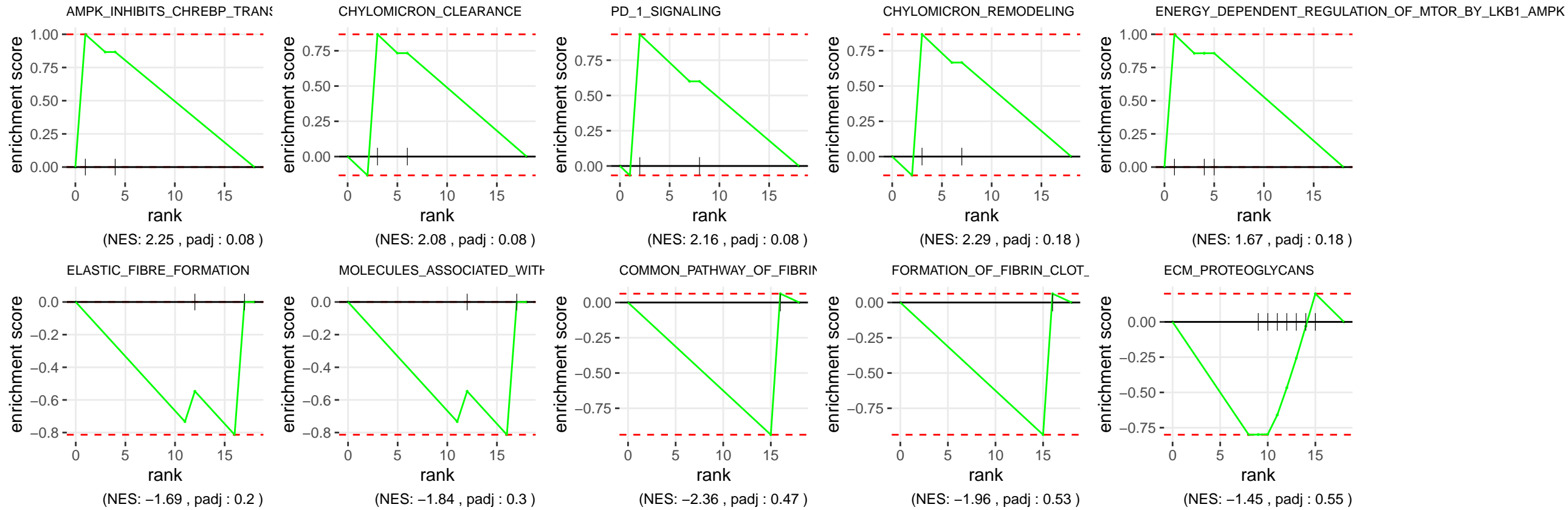


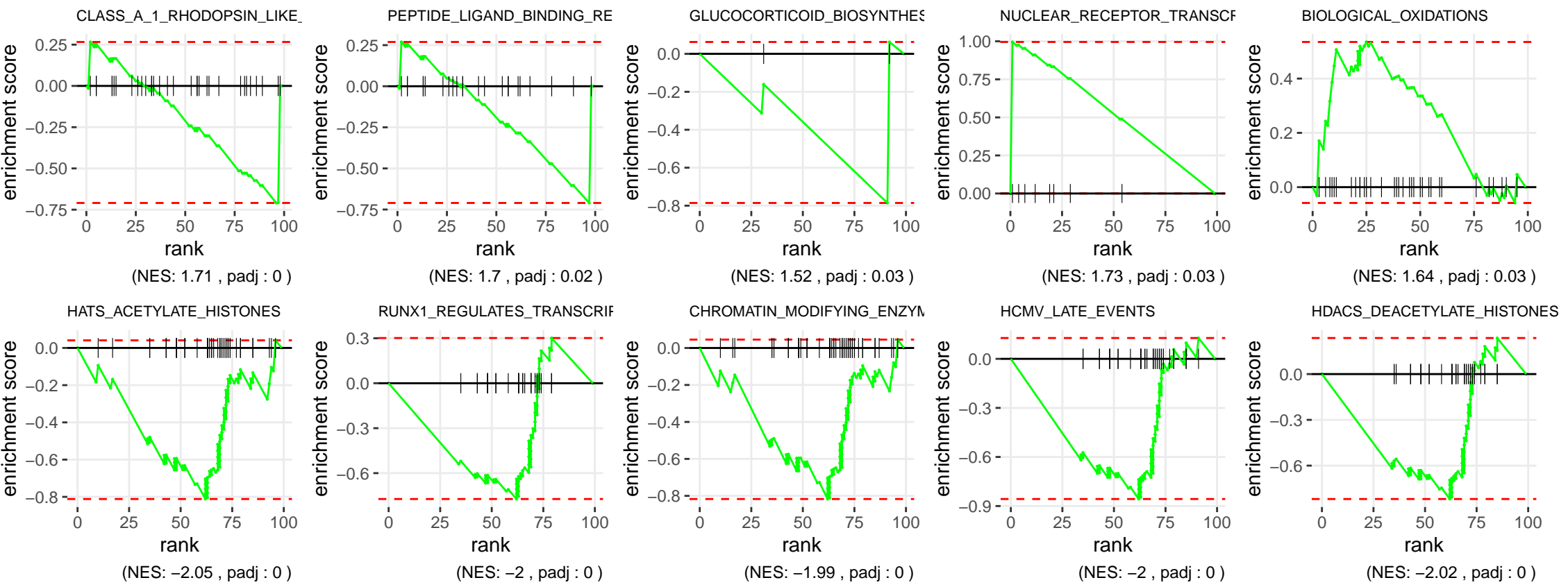
D2 ECs : Top enriched Pathways (GSEA), Old vs Young

