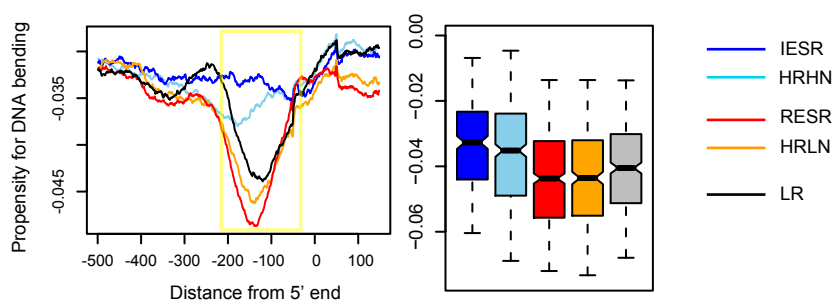
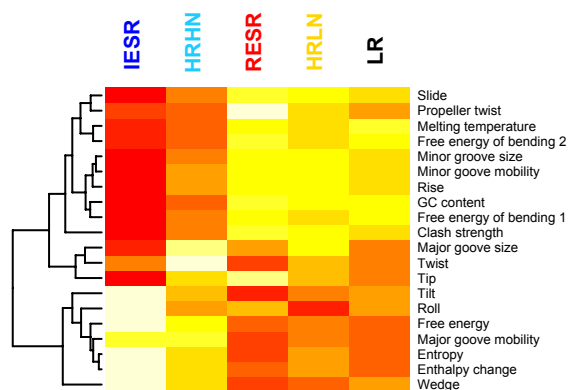


Supplementary Fig. 1

A



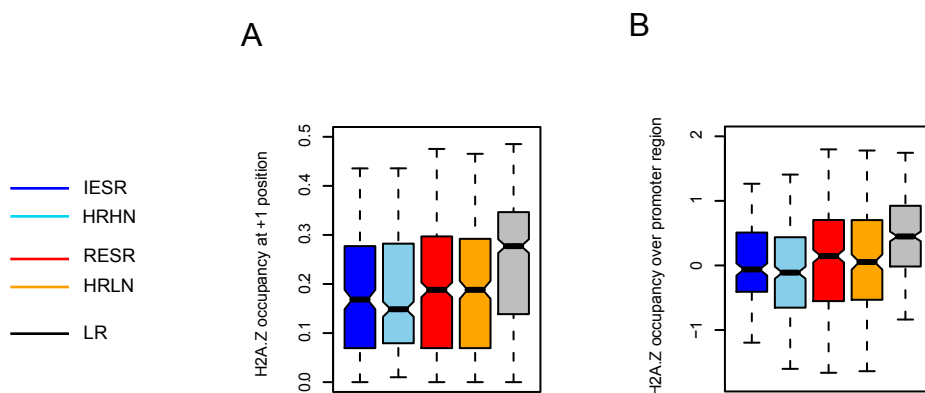
B



(A) Propensity for DNA bending was calculated based on sequence composition as described in Materials and Methods and plotted as a function of the distance from the start codon. The box plot shows nucleosome level at the critical region outlined in yellow.

(B) Structural properties of DNA were calculated based on sequence composition as described in Materials and Methods and compared among different gene groups. Red, white and yellow cells indicate high, intermediate and low level, respectively. For example, free energy binding is significantly higher for the IESR and HRHN group.

