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.

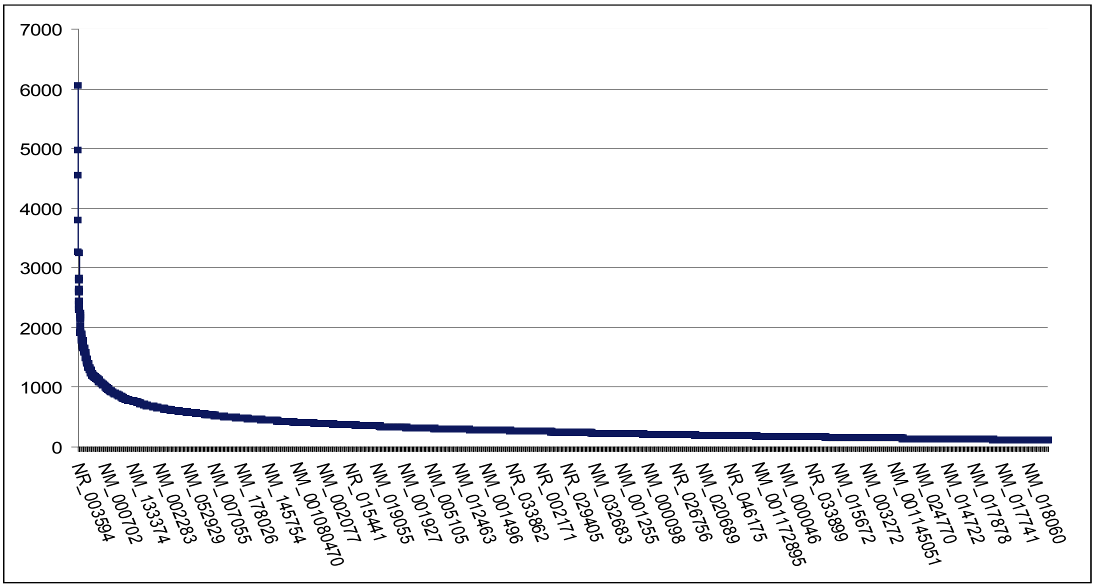

Table 1a lists the ROS affected genes offering the highest read count number. The right column lists the OMIM Ids. (Details are described in the part G)

Refseq ID	**Read Counts**		**Gene Symbol**	**Description**	**OMIM ID**
	30 min	**60 min**			
NR_003594	6,824	6,039	***REXO1L2P***	RNA exonuclease 1 homologue-like 2 (pseudog)	609614
NM_003482	6,806	4,973	***MLL2***	histone-lysine N-methyltransferase MLL2	602113
NM_005560	5,420	3,793	***LAMA5***	laminin subunit alpha-5 precursor	601033
NM_001164462	4,688	4,544	***MUC12***	mucin-12 precursor	604609

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.

Annotatation Cluster 1	Enrichment Score: 1.37			
Category	**Term**	**Count**	**p_value**	**Benjamini**
GOTERM_MF_FAT	structural molecule activity	10	3.0E-3	4.0E-1
KEGG_PATHWAY	Focal adhesion	5	5.8E-3	1.6E-1

Annotatation Cluster 2	Enrichment Score: 0.99			
Category	**Term**	**Count**	**p_value**	**Benjamini**
GOTERM_CC_FAT	cytoskeleton	13	4.4E-2	6.2E-1

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.

Annotatation Cluster 1	Enrichment Score: 1.37			
Category	**Term**	**Count**	**p_value**	**Benjamini**
GOTERM_MF_FAT	ATP binding	17	7.1E-3	8.0E-1
GOTERM_MF_FAT	adenyl ribonucleotide binding	17	8.0E-3	6.0E-1

Annotatation Cluster 2	Enrichment Score: 1.18			
Category	**Term**	**Count**	**p_value**	**Benjamini**
GOTERM_MF_FAT	motor activity	5	8.3E-3	4.7E-1
GOTERM_MF_FAT	microtubule motor activity	4	9.3E-3	4.1E-1

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.

