**S1 Table. Summary of  test in nuclear families after ascertainment correction.** This is under the hypothesis of a single dominant gene controlled transmission.

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Parent  Geno. | Parent pairs | in Offs. | in Offs. | in Off. | Obs. No. | | Exp. No. | |  | *P-* value |
| **WG** | **BB** | **WG** | **BB** |
| *Aa, aa* | (103, 104),(107, 108),(301, 302),(305, 306),(309, 310),(311, 312),(313, 314) | 0 |  |  | 6 | 7 | 6.5 | 6.5 | 0.08 | 0.78 |
| *Aa, Aa* | (105, 106),(307, 308),(403, 404) |  |  |  | 3 | 3 | 4.5 | 1.5 | 2.00 | 0.16 |
| *aa, aa* | (120, 121),(122, 123),(315, 316), (405, 406) | 0 | 0 | 1 | 0 | 5 | 0 | 5 | 0 | 1 |
| *A\_, aa* | (111, 112), (201, 202) | 0 |  |  | 4 | 0 |  |  | 1.37 | 0.24 |
| *a\_, aa* | (113, 114),(303, 304) | 0 |  |  | 0 | 4 |  |  | 1.30 | 0.25 |
| *Aa, A\_* | (203, 204), (401, 402) |  |  |  | 2 | 0 |  |  | 0.29 | 0.59 |
| *A\_, A\_* | (407, 408) |  |  |  | 1 | 0 |  |  | 0.07 | 0.79 |
| Total Chi-square | | | | | | | | | 5.11 | 0.53 |

Geno=Genotypes; Offs=Offspring; Obs. No.= Observed number; Exp. No.= Expected number;

BB: blue-black; WG: white-gold; *q* is the estimated probability of allele *a* in the population.