









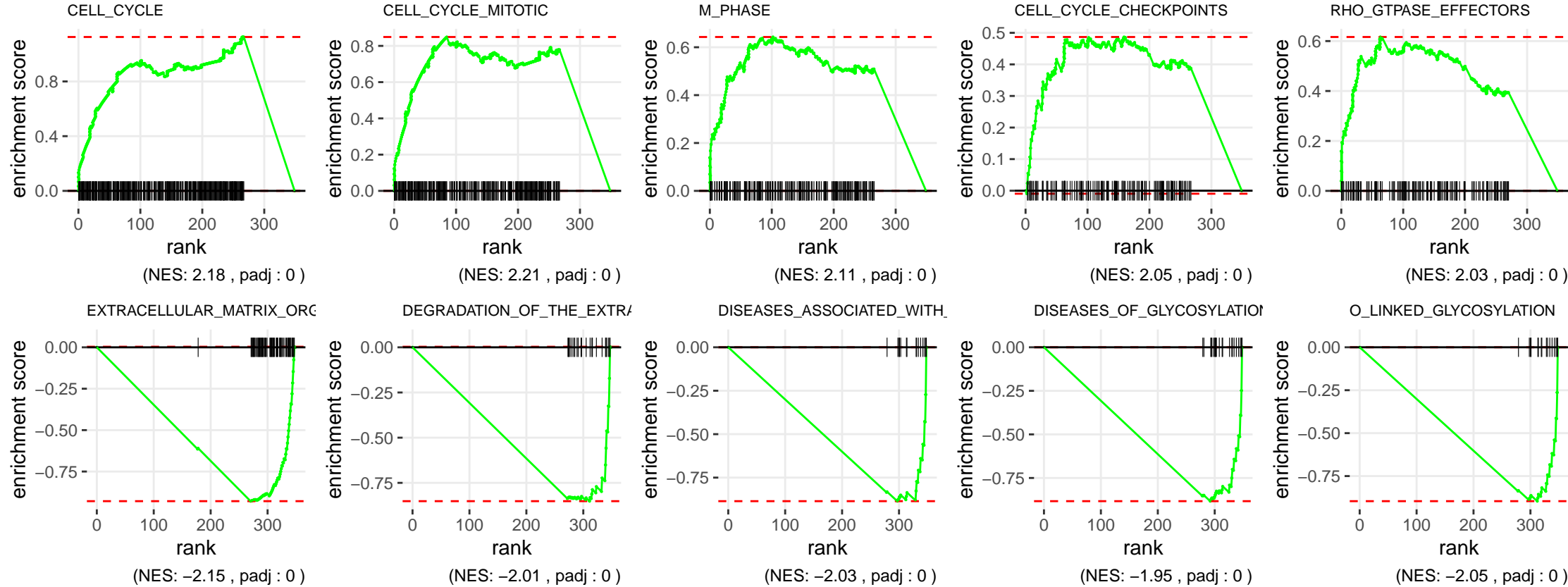


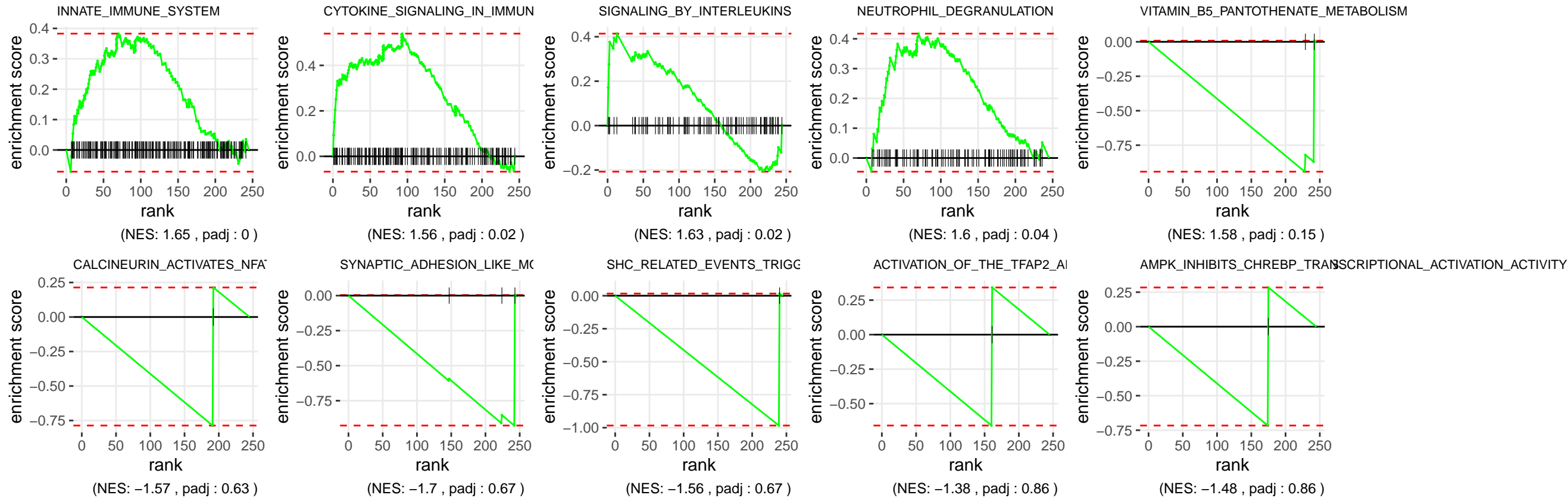
D4 ECs : Top enriched Pathways (GSEA), Old vs Young

Pathway	Gene ranks	NES	pval	padj
REACTOME_CELL_CYCLE		2.18	9.0e-27	1.4e-23
REACTOME_CELL_CYCLE_MITOTIC		2.21	1.8e-23	1.4e-20
REACTOME_M_PHASE		2.11	9.6e-15	4.9e-12
REACTOME_CELL_CYCLE_CHECKPOINTS		2.05	5.1e-10	1.3e-07
REACTOME_RHO_GTPASE_EFFECTORS		2.03	5.1e-10	1.3e-07
REACTOME_O_LINKED_GLYCOSYLATION		-2.05	1.6e-06	1.2e-04
REACTOME_DISEASES_OF_GLYCOSYLATION		-1.95	1.5e-06	1.2e-04
REACTOME_DISEASES_ASSOCIATED_WITH_O_GLYCOSYLATION_OF_PROTEINS		-2.03	6.4e-07	6.8e-05
REACTOME_DEGRADATION_OF_THE_EXTRACELLULAR_MATRIX		-2.01	4.3e-07	6.1e-05
REACTOME_EXTRACELLULAR_MATRIX_ORGANIZATION		-2.15	1.0e-11	4.0e-09

