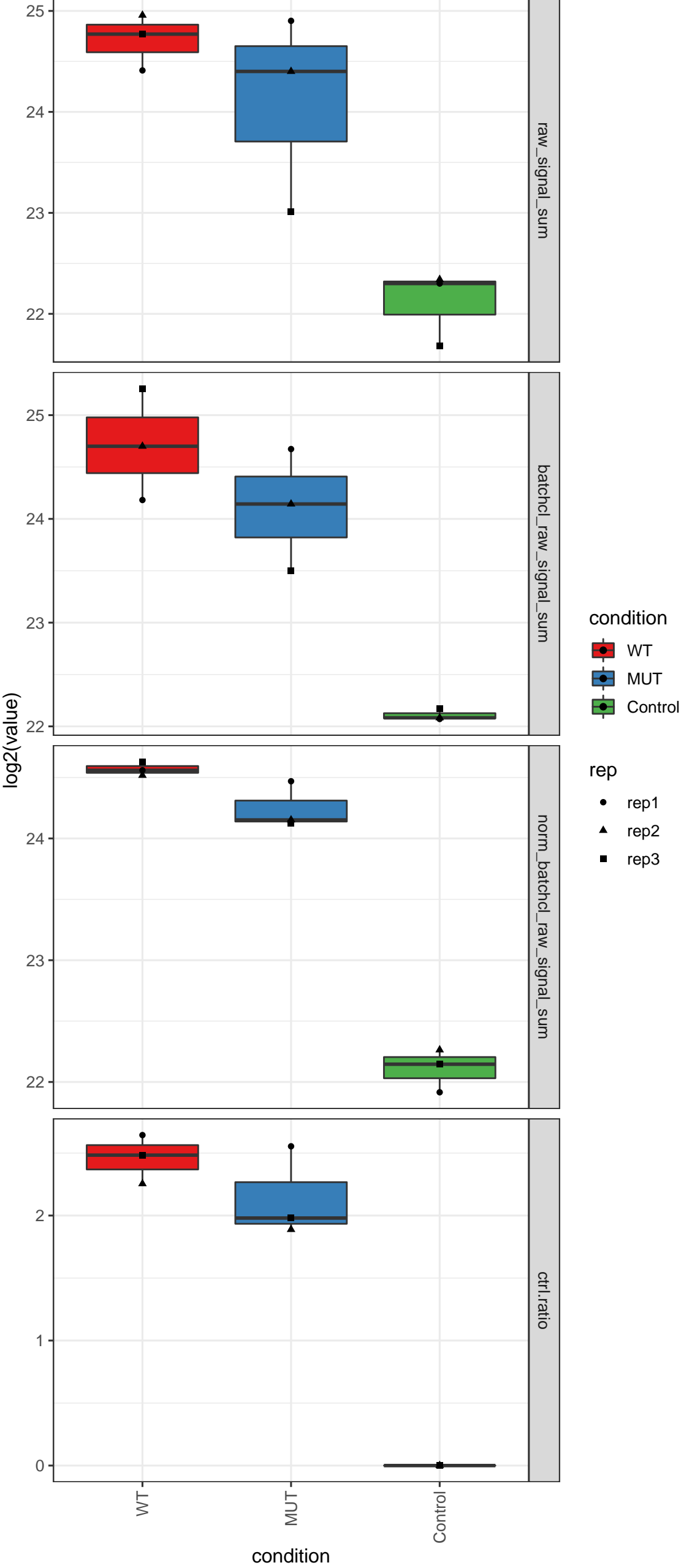


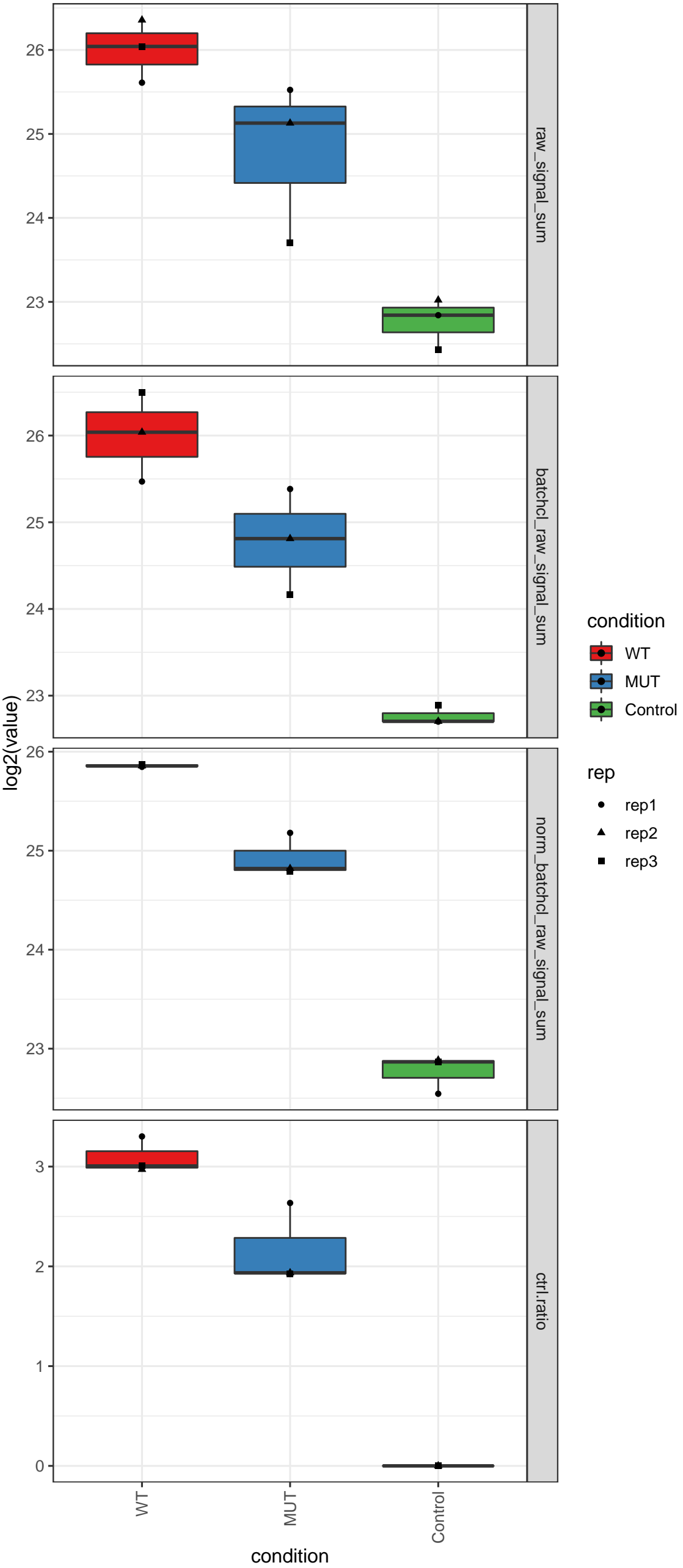
ABF1 – P14164

ARS-binding factor 1 OS=*Saccharomyces cerevisiae* (strain ATCC 204508)



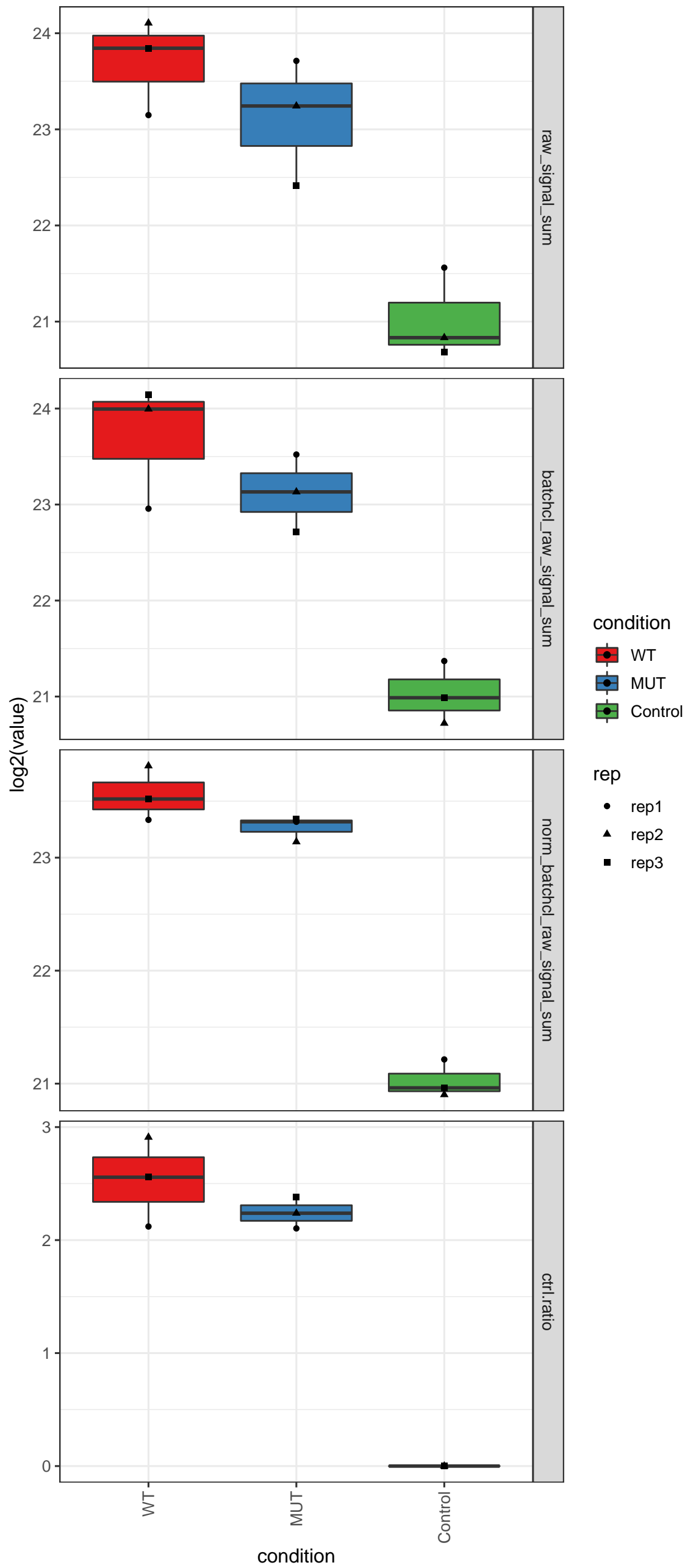
ABF2 – Q02486

ARS-binding factor 2, mitochondrial OS=*Saccharomyces cerevisiae* (strain



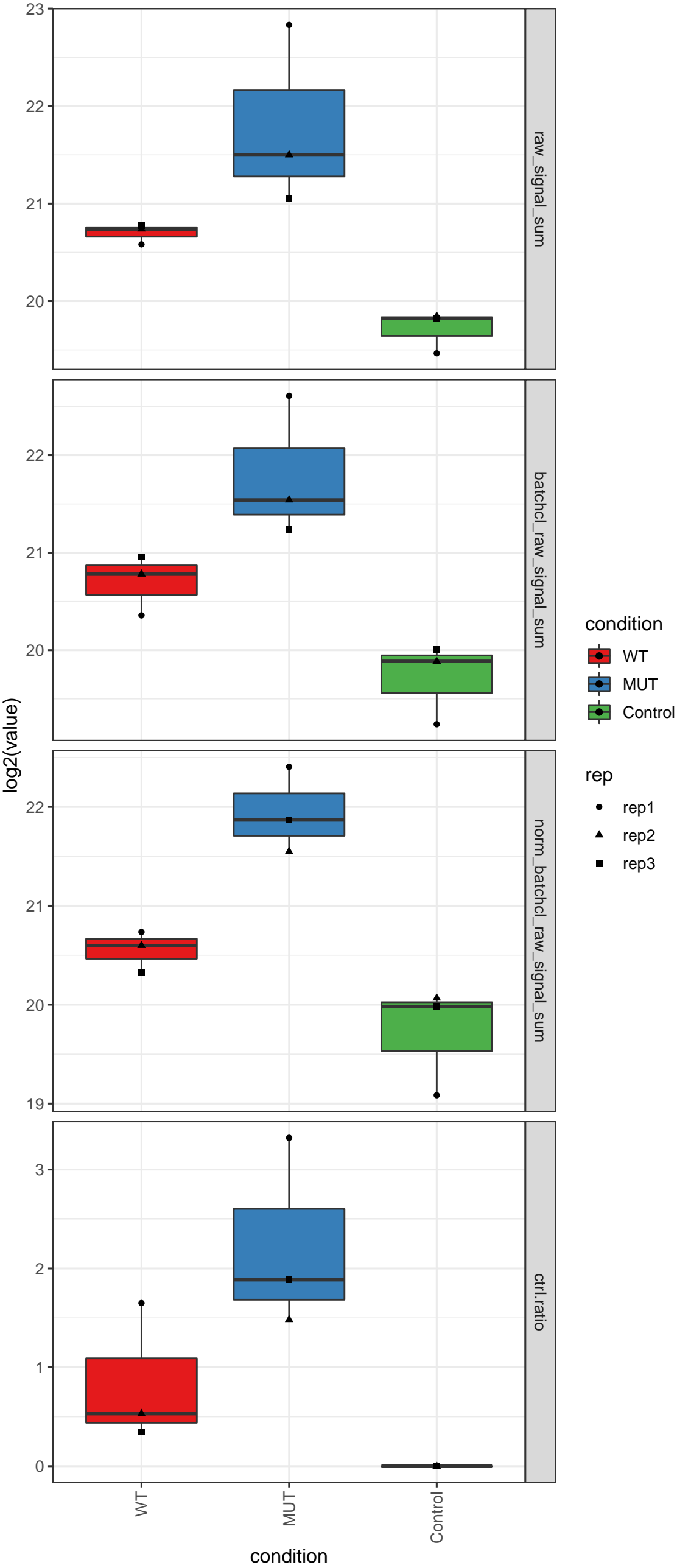
ACC1 – Q00955

Acetyl-CoA carboxylase OS=*Saccharomyces cerevisiae* (strain ATCC 204



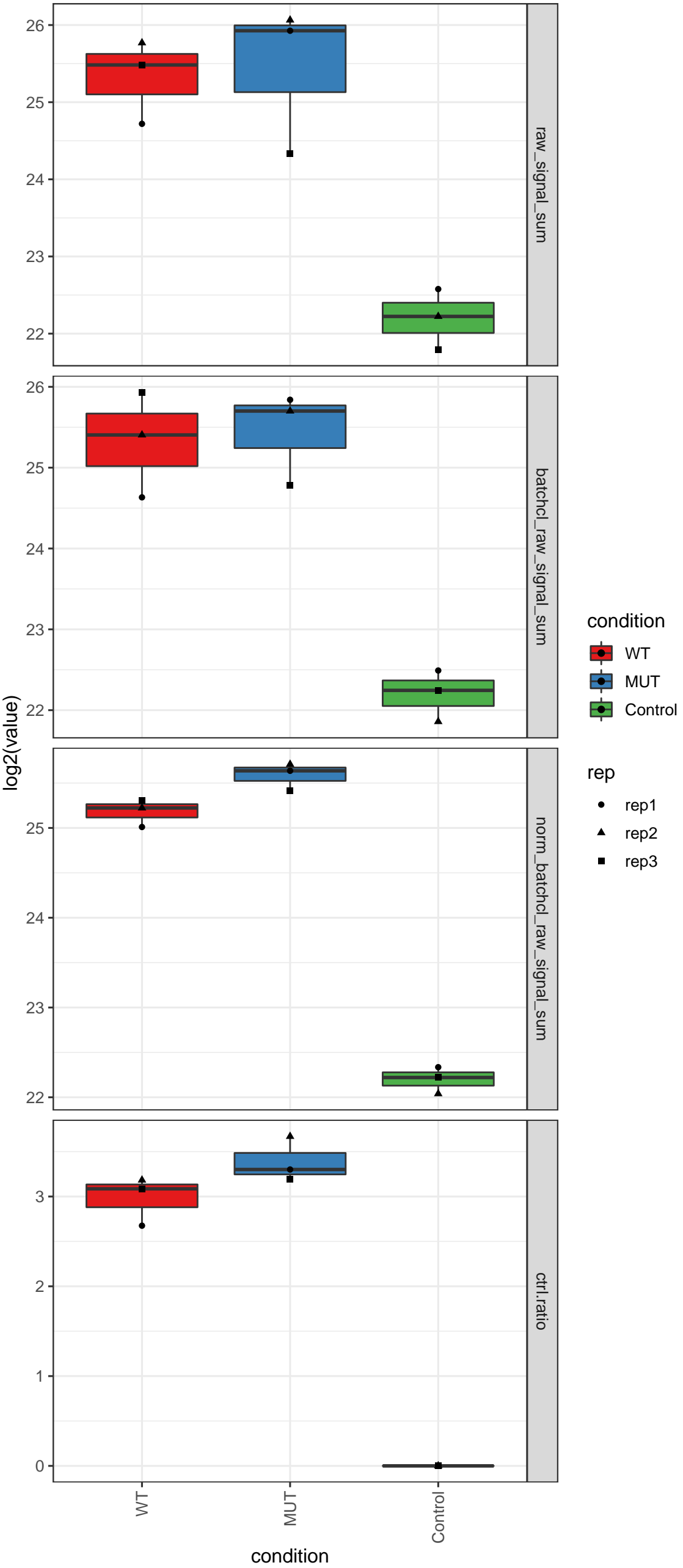
ACF2 – Q12168

Endo-1,3(4)-beta-glucanase 2 OS=*Saccharomyces cerevisiae* (strain ATC



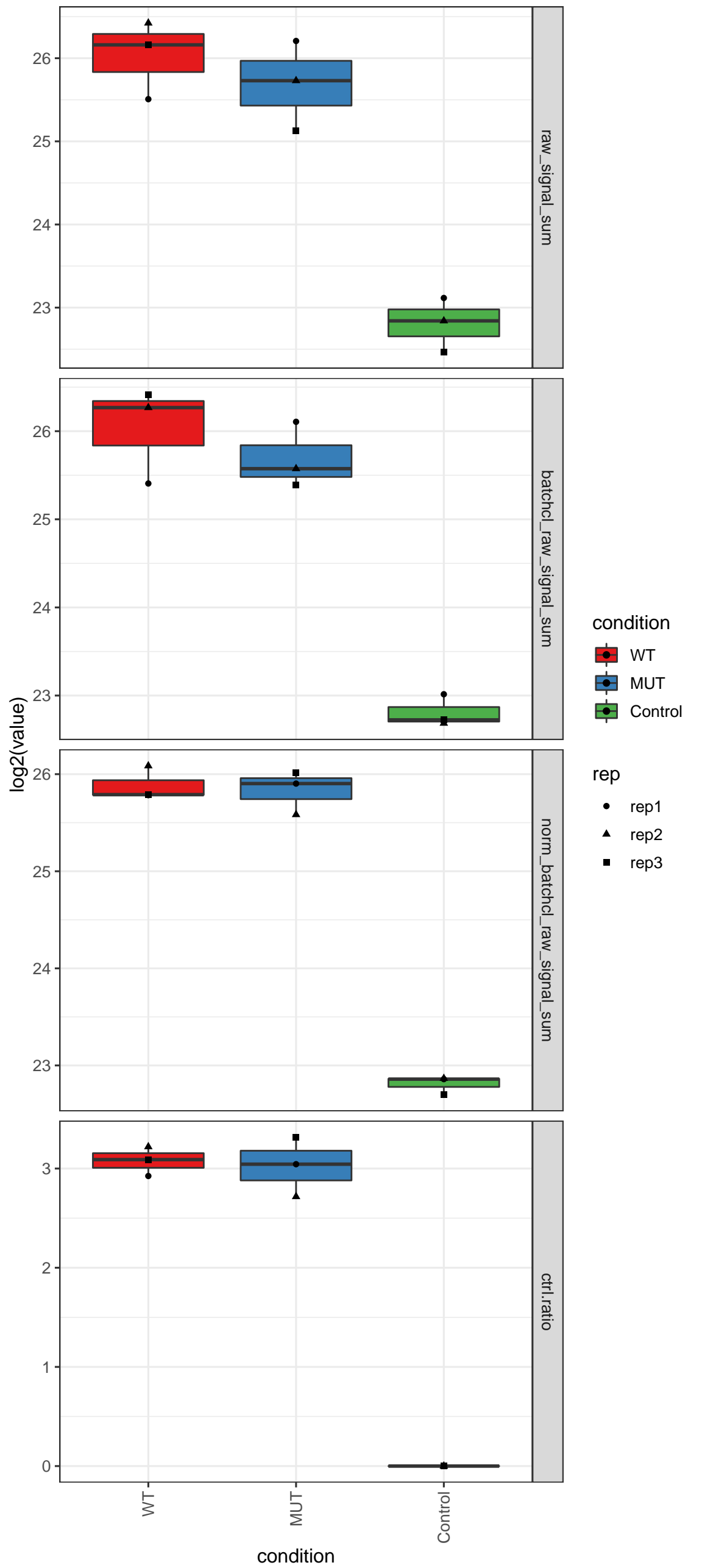
ACH1 – P32316

Acetyl-CoA hydrolase OS=*Saccharomyces cerevisiae* (strain ATCC 20450)



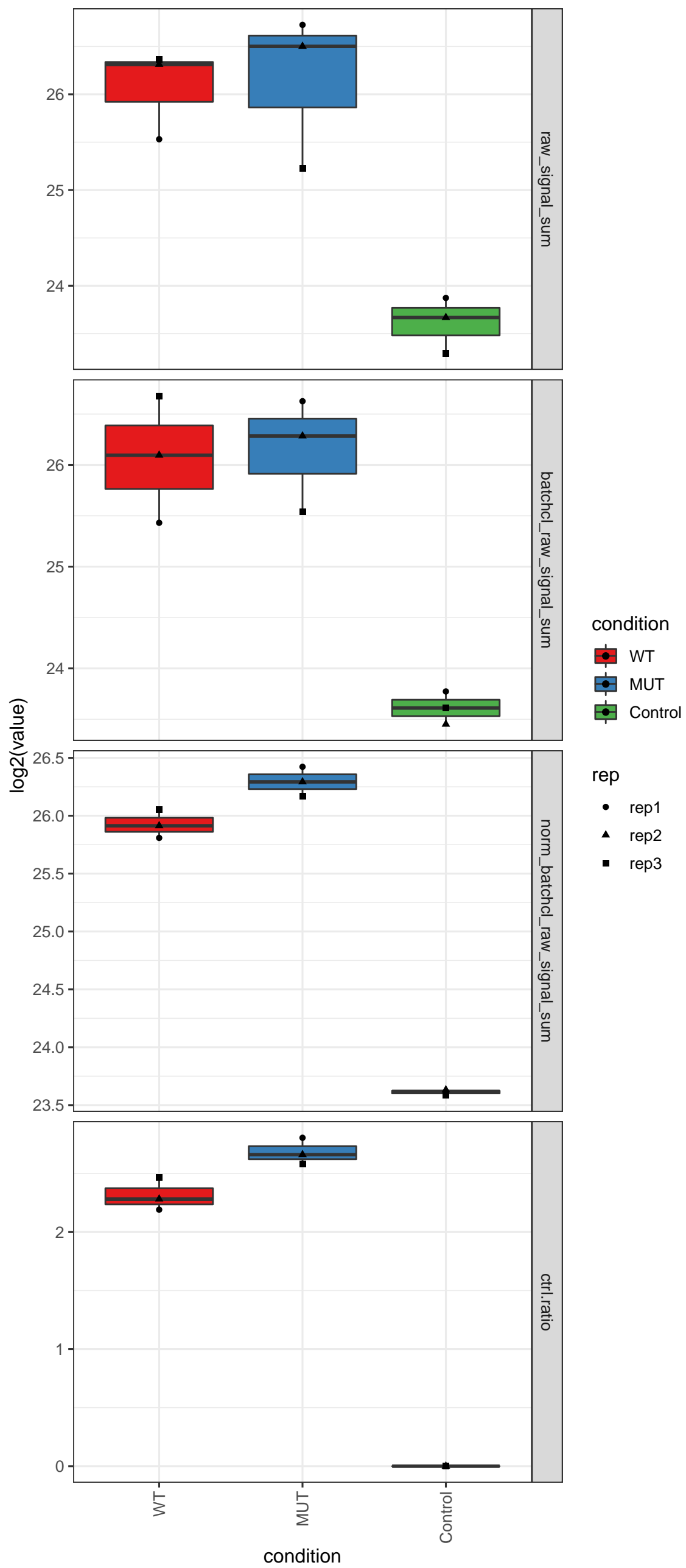
ACO1 – P19414

Aconitate hydratase, mitochondrial OS=*Saccharomyces cerevisiae* (strain /



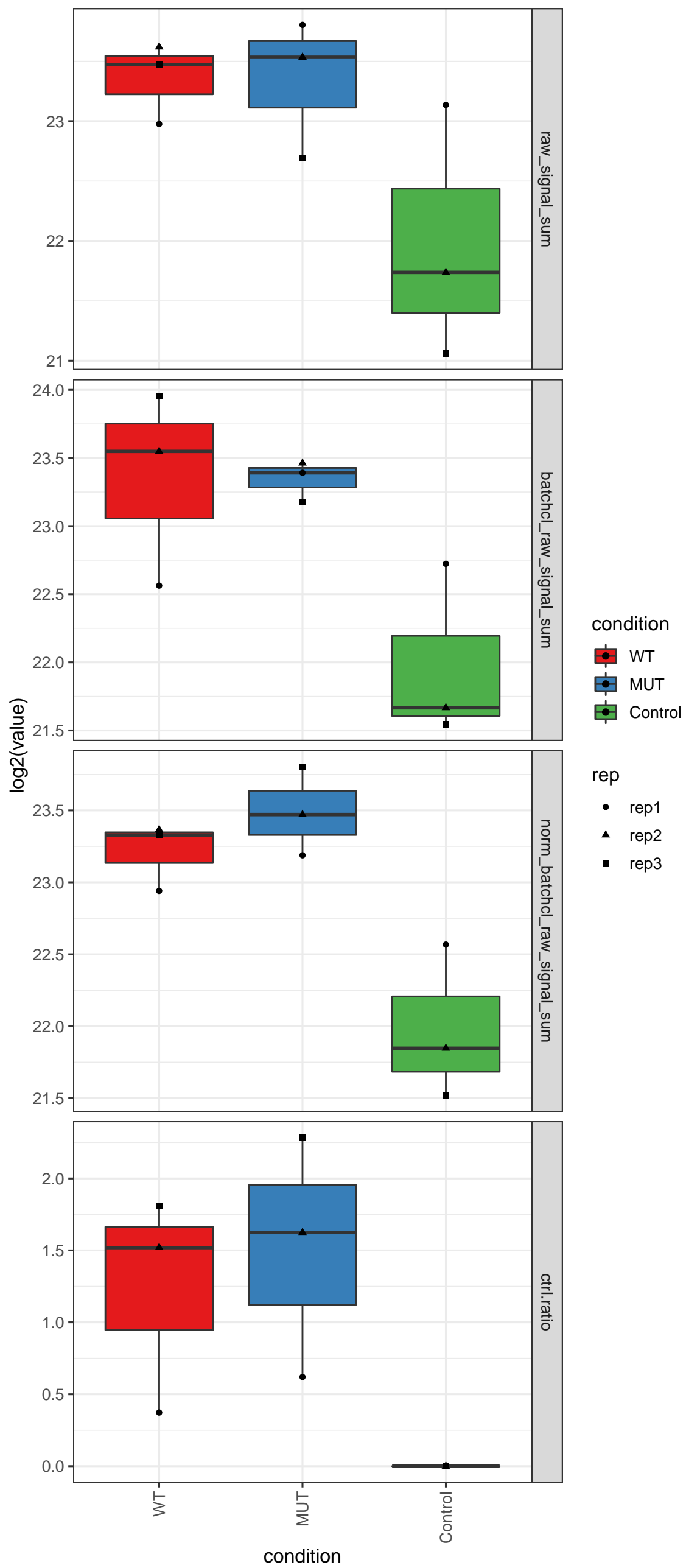
ACS1 – Q01574

Acetyl-coenzyme A synthetase 1 OS=*Saccharomyces cerevisiae* (strain



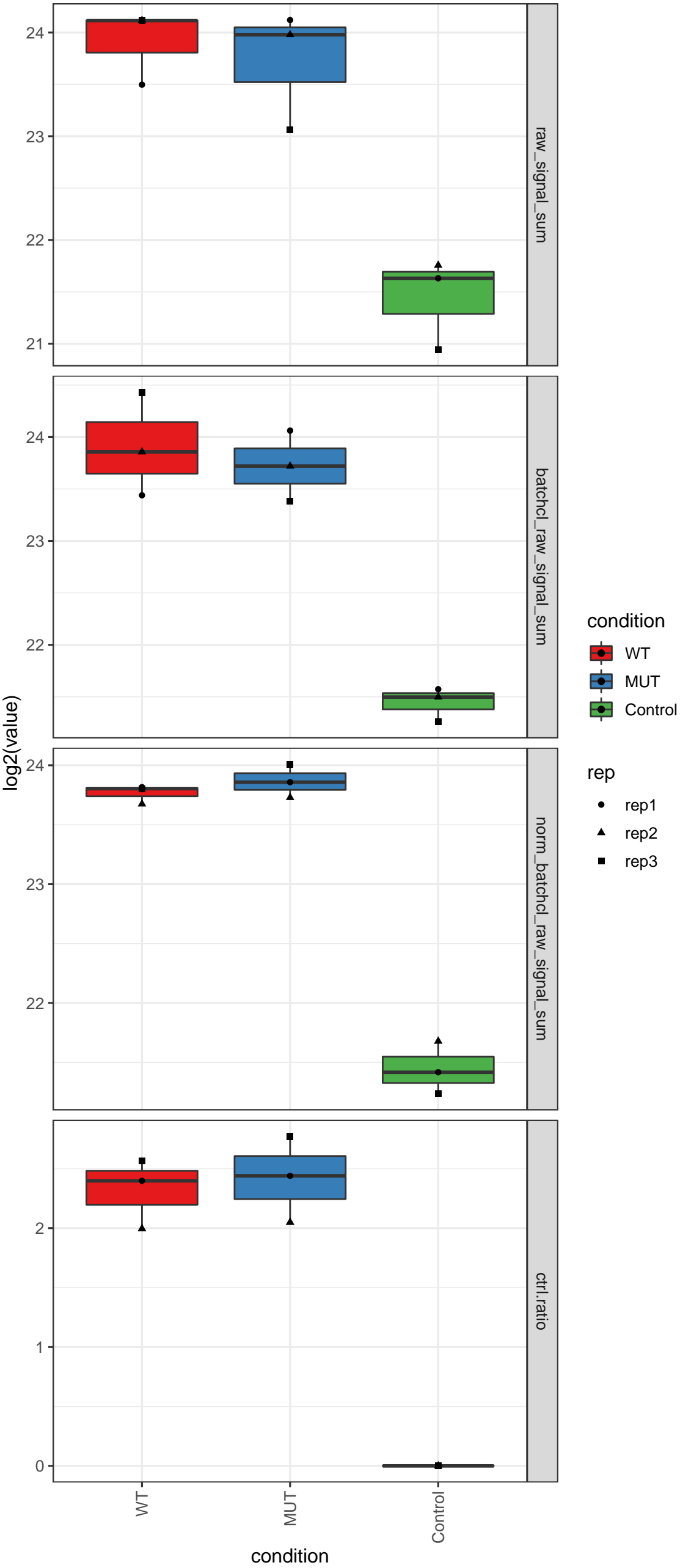
ACS2 – P52910

Acetyl-coenzyme A synthetase 2 OS=*Saccharomyces cerevisiae* (strain



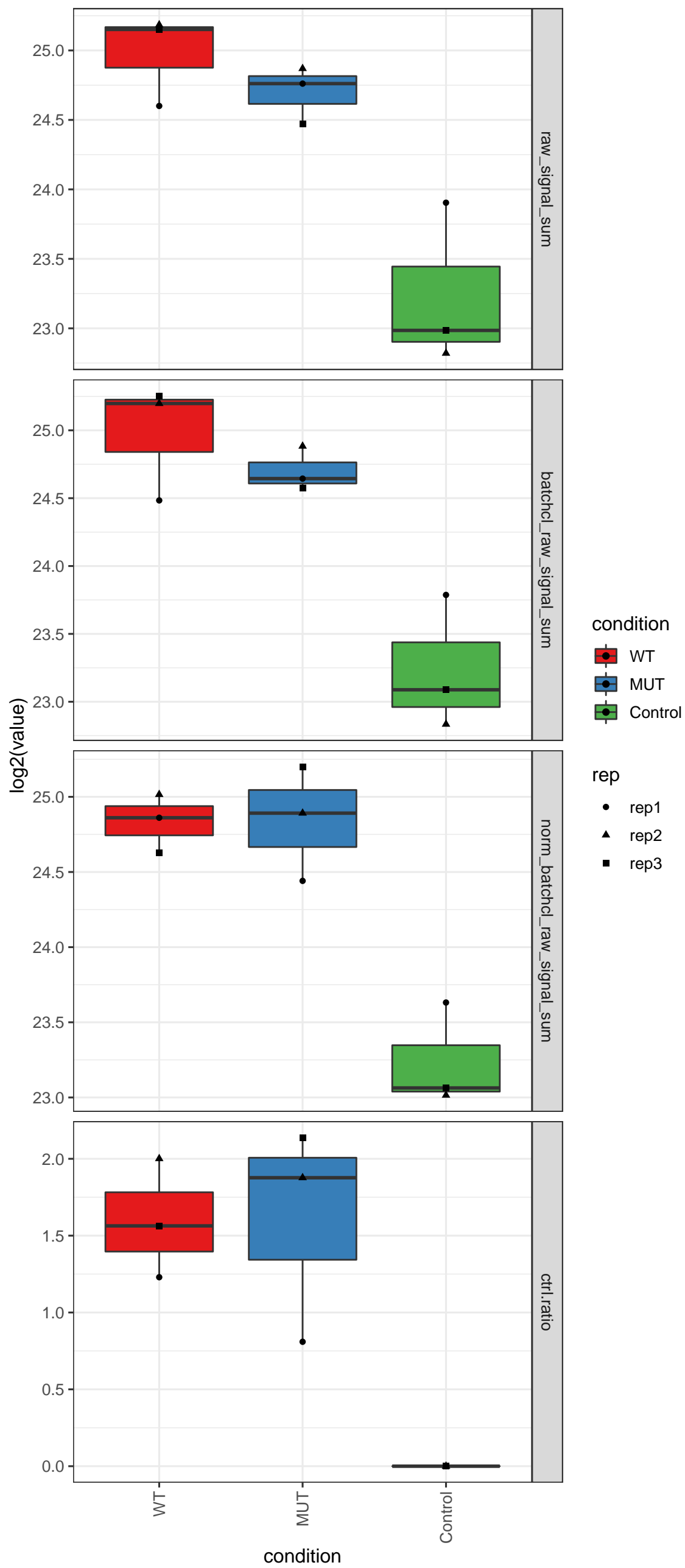
ACT1 – P60010

Actin OS=*Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN=A



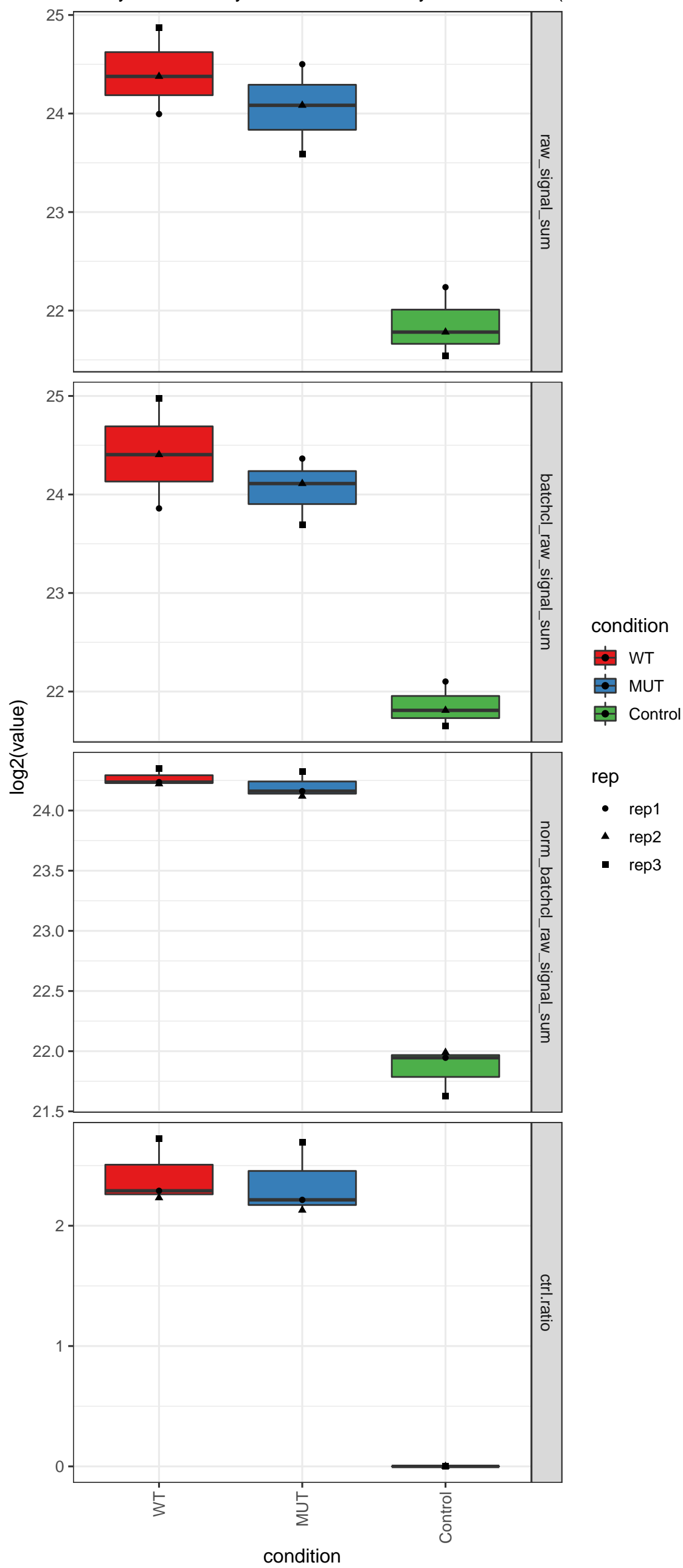
ADE12 – P80210

Adenylosuccinate synthetase OS=*Saccharomyces cerevisiae* (strain ATC



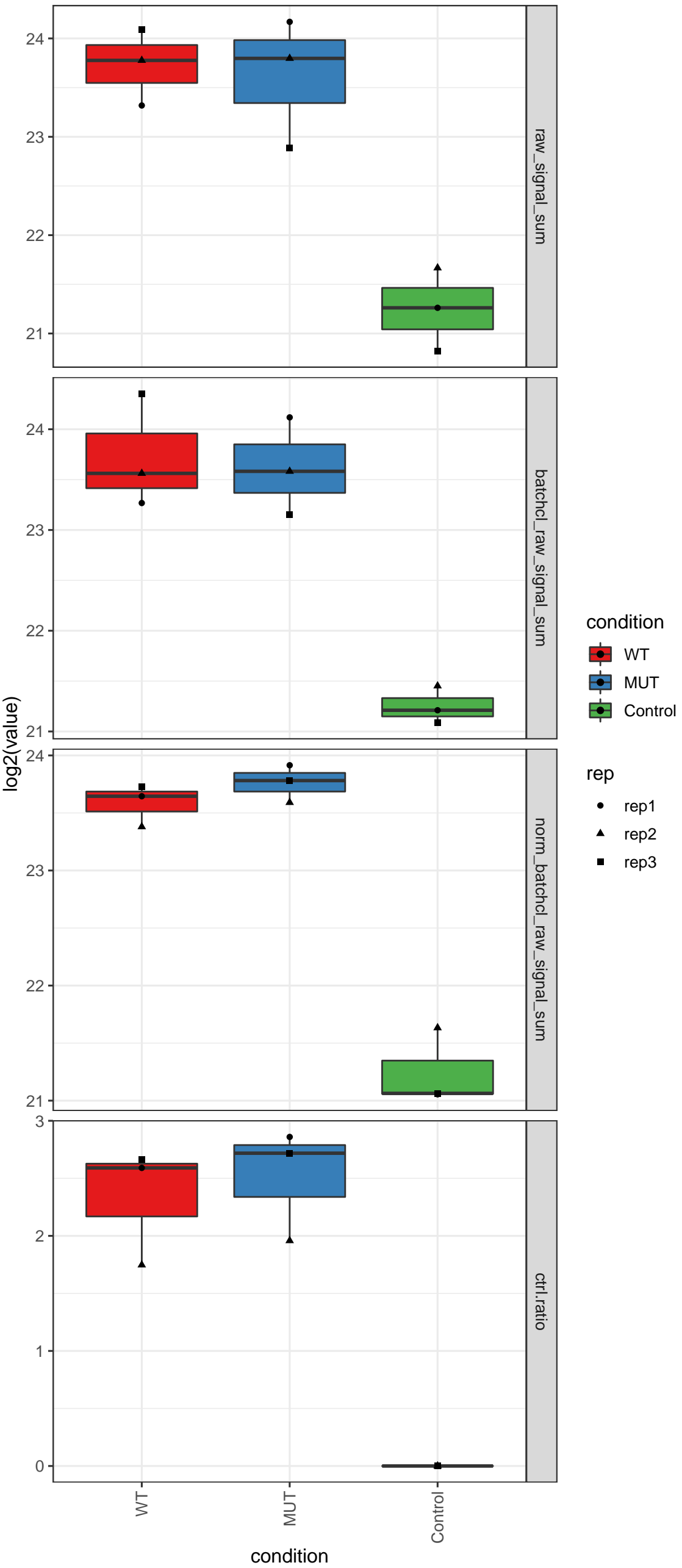
ADE13 – Q05911

Adenylosuccinate lyase OS=*Saccharomyces cerevisiae* (strain ATCC 204



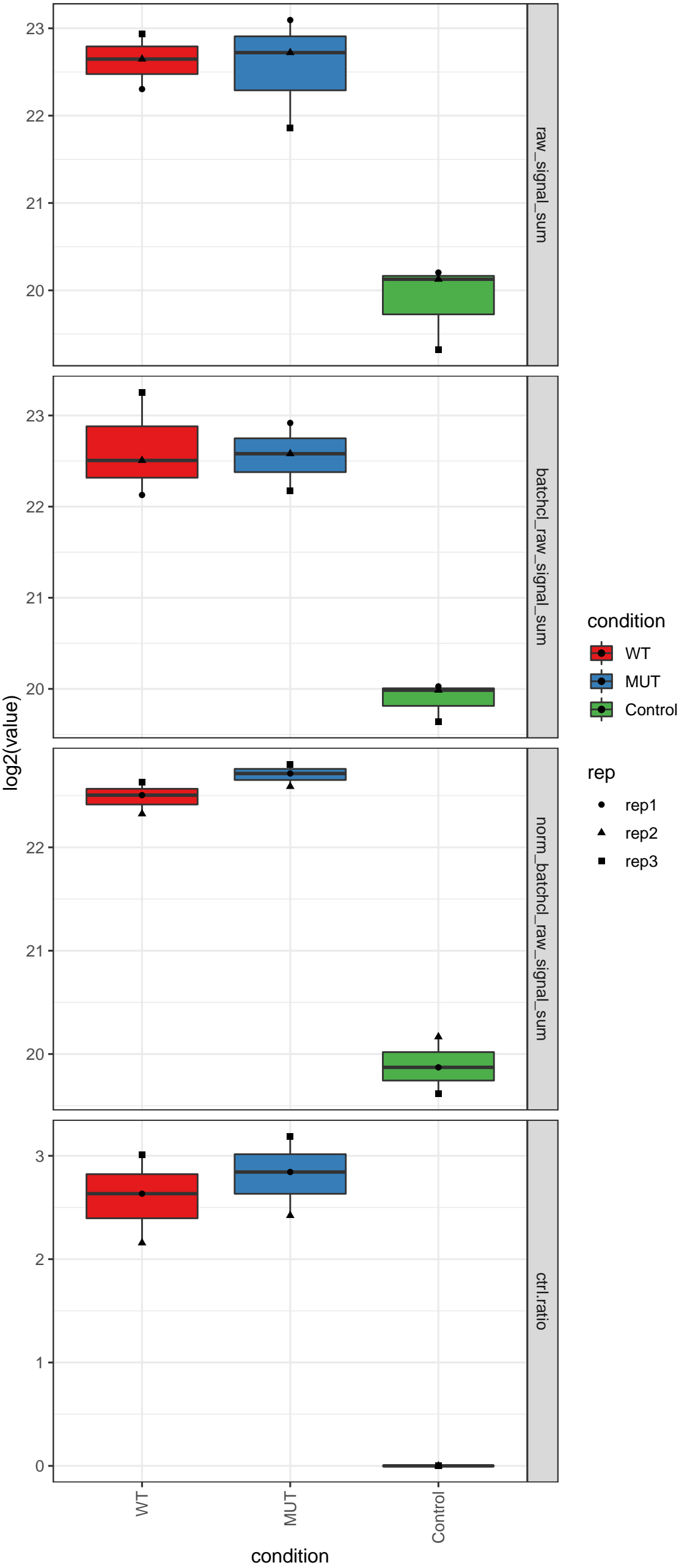
ADE17 – P38009

Bifunctional purine biosynthesis protein ADE17 OS=*Saccharomyces cerevisiae*



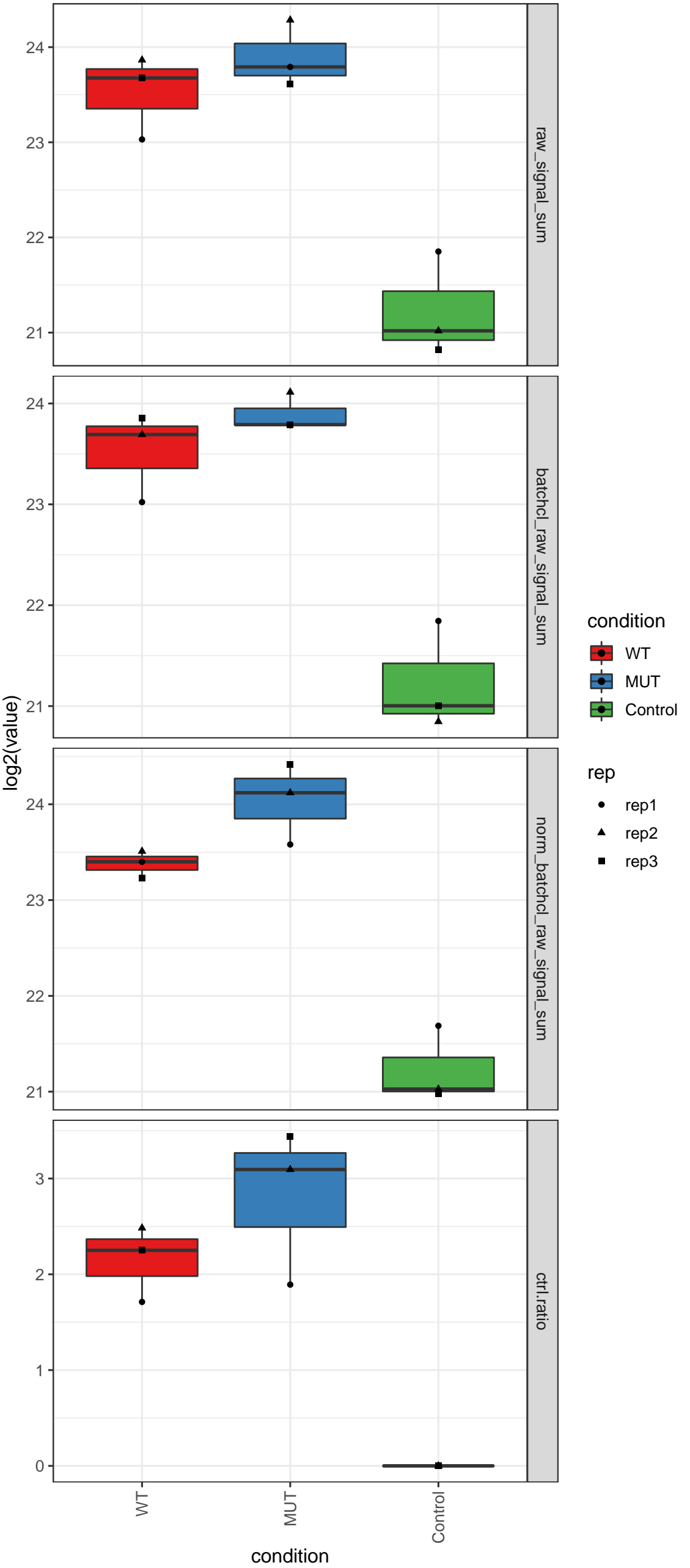
ADE2 – P21264

Phosphoribosylaminoimidazole carboxylase OS=*Saccharomyces cerevisia*



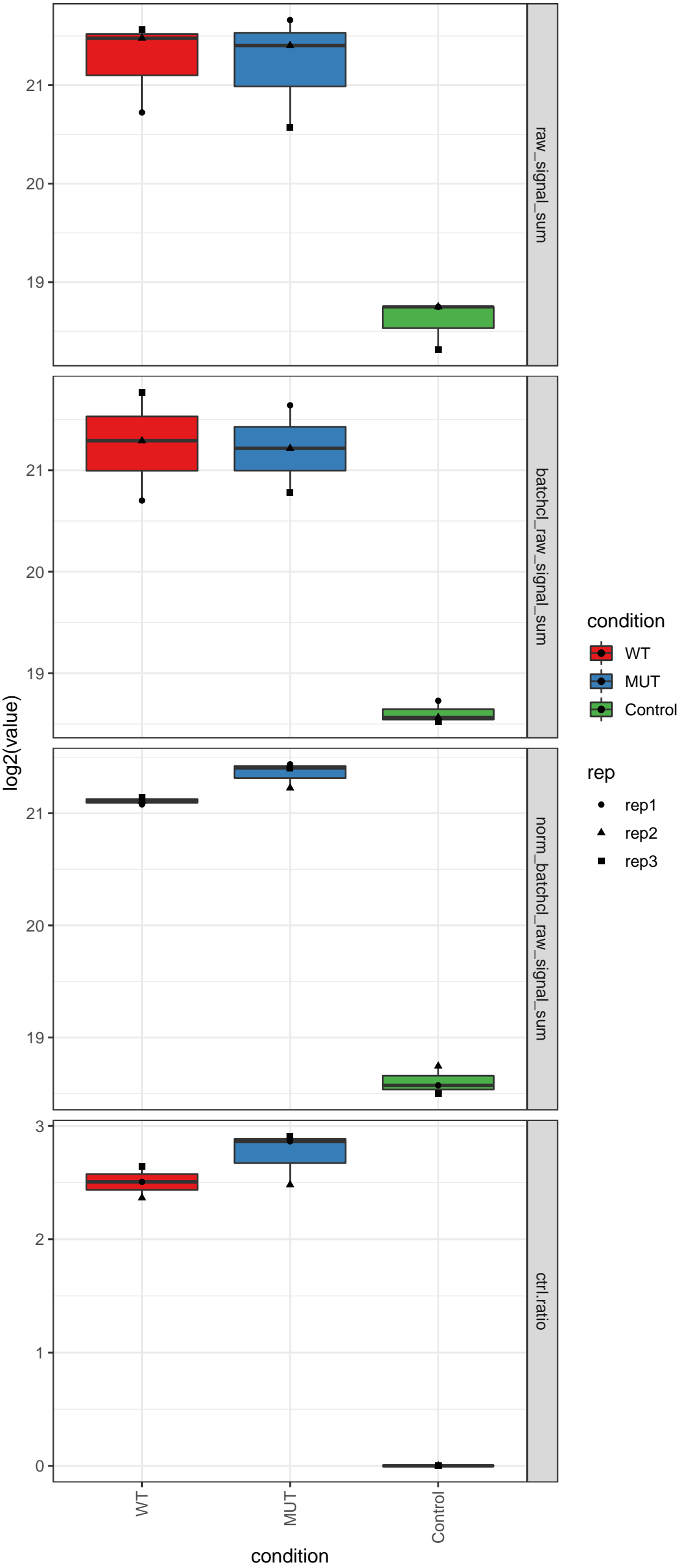
ADE3 – P07245

C-1-tetrahydrofolate synthase, cytoplasmic OS=*Saccharomyces cerevisia*



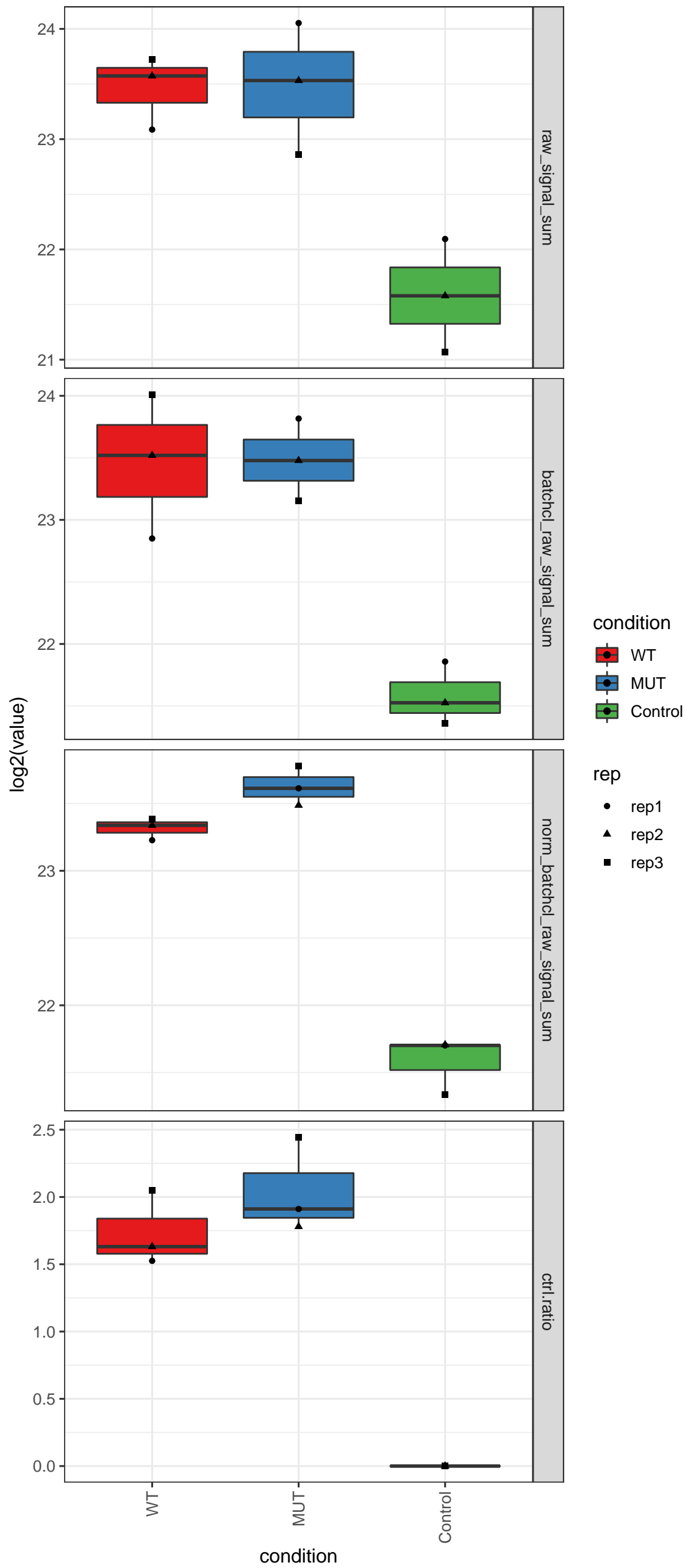
ADE4 – P04046

Amidophosphoribosyltransferase OS=*Saccharomyces cerevisiae* (strain ATCC 25768)



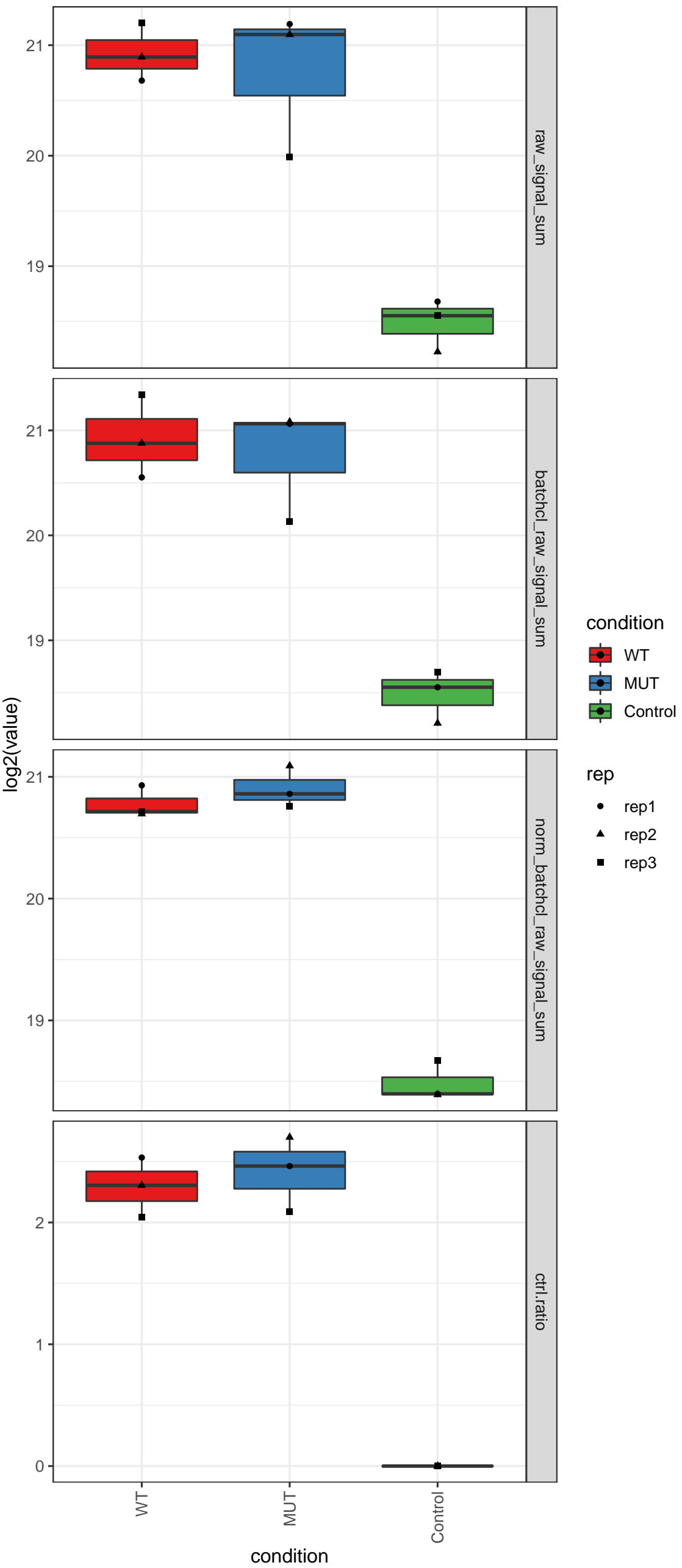
ADE5,7 – P07244

Bifunctional purine biosynthetic protein ADE5,7 OS=*Saccharomyces cerevisiae*



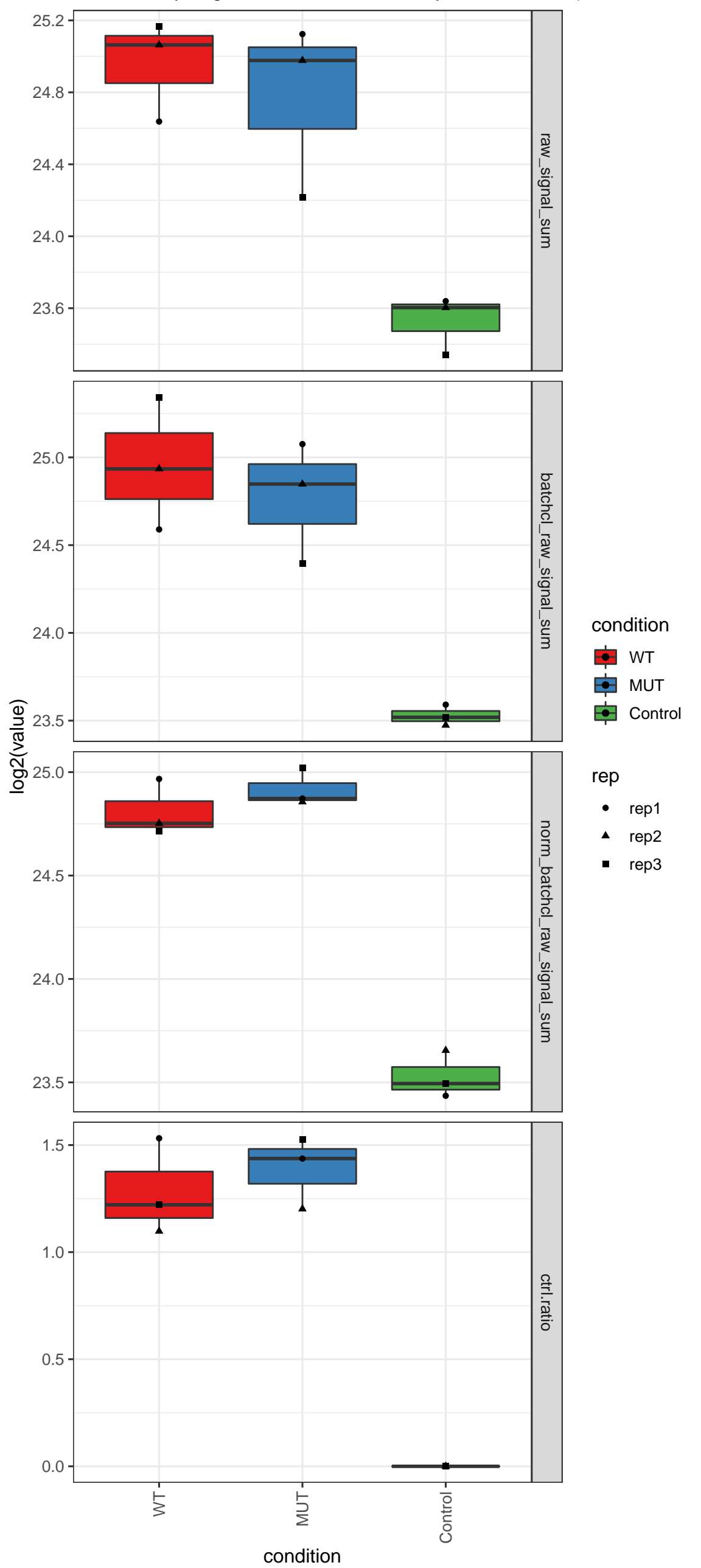
ADE6 – P38972

Phosphoribosylformylglycinamidine synthase OS=*Saccharomyces cerevisiae*



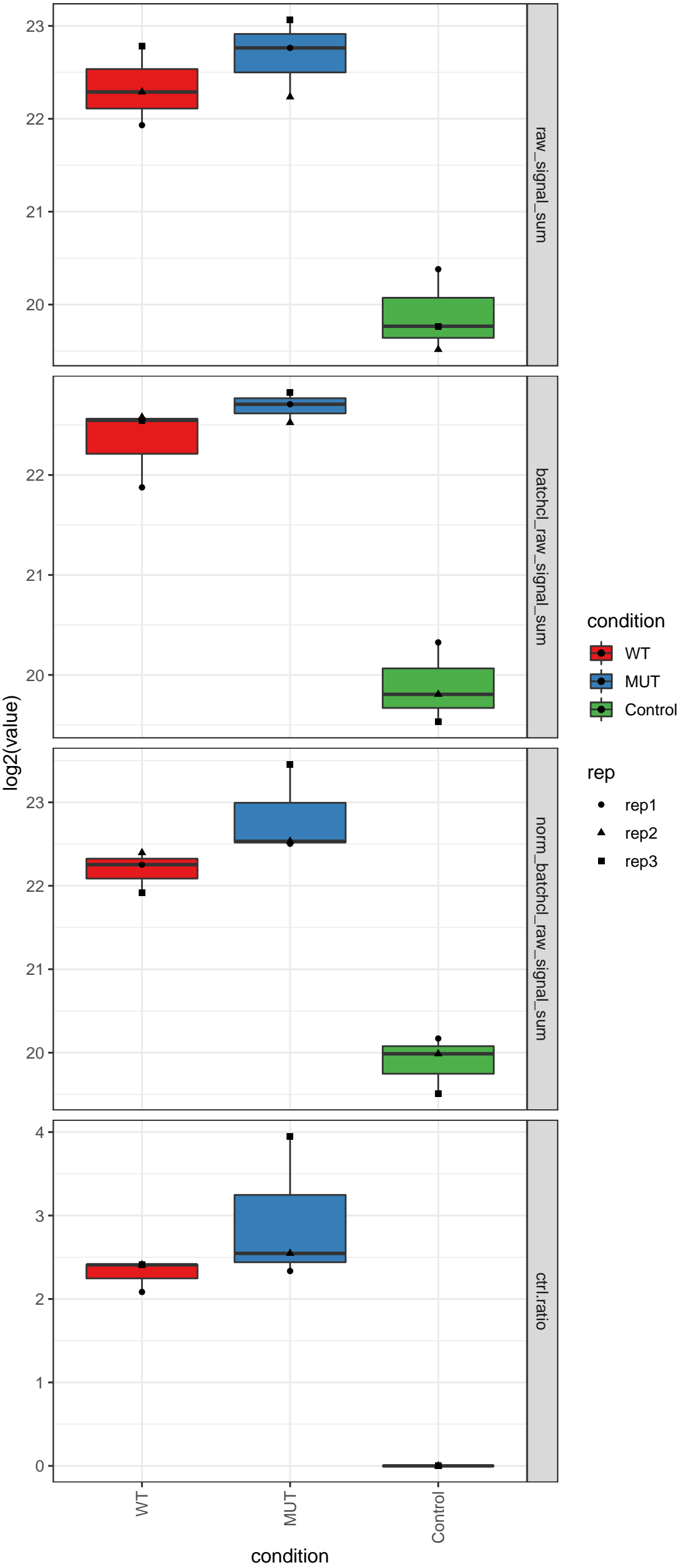
ADH1 – P00330

Alcohol dehydrogenase 1 OS=*Saccharomyces cerevisiae* (strain ATCC 25620)



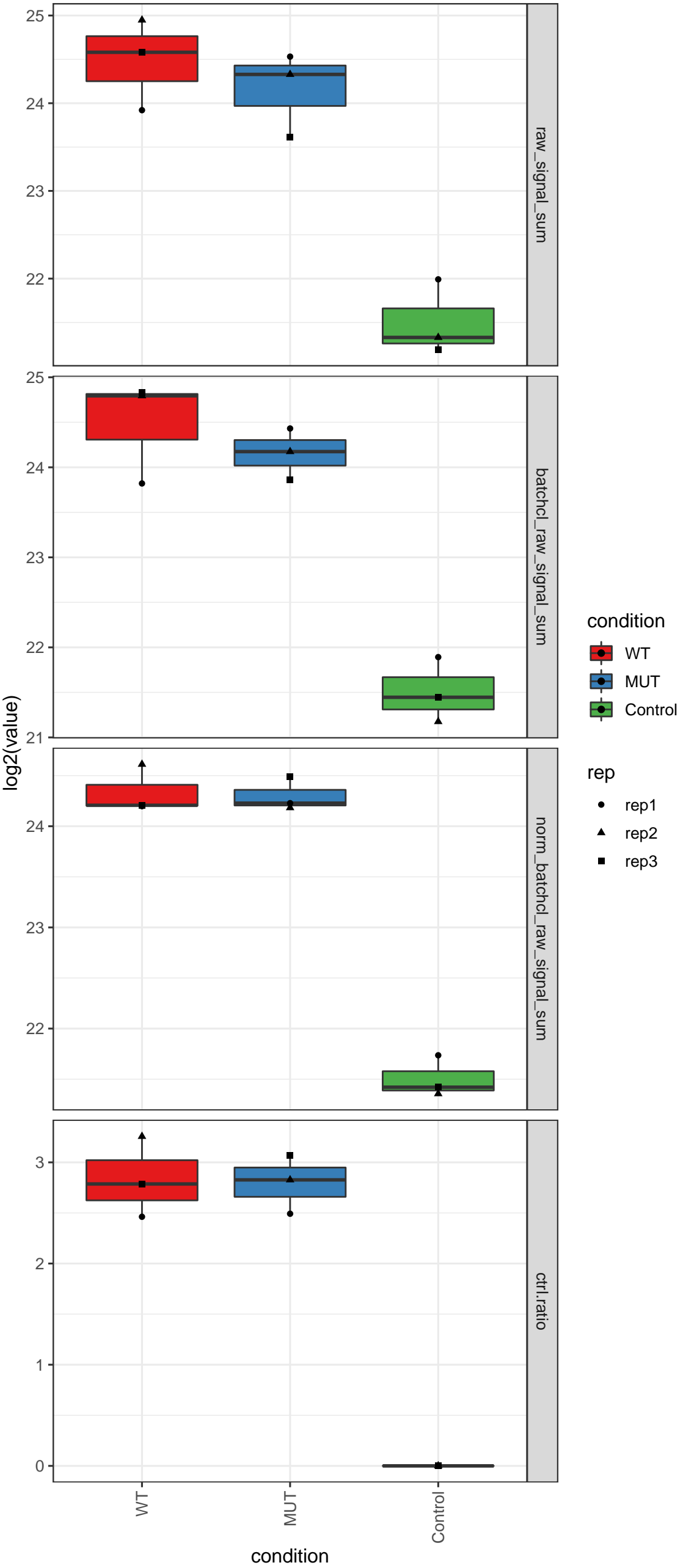
ADH2 – P00331

Alcohol dehydrogenase 2 OS=Saccharomyces cerevisiae (strain ATCC 204



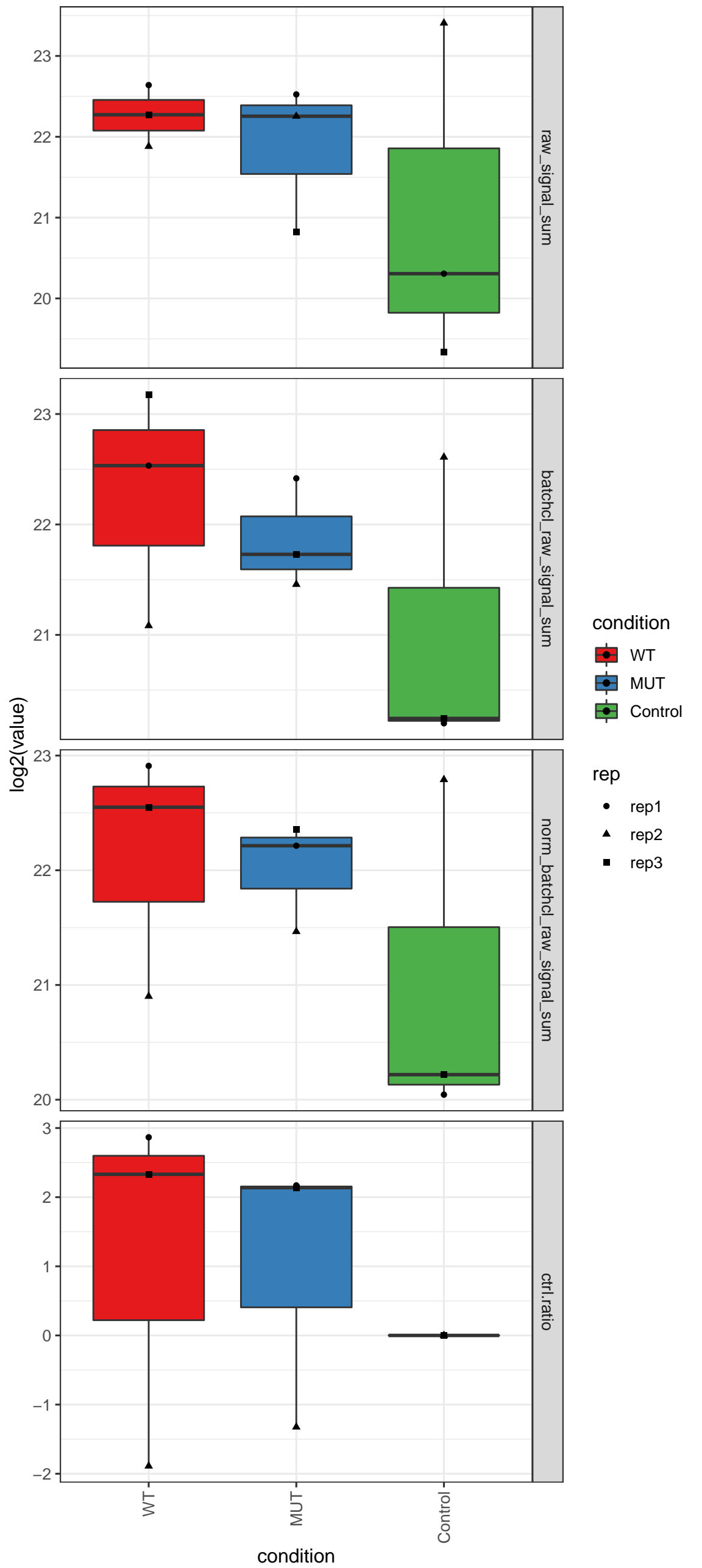
ADH3 – P07246

Alcohol dehydrogenase 3, mitochondrial OS=Saccharomyces cerevisiae (s



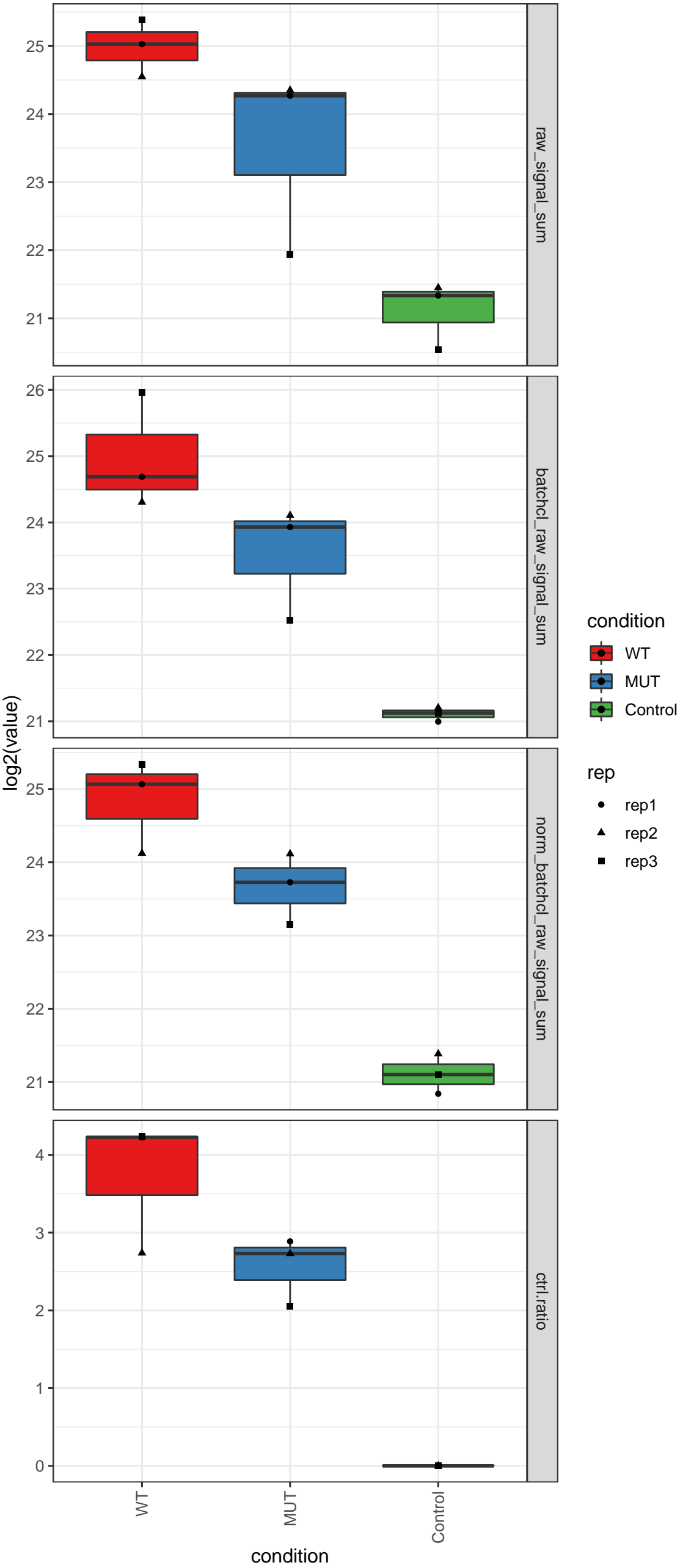
ADO1 – P47143

Adenosine kinase OS=*Saccharomyces cerevisiae* (strain ATCC 204508 / S



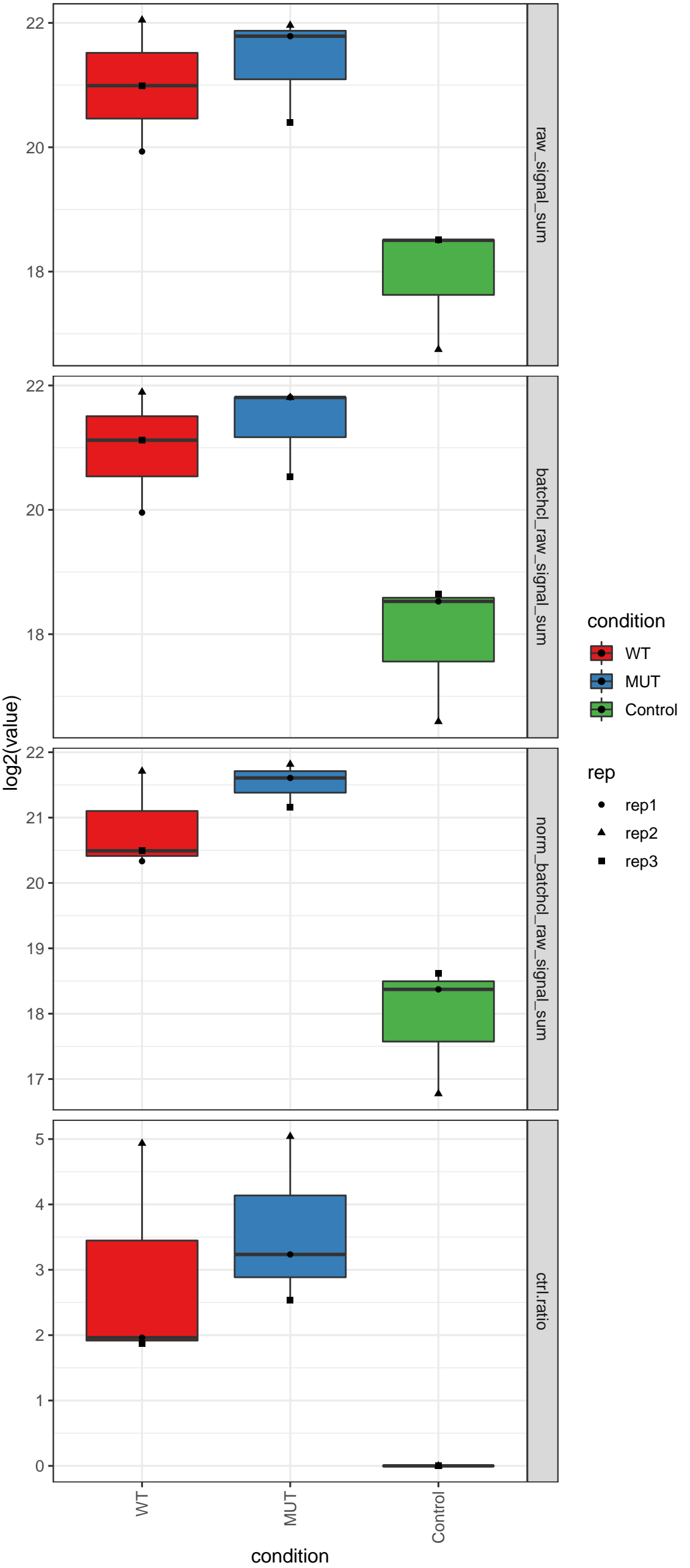
ADR1 – P07248

Regulatory protein ADR1 OS=*Saccharomyces cerevisiae* (strain ATCC 204



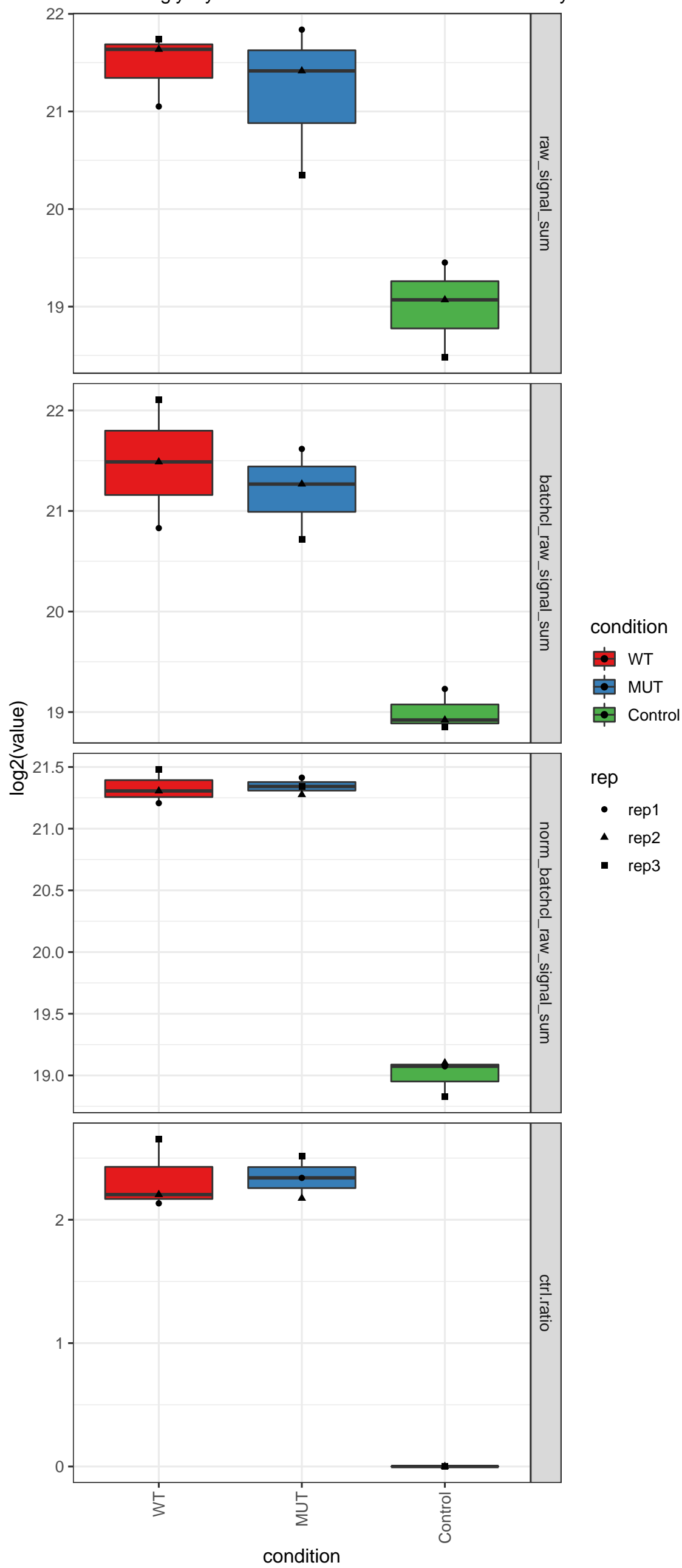
ADY3 – Q07732

Accumulates dyads protein 3 OS=*Saccharomyces cerevisiae* (strain ATCC



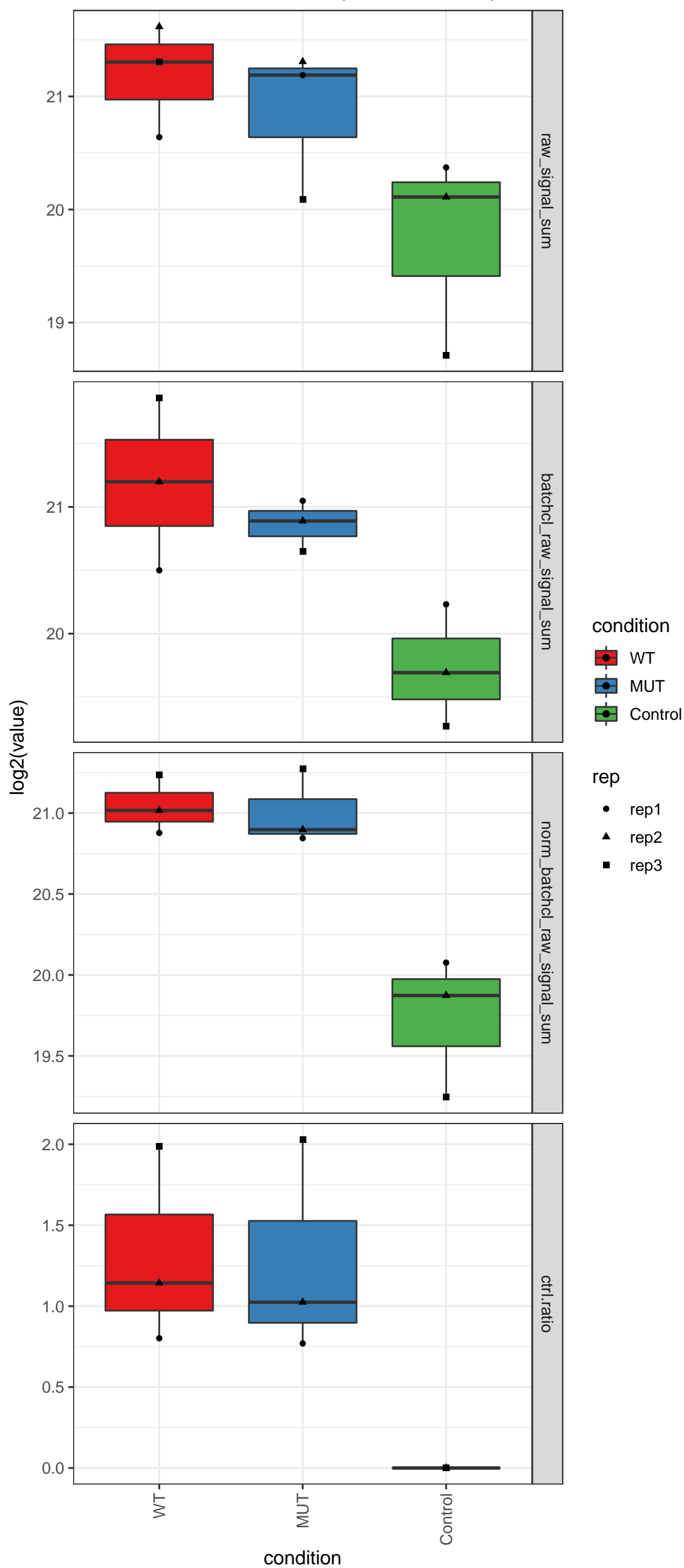
AGX1 – P43567

Alanine--glyoxylate aminotransferase 1 OS=Saccharomyces cerevisiae



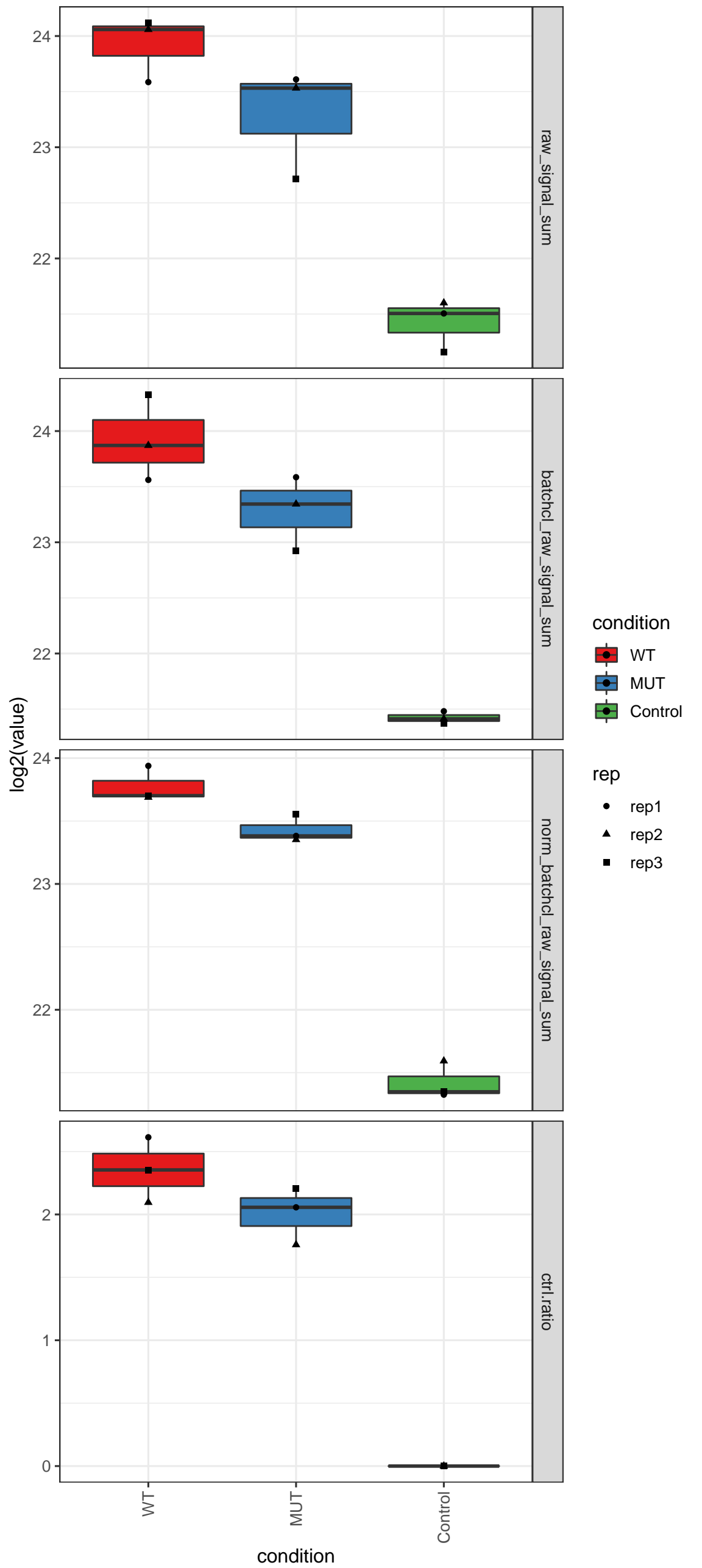
AIM45 – Q12480

Probable electron transfer flavoprotein subunit alpha, mitochondrial OS=S



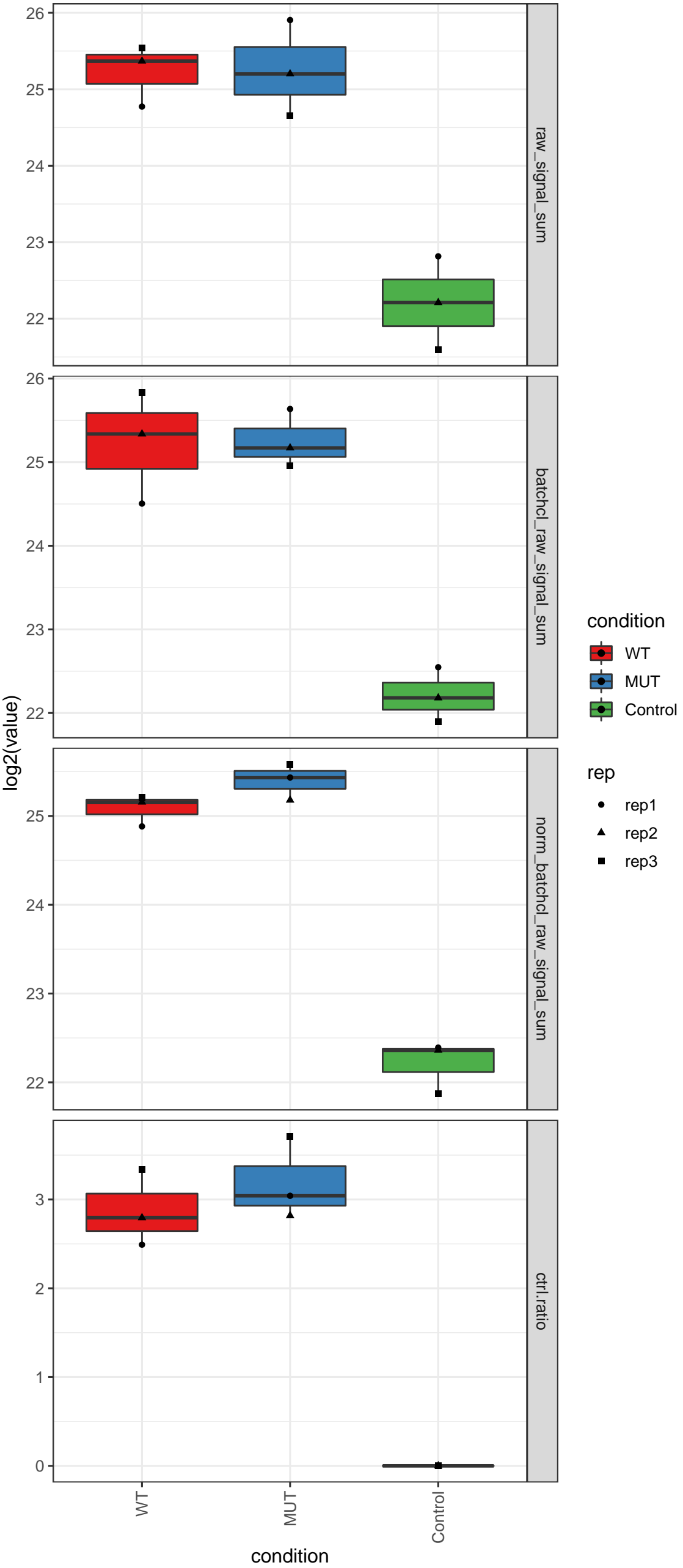
ALA1 – P40825|P40825–2

Alanine--tRNA ligase, mitochondrial OS=Saccharomyces cerevisiae (strain



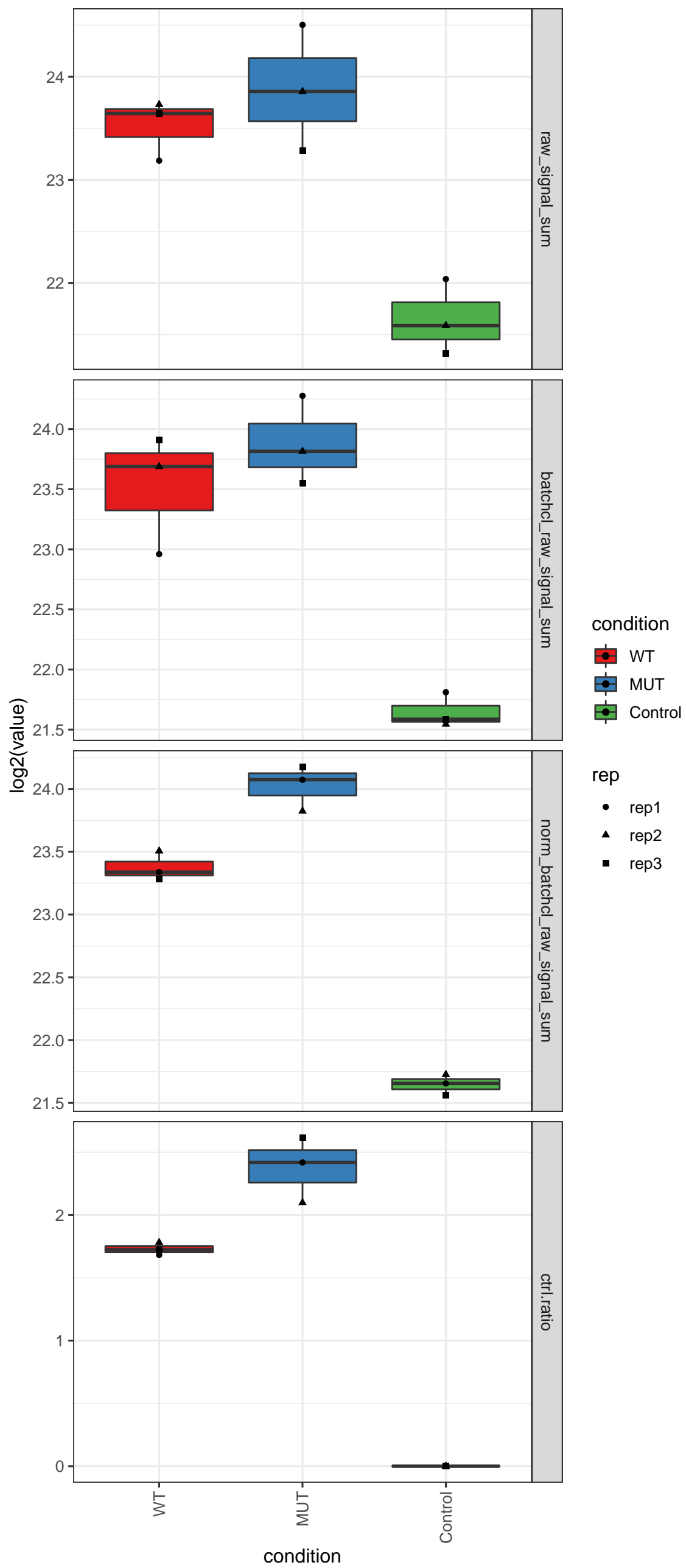
ALD4 – P46367

Potassium-activated aldehyde dehydrogenase, mitochondrial OS=Sacchar



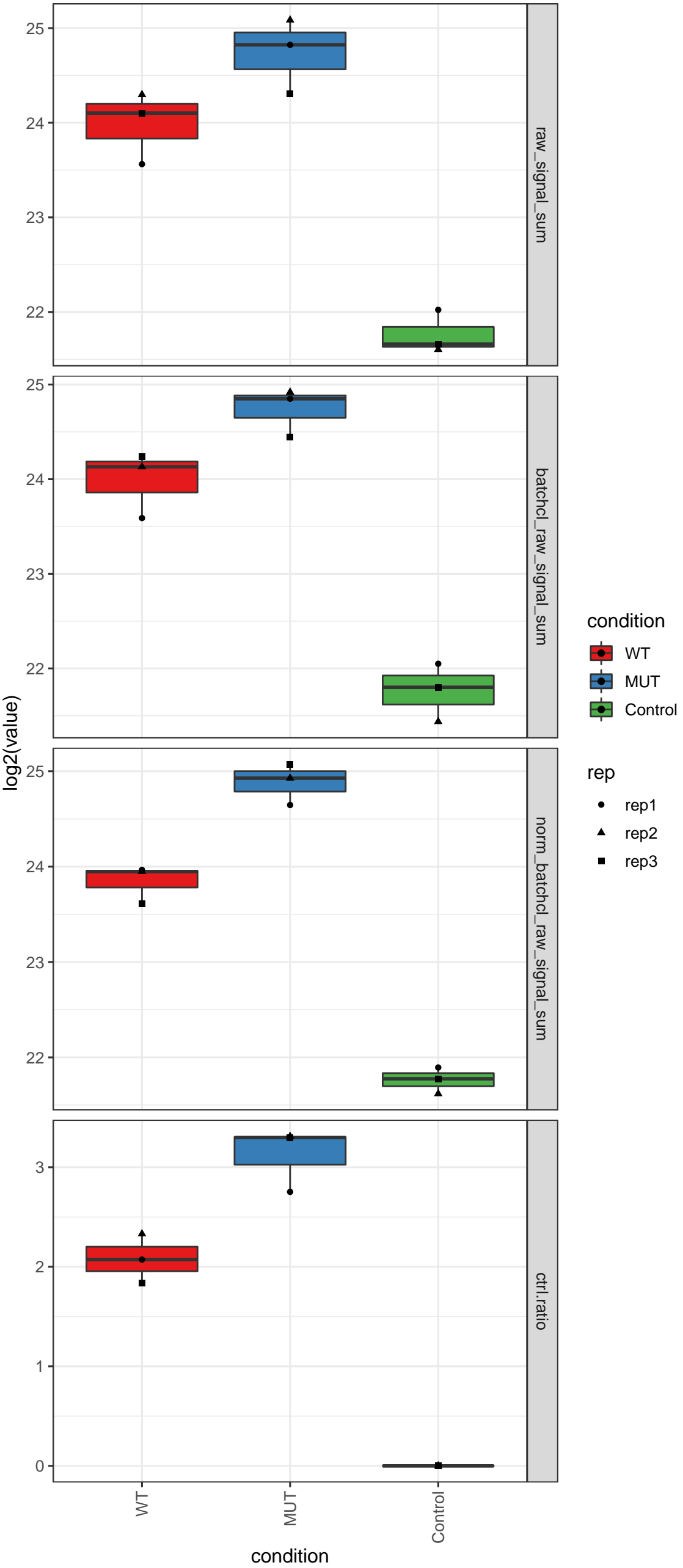
ALD6 – P54115

Magnesium-activated aldehyde dehydrogenase, cytosolic OS=Saccharo



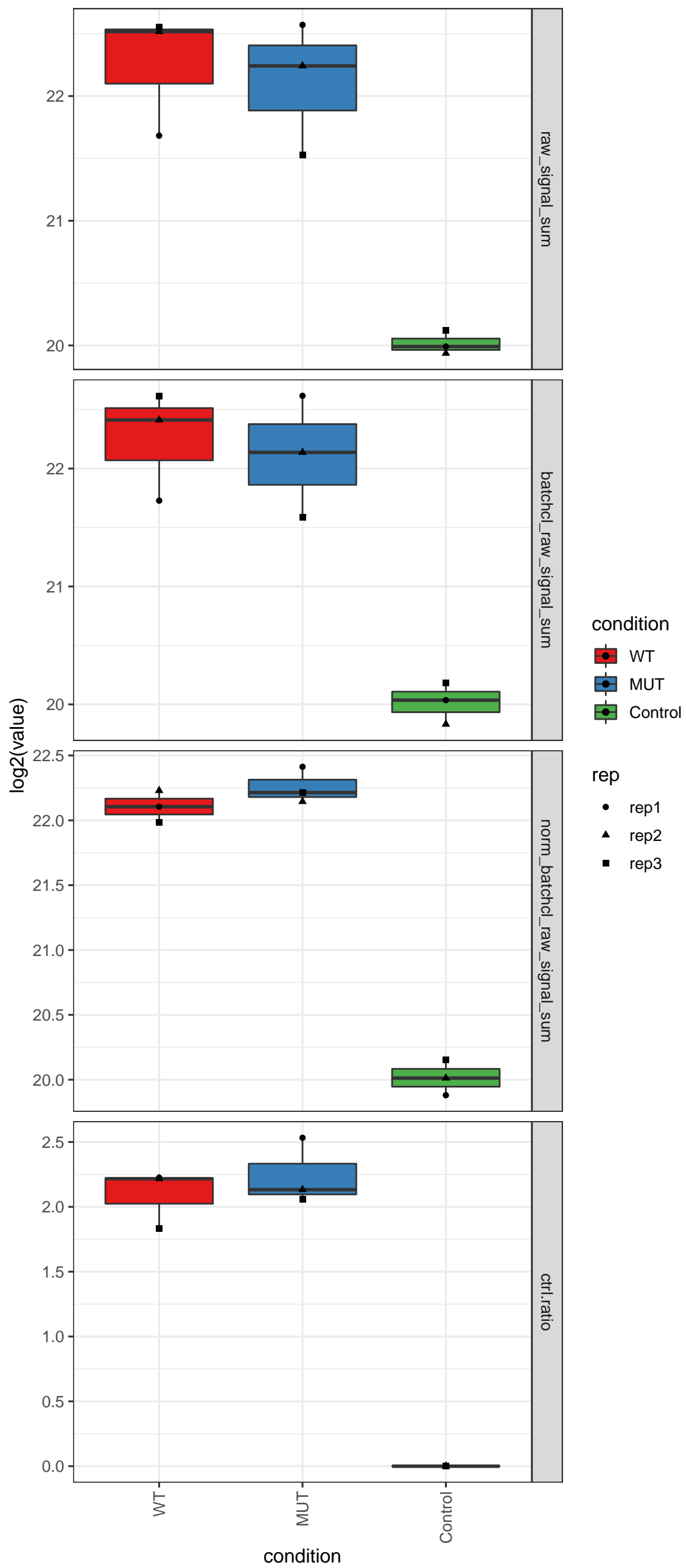
AMD1 – P15274

AMP deaminase OS=*Saccharomyces cerevisiae* (strain ATCC 204508 / S288c)



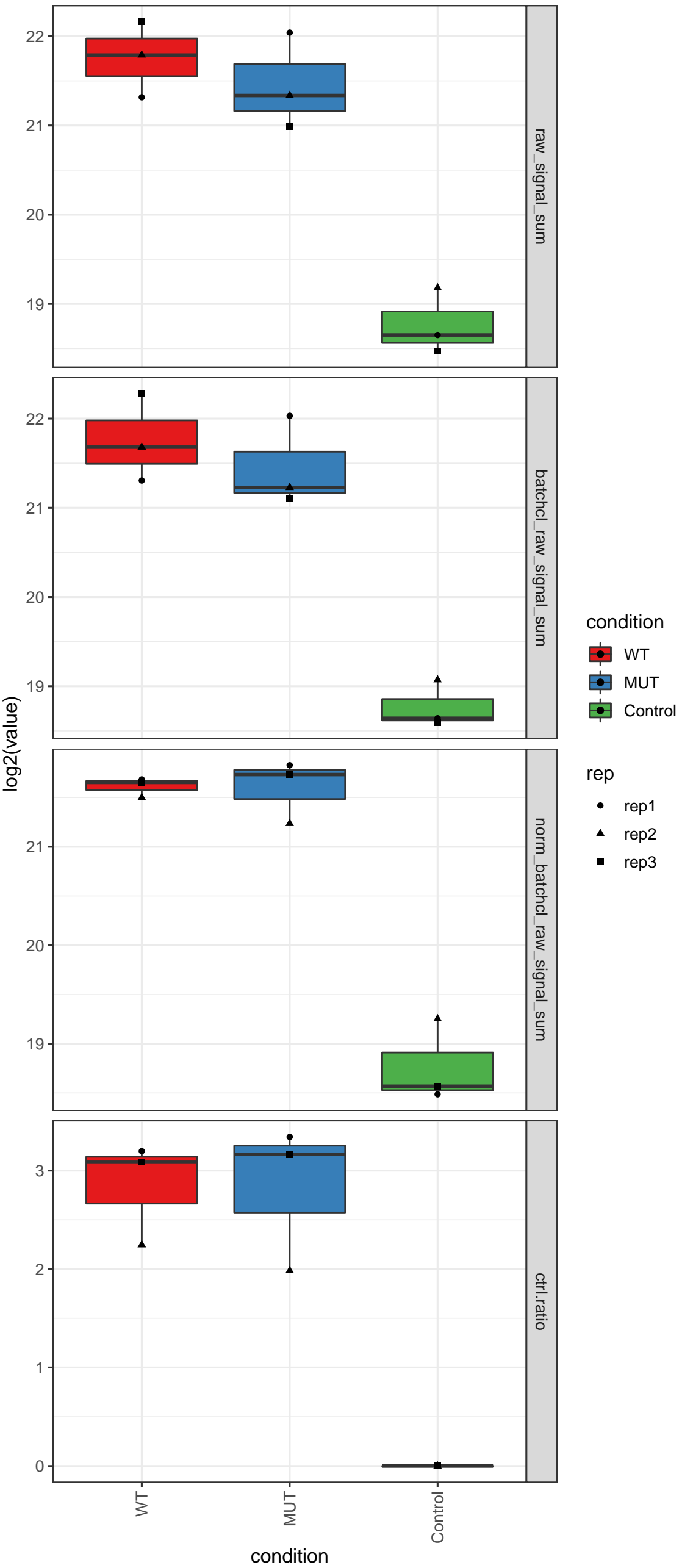
AMS1 – P22855

Alpha-mannosidase OS=*Saccharomyces cerevisiae* (strain ATCC 20450)



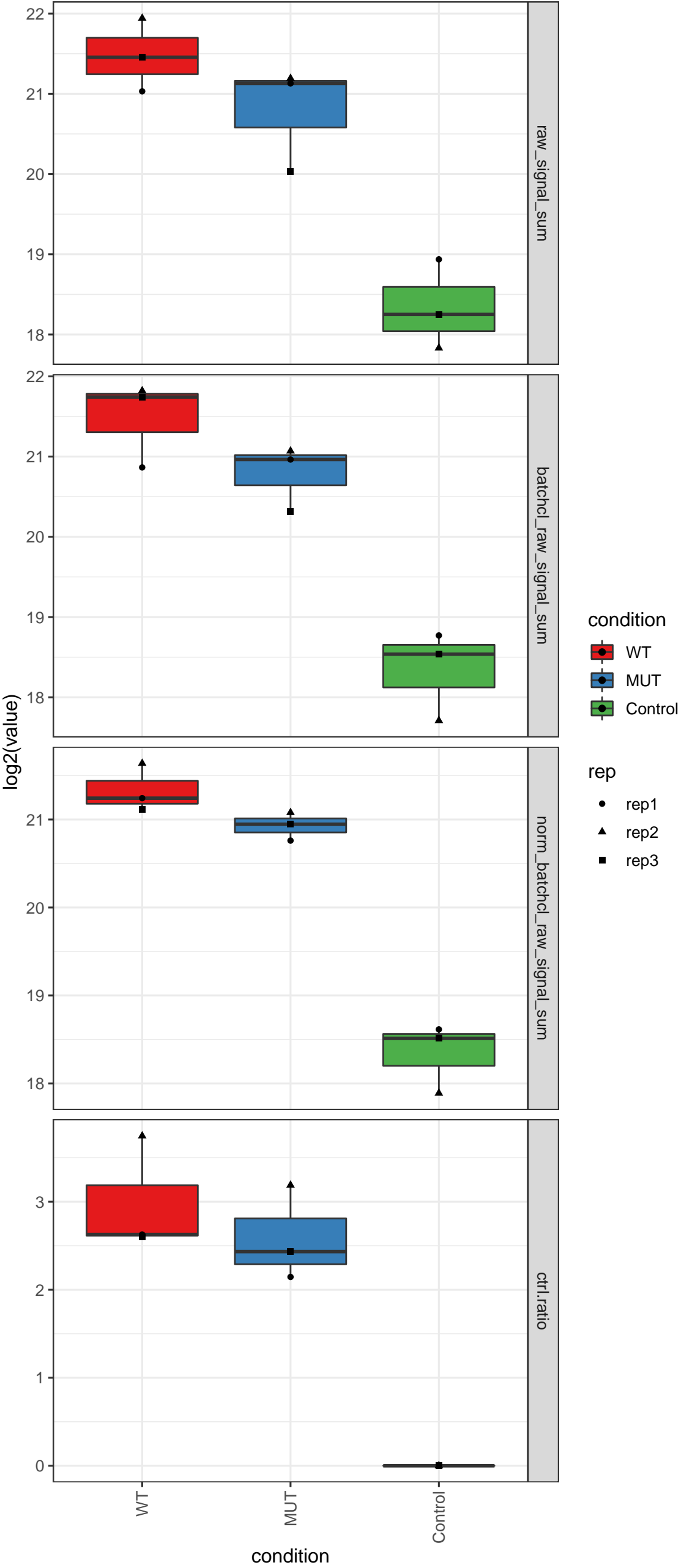
APE2 – P32454

Aminopeptidase 2, mitochondrial OS=*Saccharomyces cerevisiae* (strain ATCC 22016 / *D*6158)



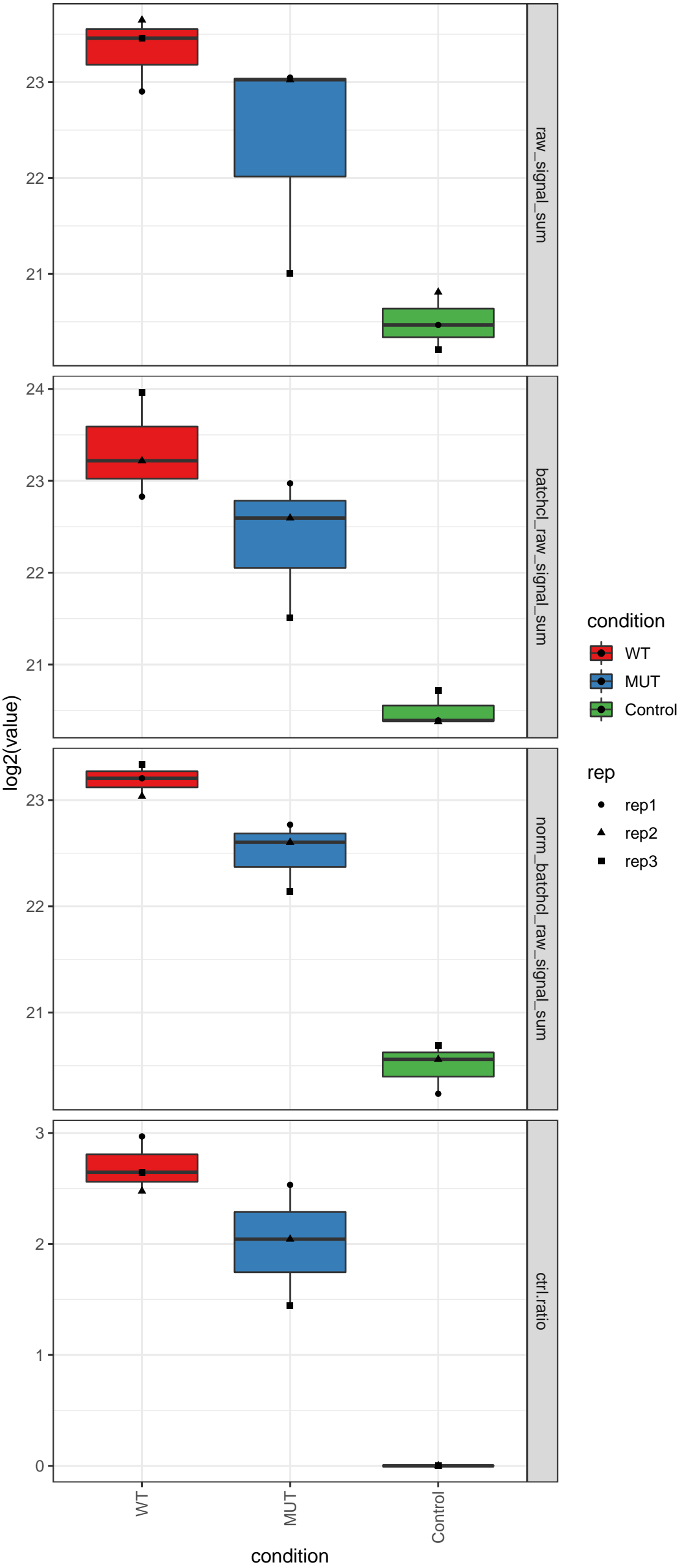
APL2 – P36000

AP-1 complex subunit beta-1 OS=Saccharomyces cerevisiae (strain ATCC



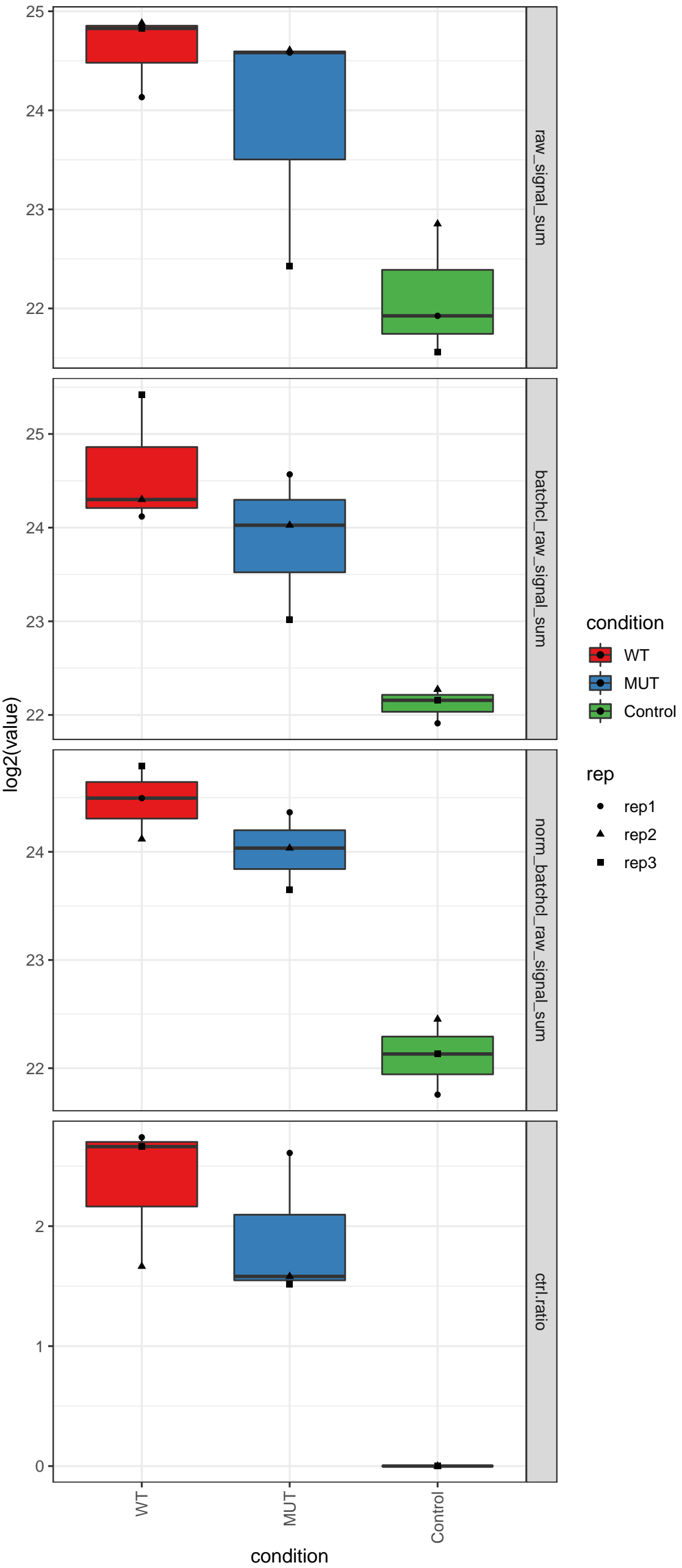
APN1 – P22936

DNA–(apurinic or apyrimidinic site) lyase 1 OS=*Saccharomyces cerevisiae*

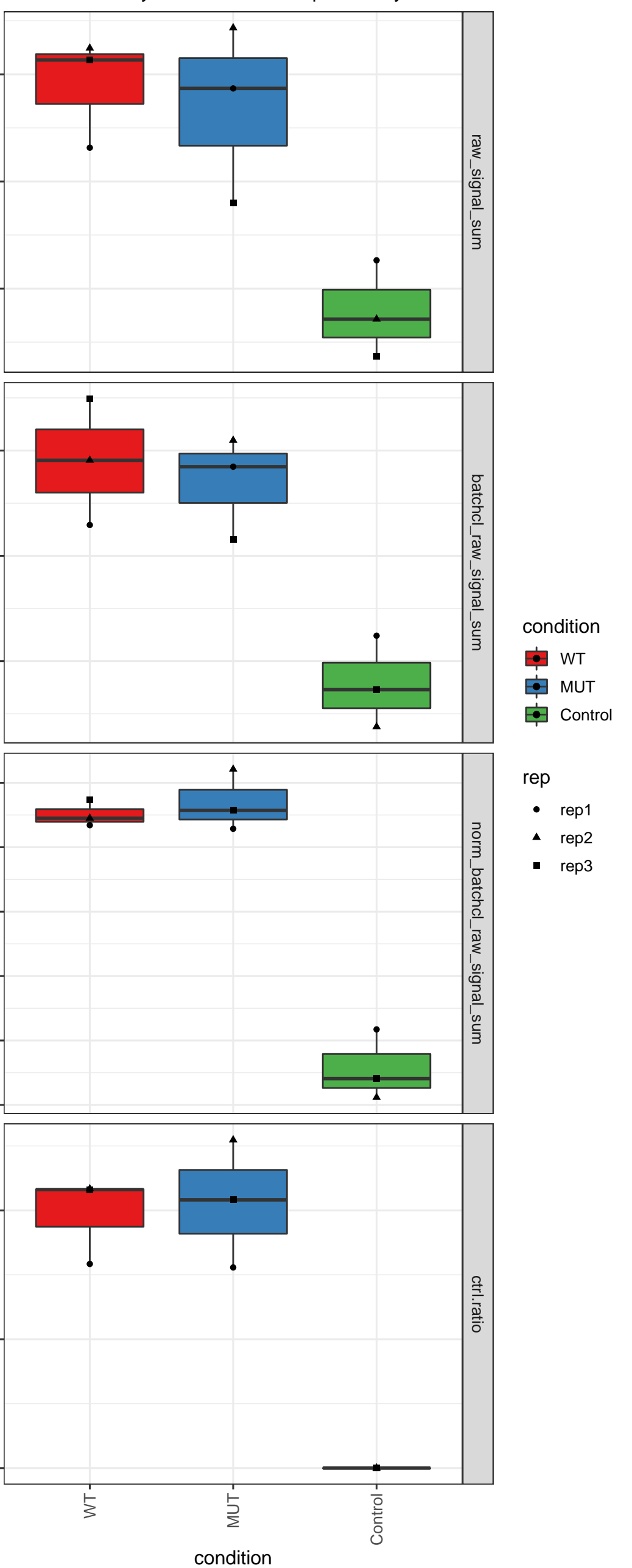


ARB1 – P40024

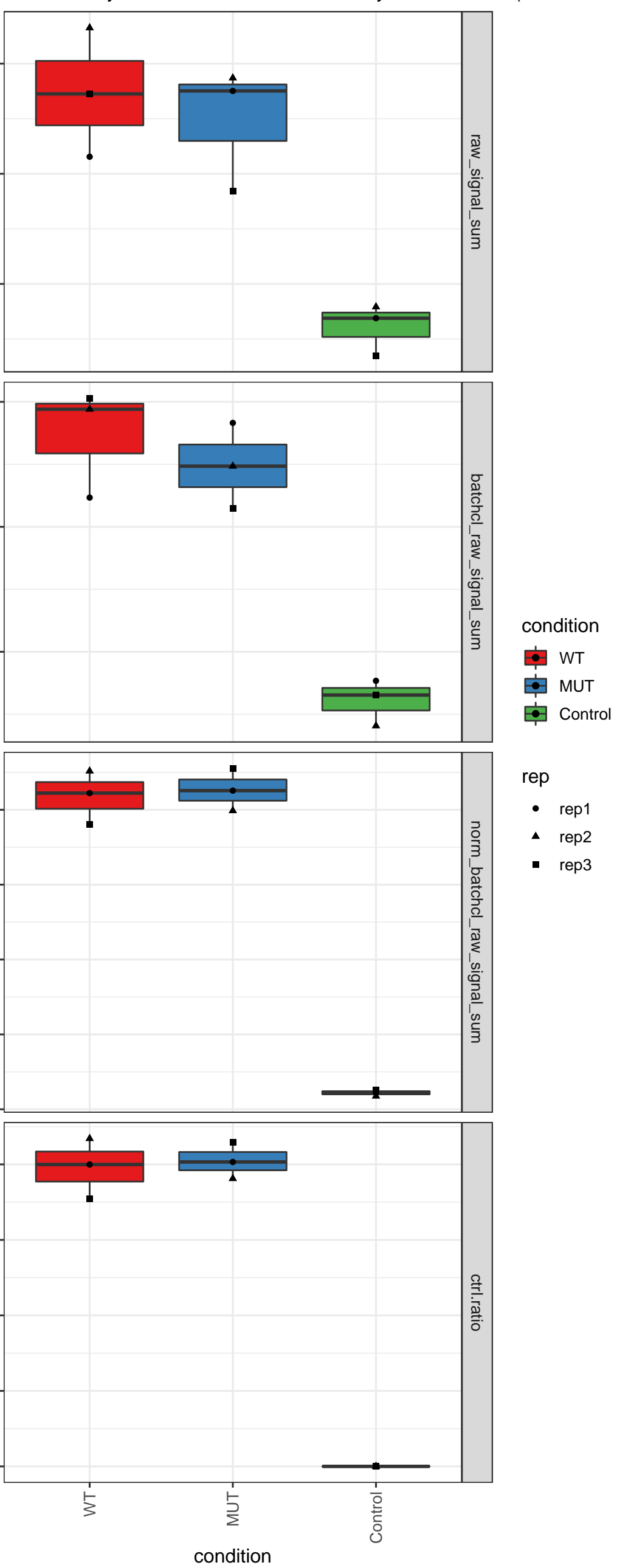
ABC transporter ATP-binding protein ARB1 OS=*Saccharomyces cerevisia*



N-terminal acetyltransferase A complex catalytic subunit ARD1 OS=Saccharomyces cerevisiae

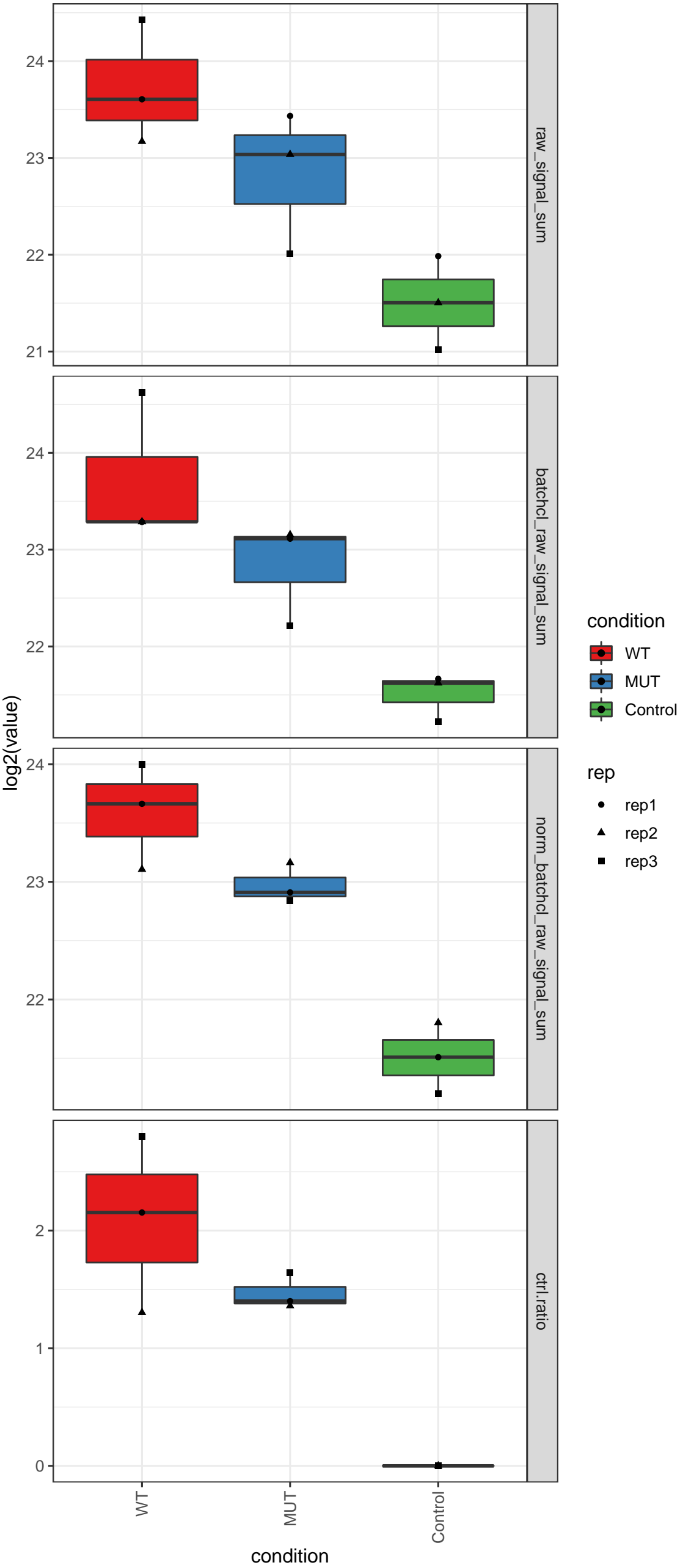


Sterol O-acyltransferase 2 OS=Saccharomyces cerevisiae (strain ATCC 25716)



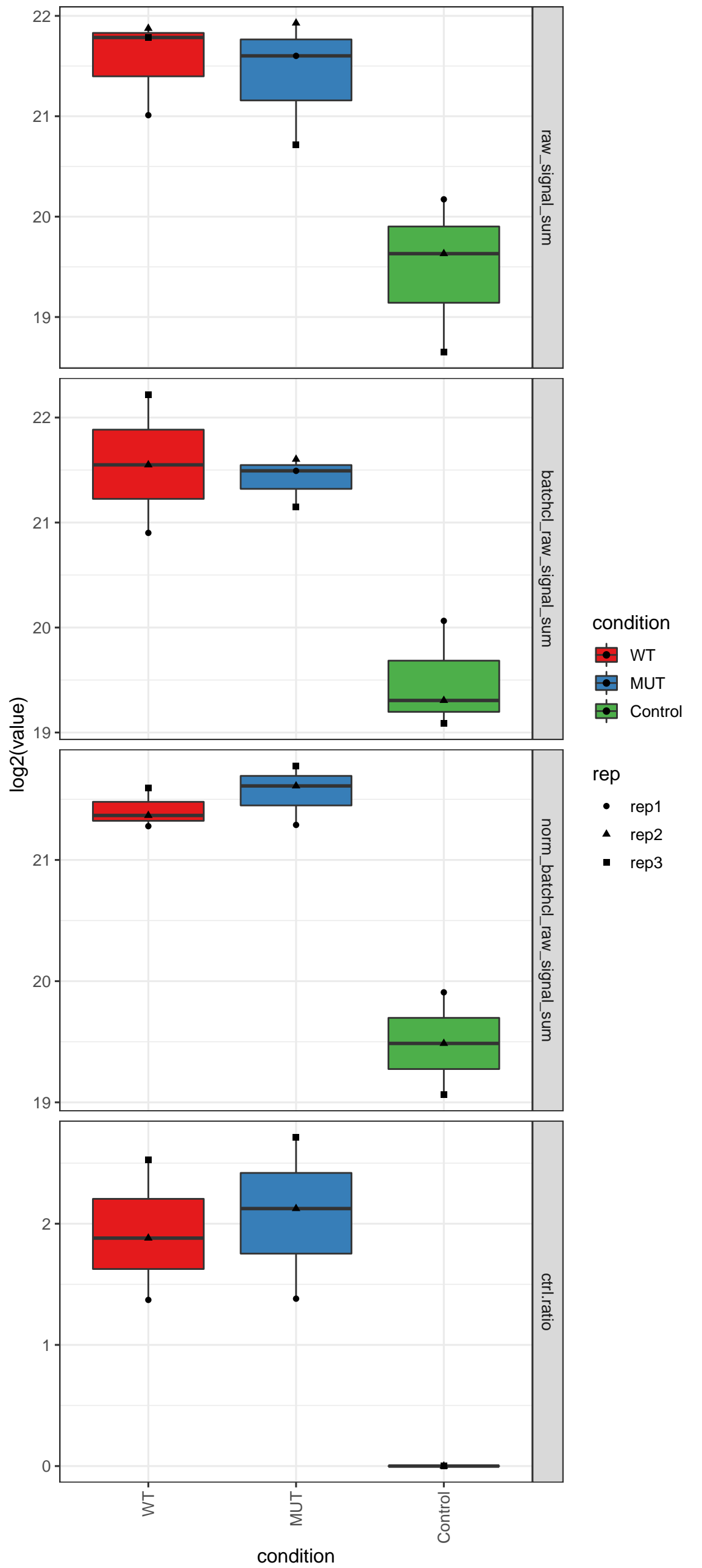
ARG1 – P22768

Argininosuccinate synthase OS=*Saccharomyces cerevisiae* (strain ATCC 2



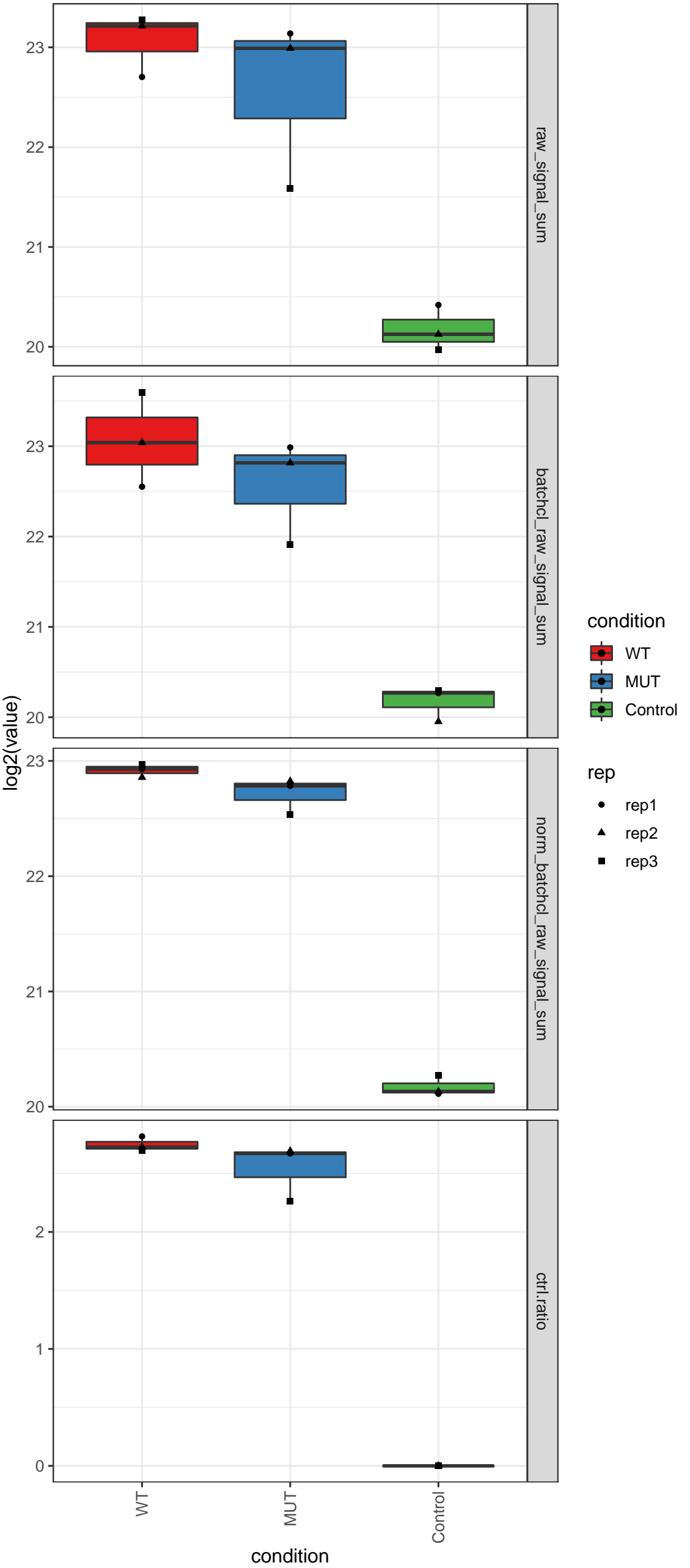
ARL1 – P38116

ADP-ribosylation factor-like protein 1 OS=*Saccharomyces cerevisiae* (stra



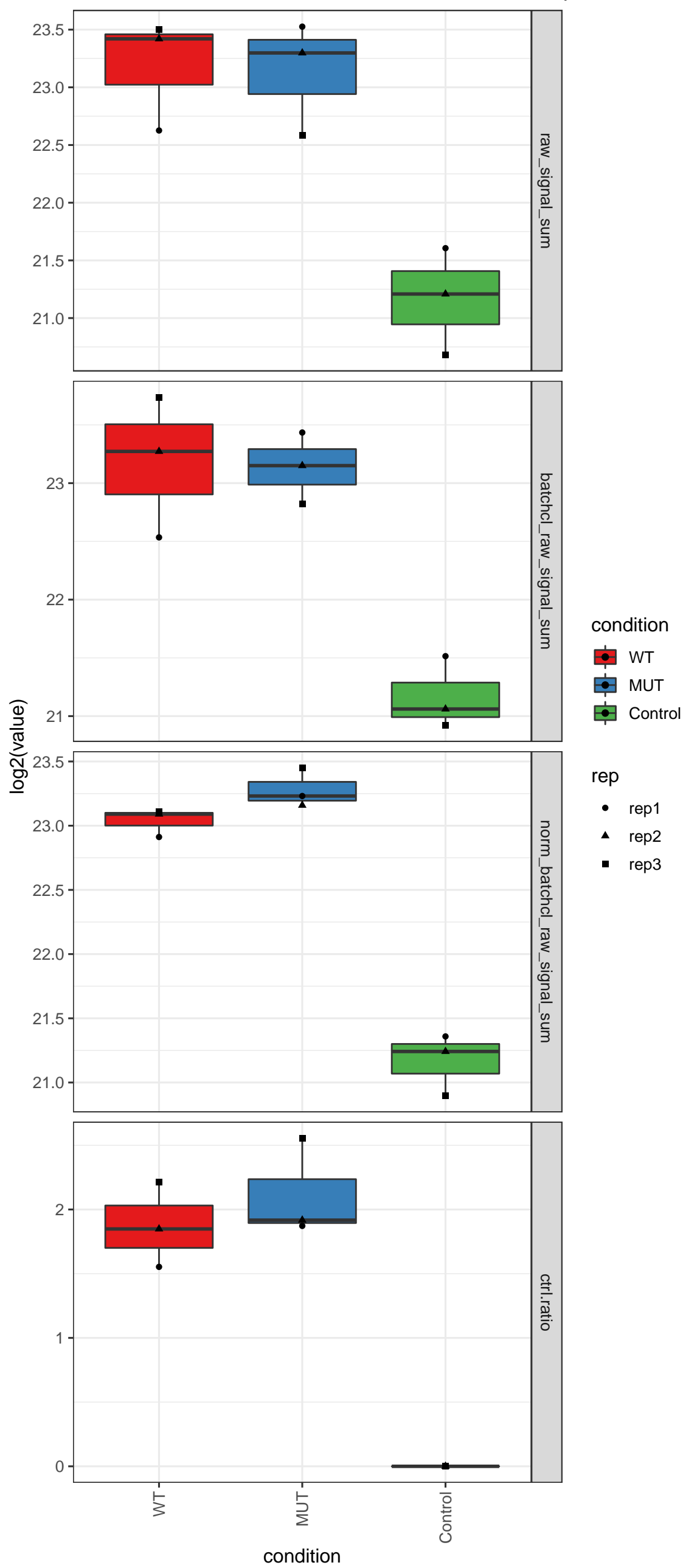
ARO4 – P32449

Phospho-2-dehydro-3-deoxyheptonate aldolase, tyrosine-inhibited OS=3



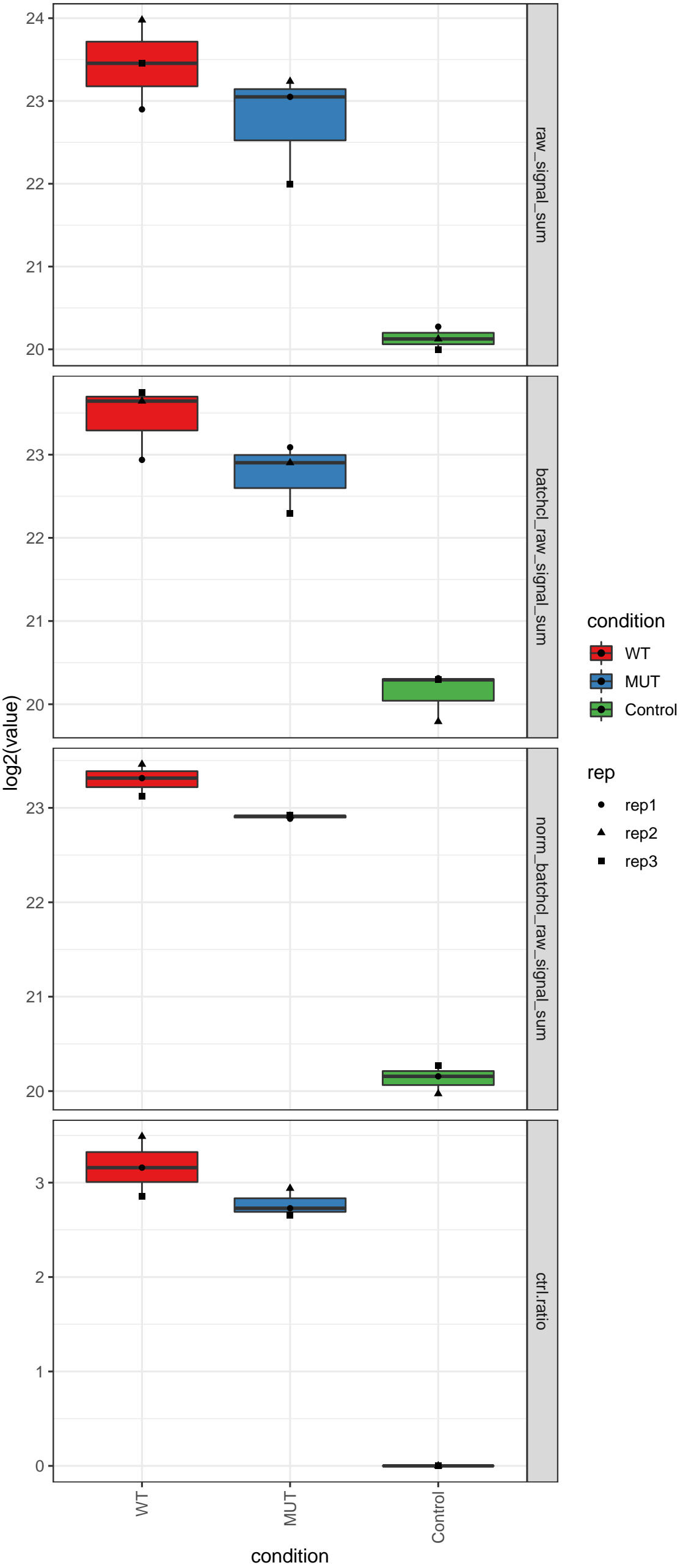
ARO9 – P38840

Aromatic amino acid aminotransferase 2 OS=*Saccharomyces cerevisiae*



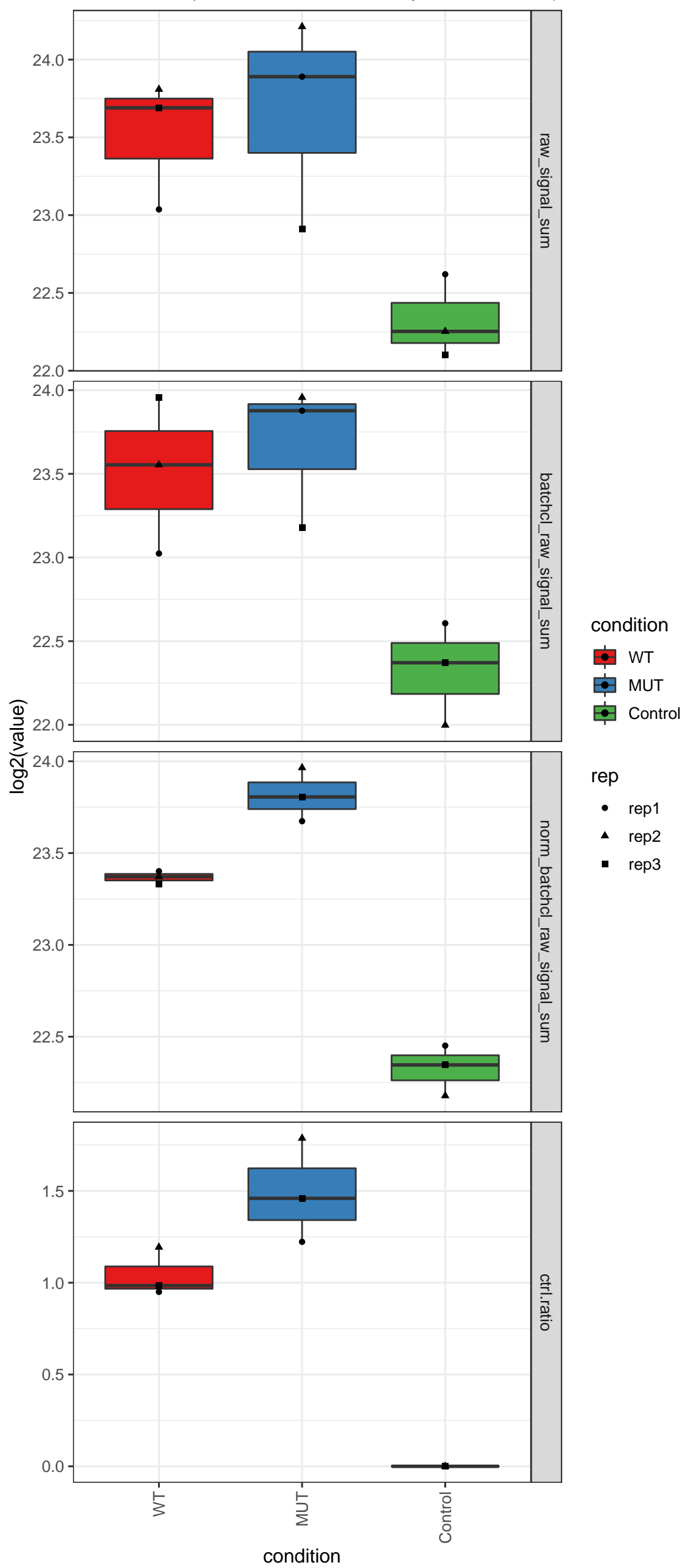
ARP4 – P80428

Actin-related protein 4 OS=Saccharomyces cerevisiae (strain ATCC 20450)



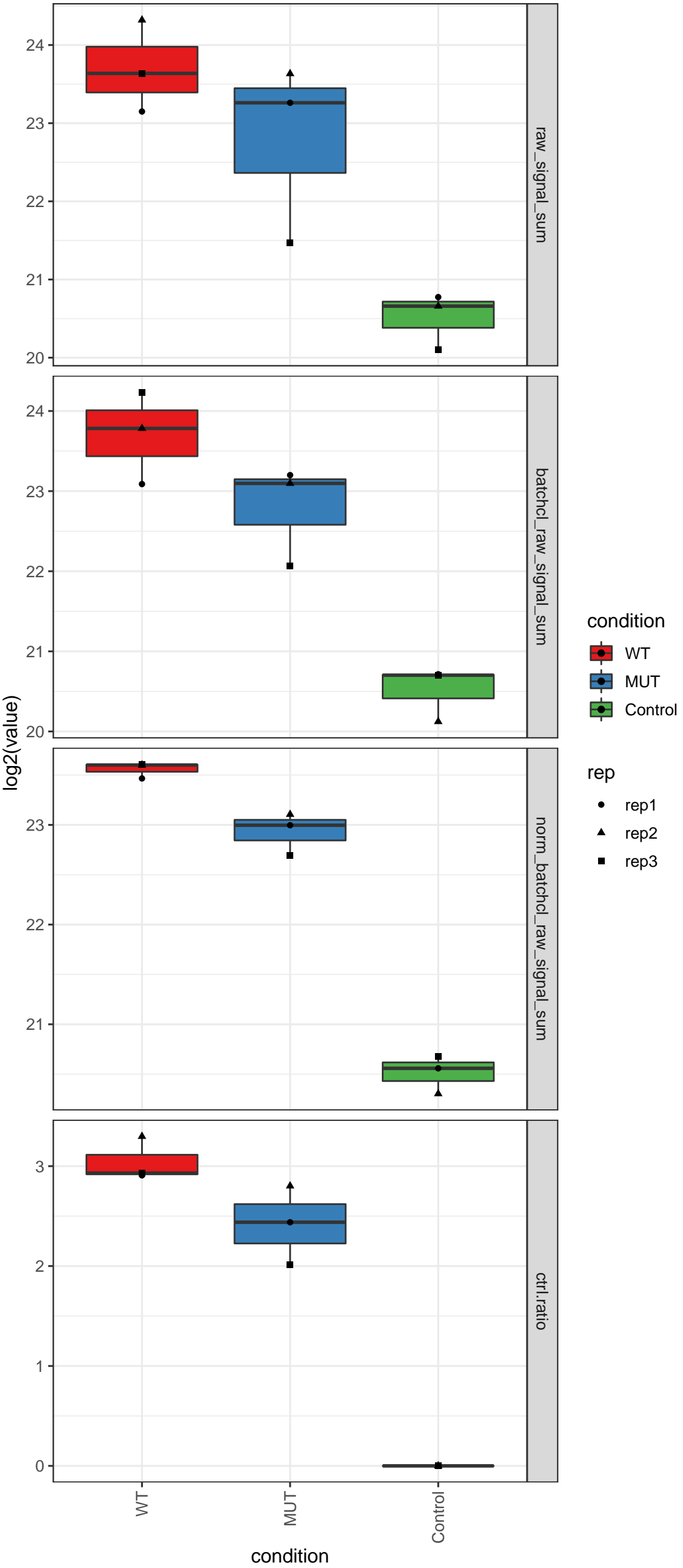
ARP7 – Q12406

Actin-related protein 7 OS=*Saccharomyces cerevisiae* (strain ATCC 20454)



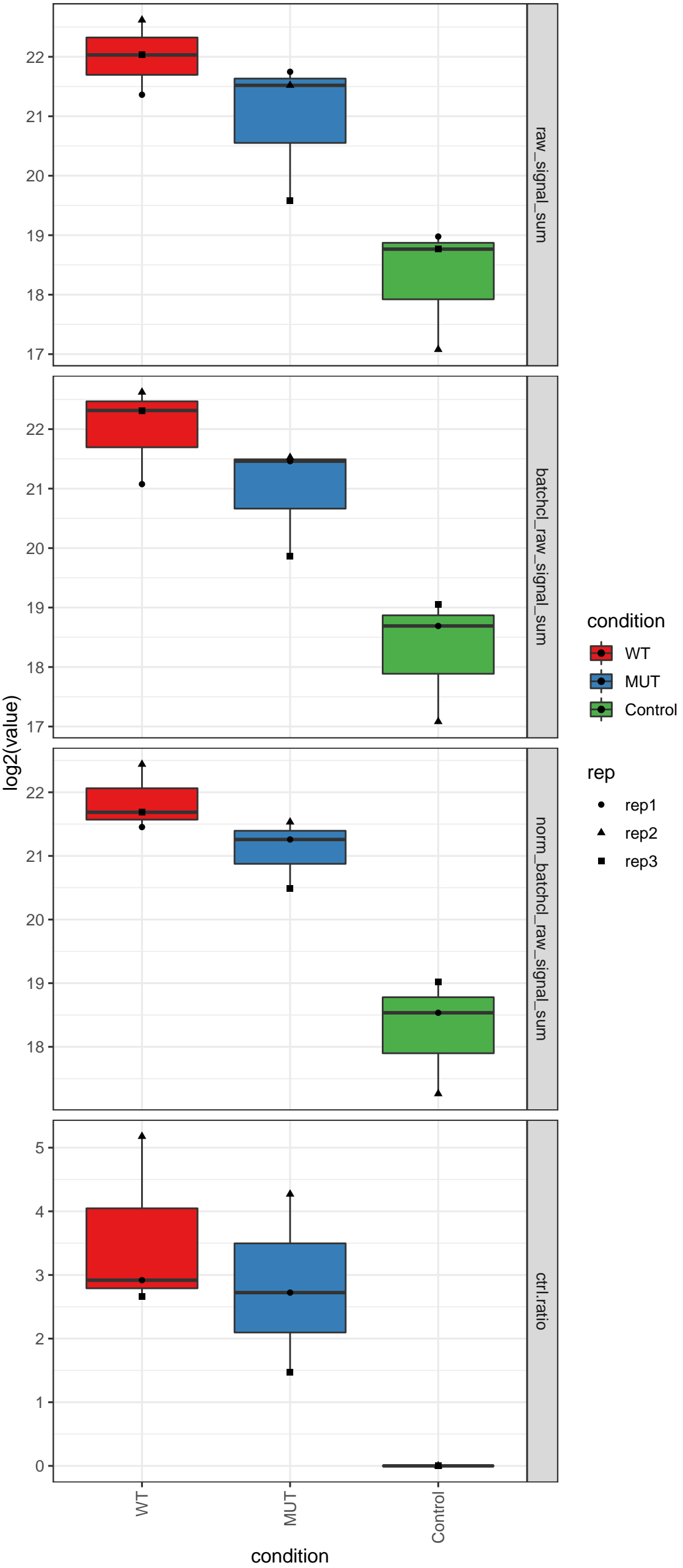
ARP8 – Q12386

Actin-like protein ARP8 OS=*Saccharomyces cerevisiae* (strain ATCC 2045



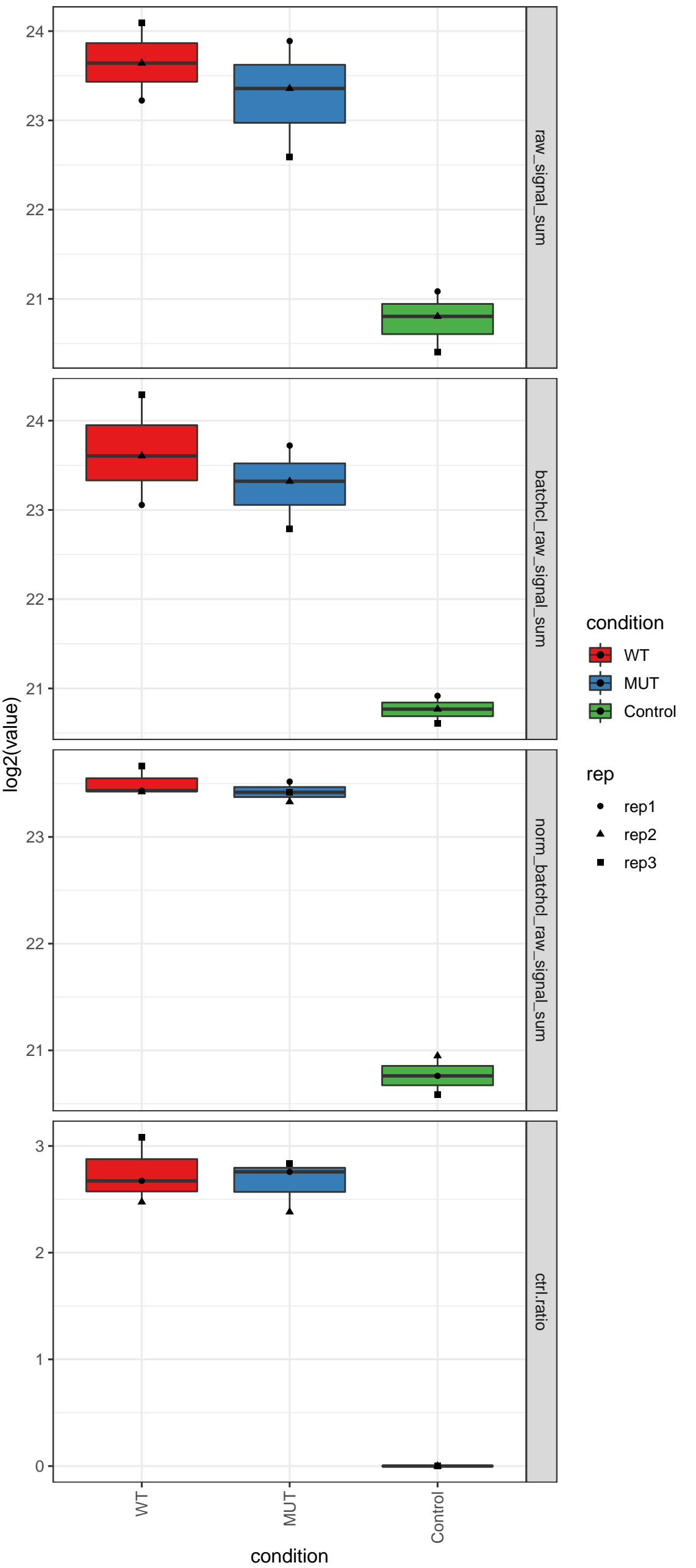
ARX1 – Q03862

Probable metalloprotease ARX1 OS=*Saccharomyces cerevisiae* (strain ATCC 25716)



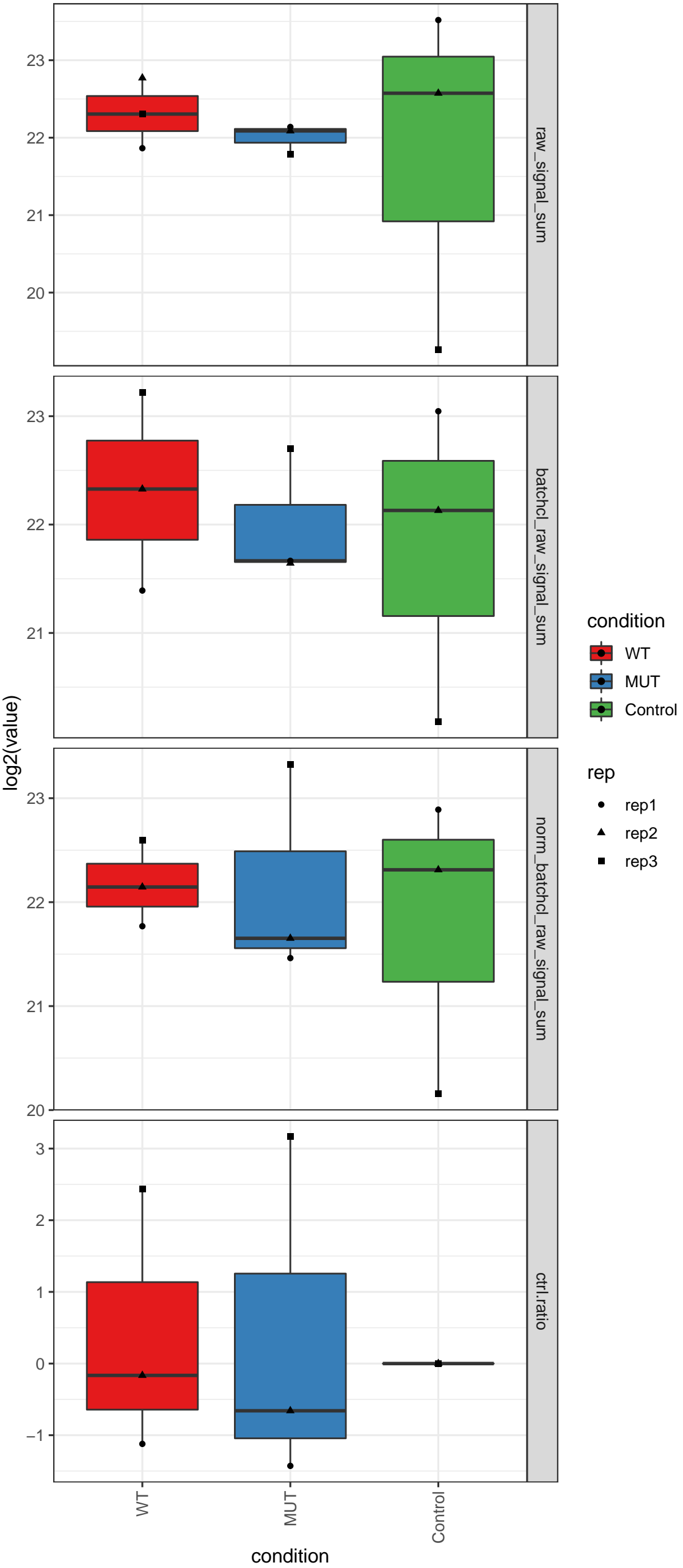
ASC1 – P38011

Guanine nucleotide-binding protein subunit beta-like protein OS=Sacchar



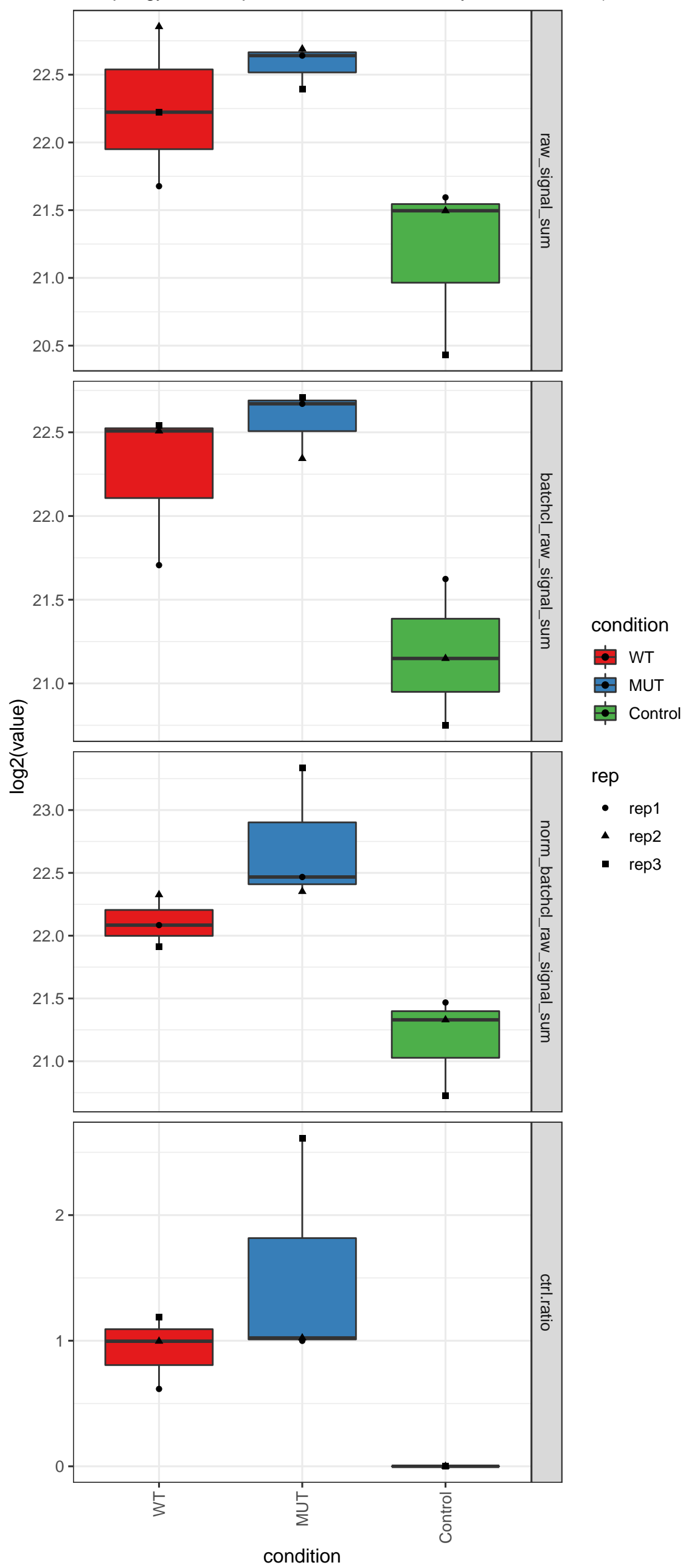
ASG1 – P40467

Activator of stress genes 1 OS=*Saccharomyces cerevisiae* (strain ATCC 20467)



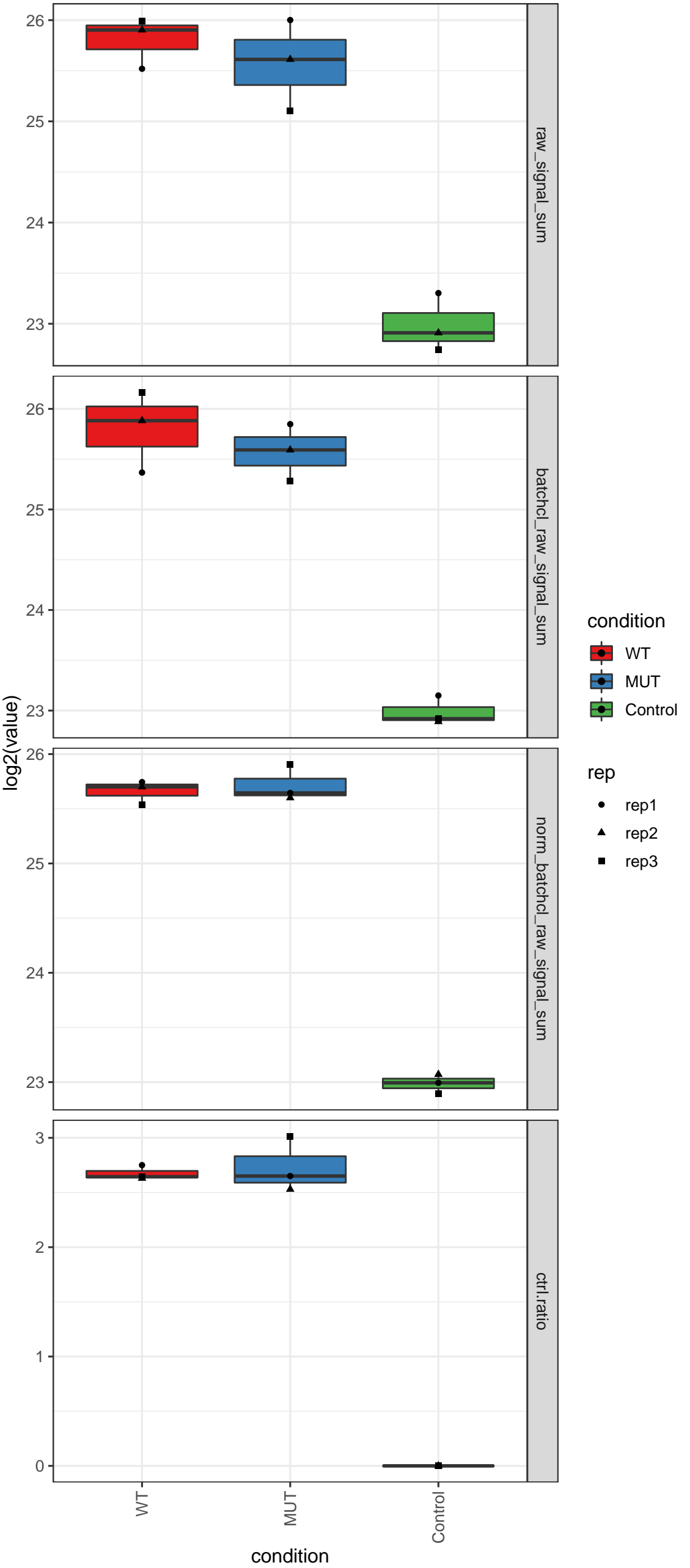
ATG8 – P38182

Autophagy-related protein 8 OS=*Saccharomyces cerevisiae* (strain ATCC 22016 / DSM 5780 / Kaz 5160)



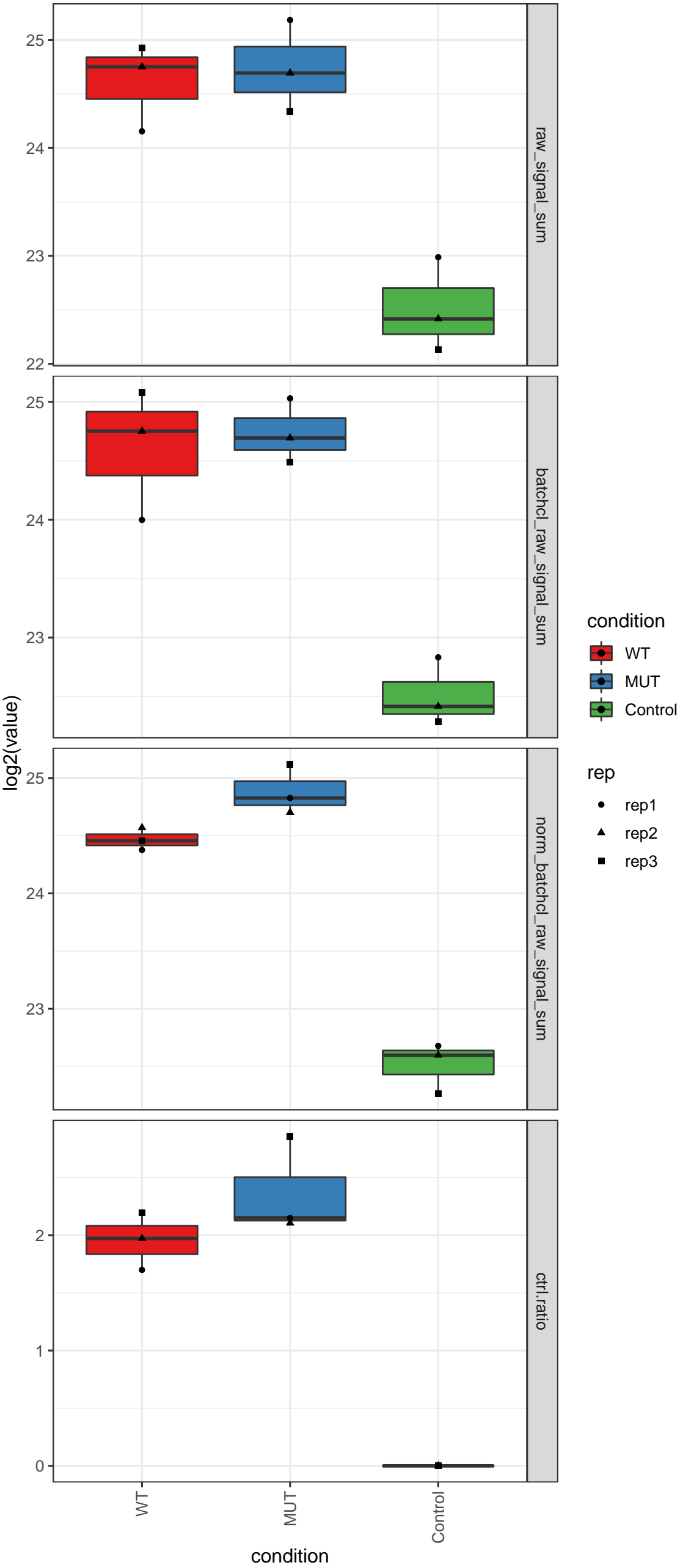
ATP1 – P07251

ATP synthase subunit alpha, mitochondrial OS=Saccharomyces cerevisiae



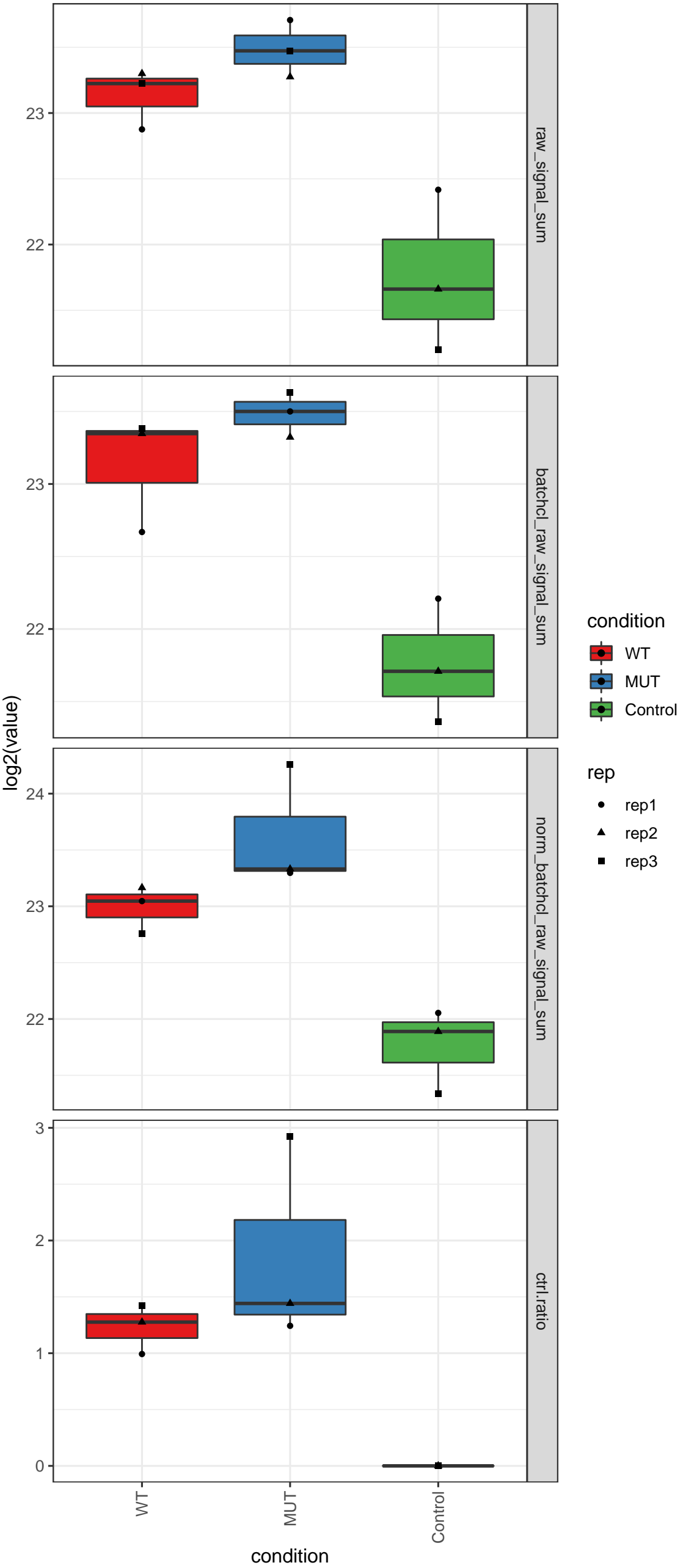
ATP2 – P00830

ATP synthase subunit beta, mitochondrial OS=Saccharomyces cerevisiae (



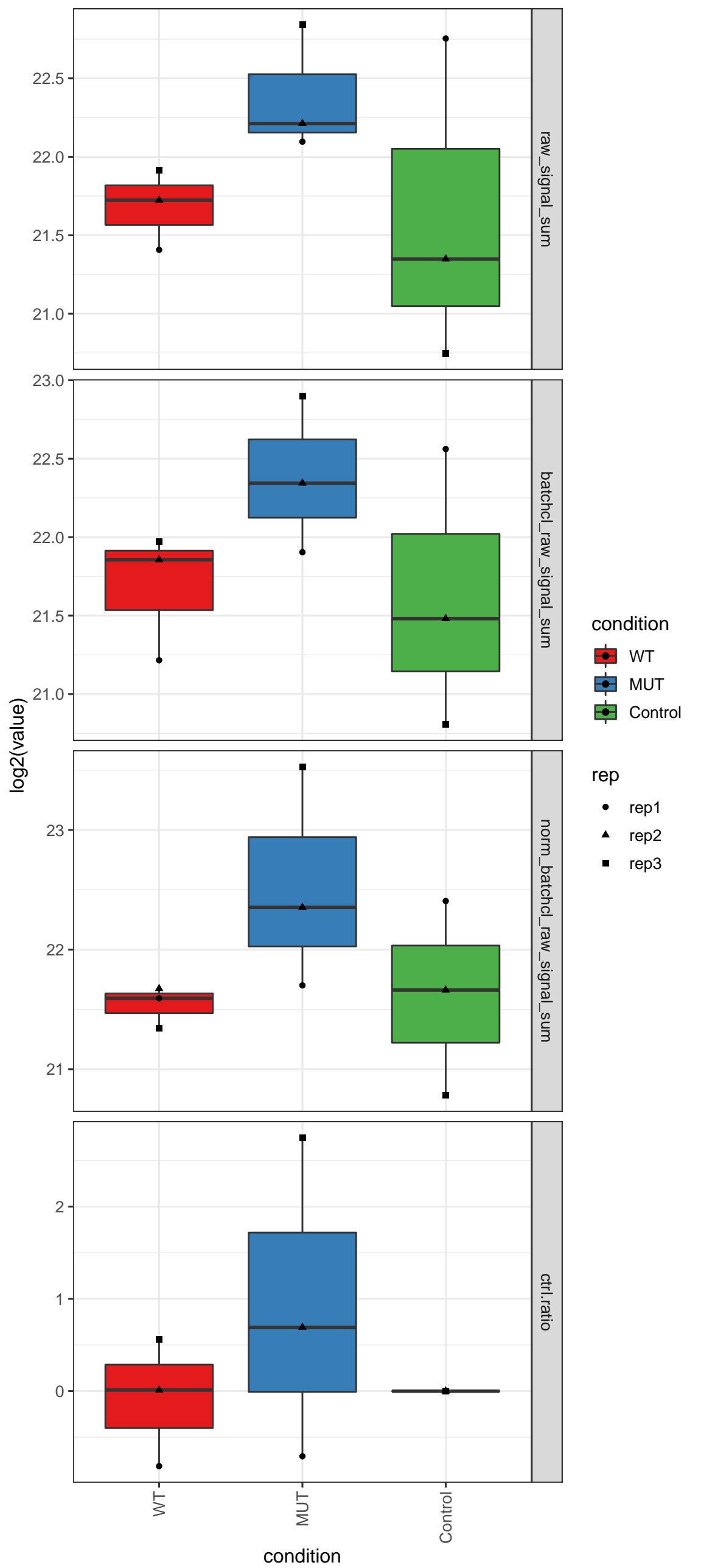
ATP3 – P38077

ATP synthase subunit gamma, mitochondrial OS=Saccharomyces cerevisia



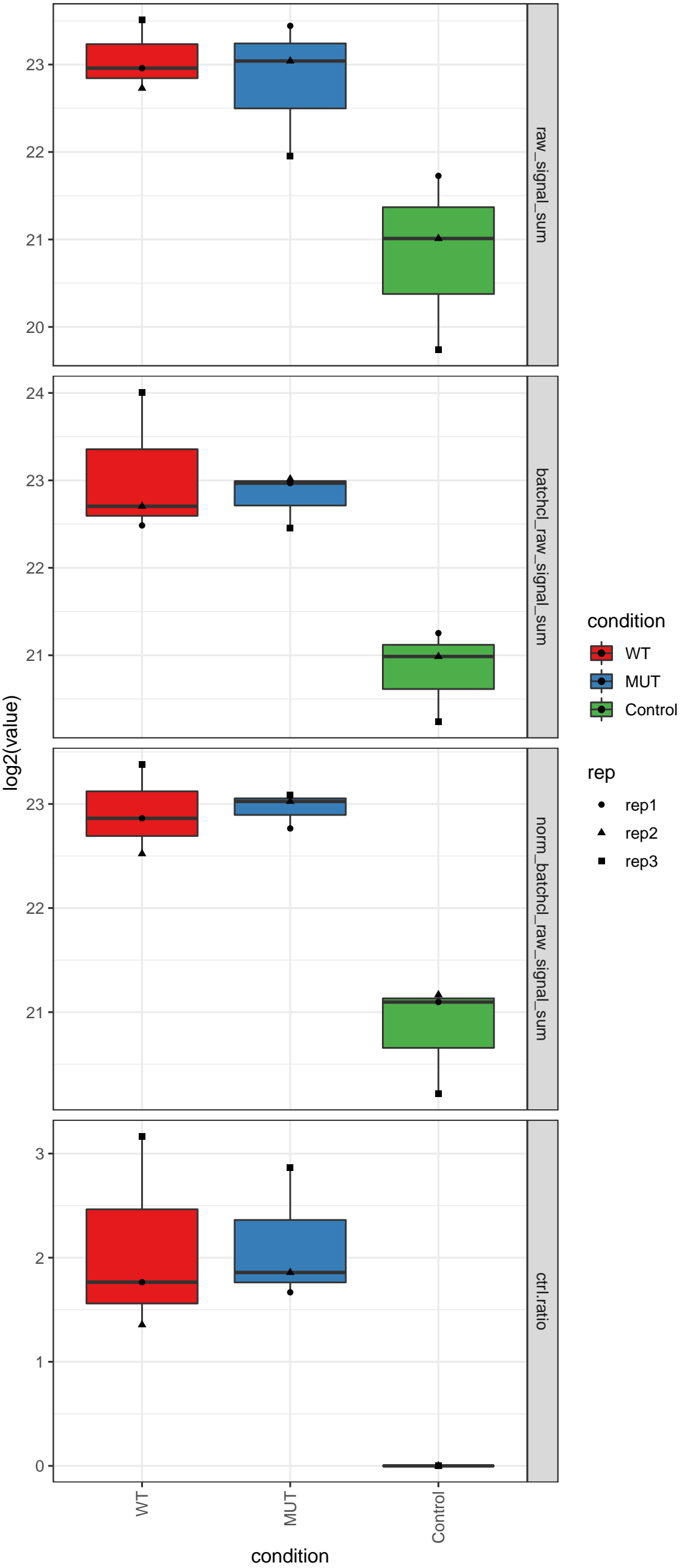
ATP5 – P09457

ATP synthase subunit 5, mitochondrial OS=*Saccharomyces cerevisiae* (s



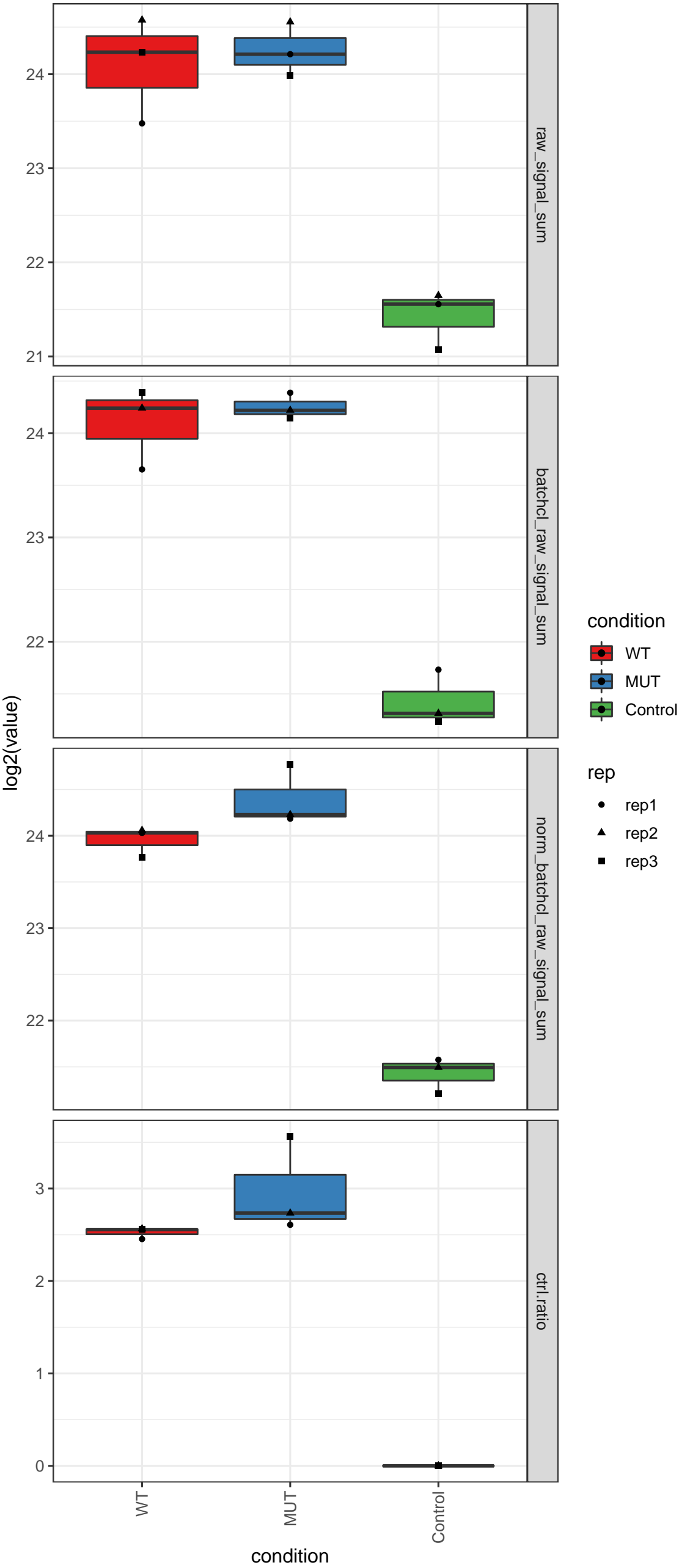
BAT2 – P47176

Branched-chain-amino-acid aminotransferase, cytosolic OS=Saccharomy



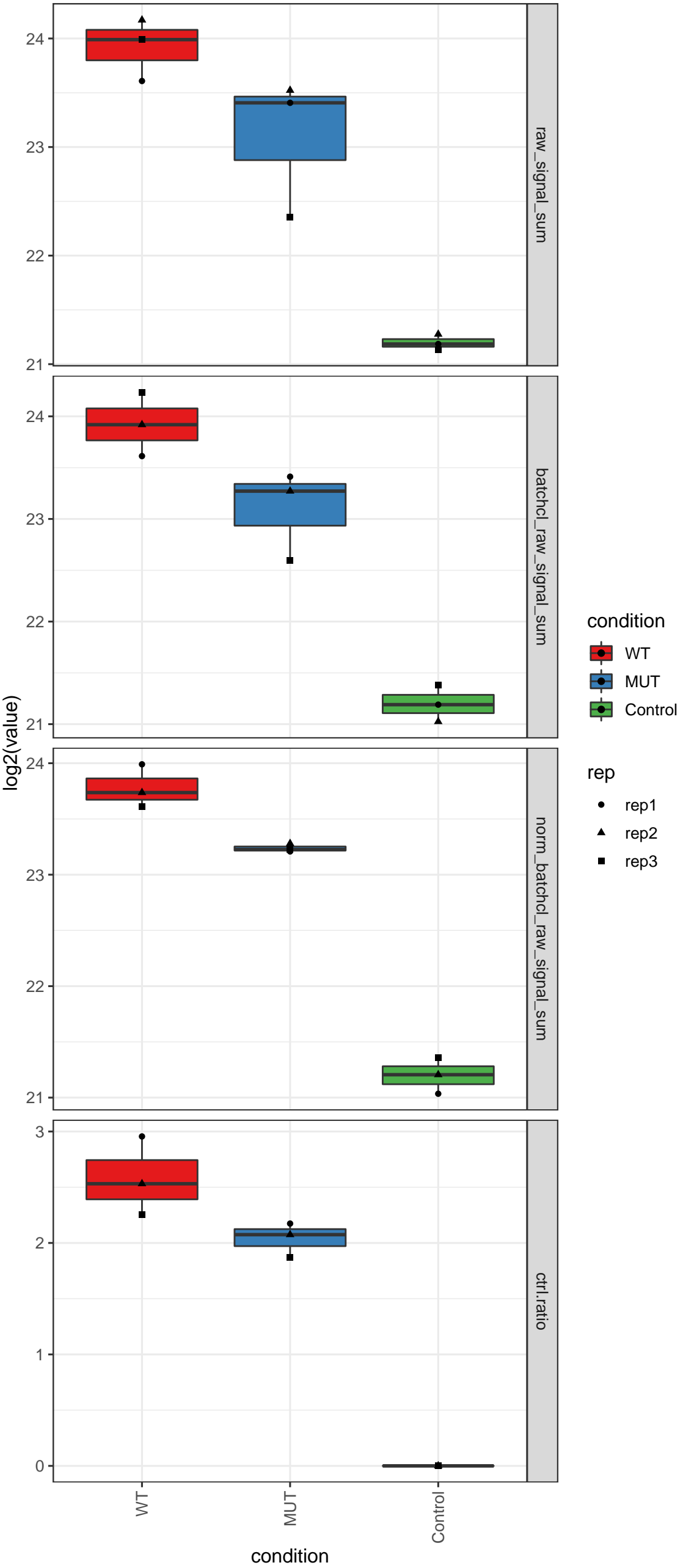
BBC1 – P47068

Myosin tail region–interacting protein MTI1 OS=*Saccharomyces cerevisiae*



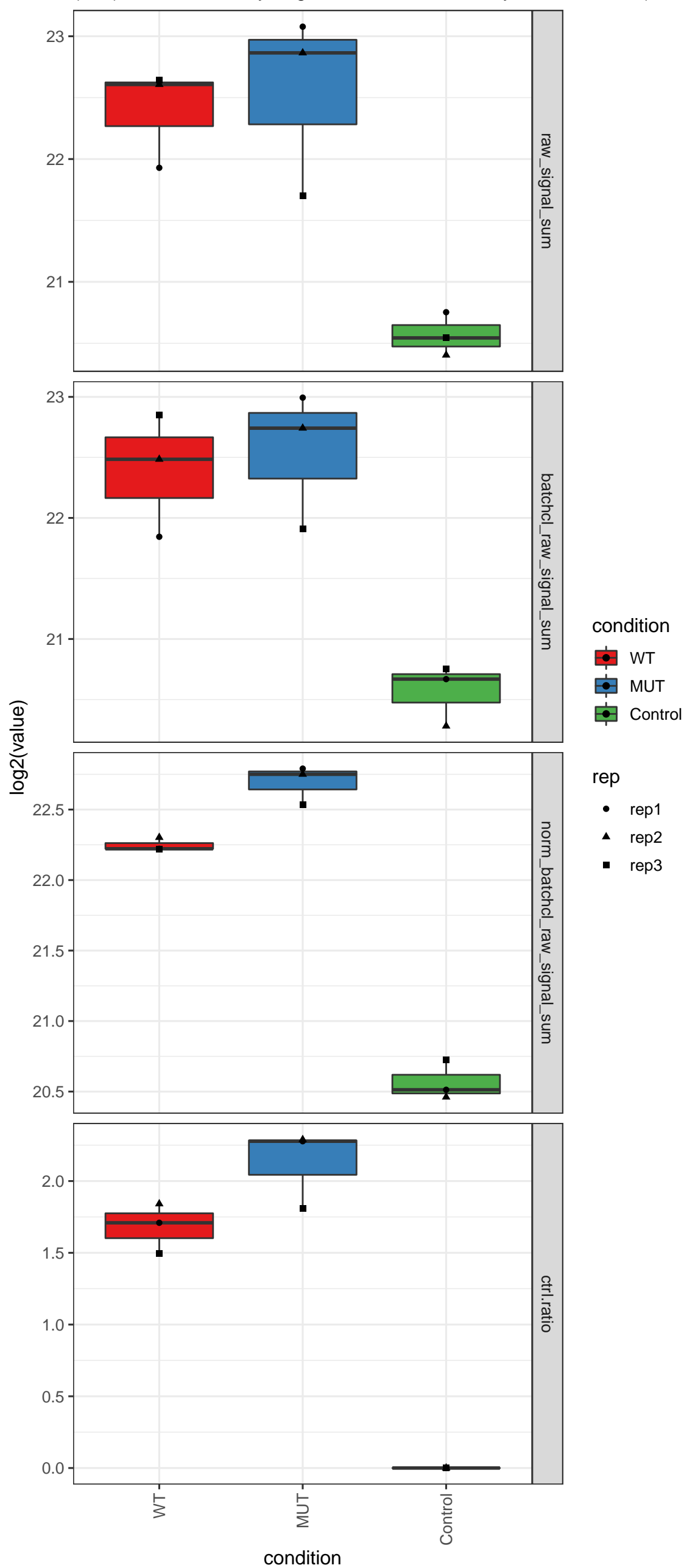
BDF1 – P35817

Bromodomain-containing factor 1 OS=*Saccharomyces cerevisiae* (strain A



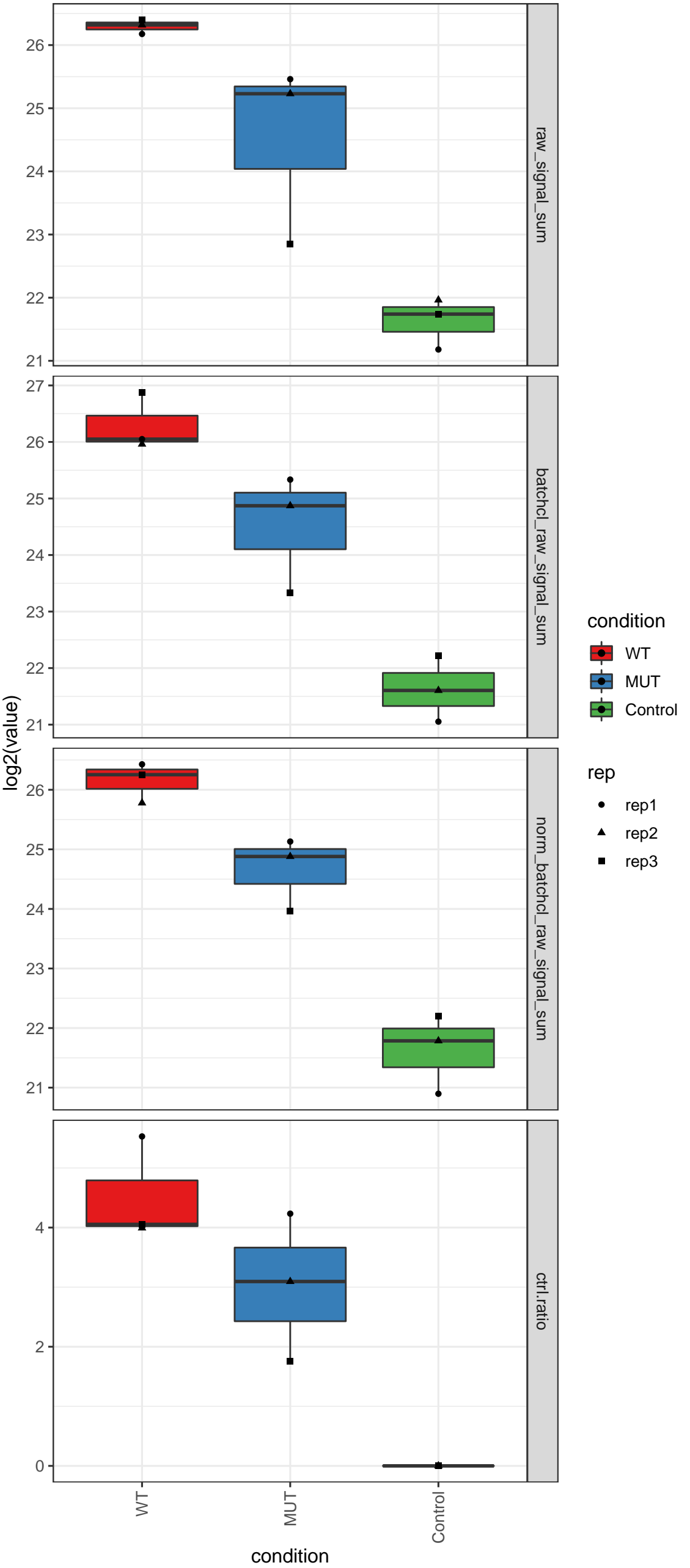
BDH1 – P39714

(R,R)–butanediol dehydrogenase OS=*Saccharomyces cerevisiae* (strain



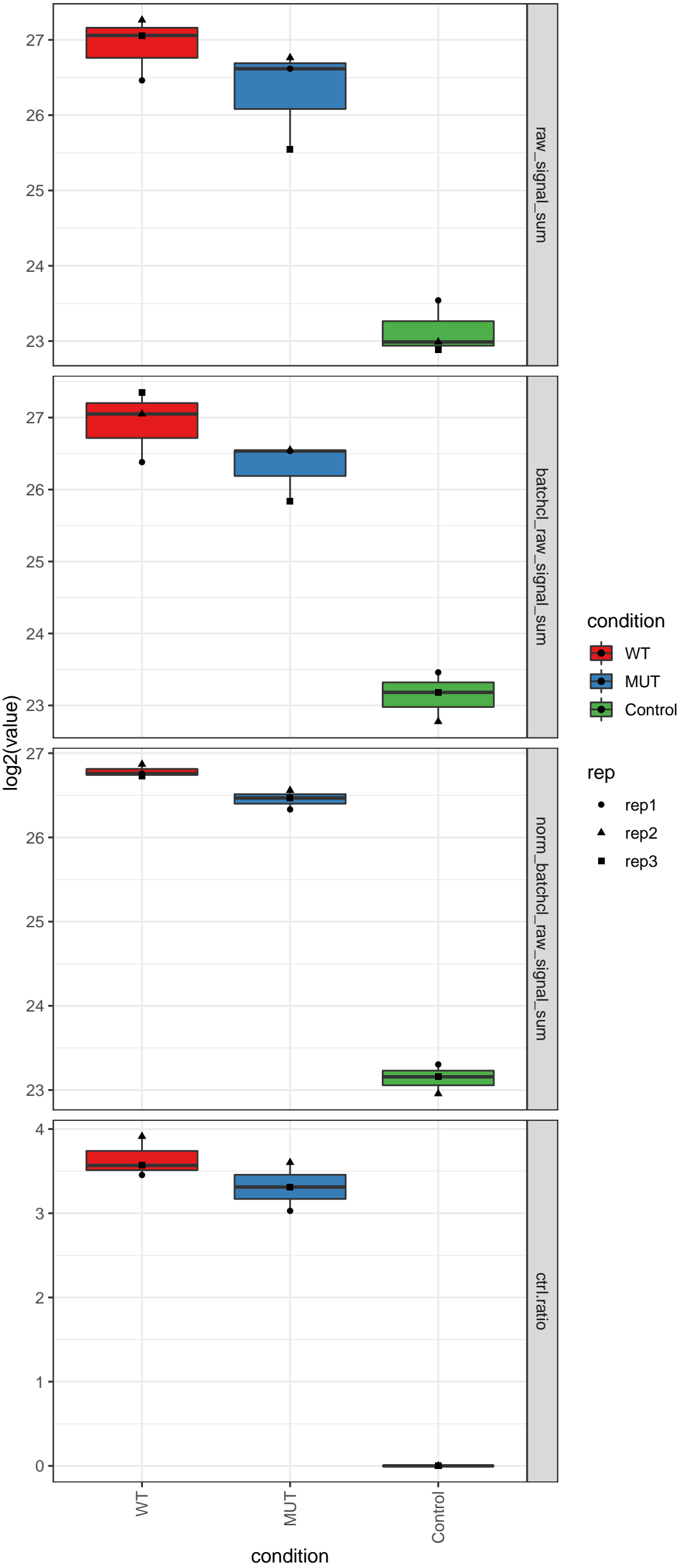
BDP1 – P46678

Transcription factor TFIIIB component B" OS=Saccharomyces cerevisiae (S



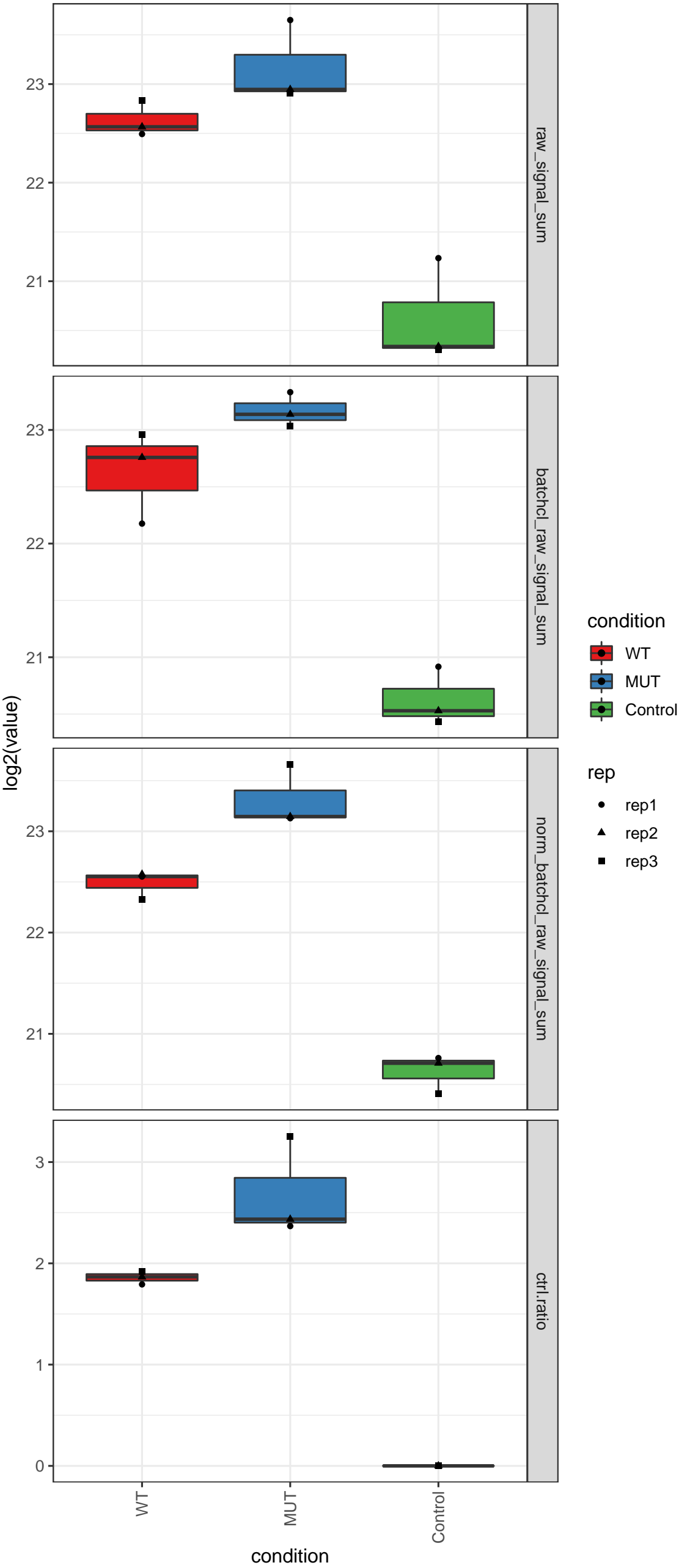
BFR1 – P38934

Nuclear segregation protein BFR1 OS=*Saccharomyces cerevisiae* (strain *A*)



