Participant flow diagram:
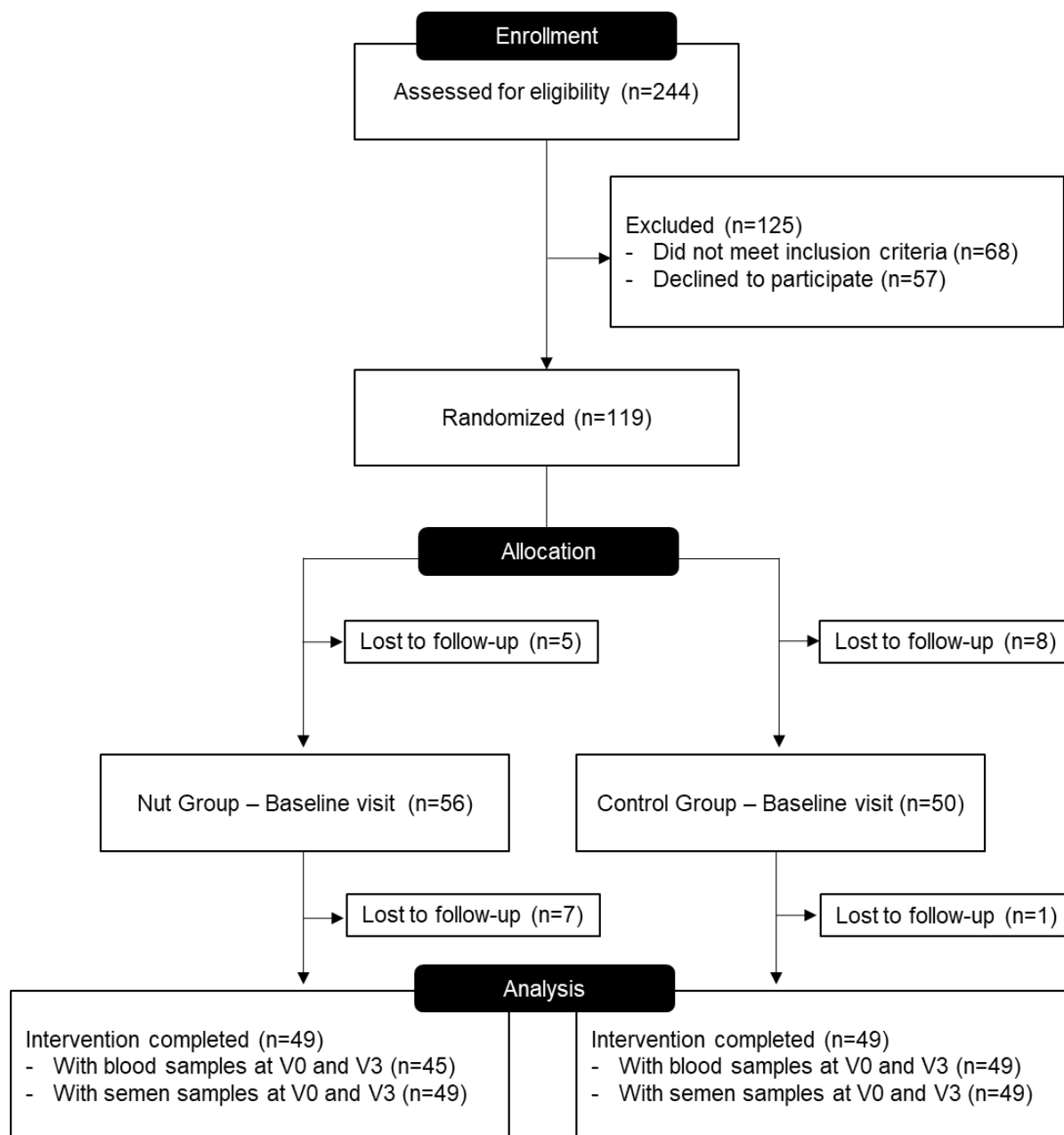
Baseline characteristics:

Baseline characteristics	Nut group (n=56)	Control group (n=50)
Age (years)	24 (4.6)	25 (4.7)
Weight (kg)	73.79 (9.74)	76.36 (11.52)
BMI (kg/m2)	23.55 (2.84)	24.09 (3.43)
Waist circumference (cm)	79.95 (7.37)	83.04 (8.57)
Systolic blood pressure (mmHg)	129.30 (11.56)	125.96 (11.46)
Diastolic blood pressure (mmHg)	73.04 (7.89)	71.63 (8.36)

Values are expressed as mean ± SD.