Pathway	Gene ranks	NES	pval	padj
REACTOME_AMPK_INHIBITS_CHREBP_TRANSCRIPTIONAL_ACTIVATION_ACTIVITY		2.25	7.3e-05	7.7e-02
REACTOME_CHYLOMICRON_CLEARANCE		2.08	1.4e-04	7.7e-02
REACTOME_PD_1_SIGNALING		2.16	1.5e-04	7.7e-02
REACTOME_CHYLOMICRON_REMODELING		2.29	5.6e-04	1.8e-01
REACTOME_ENERGY_DEPENDENT_REGULATION_OF_MTOR_BY_LKB1_AMPK		1.67	5.4e-04	1.8e-01
REACTOME_ECM_PROTEOGLYCANS		-1.45	4.8e-03	5.5e-01
REACTOME_FORMATION_OF_FIBRIN_CLOT_CLOTTING_CASCADE		-1.96	4.3e-03	5.3e-01
REACTOME_COMMON_PATHWAY_OF_FIBRIN_CLOT_FORMATION		-2.36	2.9e-03	4.7e-01
REACTOME_MOLECULES_ASSOCIATED_WITH_ELASTIC_FIBRES		-1.84	1.3e-03	3.0e-01
REACTOME_ELASTIC_FIBRE_FORMATION		-1.69	7.5e-04	2.0e-01



