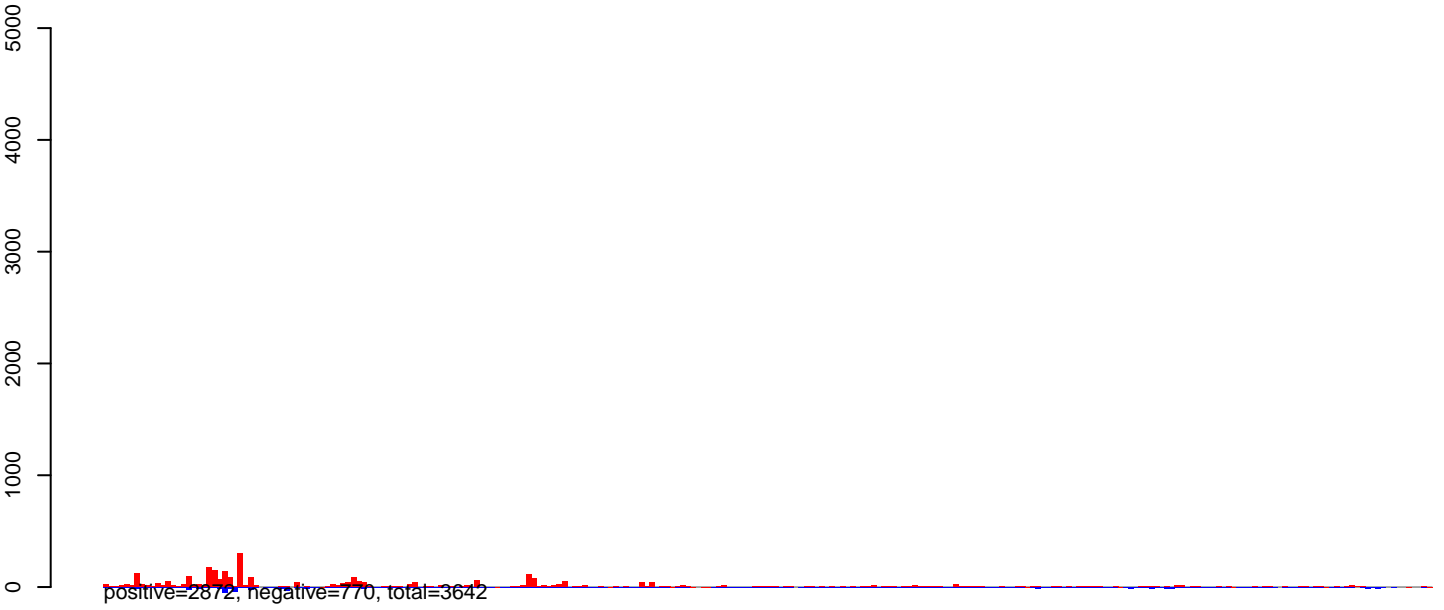
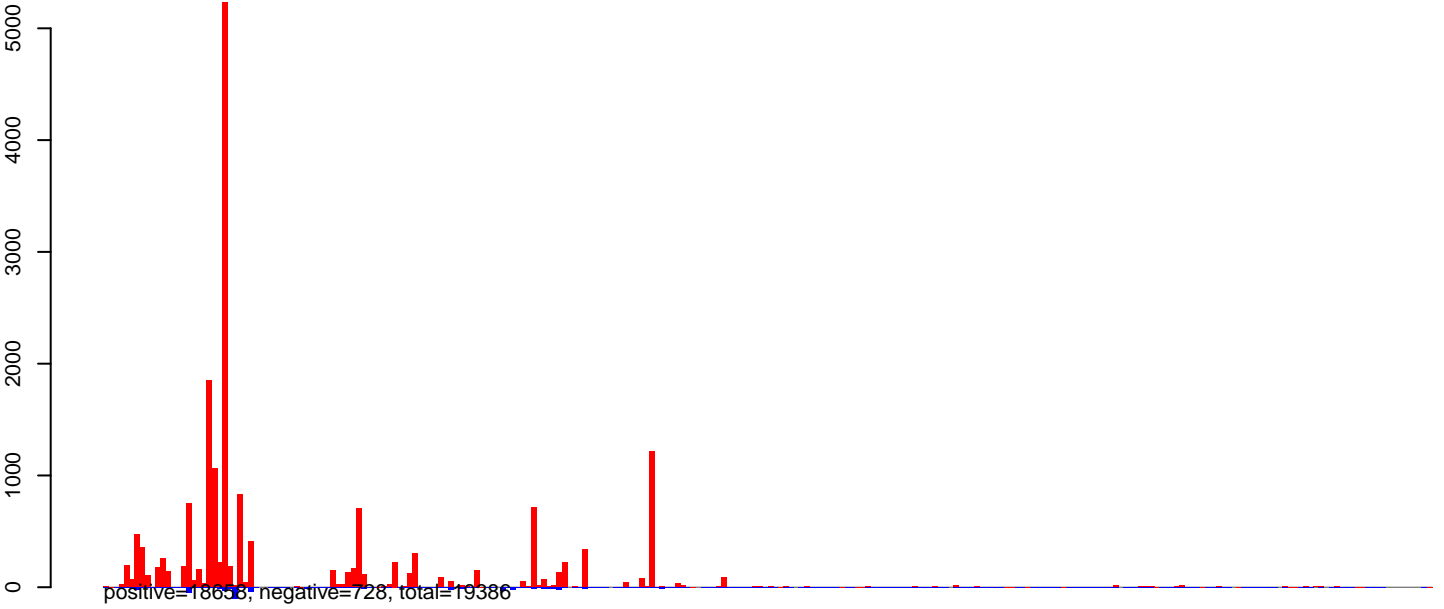


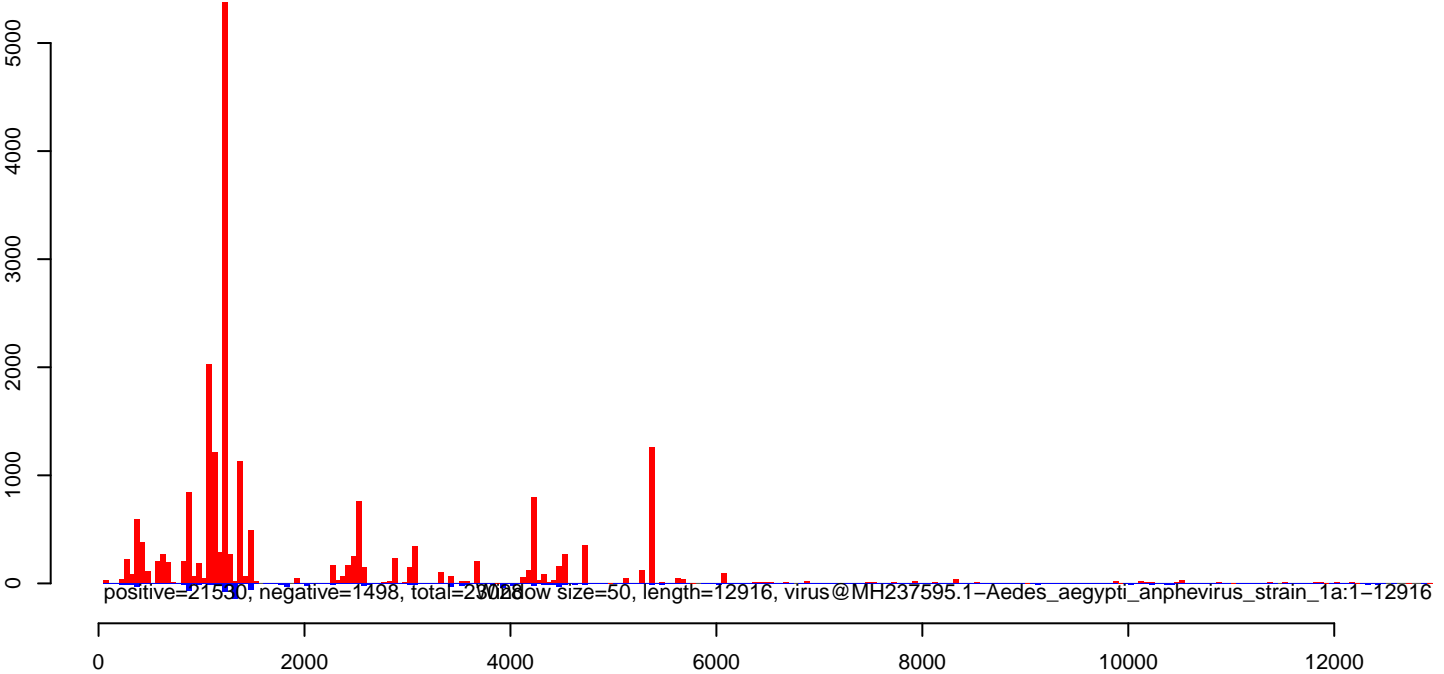
AeAeg_CCL.125_cells.18_23.rep



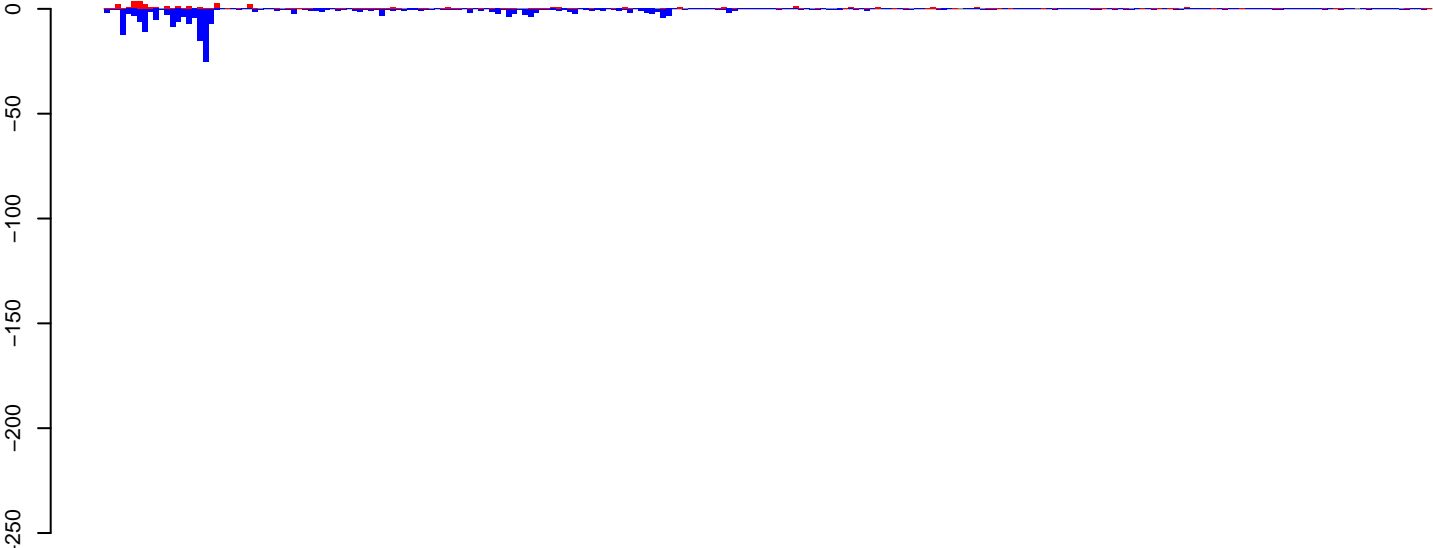
AeAeg_CCL.125_cells.24_35.rep



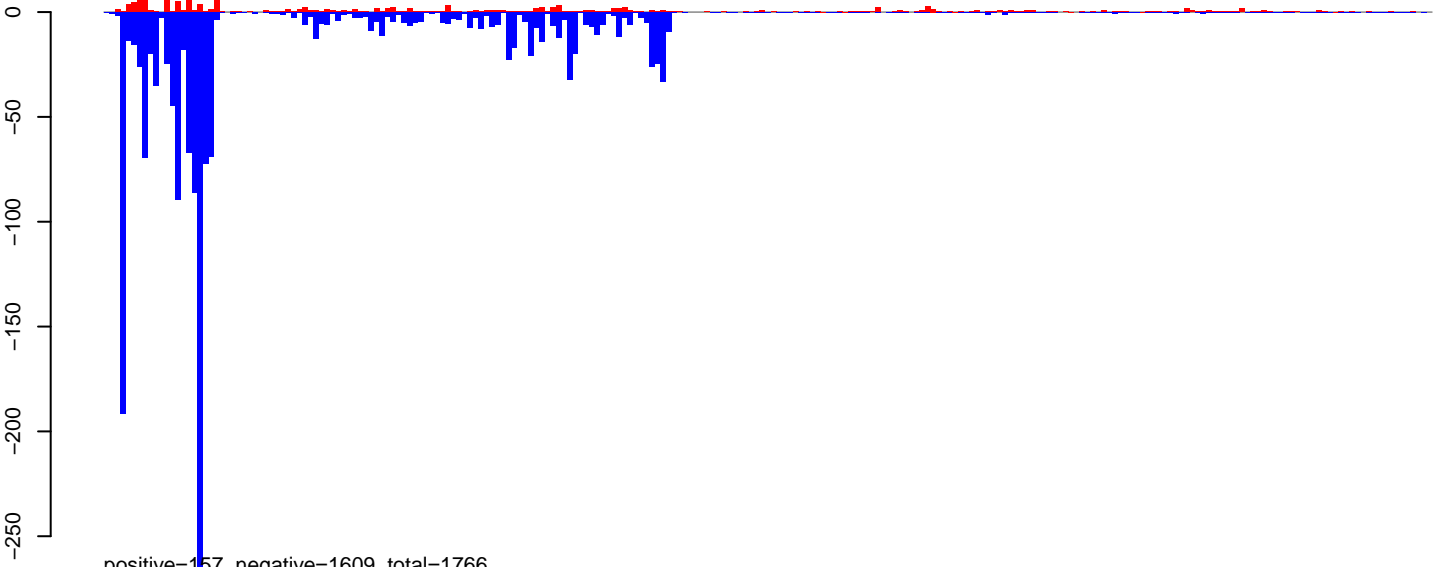
AeAeg_CCL.125_cells.rep



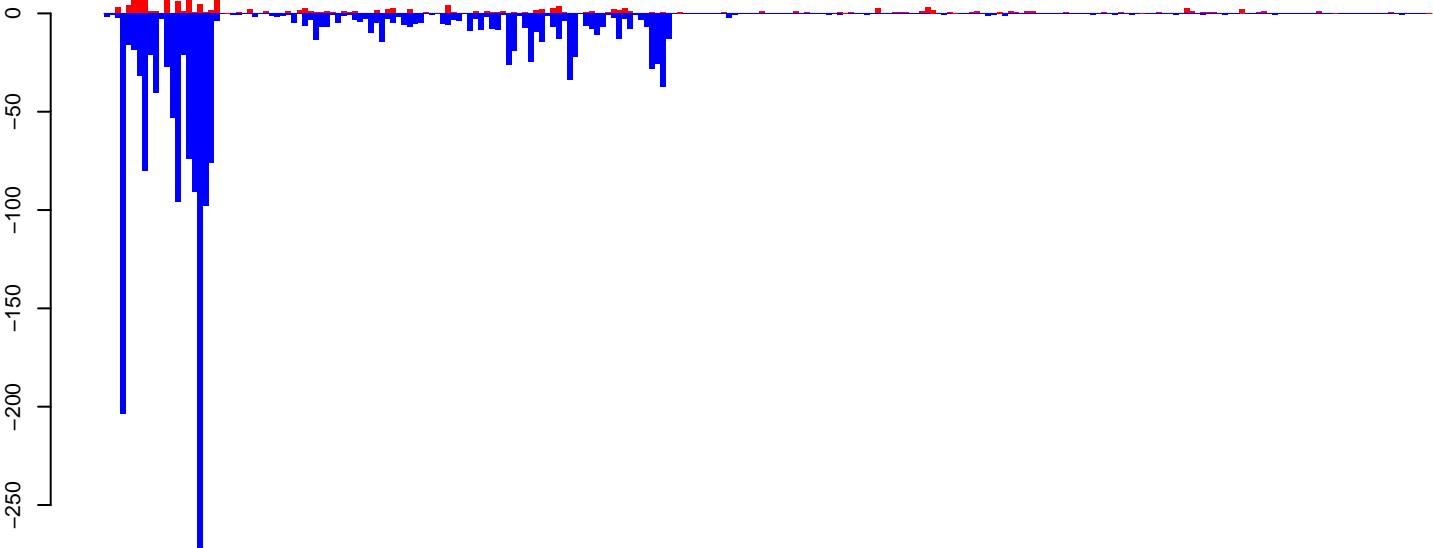
AeAeg_CCL.125_cells.18_23.rep



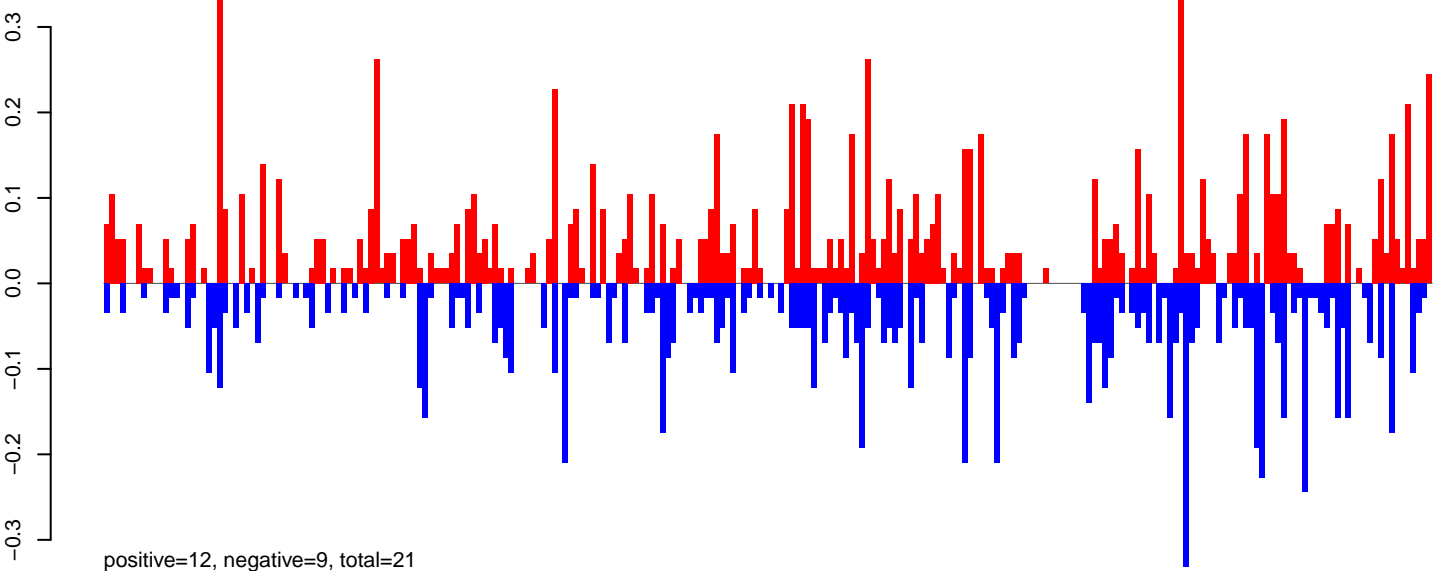
AeAeg_CCL.125_cells.24_35.rep



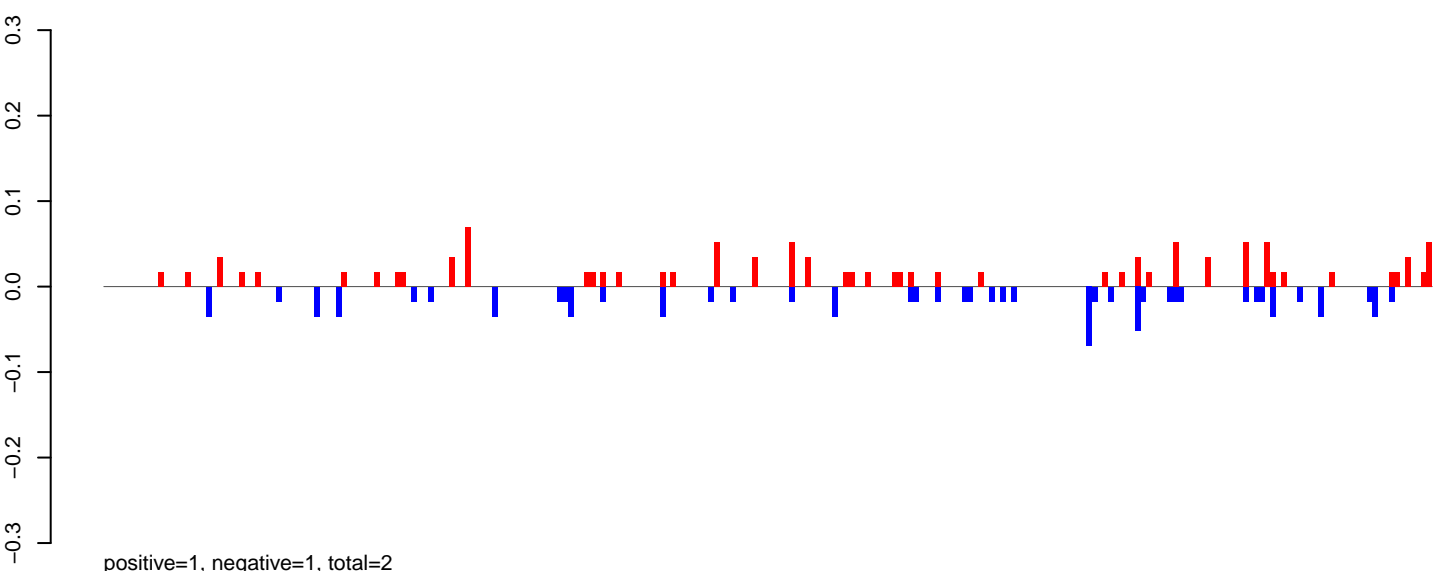
AeAeg_CCL.125_cells.rep



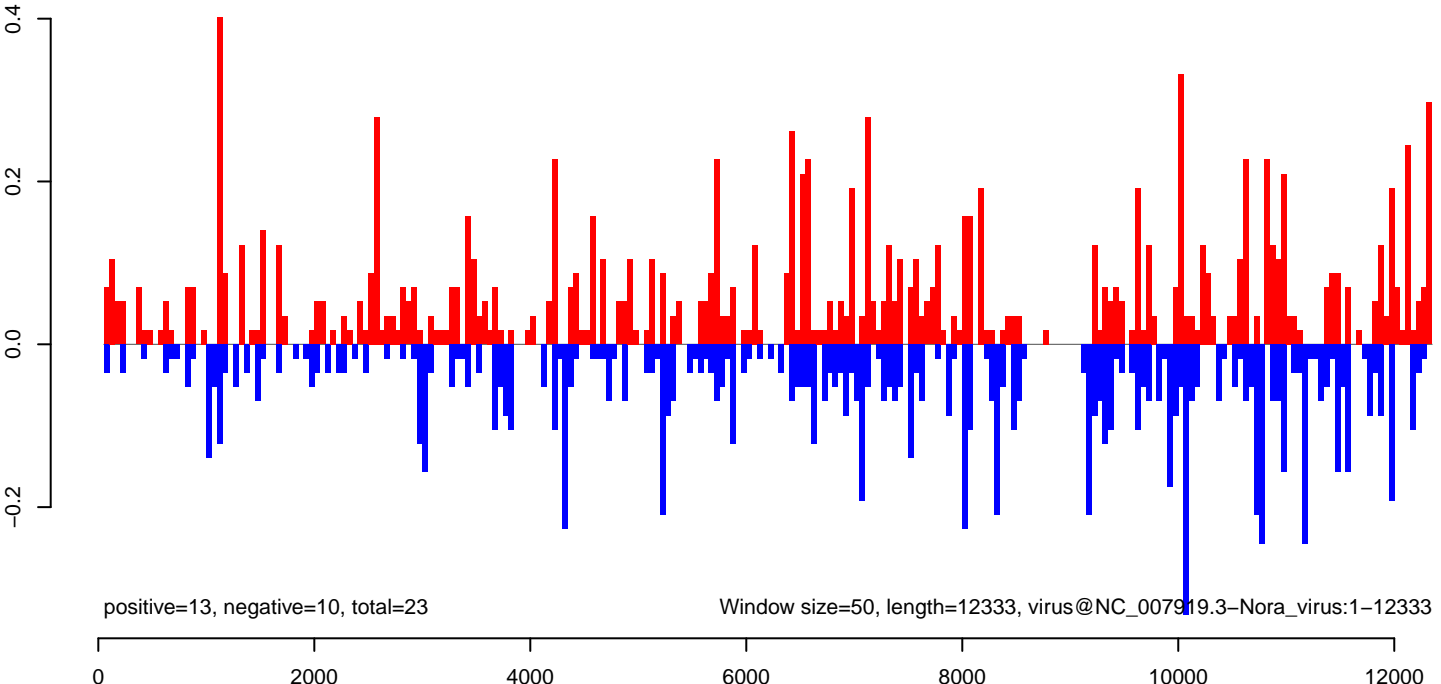
AeAeg_CCL.125_cells.18_23.rep



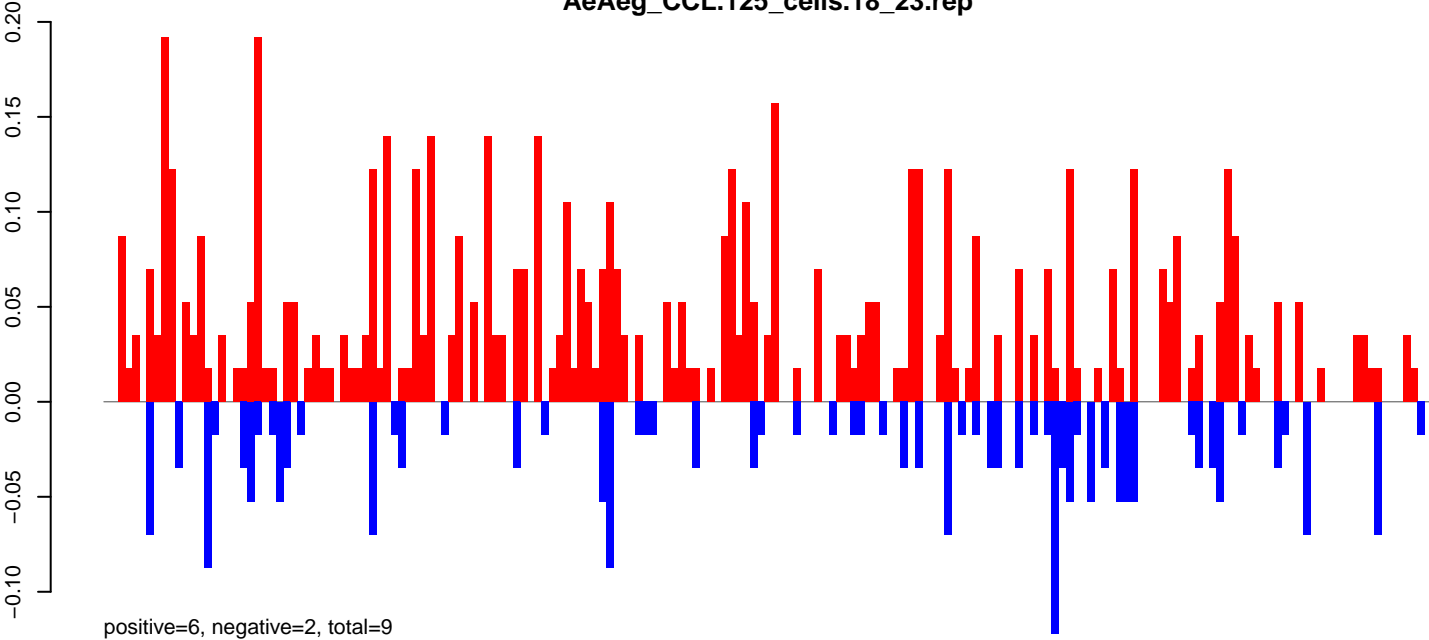
AeAeg_CCL.125_cells.24_35.rep



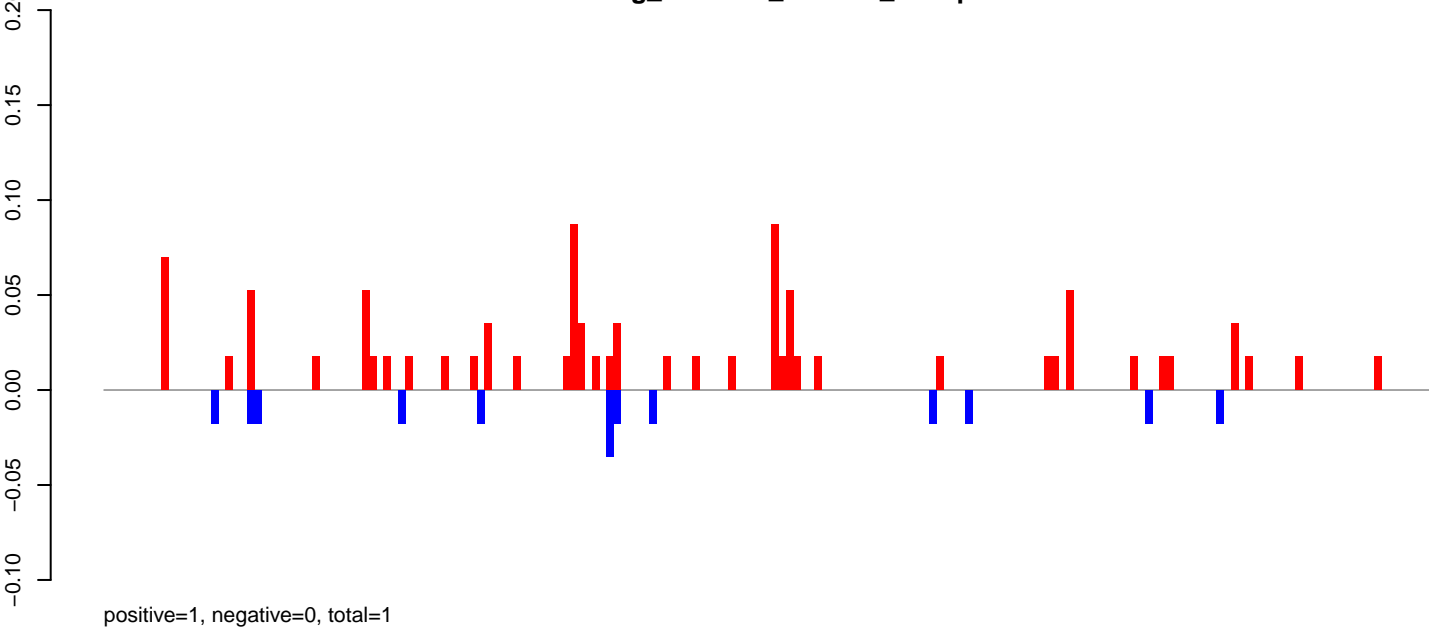
AeAeg_CCL.125_cells.rep



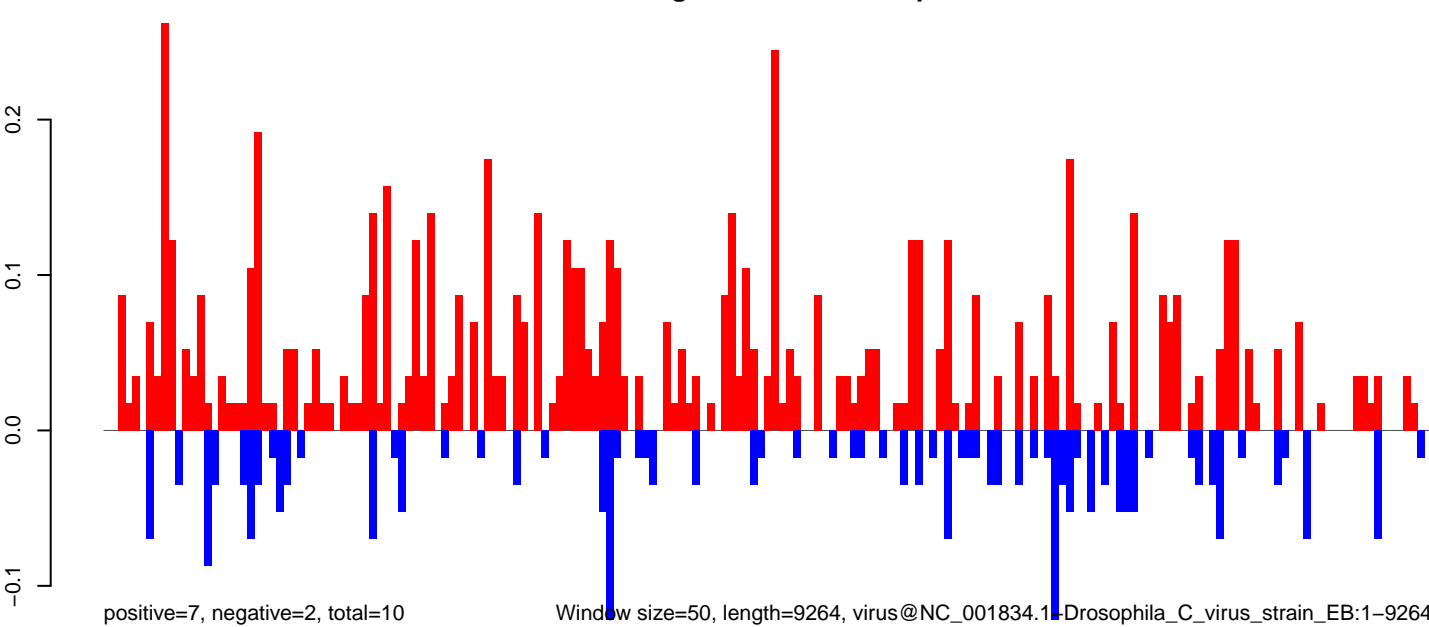
AeAeg_CCL.125_cells.18_23.rep



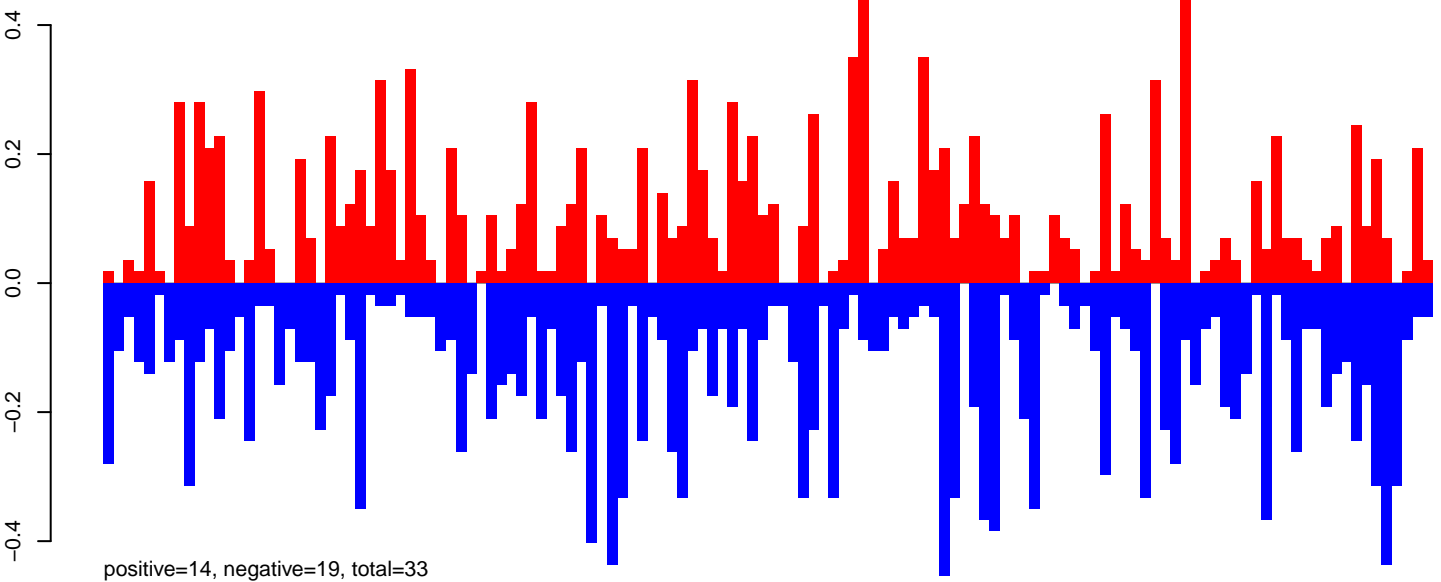
AeAeg_CCL.125_cells.24_35.rep



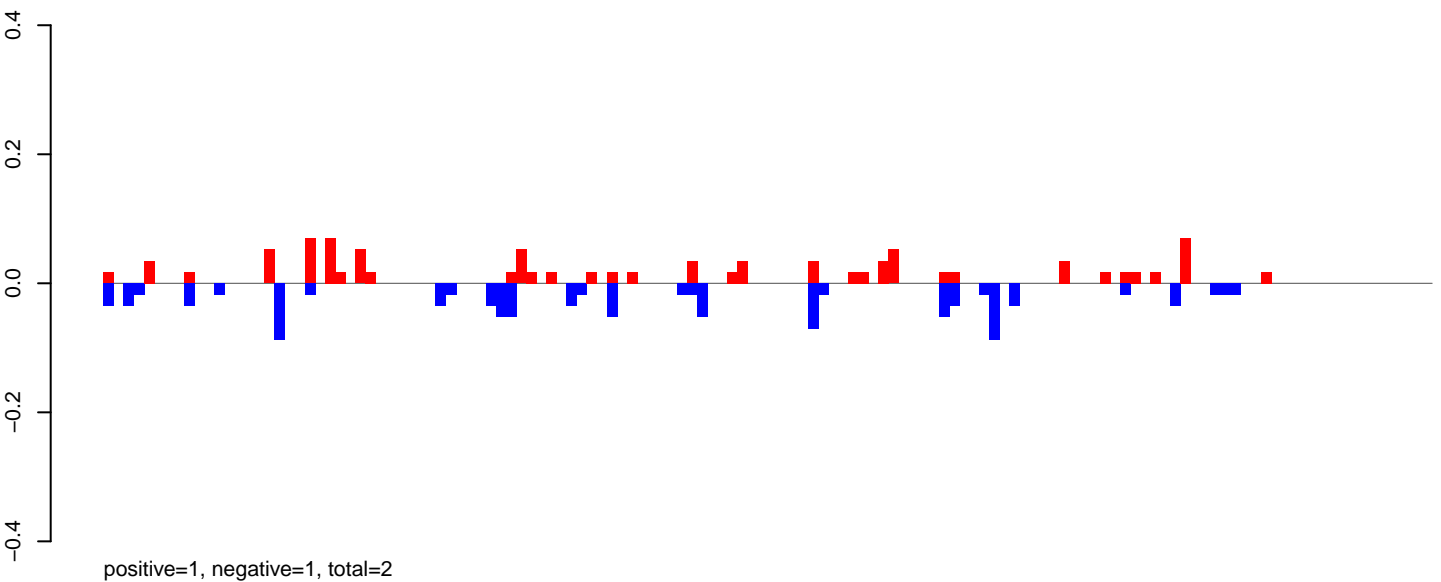
AeAeg_CCL.125_cells.rep



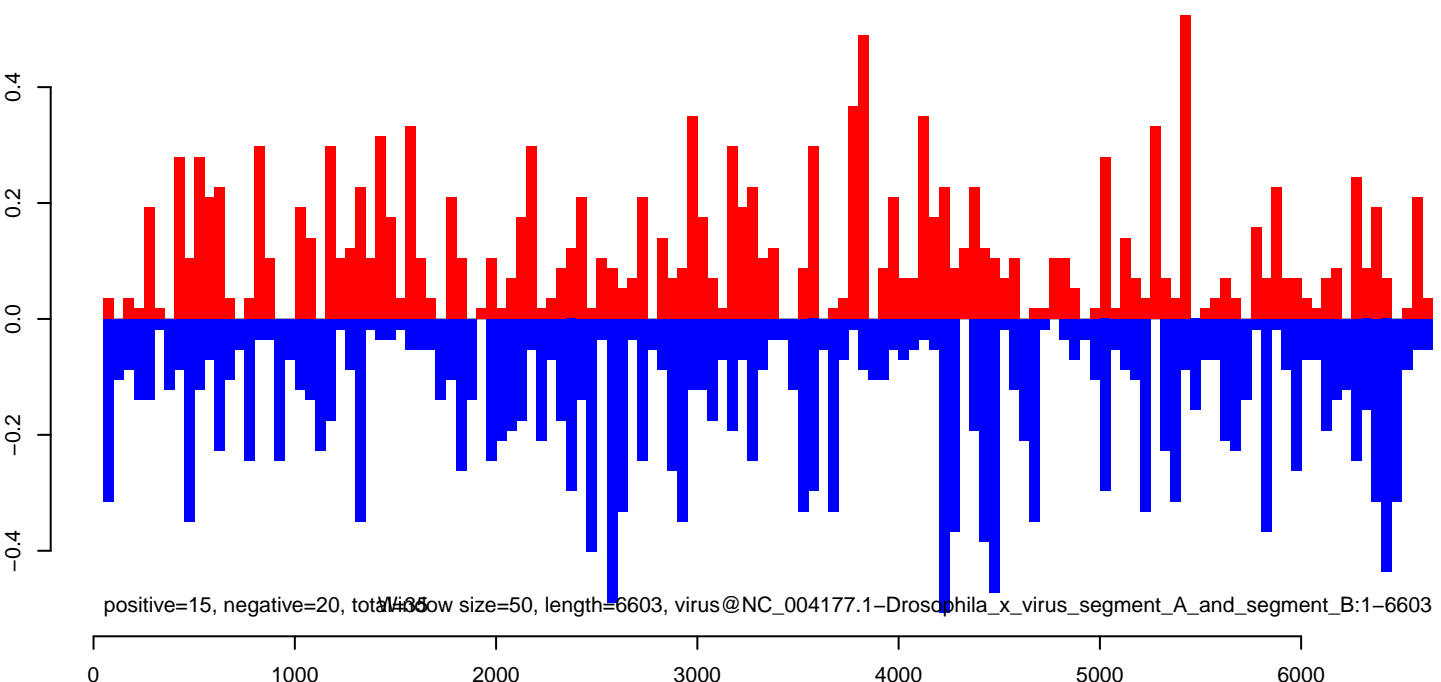
AeAeg_CCL.125_cells.18_23.rep



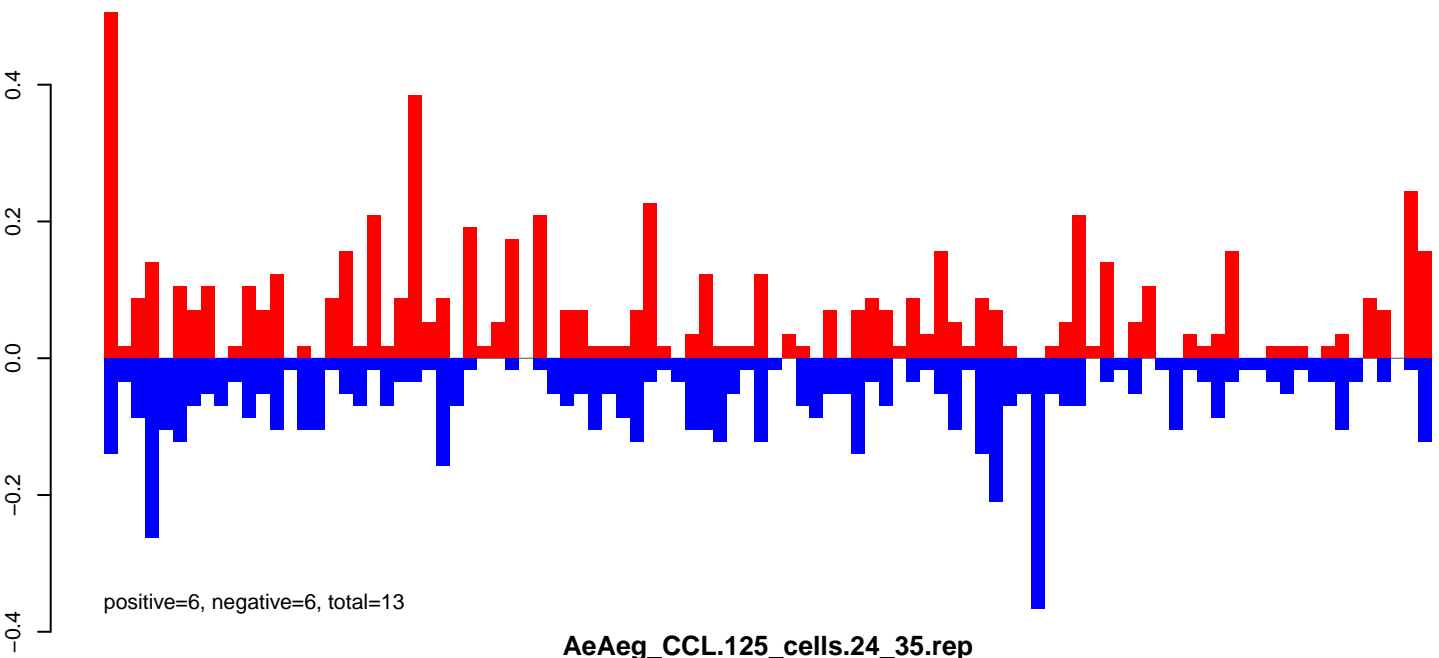
AeAeg_CCL.125_cells.24_35.rep



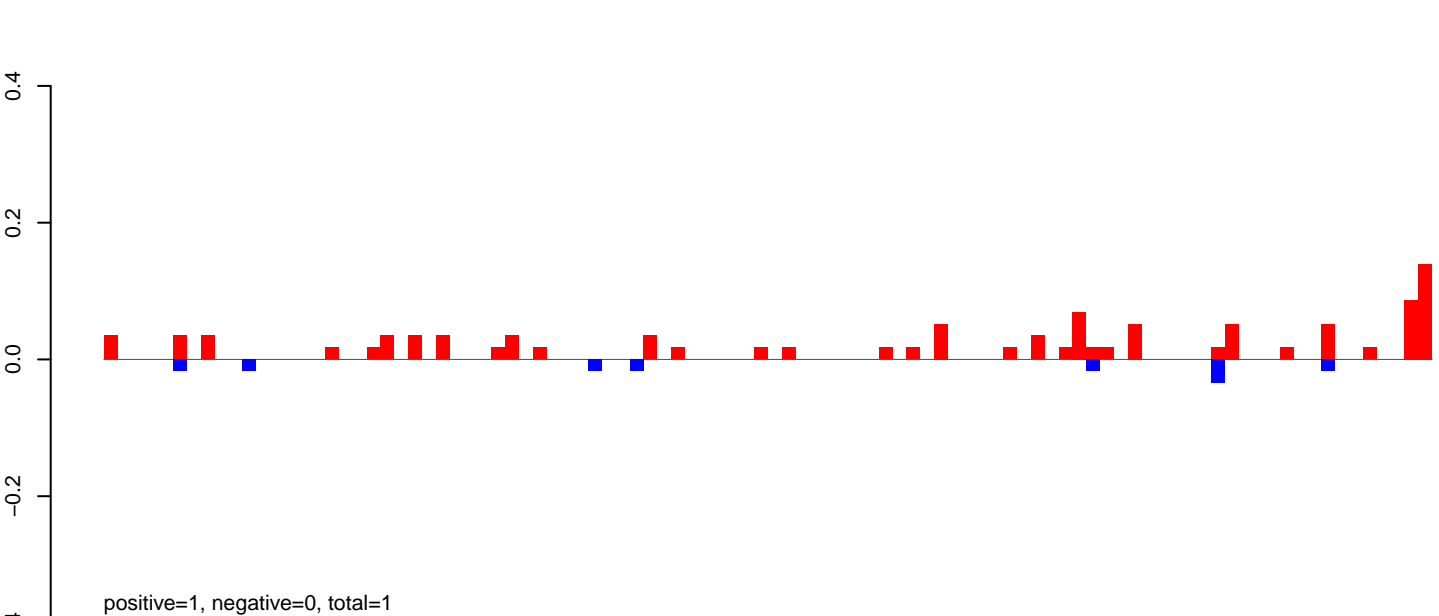
AeAeg_CCL.125_cells.rep



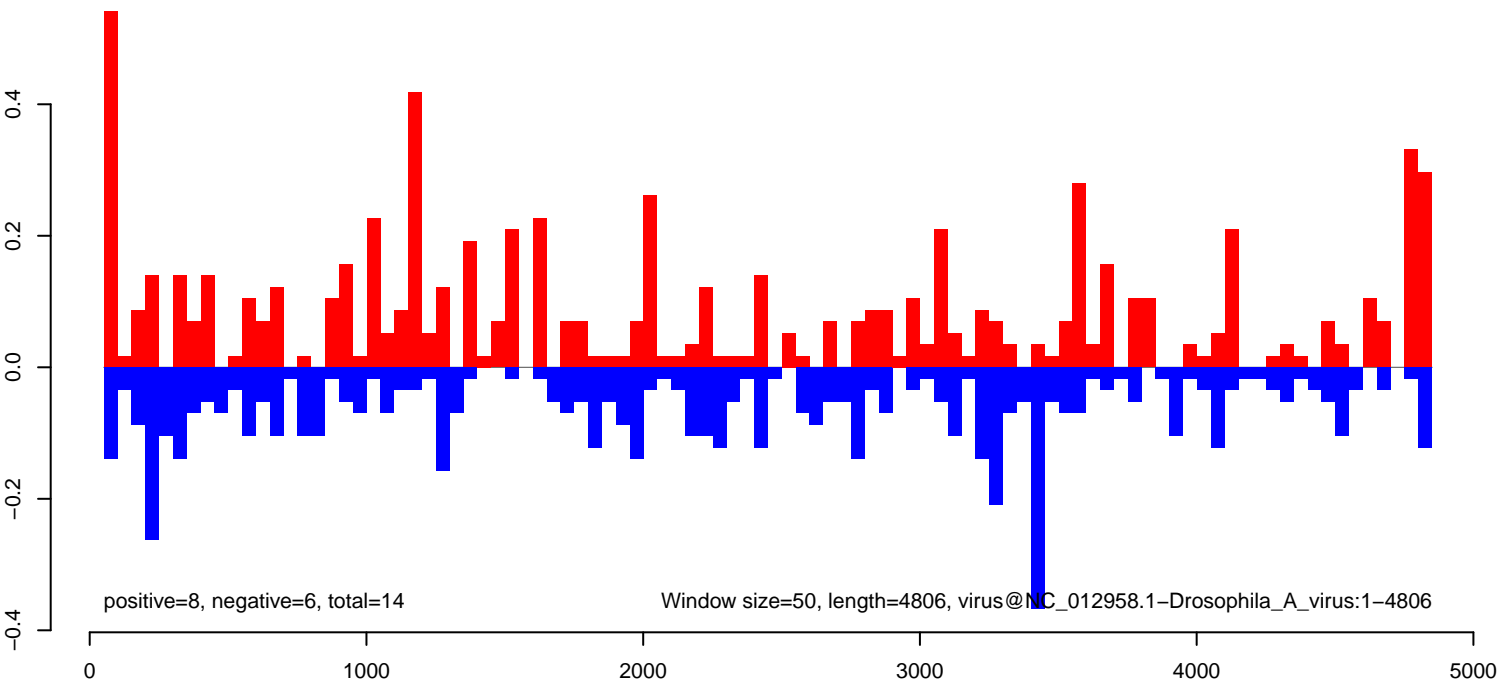
AeAeg_CCL.125_cells.18_23.rep



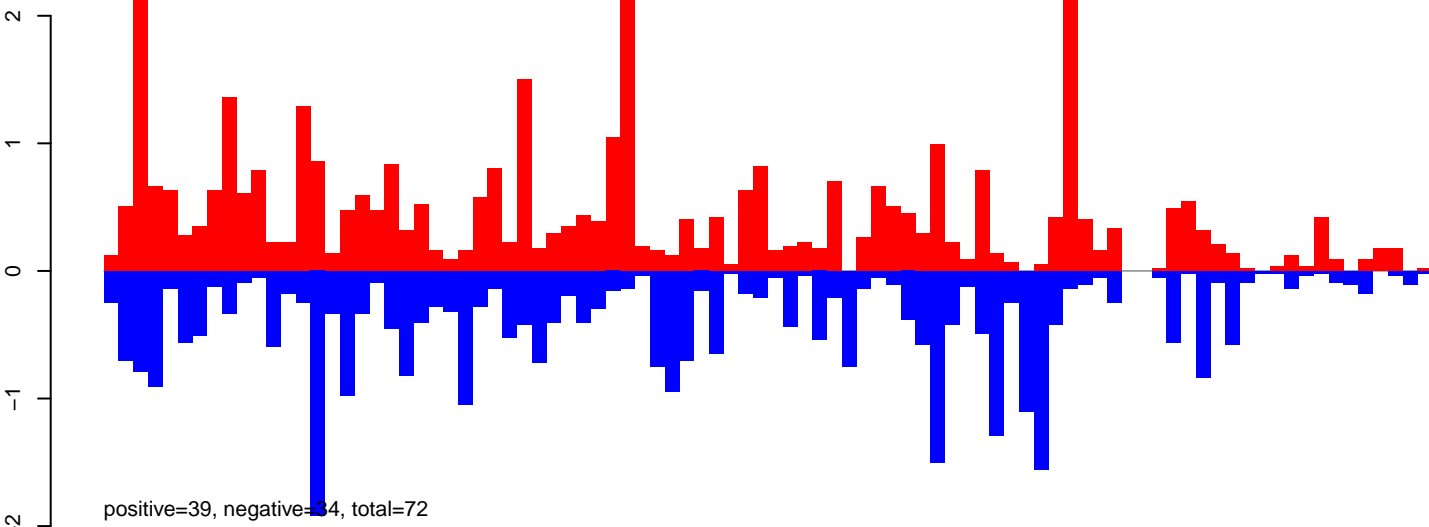
AeAeg_CCL.125_cells.24_35.rep



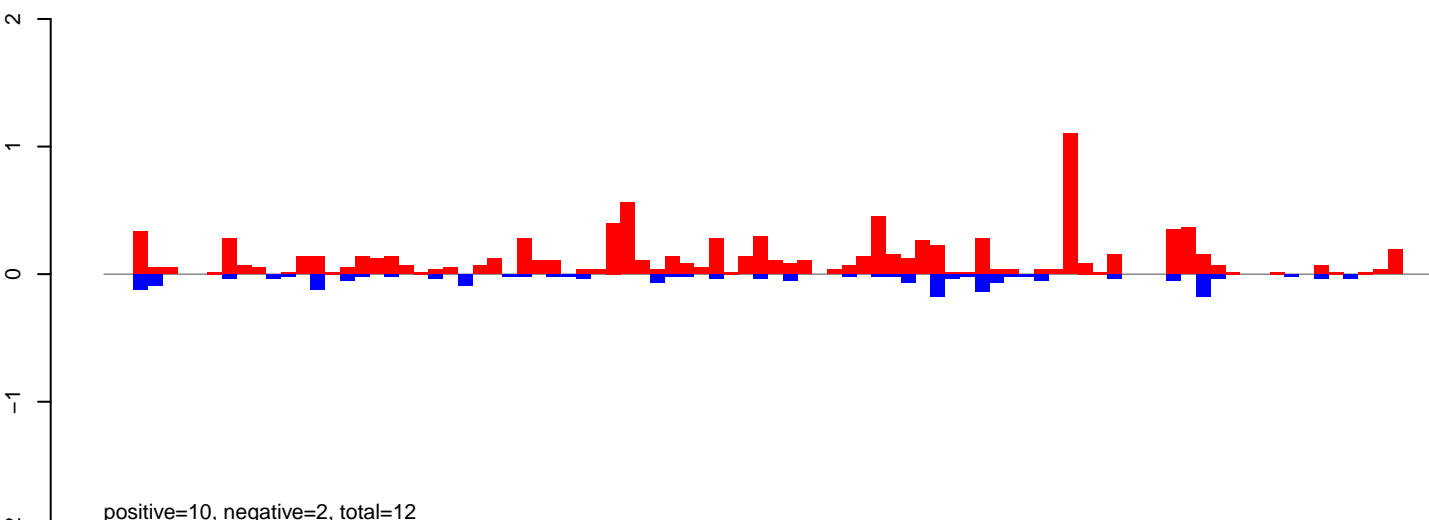
AeAeg_CCL.125_cells.rep



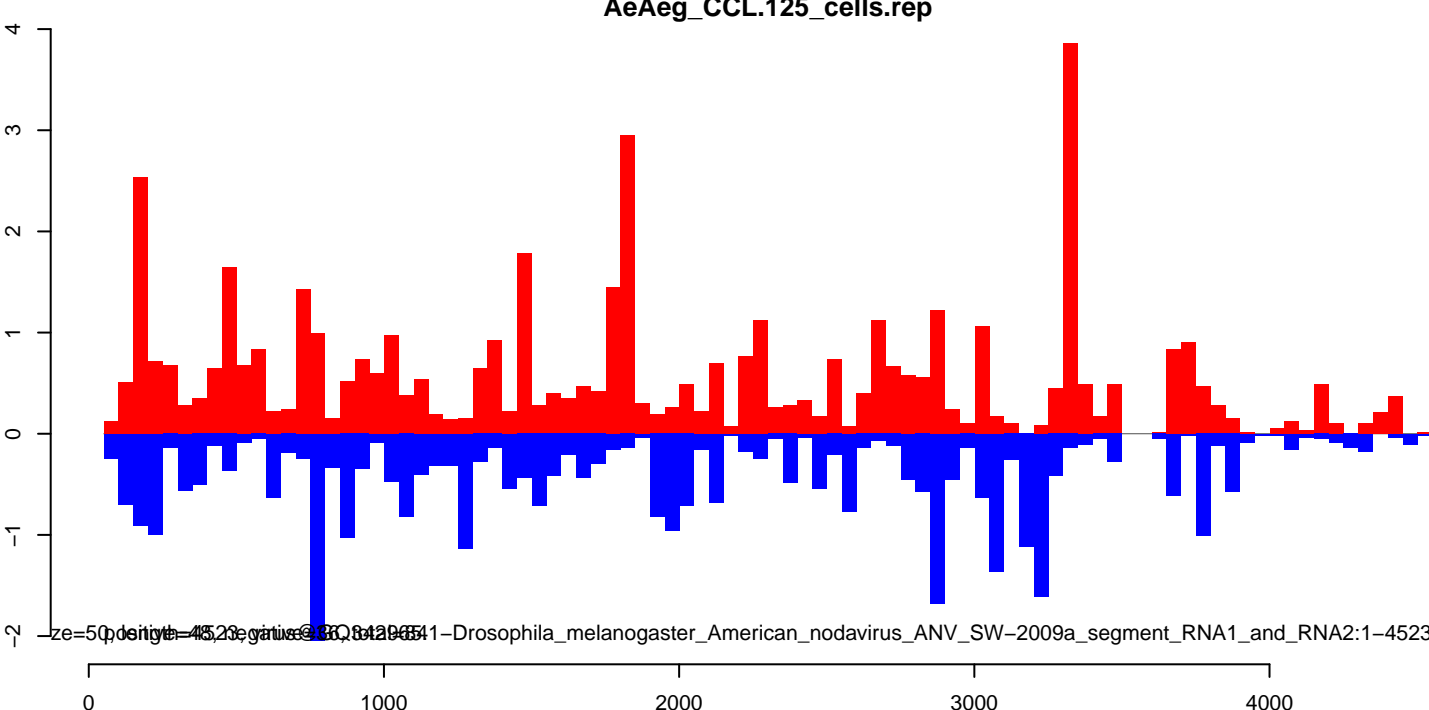
AeAeg_CCL.125_cells.18_23.rep



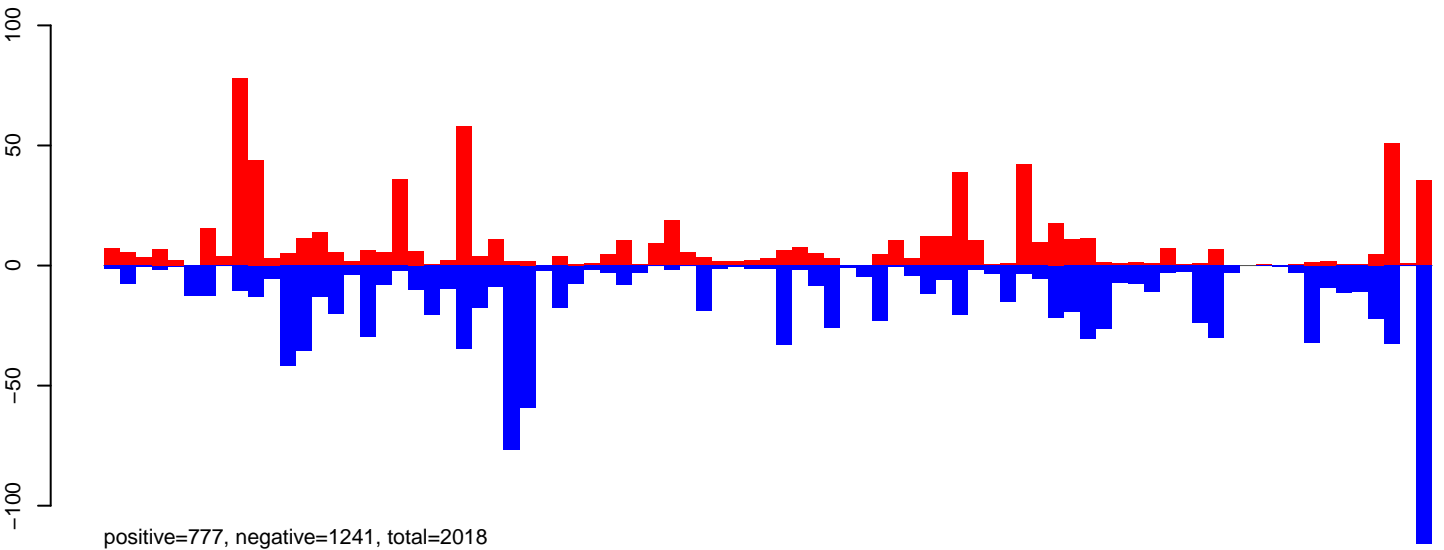
AeAeg_CCL.125_cells.24_35.rep



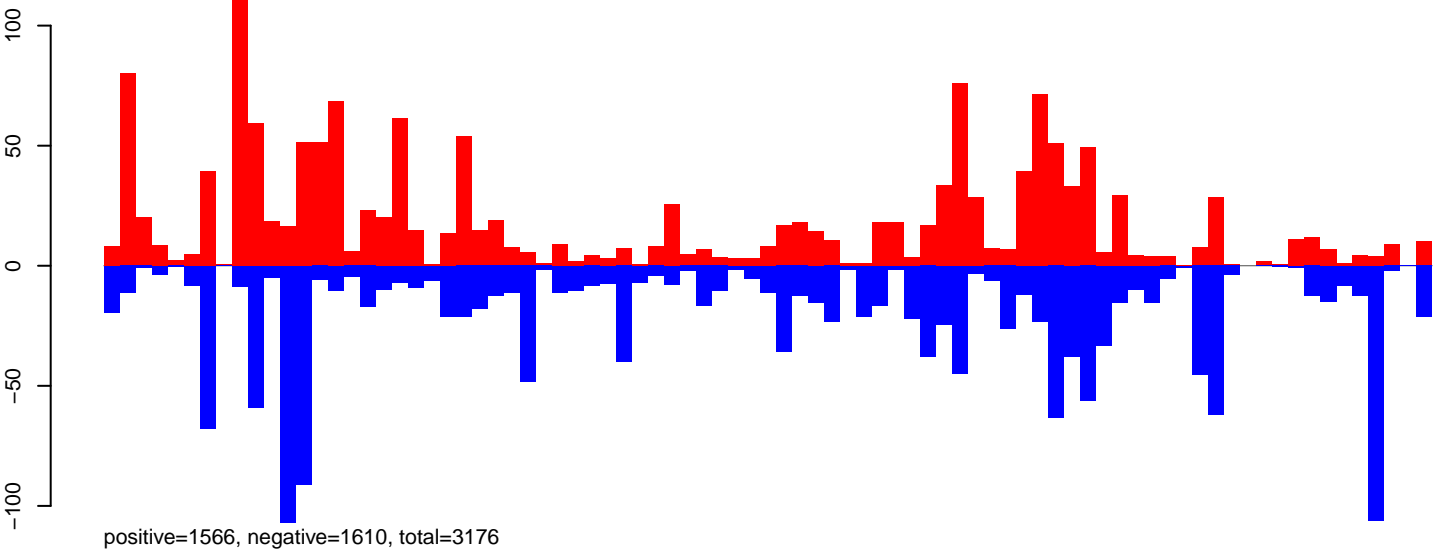
AeAeg_CCL.125_cells.rep



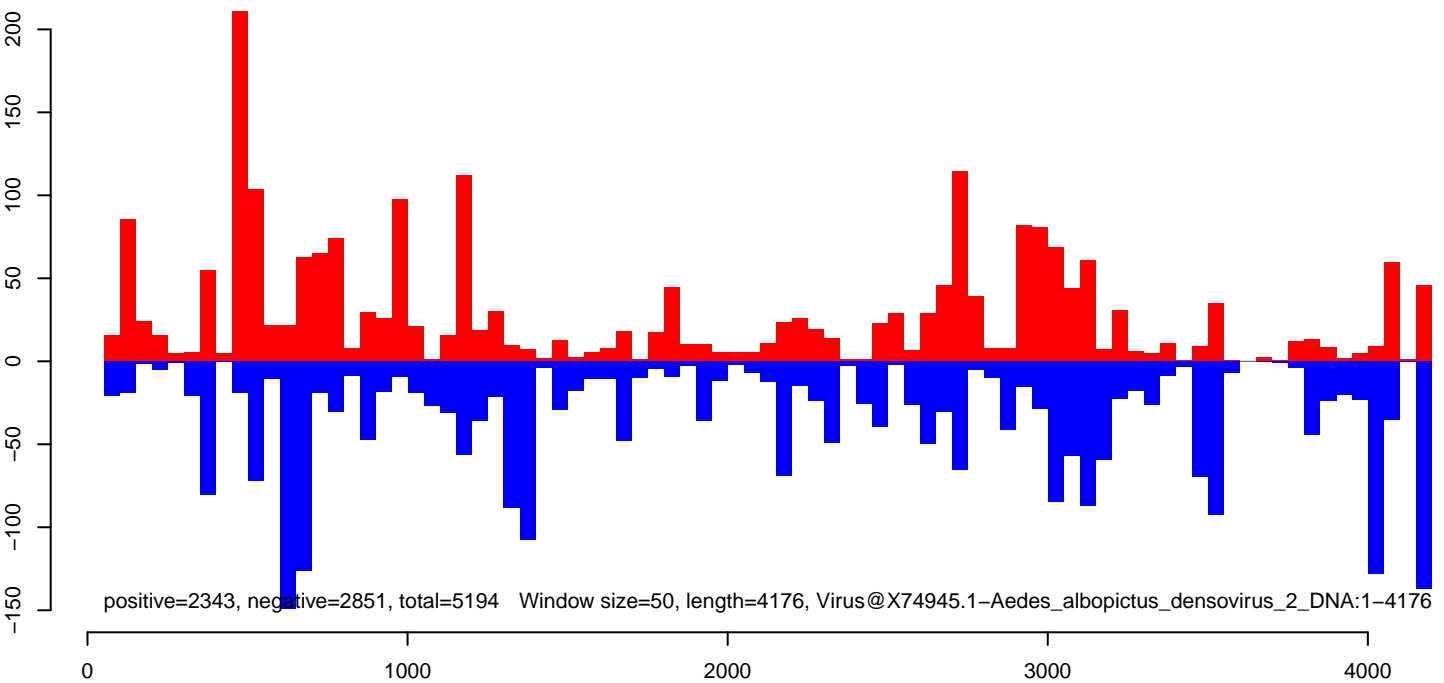
AeAeg_CCL.125_cells.18_23.rep



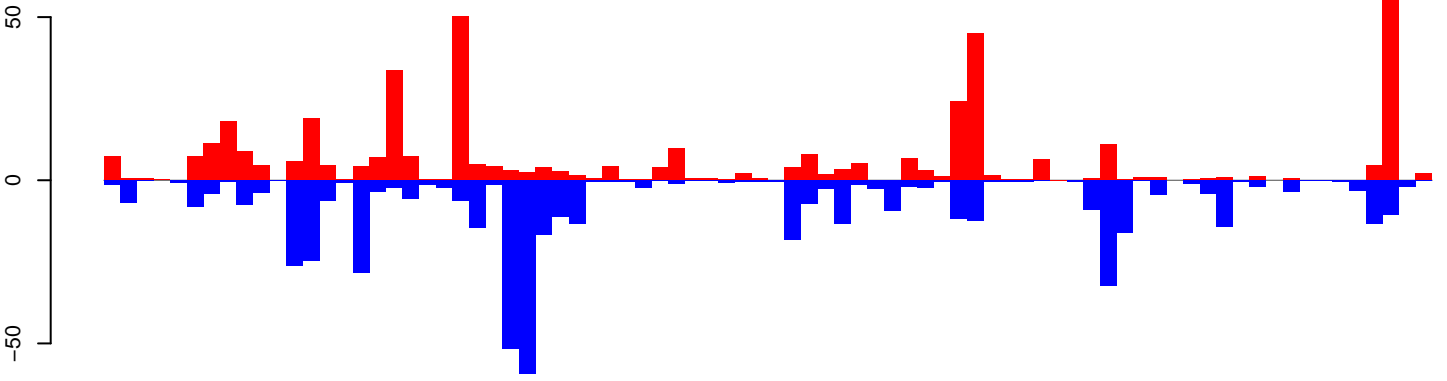
AeAeg_CCL.125_cells.24_35.rep



AeAeg_CCL.125_cells.rep

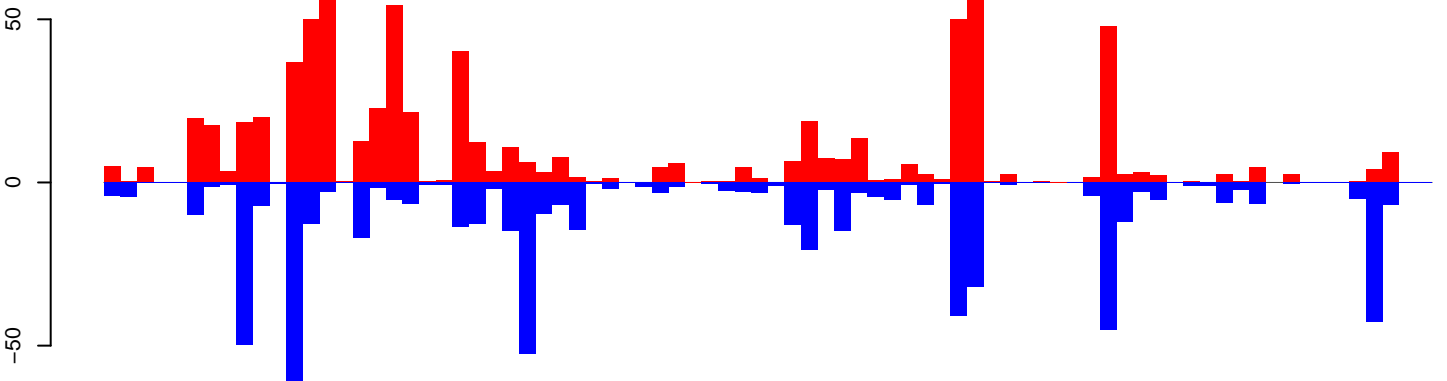


AeAeg_CCL.125_cells.18_23.rep



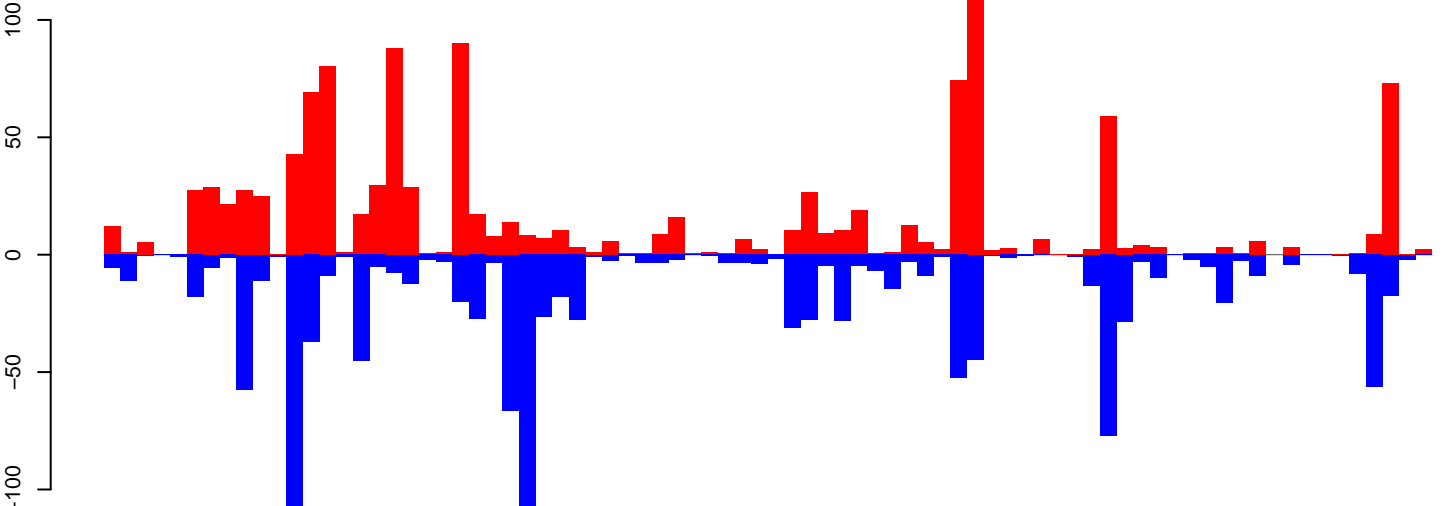
positive=440, negative=520, total=959

AeAeg_CCL.125_cells.24_35.rep



positive=764, negative=654, total=1419

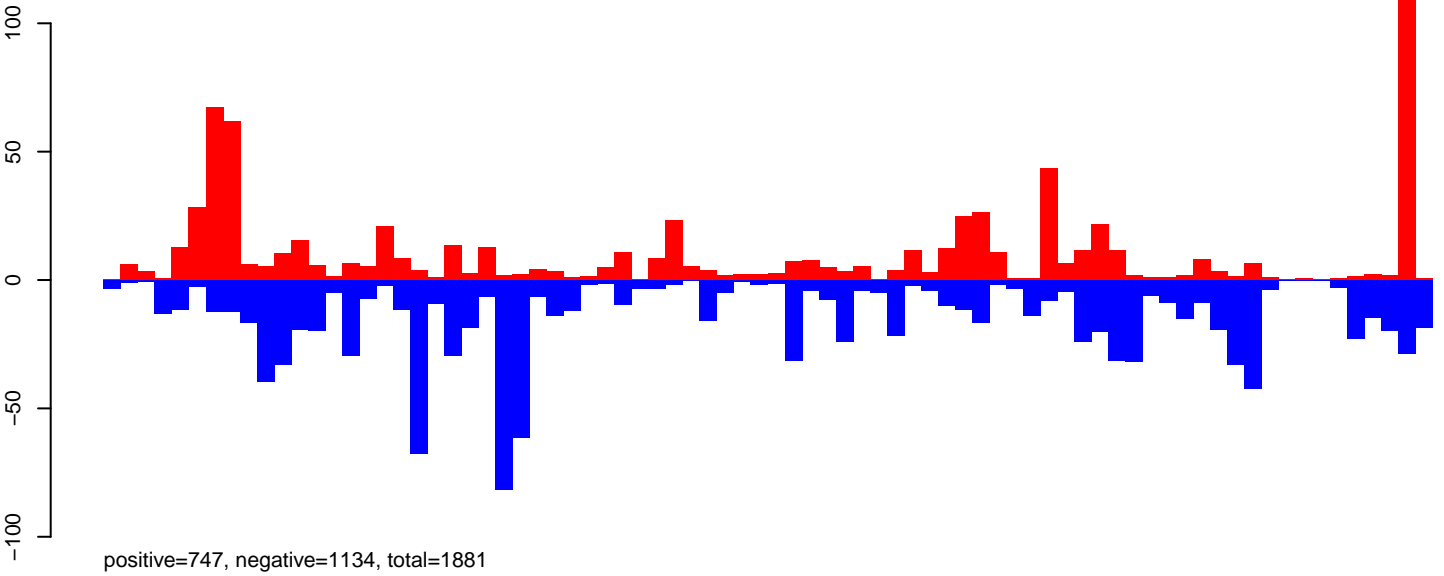
AeAeg_CCL.125_cells.rep



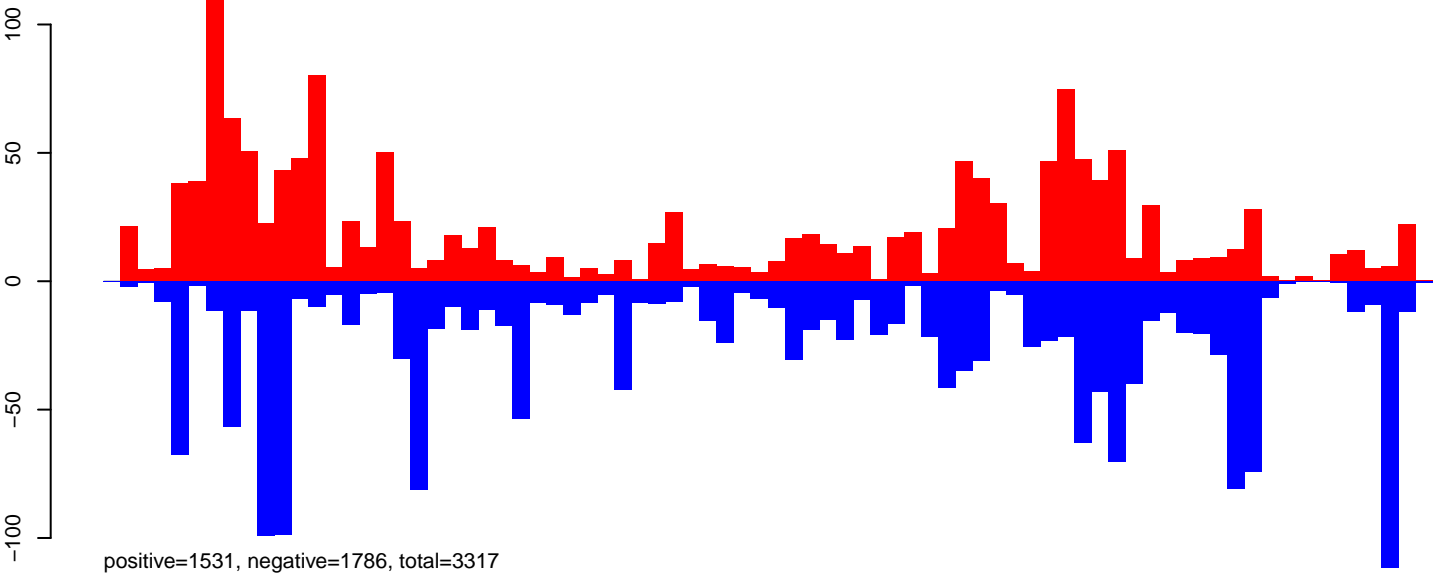
AY310871-A204; negative=1706; positive=2876; senseovirus_non-structural_protein_1_non-structural_protein_2_and_capsid_protein_genes:1-4006

0 1000 2000 3000 4000

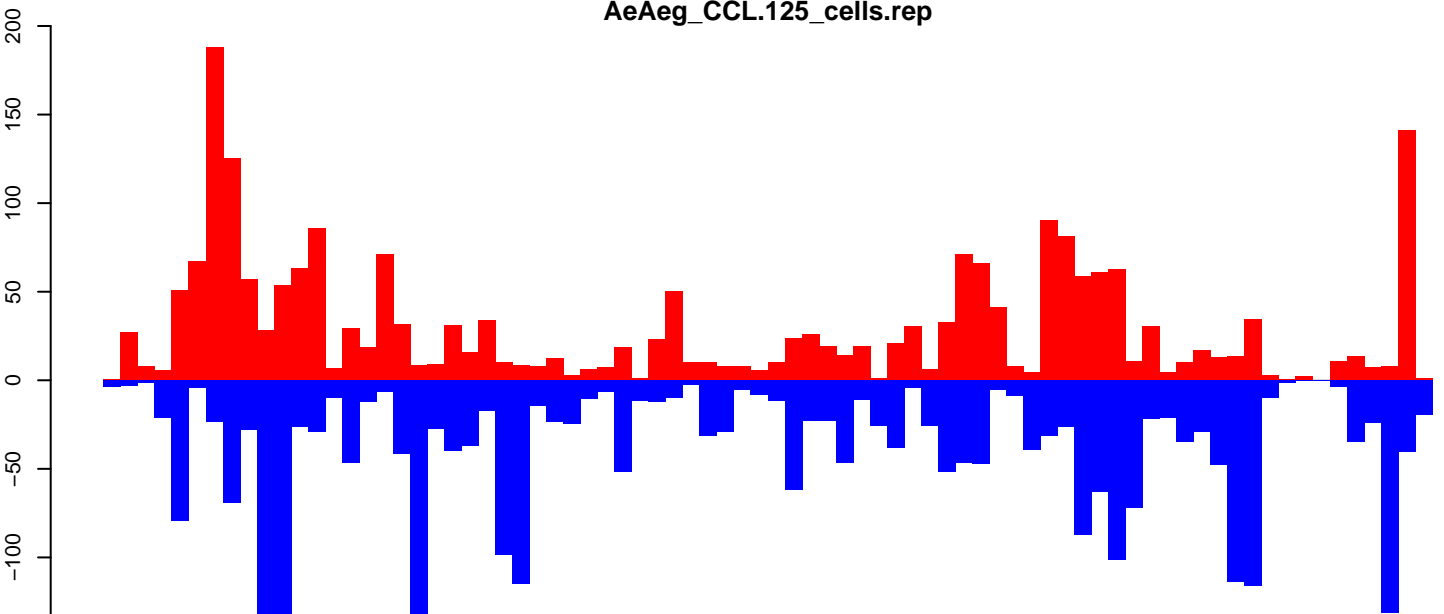
AeAeg_CCL.125_cells.18_23.rep



AeAeg_CCL.125_cells.24_35.rep

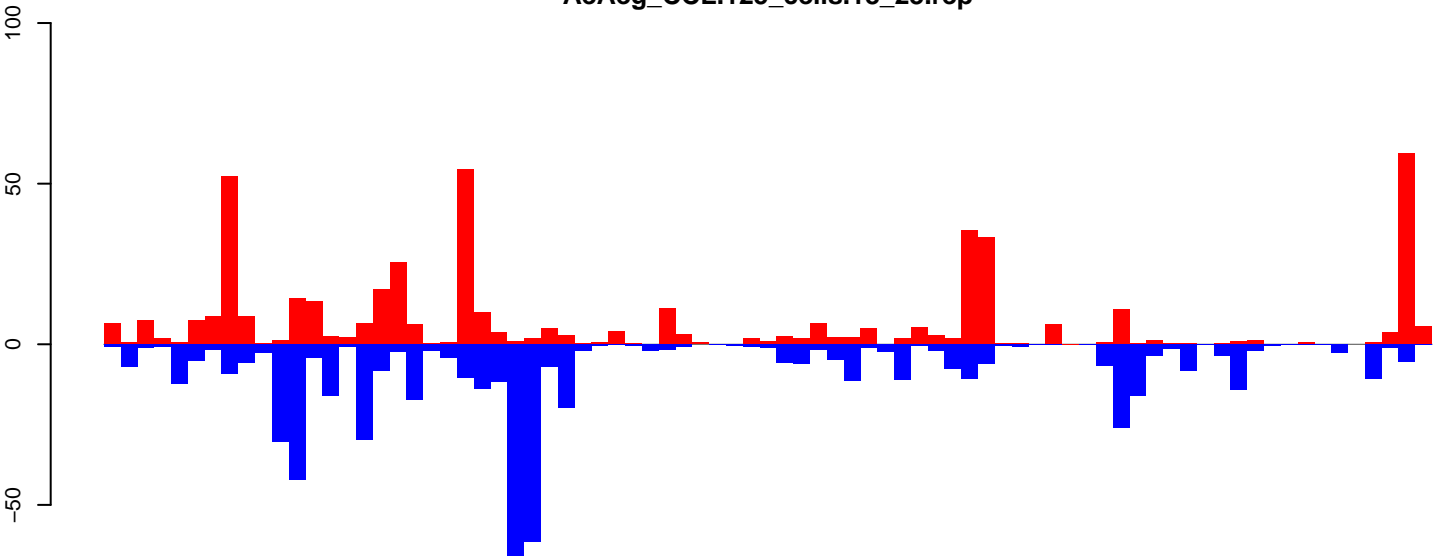


AeAeg_CCL.125_cells.rep



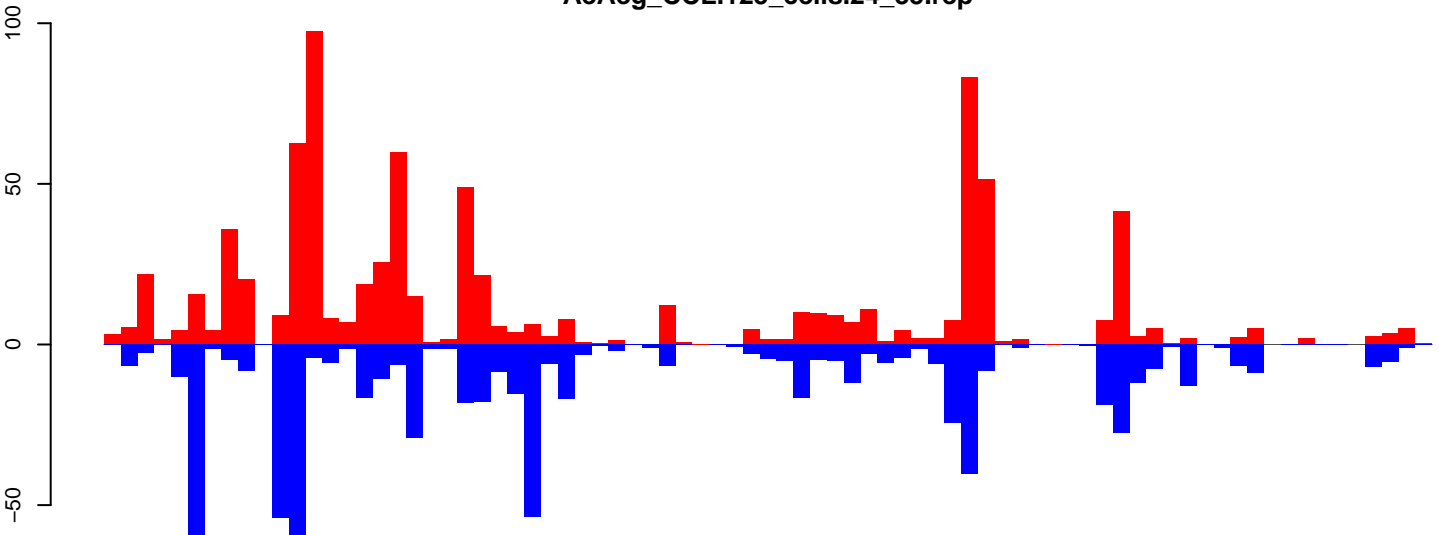
NC01550148.1-Aedes albopictus_densovirus_isolate_NC01_L3_1_trimmed_contig_5889-RC:1-3937

AeAeg_CCL.125_cells.18_23.rep



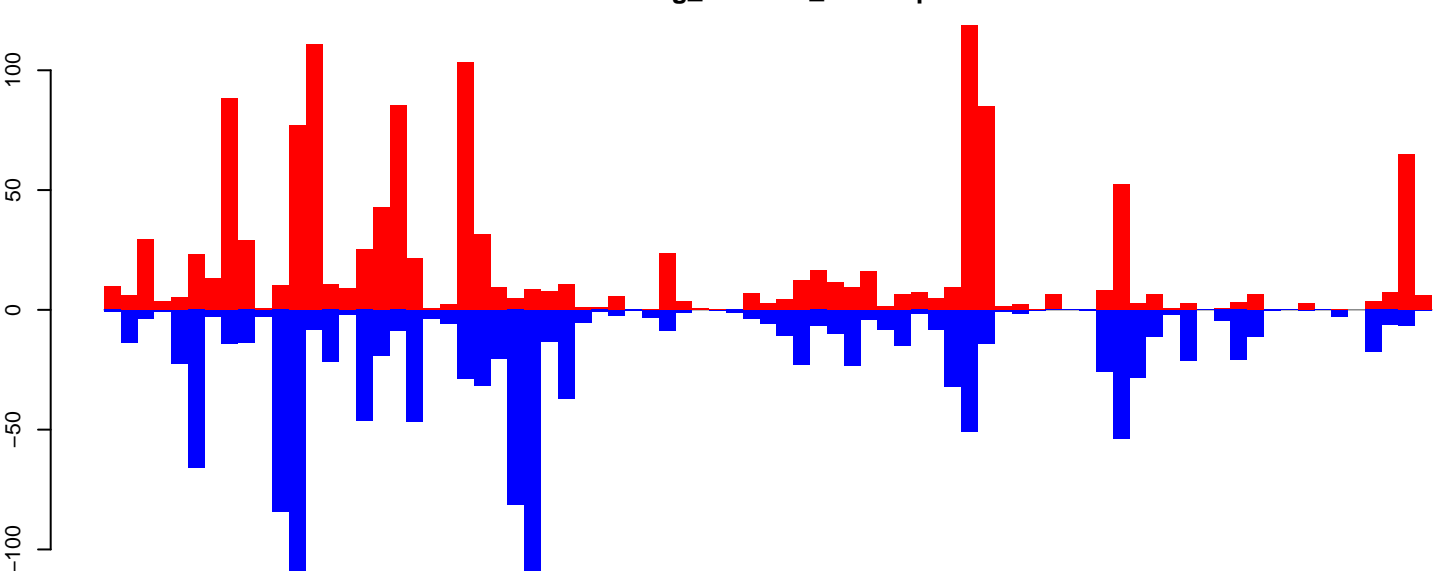
positive=487, negative=579, total=1067

AeAeg_CCL.125_cells.24_35.rep



positive=826, negative=723, total=1549

AeAeg_CCL.125_cells.rep



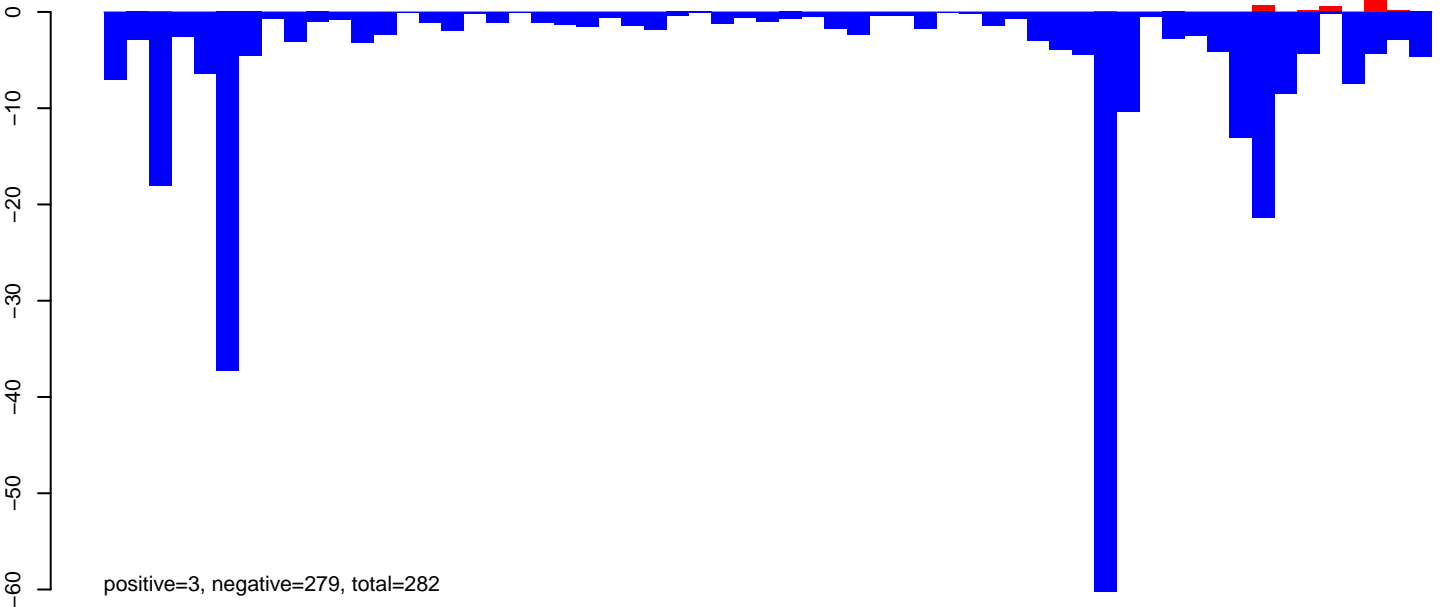
86, Virus: AeAeg_CCL.125_cells.rep, total=2616
positive=1035, negative=1581

AeAeg_CCL.125_cells.18_23.rep



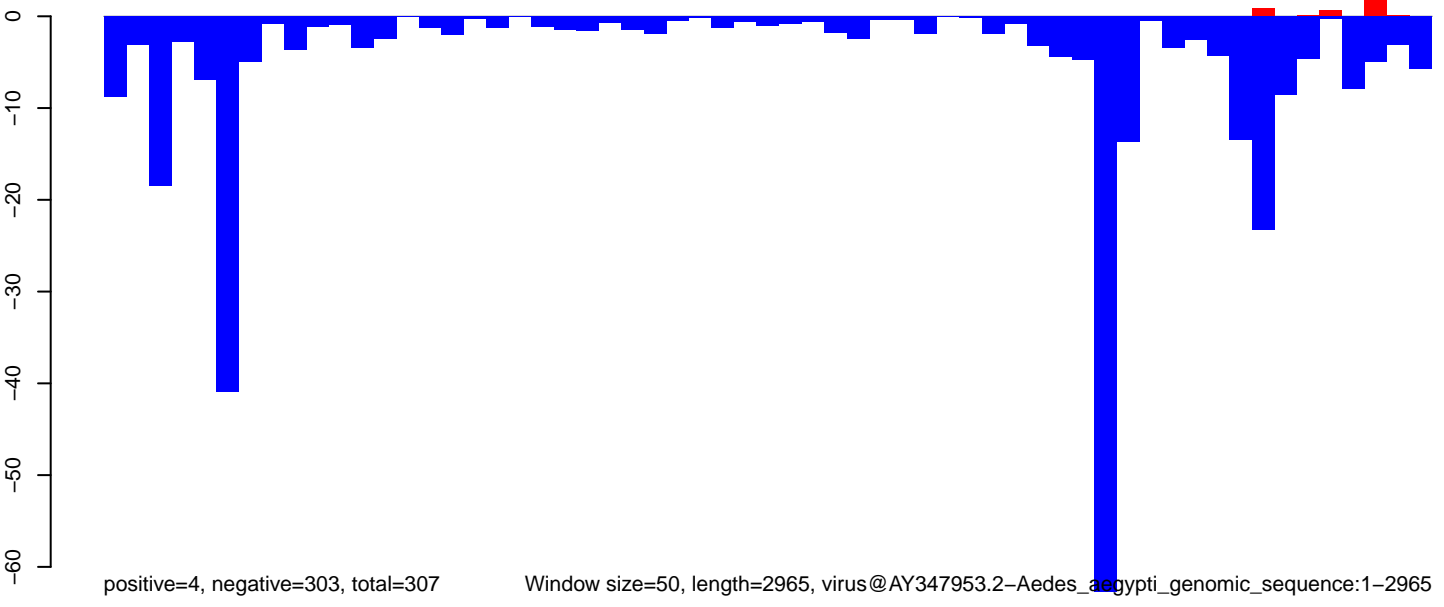
positive=1, negative=24, total=25

AeAeg_CCL.125_cells.24_35.rep



positive=3, negative=279, total=282

AeAeg_CCL.125_cells.rep

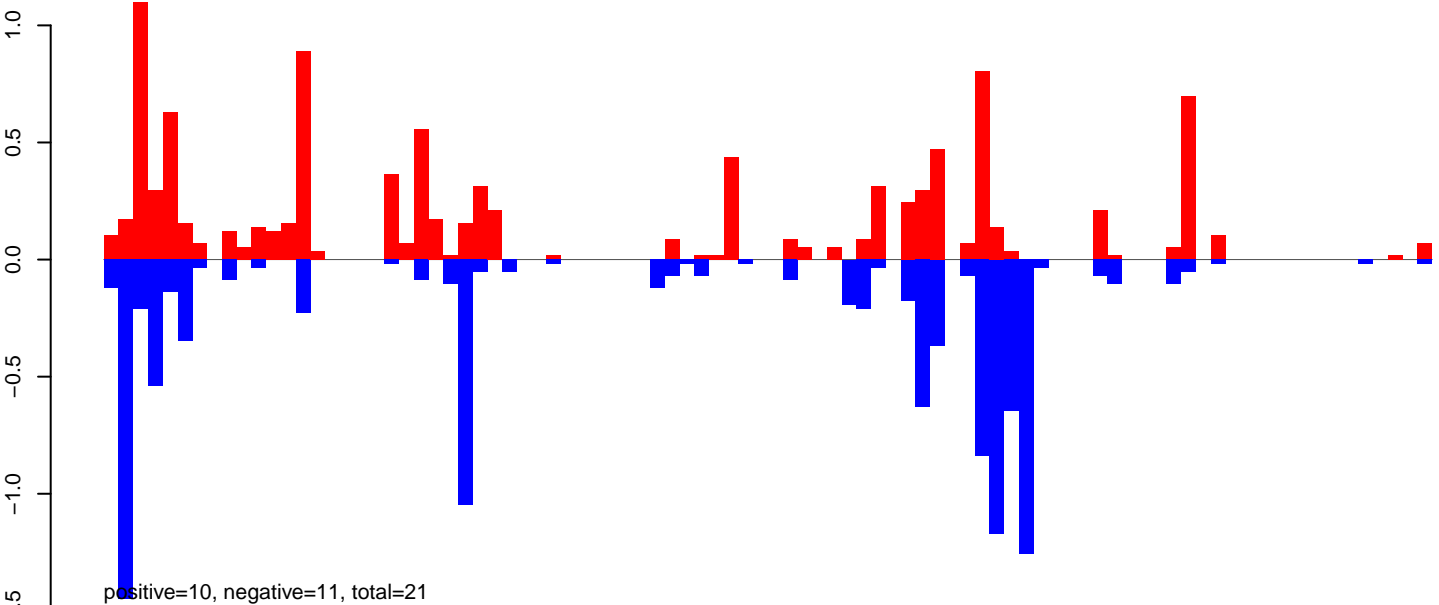


positive=4, negative=303, total=307

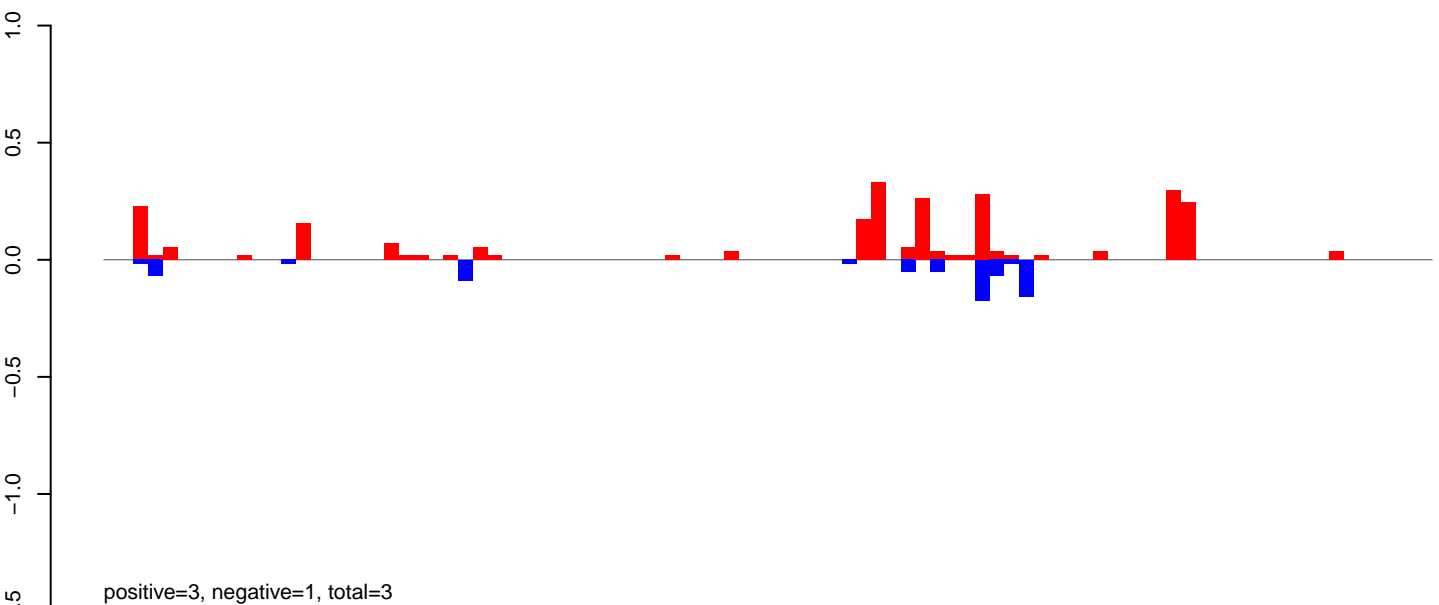
Window size=50, length=2965, virus@AY347953.2-Aedes_aegypti_genomic_sequence:1-2965

0 500 1000 1500 2000 2500 3000

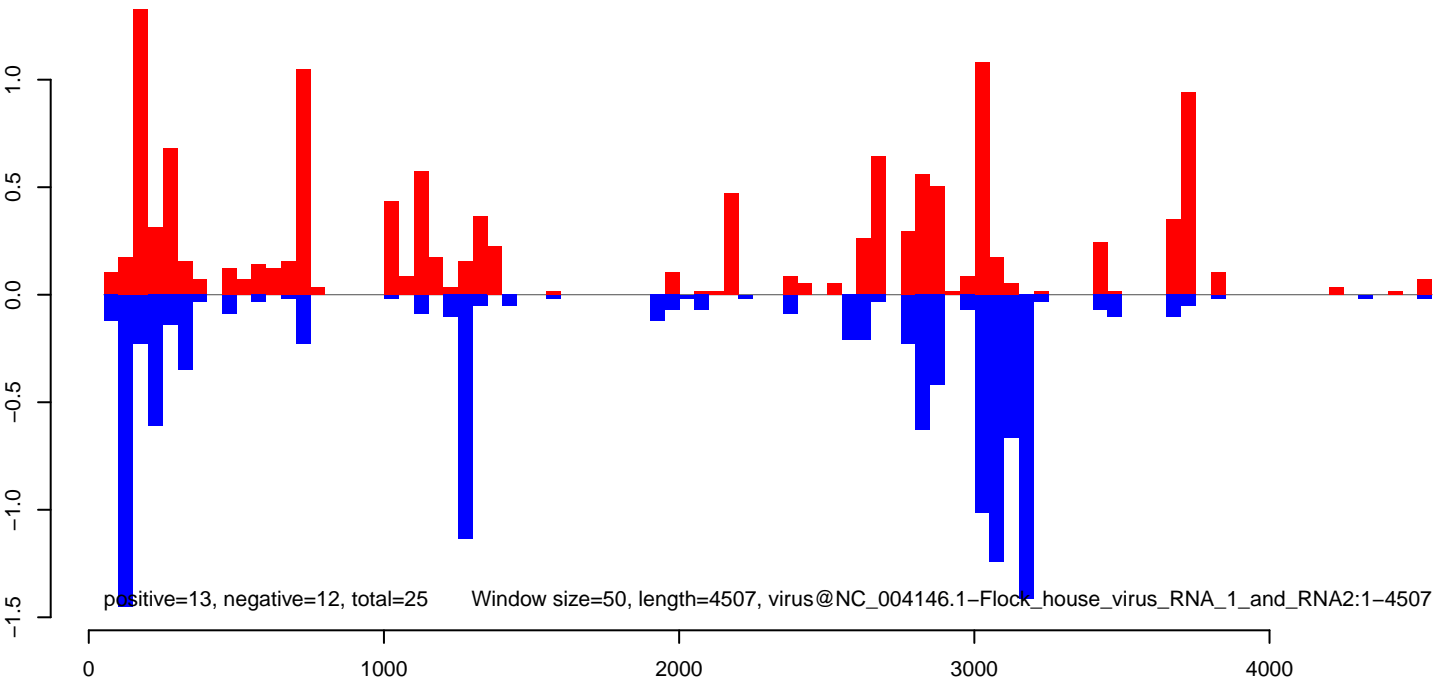
AeAeg_CCL.125_cells.18_23.rep



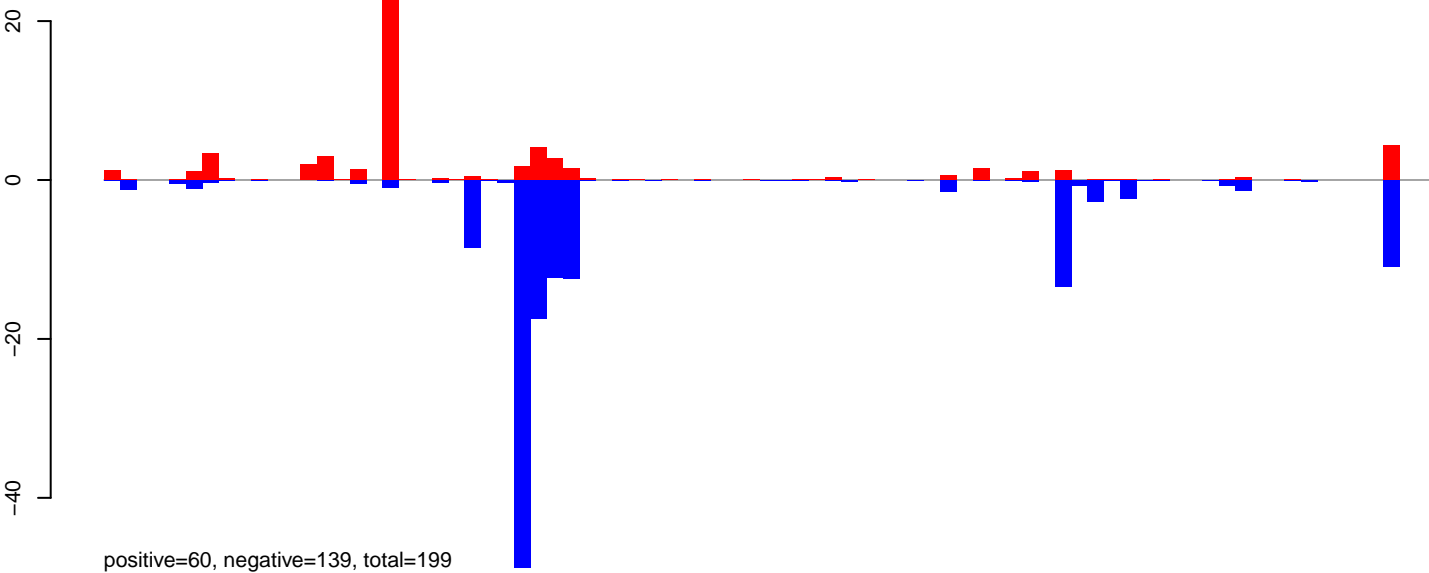
AeAeg_CCL.125_cells.24_35.rep



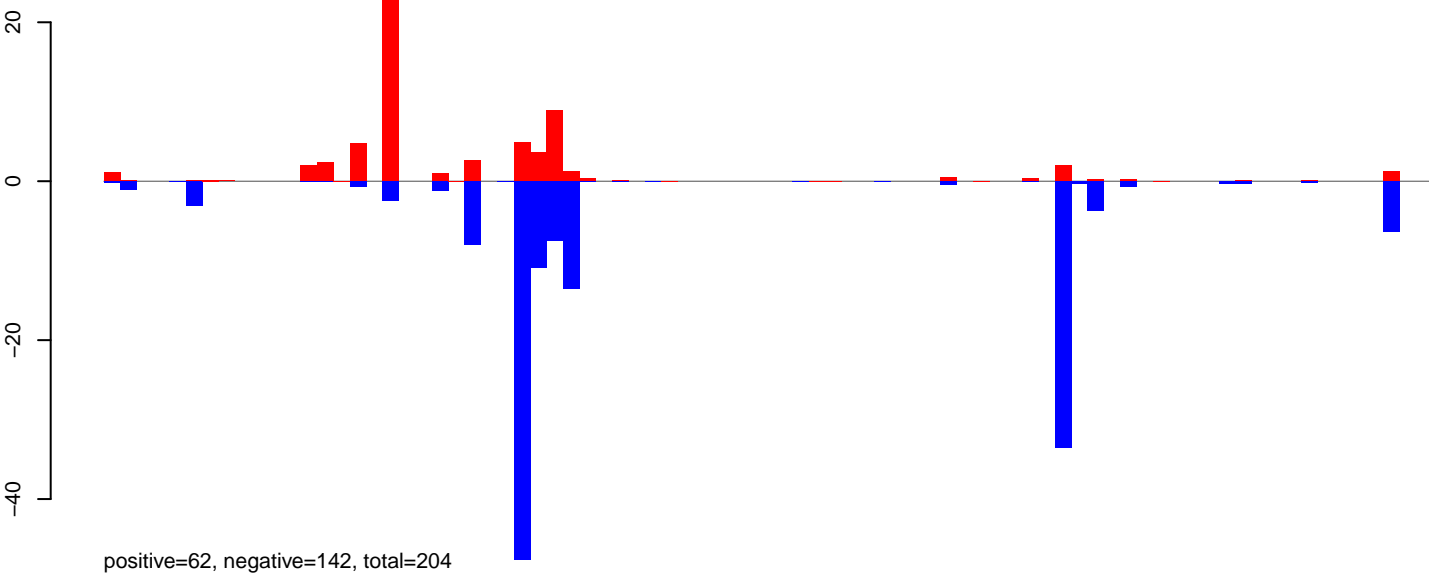
AeAeg_CCL.125_cells.rep



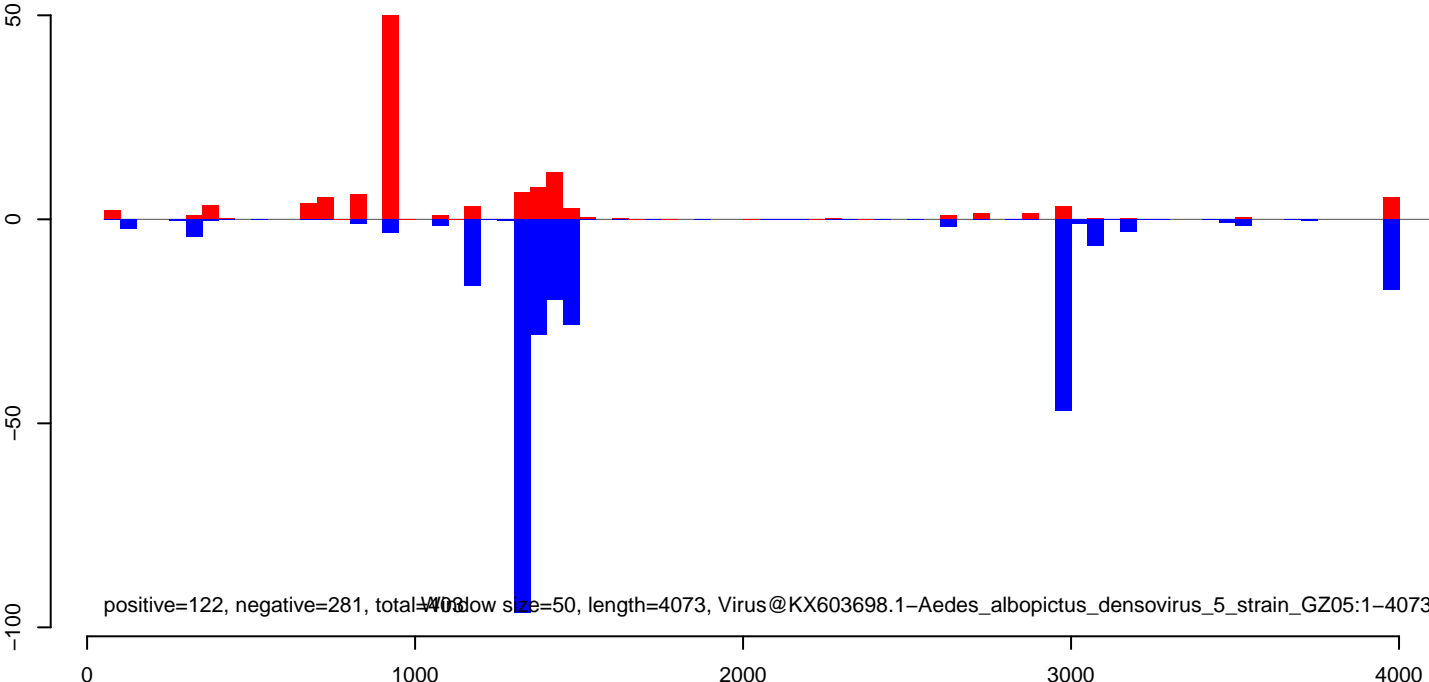
AeAeg_CCL.125_cells.18_23.rep



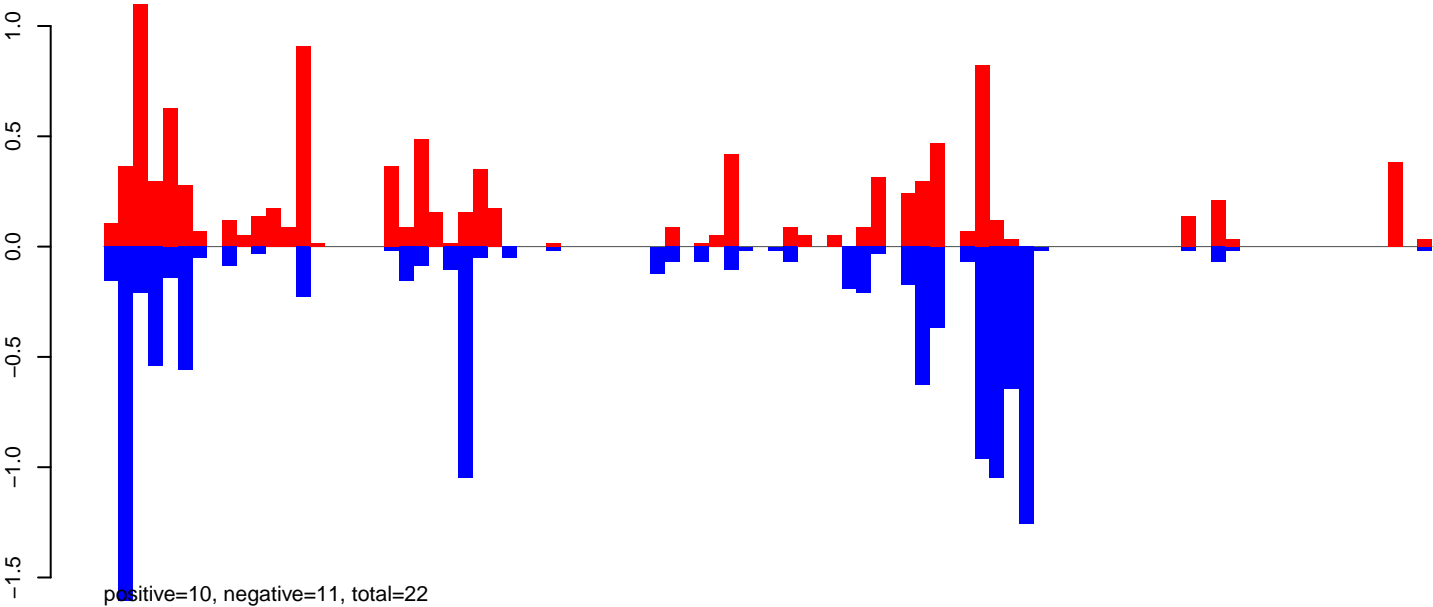
AeAeg_CCL.125_cells.24_35.rep



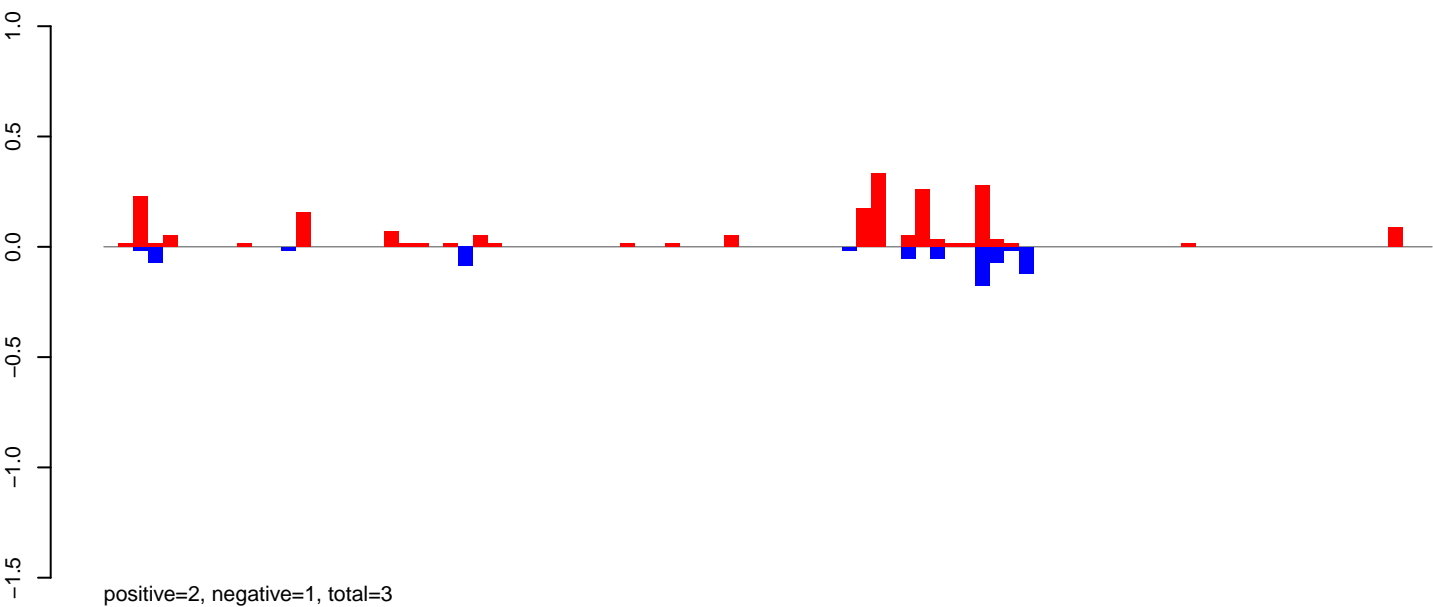
AeAeg_CCL.125_cells.rep



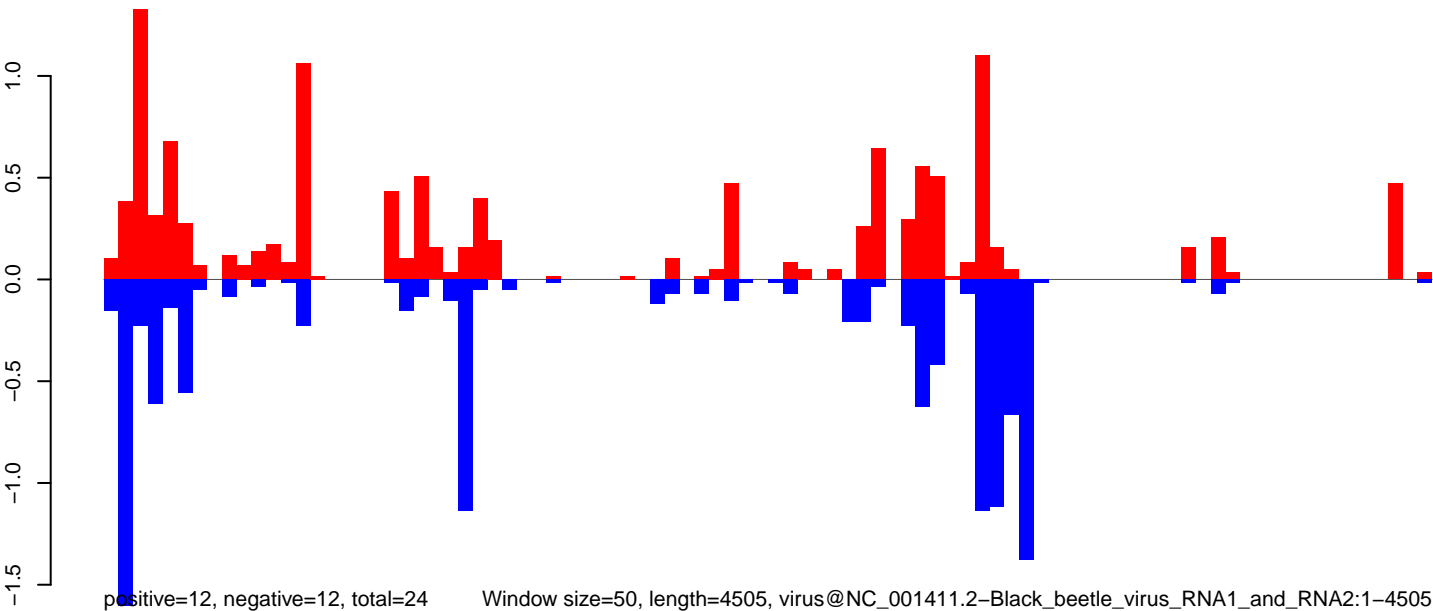
AeAeg_CCL.125_cells.18_23.rep



AeAeg_CCL.125_cells.24_35.rep



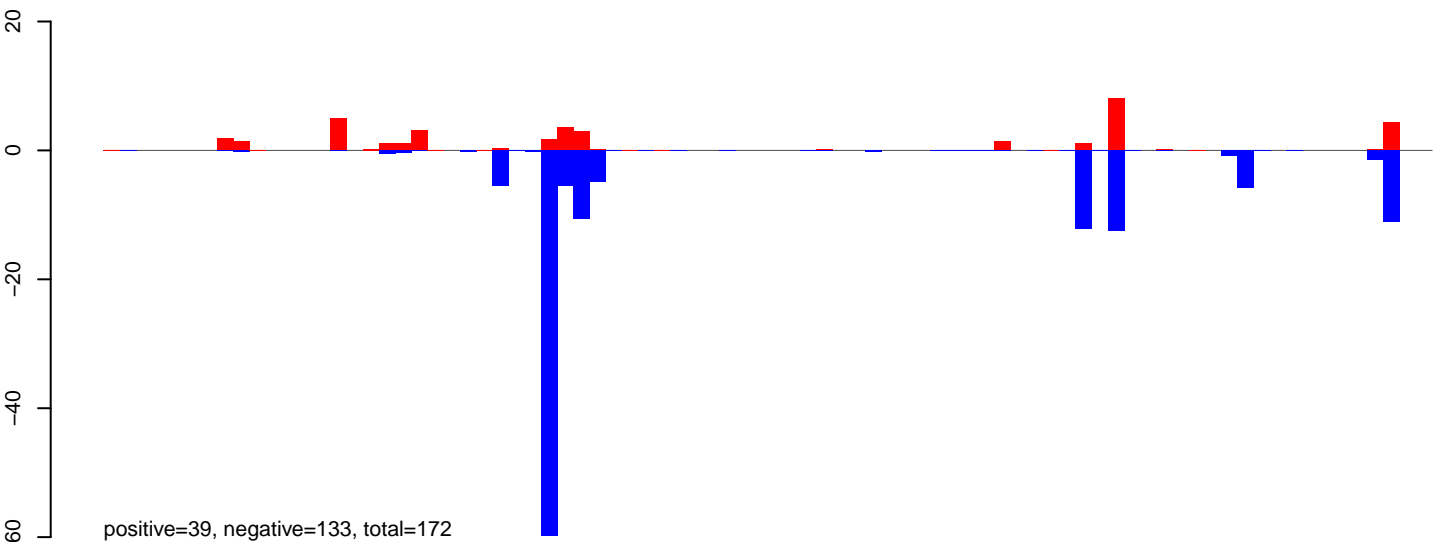
AeAeg_CCL.125_cells.rep



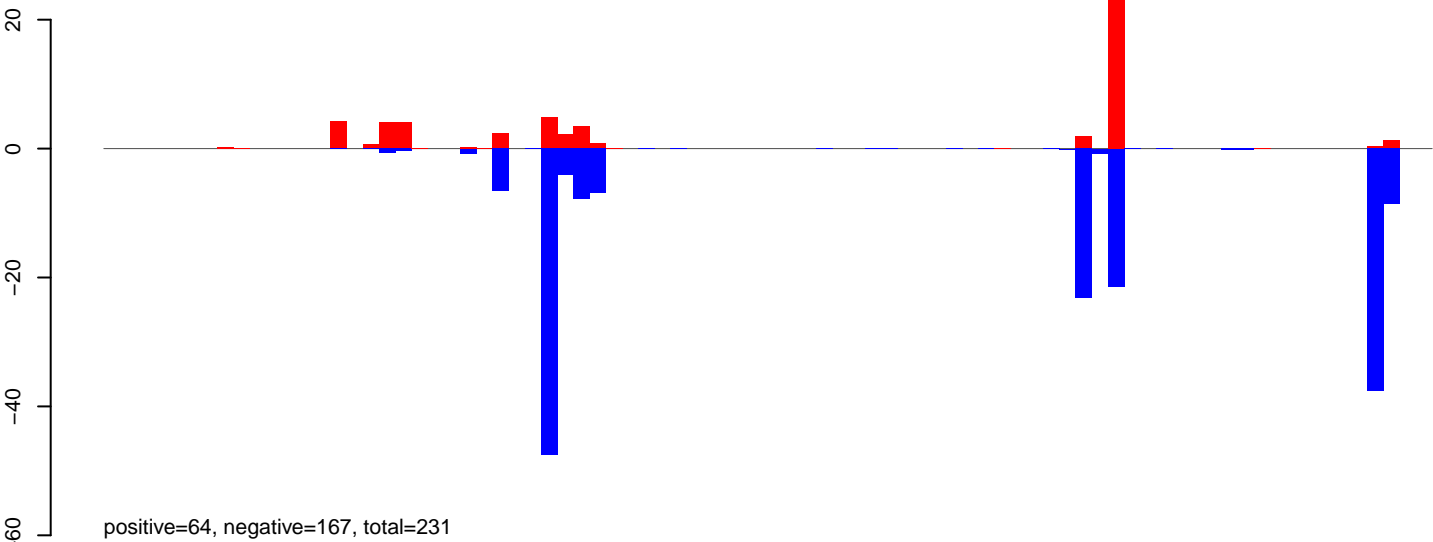
Window size=50, length=4505, virus@NC_001411.2-Black_beetle_virus_RNA1_and_RNA2:1-4505

0 1000 2000 3000 4000

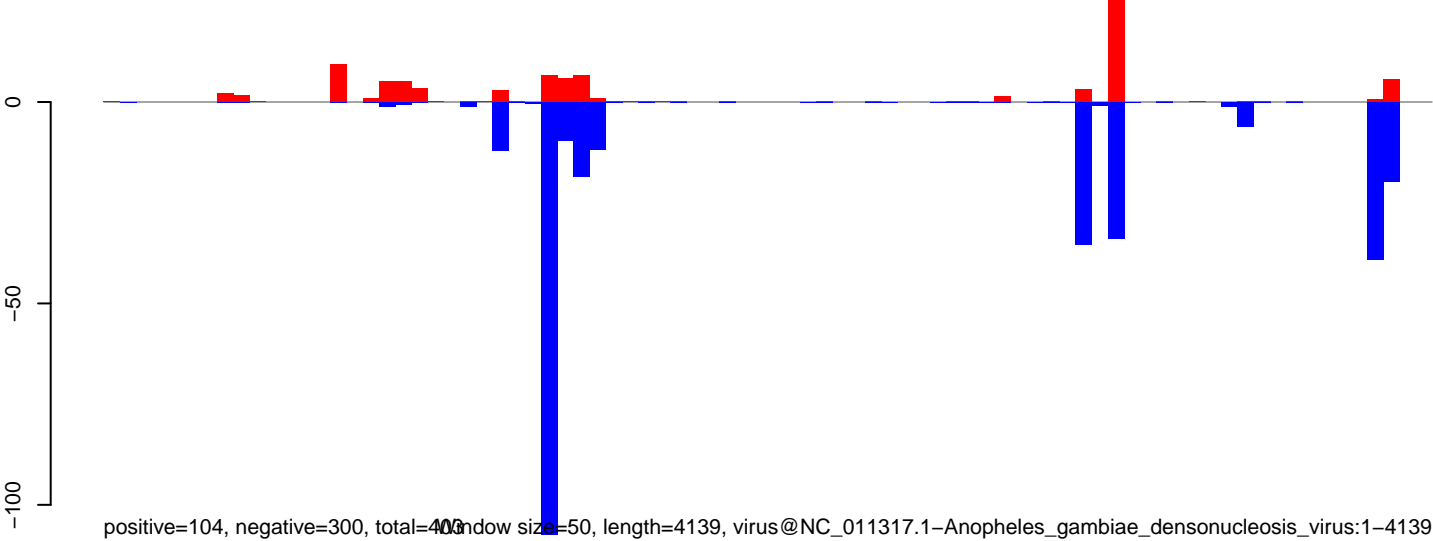
AeAeg_CCL.125_cells.18_23.rep



AeAeg_CCL.125_cells.24_35.rep



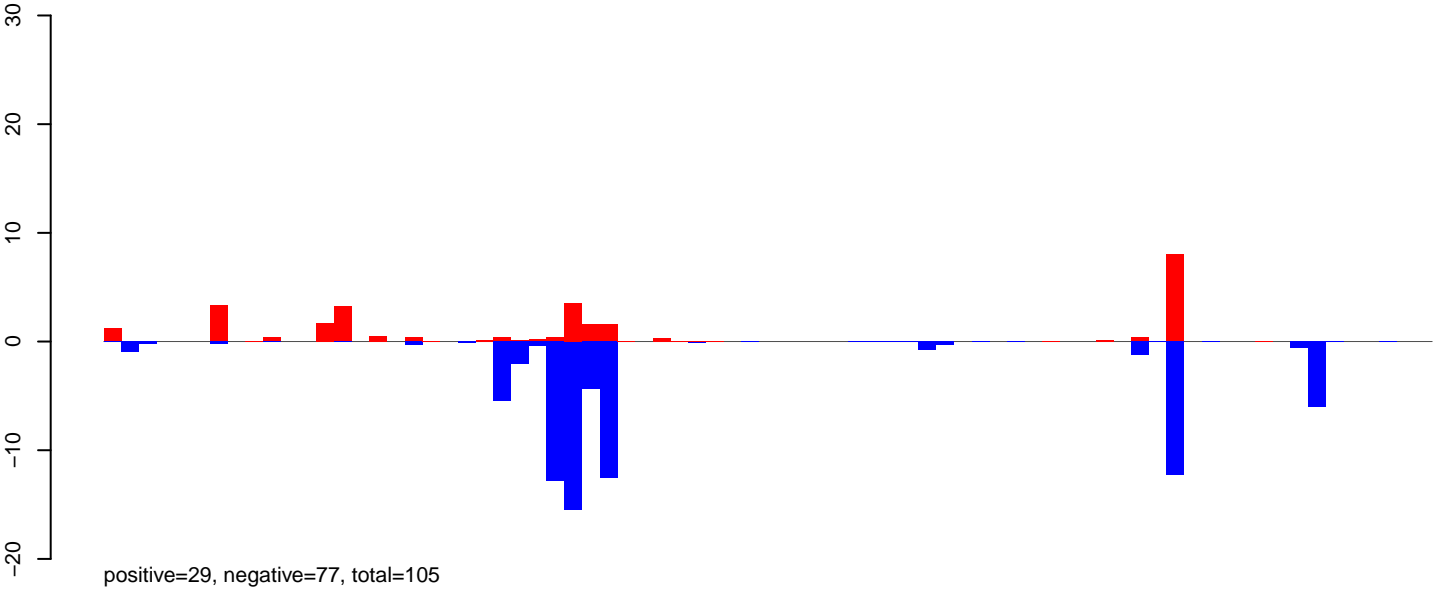
AeAeg_CCL.125_cells.rep



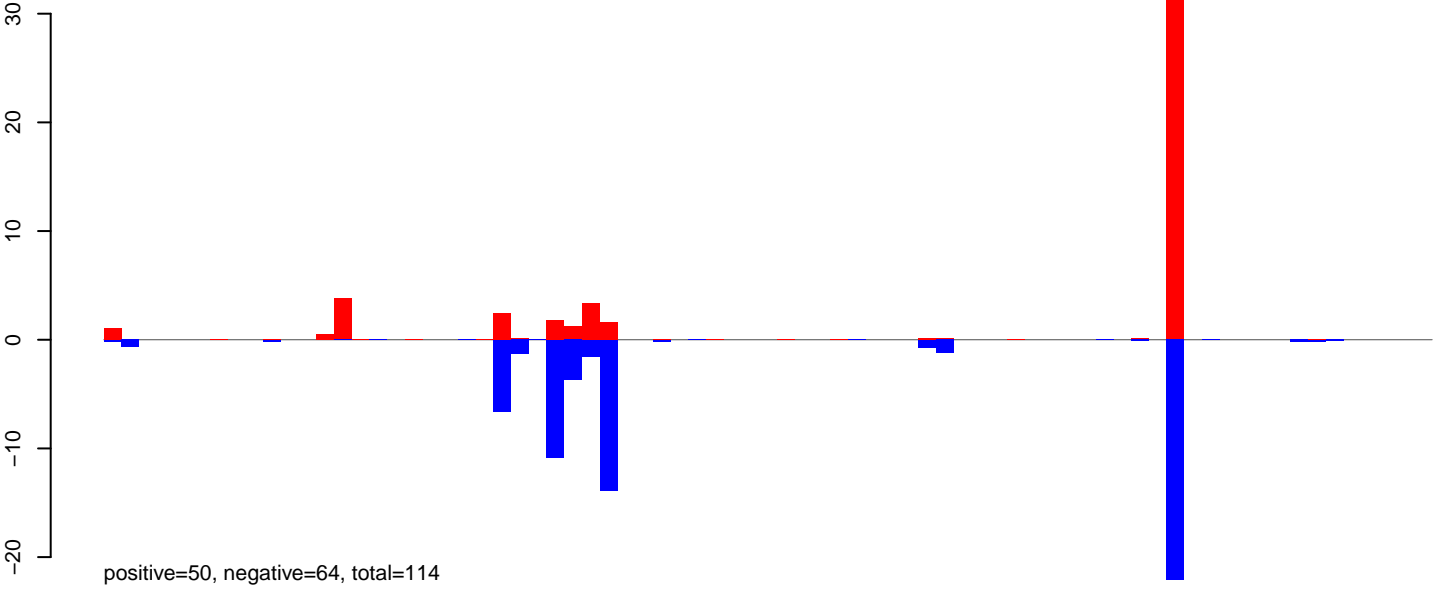
Window size=50, length=4139, virus@NC_011317.1-Anopheles_gambiae_densonucleosis_virus:1-4139

0 1000 2000 3000 4000

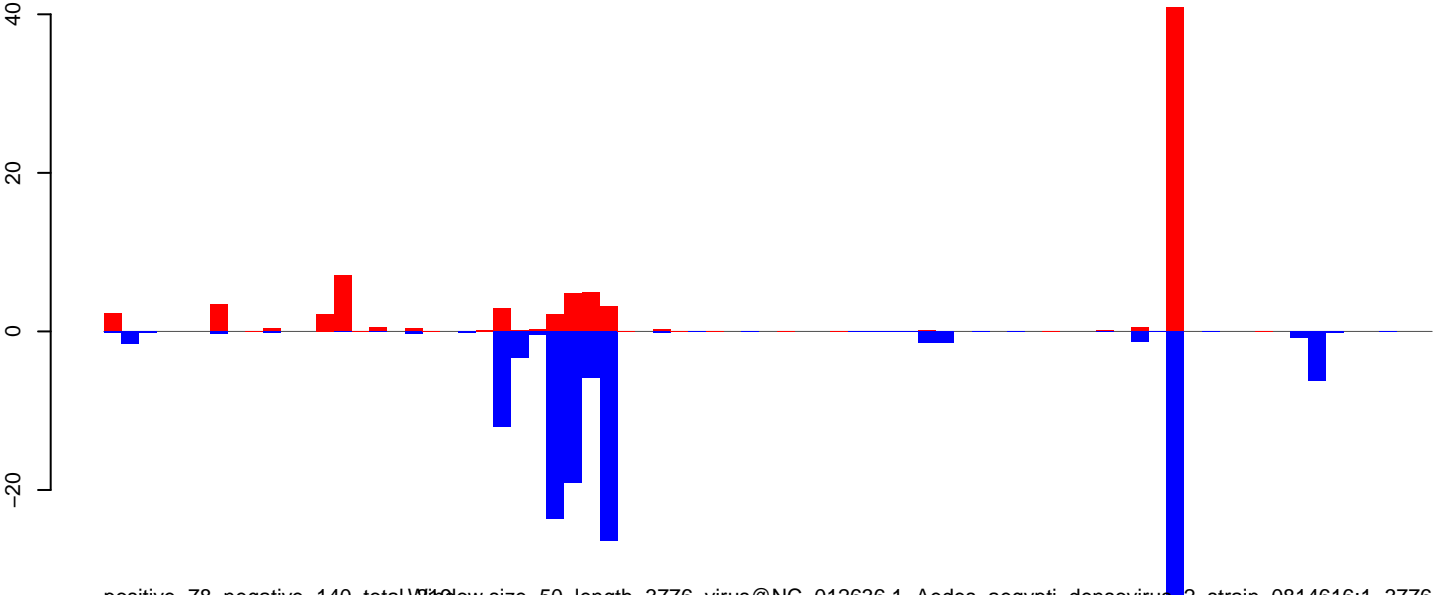
AeAeg_CCL.125_cells.18_23.rep



AeAeg_CCL.125_cells.24_35.rep



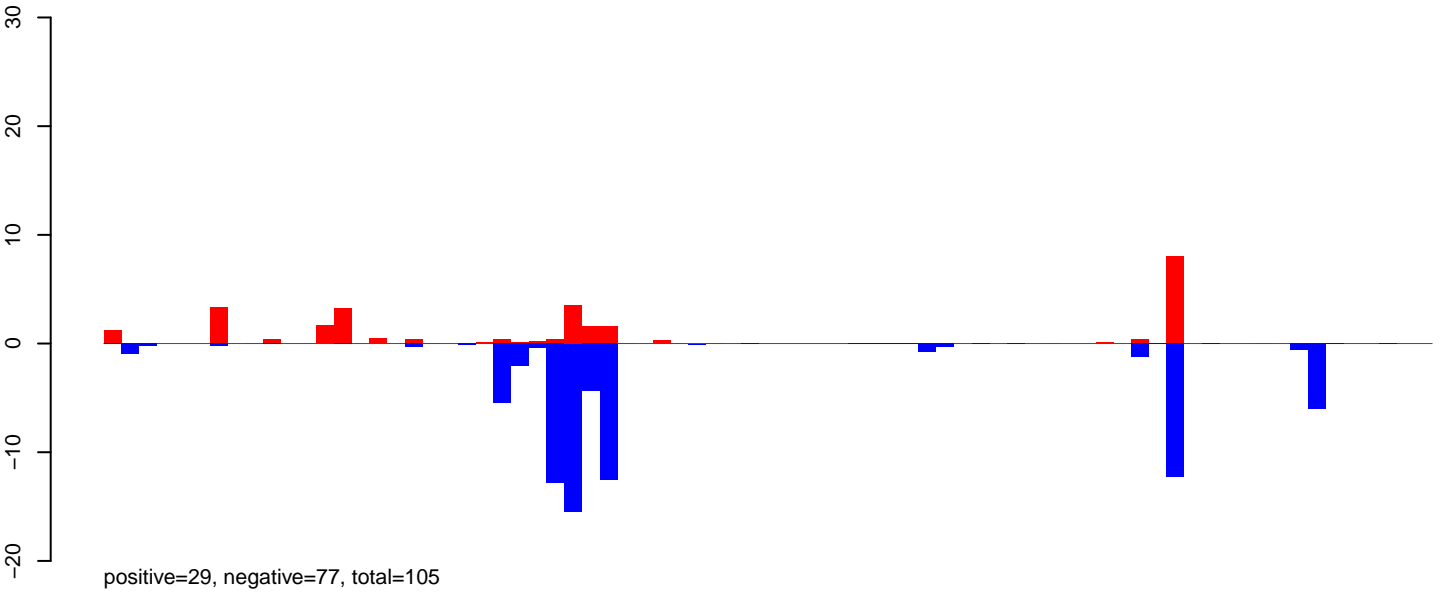
AeAeg_CCL.125_cells.rep



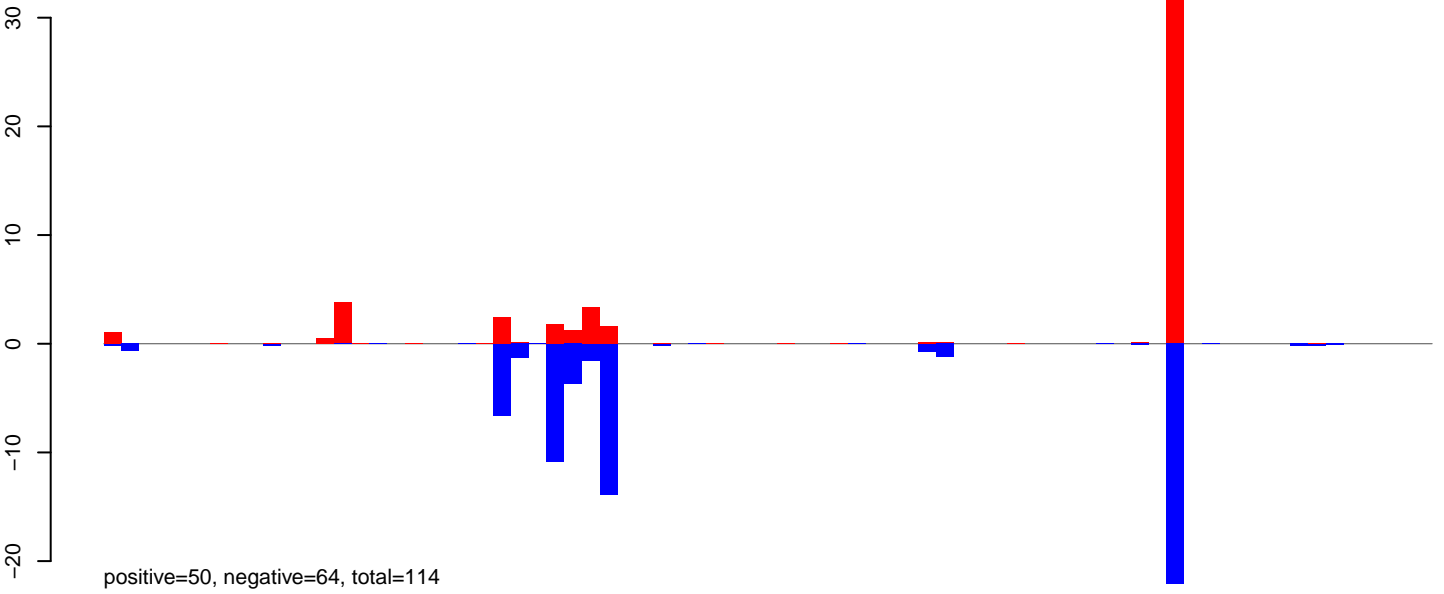
Window size=50, length=3776, virus@NC_012636.1-Aedes_aegypti_densovirus_2_strain_0814616:1-3776

0 1000 2000 3000

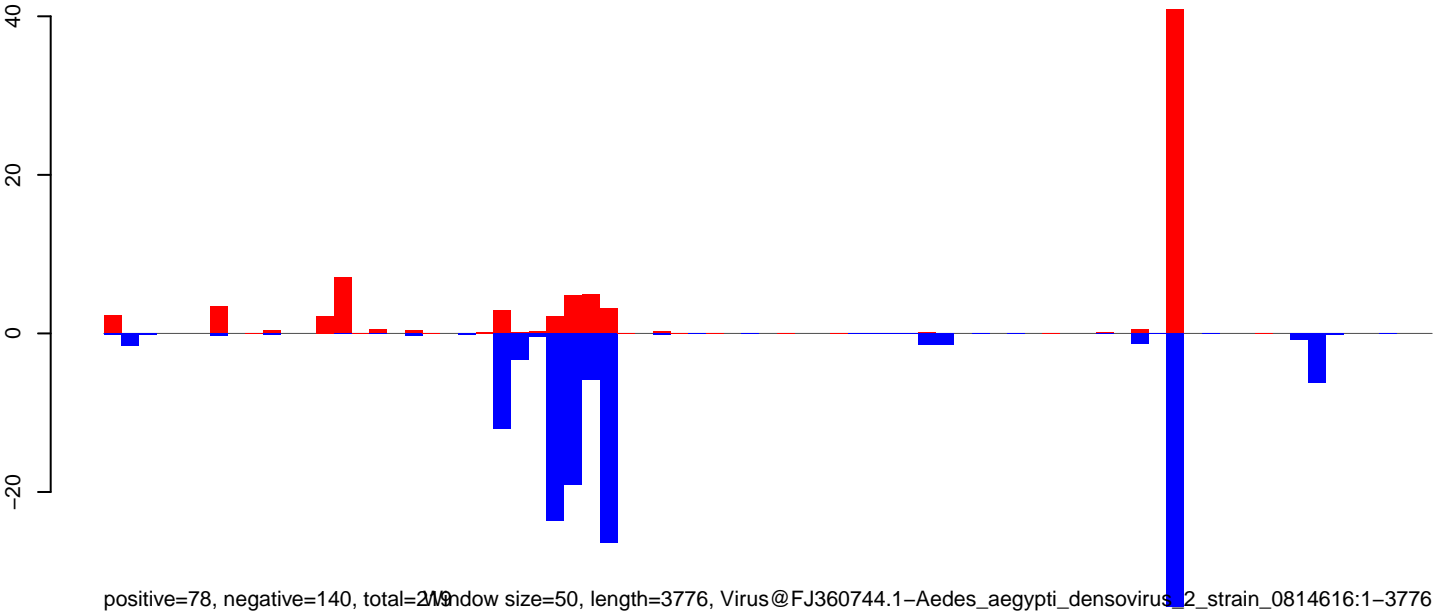
AeAeg_CCL.125_cells.18_23.rep



AeAeg_CCL.125_cells.24_35.rep

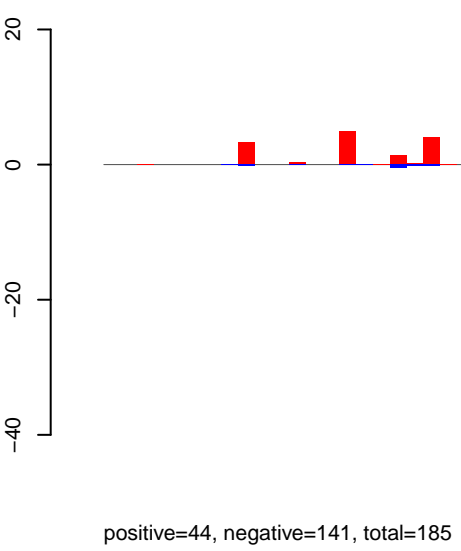


AeAeg_CCL.125_cells.rep

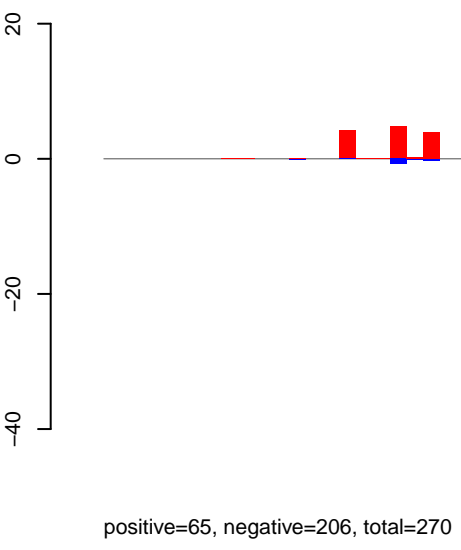


Window size=50, length=3776, Virus@FJ360744.1-Aedes_aegypti_densovirus_2_strain_0814616:1-3776

