

**A gene expression panel for estimating age in males
and females of the disease vector *Glossina morsitans***

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Electronic Supplementary Material

S2 Text

Results of WGCNA analysis

Thirty modules were identified by Weighted Gene Network Clustering Analysis (WGCNA), many of which showed signs of change with age (Fig. **S2.1**). The largest module in terms of number of genes (MEturquoise module, Fig. **S2.1**) displays very strong correlation with age, particularly at young ages, and little or no difference between sexes. In fact, when simply looking at the list of genes most strongly correlated with age, the large majority belong to this module. In order to avoid our panel containing too much redundant information, we consciously aimed to include genes from other modules (Fig. **S2.2**).

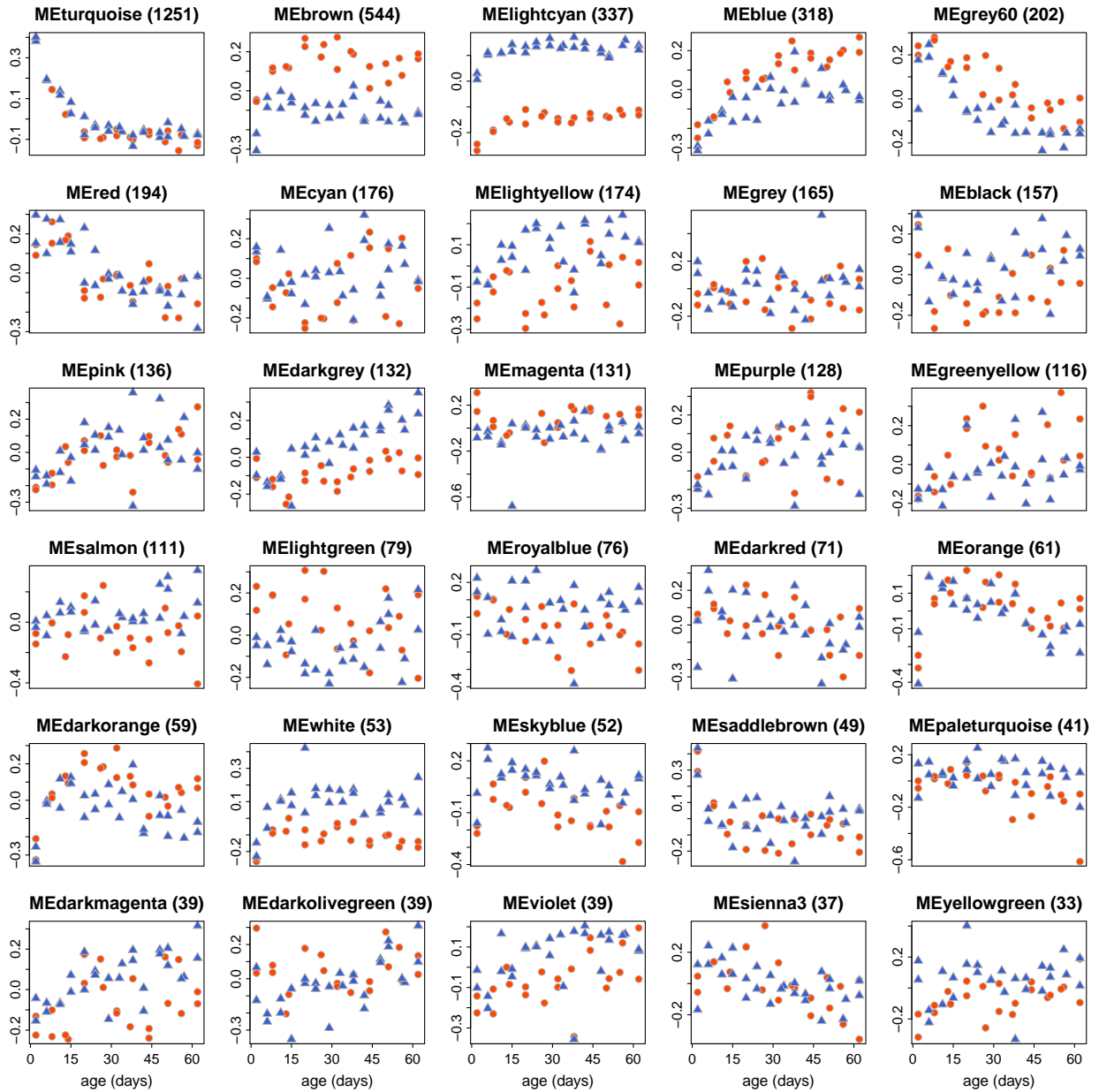


Fig. S2.1: Each plot shows represents one of the modules determined by WGCNA, plotting the value of that module's eigengene (combination of all genes that are members of the module) for each of the samples. Blue triangles are females; orange circles are males. The title of each plot shows the name of the module (assigned as a colour by WGCNA) followed by the number of genes in the module in brackets. Y axes are in arbitrary units of the eigengenes. Modules are sorted in order of number of genes contained within.

GMOY000749	GMOY001603	GMOY002920	GMOY003090	GMOY003371	GMOY003588	GMOY005053	GMOY005321	GMOY009908	GMOY011979
MEturquoise	MEgrey60	MEturquoise	MEred	MEturquoise	MEgrey60	MEturquoise	MEturquoise	MEturquoise	MEgrey60

Fig. S2.2: Module assignment of the 10 genes chosen for the final qPCR panel. Names refer to modules in Fig. S2.1.