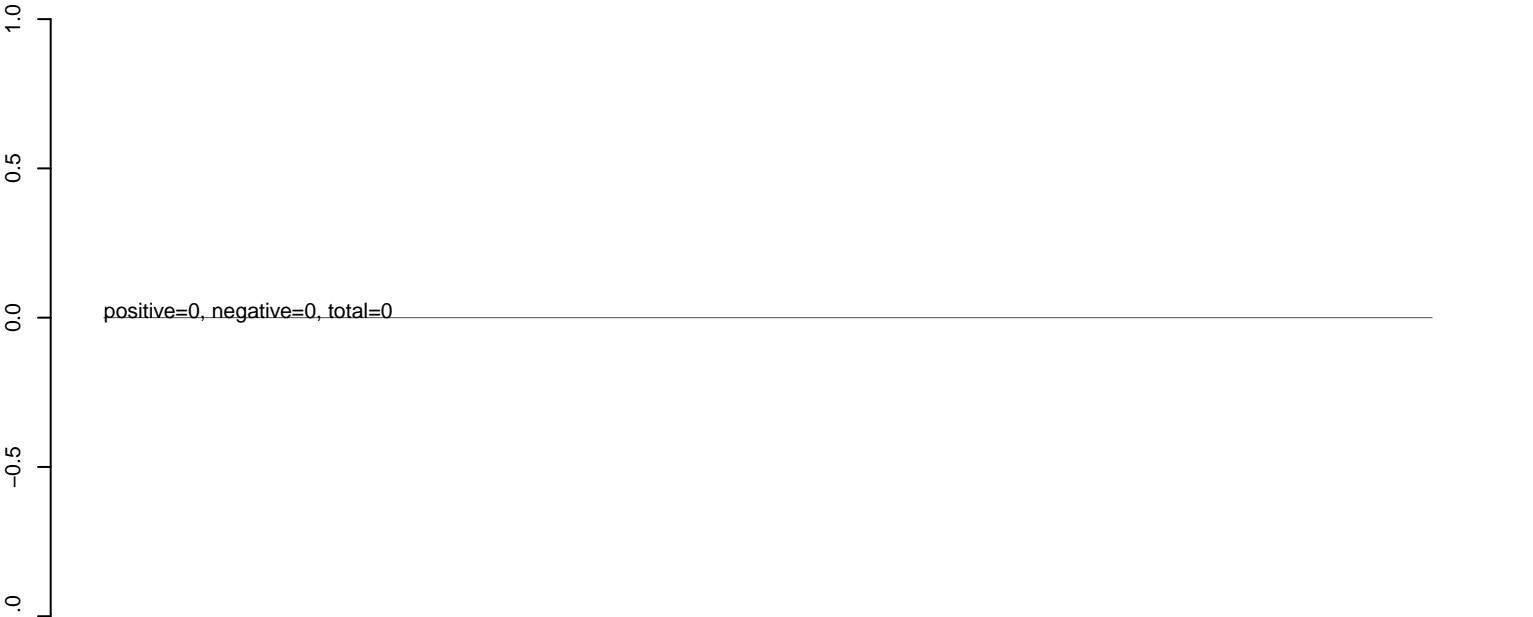


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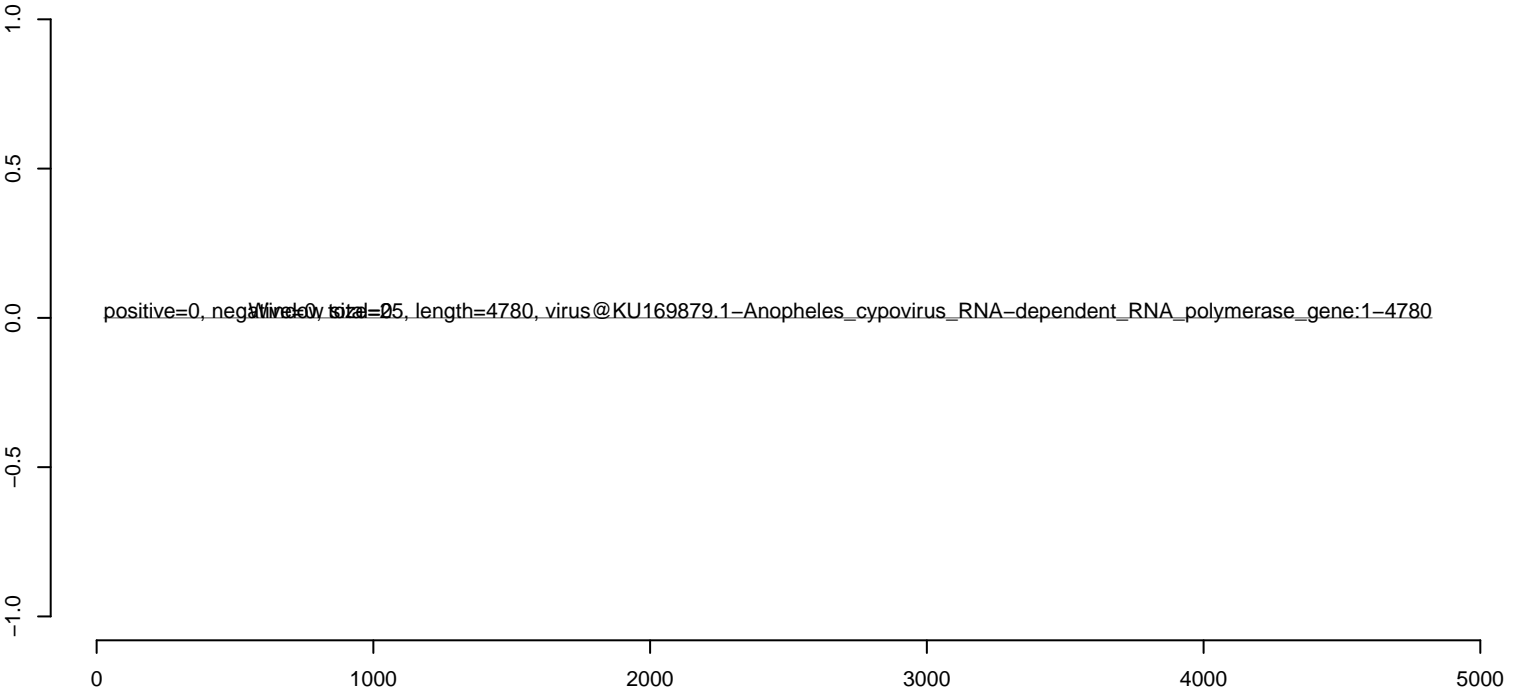
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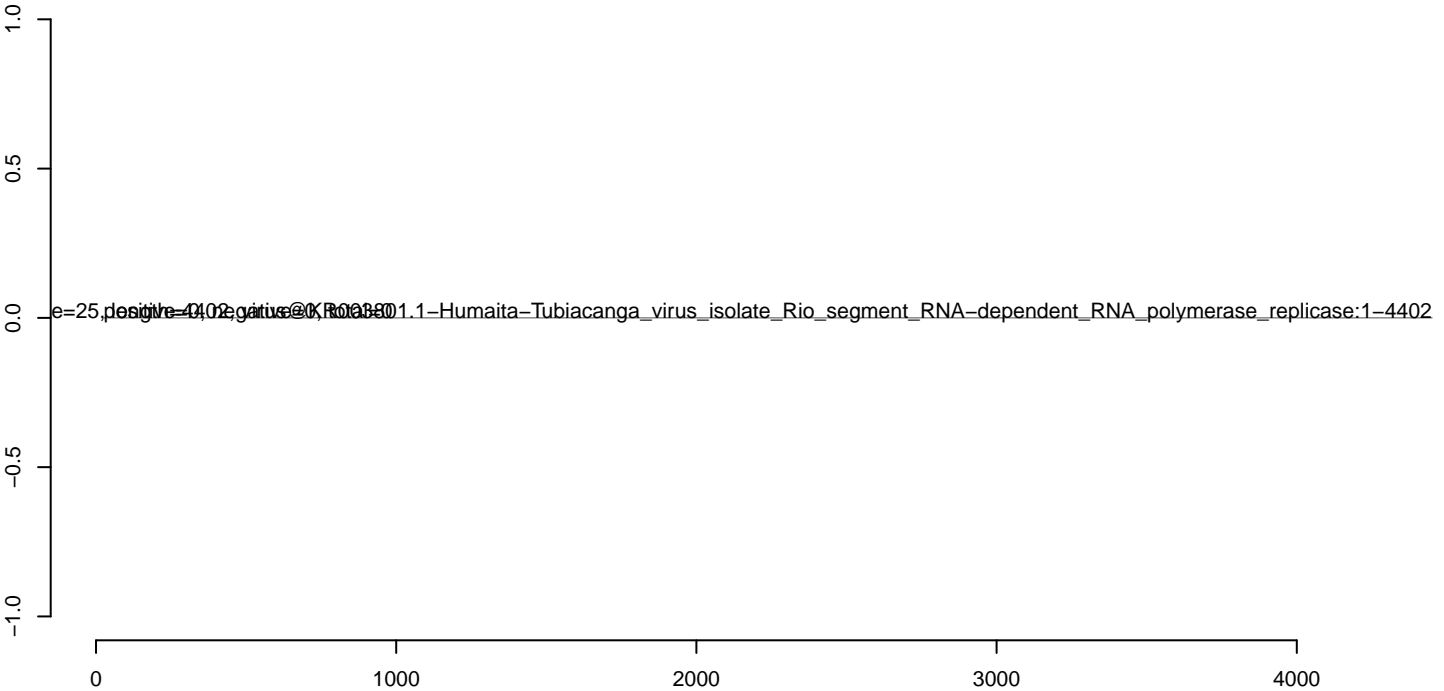
