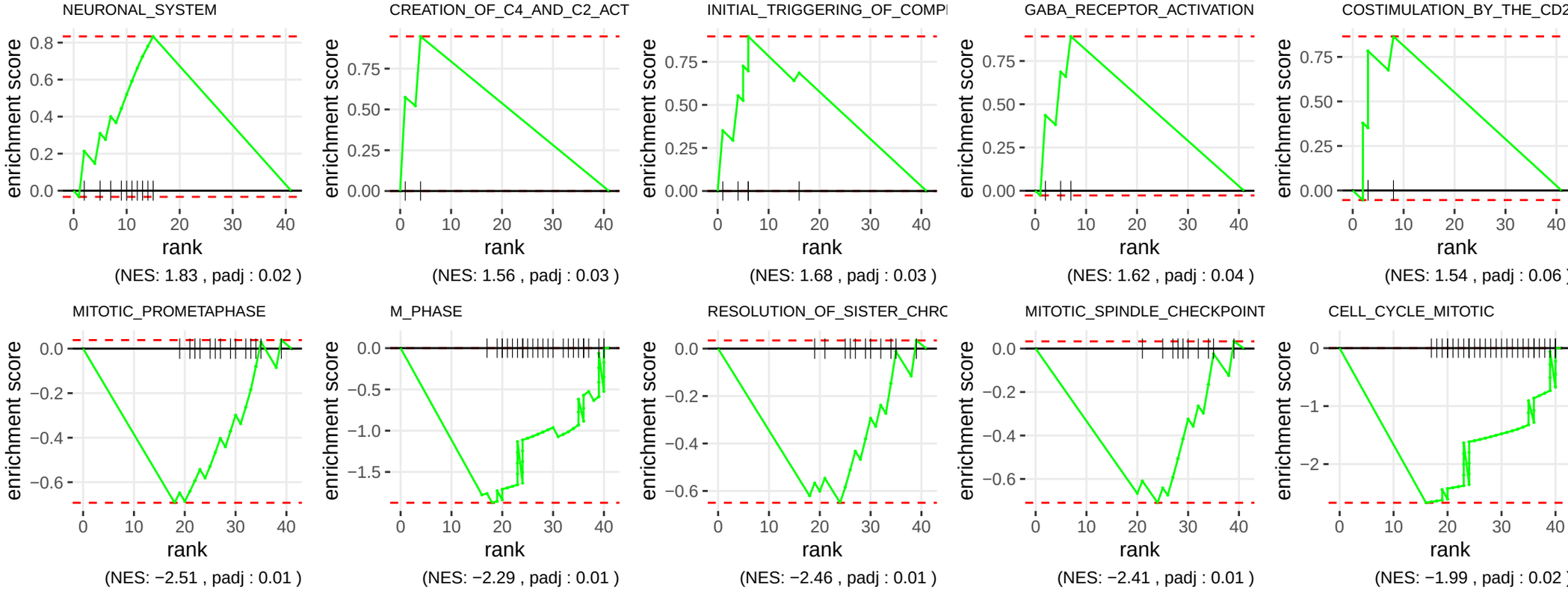
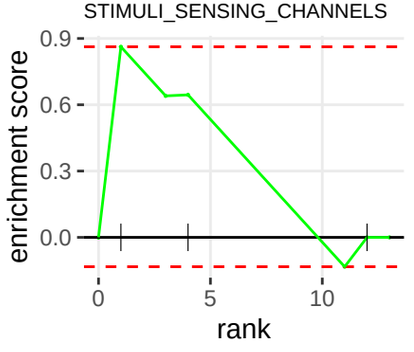
D7 ECs : Top enriched Pathways (GSEA), Old vs Young