Annotatation Cluster 1	Enrichment Score: 2.81			
Category	**Term**	**Count**	**p_value**	**Benjamini**
GOTERM_CC_FAT	actin cytoskeleton	9	5.5E-5	1.1E-2
GOTERM_CC_FAT	myosin complex	5	3.1E-4	3.0E-2
GOTERM_CC_FAT	cytoskeleton	18	3.3E-4	2.2E-2
GOTERM_MF_FAT	actin binding	9	4.7E-4	1.0E-1
GOTERM_MF_FAT	cytoskeletal protein binding	10	2.0E-3	2.0E-3
GOTERM_CC_FAT	cytoskeletal part	12	7.1E-3	3.0E-1
GOTERM_MF_FAT	motor activity	5	8.3E-3	2.1E-1
Annotatation Cluster 2	Enrichment Score: 2.36			
Category	**Term**	**Count**	**p_value**	**Benjamini**
GOTERM_BP_FAT	cytoskeletal anchoring at plasma membrane	3	6.6E-4	4.1E-1
GOTERM_BP_FAT	maintenance of protein location in cell	4	1.1E-3	3.5E-1
GOTERM_BP_FAT	maintenance of location in cell	4	1.7E-3	2.4E-1
GOTERM_BP_FAT	maintenance of protein location	4	1.7E-3	2.4E-1
GOTERM_BP_FAT	maintenance of location	4	3.9E-3	2.9E-1

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.

Annotatation Cluster 1	Enrichment Score: 1.87			
Category	**Term**	**Count**	**p_value**	**Benjamini**
GOTERM_MF_FAT	ATP binding	15	5.5E-3	6.7E-1
GOTERM_MF_FAT	adenyl ribonucleotide binding	15	6.2E-3	4.6E-1
GOTERM_MF_FAT	adenyl nucleotide binding	15	9.7E-3	4.8E-1
Annotatation Cluster 2	Enrichment Score: 1.12			
Category	**Term**	**Count**	**p_value**	**Benjamini**
GOTERM_BP_FAT	cell projection morphogenesis	6	6.8E-3	9.3E-1
GOTERM_BP_FAT	cell morphogenesis	7	7.7E-3	8.6E-1
GOTERM_BP_FAT	cell part morphogenesis	6	8.2E-3	7.9E-1

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.

Annotatation Cluster 1	Enrichment Score: 1.96			
Category	**Term**	**Count**	**p_value**	**Benjamini**
GOTERM_MF_FAT	adenyl nucleotide binding	16	3.8E-3	5.5E-1
GOTERM_MF_FAT	purine nucleoside binding	16	4.4E-3	3.7E-1
GOTERM_MF_FAT	nucleoside binding	16	4.7E-3	2.8E-1
GOTERM_MF_FAT	ATP binding	15	5.5E-3	2.5E-1
GOTERM_MF_FAT	adenyl ribonucleotide binding	15	6.2E-3	2.3E-1
Annotatation Cluster 2	Enrichment Score: 1.54			
Category	**Term**	**Count**	**p_value**	**Benjamini**
GOTERM_BP_FAT	actin cytoskeleton organization	5	2.0E-2	9.6E-1
GOTERM_BP_FAT	actin filament-based process	5	2.4E-2	9.6E-1
GOTERM_BP_FAT	cytoskeleton organization	6	4.9E-2	9.9E-1
Annotatation Cluster 3	Enrichment Score: 1.52			
Category	**Term**	**Count**	**p_value**	**Benjamini**
GOTERM_BP_FAT	cell-matrix adhesion	4	7.9E-3	9.2E-1
GOTERM_BP_FAT	cell-substrate adhesion	4	1.0E-2	8.9E-1

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.

Annotatation Cluster 1	Enrichment Score: 3.28			
Category	**Term**	**Count**	**p_value**	**Benjamini**
GOTERM_BP_FAT	cell adhesion	19	3.8E-9	2.5E-6
GOTERM_BP_FAT	biological adhesion	19	3.8E-9	1.3E-6
GOTERM_MF_FAT	extracellular matrix structural constituent	7	2.9E-6	5.9E-4
GOTERM_MF_FAT	structural molecule activity	14	6.0E-6	4.0E-4
GOTERM_CC_FAT	proteinaceous extracellular matrix	9	2.8E-4	4.0E-2
GOTERM_CC_FAT	extracellular matrix part	6	3.9E-4	2.8E-2
GOTERM_CC_FAT	extracellular matrix	9	4.7E-4	2.3E-2
KEGG_PATHWAY	ECM-receptor interaction	5	5.7E-4	2.2E-2
GOTERM_CC_FAT	basement membrane	5	7.8E-4	2.8E-2
Annotatation Cluster 2	Enrichment Score: 2.16			
Category	**Term**	**Count**	**p_value**	**Benjamini**
GOTERM_MF_FAT	motor activity	7	5.2E-5	2.6E-3
GOTERM_BP_FAT	microtubule-based process	7	1.4E-3	1.7E-1
GOTERM_CC_FAT	cytoskeletal part	13	4.1E-3	7.2E-2
GOTERM_CC_FAT	cytoskeleton	16	5.2E-3	8.2E-2

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.

