

SAGE

The Cancer Genome Anatomy Project (CGAP) has a web interface for comparing SAGE gene expression data between normal and cancerous tissues:

<http://cgap.nci.nih.gov/SAGE>

One useful tool is the SAGE Anatomic Viewer (SAV) that visually displays the relative expression of a given gene in normal and malignant tissues of the human body. Use SAV to answer the following questions:

A. SOD2

1. What is the sequence of the short (10 bp) tag of the gene SOD2?
2. What type of protein does SOD2 encode?
3. Which human tissues show a difference in SOD2 expression between normal and cancerous samples?
4. How many SOD2 tags (per 200,000 in the total library) are found in a normal breast epithelium library? How many in a breast carcinoma epithelium library?
5. What does this mean? Is SOD2 over- or under-expressed in breast cancer?

B. SPINK1

1. What is the sequence of the short (10 bp) tag of the gene SPINK1?
2. What type of protein does SPINK1 encode?
3. Which human tissues show a difference in SPINK1 expression between normal and cancerous samples?
4. How many SPINK1 tags (per 200,000 in the total library) are found in a normal prostate tissue library? How many in a prostate carcinoma library?
5. What does this mean? Is SPINK1 over- or under-expressed in prostate cancer?