Pathway	Gene ranks	NES	pval	padj
REACTOME_NEURONAL_SYSTEM		1.83	2.7e−04	2.1e−02
REACTOME_CREATION_OF_C4_AND_C2_ACTIVATORS		1.56	4.7e−04	2.8e−02
REACTOME_INITIAL_TRIGGERING_OF_COMPLEMENT		1.68	6.3e−04	3.5e−02
REACTOME_GABA_RECEPTOR_ACTIVATION		1.62	7.8e−04	3.9e−02
REACTOME_COSTIMULATION_BY_THE_CD28_FAMILY		1.54	1.6e−03	5.5e−02
REACTOME_CELL_CYCLE_MITOTIC		−1.99	1.9e−04	2.1e−02
REACTOME_MITOTIC_SPINDLE_CHECKPOINT		−2.41	1.0e−04	1.4e−02
REACTOME_RESOLUTION_OF_SISTER_CHROMATID_COHESION		−2.46	4.8e−05	8.7e−03
REACTOME_M_PHASE		−2.29	2.9e−05	8.0e−03
REACTOME_MITOTIC_PROMETAPHASE		−2.51	2.7e−05	8.0e−03

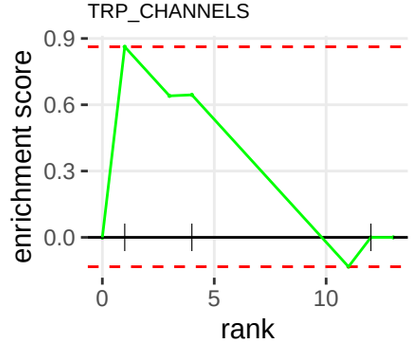


D7 FAPs : Top enriched Pathways (GSEA), Old vs Young

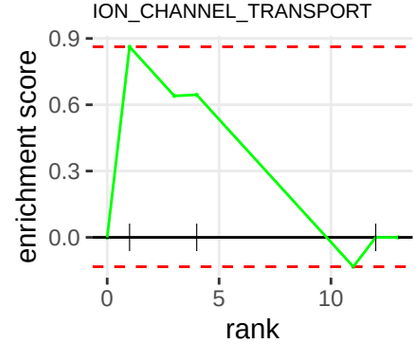
Pathway	Gene ranks	NES	pval	padj
REACTOME_STIMULI_SENSING_CHANNELS		1.82	1.8e−03	4.8e−01
REACTOME_TRP_CHANNELS		1.76	3.3e−03	4.8e−01
REACTOME_ION_CHANNEL_TRANSPORT		1.61	1.8e−02	5.3e−01
REACTOME_ACTIVATION_OF_BH3_ONLY_PROTEINS		1.46	3.8e−02	5.5e−01
REACTOME_ARACHIDONIC_ACID_METABOLISM		1.53	4.4e−02	5.5e−01
REACTOME_DNA_DAMAGE_TELOMERE_STRESS_INDUCED_SENESCENCE		−1.62	1.5e−02	4.8e−01
REACTOME_DEPOSITION_OF_NEW_CENPA_CONTAINING_NUCLEOSOMES_AT_THE_CENTROMERE		−1.62	1.5e−02	4.8e−01
REACTOME_CONDENSATION_OF_PROPHASE_CHROMOSOMES		−1.62	1.5e−02	4.8e−01
REACTOME_CHROMOSOME_MAINTENANCE		−1.62	1.5e−02	4.8e−01
REACTOME_BASE_EXCISION_REPAIR_AP_SITE_FORMATION		−1.62	1.5e−02	4.8e−01



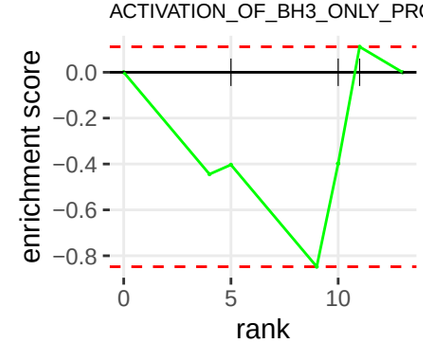
(NES: 1.82 , padj : 0.48)



(NES: 1.76 , padj : 0.48)



(NES: 1.61 , padj : 0.53)



