Figure S1 The most enriched GO terms between HP_C and nHP_C. a, biological process; b, molecular function.
Figure S2 The most enriched GO terms between HP_M and nHP_M. a, biological process; b, cellular component; c, molecular function.
Figure S3 The most enriched GO terms between nHP_M and nHP_C. a, biological process; b, cellular component; c, molecular function.
Figure S5 The quality and the quantity of the RNA samples were checked by using Agilent 2100 Bioanalyzer System, agarose gel electrophoresis and NanoDrop Lite Spectrophotometer.
### Overall Results for sample 10: R14040063

<table>
<thead>
<tr>
<th>RNA Area:</th>
<th>150.7</th>
</tr>
</thead>
<tbody>
<tr>
<td>RNA Concentration:</td>
<td>135 ng/μl</td>
</tr>
<tr>
<td>rRNA Ratio [25s / 18s]:</td>
<td>2.1</td>
</tr>
<tr>
<td>RNA Integrity Number (RIN):</td>
<td>9.1 (B.02.08)</td>
</tr>
</tbody>
</table>

### Overall Results for sample 7: R14030315

<table>
<thead>
<tr>
<th>RNA Area:</th>
<th>126.2</th>
</tr>
</thead>
<tbody>
<tr>
<td>RNA Concentration:</td>
<td>77 ng/μl</td>
</tr>
<tr>
<td>rRNA Ratio [25s / 18s]:</td>
<td>2.1</td>
</tr>
<tr>
<td>RNA Integrity Number (RIN):</td>
<td>9.6 (B.02.08)</td>
</tr>
</tbody>
</table>

### Fragment table for sample 10: R14040063

<table>
<thead>
<tr>
<th>Name</th>
<th>Start Time [s]</th>
<th>End Time [s]</th>
<th>Area</th>
<th>% of total Area</th>
</tr>
</thead>
<tbody>
<tr>
<td>18S</td>
<td>41.61</td>
<td>43.08</td>
<td>27.3</td>
<td>18.1</td>
</tr>
<tr>
<td>25S</td>
<td>45.45</td>
<td>48.03</td>
<td>56.3</td>
<td>37.4</td>
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</table>

### Fragment table for sample 7: R14030315

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<th>End Time [s]</th>
<th>Area</th>
<th>% of total Area</th>
</tr>
</thead>
<tbody>
<tr>
<td>18S</td>
<td>40.54</td>
<td>42.04</td>
<td>25.5</td>
<td>20.2</td>
</tr>
<tr>
<td>25S</td>
<td>44.76</td>
<td>46.84</td>
<td>54.1</td>
<td>42.9</td>
</tr>
</tbody>
</table>
Sample: nHP_C-1

Overall Results for sample 7: R14040060

RNA Area: 150.2
RNA Concentration: 135 ng/µl
rRNA Ratio [25s/18s]: 2.0
RNA Integrity Number (RIN): 9.2 (B.02.08)
Result Flagging Color: 
Result Flagging Label: RIN: 9.20

Fragment table for sample 7: R14040060

<table>
<thead>
<tr>
<th>Name</th>
<th>Start Time [s]</th>
<th>End Time [s]</th>
<th>Area</th>
<th>% of total Area</th>
</tr>
</thead>
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<tr>
<td>18S</td>
<td>41.66</td>
<td>43.20</td>
<td>27.4</td>
<td>18.2</td>
</tr>
<tr>
<td>25S</td>
<td>46.01</td>
<td>48.21</td>
<td>54.9</td>
<td>36.6</td>
</tr>
</tbody>
</table>

Sample: nHP_C-2

Overall Results for sample 8: R14040061

RNA Area: 154.5
RNA Concentration: 138 ng/µl
rRNA Ratio [25s/18s]: 2.0
RNA Integrity Number (RIN): 8.9 (B.02.08)
Result Flagging Color: 
Result Flagging Label: RIN: 8.90

Fragment table for sample 8: R14040061

<table>
<thead>
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<th>Name</th>
<th>Start Time [s]</th>
<th>End Time [s]</th>
<th>Area</th>
<th>% of total Area</th>
</tr>
</thead>
<tbody>
<tr>
<td>18S</td>
<td>41.66</td>
<td>43.15</td>
<td>26.7</td>
<td>17.3</td>
</tr>
<tr>
<td>25S</td>
<td>45.92</td>
<td>47.90</td>
<td>52.2</td>
<td>33.8</td>
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### Overall Results for sample 5: R14040058