D2 FAPs : Top enriched Pathways (GSEA), Old vs Young

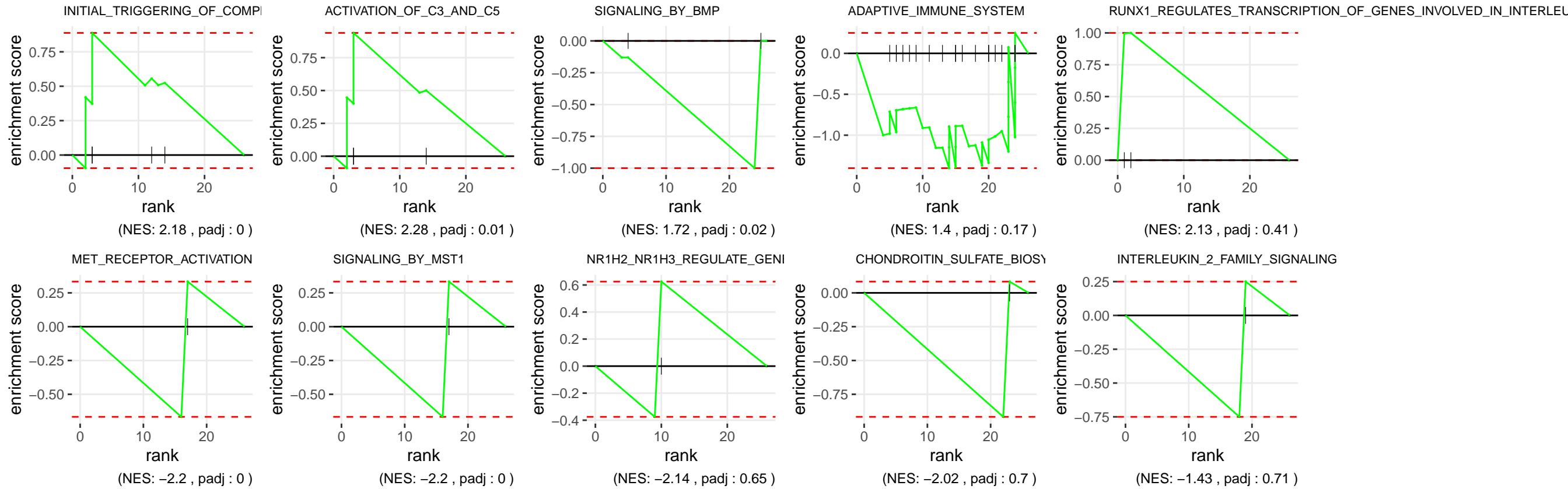
	Pathway	Gene ranks	NES	pval	padj
	REACTOME_CLASS_A_1_RHODOPSIN_LIKE_RECEPTORS	1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100	1.71	1.5e-04	4.4e-03
	REACTOME_PEPTIDE_LIGAND_BINDING_RECEPTORS	1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100	1.70	7.4e-04	1.8e-02
	REACTOME_GLUCOCORTICOID_BIOSYNTHESIS	1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100	1.52	1.3e-03	3.1e-02
	REACTOME_NUCLEAR_RECEPTOR_TRANSCRIPTION_PATHWAY	1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100	1.73	1.4e-03	3.2e-02
	REACTOME_BIOLOGICAL_OXIDATIONS	1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100	1.64	1.6e-03	3.5e-02
	REACTOME_HDACS_DEACETYLATE_HISTONES	1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100	-2.02	7.3e-08	3.8e-05
	REACTOME_HCMV_LATE_EVENTS	1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100	-2.00	1.2e-07	3.8e-05
	REACTOME_CHROMATIN_MODIFYING_ENZYMES	1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100	-1.99	9.7e-08	3.8e-05
	REACTOME_RUNX1_REGULATES_TRANSCRIPTION_OF_GENES_INVOLVED_IN_DIFFERENTIATION_OF_HSCS	1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100	-2.00	4.0e-08	3.2e-05
	REACTOME_HATS_ACETYLATE_HISTONES	1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100	-2.05	2.8e-09	4.4e-06



D2 M1 : Top enriched Pathways (GSEA), Old vs Young

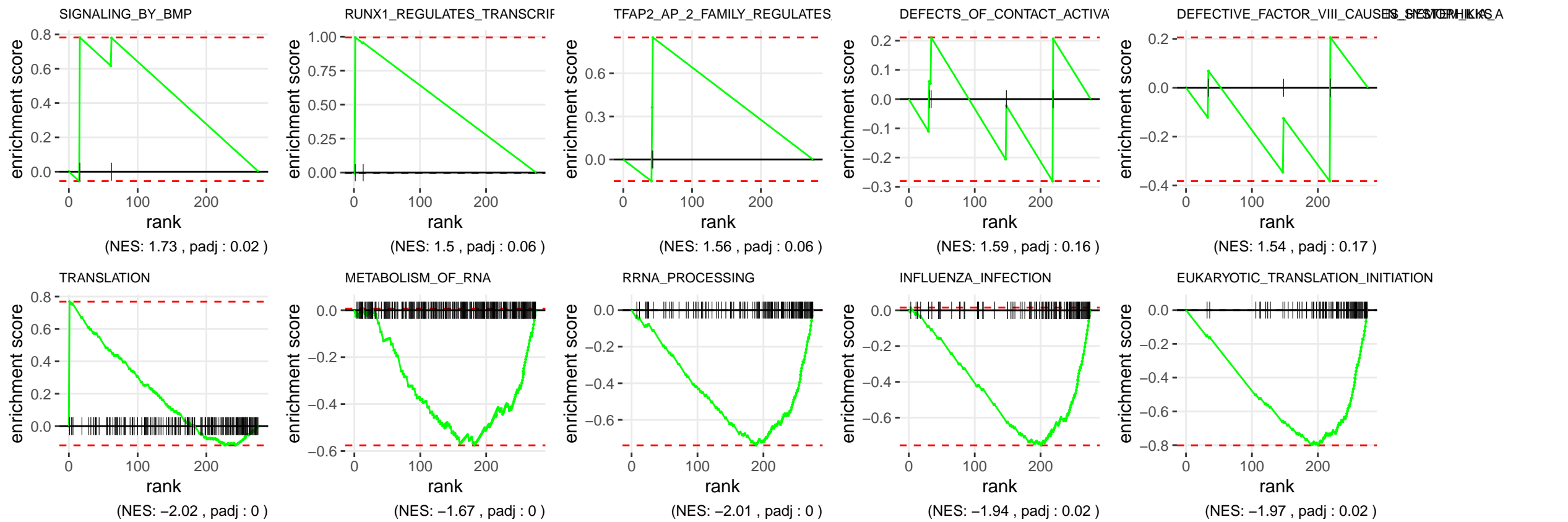
	Pathway	Gene ranks	NES	pval	padj
	REACTOME_INITIAL_TRIGGERING_OF_COMPLEMENT		2.18	4.0e-07	2.1e-04
	REACTOME_ACTIVATION_OF_C3_AND_C5		2.28	1.3e-05	5.3e-03
	REACTOME_SIGNALING_BY_BMP		1.72	5.4e-05	1.7e-02
	REACTOME_ADAPTIVE_IMMUNE_SYSTEM		1.40	6.6e-04	1.7e-01
REACTOME_RUNX1_REGULATES_TRANSCRIPTION_OF_GENES_INVOLVED_IN_INTERLEUKIN_SIGNALING			2.13	2.0e-03	4.1e-01
	REACTOME_INTERLEUKIN_2_FAMILY_SIGNALING		-1.43	8.2e-03	7.1e-01
	REACTOME_CHONDROITIN_SULFATE_BIOSYNTHESIS		-2.02	5.8e-03	7.0e-01
REACTOME_NR1H2_NR1H3_REGULATE_GENE_EXPRESSION_LINKED_TO_GLUONEOGENESIS			-2.14	4.5e-03	6.5e-01
	REACTOME_SIGNALING_BY_MST1		-2.20	1.1e-07	8.8e-05
	REACTOME_MET_RECEPTOR_ACTIVATION		-2.20	1.1e-07	8.8e-05

