

Gene ID	Assay ID	Gene ID	Assay ID
<i>Itgb1</i>	Mm01253230_m1	<i>Col4a3</i>	Mm00483656_m1
<i>Itga2</i>	Mm00434371_m1	<i>Col4a4</i>	Mm00801574_m1
<i>Itga3</i>	Mm00442890_m1	<i>Col4a5</i>	Mm00801606_m1
<i>Itga5</i>	Mm00439797_m1	<i>Col4a6</i>	Mm00474735_m1
<i>Itga6</i>	Mm00434375_m1	<i>Lama3</i>	Mm01254735_m1
<i>Itga8</i>	Mm01324958_m1	<i>Lama5</i>	Mm01222029_m1
<i>Itga9</i>	Mm01348480_m1	<i>Lama2</i>	Mm00550083_m1
<i>Itgav</i>	Mm00434506_m1	<i>Mmp1a</i>	Mm00473485_m1
<i>Itgb4</i>	Mm01266840_m1	<i>Mmp1b</i>	Mm00473493_g1
<i>Itgb5</i>	Mm00439825_m1	<i>Mmp2</i>	Mm00439498_m1
<i>Itgb6</i>	Mm01269869_m1	<i>Mmp3</i>	Mm00440295_m1
<i>Itgb8</i>	Mm00623991_m1	<i>Mmp8</i>	Mm00439509_m1
<i>Actb</i>	Mm01205647_g1	<i>Mmp9</i>	Mm00442991_m1
<i>Ccnd1</i>	Mm00432359_m1	<i>Mmp10</i>	Mm01168399_m1
<i>Krt5</i>	Mm00503549_m1	<i>Mmp13</i>	Mm00439491_m1
<i>Krt14</i>	Mm00516876_m1	<i>Mmp14</i>	Mm00485054_m1
<i>Col1a2</i>	Mm01165187_m1	<i>Mmp19</i>	Mm00491300_m1
<i>Fak</i>	Mm00433205_m1	<i>Mmp28</i>	Mm00712992_m1
<i>Ptk2b</i>	Mm00552827_m1	<i>Timp1</i>	Mm00441818_m1
<i>Bcar1</i>	Mm00487210_m1	<i>Timp2</i>	Mm00441825_m1
<i>Src</i>	Mm00436785_m1	<i>Timp4</i>	Mm00446568_m1
<i>Pxn</i>	Mm00448533_m1	<i>Timp3</i>	Mm00441826_m1
<i>Cd151</i>	Mm00515411_m1	<i>Cd44</i>	Mm01277163_m1
<i>Col4a1</i>	Mm01210125_m1	<i>Col4a3</i>	Mm00483656_m1

Figure S1. TaqMan assay primer sets. TaqMan assays used to interrogate gene expression within murine keratinocytes. All assays were obtained from Applied Biosystems (Foster City, CA).

