Table 1. Genes modulated by C3 (*Z* score > 3 or < -3)

GenBank accession number	Gene name	Gene function	*Z* score	Folds of induction
Growth and adhesion				
X15202	Integrin β1 (fibronectin receptor β) - *Itgb1*	Receptor activity; protein binding; oxidoreductase activity	-3.738	0.346
M64403	Cyclin D1 - *Ccnd1*	Protein kinase activity; protein binding; kinase activity; cyclin-dependent protein kinase regulator activity	-3.479	0.321
AI849928	Cyclin D1 - *Ccnd1*	Protein kinase activity; protein binding; kinase activity; cyclin-dependent protein kinase regulator activity	-3.980	0.315
M83749	Cyclin D2 - *Ccnd2*	Protein binding; cyclin-dependent protein kinase regulator activity	-5.182	0.191
X66032	Cyclin B2 - *Ccnb2*	Cyclin-dependent protein kinase regulator activity	-5.494	0.184
AA681998	CDC28 protein kinase regulatory subunit 2 - *Cks2*	Cyclin-dependent protein kinase activity	-4.419	0.245
AB025409	CDC28 protein kinase 1 - *Cks1*	Cyclin-dependent protein kinase activity; kinase activity	-4.928	0.232
AI848299	Replication protein A3 - *Rpa3*	Nucleic acid binding	-3.841	0.287
Differentiation markers				
V00830	Keratin complex 1, acidic, gene 10 - *Krt1-10*	Structural molecule activity; structural constituent of cytoskeleton	9.108	10.863
X97986	Desmocollin 1 - *Dsc1*	Calcium ion binding; protein binding	7.443	6.886
AW228162	Desmocollin 2 - *Dsc2*	Calcium ion binding; protein binding	5.166	3.895
Y11169	Desmocollin 3 - *Dsc3*	Calcium ion binding; protein binding	3.591	2.460
AJ005564	Small proline-rich protein 2F - *Sprr2f*	Structural molecule activity	3.234	2.214
J03458	Filaggrin -	Cytoskeleton organization and biogenesis	5.124	3.535
L10385	Transglutaminase 3, E polipeptide - *Tgm3*	Protein-glutamine γ -glutamyltransferase activity; calcium ion binding; acyltransferase activity; transferase activity	10.261	18.694
Transcription factors				
X12761	Jun oncogene - *Jun*	DNA binding; transcription factor activity; protein binding	3.788	2.658
AF006602	Histone deacetylase 5 - *Hdac5*	Transcription corepressor activity; histone deacetylase activity; protein binding; transcriptional repressor activity; hydrolase activity	3.576	2.460
U41739	Four and a half LIM domains 1 – *Fhl1*	Cell differentiation; cell growth; development; muscle development	-6.649	0.139
AI839950	Four and a half LIM domains 1 - *Fhl1*	Cell differentiation; cell growth; development; muscle development	-3.590	0.318

Table 1. Genes modulated by C3 in keratinocytes. PolyA+ RNA was prepared from primary mouse keratinocytes in low calcium medium after 6-h treatment with a GST-C3 fusion protein or GST control. cRNA probes were tested in duplicate by hybridization to Affimetrix U74A gene chips according to the manufacturer's recommendations. Probe sets with absent and/or marginal calls in both treated and controls were filtrated out. Probe sets with only one present call (either in treated or in control) were filtrated out if the present intensity value was less than 1,000 arbitrary units. Variations in gene expression between treated and controls were statistically analyzed by *Z* score determination (i.e., a measure of significance of variations in gene expression levels after local variance correction across the range of gene expression intensities) (1). Local *Z* scores were calculated for each replication and then averaged. Using relatively stringent criteria (average *Z* score >3 or < -3), 166 genes were identified which were induced and 109 genes that were suppressed in keratinocytes as a consequence of C3 treatment. Shown is a set of more relevant genes discussed in the text, together with corresponding average *Z* score values as well as folds of induction or suppression. A more detailed list can be provided upon request.

1. Colantuoni, C., Henry, G., Zeger, S., and Pevsner, J. (2002) *Bioinformatics* **18**, 1540-1541.