

Supplementary File 3. ANOVA output for melanosome roundness analysis in Fig. 3D.

```
> Dataset
  geno dv roundness
1     1  1    0.752
2     1  1    0.696
3     1  1    0.777
4     1  1    1.000
5     1  1    1.000
6     1  1    0.581
7     1  1    0.939
8     1  1    0.799
9     1  1    1.000
10    1  1    0.834
...
9728  2  2    0.517
```

where
geno = genotypes; 1 = WT, 2 = smarca4
dv = dorsal (1) or ventral (2) RPE
roundness = round (1) to elongated (0)

model 1: full model

```
> roundness.model1 <- lm(roundness^4~geno*dv, data = Dataset)
```

* raw data were transformed to normalize the distribution

```
> anova(roundness.model1)
```

Analysis of Variance Table

Response: roundness^4

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
geno.f	1	0.02	0.017241	0.1863	0.66601
dv.f	1	0.31	0.307230	3.3201	0.06847 .
geno.f:dv.f	1	0.15	0.150406	1.6254	0.20237
Residuals	9724	899.81	0.092535		

Signif. codes: 0 '****' 0.001 '***' 0.01 '**' 0.05 '.' 0.1 ' ' 1

Interpretation of results

None of the coefficient is significant. Thus, neither genotype or dorsal vs. ventral RPE position affected the roundness of melanosomes.