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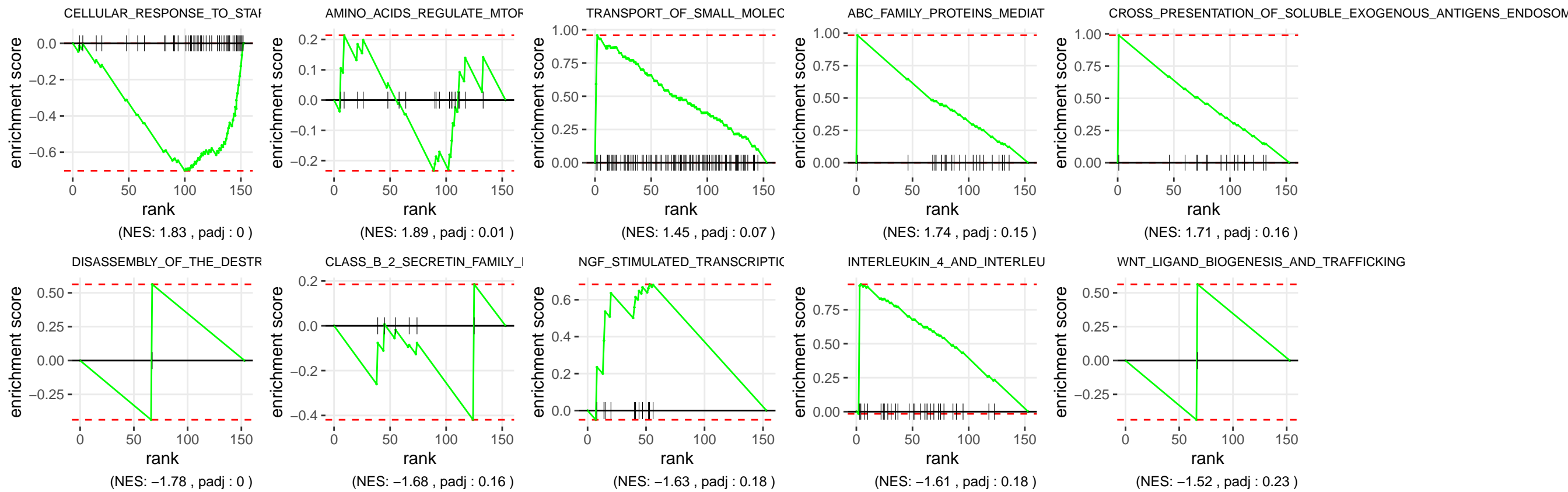
D2 M2 : Top enriched Pathways (GSEA), Old vs Young