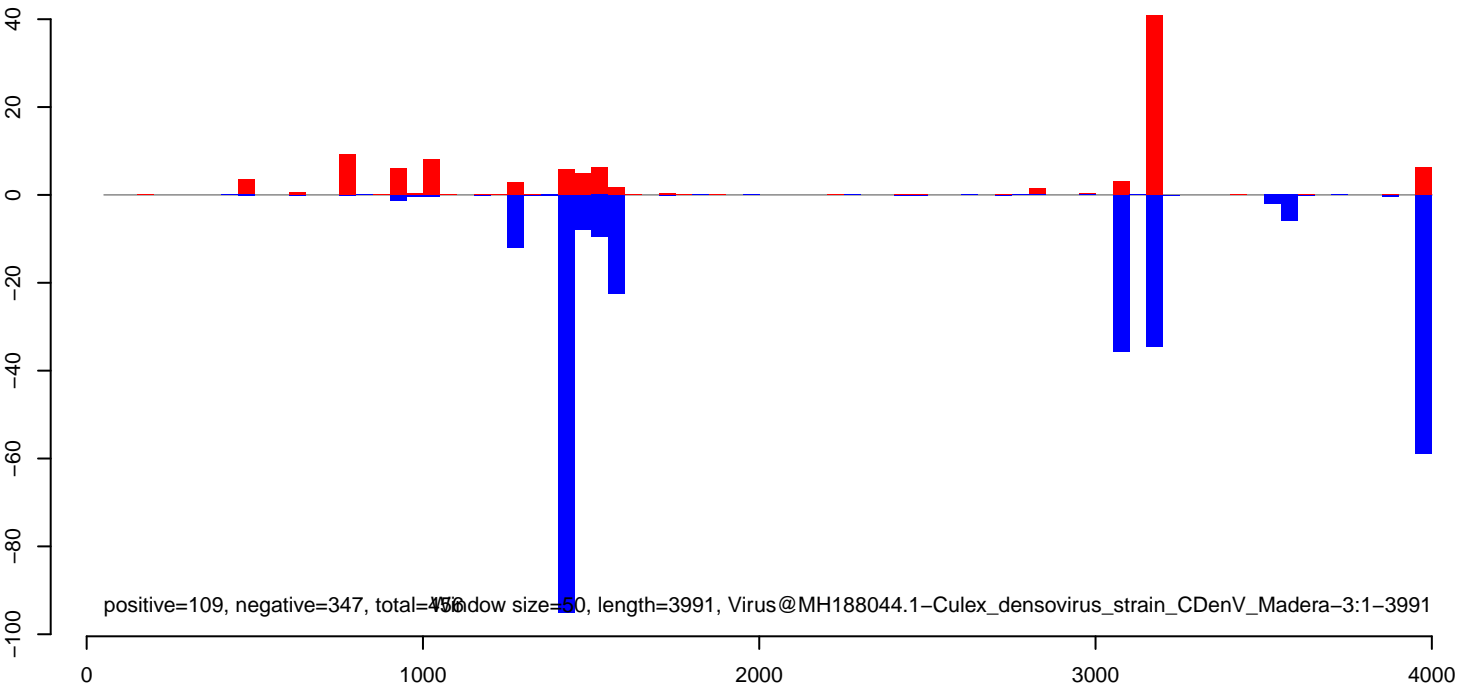
AeAeg_CCL.125_cells.18_23.rep



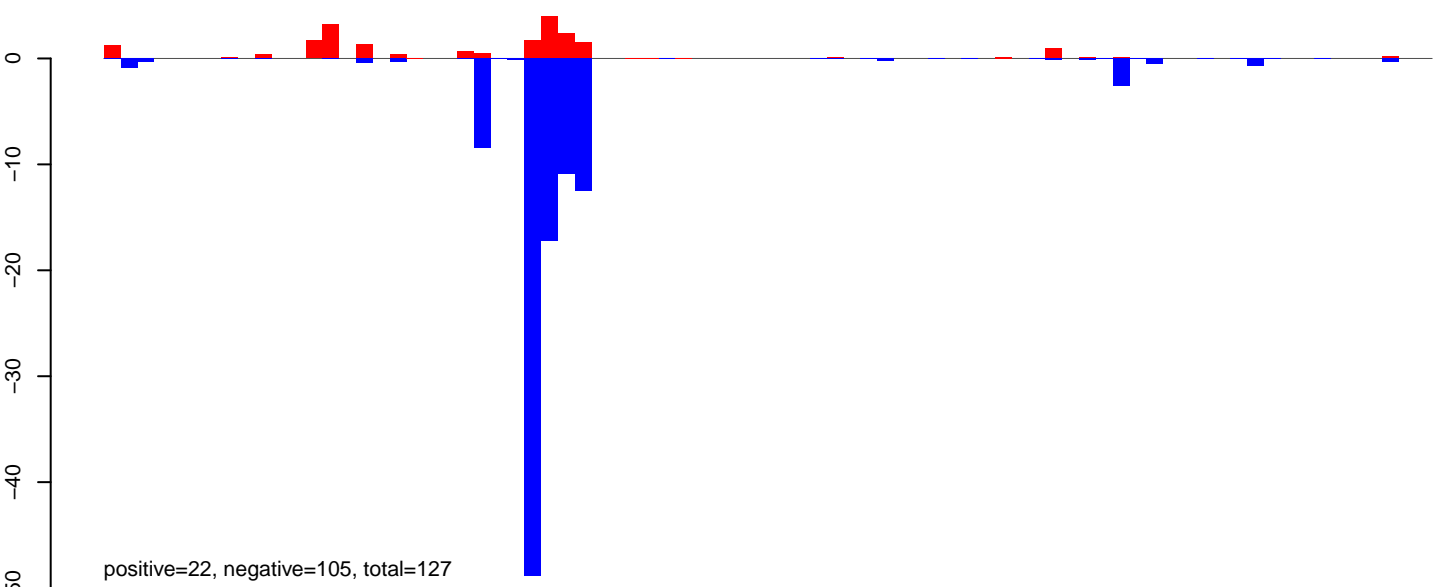
AeAeg_CCL.125_cells.24_35.rep



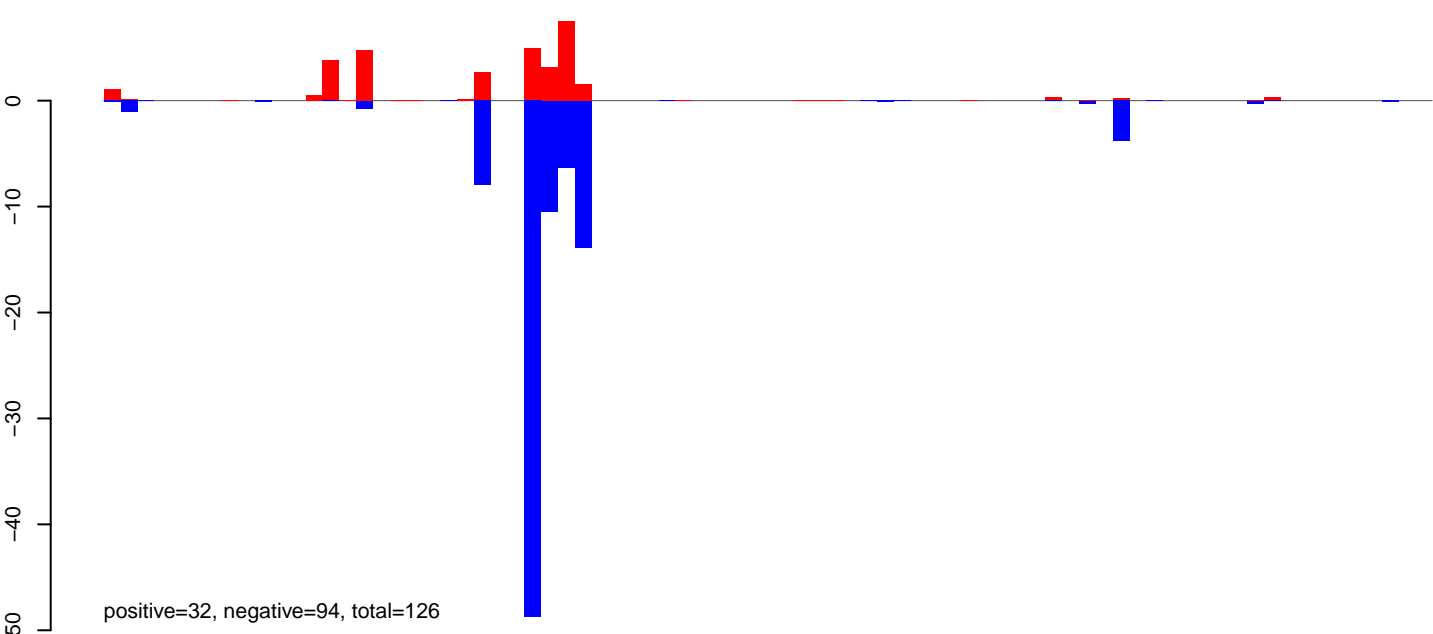
AeAeg_CCL.125_cells.rep



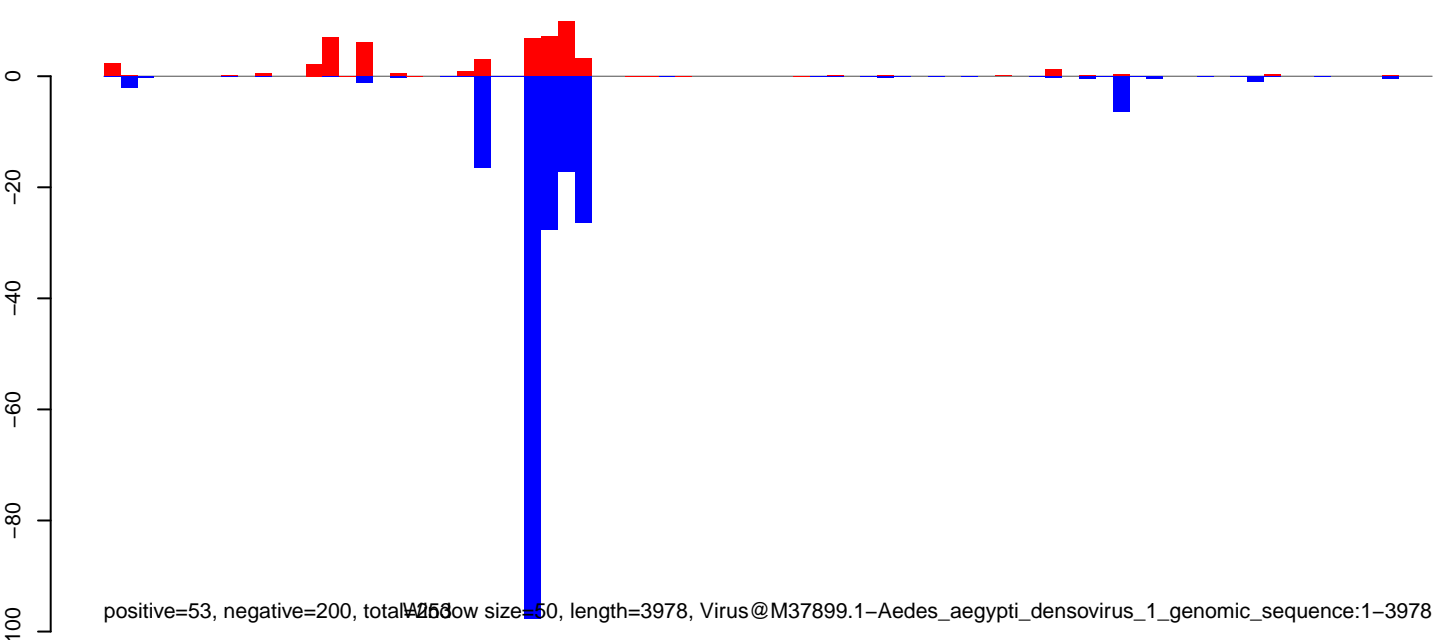
AeAeg_CCL.125_cells.18_23.rep



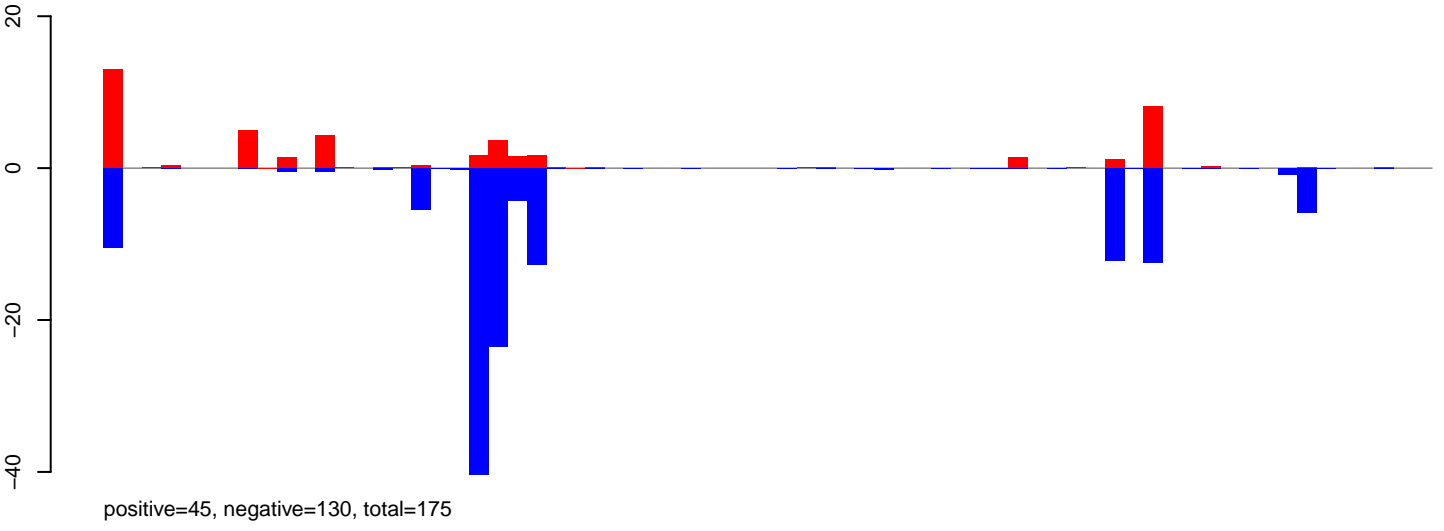
AeAeg_CCL.125_cells.24_35.rep



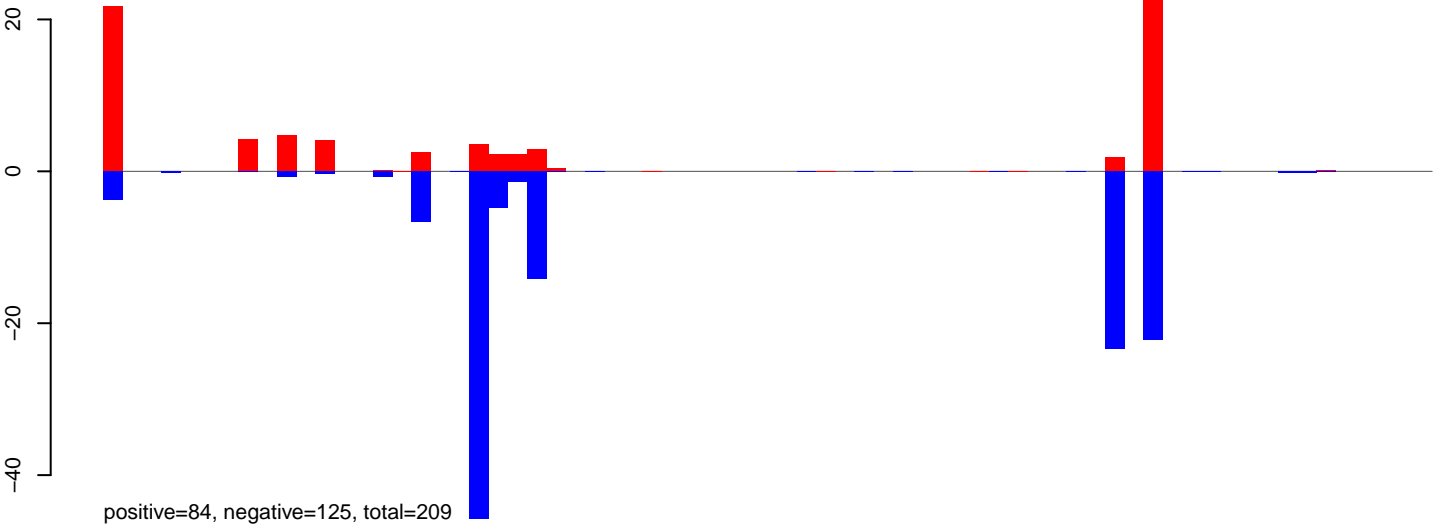
AeAeg_CCL.125_cells.rep



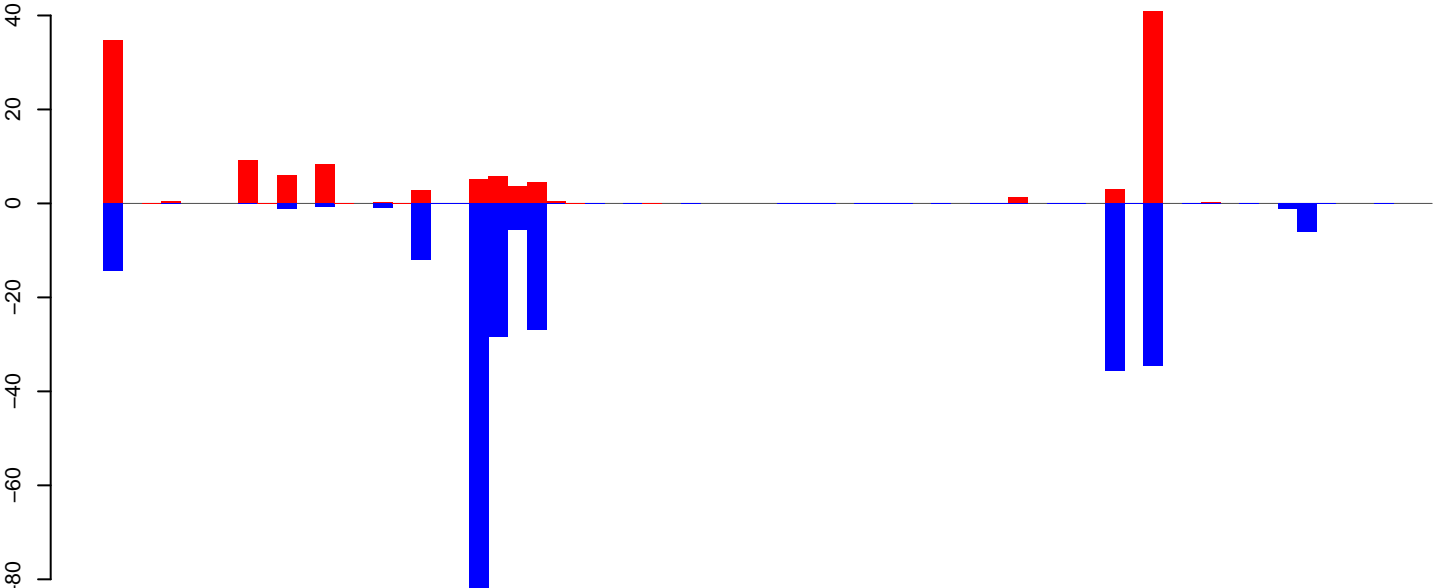
AeAeg_CCL.125_cells.18_23.rep



AeAeg_CCL.125_cells.24_35.rep



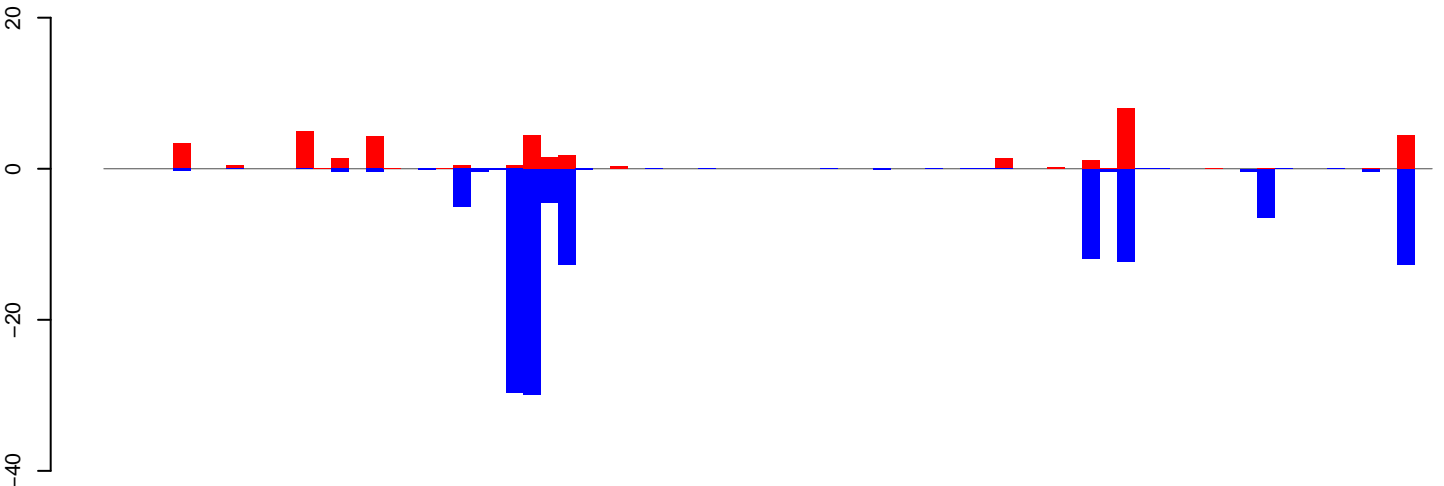
AeAeg_CCL.125_cells.rep



ipiensis_125_cells_18_23_rep_structural_protein_1_NS1_non-structural_protein_2_NS2_and_capsid_protein_VP_genes:1-3498

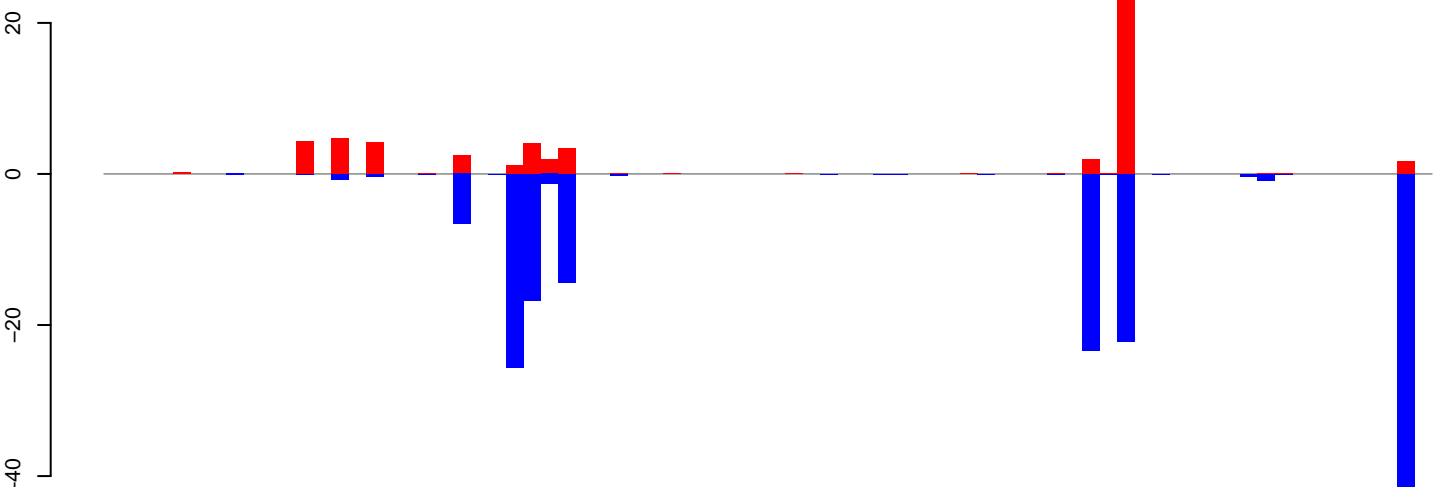
0 500 1000 1500 2000 2500 3000 3500

AeAeg_CCL.125_cells.18_23.rep



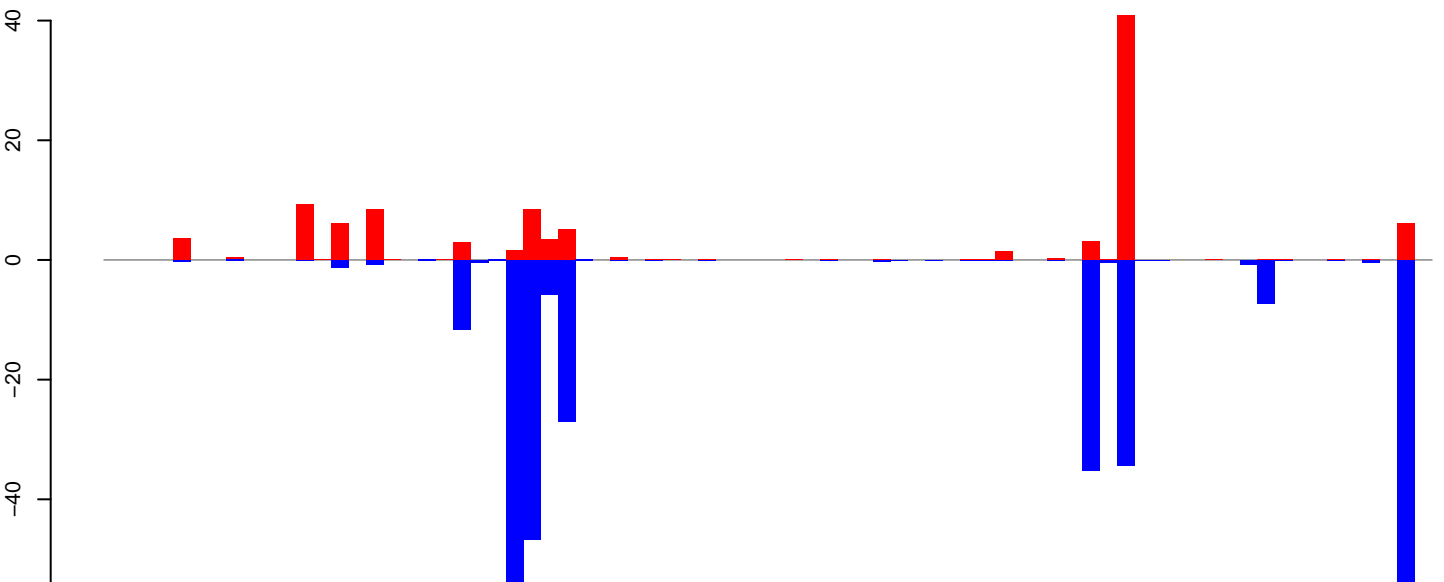
positive=39, negative=129, total=168

AeAeg_CCL.125_cells.24_35.rep



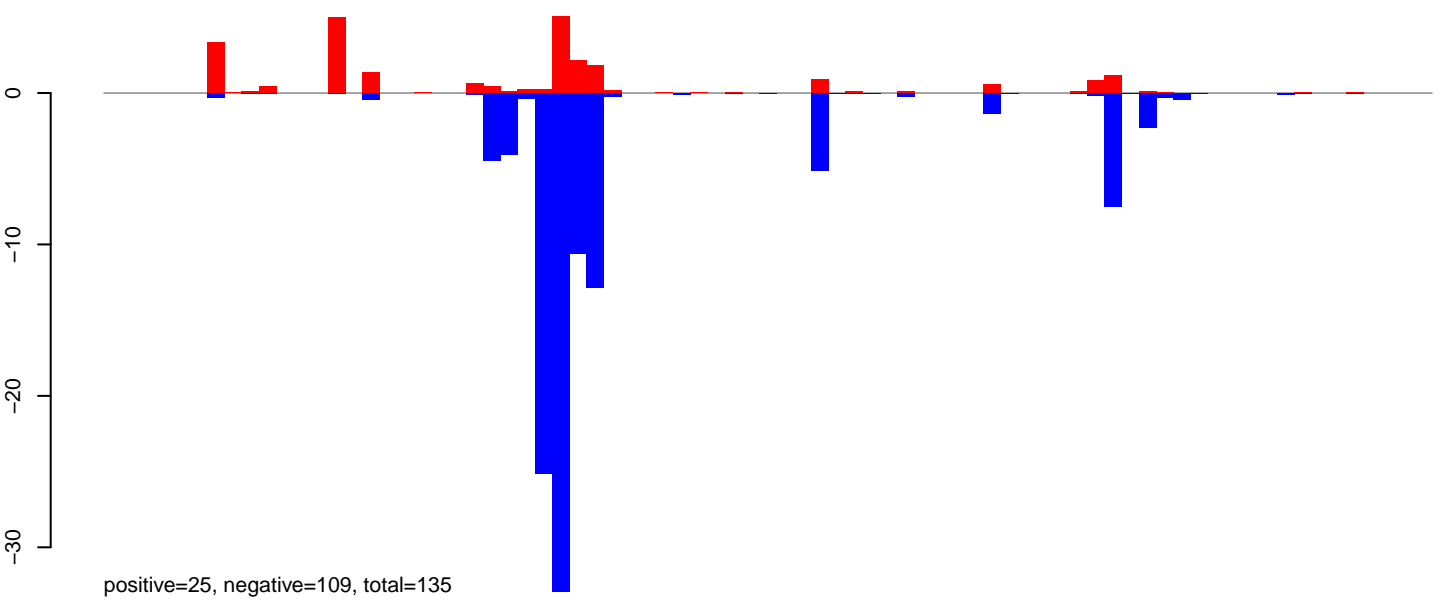
positive=63, negative=159, total=222

AeAeg_CCL.125_cells.rep

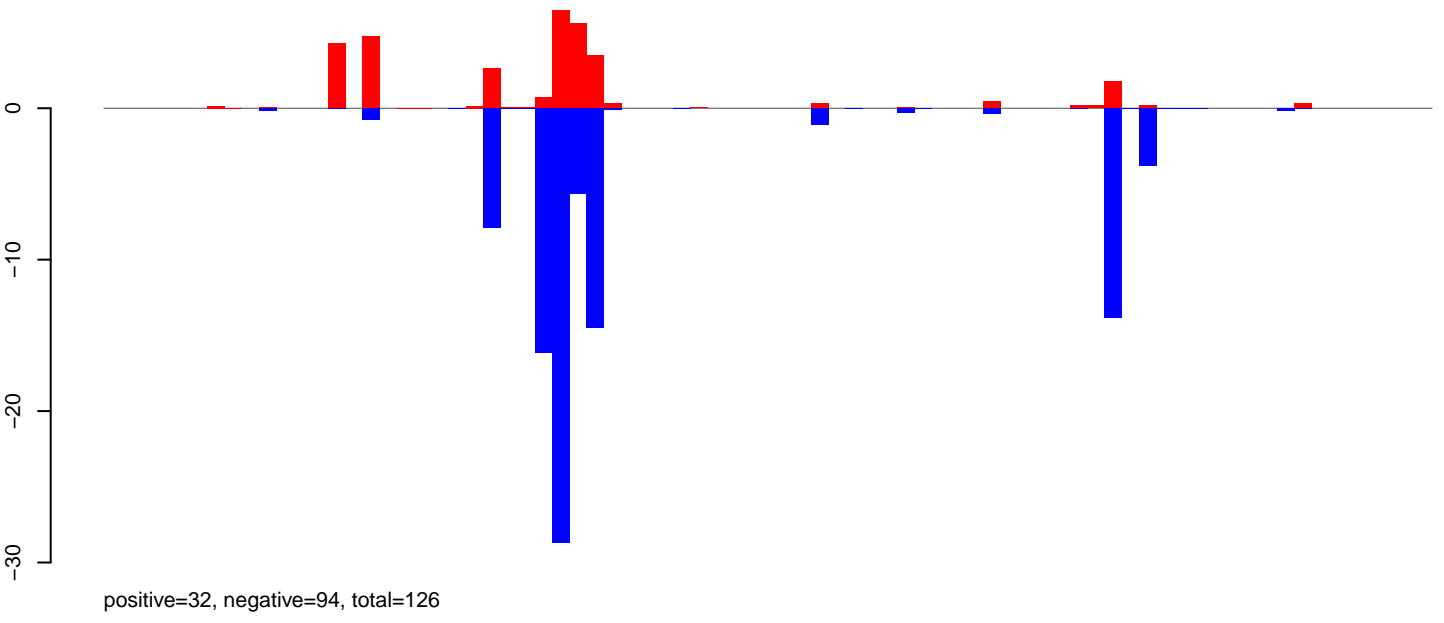


positive=102, negative=288, total=390 window size=50, length=3805, Virus@MH188045.1-Culex_densovirus_strain_CDENV_Madera-4:1-3805

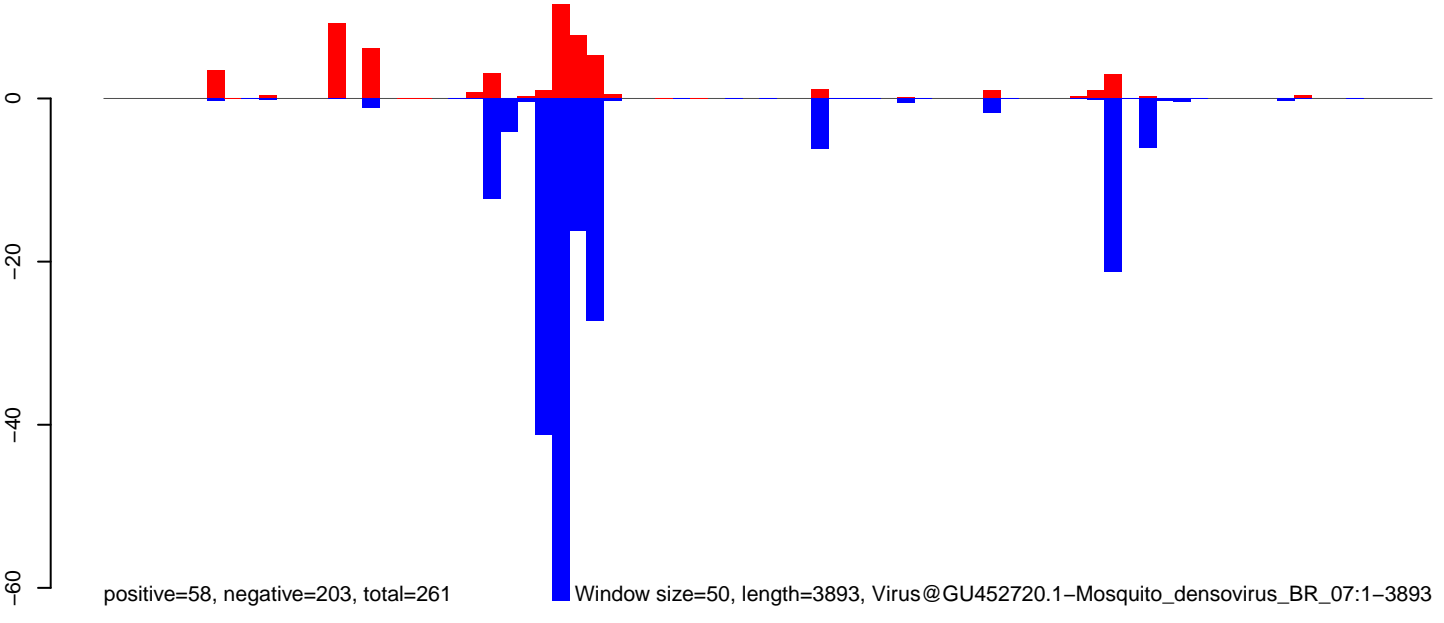
AeAeg_CCL.125_cells.18_23.rep



AeAeg_CCL.125_cells.24_35.rep

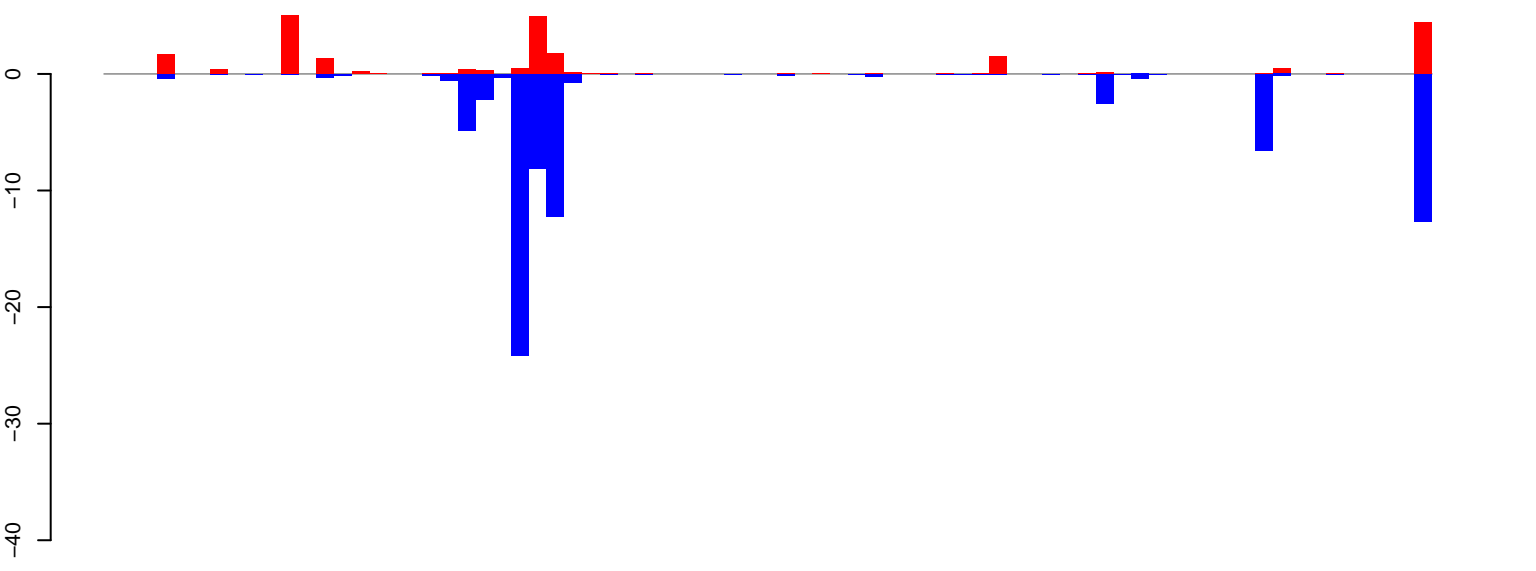


AeAeg_CCL.125_cells.rep



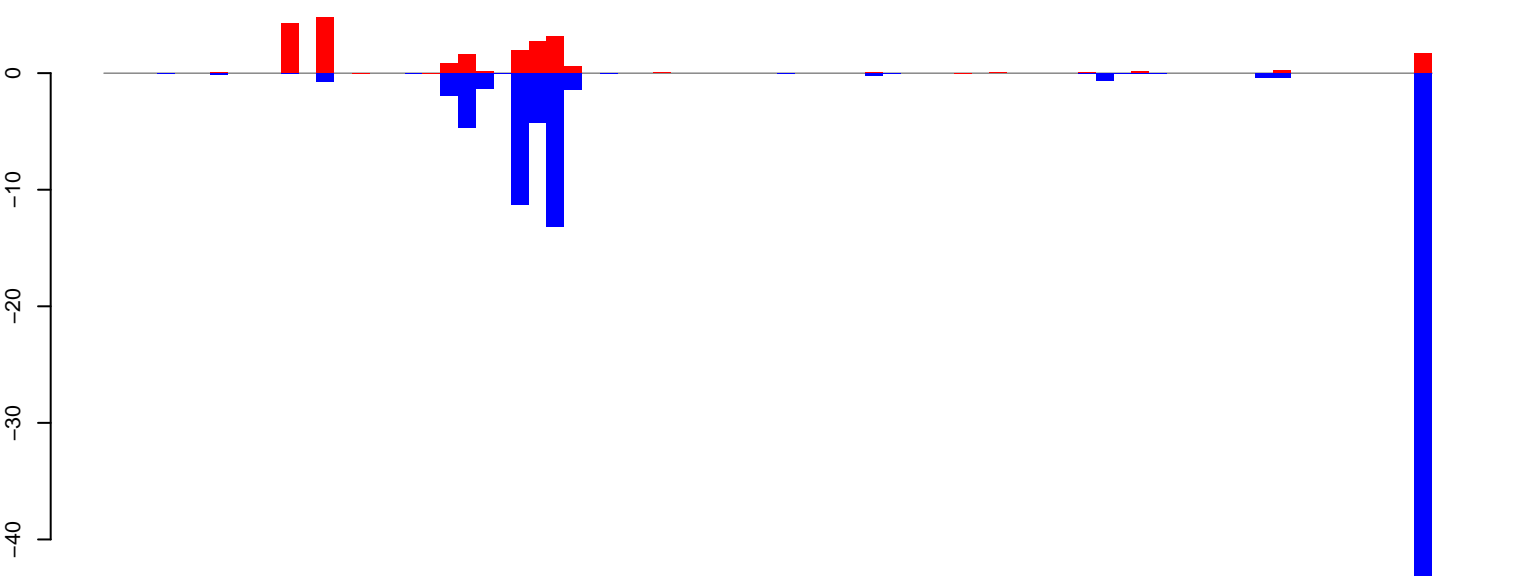
0 1000 2000 3000 4000

AeAeg_CCL.125_cells.18_23.rep



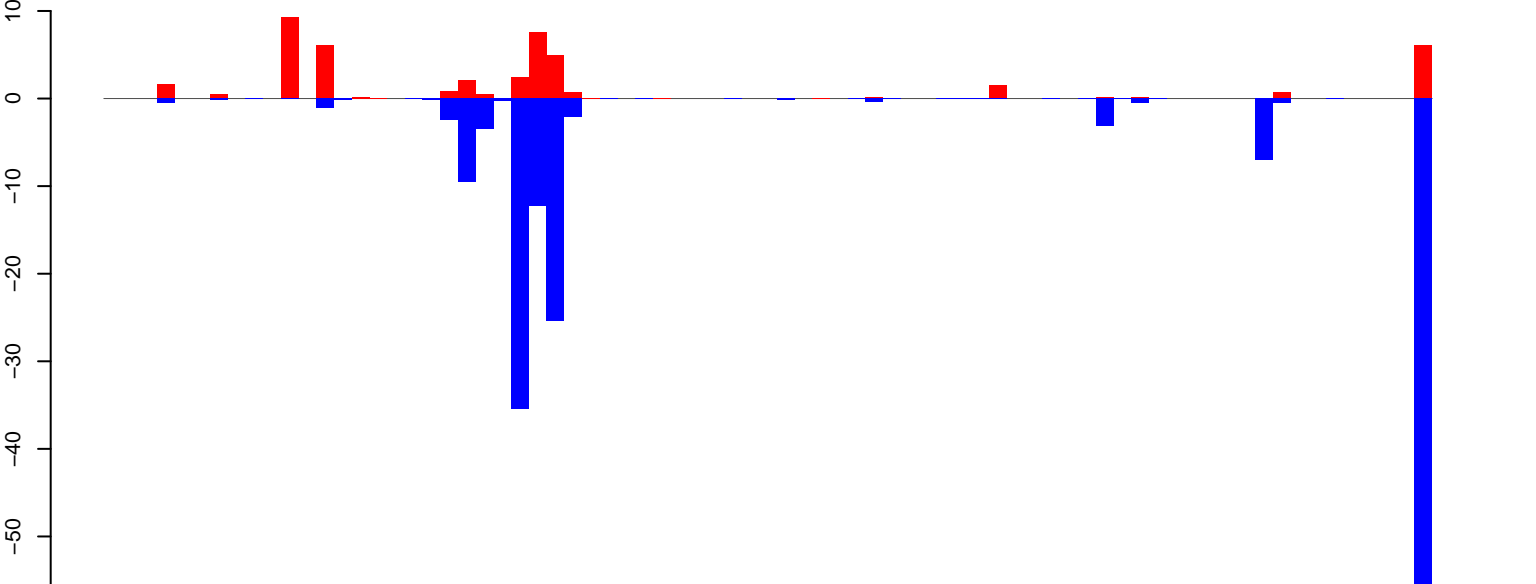
positive=28, negative=90, total=118

AeAeg_CCL.125_cells.24_35.rep



positive=24, negative=133, total=158

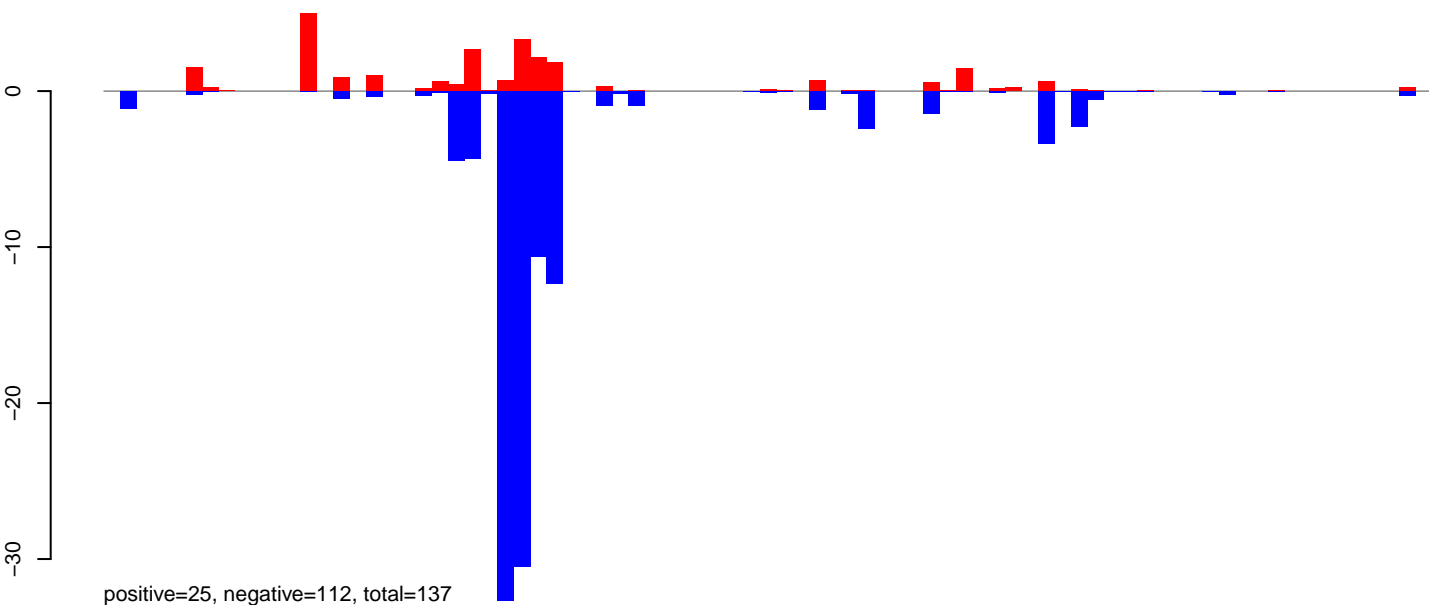
AeAeg_CCL.125_cells.rep



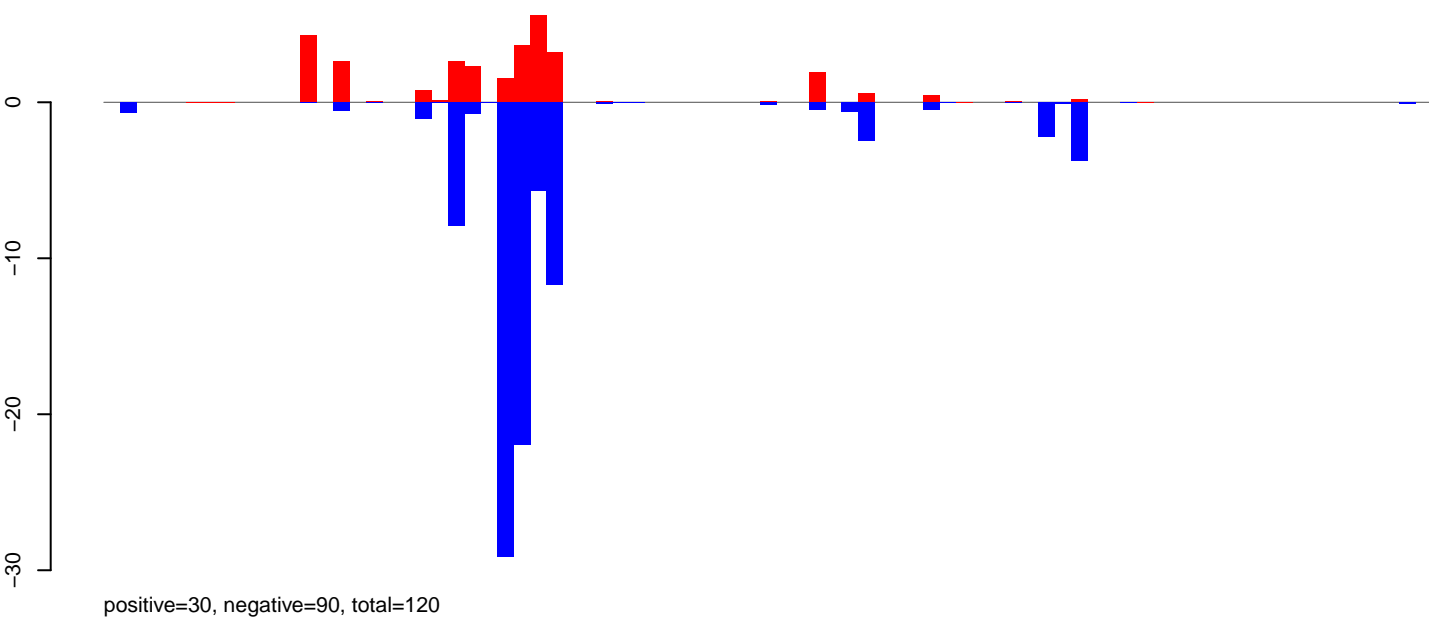
positive=53, negative=223, total=276

Window size=50, length=3790, Virus@AeAeg_Thai_Densovirus_c30446_g1_i1_len=3790:1-3790

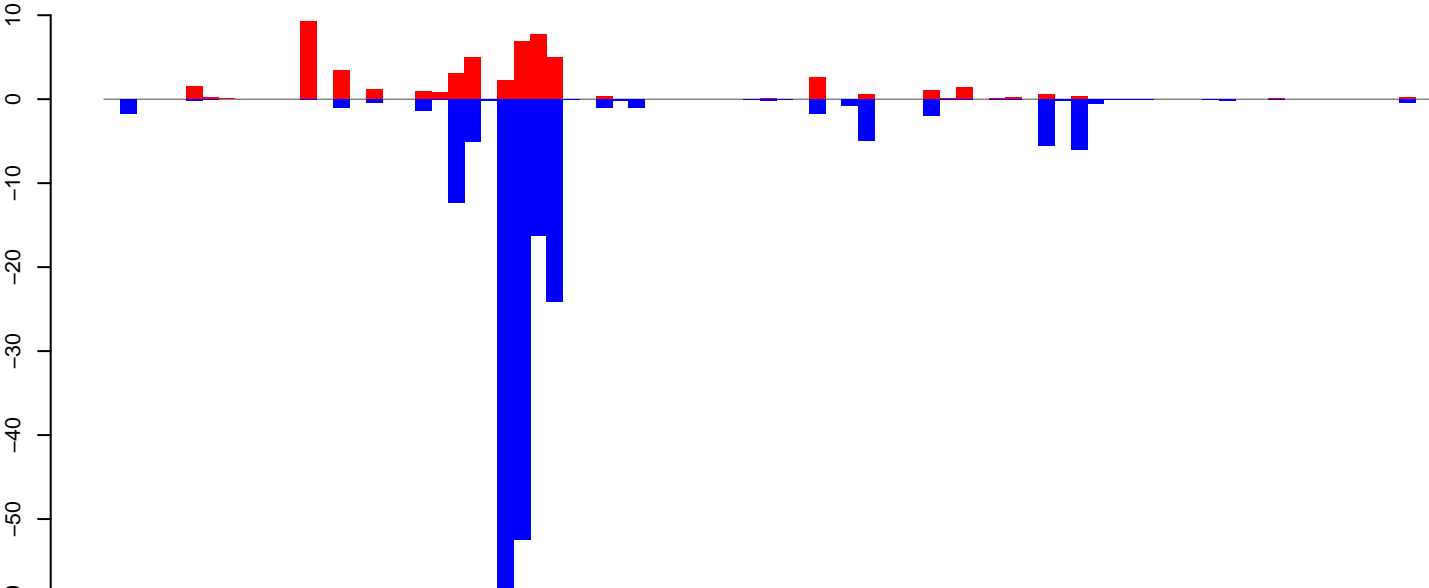
AeAeg_CCL.125_cells.18_23.rep



AeAeg_CCL.125_cells.24_35.rep



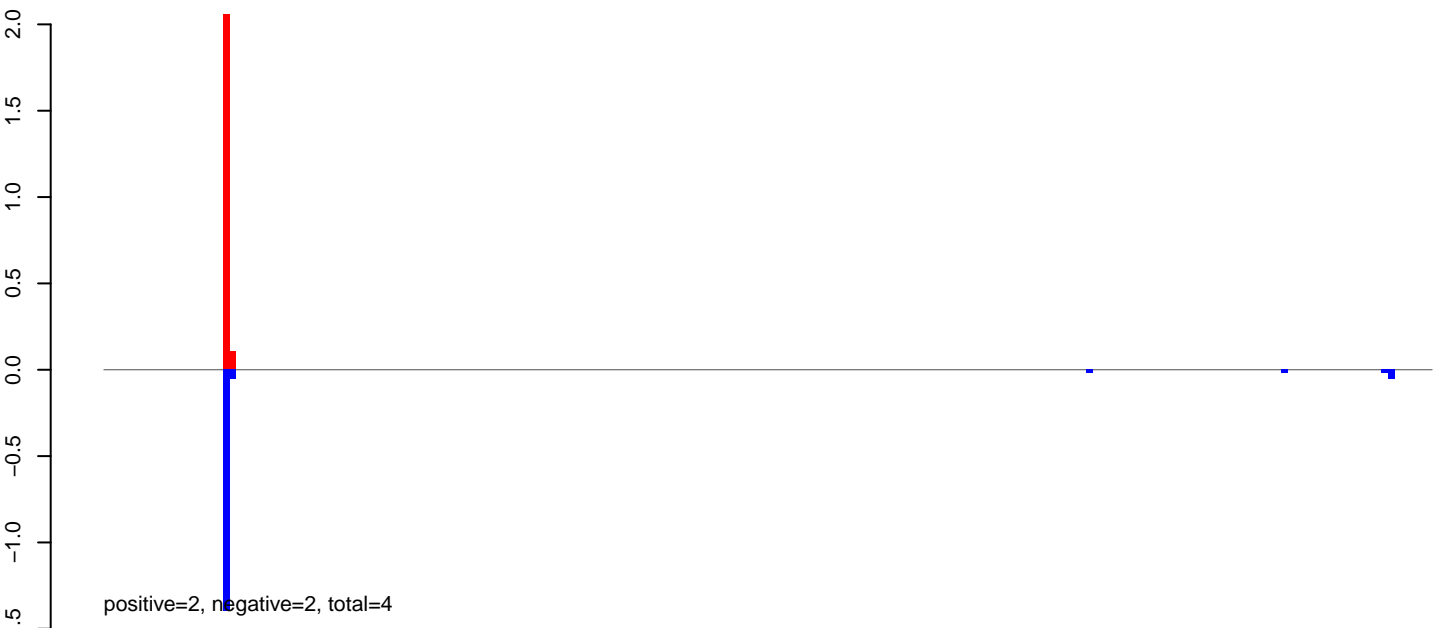
AeAeg_CCL.125_cells.rep



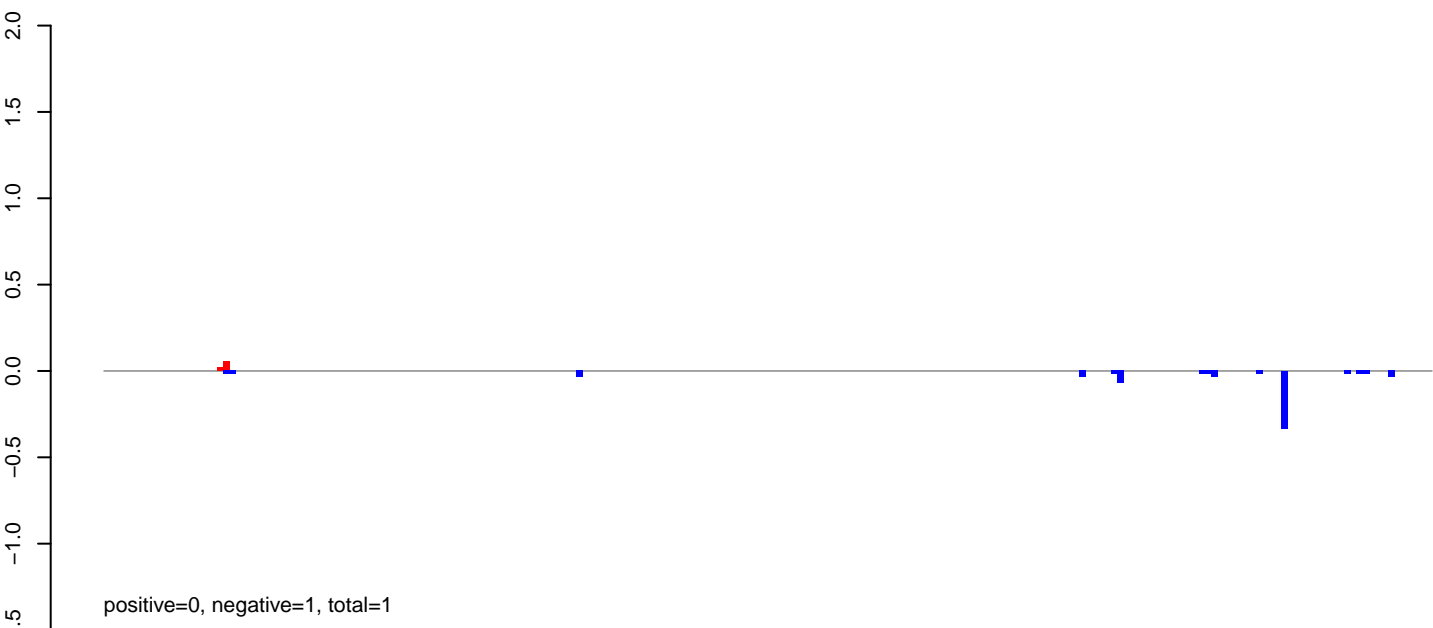
les_alp...non-structural_protein_1_NS-1_non-structural_protein_2_NS-2_and_capsid_protein_VP_genes:1-4094

0 1000 2000 3000 4000

AeAeg_CCL.125_cells.18_23.rep



AeAeg_CCL.125_cells.24_35.rep

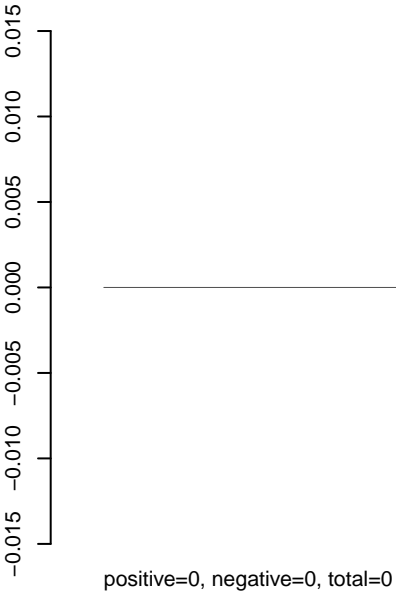


AeAeg_CCL.125_cells.rep

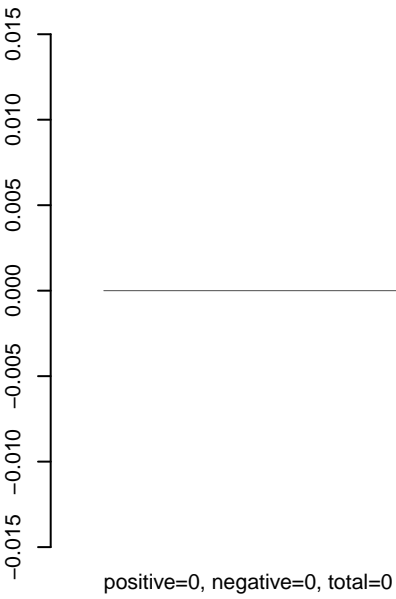


AF416352.2: Aedes albopictus cell_fusing_agent_virus_polyprotein-like_protein_gene_and_agCP8252-like_protein_gene_partial_cds:1-10587

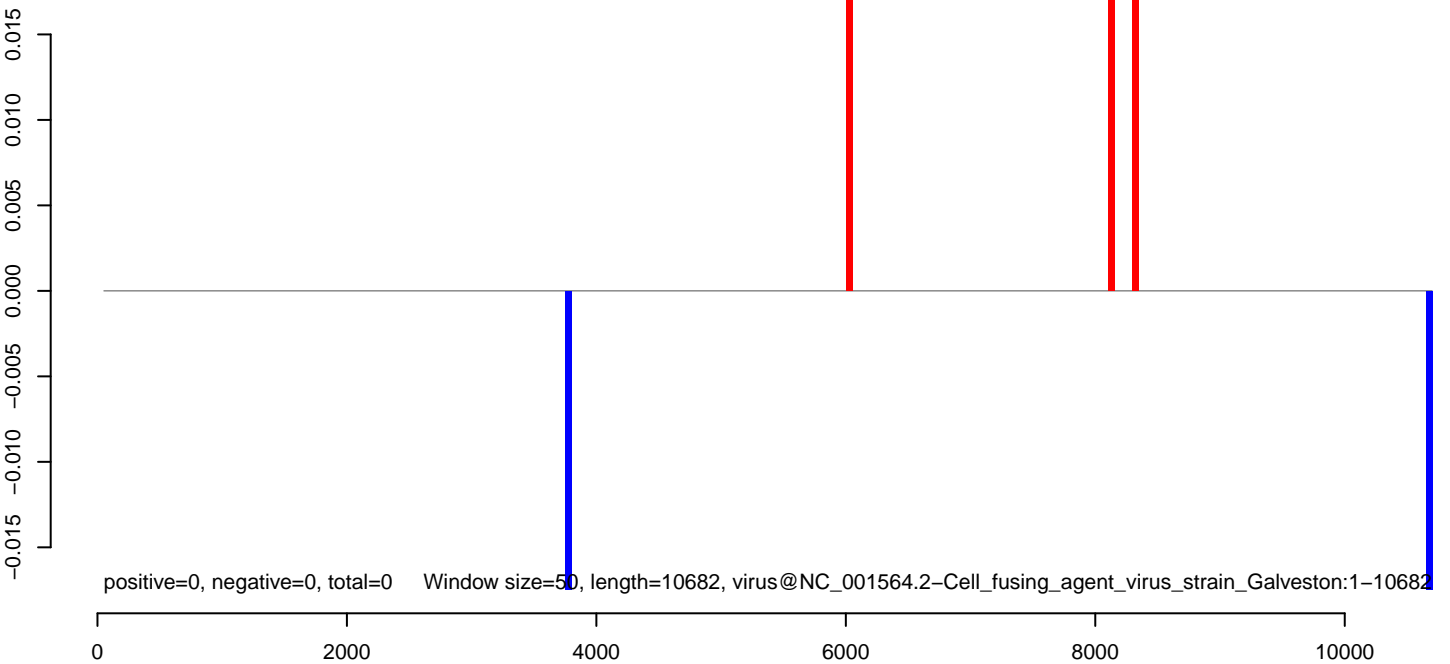
AeAeg_CCL.125_cells.18_23.rep



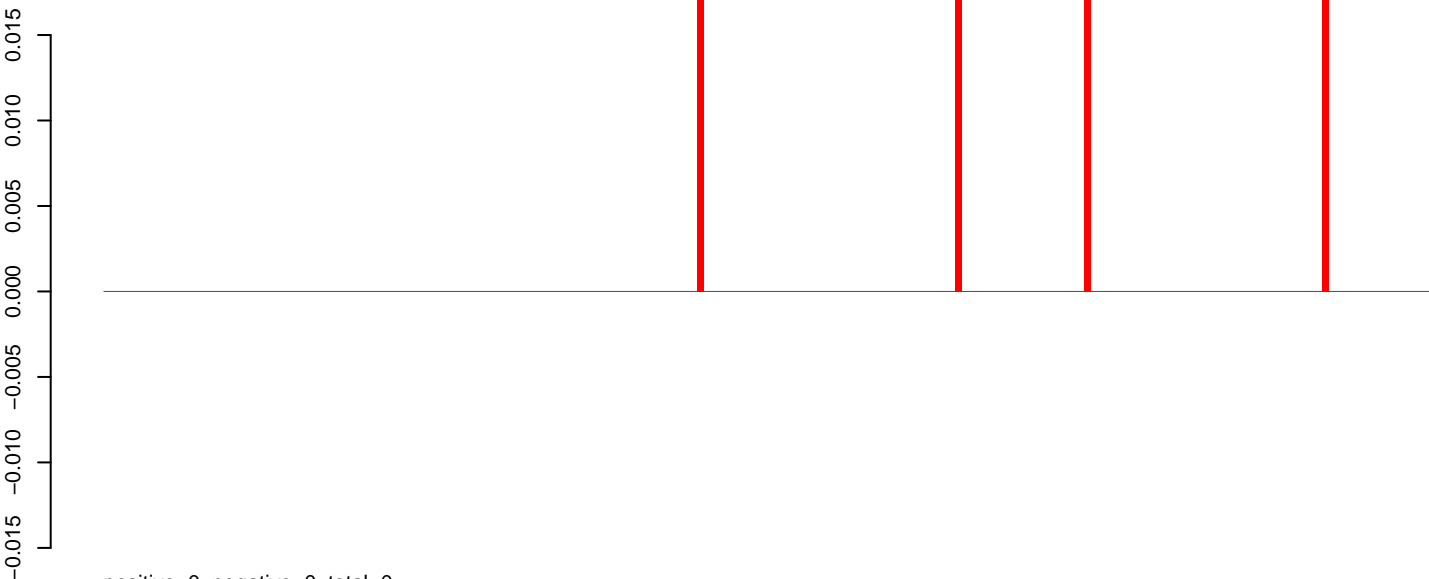
AeAeg_CCL.125_cells.24_35.rep



AeAeg_CCL.125_cells.rep

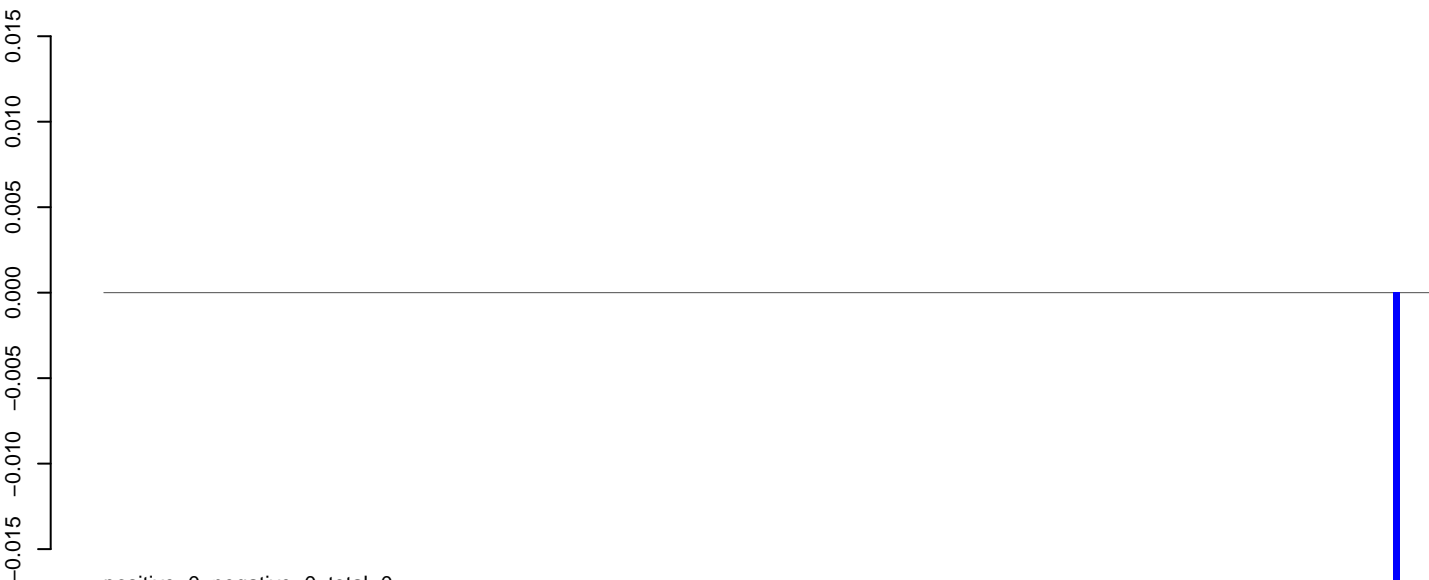


AeAeg_CCL.125_cells.18_23.rep



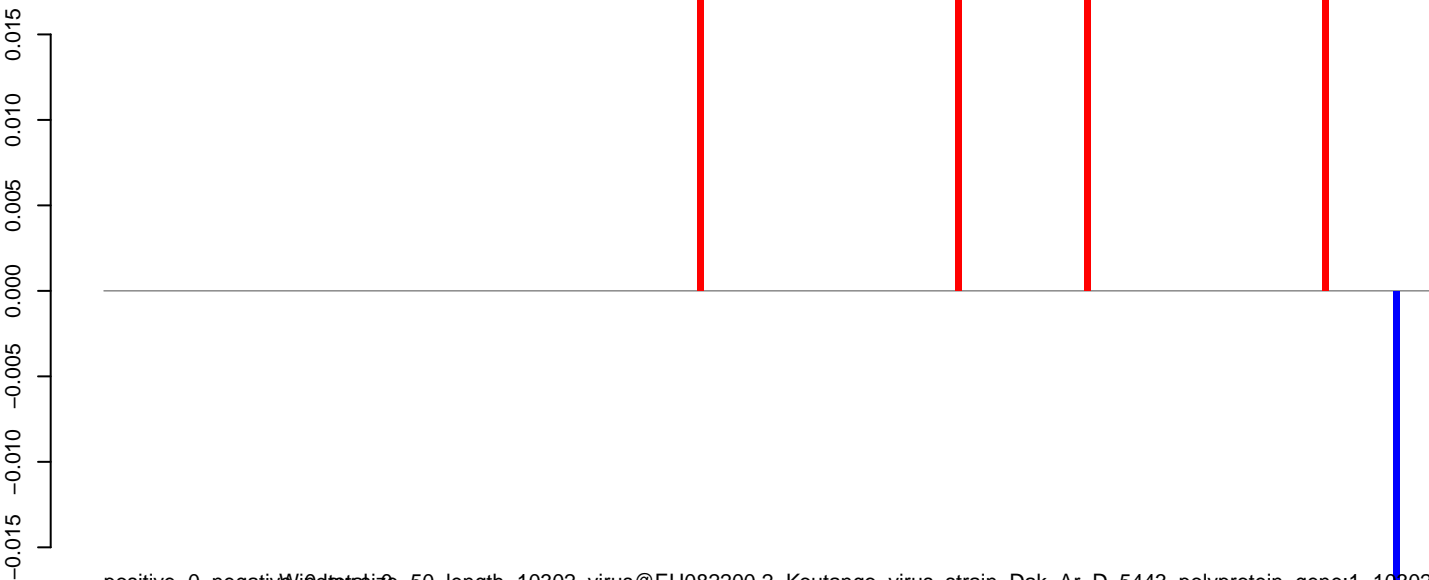
positive=0, negative=0, total=0

AeAeg_CCL.125_cells.24_35.rep



positive=0, negative=0, total=0

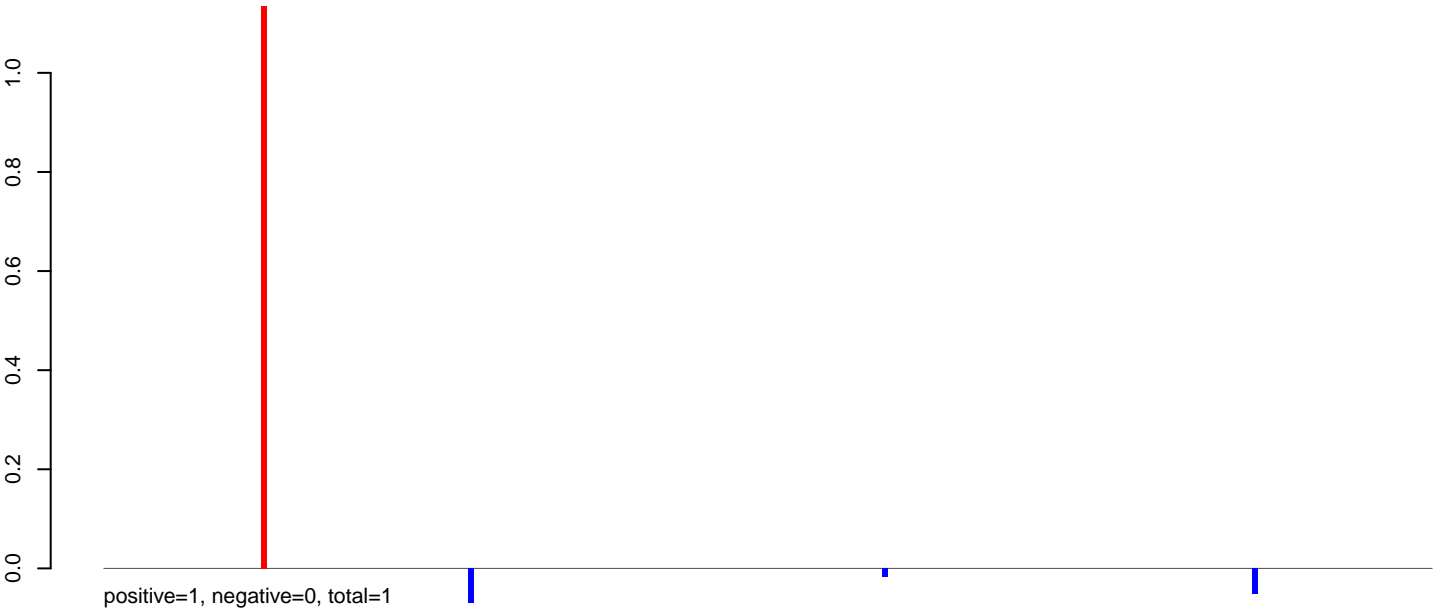
AeAeg_CCL.125_cells.rep



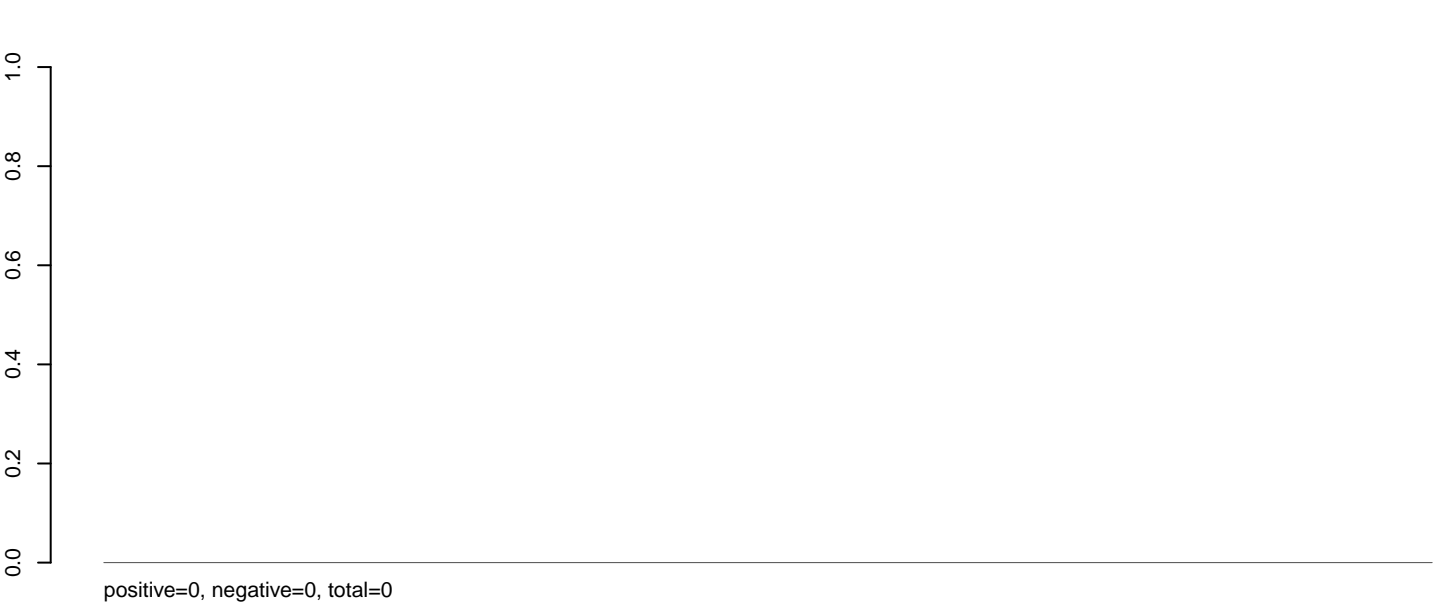
positive=0, negative=0, total=0
Window size=50, length=10302, virus@EU082200.2-Koutango_virus_strain_Dak_Ar_D_5443_polyprotein_gene:1-10302

0 2000 4000 6000 8000 10000

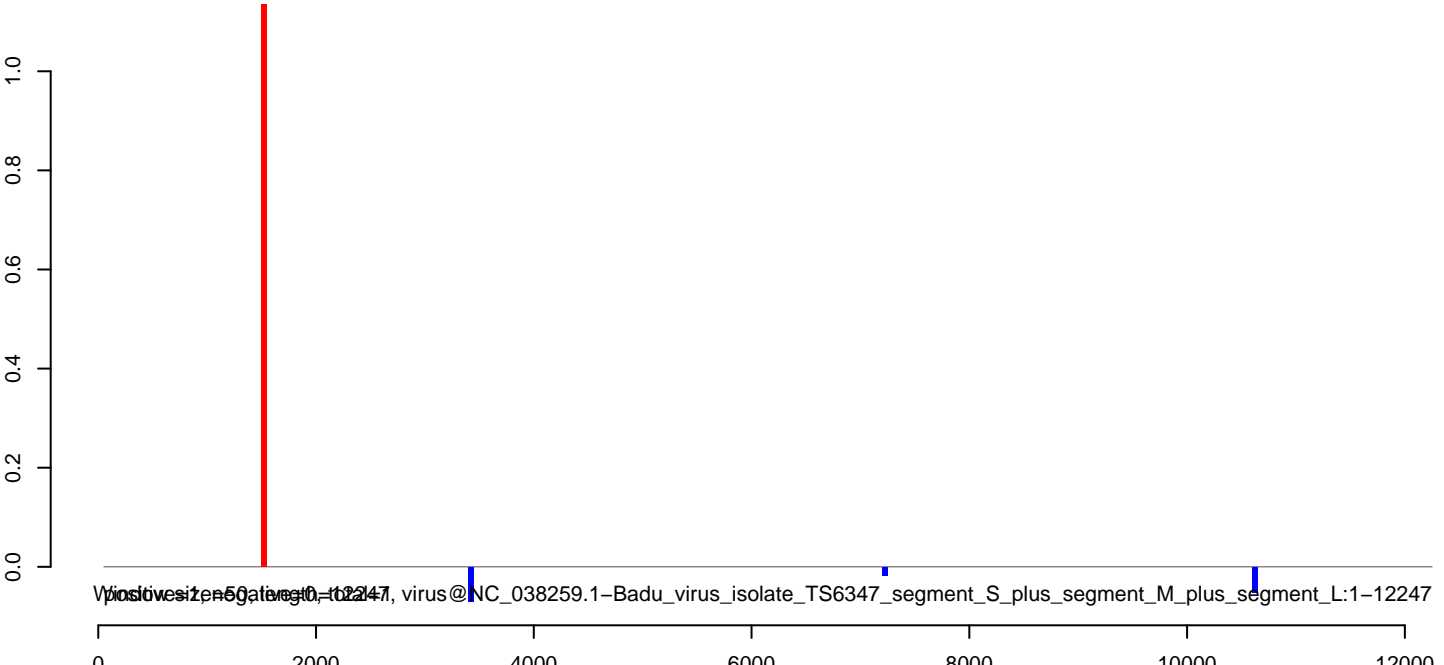
AeAeg_CCL.125_cells.18_23.rep



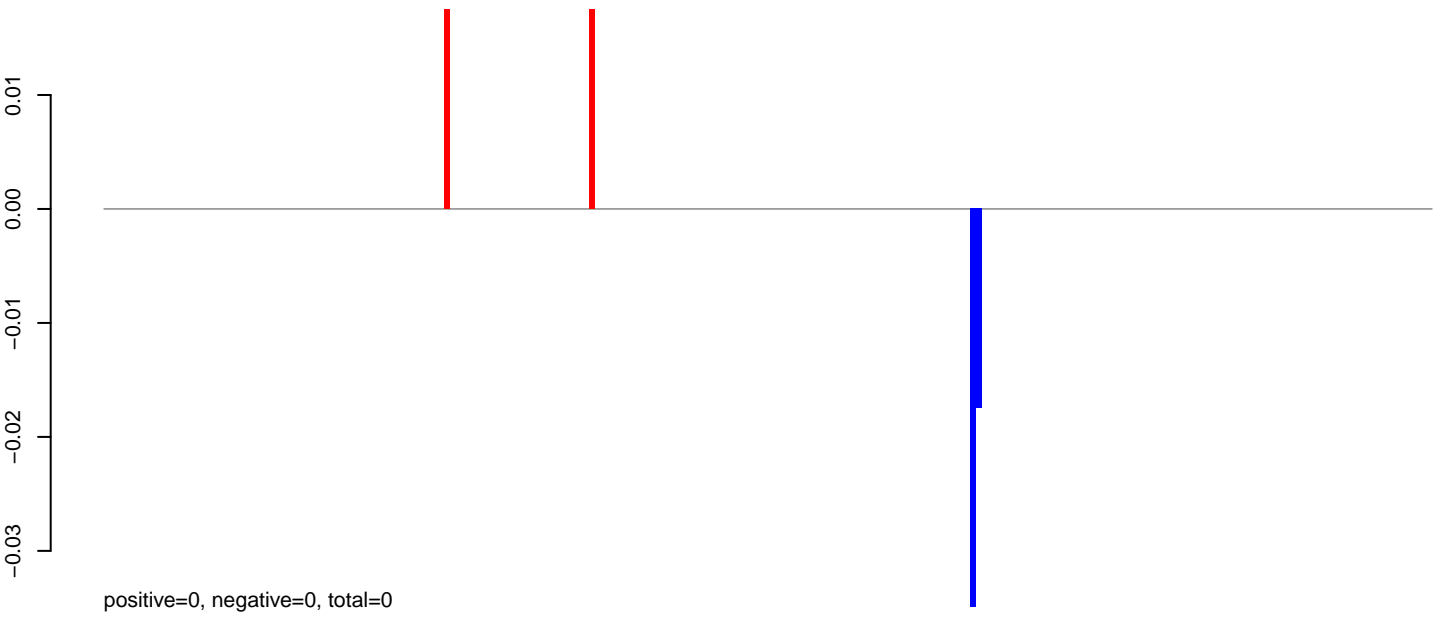
AeAeg_CCL.125_cells.24_35.rep



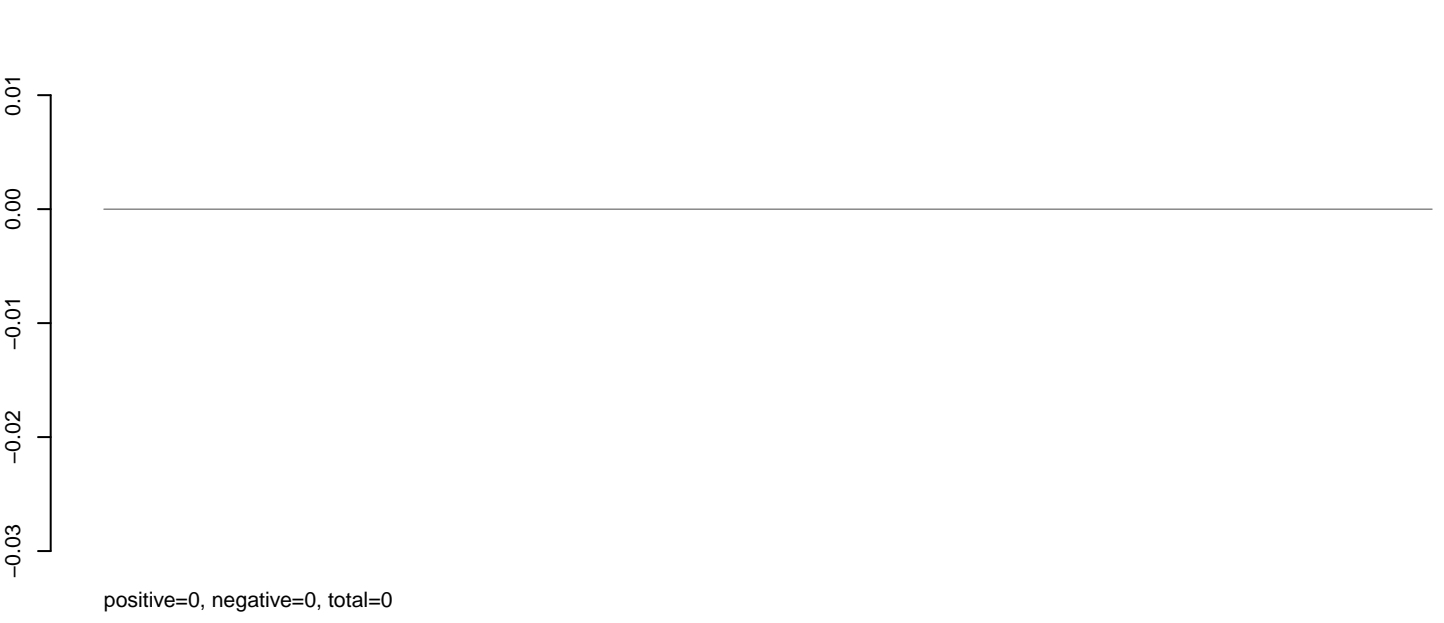
AeAeg_CCL.125_cells.rep



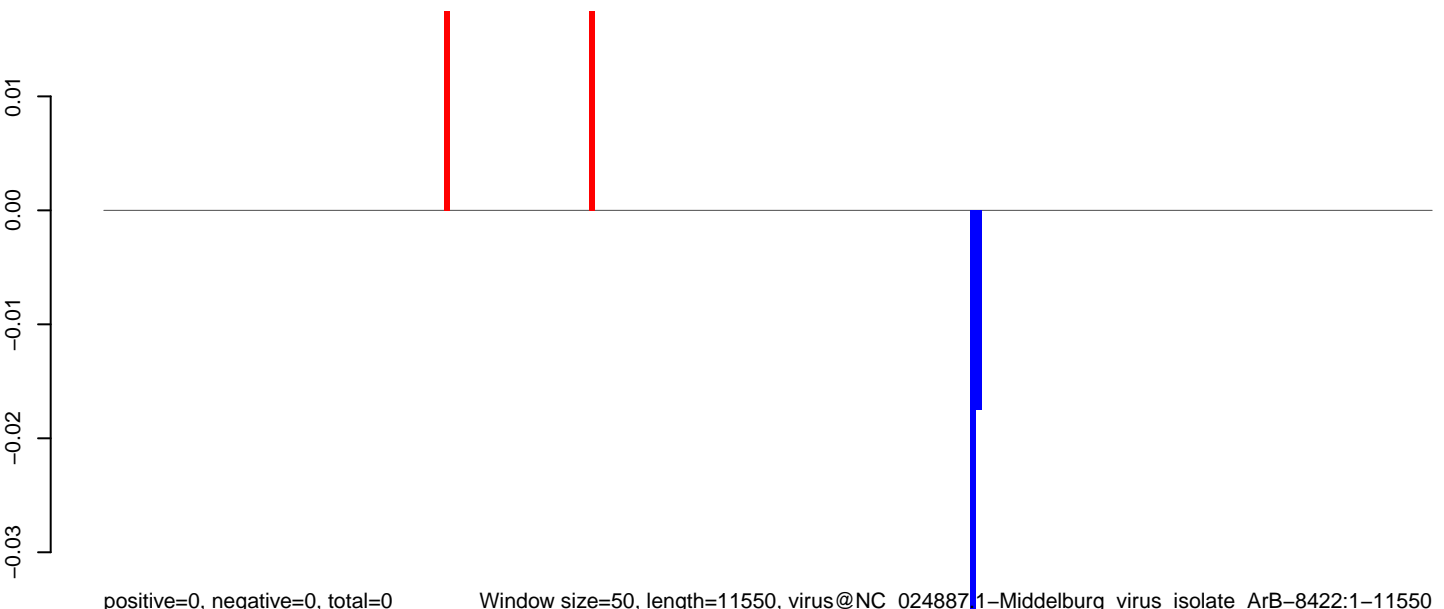
AeAeg_CCL.125_cells.18_23.rep



AeAeg_CCL.125_cells.24_35.rep



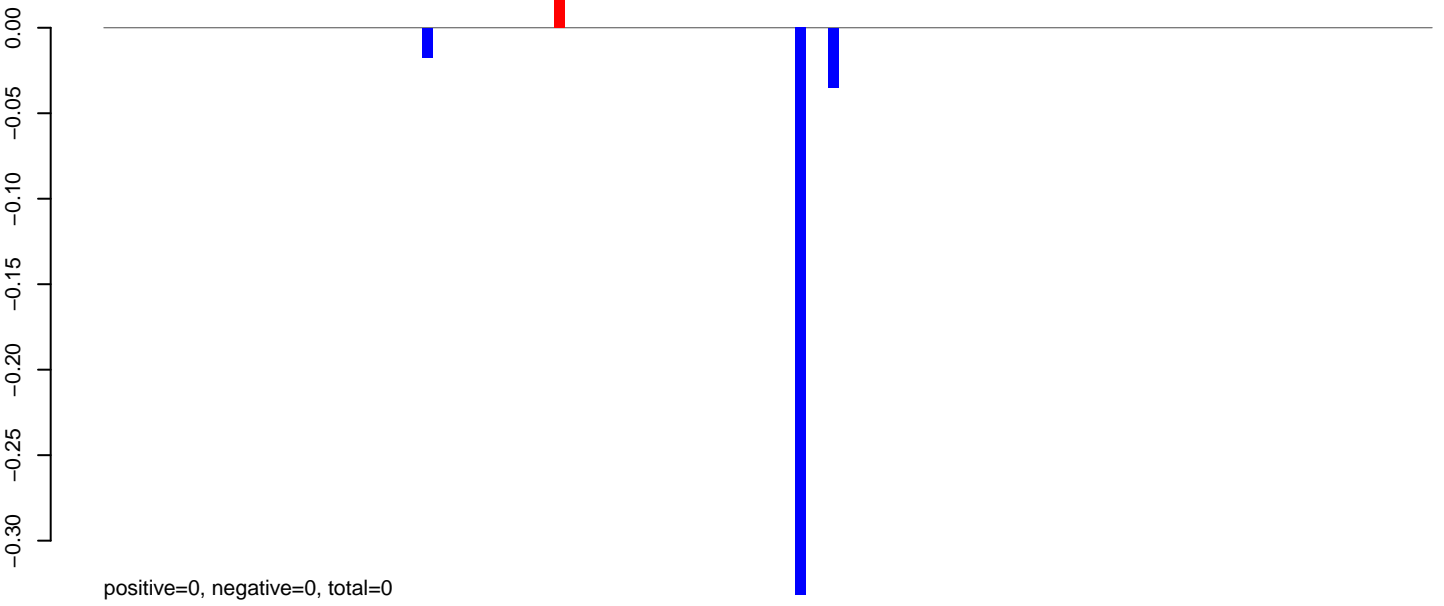
AeAeg_CCL.125_cells.rep



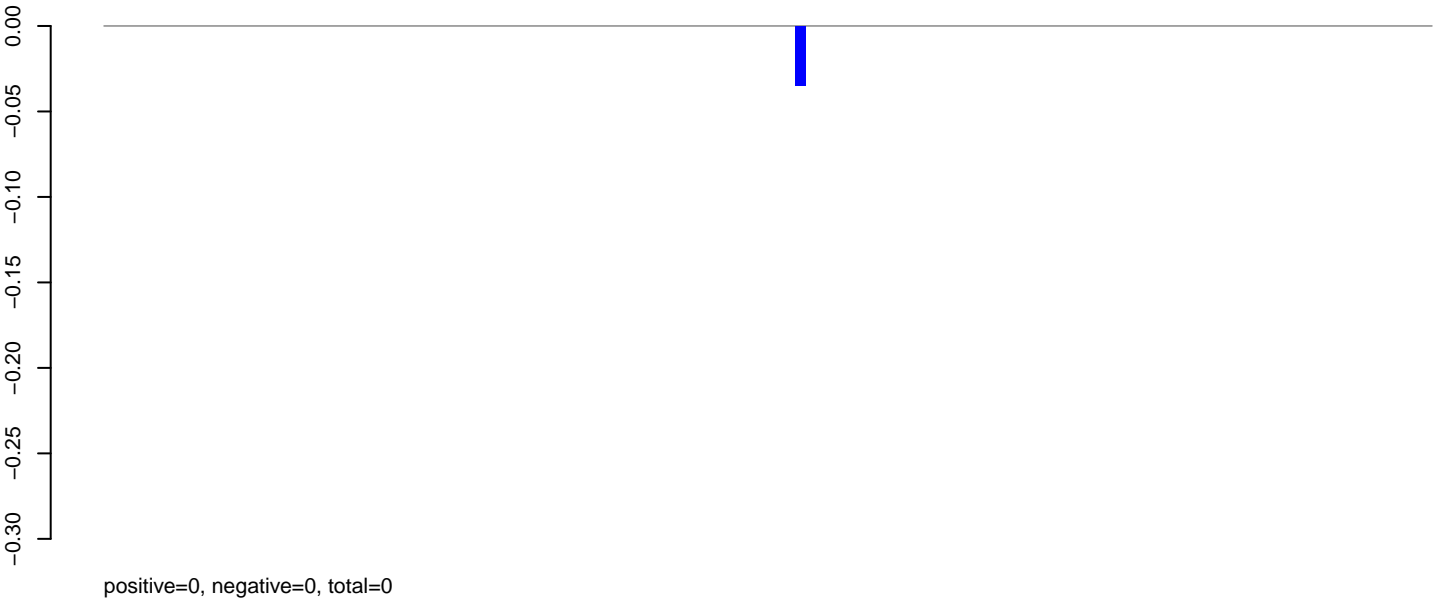
Window size=50, length=11550, virus@NC_024887.1-Middelburg_virus_isolate_ArB-8422:1-11550

0 2000 4000 6000 8000 10000 12000

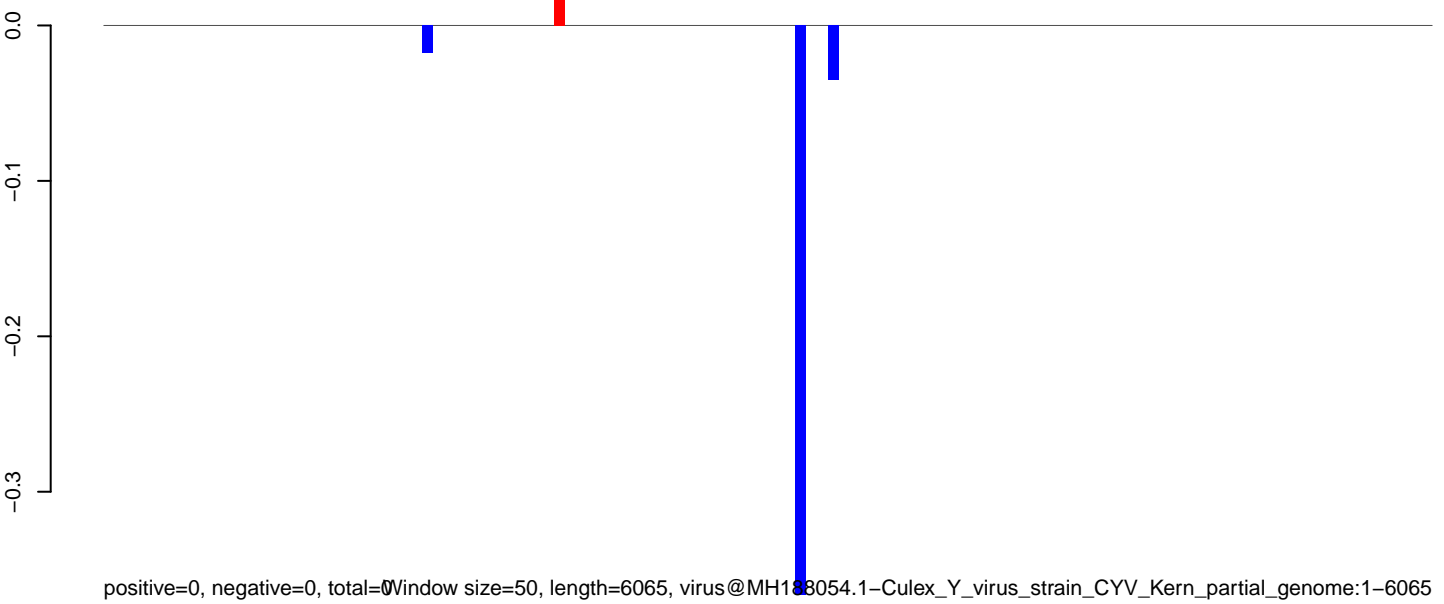
AeAeg_CCL.125_cells.18_23.rep



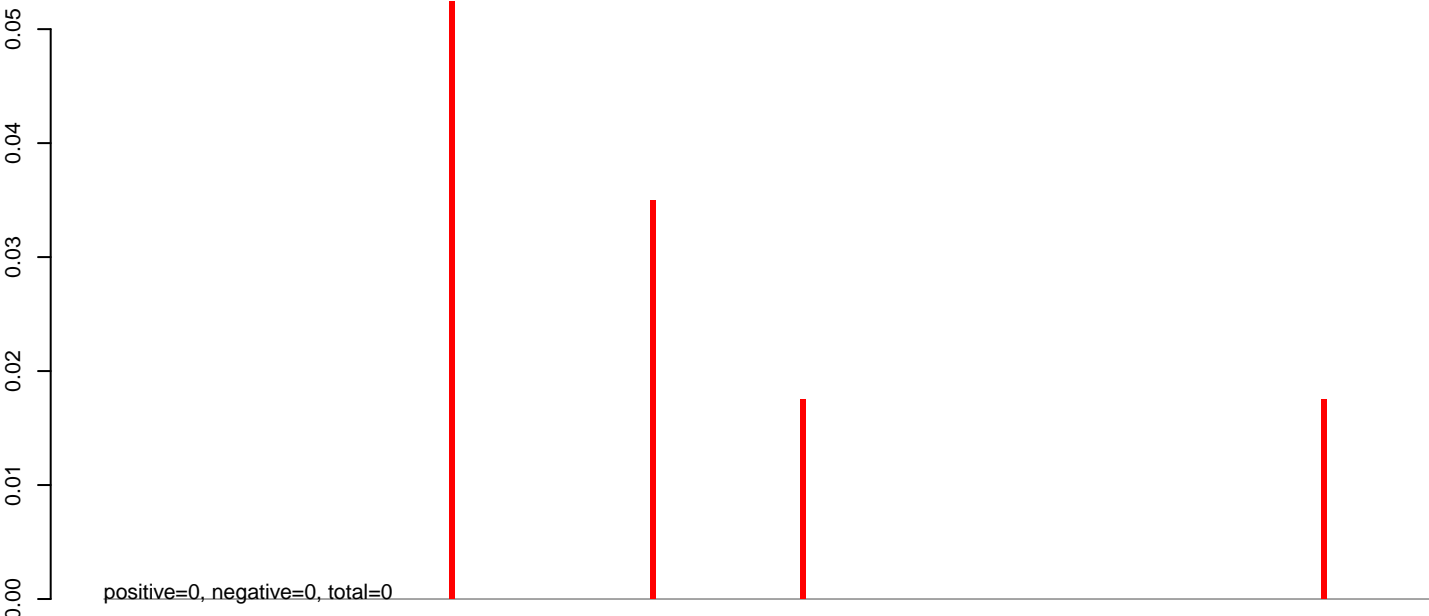
AeAeg_CCL.125_cells.24_35.rep



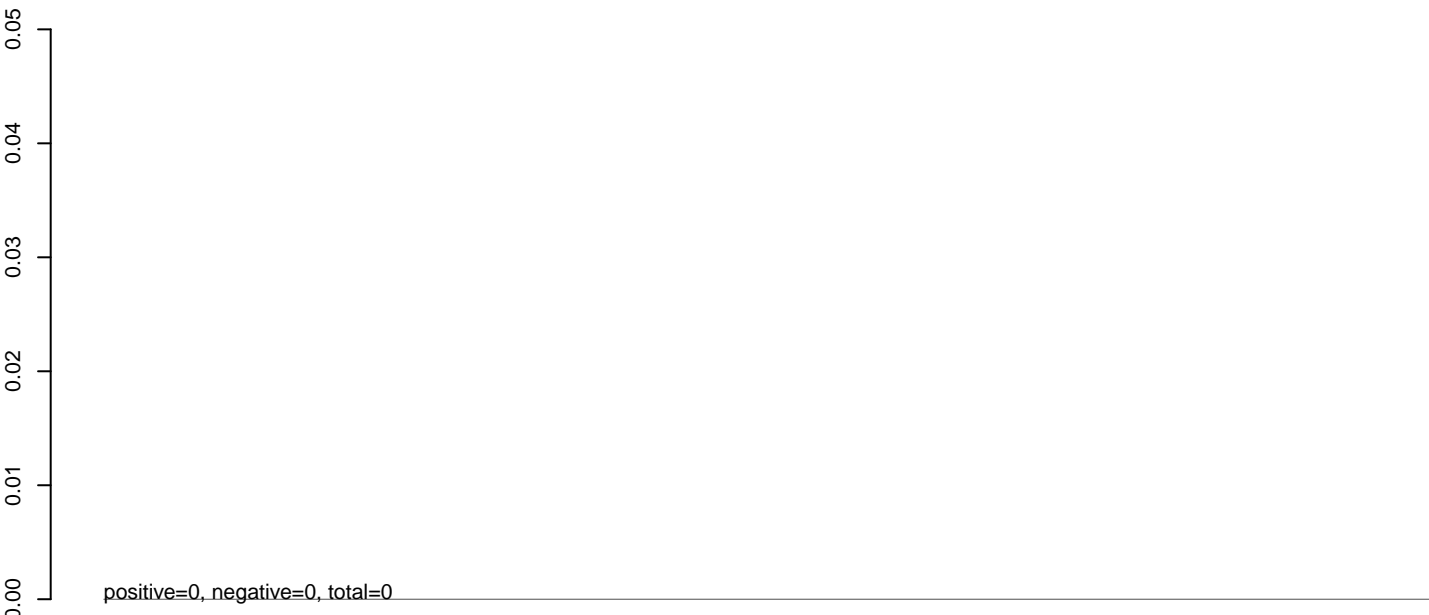
AeAeg_CCL.125_cells.rep



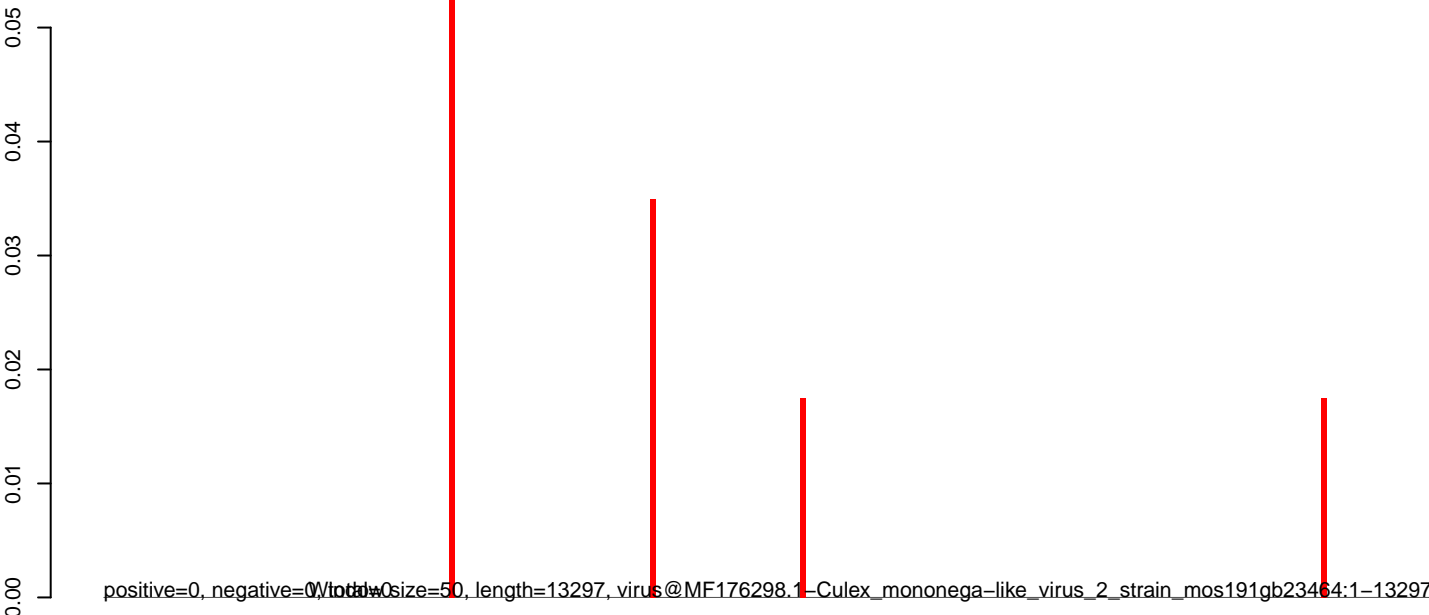
AeAeg_CCL.125_cells.18_23.rep



AeAeg_CCL.125_cells.24_35.rep



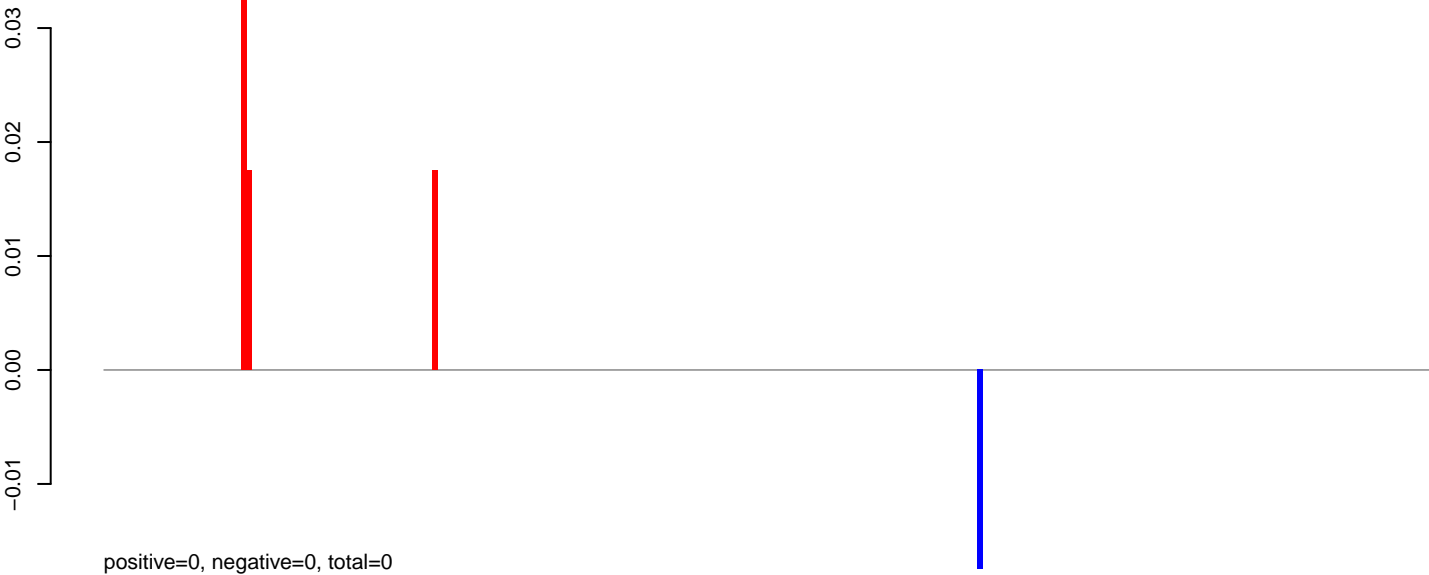
AeAeg_CCL.125_cells.rep



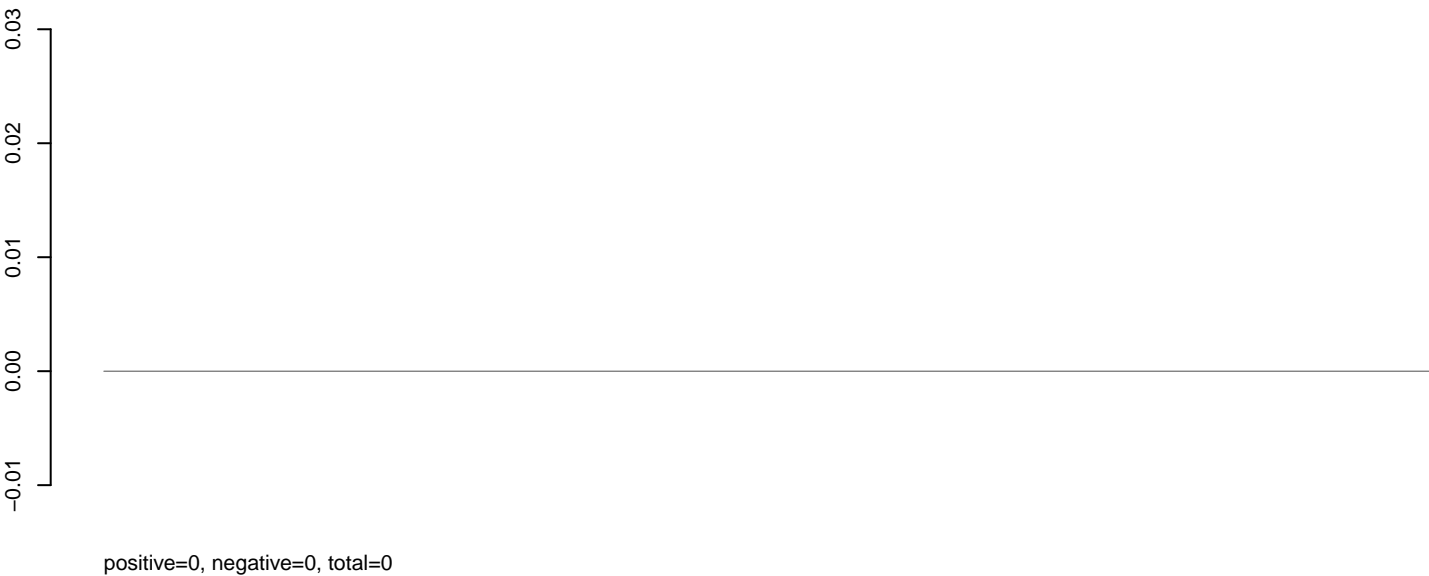
0 2000 4000 6000 8000 10000 12000

width=50, length=13297, virus@MF176298.1=Culex_mononega-like_virus_2_strain_mos191gb2346:1-13297

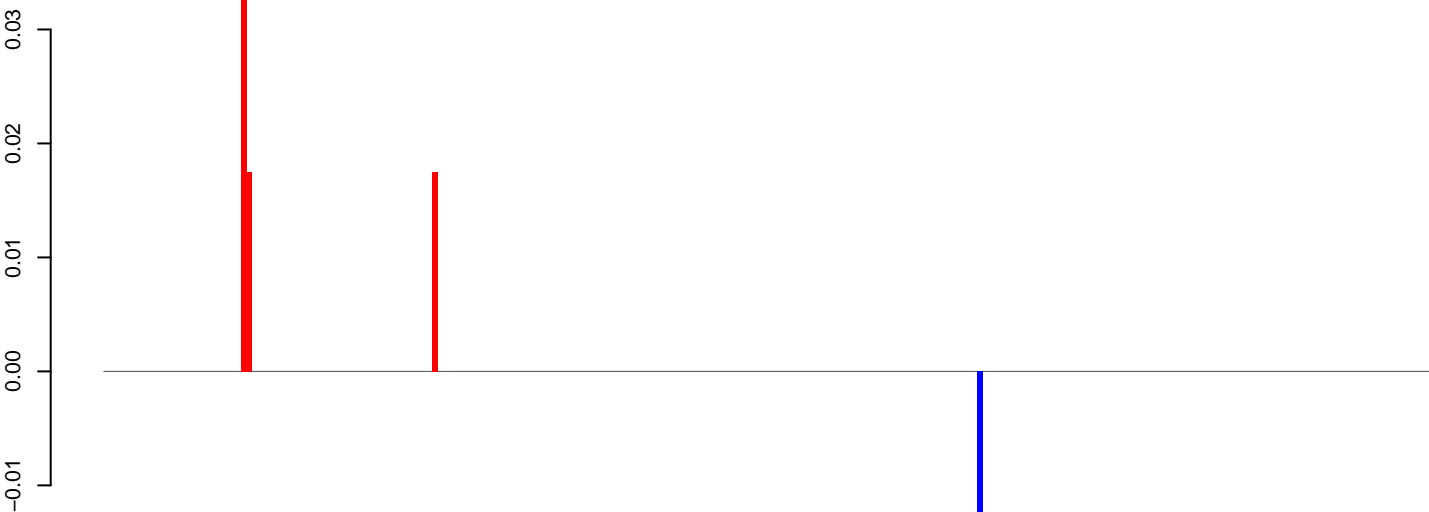
AeAeg_CCL.125_cells.18_23.rep



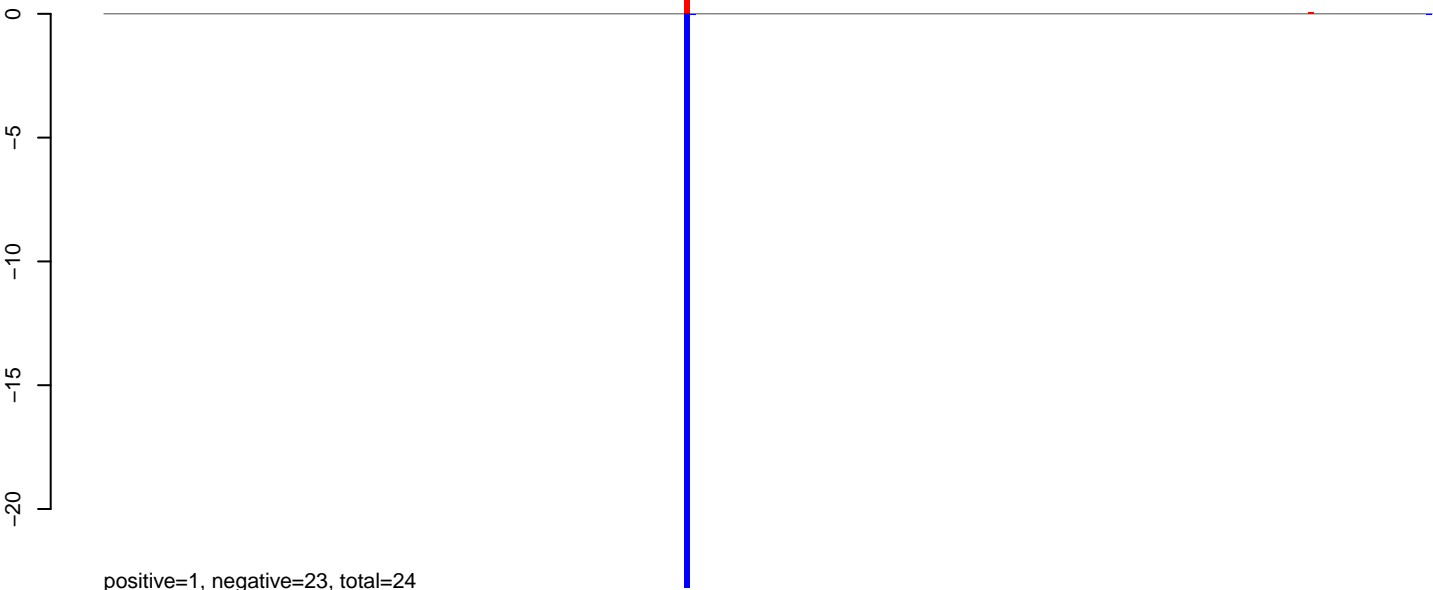
AeAeg_CCL.125_cells.24_35.rep



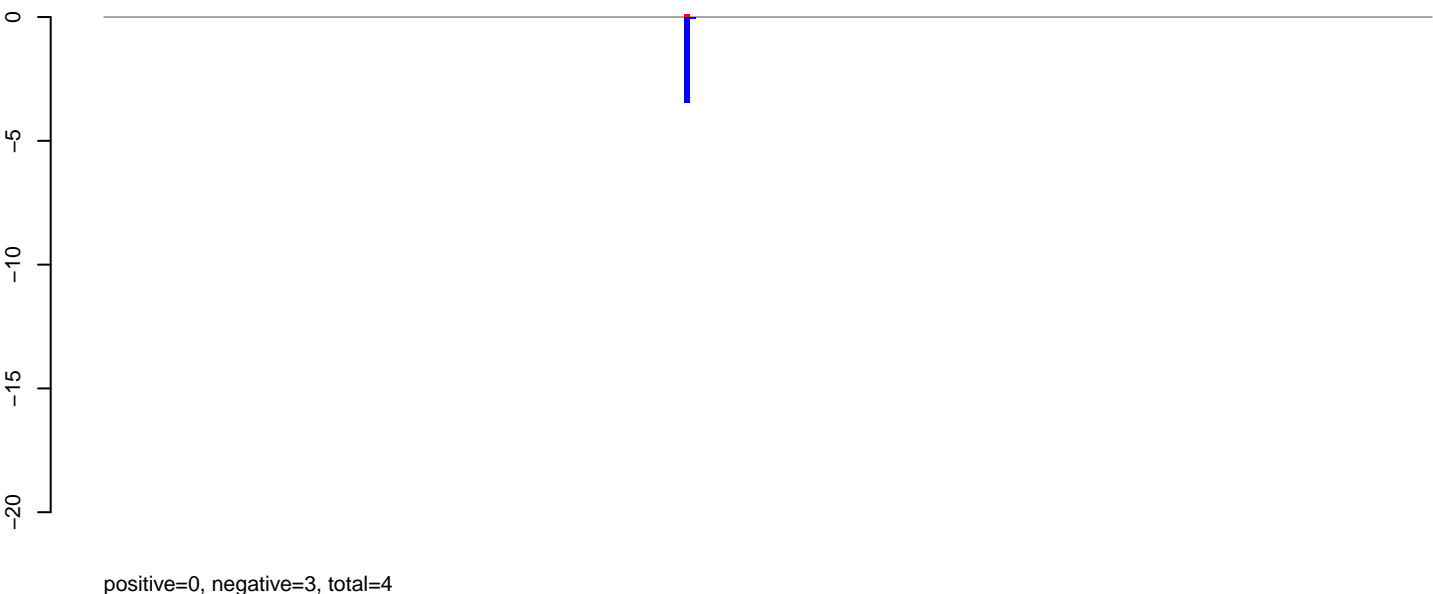
AeAeg_CCL.125_cells.rep



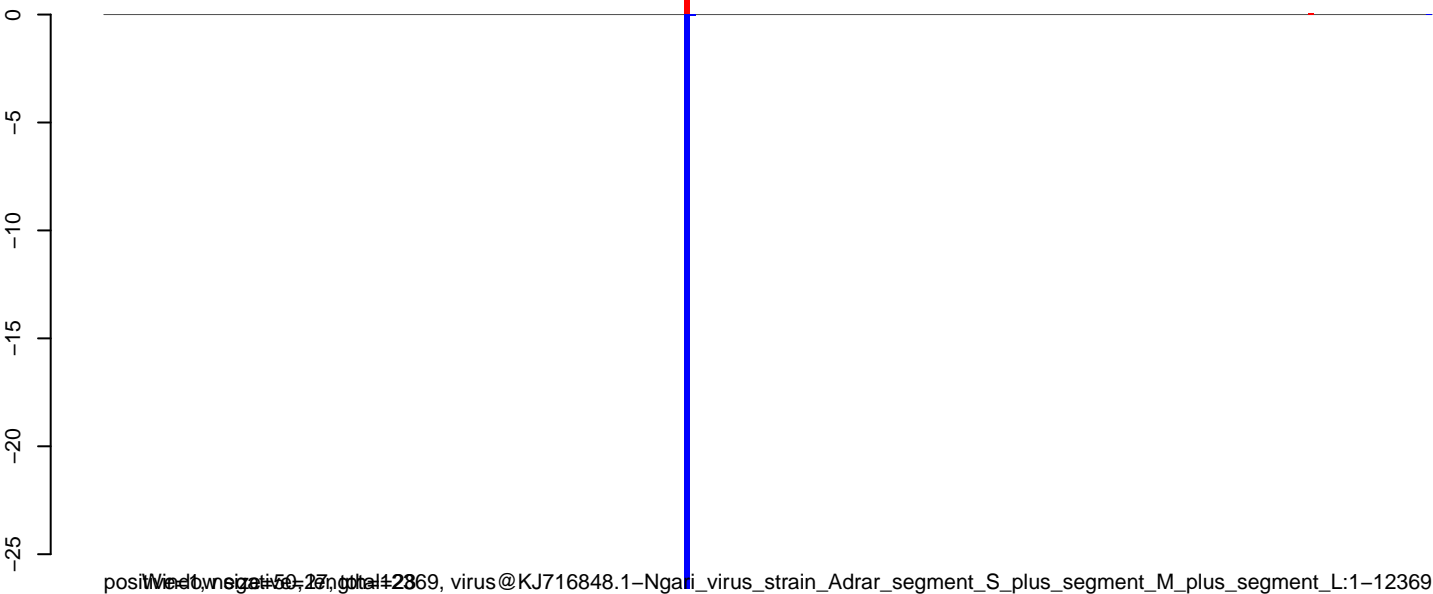
AeAeg_CCL.125_cells.18_23.rep



AeAeg_CCL.125_cells.24_35.rep



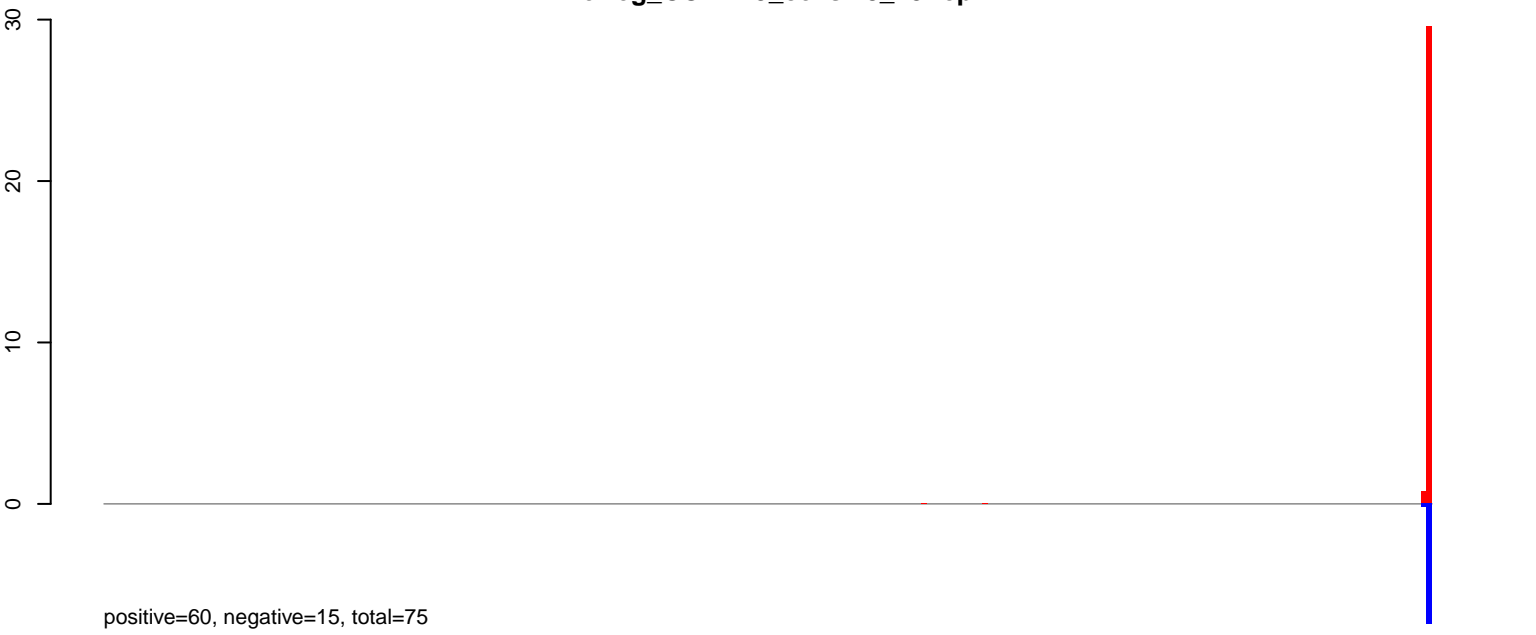
AeAeg_CCL.125_cells.rep



Ward, N. et al. (2019), virus@KJ716848.1-Ngali_virus_strain_Adrar_segment_S_plus_segment_M_plus_segment_L:1-12369

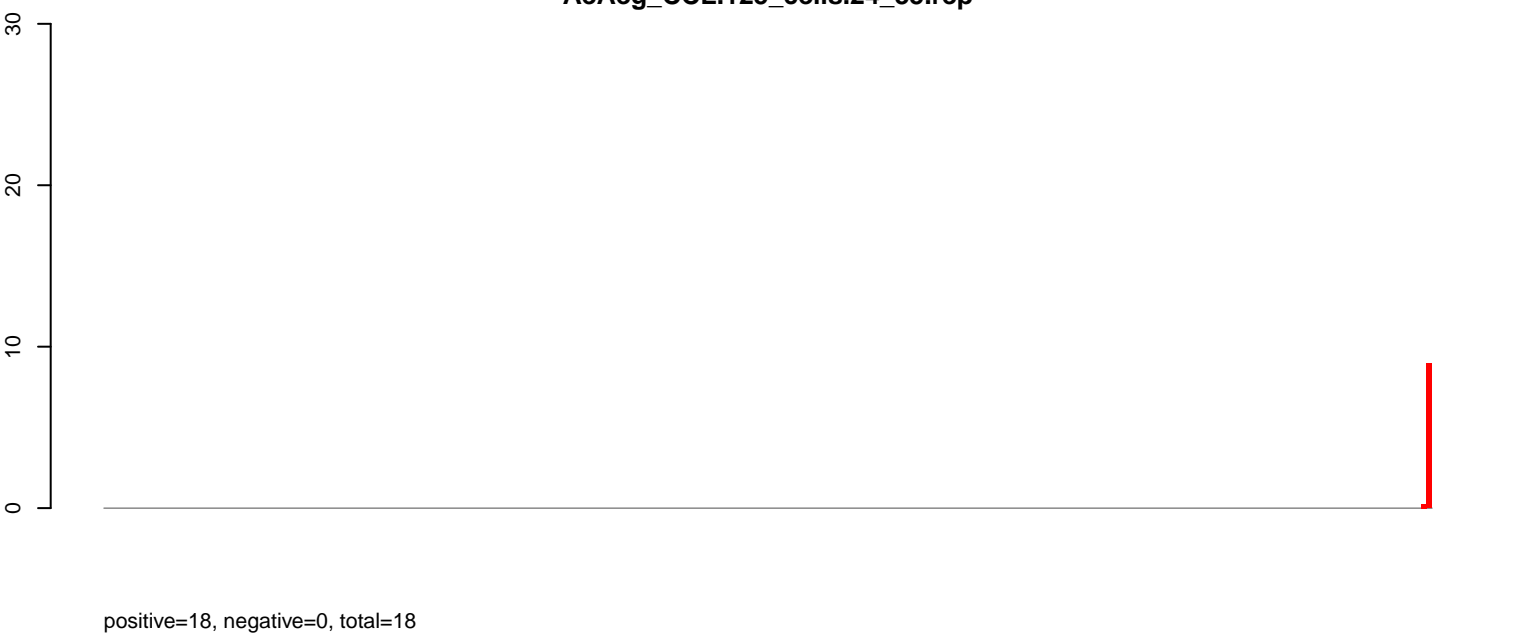
0 2000 4000 6000 8000 10000 12000

AeAeg_CCL.125_cells.18_23.rep



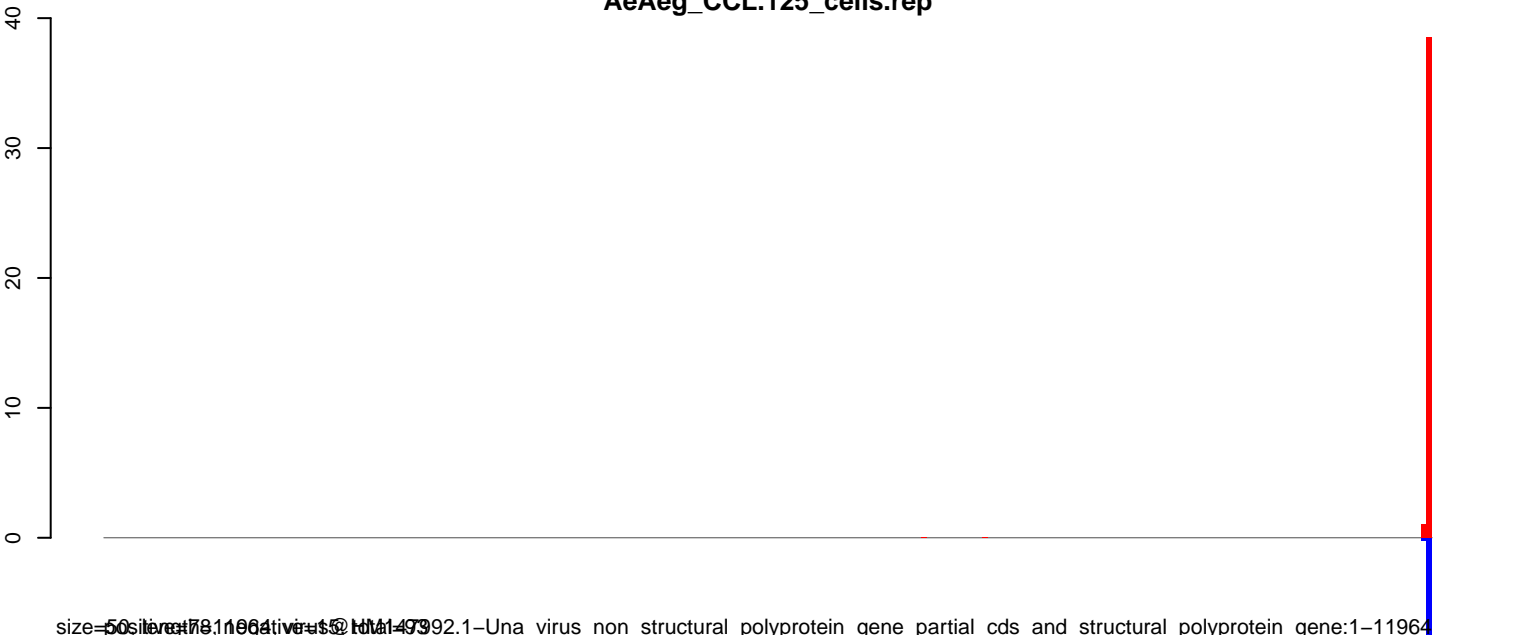
positive=60, negative=15, total=75

AeAeg_CCL.125_cells.24_35.rep



positive=18, negative=0, total=18

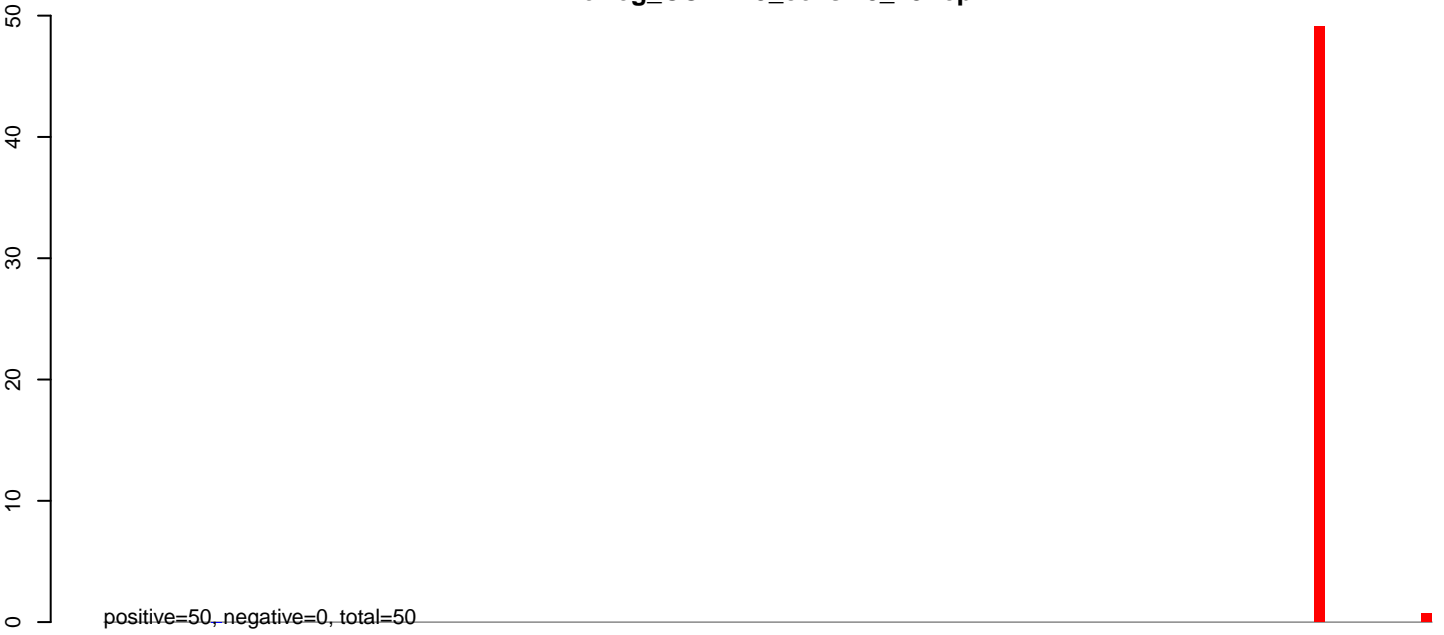
AeAeg_CCL.125_cells.rep



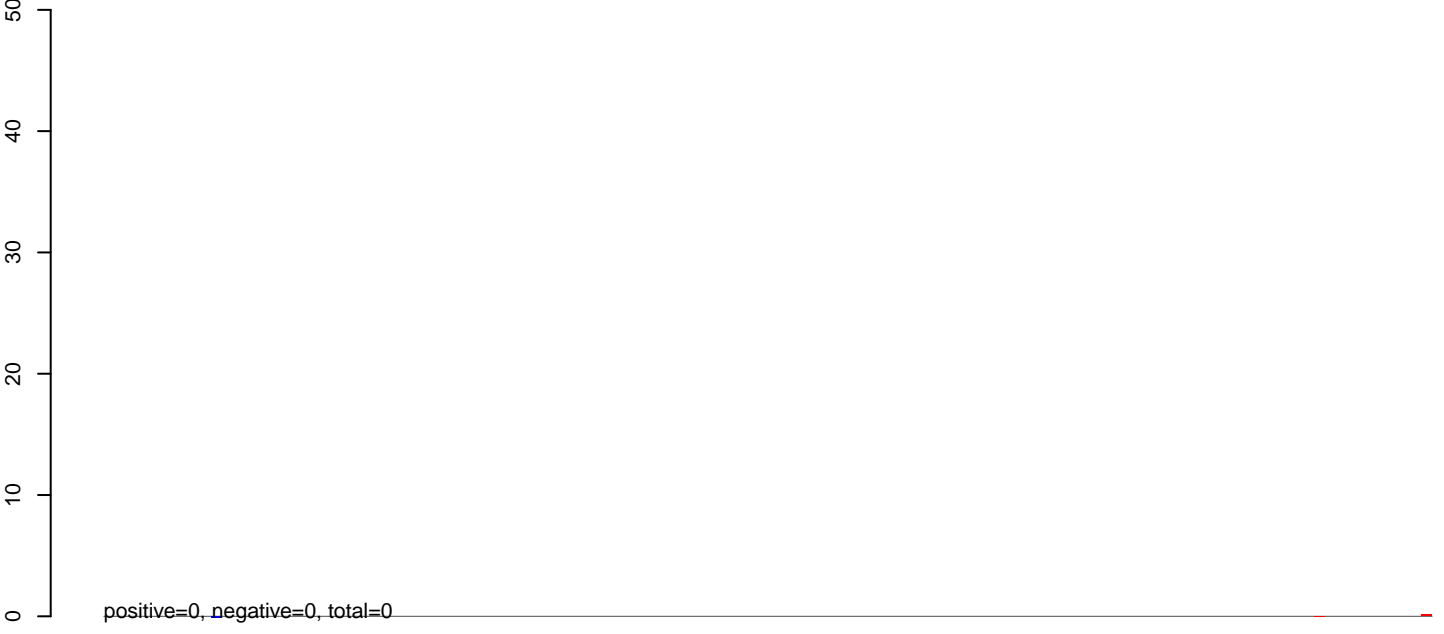
size=50, length=75,11964, positive=50, total=99
11964-Una_virus_non_structural_polyprotein_gene_partial_cds_and_structural_polyprotein_gene:1-11964

0 2000 4000 6000 8000 10000 12000

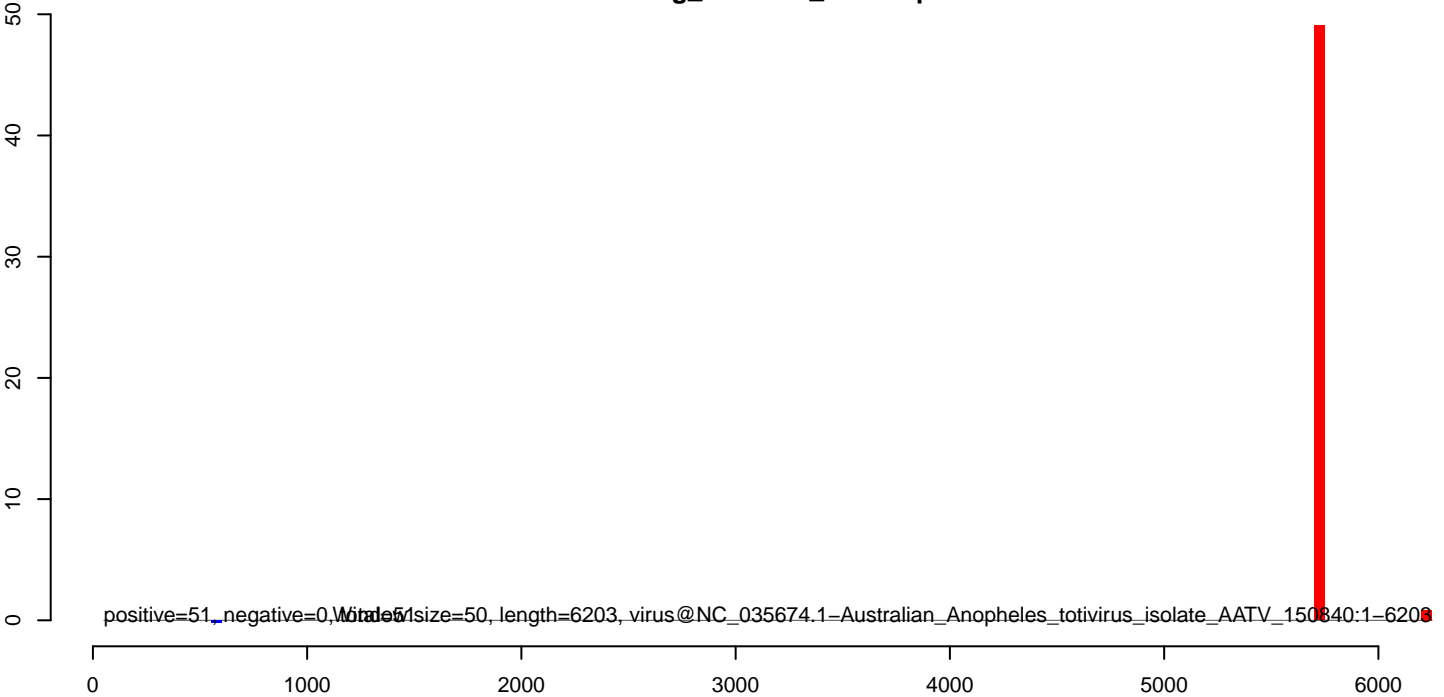
AeAeg_CCL.125_cells.18_23.rep



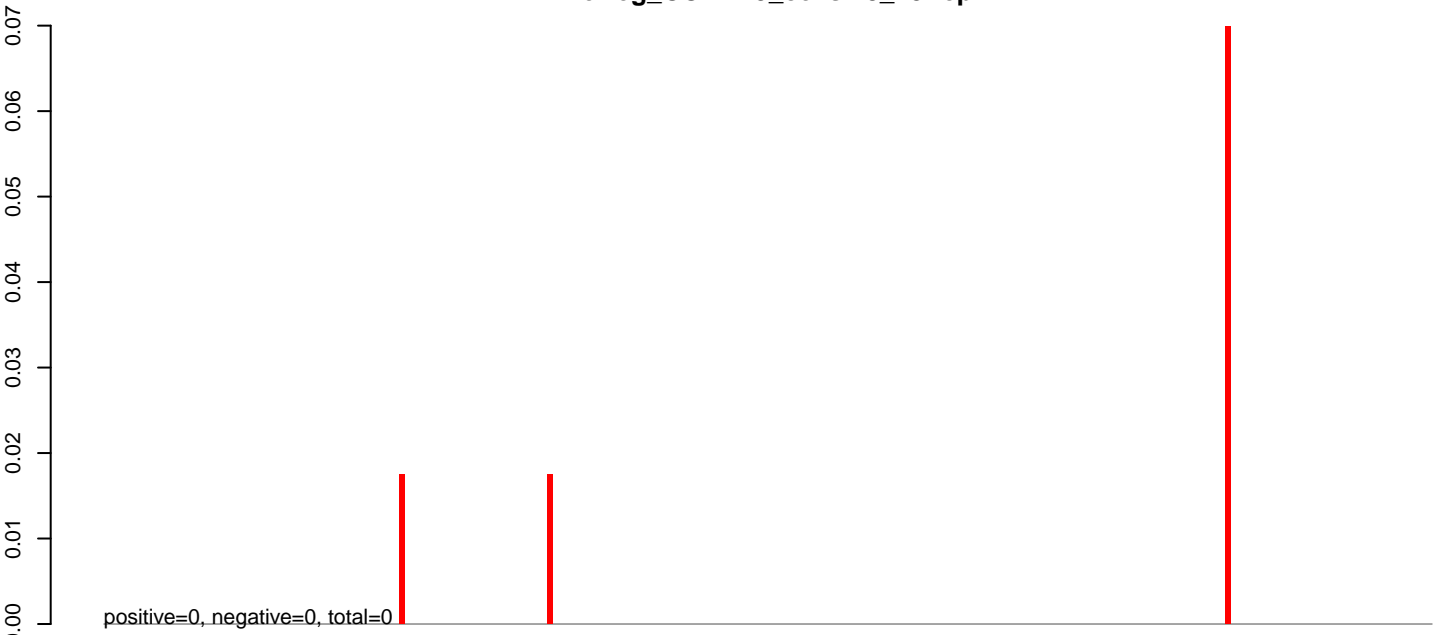
AeAeg_CCL.125_cells.24_35.rep



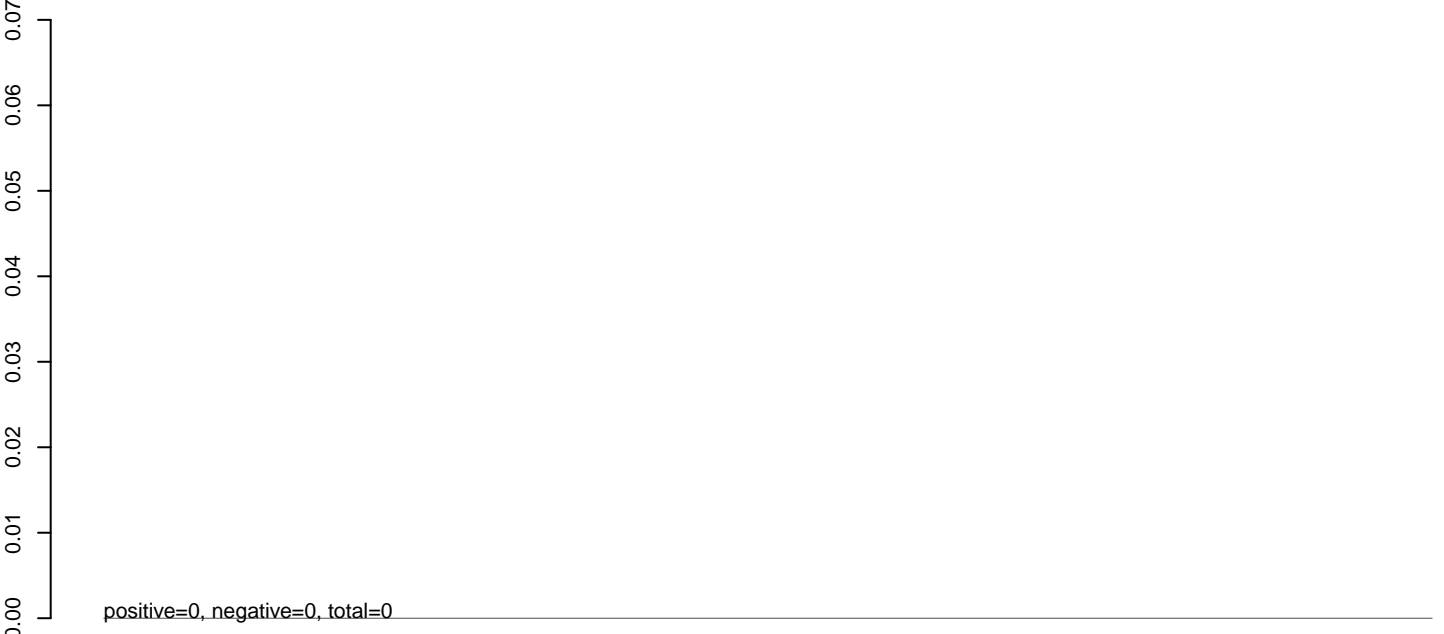
AeAeg_CCL.125_cells.rep



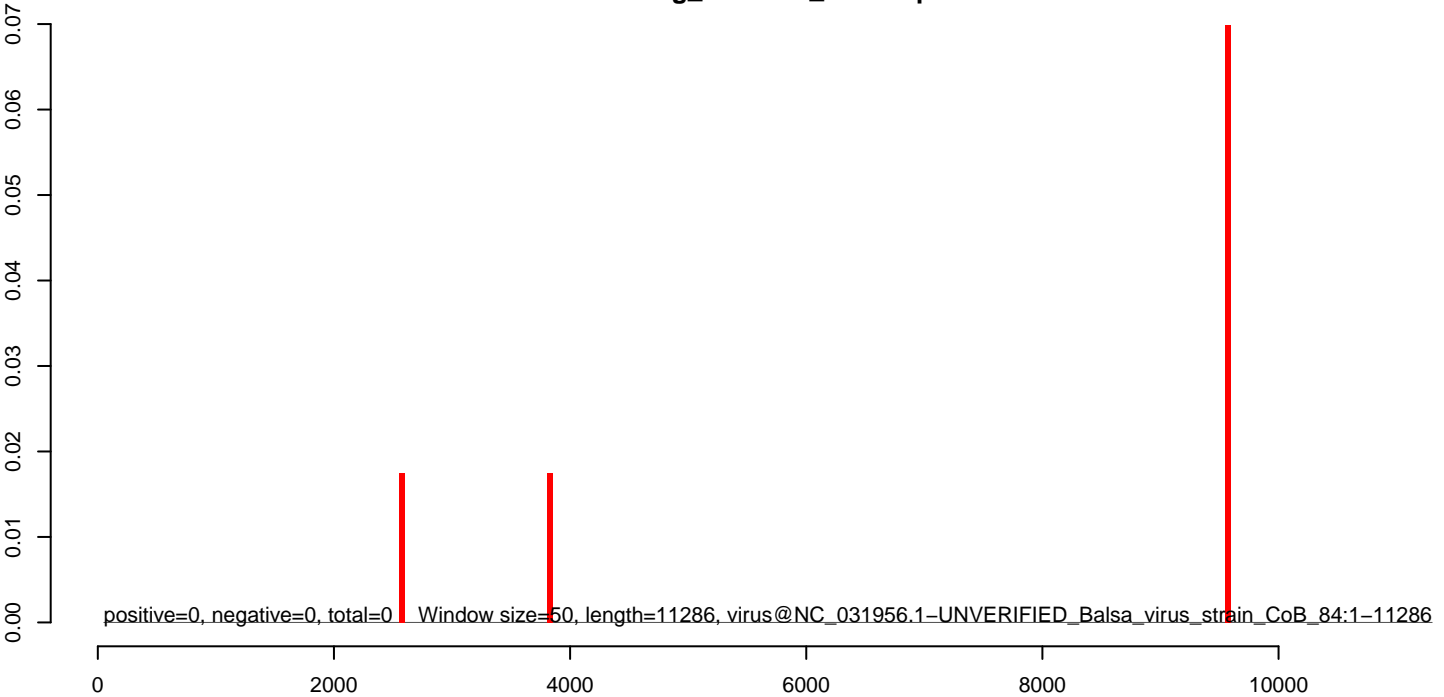
AeAeg_CCL.125_cells.18_23.rep



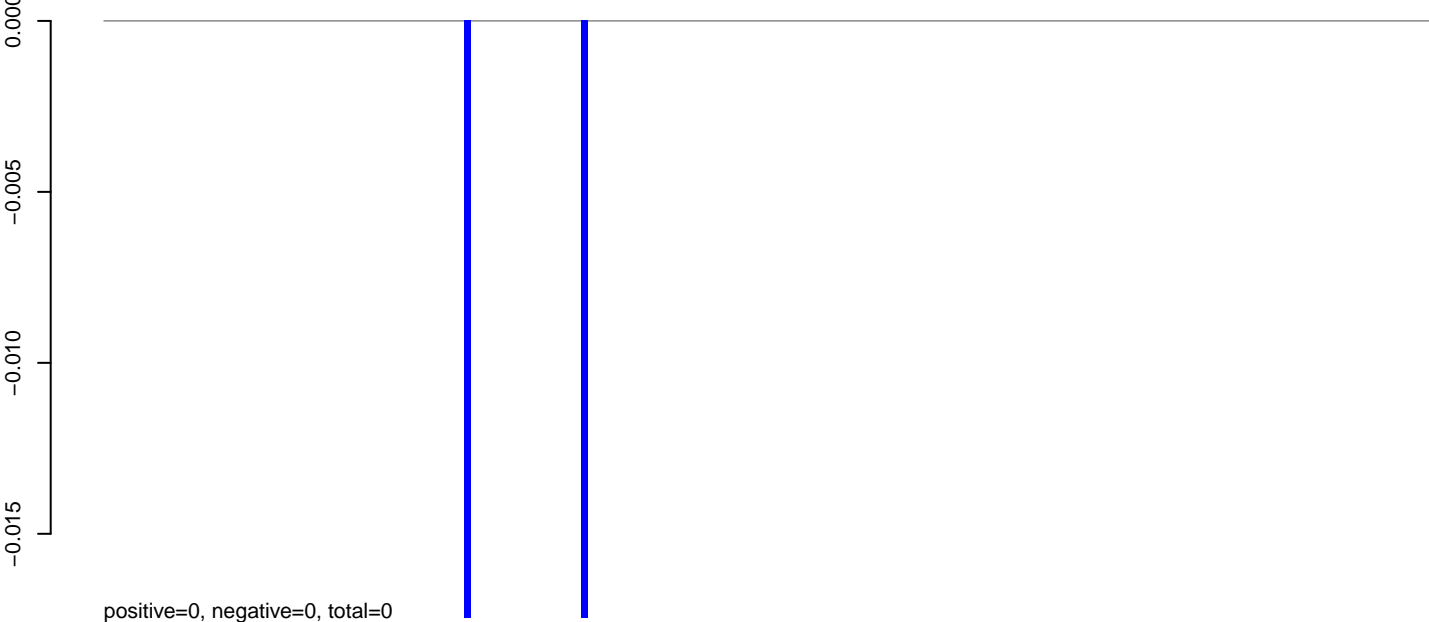
AeAeg_CCL.125_cells.24_35.rep



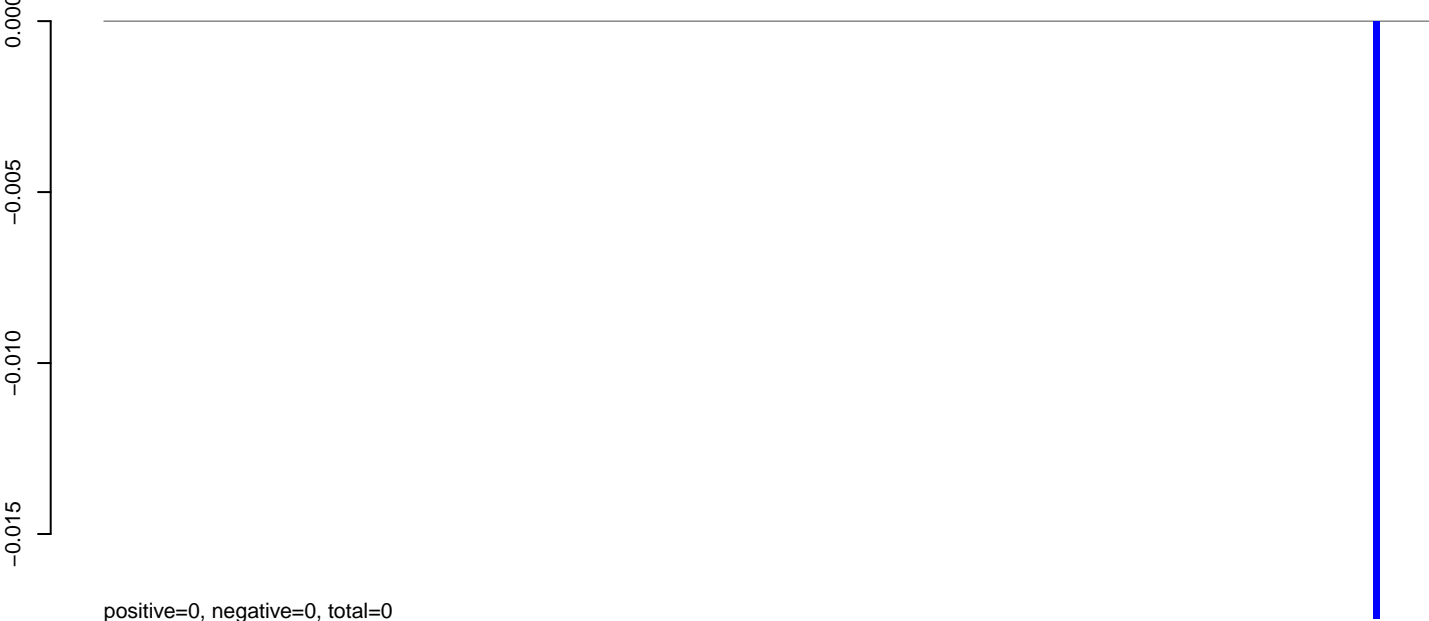
AeAeg_CCL.125_cells.rep



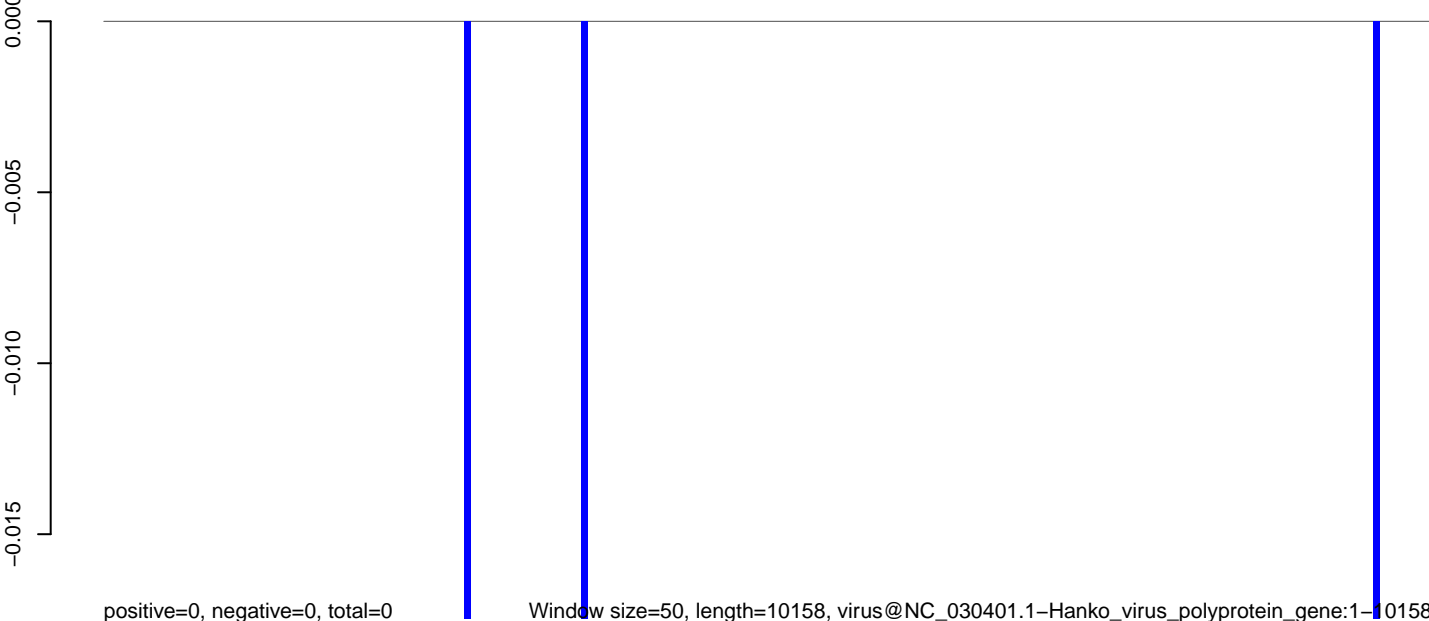
AeAeg_CCL.125_cells.18_23.rep



AeAeg_CCL.125_cells.24_35.rep



AeAeg_CCL.125_cells.rep

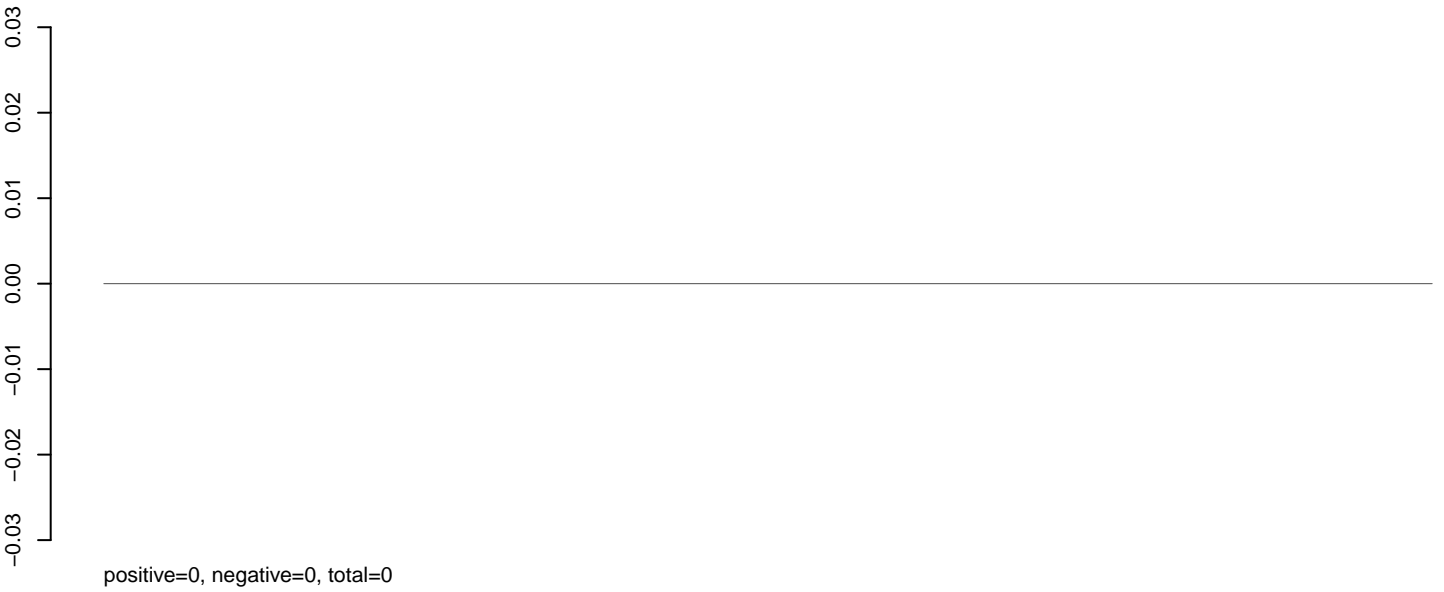


0 2000 4000 6000 8000 10000

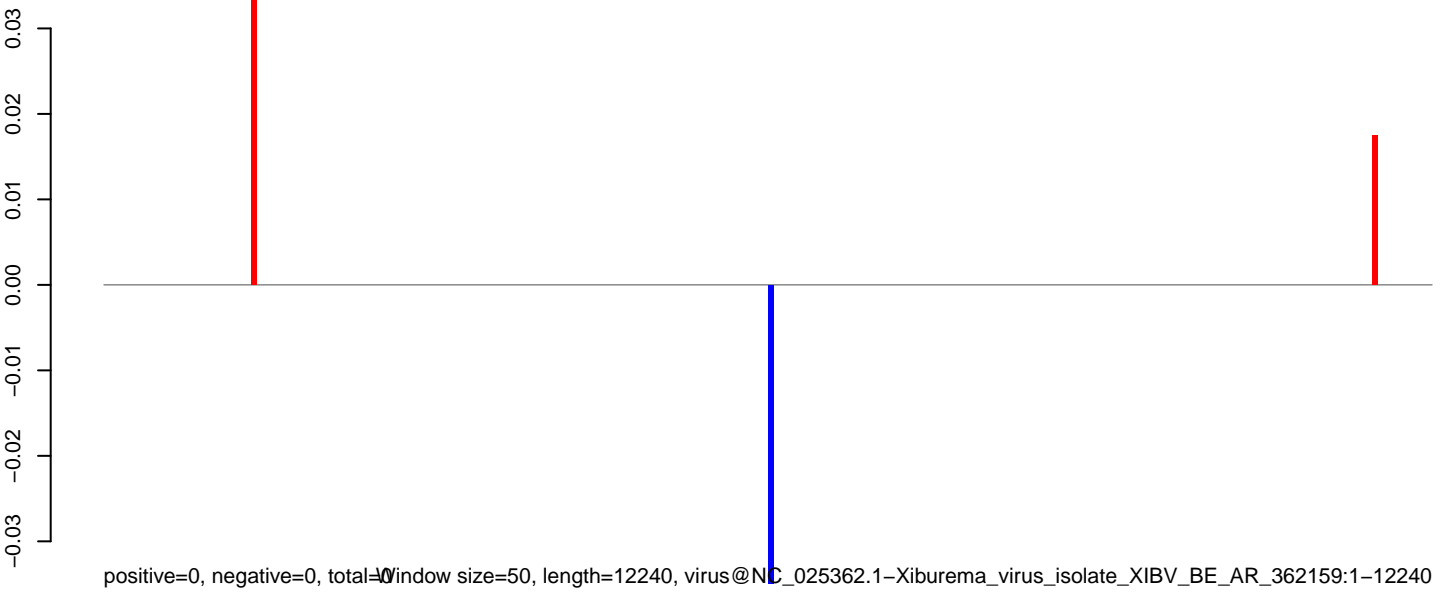
AeAeg_CCL.125_cells.18_23.rep



AeAeg_CCL.125_cells.24_35.rep



AeAeg_CCL.125_cells.rep



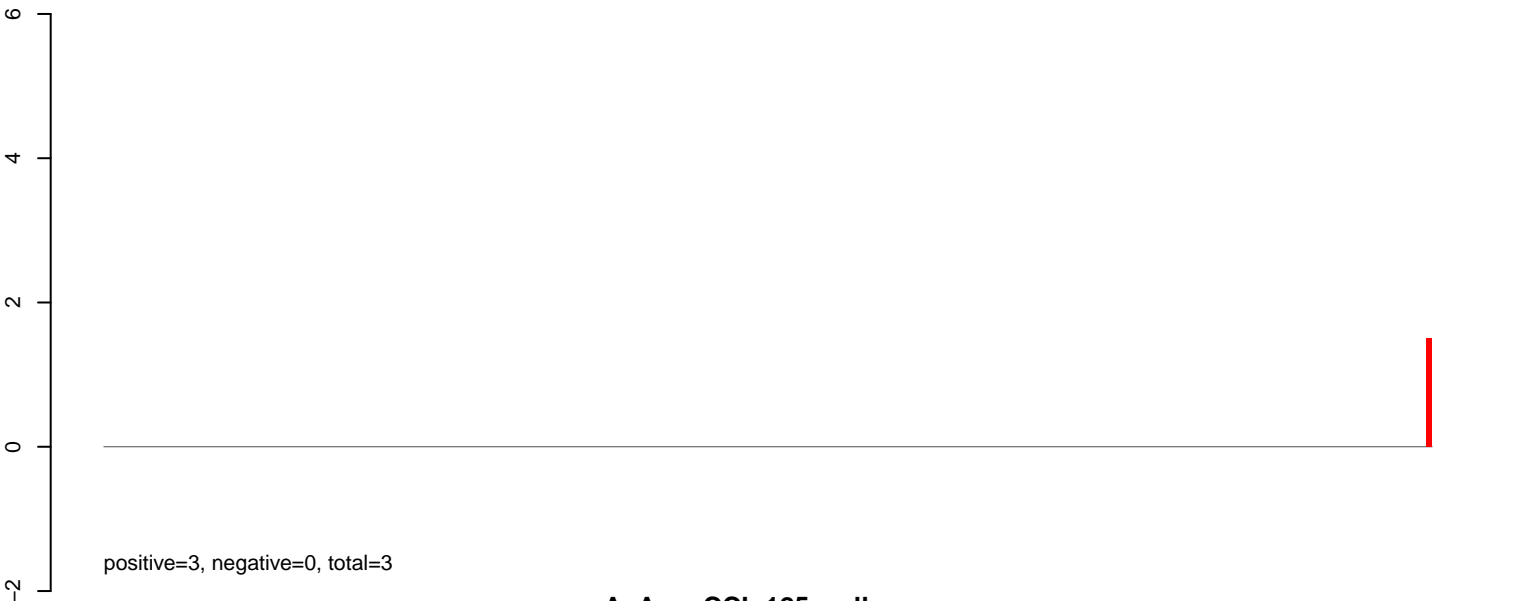
Window size=50, length=12240, virus@NC_025362.1-Xiburema_virus_isolate_XIBV_BE_AR_362159:1-12240

