Supplementary figure S7: transcript profiles of the pro-apoptotic genes BAK and BAX of *S. mansoni*

A

![Graph A](image)

B

![Graph B](image)

Suppl. Fig. S7

A, qPCR analyses (*n* = 4) of the *S. mansoni* orthologs of the pro-apoptotic genes BAK (Smp_095190) and BAX (Smp_072180) following treatment with QLT-0267 (left columns, light grey) or dsRNA against SmILK (right columns, grey).

B, result of a comparative RNA-seq analysis [1] in adults and isolated gonads on the basis of normalized, relative expression values (Avg exp (RPKM)) investigating the transcript profiles of BAK (left) and BAX (right) in: bM, bisex (paired) males; sM, single-sex (unpaired) males; bT, testes from bisex males; sT, testes from single-sex males; bF, bisex (paired) females; sF, single-sex (unpaired) females; bO, ovaries from bisex females; sO, ovaries from single-sex females (in each case *n* = 3, except sO: *n* = 2; [1]). One important finding in the context of the paper is that with respect to the expression of both genes sO > bO tendencies were found. This reveals an up-regulation of the pro-apoptotic genes BAK and BAX in ovaries isolated from unpaired, sexually immature females.
References