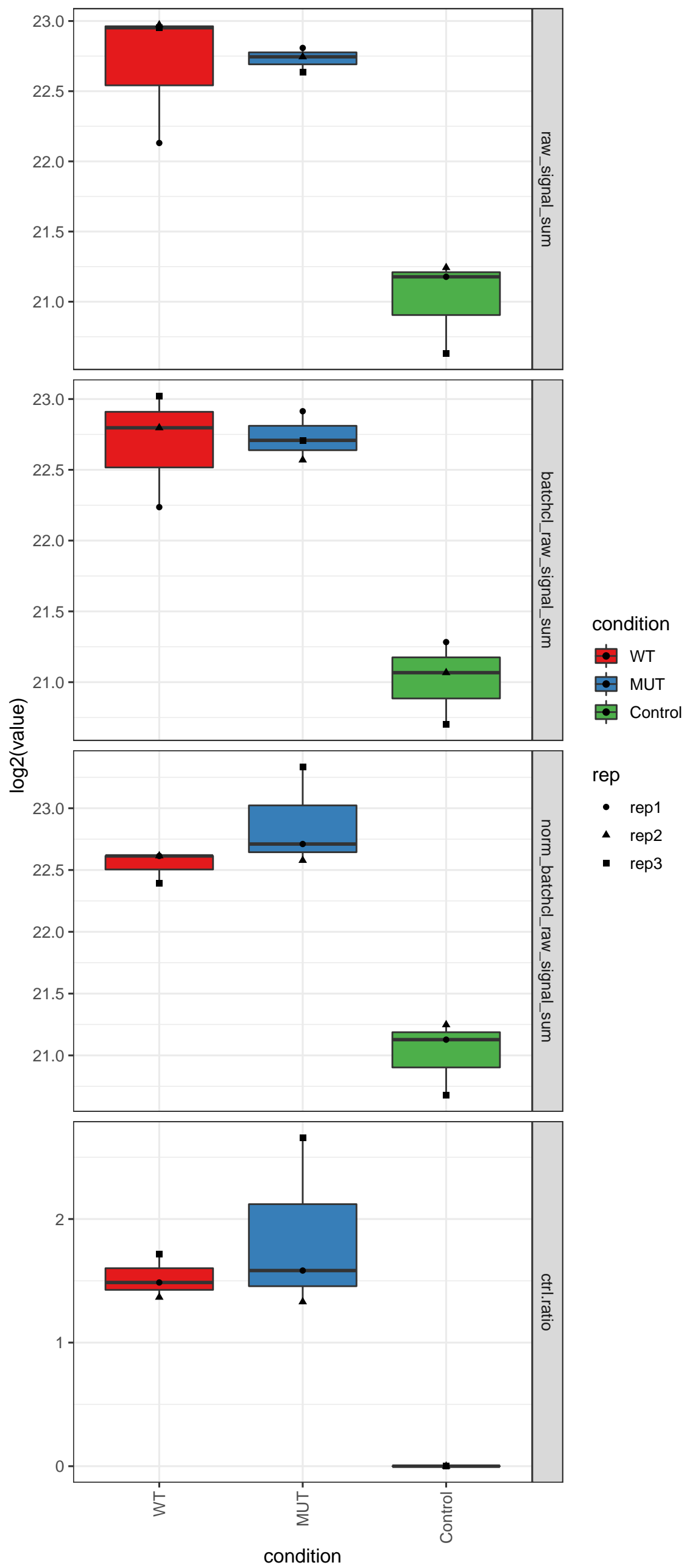
BGL2 – P15703

Glucan 1,3–beta–glucosidase OS=*Saccharomyces cerevisiae* (strain ATCC



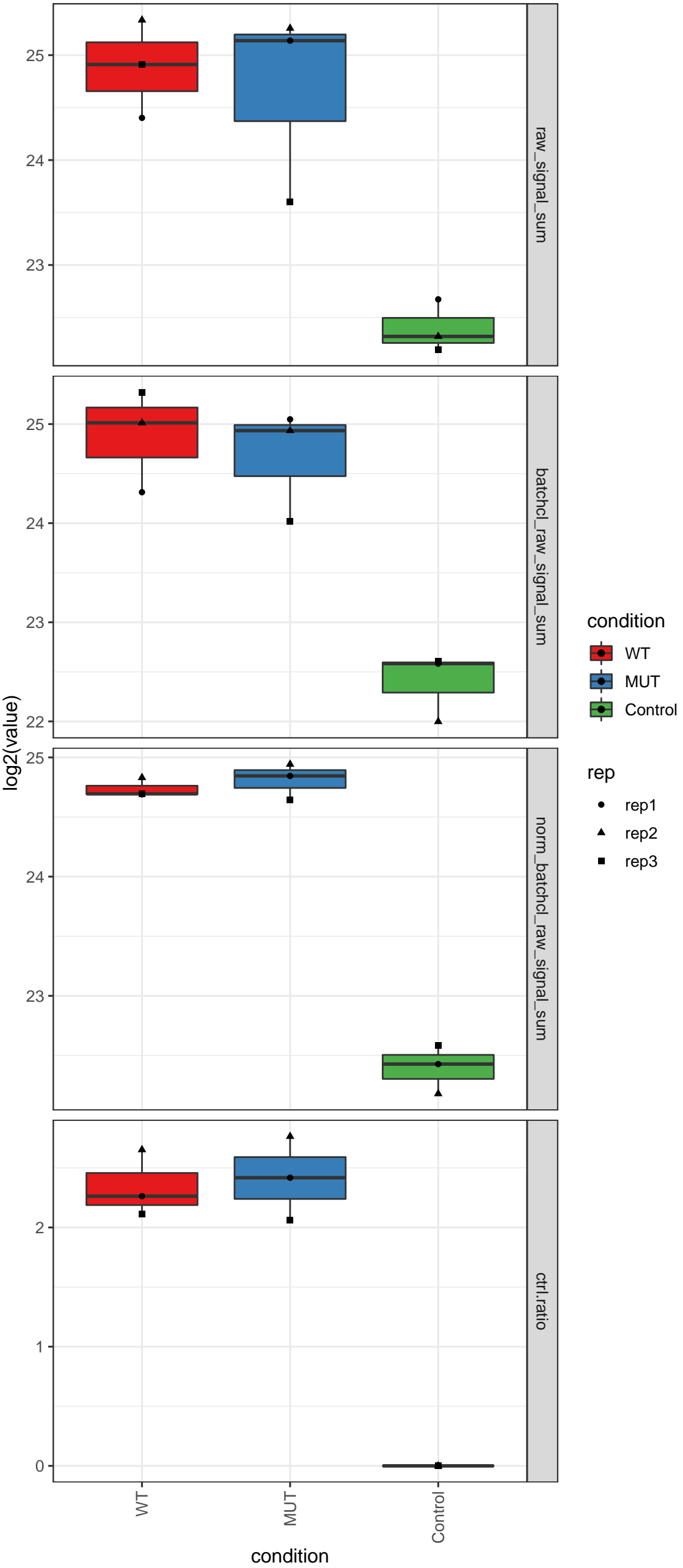
BMH1 – P29311

Protein BMH1 OS=*Saccharomyces cerevisiae* (strain ATCC 204508 / S288c)



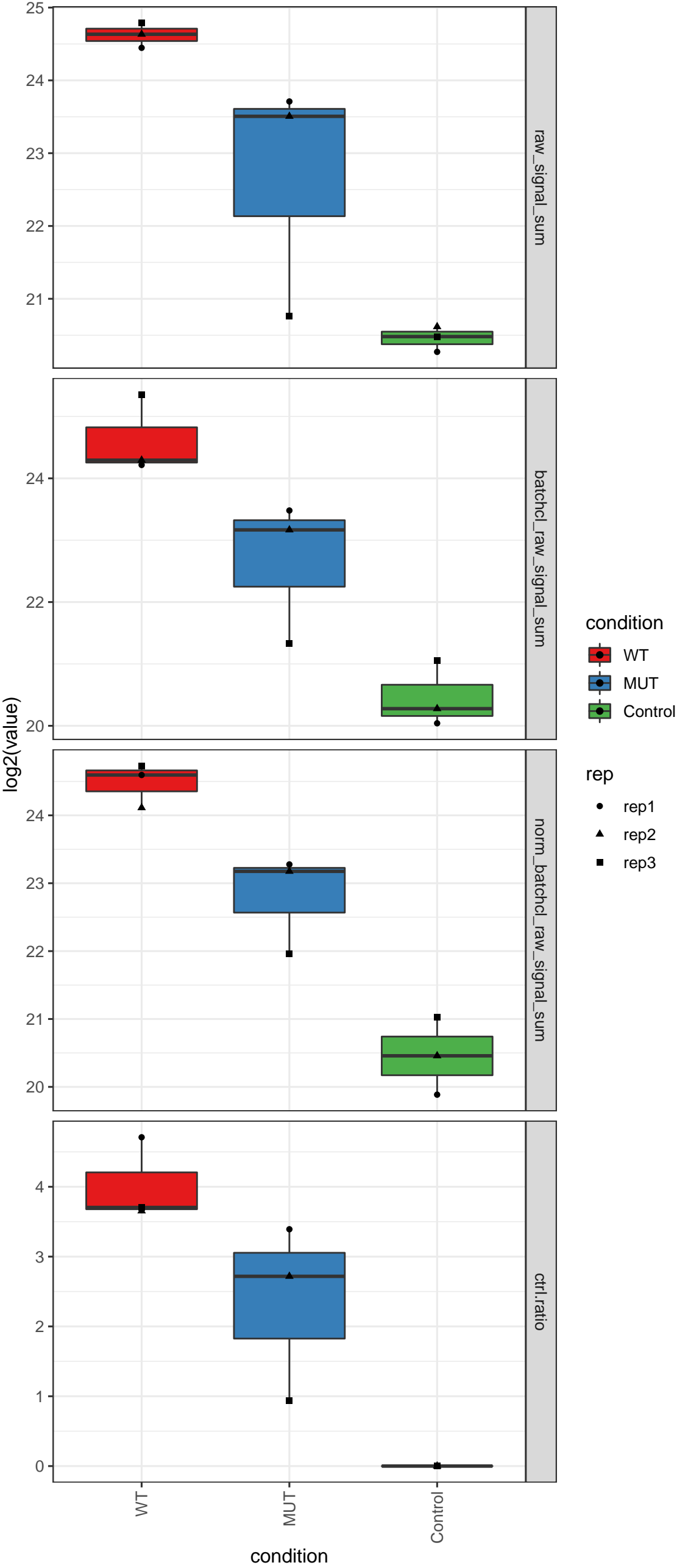
BRE1 – Q07457

E3 ubiquitin–protein ligase BRE1 OS=*Saccharomyces cerevisiae* (strain ATCC 24843)



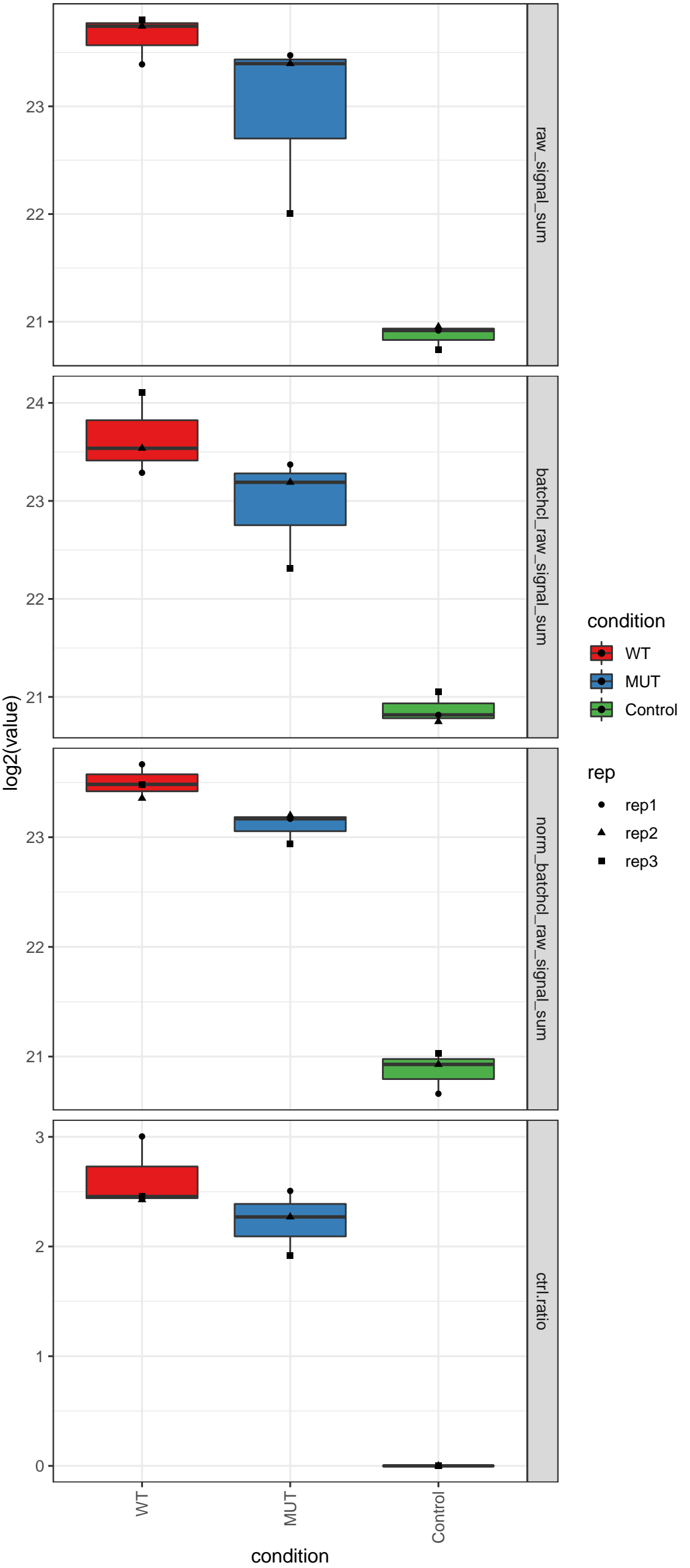
BRF1 – P29056

Transcription factor IIIB 70 kDa subunit OS=Saccharomyces cerevisiae (str



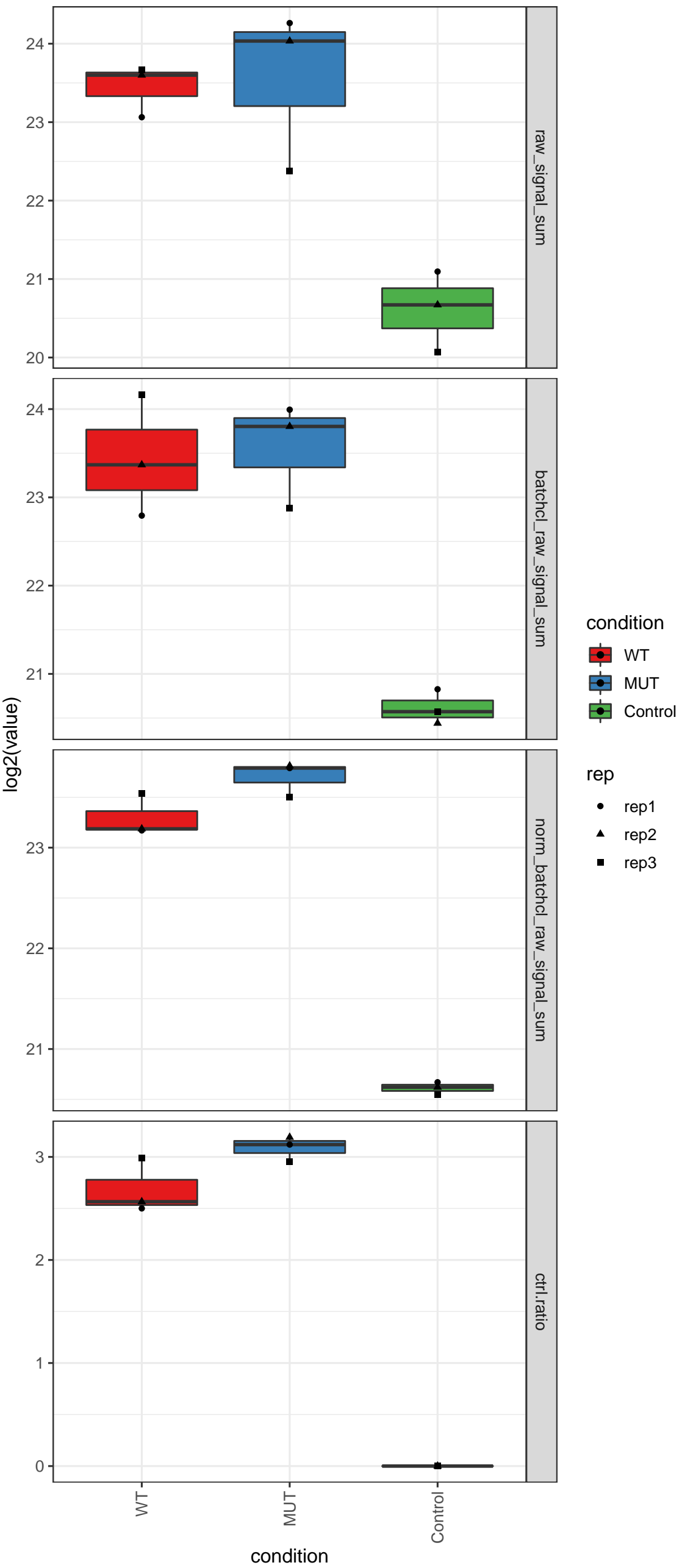
BRN1 – P38170

Condensin complex subunit 2 OS=*Saccharomyces cerevisiae* (strain ATCC



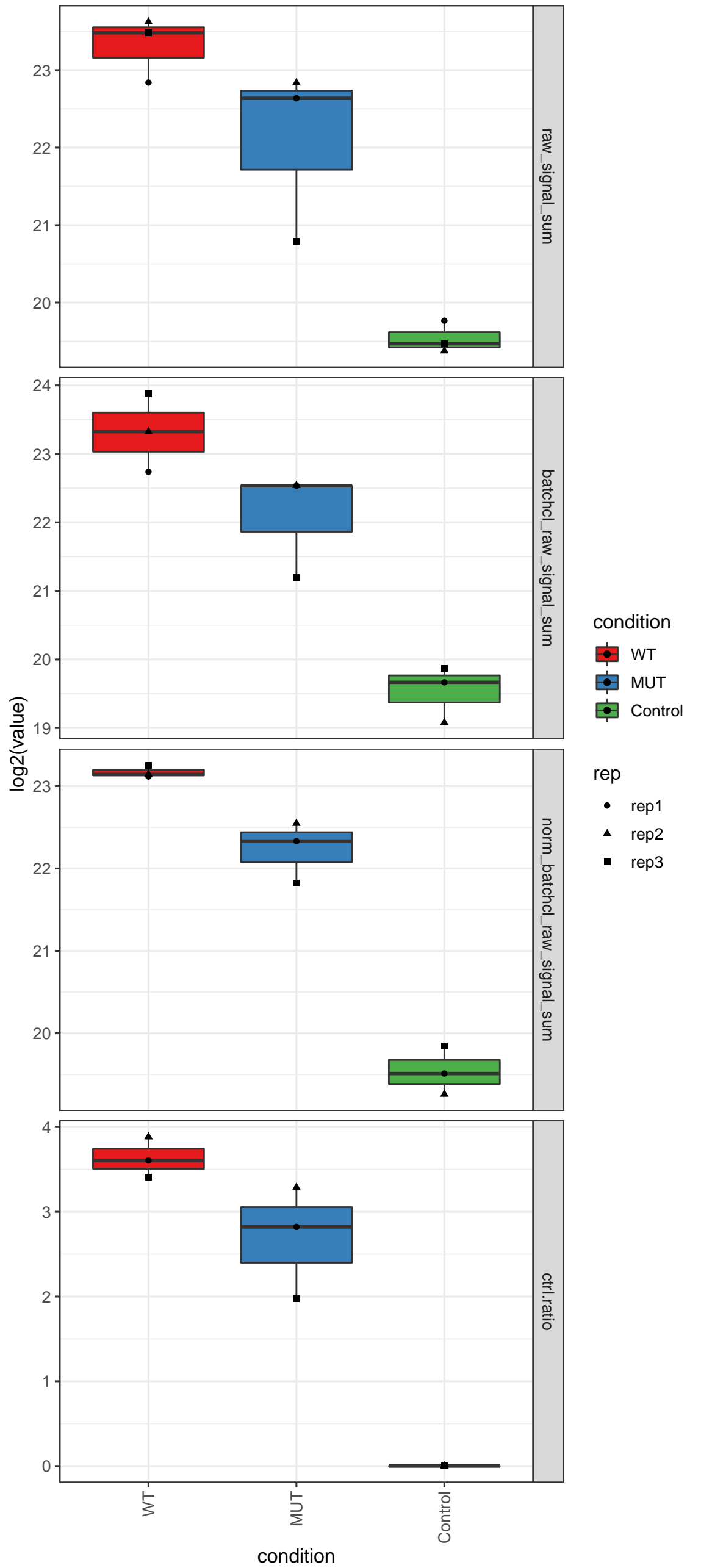
BRX1 – Q08235

Ribosome biogenesis protein BRX1 OS=*Saccharomyces cerevisiae* (strain



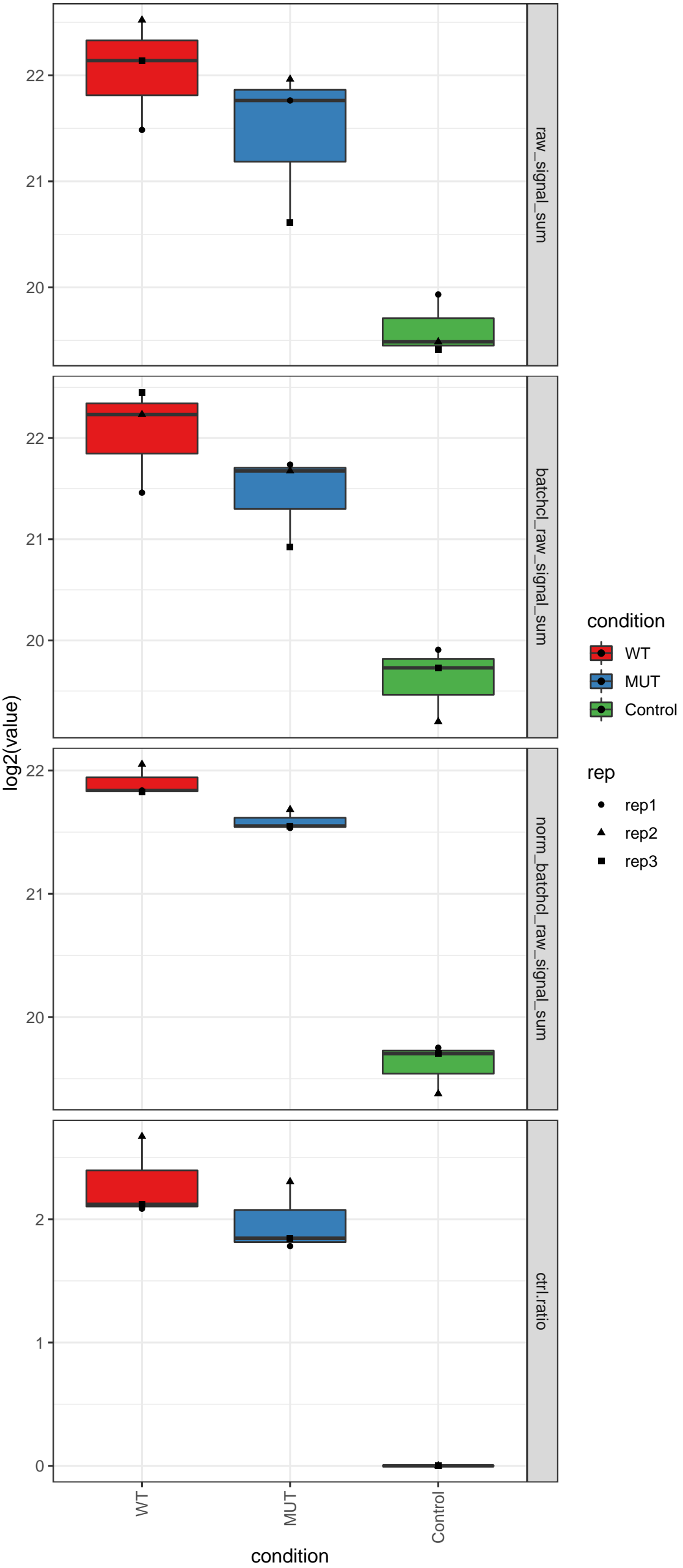
CAD1 – P24813

AP-1-like transcription activator YAP2 OS=Saccharomyces cerevisiae (str



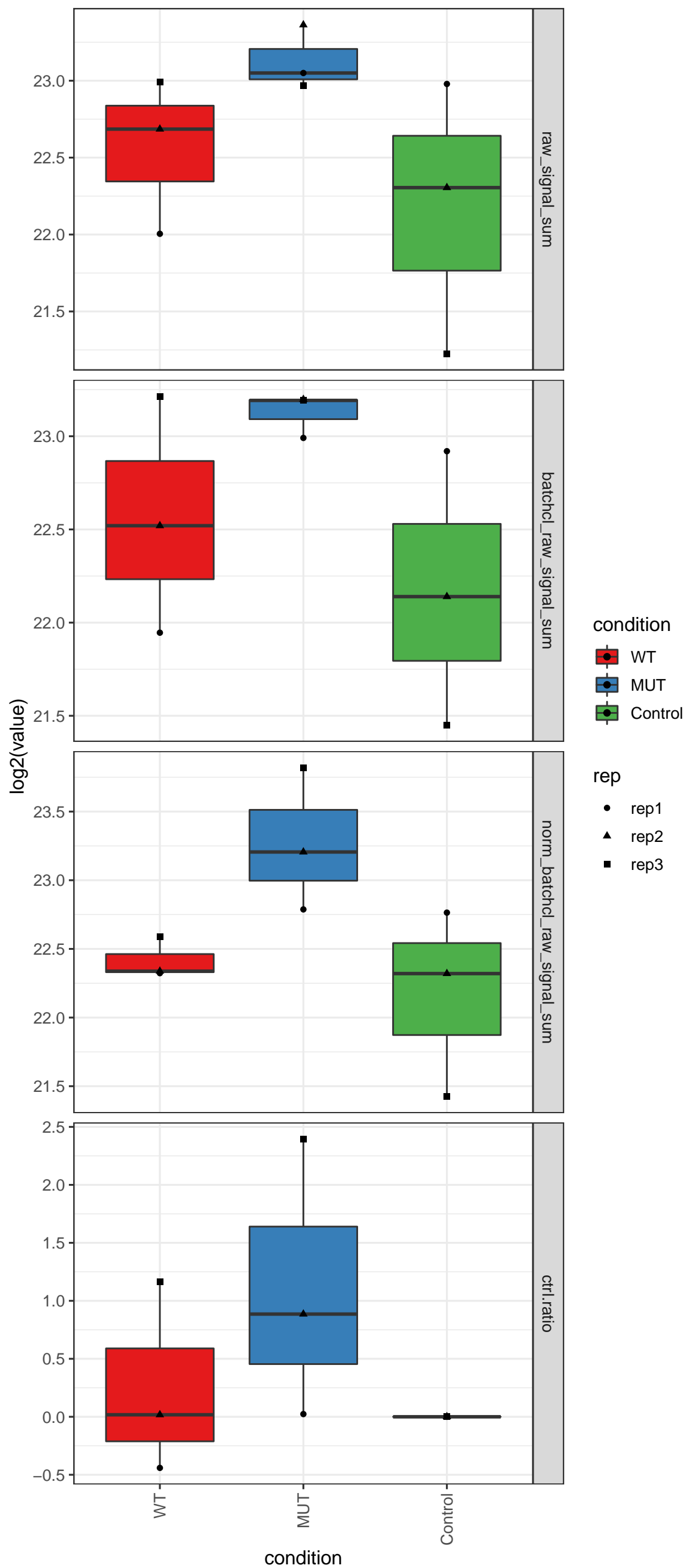
CAM1 – P29547

Elongation factor 1–gamma 1 OS=Saccharomyces cerevisiae (strain ATCC



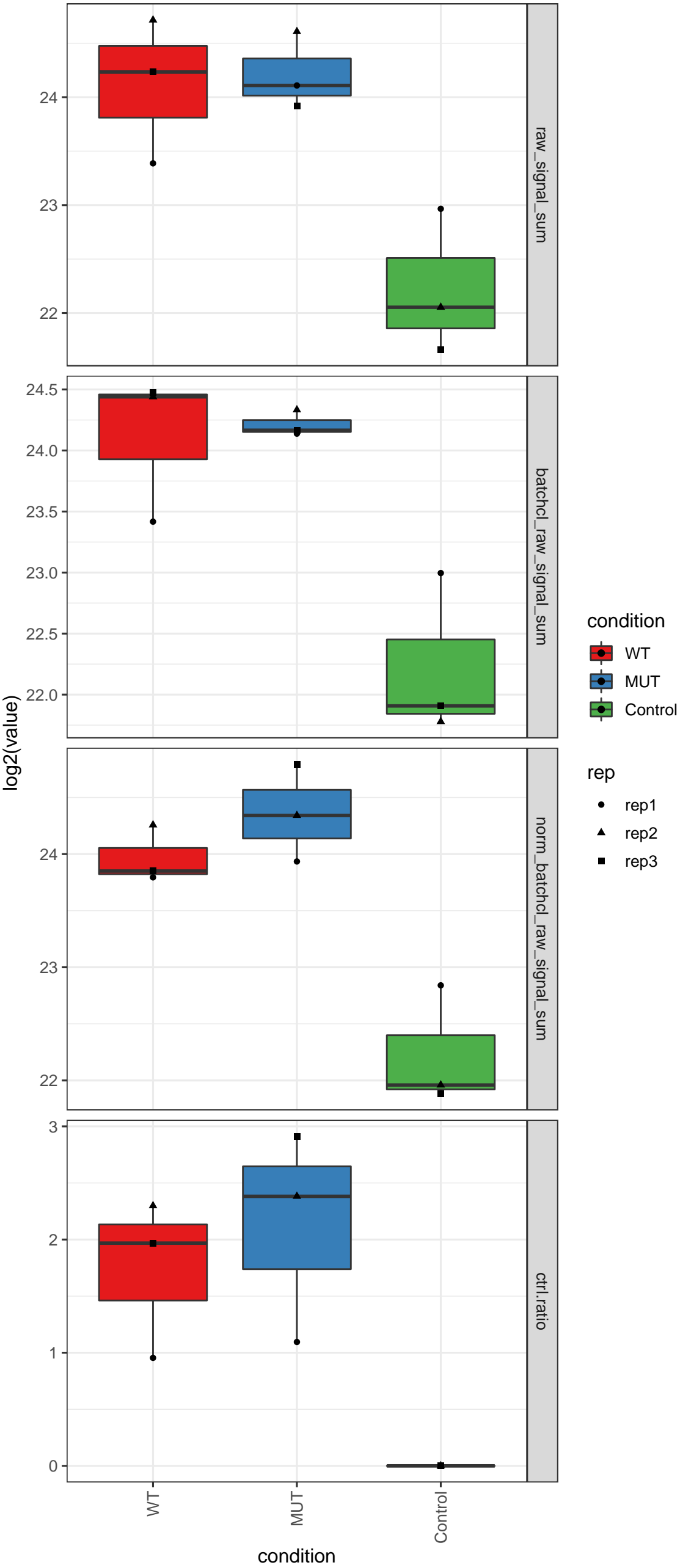
CAR1 – P00812

Arginase OS=*Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) C



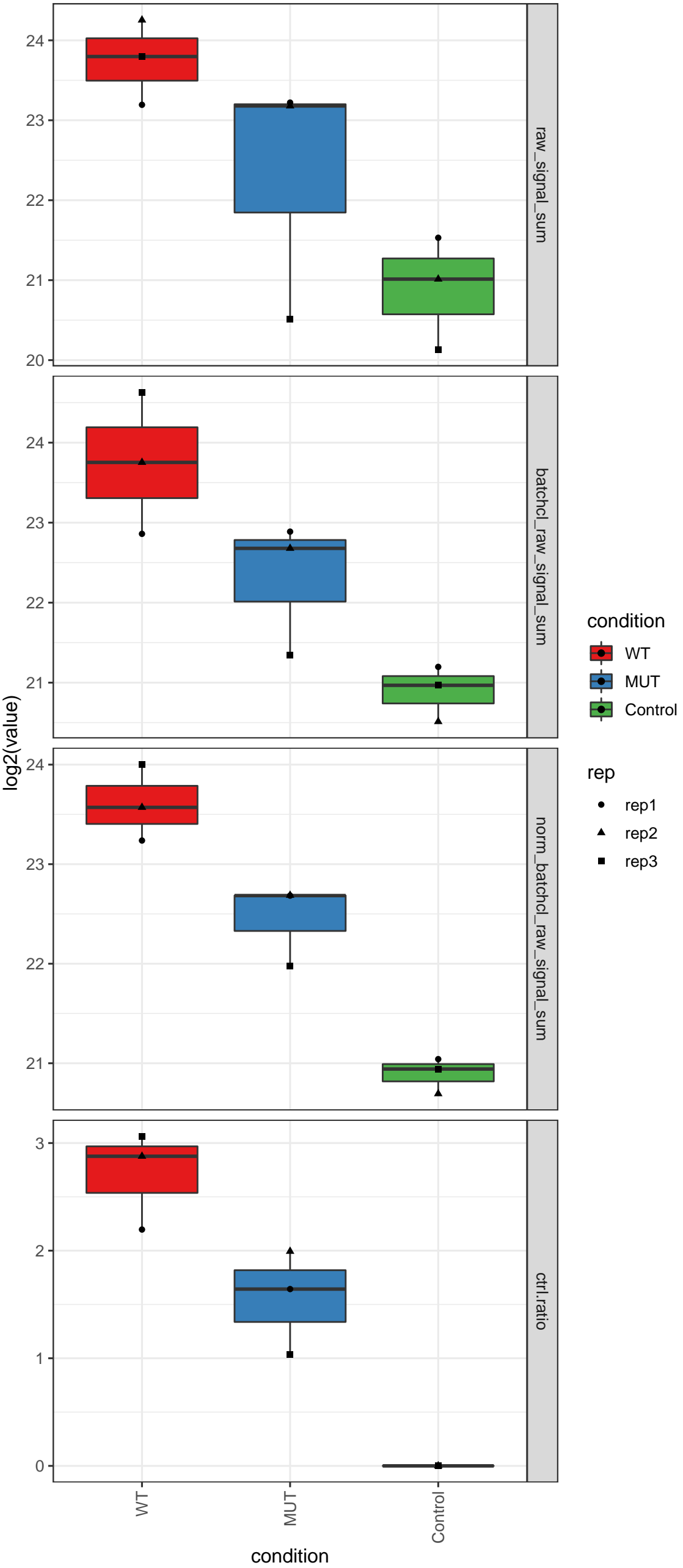
CAT2 – P32796|P32796–2

Carnitine O–acetyltransferase, mitochondrial OS=Saccharomyces cerevis



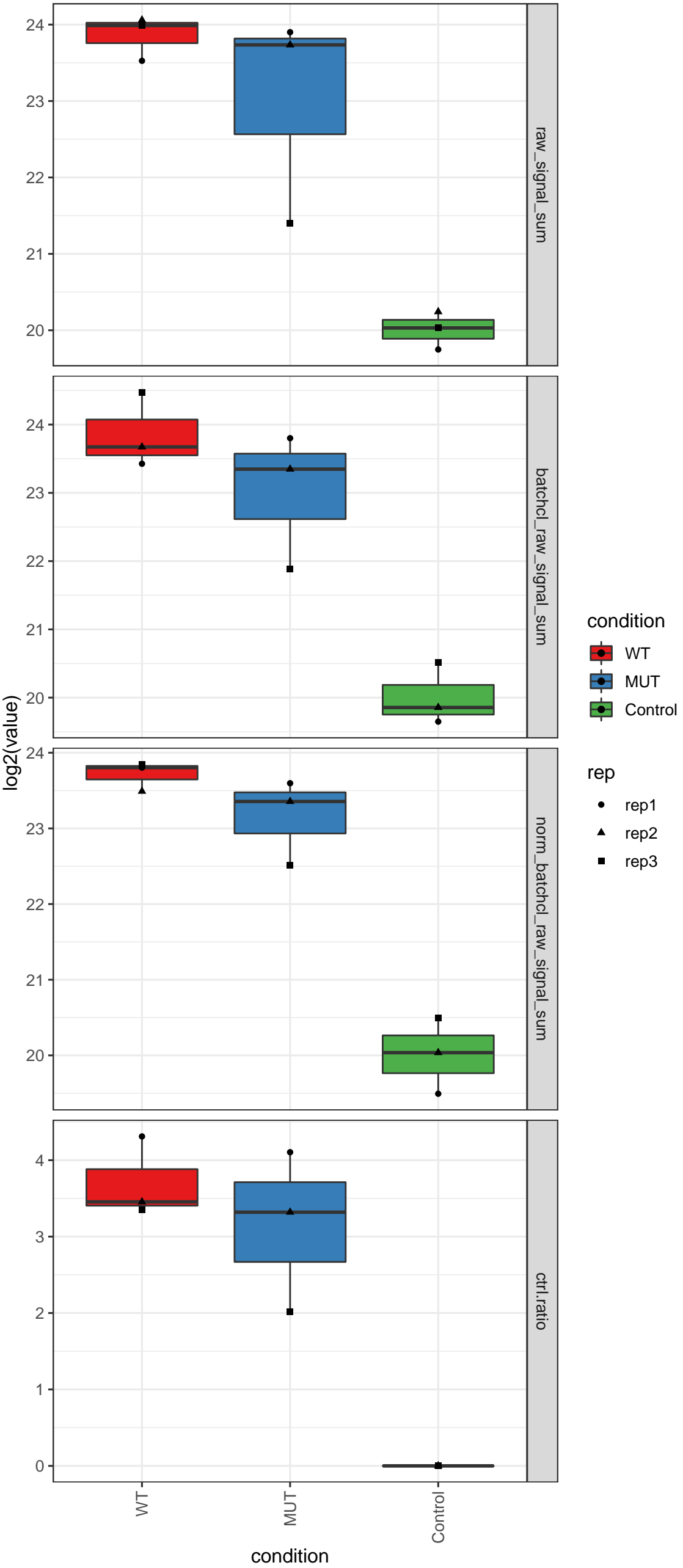
CBF1 – P17106

Centromere-binding protein 1 OS=*Saccharomyces cerevisiae* (strain ATCC 25716)



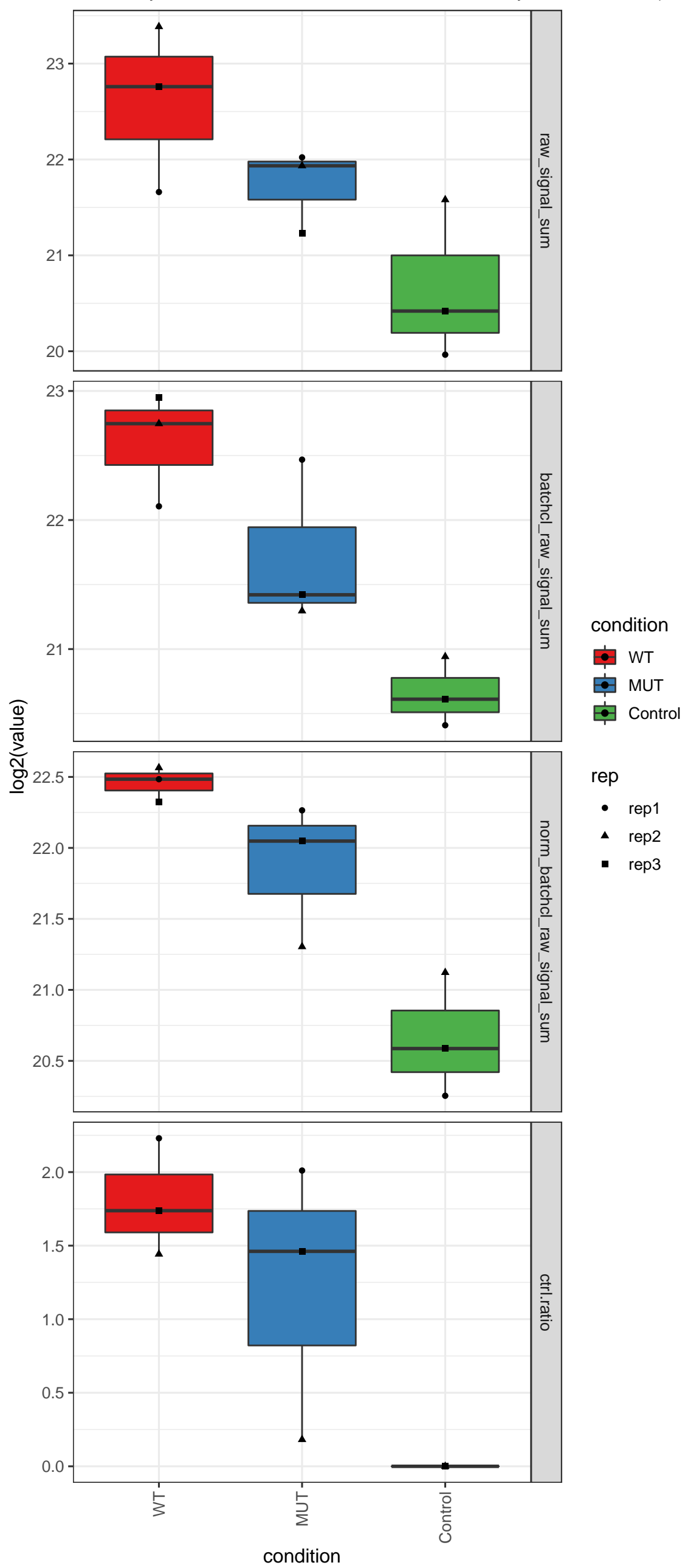
CBF5 – P33322

H/ACA ribonucleoprotein complex subunit 4 OS=*Saccharomyces cerevisiae*



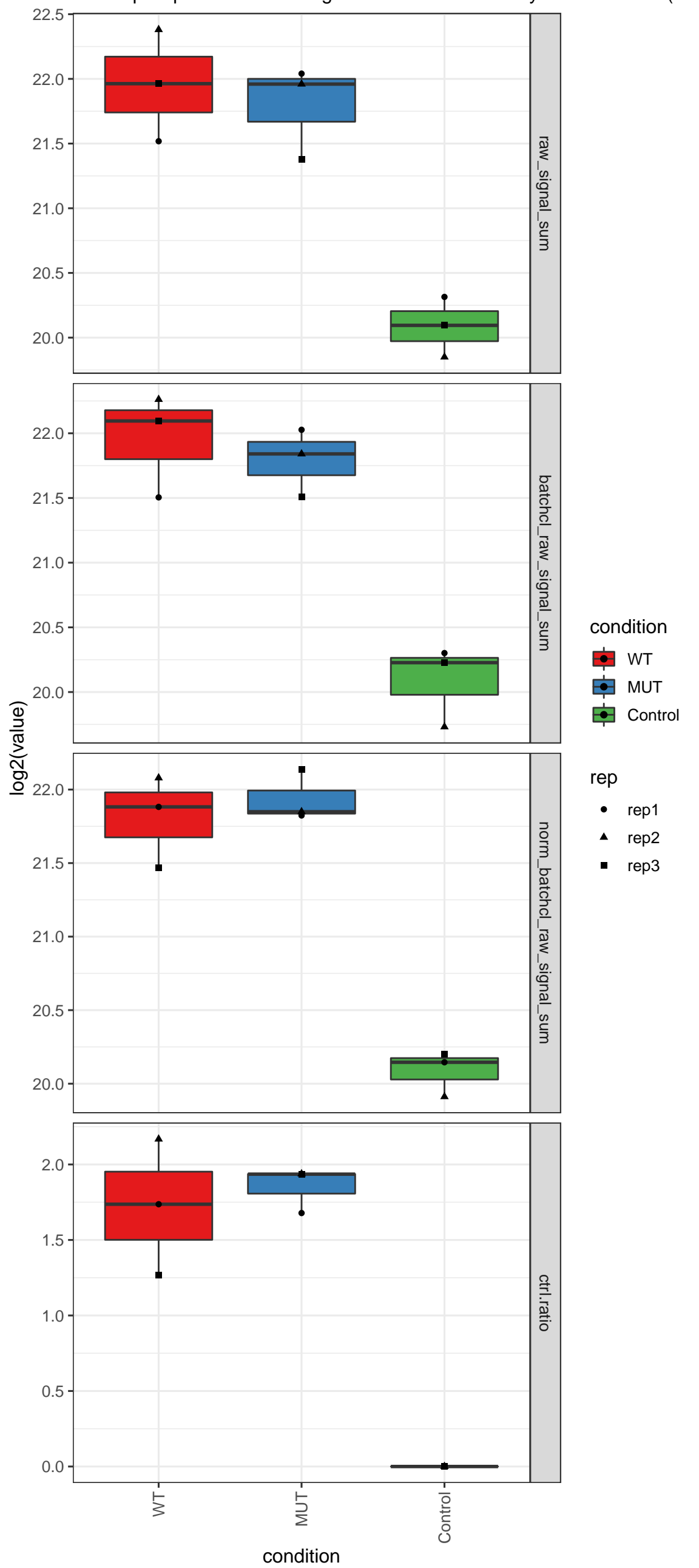
CBR1 – P38626

NADH-cytochrome b5 reductase 1 OS=*Saccharomyces cerevisiae* (strain



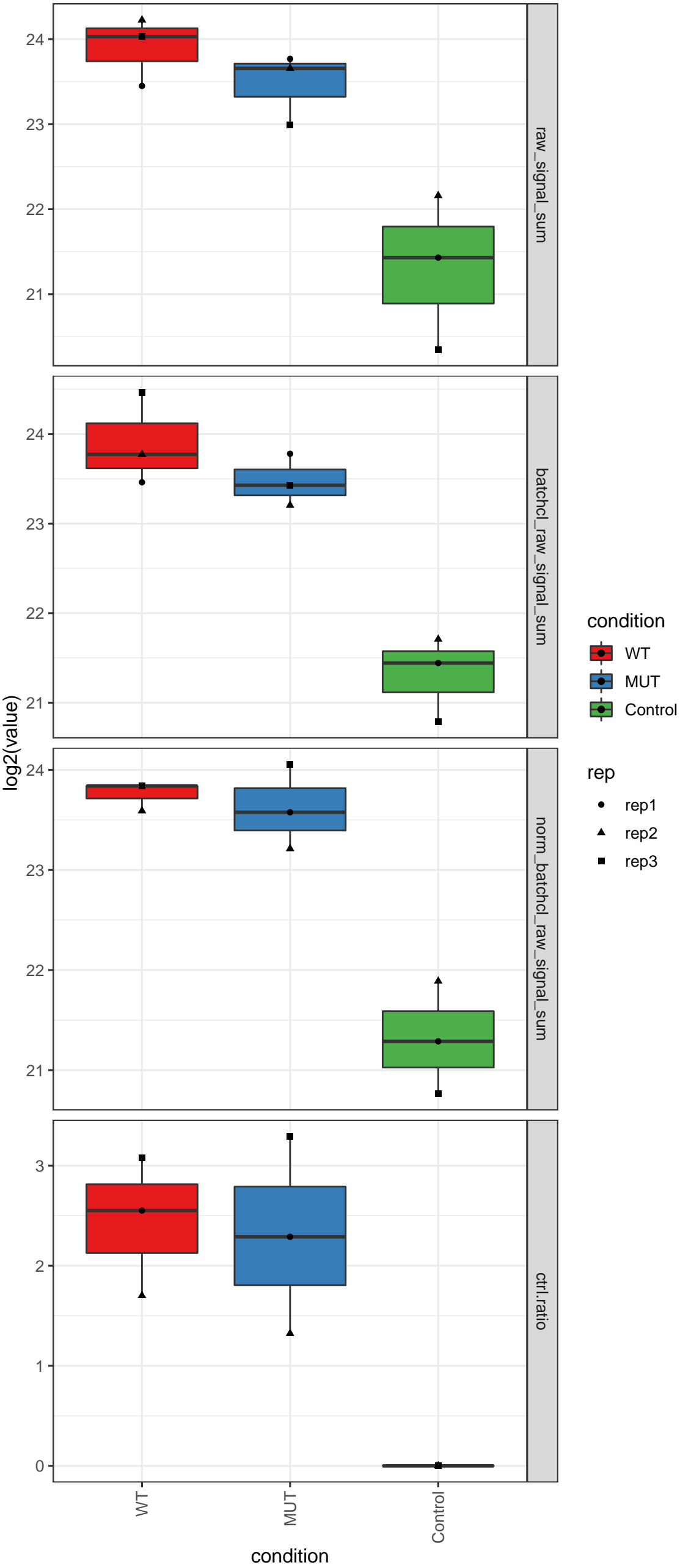
CCT3 – P39077

T-complex protein 1 subunit gamma OS=*Saccharomyces cerevisiae* (strain



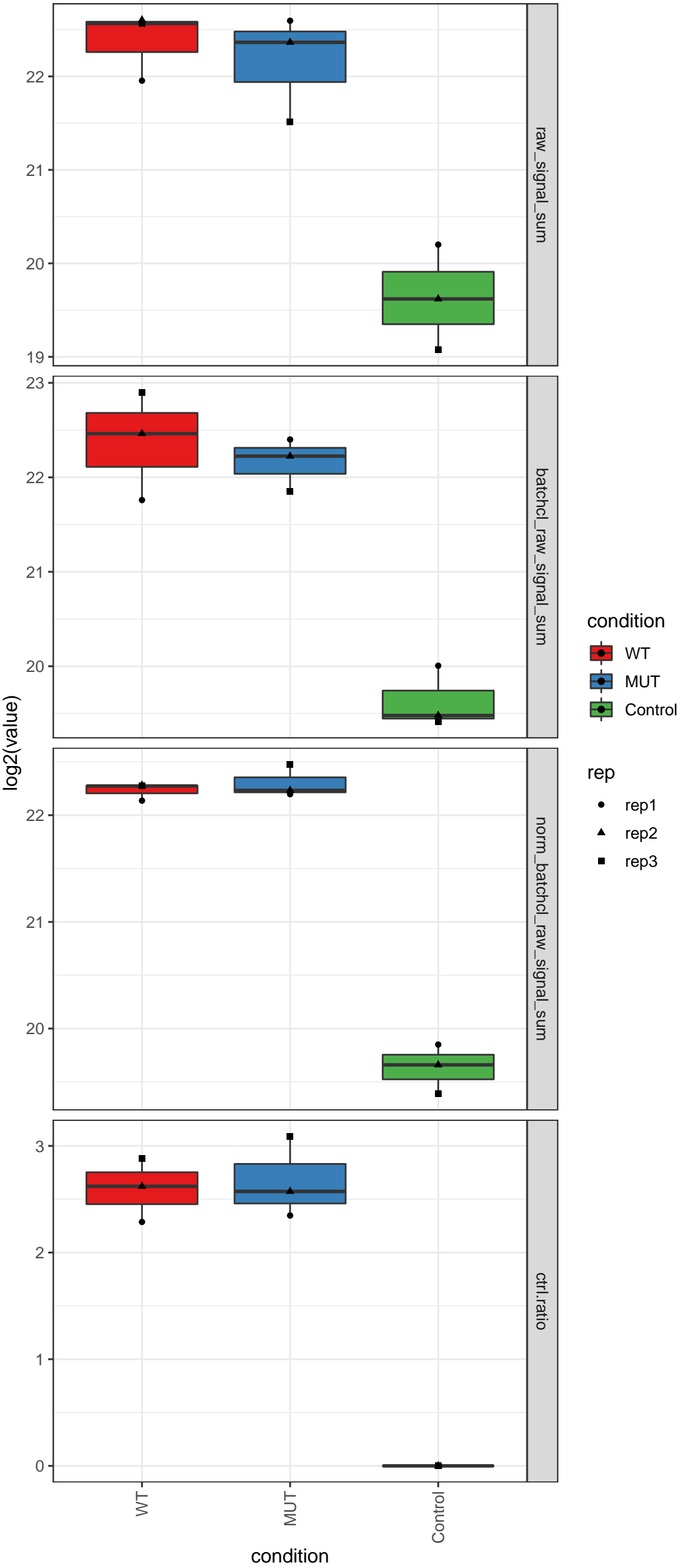
CCT4 – P39078

T-complex protein 1 subunit delta OS=*Saccharomyces cerevisiae* (strain A



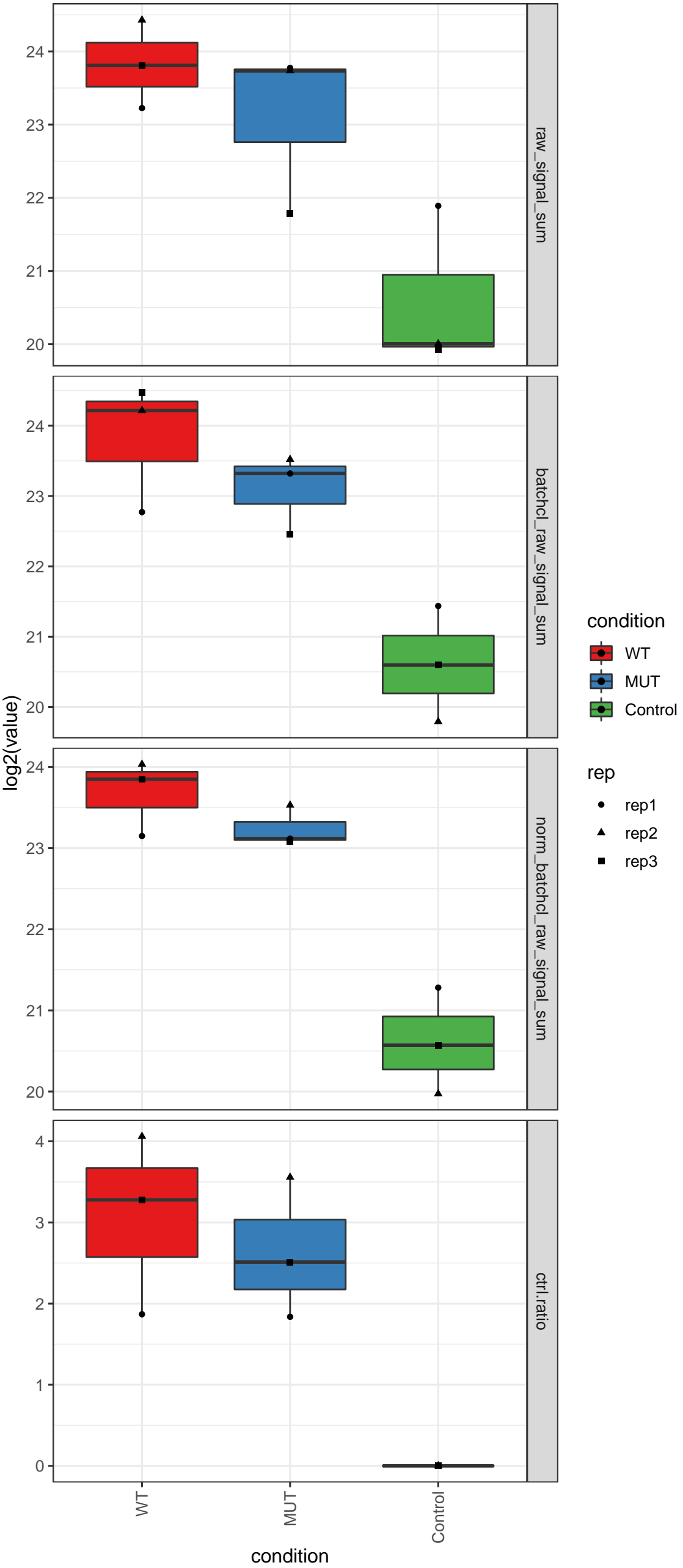
CCT8 – P47079

T-complex protein 1 subunit theta OS=*Saccharomyces cerevisiae* (strain A



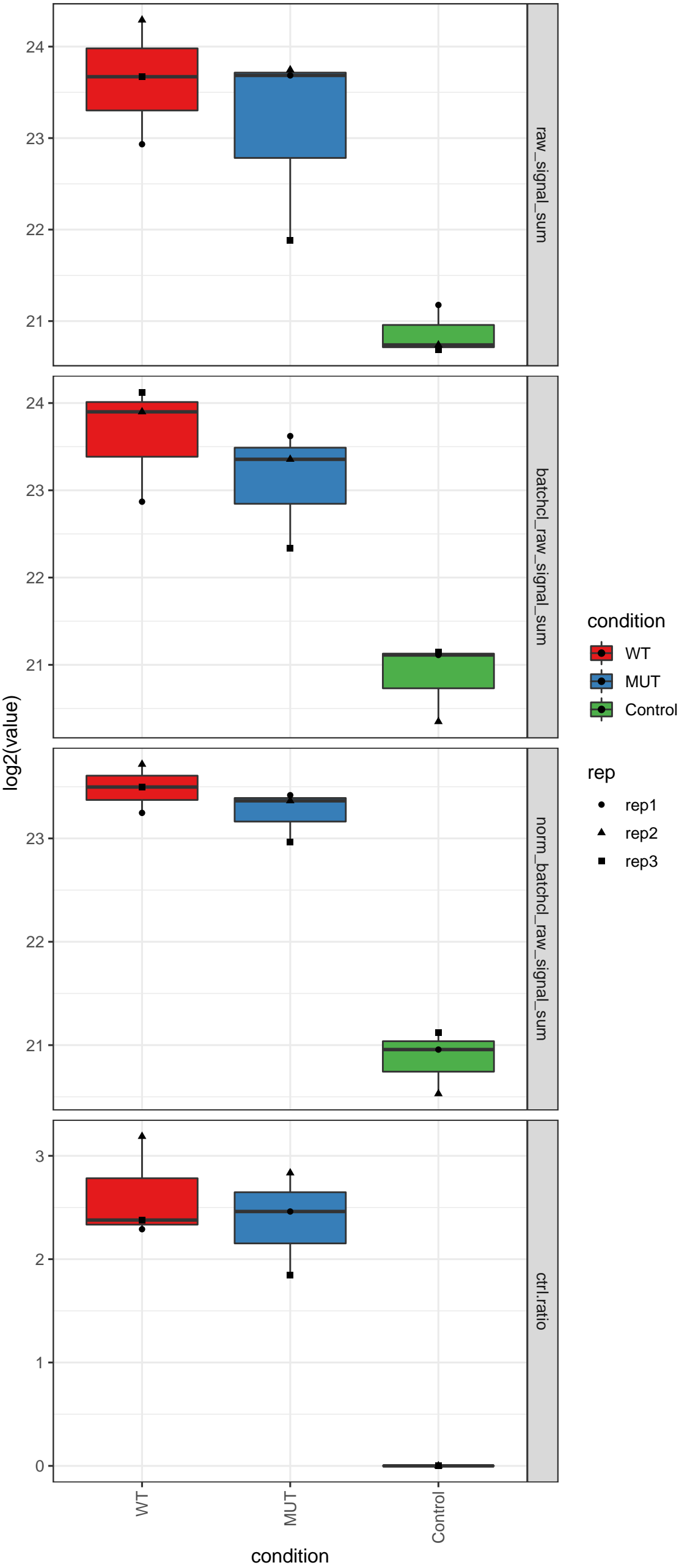
CDC10 – P25342

Cell division control protein 10 OS=*Saccharomyces cerevisiae* (strain ATCC 25465)



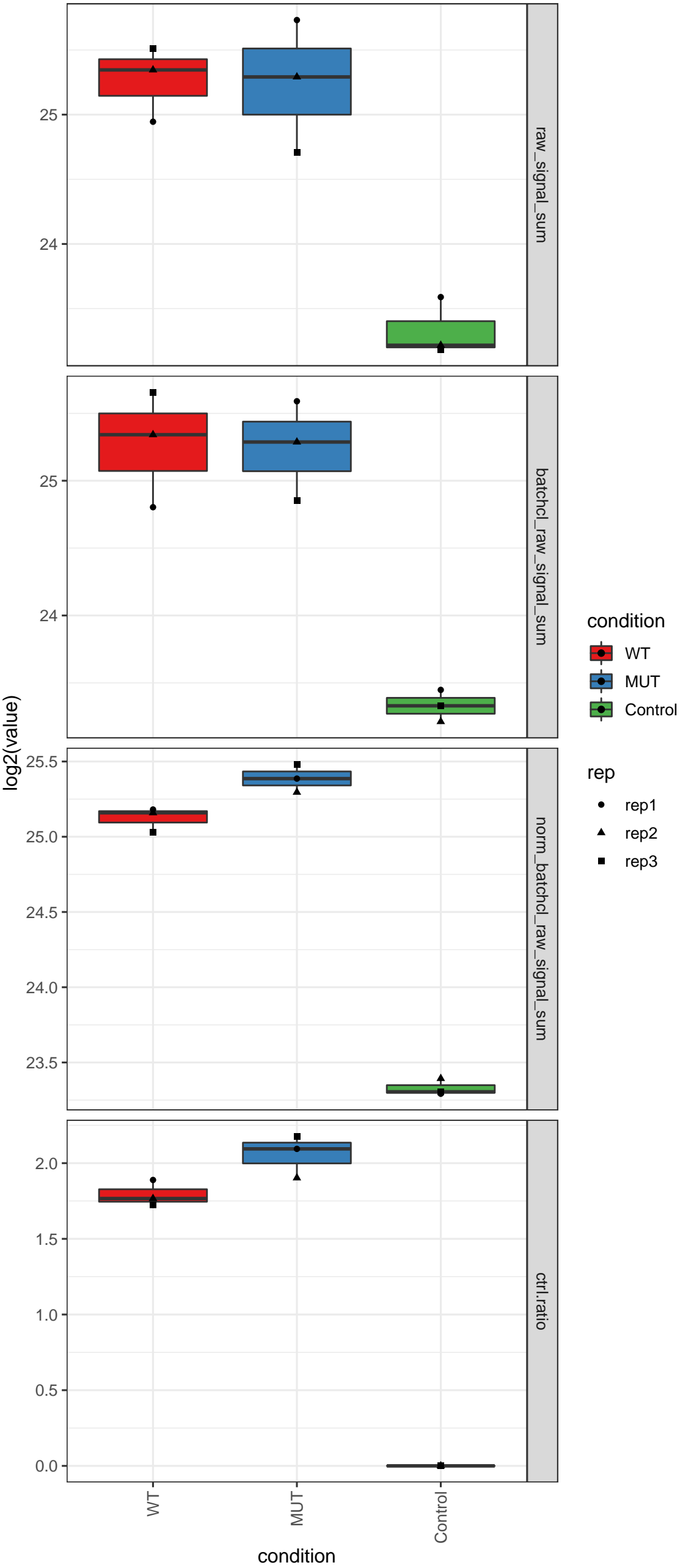
CDC12 – P32468

Cell division control protein 12 OS=*Saccharomyces cerevisiae* (strain ATCC 25796)



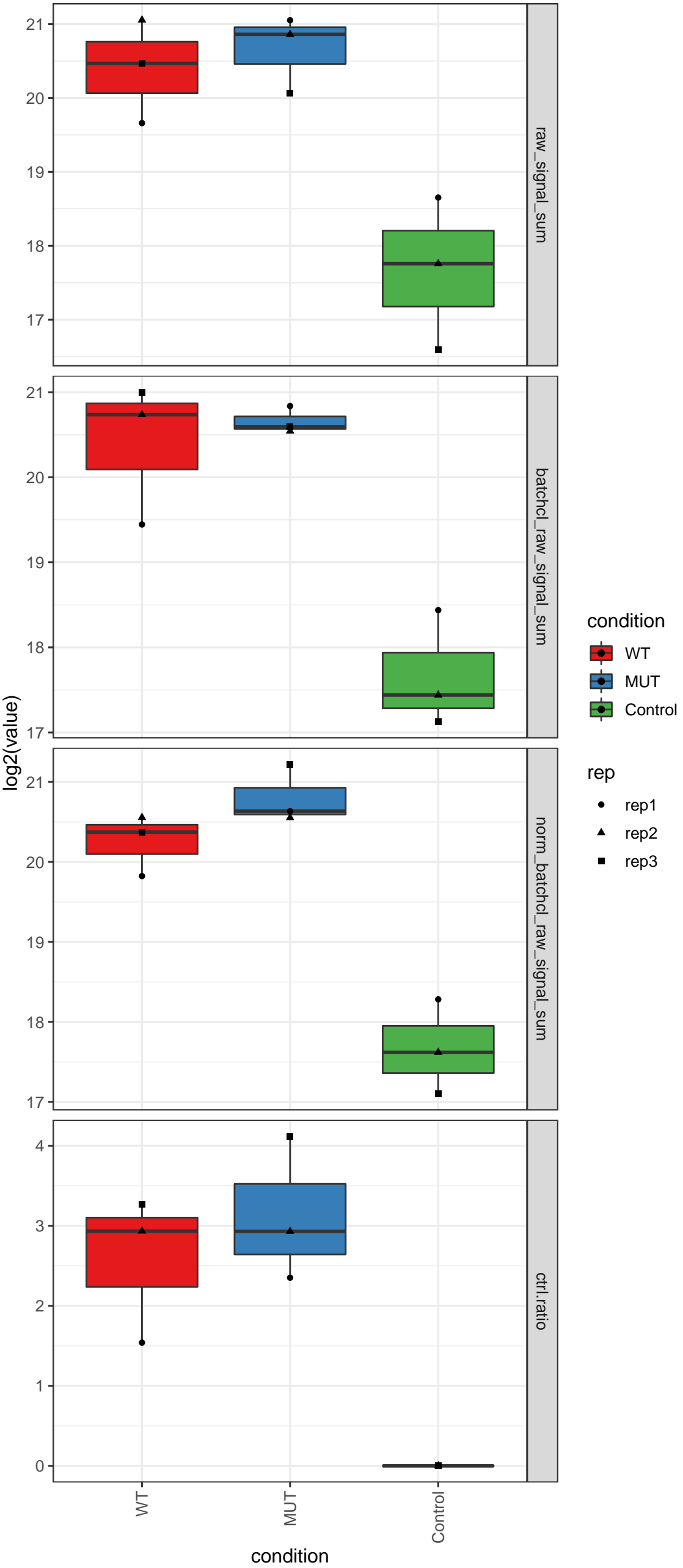
CDC19 – P00549

Pyruvate kinase 1 OS=*Saccharomyces cerevisiae* (strain ATCC 204508 /



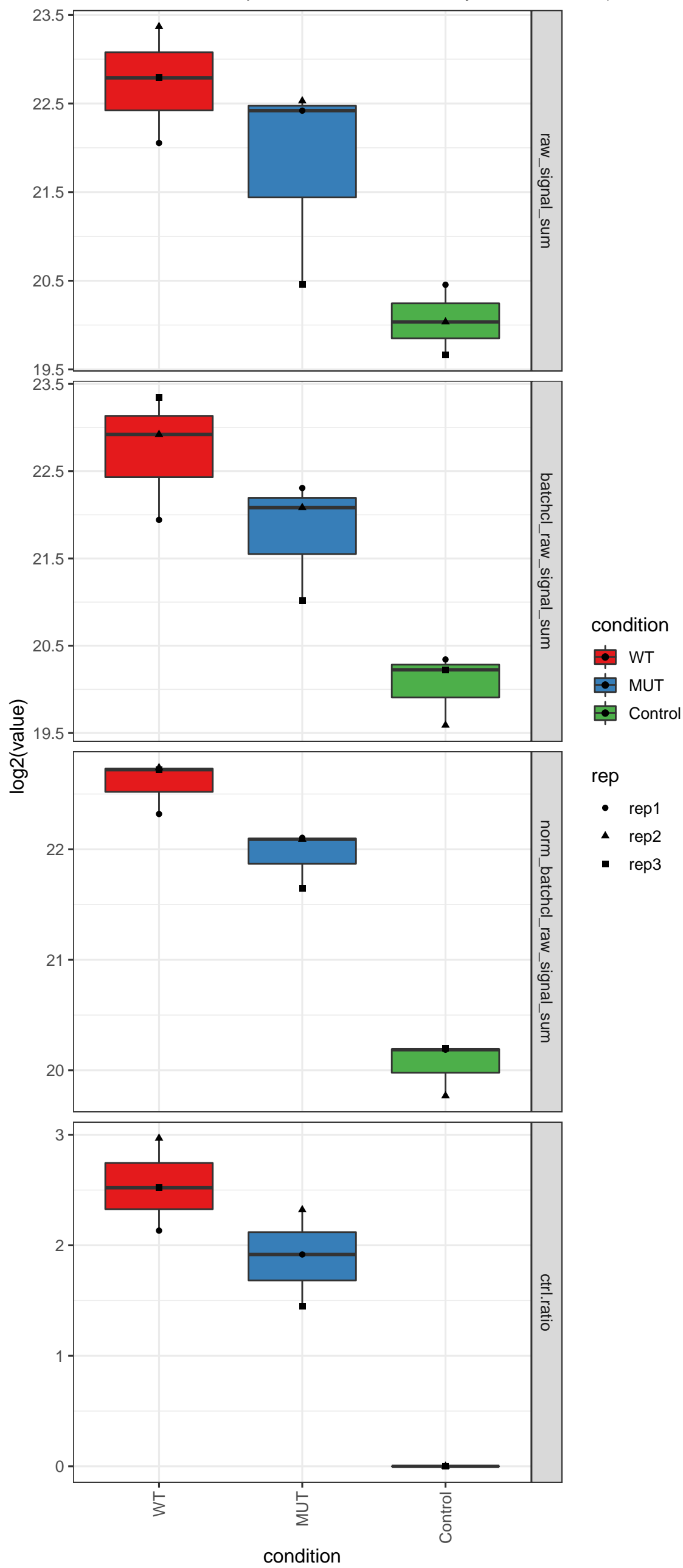
CDC24 – P11433

Cell division control protein 24 OS=*Saccharomyces cerevisiae* (strain ATCC 24843)



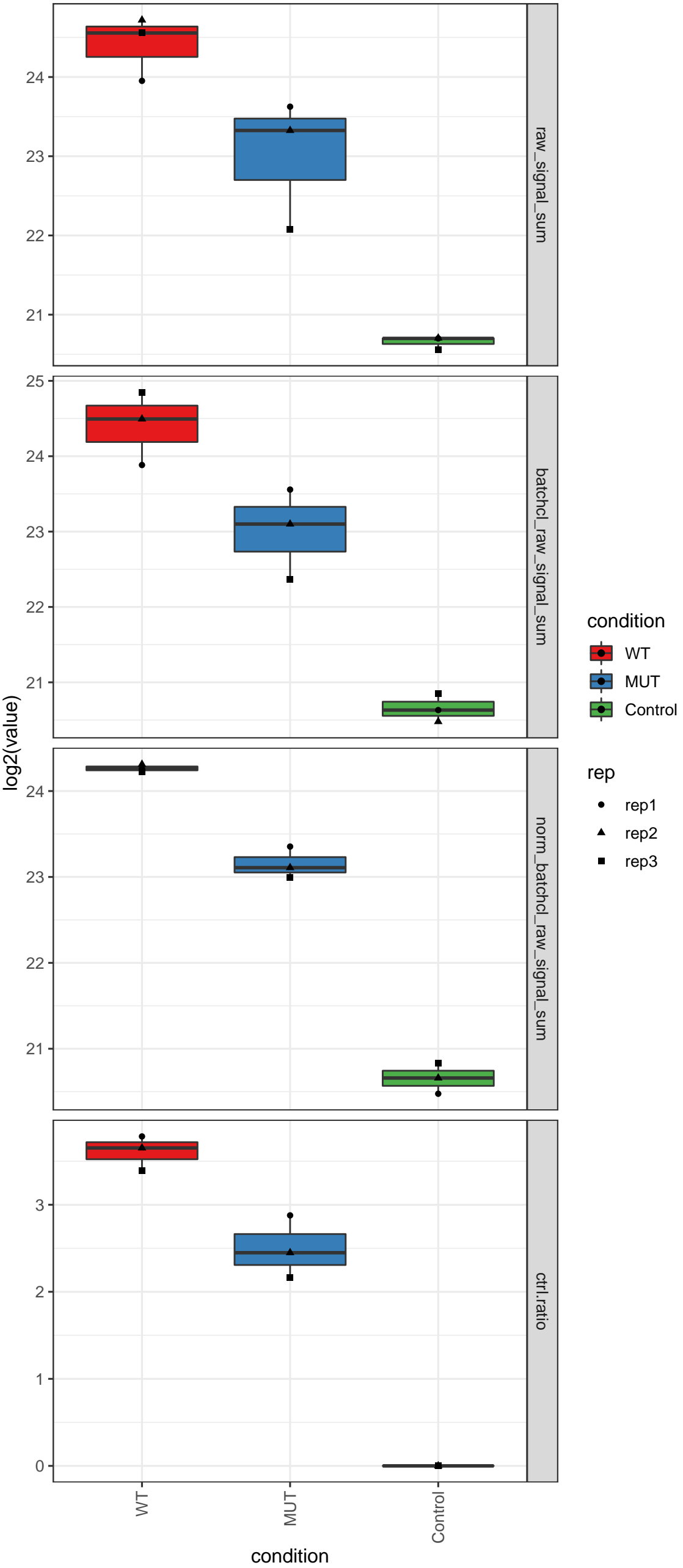
CDC3 – P32457

Cell division control protein 3 OS=*Saccharomyces cerevisiae* (strain ATCC 24843)



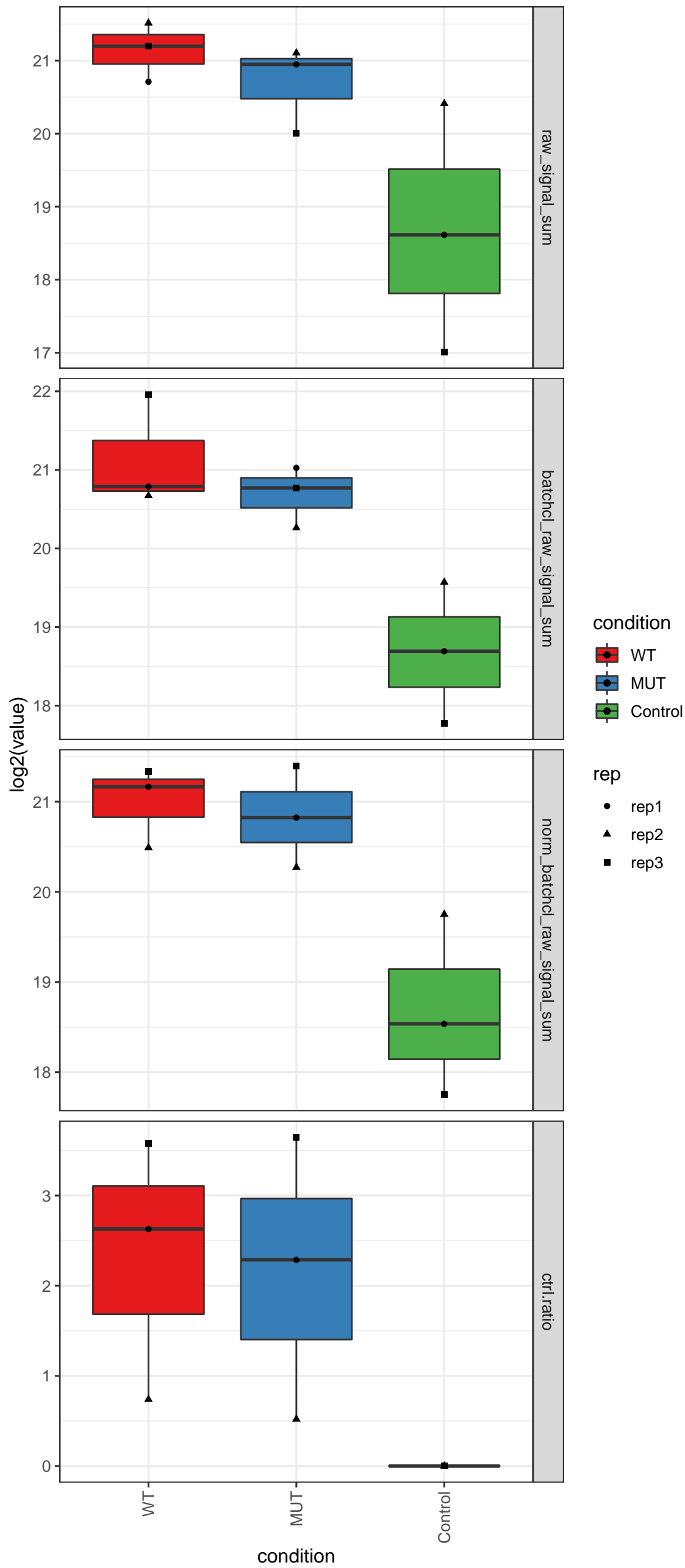
CDC60 – P26637

Leucine--tRNA ligase, cytoplasmic OS=*Saccharomyces cerevisiae* (strain



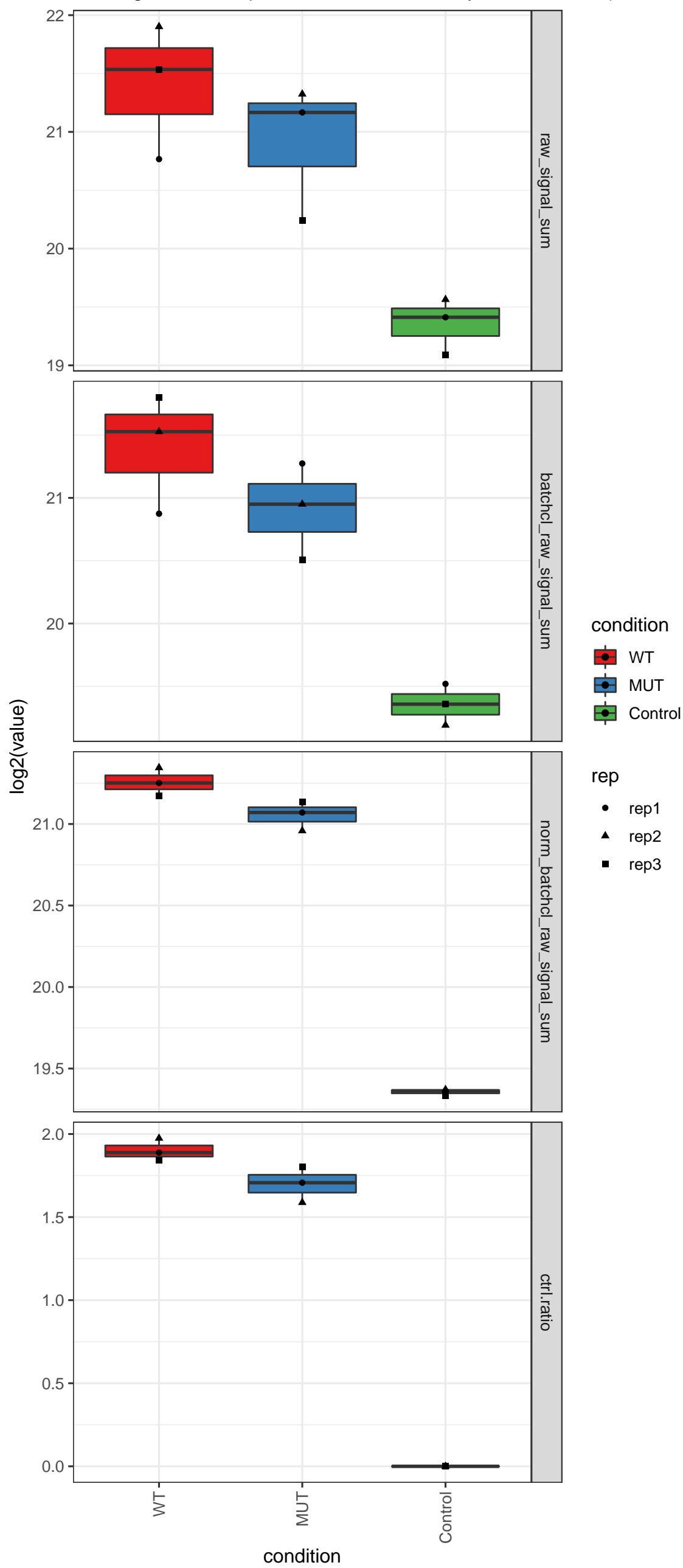
CDS1 – P38221

Phosphatidate cytidyltransferase OS=*Saccharomyces cerevisiae* (strain *A*)



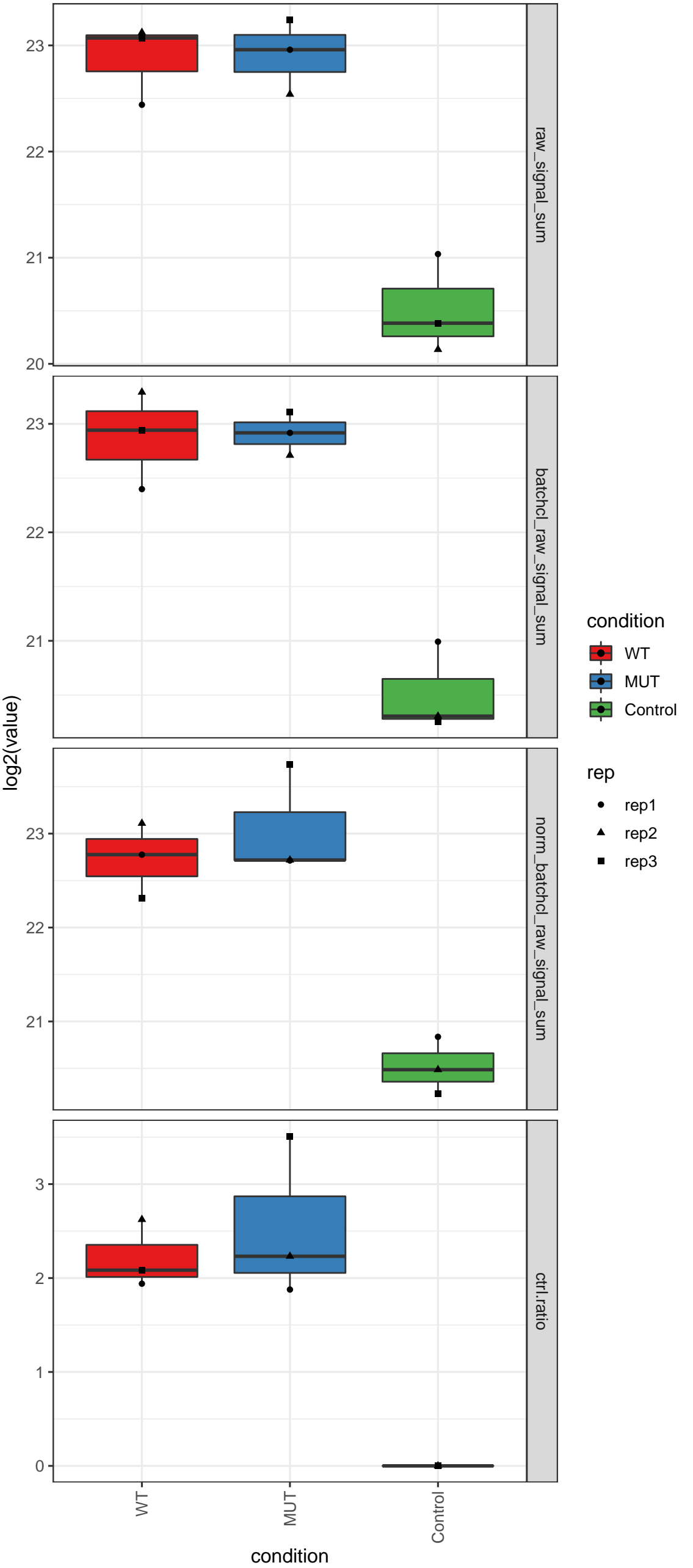
CFT2 – Q12102

Cleavage factor two protein 2 OS=Saccharomyces cerevisiae (strain ATC



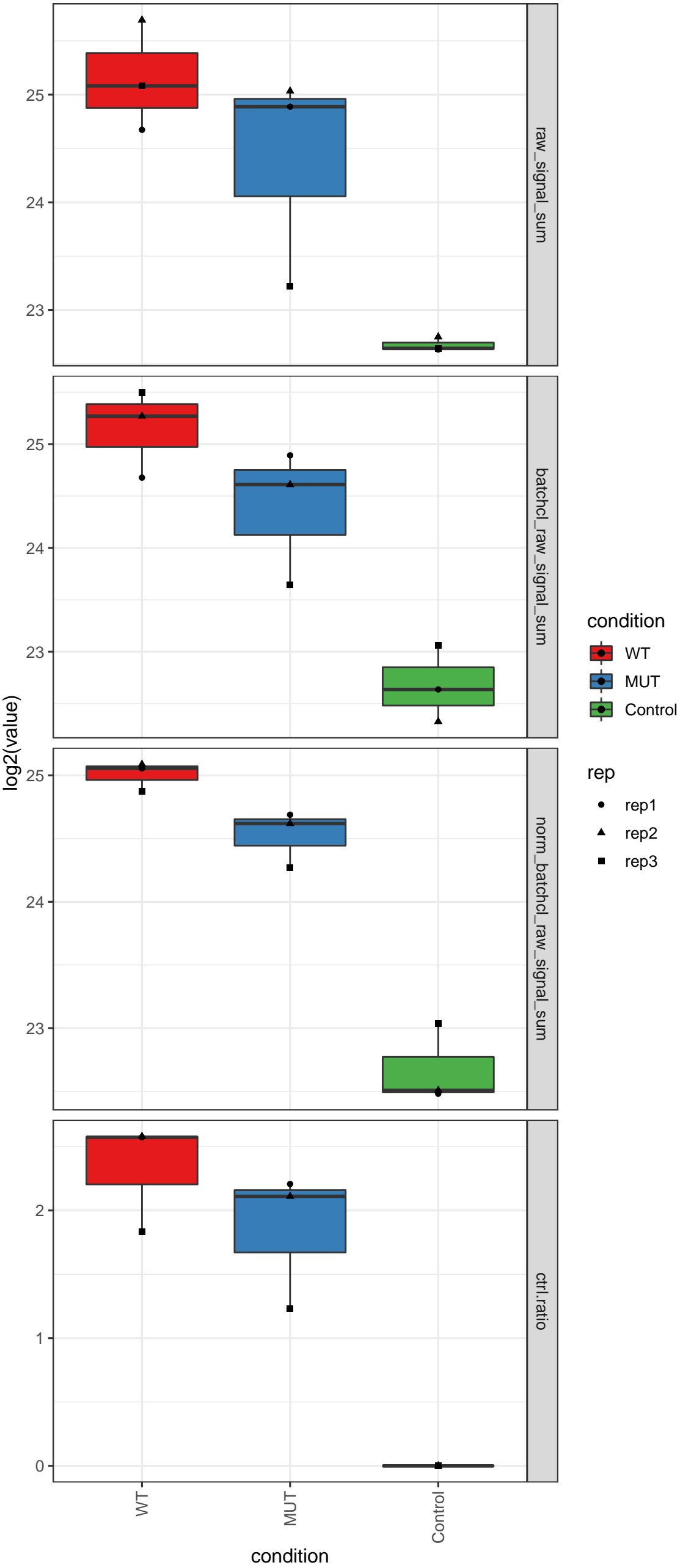
CHC1 – P22137

Clathrin heavy chain OS=*Saccharomyces cerevisiae* (strain ATCC 204508)



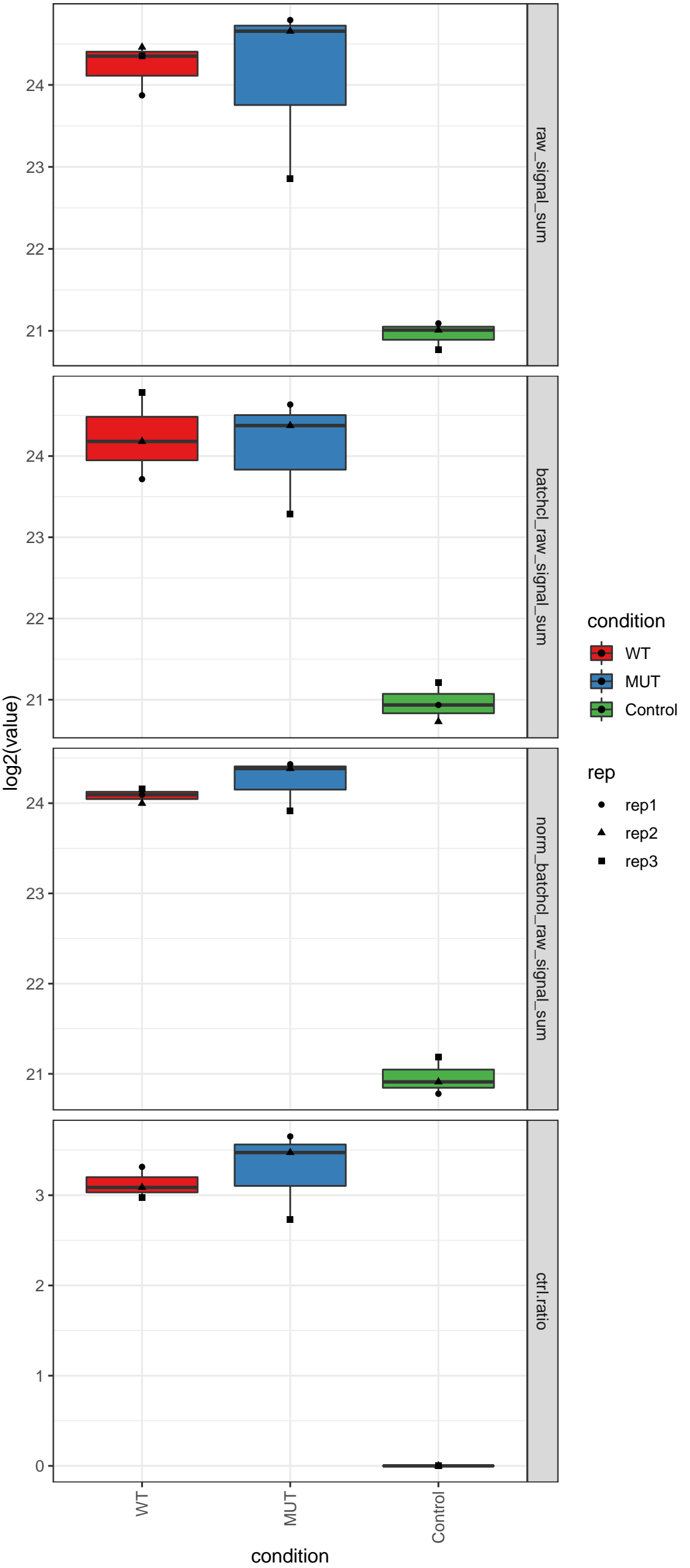
CHD1 – P32657

Chromo domain-containing protein 1 OS=Saccharomyces cerevisiae (strain



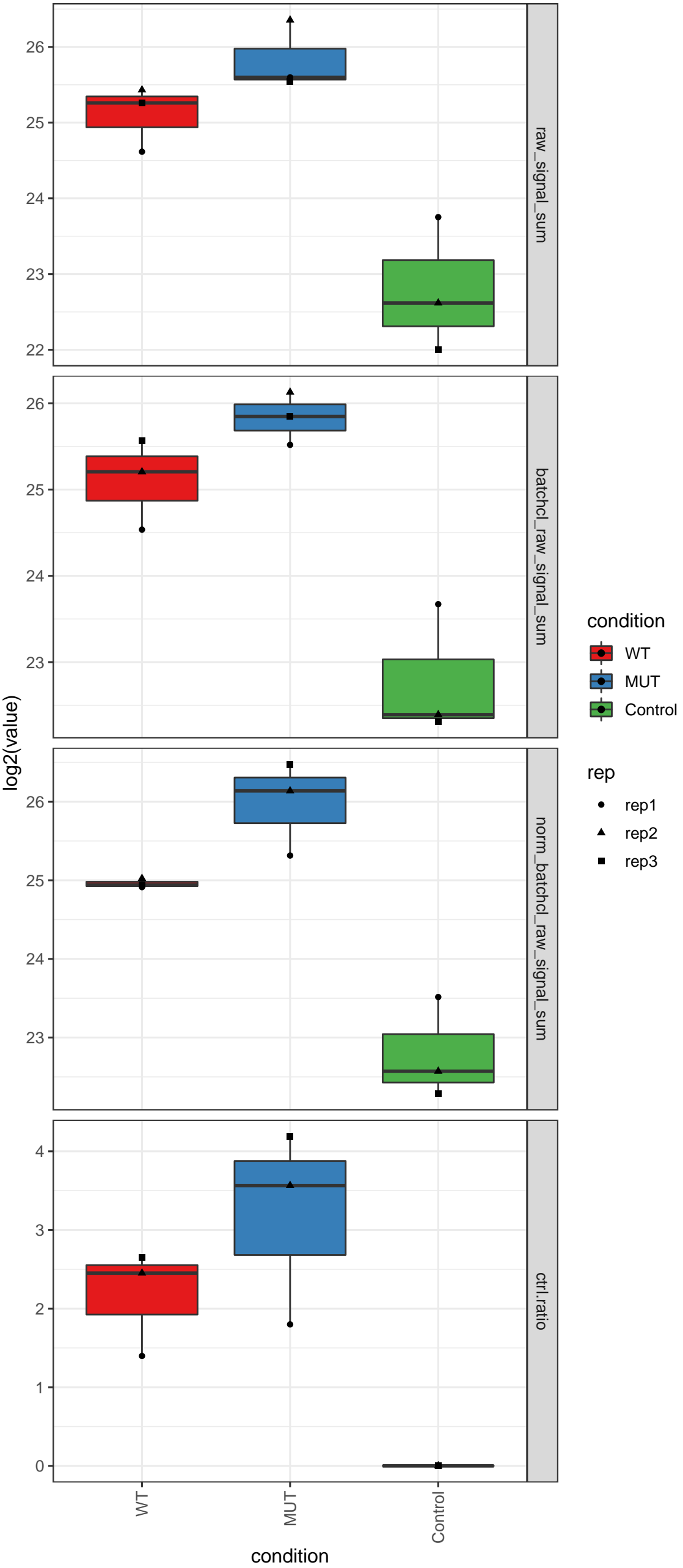
CIC1 – P38779

Proteasome–interacting protein CIC1 OS=*Saccharomyces cerevisiae* (stra



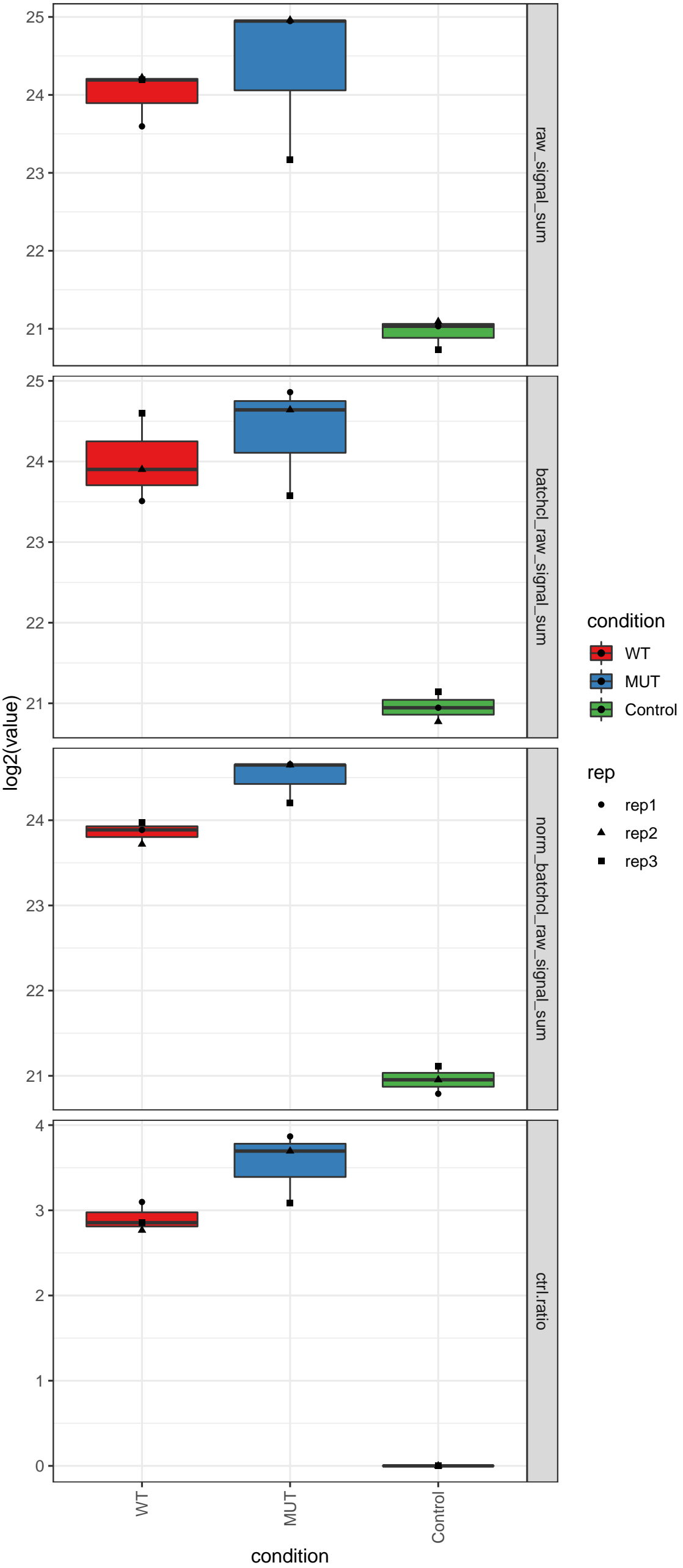
CIT1 – P00890

Citrate synthase, mitochondrial OS=*Saccharomyces cerevisiae* (strain ATCC 22016 / DSM 1151)



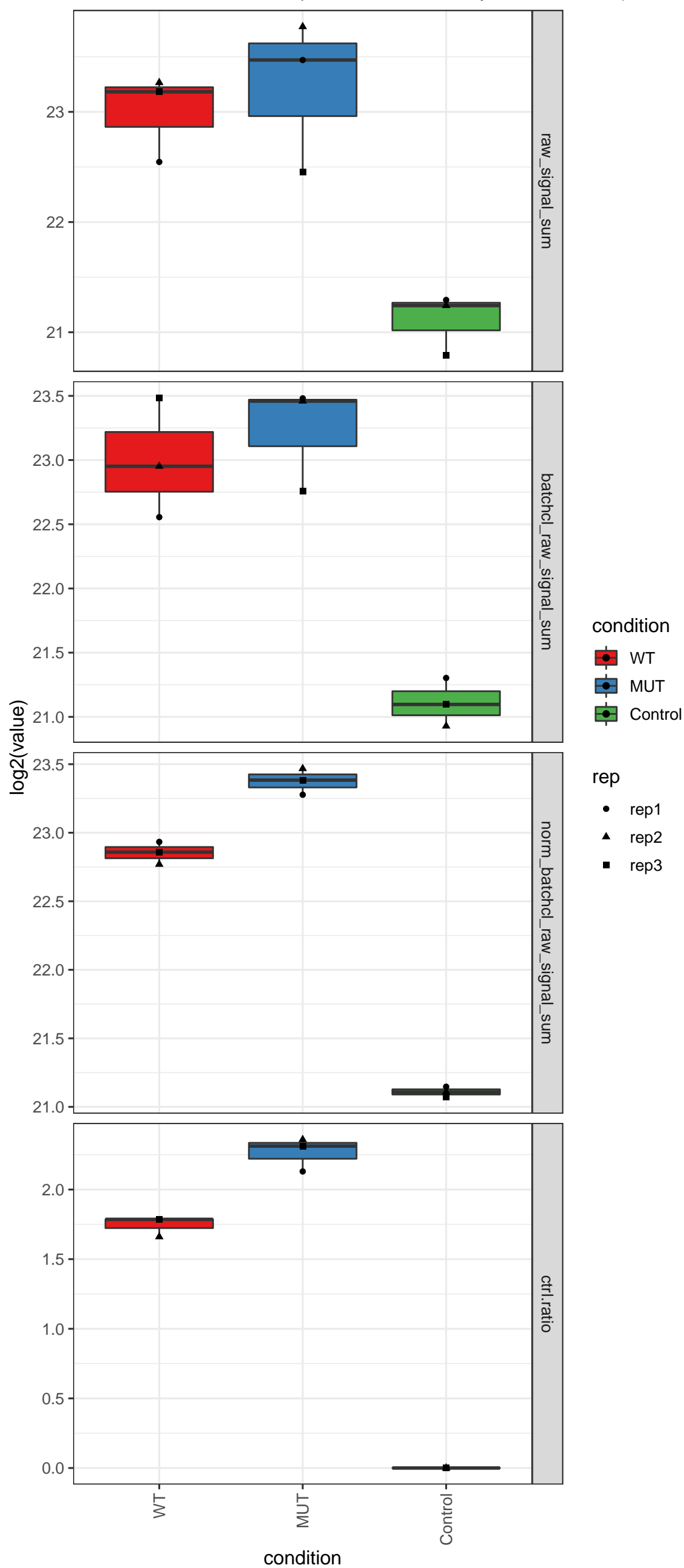
CKA1 – P15790

Casein kinase II subunit alpha OS=Saccharomyces cerevisiae (strain ATCC

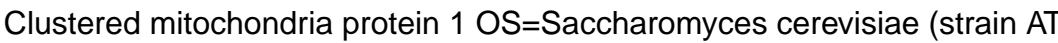


CKA2 – P19454

Casein kinase II subunit alpha' OS=Saccharomyces cerevisiae (strain ATCC 25791)

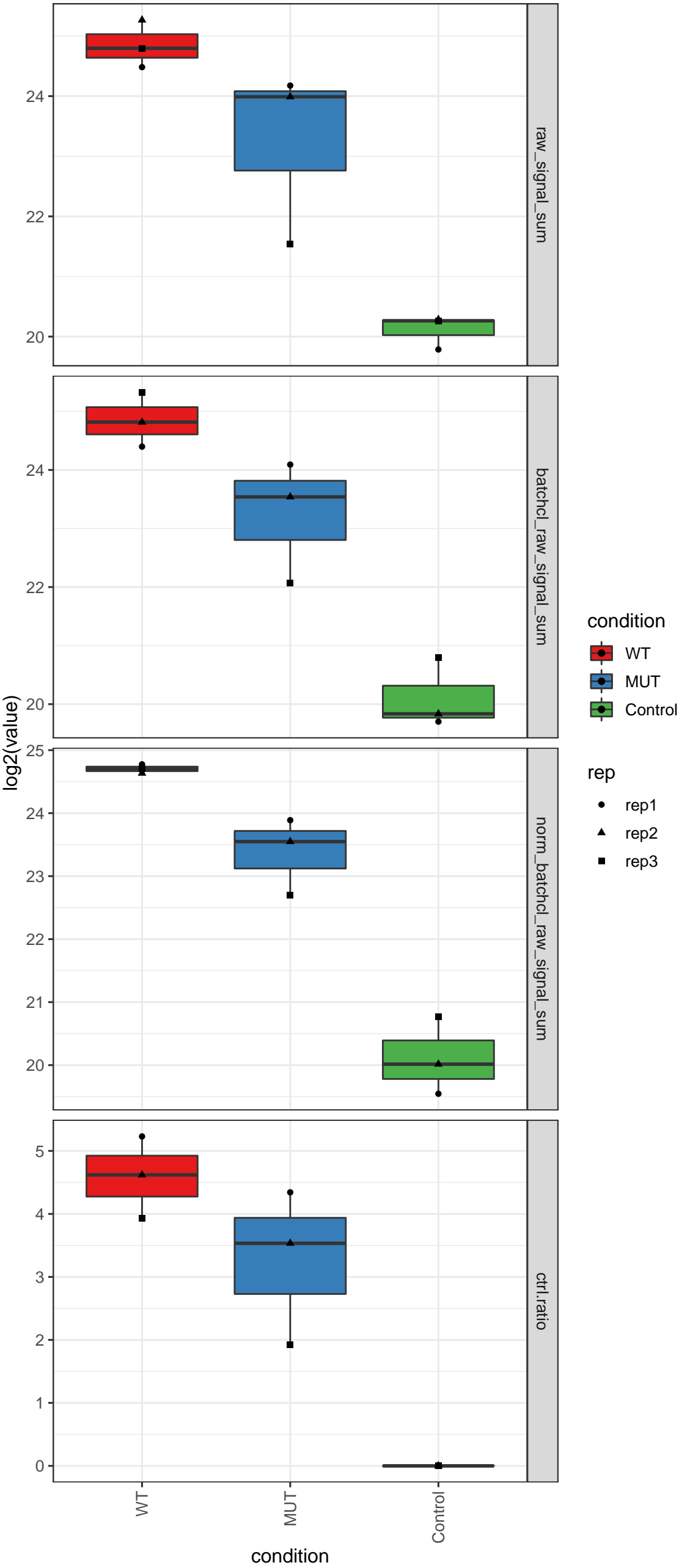


Clustered mitochondria protein 1 OS=Saccharomyces cerevisiae (strain AT



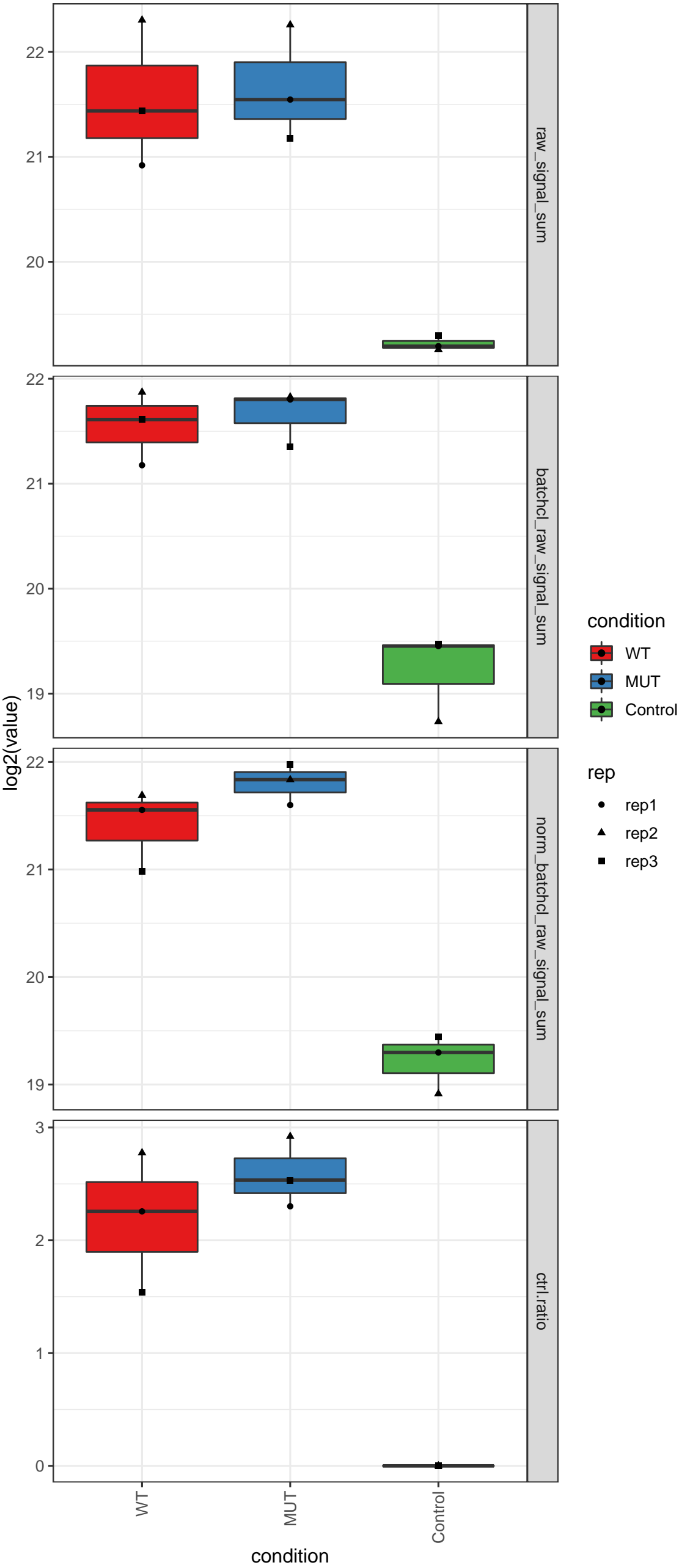
CMR1 – Q12510

DNA damage-binding protein CMR1 OS=*Saccharomyces cerevisiae* (strain



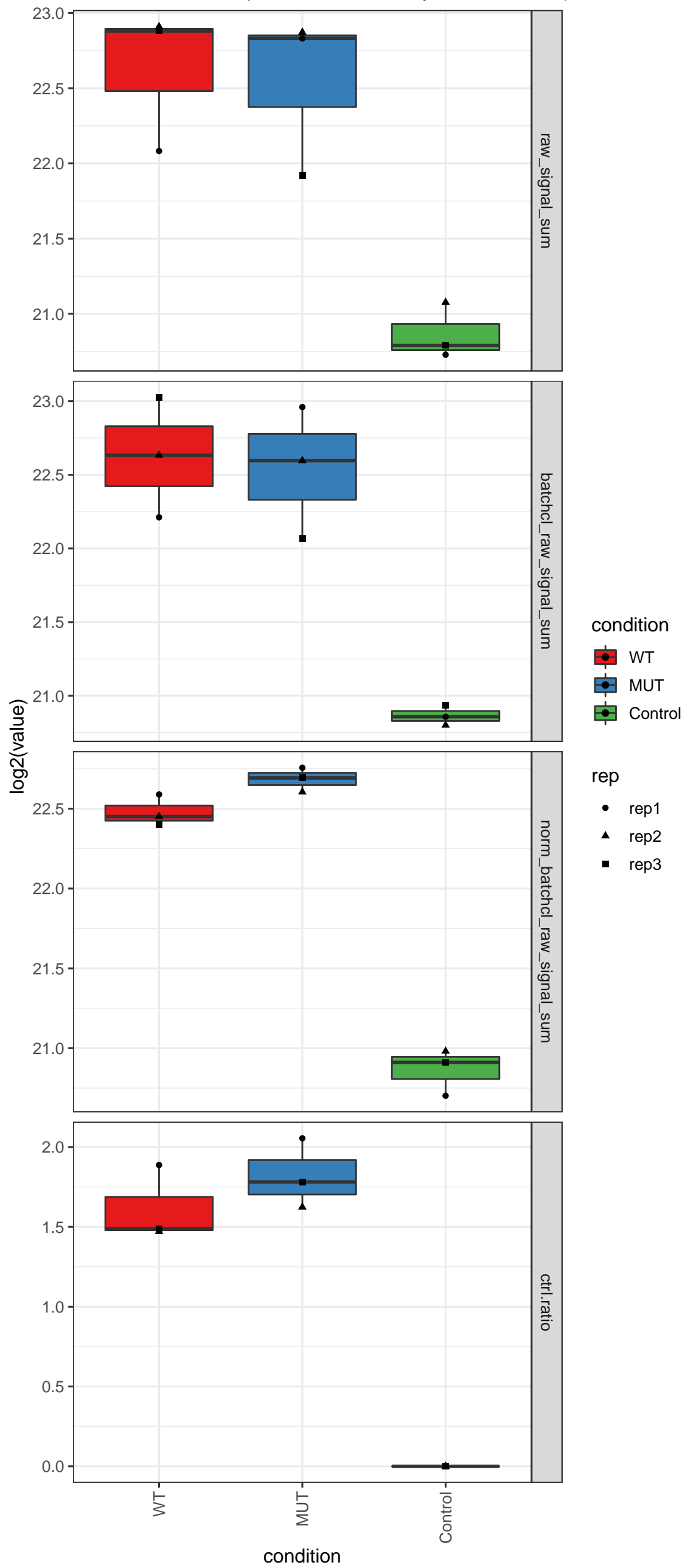
CNM67 – P53865

Chaotic nuclear migration protein 67 OS=*Saccharomyces cerevisiae* (strain



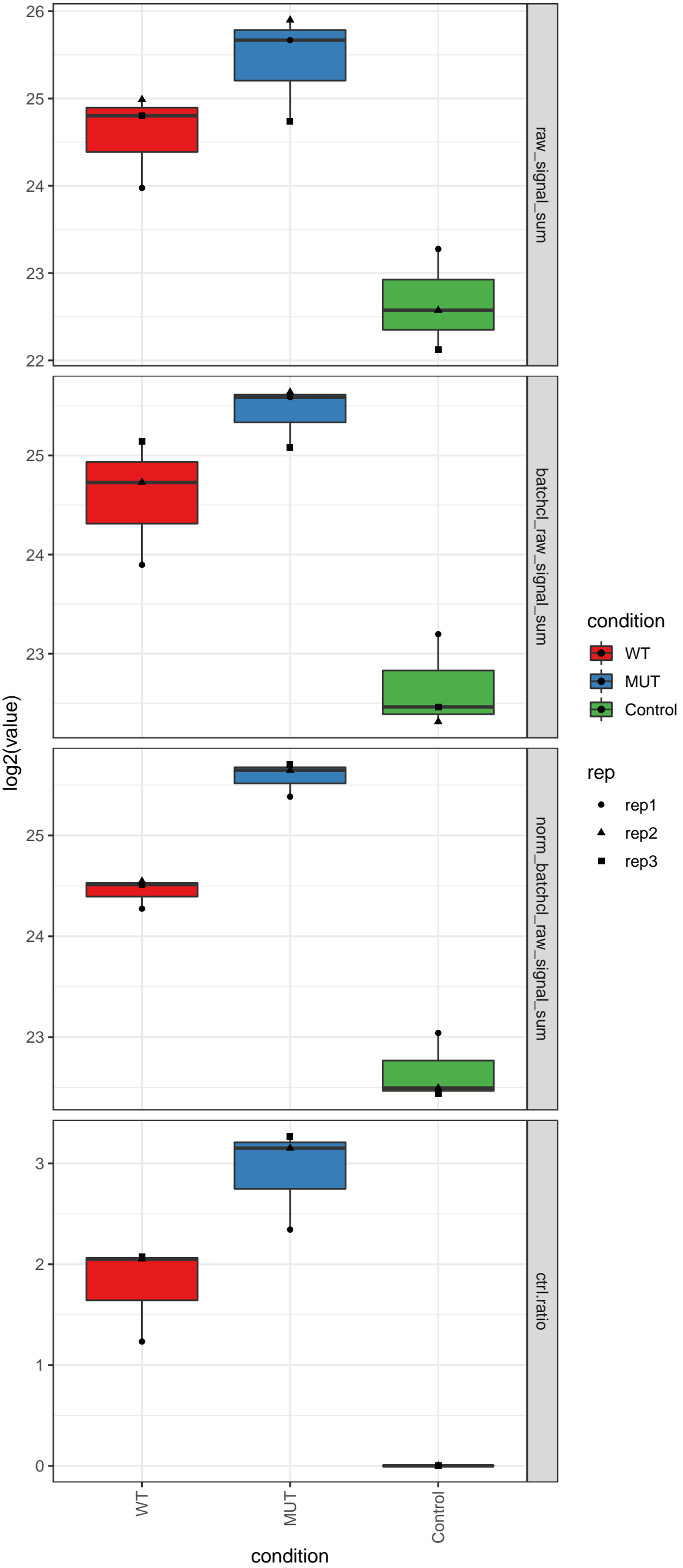
COP1 – P53622

Coatomer subunit alpha OS=*Saccharomyces cerevisiae* (strain ATCC 204



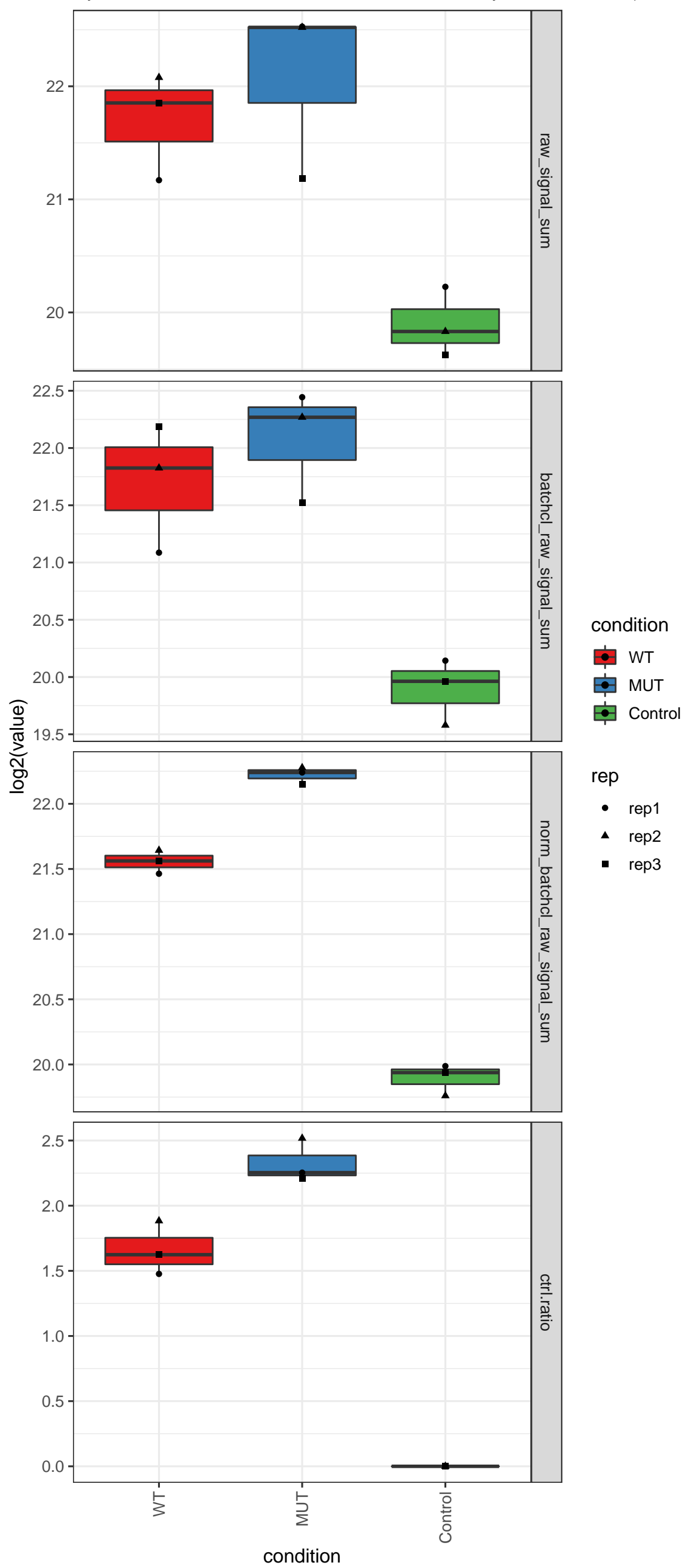
COR1 – P07256

Cytochrome b–c1 complex subunit 1, mitochondrial OS=Saccharomyces c



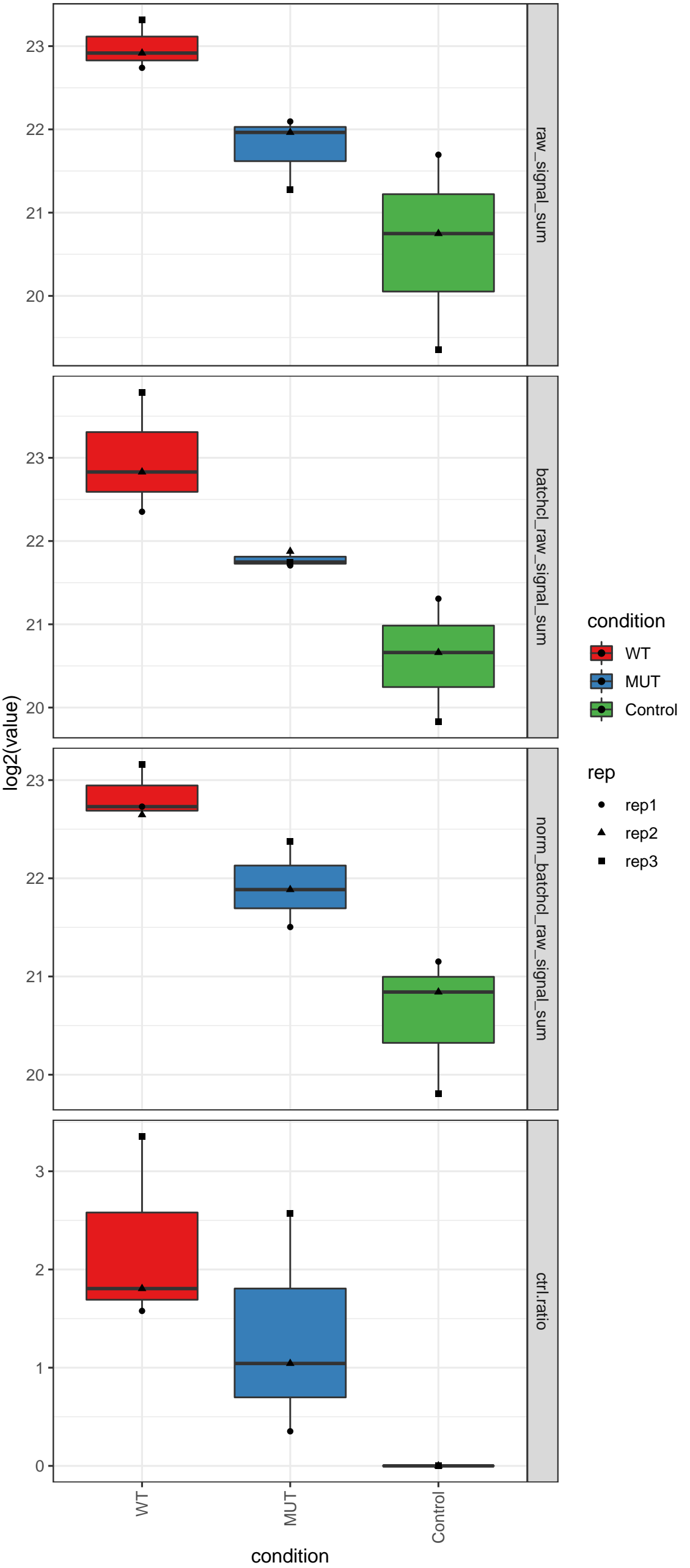
COX2 – P00410

Cytochrome c oxidase subunit 2 OS=*Saccharomyces cerevisiae* (strain A



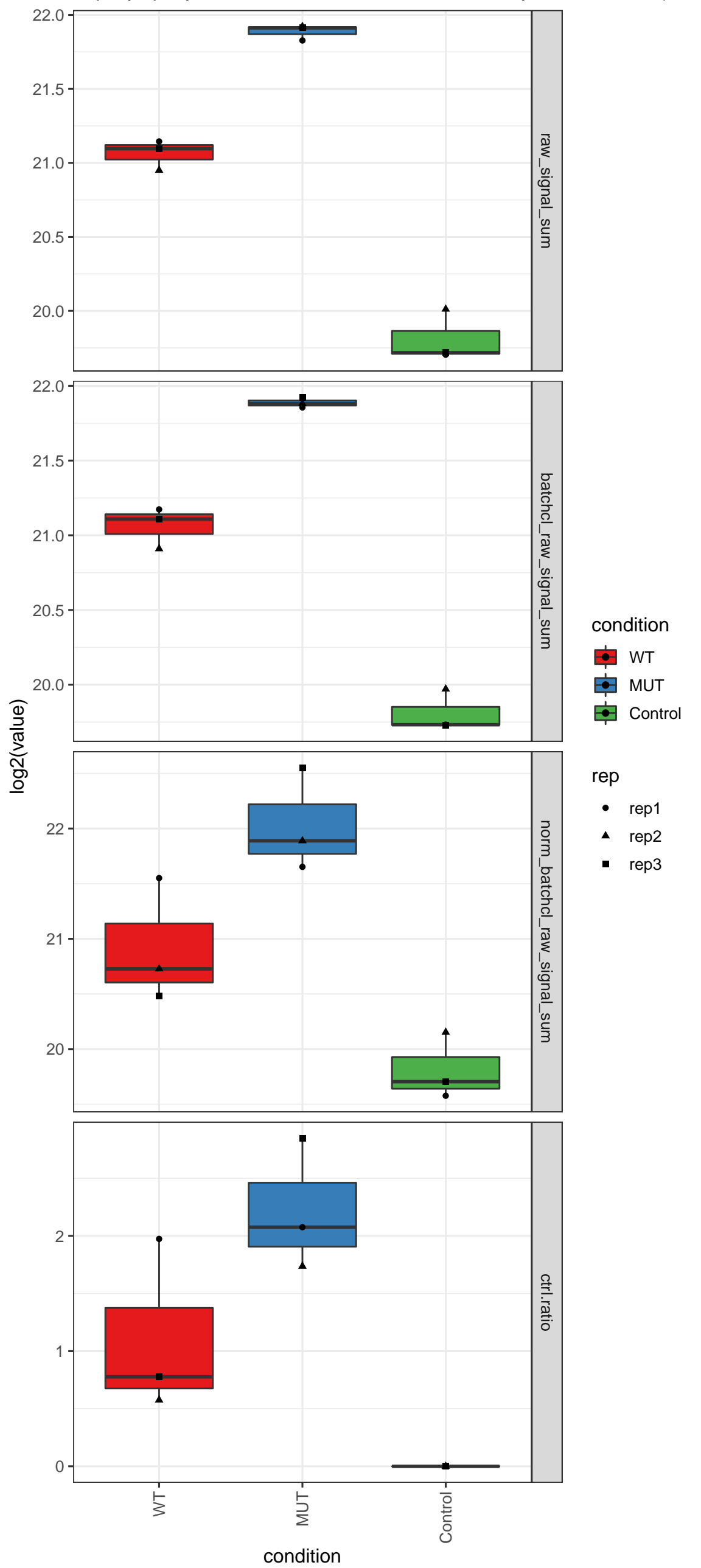
CPA2 – P03965

Carbamoyl-phosphate synthase arginine-specific large chain OS=Saccha



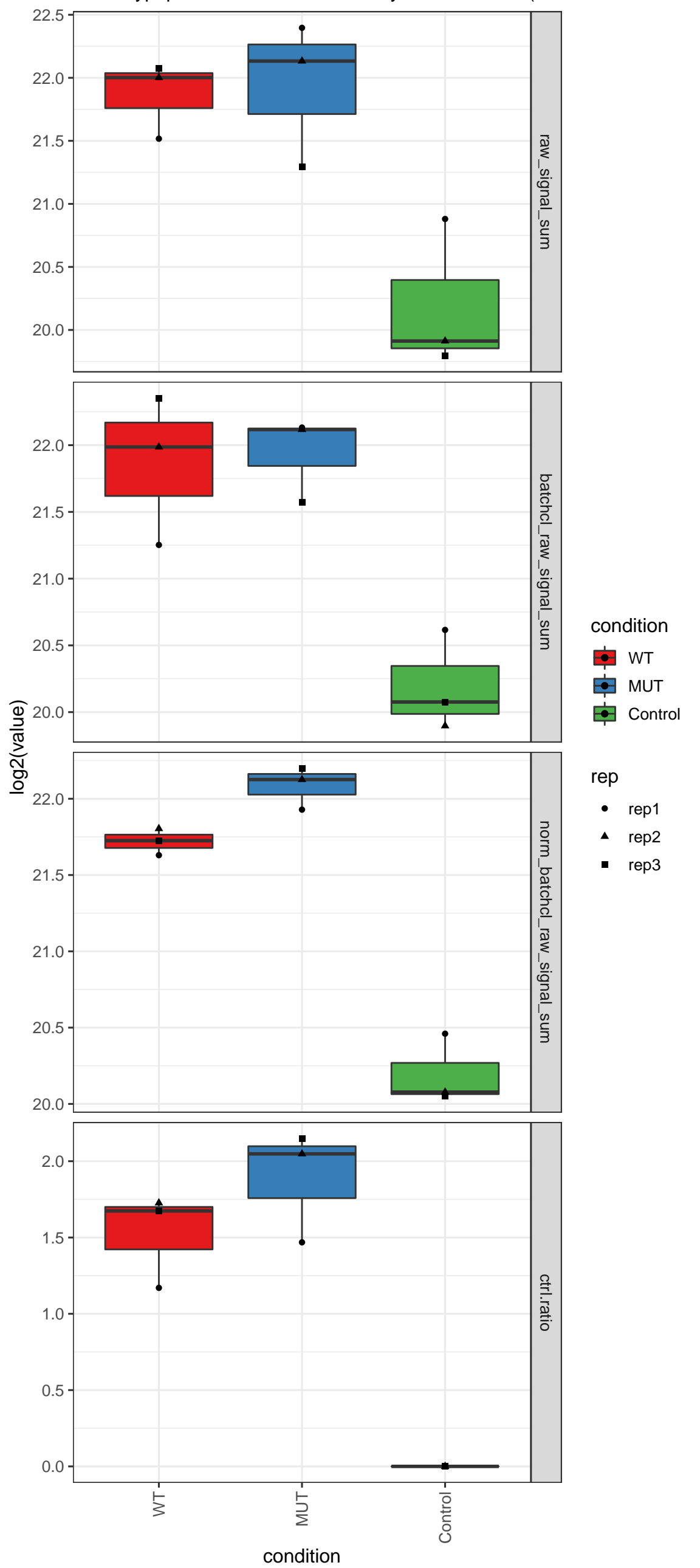
CPR1 – P14832

Peptidyl–prolyl cis–trans isomerase OS=Saccharomyces cerevisiae (strain



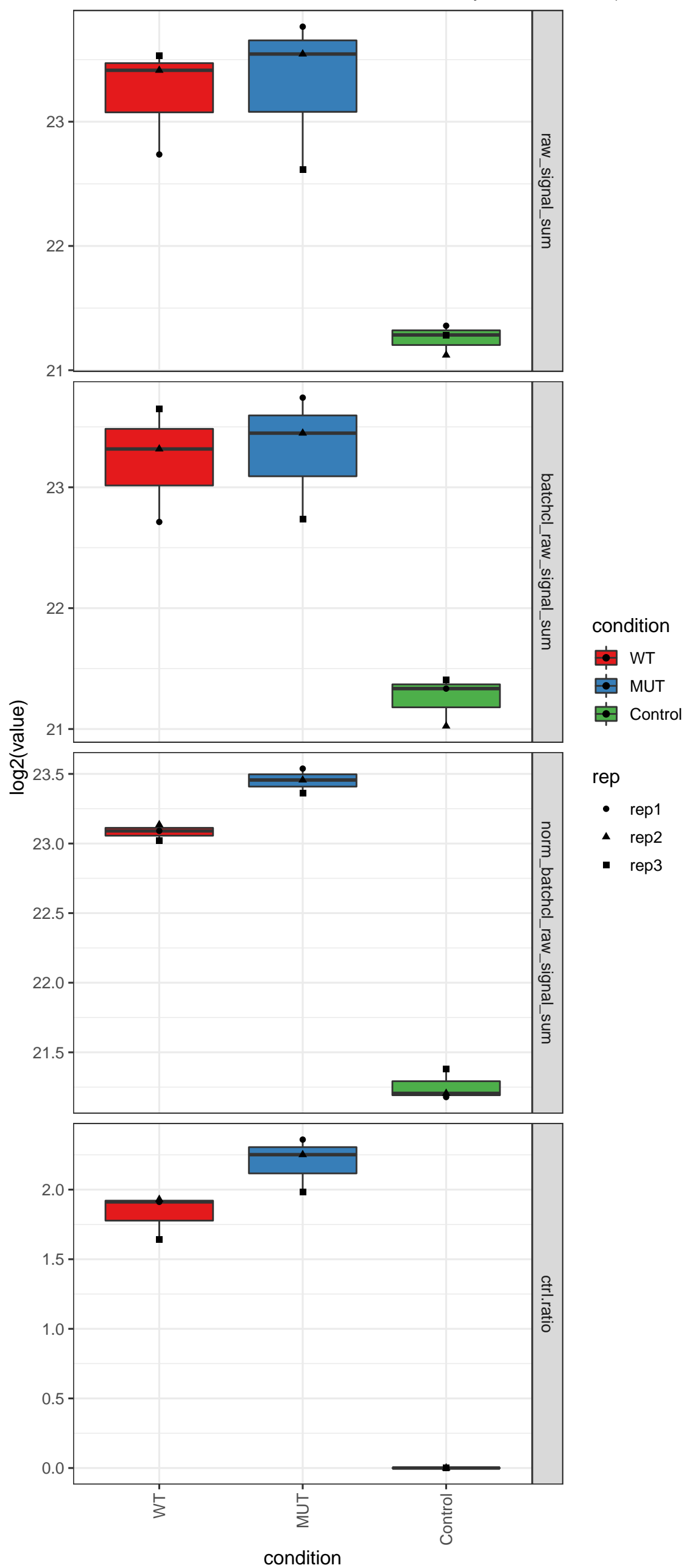
CPS1 – P27614

Carboxypeptidase S OS=Saccharomyces cerevisiae (strain ATCC 20450)



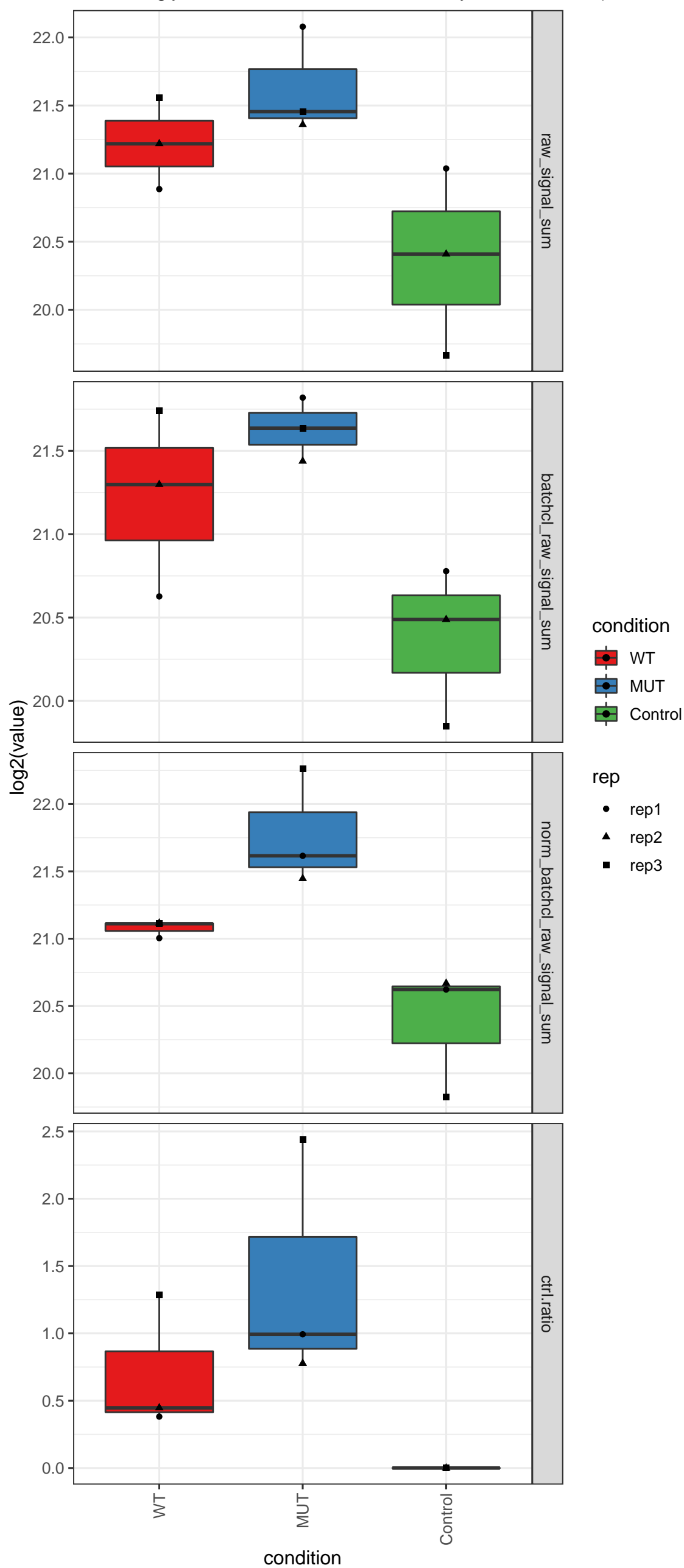
CRC1 – Q12289

Mitochondrial carnitine carrier OS=*Saccharomyces cerevisiae* (strain ATC



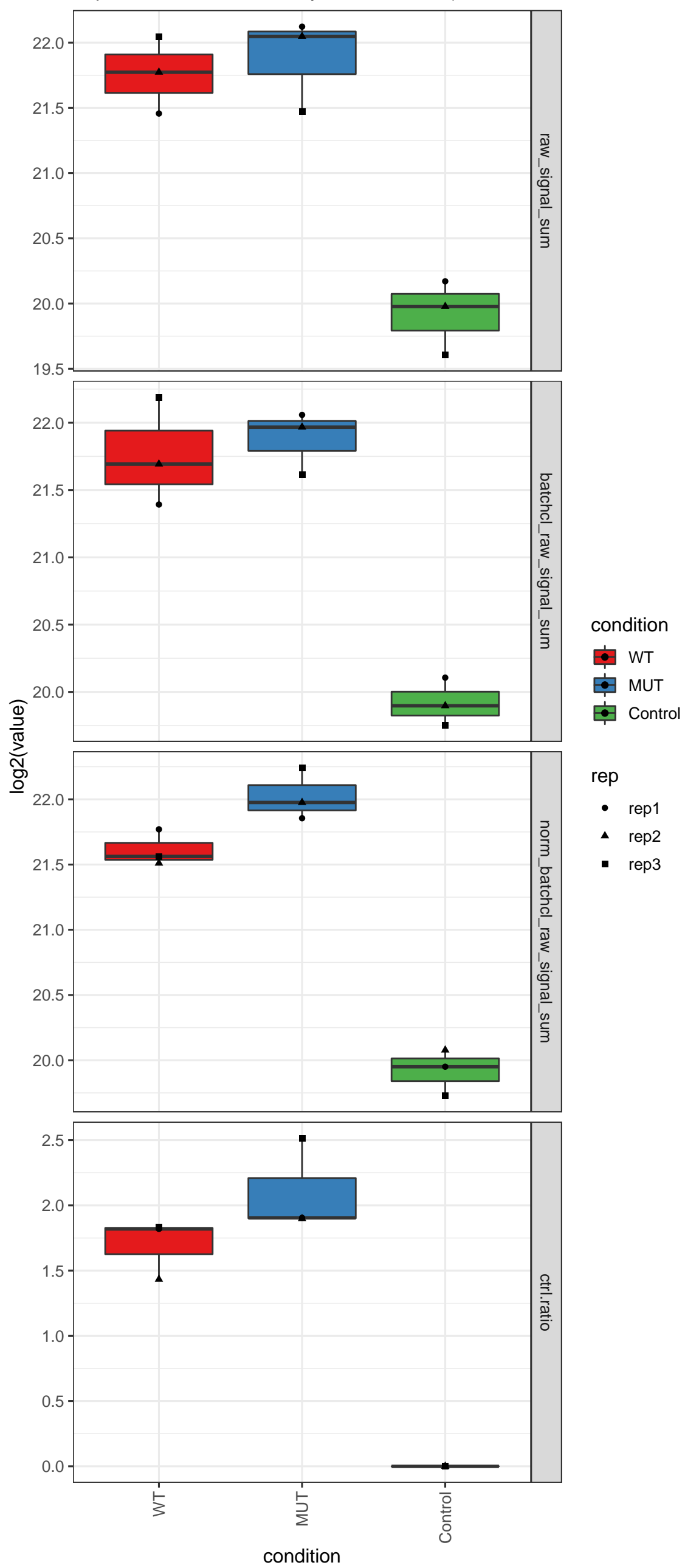
CRH1 – P53301

Probable glycosidase CRH1 OS=*Saccharomyces cerevisiae* (strain ATCC 25716)



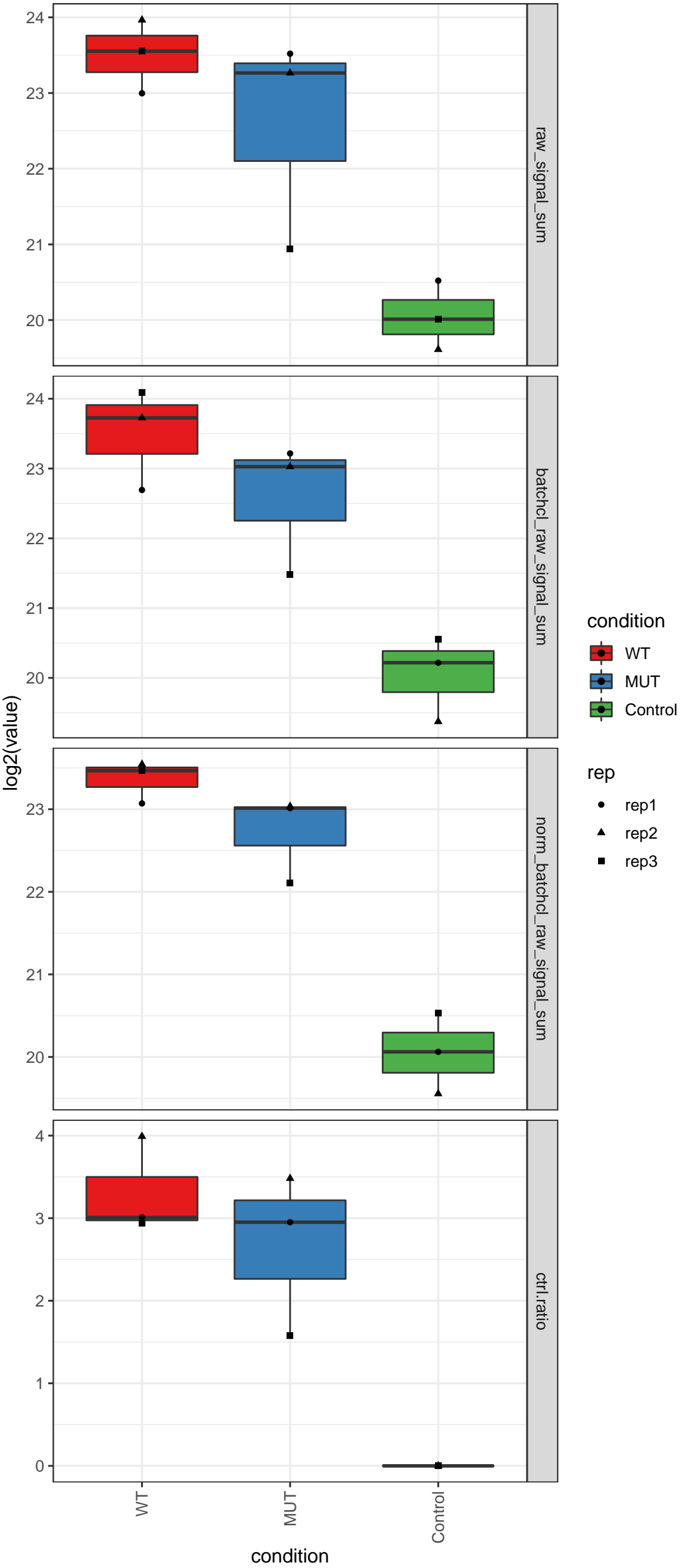
CRM1 – P30822

Exportin-1 OS=*Saccharomyces cerevisiae* (strain ATCC 204508 / S288c)



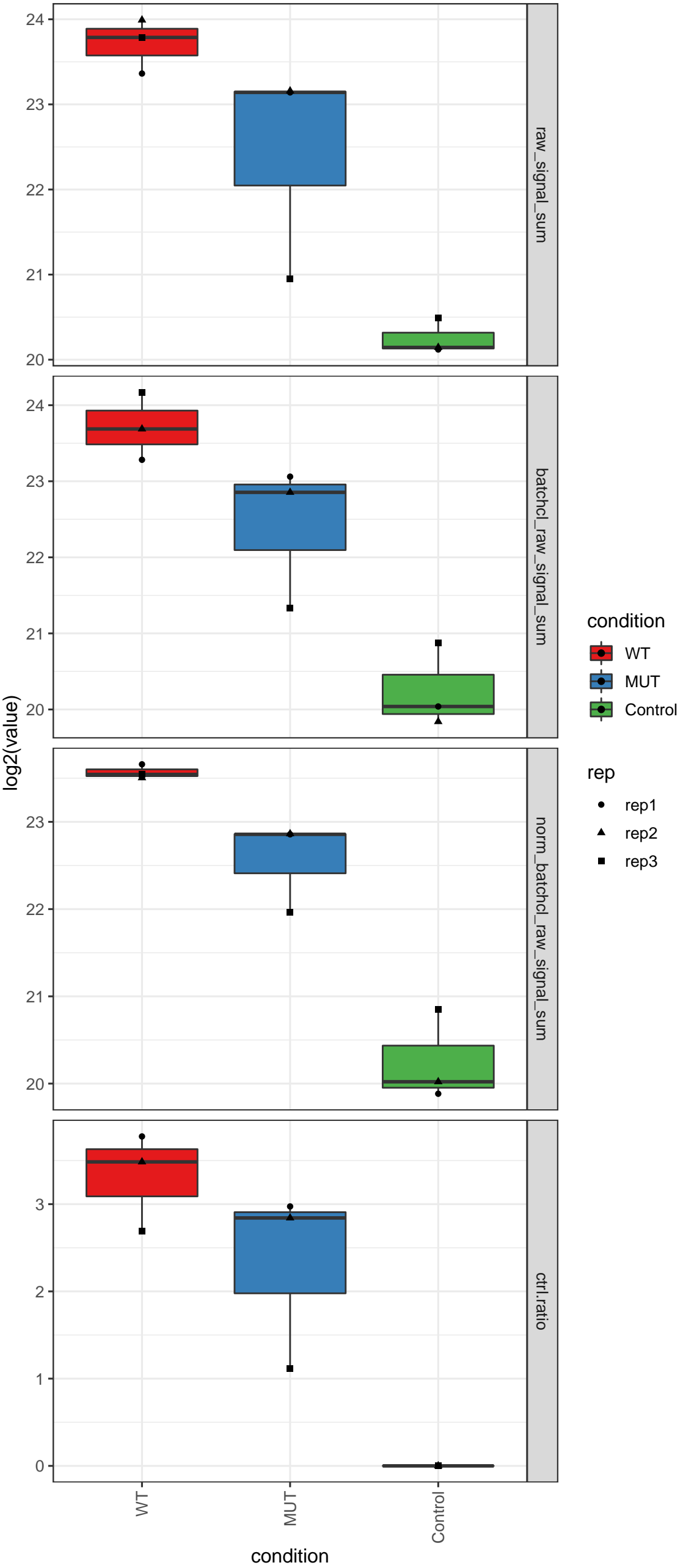
CRP1 – P38845

Cruciform DNA-recognizing protein 1 OS=*Saccharomyces cerevisiae* (stra



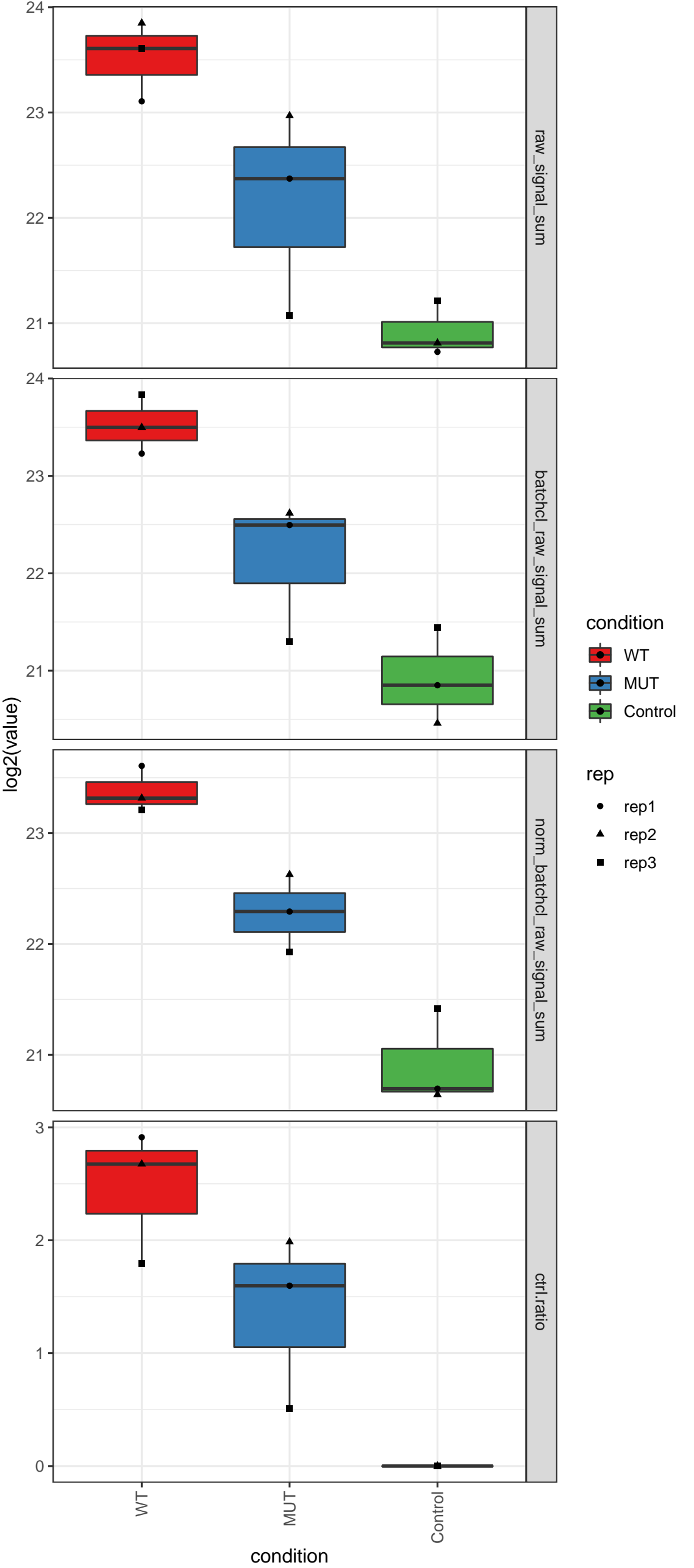
CRZ1 – P53968

Transcriptional regulator CRZ1 OS=*Saccharomyces cerevisiae* (strain ATC



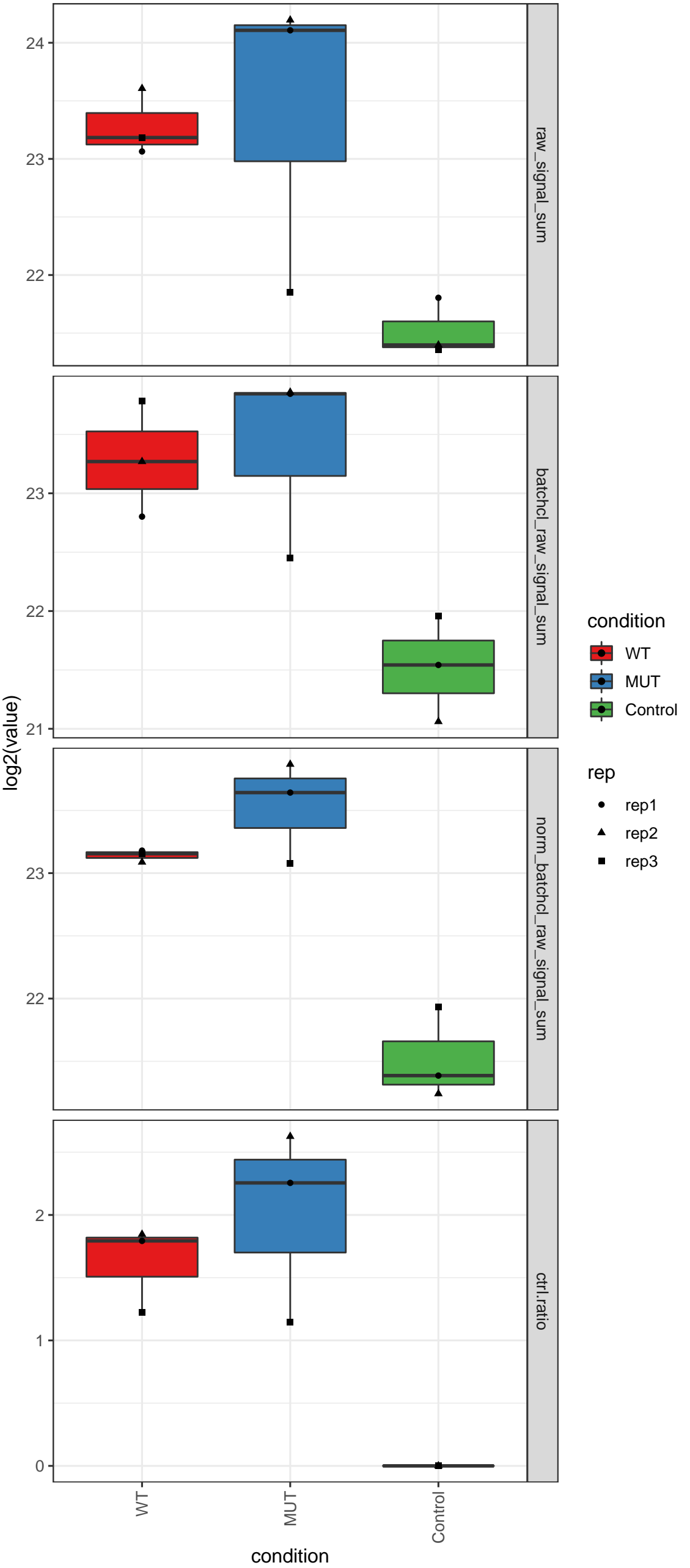
CSE4 – P36012

Histone H3–like centromeric protein CSE4 OS=*Saccharomyces cerevisiae*



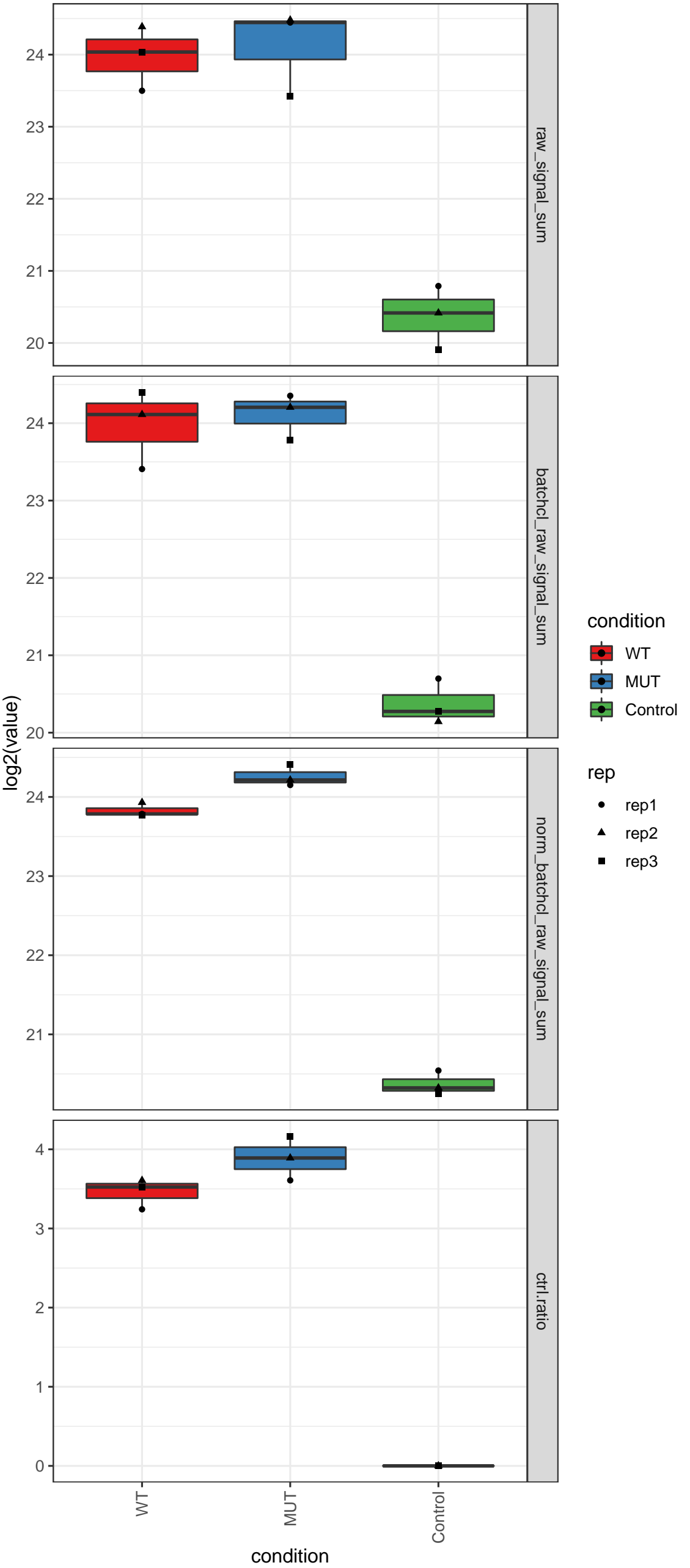
CST6 – P40535

ATF/CREB activator 2 OS=*Saccharomyces cerevisiae* (strain ATCC 20450)



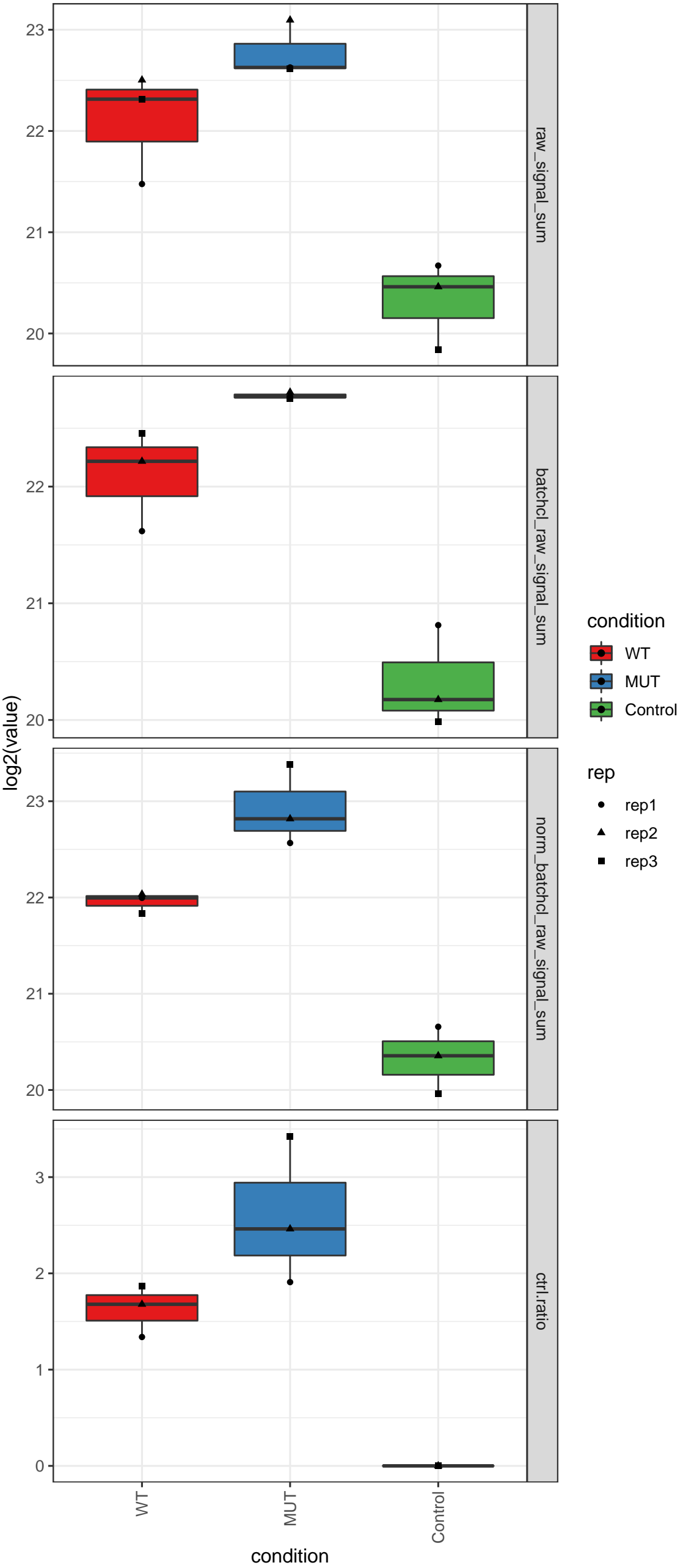
CTA1 – P15202

Peroxisomal catalase A OS=*Saccharomyces cerevisiae* (strain ATCC 2045



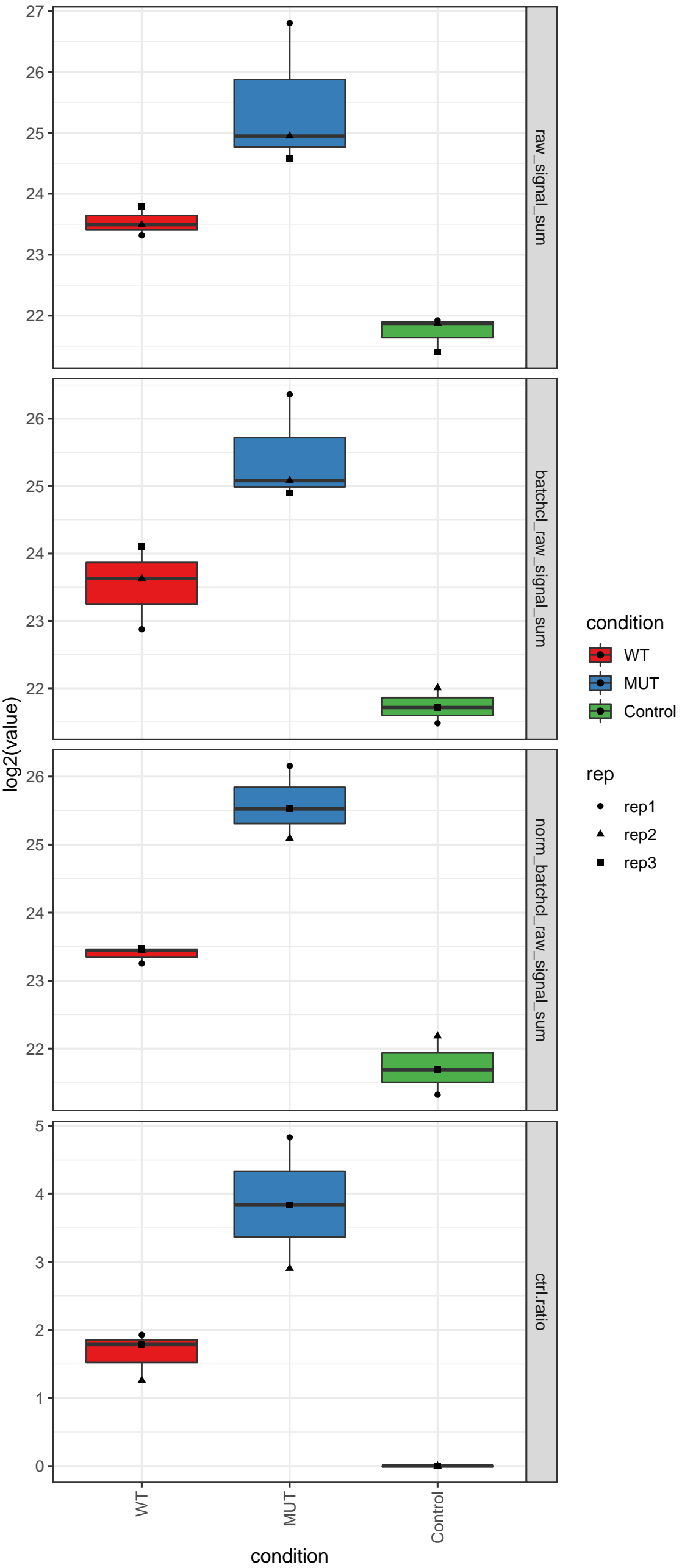
CUE5 – Q08412

Ubiquitin-binding protein CUE5 OS=*Saccharomyces cerevisiae* (strain ATCC 22016 / S288c)

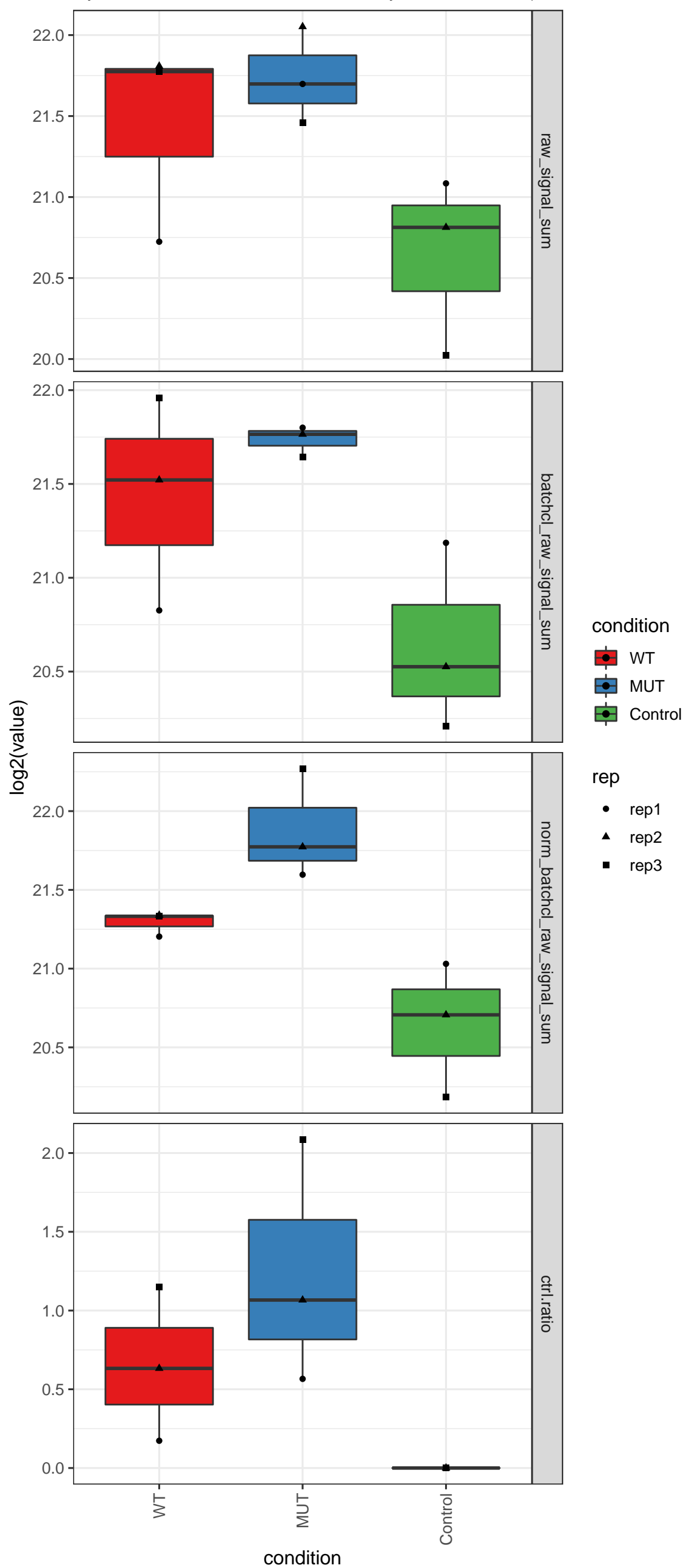


CWP1 – P28319

Cell wall protein CWP1 OS=*Saccharomyces cerevisiae* (strain ATCC 2045

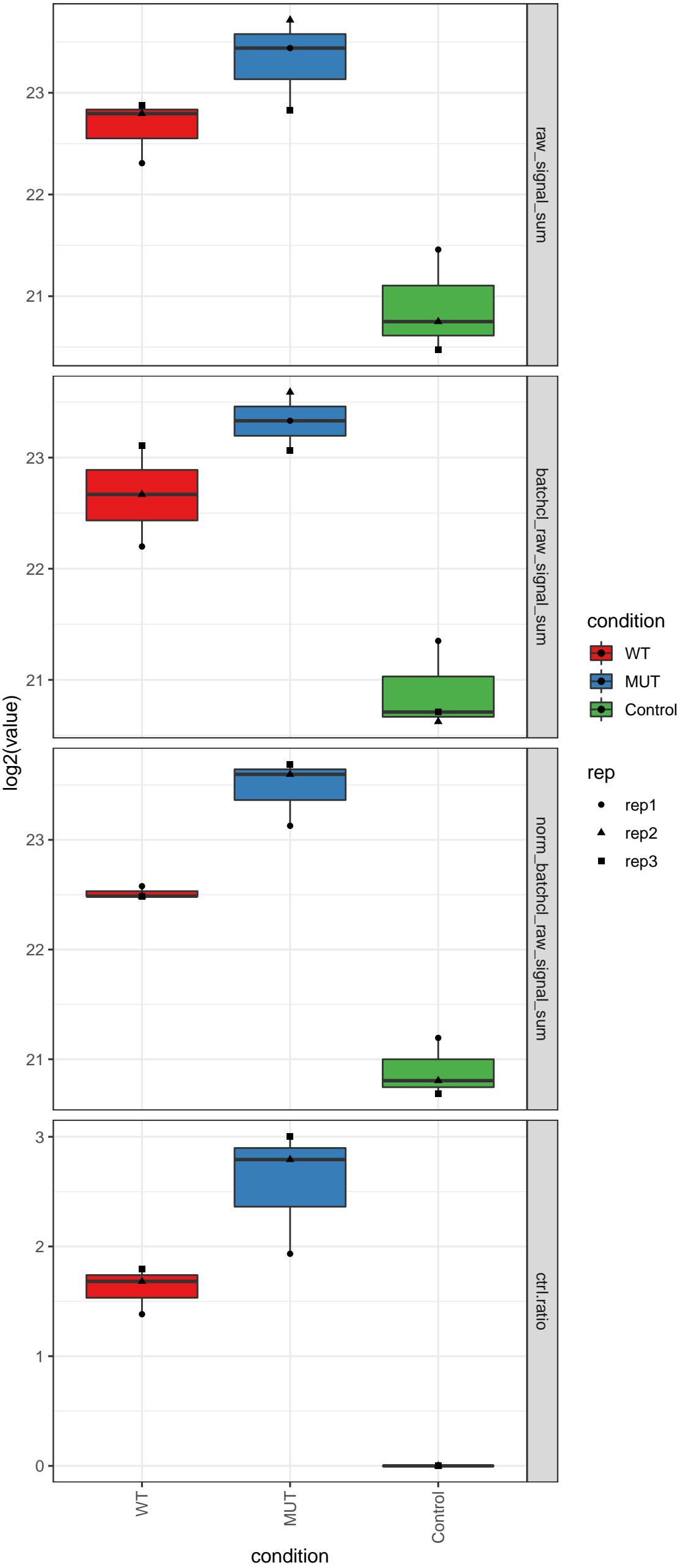


CYC1 – P00044

Cytochrome c iso-1 OS=*Saccharomyces cerevisiae* (strain ATCC 204508)