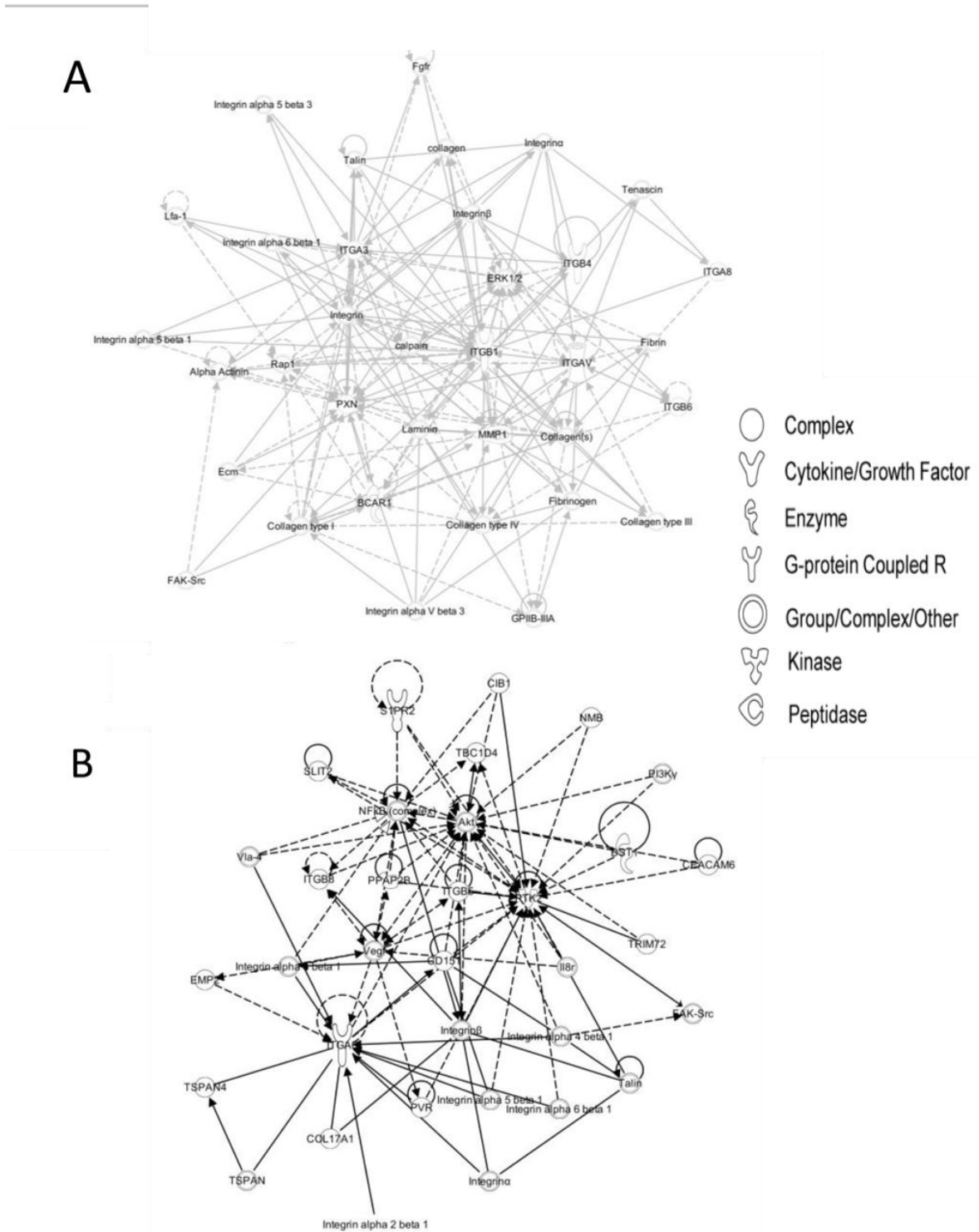
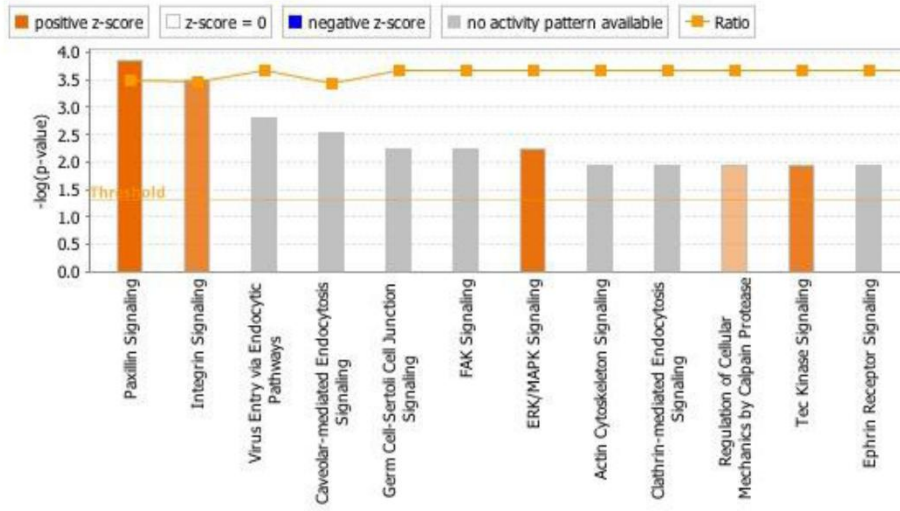


Figure S2. Merged network analysis of wildtype and FAK-deleted keratinocytes. Top scoring Ingenuity Pathway Analysis (IPA)-constructed transcriptome networks based genes that were significantly up-regulated (A) or down-regulated (B) in FAK-deleted keratinocytes compared to wildtype cells. Direct relationships are indicated by solid lines, and dashed lines represent indirect relationships.

A



B

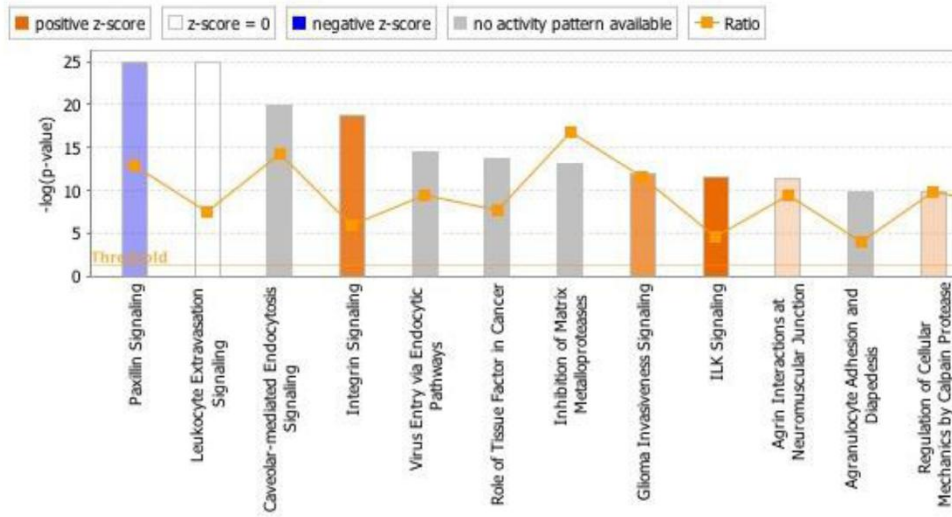


Figure S3. Canonical pathway analysis of keratinocyte subpopulations. Canonical pathways significantly enriched for among genes whose expression was significantly up-regulated in cluster 1 (A) and cluster 2 (B) cells based on the partitions delineated in Figure 3.