

Supplemental Material: Results of Multivariable^a Linear Regression by semen outcome, with exposure dichotomized as low (bottom 50th percentile) or high (top 25th percentile) for individual species of DBPs

	Br ₂ AA β (95% CL)	Br ₂ CIAA β (95% CL)	Br ₃ AA β (95% CL)	BrAA β (95% CL)	BrCl ₂ AA β (95% CL)	BrClAA β (95% CL)
Outcome ^b						
Sperm Count ^c	0.05 (-0.34-0.45)	-0.22 (-0.58-0.15)	-0.19 (-0.59-0.21)	0.18 (-0.15-0.51)	0.08 (-0.26-0.42)	-0.40 (-0.73- -0.08) ^d
Sperm Concentration ^c	-0.14 (-0.46-0.18)	-0.28 (-0.59-0.03)	-0.18 (-0.53-0.17)	-0.08 (-0.38-0.22)	-0.22 (-0.53-0.10)	-0.48 (-0.78- -0.17) ^d
% Normal Morphology ^e	0.00 (-0.30-0.31)	-0.15 (-0.45-0.15)	-0.20 (-0.53-0.12)	0.35 (0.05-0.65) ^d	0.27 (-0.05-0.58)	0.07 (-0.25-0.39)
% Abnormal Head ^e	0.08 (-0.25-0.40)	0.35 (0.04-0.66) ^d	0.21 (-0.15-0.56)	-0.06 (-0.37-0.24)	0.08 (-0.24-0.40)	0.27 (-0.06-0.60)
% Abnormal Midsection ^e	0.18 (-0.14-0.51)	0.22 (-0.11-0.55)	0.40 (0.05-0.75) ^d	-0.09 (-0.39-0.21)	-0.01 (-0.34-0.32)	0.12 (-0.22-0.46)
% Abnormal Tail ^e	-0.19 (-0.53-0.14)	-0.16 (-0.48-0.17)	0.16 (-0.20-0.51)	-0.44 (-0.74- -0.14) ^d	-0.39 (-0.72- -0.06) ^d	-0.42 (-0.75- -0.09) ^d
% Abnormal Cytoplasmic Drop ^e	-0.07 (-0.39-0.26)	-0.15 (-0.45-0.15)	-0.12 (-0.44-0.21)	-0.02 (-0.33-0.30)	-0.05 (-0.35-0.24)	-0.08 (-0.38-0.23)
% Chromomycin A3 (CMA)	-0.08 (-0.41-0.24)	-0.05 (-0.37-0.27)	-0.13 (-0.48-0.21)	0.14 (-0.17-0.45)	-0.05 (-0.37-0.28)	-0.08 (-0.40-0.23)
% DNA Fragmentation Index (DFI)	-0.09 (-0.43-0.24)	-0.07 (-0.42-0.28)	-0.02 (-0.39-0.35)	-0.15 (-0.47-0.17)	-0.22 (-0.56-0.13)	-0.19 (-0.52-0.14)
	ChBrCl ₂ β (95% CL)	ChBr ₂ Cl β (95% CL)	ChBr ₃ β (95% CL)	ChCl ₃ β (95% CL)	Cl ₂ AA β (95% CL)	Cl ₃ AA β (95% CL)
Outcome ^b						
Sperm Count ^c	0.03 (-0.39-0.45)	0.02 (-0.37-0.41)	-0.26 (-0.64-0.13)	0.11 (-0.27-0.49)	0.27 (-0.13-0.66)	0.25 (-0.11-0.62)
Sperm Concentration ^c	-0.31 (-0.63-0.00)	-0.16 (-0.47-0.15)	-0.22 (-0.55-0.11)	-0.14 (-0.46-0.18)	-0.03 (-0.36-0.30)	-0.04 (-0.36-0.28)
% Normal Morphology ^e	0.36 (0.05-0.66) ^d	0.02 (-0.25-0.30)	-0.44 (-0.78- -0.11) ^d	0.62 (0.31-0.92) ^d	0.69 (0.38-0.99) ^d	0.69 (0.38-1.00) ^d
% Abnormal Head ^e	0.26 (-0.07-0.59)	0.10 (-0.21-0.41)	0.17 (-0.18-0.52)	0.33 (-0.01-0.67)	0.31 (-0.02-0.65)	0.28 (-0.06-0.61)
% Abnormal Midsection ^e	-0.31 (-0.65-0.03)	0.14 (-0.18-0.45)	0.61 (0.27-0.96) ^d	-0.82 (-1.13- -0.51) ^d	-0.91 (-1.23- -0.60) ^d	-0.87 (-1.17- -0.57) ^d
% Abnormal Tail ^e	-0.76 (-1.08- -0.44) ^d	-0.26 (-0.58-0.07)	0.52 (0.17-0.86) ^d	-1.30 (-1.59- -1.01) ^d	-1.34 (-1.63- -1.05) ^d	-1.27 (-1.55- -0.99) ^d
% Abnormal Cytoplasmic Drop ^e	0.12 (-0.19-0.43)	-0.05 (-0.36-0.26)	-0.39 (-0.72- -0.07) ^d	0.50 (0.17-0.83) ^d	0.48 (0.14-0.82)	0.39 (0.09-0.70)
% Chromomycin A3 (CMA)	0.18 (-0.13-0.50)	0.02 (-0.30-0.34)	0.08 (-0.29-0.45)	-0.11 (-0.46-0.23)	-0.17 (-0.51-0.17)	-0.09 (-0.41-0.24)
% DNA Fragmentation Index (DFI)	-0.34 (-0.68-0.00)	-0.14 (-0.46-0.19)	0.15 (-0.22-0.51)	-0.56 (-0.99- -0.13) ^d	-0.50 (-0.90- -0.10) ^d	-0.53 (-0.88- -0.19) ^d
	CIAA β (95% CL)					
Outcome ^b						
Sperm Count ^c	0.28 (-0.11-0.67)					
Sperm Concentration ^c	-0.08 (-0.41-0.26)					
% Normal Morphology ^e	0.83 (0.52-1.15) ^d					
% Abnormal Head ^e	0.12 (-0.22-0.47)					
% Abnormal Midsection ^e	-1.03 (-1.35- -0.71) ^d					
% Abnormal Tail ^e	-1.31 (-1.60- -1.02) ^d					
% Abnormal Cytoplasmic Drop ^e	0.33 (0.01-0.65) ^d					
% Chromomycin A3 (CMA)	0.07 (-0.26-0.40)					
% DNA Fragmentation Index (DFI)	-0.53 (-0.97- -0.19) ^d					

^a All models adjusted for age, days abstaining, and education level

^b All outcomes standardized such that standard deviation=variance=1.00

^c Natural log transformation applied

^d p<0.05

^e Arc Sine transformation applied