0 2000 4000 6000 8000 10000 12000

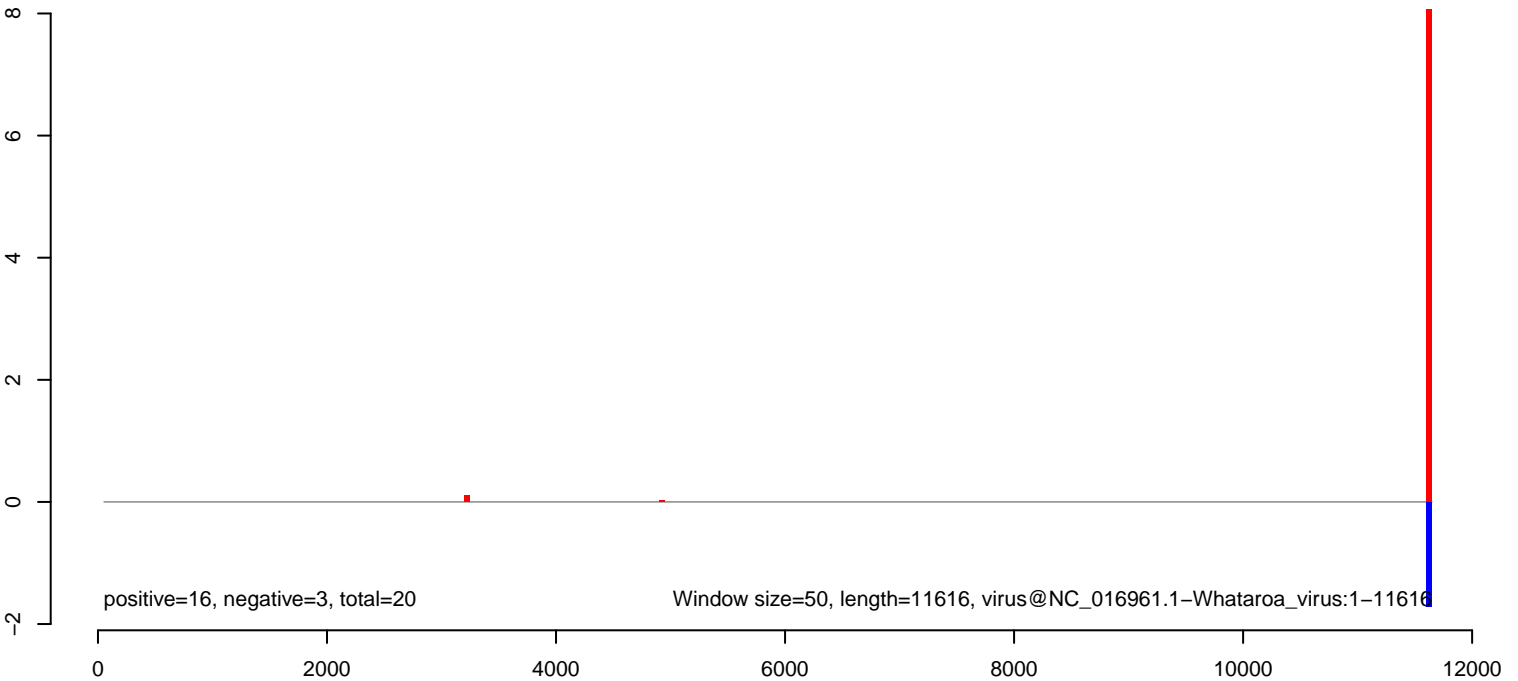
AeAeg_CCL.125_cells.18_23.rep



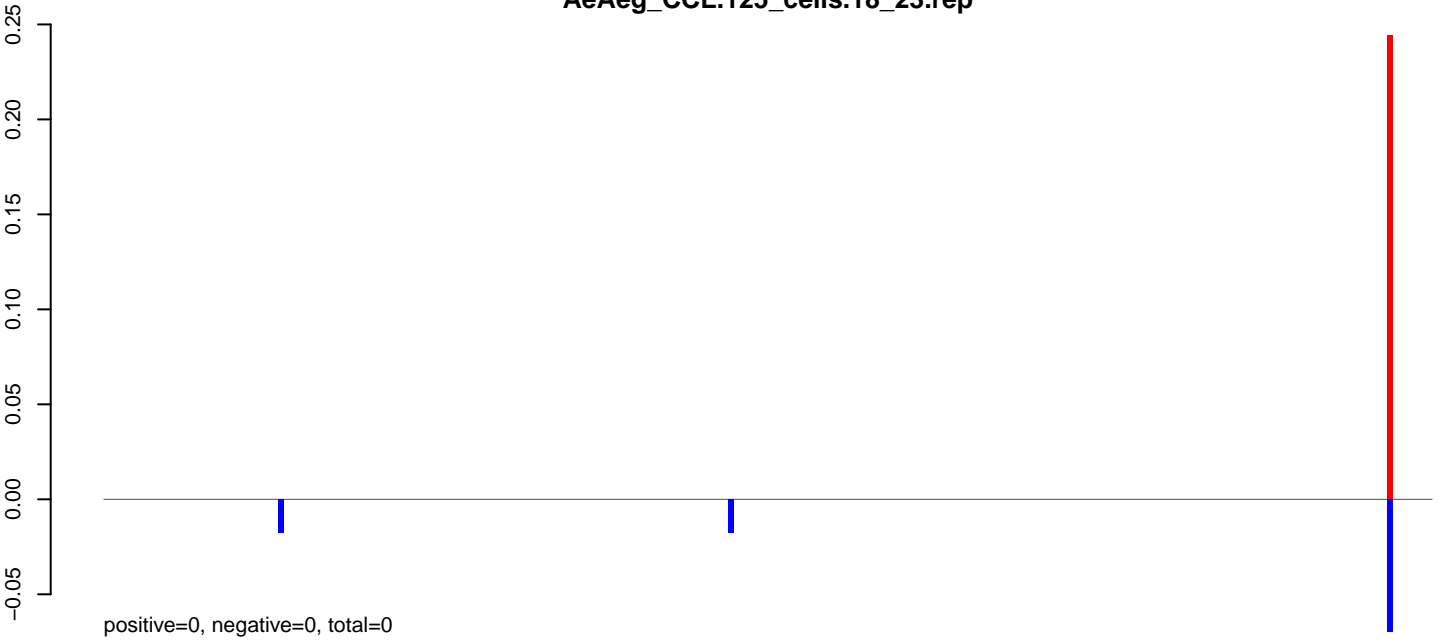
AeAeg_CCL.125_cells.24_35.rep



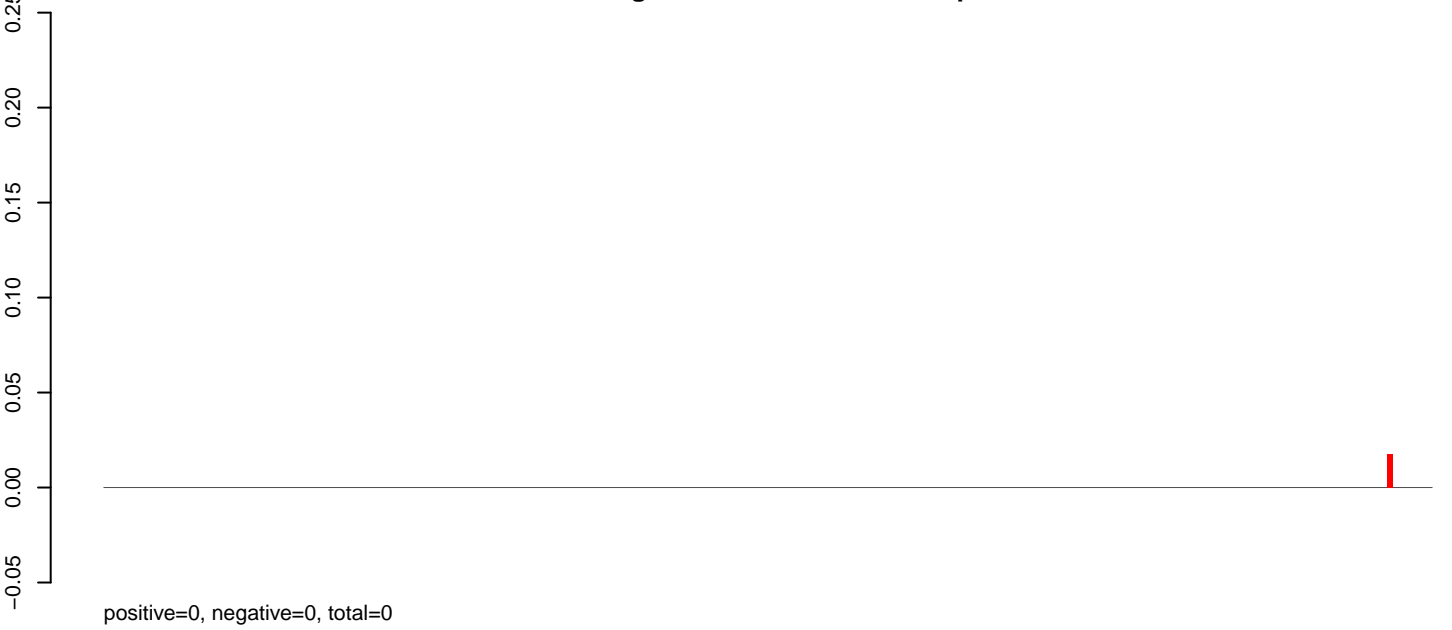
AeAeg_CCL.125_cells.rep



AeAeg_CCL.125_cells.18_23.rep



AeAeg_CCL.125_cells.24_35.rep



AeAeg_CCL.125_cells.rep



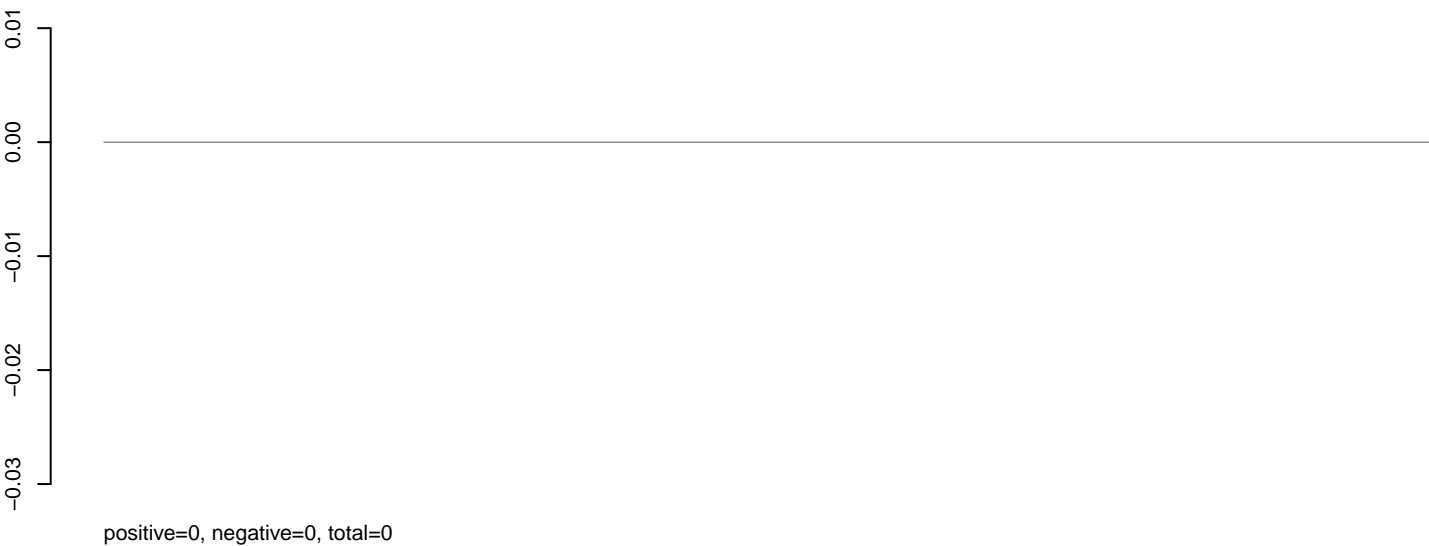
Window size=50, length=11826, virus@NC_004162.2-Chikungunya_virus:1-11826

0 2000 4000 6000 8000 10000 12000

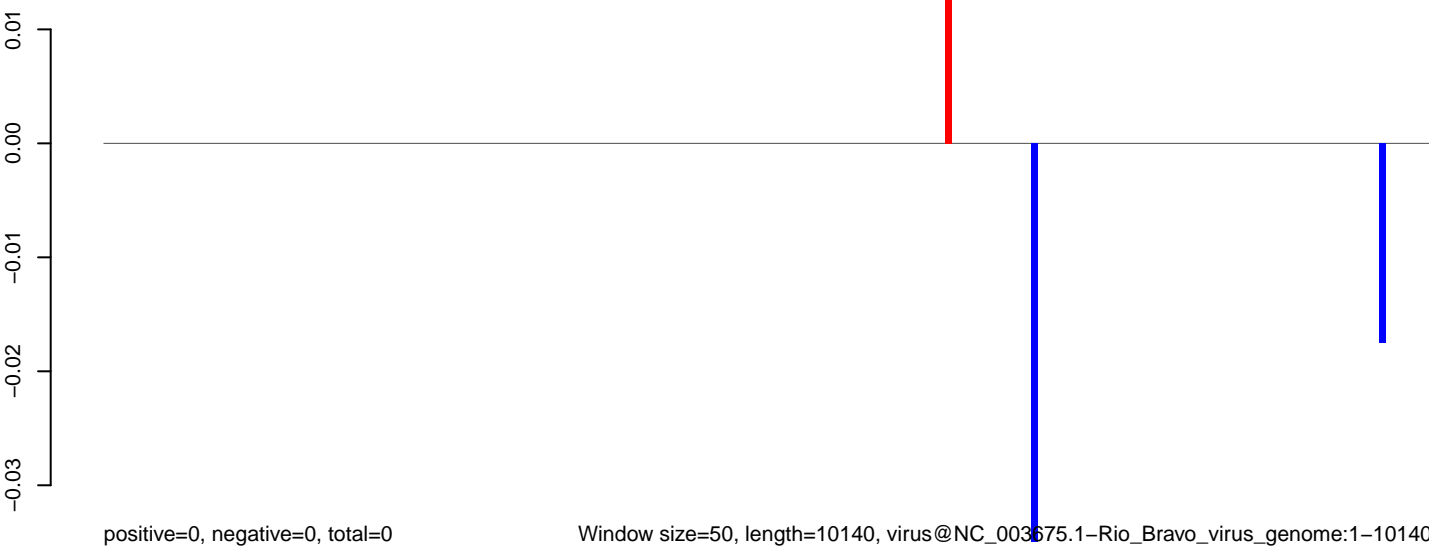
AeAeg_CCL.125_cells.18_23.rep



AeAeg_CCL.125_cells.24_35.rep



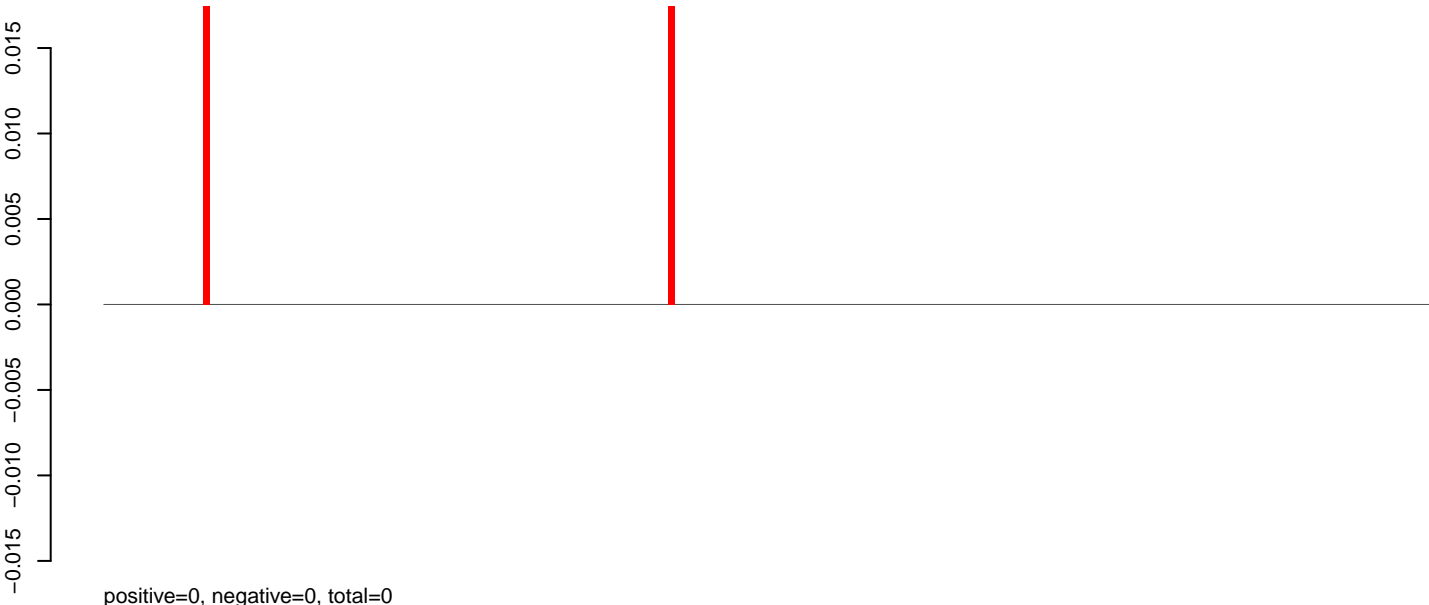
AeAeg_CCL.125_cells.rep



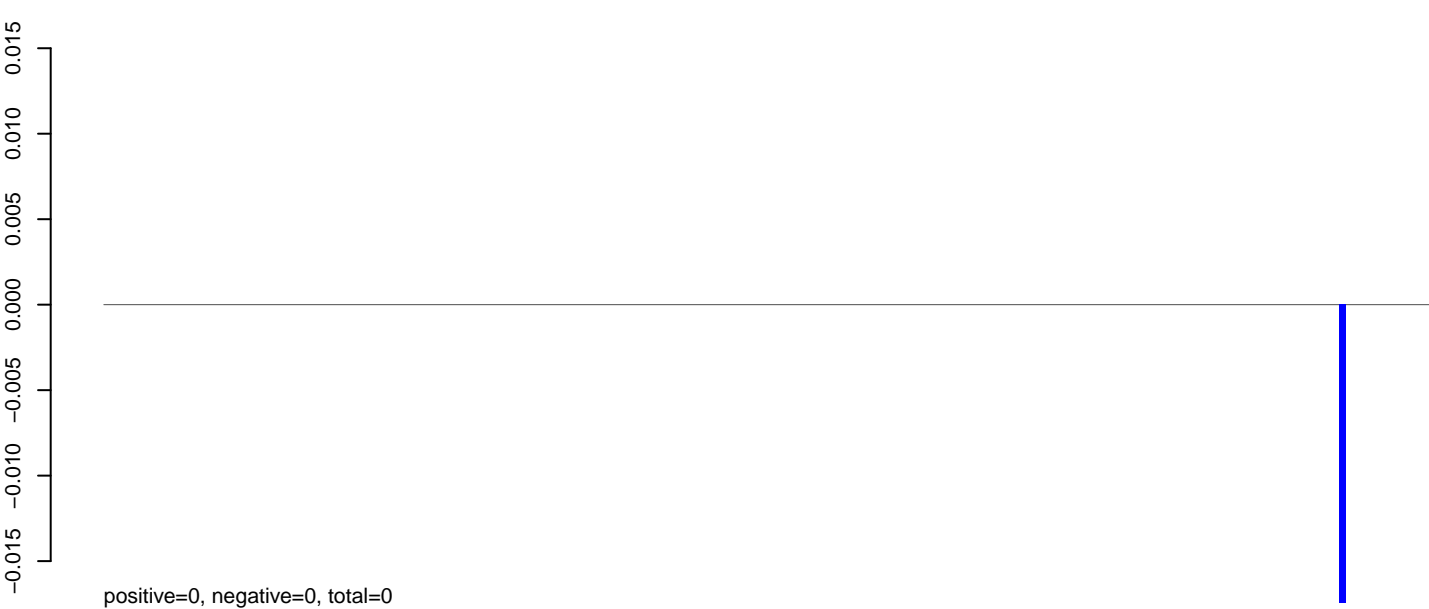
Window size=50, length=10140, virus@NC_003675.1-Rio_Bravo_virus_genome:1-10140

0 2000 4000 6000 8000 10000

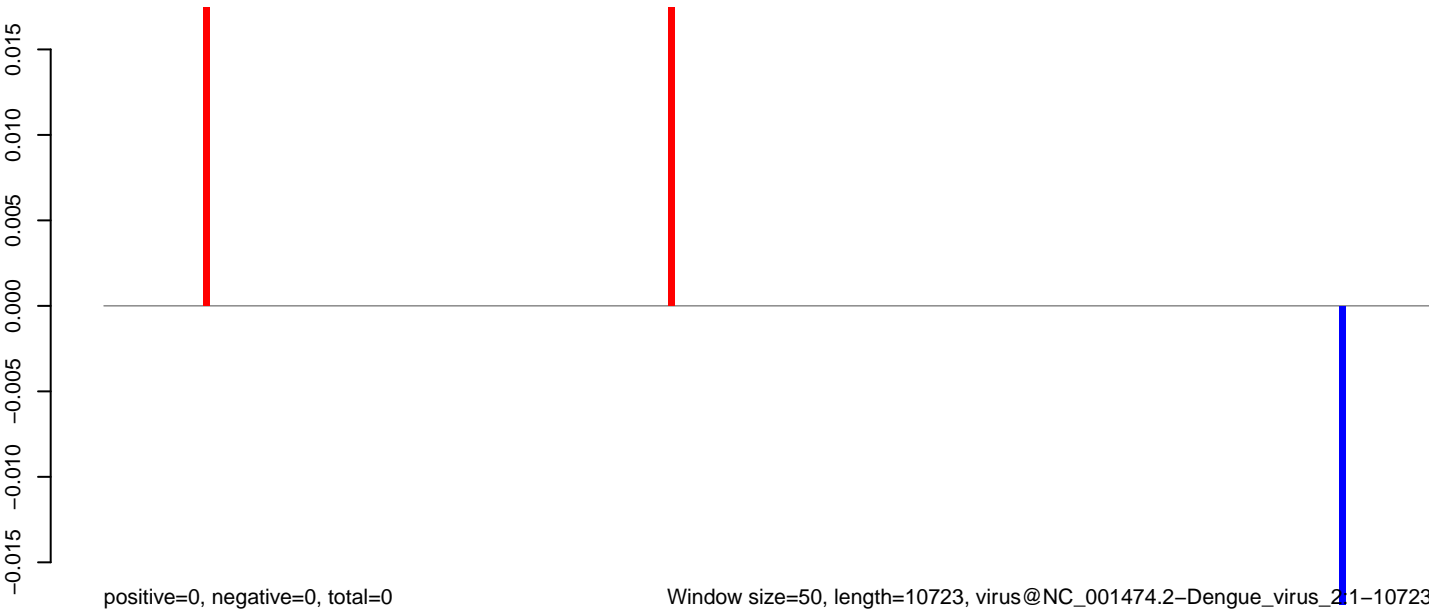
AeAeg_CCL.125_cells.18_23.rep



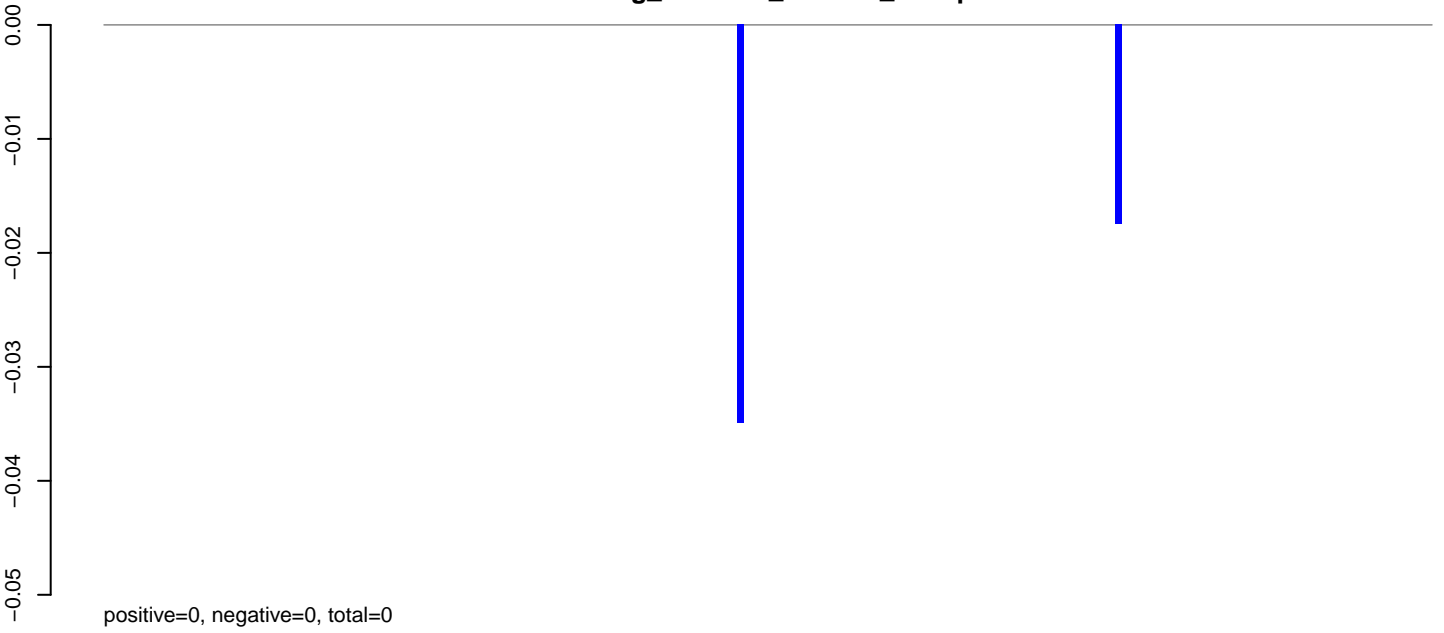
AeAeg_CCL.125_cells.24_35.rep



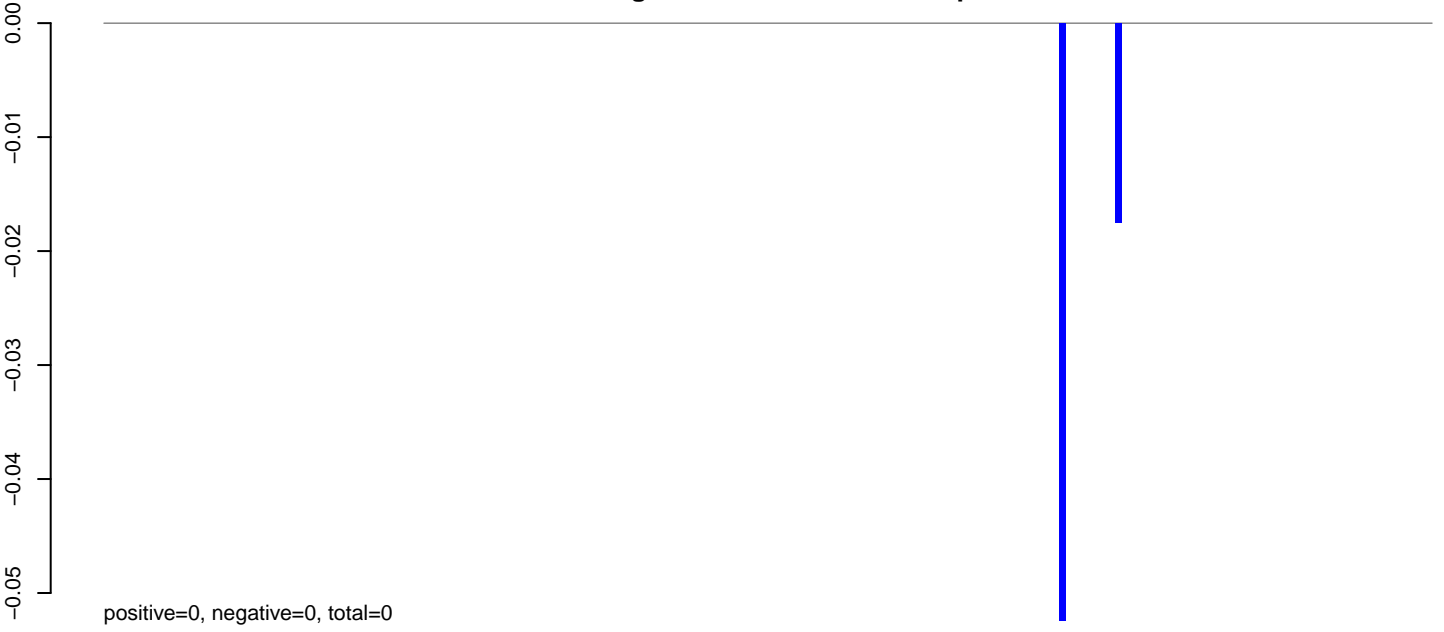
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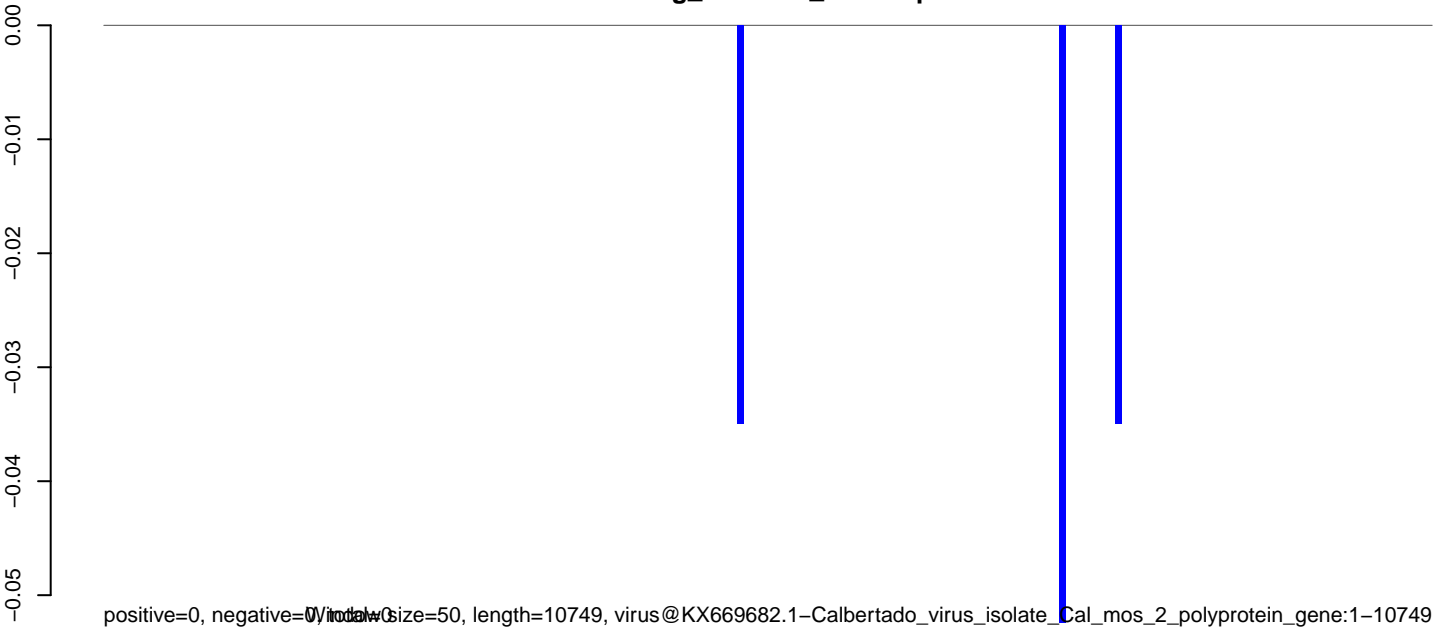
AeAeg_CCL.125_cells.18_23.rep



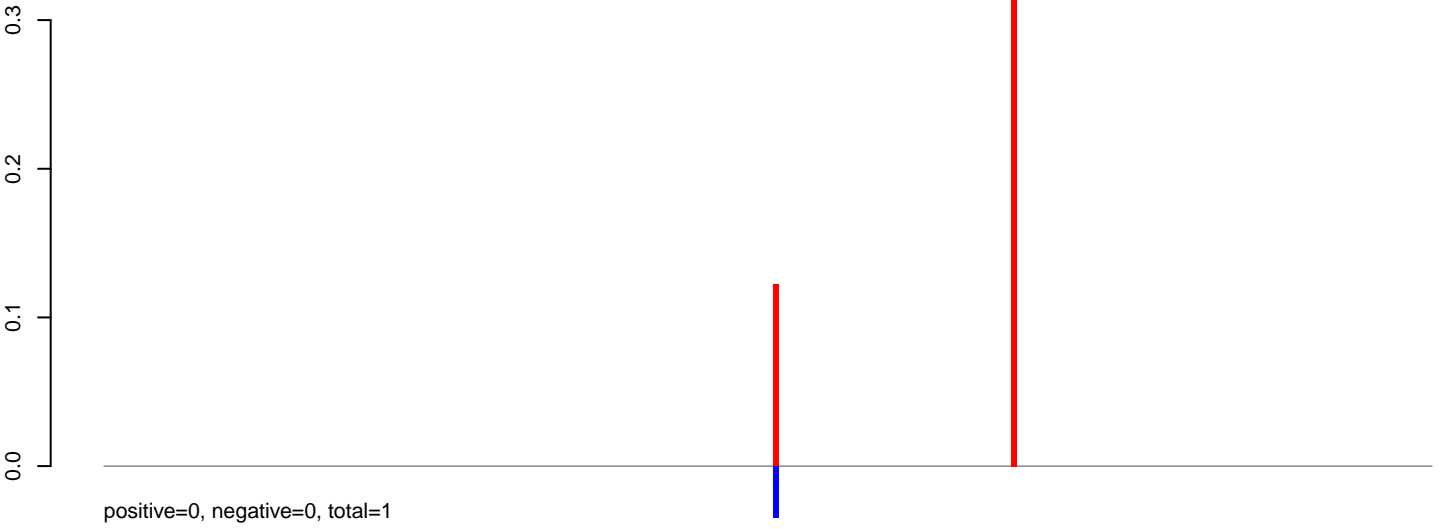
AeAeg_CCL.125_cells.24_35.rep



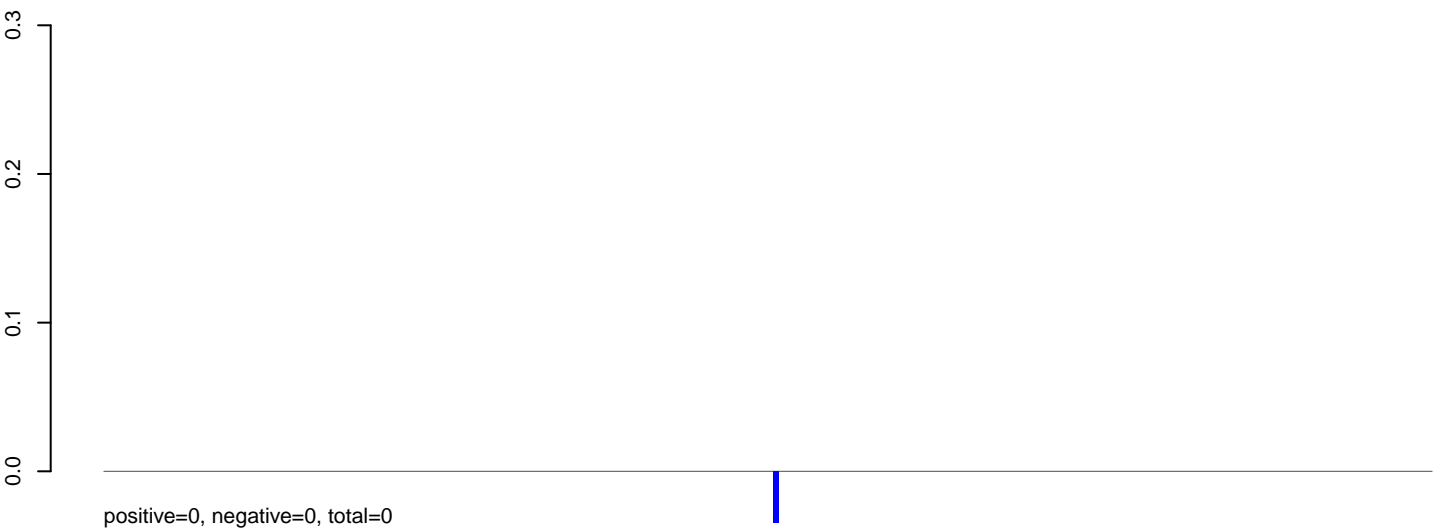
AeAeg_CCL.125_cells.rep



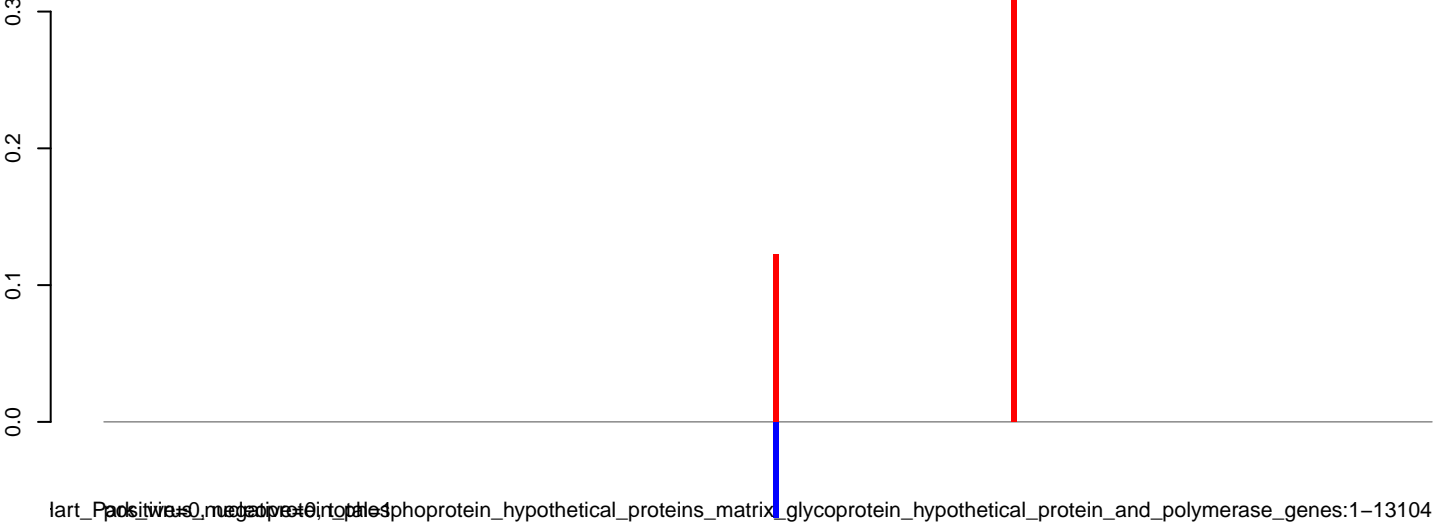
AeAeg_CCL.125_cells.18_23.rep



AeAeg_CCL.125_cells.24_35.rep

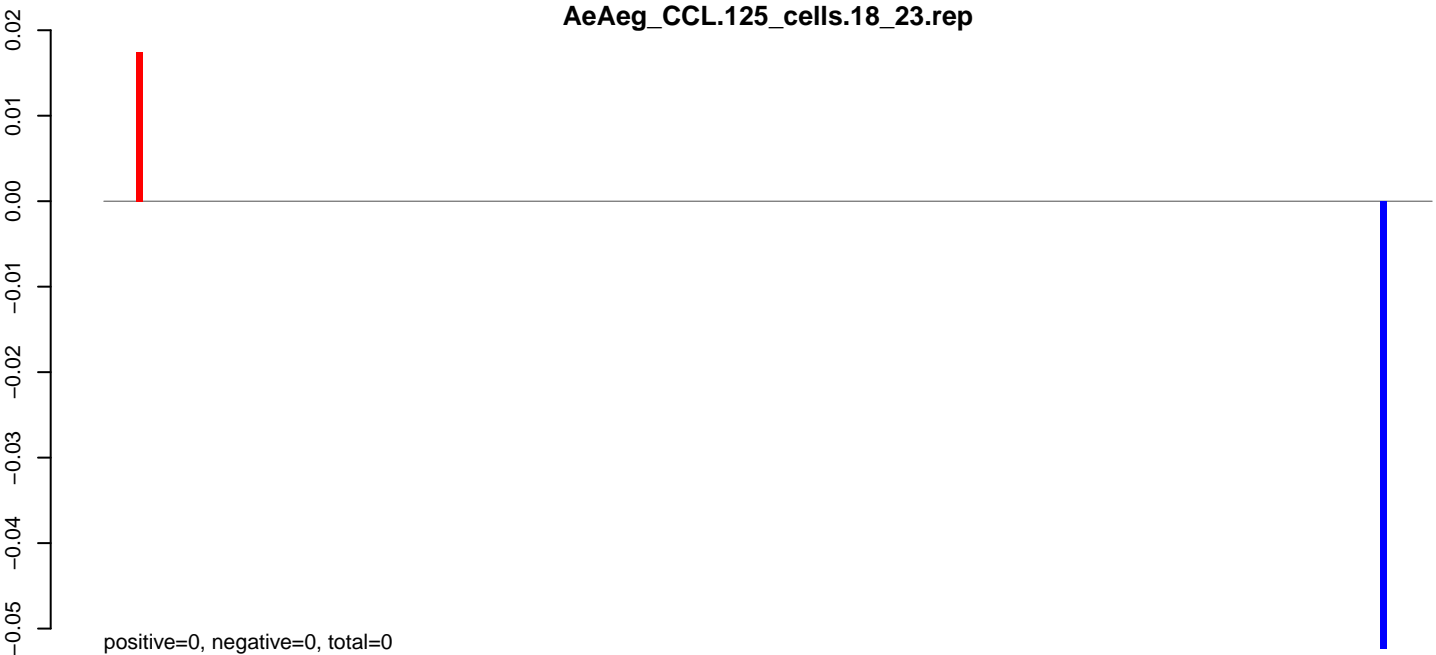


AeAeg_CCL.125_cells.rep

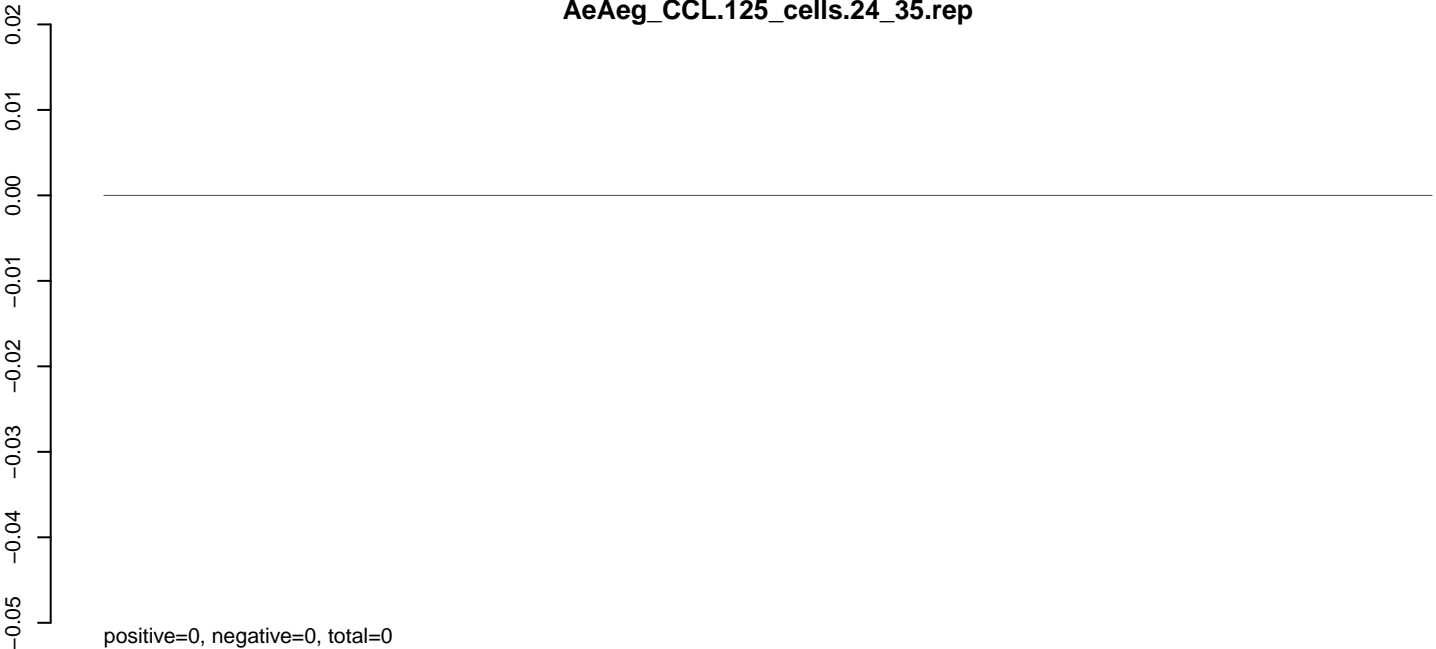


0 2000 4000 6000 8000 10000 12000

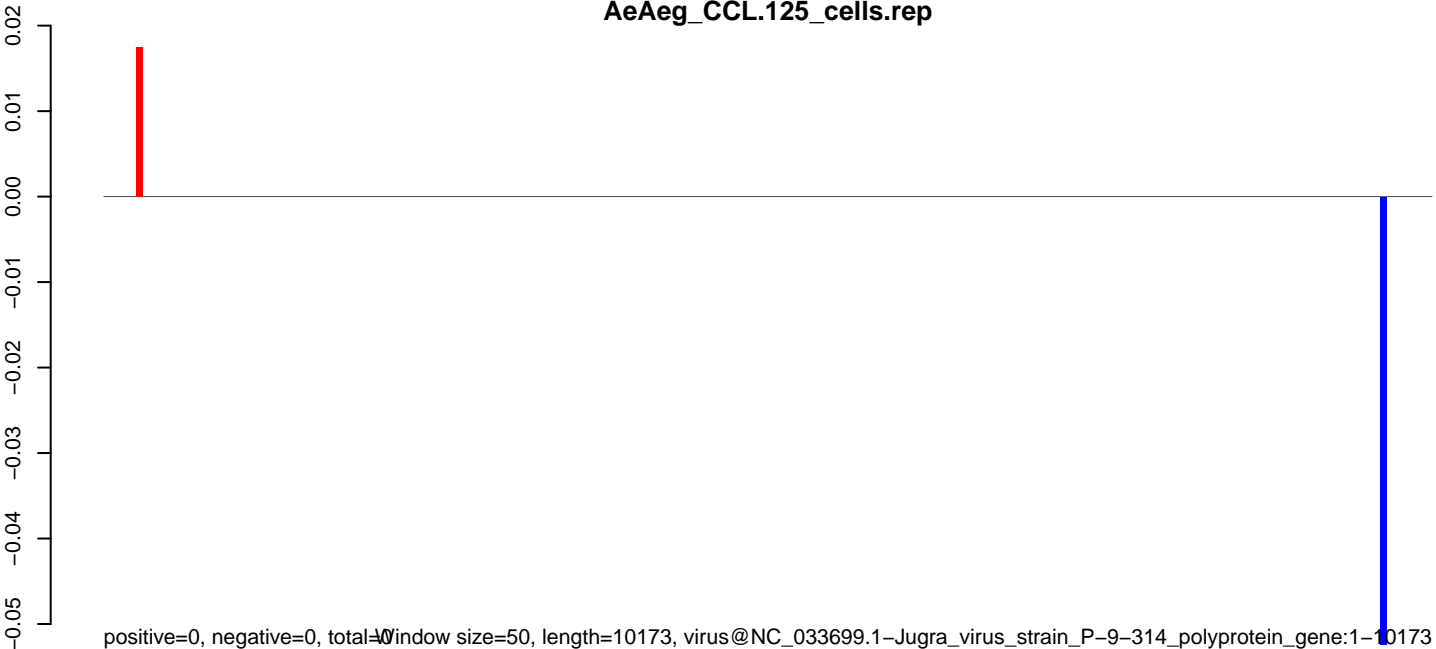
AeAeg_CCL.125_cells.18_23.rep



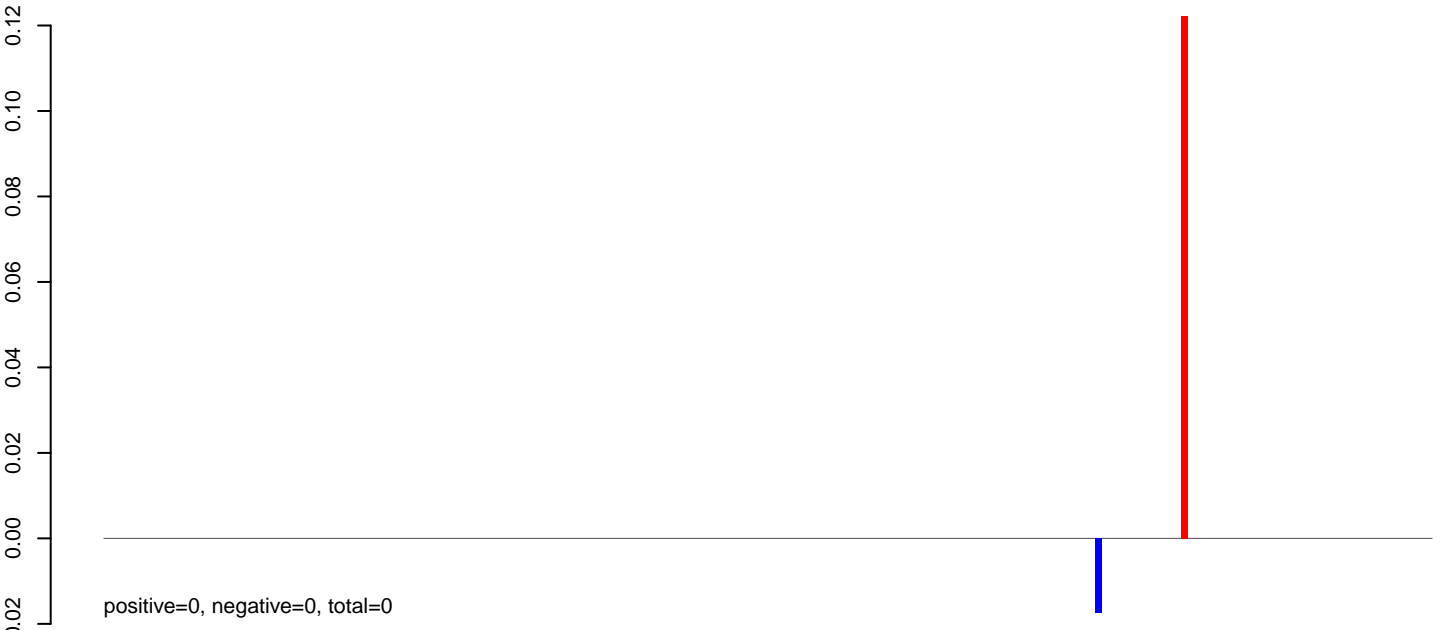
AeAeg_CCL.125_cells.24_35.rep



AeAeg_CCL.125_cells.rep



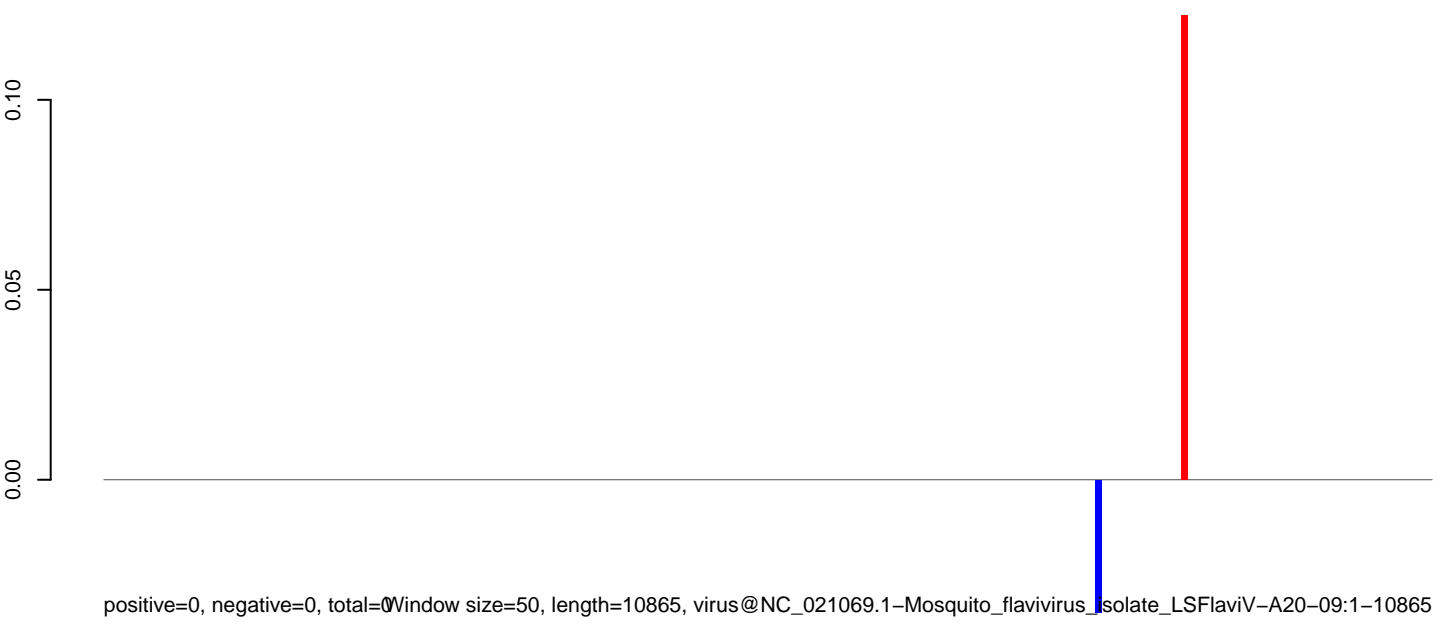
AeAeg_CCL.125_cells.18_23.rep



AeAeg_CCL.125_cells.24_35.rep



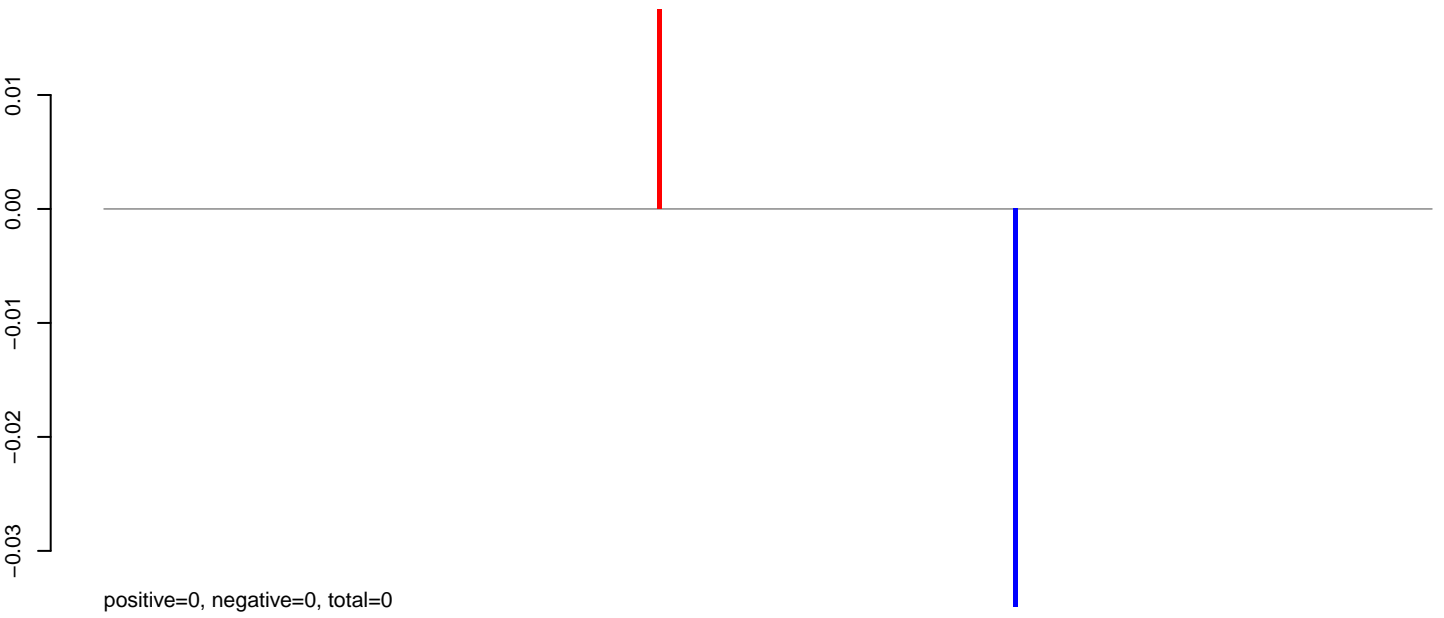
AeAeg_CCL.125_cells.rep



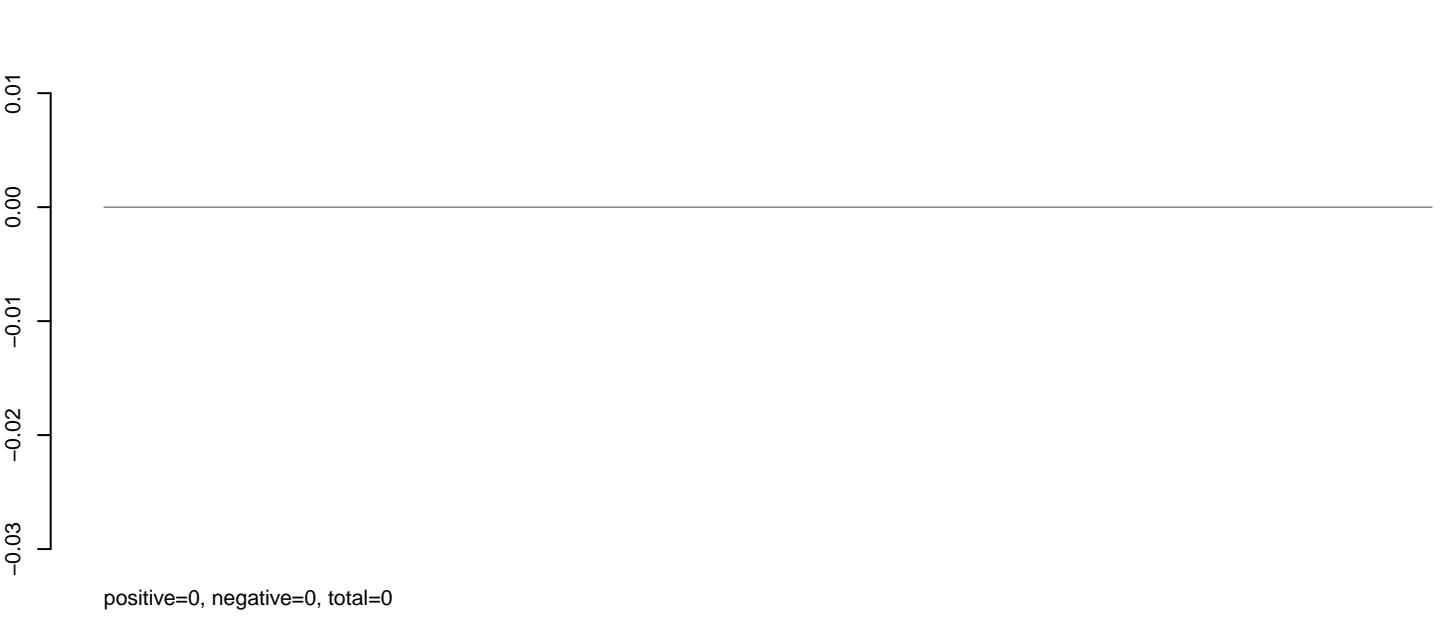
Window size=50, length=10865, virus@NC_021069.1-Mosquito_flavivirus_isolate_LSFlaviV-A20-09:1-10865

0 2000 4000 6000 8000 10000

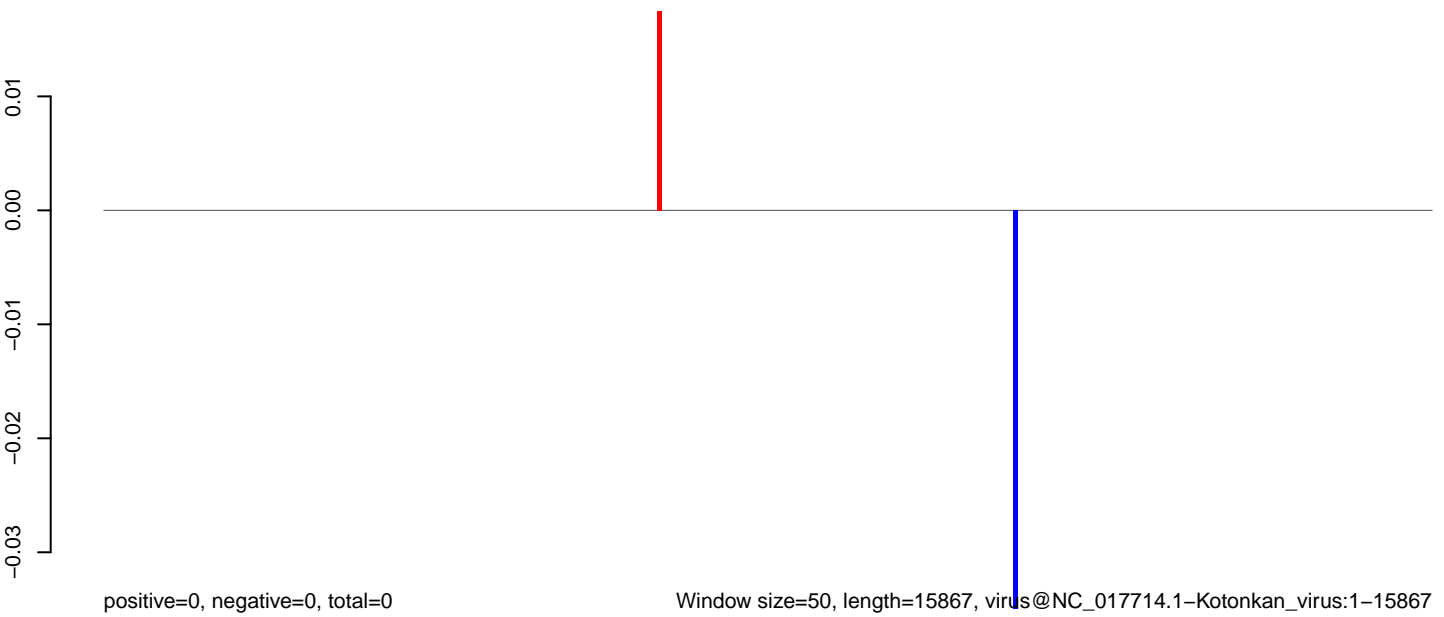
AeAeg_CCL.125_cells.18_23.rep



AeAeg_CCL.125_cells.24_35.rep



AeAeg_CCL.125_cells.rep



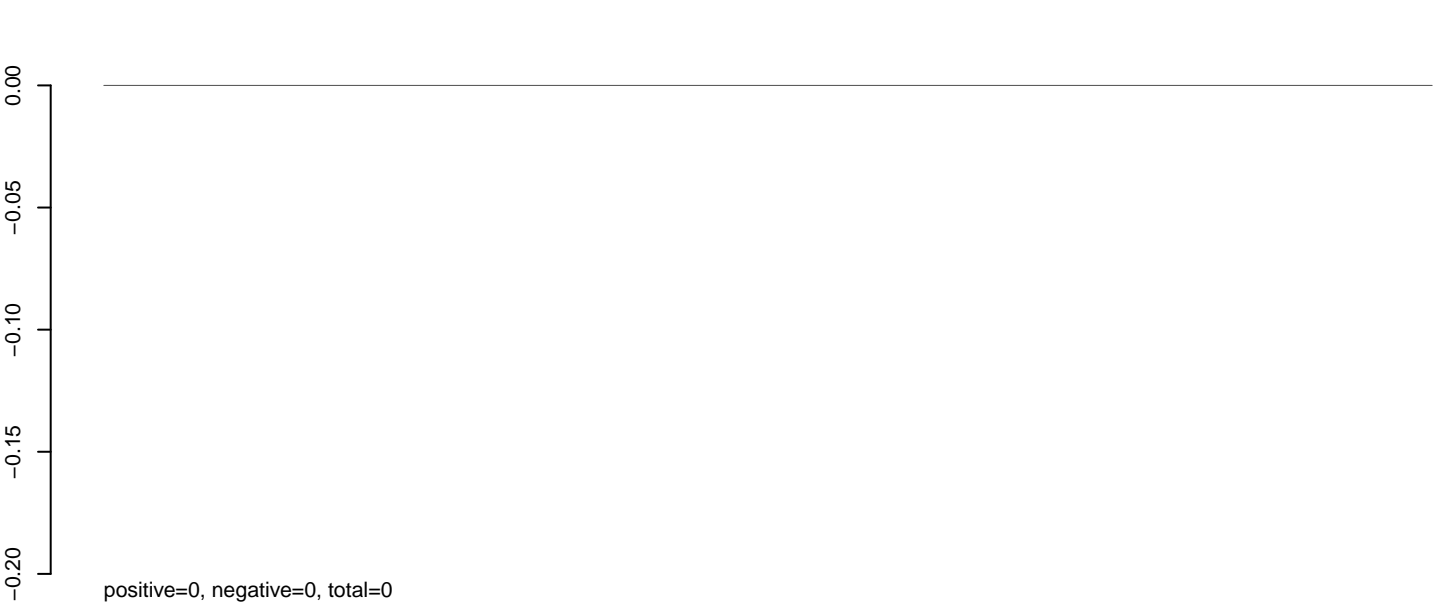
Window size=50, length=15867, virus@NC_017714.1-Kotonkan_virus:1-15867

0 5000 10000 15000

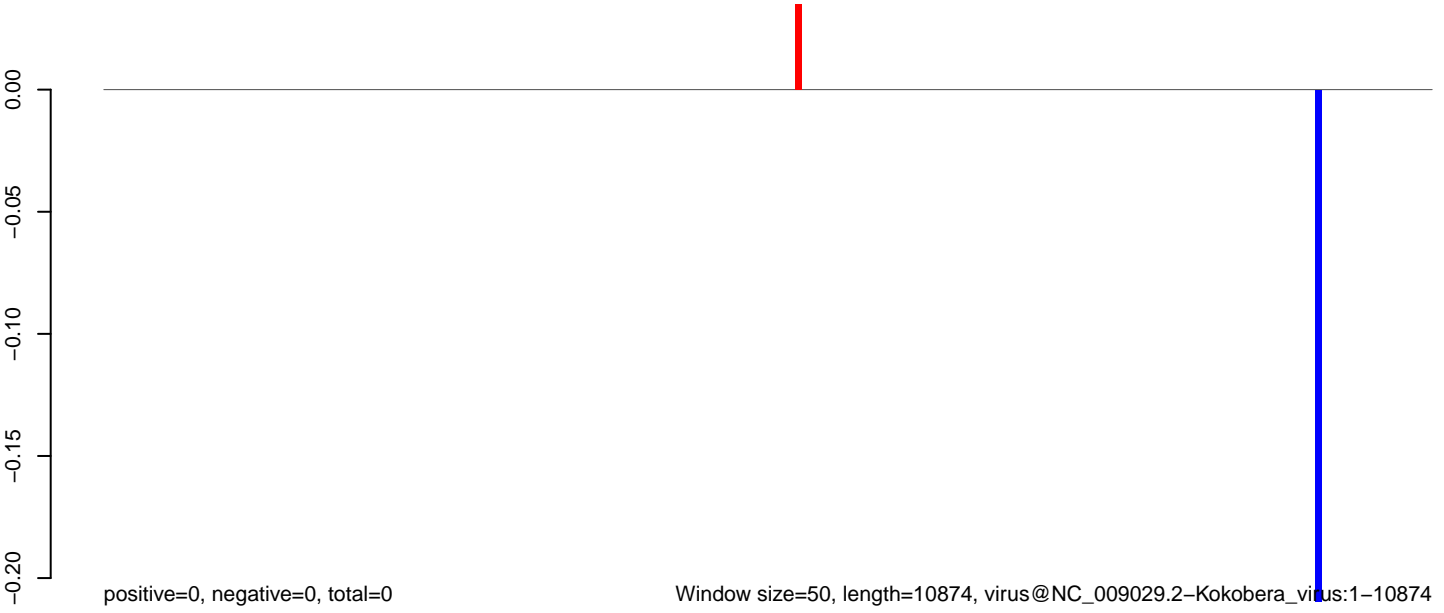
AeAeg_CCL.125_cells.18_23.rep



AeAeg_CCL.125_cells.24_35.rep

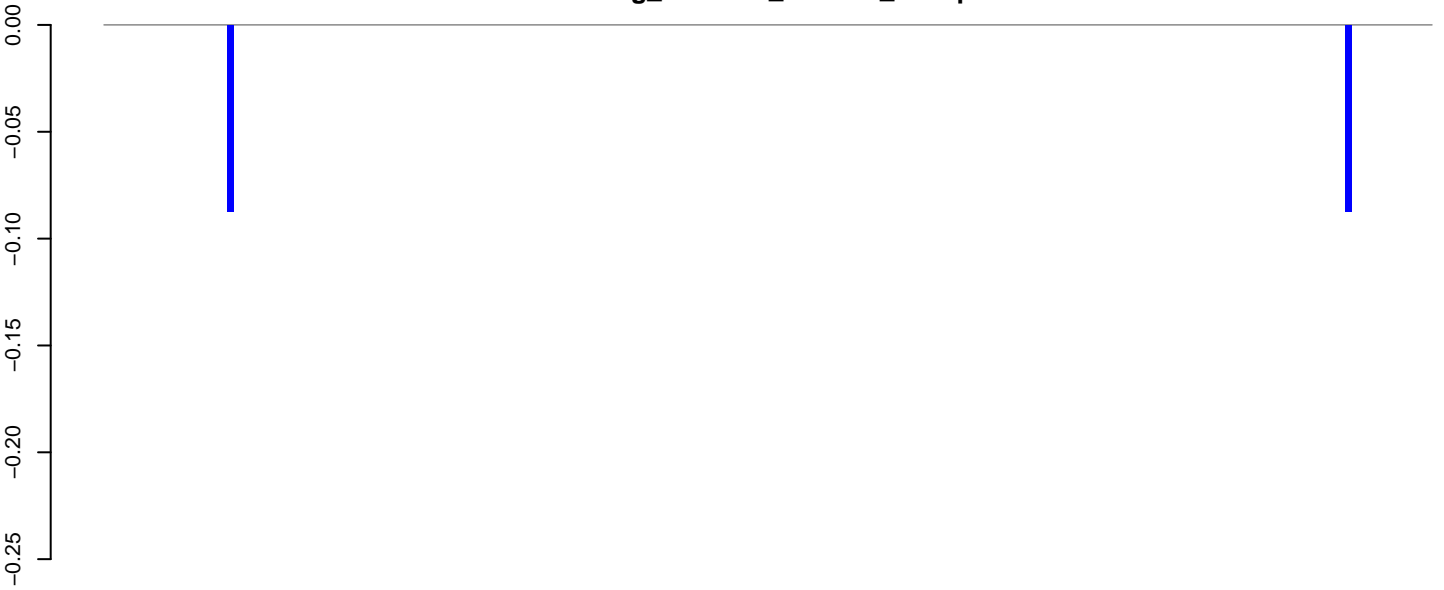


AeAeg_CCL.125_cells.rep

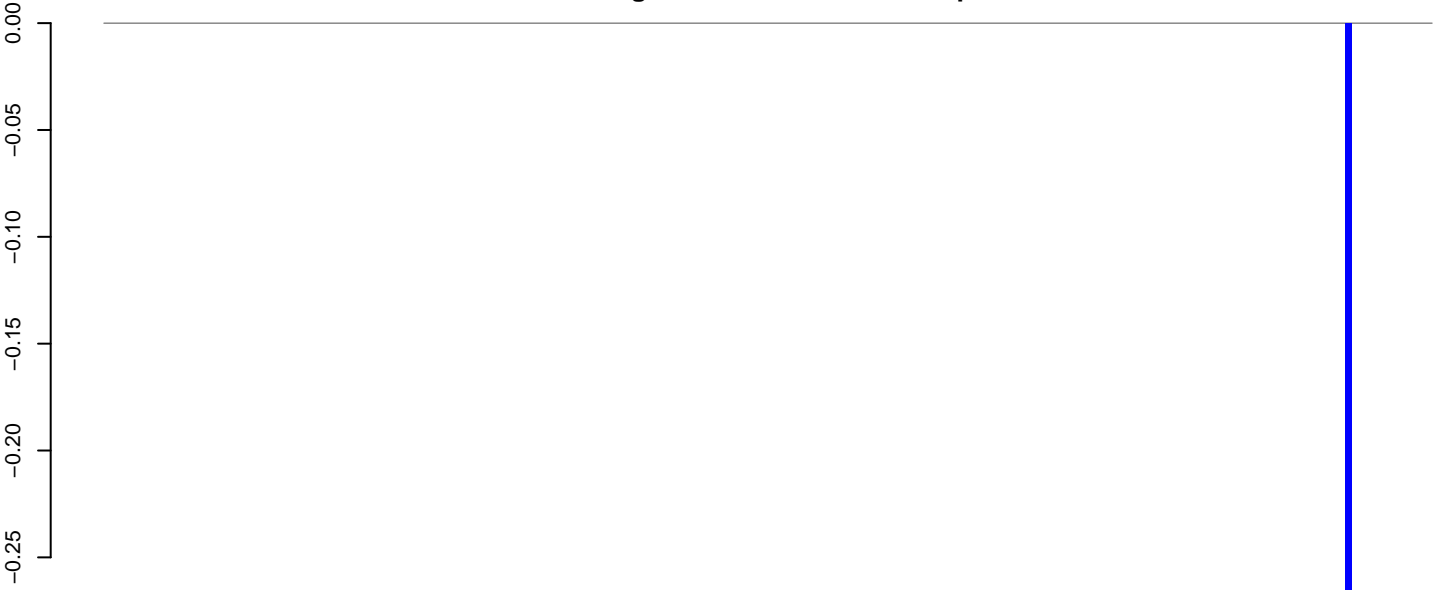


0 2000 4000 6000 8000 10000

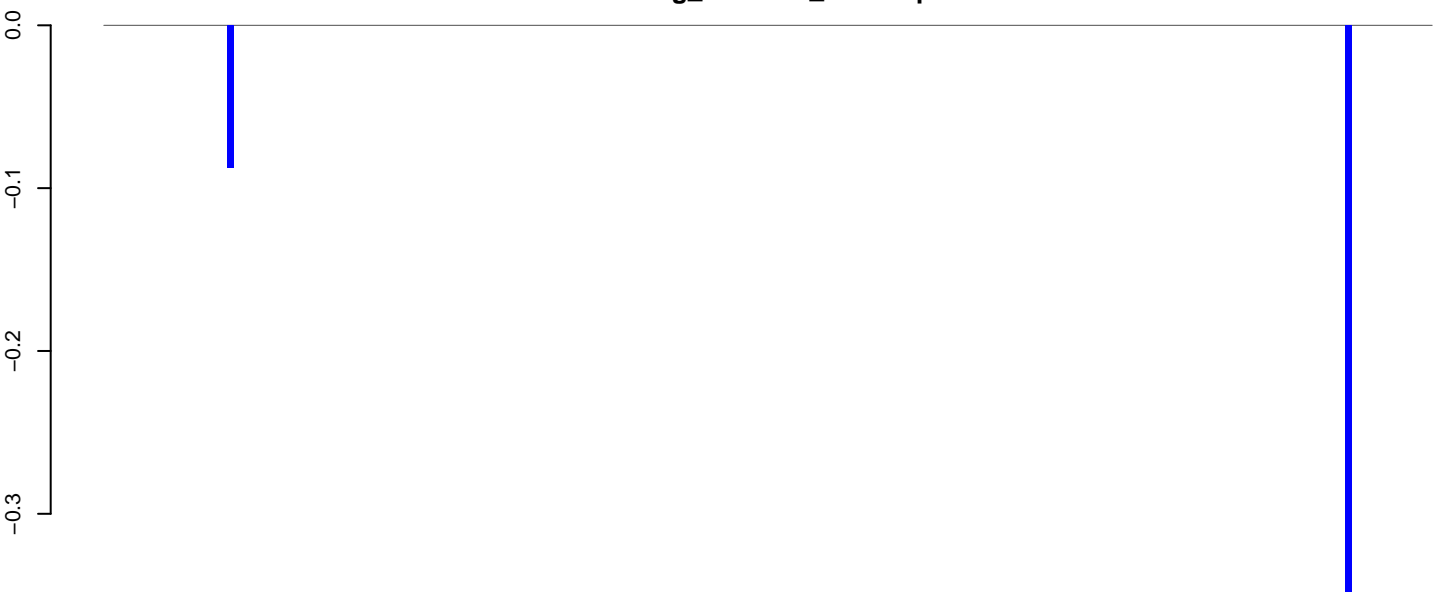
AeAeg_CCL.125_cells.18_23.rep



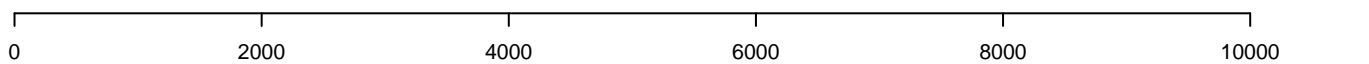
AeAeg_CCL.125_cells.24_35.rep



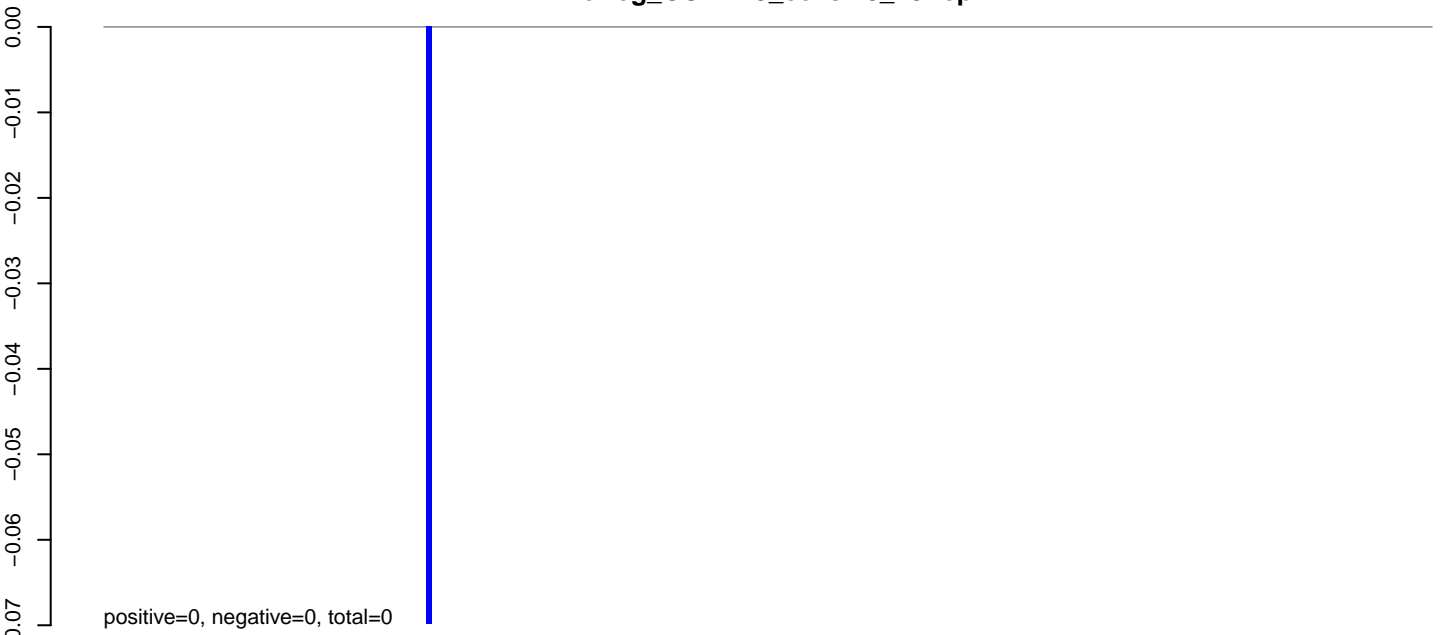
AeAeg_CCL.125_cells.rep



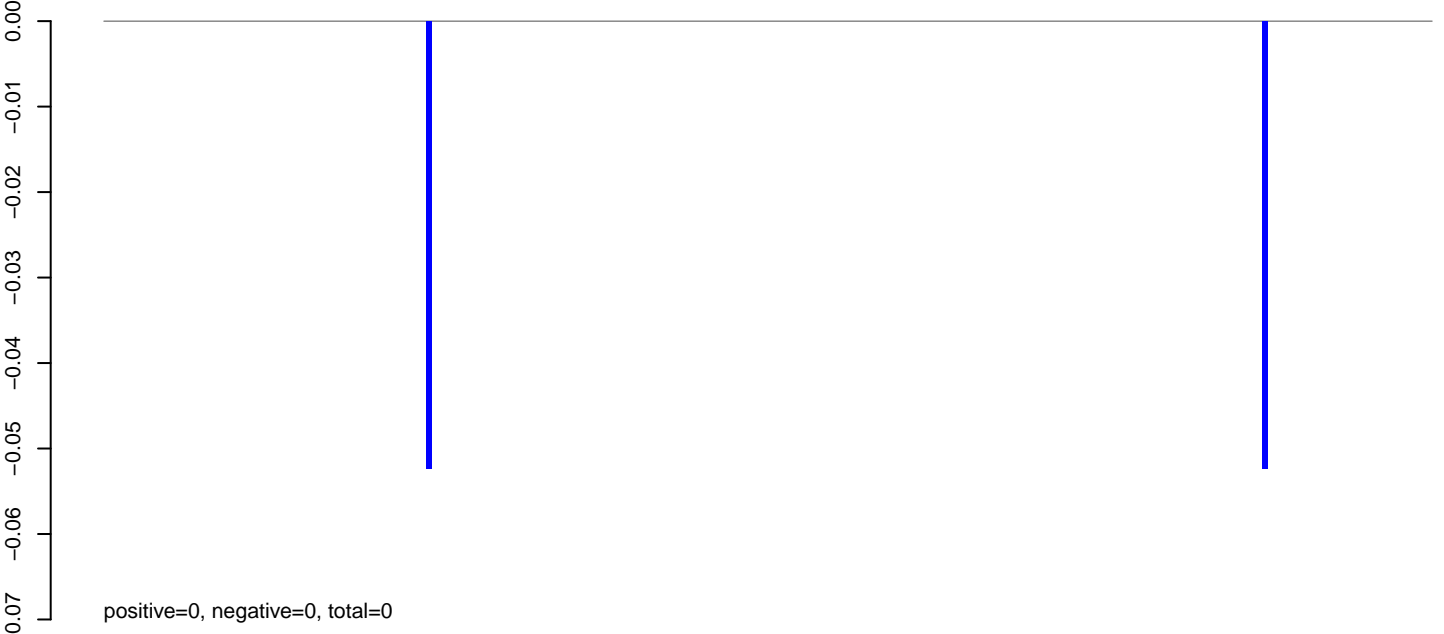
Window size=50, length=10755, virus@NC_009028.2-Ilheus_virus1-10755



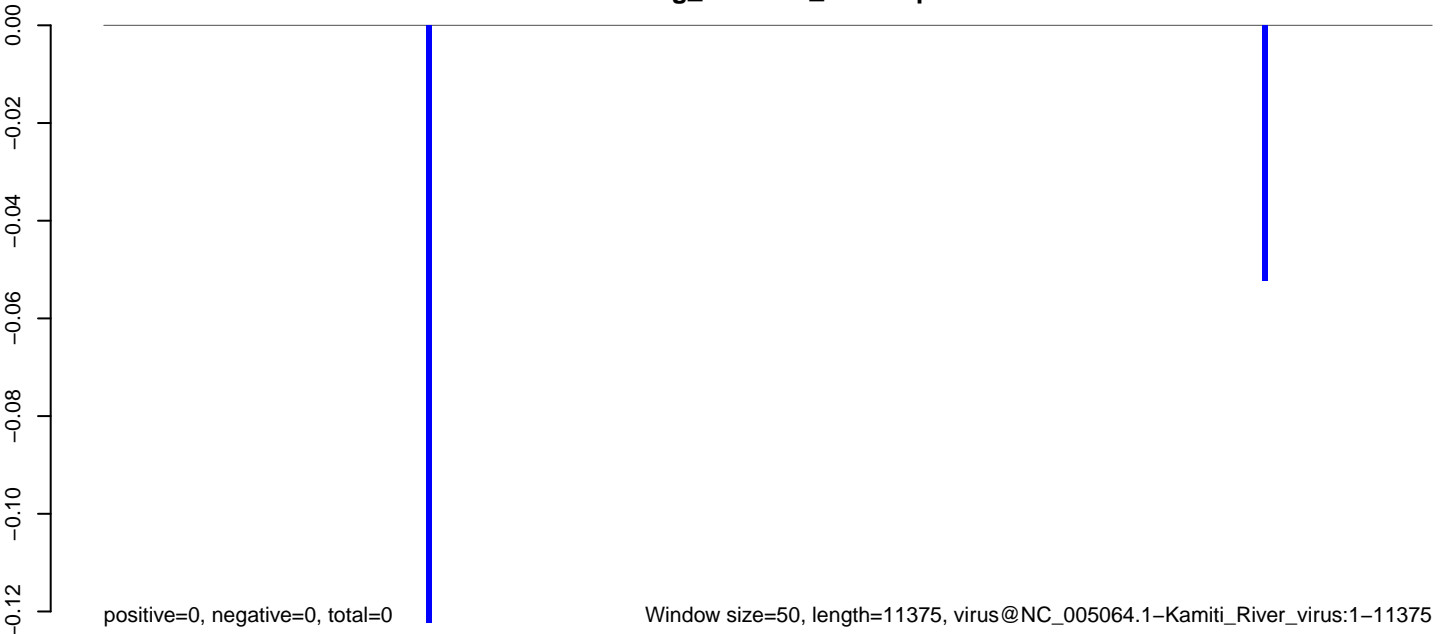
AeAeg_CCL.125_cells.18_23.rep



AeAeg_CCL.125_cells.24_35.rep

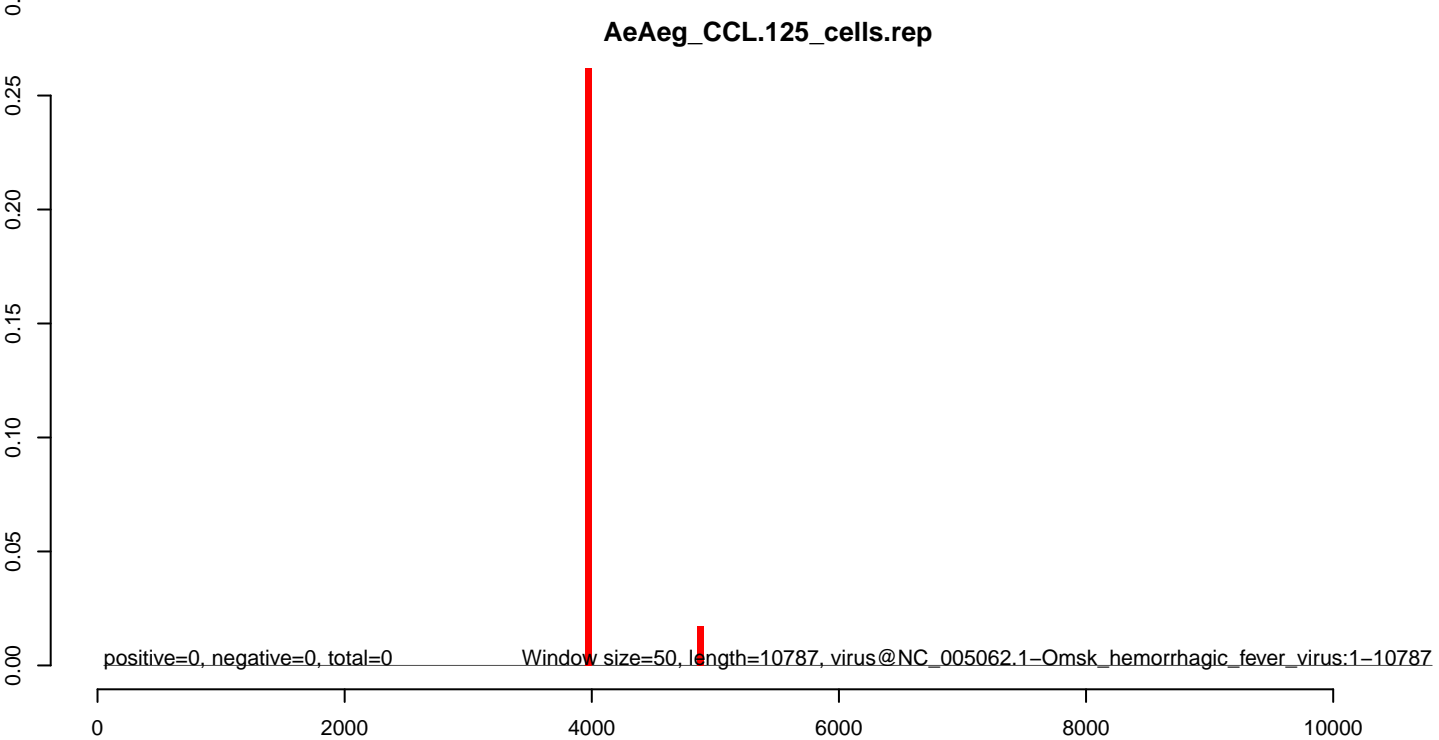
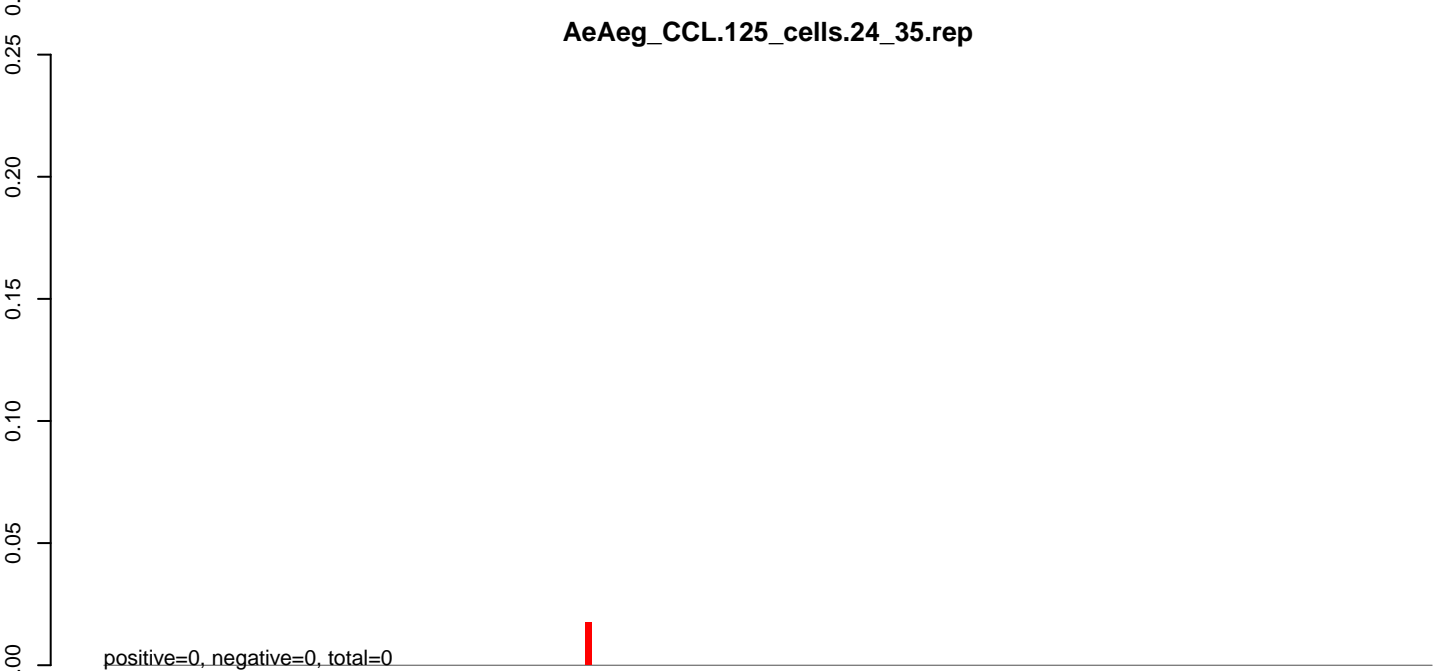
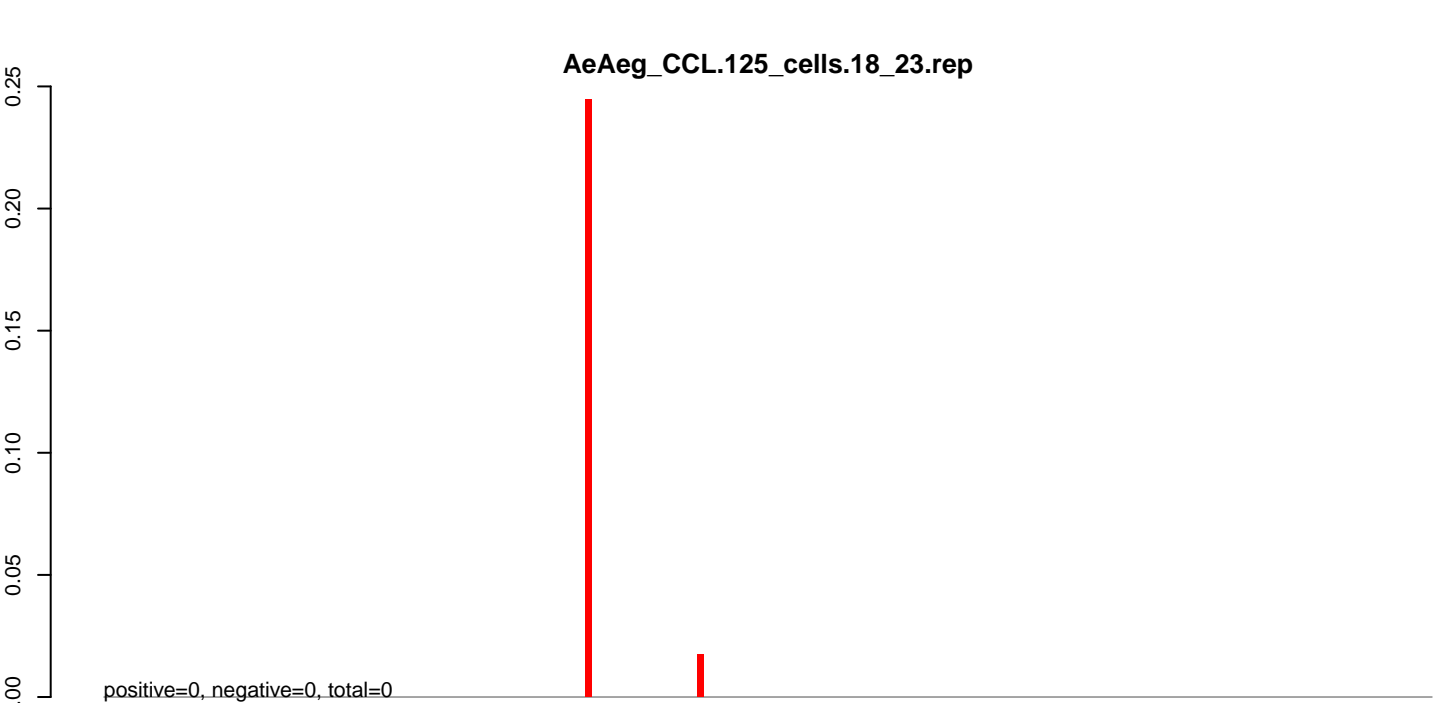


AeAeg_CCL.125_cells.rep

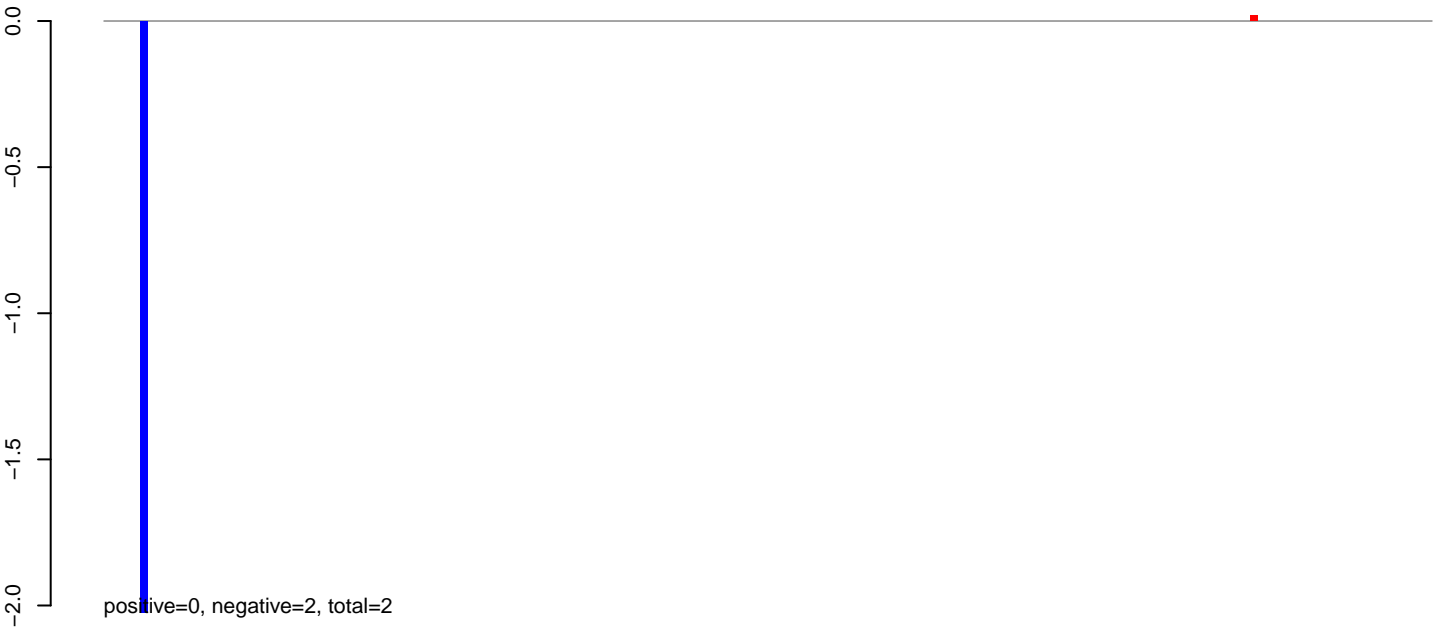


Window size=50, length=11375, virus@NC_005064.1-Kamiti_River_virus:1-11375

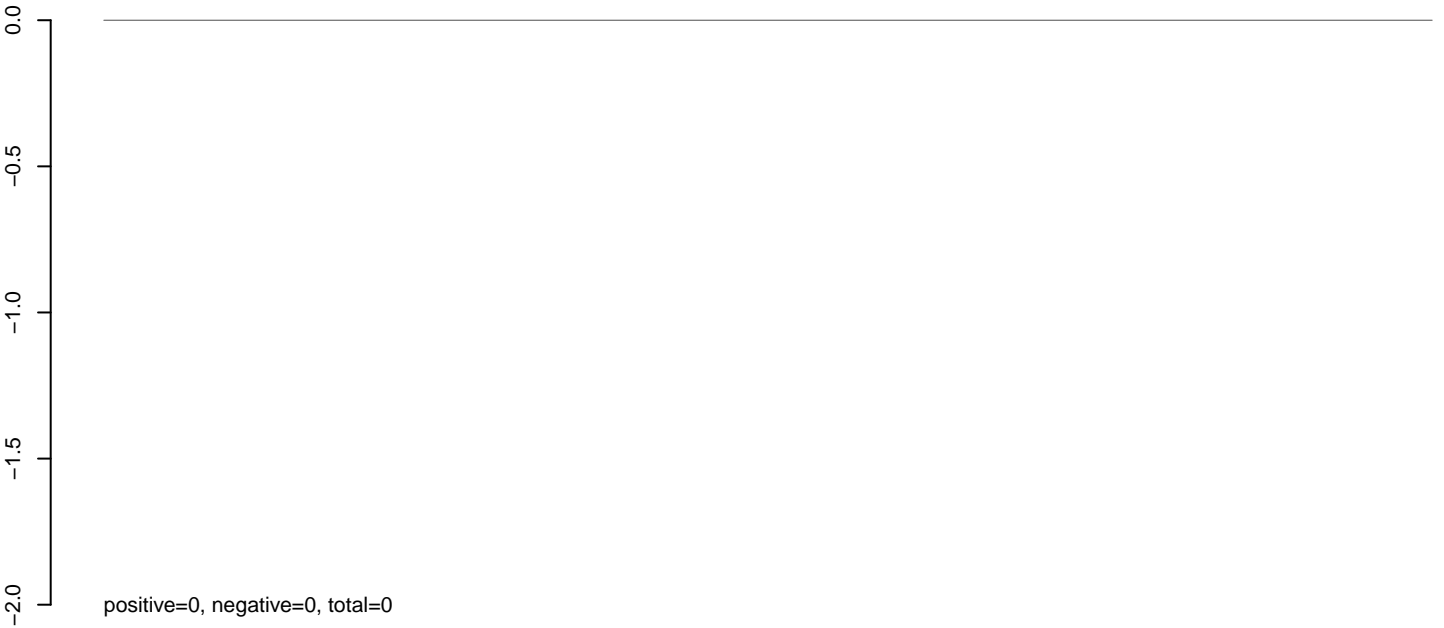
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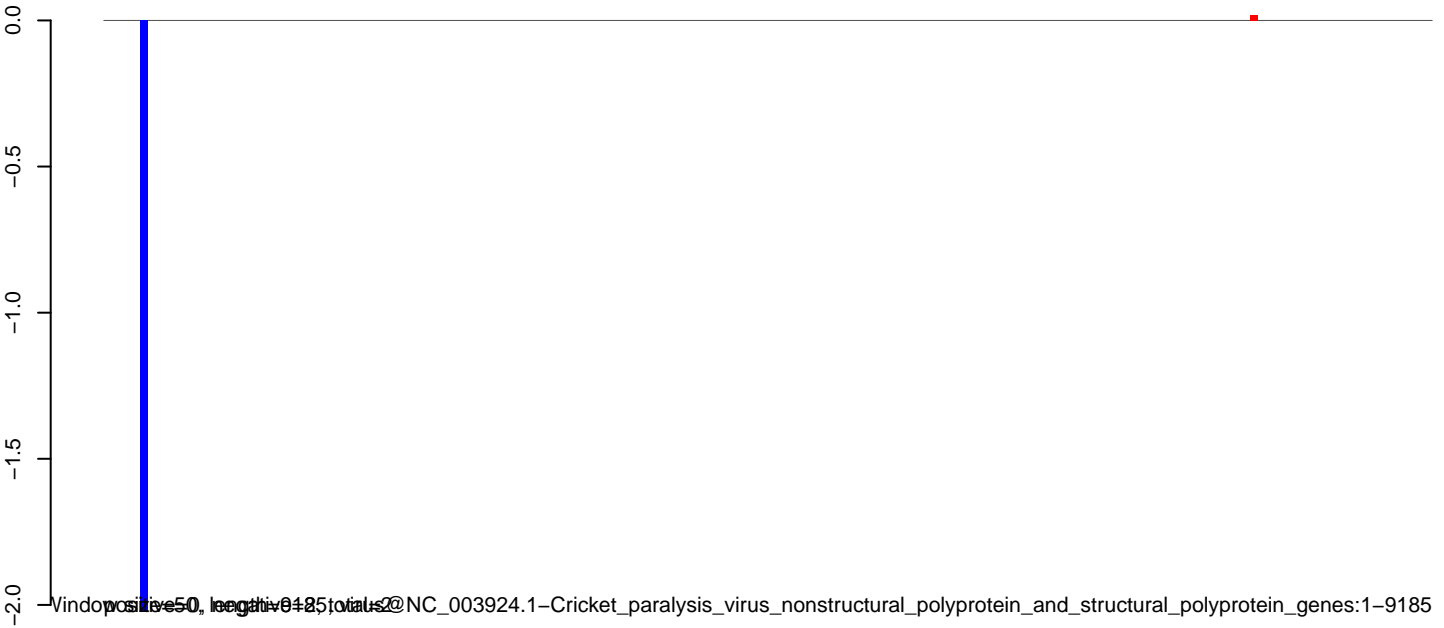
AeAeg_CCL.125_cells.18_23.rep



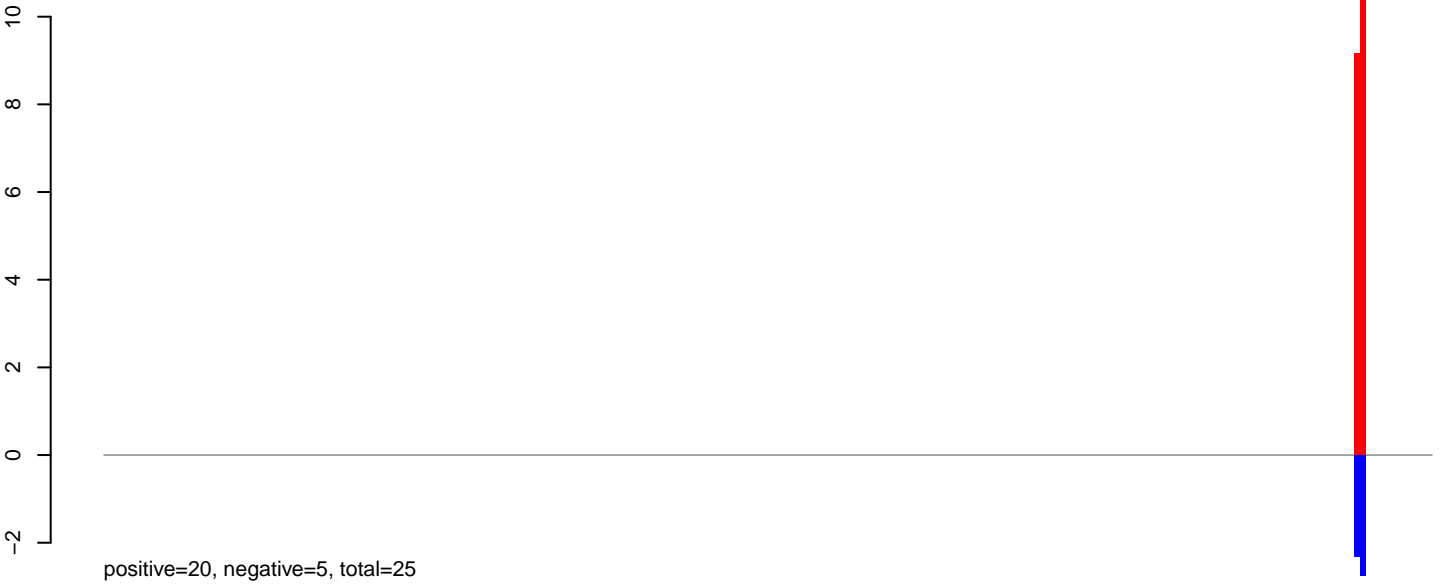
AeAeg_CCL.125_cells.24_35.rep



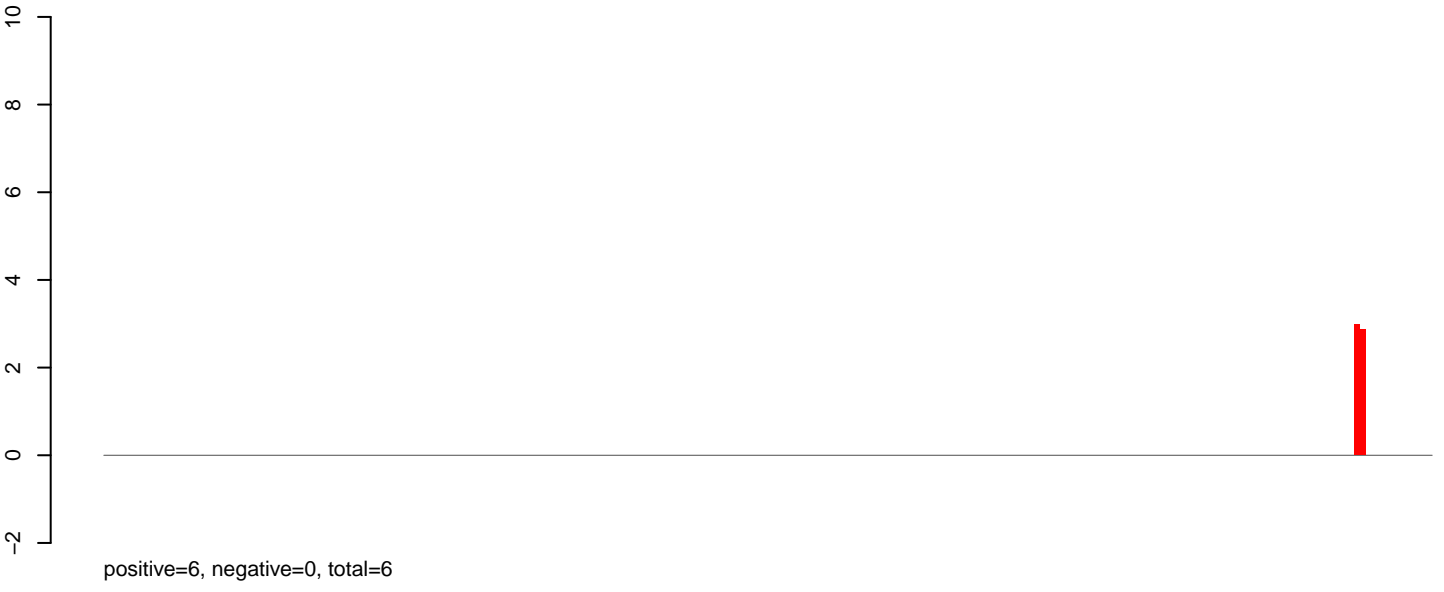
AeAeg_CCL.125_cells.rep



AeAeg_CCL.125_cells.18_23.rep



AeAeg_CCL.125_cells.24_35.rep



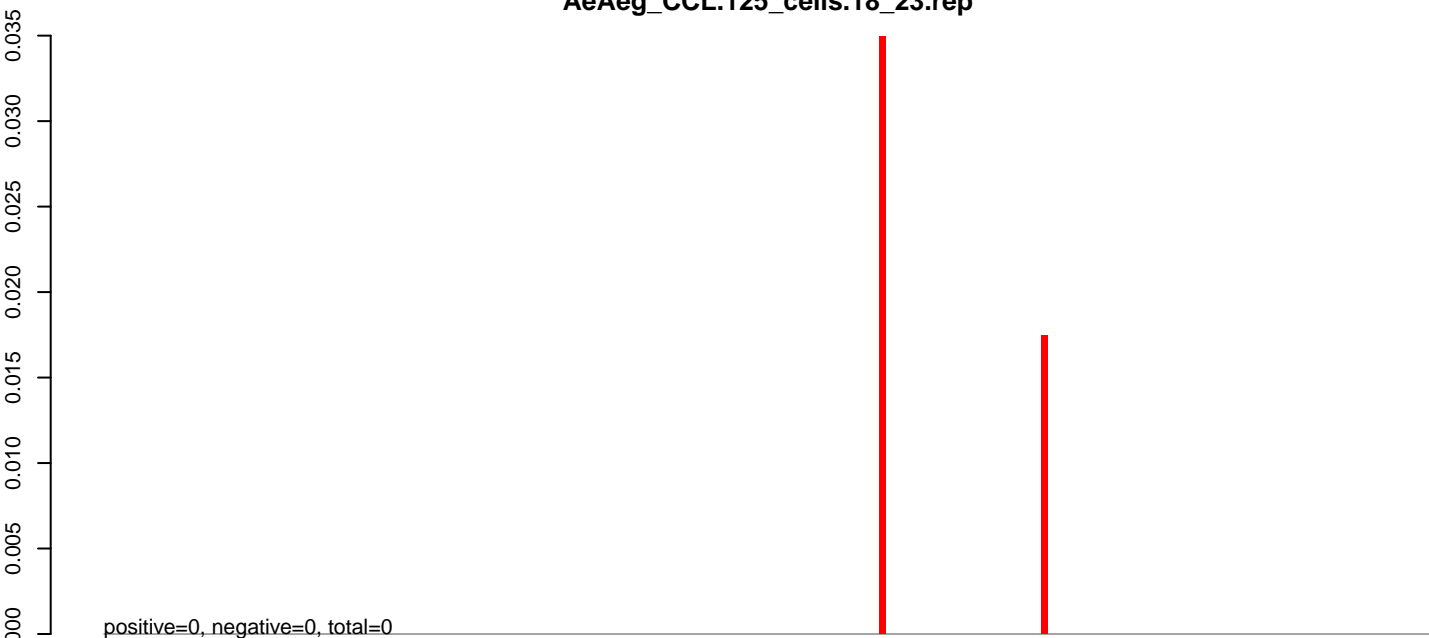
AeAeg_CCL.125_cells.rep



Window size=50, length=11141, virus@NC_001672.1-Tick-borne_encephalitis_virus:1-11141

0 2000 4000 6000 8000 10000

AeAeg_CCL.125_cells.18_23.rep



AeAeg_CCL.125_cells.24_35.rep

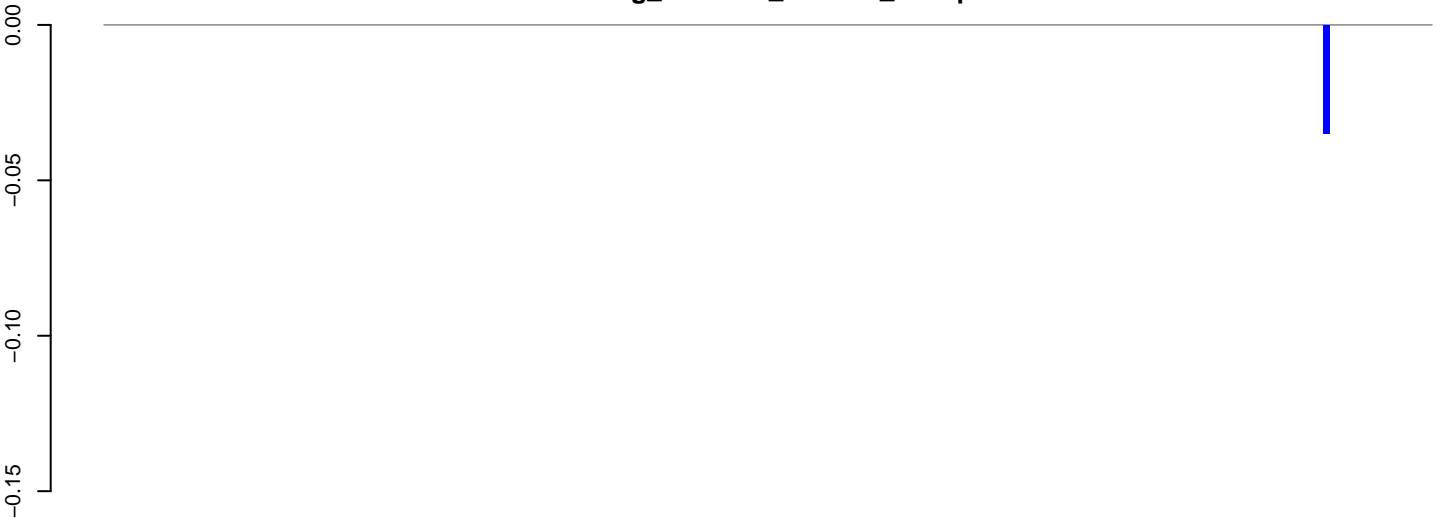


AeAeg_CCL.125_cells.rep



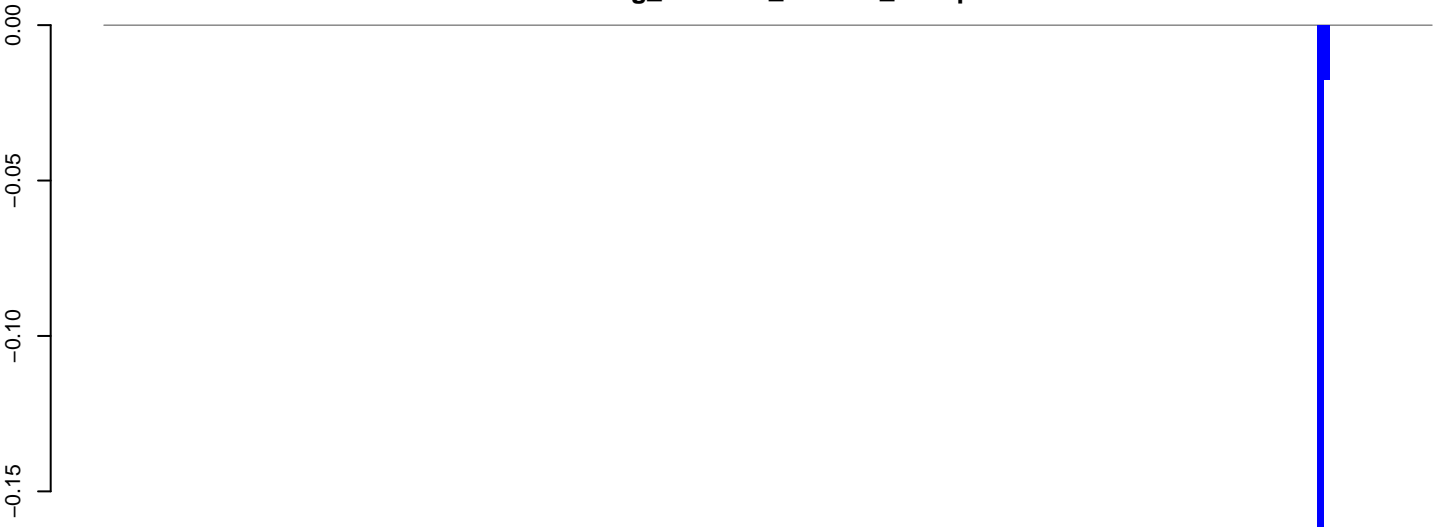
0 2000 4000 6000 8000 10000

AeAeg_CCL.125_cells.18_23.rep



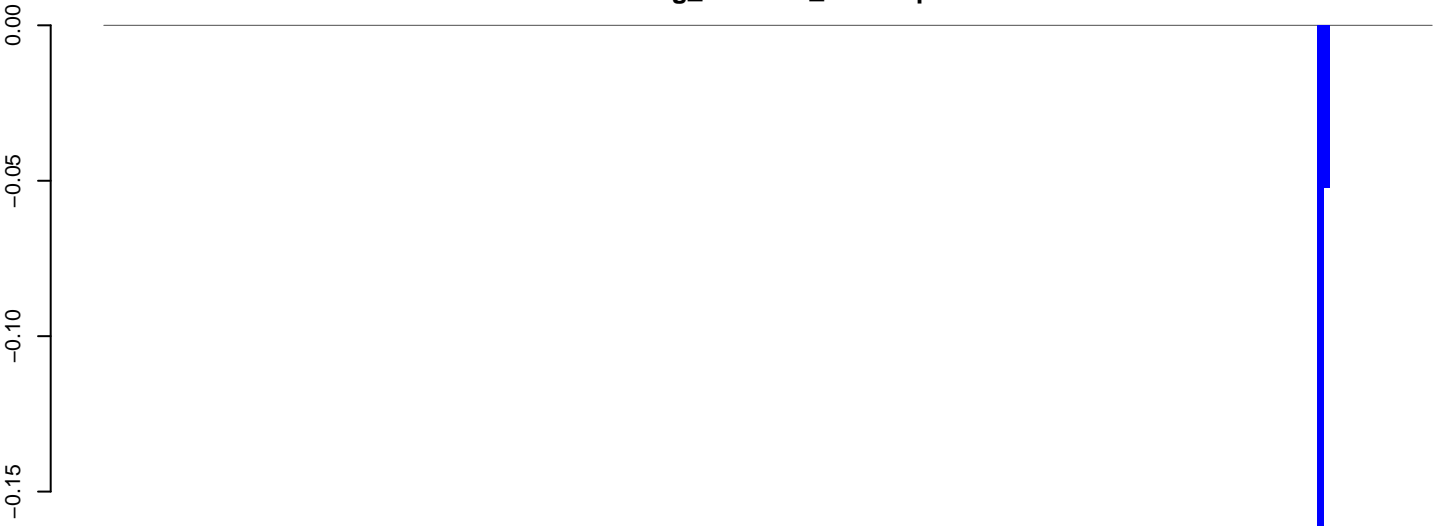
positive=0, negative=0, total=0

AeAeg_CCL.125_cells.24_35.rep



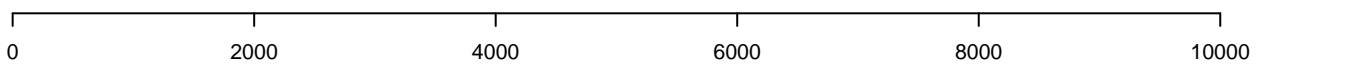
positive=0, negative=0, total=0

AeAeg_CCL.125_cells.rep

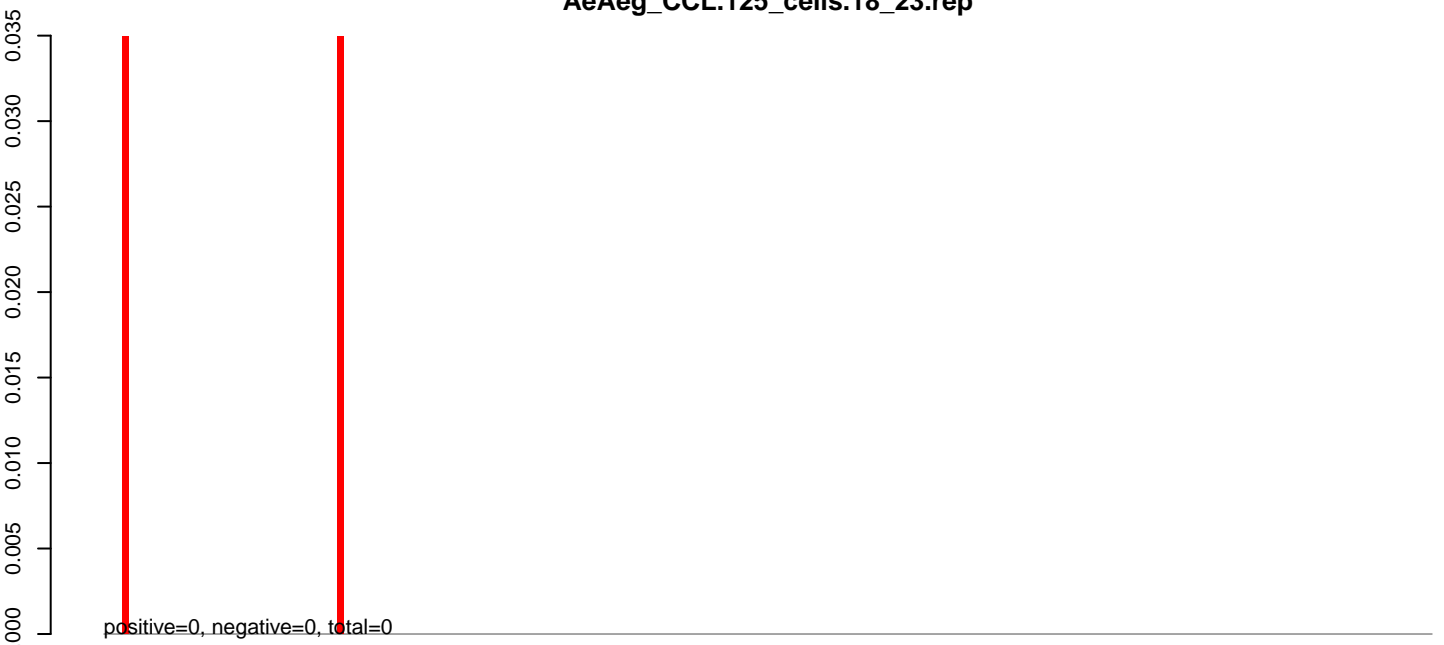


positive=0, negative=0, total=0

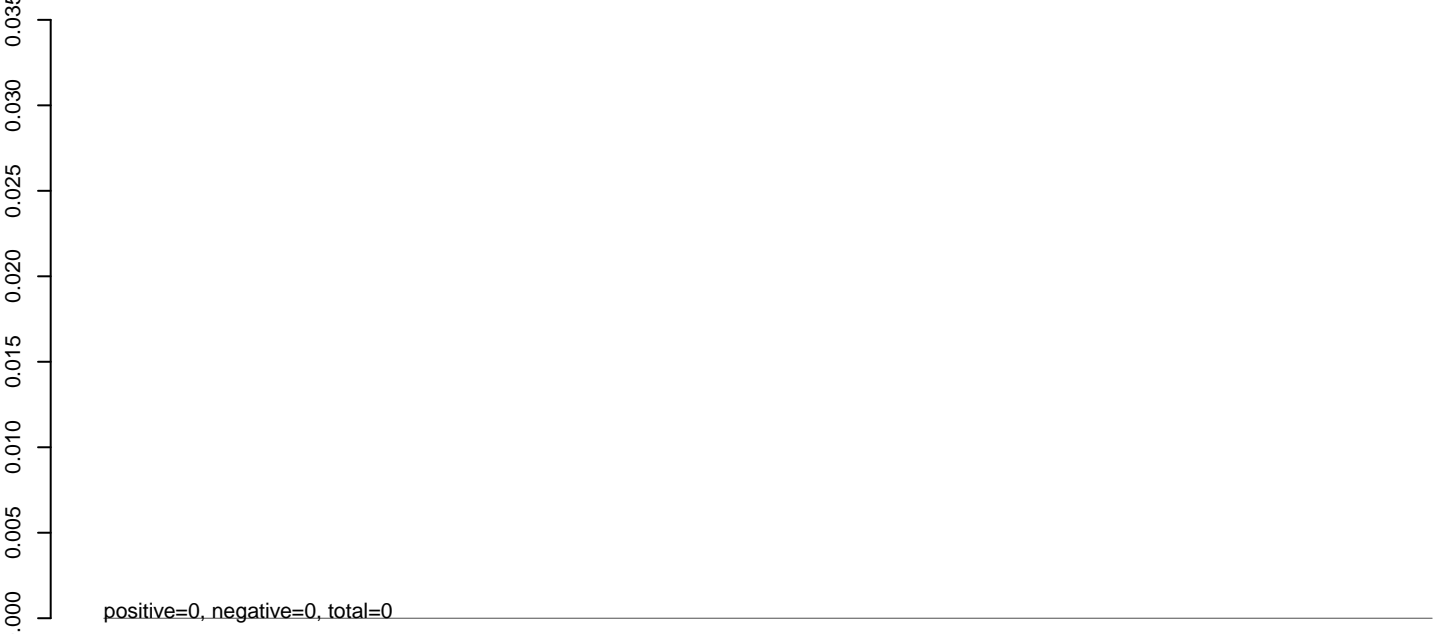
Window size=50, length=11014, virus@NC_000943.1-Murray_Valley_encephalitis_virus:1-11014



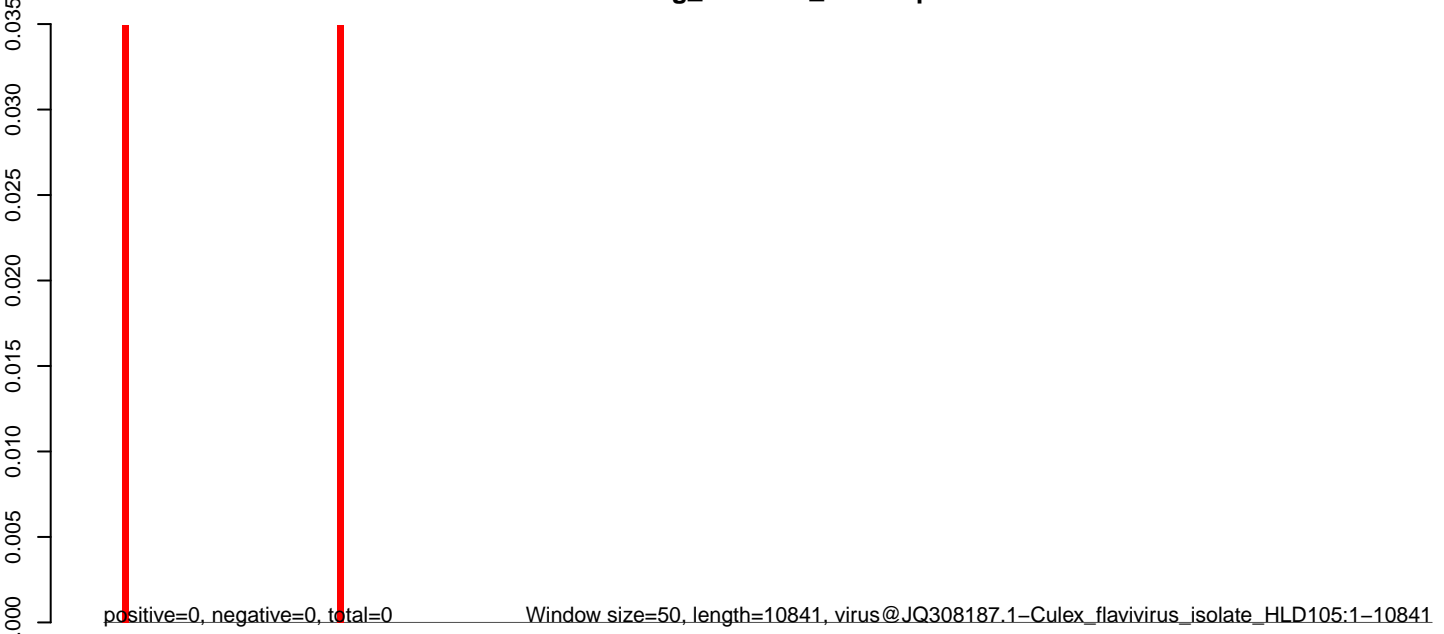
AeAeg_CCL.125_cells.18_23.rep



AeAeg_CCL.125_cells.24_35.rep

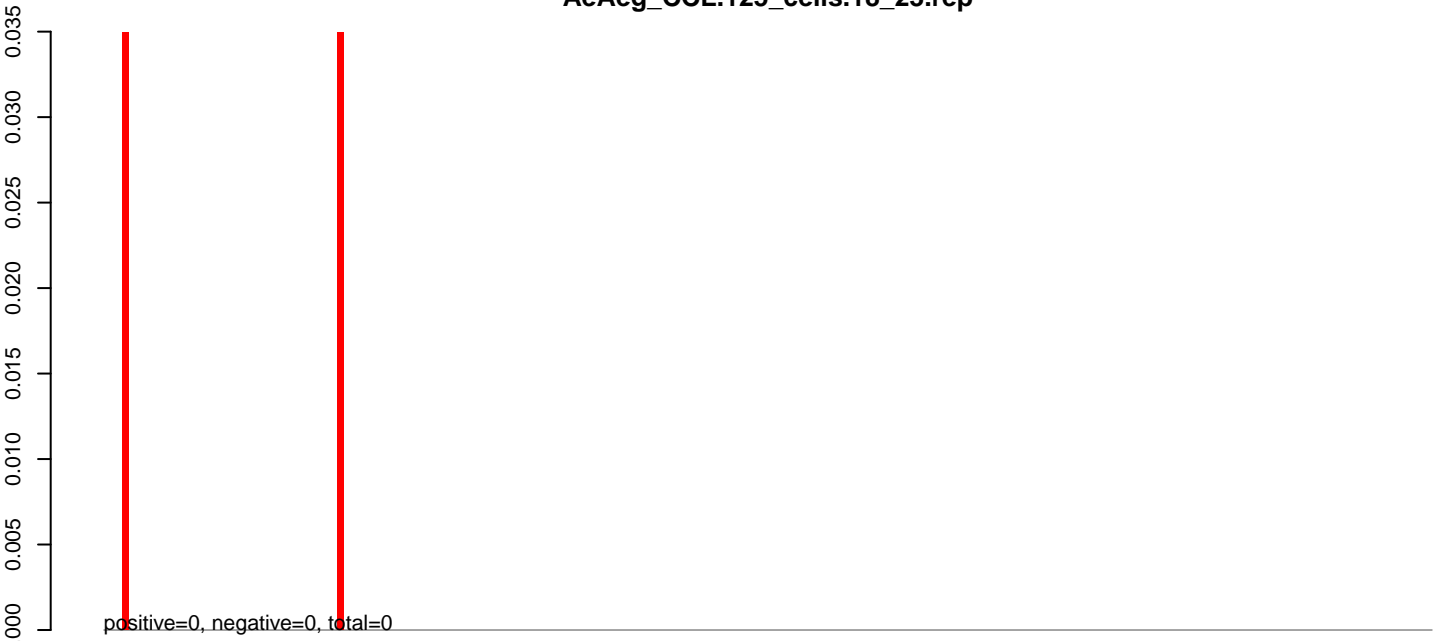


AeAeg_CCL.125_cells.rep

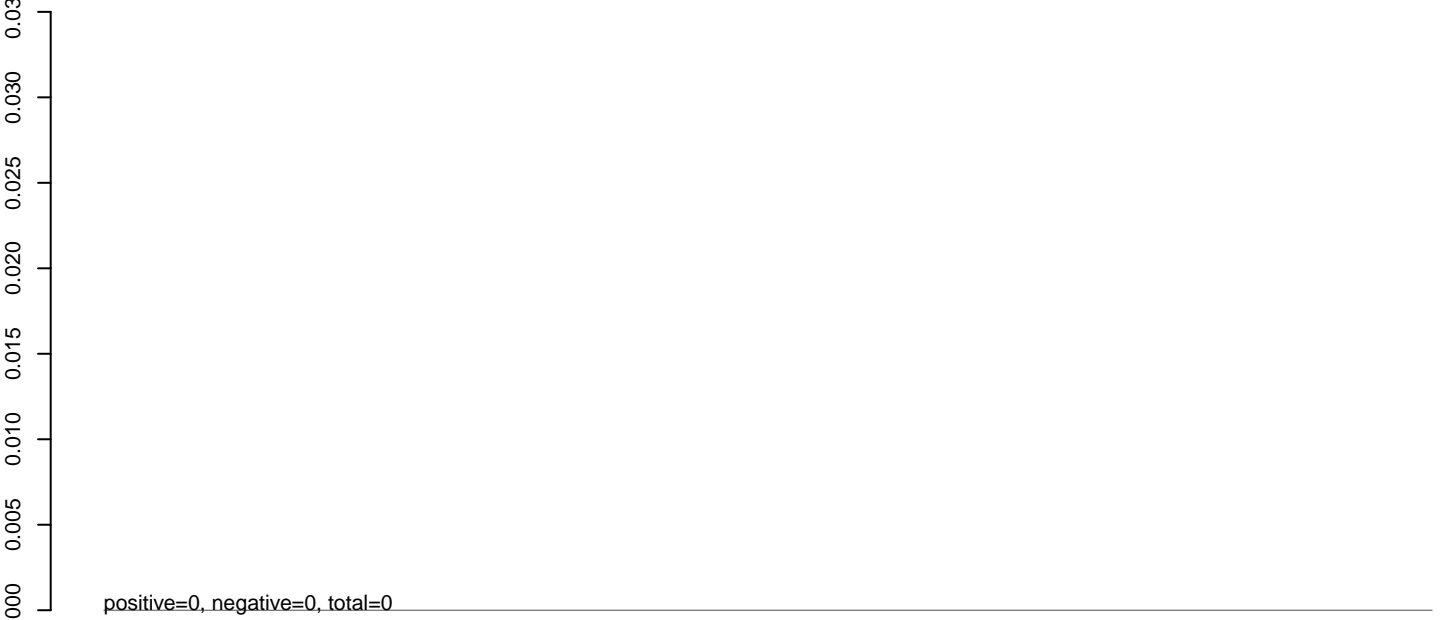


0 2000 4000 6000 8000 10000

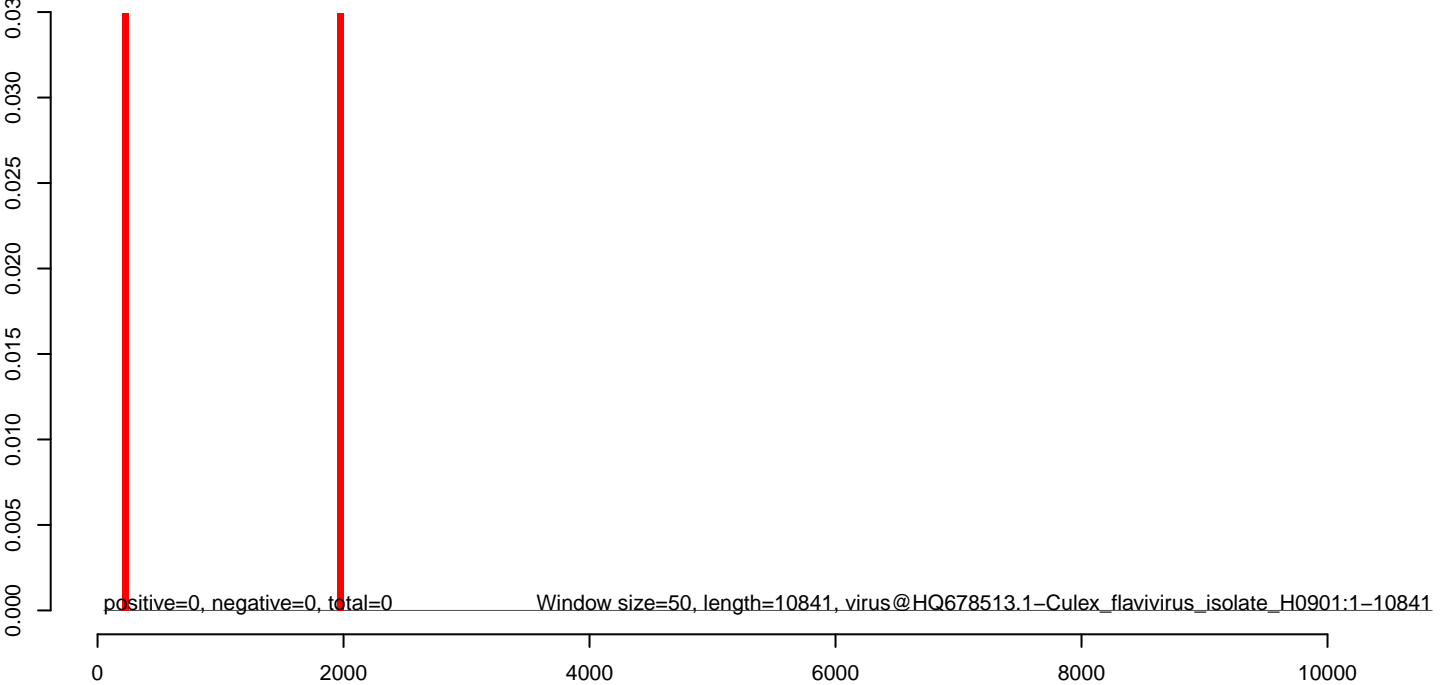
AeAeg_CCL.125_cells.18_23.rep



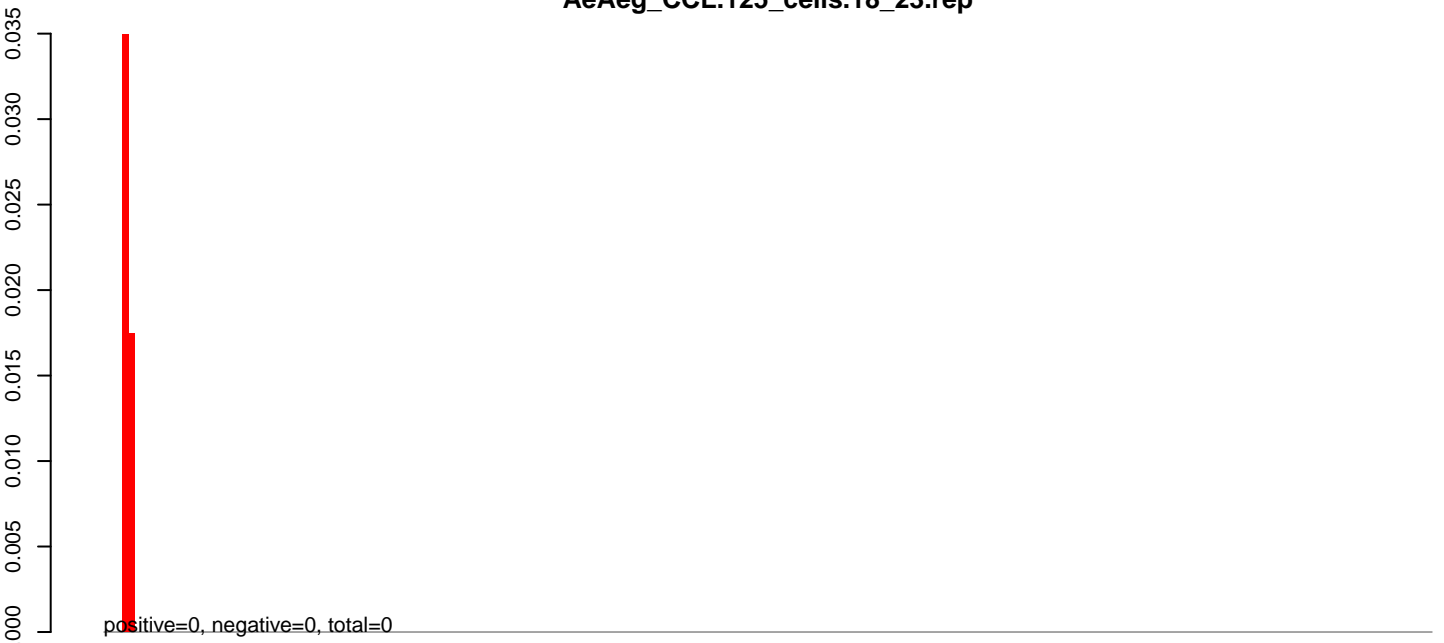
AeAeg_CCL.125_cells.24_35.rep



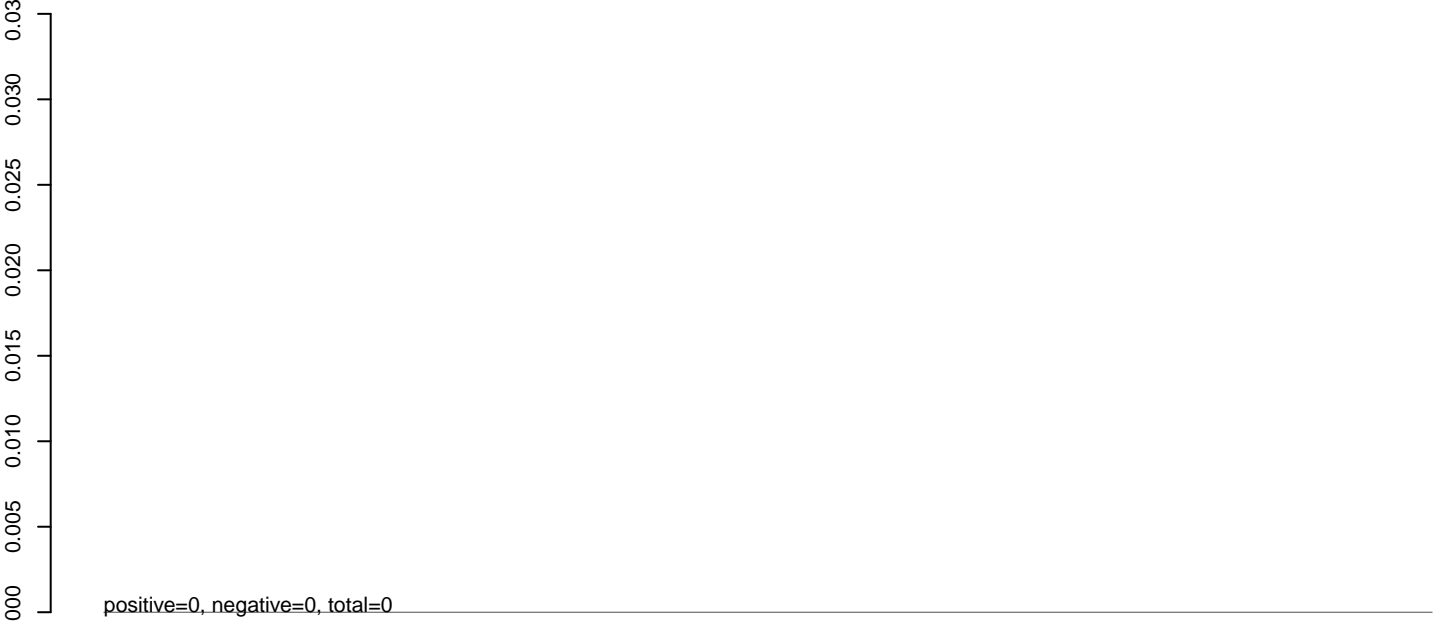
AeAeg_CCL.125_cells.rep



AeAeg_CCL.125_cells.18_23.rep



AeAeg_CCL.125_cells.24_35.rep



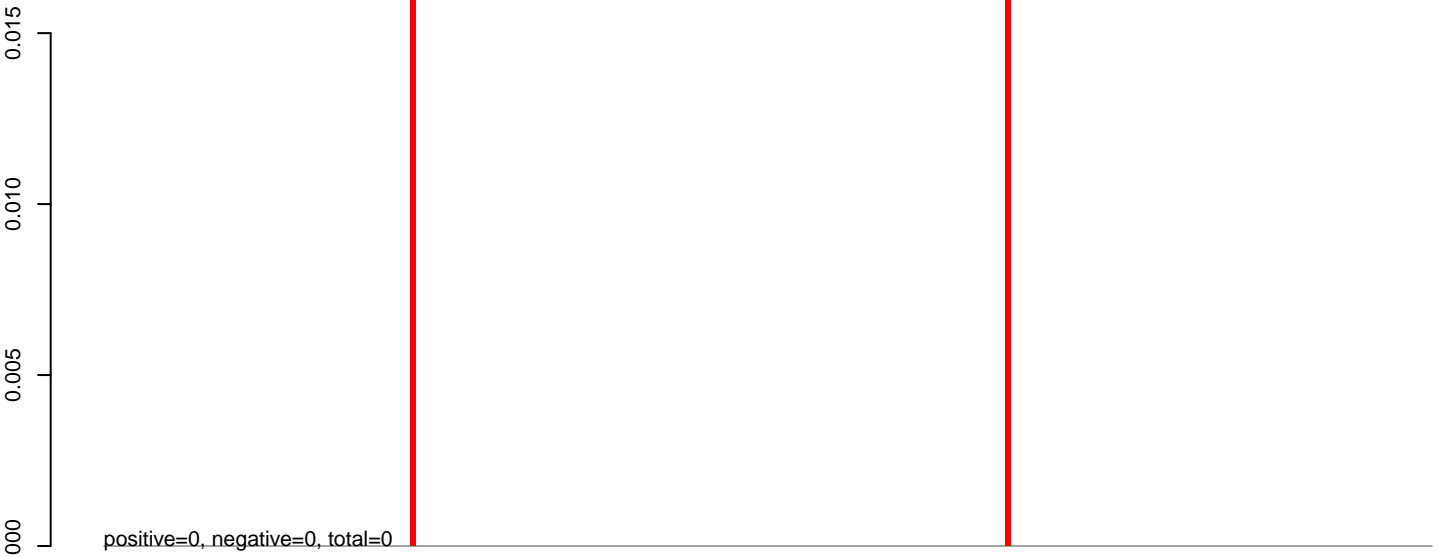
AeAeg_CCL.125_cells.rep



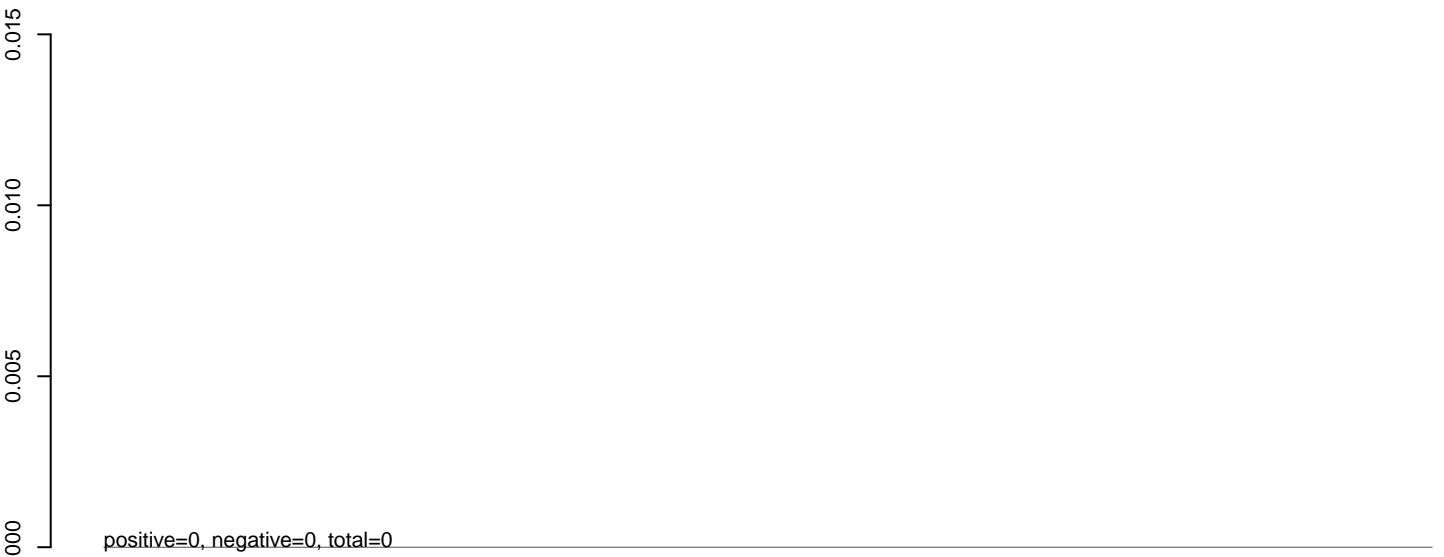
Window size=50, length=10837, virus@EU879060.1-Culex_flavivirus_strain_CxFV-Mex07:1-10837