Primary outcome measures:

Semen parameters	Nut group (n=56)		Control group (n=50)		Treatment effect
	Baseline	Changes	Baseline	Changes	P-value
pH	8.0 (8.0, 8.5)	0.0 (0.0, 0.0)	8.0 (8.0, 8.5)	0.0 (0.0, 0.0)	0.089
Volume (ml)	3.00 (1.98, 4.15)	0.00 (-0.83, 0.50)	3.15 (2.05, 4.99)	-0.65 (-1.38, 0.15)	0.112
Total spermatozoa (x10^6)	75.55 (29.95, 111.25)	4.45 (-15.60, 34.95)	69.75 (29.25, 123.25)	-15.15 (-42.05, 7.15)	**0.002**
Spermatozoa concentration (x10^6)	26.20 (14.85, 44.30)	0.10 (-2.11, 10.35)	21.20 (9.80, 37.60)	0.00 (-4.05, 4.14)	0.086
Vitality (%)	78.66 (71.03, 82.36)	3.42 (0.00, 7.44)	80.00 (73.93, 86.18)	-0.20 (-3.18, 3.59)	**0.003**
Motility:					
Total motility (progressive and non-progressive motility) (%)	64.23 (44.44, 70.45)	3.41 (-0.87, 13.14)*	67.96 (60.42, 77.93)	0.00 (-4.93, 6.30)	**0.006**
Progressive motility (%)	43.03 (27.19, 53.48)	3.78 (0.00, 15.14)*	49.72 (35.00, 61.22)	1.70 (-2.18, 5.93)	**0.036**
Non-progressive motility (%)	12.06 (9.13, 16.14)	-2.38 (-5.24, 0.06)	11.30 (7.36, 13.64)	-0.28 (-3.94, 2.66)	0.727
Immotile spermatozoa (%)	35.77 (29.05, 53.02)	-3.41 (-13.71, 0.88)*	32.04 (22.07, 39.59)	-0.92 (-5.73, 4.46)	**0.006**
Morphology:					
Normal forms (%)	6.55 (5.00, 8.08)	0.82 (-0.17, 2.12)	6.32 (5.47, 7.74)	-0.04 (-1.06, 0.65)	**0.008**
Abnormal head (%)	54.56 (45.10, 66.46)	0.00 (-2.32, 9.82)	52.43 (40.77, 66.19)	0.91 (-2.14, 8.53)	0.936
Abnormal midpiece (%)	10.79 (8.78, 15.03)	-0.21 (-2.86, 1.59)	11.83 (7.80, 14.44)	0.95 (-3.26, 2.93)	0.207
Abnormal principal piece (%)	11.27 (5.10, 27.43)	-0.46 (-3.90, 0.33)	14.49 (5.25, 30.85)	-1.15 (-4.22, 0.84)	0.829
Combined abnormality (%)	8.84 (6.46, 13.14)	0.14 (-3.39, 0.65)	7.59 (6.55, 13.46)	0.29 (-2.35, 2.20)	0.570

ANCOVA models were used to assess differences between intervention groups. Changes in seminogram variables were adjusted for baseline values of each seminogram variable. A paired Wilcoxon test was used to assess differences within intervention groups. Values are expressed as median and interquartile rank.
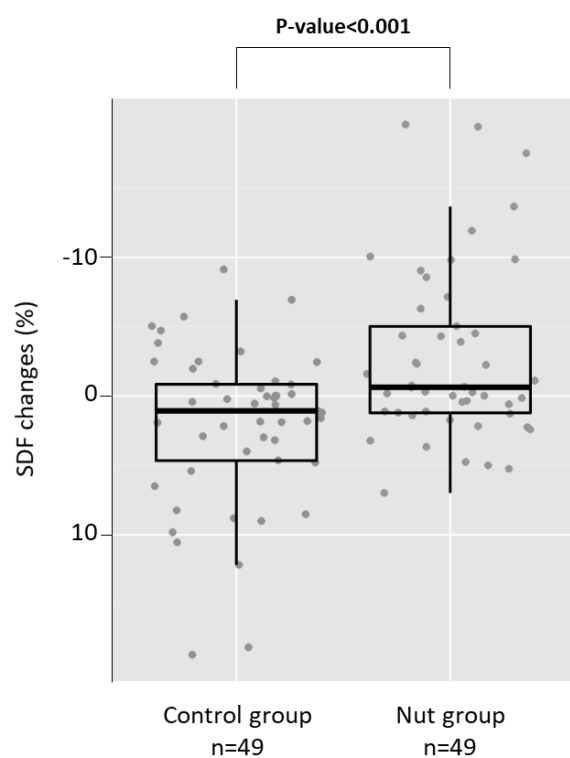∗Significant difference ($P < 0.05$) between baseline and the end of a particular intervention period.
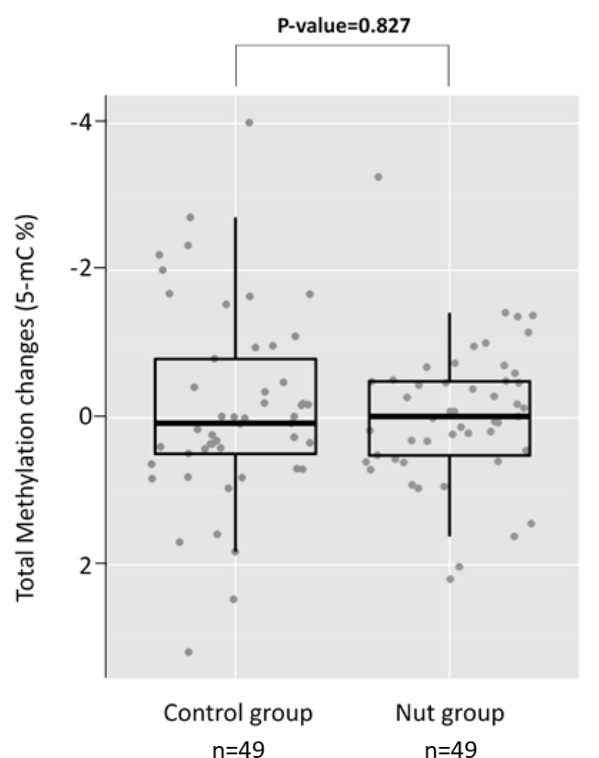
Secondary outcome measures:

