**Supplementary Table S1. Quantitative PCR Primer Sequences**

| Gene | Orientation | Primer Sequence |
|---|---|---|
| SmSULT | Forward | 5'-ATT GGA TGG TTA CAT AGC AAC TAC -3' |
| | Reverse | 5'-CCA TGG ATC ATT TGA TTT GGG T -3' |
| ShSULT | Forward | 5'- ATA GCT ACA ACA GAT CTA CCA TCA -3' |
| | Reverse | 5'- TAA GTT TCC ATG GAT CCG TAG AT-3' |
| SjSULT | Forward | 5'- TGATTGGTTGACAAGTTTTCG-3' |
| | Reverse | 5'- CACTAAAAGACGTTCGGATGG-3' |
| SmGAPDH | Forward | 5'- GTG AAA GAG ATC CAG CAA ACA T -3' |
| | Reverse | 5'- ATA TGA GCC TGA GCT TTA TCA ATG-3' |
| ShGAPDH | Forward | 5'- GAT CAA ATT AAG GCT GTG GTC A -3' |
| | Reverse | 5'- CCA AAC TCA TTA TCG TAC CAT GAA -3' |
| SjGAPDH | Forward | 5'- TCA GCT CAG ACT TTA TTG GAT GTA -3' |
| | Reverse | 5'- TTG TCG TAC CAT GAA ACC AGT –3' |
| SmACTIN | Forward | 5'- TGTTGTTGATAATGGATCAGGGA-3' |
| | Reverse | 5'- CAGTTCGTCACAATACCGTG-3' |
| ShACTIN | Forward | 5'- GACGAAGAAGTTCAAGCCCT-3' |
| | Reverse | 5'- CGTGTTCGATTGGGTATTTCAG-3' |
| SjACTIN | Forward | 5'- AGAGCTGTATTCCCTTCCATC-3' |

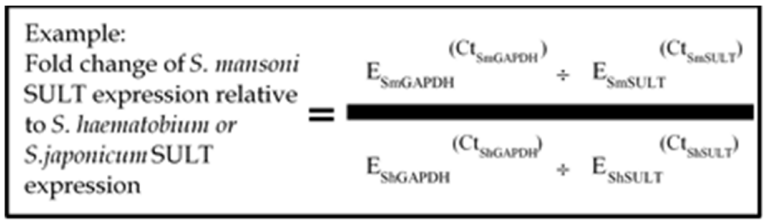
| | | |
|---|---|---|
| | Reverse | 5’- TCTTCTCCATATCATCCCAGTTTG-3’ |
| SmTUBULIN | Forward | 5’- CGGAATGGGAACACTACTCA-3’ |
| | Reverse | 5’- GACGACTGTATCAGAGACCTTAG-3’ |
| ShTUBULIN | Forward | 5’- TTGGTTGATTCCGTCTTAGATGT-3’ |
| | Reverse | 5’- TGTCAGATACTTTAGGCGATGG-3’ |
| SjTUBULIN | Forward | 5’- AATCAAATTGGTGCTAAGTTCTGG-3’ |
| | Reverse | 5’- CGTACACTGTCCATAGTTCCC-3’ |

**Supplementary Table S2. Digital PCR Primer Sets**

| Gene | Orientation | Primer Sequence |
|---|---|---|
| SmSULT | Forward | 5’-ATT GGA TGG TTA CAT AGC AAC TAC -3’ |
| | Reverse | 5’-CCA TGG ATC ATT TGA TTT GGG T -3’ |
| ShSULT | Forward | 5’- ATA GCT ACA ACA GAT CTA CCA TCA -3’ |
| | Reverse | 5’- TAA GTT TCC ATG GAT CCG TAG AT-3’ |
| SjSULT | Forward | 5’- TGATTGGTTGACAAGTTTTCG-3’ |
| | Reverse | 5’- CACTAAAAGACGTTCGGATGG-3’ |

**Supplementary Table S3: SULT T7 Primer Sequences**

| Gene | Orientation | Primer Sequence | Size |
|---|---|---|---|
| SmSULT | Forward | 5'- (T7) TCT CAG CTG GTC TAC CGA GAA-3' | 591 bp sequence nt 41-606 |
| | Reverse | 5'- (T7)TCCCAACCATCACCAAGACG-3' | |
| ShSULT | Forward | 5'- (T7)GGCCTACCAAGAACAGGTACAA-3' | 569 bp sequence nt 85-654 |
| | Reverse | 5'- (T7)TGATTCCCAACCATCACCAAG-3' | |
| SjSULT | Forward | 5'- (T7)GATACCTATAAAGAAGAAGTAGATAAAGTC-3' | 197 bp sequence nt 436-633 |
| | Reverse | 5'- (T7)AGA CGT TCG GAT GT ACA -3' | |




**Supplementary Figure S1**. Formula for Cross Species *SULT* Transcript Comparison. The method above is algebraically equivalent to the ΔΔCt method for determining relative transcript quantities. In the example given, the fold change of *S. mansoni SULT* expression is determined relative to *S. haematobium or S. japonicum SULT*. $E_{SxGAPDH}$ , $E_{SxActin}$ & $E_{SxTub}$: Efficiency of Internal Reference. $E_{SxSULT}$ : Efficiency of SULT Primers. $Ct_{SxGAPDH}$ , $Ct_{SxActin}$ & $Ct_{SxTub}$: Critical threshold of Internal Reference Primers. $Ct_{SxSULT}$: Critical threshold of SULT Primers. x = m,h, or j (*S. mansoni, S. haematobium, or S. japonicum*).

**Video S1. Fluorescence *in situ* hybridization of *SmSULT*.**

Head of *S. mansoni* male. Please see attached video.

Cells positive for *SmSULT* stained positive for TAMRA-Tyramide, magenta. DAPI (blue) was used at a final concentration of 1 ug/mL to stain cell nuclei. FITC-positive cells are *Schistosoma* stem cells, positive for *Schistosoma histone H2B* [30, 31]. *SmSULT* and *H2B* probes were used at a final concentration of 150 ng/mL. FISH was performed on whole worms. This picture is represented of 4 male worms.

h2b_sult_MG copy.mov