Mapping the Genomic Landscape of TNBC and COVID-19

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Introduction

• Triple-negative breast cancer (TNBC) is the most aggressive form of breast cancer, representing 15 to 20% of all newly diagnosed breast cancers annually.
• Clinically, it is defined as tumors lacking expression of the estrogen receptor (ER), progesterone receptor (PR), and the human epidermal growth factor-2 (HER-2).
• TNBC patients are at high risk of COVID-19, and those affected tend to have poorer clinical outcomes.
• Sadly, the molecular mechanisms linking TNBC and COVID-19 have not been characterized.

Objective/Hypothesis

• **Objective:** Discover a signature of genes, networks and signaling pathways associating TNBC and COVID-19.
• **Hypothesis:** Genomic alterations in women diagnosed with TNBC and COVID-19 could lead to measurable changes associating the two diseases, and these alterations affect gene regulatory networks and signaling pathways driving the association between the two diseases.

Materials/Methods

• Gene expression and clinical data on TNBC were obtained from The Cancer Genome Atlas (TCGA).
• Gene expression and clinical data on COVID-19 were obtained from the Gene Expression Omnibus (GEO).
• Immune responsive genes were obtained from Illumina.
• Figure 1 shows project design and execution workflow.

Table 1. Distribution of samples.

<table>
<thead>
<tr>
<th>Data</th>
<th>TNBC</th>
<th>COVID-19</th>
<th>Immune</th>
</tr>
</thead>
<tbody>
<tr>
<td>Genes</td>
<td>60,483</td>
<td>19,473</td>
<td>1,661</td>
</tr>
<tr>
<td># Cases</td>
<td>115</td>
<td>38</td>
<td>-</td>
</tr>
<tr>
<td># Controls</td>
<td>113</td>
<td>13</td>
<td>-</td>
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</tbody>
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