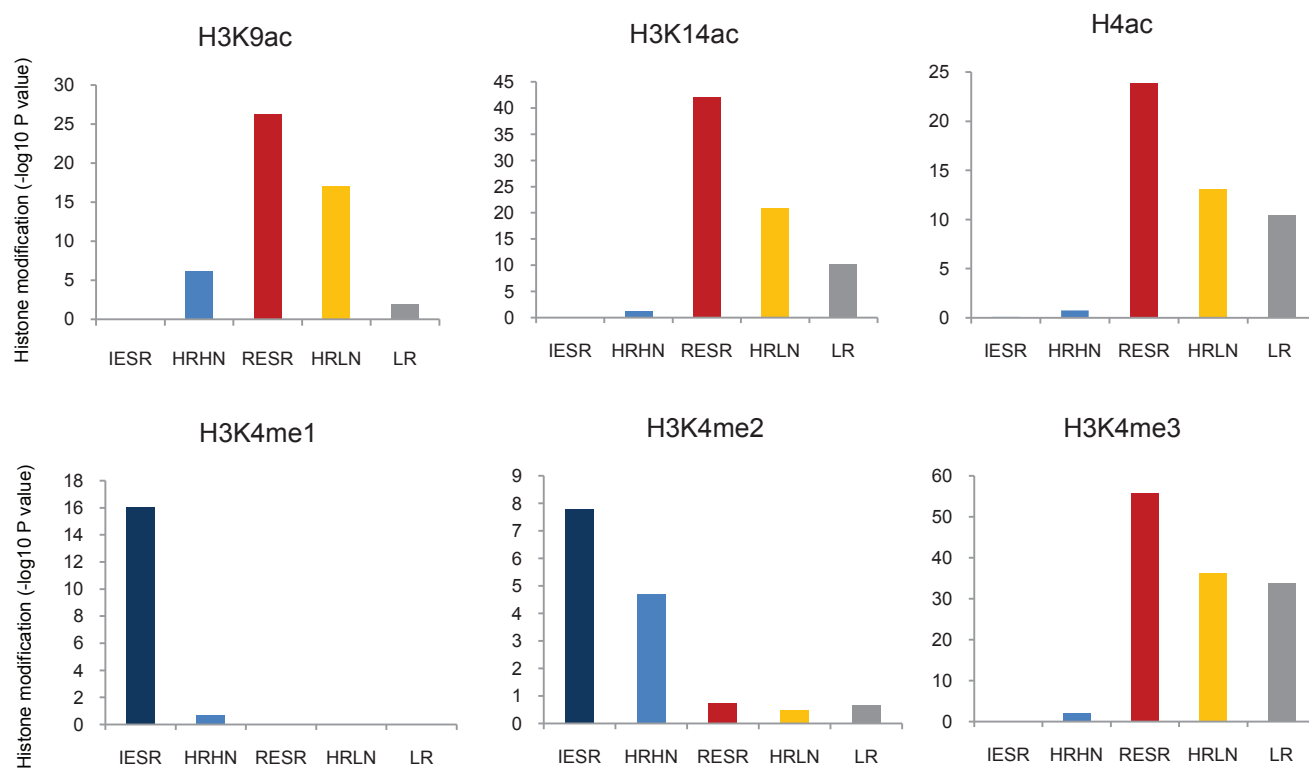
Supplementary Fig. 2



(A) H2A.Z occupancy at the first nucleosomal position downstream of the gene start site (Albert et al., 2007).