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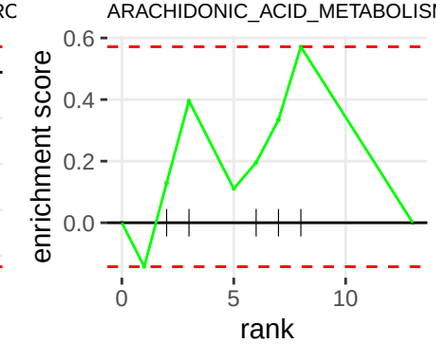

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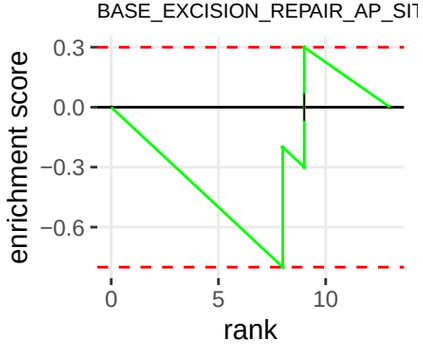
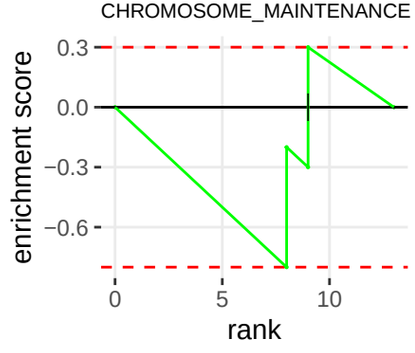
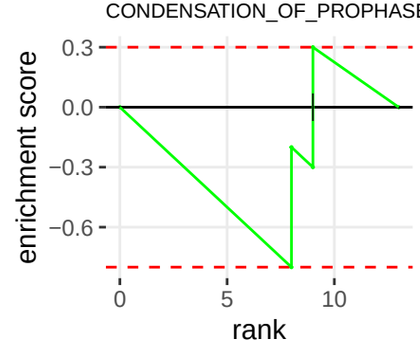


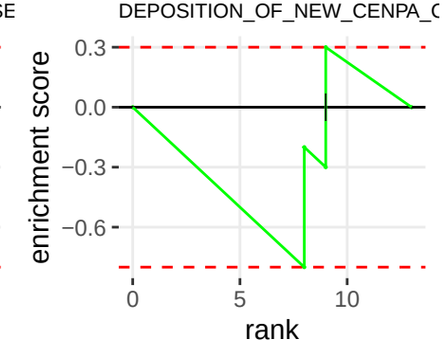
(NES: −1.62 , padj : 0.48)



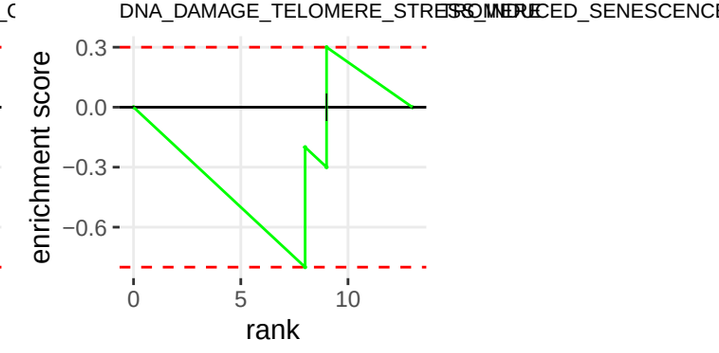
(NES: −1.62 , padj : 0.48)



(NES: −1.62 , padj : 0.48)



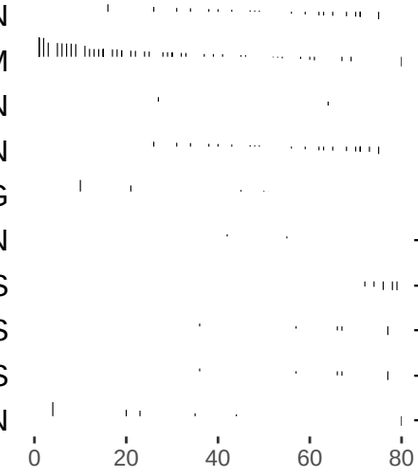
(NES: −1.62 , padj : 0.48)