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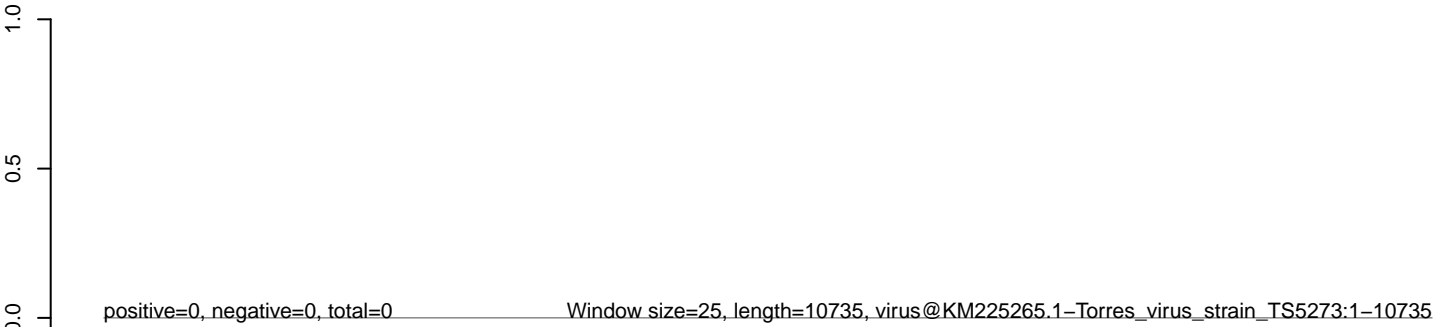
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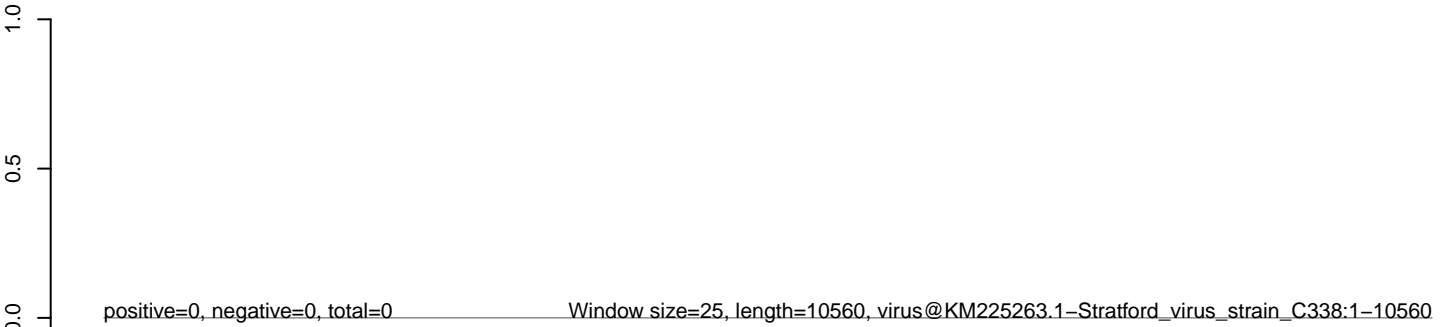
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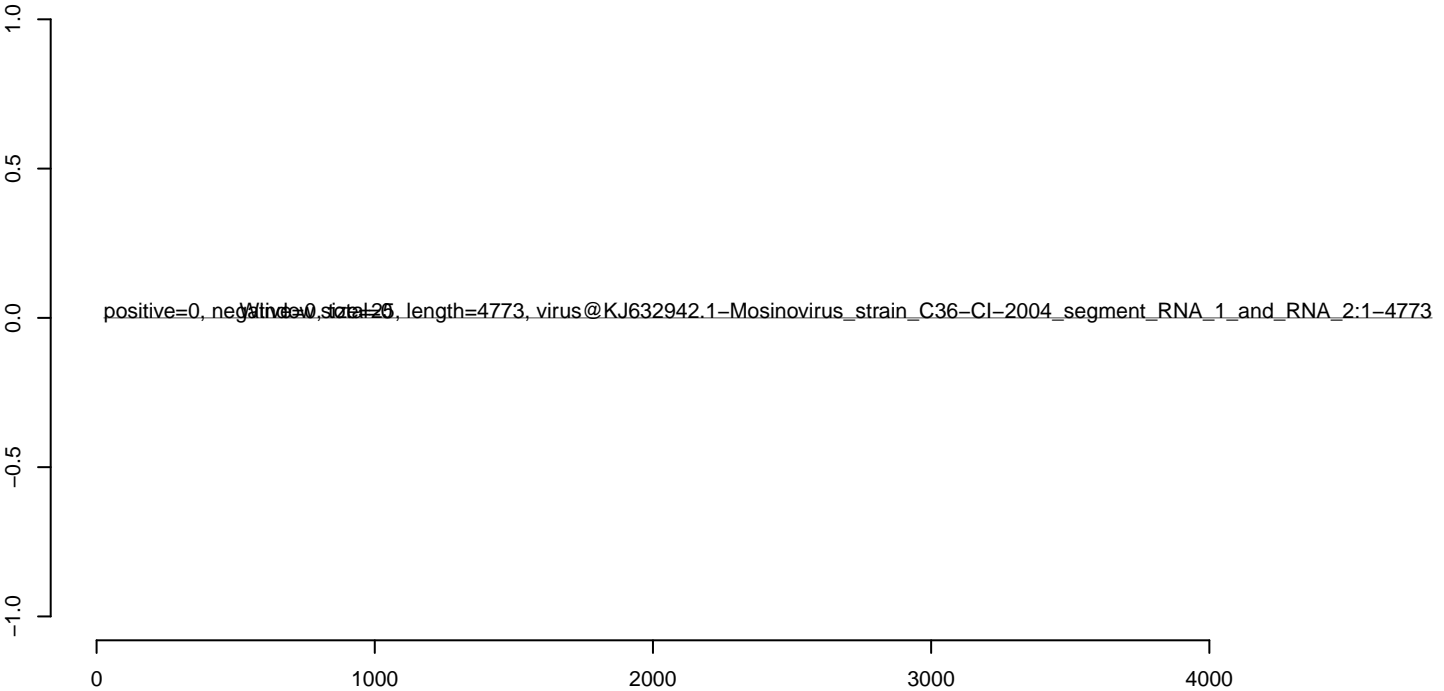