Annotatation cluster 1	Enrichment Score: 3.74			
Category	**Term**	**Count**	**p_value**	**Benjamini**
GOTERM_MF_FAT	motor activity	9	1.3E-7	2.1E-5
GOTERM_CC_FAT	dynein complex	6	6.2E-7	8.5E-5
GOTERM_BP_FAT	microtubule-based movement	8	6.3E-7	4.7E-4
GOTERM_MF_FAT	microtubule motor activity	7	8.2E-7	6.4E-5
GOTERM_BP_FAT	microtubule-based process	10	1.6E-6	5.8E-4
GOTERM_CC_FAT	axonemal dynein complex	4	2.4E-5	1.7E-3
GOTERM_BP_FAT	ciliary or flagellar motility	4	2.9E-5	4.3E-3
GOTERM_CC_FAT	axoneme	5	4.7E-5	1.6E-3
GOTERM_CC_FAT	microtubule cytoskeleton	12	6.7E-5	1.8E-3
GOTERM_CC_FAT	axoneme part	4	7.4E-5	1.7E-3
GOTERM_CC_FAT	cytoskeleton	19	8.0E-5	1.6E-3
GOTERM_CC_FAT	microtubule associated complex	6	1.4E-4	2.5E-3
GOTERM_CC_FAT	cilium axoneme	4	2.4E-4	3.7E-3
GOTERM_CC_FAT	cilium	6	4.3E-4	5.3E-3

Annotatation Cluster 2	Enrichment Score: 3.39			
Category	**Term**	**Count**	**p_value**	**Benjamini**
GOTERM_MF_FAT	motor activity	9	1.3E-7	2.1E-5
GOTERM_BP_FAT	microtubule-based movement	8	6.3E-7	4.7E-4
GOTERM_MF_FAT	microtubule motor activity	7	8.2E-7	6.4E-5
GOTERM_MF_FAT	ATPase activity	8	4.9E-4	1.9E-2
GOTERM_MF_FAT	ATP binding	16	9.3E-4	2.8E-2
GOTERM_MF_FAT	adenyl ribonucleotide binding	16	1.1E-3	2.7E-2
GOTERM_MF_FAT	adenyl nucleotide binding	16	1.8E-3	3.9E-2
GOTERM_MF_FAT	purine nucleoside binding	16	4.0E-2	2.1E-3

Annotatation Cluster 3	Enrichment Score: 2.92			
Category	**Term**	**Count**	**p_value**	**Benjamini**
GOTERM_BP_FAT	cell adhesion	14	9.2E-6	2.3E-3
GOTERM_BP_FAT	biological adhesion	14	9.4E-6	1.7E-3
GOTERM_CC_FAT	basement membrane	6	4.0E-5	1.8E-3
GOTERM_CC_FAT	extracellular matrix part	6	2.7E-4	3.7E-3

B Histone H2A-KRED - (genes localization distributed over the whole nucleus)

Table12a shows the annotation Cluster1-3 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.

