

Supplement, Table 5. Biological Processes targeted by changes in gene expression in Celecoxib-treated patients

Gene Ontology Category ^a	Number of Significant Genes in a Category ^b	Number of Genes on Array in a Category ^c	EASE Score
cell communication	342 (35)	1610	0.0002
immune response	103 (7)	421	0.0008
lymphocyte activation	16 (1)	36	0.0009
response to stress	116 (6)	489	0.0013
response to pest/pathogen/parasite	71 (3)	275	0.0014
defense response	110 (7)	462	0.0015
ER to Golgi transport	10 (1)	18	0.0022
immune cell activation	17 (1)	43	0.0025
cell activation	17 (1)	43	0.0025
response to wounding	45 (3)	166	0.0047
response to biotic stimulus	115 (7)	508	0.0070
cell-cell signaling	67 (7)	274	0.0077
cell adhesion	77 (4)	327	0.0111
cellular process	634 (73)	3283	0.0114
T-cell activation	9 (1)	19	0.0134
B-cell activation	9 (1)	19	0.0134
regulation of apoptosis	37 (2)	141	0.0181
signal transduction	260 (31)	1277	0.0186
TGFbeta receptor signaling pathway	10 (2)	24	0.0205
cell-cell adhesion	28 (1)	101	0.0213
transcription\, DNA-dependent	197 (23)	951	0.0224
response to external stimulus	154 (13)	728	0.0226
response to chemical substance	35 (5)	134	0.0232
transmembrane receptor protein serine/threonine kinase signaling pathway	11 (2)	29	0.0274
cellular defense response	17 (1)	54	0.0276
protein kinase cascade	27 (3)	100	0.0327
regulation of transcription\, DNA-dependent	188 (22)	914	0.0333
transcription	202 (23)	990	0.0367
regulation of transcription	191 (22)	933	0.0378

cell death	59 (3)	257	0.0419
death	59 (3)	257	0.0419
chemotaxis	20 (2)	71	0.0476
taxis	20 (2)	71	0.0476
innate immune response	29 (2)	113	0.0486

^aCategories are sorted by EASE score

^bTotal number of significant by SAM genes that have been Categorized in Gene Ontology is 1106; the number of genes in a category, which changes in expression are significant at $p < 0.001$, is shown in brackets (out of 125 that have been categorized)

^cTotal number of genes presented on arrays that have been Categorized in Gene Ontology is 6062