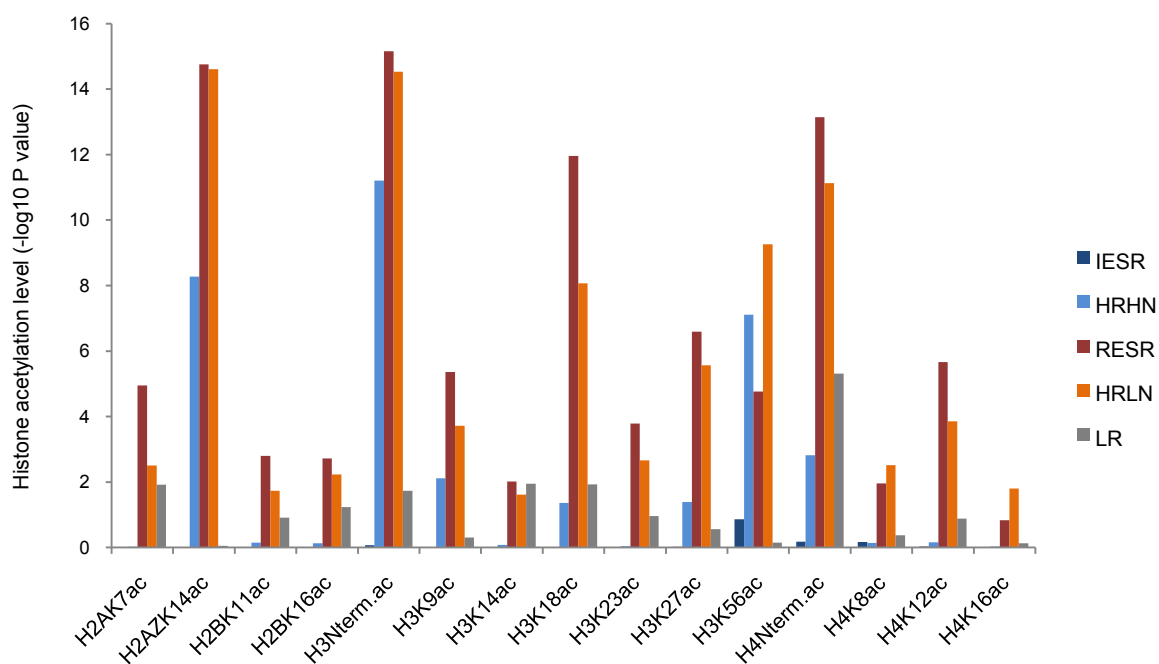
(B) H2A.Z occupancy over the promoter region (Zhang et al., 2005).

Supplementary Fig. 3



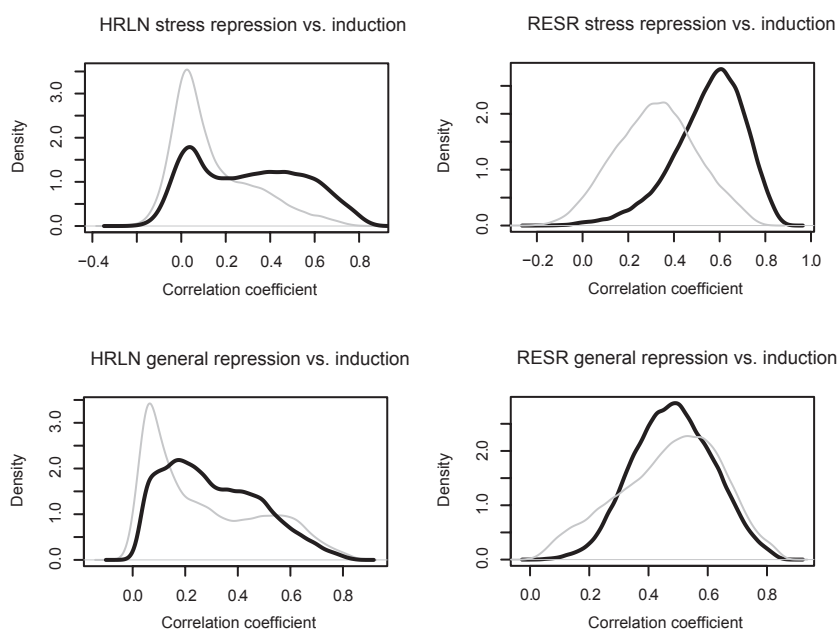
The average histone modification level was obtained for each promoter and compared between the target group of genes and the rest of genes by means of the Kolmogorov-Smirnov test. A higher $-\log_{10}(P \text{ value})$ from the test indicates a higher modification level.