Annotatation Cluster 1	Enrichment Score: 6.15			
Category	**Term**	**Count**	**p_value**	**Benjamini**
GOTERM_BP_FAT	microtubule-based movement	19	3.1E-10	5.7E-7
GOTERM_CC_FAT	dynein complex	12	4.3E-10	7.3E-8
GOTERM_MF_FAT	motor activity	21	8.5E-10	2.1E-7
GOTERM_MF_FAT	microtubule motor activity	16	1.2E-9	1.9E-7
GOTERM_BP_FAT	microtubule-based process	25	1.8E-8	1.7E-5
GOTERM_CC_FAT	axonemal dynein complex	7	2.1E-7	1.5E-5
GOTERM_CC_FAT	microtubule associated complex	15	2.9E-7	1.4E-5
GOTERM_CC_FAT	microtubule cytoskeleton	36	5.5E-7	2.3E-5
GOTERM_CC_FAT	microtubule	24	5.5E-7	2.1E-5
GOTERM_CC_FAT	axoneme	10	7.0E-7	2.4E-5
GOTERM_CC_FAT	cytoskeleton	65	1.4E-6	3.9E-5
GOTERM_MF_FAT	ATPase activity	26	2.5E-6	2.1E-4
GOTERM_CC_FAT	axoneme part	7	2.6E-6	6.3E-5
GOTERM_CC_FAT	non-membrane-bounded organelle	102	2.6E-6	6.0E-5
GOTERM_CC_FAT	intracellular non-membrane-bounded organelle	102	2.6E-6	6.0E-5
GOTERM_BP_FAT	ciliary or flagellar motility	6	1.5E-5	4.6E-3
GOTERM_CC_FAT	cilium axoneme	7	3.1E-5	6.2E-4
GOTERM_CC_FAT	cilium part	8	1.1E-4	2.1E-3
GOTERM_CC_FAT	cilium	13	1.1E-4	2.0E-3
GOTERM_CC_FAT	cytoskeletal part	44	1.7E-4	2.9E-3
GOTERM_CC_FAT	cell projection part	17	3.3E-4	5.4E-3
Annotatation Cluster 2	Enrichment Score: 5.73			
Category	**Term**	**Count**	**p_value**	**Benjamini**
GOTERM_CC_FAT	extracellular matrix part	20	1.1E-10	3.9E-8
GOTERM_MF_FAT	extracellular matrix structural constituent	17	6.6E-10	3.2E-7
KEGG_PATHWAY	ECM-receptor interaction	15	1.9E-9	1.9E-7
GOTERM_CC_FAT	basement membrane	14	7.6E-8	8.6E-6
GOTERM_CC_FAT	proteinaceous extracellular matrix	27	1.9E-7	1.6E-5
GOTERM_CC_FAT	extracellular matrix	28	2.3E-7	1.3E-5
GOTERM_CC_FAT	collagen	9	2.1E-6	5.6E-5
GOTERM_MF_FAT	structural molecule activity	36	2.6E-5	8.5E-4
Annotatation Cluster 3	Enrichment Score: 4.84			
Category	**Term**	**Count**	**p_value**	**Benjamini**
GOTERM_MF_FAT	adenyl ribonucleotide binding	71	8.9E-7	1.1E-4

GOTERM_MF_FAT	ATP binding	70	1.1E-6	1.1E-4
GOTERM_MF_FAT	adenyl nucleotide binding	71	5.8E-6	3.5E-4
GOTERM_MF_FAT	purine nucleoside binding	71	9.6E-6	4.7E-4
GOTERM_MF_FAT	nucleoside binding	71	1.2E-5	4.6E-4
GOTERM_MF_FAT	ribonucleotide binding	77	2.6E-5	9.0E-4
GOTERM_MF_FAT	purine ribonucleotide binding	77	2.6E-5	9.0E-4
GOTERM_MF_FAT	purine nucleotide binding	77	1.1E-4	2.8E-3

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).

