

Human spermatozoa quantitative proteomic signature classifies normo- and asthenozoospermia

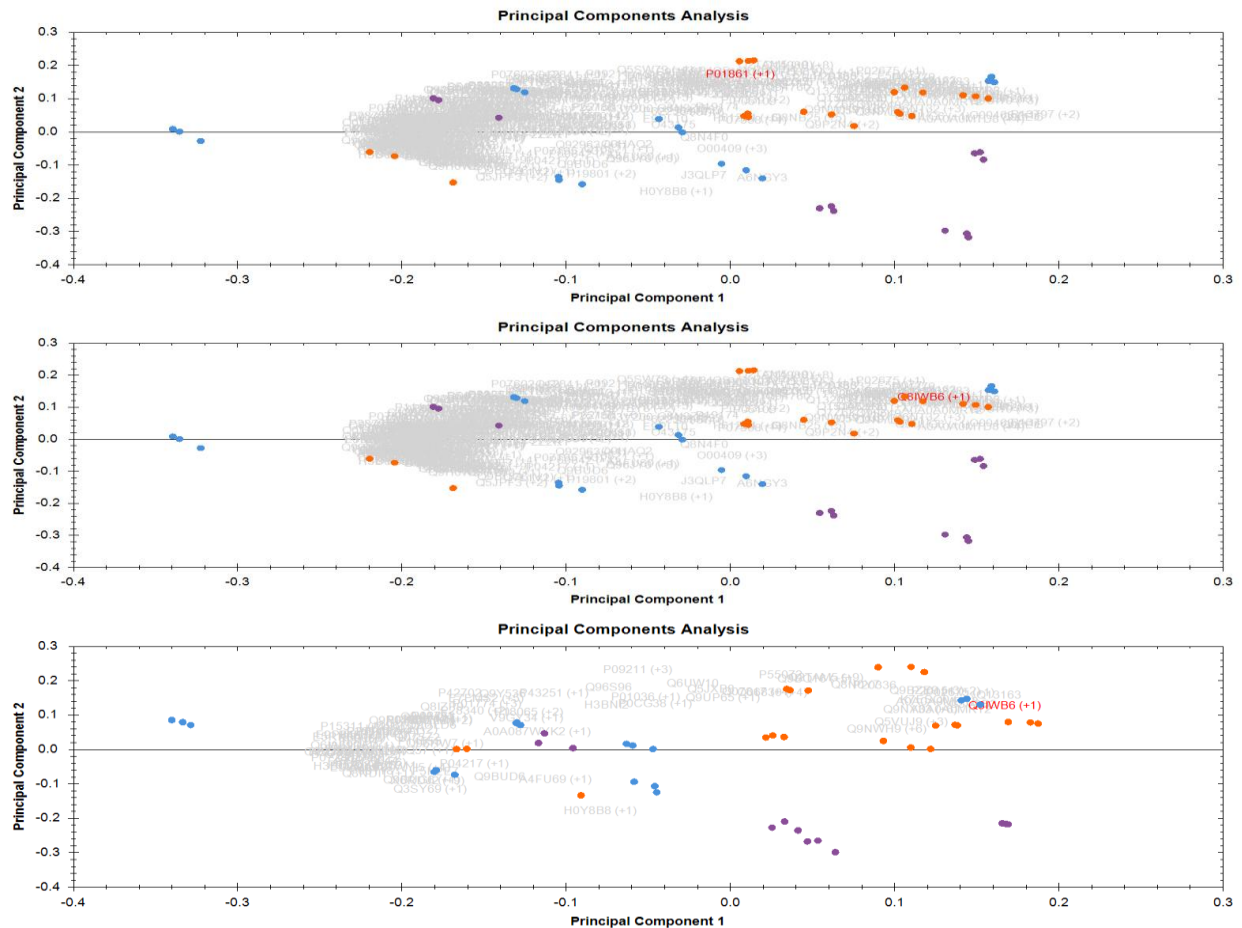
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Supplementary Table 1 and Figures

