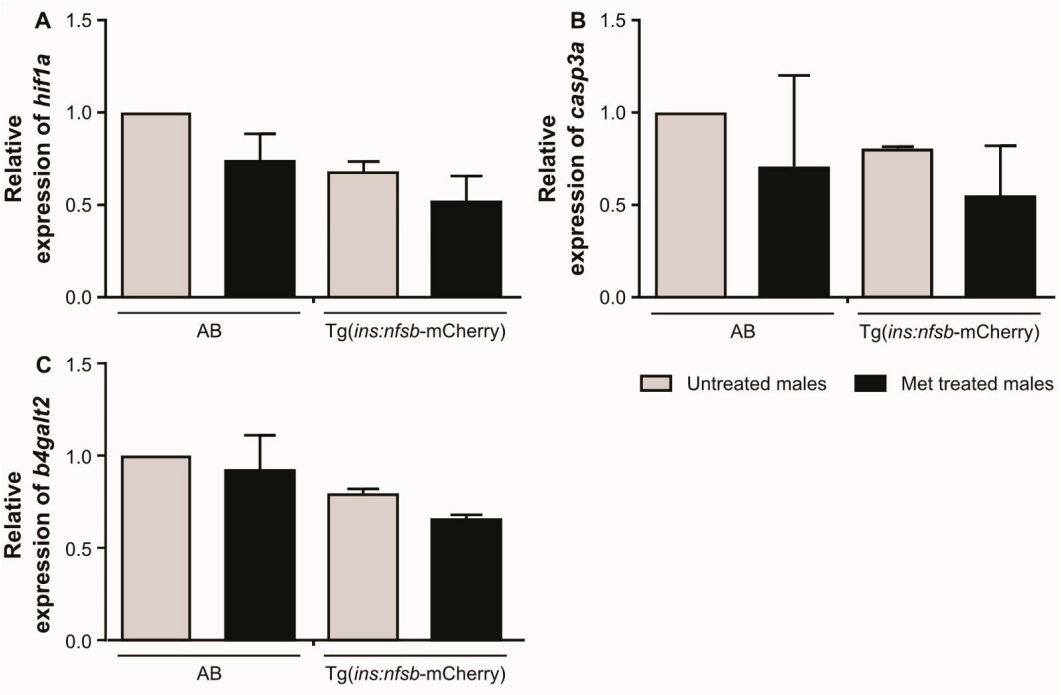
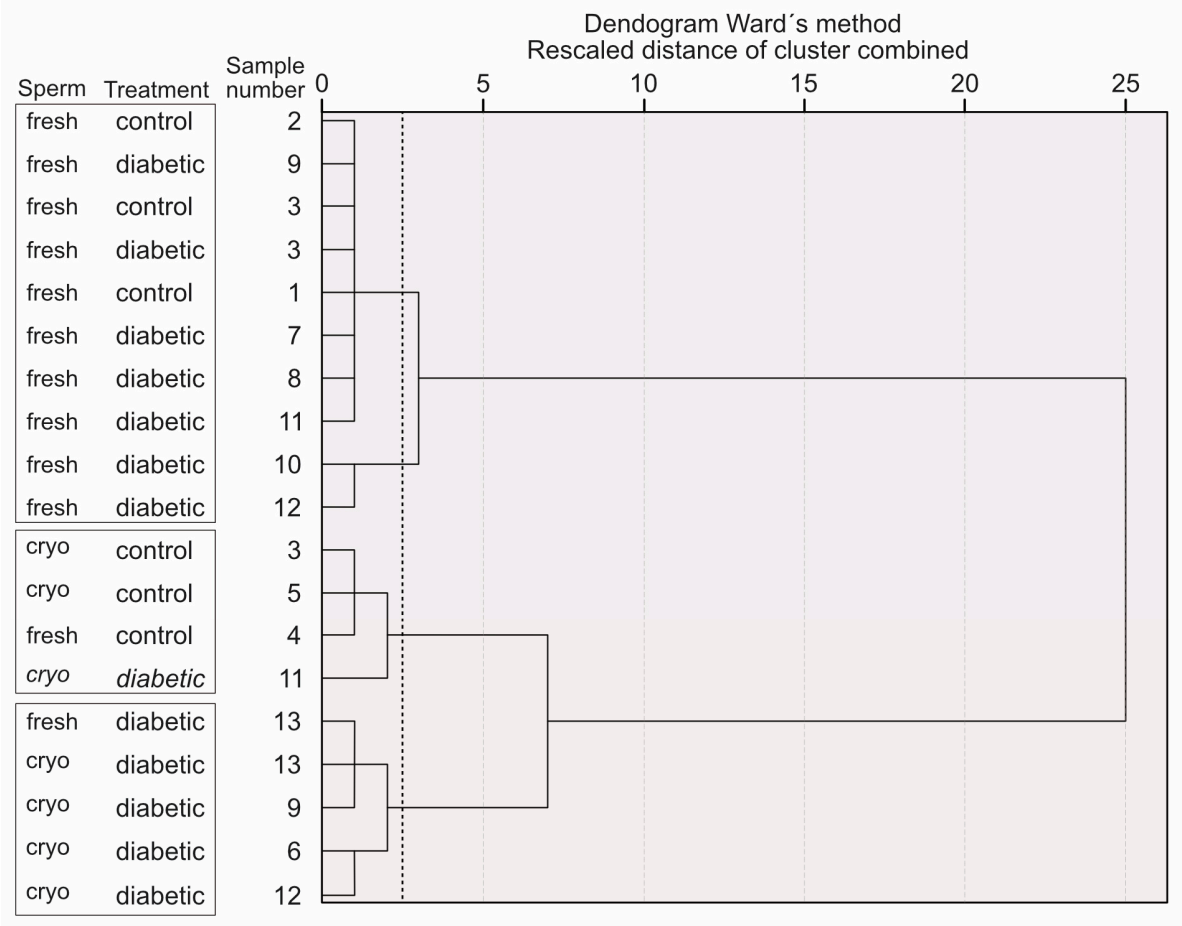
**Supplementary Table S1.** Forward and reverse primers used for target genes analysis through quantitative real-time polymerase chain reaction (qPCR).