Supplementary Fig. 4



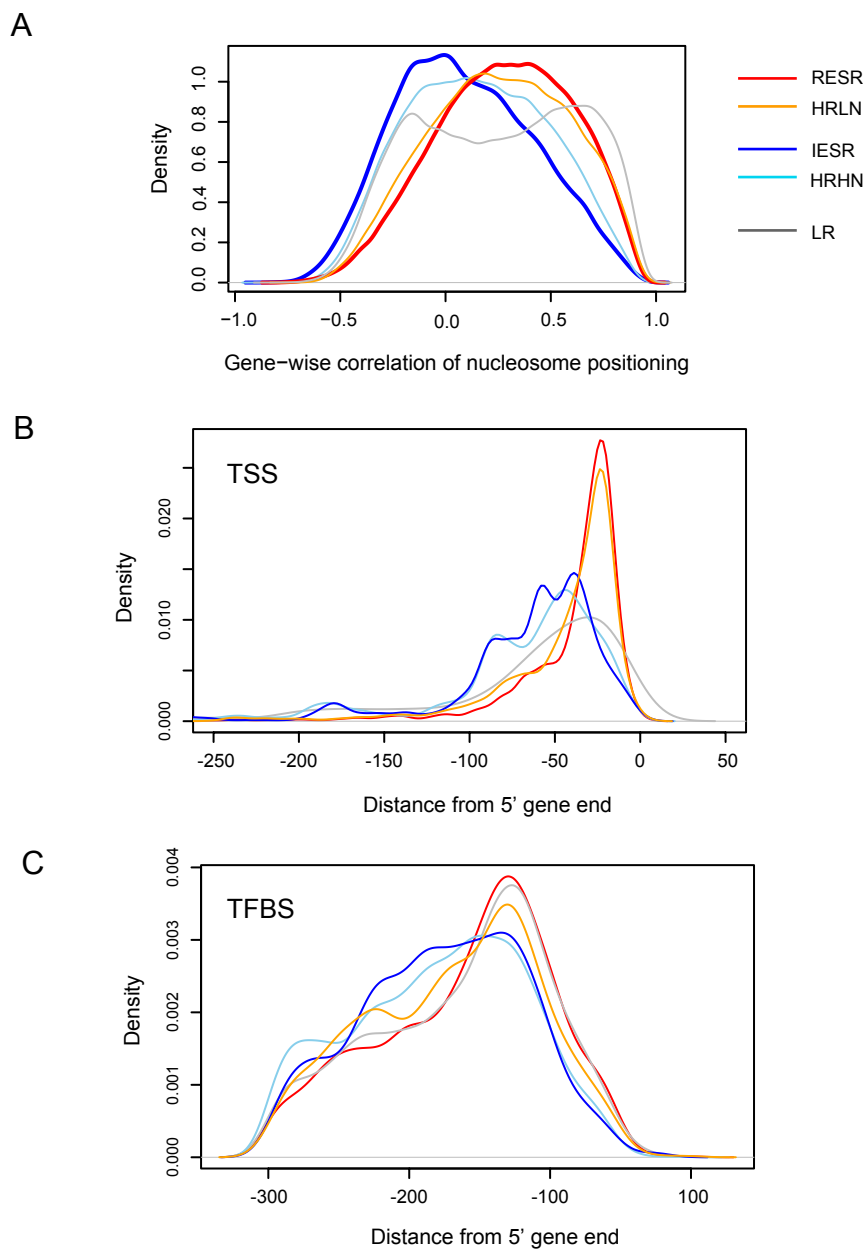
Normalized measures for various histone acetylations for each promoter were downloaded from the ChromatinDB (http://www.bioinformatics2.wsu.edu/cgi-bin/ChromatinDB/cgi/visualize_select.pl) and compared between the target group of genes and the rest of genes by means of the Kolmogorov-Smirnov test. A higher $-\log_{10}$ (P value) from the test indicates a higher modification level.

Supplementary Fig. 5



The correlation coefficients of all pairs of genes in each group were measured among induced genes (gray curve) and among repressed genes (black curve) across specific stress conditions (Gasch et al., 2000), which means the correlation of stress response, and across many different environmental perturbations (Tirosh et al., 2006), which means the correlation of general responsiveness.