Boxplot of the differences between the control group and nut group in the reactive oxygen species (ROS) analysis.
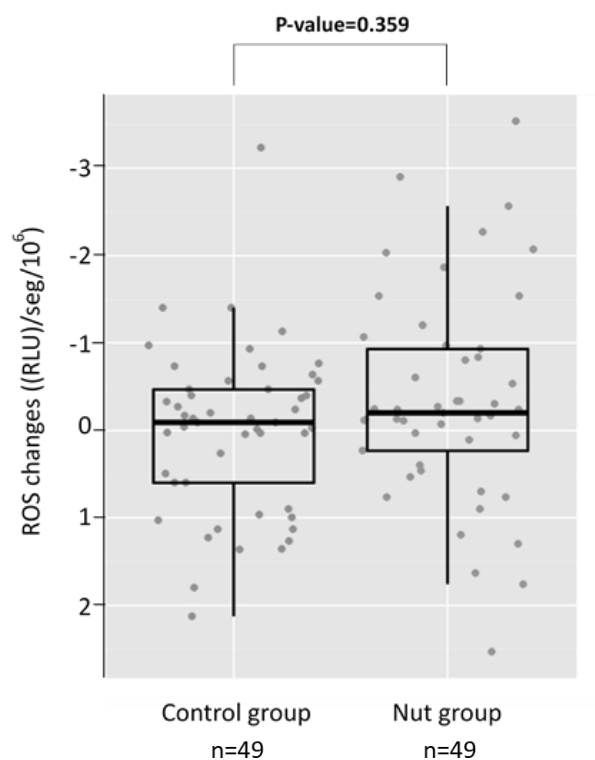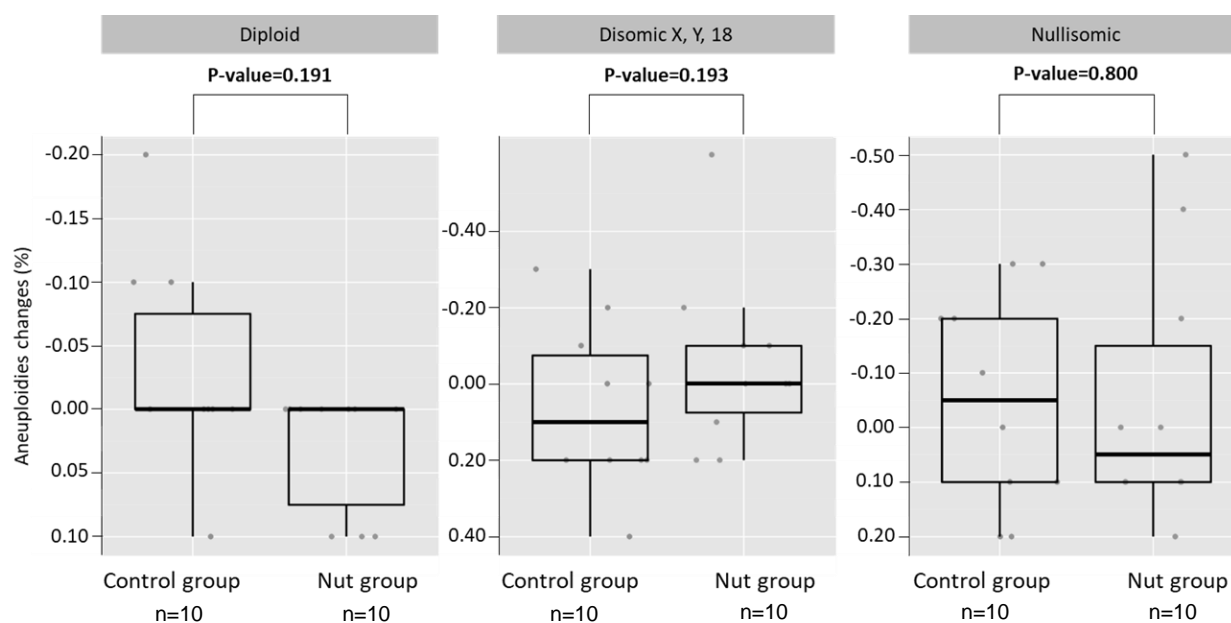

