Table S1. GO enrichment pathways.

Figure S2	Pathway Name	GO ID
Figure S2A	Regulation of division septum assembly	GO:0032955
CG *vs*. LG	Regulation of cell septum assembly	GO:1901891
	Regulation of cytokinetic process	GO:0032954
	Mitotic spindle pole body	GO:0044732
	FAR/SIN/STRIPAK complex	GO:0090443
	Actomyosin contractile ring contraction	GO:0000916
	Negative regulation of division septum assembly	GO:0010974
	Septation initiation signaling	GO:0031028
	Regulation of septation initiation signaling	GO:0031029
	Negative regulation of septation initiation signaling	GO:0031030
	Regulation of actomyosin contractile ring contraction	GO:0031991
	Contractile ring contraction	GO:0036213
	Asymmetric protein localization to old or new spindle pole body	GO:0061492
	Asymmetric protein localization to old mitotic spindle pole body	GO:0061509
	Negative regulation of cell septum assembly	GO:1901892
	Negative regulation of mitotic cytokinesis	GO:1902413
	Protein localization to mitotic spindle pole body	GO:1902440
	Negative regulation of mitotic cytokinetic process	GO:1903437
	Chromosome condensation	GO:0030261
	Regulation of hippo signaling	GO:0035330
Figure S2B	Extracellular space	GO:0005615
CG *vs*. HG	Regulation of division septum assembly	GO:0032955
	Regulation of cell septum assembly	GO:1901891
	Mitotic spindle pole body	GO:0044732
	FAR/SIN/STRIPAK complex	GO:0090443
	Regulation of cytokinetic process	GO:0032954
	Actomyosin contractile ring contraction	GO:0000916
	Negative regulation of division septum assembly	GO:0010974
	Septation initiation signaling	GO:0031028
	Regulation of septation initiation signaling	GO:0031029
	Negative regulation of septation initiation signaling	GO:0031030
	Regulation of actomyosin contractile ring contraction	GO:0031991
	Contractile ring contraction	GO:0036213
	Asymmetric protein localization to old or new spindle pole body	GO:0061492
	Asymmetric protein localization to old mitotic spindle pole body	GO:0061509
	Negative regulation of cell septum assembly	GO:1901892
	Negative regulation of mitotic cytokinesis	GO:1902413
	Protein localization to mitotic spindle pole body	GO:1902440
	Negative regulation of mitotic cytokinetic process	GO:1903437
	Regulation of hippo signaling	GO:0035330
Figure S2C	Carboxylic acid metabolic process	GO:0019752

LG *vs*. HG	Nucleotide metabolic process	GO:0009117
	Organic acid metabolic process	GO:0006082
	Nucleoside phosphate metabolic process	GO:0006753
	Oxoacid metabolic process	GO:0043436
	Nucleoside bisphosphate metabolic process	GO:0033865
	Ribonucleoside bisphosphate metabolic process	GO:0033875
	Purine nucleoside bisphosphate metabolic process	GO:0034032
	TRNA aminoacylation for protein translation	GO:0006418
	Acyl-CoA metabolic process	GO:0006637
	Thioester metabolic process	GO:0035383
	Aminoacyl-tRNA ligase activity	GO:0004812
	Ligase activity, forming carbon-oxygen bonds	GO:0016875
	Cellular amide metabolic process	GO:0043603
	Ribonucleotide metabolic process	GO:0009259
	Nucleobase-containing small molecule metabolic process	GO:0055086
	Fatty acid catabolic process	GO:0009062
	Ribose phosphate metabolic process	GO:0019693
	Purine-containing compound metabolic process	GO:0072521
	Monocarboxylic acid metabolic process	GO:0032787

Table S2. KEGG enrichment pathways.

Figure S3	Pathway Name	KEGG ID
Figure S3A	Thyroid hormone signaling pathway	Ko04919
CG *vs*. LG	Protein processing in endoplasmic reticulum	Ko04141
	Glycine, serine and threonine metabolism	Ko00260
	Phototransduction	Ko04744
	Central carbon metabolism in cancer	Ko05230
	Dilated cardiomyopathy	Ko05414
	Hypertrophic cardiomyopathy	Ko05410
	Basal cell carcinoma	Ko05217
	Cholesterol metabolism	Ko04979
	Morphine addiction	Ko05032
	Nitrogen metabolism	Ko00910
	Human cytomegalovirus infection	Ko05163
	Human immunodeficiency virus 1 infection	Ko05170
	PI3K-Akt signaling pathway	Ko04151
	Retrograde endocannabinoid signaling	Ko04723
	Kaposi sarcoma-associated herpesvirus infection	Ko05167
	Serotonergic synapse	Ko04726
	PPAR signaling pathway	Ko03320
	Citrate cycle (TCA cycle)	Ko00020
	Antigen processing and presentation	Ko04612
Figure S3B	Staphylococcus aureus infection	Ko05150
CG *vs*. HG	Complement and coagulation cascades	Ko04610
	Aminoacyl-tRNA biosynthesis	Ko00970
	PPAR signaling pathway	Ko03320
	Neuroactive ligand-receptor interaction	Ko04080
	Cortisol synthesis and secretion	Ko04927
	Vascular smooth muscle contraction	Ko04270
	Viral myocarditis	Ko05416
	Ovarian steroidogenesis	Ko04913
	Ferroptosis	Ko04216
	Bile secretion	Ko04976
	Fatty acid biosynthesis	Ko00061
	Biosynthesis of amino acids	Ko01230
	Regulation of lipolysis in adipocytes	Ko04923
	Platelet activation	Ko04611
	One carbon pool by folate	Ko00670
	Coronavirus disease - COVID-19	Ko05171
	RNA degradation	Ko03018
	Progesterone-mediated oocyte maturation	Ko04914
	Parathyroid hormone synthesis, secretion and action	Ko04928

Figure S3C	Aminoacyl-tRNA biosynthesis	Ko00970
LG *vs*. HG	Valine, leucine and isoleucine degradation	Ko00280
	Propanoate metabolism	Ko00640
	Fatty acid metabolism	Ko01212
	Fatty acid elongation	Ko00062
	Carbon metabolism	Ko01200
	Metabolic pathways	Ko01100
	Citrate cycle (TCA cycle)	Ko00020
	Fatty acid degradation	Ko00071
	Ferroptosis	Ko04216
	Biosynthesis of amino acids	Ko01230
	Glycolysis / Gluconeogenesis	Ko00010
	Huntington disease	Ko05016
	Butanoate metabolism	Ko00650
	Amyotrophic lateral sclerosis	Ko05014
	Proteasome	Ko03050
	Biosynthesis of unsaturated fatty acids	Ko01040
	PPAR signaling pathway	Ko03320
	Beta-Alanine metabolism	Ko00410
	Prion disease	Ko05020