0 2000 4000 6000 8000 10000

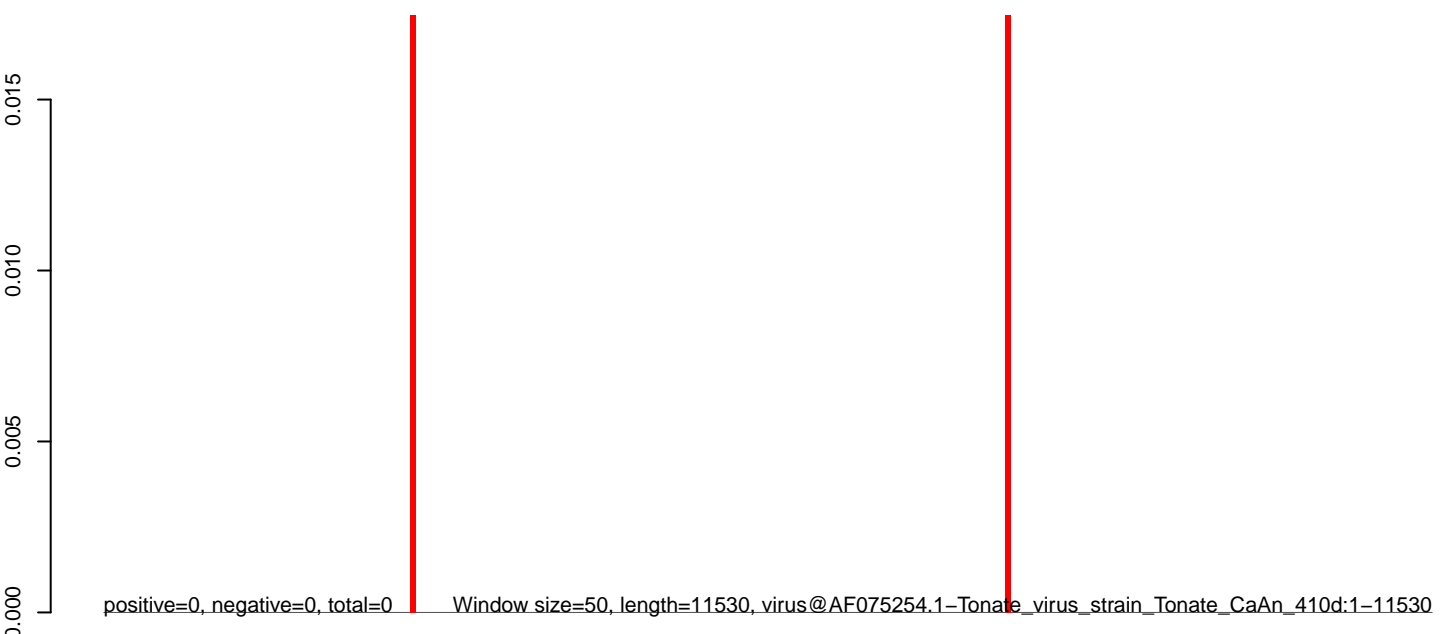
AeAeg_CCL.125_cells.18_23.rep



AeAeg_CCL.125_cells.24_35.rep

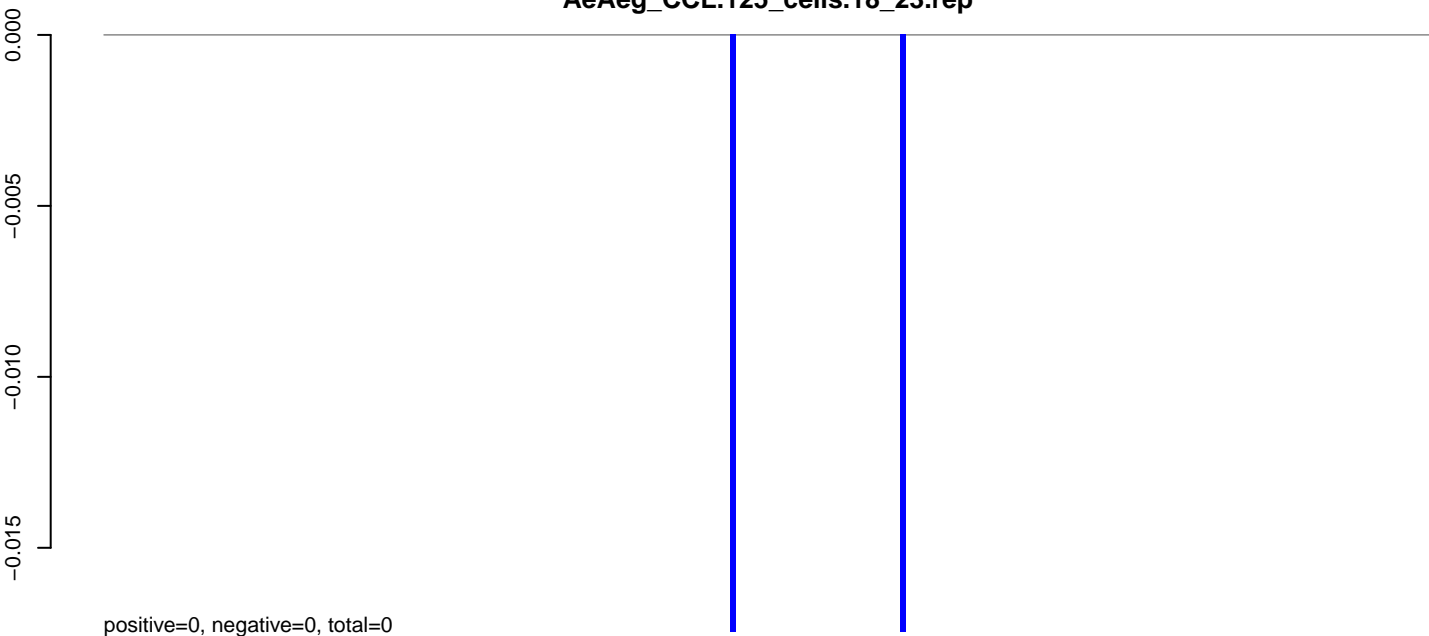


AeAeg_CCL.125_cells.rep

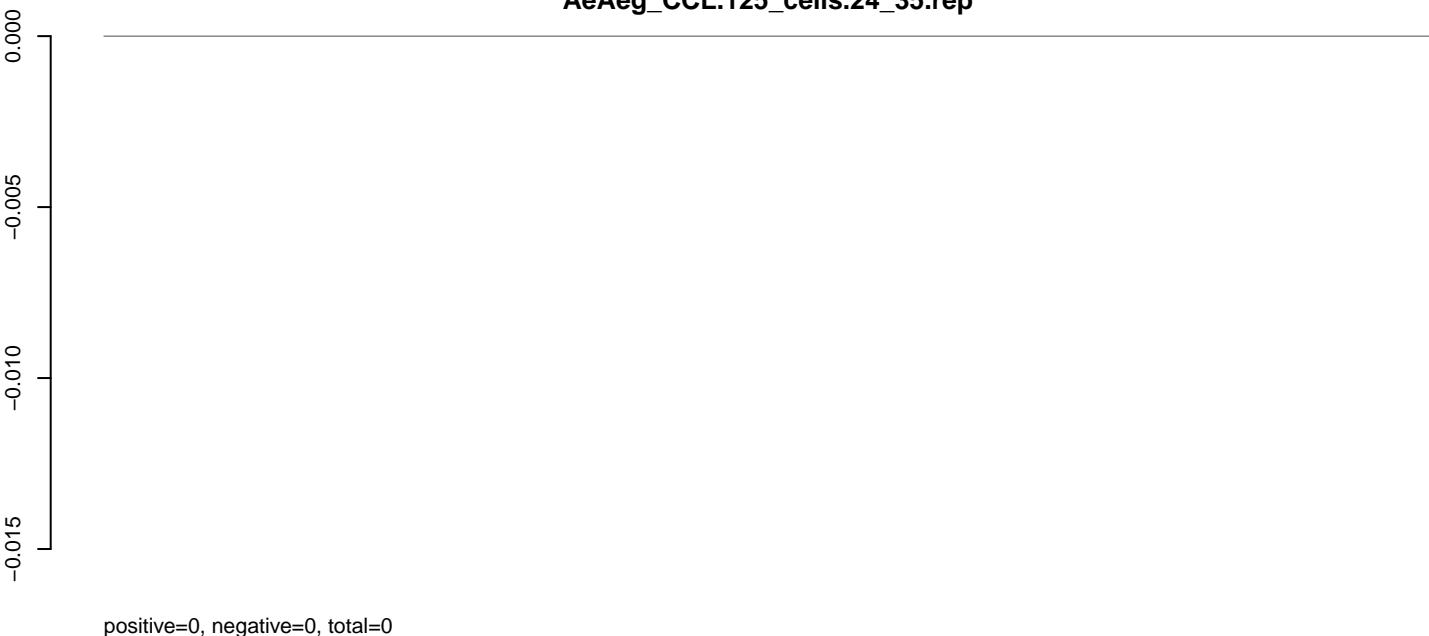


0 2000 4000 6000 8000 10000 12000

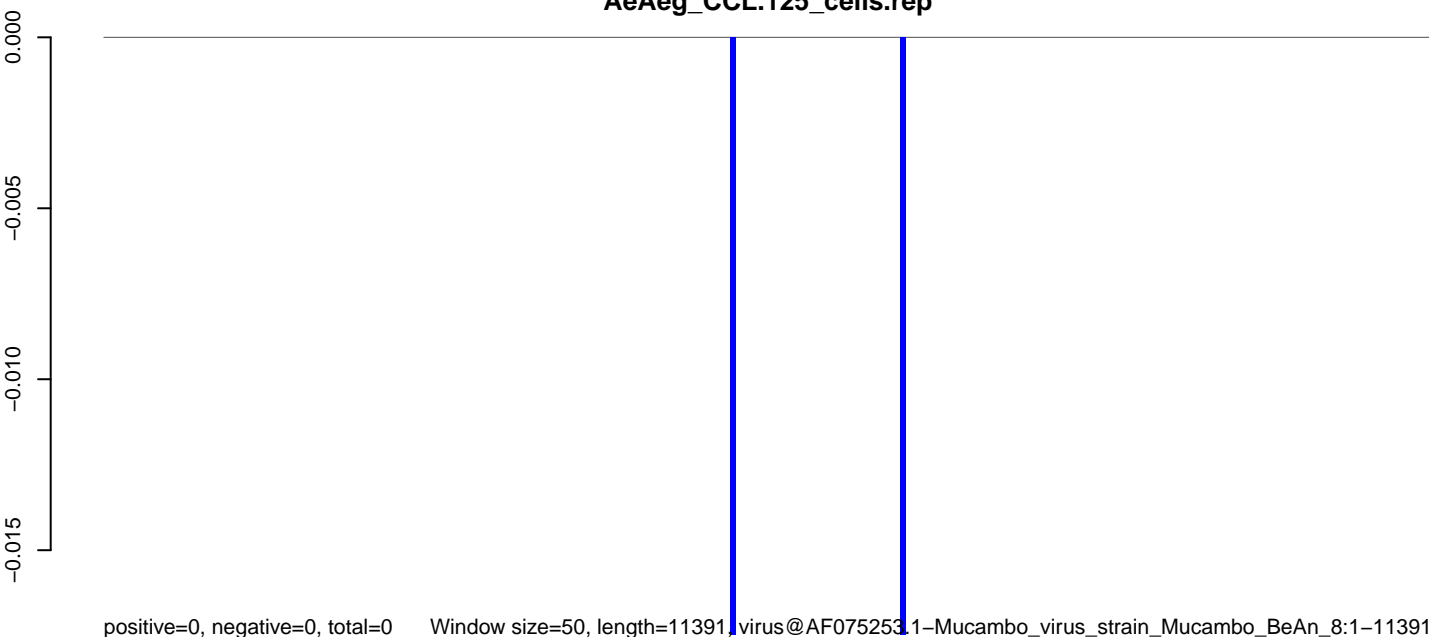
AeAeg_CCL.125_cells.18_23.rep



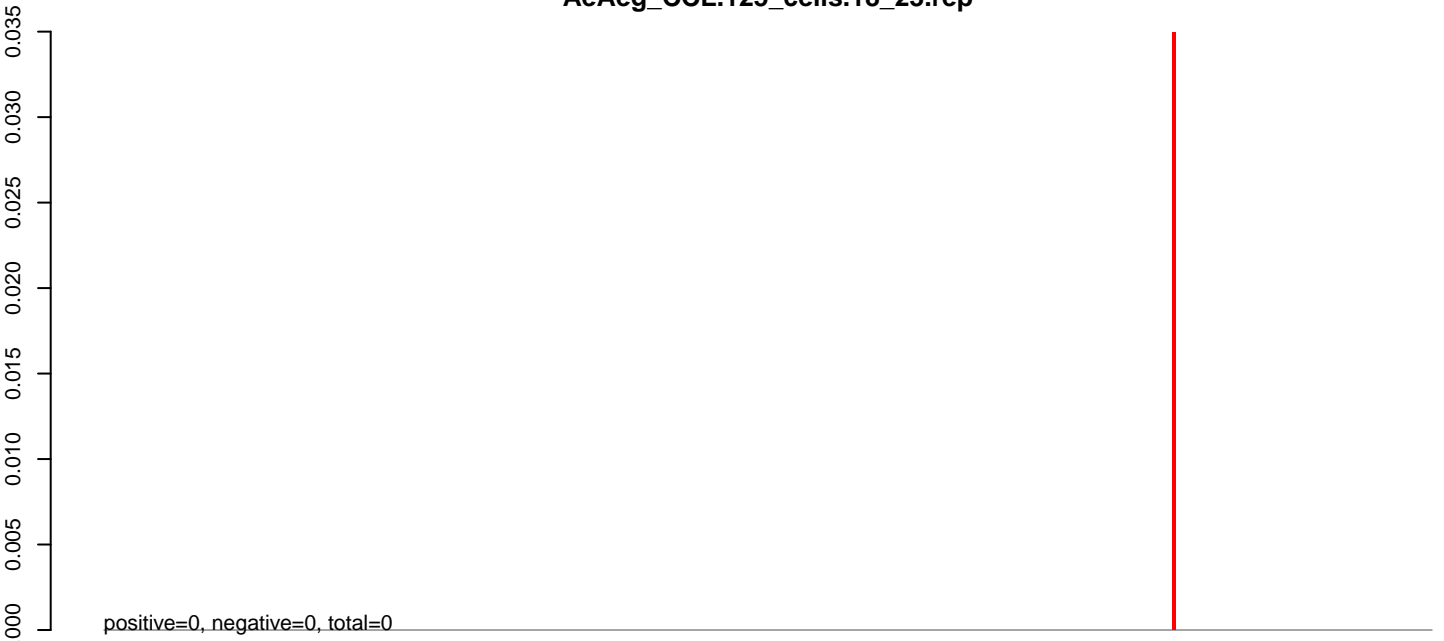
AeAeg_CCL.125_cells.24_35.rep



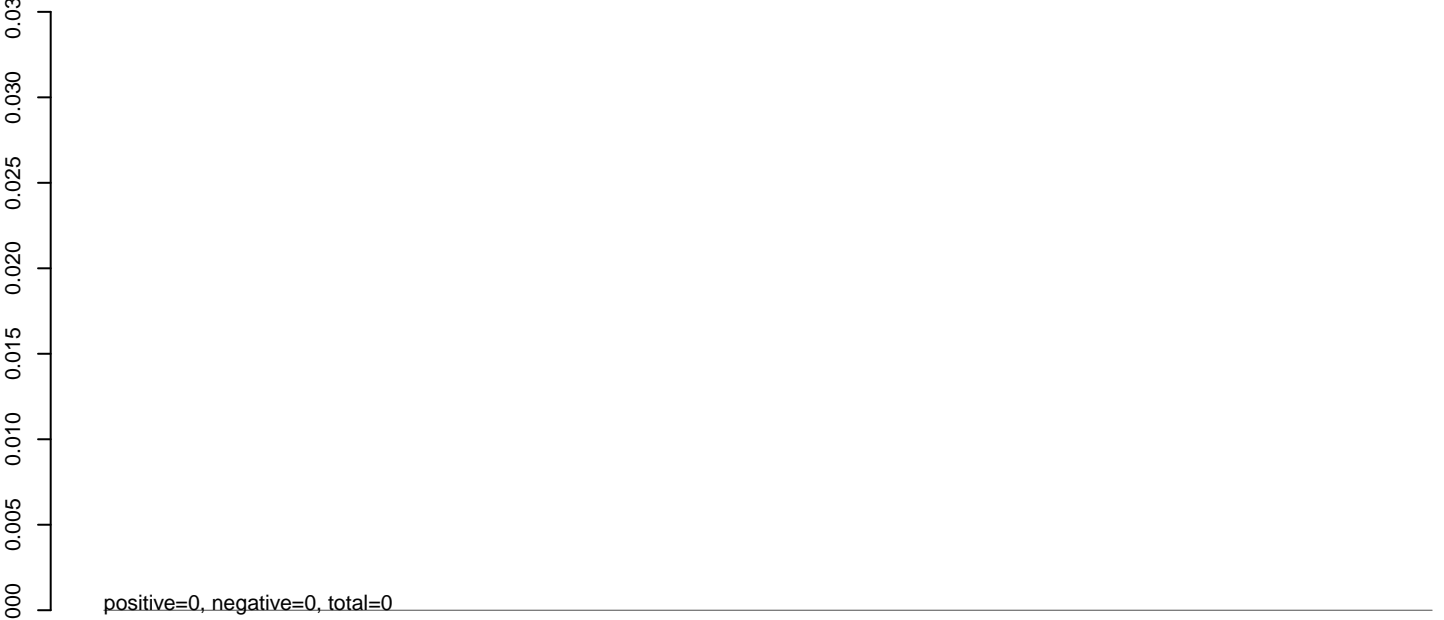
AeAeg_CCL.125_cells.rep



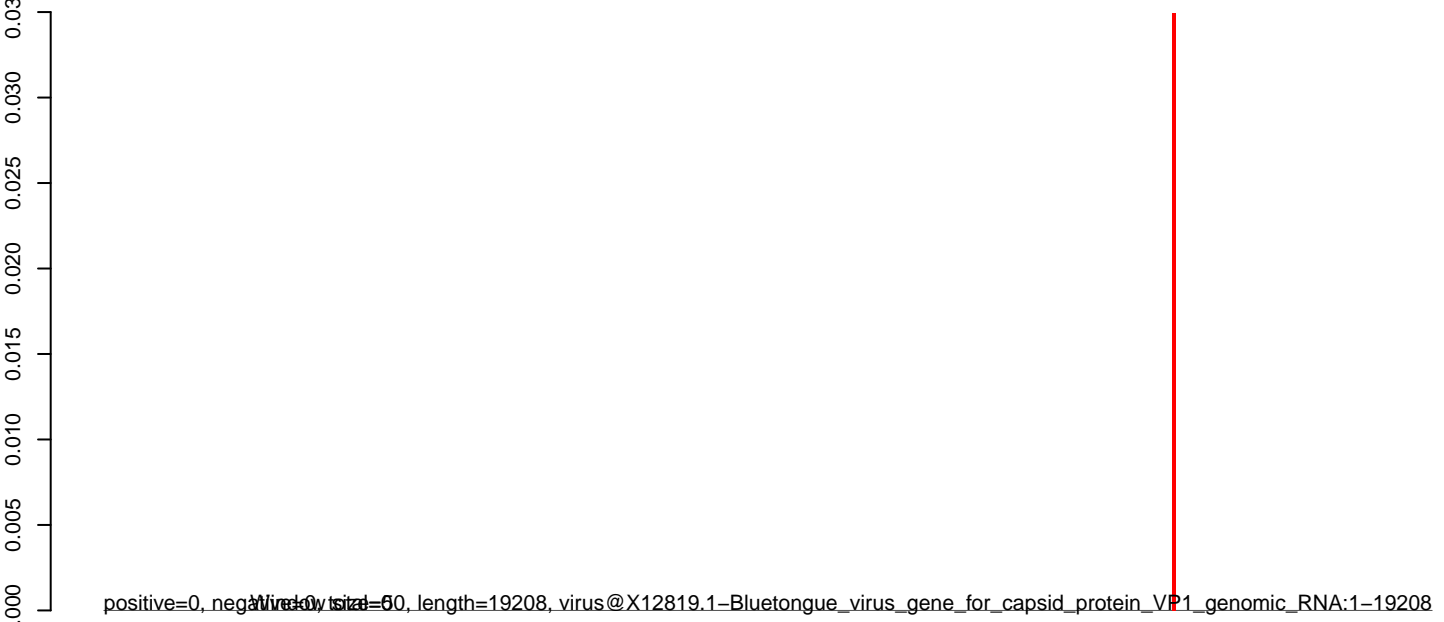
AeAeg_CCL.125_cells.18_23.rep



AeAeg_CCL.125_cells.24_35.rep



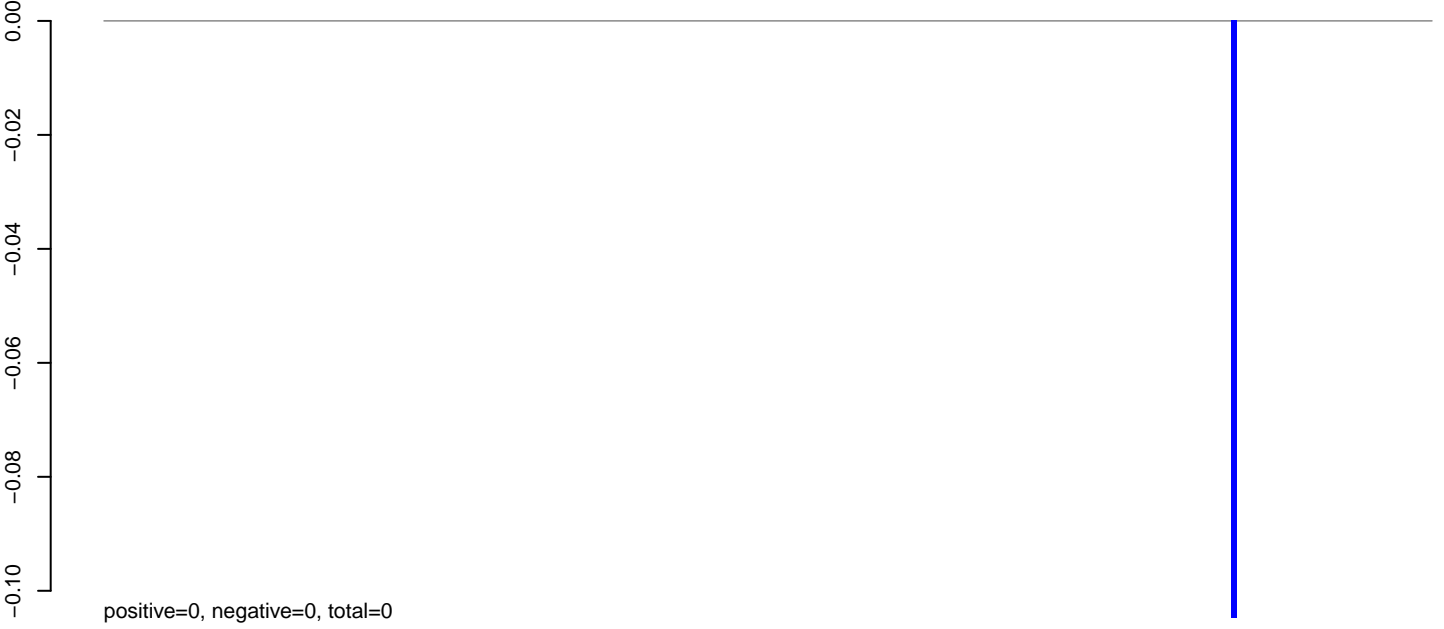
AeAeg_CCL.125_cells.rep



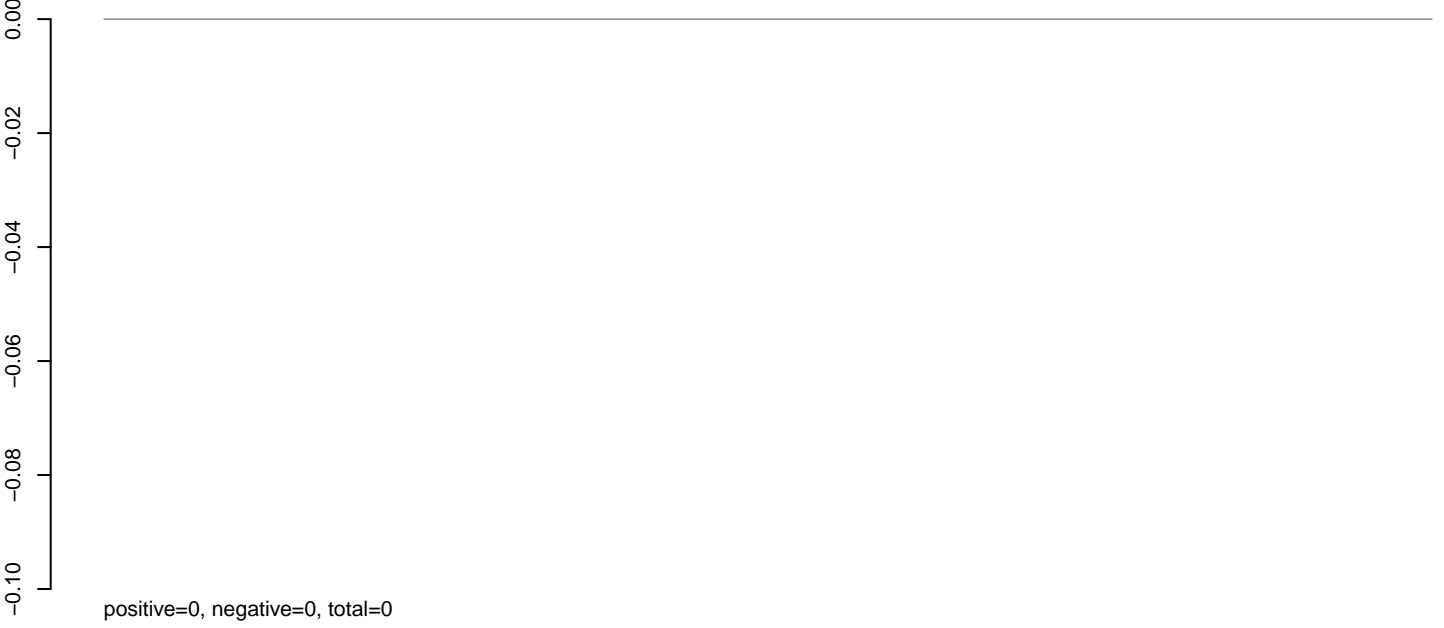
Window size=60, length=19208, virus@X12819.1-Bluetongue_virus_gene_for_capsid_protein_VP1_genomic_RNA:1-19208

0 5000 10000 15000 20000

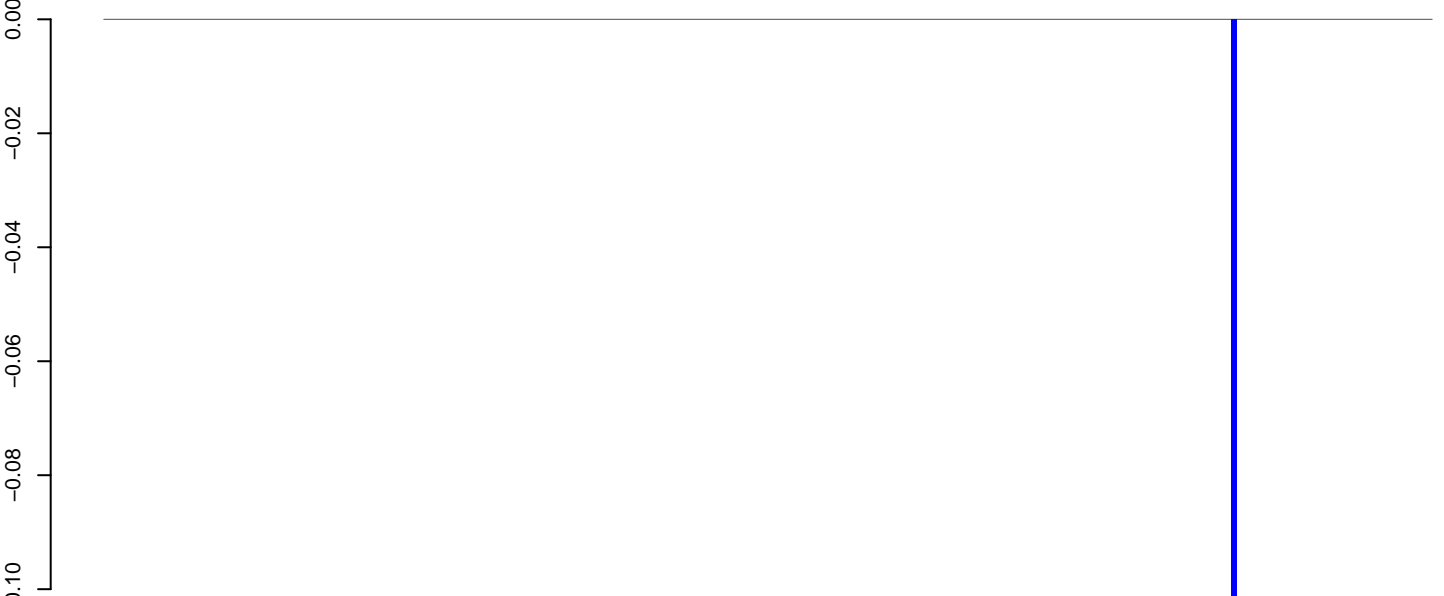
AeAeg_CCL.125_cells.18_23.rep



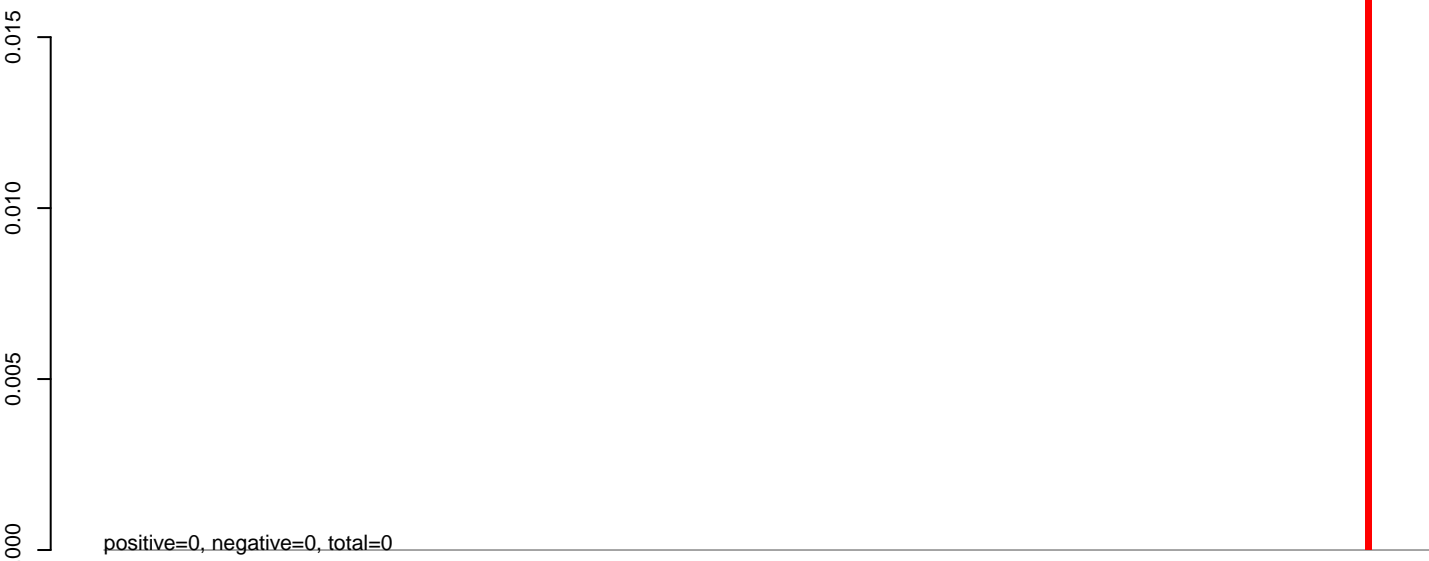
AeAeg_CCL.125_cells.24_35.rep



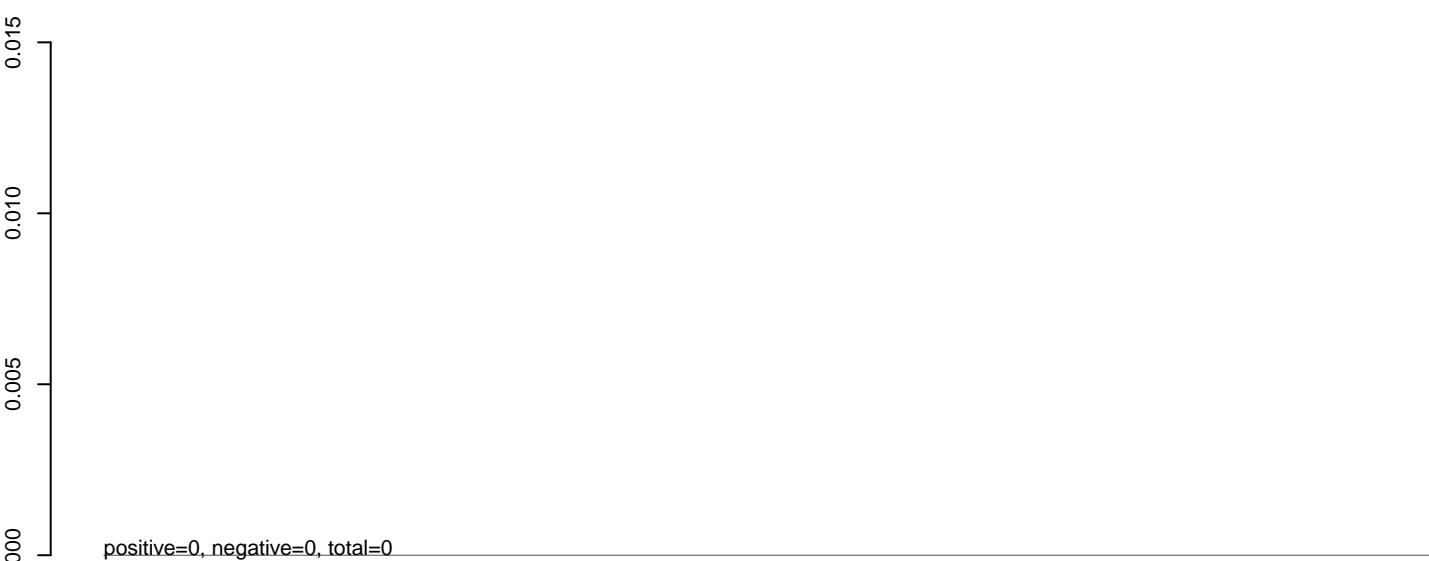
AeAeg_CCL.125_cells.rep



AeAeg_CCL.125_cells.18_23.rep



AeAeg_CCL.125_cells.24_35.rep

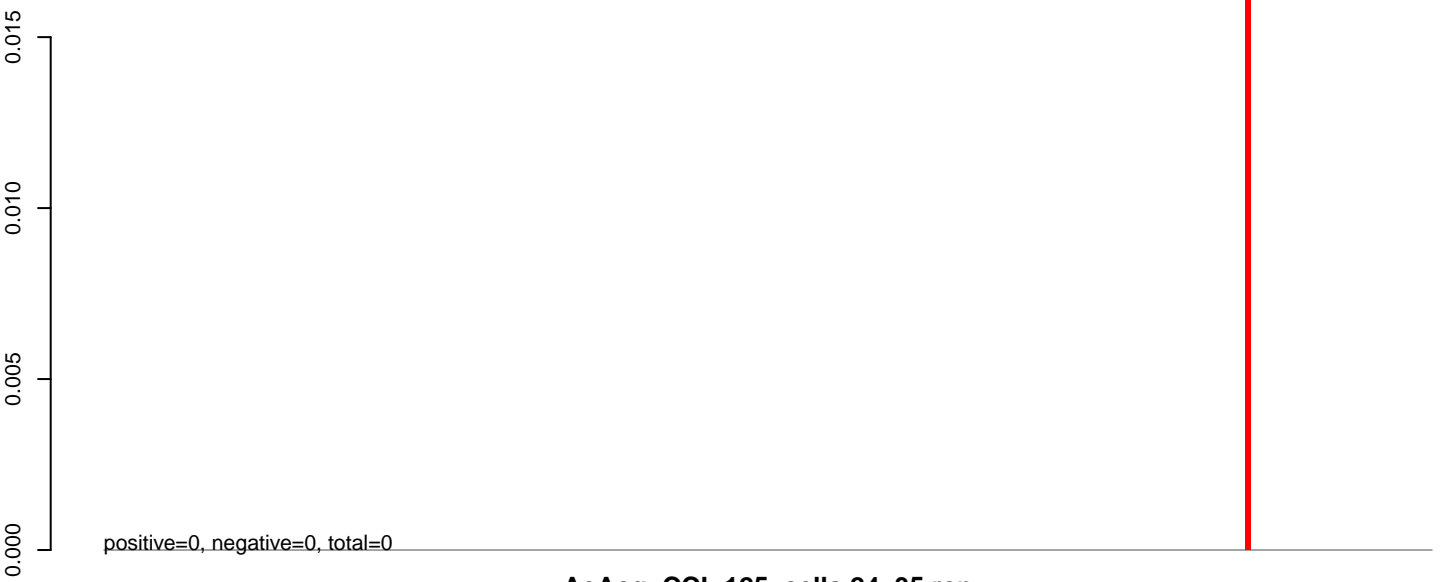


AeAeg_CCL.125_cells.rep

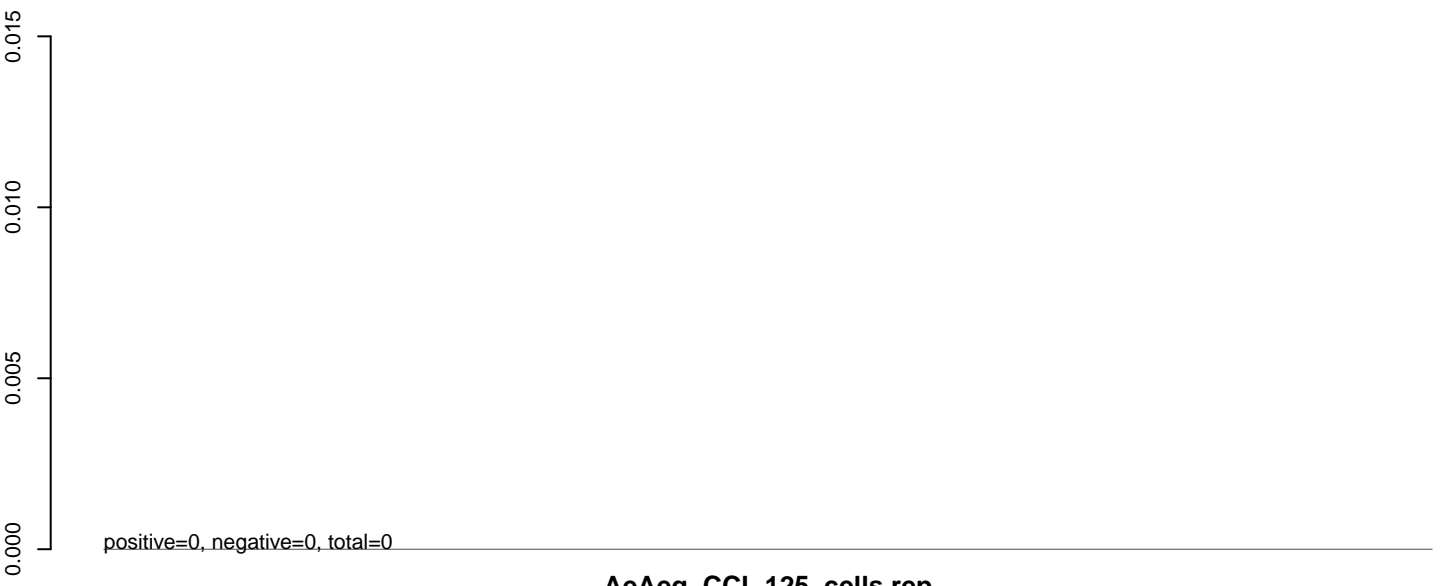


50, length=10968, gene=NC_068463.1-Nkolbisson_virus_nucleoprotein_phosphoprotein_matrix_glycoprotein_and_polymerase_genes:1-10968

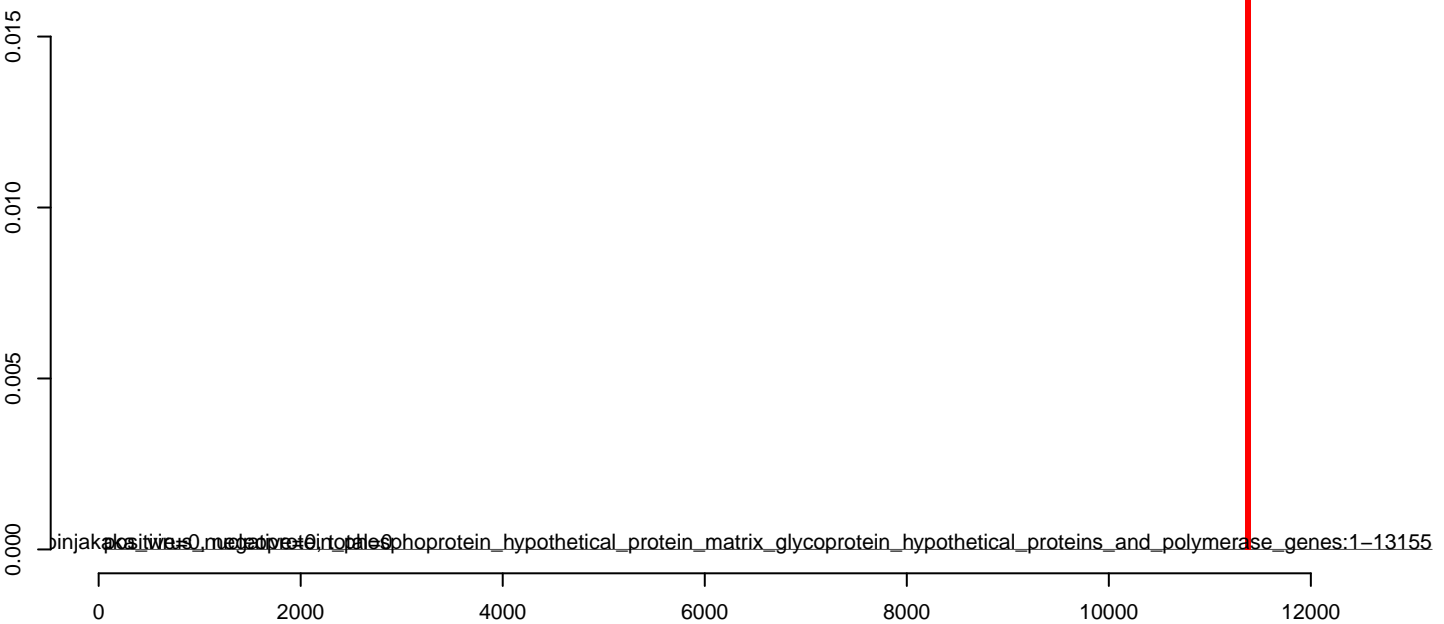
AeAeg_CCL.125_cells.18_23.rep



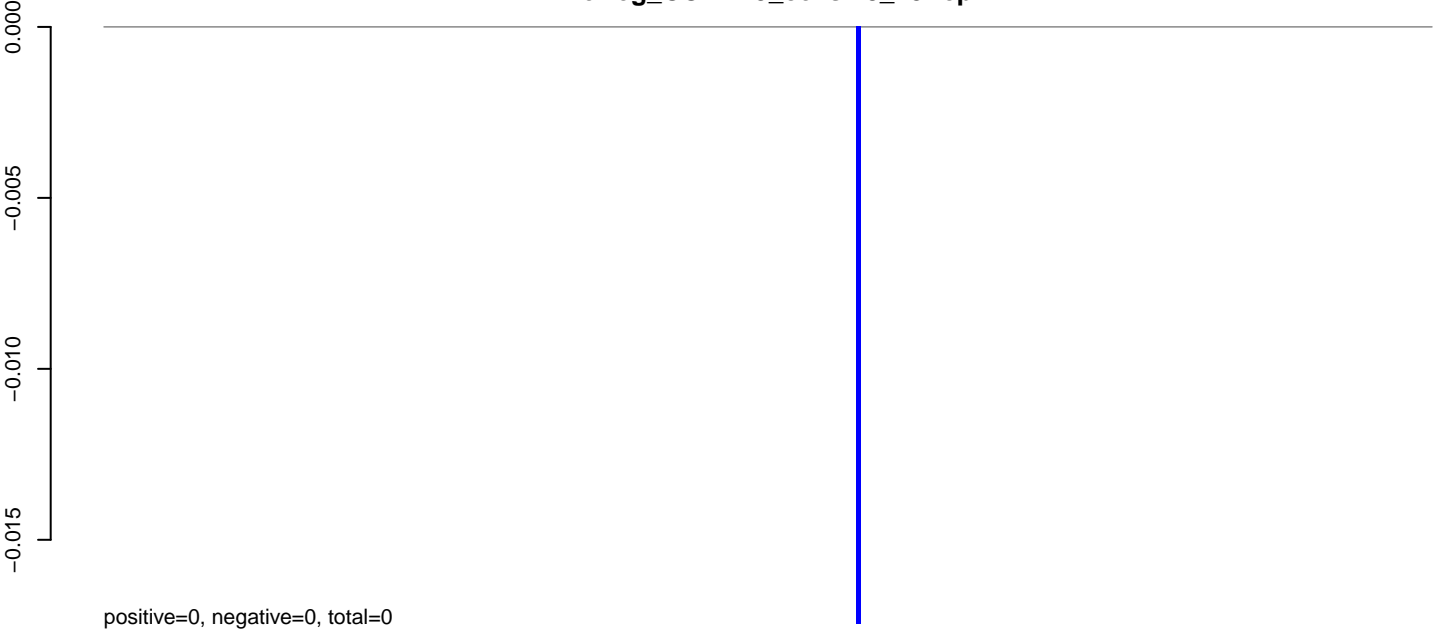
AeAeg_CCL.125_cells.24_35.rep



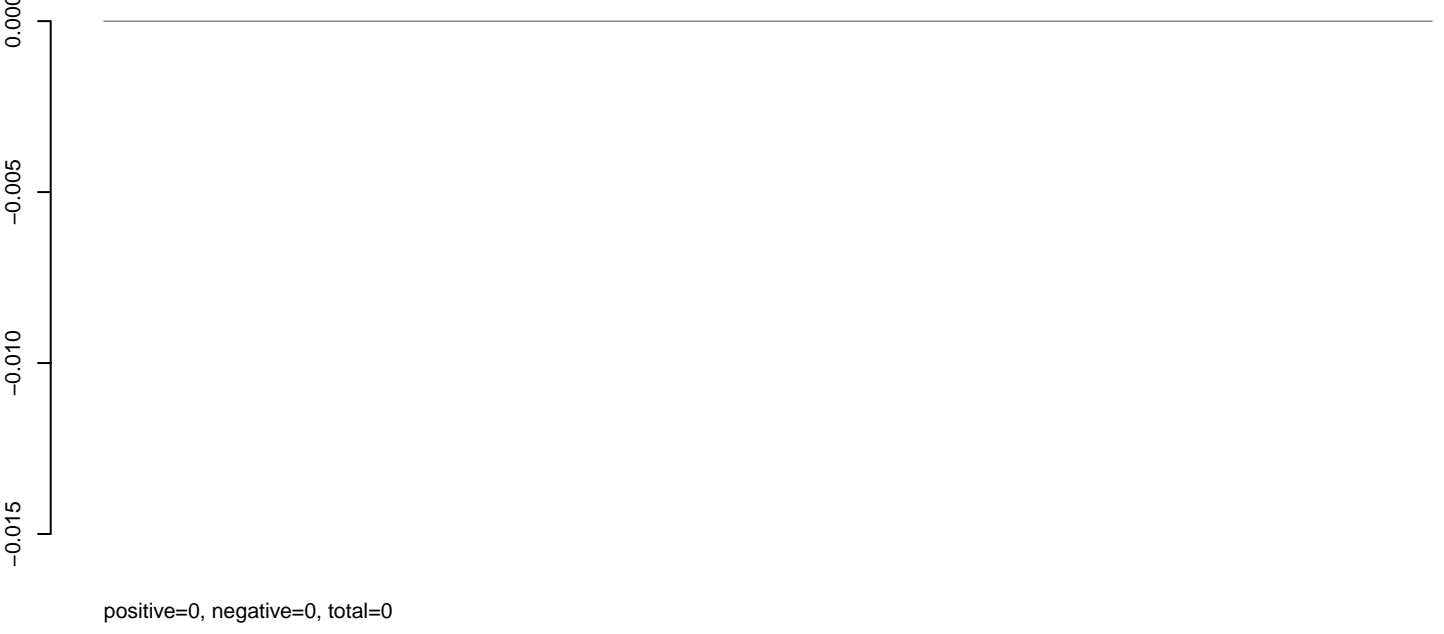
AeAeg_CCL.125_cells.rep



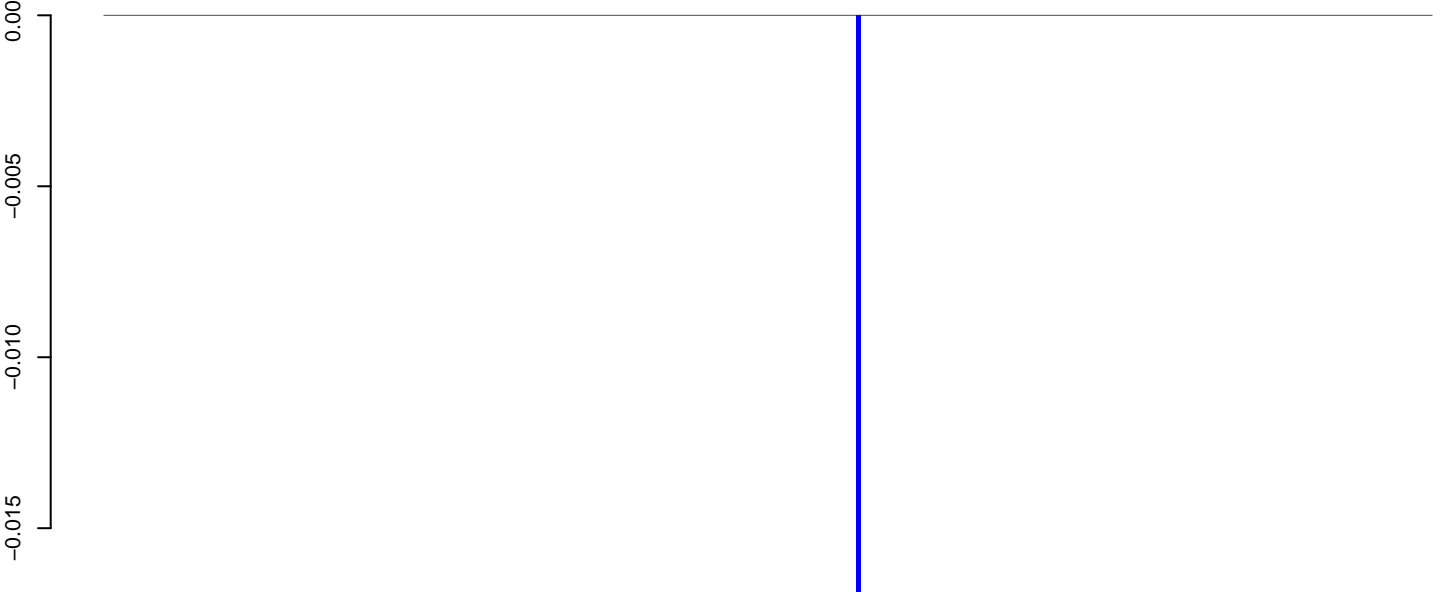
AeAeg_CCL.125_cells.18_23.rep



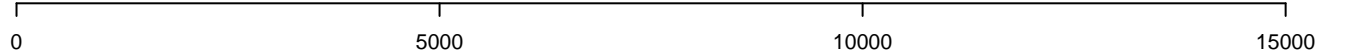
AeAeg_CCL.125_cells.24_35.rep



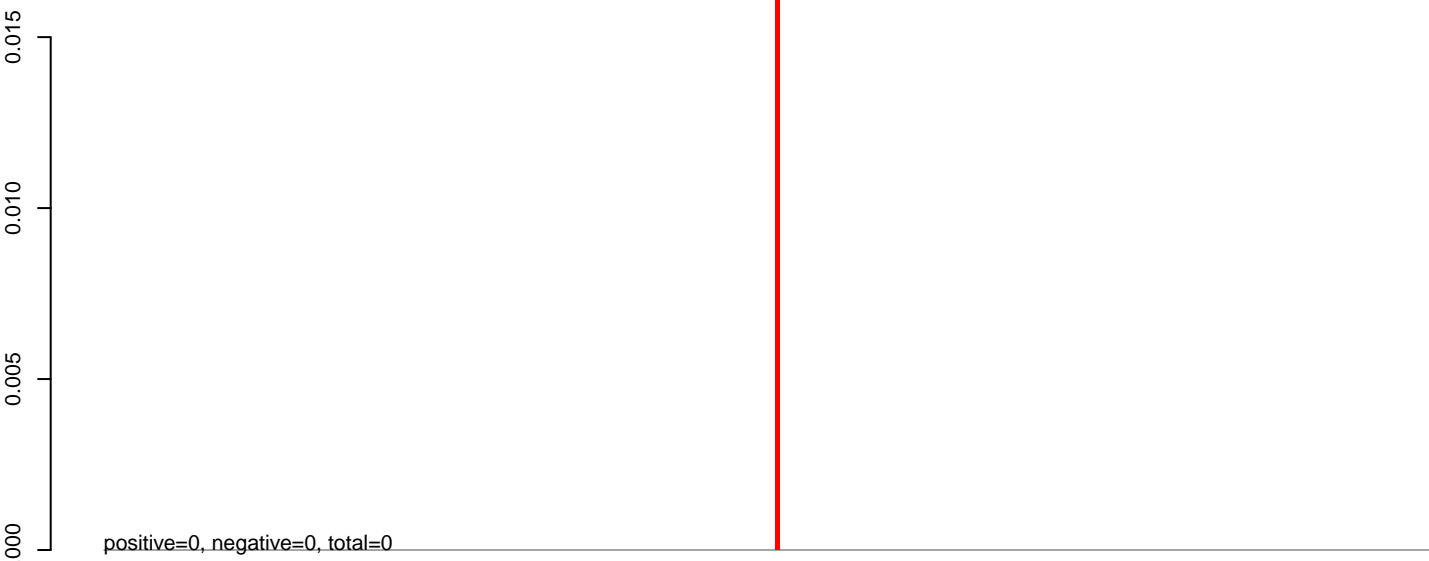
AeAeg_CCL.125_cells.rep



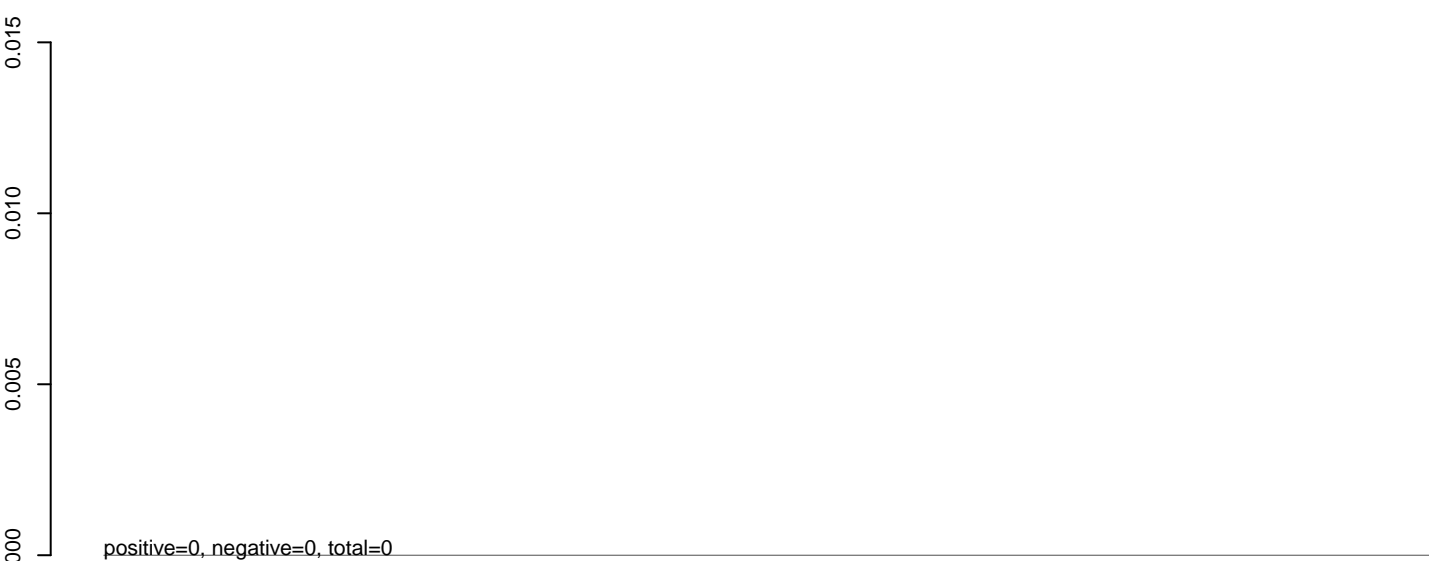
rotp...positive=0, negative=0, total=0..._proteins_matrix_hypothetical_proteins_glycoprotein_hypothetical_proteins_and_polymerase_genes:1-15721



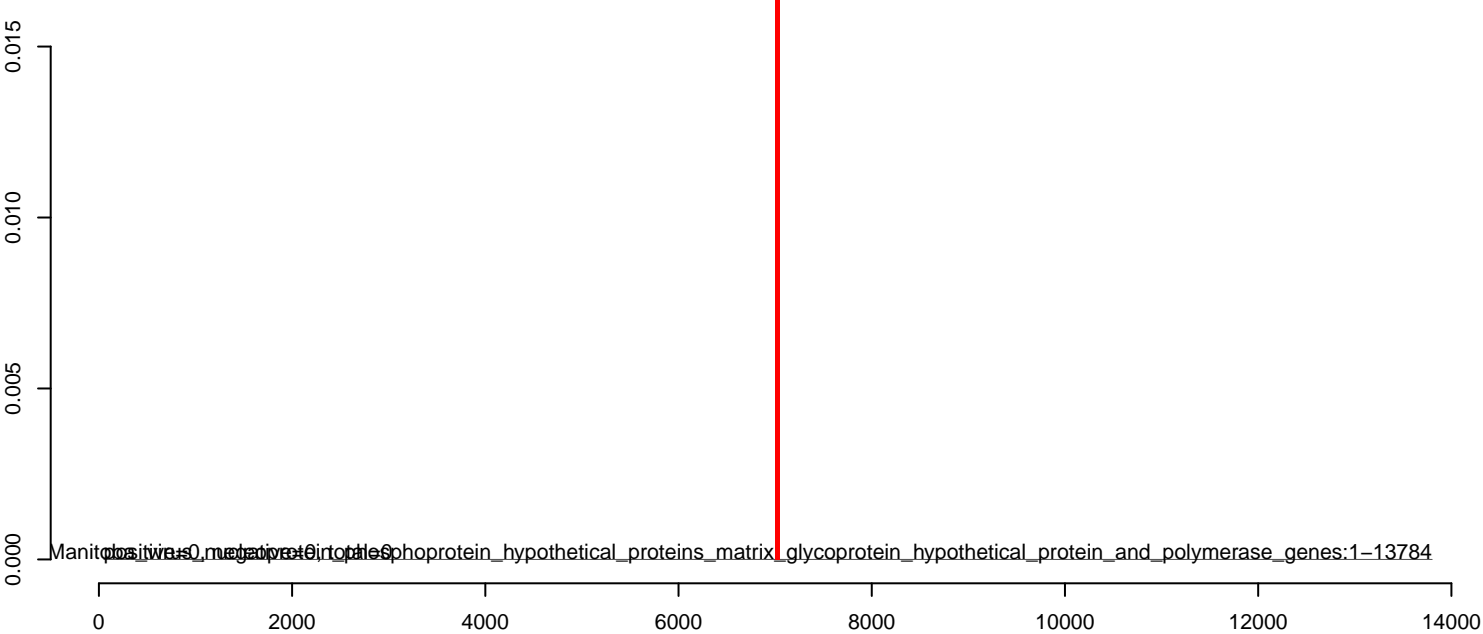
AeAeg_CCL.125_cells.18_23.rep



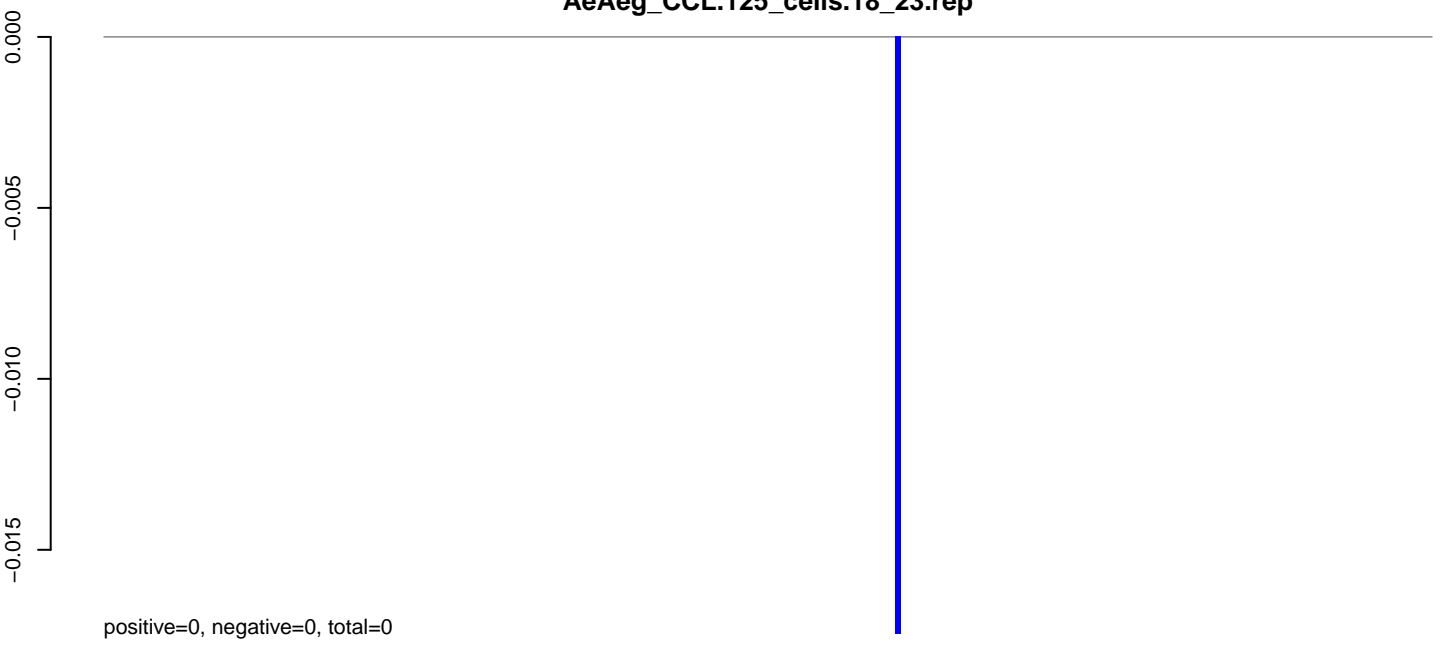
AeAeg_CCL.125_cells.24_35.rep



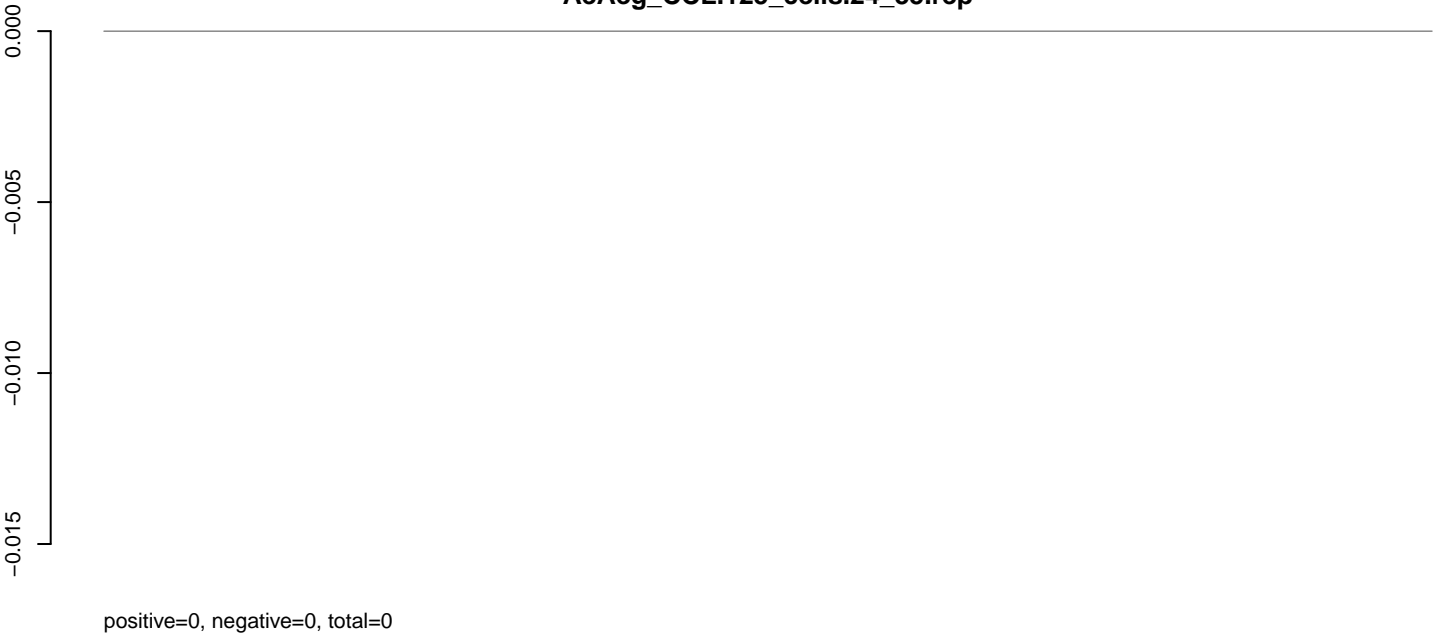
AeAeg_CCL.125_cells.rep



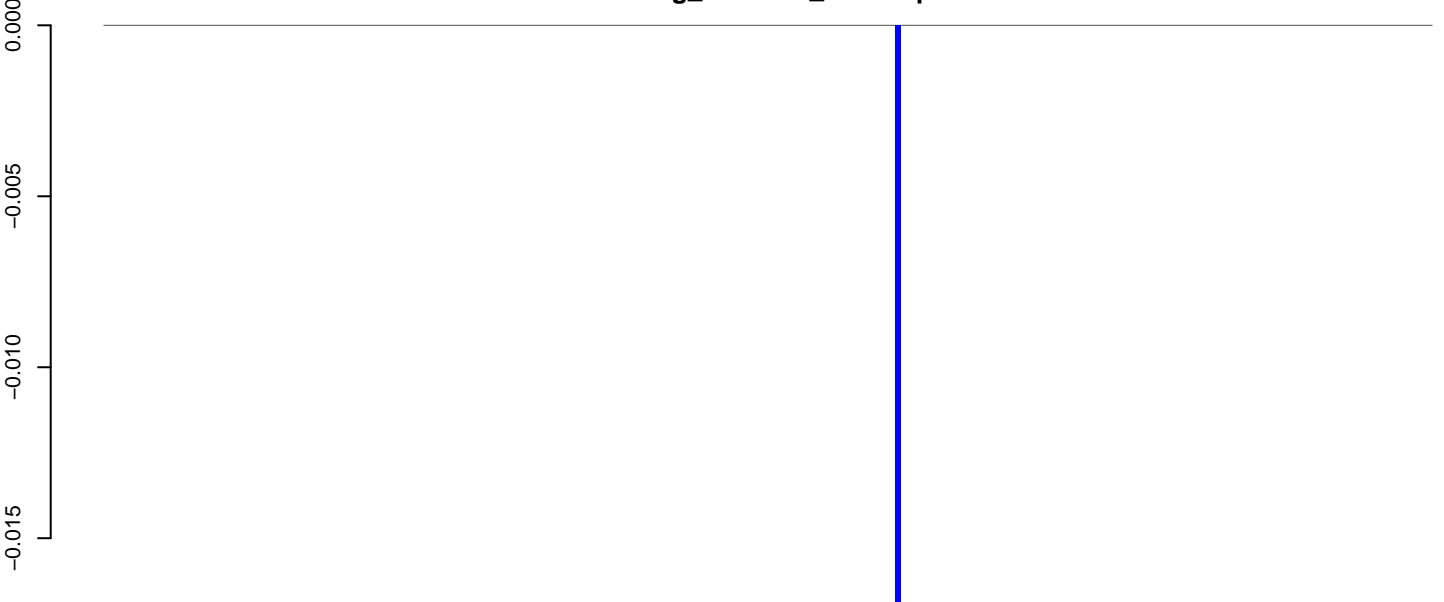
AeAeg_CCL.125_cells.18_23.rep



AeAeg_CCL.125_cells.24_35.rep



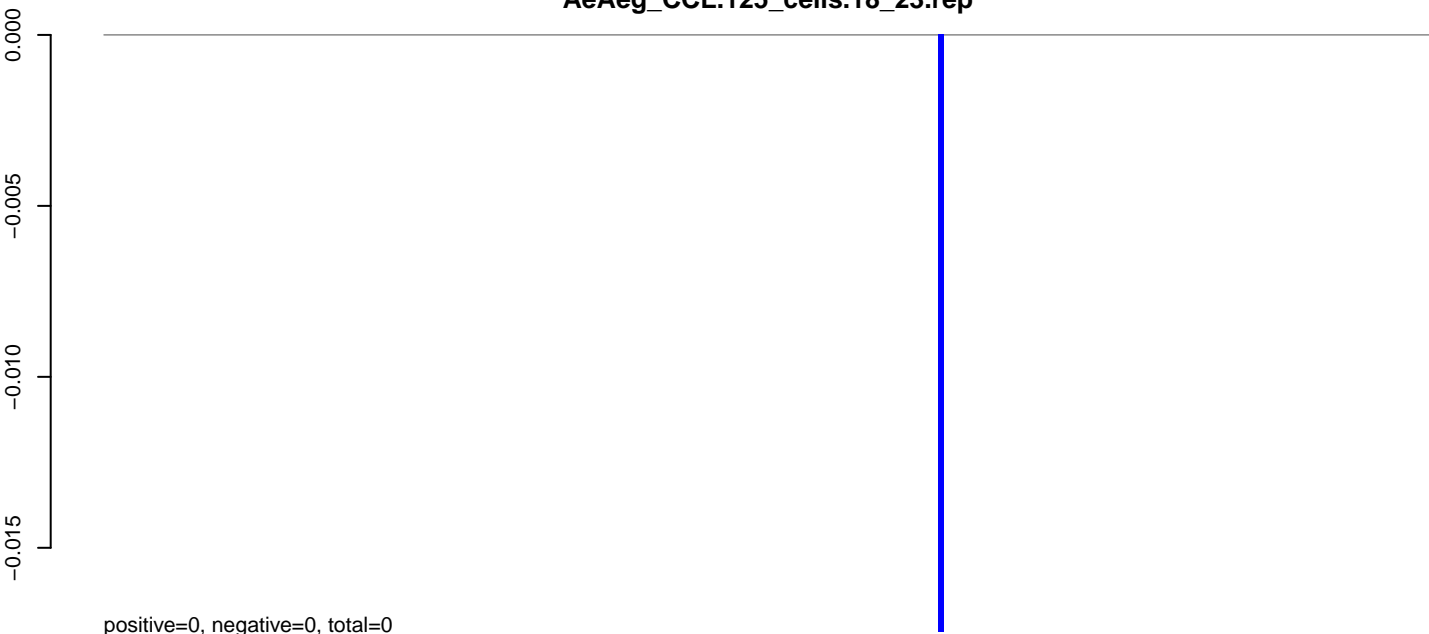
AeAeg_CCL.125_cells.rep



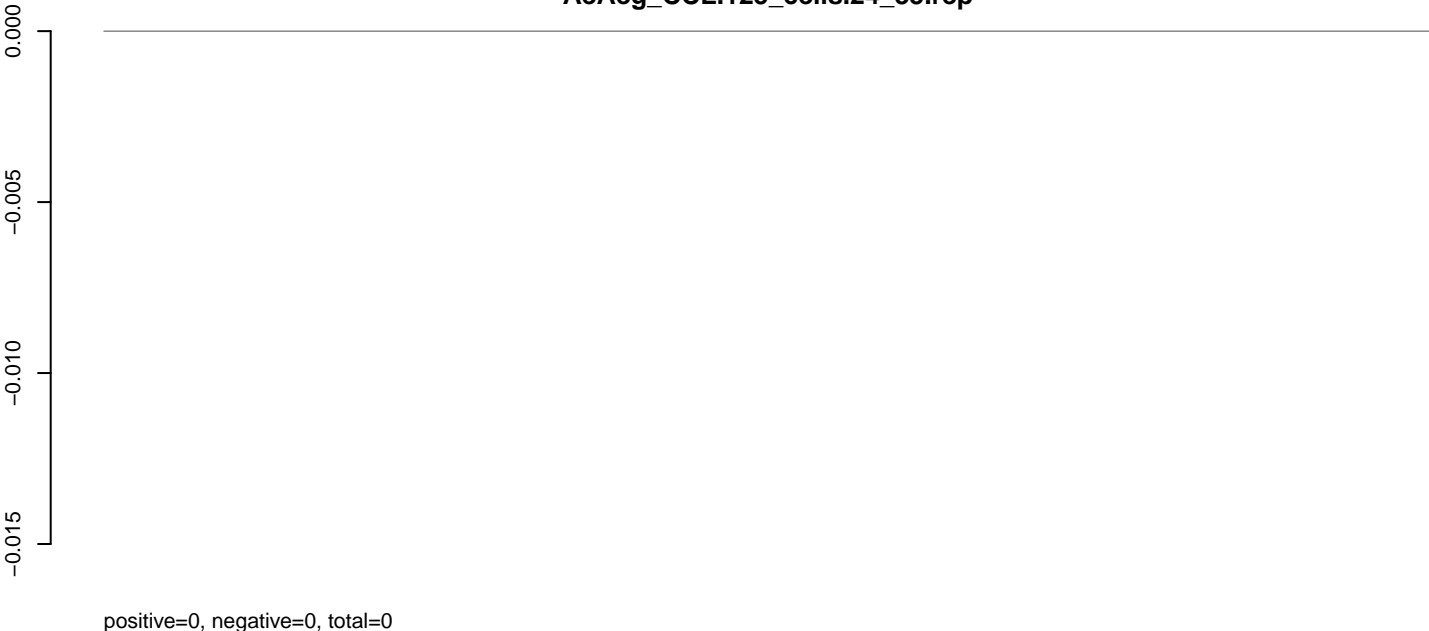
1, virus_G10_004580, nucleoprotein_phosphoprotein_matrix_glycoprotein_hypothetical_proteins_and_polymerase_genes:1-13294

0 2000 4000 6000 8000 10000 12000

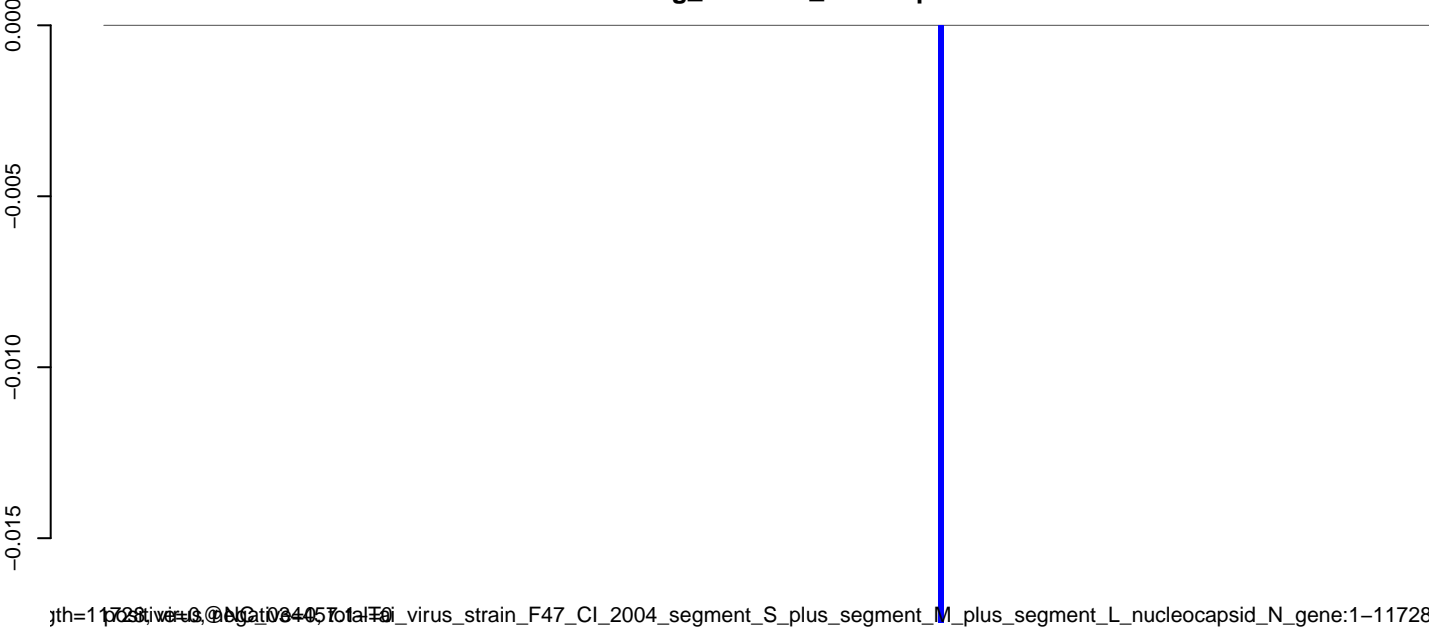
AeAeg_CCL.125_cells.18_23.rep



AeAeg_CCL.125_cells.24_35.rep



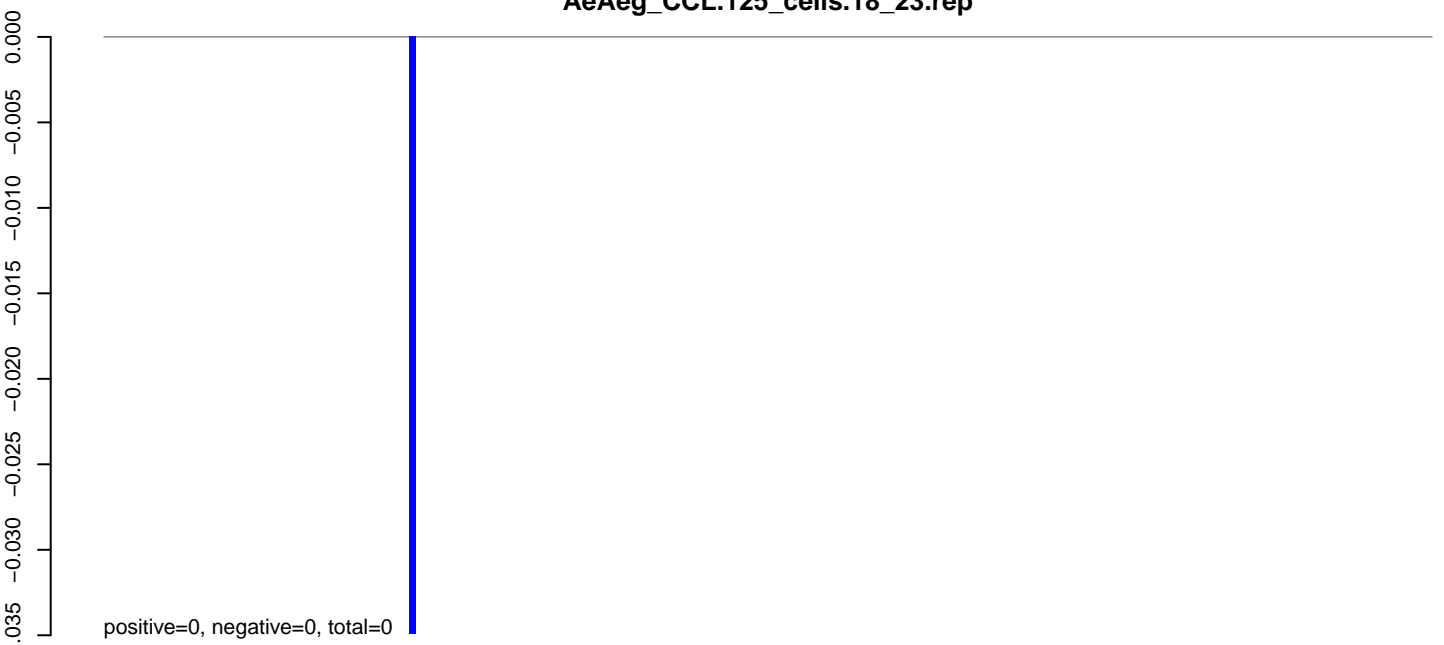
AeAeg_CCL.125_cells.rep



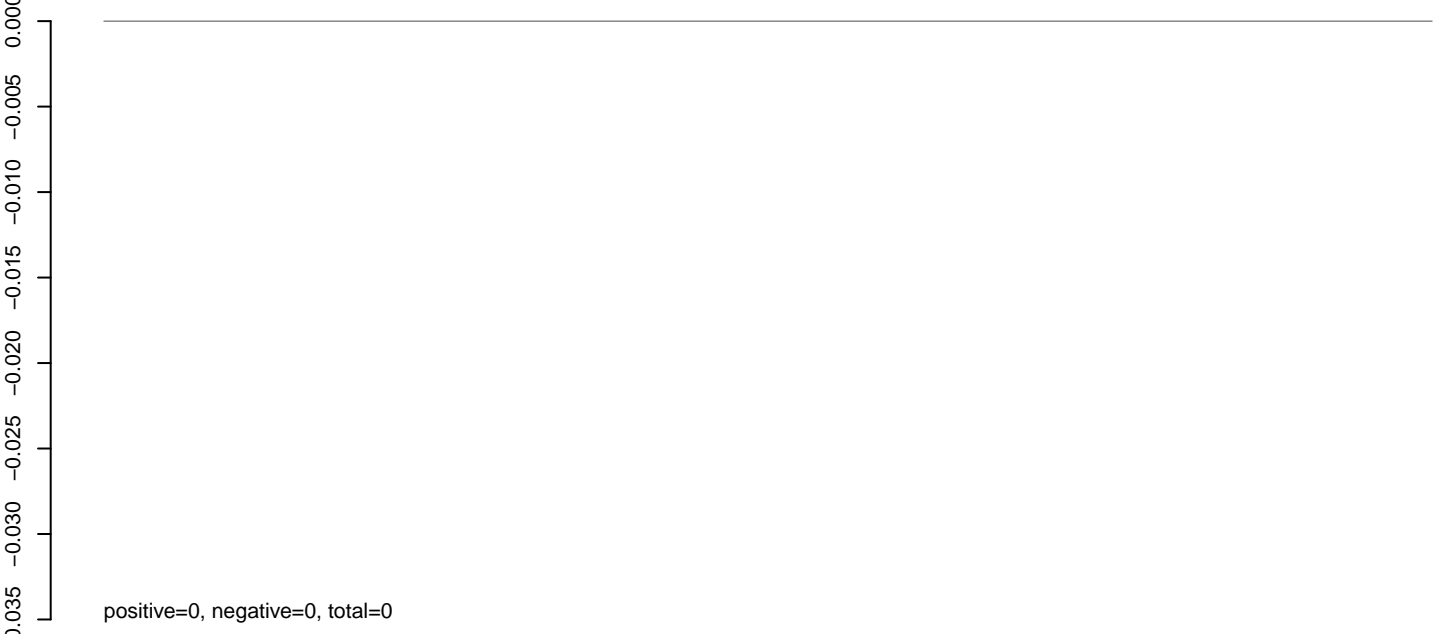
path=11728_virus_01020340570140_virus_strain_F47_CI_2004_segment_S_plus_segment_M_plus_segment_L_nucleocapsid_N_gene:1-11728

0 2000 4000 6000 8000 10000 12000

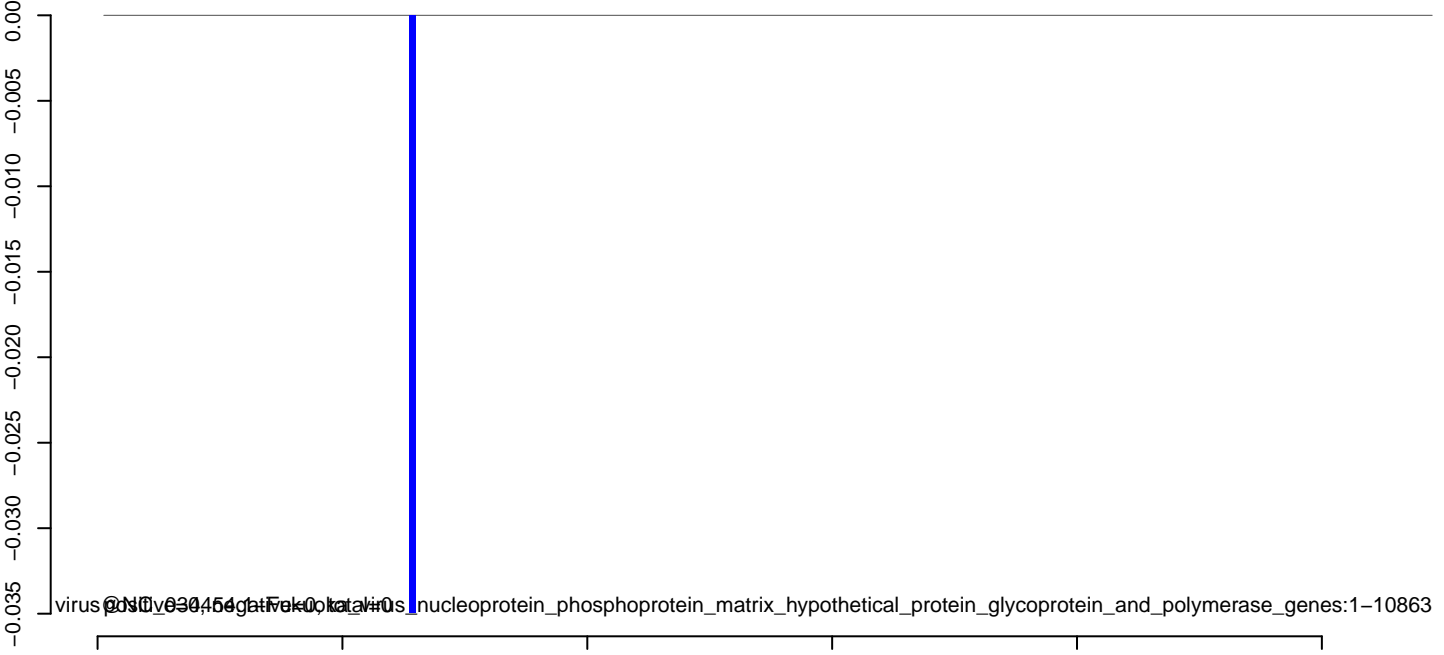
AeAeg_CCL.125_cells.18_23.rep



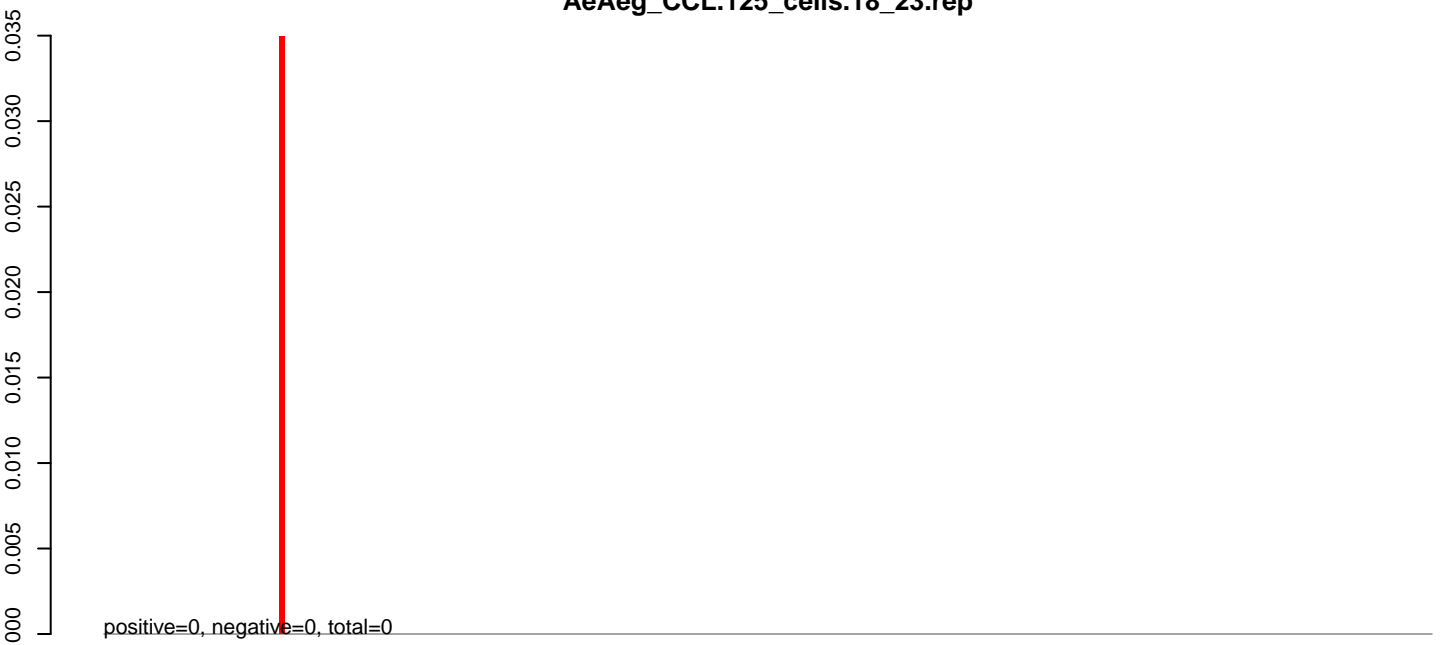
AeAeg_CCL.125_cells.24_35.rep



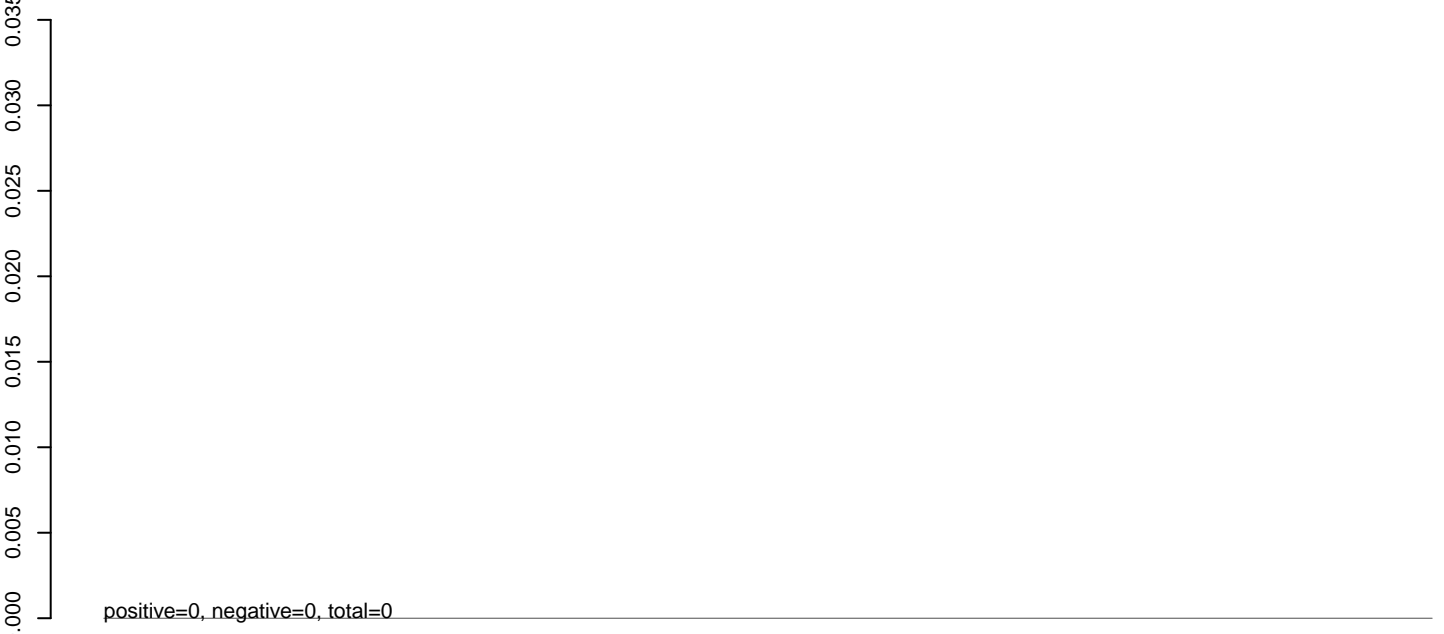
AeAeg_CCL.125_cells.rep



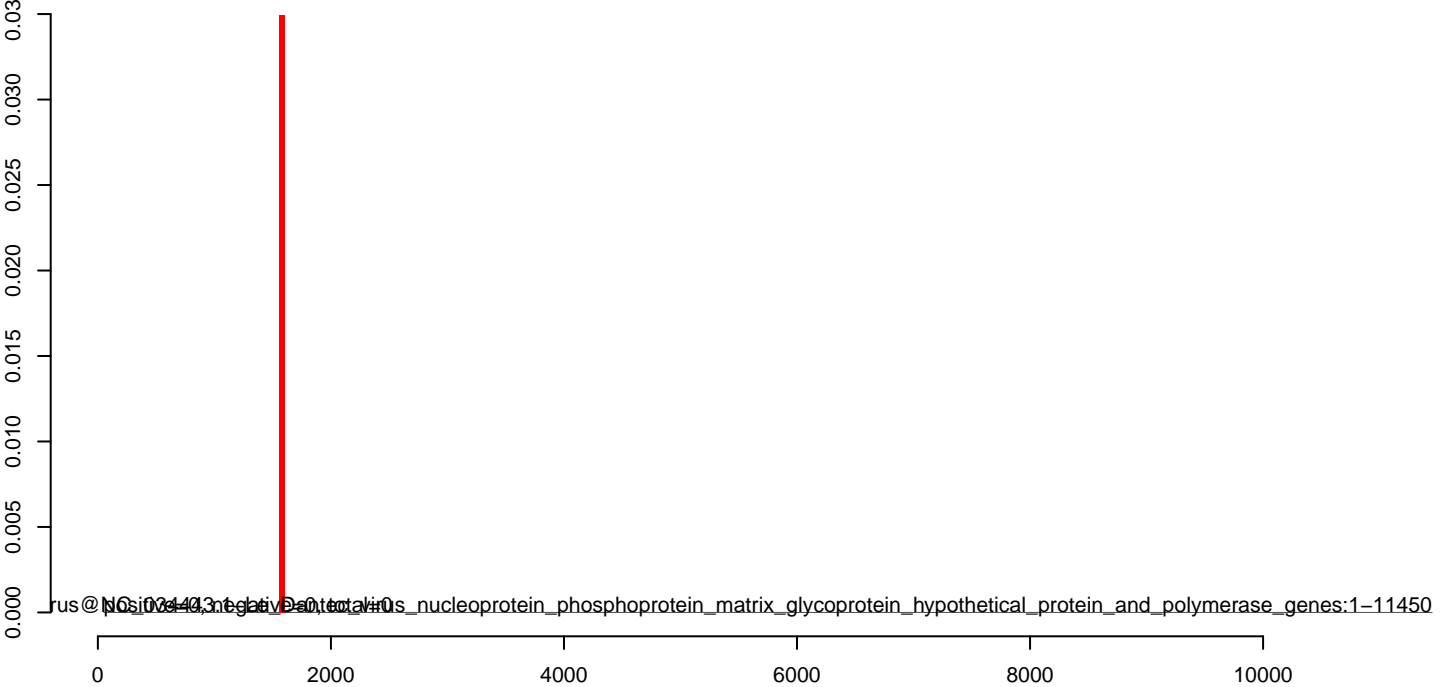
AeAeg_CCL.125_cells.18_23.rep



AeAeg_CCL.125_cells.24_35.rep

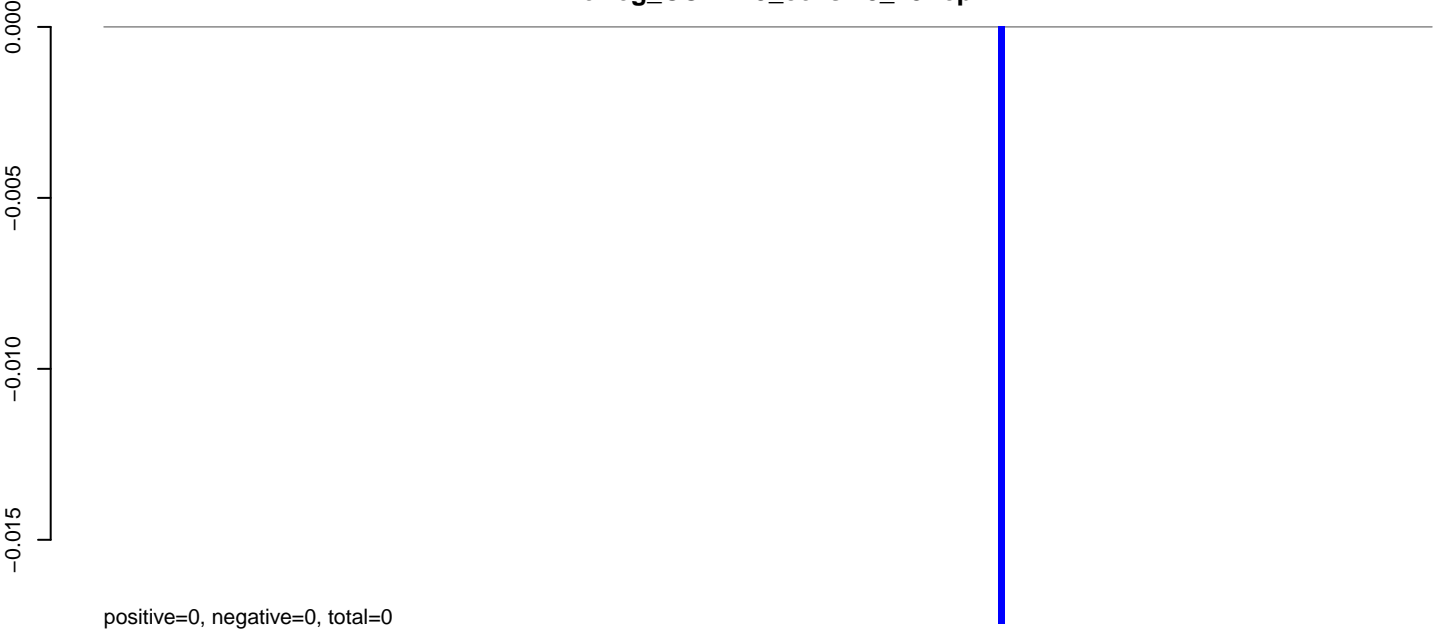


AeAeg_CCL.125_cells.rep

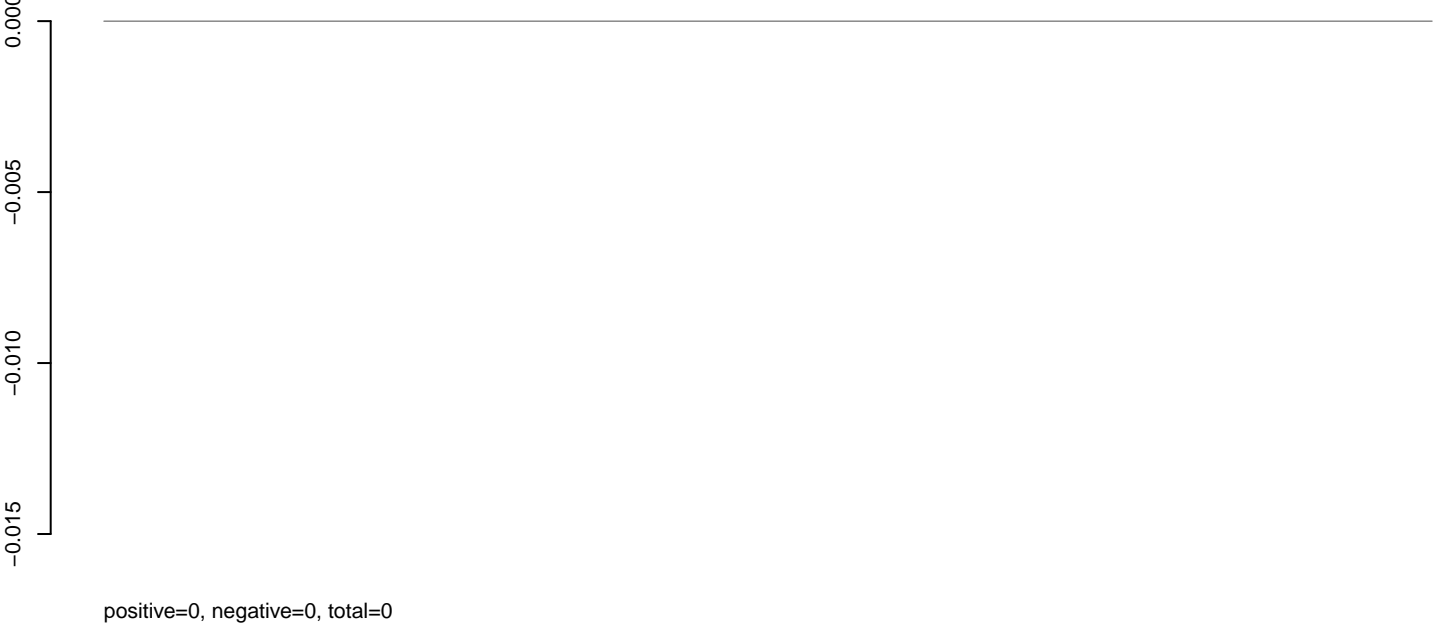


NC_024403.1:1-11450:1 nucleoprotein_phosphoprotein_matrix_glycoprotein_hypothetical_protein_and_polymerase_genes:1-11450

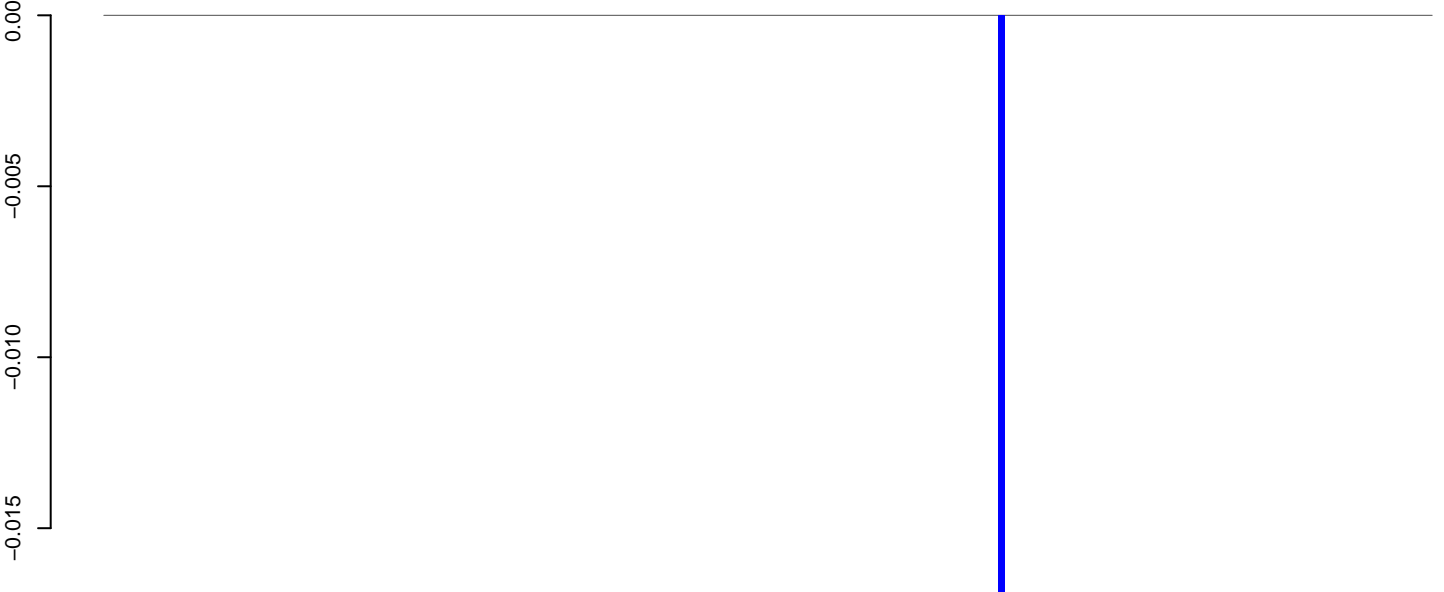
AeAeg_CCL.125_cells.18_23.rep



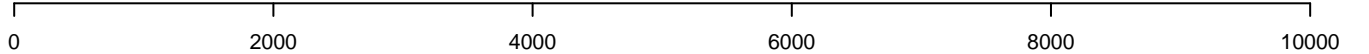
AeAeg_CCL.125_cells.24_35.rep



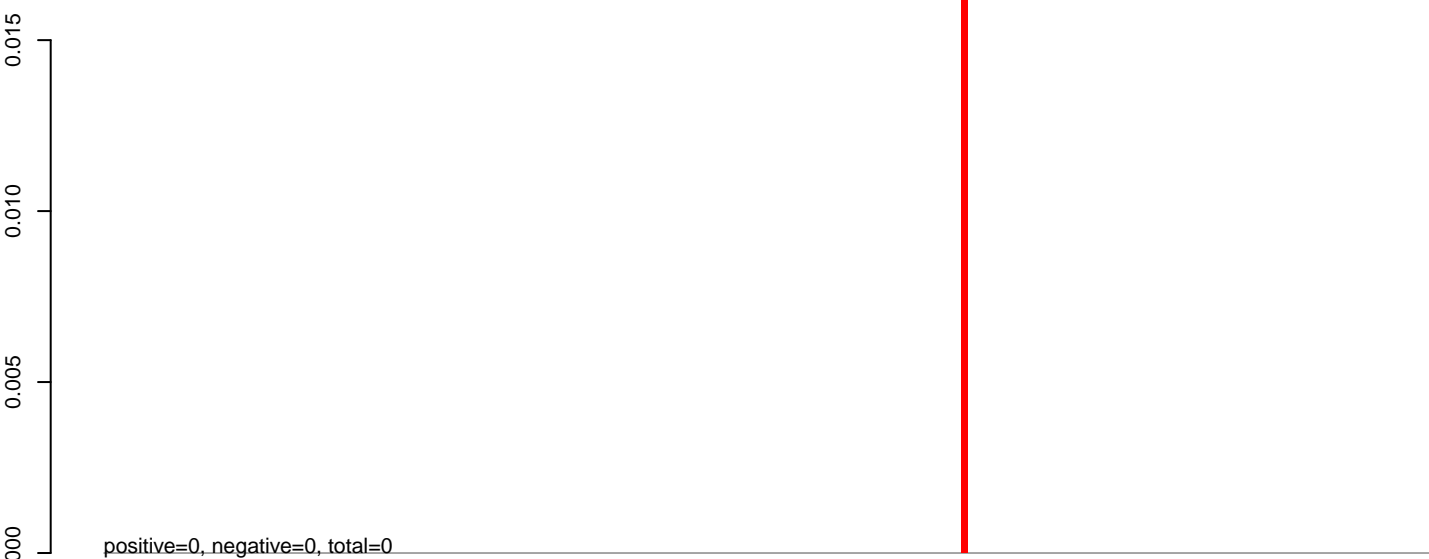
AeAeg_CCL.125_cells.rep



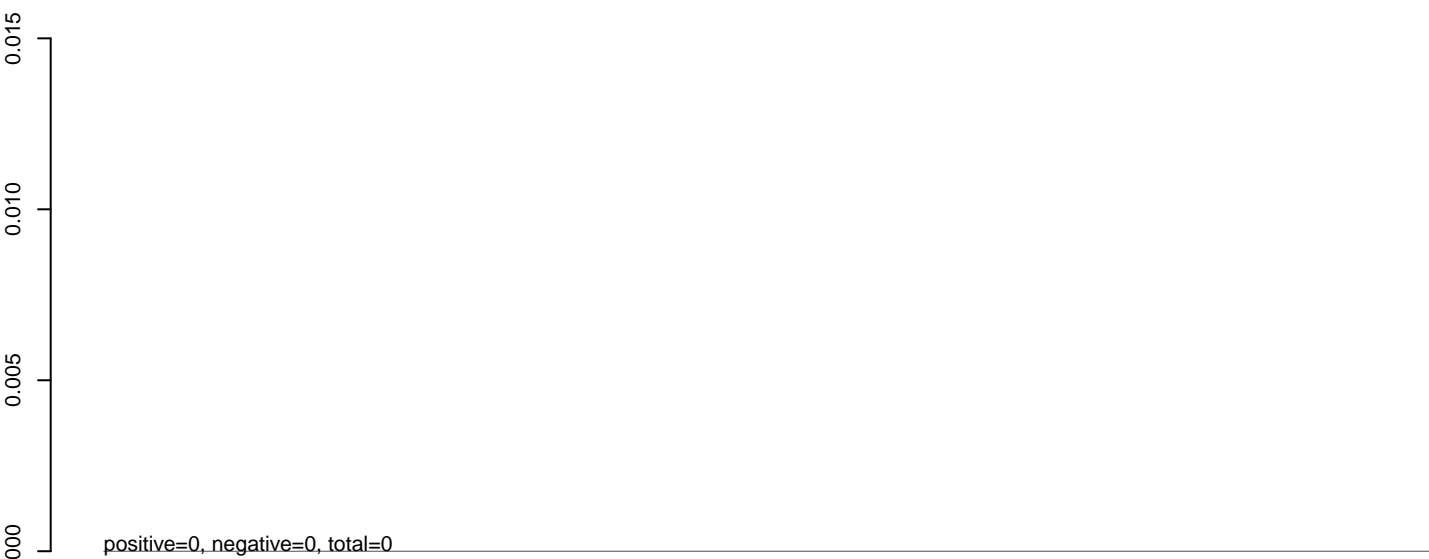
Window=6, index=6, positive=0, negative=0, total=0, length=10293, virus@NC_034018.1-Yaounde_virus_strain_Dak_Ar_Y276_polyprotein_gene:1-10293



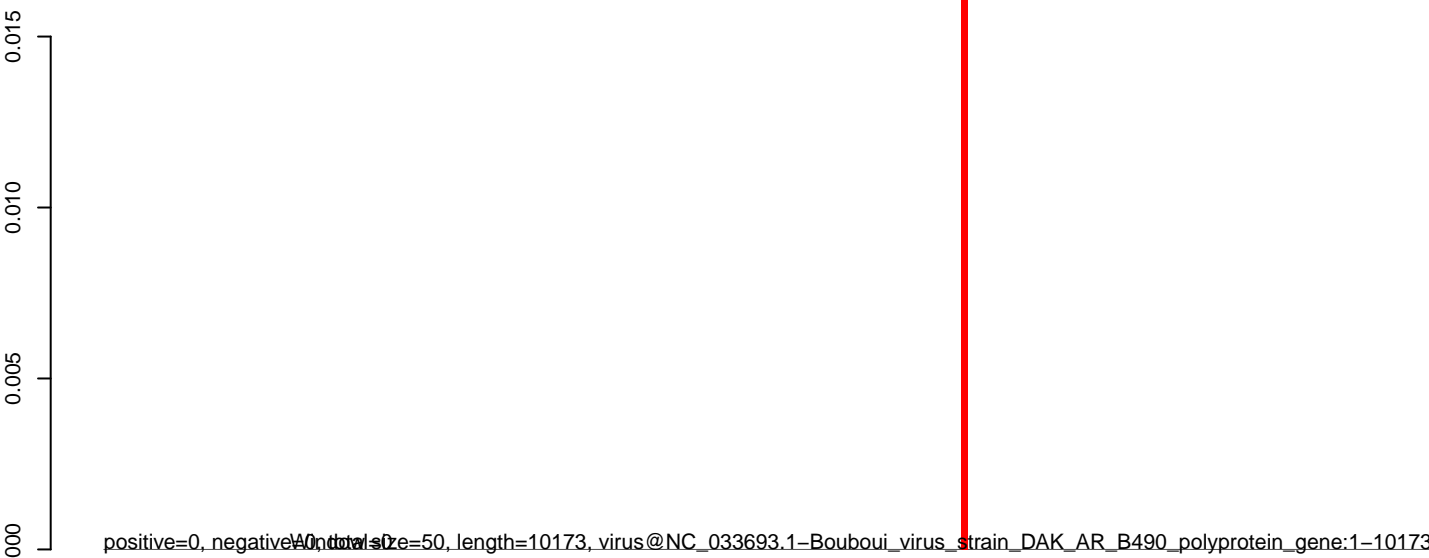
AeAeg_CCL.125_cells.18_23.rep



AeAeg_CCL.125_cells.24_35.rep

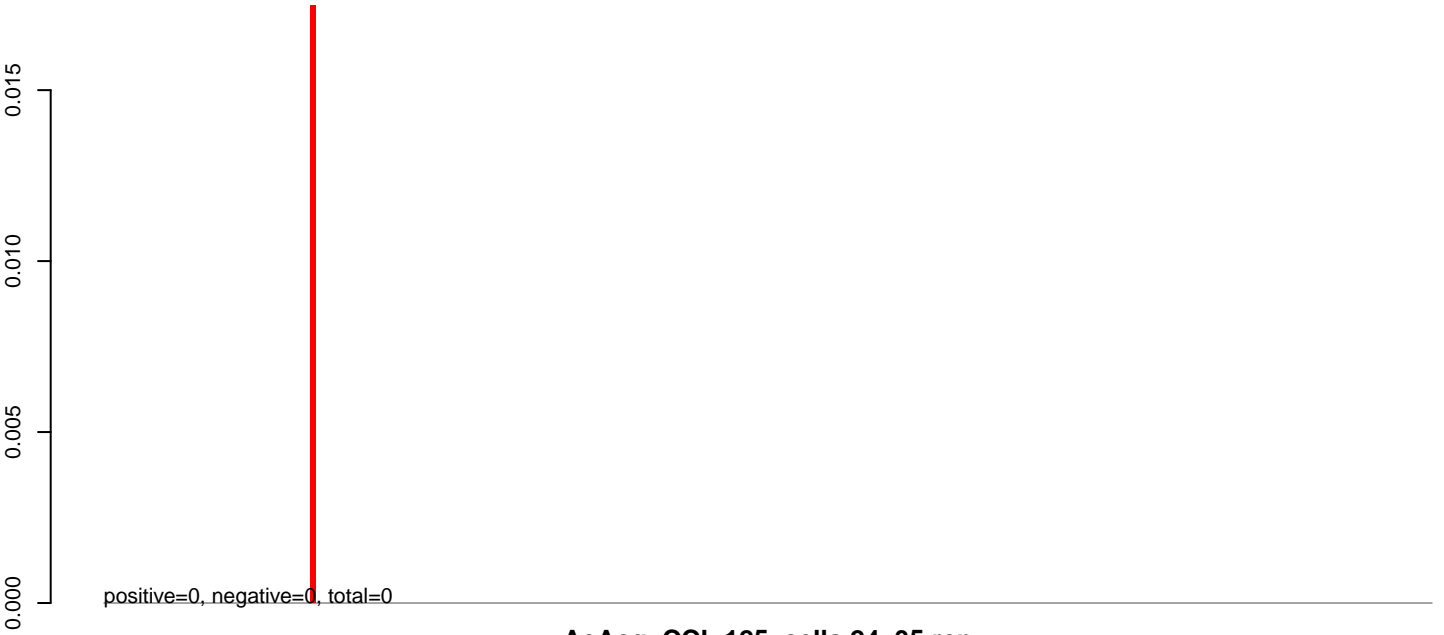


AeAeg_CCL.125_cells.rep

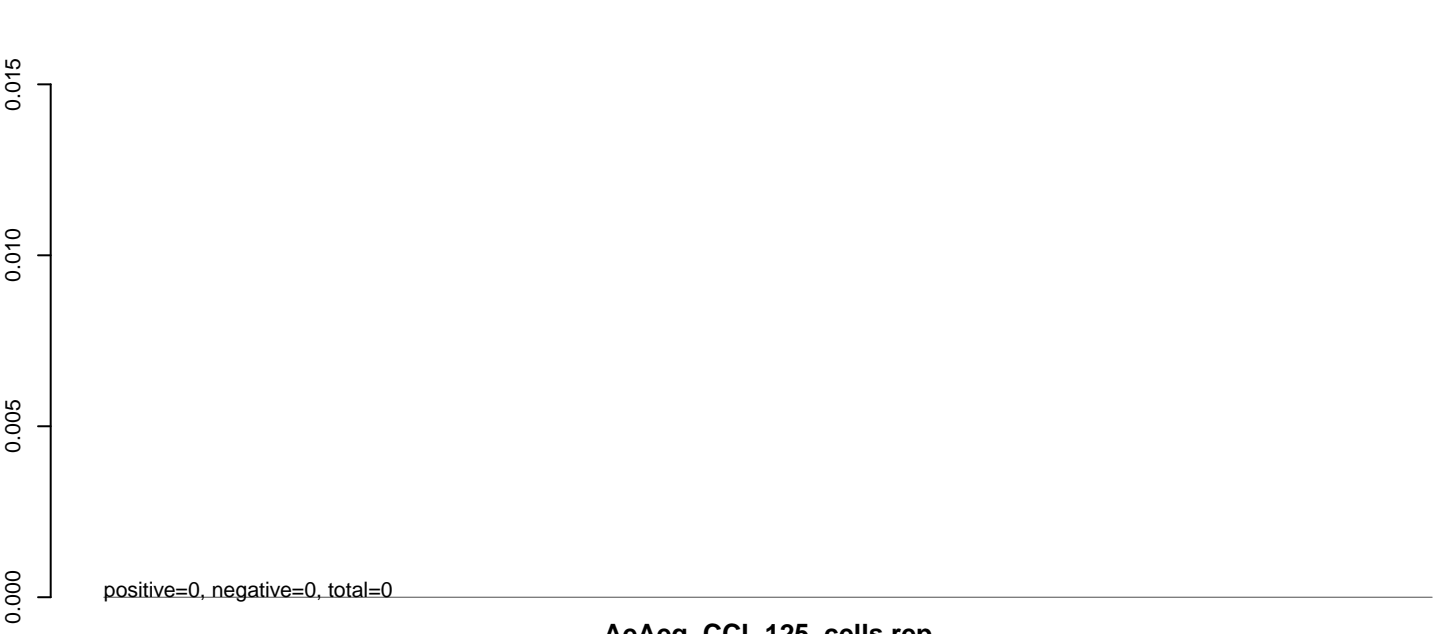


0 2000 4000 6000 8000 10000

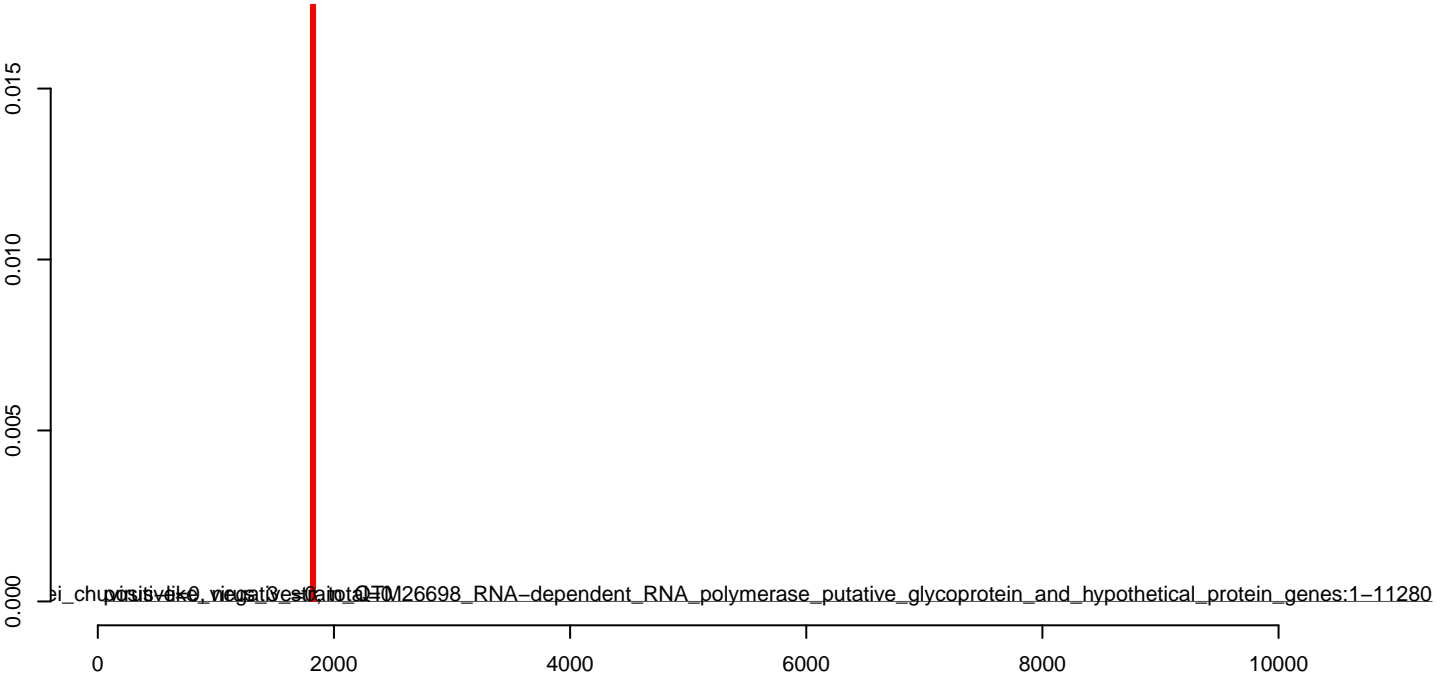
AeAeg_CCL.125_cells.18_23.rep



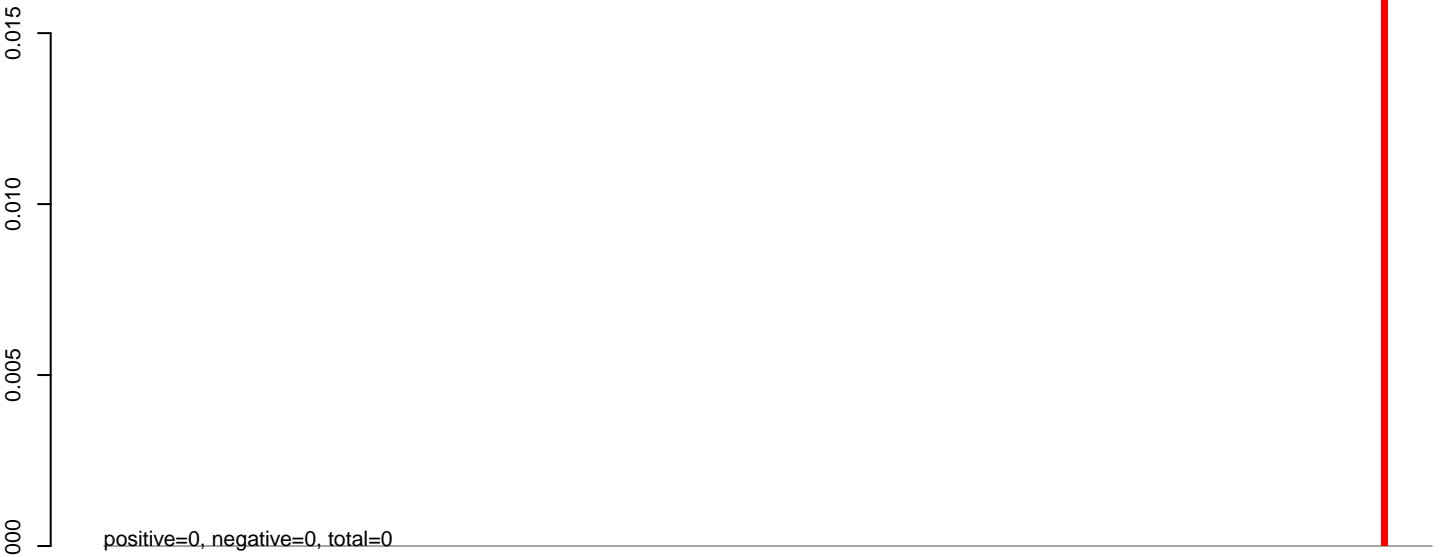
AeAeg_CCL.125_cells.24_35.rep



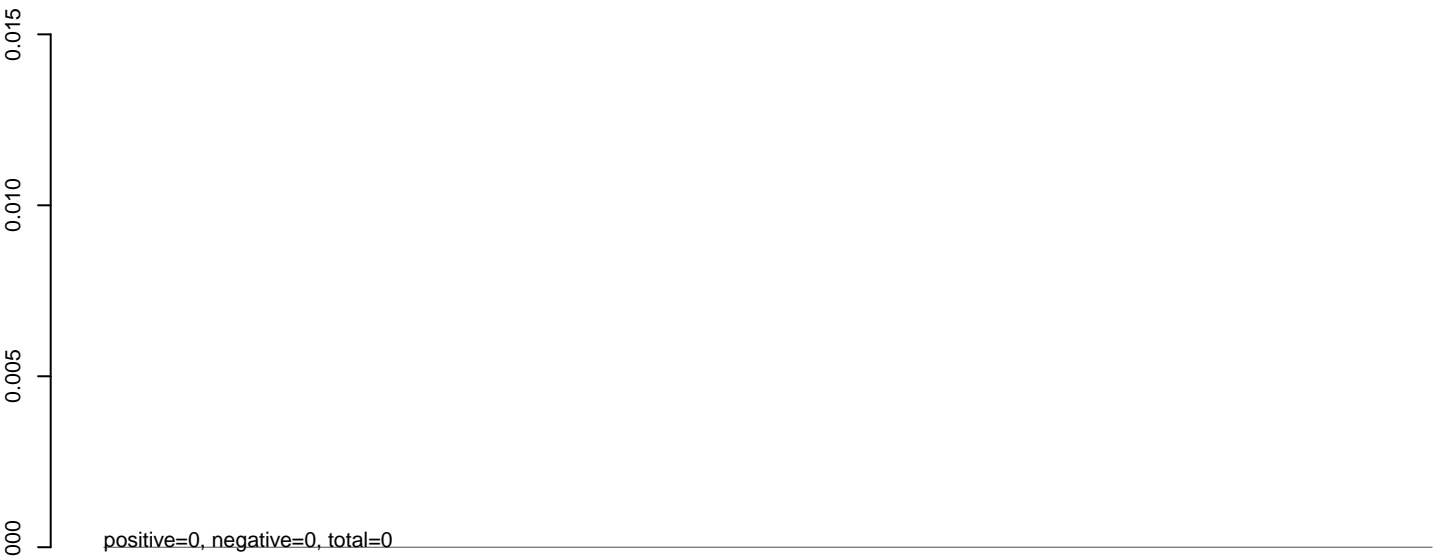
AeAeg_CCL.125_cells.rep



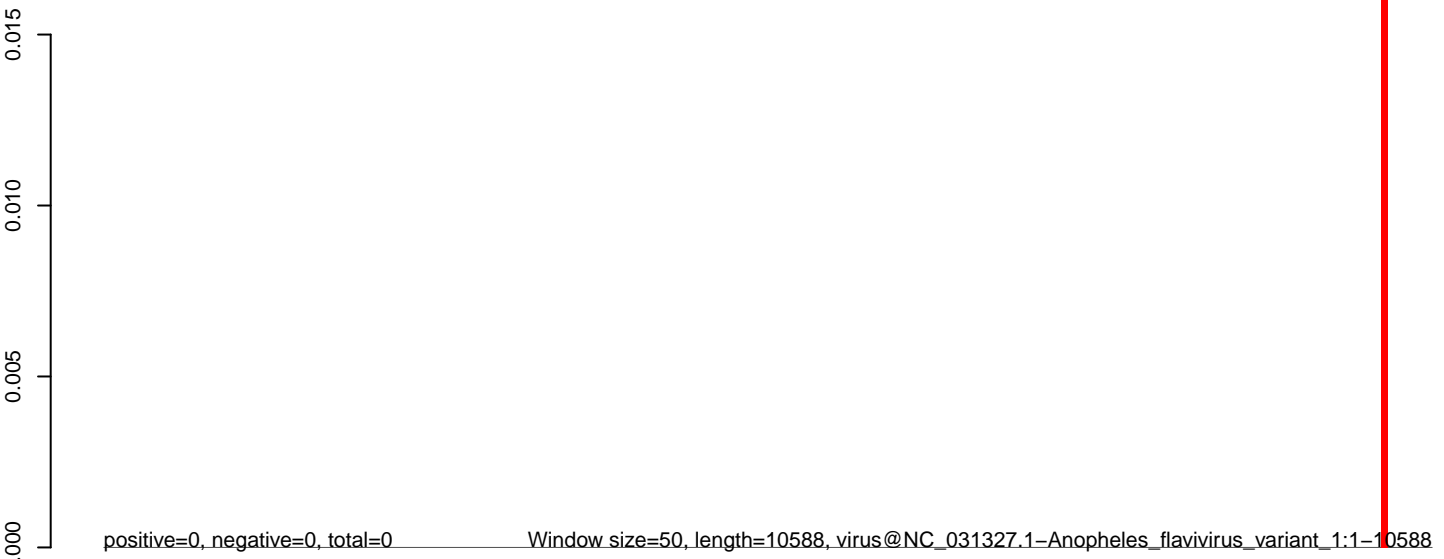
AeAeg_CCL.125_cells.18_23.rep



AeAeg_CCL.125_cells.24_35.rep

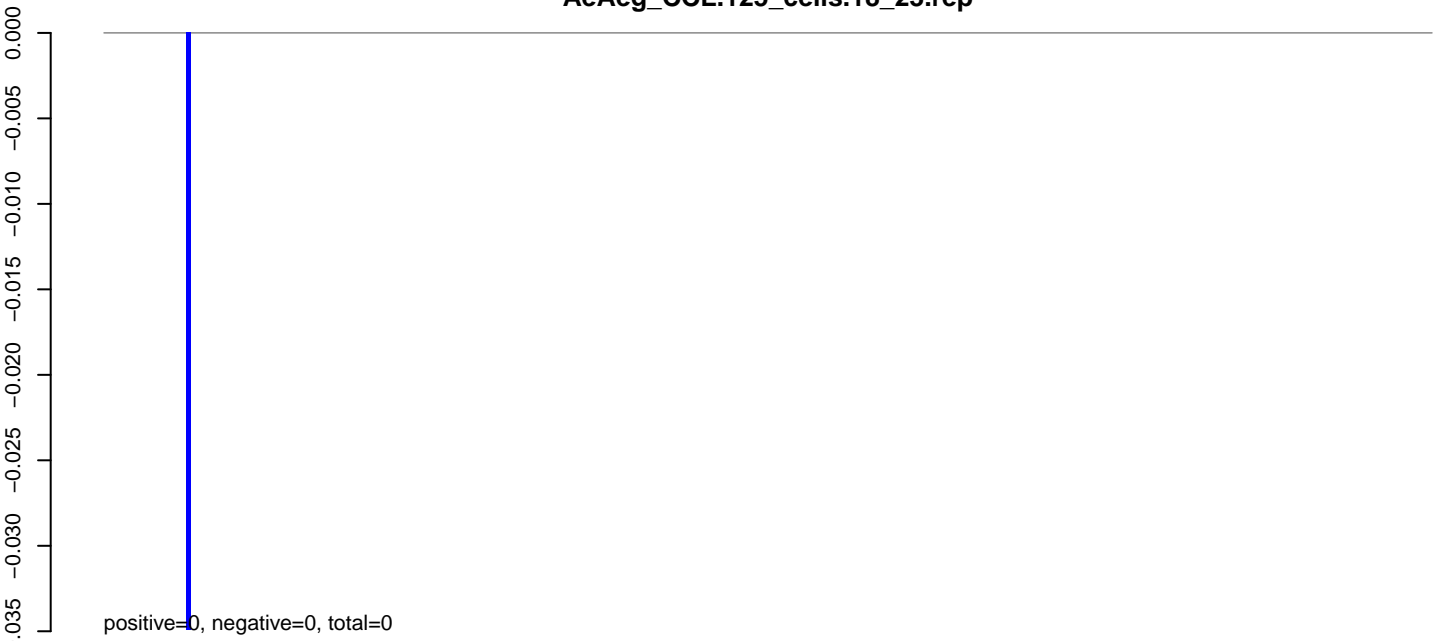


AeAeg_CCL.125_cells.rep

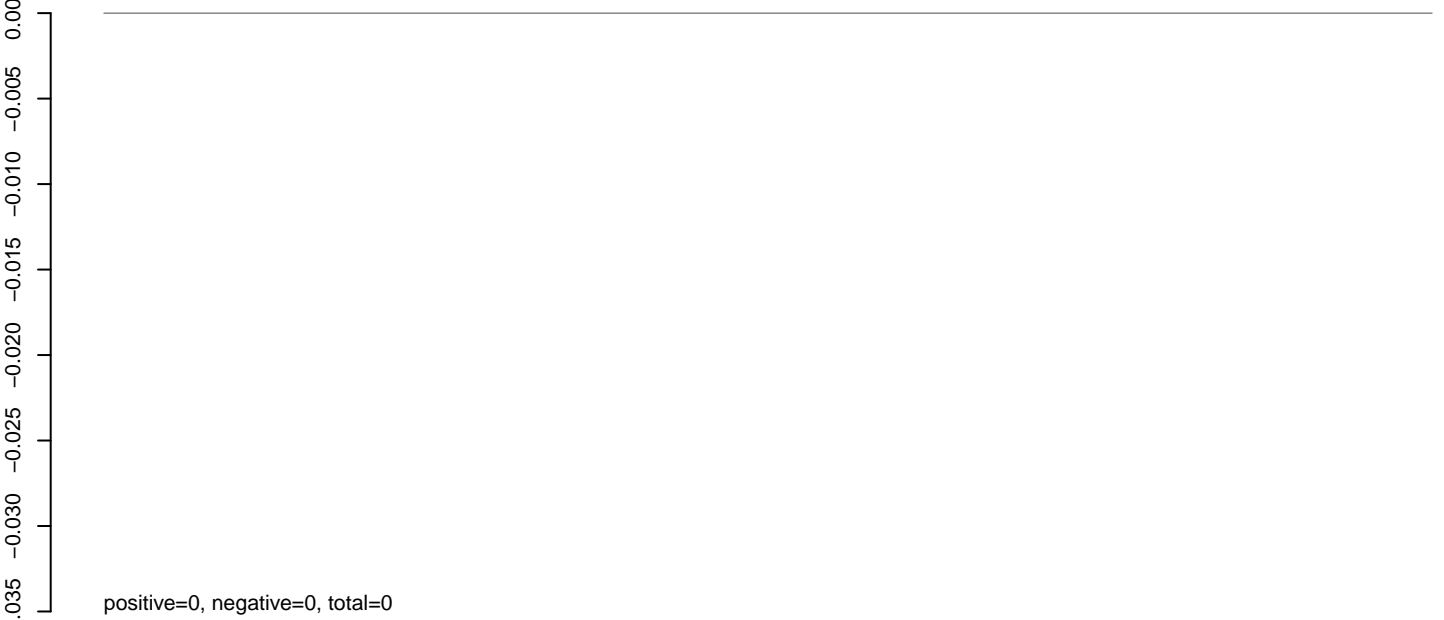


0 2000 4000 6000 8000 10000

AeAeg_CCL.125_cells.18_23.rep



AeAeg_CCL.125_cells.24_35.rep



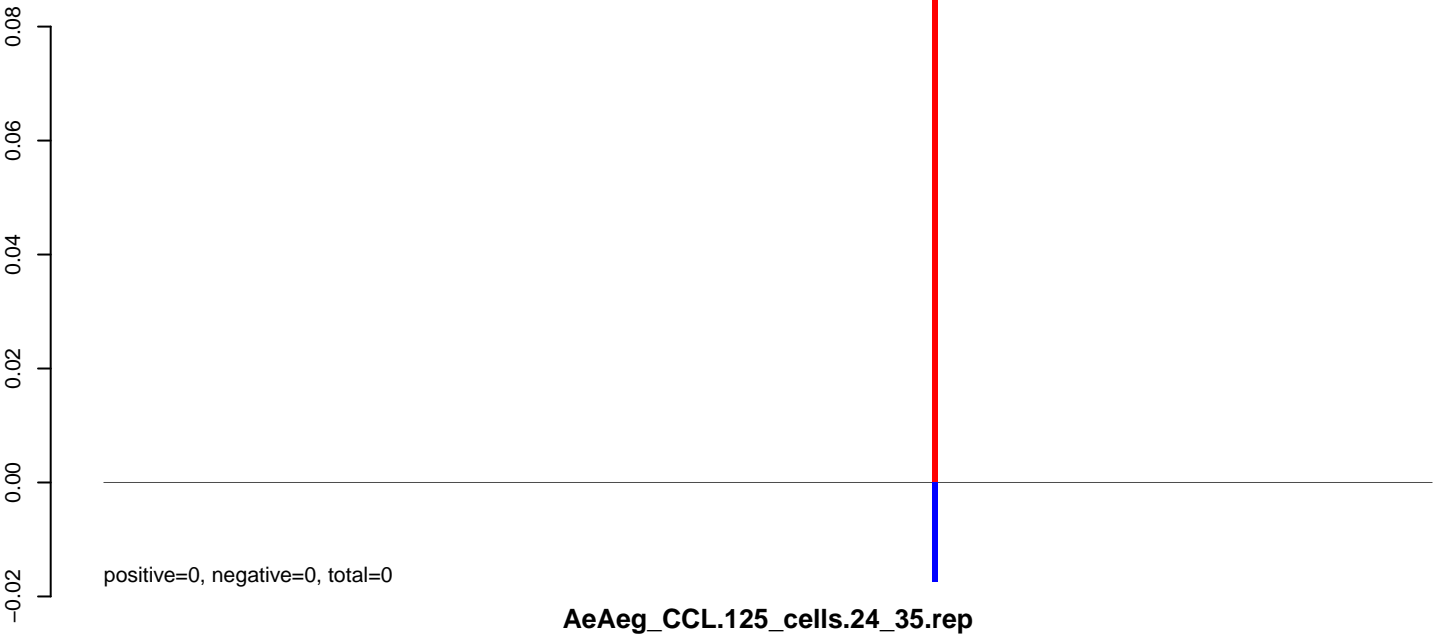
AeAeg_CCL.125_cells.rep



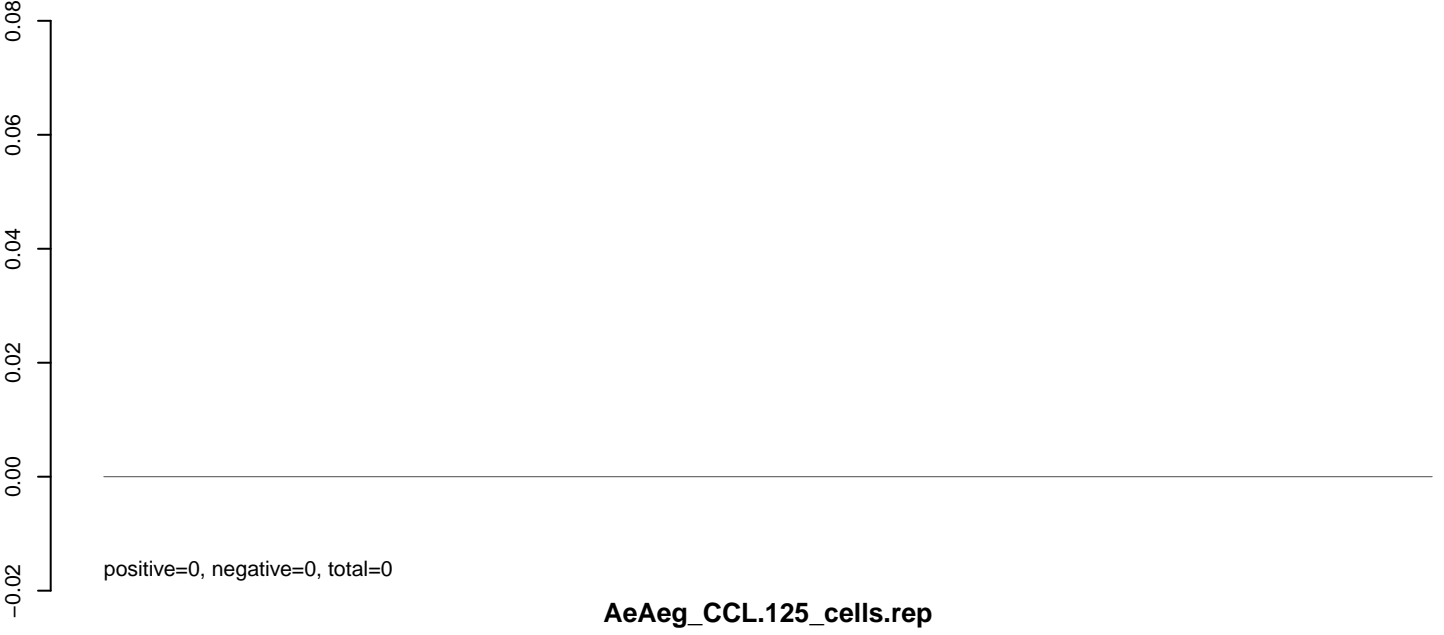
o_Virus_13-ORF1-ORF1-ORF2-ORF2-ORF3-ORF3-glycoprotein_G_and_RNA-dependent_RNA_polymerases_genes:1-13706

0 2000 4000 6000 8000 10000 12000 14000

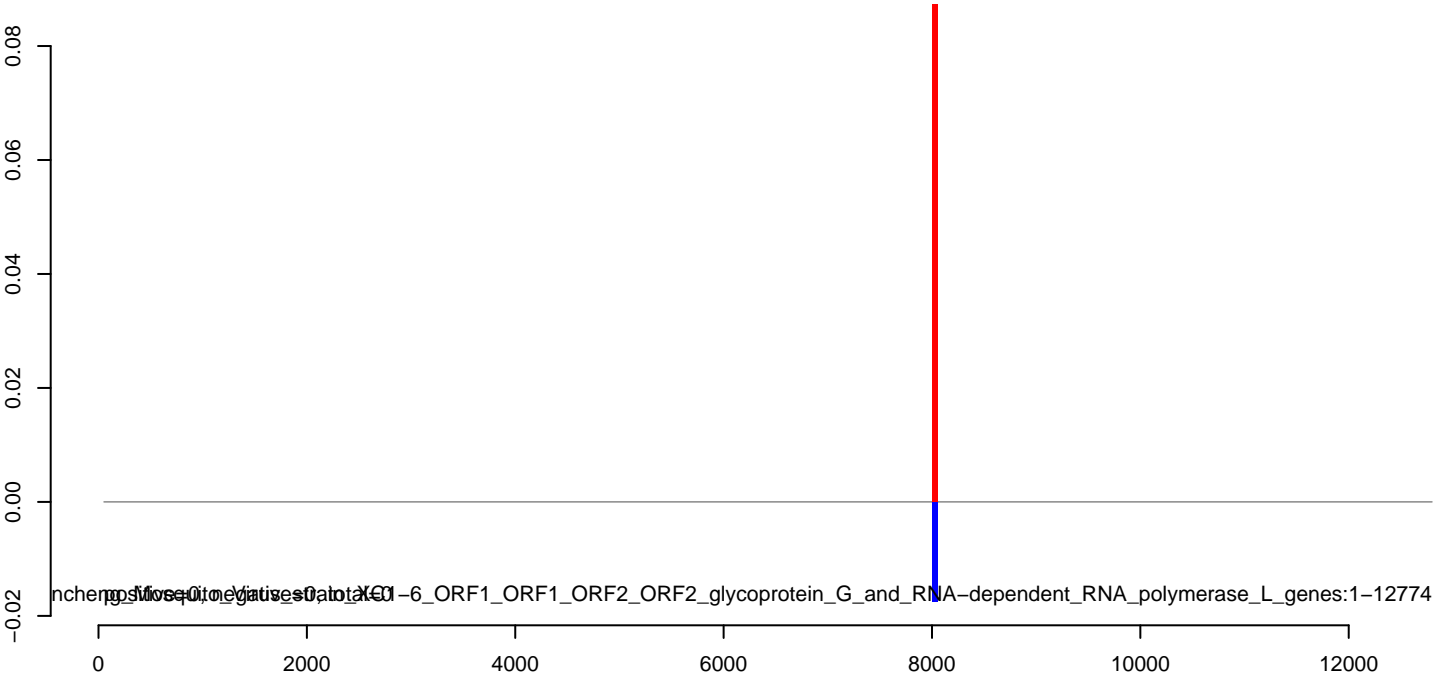
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AeAeg_CCL.125_cells.24_35.rep

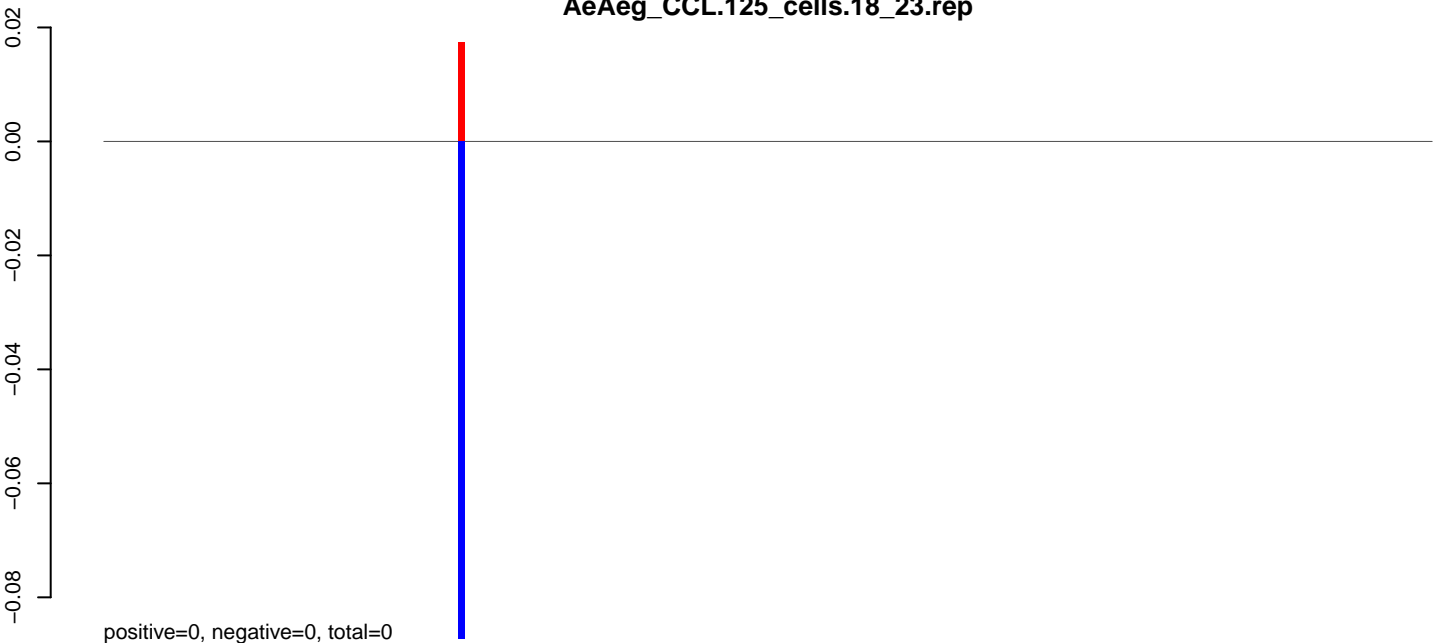


AeAeg_CCL.125_cells.rep

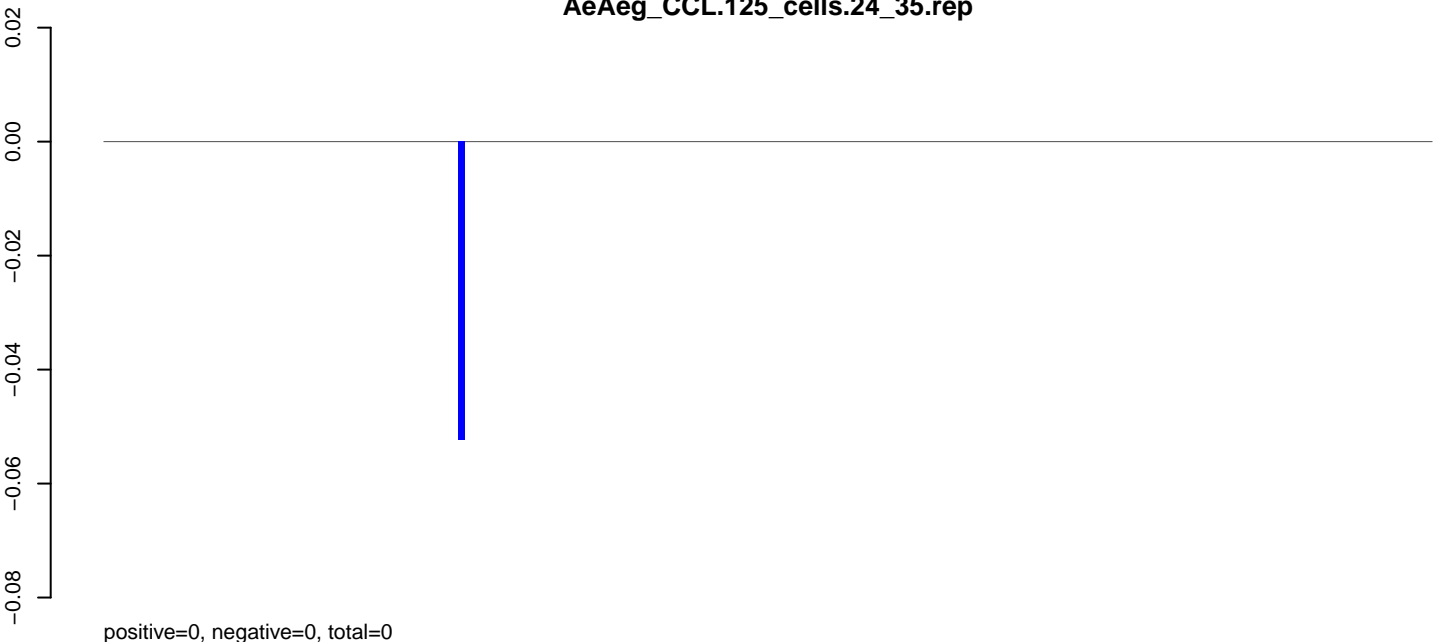


inchembiosciencejournal.com/doi/10.1002/ajb.10001-6_ORF1_ORF1_ORF2_ORF2_glycoprotein_G_and_RNA-dependent_RNA_polymerase_L_genes:1-12774

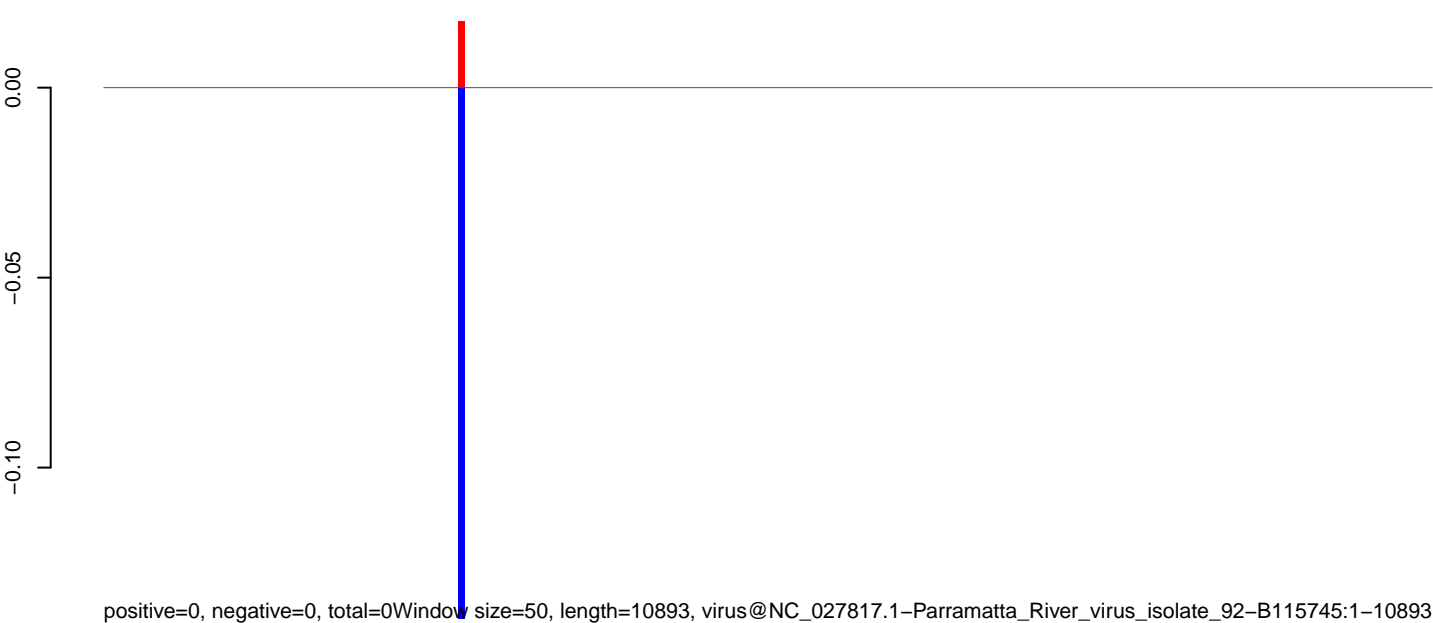
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AeAeg_CCL.125_cells.24_35.rep



