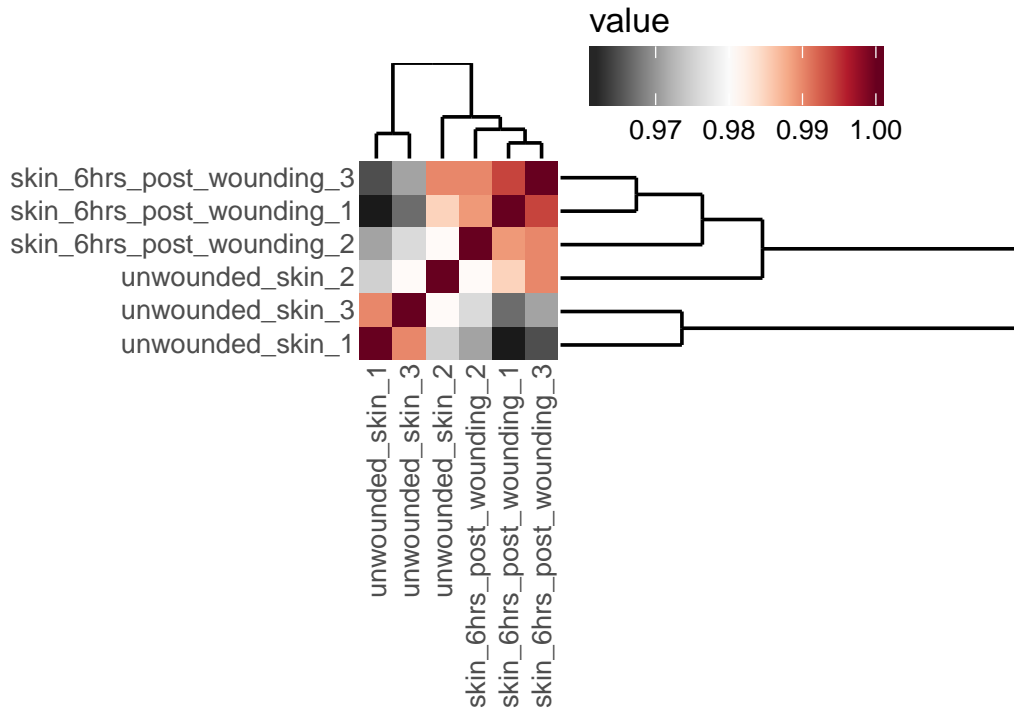


# Mouse - 6h post-wounding skin regeneration (GSE23006)

Chen et al. BMC Genomics 2010 - PMID: 20704739

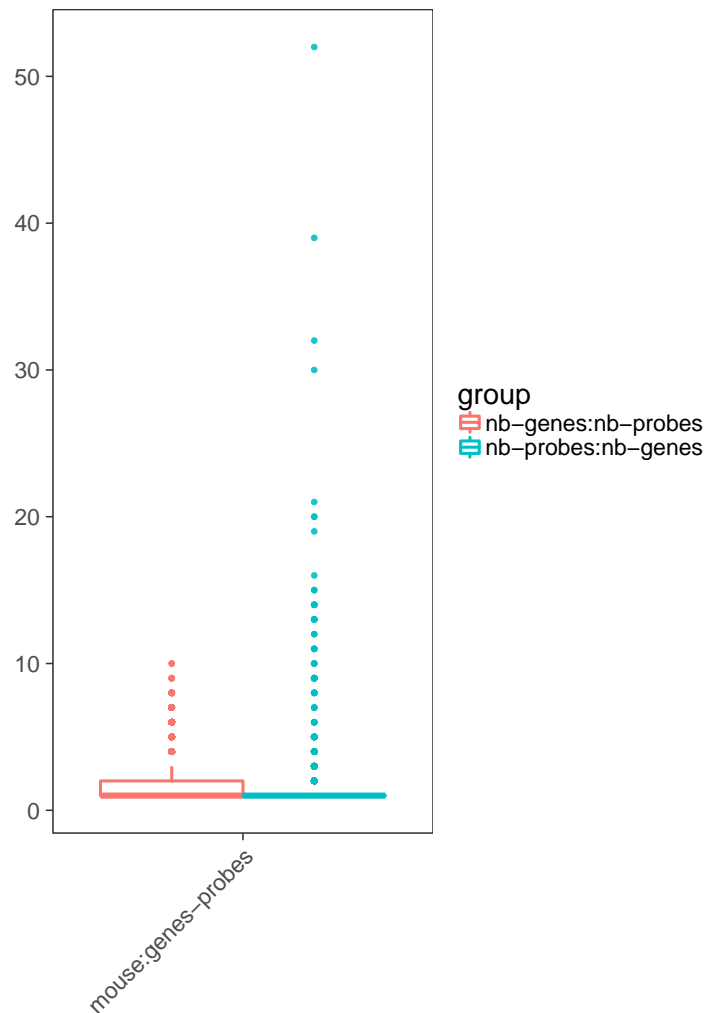
Two best replicates were selected based on clustering of probe signal (pearson correlation). Average signal between replicates was used for the analysis.