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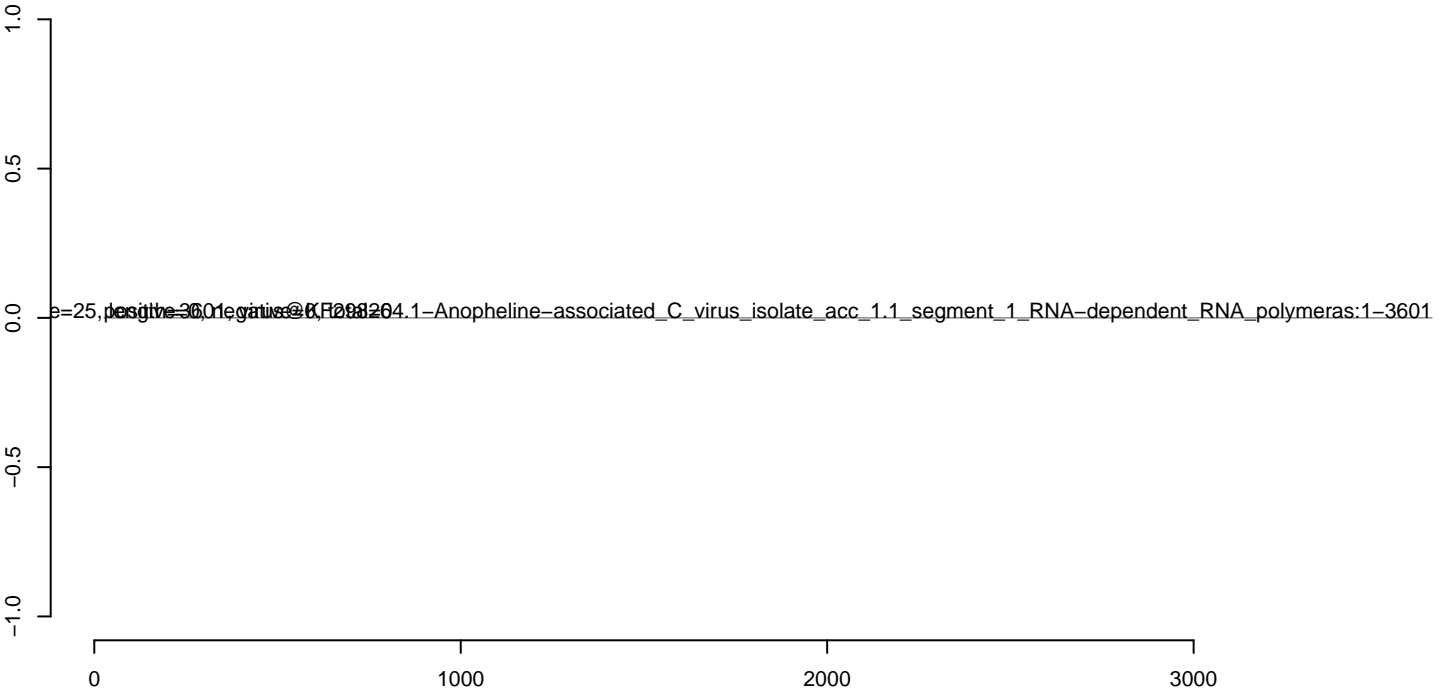
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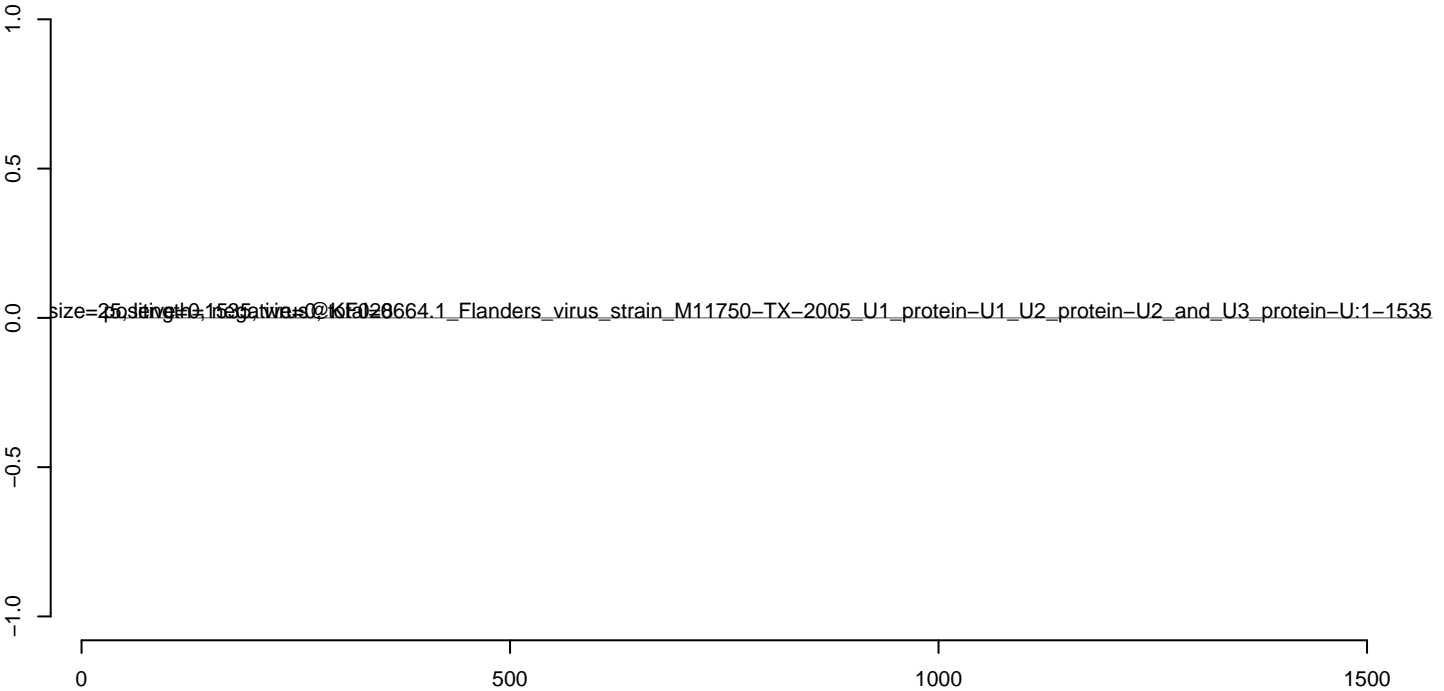
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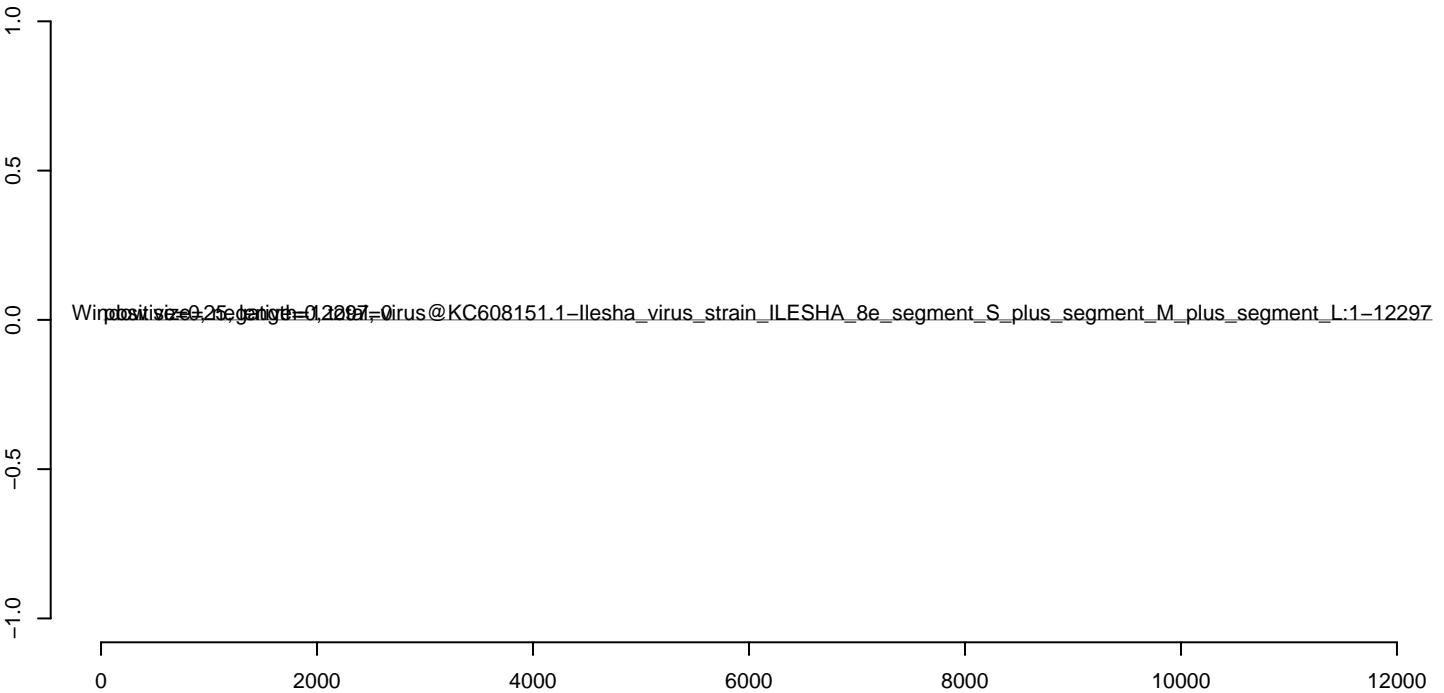