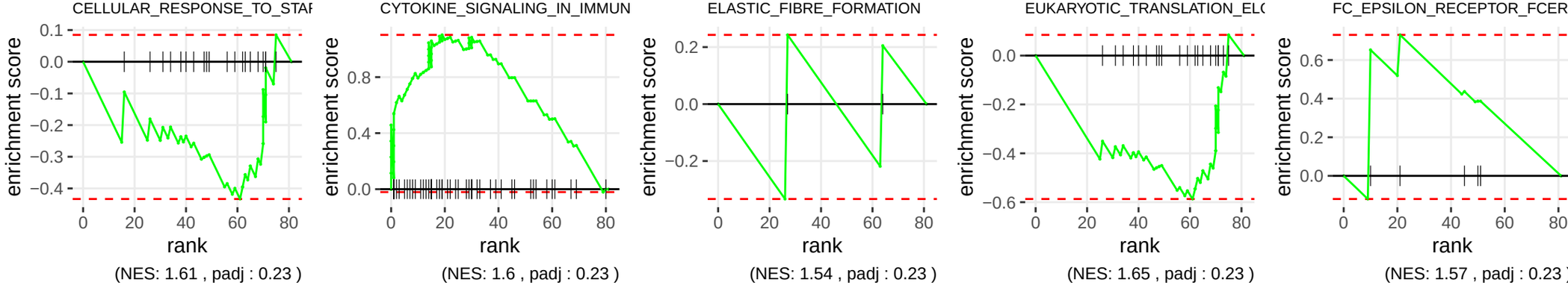


(NES: −1.62 , padj : 0.48)

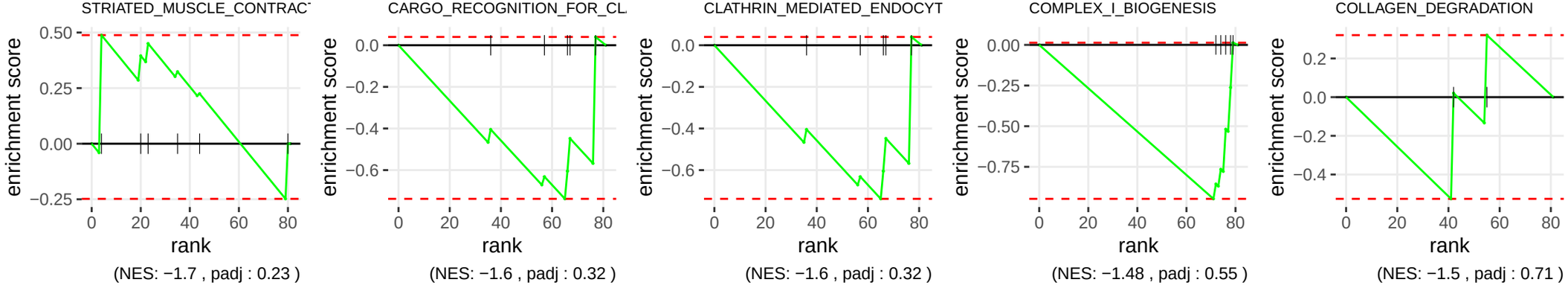
D7 M2 : Top enriched Pathways (GSEA), Old vs Young

Pathway	Gene ranks	NES	pval	padj
REACTOME_CELLULAR_RESPONSE_TO_STARVATION		1.61	6.8e−03	2.3e−01
REACTOME_CYTOKINE_SIGNALING_IN_IMMUNE_SYSTEM		1.60	1.9e−03	2.3e−01
REACTOME_ELASTIC_FIBRE_FORMATION		1.54	3.8e−03	2.3e−01
REACTOME_EUKARYOTIC_TRANSLATION_ELONGATION		1.65	3.8e−03	2.3e−01
REACTOME_FC_EPSILON_RECEPTOR_FCERI_SIGNALING		1.57	7.0e−03	2.3e−01
REACTOME_COLLAGEN_DEGRADATION		−1.50	3.2e−02	7.1e−01
REACTOME_COMPLEX_I_BIOGENESIS		−1.48	2.4e−02	5.5e−01
REACTOME_CLATHRIN_MEDIATED_ENDOCYTOSIS		−1.60	1.2e−02	3.2e−01
REACTOME_CARGO_RECOGNITION_FOR_CLATHRIN_MEDIATED_ENDOCYTOSIS		−1.60	1.2e−02	3.2e−01
REACTOME_STRIATED_MUSCLE_CONTRACTION		−1.70	4.7e−03	2.3e−01





