S2 Fig. Exon structure of *SLC2A11B* from one wild-type and one pearl-eye homozygous pigeons that were used for transcriptome assembly. **(A)** Alignment of assembled transcripts of *SLC2A11B* to zebra finch and chicken transcripts from the *Ensembl* database (retrieved on November 2020). The putative canonical transcript of *SLC2A11B* in pigeons, and its respective predicted open reading frame, is shown on top. Of all the transcripts that were assembled, we only considered those that represented more than 10% of the overall transcripts mapping to the candidate region. Colors indicate the base content of each sequence: adenine – green; guanine – black; cytosine – blue; thymine – red. **(B)** Sashimi plots based on reads mapping to the genomic interval containing *SLC2A11B* for the two pigeons. Compared to the wild-type, the pearl-eye individual has a relatively decreased amount of reads in the 5' end of the gene, different proportions of reads along the transcript and relatively increased amount of reads in intronic regions.