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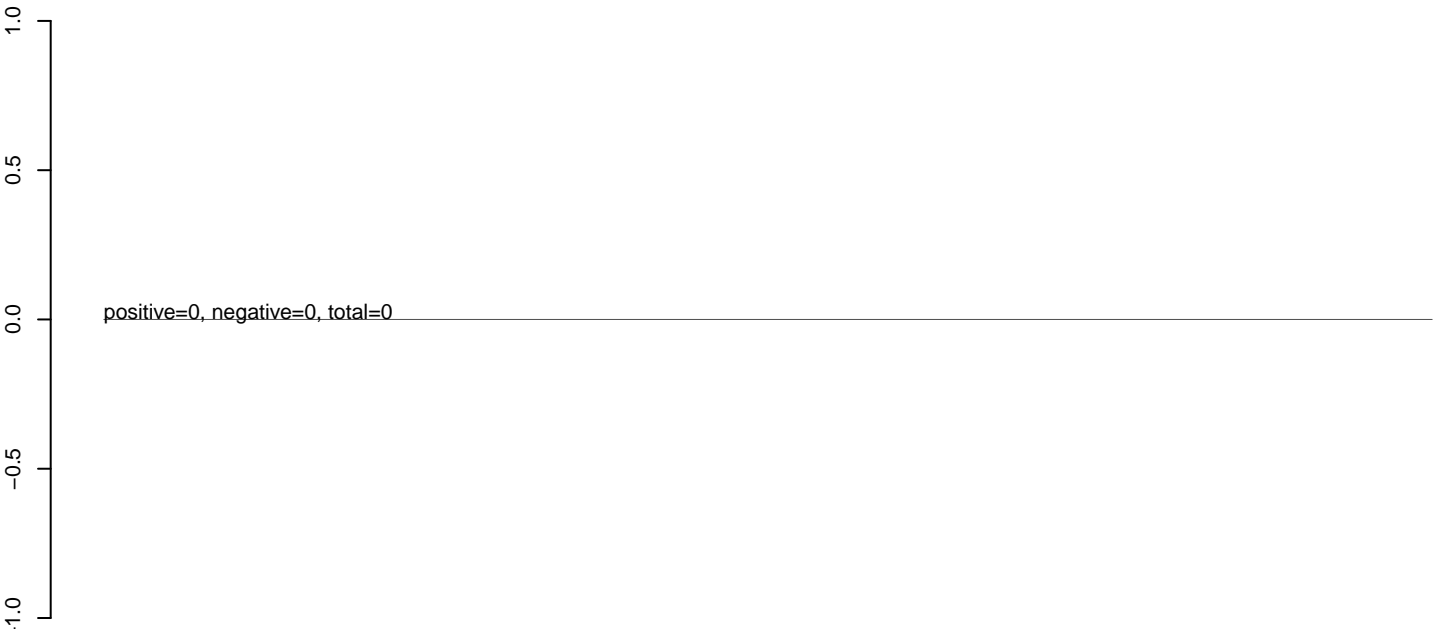
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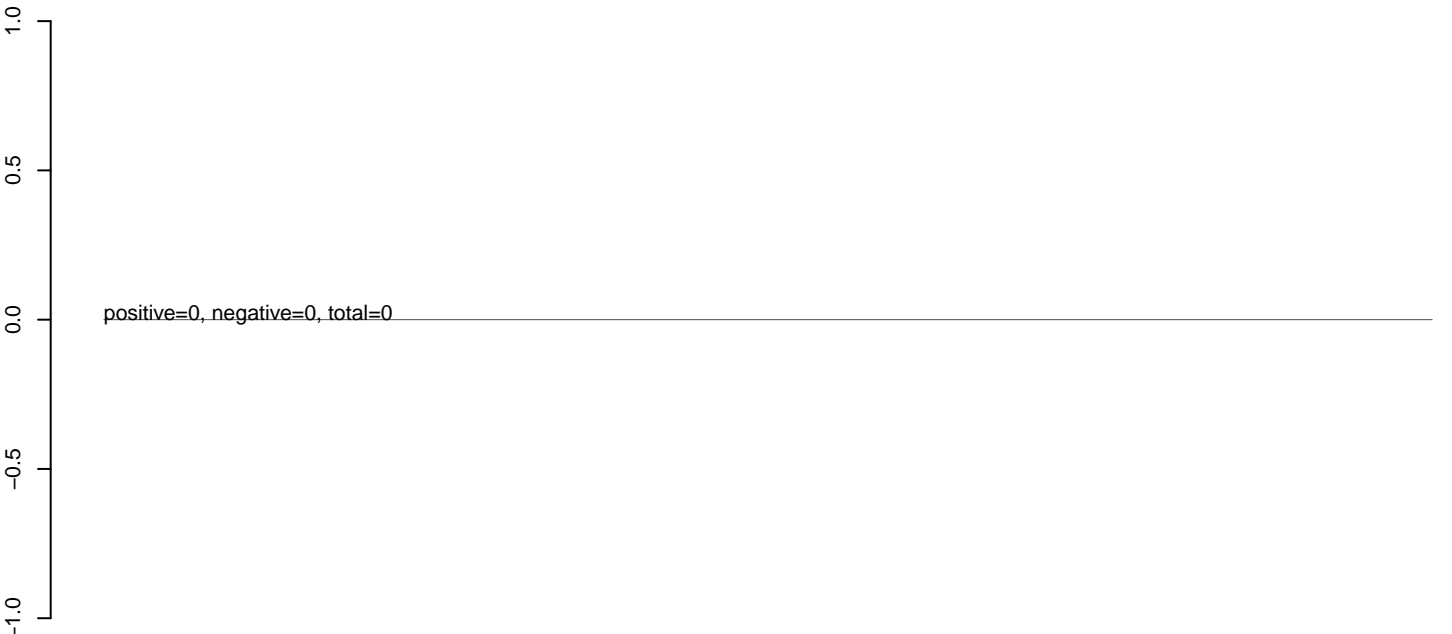
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