Supplementary Material

A  KRED-Lamin B1 fusion protein - genes in the immediate vicinity of the Lamina

Figure 3a  the plots represent the curves of the read counts (ordinate) 60 min after light exposition; the axis of abscissae lists the affected genes in descending read counts order up to 100. (■ = read count). The ordinate shows the number of counts.

Table 1a  lists the ROS affected genes offering the highest read count number. The right column lists the OMIM Ids. (Details are described in the part G)

<table>
<thead>
<tr>
<th>Refseq ID</th>
<th>Read Counts</th>
<th>Gene Symbol</th>
<th>Description</th>
<th>OMIM ID</th>
</tr>
</thead>
<tbody>
<tr>
<td>NR_003594</td>
<td>6,824</td>
<td>REXO1L2P</td>
<td>RNA exonuclease 1 homologue-like 2 (pseudog)</td>
<td>609514</td>
</tr>
<tr>
<td>NM_003482</td>
<td>6,806</td>
<td>MLL2</td>
<td>histone-lysine N-methyltransferase MLL2</td>
<td>602113</td>
</tr>
<tr>
<td>NM_005580</td>
<td>5,420</td>
<td>LAMAS</td>
<td>laminin subunit alpha-5 precursor</td>
<td>601033</td>
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<tr>
<td>NM_001164462</td>
<td>4,688</td>
<td>MUC12</td>
<td>mucin-12 precursor</td>
<td>604609</td>
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</table>

Table 3a  shows the annotation clusters 1 and 2 with the enrichment scores 1.37 and 0.99 of the gene bundle with the entries from 101 to 200 affected genes in DAVID functional annotations analysis indicating the clusters of GO term enrichment.

<table>
<thead>
<tr>
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<tbody>
<tr>
<td>Category</td>
<td>Term</td>
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<tr>
<td>GOTERM_MF_FAT</td>
<td>structural molecule activity</td>
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<tr>
<td>KEGG_PATHWAY</td>
<td>Focal adhesion</td>
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<table>
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<tr>
<td>Category</td>
<td>Term</td>
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<tr>
<td>GOTERM_CC_FAT</td>
<td>cytoskeleton</td>
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Table 4a shows the annotation clusters 1-2 with the enrichment scores 1.37 and 1.18 of the gene bundle with the entries from 201 to 300 affected genes in DAVID functional annotations analysis indicating the clusters of GO term enrichment.

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<th>Annotatation Cluster 1</th>
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<th>Category</th>
<th>Term</th>
<th>Count</th>
<th>p_value</th>
<th>Benjamini</th>
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</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>GOTERM_MF_FAT</td>
<td>ATP binding</td>
<td>17</td>
<td>7.1E-3</td>
<td>8.0E-1</td>
</tr>
<tr>
<td></td>
<td></td>
<td>GOTERM_MF_FAT</td>
<td>adenyl ribonucleotide binding</td>
<td>17</td>
<td>8.0E-3</td>
<td>6.0E-1</td>
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</tbody>
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Annotatation Cluster 2 | Enrichment Score: 1.18 | Category | Term                           | Count | p_value  | Benjamini |
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<tbody>
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<td></td>
<td></td>
<td>GOTERM_MF_FAT</td>
<td>motor activity</td>
<td>5</td>
<td>8.3E-3</td>
<td>4.7E-1</td>
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<tr>
<td></td>
<td></td>
<td>GOTERM_MF_FAT</td>
<td>microtubule motor activity</td>
<td>4</td>
<td>9.3E-3</td>
<td>4.1E-1</td>
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Table 5a shows the annotation clusters 1-2 with the enrichment scores 2.81 and 2.36 of the gene bundle with the entries from 301 to 400 affected genes in DAVID functional annotations analysis indicating the clusters of GO term enrichment.