(NES: 1.61 , padj : 0.23) (NES: 1.6 , padj : 0.23) (NES: 1.54 , padj : 0.23) (NES: 1.65 , padj : 0.23) (NES: 1.57 , padj : 0.23)



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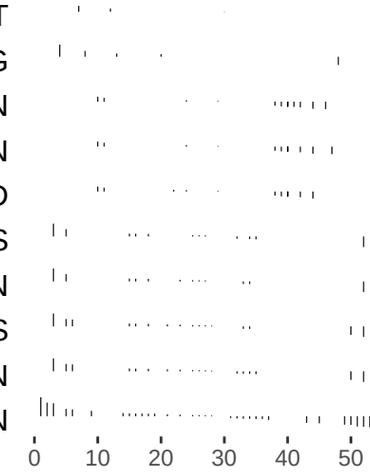
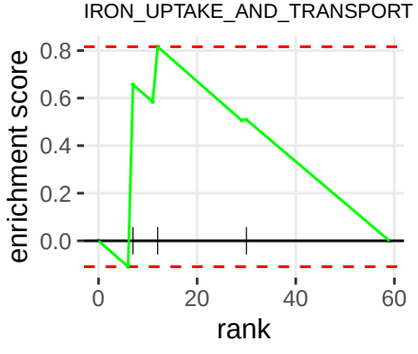
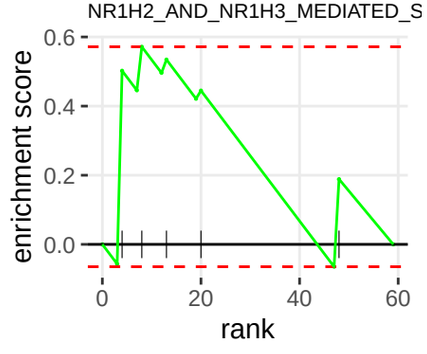
D7 sCs : Top enriched Pathways (GSEA), Old vs Young

Pathway	Gene ranks	NES	pval	padj
REACTOME_IRON_UPTAKE_AND_TRANSPORT		1.66	1.9e−02	4.4e−01
REACTOME_NR1H2_AND_NR1H3_MEDIATED_SIGNALING		1.75	3.0e−02	5.3e−01
REACTOME_EUKARYOTIC_TRANSLATION_ELONGATION		1.67	3.7e−02	5.5e−01
REACTOME_EUKARYOTIC_TRANSLATION_INITIATION		1.59	3.4e−02	5.5e−01
REACTOME_NONSENSE_MEDIATED_DECAY_NMD		1.59	3.4e−02	5.5e−01
REACTOME_ASSEMBLY_OF_COLLAGEN_FIBRILS_AND_OTHER_MULTIMERIC_STRUCTURES		−2.18	1.5e−04	1.7e−02
REACTOME_COLLAGEN_CHAIN_TRIMERIZATION		−2.27	2.3e−05	3.3e−03
REACTOME_COLLAGEN_BIOSYNTHESIS_AND_MODIFYING_ENZYMES		−2.38	8.7e−06	1.6e−03
REACTOME_COLLAGEN_FORMATION		−2.44	3.1e−07	8.8e−05
REACTOME_EXTRACELLULAR_MATRIX_ORGANIZATION		−2.45	6.5e−09	3.7e−06





(NES: 1.66 , padj : 0.44)



