

Additional File 3. CTL sample expression among mouse strains and comparison to normal human skin. (A – G) Spearman correlation of average expression (FPKM) in CTL mouse skin ($n = 4$ per strain, males + females) and normal human skin ($n = 90$ subjects; GSE54456). Dashed lines represent robust linear regression estimates. (H) Overlap of robust regression estimates for each strain. (I) Genes with highest expression in normal human skin (bottom margin parentheses: average FPKM). Heatmap colors depict average FPKM in CTL mouse skin for each strain (see legend). Relative FPKM across strains is indicated by values within the heatmap (1 = strain with highest expression; left margin parentheses: average relative expression across genes). (J) Number of genes differentially expressed between CTL samples (FDR < 0.10; FC > 2.0 or FC < 0.50; all 21 possible strain comparisons; red: higher expression in first strain listed; blue: higher expression in second strain listed). (K – N) Genes with different expression in CTL samples from B6 and MOLF mice. Groups without the same letter differ significantly ($P < 0.05$, Tukey honest significant difference; Error bars: standard error of the mean).