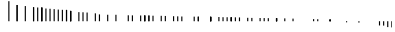











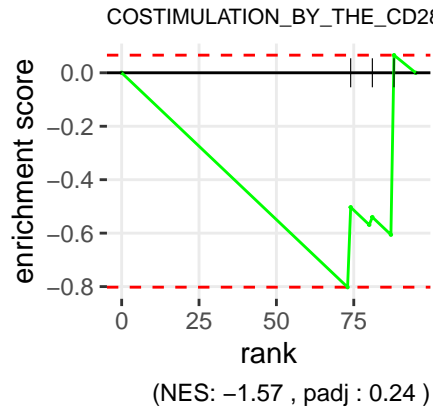
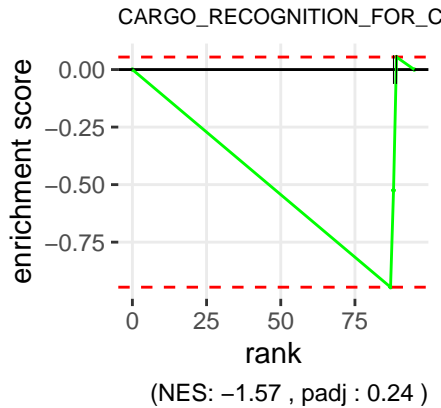
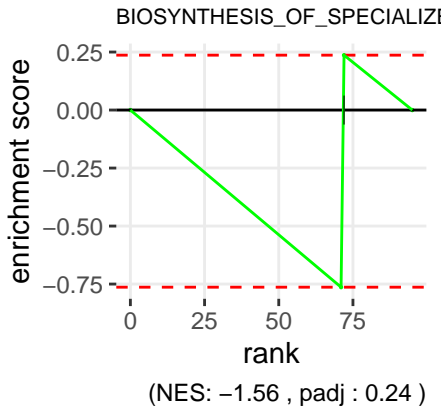
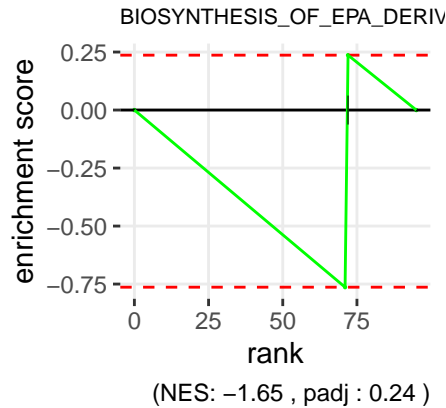
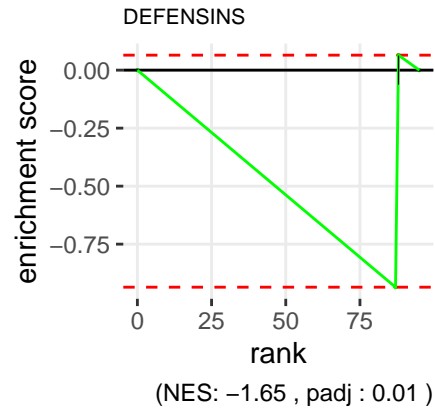
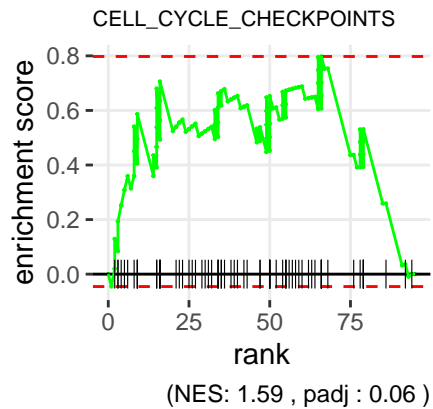
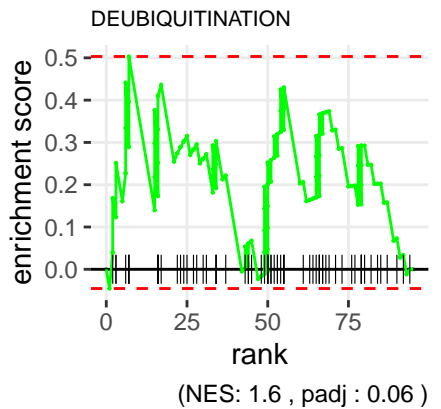
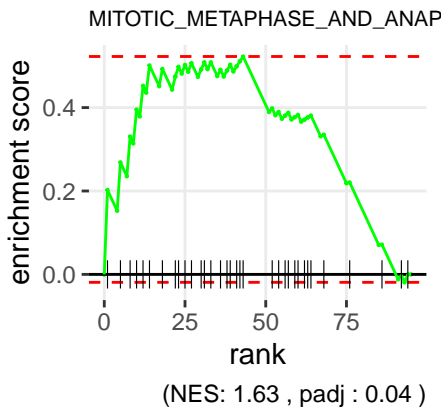
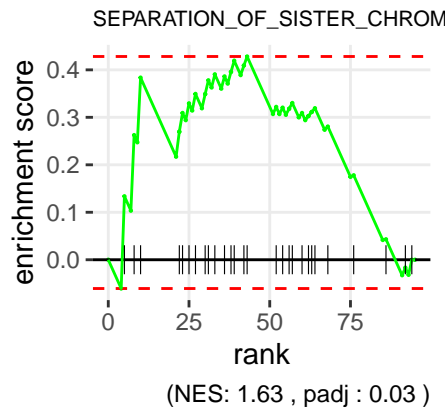
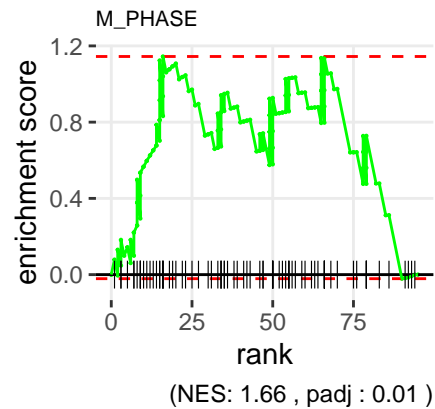
D4 FAPs : Top enriched Pathways (GSEA), Old vs Young