Supplementary Fig. 6

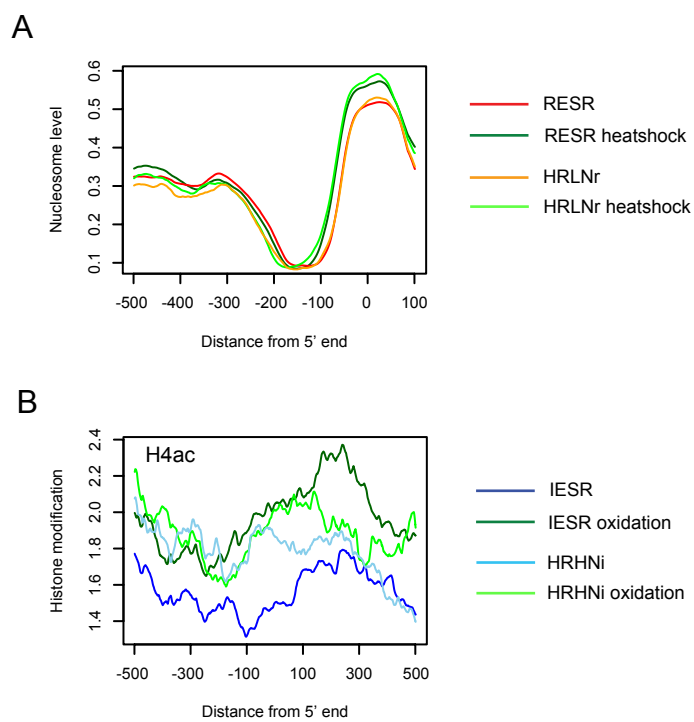


(A) Nucleosome occupancy pattern across the promoter was compared between two genes in each group in terms of correlation coefficient.

(B) The distribution of transcription start sites as a function of distance from the 5' gene end.

(C) The distribution of transcription-factor binding sites as a function of distance from the 5' gene end.

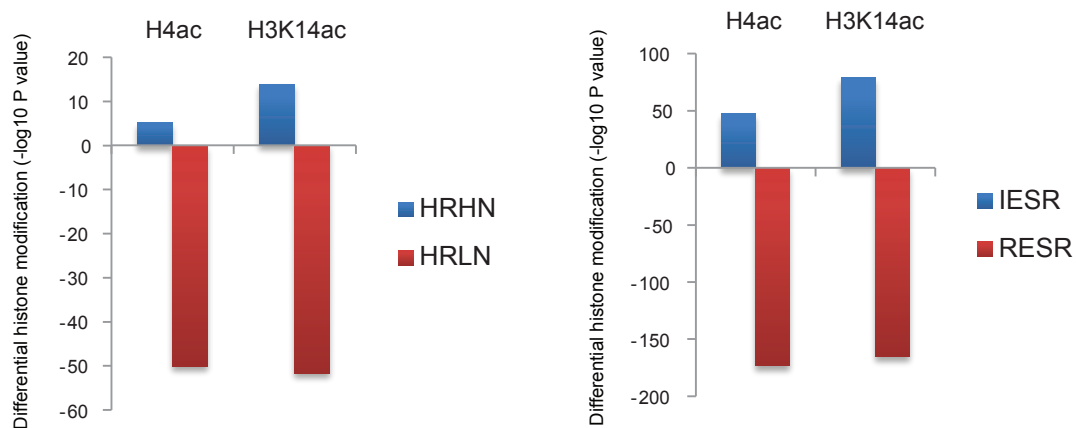
Supplementary Fig. 7



(A) Changes in nucleosome occupancy upon heat shock for the RESR genes and the HRLN genes that are repressed in expression level.