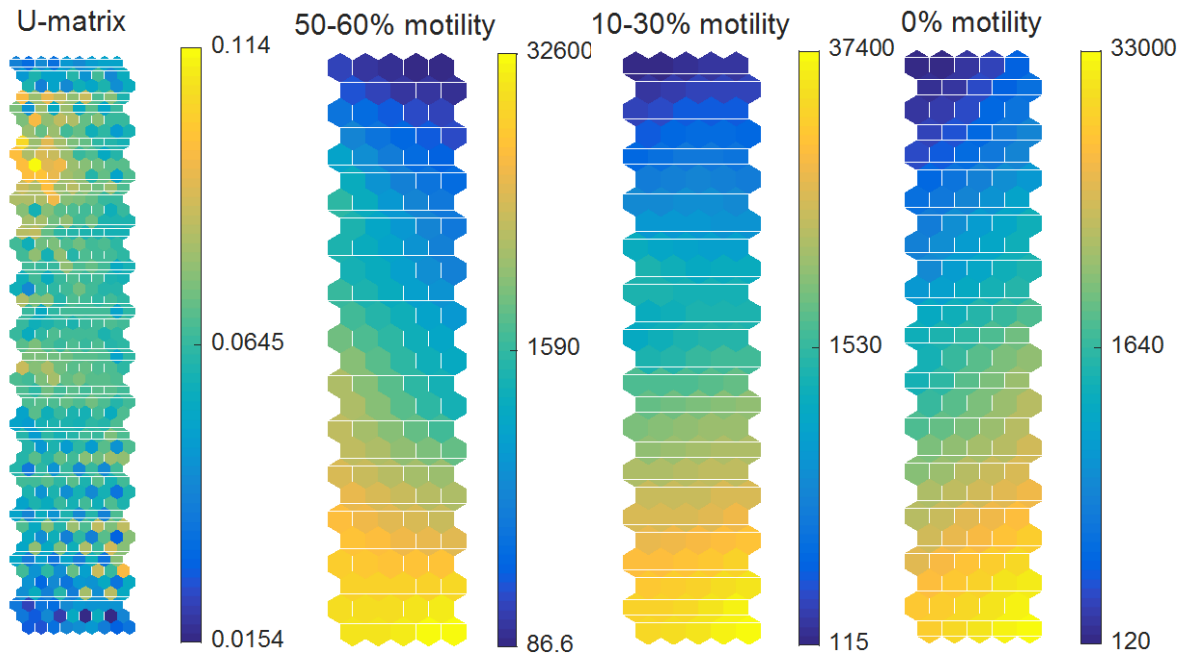
Supplementary Table 1: Metadata for samples included in the study. Coded sample names, disease categorization, sperm count and sperm motility in percentage is given in the table. Which sperm and seminal plasma samples were used in the study are also indicated in separate columns.

Sample Name	Disease class	Sperm	Seminal plasma	Sperm Count million/mL	Sperm Motility (% Motile sperm)
N2	Normal	x	x	160	60
N3	Normal	x	x	116	50
N11	Normal	x	x	102	55
N12	Normal	x	x	78	50
N13	Normal	x	x	60	55
N21	Normal	N/A	x	86	50
N22	Normal	N/A	x	185	60
A1	Asthenozoospermia	X	x	224	10
A2	Asthenozoospermia	X	x	60	20
A3	Asthenozoospermia	X	x	50	0
A4	Asthenozoospermia	N/A	x	2	0
A5	Asthenozoospermia	X	x	70	0
A12	Asthenozoospermia	X	x	55	30
A13	Asthenozoospermia	X	x	78	30
A21	Asthenozoospermia	X	x	160	0
A22	Asthenozoospermia	N/A	x	105	10
A23	Asthenozoospermia	X	x	72	10