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<th>Term</th>
<th>Count</th>
<th>p_value</th>
<th>Benjamini</th>
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<tbody>
<tr>
<td></td>
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<td>GOTERM_CC_FAT</td>
<td>actin cytoskeleton</td>
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<td></td>
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<td>GOTERM_CC_FAT</td>
<td>myosin complex</td>
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<td>3.1E-4</td>
<td>3.0E-2</td>
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<td></td>
<td></td>
<td>GOTERM_CC_FAT</td>
<td>cytoskeleton</td>
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<td></td>
<td></td>
<td>GOTERM_MF_FAT</td>
<td>actin binding</td>
<td>9</td>
<td>4.7E-4</td>
<td>1.0E-1</td>
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<td>2.0E-3</td>
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<td>GOTERM_CC_FAT</td>
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<td>3.0E-1</td>
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<tr>
<td></td>
<td></td>
<td>GOTERM_MF_FAT</td>
<td>motor activity</td>
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<td>8.3E-3</td>
<td>2.1E-1</td>
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Annotatation Cluster 2 | Enrichment Score: 2.36 | Category | Term                           | Count | p_value  | Benjamini |
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<td>GOTERM_BP_FAT</td>
<td>cytoskeletal anchoring at plasma membrane</td>
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<td>4.1E-1</td>
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<tr>
<td></td>
<td></td>
<td>GOTERM_BP_FAT</td>
<td>maintenance of protein location in cell</td>
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<td>1.1E-3</td>
<td>3.5E-1</td>
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<tr>
<td></td>
<td></td>
<td>GOTERM_BP_FAT</td>
<td>maintenance of location in cell</td>
<td>4</td>
<td>1.7E-3</td>
<td>2.4E-1</td>
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<td></td>
<td></td>
<td>GOTERM_BP_FAT</td>
<td>maintenance of protein location</td>
<td>4</td>
<td>1.7E-3</td>
<td>2.4E-1</td>
</tr>
<tr>
<td></td>
<td></td>
<td>GOTERM_BP_FAT</td>
<td>maintenance of location</td>
<td>4</td>
<td>3.9E-3</td>
<td>2.9E-1</td>
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</table>
Table 6a shows the annotation clusters 1-2 with the enrichment scores 1.87 and 1.12 of the gene bundle with the entries from 401 to 500 affected genes in DAVID functional annotations analysis indicating the clusters of GO term enrichment.

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<th>Benjamini</th>
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</thead>
<tbody>
<tr>
<td>Category</td>
<td>Term</td>
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<td></td>
<td></td>
</tr>
<tr>
<td>GOTERM_MF_FAT</td>
<td>ATP binding</td>
<td>15</td>
<td>5.5E-3</td>
<td>6.7E-1</td>
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<tr>
<td>GOTERM_MF_FAT</td>
<td>adenyl ribonucleotide binding</td>
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<td>6.2E-3</td>
<td>4.6E-1</td>
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<tr>
<td>GOTERM_MF_FAT</td>
<td>adenyl nucleotide binding</td>
<td>15</td>
<td>9.7E-3</td>
<td>4.8E-1</td>
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<table>
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<td>Term</td>
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<td>GOTERM_BP_FAT</td>
<td>cell projection morphogenesis</td>
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<td>6.8E-3</td>
<td>9.3E-1</td>
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<tr>
<td>GOTERM_BP_FAT</td>
<td>cell morphogenesis</td>
<td>7</td>
<td>7.7E-3</td>
<td>8.6E-1</td>
</tr>
<tr>
<td>GOTERM_BP_FAT</td>
<td>cell part morphogenesis</td>
<td>6</td>
<td>8.2E-3</td>
<td>7.9E-1</td>
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</tbody>
</table>

Table 7a shows the annotation clusters 1-3 with the enrichment scores 1.96; 1.54; and 1.52 of the gene bundle with the entries from 501 to 600 affected genes in DAVID functional annotations analysis indicating the clusters of GO term enrichment.

<table>
<thead>
<tr>
<th>Annotation Cluster 1</th>
<th>Enrichment Score: 1.96</th>
<th>Count</th>
<th>p_value</th>
<th>Benjamini</th>
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<tbody>
<tr>
<td>Category</td>
<td>Term</td>
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<tr>
<td>GOTERM_MF_FAT</td>
<td>adenyl nucleotide binding</td>
<td>16</td>
<td>3.8E-3</td>
<td>5.5E-1</td>
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<tr>
<td>GOTERM_MF_FAT</td>
<td>purine nucleoside binding</td>
<td>16</td>
<td>4.4E-3</td>
<td>3.7E-1</td>
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<tr>
<td>GOTERM_MF_FAT</td>
<td>nucleoside binding</td>
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<td>4.7E-3</td>
<td>2.8E-1</td>
</tr>
<tr>
<td>GOTERM_MF_FAT</td>
<td>ATP binding</td>
<td>15</td>
<td>5.5E-3</td>
<td>2.5E-1</td>
</tr>
<tr>
<td>GOTERM_MF_FAT</td>
<td>adenyl ribonucleotide binding</td>
<td>15</td>
<td>6.2E-3</td>
<td>2.3E-1</td>
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<table>
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<th>Count</th>
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<th>Benjamini</th>
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<tbody>
<tr>
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<td>Term</td>
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<tr>
<td>GOTERM_BP_FAT</td>
<td>actin cytoskeleton organization</td>
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<td>2.0E-2</td>
<td>9.6E-1</td>
</tr>
<tr>
<td>GOTERM_BP_FAT</td>
<td>actin filament-based process</td>
<td>5</td>
<td>2.4E-2</td>
<td>9.6E-1</td>
</tr>
<tr>
<td>GOTERM_BP_FAT</td>
<td>cytoskeleton organization</td>
<td>6</td>
<td>4.9E-2</td>
<td>9.9E-1</td>
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<table>
<thead>
<tr>
<th>Annotation Cluster 3</th>
<th>Enrichment Score: 1.52</th>
<th>Count</th>
<th>p_value</th>
<th>Benjamini</th>
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<tbody>
<tr>
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<td>Term</td>
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</tr>
<tr>
<td>GOTERM_BP_FAT</td>
<td>cell-matrix adhesion</td>
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<td>7.9E-3</td>
<td>9.2E-1</td>
</tr>
<tr>
<td>GOTERM_BP_FAT</td>
<td>cell-substrate adhesion</td>
<td>4</td>
<td>1.0E-2</td>
<td>8.9E-1</td>
</tr>
</tbody>
</table>
Table 9a lists the annotation clusters 1-2 with the enrichment scores 3.28 and 2.16 of the gene bundle of the first 100 entries with the highest counts of the probe 60 min after illumination in DAVID functional annotations analysis which gave clusters of GO term enrichment.

