



**Supplemental Fig. 3. Validation of microarray data by Q-PCR.** Six genes from different GO groups representing typical pattern of glucocorticoid-induced differential gene expression in epidermis in w.t. and REDD1 KO milieu were selected for validation. **A.** Microarray data for the selected genes. **B.** Q-PCR data for the selected genes. **C.** Pearson correlation coefficients (PCC) between microarray and Q-PCR data for the corresponding genes. Bars represent mean  $\pm$  SD calculated for two individual skin samples.