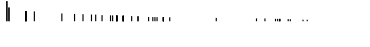
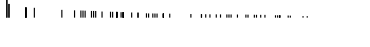
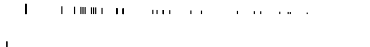

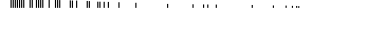





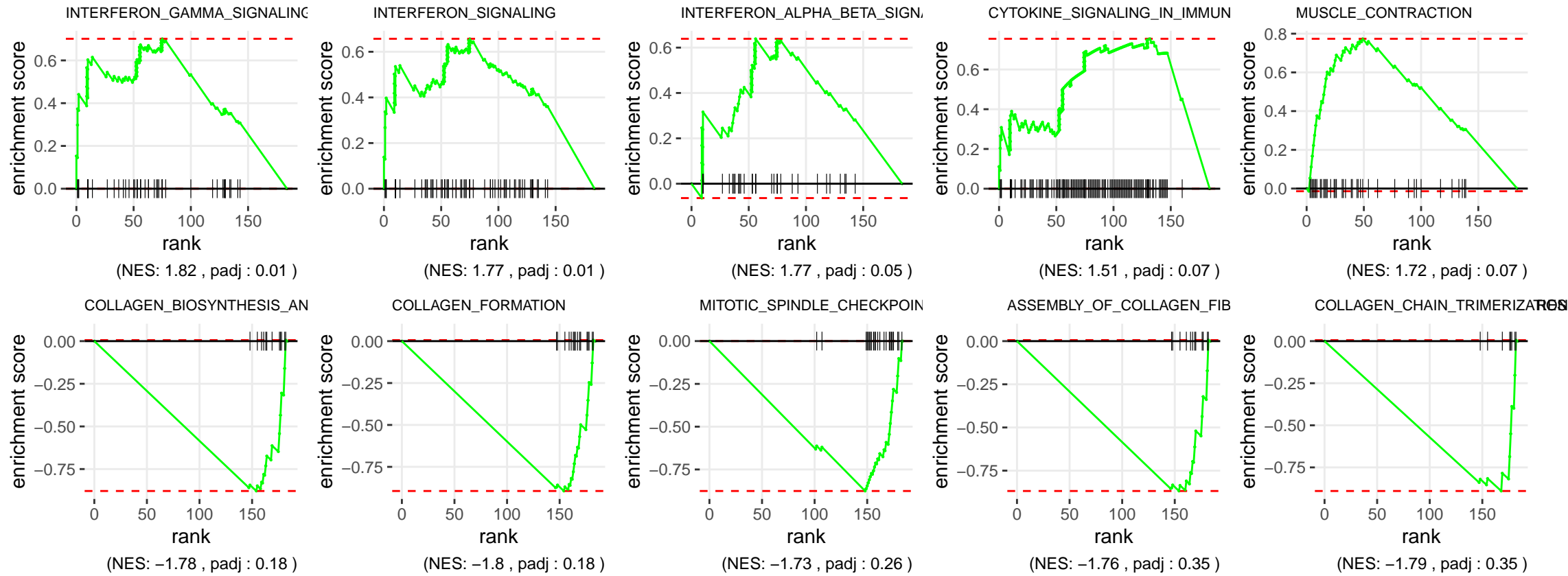


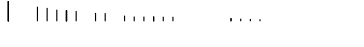









D7 ECs : Top enriched Pathways (GSEA), Old vs Young

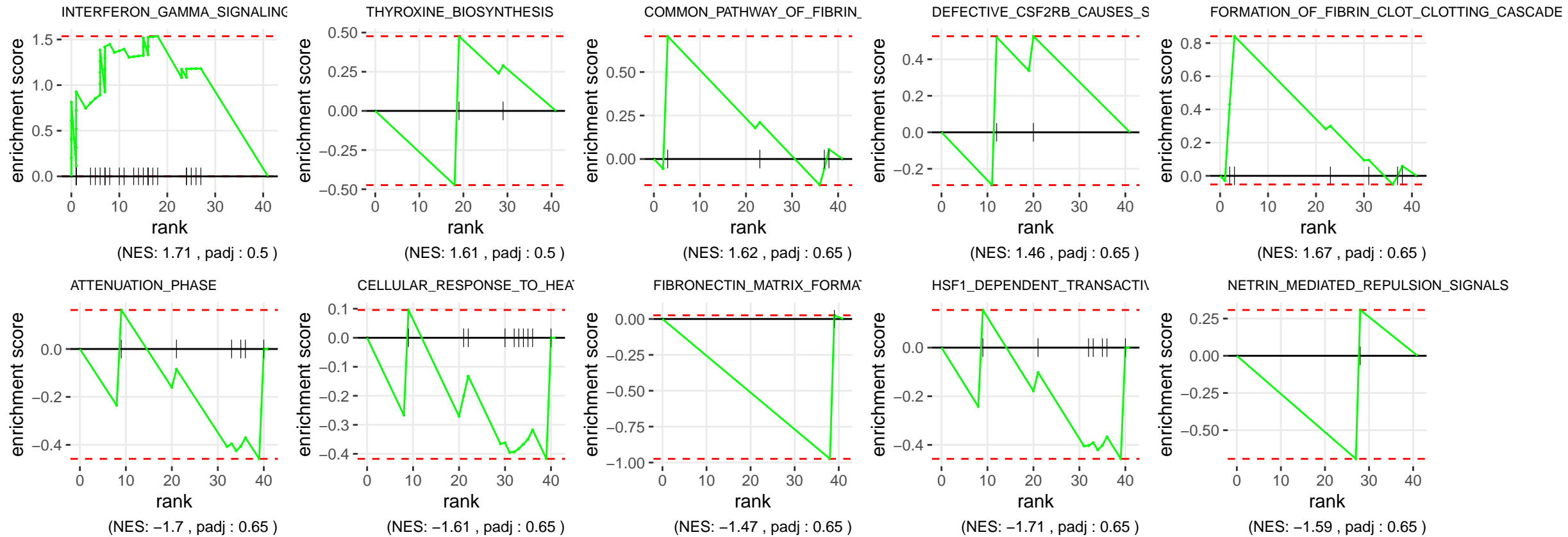
	Pathway	Gene ranks	NES	pval	padj
	REACTOME_INTERFERON_GAMMA_SIGNALING		1.82	1.4e-05	1.2e-02
	REACTOME_INTERFERON_SIGNALING		1.77	1.5e-05	1.2e-02
	REACTOME_INTERFERON_ALPHA_BETA_SIGNALING		1.77	9.3e-05	4.9e-02
	REACTOME_CYTOKINE_SIGNALING_IN_IMMUNE_SYSTEM		1.51	2.1e-04	7.0e-02
	REACTOME_MUSCLE_CONTRACTION		1.72	2.2e-04	7.0e-02
	REACTOME_COLLAGEN_CHAIN_TRIMERIZATION		-1.79	6.1e-03	3.5e-01
	REACTOME_ASSEMBLY_OF_COLLAGEN_FIBRILS_AND_OTHER_MULTIMERIC_STRUCTURES		-1.76	5.3e-03	3.5e-01
	REACTOME_MITOTIC_SPINDLE_CHECKPOINT		-1.73	3.1e-03	2.6e-01
	REACTOME_COLLAGEN_FORMATION		-1.80	1.3e-03	1.8e-01
