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Supplemental information

The role of HnrnpF/H as a driver of oligoteratozoospermia

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Table S1. Semen parameters used for this study, related to Table 1.

A) Semen analysis of individual infertile donors.

B) Semen analysis of individual fertile donors.

Panel A

Infertile			
VOLUME	MOTILITY	COUNT (10 ⁶ /mL)	MORPHOLOGY (% Normal)
4.0	32	33.75	6
4.0	53	45.03	5
4.0	49	13	8
5.0	39	20.7	7
3.8	53	14.145	4
2.5	53	42.9	7
4.5	37	8.05	7
2.5	45	36.63	6
4.0	44	5.535	4
5.5	39	18.9	4
1.5	45	33.75	4

Panel B

Fertile			
VOLUME	MOTILITY	COUNT (10 ⁶ /mL)	MORPHOLOGY (% Normal)
5	66	128	29
8	77	72	25
3	69	227	39
2	81	145	50
3	61	224	35
5	63	340	24
3.5	83	190	47
0.5	53	164	30
1.5	88	186	47
4	75	138	32

Table S3. Gene ontology analysis, related to Figures 1 and 2.

A) Shows the Sub-cellular compartment.

B) Shows the Biological Process.

c) Shows the Molecular Function of changing proteins.

Panel A

Sub Cellular compartment	# Proteins	%	P-Value	Benjamaini-corrected
Mitochondrion	75	20.3	2.60E-18	1.20E-16
Nucleosome core	17	4.6	1.10E-11	2.60E-10
Cytoplasm	161	43.5	4.90E-11	7.50E-10
Proteasome	10	2.7	6.40E-07	7.30E-06
Cilium	17	4.6	1.80E-04	1.60E-03
Mitochondrion inner membrane	18	4.9	2.30E-04	1.80E-03
Flagellum	10	2.7	8.50E-04	5.60E-03
Cytoskeleton	41	11.1	2.40E-03	1.40E-02
Intermediate filament	7	1.9	3.40E-03	1.60E-02
Dynein	5	1.4	3.60E-03	1.60E-02
CF(1)	3	0.8	5.00E-03	2.10E-02
Chromosome	20	5.4	1.60E-02	6.10E-02
Virion	5	1.4	1.70E-02	6.10E-02
Cytoplasmic vesicle	21	5.7	3.90E-02	1.30E-01
Keratin	7	1.9	8.40E-02	2.60E-01

Panel B

Biological Process	# Proteins	%	P-Value	Benjamini-corrected
RNA binding	82	4.6	1.20E-07	8.40E-06
structural constituent of chromatin	16	4.3	3.40E-10	1.00E-07
unfolded protein binding	17	4.6	2.80E-09	5.50E-07
protein domain specific binding	22	5.9	8.70E-09	1.30E-06
protein binding	284	76.8	2.20E-08	2.60E-06
chaperone binding	14	3.8	1.30E-07	1.30E-05
protein heterodimerization activity	23	6.2	2.40E-06	2.00E-04
structural molecule activity	16	4.3	3.90E-06	2.90E-04
structural constituent of ribosome	15	4.1	1.40E-05	9.30E-04
cadherin binding	19	5.1	3.20E-05	1.90E-03
protein binding involved in protein folding	8	2.2	4.30E-05	2.10E-03
identical protein binding	56	15.1	4.30E-05	2.10E-03
ATP binding	52	14.1	4.70E-05	2.10E-03
ADP binding	7	1.9	4.90E-05	2.10E-03
ubiquitin protein ligase binding	16	4.3	8.30E-04	3.30E-02
heat shock protein binding	7	1.9	1.00E-03	3.90E-02
magnesium ion binding	13	3.5	1.50E-03	5.30E-02
flavin adenine dinucleotide binding	7	1.9	1.70E-03	5.60E-02
serine-type carboxypeptidase activity	3	0.8	3.40E-03	1.00E-01
oxidoreductase activity	12	3.2	3.70E-03	1.10E-01
catalytic activity	9	2.4	4.50E-03	1.20E-01
pyruvate dehydrogenase (NAD ⁺) activity	3	0.8	5.00E-03	1.20E-01
L-lactate dehydrogenase activity	3	0.8	5.00E-03	1.20E-01
proton-transporting ATP synthase activity, rotational mechanism	4	1.1	5.00E-03	1.20E-01
MHC class I protein binding	4	1.1	5.80E-03	1.30E-01
nuclear import signal receptor activity	4	1.1	5.80E-03	1.30E-01
peroxiredoxin activity	3	0.8	6.90E-03	1.50E-01
ligase activity	5	1.4	7.70E-03	1.60E-01

Panel C

Molecular function	# Proteins	%	P-Value	Benjamini-corrected
Isomerase		4.6	1.20E-07	8.40E-06
Oxidoreductase	32	8.6	4.50E-06	1.60E-04
Chaperone	18	4.9	8.20E-06	1.90E-04
Ligase	14	3.8	2.50E-05	4.30E-04
Ribonucleoprotein	19	5.1	8.50E-05	1.20E-03
Aminoacyl-tRNA synthetase	7	1.9	1.50E-04	1.80E-03
Ribosomal protein	14	3.8	2.30E-04	2.30E-03
tRNA-binding	4	1.1	2.10E-02	1.50E-01
Elongation factor	4	1.1	2.10E-02	1.50E-01
Viral nucleoprotein	4	1.1	2.10E-02	1.50E-01
Antioxidant	3	0.8	3.40E-02	2.20E-01
Carboxypeptidase	4	1.1	4.60E-02	2.70E-01
Motor protein	7	1.9	7.10E-02	3.80E-01
Peroxidase	3	0.8	9.70E-02	4.90E-01

Figure S1. R-Script for identifying protein isoforms, related to Fig. 3.

```
# choose Swath library text file
df = read.table(file=file.choose(), header = T)
df1 = df[,c(1:2)]

library(dplyr)
IsoGroup = df1 %>% group_by(Sequence) %>%
  summarise(ProteinGroup = paste(Protein_Name, collapse=","))

write.table(IsoGroup, file = "IsoGroup.txt", sep = "\t", quote = F, row.names = F, col.names = F)

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```