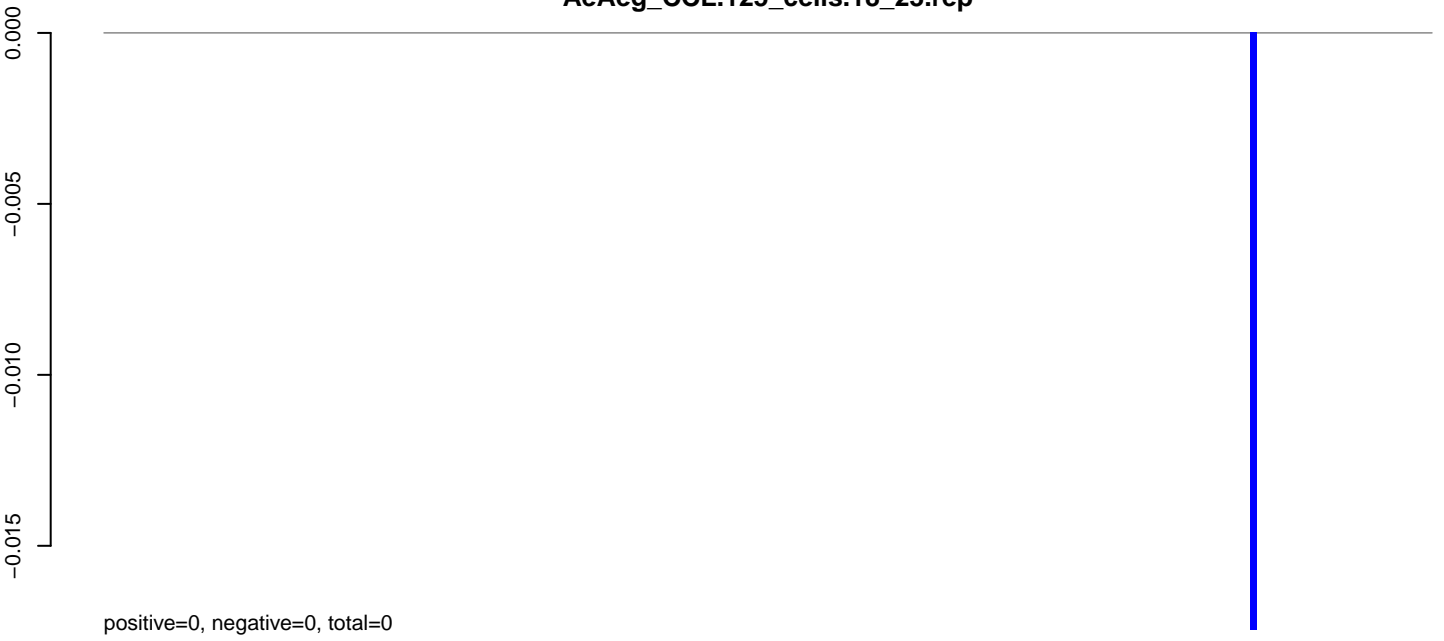
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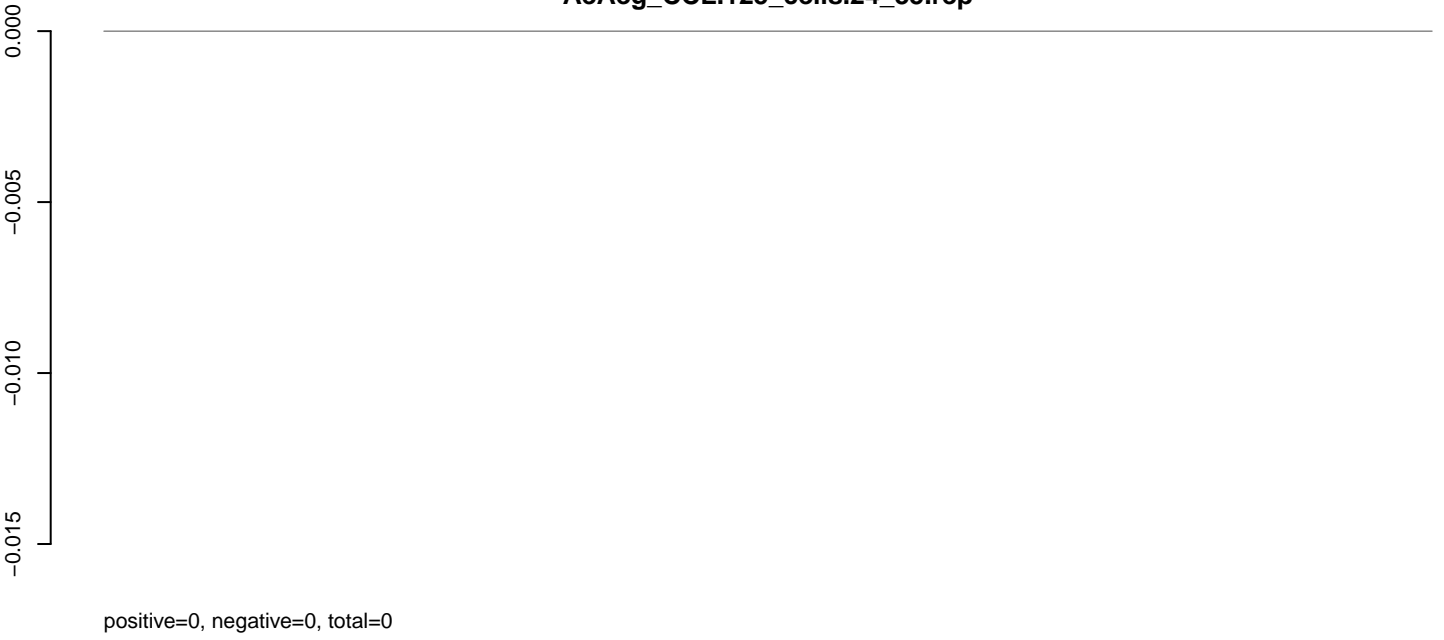
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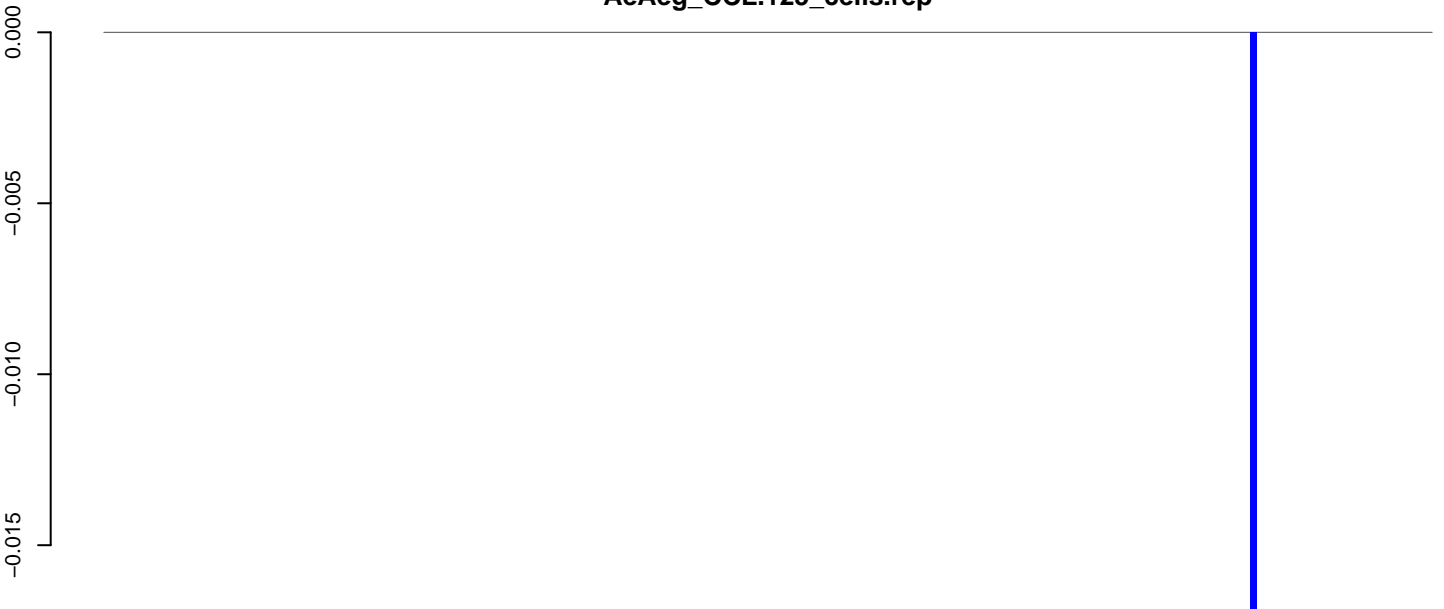
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AeAeg_CCL.125_cells.24_35.rep



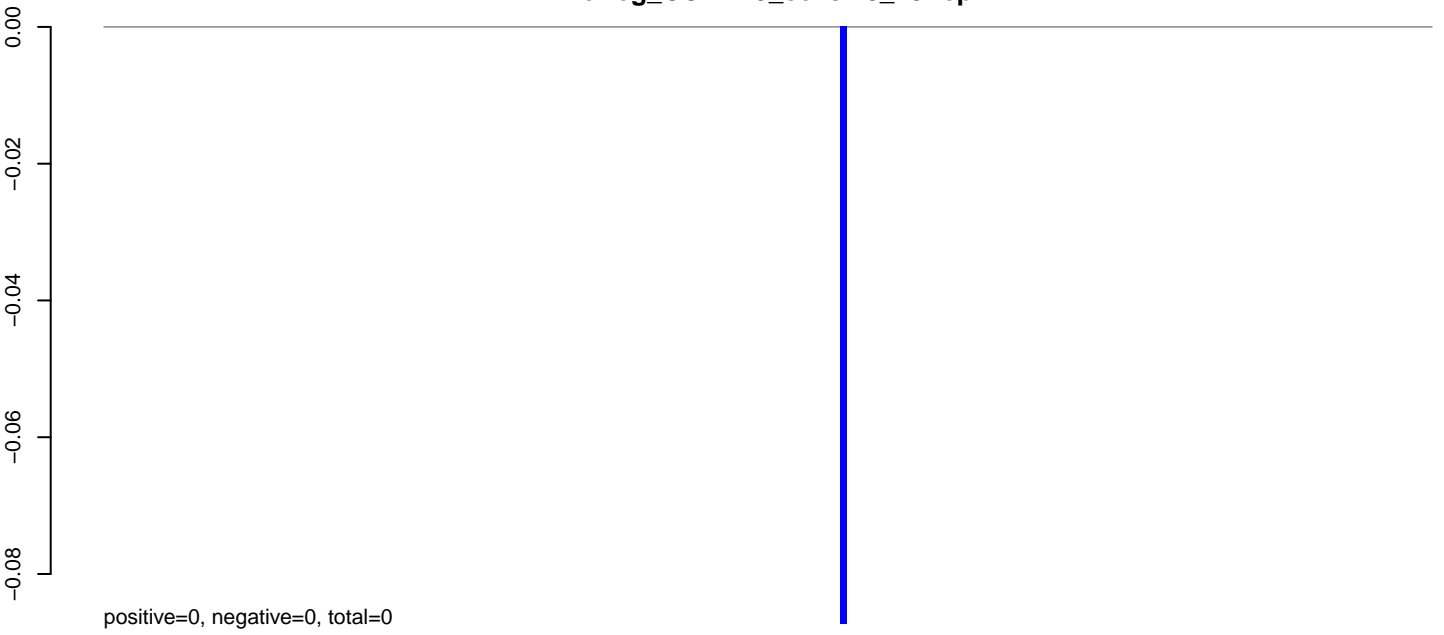
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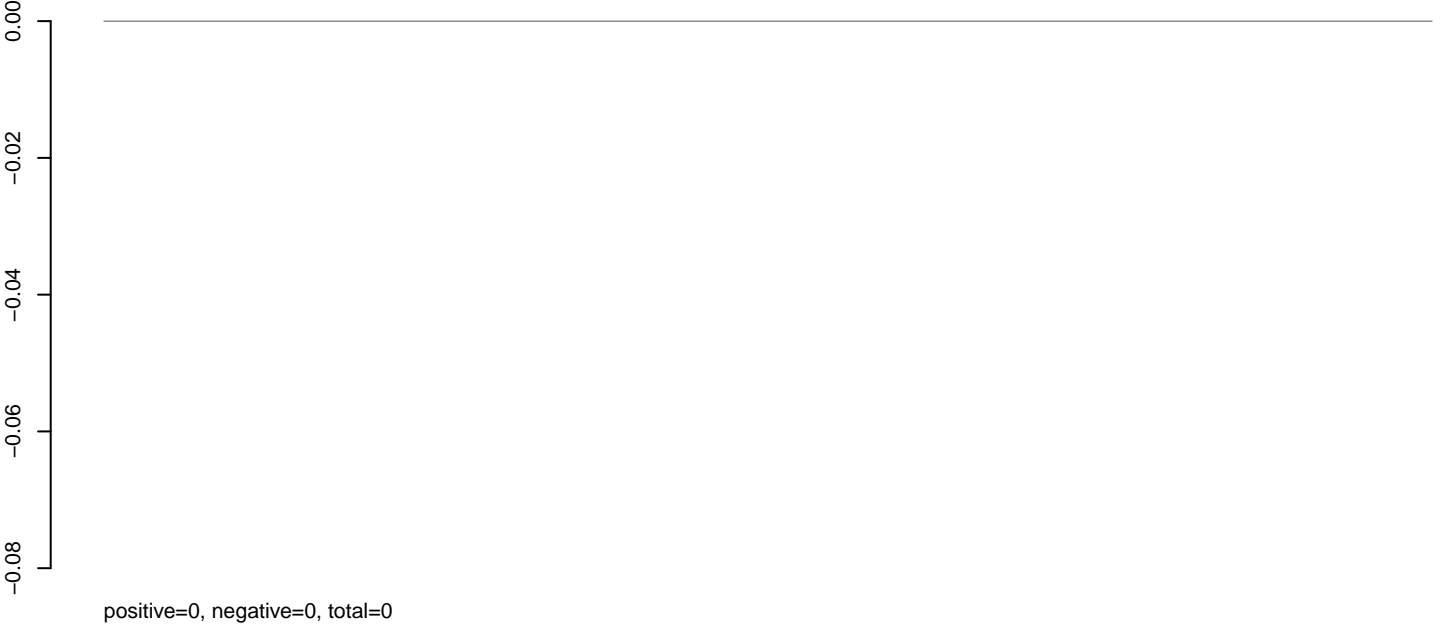
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0 2000 4000 6000 8000 10000

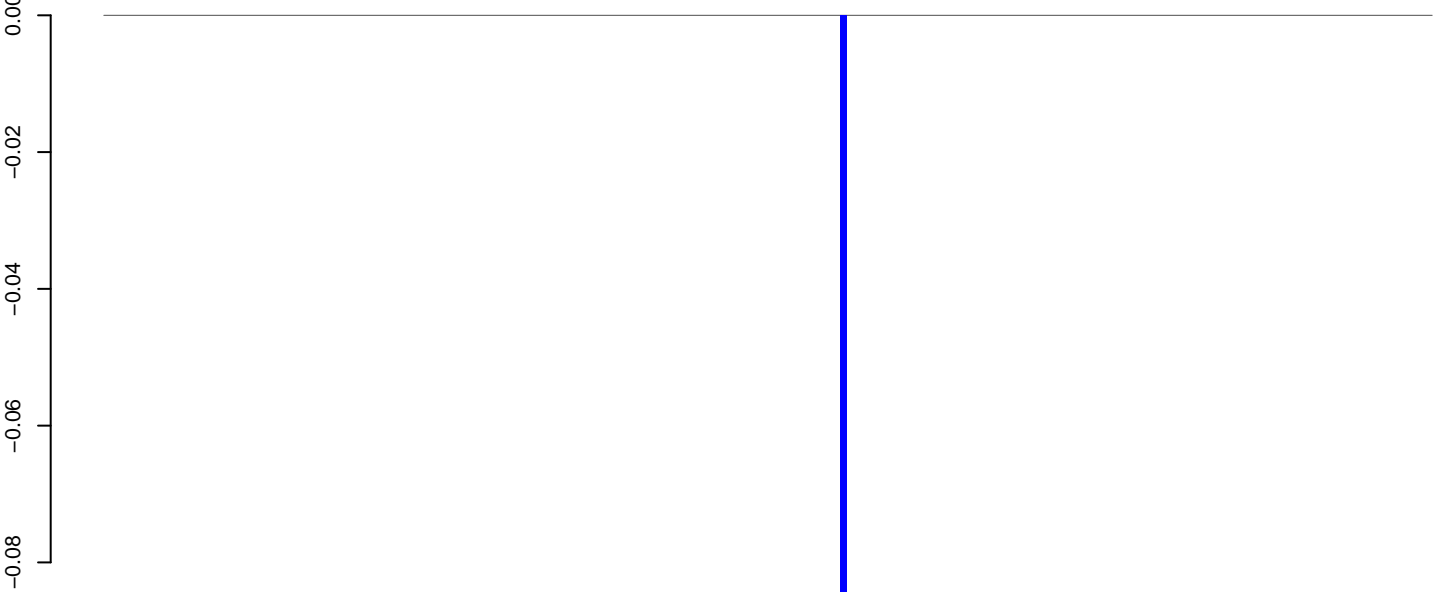
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AeAeg_CCL.125_cells.24_35.rep



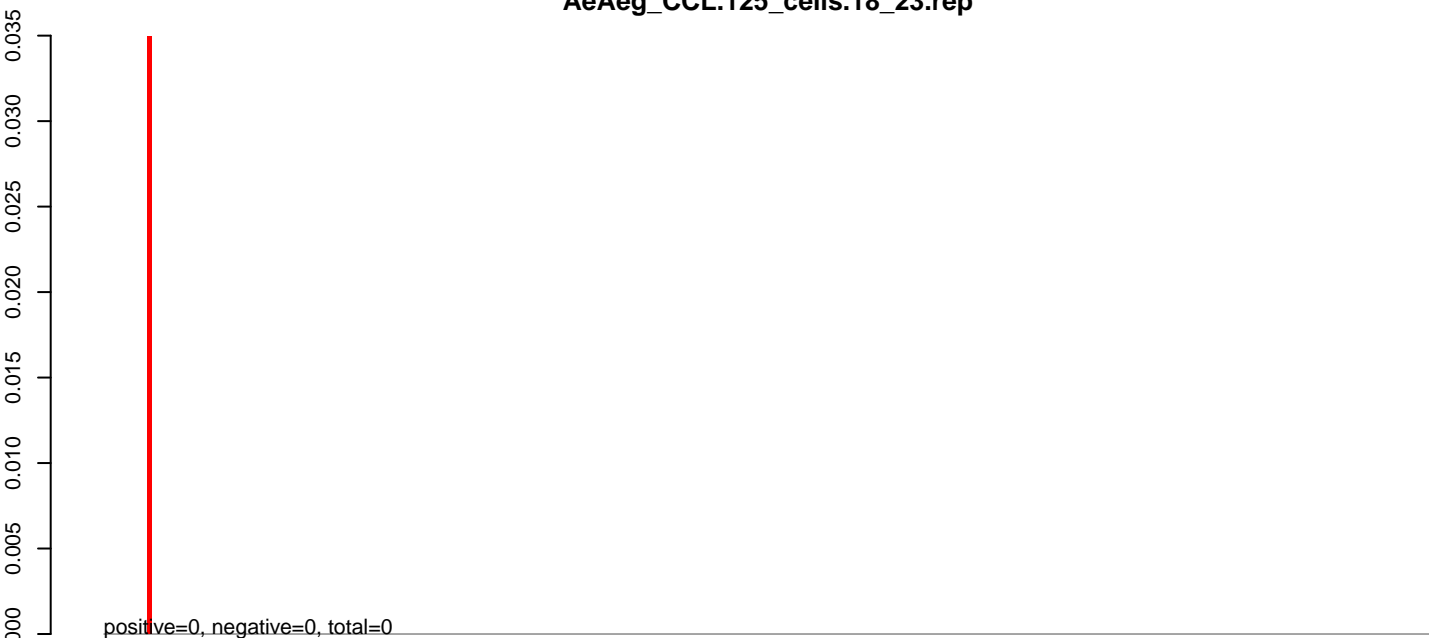
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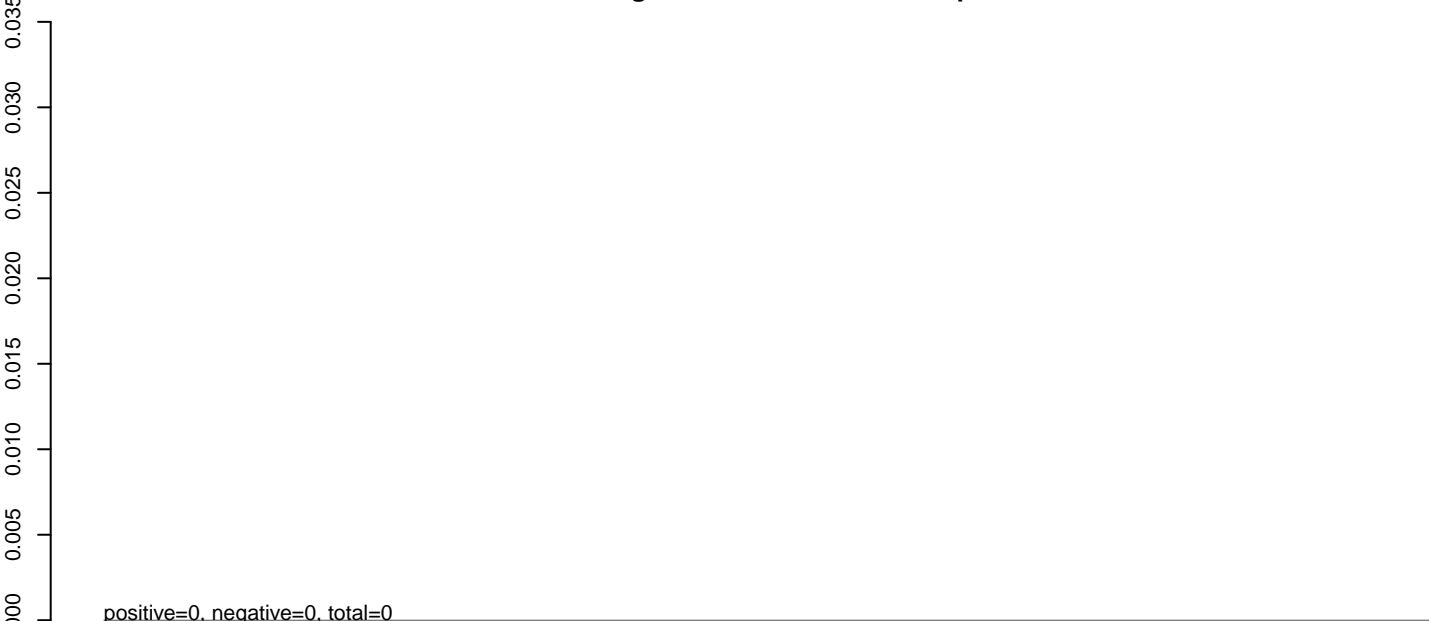
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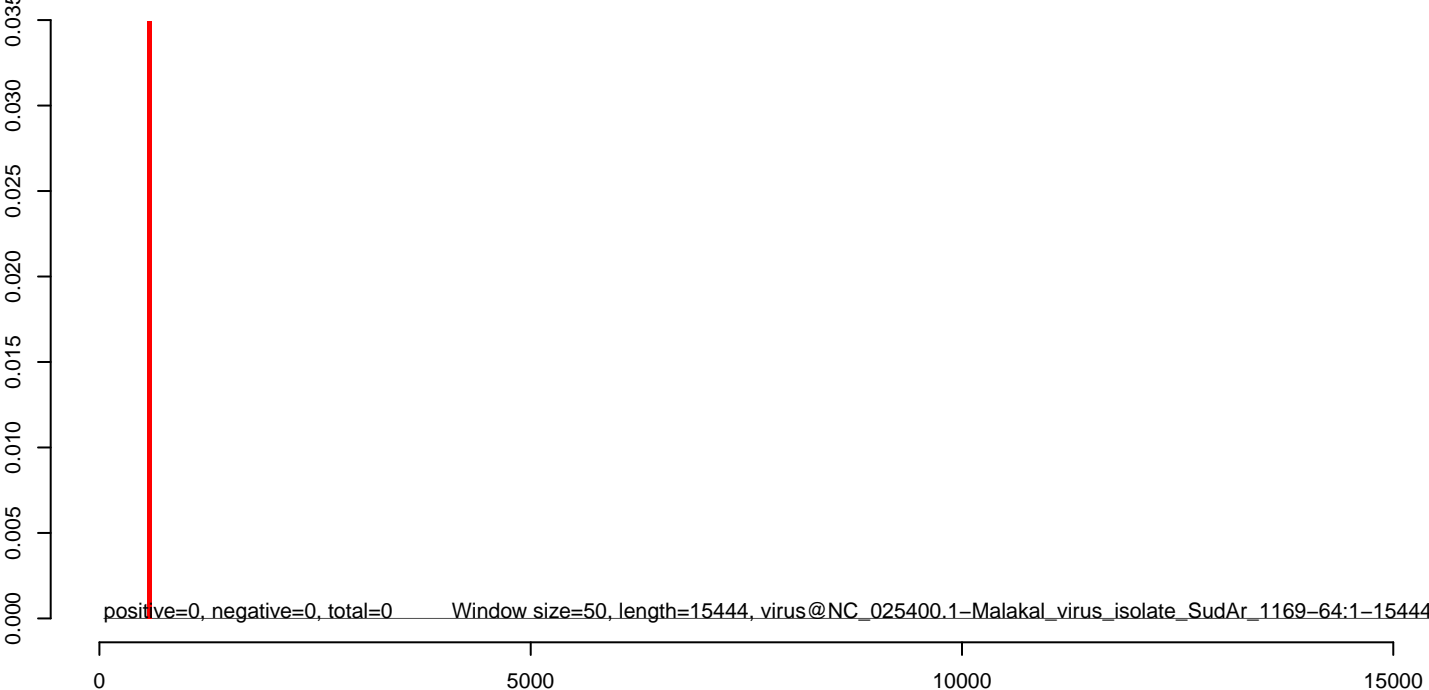
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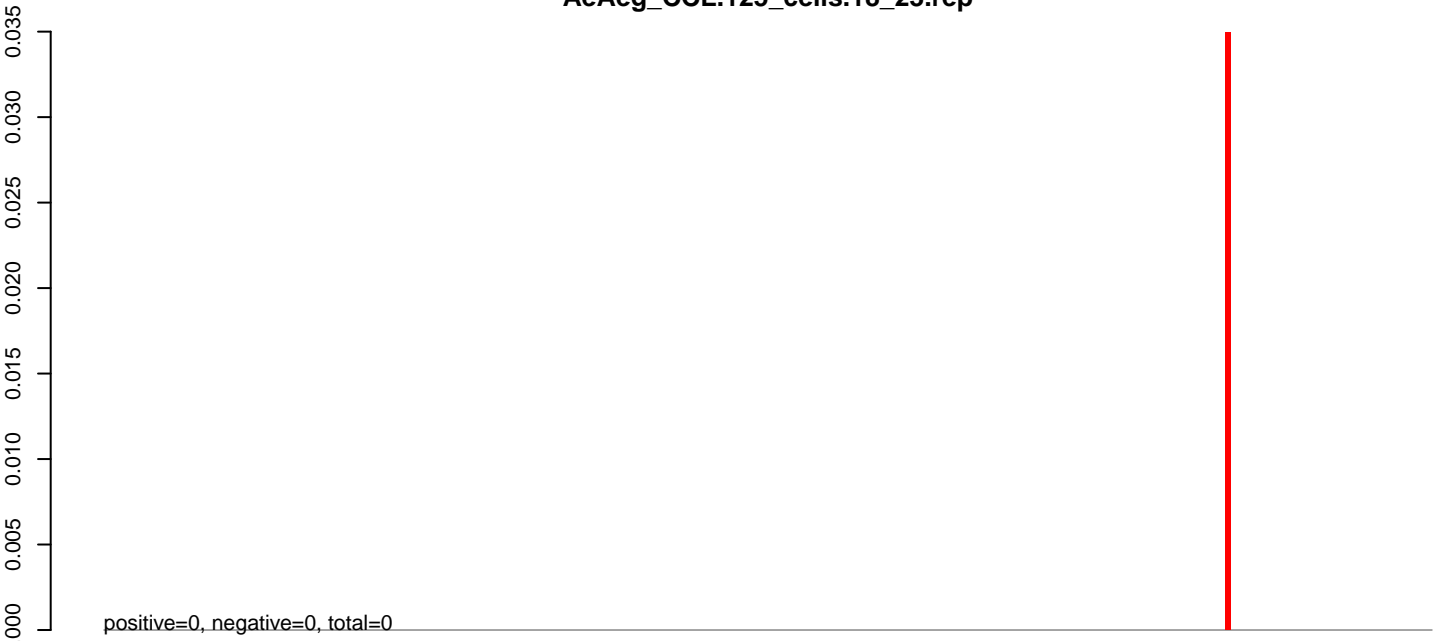
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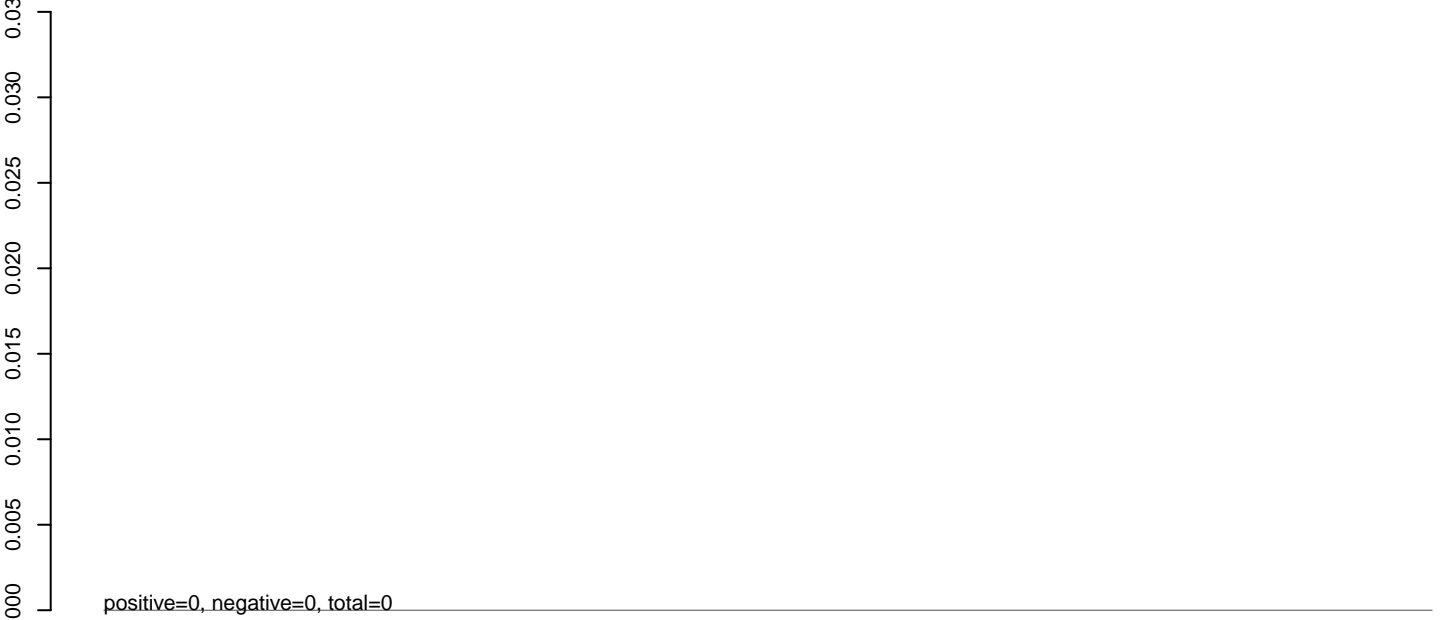
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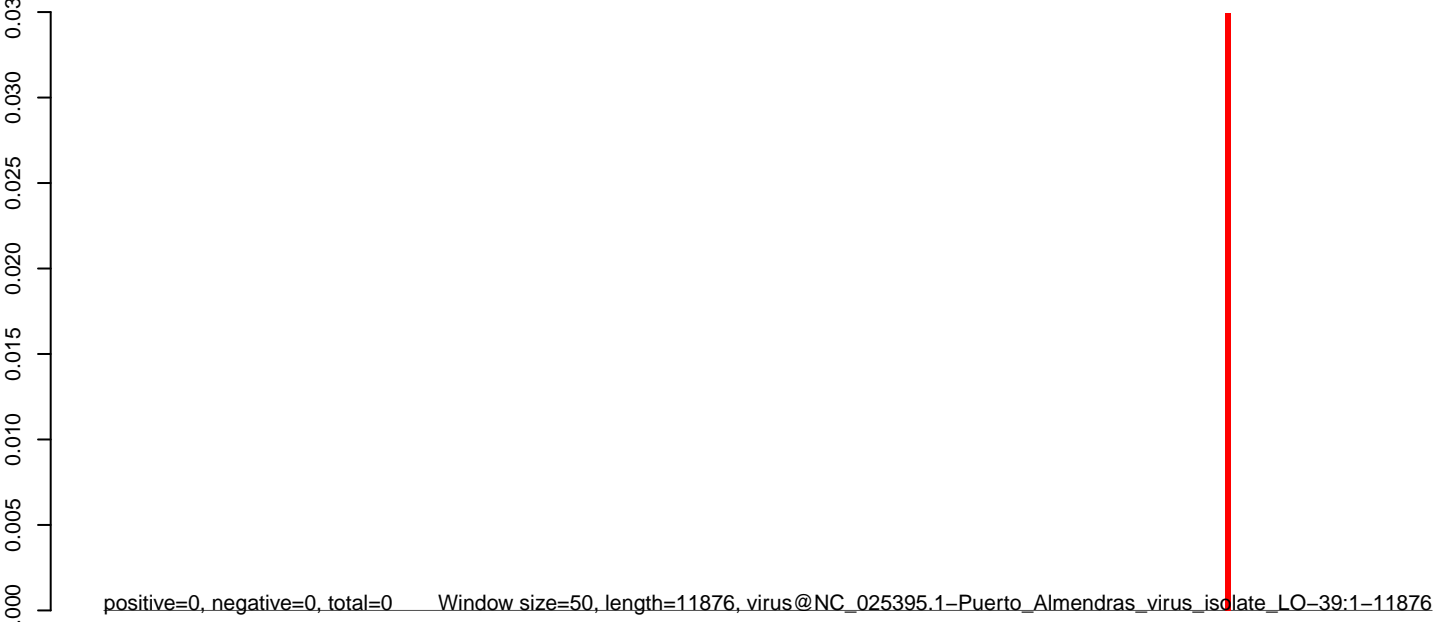
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AeAeg_CCL.125_cells.24_35.rep

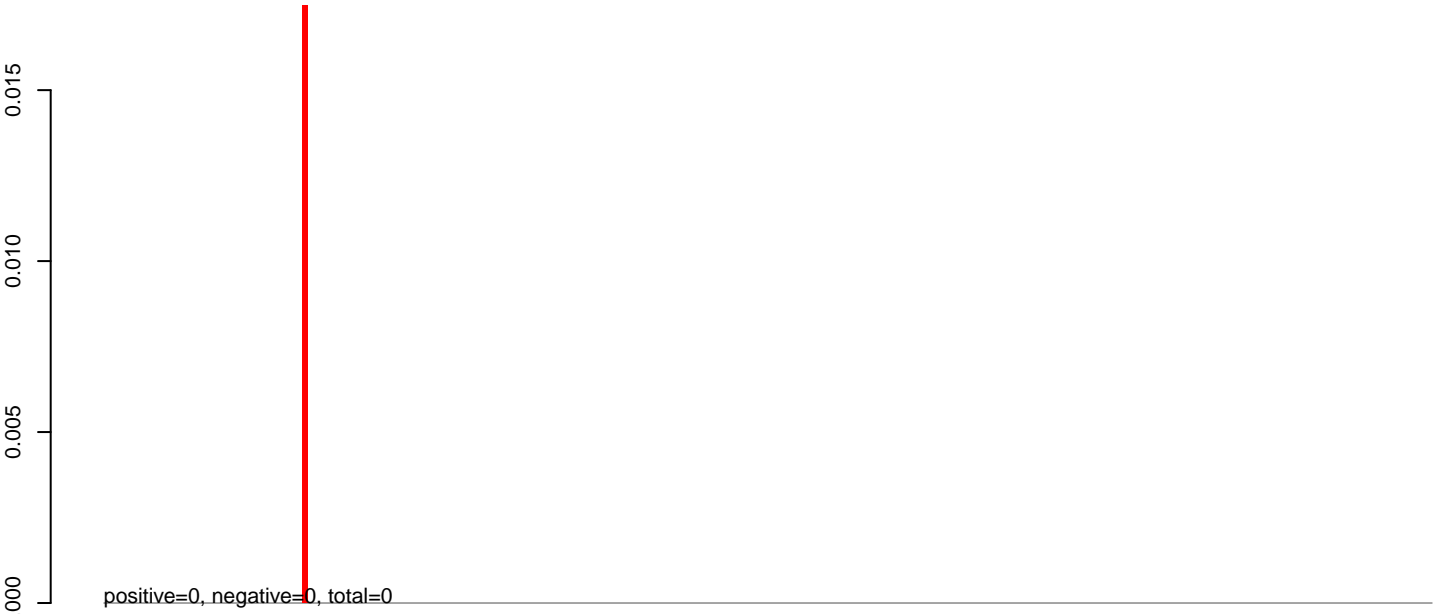


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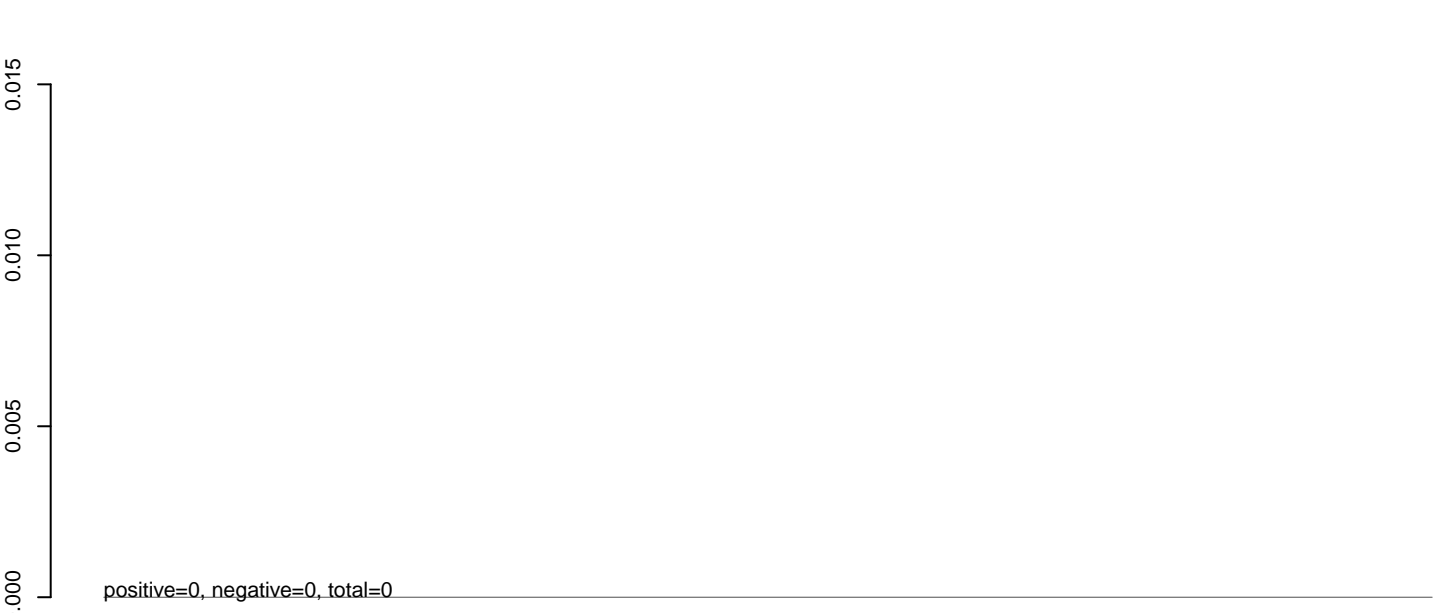


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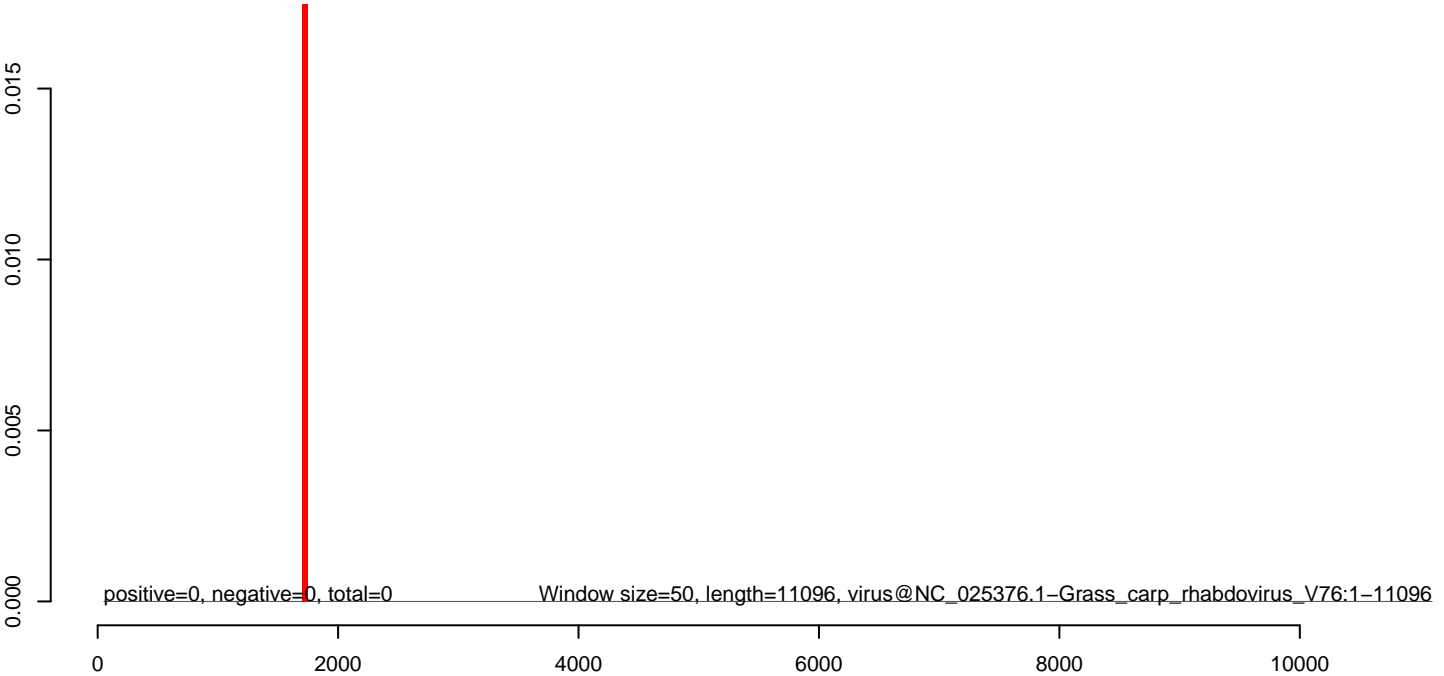
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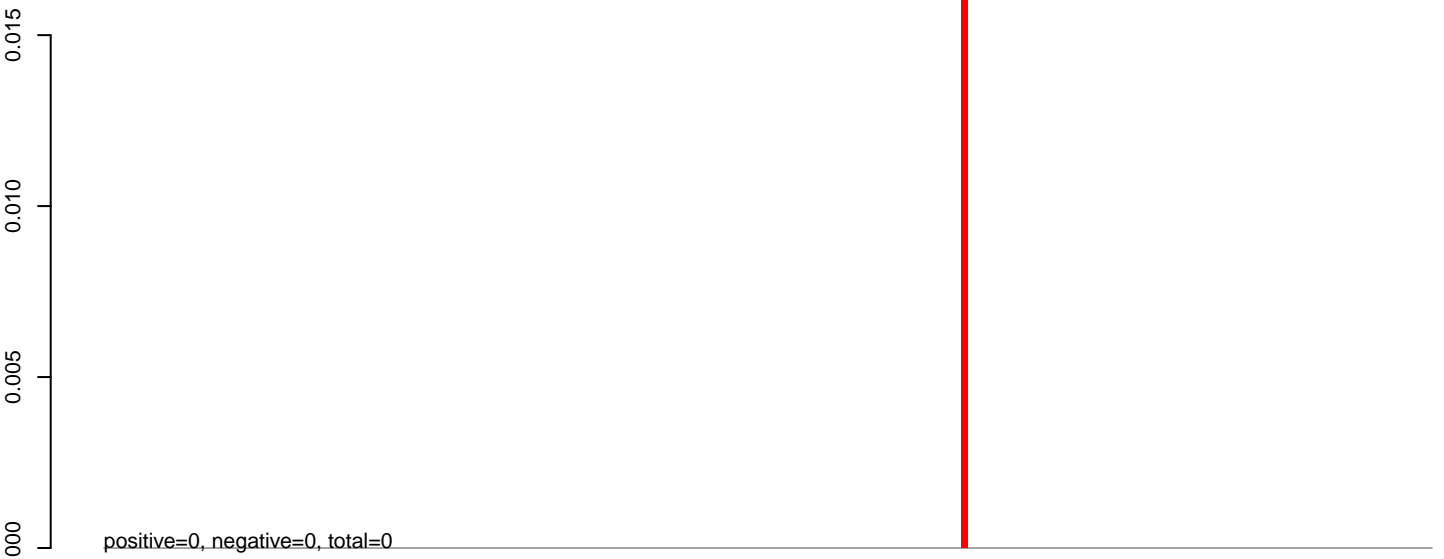
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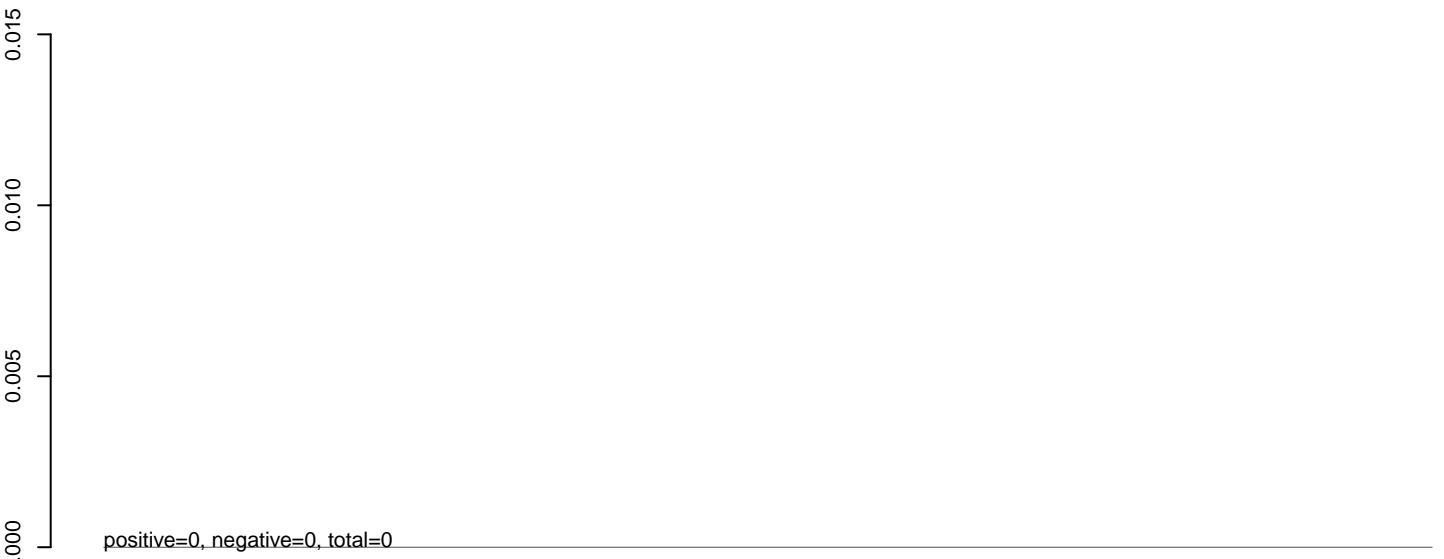
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AeAeg_CCL.125_cells.18_23.rep



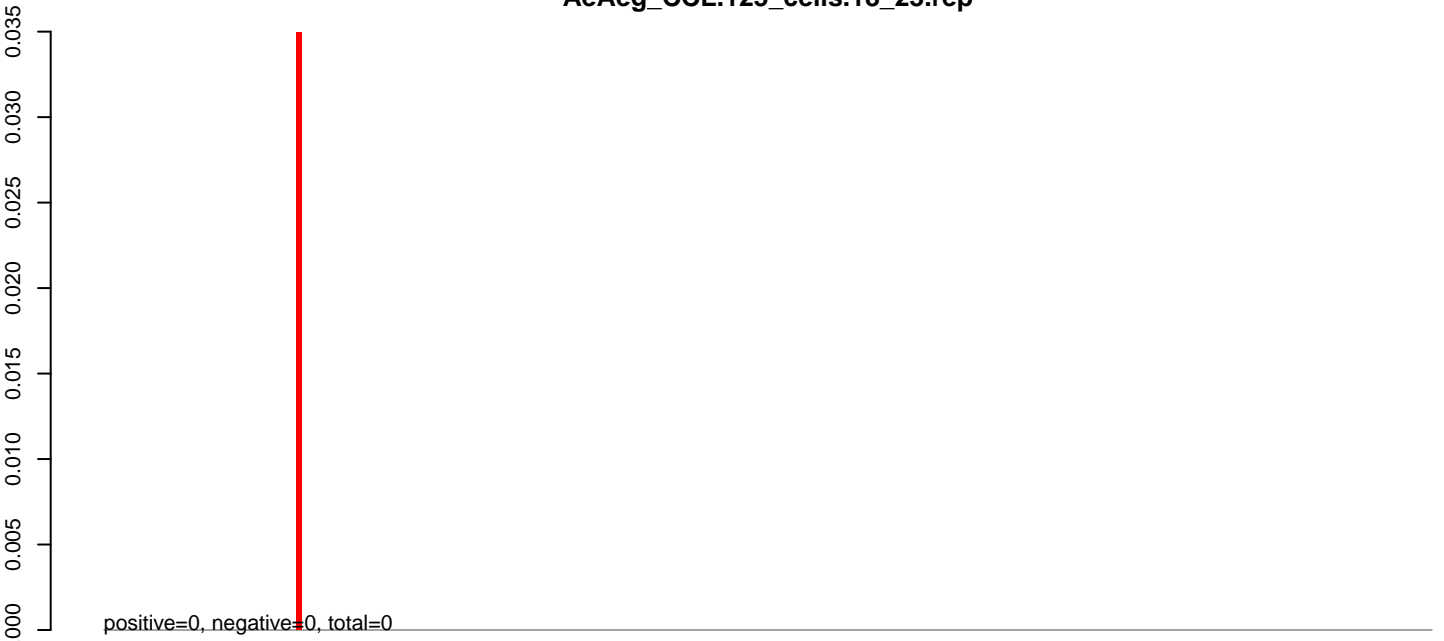
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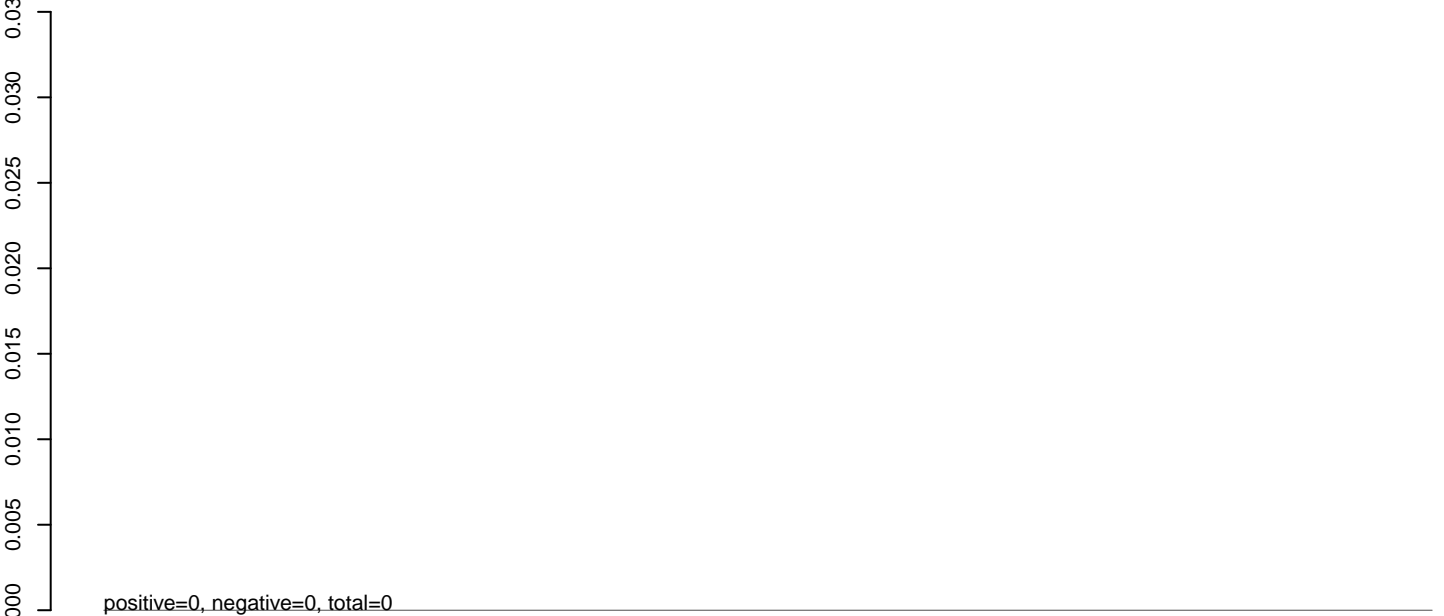
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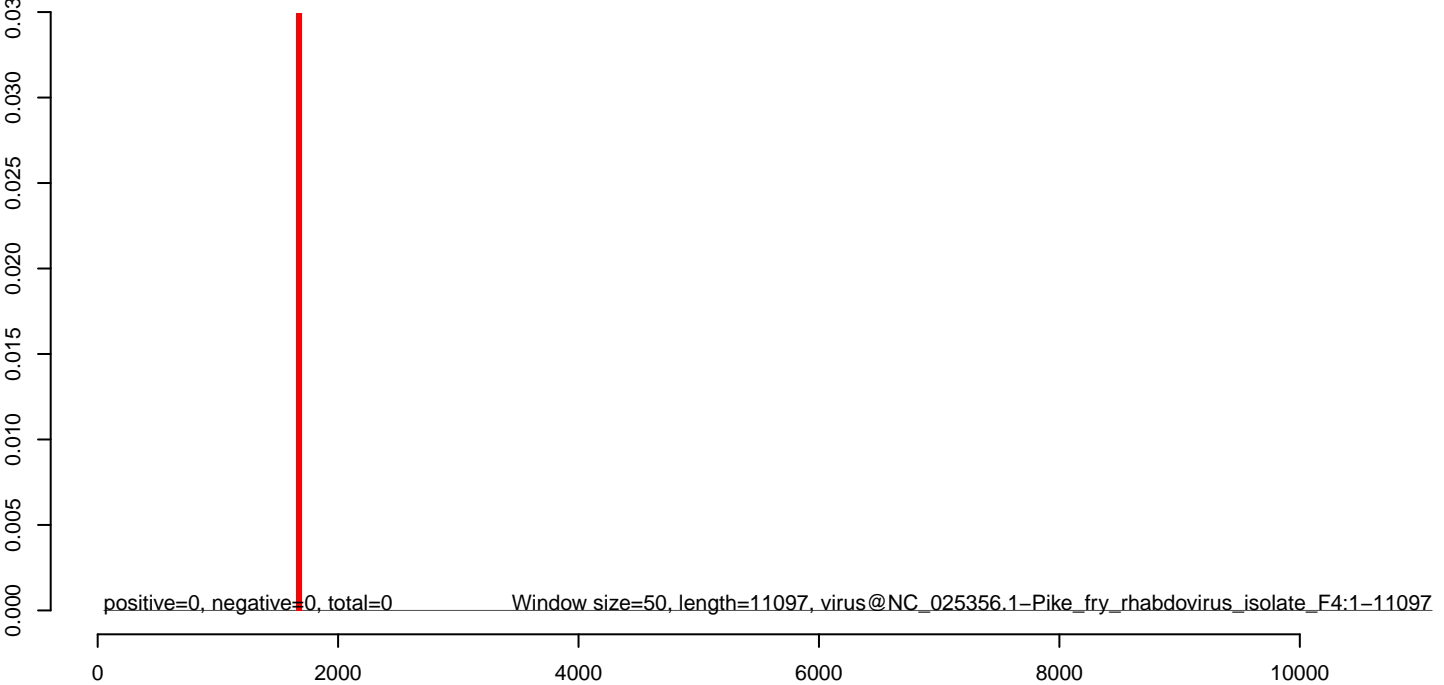
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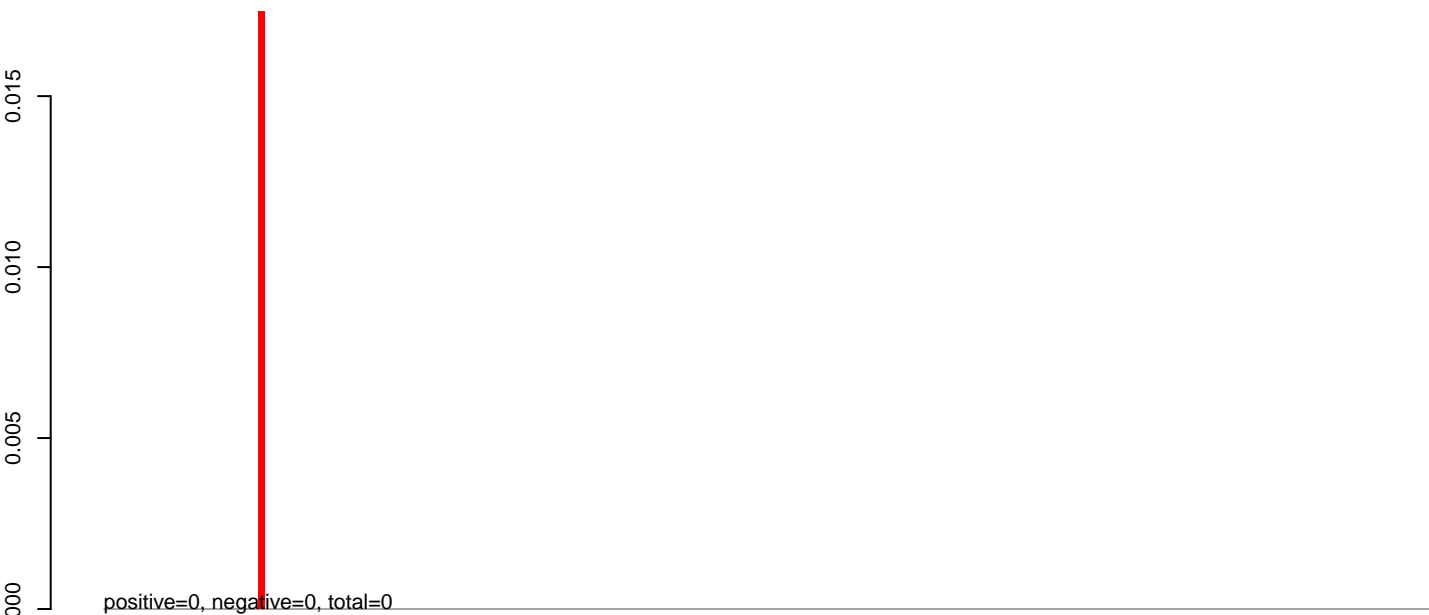
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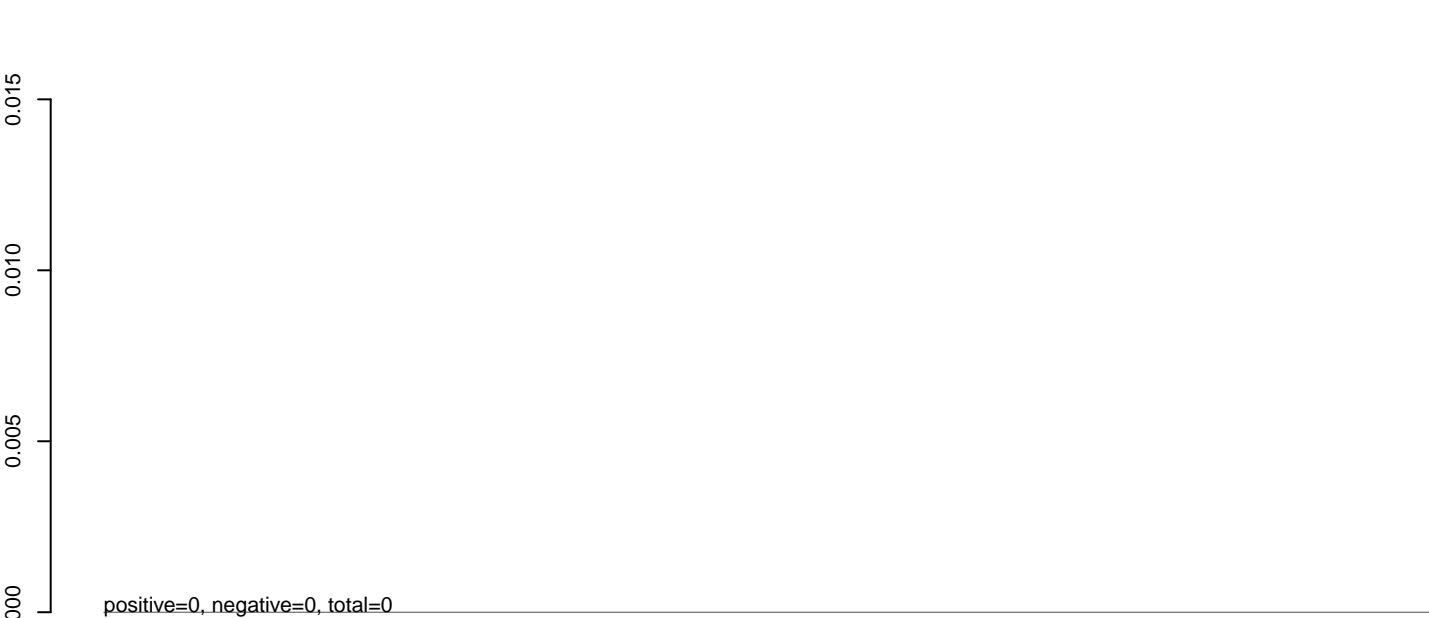
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AeAeg_CCL.125_cells.18_23.rep



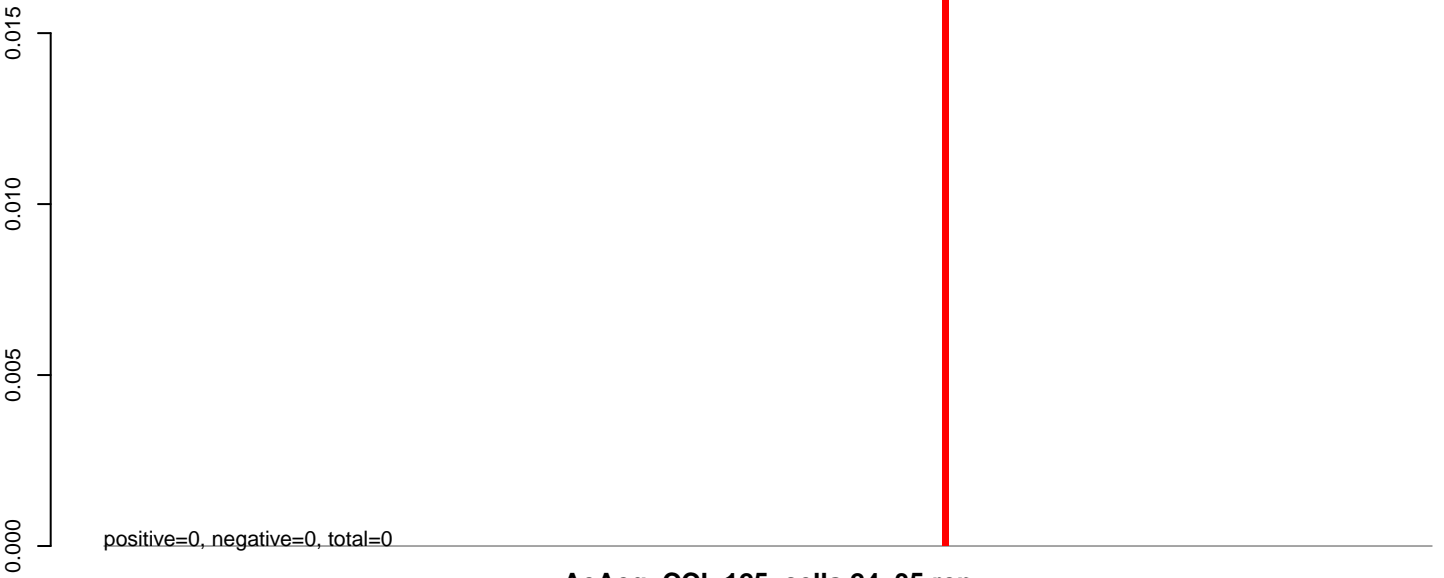
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AeAeg_CCL.125_cells.rep



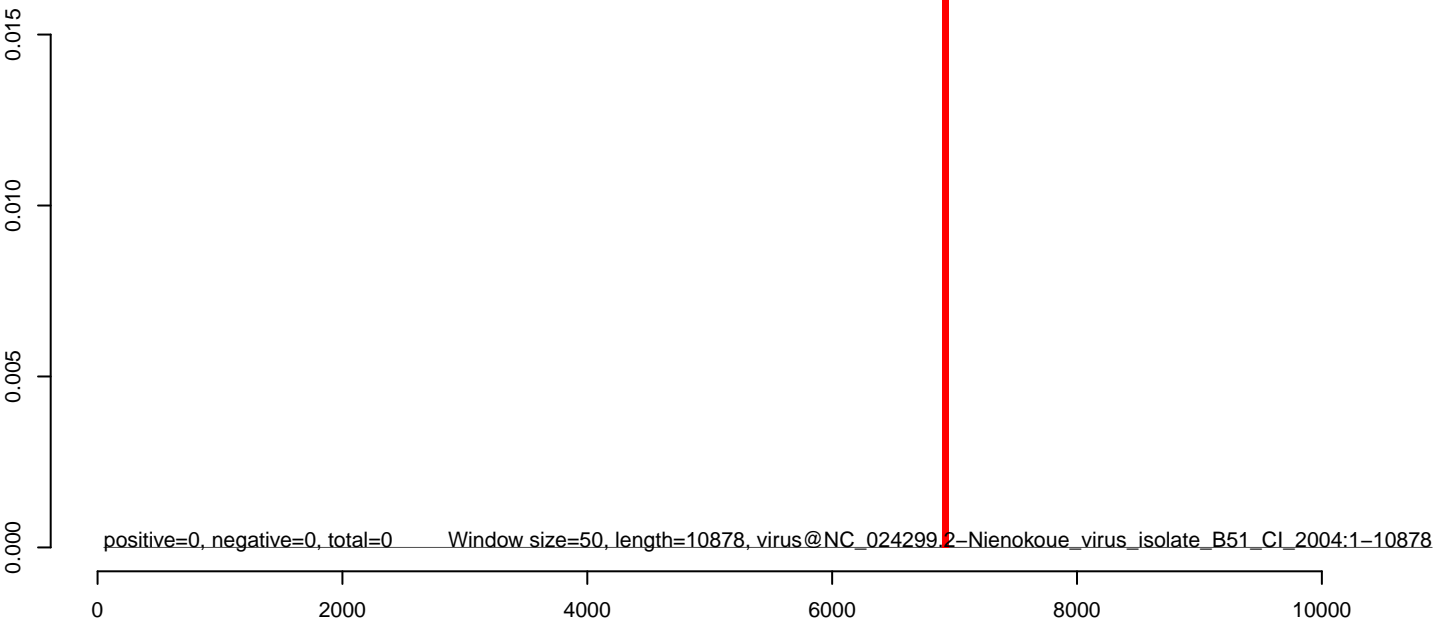
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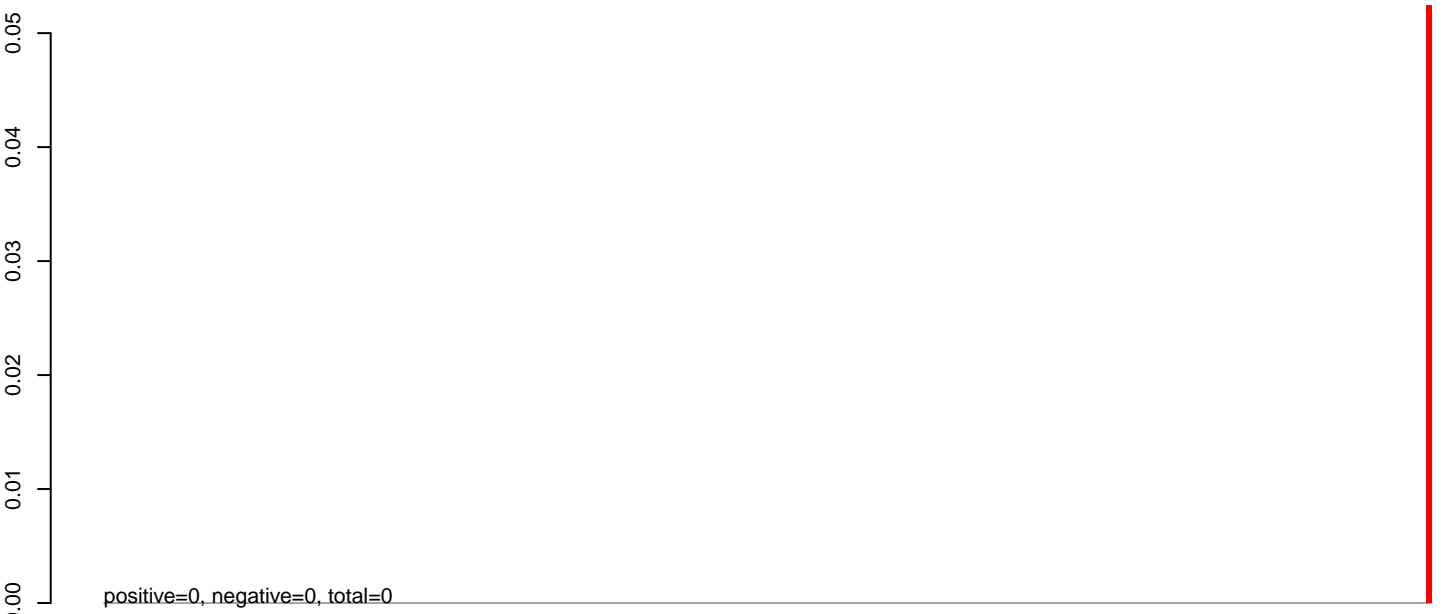
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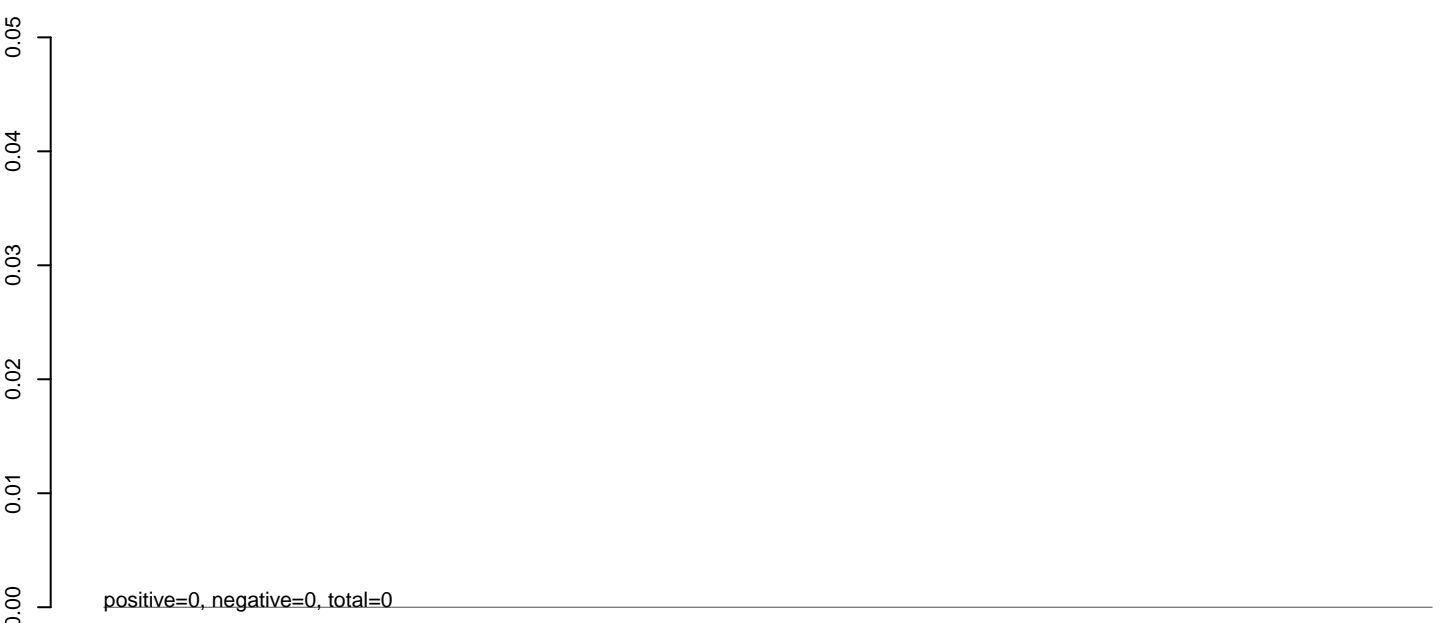
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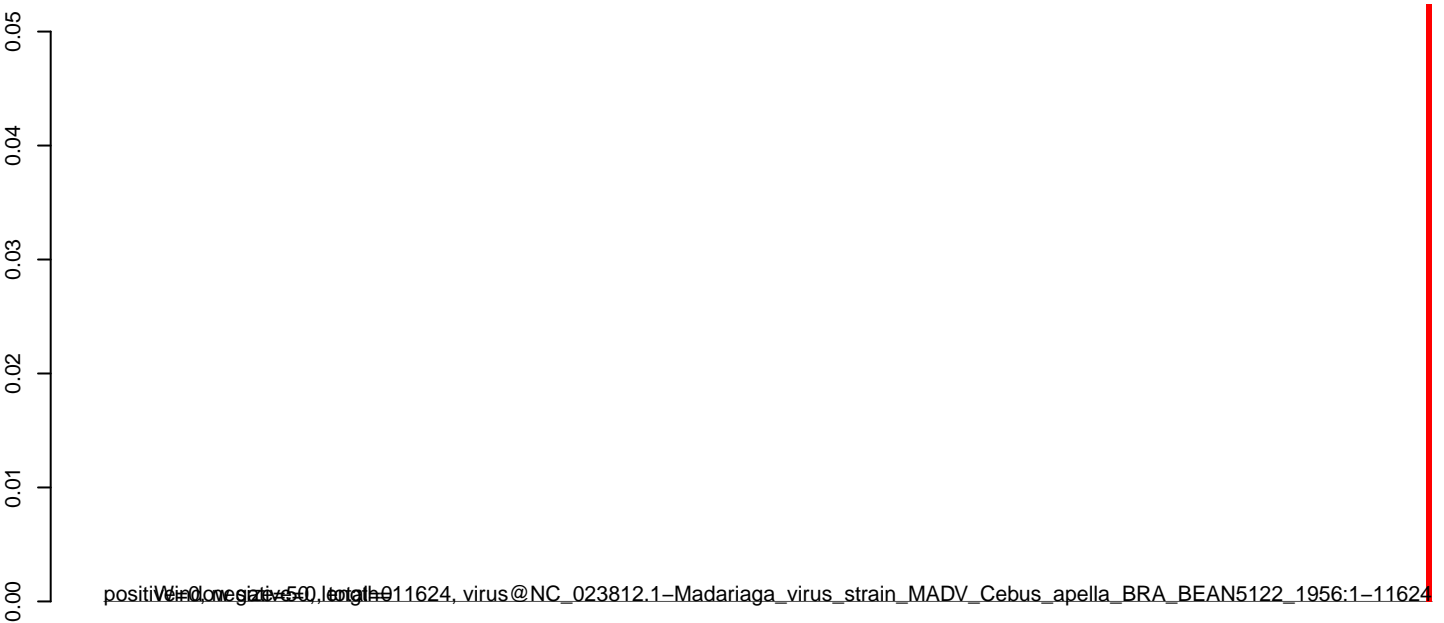
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AeAeg_CCL.125_cells.24_35.rep

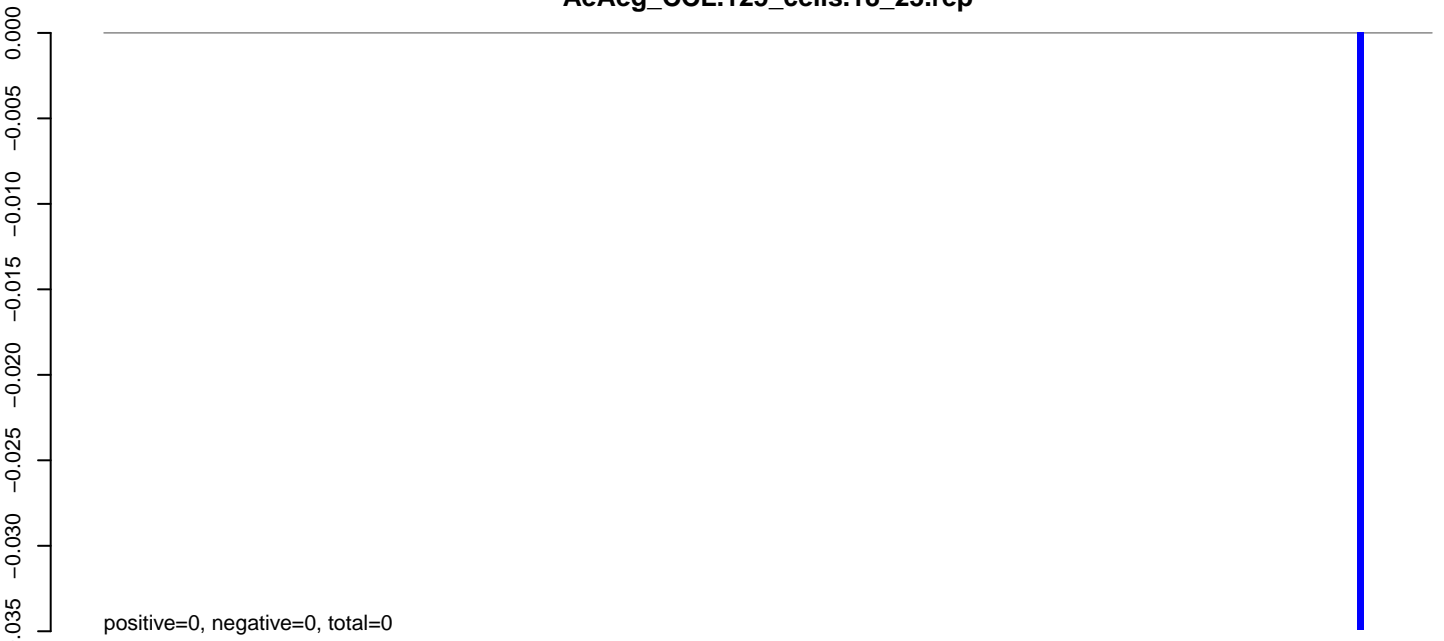


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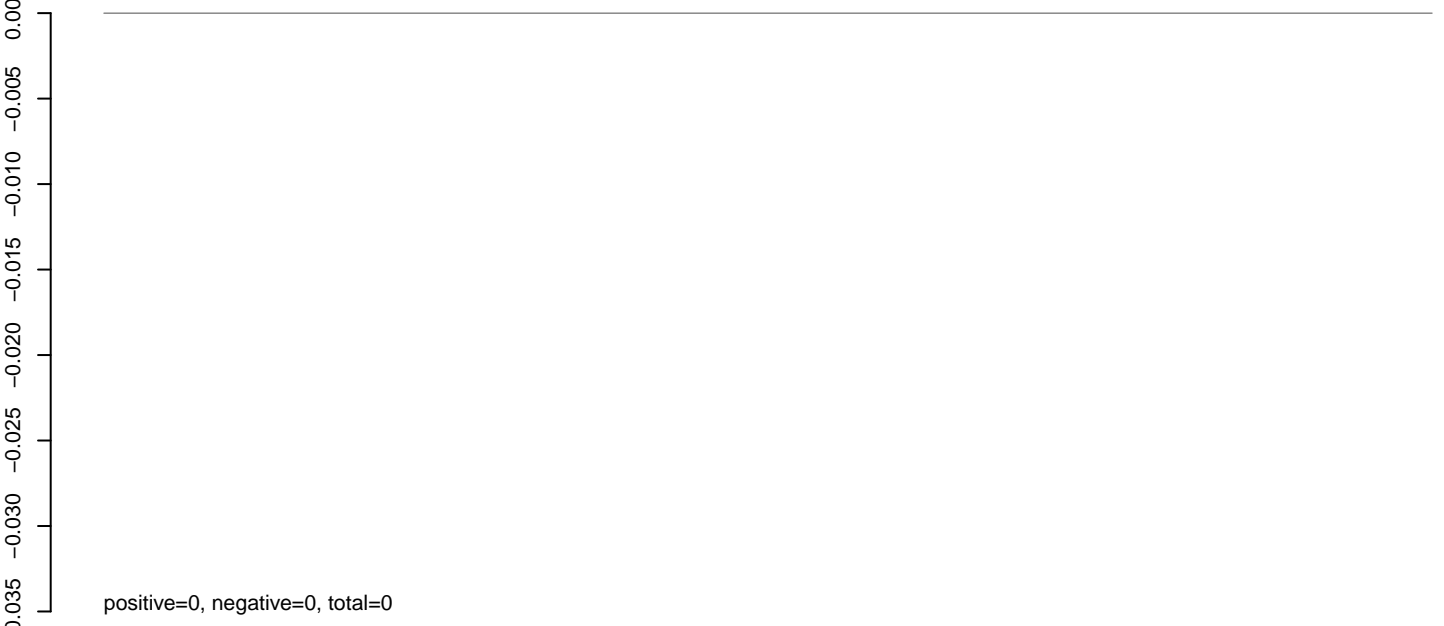


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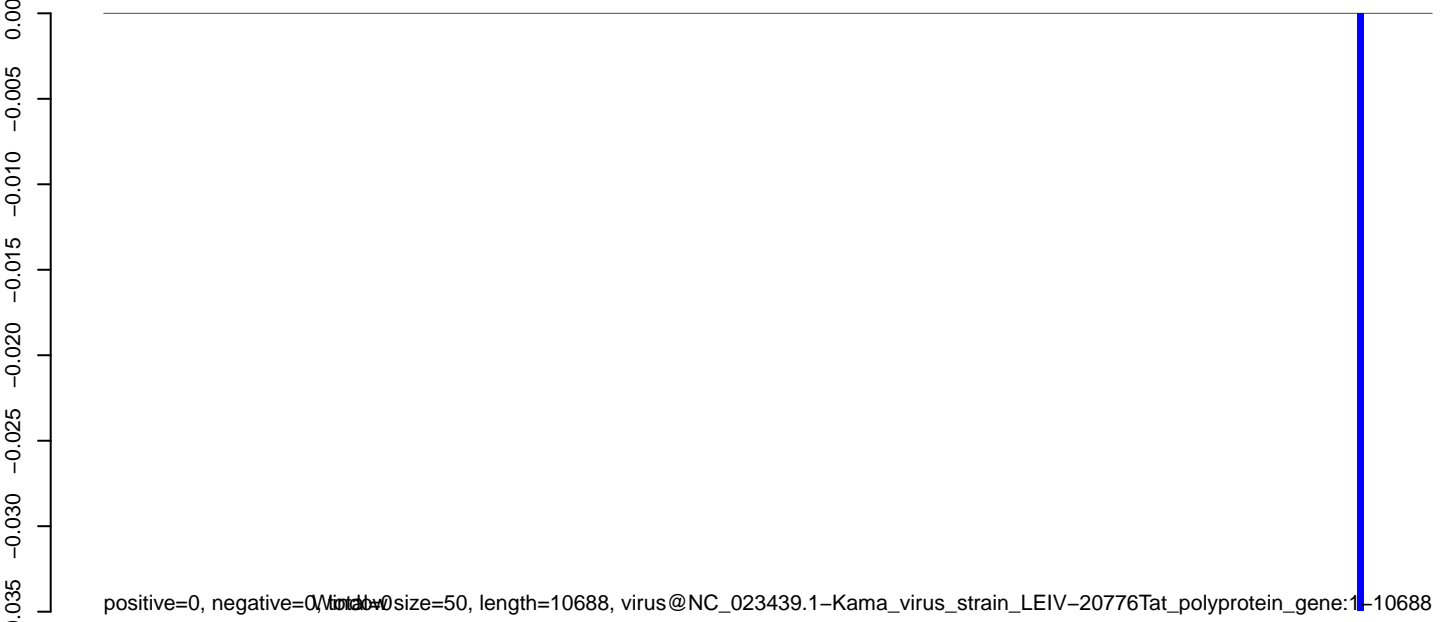
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AeAeg_CCL.125_cells.24_35.rep



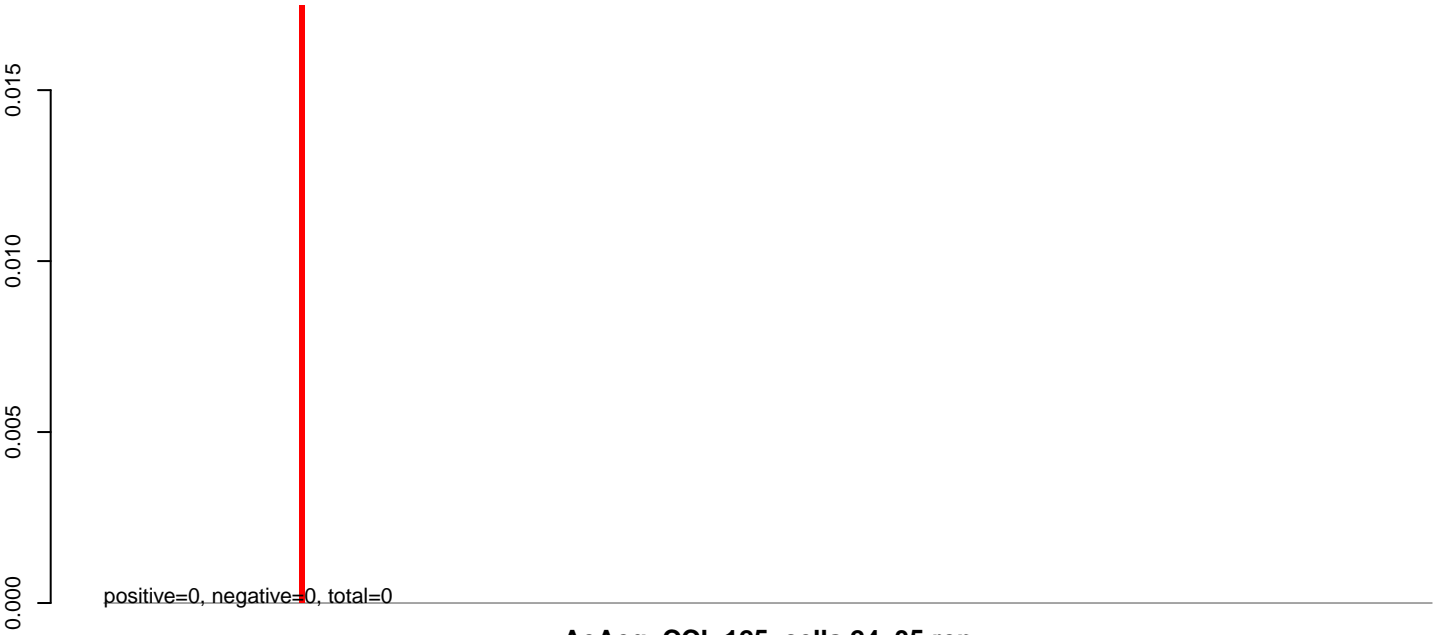
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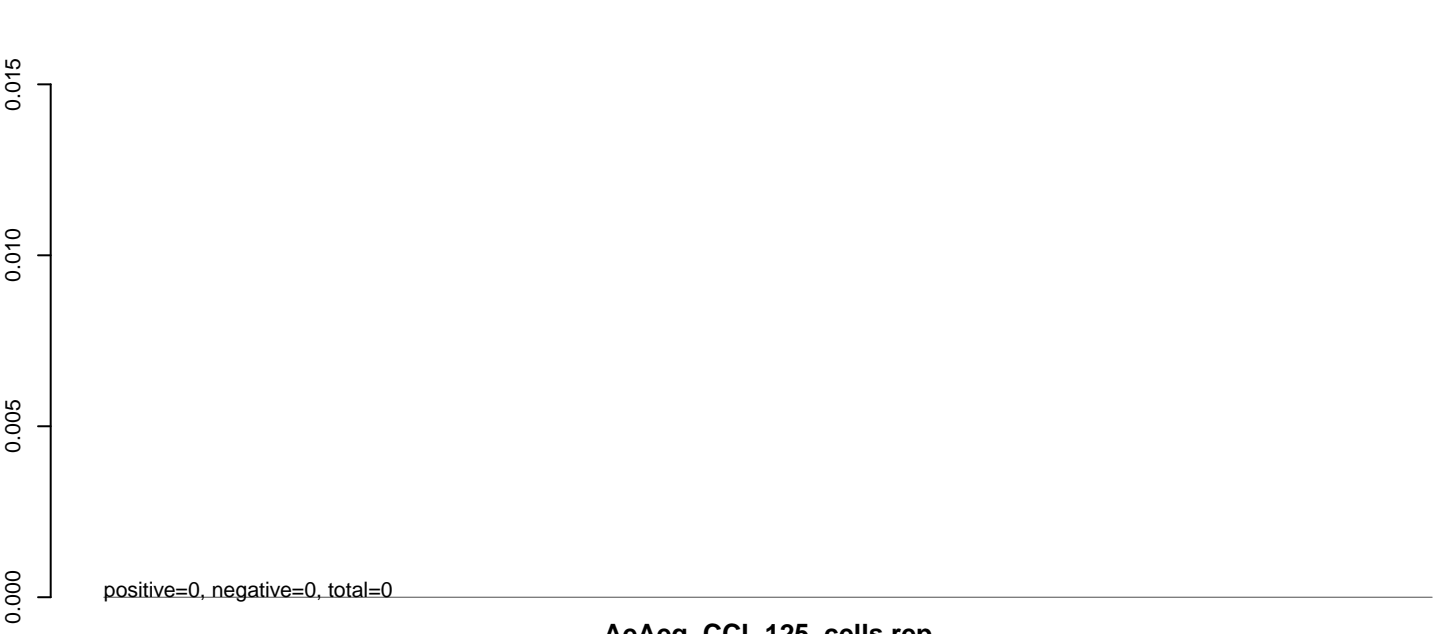
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0 2000 4000 6000 8000 10000

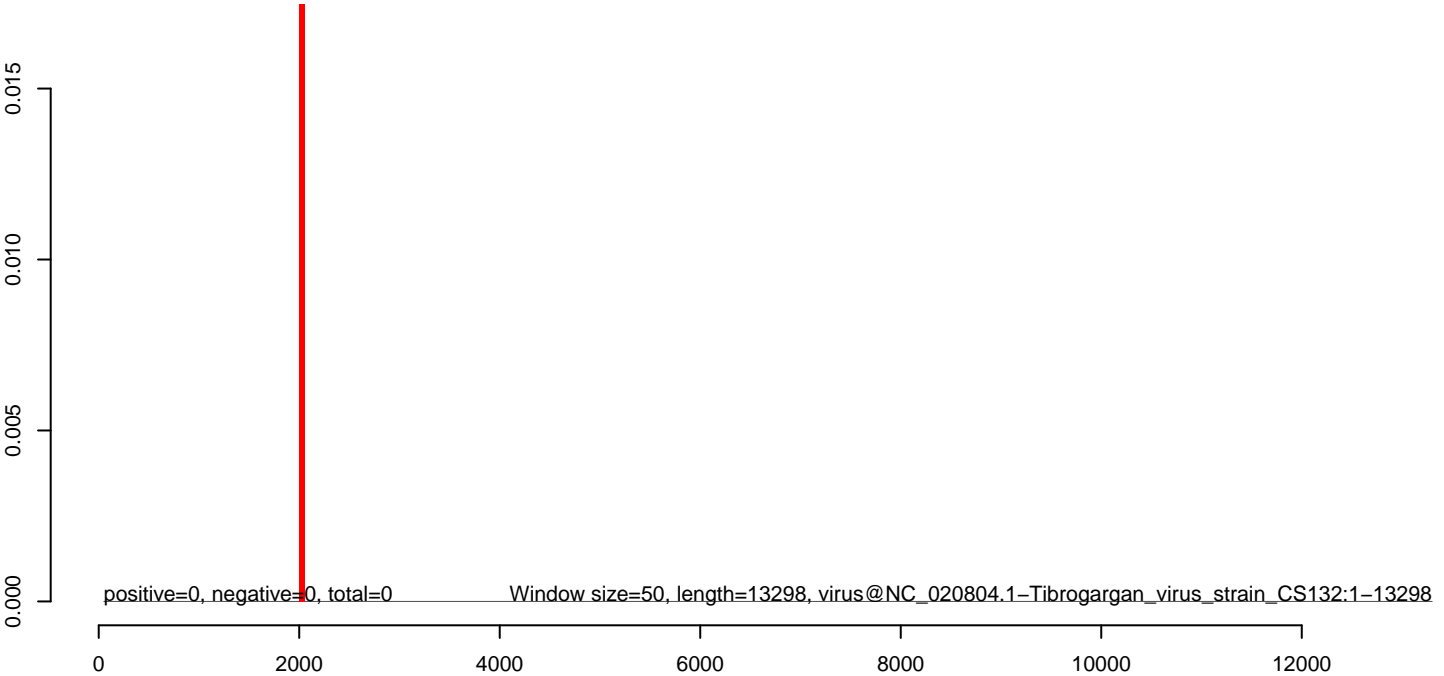
AeAeg_CCL.125_cells.18_23.rep



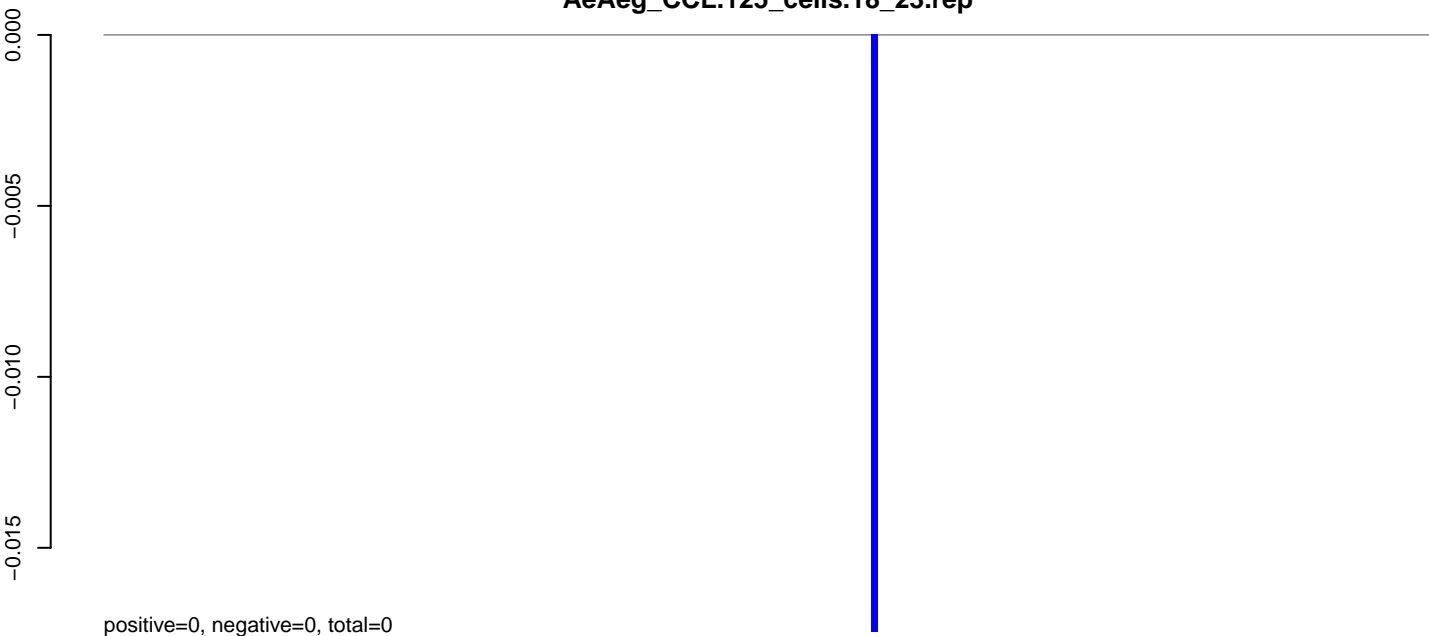
AeAeg_CCL.125_cells.24_35.rep



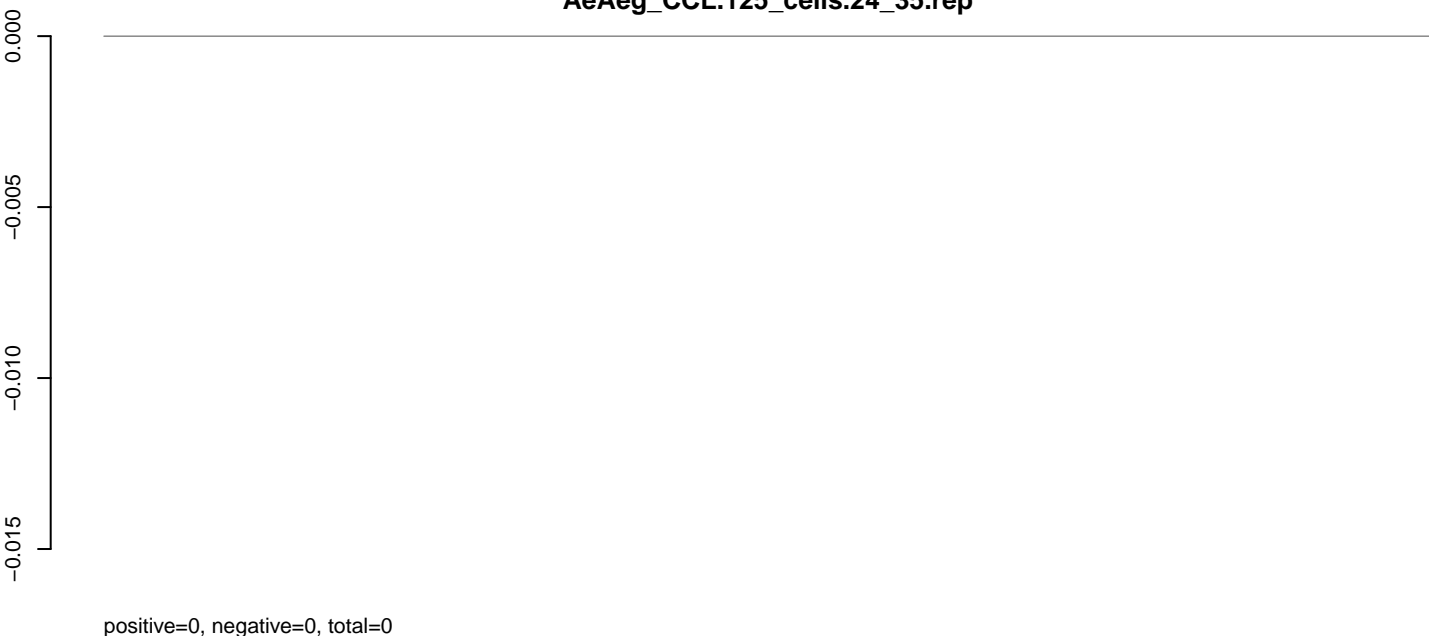
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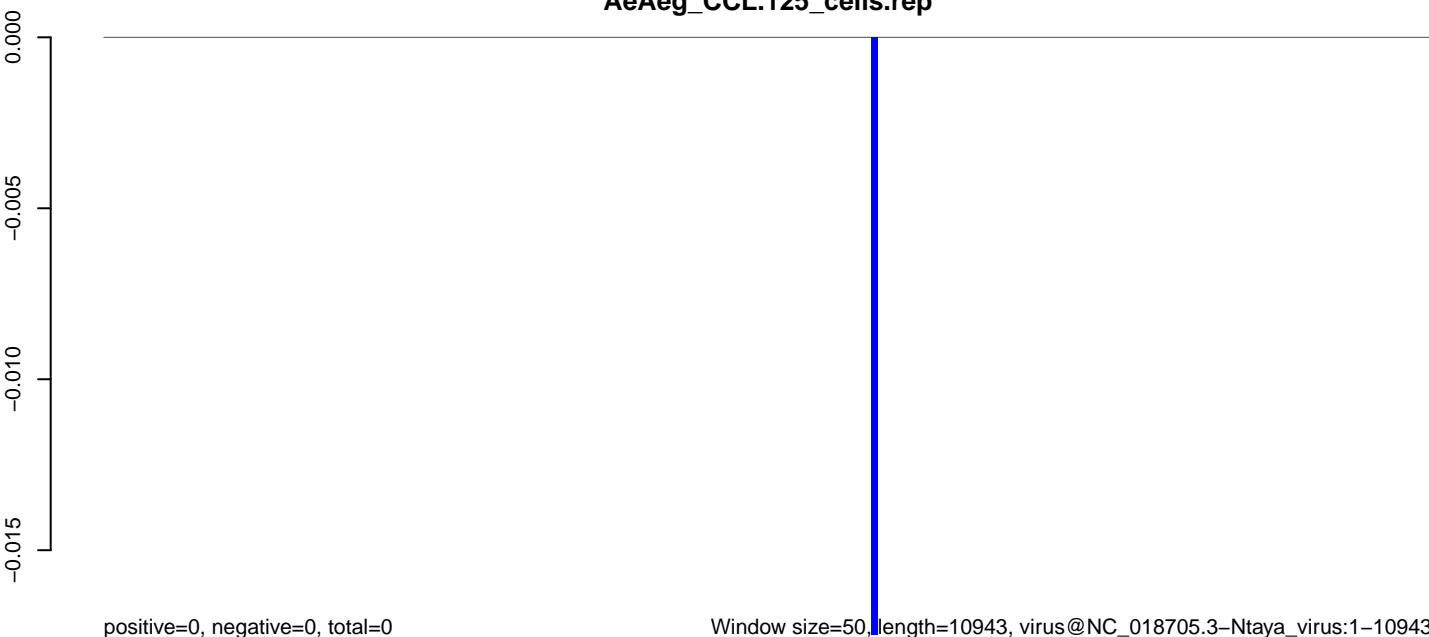
AeAeg_CCL.125_cells.18_23.rep



AeAeg_CCL.125_cells.24_35.rep

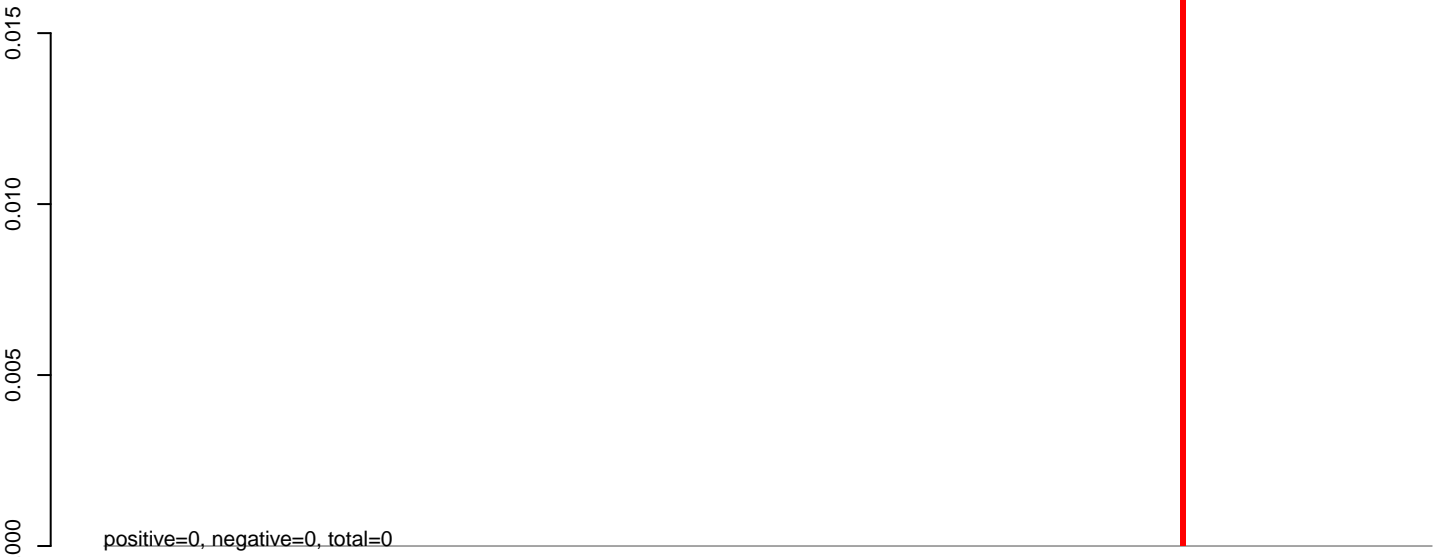


AeAeg_CCL.125_cells.rep

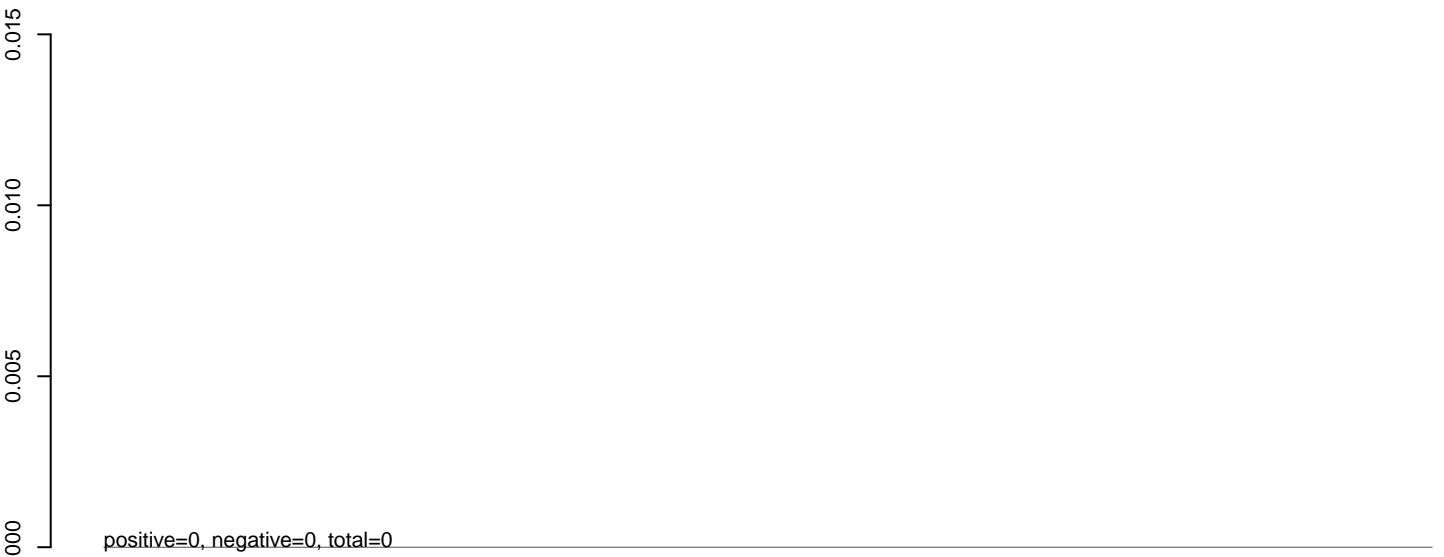


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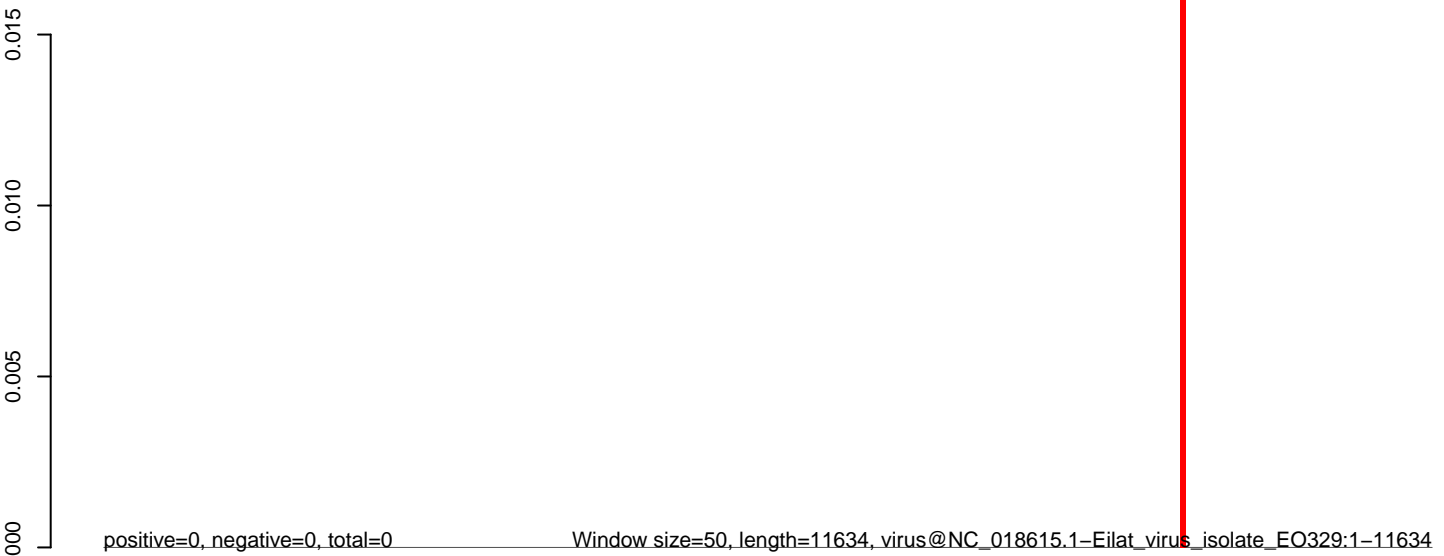
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AeAeg_CCL.125_cells.24_35.rep

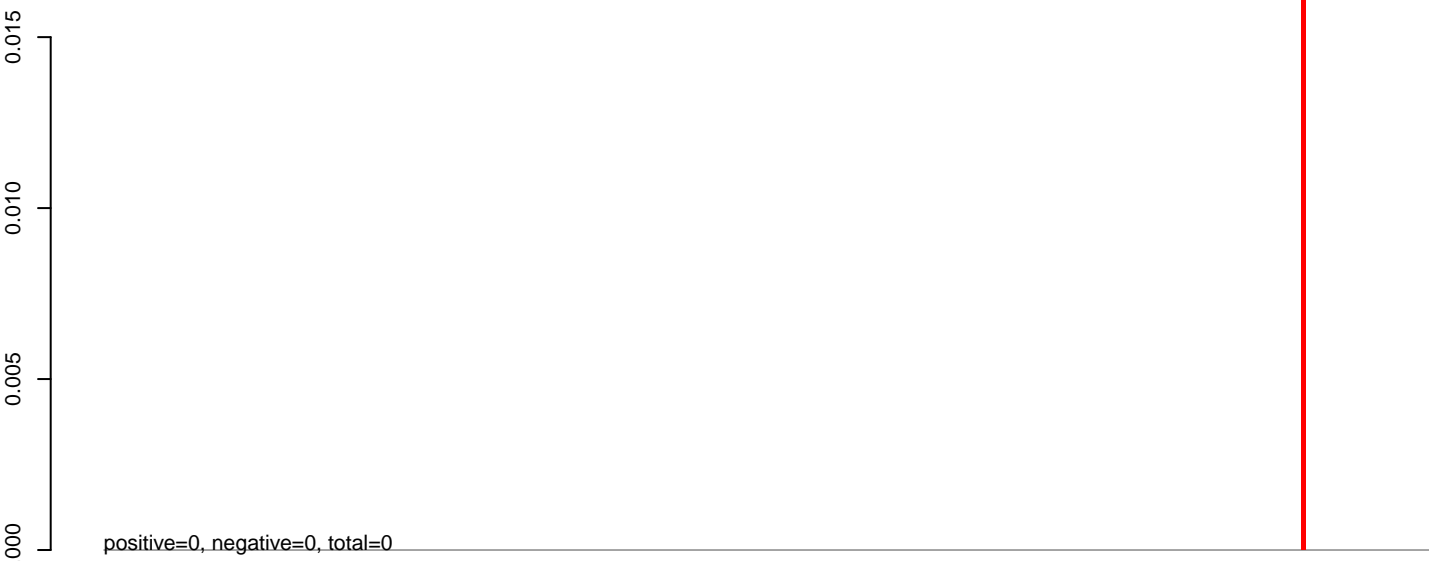


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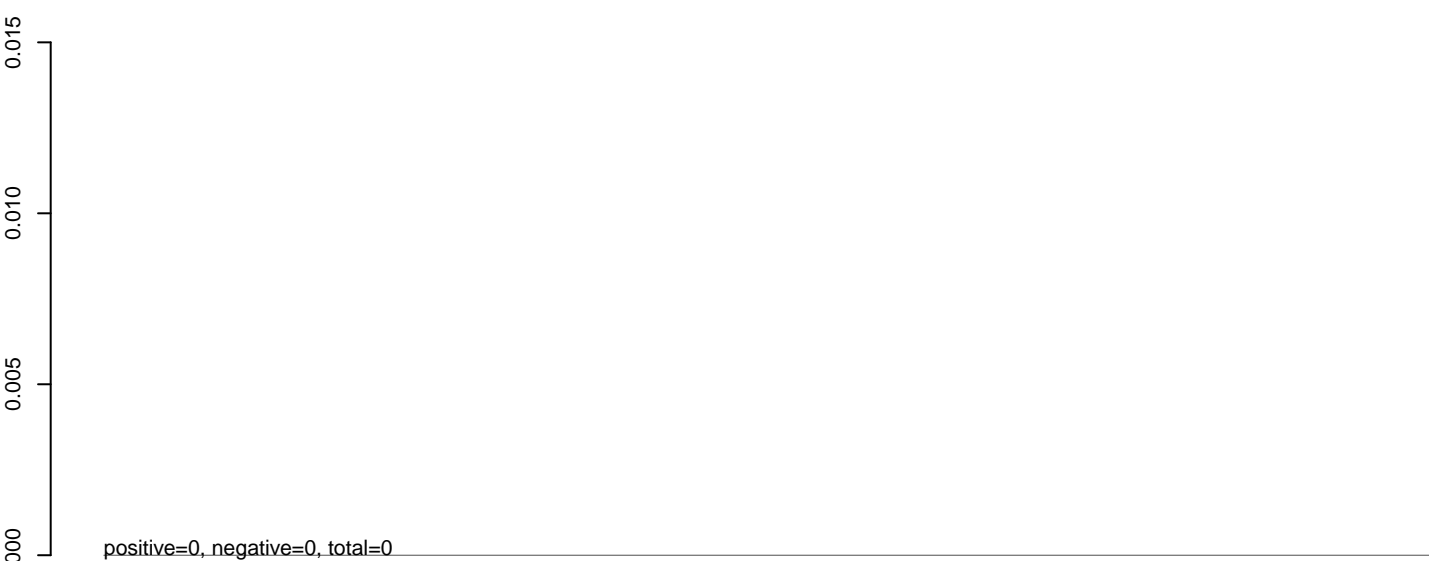


0 2000 4000 6000 8000 10000 12000

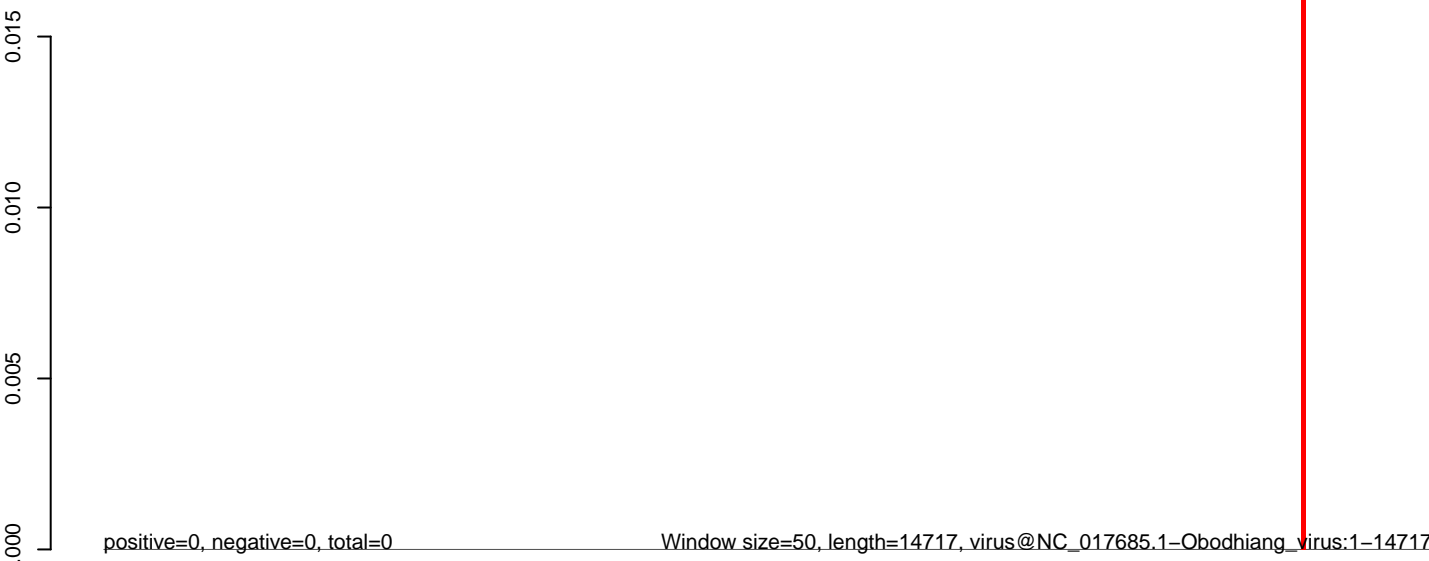
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AeAeg_CCL.125_cells.24_35.rep



AeAeg_CCL.125_cells.rep



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AeAeg_CCL.125_cells.18_23.rep

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-0.005
-0.010
-0.015
-0.020
-0.025
-0.030
-0.035

positive=0, negative=0, total=0

AeAeg_CCL.125_cells.24_35.rep

0.000
-0.005
-0.010
-0.015
-0.020
-0.025
-0.030
-0.035

positive=0, negative=0, total=0

AeAeg_CCL.125_cells.rep

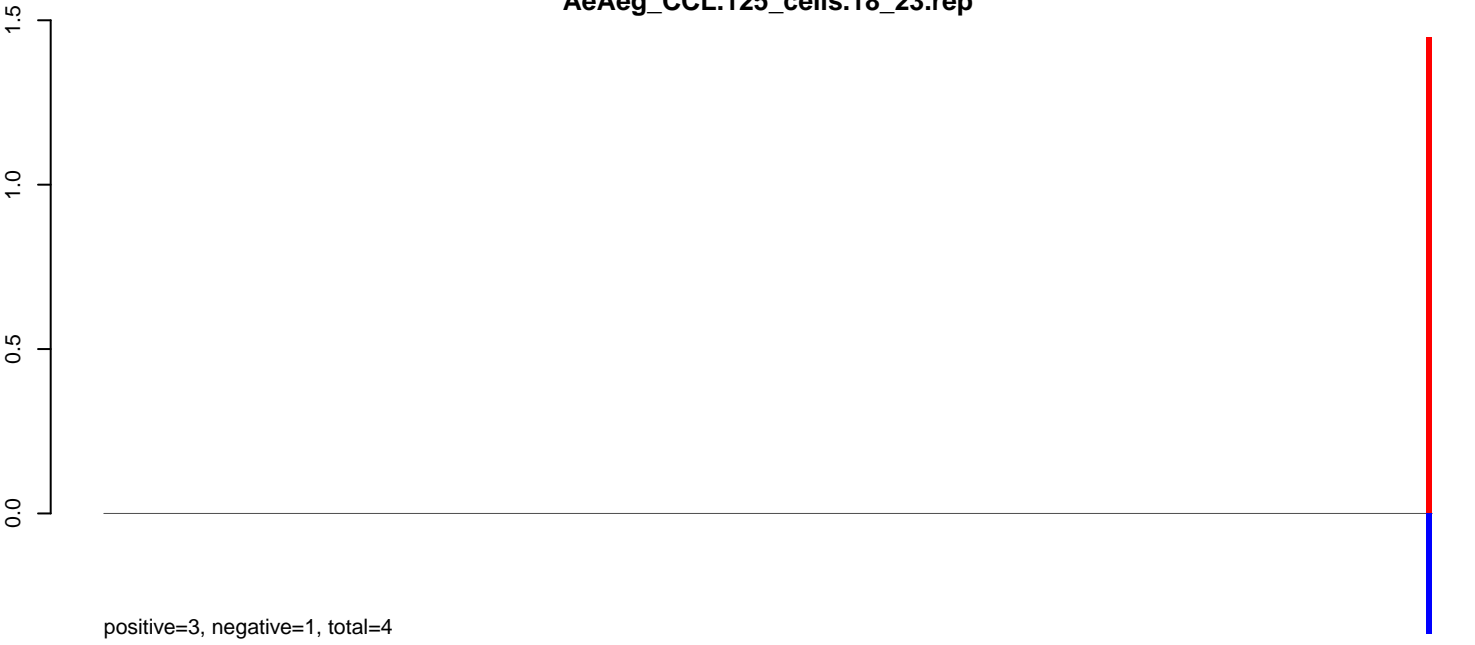
0.000
-0.005
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-0.025
-0.030
-0.035

positive=0, negative=0, total=0

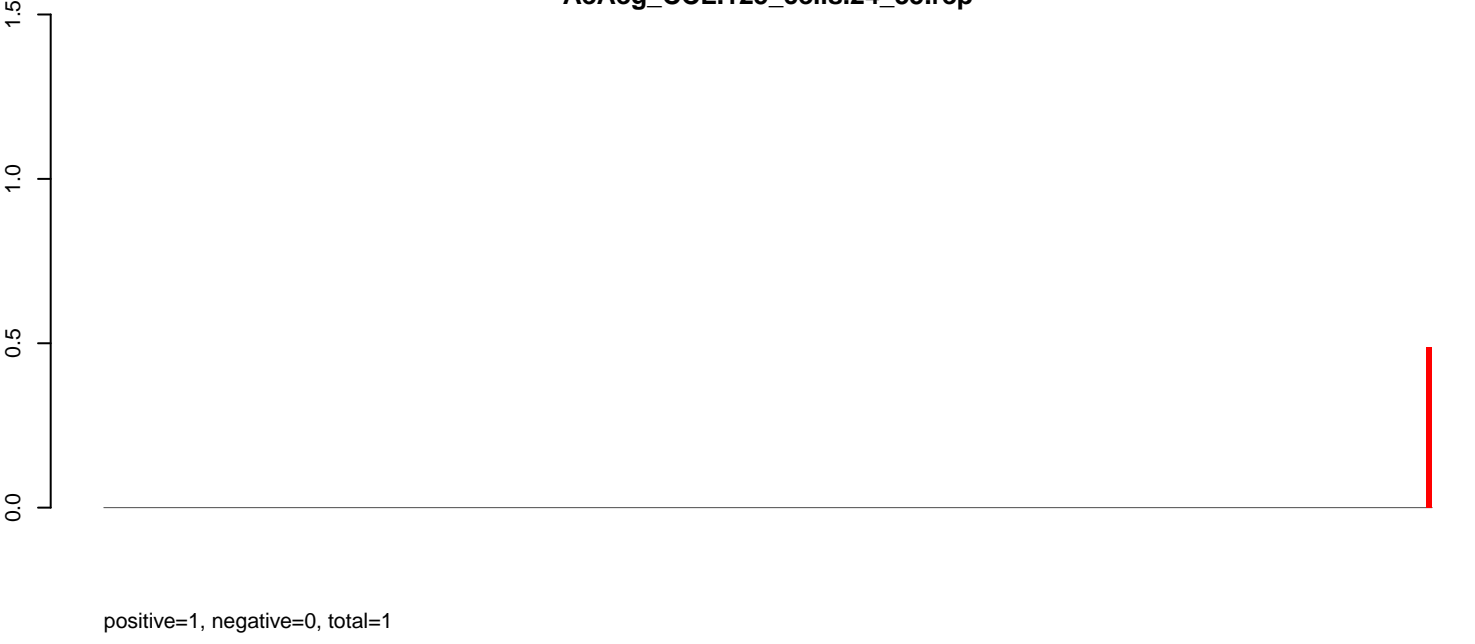
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0 2000 4000 6000 8000 10000

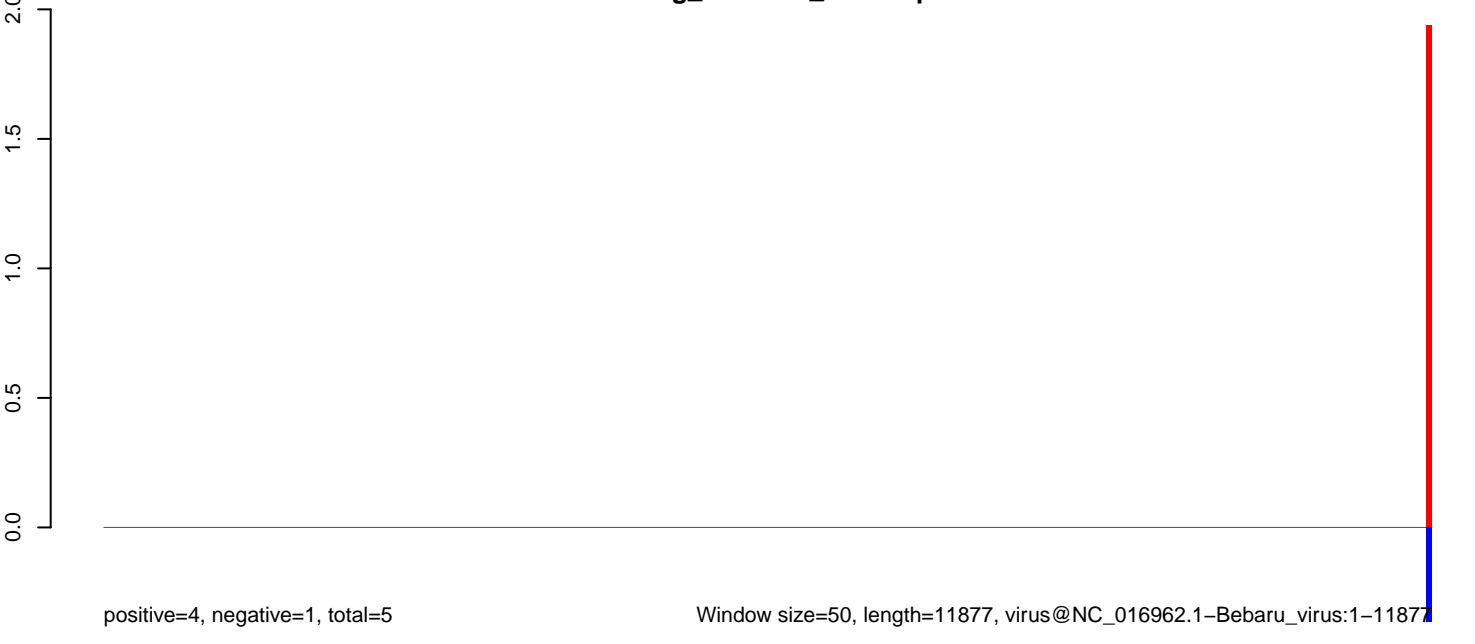
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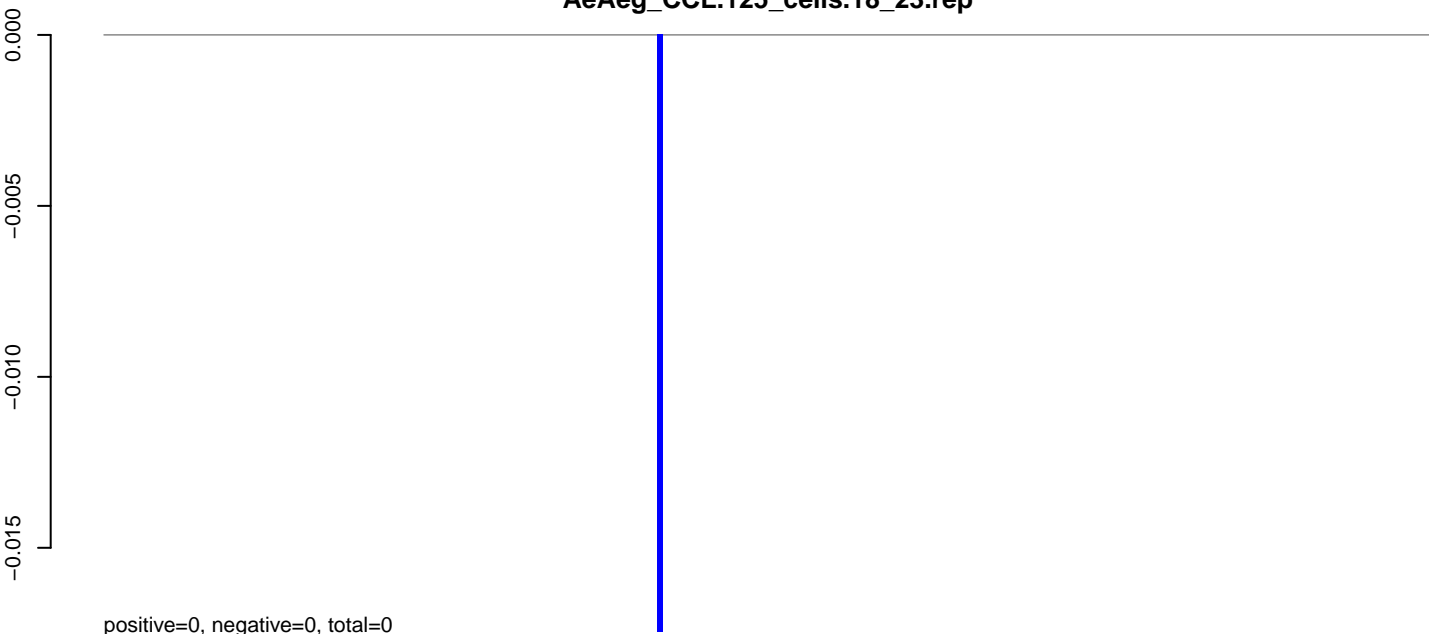
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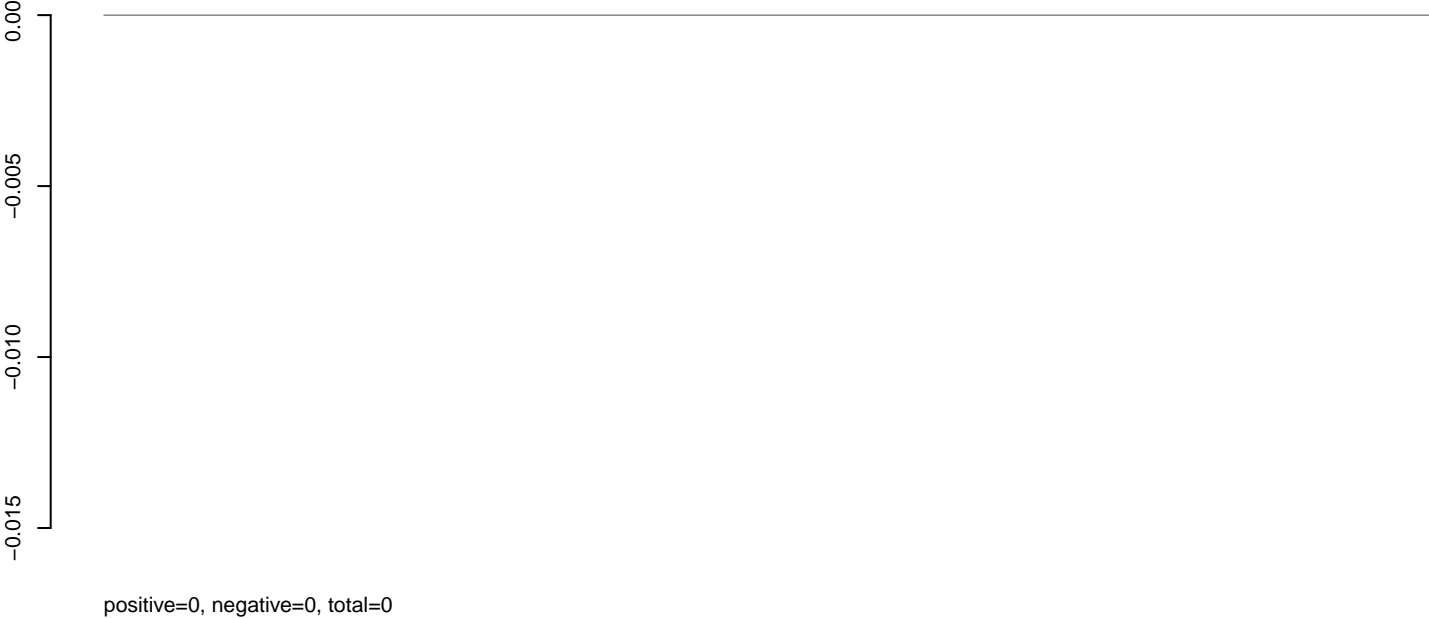
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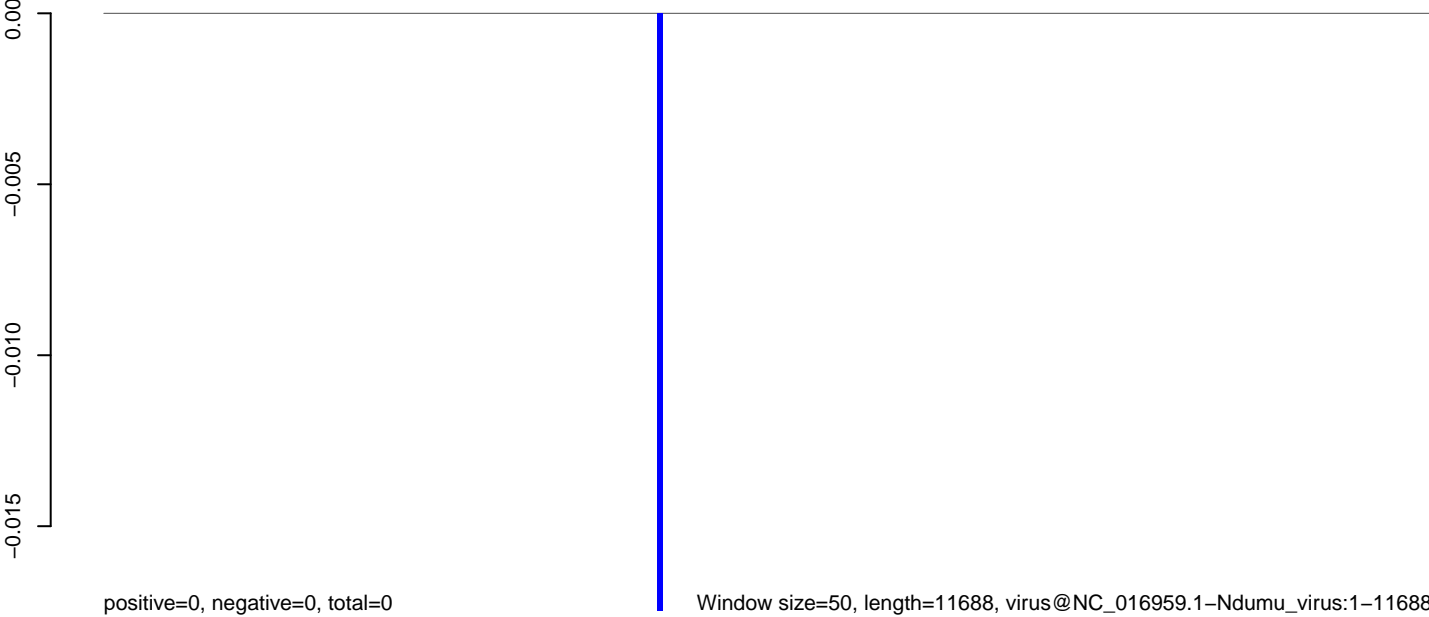
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AeAeg_CCL.125_cells.24_35.rep

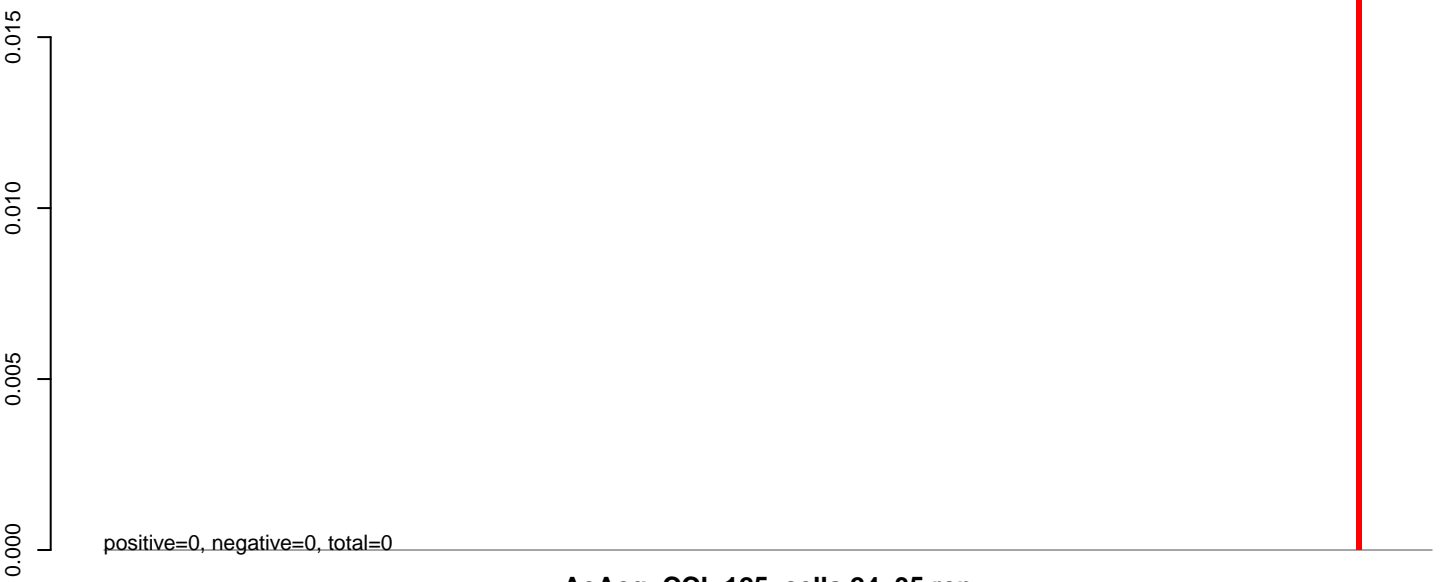


AeAeg_CCL.125_cells.rep

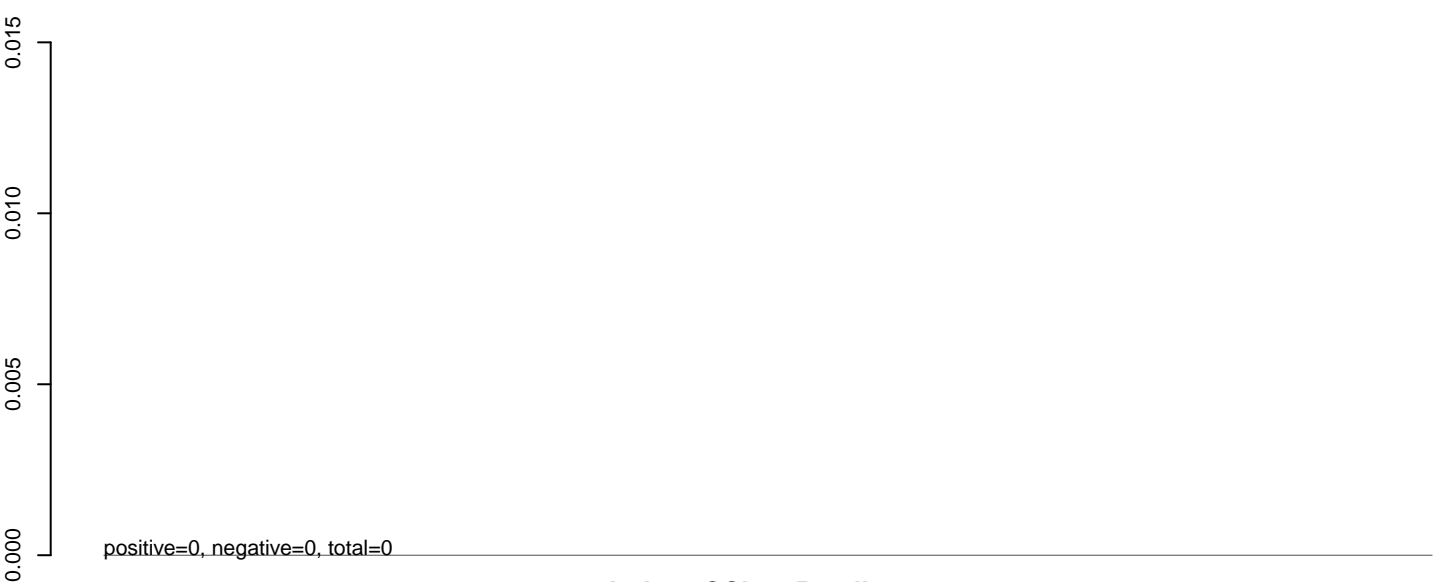


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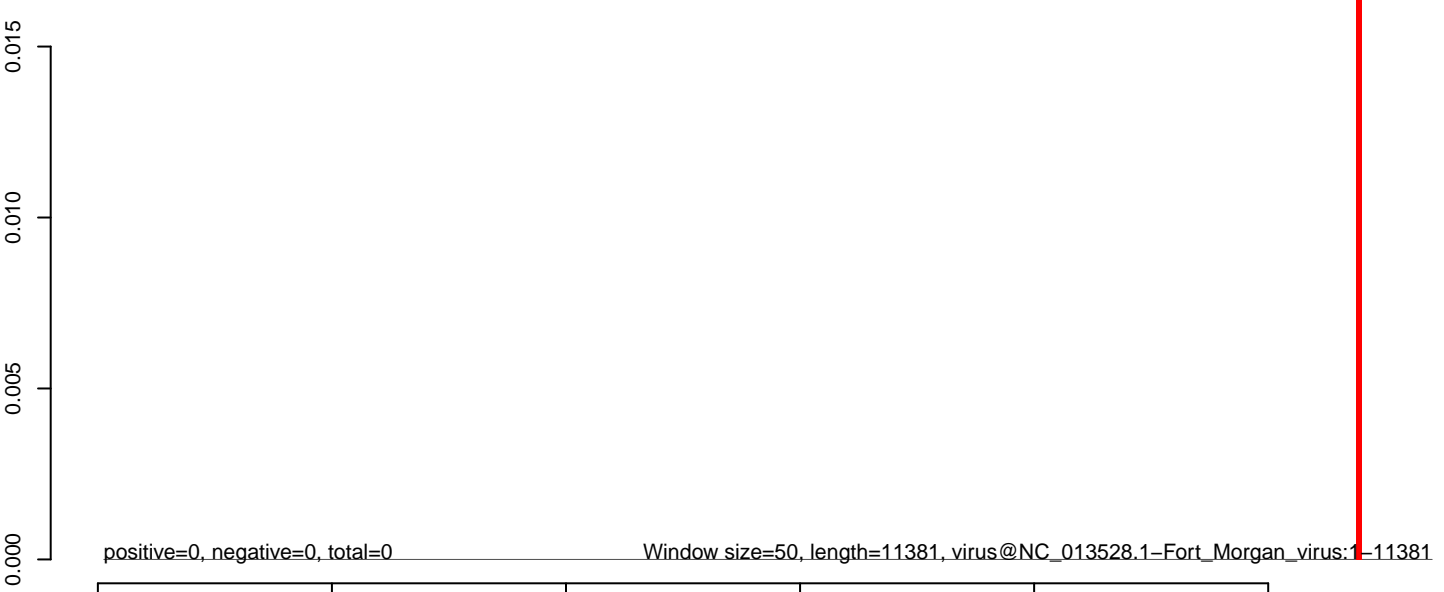
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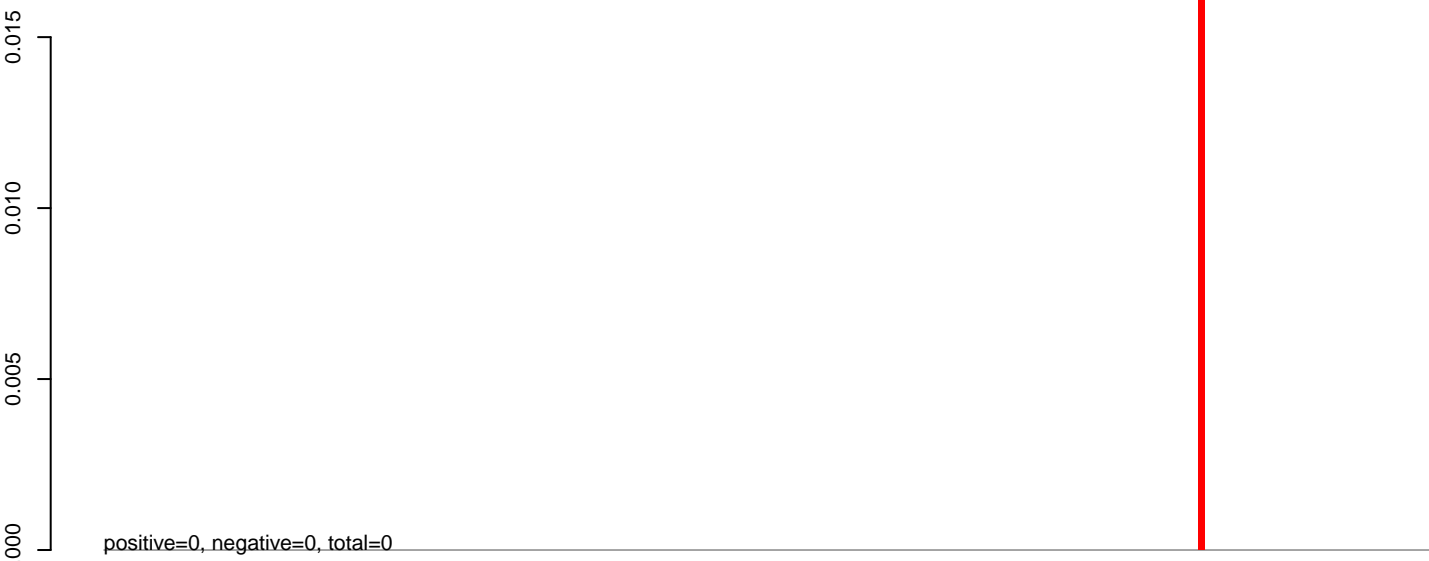
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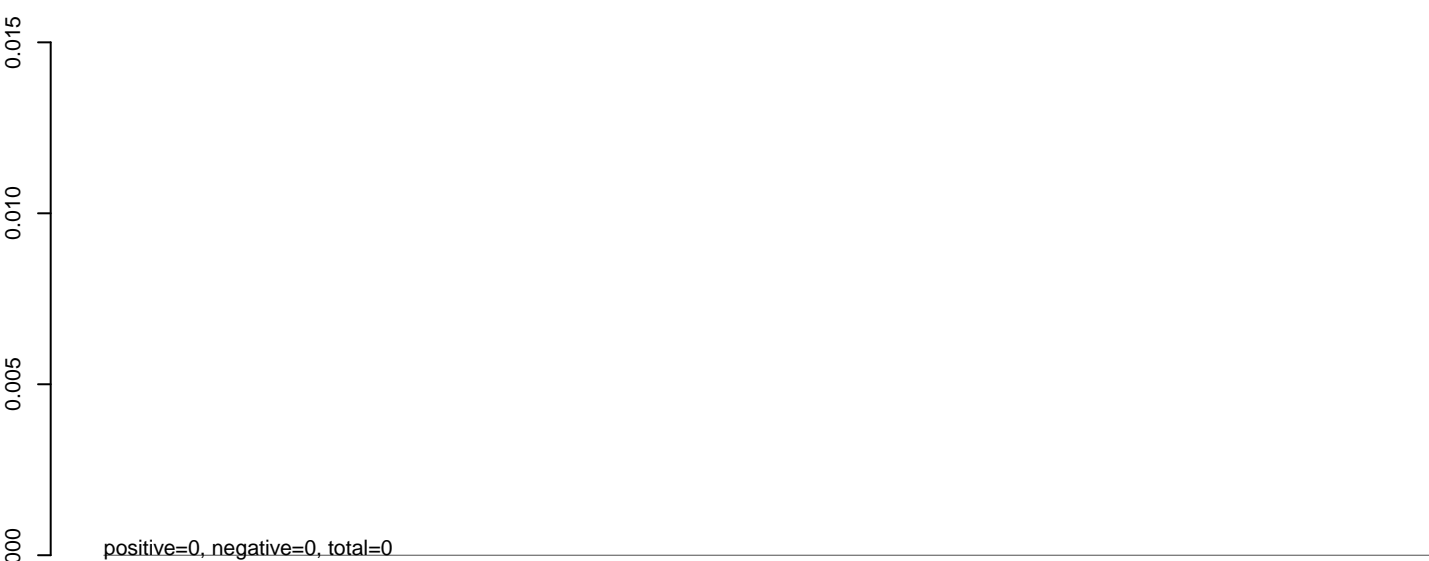
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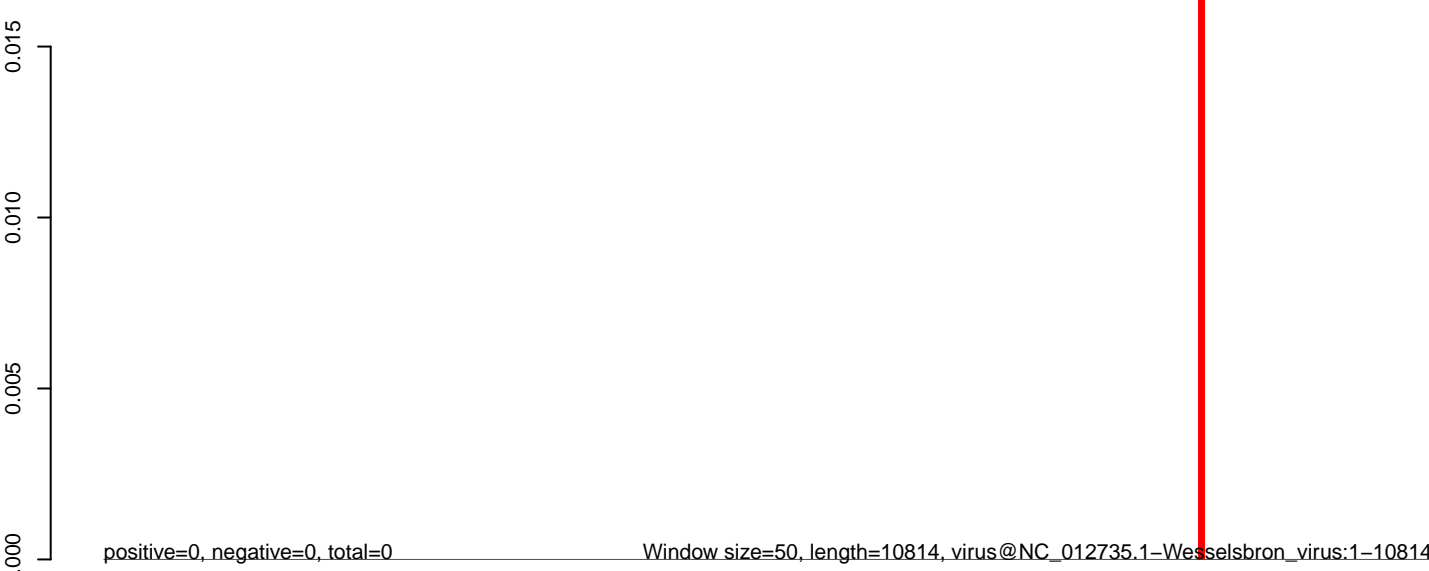
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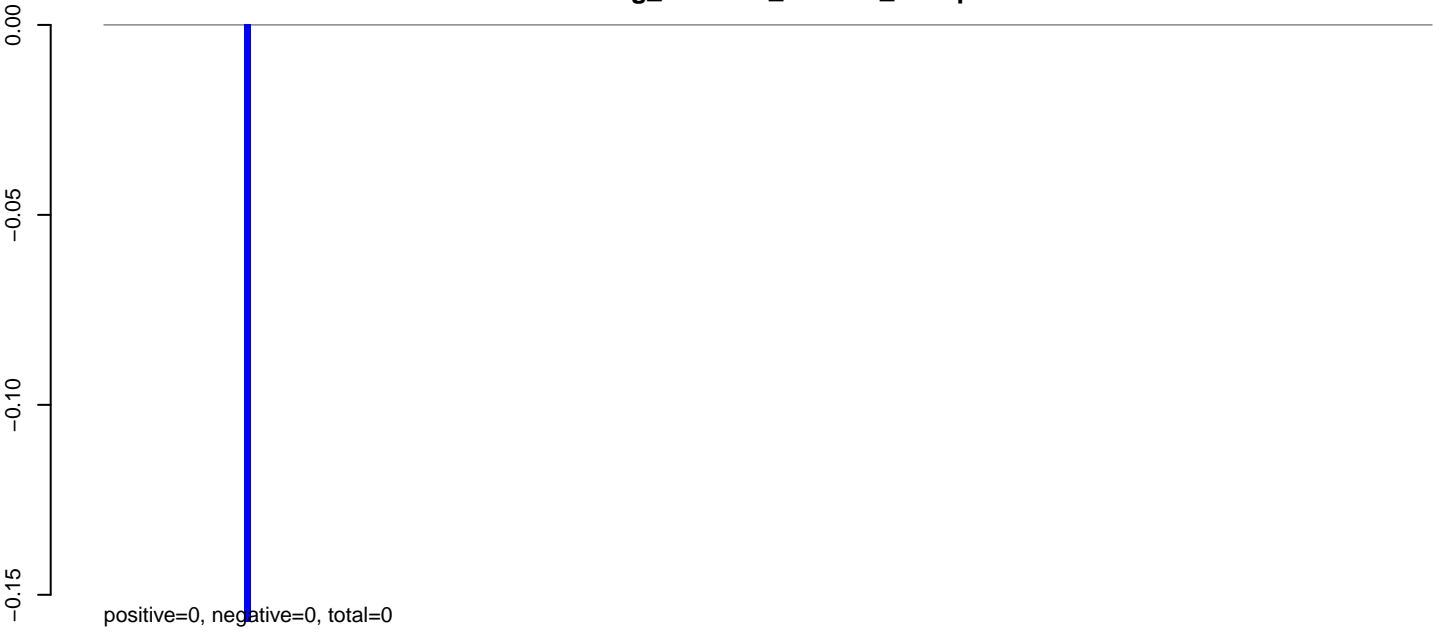