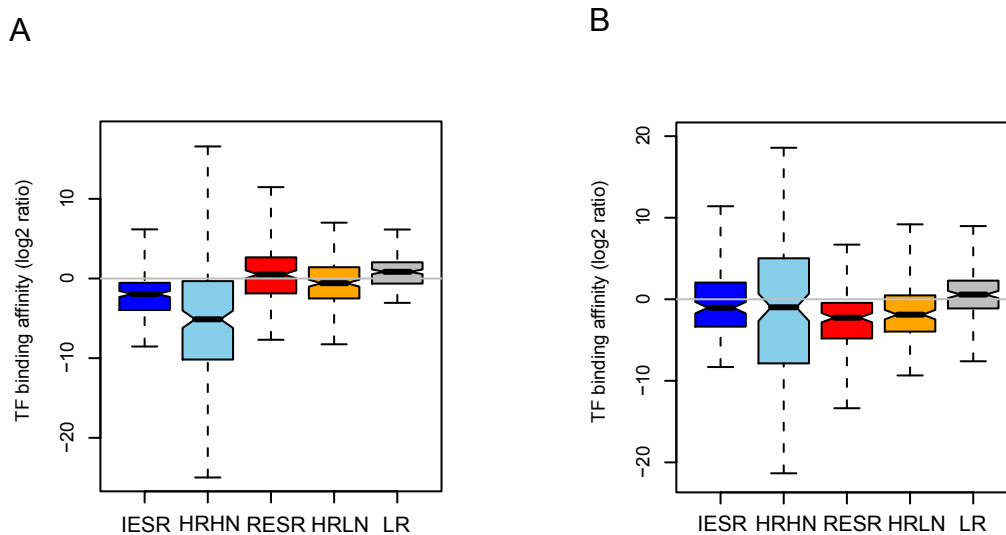
(B) Changes in H4ac level upon oxidative stress for the IESR genes and the HRHN genes that are induced in expression level.

Supplementary Fig. 8



Changes in H4ac and H3K14ac level upon oxidative stress were statistically tested by means of the Kolmogorov-Smirnov test. A large negative value of $-\log_{10}$ (P value) indicates a significant loss of histone modification in response to oxidative stress.

Supplementary Fig. 9



Binding affinity of 203 transcription factors in rich media conditions (A) and that of 84 transcription factors in one of 12 different stressful environmental conditions (B) onto different groups of promoters. Increased affinity toward stress genes and decreased affinity toward growth genes are observed.

Supplementary Table 1. Functional enrichment of the HRHN genes

GO_term	P-value
carboxylic acid metabolic process	5.37E-20
organic acid metabolic process	5.37E-20
generation of precursor metabolites and energy	2.08E-15
amino acid biosynthetic process	2.50E-15
amino acid metabolic process	8.26E-15
cellular nitrogen compound metabolic process	1.70E-14
nitrogen compound metabolic process	2.89E-14
amine biosynthetic process	3.88E-14
oxidative phosphorylation	4.56E-14
cellular amine metabolic process	4.77E-14
nitrogen compound biosynthetic process	5.36E-14
cellular amino acid and derivative metabolic process	5.90E-14
nucleobase, nucleoside and nucleotide metabolic process	4.26E-12
nucleoside phosphate metabolic process	3.48E-11
nucleotide metabolic process	3.48E-11
purine ribonucleotide biosynthetic process	1.17E-09
purine nucleotide biosynthetic process	4.32E-09
purine ribonucleotide metabolic process	4.32E-09
ribonucleotide biosynthetic process	7.94E-09
ribonucleotide metabolic process	2.46E-08
transmembrane ion transport	3.71E-08
electron transport chain	5.02E-08
respiratory electron transport chain	5.02E-08
ATP synthesis coupled electron transport	5.02E-08
mitochondrial ATP synthesis coupled electron transport	5.02E-08
oxidation reduction	5.02E-08
cofactor metabolic process	6.11E-08
purine nucleotide metabolic process	6.99E-08
metabolic process	2.56E-07
transmembrane transport	3.20E-07
nucleotide biosynthetic process	3.64E-07
coenzyme metabolic process	7.65E-07
cellular metabolic process	1.81E-06
energy derivation by oxidation of organic compounds	1.82E-06
glutamine family amino acid metabolic process	9.54E-06
glutamine family amino acid biosynthetic process	1.13E-05
cellular alcohol metabolic process	1.48E-05
mitochondrial electron transport, ubiquinol to cytochrome c	1.73E-05
acetyl-CoA metabolic process	2.43E-05
coenzyme catabolic process	2.43E-05
purine nucleoside triphosphate metabolic process	2.43E-05
purine nucleoside triphosphate biosynthetic process	2.43E-05
purine ribonucleoside triphosphate metabolic process	2.43E-05
purine ribonucleoside triphosphate biosynthetic process	2.43E-05
acetyl-CoA catabolic process	2.64E-05
tricarboxylic acid cycle	2.64E-05
cellular aromatic compound metabolic process	2.73E-05
nucleoside triphosphate biosynthetic process	3.10E-05
cofactor catabolic process	4.61E-05
proton transport	8.34E-05