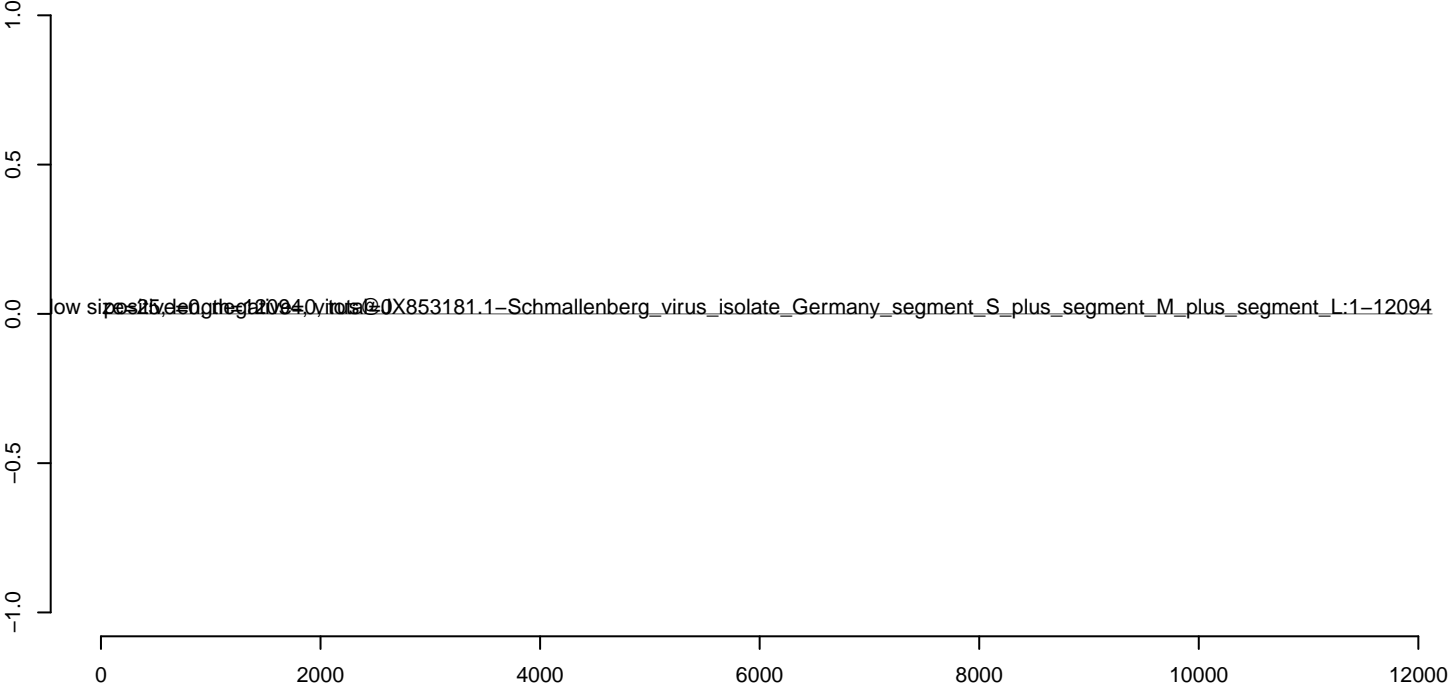
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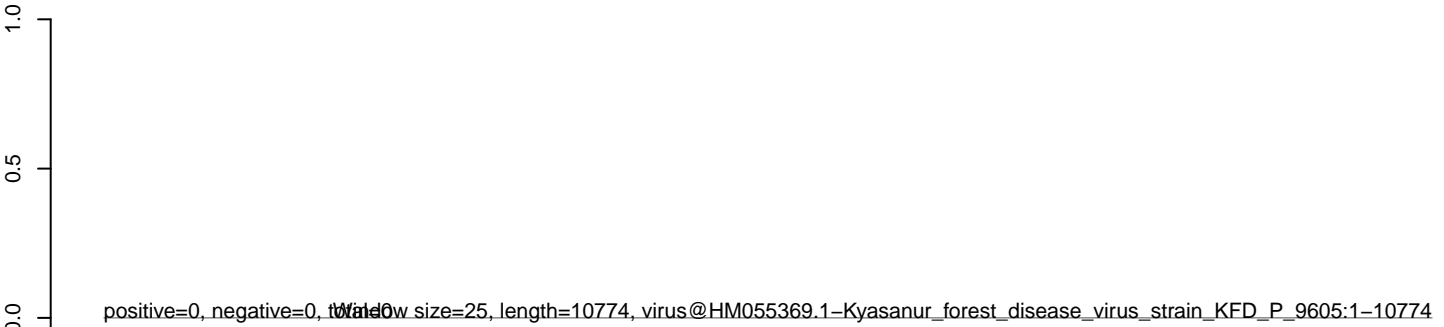
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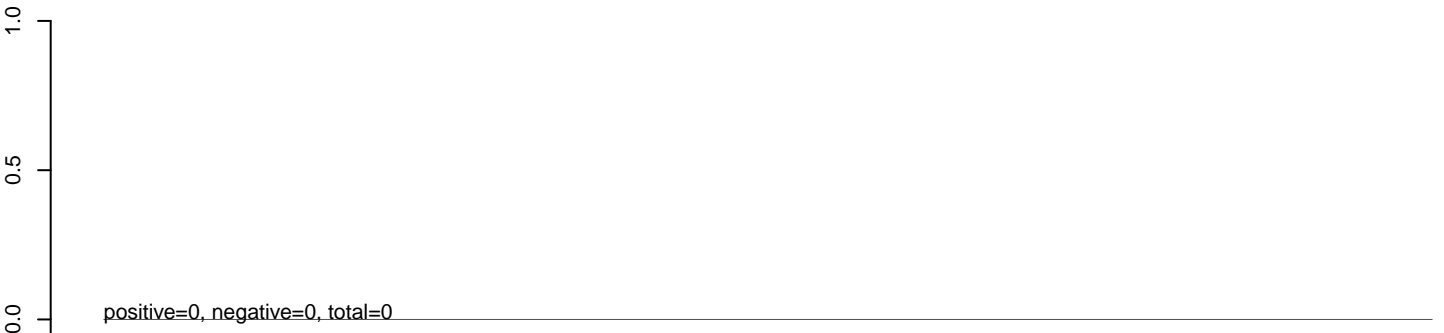
