

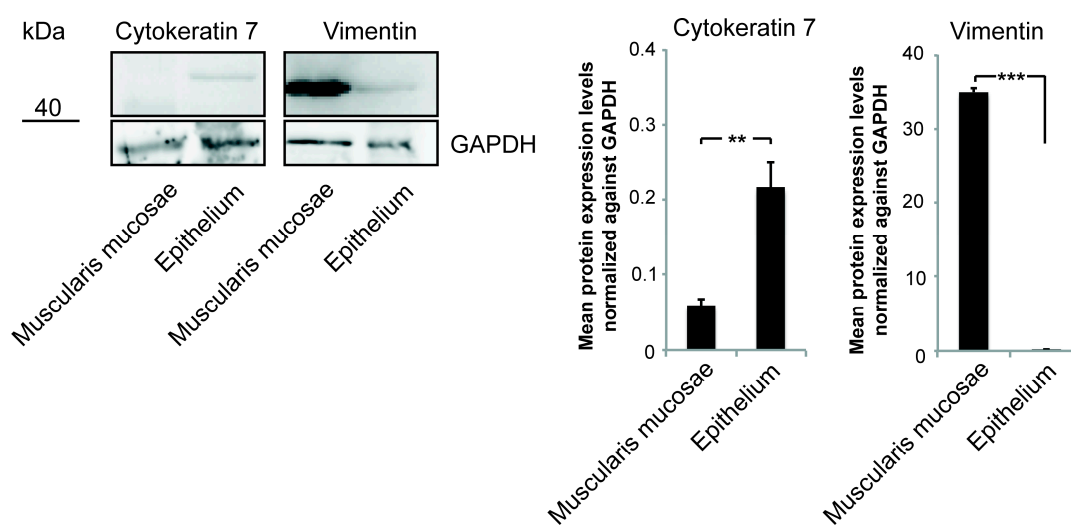


Article

# Altered intestinal morphology and microbiota composition in the Autism Spectrum Disorders associated SHANK3 mouse model

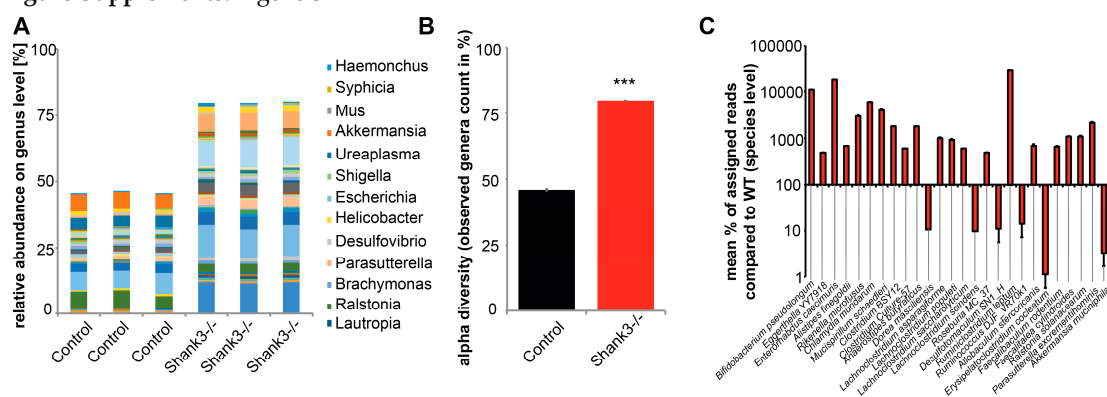
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Figure Supplements: Figure S1



**Figure supplement 1.** Purification and analysis of GI epithelium of wildtype and *Shank3 $\alpha\beta$*  KO mice. Western Blot analysis for the expression of Vimentin, and Cytokeratin 7 shows that epithelium can be successfully separated from gut muscle (t-test, *Cytokeratin7*:  $p < 0.01$ ; *Vimentin*:  $p < 0.001$  ( $n = 3$  western blot bands were analyzed from 3 animals)). \*\*  $p < 0.01$ ; \*\*\*  $p < 0.001$

Figure Supplements: Figure S2



**Figure supplement 2. (A)** Bar plot graph comparing Control and *Shank3 $\alpha\beta$*  KO mice on genus level. Within group sample differences were small compared to between group differences. **(B)** Measurement of alpha diversity reveals a significant difference between Controls and *Shank3 $\alpha\beta$*  KO mice (*t*-test,  $p < 0.0001$ ). **(C)** Identification of species by 16S rRNA sequencing can only be done with low confidence. Species with more than 5 fold increase or decrease in *Shank3 $\alpha\beta$*  KO mice compared to Control are shown. Among those highly upregulated are: *Bifidobacterium pseudolongum*, *Eggerthella* YY7918, *Enterorhabdus caecimuris*, *Alistipes finegoldii*, *Rikenella microfusus*, *Chlamydia muridarum*, *Mucispirillum schaedleri*, *Clostridium* BSY12, *Clostridium* Culture-57, *Anaerostipes butyraticus*, *Lachnospirillum asparagiforme*, *Lachnospirillum populeti*, *Lachnospirillum saccharolyticum*, *Roseburia* MC\_37, *Ruminiclostridium leptum*, *Allobaculum stercoricanis*, *Faecalibaculum rodentium*, *Faecalitalea cylindroides*, *Ralstonia solanacearum*, *Parasutterella excrementihominis*. Species significantly downregulated include: *Dorea massiliensis*, *Lachnospirillum scindens*, *Desulfotomaculum* SN1\_H, *Ruminococcus* DJF\_VR70k1, *Erysipelatoclostridium cocleatum*, *Akkermansia muciniphila*. \*\*\*  $p < 0.001$