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**Fig. S1. Wild type cohorts from the *Asc-/-* and *Nlrp1b-/-* evaluations are comparable. (A)** All samples were normalized at the same level (20000 reads) and PCoA analysis of the four groups show the microbiota composition among these four groups was significantly different (ANOSIM R=0.8418, *P*=0.001, 999 permutations). **(B)** Clustering analysis based on Bray-Curtis distance showed that *Nlrp1b-/-* and *Asc-/-* group clustered separately from WT1 and WT2, but WT1 and WT2 clustered together.