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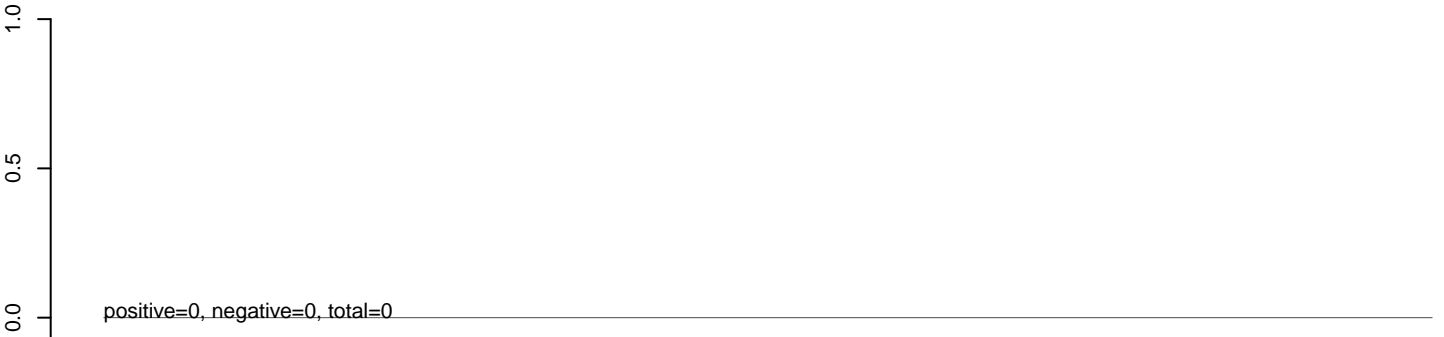
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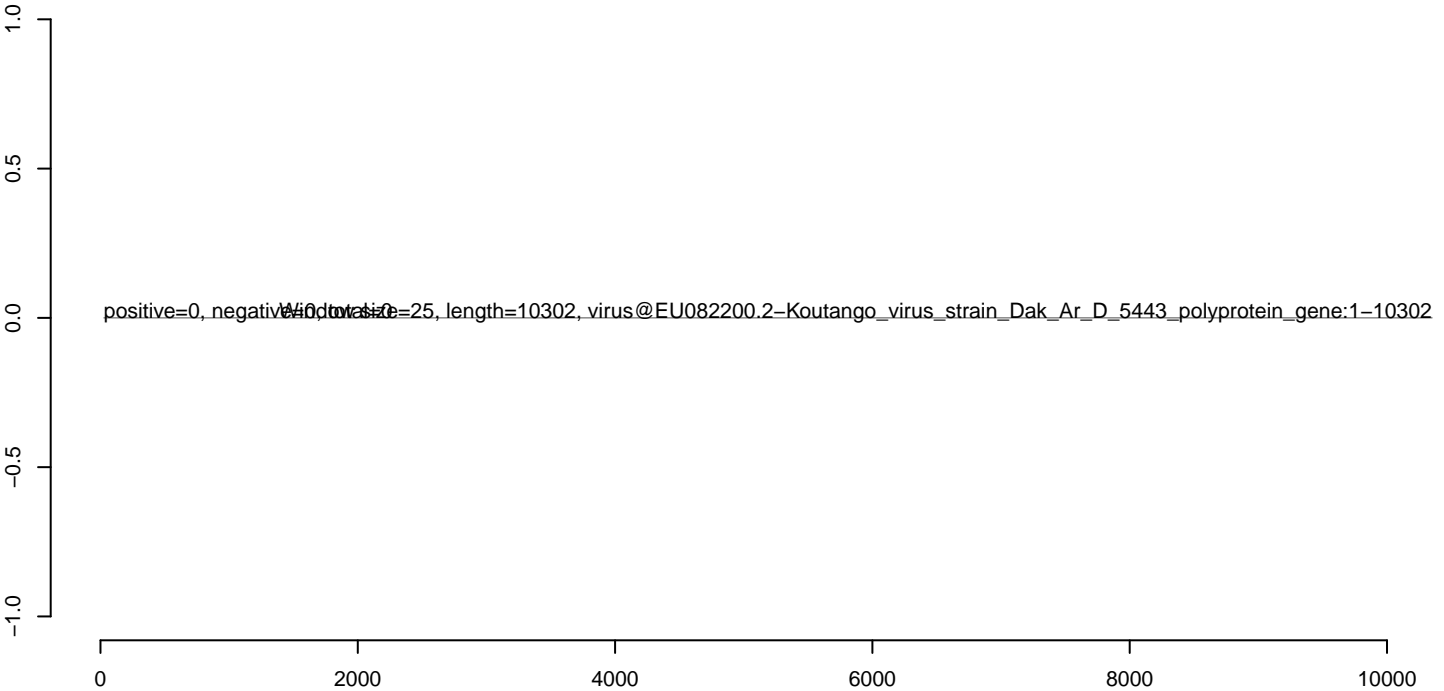
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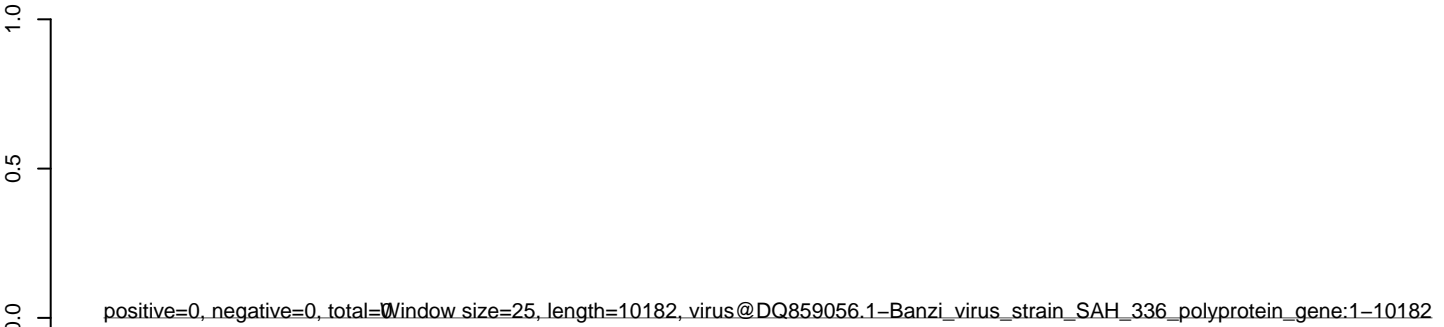