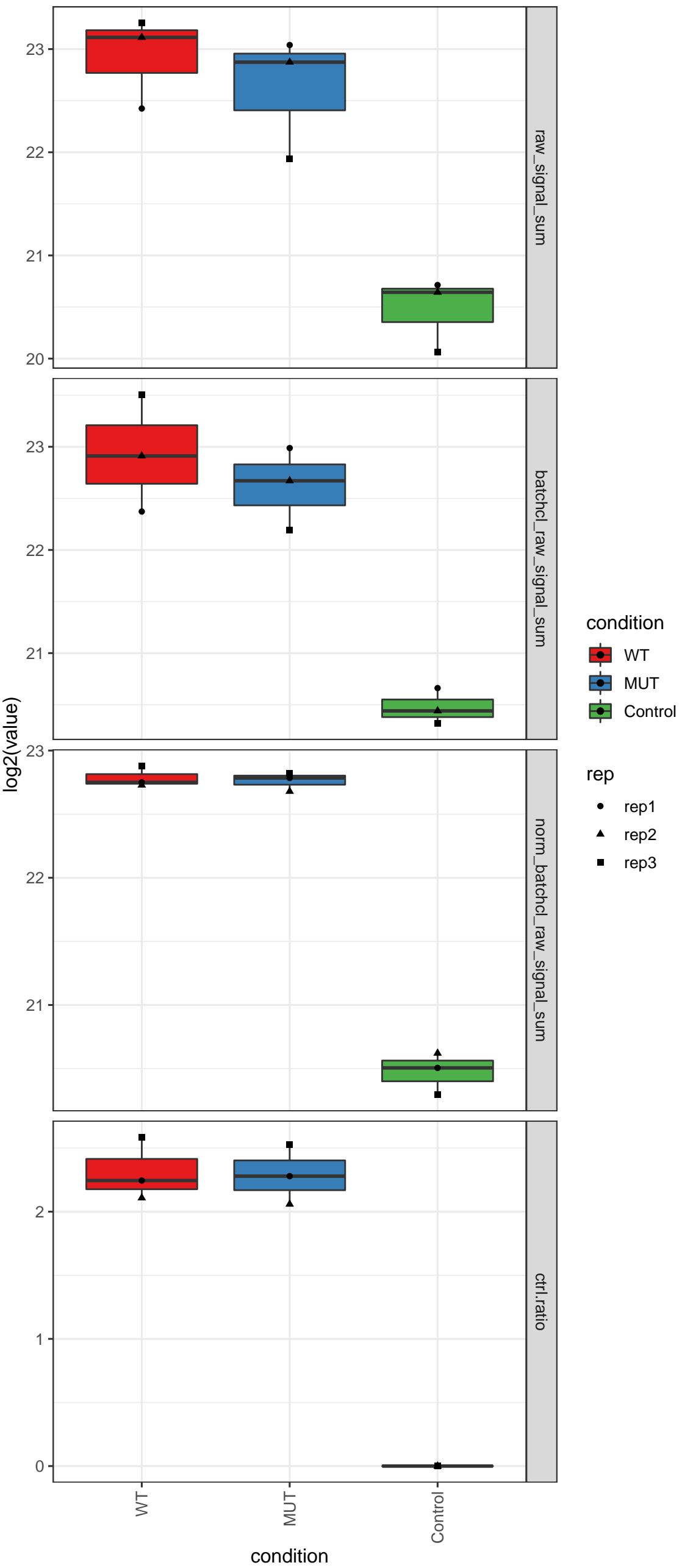
CYT1 – P07143

Cytochrome c1, heme protein, mitochondrial OS=*Saccharomyces cerevisiae*



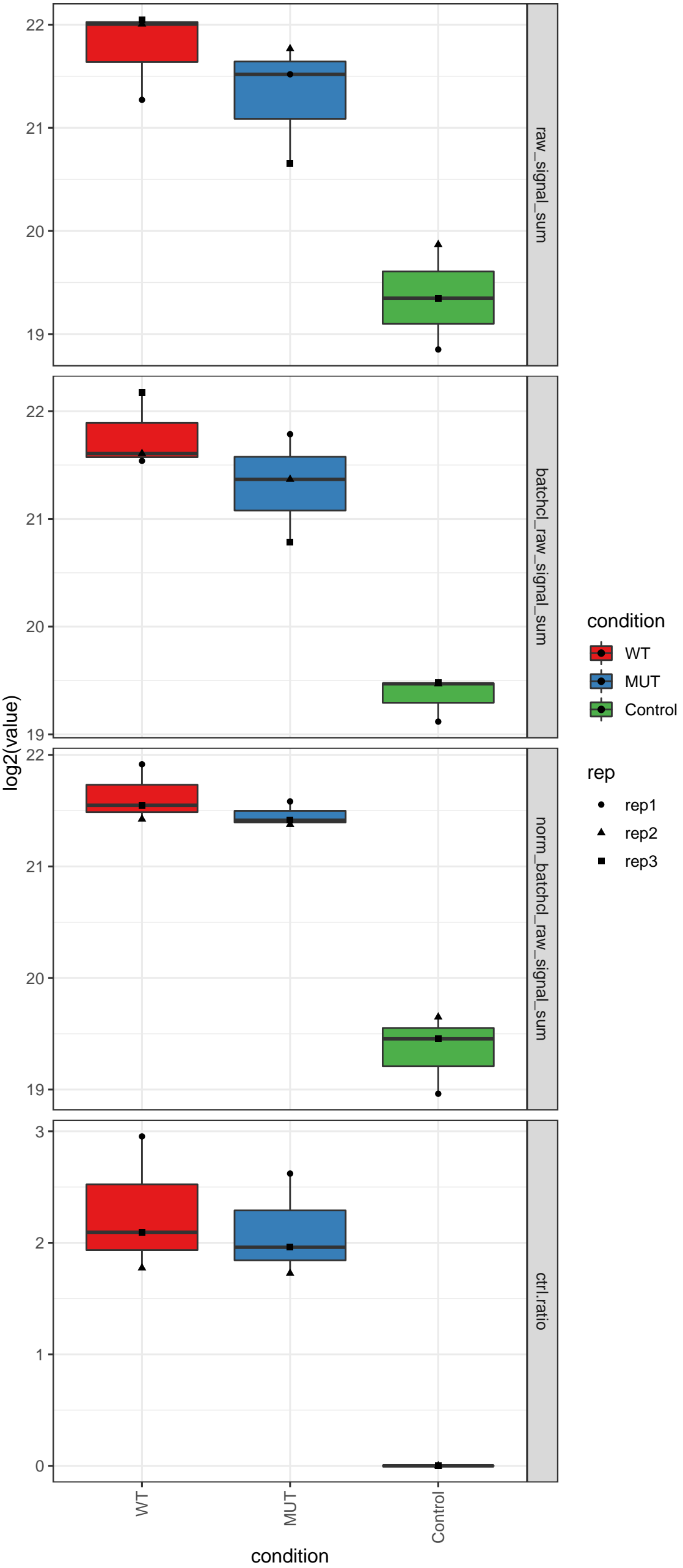
DBP2 – P24783

ATP-dependent RNA helicase DBP2 OS=*Saccharomyces cerevisiae* (strain



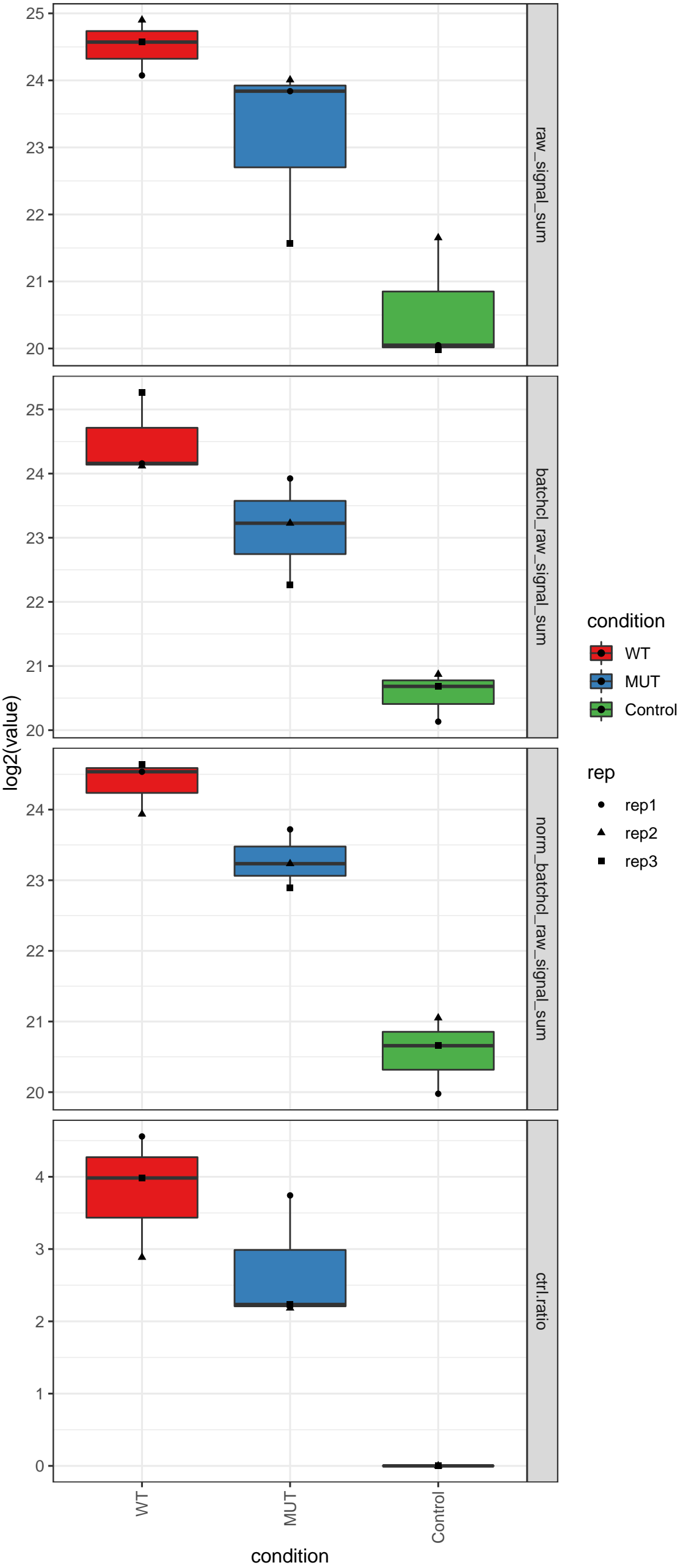
DBP3 – P20447

ATP-dependent RNA helicase DBP3 OS=*Saccharomyces cerevisiae* (strain



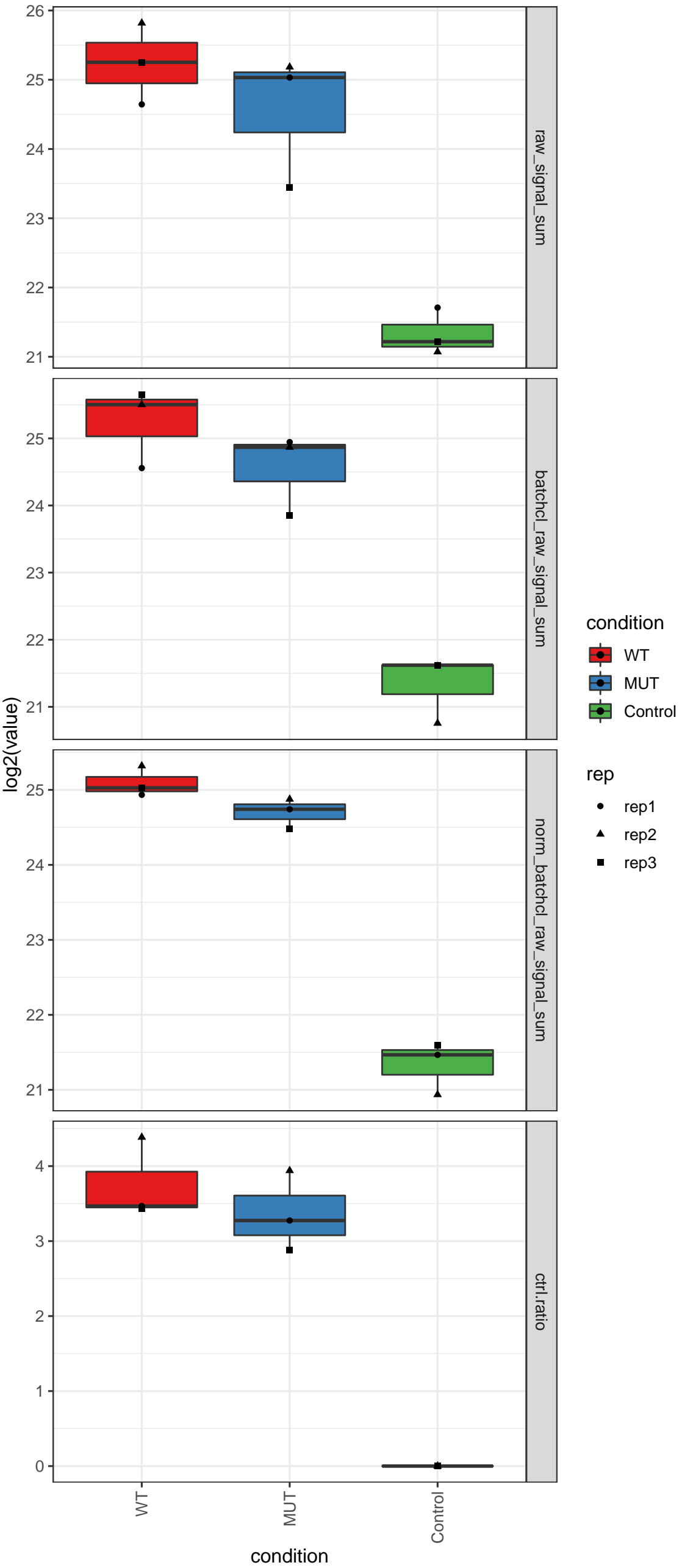
DBP5 – P20449

ATP-dependent RNA helicase DBP5 OS=Saccharomyces cerevisiae (strain



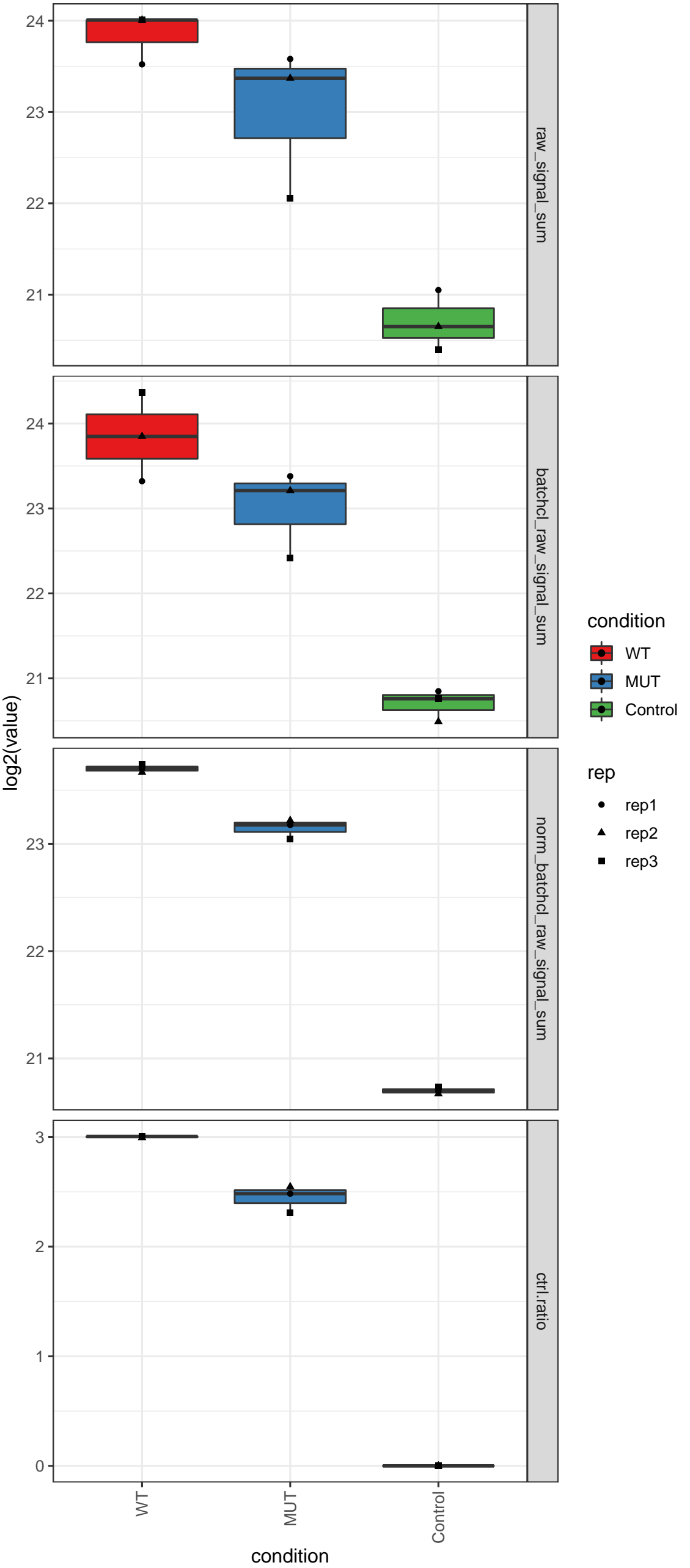
DED1 – P06634

ATP-dependent RNA helicase DED1 OS=*Saccharomyces cerevisiae* (strain



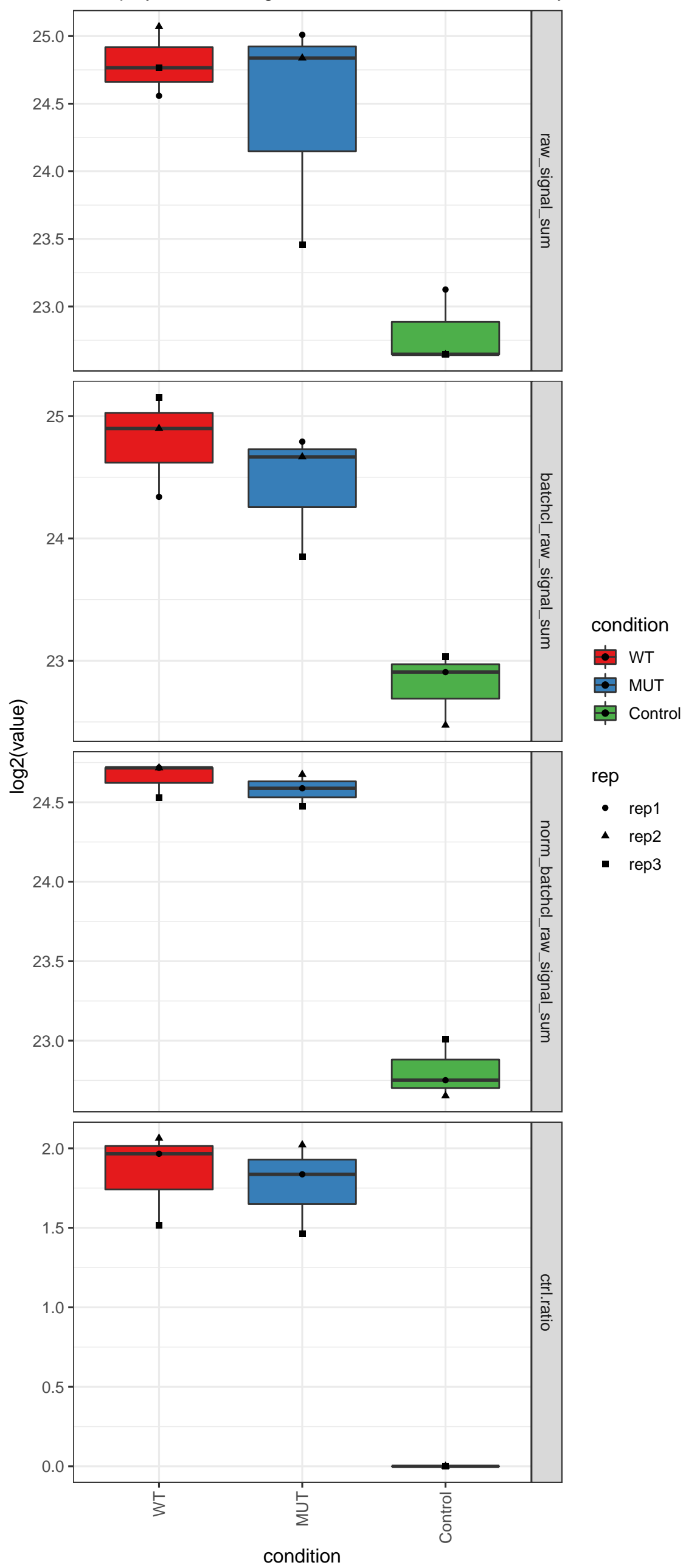
DED81 – P38707

Asparagine--tRNA ligase, cytoplasmic OS=*Saccharomyces cerevisiae* (str



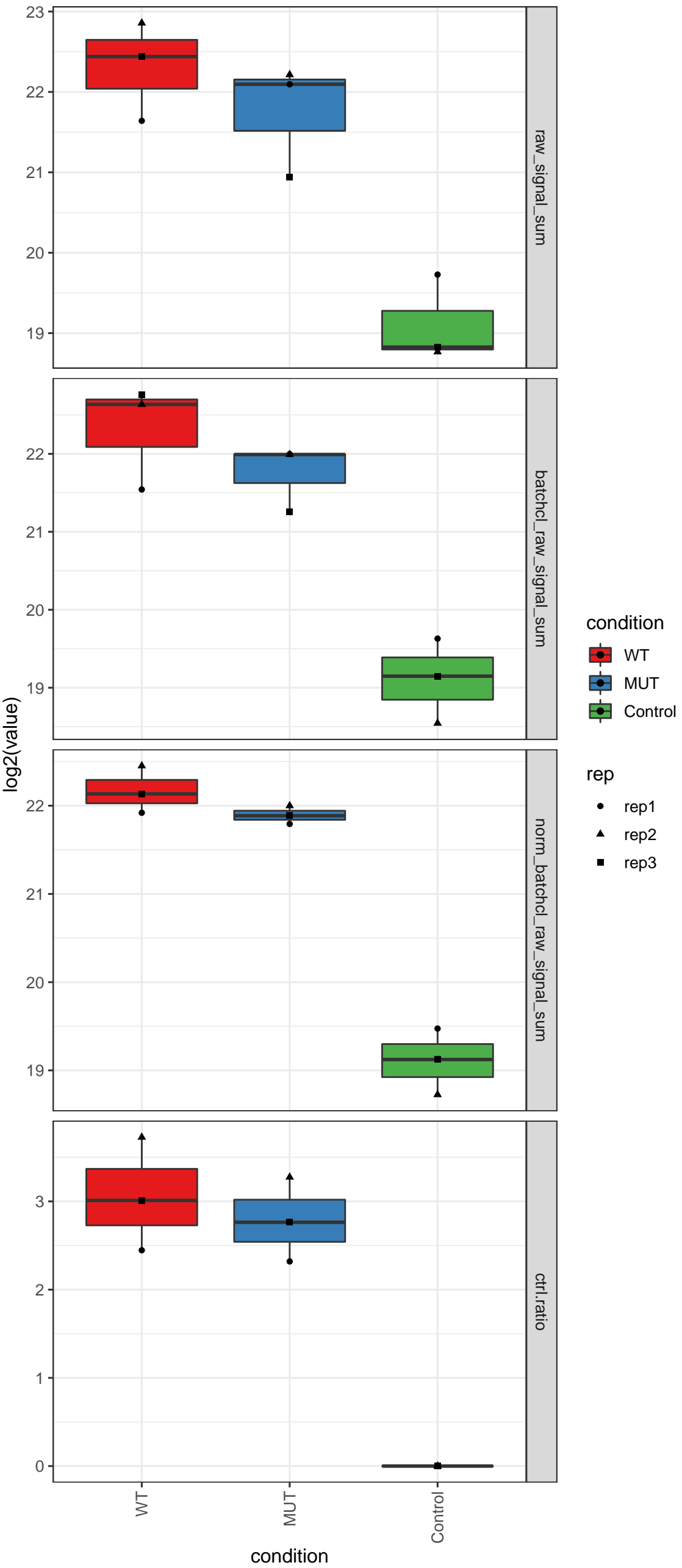
DEF1 – P35732

RNA polymerase II degradation factor 1 OS=*Saccharomyces cerevisiae* (



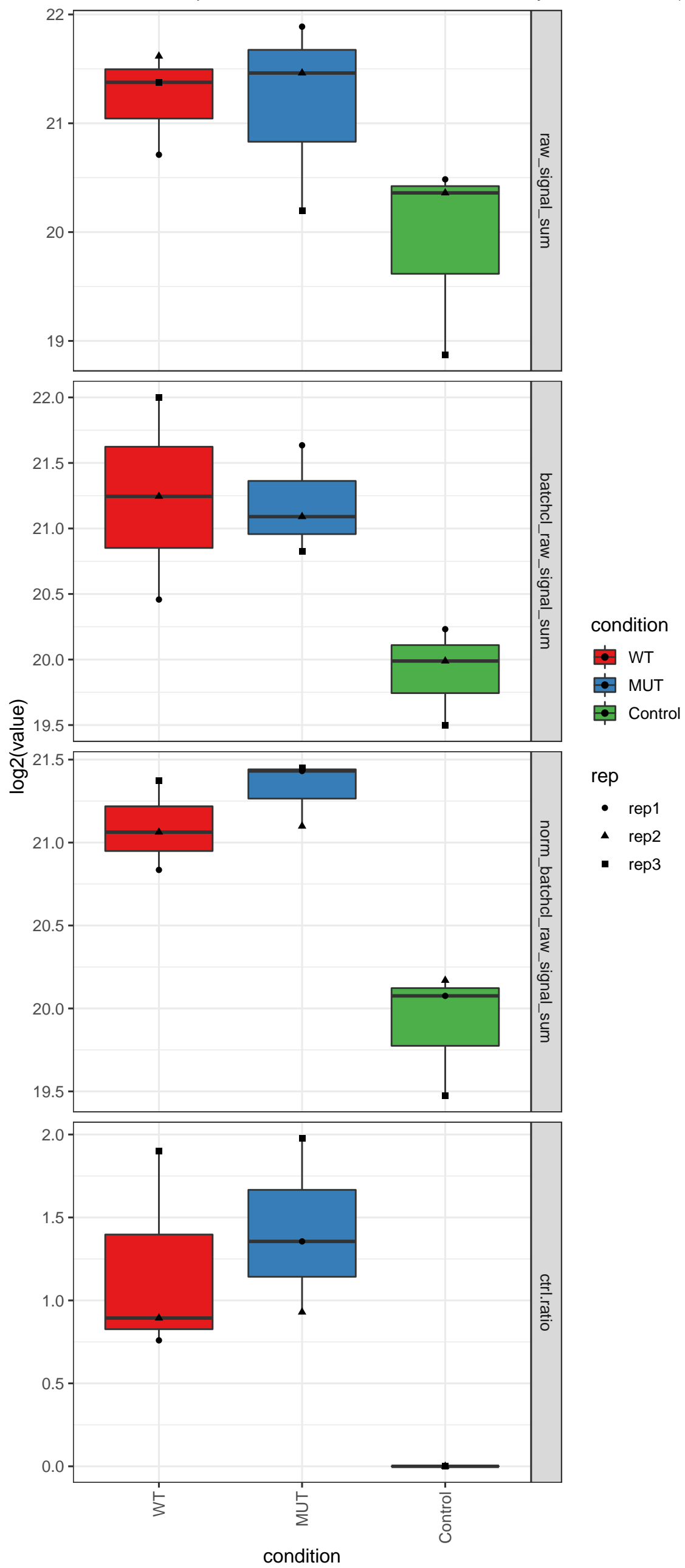
DHH1 – P39517

ATP-dependent RNA helicase DHH1 OS=*Saccharomyces cerevisiae* (stra



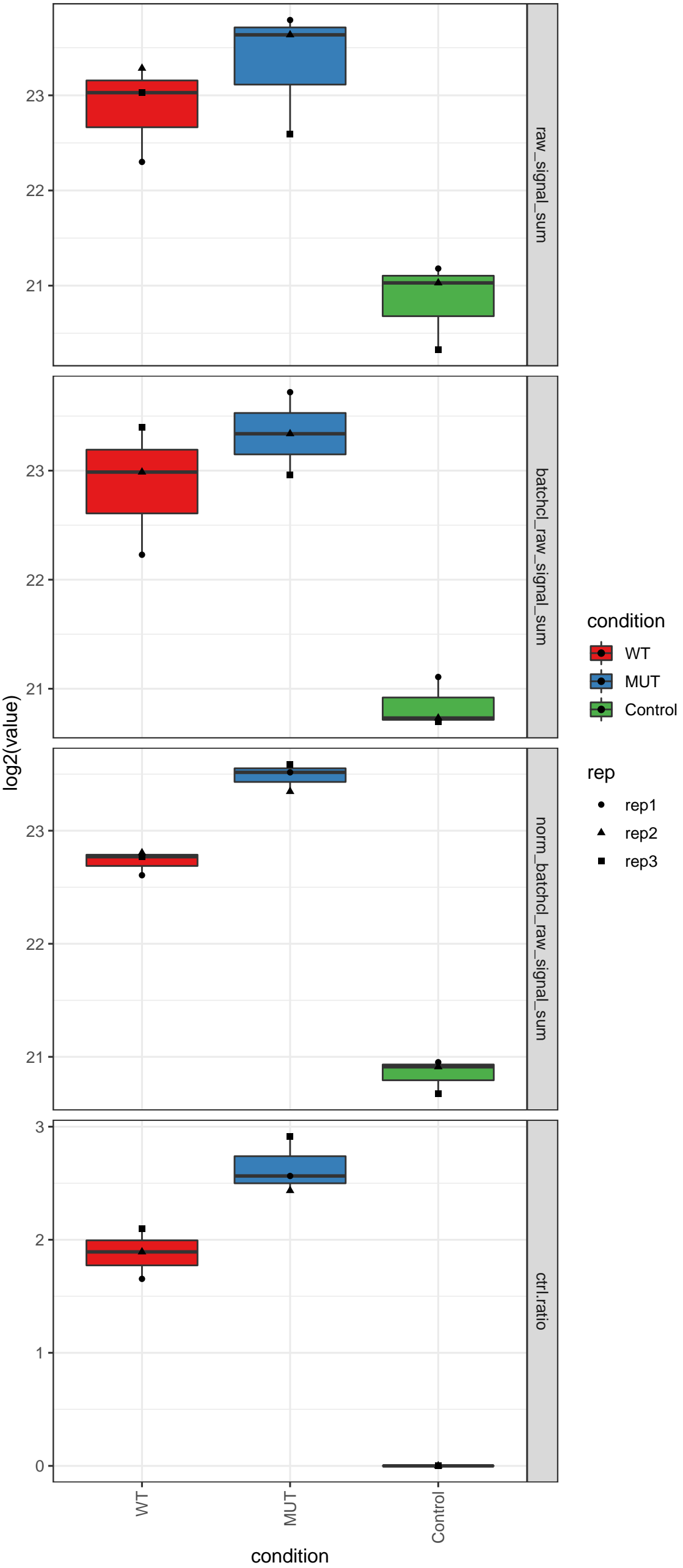
DIS3 – Q08162

Exosome complex exonuclease DIS3 OS=*Saccharomyces cerevisiae* (strain



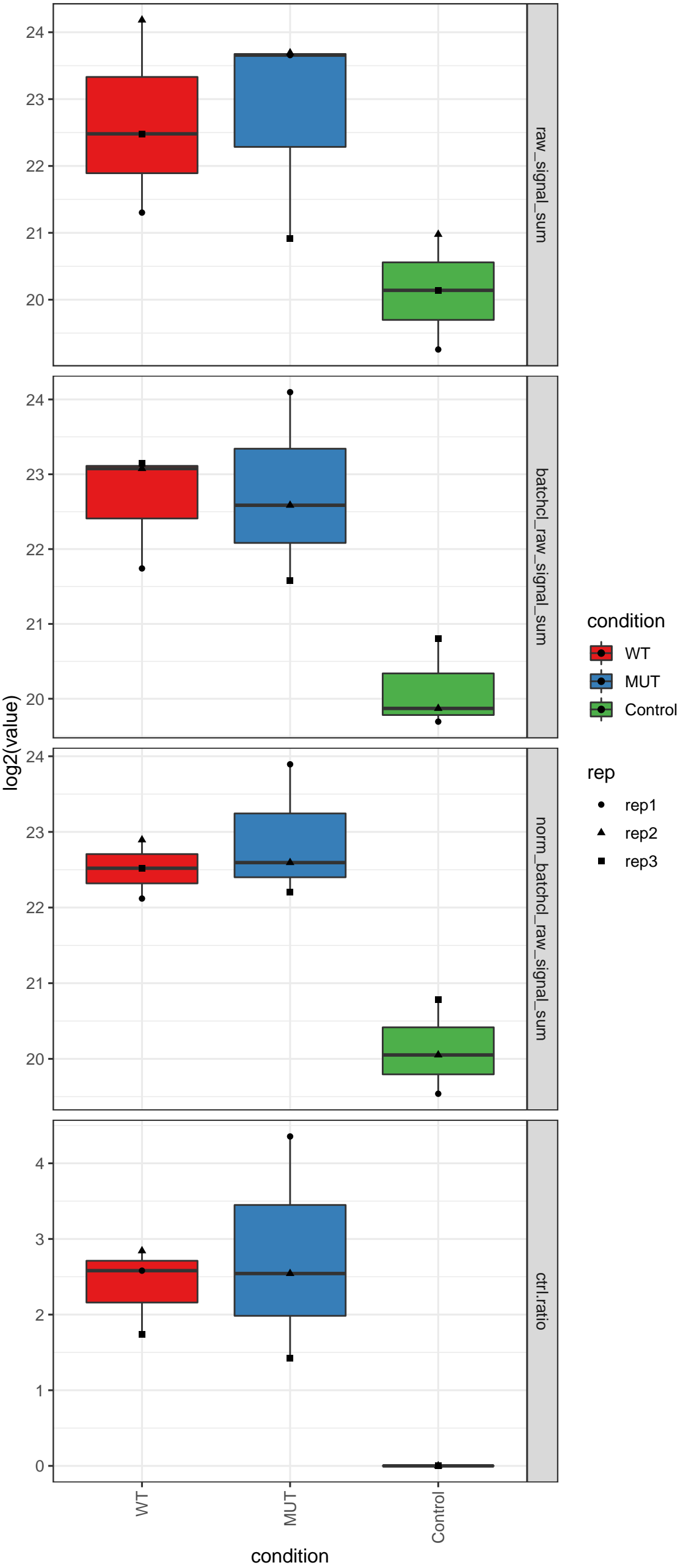
DLD1 – P32891

D-lactate dehydrogenase [cytochrome] 1, mitochondrial OS=Saccharomy



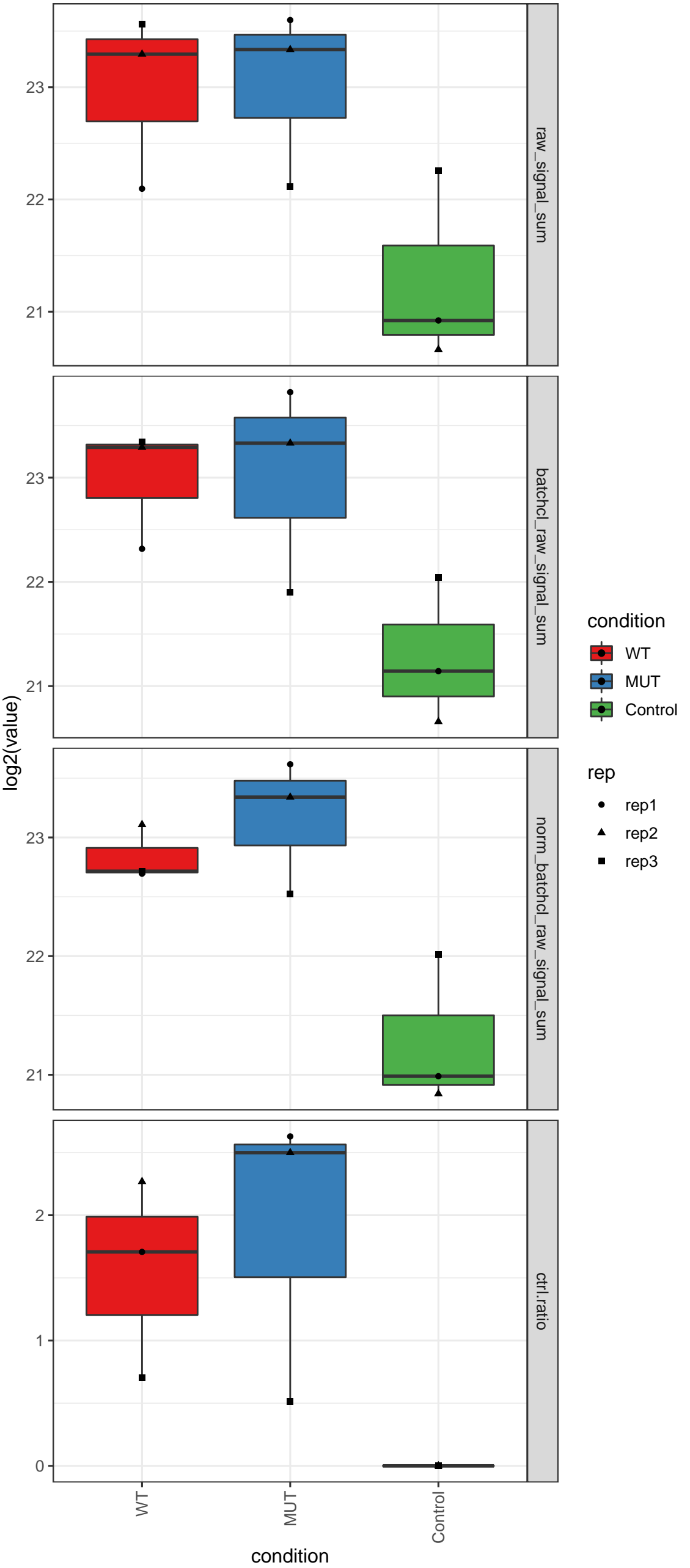
DMA2 – P53924

E3 ubiquitin–protein ligase DMA2 OS=*Saccharomyces cerevisiae* (strain A



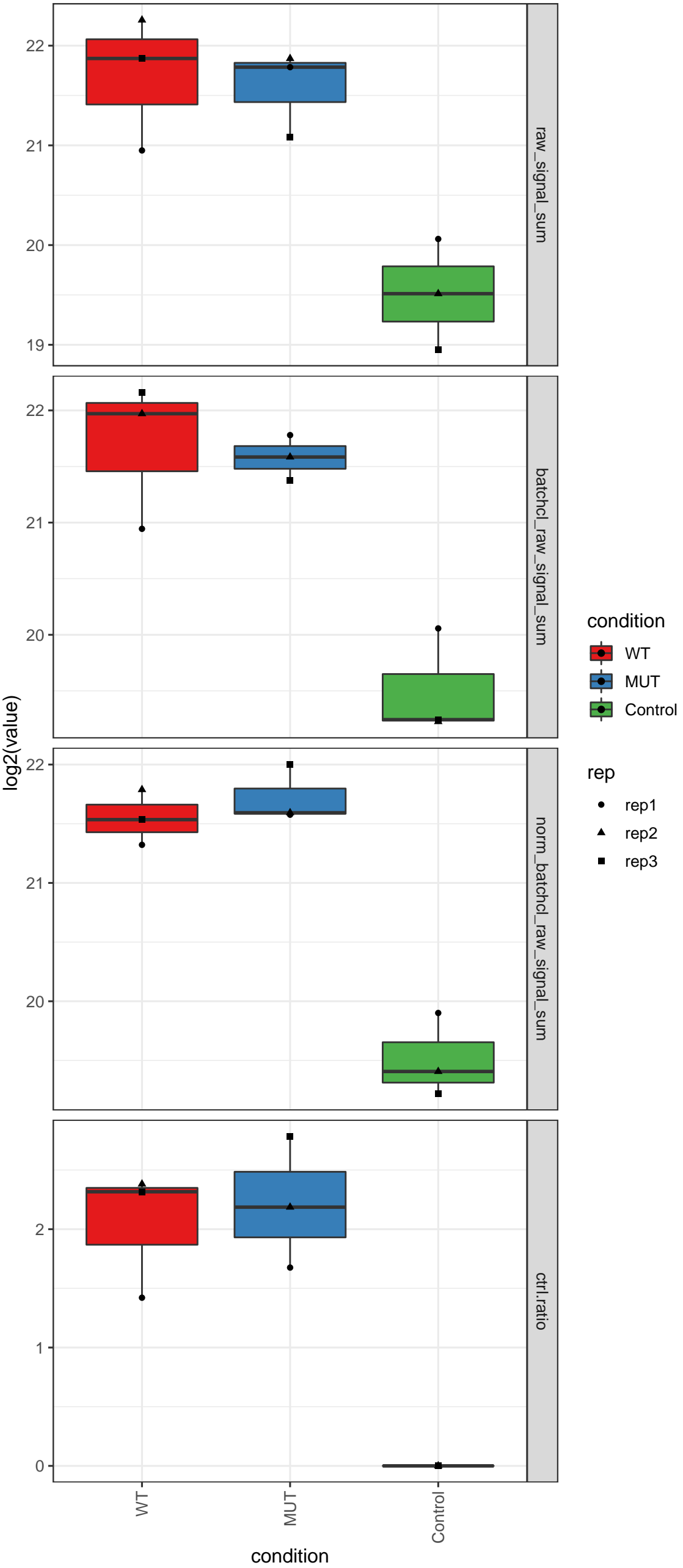
DMC1 – P25453

Meiotic recombination protein DMC1 OS=*Saccharomyces cerevisiae* (strain



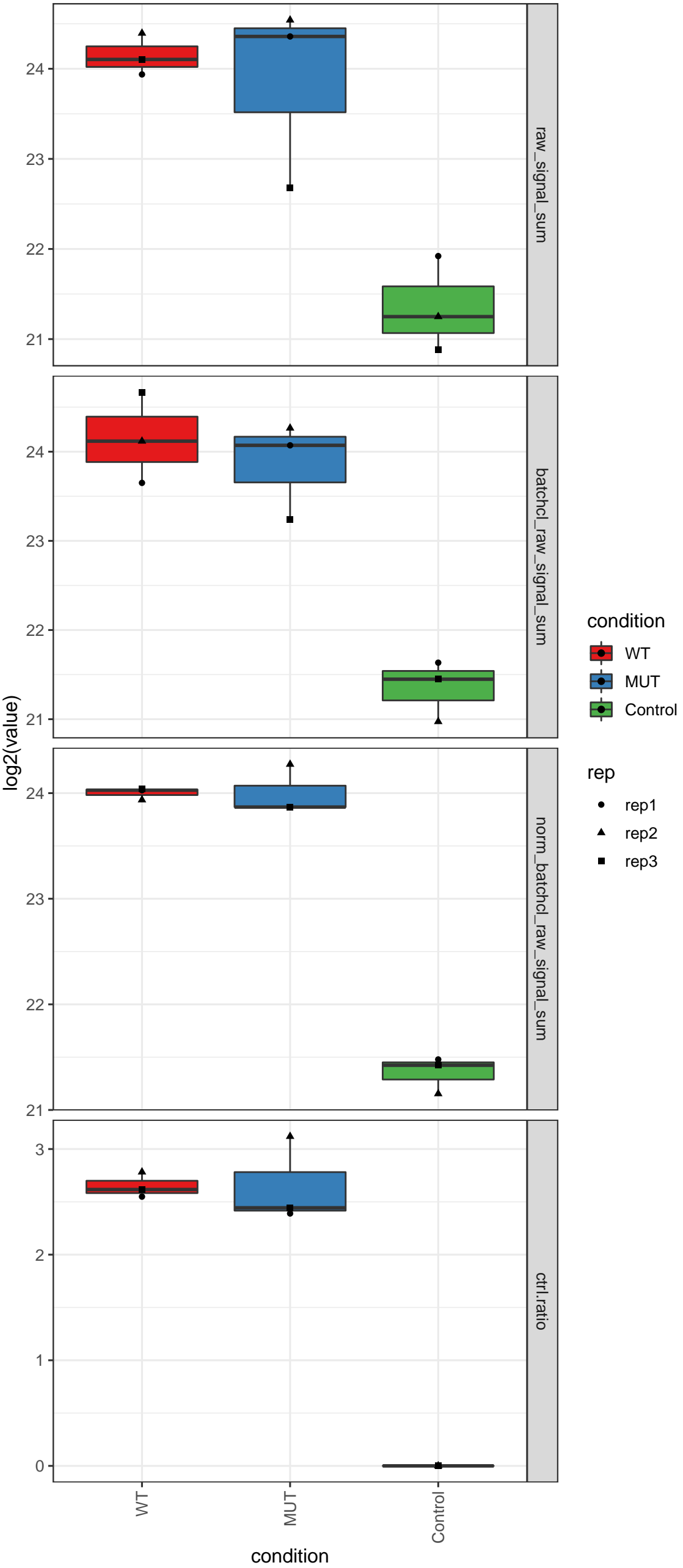
DNM1 – P54861

Dynamin-related protein DNM1 OS=*Saccharomyces cerevisiae* (strain ATCC 22016 / S288c)



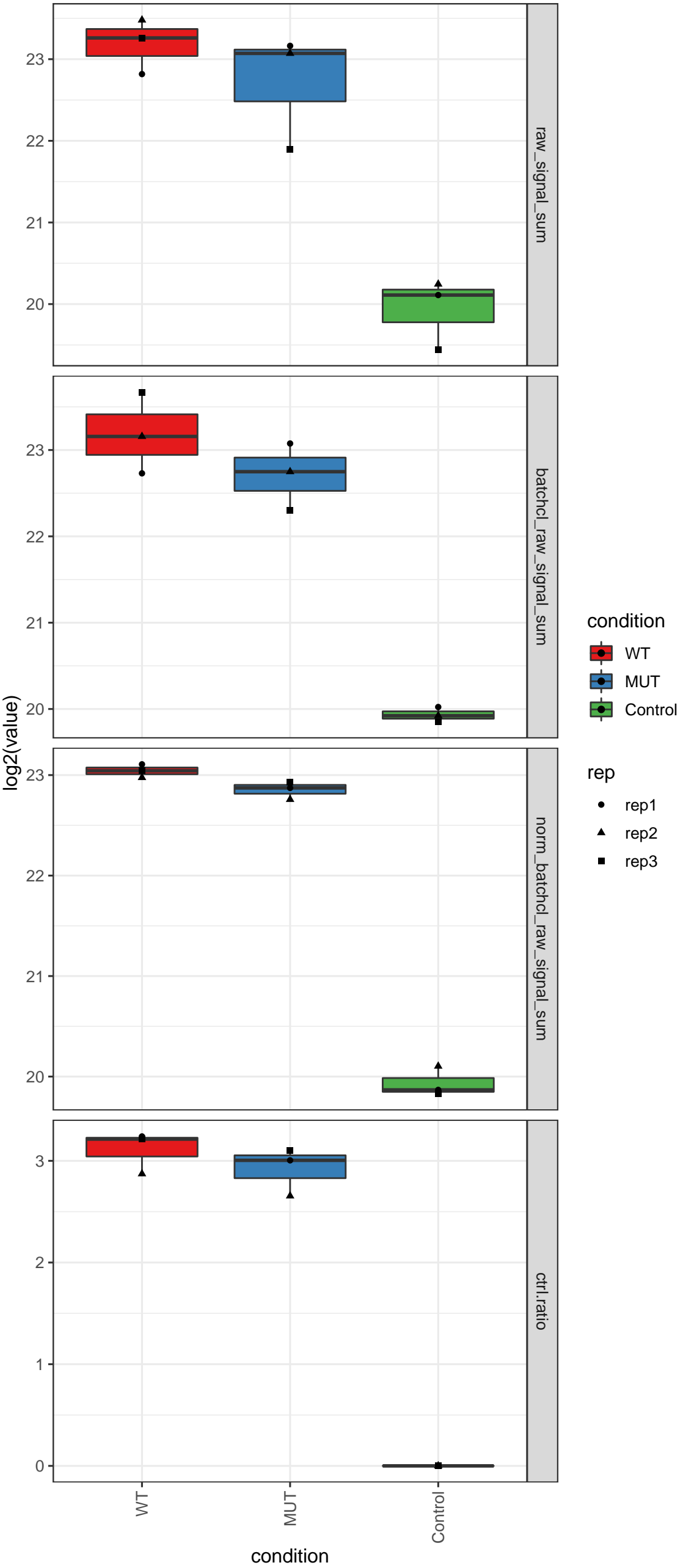
DOT5 – P40553

Peroxisredoxin DOT5 OS=*Saccharomyces cerevisiae* (strain ATCC 204508)



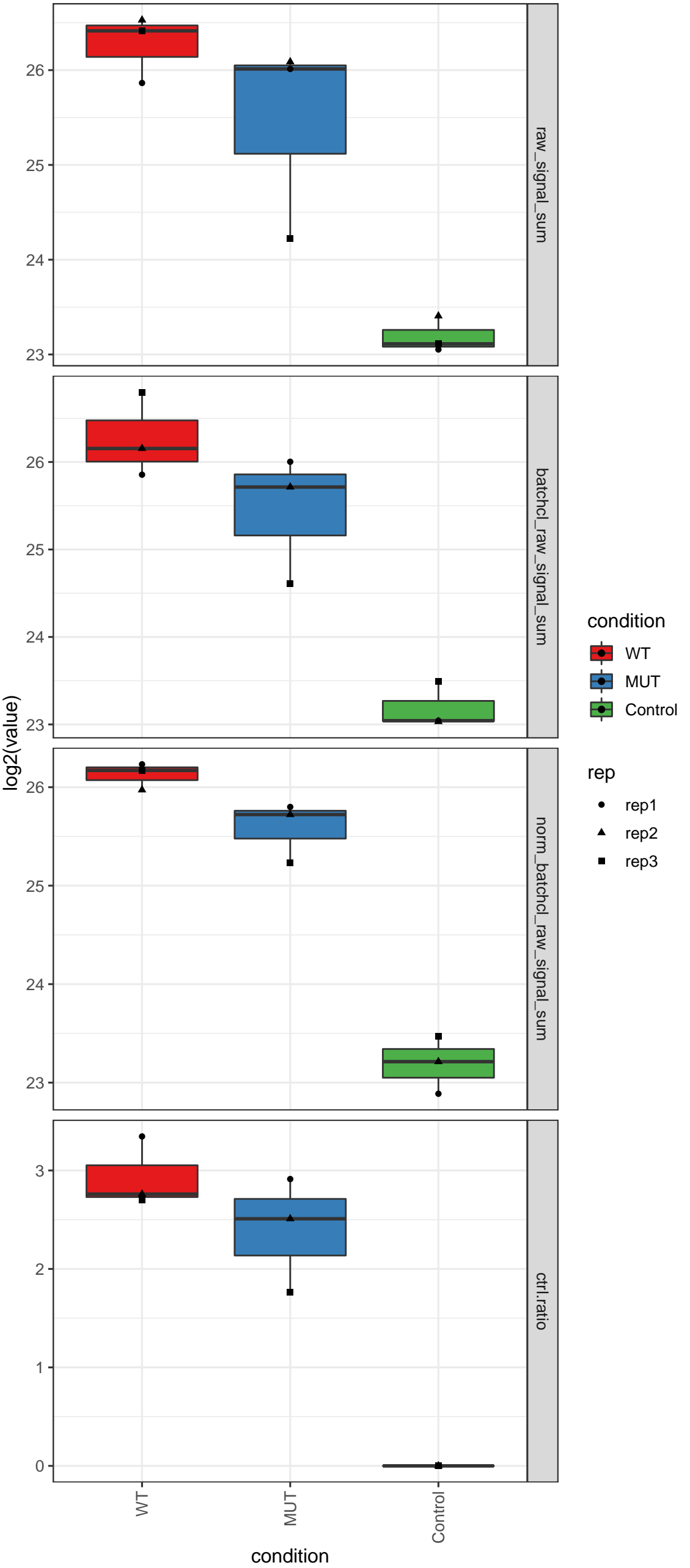
DPM1 – P14020

Dolichol-phosphate mannosyltransferase OS=*Saccharomyces cerevisiae* (



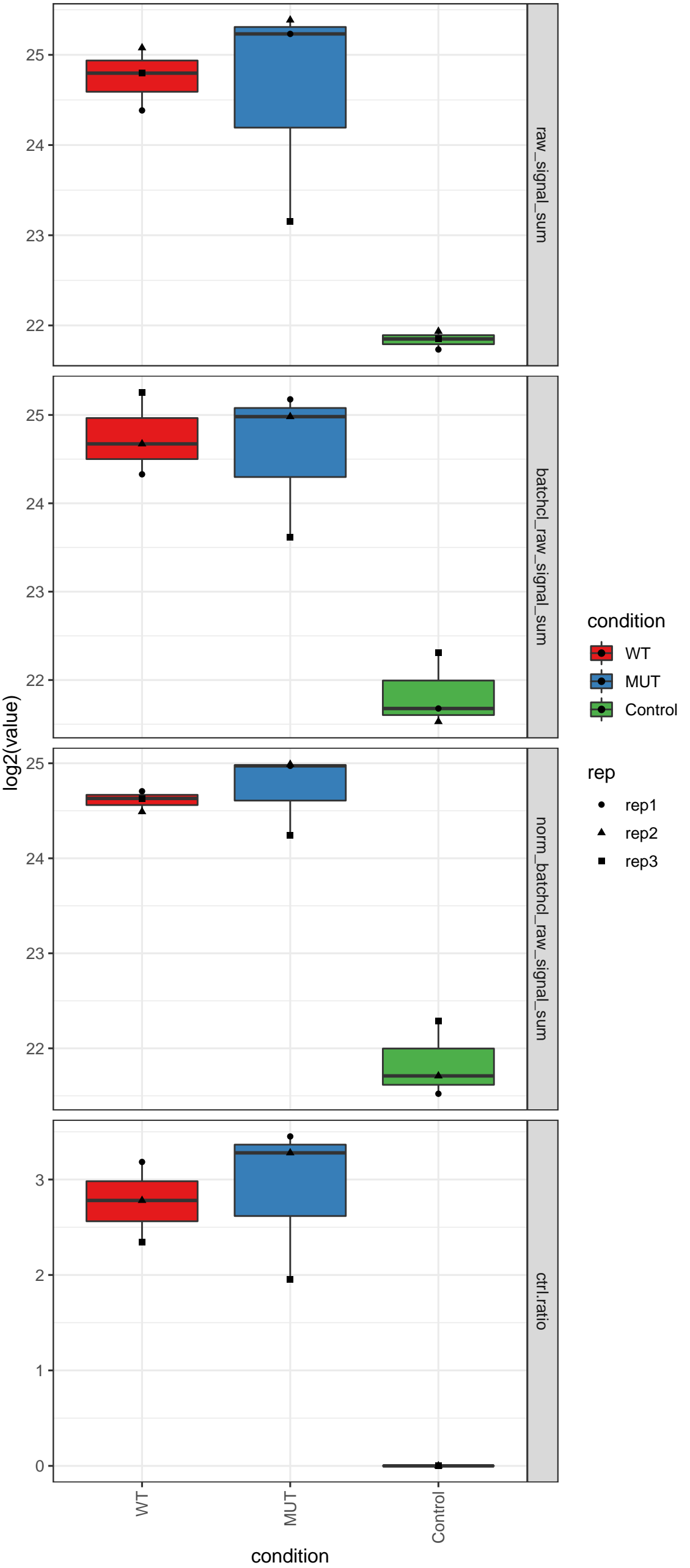
DPS1 – P04802

Aspartate--tRNA ligase, cytoplasmic OS=*Saccharomyces cerevisiae* (stra



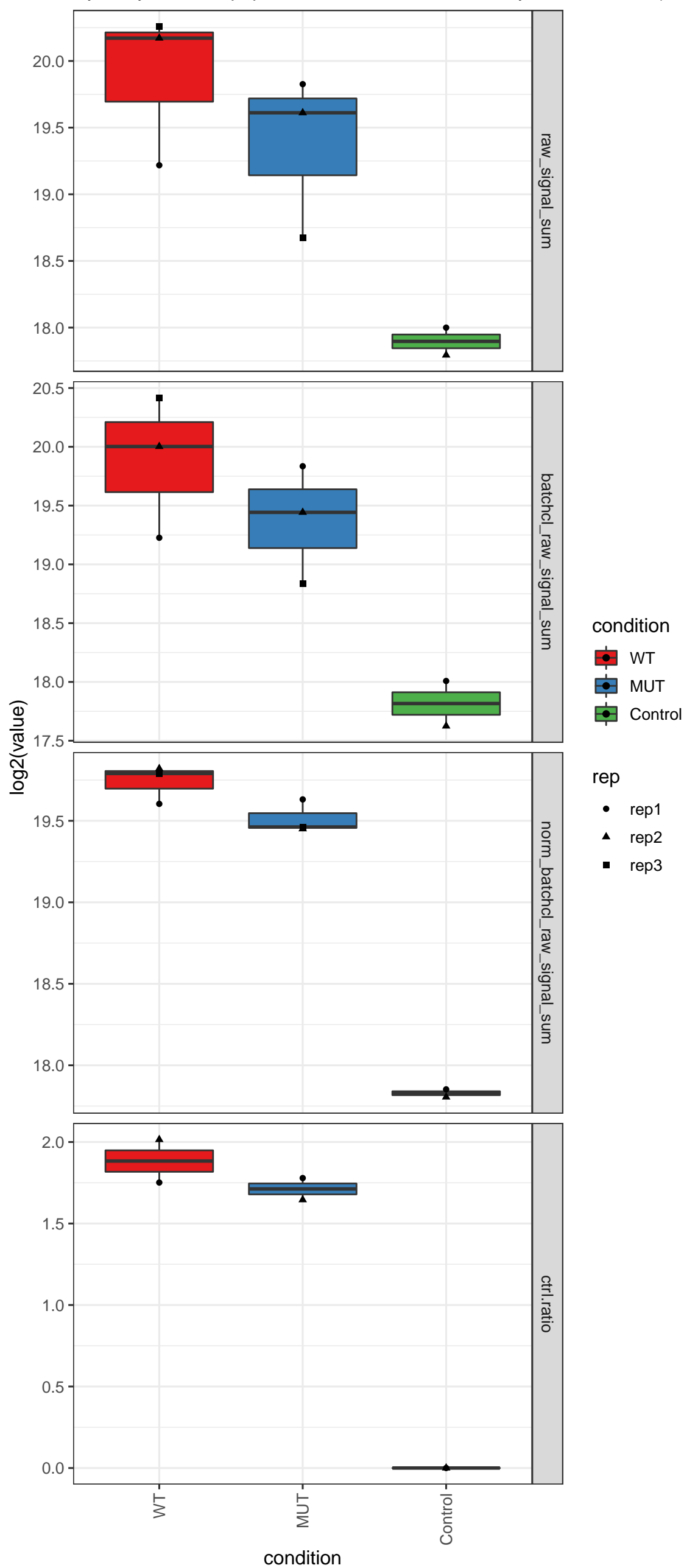
DST1 – P07273

Transcription elongation factor S-II OS=*Saccharomyces cerevisiae* (strain



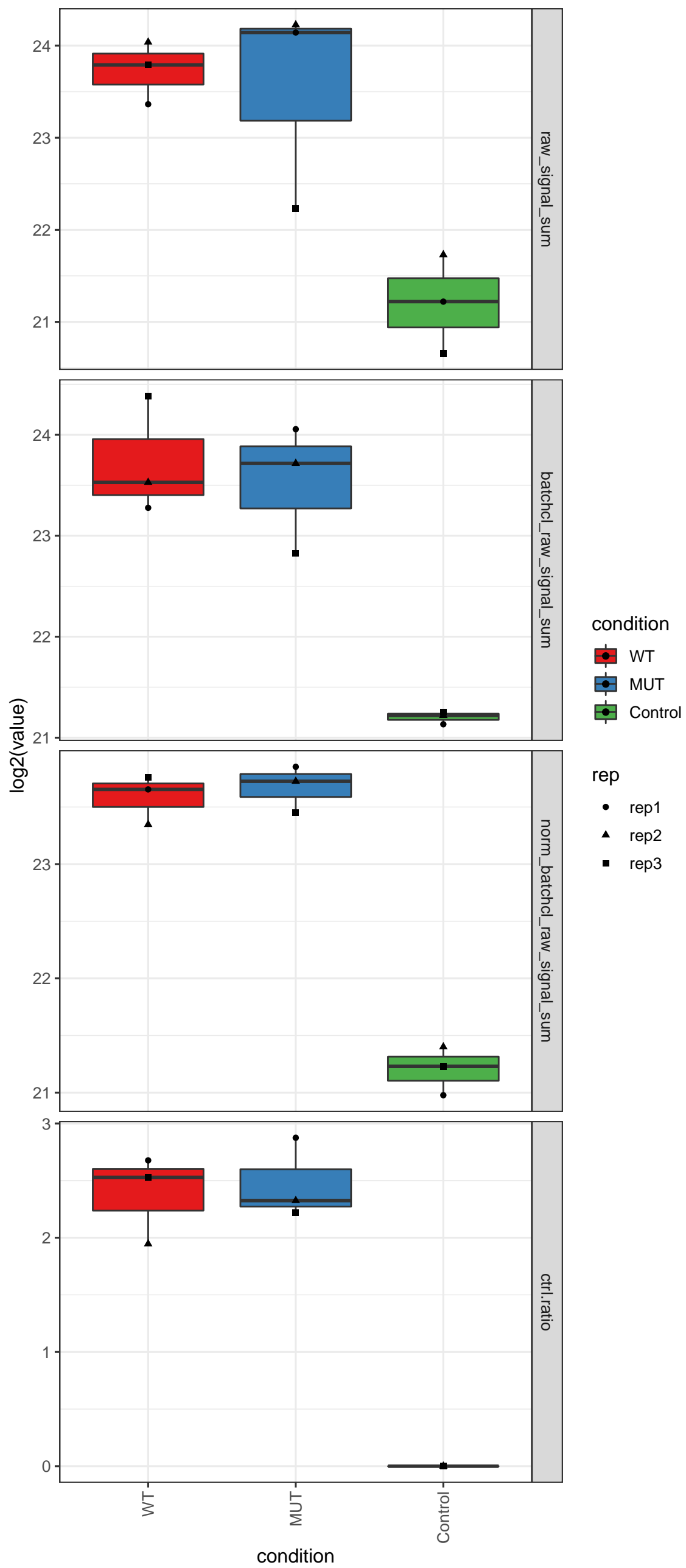
DUG1 – P43616

Cys–Gly metallodipeptidase DUG1 OS=*Saccharomyces cerevisiae* (strain



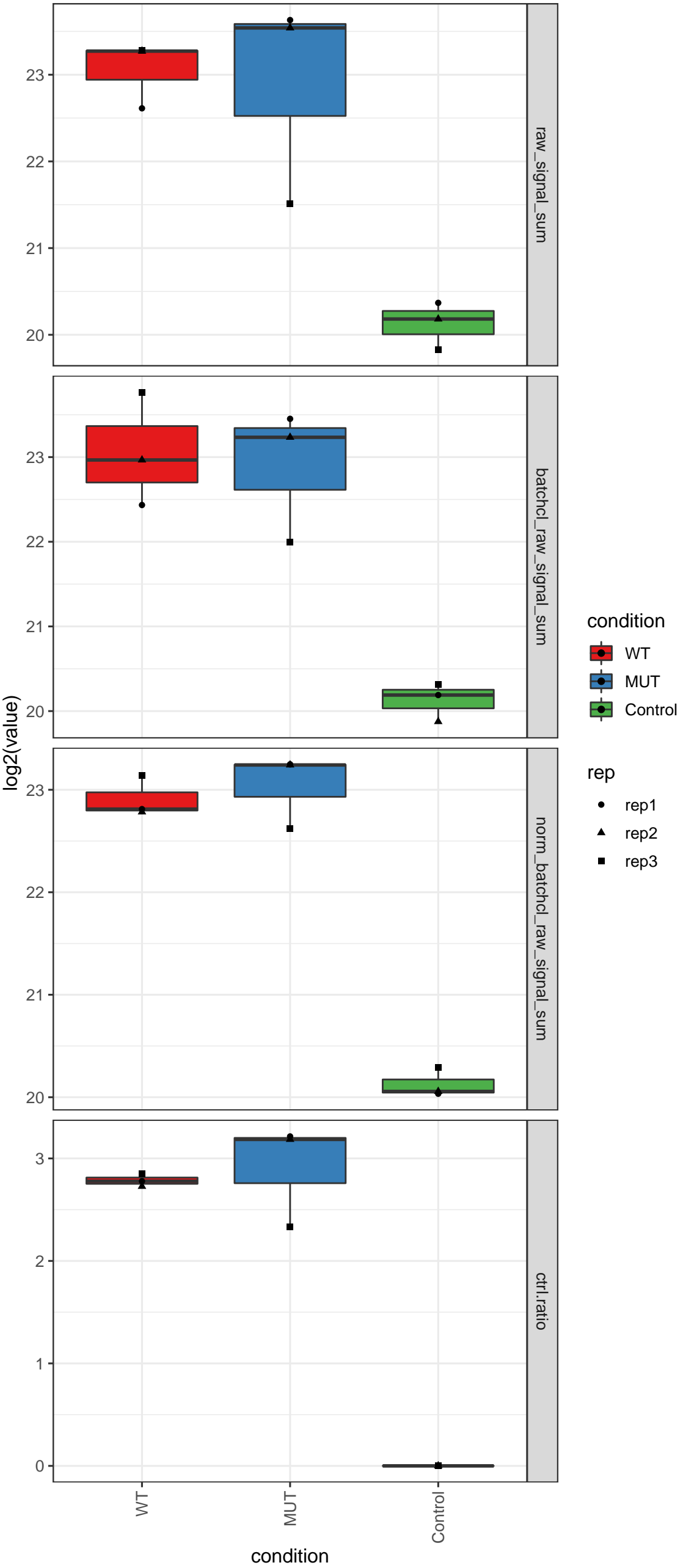
EAF3 – Q12432

Chromatin modification–related protein EAF3 OS=*Saccharomyces cerevisiae*



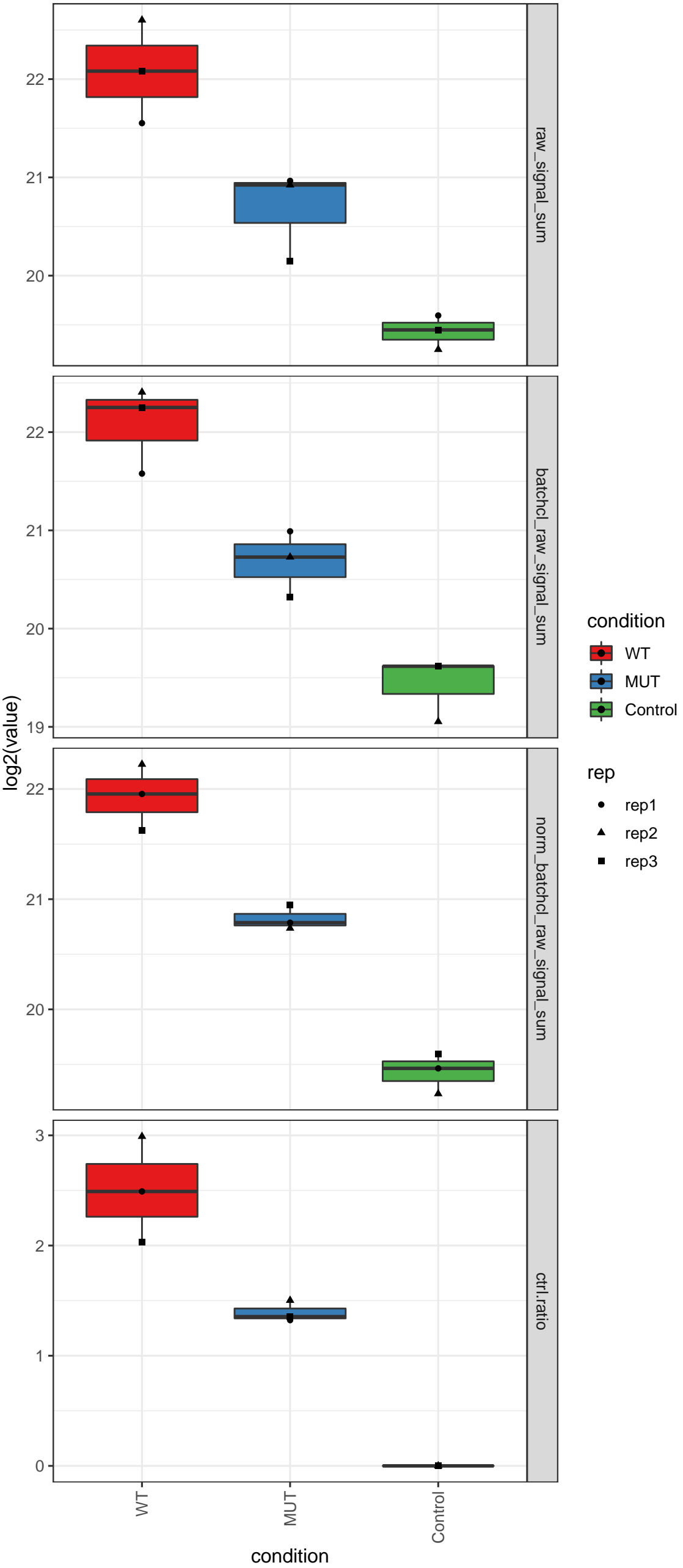
EBP2 – P36049

rRNA-processing protein EBP2 OS=*Saccharomyces cerevisiae* (strain ATC



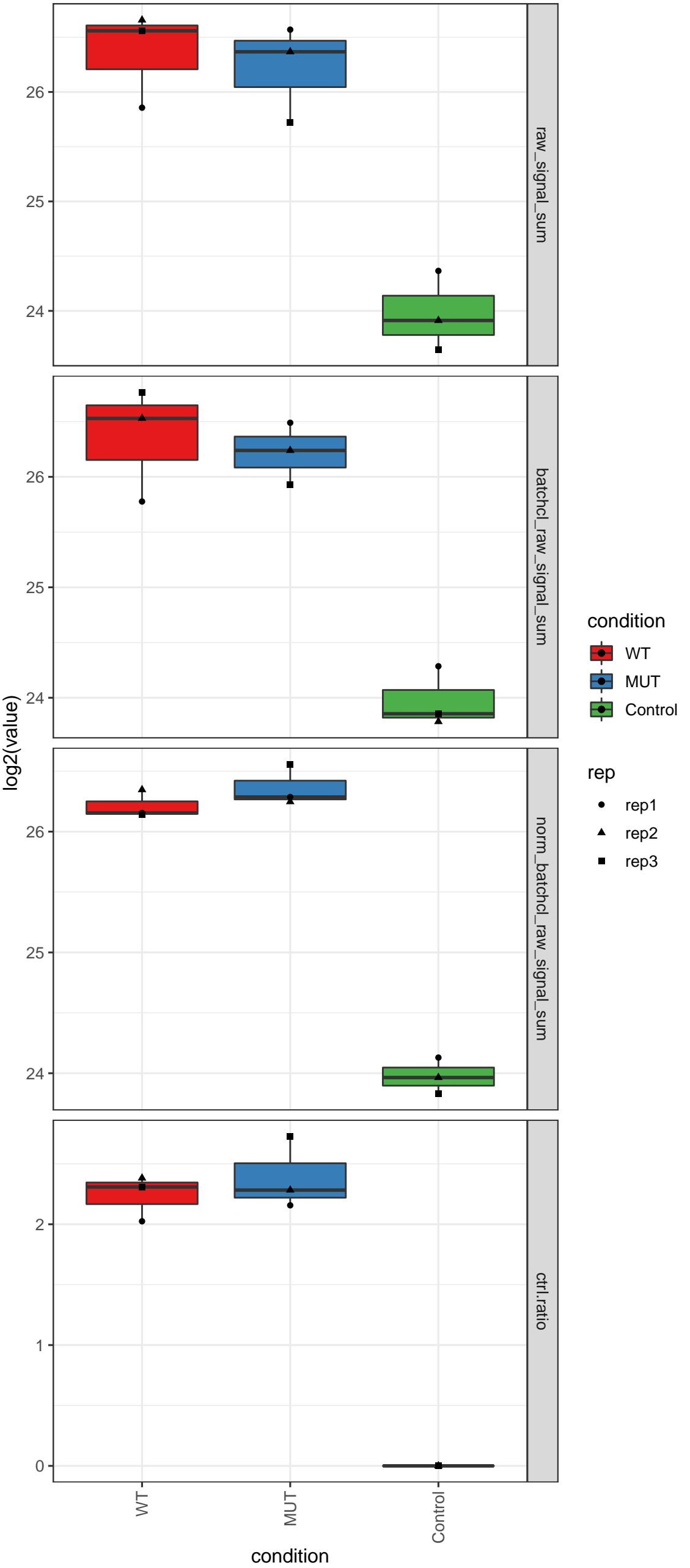
EDE1 – P34216

EH domain-containing and endocytosis protein 1 OS=*Saccharomyces cerevisiae*



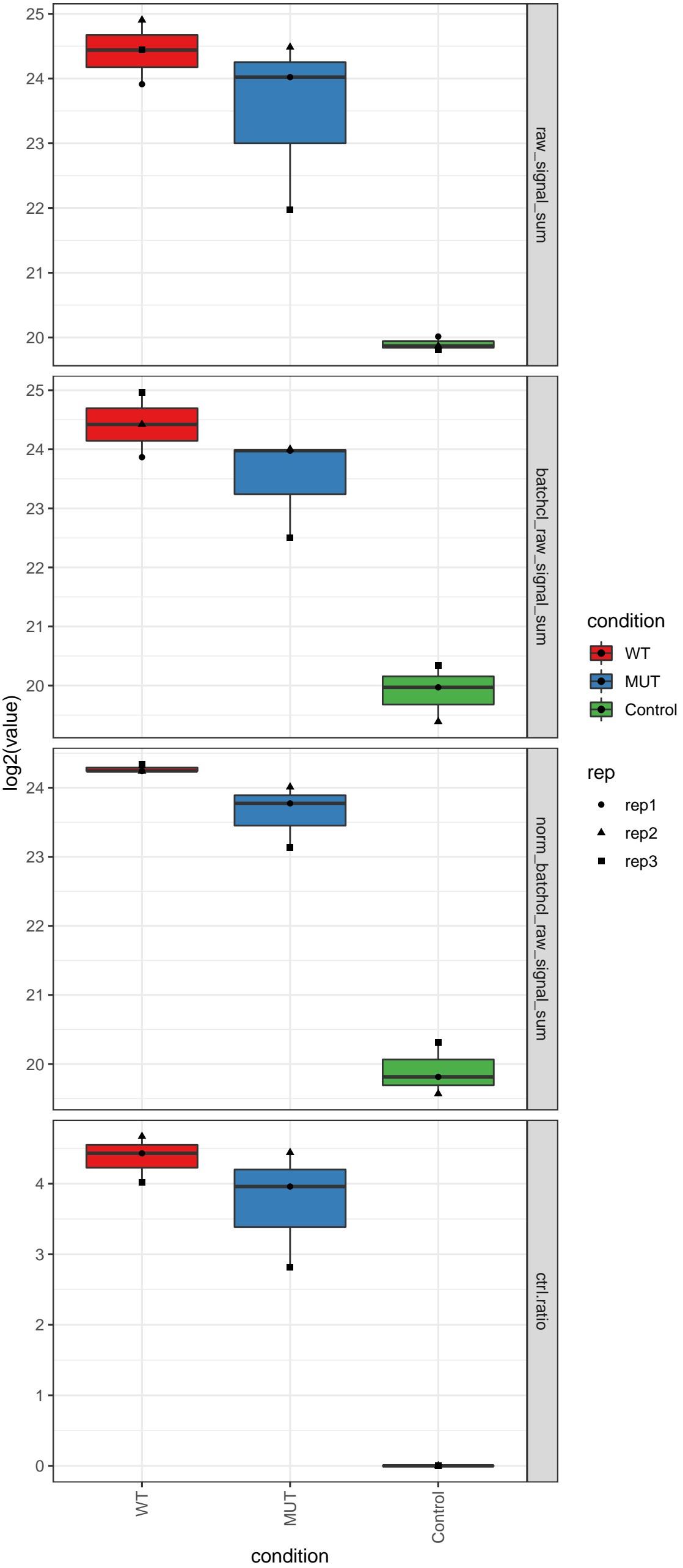
EFT1 – P32324

Elongation factor 2 OS=*Saccharomyces cerevisiae* (strain ATCC 204508 /



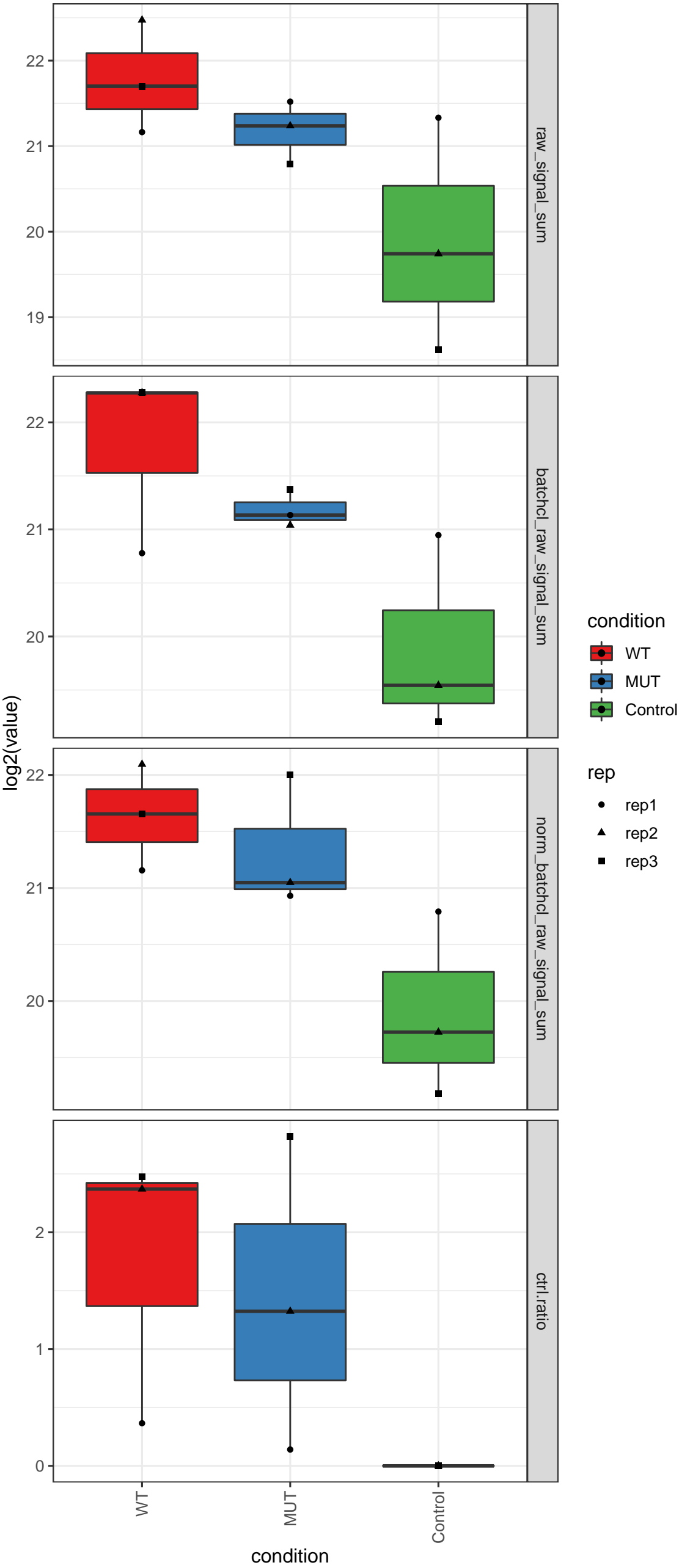
EGD1 – Q02642

Nascent polypeptide-associated complex subunit beta-1 OS=Saccharomyces cerevisiae



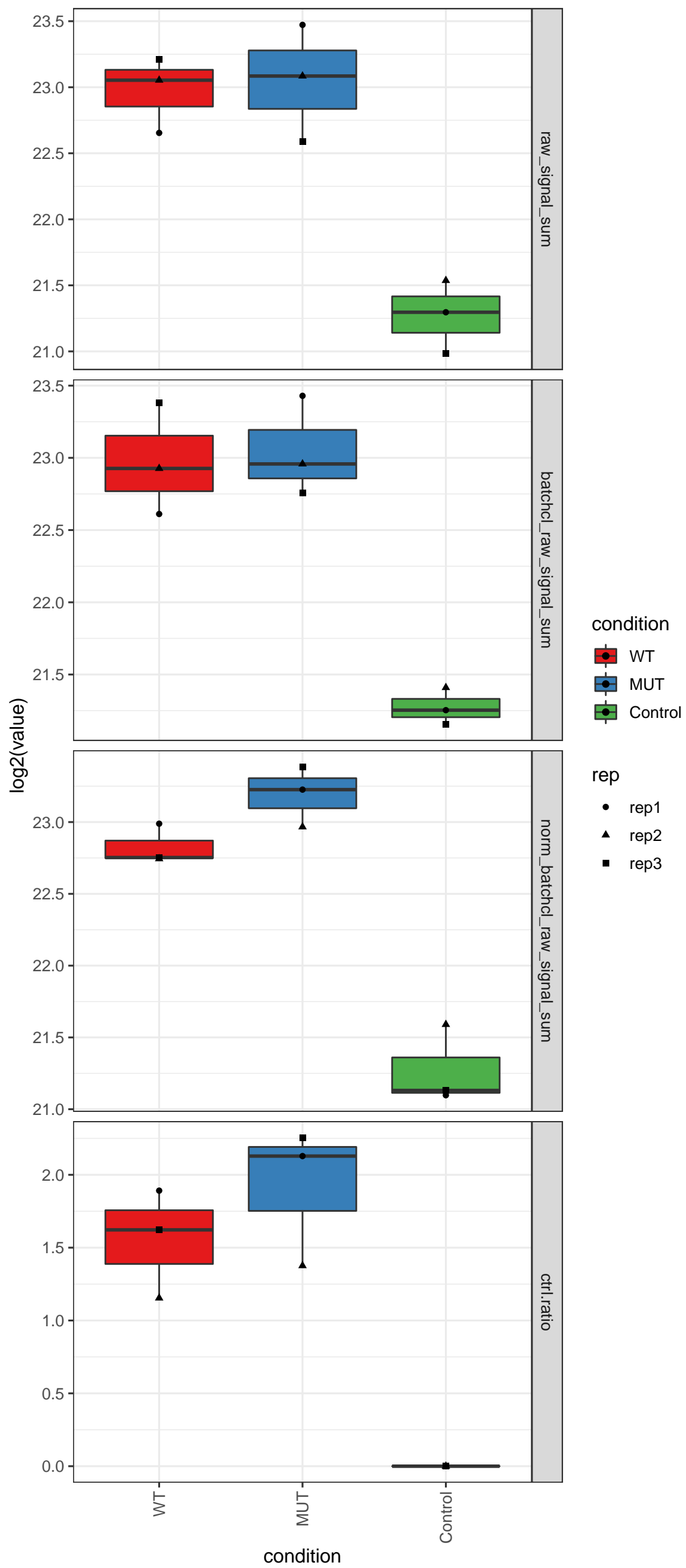
EHT1 – P38295

Medium-chain fatty acid ethyl ester synthase/esterase 2 OS=Saccharomyces cerevisiae



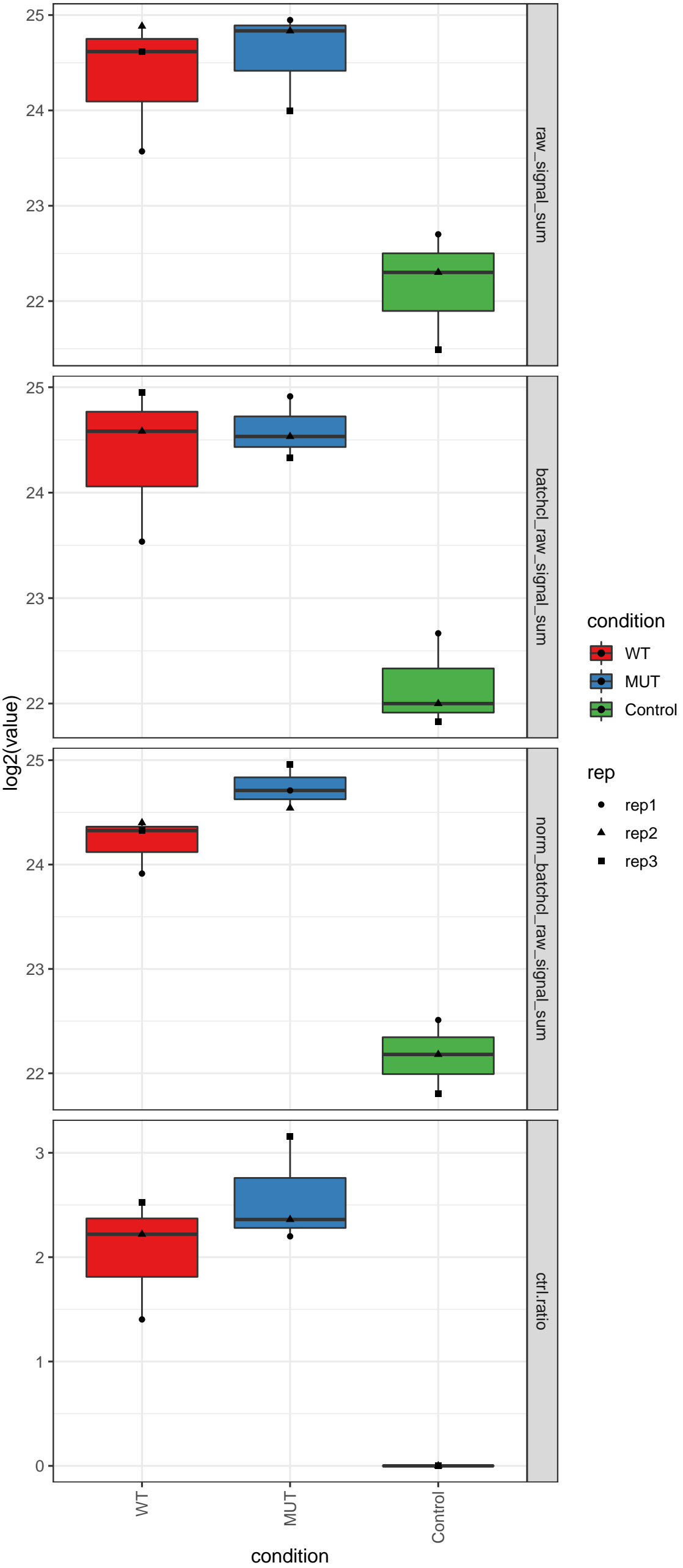
EIS1 – Q05050

Eisosome protein 1 OS=*Saccharomyces cerevisiae* (strain ATCC 204508)



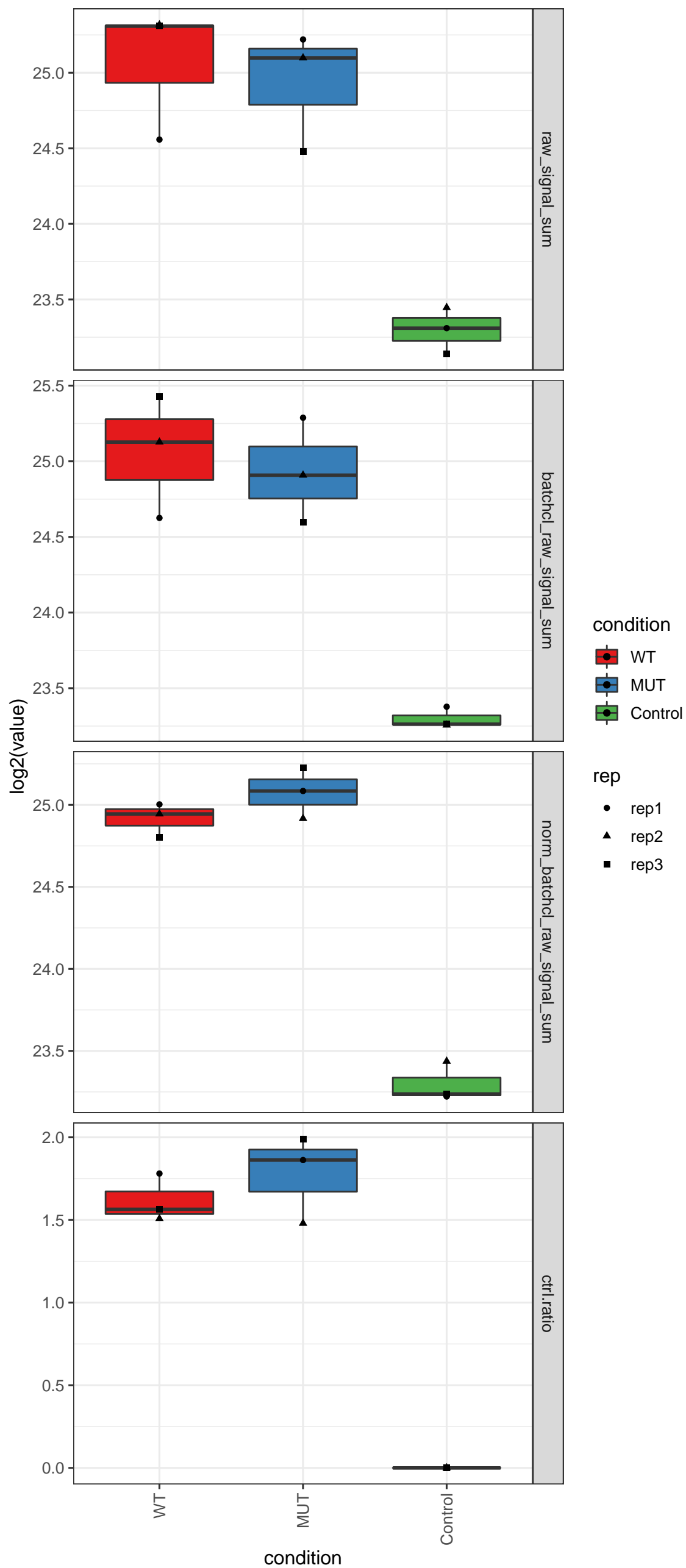
ENO1 – P00924

Enolase 1 OS=*Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) G



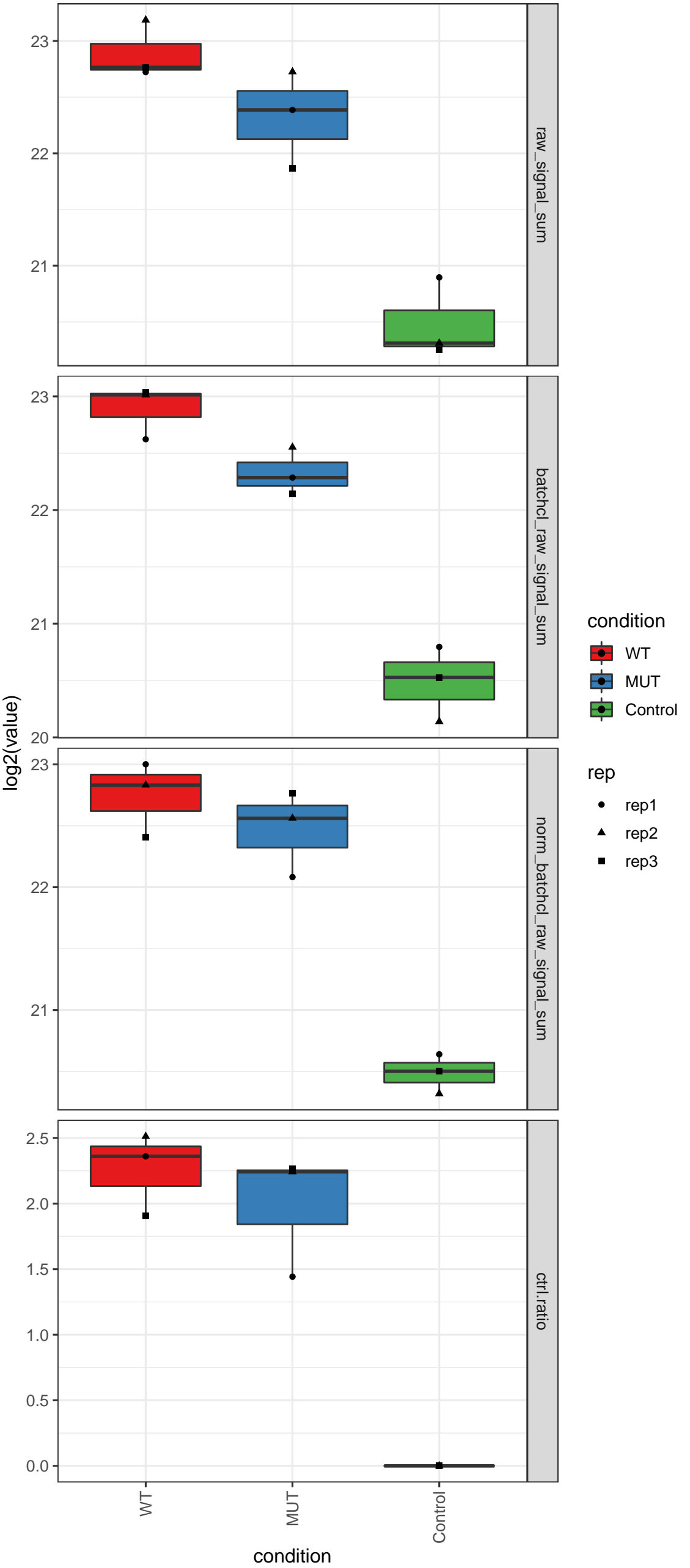
ENO2 – P00925

Enolase 2 OS=*Saccharomyces cerevisiae* (strain ATCC 204508 / S288c)



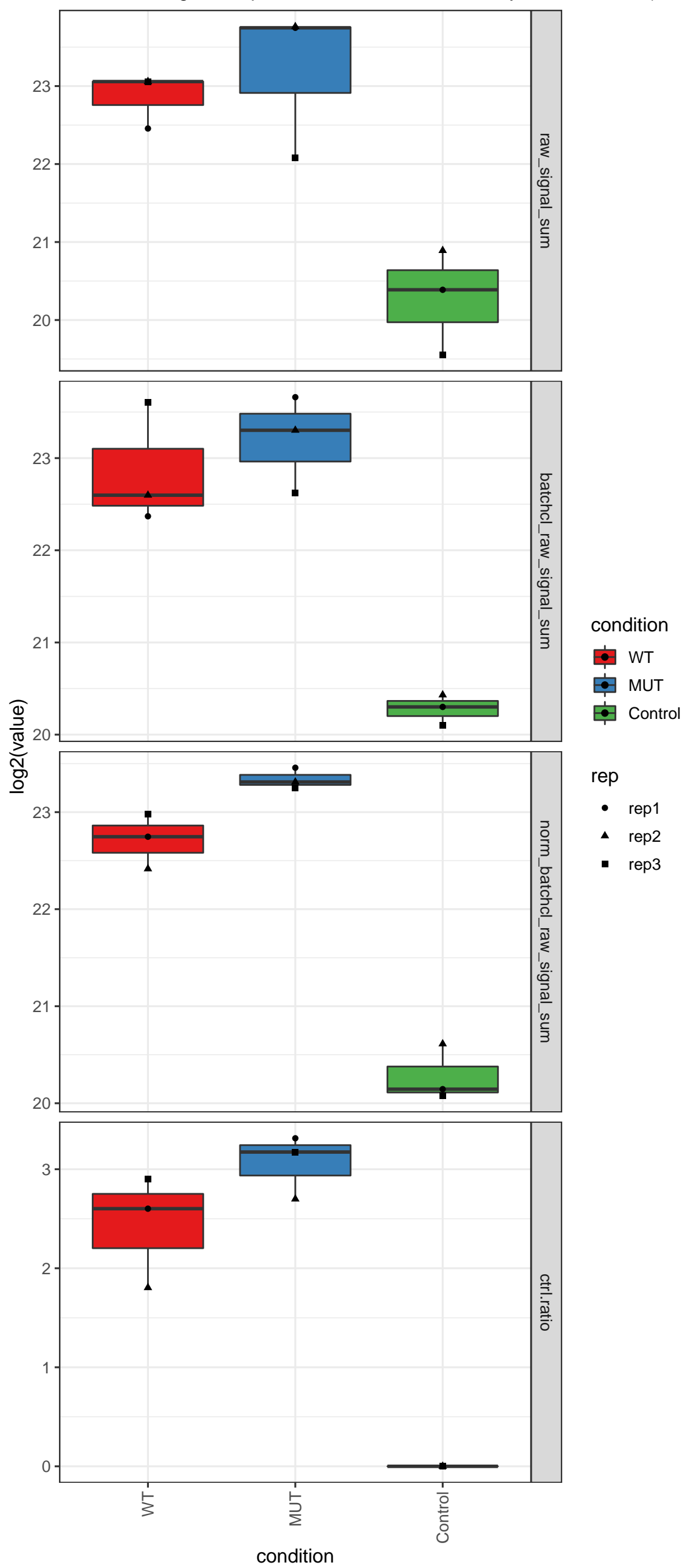
EPL1 – P43572

Enhancer of polycomb-like protein 1 OS=Saccharomyces cerevisiae (strain



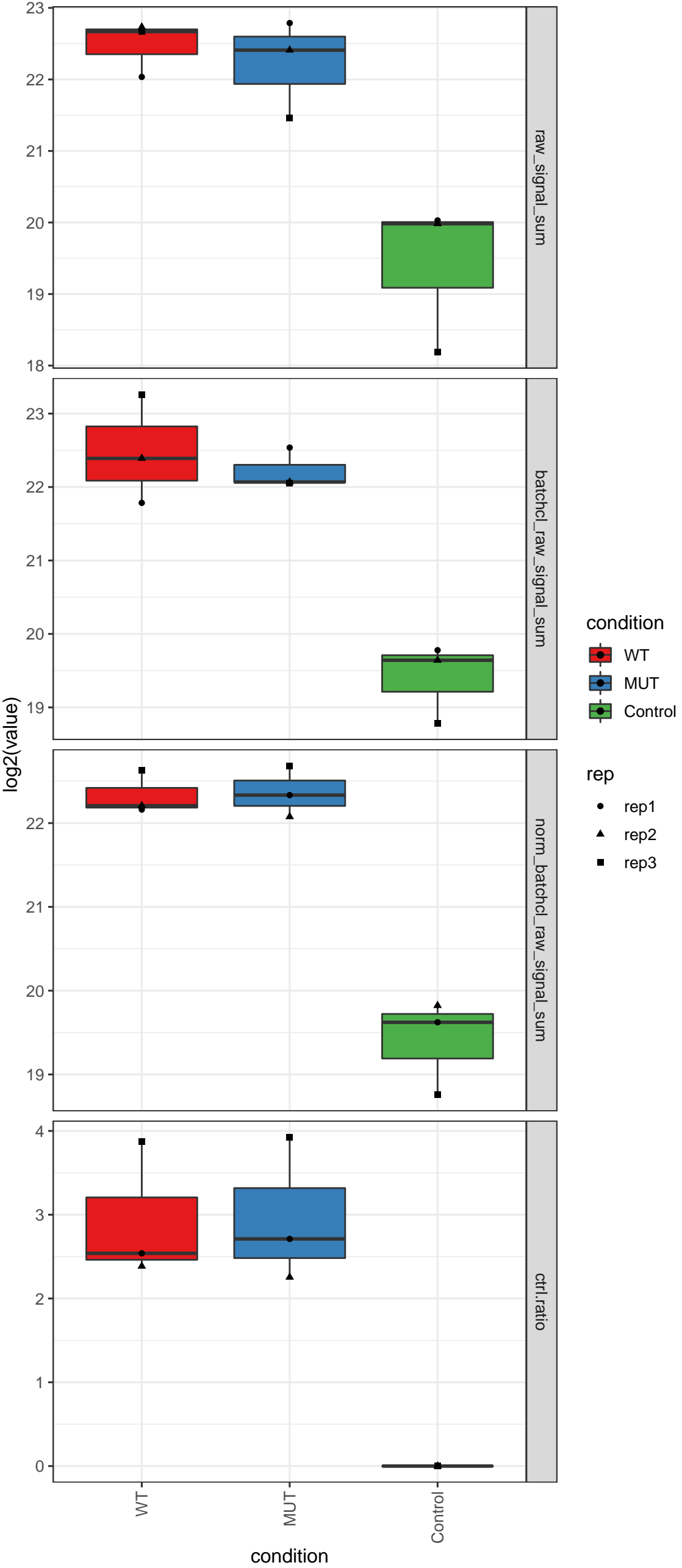
ERB1 – Q04660

Ribosome biogenesis protein ERB1 OS=*Saccharomyces cerevisiae* (strain



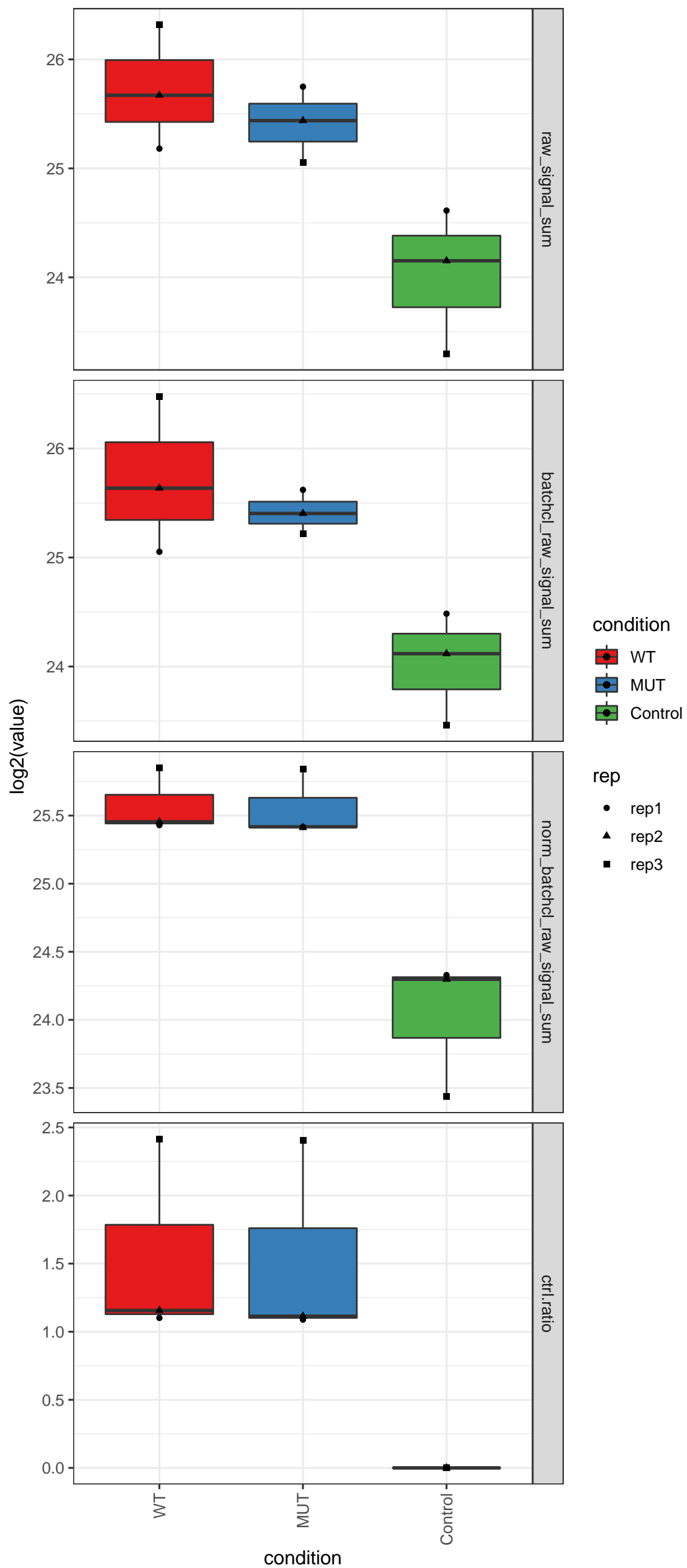
ERG10 – P41338

Acetyl-CoA acetyltransferase OS=*Saccharomyces cerevisiae* (strain ATCC



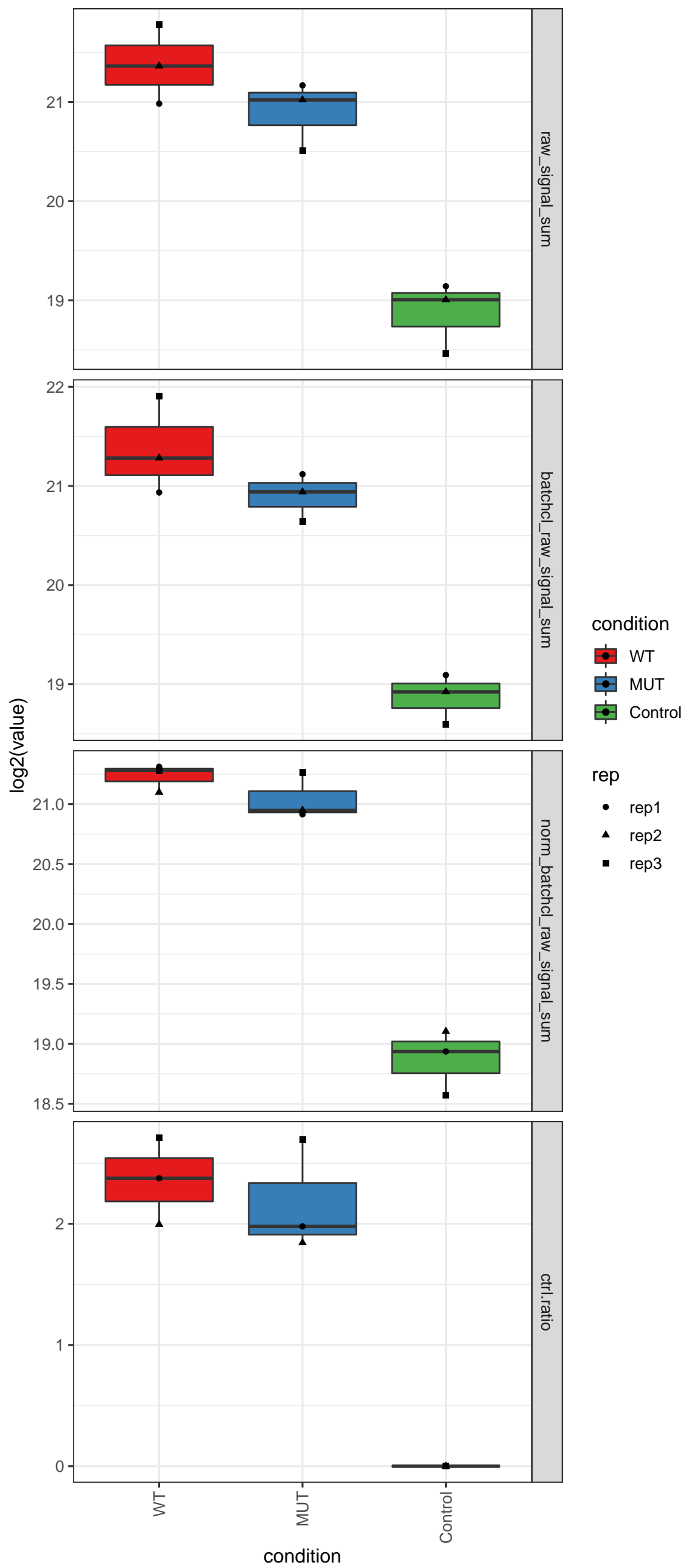
ERG13 – P54839

Hydroxymethylglutaryl–CoA synthase OS=*Saccharomyces cerevisiae* (strain ATCC 25716 / S288c)



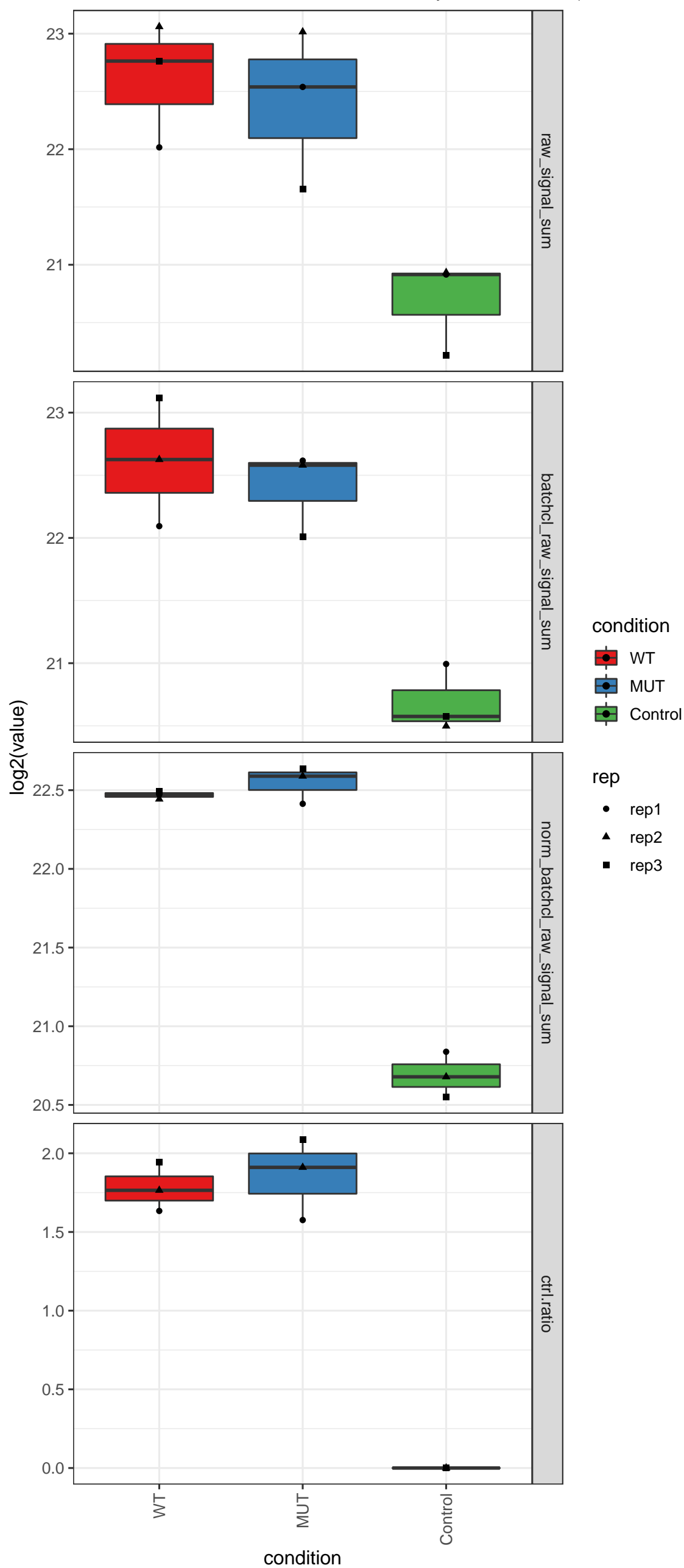
ERG20 – P08524

Farnesyl pyrophosphate synthase OS=*Saccharomyces cerevisiae* (strain



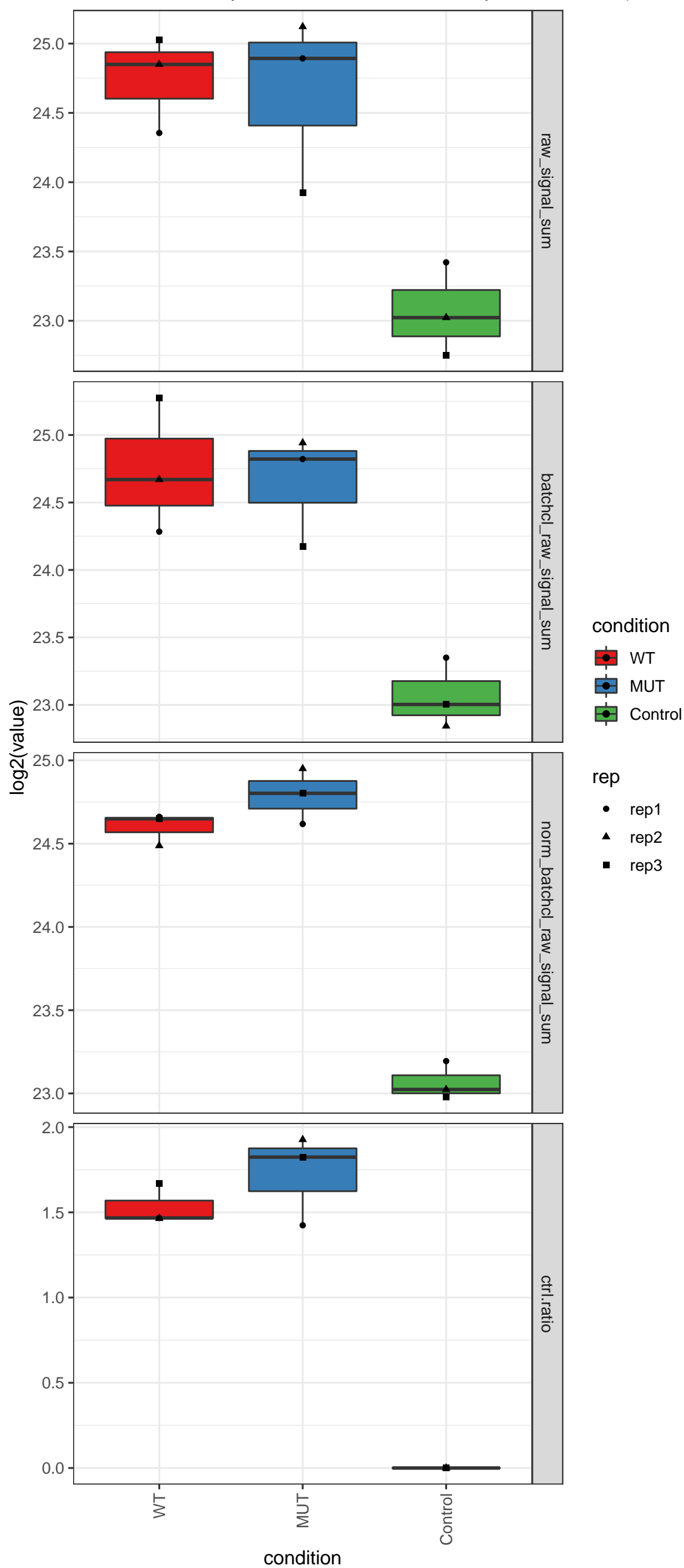
ERG27 – Q12452

3-keto-steroid reductase OS=*Saccharomyces cerevisiae* (strain ATCC 20452)



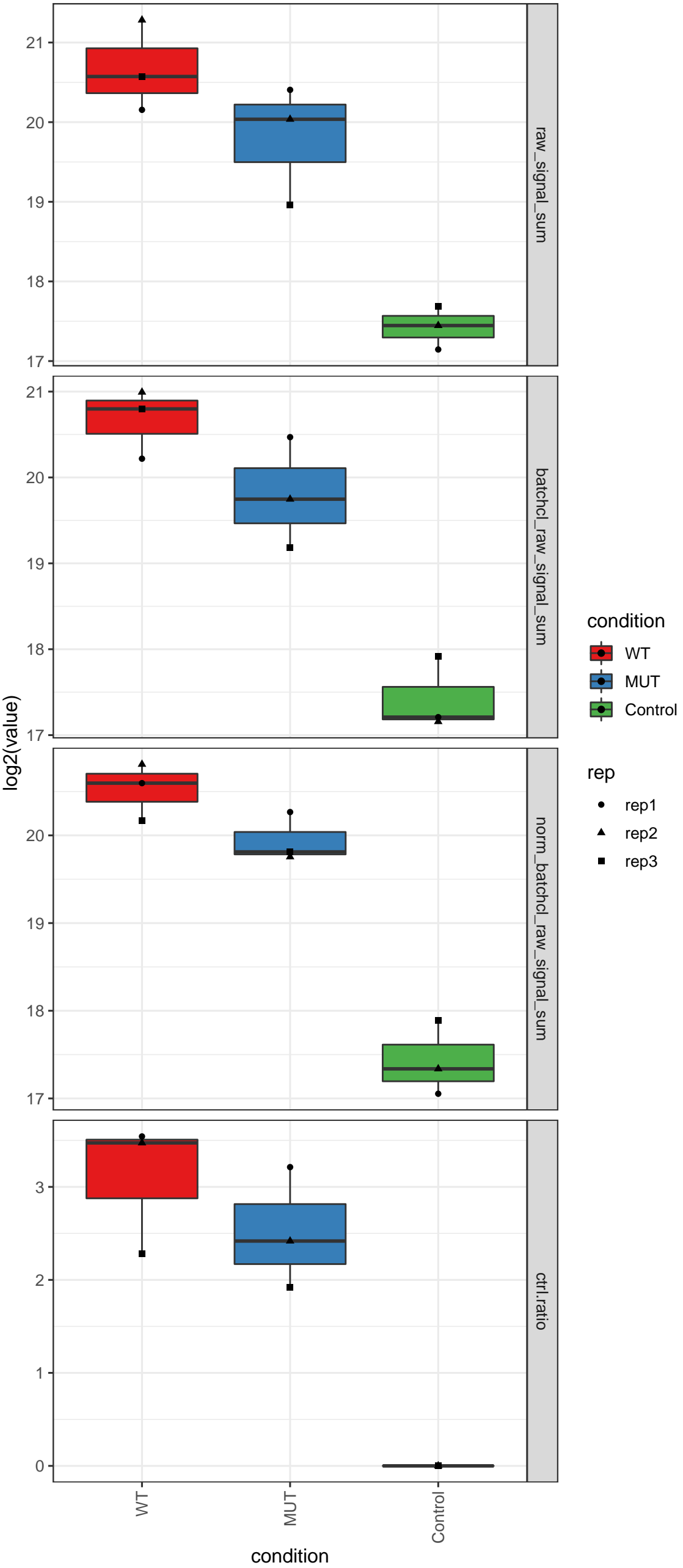
ERG6 – P25087

Sterol 24-C-methyltransferase OS=*Saccharomyces cerevisiae* (strain ATCC 25916)



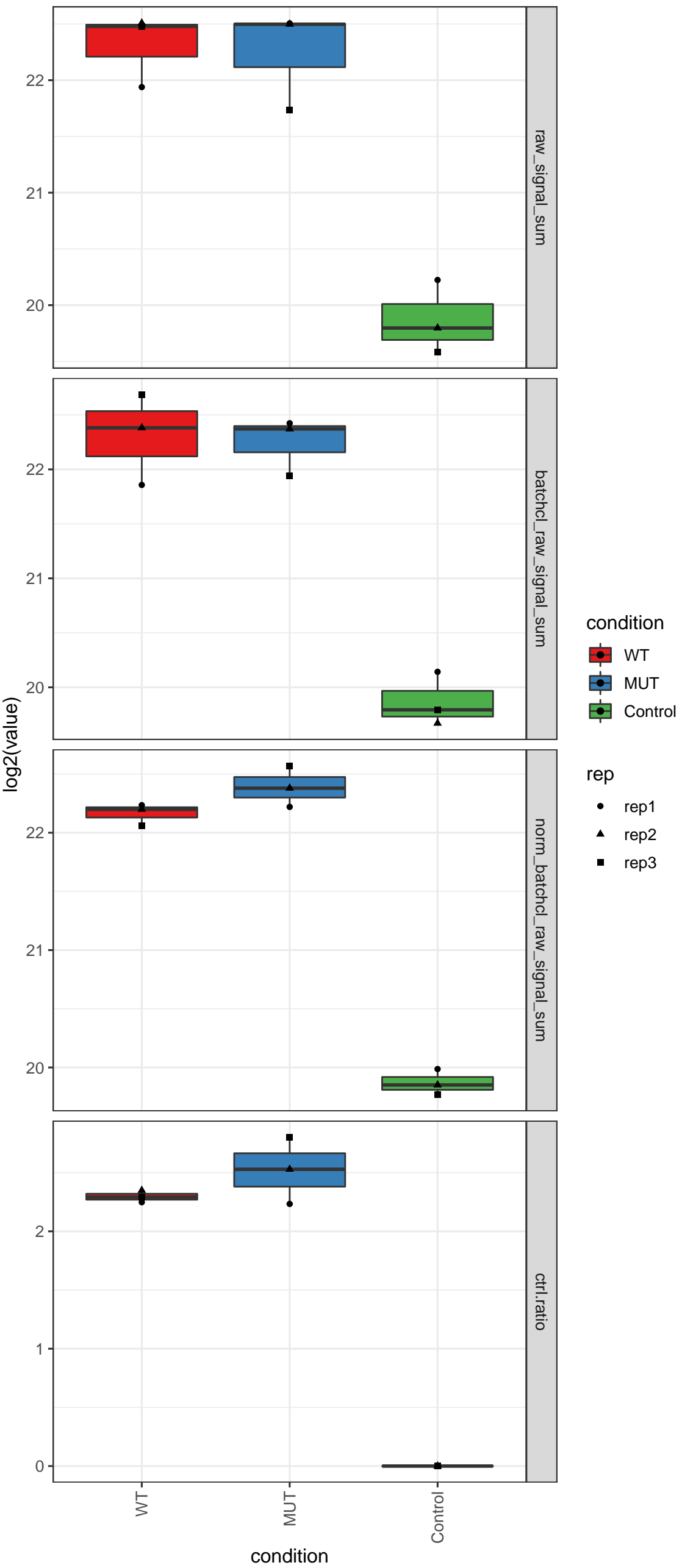
ERV29 – P53337

ER-derived vesicles protein ERV29 OS=Saccharomyces cerevisiae (strain



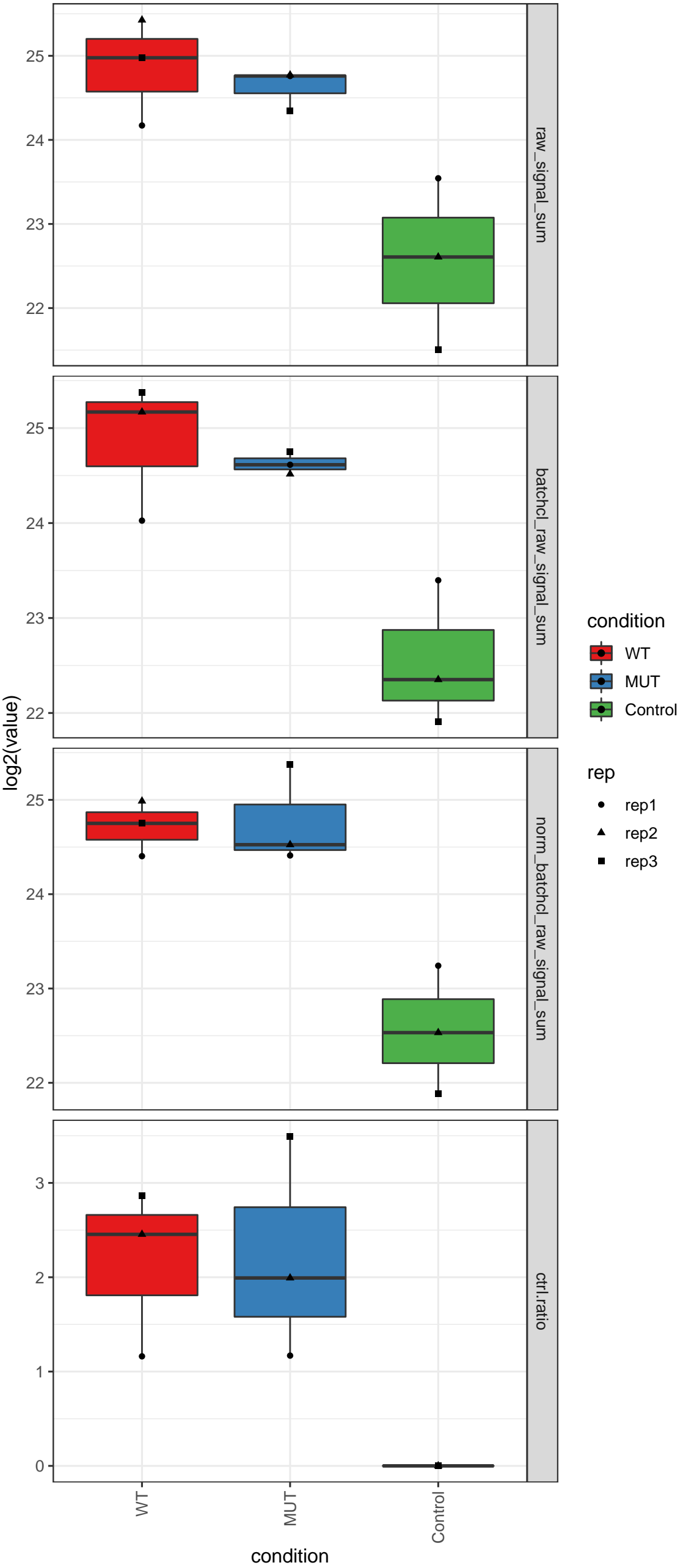
ETR1 – P38071

Enoyl-[acyl-carrier protein] reductase [NADPH, B-specific], mitochondrial



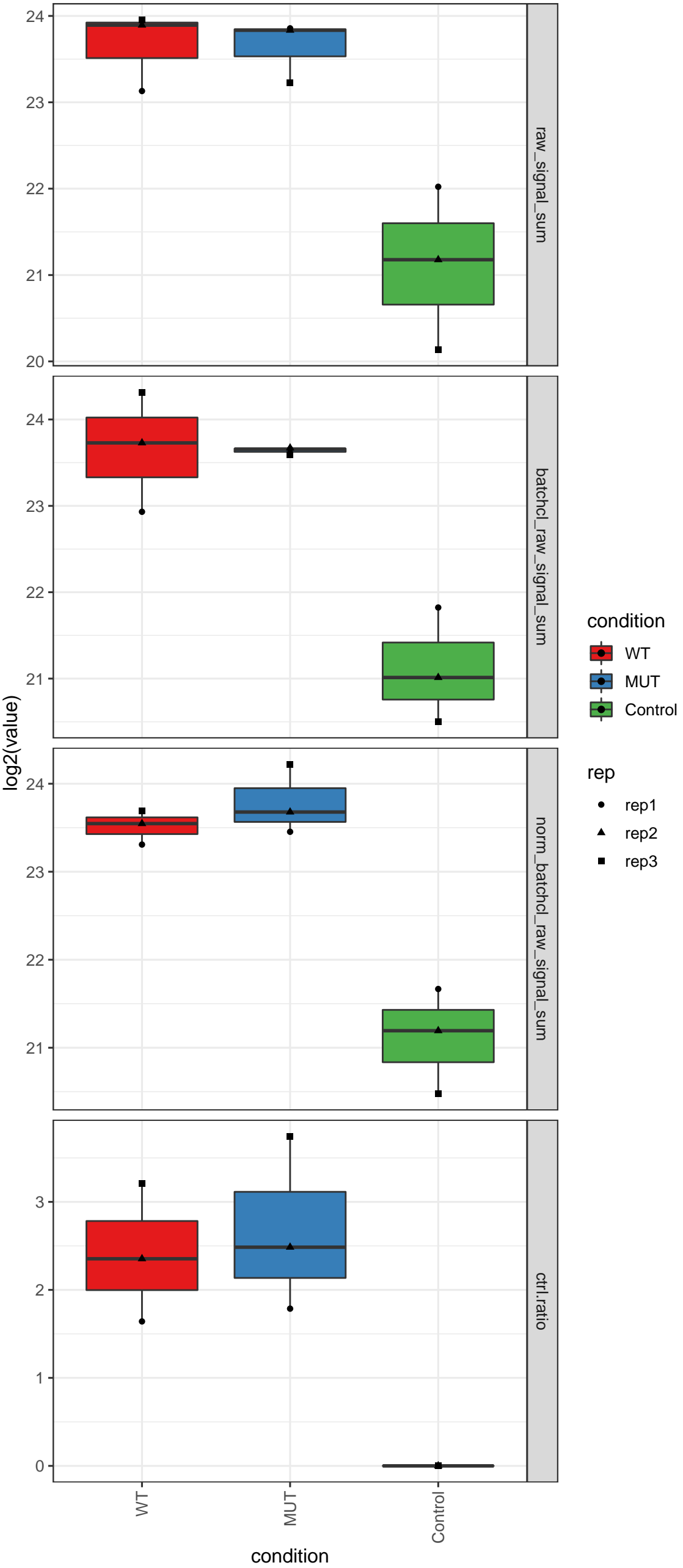
FAA1 – P30624

Long-chain-fatty-acid--CoA ligase 1 OS=Saccharomyces cerevisiae (stra



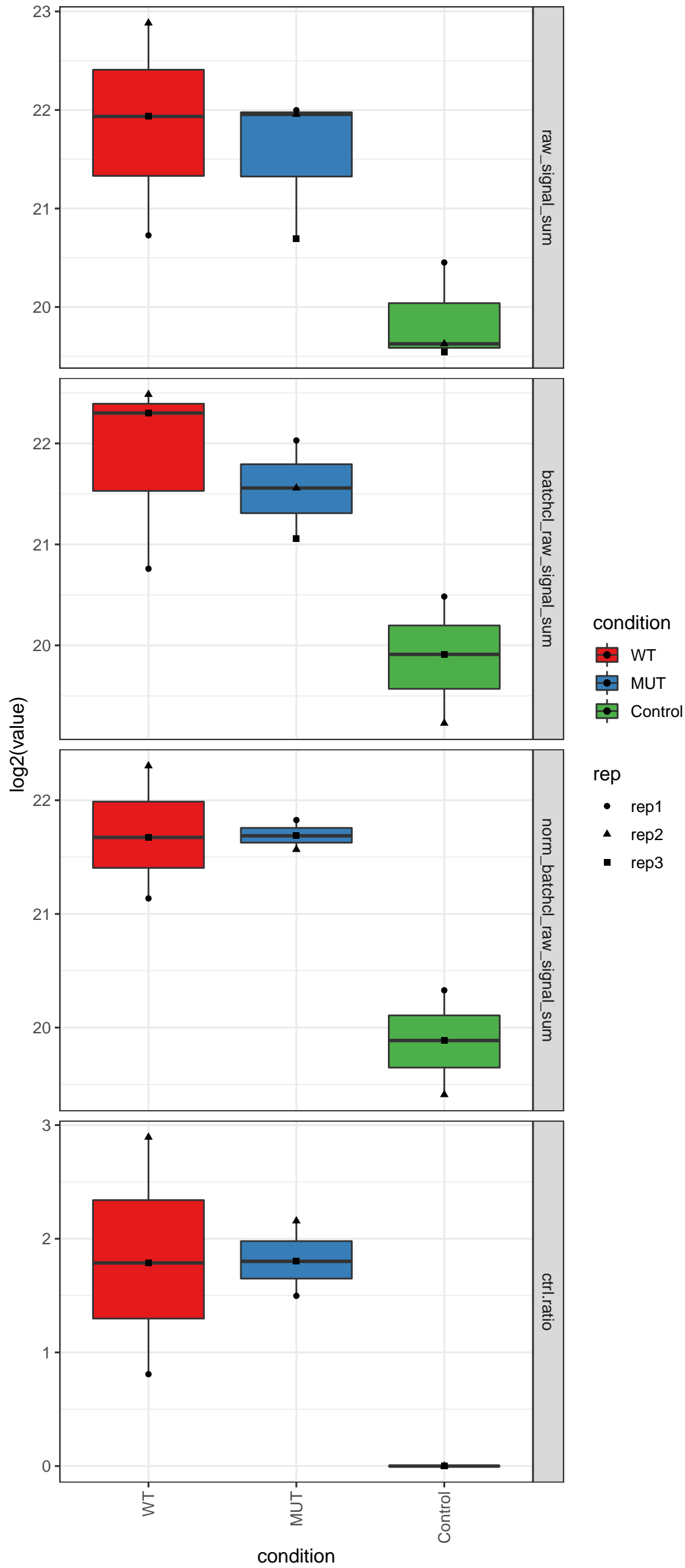
FAA2 – P39518

Long-chain-fatty-acid--CoA ligase 2 OS=Saccharomyces cerevisiae (stra



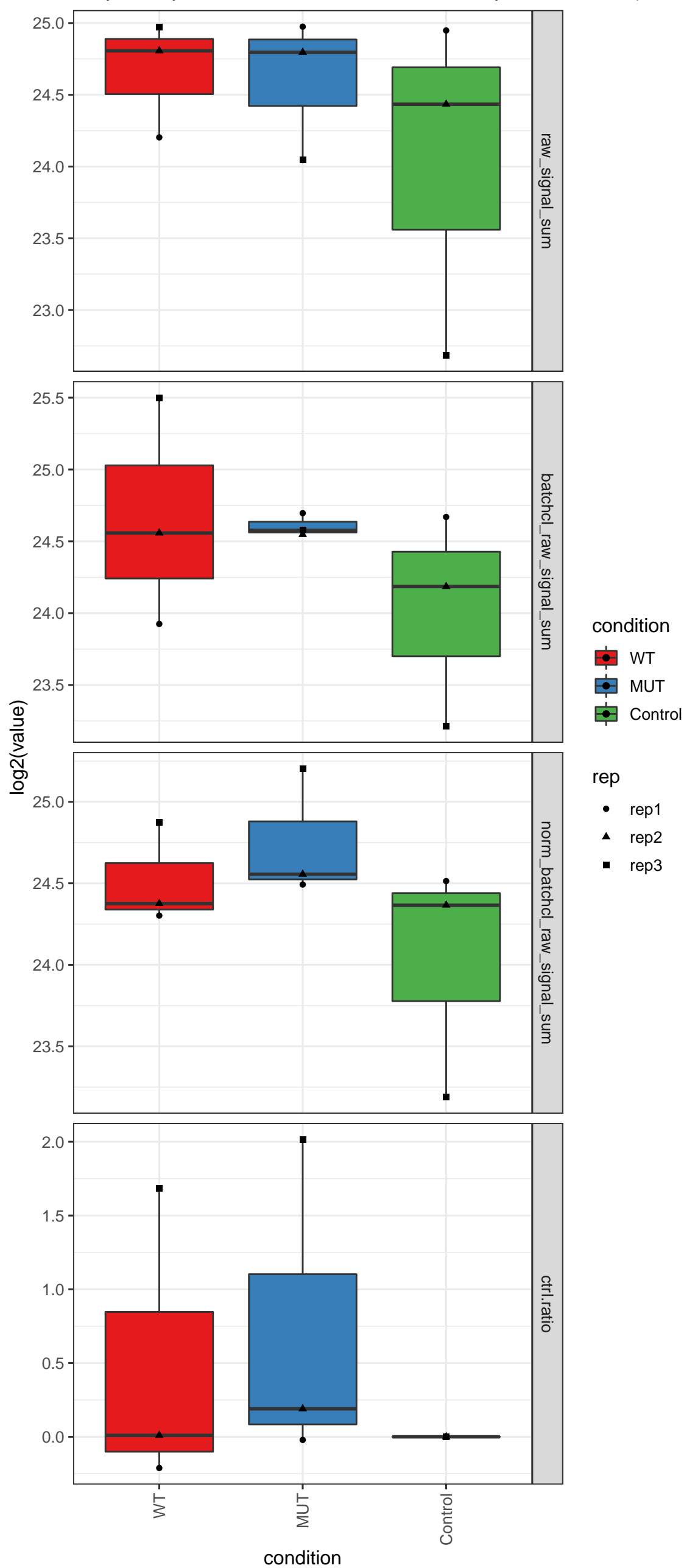
FAA4 – P47912

Long-chain-fatty-acid--CoA ligase 4 OS=Saccharomyces cerevisiae (stra



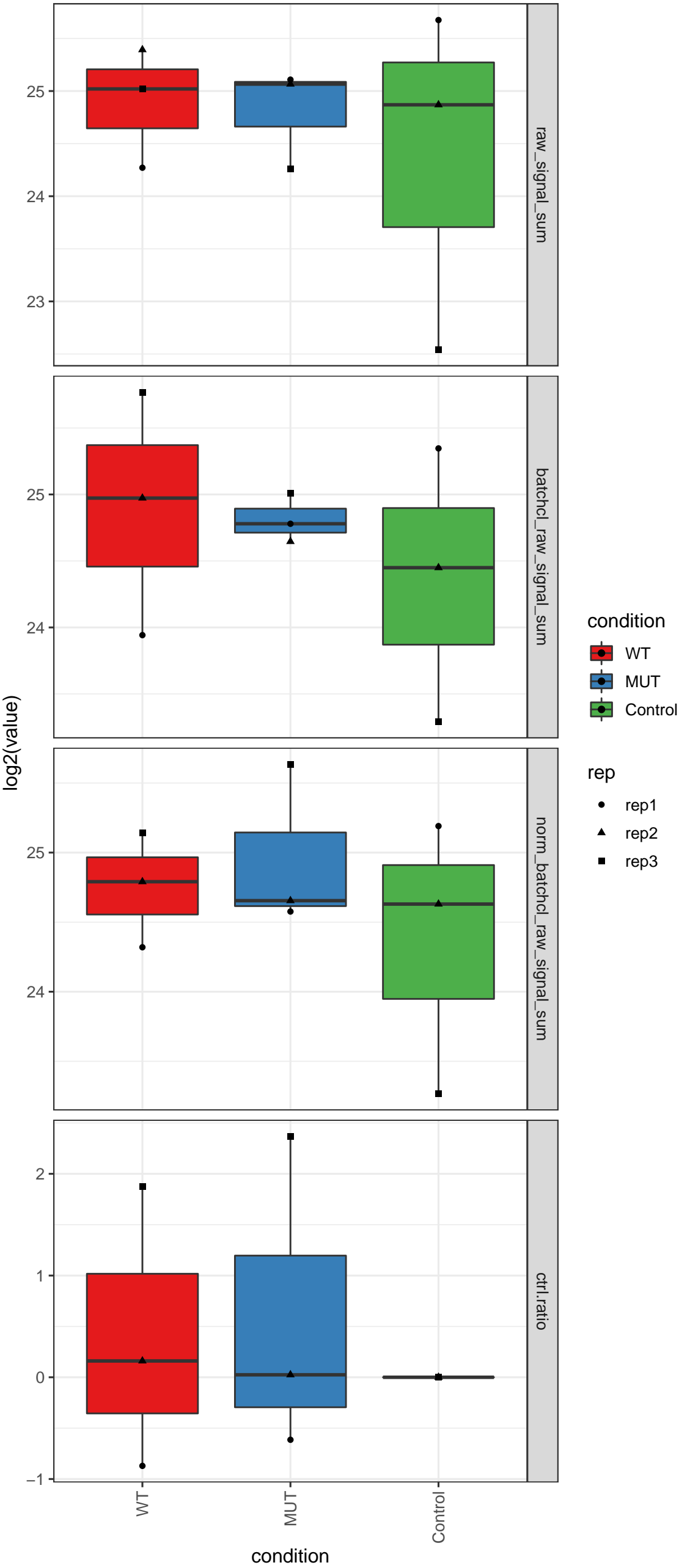
FAS1 – P07149

Fatty acid synthase subunit beta OS=Saccharomyces cerevisiae (strain A



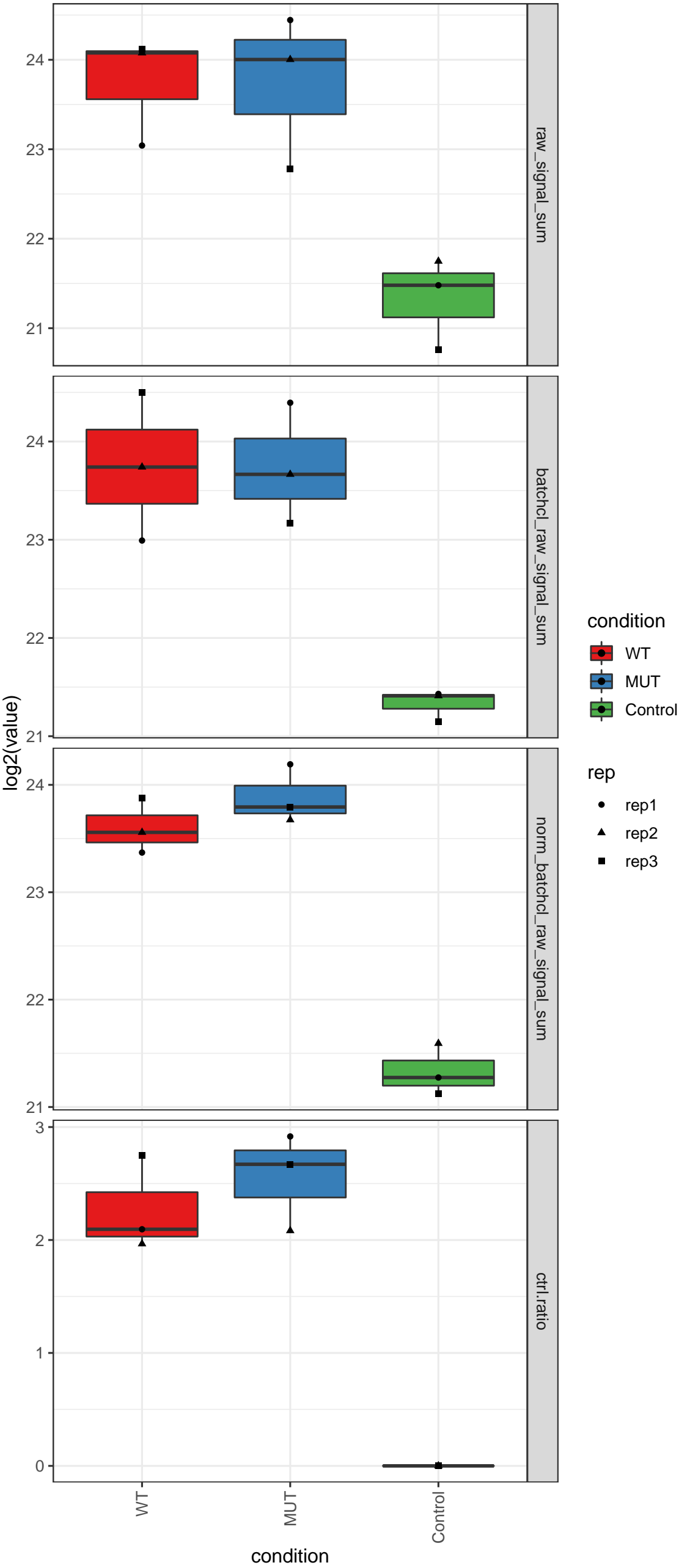
FAS2 – P19097

Fatty acid synthase subunit alpha OS=Saccharomyces cerevisiae (strain A



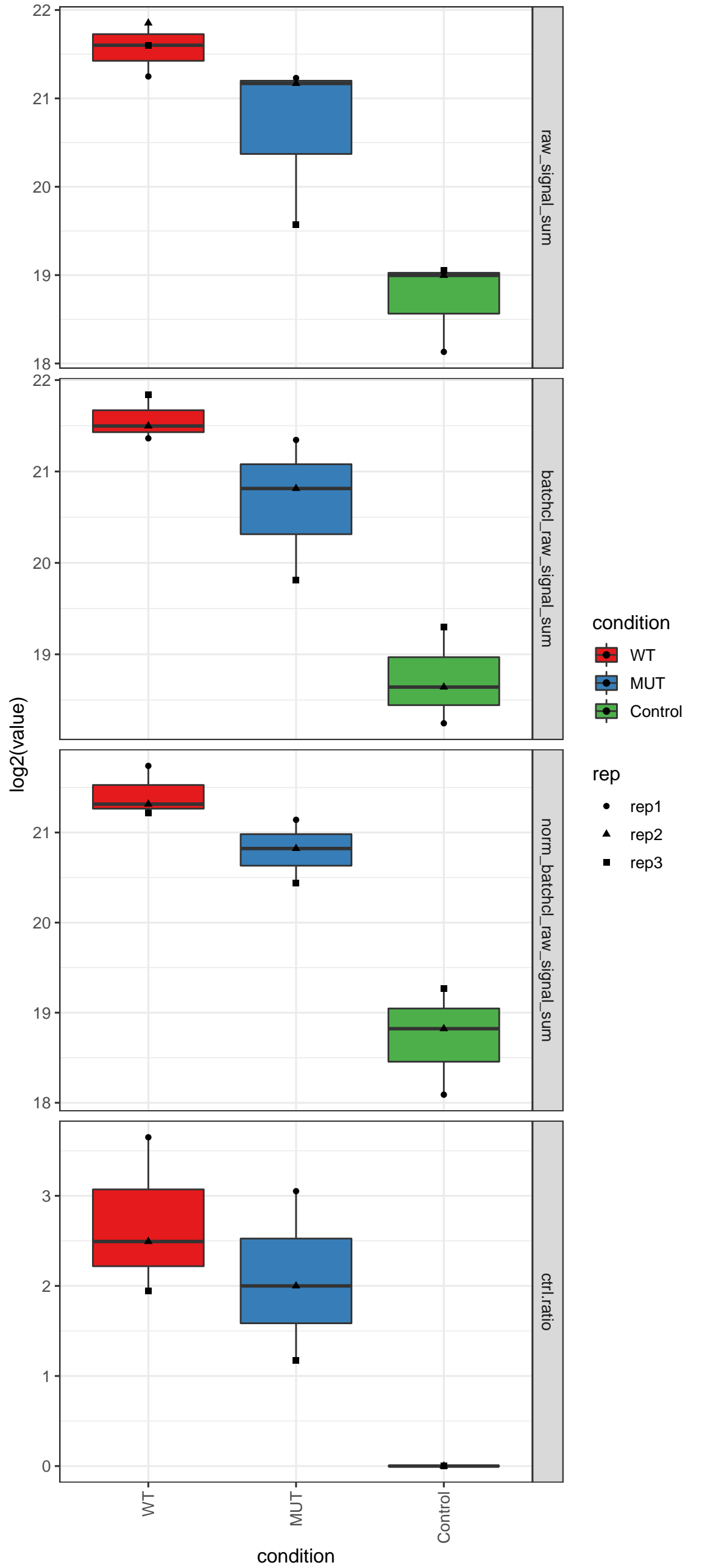
FBP1 – P09201

Fructose-1,6-bisphosphatase OS=*Saccharomyces cerevisiae* (strain ATCC 25620)



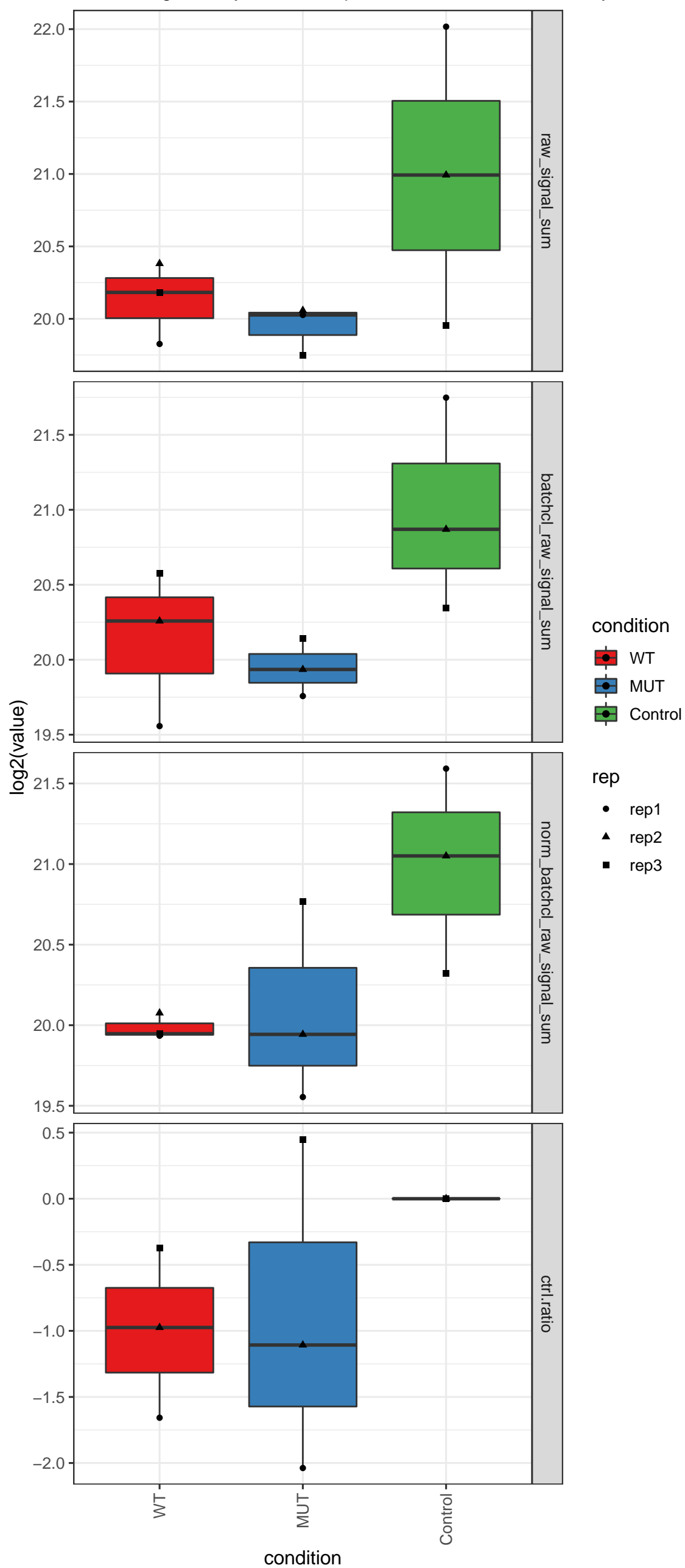
FHL1 – P39521

Pre-rRNA-processing protein FHL1 OS=*Saccharomyces cerevisiae* (strain



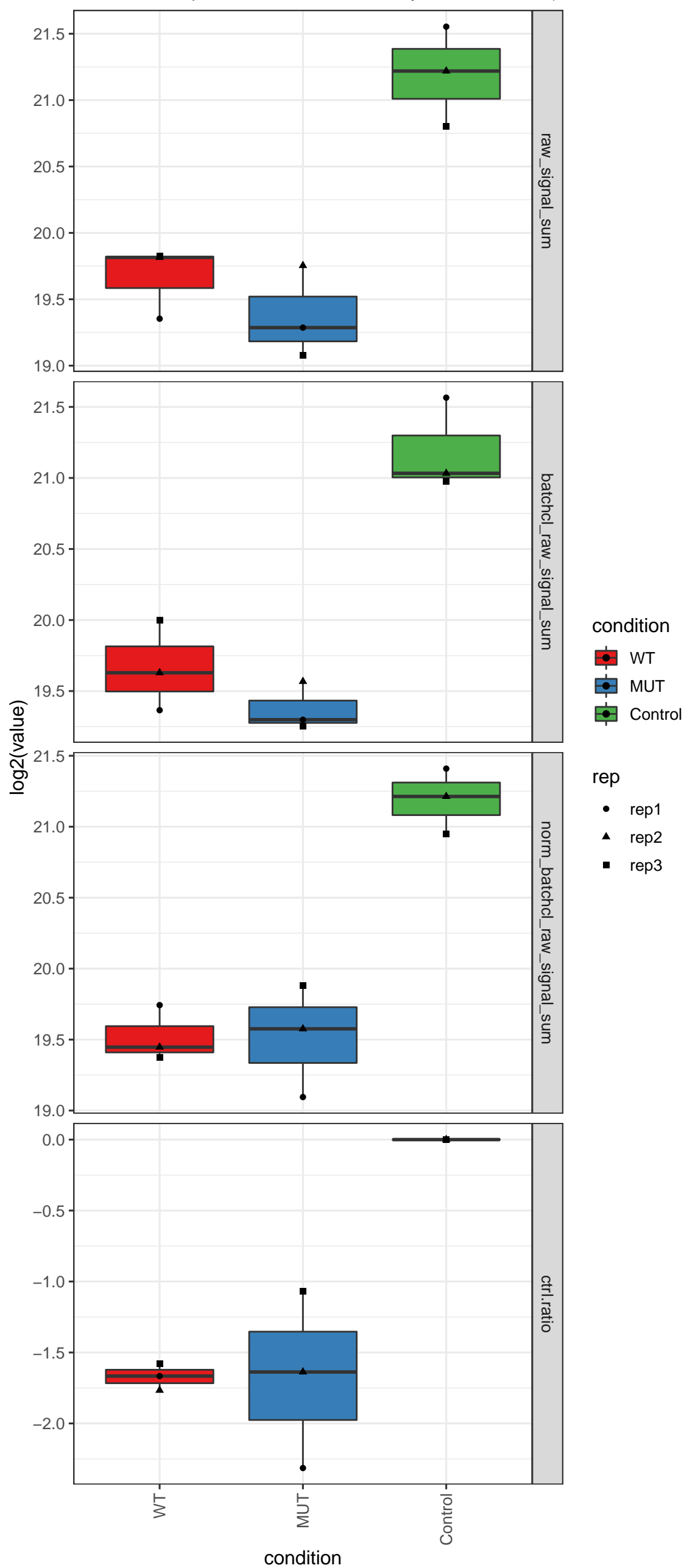
FKS1 – P38631

1,3-beta-glucan synthase component FKS1 OS=*Saccharomyces cerevisiae*



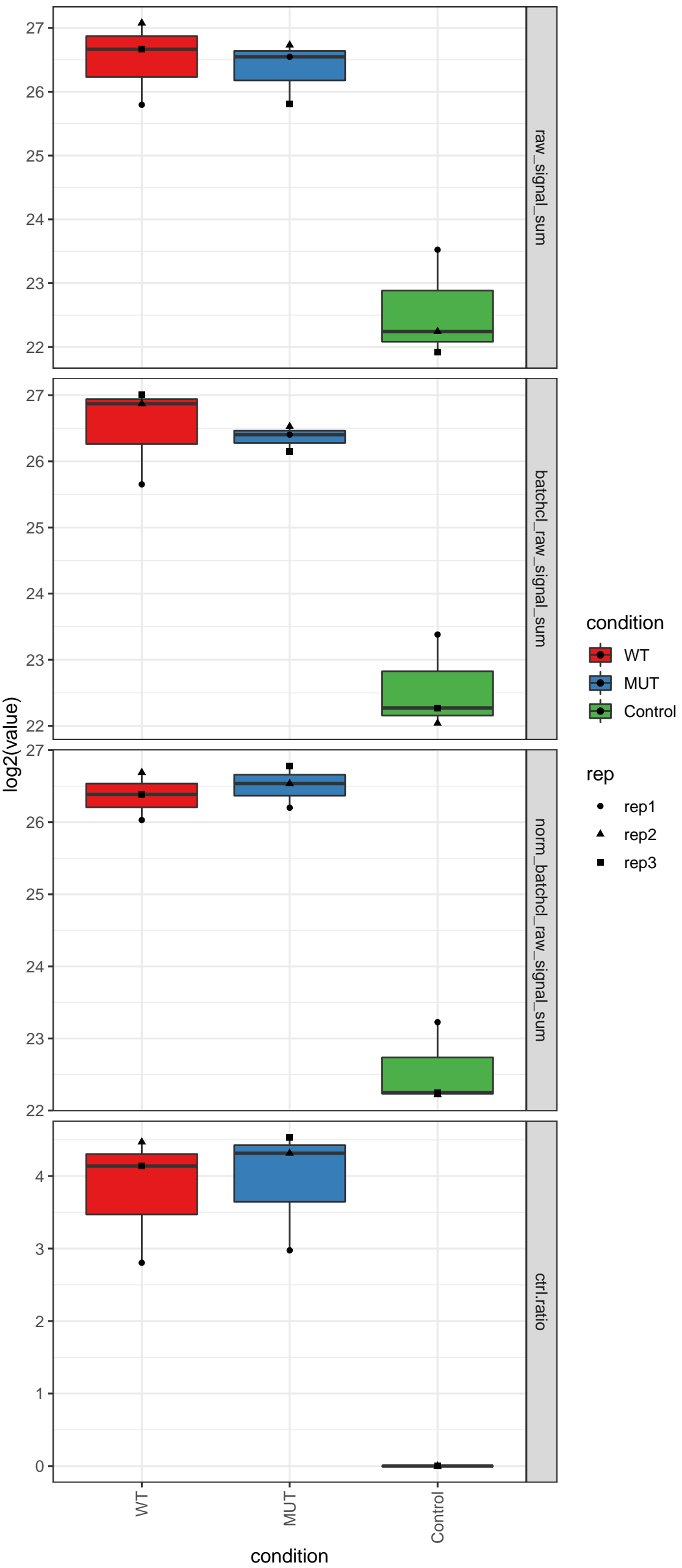
FLC2 – P39719

Flavin carrier protein 2 OS=Saccharomyces cerevisiae (strain ATCC 20454)



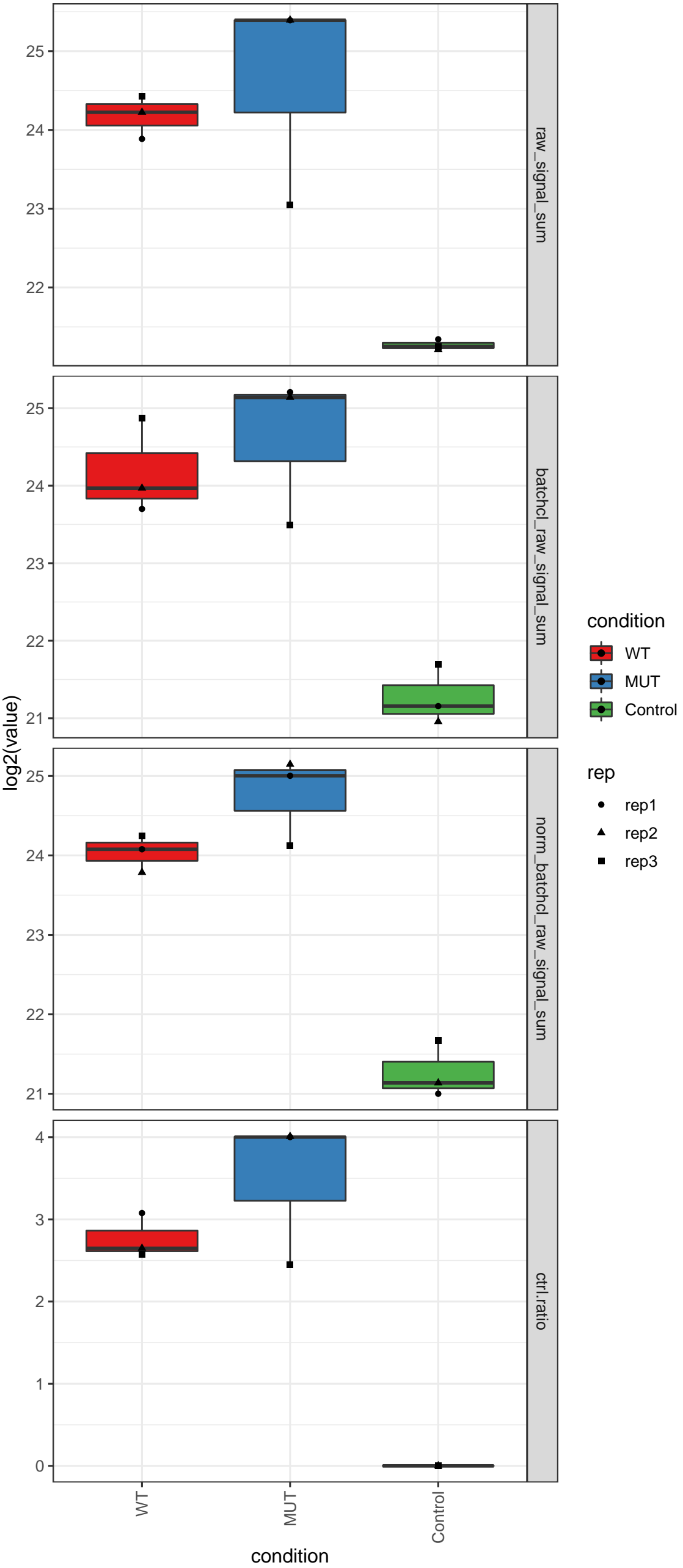
FOX2 – Q02207

Peroxisomal hydratase–dehydrogenase–epimerase OS=*Saccharomyces cerevisiae*



FPR3 – P38911

FK506-binding nuclear protein OS=*Saccharomyces cerevisiae* (strain ATC

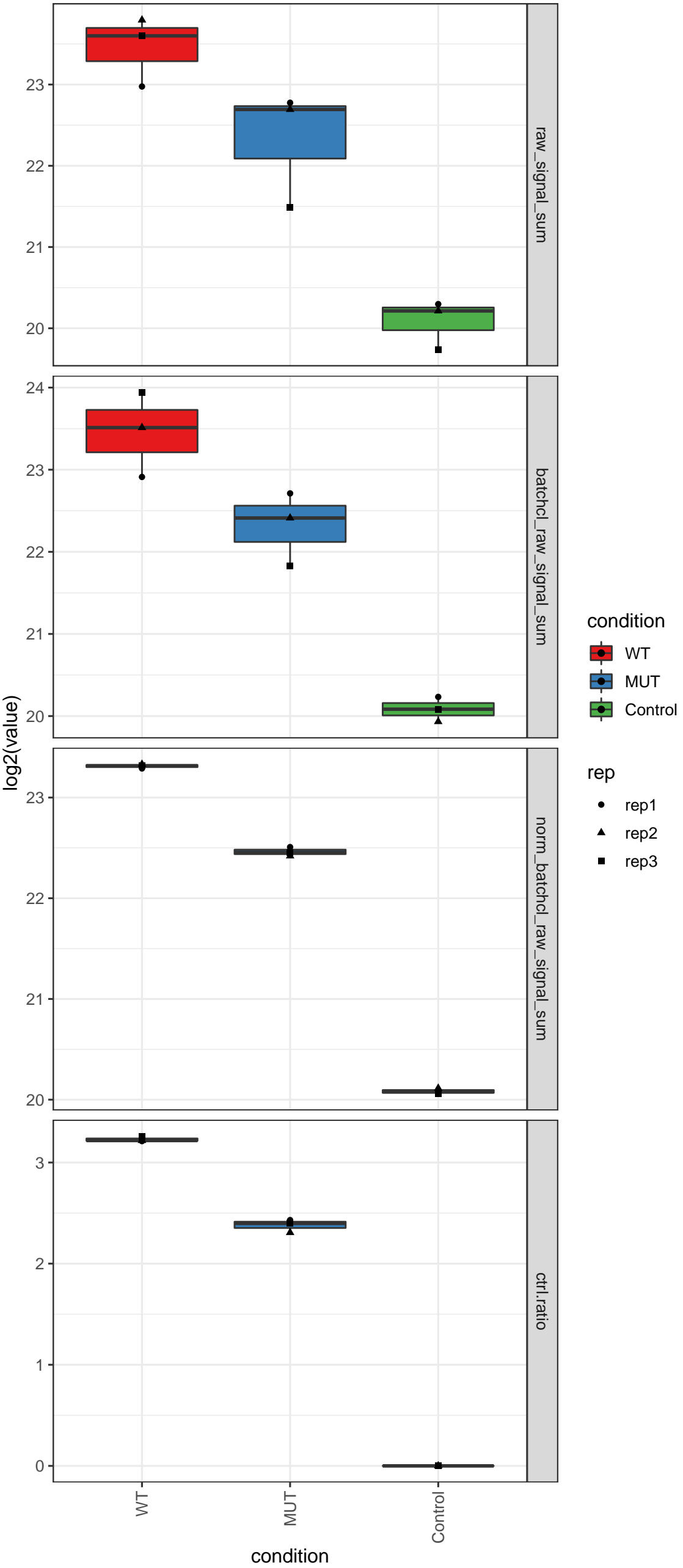


Putative Xaa-Pro aminopeptidase FRA1 OS=Saccharomyces cerevisiae



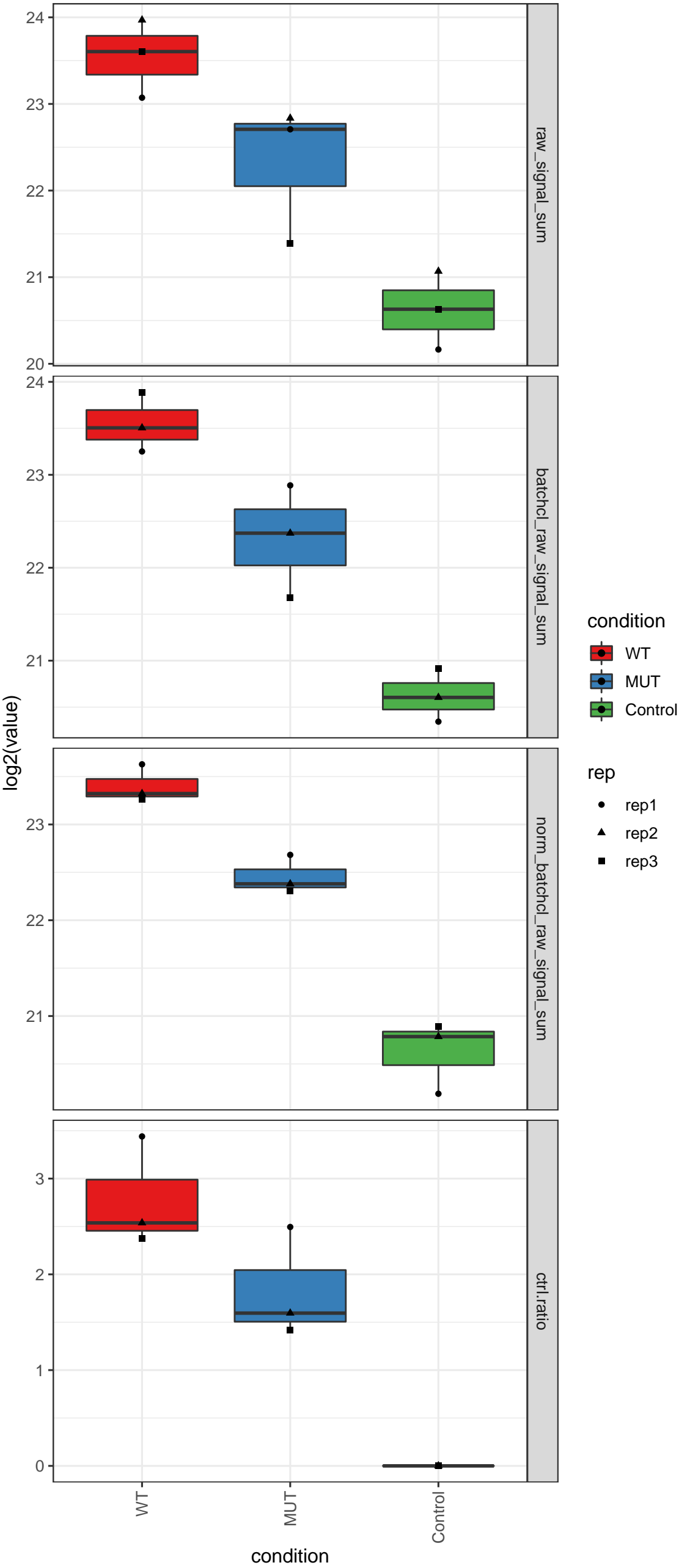
FRS1 – P15624

Phenylalanine--tRNA ligase beta subunit OS=Saccharomyces cerevisiae



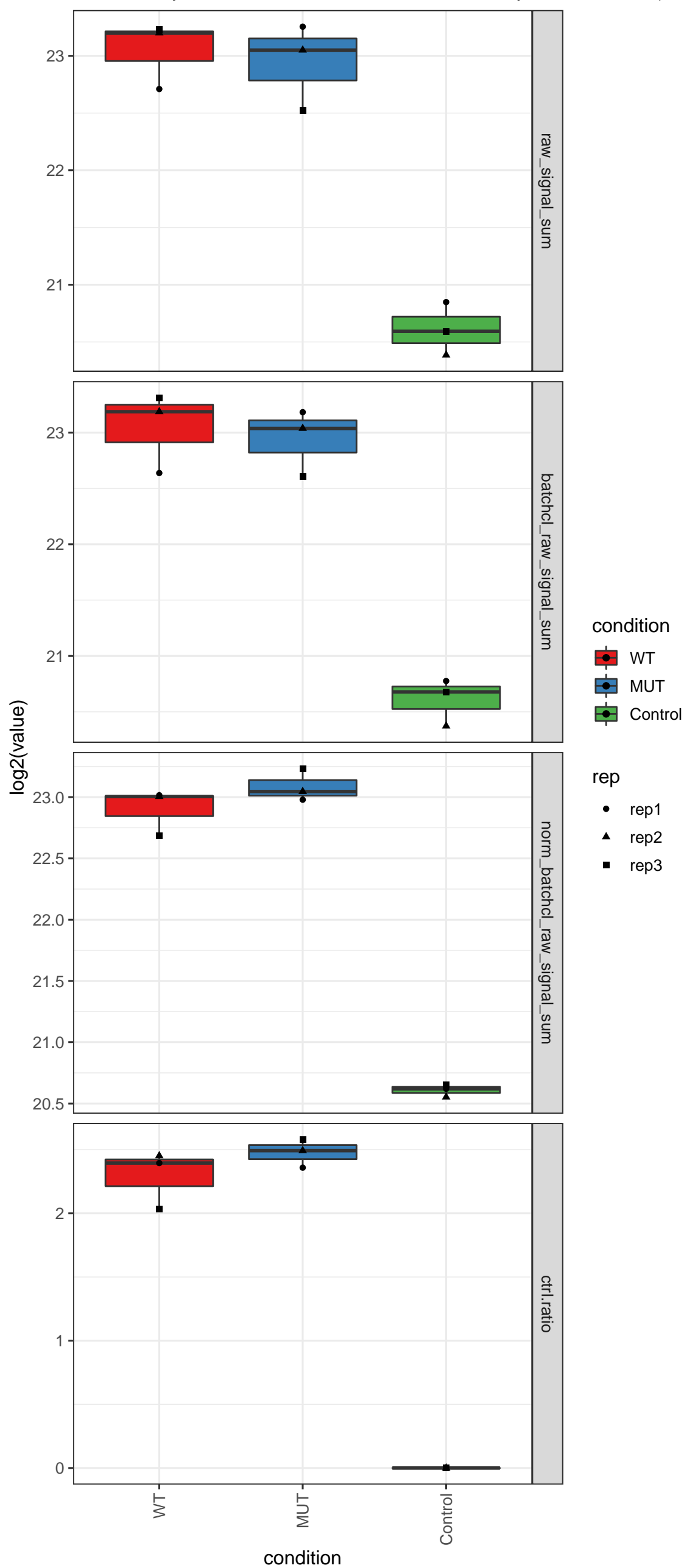
FRS2 – P15625

Phenylalanine--tRNA ligase alpha subunit OS=Saccharomyces cerevisiae



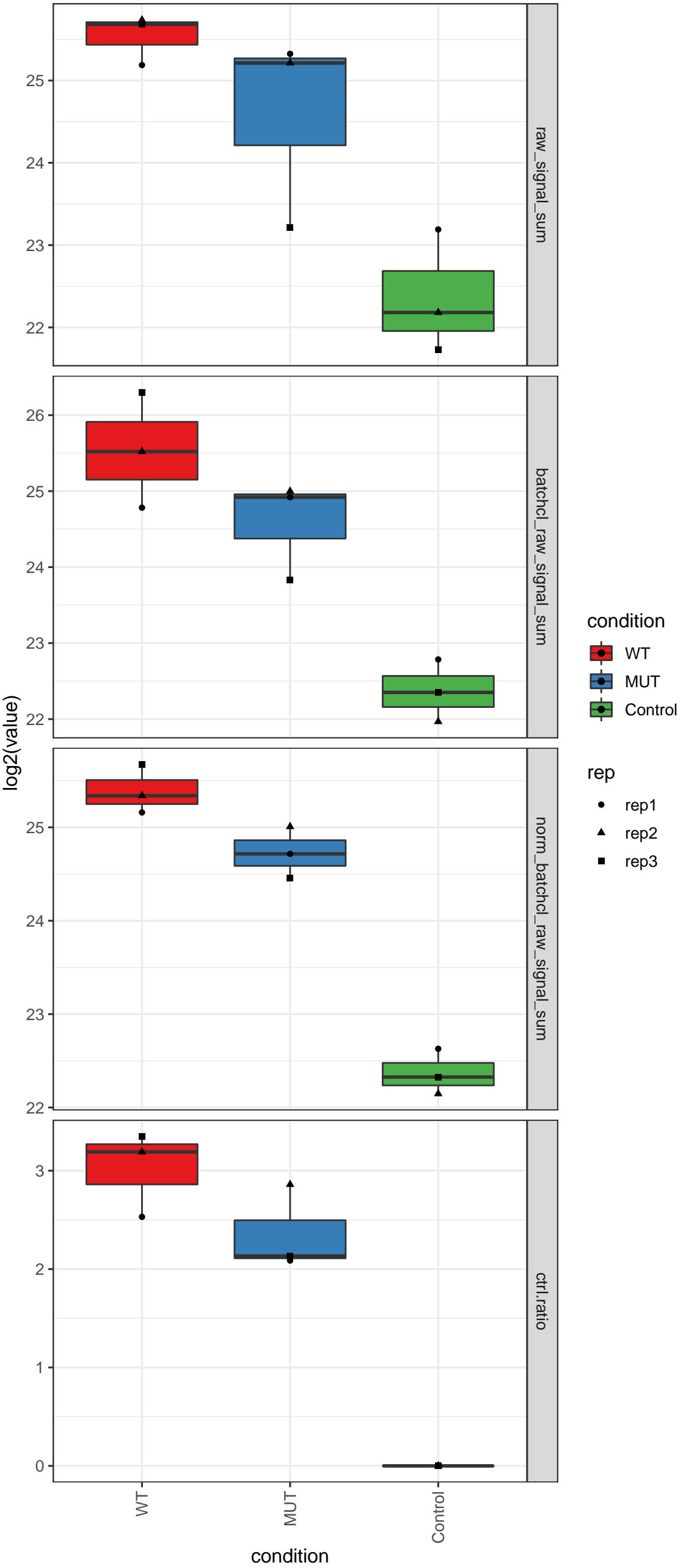
FUM1 – P08417

Fumarate hydratase, mitochondrial OS=*Saccharomyces cerevisiae* (strain



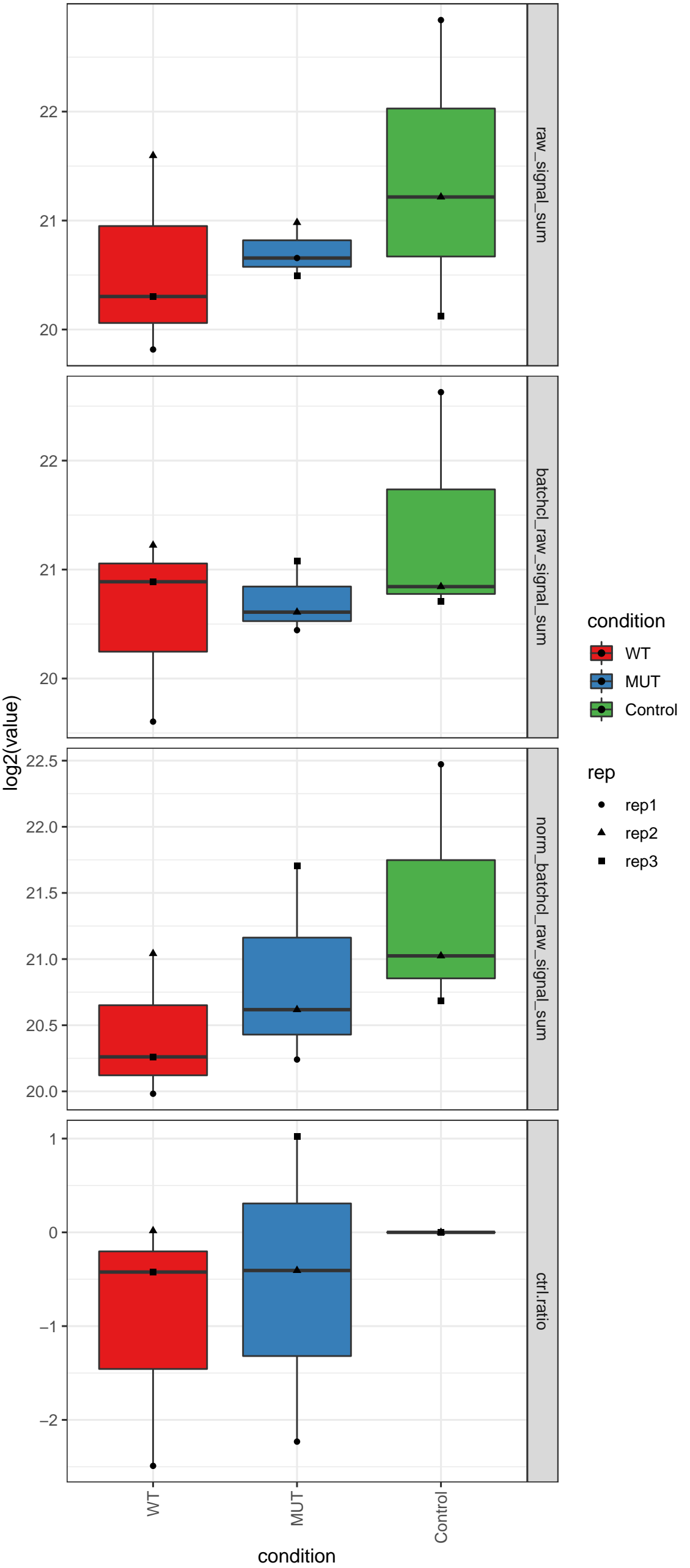
FUN12 – P39730

Eukaryotic translation initiation factor 5B OS=*Saccharomyces cerevisiae* (s



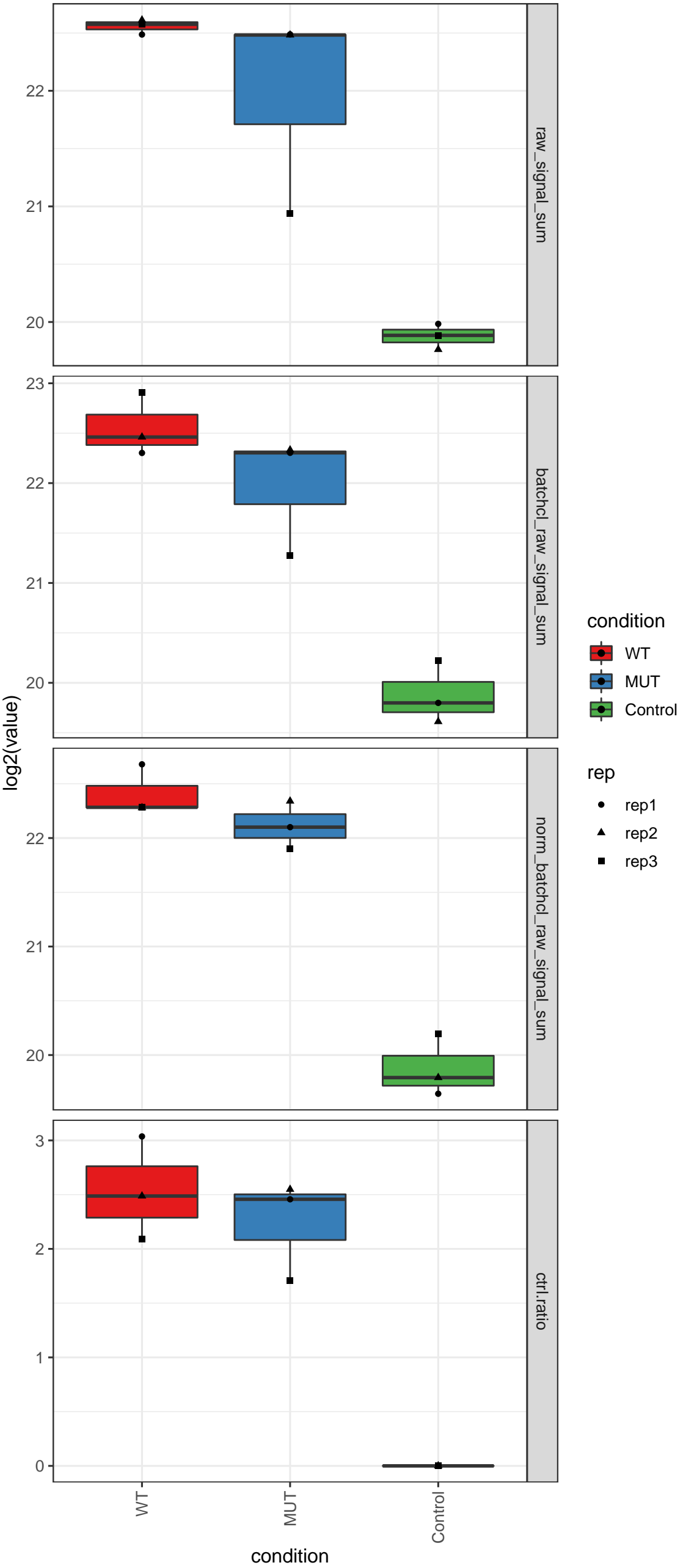
GAP1 – P19145

General amino–acid permease GAP1 OS=*Saccharomyces cerevisiae* (str. *S. cerevisiae*)



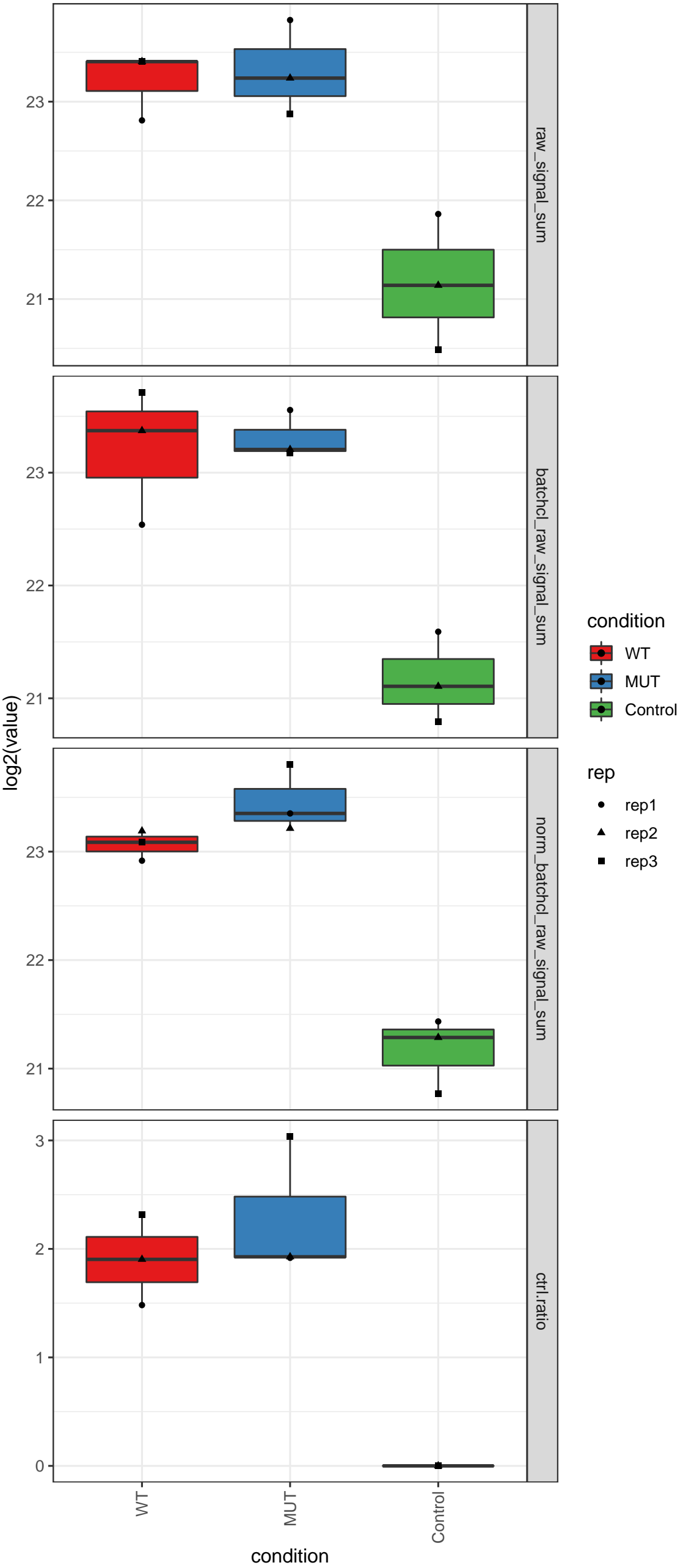
GAR1 – P28007

H/ACA ribonucleoprotein complex subunit 1 OS=*Saccharomyces cerevisiae*



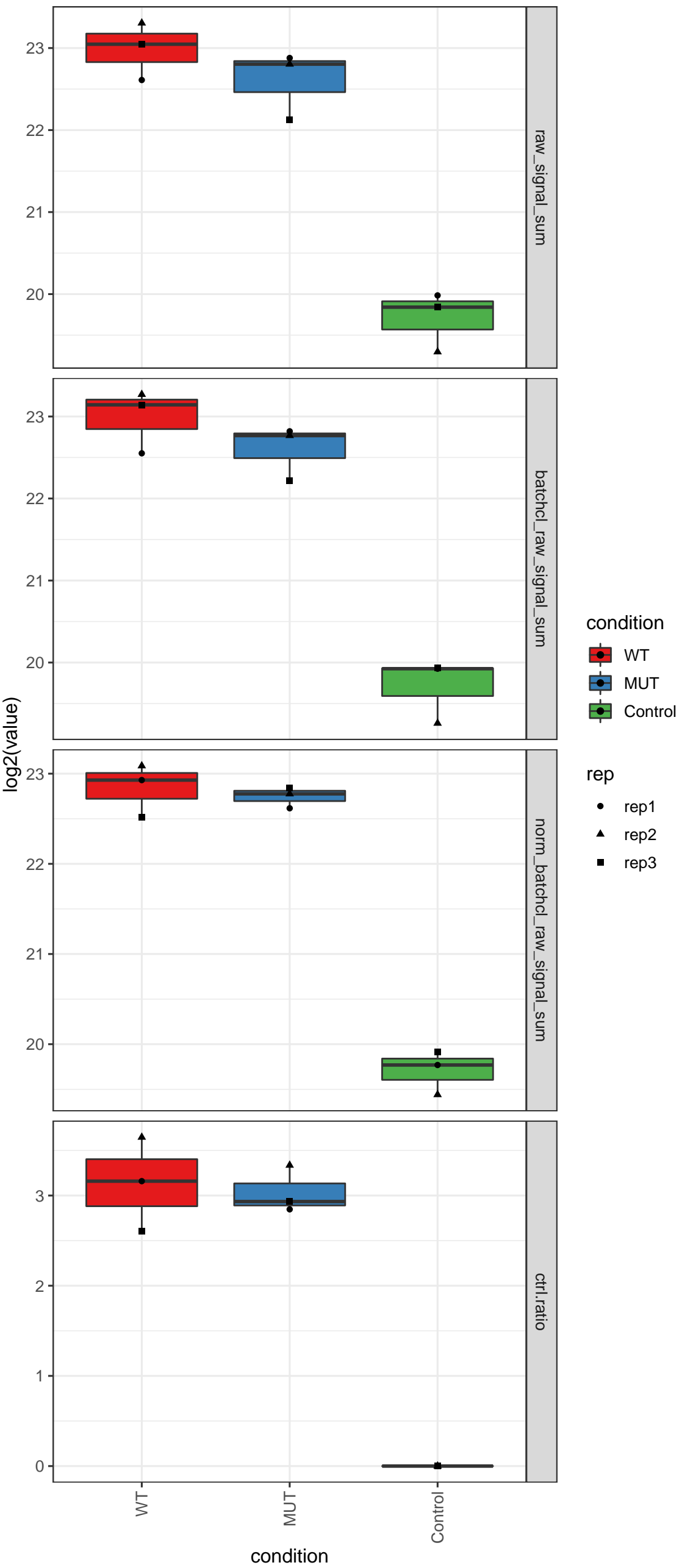
GAS1 – P22146

1,3-beta-glucanosyltransferase GAS1 OS=Saccharomyces cerevisiae (str



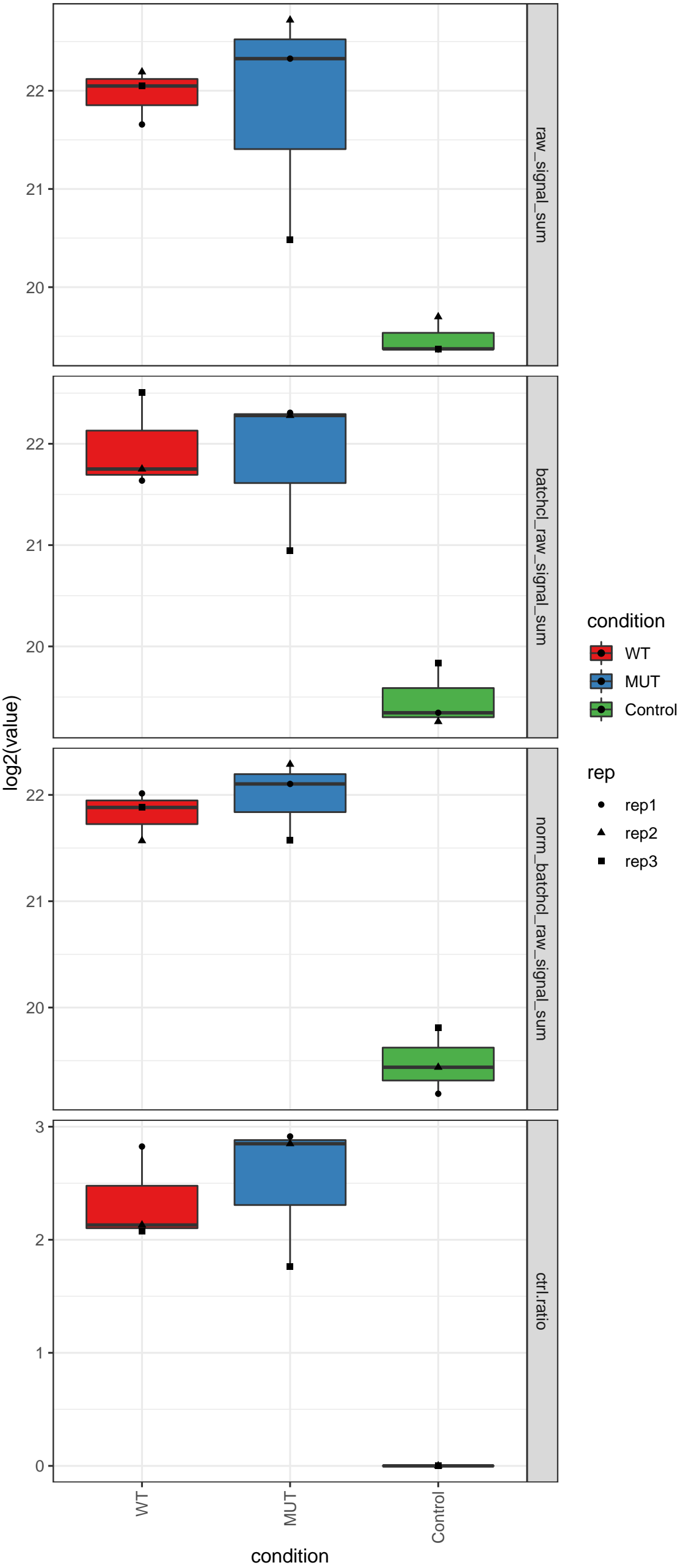
GCD11 – P32481

Eukaryotic translation initiation factor 2 subunit gamma OS=Saccharomyce



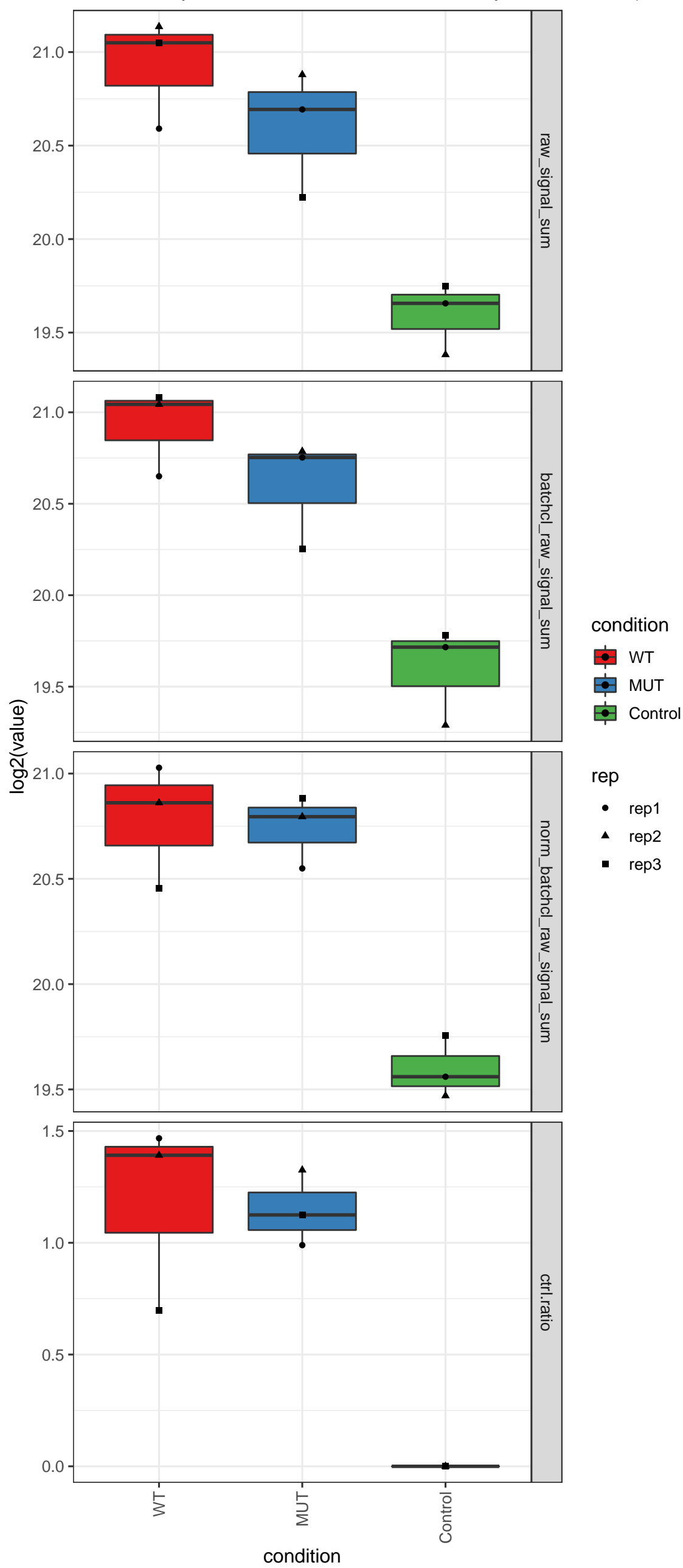
GCN2 – P15442

eIF-2- α kinase GCN2 OS=*Saccharomyces cerevisiae* (strain ATCC 20454)



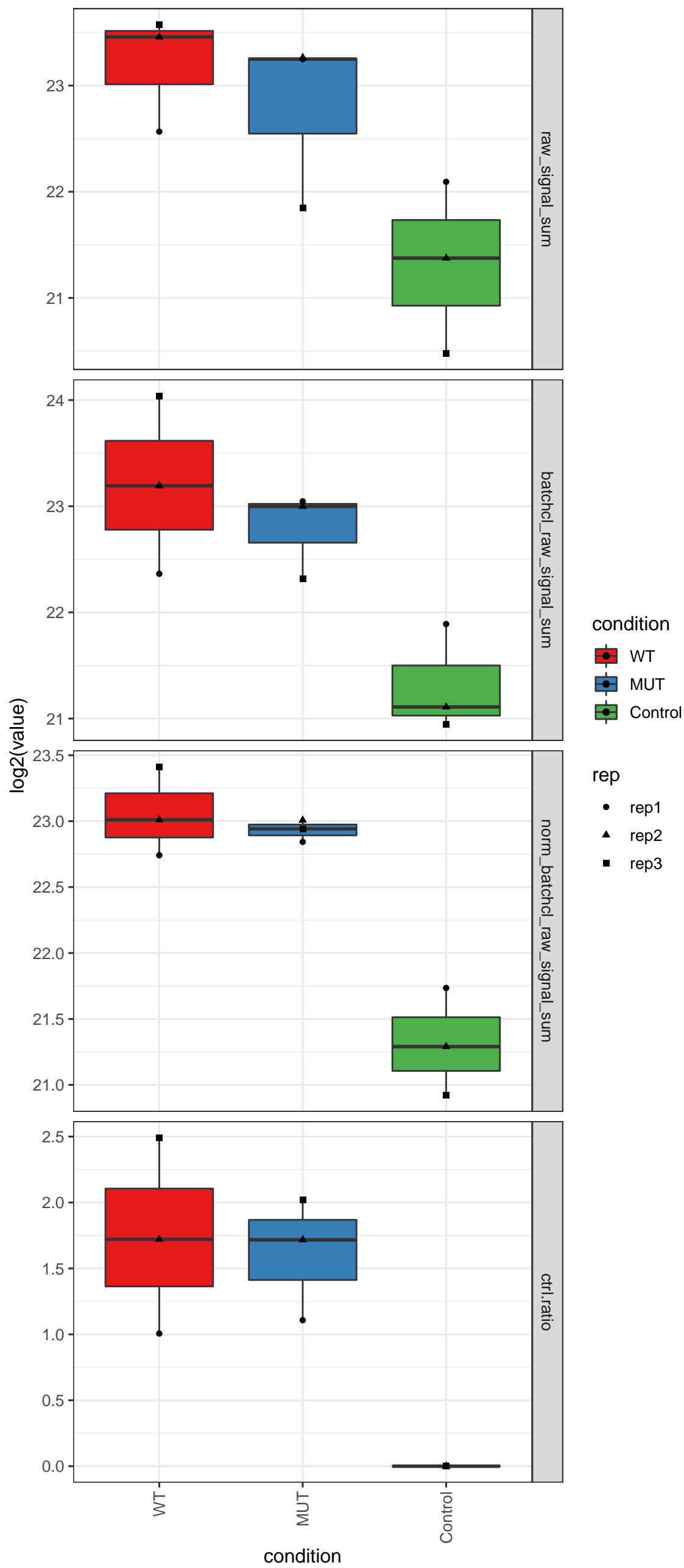
GCN5 – Q03330

Histone acetyltransferase GCN5 OS=*Saccharomyces cerevisiae* (strain A



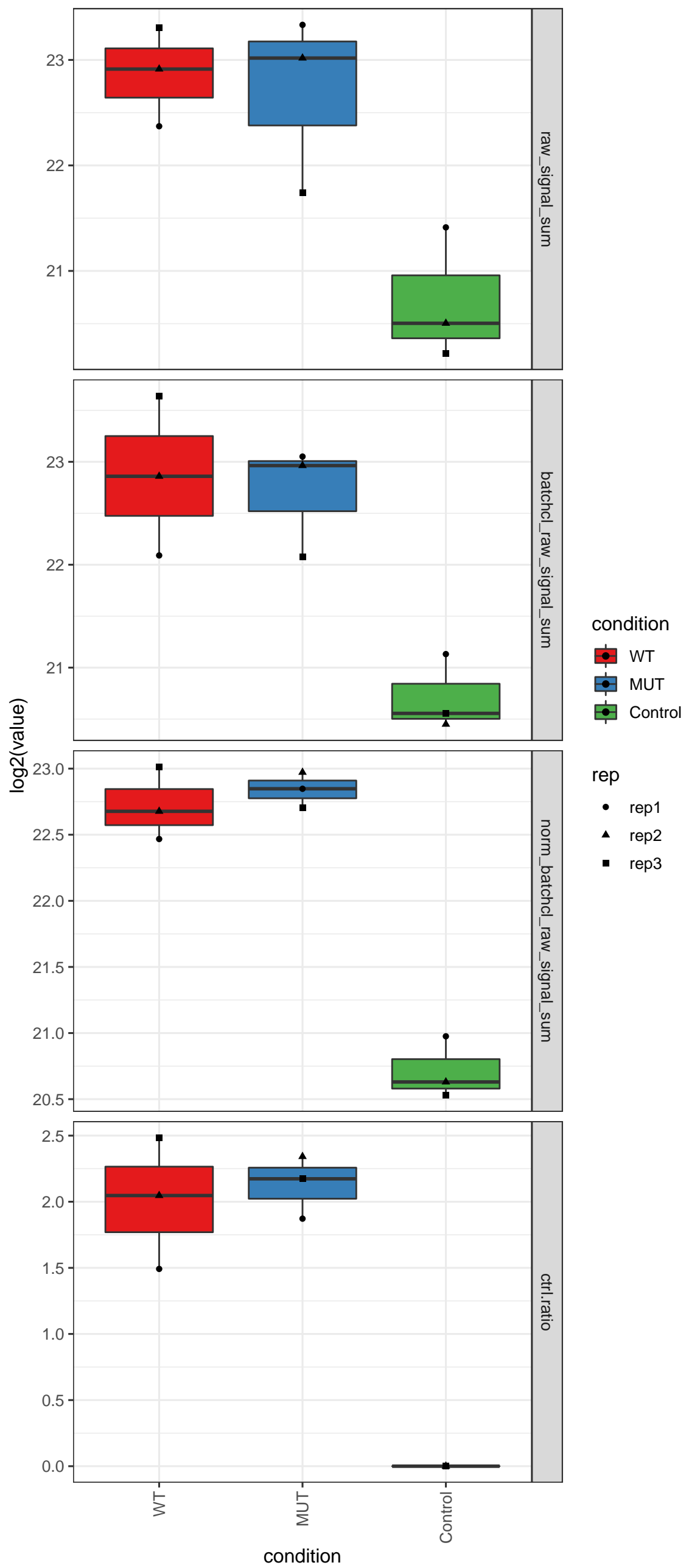
GCV1 – P48015

Aminomethyltransferase, mitochondrial OS=Saccharomyces cerevisiae (S



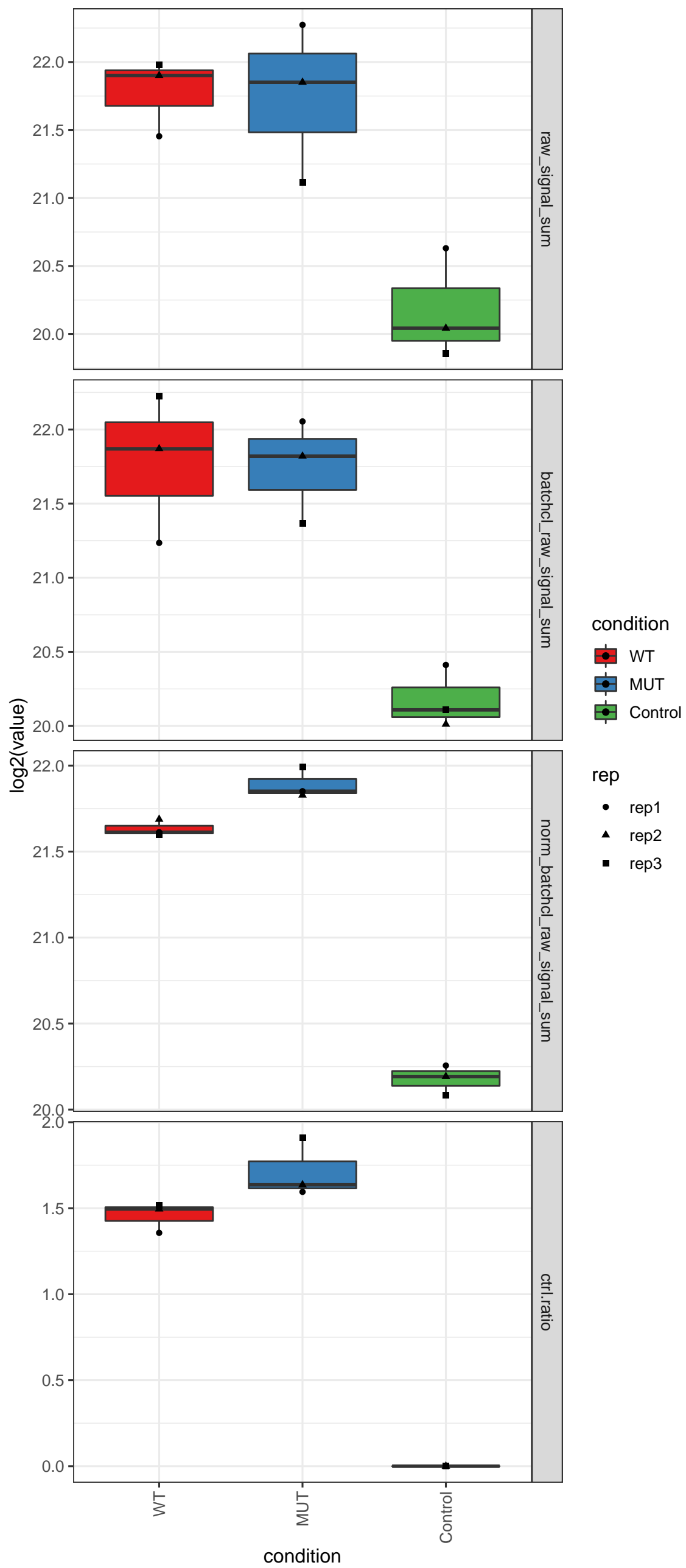
GCV2 – P49095

Glycine dehydrogenase (decarboxylating), mitochondrial OS=Saccharom



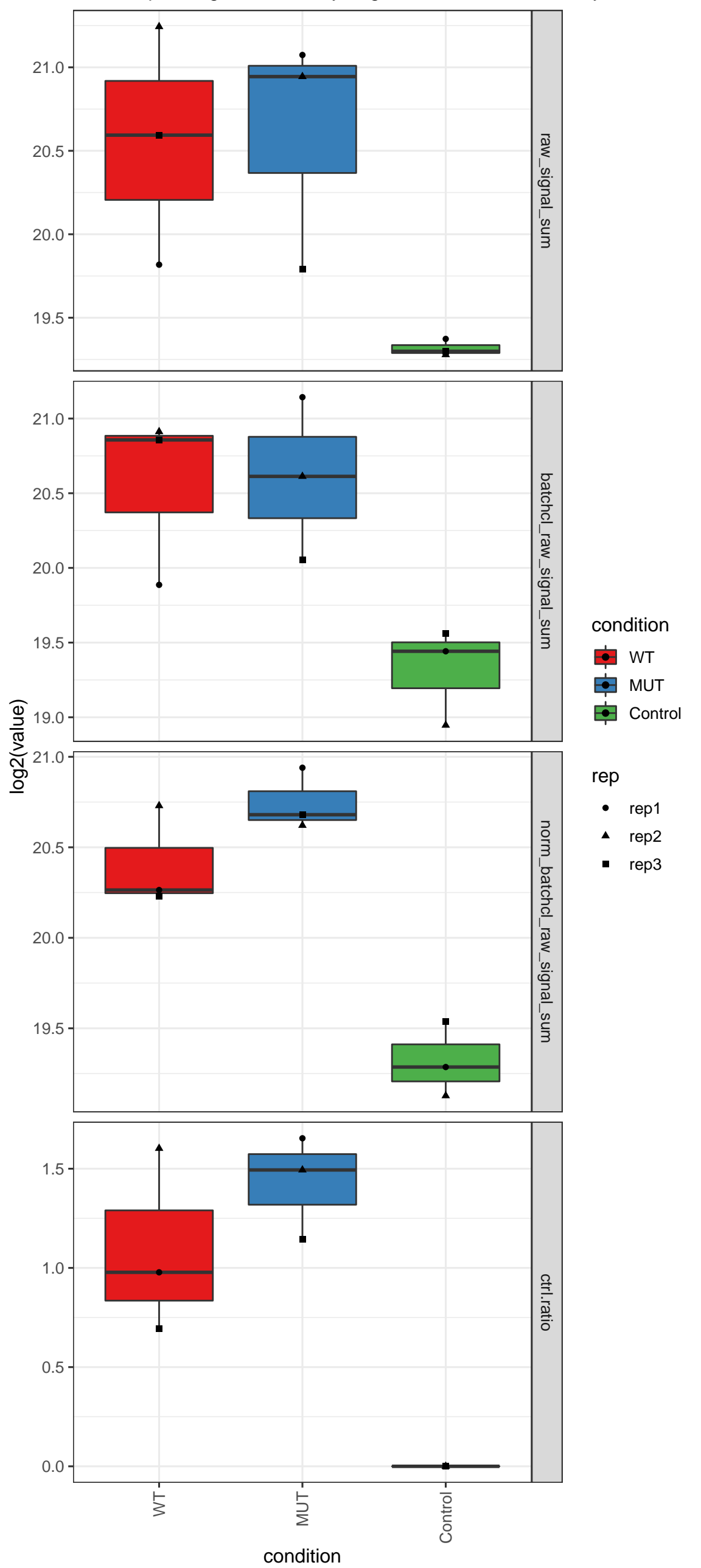
GDB1 – Q06625

Glycogen debranching enzyme OS=*Saccharomyces cerevisiae* (strain ATCC 22016 / DSM 1840 / S288c)



