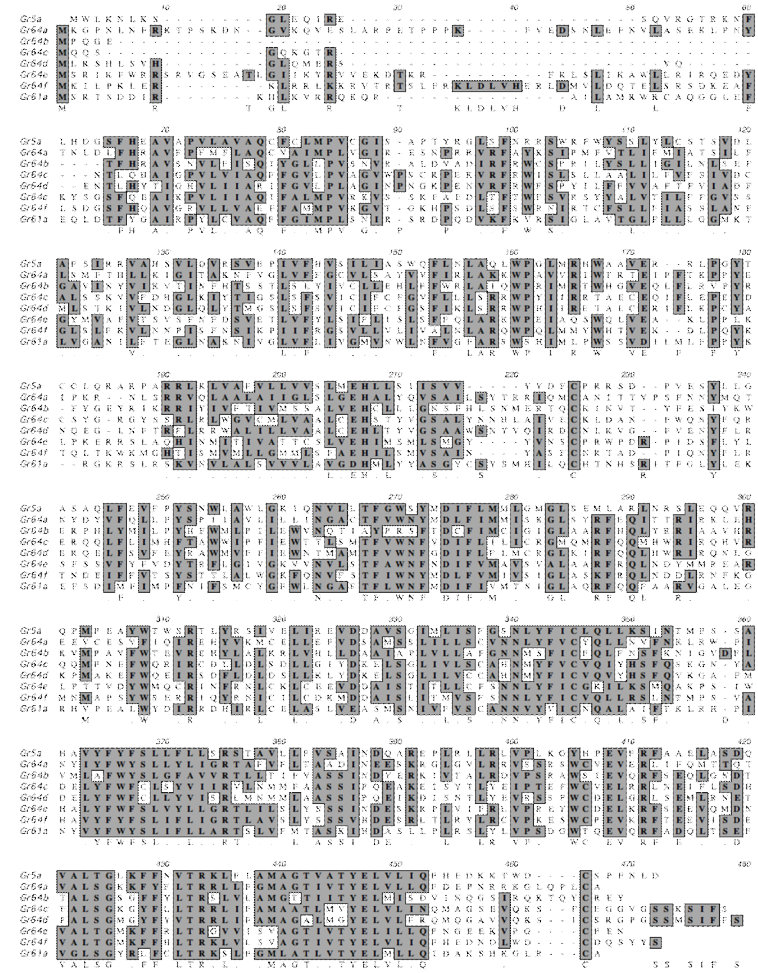
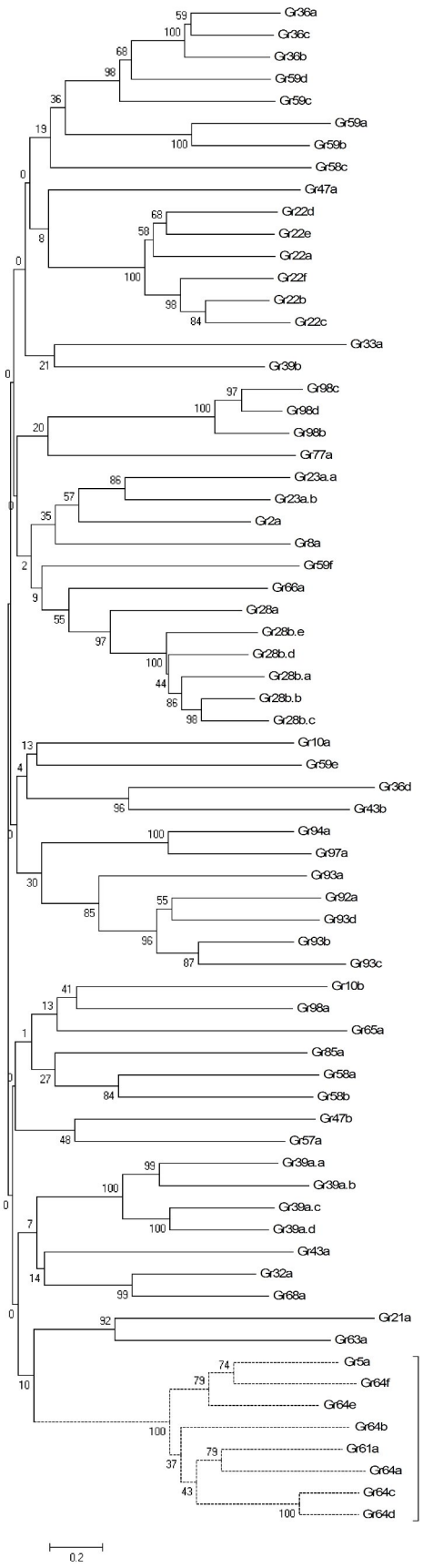
S1A **S1B**

