

ANOVA - BMI

								95% CI for η^2	
Homogeneity Correction	Cases	Sum of Squares [*]	df	Mean Square	F	p	η^2	Lower	Upper
None	MASMALI classification	376.460	2.000	188.230	3.854	0.027	0.117	0.000	0.272
	Residuals	2833.090	58.000	48.846					
Brown-Forsythe	MASMALI classification	376.460	2.000	188.230	3.934	0.026	0.117	0.000	0.272
	Residuals	2833.090	46.900	60.407					
Welch	MASMALI classification	376.460	2.000	188.230	3.617	0.038	0.117	0.000	0.272
	Residuals	2833.090	31.602	89.648					

*Type III Sum of Squares

Test for Equality of Variances (Levene's)

F	df1	df2	p
0.402	2.000	58.000	0.671

Kruskal-Wallis Test

Factor	Statistic	df	p	Rank η^2	95% CI for Rank η^2	
					Lower	Upper
MASMALI classification	7.448	2	0.024	0.094	0.000	0.362

Dunn's Post Hoc Comparisons - MASMALI classification*

Comparison	z	Wi	Wj	rrb	p	pbonf	pholm
0 - 1	-0.944	22.167	28.188	0.208	0.345	1.000	0.345
0 - 2	-2.628	22.167	36.917	0.478	0.009	0.026	0.026
1 - 2	-1.588	28.188	36.917	0.292	0.112	0.337	0.224

Standard (HSD). Bootstrapped Post Hoc Comparisons - MASMALI classification

95% bcat CI									
		Mean Difference	Lower	Upper	SE	df	bias	t	p _{tukey}
0	1	1009.092	- 1550.934	3686.516	1325.361	58	- 54.349	0.837	0.682
	2	4449.819	2625.072	6851.757	1057.607	58	- 35.468	4.109	< .001***
1	2	3519.710	1051.128	5836.095	1152.185	58	18.881	3.226	0.006 **

** p < .01, *** p < .001

† Bias corrected accelerated.

Note. Bootstrapping based on 1000 successful replicates.

Note. Mean Difference estimate is based on the median of the bootstrap distribution.

Note. P-value adjusted for comparing a family of 3 estimates.