Boxplot of the differences between the control group and nut group in the sperm DNA fragmentation (SDF) analysis.

Boxplot of the differences between the control group and nut group in the total methylation analysis.


Boxplot of the differences between the control group and nut group in the aneuploidy analysis.

For all the boxplot graphs: ANCOVA models were used to assess differences between intervention groups. Changes were adjusted for baseline values. A horizontal line in the boxplot illustrates the median value. The upper and lower bars indicate the 3rd and 1st percentiles, respectively.

Bar plot of the differences between the control group and nut group for the analyzed miRNAs.
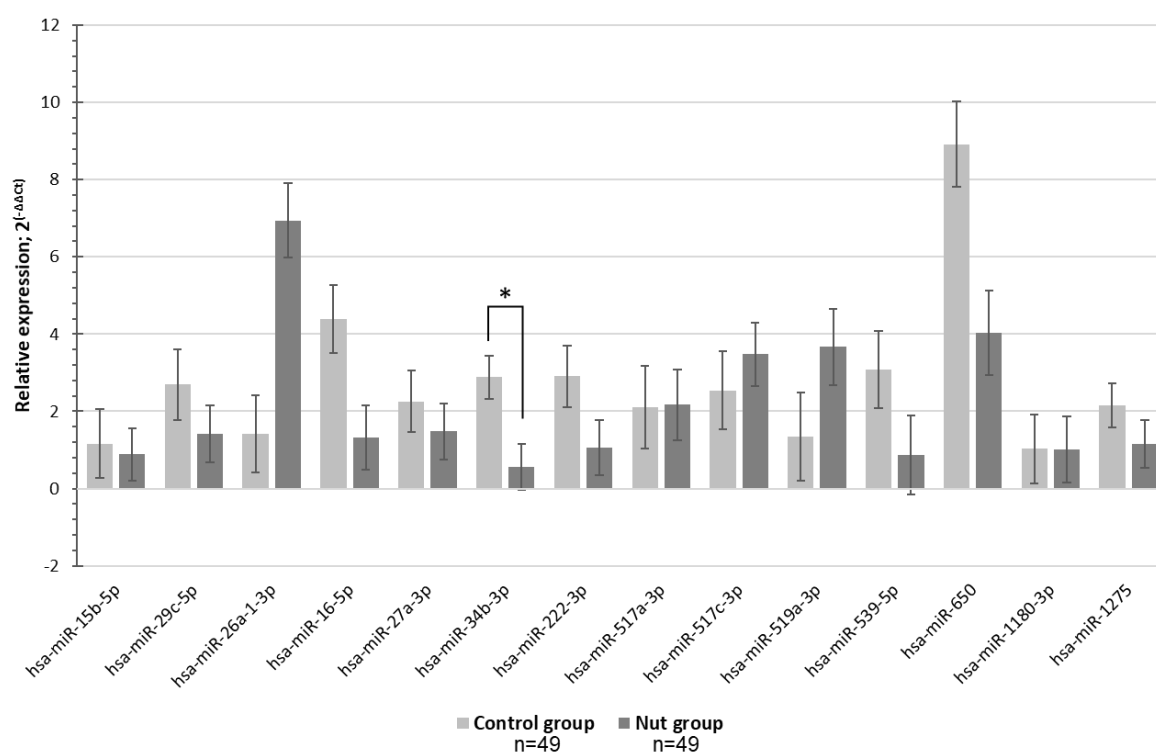
Legend: We evaluated the differences with a Wilcoxon analysis for normality distribution reasons. The grey bars illustrate the mean value and the vertical lines the standard error. *Significant difference (P<0.05) between the nut supplemented group and the control group after the 14-wk intervention period.

Adverse events:

There were no adverse events associated with this trial.