**S1 Table.** Average number of MITF+, MART1+, *TYR*+ and *CDKN2A*+ cells/mm2 in different parts of the feather in different genotypes. Significant differences from the value obtained for *N/N* are indicated by stars (one-way ANOVA, Tukey’s multi-comparison post-hoc test; \* *P*<0.05, \*\* *P*<0.01, \*\*\* *P*<0.001).

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Regiona | MITF cells/mm2 |  | Regiona | MART1 cells/ mm2 |
|   | ***N/N*** | ***B0/W*** | ***B2/N*** |  |  | ***N/N*** | ***B0/W*** | ***B2/N*** |
| BA | 3470±454 | 1070±419\*\* | 2090±648\* |  | **BA** | 1970±207 | 790±209\*\*\* | 1740±109 |
| RGZ | 2500±246 | 742±442\*\*\* | 1650±618 |  | **RGZ** | 1180±159 | 642±207 | 798±326 |
| UB | 1160±132 | 0±0\* | 675±273 |  | **UB** | 0±0 | 276±76 | 484±203 |
| MB | 625±84 | 0±0 | 0±0 |  | **MB** | 0±0 | 0±0 | 0±0 |
| LB | 69±120 | 0±0 | 0±0 |  | **LB** | 0±0 | 0±0 | 0±0 |
| PE | 0±0 | 0±0 | 0±0 |  | **PE** | 0±0 | 0±0 | 0±0 |
|  |  |  |  |  |  |  |  |  |
|  | ***TYR* cells/mm2** |  |  | ***CDKN2A* cells/mm2** |
|   | ***N/N*** | ***B0/W*** | ***B2/N*** |  |  | ***N/N*** | ***B0/W*** | ***B2/N*** |
| BA | 2130±323 | 481±113\*\*\* | 1310±531 |  | **BA** | 292±70 | 1130±345\* | 920±194\* |
| RGZ | 1270±238 | 398±176\*\* | 1060±256 |  | **RGZ** | 0±0 | 246±213 | 155±136 |
| UB | 0±0 | 104±181 | 0±0 |  | **UB** | 0±0 | 0±0 | 0±0 |
| MB | 0±0 | 0±0 | 0±0 |  | **MB** | 0±0 | 0±0 | 0±0 |
| LB | 0±0 | 0±0 | 0±0 |  | **LB** | 0±0 | 0±0 | 0±0 |
| PE | 0±0 | 0±0 | 0±0 |  | **PE** | 0±0 | 0±0 | 0±0 |
| aBA=barb, RGZ=ramogenic zone, UB=upper bulge, MB=middle bulge, LB=lower bulge, PE=papilla ectoderm. |