Using Microarrays to Study Leukemia
Microarray data to identify the type of cancer cell.

Summary
In the activity “ALL Subtypes” you used microarrays to identify two different forms of ALL.

ALL (ALL1 in the DVD) is typical acute lymphocytic leukemia. Patients with this form of the disease respond well to treatment.

MLL (ALL2 in the DVD) is mixed lineage leukemia. These patients do not respond well to typical ALL treatment.

Further, you identified a series of genes whose expression pattern can be used to identify which type of ALL a patient is suffering. We will now use these gene expression patterns to further examine cellular defects in the different types of cancers.

Remember that in leukemia, the white blood cells are stopped at a particular stage of their development and never reach full maturity. In this activity, you will use the microarray expression data from the previous activity, as well as data presented in this activity, to look at where the development of cells is stopped in ALL vs MLL.
**Background**

Below is a figure diagramming the pathway of white blood cell maturation. Below each cell type in the B-cell lineage is a summary of the molecules expressed on the surface of each cell stage. These markers are described and outlined in more detail in Table 1 on the next page.

![Diagram of B-cell lineage](image)

Figure 1: Marker expression in various B-cell precursors.

Cells from ALL patients are stopped in the Pre B-Cell stage. You will be determining whether cells from MLL patients are stopped earlier or later in the B cell developmental pathway by comparing levels of expression of various markers.
Table 1: Markers expressed in ALL vs MLL

<table>
<thead>
<tr>
<th>Marker Name</th>
<th>Cells that normally express this marker</th>
<th>Function (if known)</th>
<th>Expression in ALL and MLL</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>CD19</strong></td>
<td>B-cell specific, indicates a cell that will become a B-cell</td>
<td>B-cell development?</td>
<td>CD19 is expressed in equal amounts on cells from both ALL and MLL patients.</td>
</tr>
<tr>
<td><strong>CD24</strong></td>
<td>B-cells and myeloid cells. Expression of CD24 increases as B-cells mature.</td>
<td>Its function may be to help activate T cells.</td>
<td></td>
</tr>
<tr>
<td><strong>CD44</strong></td>
<td>WBCs and RBCs. In B-cells, its expression decreases as B-cells mature.</td>
<td>Receptor for extracellular matrix components</td>
<td></td>
</tr>
<tr>
<td><strong>CD79B</strong></td>
<td>Found on the surface of B-cells and expression increases as B-cells mature. Presence of this marker indicates commitment to the B-cell lineage.</td>
<td>This marker is an antibody. It functions as the antigen receptor for the B-cells and determines the specificity of the antigen that will be recognized by the B-cell.</td>
<td></td>
</tr>
<tr>
<td><strong>SPN</strong></td>
<td>Expression of CD43 decreases as B-cells mature</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Questions
1. Look at your results from the “ALL Subtypes” activity. Note whether the expression of CD24, CD44, CD79B and SPN is higher in ALL or MLL. Write your answers in the far right column of the table above.
2. Cells from patients with ALL are arrested at the Pre B-Cell stage. At which stage do you think cells from MLL are stopped? You will need to use both table 1 and figure 1 to answer this question. Hint: Are the MLL cells stopped before or after the ALL cells?
3. Explain your answer by describing the levels of expression of the different markers.