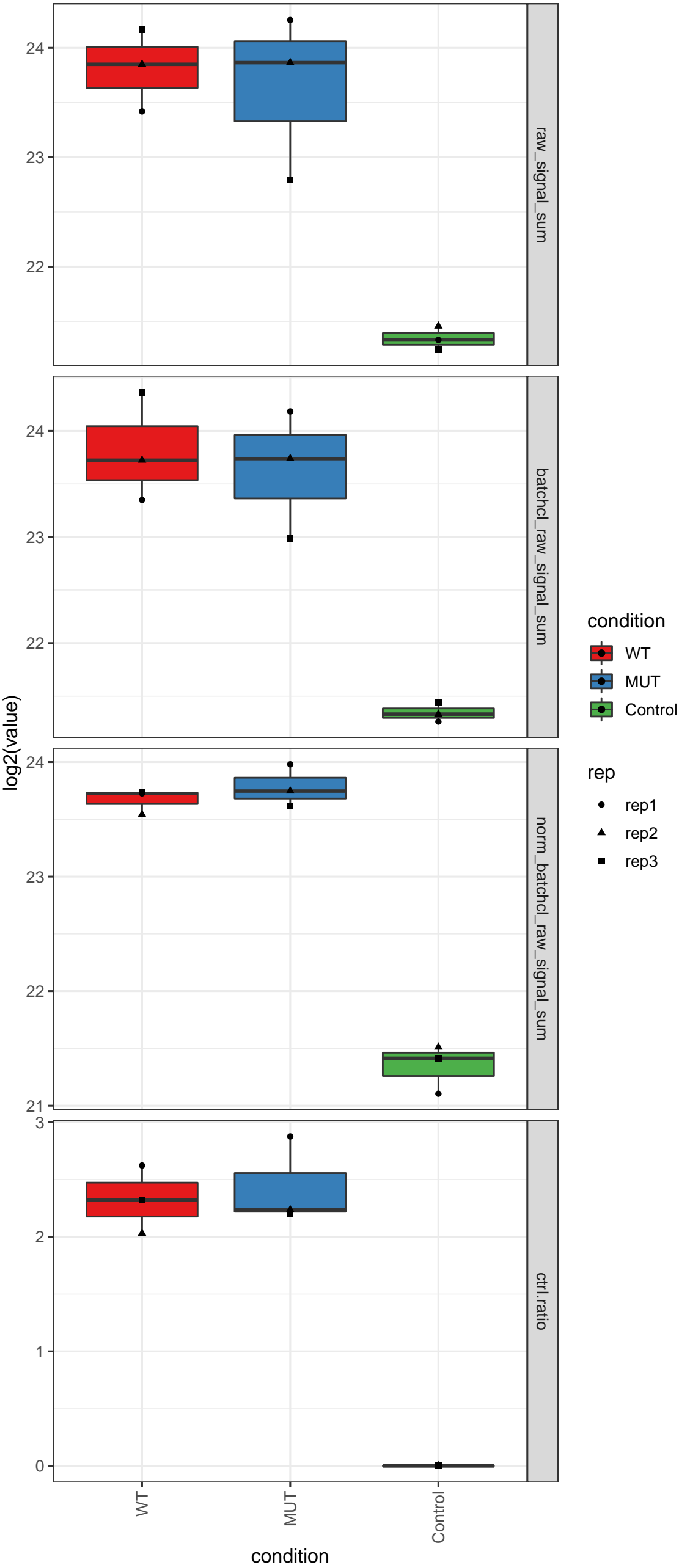
GDH1 – P07262

NADP-specific glutamate dehydrogenase 1 OS=*Saccharomyces cerevisiae*



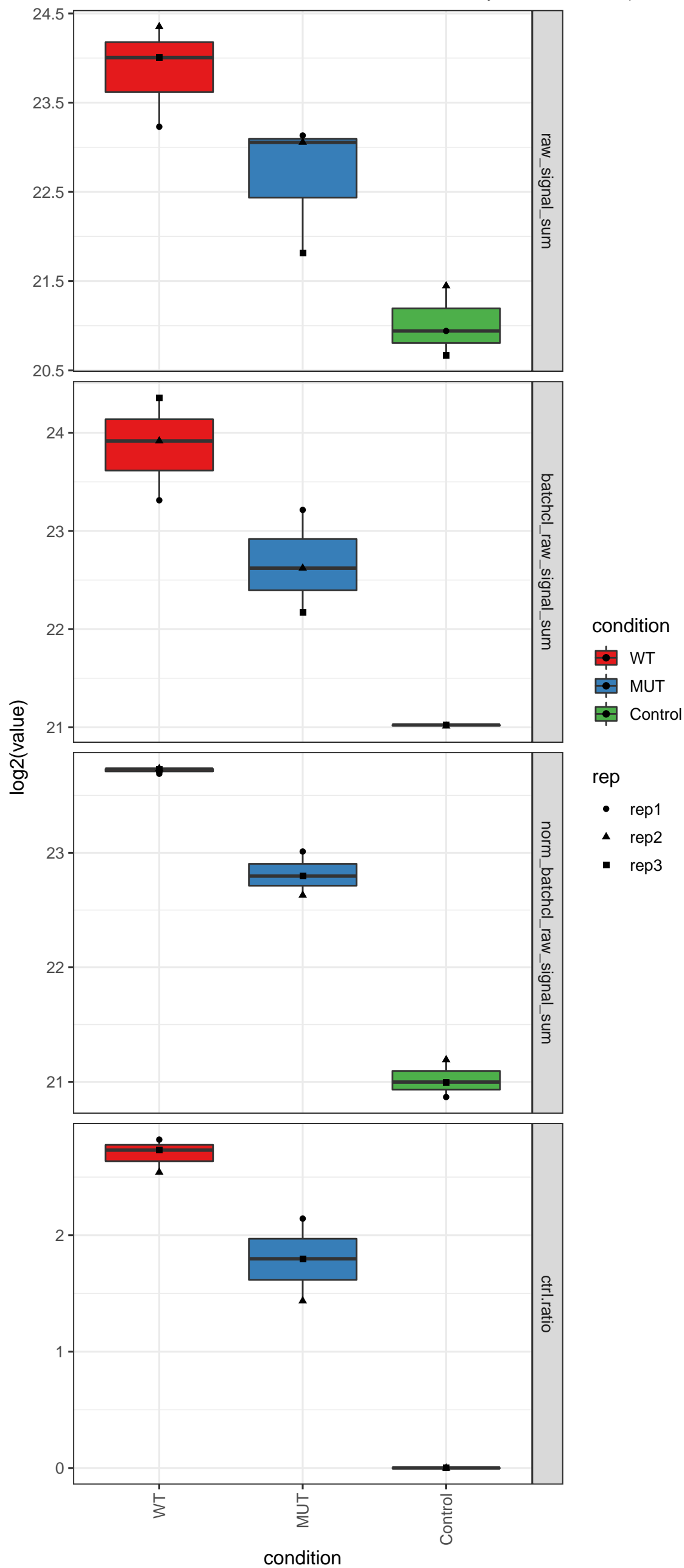
GDH2 – P33327

NAD-specific glutamate dehydrogenase OS=*Saccharomyces cerevisiae* (S288C)



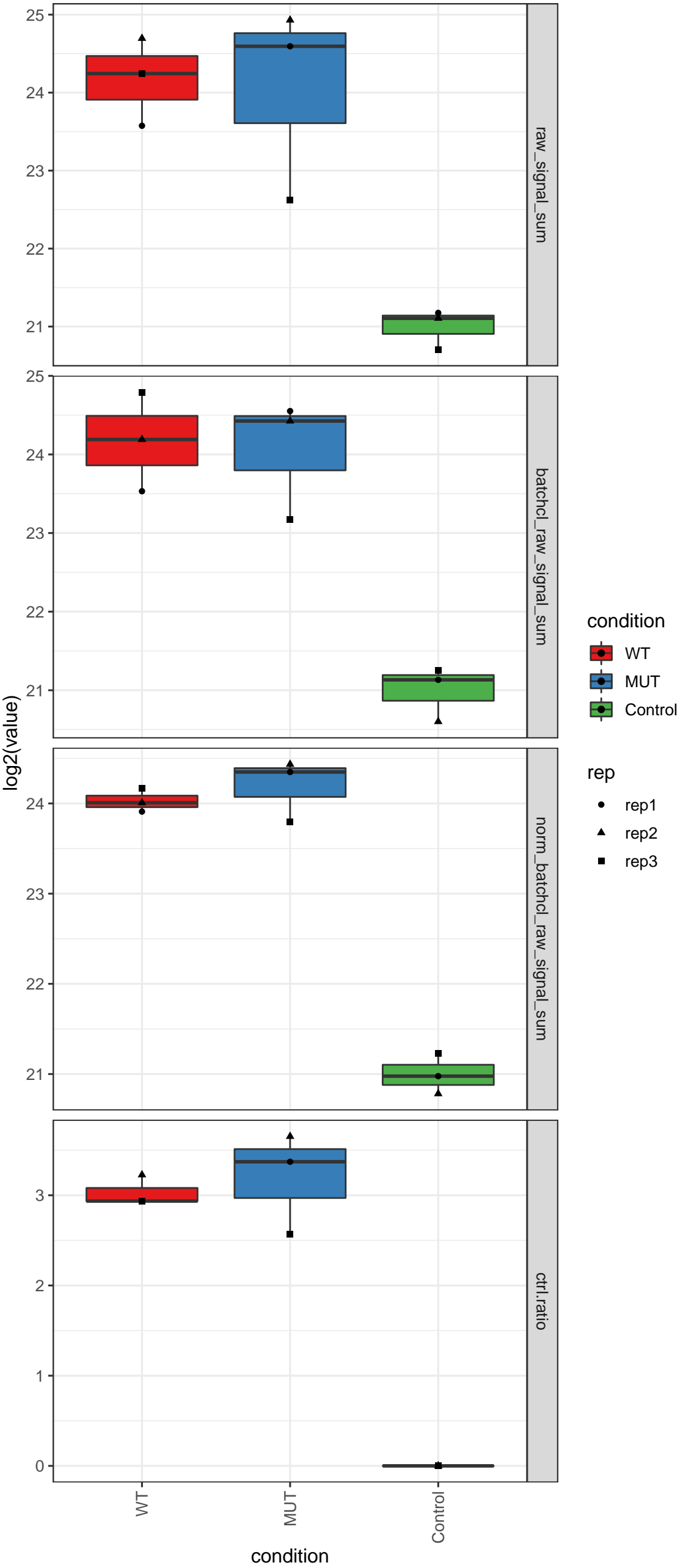
GDI1 – P39958

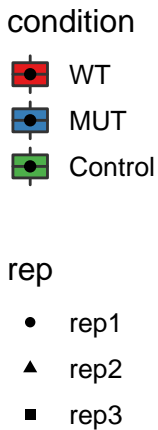
Rab GDP–dissociation inhibitor OS=*Saccharomyces cerevisiae* (strain ATCC 22016 / *D6158*)



GET4 – Q12125

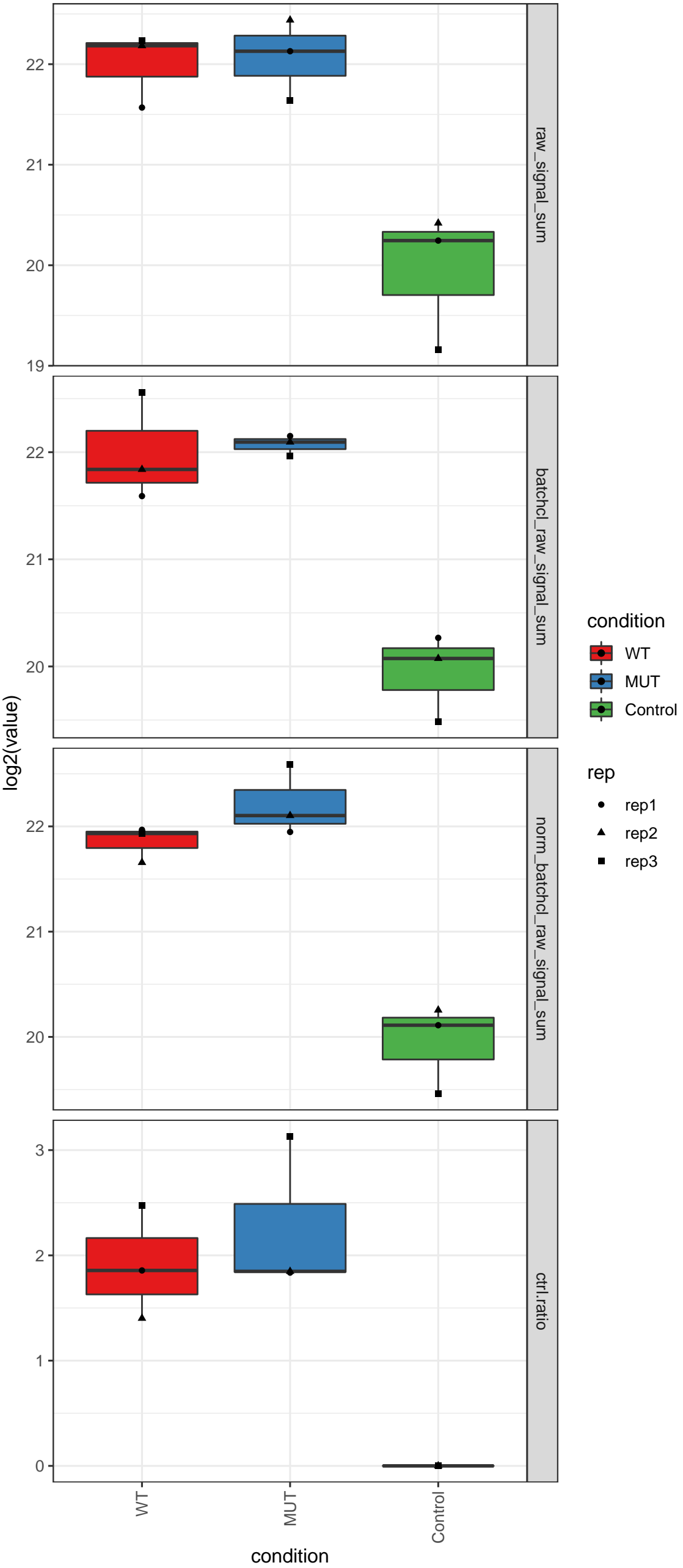
Golgi to ER traffic protein 4 OS=*Saccharomyces cerevisiae* (strain ATCC 2



ADP-ribosylation factor-binding protein GGA1 OS=*Saccharomyces cere*

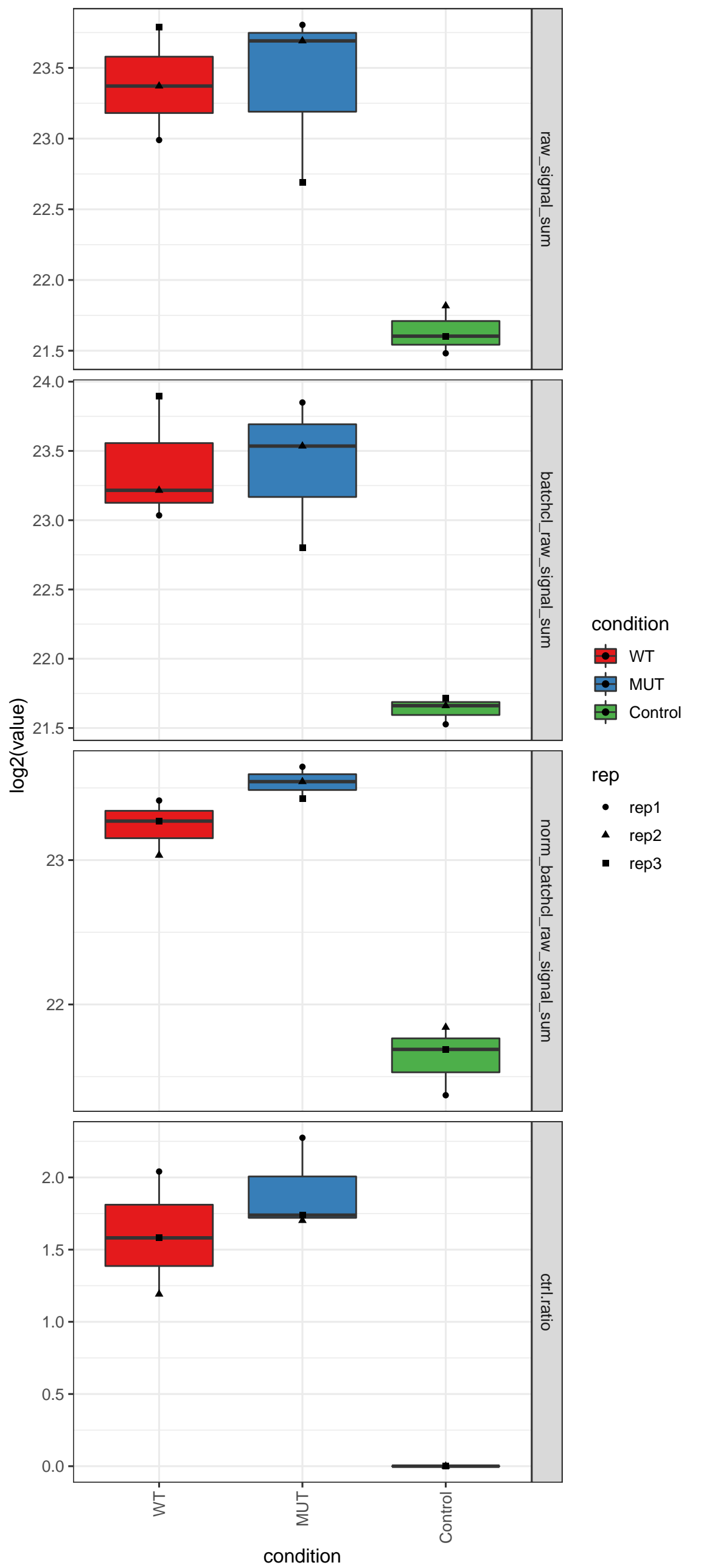
GGA2 – P38817

ADP-ribosylation factor-binding protein GGA2 OS=Saccharomyces cerevisiae



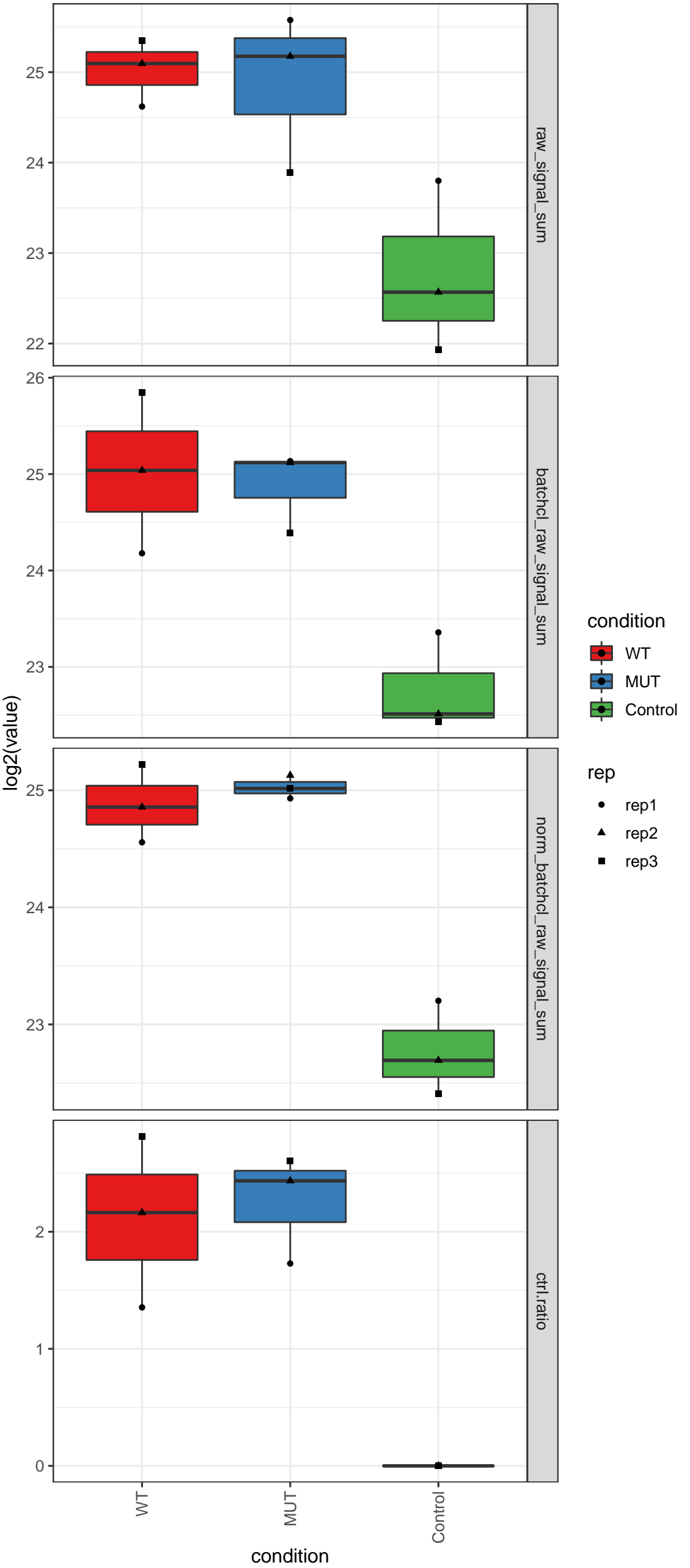
GLC3 – P32775

1,4-alpha-glucan-branching enzyme OS=Saccharomyces cerevisiae (strain



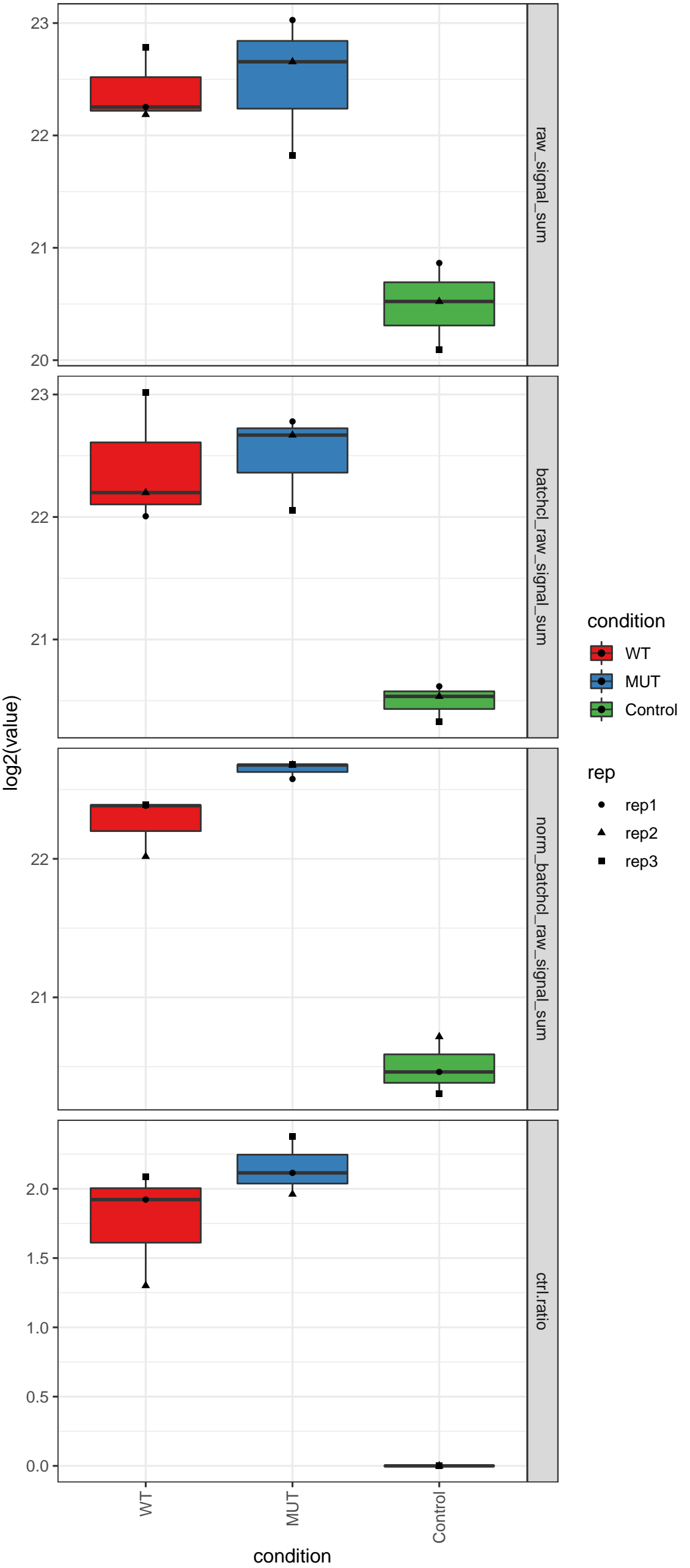
GLK1 – P17709

Glucokinase-1 OS=*Saccharomyces cerevisiae* (strain ATCC 204508 / S28



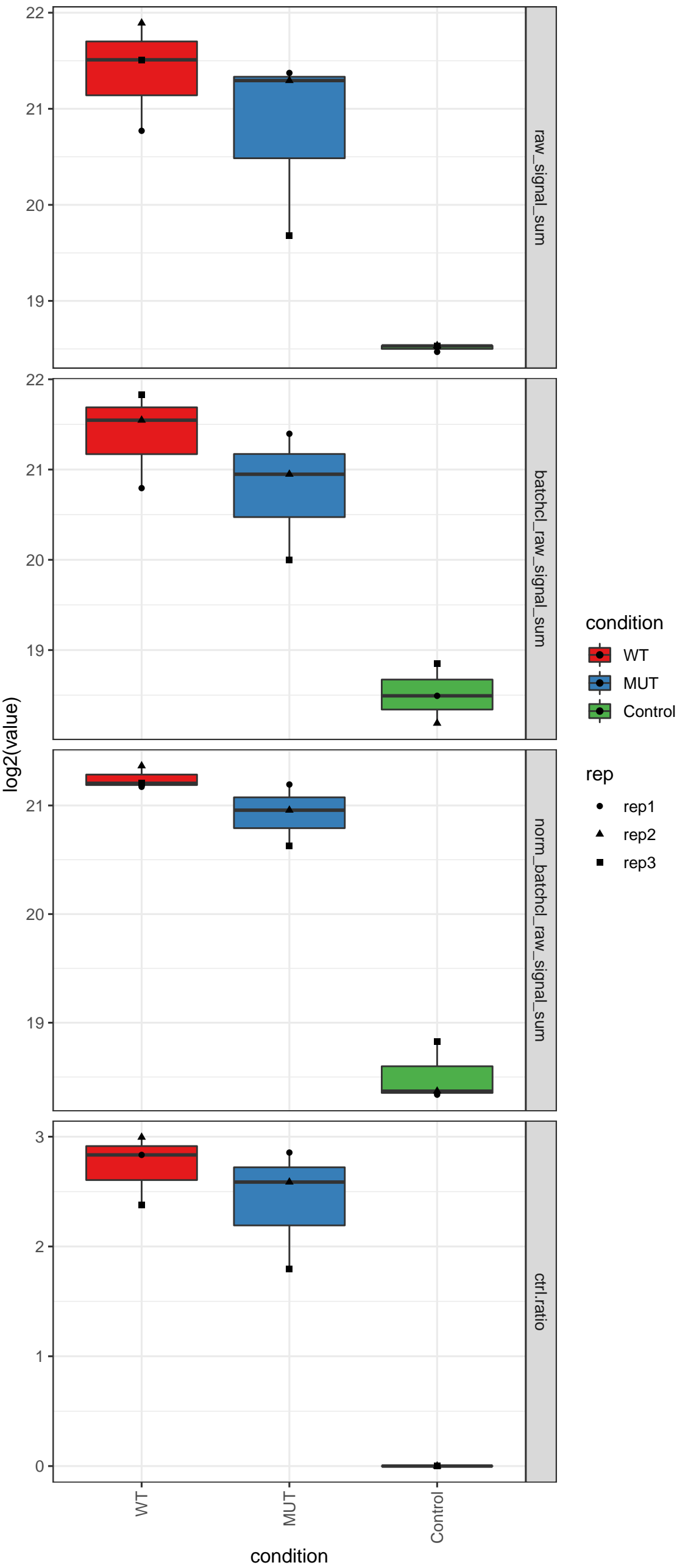
GLN1 – P32288

Glutamine synthetase OS=*Saccharomyces cerevisiae* (strain ATCC 20450)



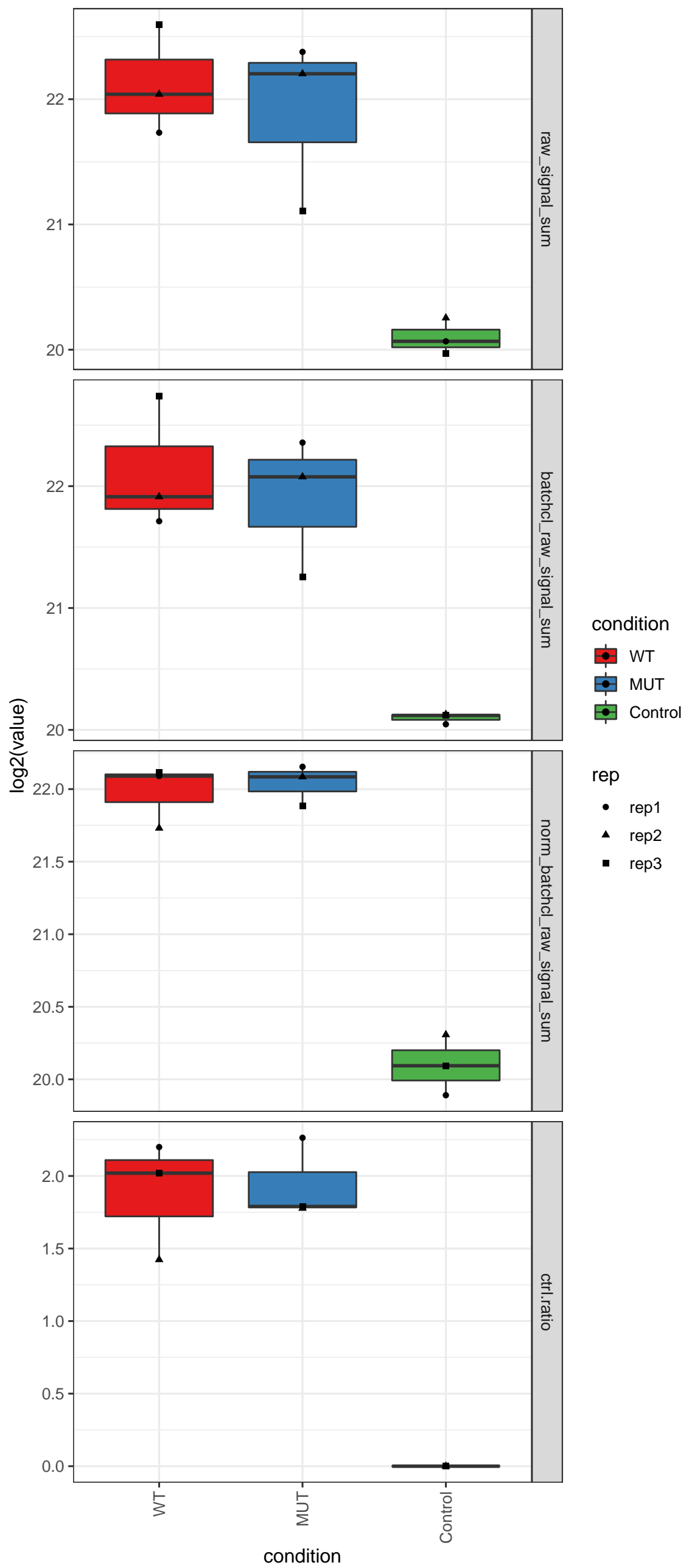
GLO3 – P38682

ADP-ribosylation factor GTPase-activating protein GLO3 OS=Saccharomy



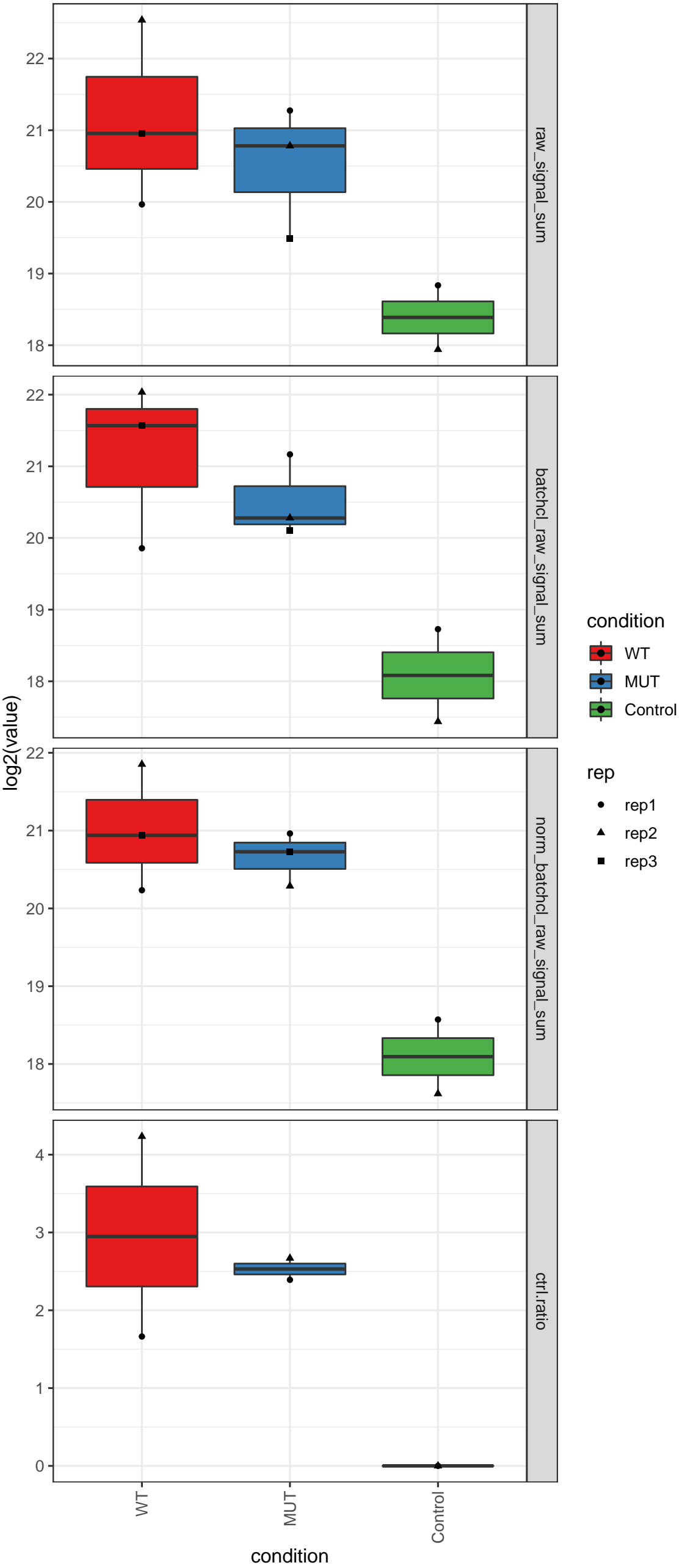
GLR1 – P41921|P41921–2

Glutathione reductase OS=Saccharomyces cerevisiae (strain ATCC 2045



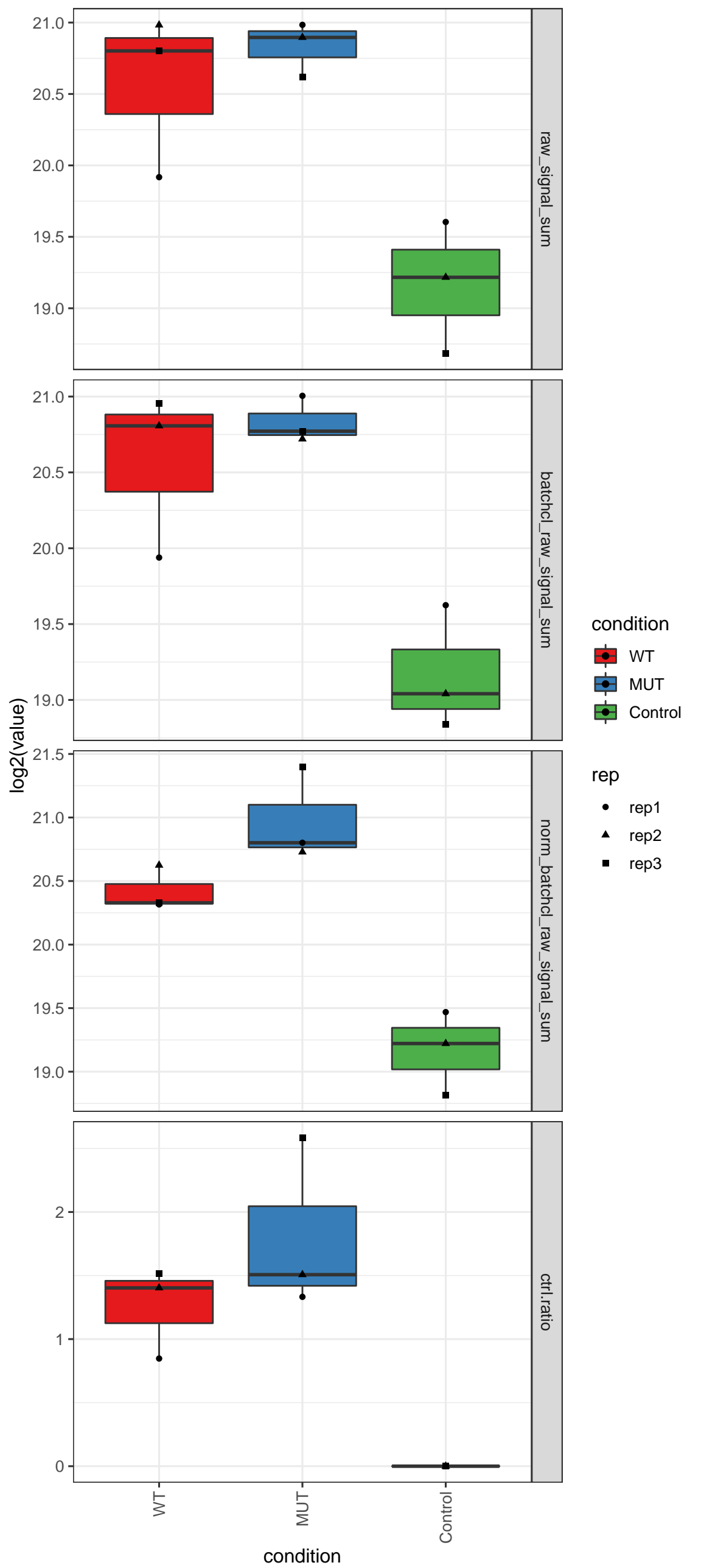
GLT1 – Q12680

Glutamate synthase [NADH] OS=Saccharomyces cerevisiae (strain ATCC



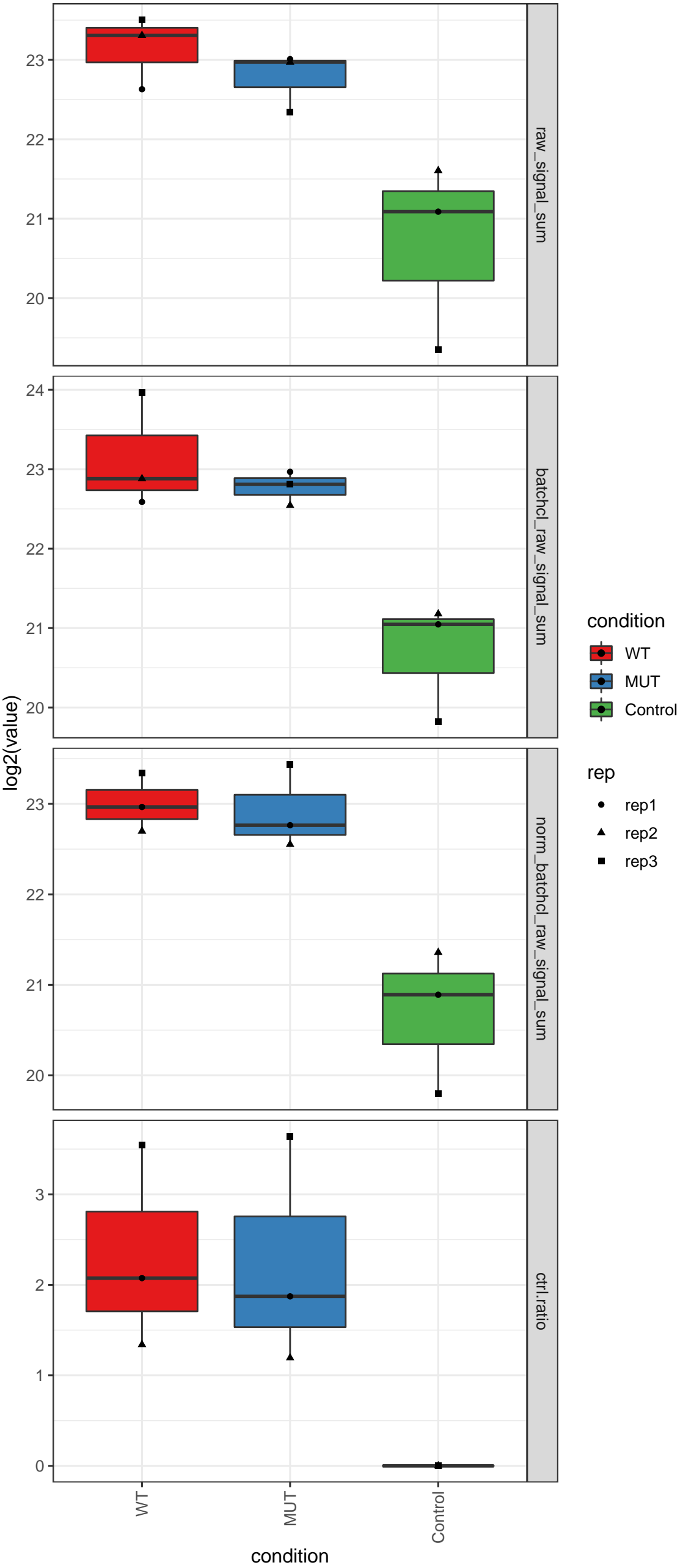
GND1 – P38720

6-phosphogluconate dehydrogenase, decarboxylating 1 OS=Saccharomy



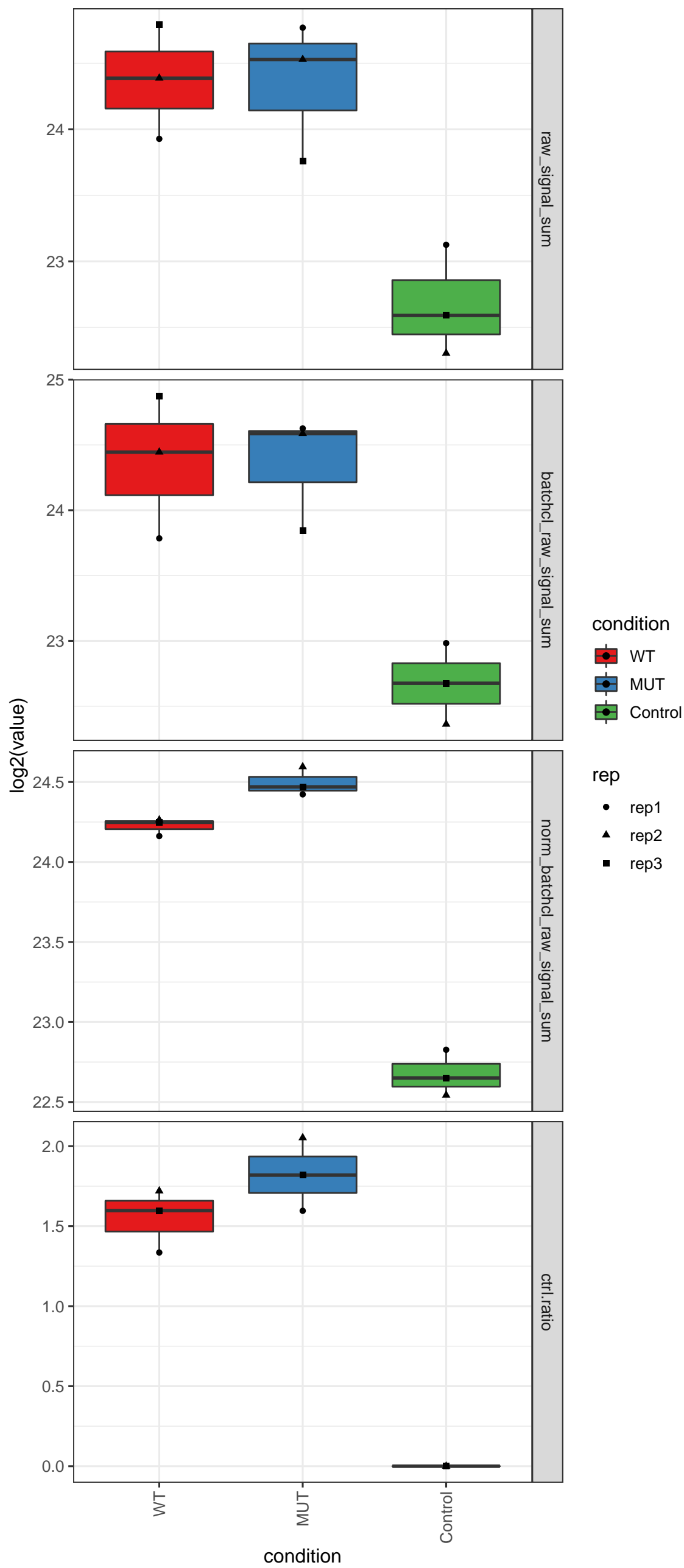
GPD1 – Q00055

Glycerol-3-phosphate dehydrogenase [NAD(+)] 1 OS=Saccharomyces cerevisiae



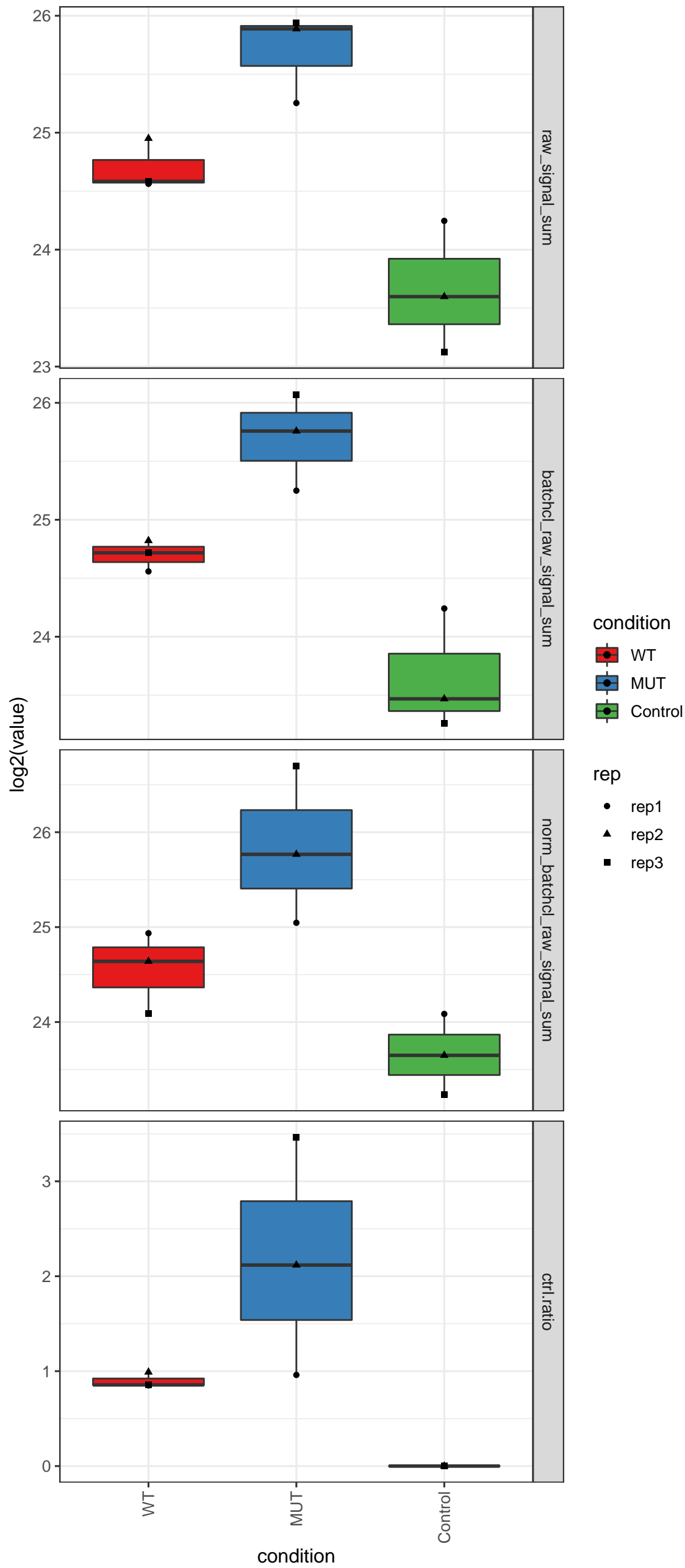
GPH1 – P06738

Glycogen phosphorylase OS=*Saccharomyces cerevisiae* (strain ATCC 20454) [taxid:4914]



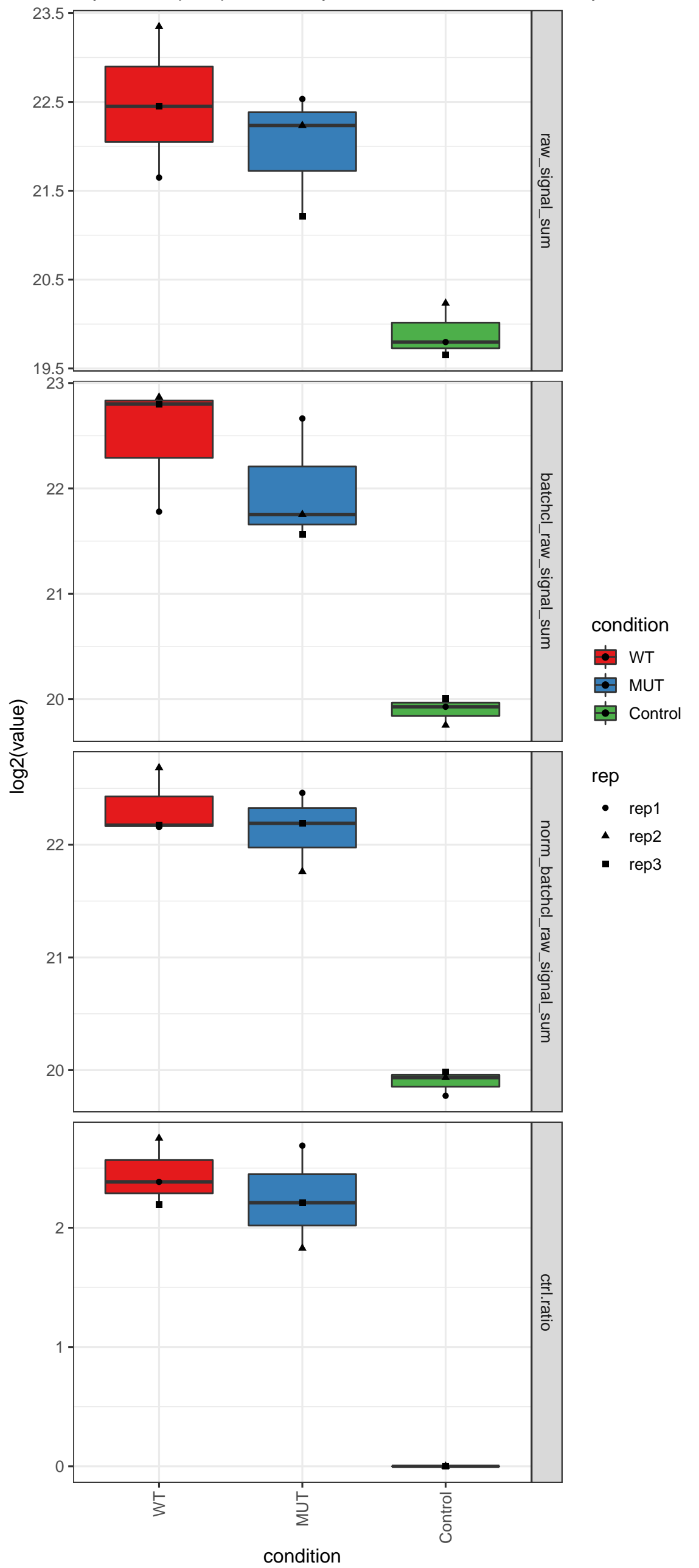
GPM1 – P00950

Phosphoglycerate mutase 1 OS=*Saccharomyces cerevisiae* (strain ATCC 2



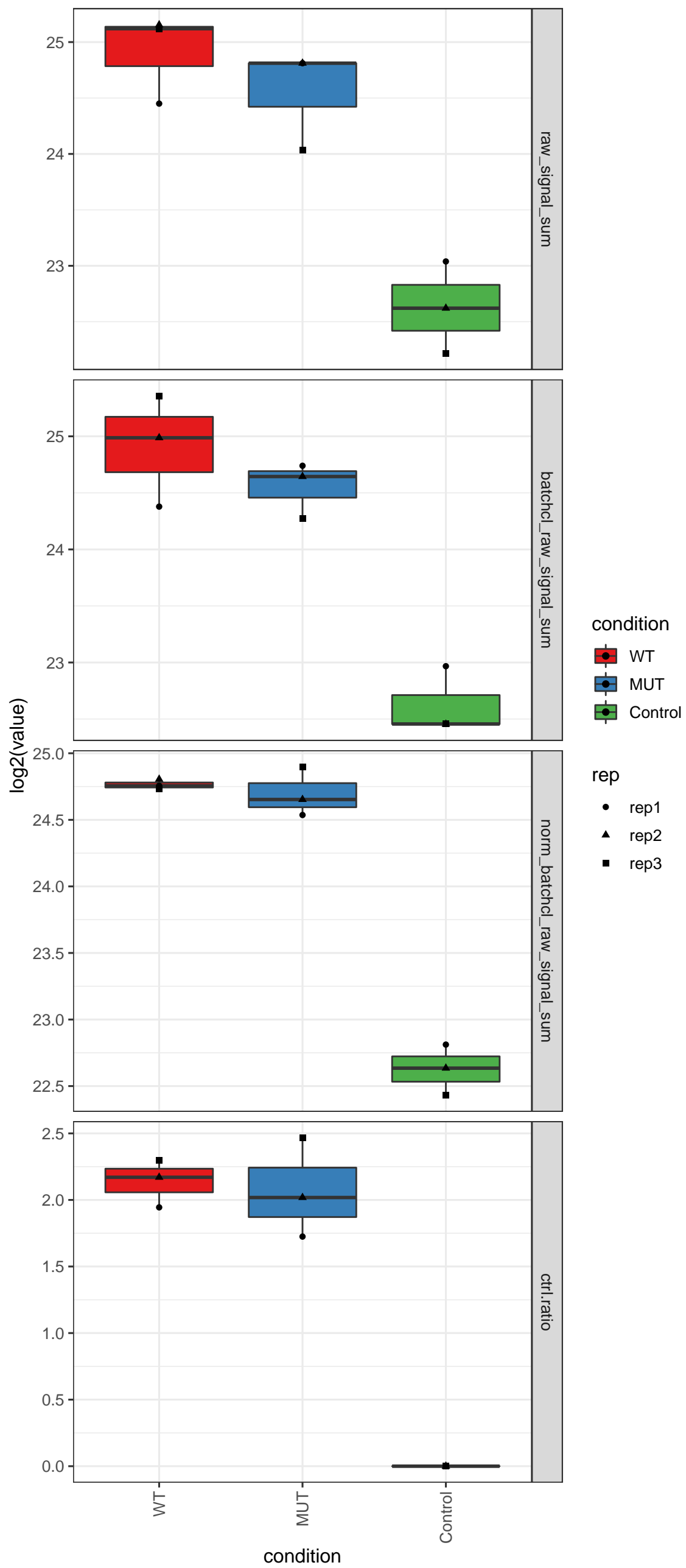
GPT2 - P36148

Glycerol-3-phosphate O-acyltransferase 2 OS=Saccharomyces cerevisiae



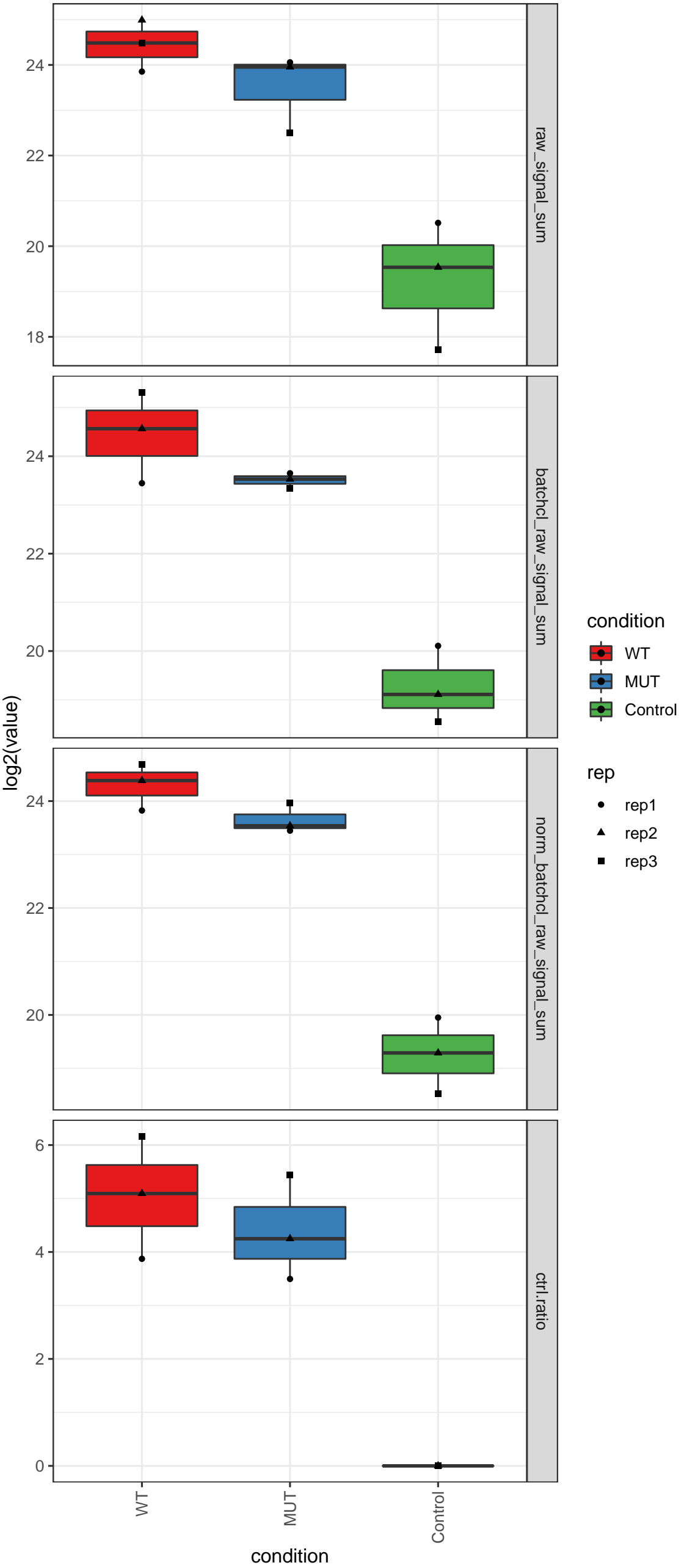
GRS1 – P38088–2

Isoform Cytoplasmic of Glycine--tRNA ligase 1, mitochondrial OS=Sacchar



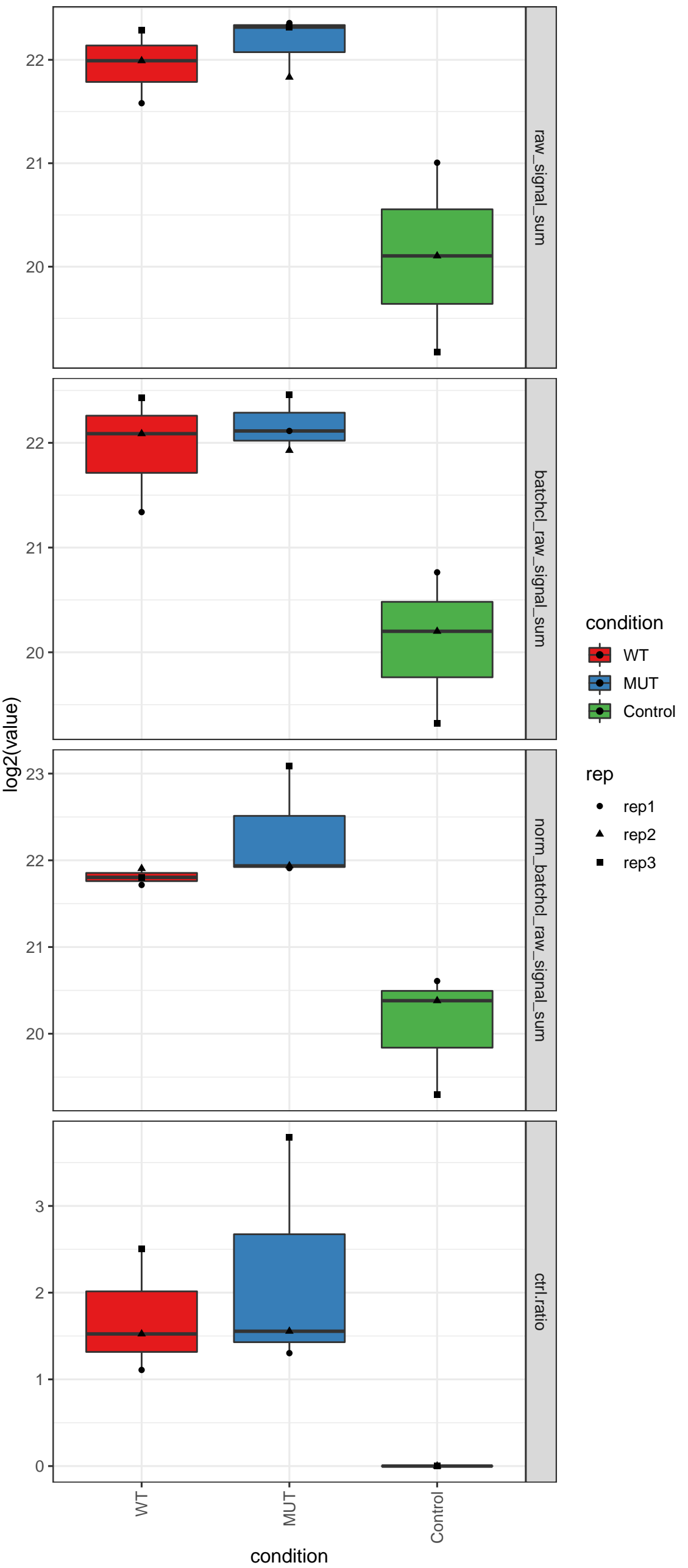
GSP2 – P32836

GTP-binding nuclear protein GSP2/CNR2 OS=*Saccharomyces cerevisiae*



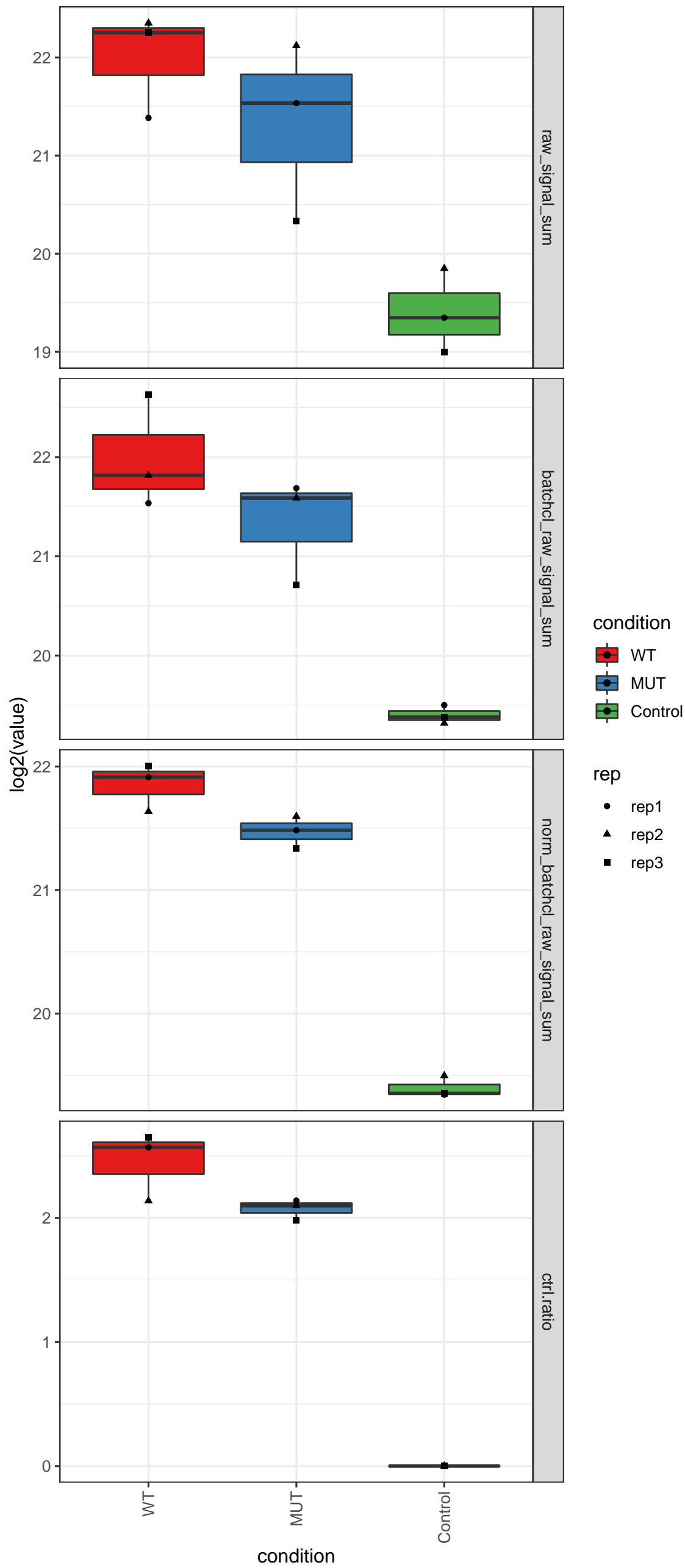
GSY1 – P23337

Glycogen [starch] synthase isoform 1 OS=*Saccharomyces cerevisiae* (strain



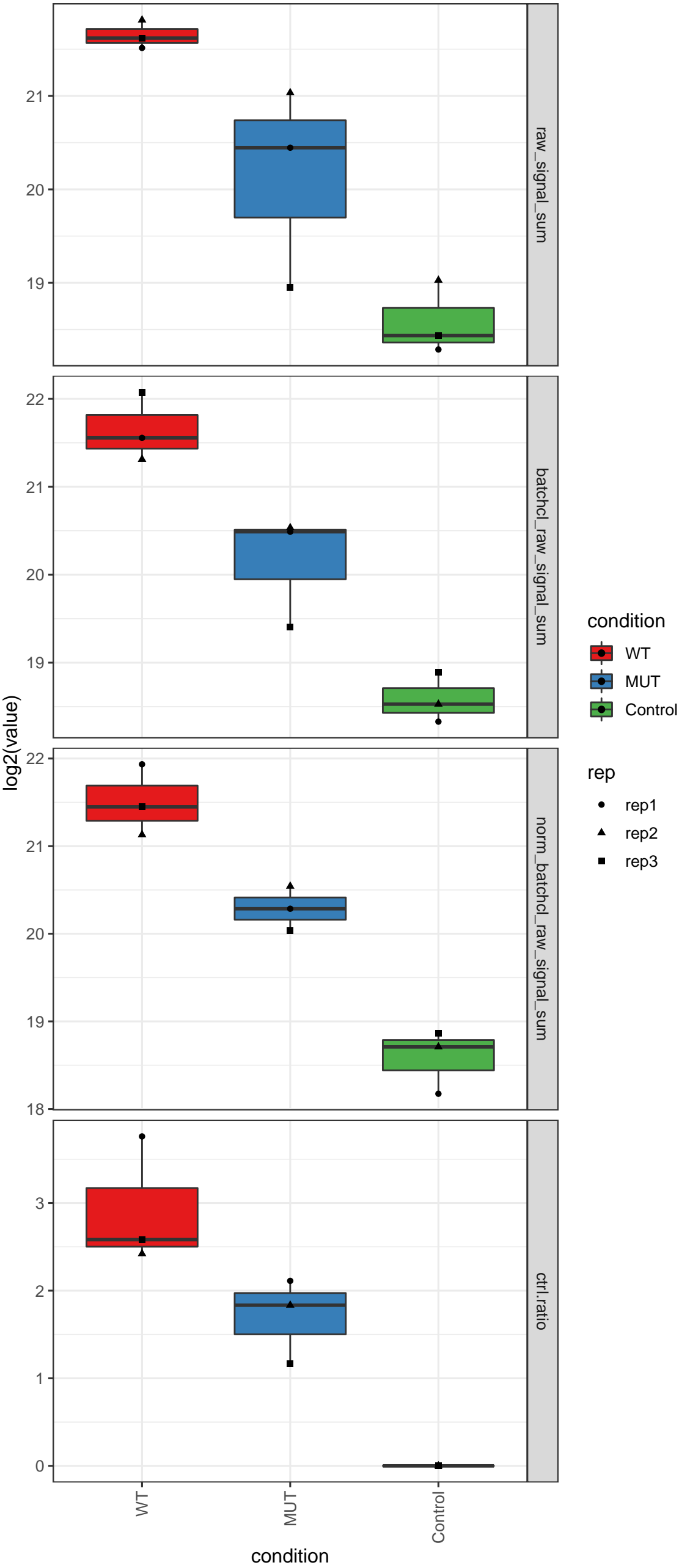
GTS1 – P40956

Protein GTS1 OS=*Saccharomyces cerevisiae* (strain ATCC 204508 / S288



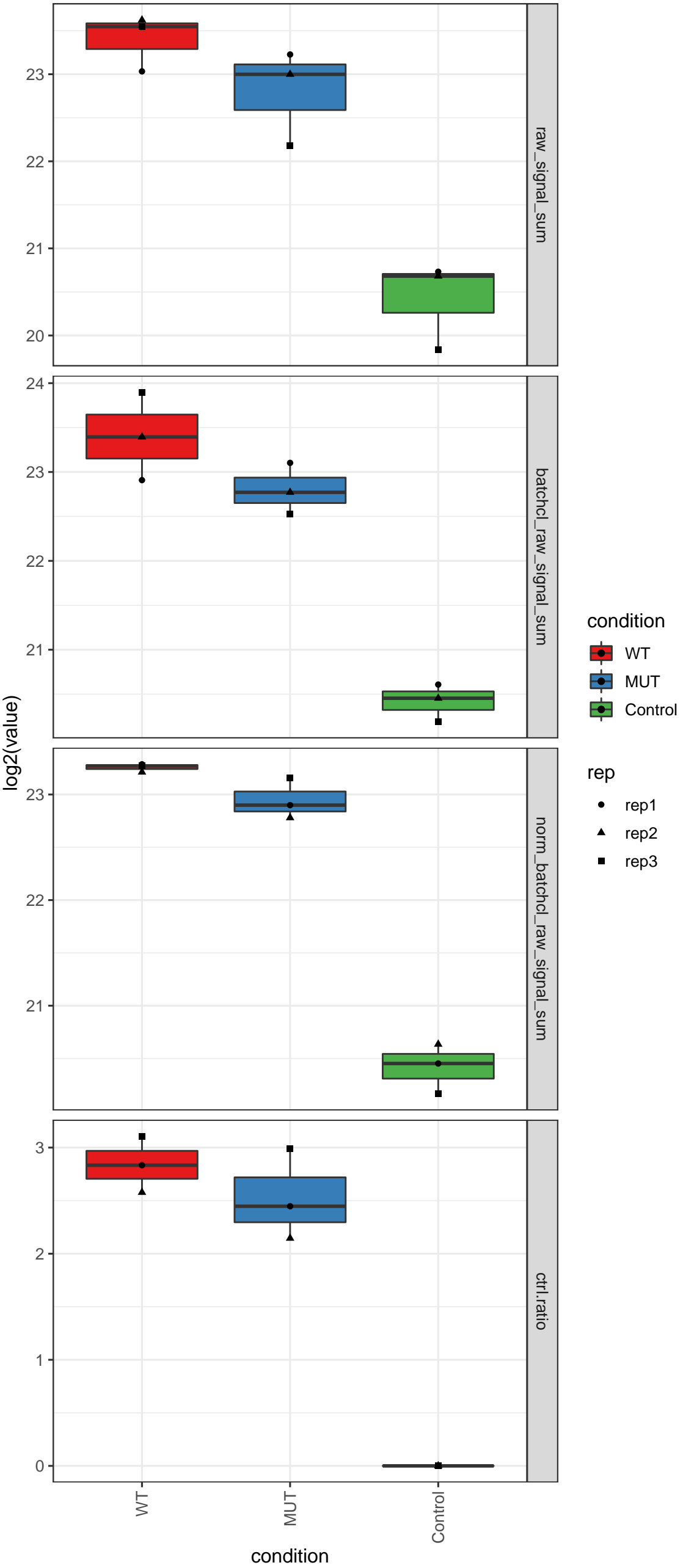
GTT3 – P39996

Glutathione transferase 3 OS=Saccharomyces cerevisiae (strain ATCC 204



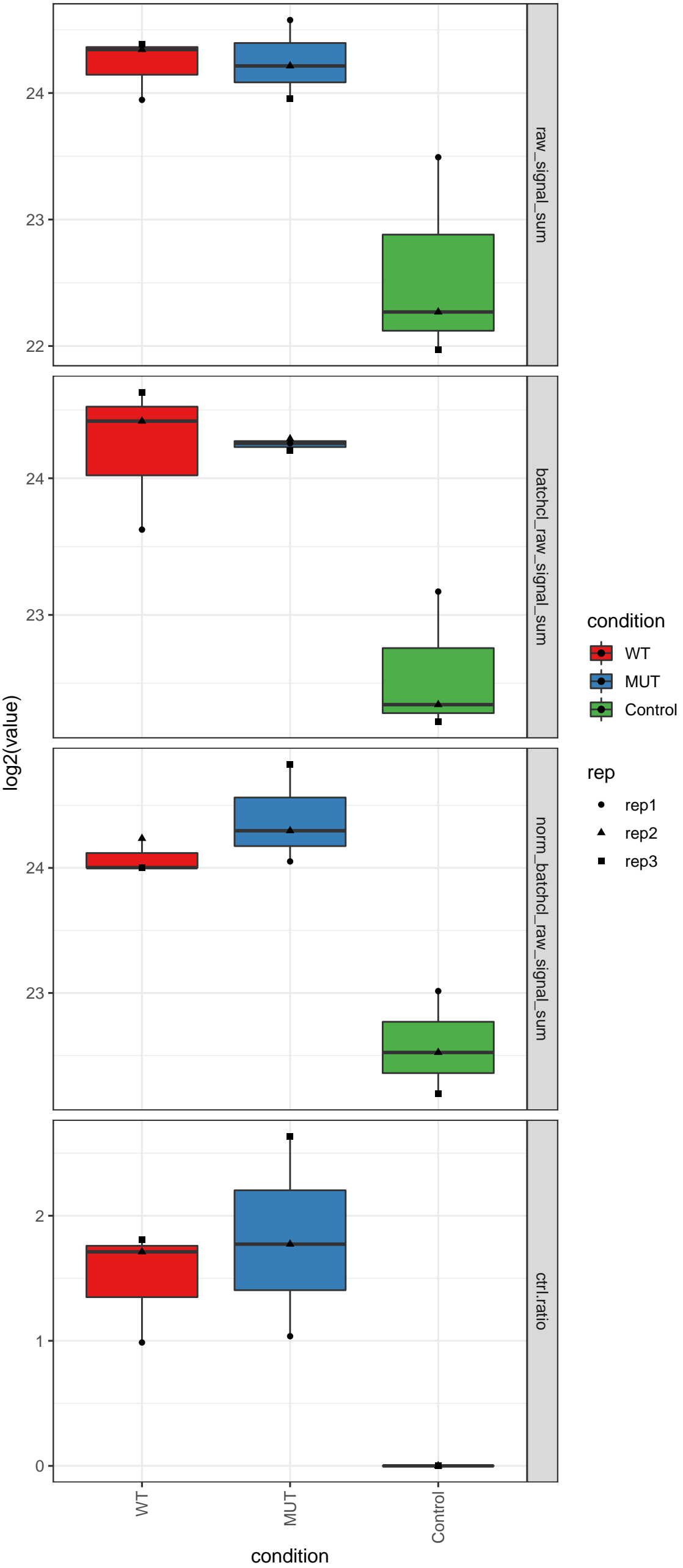
GUS1 – P46655

Glutamate--tRNA ligase, cytoplasmic OS=*Saccharomyces cerevisiae* (stra



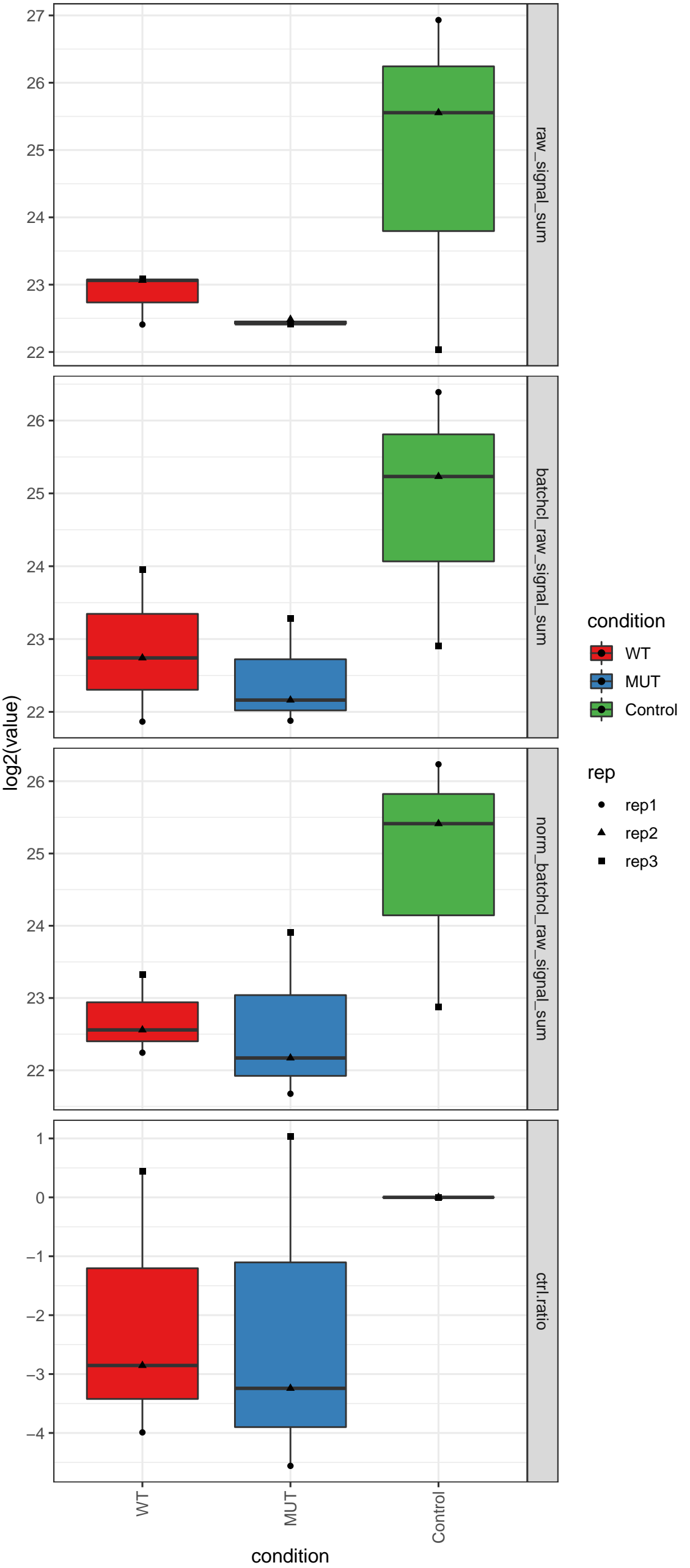
GUT2 – P32191

Glycerol-3-phosphate dehydrogenase, mitochondrial OS=Saccharomyces



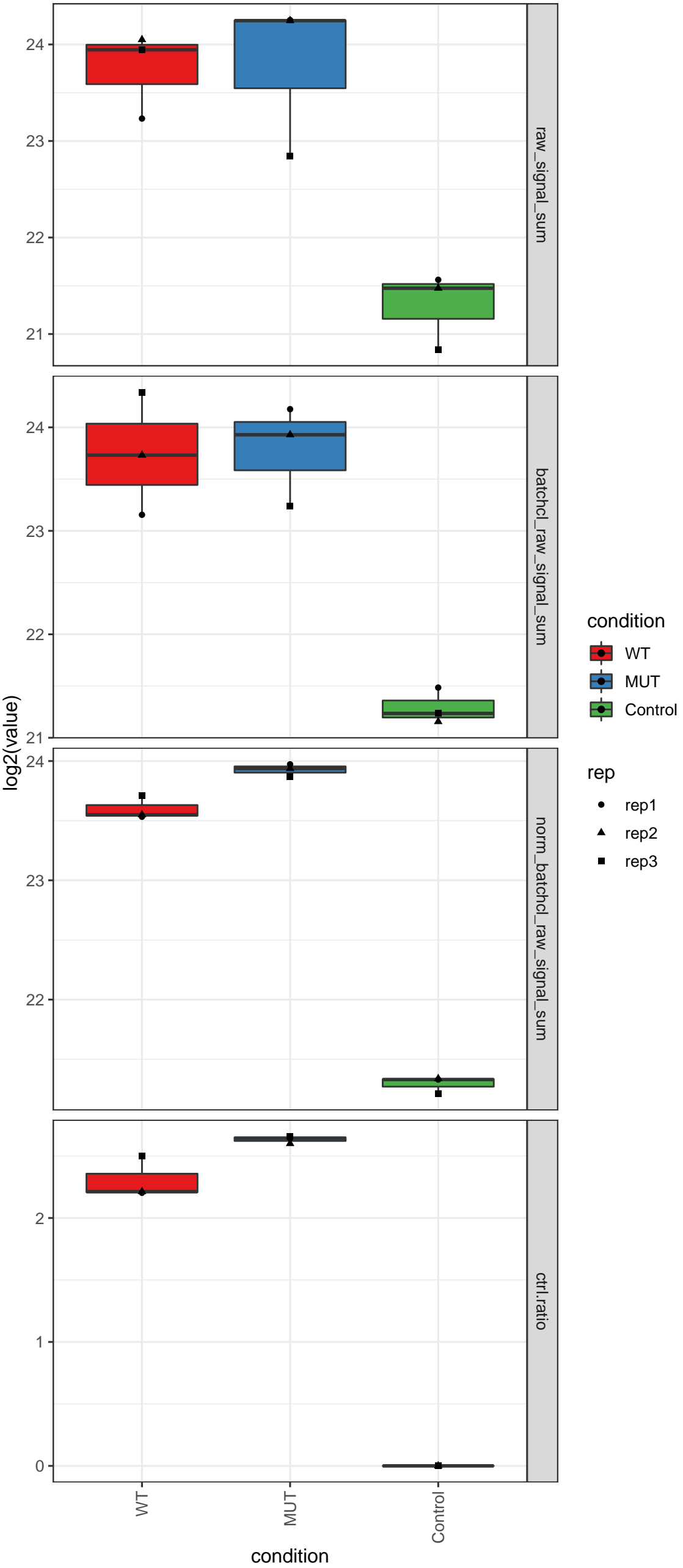
GVP36 – P40531

Protein GVP36 OS=*Saccharomyces cerevisiae* (strain ATCC 204508 / S28



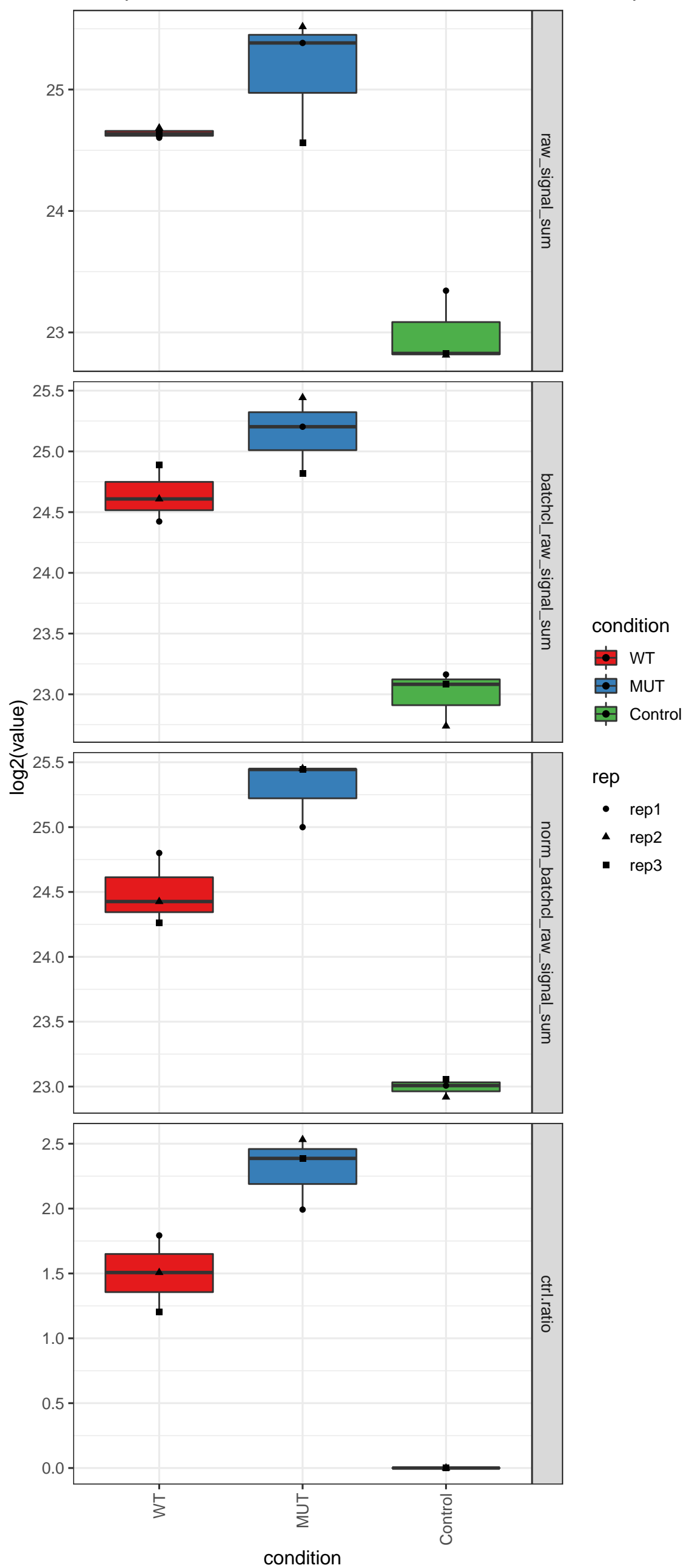
HAS1 – Q03532

ATP-dependent RNA helicase HAS1 OS=*Saccharomyces cerevisiae* (strain



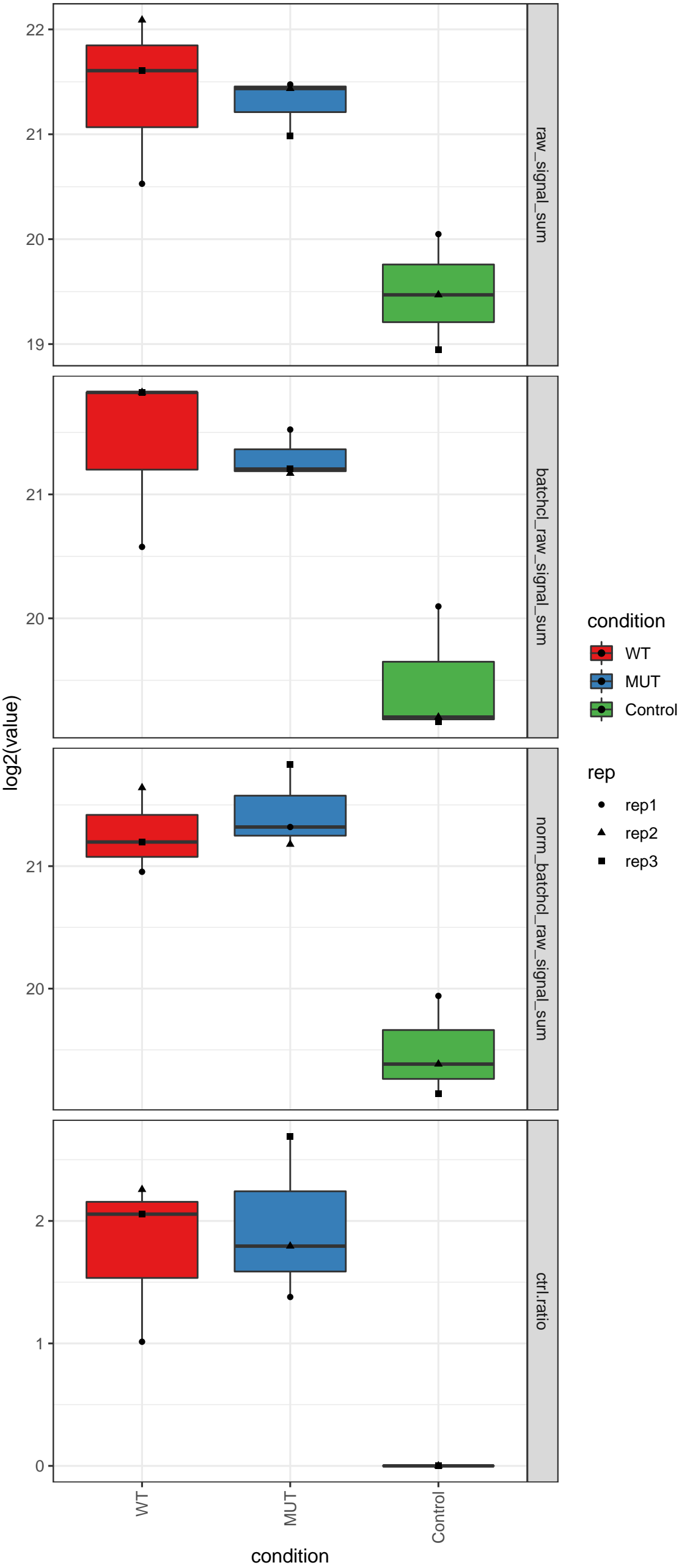
HCR1 – Q05775

Eukaryotic translation initiation factor 3 subunit J OS=Saccharomyces cerevisiae



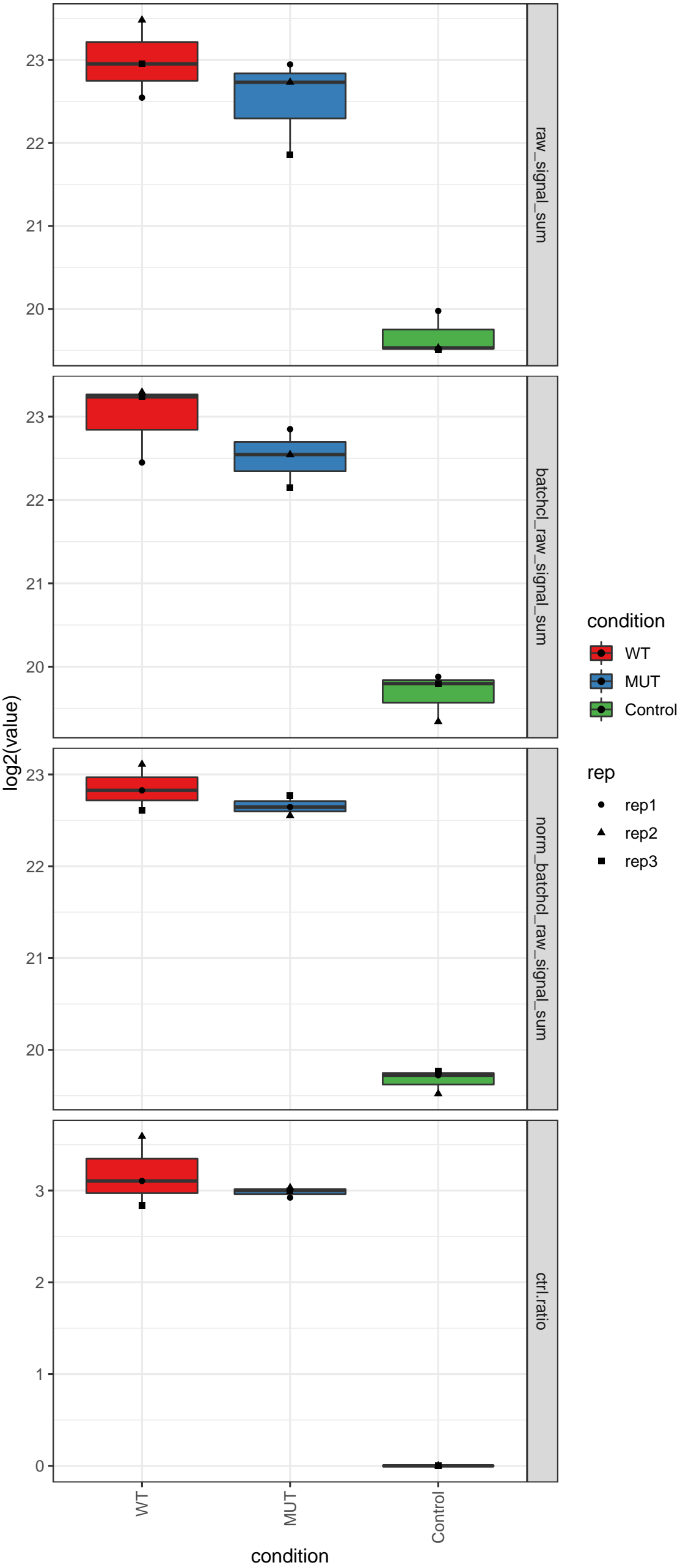
HEF3 – P53978

Elongation factor 3B OS=*Saccharomyces cerevisiae* (strain ATCC 204508)



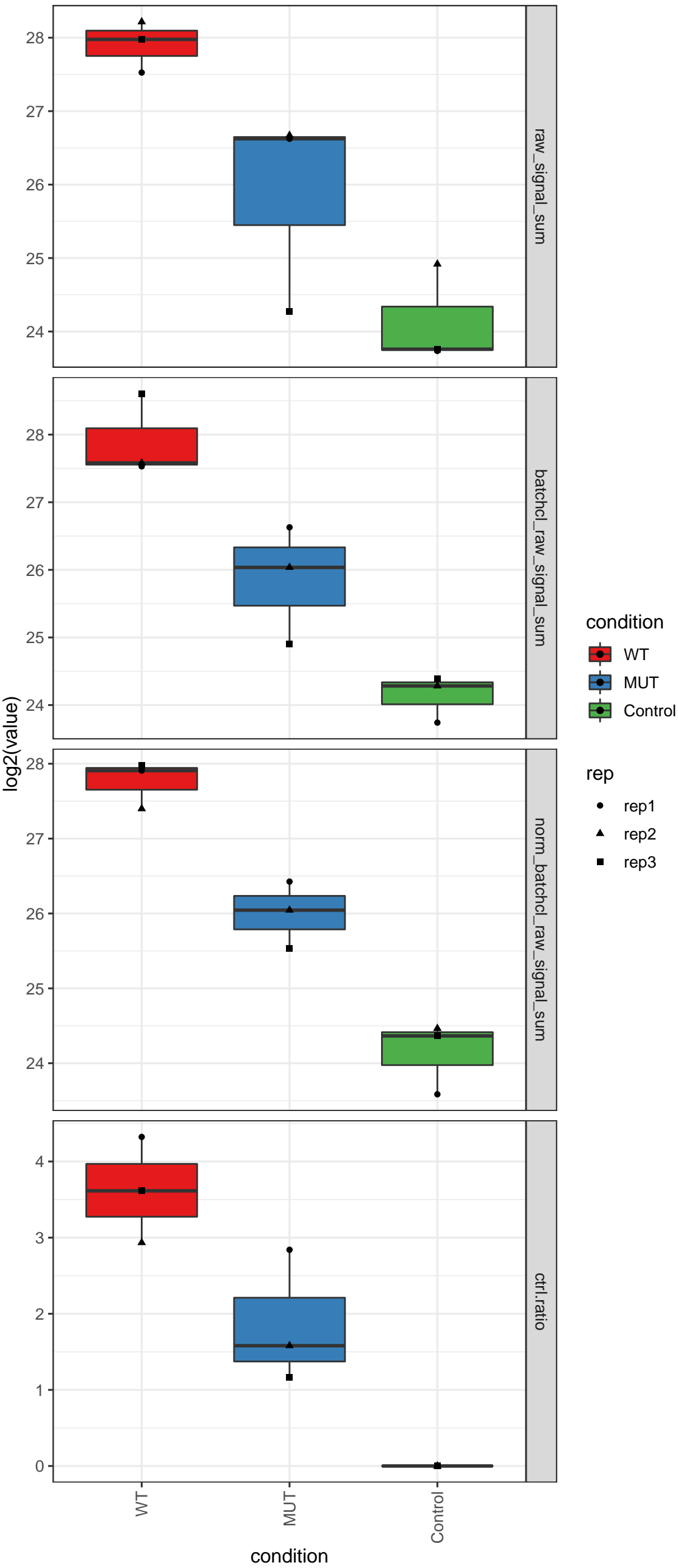
HFD1 – Q04458

Fatty aldehyde dehydrogenase HFD1 OS=*Saccharomyces cerevisiae* (stra



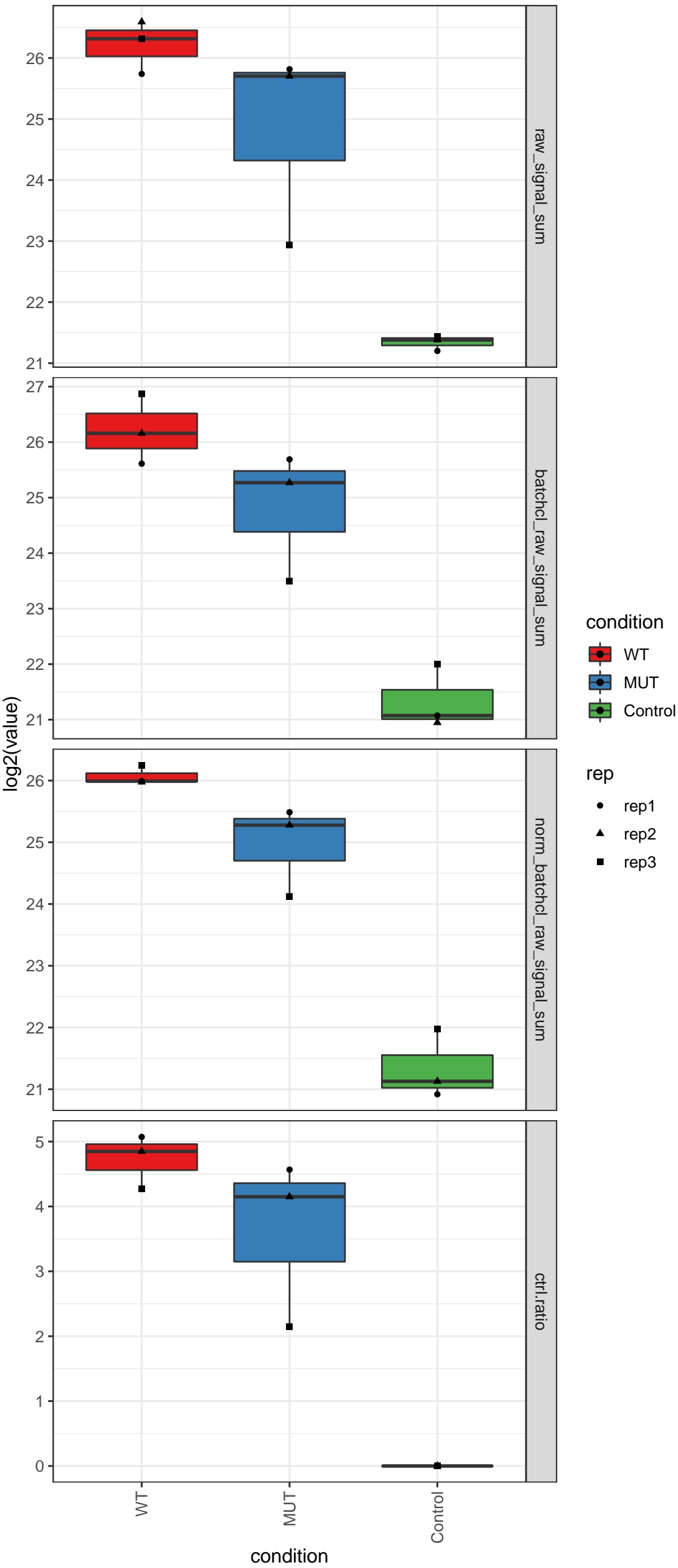
HHF1 – P02309

Histone H4 OS=*Saccharomyces cerevisiae* (strain ATCC 204508 / S288c)



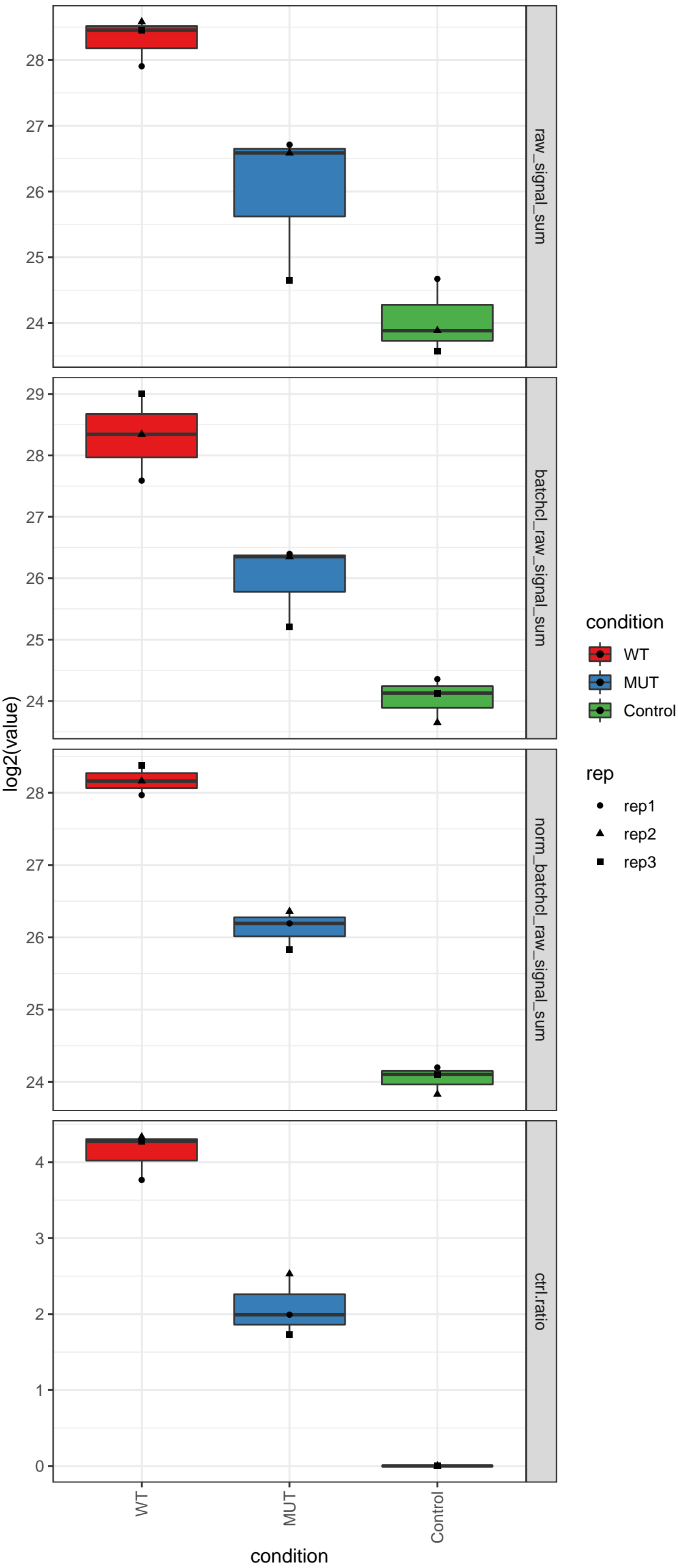
HHO1 – P53551

Histone H1 OS=*Saccharomyces cerevisiae* (strain ATCC 204508 / S288c)



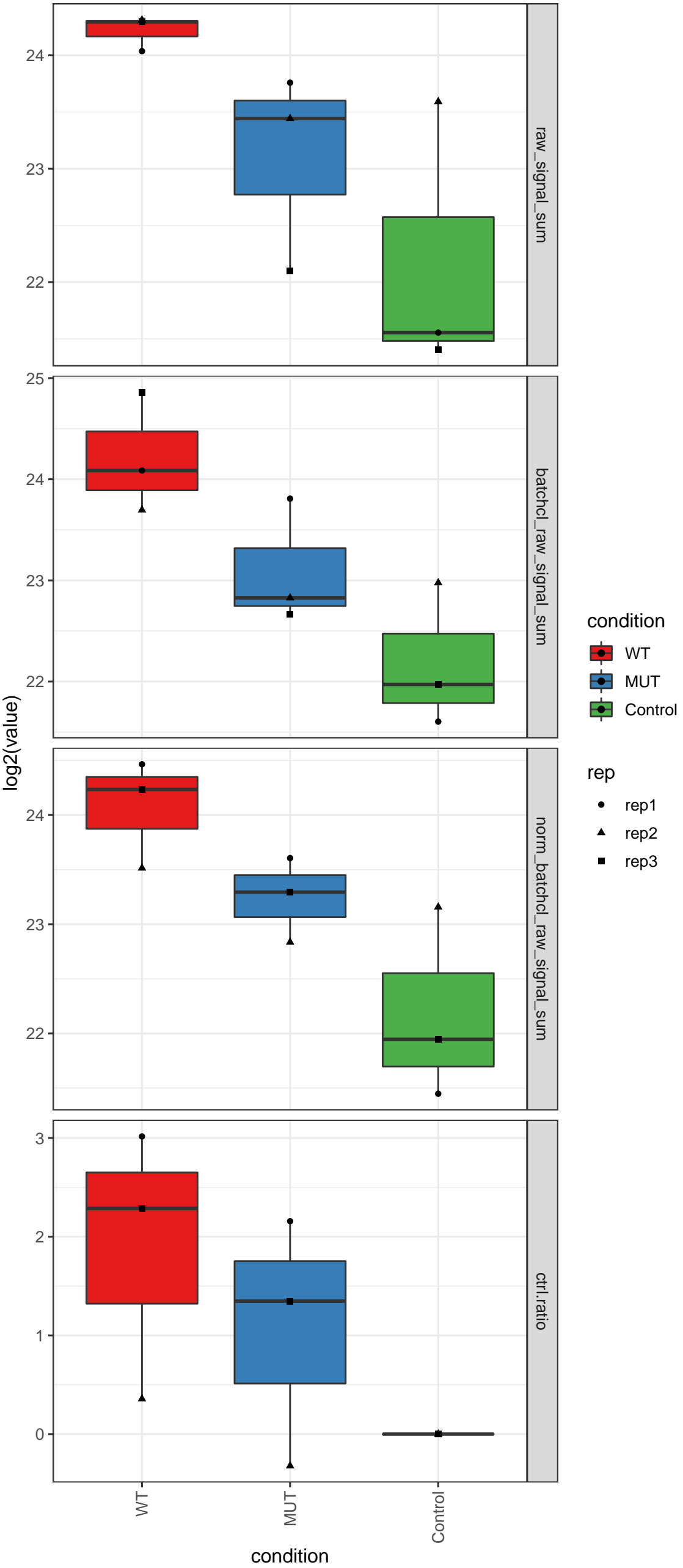
HHT1 – P61830

Histone H3 OS=*Saccharomyces cerevisiae* (strain ATCC 204508 / S288c)



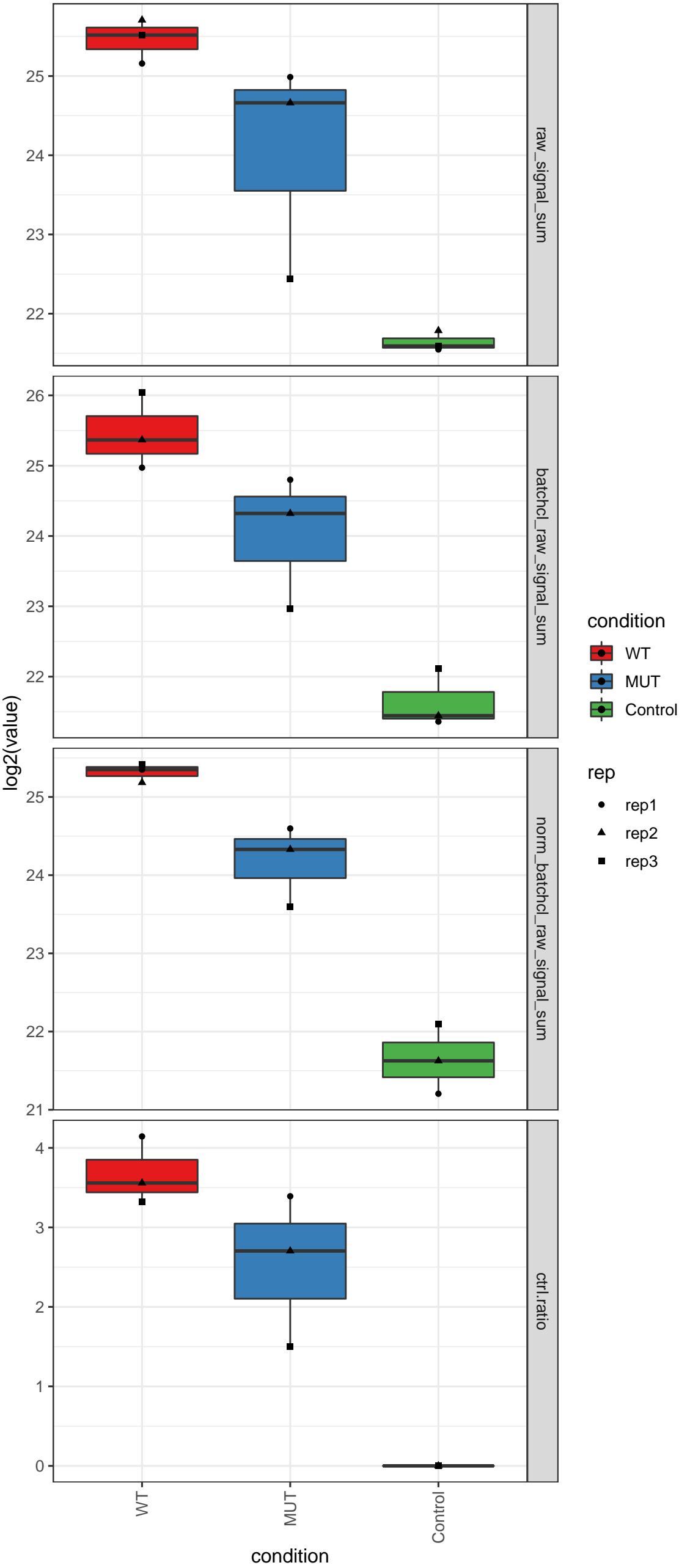
HIR1 – P32479

Protein HIR1 OS=*Saccharomyces cerevisiae* (strain ATCC 204508 / S288c)



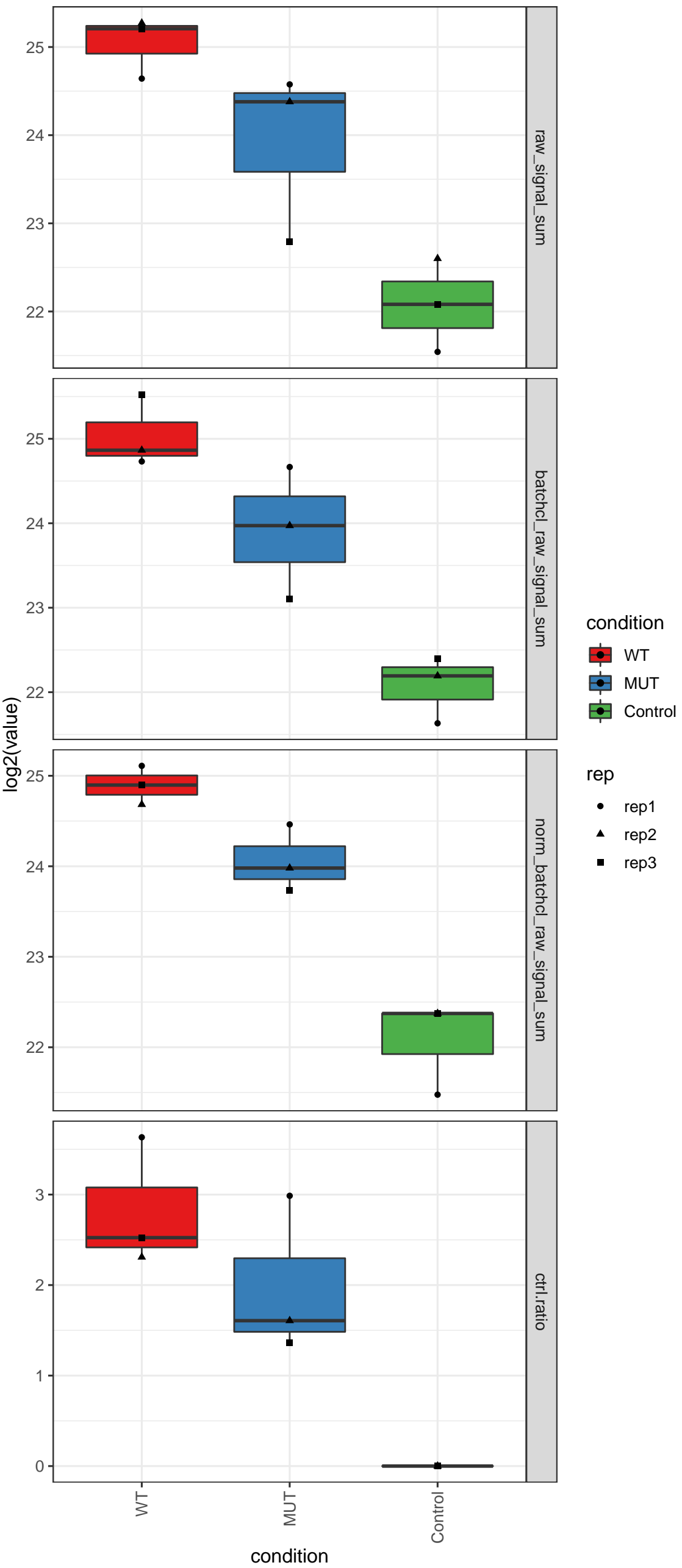
HIR2 – P32480

Protein HIR2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c)

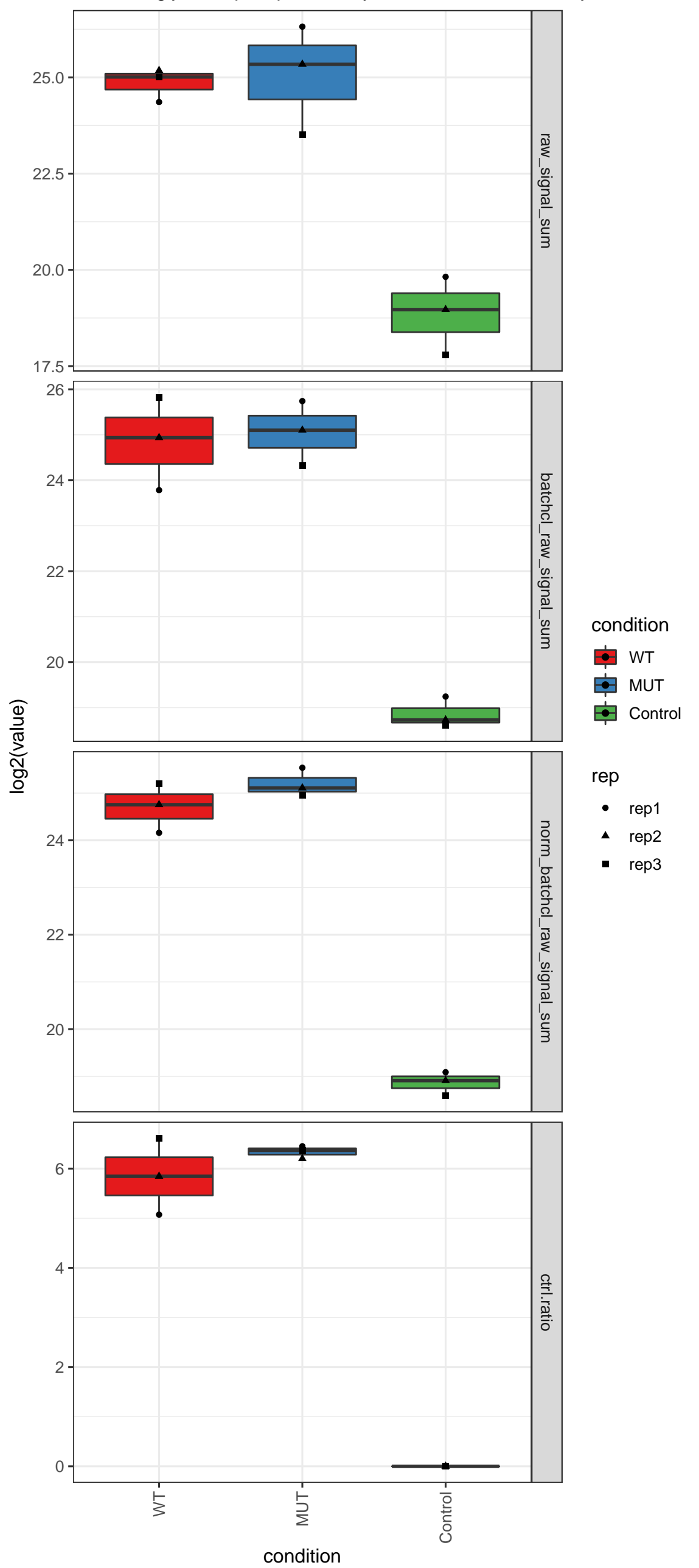


HIR3 – P47171

Histone transcription regulator 3 OS=*Saccharomyces cerevisiae* (strain ATCC 25716)

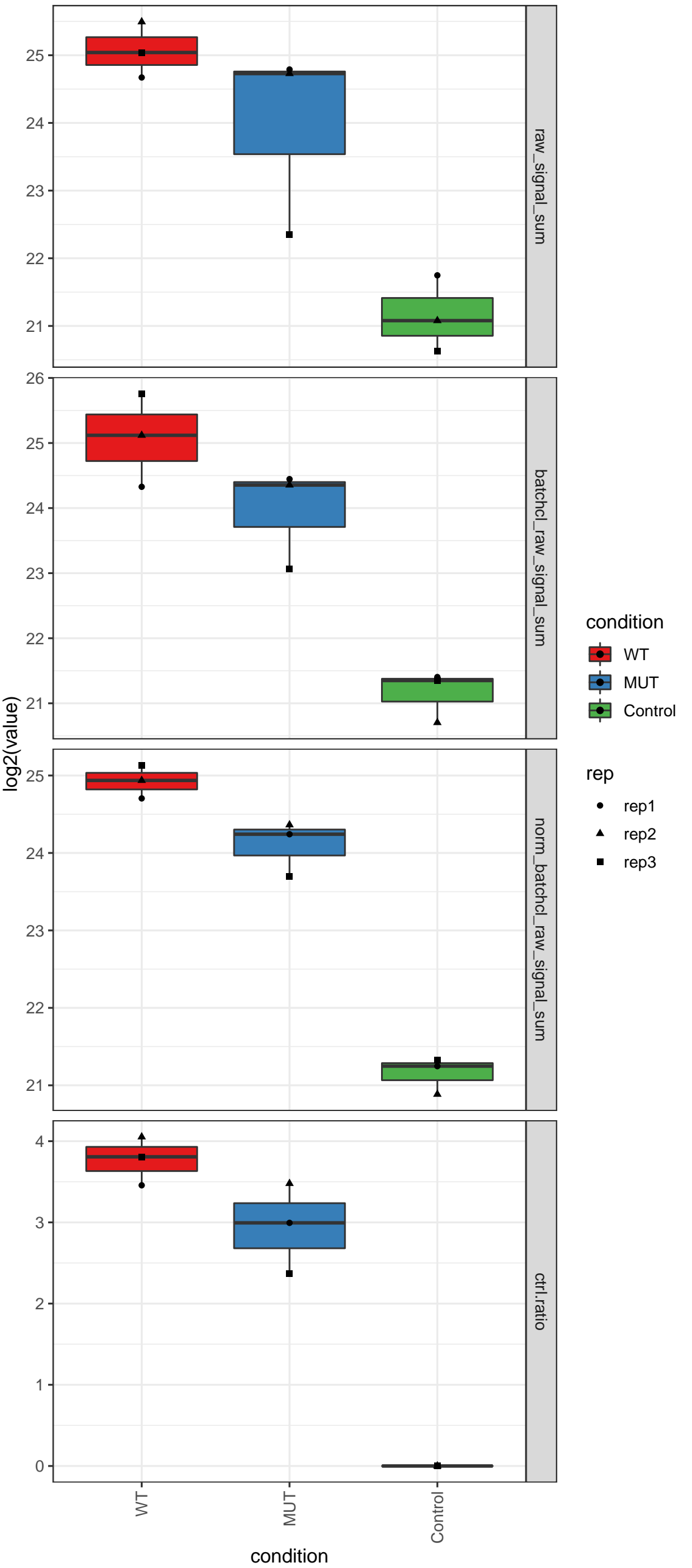


Imidazoleglycerol-phosphate dehydratase OS=Saccharomyces cerevisia



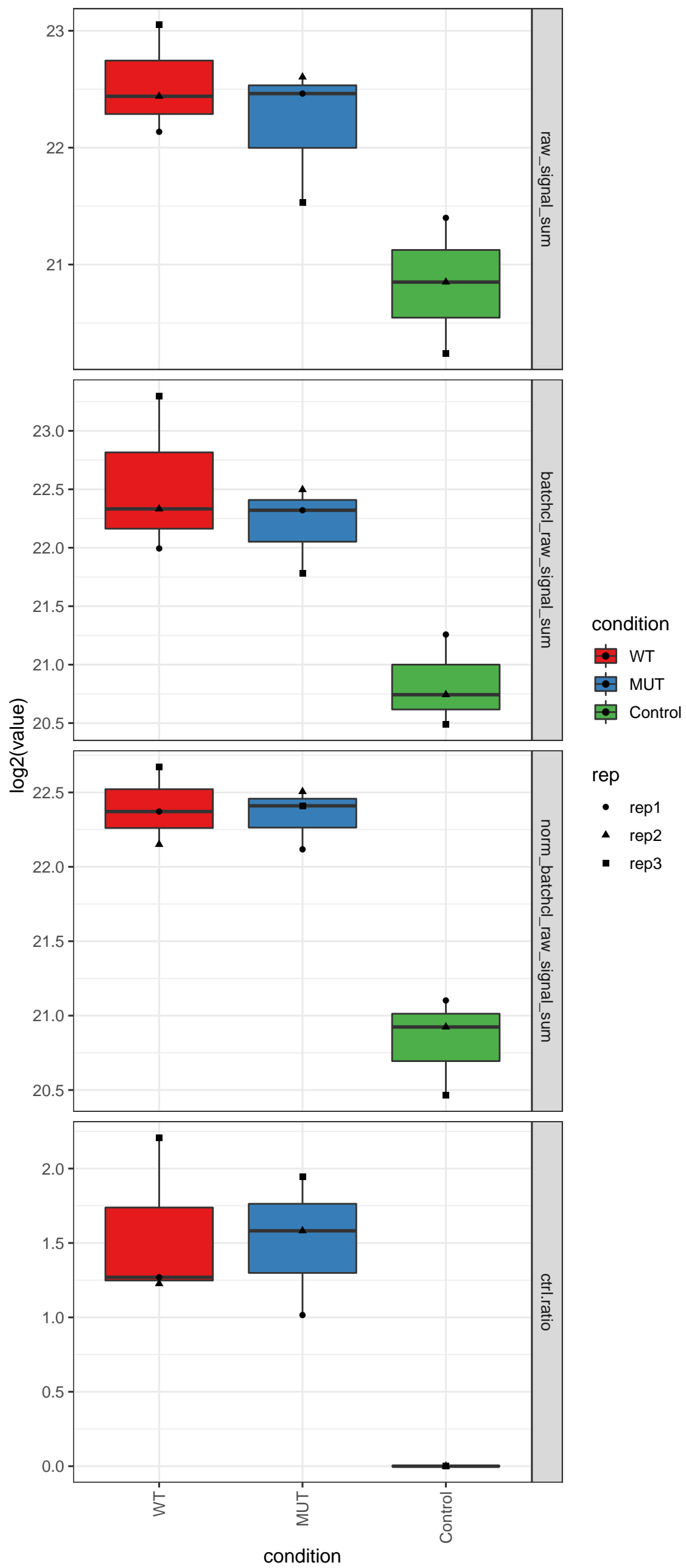
HMO1 – Q03973

High mobility group protein 1 OS=*Saccharomyces cerevisiae* (strain ATCC



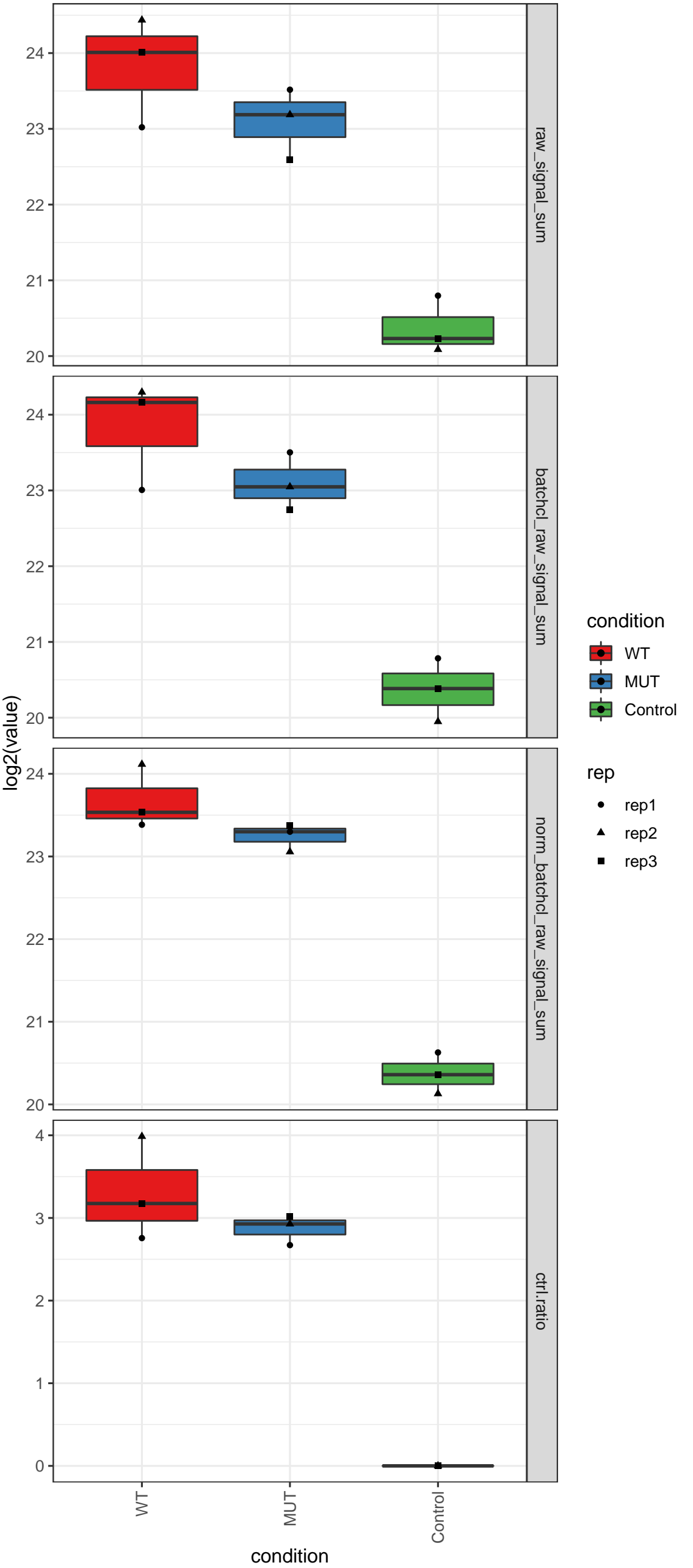
HOM2 – P13663

Aspartate-semialdehyde dehydrogenase OS=Saccharomyces cerevisiae



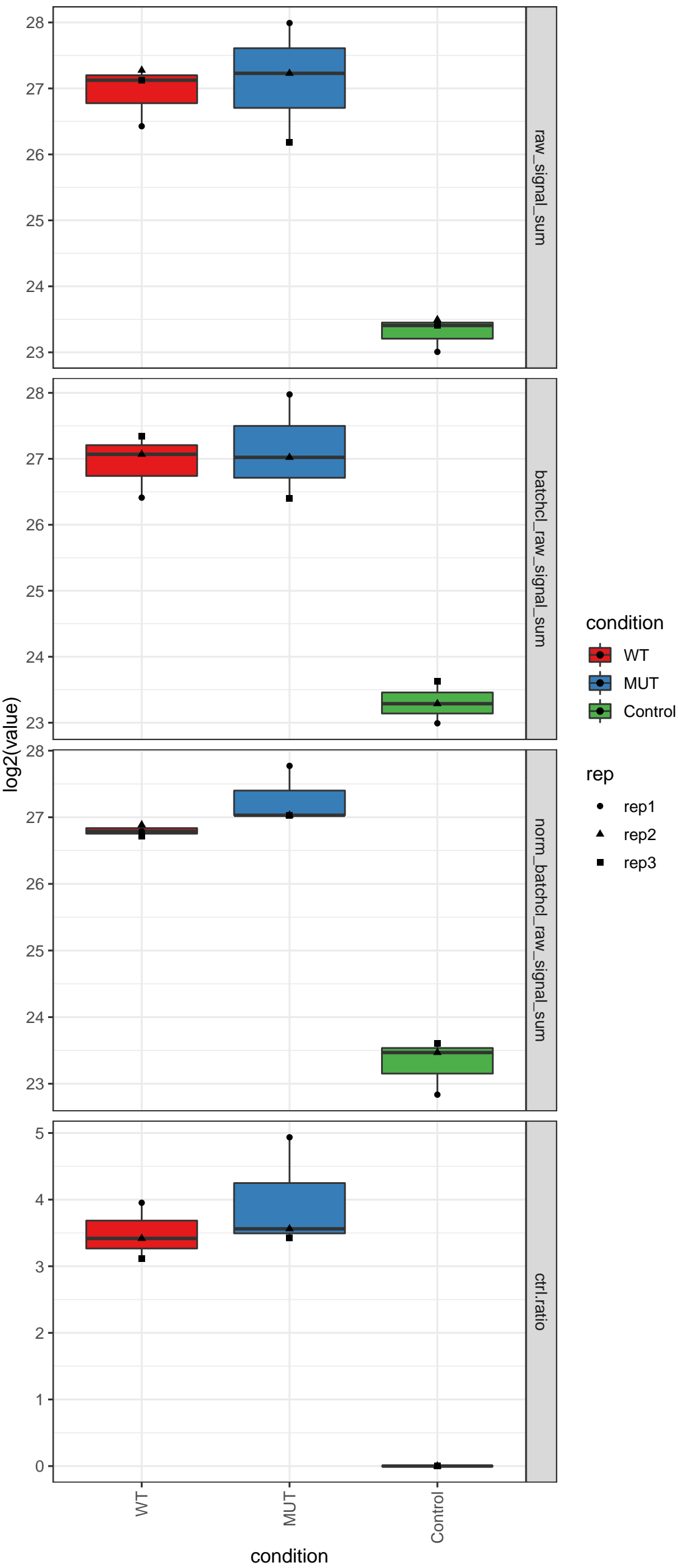
HOM6 – P31116

Homoserine dehydrogenase OS=*Saccharomyces cerevisiae* (strain ATCC



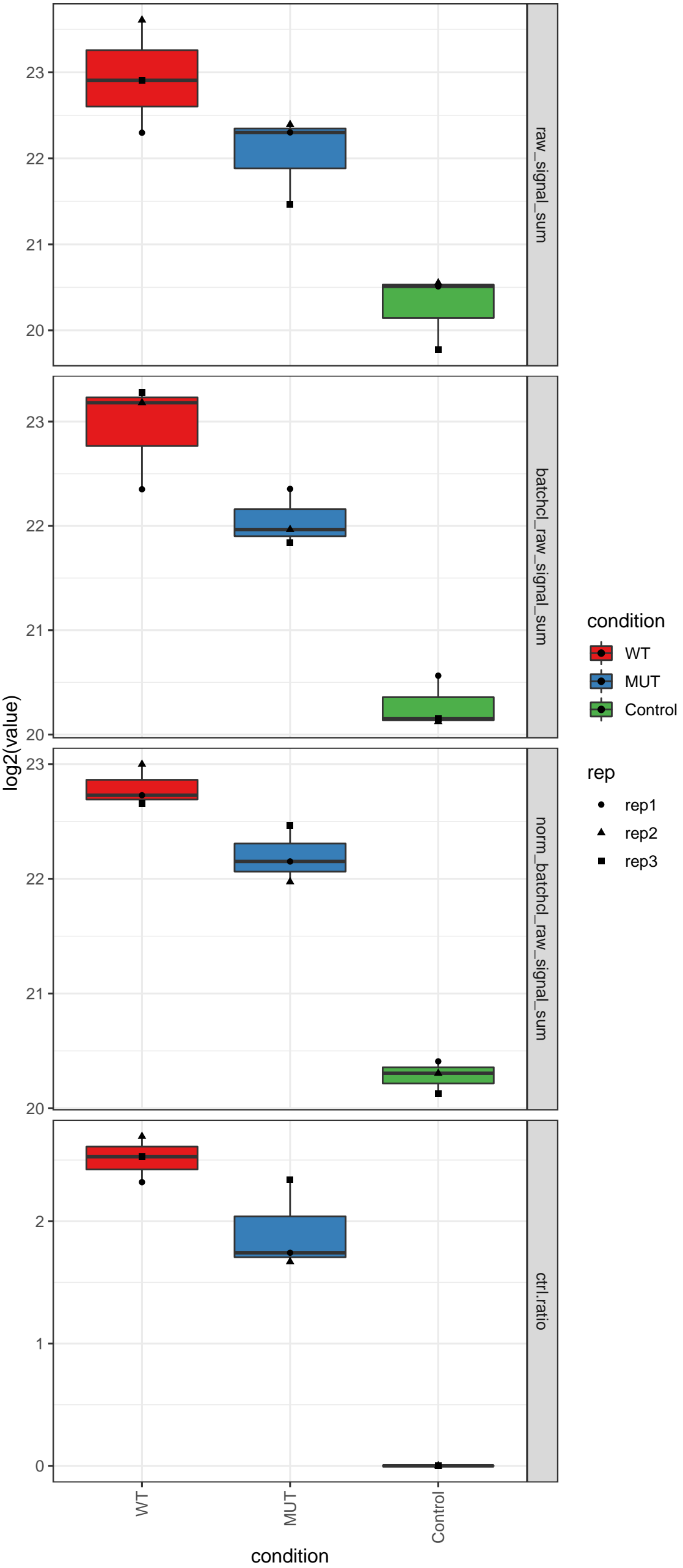
HOP1 – P20050

Meiosis-specific protein HOP1 OS=*Saccharomyces cerevisiae* (strain ATC



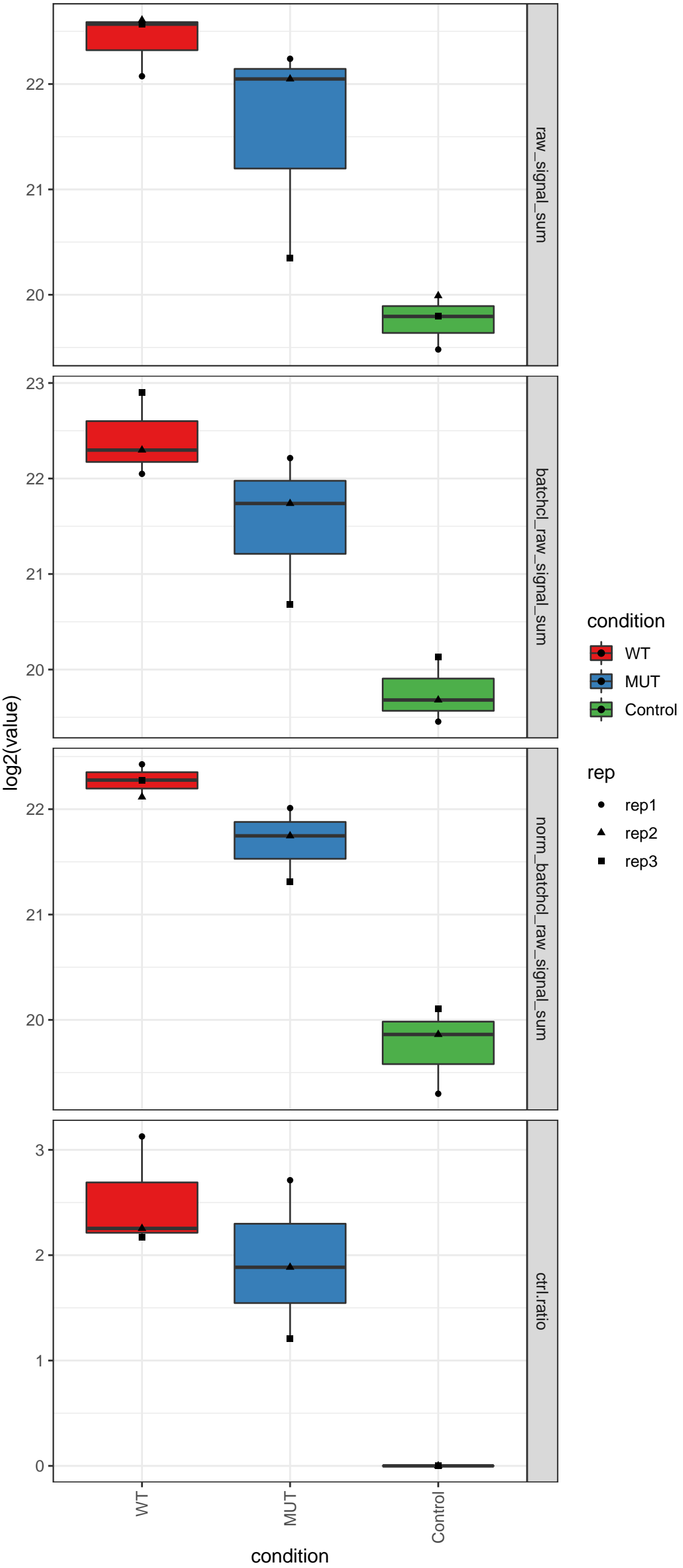
HOS3 – Q02959

Histone deacetylase HOS3 OS=*Saccharomyces cerevisiae* (strain ATCC 25791)



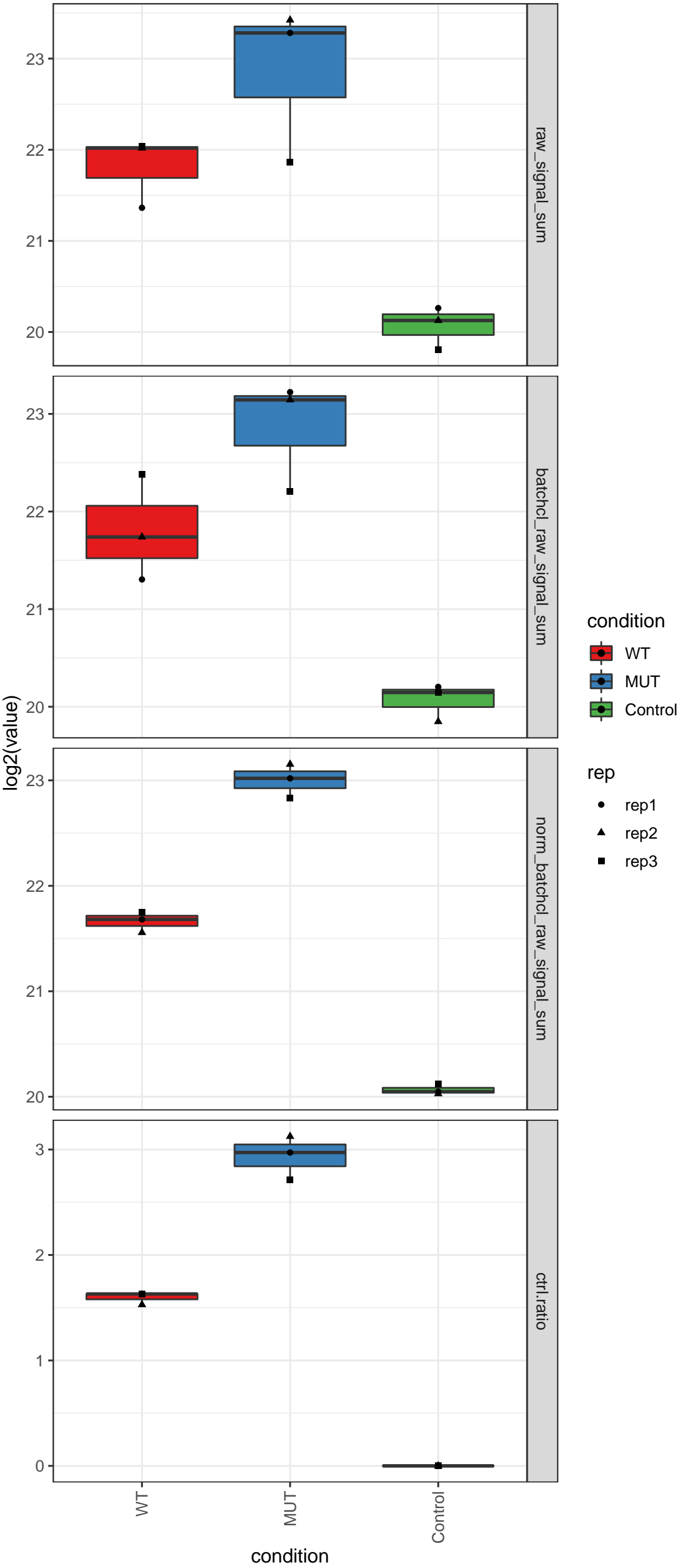
HPC2 – Q01448

Histone promoter control protein 2 OS=*Saccharomyces cerevisiae* (strain A



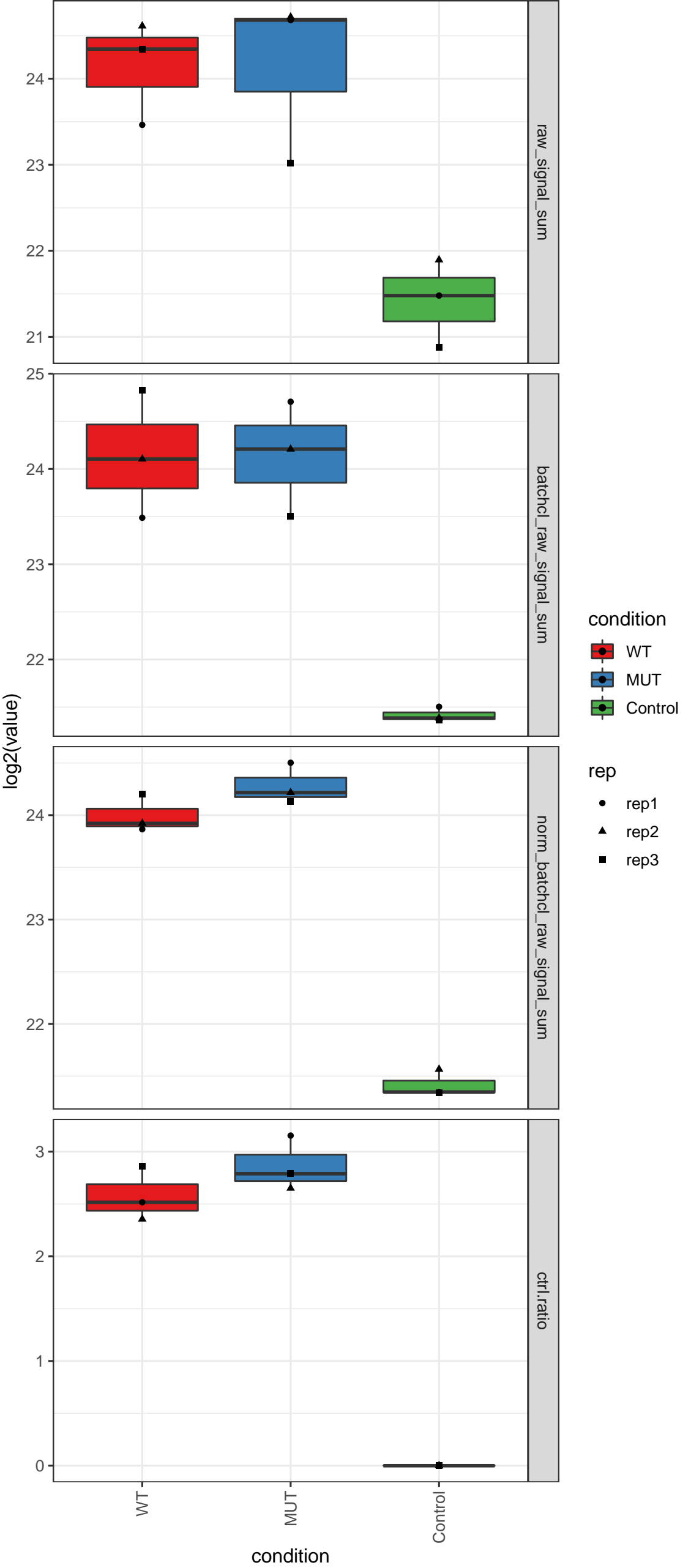
HRK1 – Q08732

Serine/threonine–protein kinase HRK1 OS=*Saccharomyces cerevisiae* (str



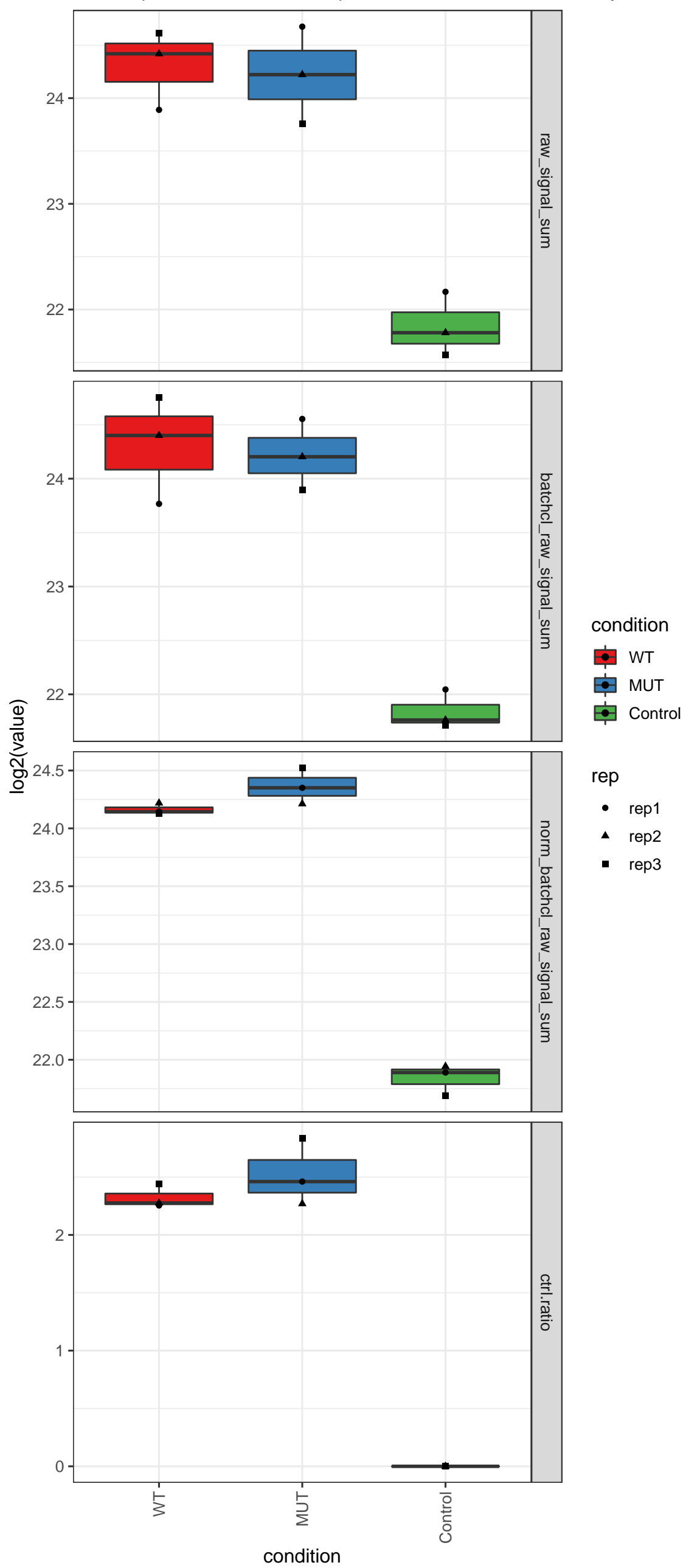
HRR25 – P29295

Casein kinase I homolog HRR25 OS=*Saccharomyces cerevisiae* (strain ATCC 22016 / *D6158*)



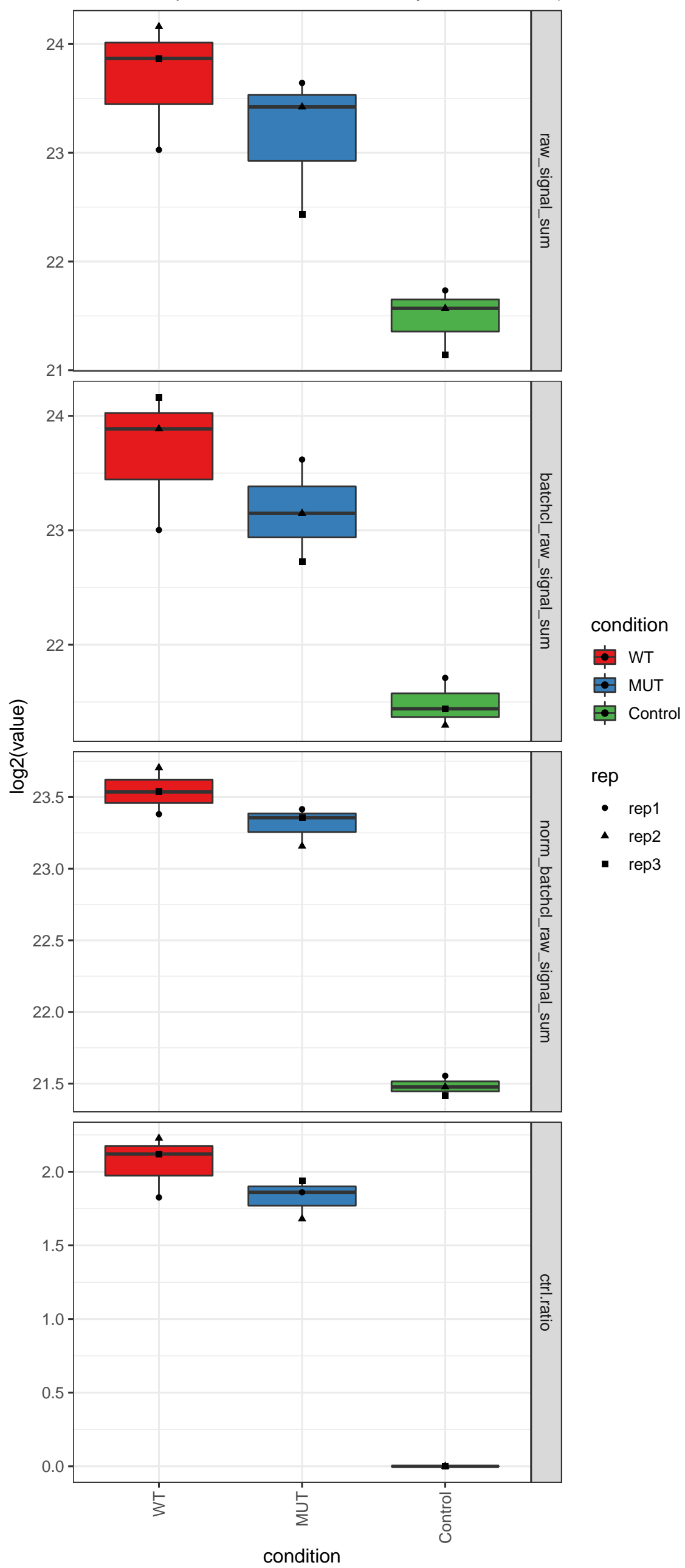
HSC82 – P15108

ATP-dependent molecular chaperone HSC82 OS=*Saccharomyces cerevisiae*



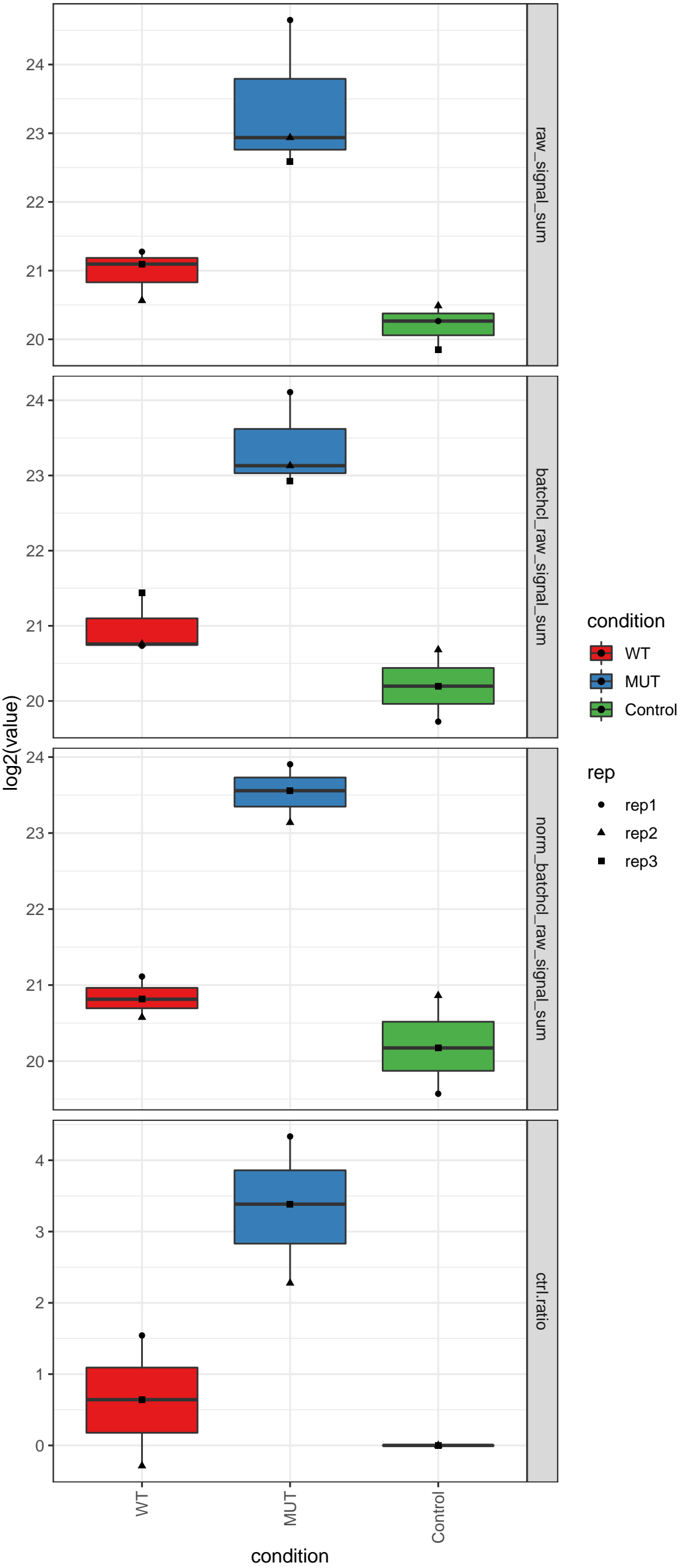
HSP104 – P31539

Heat shock protein 104 OS=*Saccharomyces cerevisiae* (strain ATCC 204



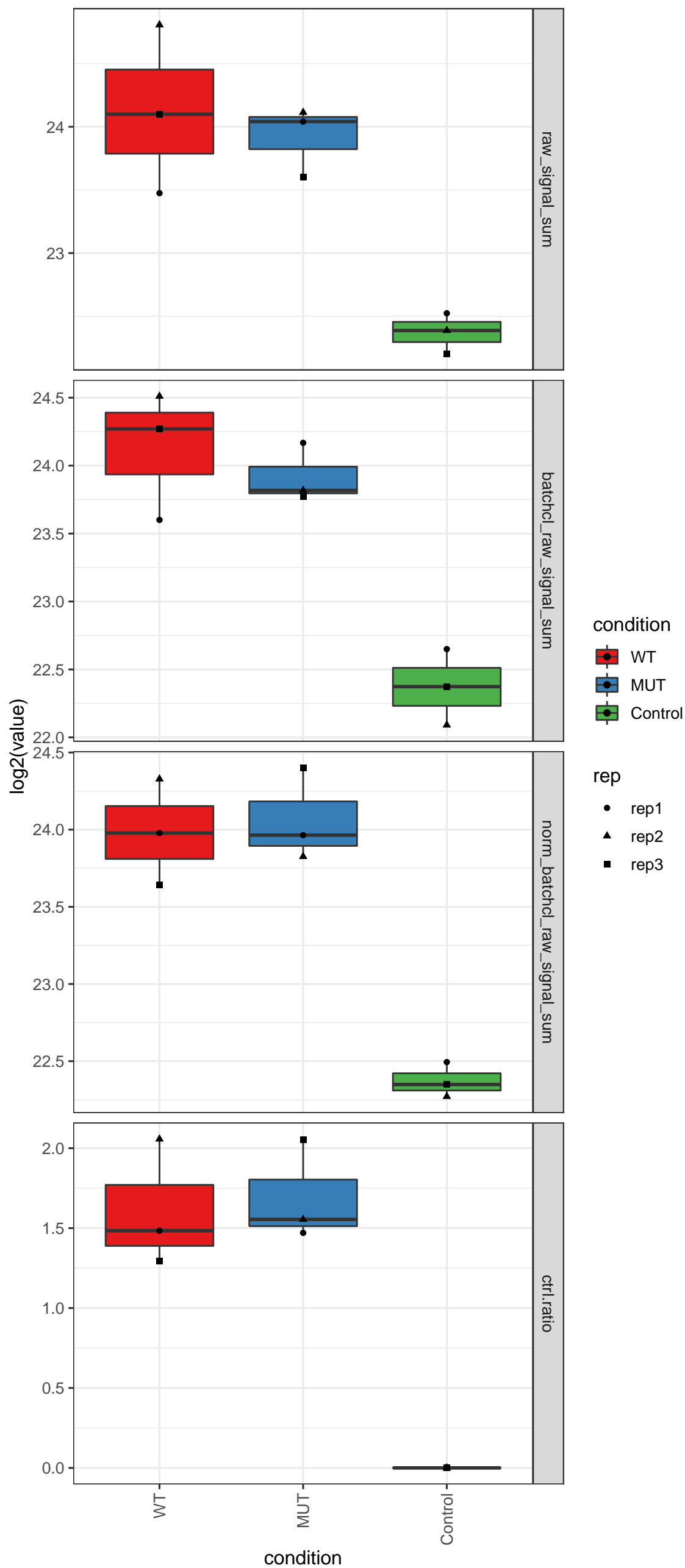
HSP150 – P32478

Cell wall mannoprotein HSP150 OS=*Saccharomyces cerevisiae* (strain ATC



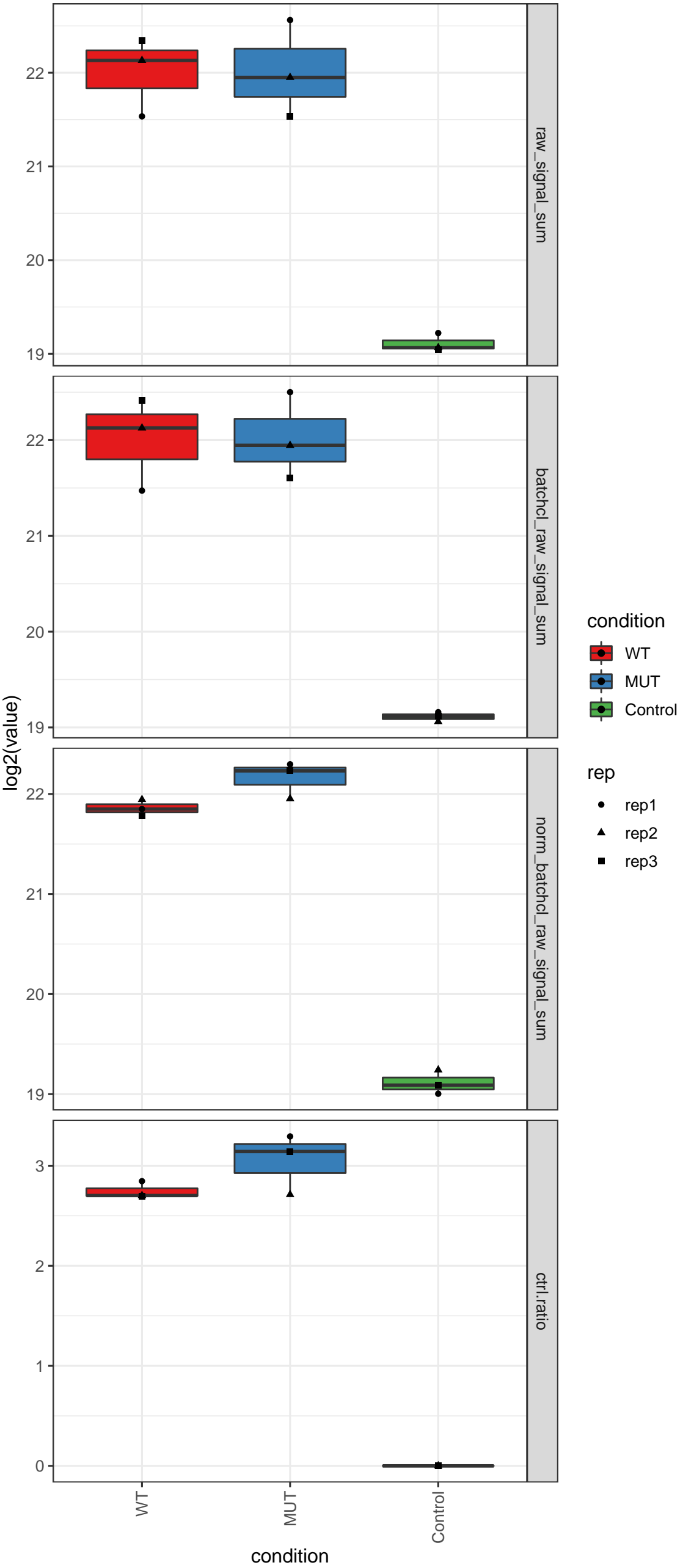
HSP60 – P19882

Heat shock protein 60, mitochondrial OS=Saccharomyces cerevisiae (str



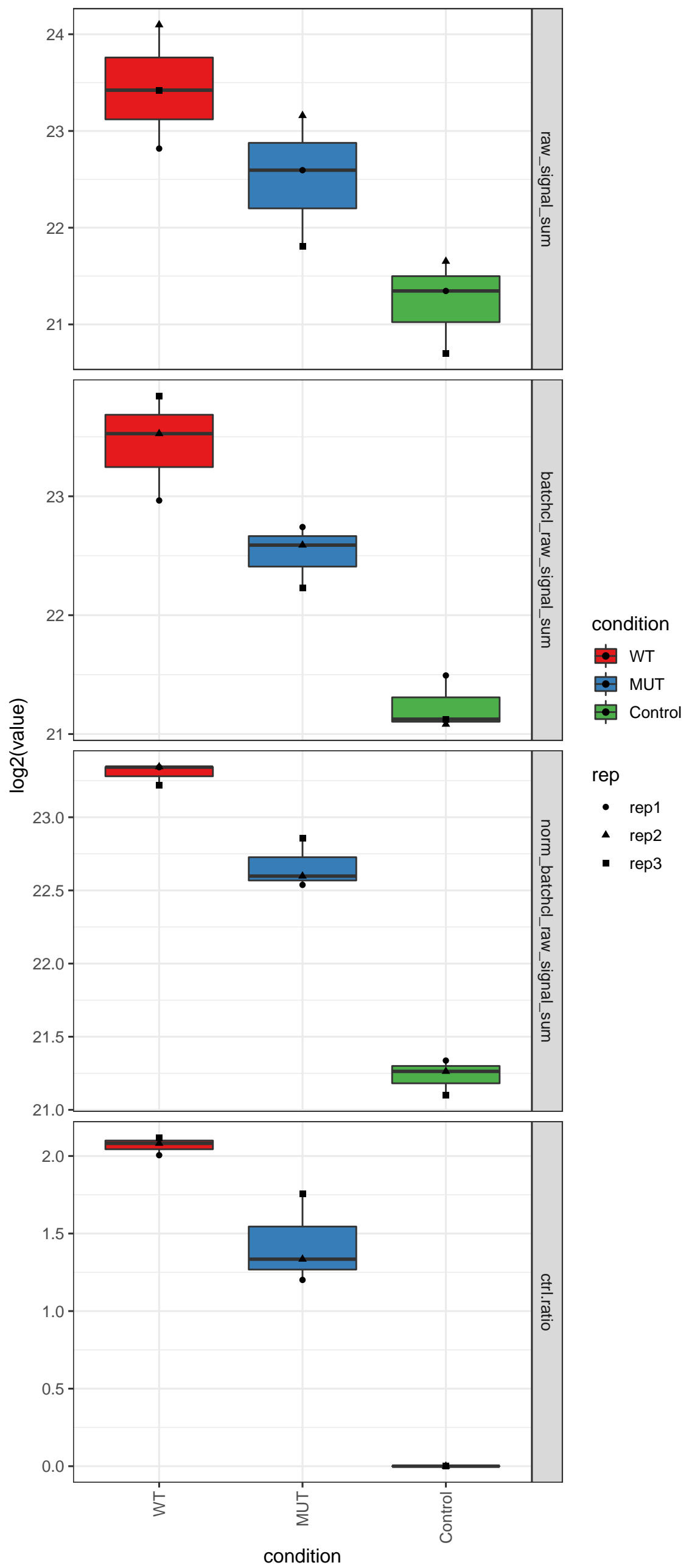
HSP82 – P02829

ATP-dependent molecular chaperone HSP82 OS=*Saccharomyces cerevisiae*



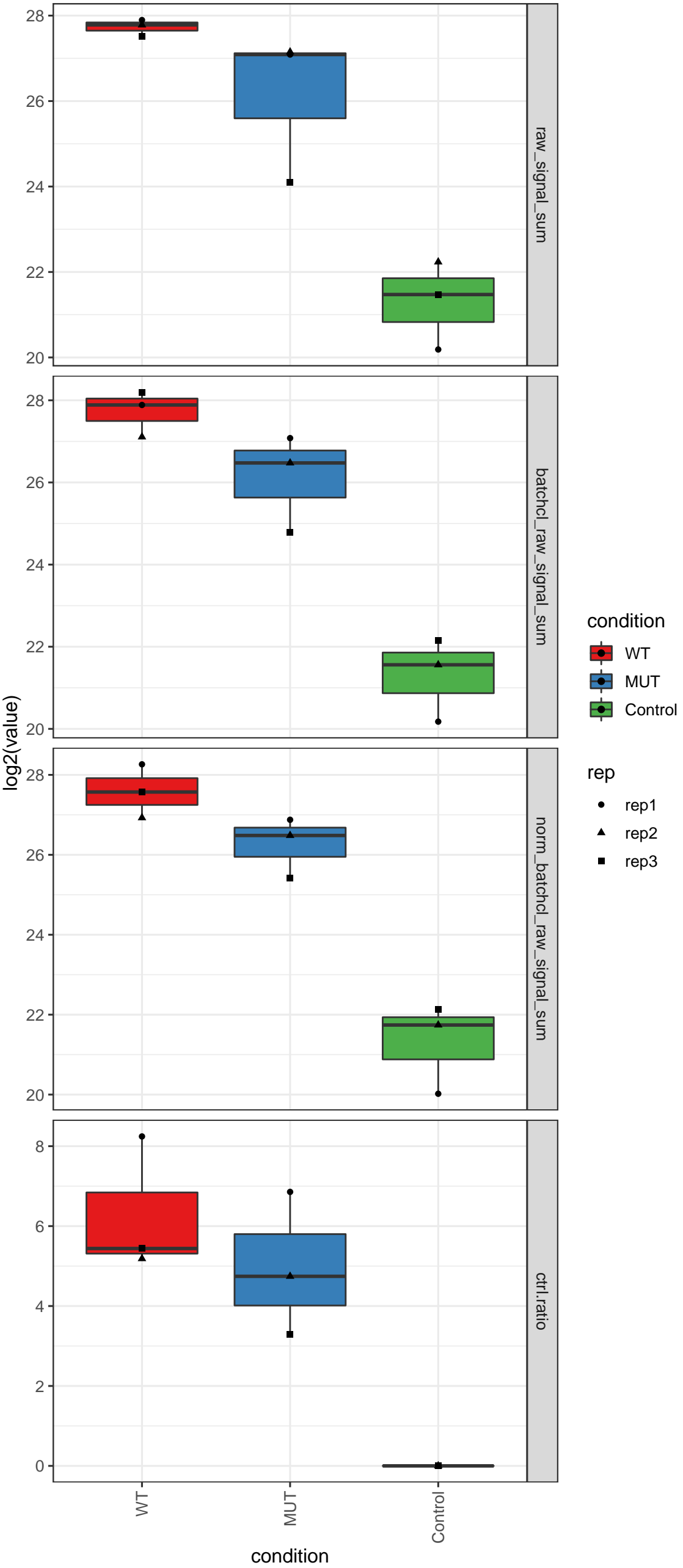
HSV2 – P50079

SVP1-like protein 2 OS=*Saccharomyces cerevisiae* (strain ATCC 204508)



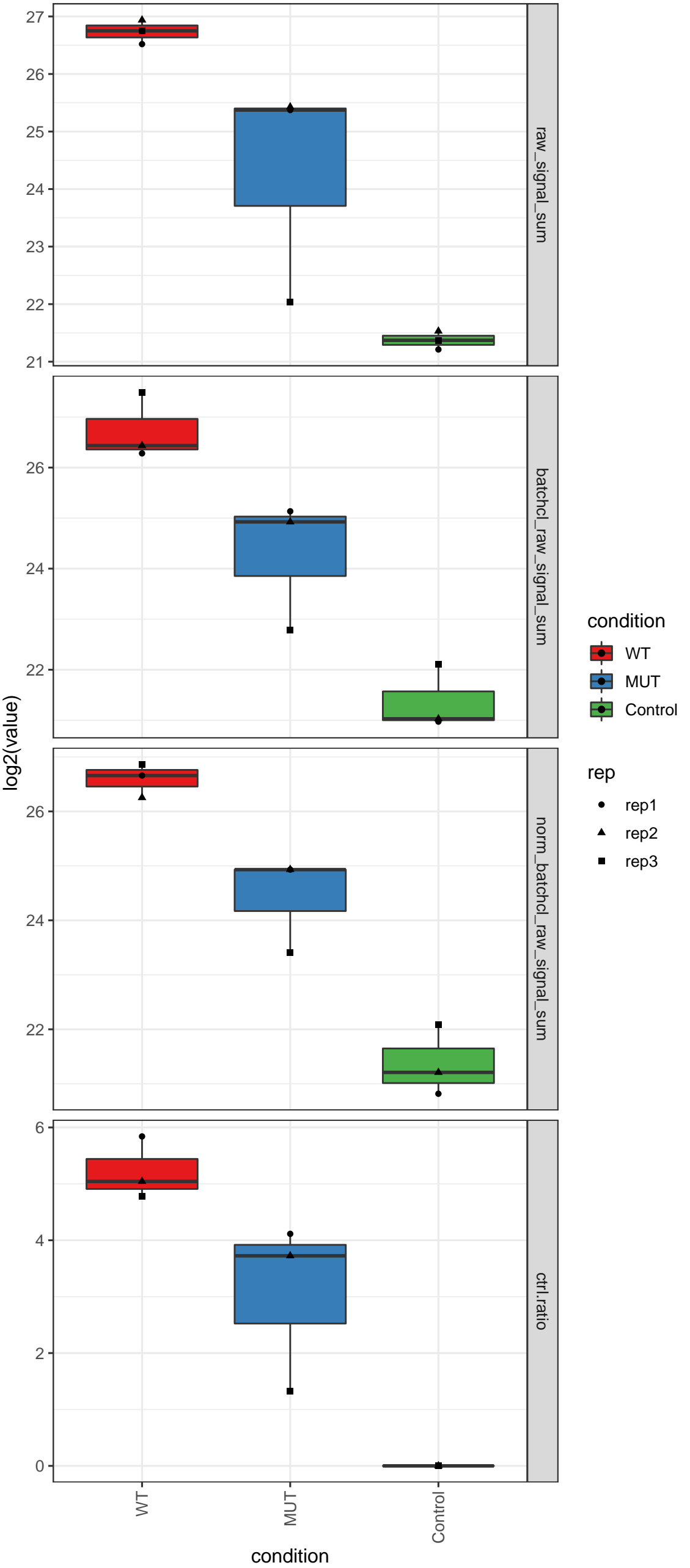
HTA1|HTA2 – P04911|P04912

Histone H2A.1 OS=*Saccharomyces cerevisiae* (strain ATCC 204508 / S288c)



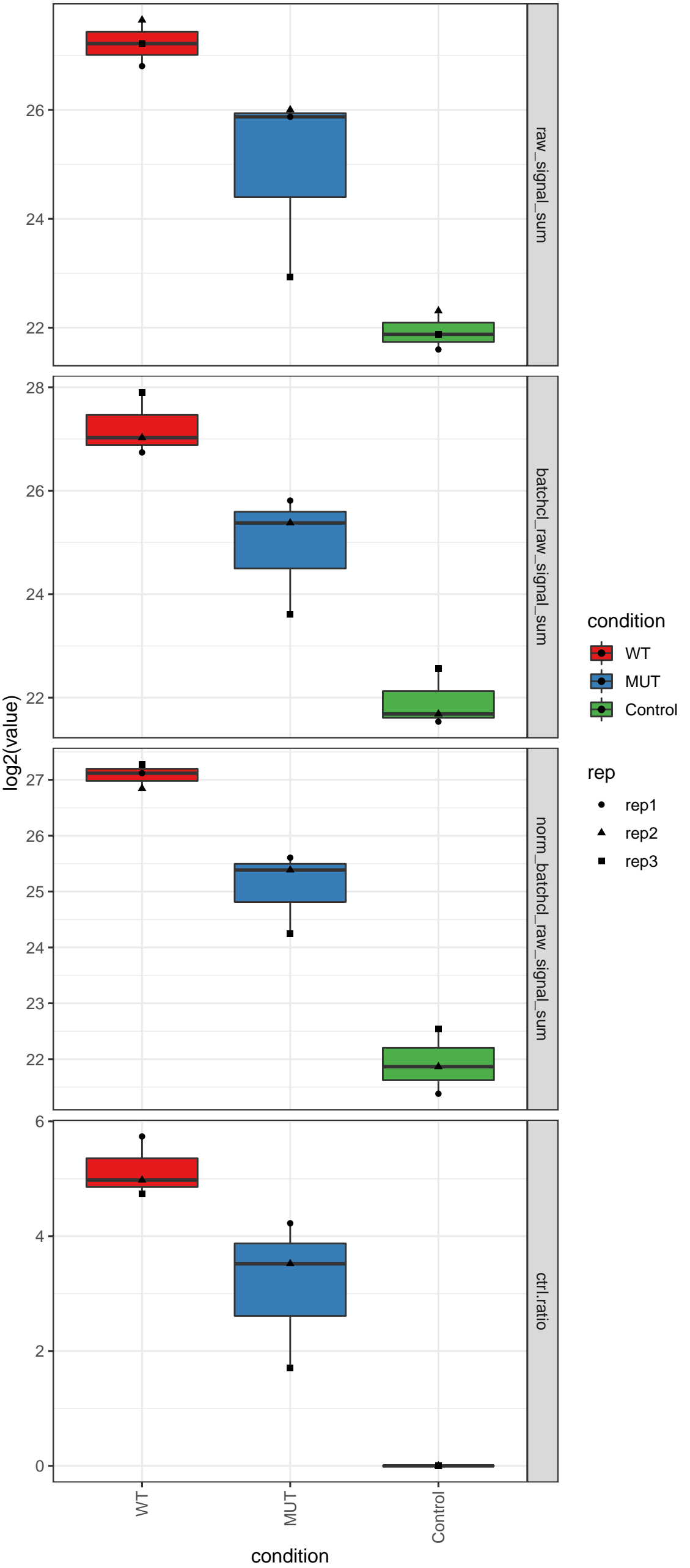
HTB1 – P02293

Histone H2B.1 OS=*Saccharomyces cerevisiae* (strain ATCC 204508 / S288c)



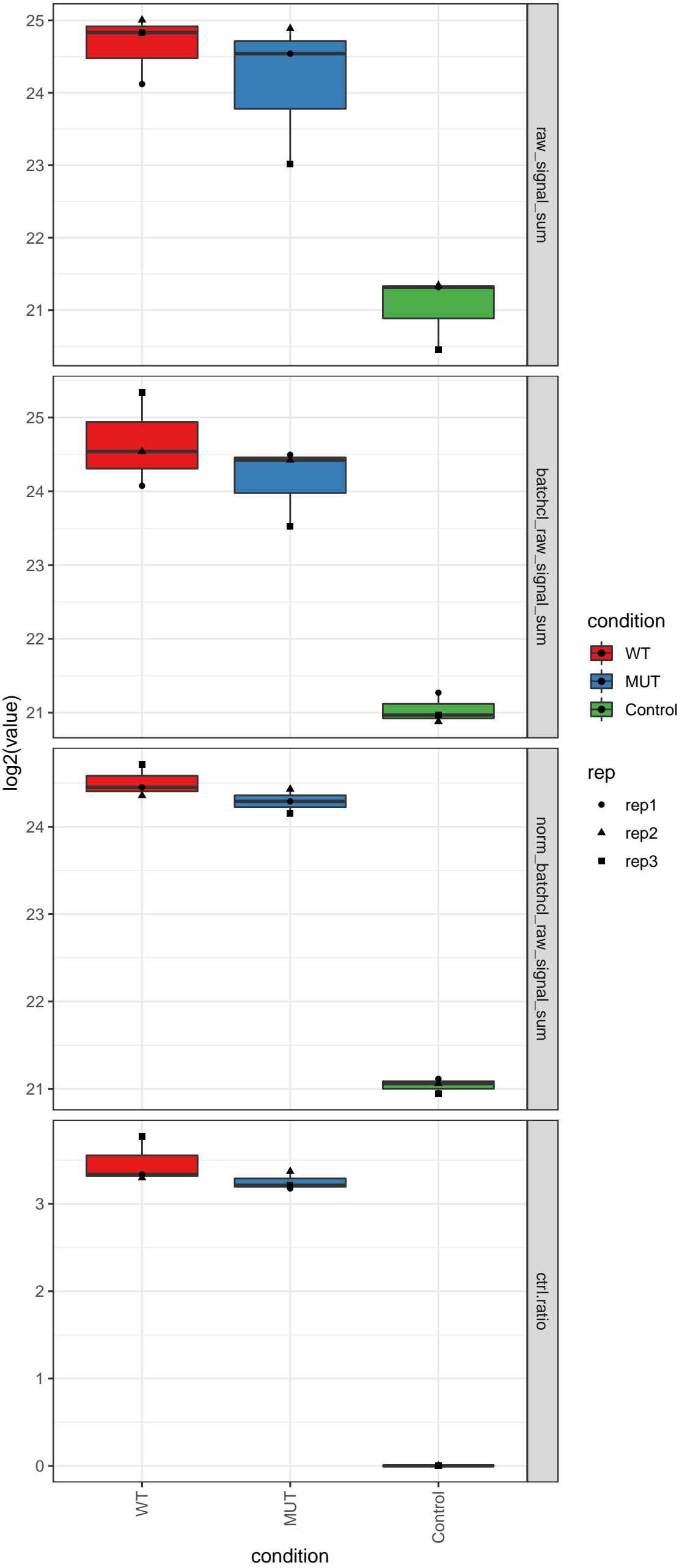
HTB2 – P02294

Histone H2B.2 OS=*Saccharomyces cerevisiae* (strain ATCC 204508 / S288c)



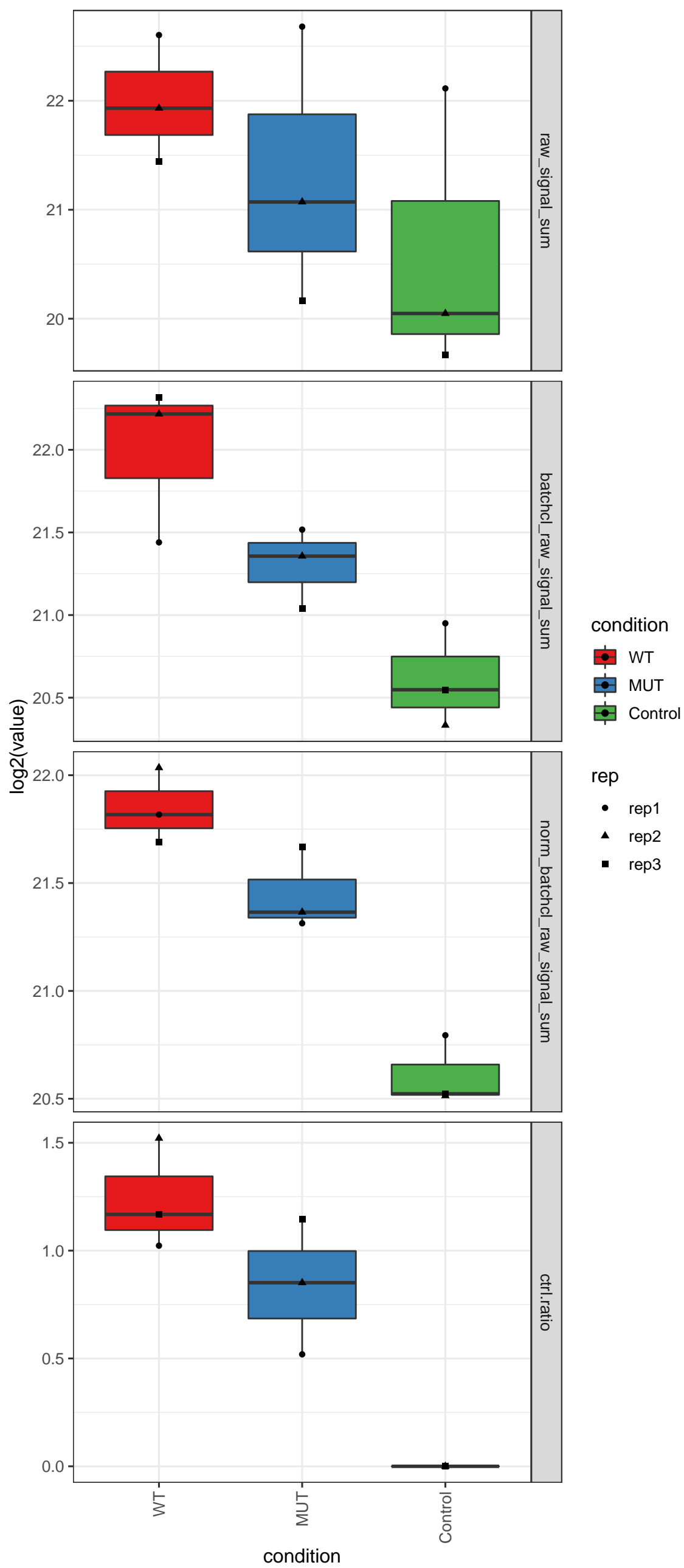
HTS1 – P07263|P07263–2

Histidine--tRNA ligase, mitochondrial OS=Saccharomyces cerevisiae (stra



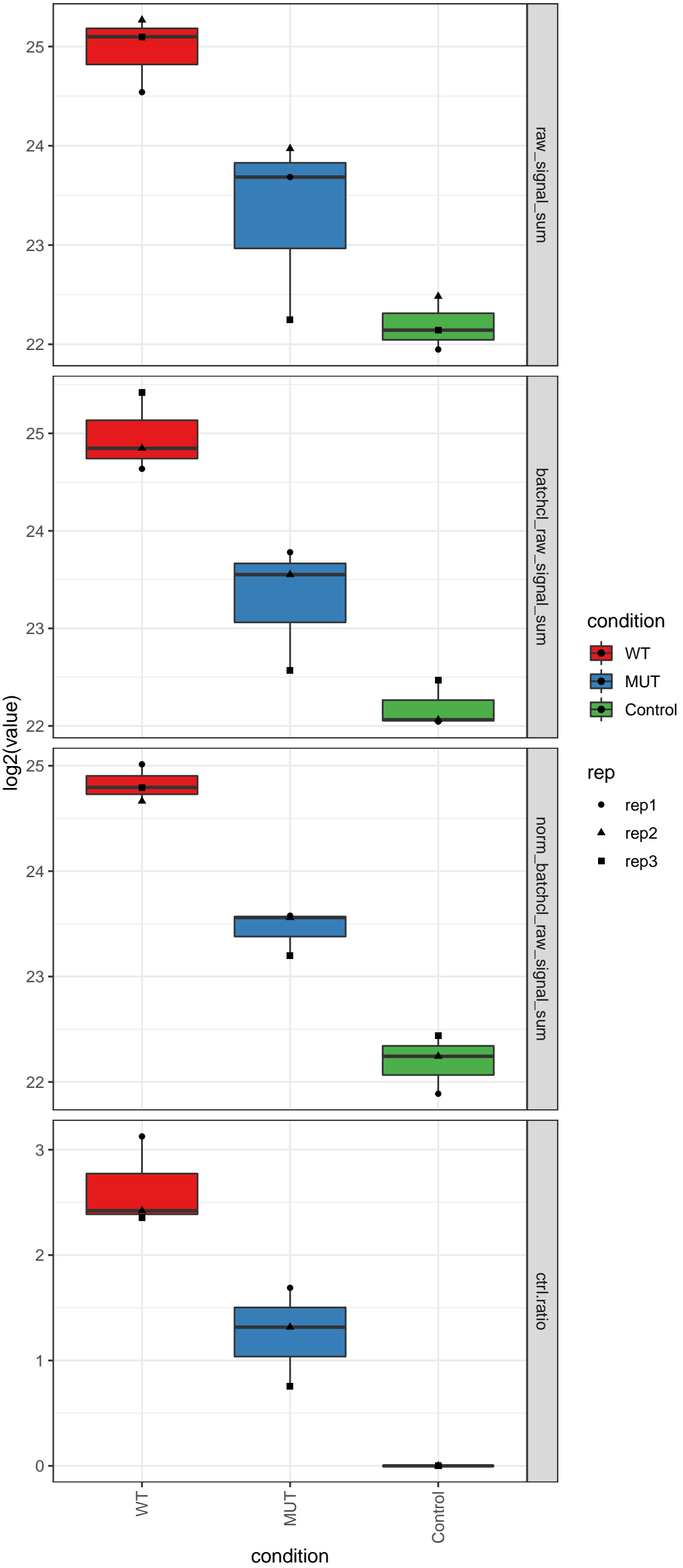
HttQx_EGFP – HttQx_EGFP

NA



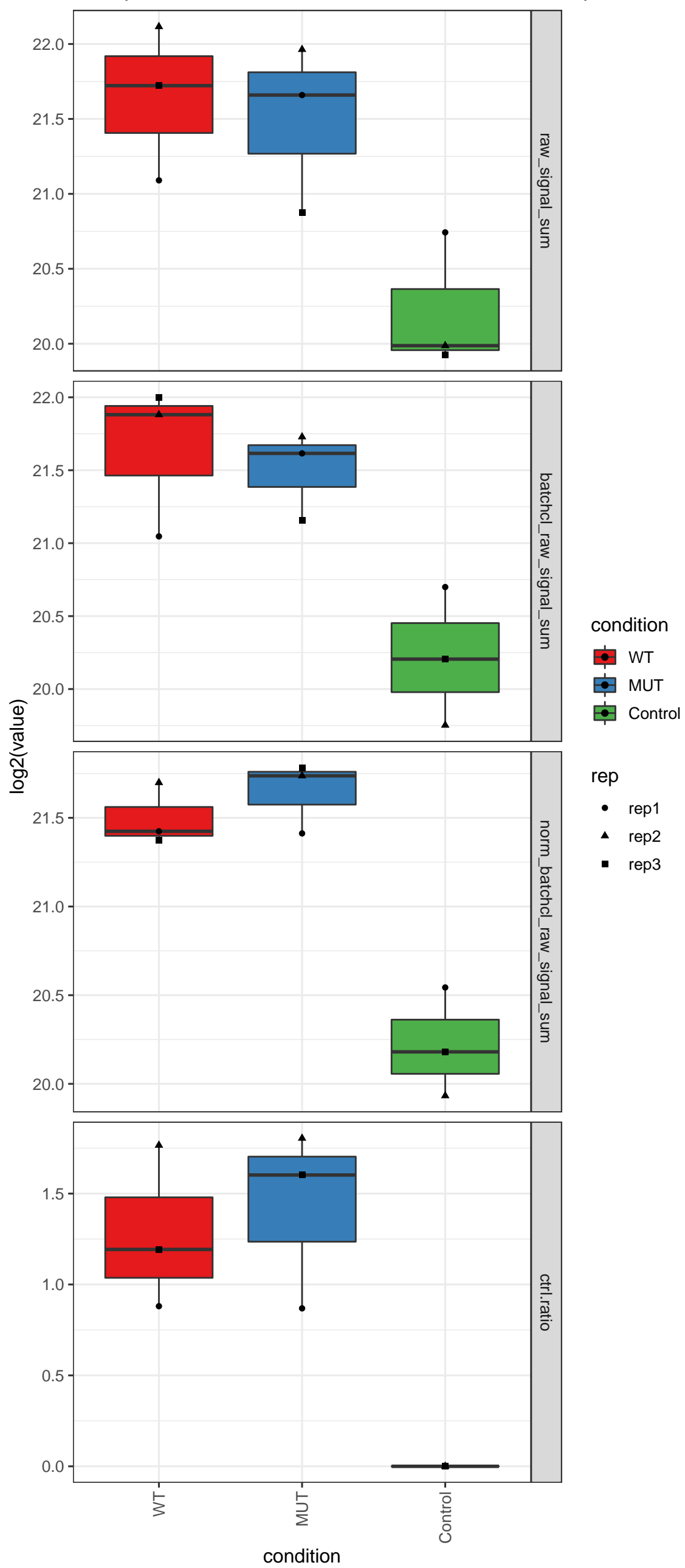
HTZ1 – Q12692

Histone H2A.Z OS=*Saccharomyces cerevisiae* (strain ATCC 204508 / S288c)



