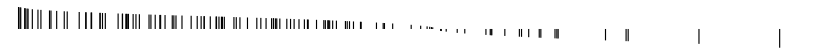
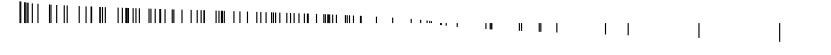
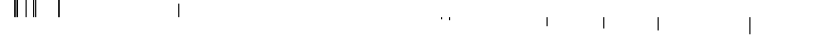
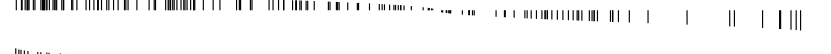
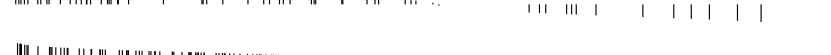

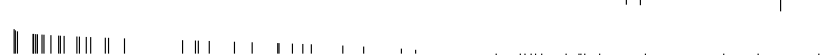





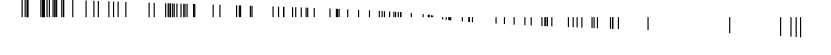
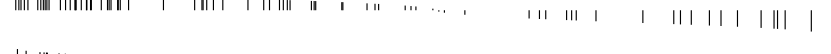





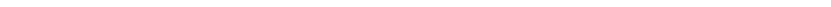


Pathway	Gene ranks	NES	pval	padj
GO_PROTEIN_LOCALIZATION_TO_ENDOPLASMIC_RETICULUM		2.40	2.6e-05	2.0e-03
GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_ENDOPLASMIC_RETICULUM		2.37	2.5e-05	2.0e-03
GO_CELL_MIGRATION_INVOLVED_IN_SPROUTING_ANGIOGENESIS		2.22	6.5e-05	3.2e-03
GO_RESPONSE_TO_TOPOLOGICALLY_INCORRECT_PROTEIN		2.20	2.7e-05	2.0e-03
GO_POSITIVE_REGULATION_OF_SYNAPSE_ASSEMBLY		2.16	4.7e-05	2.6e-03
GO_TRANSLATIONAL_INITIATION		2.16	2.6e-05	2.0e-03
GO_PHARYNGEAL_SYSTEM_DEVELOPMENT		2.13	1.3e-04	4.8e-03
GO_EXTRACELLULAR_MATRIX_BINDING		2.13	4.6e-05	2.5e-03
GO_REGULATION_OF_POSITIVE_CHEMOTAXIS		2.10	2.4e-04	7.2e-03
EAR_TRANSCRIBED_MRNA_CATABOLIC_PROCESS_NONSENSE_MEDIATED_DECAY		2.10	2.5e-05	2.0e-03
GO_COCHLEA_MORPHOGENESIS		2.10	3.7e-04	9.8e-03
GO_POSITIVE_REGULATION_OF_INFLAMMATORY_RESPONSE		2.09	2.5e-05	2.0e-03
GO_MESODERMAL_CELL_DIFFERENTIATION		2.09	2.7e-04	7.6e-03
GO_CELLULAR_RESPONSE_TO_TOPOLOGICALLY_INCORRECT_PROTEIN		2.08	2.6e-05	2.0e-03
GO_REGULATION_OF_SYNAPSE_ASSEMBLY		2.06	7.3e-05	3.4e-03
GO_POSITIVE_CHEMOTAXIS		2.06	3.1e-04	8.7e-03
GO_HEMIDESMOSOME_ASSEMBLY		2.05	3.6e-04	9.7e-03
GO_CYTOSOLIC_LARGE_RIBOSOMAL_SUBUNIT		2.04	9.4e-05	4.0e-03
GO_MORPHOGENESIS_OF_AN_EPITHELIAL_SHEET		2.04	1.4e-04	4.9e-03
GO_MUSCLE_ORGAN_MORPHOGENESIS		2.03	7.2e-05	3.4e-03
	050001000015000			