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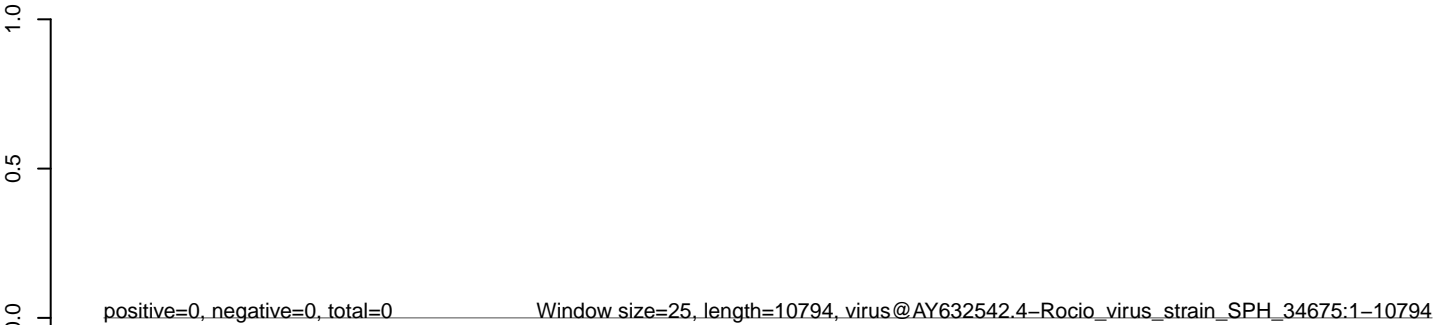
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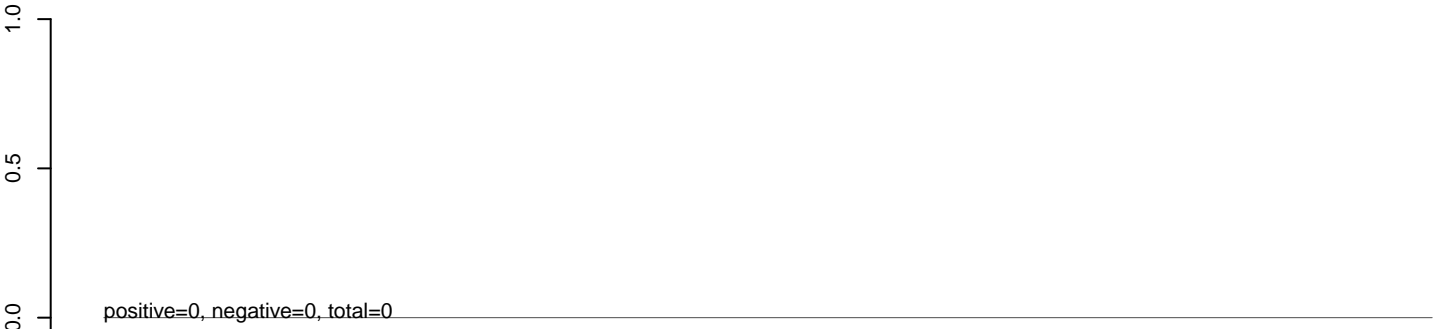


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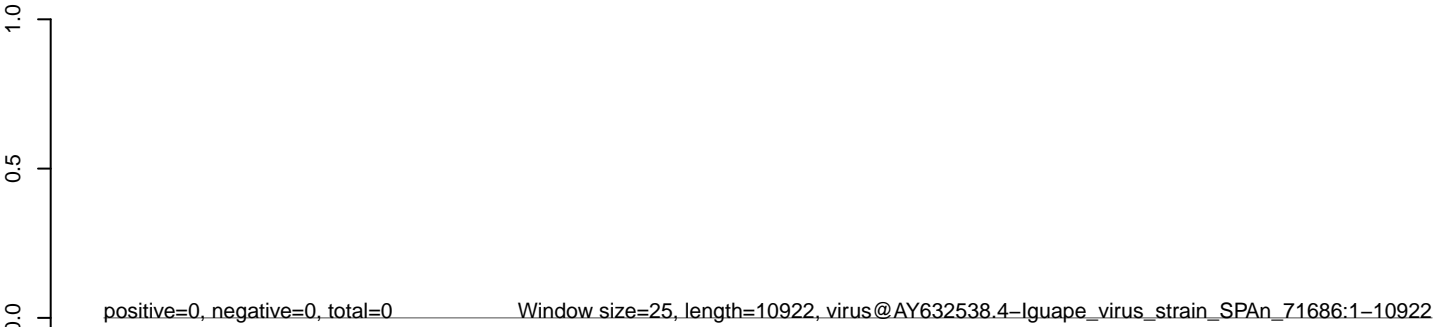