hydrogen transport	8.34E-05
ribonucleoside triphosphate metabolic process	8.34E-05
ribonucleoside triphosphate biosynthetic process	8.34E-05
response to oxidative stress	0.0001
energy coupled proton transport, down electrochemical gradient	0.00011
ATP synthesis coupled proton transport	0.00011
ATP metabolic process	0.00011
ATP biosynthetic process	0.00011
branched chain family amino acid metabolic process	0.00011
nucleoside triphosphate metabolic process	0.00014
alcohol catabolic process	0.00015
ion transport	0.00019
trehalose metabolic process	0.00021
disaccharide biosynthetic process	0.00023
trehalose biosynthetic process	0.00023
aerobic respiration	0.00029
monovalent inorganic cation transport	0.00033
cellular catabolic process	0.00043
monosaccharide catabolic process	0.00045
catabolic process	0.00049
serine family amino acid catabolic process	0.00058
cation transport	0.00059
heterocycle metabolic process	0.00076
phosphorylation	0.00084
amino acid catabolic process	0.00096
cellular respiration	0.00108
carbohydrate metabolic process	0.00201
response to chemical stimulus	0.00229
phosphorus metabolic process	0.00233
phosphate metabolic process	0.00233
nitrogen compound catabolic process	0.00237
amine catabolic process	0.00237
glutamate biosynthetic process	0.00259
branched chain family amino acid biosynthetic process	0.00259
glucose metabolic process	0.0031
cellular process	0.00399
cellular carbohydrate metabolic process	0.00467
NADPH regeneration	0.00491
dicarboxylic acid metabolic process	0.00515
hexose catabolic process	0.00519
purine ribonucleoside monophosphate biosynthetic process	0.00594
pyridine nucleotide metabolic process	0.00887
glycine catabolic process	0.00977

Supplementary Table 2. Functional enrichment of the HRLN genes

GO_term	P-value
ribosome biogenesis	8.21E-33
ribonucleoprotein complex biogenesis and assembly	8.18E-32
cellular process	1.41E-20
primary metabolic process	1.40E-16
cellular metabolic process	4.19E-13
gene expression	8.30E-13
metabolic process	1.43E-12
ncRNA metabolic process	2.11E-12
ribosomal large subunit biogenesis	2.34E-12
translation	2.88E-12
cellular biosynthetic process	1.19E-11
biosynthetic process	1.79E-11
cellular biopolymer metabolic process	3.88E-10
organelle organization	6.54E-10
rRNA metabolic process	8.40E-10
ncRNA processing	2.71E-09
rRNA processing	4.78E-09
cellular macromolecule metabolic process	7.81E-09
maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	1.25E-08
macromolecule metabolic process	1.68E-08
cellular component organization	2.20E-08
maturation of SSU-rRNA	2.39E-08
biopolymer metabolic process	2.60E-08
cellular macromolecule biosynthetic process	1.25E-07
macromolecule biosynthetic process	1.25E-07
cellular biopolymer biosynthetic process	1.63E-07
biopolymer biosynthetic process	1.71E-07
ribosome localization	5.20E-07
establishment of ribosome localization	5.20E-07
ribosome export from nucleus	5.20E-07
ribonucleoprotein complex assembly	8.54E-07
ribosome assembly	2.05E-06
cellular protein metabolic process	5.17E-06
protein metabolic process	9.37E-06
ribosomal large subunit assembly and maintenance	4.54E-05
maturation of 5.8S rRNA	6.22E-05
maturation of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	6.22E-05
ribosomal subunit assembly	7.24E-05
organelle localization	0.00015
establishment of organelle localization	0.00095
RNA processing	0.00146
endonucleolytic cleavage in ITS1 to separate SSU-rRNA from 5.8S rRNA and LSU-rRNA from tric	0.00176
endonucleolytic cleavages during rRNA processing	0.00176
endonucleolytic cleavage of tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	0.00176
RNA metabolic process	0.00184
endonucleolytic cleavage in 5'-ETS of tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rF	0.00306
cleavages during rRNA processing	0.00575
endonucleolytic cleavage to generate mature 5'-end of SSU-rRNA from (SSU-rRNA, 5.8S rRNA,	0.00813
transcription from RNA polymerase I promoter	0.00974