AeAeg_CCL.125_cells.rep

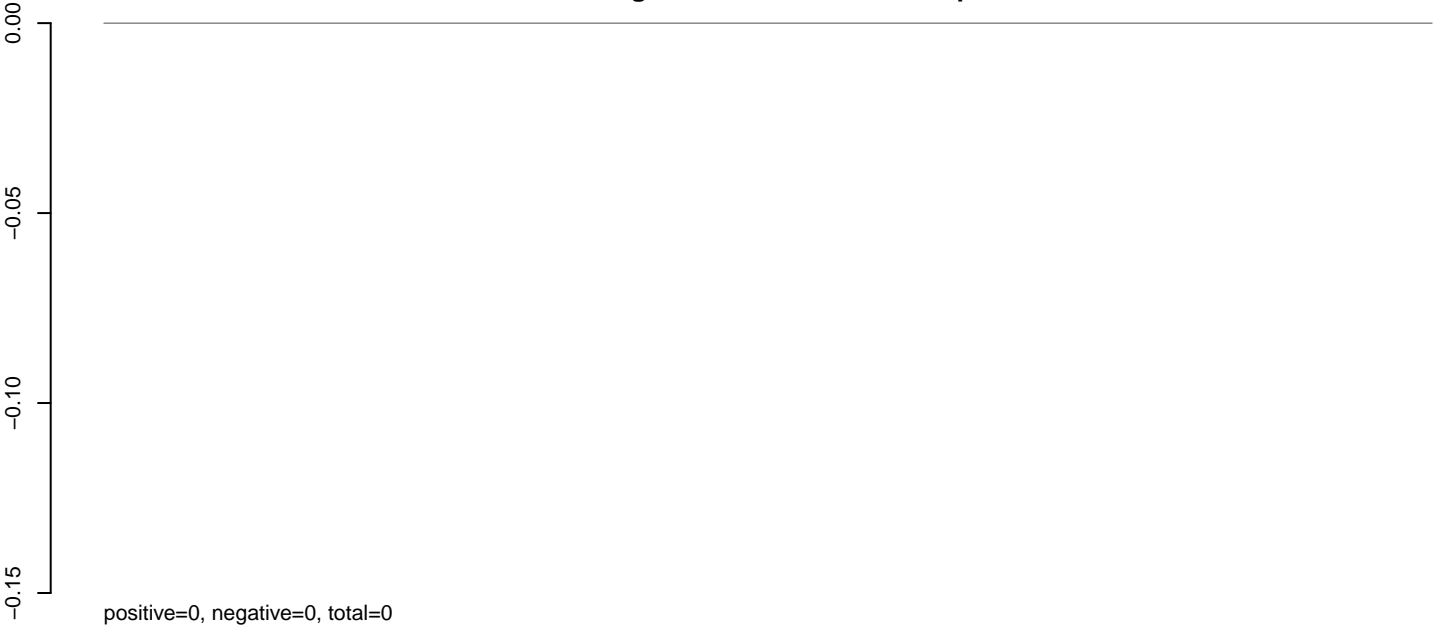


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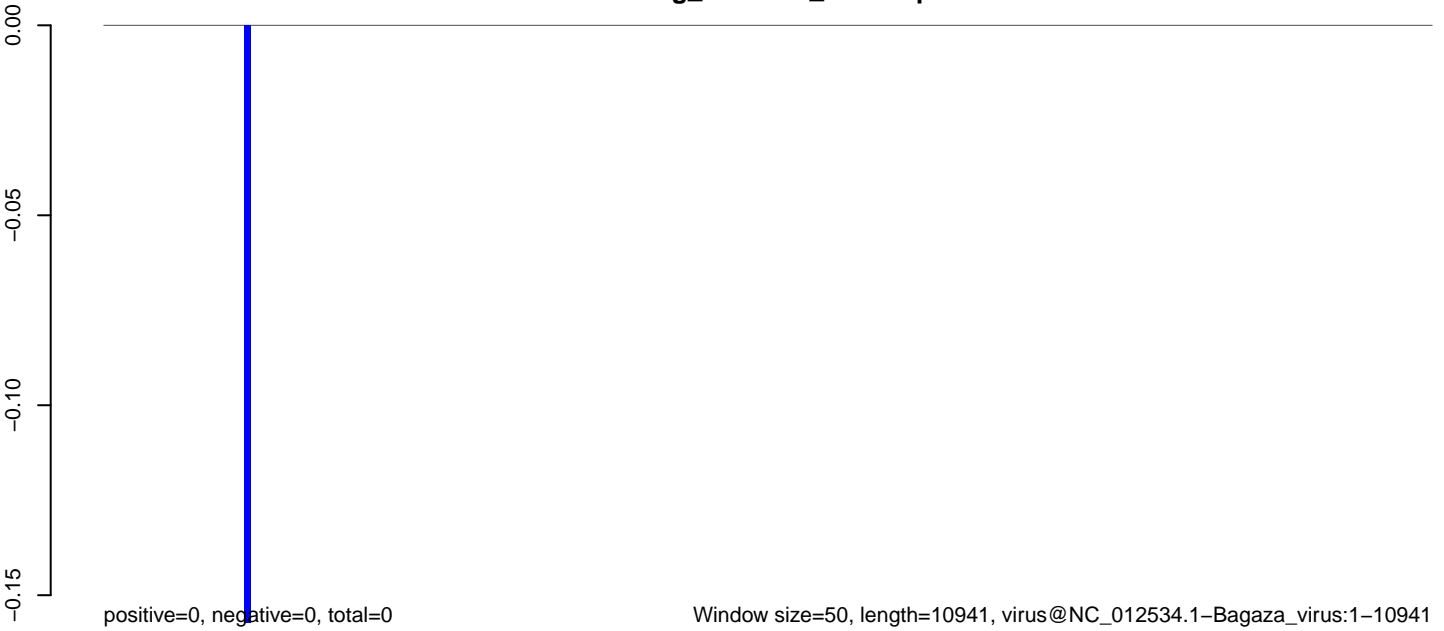
AeAeg_CCL.125_cells.18_23.rep



AeAeg_CCL.125_cells.24_35.rep



AeAeg_CCL.125_cells.rep



0 2000 4000 6000 8000 10000

AeAeg_CCL.125_cells.18_23.rep

0.00
-0.01
-0.02
-0.03
-0.04
-0.05

positive=0, negative=0, total=0

AeAeg_CCL.125_cells.24_35.rep

0.00
-0.01
-0.02
-0.03
-0.04
-0.05

positive=0, negative=0, total=0

AeAeg_CCL.125_cells.rep

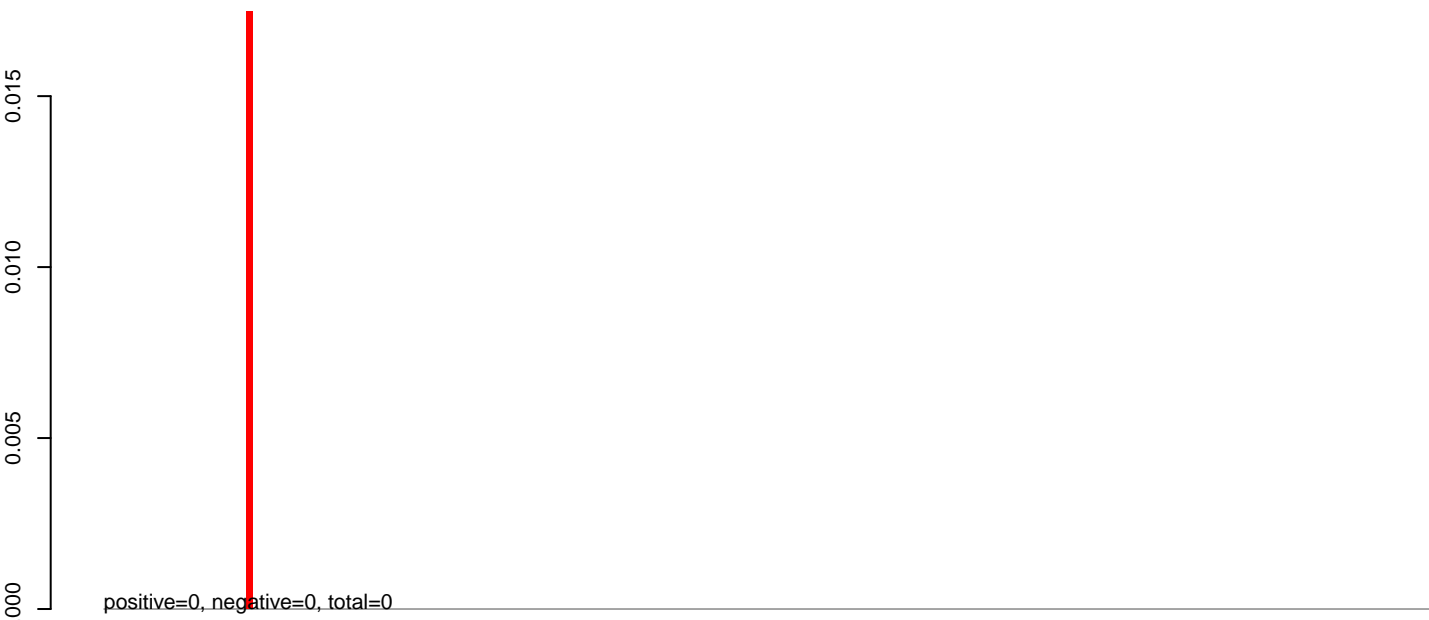
0.00
-0.01
-0.02
-0.03
-0.04
-0.05

positive=0, negative=0, total=0

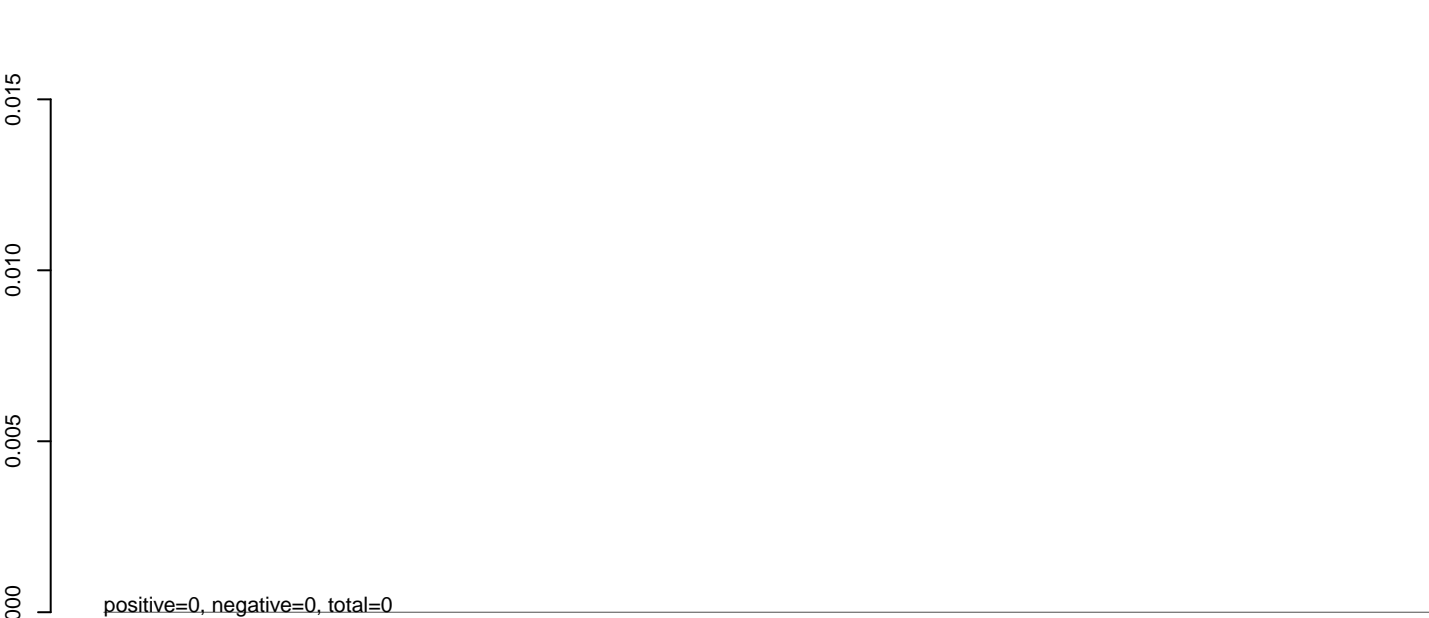
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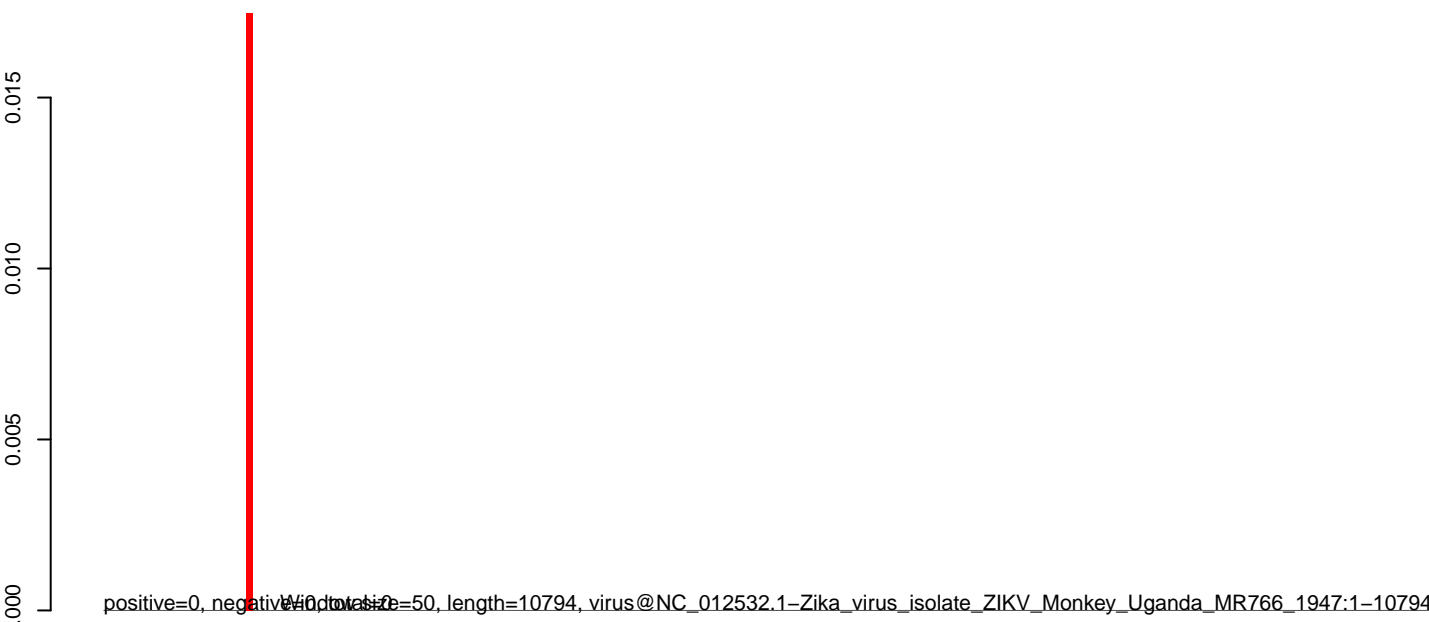
AeAeg_CCL.125_cells.18_23.rep



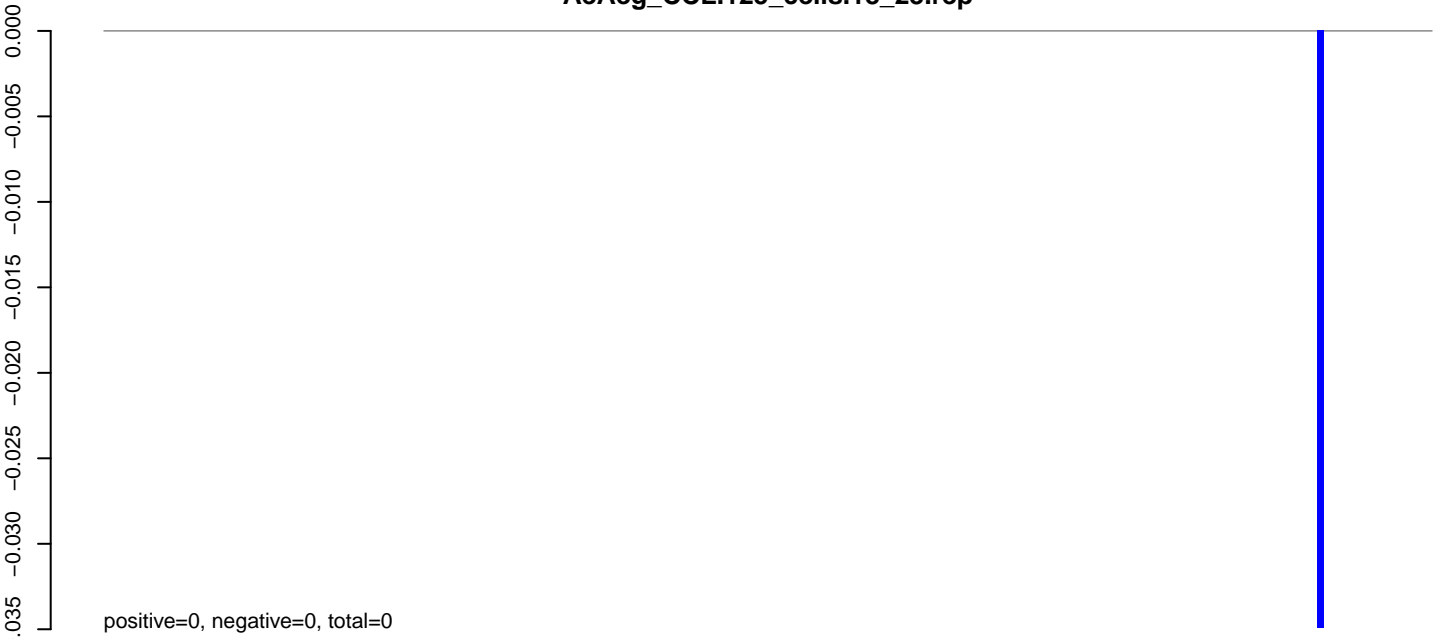
AeAeg_CCL.125_cells.24_35.rep



AeAeg_CCL.125_cells.rep

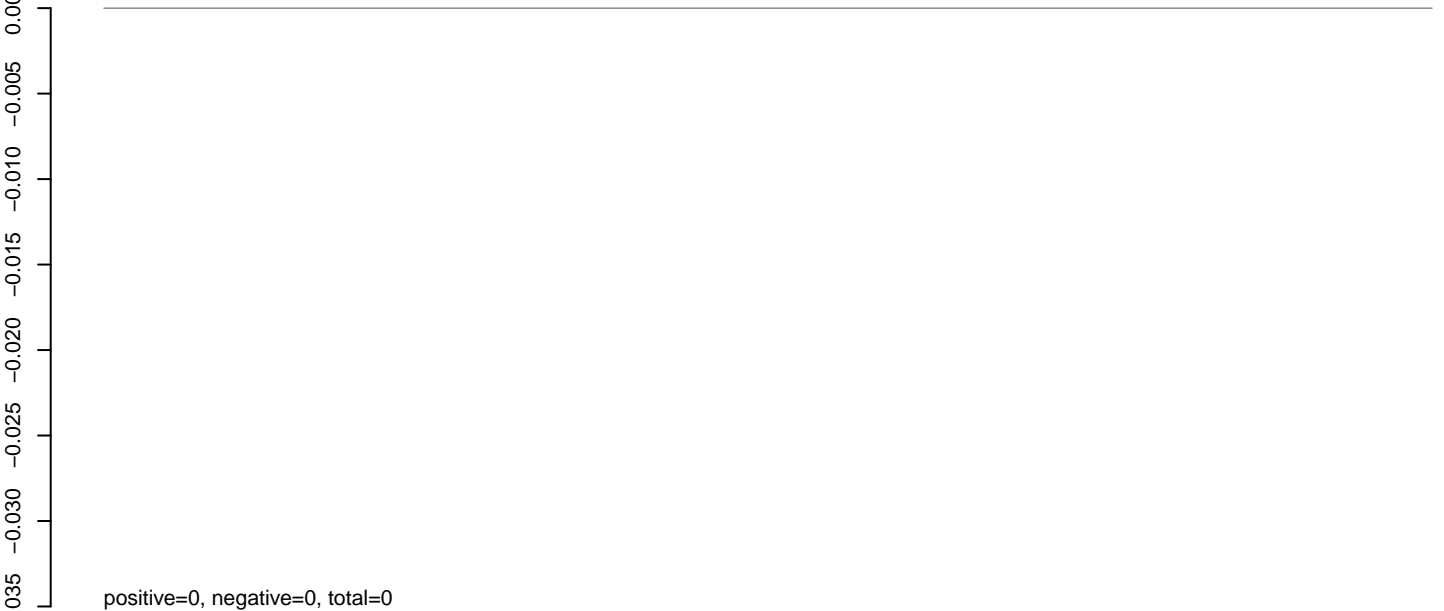


AeAeg_CCL.125_cells.18_23.rep



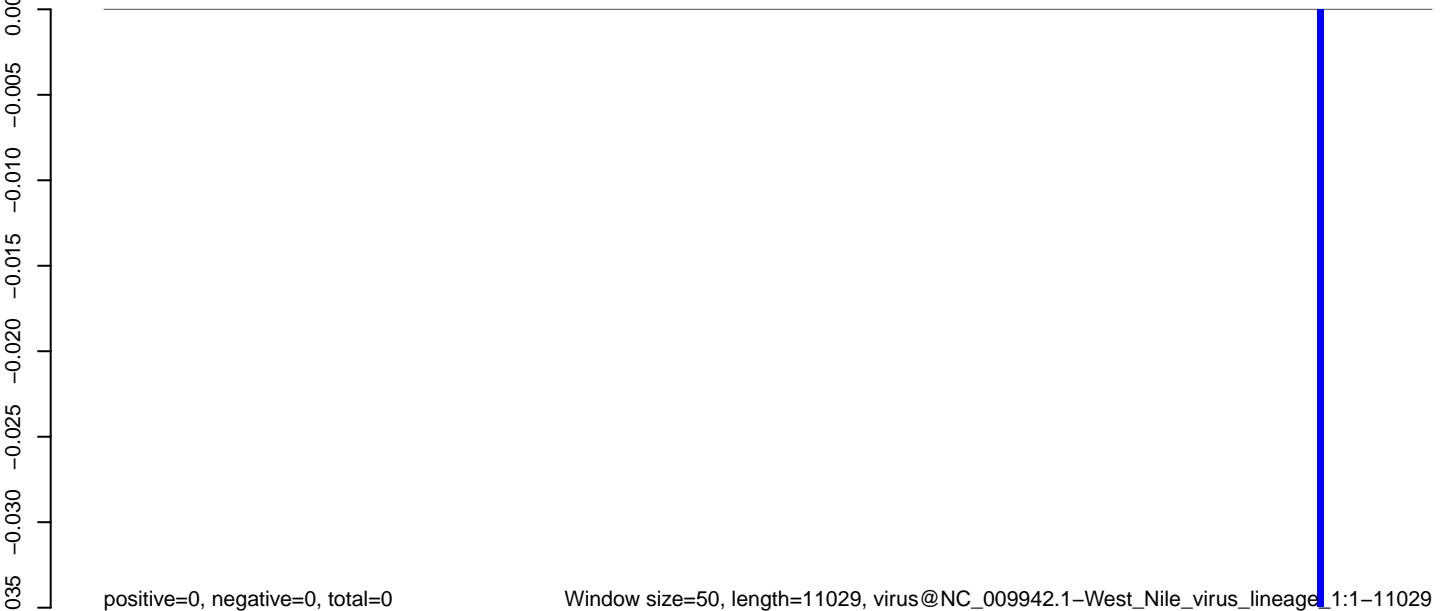
positive=0, negative=0, total=0

AeAeg_CCL.125_cells.24_35.rep



positive=0, negative=0, total=0

AeAeg_CCL.125_cells.rep

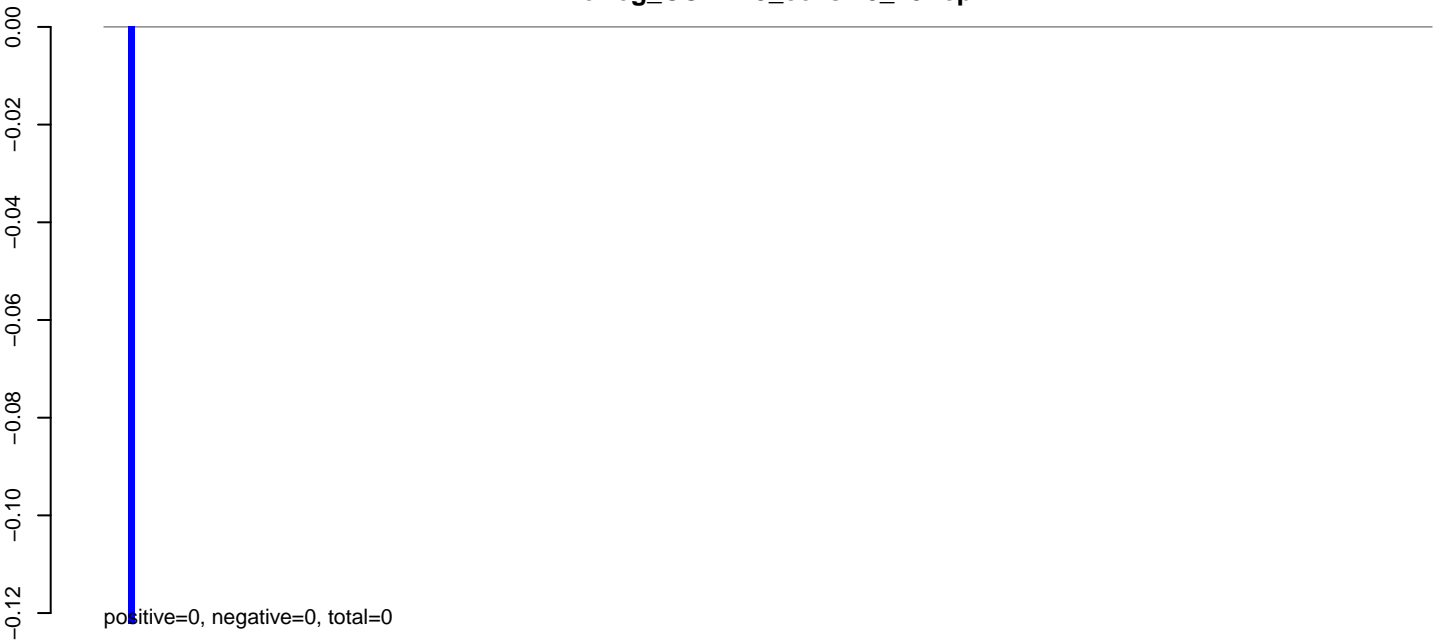


positive=0, negative=0, total=0

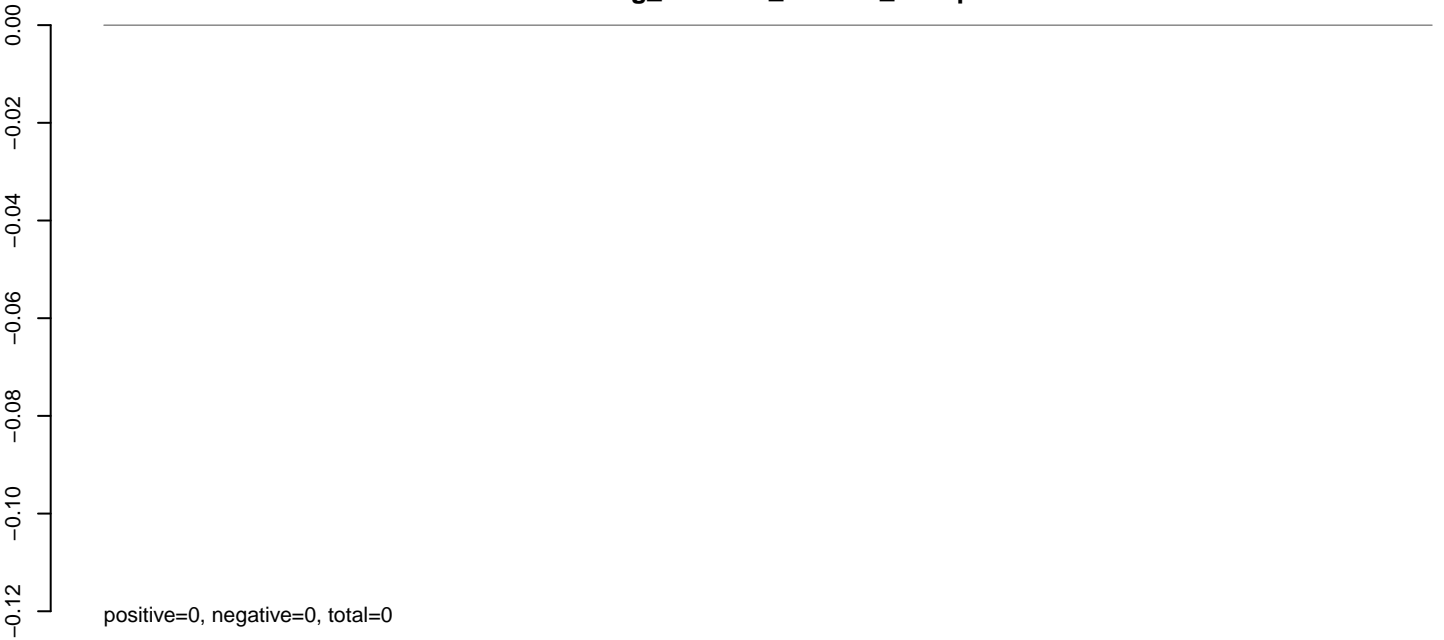
Window size=50, length=11029, virus@NC_009942.1-West_Nile_virus_lineage_1:1-11029

0 2000 4000 6000 8000 10000

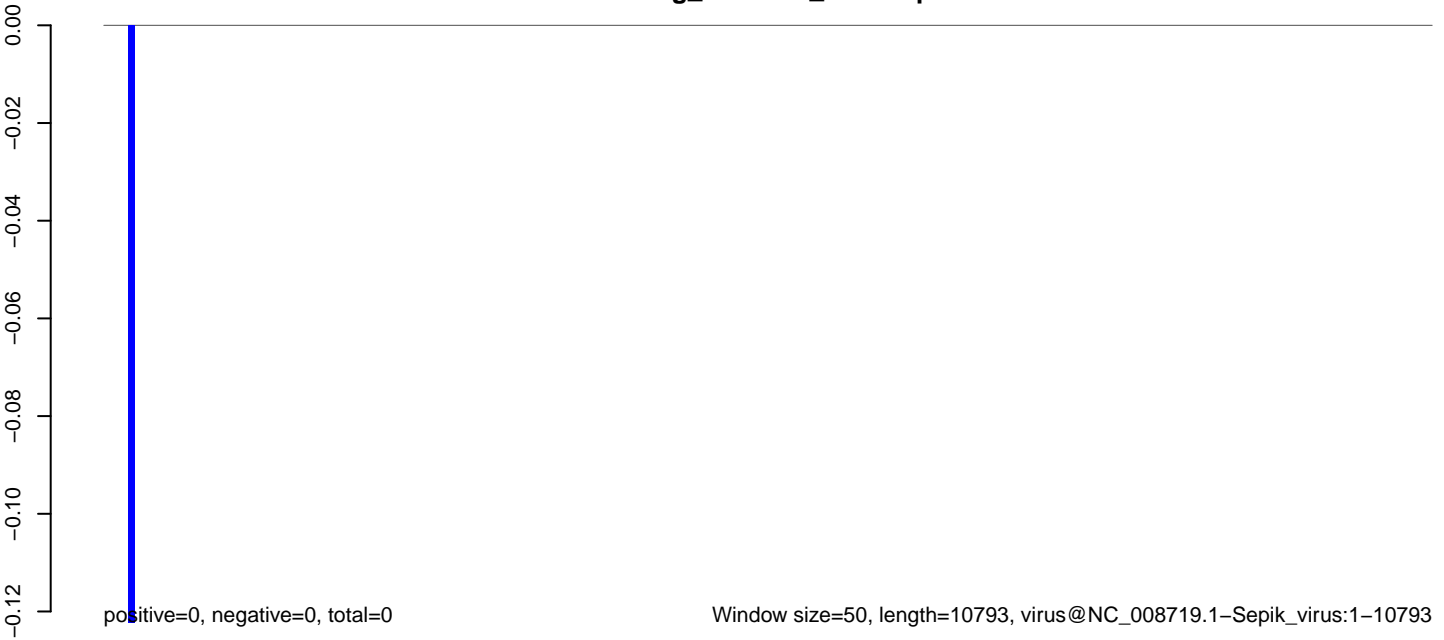
AeAeg_CCL.125_cells.18_23.rep



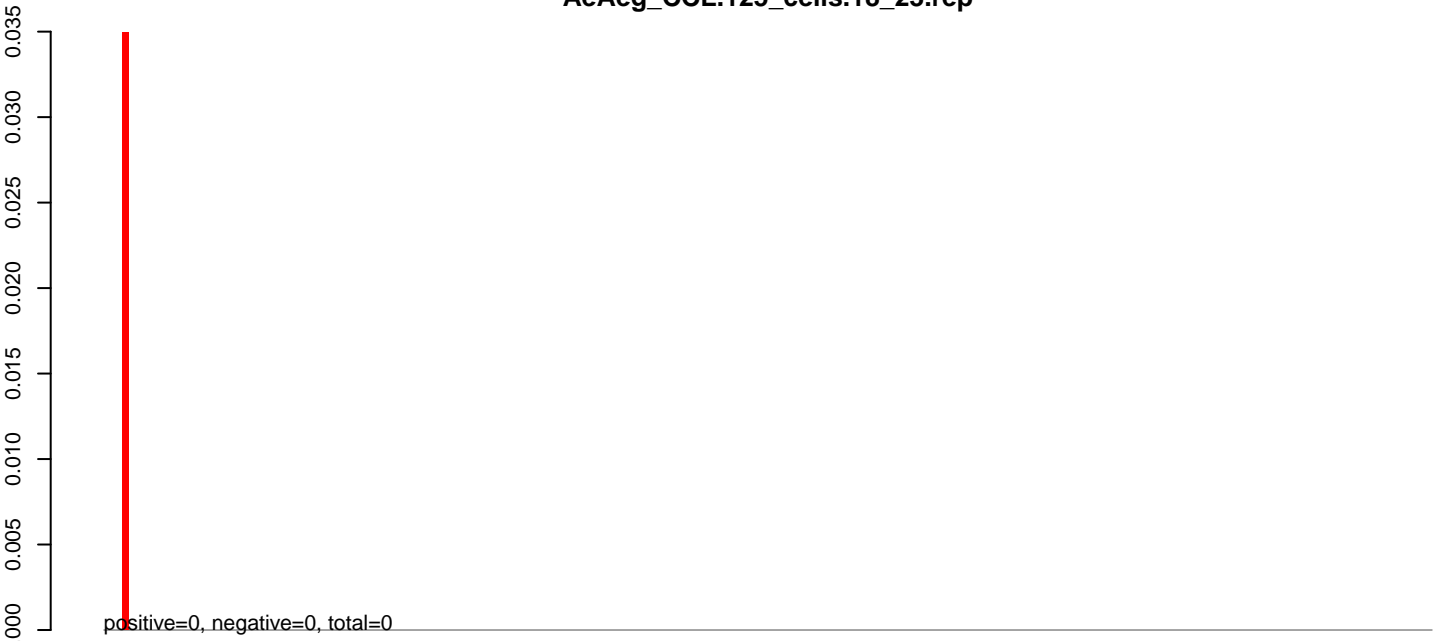
AeAeg_CCL.125_cells.24_35.rep



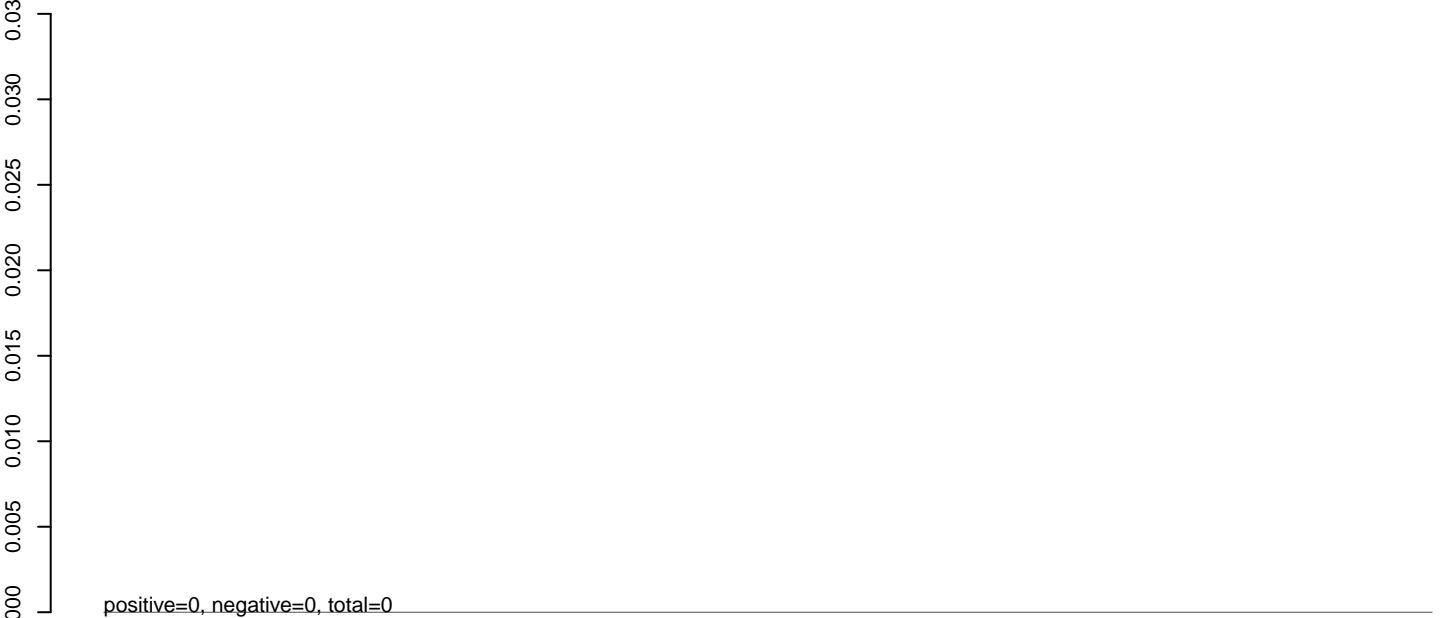
AeAeg_CCL.125_cells.rep



AeAeg_CCL.125_cells.18_23.rep



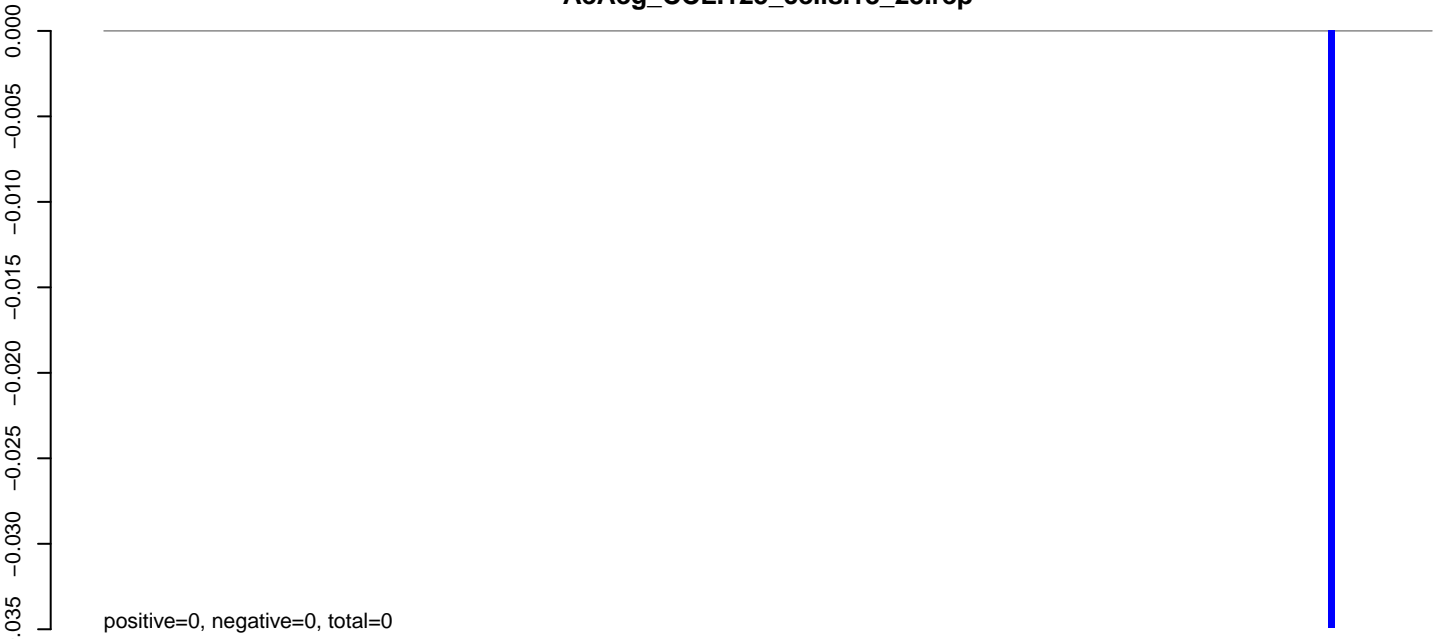
AeAeg_CCL.125_cells.24_35.rep



AeAeg_CCL.125_cells.rep

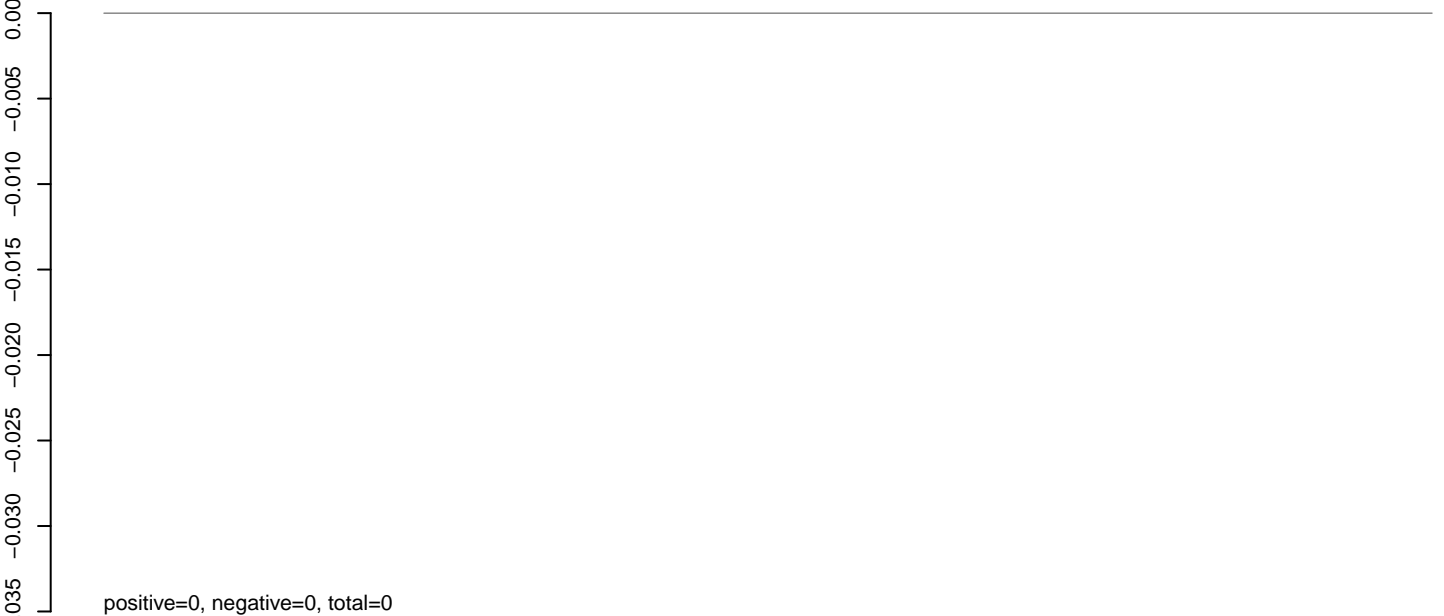


AeAeg_CCL.125_cells.18_23.rep



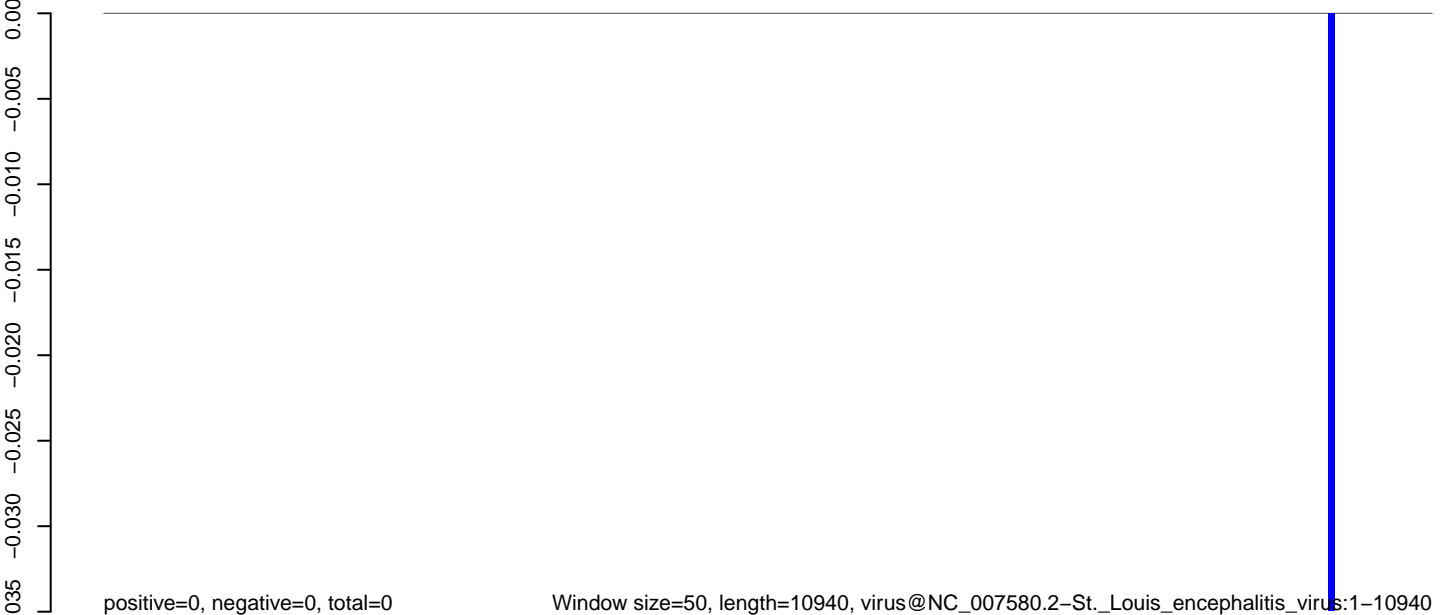
positive=0, negative=0, total=0

AeAeg_CCL.125_cells.24_35.rep



positive=0, negative=0, total=0

AeAeg_CCL.125_cells.rep

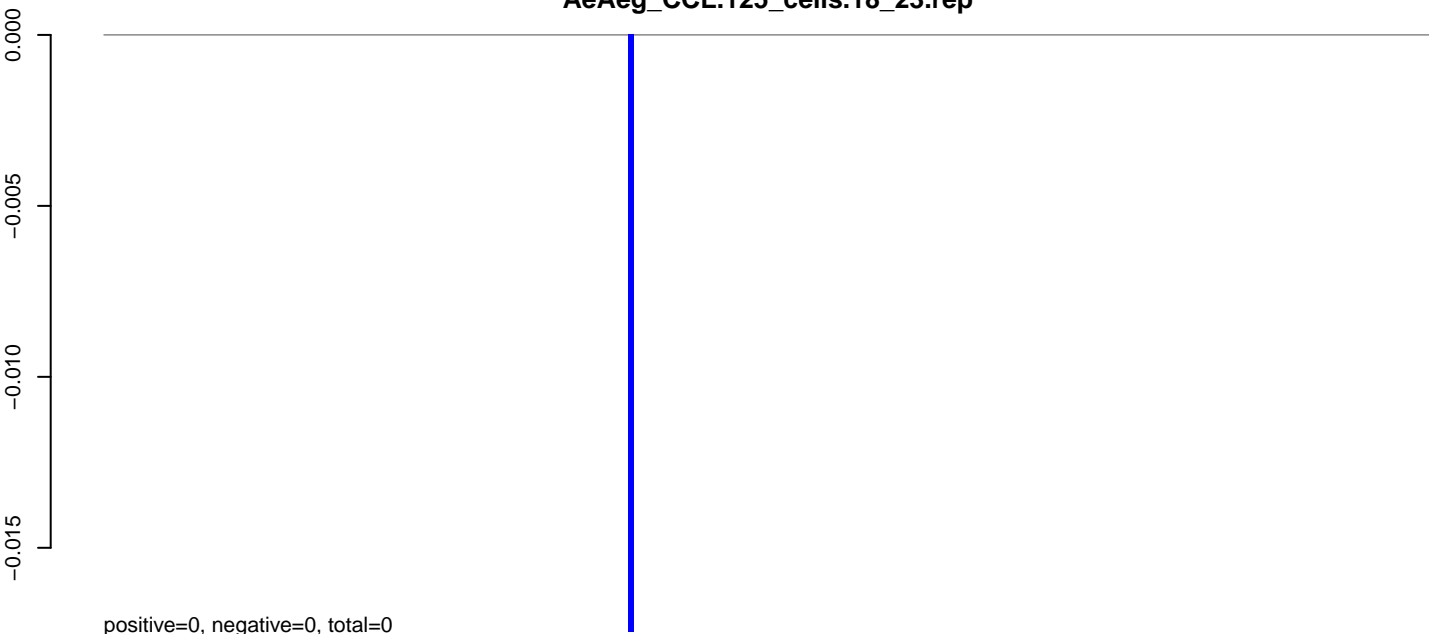


positive=0, negative=0, total=0

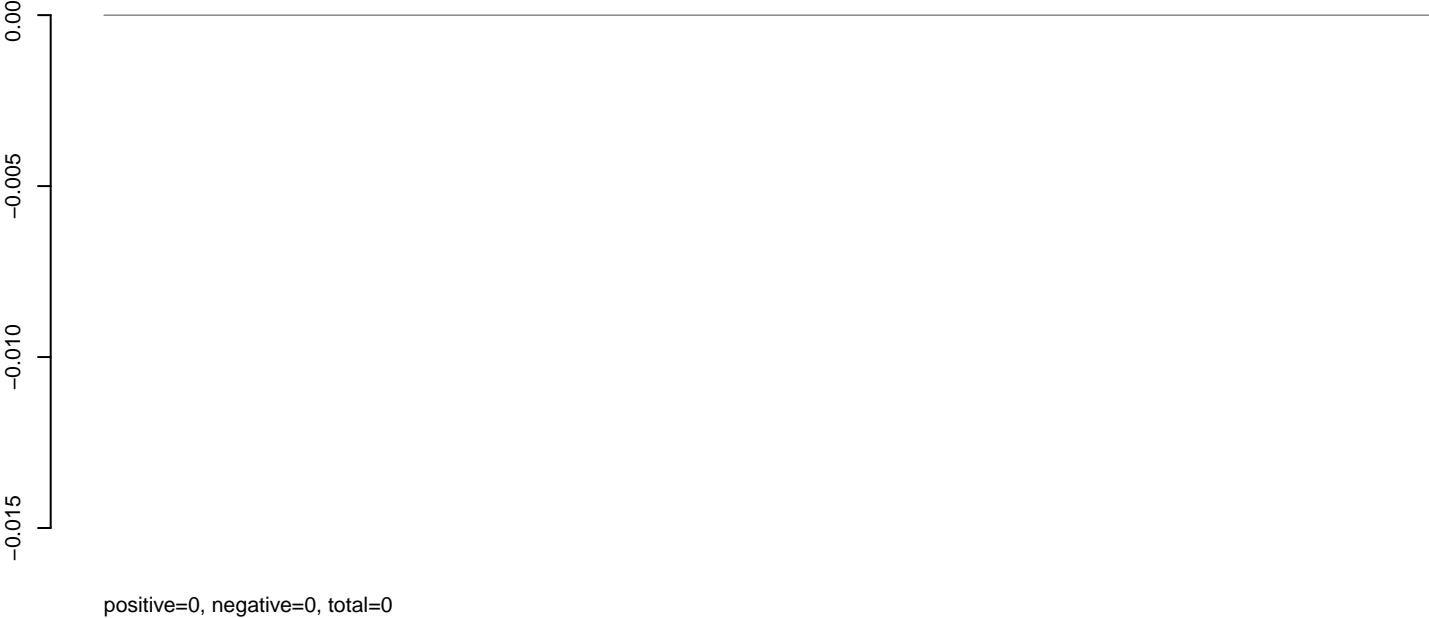
Window size=50, length=10940, virus@NC_007580.2-St._Louis_encephalitis_virus:1-10940

0 2000 4000 6000 8000 10000

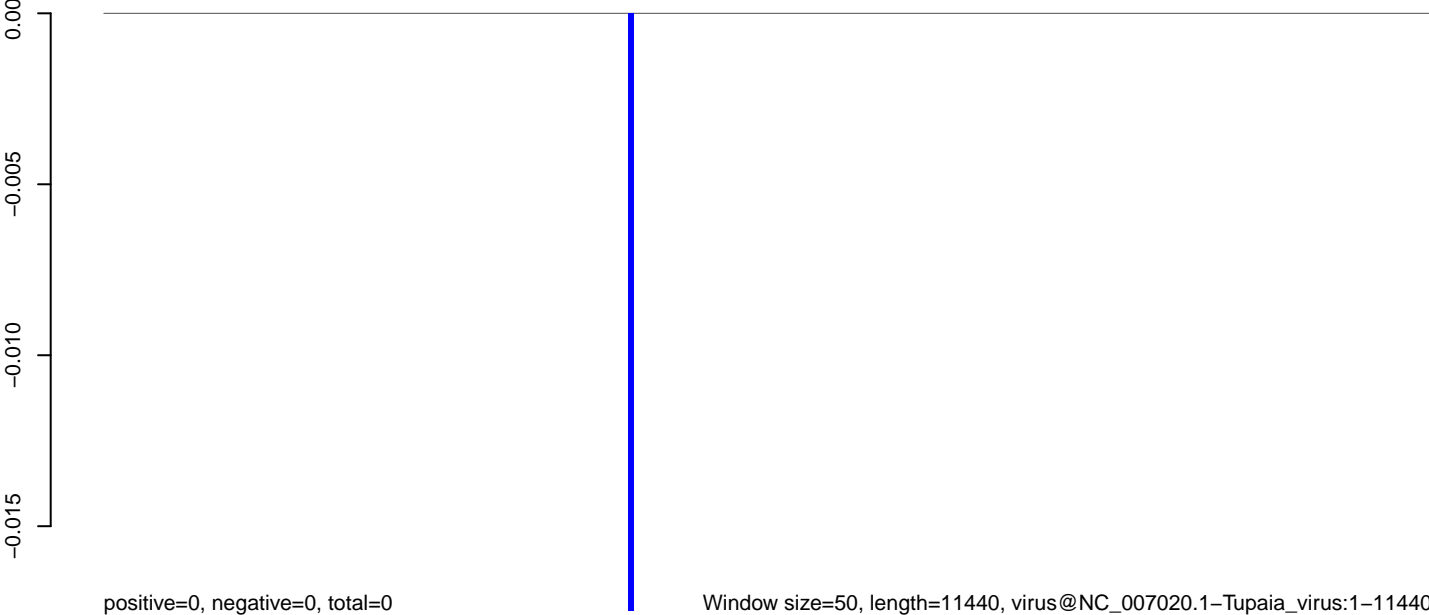
AeAeg_CCL.125_cells.18_23.rep



AeAeg_CCL.125_cells.24_35.rep

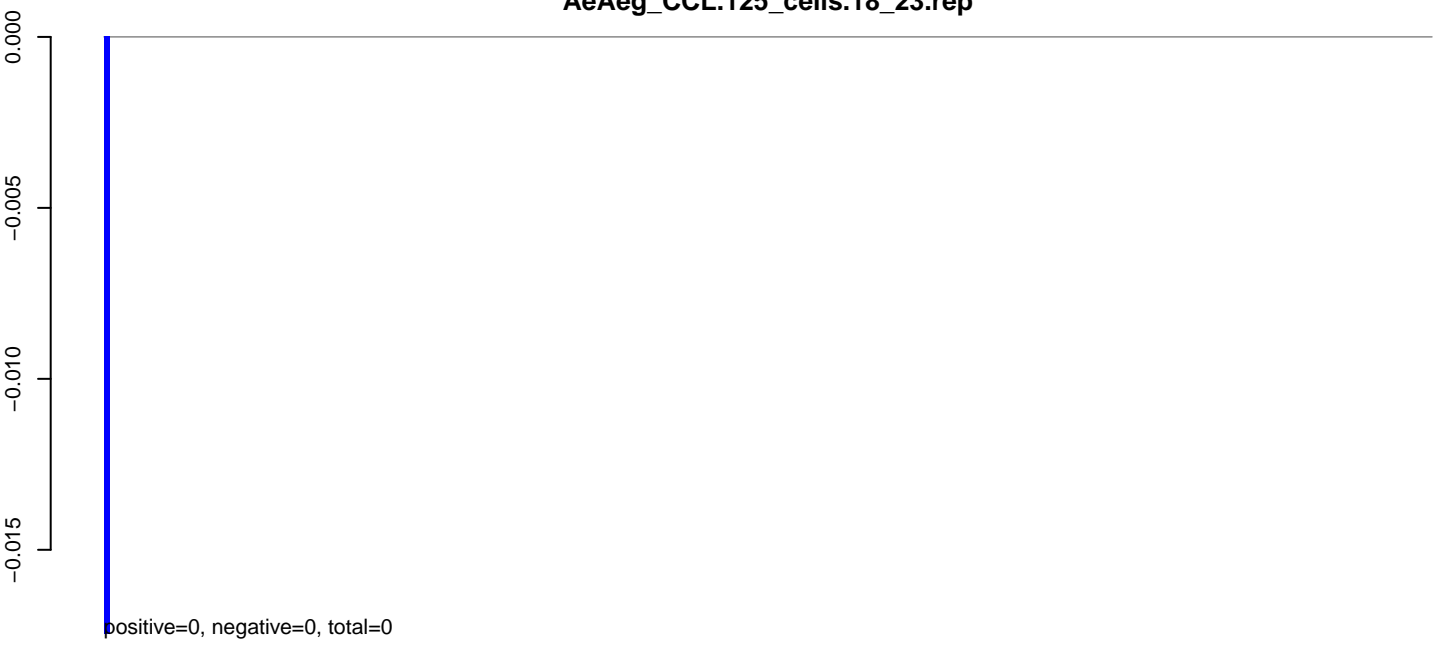


AeAeg_CCL.125_cells.rep

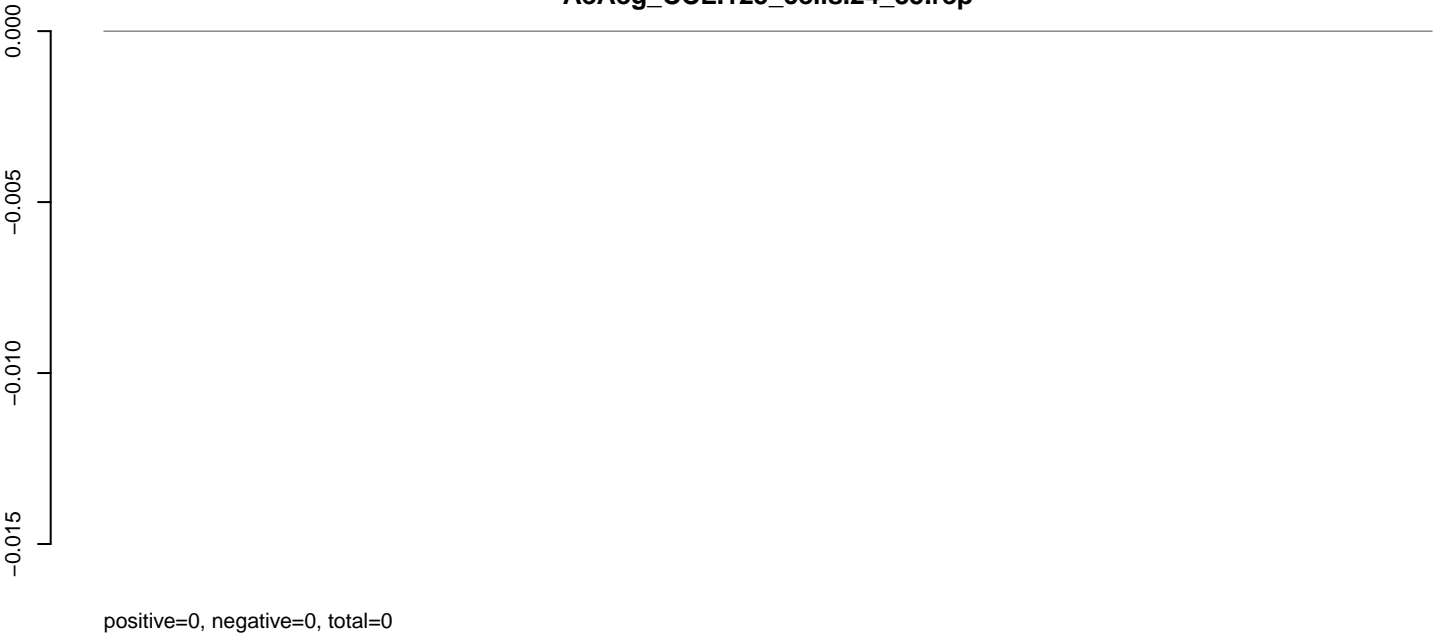


0 2000 4000 6000 8000 10000

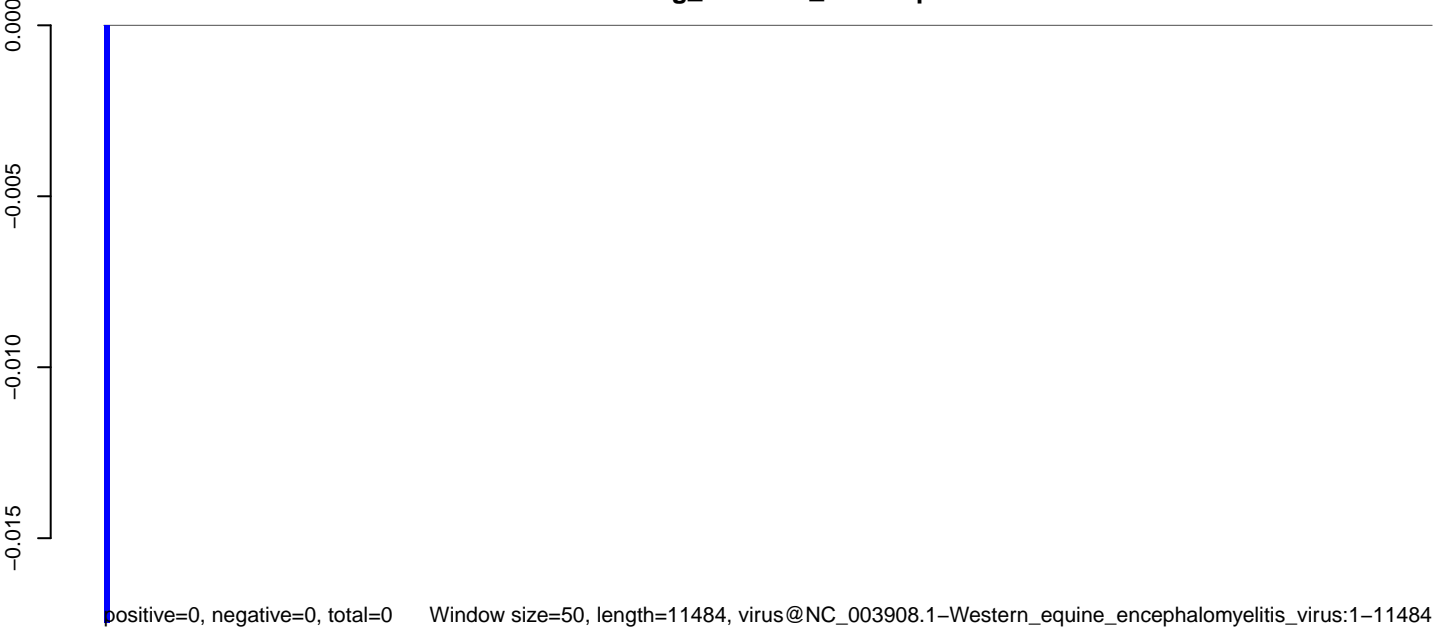
AeAeg_CCL.125_cells.18_23.rep



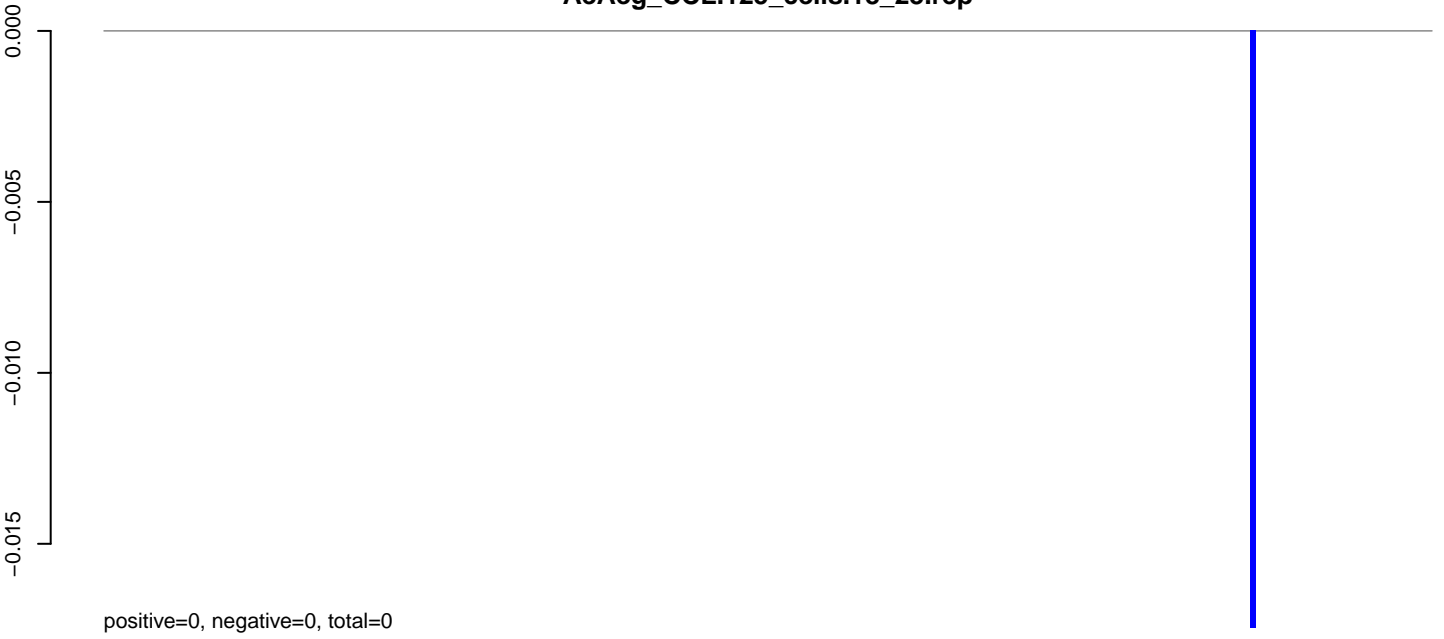
AeAeg_CCL.125_cells.24_35.rep



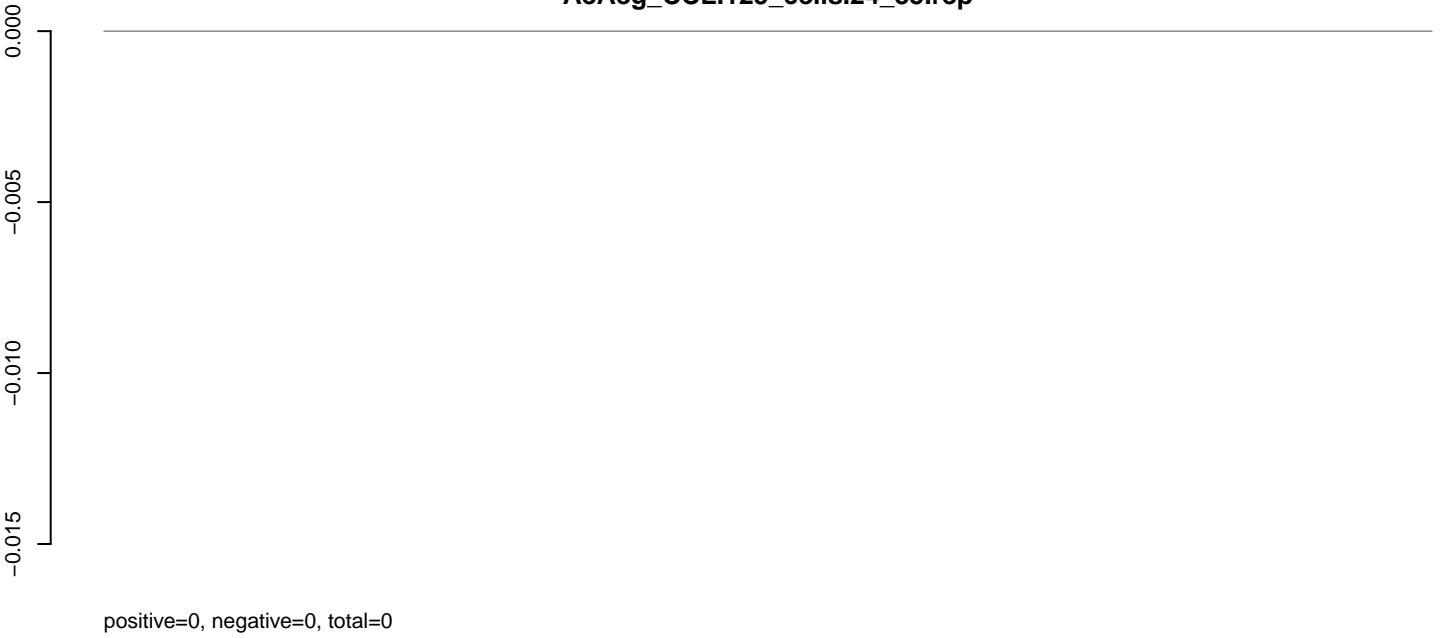
AeAeg_CCL.125_cells.rep



AeAeg_CCL.125_cells.18_23.rep



AeAeg_CCL.125_cells.24_35.rep



AeAeg_CCL.125_cells.rep

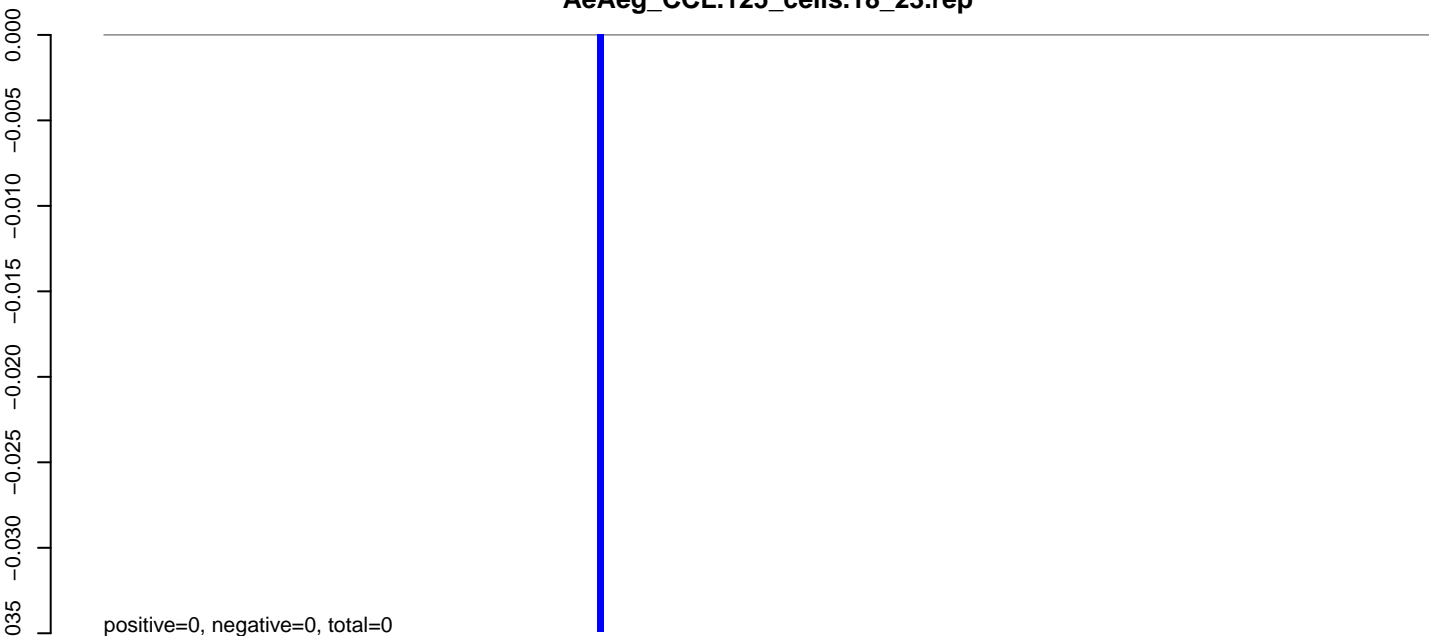


positive=0, negative=0, total=0

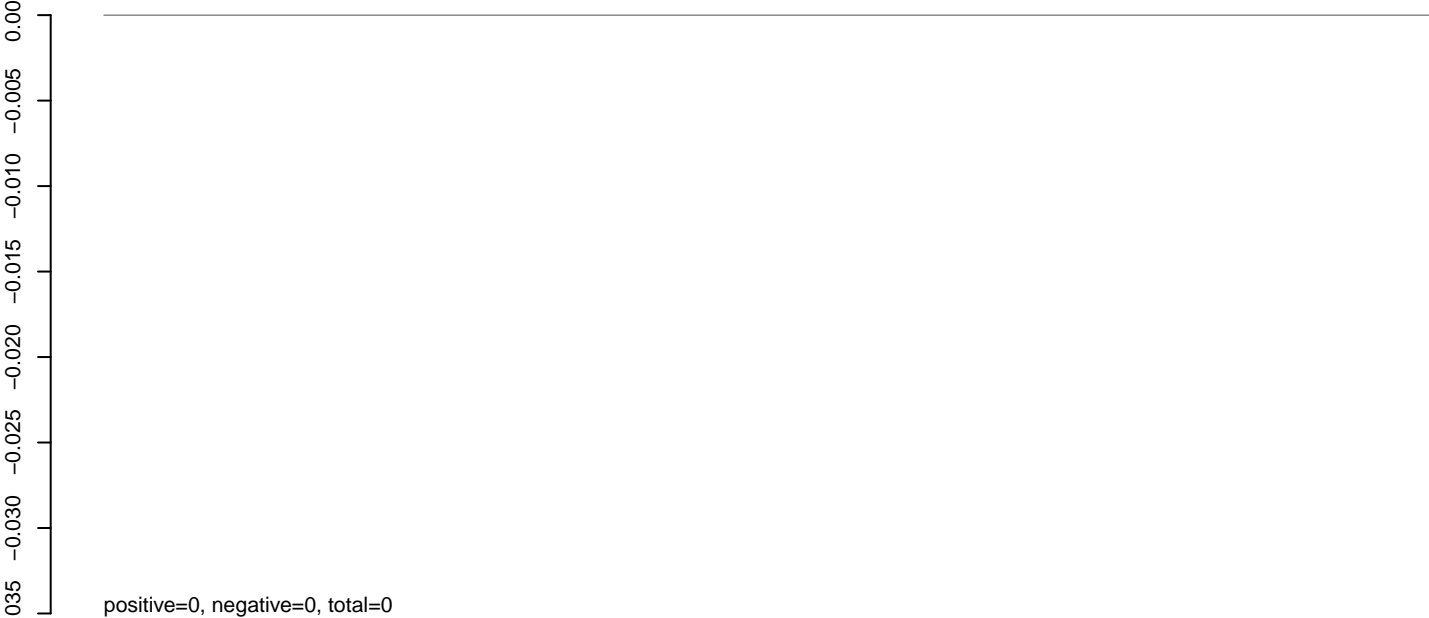
Window size=50, length=11675, virus@NC_003899.1-Eastern_equine_encephalitis_virus:1-11675

0 2000 4000 6000 8000 10000 12000

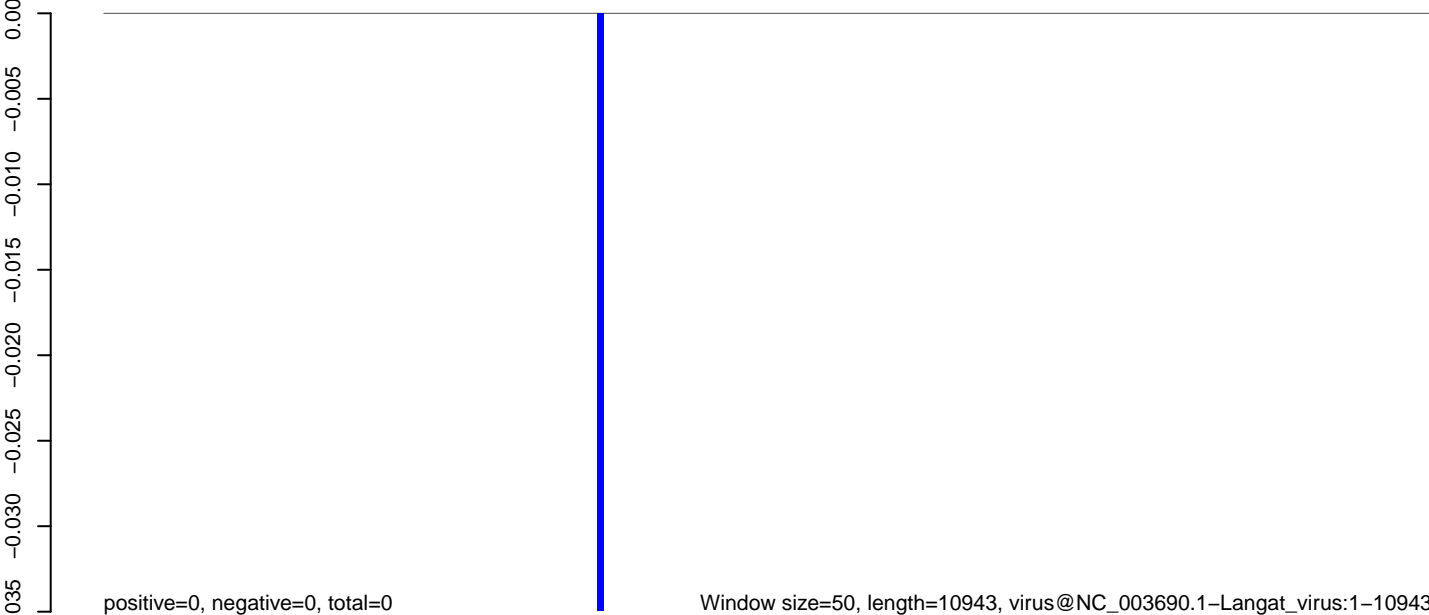
AeAeg_CCL.125_cells.18_23.rep



AeAeg_CCL.125_cells.24_35.rep



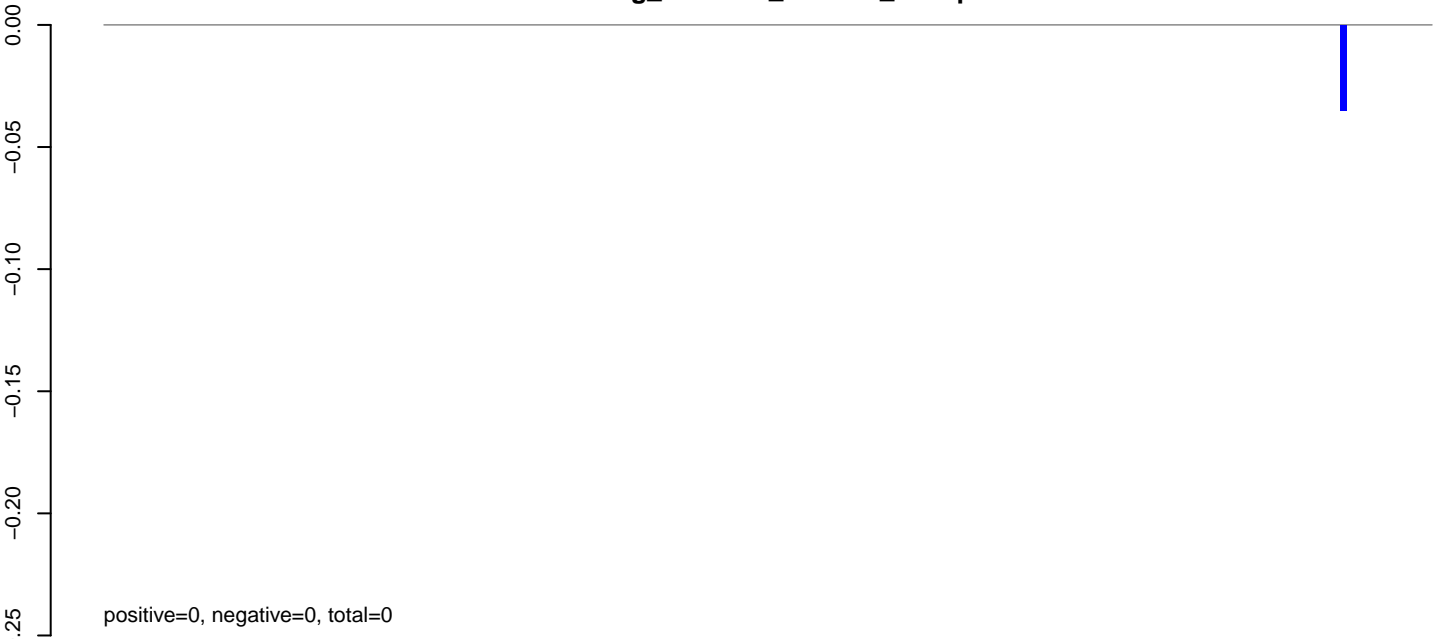
AeAeg_CCL.125_cells.rep



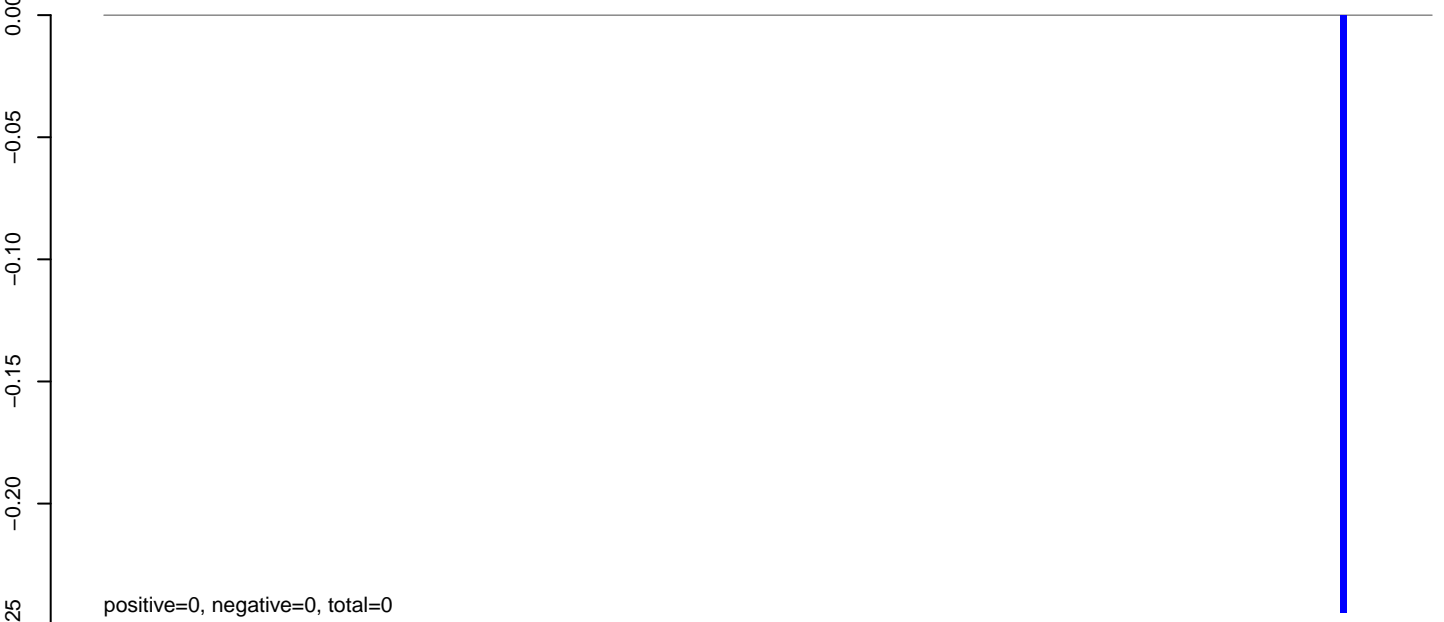
Window size=50, length=10943, virus@NC_003690.1-Langat_virus:1-10943

0 2000 4000 6000 8000 10000

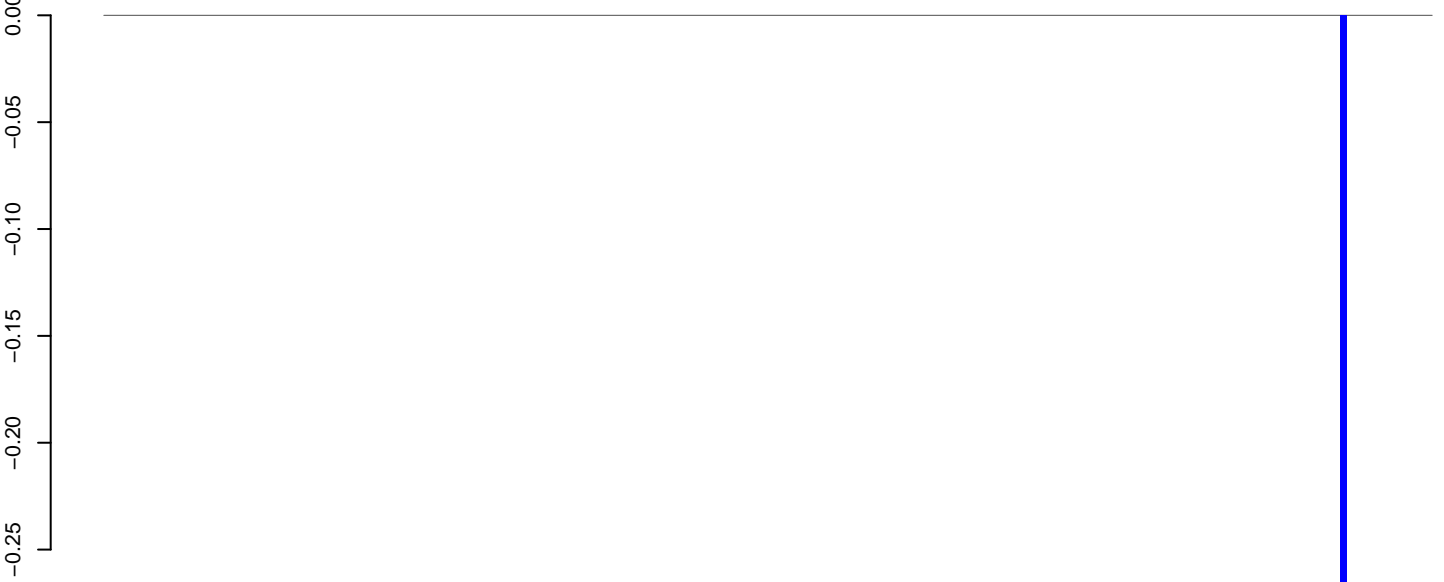
AeAeg_CCL.125_cells.18_23.rep



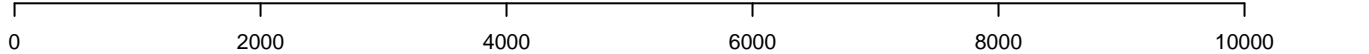
AeAeg_CCL.125_cells.24_35.rep



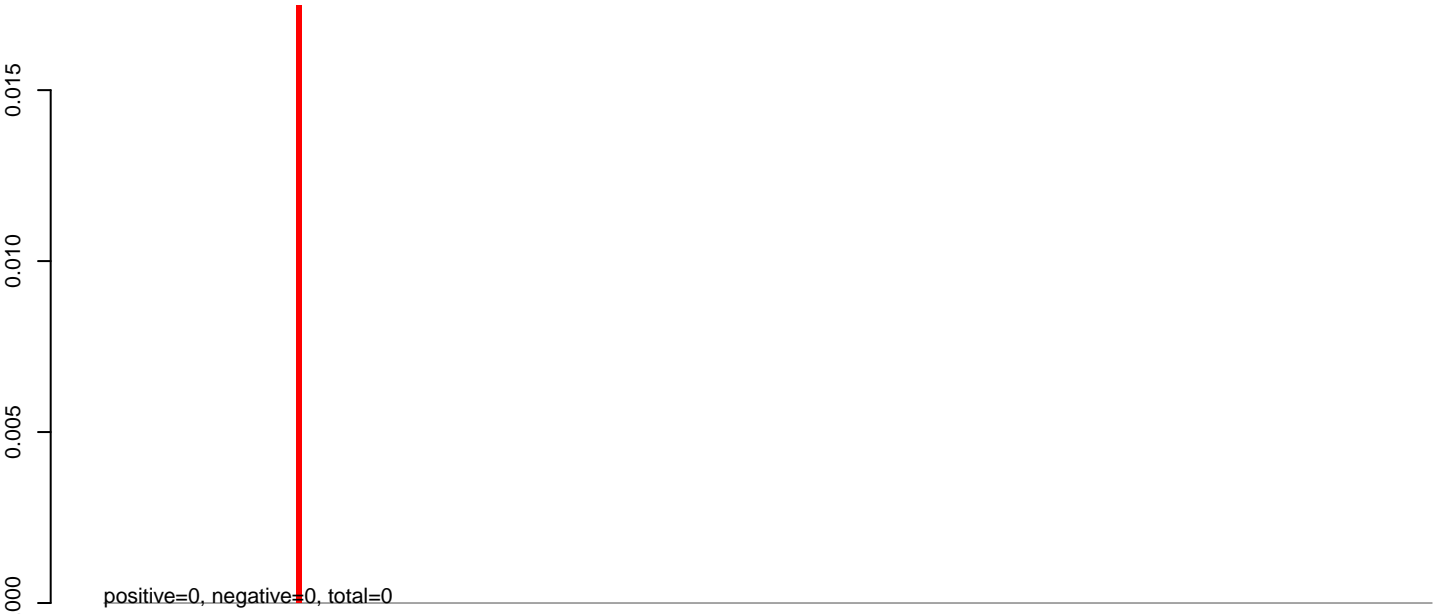
AeAeg_CCL.125_cells.rep



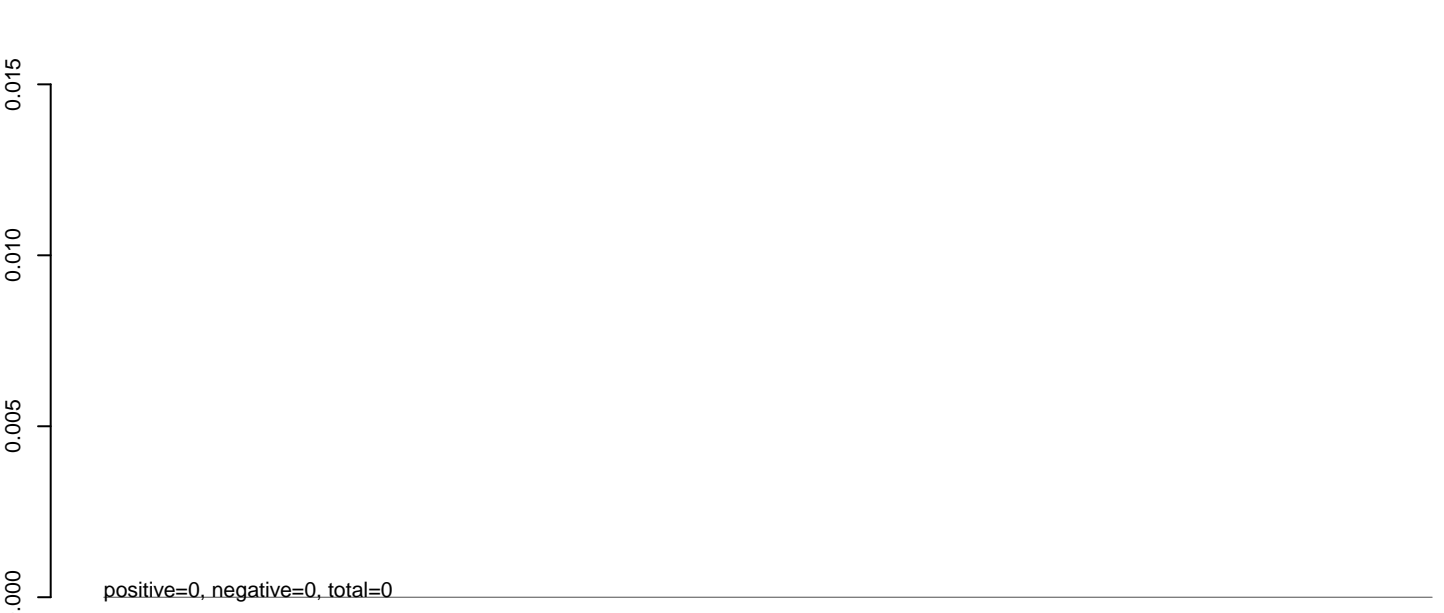
Window size=50, length=10839, virus@NC_003687.1-Powassan_virus_1-10839



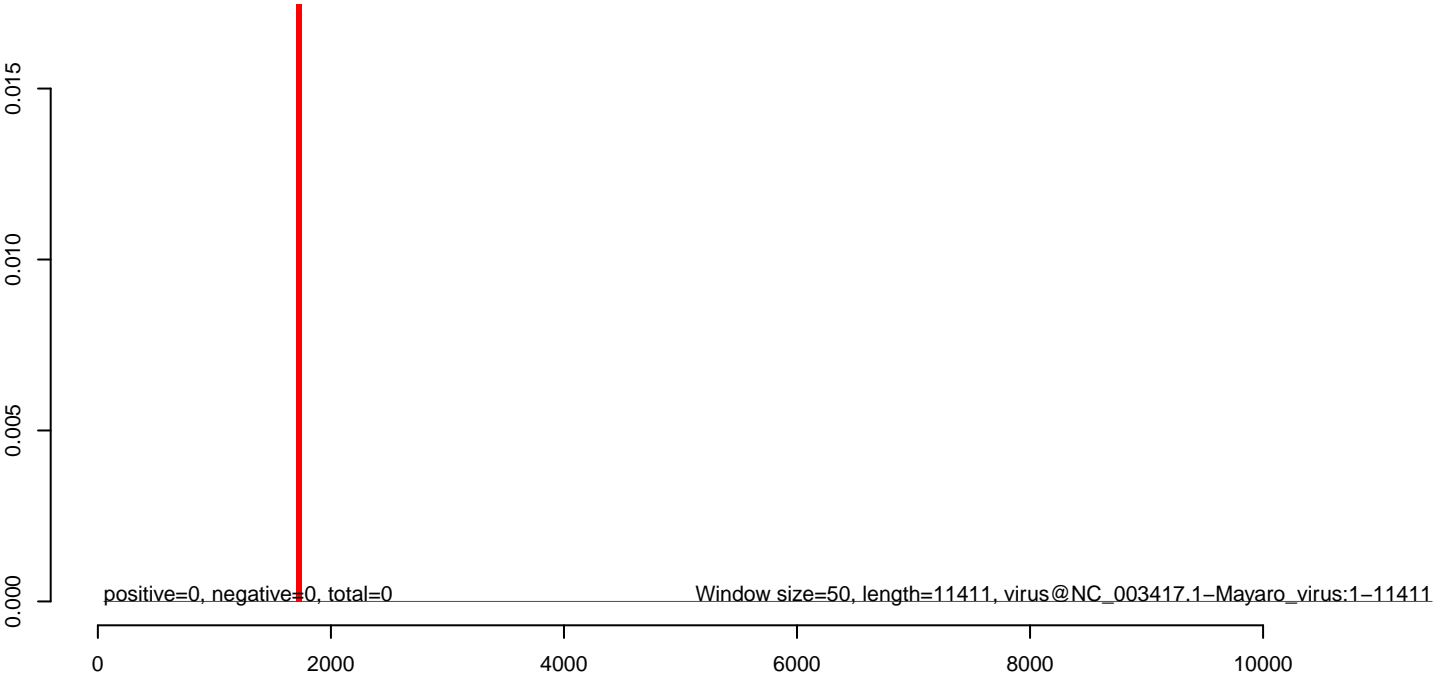
AeAeg_CCL.125_cells.18_23.rep



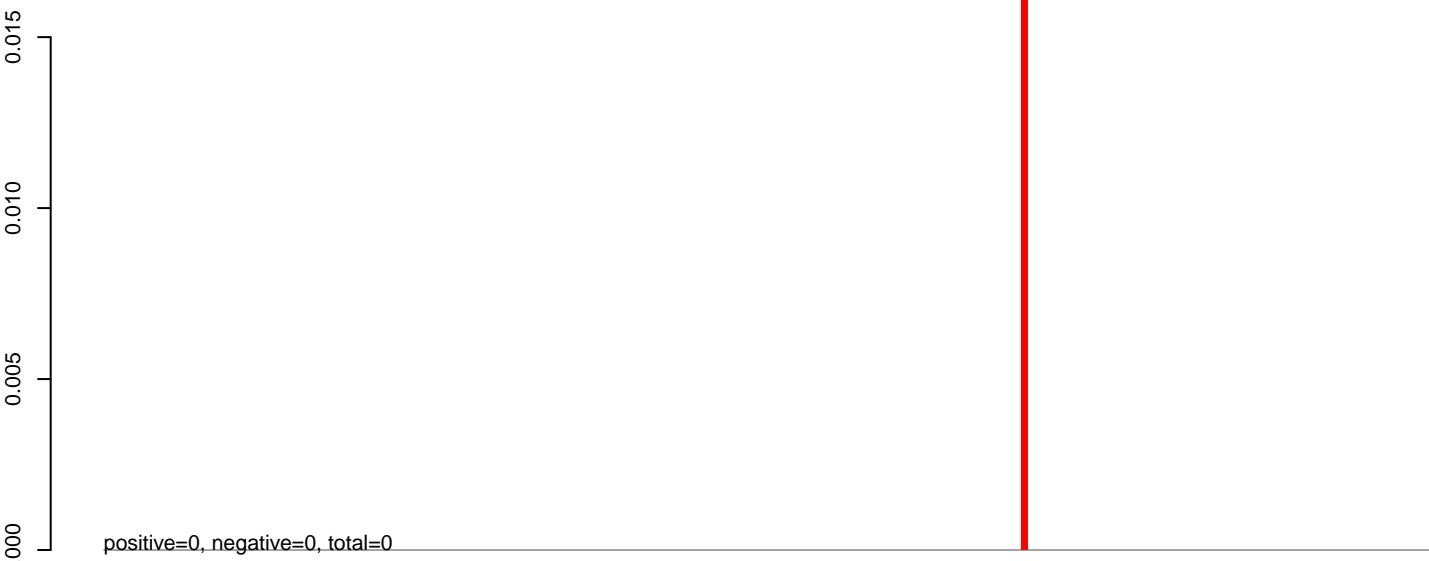
AeAeg_CCL.125_cells.24_35.rep



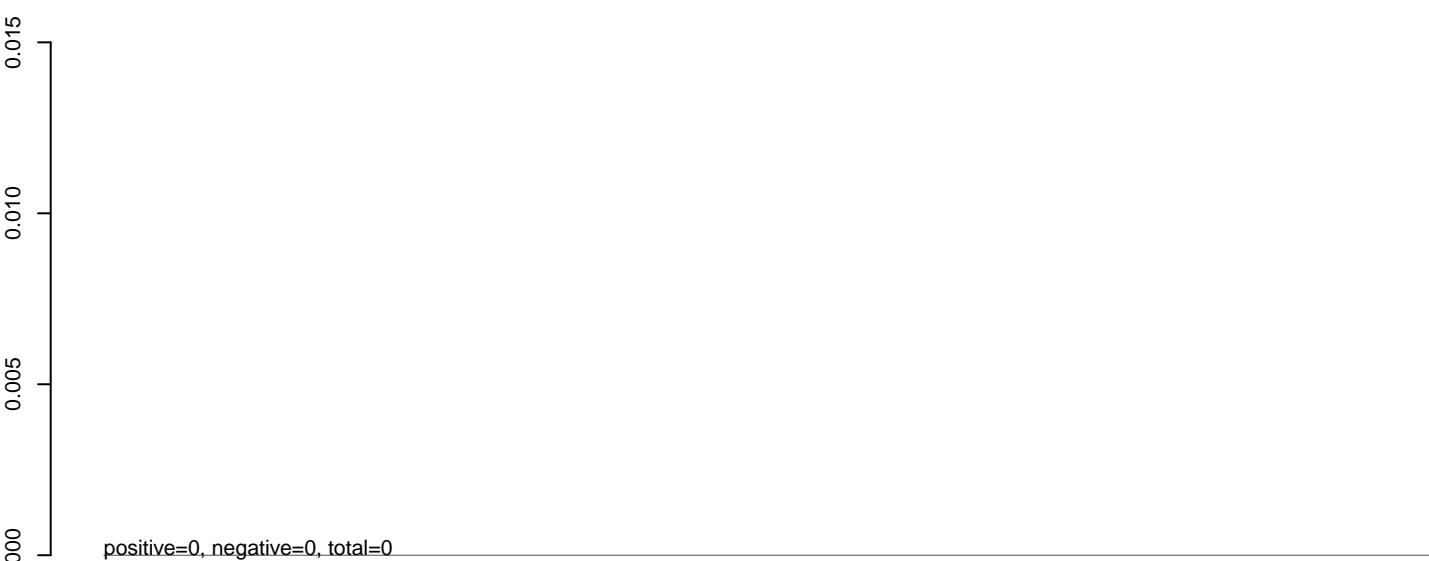
AeAeg_CCL.125_cells.rep



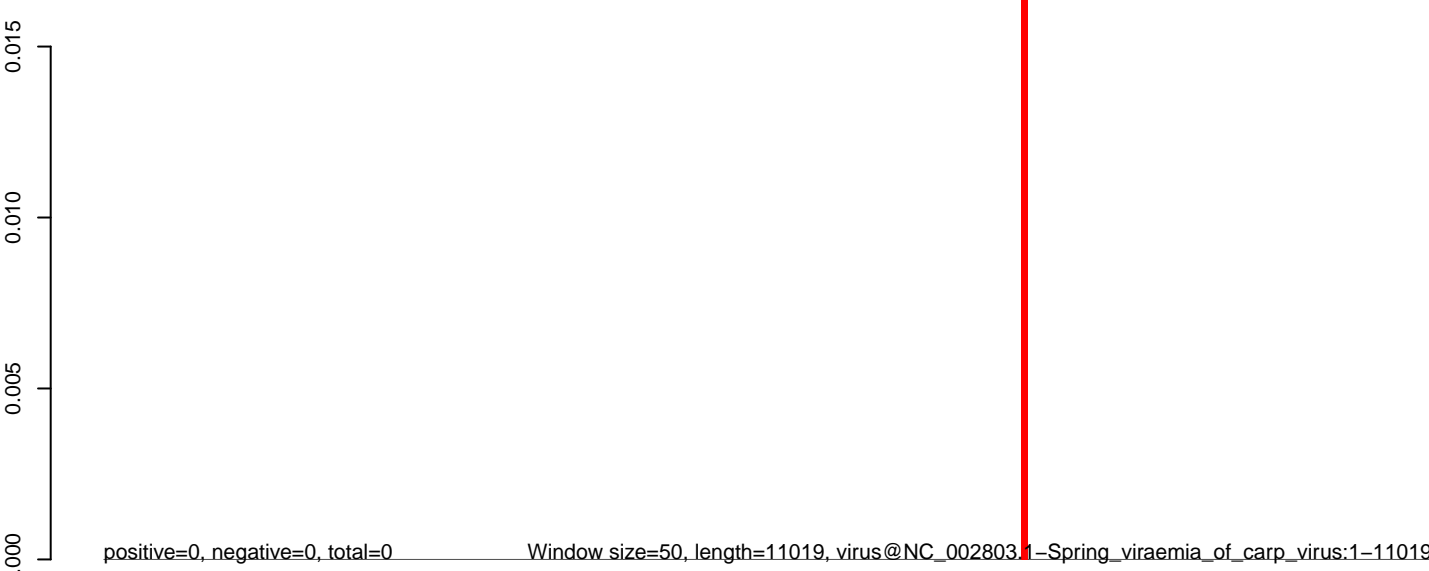
AeAeg_CCL.125_cells.18_23.rep



AeAeg_CCL.125_cells.24_35.rep

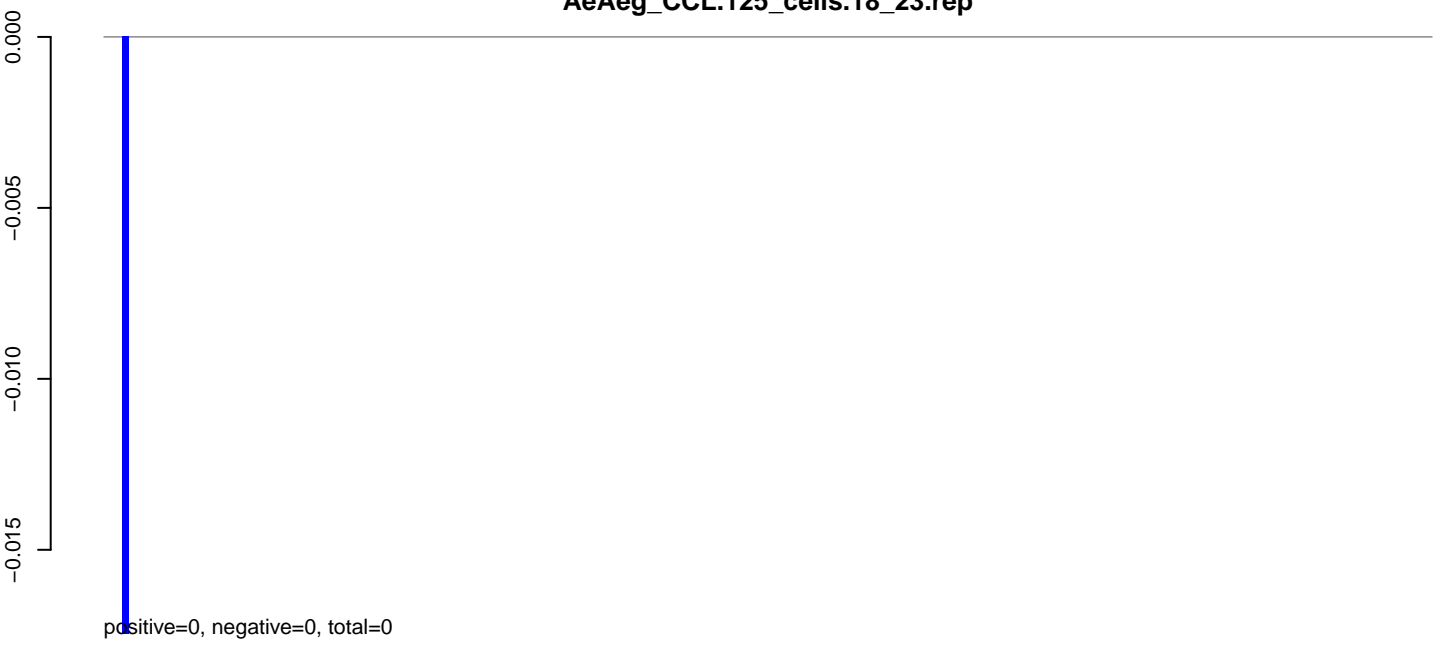


AeAeg_CCL.125_cells.rep

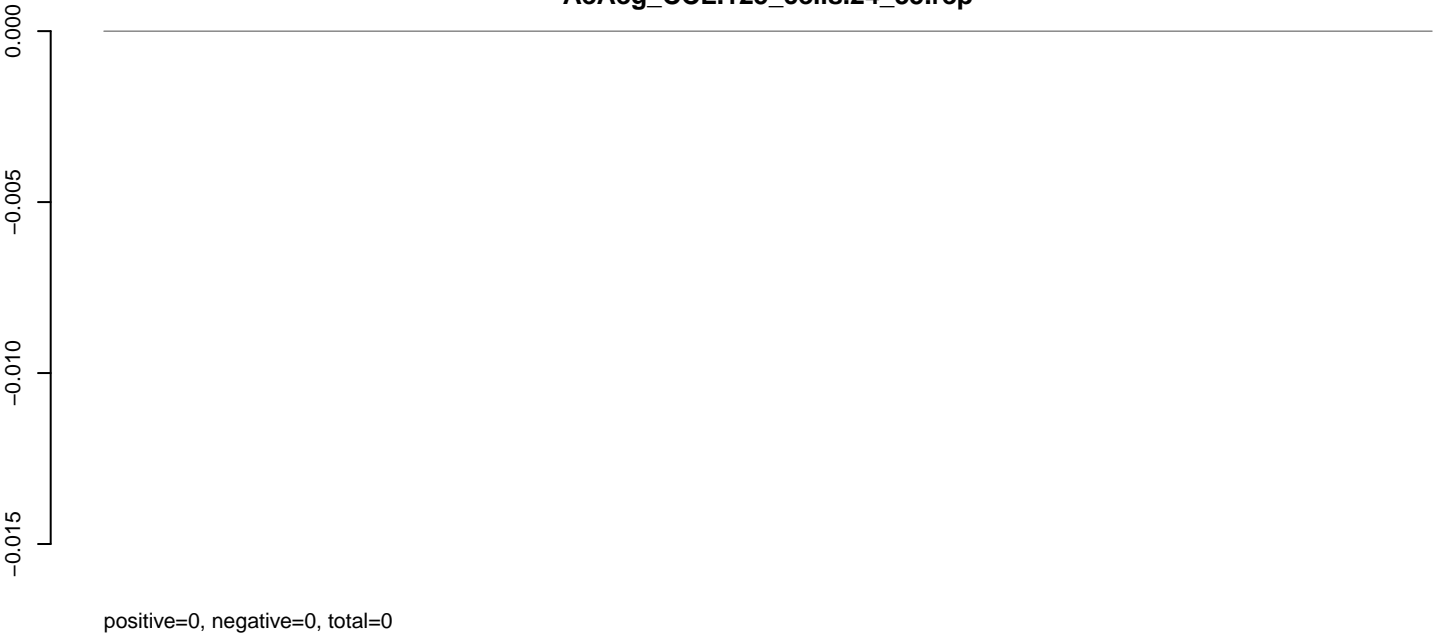


0 2000 4000 6000 8000 10000

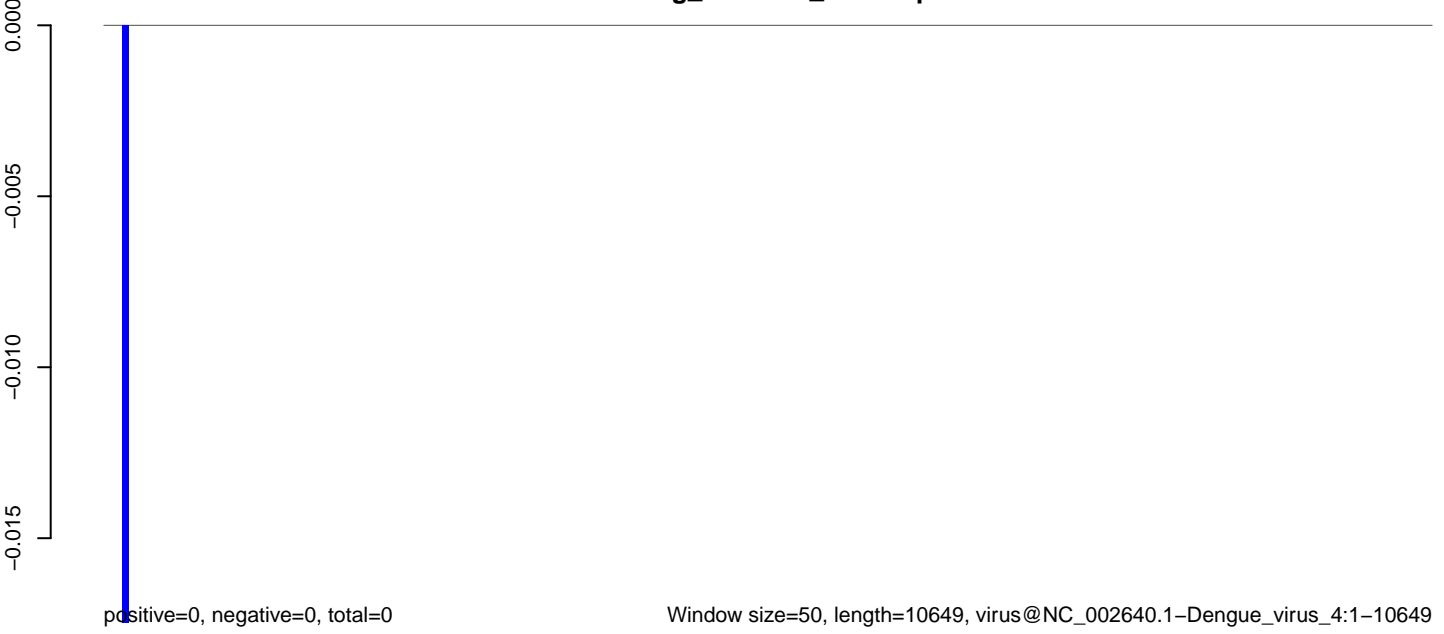
AeAeg_CCL.125_cells.18_23.rep



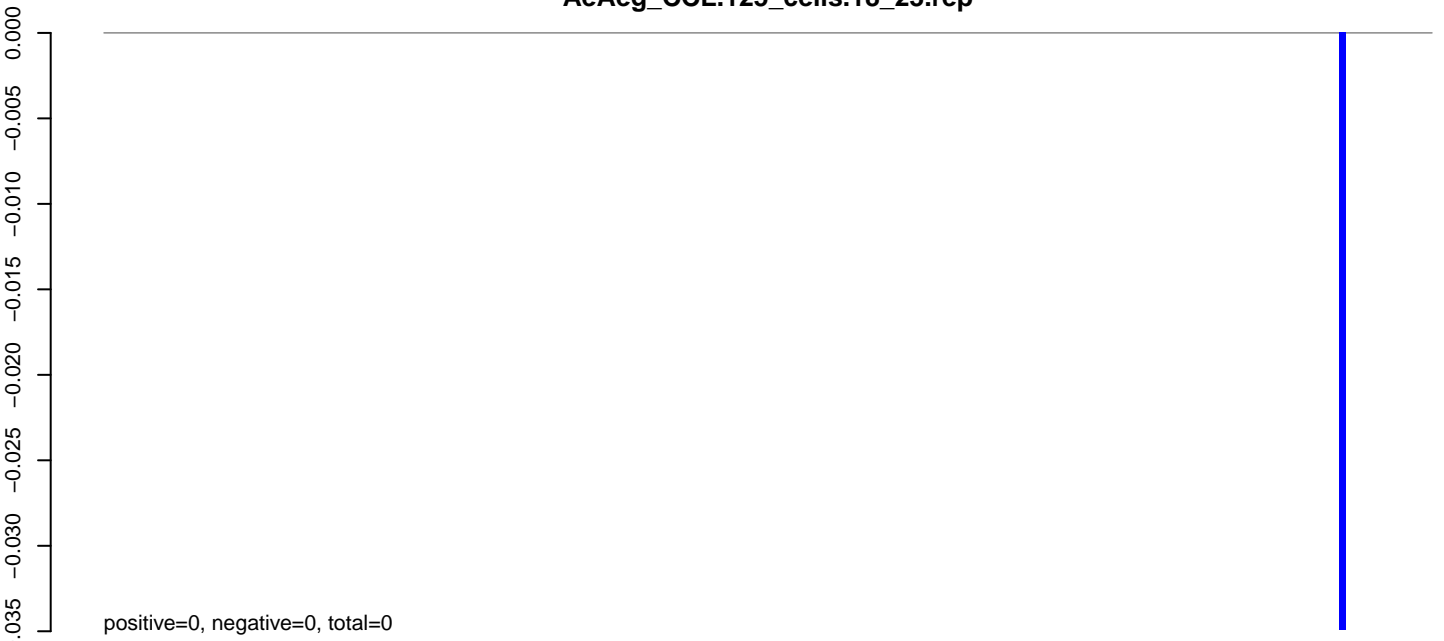
AeAeg_CCL.125_cells.24_35.rep



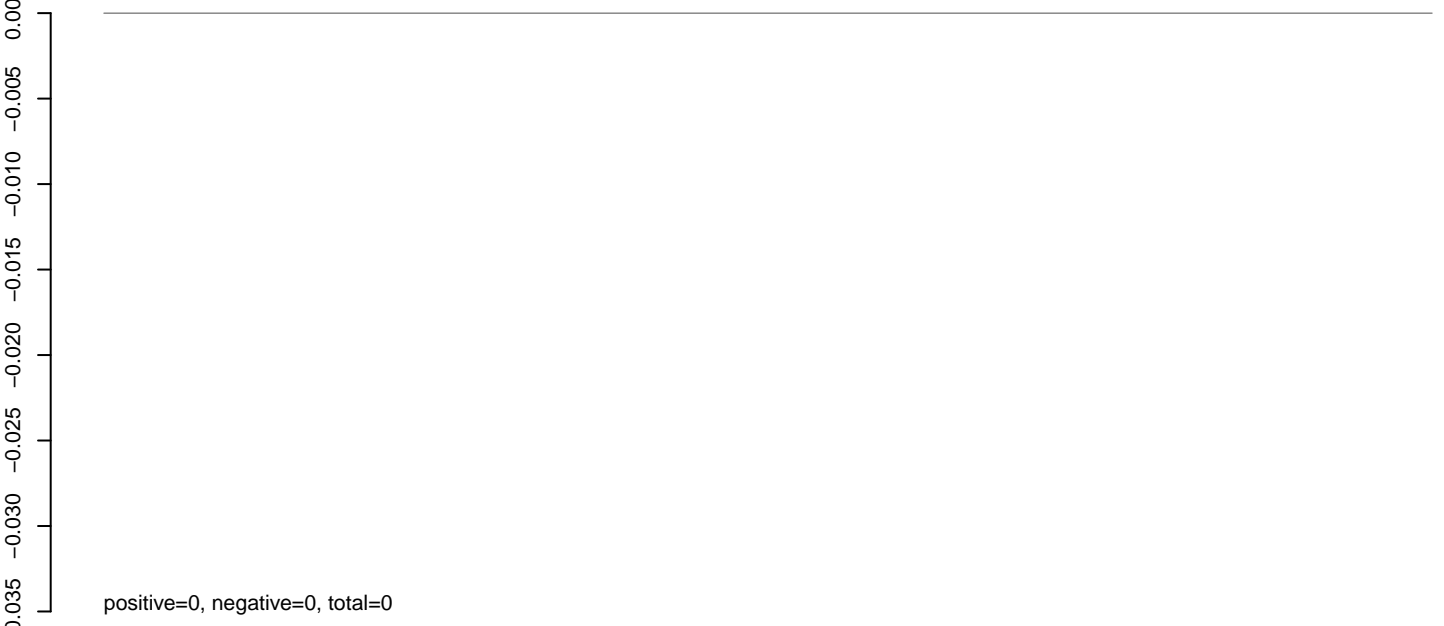
AeAeg_CCL.125_cells.rep



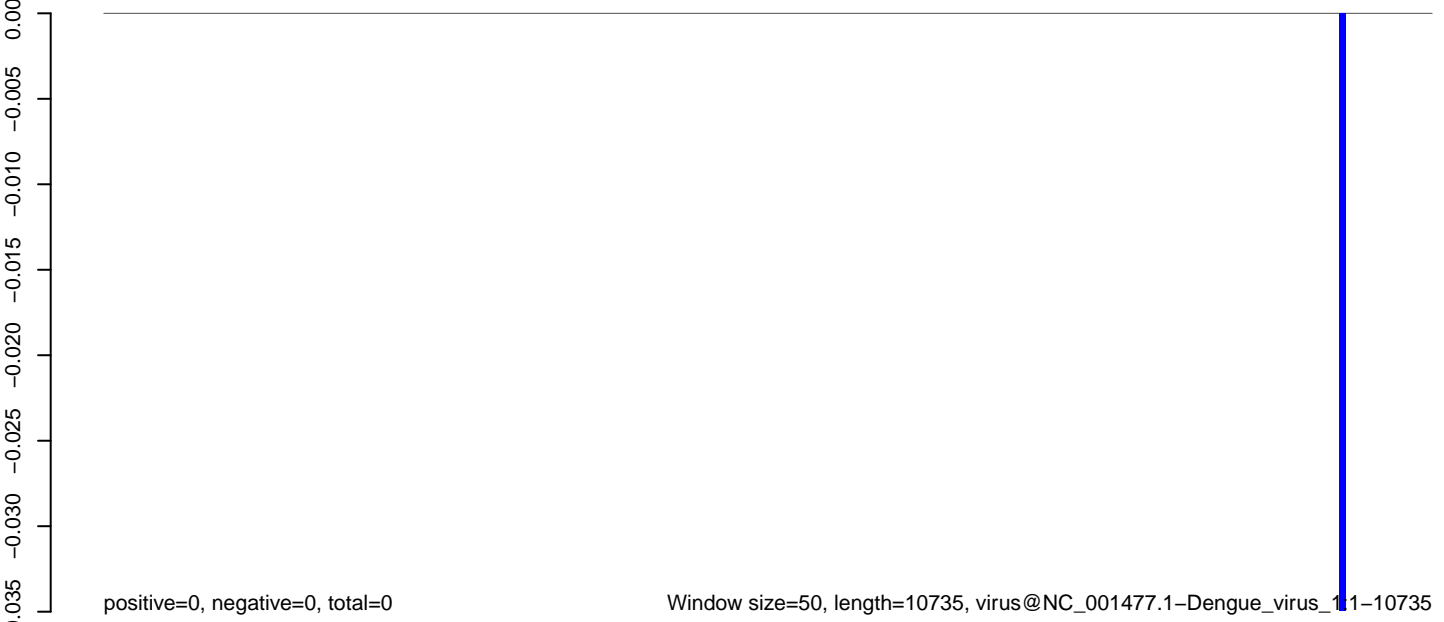
AeAeg_CCL.125_cells.18_23.rep



AeAeg_CCL.125_cells.24_35.rep



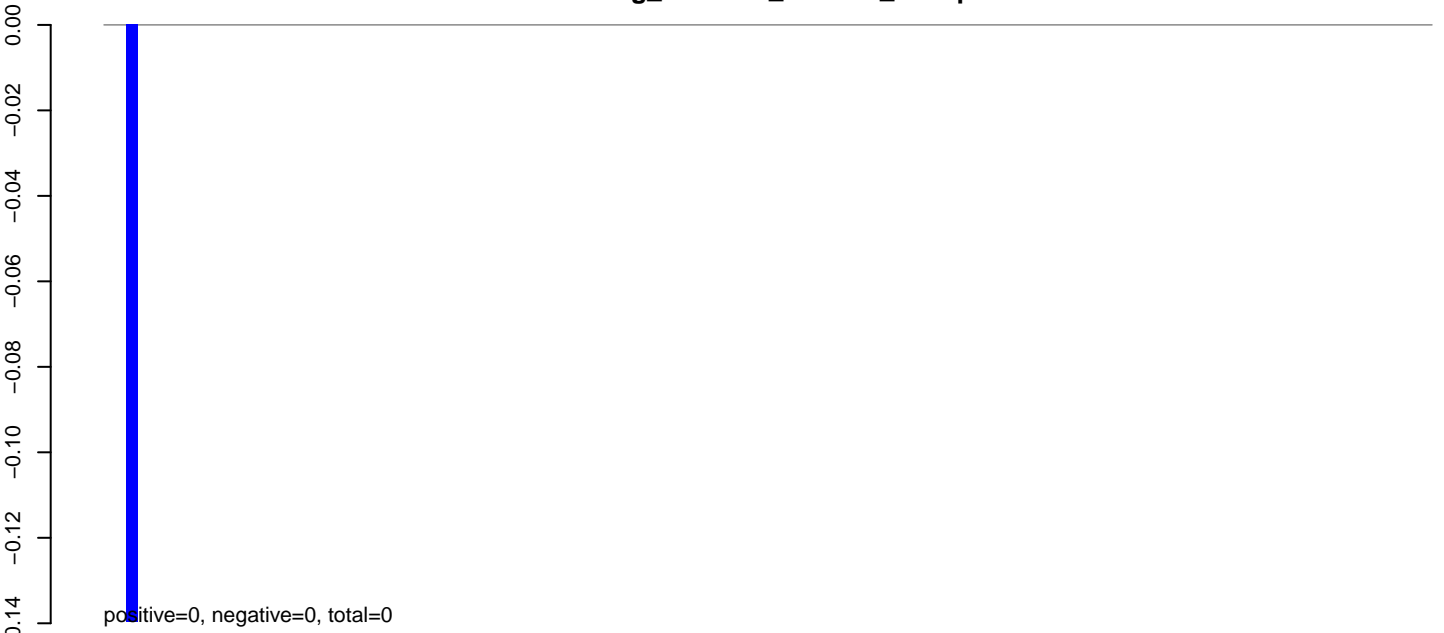
AeAeg_CCL.125_cells.rep



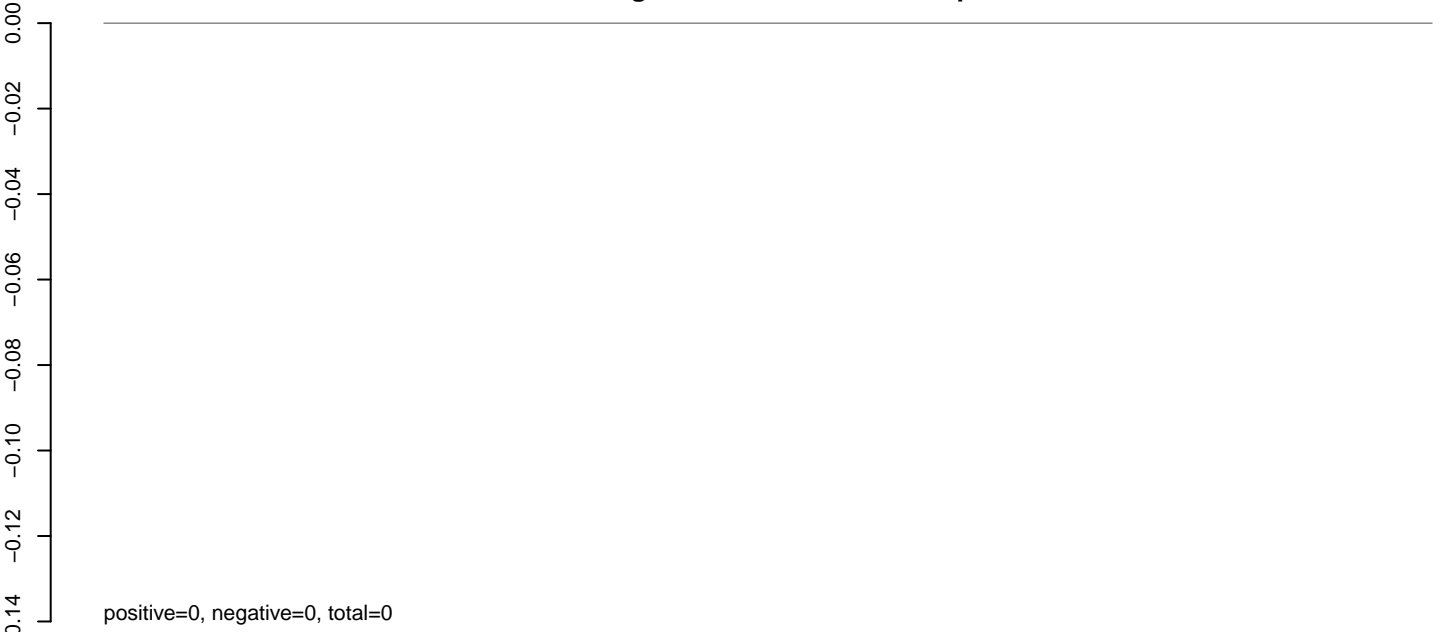
Window size=50, length=10735, virus@NC_001477.1-Dengue_virus_11-10735

0 2000 4000 6000 8000 10000

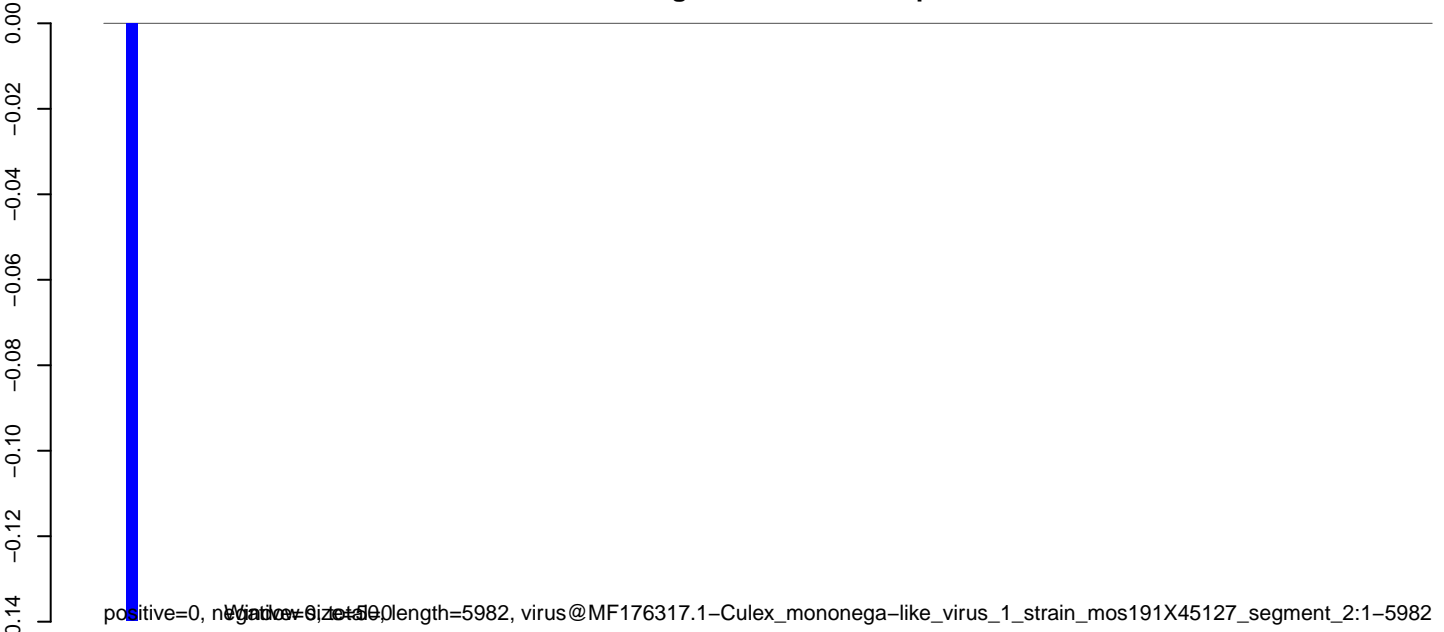
AeAeg_CCL.125_cells.18_23.rep



AeAeg_CCL.125_cells.24_35.rep



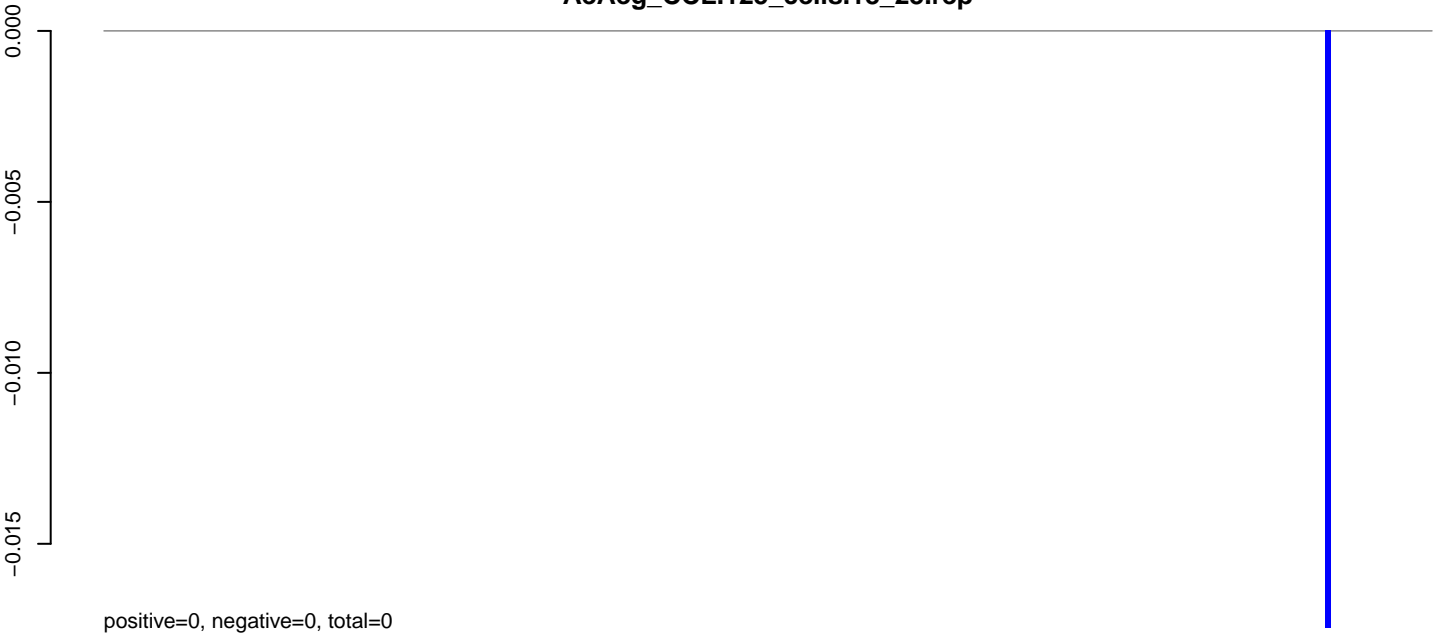
AeAeg_CCL.125_cells.rep



Wiggle Size: length=5982, virus@MF176317.1-Culex_mononega-like_virus_1_strain_mos191X45127_segment_2:1-5982

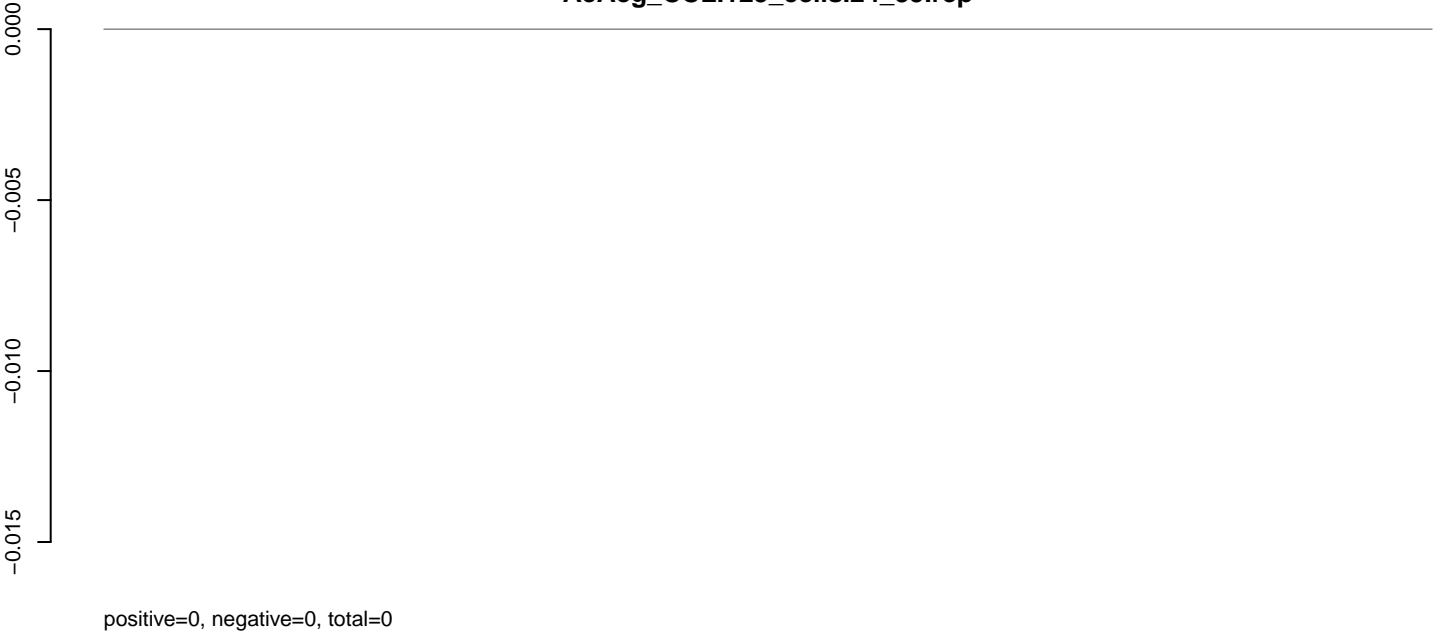
0 1000 2000 3000 4000 5000 6000

AeAeg_CCL.125_cells.18_23.rep



positive=0, negative=0, total=0

AeAeg_CCL.125_cells.24_35.rep



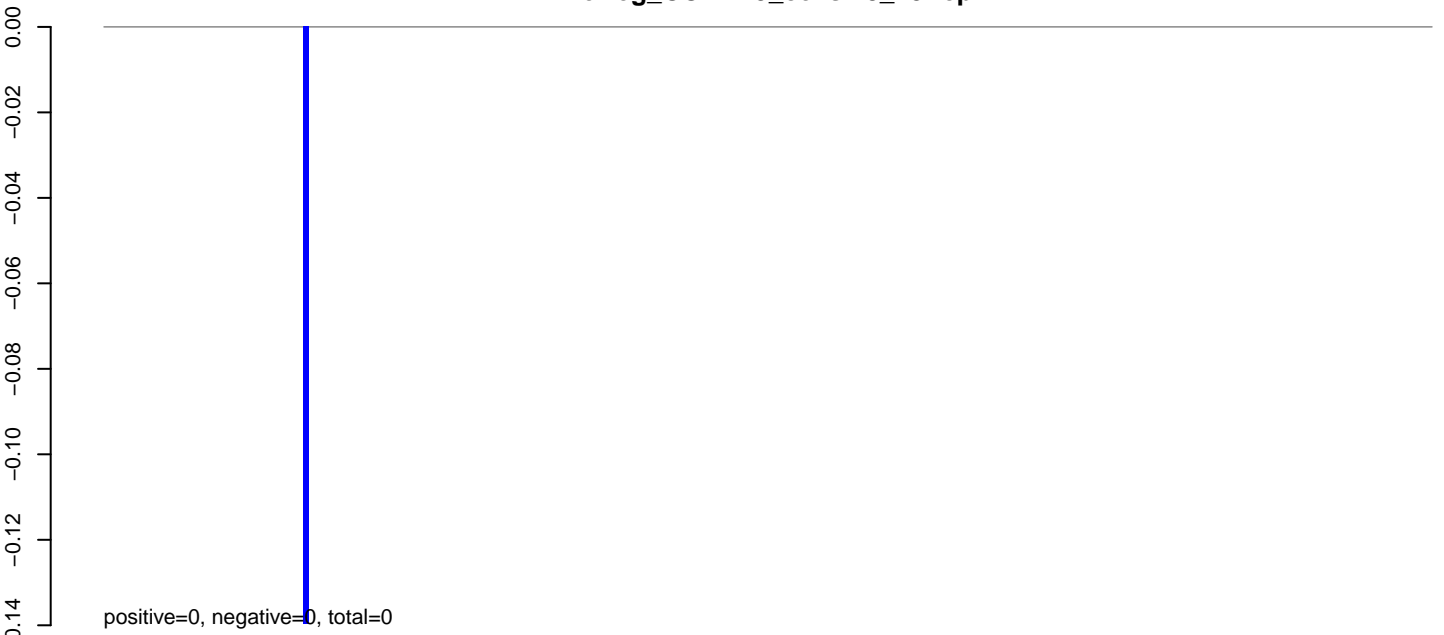
positive=0, negative=0, total=0

AeAeg_CCL.125_cells.rep

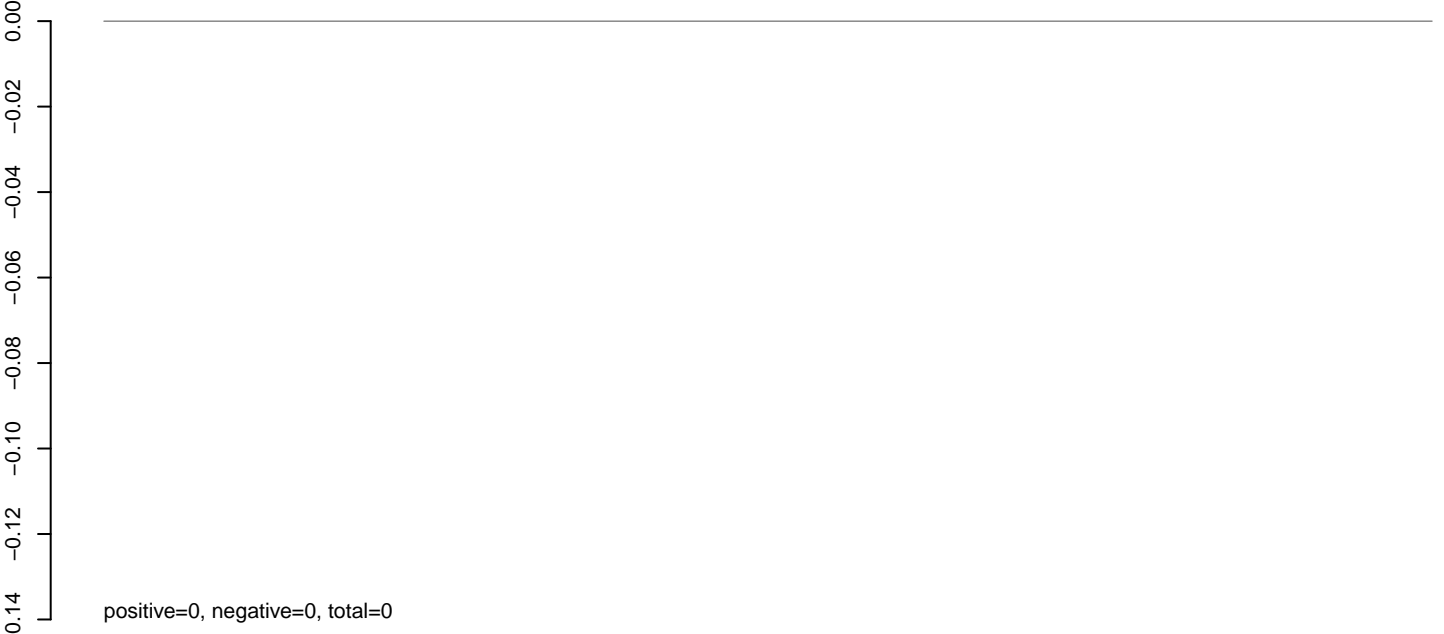


positive=0, negative=0, total=0, window size=50, length=11835, virus@M20303.1-O-Nyong-nyong_virus_Gulu_strain_complete_genome:1-11835

