

Title	Functional environmental screening of a metagenomic library identifies stlA; a unique salt tolerance locus from the human gut microbiome
Authors	Culligan, Eamonn P.;Sleator, Roy D.;Marchesi, Julian R.;Hill, Colin
Publication date	2013
Original Citation	Culligan EP, Sleator RD, Marchesi JR, Hill C (2013) Functional Environmental Screening of a Metagenomic Library Identifies stlA; A Unique Salt Tolerance Locus from the Human Gut Microbiome . PLoS ONE 8(12): e82985. doi:10.1371/journal.pone.0082985
Type of publication	Article (peer-reviewed)
Link to publisher's version	10.1371/journal.pone.0082985
Rights	© 2015 Culligan et al. This is an open access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited - http://creativecommons.org/licenses/by/4.0/
Download date	2026-08-03 06:14:22
Item downloaded from	https://hdl.handle.net/10468/2350

Figure S4. Comparisons of gene arrangement on SMG 25 fosmid insert and scaffolds with *sttA* homologues from Human Microbiome Project.

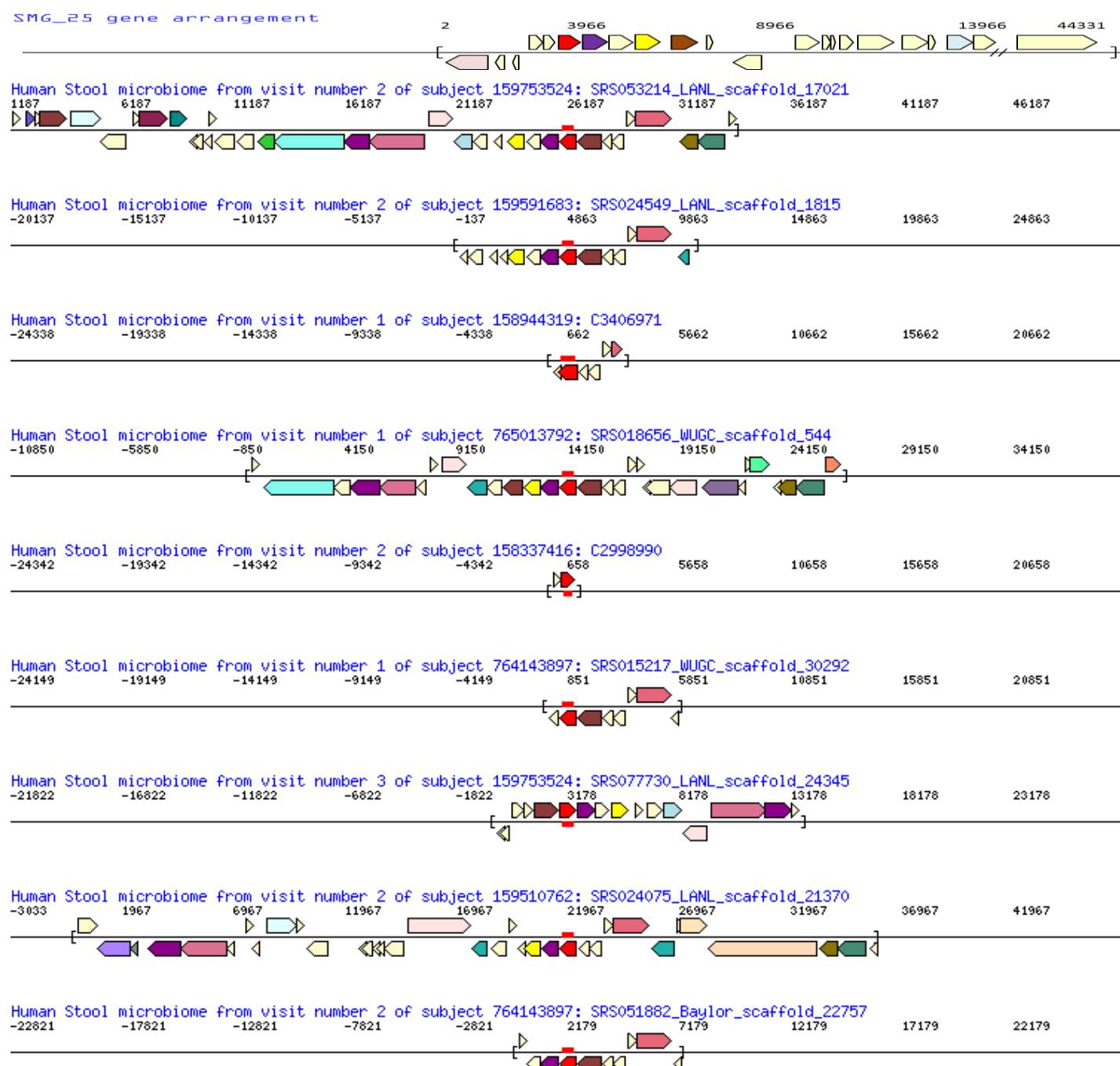


Figure S4. The gene neighbourhood region of the *sttA* gene from SMG 25 is compared with gene neighbourhoods from scaffolds with an *sttA* homologue. Homologues of *sttA* were identified through similarity searches (BLASTP; $1e^{-50}$ cut-off) to the Human Microbiome Project (HMP) datasets. Ten *sttA* homologues were identified and only from the stool microbiome. A legend describing putative

gene functions is presented below datasets. Ten *stlA* homologues were identified and only from the stool microbiome. A legend describing putative gene functions is presented below.

Legend: Red = Hypothetical/membrane protein (*stlA* and homologues); Cream = Hypothetical protein; Dark purple = NADH:ubiquinone oxidoreductase (COG0838); Medium brown = Fucose permease (COG0838); Light blue = Site-specific recombinase, XerD (COG4974); Dark brown = Uncharacterized protein related to capsule biosynthesis enzymes (COG3550); Dark blue/grey = Predicted restriction endonuclease (COG3183); Green = Predicted metal-dependent hydrolase (COG1451); Light-medium blue = Type I site-specific restriction-modification system (COG0610); Light purple = Restriction endonuclease (COG0732); Light maroon = Type I restriction-modification system methyltransferase subunit (COG0286); Light pink = Restriction endonuclease (COG1715); Medium blue = ATP-dependent nuclease (COG3857); Yellow = Predicted membrane protein (TM2 domain) (COG2314); Purple = DnaJ-class molecular chaperone with C-terminal Zn finger domain (COG0484); Brown = Ankyrin repeat protein (COG0666); Dark pink = Serine/threonine protein kinase (COG0515); Olive = Uncharacterized protein with von Willebrand factor (vWF) domain (COG4245); Dark blue = Uncharacterized protein with protein kinase and helix-hairpin-helix DNA-binding domains (COG4248); Light mint green = Virulence protein (COG3943); Mint green = RecB family exonuclease (COG2887); Pink = Predicted oxidoreductase (COG0667); Purple/grey = Hydrolases of the alpha/beta superfamily (COG1073); Light green = Transcriptional regulator, AraC-type DNA-binding domain-containing proteins (COG2207); Orange = Predicted ATPase (AAA+ superfamily) (COG1373); Light grey = Site-specific recombinase, DNA invertase Pin homologs (COG1961); Dark cream = Filamentation induced by cAMP protein (COG3177); Light orange = Predicted helicase (COG4889).