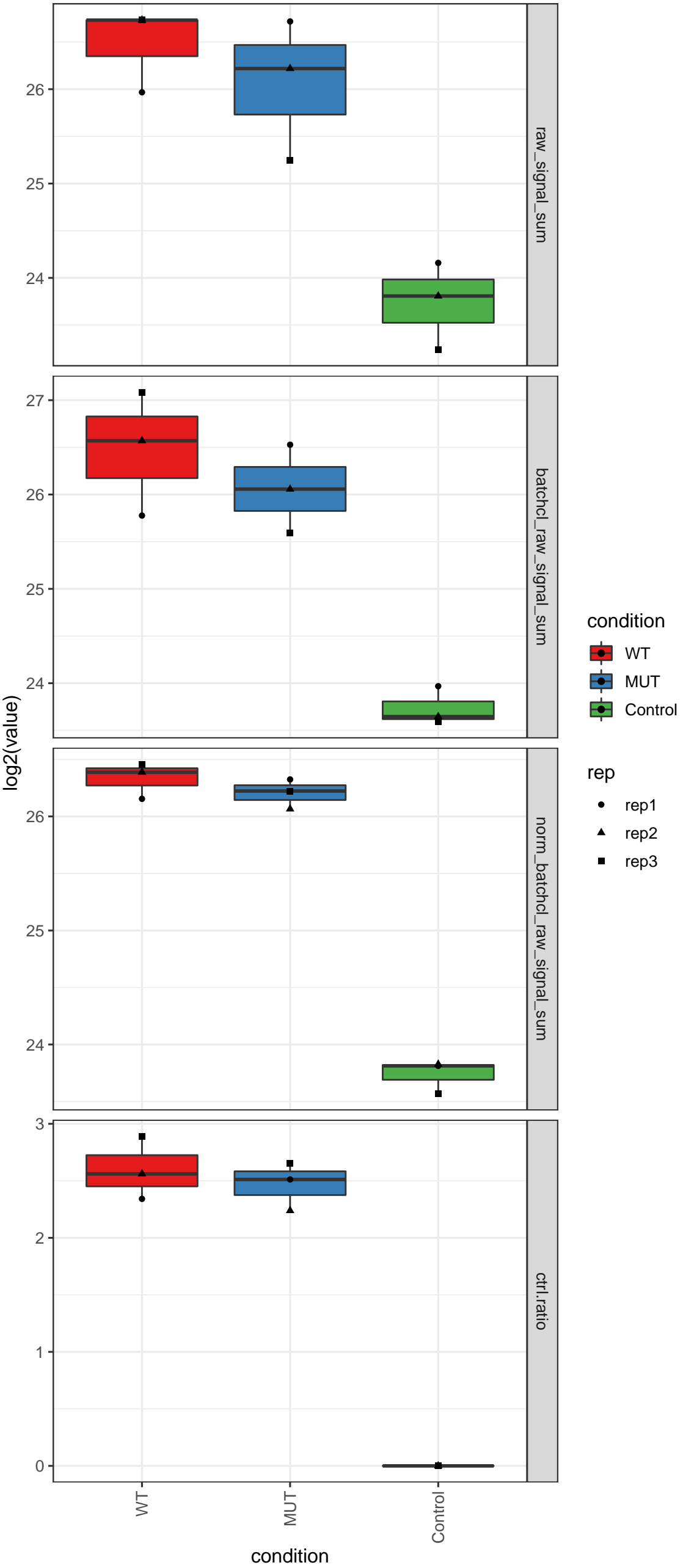
HYP2 – P23301

Eukaryotic translation initiation factor 5A-1 OS=*Saccharomyces cerevisiae*



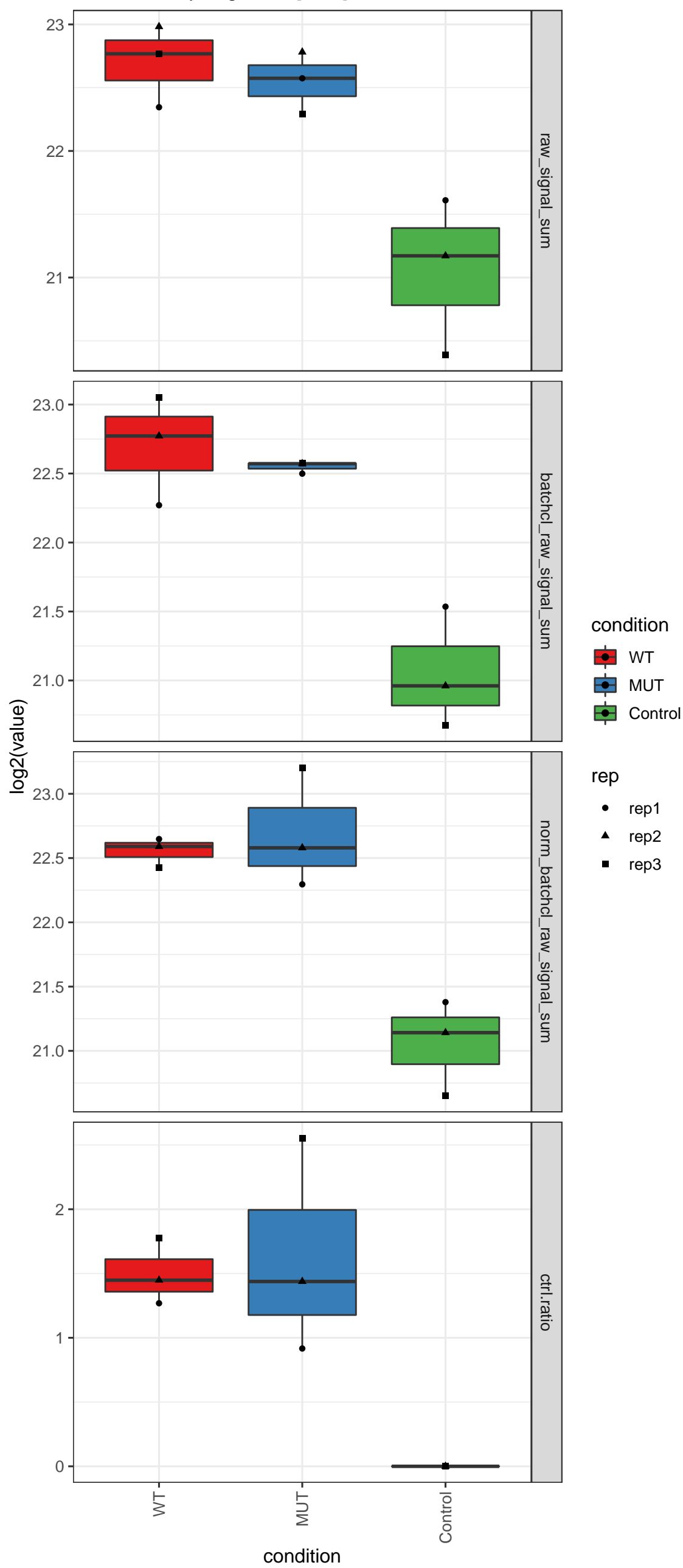
ICL1 – P28240

Isocitrate lyase OS=*Saccharomyces cerevisiae* (strain ATCC 204508 / S28



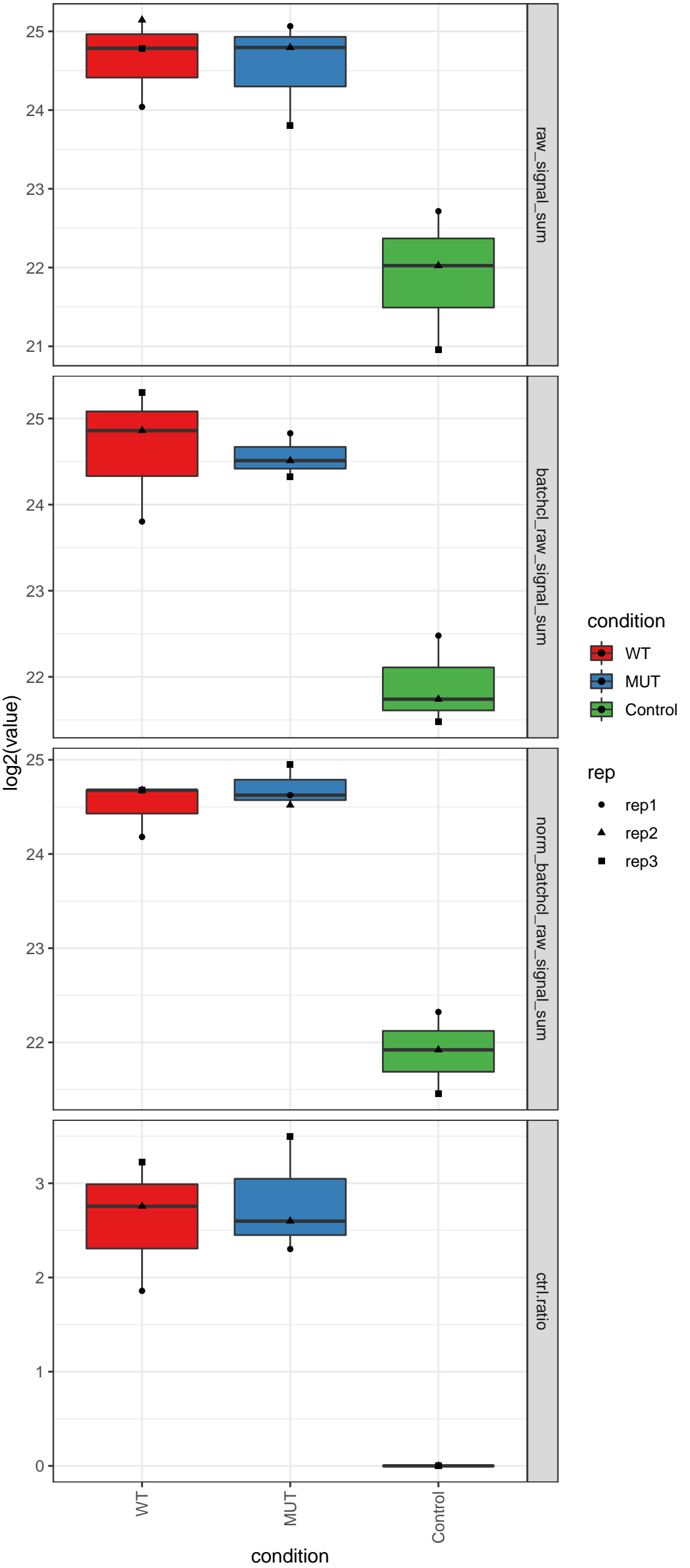
IDH1 – P28834

Isocitrate dehydrogenase [NAD] subunit 1, mitochondrial OS=Saccharom



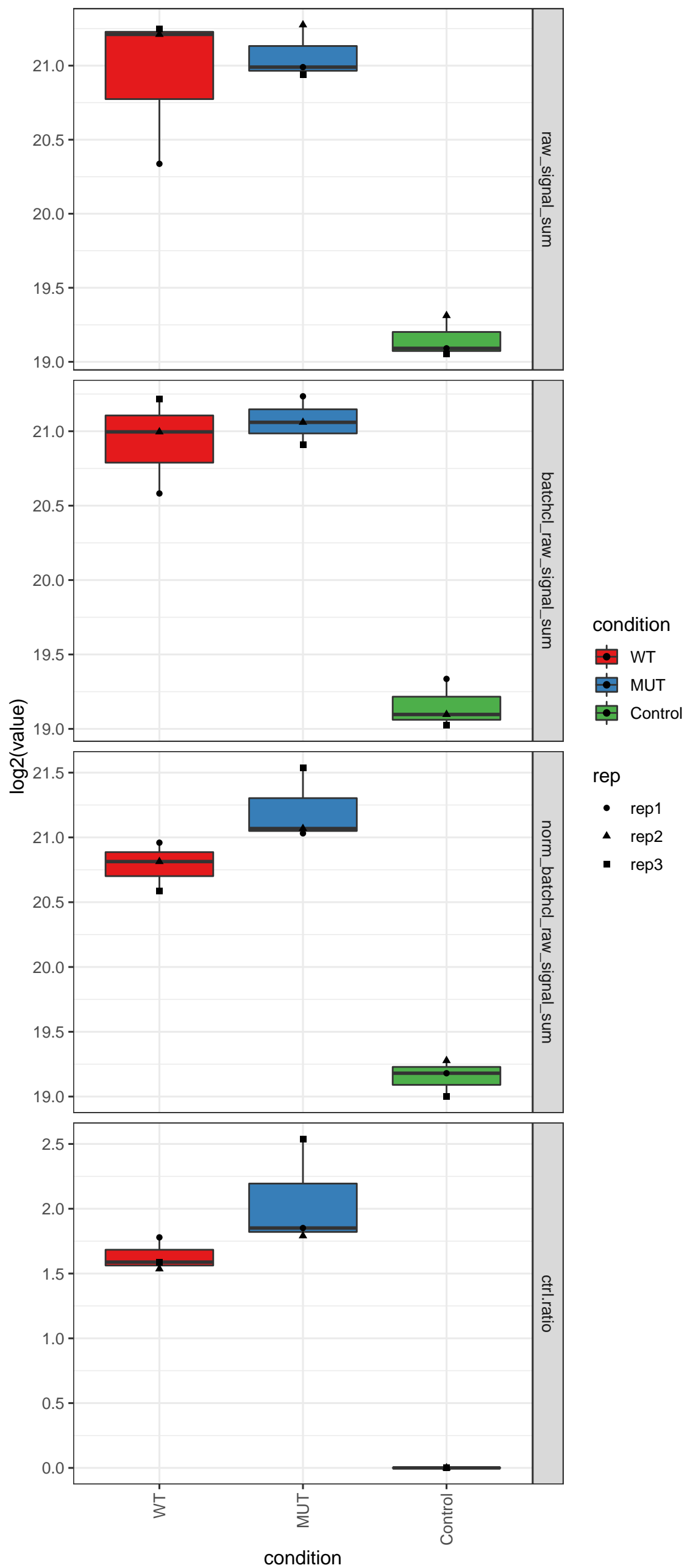
IDP2 – P41939

Isocitrate dehydrogenase [NADP] cytoplasmic OS=*Saccharomyces cerevisiae*



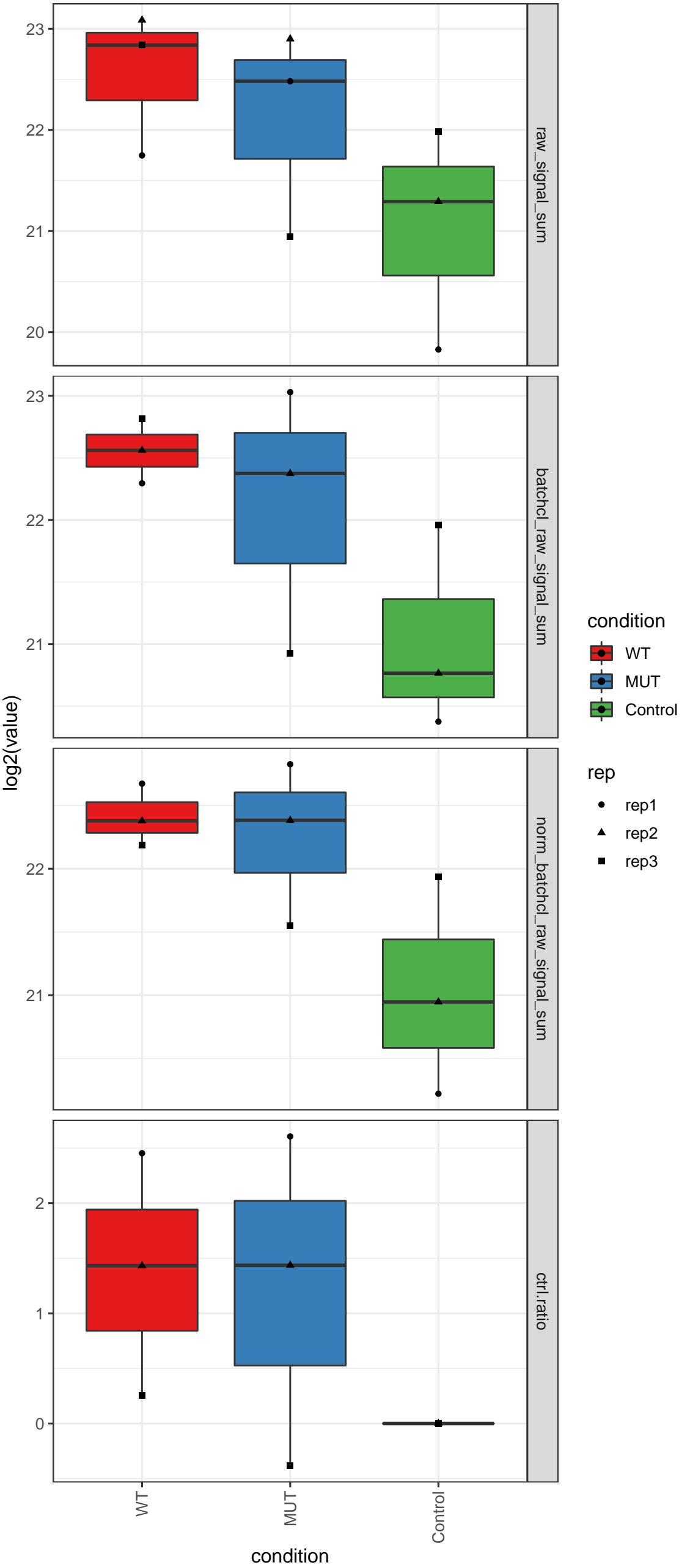
IDP3 – P53982

Isocitrate dehydrogenase [NADP] OS=*Saccharomyces cerevisiae* (strain



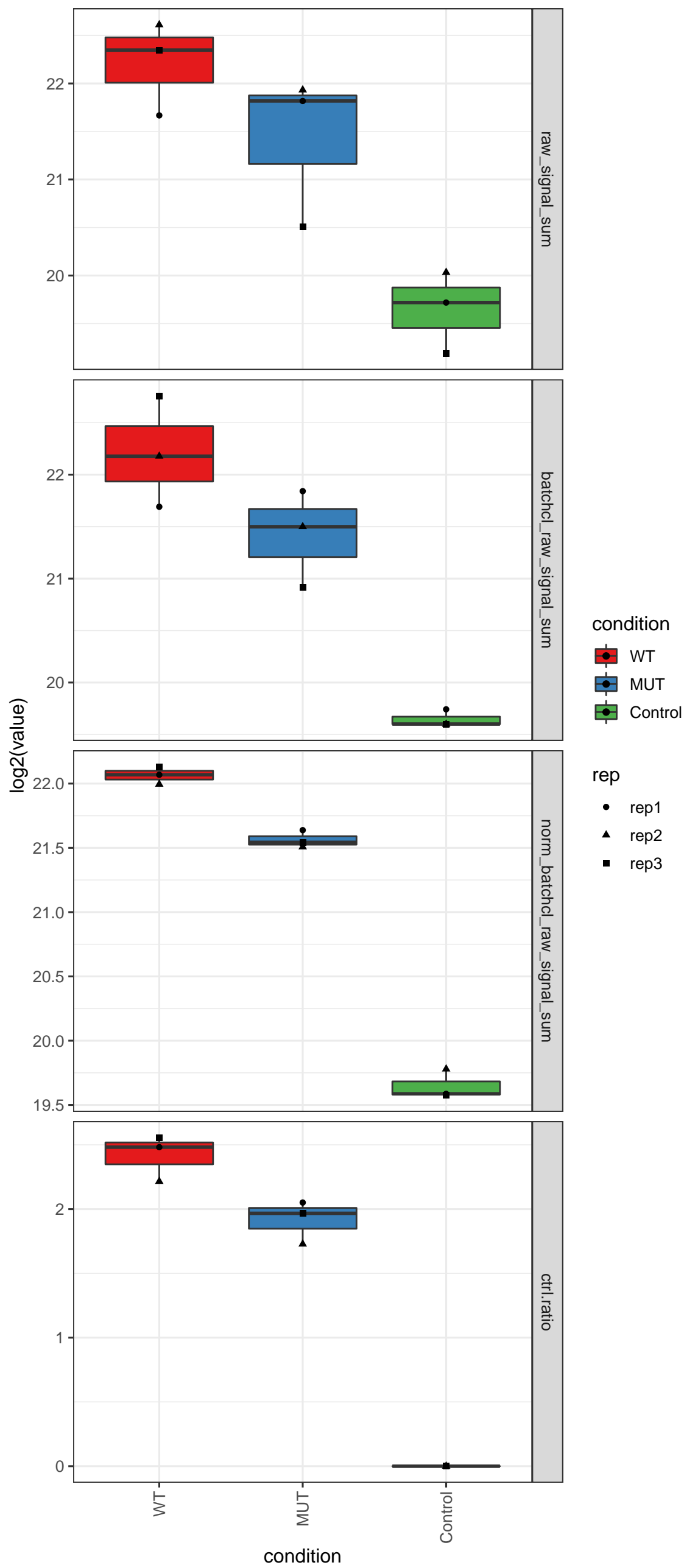
IES1 – P43579

Ino eighty subunit 1 OS=*Saccharomyces cerevisiae* (strain ATCC 204508 /



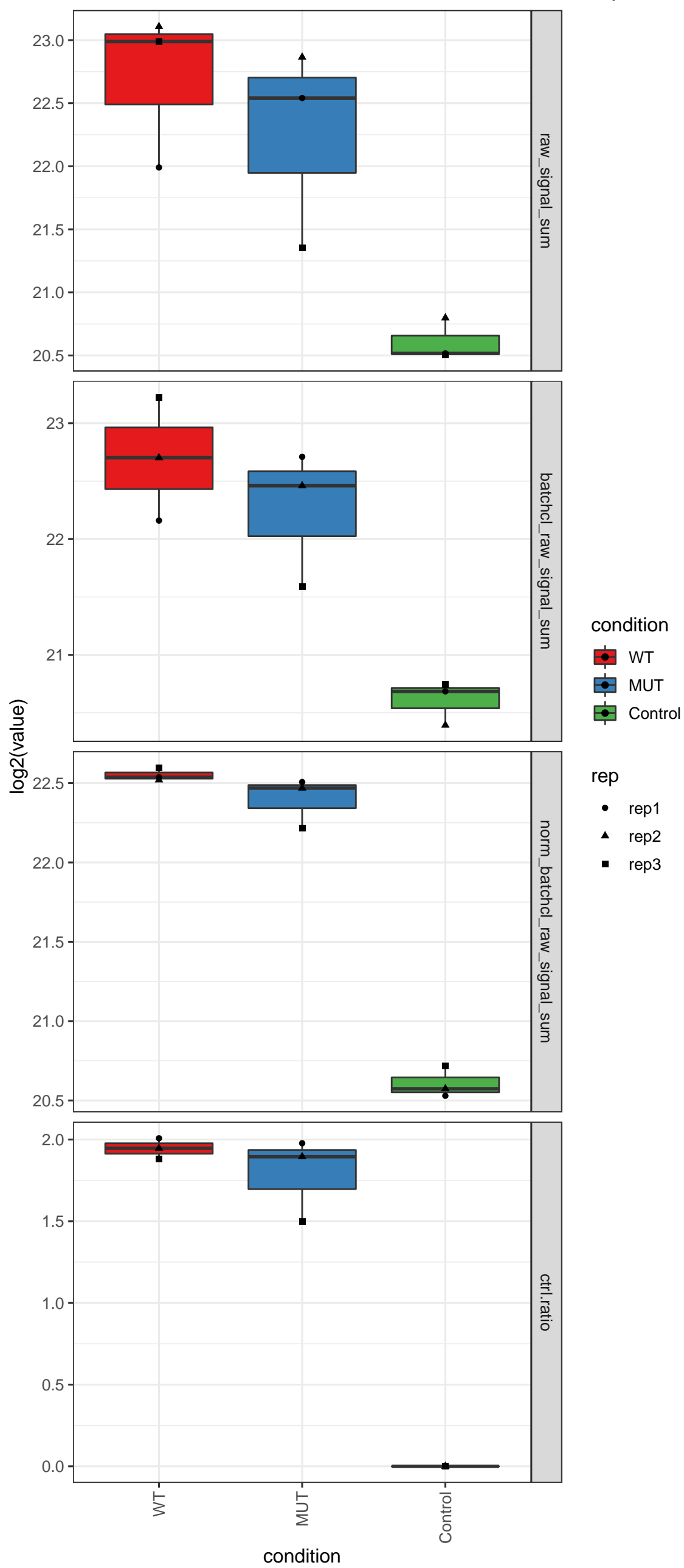
IES2 – P40154

Ino eighty subunit 2 OS=*Saccharomyces cerevisiae* (strain ATCC 204508



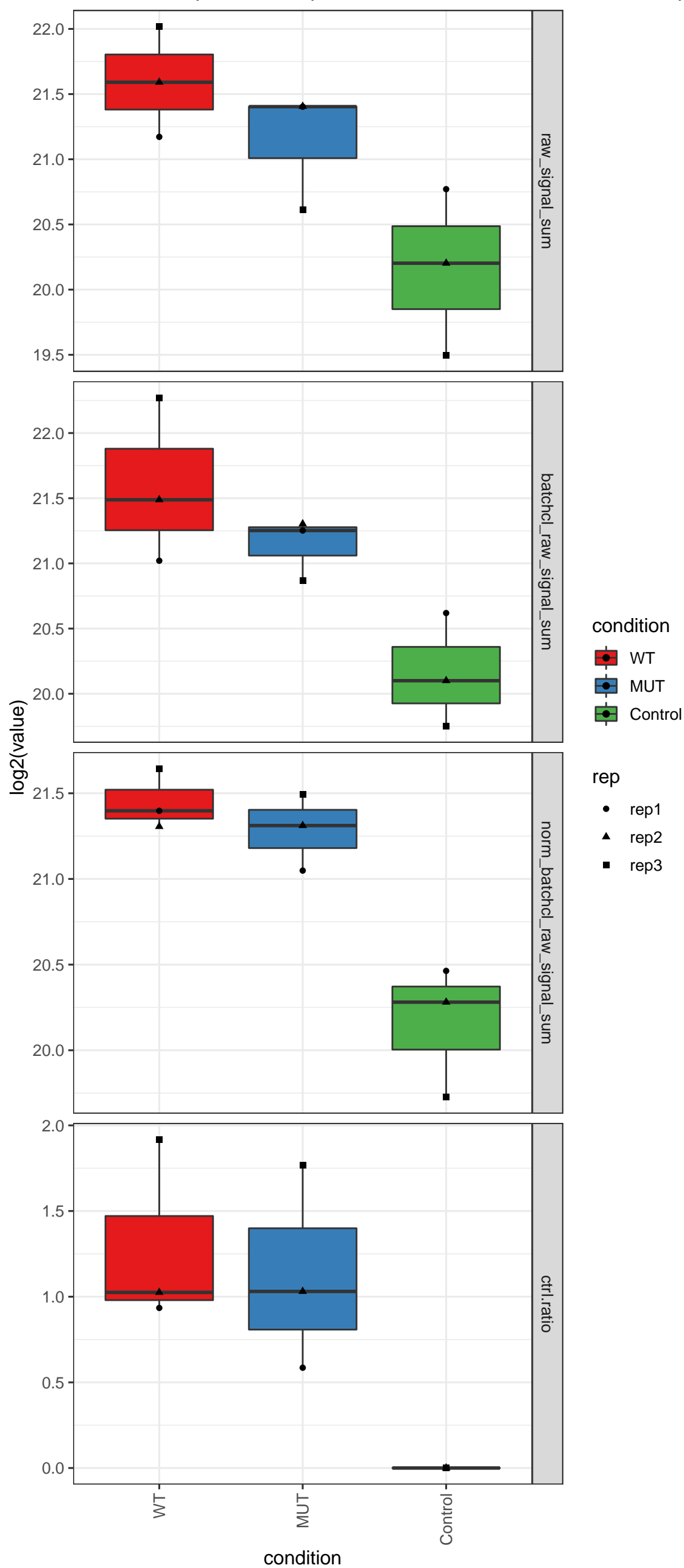
IFM1 – P25038

Translation initiation factor IF-2, mitochondrial OS=*Saccharomyces cerevisiae*



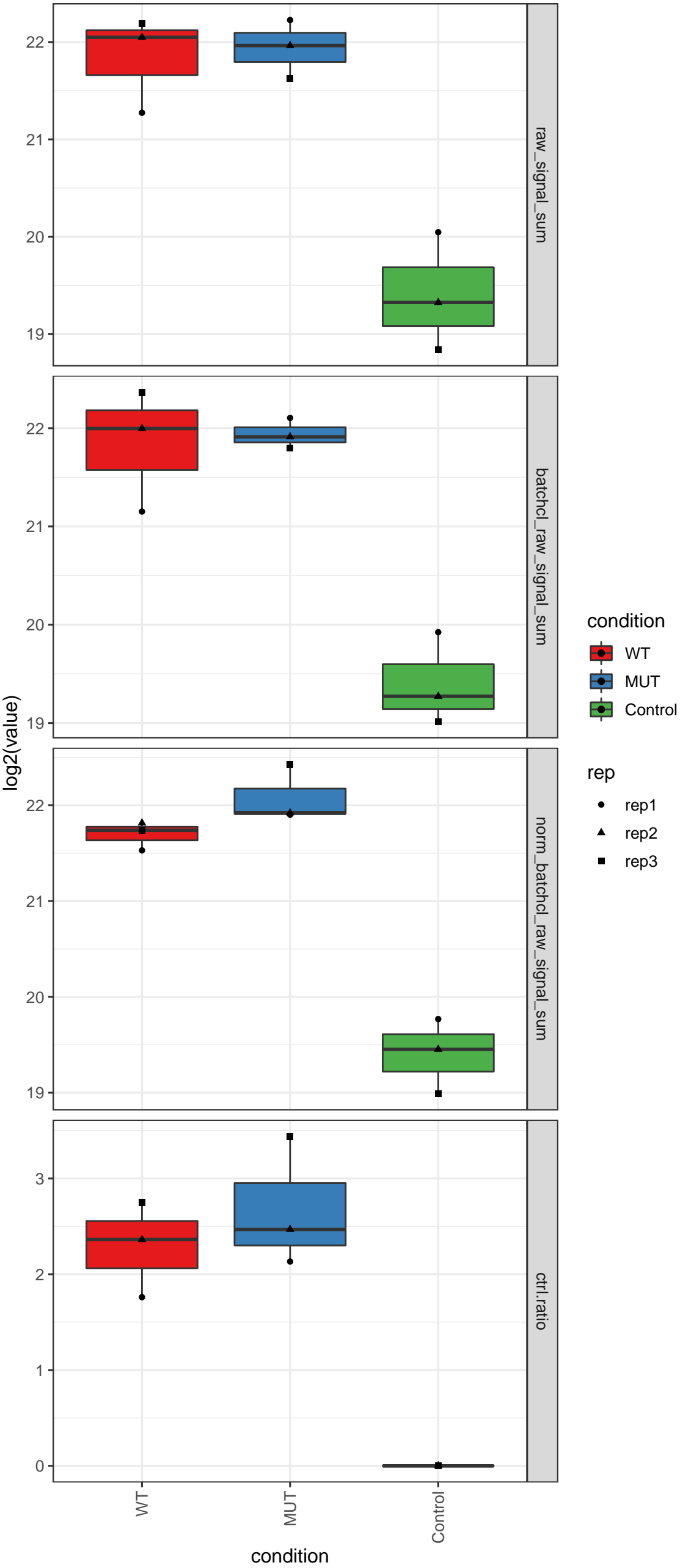
ILV2 – P07342

Acetolactate synthase catalytic subunit, mitochondrial OS=Saccharomyces cerevisiae



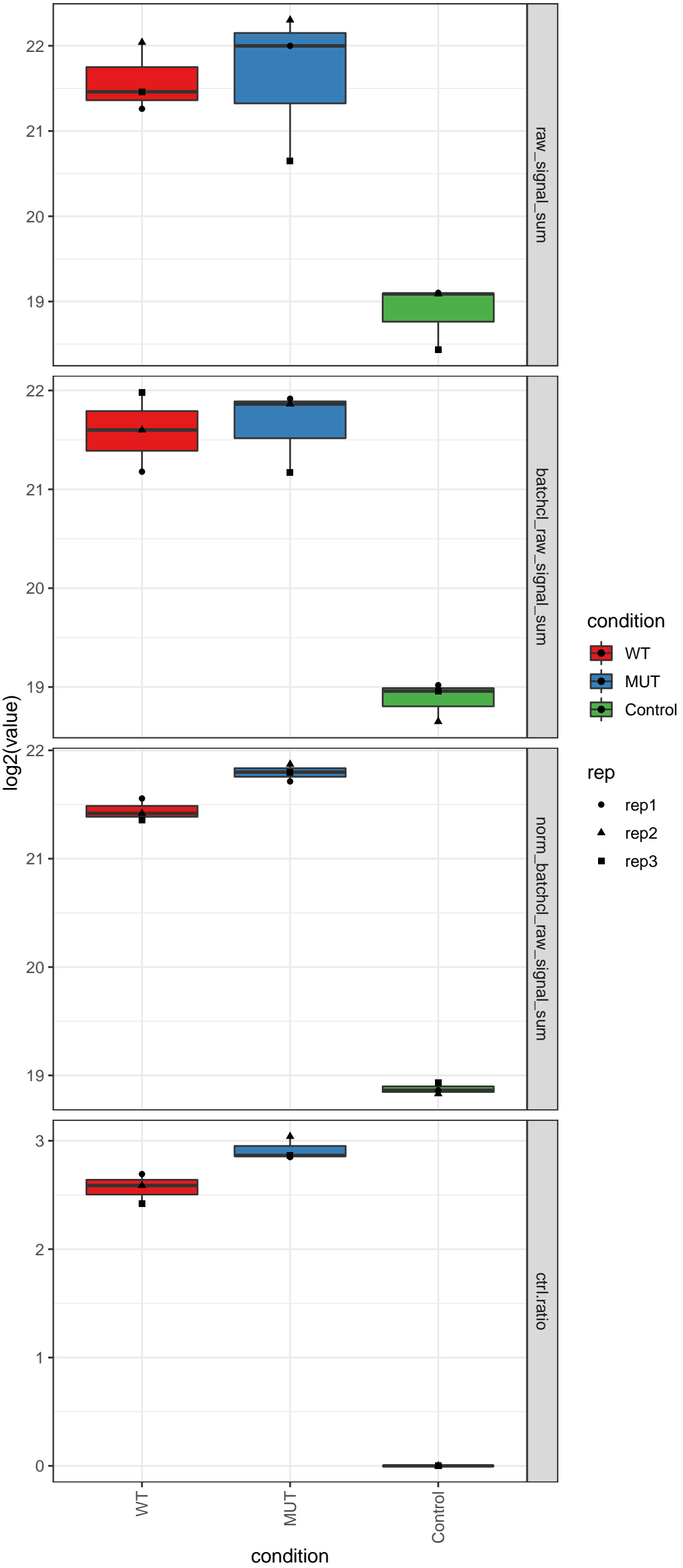
IMD4 – P50094

Inosine-5'-monophosphate dehydrogenase 4 OS=*Saccharomyces cerevisiae*



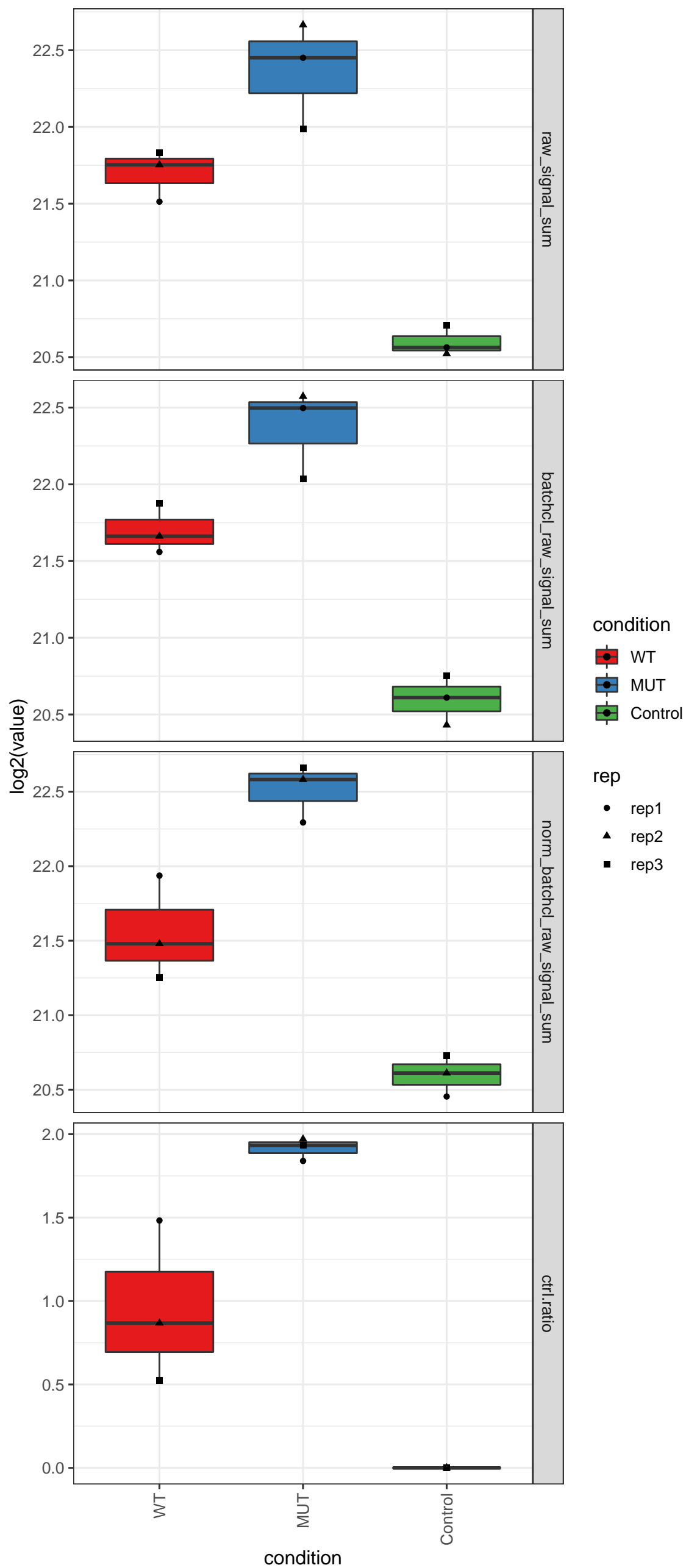
IMG1 – P25626

54S ribosomal protein IMG1, mitochondrial OS=*Saccharomyces cerevisiae*



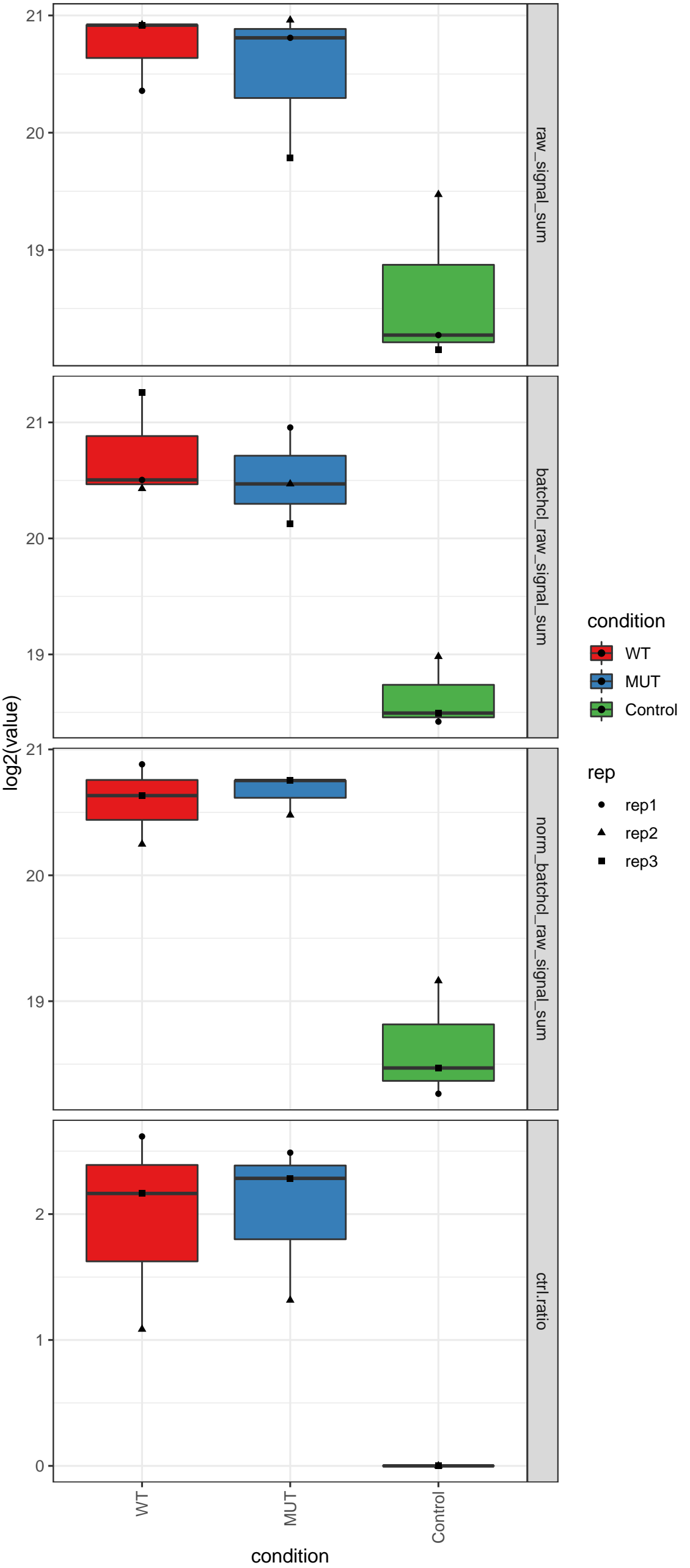
IMG2 – P25642

54S ribosomal protein IMG2, mitochondrial OS=*Saccharomyces cerevisiae*



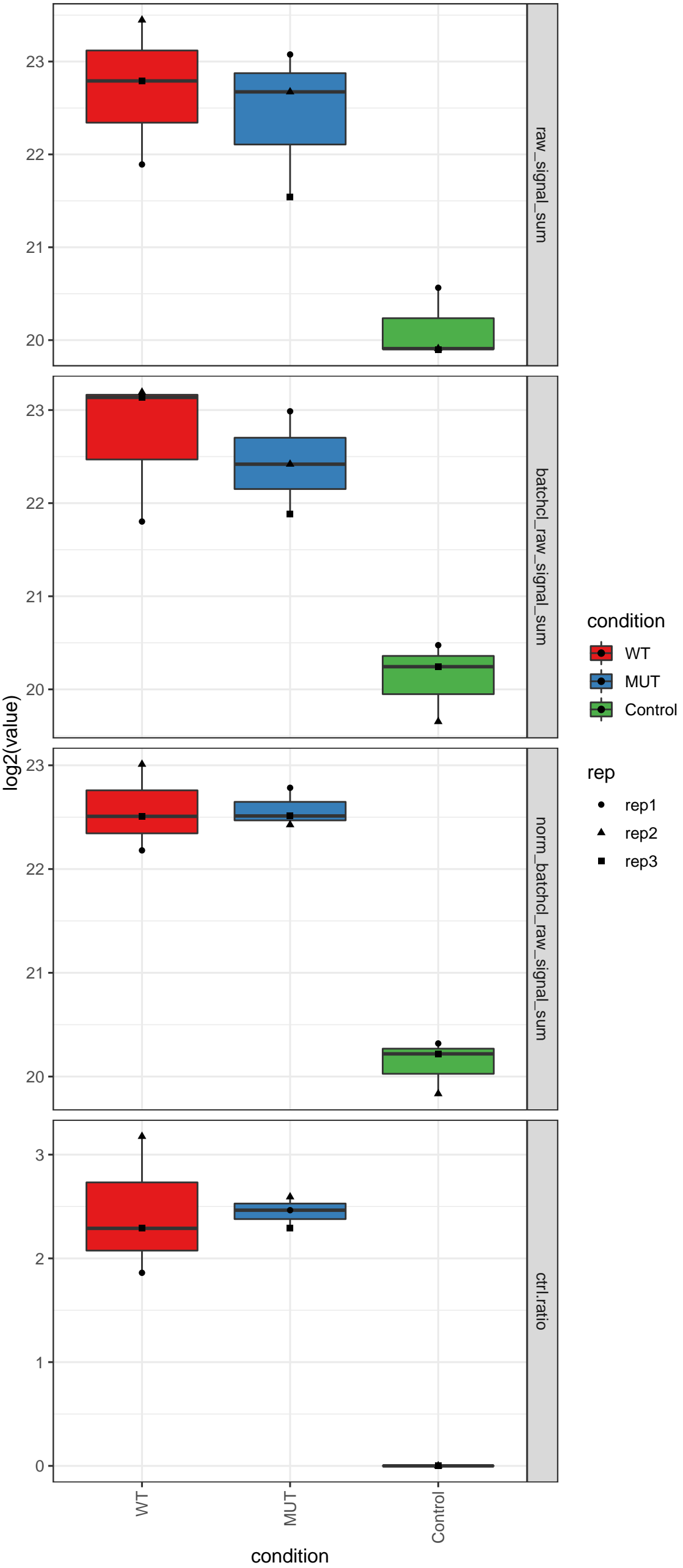
IMH1 – Q06704

Golgin IMH1 OS=*Saccharomyces cerevisiae* (strain ATCC 204508 / S288c)



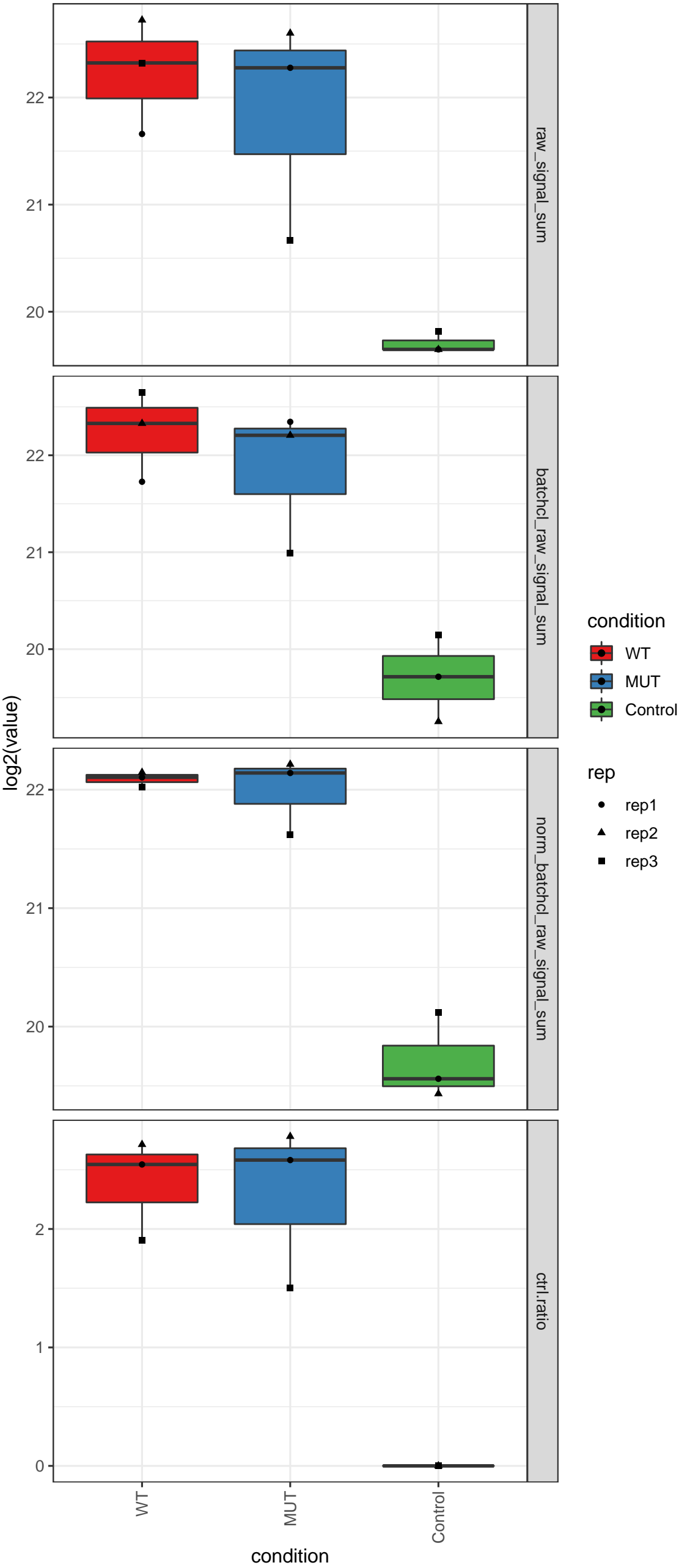
INO1 – P11986

Inositol-3-phosphate synthase OS=*Saccharomyces cerevisiae* (strain ATCC 22016 / S288c)



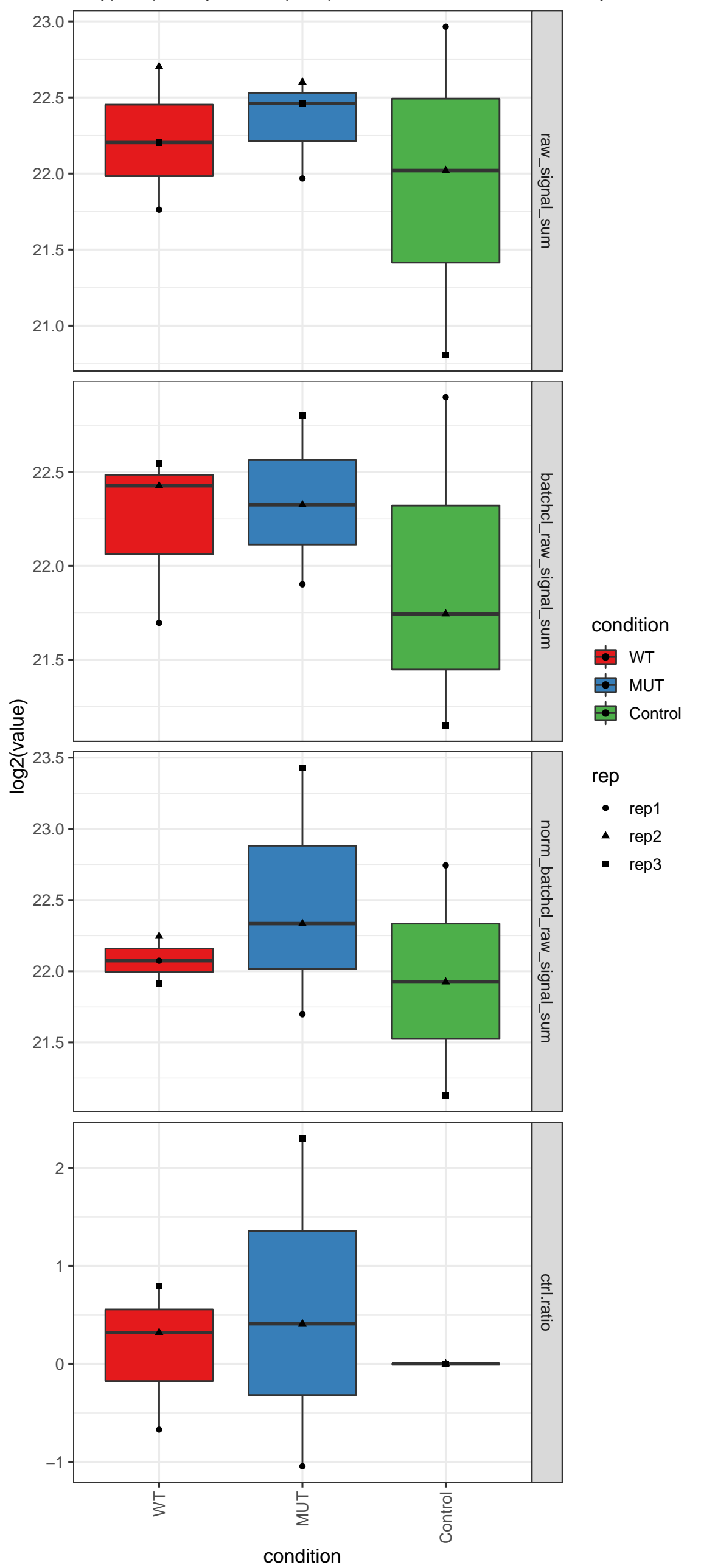
INO80 – P53115

Putative DNA helicase INO80 OS=*Saccharomyces cerevisiae* (strain ATCC 24843)



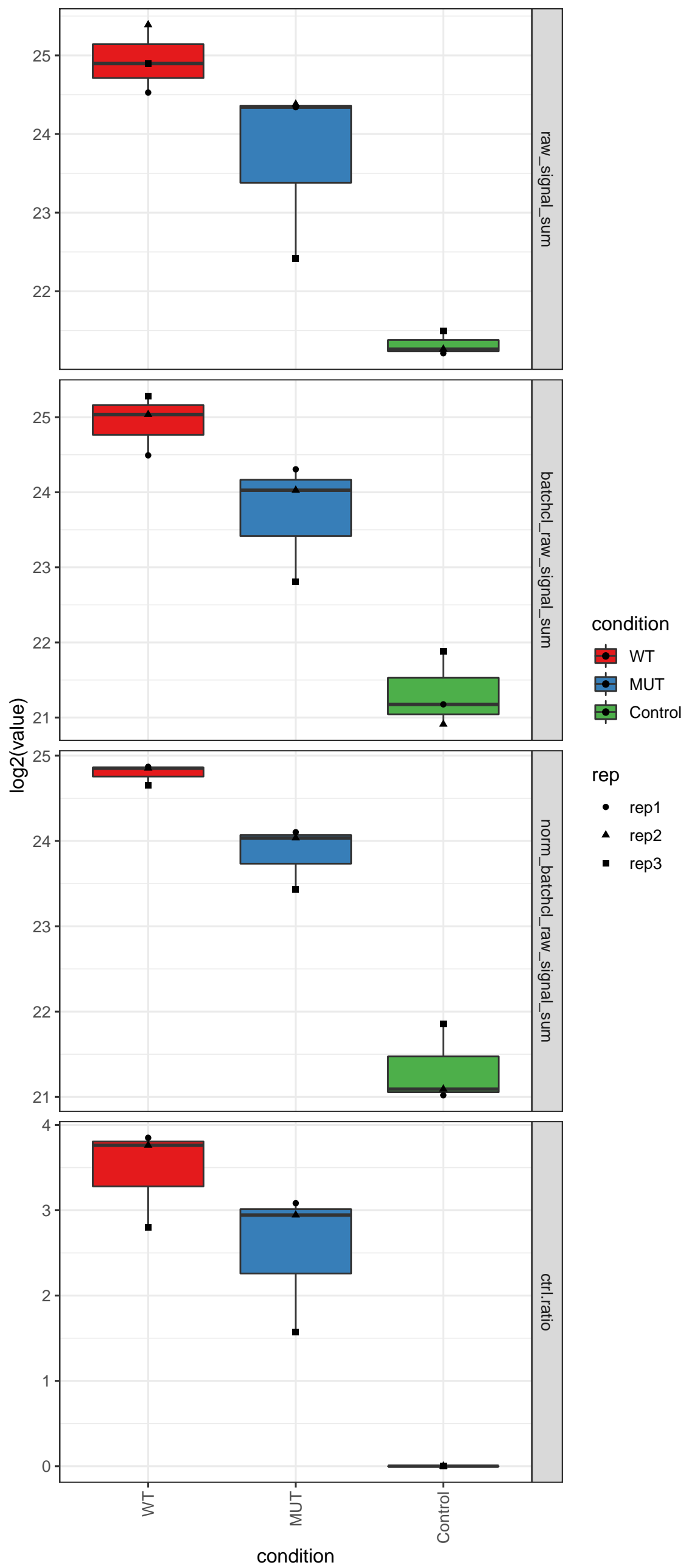
INP52 – P50942

Polyphosphatidylinositol phosphatase INP52 OS=*Saccharomyces cerevisiae*



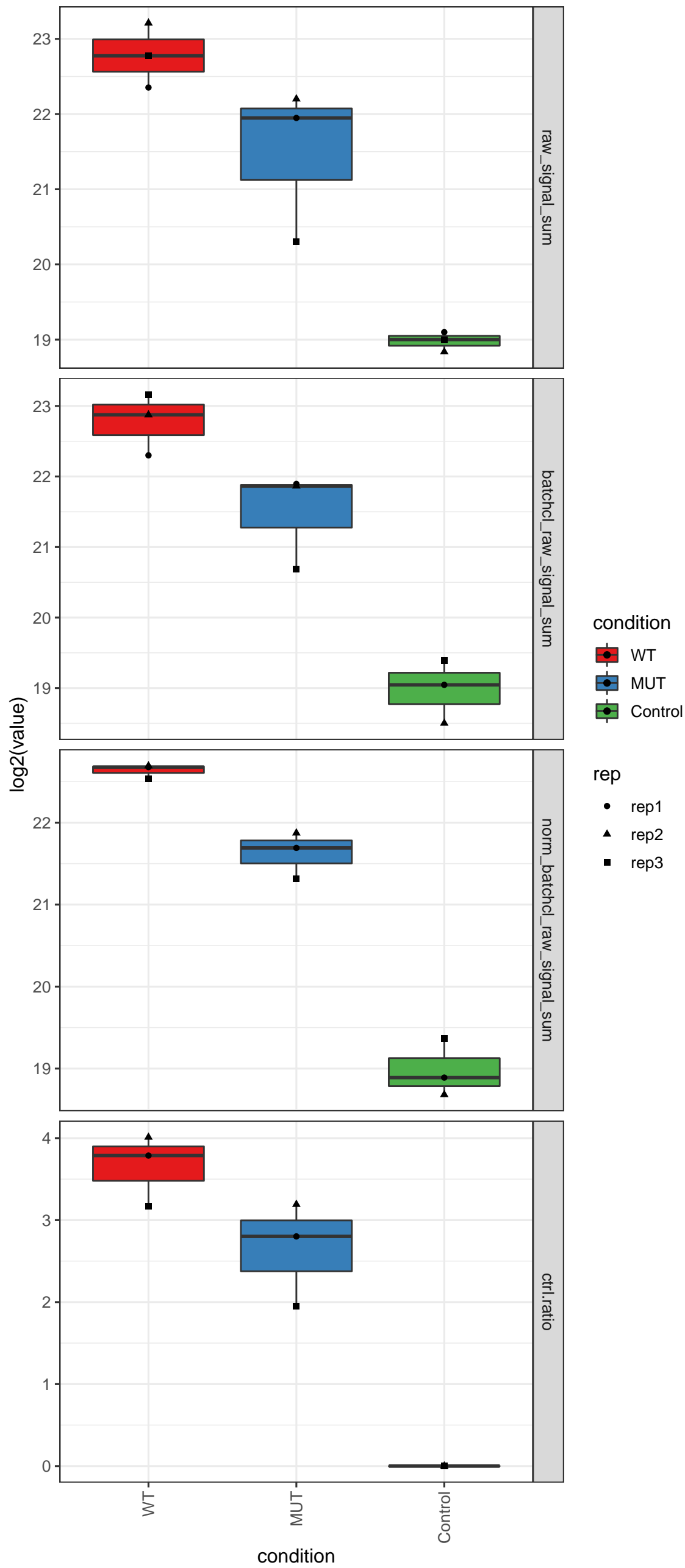
IOC2 – Q12072

ISWI one complex protein 2 OS=*Saccharomyces cerevisiae* (strain ATCC 24843)



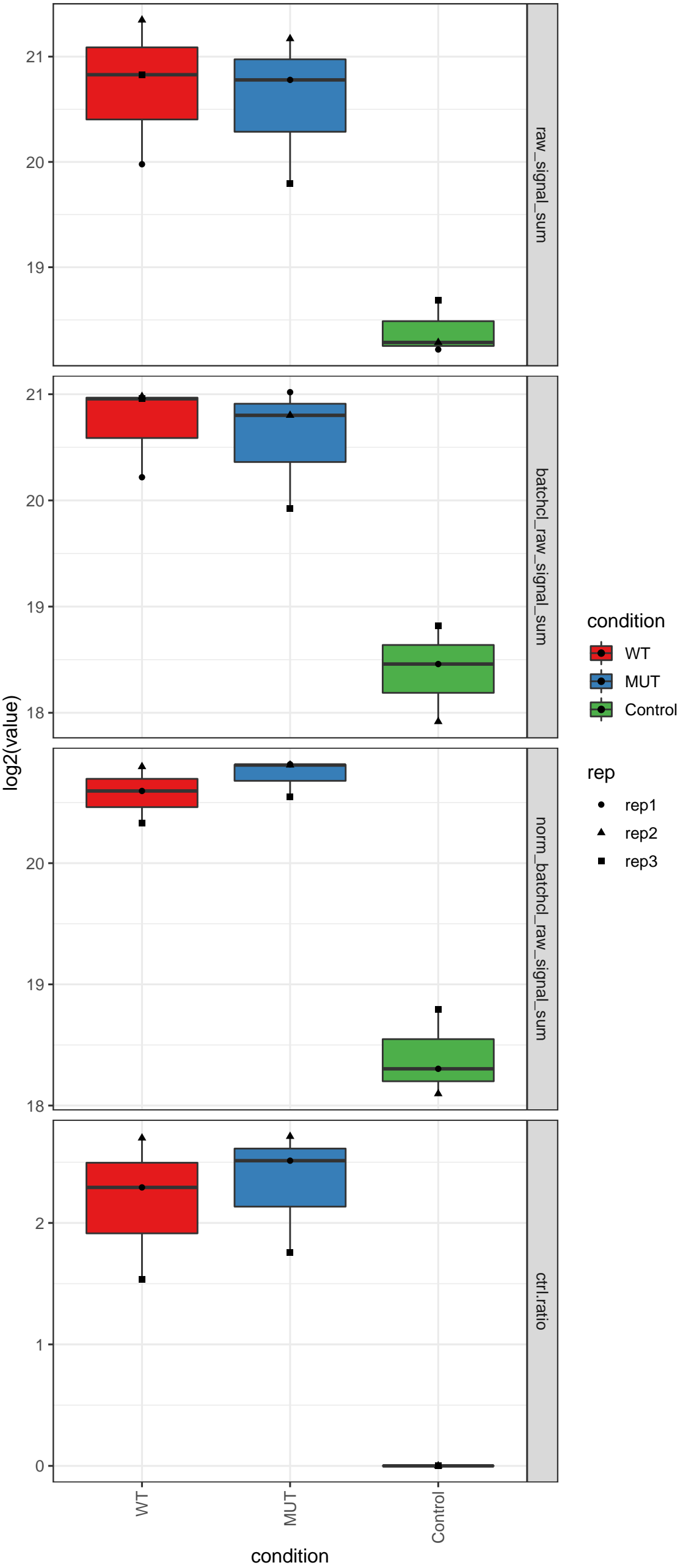
IOC3 – P43596

ISWI one complex protein 3 OS=*Saccharomyces cerevisiae* (strain ATCC 24843)



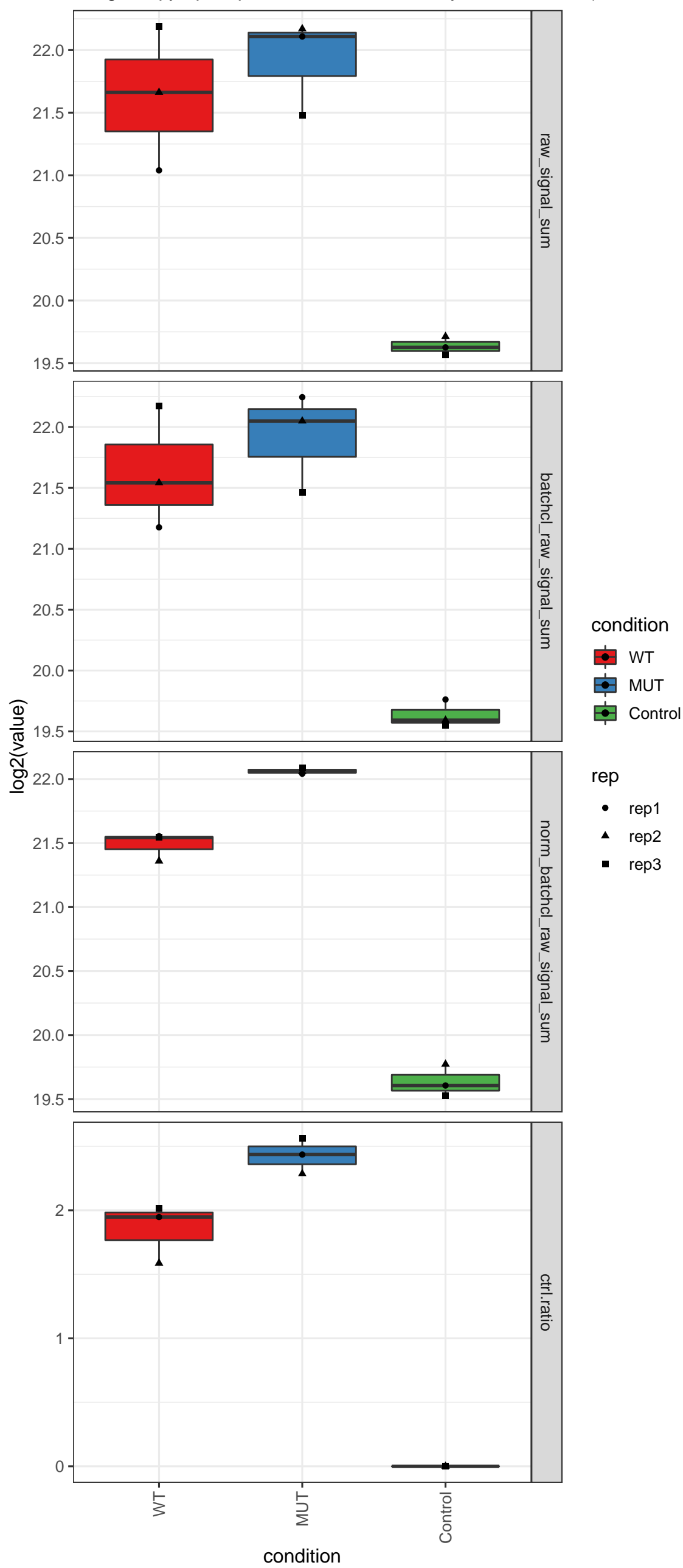
IPI3 – P53877

Pre-rRNA-processing protein IPI3 OS=*Saccharomyces cerevisiae* (strain



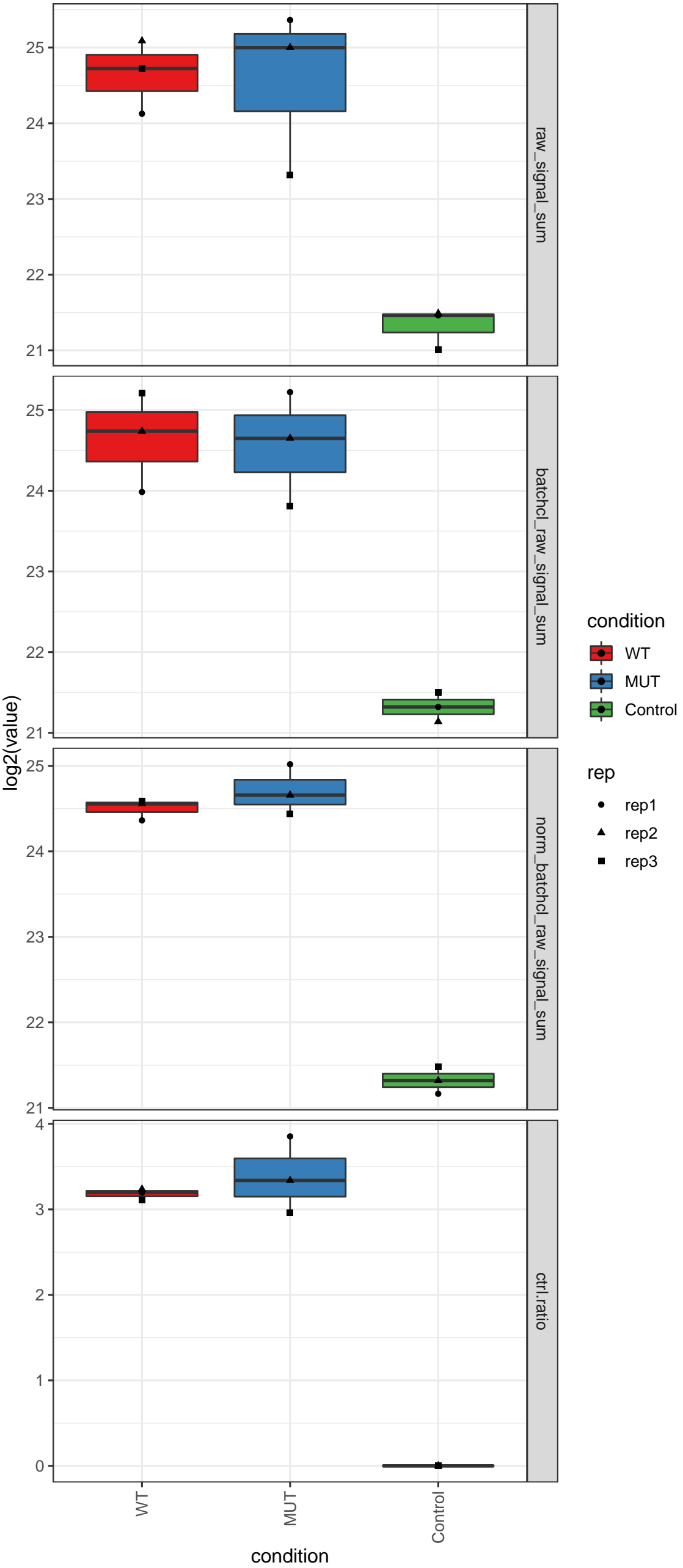
IPP1 – P00817

Inorganic pyrophosphatase OS=*Saccharomyces cerevisiae* (strain ATCC



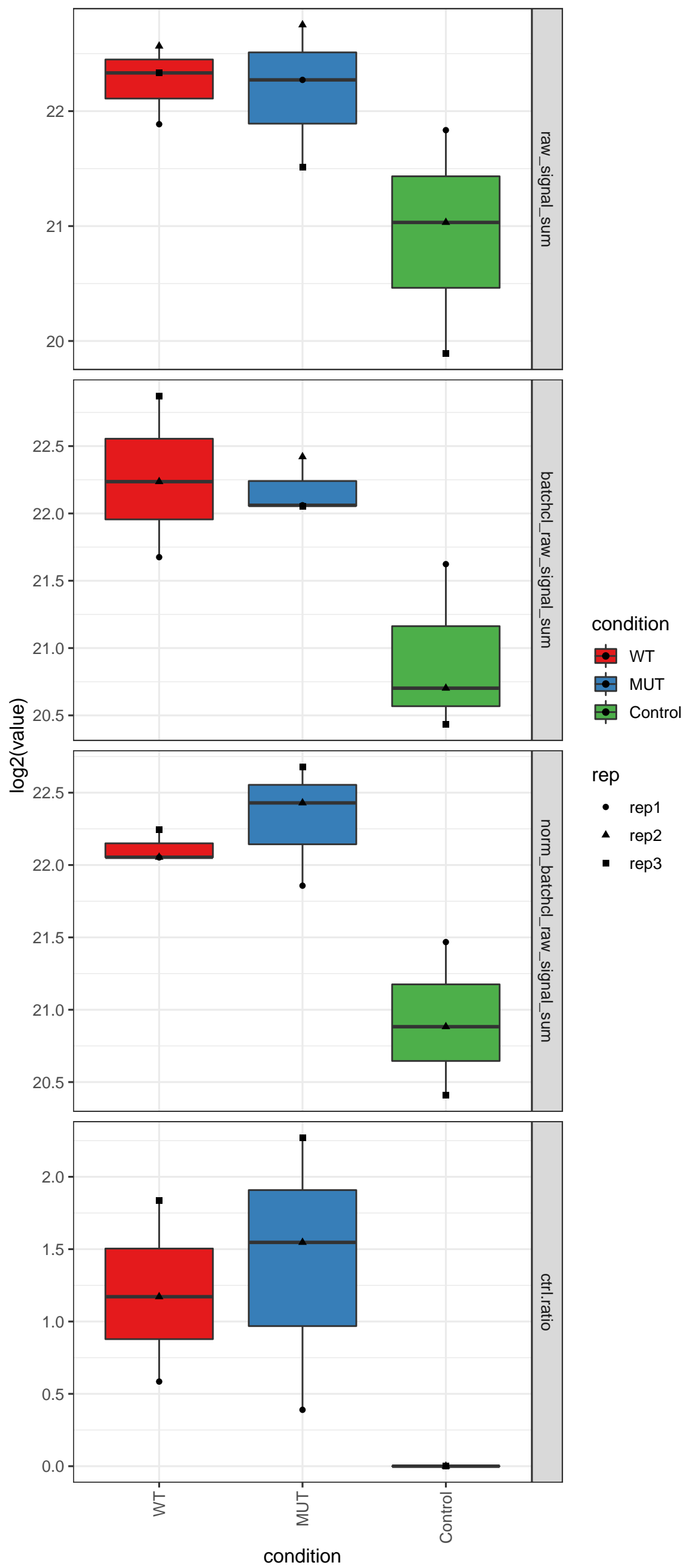
IRR1 – P40541

Cohesin subunit SCC3 OS=*Saccharomyces cerevisiae* (strain ATCC 20450)



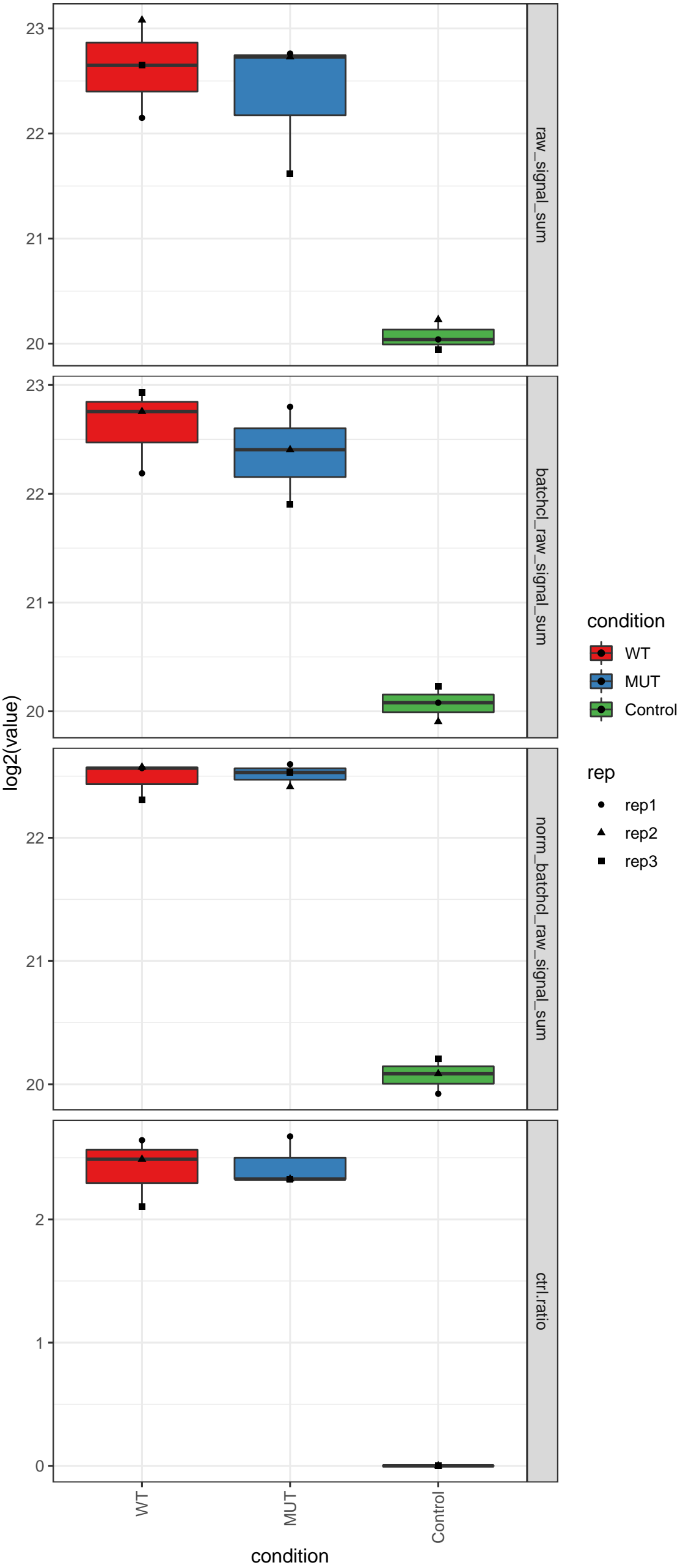
IST1 – P53843

Vacuolar protein sorting–associated protein IST1 OS=*Saccharomyces cerevisiae*



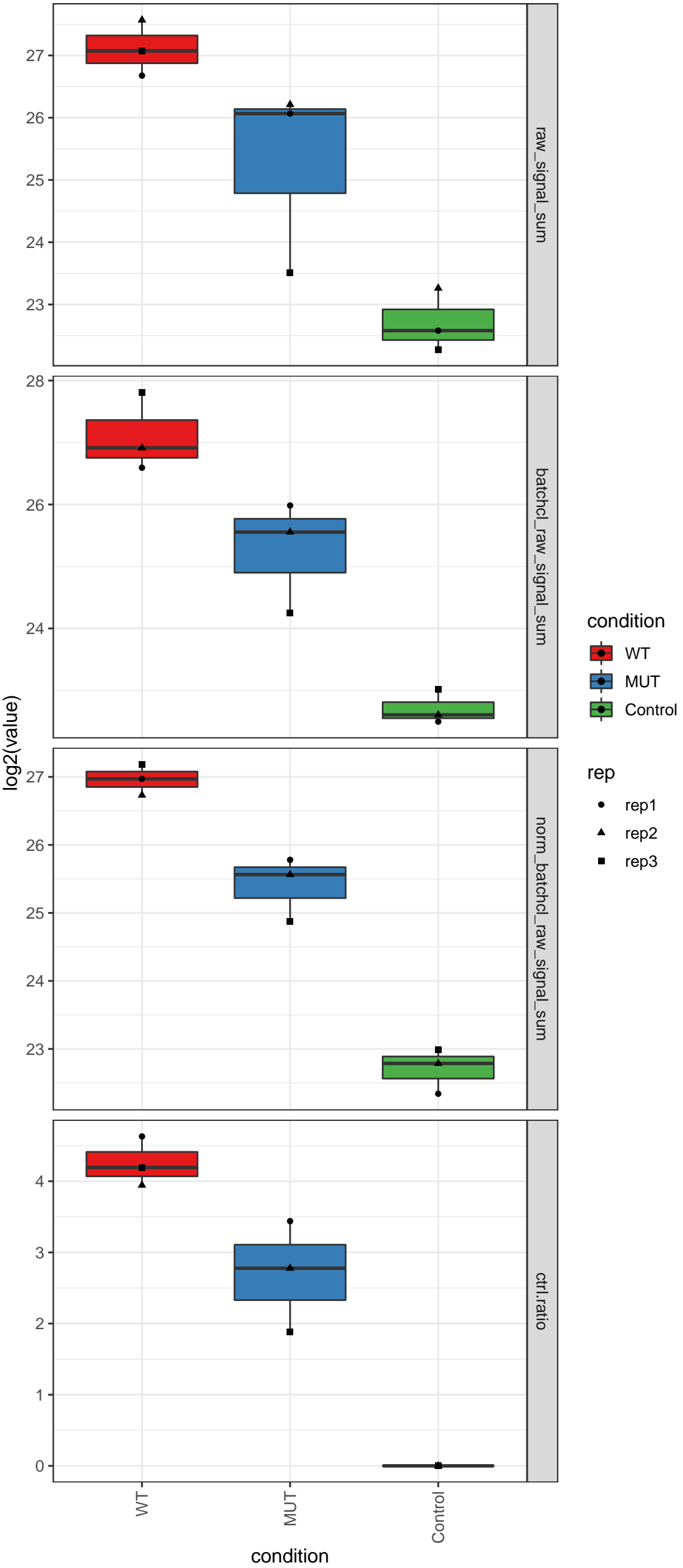
IST2 – P38250

Increased sodium tolerance protein 2 OS=*Saccharomyces cerevisiae* (strain



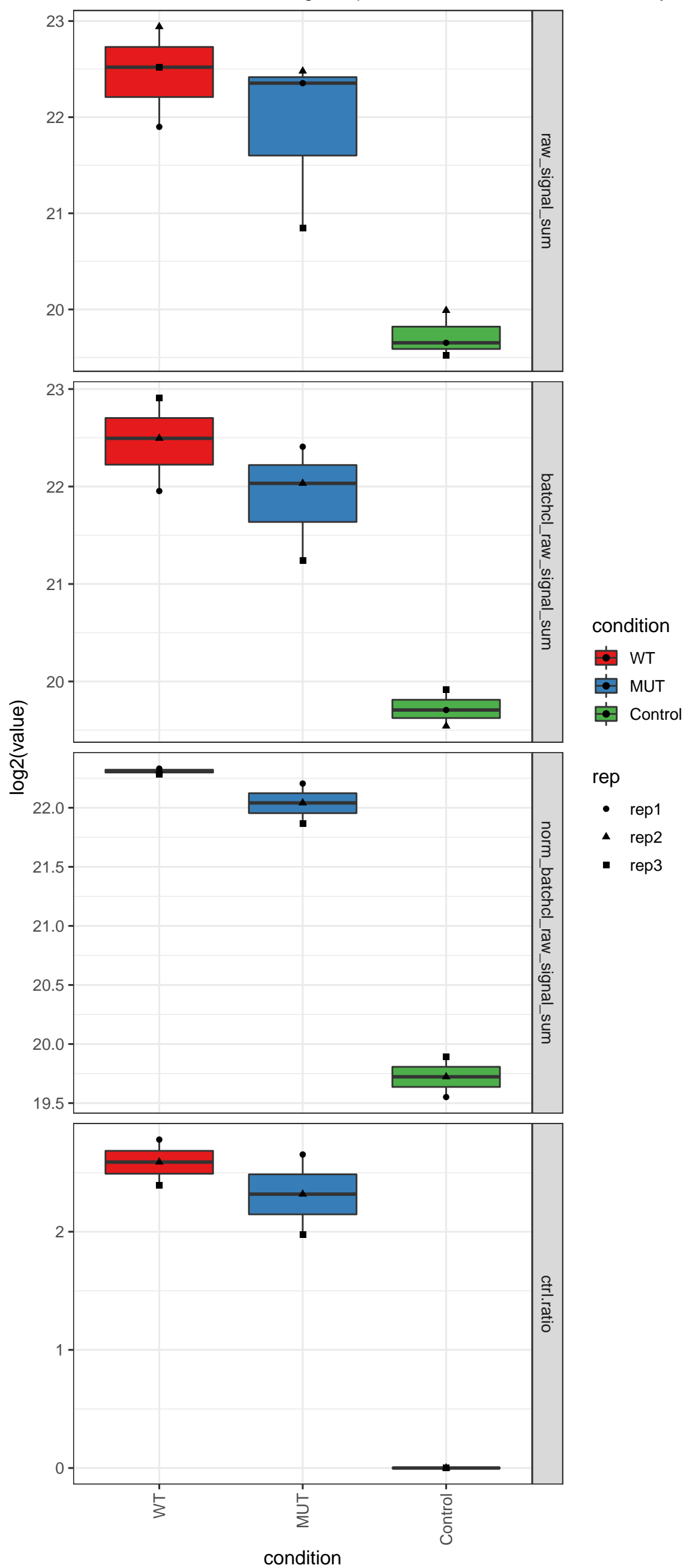
ISW1 – P38144

ISWI chromatin–remodeling complex ATPase ISW1 OS=Saccharomyces c



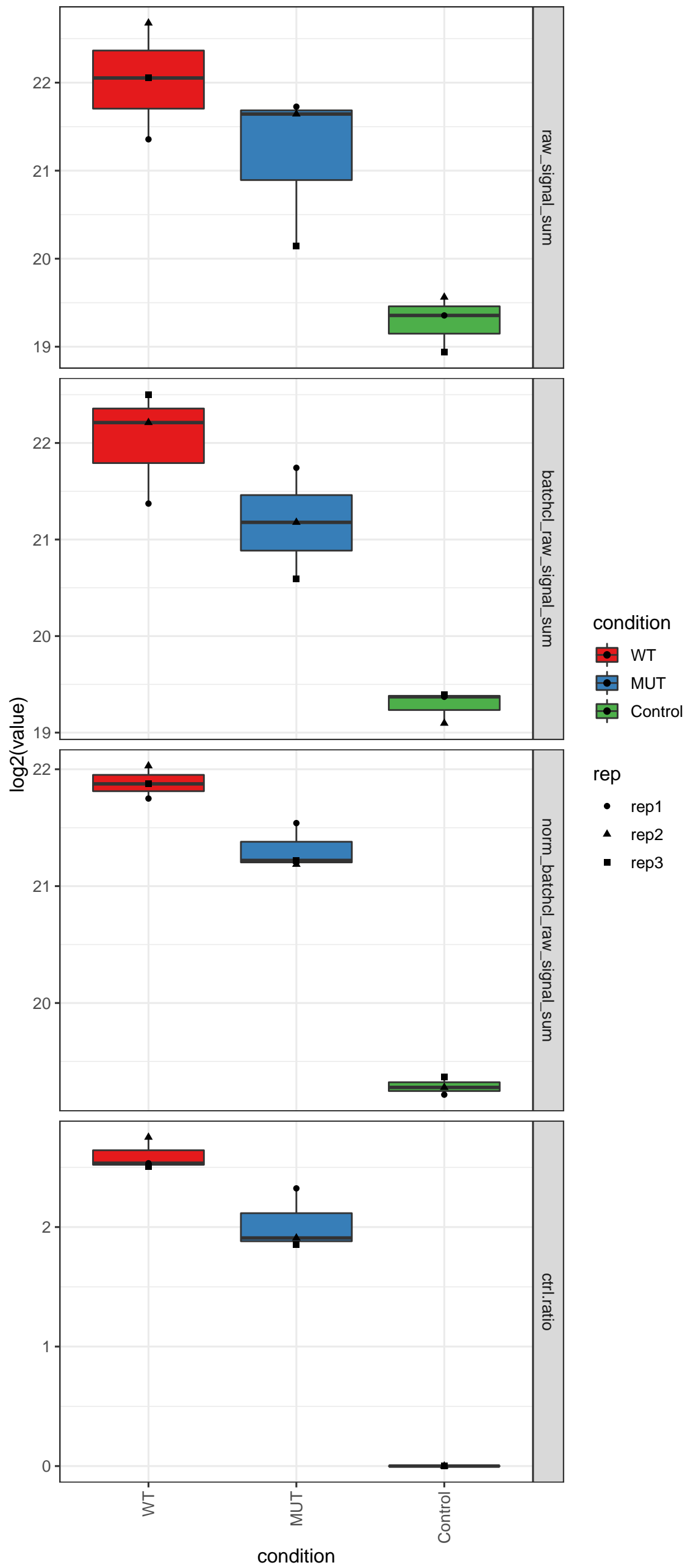
ISW2 – Q08773

ISWI chromatin–remodeling complex ATPase ISW2 OS=Saccharomyces



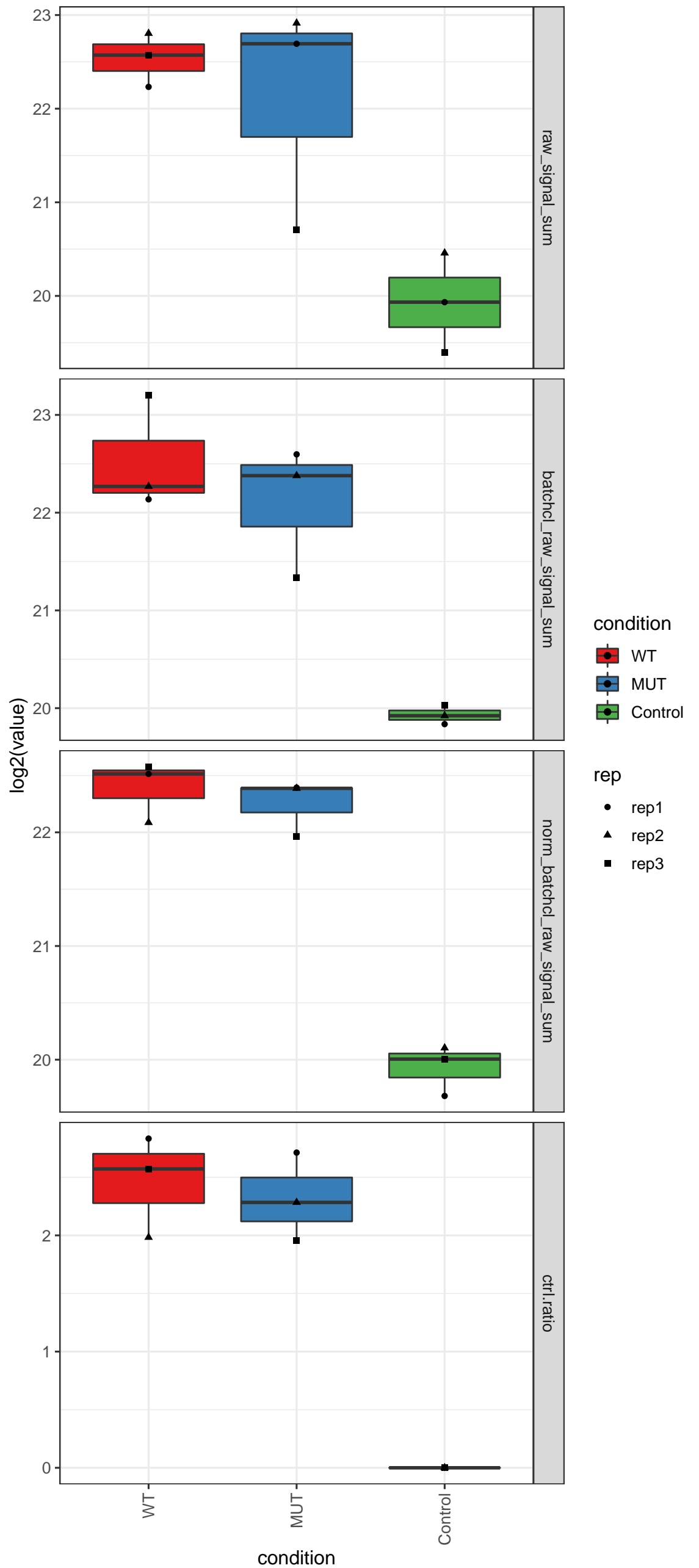
JHD1 – P40034

JmjC domain-containing histone demethylation protein 1 OS=Saccharomy



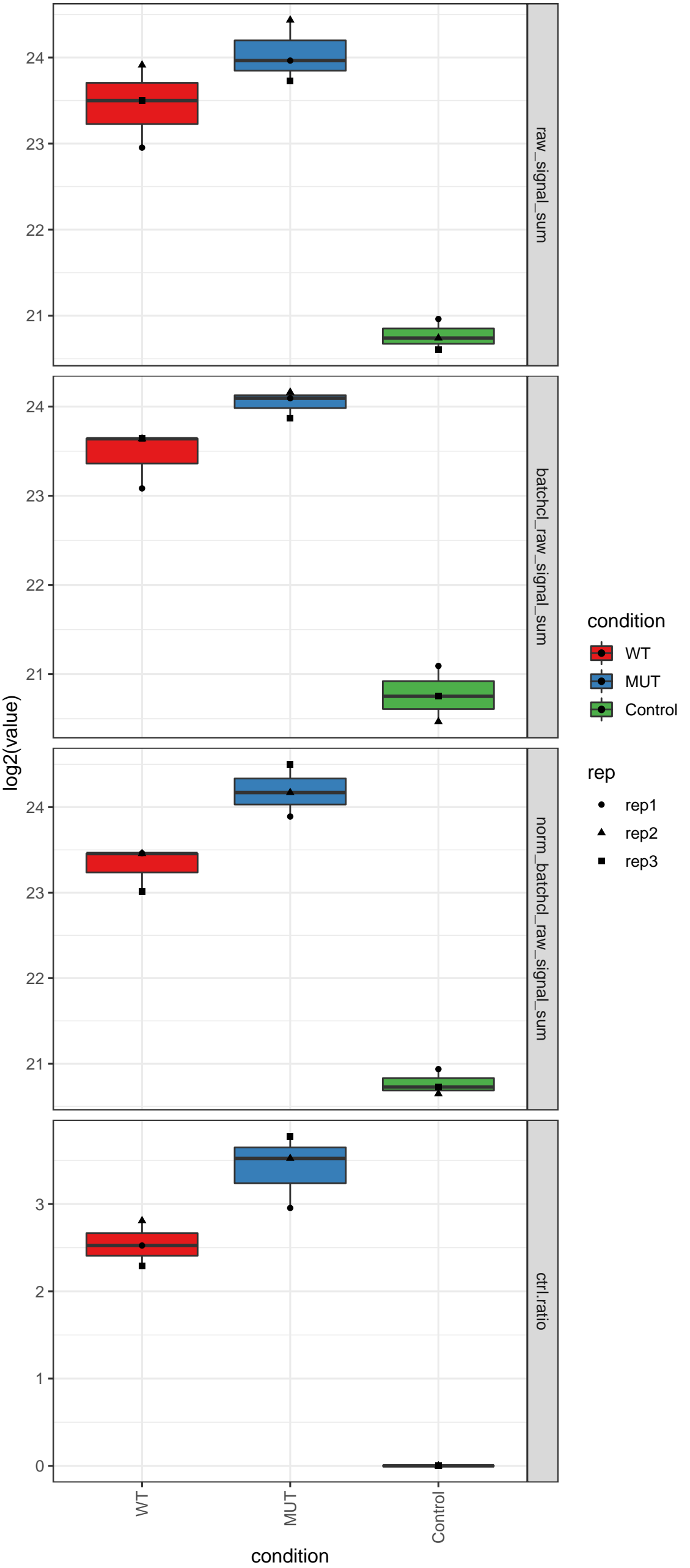
JIP5 – Q06214

WD repeat-containing protein JIP5 OS=*Saccharomyces cerevisiae* (strain



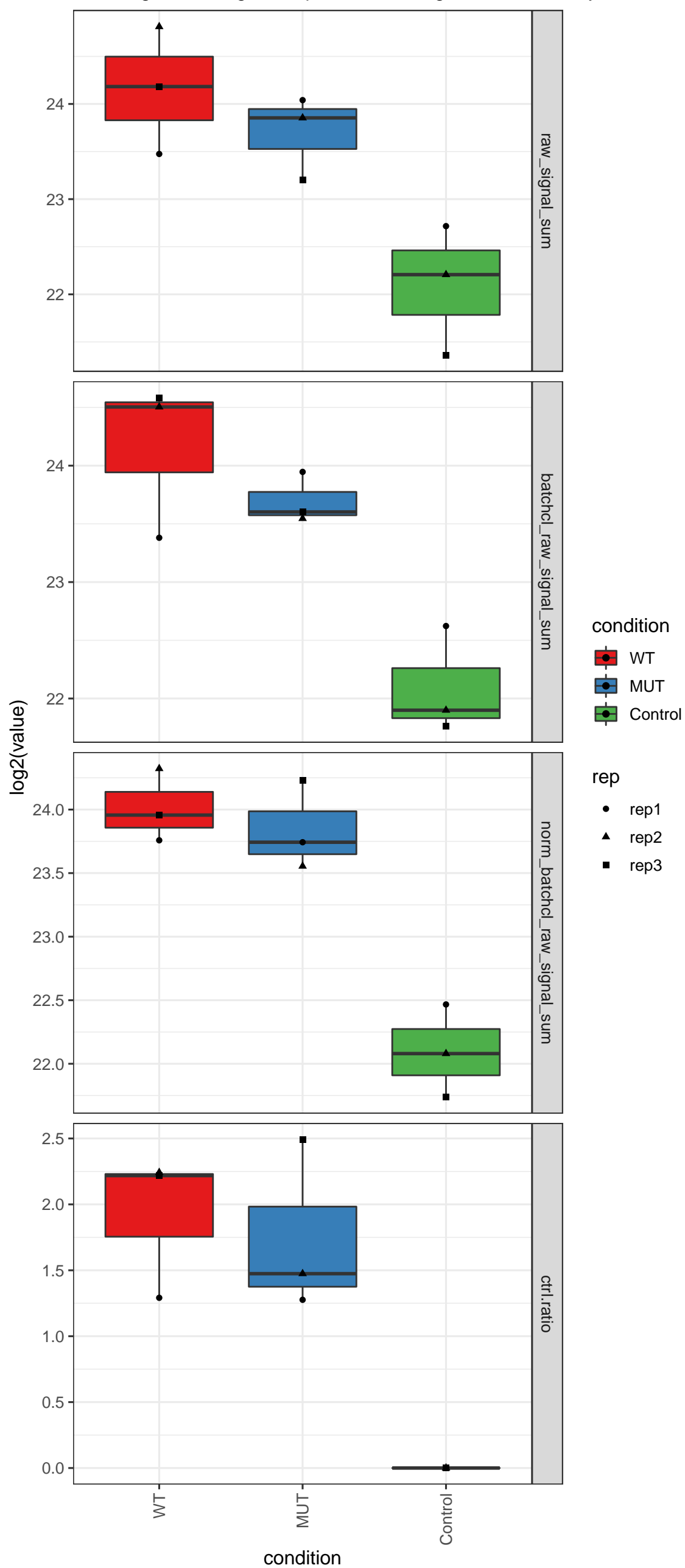
KAP95 – Q06142

Importin subunit beta-1 OS=Saccharomyces cerevisiae (strain ATCC 2045



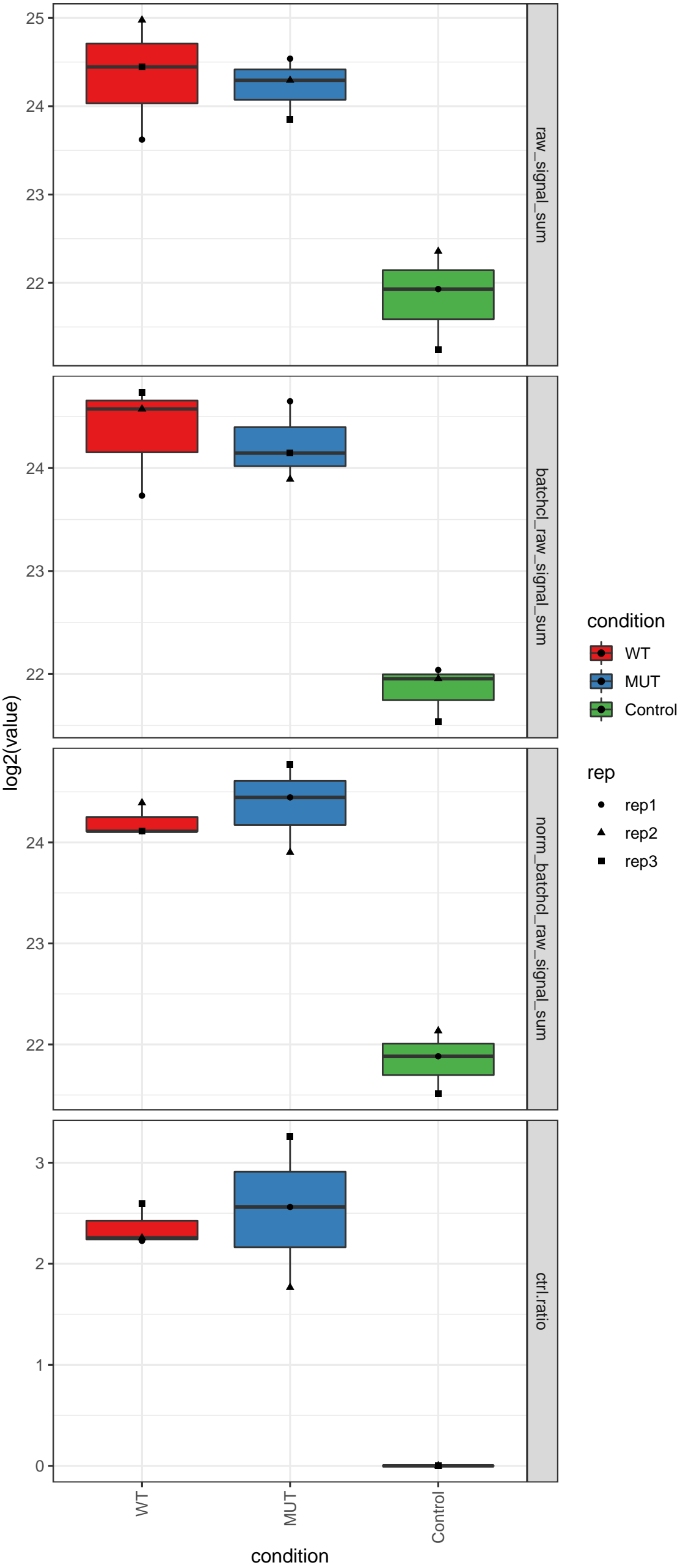
KAR2 – P16474

78 kDa glucose-regulated protein homolog OS=Saccharomyces cerevisiae



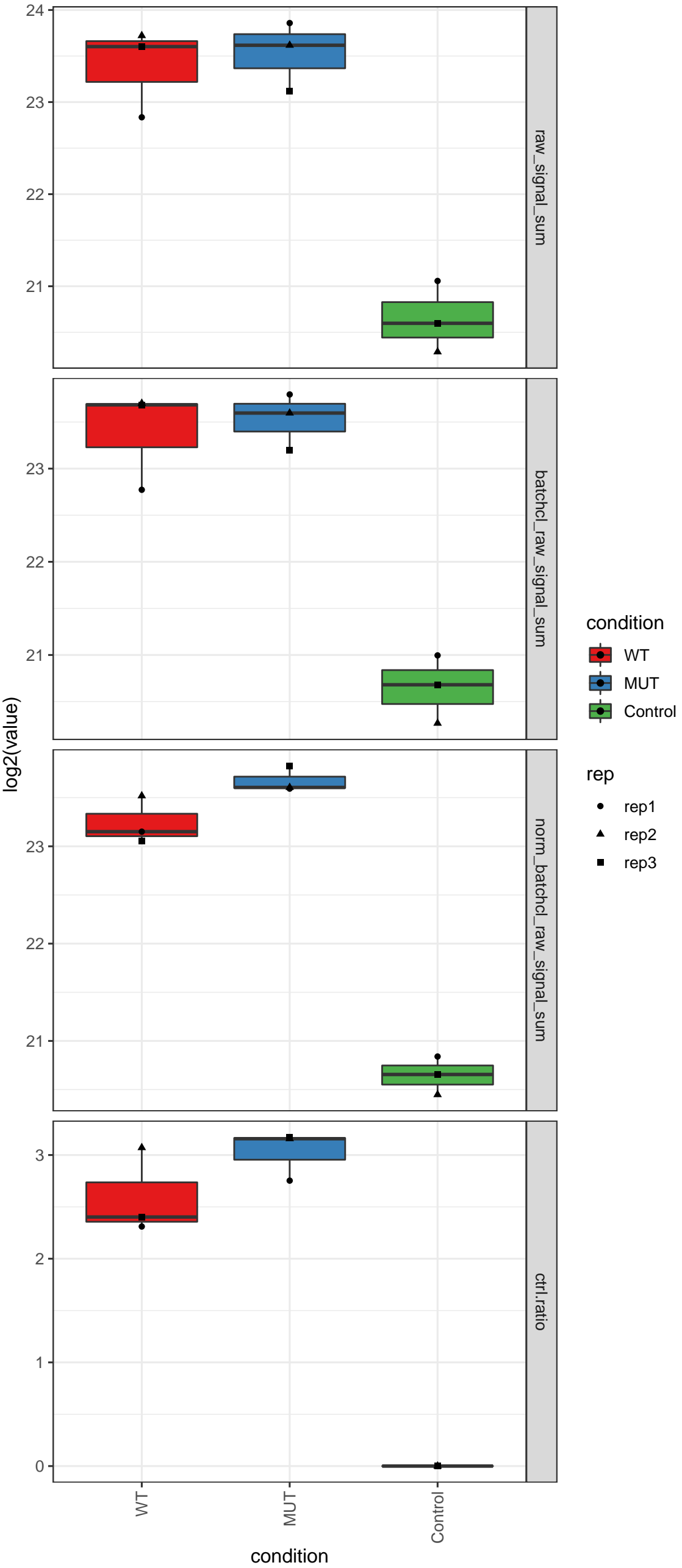
KGD1 – P20967

2-oxoglutarate dehydrogenase, mitochondrial OS=Saccharomyces cerevis



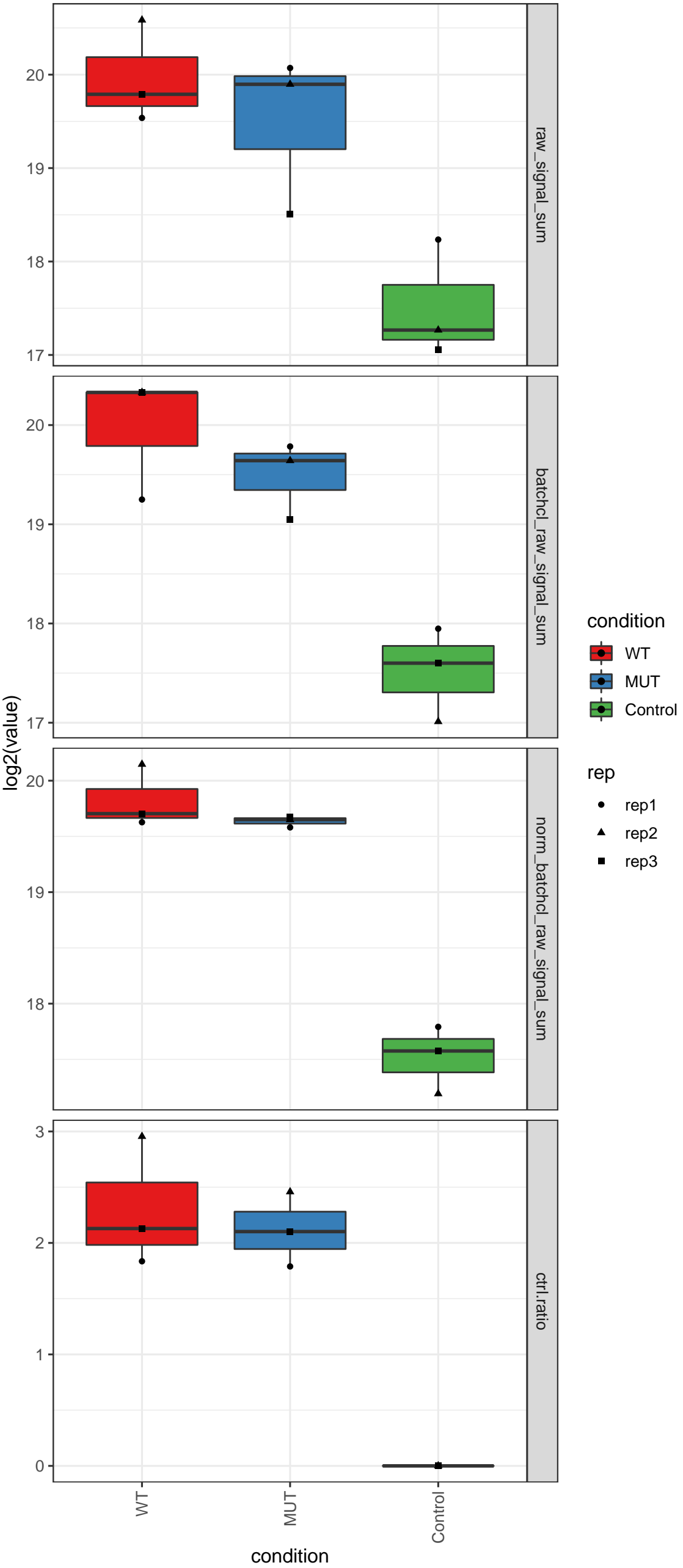
KGD2 – P19262

Dihydrolipoyllysine–residue succinyltransferase component of 2–oxoglutarate dehydrogenase complex



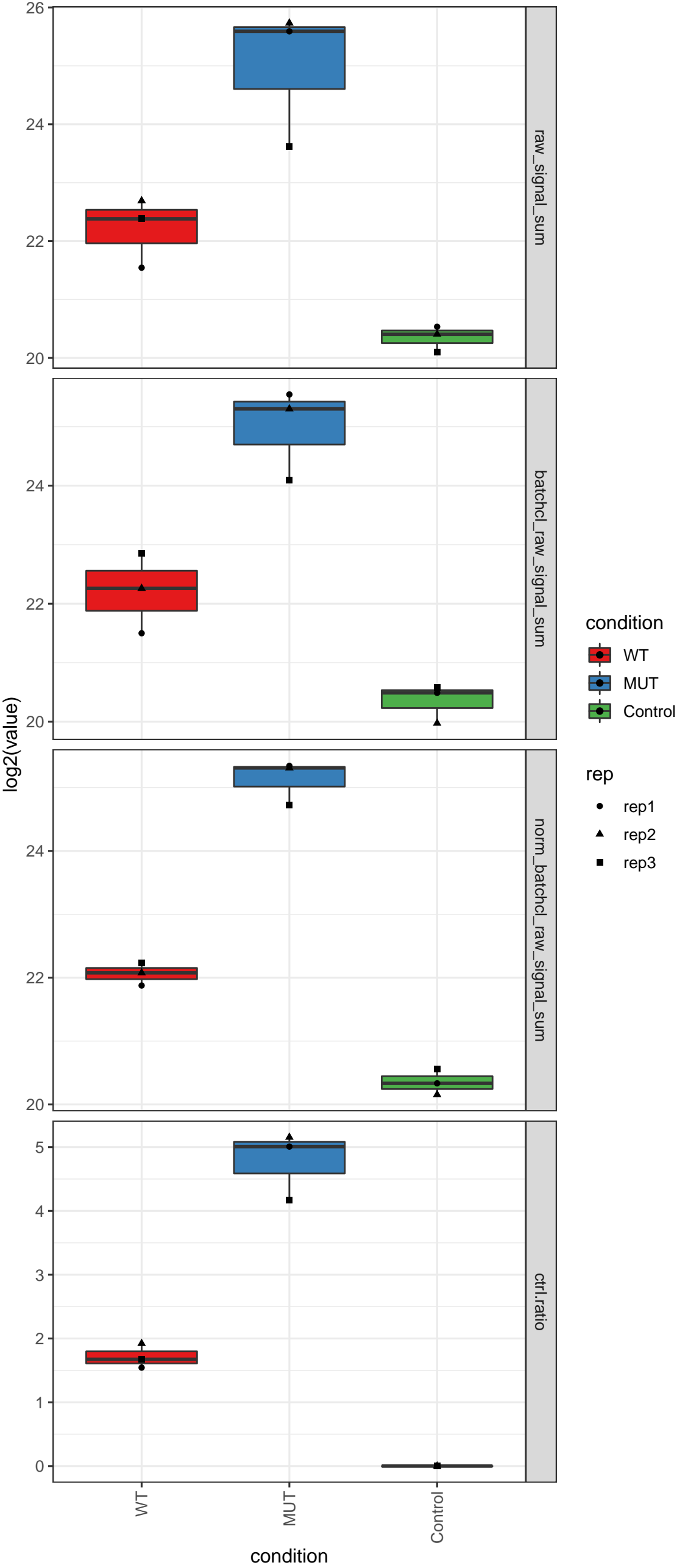
KIN1 – P13185

Serine/threonine protein kinase KIN1 OS=*Saccharomyces cerevisiae* (strain



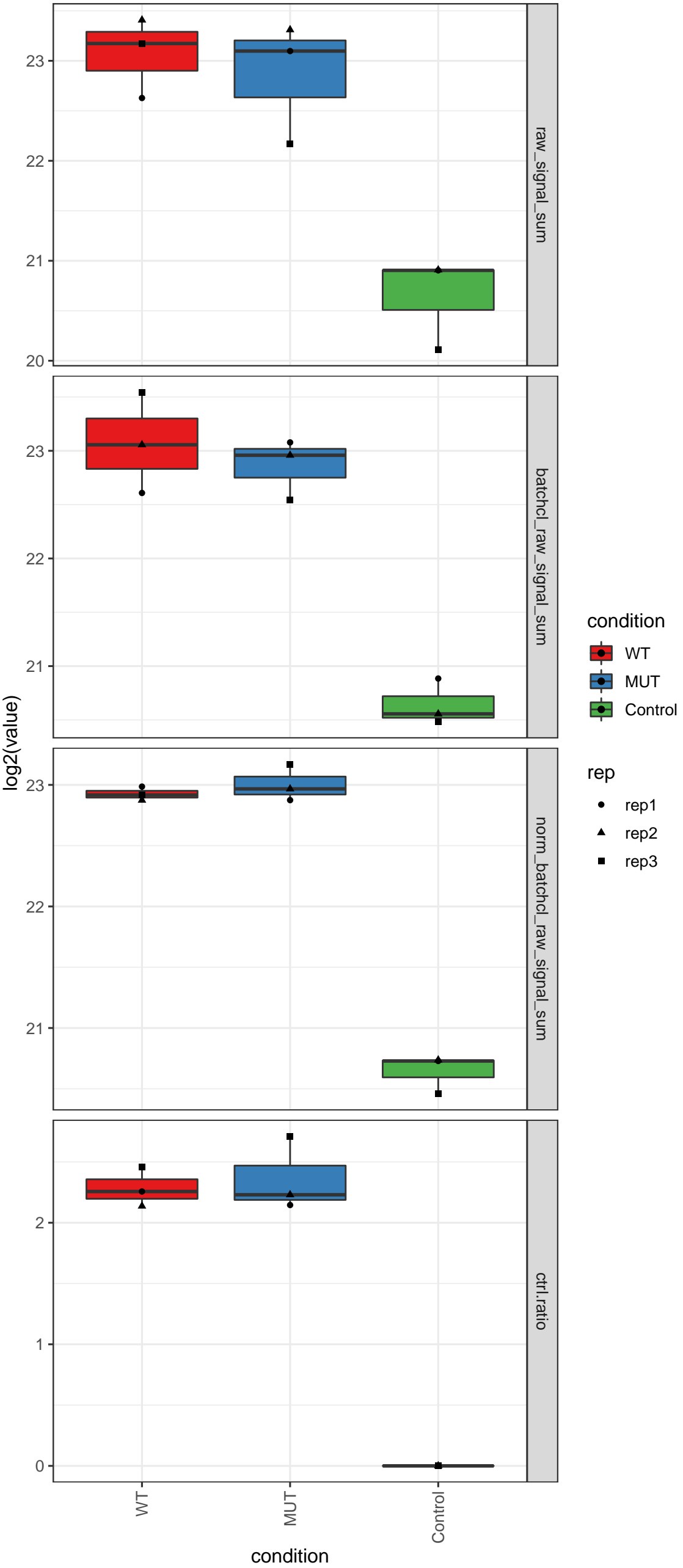
KIN2 – P13186

Serine/threonine–protein kinase KIN2 OS=*Saccharomyces cerevisiae* (stra



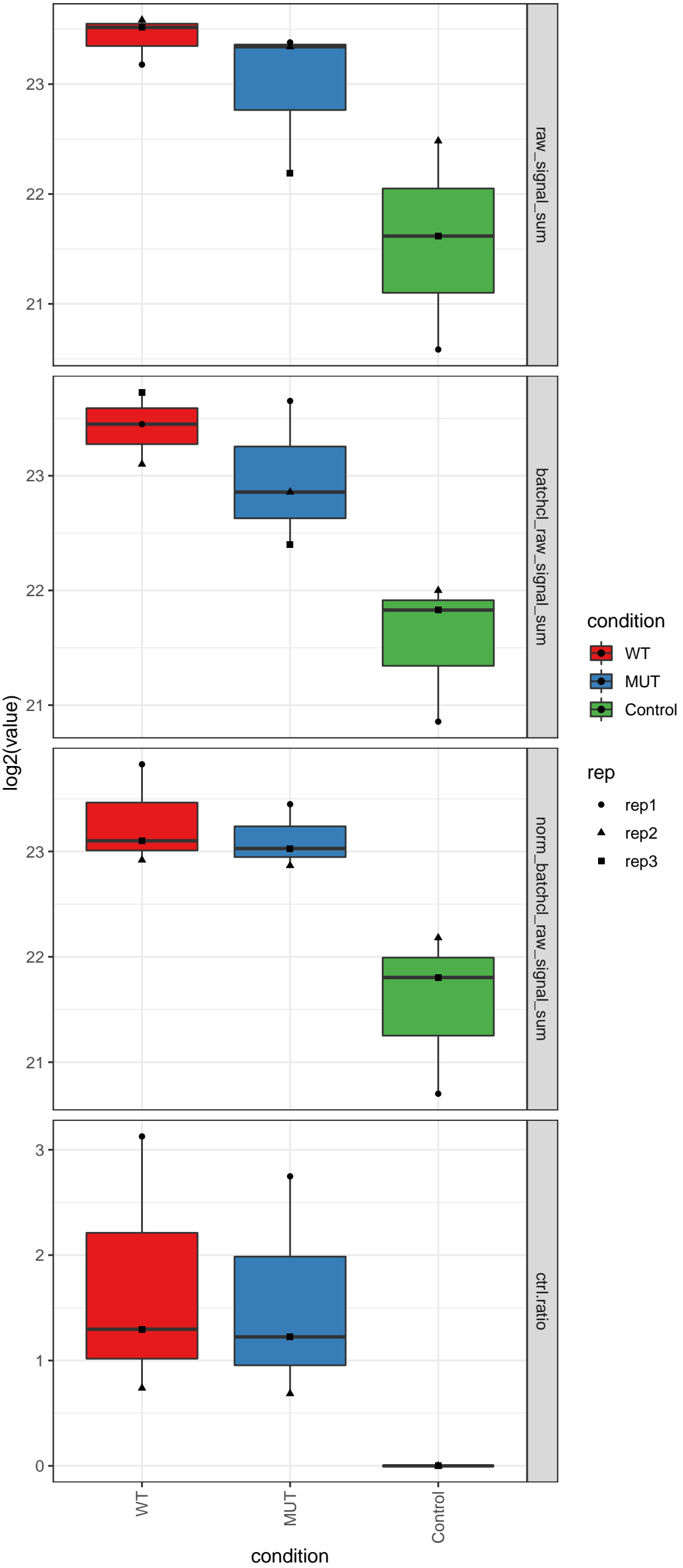
KNS1 – P32350

Dual specificity protein kinase KNS1 OS=*Saccharomyces cerevisiae* (strain



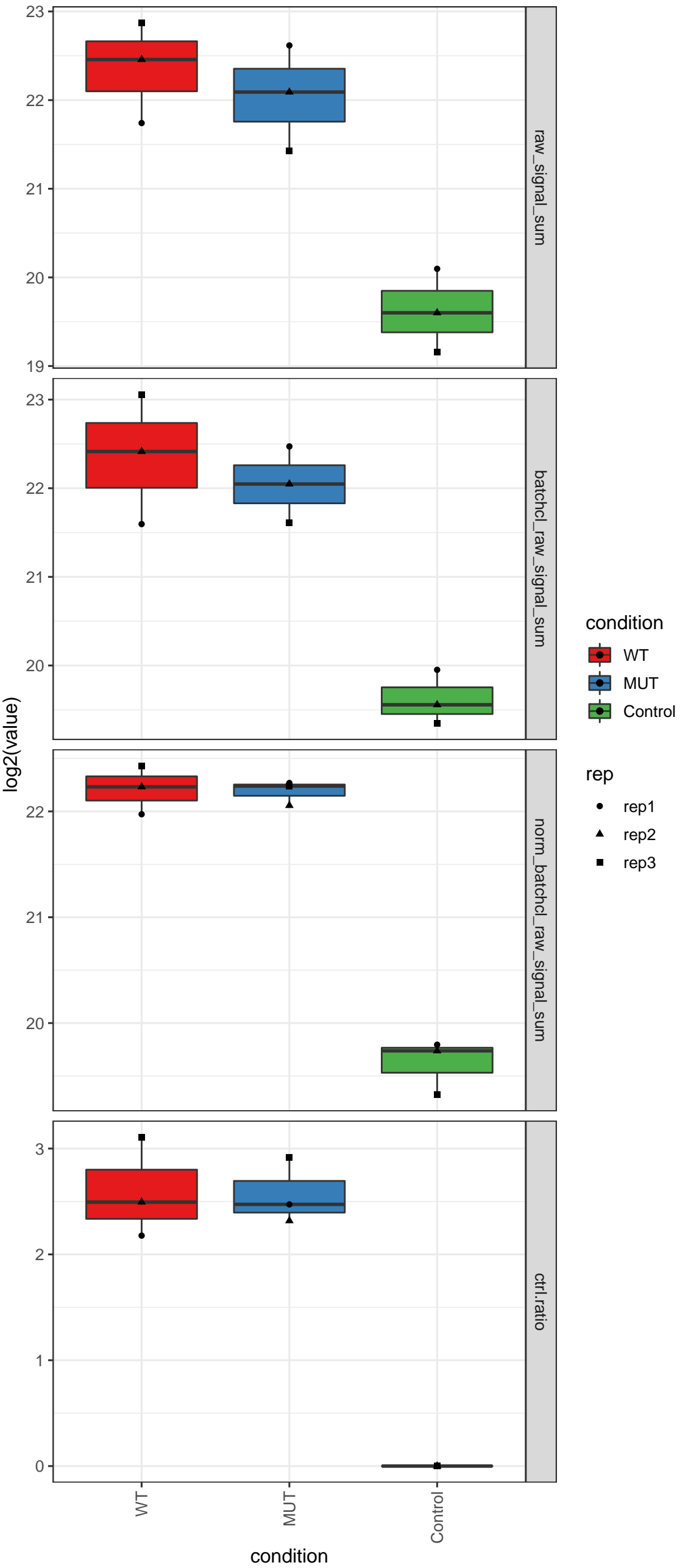
KRS1 – P15180

Lysine--tRNA ligase, cytoplasmic OS=*Saccharomyces cerevisiae* (strain A



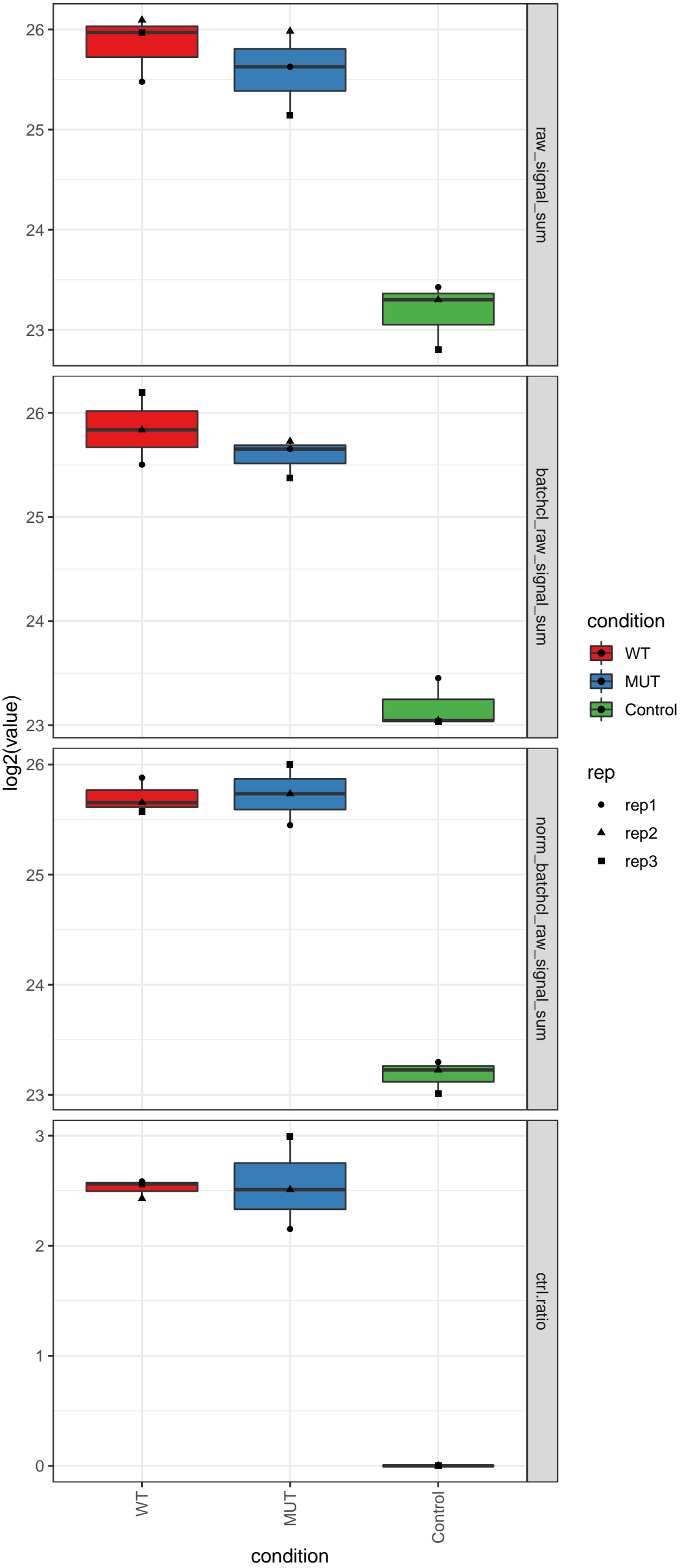
LAP3 – Q01532|Q01532-2

Cysteine proteinase 1, mitochondrial OS=*Saccharomyces cerevisiae* (strain



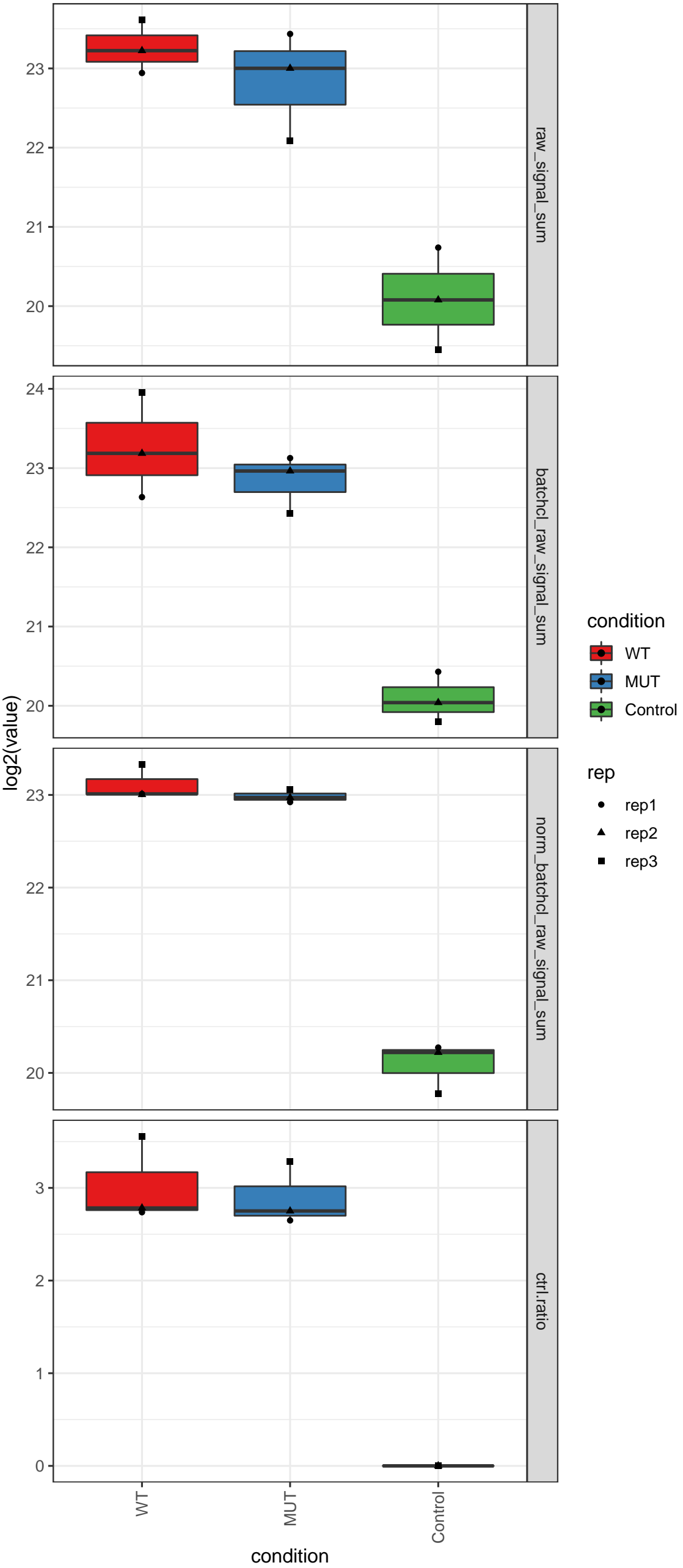
LAT1 – P12695

Dihydrolipoyllysine–residue acetyltransferase component of pyruvate dehydrogenase complex



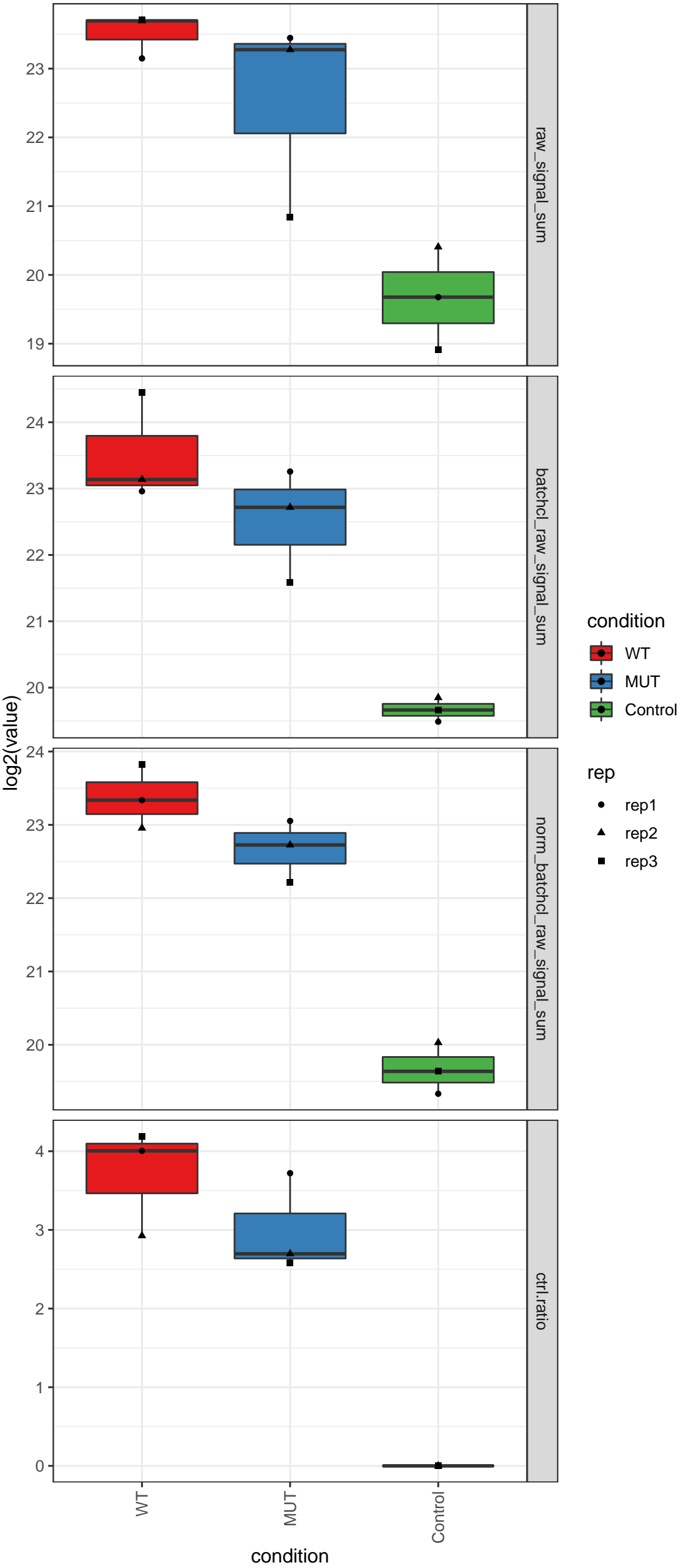
LEU4 – P06208|P06208–2

2-isopropylmalate synthase OS=*Saccharomyces cerevisiae* (strain ATCC 20464)



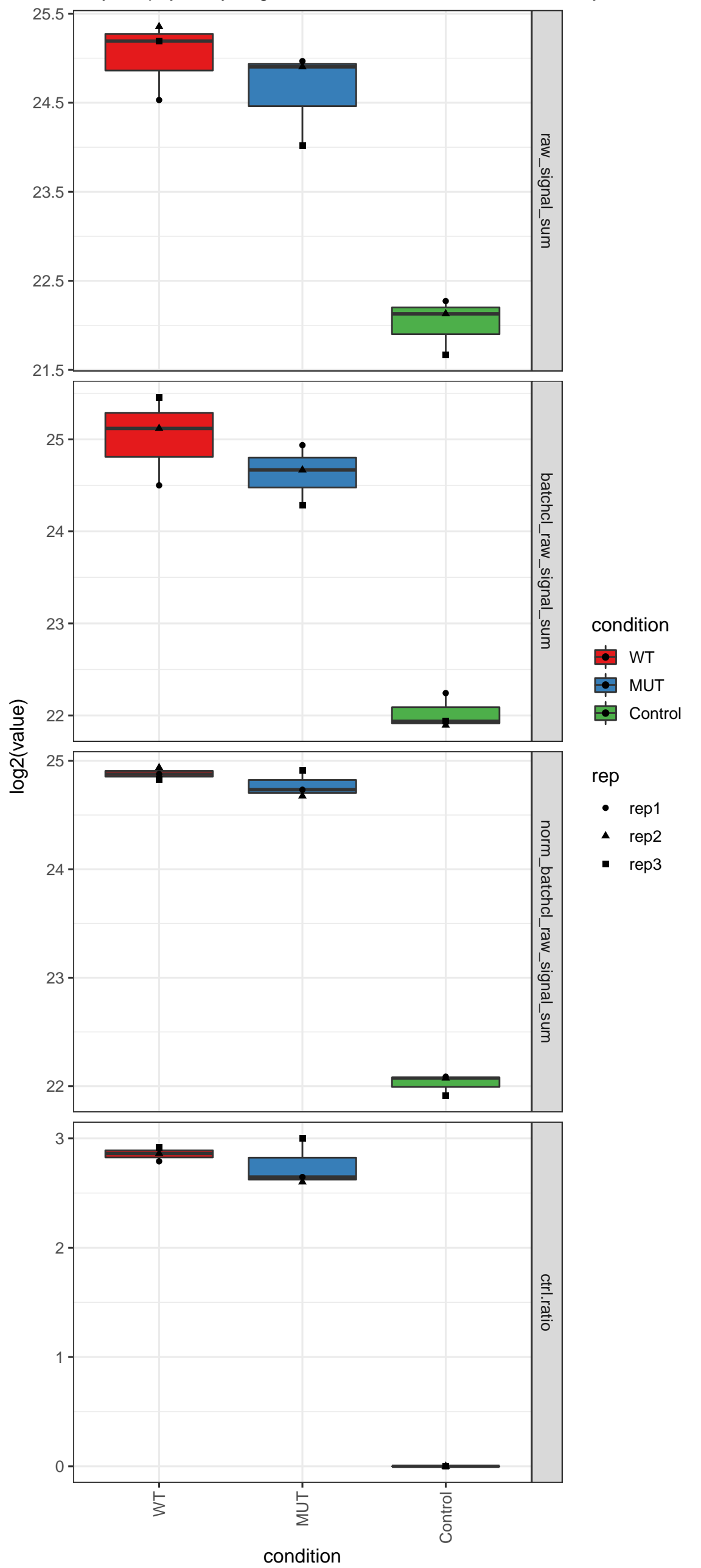
LOC1 – P43586

60S ribosomal subunit assembly/export protein LOC1 OS=Saccharomyces



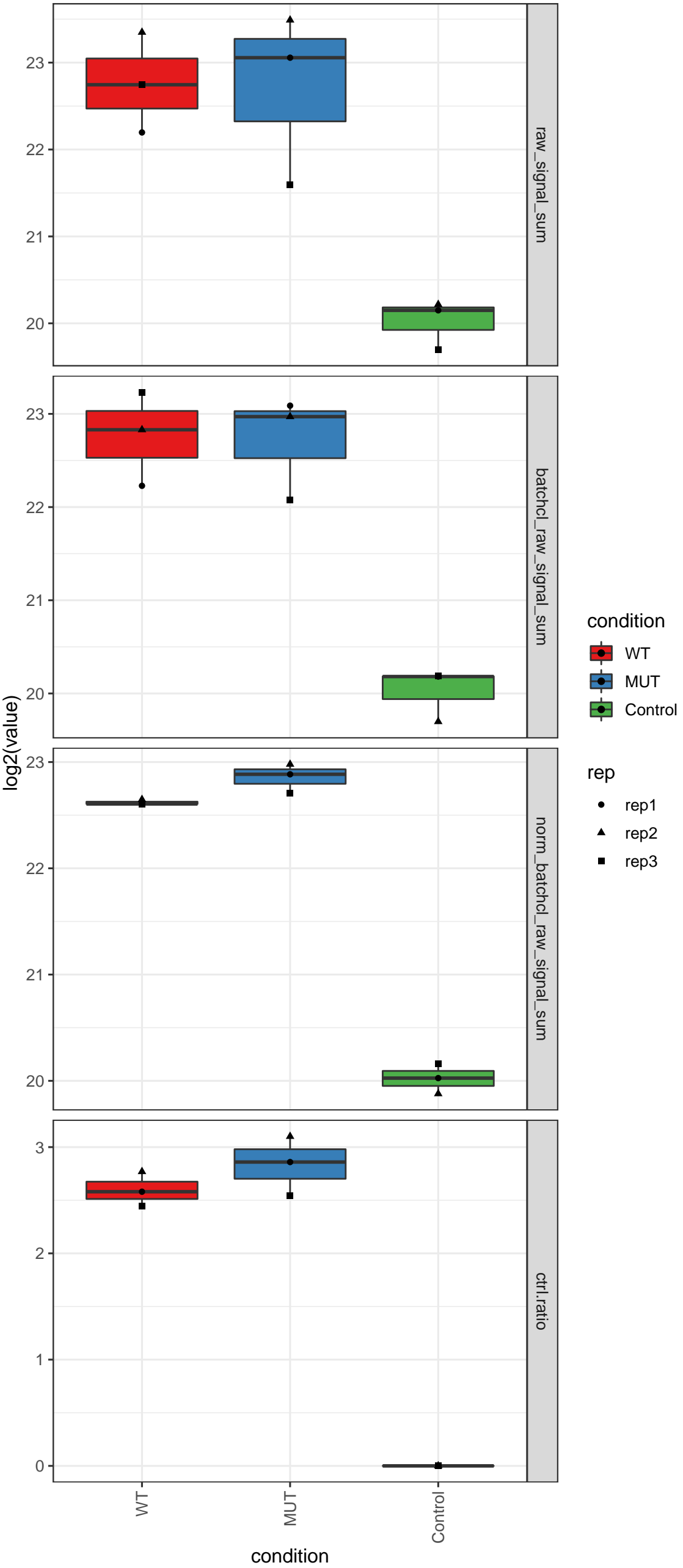
LPD1 – P09624

Dihydrolipoyl dehydrogenase, mitochondrial OS=Saccharomyces cerevisi



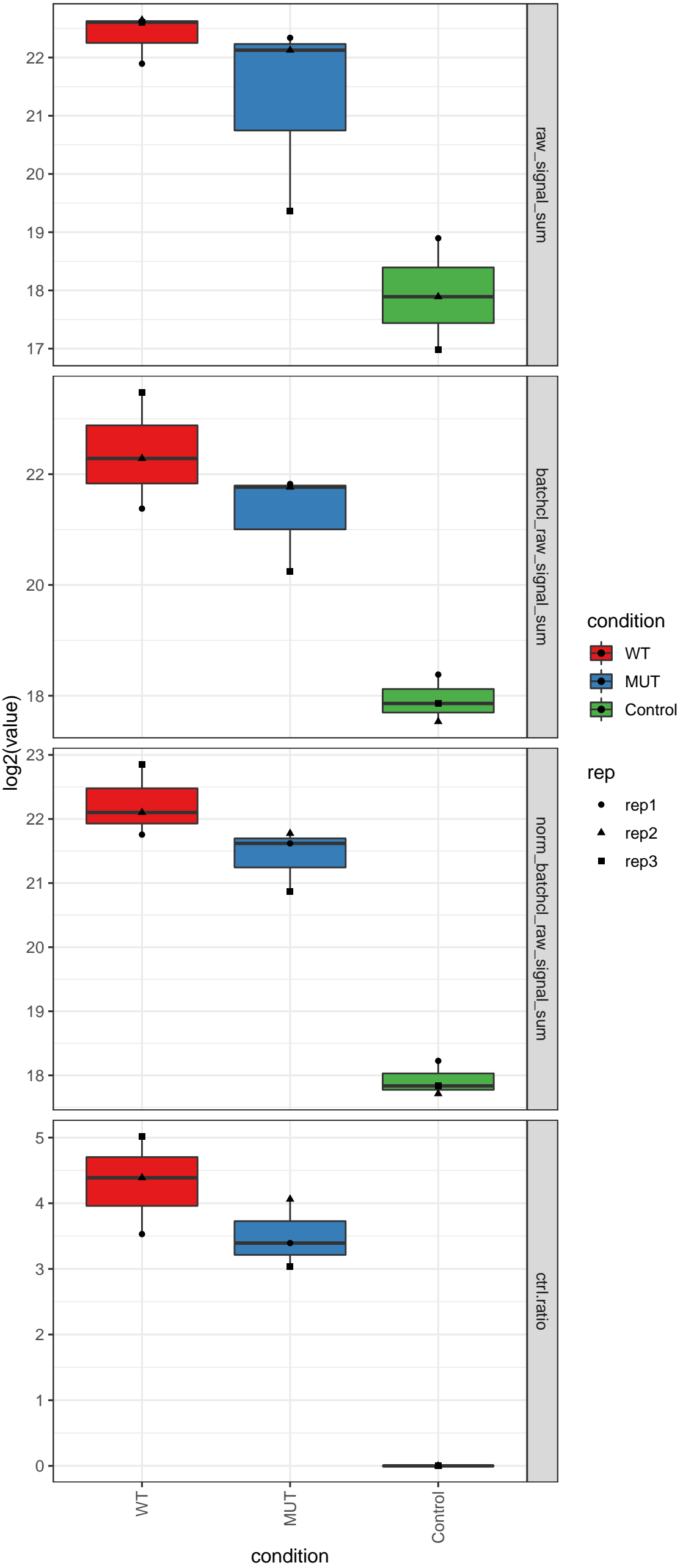
LPX1 – Q12405

Peroxisomal membrane protein LPX1 OS=*Saccharomyces cerevisiae* (strain



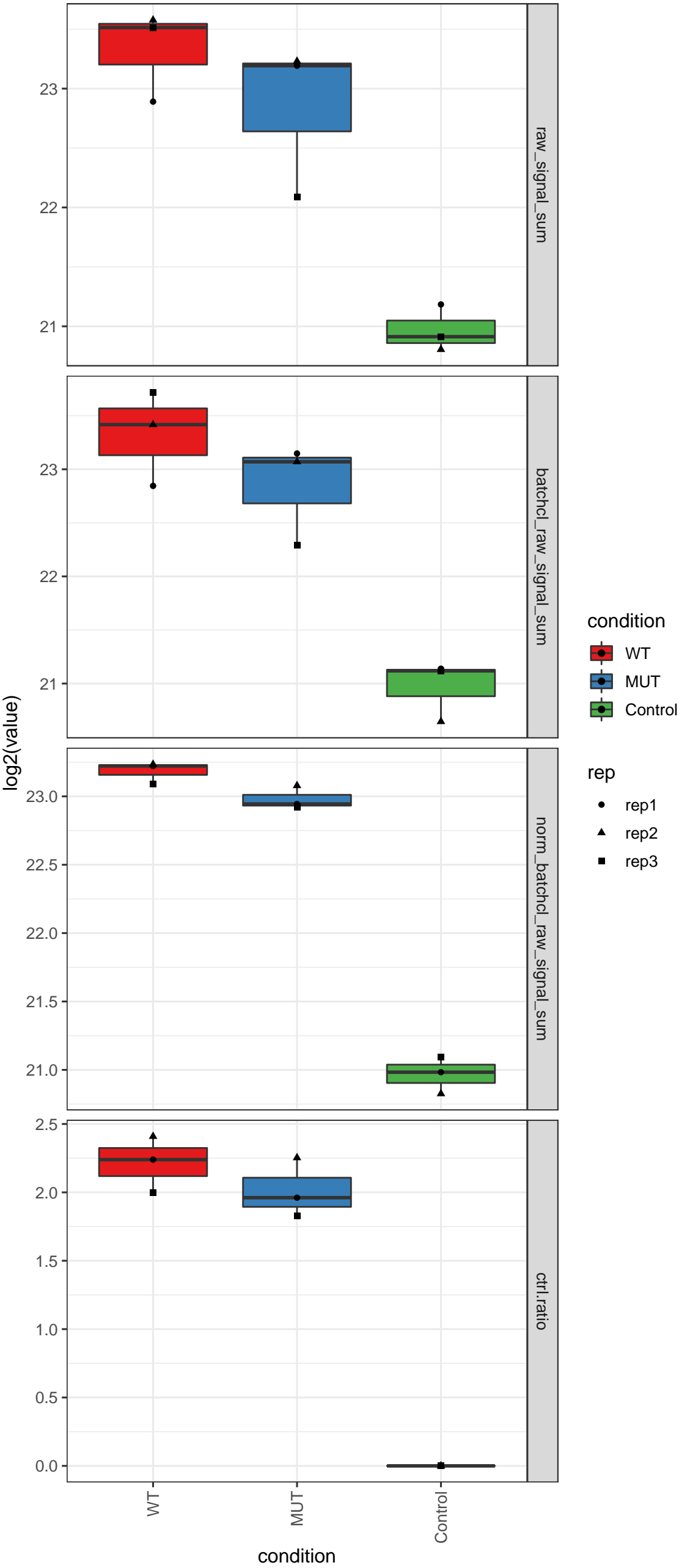
LSB3 – P43603

LAS seventeen-binding protein 3 OS=Saccharomyces cerevisiae (strain ATCC 25716)



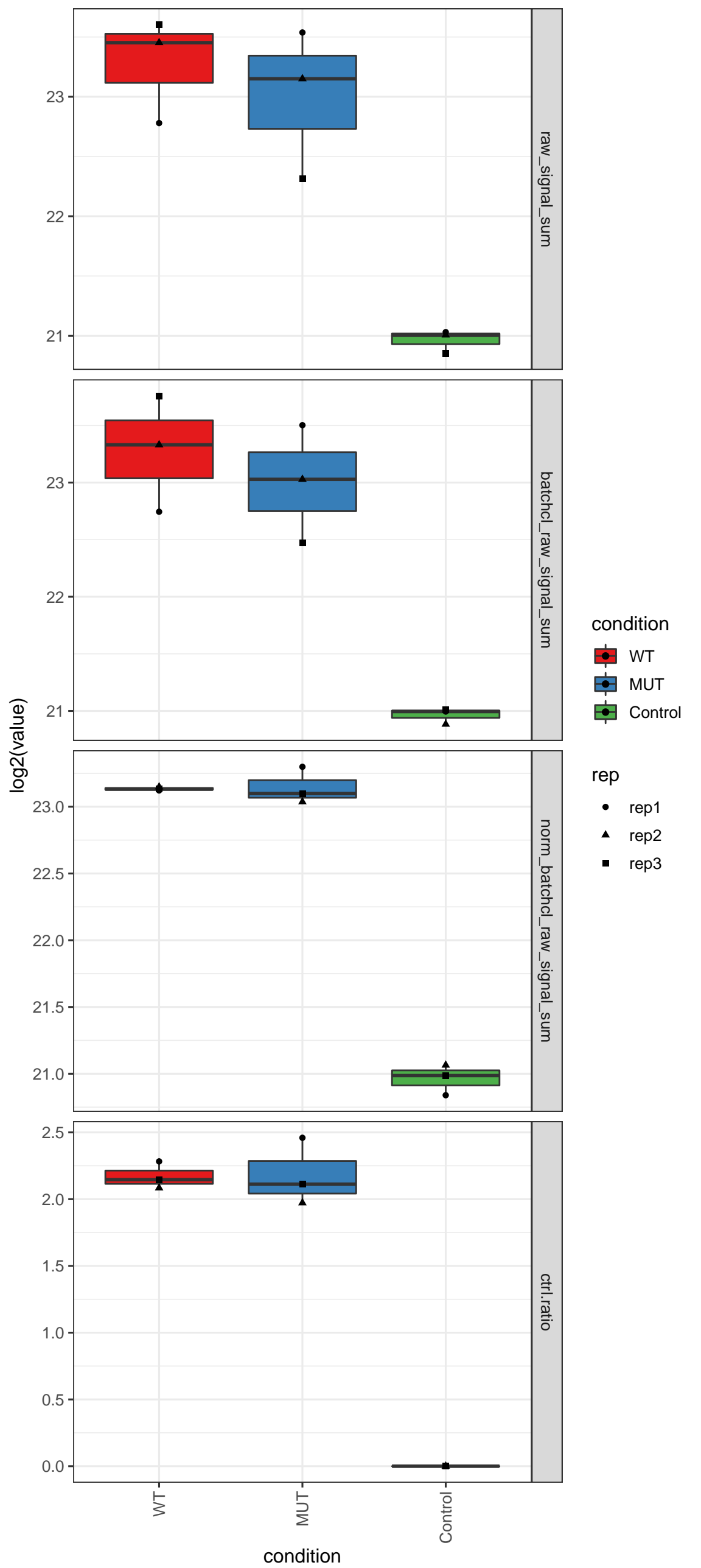
LSC1 – P53598

Succinyl-CoA ligase [ADP-forming] subunit alpha, mitochondrial OS=Sa



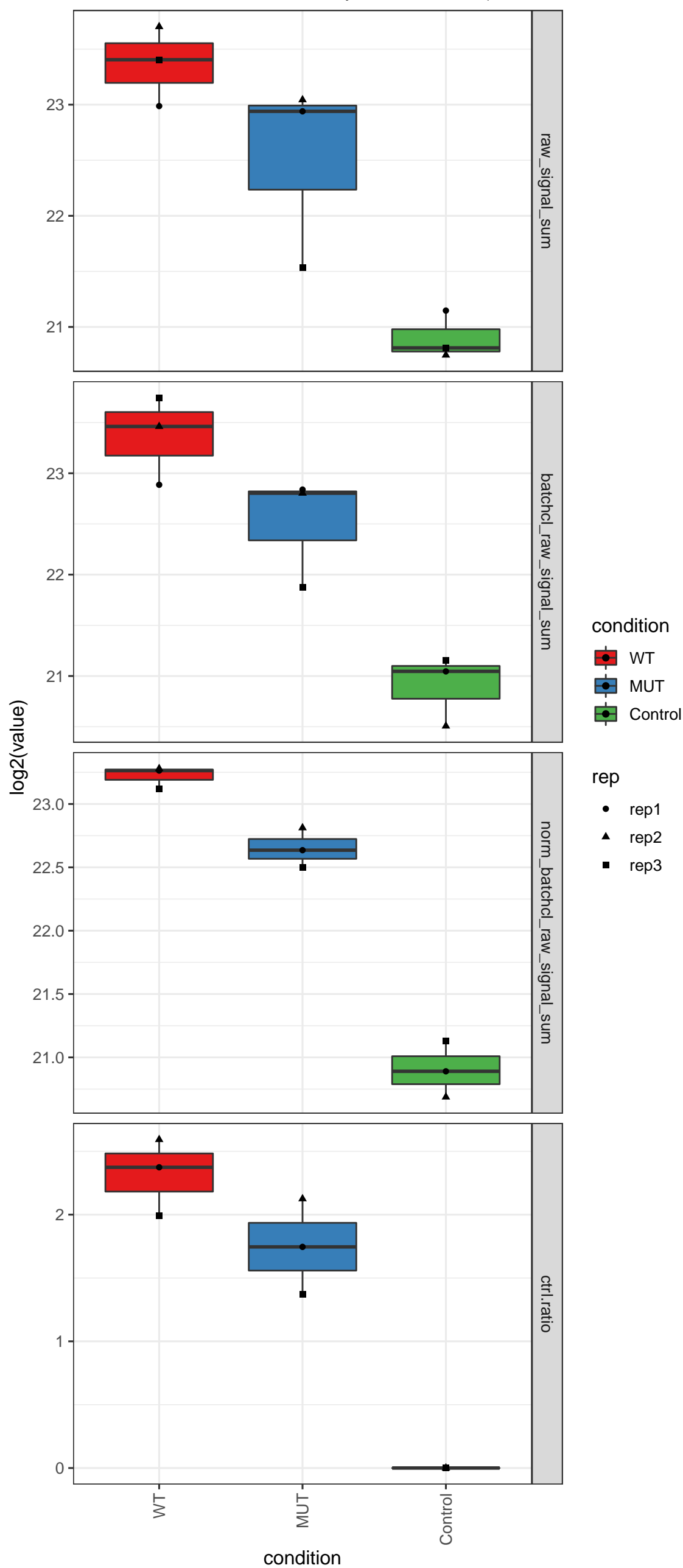
LSC2 – P53312

Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial OS=Sac



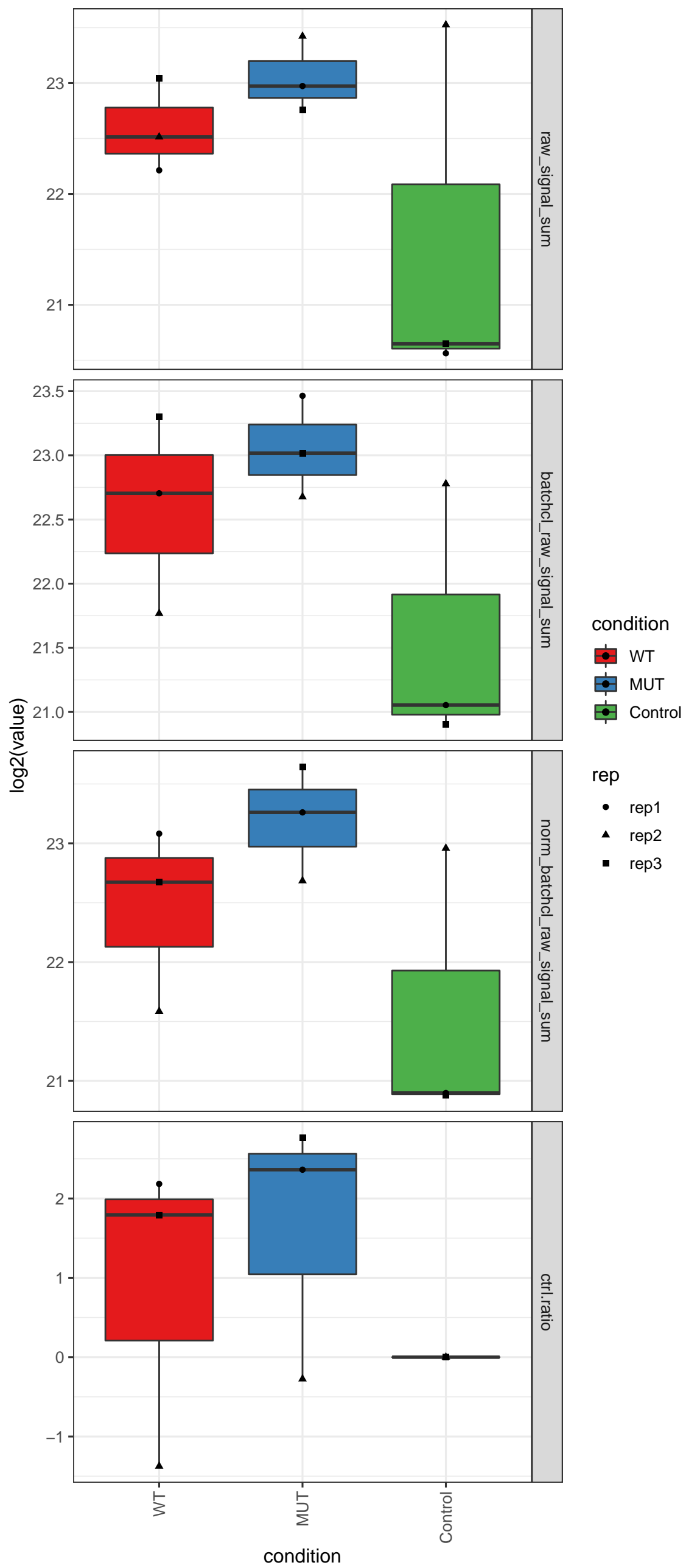
LSM12 – P38828

Protein LSM12 OS=*Saccharomyces cerevisiae* (strain ATCC 204508 / S288c)



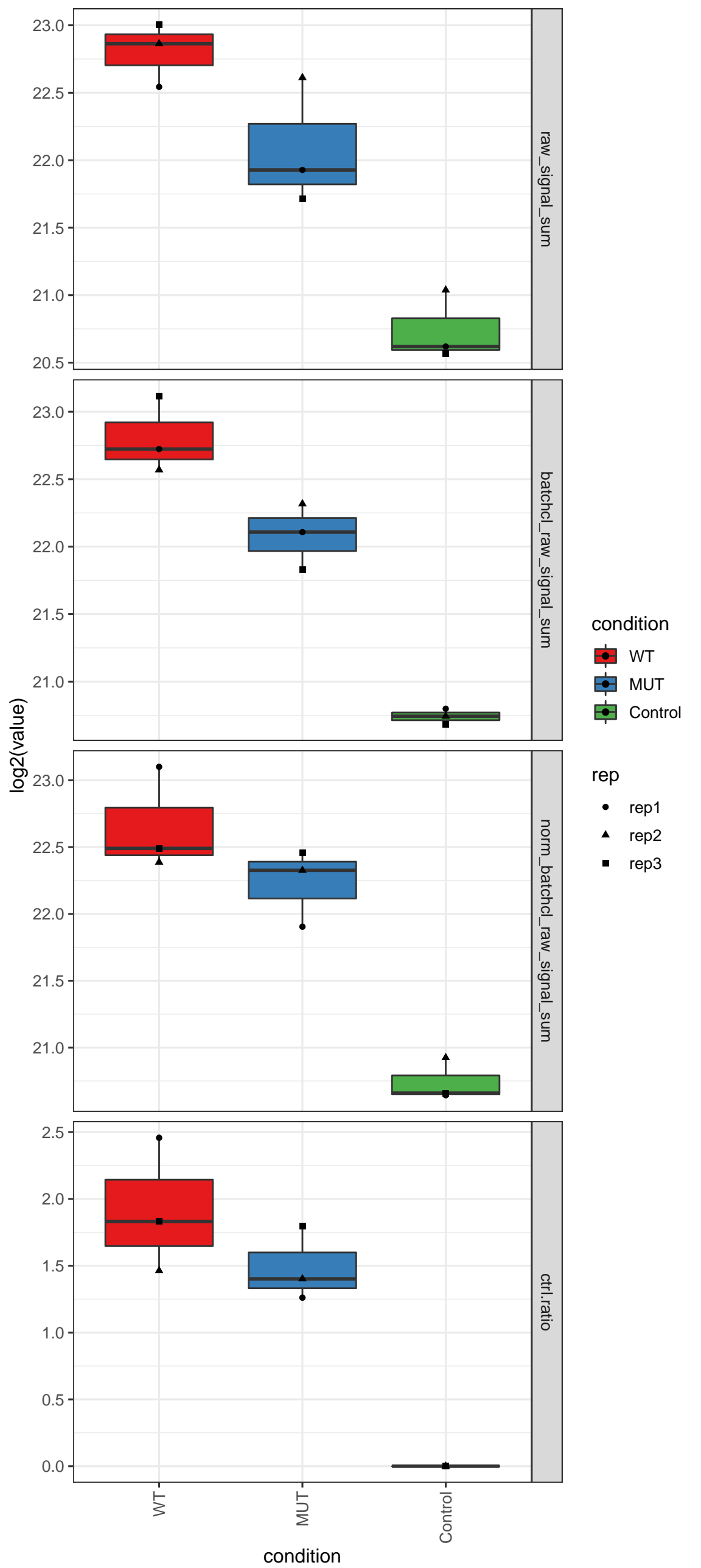
LSP1 – Q12230

Sphingolipid long chain base–responsive protein LSP1 OS=Saccharomyces cerevisiae



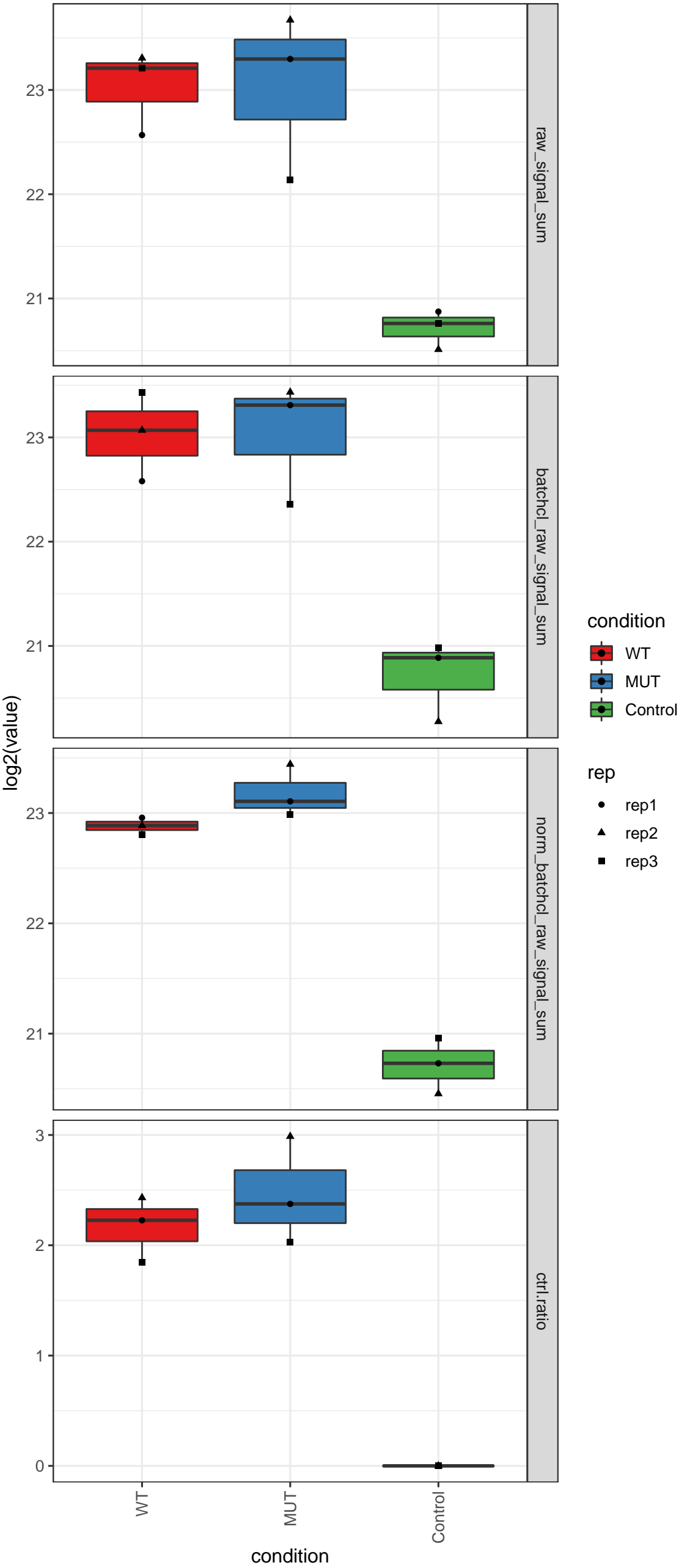
LYS1 – P38998

Saccharopine dehydrogenase [NAD(+), L-lysine-forming] OS=Saccharo



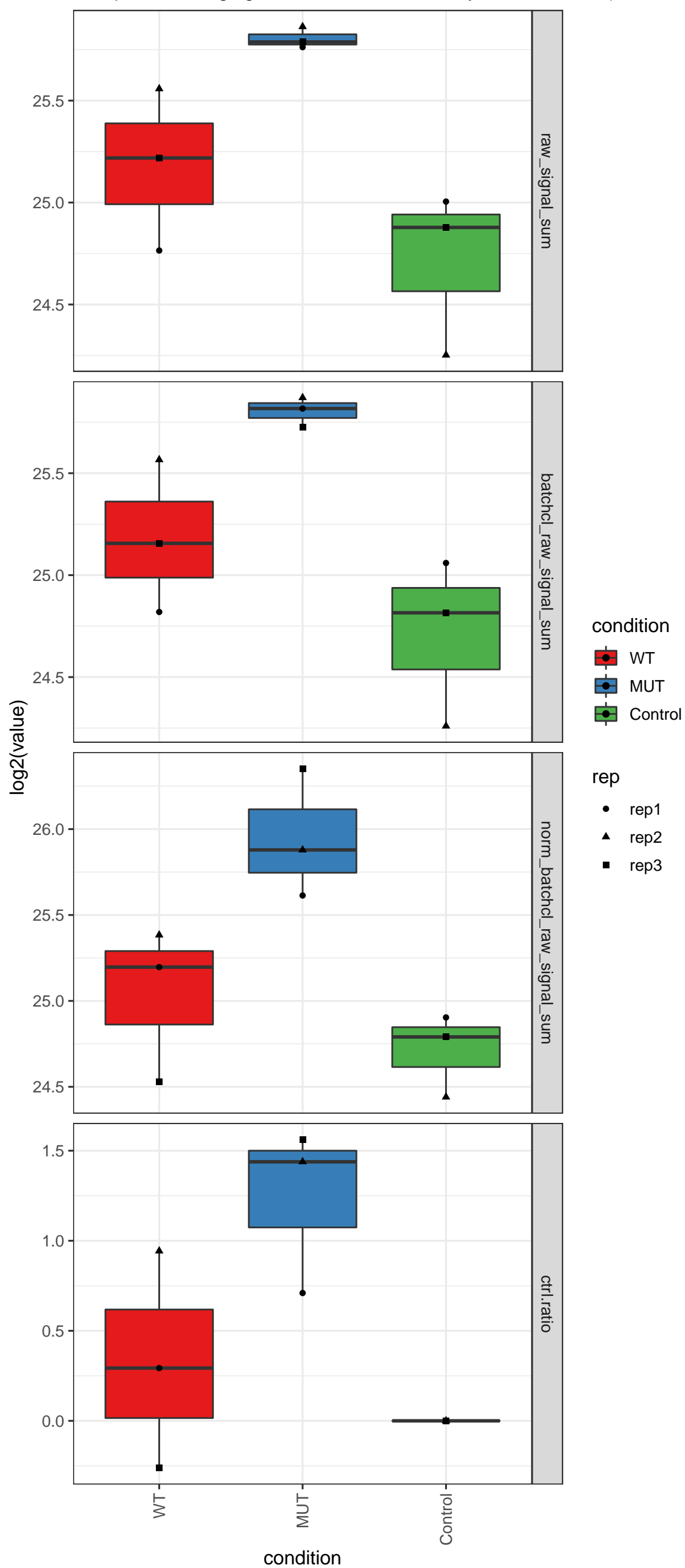
MAK21 – Q12176

Ribosome biogenesis protein MAK21 OS=*Saccharomyces cerevisiae* (strain



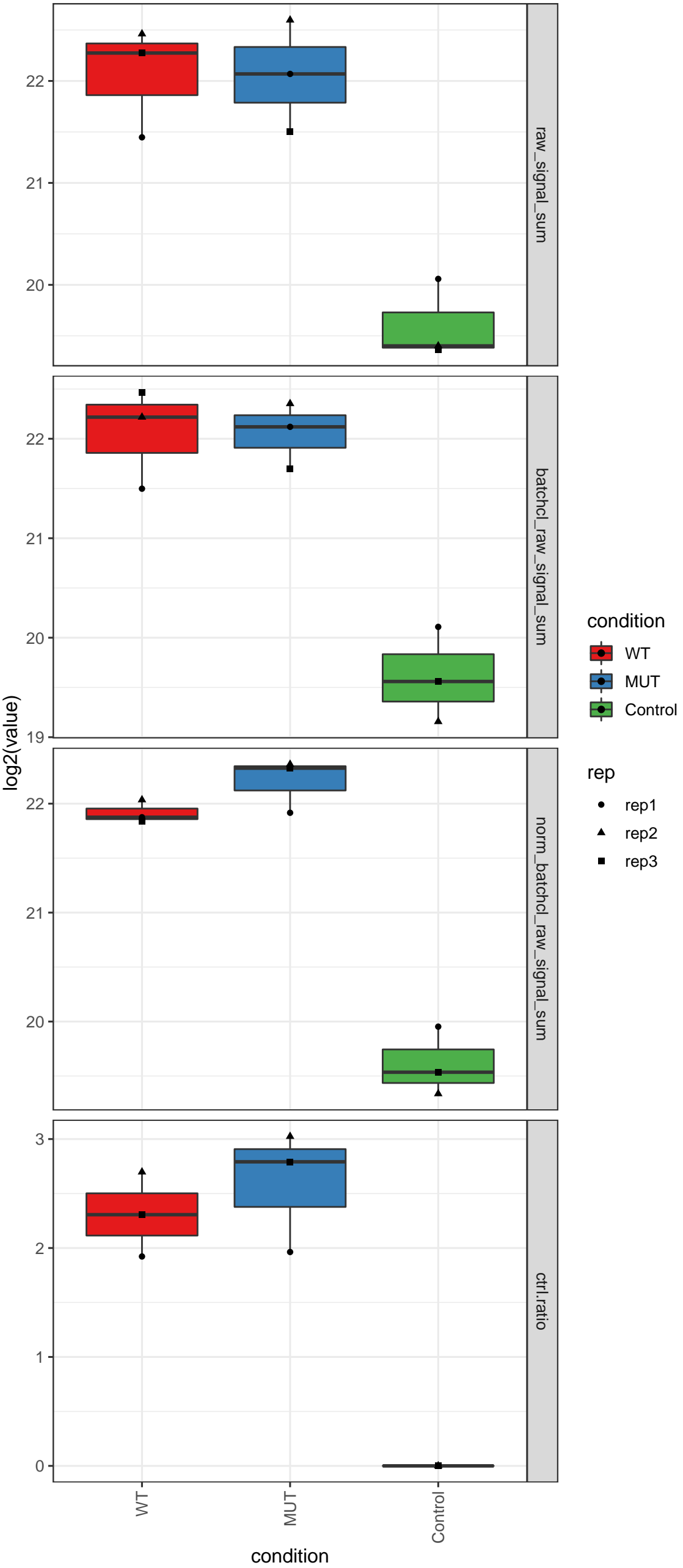
MBF1 – O14467

Multiprotein-bridging factor 1 OS=*Saccharomyces cerevisiae* (strain ATC



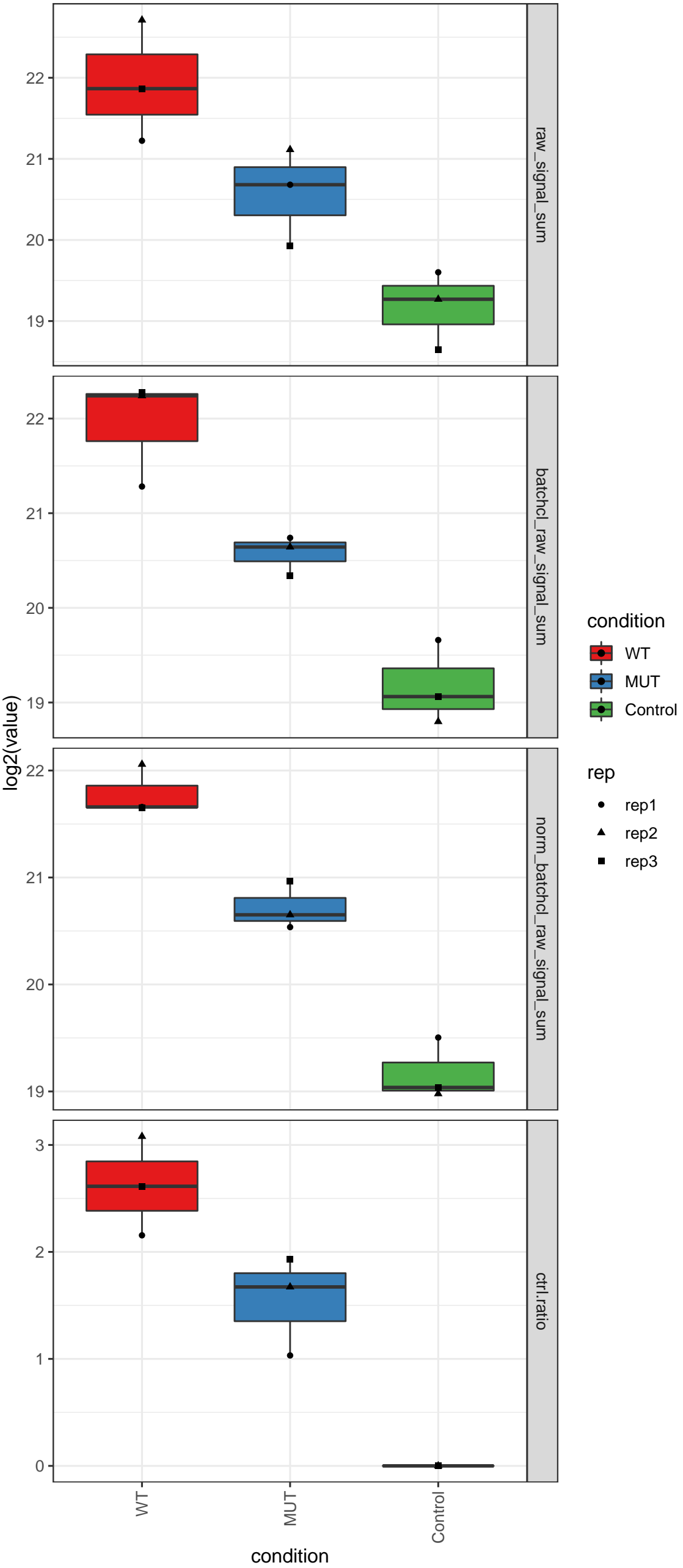
MCK1 – P21965

Protein kinase MCK1 OS=*Saccharomyces cerevisiae* (strain ATCC 204508)



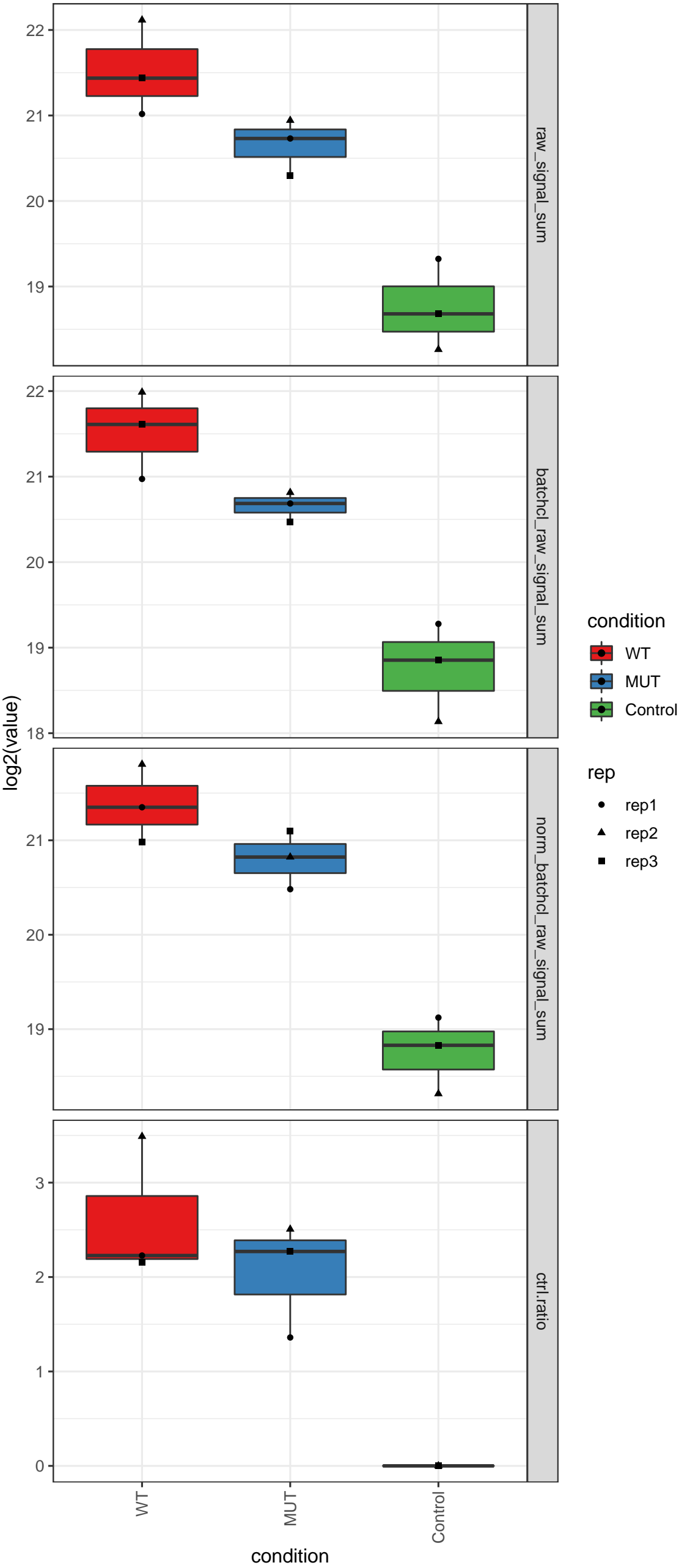
MCM3 – P24279

DNA replication licensing factor MCM3 OS=*Saccharomyces cerevisiae* (str



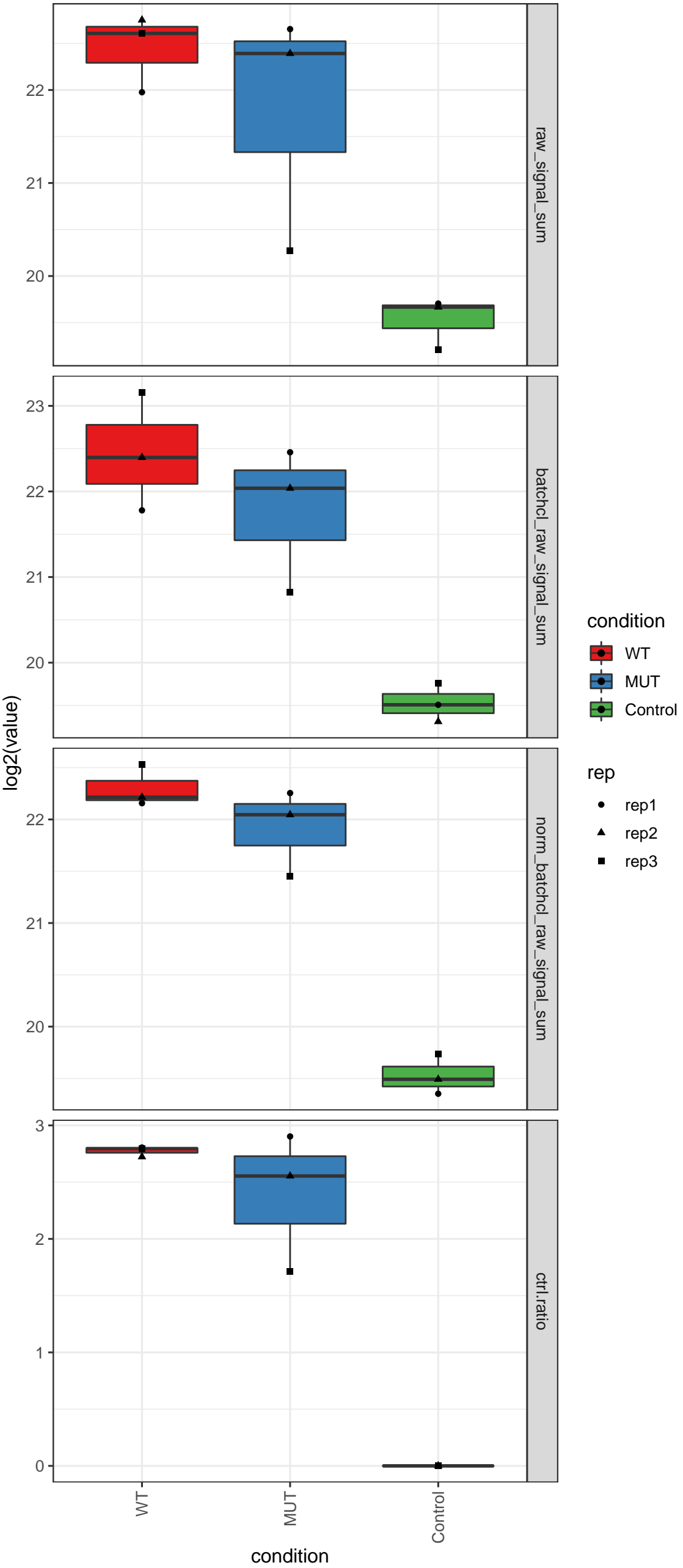
MCM4 – P30665

DNA replication licensing factor MCM4 OS=*Saccharomyces cerevisiae* (str



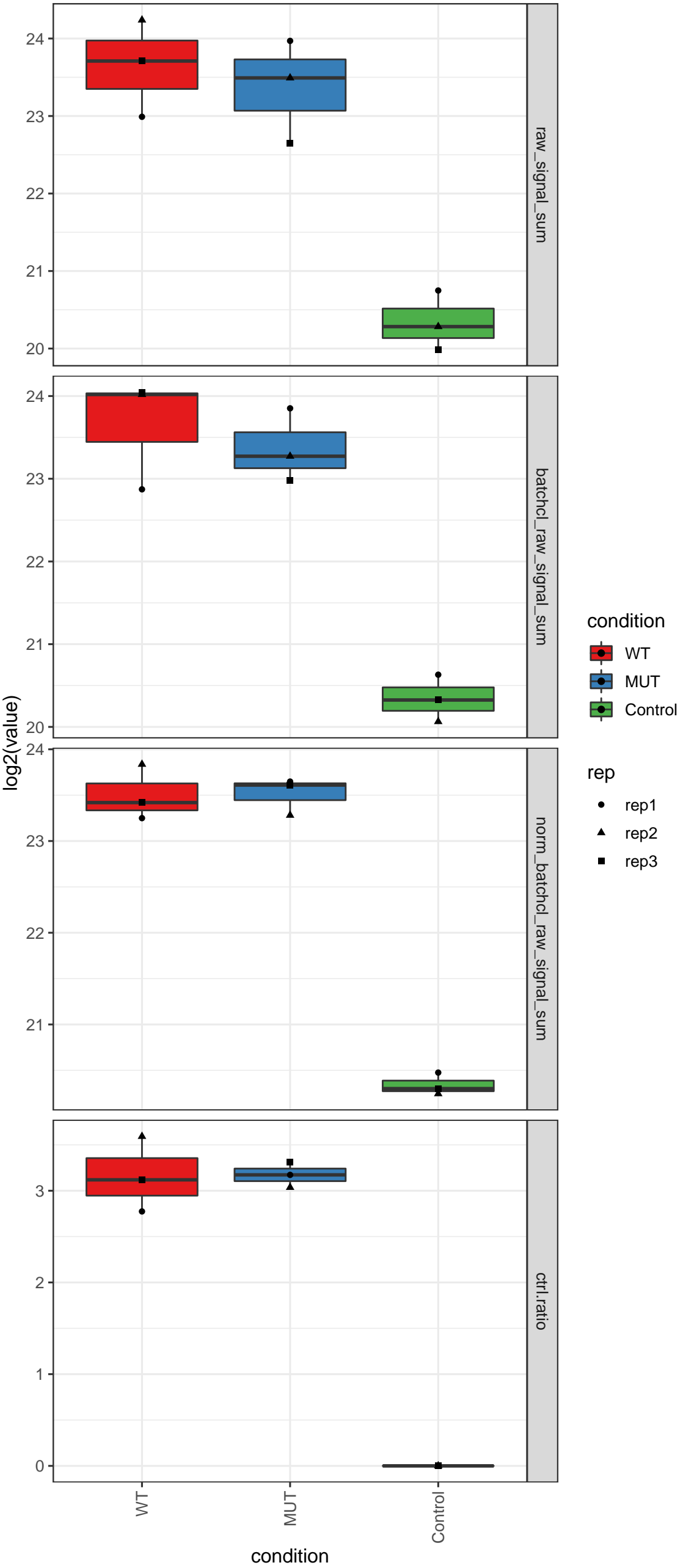
MDG1 – P53885

Signal transduction protein MDG1 OS=*Saccharomyces cerevisiae* (strain A



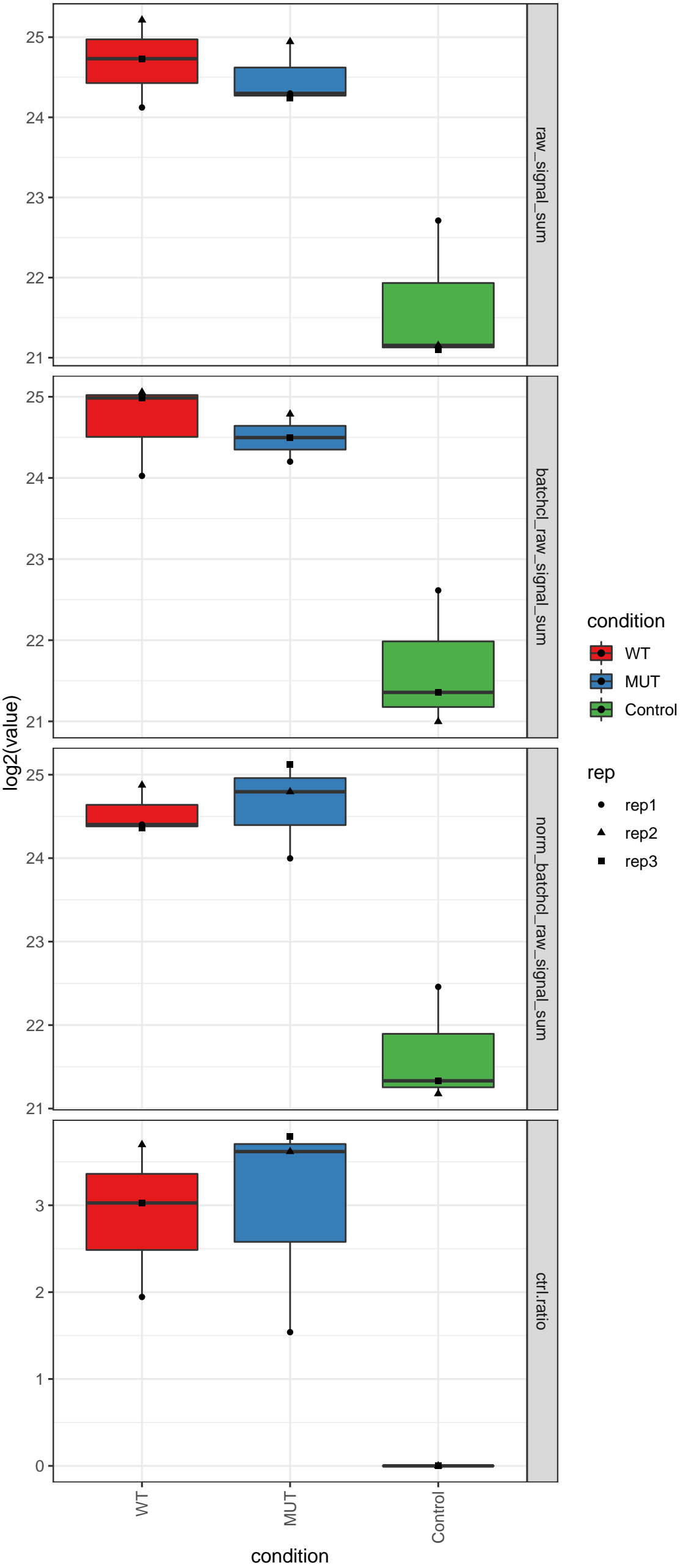
MDH2 – P22133

Malate dehydrogenase, cytoplasmic OS=*Saccharomyces cerevisiae* (strain



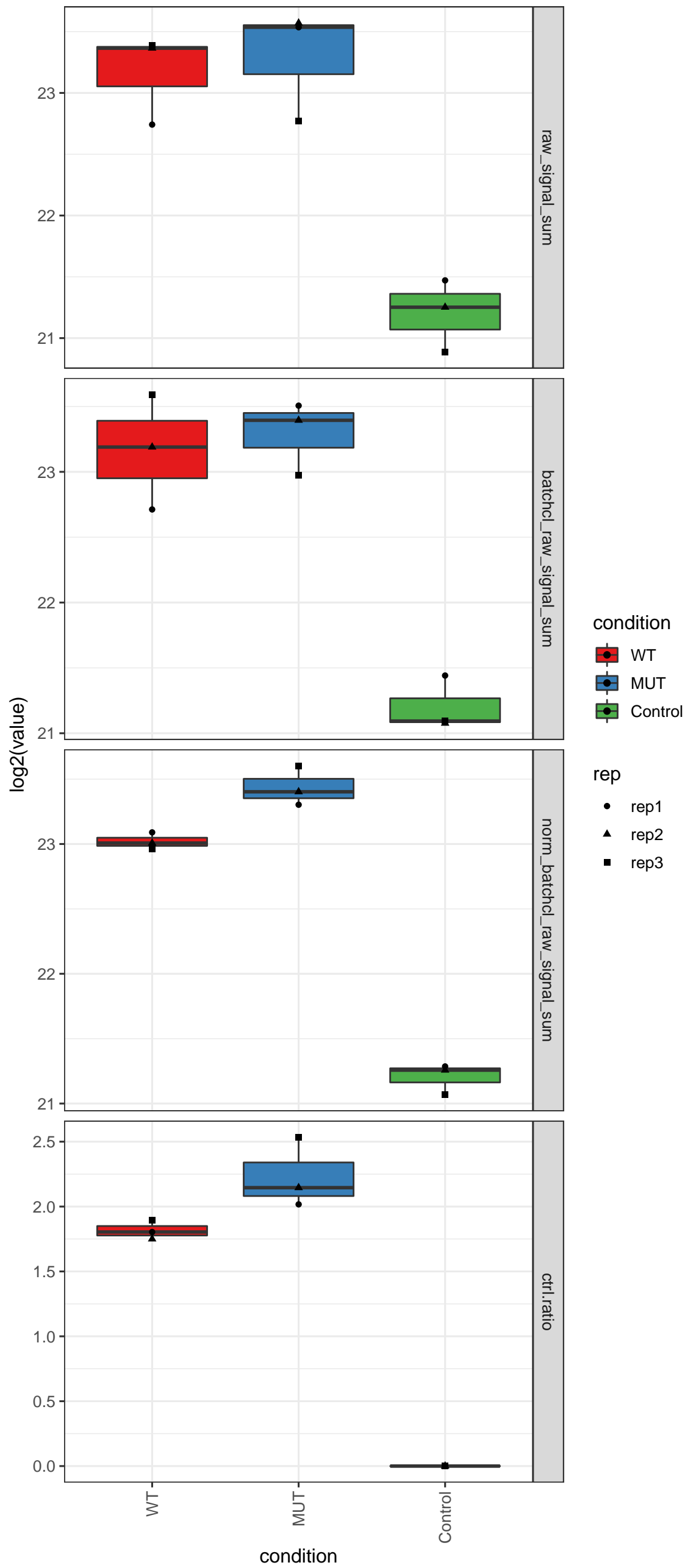
MDH3 – P32419

Malate dehydrogenase, peroxisomal OS=*Saccharomyces cerevisiae* (strain



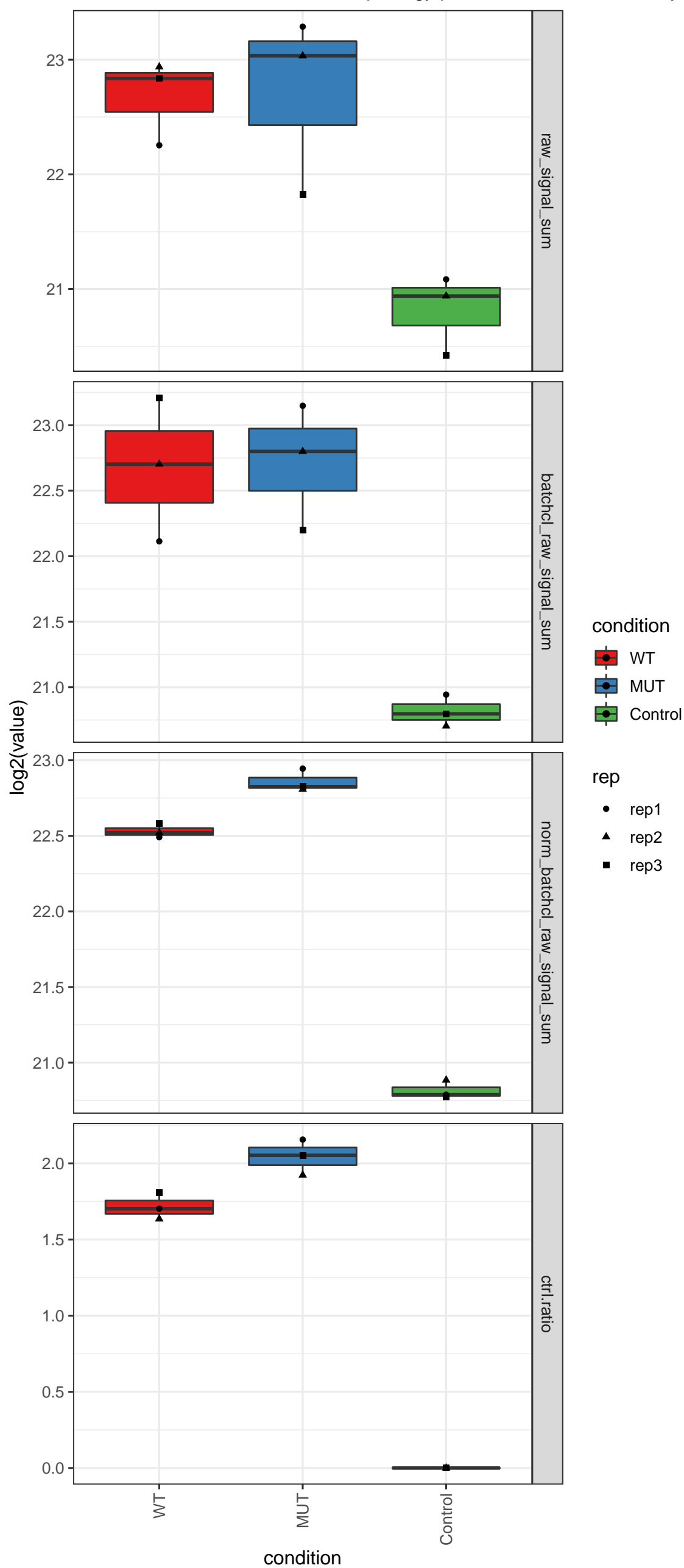
MDJ1 – P35191

DnaJ homolog 1, mitochondrial OS=*Saccharomyces cerevisiae* (strain ATCC 22016 / DSM 5780 / EC 1116)



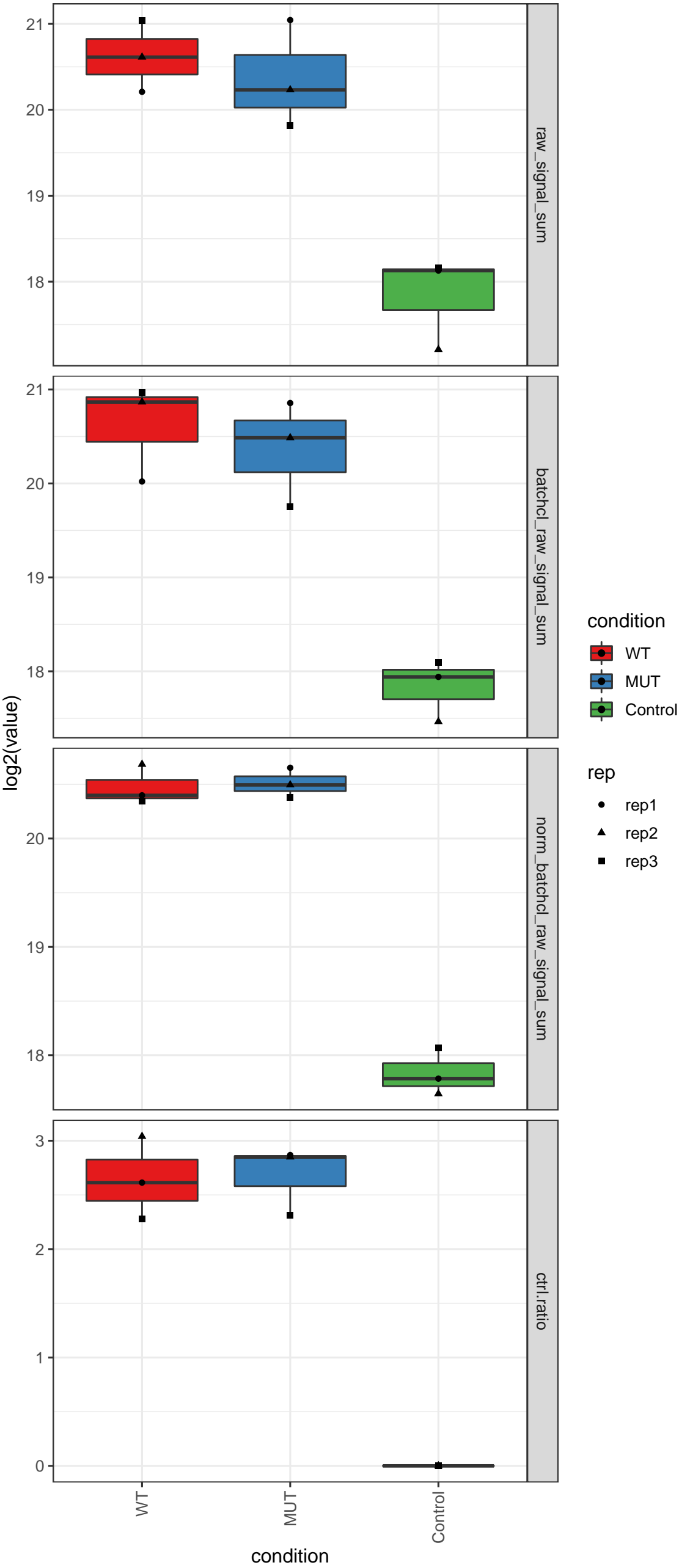
MDM38 – Q08179

Mitochondrial distribution and morphology protein 38 OS=Saccharomyce



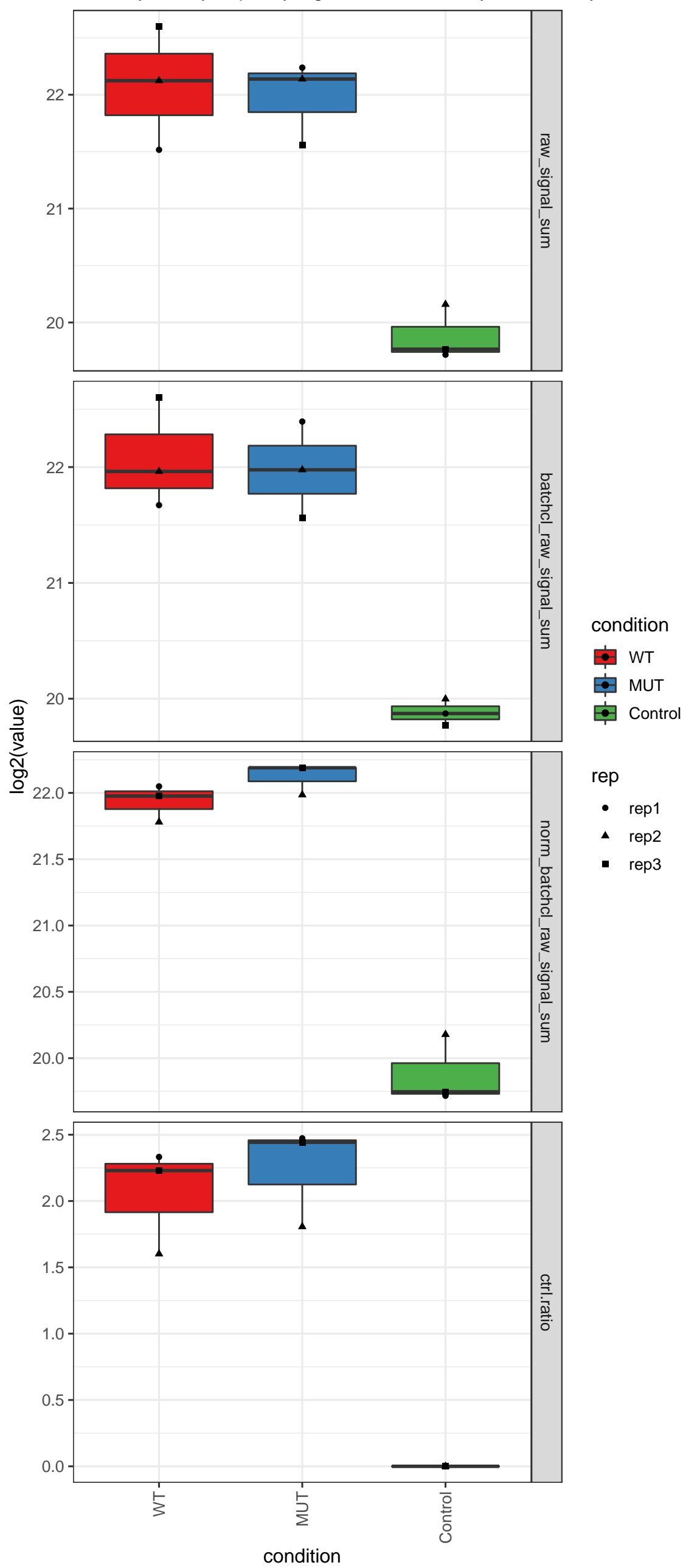
MET17 – P06106

Homocysteine/cysteine synthase OS=*Saccharomyces cerevisiae* (strain ATCC 25465)



