

Supplemental Data File

Table S1. Image Feature Definitions, from IDEAS[®] Software Version 6.2 (Luminex Corp., Seattle, WA, USA).

Image Feature	Definition
<i>Angle Intensity</i>	Angle is the angle of the major axis from a horizontal plane in radians.
<i>Area</i>	The number of microns squared in a mask is equal to the Area. 1 pixel = 1.0 μm^2 .
<i>Aspect Ratio</i>	Aspect Ratio is the Minor Axis divided by the Major Axis and describes how round or oblong an object is.
<i>Aspect Ratio Intensity</i>	Aspect Ratio Intensity is the Minor Axis Intensity divided by the Major Axis Intensity.
<i>Bright Detail Intensity R3</i>	The Bright Detail Intensity R3 feature computes the intensity of localized bright spots within the masked area in the image. The intensity of bright spots that are 3 pixels in radius or less are included and the local background around the spots is removed before the intensity computation.
<i>Centriod Y</i>	Centroid Y is the number of pixels in the vertical axis from the upper, left corner of the image to the center of the mask.
<i>Circularity</i>	Circularity measures the degree of the mask's deviation from a circle. Its measurement is based on the average distance of the object boundary from its center divided by the variation of this distance. Thus, the closer the object to a circle, the smaller the variation and therefore the feature value will be high. Vice versa, the more the shape deviates from a circle, the higher the variation and therefore the Circularity value will be low.
<i>Diameter</i>	The Diameter feature provides the diameter of the circle that has the same area as the object.
<i>Gradient RMS</i>	The Gradient RMS feature measures the sharpness of an image by detecting large changes of pixel values in the image. It is computed using the average gradient of a pixel normalized for variations in intensity levels.
<i>H Correlation</i>	The Haralick (H) texture features are a set of texture features based on the second order statistics computed from the joint 2-D probability distribution of pixel intensities in the image. This distribution is referred to as the Gray Level Co-occurrence Matrix (GLCM). Correlation measures how similar pixel pairs are, and is the opposite of contrast. Images with high correlation are very uniform and lack variant texture.
<i>H Energy</i>	Energy is a measure of intensity concentration in the cell. At one extreme is the case of a uniform distribution with all probabilities being equal. This image has several intensity variations with no noticeable concentration of high intensity and thus has low energy. At the other extreme is the case of a very narrow distribution with a few elements having high values. This image will have notable intensity concentrations and thus, has high energy.
<i>H Entropy</i>	Entropy is also a measure of high intensity concentration in the cell. However, this feature relates to the randomness of the intensities in the image. Images that have distinct areas of intensity concentration are less random and thus, have low entropy. Images that have a range of equally likely intensity pairings have less distinct intensity concentrations, and correspondingly, have higher entropy. Entropy is the opposite of energy.
<i>Height</i>	Using the bounding rectangle, Height is the number of microns of the longer side.
<i>Length</i>	Length measures the longest part of an object. Unlike the Major Axis feature, Length can measure the object's length even if it folds to form a cashew, banana, or doughnut shape, where in many of these cases the major or minor axis features would not be able to differentiate these with true circular shaped objects with no hole.
<i>Symmetry 3</i>	The Symmetry 3 feature measures the tendency of the object to have a three-fold axis of symmetry.

Table S2. Correlations of semen parameters found not significant.

PARAMETERS	<i>r</i>	<i>P-value</i>
<i>Not Significant:</i>		
% Normal Morphology: Conception Rate	0.206	0.175
% Normal Morphology: Total Born	0.001	0.994
% Mero Negative: Conception Rate	-0.033	0.828
% Mero Negative: Total Born	0.286	0.057
% Depolarized Mitochondria: Conception Rate	-0.017	0.911
% Viable with Intact Acrosome: Conception Rate	0.219	0.148
% Viable with Intact Acrosome: Total Born	0.266	0.078
Oxidation (Basal:Induced Ratio):Conception Rate	-0.078	0.612
Oxidation (Basal:Induced Ratio):Total Born	0.064	0.676
CompDNA: Conception Rate	-0.062	0.685
Mean Length MS: Conception Rate	-0.038	0.806
Std Dev Length MS: Conception Rate	0.074	0.628
Std Dev Length MS: Total Born	-0.264	0.080
Range Length MS: Conception Rate	0.117	0.444
Range Length MS: Total Born	-0.177	0.244
Minimum MS Length: Conception Rate	-0.227	0.133
Minimum MS Length: Total Born	-0.085	0.578
Maximum MS Length: Conception Rate	-0.113	0.461
% Depolarized Mitochondria: Minimum MS Length	0.067	0.662
% Depolarized Mitochondria: Maximum MS Length	0.146	0.339
% Viable with Intact Acrosome: Minimum MS Length	-0.241	0.111

Table S3. Assorted correlations of IBFC with fertility/AI service outcomes and laboratory semen parameters found in spermatozoa of 45 boars.

