

6. Housekeeping genes encode proteins involved in universally important processes such as transcription, translation, and glycolysis. Because these genes appear to be expressed in all cells at constant levels, the expression of housekeeping genes is often used as a control when comparing how the expression of other genes varies under different conditions.

Researchers studying the effect of pesticides on declining bee populations wanted to determine whether the expression of four housekeeping genes (*GAPDH*, *RPL32*, *RPS5*, and *TBP-AF*) was in fact constant in bees across different variables. The researchers collected samples of mRNA for each of the four genes and compared how their expression varied across the developmental stage of the bee, the sex of the bee, and the cell type from which the sample was taken. The mRNA from the samples was reverse transcribed to produce DNA copies of each gene. PCR was then used to amplify the DNA, and the Cq value was determined. The Cq value is the number of PCR cycles needed to produce a specified number of DNA copies. A high Cq value for a sample indicates the gene was expressed at a low level.

To analyze whether any of the examined variables affected expression of the housekeeping genes, researchers examined the range of Cq values for each gene in response to each variable. Genes with a wide range of Cq values were determined to be affected by the variable, while genes with a narrow range of Cq values were determined to be unaffected by the variable.

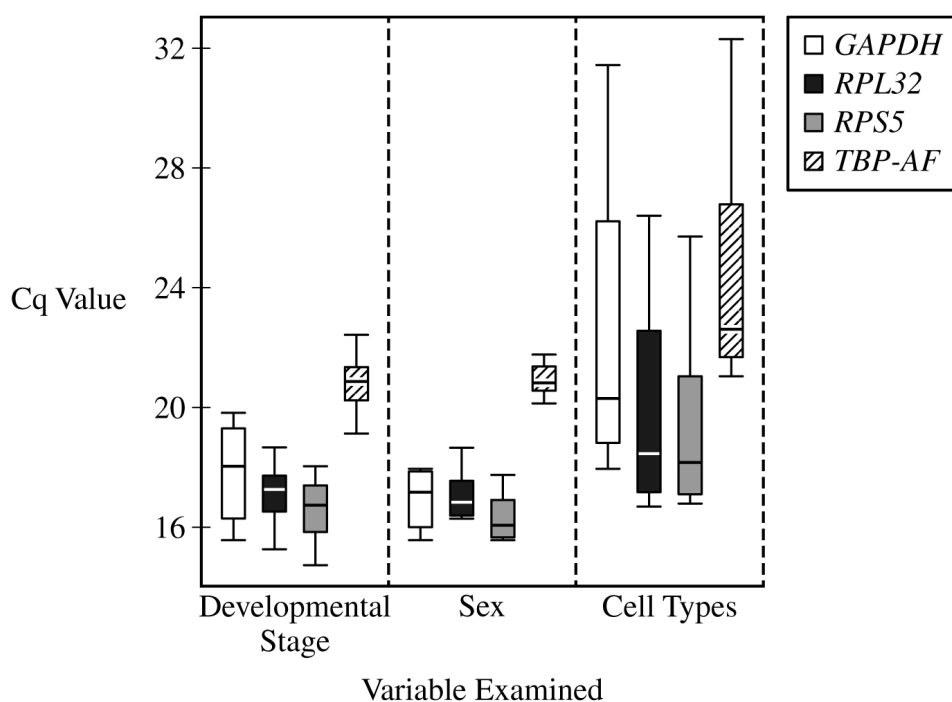


Figure 1. The effect of developmental stage, sex, and cell type on the Cq value of four housekeeping genes

- (a) Based on the data in Figure 1, **identify** the gene that had the lowest median Cq value when bees of different developmental stages were compared.
- (b) The Cq value is inversely proportional to the amount of mRNA from that gene in the starting sample. Based on the data in Figure 1, **identify** the gene that has the lowest level of gene expression regardless of variable.
- (c) The scientists investigated the effect of pesticides on the expression of other genes in one cell type of a group of bees containing males and females of the same developmental stage. They hypothesized that *TBP-AF* would serve as the best control gene for this experiment. Use the data to **evaluate** their hypothesis.
- (d) **Explain** how expression of a gene such as *GAPDH* can vary from one cell type to another within the same bee.
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Write your responses to this question only on the designated pages in the separate Free Response booklet.