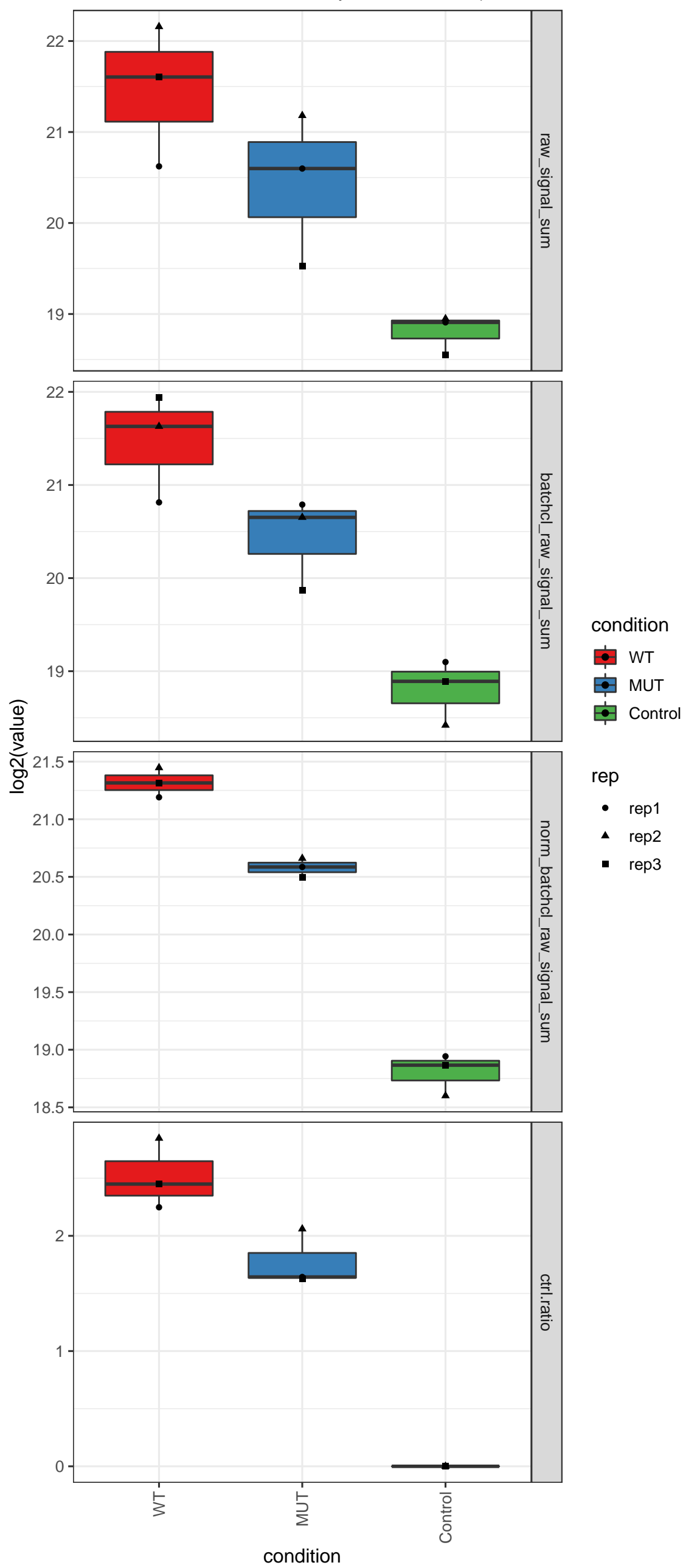
MET6 – P05694

5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase



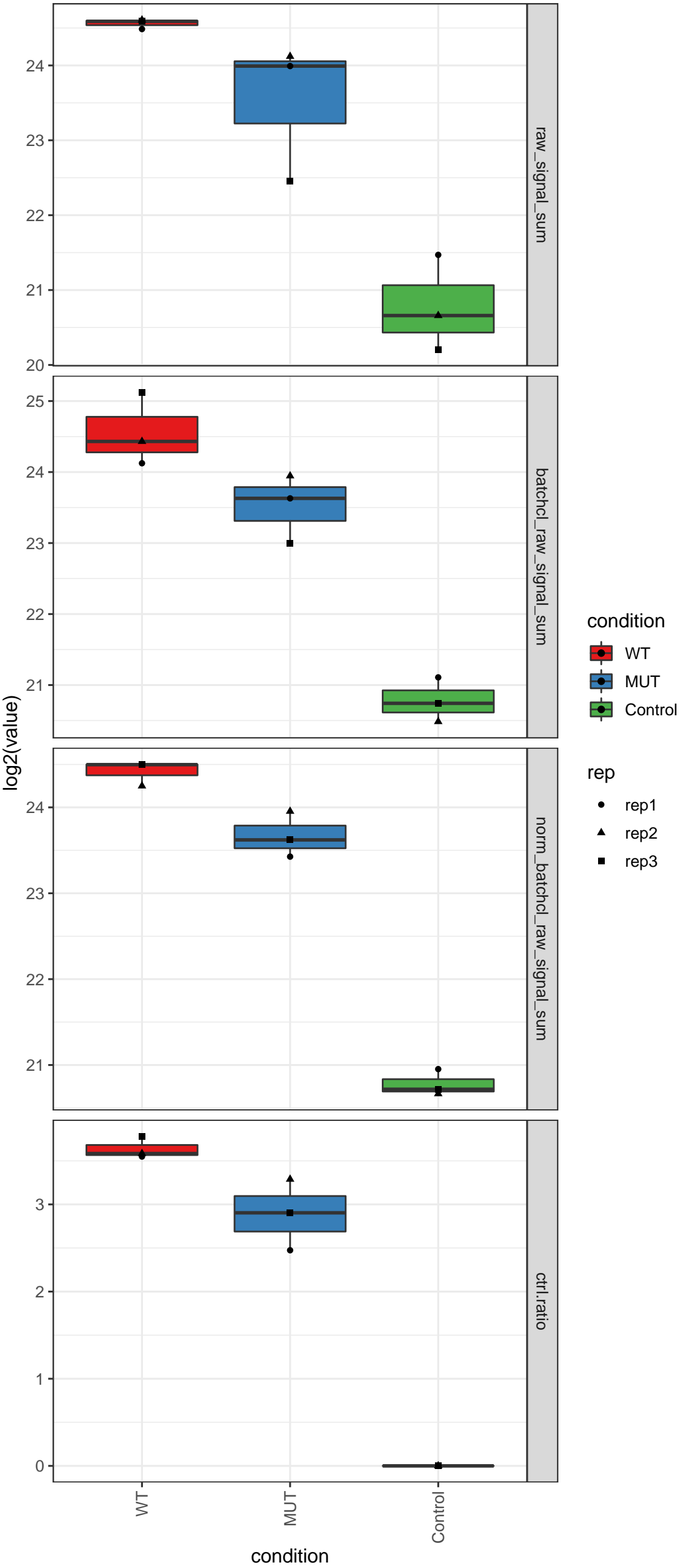
MGA2 – P40578

Protein MGA2 OS=*Saccharomyces cerevisiae* (strain ATCC 204508 / S288c)



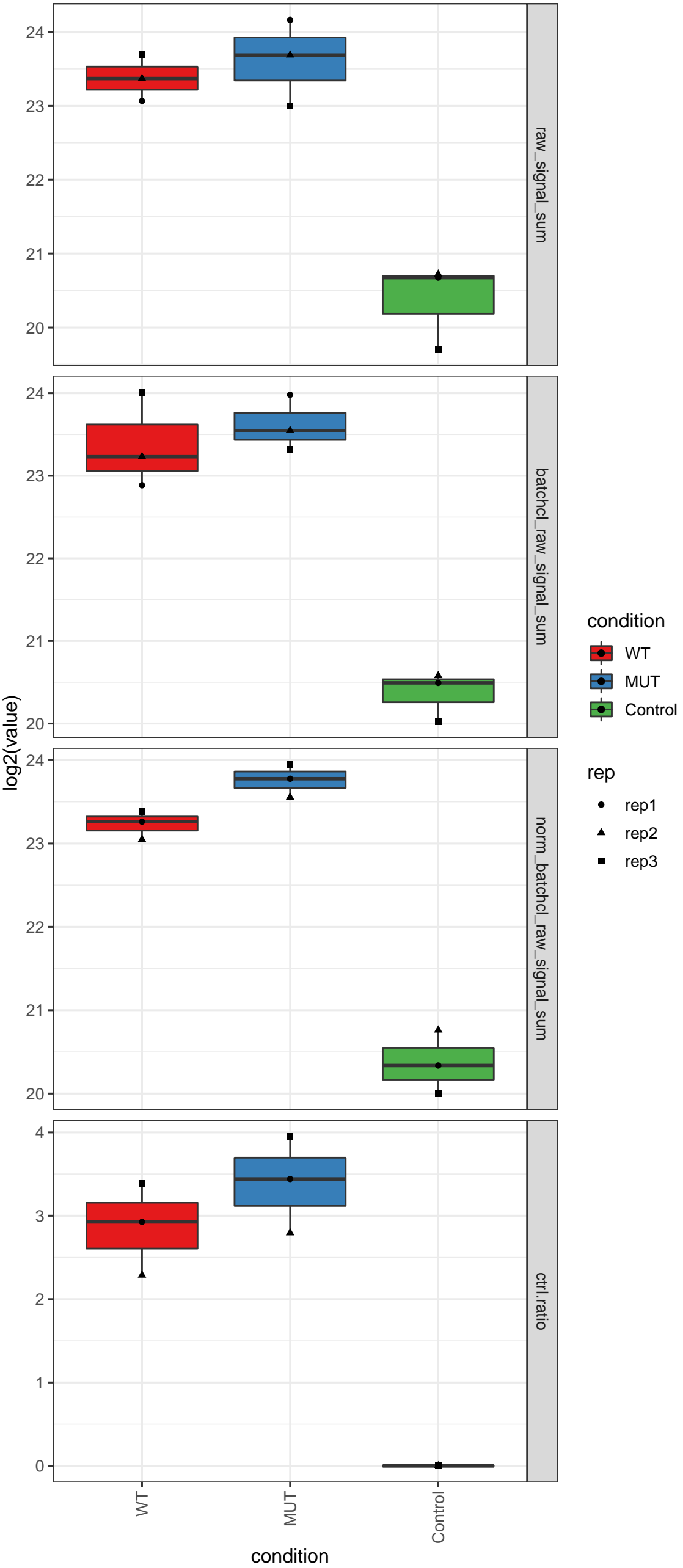
MGM101 – P32787

Mitochondrial genome maintenance protein MGM101 OS=Saccharomyces



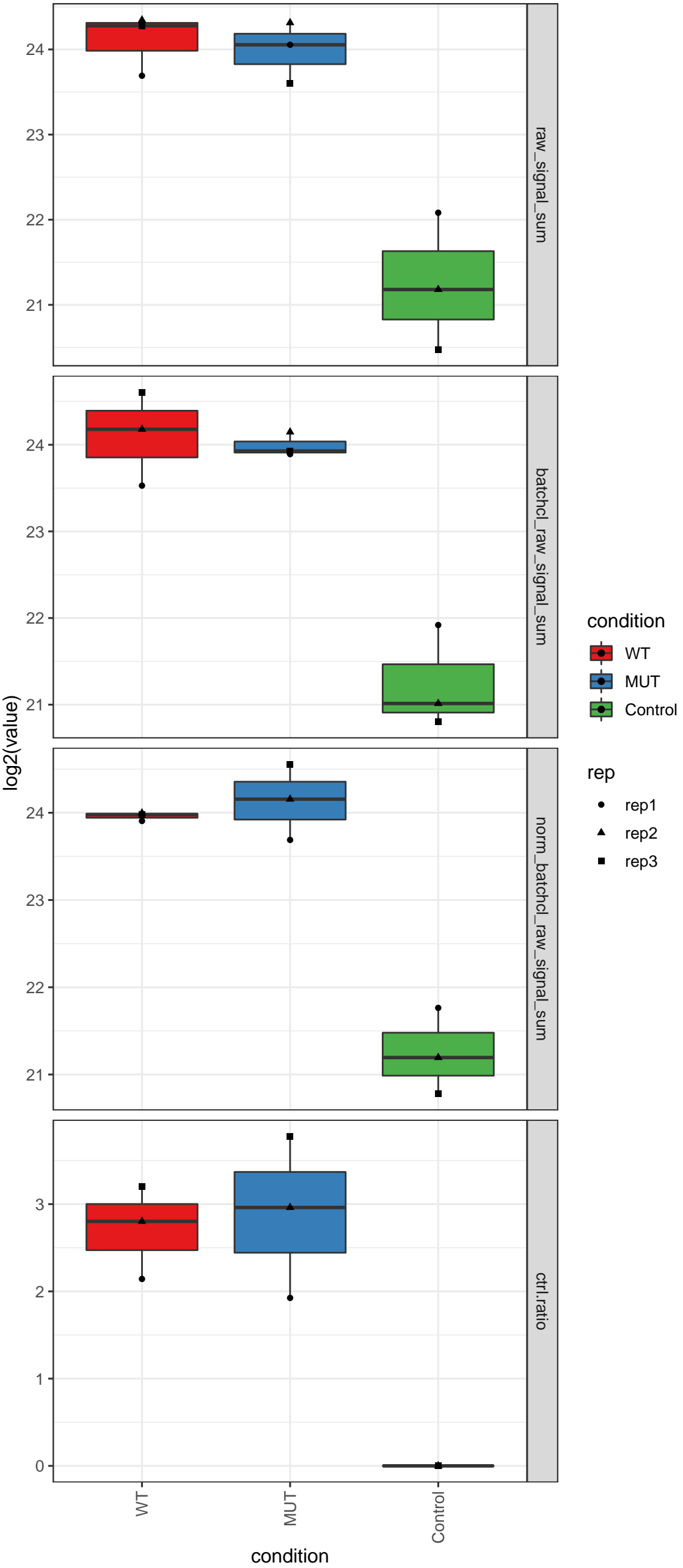
MIR1 – P23641

Mitochondrial phosphate carrier protein OS=Saccharomyces cerevisiae (st



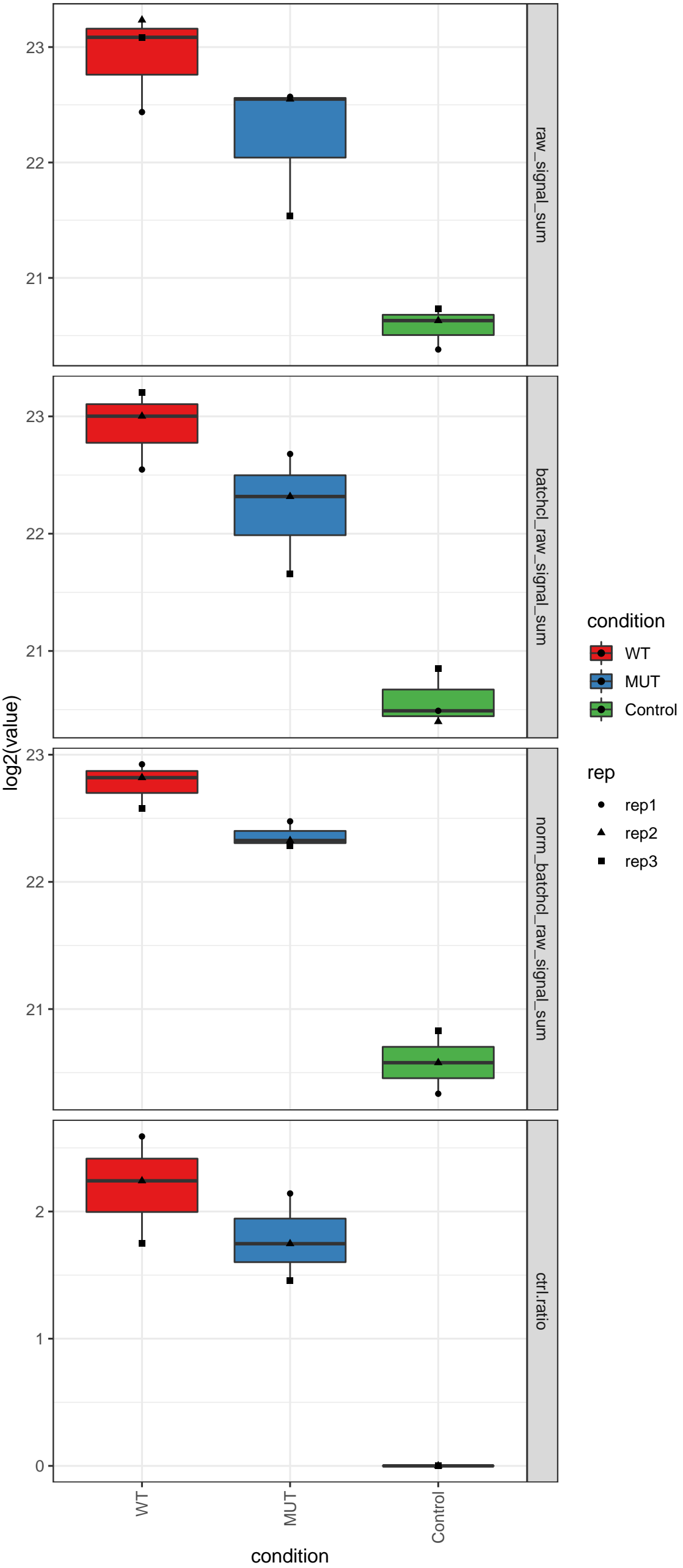
MIS1 – P09440

C-1-tetrahydrofolate synthase, mitochondrial OS=Saccharomyces cerevis



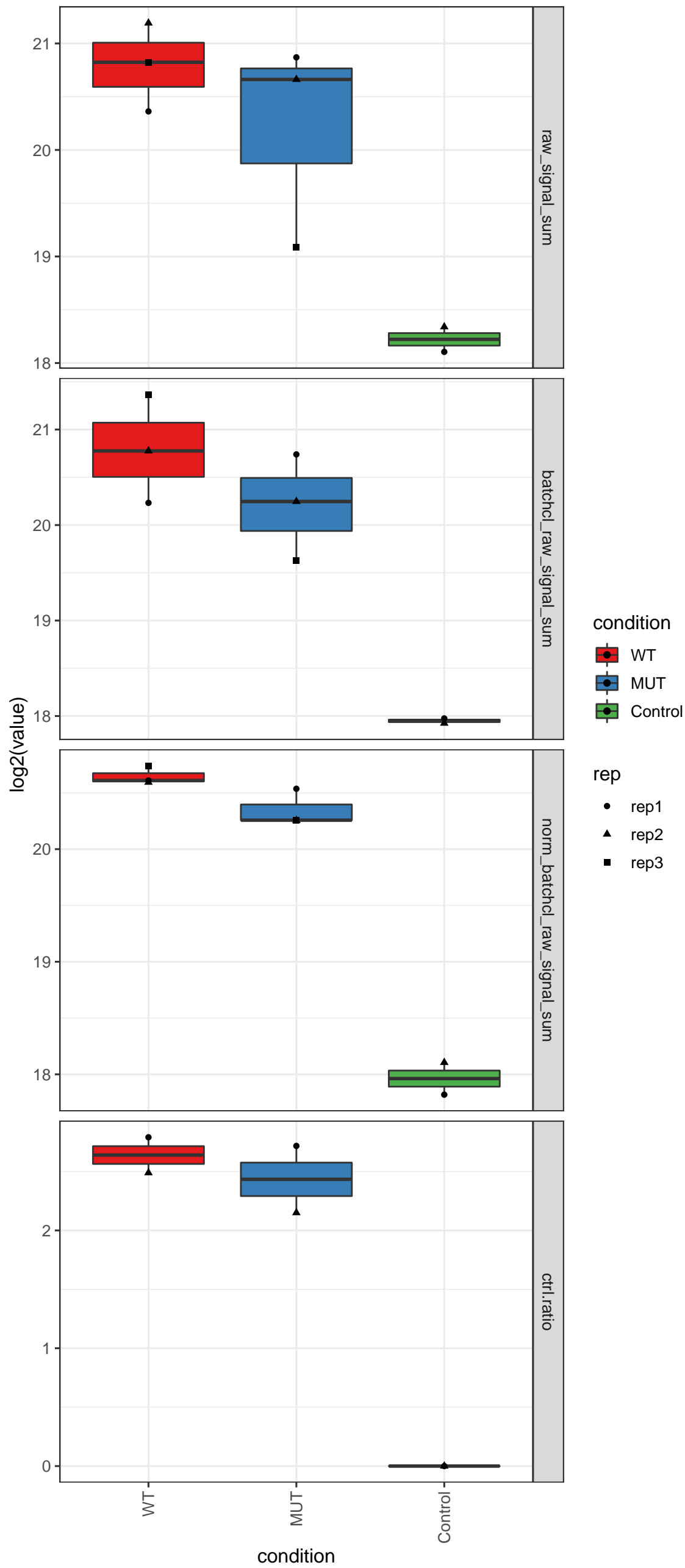
MKT1 – P40850

Protein MKT1 OS=*Saccharomyces cerevisiae* (strain ATCC 204508 / S288



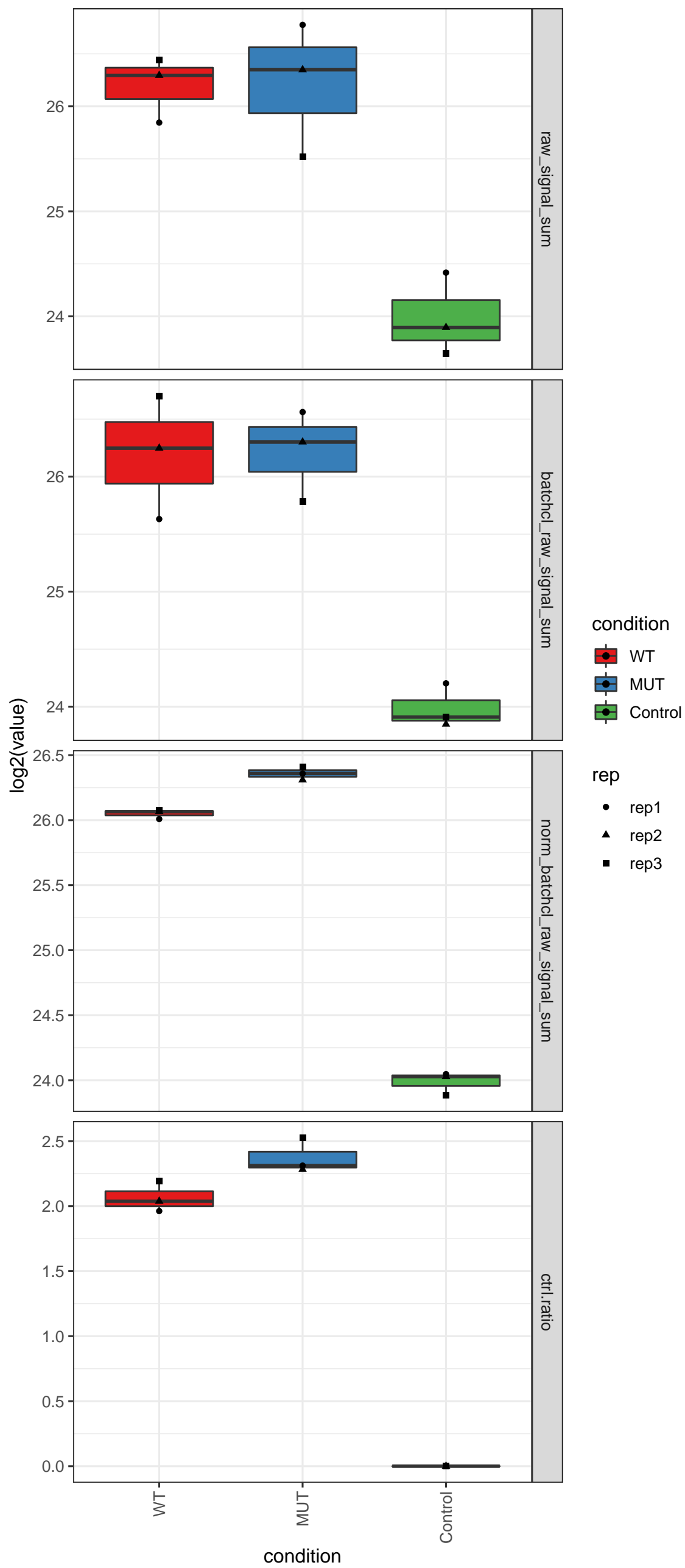
MLH1 – P38920

DNA mismatch repair protein MLH1 OS=*Saccharomyces cerevisiae* (strain



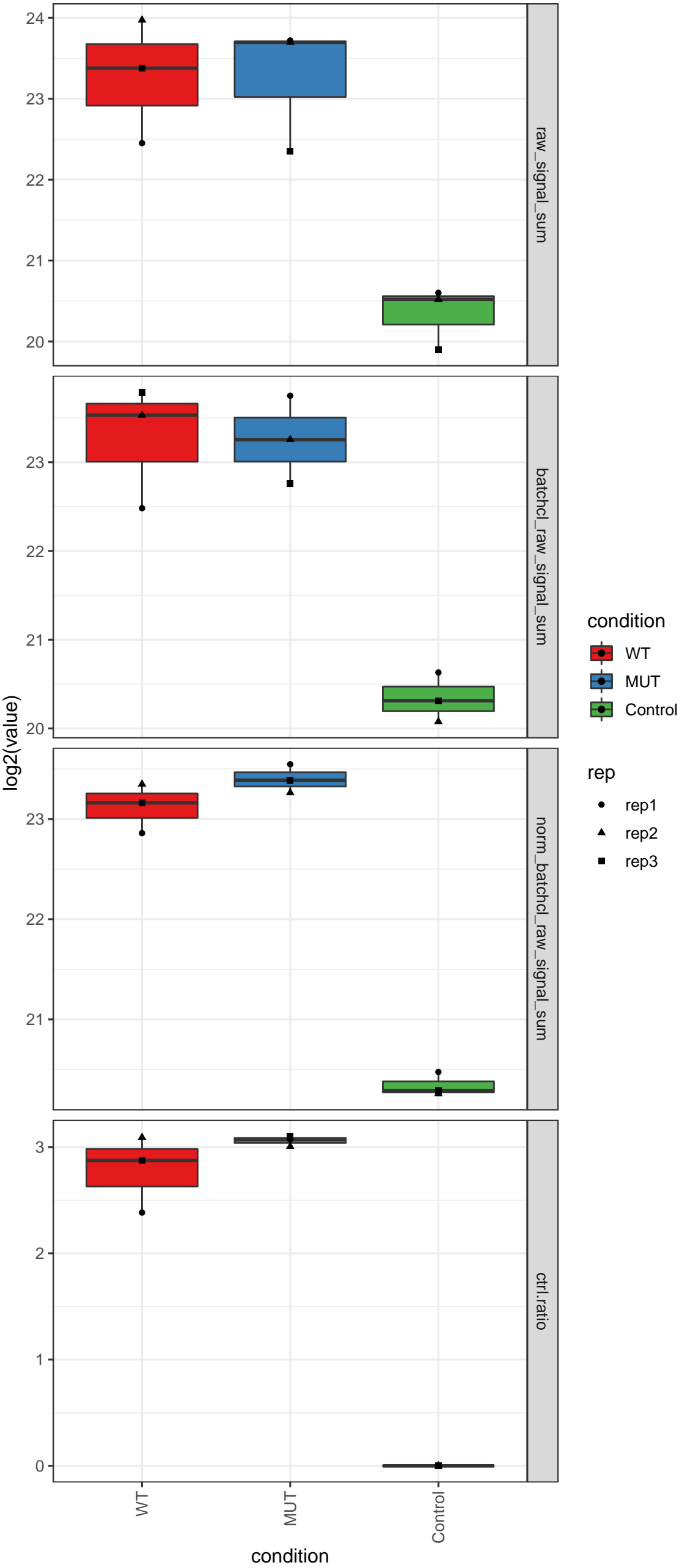
MLS1 – P30952

Malate synthase 1, glyoxysomal OS=*Saccharomyces cerevisiae* (strain A



MND1 – P53102

Meiotic nuclear division protein 1 OS=*Saccharomyces cerevisiae* (strain ATCC 24843)

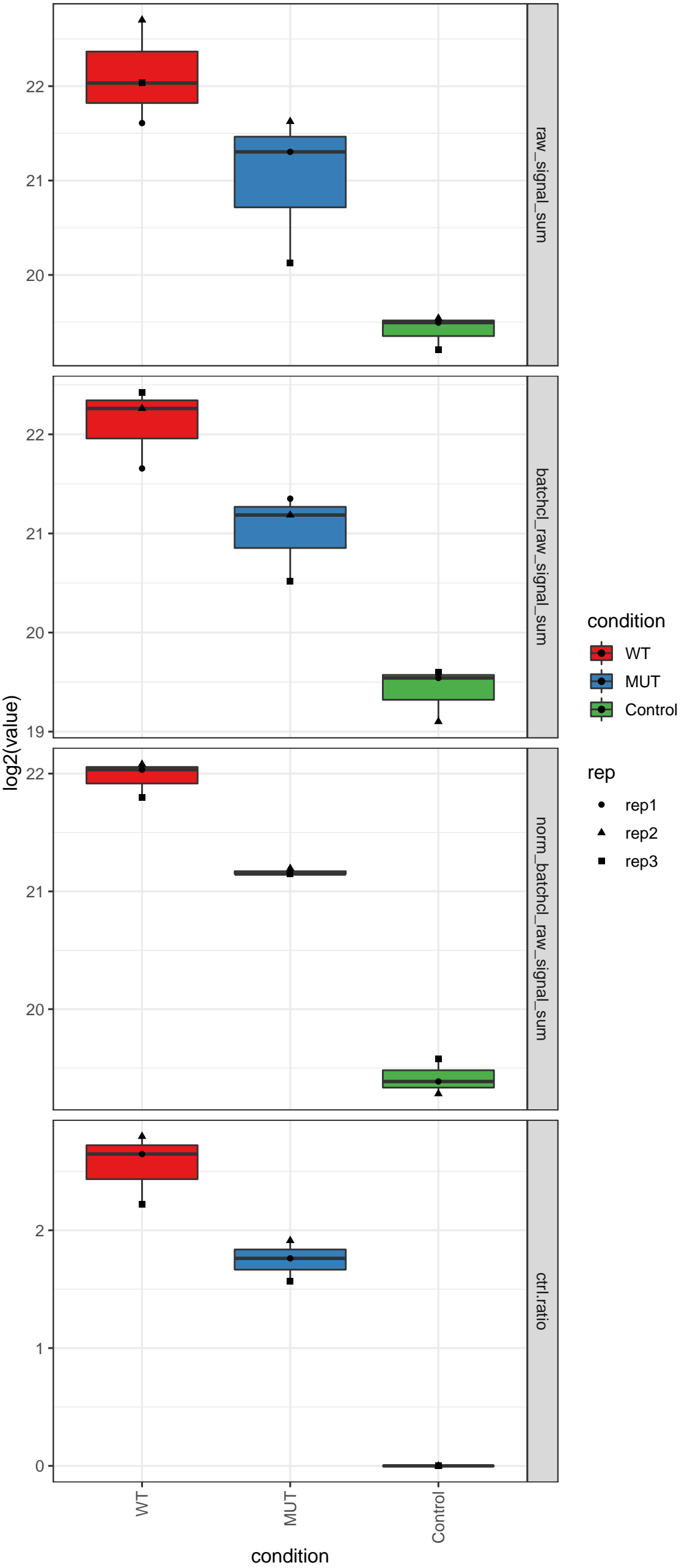


TATA-binding protein-associated factor MOT1 OS=Saccharomyces cerevis



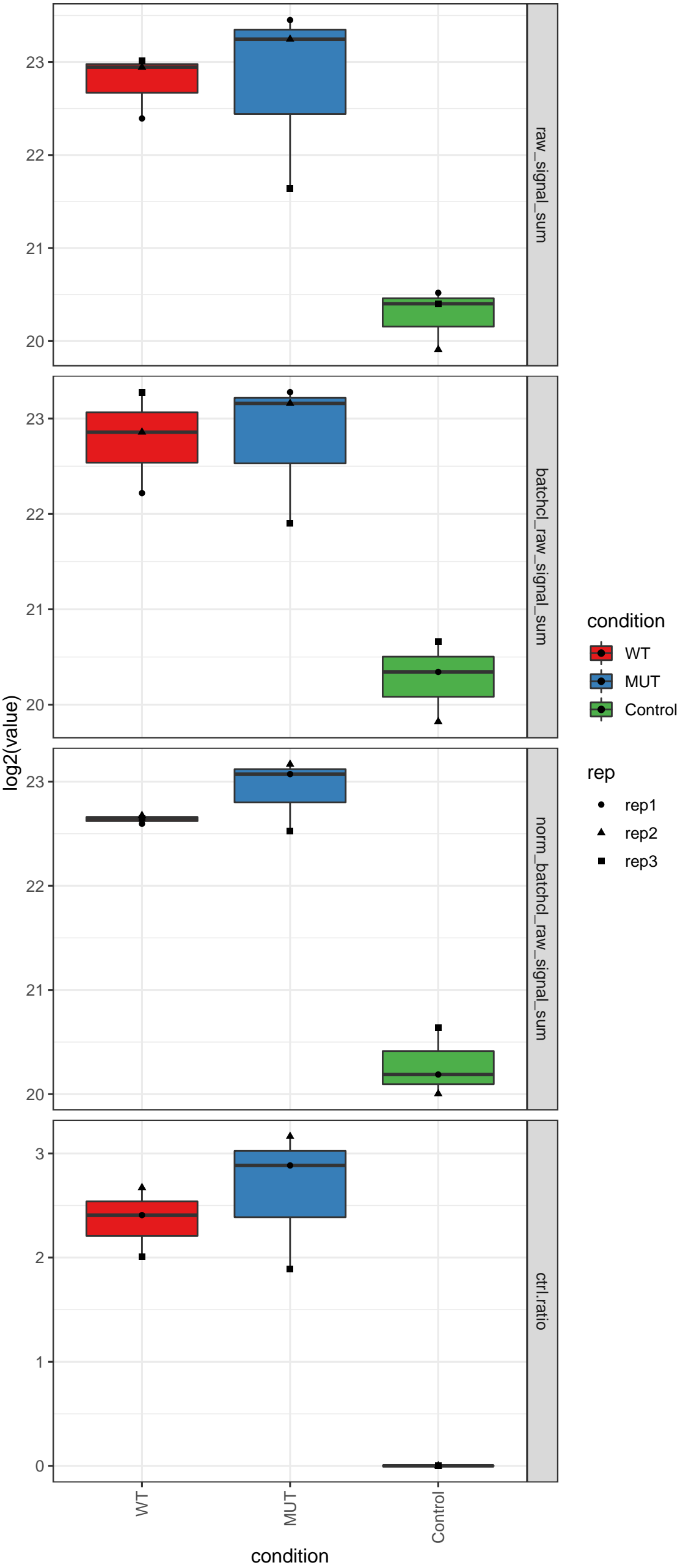
MPH1 – P40562

ATP-dependent DNA helicase MPH1 OS=*Saccharomyces cerevisiae* (strain



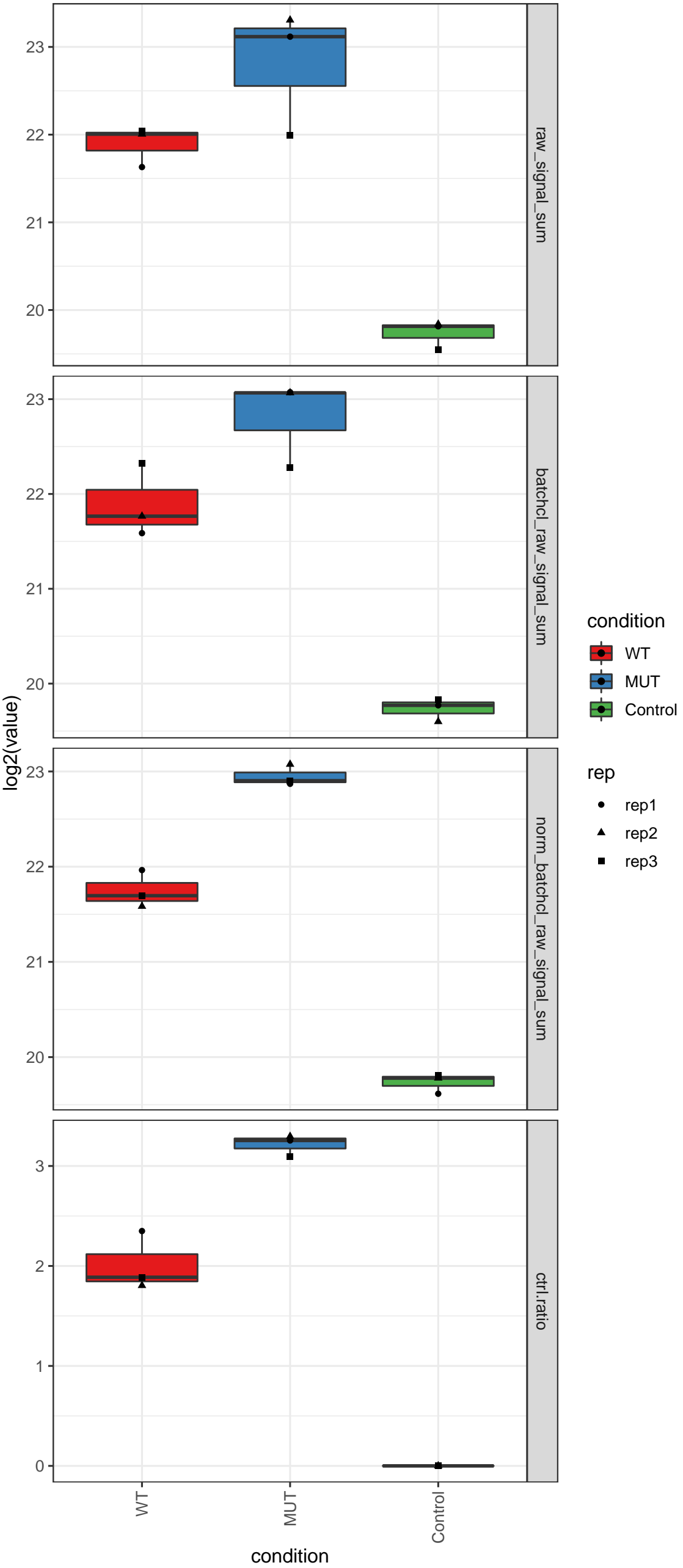
MRM1 – P25270

rRNA methyltransferase 1, mitochondrial OS=*Saccharomyces cerevisiae* (S)



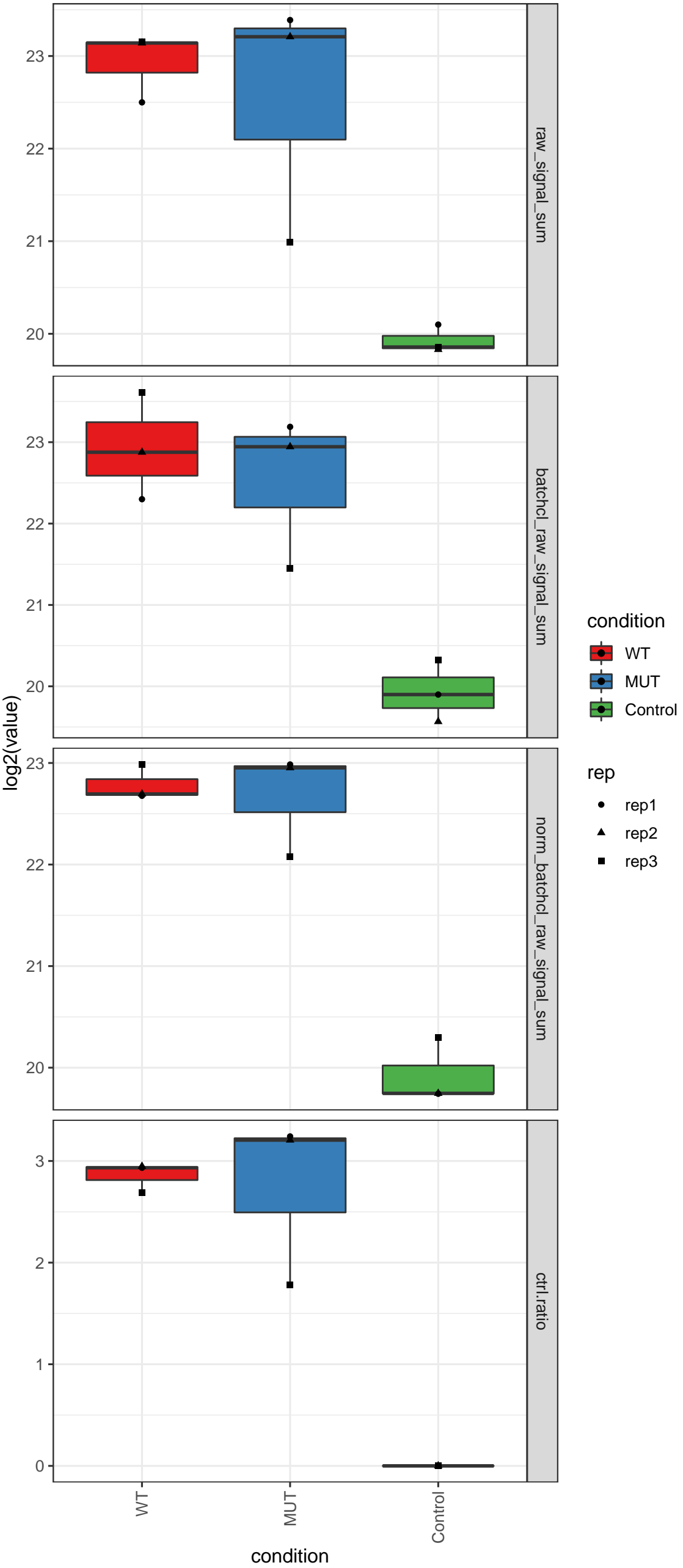
MRP20 – P32387

54S ribosomal protein L41, mitochondrial OS=*Saccharomyces cerevisiae* (



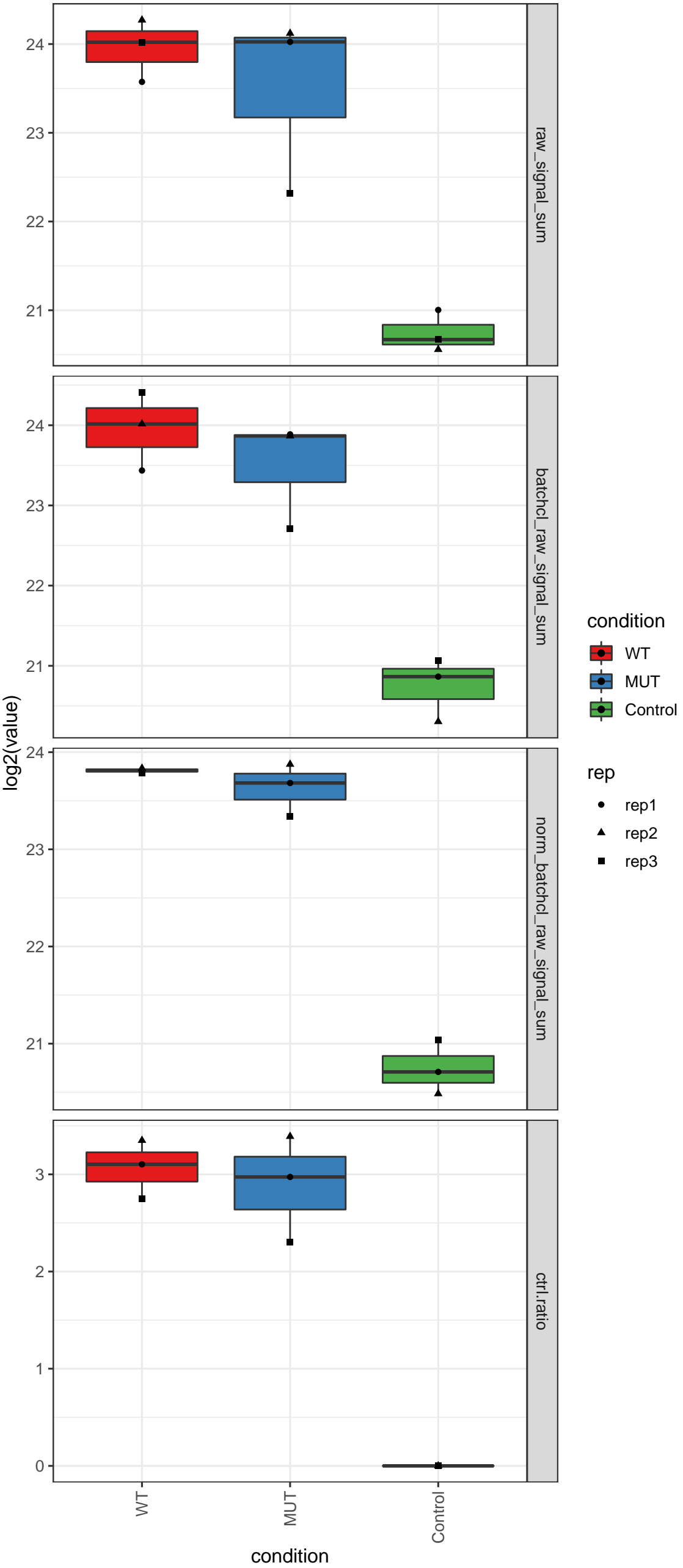
MRP7 – P12687

54S ribosomal protein L2, mitochondrial OS=*Saccharomyces cerevisiae* (s



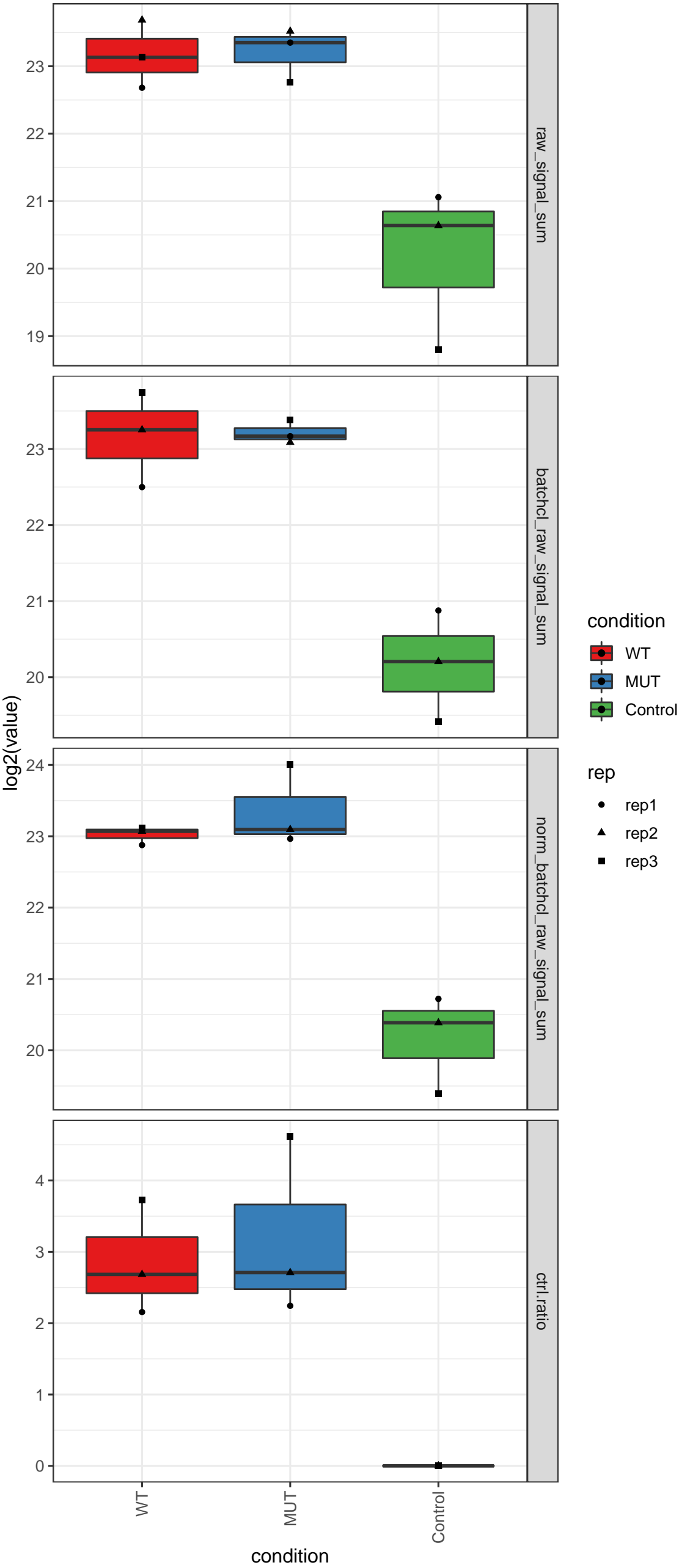
MRPL10 – P36520

54S ribosomal protein L10, mitochondrial OS=Saccharomyces cerevisiae (



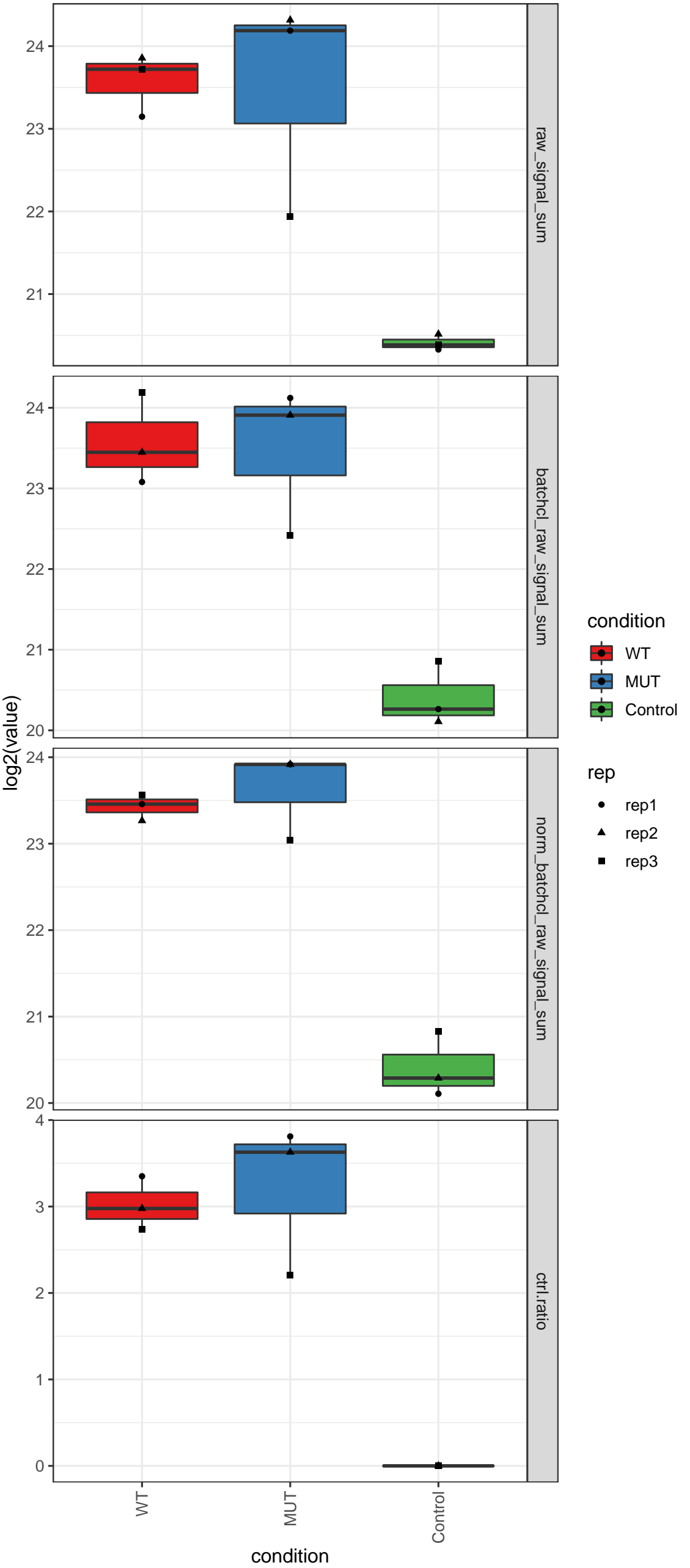
MRPL11 – P36521

54S ribosomal protein L11, mitochondrial OS=*Saccharomyces cerevisiae* (



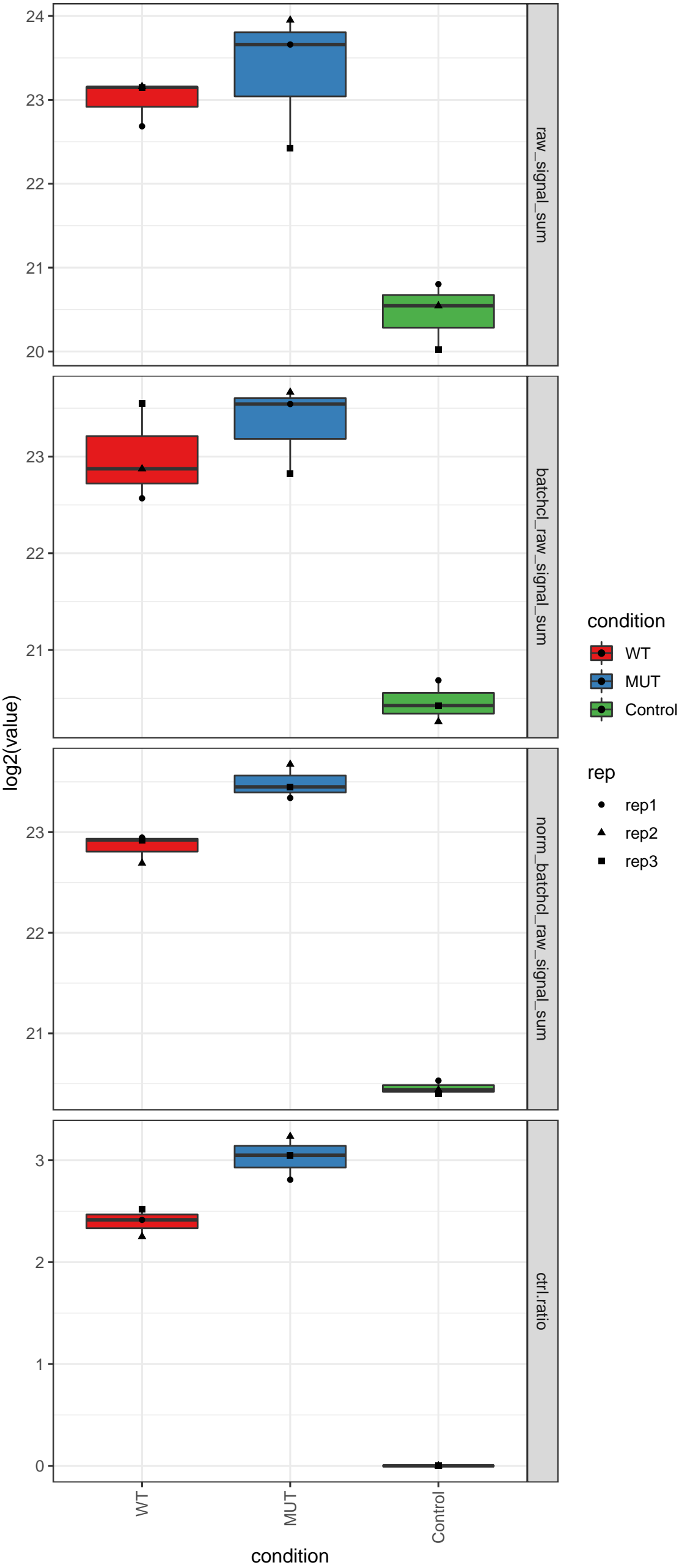
MRPL16 – P38064

54S ribosomal protein L16, mitochondrial OS=*Saccharomyces cerevisiae* (



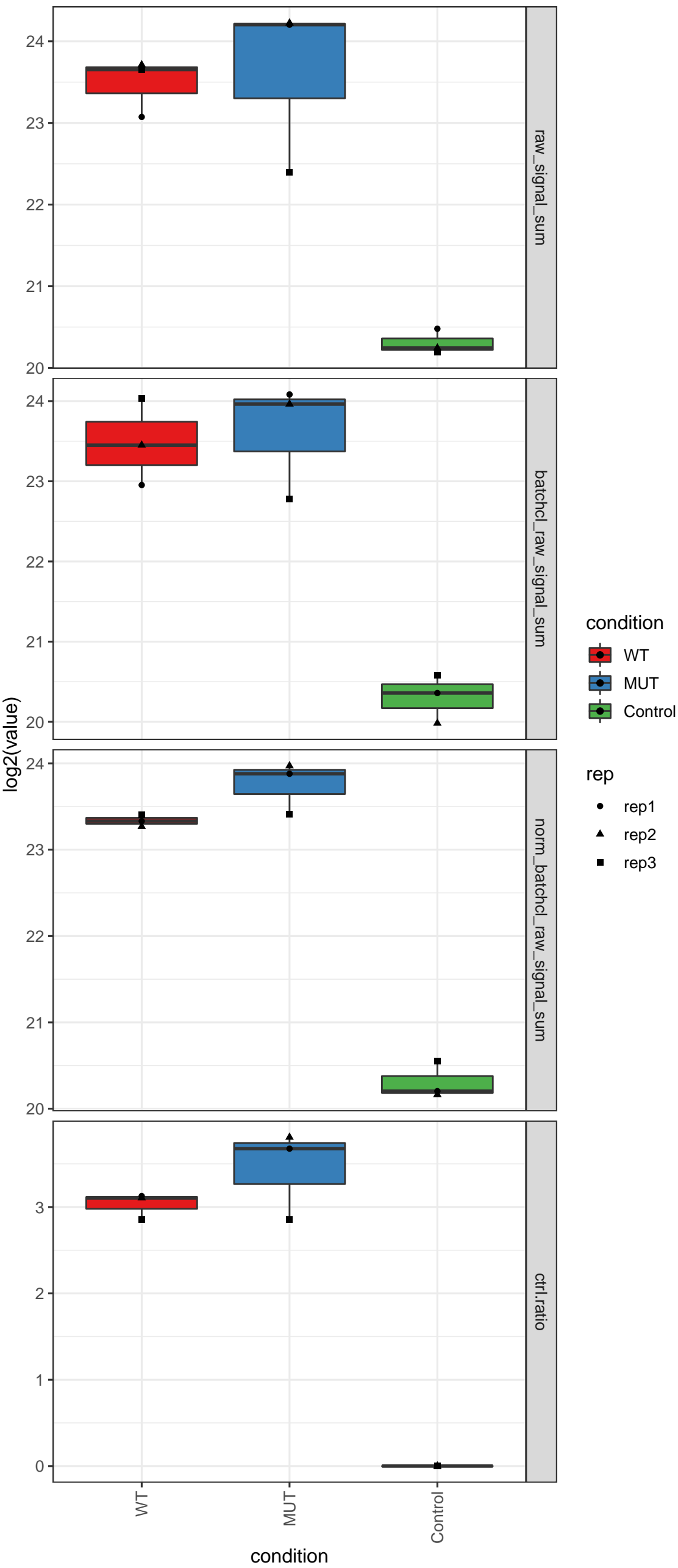
MRPL17 – P36528

54S ribosomal protein L17, mitochondrial OS=Saccharomyces cerevisiae (



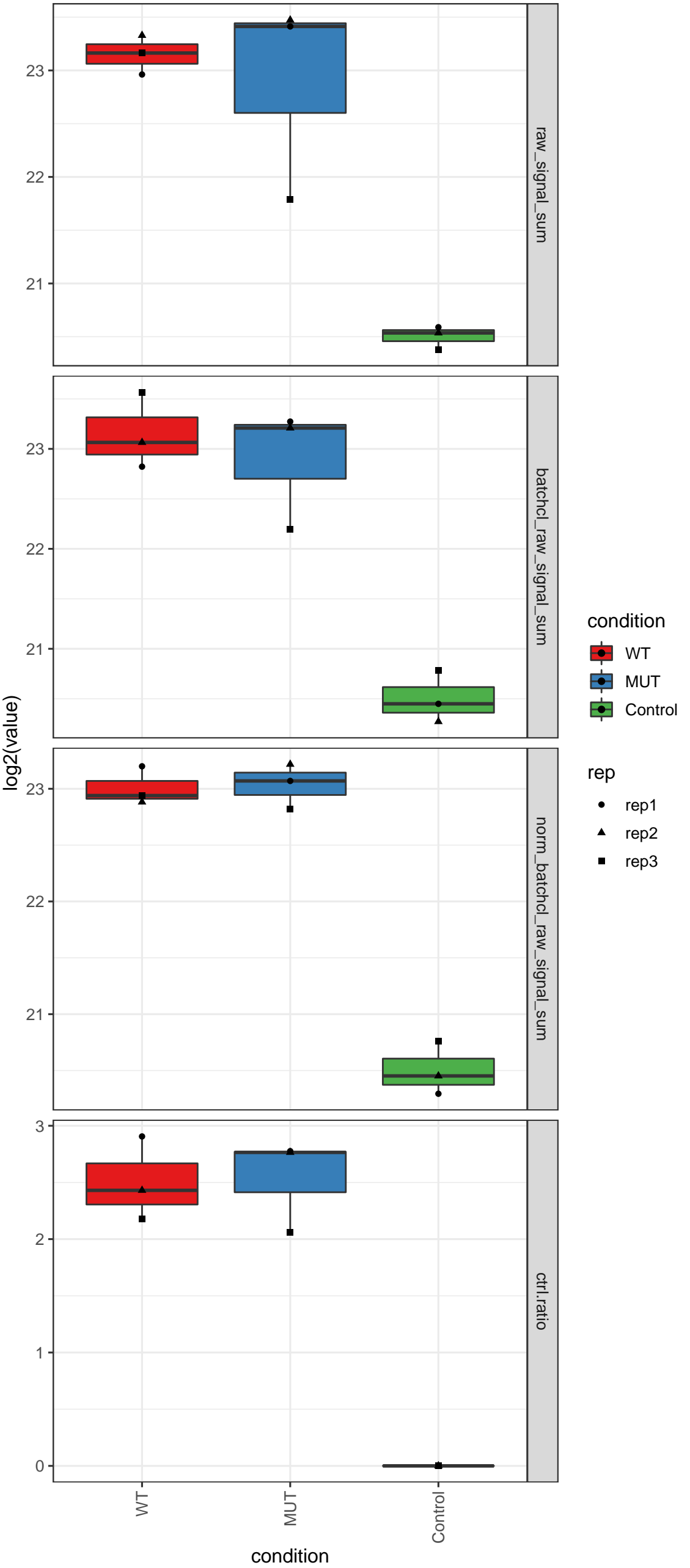
MRPL22 – P53881

54S ribosomal protein L22, mitochondrial OS=Saccharomyces cerevisiae (



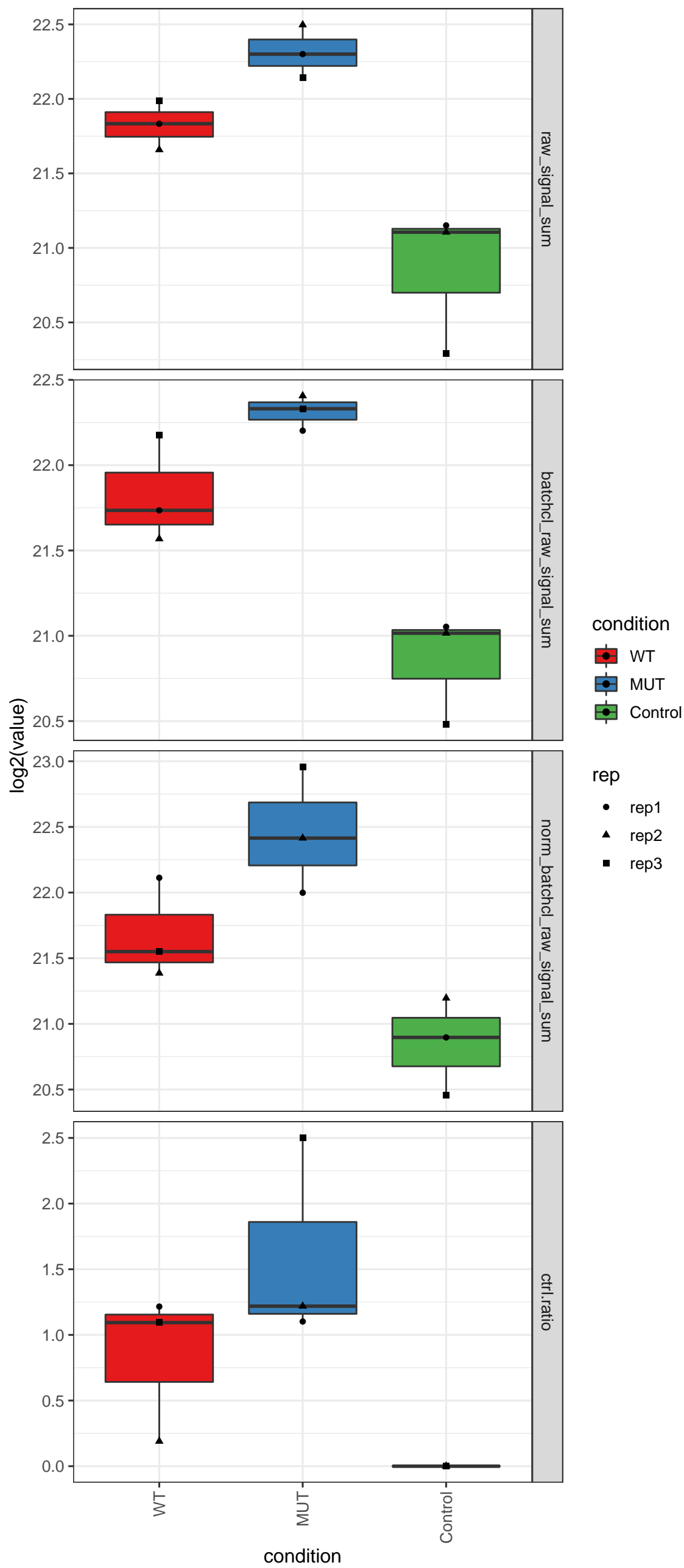
MRPL24 – P36525

54S ribosomal protein L24, mitochondrial OS=*Saccharomyces cerevisiae* (



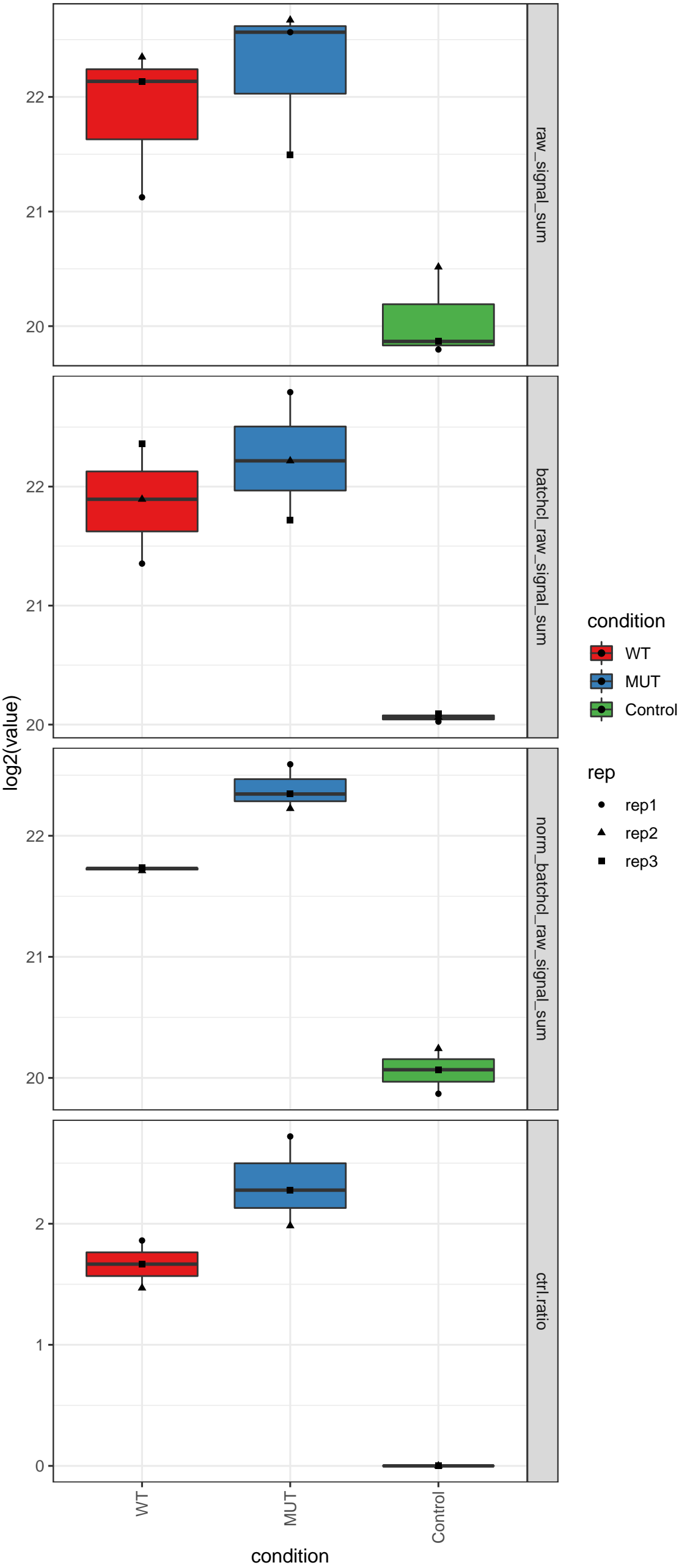
MRPL25 – P23369

54S ribosomal protein L25, mitochondrial OS=*Saccharomyces cerevisiae*



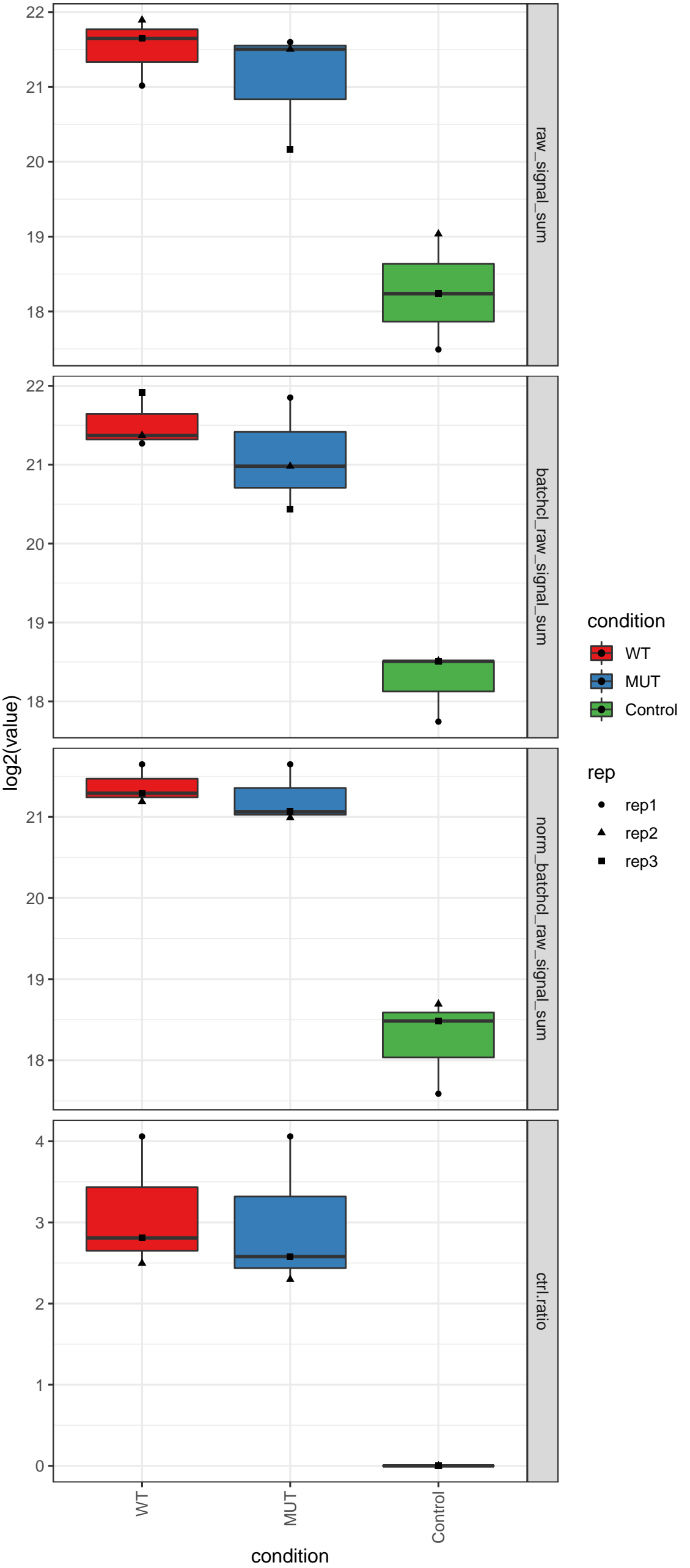
MRPL3 – P36516

54S ribosomal protein L3, mitochondrial OS=*Saccharomyces cerevisiae* (s



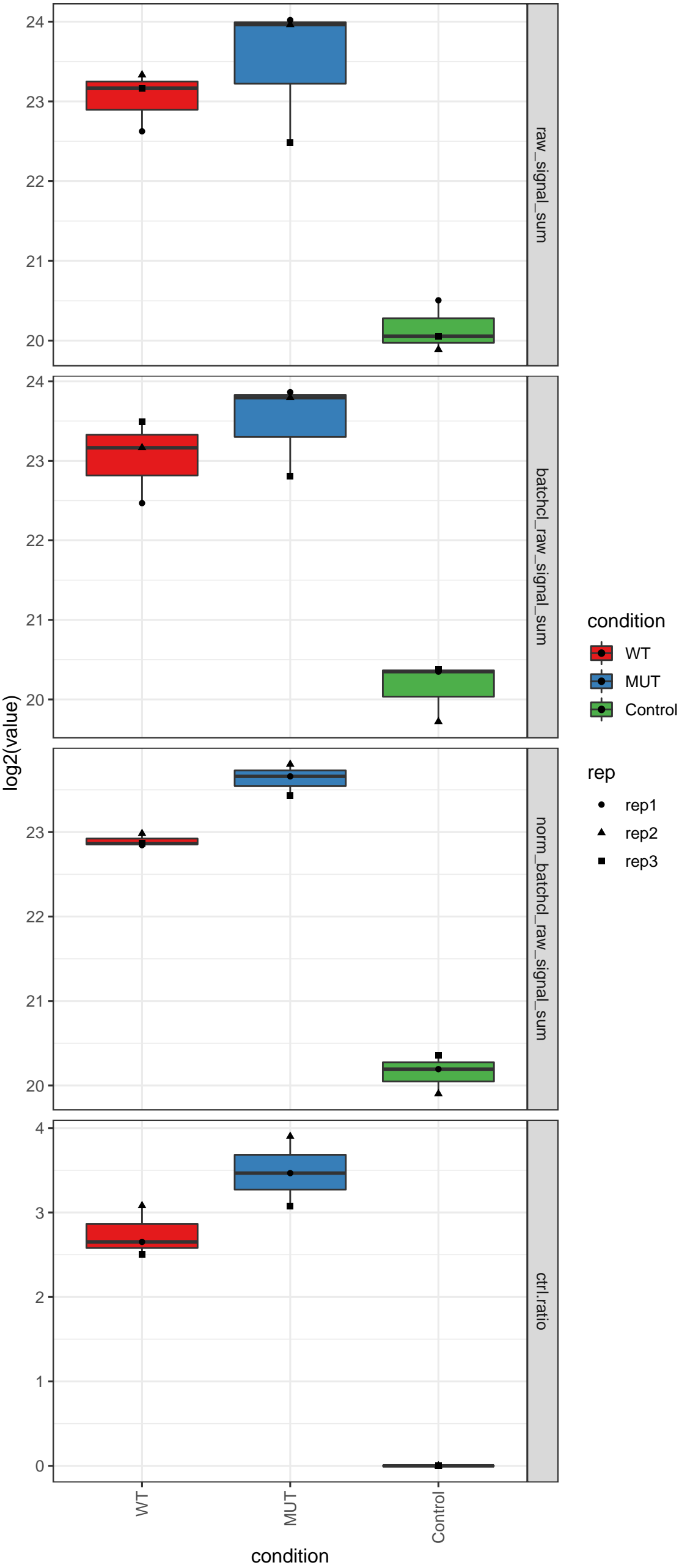
MRPL32 – P25348

54S ribosomal protein L32, mitochondrial OS=*Saccharomyces cerevisiae* (



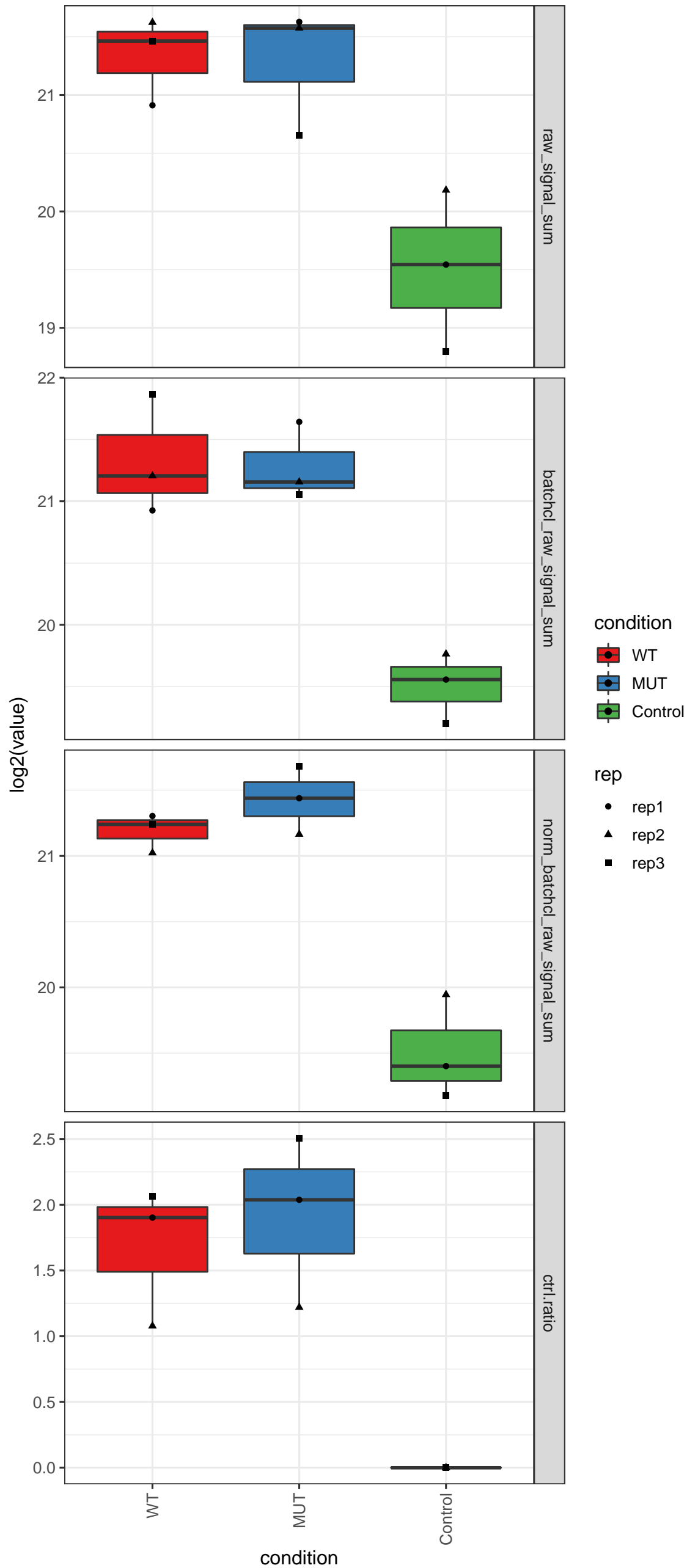
MRPL35 – Q06678

54S ribosomal protein L35, mitochondrial OS=Saccharomyces cerevisiae (



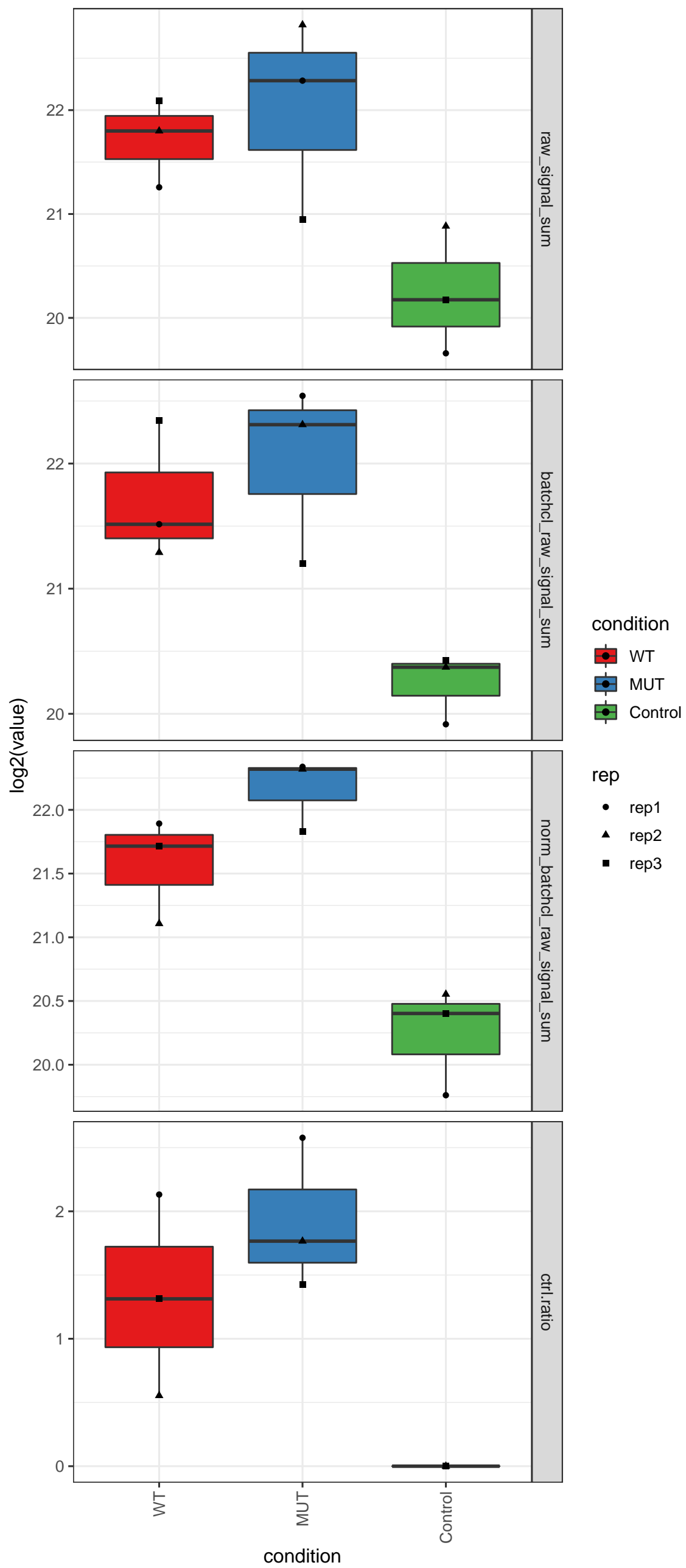
MRPL36 – P36531

54S ribosomal protein L36, mitochondrial OS=Saccharomyces cerevisiae



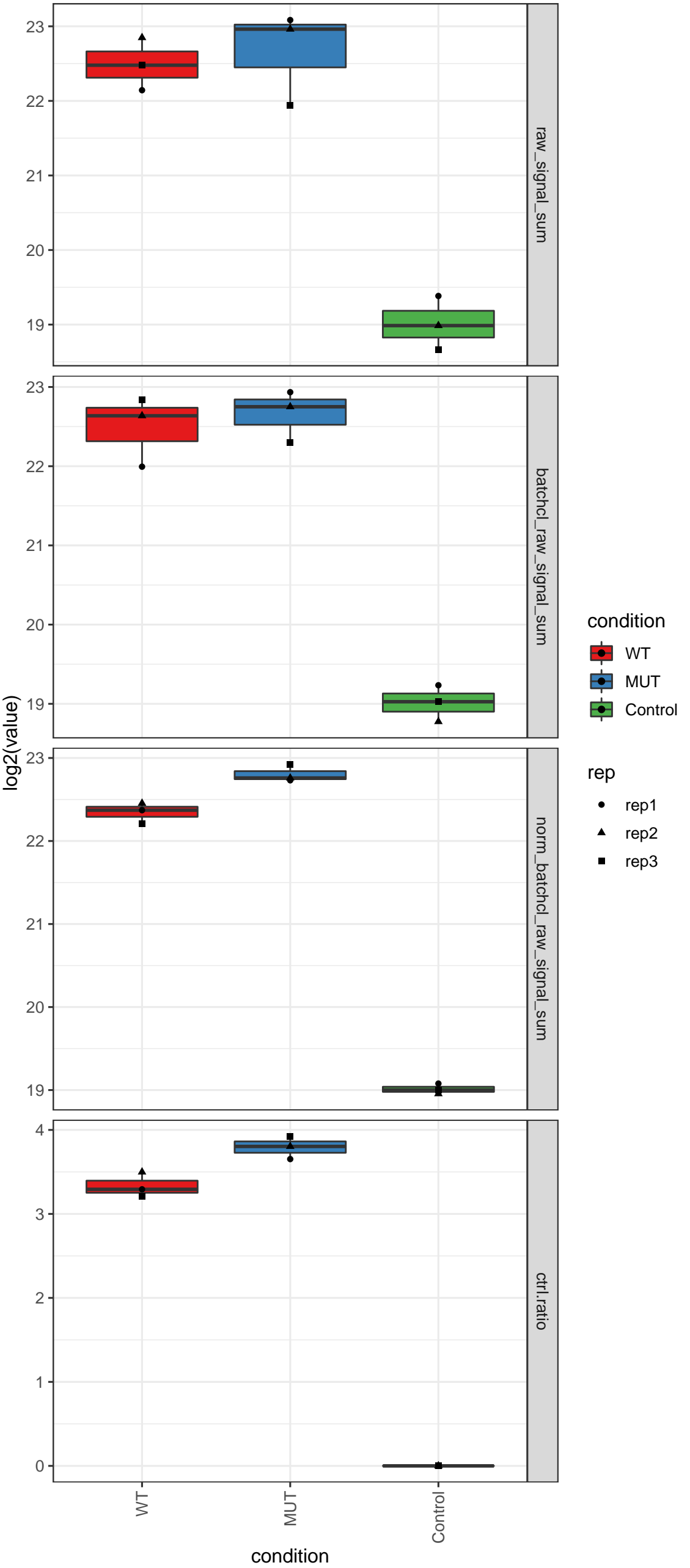
MRPL40 – P36534

54S ribosomal protein L40, mitochondrial OS=*Saccharomyces cerevisiae*



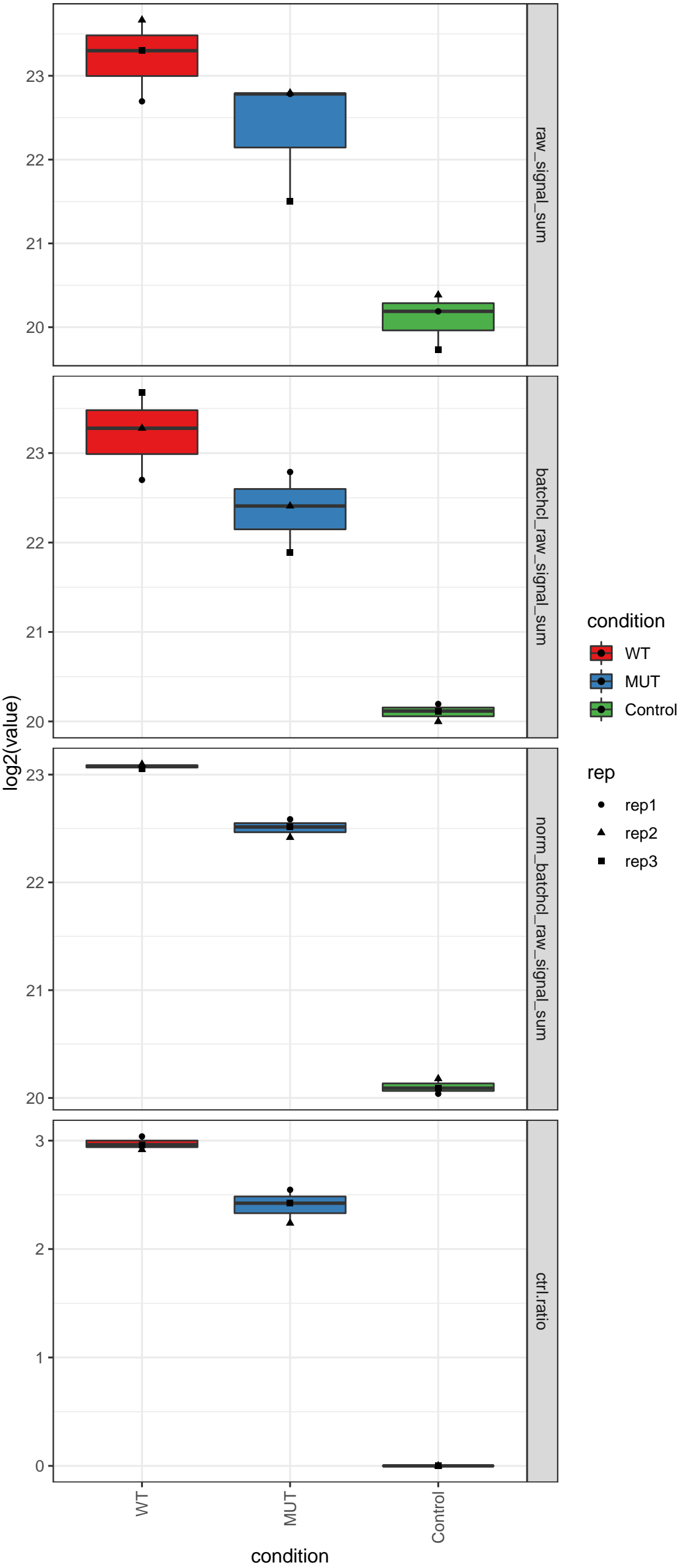
MRPL9 – P31334

54S ribosomal protein L9, mitochondrial OS=Saccharomyces cerevisiae (s



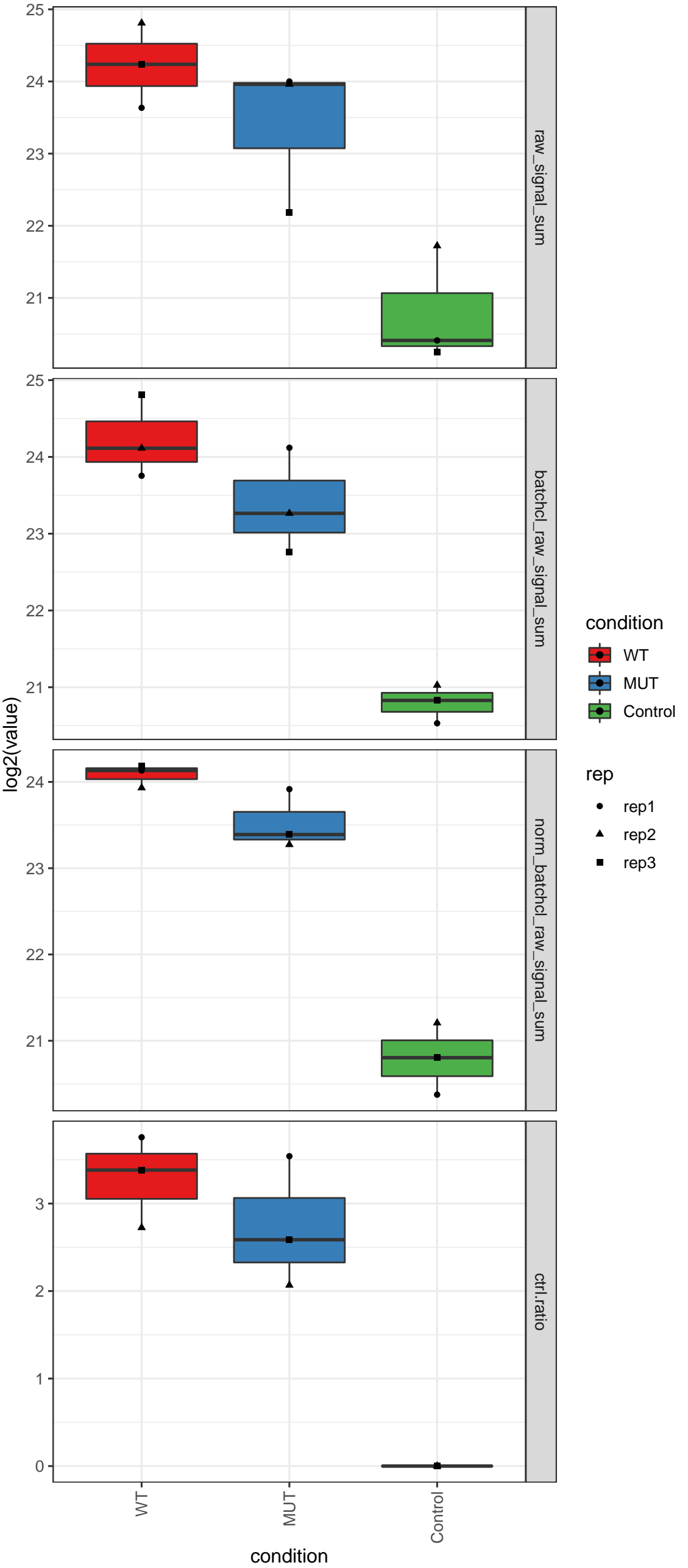
MRPS17 – Q03246

37S ribosomal protein S17, mitochondrial OS=Saccharomyces cerevisiae (



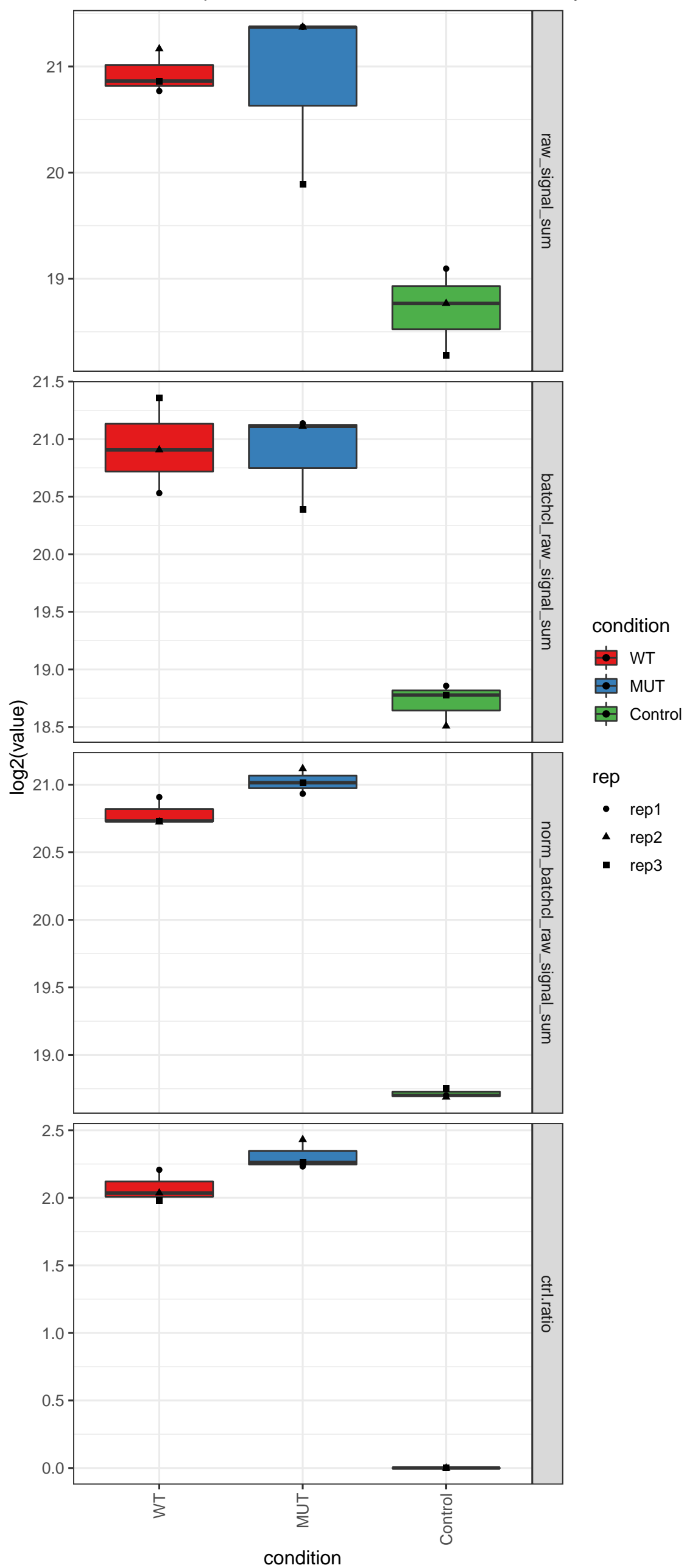
MRPS28 – P21771

37S ribosomal protein S28, mitochondrial OS=Saccharomyces cerevisiae (



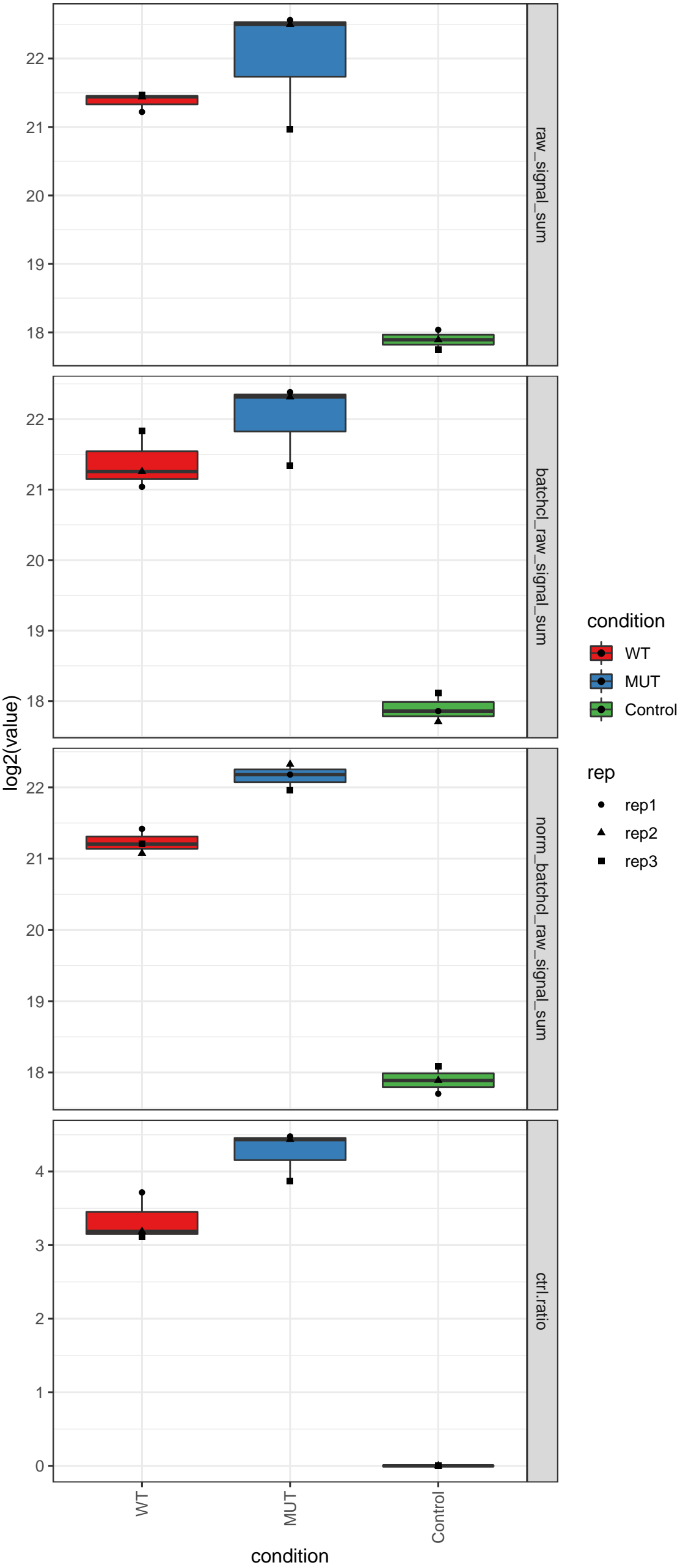
MRPS35 – P53292

37S ribosomal protein S35, mitochondrial OS=*Saccharomyces cerevisiae*



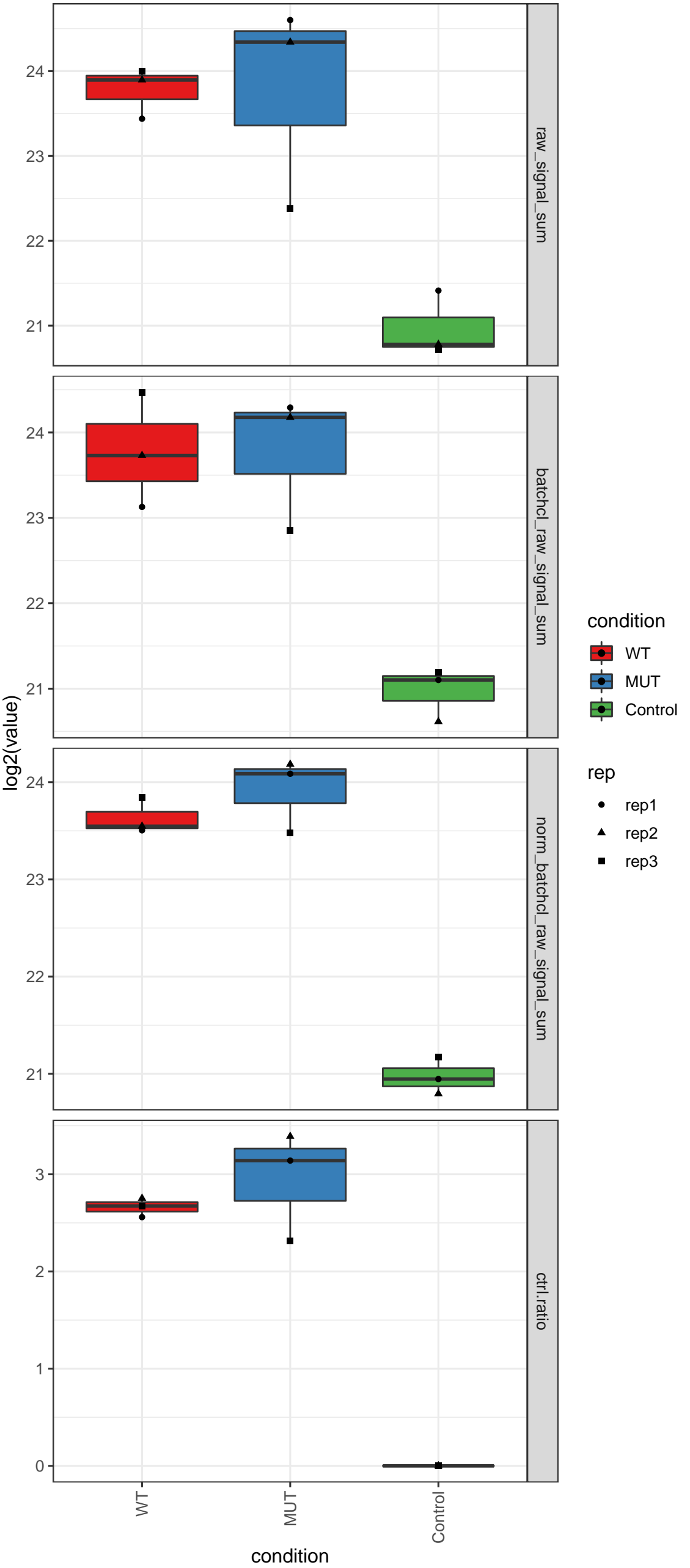
MRPS5 – P33759

37S ribosomal protein S5, mitochondrial OS=Saccharomyces cerevisiae (s



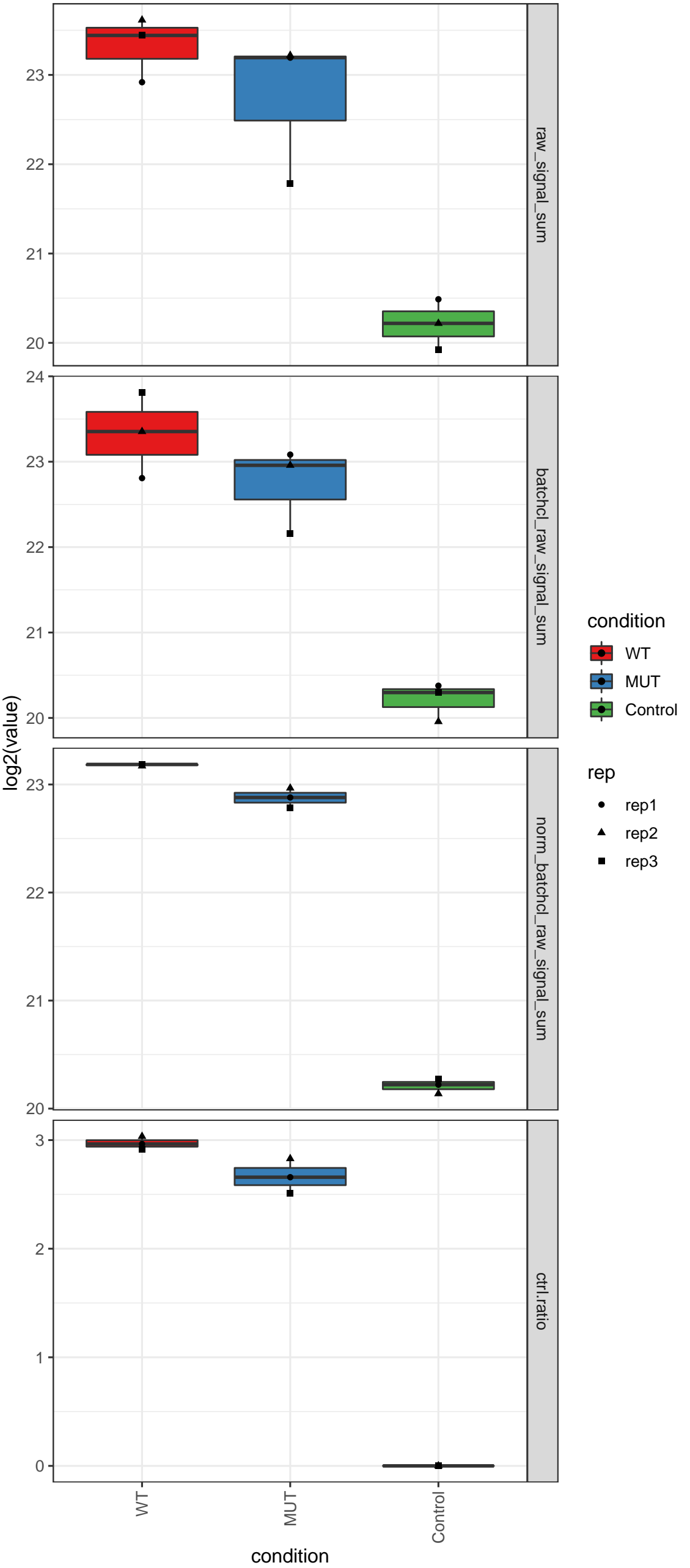
MRPS9 – P38120

37S ribosomal protein S9, mitochondrial OS=Saccharomyces cerevisiae (s



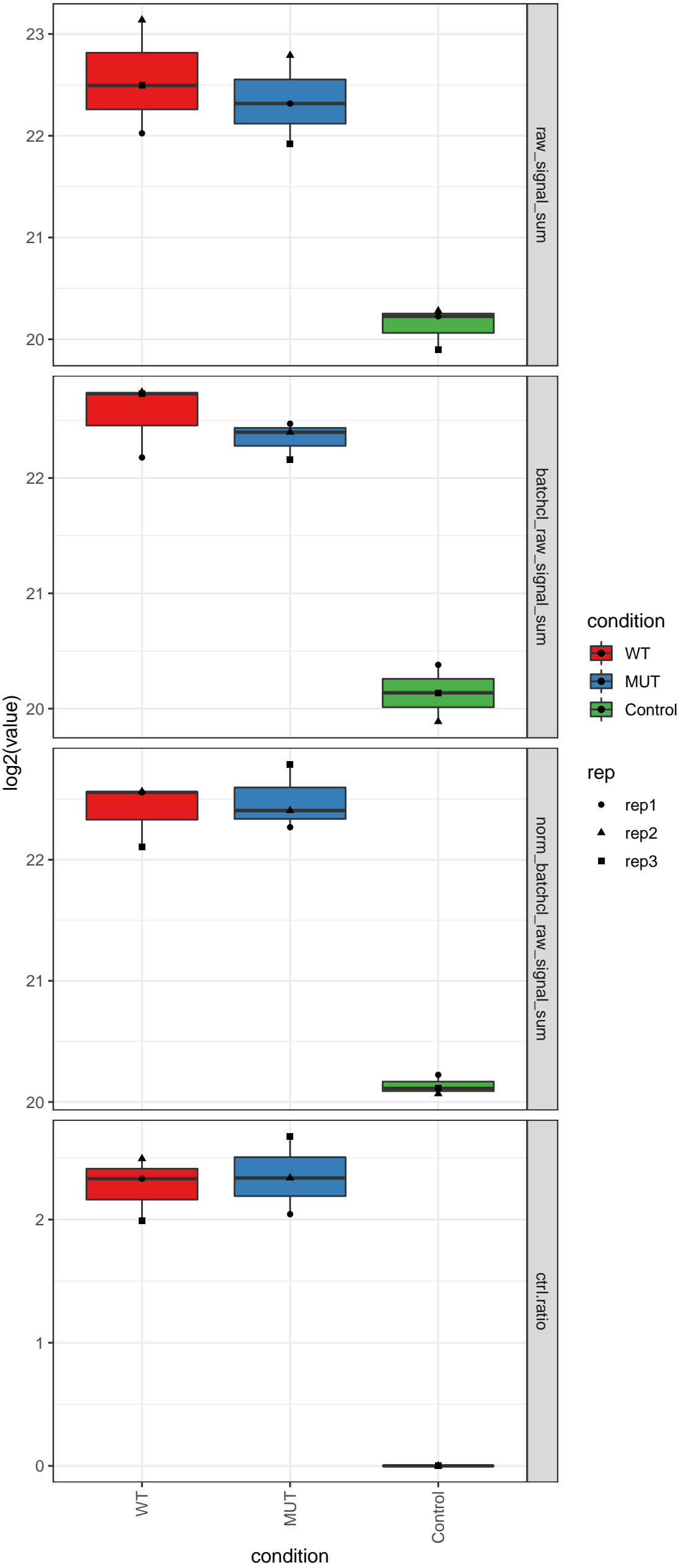
MRT4 – P33201

Ribosome assembly factor MRT4 OS=*Saccharomyces cerevisiae* (strain ATCC 25796)



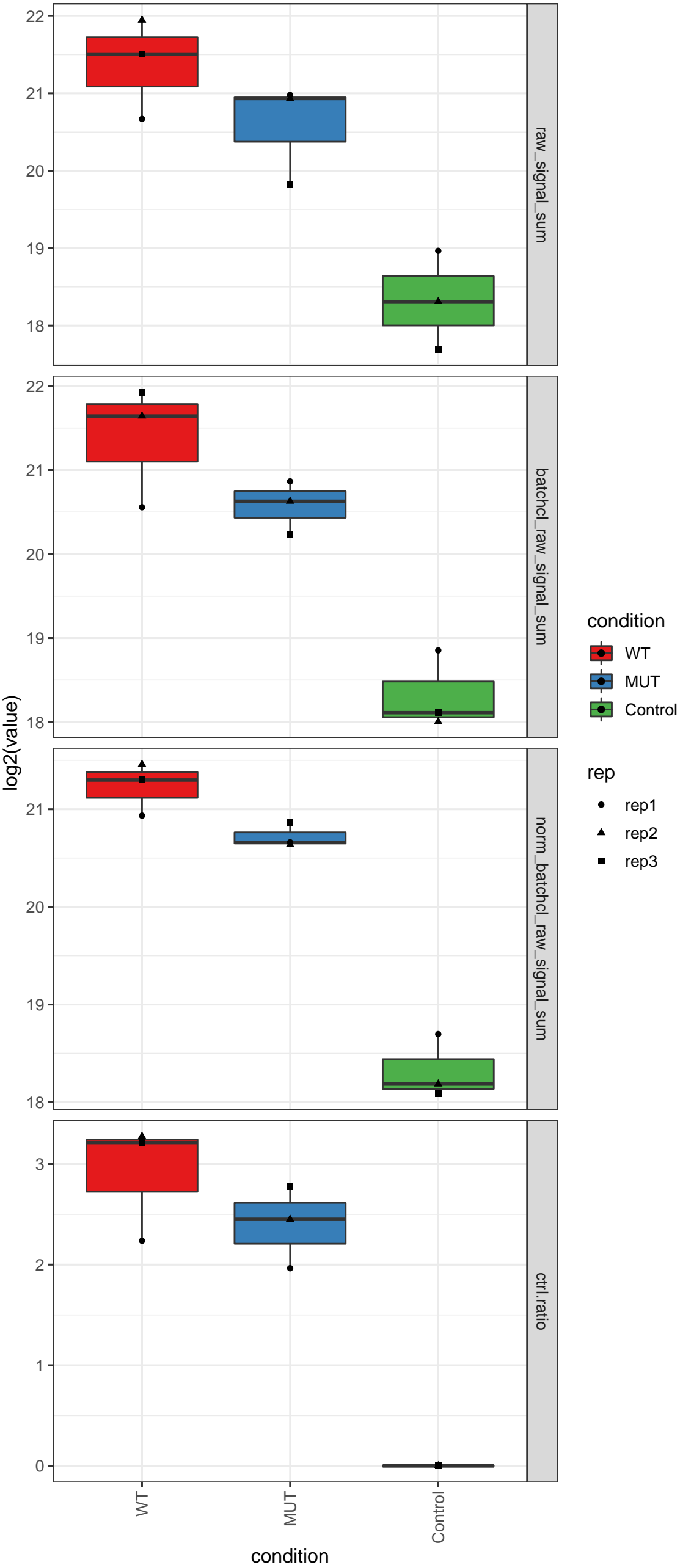
MSD1 – P15179

Aspartate--tRNA ligase, mitochondrial OS=Saccharomyces cerevisiae (str



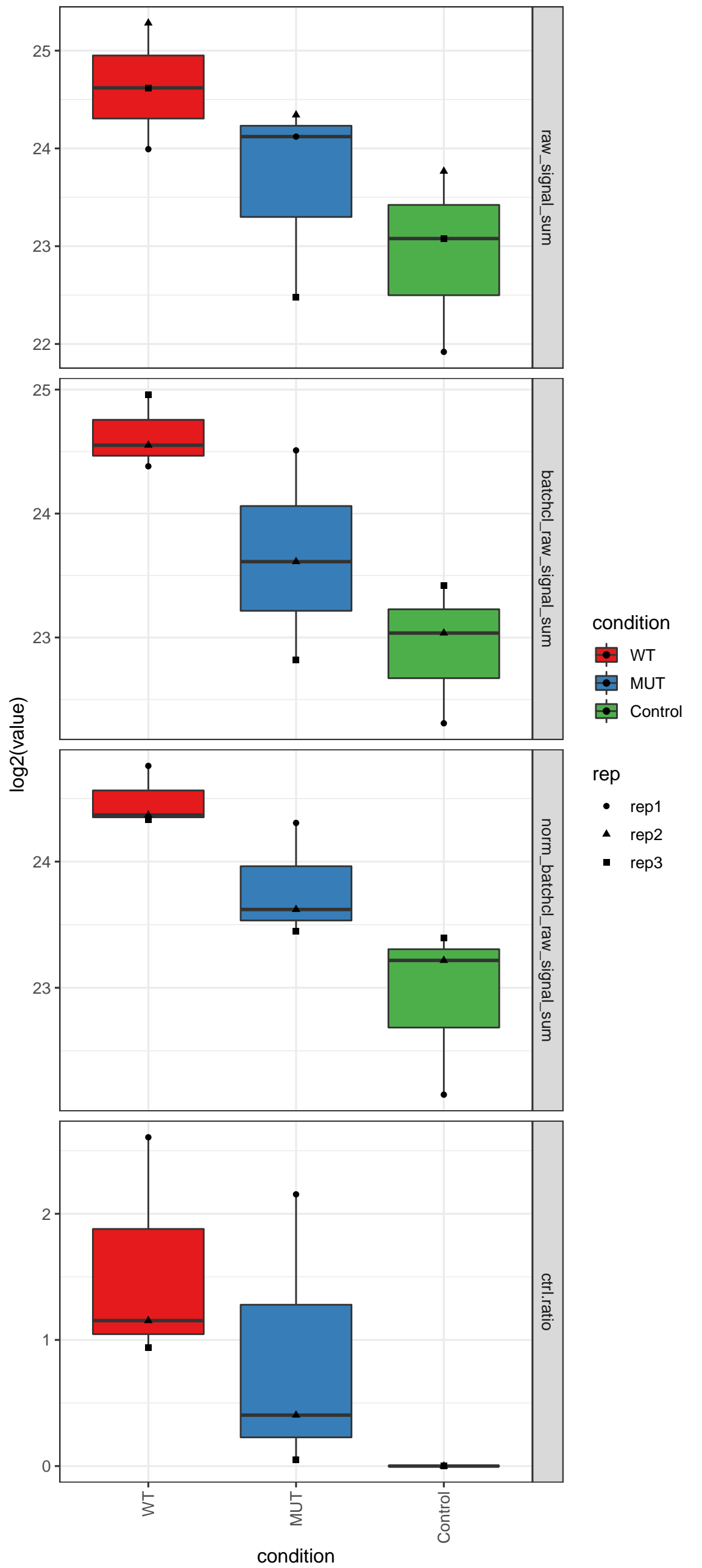
MSH1 – P25846

DNA mismatch repair protein MSH1, mitochondrial OS=*Saccharomyces cerevisiae*



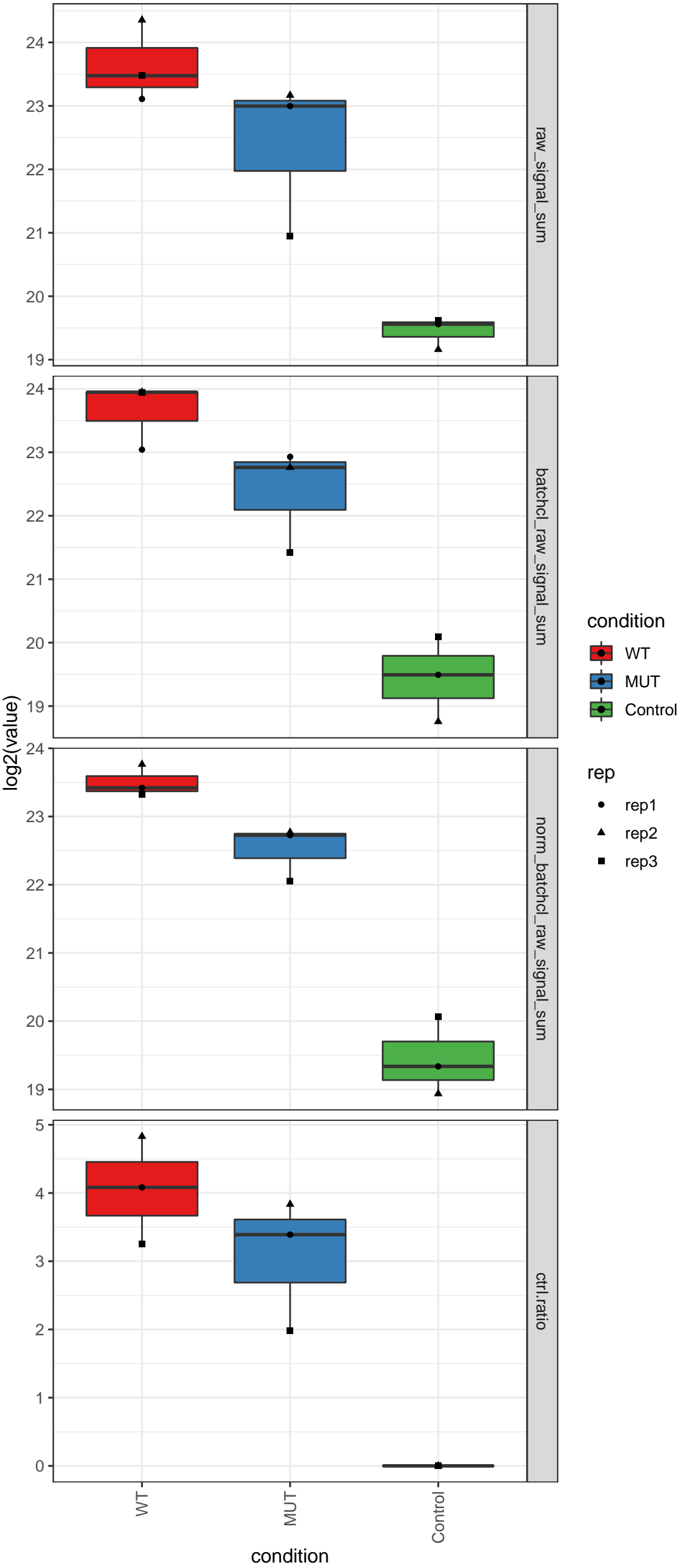
MSH2 – P25847

DNA mismatch repair protein MSH2 OS=*Saccharomyces cerevisiae* (strain



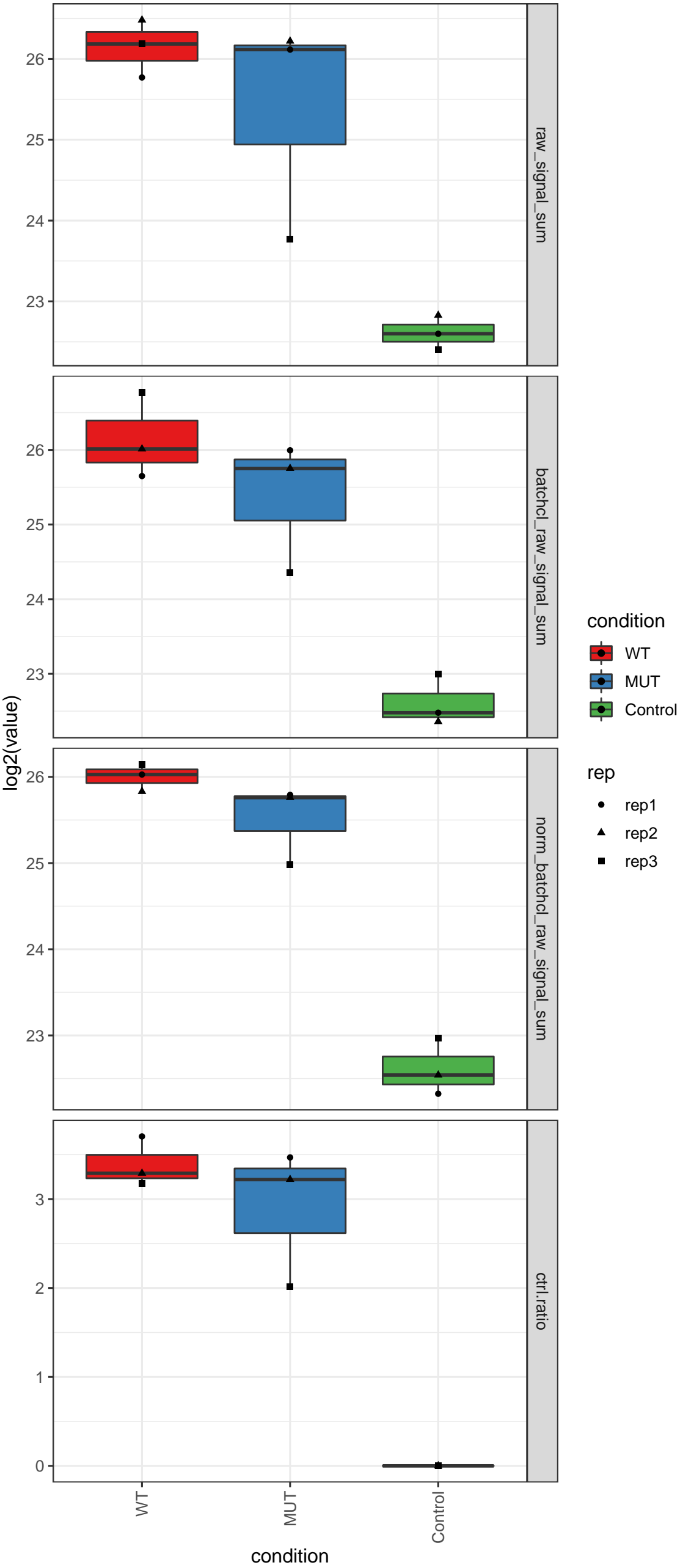
MSH6 – Q03834

DNA mismatch repair protein MSH6 OS=*Saccharomyces cerevisiae* (strain



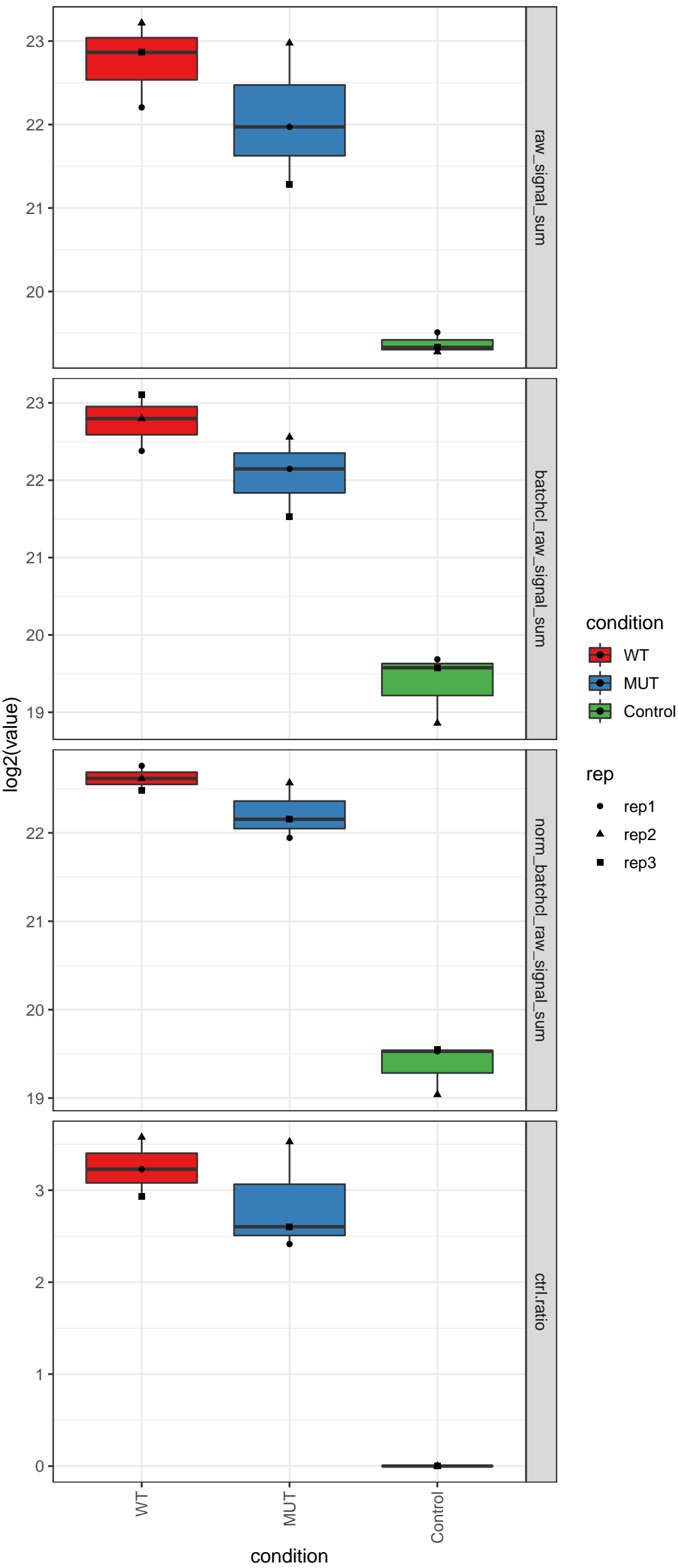
MSS116 – P15424

ATP-dependent RNA helicase MSS116, mitochondrial OS=Saccharomyce



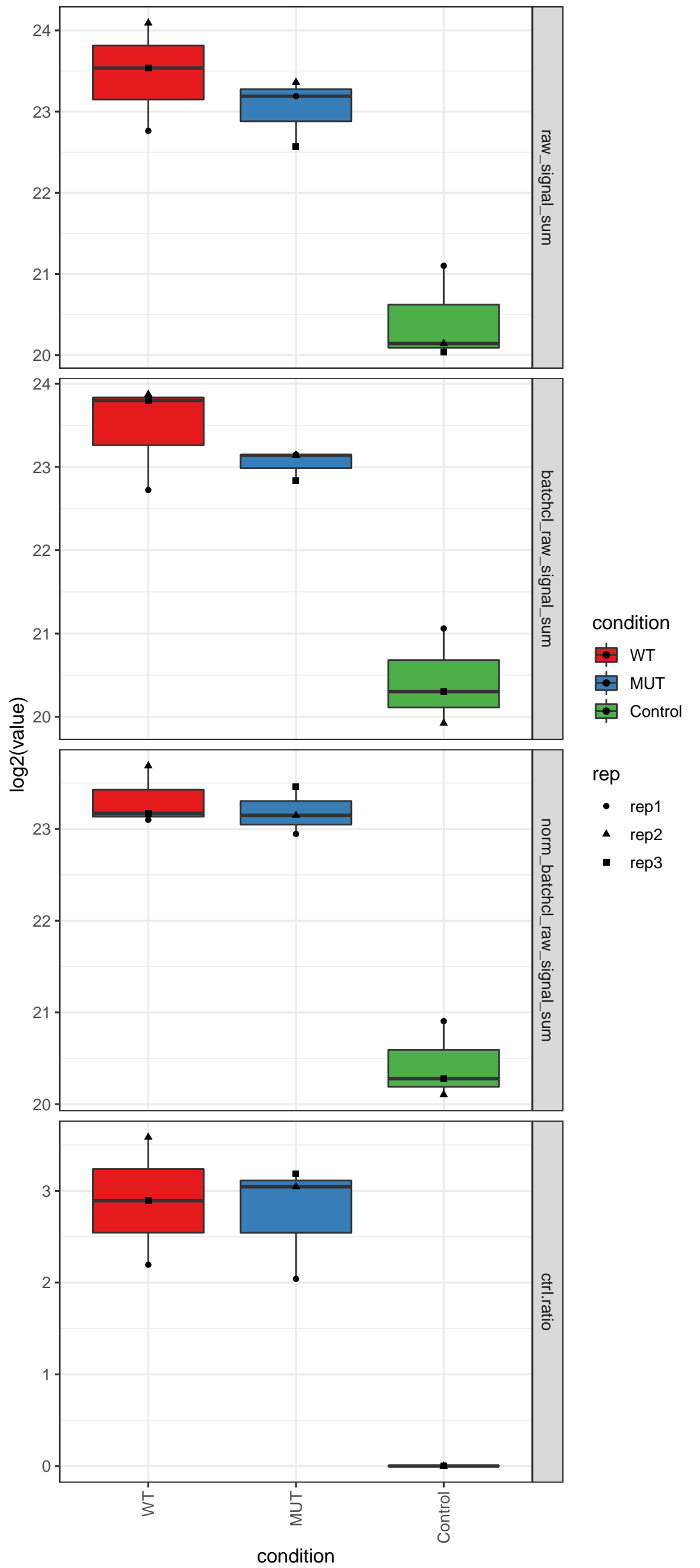
MST1 – P07236

Threonine--tRNA ligase, mitochondrial OS= *Saccharomyces cerevisiae* (strain ATCC 22016 / DSM 5780 /



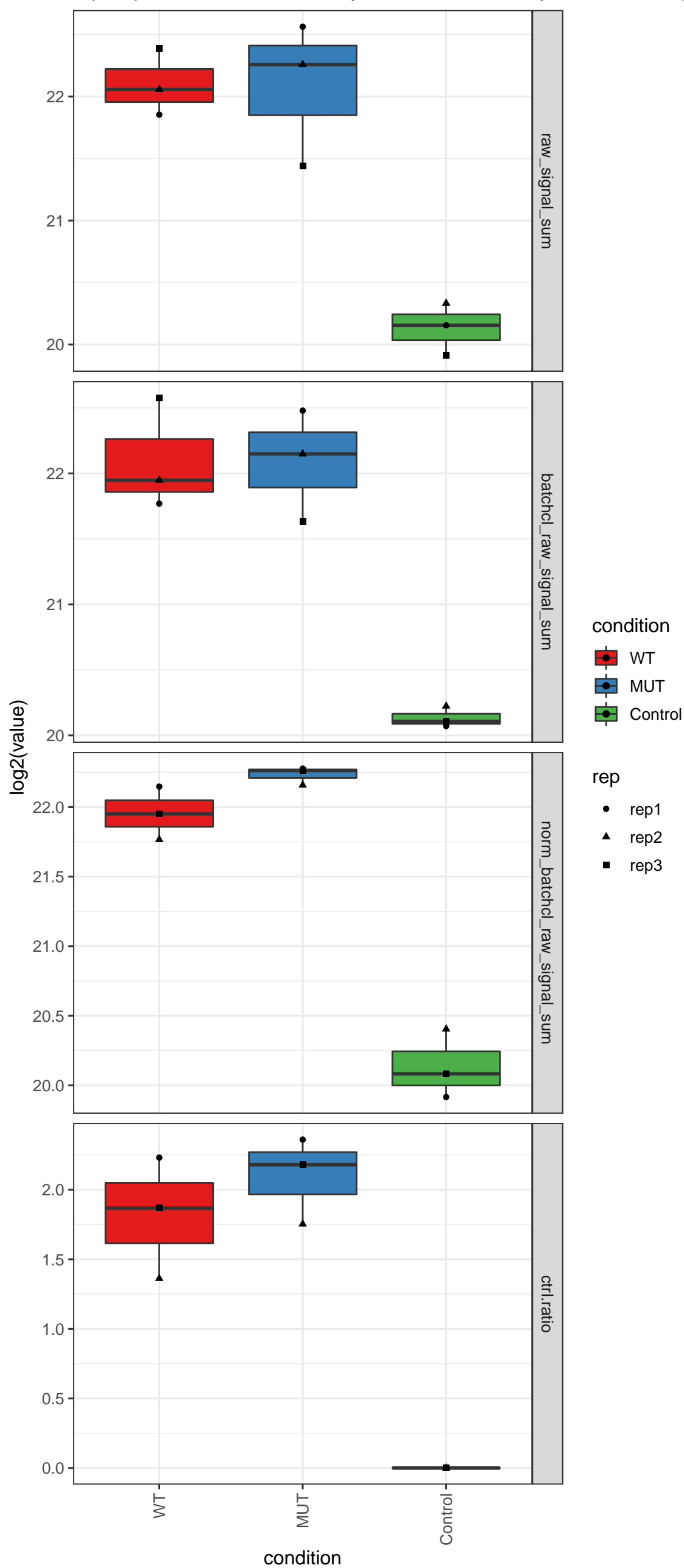
MSY1 – P48527

Tyrosine--tRNA ligase, mitochondrial OS=*Saccharomyces cerevisiae* (stra



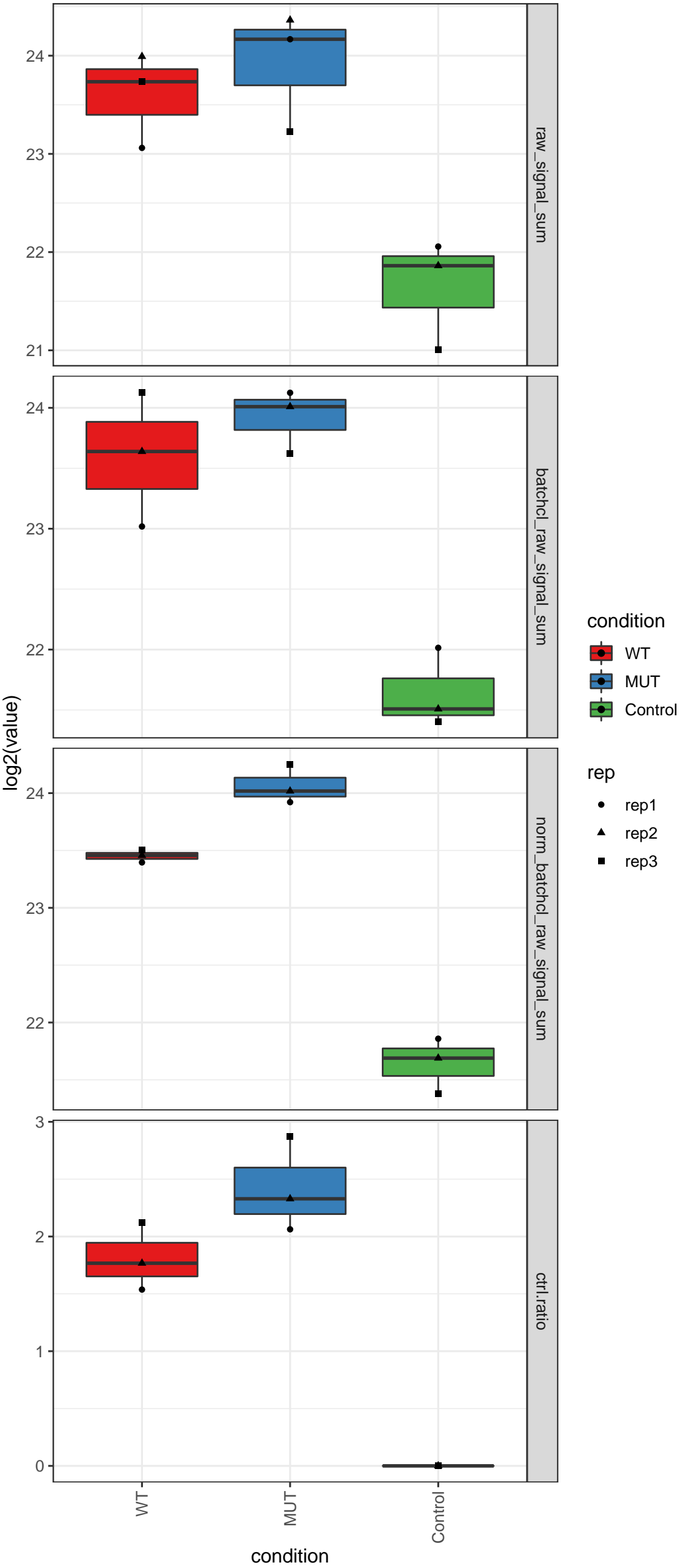
MVD1 – P32377

Diphosphomevalonate decarboxylase OS=*Saccharomyces cerevisiae* (strain

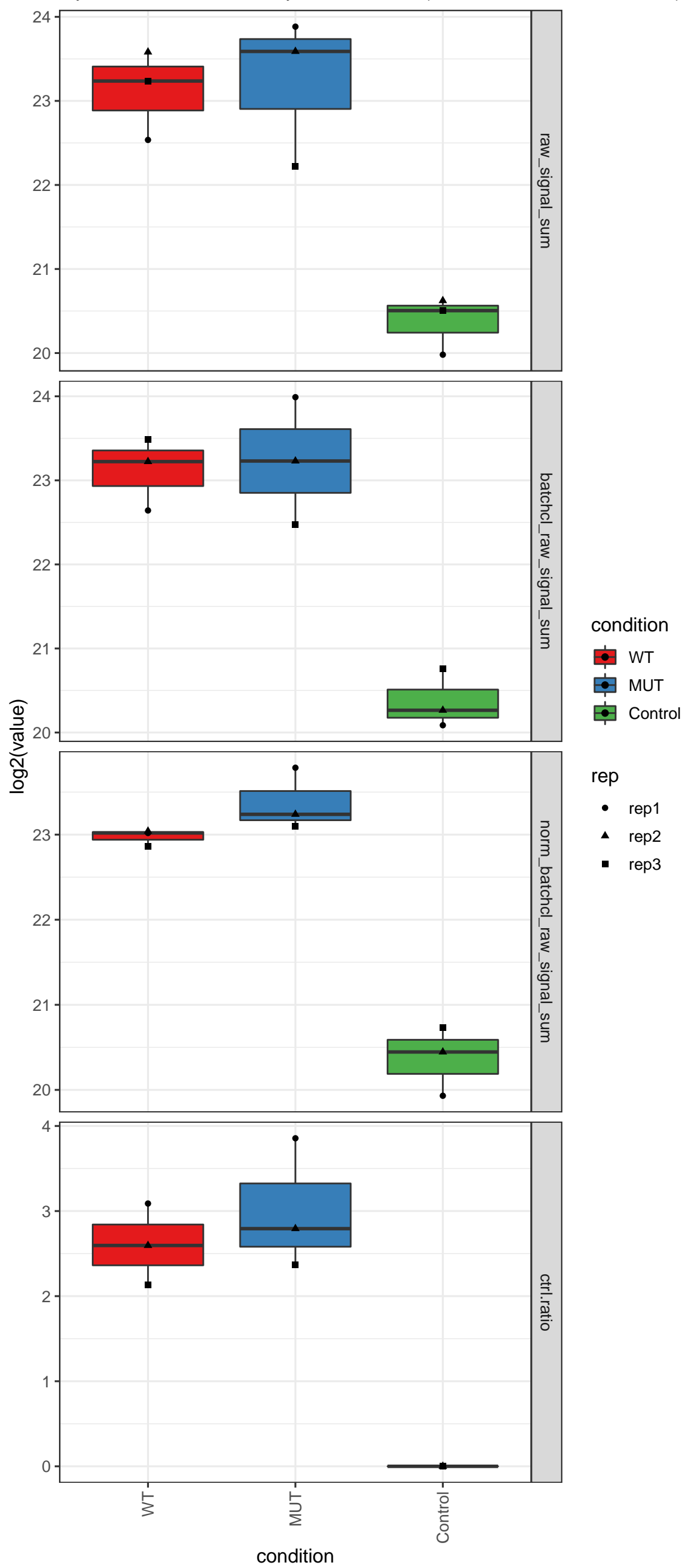


MYO2 – P19524

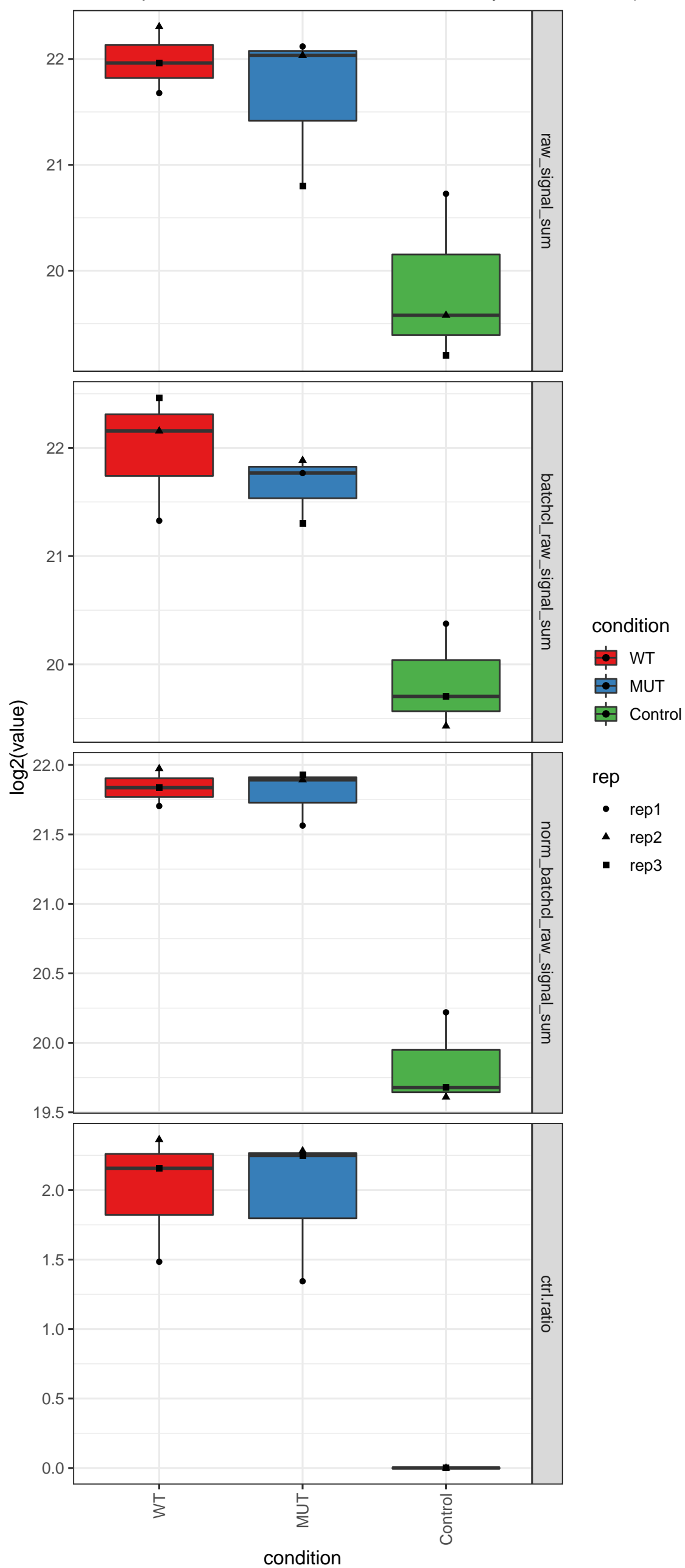
Myosin-2 OS=*Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) G



Myosin-3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) G

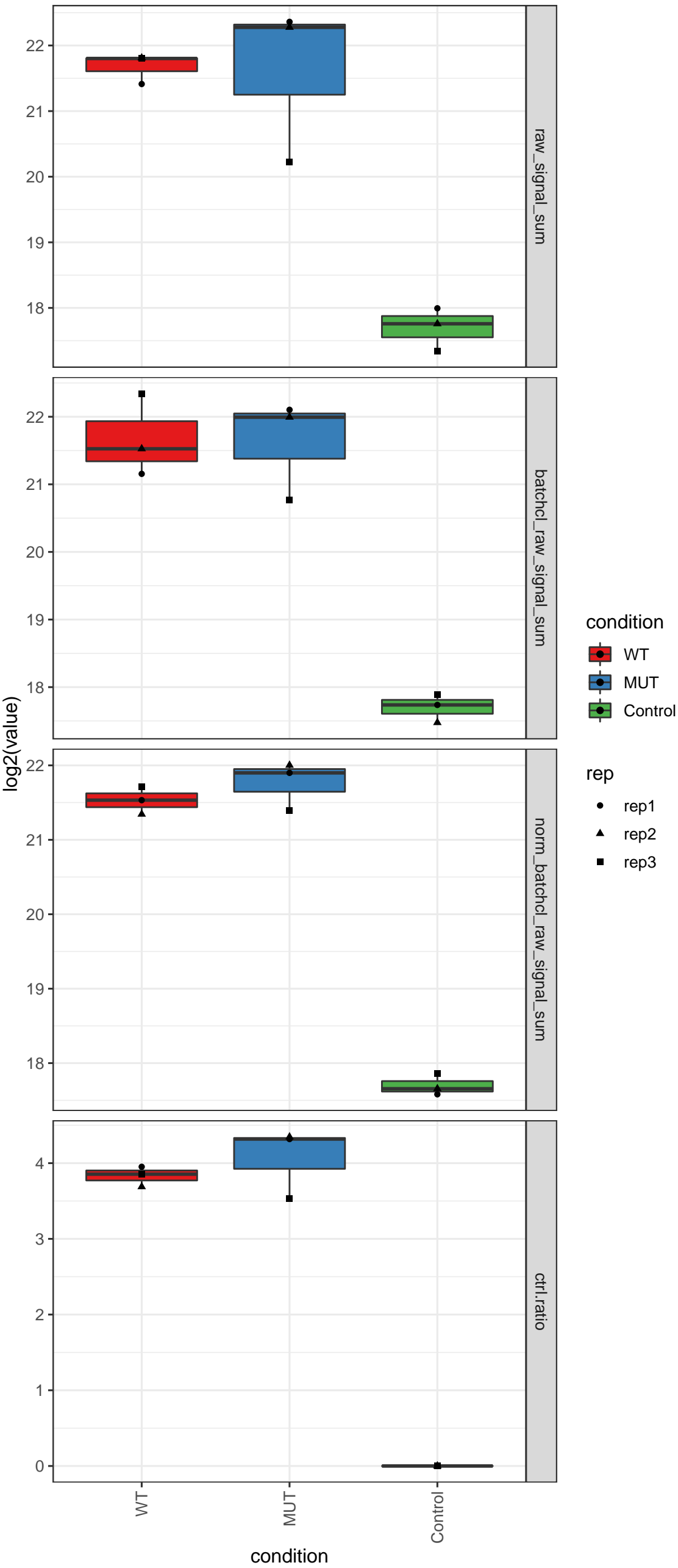


NAM7 – P30771

ATP-dependent helicase NAM7 OS=*Saccharomyces cerevisiae* (strain A

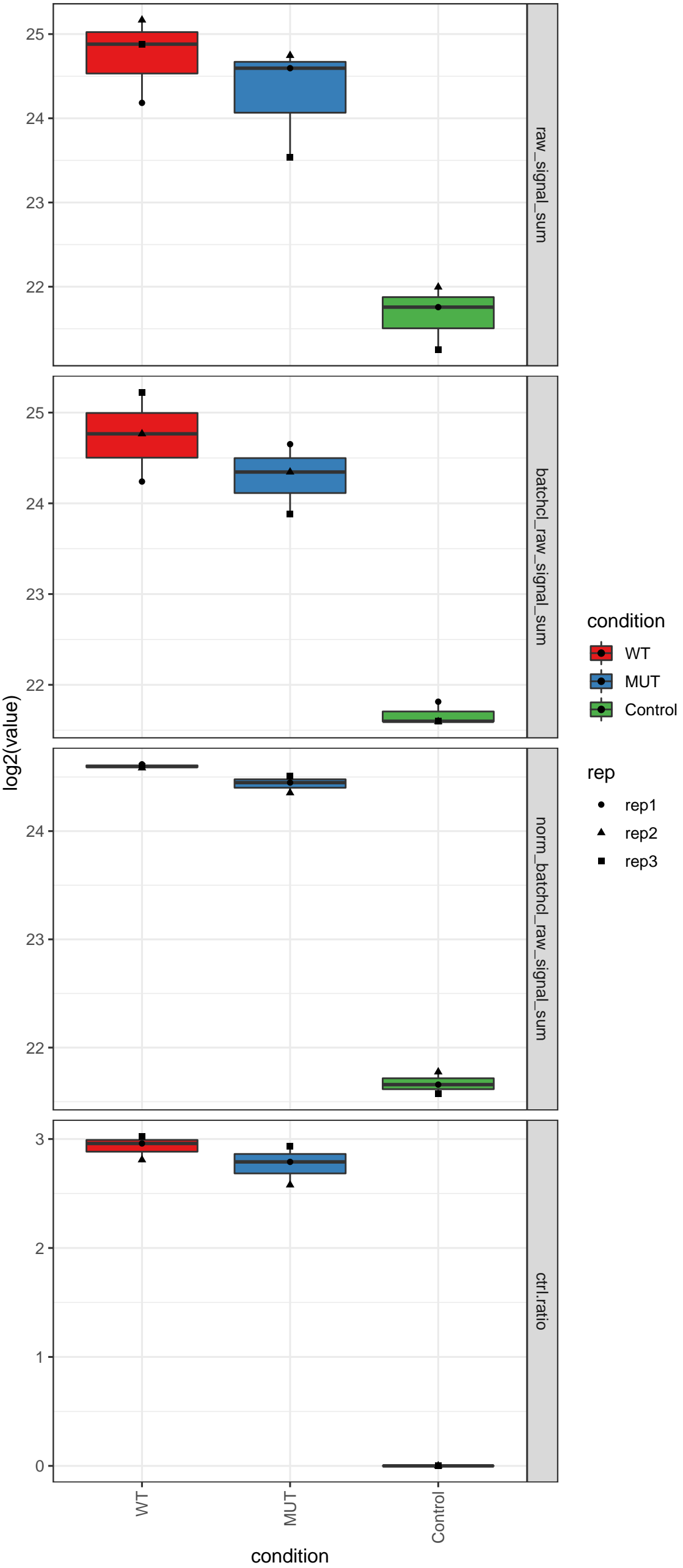
NAM9 – P27929

37S ribosomal protein NAM9, mitochondrial OS=*Saccharomyces cerevisia*



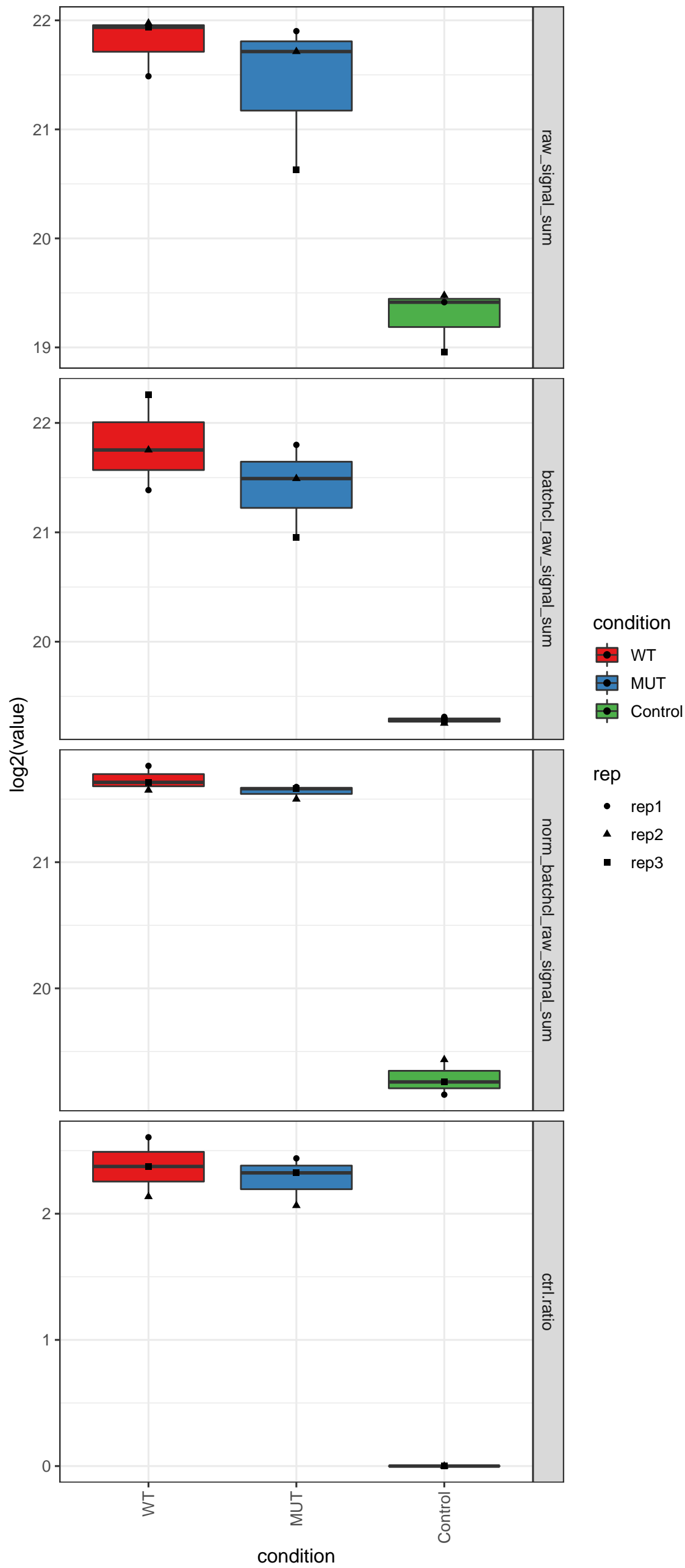
NAT1 – P12945

N-terminal acetyltransferase A complex subunit NAT1 OS=Saccharomyces



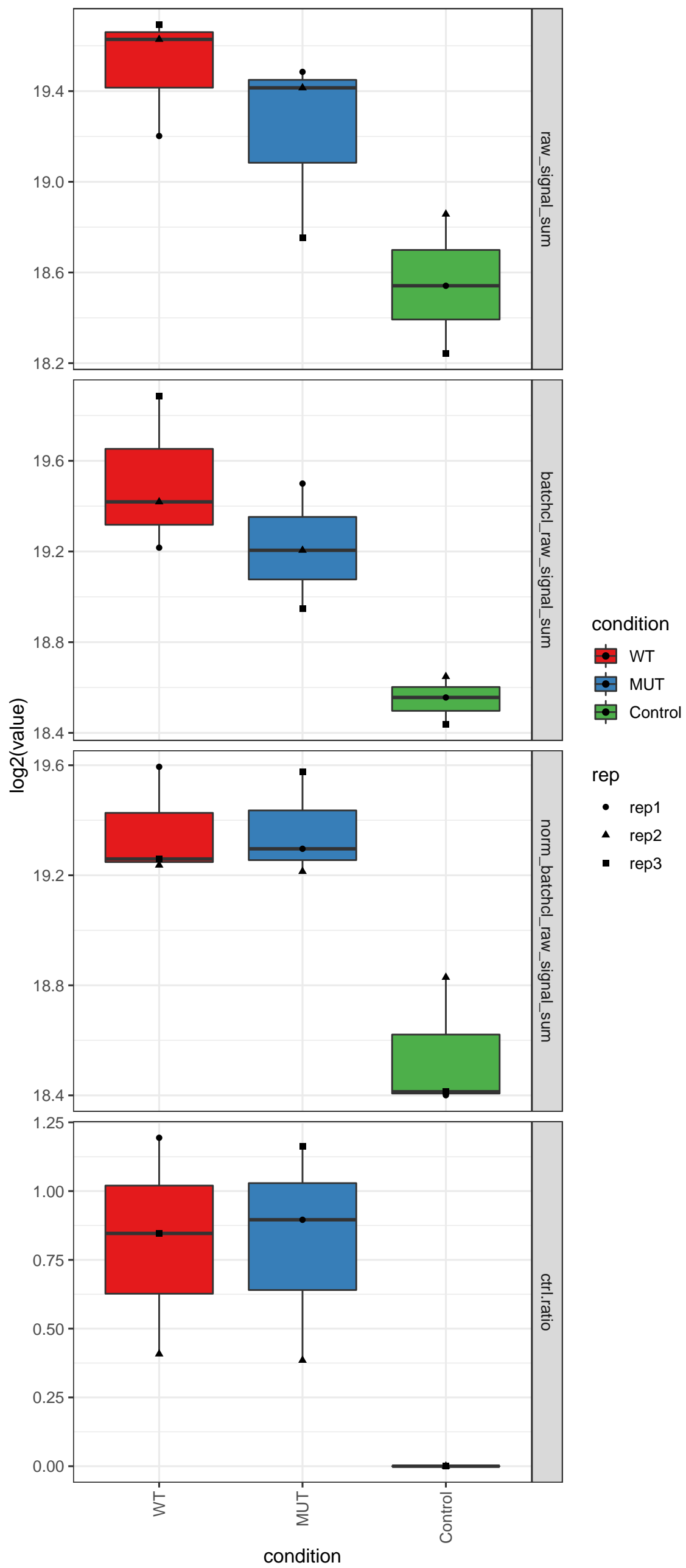
NAT10 – P53914

RNA cytidine acetyltransferase OS=*Saccharomyces cerevisiae* (strain ATC



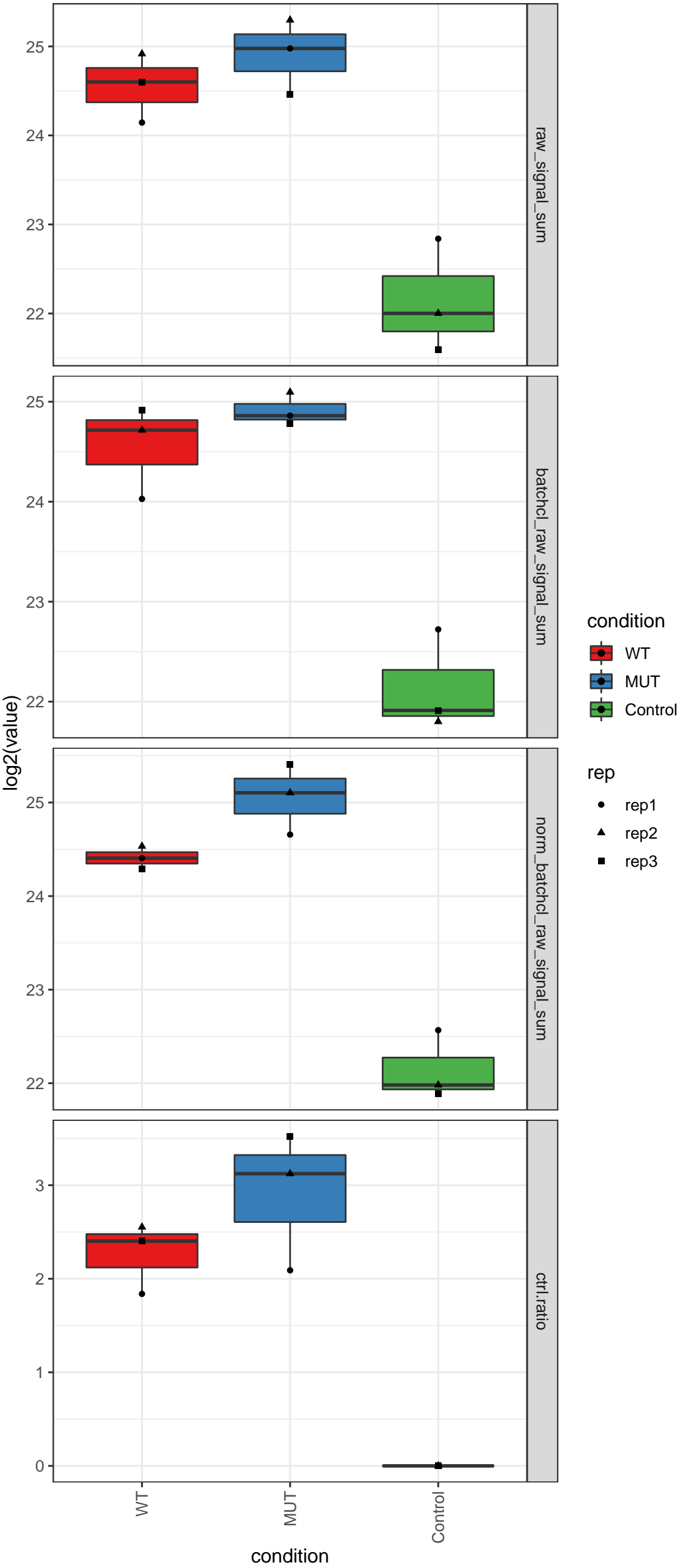
NCE102 – Q12207

Non-classical export protein 2 OS=*Saccharomyces cerevisiae* (strain ATCC 22016 / DSM 5780 / S288C)



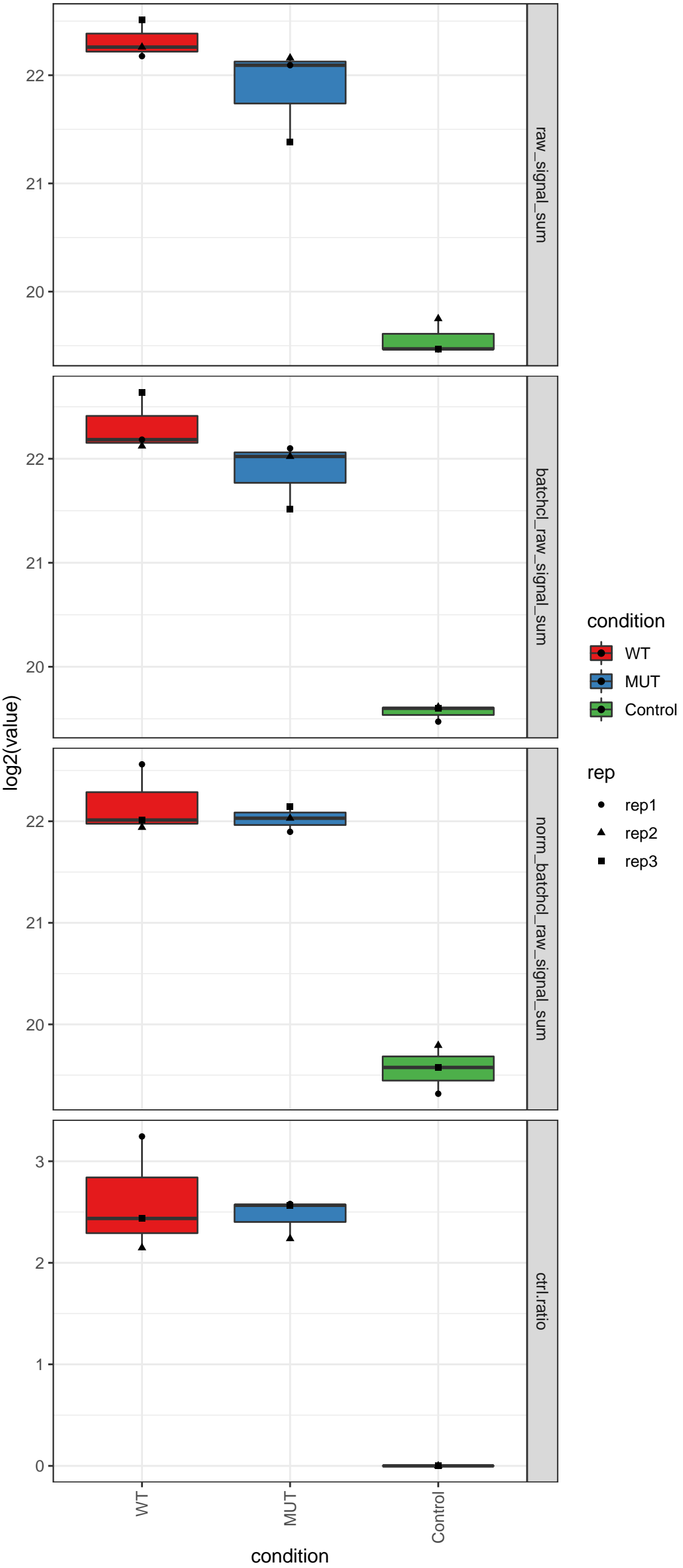
NDI1 – P32340

Rotenone-insensitive NADH-ubiquinone oxidoreductase, mitochondrial O



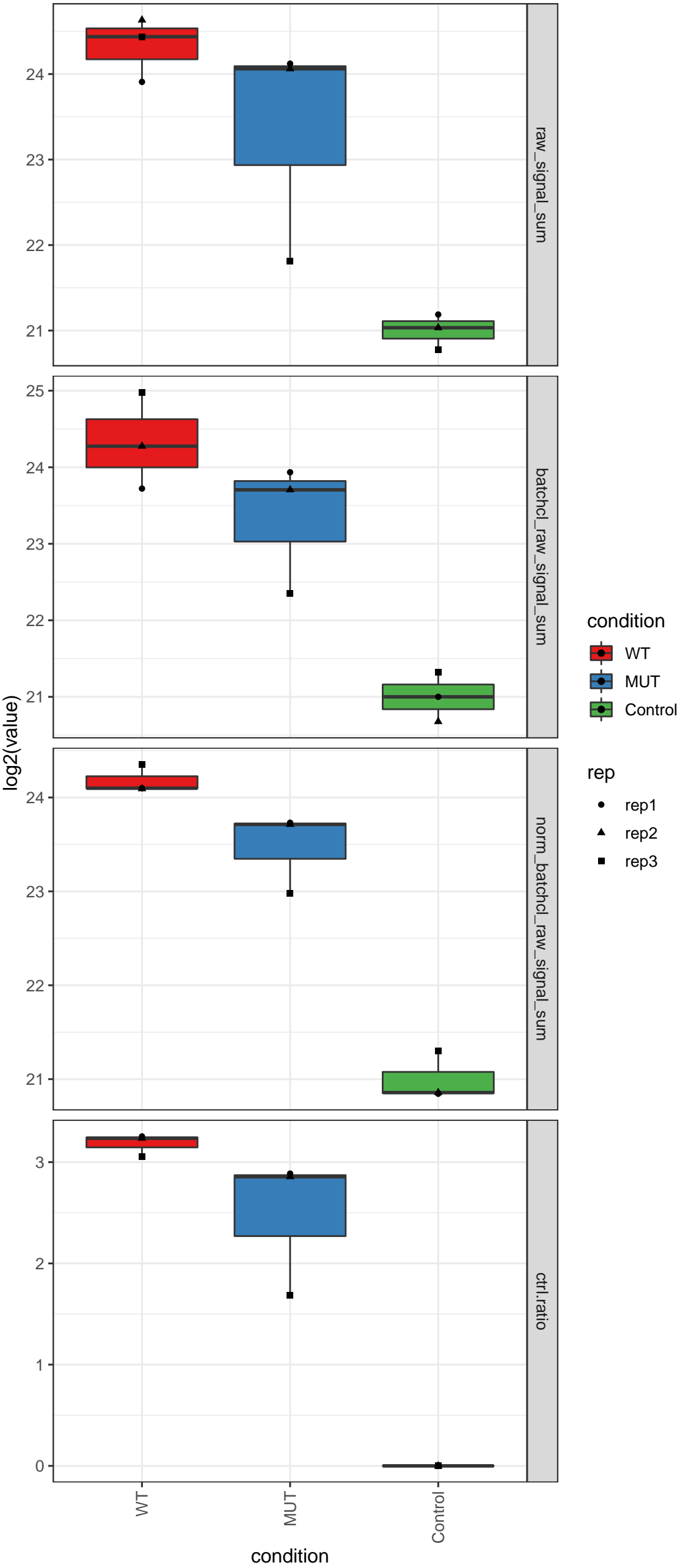
NGG1 – P32494

Chromatin-remodeling complexes subunit NGG1 OS=*Saccharomyces cerevisiae*



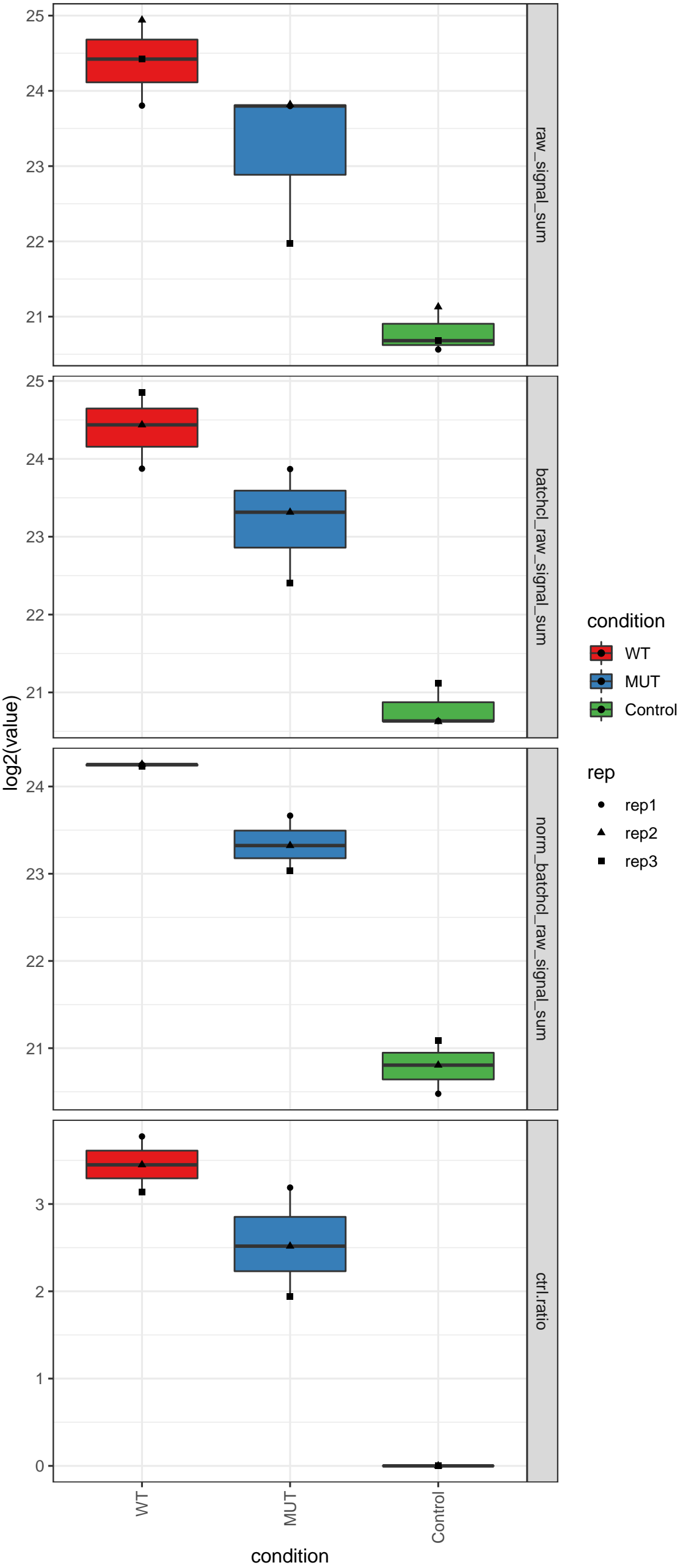
NHP2 – P32495

H/ACA ribonucleoprotein complex subunit 2 OS=*Saccharomyces cerevisiae*



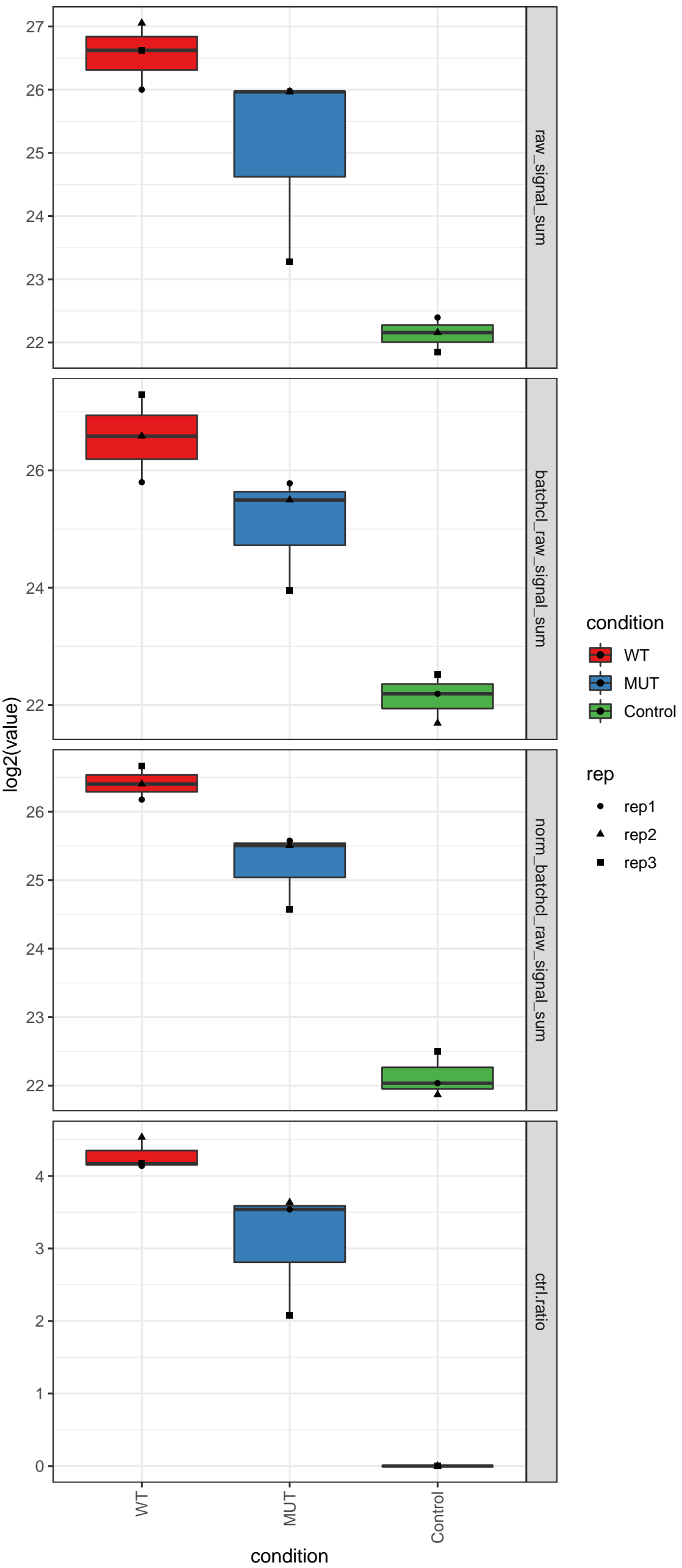
NHP6A – P11632

Non-histone chromosomal protein 6A OS=*Saccharomyces cerevisiae* (stra



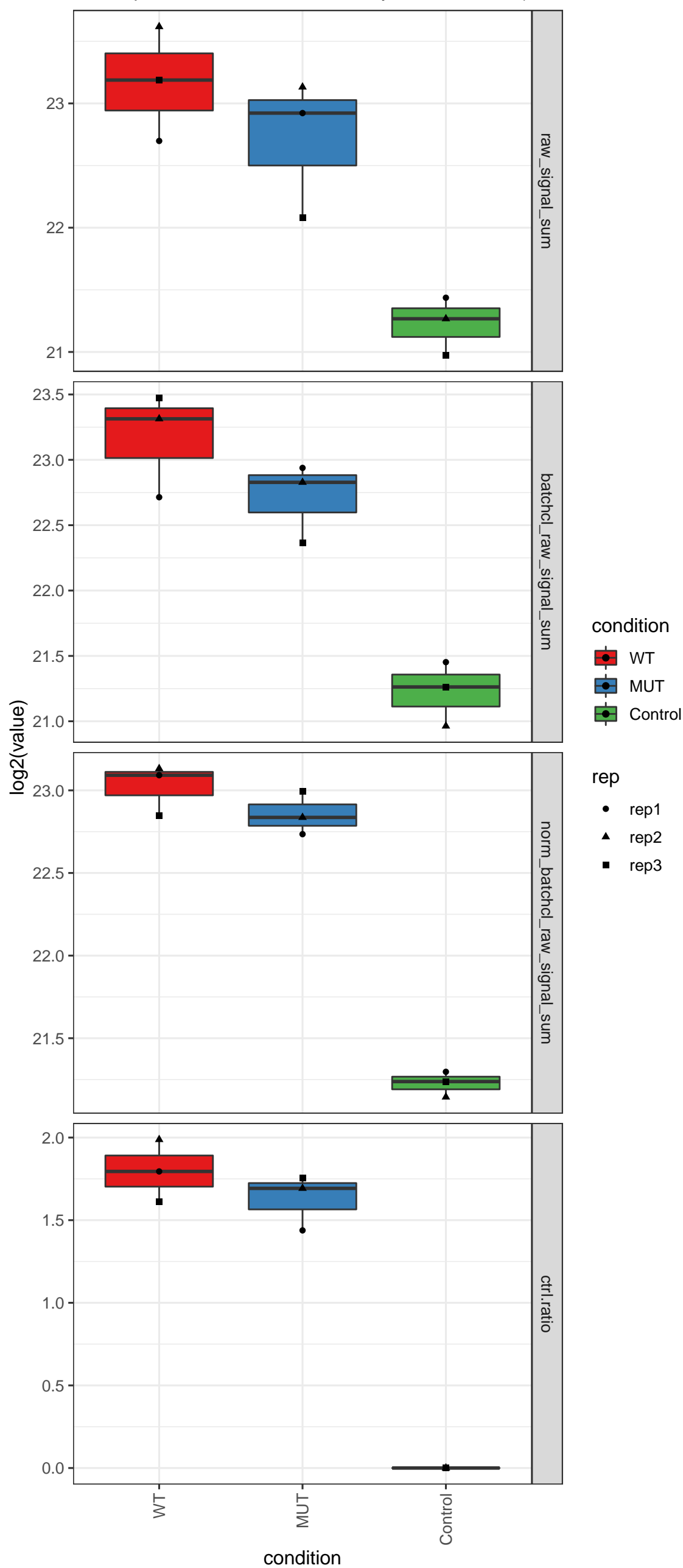
NHP6B – P11633

Non-histone chromosomal protein 6B OS=*Saccharomyces cerevisiae* (strain



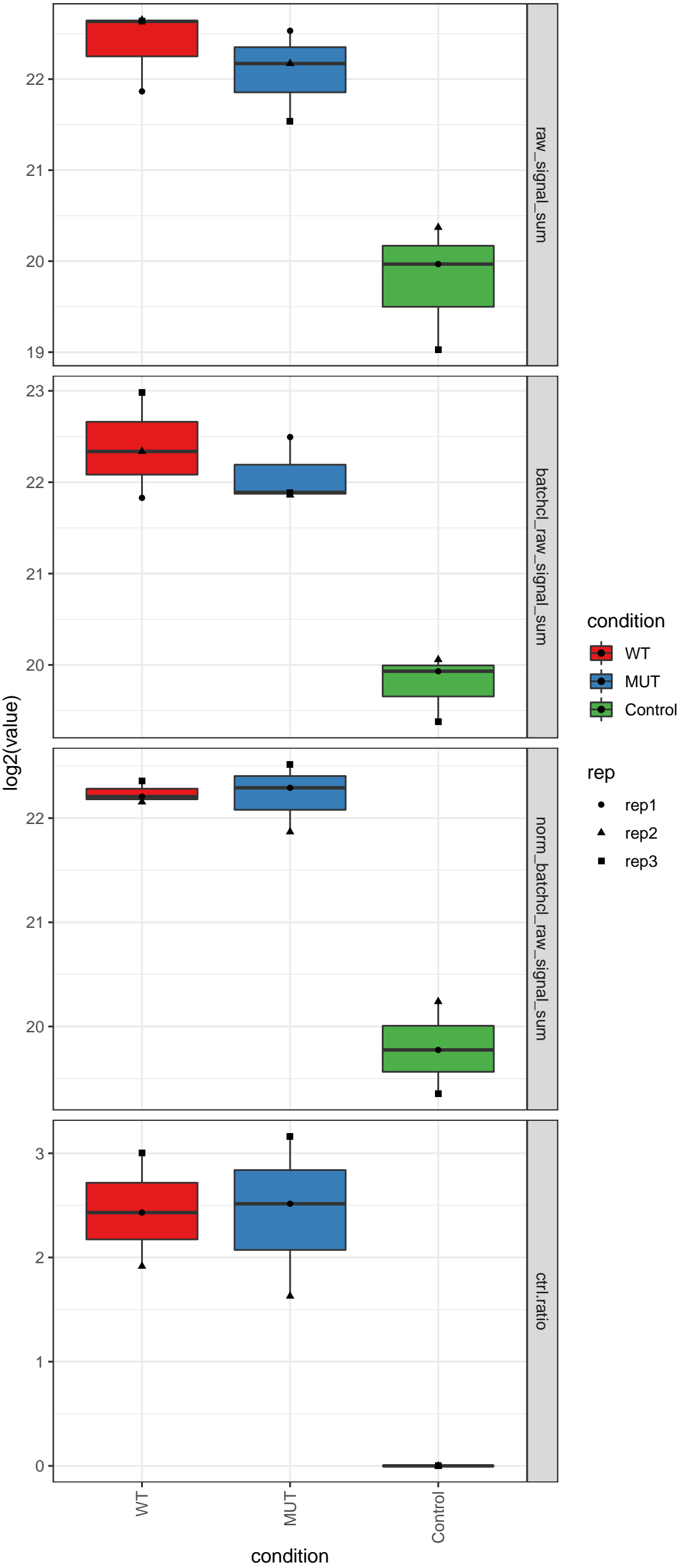
NIC96 – P34077

Nucleoporin NIC96 OS=*Saccharomyces cerevisiae* (strain ATCC 204508)



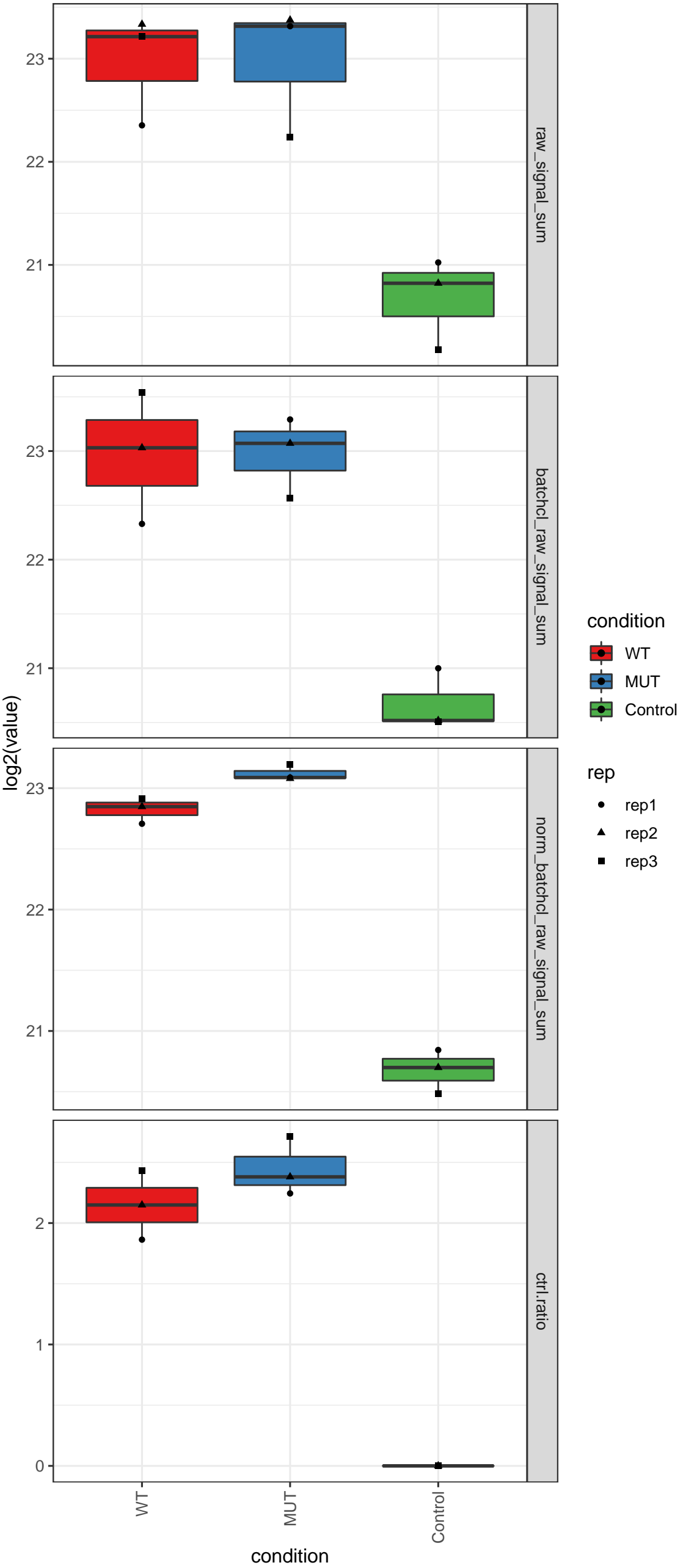
NIP1 – P32497

Eukaryotic translation initiation factor 3 subunit C OS=*Saccharomyces cere*



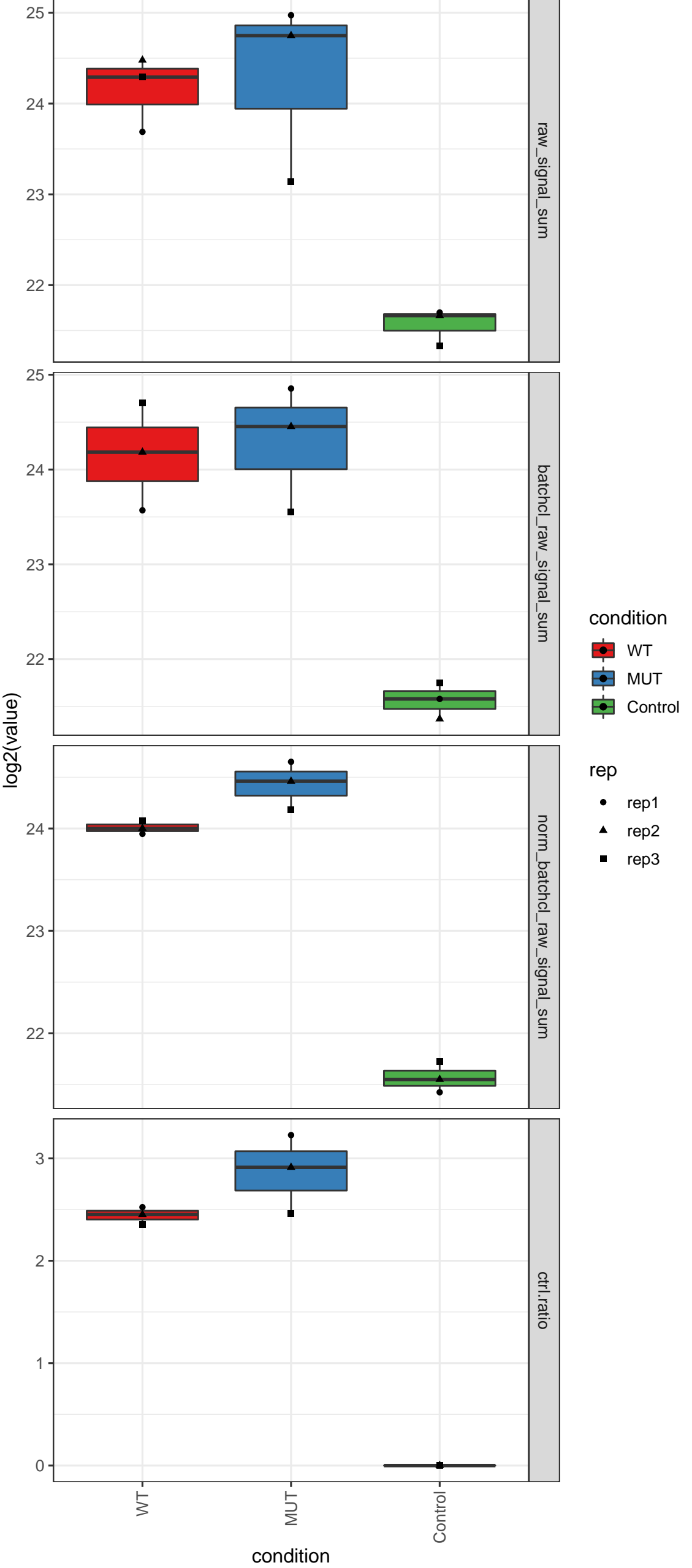
NOC2 – P39744

Nucleolar complex protein 2 OS=*Saccharomyces cerevisiae* (strain ATCC 2



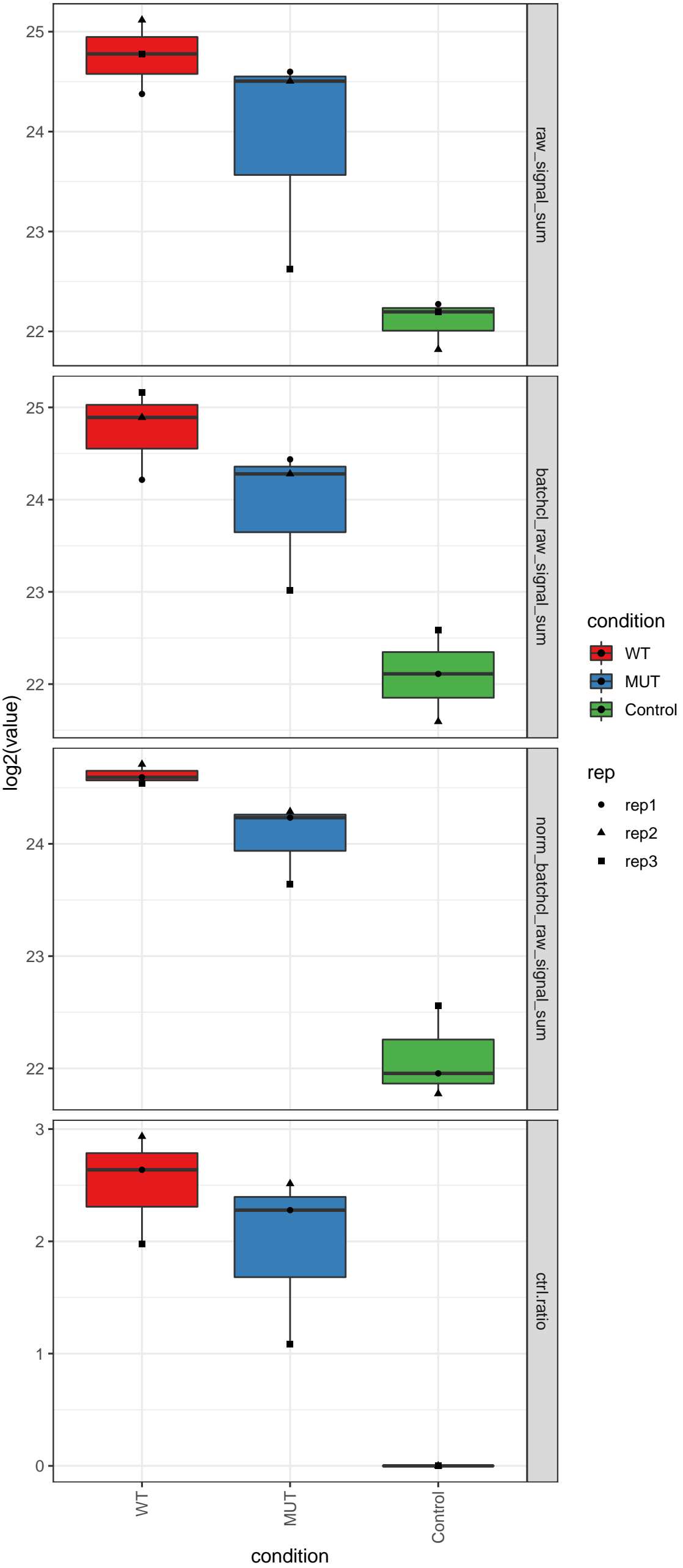
NOG1 – Q02892

Nucleolar GTP-binding protein 1 OS=*Saccharomyces cerevisiae* (strain ATCC 24843)