PARAMETERS	<i>r</i>	<i>P-value</i>
Fertility Related		
Bright Detail Intensity R3_mH33342_iAGG, Median Absolute Deviation (MAD), Head High AGG: Total Born	-0.423	0.004
Sperm Trait Related		
H Energy Mean_mSSC_iSSC_5, Median: % Viable with Intact Acrosome	0.621	< 0.00001
Centroid Y Intensity_mSSC_iSSC, MAD: % Viable with Intact Acrosome	-0.607	< 0.00001
Bright Detail Intensity R3_mSSC_iSSC, Median: % Viable with Intact Acrosome	0.531	0.0002
Bright Detail Intensity R3_mH33342_iAGG, Median, Head High AGG: CompDNA	0.496	0.0005

Bright Detail Intensity R3_mH33342_iAGG, Mean, Head: Low AGG: Mean Length MS	0.442	0.002
Symmetry 3_mSSC_iSSC, Median: % Normal Morphology	0.441	0.002
Length_mH33342, Mean: % Viable with Intact Acrosome	0.420	0.004
Height_mH33342, Mean: % Viable with Intact Acrosome	0.413	0.005
% Head No AGG [gated]: % Viable with Intact Acrosome	-0.377	0.011
% Head: Mid AGG [gated]: % Viable with Intact Acrosome	0.351	0.018
% Head Low AGG [gated]: % Viable with Intact Acrosome	0.339	0.023
Mitochondria Related		
Symmetry 3_mSSC_iSSC, Std. Dev.: % Depolarized Mitochondria	0.650	0.000002
Aspect Ratio_mSSC, MAD: % Depolarized Mitochondria	0.516	0.0003
Angle Intensity_mSSC_iSSC, Mean: % Depolarized Mitochondria	-0.515	0.0003
Bright Detail Intensity R3_mSSC_iSSC, Median: % Depolarized Mitochondria	-0.477	0.001
Symmetry 3_mSSC_iSSC, Mean: Oxidation (Basal:Induced Ratio)	-0.440	0.002
Area_mSSC, Median: % Depolarized Mitochondria	-0.406	0.006
Aspect Ratio Intensity_mSSC_iSSC, Mean: % Depolarized Mitochondria	0.403	0.006
% Head: No AGG [gated]: Oxidation (Basal:Induced Ratio)	0.321	0.032
% Head Low AGG [gated]: Oxidation (Basal:Induced Ratio)	-0.334	0.025
% Head: Mid AGG [gated]: Oxidation (Basal:Induced Ratio)	-0.315	0.035
Semen Parameter Related		
CompDNA: Total Born	-0.327	0.028
% Depolarized Mitochondria: Total Born	-0.322	0.031
Mean Length MS: Total Born	-0.299	0.046
Maximum MS Length: Total Born	-0.322	0.031
Mean Length MS: Oxidation (Basal:Induced Ratio)	-0.464	0.001
% Normal Morphology: Maximum MS Length	-0.368	0.013
Not Significant:		
Circularity_mH33342, Mean: Conception Rate	-0.233	0.123
Circularity_mH33342, Mean: Total Born	-0.210	0.165

Table S4. Correlations of terminal index with fertility/AI service outcomes and laboratory semen parameters of interest that were not found significant corresponding with manuscript **Figure 5**.

PARAMETERS	<i>r</i>	<i>P-value</i>
Sperm Trait Related		
Not Significant:		
CompDNA: Terminal Index	0.202	0.183
% Mero Negative: Terminal Index	0.142	0.351
% Depolarized Mitochondria: Terminal Index	-0.223	0.142
% Normal Morphology: Terminal Index	-0.041	0.787
% Viable with Intact Acrosome: Terminal Index	-0.037	0.809

Fertility Related		
<i>Not Significant:</i>		
<i>Total Born: Terminal Index</i>	0.071	0.600
<i>Conception Rate: Terminal Index</i>	0.036	0.812

Table S5. Correlations of terminal index with fertility/AI service outcomes and laboratory semen parameters with significance found in spermatozoa of 45 boars.