Supplementary Table 3. Functional enrichment of the LR genes

GO_term	P-value
establishment of localization in cell	2.46E-29
cellular localization	1.47E-28
intracellular transport	1.18E-27
vesicle-mediated transport	1.78E-26
Golgi vesicle transport	1.92E-18
localization	2.25E-18
transport	5.60E-18
establishment of localization	7.72E-18
cellular process	1.42E-15
macromolecule localization	4.03E-12
retrograde vesicle-mediated transport, Golgi to ER	8.86E-11
protein localization	1.87E-08
endosome transport	2.39E-08
rRNA transport	1.77E-07
rRNA export from nucleus	1.77E-07
RNA localization	2.64E-07
intracellular protein transport	2.75E-07
post-Golgi vesicle-mediated transport	3.08E-07
protein transport	4.91E-07
tRNA export from nucleus	5.75E-07
establishment of protein localization	8.84E-07
tRNA transport	9.90E-07
cellular component organization	1.24E-06
nuclear import	3.24E-06
protein import into nucleus	3.24E-06
RNA export from nucleus	3.44E-06
nucleic acid transport	4.39E-06
RNA transport	4.39E-06
establishment of RNA localization	4.39E-06
snRNA transport	8.10E-06
snRNA export from nucleus	8.10E-06
NLS-bearing substrate import into nucleus	8.10E-06
snRNP protein import into nucleus	8.10E-06
ribosomal protein import into nucleus	8.10E-06
protein targeting	1.24E-05
nuclear pore organization and biogenesis	1.31E-05
mRNA-binding (hnRNP) protein import into nucleus	2.41E-05
nuclear transport	2.71E-05
nucleocytoplasmic transport	2.71E-05
biological regulation	3.58E-05
membrane organization	3.91E-05
mRNA transport	5.71E-05
mRNA export from nucleus	5.71E-05
nucleobase, nucleoside, nucleotide and nucleic acid transport	6.02E-05
mRNA metabolic process	0.0001
ER to Golgi vesicle-mediated transport	0.00012
RNA elongation	0.00013
cellular structure morphogenesis	0.00023
anatomical structure development	0.00023
cell morphogenesis	0.00023
anatomical structure morphogenesis	0.00023

protein import	0.00032
vacuolar transport	0.00042
nuclear-transcribed mRNA catabolic process	0.00043
protein export from nucleus	0.00049
nuclear export	0.00052
establishment or maintenance of cell polarity	0.00077
RNA elongation from RNA polymerase II promoter	0.00119
mRNA catabolic process	0.00153
protein modification process	0.002
exocytosis	0.00246
regulation of biological process	0.00379
nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay	0.00482
intra-Golgi vesicle-mediated transport	0.00699
endoplasmic reticulum organization and biogenesis	0.00774
late endosome to vacuole transport	0.00775
asexual reproduction	0.00994
endocytosis	0.00994
cell budding	0.00994