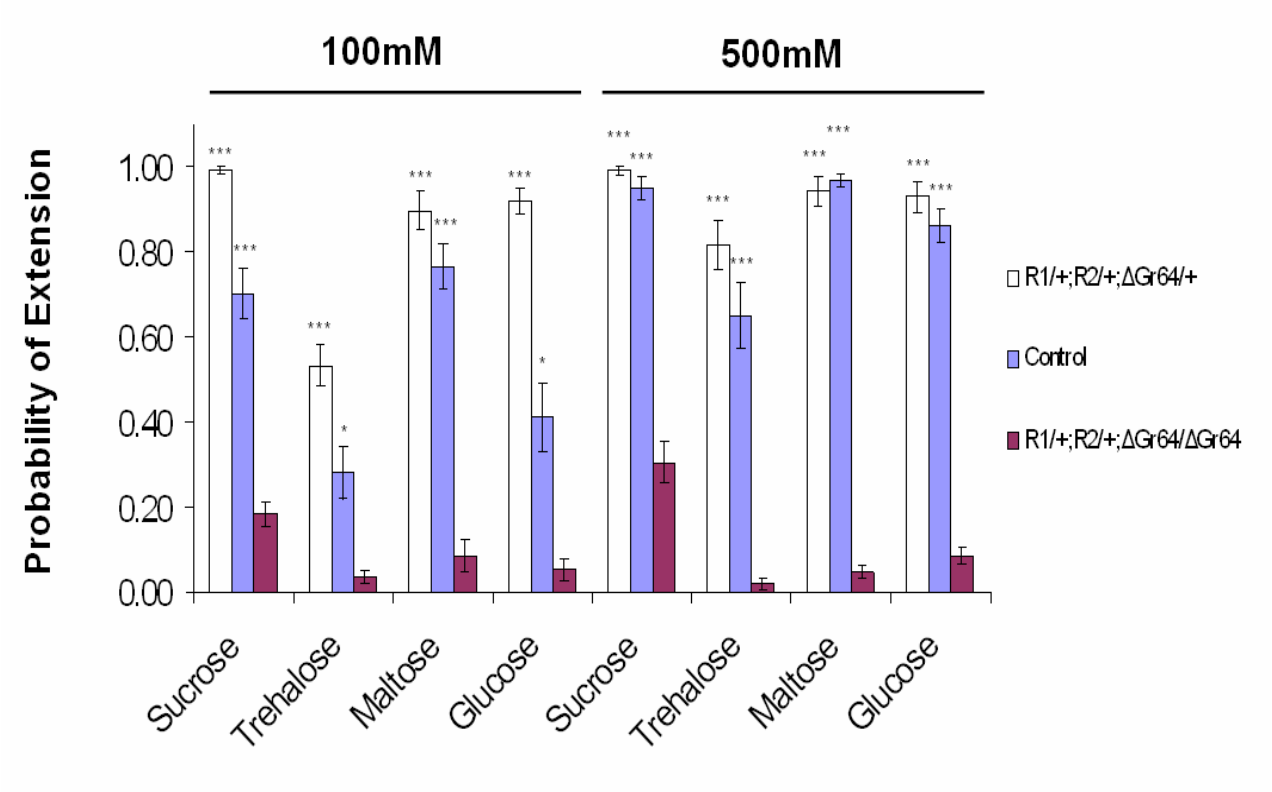




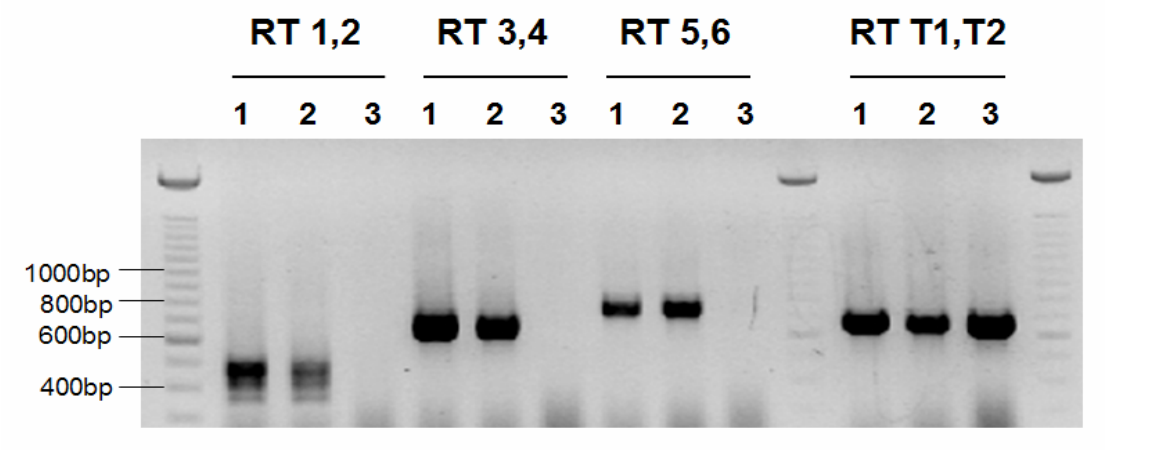
Supplementary Figure S1: Sequence conservation of th
Drosophila melanogaster

(A) Alignment of the eight putative sugar receptors. Alignme
the Multiple Alignment feature of MacVector, using a BLOSUI
default parameter settings.

(B) Evolutionary relationship between GR proteins. The
generated in MEGA4, using the Neighbor-Joining method [32
indicated next to the branches. The eight sugar receptors are at th
bracket) and have bootstrap support of 100%.



Supplementary Figure S2: Flies with R1 and R2 transgenes show normal PER response. The graph shows PER responses for three different sugars of flies containing the two transgenes R1 and R2 and a wild type copy of the *Gr64* gene (*R1/+;R2/+;ΔGR64/+*), in comparison to control flies (see Figure 2), as well as homozygous *ΔGR64* mutants. *R1/+;R2/+;ΔGR64/+* flies show normal response to these sugars, compared to the highly reduced or lost response in mutants. At 500 mM, the response of *R1/+;R2/+;ΔGR64/+* flies is the same as that observed in the control strain, while at 100 mM, the response appears slightly higher. Asterisks indicate a significant difference between the mutant and control strains, as determined by Student's t-test (* indicates $p<0.05$, *** indicates $p<0.0001$).



Supplementary Figure S3: Expression of the *Gr64* genes in flies containing the rescue Gr64 construct

Flies containing the *UAS-Gr64abcd_GFP_f* transgene express the *Gr64* genes, both in the absence (lanes 1) and presence (lanes 2) of the *Gr5a-Gal4* driver. In lanes 3, RNA from homozygous *ΔGr64a* mutants flies (*R1/+;R2/+;ΔGR64/ΔGR64*) was loaded. RT-PCR analysis of RNA isolated from heads and legs (not shown) was carried out for the first four genes. Integrity of cDNA was confirmed using primers against the tubulin gene. The same primers were used as in Figure 1D (1-6, T1 and TR2).