Pathway	Gene ranks	NES	pval	padj
REACTOME_INNATE_IMMUNE_SYSTEM		1.65	4.9e-09	7.8e-06
REACTOME_CYTOKINE_SIGNALING_IN_IMMUNE_SYSTEM		1.56	3.7e-05	2.0e-02
REACTOME_SIGNALING_BY_INTERLEUKINS		1.63	2.9e-05	2.0e-02
REACTOME_NEUTROPHIL_DEGRANULATION		1.60	1.0e-04	4.0e-02
REACTOME_VITAMIN_B5_PANTOTHENATE_METABOLISM		1.58	4.7e-04	1.5e-01
REACTOME_AMPK_INHIBITS_CHREBP_TRANSCRIPTIONAL_ACTIVATION_ACTIVITY		-1.48	7.6e-02	8.6e-01
REACTOME_ACTIVATION_OF_THE_TFAP2_AP_2_FAMILY_OF_TRANSCRIPTION_FACTORS		-1.38	1.1e-01	8.6e-01
REACTOME_SHC_RELATED_EVENTS_TRIGGERED_BY_IGF1R		-1.56	1.1e-02	6.7e-01
REACTOME_SYNAPTIC_ADHESION_LIKE_MOLECULES		-1.70	1.1e-02	6.7e-01
REACTOME_CALCINEURIN_ACTIVATES_NFAT		-1.57	9.4e-03	6.3e-01



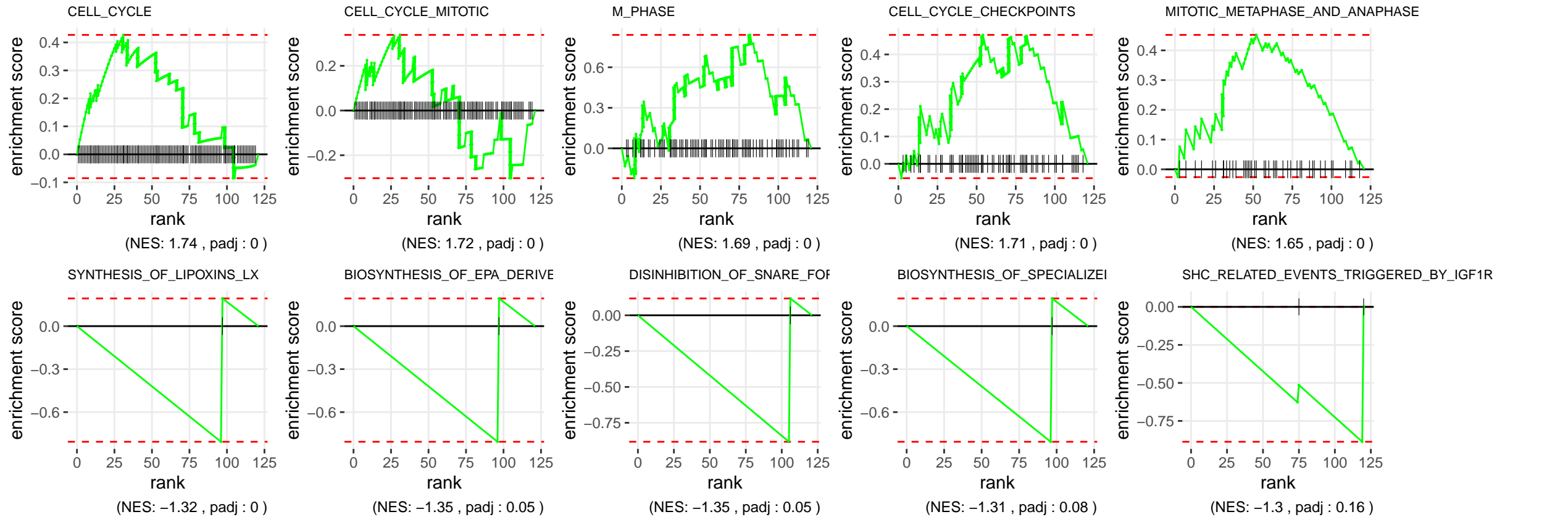
D4 M1 : Top enriched Pathways (GSEA), Old vs Young