Refseq_ID	**Gene symbol**	**Read counts**	**physical map**
NM_001127482	***SPRYD7***	12550	13q14.2 [R]
NM_001003796	***NHP2L1***	6584	22q13.2 [G]
NM_001039210	***ALG13***	6428	Xq23 [G]
NM_001004333	***RNASEK***	6331	17p13.1 [R]
NM_001035223	***RGL3***	5688	19p13.2 [G]
NM_001114106	***SLC44A3***	5055	1p21.3 [G]
NM_001099410	***GPRASP1***	4953	Xq22.1 [R]
NM_001105538	***MYBBP1A***	4826	17p13.2 [G]
NM_001124759	***FRG2C***	4339	3p12.3 [G]
NM_001099455	***CPPED1***	4305	16p13.12 [G]
NM_001171799	***TRIQK***	3906	8q22.1 [R]
NM_001134364	***MAP4***	3613	3p21.31 [R]
NM_001139518	***PRKRA***	3409	2q31.2 [G]
NM_001042680	***MFSD12***	3312	19p13.3 [R]
NM_001145400	***ADAD2***	3282	16q24.1 [R]
NM_001031710	***KLHL7***	3224	7p15.3 [R]
NM_001145212	***SLCO2B1***	3170	11q13.4 [R]
NM_001145123	***PPP1R17***	3141	7p14.3 [G]
NM_001261467	***NSRP1***	2912	17q11.2 [R]
NM_001037535	***SCML1***	2854	Xp22.13 [R]
NM_001006605	***FAM69A***	2844	1p22.1 [R]
NM_001098424	***DLG1***	2820	3q29 [R]
NM_001012320	***ZNF302***	2703	19q13.11 [R]
NM_001099437	***ZNF30***	2630	19q13.11 [R]
NM_001004340	***FCGR1B***	2605	1p11.2 [R]
NM_001099431	***CLEC1B***	2542	12p13.2 [G]
NM_001031666	***MS4A3***	2333	11q12.1 [R]
NM_001242758	***HLA-A***	2318	6p22.1 [R]
NM_001042370	***TROVE2***	2235	1q31.2 [R]
NM_001100431	***VSIG4***	2230	Xq12 [G]
NM_001145114	***RRP12***	2162	10q24.1 [G]
NM_001004353	***C9orf173***	2143	9q34.3 [R]
NM_001170331	***LANCL3***	1899	Xp21.1 [R]
NM_001267544	***ARFRP1***	1846	20q13.33 [R]
NM_001012270	***BIRC5***	1821	17q25.3 [R]
NM_001097612	***GPR89A***	1797	1q21.1 [R]
NM_001145345	***ZNF566***	1597	19q13.12 [G]
NM_001163297	***MARK2***	1539	11q13.1 [R]
NM_001105580	***GABRR3***	1519	3q11.2 [G]
NM_001083539	***KIR3DS1***	1495	19q13.4 [G]
NM_001012288	***CRLF2***	1466	Xp22.33 [R]
NM_001242307	***PITRM1***	1403	10p15.2 [G]
NM_001267727	***ARSG***	1364	17q24.2 [R]
NM_001145311	***PLIN1***	1354	15q26.1 [R]
NM_001139441	***BCAP31***	1291	Xq28 [R]
NM_001042635	***NGDN***	1222	14q11.2 [R]
NM_001097577	***ANG***	1208	14q11.2 [R]
NM_001084392	***DDT***	1183	22q11.23 [R]
NM_001169574	***CXorf58***	1183	Xp22.11 [R]

NM_001202449	***ADK***	1110	10q22.2 [G]
NM_001004426	***PLA2G6***	1101	22q13.1 [R]
NM_001242350	***VNN2***	1067	6q23.2 [G]
NM_001098637	***PWWP2B***	1052	10q26.3 [R]
NM_001145201	***PRAP1***	1023	10q26.3 [R]
NM_001242886	***DDC***	1023	7p12.1 [G]
NM_001031702	***SEMA5B***	1013	3q21.1 [R]
NM_001145	***ANG***	1003	14q11.2 [R]

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.

Refseq_ID	**Gene symbol**	**Read counts**	**physical map**
NM_001146197	***CCDC168***	3804	13q33.1 [G]
NM_001127464	***ZNF469***	3247	16q24.2 [R]
NM_001042603	***KDM5A***	2974	12p13.33 [R]
NM_001110781	***SLC35E2B***	2580	1p36.33 [R]
NM_001114132	***NBEAL1***	2454	
NM_001037165	***FOXK1***	2427	
NM_001044	***SLC6A3***	2081	
NM_001012418	***MYLK4***	1739	
NM_001159	***AOX1***	1681	
NM_001271	***CHD2***	1560	
NM_001031701	***NT5DC3***	1450	
NM_001201380	***CNTNAP3B***	1382	
NM_001145124	***SPATA31C1***	1377	
NM_001270	***CHD1***	1356	
NM_001031617	***COX19***	1292	
NM_001084	***PLOD3***	1235	
NM_001037335	***HELZ2***	1203	
NM_001110199	***SRRM3***	1156	
NM_001145399	***MPPED2***	1124	
NM_001042573	***ENGASE***	1119	
NM_001085429	***TMEM213***	1019	
NM_001031713	***CCDC90A***	1014	
NM_001097615	***POLR2J3***	1009	
NM_001099415	***POM121C***	1009	
NM_001146106	***PARP9***	1009	