

Table 3a. Early up-regulated genes: enriched annotation terms

Terms	Skin		Tongue	
	Member (#)	p value	Member (#)	p value
Response to wounding	52	3.3E-16	25	5.8E-9
Inflammatory response	43	1.2E-15	24	5.7E-11
Cytokine	39	1.0E-15	16	6.1E-6
Toll-like receptor signaling pathway	31	4.5E-12		
Receptor binding	73	1.2E-11	28	3.6E-4
Cytokine-cytokine receptor interaction	47	1.2E-11	18	9.1E-4
Jak-STAT signaling pathway	29	1.8E-6		
Chemotaxis	25	4.0E-10	11	6.4E-4

Table contains a list of top significant annotation terms and p values derived from DAVID functional annotation analysis.

Terms: biological description associated with a particular entry in the database.

Member (#): number of Affymetrix probe set IDs differentially expressed in each term

P value: modified Fisher Exact p-value, FDR adjusted.

Table 3b. Early up-regulated genes: enriched groups of functionally related genes

Terms	Skin		Tongue	
	Member (#)	Score	Member (#)	Score
Interferon α , β and δ /cytokine	16 (Group 1)	9.77		
Chemokine	12 (Group 2)	9.58	10 (Group 1)	6.46
Cell differentiation/apoptosis	8 (Group 3)	3.85	1	
Positive regulation of protein kinase activity	4 (Group 4)	3.68		
Regulation of metabolic/biological process	4 (Group 5)	2.91		
Pattern recognition receptors (TLR related)	7 (Group 6)	2.82		
Ribosome/organelle organization	8 (Group 7)	2.5		
Matrix metalloproteinase (MMP)	6 (Group 8)	2.04		
Negative regulation of cell proliferation			4 (Group 2)	3.34
GTP binding			14 (Group 3)	3.08
Keratinization/epidermal development			4 (Group 4)	2.27

Table contains a list of top enriched groups of annotation terms and enrichment scores derived from DAVID gene functional classification analysis.

Term: consensus annotation terms shared by a group of genes.

Member (#): number of Affymetrix probe set IDs differentially expressed in each group.

Score: biological significance of the gene groups based on overall EASE scores for all enriched annotation terms.