

# Supplementary: Changes in Bull Semen Metabolome in Relation to Cryopreservation and Fertility

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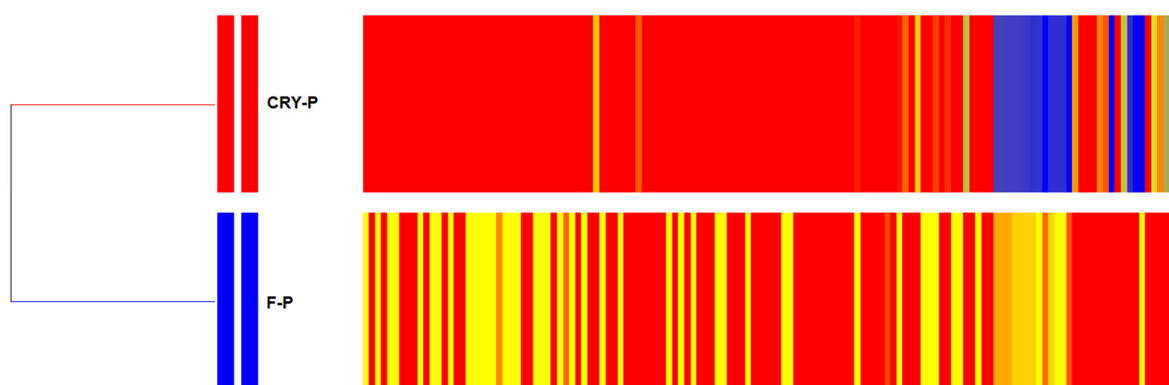
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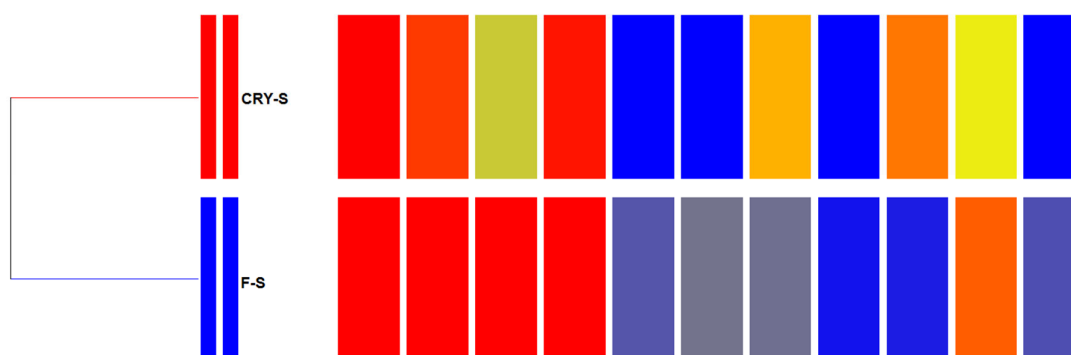
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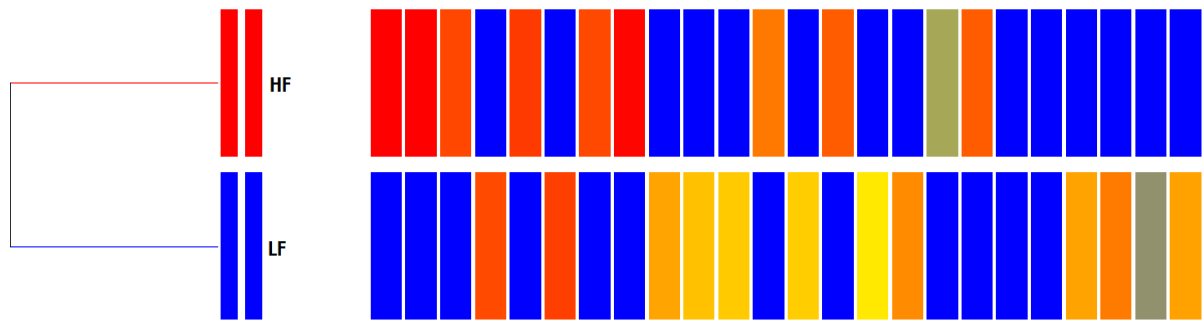
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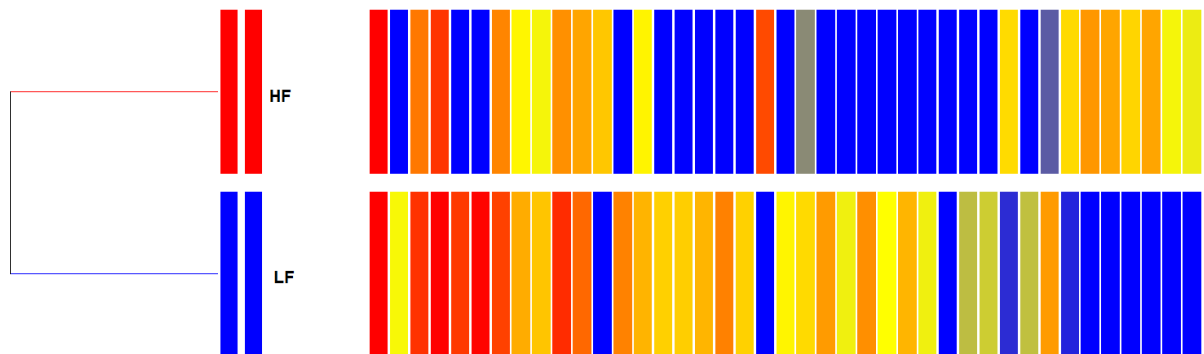
**Figure S1.** Hierarchical clustering analysis of fresh (in blue; F-P) and cryopreserved (in red; CRY-P) seminal plasma. Differentially expressed metabolites were obtained from T-test  $p\text{-value} < 0.05$  and fold change  $> 2.0$ .