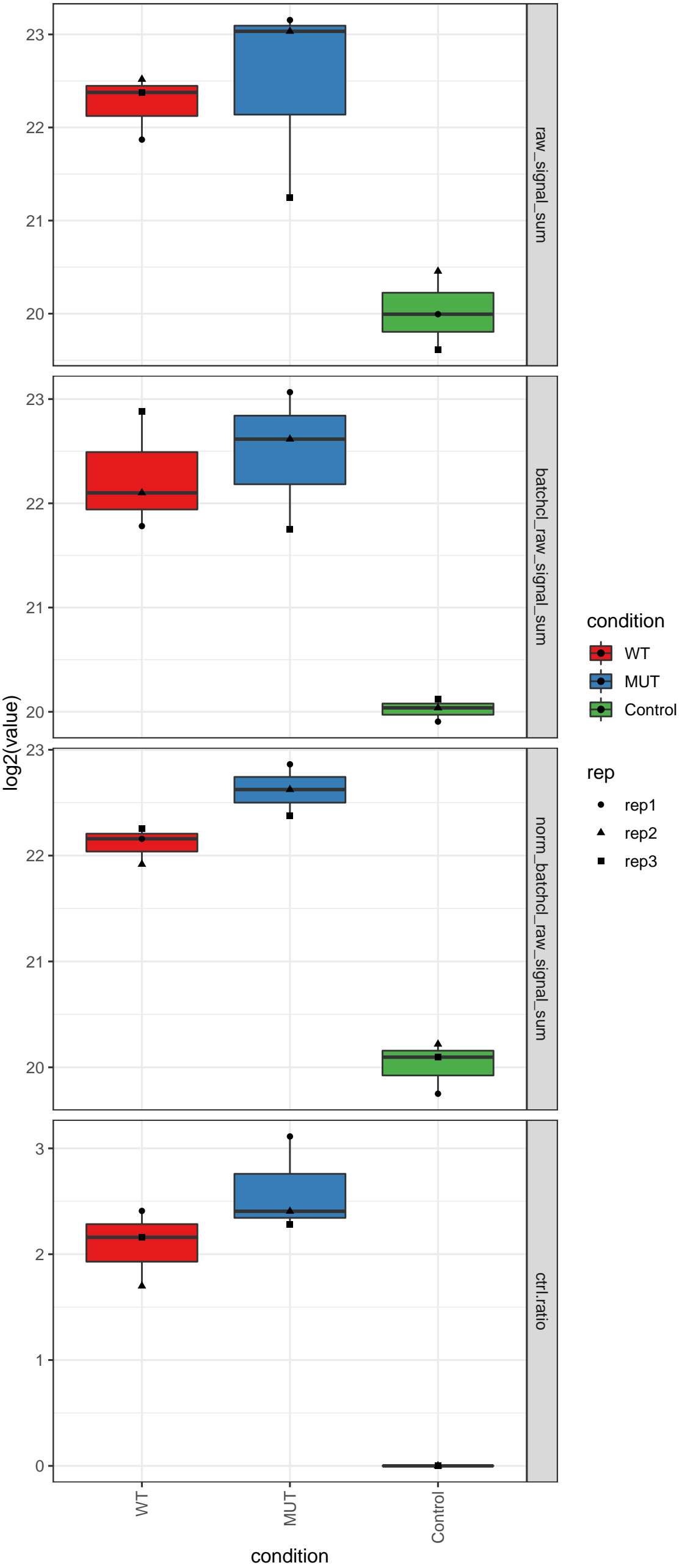
NOP1 – P15646

rRNA 2'-O-methyltransferase fibrillarin OS=*Saccharomyces cerevisiae* (strain



NOP12 – Q08208

Nucleolar protein 12 OS=*Saccharomyces cerevisiae* (strain ATCC 204508)

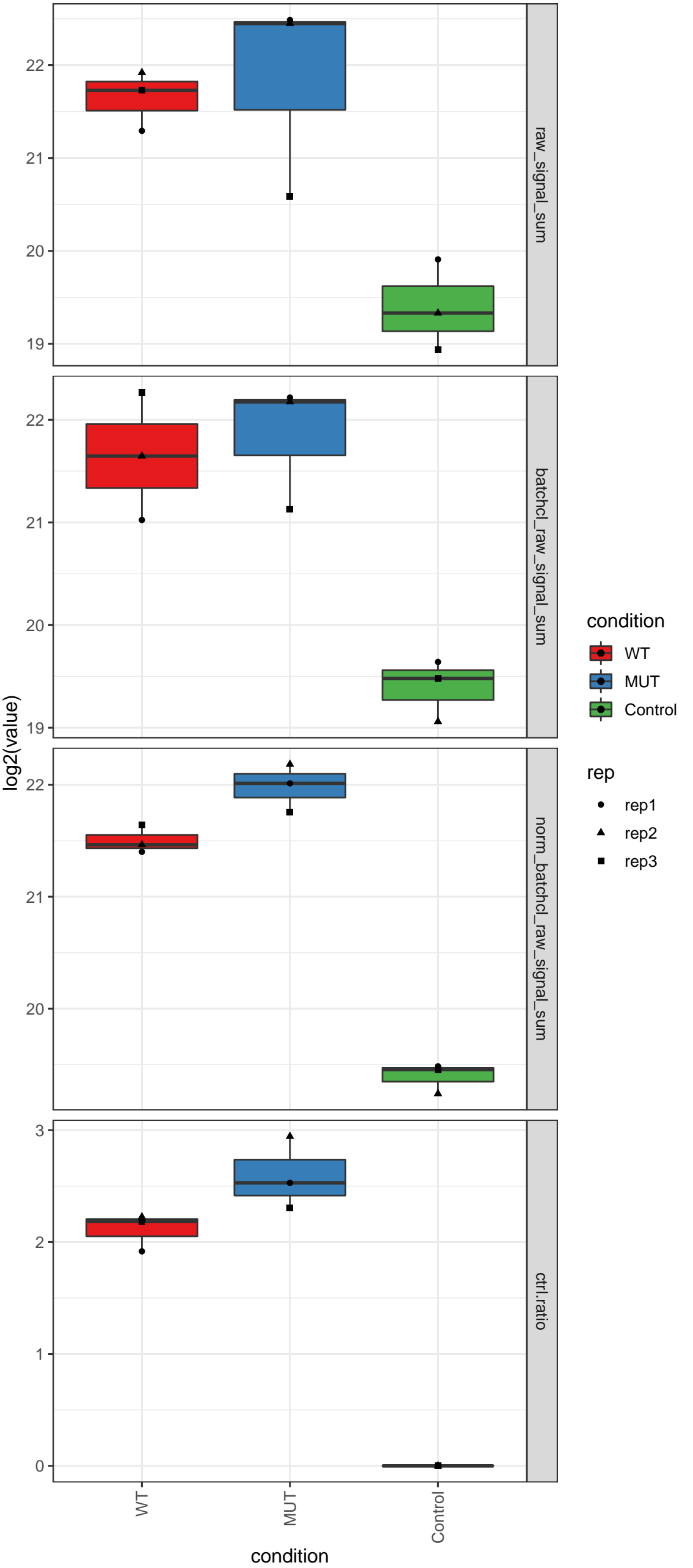


Nucleolar protein 13 OS=*Saccharomyces cerevisiae* (strain ATCC 20450)



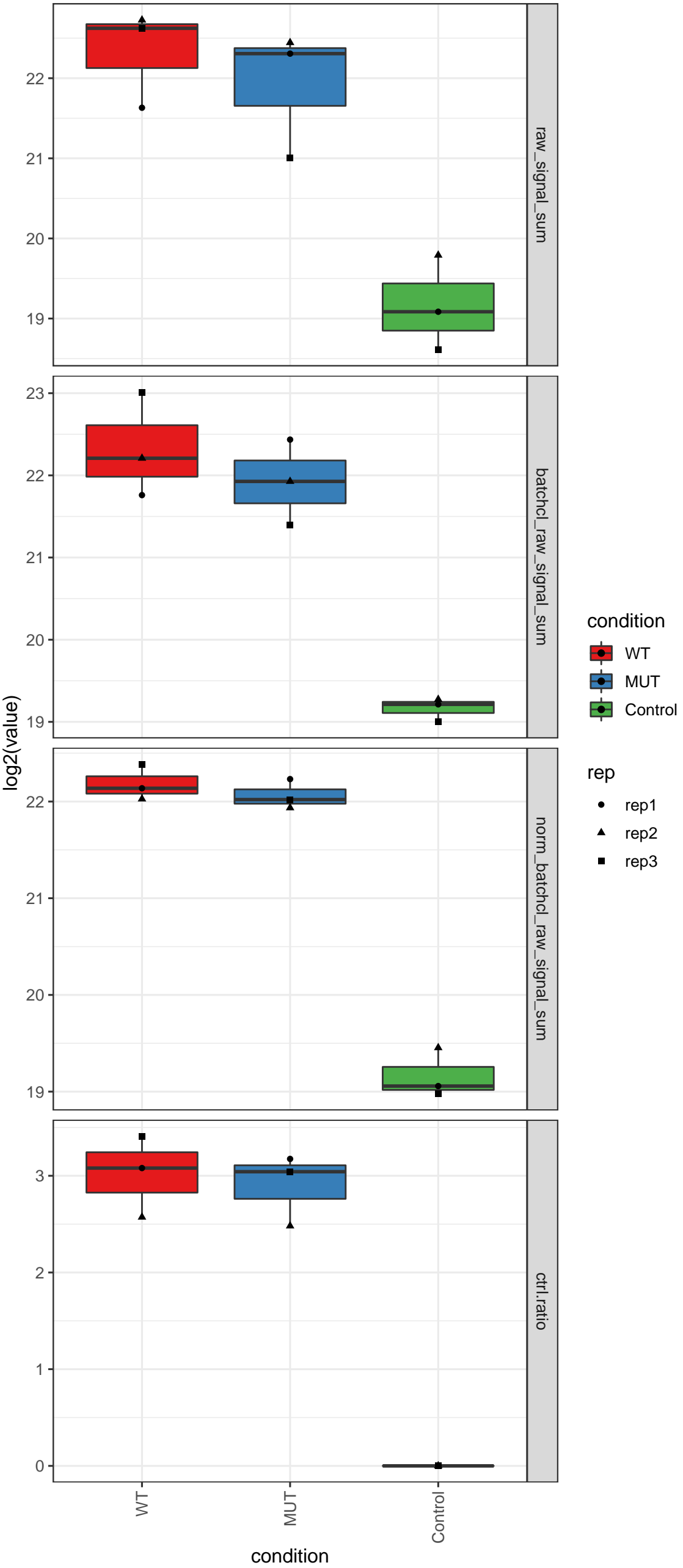
NOP16 – P40007

Nucleolar protein 16 OS=*Saccharomyces cerevisiae* (strain ATCC 204508)



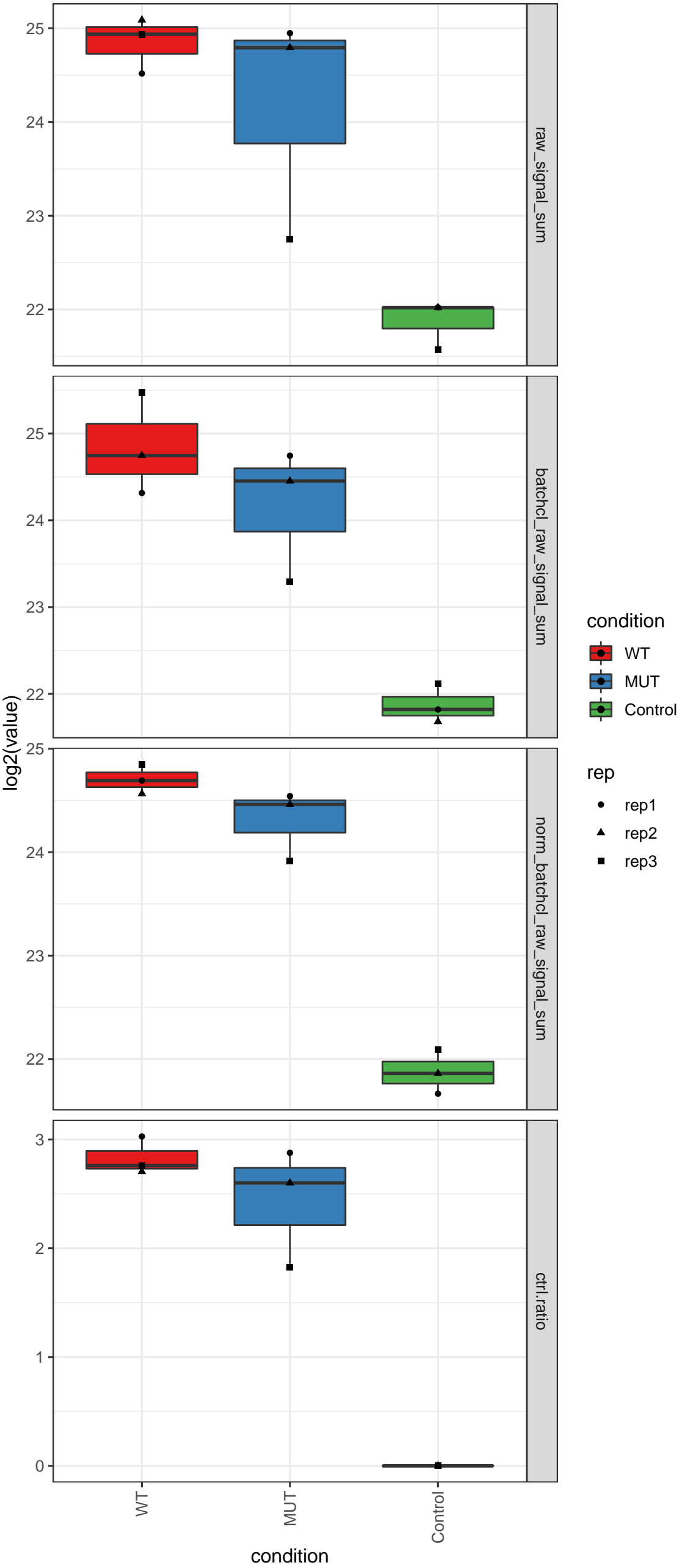
NOP2 – P40991

25S rRNA (cytosine(2870)–C(5))–methyltransferase OS=Saccharomyces cerevisiae



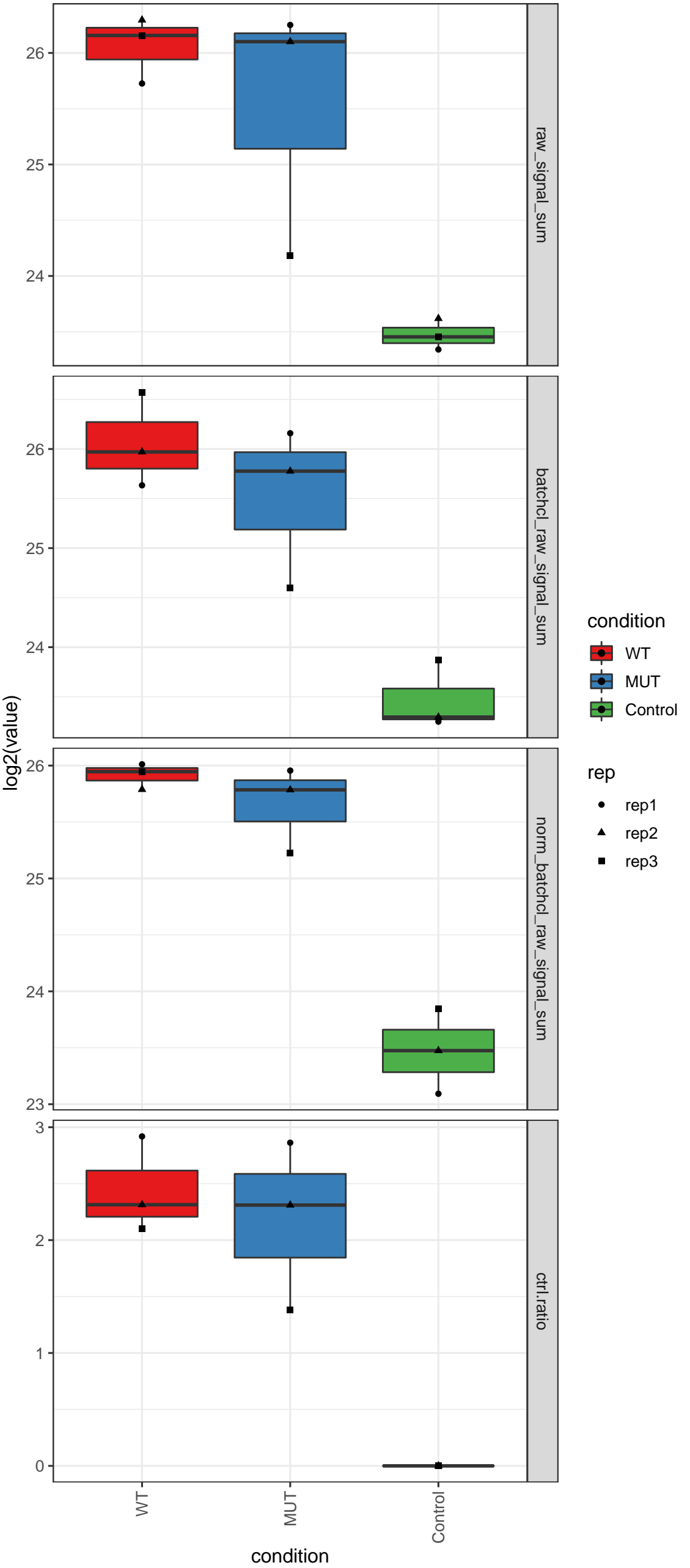
NOP56 – Q12460

Nucleolar protein 56 OS=*Saccharomyces cerevisiae* (strain ATCC 204508)



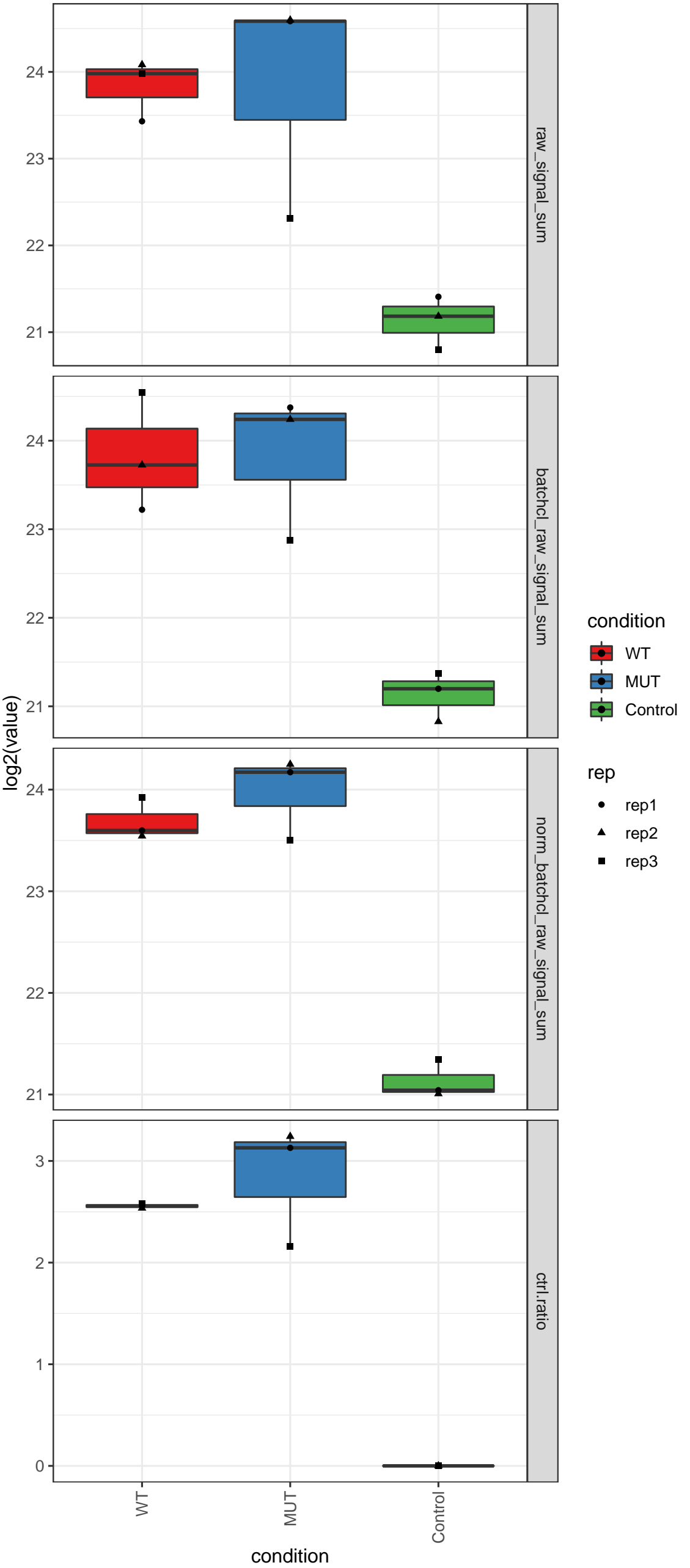
NOP58 – Q12499

Nucleolar protein 58 OS=*Saccharomyces cerevisiae* (strain ATCC 204508)



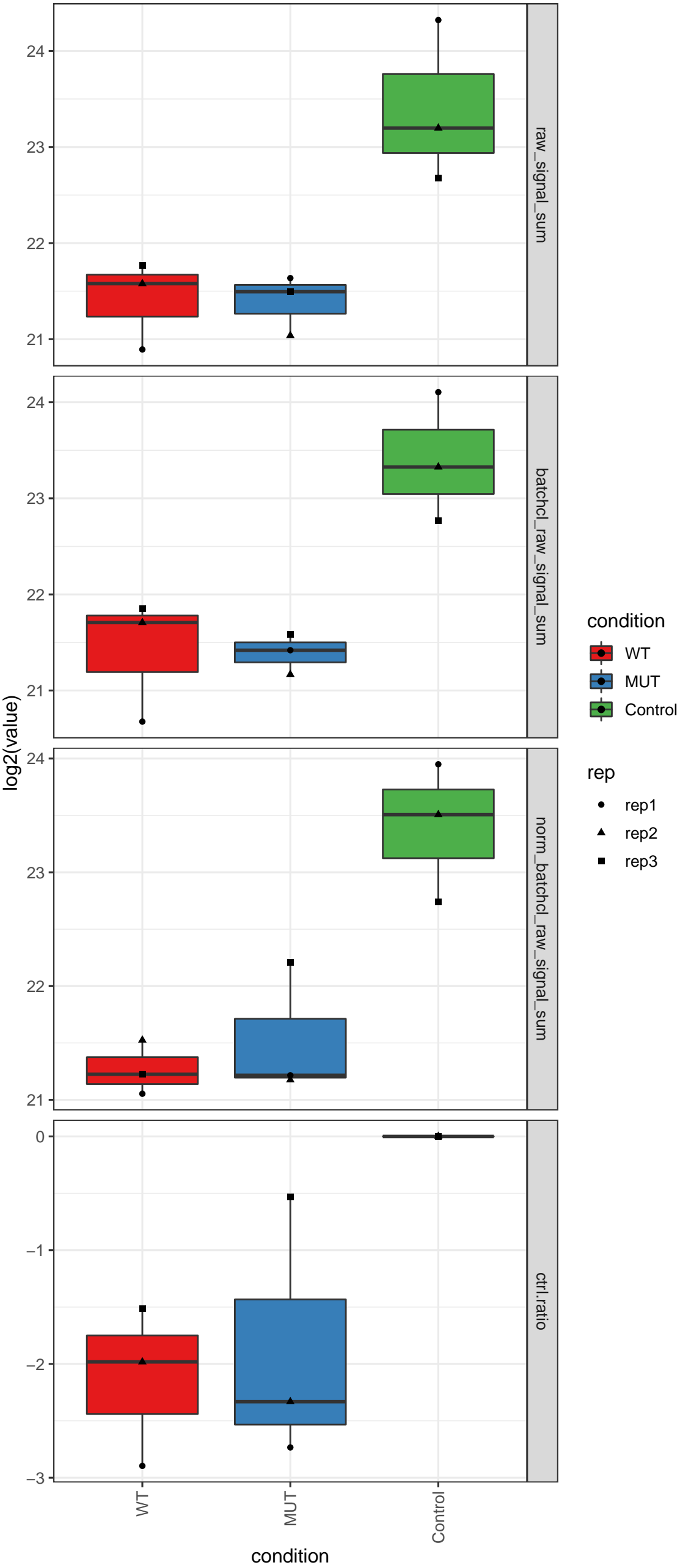
NOP7 – P53261

Pescadillo homolog OS=*Saccharomyces cerevisiae* (strain ATCC 204508 /



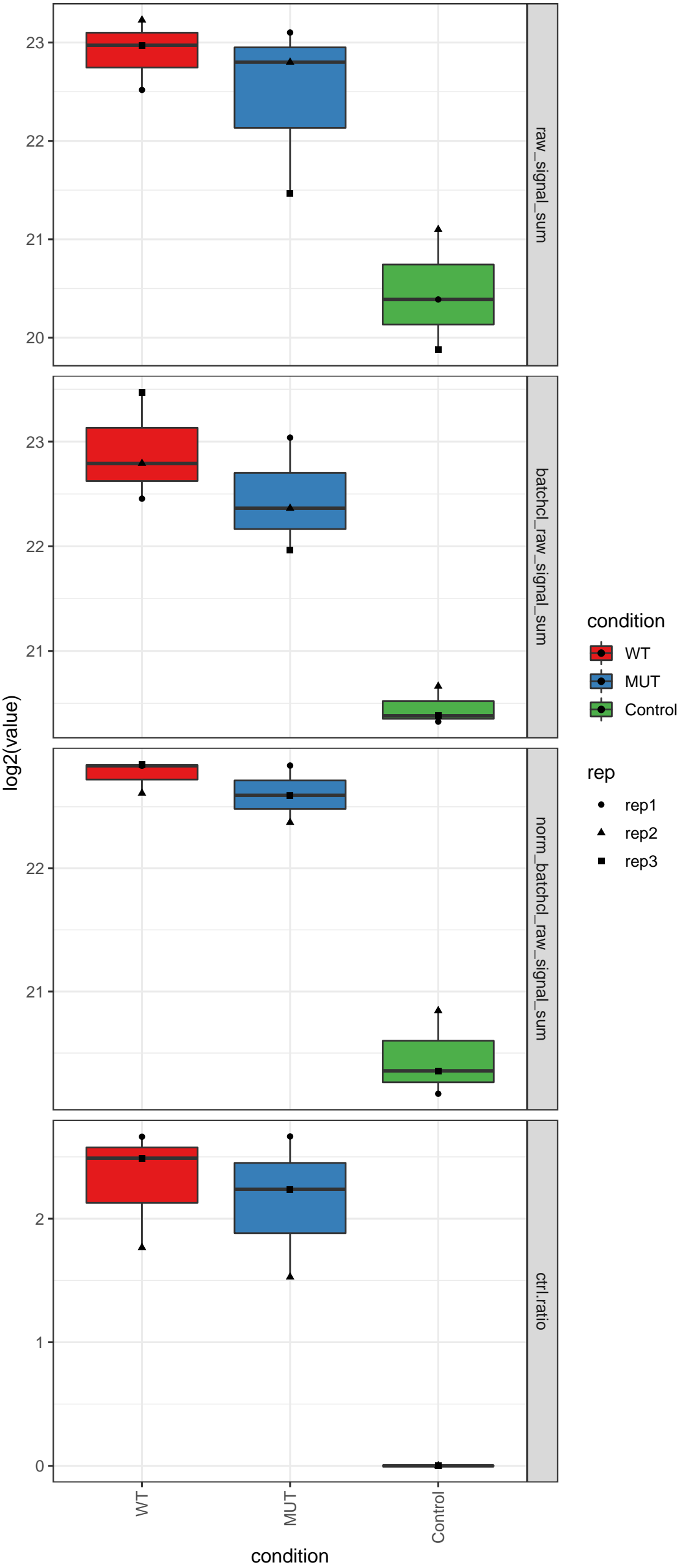
NOT5 – Q12514

General negative regulator of transcription subunit 5 OS=Saccharomyces cerevisiae



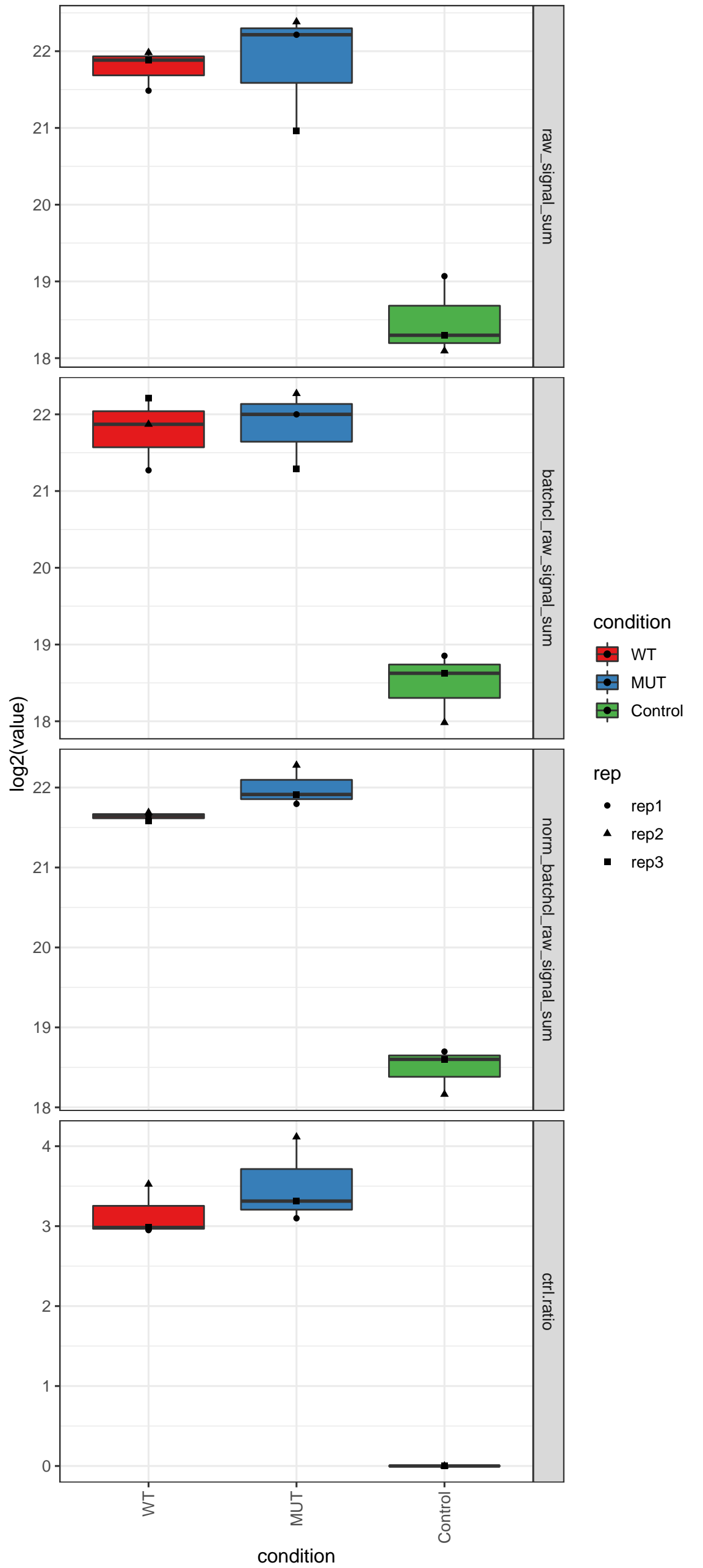
NPL6 – P32832

Chromatin structure–remodeling complex subunit RSC7 OS=*Saccharomyces cerevisiae*



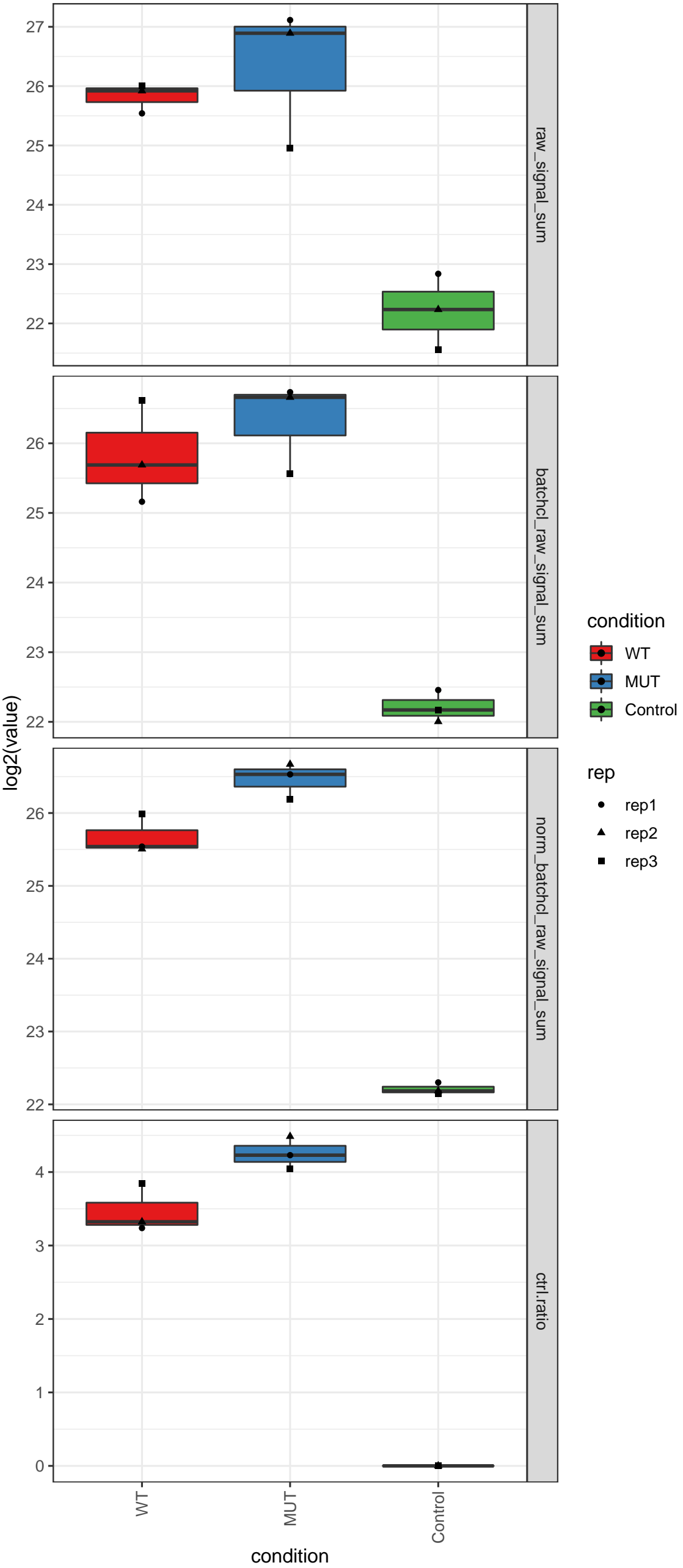
NSA1 – P53136

Ribosome biogenesis protein NSA1 OS=*Saccharomyces cerevisiae* (strain



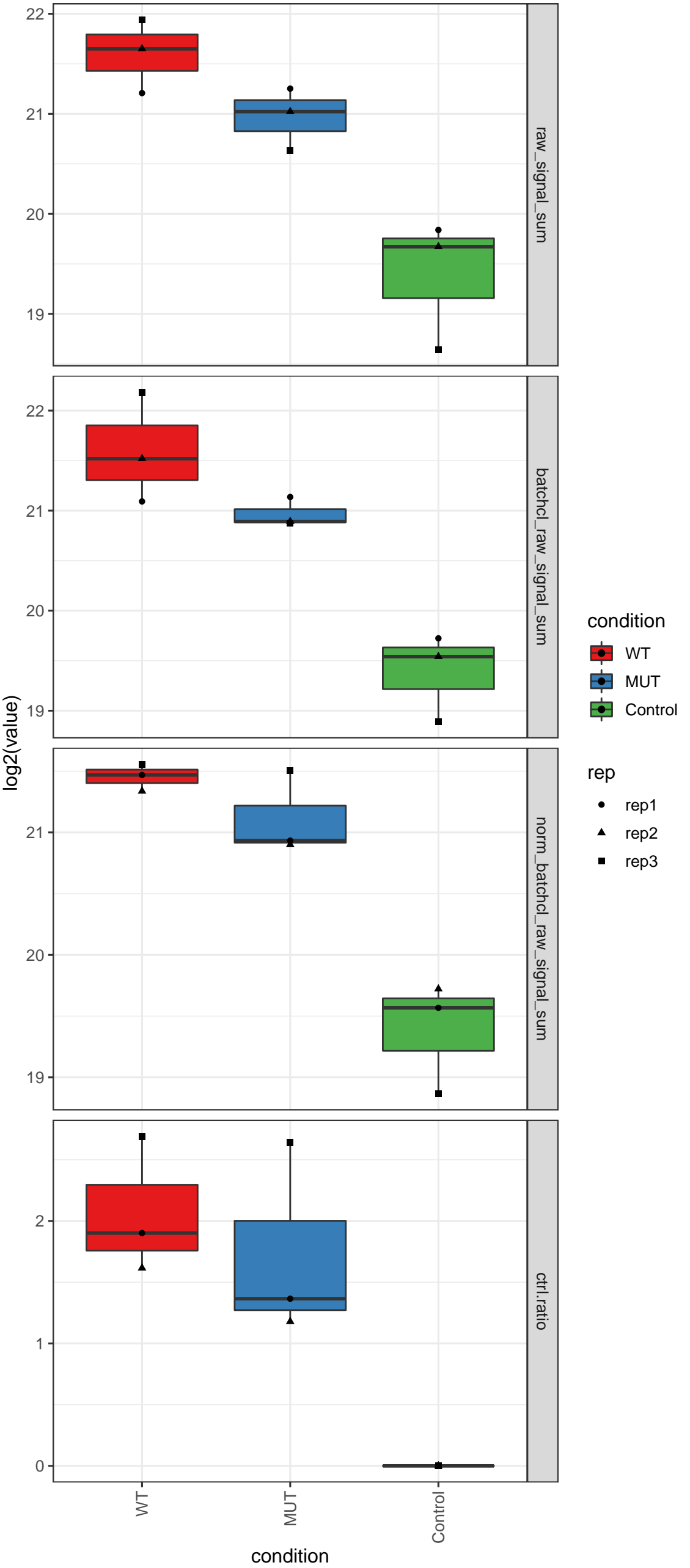
NSR1 – P27476

Nuclear localization sequence-binding protein OS=*Saccharomyces cerevisiae*



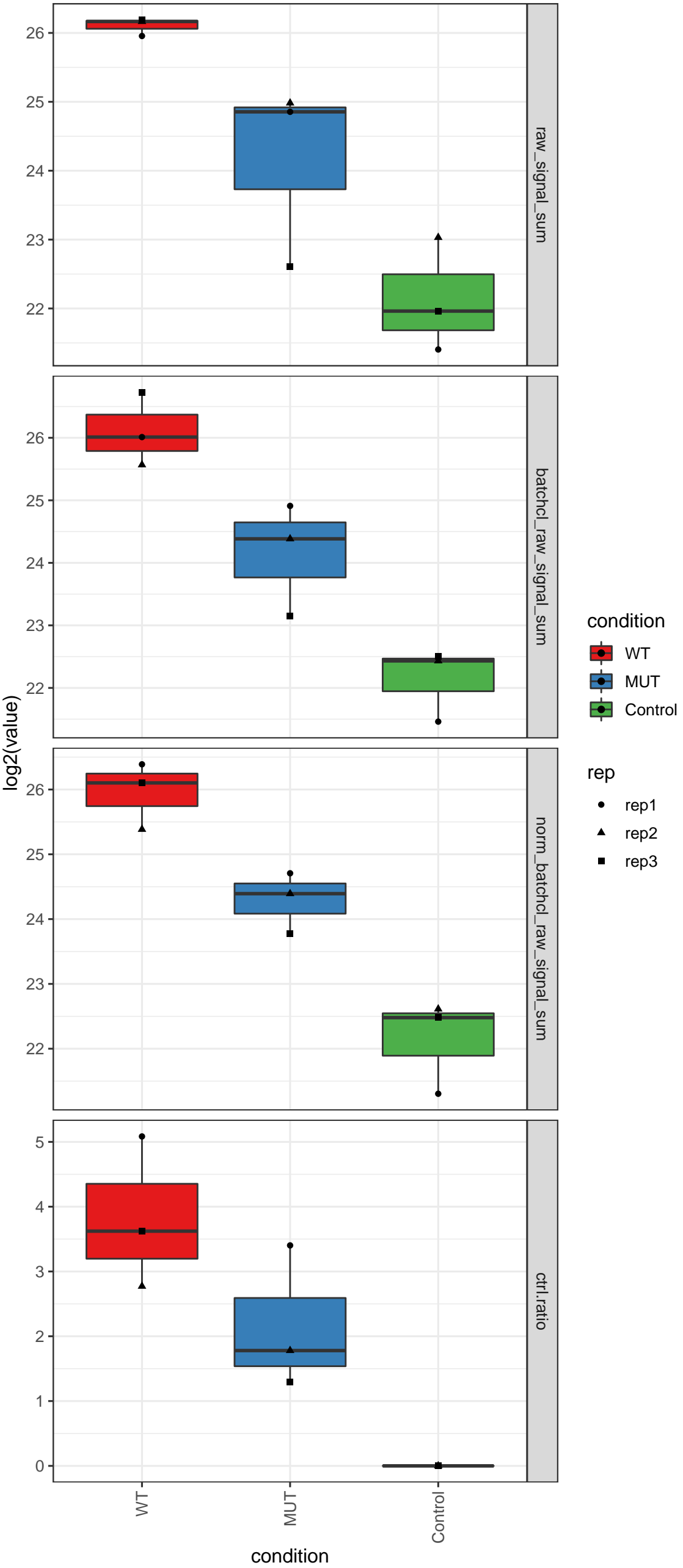
NTH1 – P32356

Neutral trehalase OS=*Saccharomyces cerevisiae* (strain ATCC 204508 / S



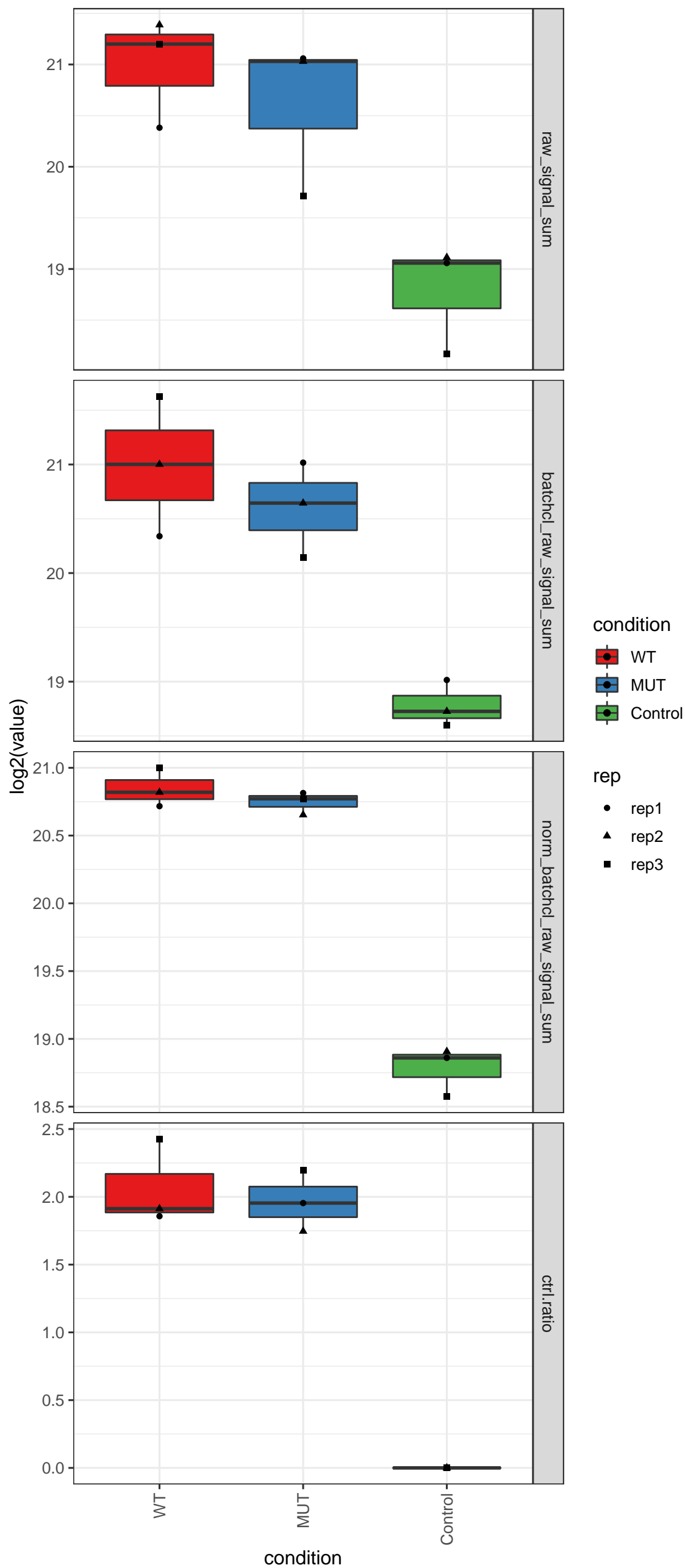
NTO1 – Q12311

NuA3 HAT complex component NTO1 OS=Saccharomyces cerevisiae (stra



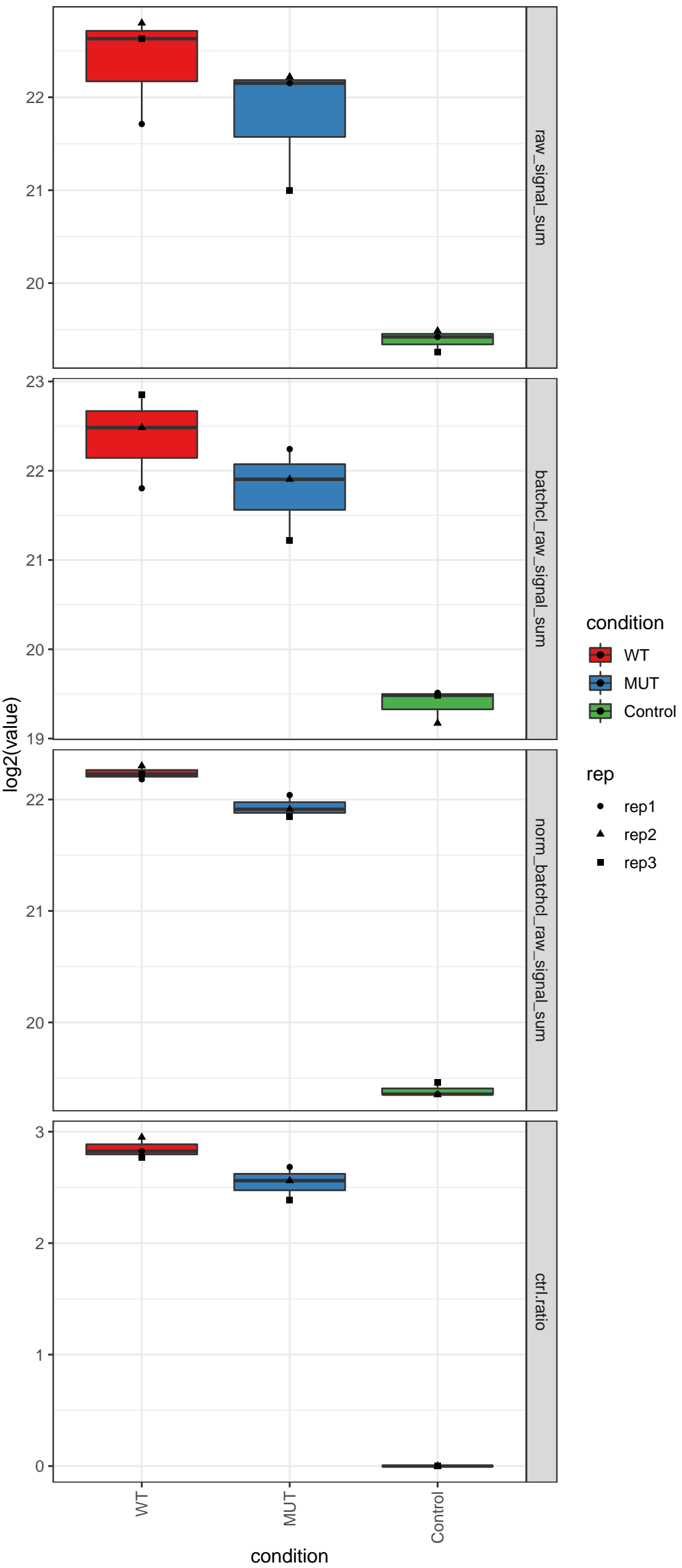
NUP145 – P49687

Nucleoporin NUP145 OS=*Saccharomyces cerevisiae* (strain ATCC 20450)



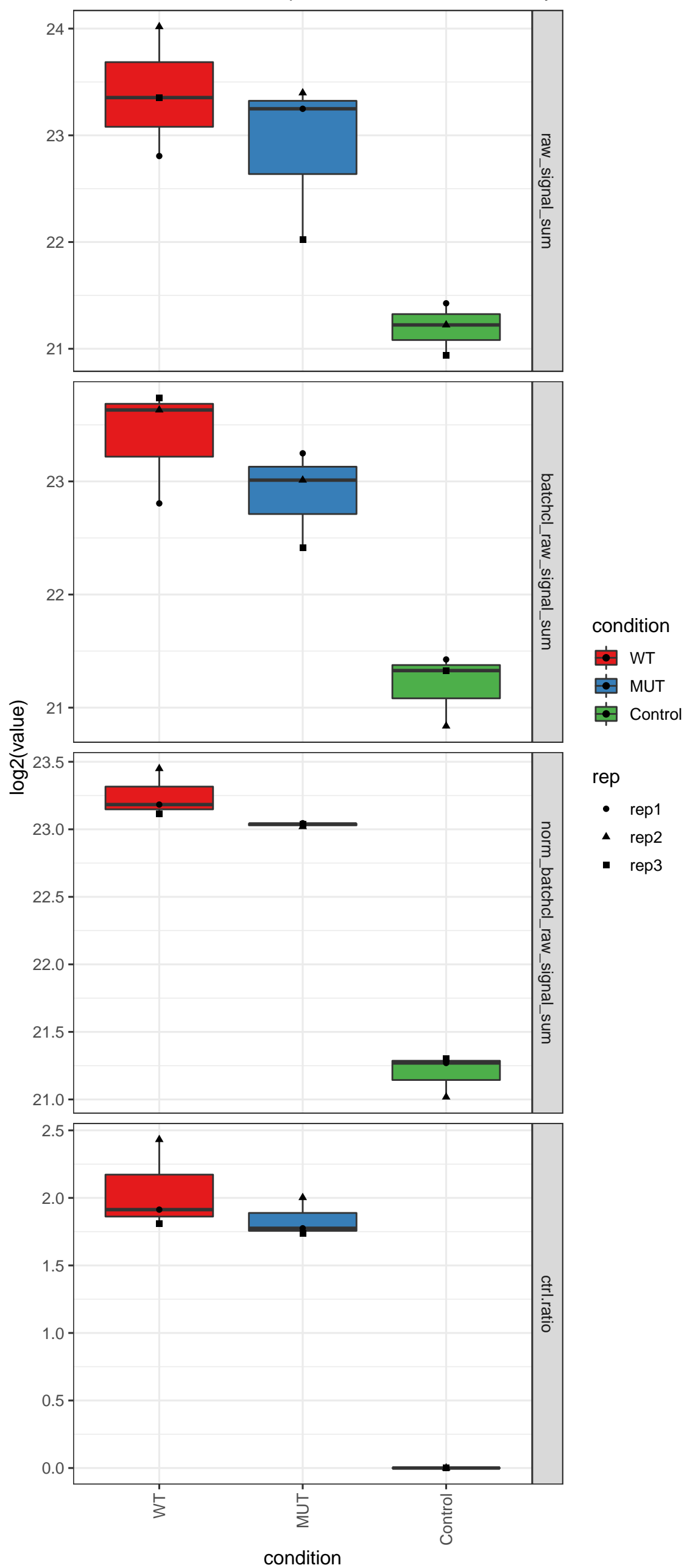
NUS1 – Q12063

Dehydrololichyl diphosphate synthase complex subunit NUS1 OS=Saccha

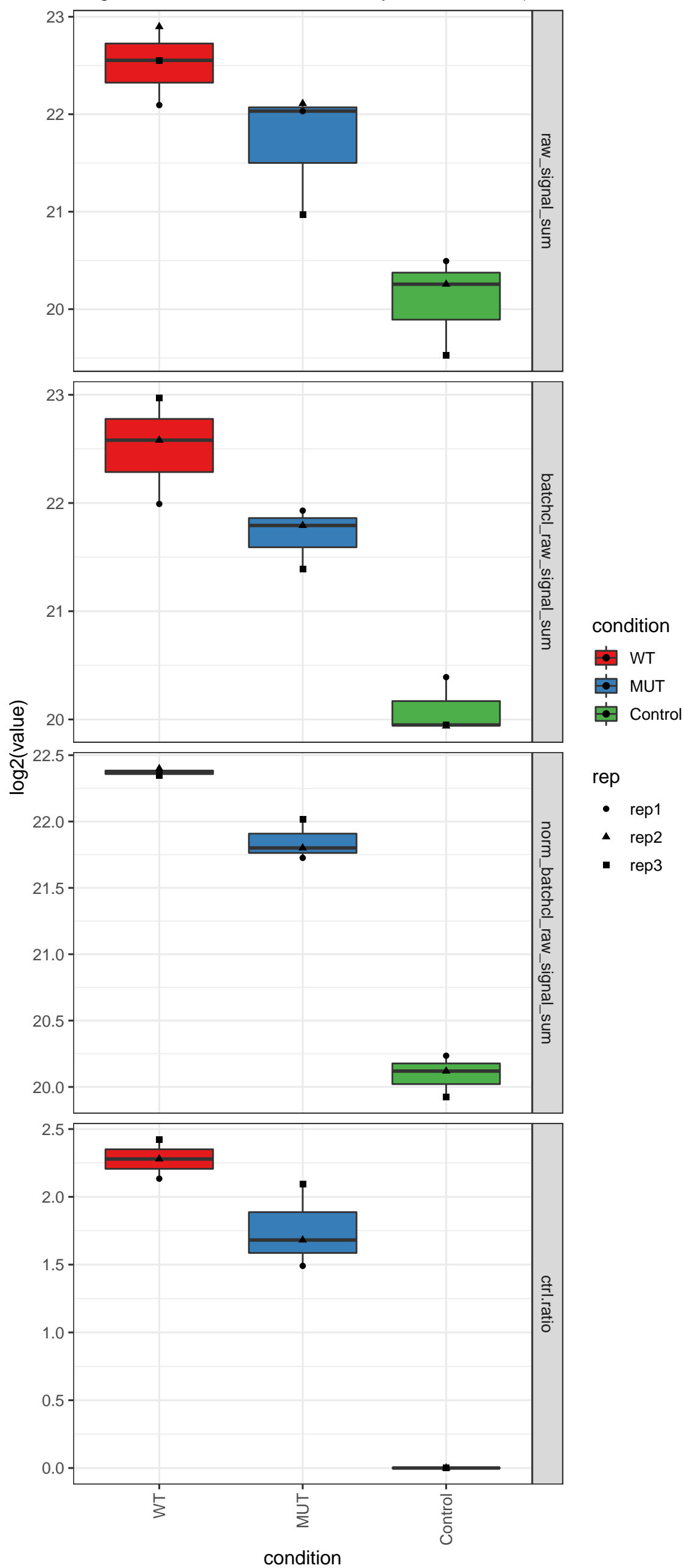


OAF1 – P39720

Oleate-activated transcription factor 1 OS=Saccharomyces cerevisiae (strain

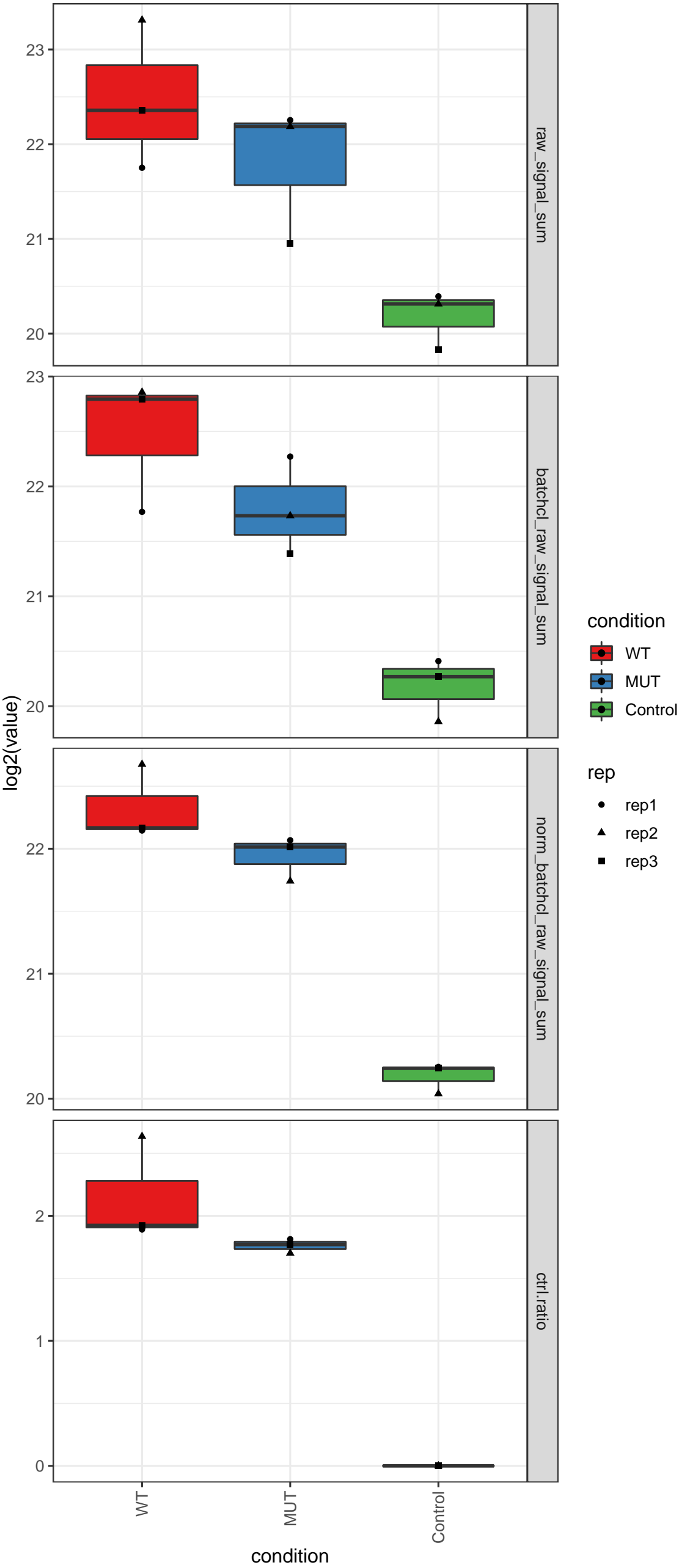


OLA1 – P38219

Obg-like ATPase 1 OS=*Saccharomyces cerevisiae* (strain ATCC 204508)

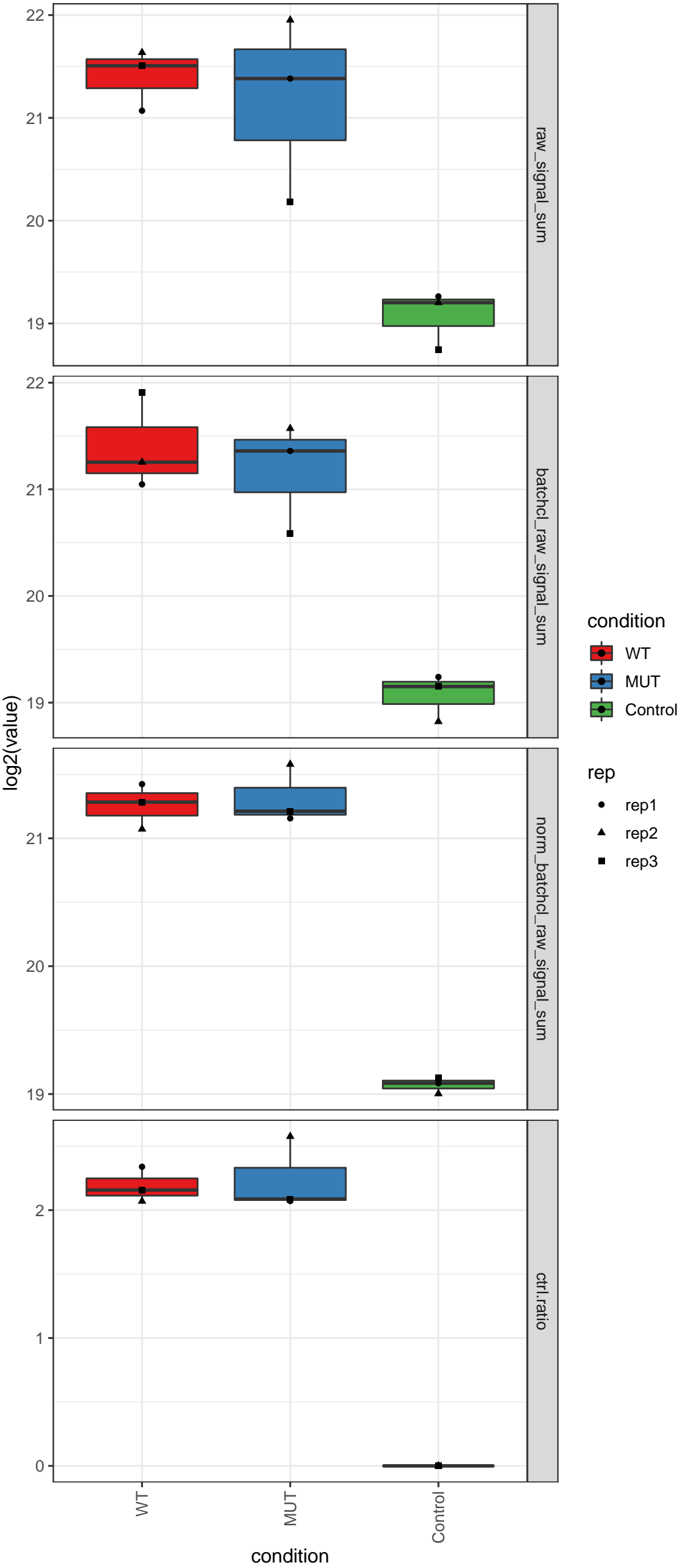
OLE1 – P21147

Acyl-CoA desaturase 1 OS=Saccharomyces cerevisiae (strain ATCC 2045



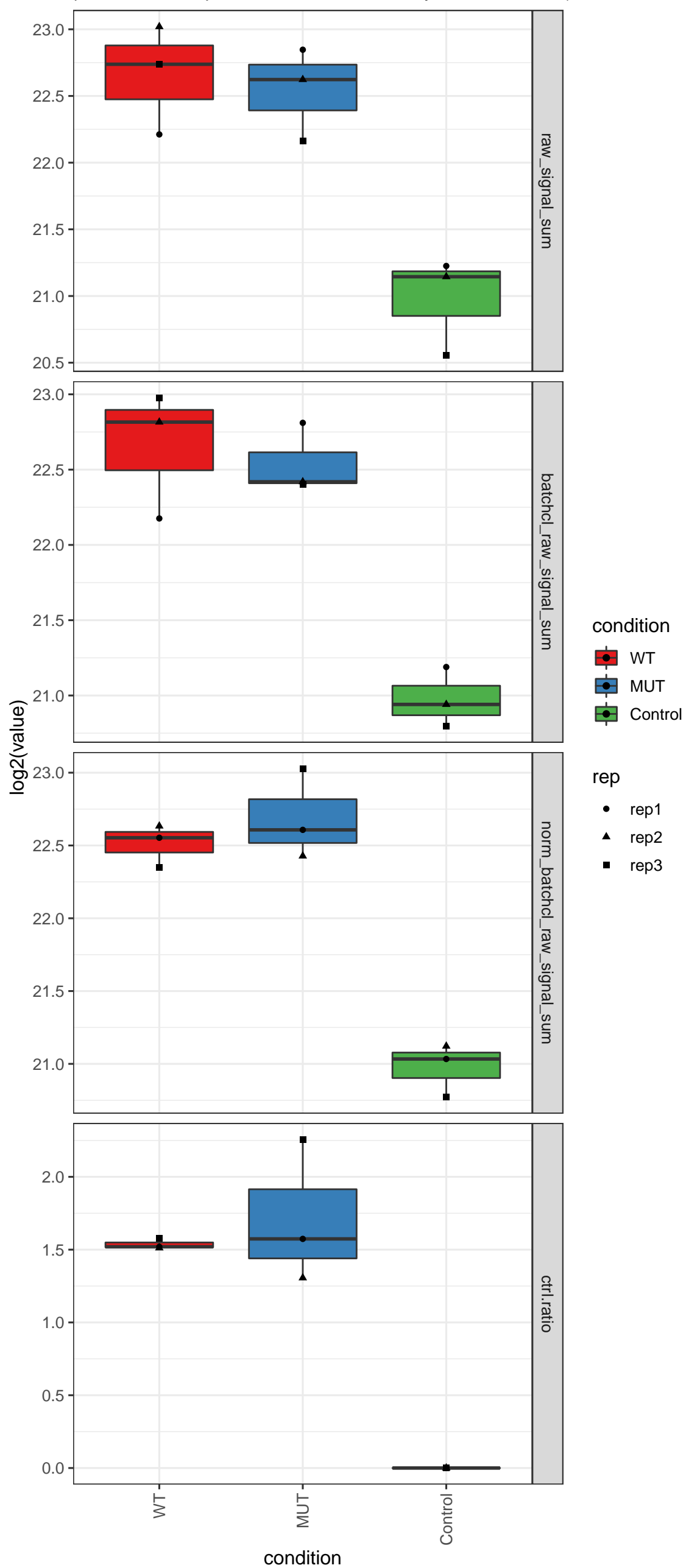
OSM1 – P21375

Fumarate reductase 2 OS=*Saccharomyces cerevisiae* (strain ATCC 20450)



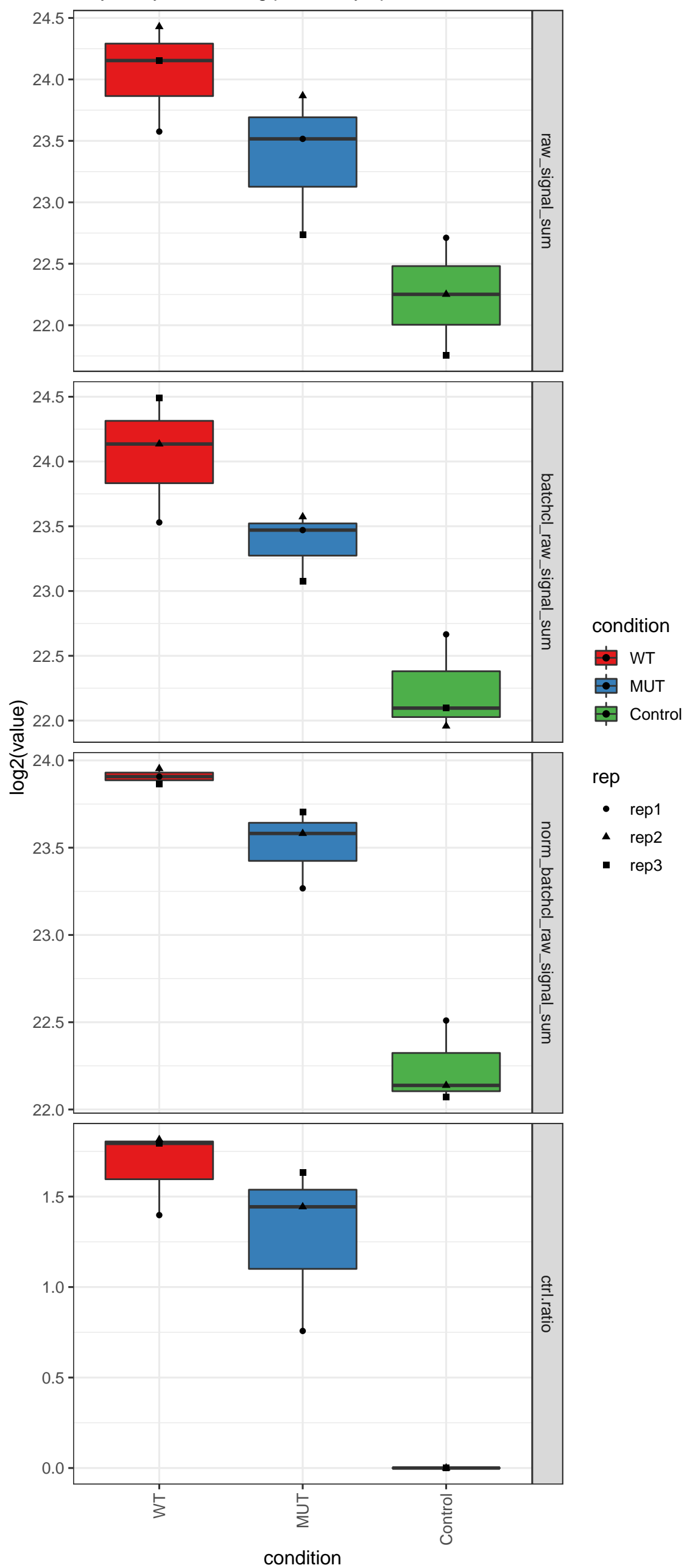
P1707_RE|RTN1 – P1707_RE|Q04947

|Reticulon-like protein 1 OS=Saccharomyces cerevisiae (strain ATCC 20456) EC=3.6.1.1



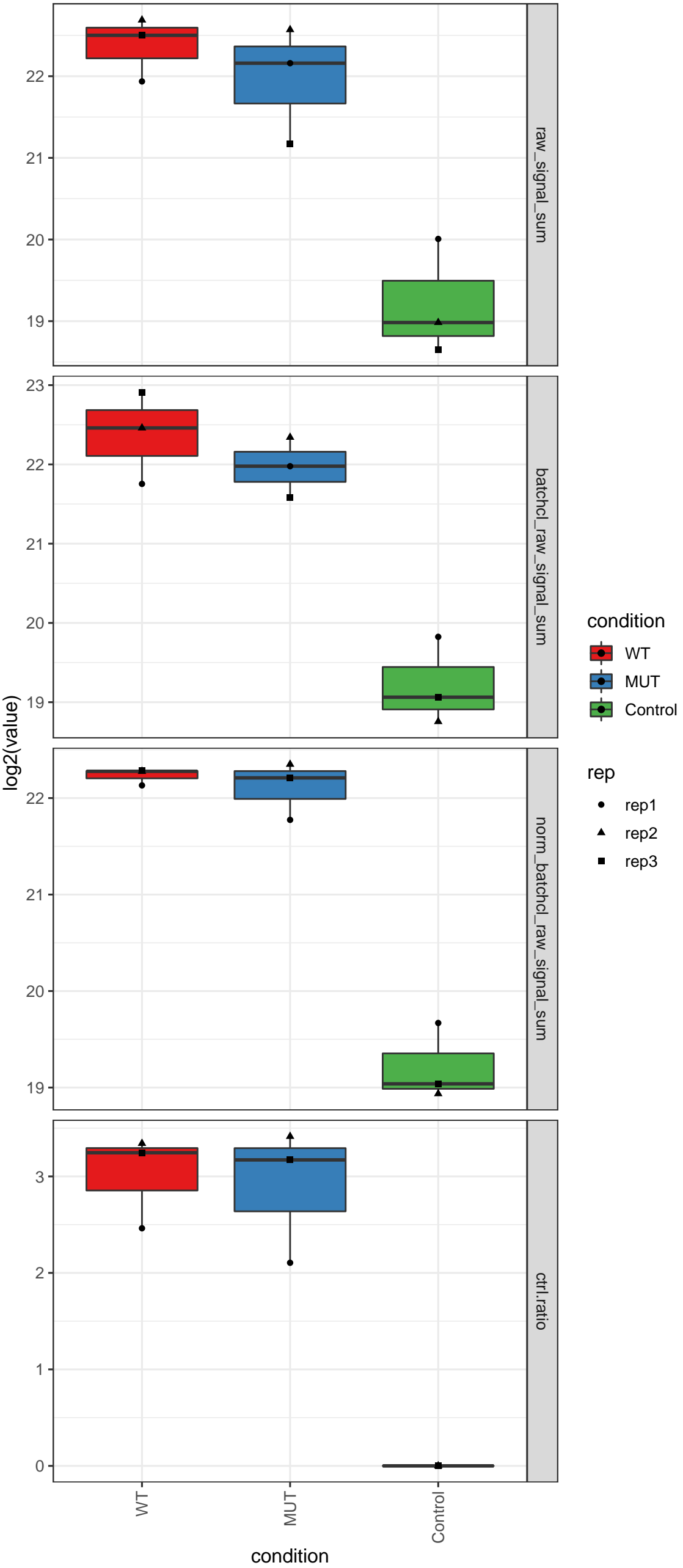
PAB1 – P04147

Polyadenylate-binding protein, cytoplasmic and nuclear OS=Saccharomy



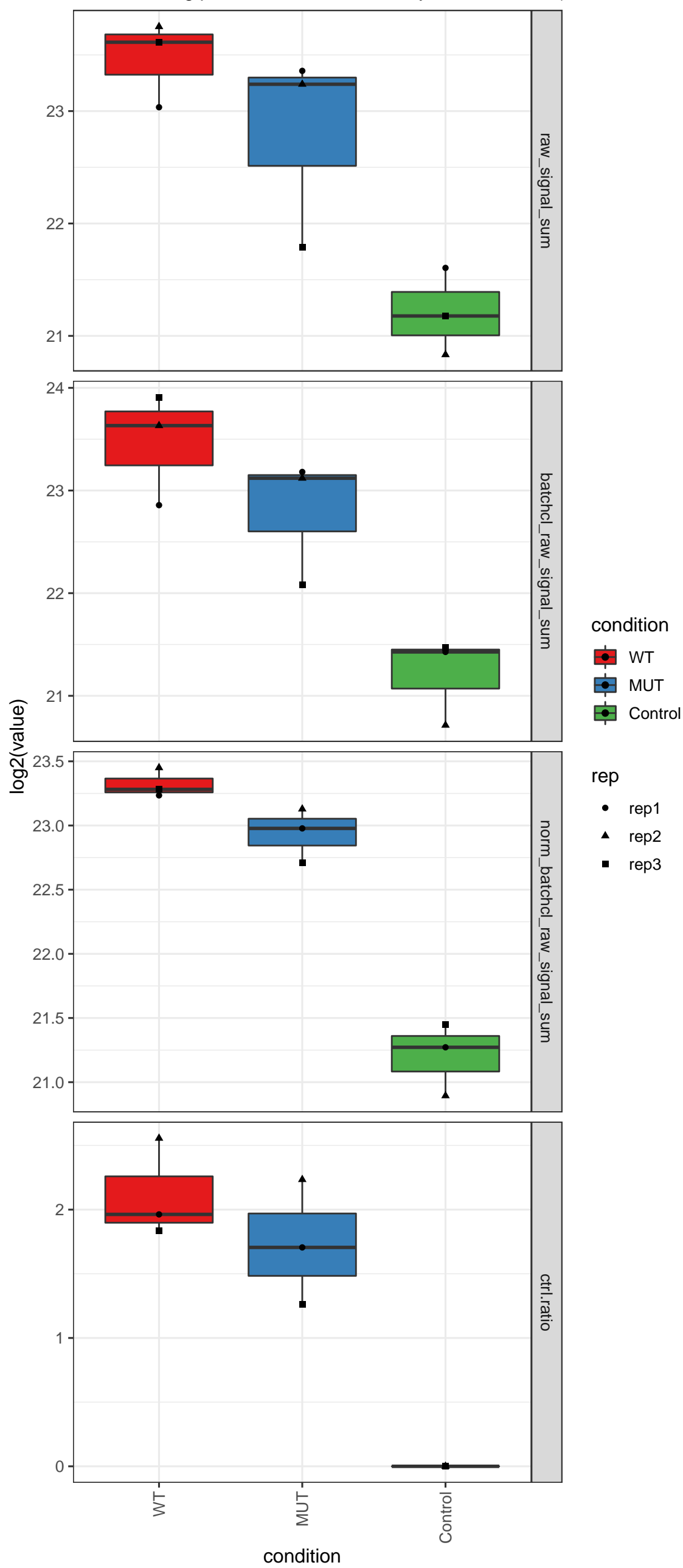
PAT1 – P25644

DNA topoisomerase 2–associated protein PAT1 OS=*Saccharomyces cerevisiae*



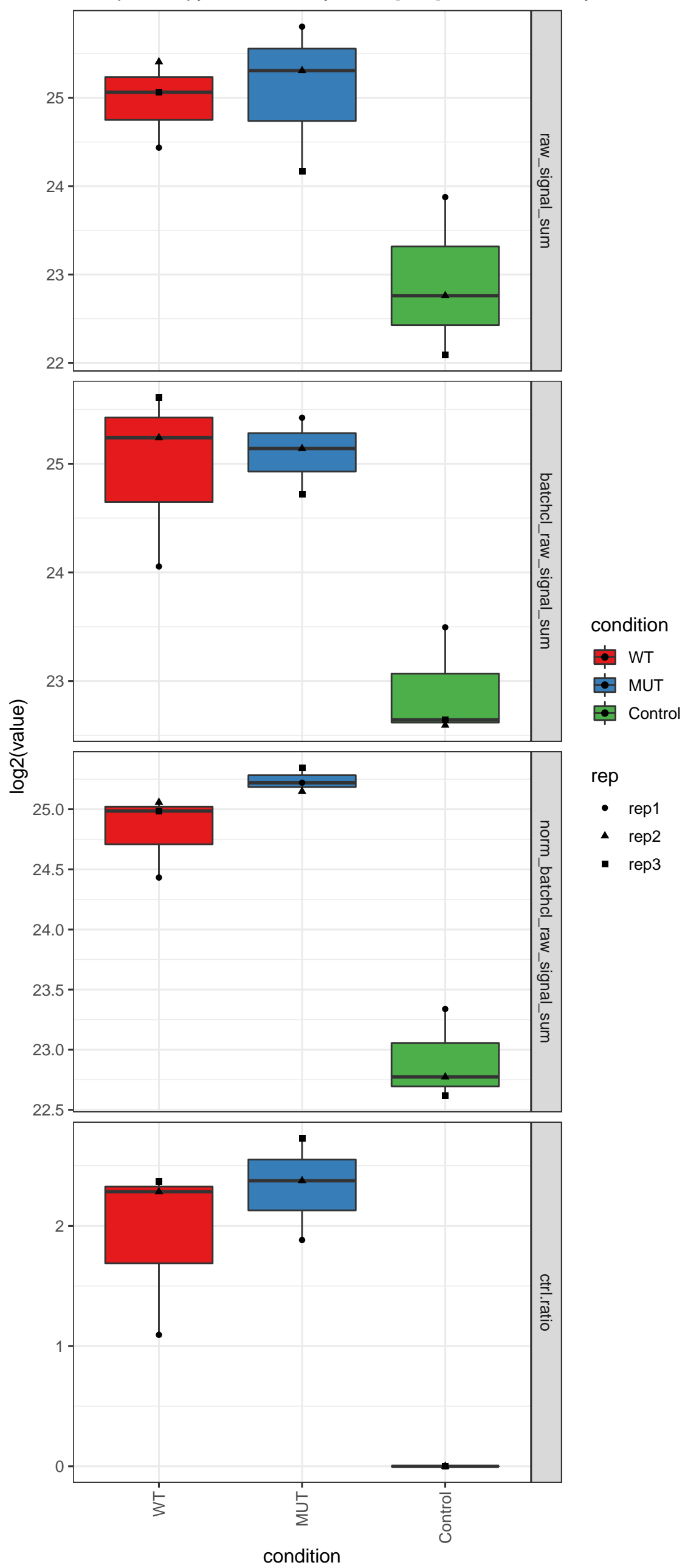
PBP1 – P53297

PAB1-binding protein 1 OS=*Saccharomyces cerevisiae* (strain ATCC 204



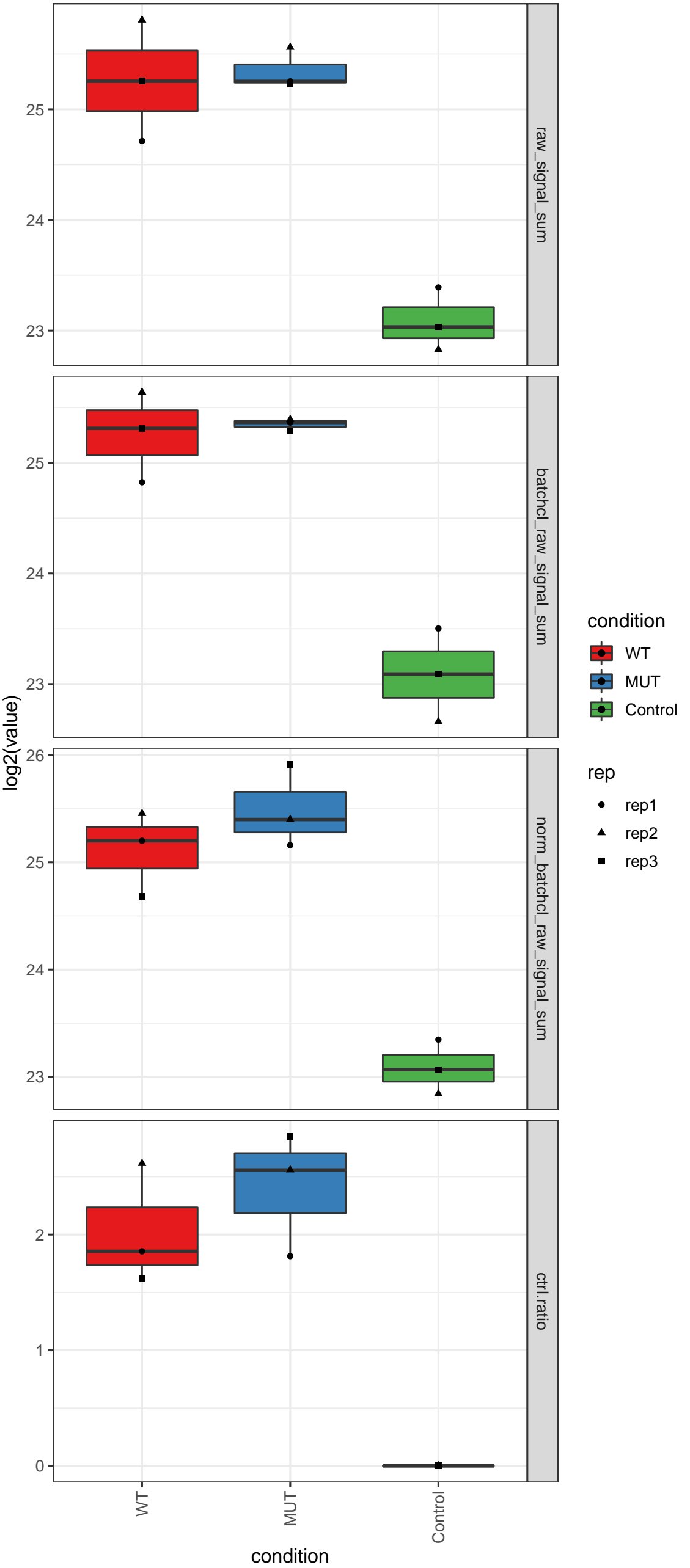
PCK1 – P10963

Phosphoenolpyruvate carboxykinase [ATP] OS=Saccharomyces cerevisia



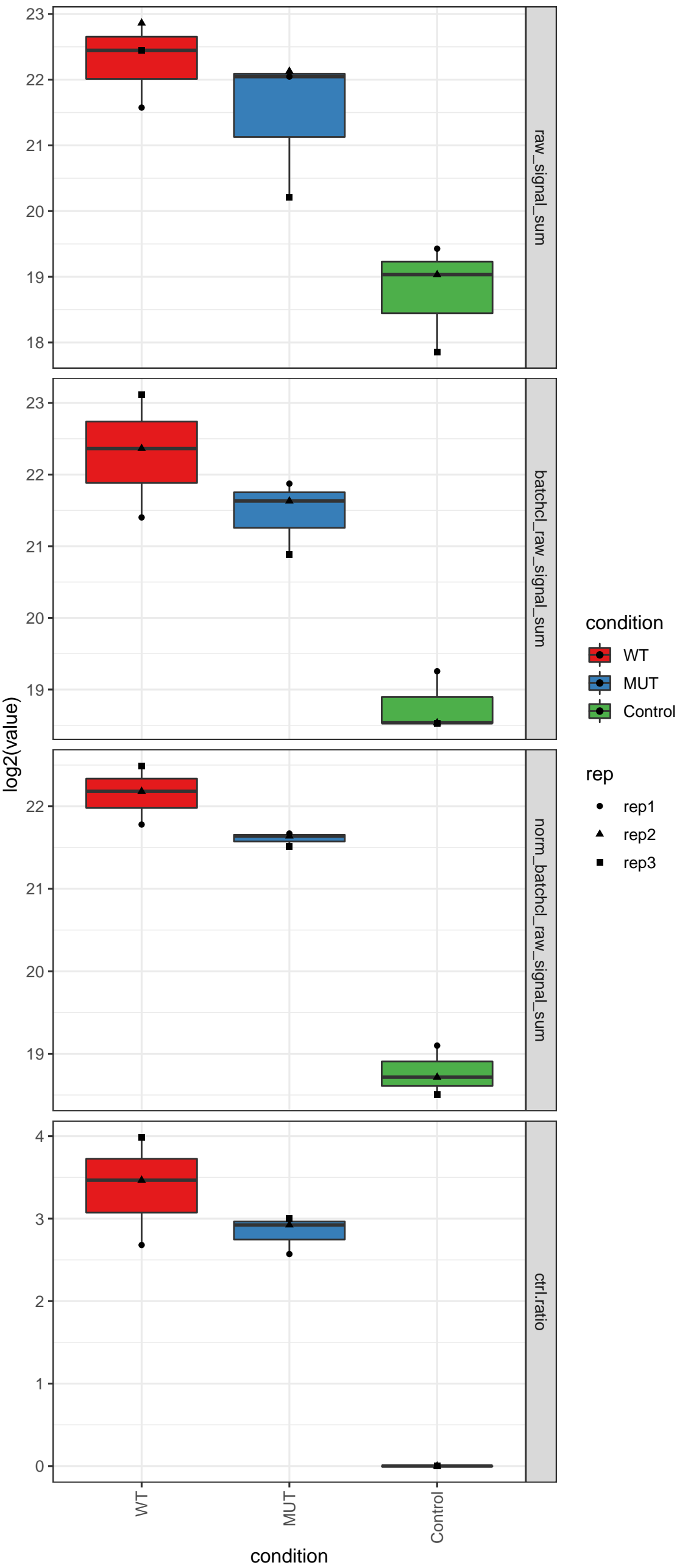
PCS60 – P38137

Peroxisomal-coenzyme A synthetase OS=*Saccharomyces cerevisiae* (stra



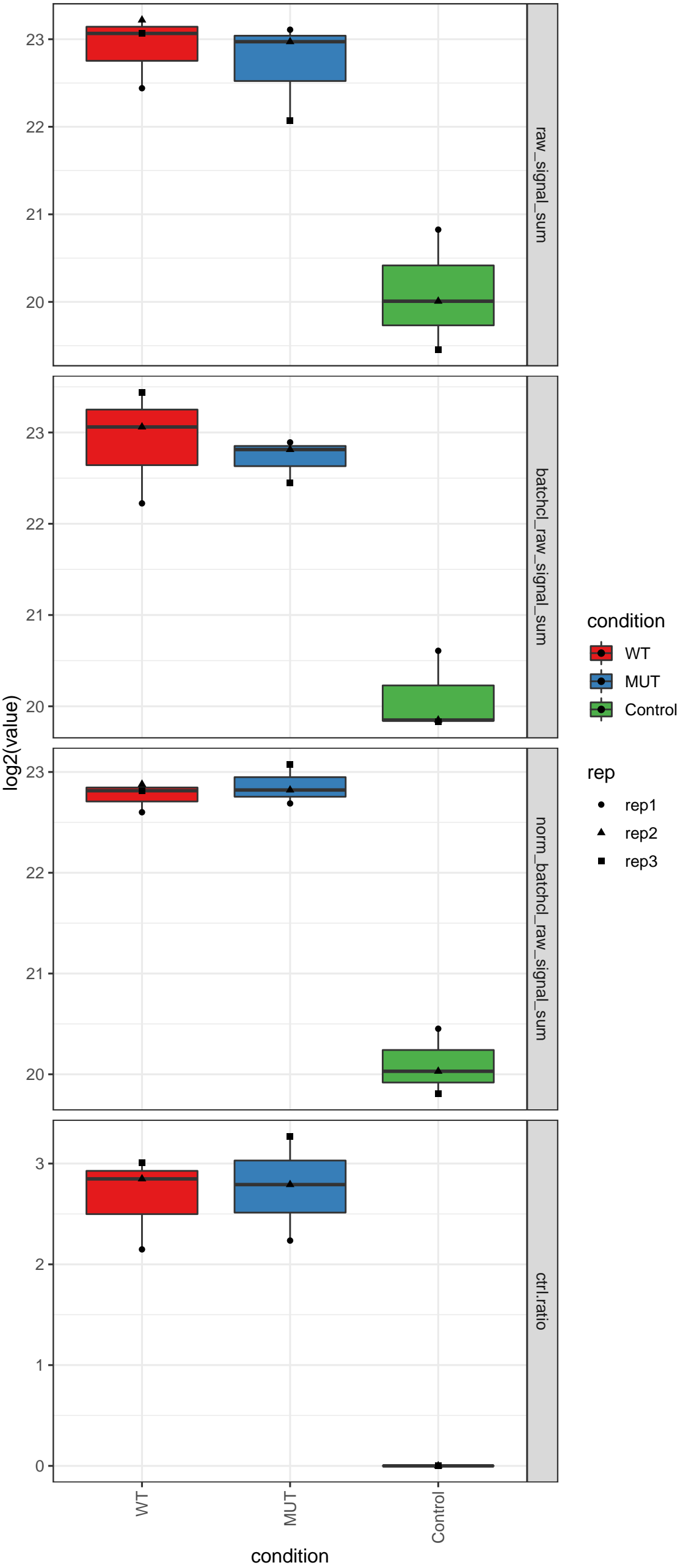
PCT1 – P13259

Choline-phosphate cytidyltransferase OS=Saccharomyces cerevisiae (str. *S. cerevisiae*)



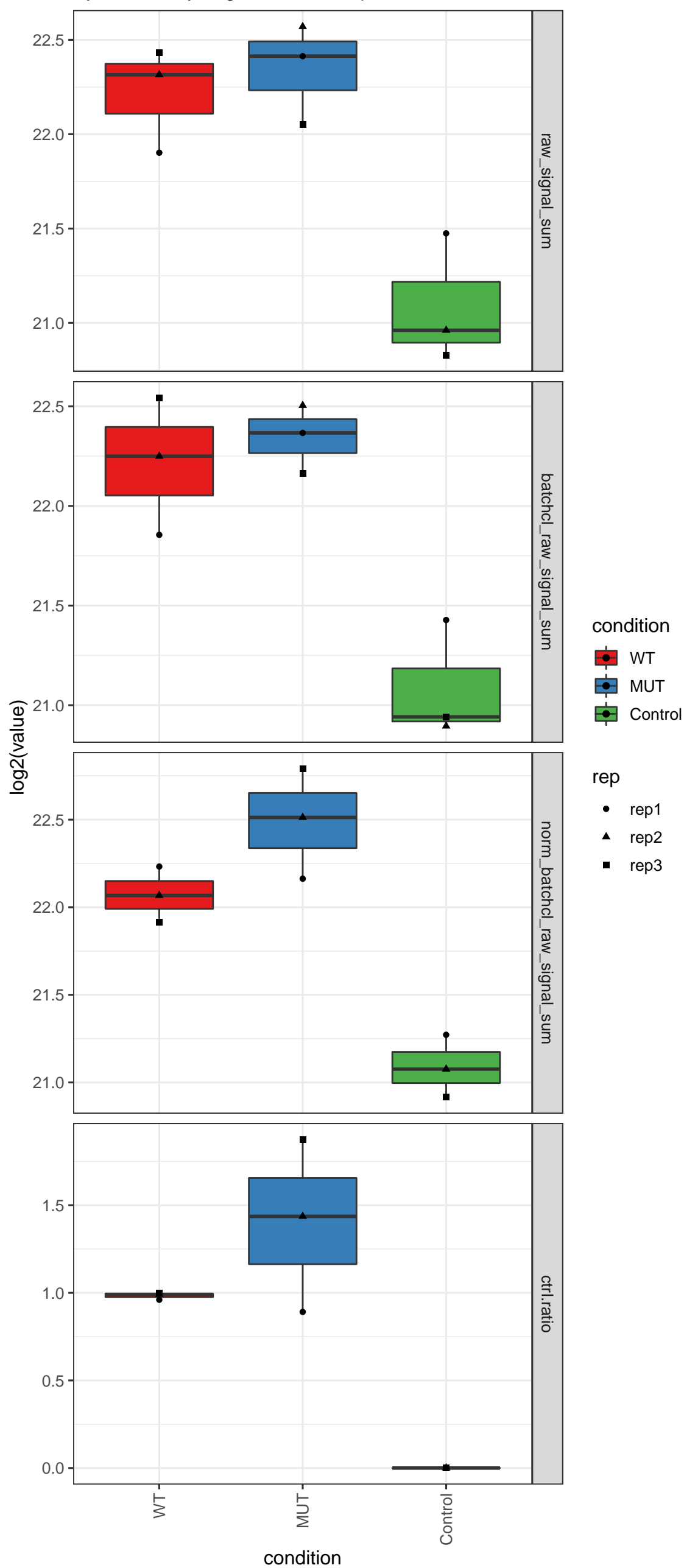
PDA1 – P16387

Pyruvate dehydrogenase E1 component subunit alpha, mitochondrial OS=



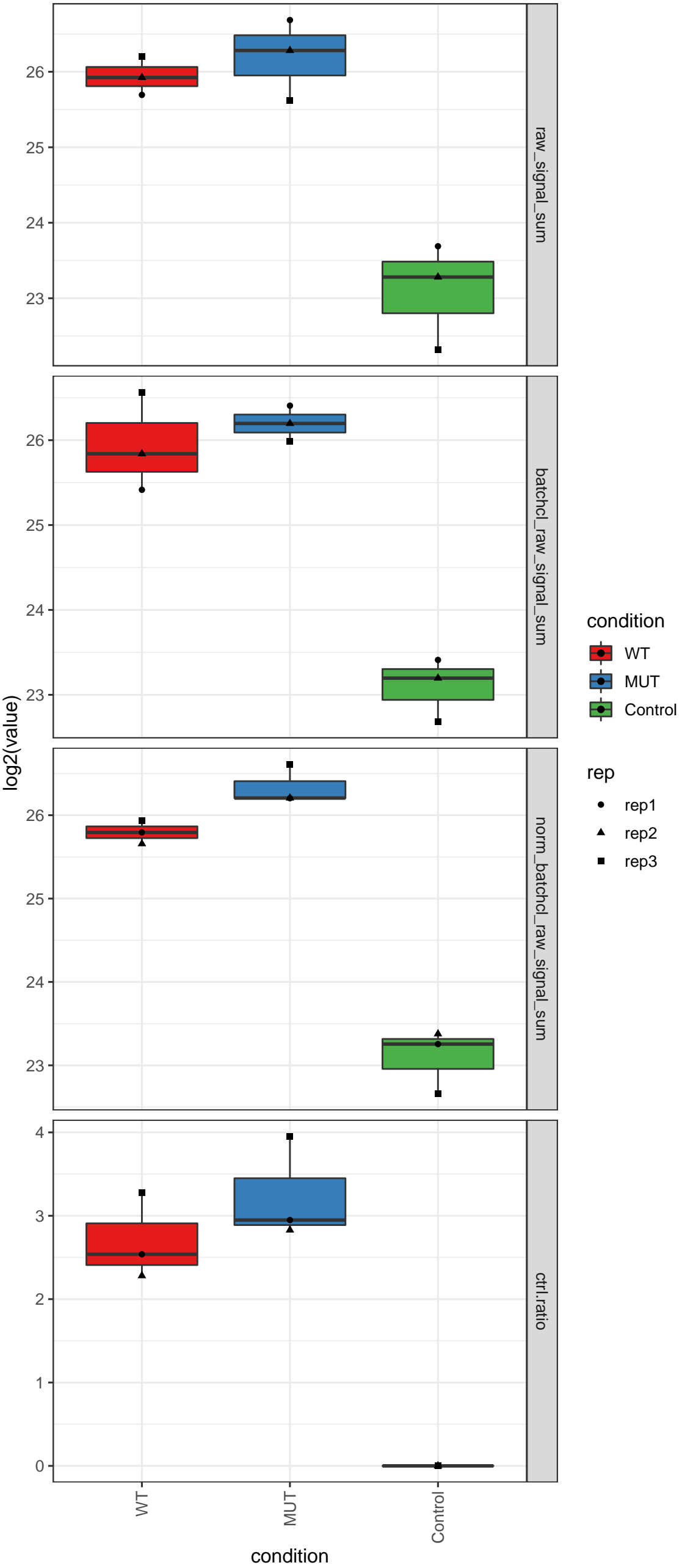
PDB1 – P32473

Pyruvate dehydrogenase E1 component subunit beta, mitochondrial OS=



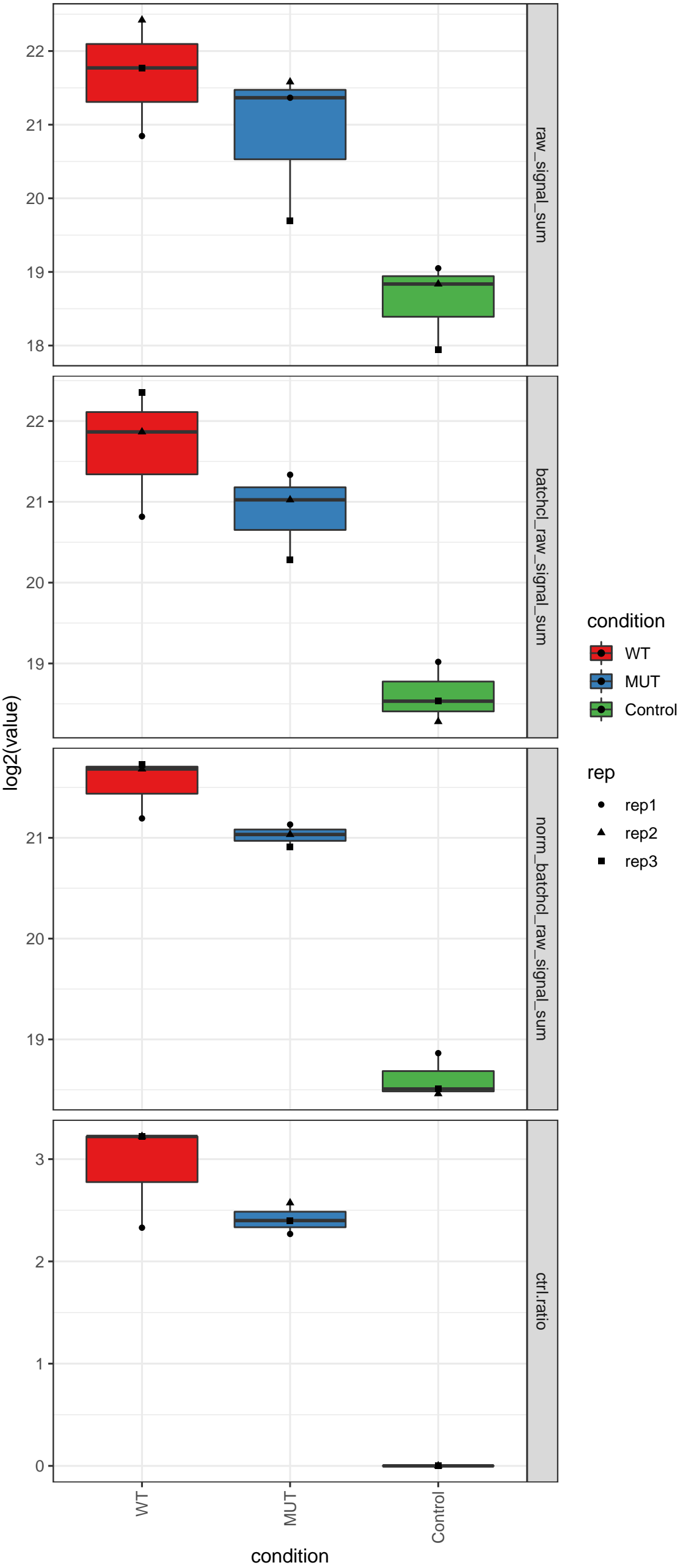
PDC1 – P06169

Pyruvate decarboxylase isozyme 1 OS=*Saccharomyces cerevisiae* (strain



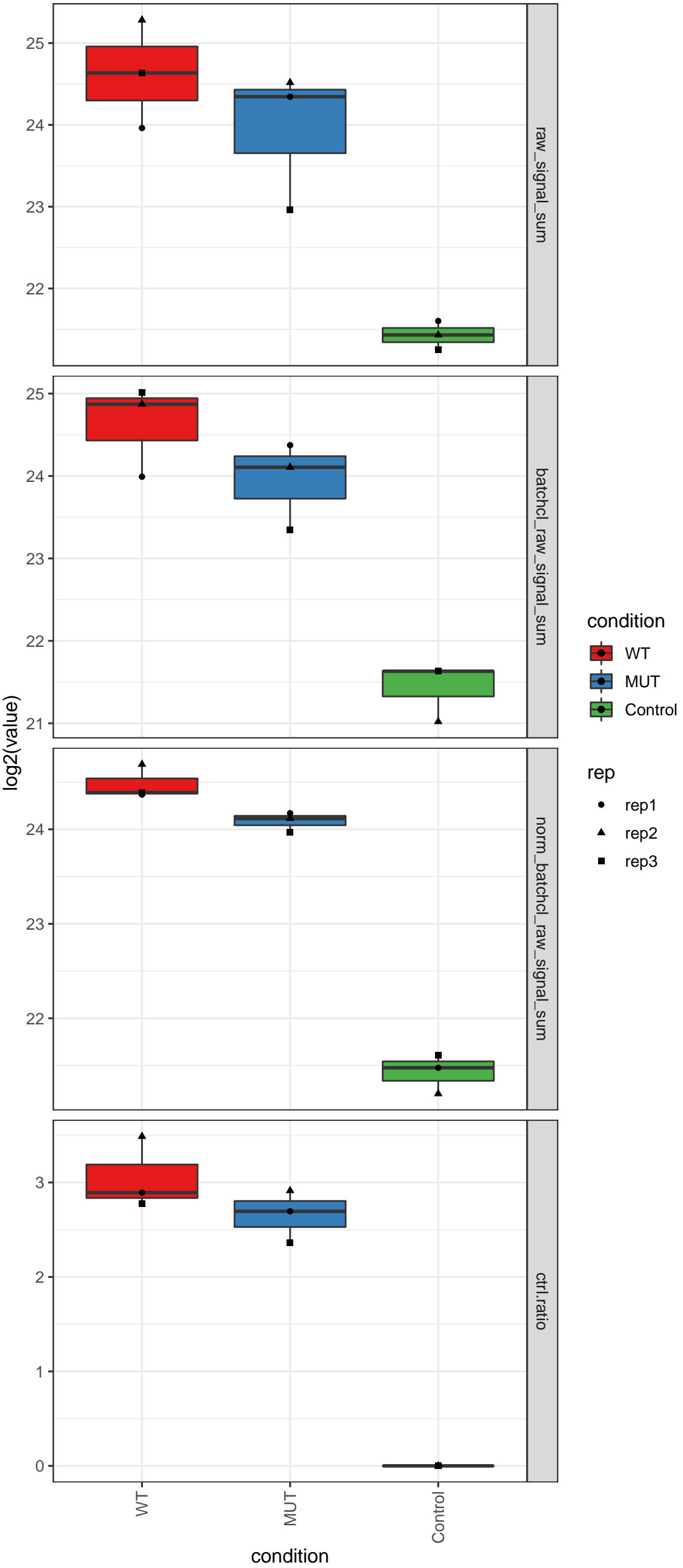
PDE2 – P06776

3',5'-cyclic-nucleotide phosphodiesterase 2 OS=Saccharomyces cerevisia



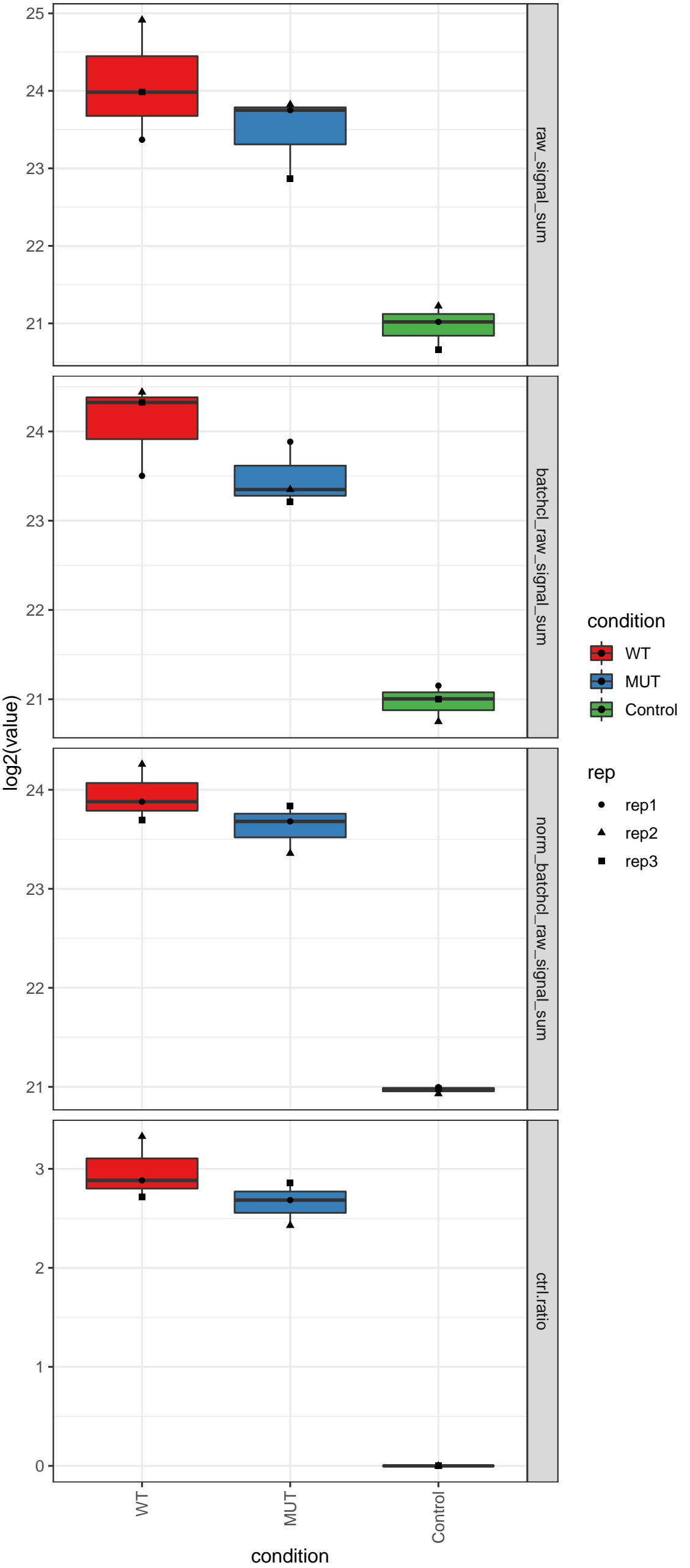
PDH1 – Q12428

Probable 2-methylcitrate dehydratase OS=*Saccharomyces cerevisiae* (strain

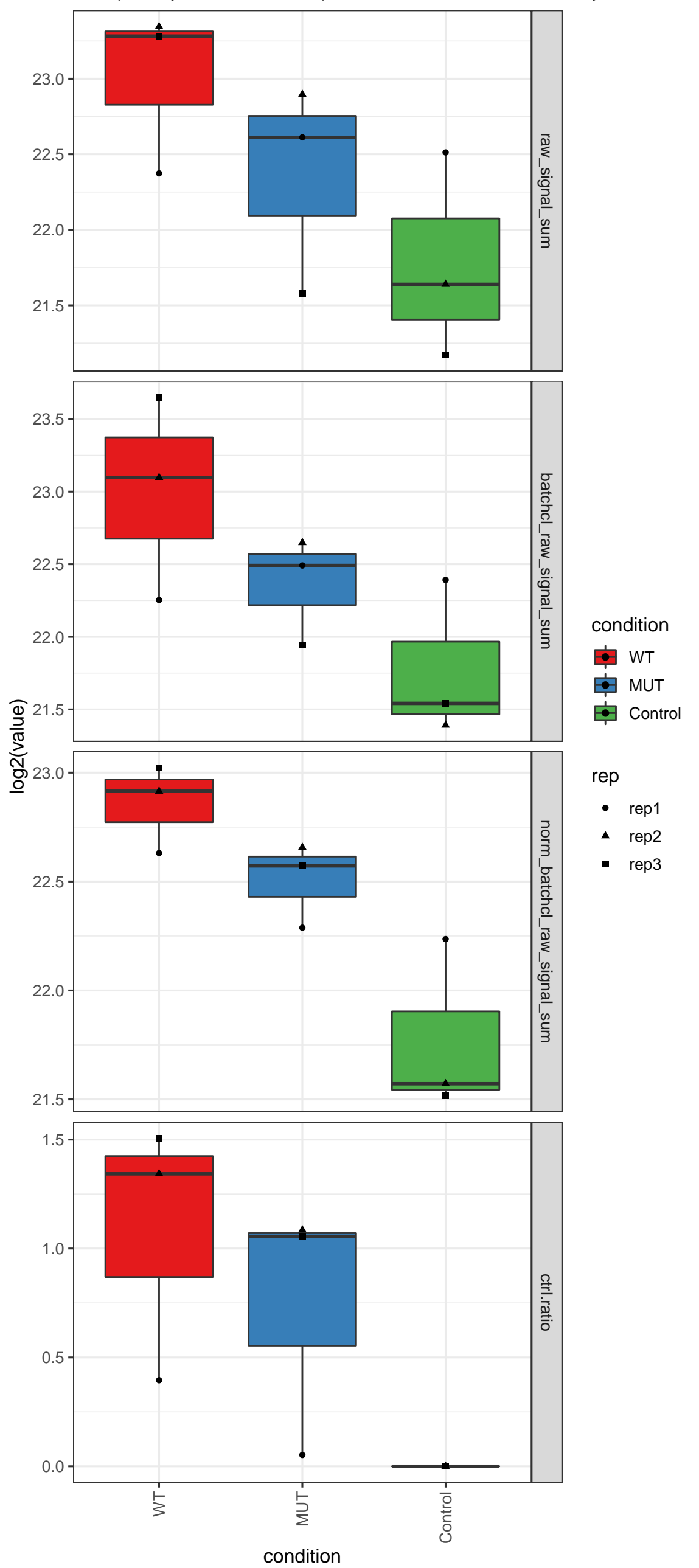


PDI1 – P17967

Protein disulfide–isomerase OS=*Saccharomyces cerevisiae* (strain ATCC 2

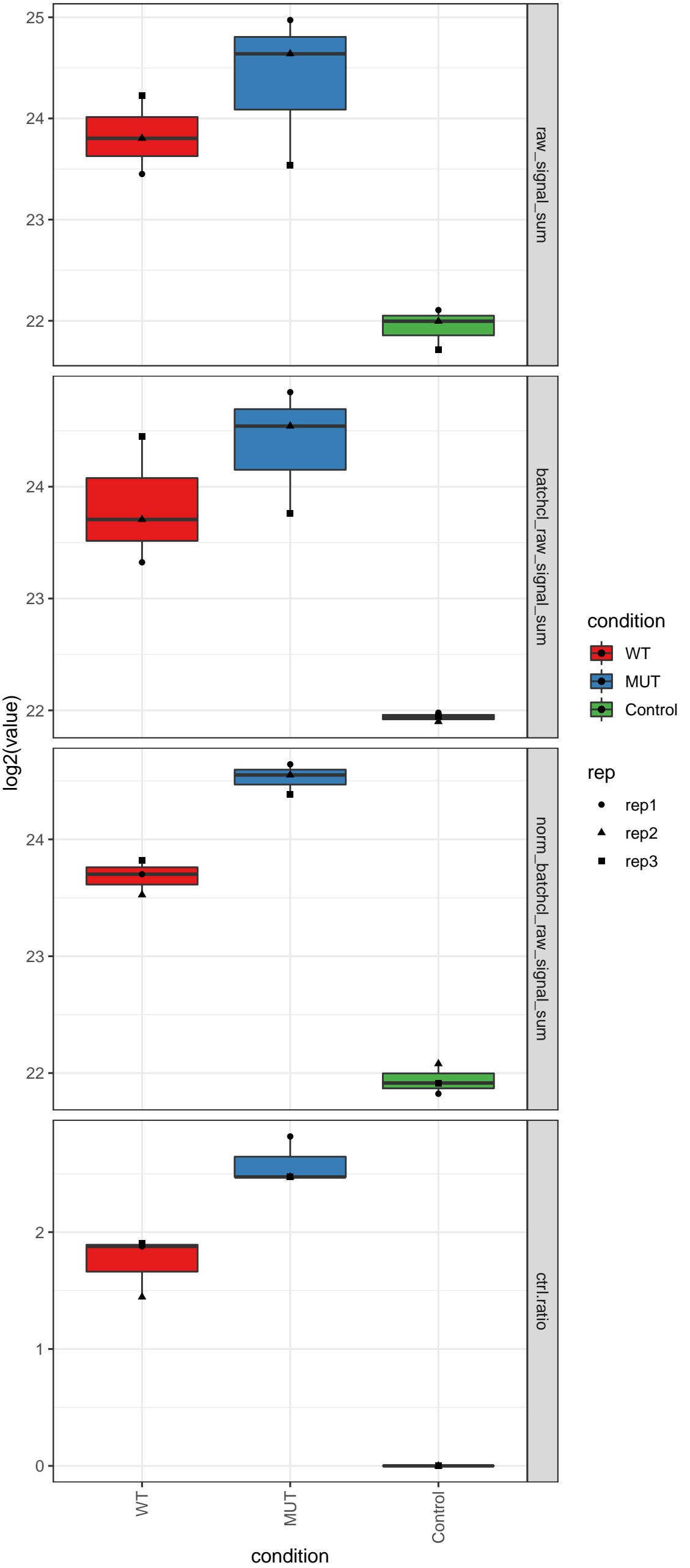


Phosphatidylinositol transfer protein PDR16 OS=Saccharomyces cerevisiae



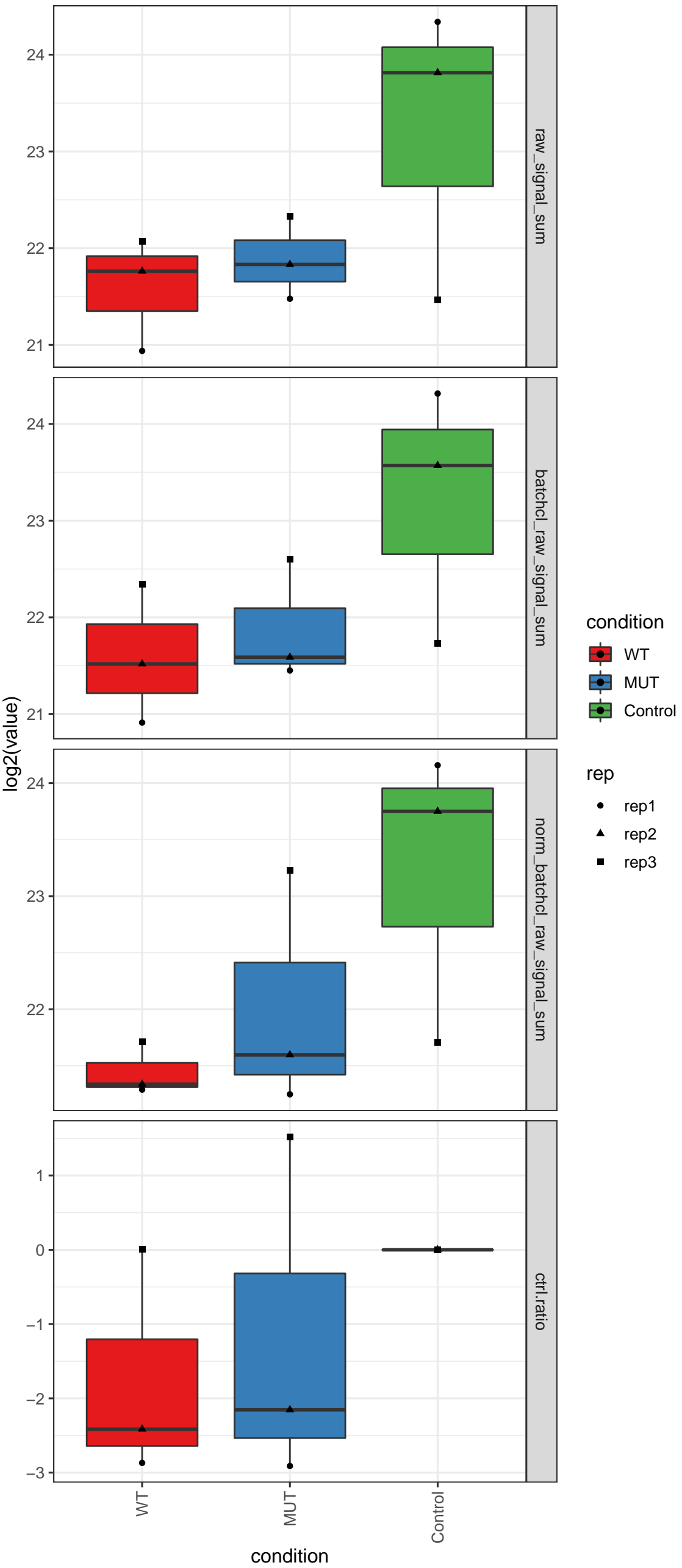
PDS5 – Q04264

Sister chromatid cohesion protein PDS5 OS=*Saccharomyces cerevisiae* (s



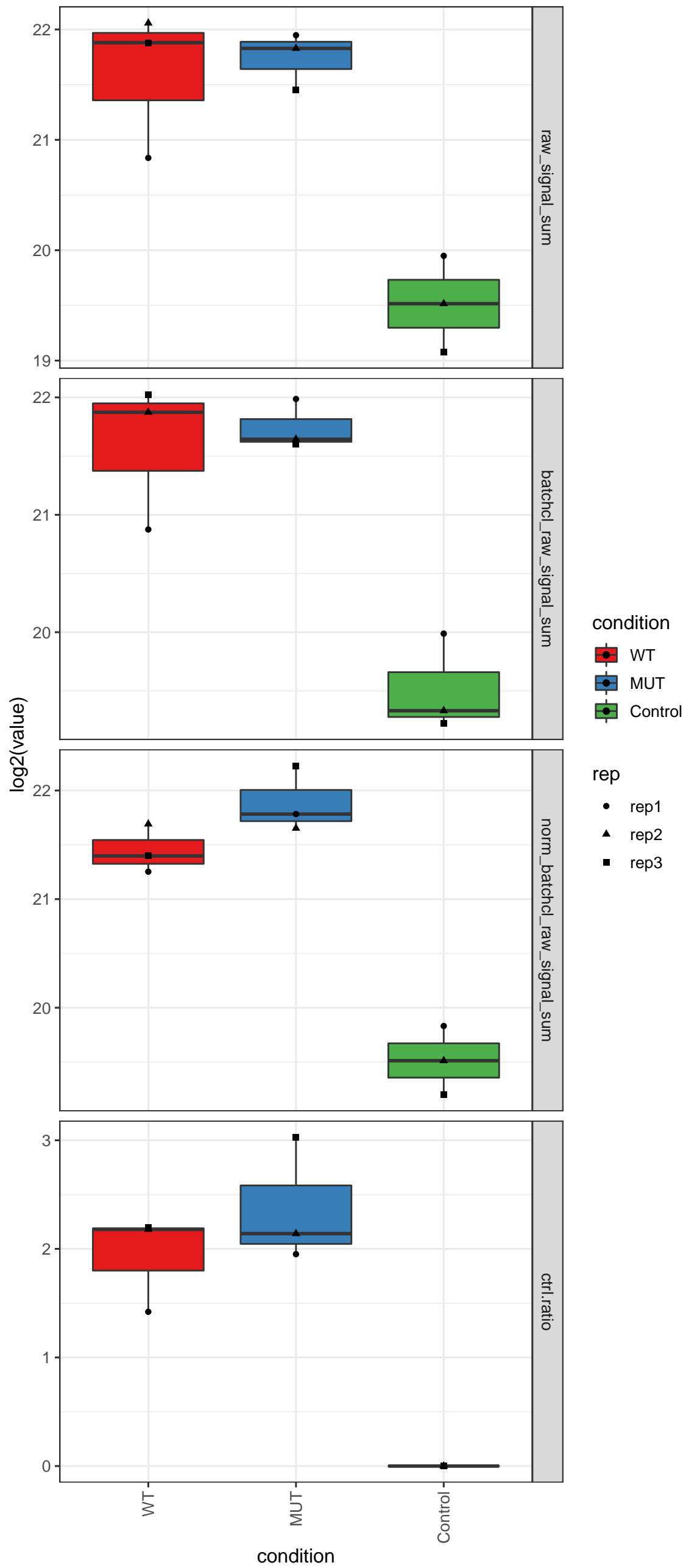
PEA2 – P40091

Protein PEA2 OS=*Saccharomyces cerevisiae* (strain ATCC 204508 / S288



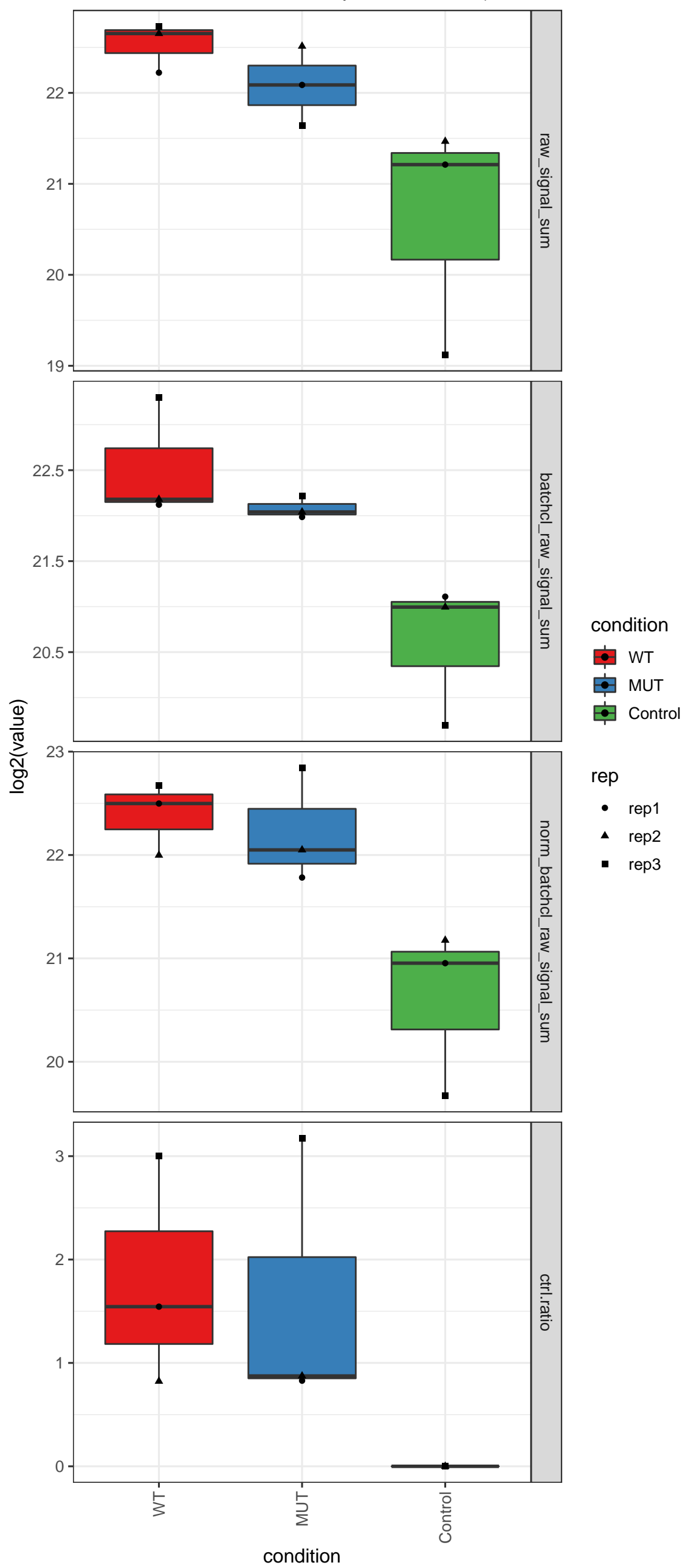
PEP4 – P07267

Saccharopepsin OS=Saccharomyces cerevisiae (strain ATCC 204508 / S2



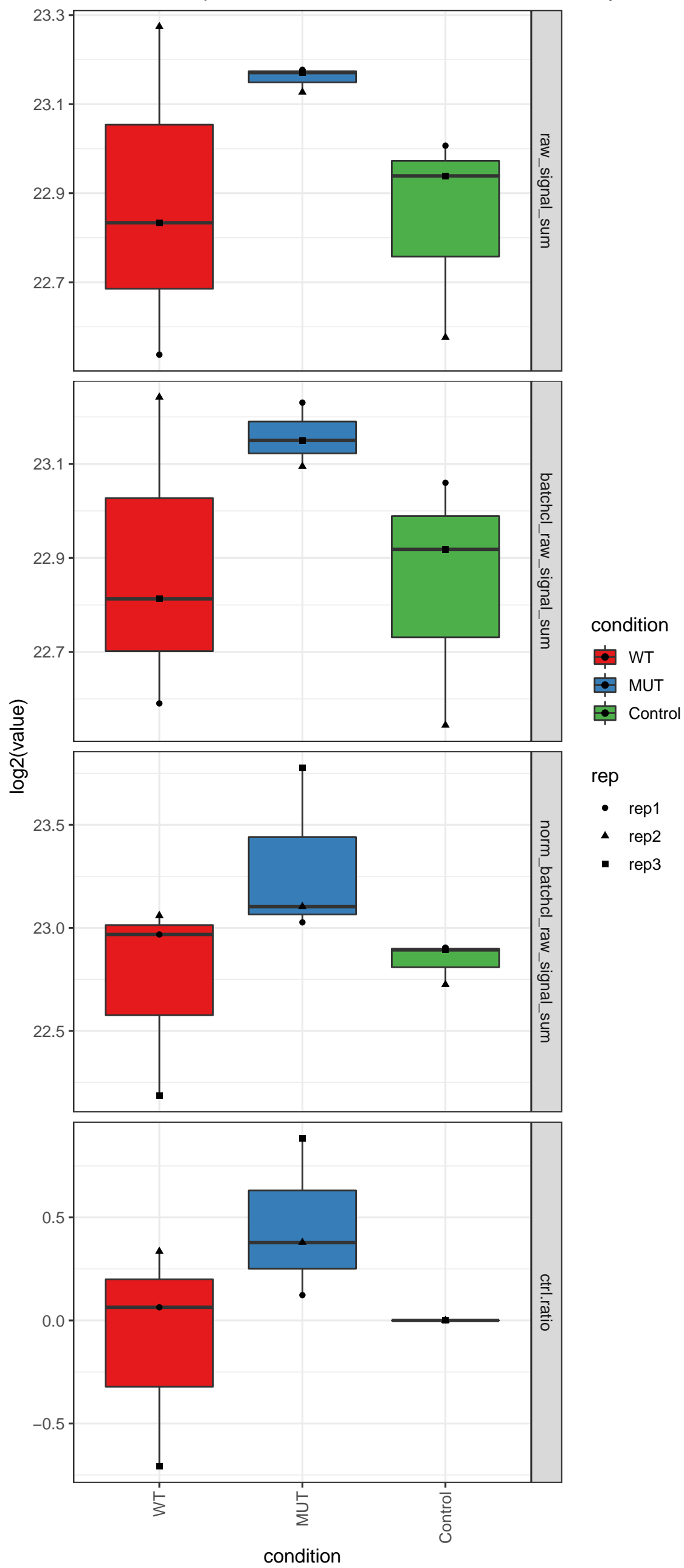
PET10 – P36139

Protein PET10 OS=*Saccharomyces cerevisiae* (strain ATCC 204508 / S2



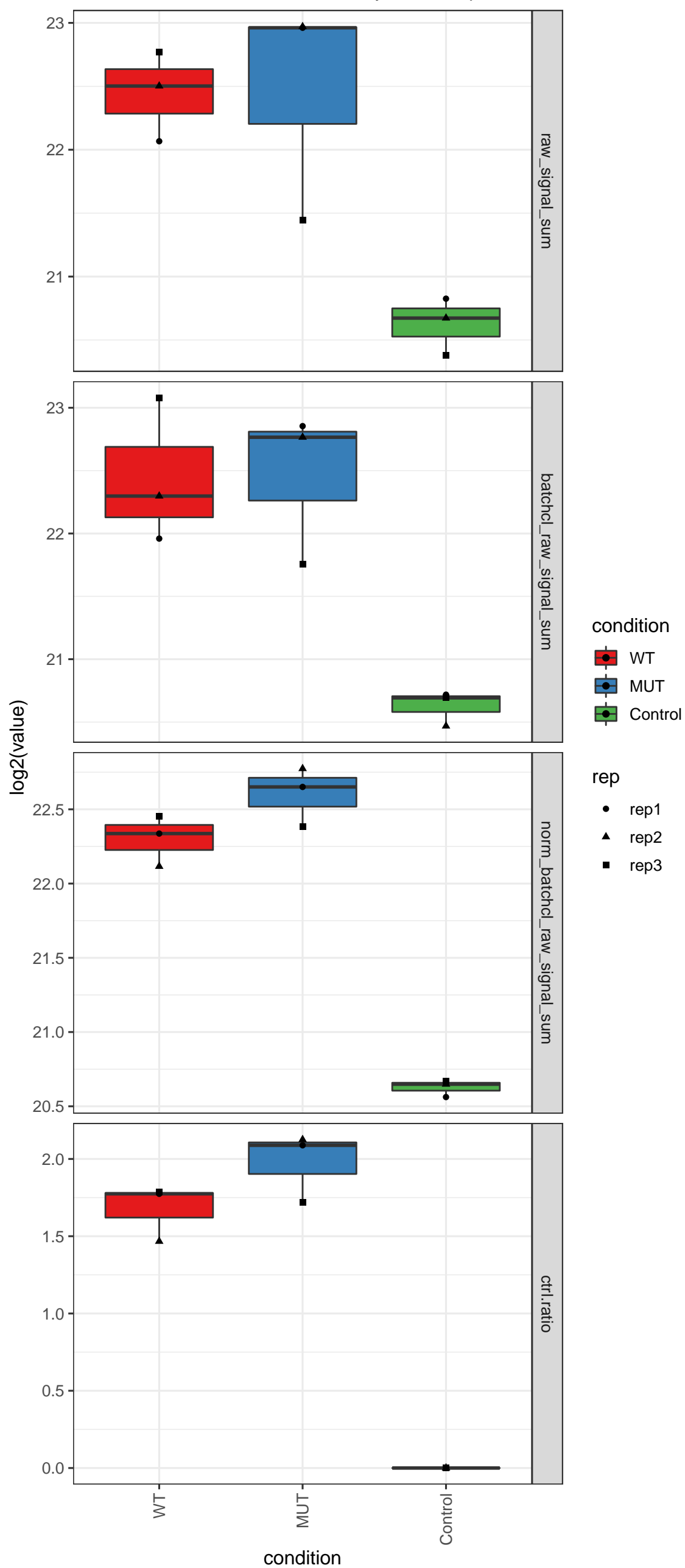
PET123 – P17558

37S ribosomal protein PET123, mitochondrial OS=*Saccharomyces cerevisiae*



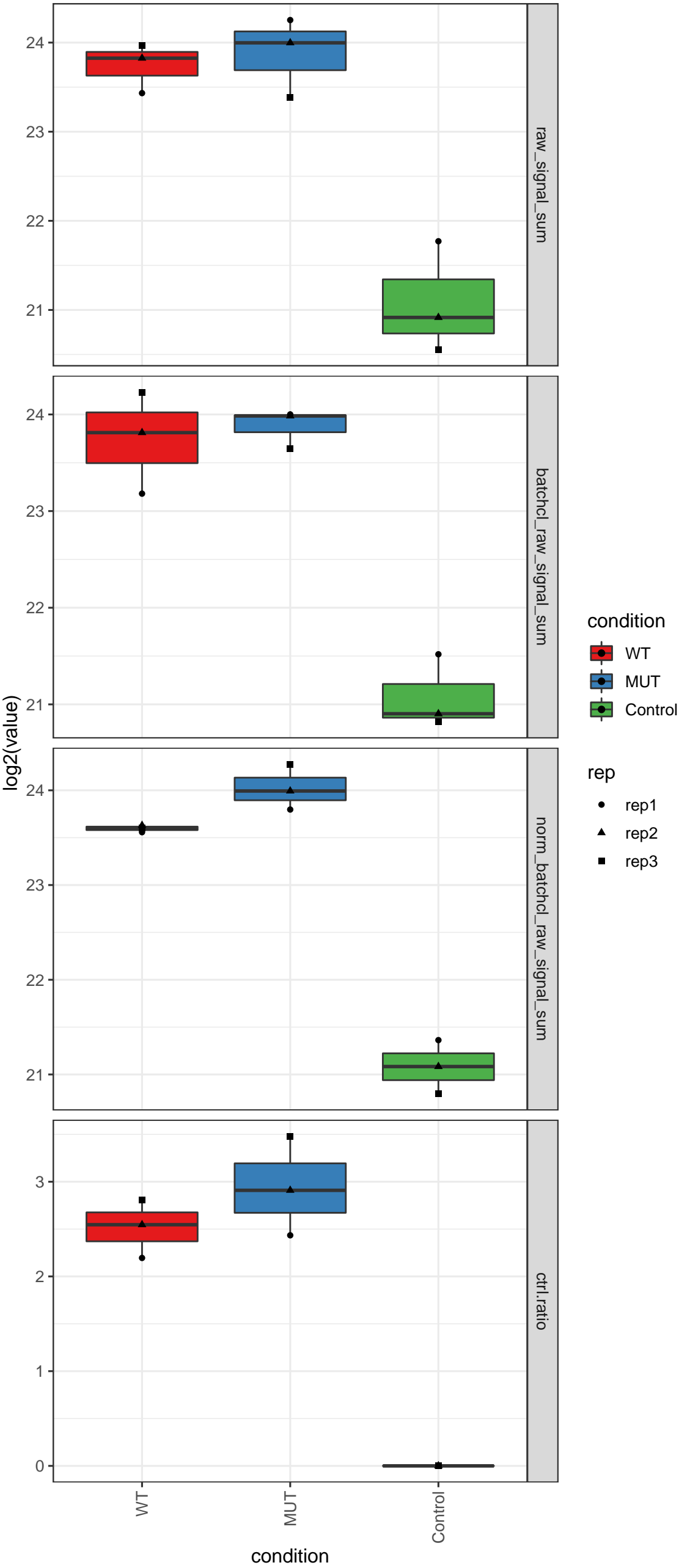
PET127 – P32606

Putative mitochondrial translation system component PET127 OS=Saccharomyces cerevisiae



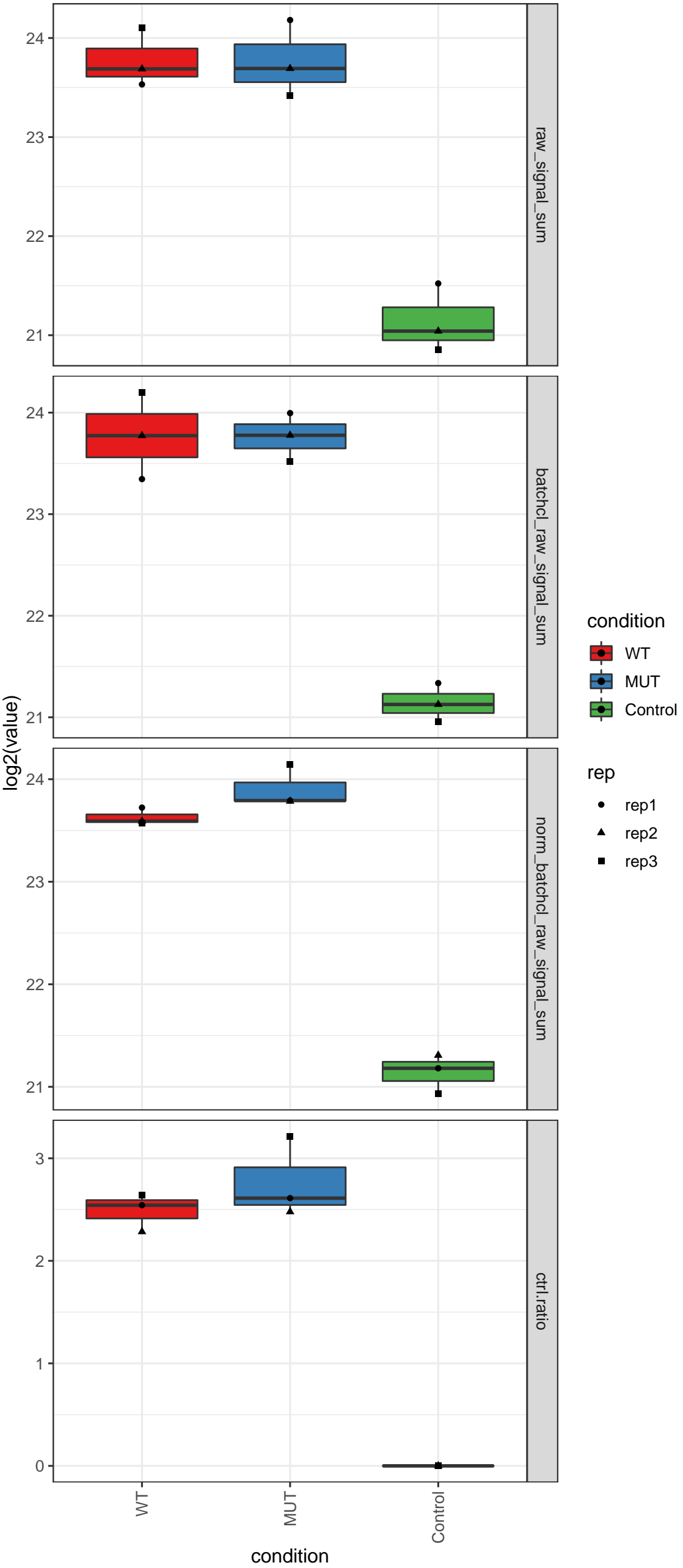
PET9 – P18239

ADP,ATP carrier protein 2 OS=*Saccharomyces cerevisiae* (strain ATCC 204



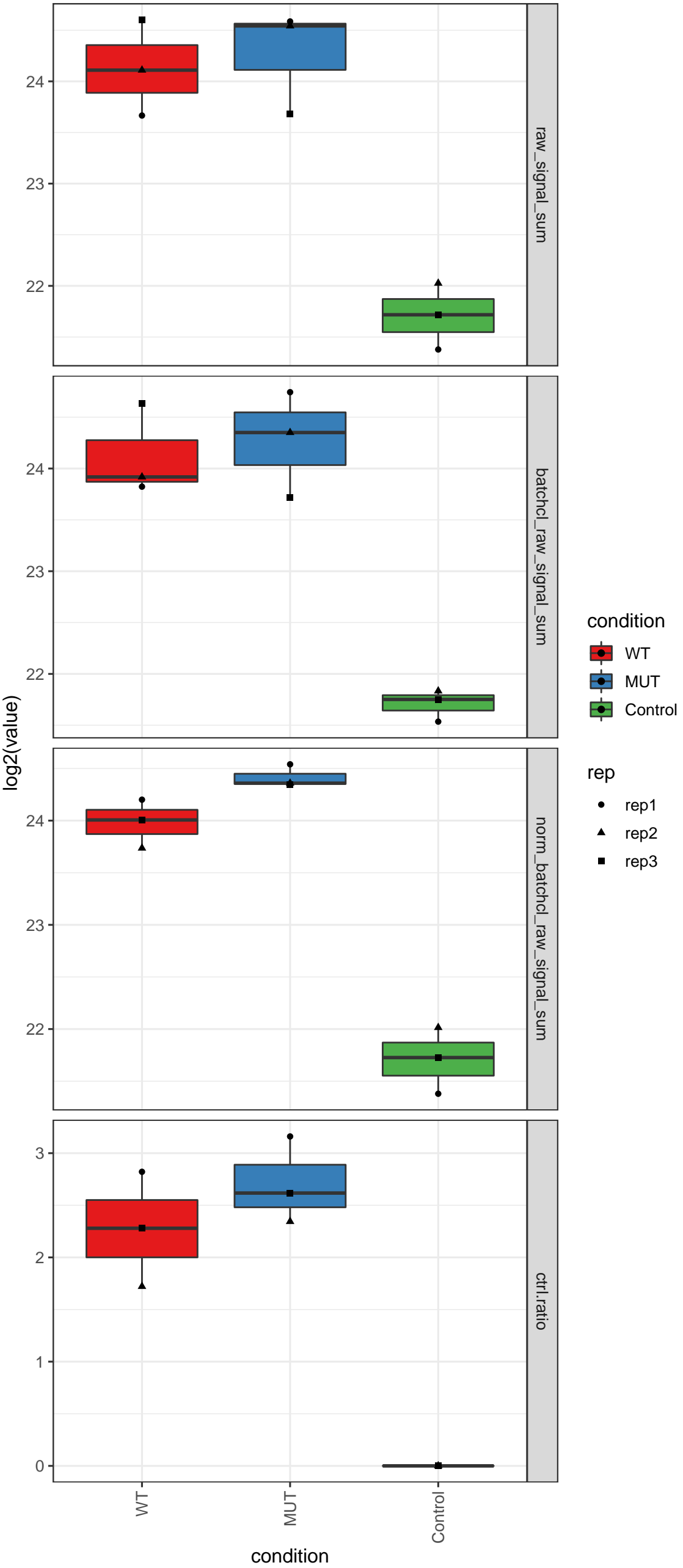
PFK1 – P16861

ATP-dependent 6-phosphofructokinase subunit alpha OS=Saccharomyce



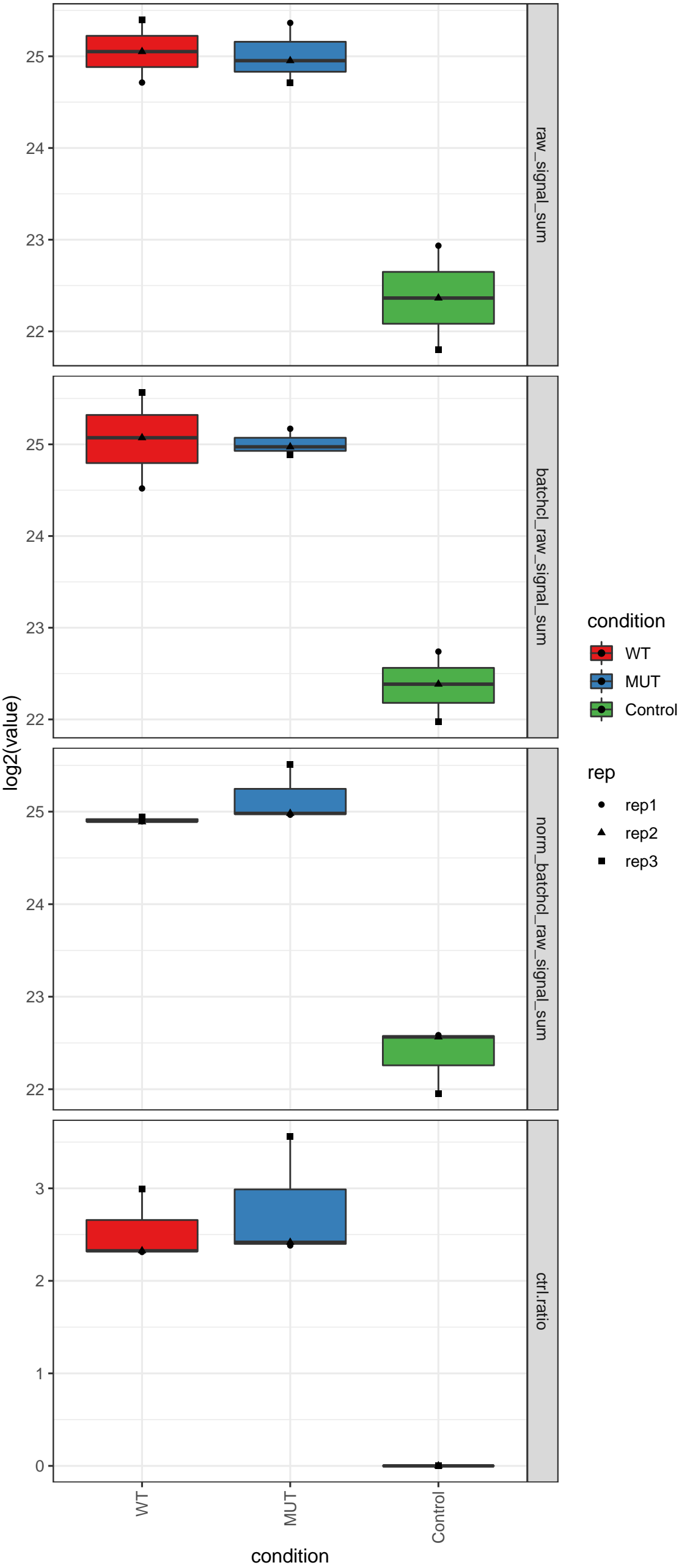
PFK2 – P16862

ATP-dependent 6-phosphofructokinase subunit beta OS=Saccharomyces



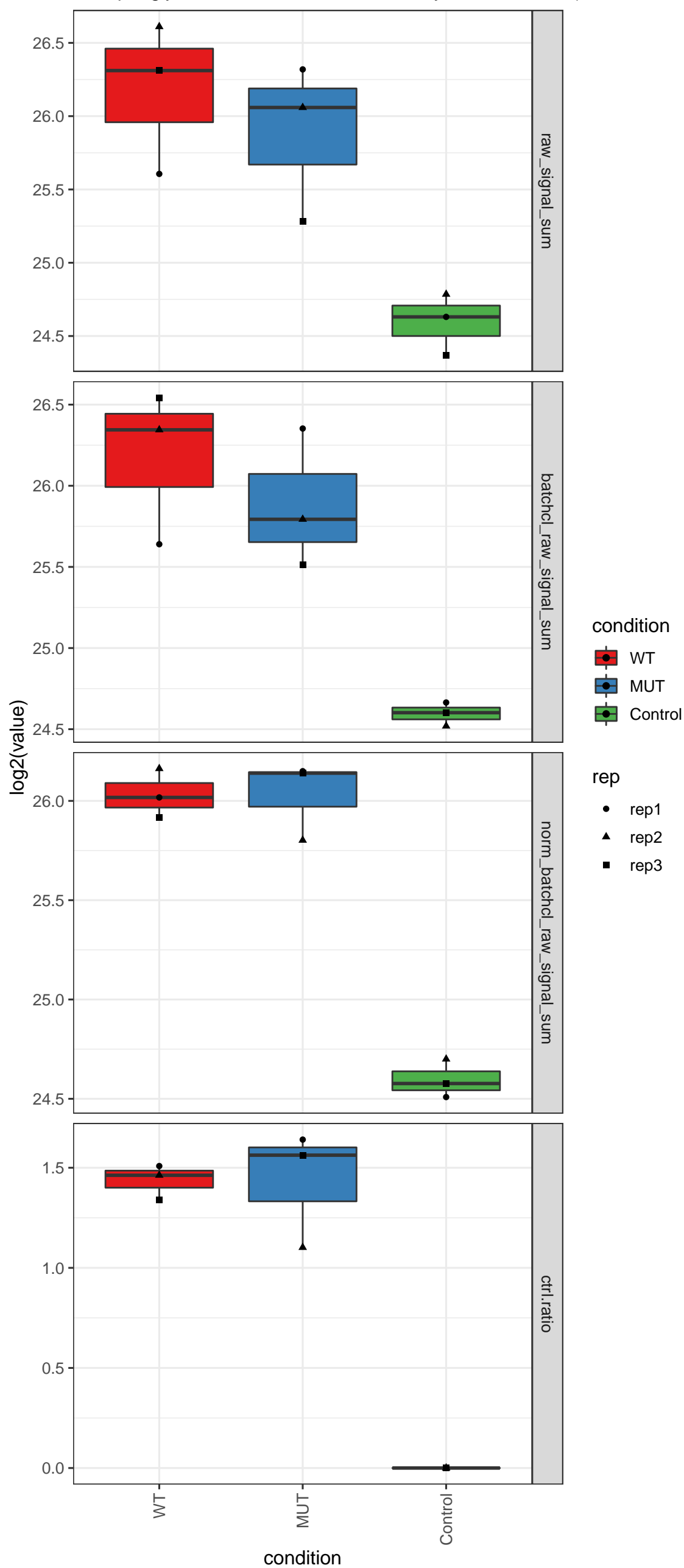
PGI1 – P12709

Glucose-6-phosphate isomerase OS=*Saccharomyces cerevisiae* (strain A



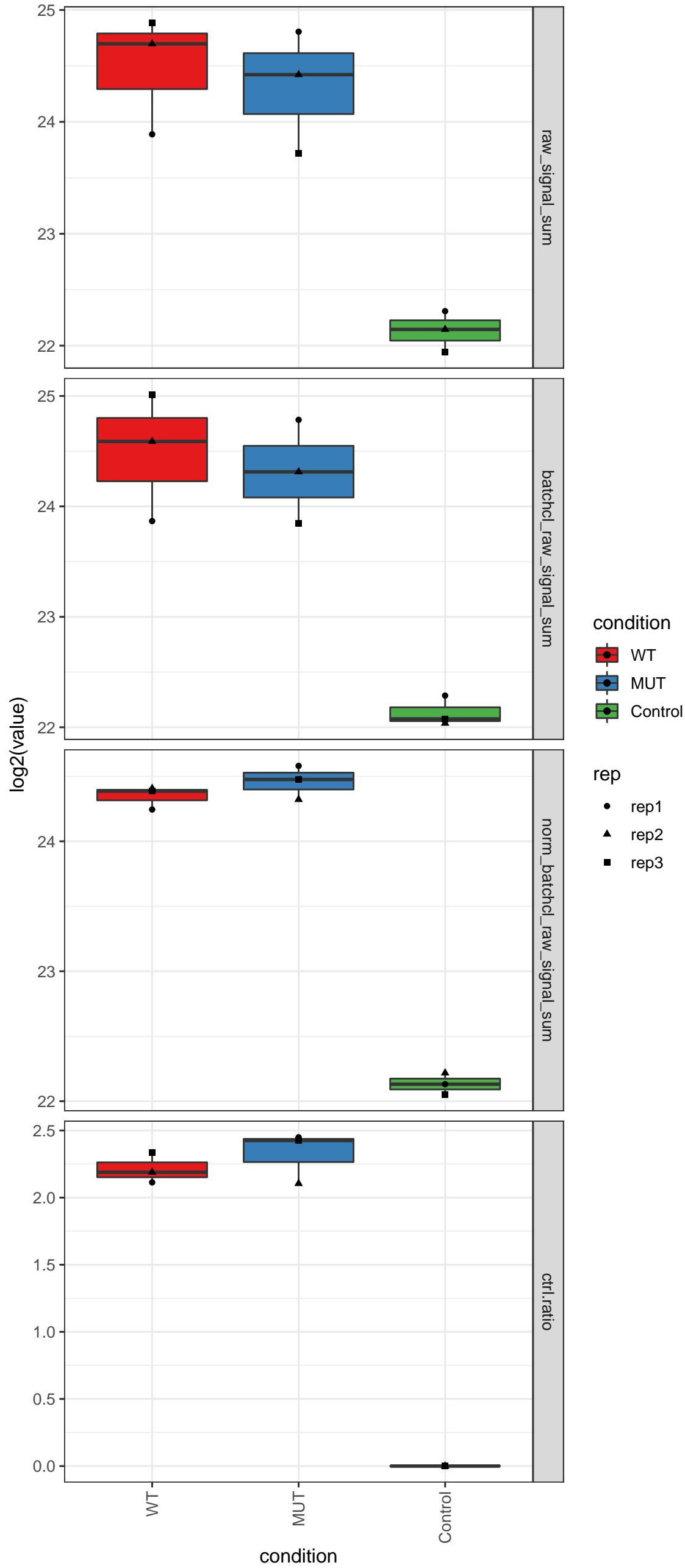
PGK1 – P00560

Phosphoglycerate kinase OS=*Saccharomyces cerevisiae* (strain ATCC 20454)



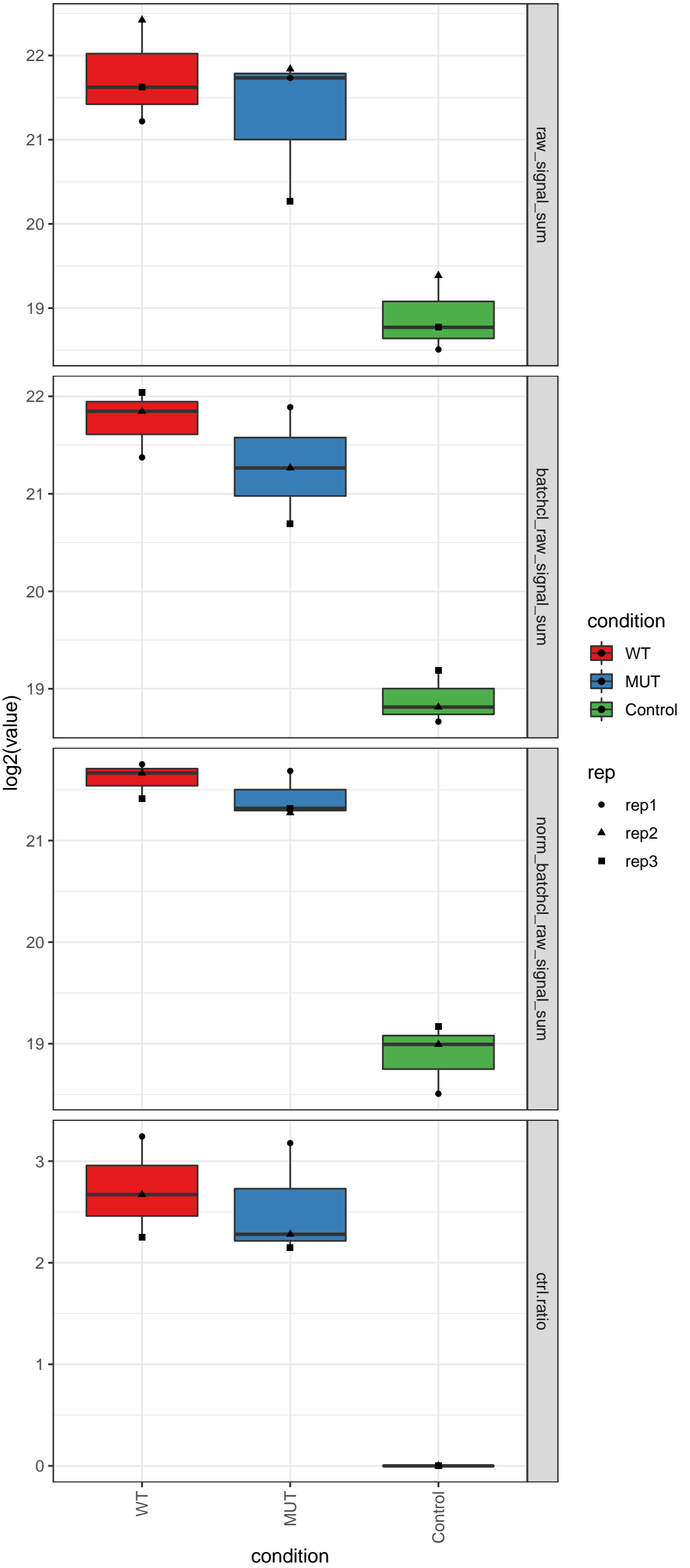
PGM2 – P37012

Phosphoglucomutase 2 OS=*Saccharomyces cerevisiae* (strain ATCC 20454)



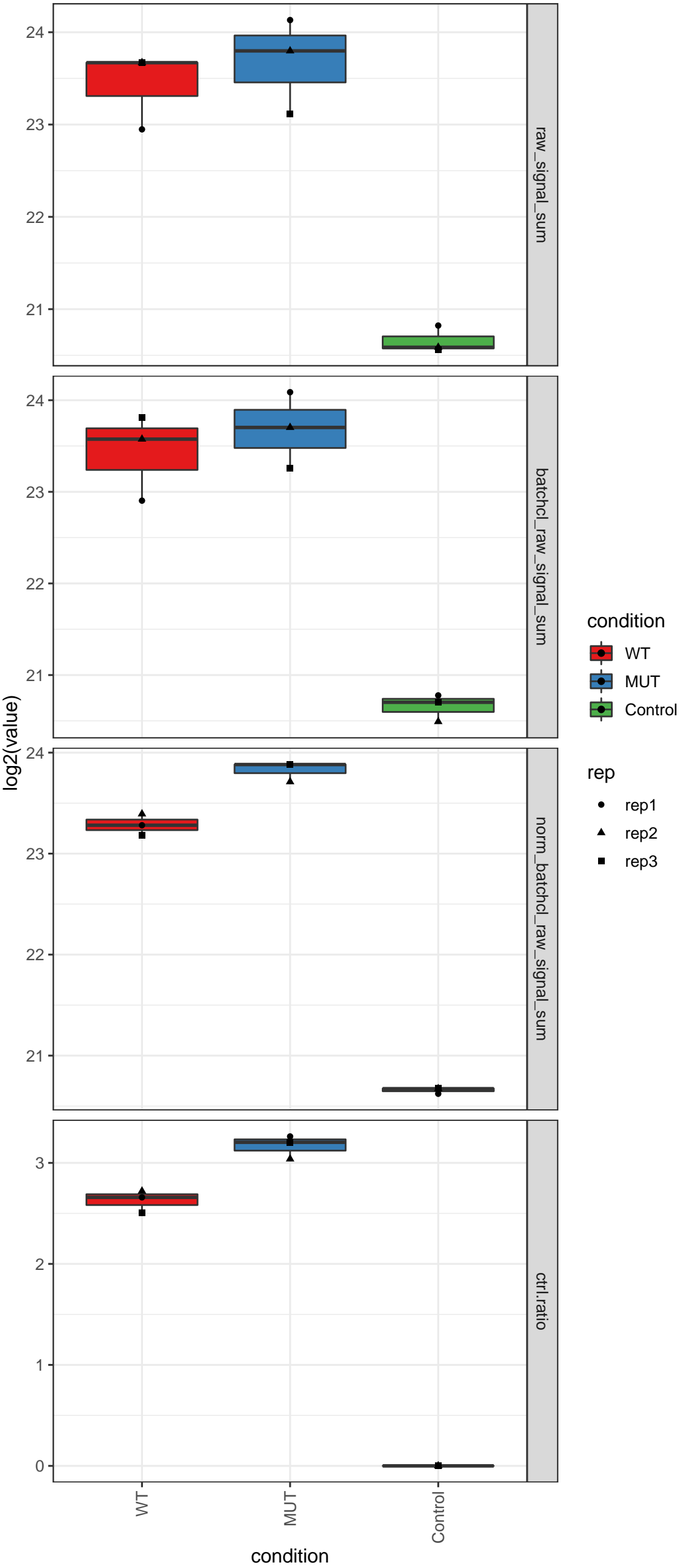
PHO2 – P07269

Regulatory protein PHO2 OS=*Saccharomyces cerevisiae* (strain ATCC 204



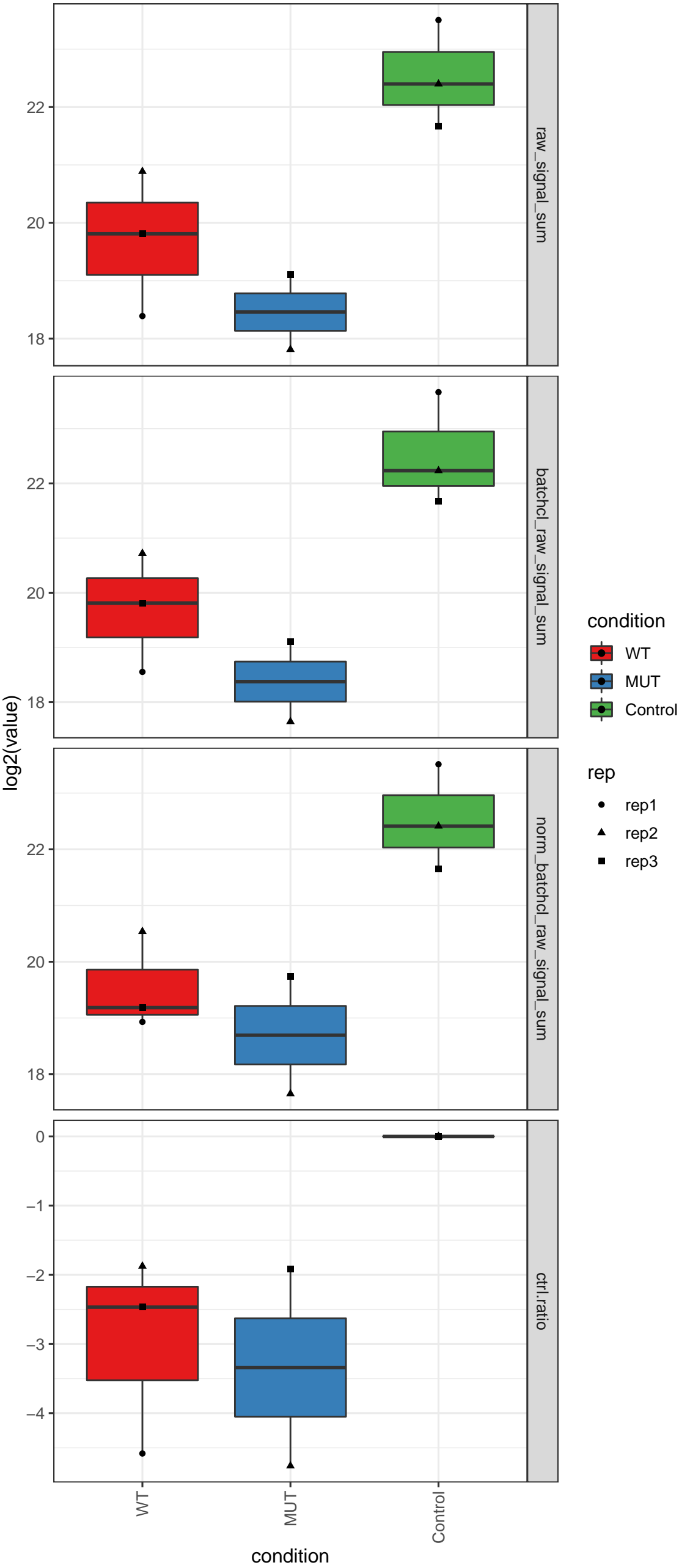
PIL1 – P53252

Sphingolipid long chain base-responsive protein PIL1 OS=Saccharomyces



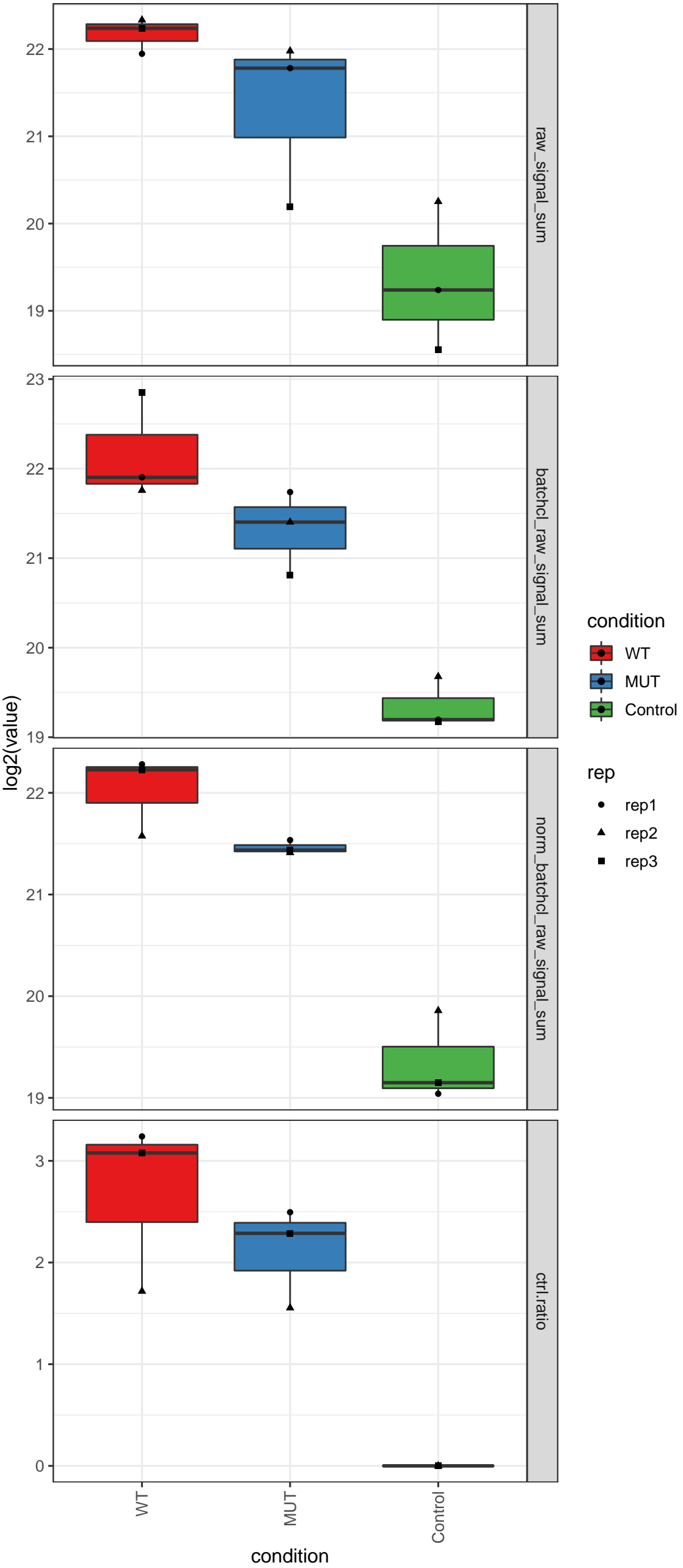
PIN2 – Q12057

[PSI+] induction protein 2 OS=*Saccharomyces cerevisiae* (strain ATCC 204



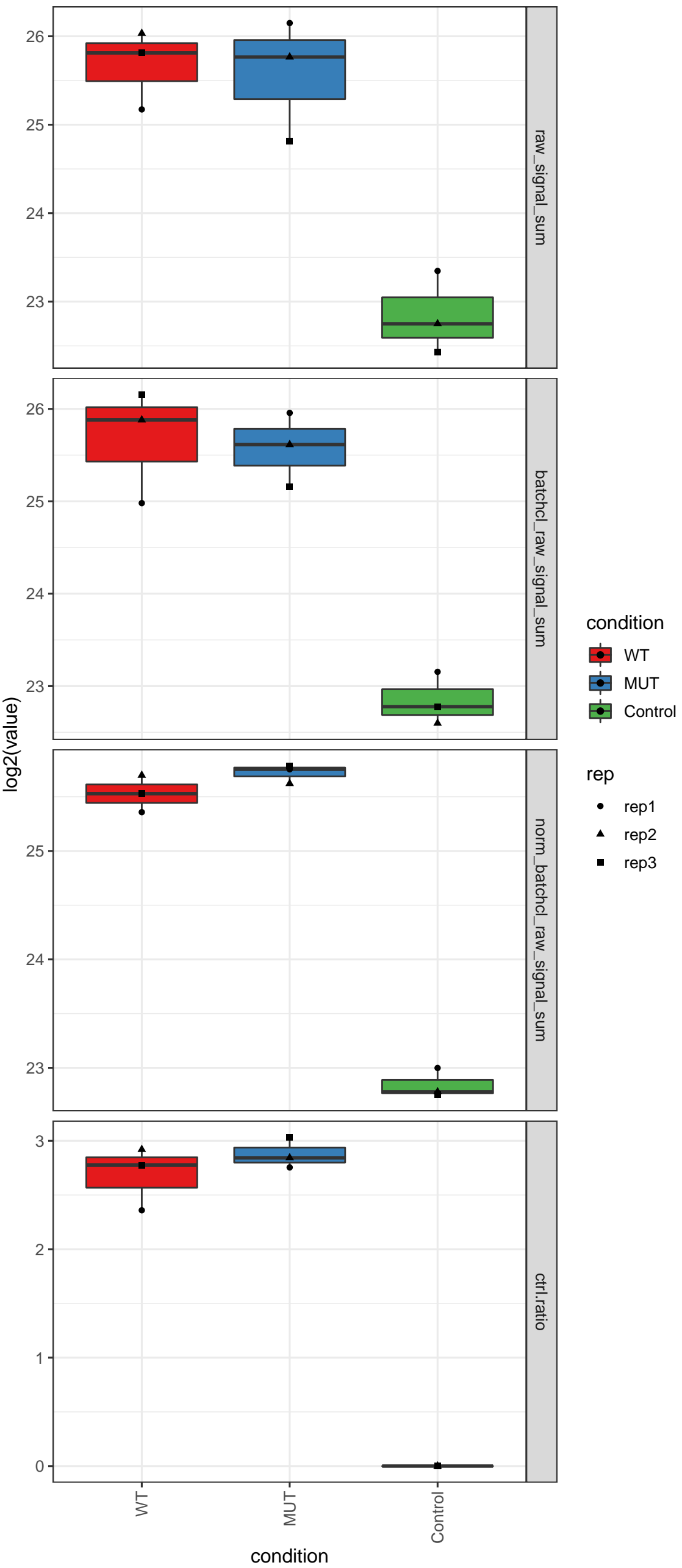
PIP2 – P52960

Peroxisome proliferation transcriptional regulator OS=*Saccharomyces cere*



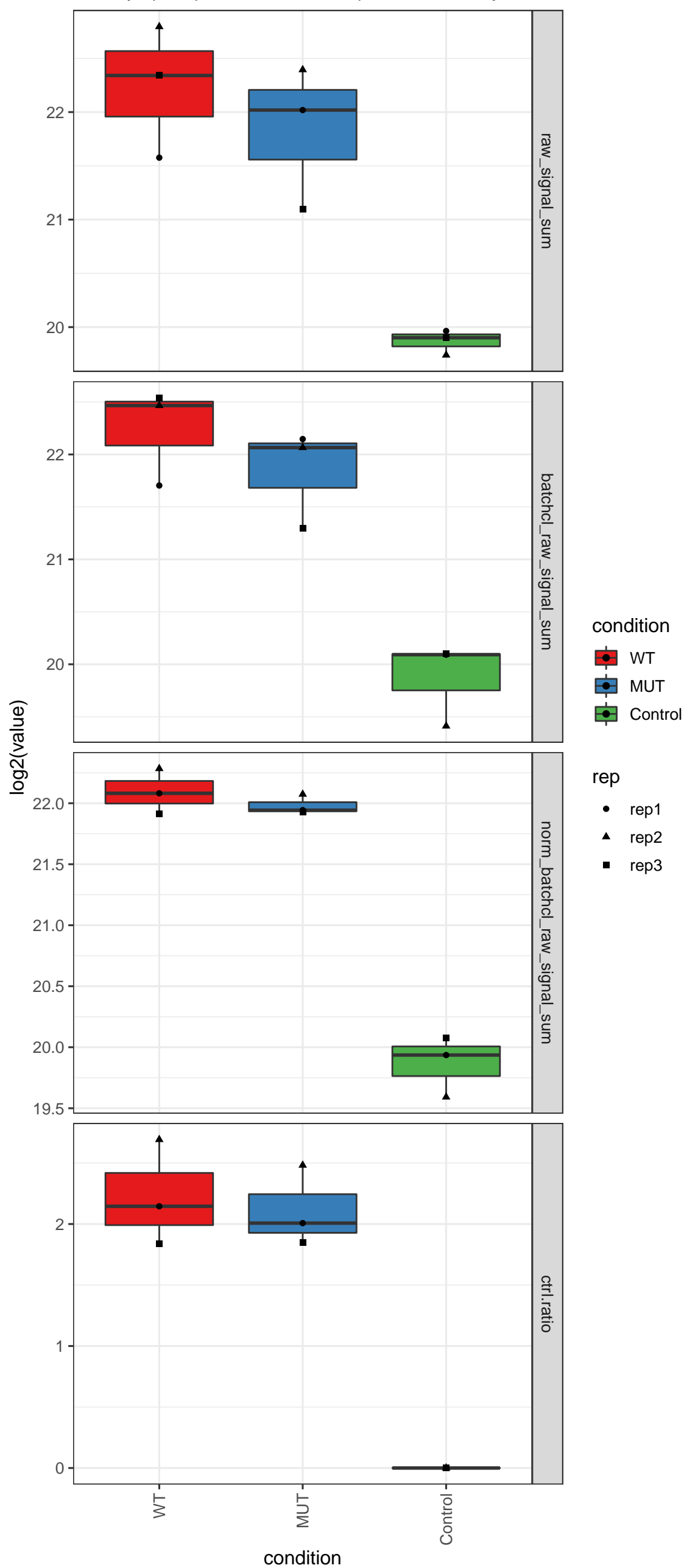
PMA1 – P05030

Plasma membrane ATPase 1 OS=*Saccharomyces cerevisiae* (strain ATCC



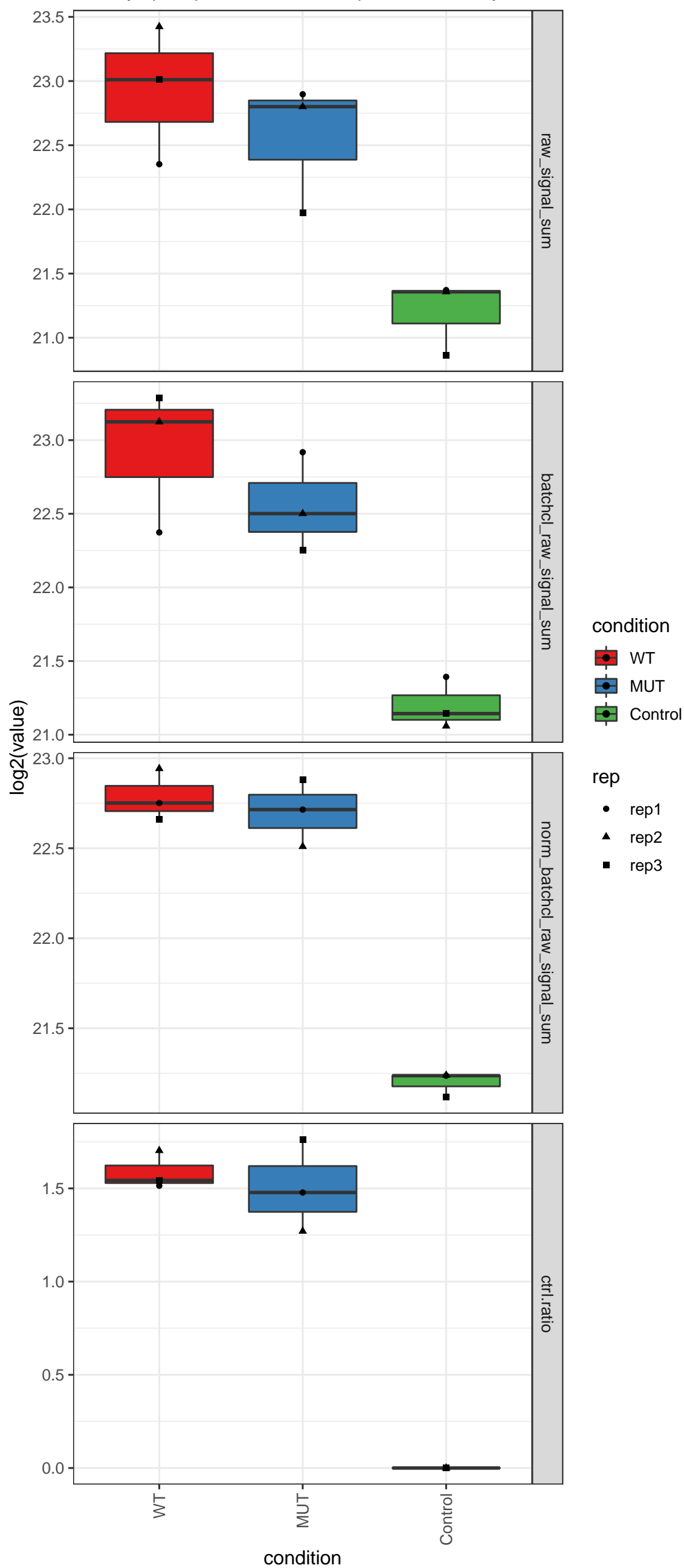
PMT1 – P33775

Dolichyl–phosphate–mannose--protein mannosyltransferase 1 OS=Sac



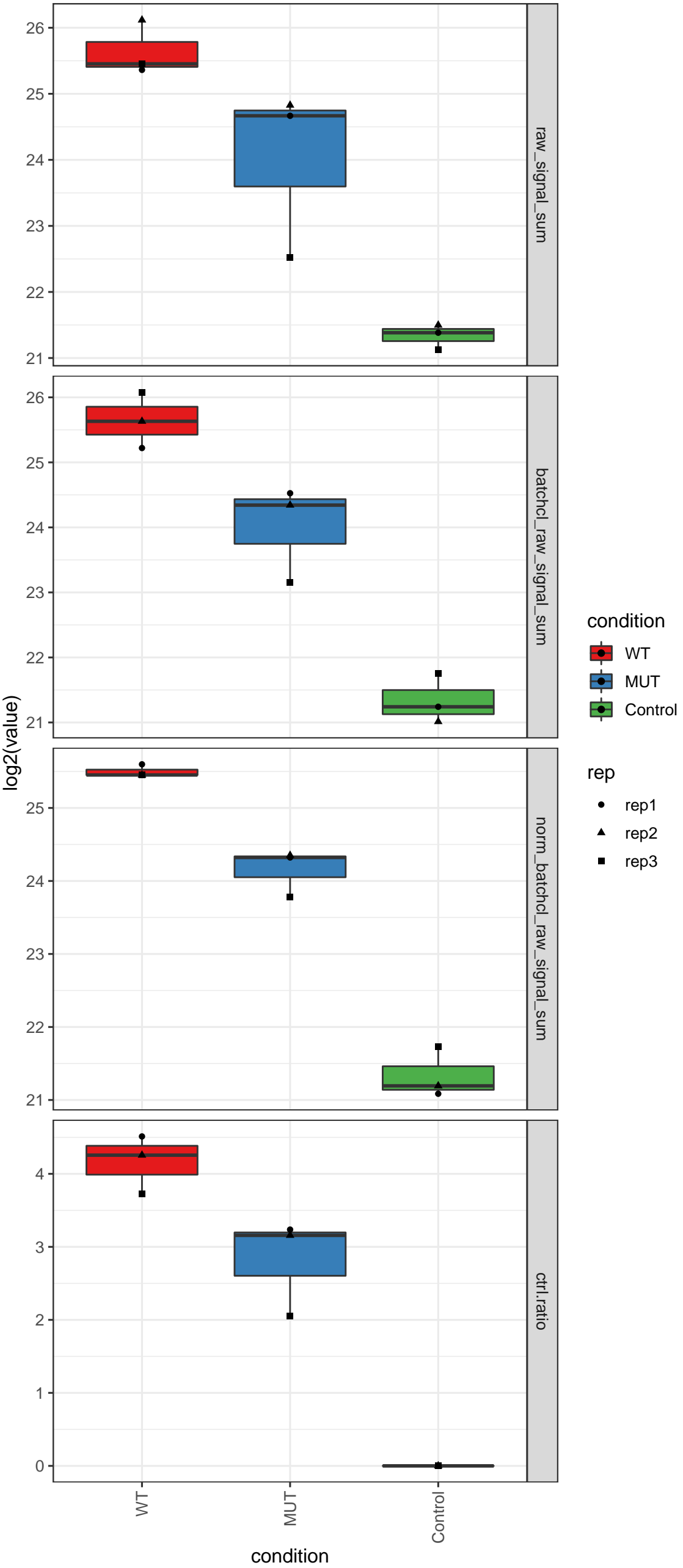
PMT2 – P31382

Dolichyl–phosphate–mannose--protein mannosyltransferase 2 OS=Sac



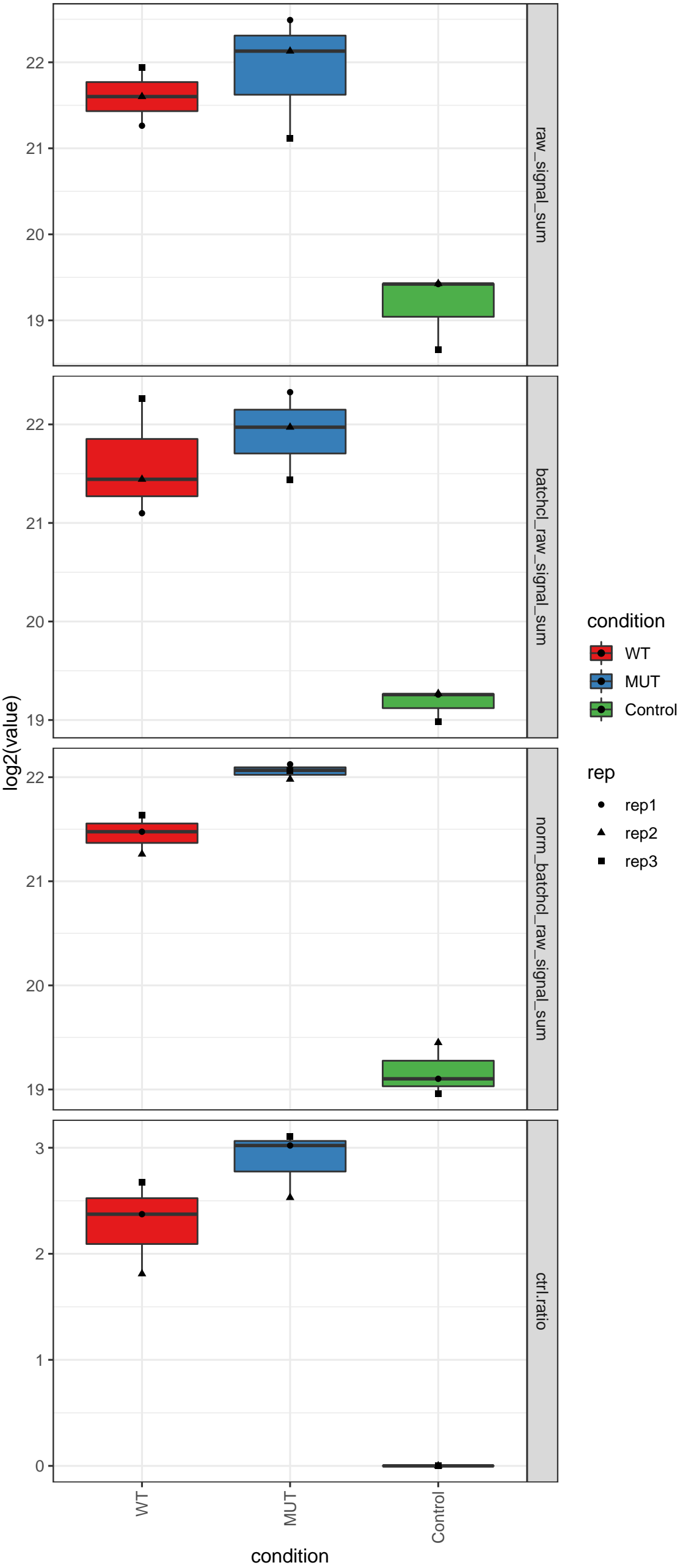
POB3 – Q04636

FACT complex subunit POB3 OS=*Saccharomyces cerevisiae* (strain ATCC



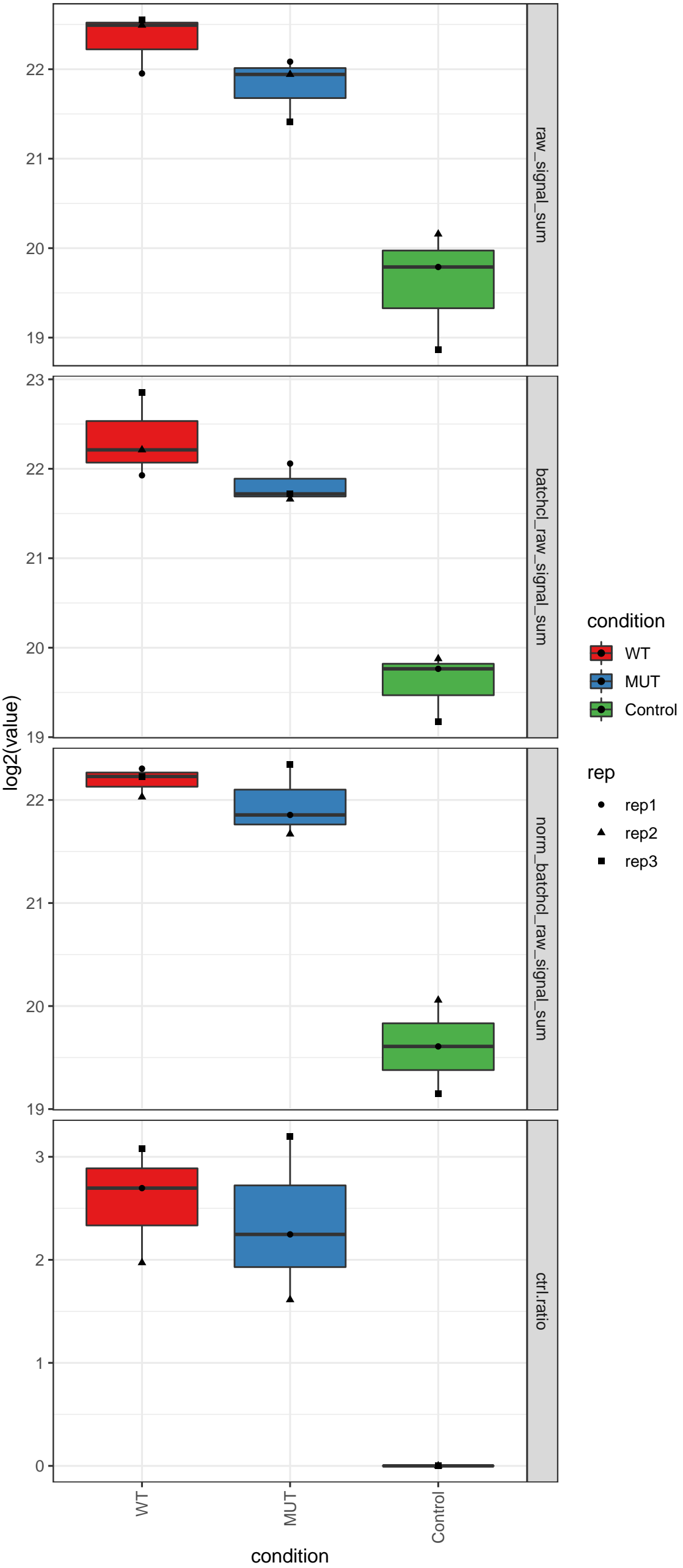
POL30 – P15873

Proliferating cell nuclear antigen OS=*Saccharomyces cerevisiae* (strain ATCC 22016)



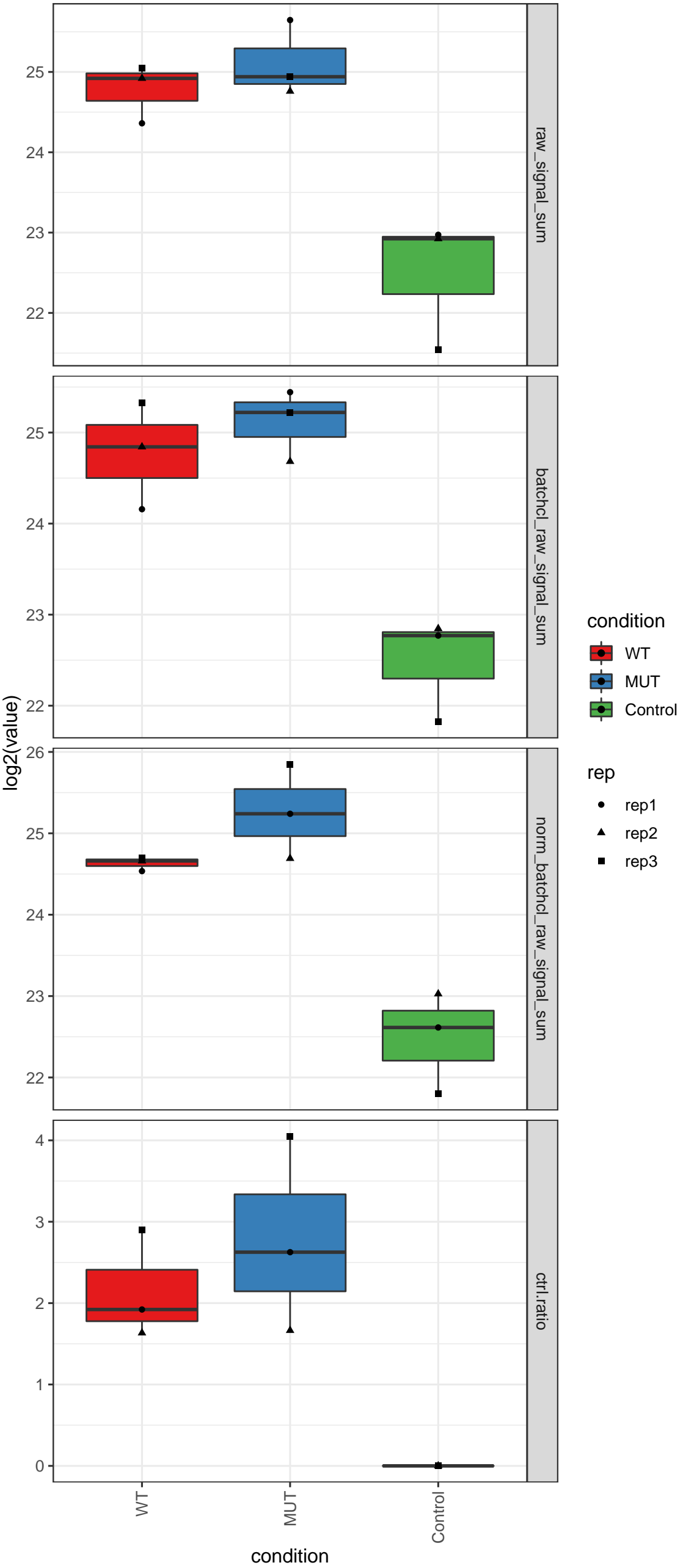
POM33 – Q12164

Pore membrane protein of 33 kDa OS=*Saccharomyces cerevisiae* (strain A



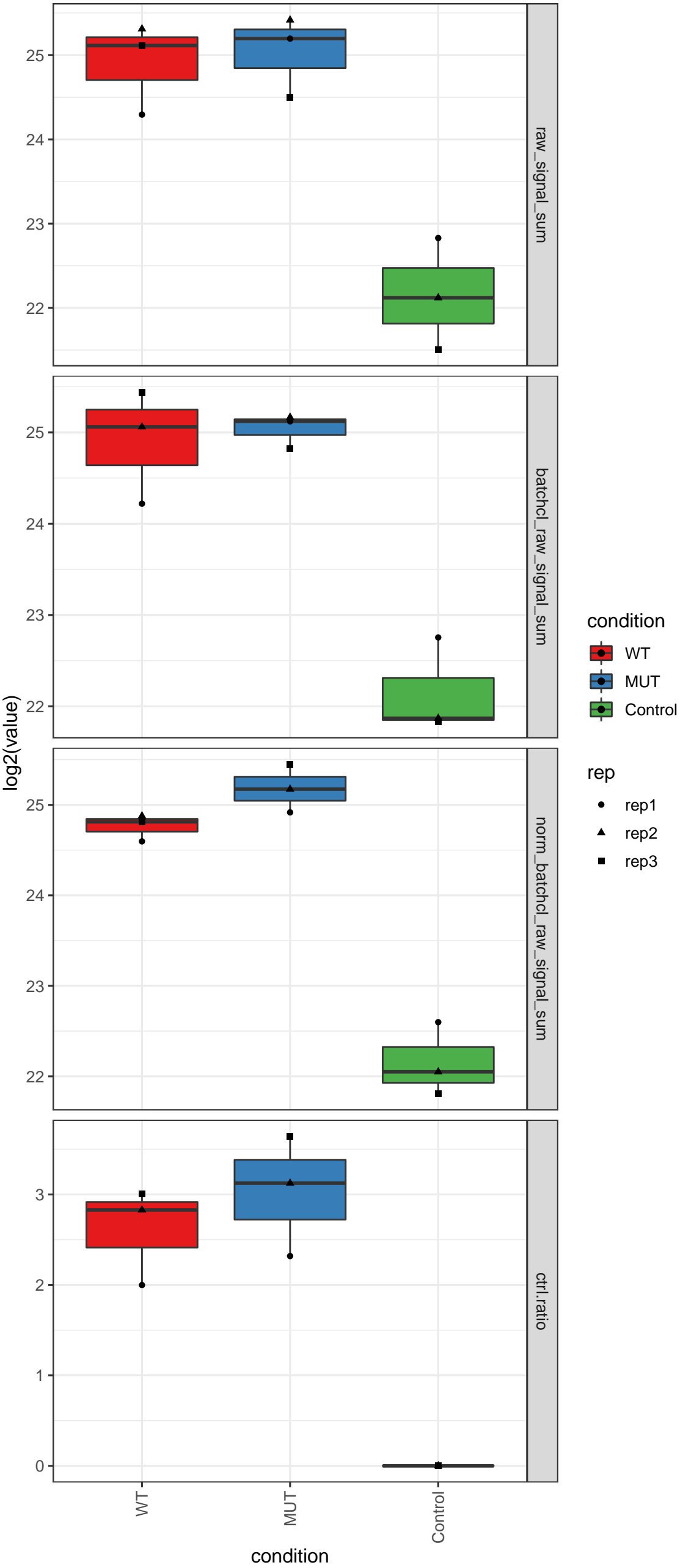
POR1 – P04840

Mitochondrial outer membrane protein porin 1 OS=*Saccharomyces cerevisiae*



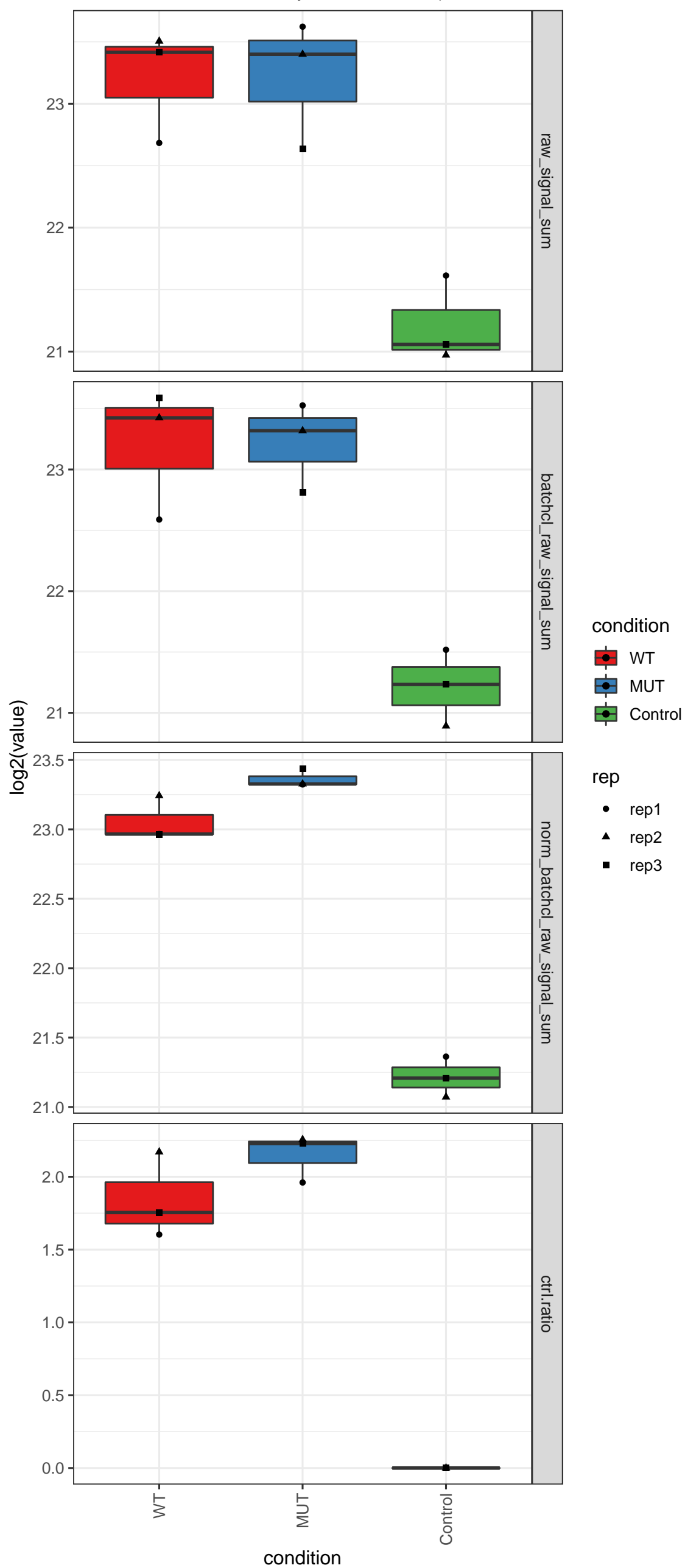
POX1 – P13711

Acyl-coenzyme A oxidase OS=*Saccharomyces cerevisiae* (strain ATCC 20454)