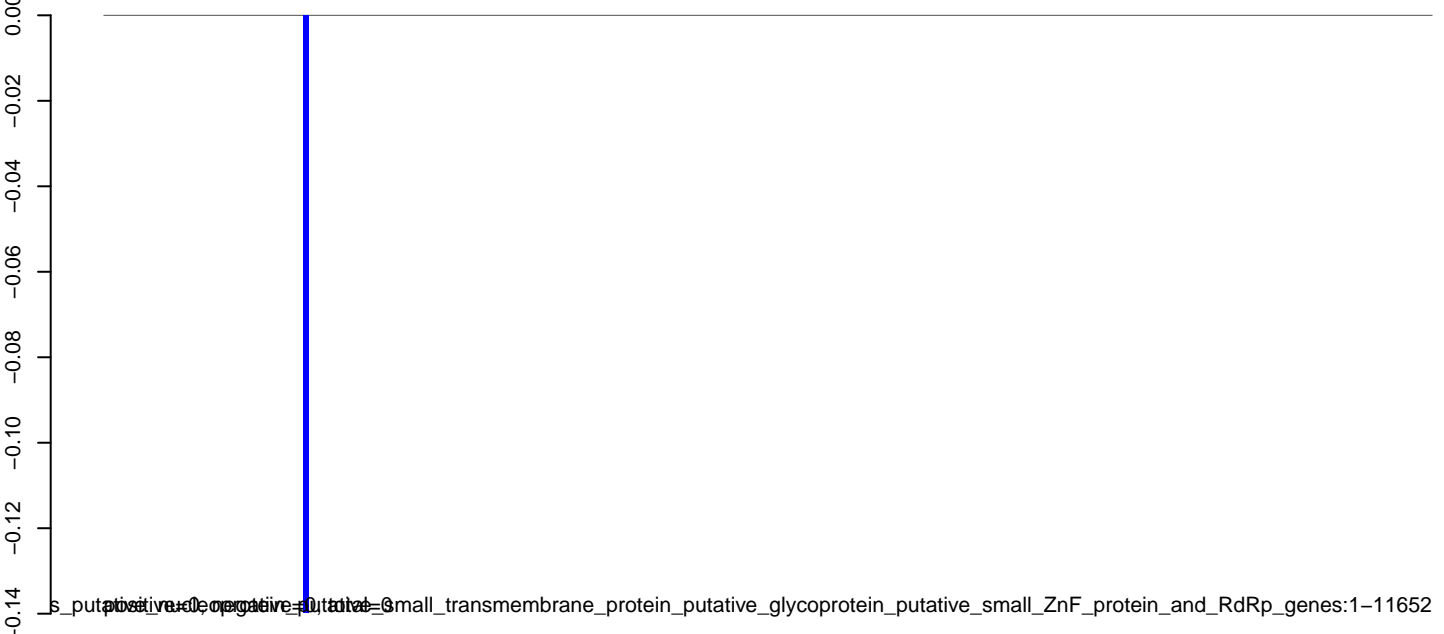
AeAeg_CCL.125_cells.18_23.rep



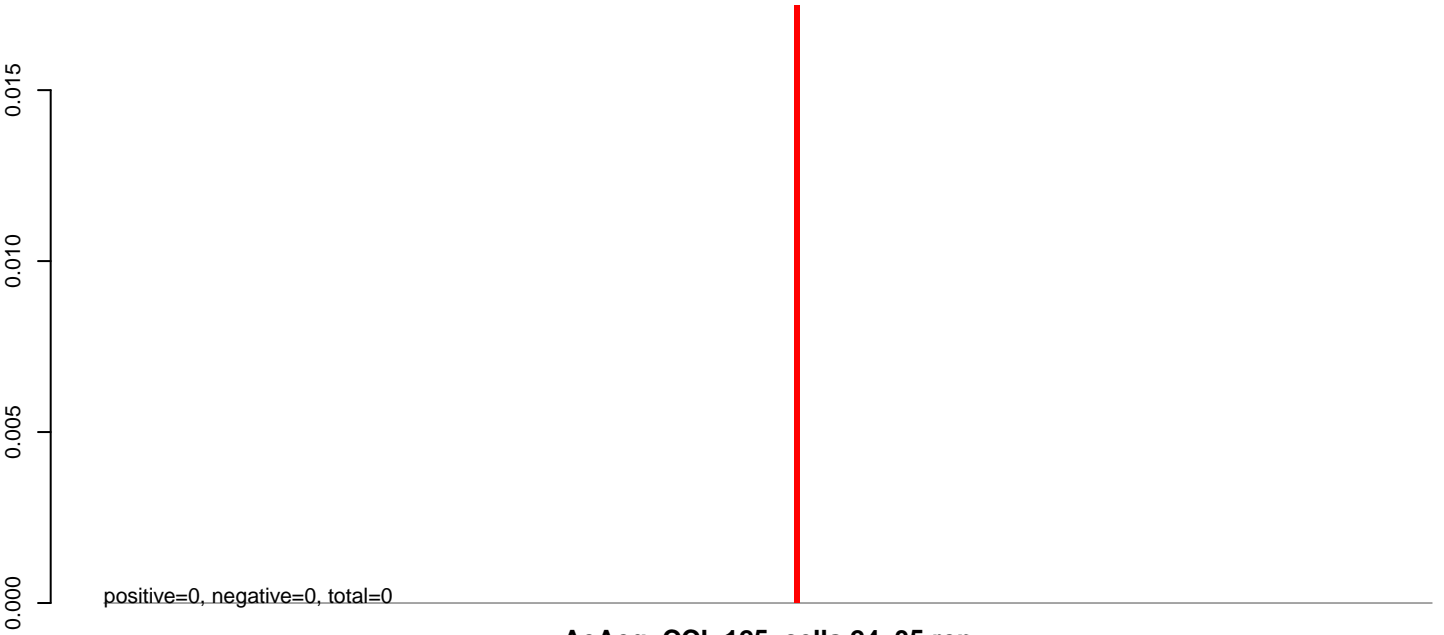
AeAeg_CCL.125_cells.24_35.rep



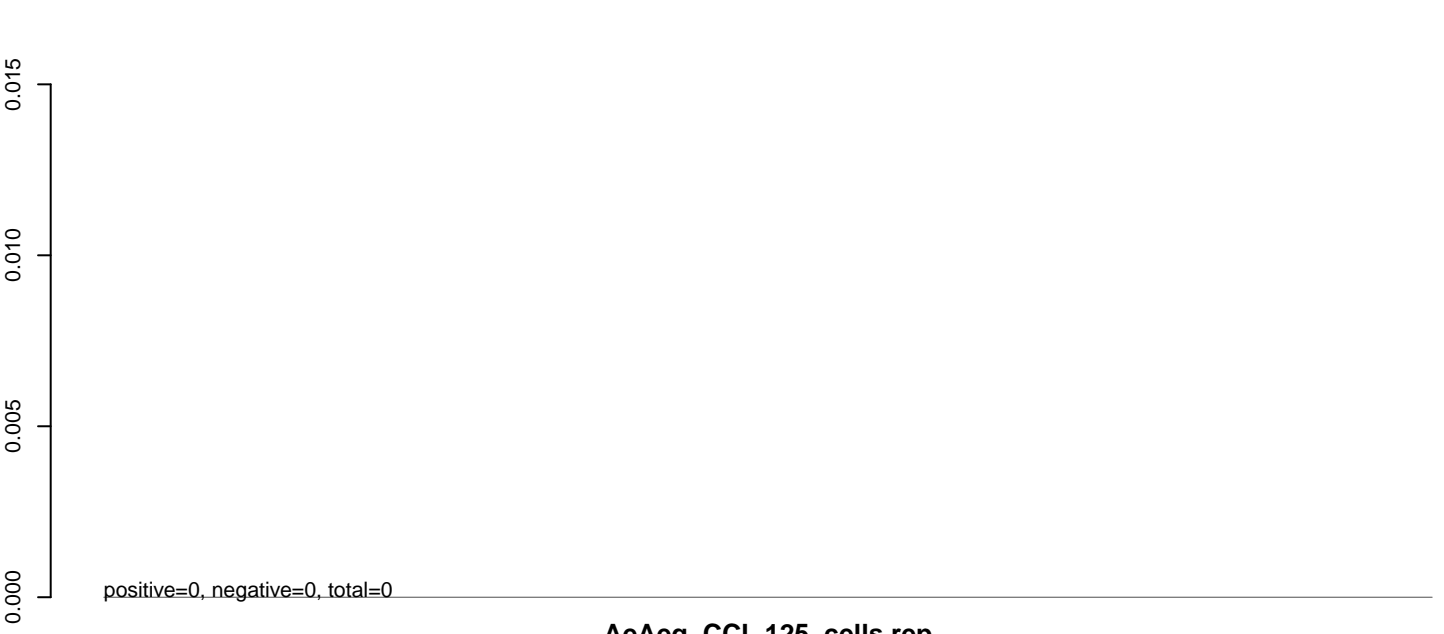
AeAeg_CCL.125_cells.rep



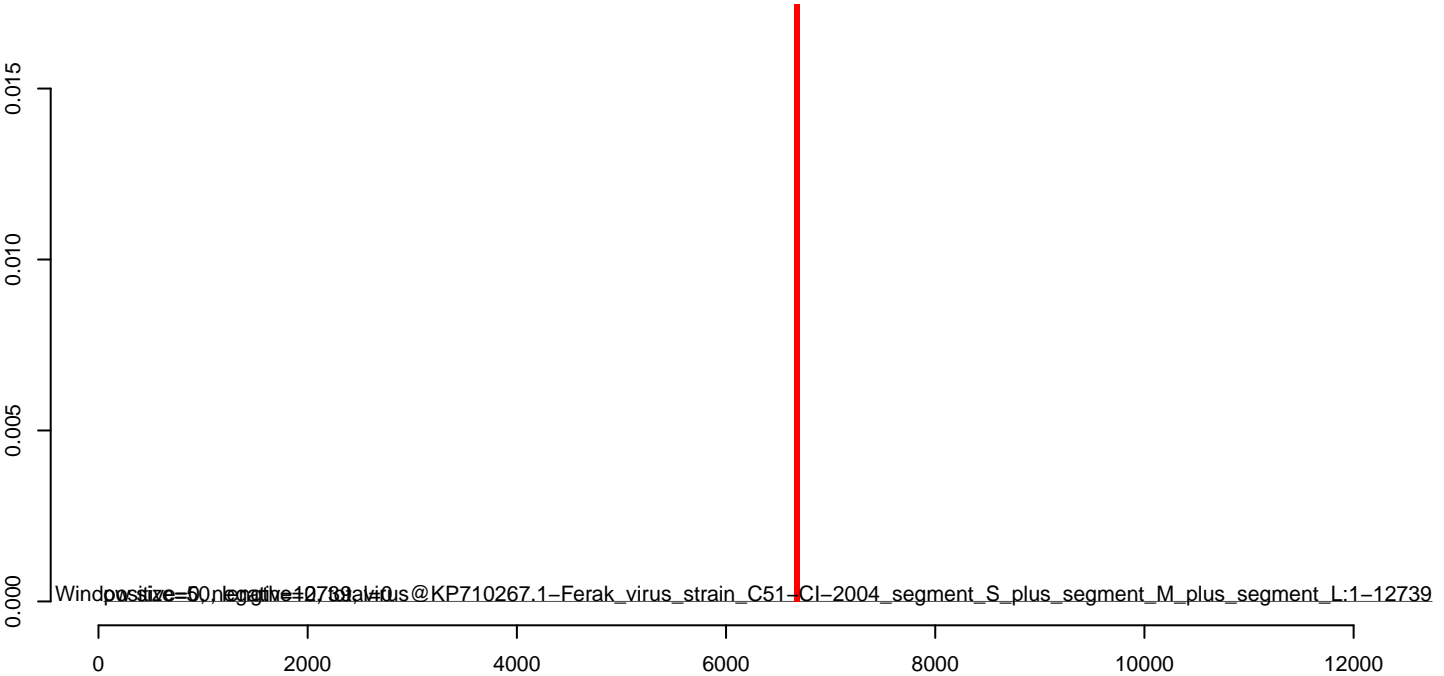
AeAeg_CCL.125_cells.18_23.rep



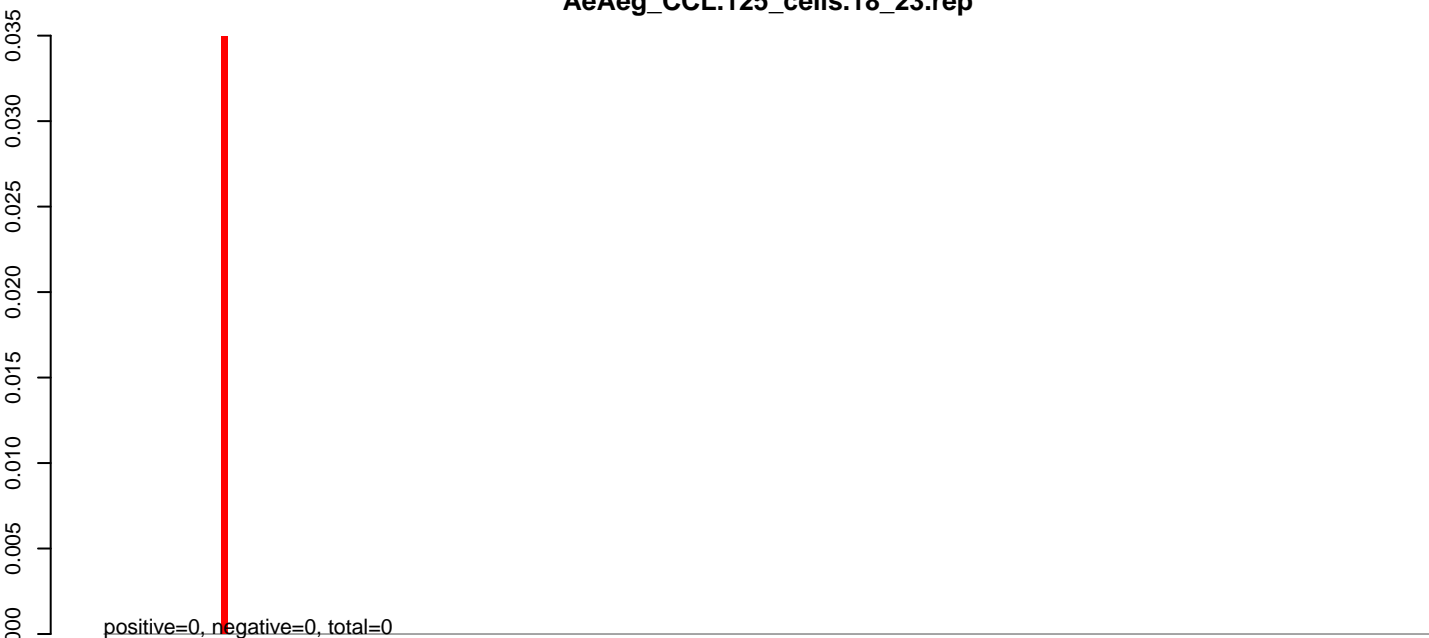
AeAeg_CCL.125_cells.24_35.rep



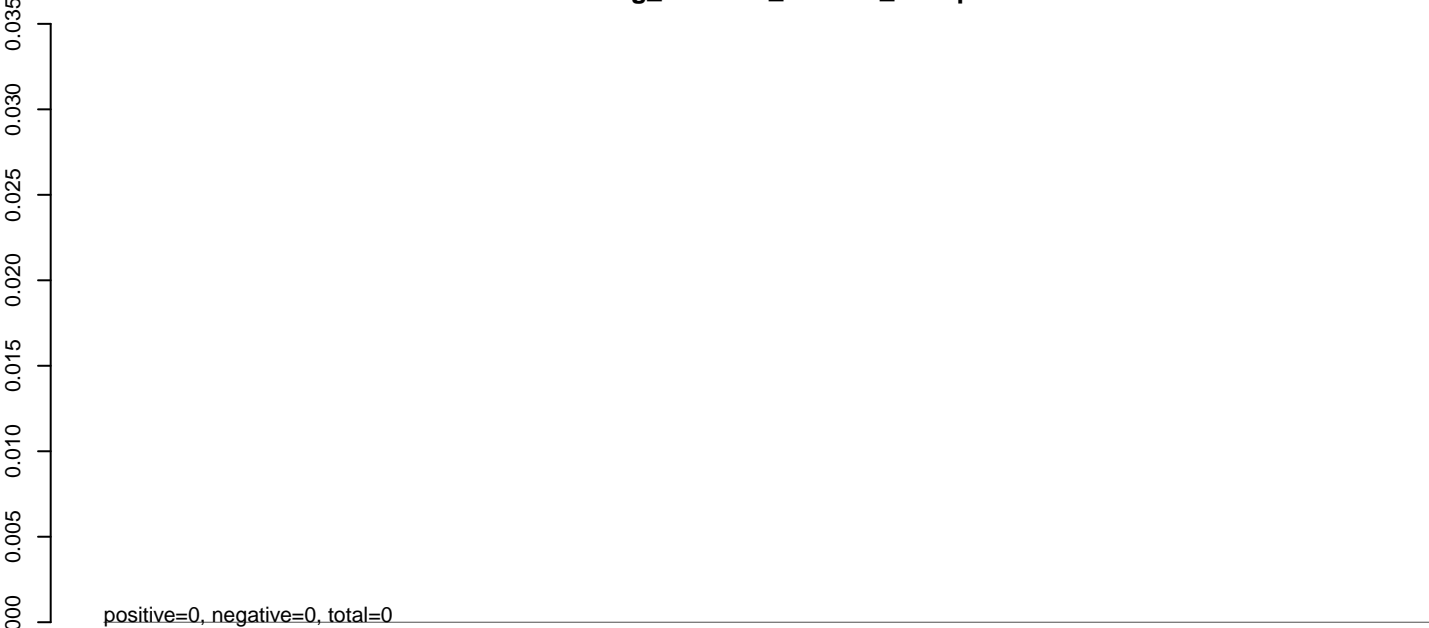
AeAeg_CCL.125_cells.rep



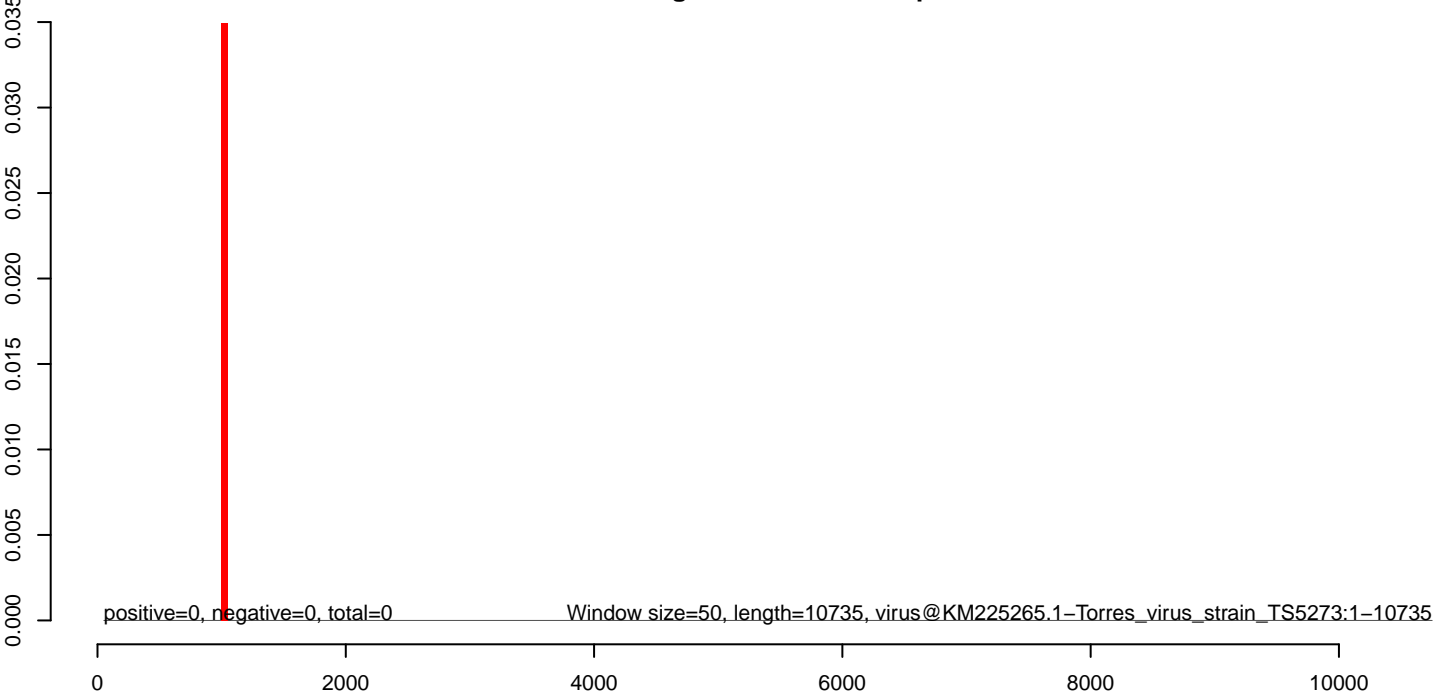
AeAeg_CCL.125_cells.18_23.rep



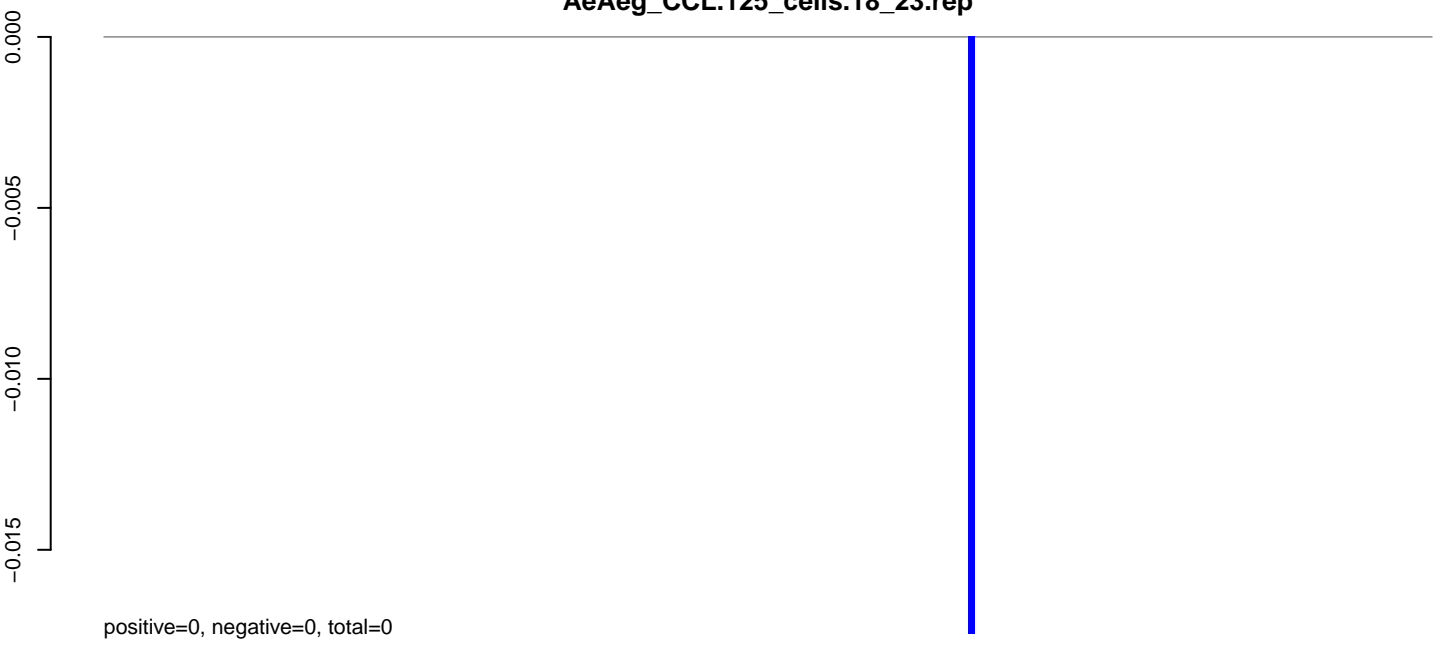
AeAeg_CCL.125_cells.24_35.rep



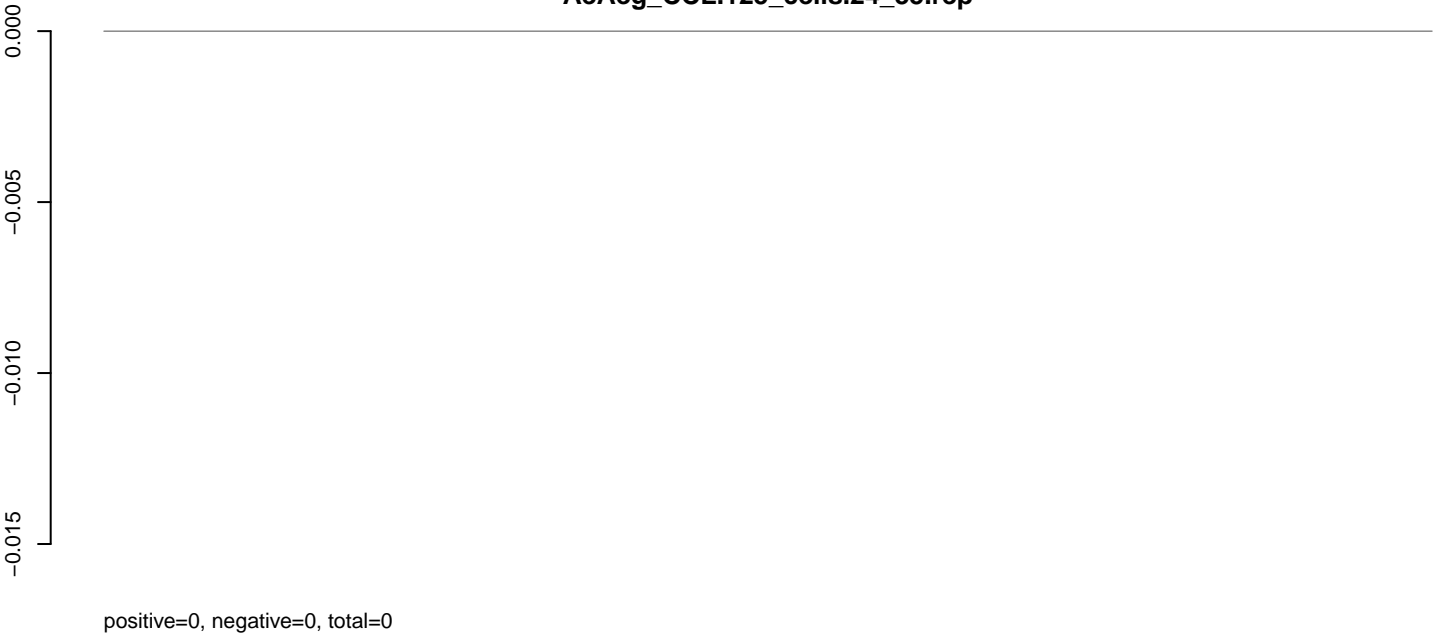
AeAeg_CCL.125_cells.rep



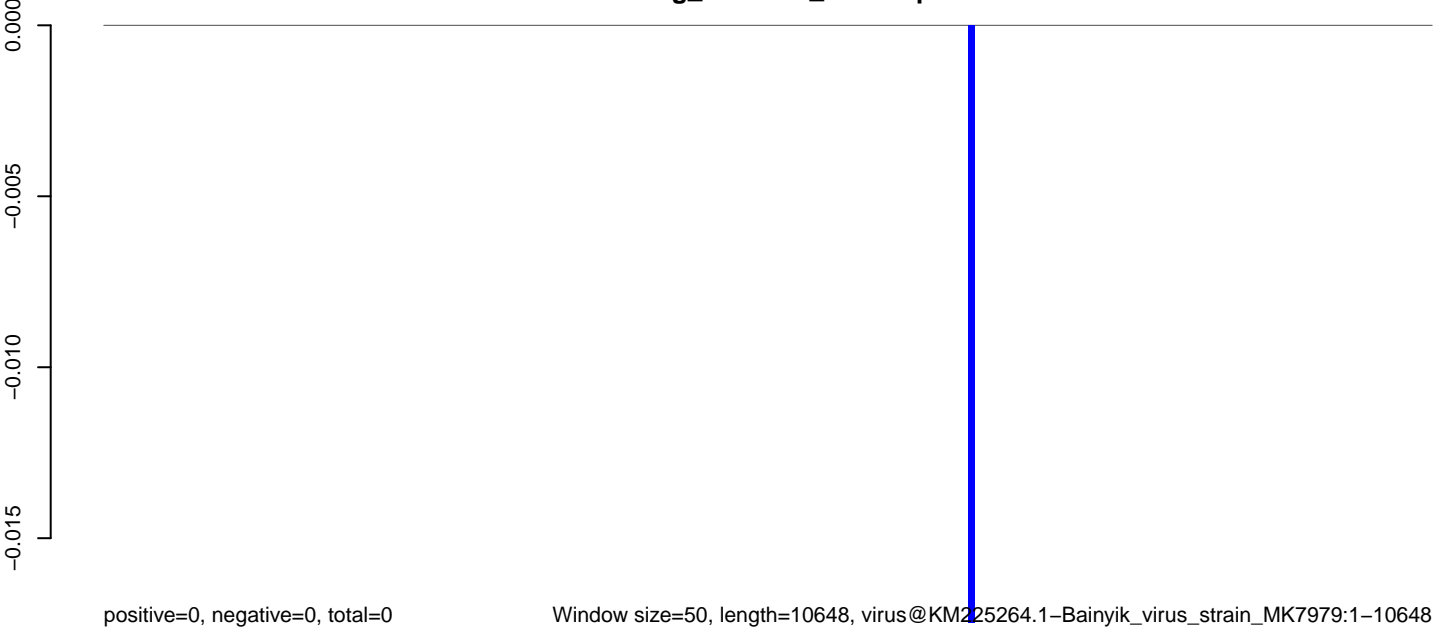
AeAeg_CCL.125_cells.18_23.rep



AeAeg_CCL.125_cells.24_35.rep



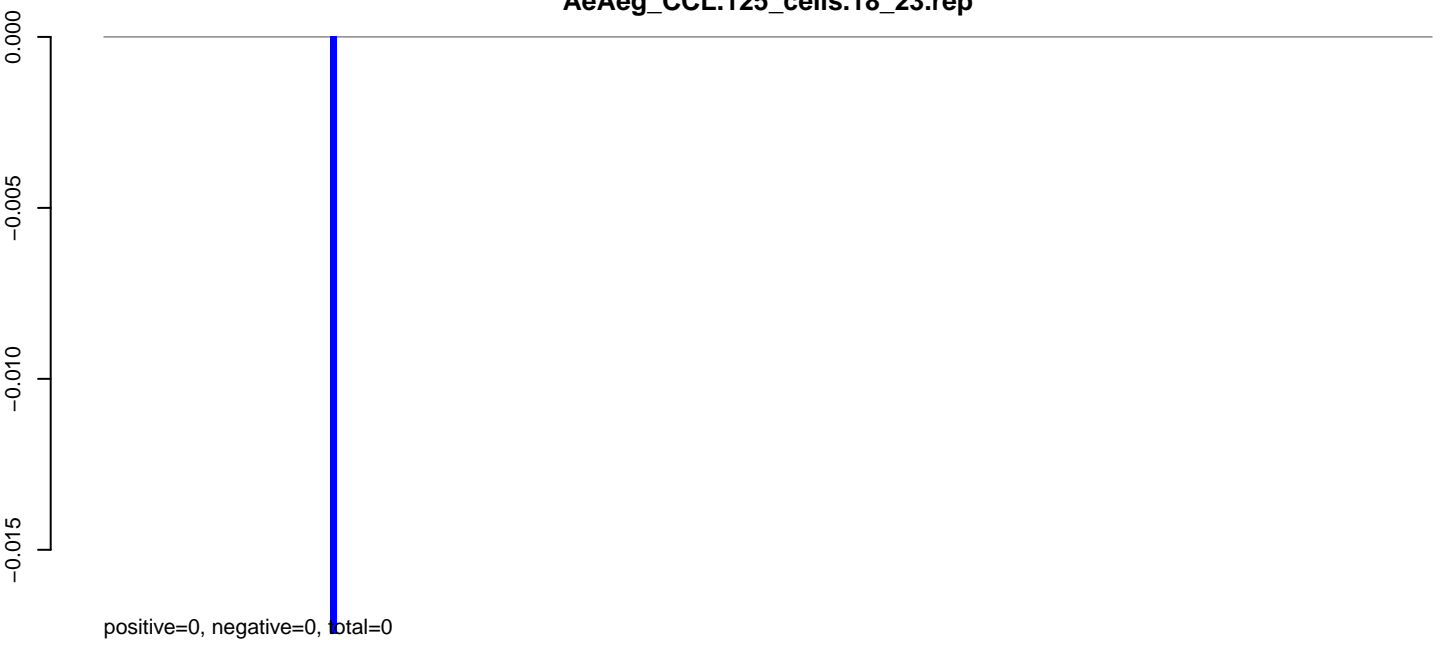
AeAeg_CCL.125_cells.rep



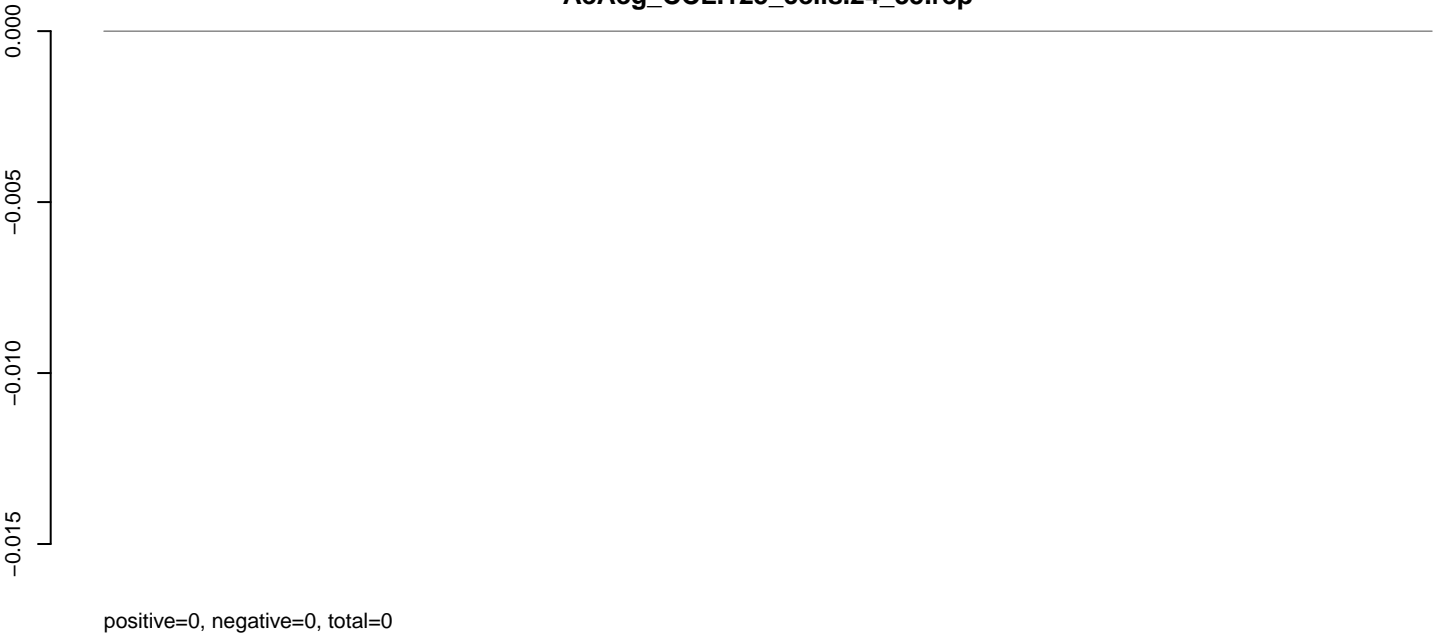
Window size=50, length=10648, virus@KM225264.1-Bainyik_virus_strain_MK7979:1-10648

0 2000 4000 6000 8000 10000

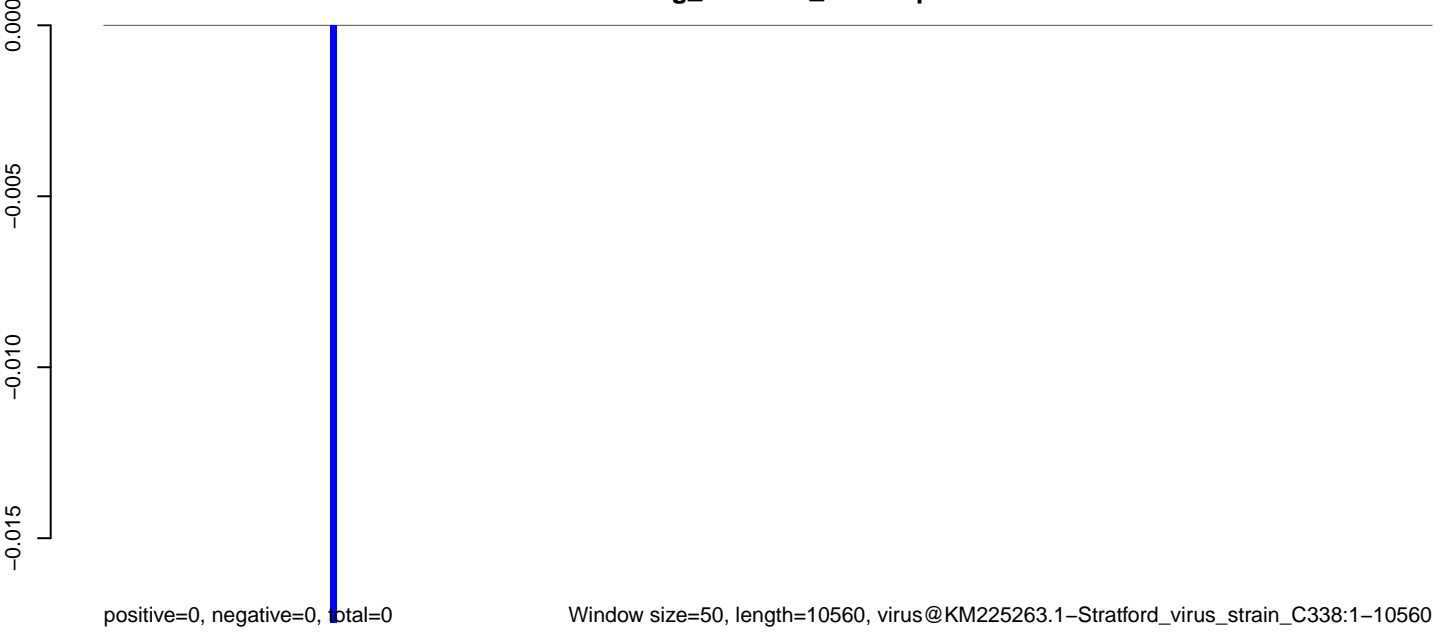
AeAeg_CCL.125_cells.18_23.rep



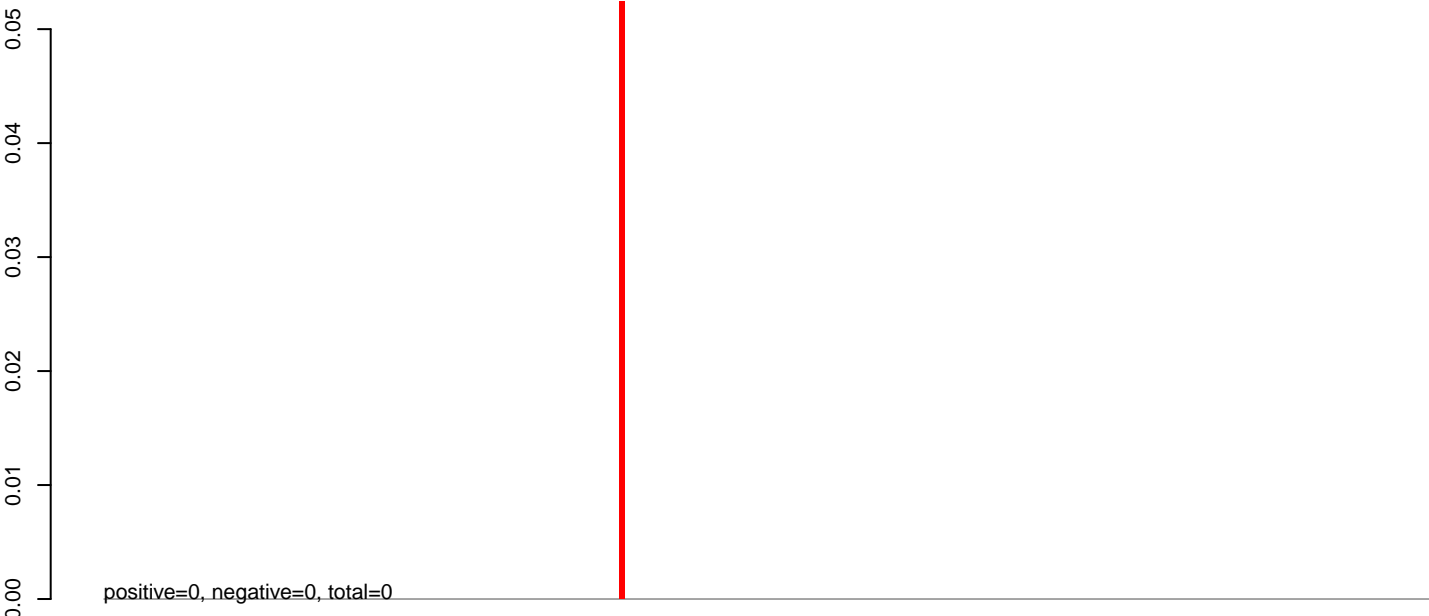
AeAeg_CCL.125_cells.24_35.rep



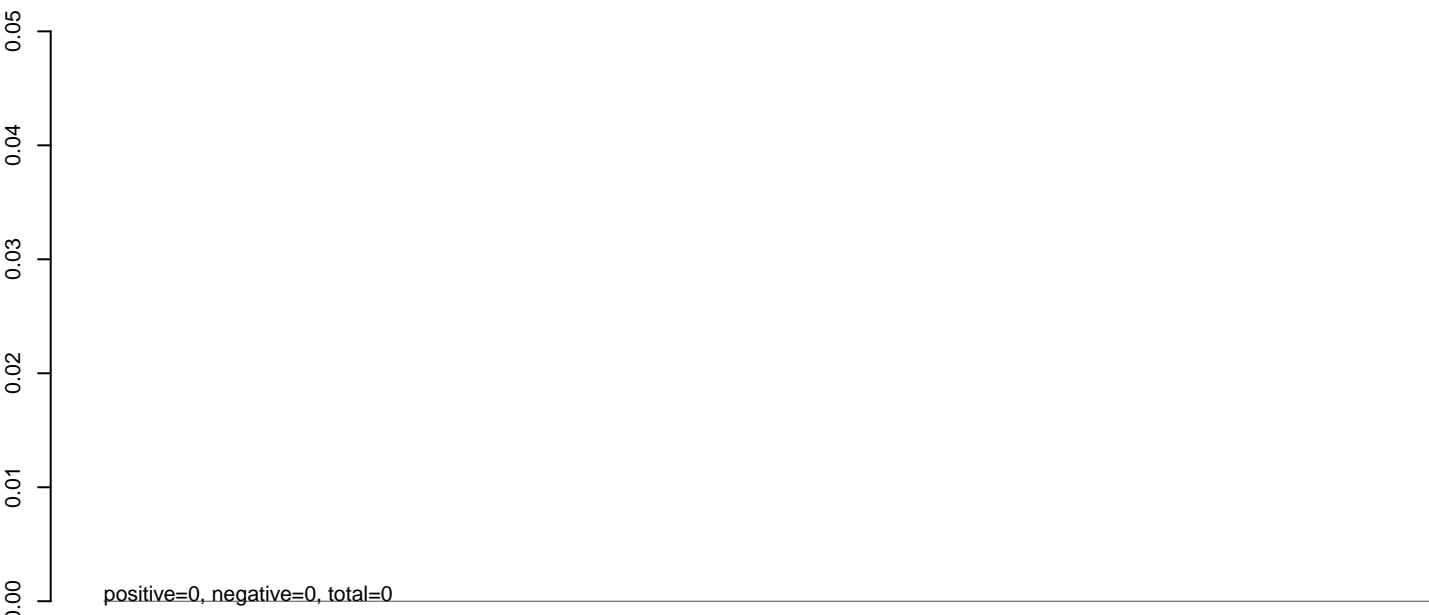
AeAeg_CCL.125_cells.rep



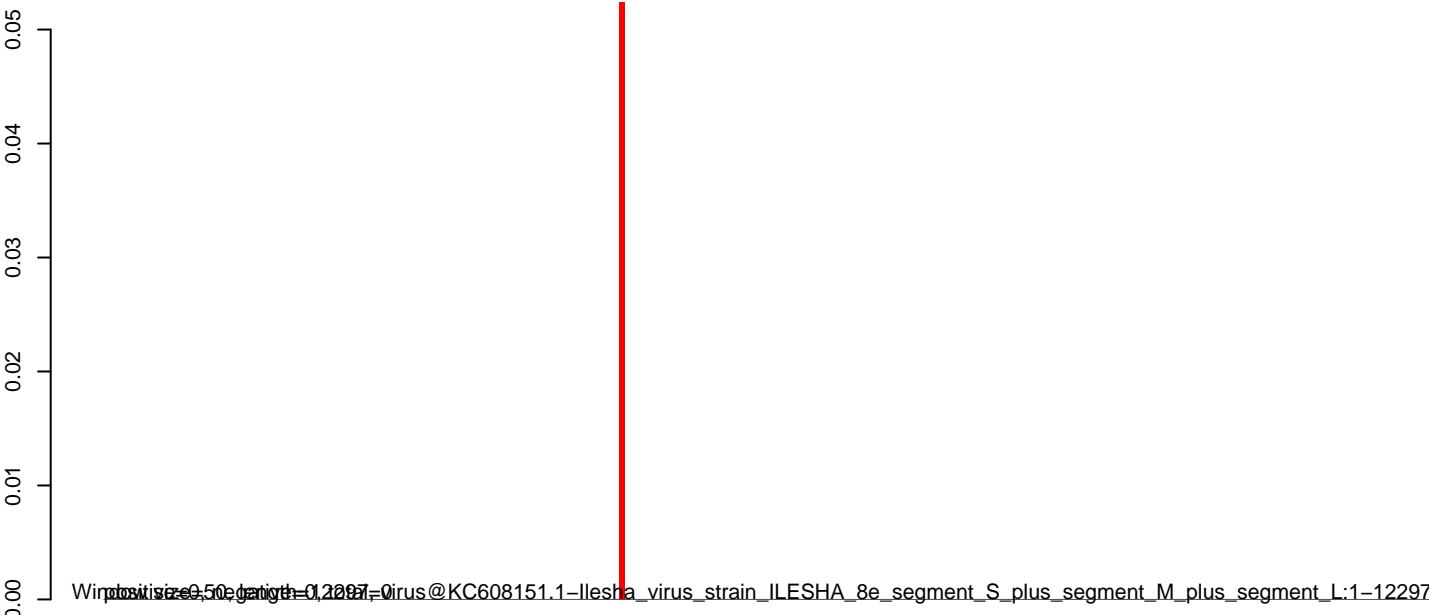
AeAeg_CCL.125_cells.18_23.rep



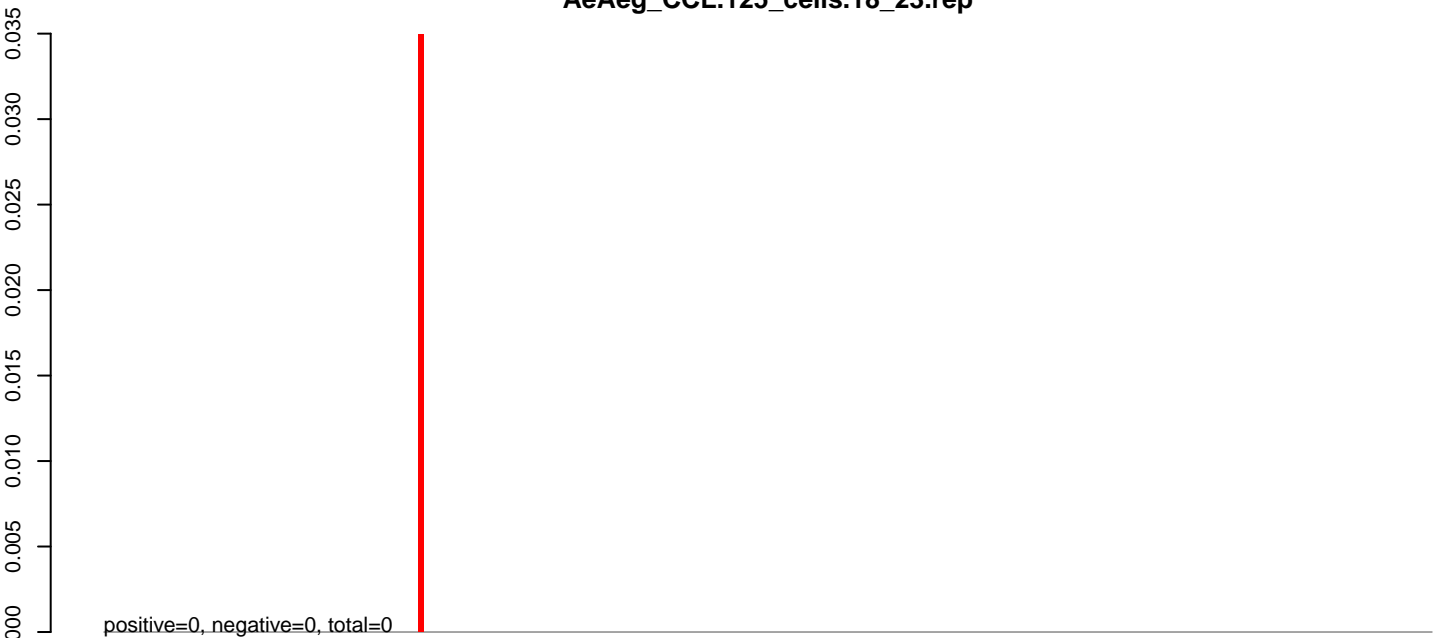
AeAeg_CCL.125_cells.24_35.rep



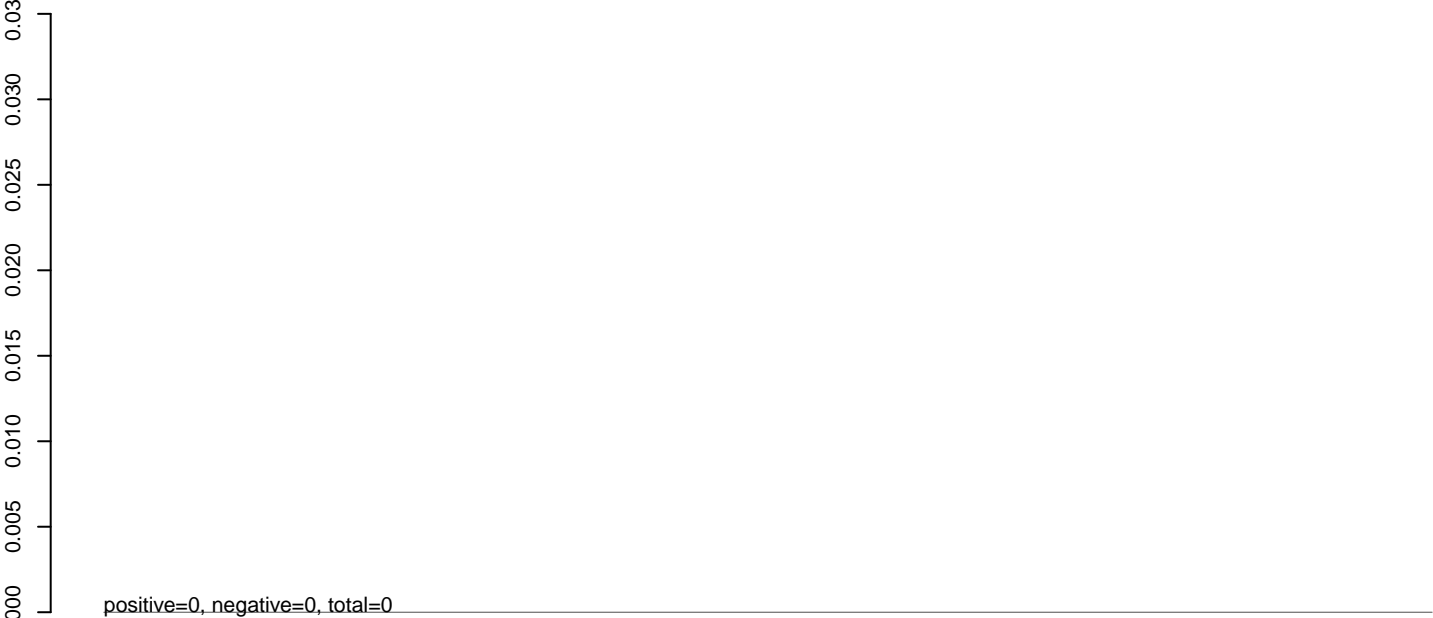
AeAeg_CCL.125_cells.rep



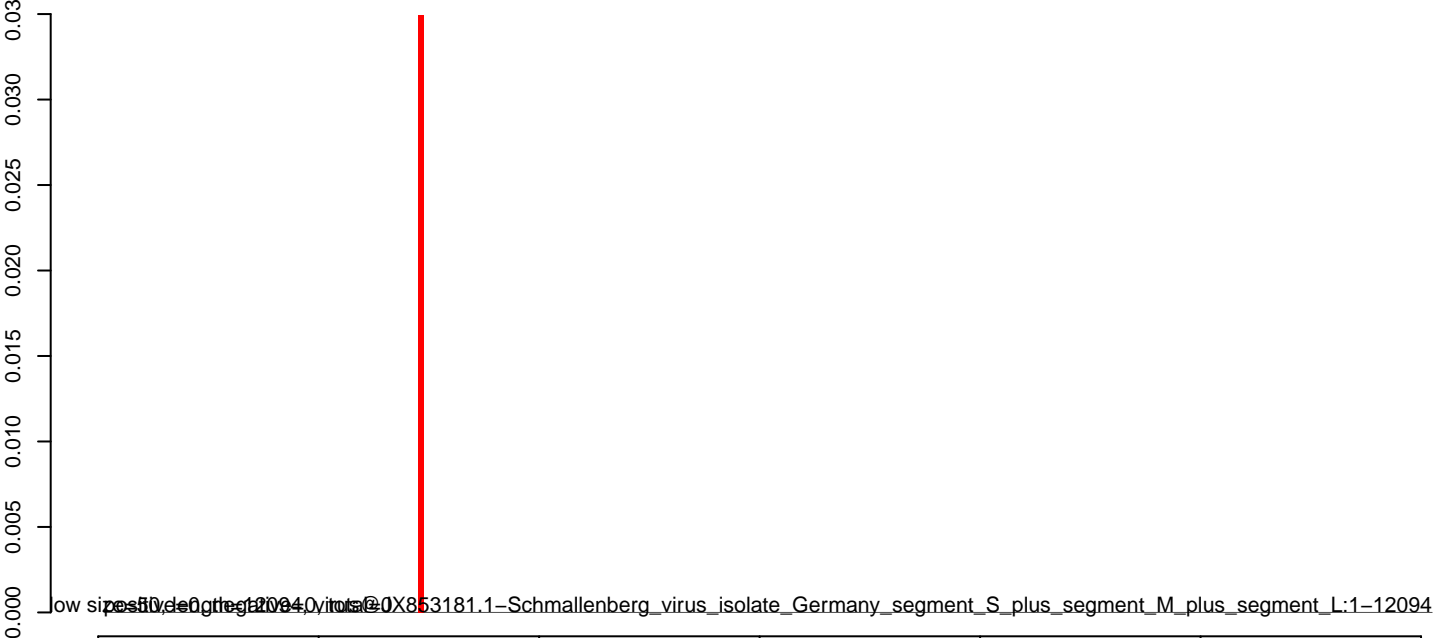
AeAeg_CCL.125_cells.18_23.rep



AeAeg_CCL.125_cells.24_35.rep



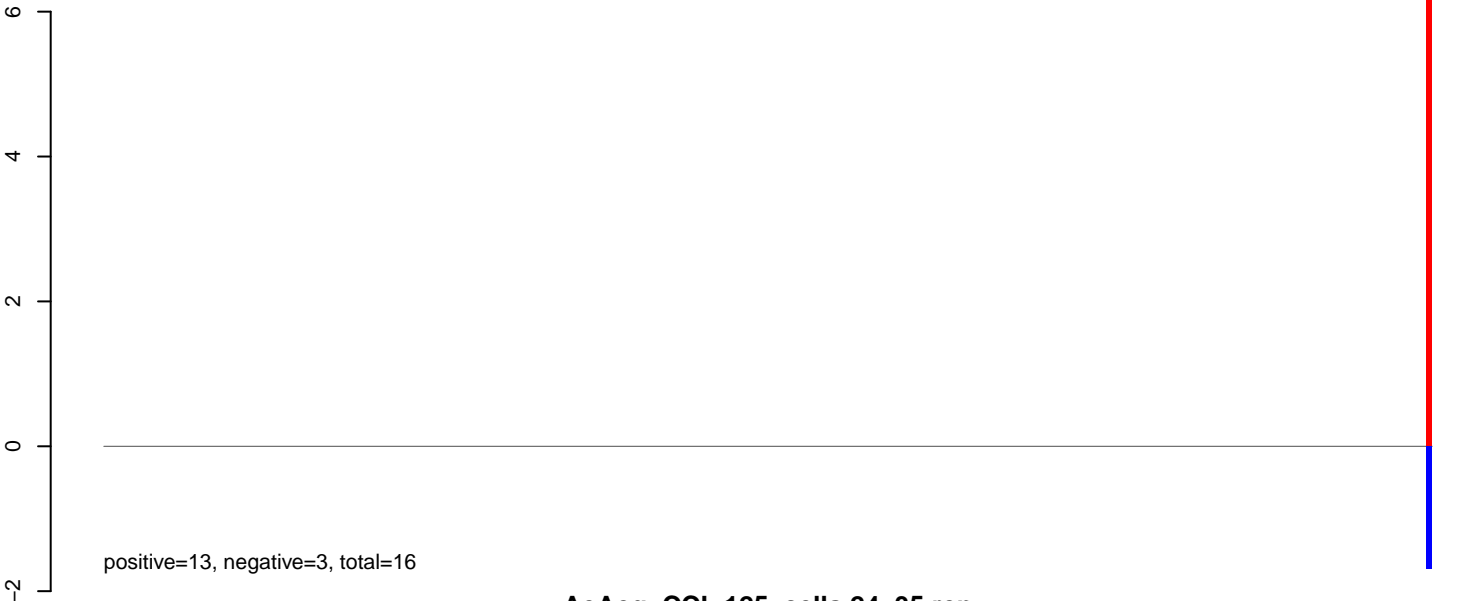
AeAeg_CCL.125_cells.rep



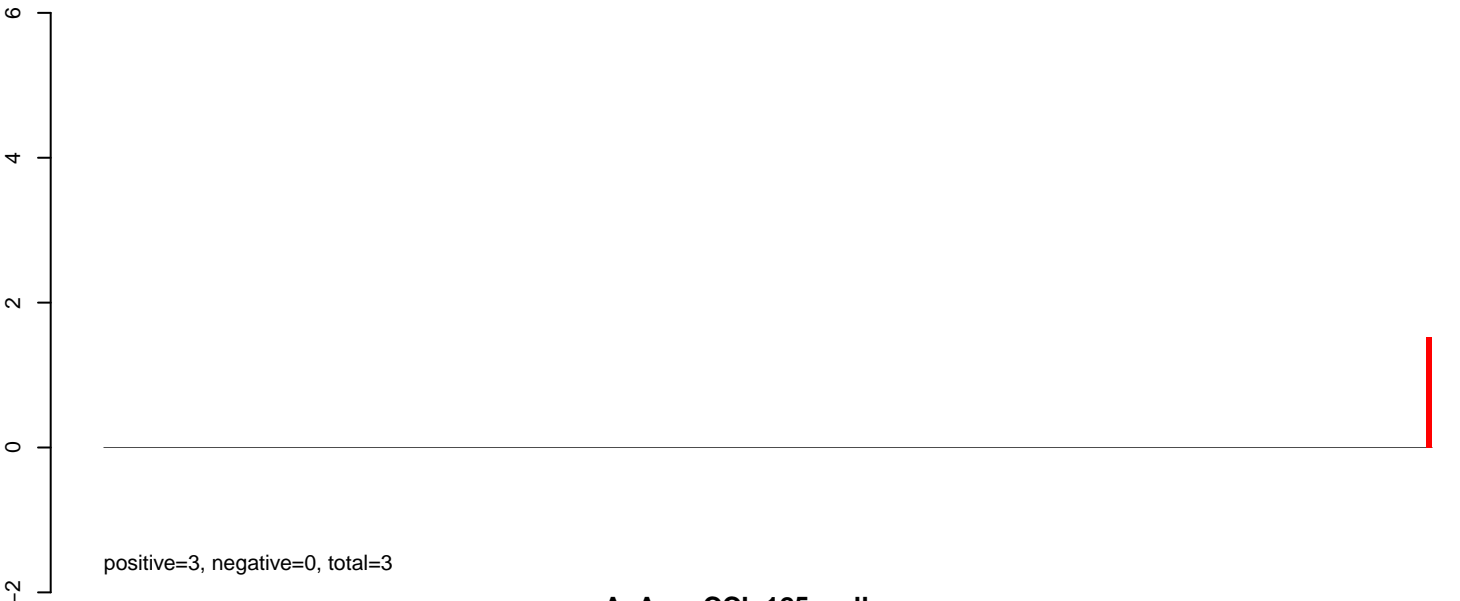
low size of the genome of the 2004/01/06/X853181.1-Schmallenberg_virus_isolate_Germany_segment_S_plus_segment_M_plus_segment_L:1-12094

0 2000 4000 6000 8000 10000 12000

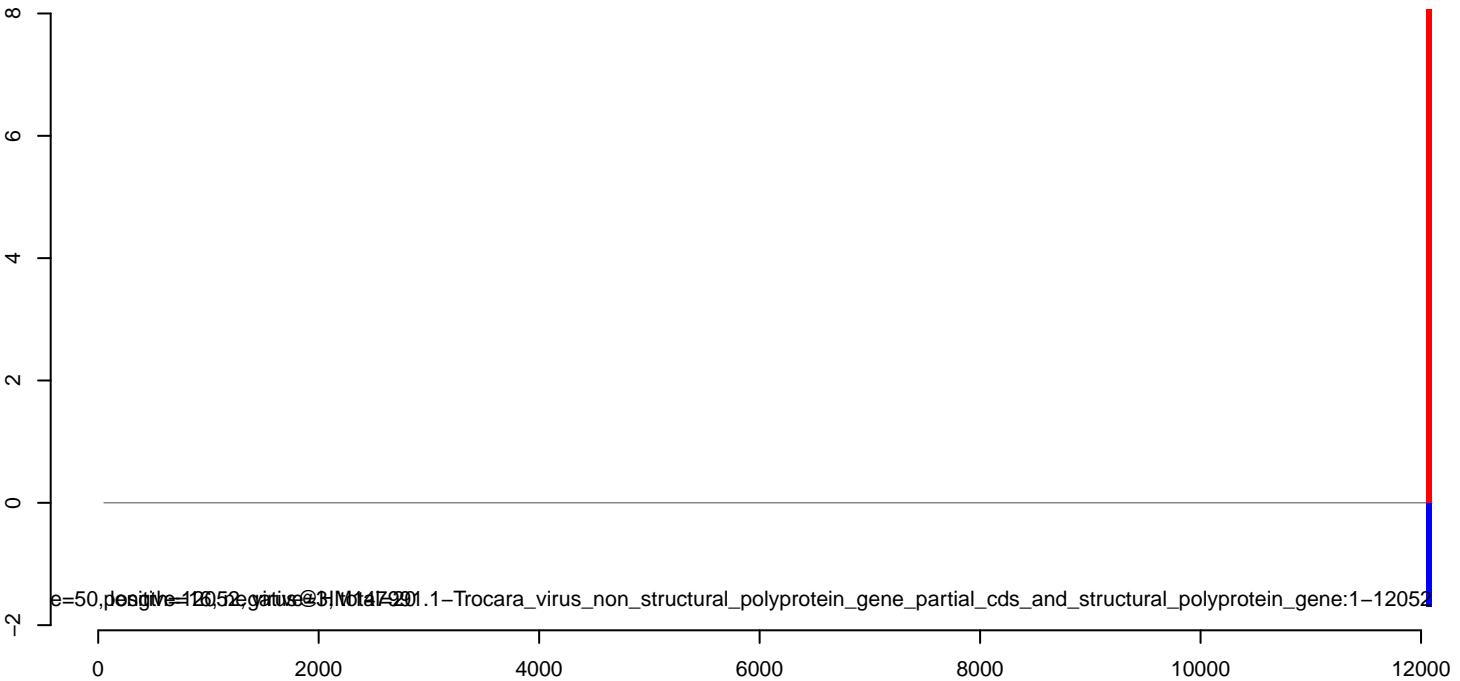
AeAeg_CCL.125_cells.18_23.rep



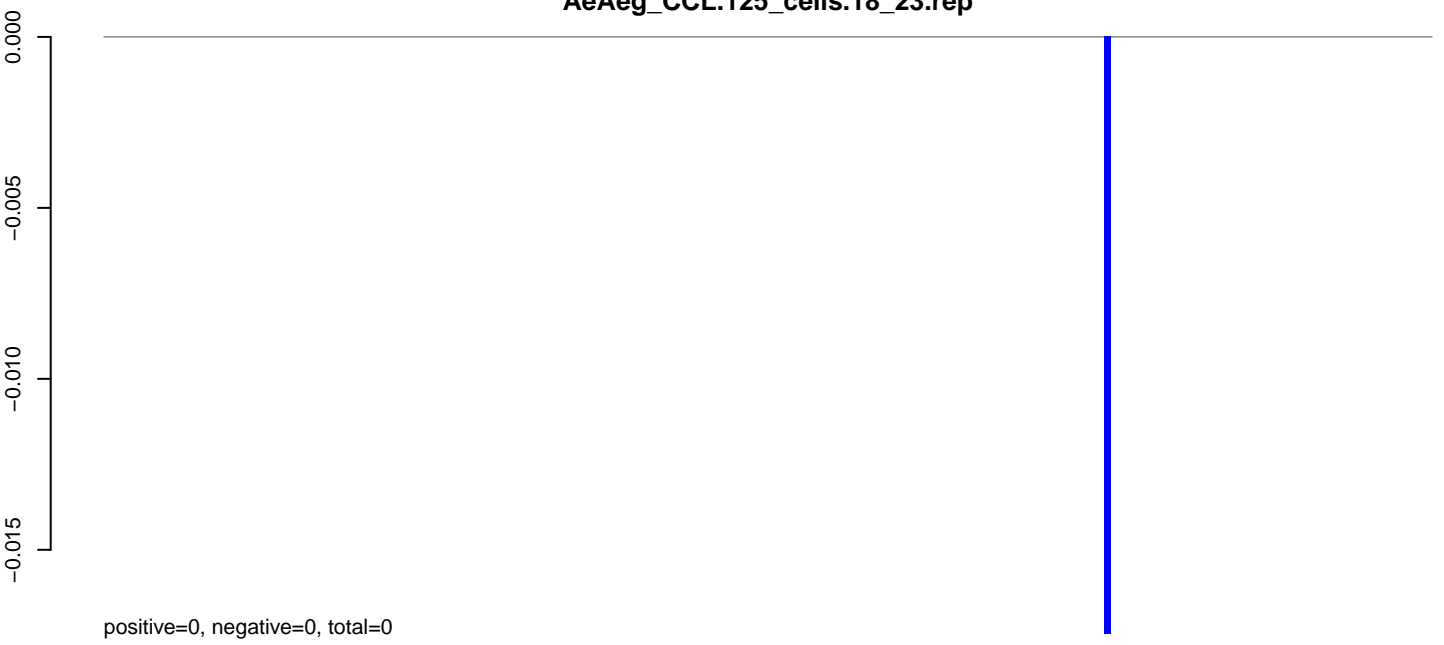
AeAeg_CCL.125_cells.24_35.rep



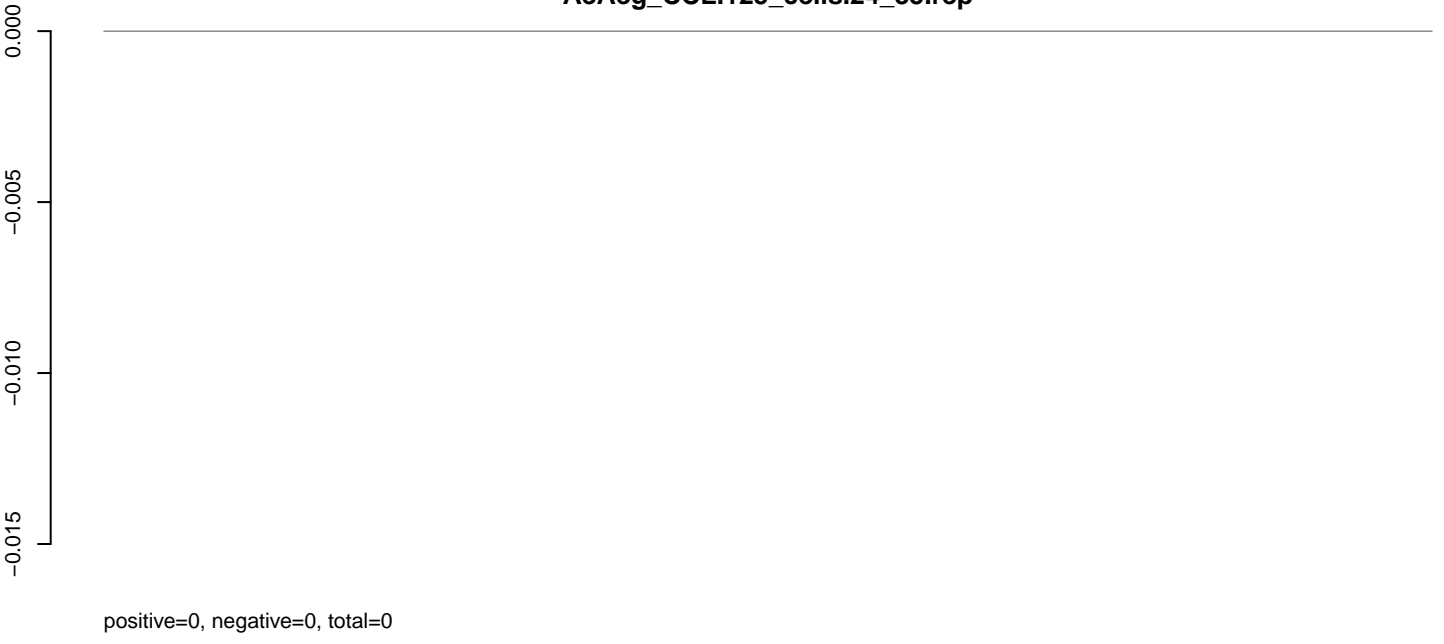
AeAeg_CCL.125_cells.rep



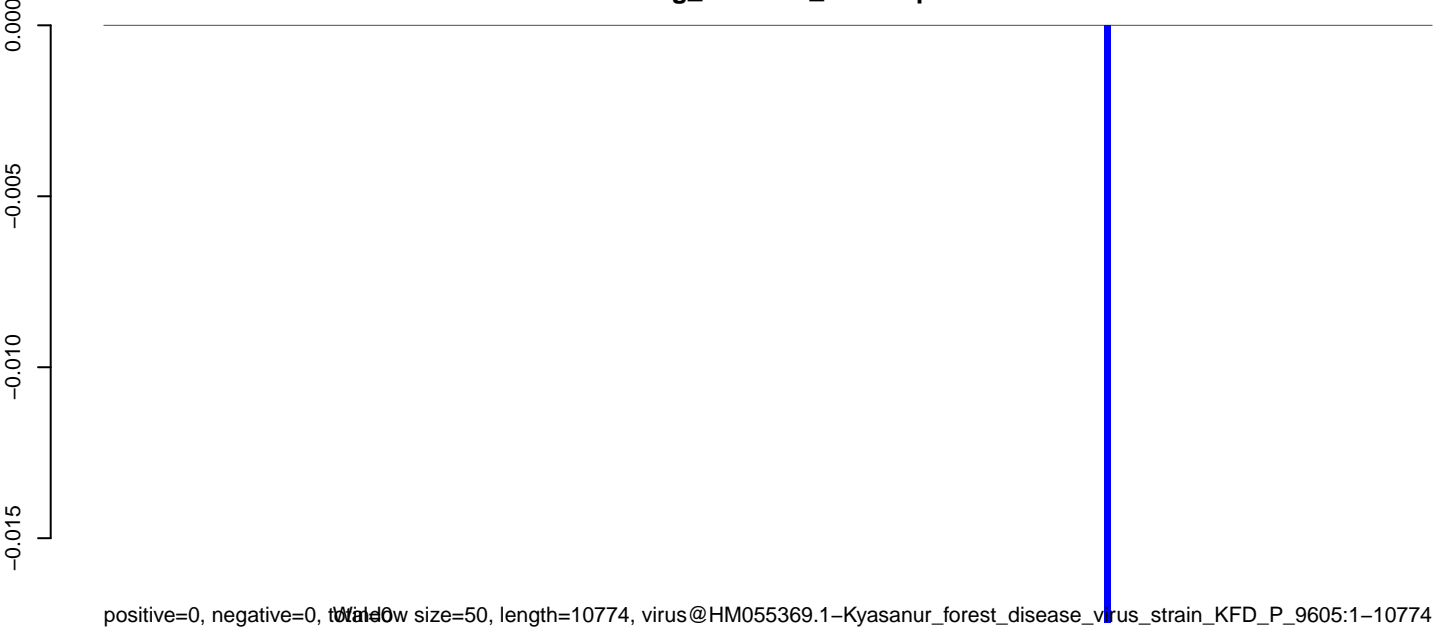
AeAeg_CCL.125_cells.18_23.rep



AeAeg_CCL.125_cells.24_35.rep

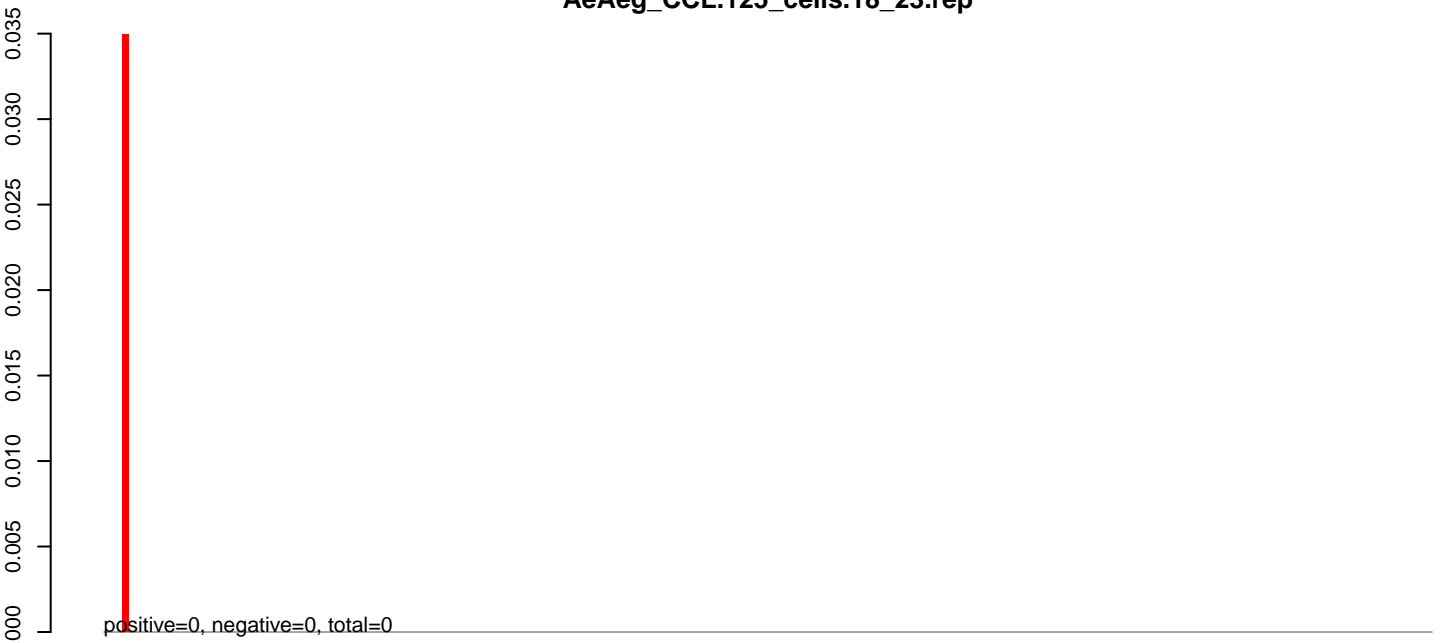


AeAeg_CCL.125_cells.rep

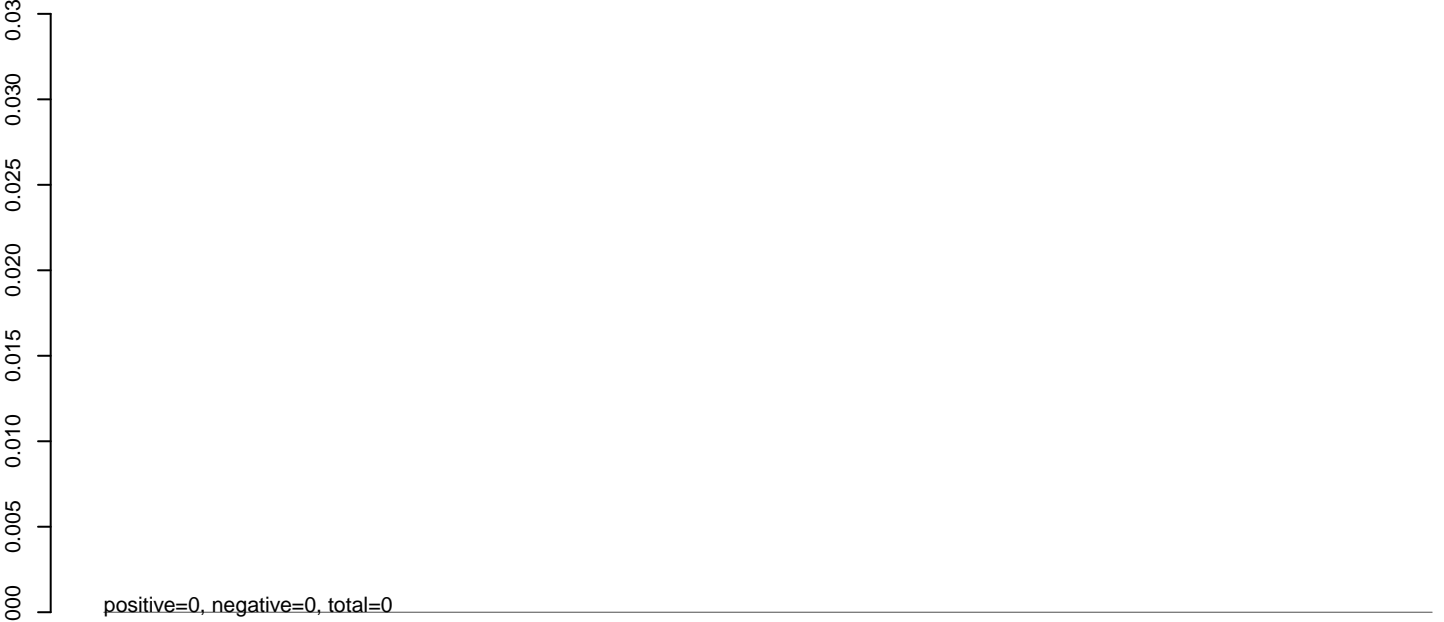


0 2000 4000 6000 8000 10000

AeAeg_CCL.125_cells.18_23.rep



AeAeg_CCL.125_cells.24_35.rep



AeAeg_CCL.125_cells.rep



Window size=50, length=10837, virus@FJ663034.1-Culex_flavivirus_isolate_lowa07:1-10837

0 2000 4000 6000 8000 10000

AeAeg_CCL.125_cells.18_23.rep

0.000
-0.005
-0.010
-0.015
-0.020
-0.025
-0.030
-0.035

positive=0, negative=0, total=0

AeAeg_CCL.125_cells.24_35.rep

0.000
-0.005
-0.010
-0.015
-0.020
-0.025
-0.030
-0.035

positive=0, negative=0, total=0

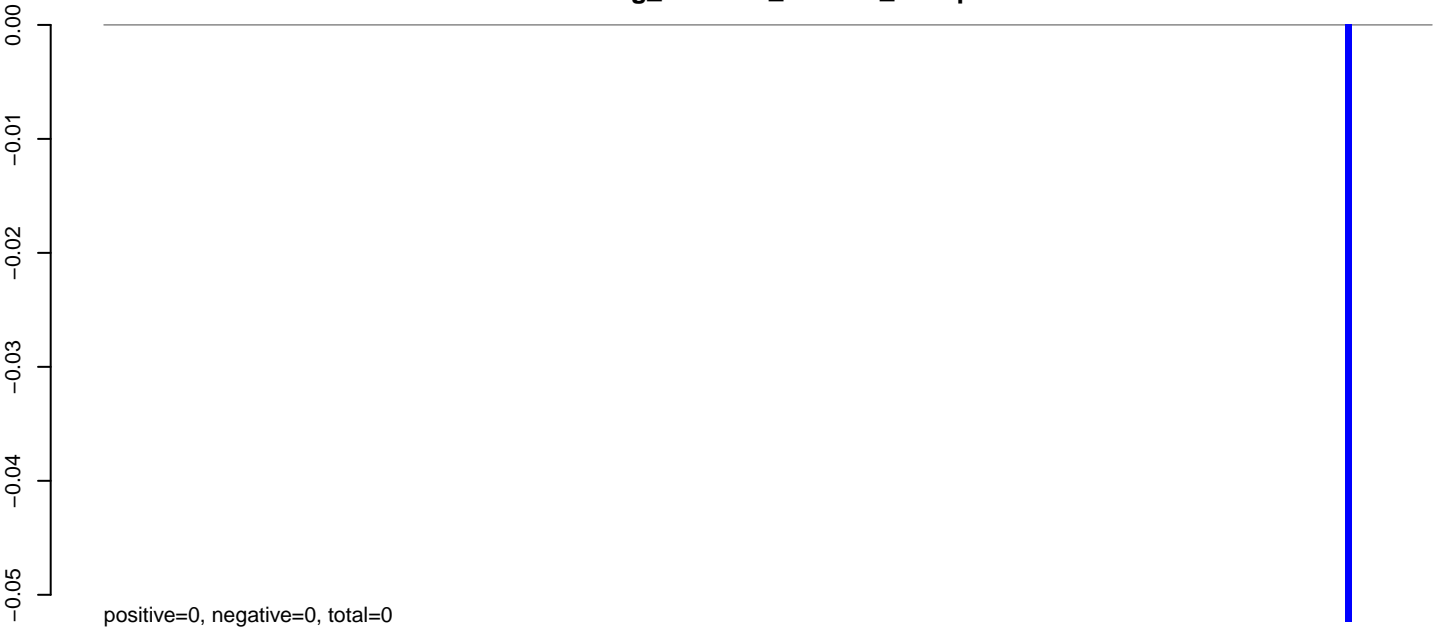
AeAeg_CCL.125_cells.rep

0.000
-0.005
-0.010
-0.015
-0.020
-0.025
-0.030
-0.035

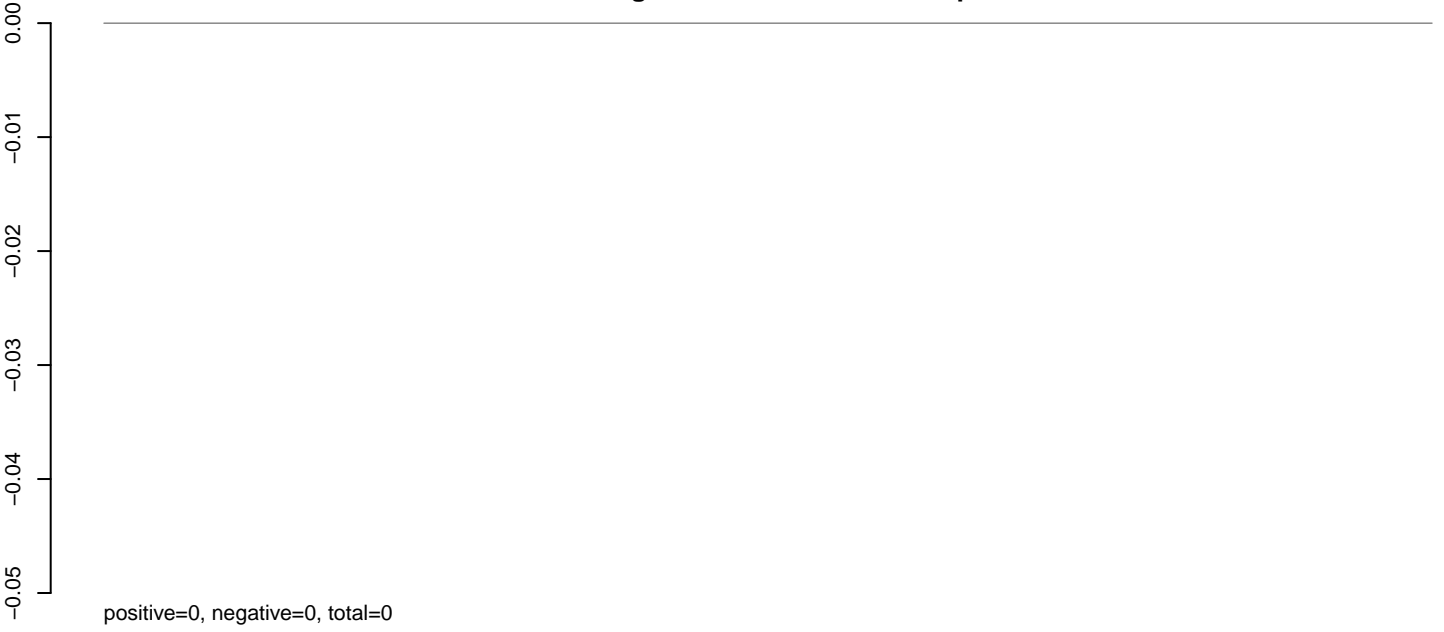
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Window size=50, length=10254, virus@DQ235149.1-Royal_Farm_virus_from_Afghanistan_polyprotein_gene:1-10254

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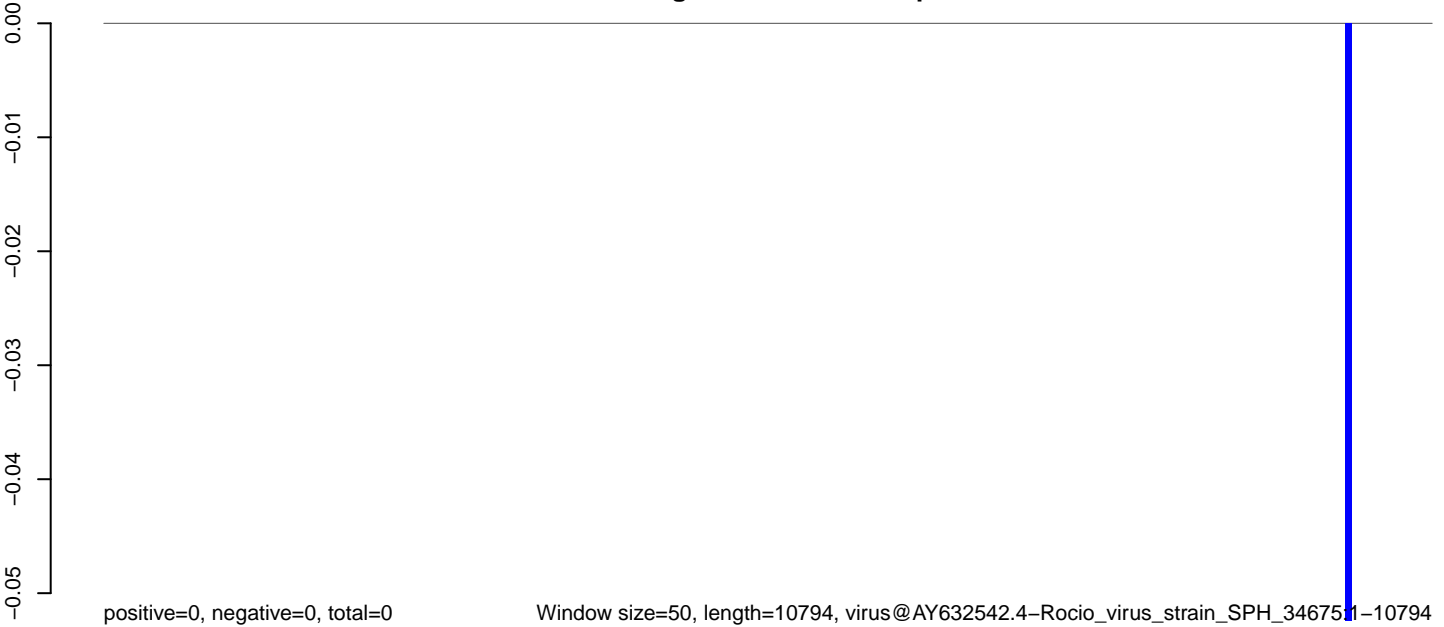
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AeAeg_CCL.125_cells.24_35.rep

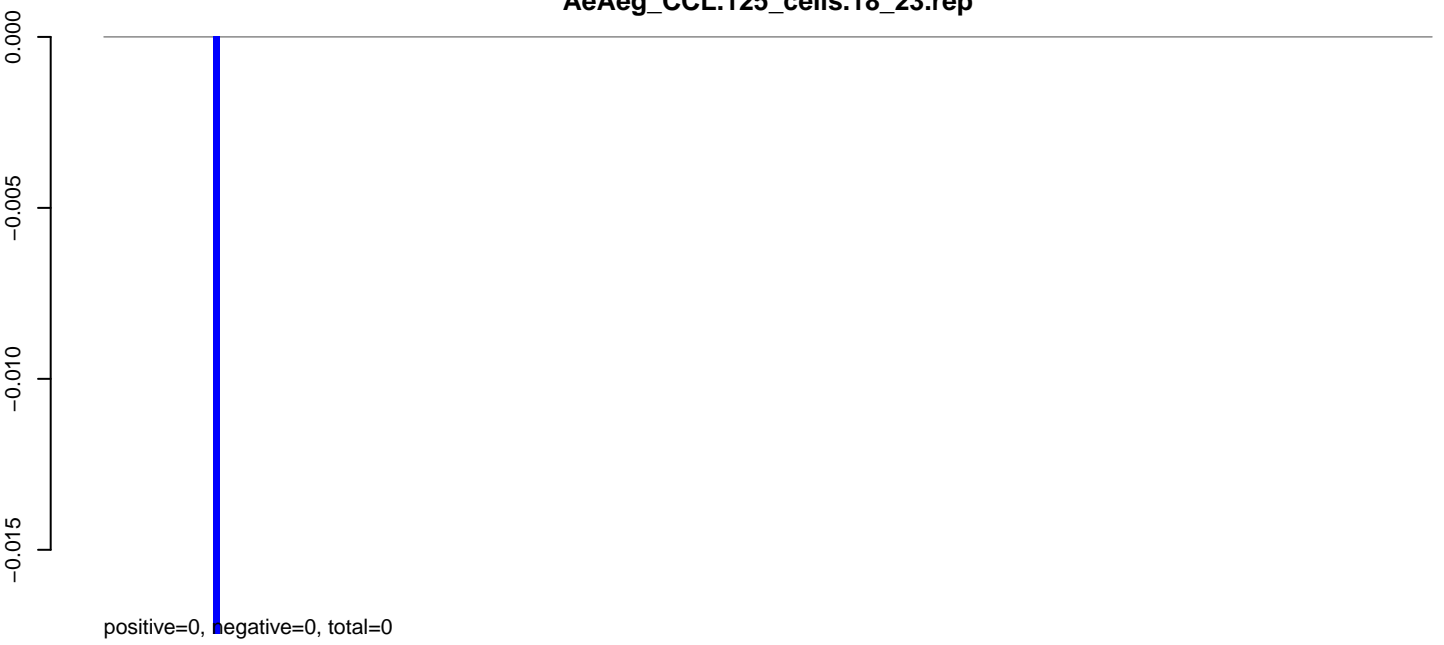


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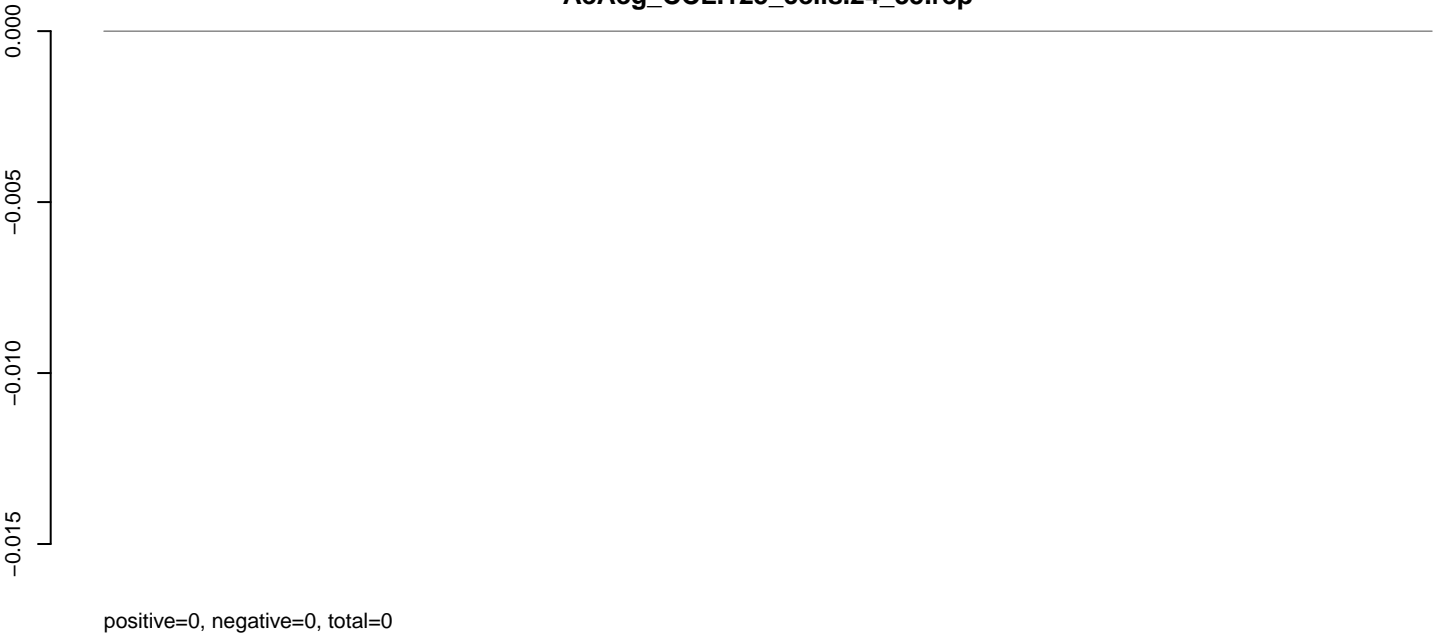


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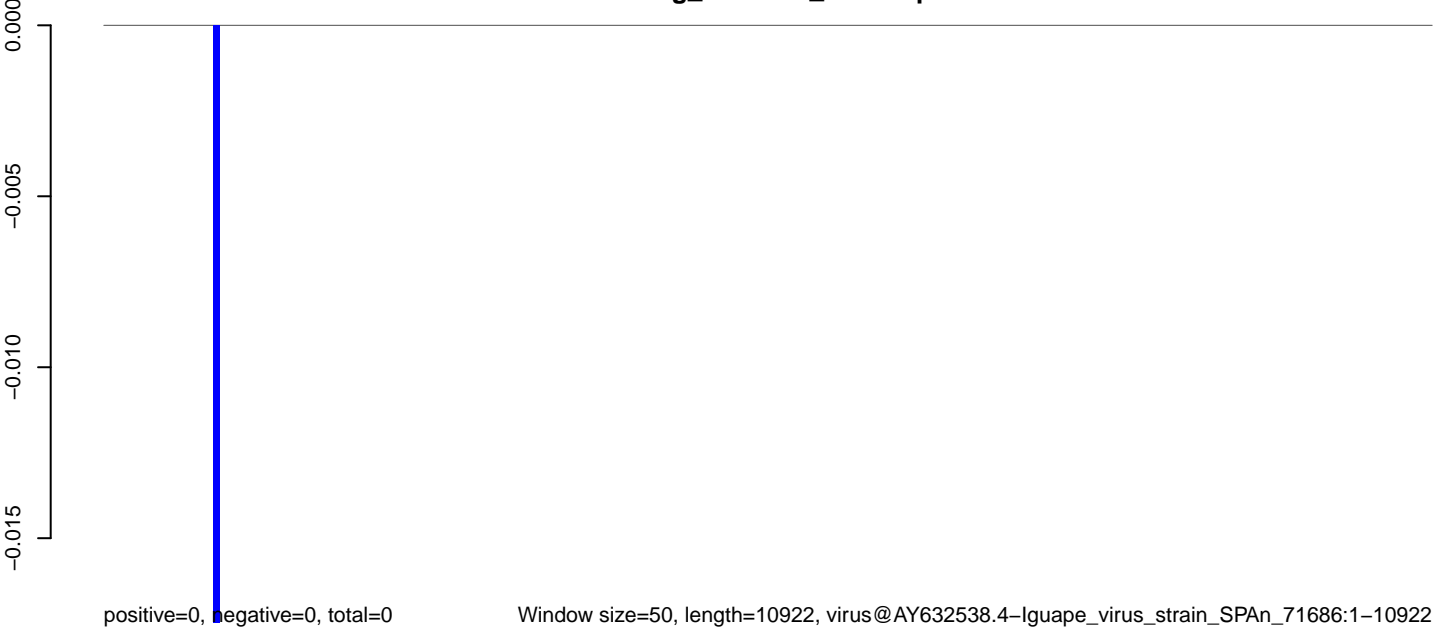
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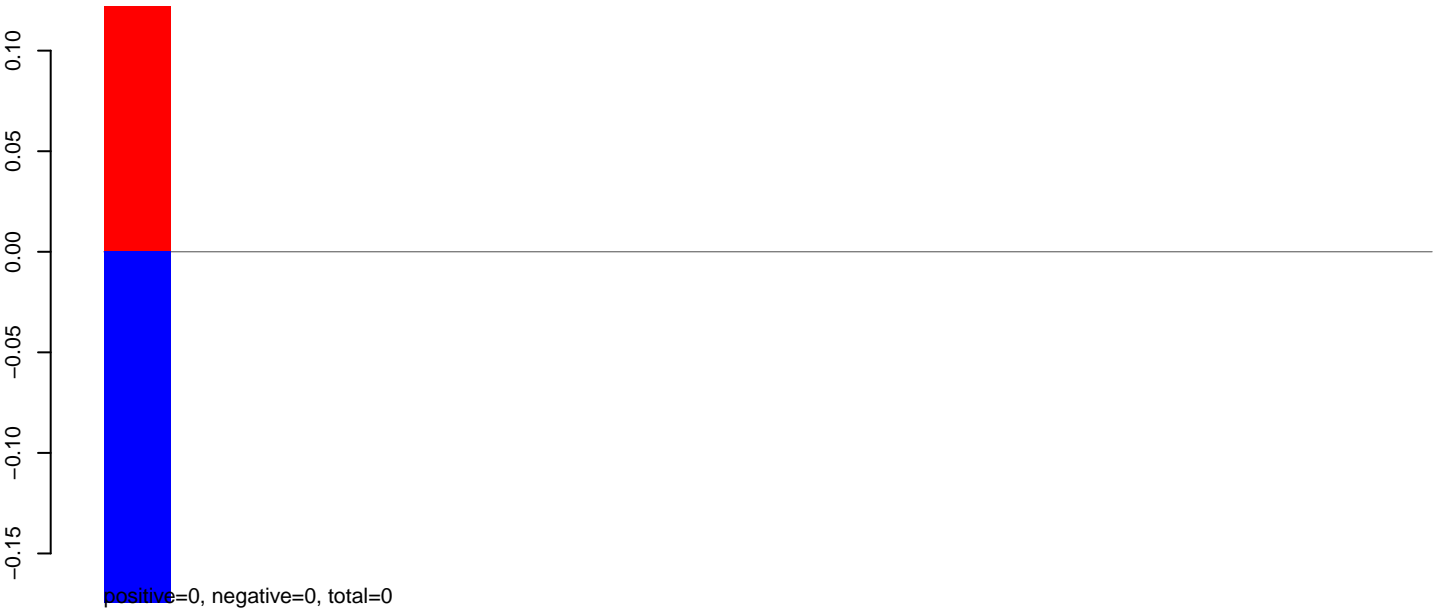
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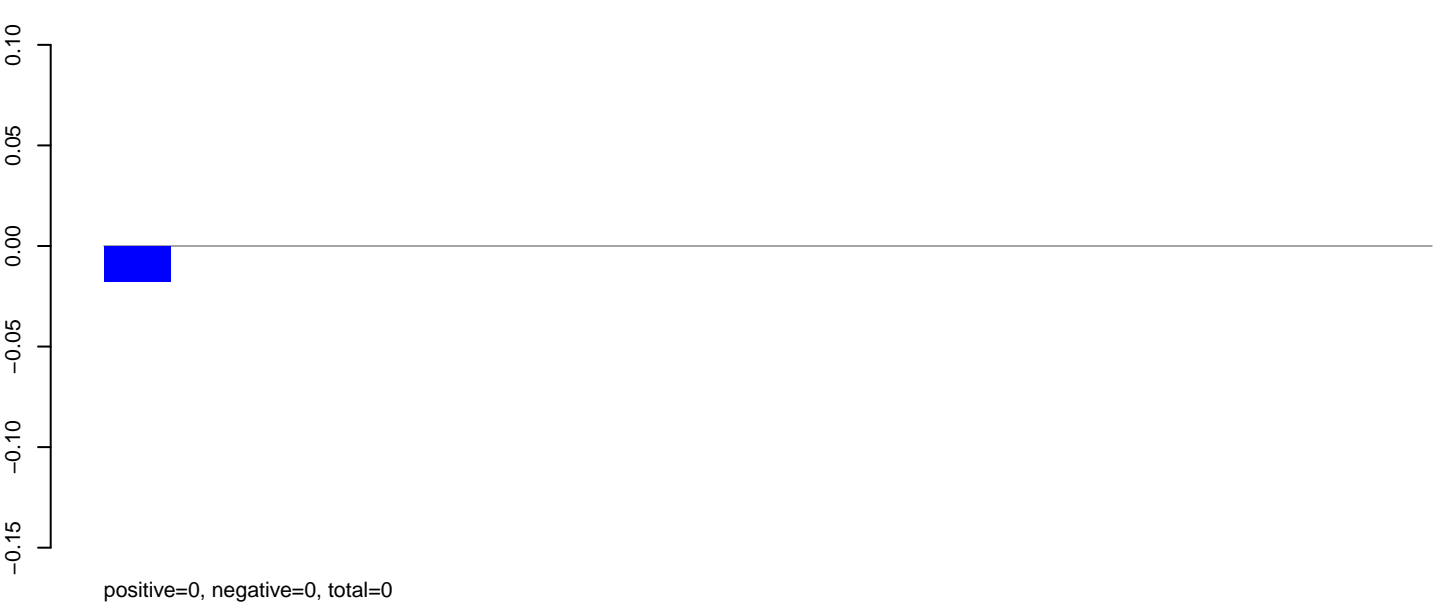
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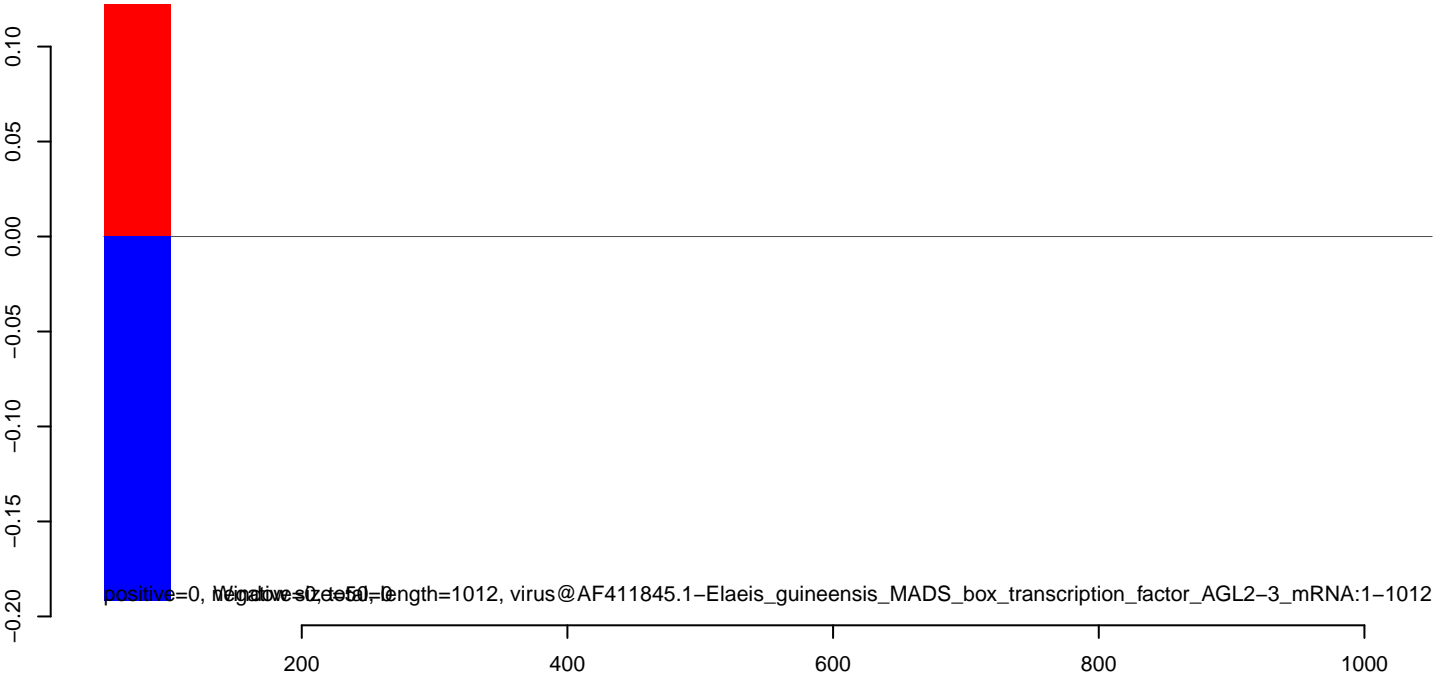
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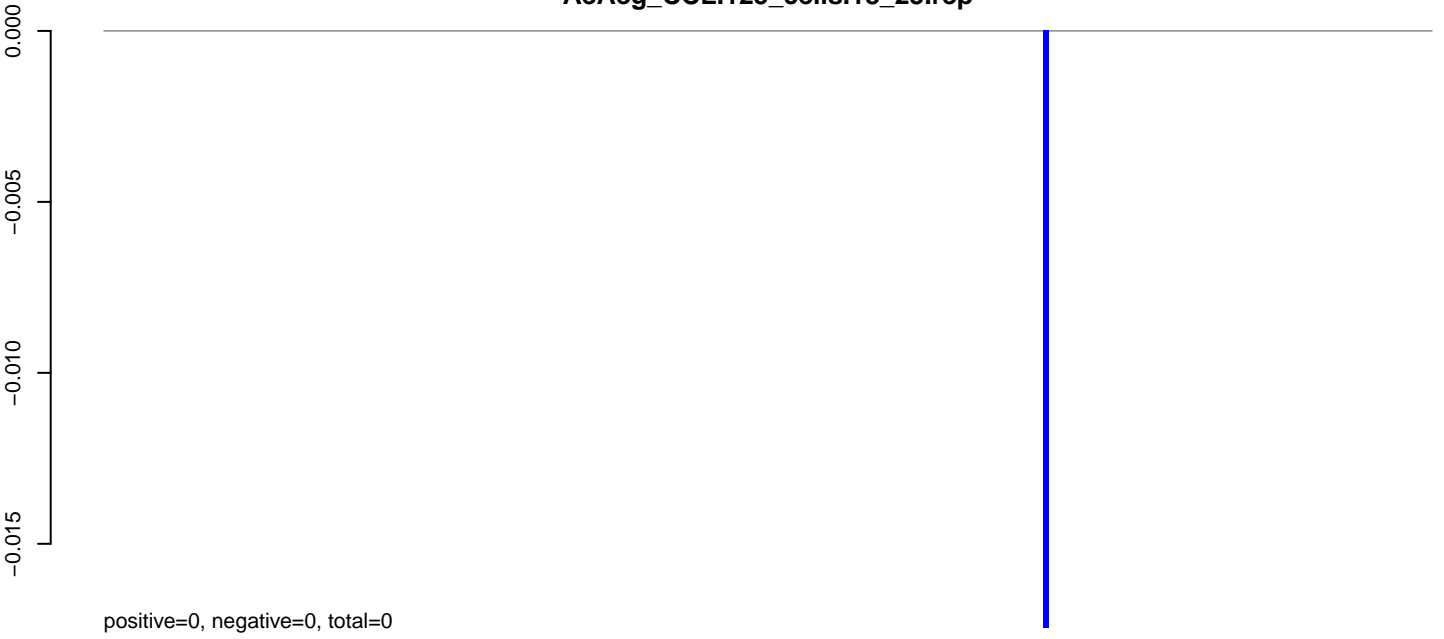
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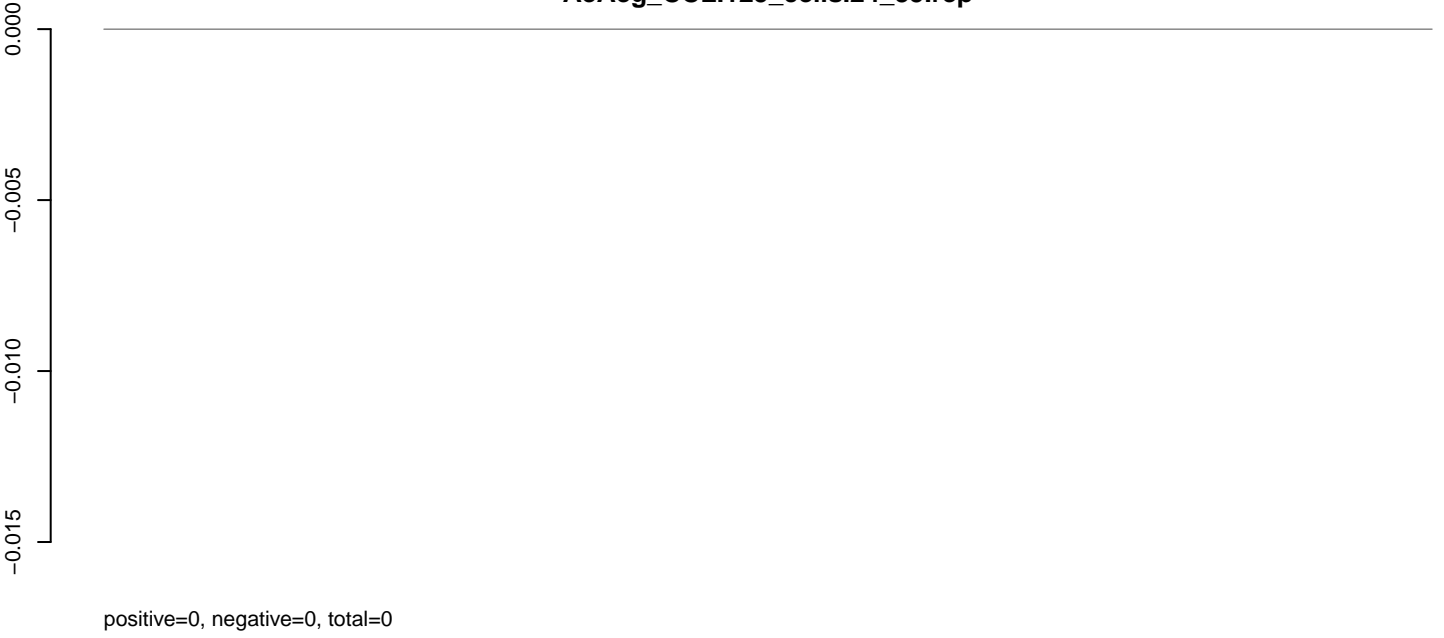
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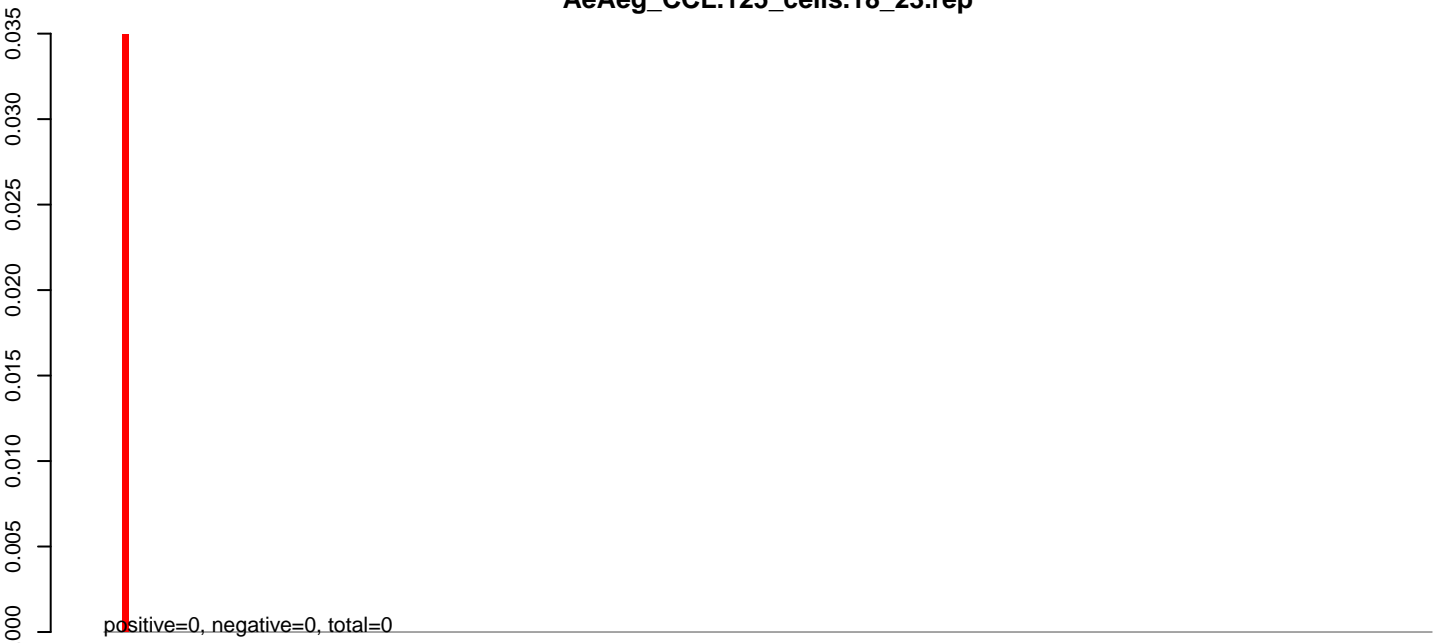
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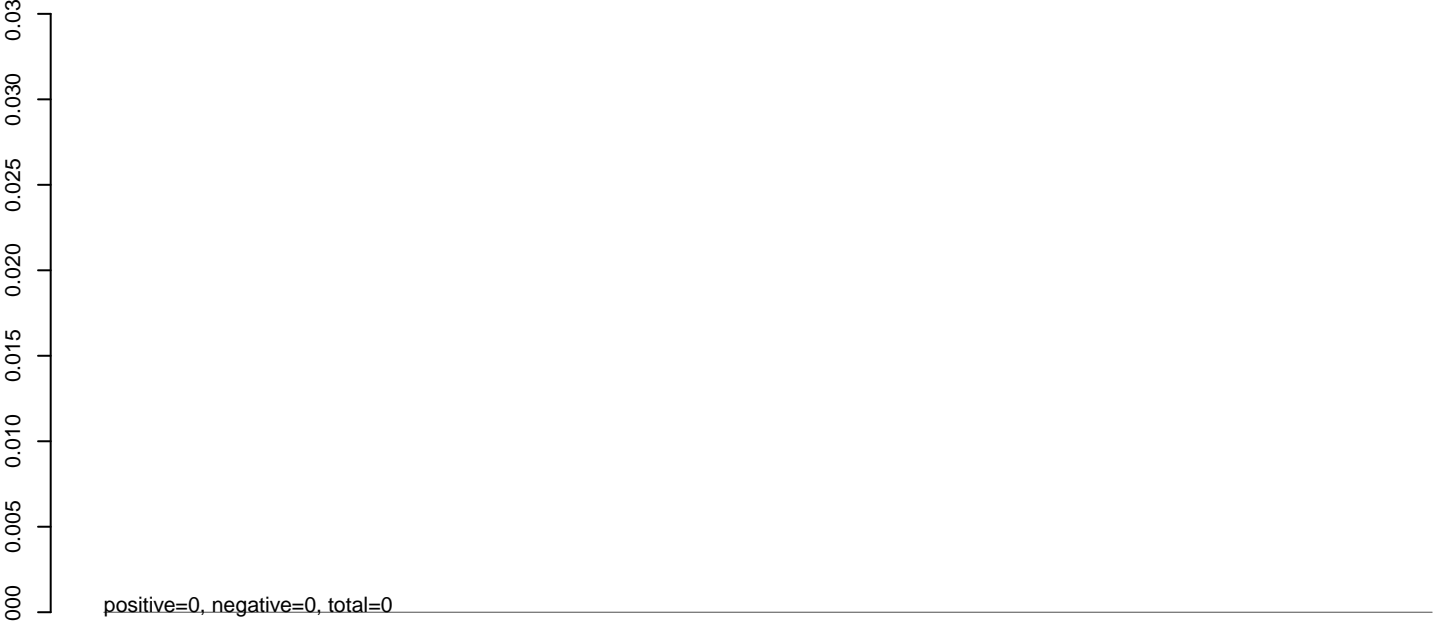
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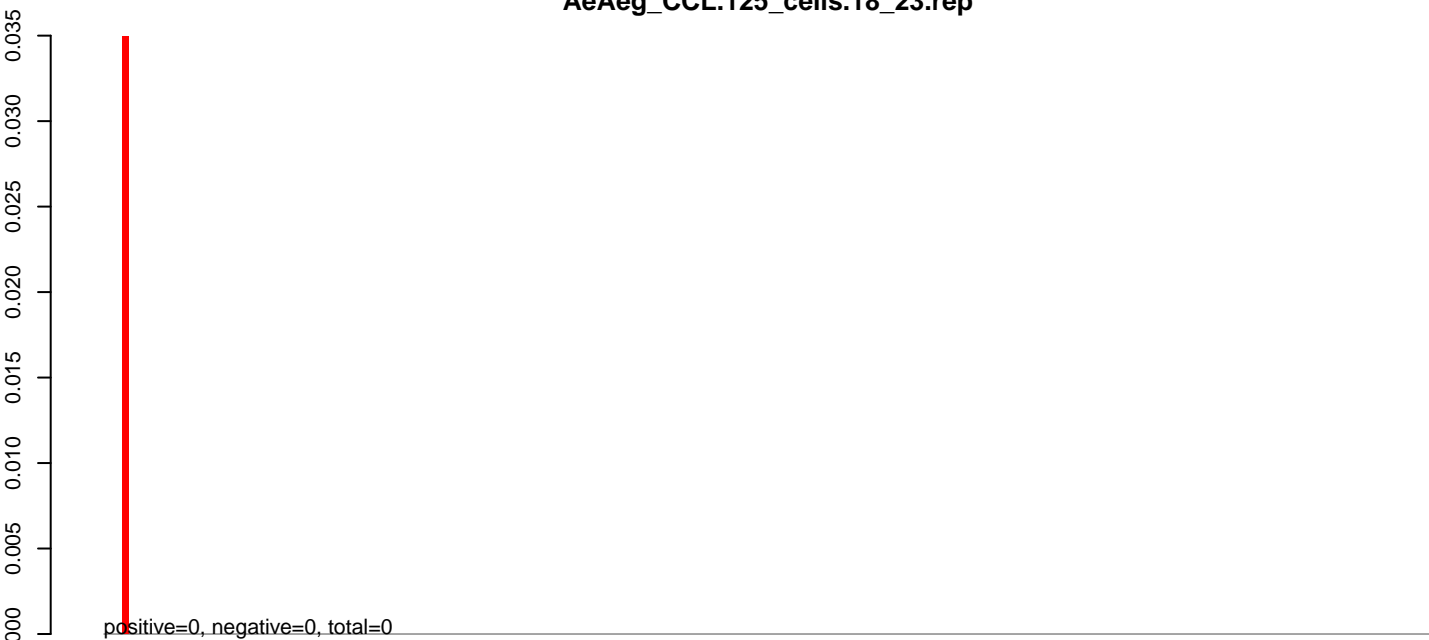
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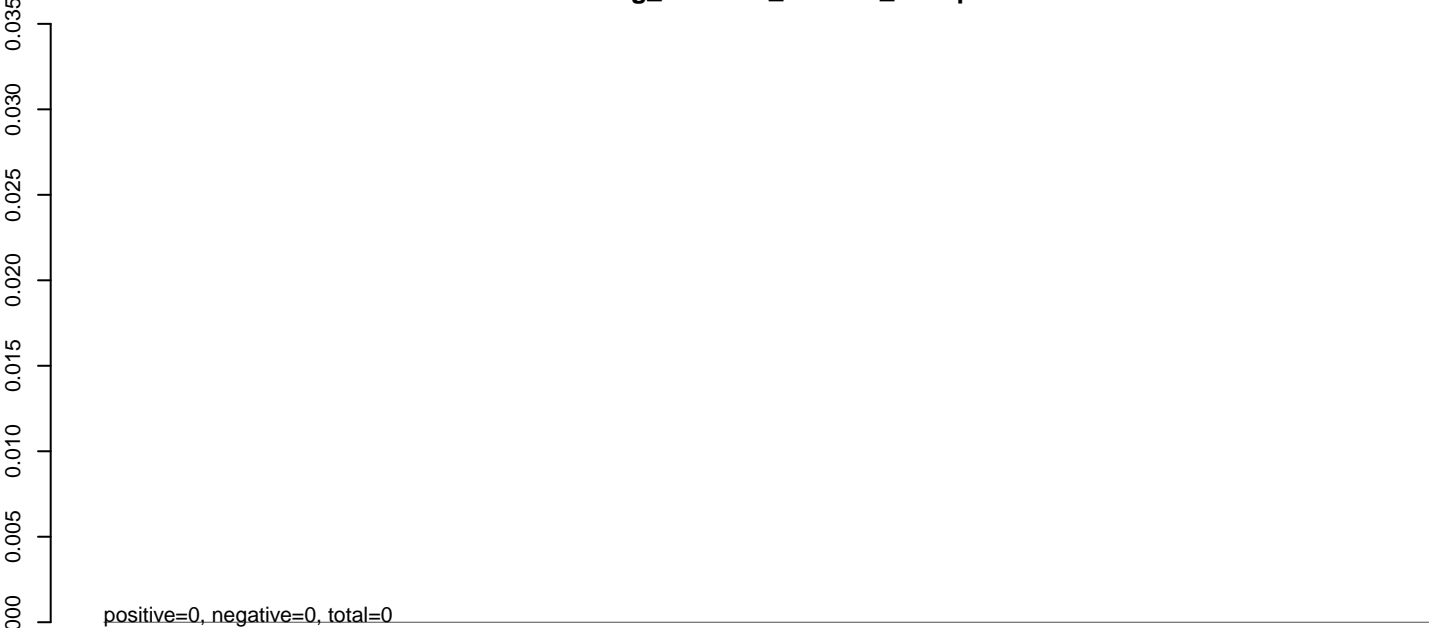
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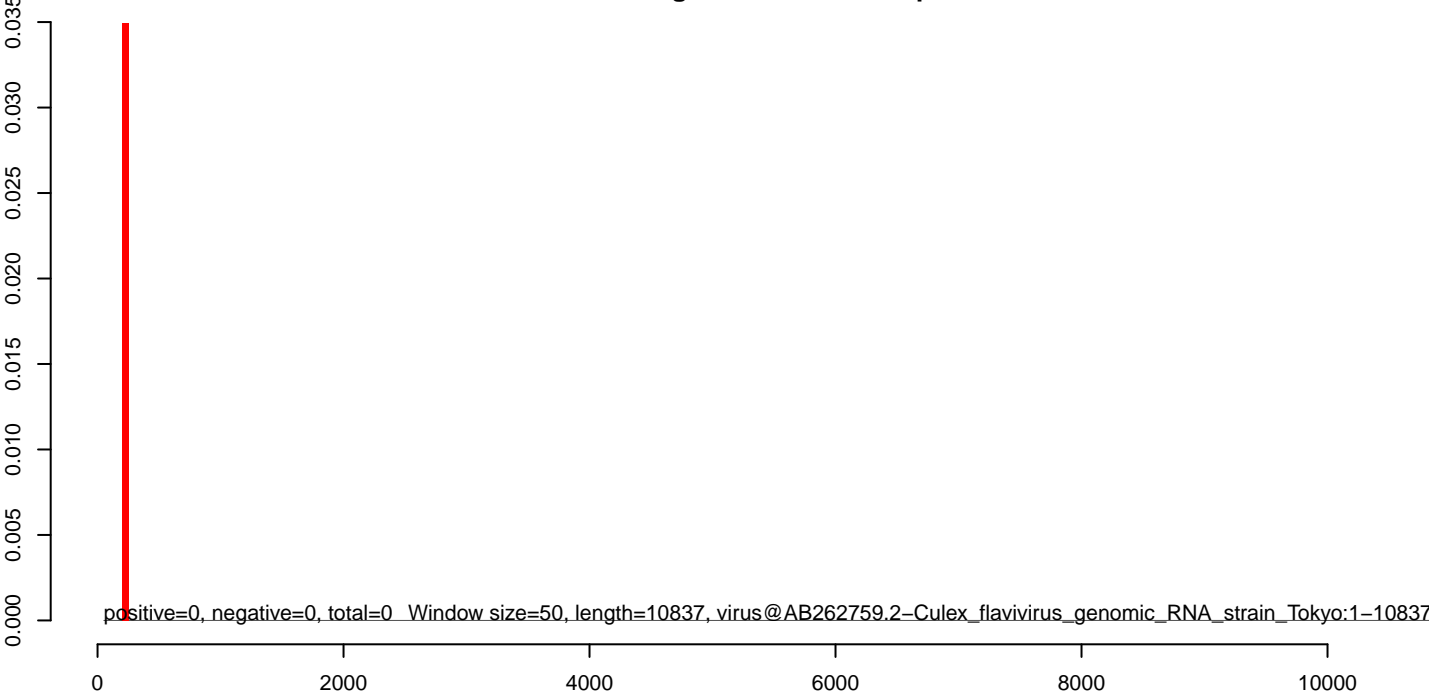
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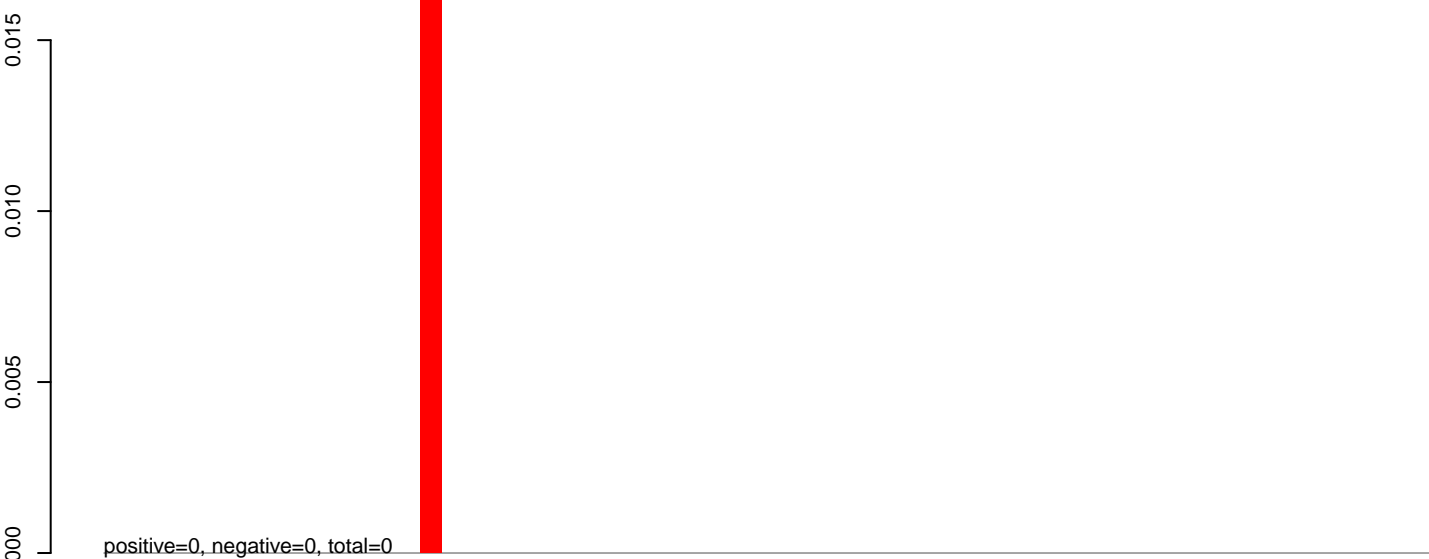
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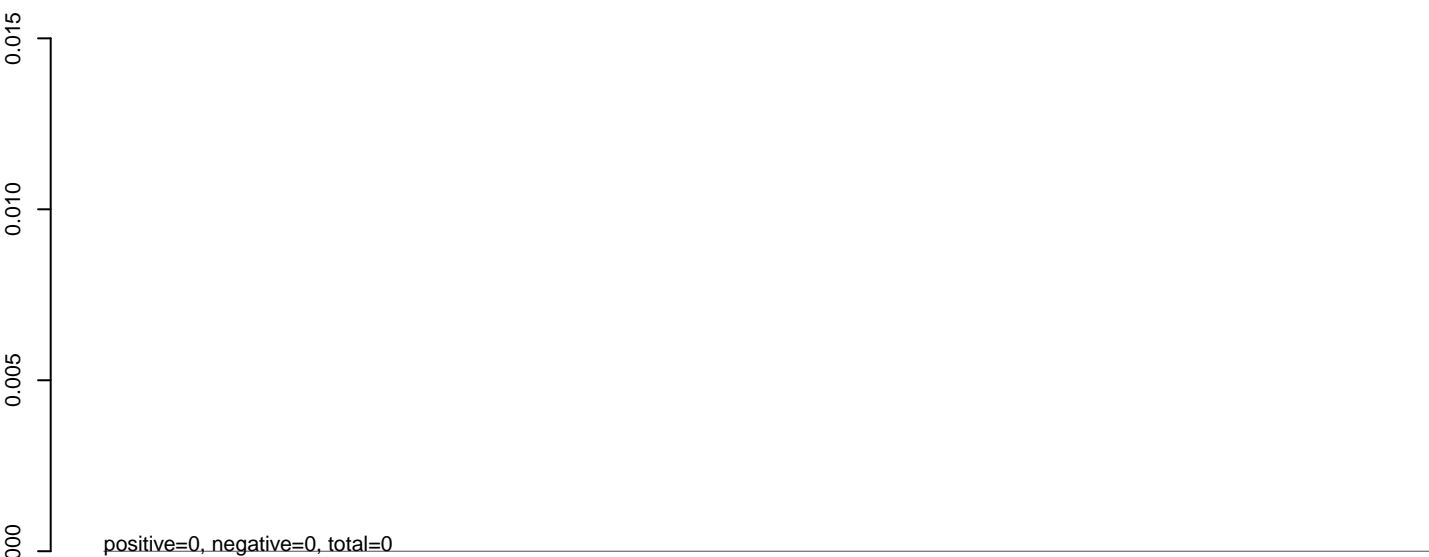
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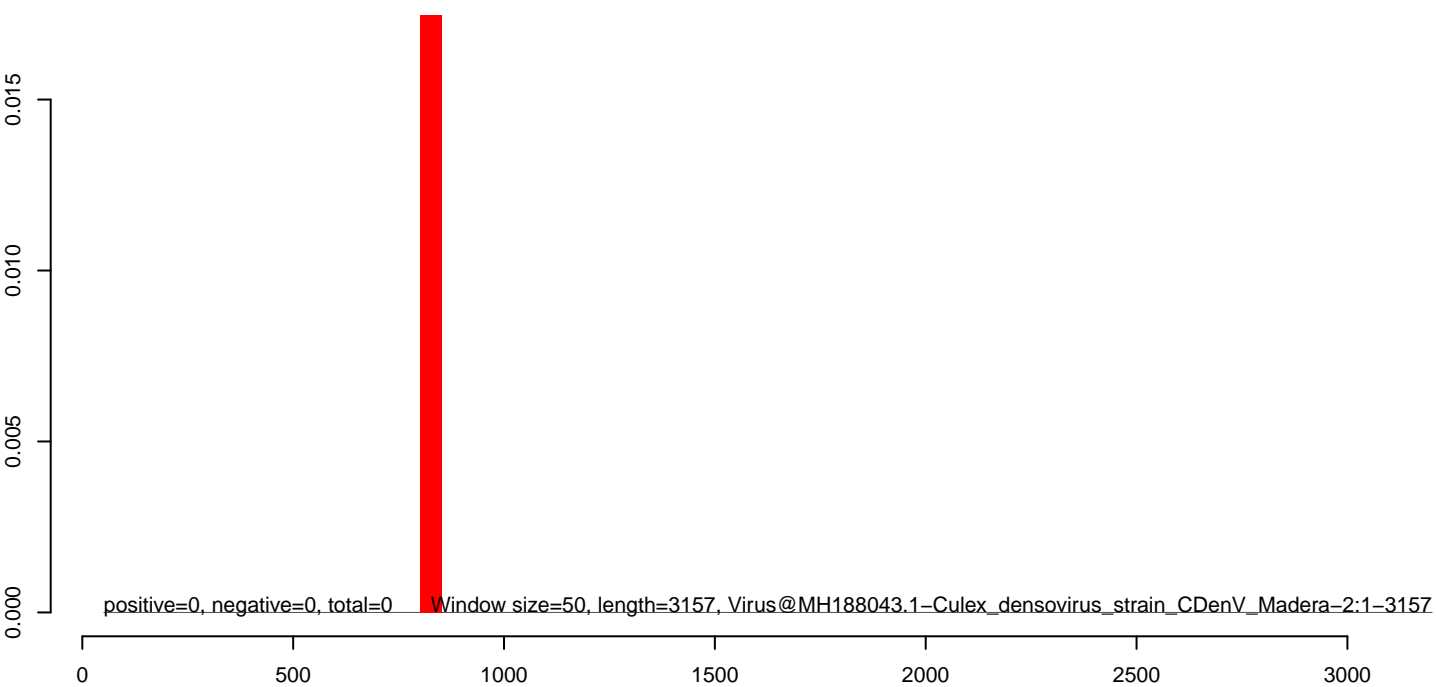
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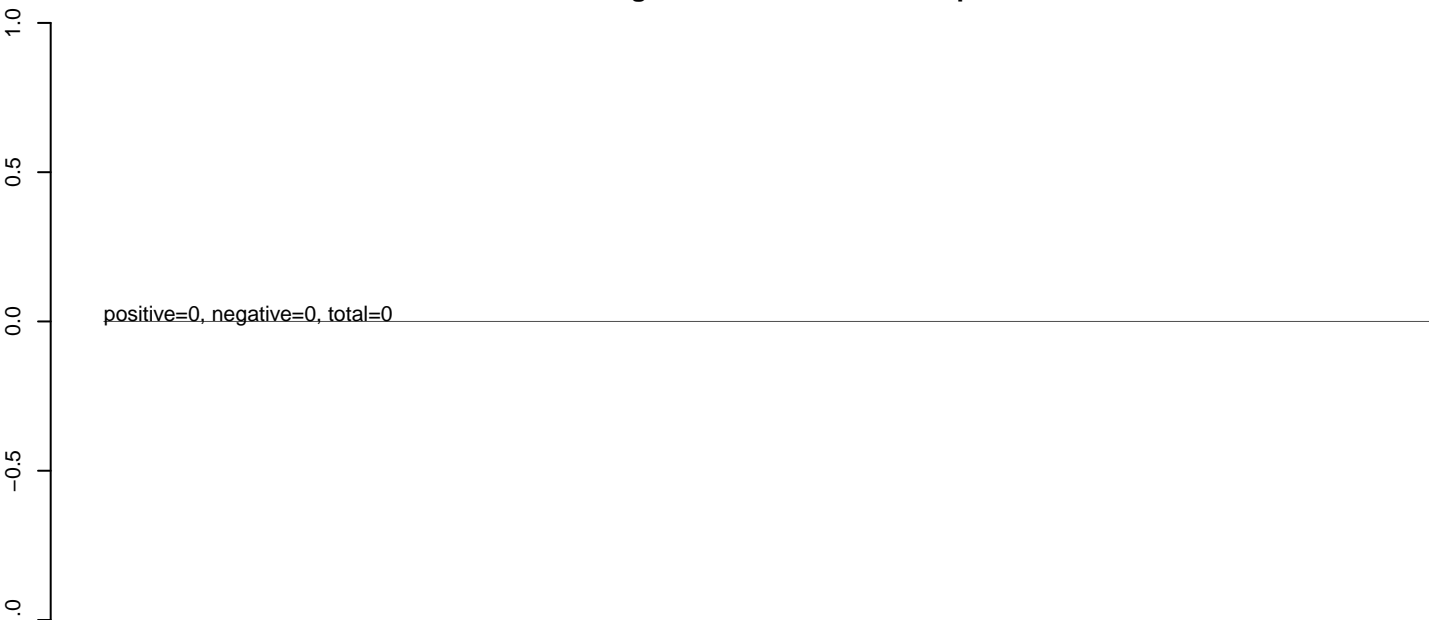
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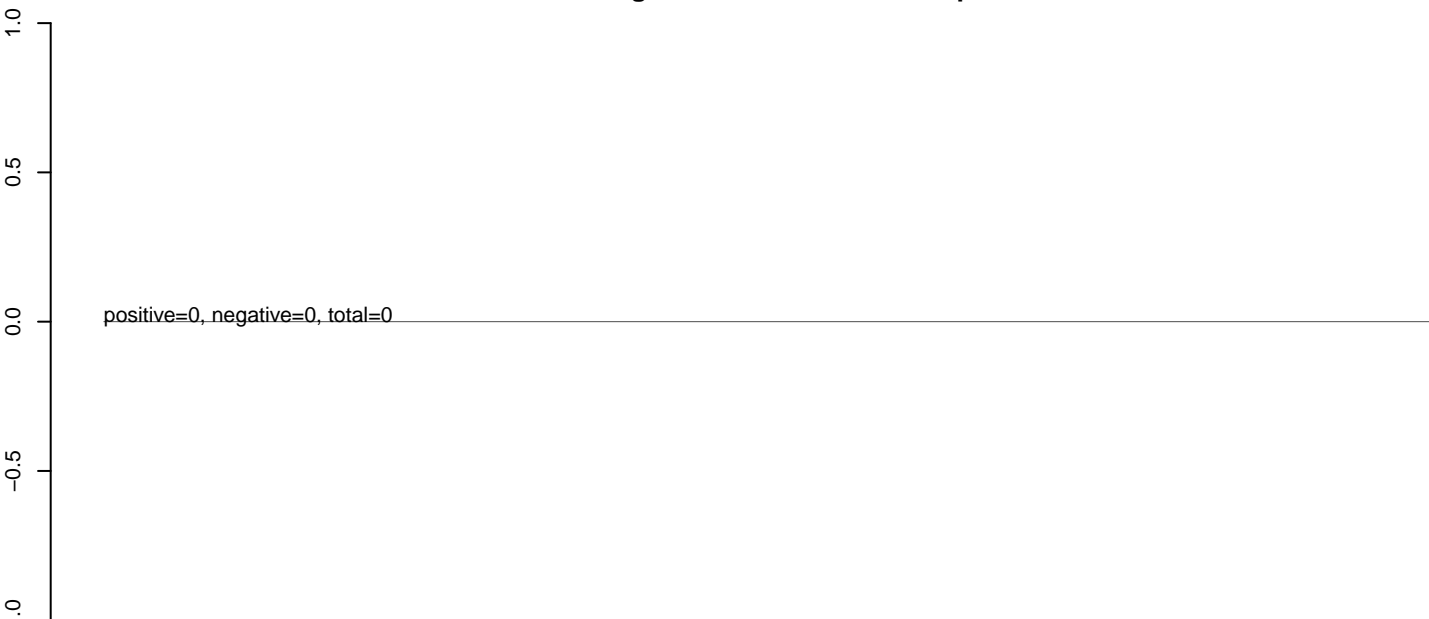
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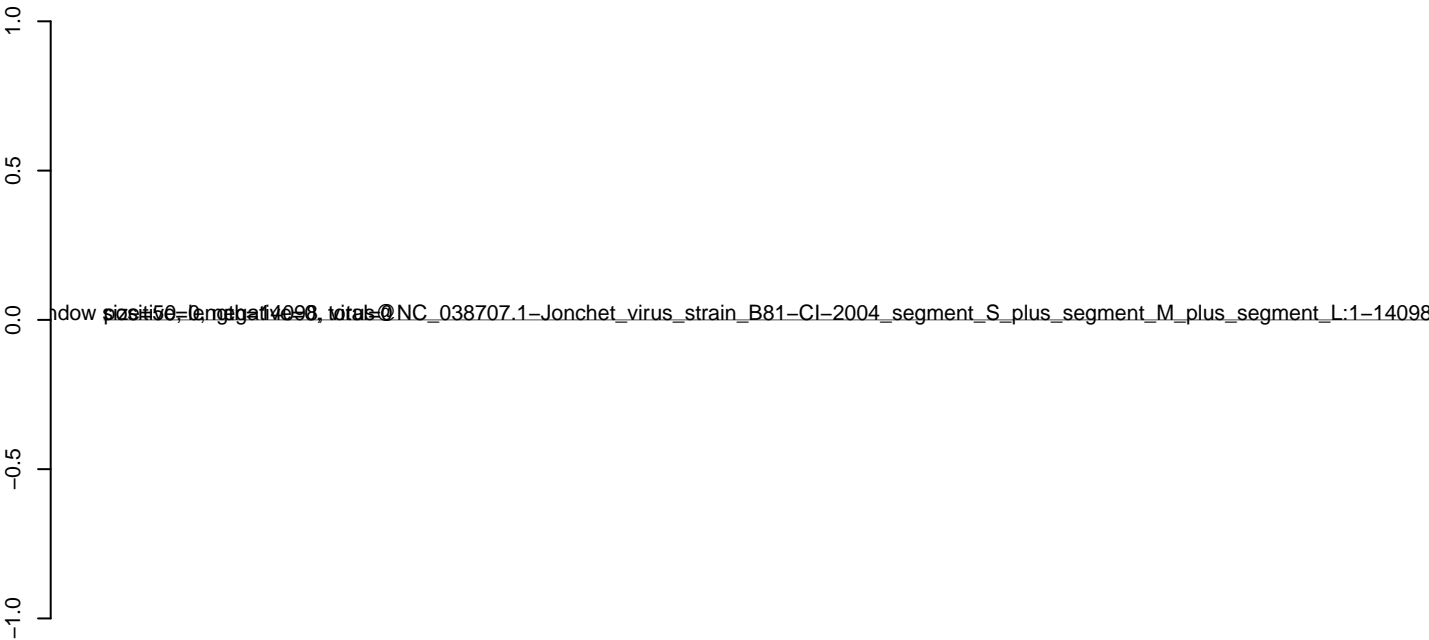
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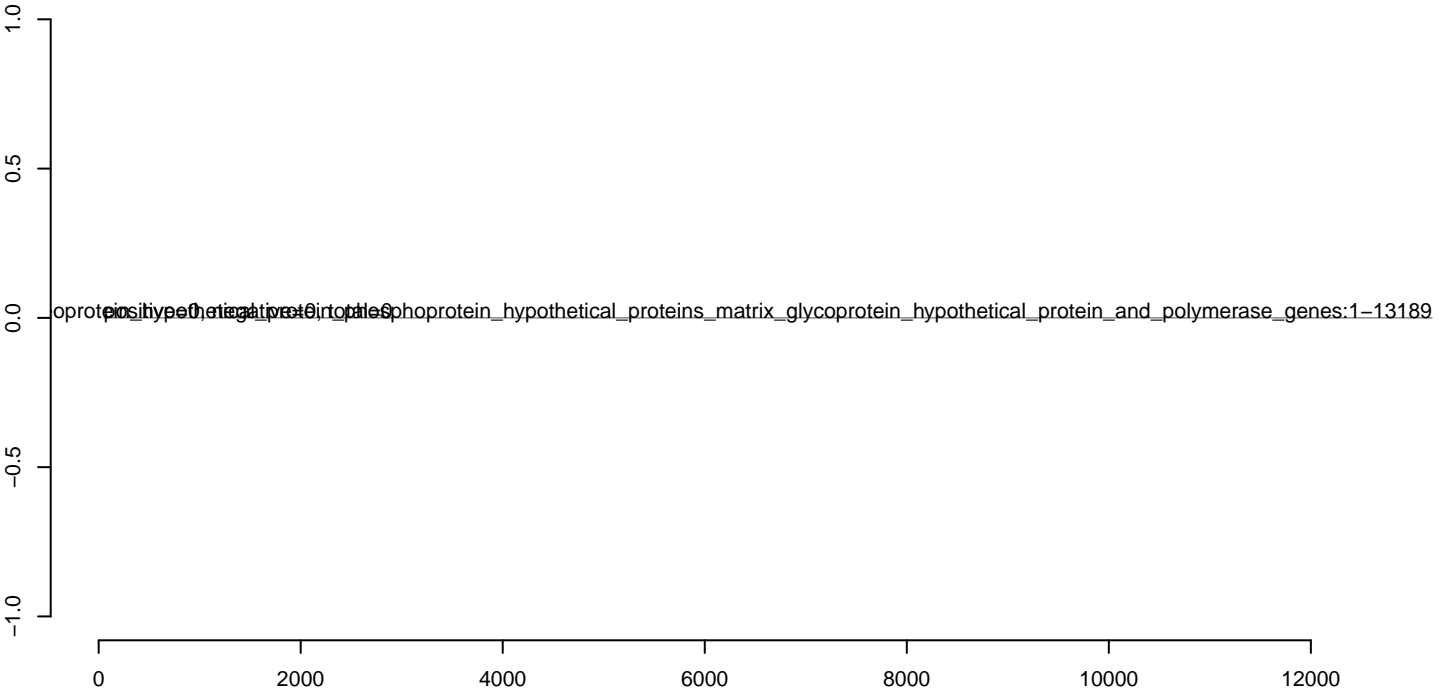
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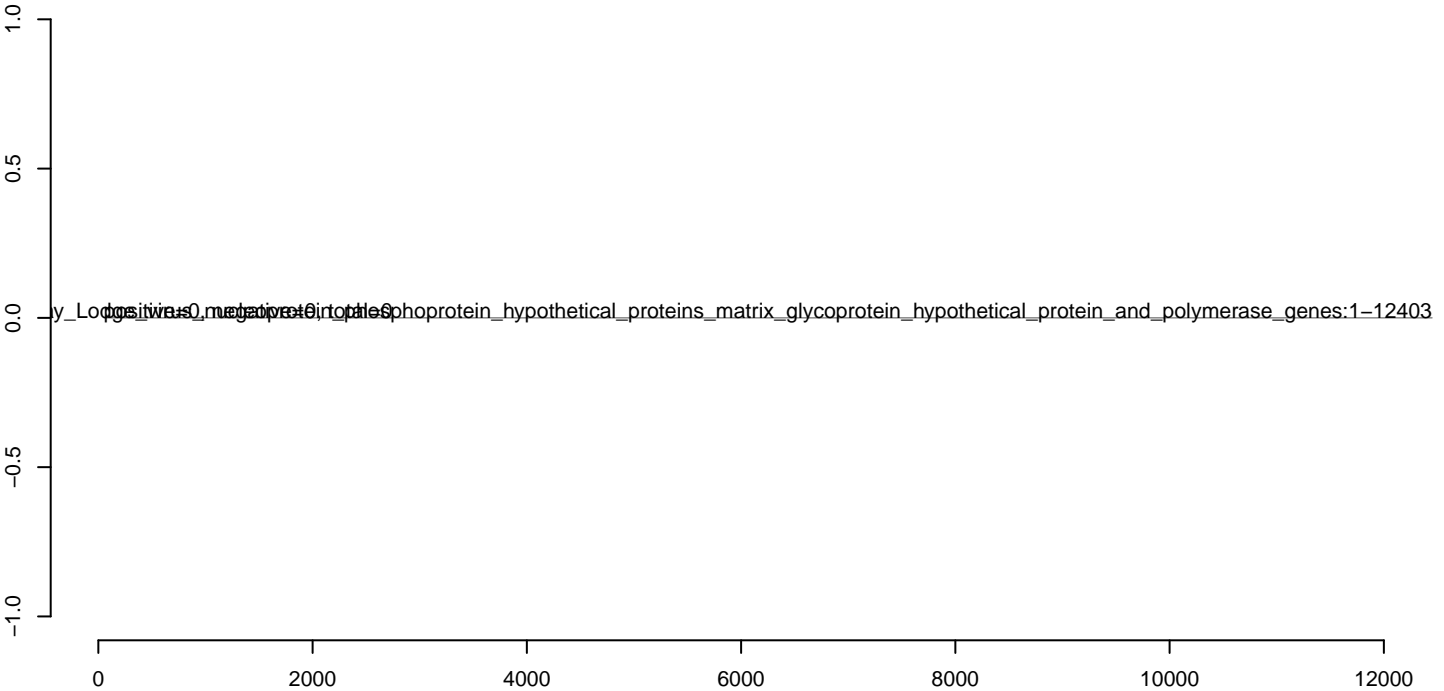
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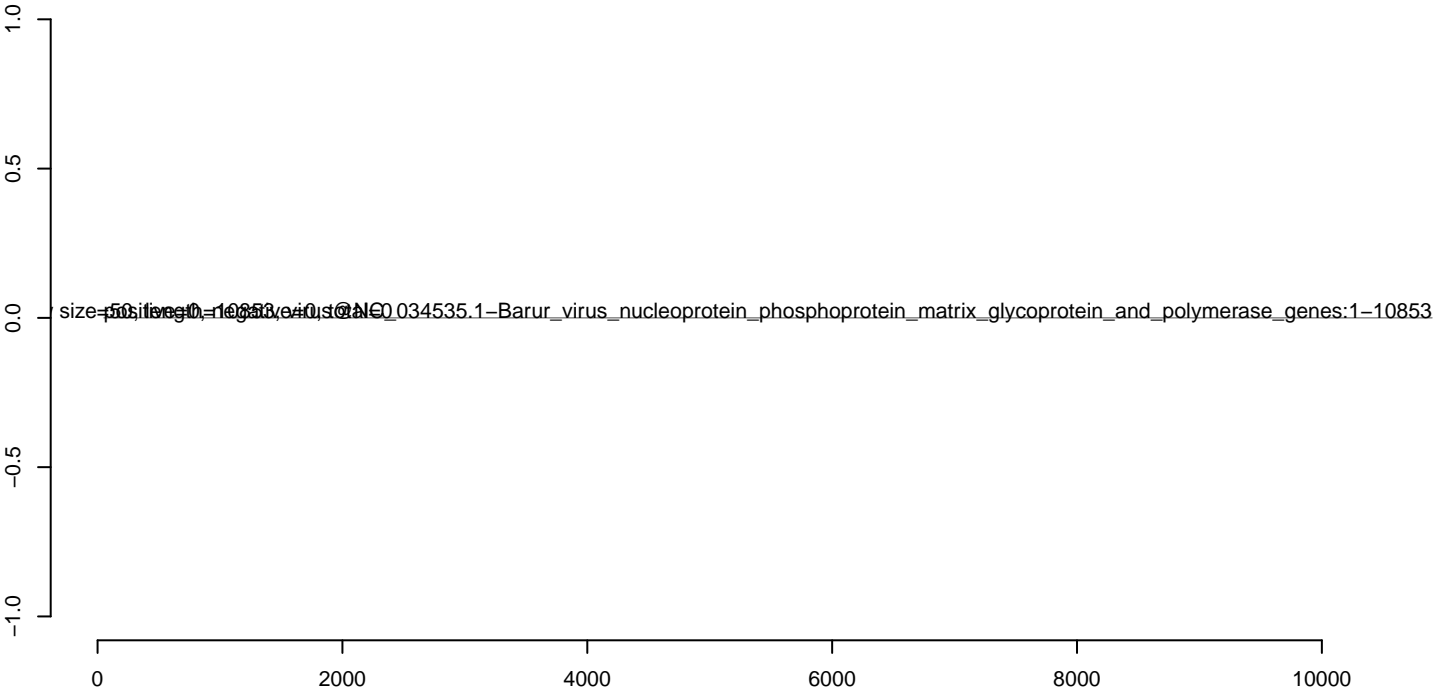
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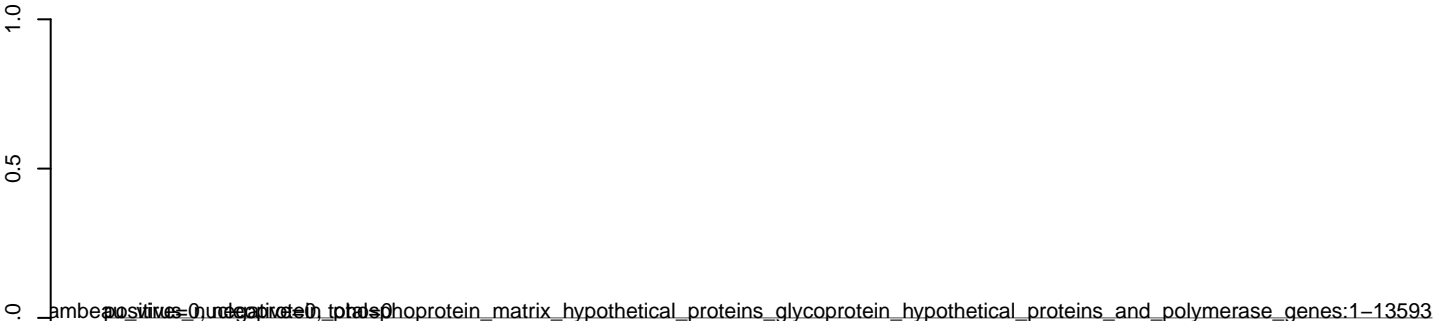
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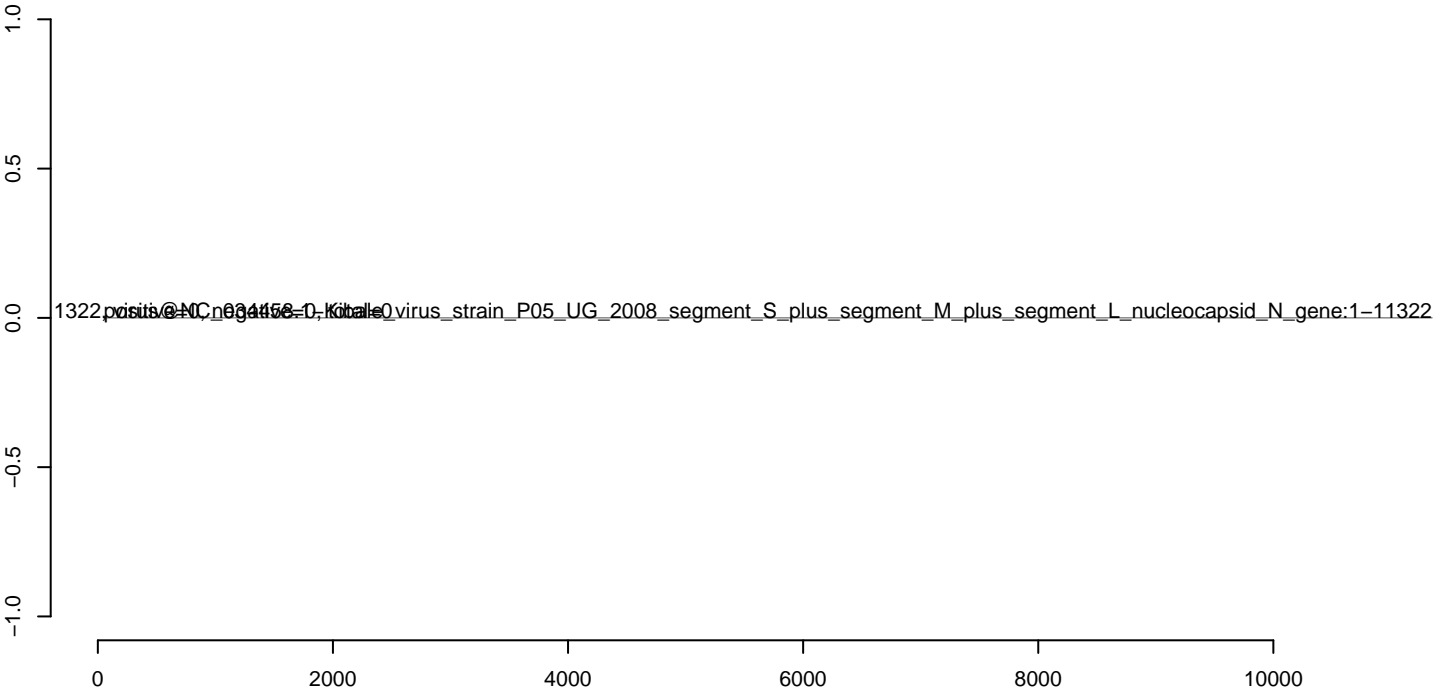
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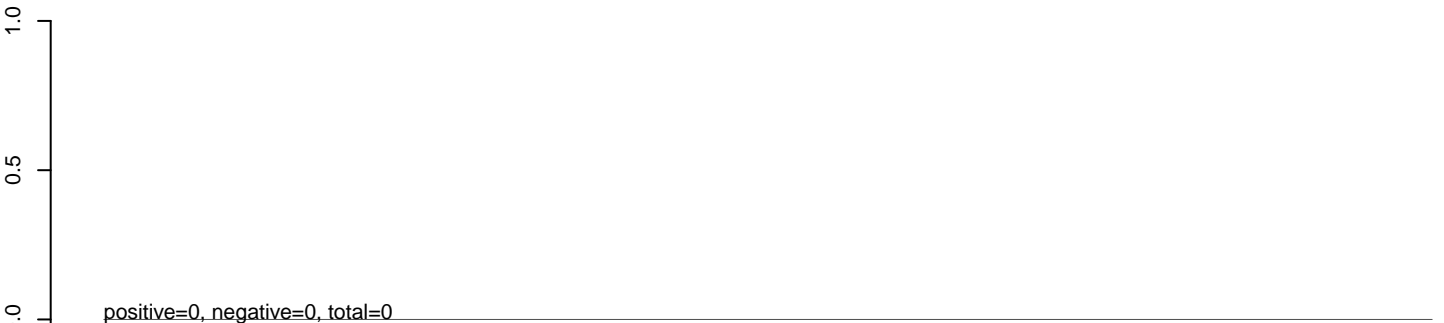
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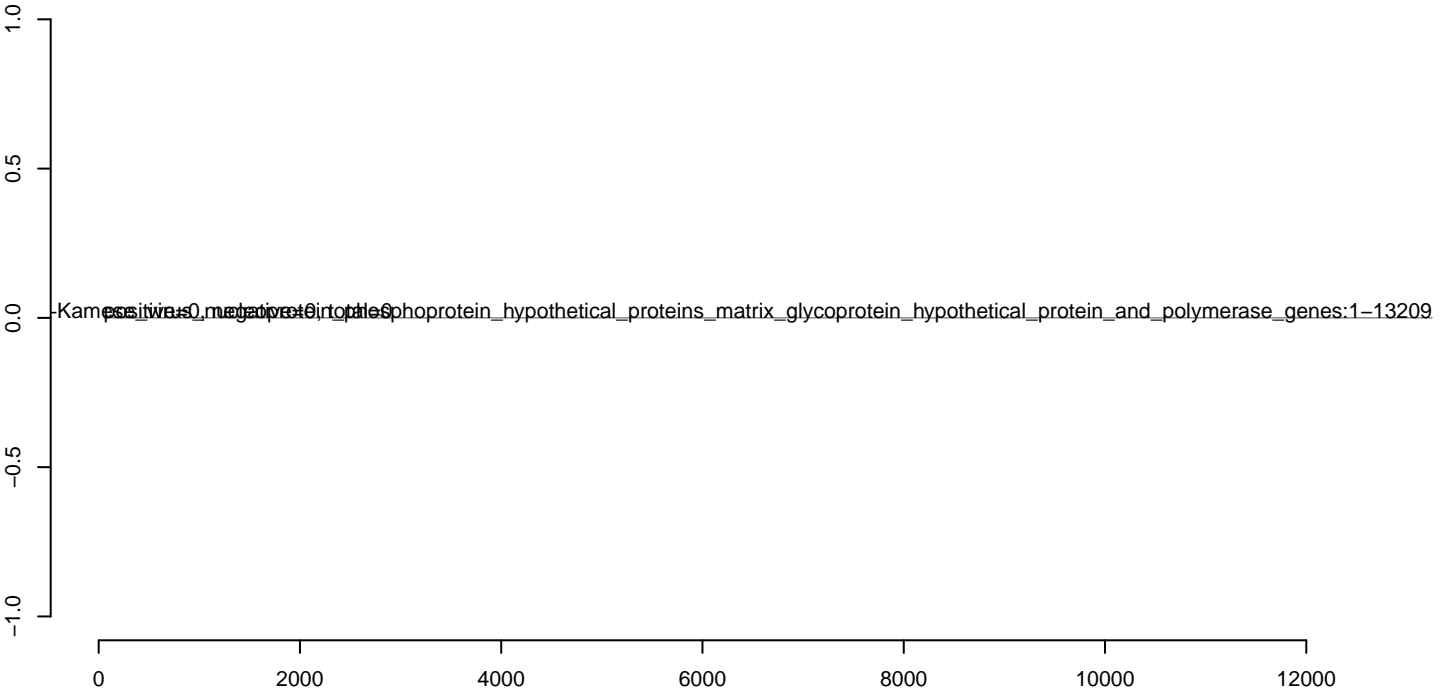
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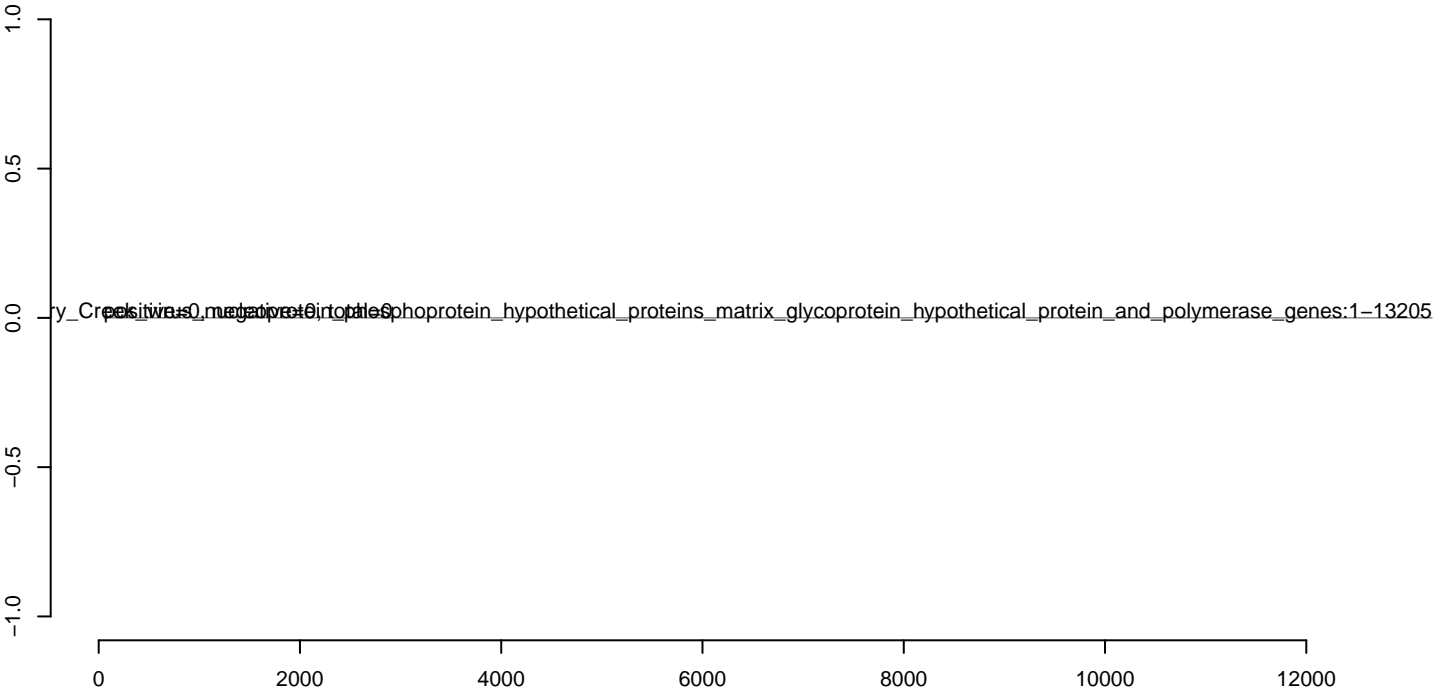
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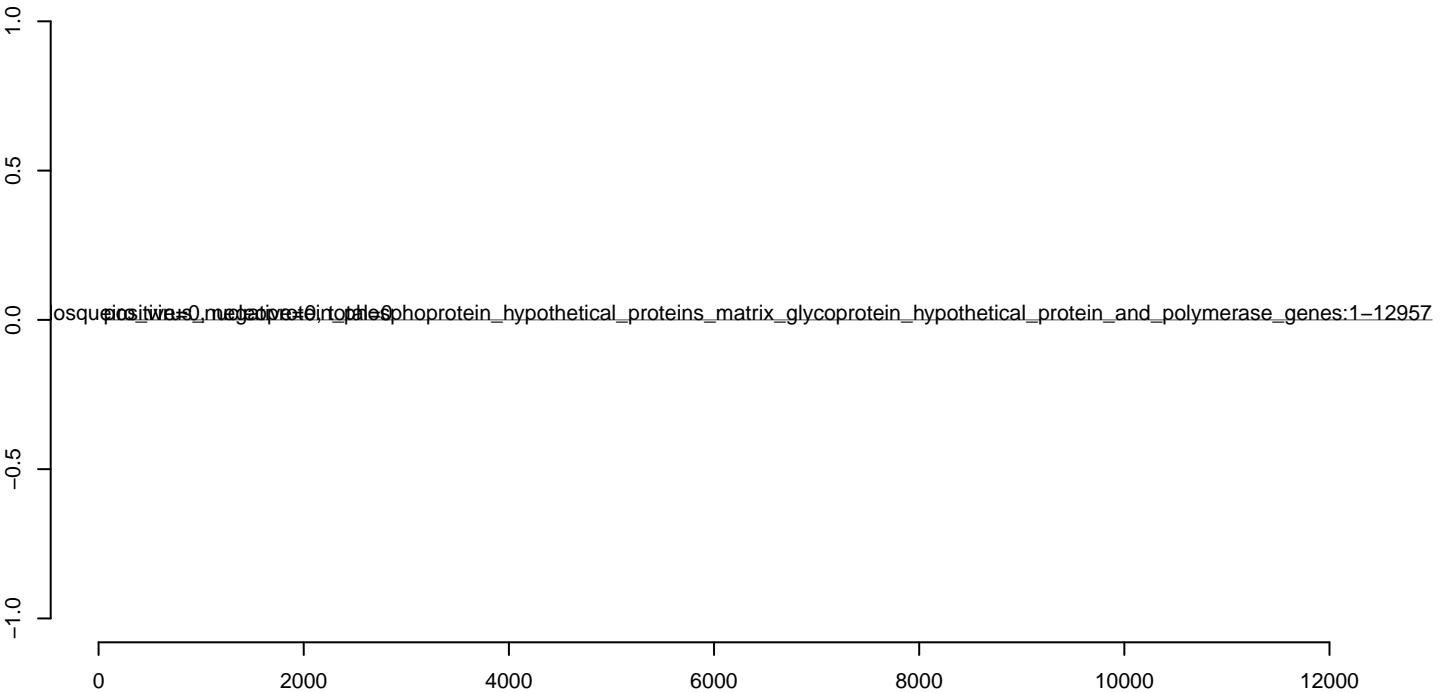
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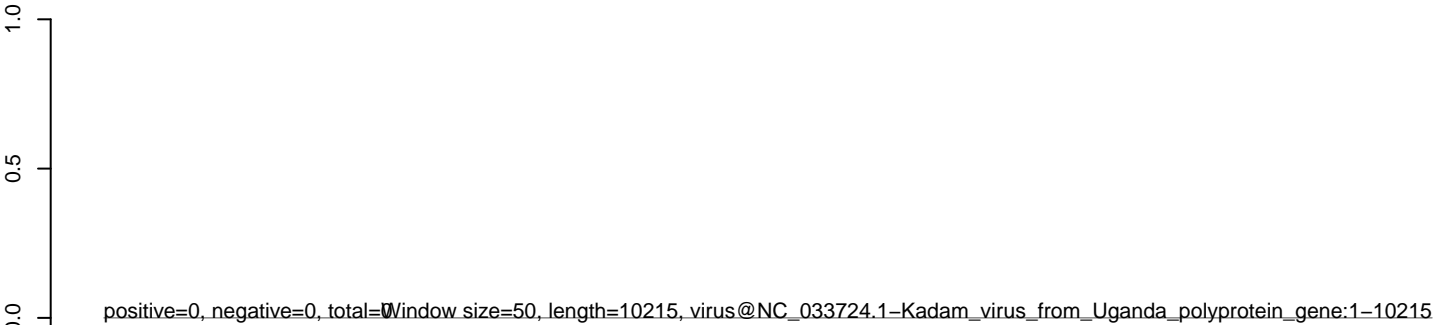
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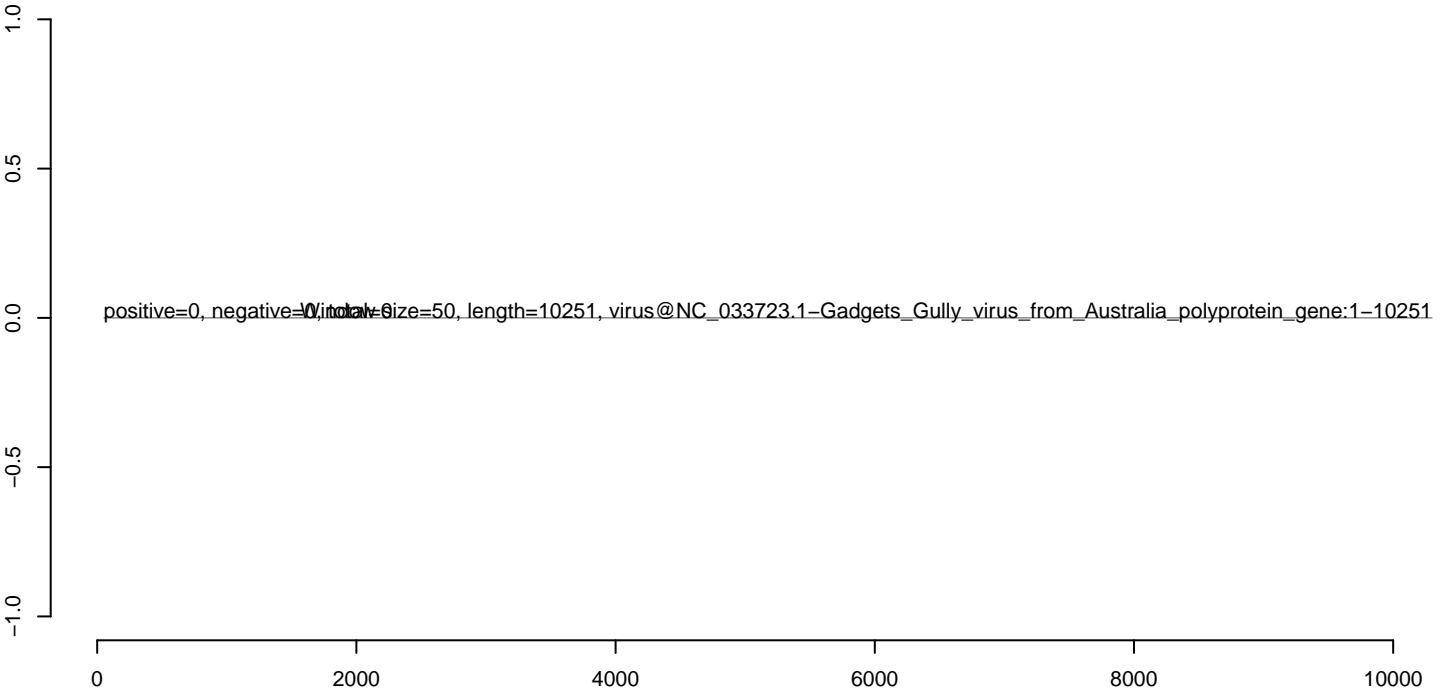
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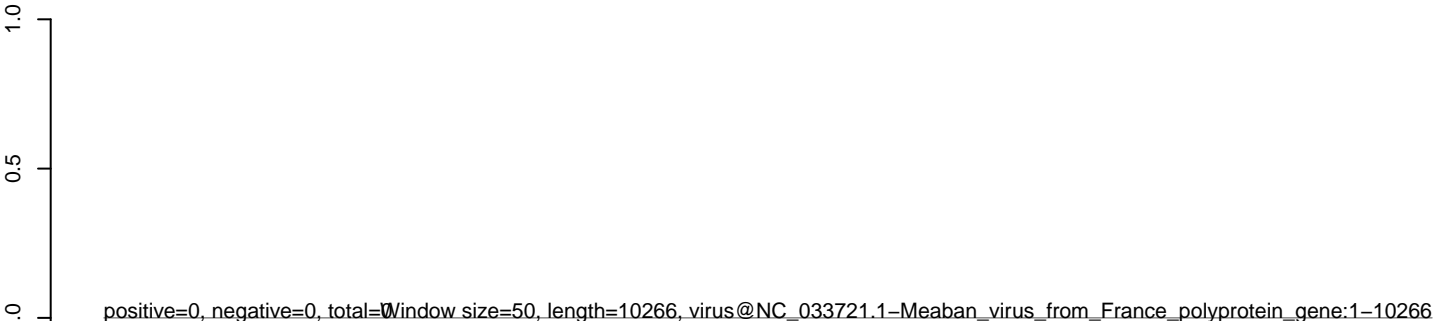
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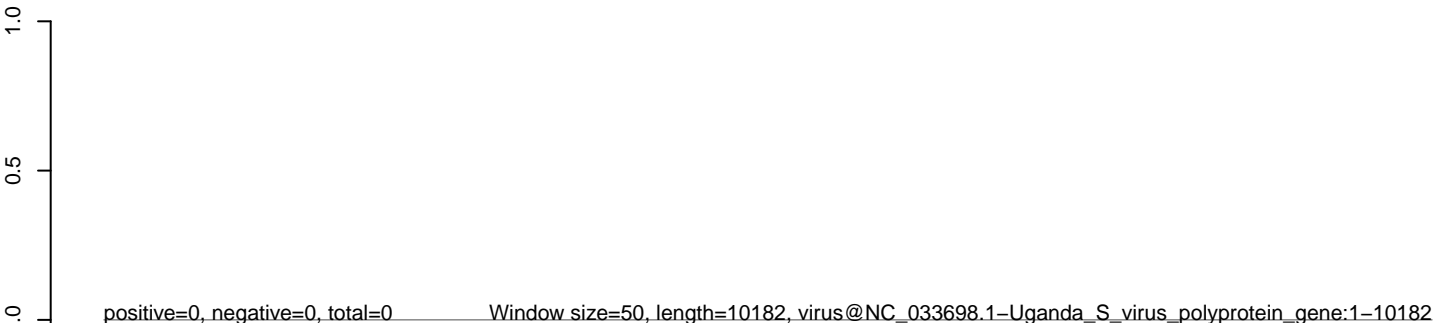
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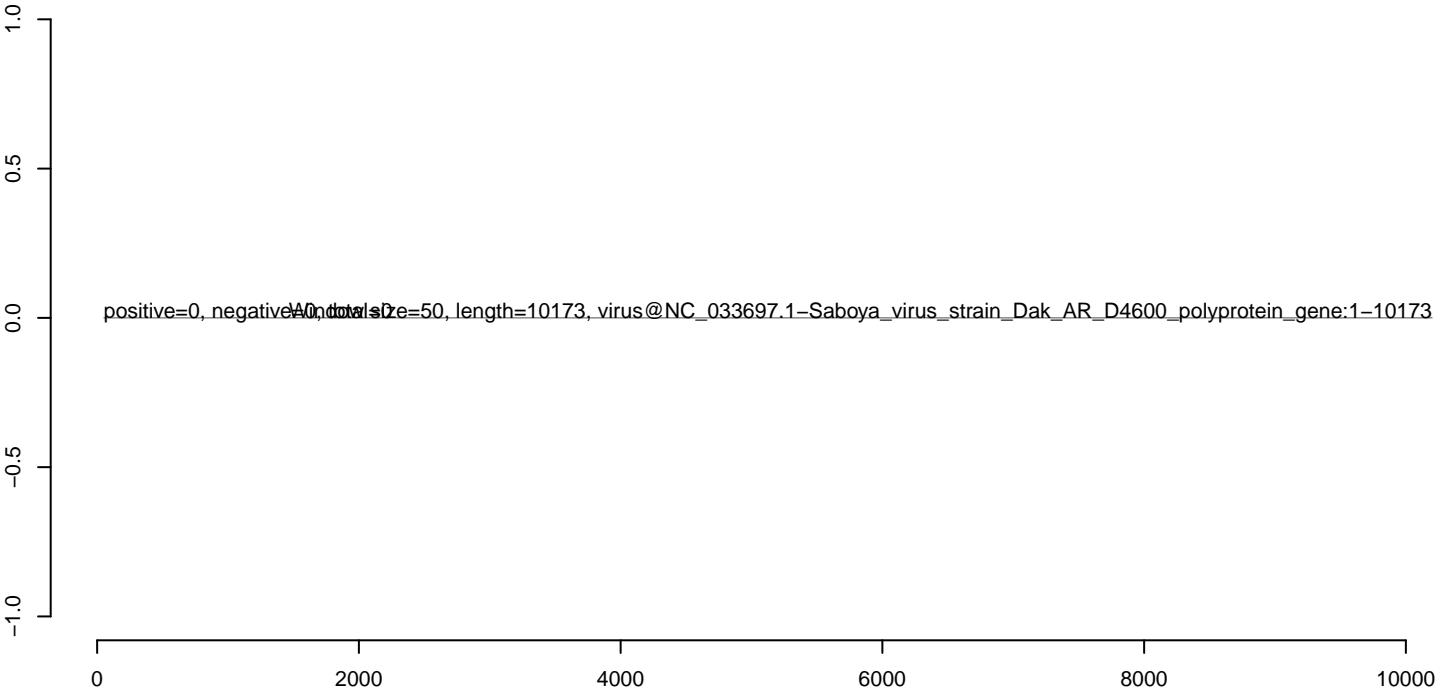
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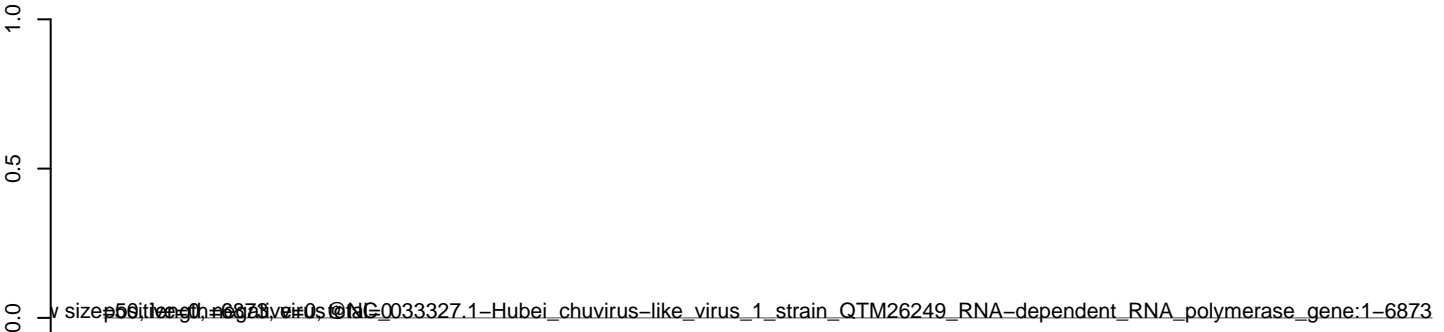
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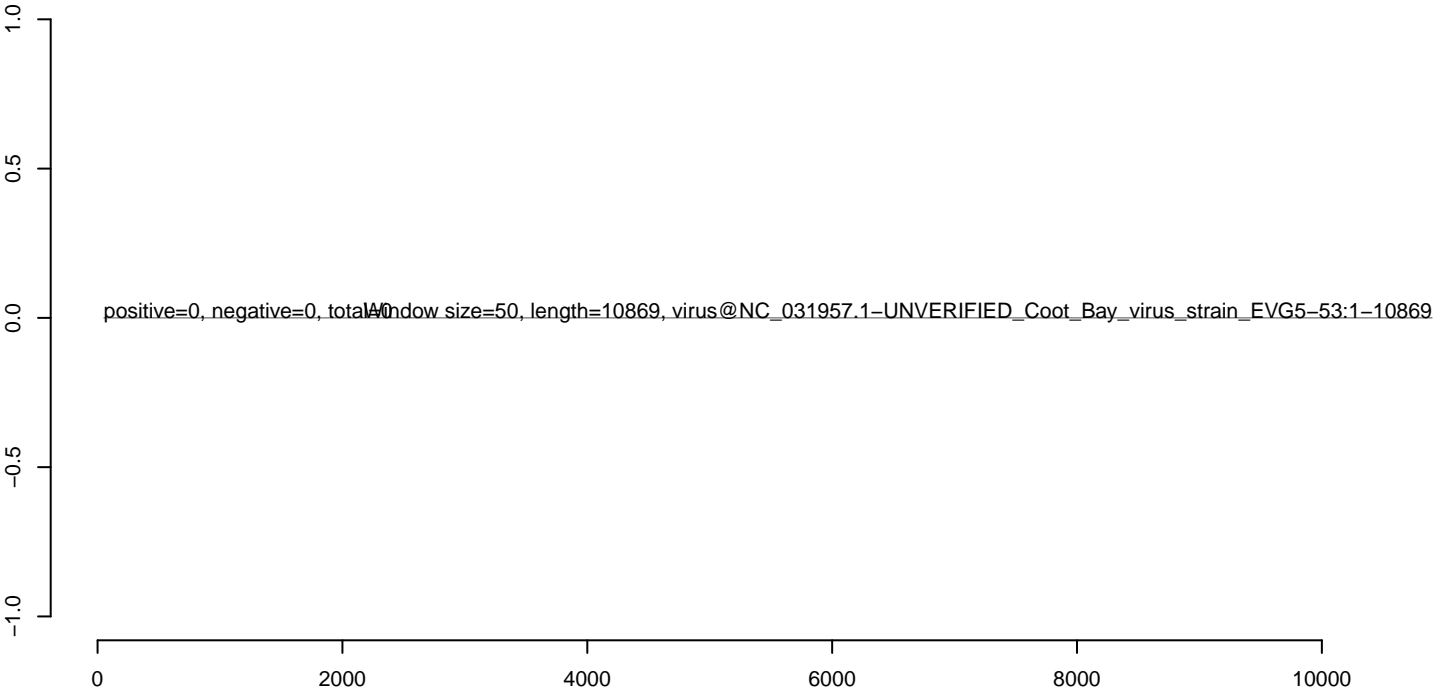
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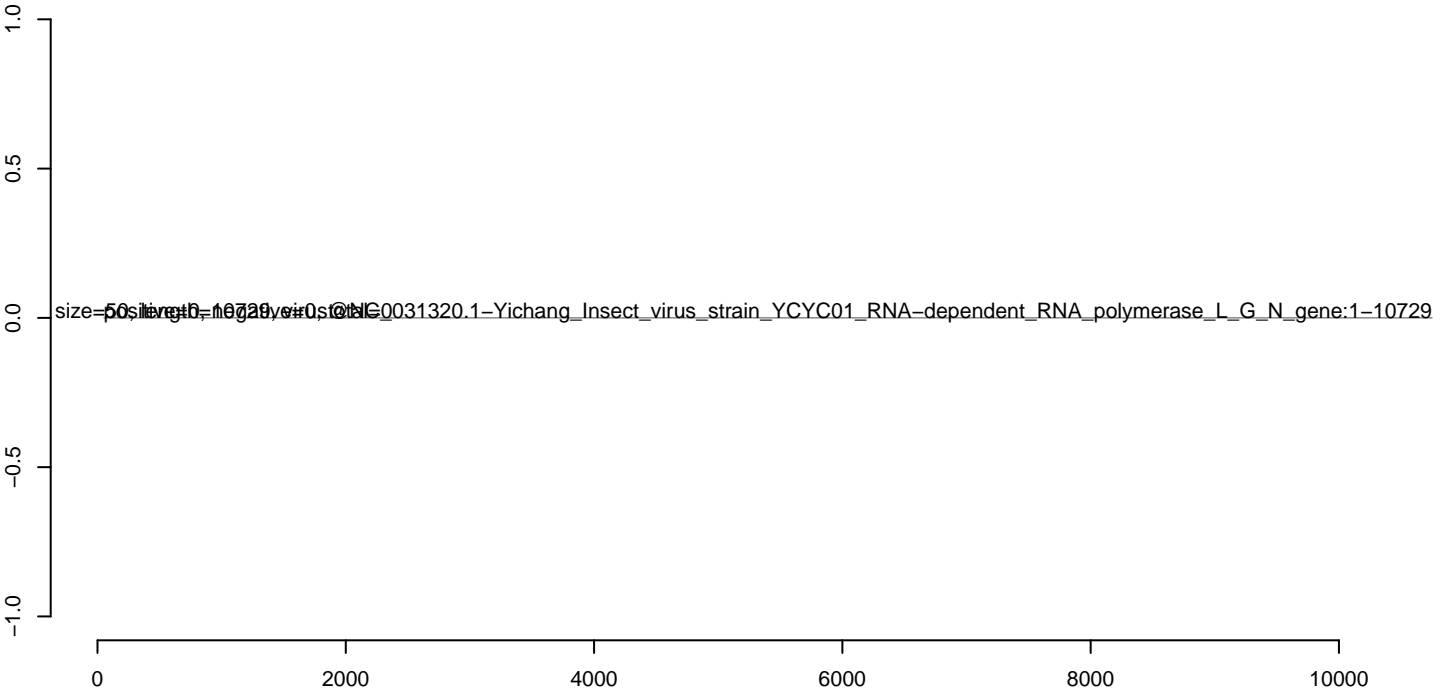
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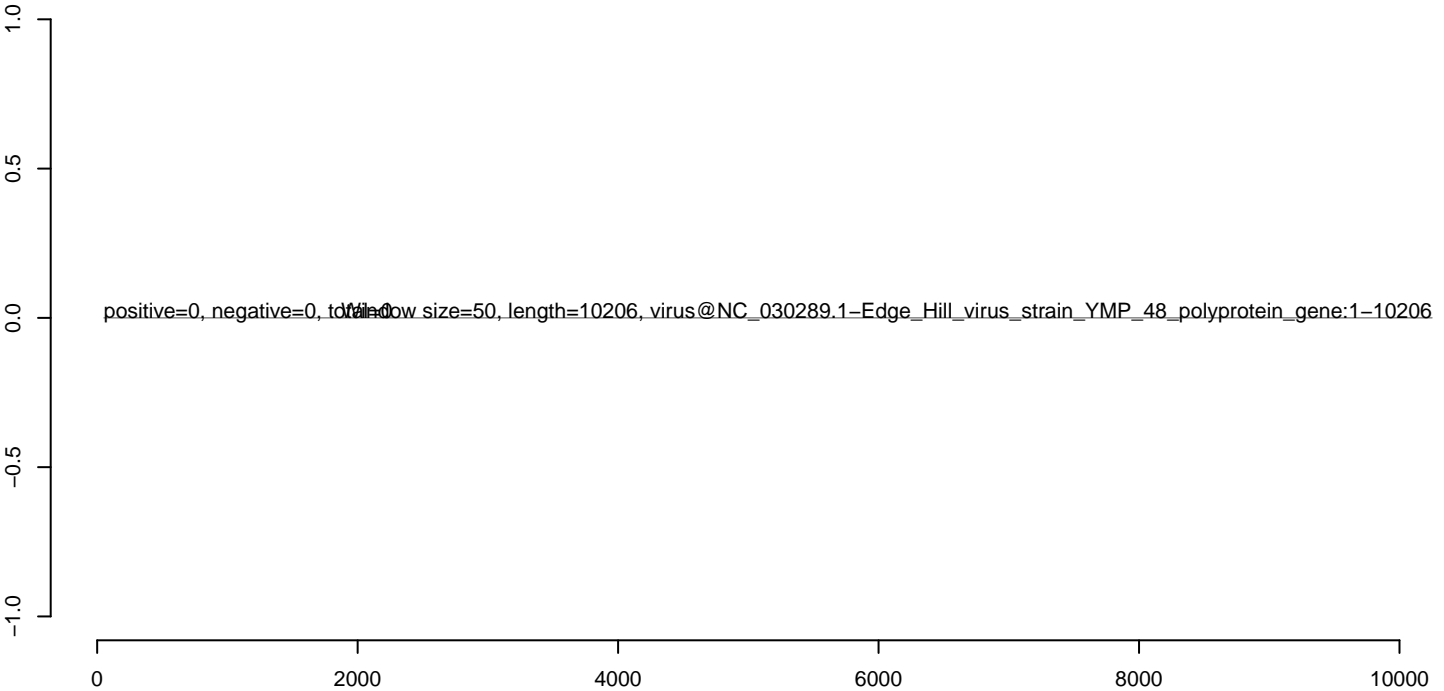
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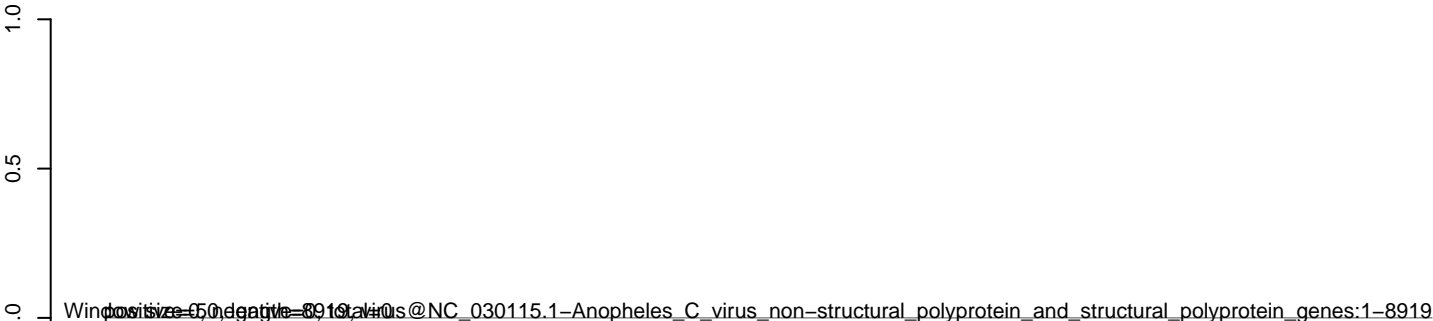
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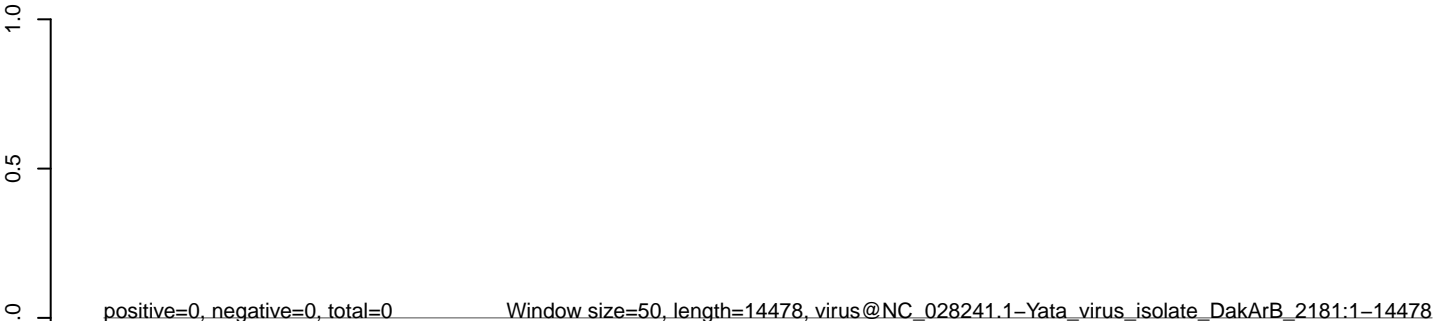
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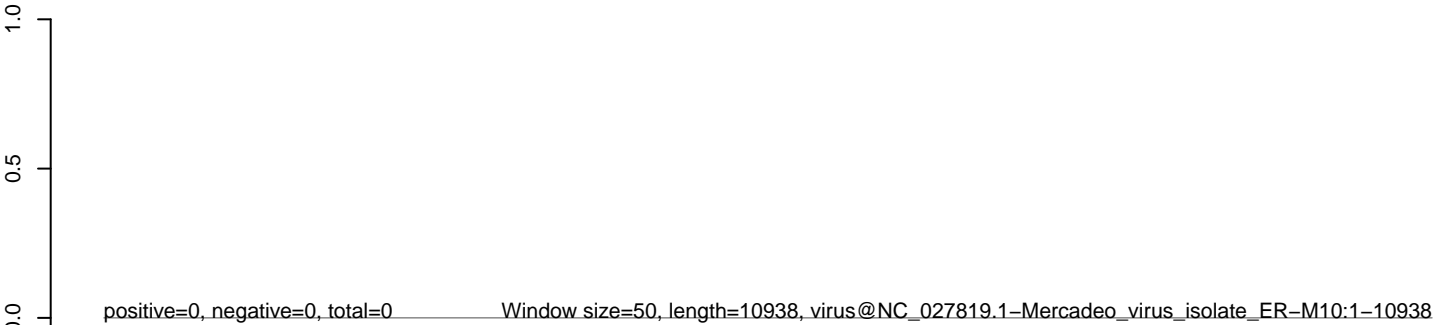
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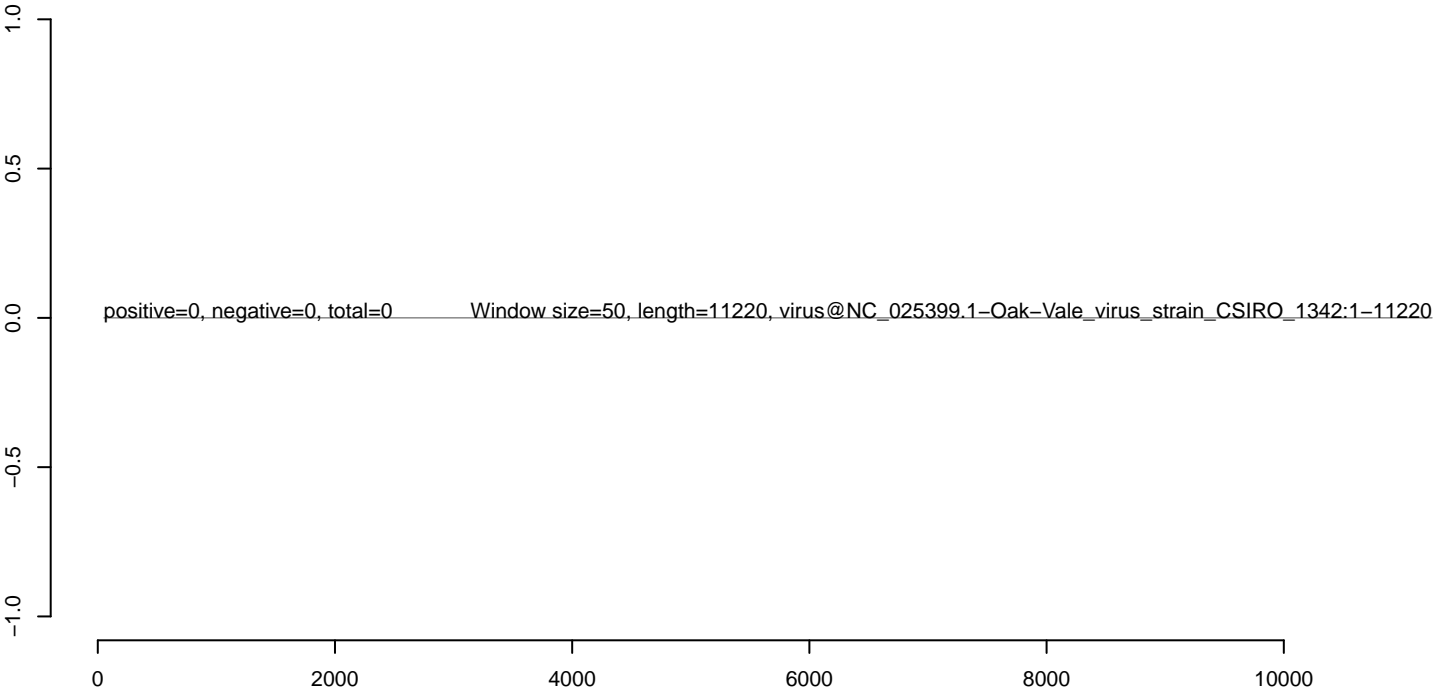
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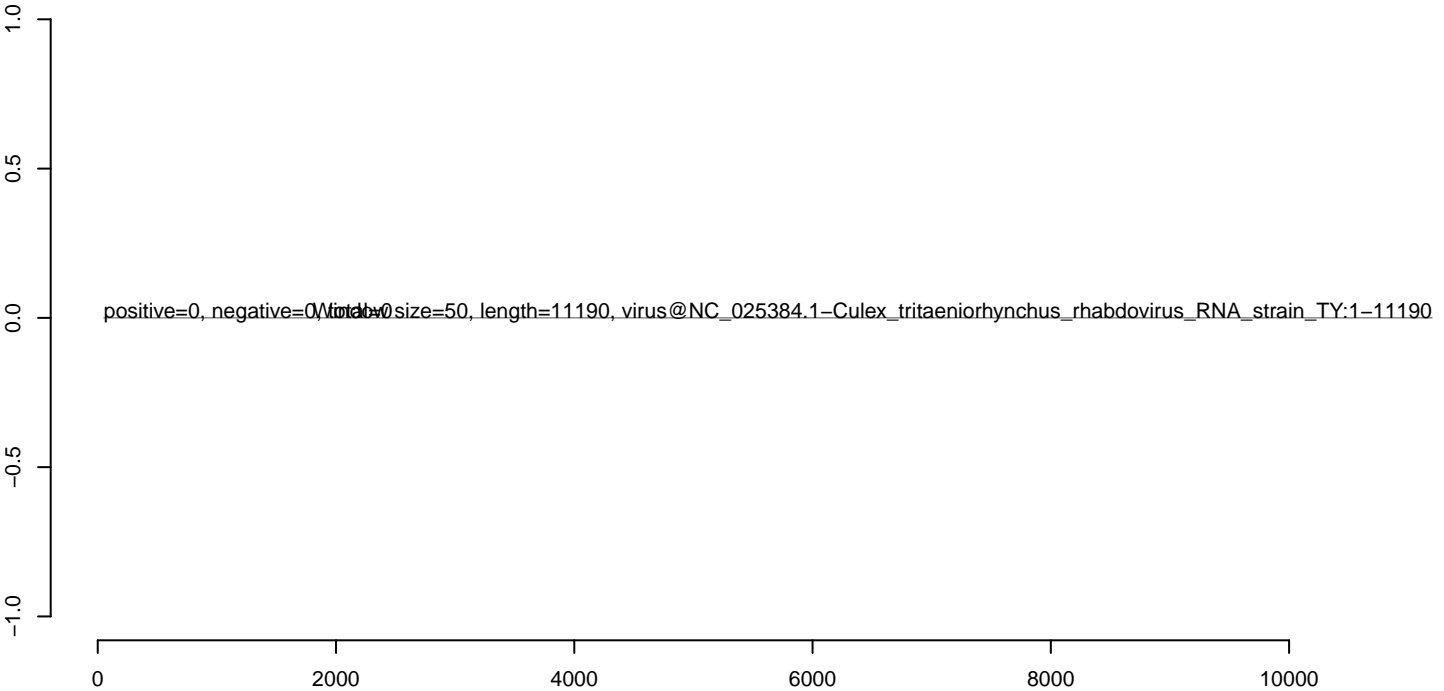
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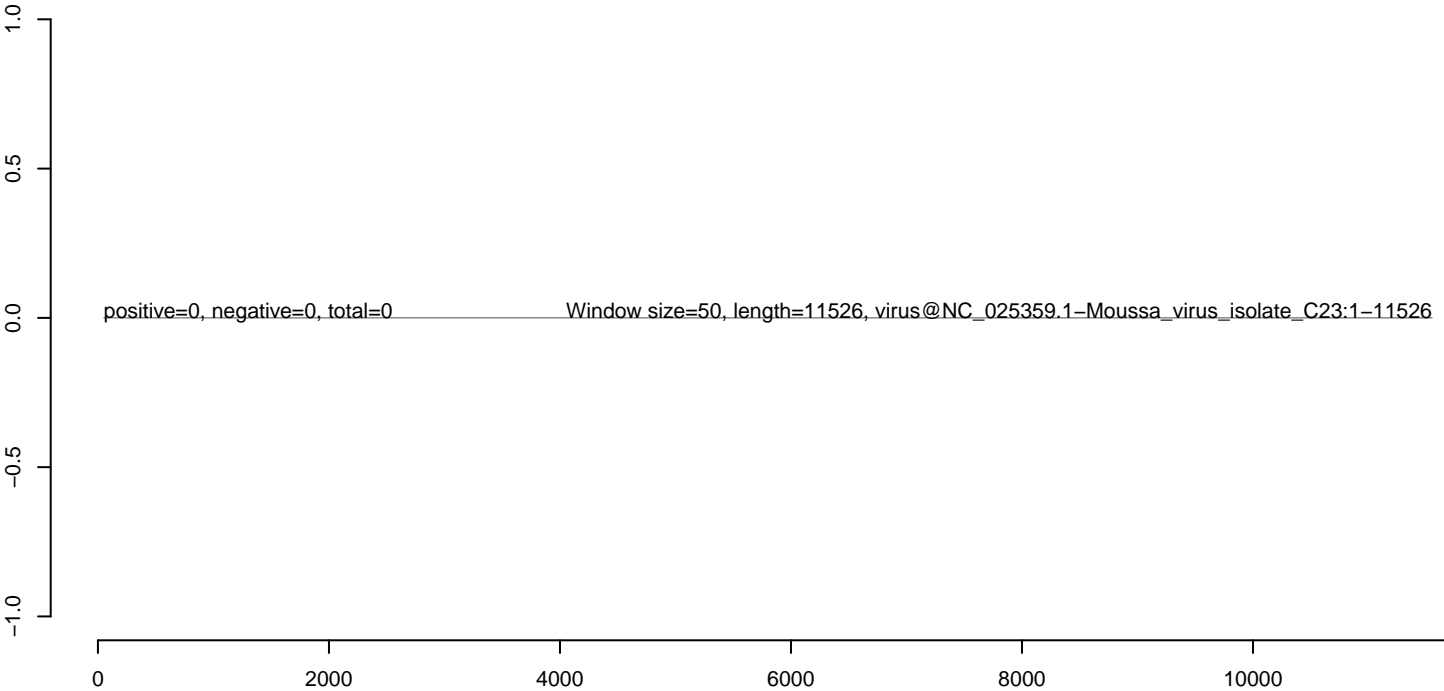
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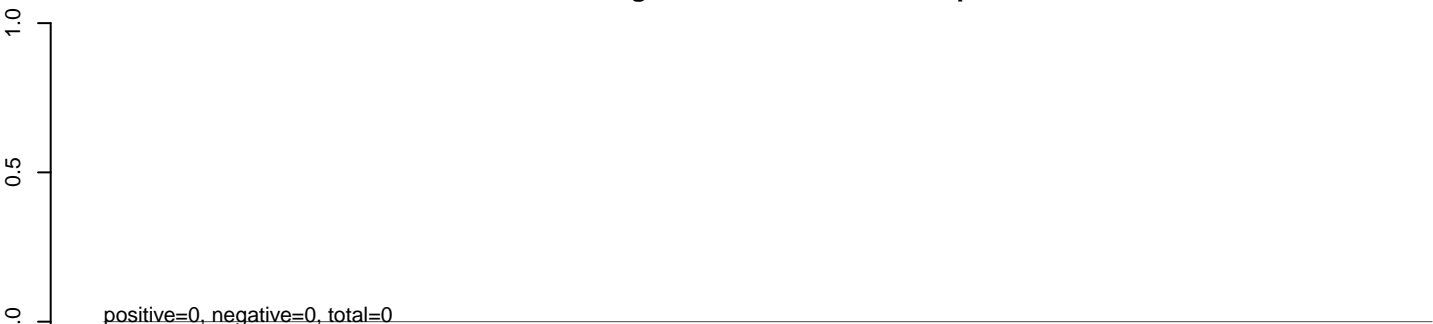
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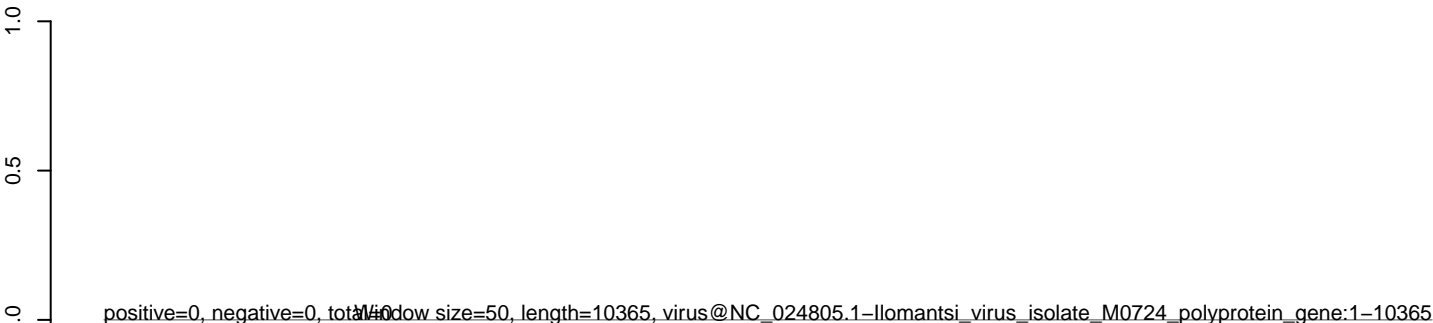
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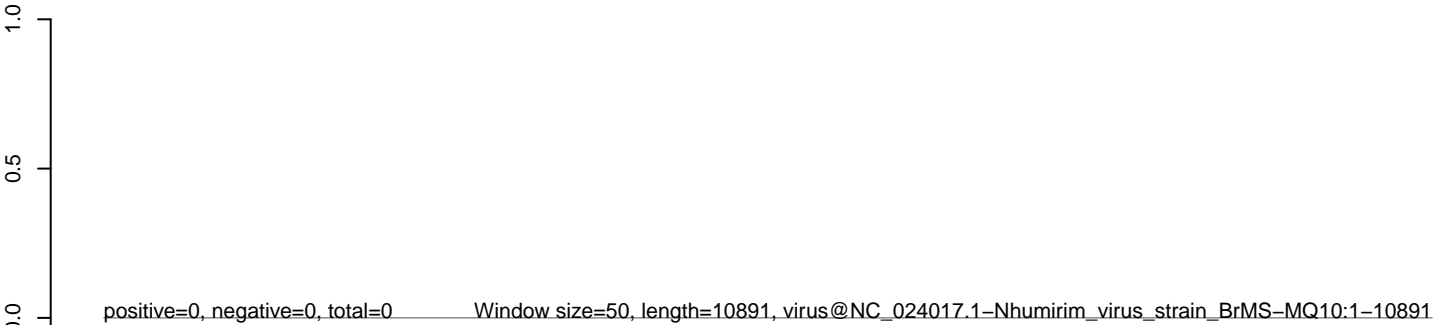
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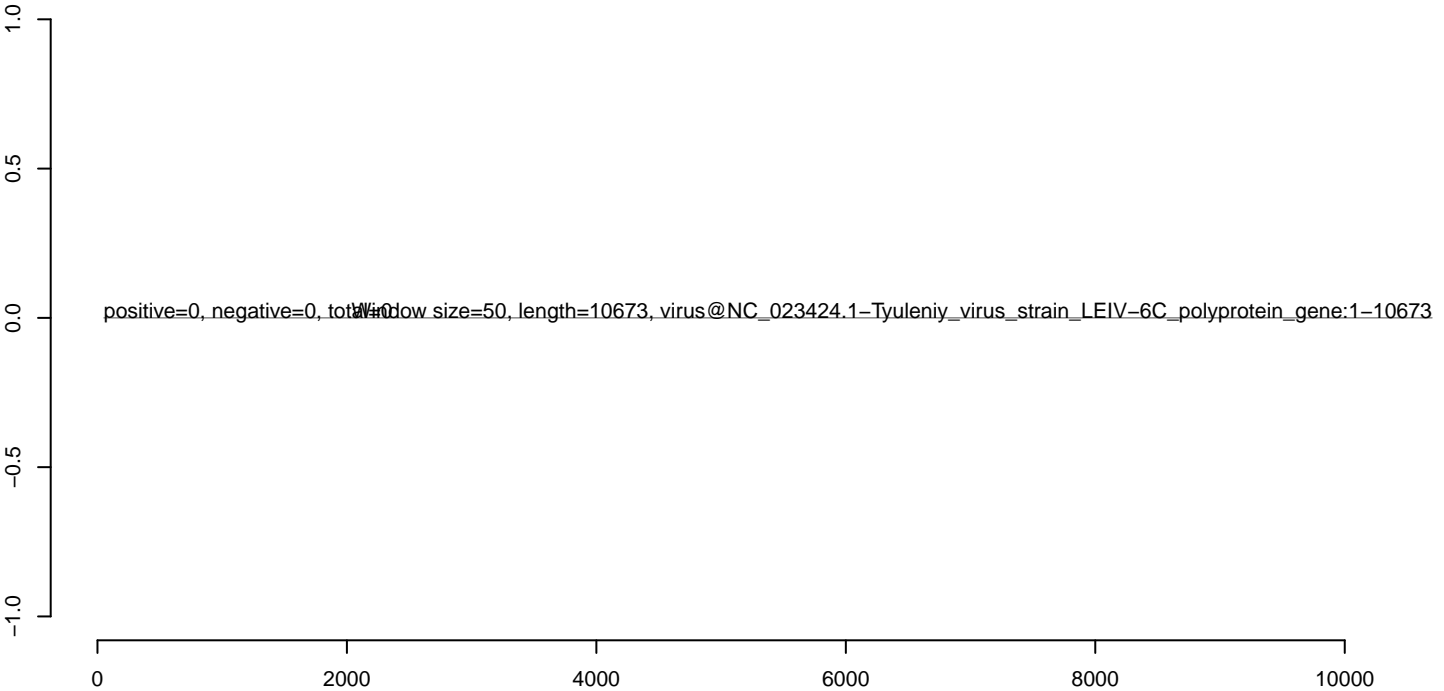
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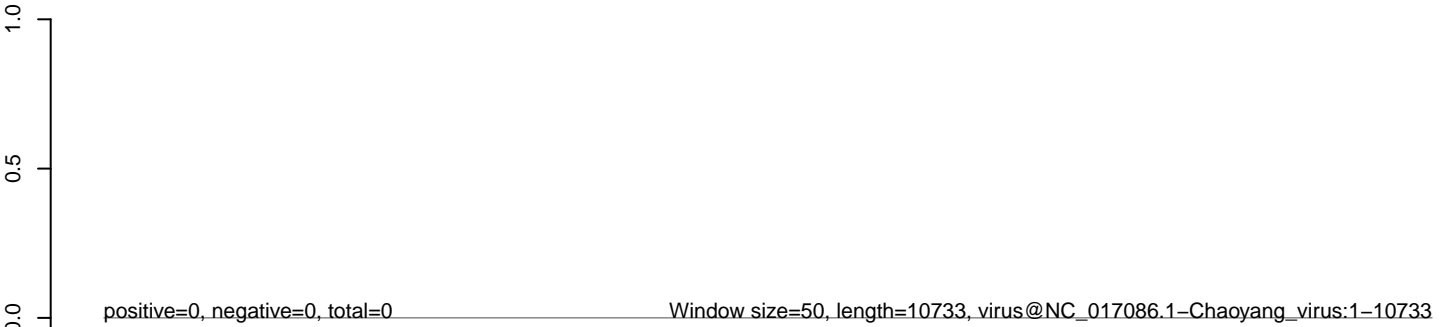
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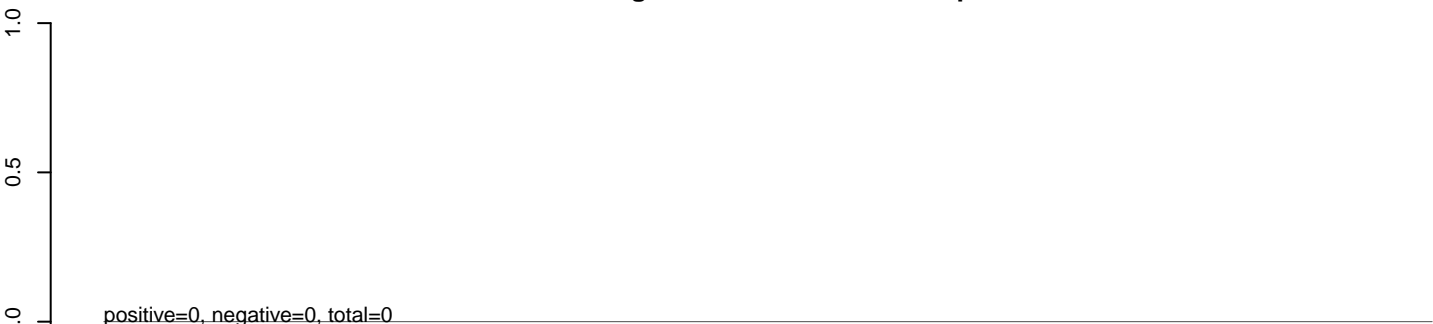