	Pathway	Gene ranks	NES	pval	padj
	REACTOME_M_PHASE		1.66	4.6e-06	7.1e-03
	REACTOME_SEPARATION_OF_SISTER_CHROMATIDS		1.63	6.7e-05	3.4e-02
	REACTOME_MITOTIC_METAPHASE_AND_ANAPHASE		1.63	1.1e-04	4.3e-02
	REACTOME_DEUBIQUITINATION		1.60	2.0e-04	6.2e-02
	REACTOME_CELL_CYCLE_CHECKPOINTS		1.59	4.1e-04	6.4e-02
	REACTOME_COSTIMULATION_BY_THE_CD28_FAMILY		-1.57	3.7e-03	2.4e-01
	REACTOME_CARGO_RECOGNITION_FOR_CLATHRIN_MEDIATED_ENDOCYTOSIS		-1.57	2.9e-03	2.4e-01
	REACTOME_BIOSYNTHESIS_OF_SPECIALIZED_PRORESOLVING_MEDIATORS_SPMS		-1.56	2.6e-03	2.4e-01
	REACTOME_BIOSYNTHESIS_OF_EPA_DERIVED_SPMS		-1.65	3.3e-03	2.4e-01
	REACTOME_DEFENSINS		-1.65	9.6e-06	7.4e-03
		0255075			













D4 M2 : Top enriched Pathways (GSEA), Old vs Young

Pathway	Gene ranks	NES	pval	padj
REACTOME_CELL_CYCLE		1.74	2.7e-11	4.2e-08
REACTOME_CELL_CYCLE_MITOTIC		1.72	2.4e-09	1.9e-06
REACTOME_M_PHASE		1.69	9.0e-08	4.7e-05
REACTOME_CELL_CYCLE_CHECKPOINTS		1.71	2.8e-07	1.1e-04
REACTOME_MITOTIC_METAPHASE_AND_ANAPHASE		1.65	1.9e-05	5.0e-03
REACTOME_SHC_RELATED_EVENTS_TRIGGERED_BY_IGF1R		-1.30	7.4e-03	1.6e-01
REACTOME_BIOSYNTHESIS_OF_SPECIALIZED_PRORESOLVING_MEDIATORS_SPMS		-1.31	1.4e-03	8.1e-02
REACTOME_DISINHIBITION_OF_SNARE_FORMATION		-1.35	5.2e-04	4.6e-02
REACTOME_BIOSYNTHESIS_OF_EPA_DERIVED_SPMS		-1.35	5.3e-04	4.6e-02
REACTOME_SYNTHESIS_OF_LIPOXINS_LX		-1.32	3.3e-06	1.0e-03



D4 sCs : Top enriched Pathways (GSEA), Old vs Young

Pathway	Gene ranks	NES	pval	padj
REACTOME_CELL_CYCLE		2.31	4.1e-35	6.3e-32
REACTOME_CELL_CYCLE_MITOTIC		2.30	1.4e-30	1.0e-27
REACTOME_M_PHASE		2.31	2.6e-26	1.3e-23
REACTOME_CELL_CYCLE_CHECKPOINTS		2.31	2.2e-22	8.6e-20
REACTOME_METABOLISM_OF_RNA		2.00	5.6e-17	1.7e-14
REACTOME_DEGRADATION_OF_THE_EXTRACELLULAR_MATRIX		-2.16	3.4e-08	9.6e-07
REACTOME_COLLAGEN_FORMATION		-2.14	1.9e-08	5.8e-07
REACTOME_COLLAGEN_BIOSYNTHESIS_AND_MODIFYING_ENZYMES		-2.16	1.7e-08	5.3e-07
REACTOME_ECM_PROTEOGLYCANs		-2.20	1.9e-11	1.9e-09
REACTOME_EXTRACELLULAR_MATRIX_ORGANIZATION		-2.28	2.5e-14	4.3e-12

