Table S1. **Genes identified in genome-wide screening for *fld* strains**

Categories	Genes
DNA maintenance/chromatin structure (1)	*HMO1*
Metabolic enzymes (4)	*COX5A, CYS4, DGA1, HEM14*
Protein glycosylation (1)	*CWH8*
Protein biosynthesis (5)	*RPP2B, RPL2B, RPL8B, RPL12B, RPL20A*
Hypothetical/uncharacterized ORF (1)	*YLR404W*
Miscellaneous (5)	*BUD25, LTV1, NEM1, SPO7, SSD1*

This table lists a total of 17 genes whose deletions result in decreased intracellular LDs. The number of genes in each group is indicated in parentheses. Some genes may have different designations; our choice was made based on the frequency of their use in literature. Detailed gene information can be found at the Saccharomyces Genome Database.

Table S2. **Genes identified in genome-wide screening for *mld* strains**

Categories	Genes
Channels and transporters (5)	*FUI1, VMA6, VMA8, VMA13, VMA21*
Cytoskeleton organization (5)	*ARC18, ARP1, CNM67, NUM1, SPC72*[a]
DNA maintenance/chromatin structure (9)	*EST1,*[a] *EST2,*[a] *EST3, POL32, MRE11, RAD27,*[a] *RAD50, RTT109, XRS2*
Metabolic enzymes (18)	*ADE3, ADE4, ADE5,7, ADE6, ADE8, ADE12, ELO3, ERG2, ERG3, ERG4, ERG5, ERG6, KGD1,*[a] *MET7, PFK2, RNR4, TGL3, TGL4*
Protein glycosylation (7)	*ANP1, ERD1, MNN10, MNN11, OCH1, OST4, PMR1*[a]
Protein biosynthesis (3)	*RPS12, RPS21B, RPS30B*
Protein degradation (4)	*DEF1, DOA10, HRD1, UBX1*
Protein modification (3)	*MAP1, MDM20, PPG1*
Protein/RNA transport (1)	*APQ12*
RNA modification and metabolism (3)	*DHH1, KEM1, REF2*
Signaling/transcription factors (18)	*HPR1, MFT1, NOT5, PAF1, PGD1, PHO85, RLR1, ROX3,*[a] *RPB4, SNF1, SNF2, SNF6, SNF11, SRB2,*[a] *SRB5,*[a] *SSN3, SWI3, TAF14*
Vesicular transport (22)	*CHC1, SAC1, SWA2, VAM3, VPS1, VPS11, VPS15, VPS16, VPS18, VPS19, VPS27, VPS31, VPS33, VPS34, VPS39, VPS41, VPS43, VPS45, VPS53,*[a] *VPS54, VPS64, VPS66*
Hypothetical/uncharacterized ORF (10)	*YDL073W, YDR532C, YGL168W,*[a] *YKL037W, YJL075C, YLL030C,*[a] *YLR358C, YOR041C, YPL183W-A, YPR087W*[a]
Miscellaneous (8)	*ARG82, BUD22, ELM1, GON7,*[a] *KRE6, MMS22, SPS1, TPD3*

This table lists a total of 116 genes whose deletions lead to increased intracellular LDs, among which 14 give a strong phenotype.
[a]Strong phenotype.