

Supplementary File 4. ANOVA output for melanosome area analysis in Fig. 3E.

```
> Dataset
```

```
      geno dv   area
1       1  1  0.057
2       1  1  0.164
3       1  1  0.058
4       1  1  0.022
5       1  1  0.026
6       1  1  0.121
7       1  1  0.092
8       1  1  0.060
9       1  1  0.066
10      1  1  0.145
...
9728    2  2  0.148
```

where

geno = genotypes; 1 = WT, 2 = smarca4

dv = dorsal (1) or ventral (2) RPE

area = melanosome area

```
# model 1: full model
```

```
> area.model1 <- lm(area^0.3~geno*dv, data = Dataset)
```

```
> anova(area.model1)
```

Analysis of Variance Table

Response: area^0.3

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
geno.f	1	0.239	0.238651	16.5779	4.706e-05 ***
dv.f	1	0.215	0.214566	14.9048	0.0001138 ***
geno.f:dv.f	1	0.106	0.106458	7.3951	0.0065519 **
Residuals	9724	139.985	0.014396		

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

* raw data were transformed to normalize the distribution

```
## Interpretation of results
```

```
> summary(area.model1)
```

Call:

```
lm(formula = area^0.3 ~ geno.f * dv.f, data = Dataset)
```

Residuals:

Min	1Q	Median	3Q	Max
-0.39502	-0.08596	0.00579	0.08862	0.36168

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)	
(Intercept)	0.520908	0.001830	284.627	< 2e-16	***
geno.fyng	-0.014936	0.002868	-5.207	1.96e-07	***
dv.fventral	-0.016049	0.003399	-4.722	2.37e-06	***
geno.fyng:dv.fventral	0.016387	0.006026	2.719	0.00655	**

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

Residual standard error: 0.12 on 9724 degrees of freedom

Multiple R-squared: 0.003982, Adjusted R-squared: 0.003675

F-statistic: 12.96 on 3 and 9724 DF, p-value: 1.911e-08

In the summary output of `area.model1`,

1. The coefficient `geno.fyng` has a significant negative estimate (p -value = 1.96e-07). This implies that the melanosome area was generally smaller in *smarca4* RPE.
2. The coefficient `DVventral` has a significant negative estimate (p -value = 2.37e-06). This implies that the melanosome area was smaller in the ventral RPE in both genotypes.
3. The coefficient `geno.fyng:dv.fventral` has a significant positive estimate (p -value = 0.00655). This implies that the melanosome area was comparatively larger on the ventral *smarca4* RPE.