Gene Set: RNAseq_HPC7_UP-REG

<table>
<thead>
<tr>
<th>Up-reg in phenotype</th>
<th>NES</th>
<th>p-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>HSC</td>
<td>2.99</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>CMP</td>
<td>2.97</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>GMP</td>
<td>2.82</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>B-cells</td>
<td>2.66</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>T-cells</td>
<td>2.25</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>Macrophage</td>
<td>2.25</td>
<td>&lt;0.001</td>
</tr>
</tbody>
</table>

**Table S1** – Comparison of HPC7 gene set enrichment in various haematopoietic cell types. Enrichment of HPC7 up-regulated genes was assessed by Gene Set Enrichment Analysis (GSEA) on expression data of haematopoietic progenitor as well as differentiated cell types from BioGPS. NES denotes normalized enrichment score.