PARAMETERS	<i>r</i>	<i>P-value</i>
<i>Oxidation (Basal:Induced Ratio):Terminal Index</i>	0.438	0.003
<i>H Correlation Mean_mSSC_iSSC_5, Std. Dev.: Terminal Index</i>	-0.424	0.004
<i>Symmetry 3_mSSC_iSSC, Mean: Terminal Index</i>	-0.422	0.004

Figure S1. The following graphs shows the scatter plot of conception rate by each covariate together with regression lines unweighted (blue) and weighted (orange) by logarithmic function of number of matings. Each individual circle represents a boar and is colored by blue gradient corresponding to number of matings. There are no significant differences between unweighted and weighted regression lines.

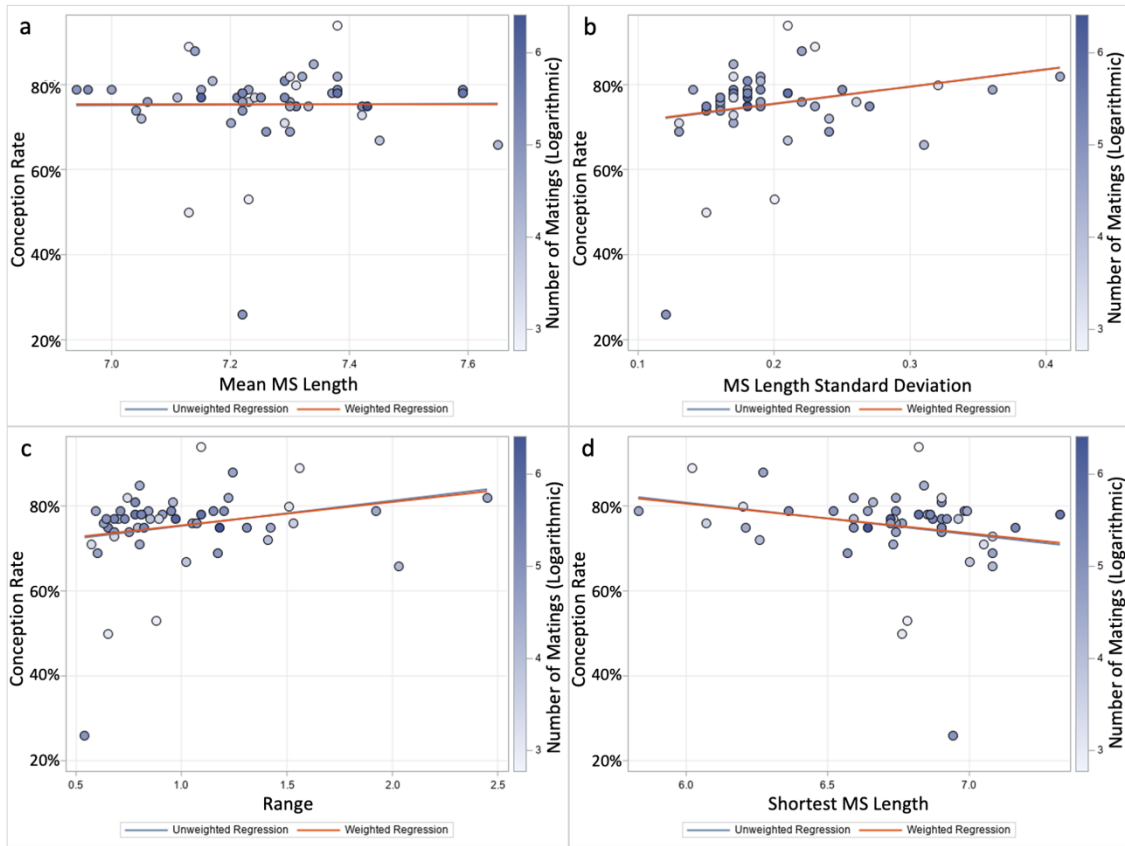


Figure S2. The following graphs shows the scatter plot of average total born by each covariate together with regression lines unweighted (blue) and weighted (orange) by logarithmic function of number of matings. Each individual circle represents a boar and is colored by blue gradient of number of matings. There are no significant differences between unweighted and weighted regression lines.