	Pathway	Gene ranks	NES	pval	padj
	REACTOME_SIGNALING_BY_BMP		1.73	6.5e-05	2.0e-02
	REACTOME_RUNX1_REGULATES_TRANSCRIPTION_OF_GENES_INVOLVED_IN_INTERLEUKIN_SIGNALING		1.50	5.6e-04	5.6e-02
	REACTOME_TFAP2_AP_2_FAMILY_REGULATES_TRANSCRIPTION_OF_GROWTH_FACTORS_AND_THEIR_RECEPTORS		1.56	5.3e-04	5.6e-02
	REACTOME_DEFECTS_OF_CONTACT_ACTIVATION_SYSTEM_CAS_AND_KALLIKREIN_KININ_SYSTEM_KKS		1.59	1.7e-03	1.6e-01
	REACTOME_DEFECTIVE_FACTOR_VIII_CAUSES_HEMOPHILIA_A		1.54	1.9e-03	1.7e-01
	REACTOME_EUKARYOTIC_TRANSLATION_INITIATION		-1.97	9.4e-05	2.3e-02
	REACTOME_INFLUENZA_INFECTION		-1.94	6.6e-05	2.0e-02
	REACTOME_RRNA_PROCESSING		-2.01	9.1e-06	4.5e-03
	REACTOME_METABOLISM_OF_RNA		-1.67	6.4e-06	4.5e-03
	REACTOME_TRANSLATION		-2.02	4.4e-08	6.6e-05









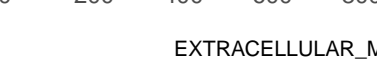



D2 Neutro : Top enriched Pathways (GSEA), Old vs Young

	Pathway	Gene ranks	NES	pval	padj
	REACTOME_CELLULAR_RESPONSE_TO_STARVATION		1.83	3.5e-06	2.6e-03
	REACTOME_AMINO_ACIDS_REGULATE_MTORC1		1.89	1.3e-05	6.3e-03
	REACTOME_TRANSPORT_OF_SMALL_MOLECULES		1.45	2.0e-04	7.3e-02
	REACTOME_ABC_FAMILY_PROTEINS_MEDIATED_TRANSPORT		1.74	4.9e-04	1.5e-01
	REACTOME_CROSS_PRESENTATION_OF_SOLUBLE_EXOGENOUS_ANTIGENS_ENDOSOMES		1.71	7.3e-04	1.6e-01
	REACTOME_WNT_LIGAND_BIOGENESIS_AND_TRAFFICKING		-1.52	4.8e-03	2.3e-01
	REACTOME_INTERLEUKIN_4_AND_INTERLEUKIN_13_SIGNALING		-1.61	3.2e-03	1.8e-01
	REACTOME_NGF_STIMULATED_TRANSCRIPTION		-1.63	3.0e-03	1.8e-01
	REACTOME_CLASS_B_2_SECRETIN_FAMILY_RECEPTORS		-1.68	1.2e-03	1.6e-01
	REACTOME_DISASSEMBLY_OF_THE_DESTRUCTION_COMPLEX_AND_RECRUITMENT_OF_AXIN_TO_THE_MEMBRANE		-1.78	4.5e-07	6.8e-04
		050100150			



D2 sCs : Top enriched Pathways (GSEA), Old vs Young

Pathway	Gene ranks	NES	pval	padj
REACTOME_MUSCLE_CONTRACTION		2.36	3.5e-14	1.9e-12
REACTOME_SIGNALING_BY_GPCR		1.81	2.1e-07	3.7e-06
REACTOME_NEURONAL_SYSTEM		1.86	2.2e-07	3.8e-06
REACTOME_CARDIAC_CONDUCTION		2.06	7.7e-07	1.2e-05
REACTOME_EXTRACELLULAR_MATRIX_ORGANIZATION		1.81	2.1e-06	2.8e-05
REACTOME_CELL_CYCLE_CHECKPOINTS		-2.65	6.0e-33	1.9e-30
REACTOME_M_PHASE		-2.62	1.3e-37	5.1e-35
REACTOME_METABOLISM_OF_RNA		-2.57	1.0e-50	5.1e-48
REACTOME_CELL_CYCLE_MITOTIC		-2.67	1.0e-50	5.1e-48
REACTOME_CELL_CYCLE		-2.65	1.0e-50	5.1e-48