	REACTOME_COLLAGEN_BIOSYNTHESIS_AND_MODIFYING_ENZYMES		-1.78	1.5e-03	1.8e-01

0 50 100 150

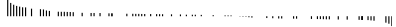
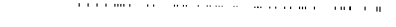







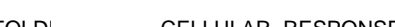


D7 FAPs : Top enriched Pathways (GSEA), Old vs Young

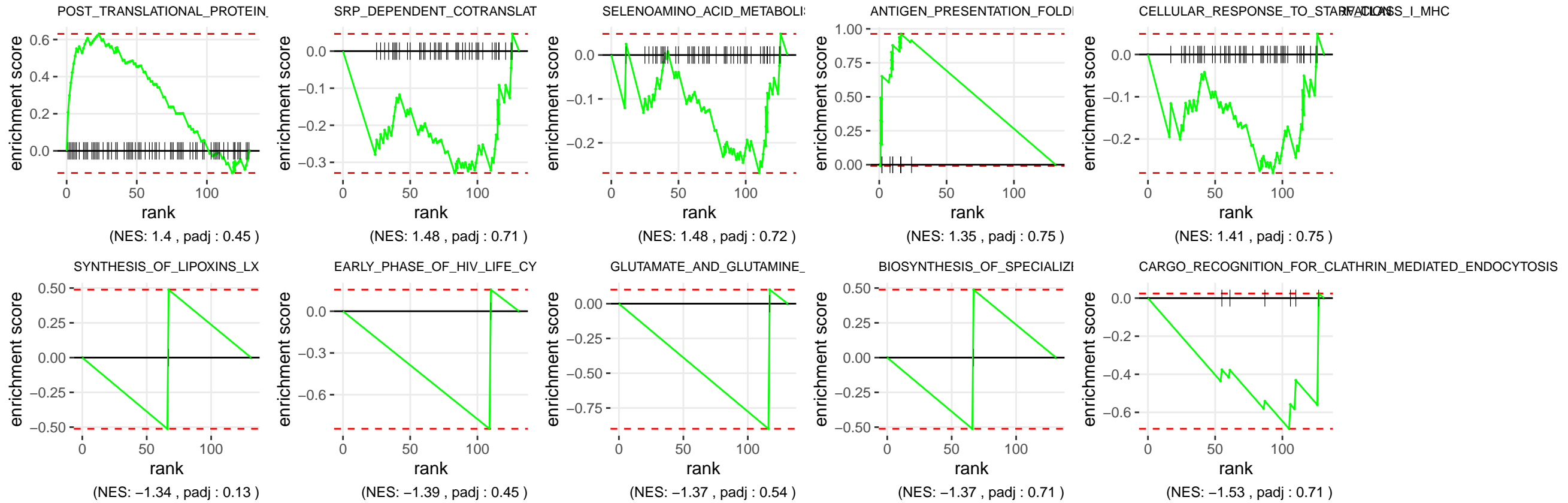
Pathway	Gene ranks	NES	pval	padj
REACTOME_INTERFERON_GAMMA_SIGNALING		1.71	6.3e-04	5.0e-01
REACTOME_THYROXINE_BIOSYNTHESIS		1.61	5.2e-04	5.0e-01
REACTOME_COMMON_PATHWAY_OF_FIBRIN_CLOT_FORMATION		1.62	7.0e-03	6.5e-01
REACTOME_DEFECTIVE_CSF2RB_CAUSES_SMDP5		1.46	7.7e-03	6.5e-01
REACTOME_FORMATION_OF_FIBRIN_CLOT_CLOTTING_CASCADE		1.67	3.0e-03	6.5e-01
REACTOME_NETRIN_MEDIATED_REPULSION_SIGNALS		-1.59	7.7e-03	6.5e-01
REACTOME_HSF1_DEPENDENT_TRANSACTIVATION		-1.71	4.2e-03	6.5e-01
REACTOME_FIBRONECTIN_MATRIX_FORMATION		-1.47	6.3e-03	6.5e-01
REACTOME_CELLULAR_RESPONSE_TO_HEAT_STRESS		-1.61	6.1e-03	6.5e-01
REACTOME_ATTENUATION_PHASE		-1.70	6.4e-03	6.5e-01



