Mouse - 6h post-wounding skin regeneration (GSE23006)

Chen et al. BMC Genomics 2010 - PMID: 20704739

Two best replicates were selected based on clustering of probe signal (pearson correlation). Average signal between replicates was used for the analysis.



Mapping probes and mouse protein-coding genes (ENSEMBL79, GENCODE vM4, march 2015):

- Probes mostly relate to one mouse protein-coding gene.
- Mouse protein-coding genes relate to approx. 2 probes on average.



Summary statistics mouse protein-coding genes:

Genes were classified using different fold change thresholds (plots below are equal, just excluded flat genes in the second plot for visualization purposes):



Using 1.7 fold change between control and regeneration as we did for our fly data:

	Genes mapped to probe(s)	Total number of annotated genes
Mouse protein-coding genes	18.153 (82%)	22.032
Mouse upregulated genes regeneration	1.588 (9%)	1.588 (7%)

Genes mapping to more than one probe, classified both as higher in regeneration and lower in regeneration were not considered.

Mapping mouse protein-coding genes and fly protein-coding genes (ENSEMBL79):

	Genes mapped	Total number of	%
	to orthologs	annotated genes	
Fly genes	7,304	13,920	52.47
Fly up-reg 0h	1,287	1,997	64.45
Mouse genes	10,241	22,032	46.48
Mouse up-reg (FC1.7)	859	1,588	54.09
Mouse up-reg (FC1.5)	1,339	2,326	57.57

GO enrichment for the 107 genes that upregulated both in fly and mouse (FC1.7) regeneration data:

cell	cell development	nervous system development	tube development	tissue development	regulation of cell communication	regulation of signali	regulation of signaling		cell migration		
differentiation					positive ulat	tion		cell			
		cellular		system		nunication		localization of cell	or subcellular component		
	tube morphogenesis		neurogenesis	development	regulation of cellular	regulation					
cellular developmental	tub	e			process	of biologica process	al	macromolecule localization			
process	animal organ morphogenesis	gland morphogenesis	metamorphosis	regulation of cell differentiation	Gell	cellular	Се	llular			
anatomical structure morphogenesis	Interprogeneata	regulation of cell development	post-embryonic development	multicellular organism development	communication	metabolism	pr	UCCESS S	localization		
	cell										
	fate commitment	animal organ development	epithelial cell differentiation	instar larval or pupal morphogenesis	cytoskeleton organization	projection organization	si	gignaliking	locomotion		

GO enrichment for the 172 genes that upregulated both in fly and mouse (FC1.5) regeneration data:

regulation of cellular process	regulation positive regulation regulation of cellular of cellular process process		regulation celli of cellular com metabolism orga		lular cell mponent development janization		cellular metabolism	cellular response to stimulus sm				sigi trar	nai 1sduction		
	nervous	cell			cell		ce pro mi				cellular protein modification al process		molecu cation	re to ex	sponse dernal limulus
regulation system of biological development process		migration		neurogen	organizatio	n		primary metabolism		nitrogen compound metabolism					
cell	cellular component biogenesis	regulation a system of cell differentiation		terre en		t in	cell communication	organic substance metabolism				phosp	horylation		
differentiation		regulation of multicellular organismal	tissue development			synapse assembly	cellular		cellular componen		nt IOCIocalization OT		union :		
cellular cell developmental ass process	cellular component assembly acti	actin	tin		tube development		process	organizat or biogenes		lon					
positive regulation of biological process	regulation of cell development	process		localization	regulation of biological quality	cell fate commitment	biological				response to stimulus				
		localization of cell		of cell or subcellular componen	celi r part t morphogenesi	epitheliai celi development	regeliation	on		ang	locemution		Mion		