<table>
<thead>
<tr>
<th>Conditiona</th>
<th>Growth collected</th>
<th>MS/MS peptides</th>
<th>Total peptides</th>
<th>Non-redundant Proteins (loge)&lt;-1</th>
<th>Proteins (loge)&lt;-3</th>
<th>Proteins (loge)&lt;-10</th>
<th>Number of genes identified</th>
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<tbody>
<tr>
<td>WG_Exp_Rep1</td>
<td>33864</td>
<td>19928</td>
<td>8315</td>
<td>1947</td>
<td>1830</td>
<td>1377</td>
<td>5193</td>
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<tr>
<td>WG_Exp_Rep2</td>
<td>34996</td>
<td>17941</td>
<td>7431</td>
<td>1836</td>
<td>1714</td>
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<td>WG_Sta_Rep1</td>
<td>36092</td>
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<td>9787</td>
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<td>WG_Sta_Rep2</td>
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<td>1975</td>
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**Average (Proteins)**

<table>
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<tr>
<th>Condition</th>
<th>Proteins</th>
<th>RNA scores</th>
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<td>WG_Exp</td>
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<tr>
<td>WG_Sta</td>
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<tr>
<td>WFA_Exp</td>
<td>1827</td>
<td>1715</td>
</tr>
</tbody>
</table>

a: WG: Waste glycerol; WFA: waste fatty acids; Exp: exponential phase; Sta: stationary phase; Rep1/2: biological replicate 1 and 2.