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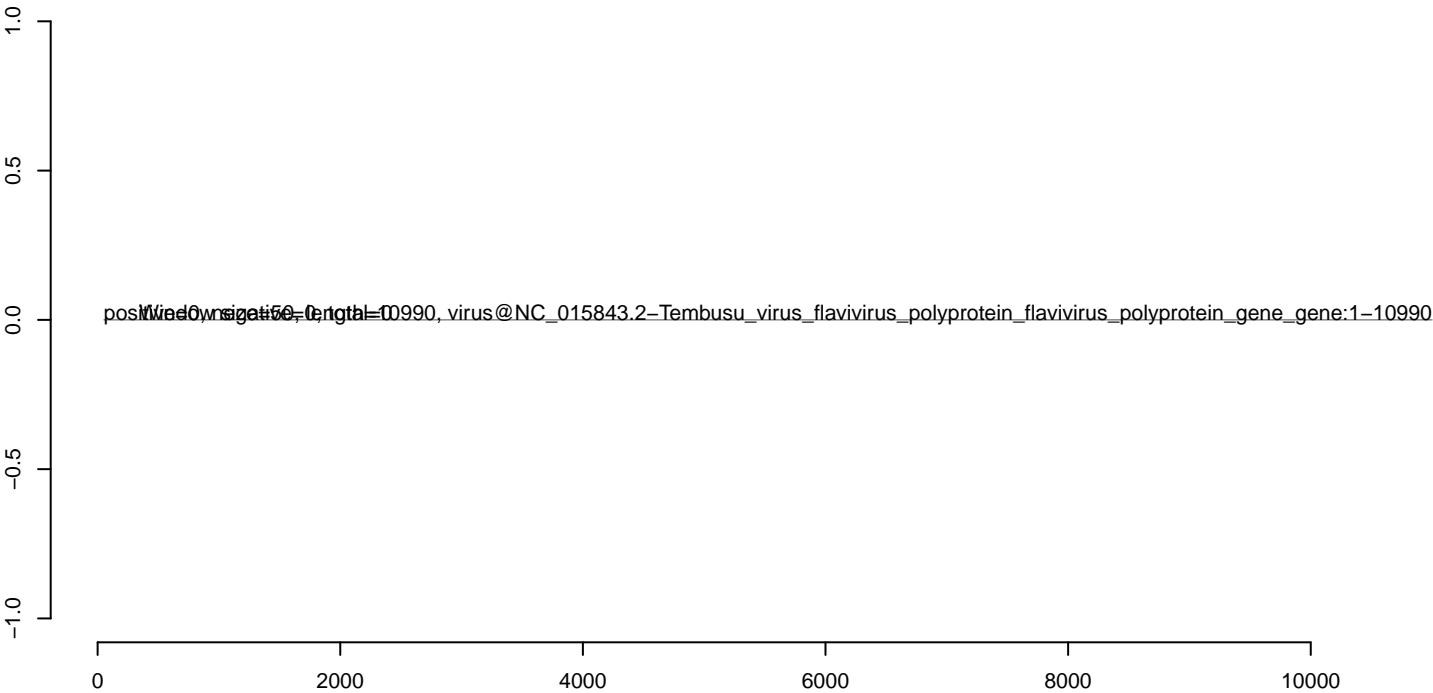
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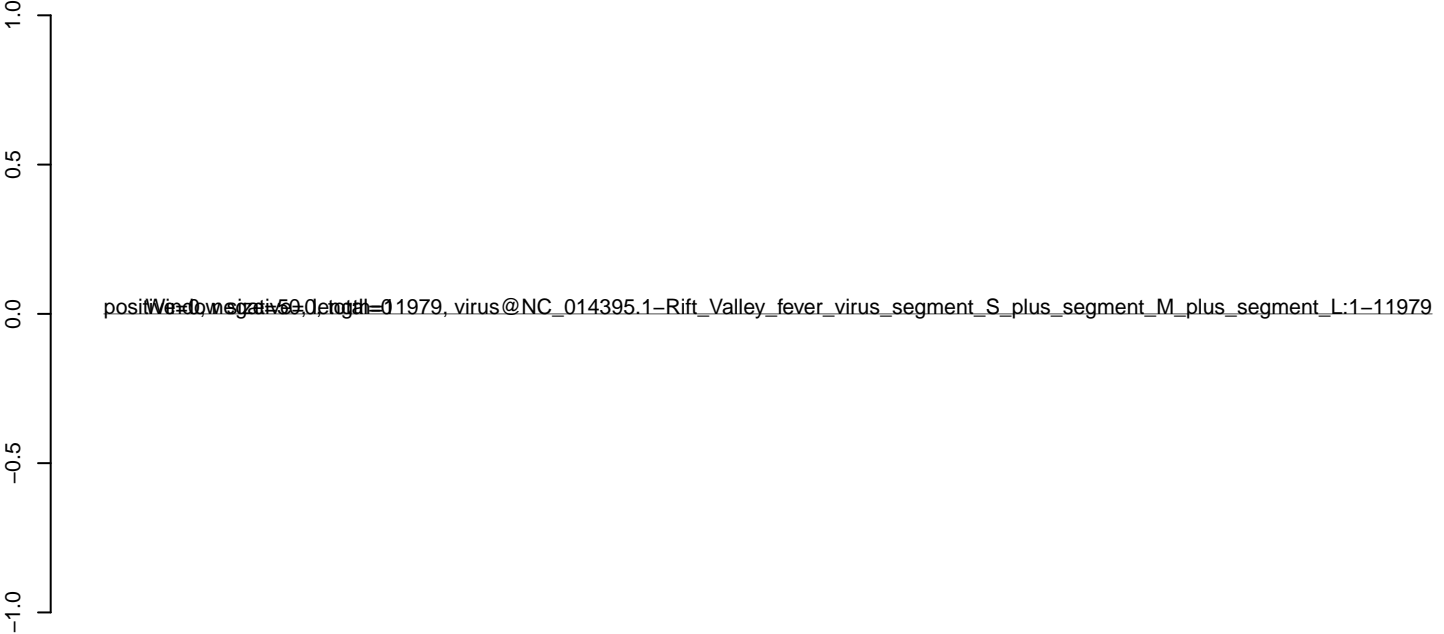
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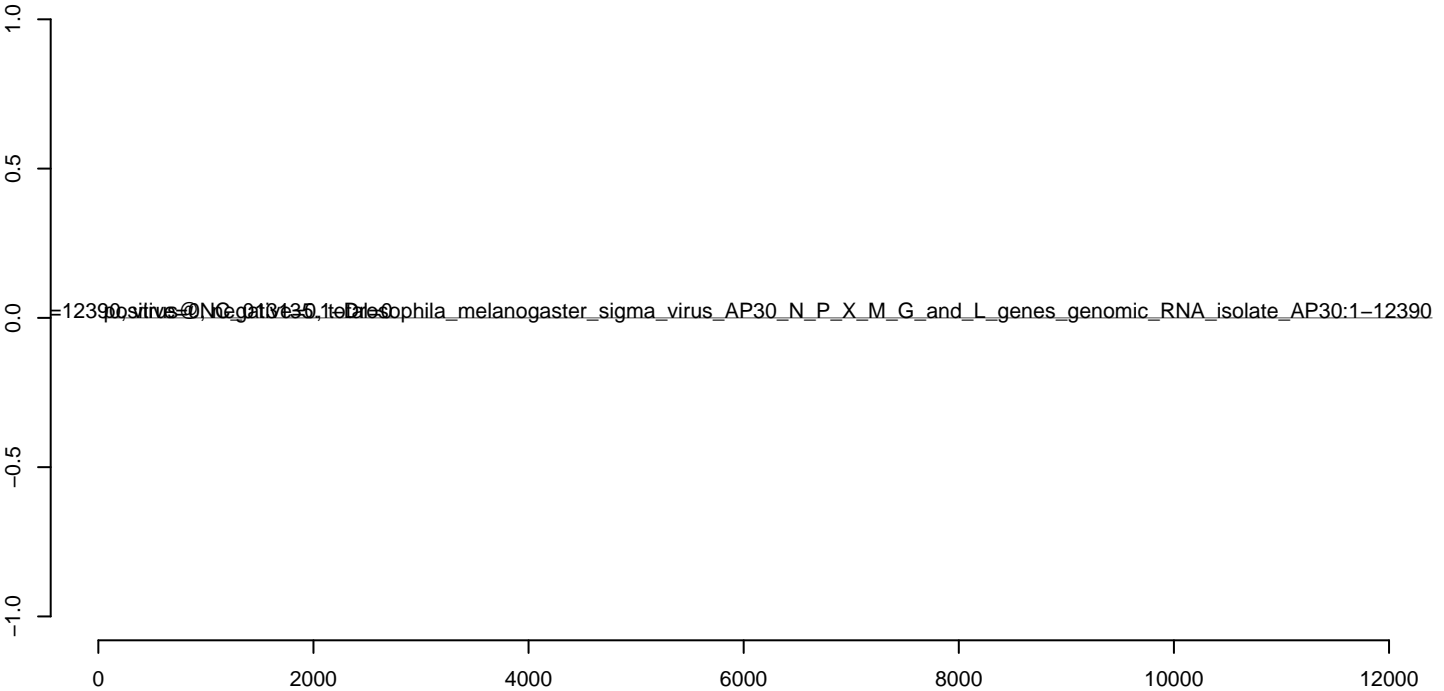
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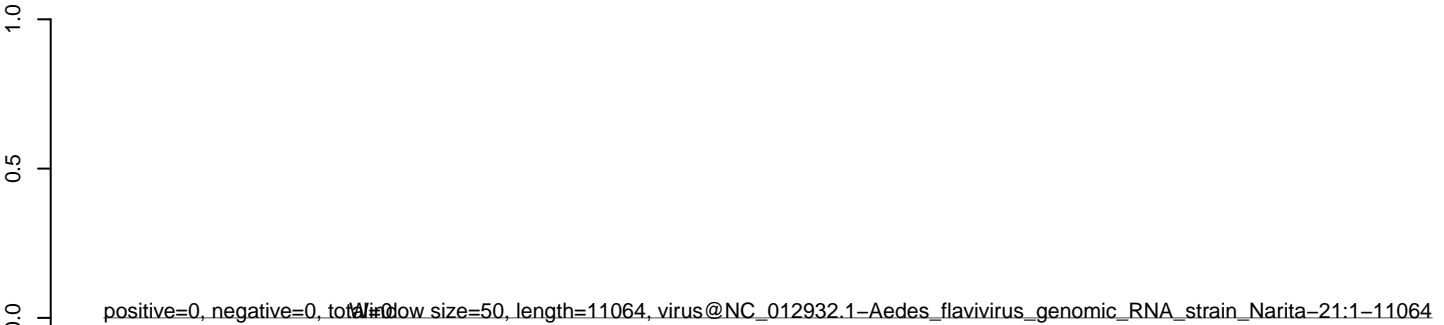
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AeAeg_CCL.125_cells.rep



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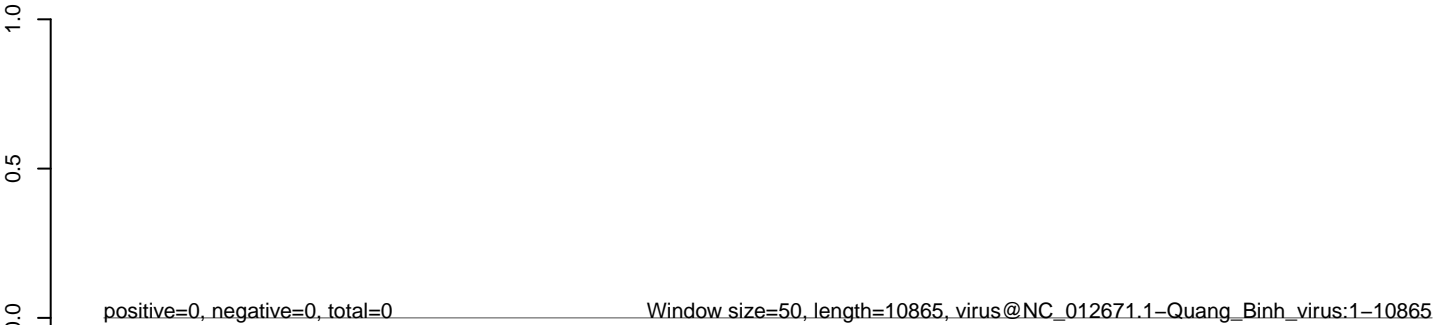
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AeAeg_CCL.125_cells.rep



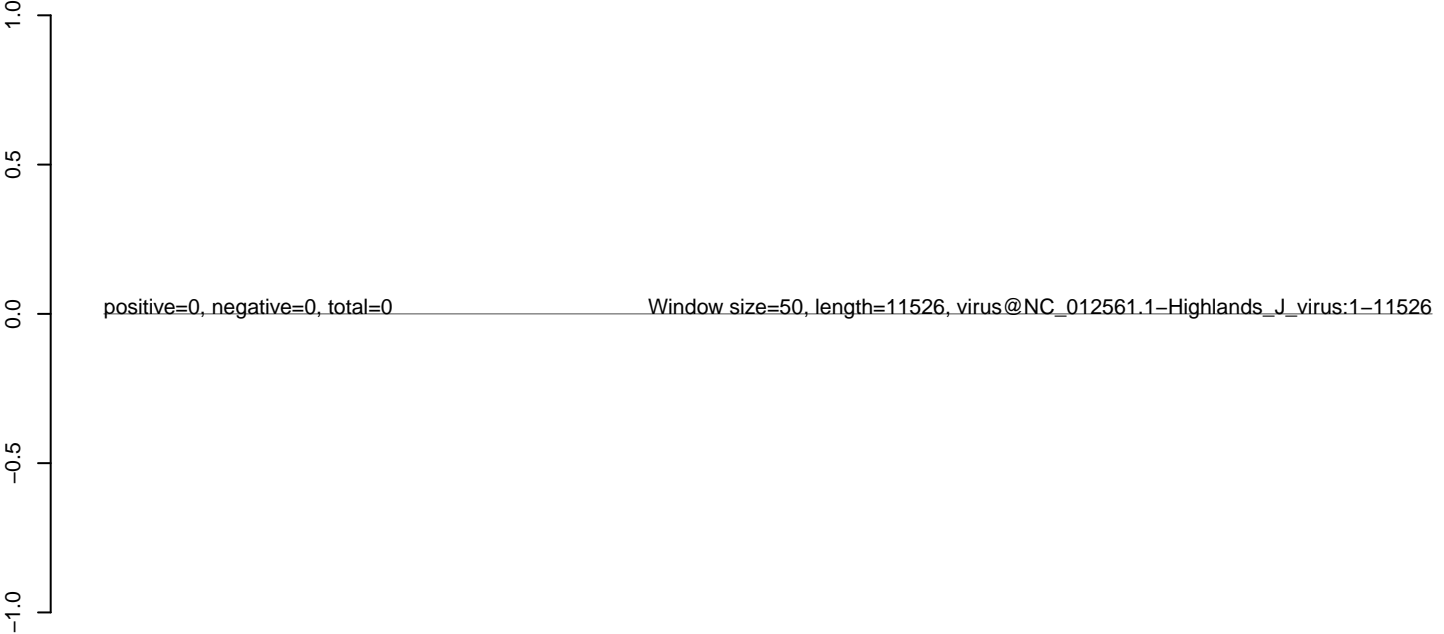
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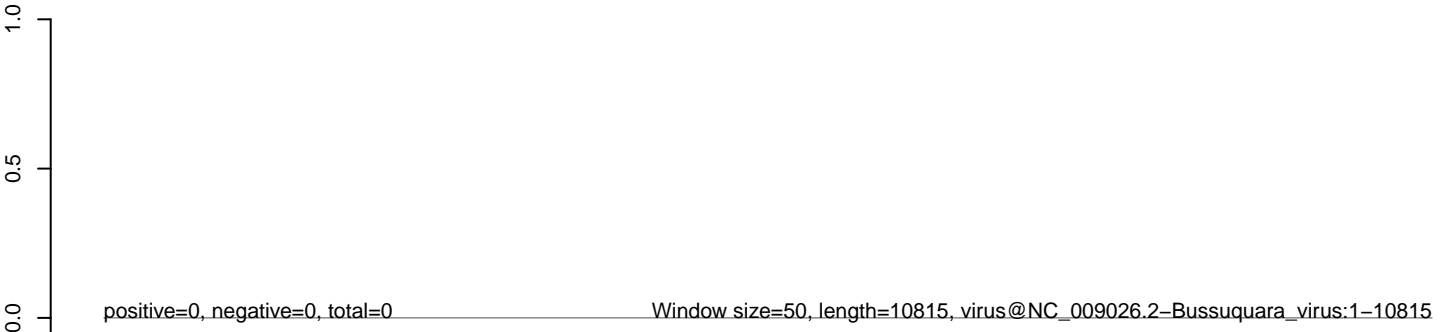
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AeAeg_CCL.125_cells.24_35.rep



AeAeg_CCL.125_cells.rep



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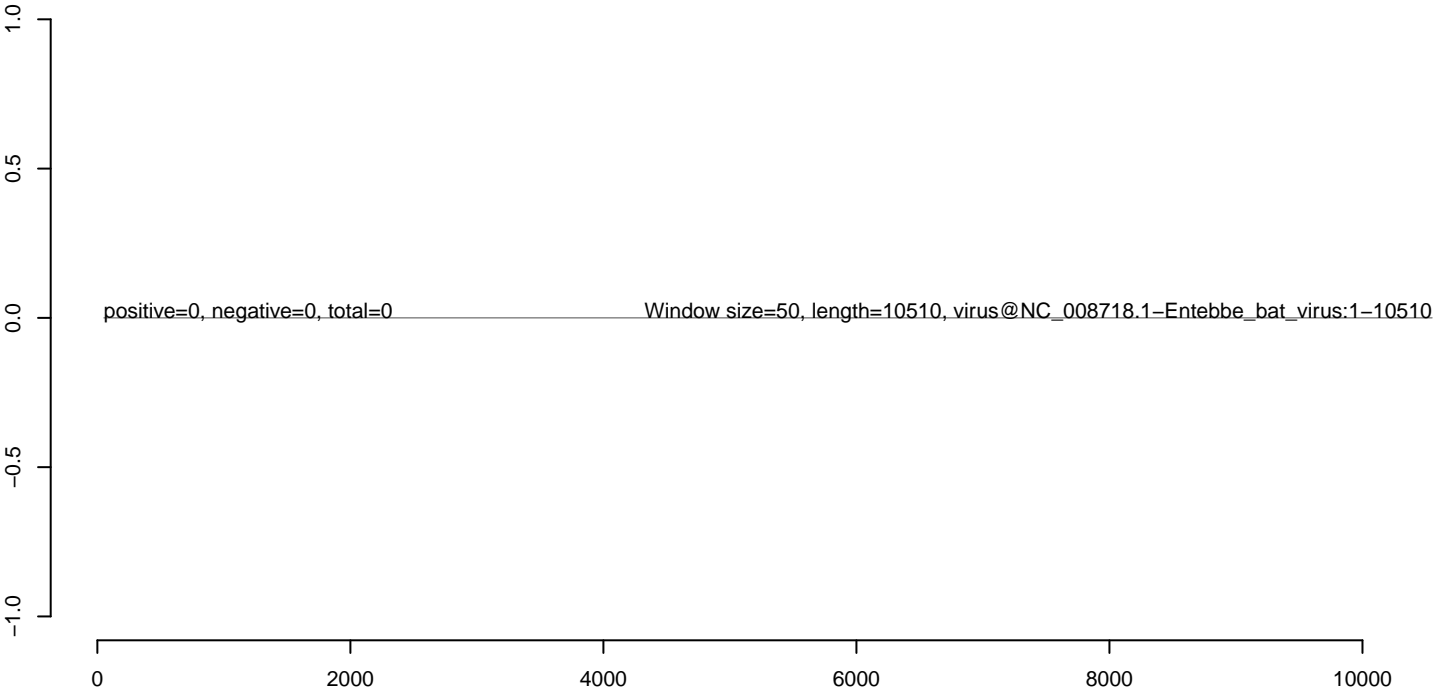
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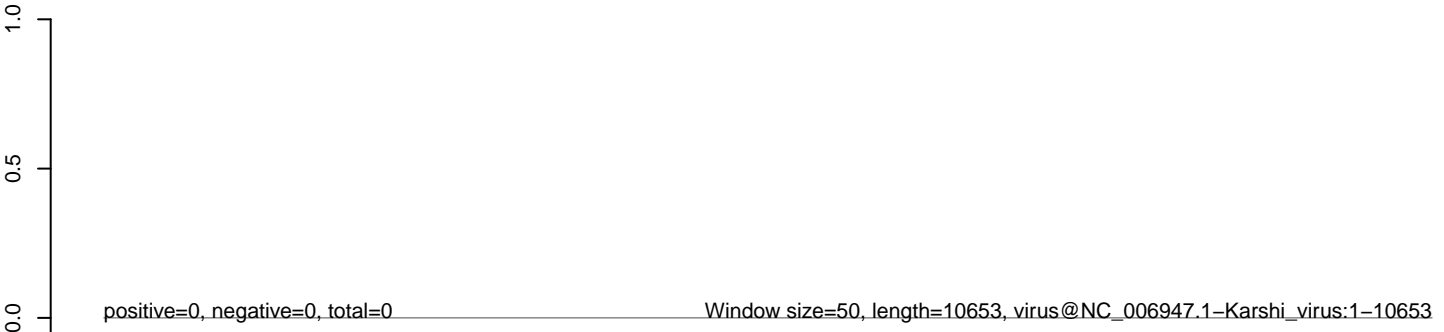
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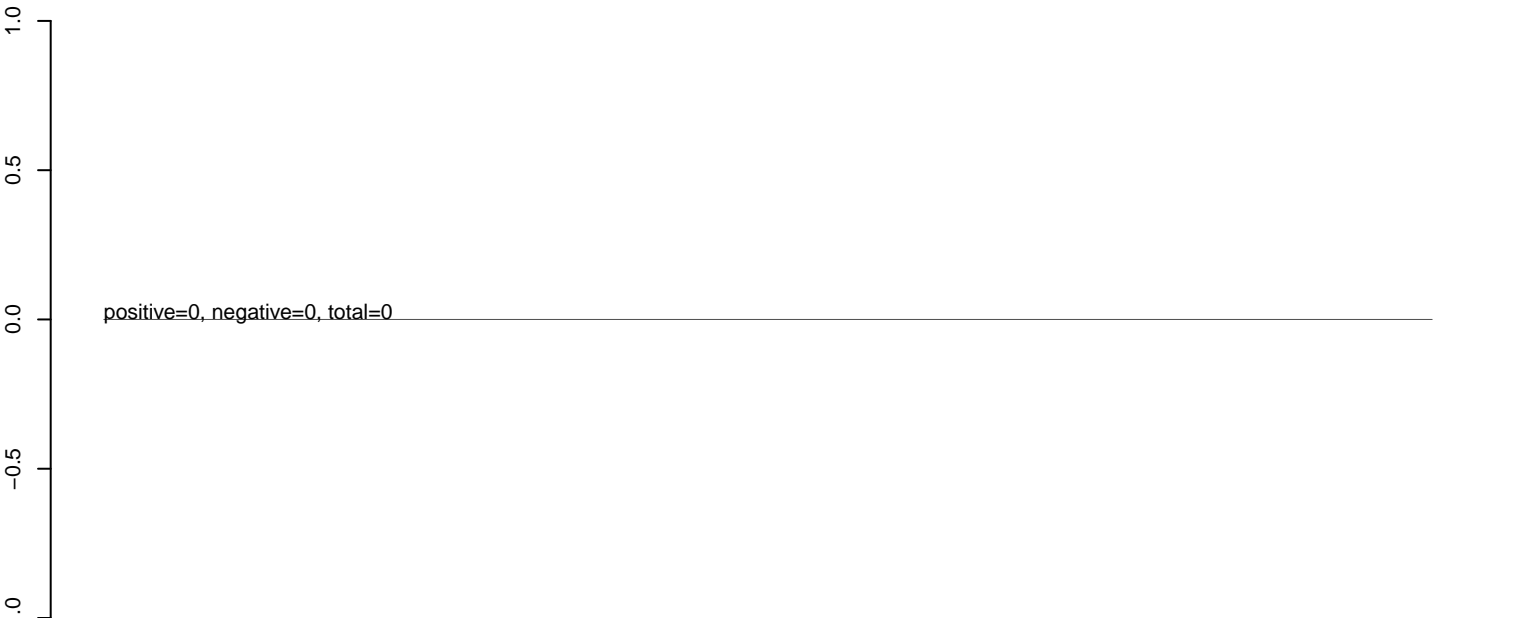


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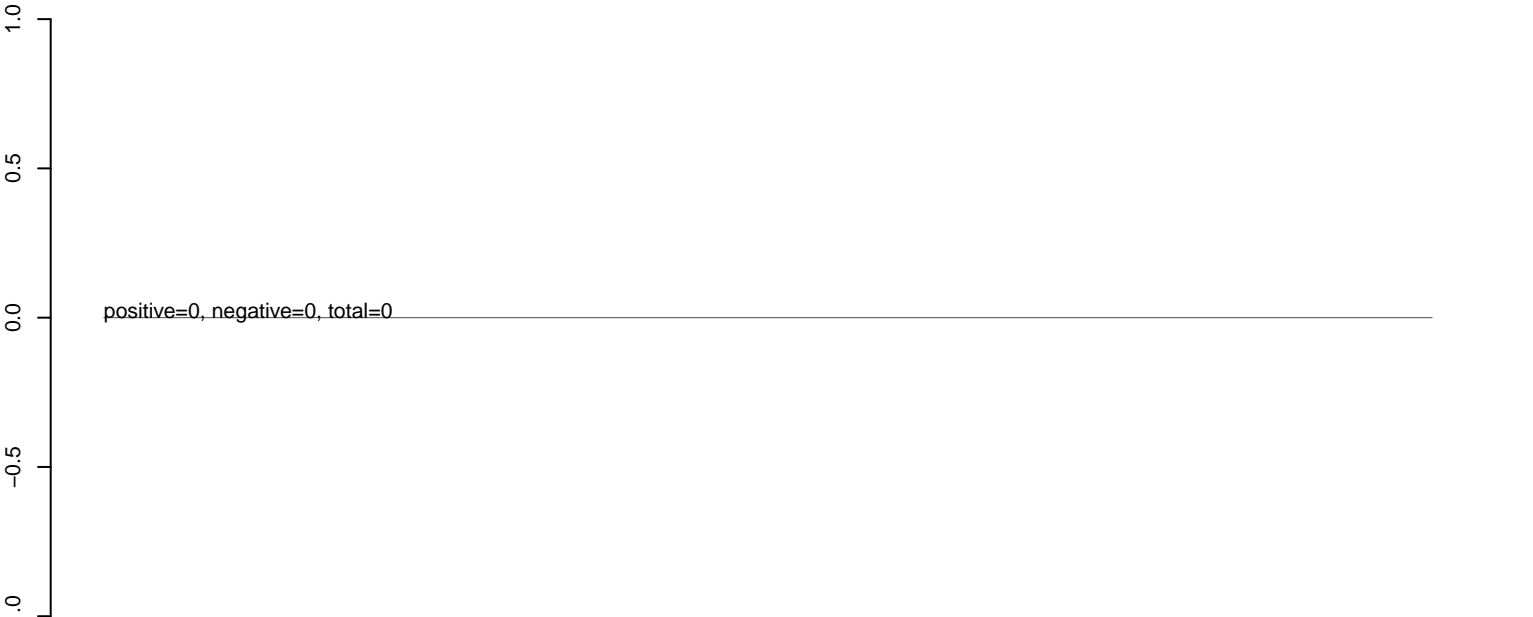


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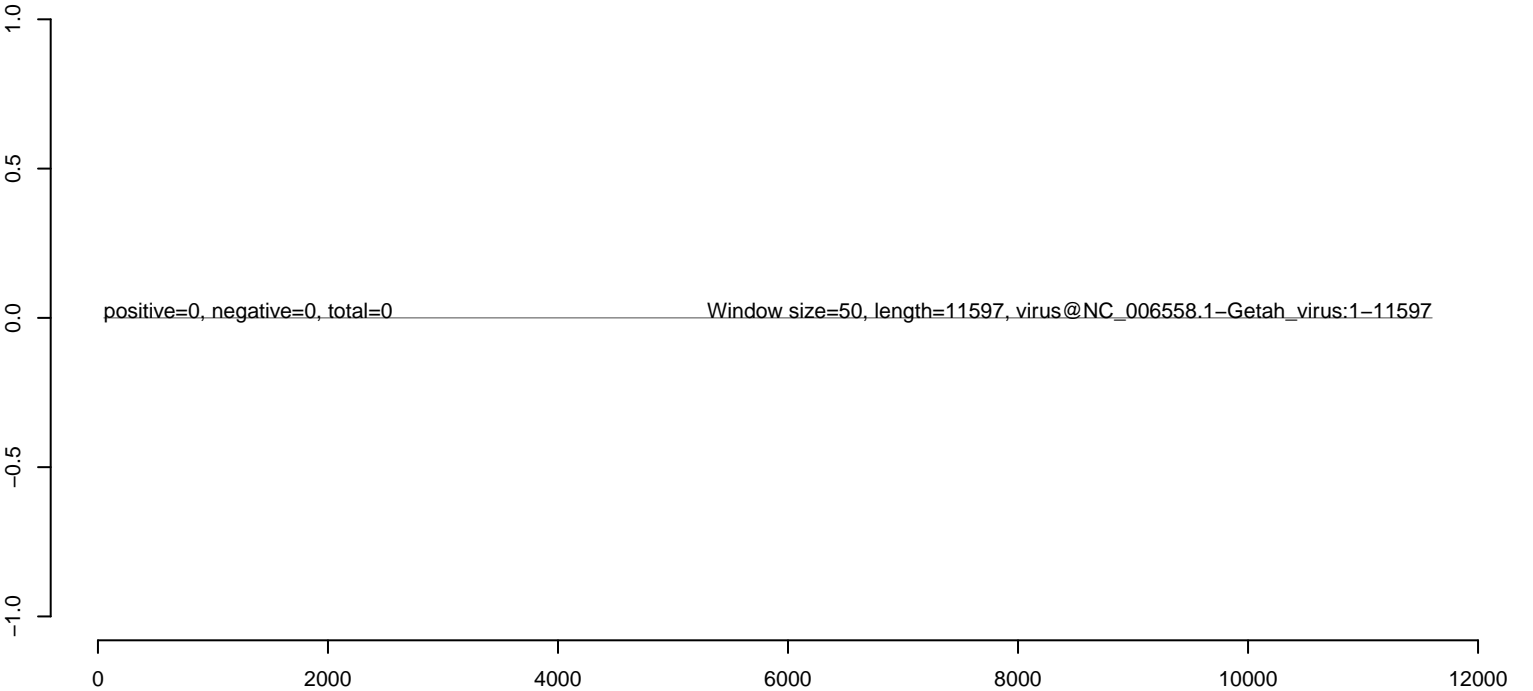
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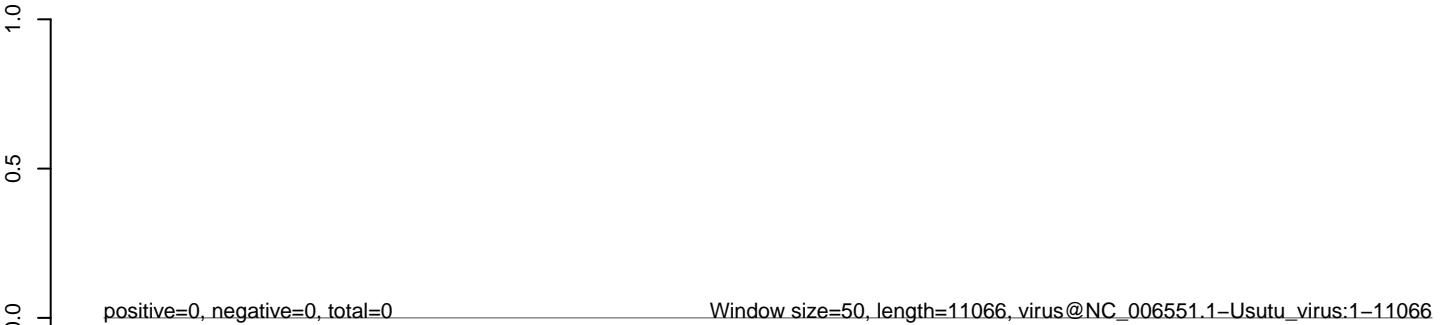
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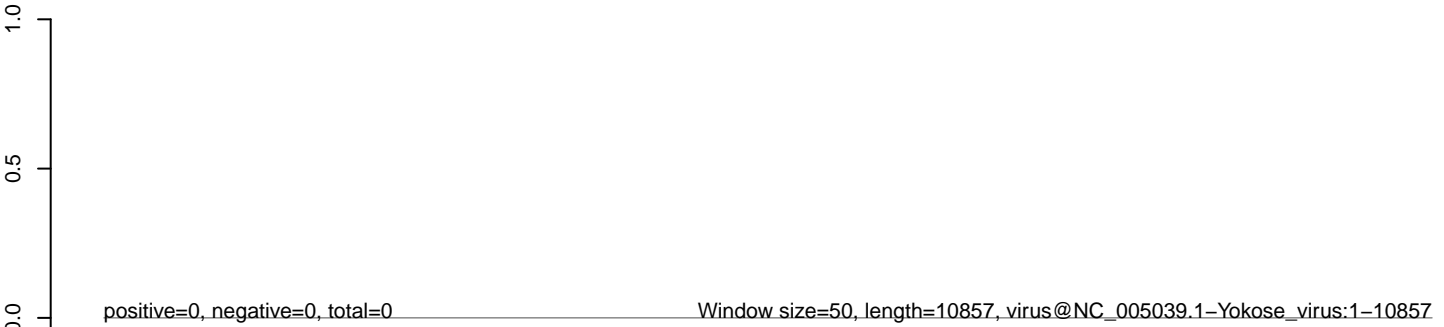
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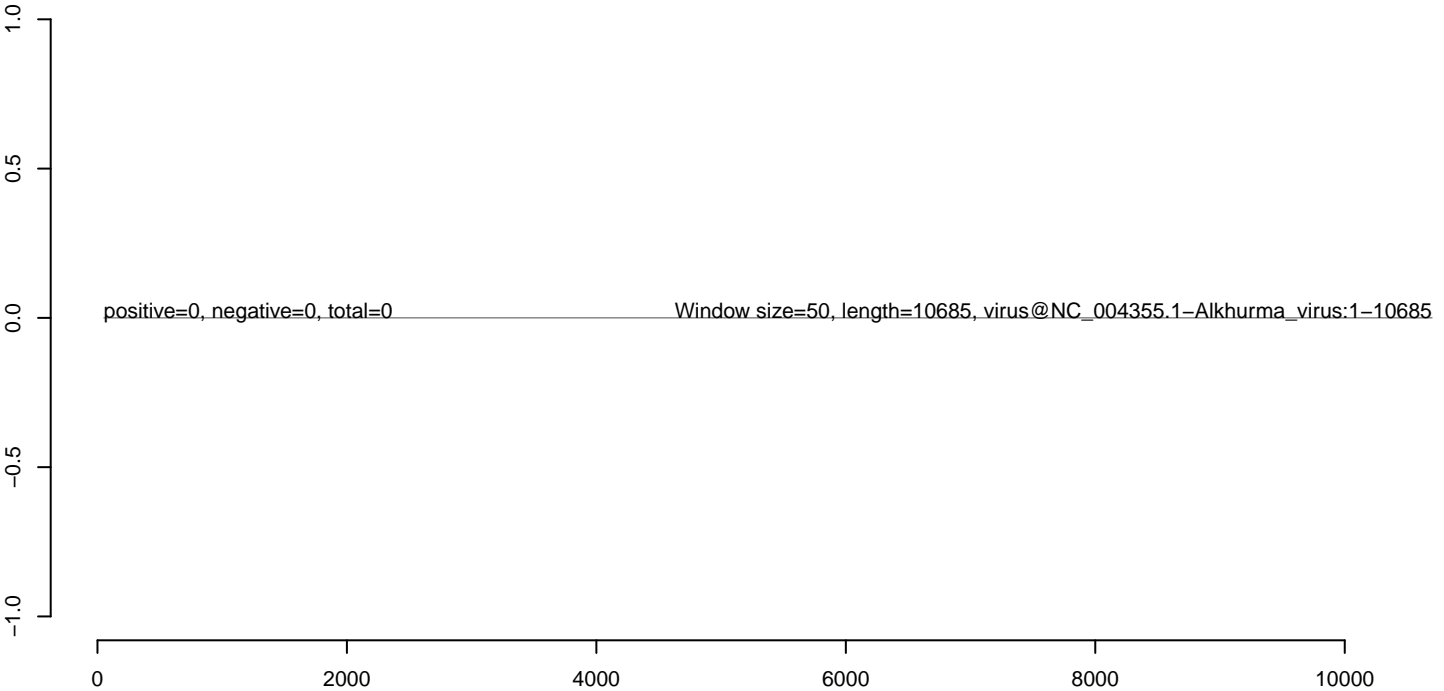
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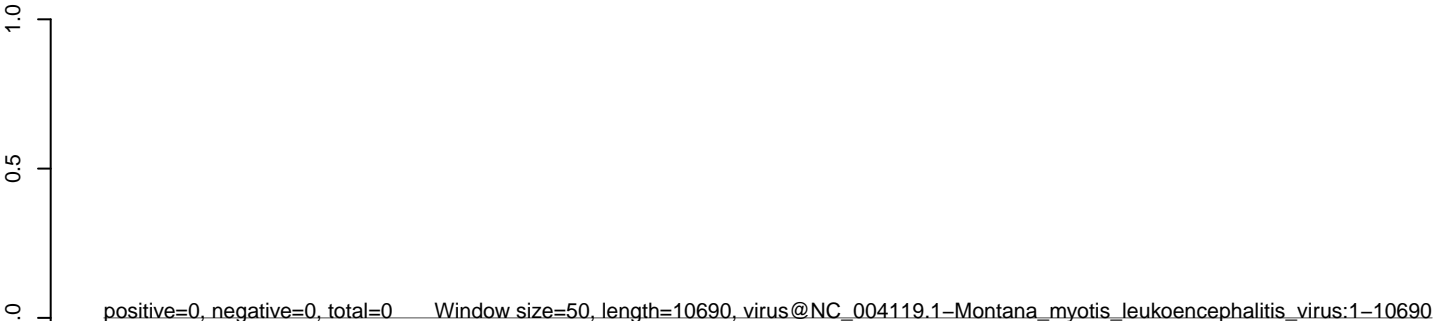
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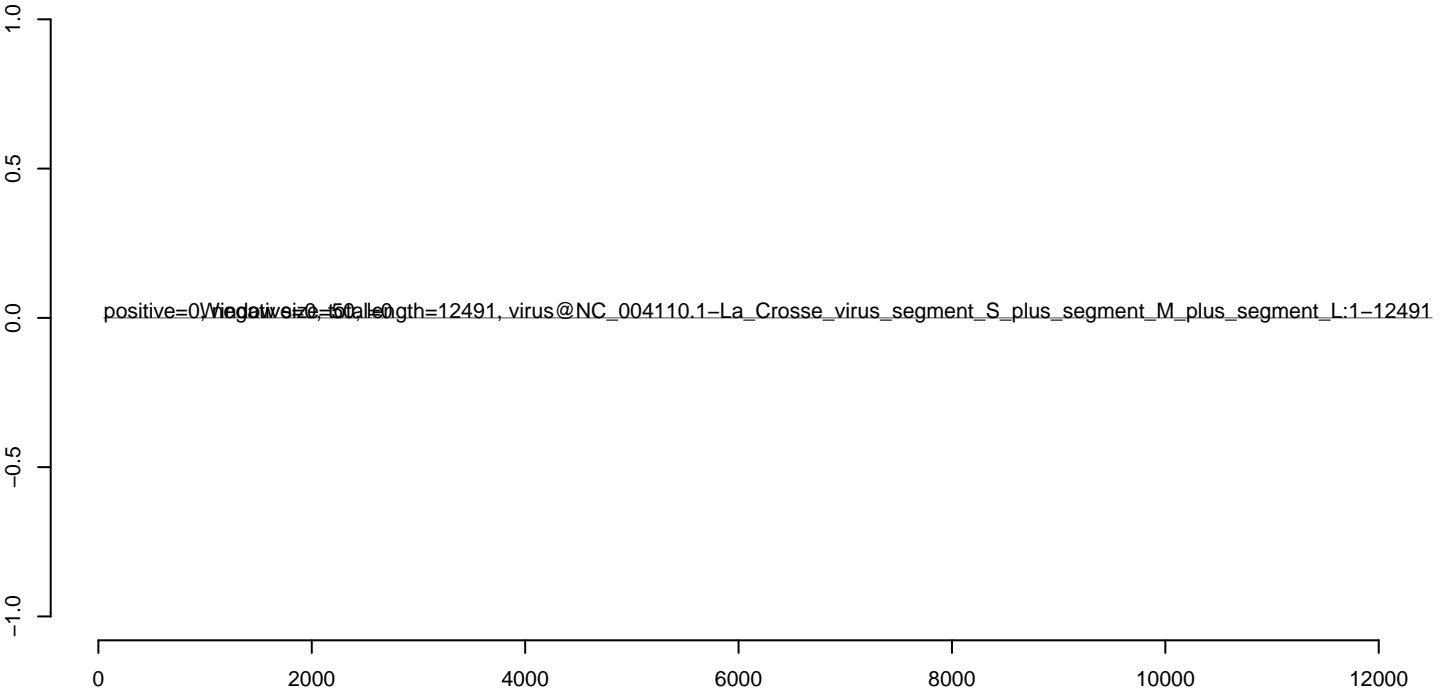
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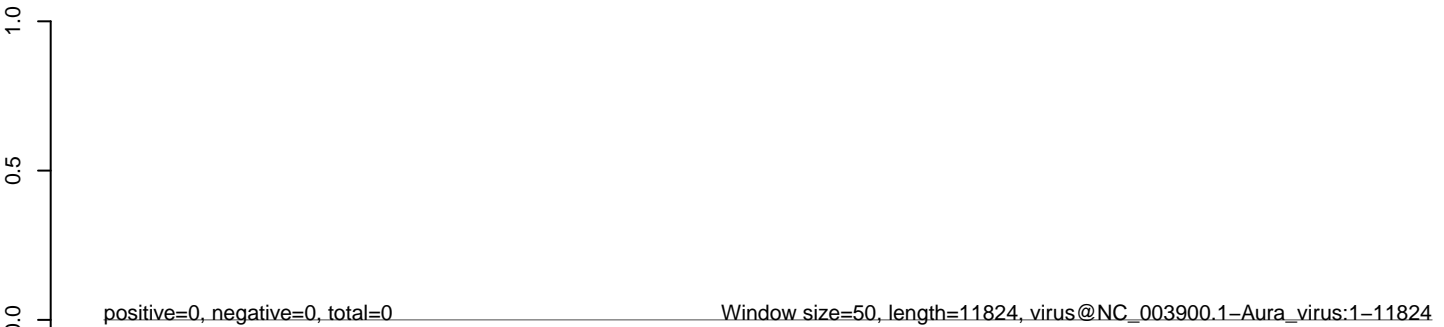
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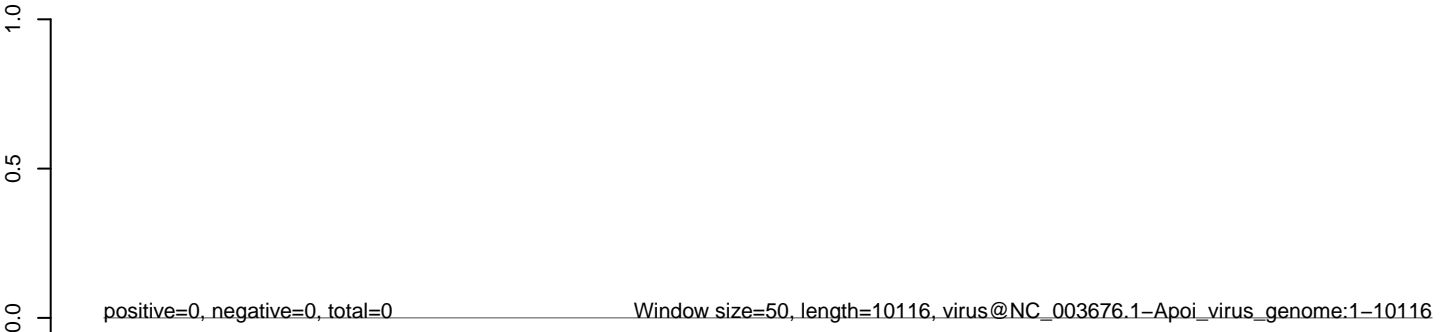
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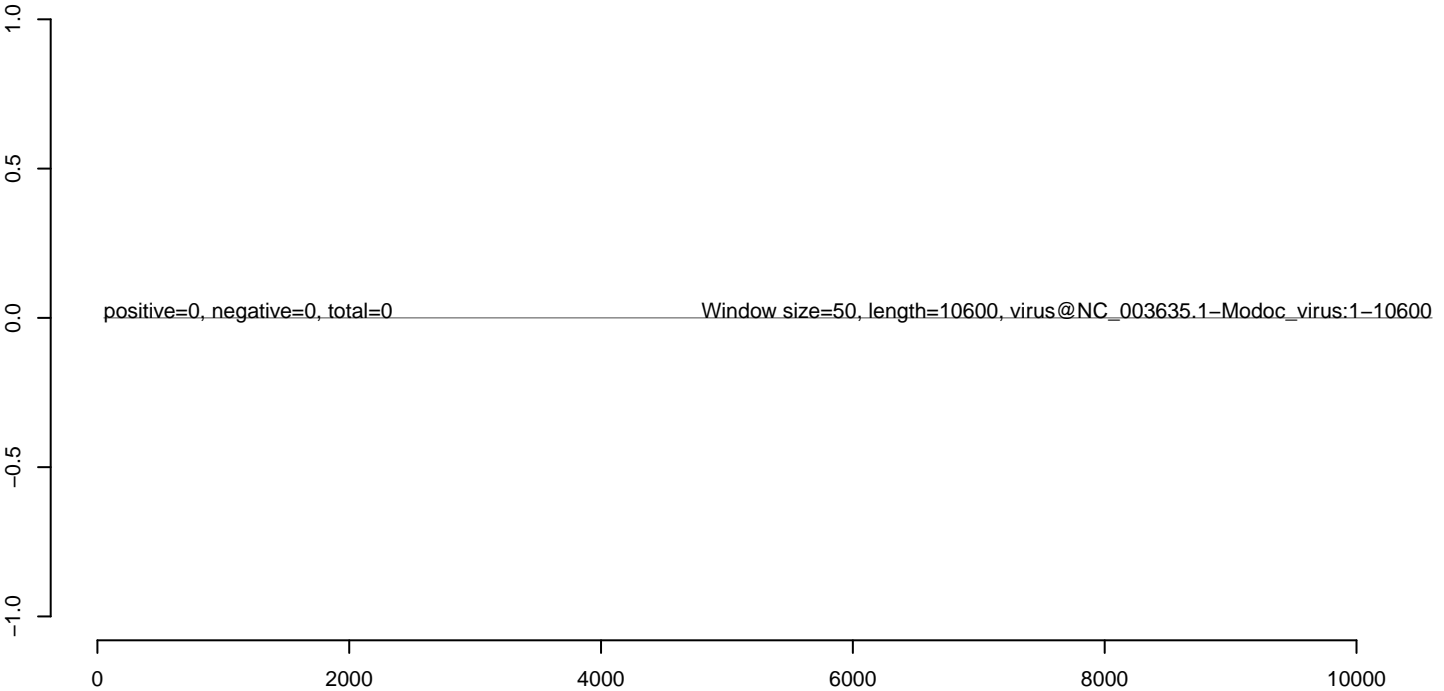
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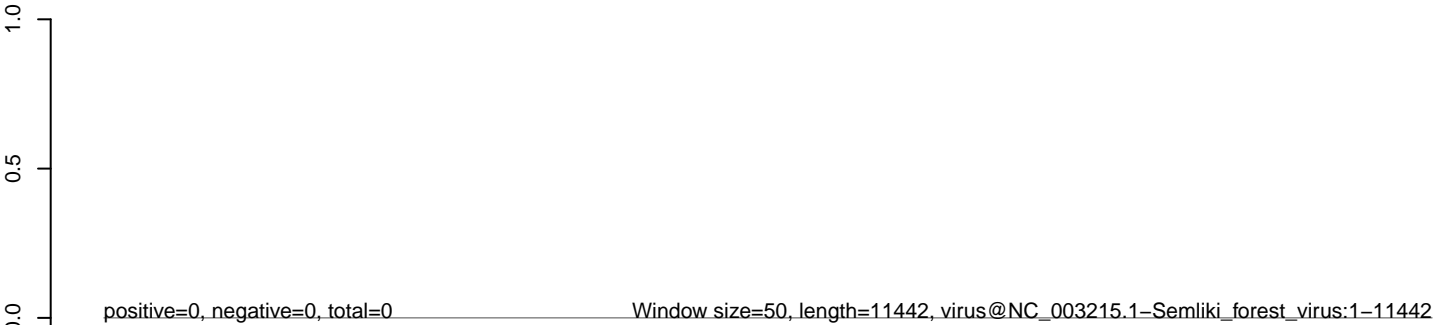
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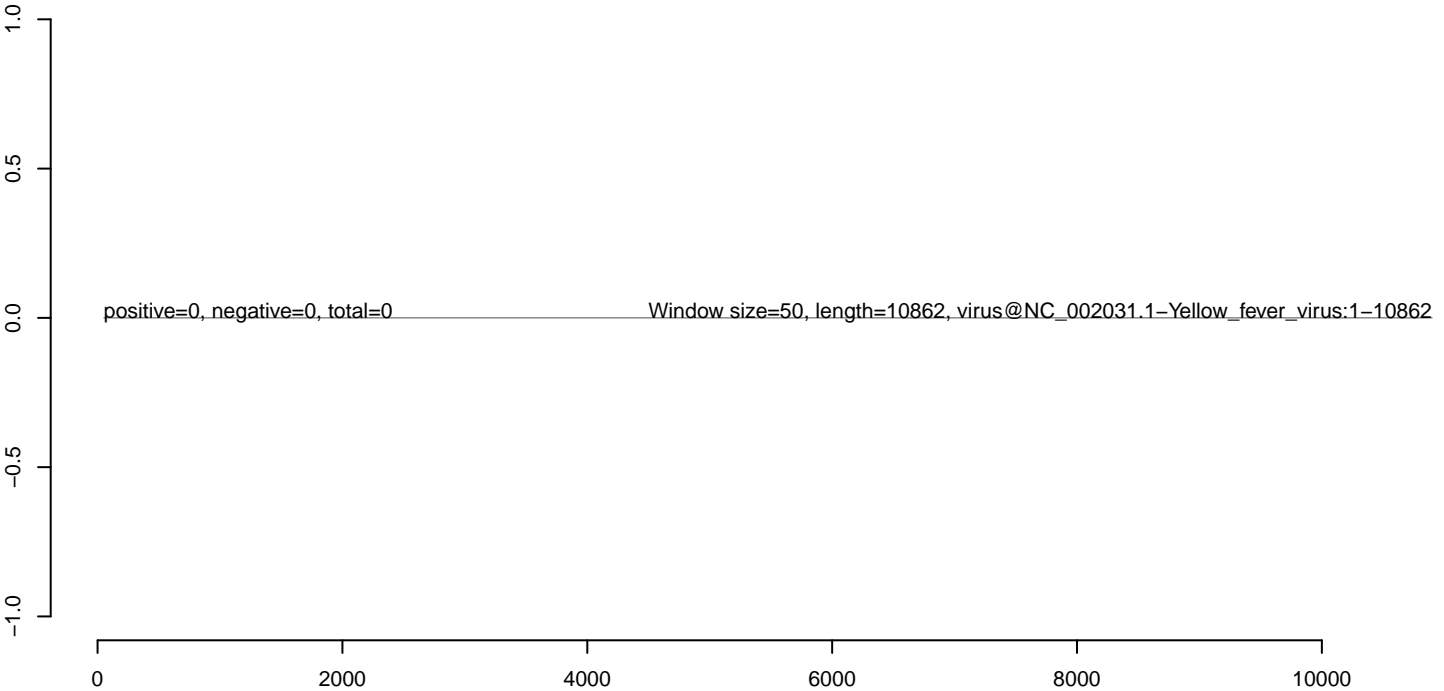
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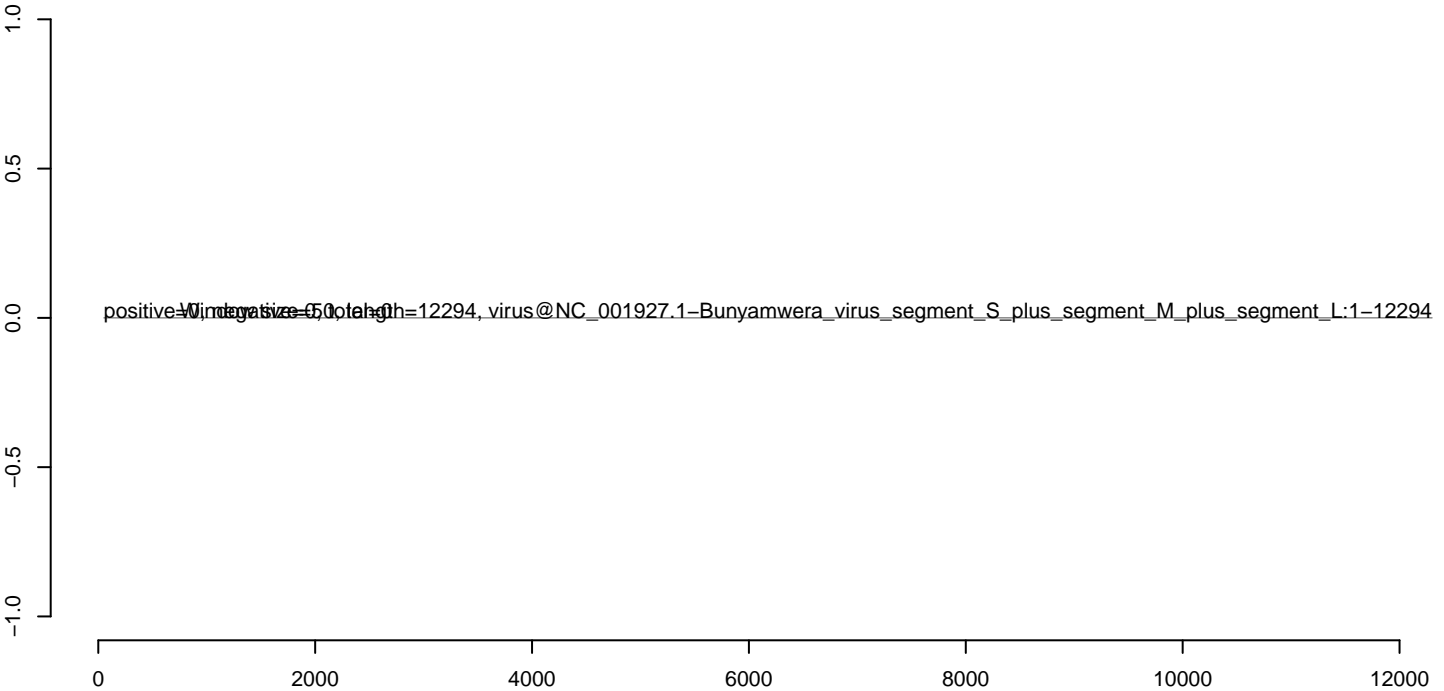
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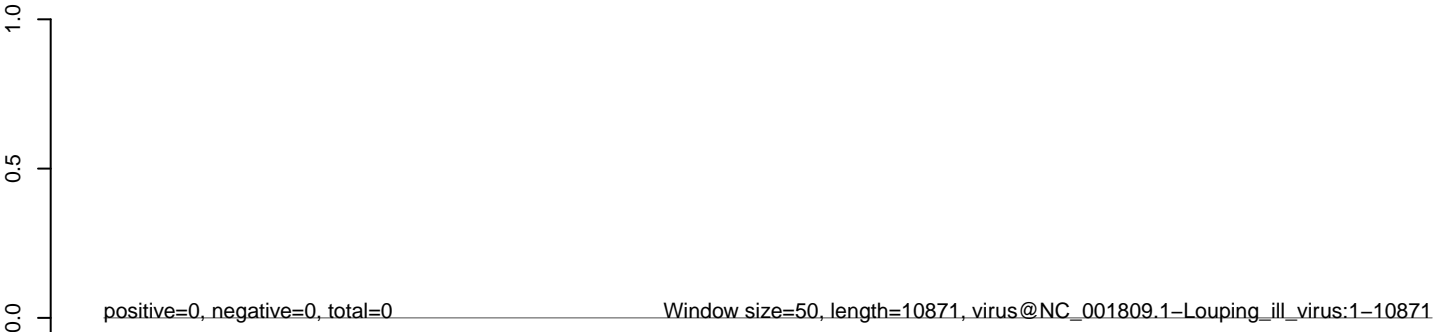
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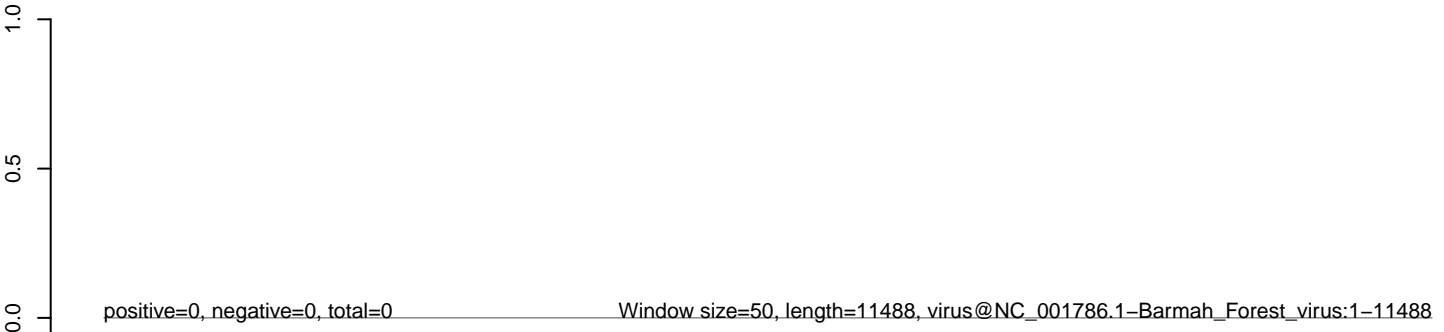
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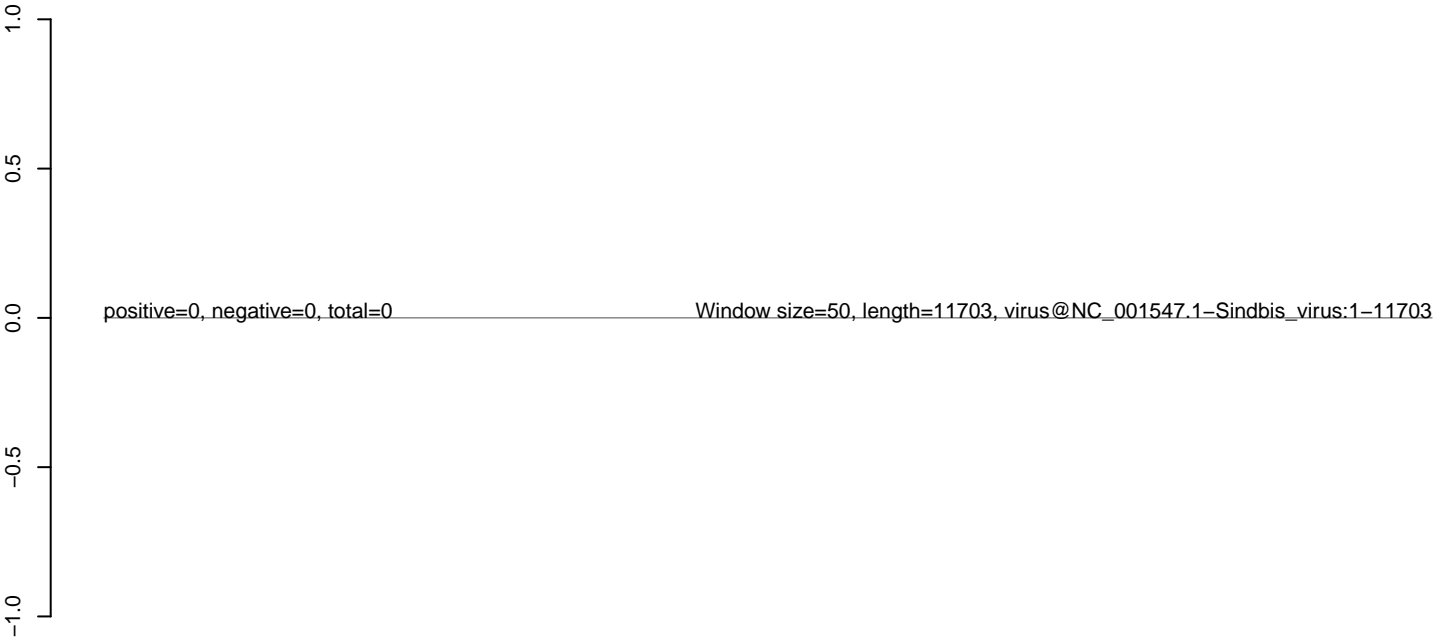
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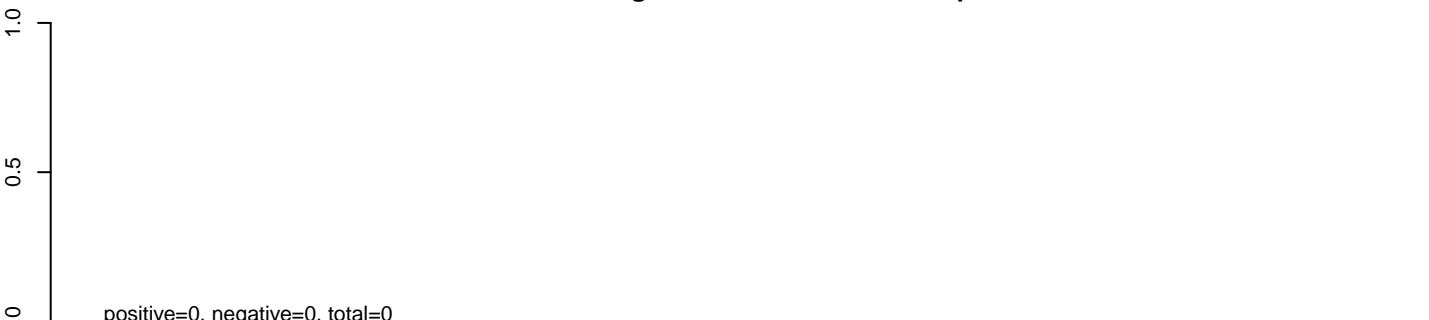
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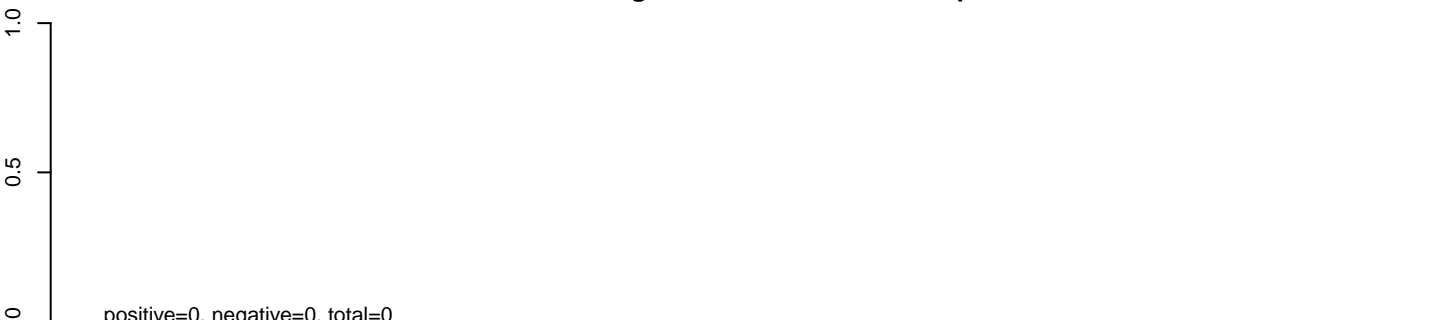
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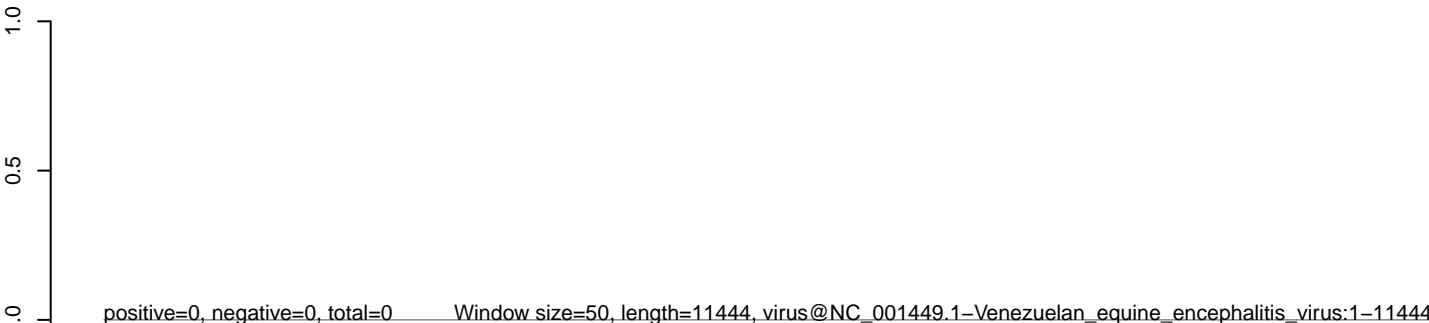
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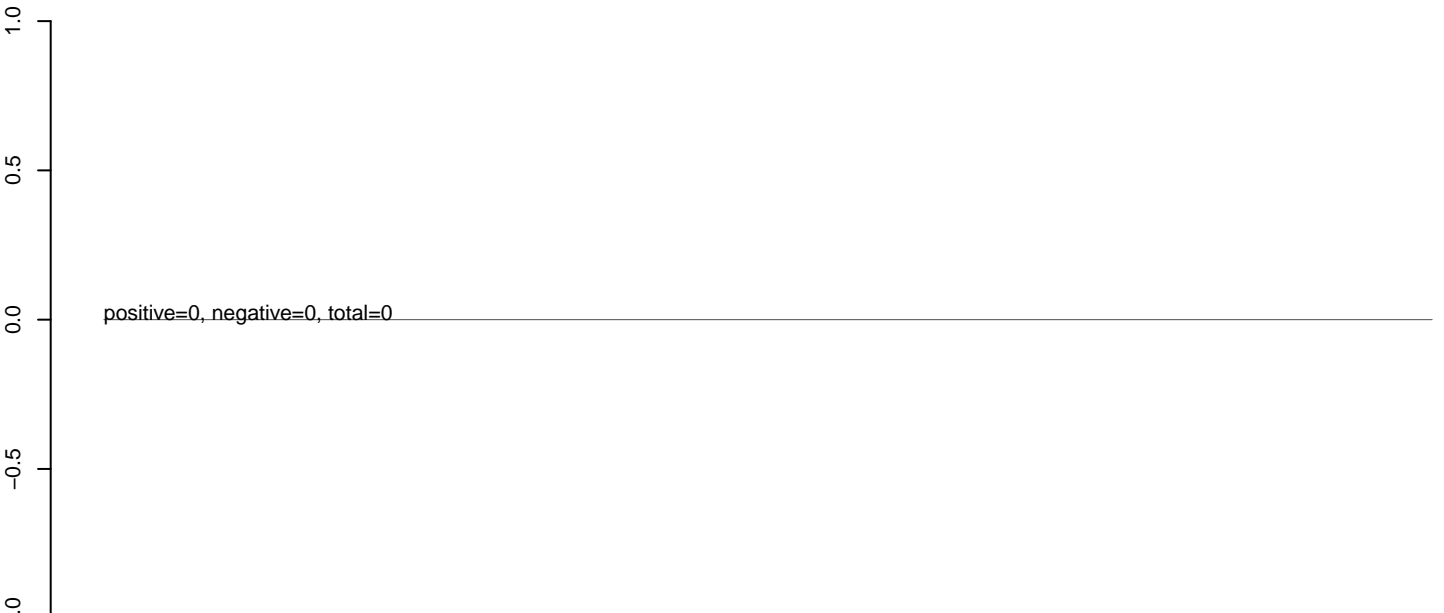


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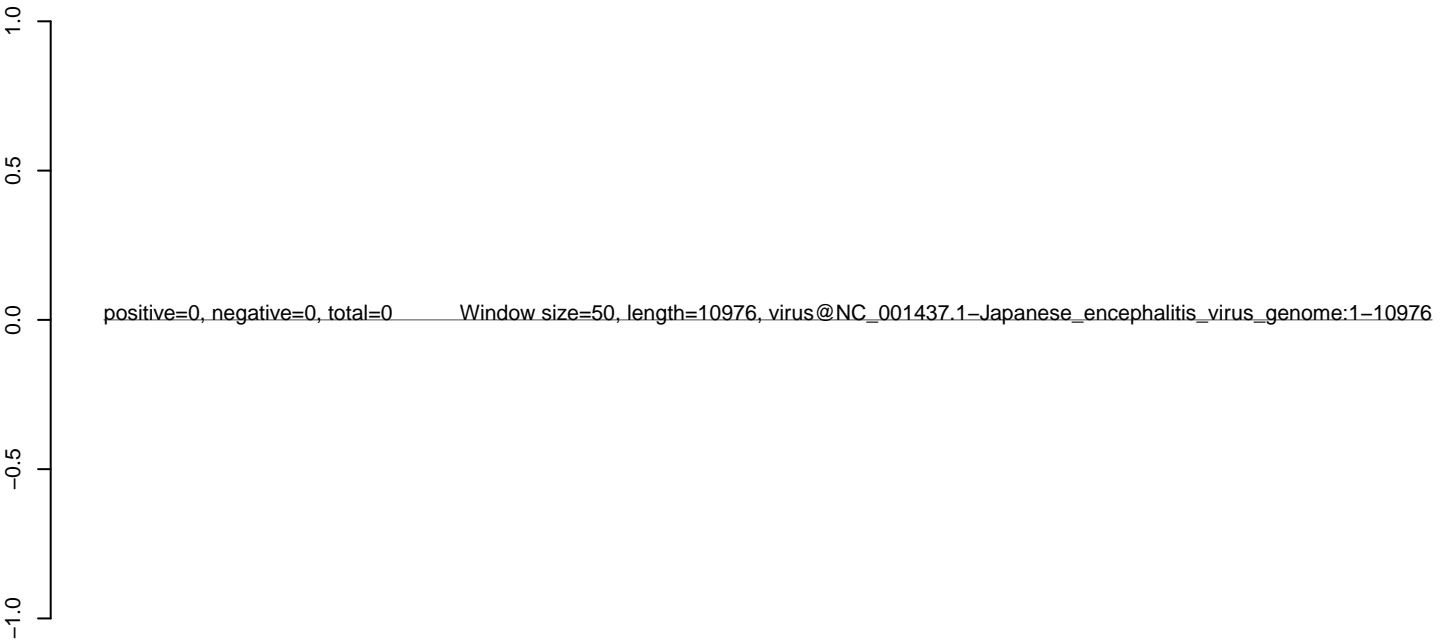
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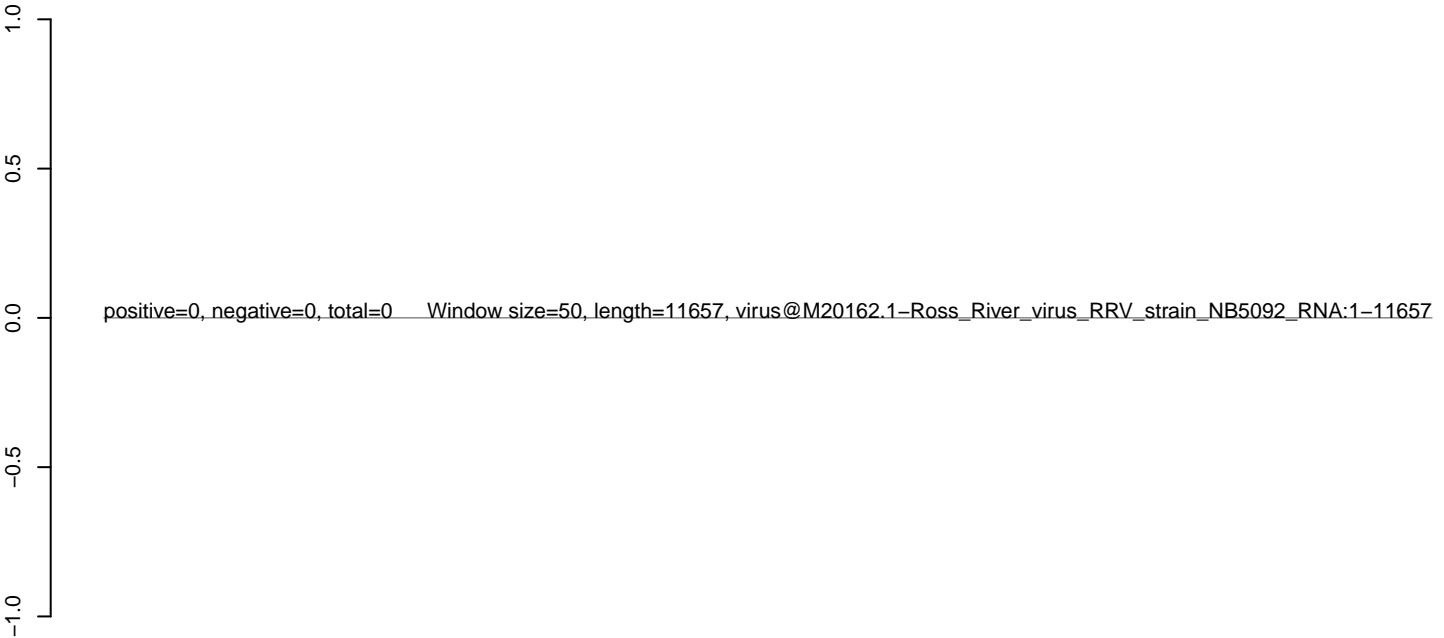
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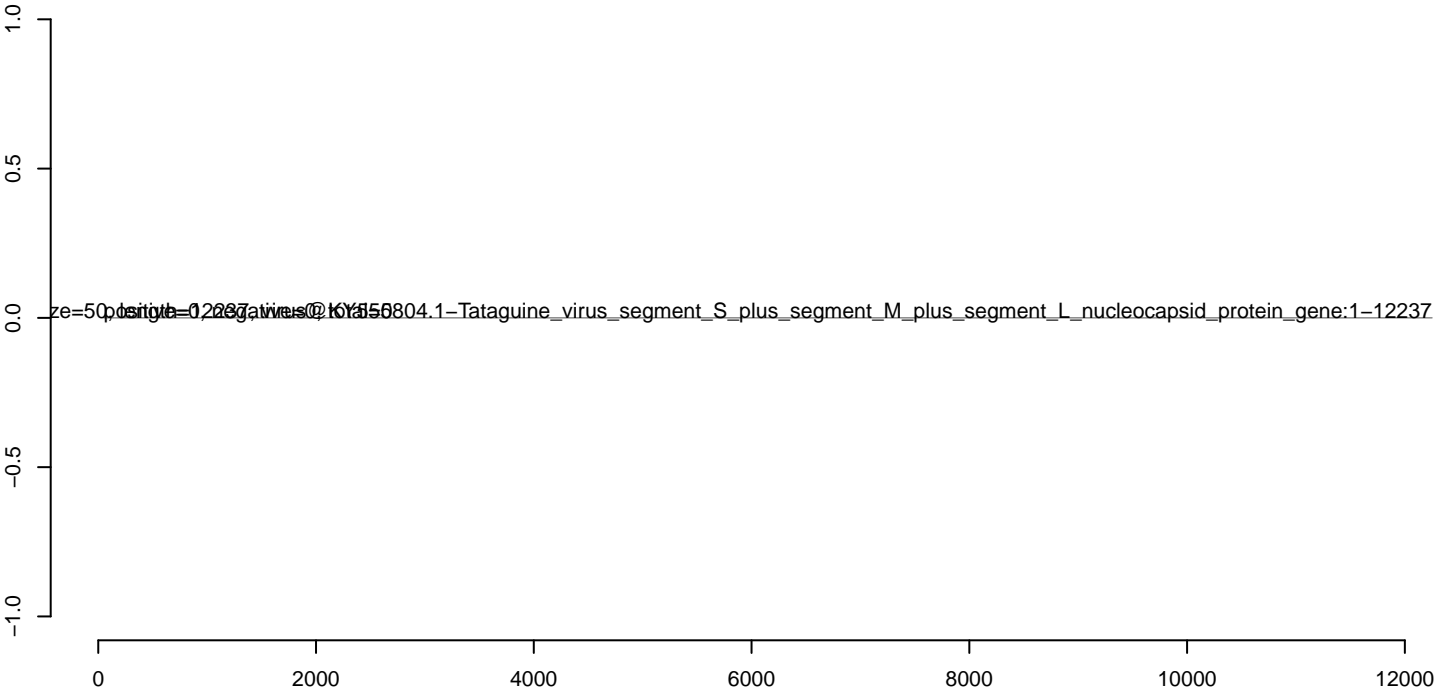
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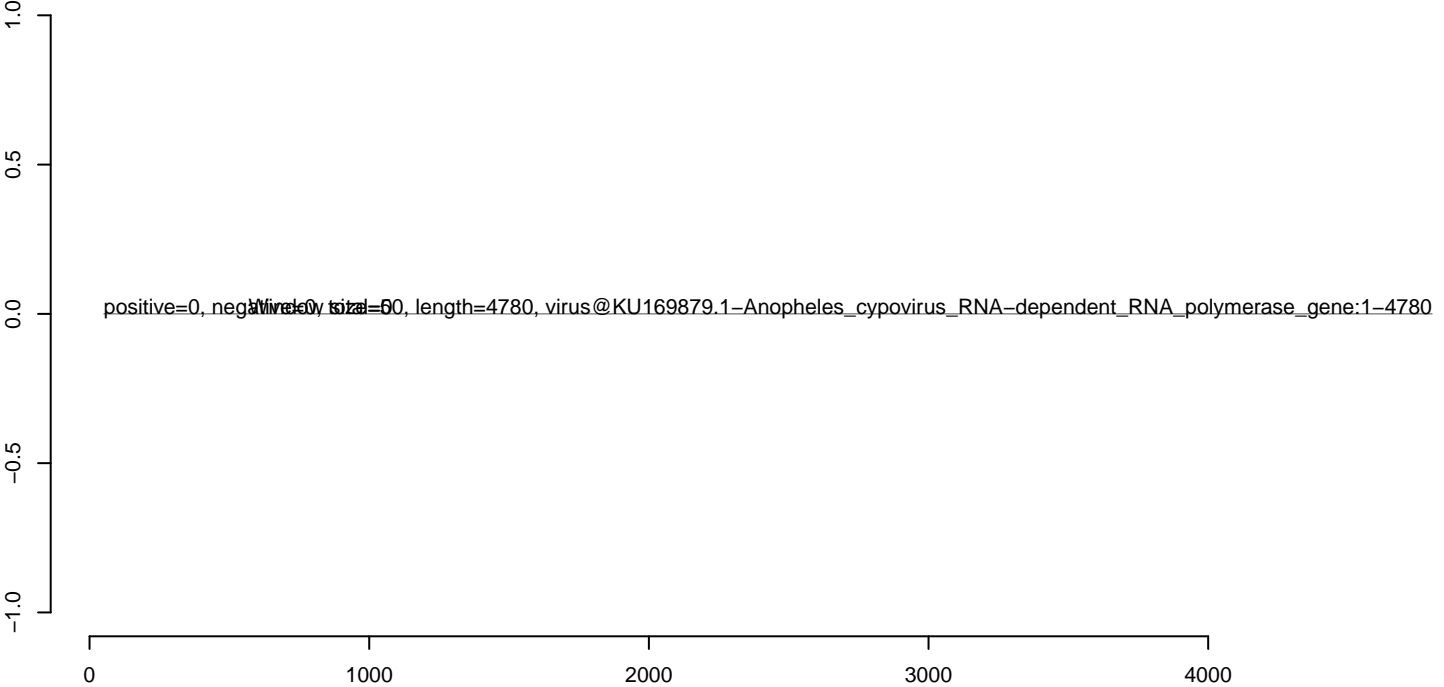
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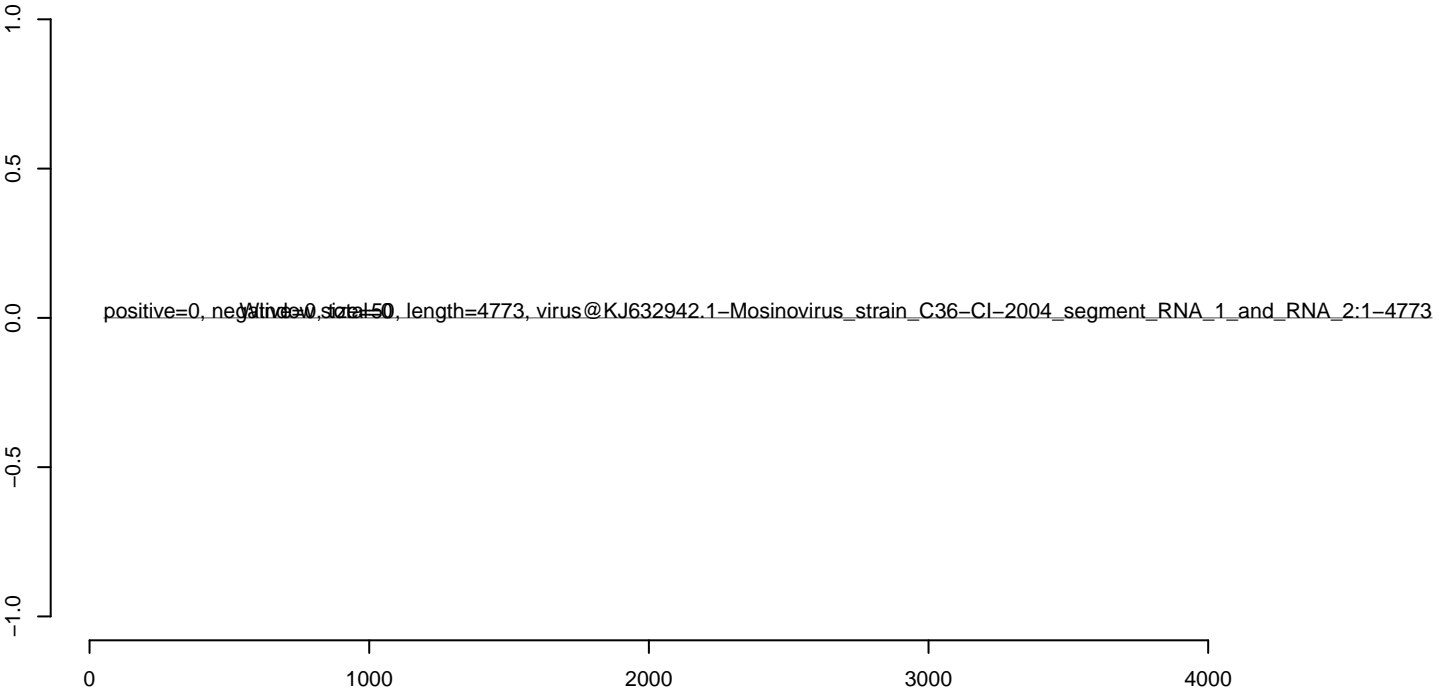
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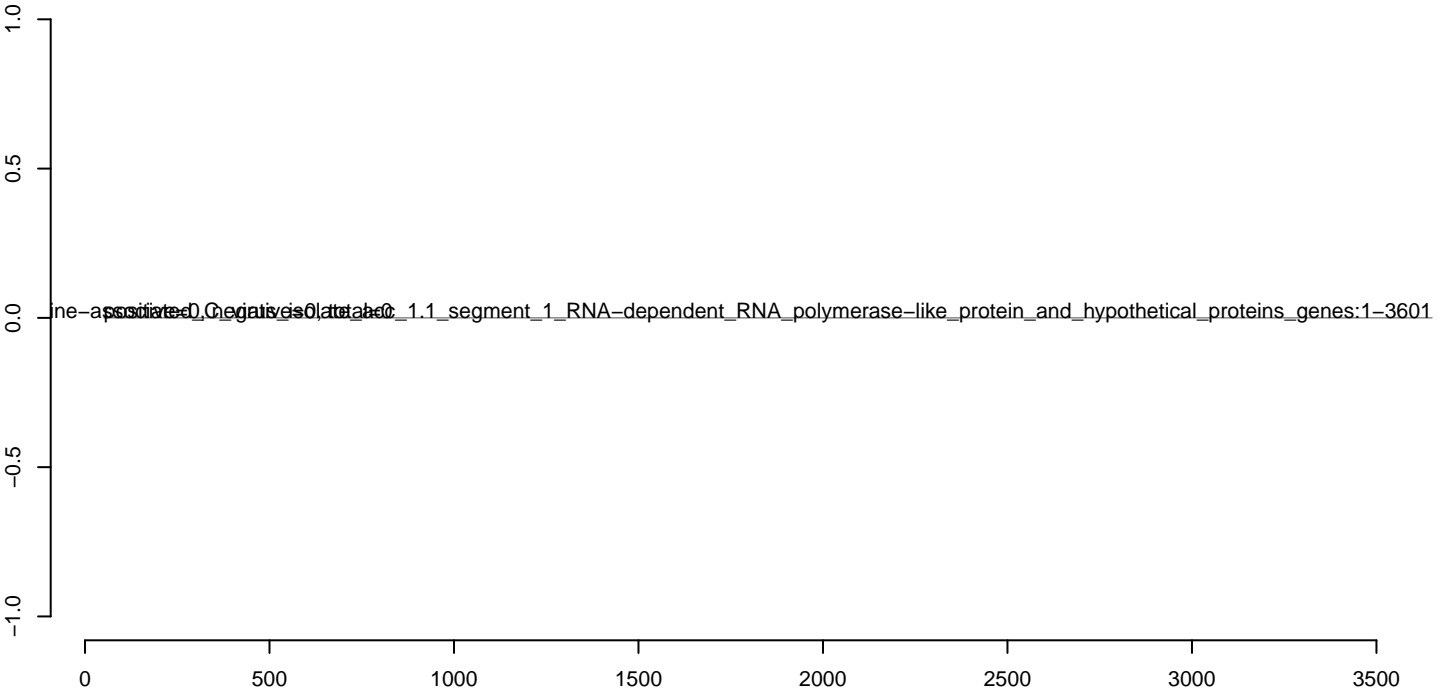
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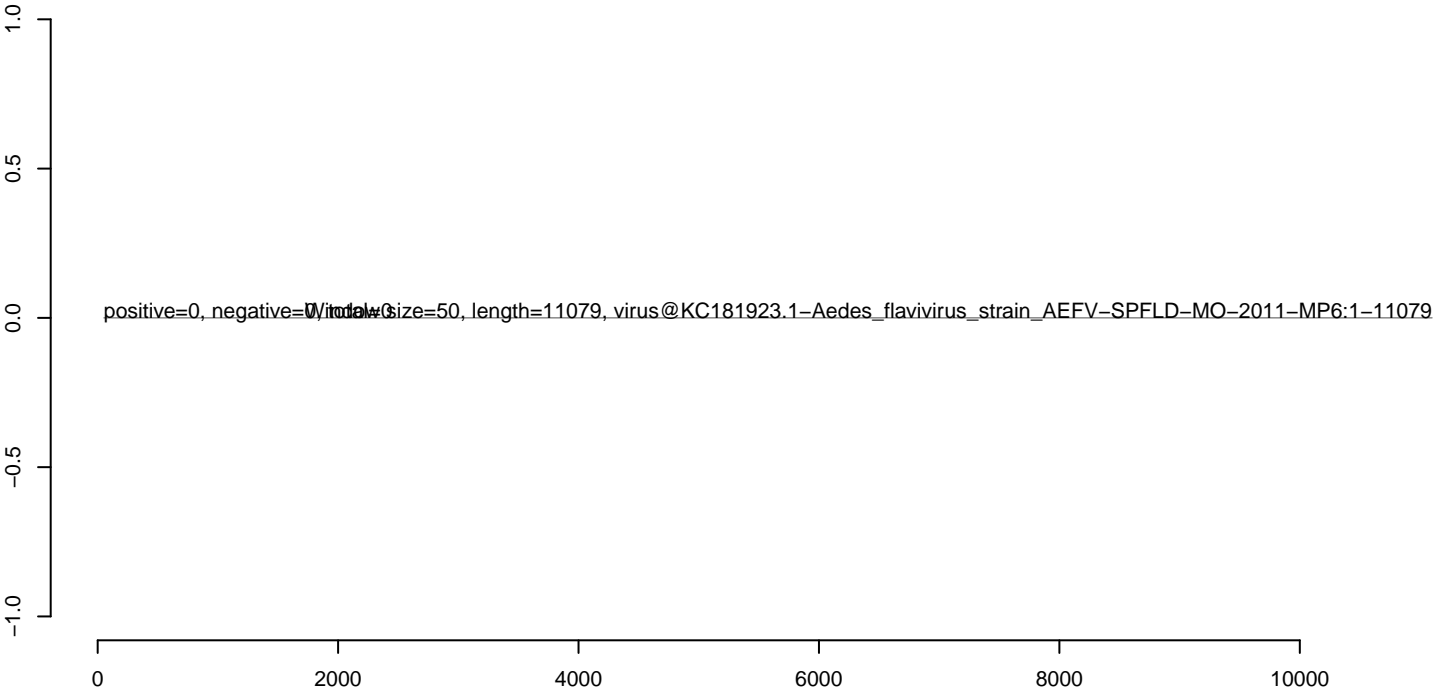
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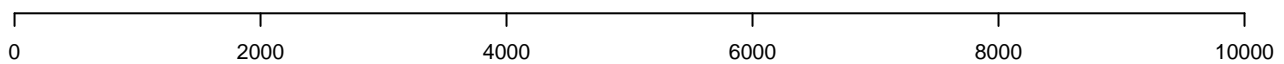
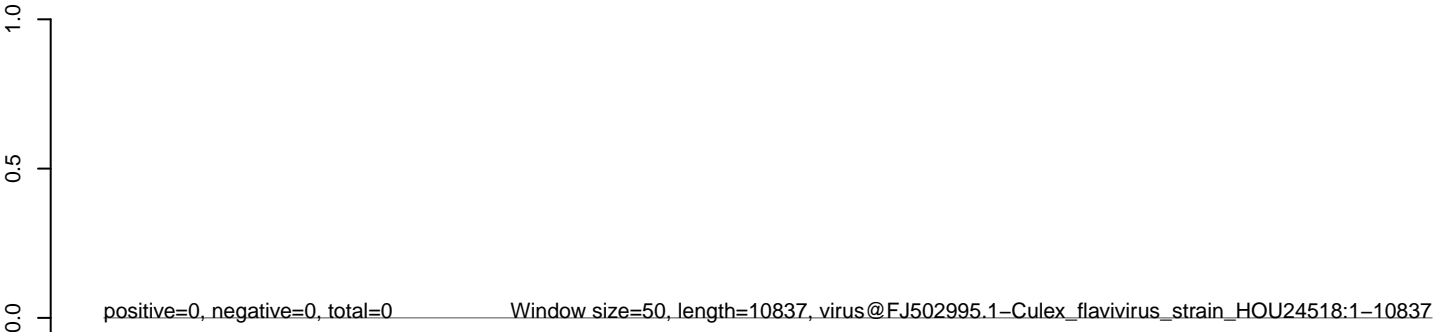
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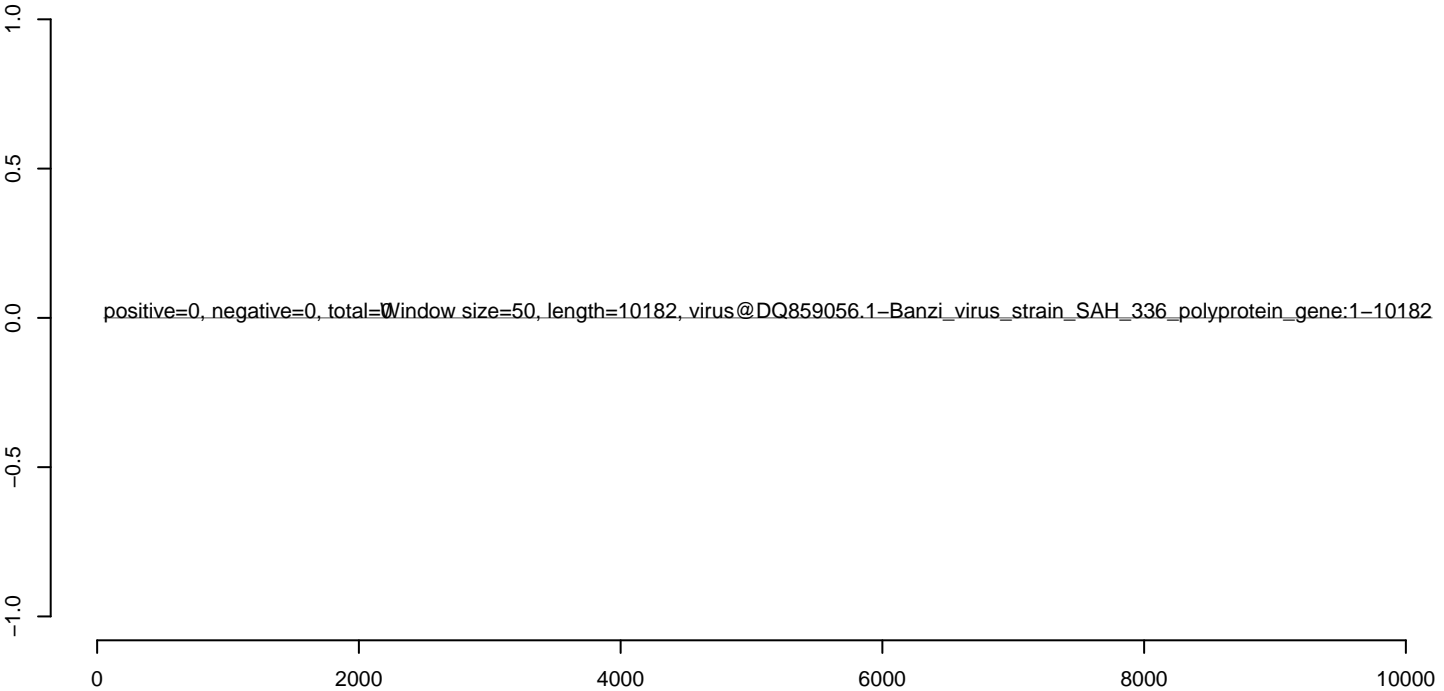
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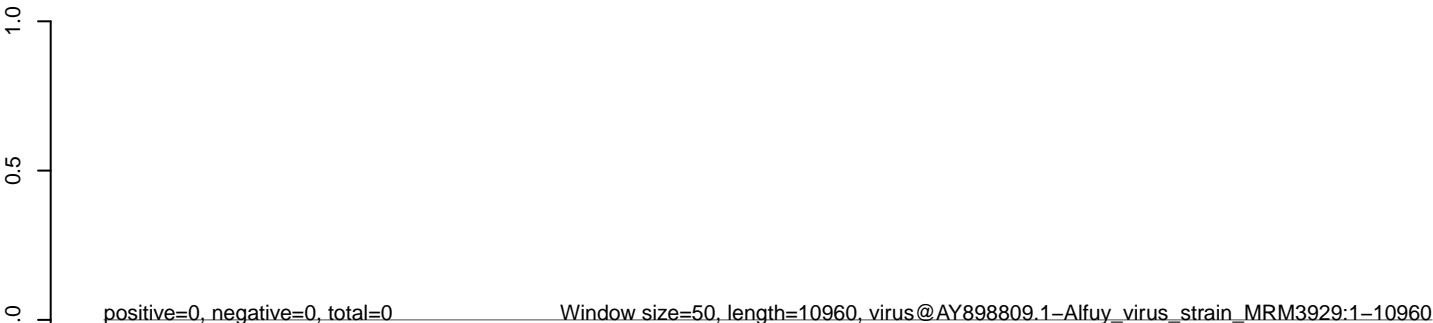
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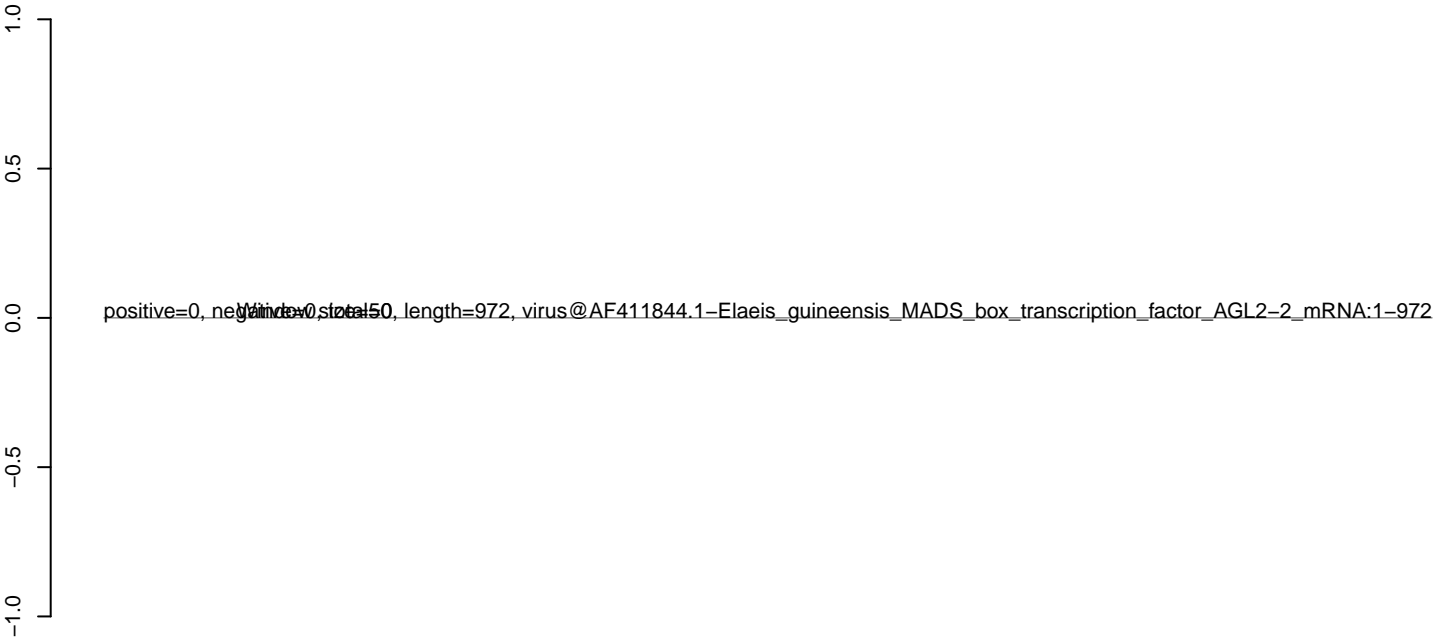
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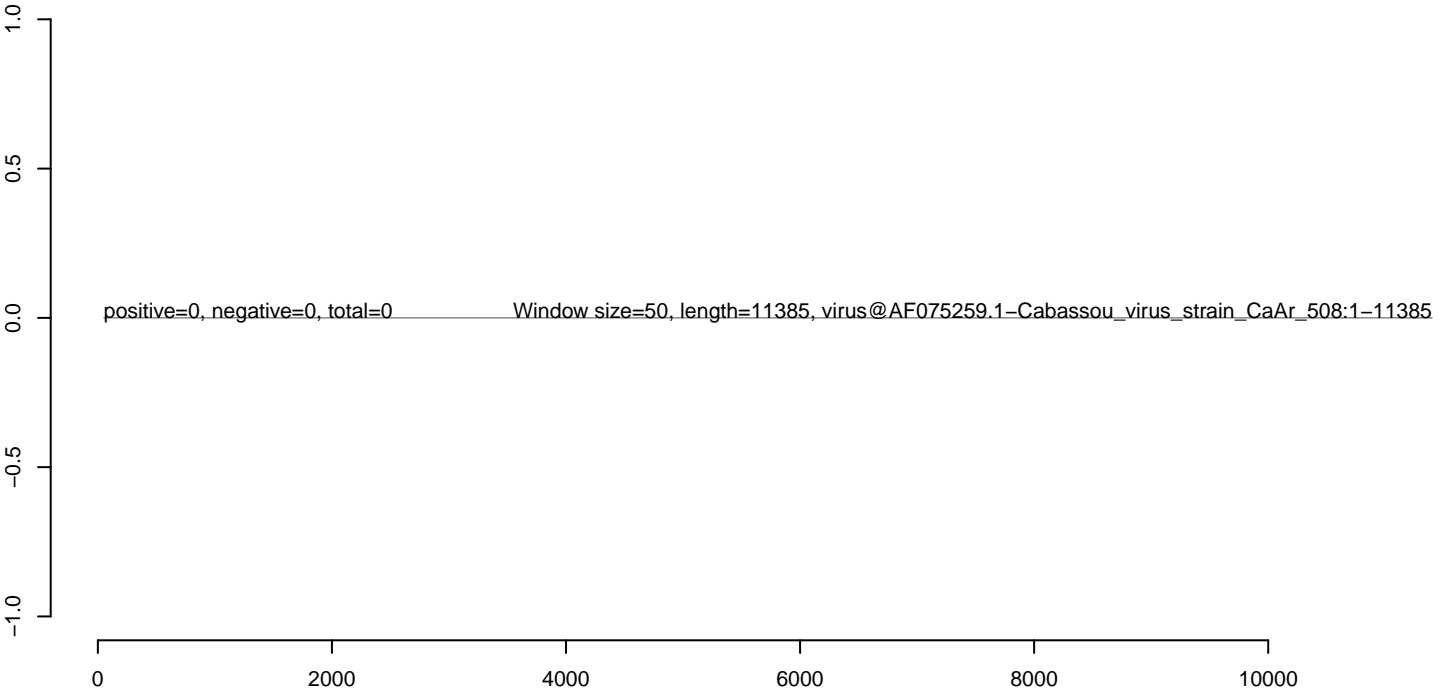
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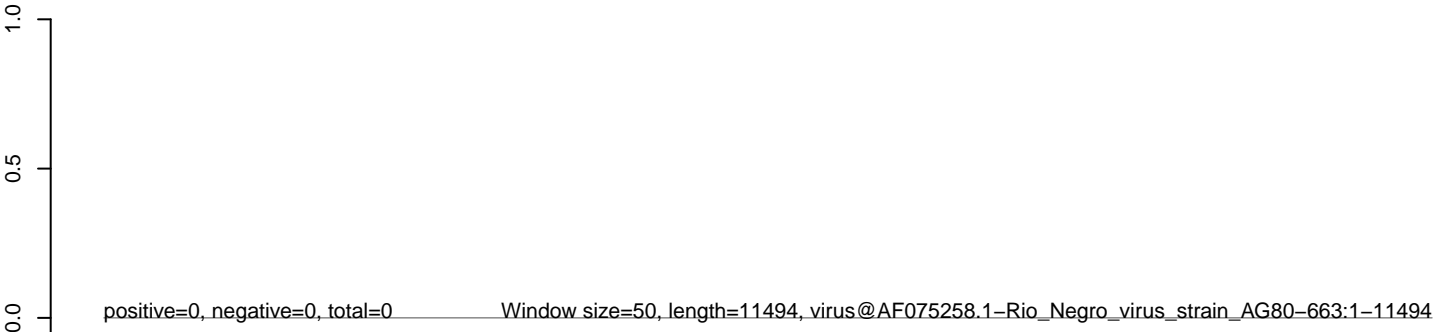
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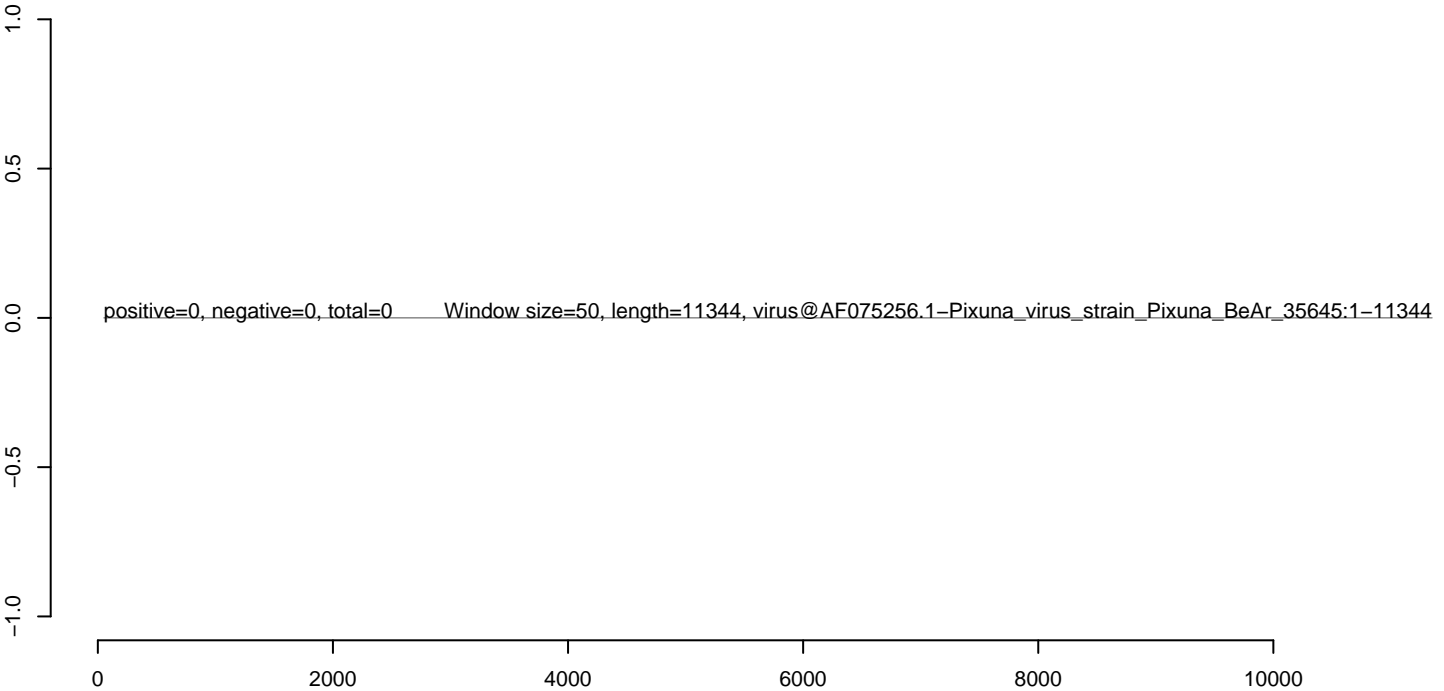
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