| Target Gene | Gene Name | Forward Primer (5′-3′) | Reverse Primer (5′-3′) | Annealing Temperature (°C) |
|---|---|---|---|---|
| *ef1a* | elongation factor 1 alpha | AGCCCCTCCTGGCTTTCACCC | TGGGACGAAGGCAACACTGGC | 60 |
| *insa* | preproinsulin | CATTCCTCGCCTCTGCTTC | TGCCTGGGTTAGTGCTTACA | 60 |
| *insra* | insulin receptor a | TCTACAGCGAGGAAAACAAGC | AGAGATAAGATGCGTCCGTTTT | 60 |
| *slc2a2* | solute carrier family 2 member 2 | GCCATAACAGCAGGACTACT | GATGACAGACCACAGTACAATCC | 60 |
| *b4galt2* | 1,4- galactosyltransferase | ACCATCTTCTGCCTAGCACCA | GAGTATATTTCCCGCCTTCTGTGAC | 60 |
| *hif1a* | hypoxia-inducible factor-1a | CAGCCTTTTTGTGAAGGGGC | TGACTGGAGAAACAGTCCGC | 60 |




**Supplementary Figure S1.** Genes relative expression to *ef1α* in zebrafish sperm pools using 2−ΔΔCt method: (**A**) *hif1a* in spermatozoa pools of AB males in control (*n* = 2) and Met treatment (*n* = 2), and Tg(*ins*:*nfsb-mCherry*) in control (*n* = 2) and Met treatment (*n* = 2) and (**B**) *caspase 3a (casp3a)* in spermatozoa pools of AB males in control (*n* = 2) and Met treatment (*n* = 2), and Tg(*ins*:*nfsb-mCherry*) in control (*n* = 2) and Met treatment (*n* = 2) and (**C**) *b4galt2* in spermatozoa pools of AB males in control (*n* = 2) and Met treatment (*n* = 2), and Tg(*ins*:*nfsb-mCherry*) in control (*n* = 2) and Met treatment (*n* = 2) The values plotted represent means ± SD.




**Supplementary Figure S2.** Dendogram of Ward´s hierarchical cluster analysis for fresh and cryopreserved sperm (of principal components resulting from motility and DNA fragmentation data) of zebrafish sperm cryopreserved with a −10 °C/min cooling rate. Rectangles discriminate clusters of samples within fresh and cryopreserved sperm from untreated and Met treated Tg(*ins:nfsb-mCherry*) males.