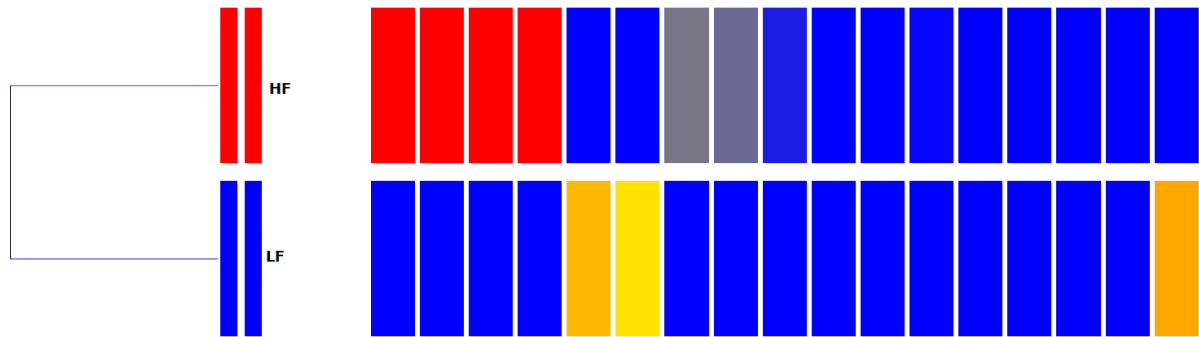
**Figure S2.** Hierarchical clustering analysis of fresh (blue; F-S) and cryopreserved (red; CRY-S) spermatozoa. Differentially expressed metabolites were obtained from T-test  $p\text{-value} < 0.05$  and fold change  $> 2.0$ .



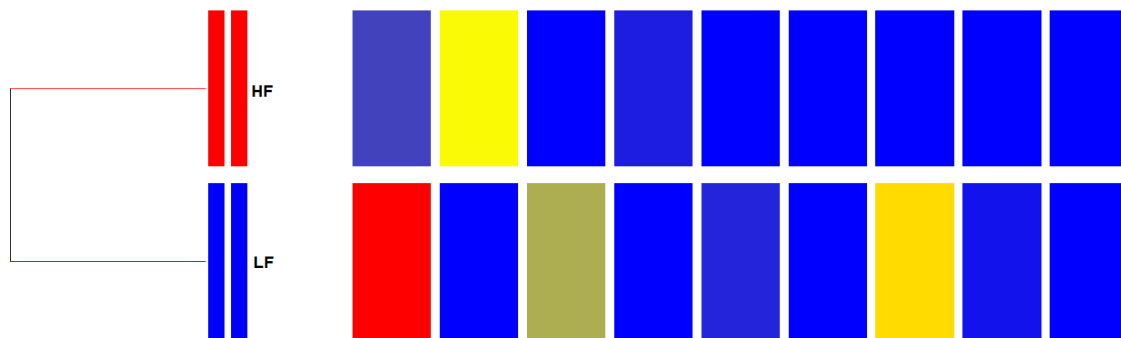
**Figure S3.** Hierarchical clustering analysis of fresh seminal plasma for high (in red; HF) and low (in blue; LF) fertility bulls. Differentially expressed metabolites were obtained from T-test  $p\text{-value} < 0.05$  and fold change  $> 2.0$ .



**Figure S4.** Hierarchical clustering analysis of cryopreserved seminal plasma for high (in red; HF) and low (in blue; LF) fertility bulls. Differentially expressed metabolites were obtained from T-test  $p\text{-value} < 0.05$  and fold change  $> 2.0$ .



**Figure S5.** Hierarchical clustering analysis of fresh spermatozoa for high (in red; HF) and low (in blue; LF) fertility bulls. Differentially expressed metabolites were obtained from T-test  $p\text{-value}<0.05$  and fold change $>2.0$ .



**Figure S6.** Hierarchical clustering analysis of cryopreserved spermatozoa for high (in red; HF) and low (in blue; LF) fertility bulls. Differentially expressed metabolites were obtained from T-test  $p\text{-value}<0.05$  and fold change $>2.0$ .