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

	Pathway	Gene ranks	NES	pval	padj
	REACTOME_POST_TRANSLATIONAL_PROTEIN_MODIFICATION		1.40	6.7e-04	4.5e-01
	REACTOME_SRP_DEPENDENT_COTRANSLATIONAL_PROTEIN_TARGETING_TO_MEMBRANE		1.48	4.2e-03	7.1e-01
	REACTOME_SELENOAMINO_ACID_METABOLISM		1.48	5.2e-03	7.2e-01
	REACTOME_ANTIGEN_PRESENTATION_FOLDING_ASSEMBLY_AND_PEPTIDE_LOADING_OF_CLASS_I_MHC		1.35	1.7e-02	7.5e-01
	REACTOME_CELLULAR_RESPONSE_TO_STARVATION		1.41	2.3e-02	7.5e-01
	REACTOME_CARGO_RECOGNITION_FOR_CLATHRIN_MEDIATED_ENDOCYTOSIS		-1.53	2.9e-03	7.1e-01
	REACTOME_BIOSYNTHESIS_OF_SPECIALIZED_PRORESOLVING_MEDIATORS_SPMS		-1.37	3.7e-03	7.1e-01
	REACTOME_GLUTAMATE_AND_GLUTAMINE_METABOLISM		-1.37	1.4e-03	5.4e-01
	REACTOME_EARLY_PHASE_OF_HIV_LIFE_CYCLE		-1.39	8.8e-04	4.5e-01
	REACTOME_SYNTHESIS_OF_LIPOXINS_LX		-1.34	8.3e-05	1.3e-01

0 25 50 75 100 125



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

Pathway	Gene ranks	NES	pval	padj
REACTOME_NONSENSE_MEDIATED_DECAY_NMD		1.94	5.1e-05	6.5e-03
REACTOME_EUKARYOTIC_TRANSLATION_ELONGATION		1.93	9.9e-05	1.1e-02
REACTOME_EUKARYOTIC_TRANSLATION_INITIATION		1.83	2.9e-04	2.5e-02
REACTOME_SELENOAMINO_ACID_METABOLISM		1.79	4.4e-04	3.4e-02
REACTOME_NR1H2_AND_NR1H3_MEDIATED_SIGNALING		1.81	1.3e-03	8.8e-02
REACTOME_ECM_PROTEOGLYCANS		-1.90	7.0e-07	2.7e-04
REACTOME_COLLAGEN_BIOSYNTHESIS_AND_MODIFYING_ENZYMES		-1.89	8.6e-07	2.7e-04
REACTOME_ASSEMBLY_OF_COLLAGEN_FIBRILS_AND_OTHER_MULTIMERIC_STRUCTURES		-1.89	6.8e-07	2.7e-04
REACTOME_COLLAGEN_FORMATION		-1.95	1.5e-08	1.2e-05
REACTOME_EXTRACELLULAR_MATRIX_ORGANIZATION		-1.98	3.5e-10	5.4e-07