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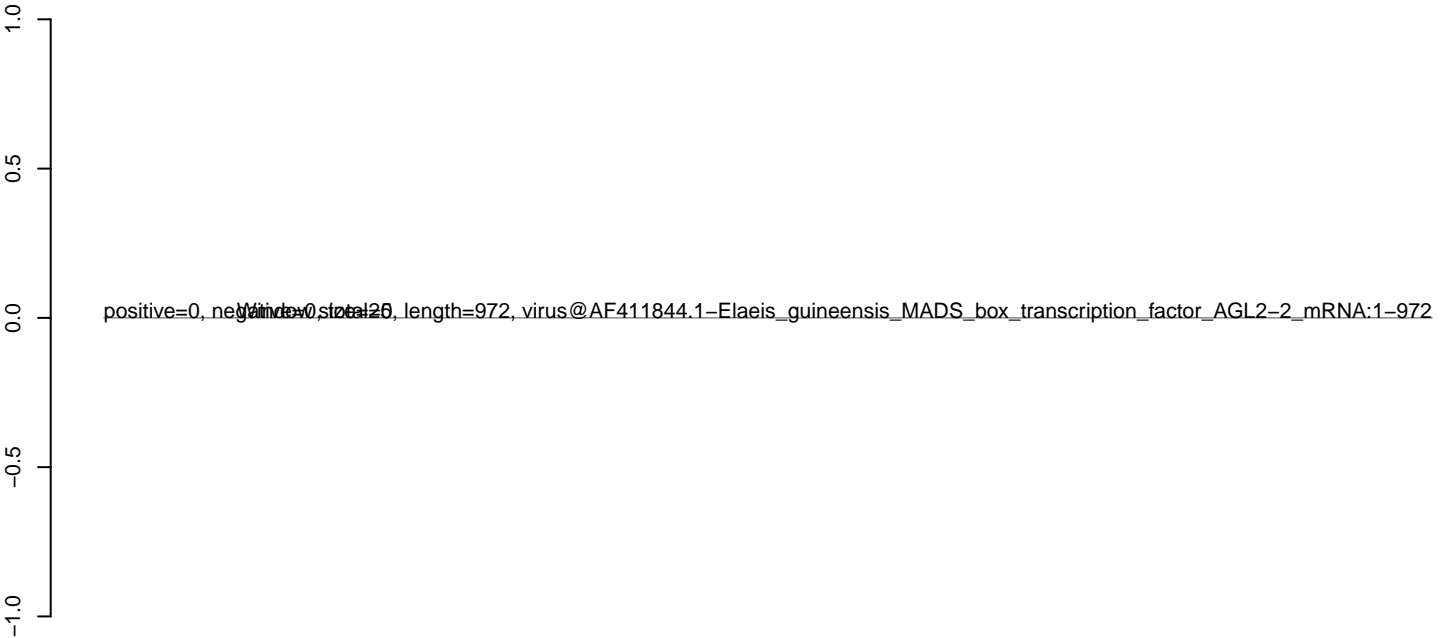
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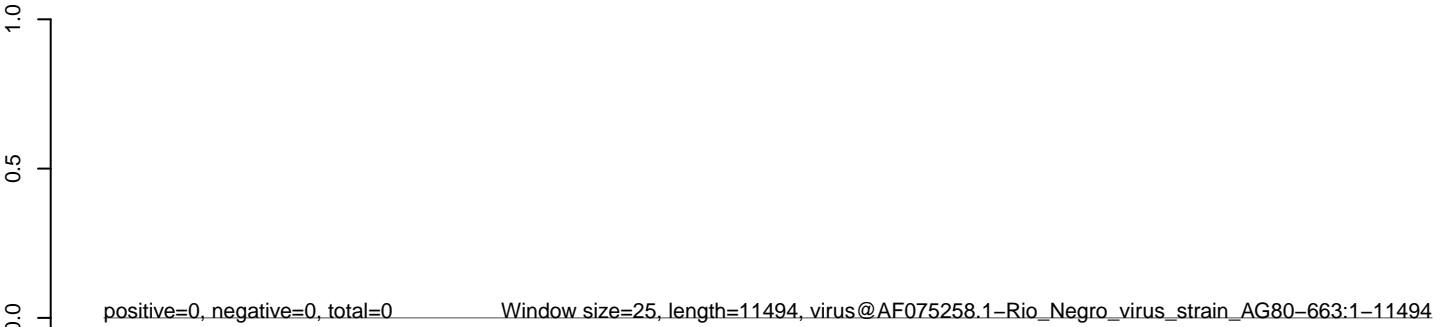
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