Additional File 9. Gene ontology (GO) biological process (BP) terms enriched among psoriasis-decreased DEGs and correspondence with IMQ responses. (A) Psoriasisenriched GO BP terms. Heatmap colors depict average IMQ responses of 10 representative mouse homologues for each GO BP term. Chosen genes are homologous to the 10 human genes associated with the listed term for which expression was most strongly decreased in psoriasis lesions (i.e., lowest p-value). (B) Psoriasis-decreased DEGs associated with homeostatic GO BP terms (blue font in part (A)). (C) Psoriasis-decreased DEGs associated with transport GO BP terms (red font in part (A)). (D, E) RT-PCR analysis of (D) Atp13a5 and (E) P2rx1 expression (n  $\geq$  4 per strain/sex/treatment group; n = 38 mice total). Groups without the same letter differ

 $\geq$  4 per strain/sex/treatment group; n=38 mice total). Groups without the same letter differ significantly (P < 0.05, Tukey honest significant difference; Error bars: standard error of the mean; p-values: strain-by-treatment interaction effect). *Rn18s* was used as an endogenous control to estimate relative gene expression.