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

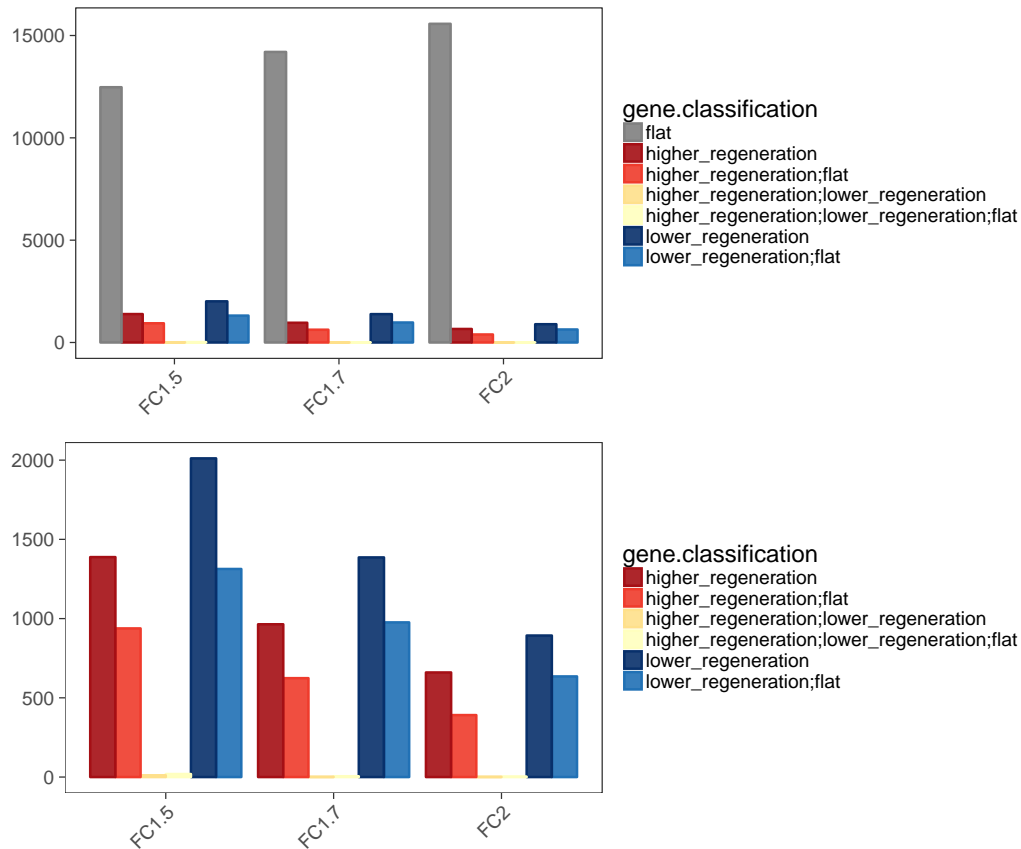
- Probes mostly relate to one mouse protein-coding gene.
- Mouse protein-coding genes relate to approx. 2 probes on average.

	number	average of mapping	median of mapping
probes	45101	1.0528	1
protein-coding genes	22032	1.7907	1



## 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:

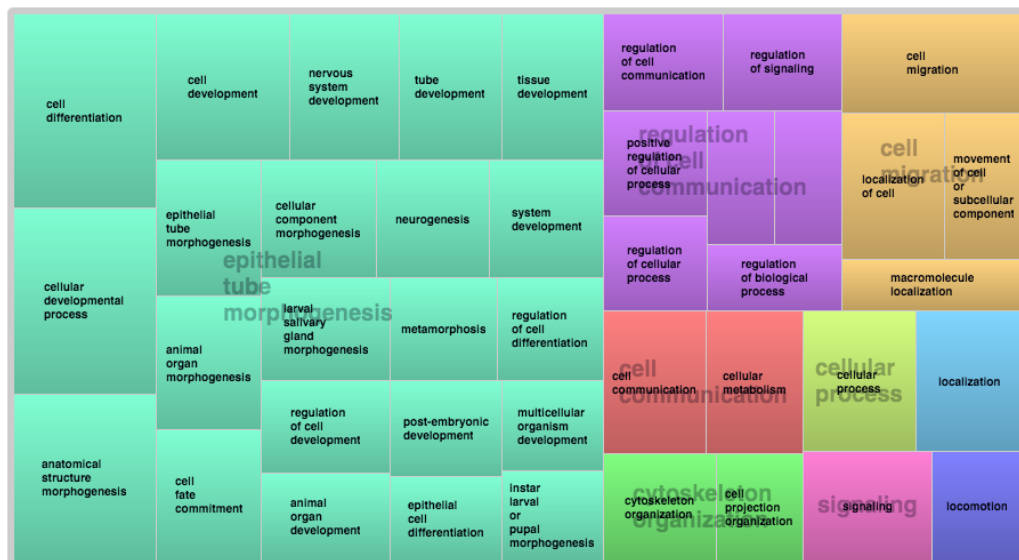
	Genes mapped to probe(s)	Total number of annotated genes
Mouse protein-coding genes	18.153 (82%)	22.032
Mouse upregulated genes regeneration	1.588 (9%)	1.588 (7%)

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 to orthologs	Total number of 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:



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

