

1 **Description of additional supplementary items**

2 The Supplementary Data 1 excel file contains the results of all RNA-seq analyses, as well as all raw data  
3 values used to generate figures in which data values are shown. The first two sheets show genes  
4 differentially regulated between white and opaque cells with relevant expression values and statistics,  
5 as well as analyses used to generate the pie charts shown in Figure 3, while the third tab specifically  
6 shows transcriptional factors differentially expressed between the two cell types. Sheet 4 shows the  
7 mapping efficiencies and average sequencing depth for the RNA seq libraries. Sheets 5-12 contain all  
8 raw data for Figure 2, Figure 4, Figure 5, and all supplemental figures in which numerical data points are  
9 plotted. All sheets are labelled clearly.

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