<table>
<thead>
<tr>
<th>Annotation Cluster 1</th>
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</thead>
<tbody>
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<td><strong>Term</strong></td>
</tr>
<tr>
<td>GOTERM_BP_FAT</td>
<td>cell adhesion</td>
</tr>
<tr>
<td>GOTERM_BP_FAT</td>
<td>biological adhesion</td>
</tr>
<tr>
<td>GOTERM_MF_FAT</td>
<td>extracellular matrix structural constituent</td>
</tr>
<tr>
<td>GOTERM_MF_FAT</td>
<td>structural molecule activity</td>
</tr>
<tr>
<td>GOTERM_CC_FAT</td>
<td>proteinaceous extracellular matrix</td>
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<tr>
<td>GOTERM_MC_FAT</td>
<td>extracellular matrix part</td>
</tr>
<tr>
<td>KEGG_PATHWAY</td>
<td>ECM-receptor interaction</td>
</tr>
<tr>
<td>GOTERM_CC_FAT</td>
<td>basement membrane</td>
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<table>
<thead>
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</thead>
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<td><strong>Term</strong></td>
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<td>motor activity</td>
</tr>
<tr>
<td>GOTERM_BP_FAT</td>
<td>microtubule-based process</td>
</tr>
<tr>
<td>GOTERM_CC_FAT</td>
<td>cytoskeletal part</td>
</tr>
<tr>
<td>GOTERM_CC_FAT</td>
<td>cytoskeleton</td>
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</tbody>
</table>
Table 11a lists the annotation clusters 1-3 with the corresponding enrichment scores of the gene bundle of most prominent 57 of the first 100 affected genes (of the histone H2A-KRED nuclei) which offer the highest count number of the control 30 min after illumination in DAVID functional annotations analysis which gave clusters of GO term enrichment.

<table>
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<td>GOTERM_BP_FAT</td>
<td>microtubule-based movement</td>
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<td></td>
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<td>cytoskeleton</td>
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<td></td>
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<td>4.7E-4</td>
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<td></td>
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<td>1.9E-2</td>
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<tr>
<td>GOTERM_MF_FAT</td>
<td>ATP binding</td>
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<td></td>
<td>16</td>
<td>9.3E-4</td>
<td>2.8E-2</td>
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<td>adenyl ribonucleotide binding</td>
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<td></td>
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<td>1.1E-3</td>
<td>2.7E-2</td>
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<td>1.8E-3</td>
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<td></td>
<td>14</td>
<td>9.2E-6</td>
<td>2.3E-3</td>
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<tr>
<td>GOTERM_BP_FAT</td>
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Table 12a shows the annotation Cluster 1-3 with the enrichment scores 6.15; 5.74, and 4.84 of the first 500 affected genes (of the histone H2A-KRED nuclei) which offer the highest count number of the control 30 min after illumination in DAVID functional annotations analysis which gave clusters of GO term enrichment.

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Table 13a lists the first 57 most affected genes which show read counts solely in the lamin B1 probe but not in the H2A-KRED control. The 13 genes which offer the highest read counts (gray highlighted) were displayed and listed in the manuscript in Table 4 and further characterized (shown in Table 6).

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D  Chromatin-localized - but not lamin B1 localized ROS-affected genes

Table 14a lists the first 25 of the most affected genes which show read counts in the H2A-KRED control but not in the lamin B1 probe.

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