





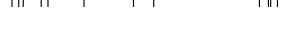
























D0 : Top enriched Pathways (GSEA), Old vs Young					
Pathway	Gene ranks	NES	pval	padj	
REACTOME_MUSCLE_CONTRACTION		2.30	3.1e-06	3.2e-05	
REACTOME_CARDIAC_CONDUCTION		2.39	1.2e-05	1.1e-04	
REACTOME_PHASE_I_FUNCTIONALIZATION_OF_COMPOUNDS		2.33	2.0e-05	1.8e-04	
REACTOME_CYTOCHROME_P450_ARRANGED_BY_SUBSTRATE_TYPE		2.29	2.7e-05	2.3e-04	
REACTOME_NEURONAL_SYSTEM		2.03	4.4e-05	3.7e-04	
REACTOME_BIOLOGICAL_OXIDATIONS		2.07	2.7e-04	2.0e-03	
REACTOME_ION_HOMEOSTASIS		2.11	2.8e-04	2.0e-03	
REACTOME_RA_BIOSYNTHESIS_PATHWAY		2.00	4.2e-04	2.8e-03	
REACTOME_PEPTIDE_HORMONE_METABOLISM		2.07	4.5e-04	3.0e-03	
REACTOME_STIMULI_SENSING_CHANNELS		2.01	5.4e-04	3.6e-03	
REACTOME_POTASSIUM_CHANNELS		2.05	5.5e-04	3.6e-03	
REACTOME_SIGNALING_BY_RETINOIC_ACID		2.02	8.7e-04	5.5e-03	
REACTOME_VOLTAGE_GATED_POTASSIUM_CHANNELS		2.02	8.9e-04	5.5e-03	
REACTOME_METABOLIC_DISORDERS_OF_BIOLOGICAL_OXIDATION_ENZYMES		1.94	1.1e-03	6.7e-03	
REACTOME_TRANSPORT_OF_SMALL_MOLECULES		1.65	1.2e-03	7.4e-03	
REACTOME_RECOGNITION_AND_ASSOCIATION_OF_DNA_GLYCOSYLASE_WITH_SITE_CONTAINING_AN_AFFECTED_PURINE		-2.67	6.0e-09	2.3e-07	
REACTOME_ERCC6_CSB_AND_EHMT2_G9A_POSITIVELY_REGULATE_RRNA_EXPRESSION		-2.63	6.2e-09	2.3e-07	
REACTOME_DEPOSITION_OF_NEW_CENPA_CONTAINING_NUCLEOSOMES_AT_THE_CENTROMERE		-2.76	6.0e-09	2.3e-07	
REACTOME_ACTIVATED_PKN1_STIMULATES_TRANSCRIPTION_OF_AR_ANDROGEN_RECEPTOR_REGULATED_GENES_KLK2_AND_KLK3		-2.63	6.2e-09	2.3e-07	
REACTOME_RESOLUTION_OF_SISTER_CHROMATID_COHESION		-2.74	3.2e-09	2.0e-07	
REACTOME_MITOTIC_PROPHASE		-2.77	2.6e-09	2.0e-07	
REACTOME_HATS_ACETYLTE_HISTONES		-2.74	2.9e-09	2.0e-07	
REACTOME_DNA_METHYLATION		-2.72	3.5e-09	2.0e-07	
REACTOME_BASE_EXCISION_REPAIR_AP_SITE_FORMATION		-2.66	2.4e-09	2.0e-07	
REACTOME_RHO_GTPASE_EFFECTORS		-2.83	1.0e-10	1.2e-08	
REACTOME_M_PHASE		-2.95	1.0e-10	1.2e-08	
REACTOME_CELL_CYCLE_MITOTIC		-3.00	1.0e-10	1.2e-08	
REACTOME_CELL_CYCLE_CHECKPOINTS		-3.00	1.0e-10	1.2e-08	
REACTOME_CELL_CYCLE		-3.00	1.0e-10	1.2e-08	
	0 50 100 150 200				

