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Author(s)	Culligan, Eamonn P.; Sleator, Roy D.; Marchesi, Julian R.; Hill, Colin
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Figure S5. Multiple sequence alignment of StIA protein sequence with HMP and MetaHit homologues.

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                10      20      30      40      50      60      70      80      90
(A) -----MDTVRQRQLGIKRSMLTALLMGFCFLFYAPEAFSQEESALPKQSGLDEDMAGVVALVKQRYGEQLRNQYMGGATTAKAYAIGALRMENDIAKABA 97
(B) -----MNTIRHVQGAWFKKRILTVLLLVGVCCLFYPHNALSQDEPSTPPQKTGMQLDMEKGMQARKRSQDQLYNQYMGGATTAGQYAIGAAQOMENATAEABR 97
(C) -----MNTVRQRQLGIKRSILTALLMGFCFLFYTPEAFSQDEPGSPPKKSGLAEDMEKGIQAQANQRYGQQLYQYMGGATTAKCAIGVLRMENATAEABG 97
(D) MQAKSYPDGINTNTNITMNTVRQRQLGIKRSILTALLMGFCFLFYAPEAFSQDEPGAPSQRTAMDDDFDKSMAQARQQYGNRLYQYMGGATTAKERAIIGVLRMENATAEABG 114
(E) -----MNTVRQRQLGIKRSILTALLMGFCFLFYTPEAFSQDEPGSPPKKSGLAEDMEKGIQAQADQRYGQQLYQYMGGATTAKCAIGVLRMENATAEABG 97
(F) -----MNTVRQRQLGIKRSILTALLMGFCFLFYTPEAFSQDEPGSPPKKSGLAEDMEKGIQAQANQRYGQQLYQYMGGATTAKCAIGVLRMENATAEABG 97
(G) -----MNTIRHVQGAWFKKRILTVLLLVGVCCLFYPHNALSQDEPSTPPQKTGMQLDMEKGMQARKRSQDQLYNQYMGGATTAGQYAIGAAQOMENATAEABR 97
(H) -----MGFCFLFYTPEAFSQDEPGSPPKKSGLDEDMKGIQAQARQQYGNRLYQYMGGATTAKERAIIGVLRMENATAEABG 76
(I) -----MNTVRQRQLGIKRSILTALLMGFCFLFYTPEAFSQDEPGSPPKKSGLAEDMEKGIQAQANQRYGQQLYQYMGGATTAKCAIGVLRMENATAEABG 97
(J) MQAKSCREAINNTNITMNTVRQRQLRIKRSILTALLMGFCFLFYTPEAFSQEESALPKQSGLDEDMAGIALAKQRYGEQLRNQYMGGATTAKAYAIGALRMENDIAKABG 114
(K) -----MQAEFDKGTQAQRNRKYGDQVYDQYMGGTTAGQRAVGAQOMENATAVABG 50
(L) -----MGFCFLFYTPEAFSQDEPGSPPKKSGLDEDMKGMQARQQYGNRLYQYMGGATTAKERAIIGALRMENATAEABG 76