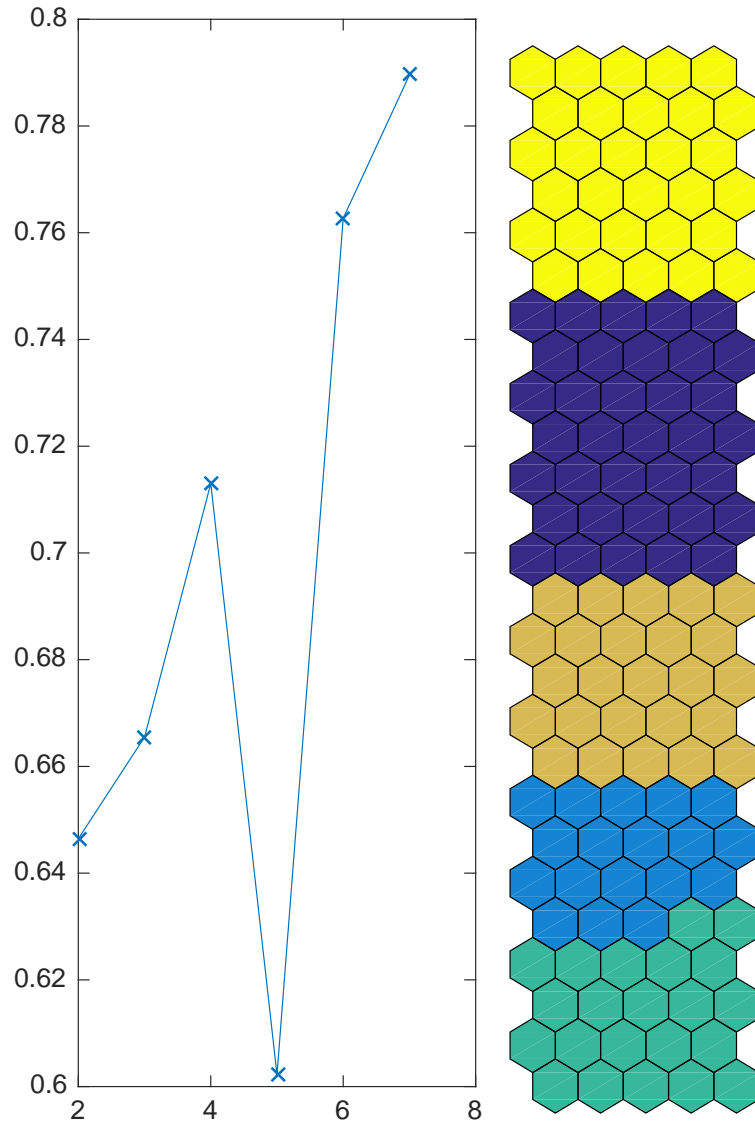
Supplementary Figures:



Supplementary Figure 1: Human seminal plasma motility classes PCA: Purple dots are samples having 0% sperm motility, blue dots are samples having 10-30% sperm motility and orange dots are samples having 50-60% sperm motility. Upper panel is the PCA when all the proteins quantitated were considered for the PCA, middle panel is when only housekeeping proteins (FC 1.0 to 1.29) were considered for PCA. Lower panel is when only the proteins having Anova p value less than 0.05 and fold change more than 2 in either condition were considered for PCA.



Supplementary Figure 2: Sperm proteomic dataset SOM analysis; The first matrix in the figure is the U-matrix calculated based on all the variables and then the component planes. Unified distance matrix (U-matrix) visualizes distances between neighboring map units, and shows the cluster structure of the map: High values of the U-matrix indicate a cluster border, uniform areas of low values indicate cluster themselves. Each component planes shows the values of one variable in each map unit.



Supplementary Figure 3: Sperm proteomic dataset SOM analysis; It illustrates the Davies-Boulding index which indicates that there are five clusters formed in SOM analysis. The clusters on the map are also shown. This cluster information enabled the respective cluster feature extraction.