

Supplementary File 1. ANOVA output for melanosome number per RPE cell area analysis in Fig. 3B

```
> Dataset
  sample geno      DV total_no  area
1    WT1   WT  Dorsal    1412 649.624
2    WT1   WT ventral     584 467.658
3    WT2   WT  Dorsal    1522 779.474
4    WT2   WT ventral     628 398.583
5    WT3   WT  Dorsal    1364 809.531
6    WT3   WT ventral     543 424.195
7   Yng1  yng  Dorsal    1013 731.764
8   Yng1  yng ventral     126 196.447
9   Yng2  yng  Dorsal     881 809.427
10  Yng2  yng ventral     305 372.191
11  Yng3  yng  Dorsal    1057 790.386
12  Yng3  yng ventral     293 334.830
```

where
Sample: Biological replicate number
Geno: genotype
DV: dorsal or ventral to optic nerve
total_no: melanosome count
area: RPE cell area

model 1: full model

```
> modeltotal1 <- lm(total_no/area~geno*DV, data = Dataset)
```

```
> anova(modeltotal1)
Analysis of Variance Table
```

Response: total_no/area

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
geno	1	1.18410	1.18410	35.7251	0.0003318 ***
DV	1	0.84312	0.84312	25.4375	0.0009972 ***
geno:DV	1	0.00451	0.00451	0.1359	0.7219171
Residuals	8	0.26516	0.03314		

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

model 2: main factor only

```
> modeltotal2 <- lm(total_no/area~geno+DV, data = Dataset)
```

```
> anova(modeltotal2)
Analysis of Variance Table
```

```

Response: total_no/area
      Df Sum Sq Mean Sq F value    Pr(>F)
geno    1 1.18410  1.18410   39.519 0.0001433 ***
DV      1 0.84312  0.84312   28.139 0.0004908 ***
Residuals 9 0.26966  0.02996
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

model comparison

```

> anova(modeltotal1,modeltotal2)
Analysis of Variance Table

```

```

Model 1: total_no/area ~ geno * DV
Model 2: total_no/area ~ geno + DV
  Res.Df    RSS Df Sum of Sq    F Pr(>F)
1      8 0.26516
2      9 0.26966 -1 -0.0045057 0.1359 0.7219

```

* Since p is not significant, so model simplification is justified and modeltotal2 is used in the result section.

Interpretation of results

```

> summary(modeltotal2)

```

```

Call:
lm(formula = total_no/area ~ geno + DV, data = Dataset)

```

```

Residuals:
      Min       1Q   Median       3Q      Max
-0.23273 -0.12309  0.04143  0.10014  0.25591

```

```

Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept)   1.91765    0.08655   22.157 3.67e-09 ***
genoyng       -0.62825    0.09994   -6.286 0.000143 ***
DVventral     -0.53013    0.09994   -5.305 0.000491 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

```

Residual standard error: 0.1731 on 9 degrees of freedom
Multiple R-squared:  0.8826,    Adjusted R-squared:  0.8565
F-statistic: 33.83 on 2 and 9 DF,  p-value: 6.51e-05

```

* In the summary output of modeltotal2,

1. The coefficient *genoyng* has a significant negative estimate (p -value = $1.43\text{e-}4$). This implies that the number of melanosome per RPE area in *smarca4* RPE was significantly lower.
2. The coefficient *DVventral* has a significant negative estimate (p -value = $4.91\text{e-}4$). This implies that the number of melanosome per RPE area was significantly lower in the ventral RPE in both genotypes.