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(A) EGNTSLANALRQQLAMAQRTINEWYNGELQOKADAGDTRAQRELD EYYAFMKTVEGSSPAGSEFFLISIIISGLLLYGYIVLLSPKDATINRKTLLPWCVGLAVFDMLGNWVNC 211
(B) NGNTGRANMLREQLARANSNNQWYLNEELKQKADAGDACAQRELD EYYELIKTSTPSLP--AVPFVVSIFGLLFYWCMLVFSPRDTIILNRKTLLPWCVGLTVEFDMLGNLTNS 209
(C) KGDTAQANALRQQLARAQSNNEWSIGHLQOKANVGDTRAQRELD EYYAFMKTVEGSSPGEAFPFLLISIIISGLLLYGYIVLLSPKDATINRKTLLPWCVGLAIFDMLGNWVNC 211
(D) KGDTAQANALRQQLAMAQSNNEWSSTGHLLQOKANA GDTRAQRELD EYYAFMKTVEGSSPGEAFPFLLISIIISGLLLYGYIVLLSPKDATINRKTLLPWCVGLAIFDMLGNWVNC 228
(E) KGDTAQANALRQQLAMAQSNNEWSIGHLQOKANVGDTRAQRELD EYYAFMKTVEGSSPGEAFPFLLISIIISGLLLYGYIVLLSPKDATINRKTLLPWCVGLAIFDMLGNWVNC 211
(F) KGDTAQANALRQQLARAQSNNEWSIGHLQOKANVGDTRAQRELD EYYAFMKTVEGSSPGEAFPFLLISIIISGLLLYGYIVLLSPKDATINRKTLLPWCVGLAIFDMLGNWVNC 211
(G) NGNTGRANMLREQLARANSNNQWYLNEELKQKADAGDACAQRELD EYYELIKTSTPSLP--AVPFVVSIFGLLFYWCMLVFSPRDTIILNRKTLLPWCVGLTVEFDMLGNLTNS 209
(H) KGDTAQANALRQQLAMAQSNNEWSSTGHLLQOKANA GDTRAQRELD EYYAFMKTVEGSSPGEAFPFLLISIIISGLLLYGYIVLLSPKDATINRKTLLPWCVGLAIFDMLGNWVNC 211
(I) KGDTAQANALRQQLARAQSNNEWSIGHLQOKANVGDTRAQRELD EYYAFMKTVEGSSPGEAFPFLLISIIISGLLLYGYIVLLSPKDATINRKTLLPWCVGLAIFDMLGNWVNC 211
(J) EGNTLANMLRQQLAAVQANQISNTELLQOKANVGDTRAQRELD EYYAFMKTVEGSSPGEAFPFLLISIIISGLLLYGYIVLLSPKDATINRKTLLPWCVGLAIFDMLGNWVNC 228
(K) KGDTAQADMLRQQLARANSNNQWYLNEELKQKADAGDACAQRELD EYYELIKTSTPSLP--AVPFVVSIFGLLFYWCMLVFSPRDTIILNRKTLLPWCVGLTVEFDMLGNLTNS 162
(L) KGDTQANALRQQLAMAQSNNEWANGKLLQOKANA GDTRAQRELD EYYAFMKTVEGSSADLFPFLISIIISGLLLYGYIVLLSPKDATINRKTLLPWCVGLAIFDMLGNWVNC 190

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(A) LFLFVEILVLLVVARNFQCSWKRSEFALGLMLVSIILIGLLPLFF 257
(B) LFLFGEVLAILLIARSEFKYSWKRTFSFLGIVLVSVLILGLLTTF 255
(C) LFLFVEILVLLVVARNFQCSWKRSEFALGLMLVSIILIGLLPLFF 257
(D) LFLFVEILVLLVVARNFQCSWKRSEFALGLMLVSIILIGLLPLFF 274
(E) LFLFVEILVLLVVARNFQCSWKRSEFALGLMLVSIILIGLLPLFF 257
(F) LFLFVEILVLLVVARNFQCSWKRSEFALGLMLVSIILIGLLPLFF 257
(G) LFLFGEVLAILLIARSEFKYSWKRTFSFLGIVLVSVLILGLLTTF 255
(H) LFLFVEILVLLVVARNFQCSWKRSEFALGLMLVSIILIGLLPLFF 236
(I) LFLFVEILVLLVVARNFQCSWKRSEFALGLMLVSIILIGLLPLFF 257
(J) LFLFVEILVLLVVARNFQCSWKRSEFALGLMLVSIILIGLLPLFF 274
(K) LFLFGEVLAILLIARSEFKYSWKRTFSFLGIVLVSVLILGLLTTF 208
(L) LFLFVEILVLLVVARNFQCSWKRSEFALGLMLVSIILIGLLPLFF 224

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Figure S5. Multiple protein sequence alignment of SttA and homologous sequences from Human Stool Microbiome from Human Microbiome Project (HMP) and MetaHit. Black shading indicates regions of 100% amino acid identity. Putative transmembrane regions for SttA, predicted by TMHMM, are indicated with red boxes. Truncated or partial sequence fragments from HMP were not included (n=4). Information on the protein sequences (A) – (L) is indicated in the legend below.

Legend:

(A) = SttA protein sequence (B) SRS053214_LANL_scaffold_17021__gene_42707 (C) SRS024549_LANL_scaffold_1815__gene_4559 (D) C3406971__gene_199744 (E) SRS018656_WUGC_scaffold_544__gene_591 (F) SRS015217_WUGC_scaffold_30292__gene_65222 (G) SRS077730_LANL_scaffold_24345__gene_72567 (H) SRS024075_LANL_scaffold_21370__gene_63545 (I) Baylor_scaffold_22757__gene_50812 (J) C2121591__gene_151559 (K) MetaHit_MH0011_GL0108025 [Complete]locus=scaffold6530_52:7938:8564 (L) MetaHit_V1_GL0100177 [Complete] locus=scaffold36986_1:2178:2888