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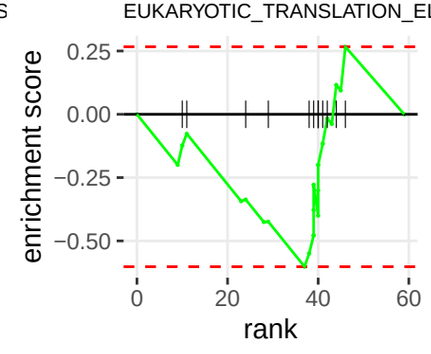
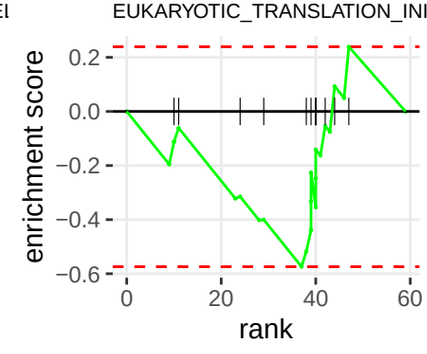
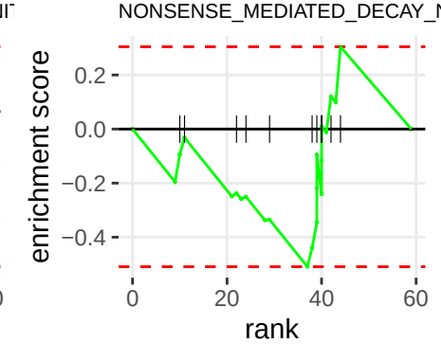


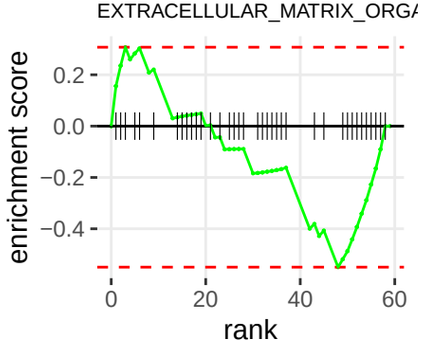
(NES: 1.67 , padj : 0.55)



(NES: 1.59 , padj : 0.55)



(NES: 1.59 , padj : 0.55)



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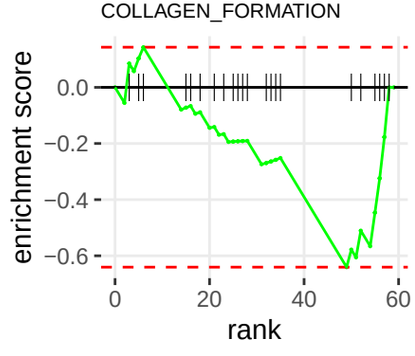
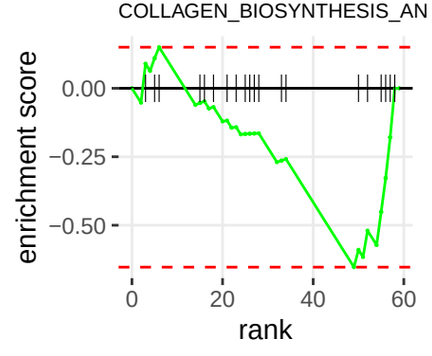


(NES: −2.44 , padj : 0)



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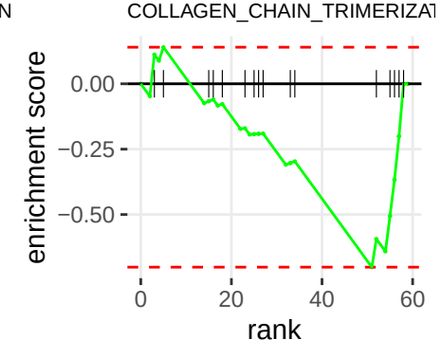
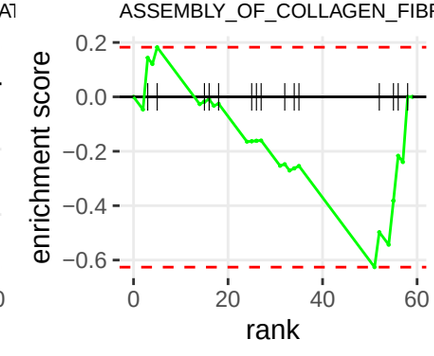


(NES: −2.27 , padj : 0)



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