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<tr>
<th>RNA Area:</th>
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<tbody>
<tr>
<td>RNA Concentration:</td>
<td>125 ng/μl</td>
</tr>
<tr>
<td>rRNA Ratio [25s / 18s]:</td>
<td>2.0</td>
</tr>
<tr>
<td>RNA Integrity Number (RIN):</td>
<td>9.6 (B.02.08)</td>
</tr>
</tbody>
</table>

**Result Flagging Color:**

| Result Flagging Label: | RIN: 9.60 |

**Fragment table for sample 5: R14040058**

<table>
<thead>
<tr>
<th>Name</th>
<th>Start Time [s]</th>
<th>End Time [s]</th>
<th>Area</th>
<th>% of total Area</th>
</tr>
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<tbody>
<tr>
<td>18S</td>
<td>41.77</td>
<td>43.25</td>
<td>28.1</td>
<td>20.1</td>
</tr>
<tr>
<td>25S</td>
<td>46.14</td>
<td>48.36</td>
<td>55.5</td>
<td>39.7</td>
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</tbody>
</table>

### Overall Results for sample 6: R14040059

<table>
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<tr>
<th>RNA Area:</th>
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<tbody>
<tr>
<td>RNA Concentration:</td>
<td>105 ng/μl</td>
</tr>
<tr>
<td>rRNA Ratio [25s / 18s]:</td>
<td>1.9</td>
</tr>
<tr>
<td>RNA Integrity Number (RIN):</td>
<td>9.6 (B.02.08)</td>
</tr>
</tbody>
</table>

**Result Flagging Color:**

| Result Flagging Label: | RIN: 9.60 |

**Fragment table for sample 6: R14040059**

<table>
<thead>
<tr>
<th>Name</th>
<th>Start Time [s]</th>
<th>End Time [s]</th>
<th>Area</th>
<th>% of total Area</th>
</tr>
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<tbody>
<tr>
<td>18S</td>
<td>41.68</td>
<td>43.43</td>
<td>23.9</td>
<td>20.3</td>
</tr>
<tr>
<td>25S</td>
<td>46.14</td>
<td>48.06</td>
<td>45.5</td>
<td>38.7</td>
</tr>
</tbody>
</table>
Agarose gel electrophoresis test

Note: Lane M, Trans2KPlus Marker; Lane 1, HP_C-1; Lane 2, HP_M-1.
Agarose gel electrophoresis test

Note: Lane M, Trans2KPlus Marker; Lane 1, nHP_M-1; Lane 2, nHP_M-2; Lane 3, nHP_C-1; Lane 4, nHP_C-2; Lane 5, HP_C-2; Lane 6, HP_M-2.
<table>
<thead>
<tr>
<th>Sample name</th>
<th>Sample ID</th>
<th>Concentration (ng/μL)</th>
<th>OD260/280</th>
<th>OD260/230</th>
<th>25S/18S</th>
<th>RNA integrity number (RIN)</th>
<th>Inspection</th>
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</thead>
<tbody>
<tr>
<td>HP_C-1</td>
<td>R14040062</td>
<td>1220</td>
<td>2.279</td>
<td>0.366</td>
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<td>9.5</td>
<td>Pass</td>
</tr>
<tr>
<td>HP_C-2</td>
<td>R14030314</td>
<td>690.00</td>
<td>2.161</td>
<td>0.926</td>
<td>2.1</td>
<td>9.4</td>
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</tr>
<tr>
<td>HP_M-1</td>
<td>R14040063</td>
<td>1984</td>
<td>2.238</td>
<td>0.563</td>
<td>2.1</td>
<td>9.1</td>
<td>Pass</td>
</tr>
<tr>
<td>HP_M-2</td>
<td>R14030315</td>
<td>1540.00</td>
<td>2.167</td>
<td>2.172</td>
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<td>9.6</td>
<td>Pass</td>
</tr>
<tr>
<td>nHP_M-1</td>
<td>R14040058</td>
<td>2074</td>
<td>1.945</td>
<td>1.087</td>
<td>2.0</td>
<td>9.6</td>
<td>Pass</td>
</tr>
<tr>
<td>nHP_M-2</td>
<td>R14040059</td>
<td>1848</td>
<td>1.929</td>
<td>0.857</td>
<td>1.9</td>
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<tr>
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<td>R14040060</td>
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<td>9.2</td>
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<tr>
<td>nHP_C-2</td>
<td>R14040061</td>
<td>1562</td>
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</tbody>
</table>