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END OF EXAM

7. A researcher is studying patterns of gene expression in mice. The researcher collected samples from six different tissues in a healthy mouse and measured the amount of mRNA from six genes. The data are shown in Figure 1.

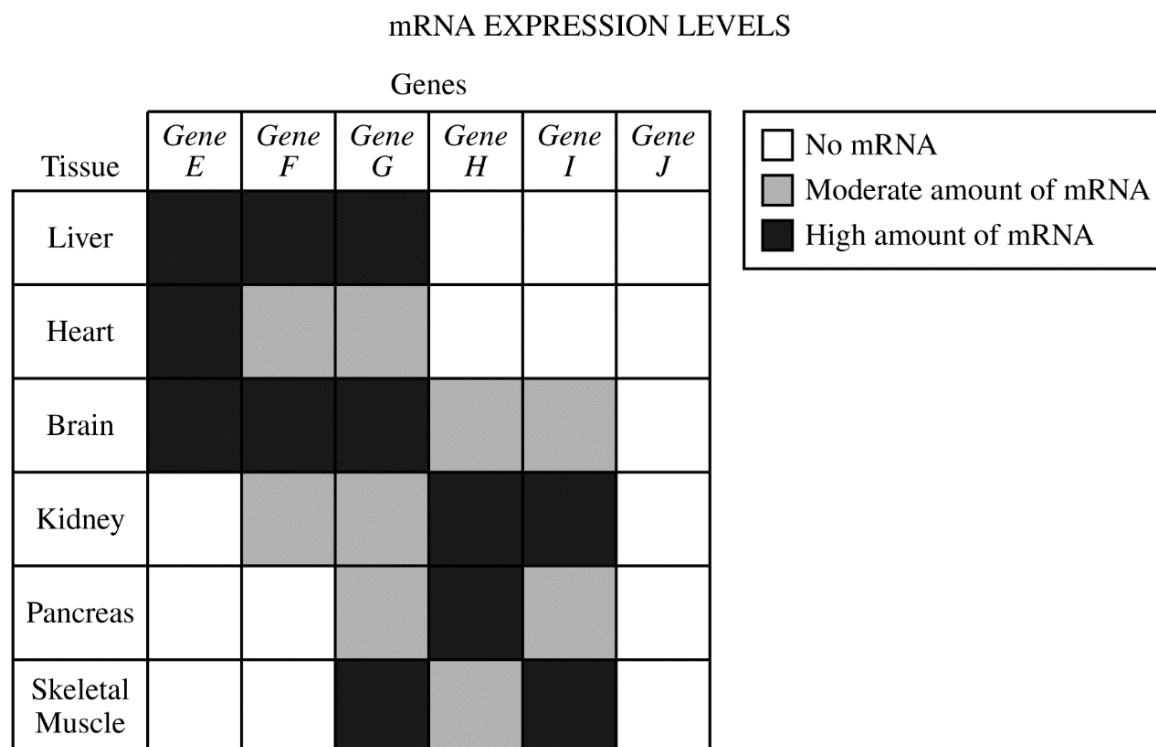


Figure 1. mRNA expression levels of six genes

- (a) Based on the data provided, **identify** the gene that is most likely to encode a protein that is an essential component of glycolysis. **Provide reasoning** to support your identification.
- (b) The researcher observed that tissues with a high level of *gene H* mRNA did not always have gene H protein. **Provide reasoning** to explain how tissues with high *gene H* mRNA levels can have no gene H protein.

7. Smell perception in mammals involves the interactions of airborne odorant molecules from the environment with receptor proteins on the olfactory neurons in the nasal cavity. The binding of odorant molecules to the receptor proteins triggers action potentials in the olfactory neurons and results in transmission of information to the brain. Mammalian genomes typically have approximately 1,000 functional odorant-receptor genes, each encoding a unique odorant receptor.
- (a) **Describe** how the signal is transmitted across the synapse from an activated olfactory sensory neuron to the interneuron that transmits the information to the brain.
- (b) **Explain** how the expression of a limited number of odorant receptor genes can lead to the perception of thousands of odors. Use the evidence about the number of odorant receptor genes to **support** your answer.
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