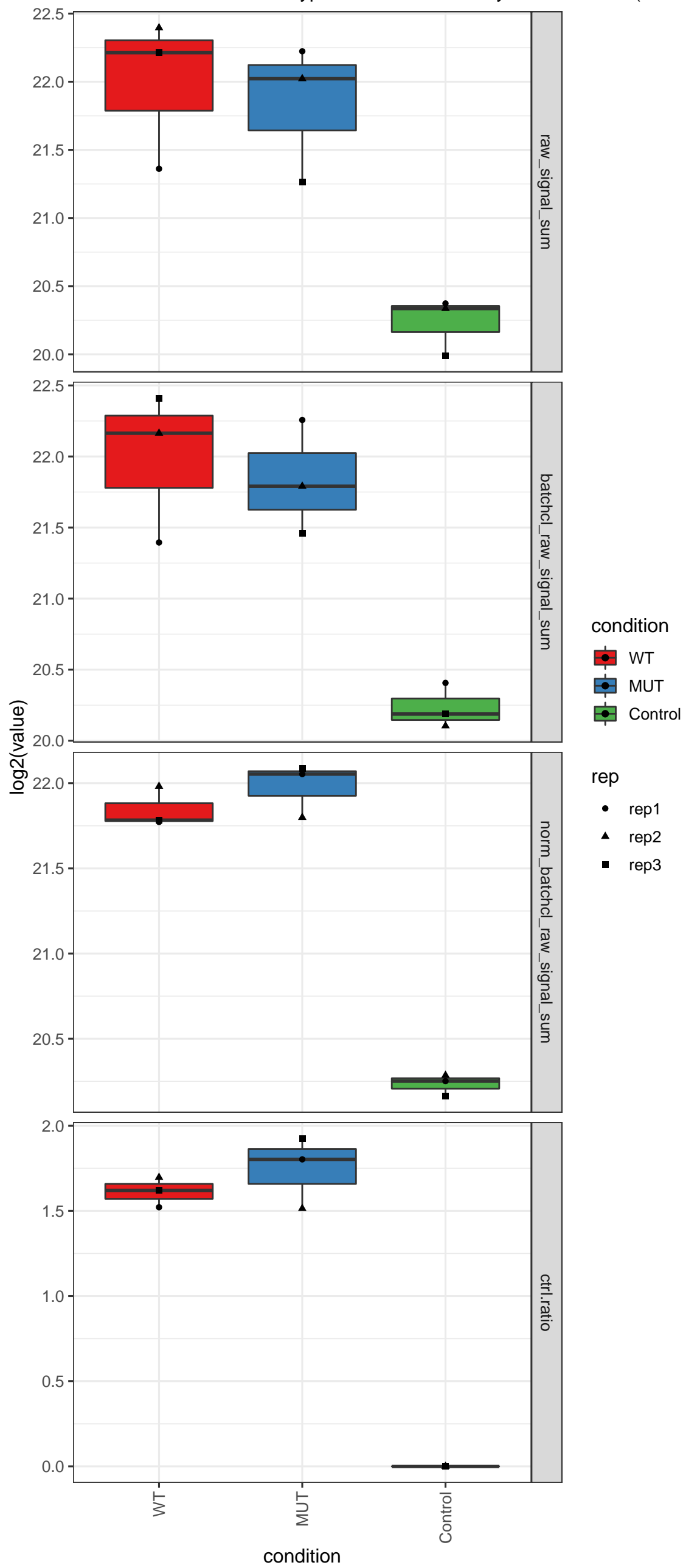
PRB1 – P09232

Cerevisin OS=*Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) (



PRE3 – P38624

Proteasome subunit beta type-1 OS=*Saccharomyces cerevisiae* (strain A)

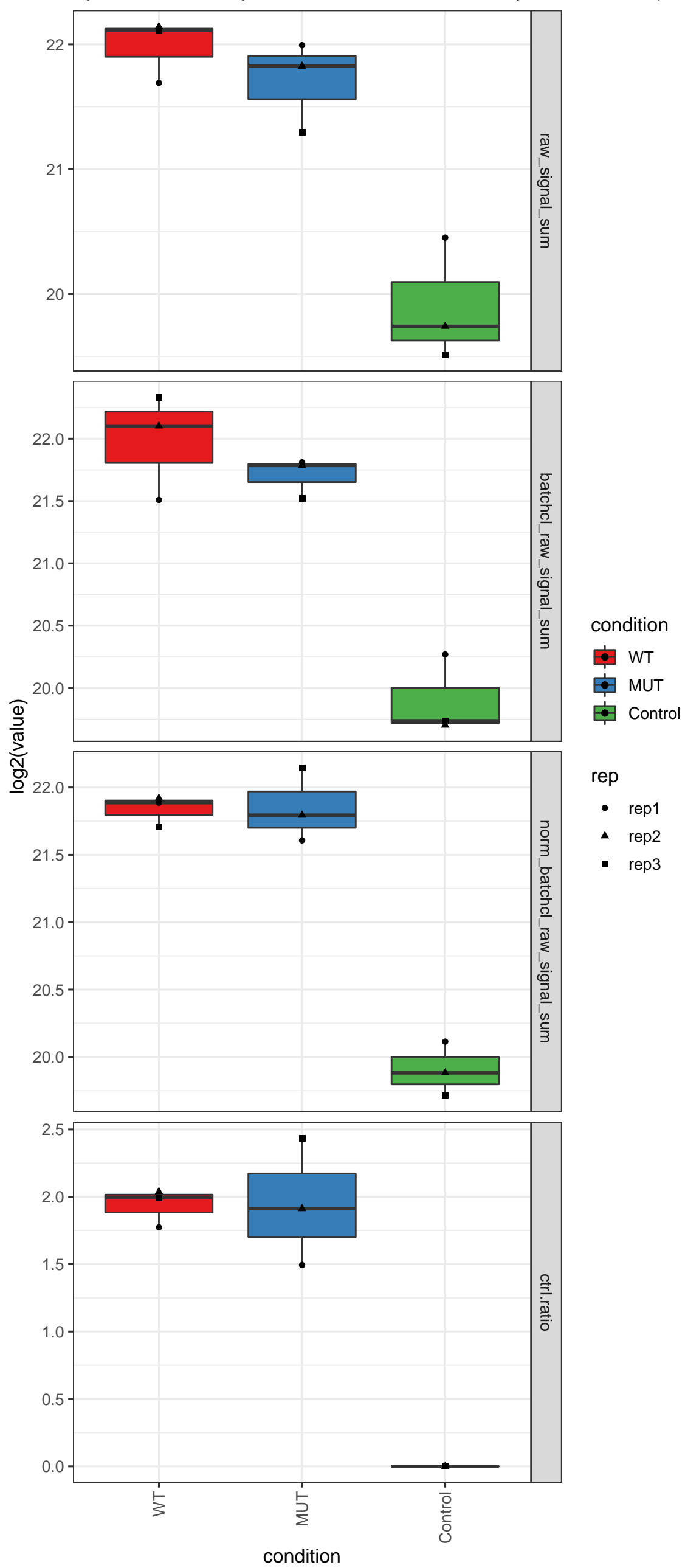


Proteasome subunit beta type-6 OS=Saccharomyces cerevisiae (strain A



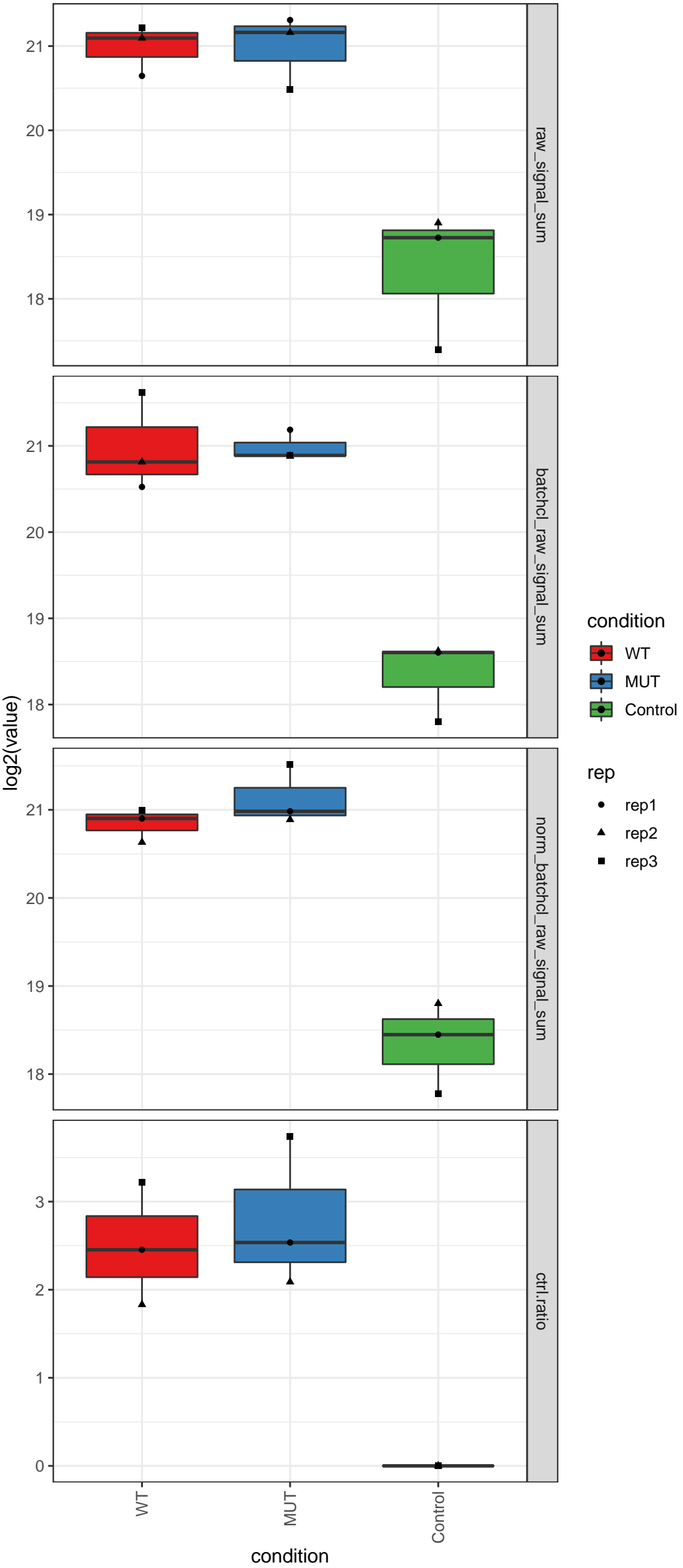
PRO3 – P32263

Pyrroline-5-carboxylate reductase OS=*Saccharomyces cerevisiae* (strain



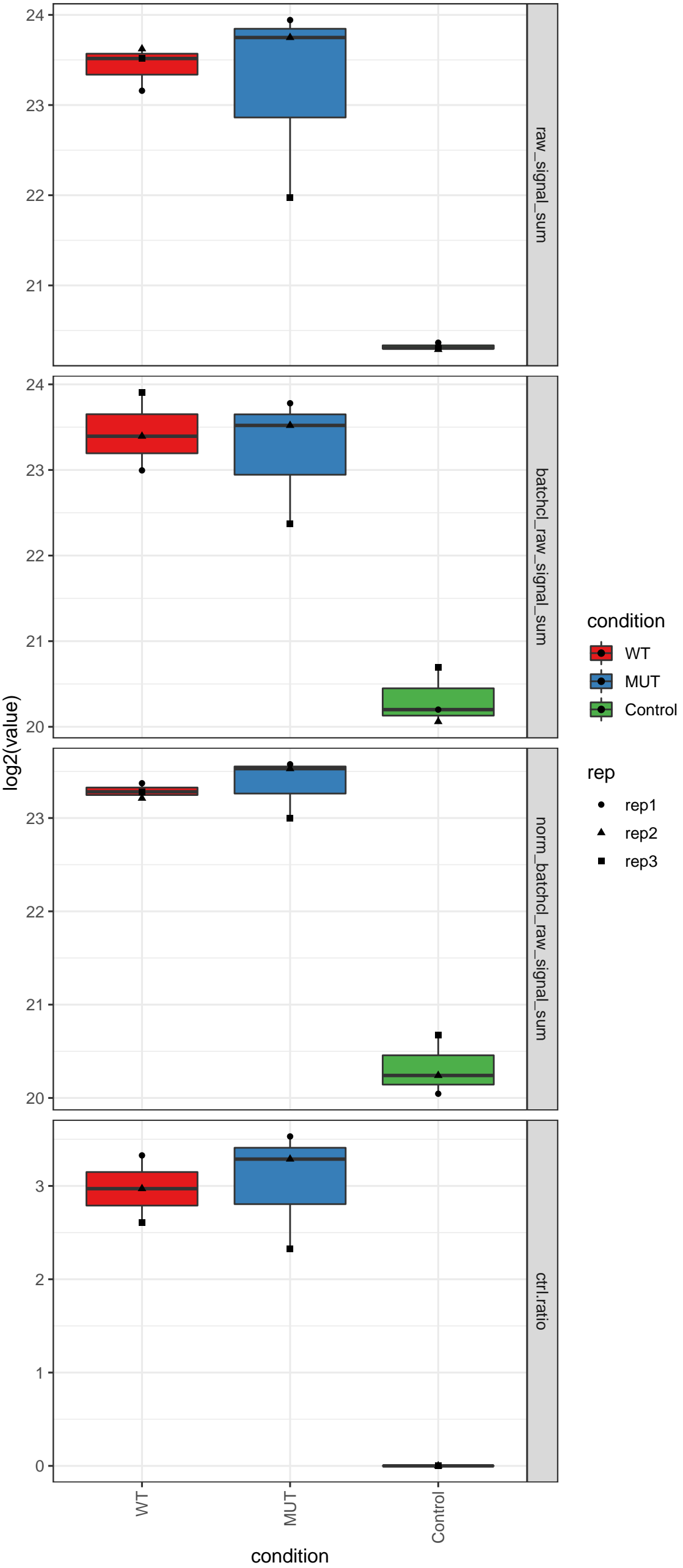
PRP19 – P32523

Pre-mRNA-processing factor 19 OS=*Saccharomyces cerevisiae* (strain ATCC 22016 / DSM 578 / Kazuo)



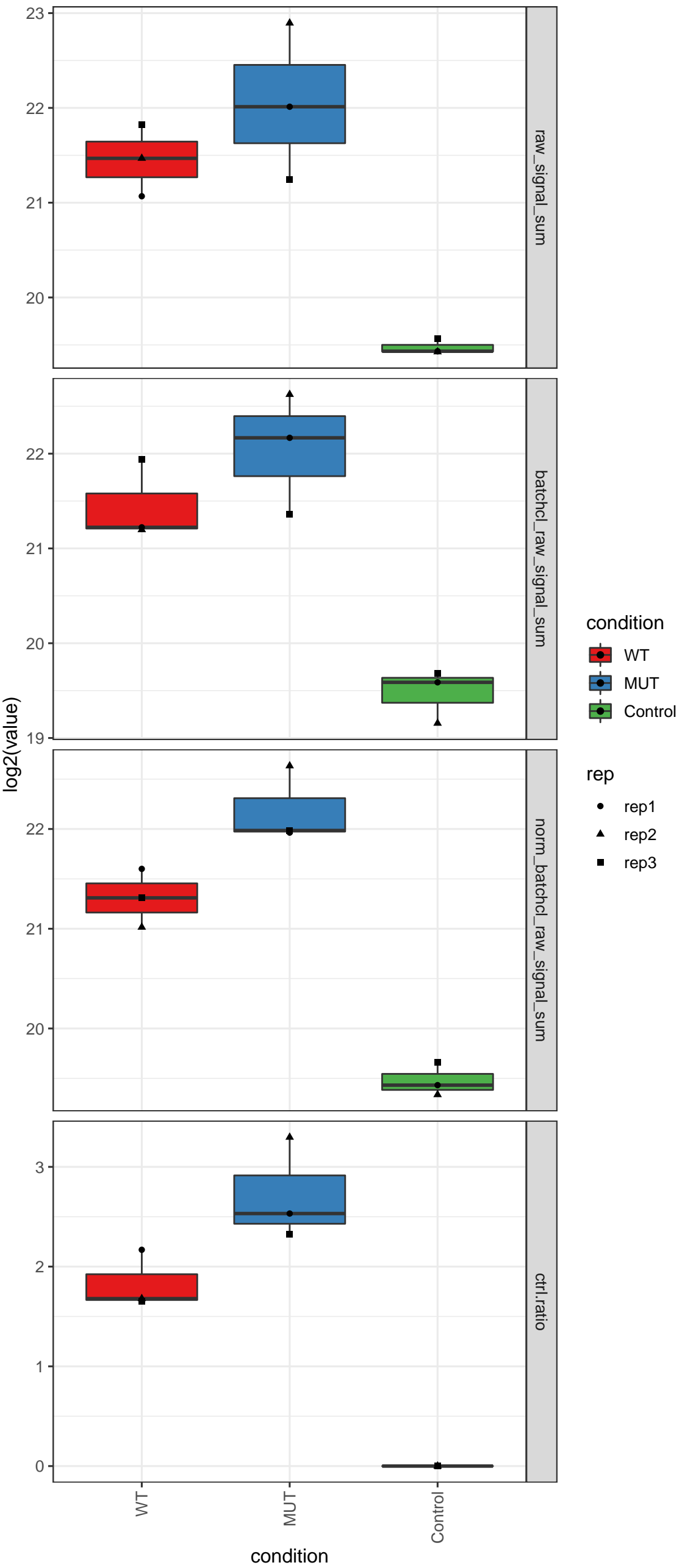
PRP43 – P53131

Pre-mRNA-splicing factor ATP-dependent RNA helicase PRP43 OS=Sac



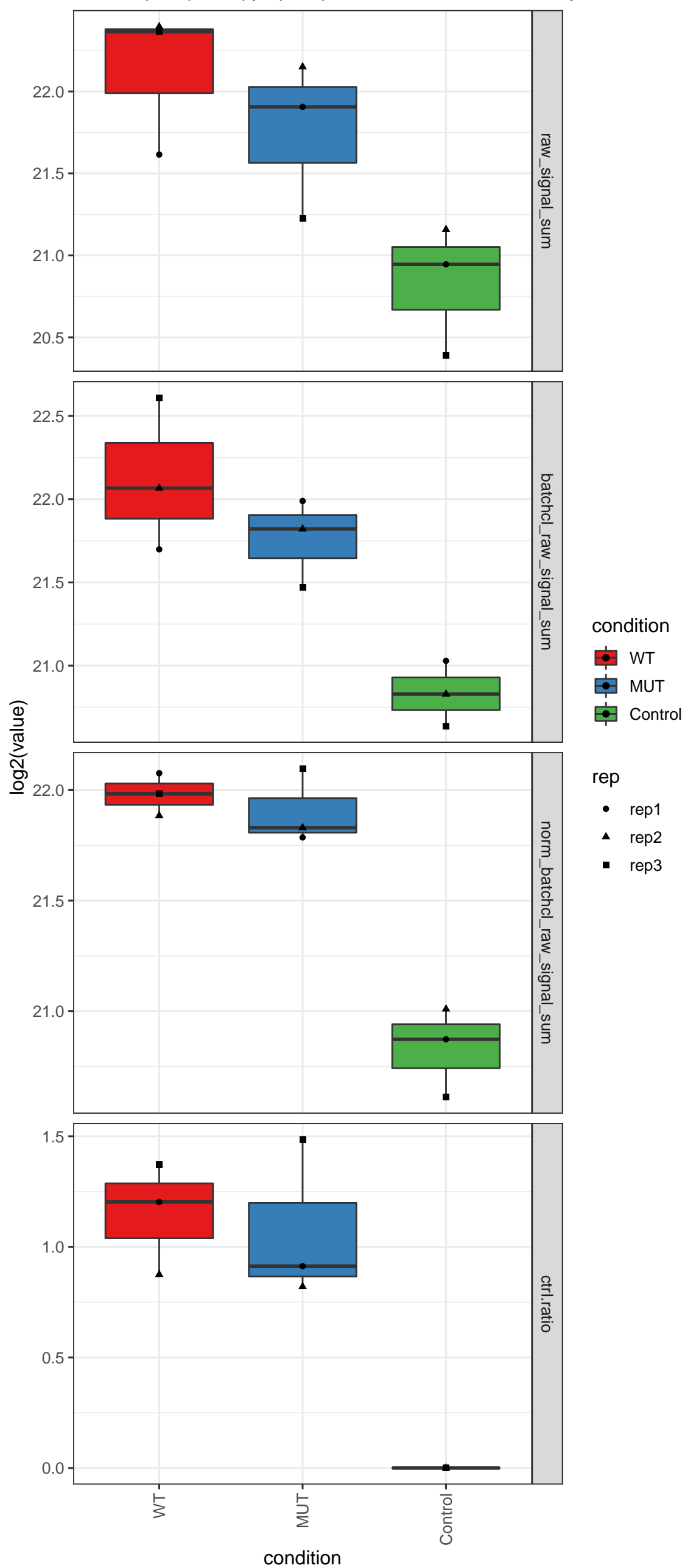
PRS1 – P32895

Ribose-phosphate pyrophosphokinase 1 OS=*Saccharomyces cerevisiae* (



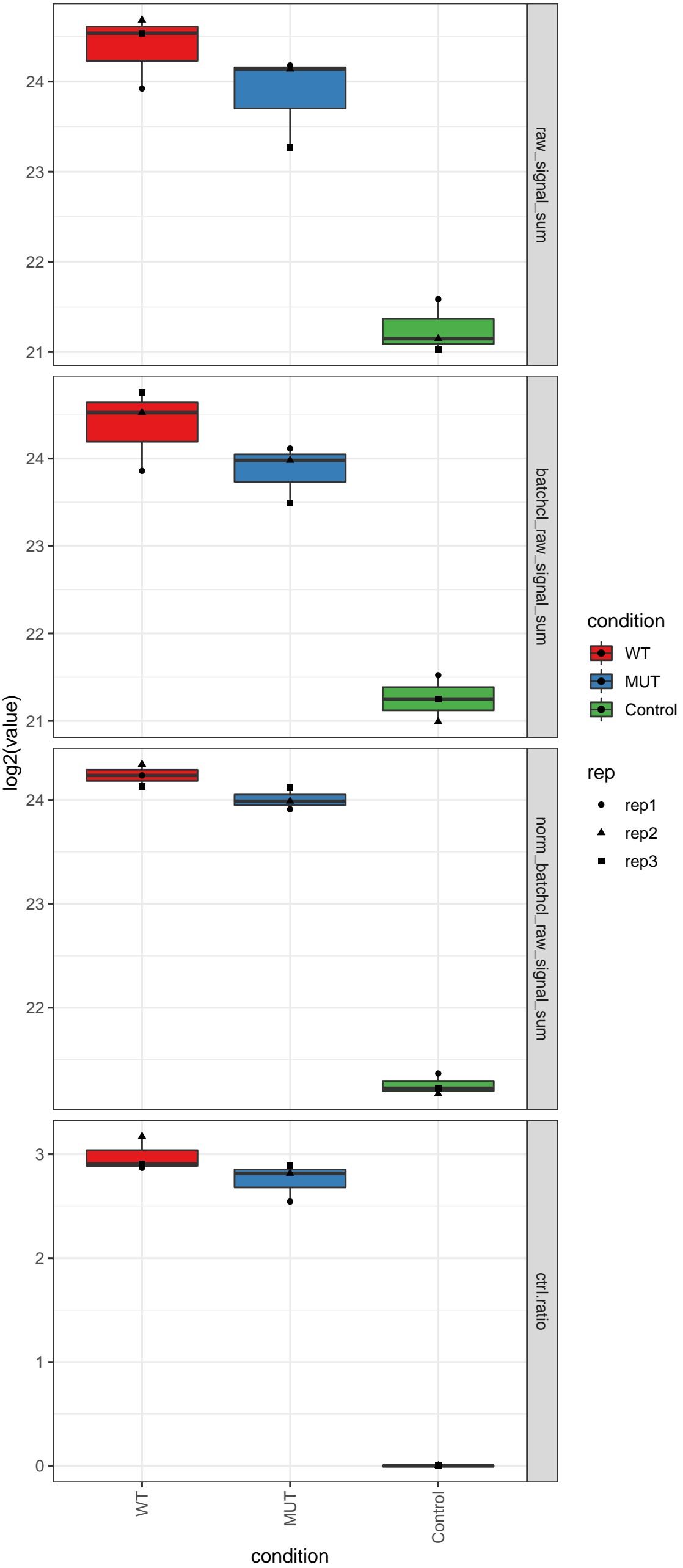
PRS3 – P38689

Ribose-phosphate pyrophosphokinase 3 OS=*Saccharomyces cerevisiae*



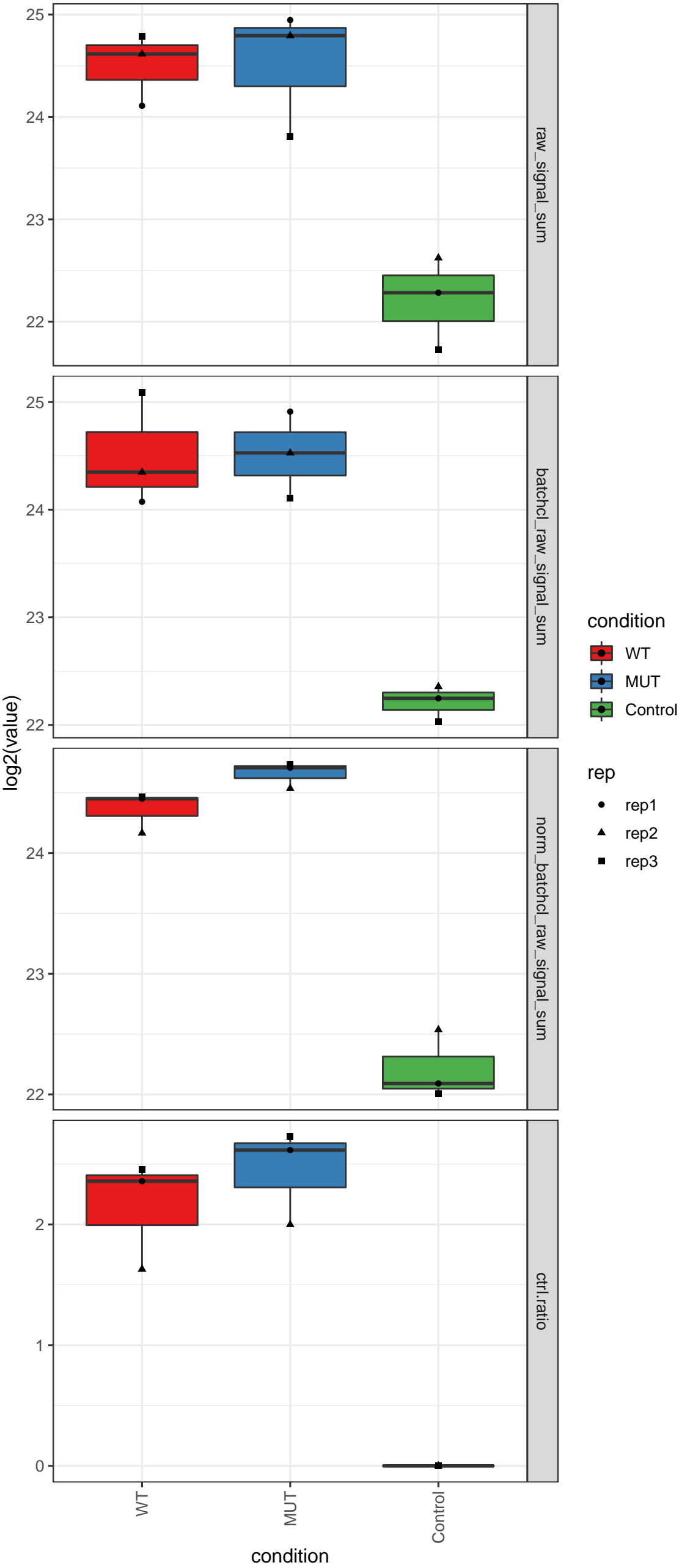
PRT1 – P06103

Eukaryotic translation initiation factor 3 subunit B OS=*Saccharomyces cerevisiae*



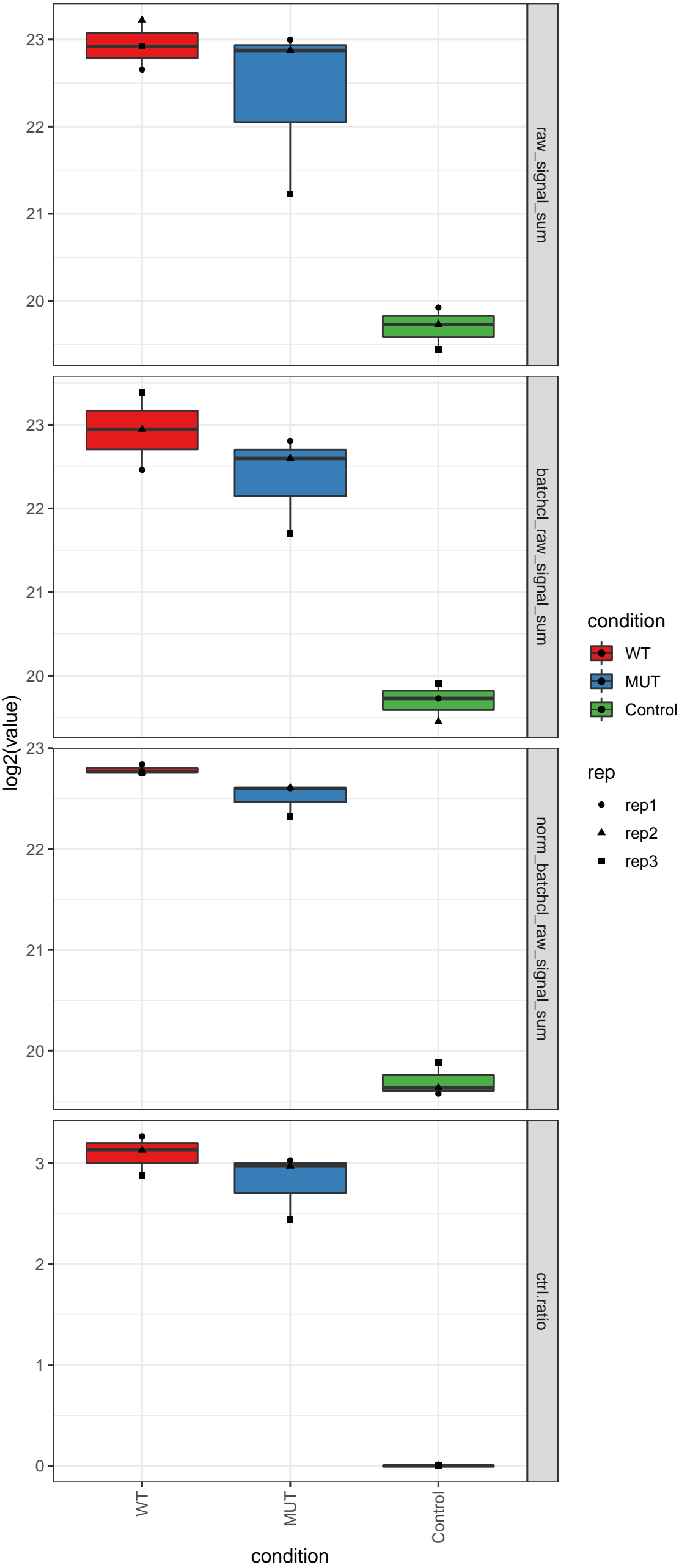
PSA1 – P41940

Mannose-1-phosphate guanyltransferase OS=*Saccharomyces cerevisiae*



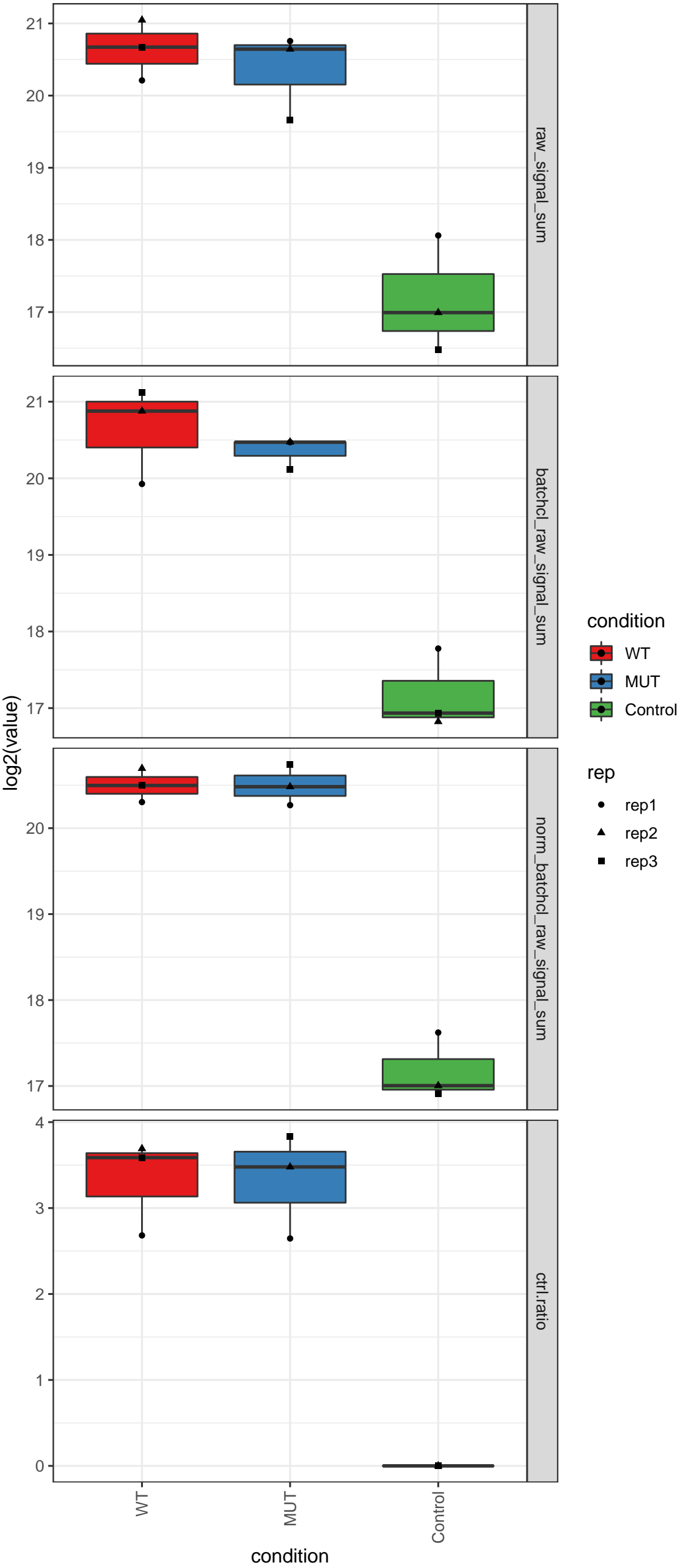
PSH1 – Q12161

RING finger protein PSH1 OS=Saccharomyces cerevisiae (strain ATCC 20



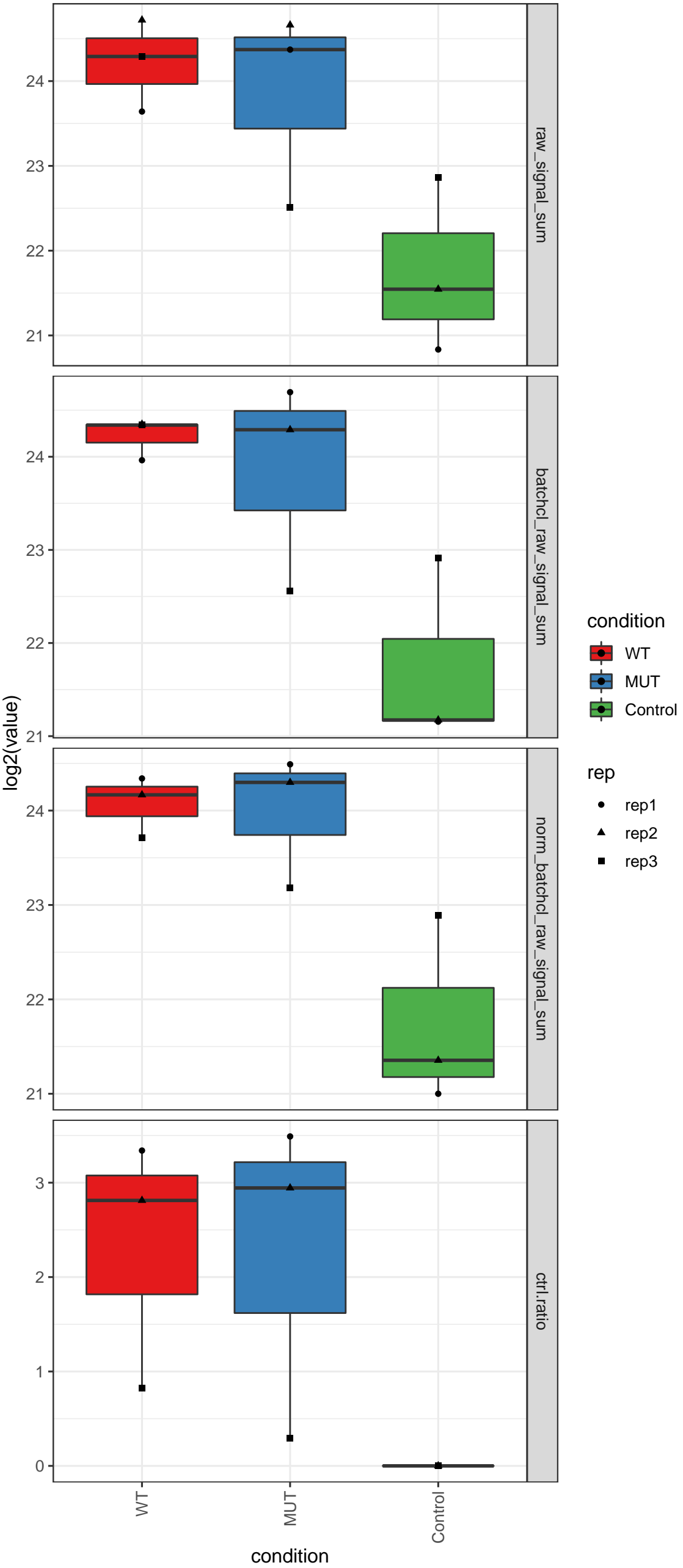
PUF3 – Q07807

mRNA-binding protein PUF3 OS=*Saccharomyces cerevisiae* (strain ATCC

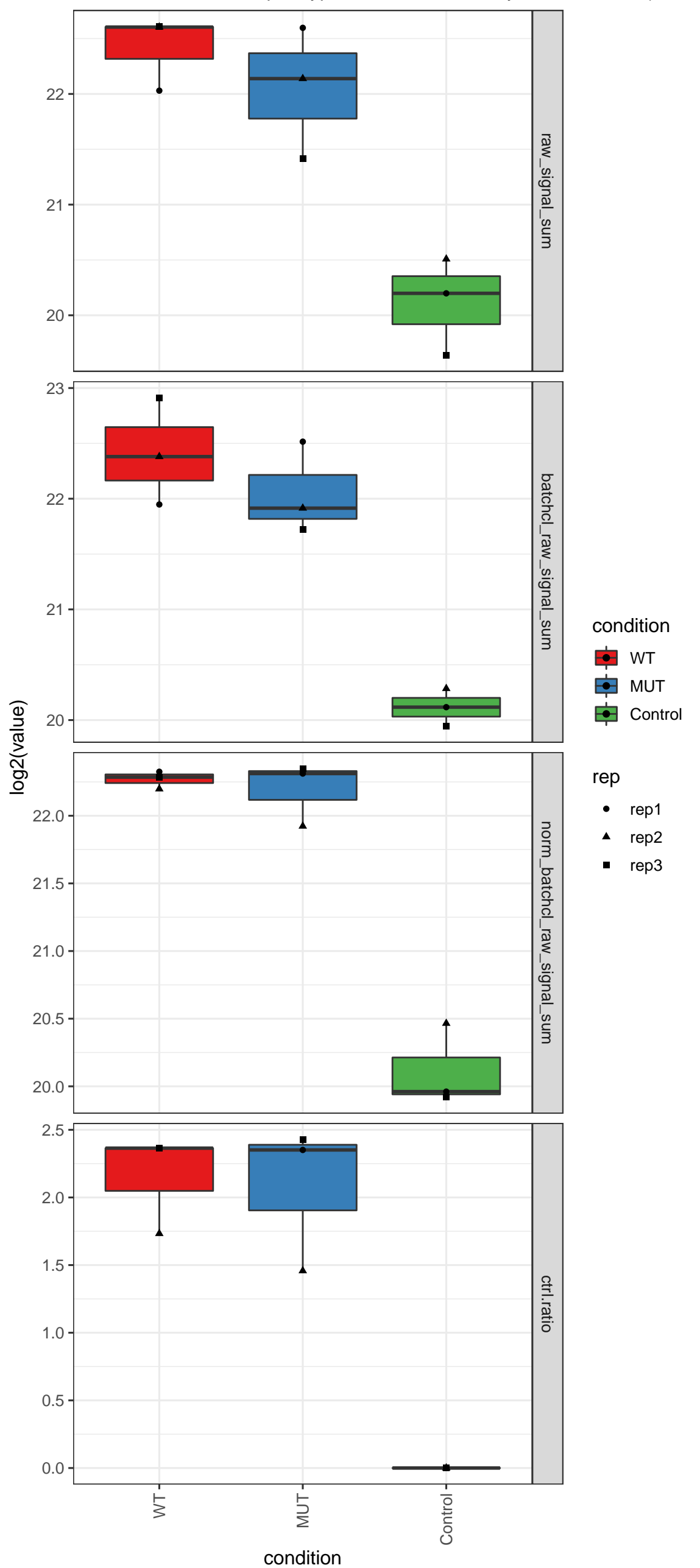


PUF6 – Q04373

Pumilio homology domain family member 6 OS=*Saccharomyces cerevisiae*

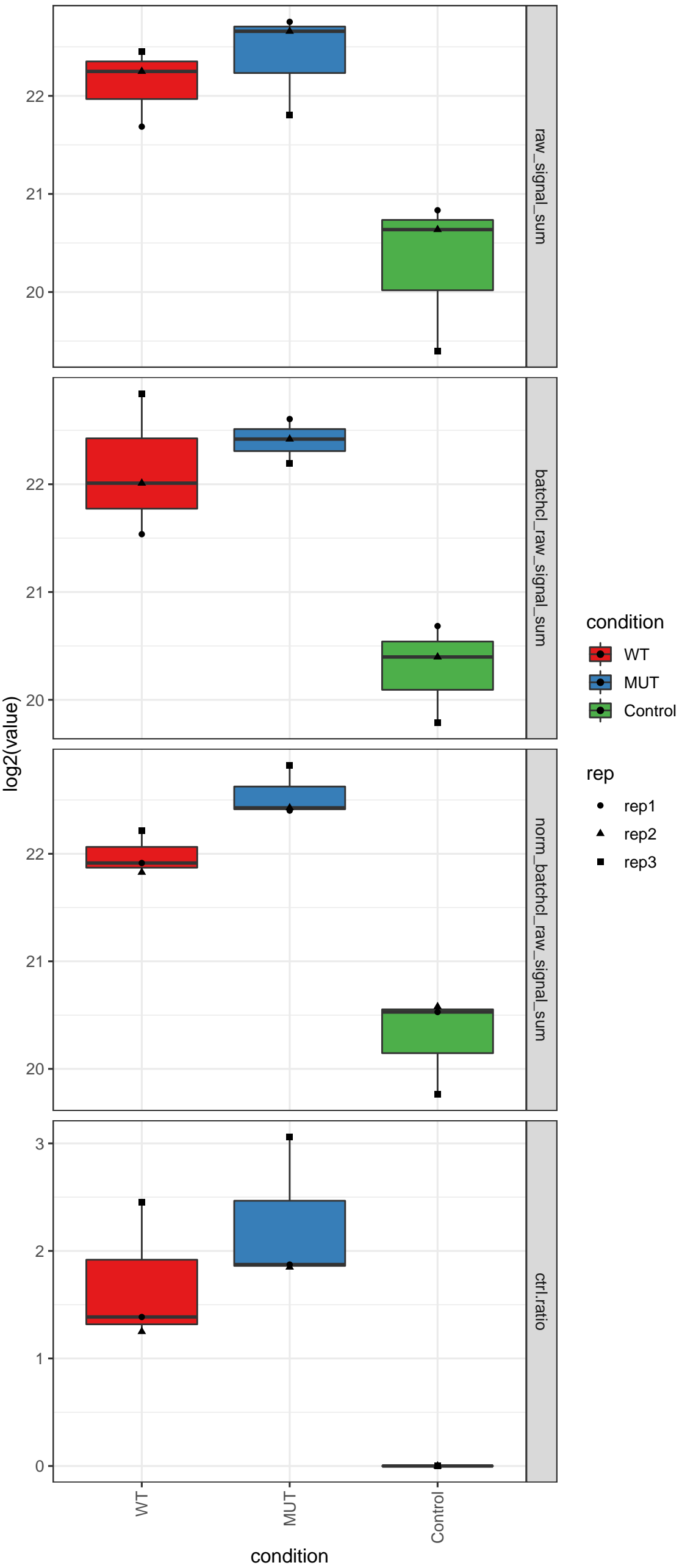


Proteasome subunit alpha type-5 OS=Saccharomyces cerevisiae (strain



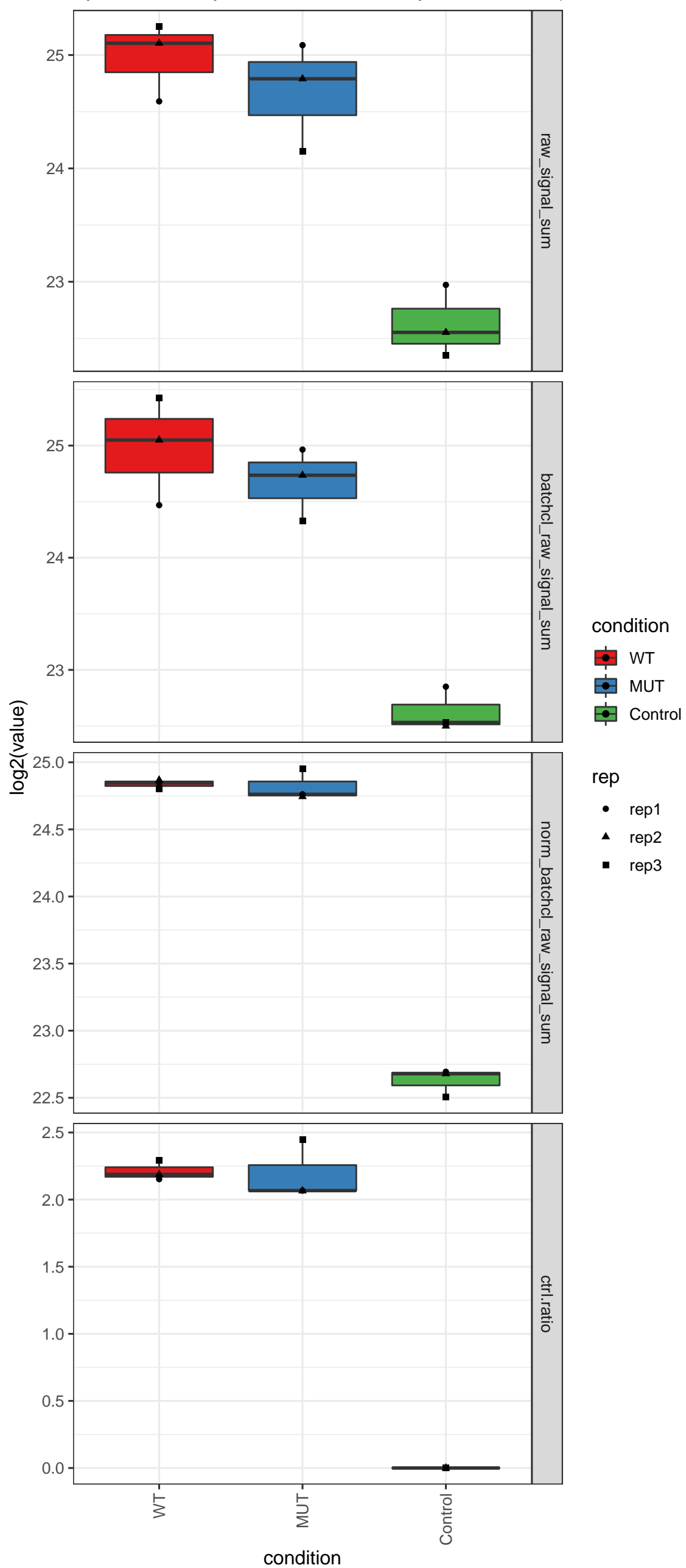
PWP1 – P21304

Periodic tryptophan protein 1 OS=*Saccharomyces cerevisiae* (strain ATCC



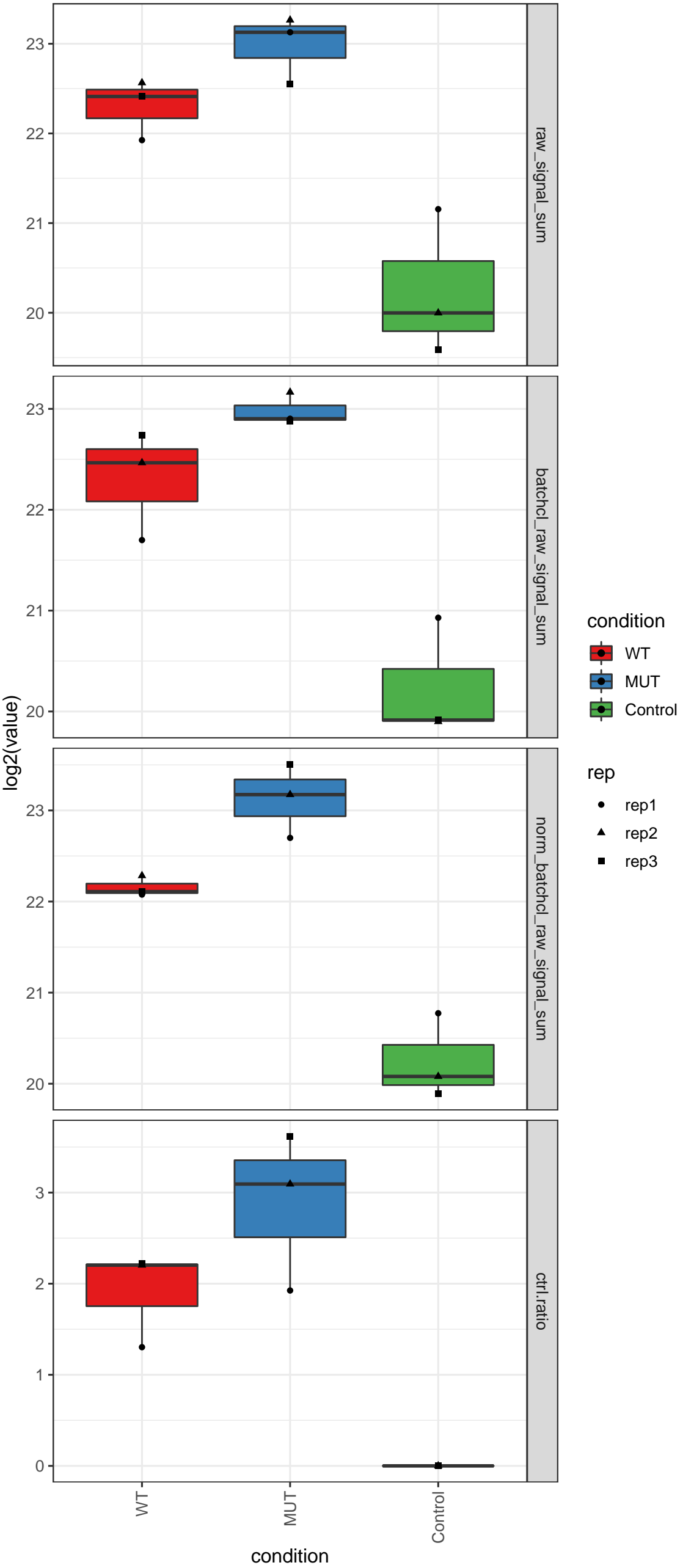
PYC1 – P11154

Pyruvate carboxylase 1 OS=*Saccharomyces cerevisiae* (strain ATCC 204



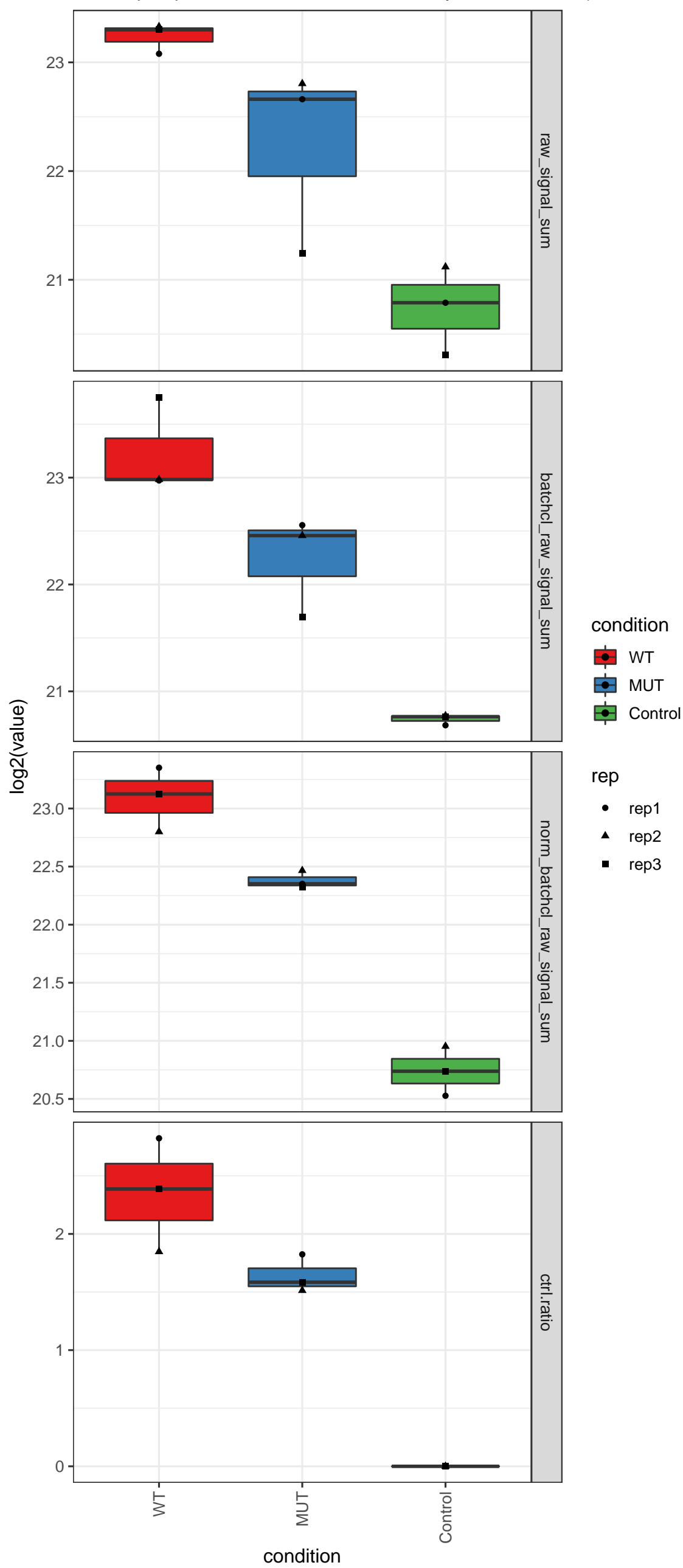
QCR2 – P07257

Cytochrome b–c1 complex subunit 2, mitochondrial OS=Saccharomyces c



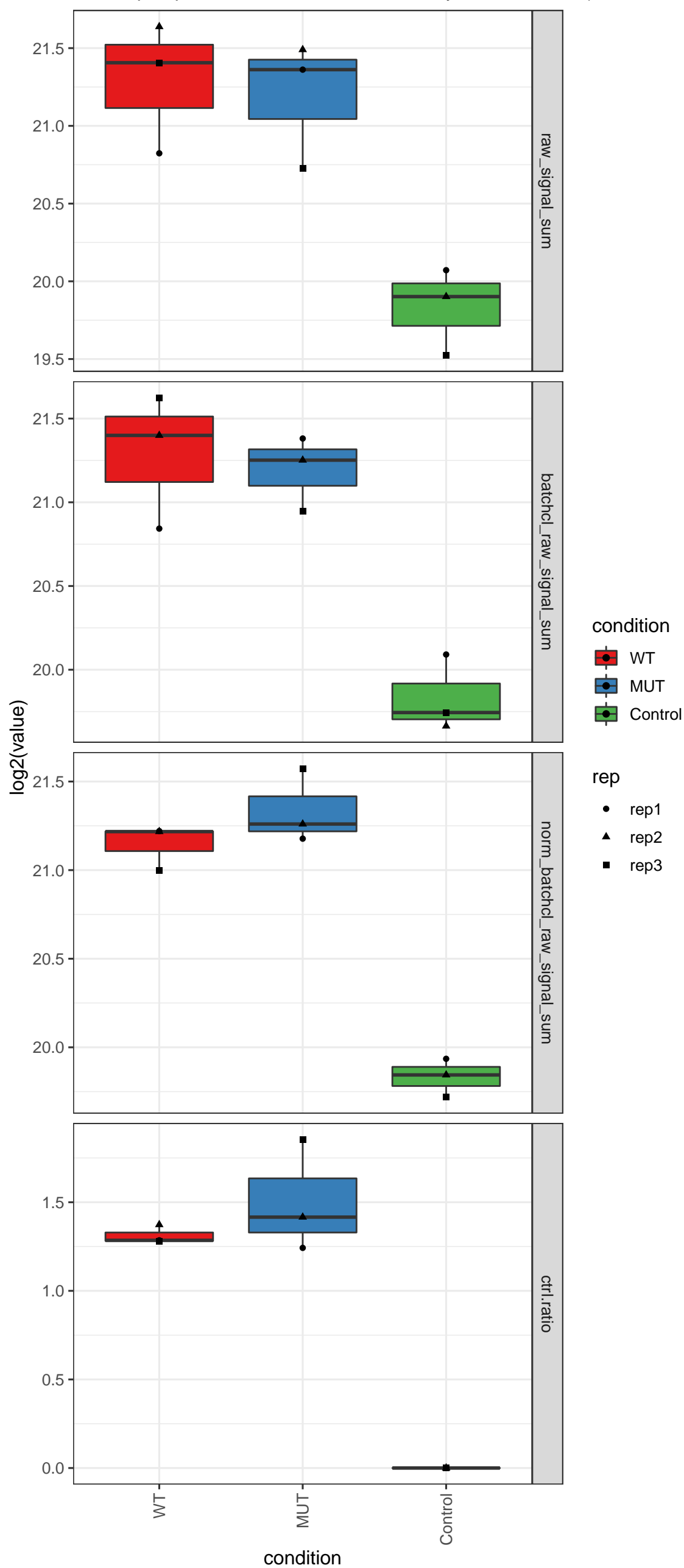
RAD16 – P31244

DNA repair protein RAD16 OS=*Saccharomyces cerevisiae* (strain ATCC 24843)

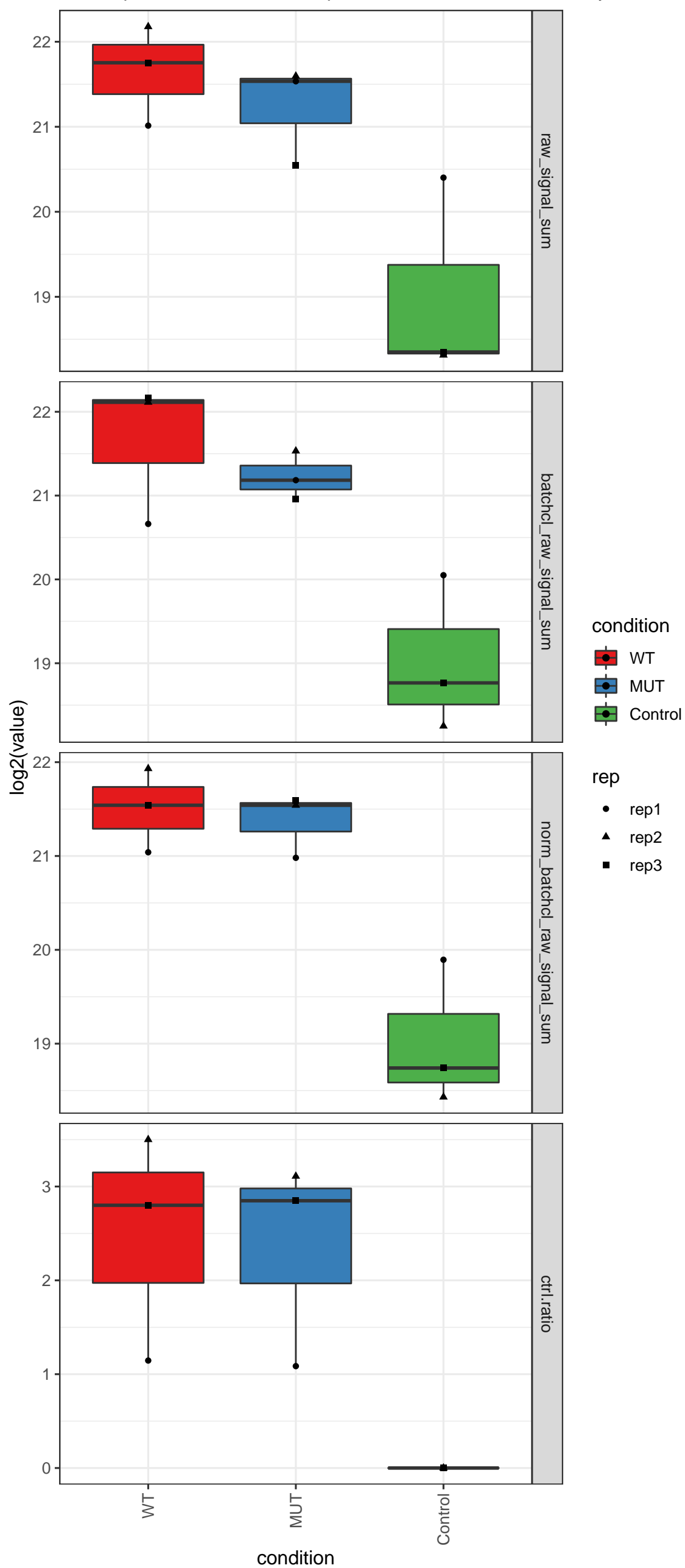


RAD51 – P25454

DNA repair protein RAD51 OS=*Saccharomyces cerevisiae* (strain ATCC 24843)

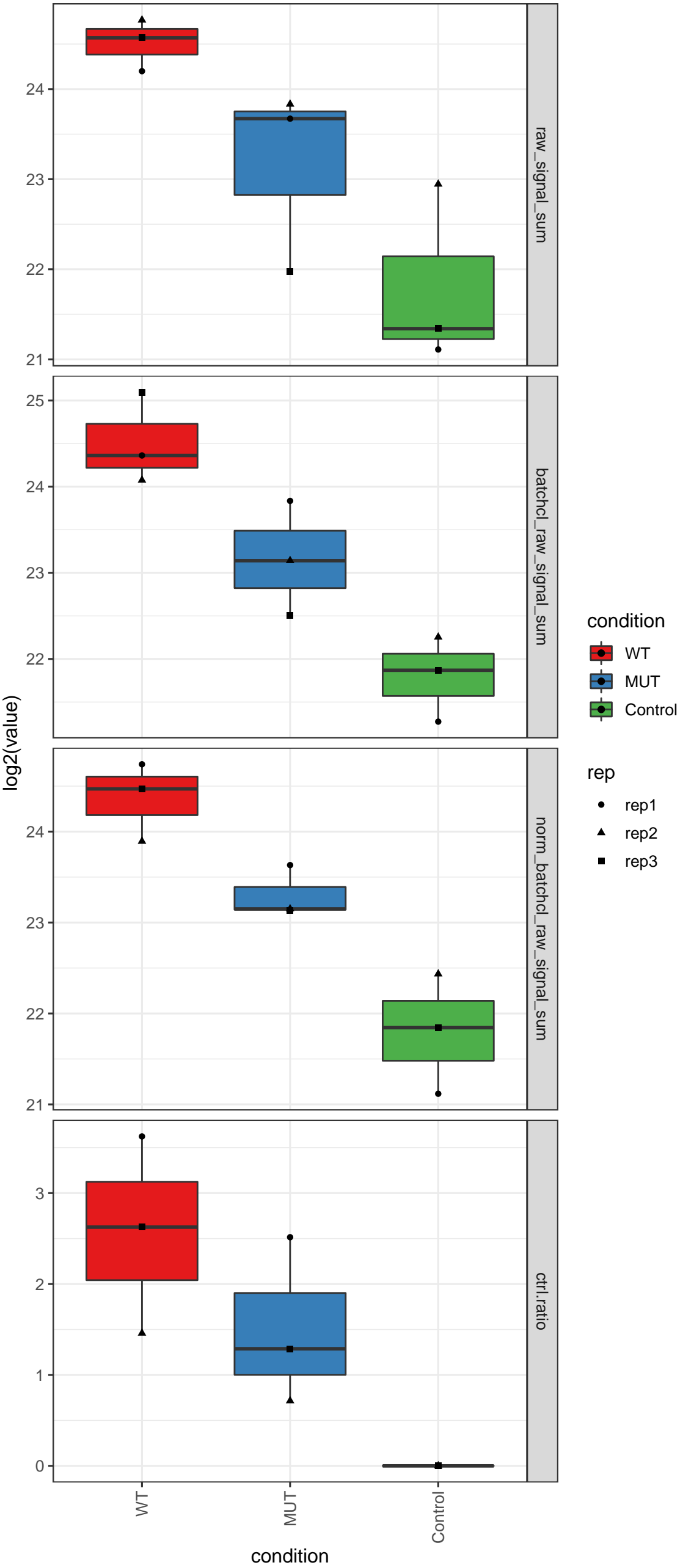


DNA repair and recombination protein RAD52 OS=Saccharomyces cerevis

[illegible]

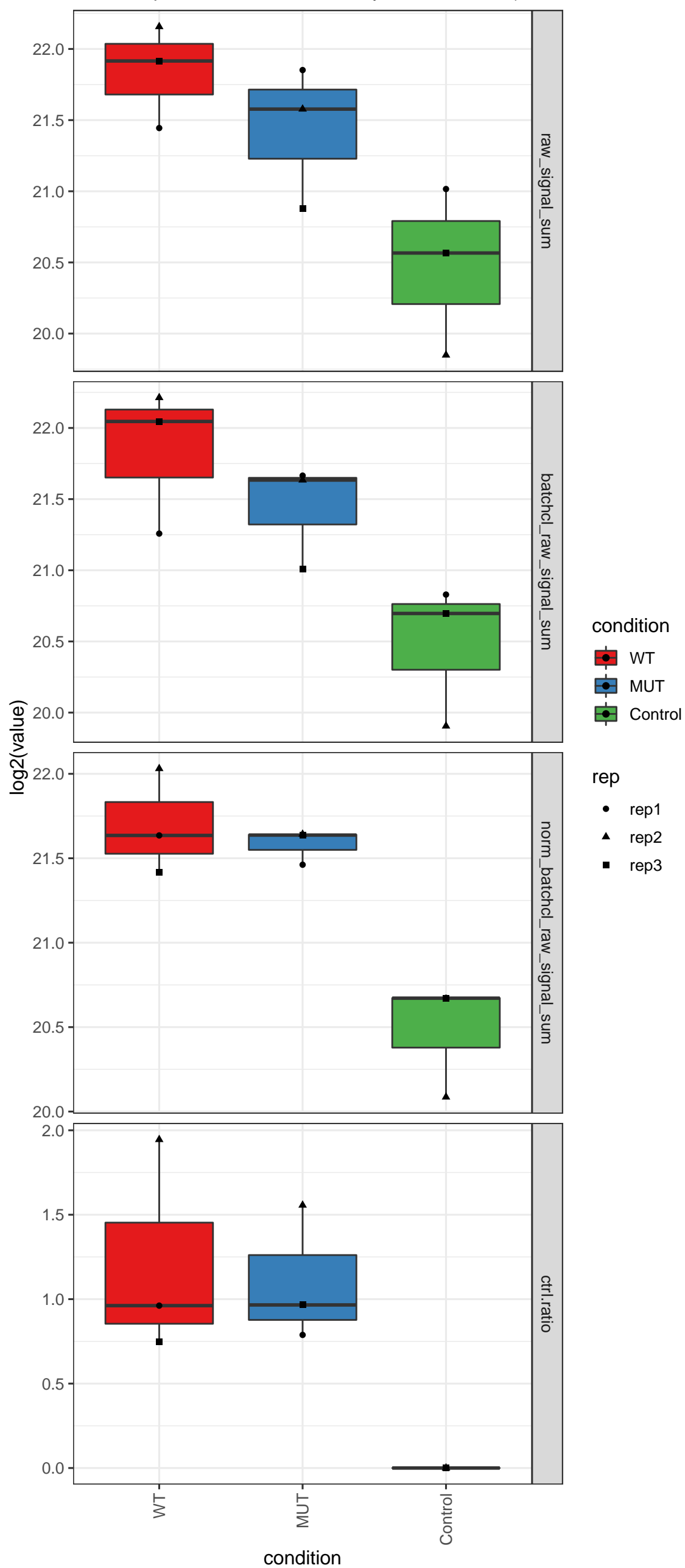
RAP1 – P11938

DNA-binding protein RAP1 OS=*Saccharomyces cerevisiae* (strain ATCC 24842)



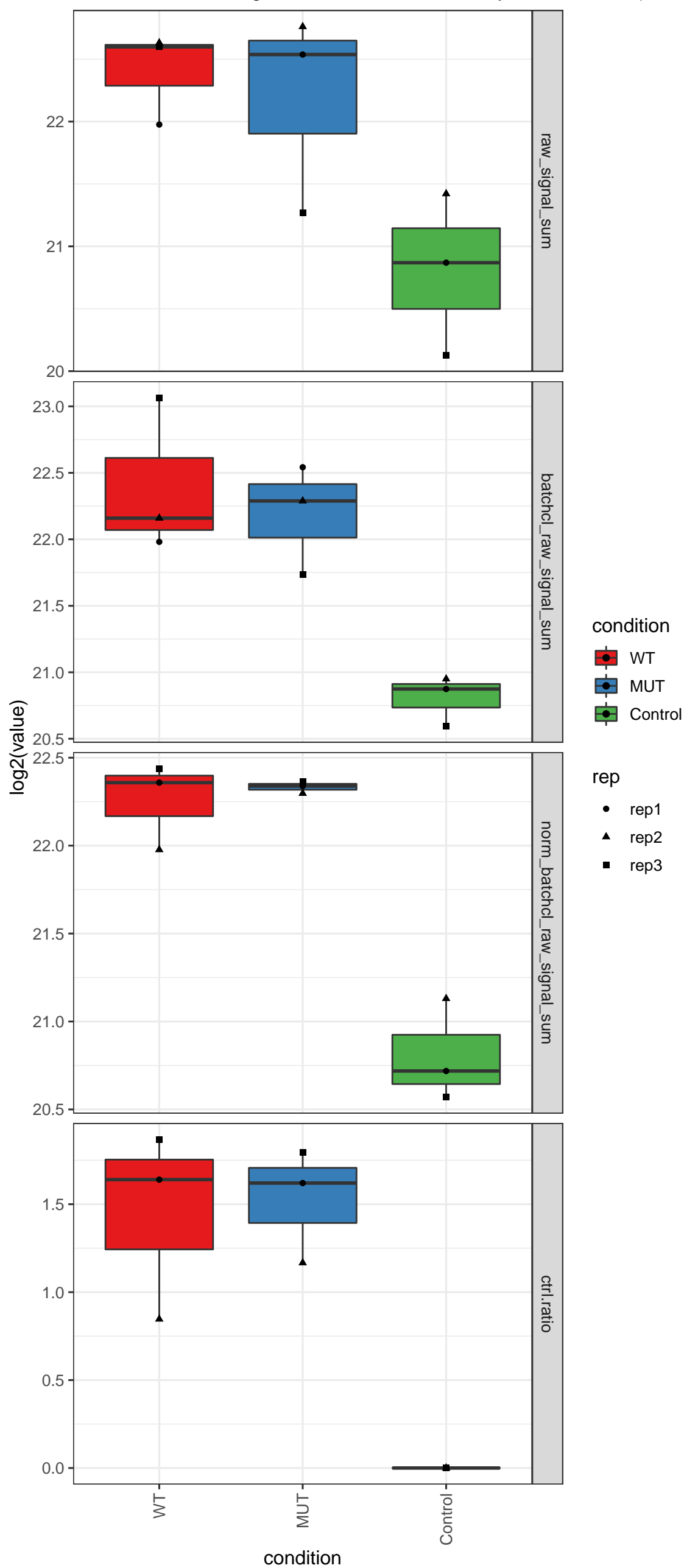
RAS2 – P01120

Ras-like protein 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 /



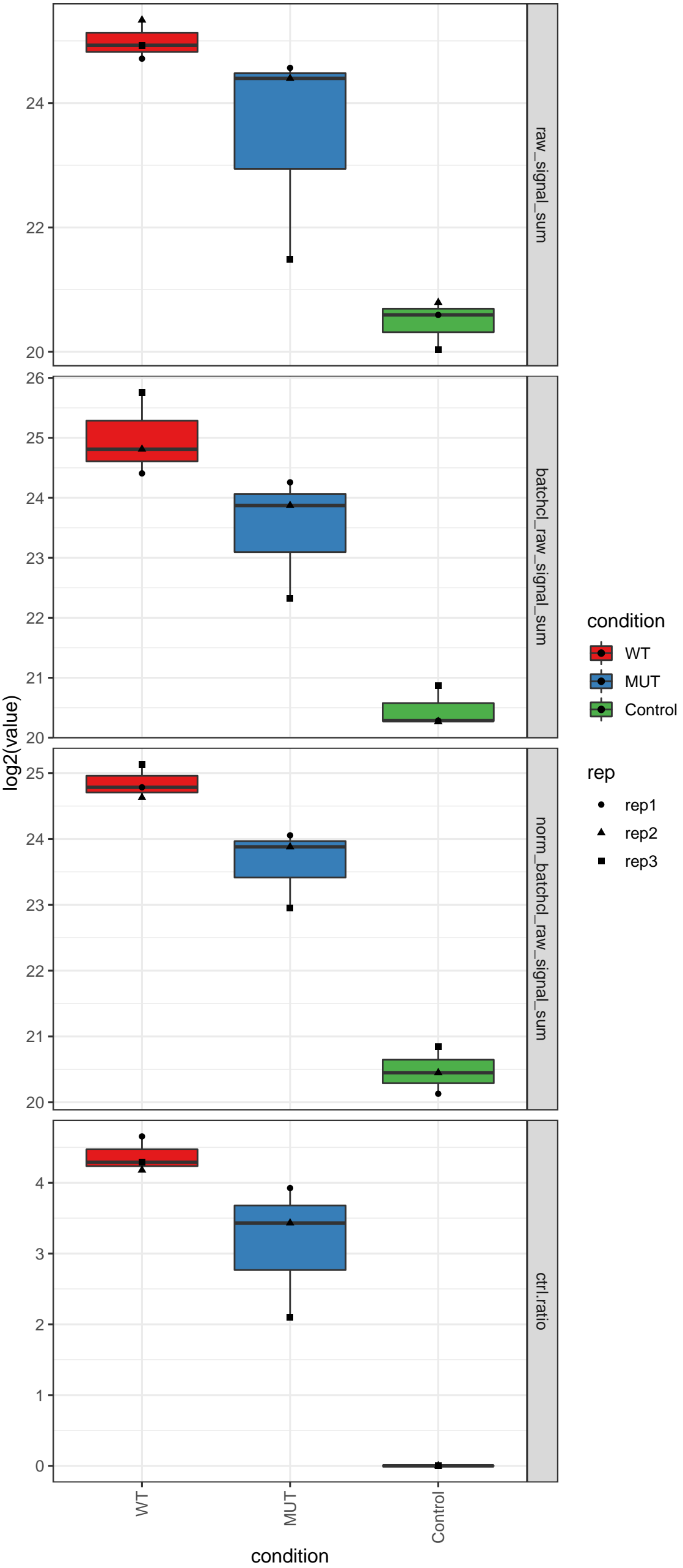
RBG1 – P39729

Ribosome-interacting GTPase 1 OS=*Saccharomyces cerevisiae* (strain A



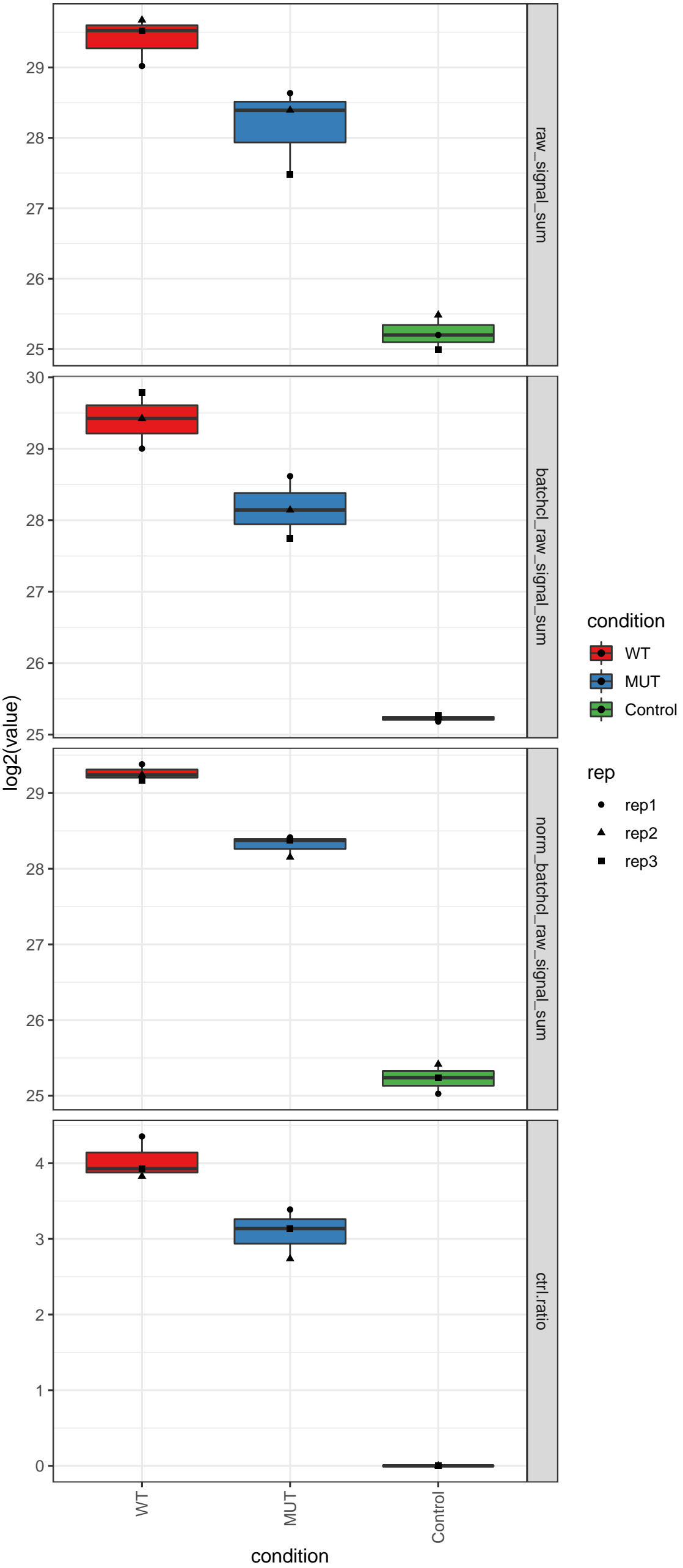
REB1 – P21538

DNA-binding protein REB1 OS=*Saccharomyces cerevisiae* (strain ATCC 2



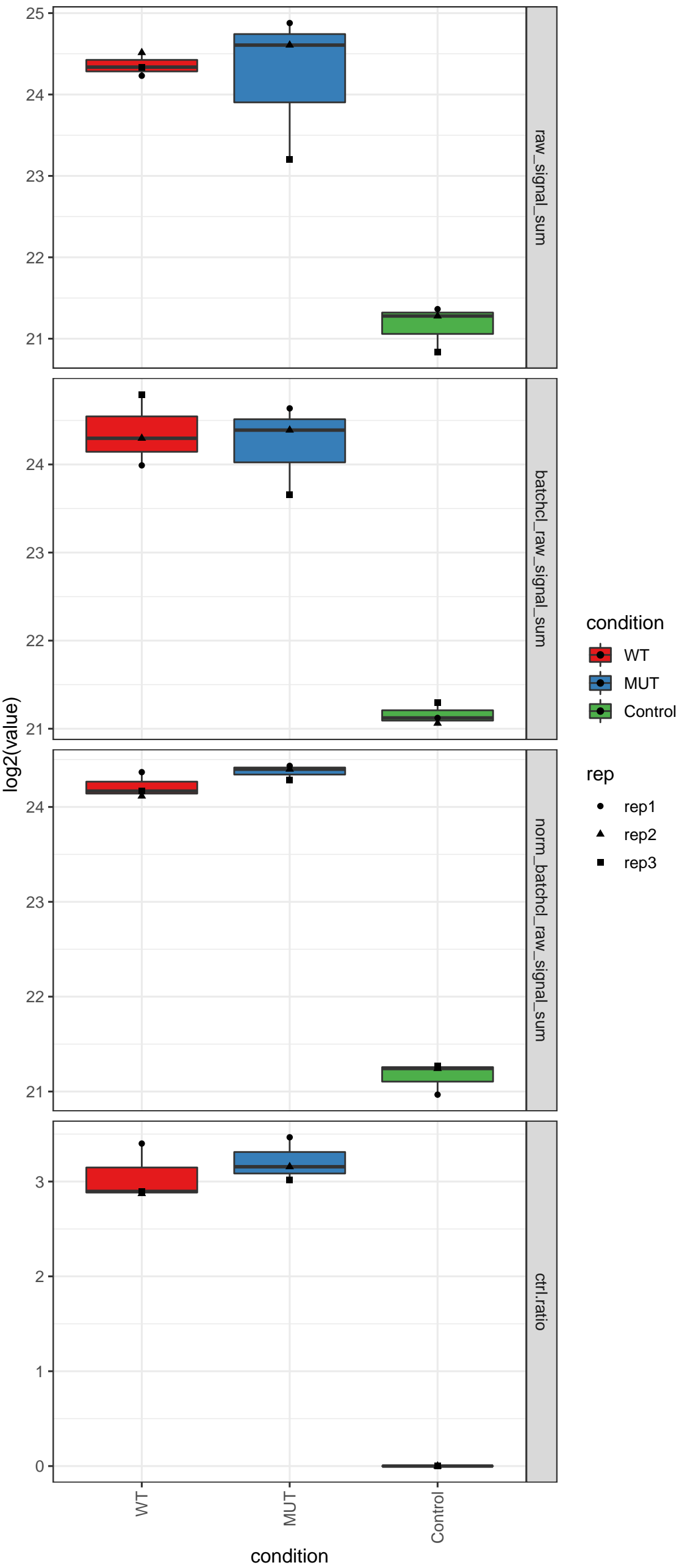
REC107 – P21651

Recombination protein 107 OS=*Saccharomyces cerevisiae* (strain ATCC 2



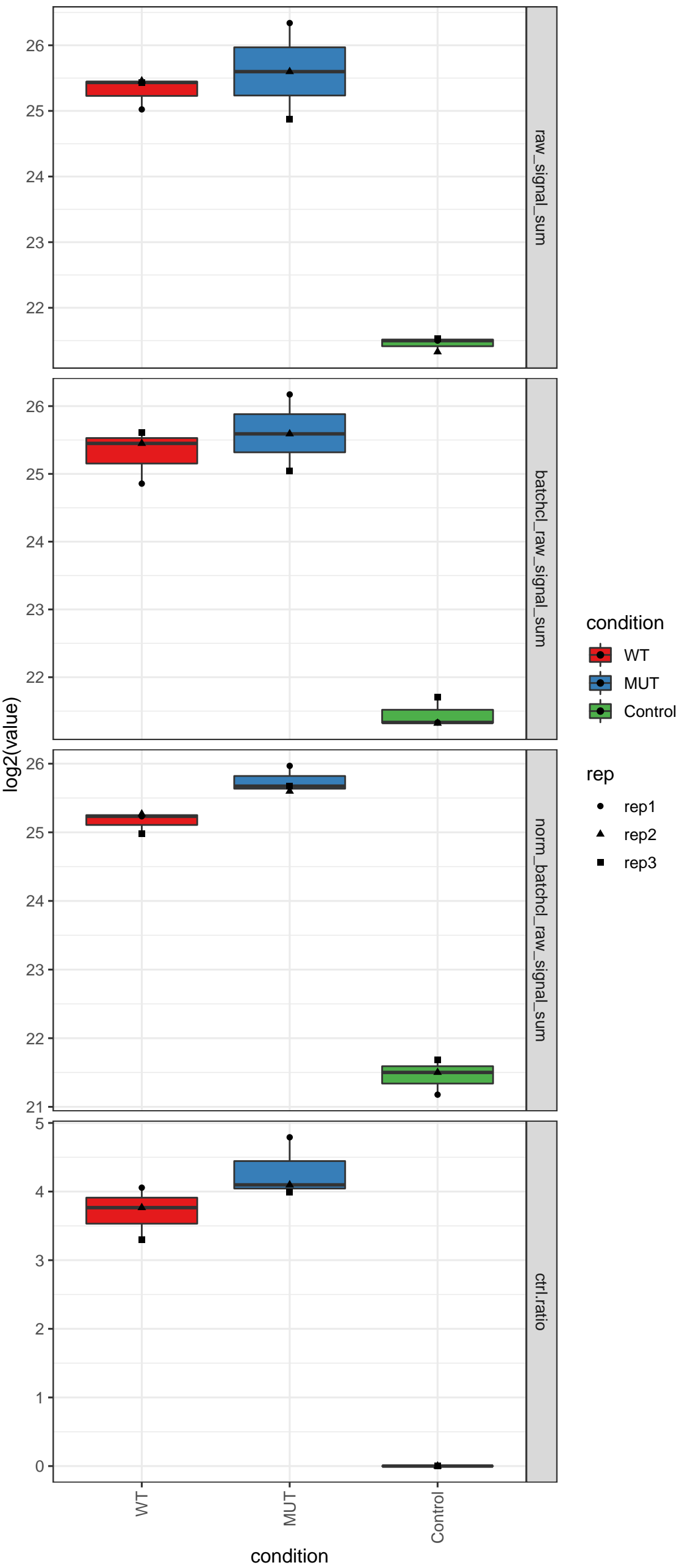
REC8 – Q12188

Meiotic recombination protein REC8 OS=*Saccharomyces cerevisiae* (strain



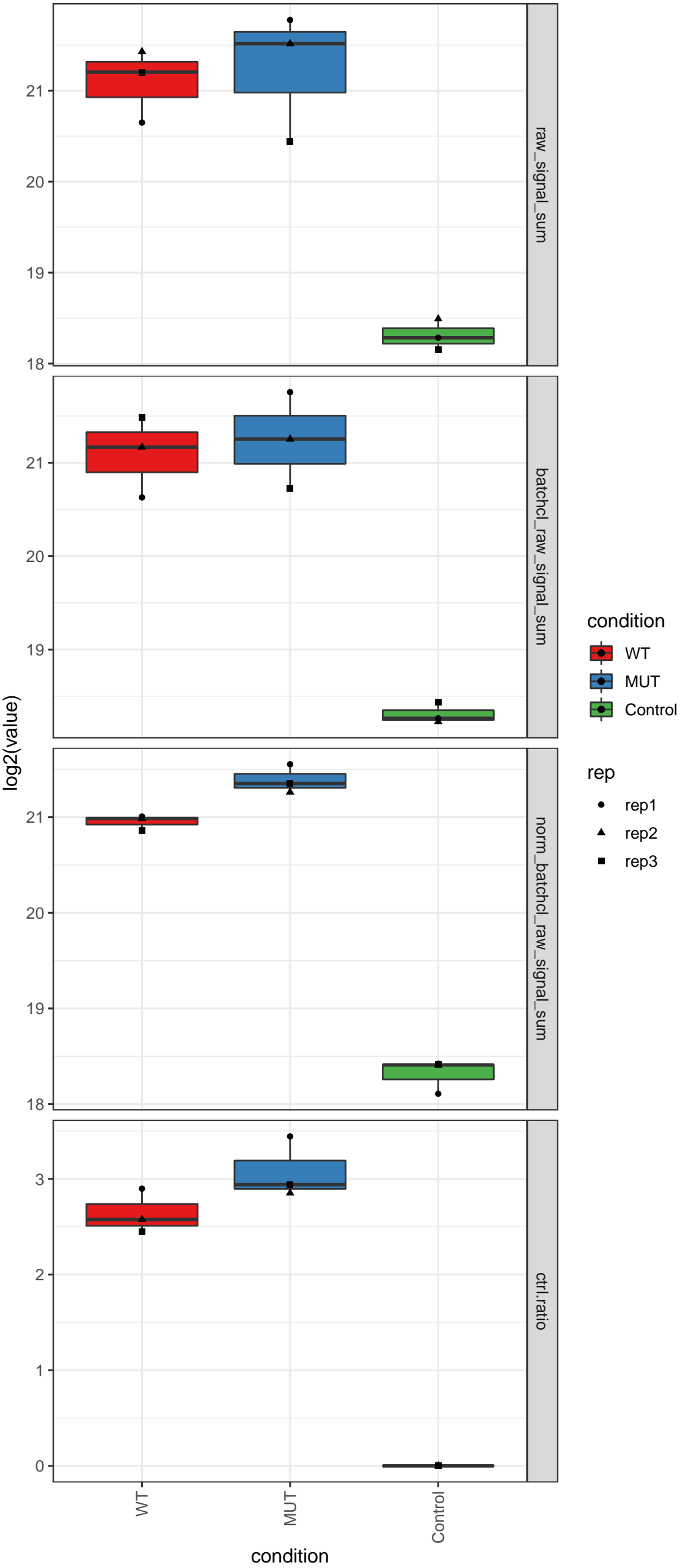
RED1 – P14291

Protein RED1 OS=*Saccharomyces cerevisiae* (strain ATCC 204508 / S288



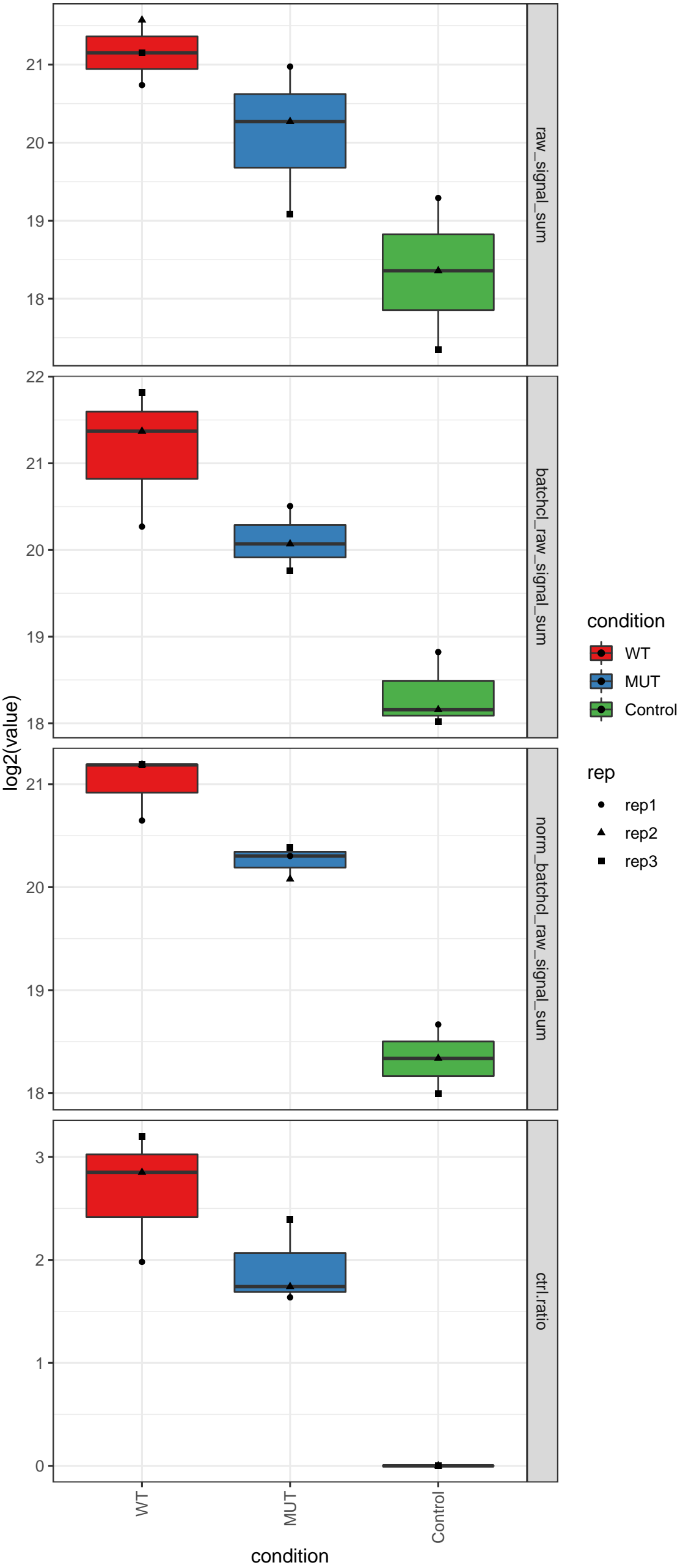
REP1 – P03871

Partitioning protein REP1 OS=*Saccharomyces cerevisiae* (strain ATCC 204



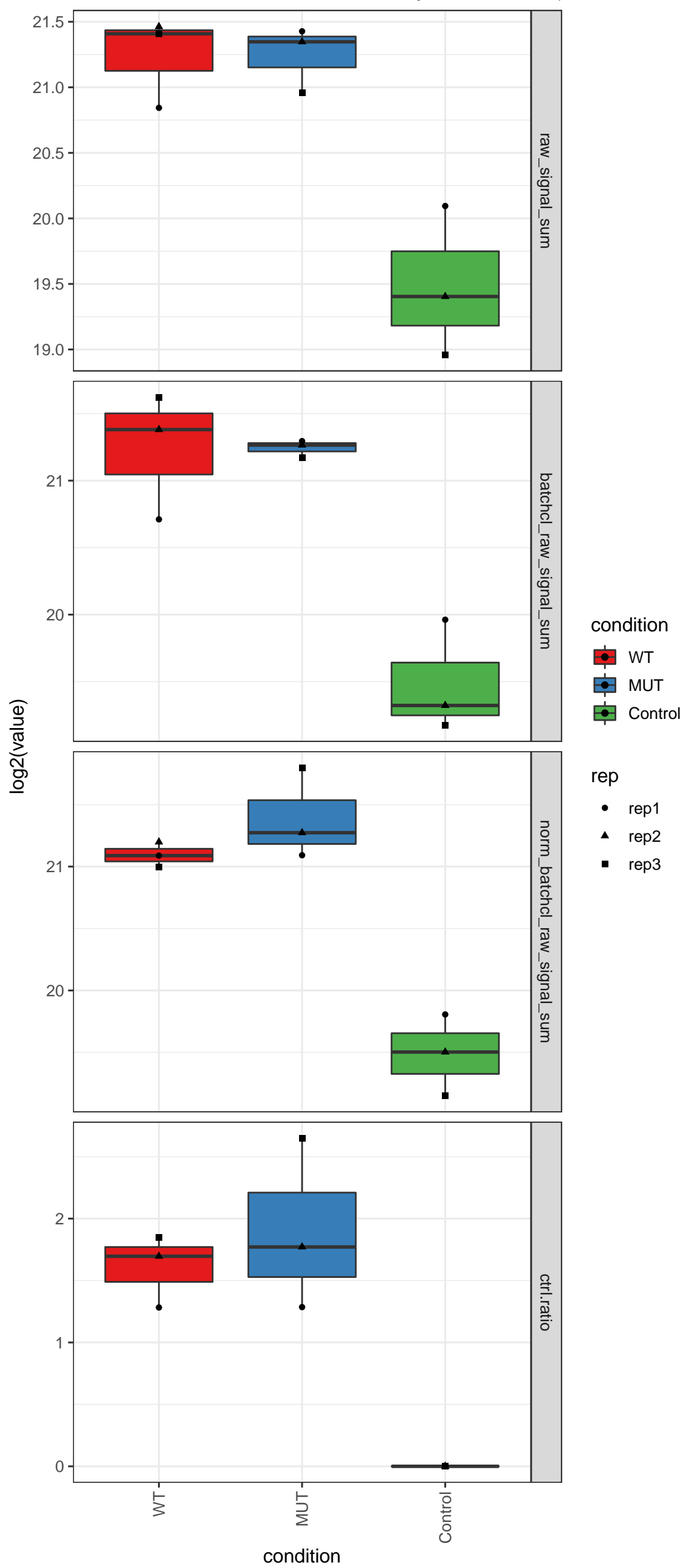
REP2 – P03872

Partitioning protein REP2 OS=*Saccharomyces cerevisiae* (strain ATCC 204



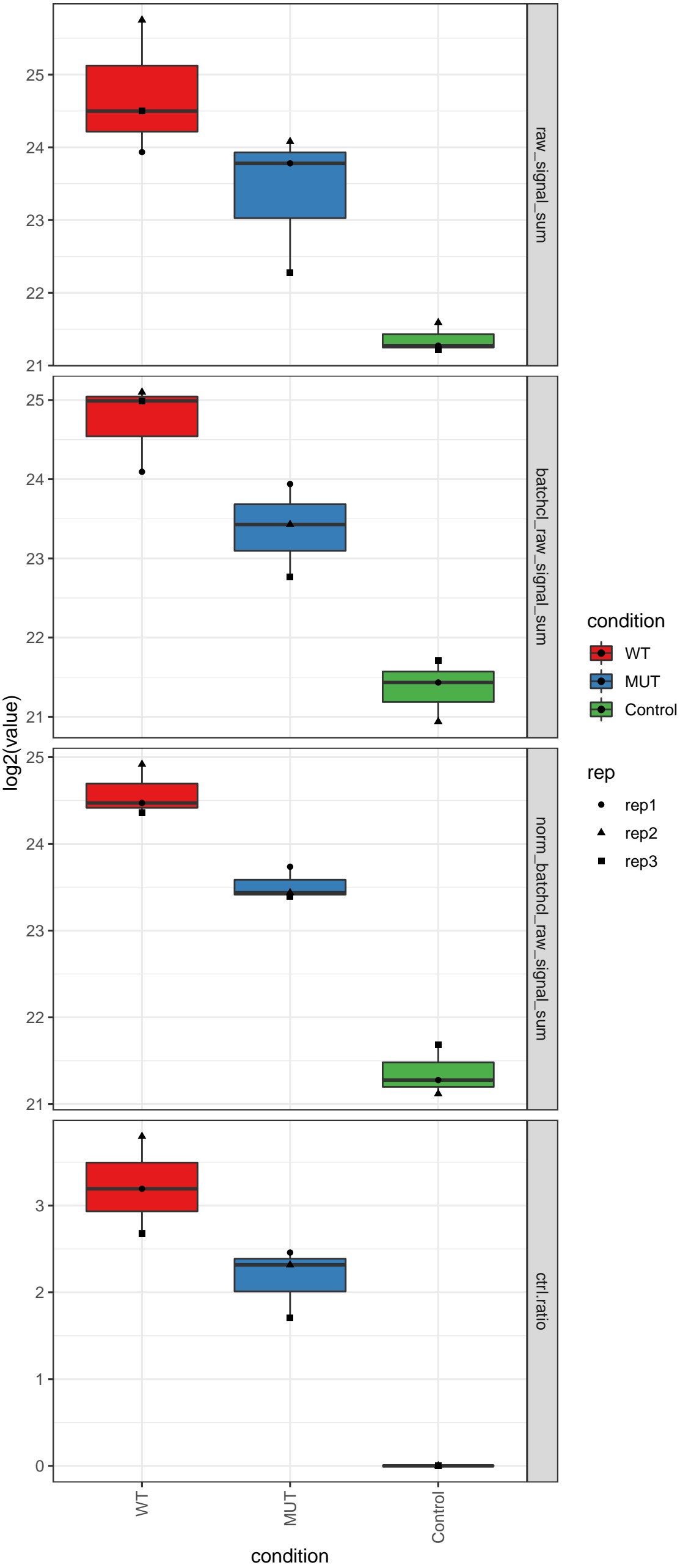
RET2 – P43621

Coatomer subunit delta OS=*Saccharomyces cerevisiae* (strain ATCC 204



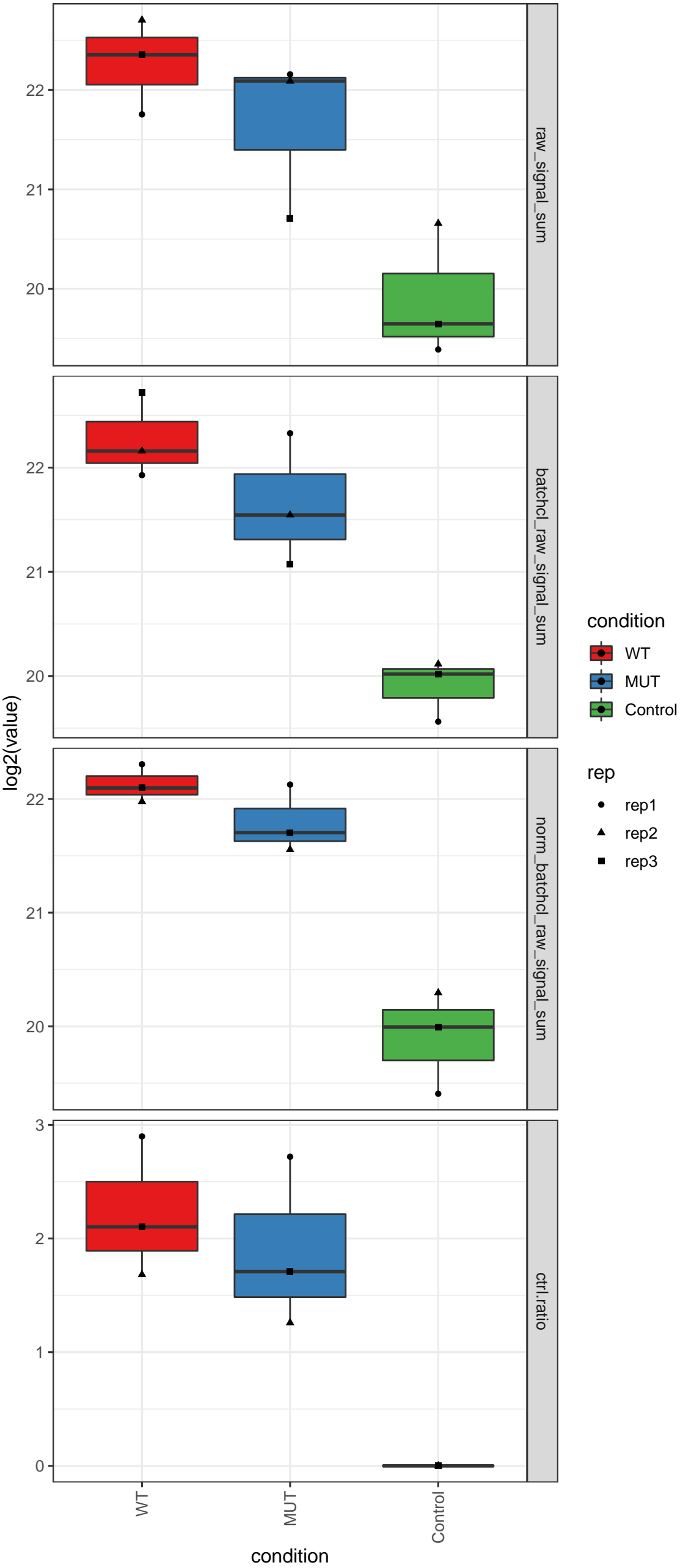
RFA1 – P22336

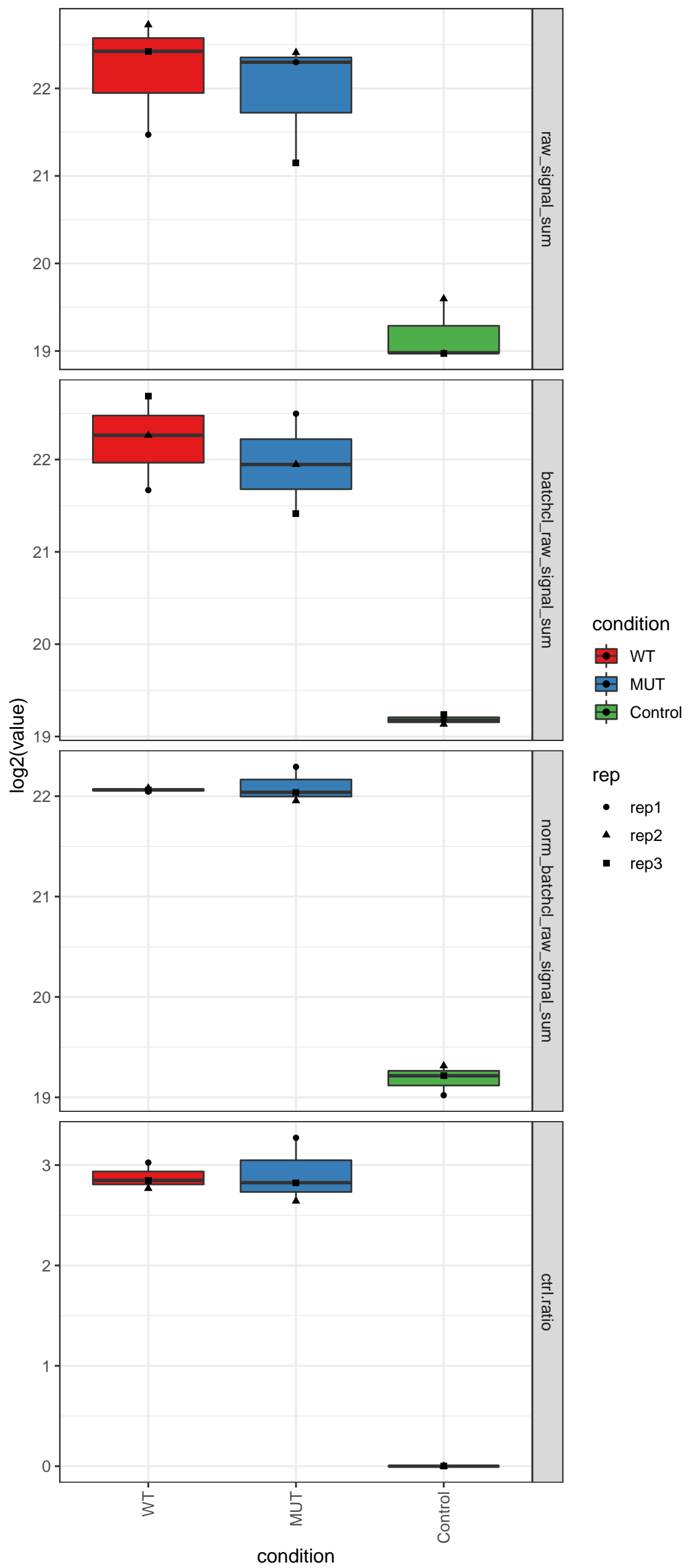
Replication factor A protein 1 OS=*Saccharomyces cerevisiae* (strain ATCC



RFC1 – P38630

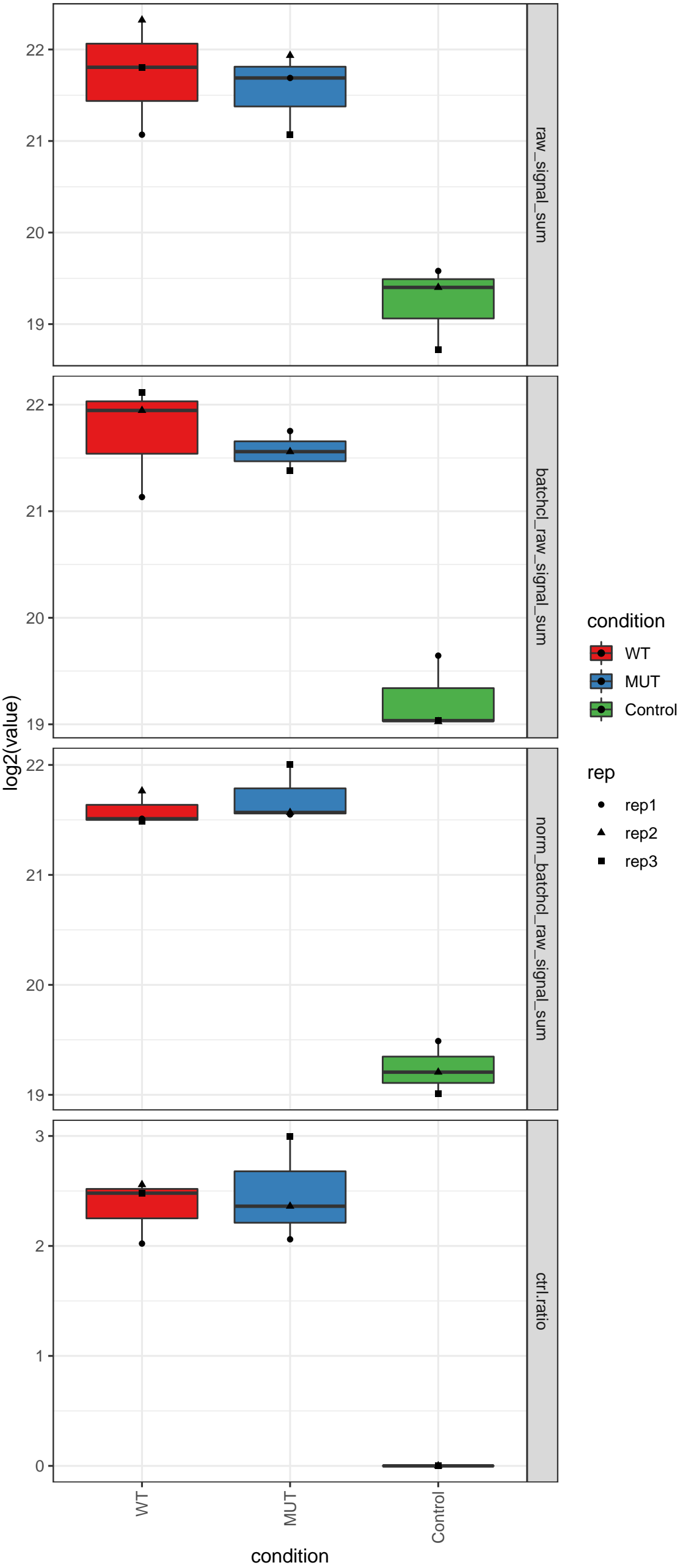
Replication factor C subunit 1 OS=*Saccharomyces cerevisiae* (strain ATCC



Replication factor C subunit 2 OS=*Saccharomyces cerevisiae* (strain ATCC)

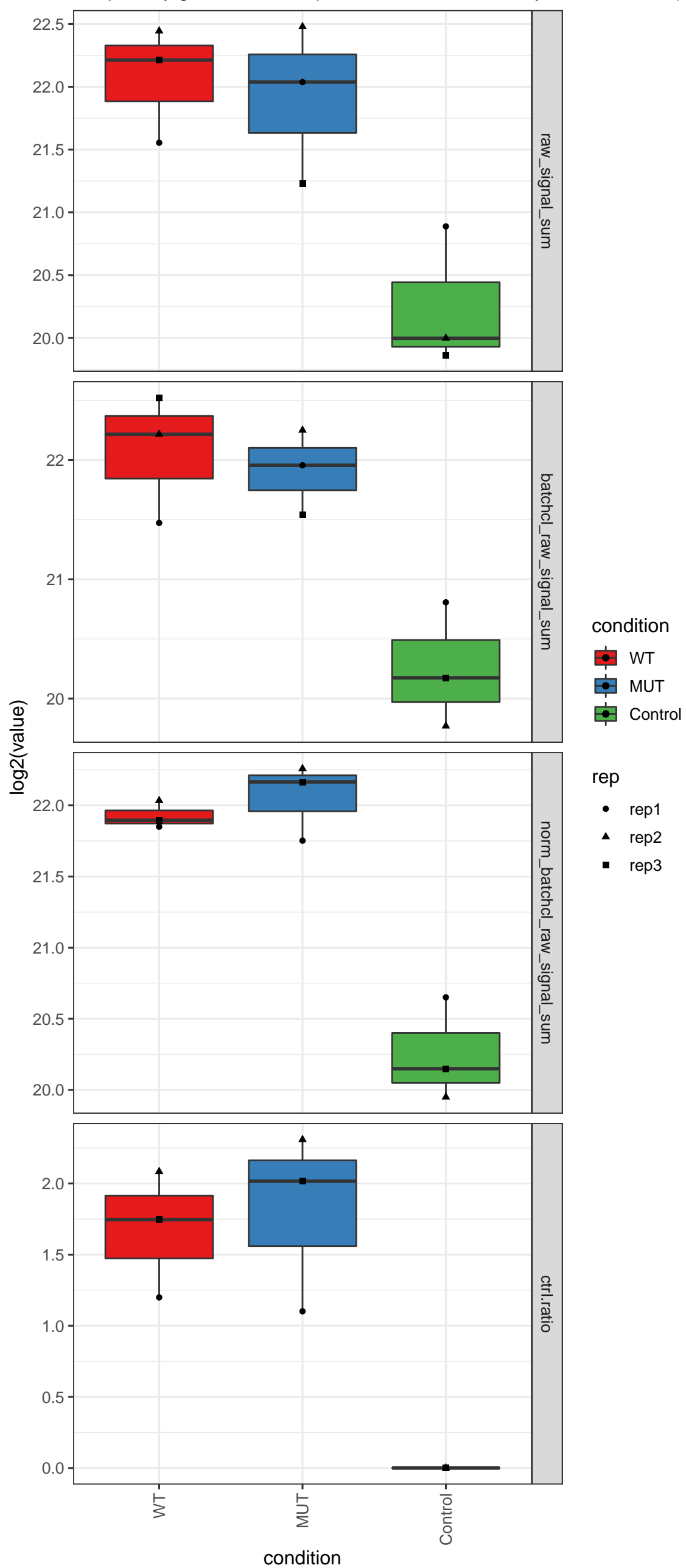
RFC3 – P38629

Replication factor C subunit 3 OS=*Saccharomyces cerevisiae* (strain ATCC



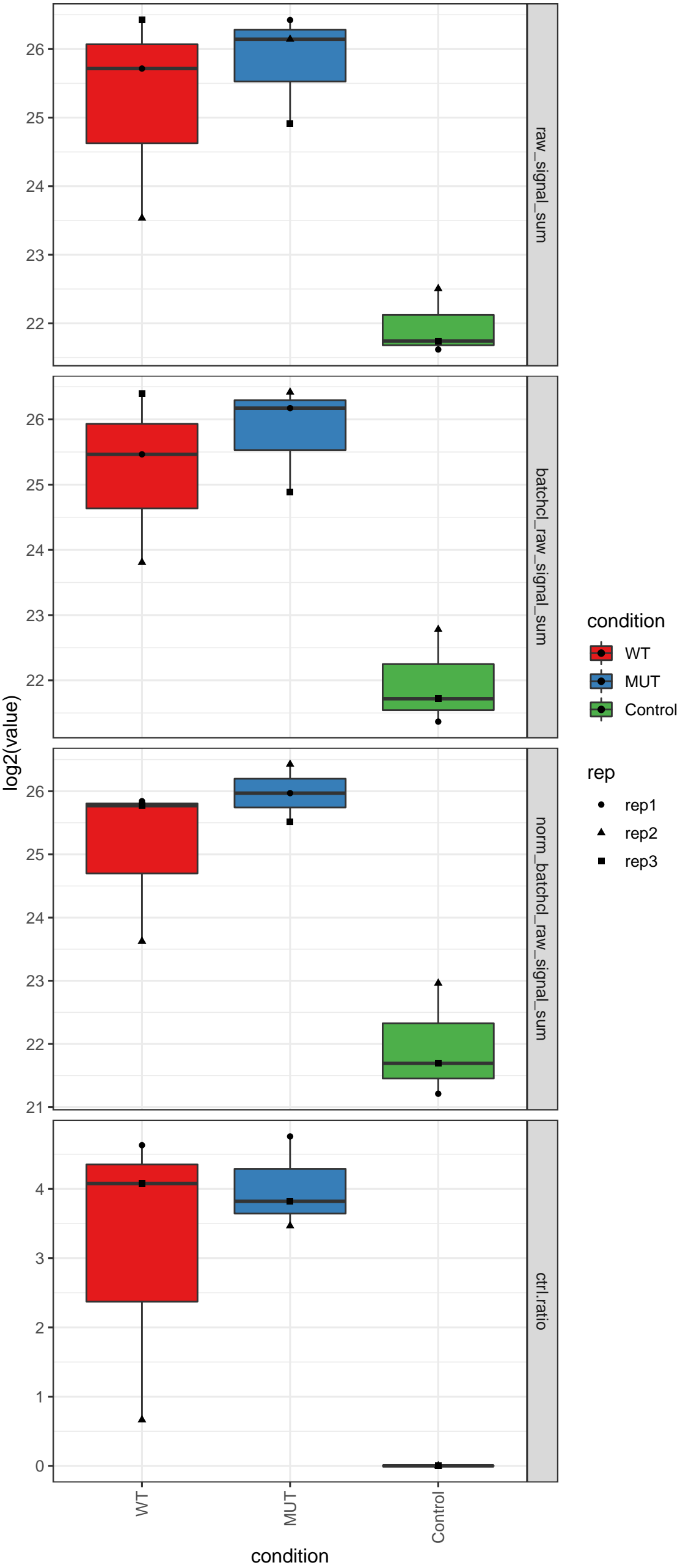
RG11 – P40043

Respiratory growth induced protein 1 OS=*Saccharomyces cerevisiae* (str



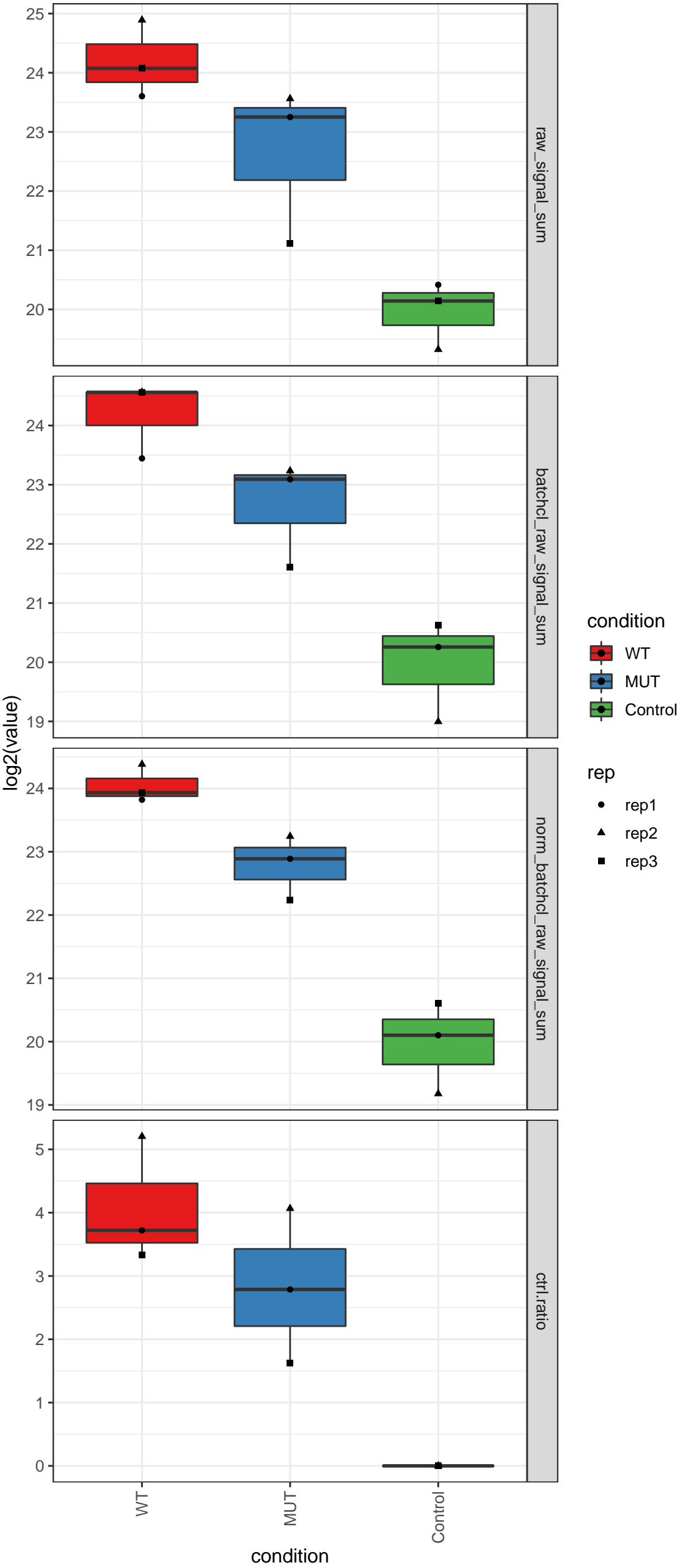
RGI2 – P40188

Respiratory growth induced protein 2 OS=*Saccharomyces cerevisiae* (strain



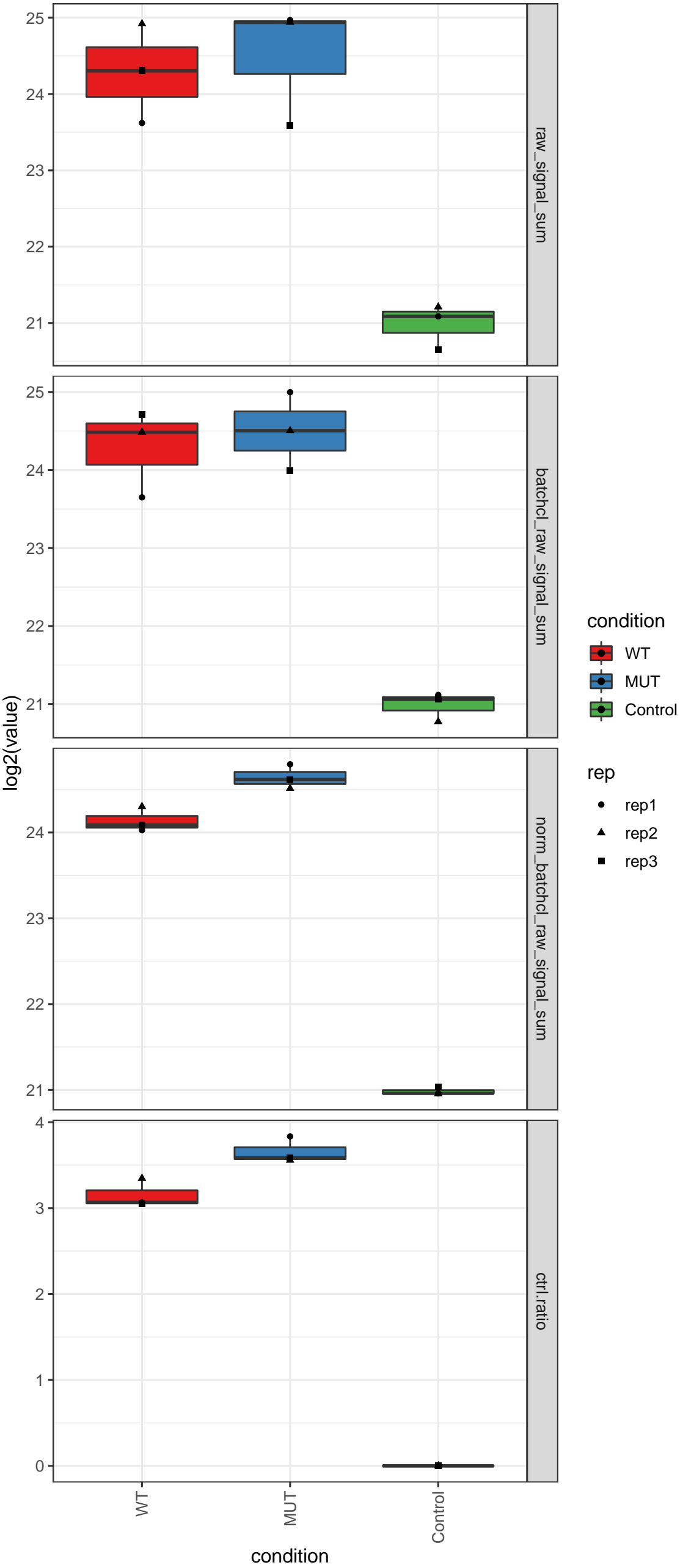
RIM1 – P32445

Single-stranded DNA-binding protein RIM1, mitochondrial OS=Saccharon



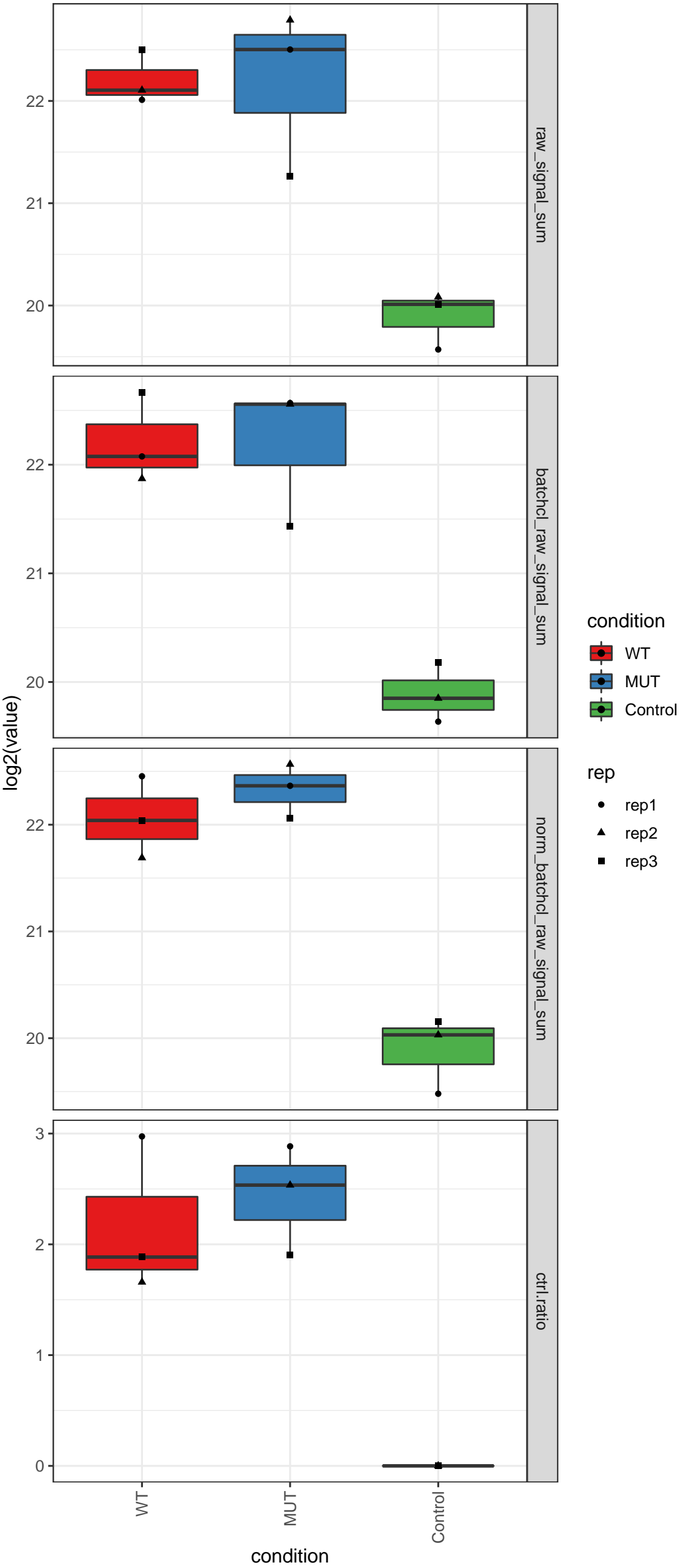
RIM4 – P38741

Meiotic activator RIM4 OS=*Saccharomyces cerevisiae* (strain ATCC 20450)



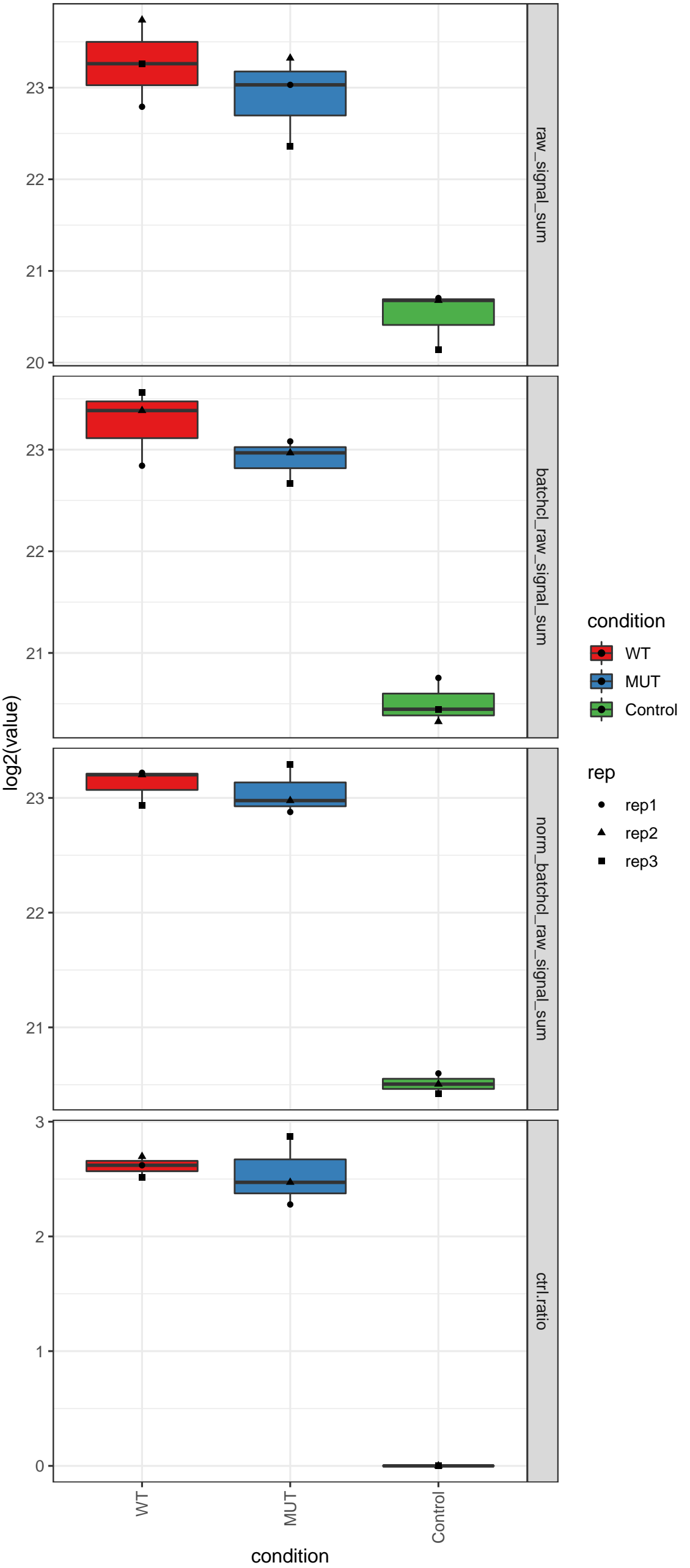
RIO2 – P40160

Serine/threonine–protein kinase RIO2 OS=Saccharomyces cerevisiae (stra



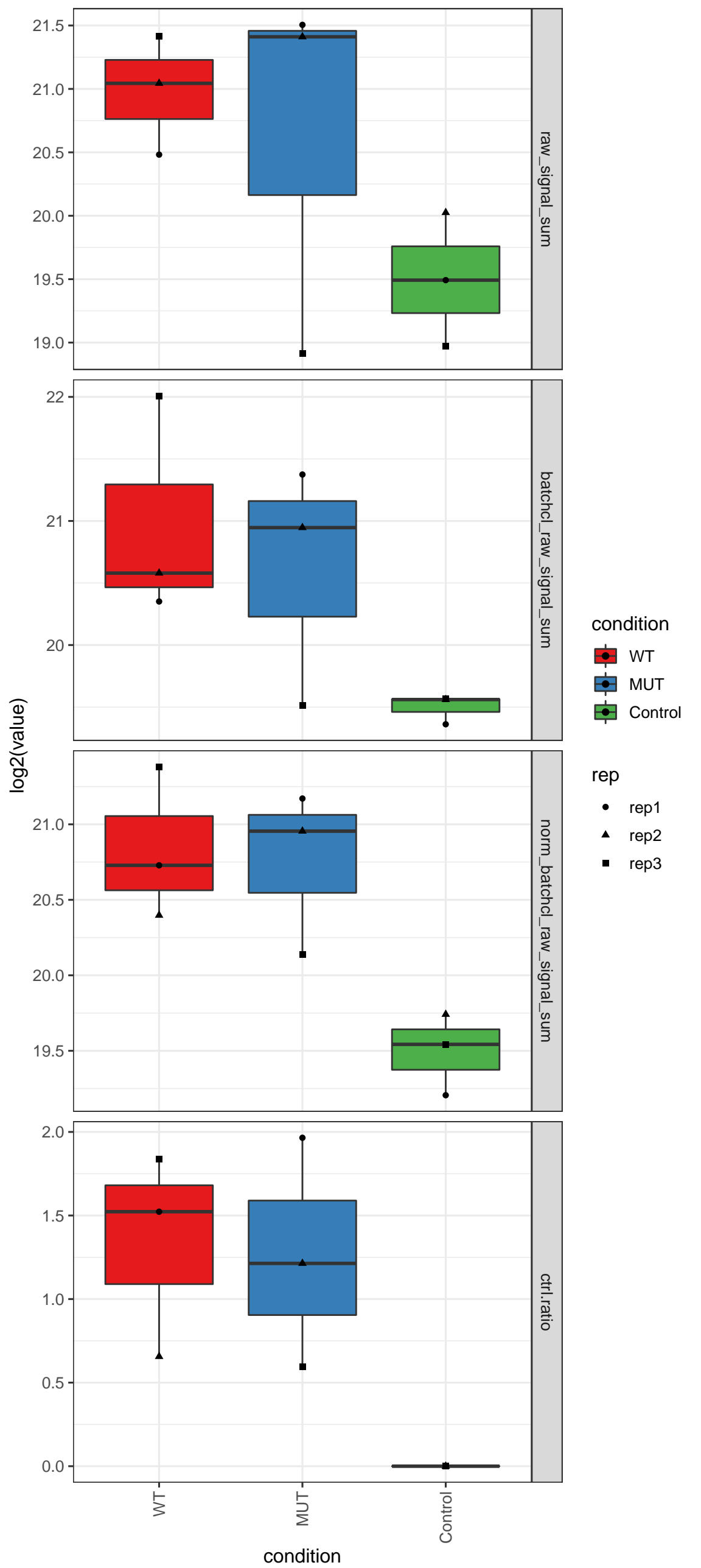
RLI1 – Q03195

Translation initiation factor RLI1 OS=*Saccharomyces cerevisiae* (strain ATCC 25716)



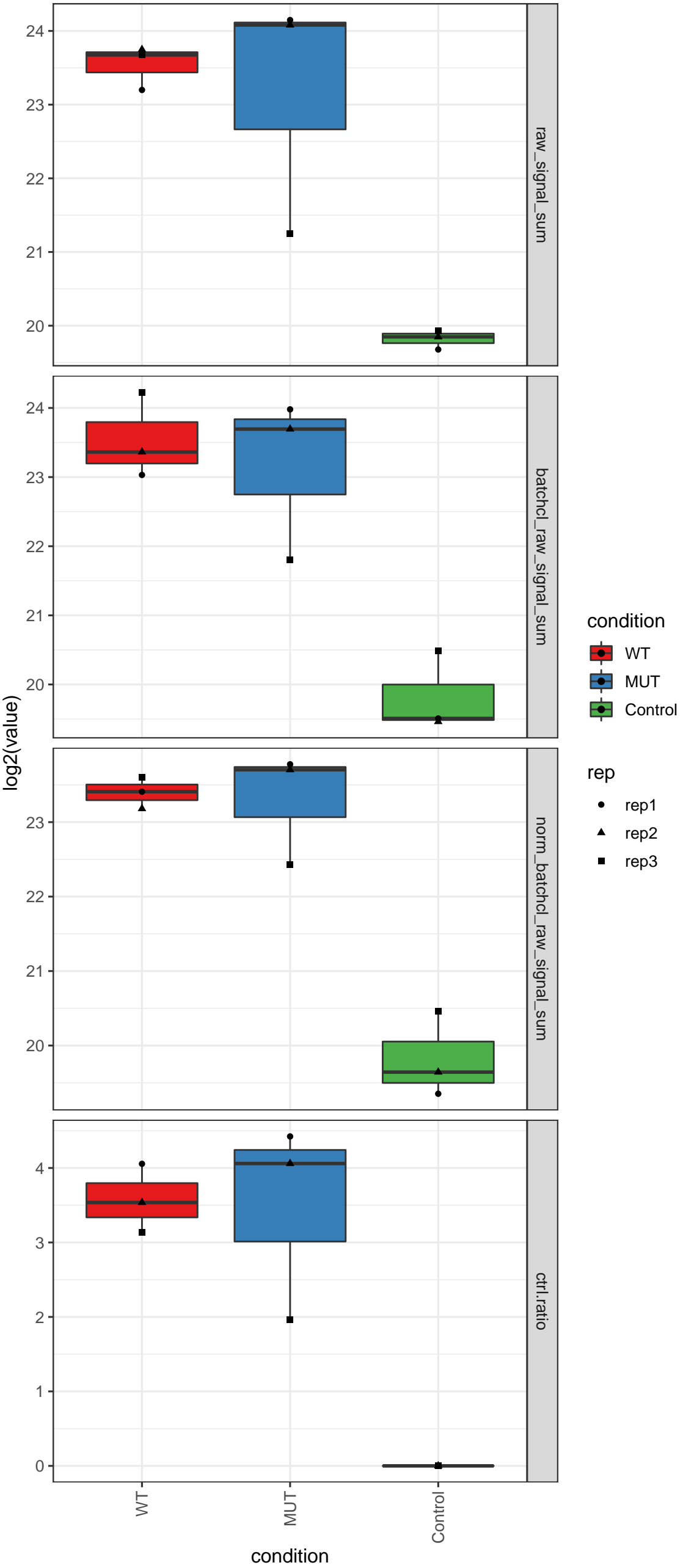
RLP7 – P40693

Ribosome biogenesis protein RLP7 OS=*Saccharomyces cerevisiae* (strain



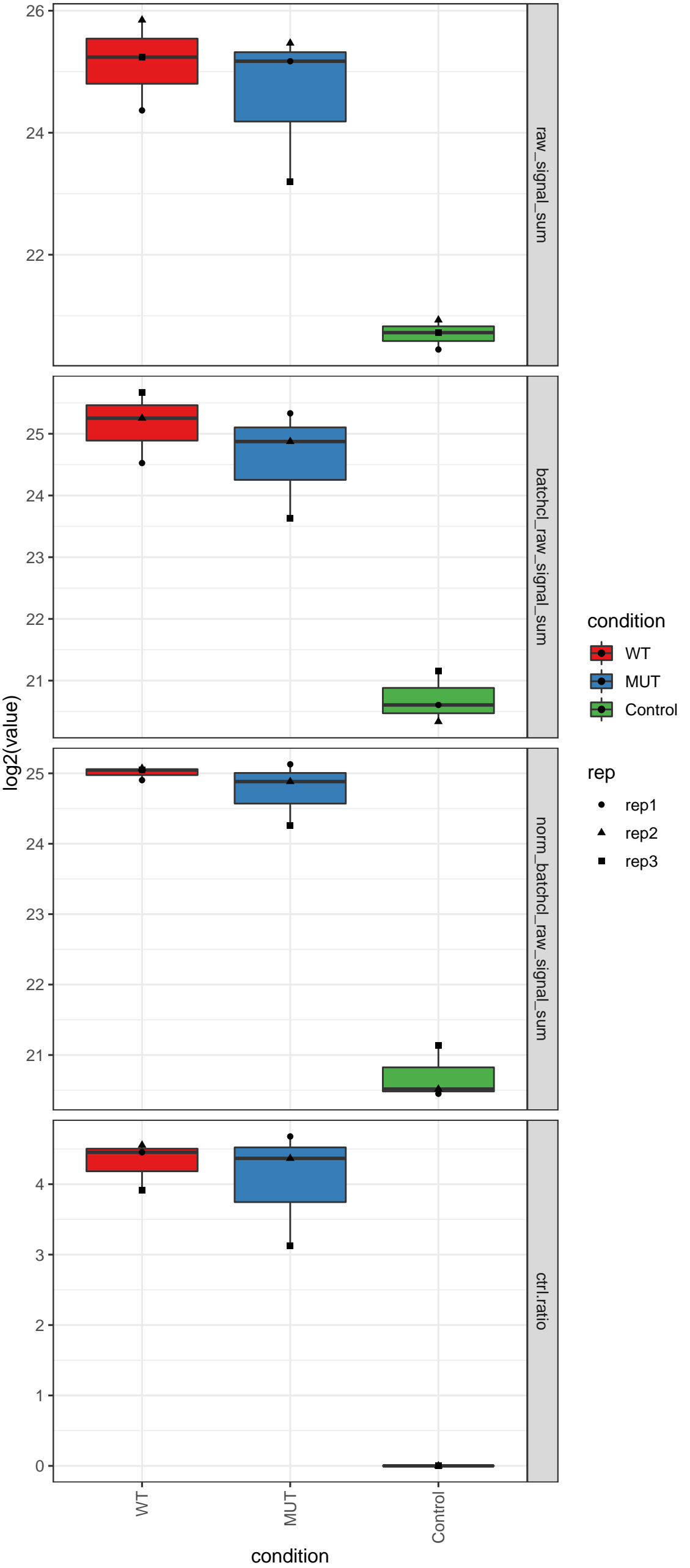
RML2 – P32611

54S ribosomal protein RML2, mitochondrial OS=*Saccharomyces cerevisiae*



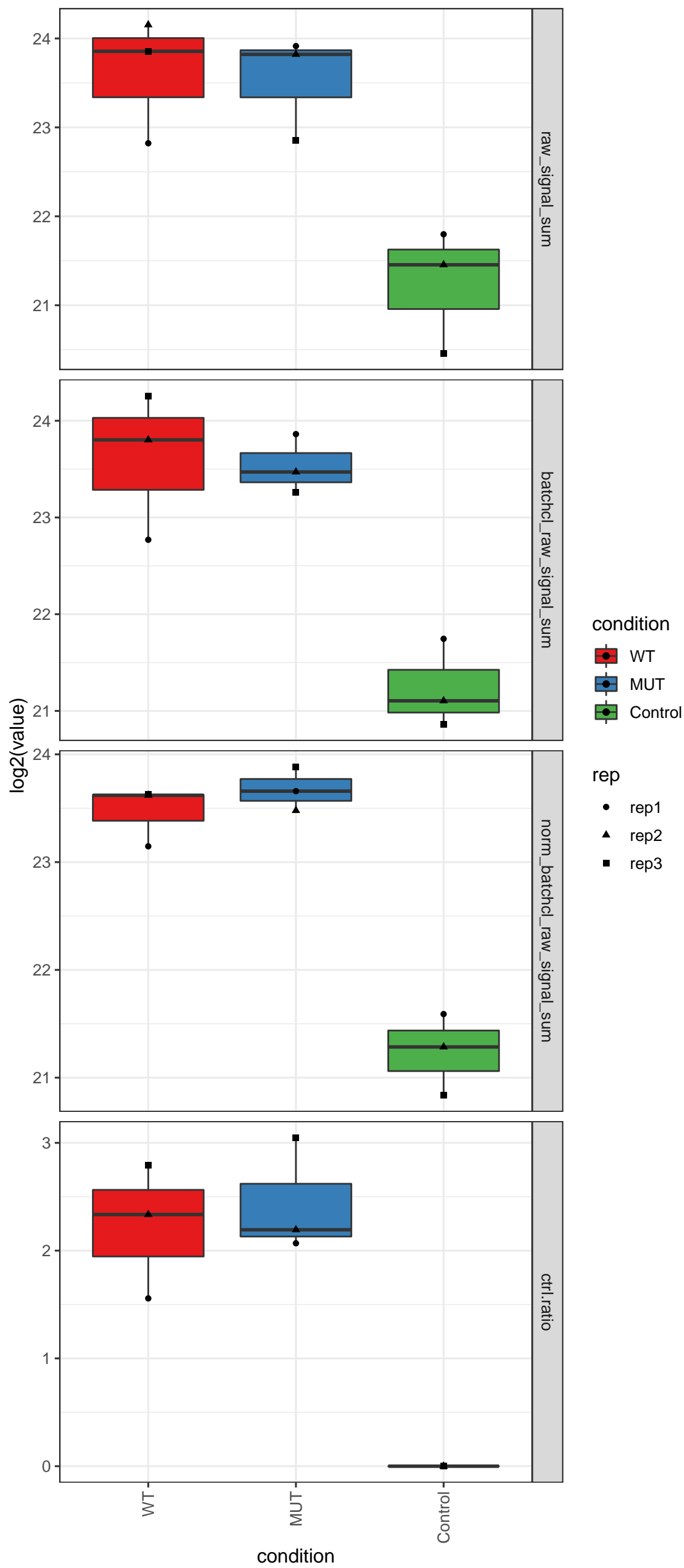
RNP1 – P32385

Ribonucleoprotein 1 OS=*Saccharomyces cerevisiae* (strain ATCC 204508)



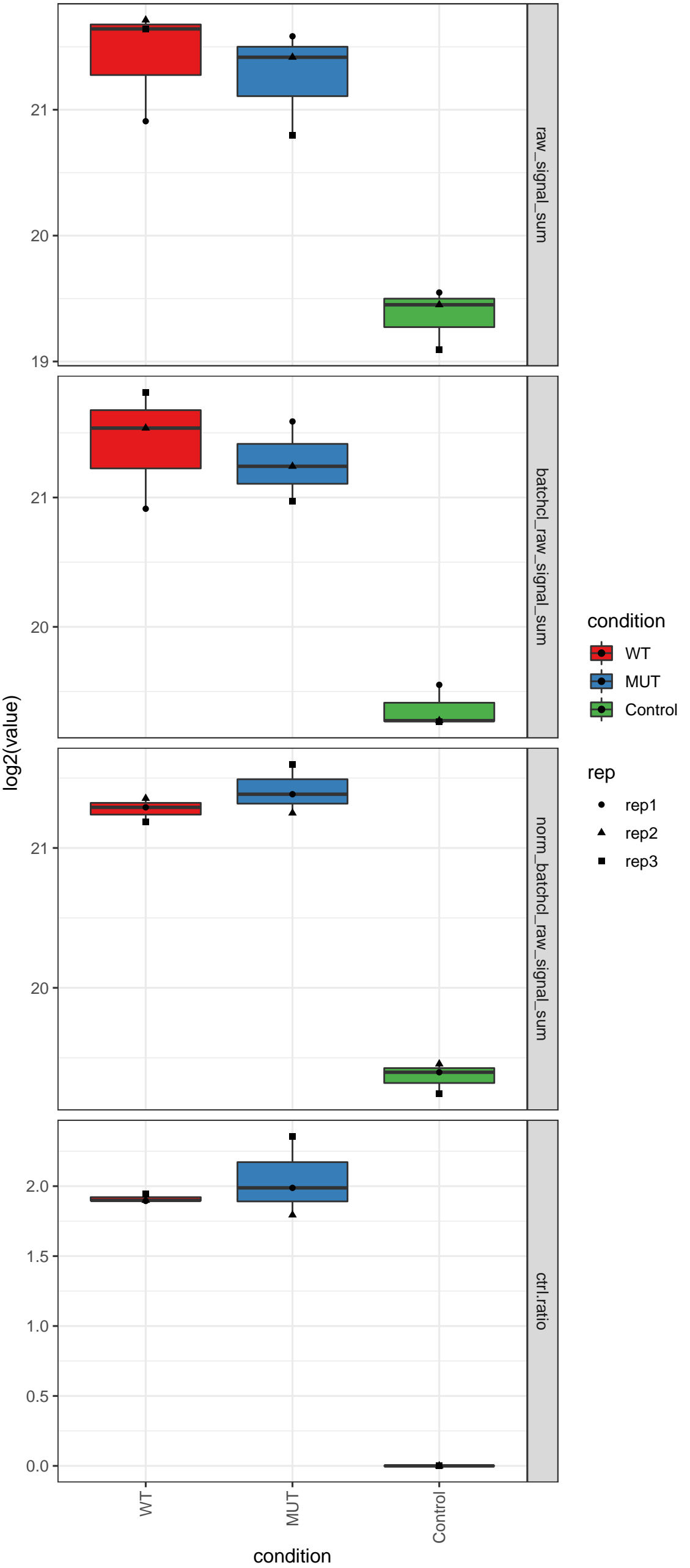
RNR1 – P21524

Ribonucleoside–diphosphate reductase large chain 1 OS=Saccharomyces



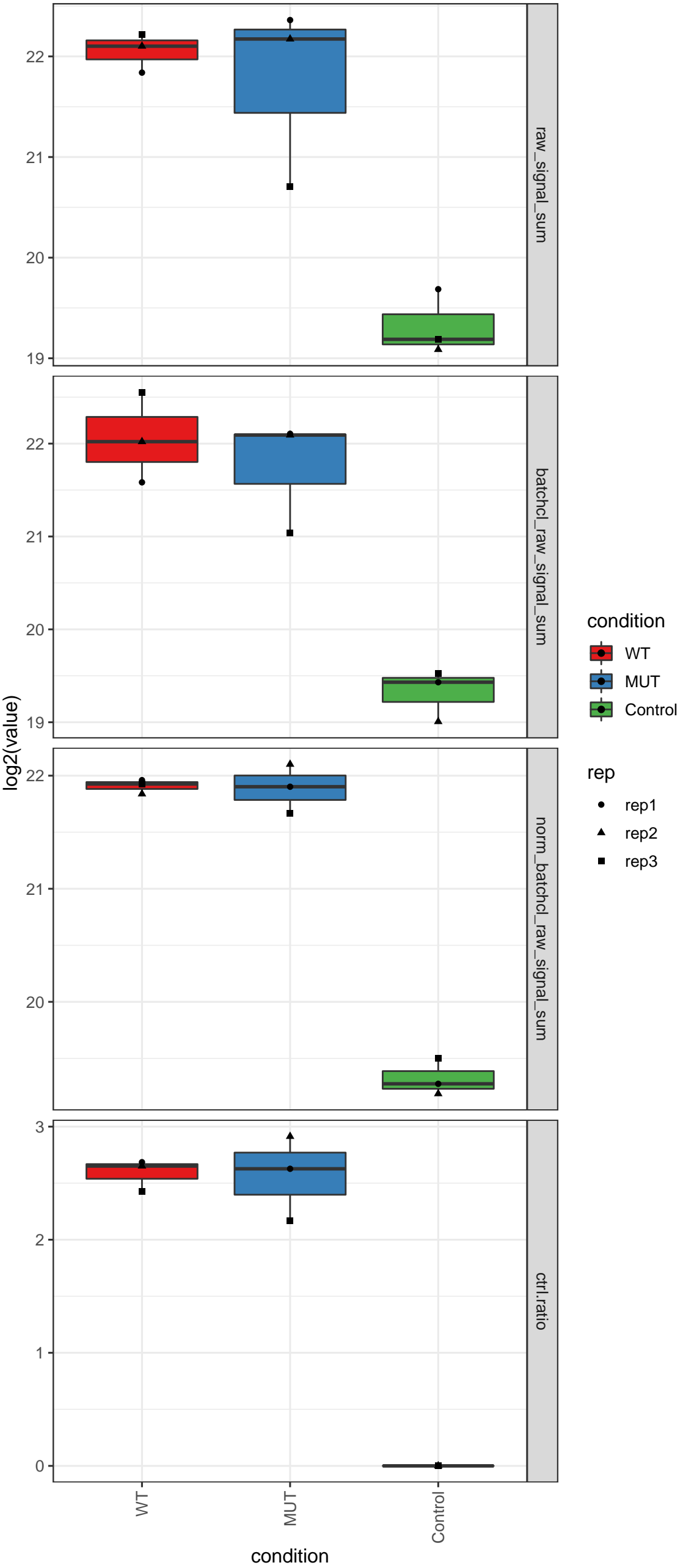
RNR4 – P49723

Ribonucleoside–diphosphate reductase small chain 2 OS=*Saccharomyces*



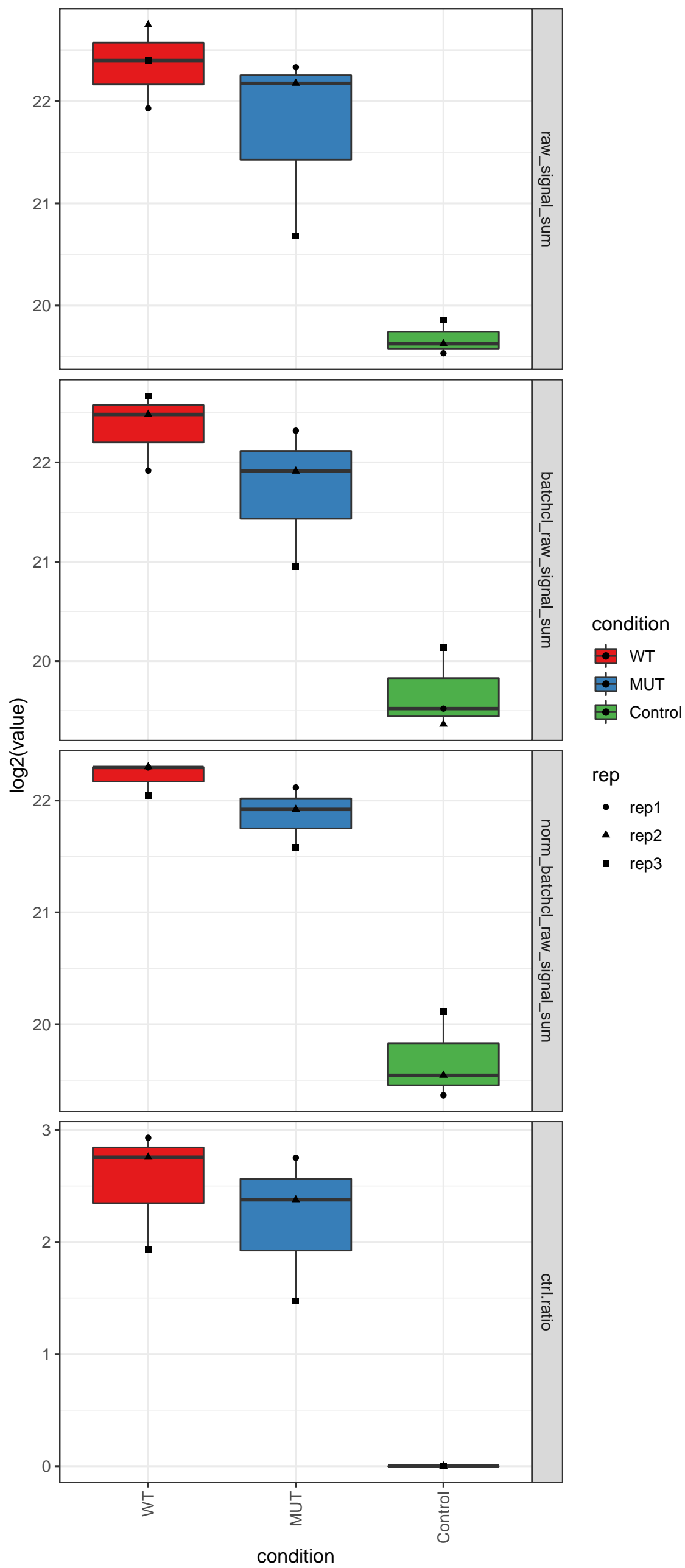
RPA135 – P22138

DNA-directed RNA polymerase I subunit RPA135 OS=*Saccharomyces cerevisiae*



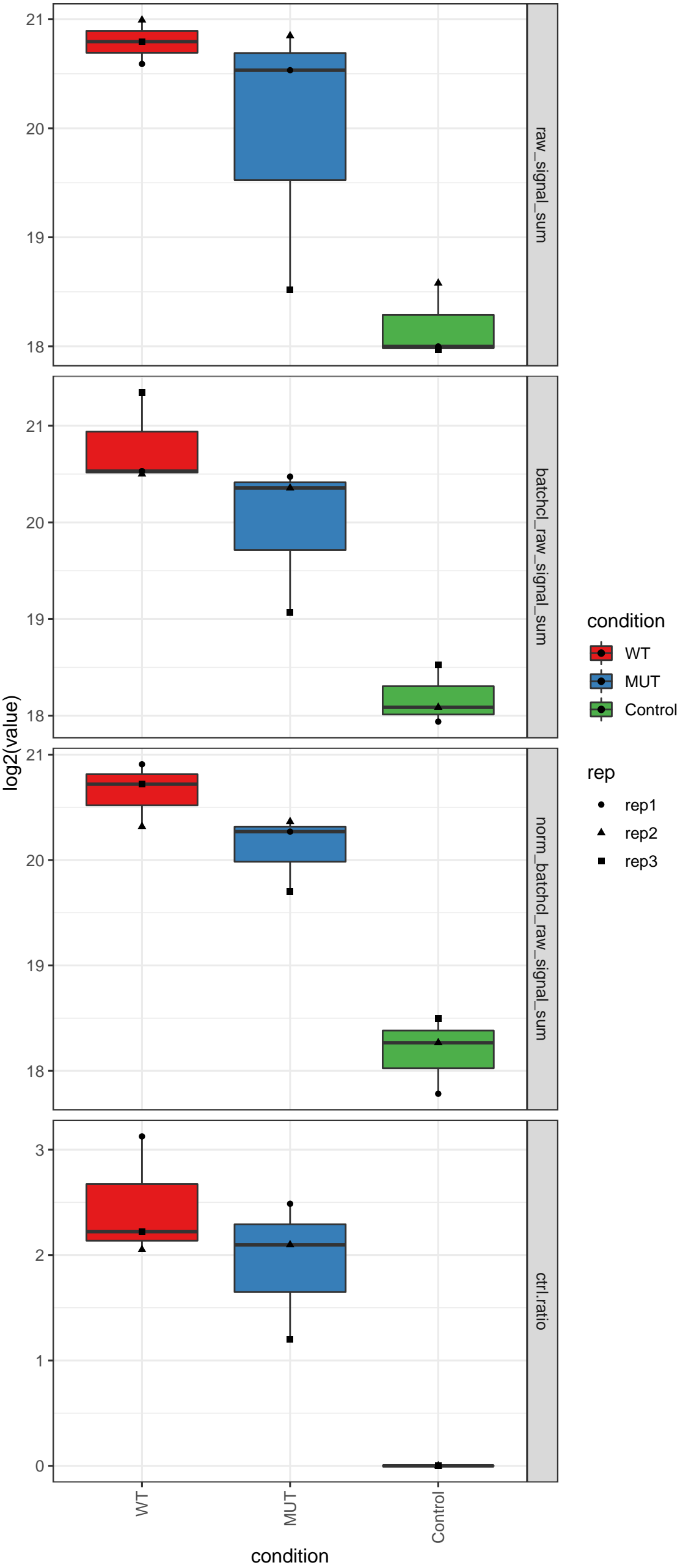
RPA190 – P10964

DNA-directed RNA polymerase I subunit RPA190 OS=*Saccharomyces cerevisiae*



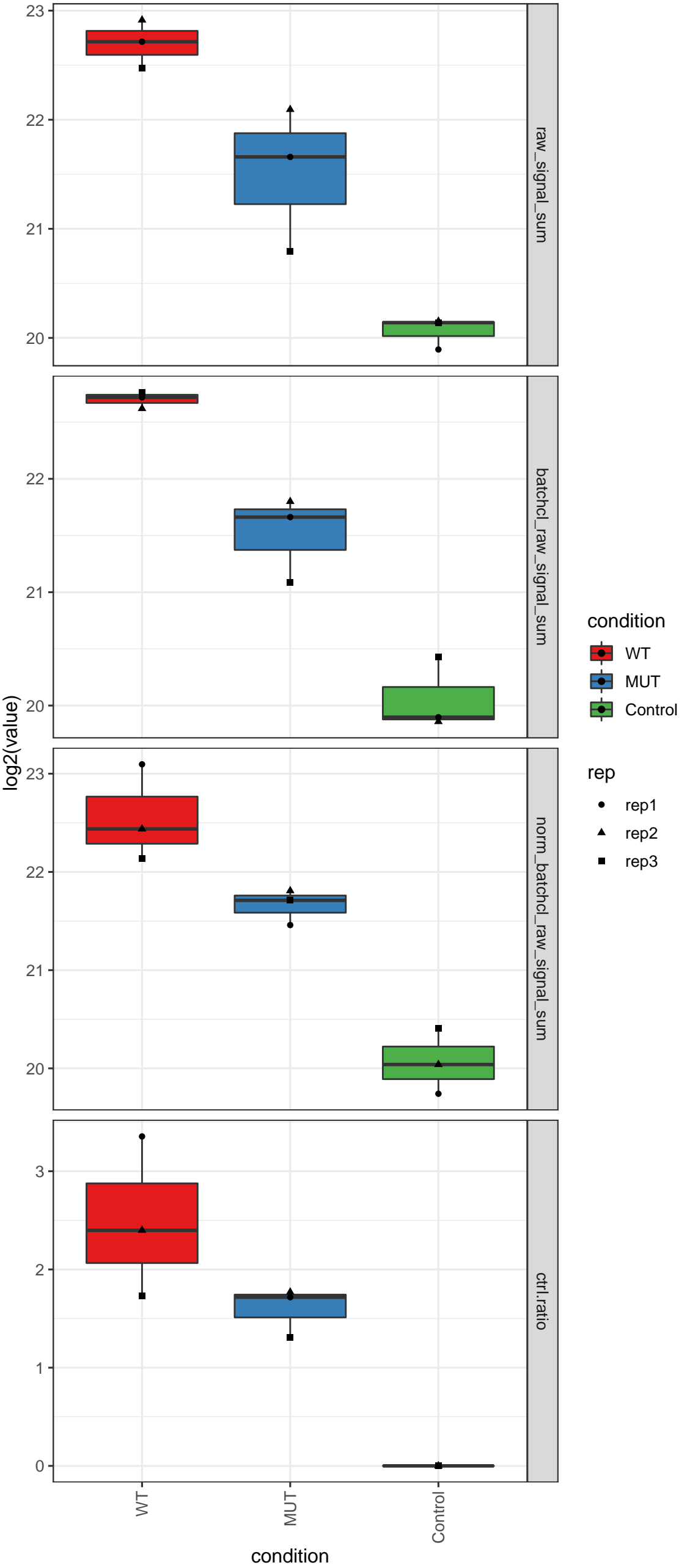
RPA49 – Q01080

DNA-directed RNA polymerase I subunit RPA49 OS=*Saccharomyces cerevisiae*



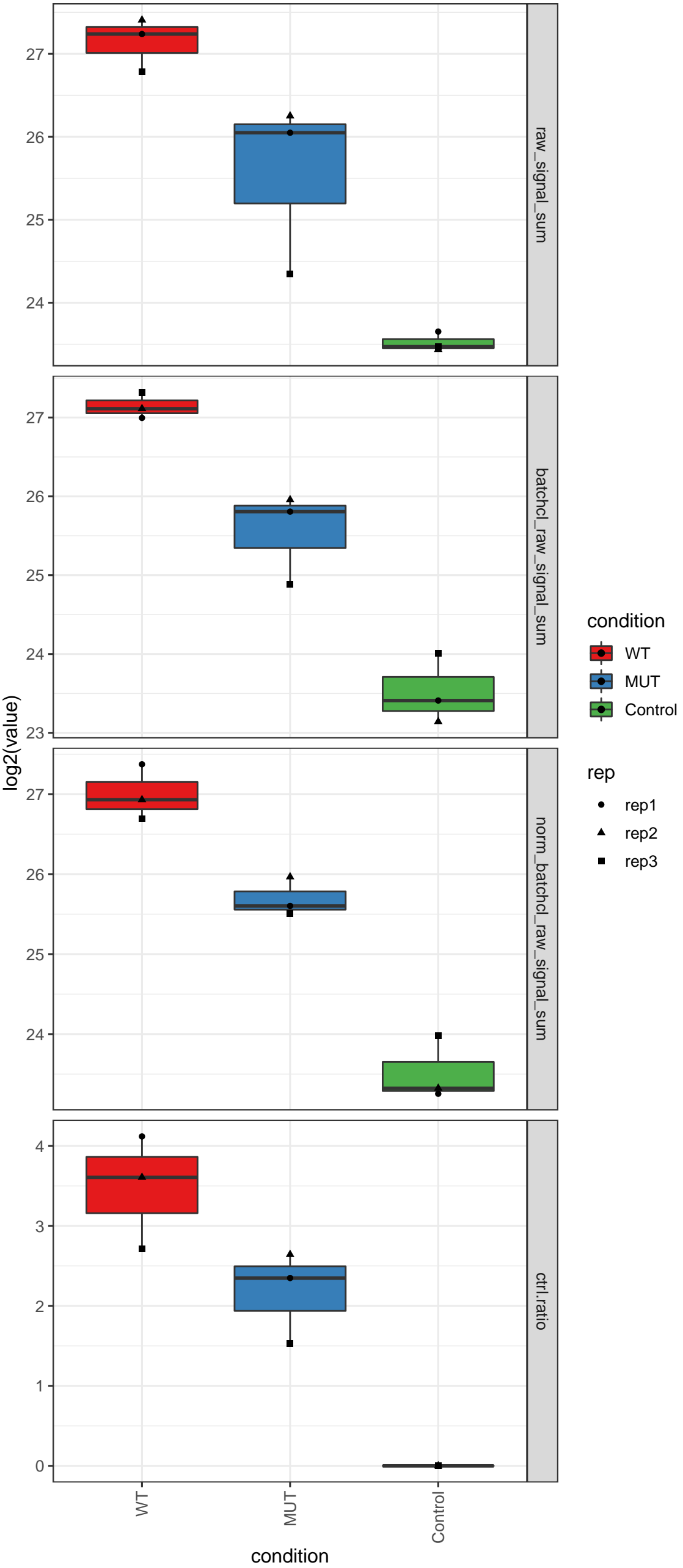
RPB11 – P38902

DNA-directed RNA polymerase II subunit RPB11 OS=*Saccharomyces cerevisiae*



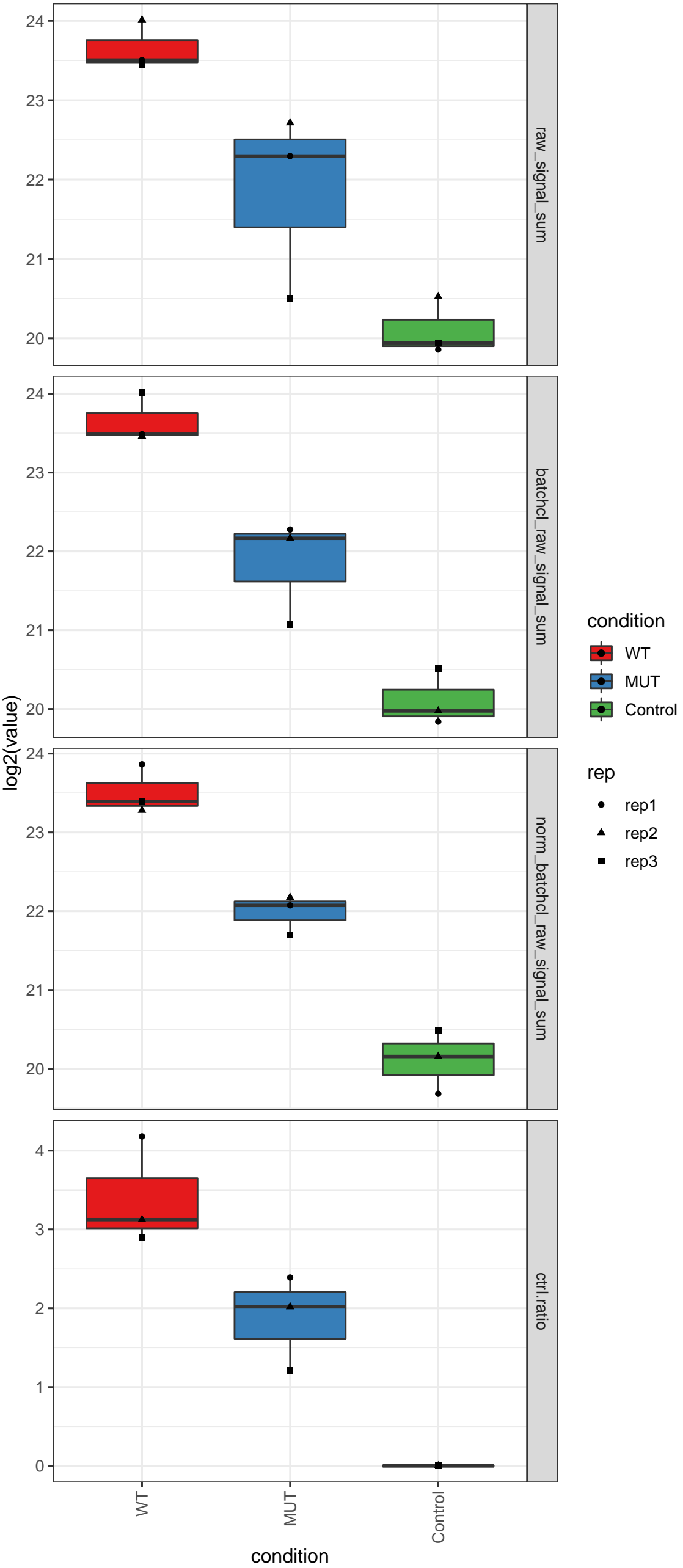
RPB2 – P08518

DNA-directed RNA polymerase II subunit RPB2 OS=*Saccharomyces cere*



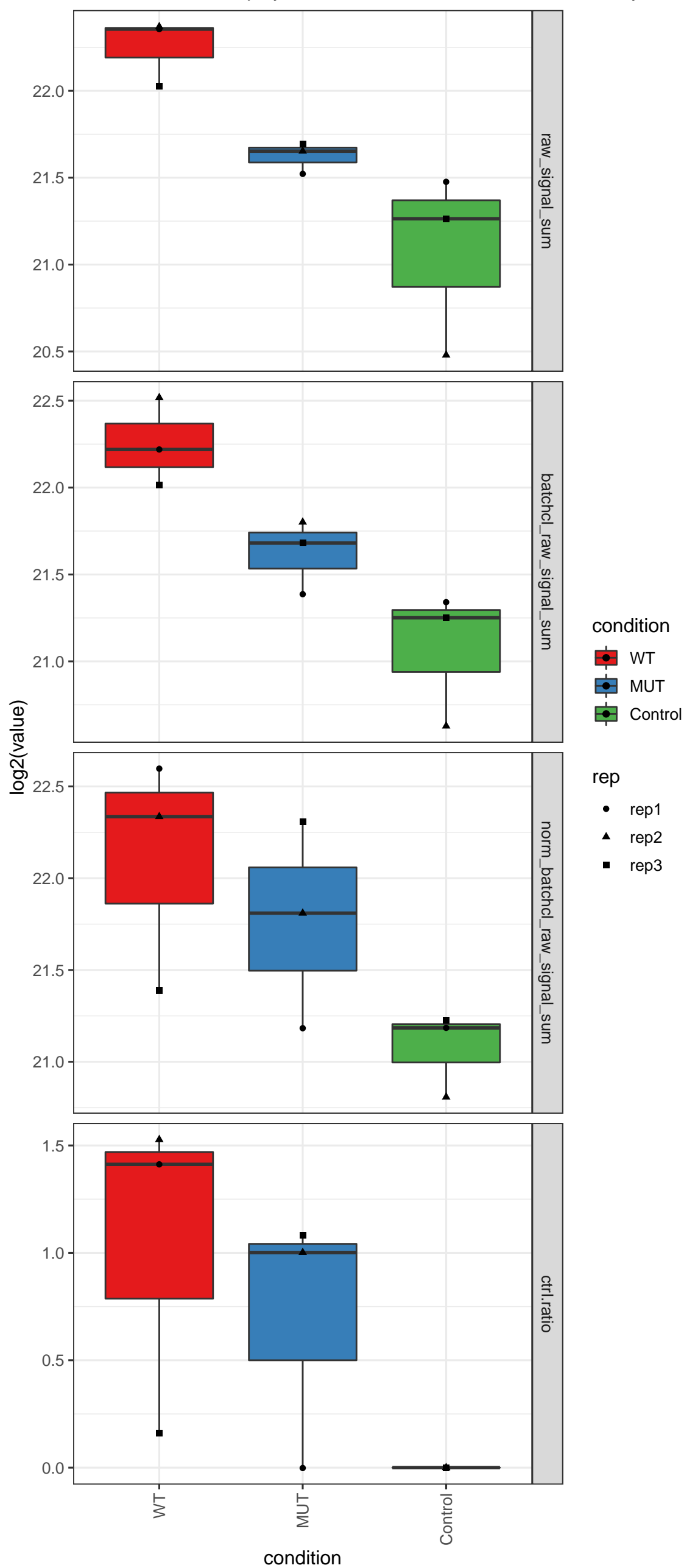
RPB3 – P16370

DNA-directed RNA polymerase II subunit RPB3 OS=*Saccharomyces cere*



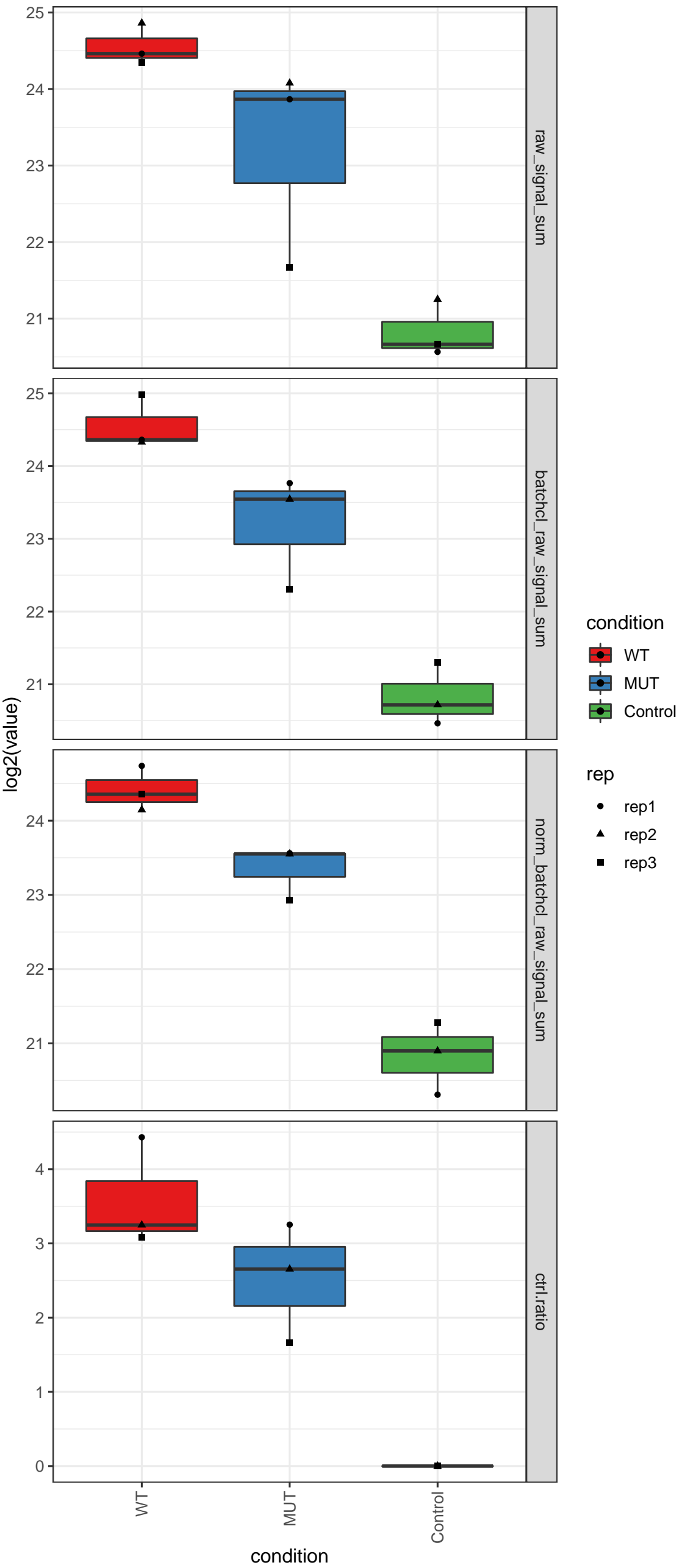
RPB4 – P20433

DNA-directed RNA polymerase II subunit RPB4 OS=*Saccharomyces cerevisiae*



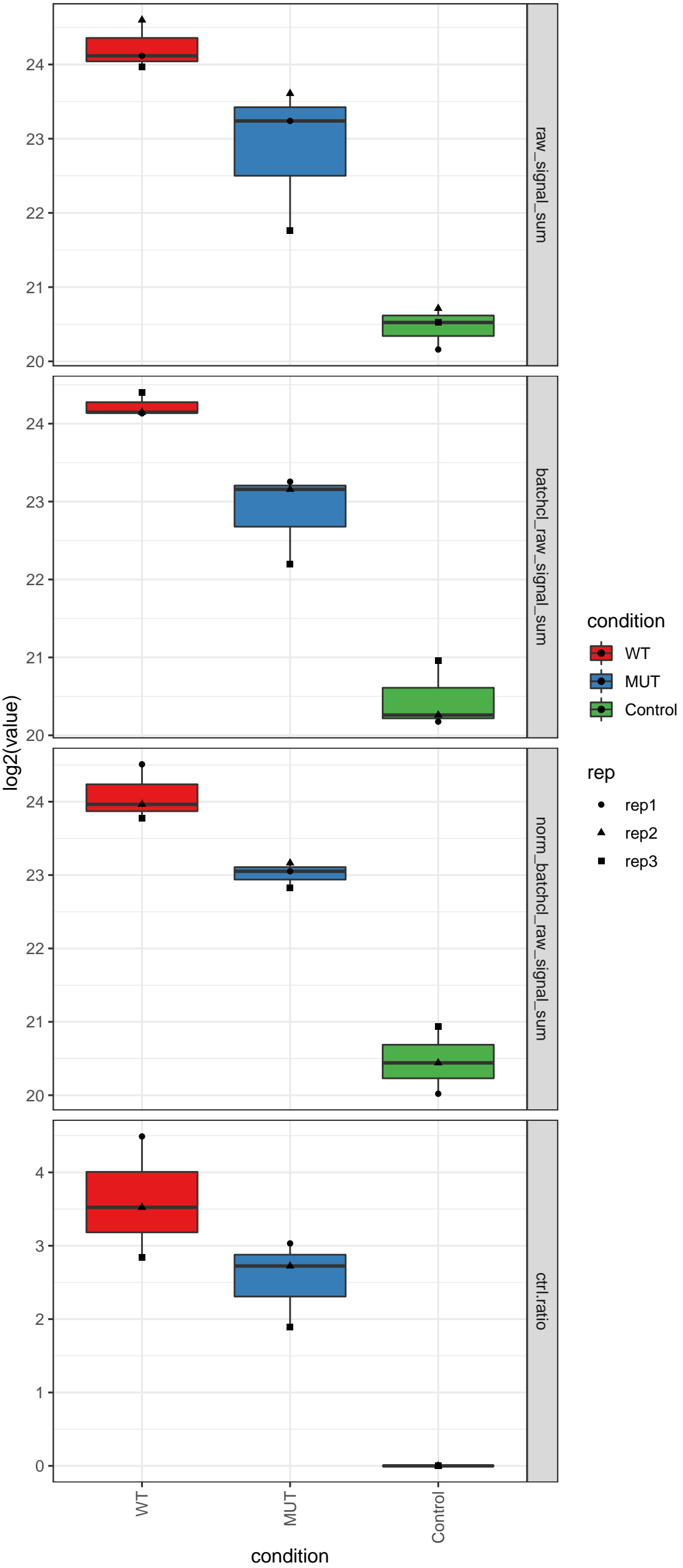
RPB5 – P20434

DNA-directed RNA polymerases I, II, and III subunit RPABC1 OS=Saccha



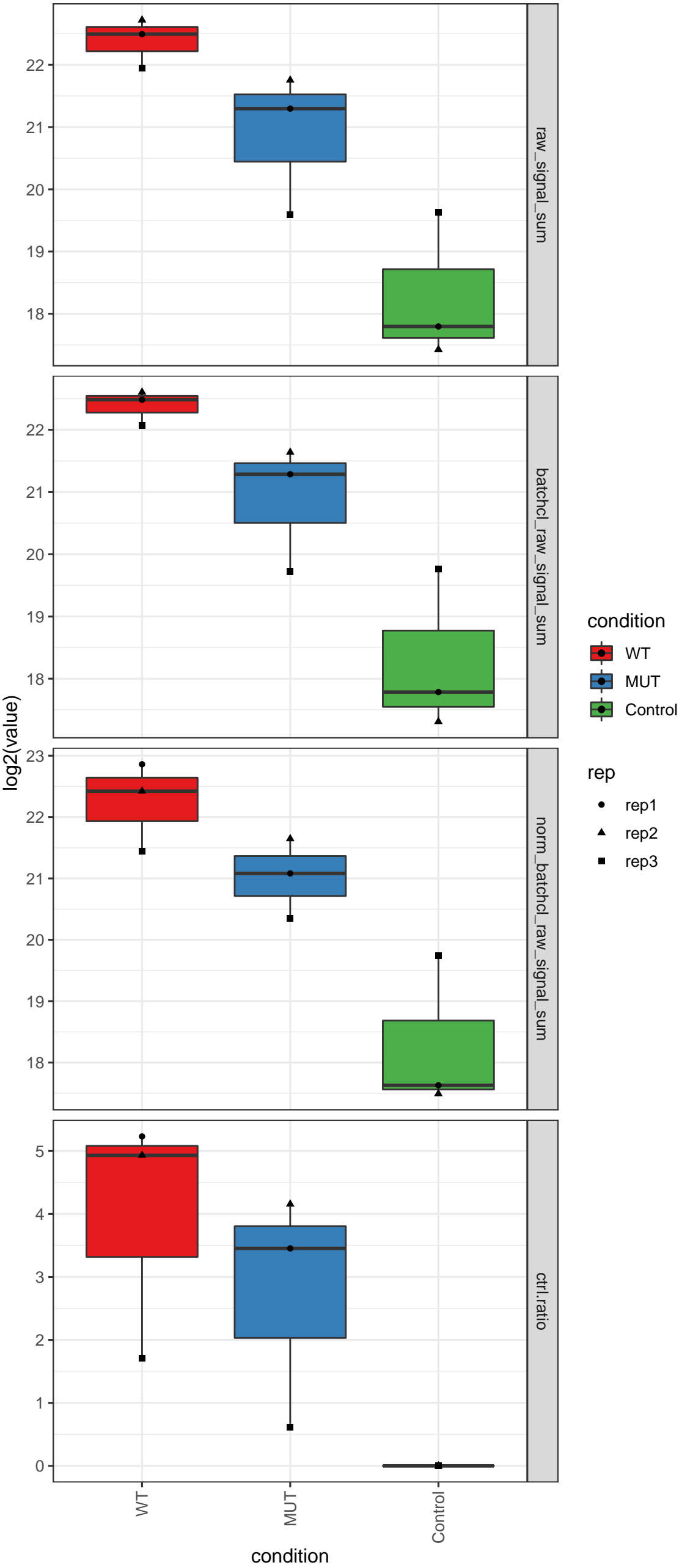
RPB8 – P20436

DNA-directed RNA polymerases I, II, and III subunit RPABC3 OS=Saccha



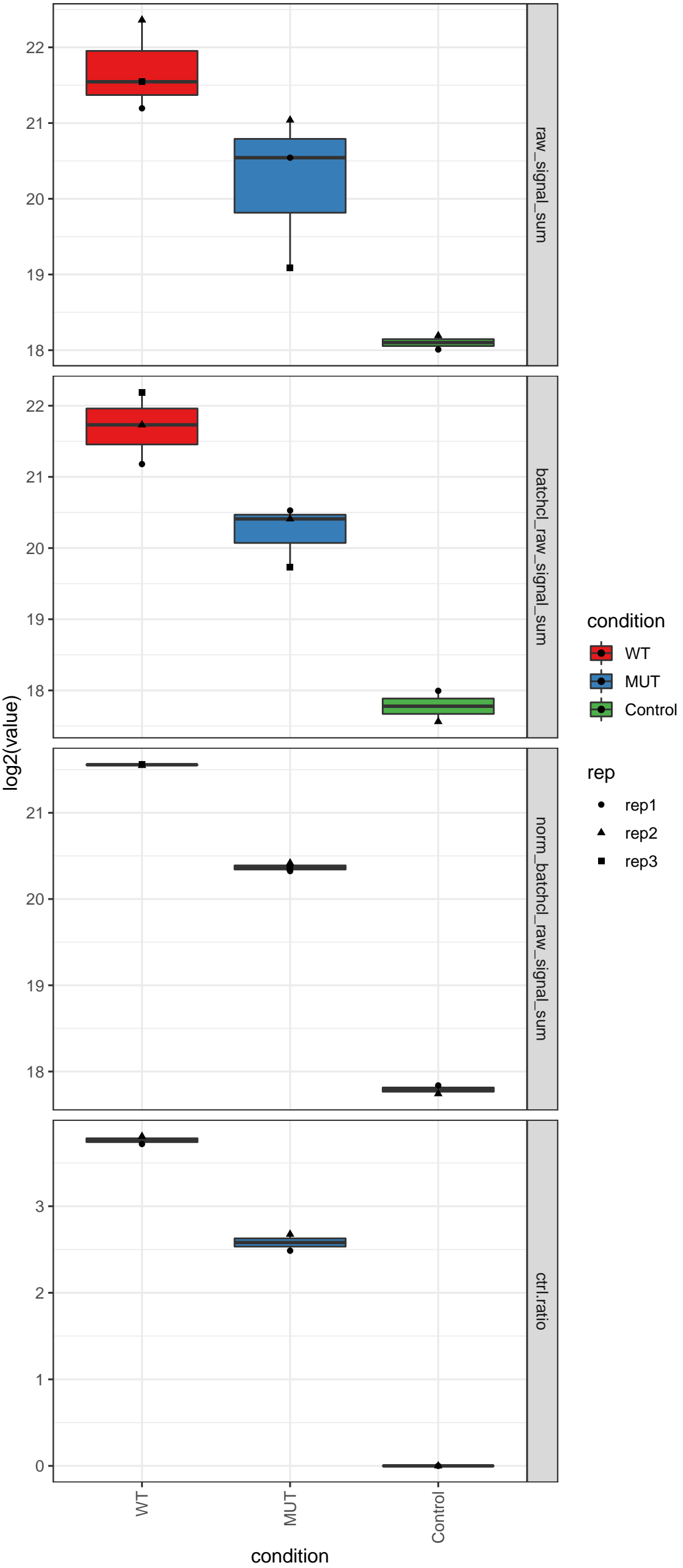
RPC10 – P40422

DNA-directed RNA polymerases I, II, and III subunit RPABC4 OS=Saccha

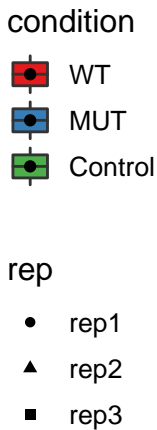


RPC82 – P32349

DNA-directed RNA polymerase III subunit RPC3 OS=*Saccharomyces cerevisiae*

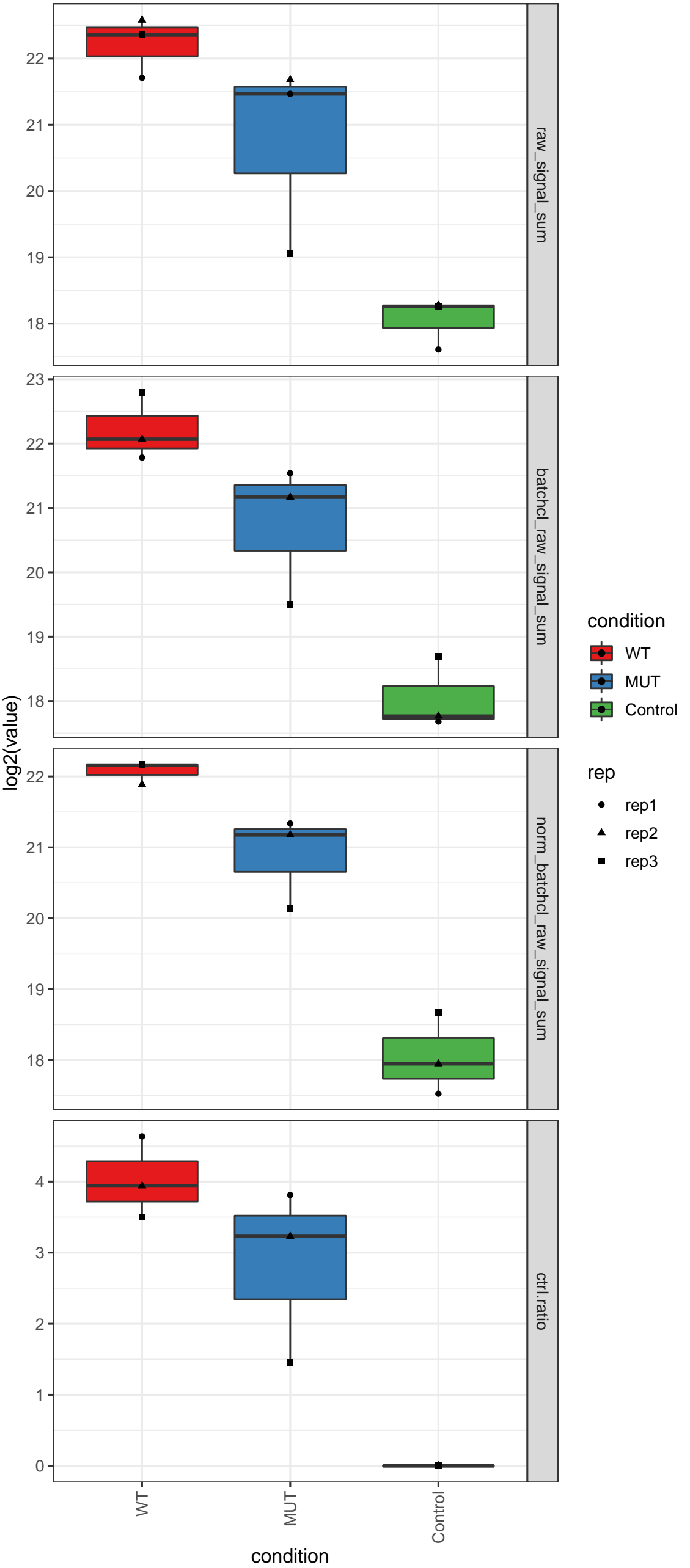


Eukaryotic translation initiation factor 3 subunit A OS=Saccharomyces ce



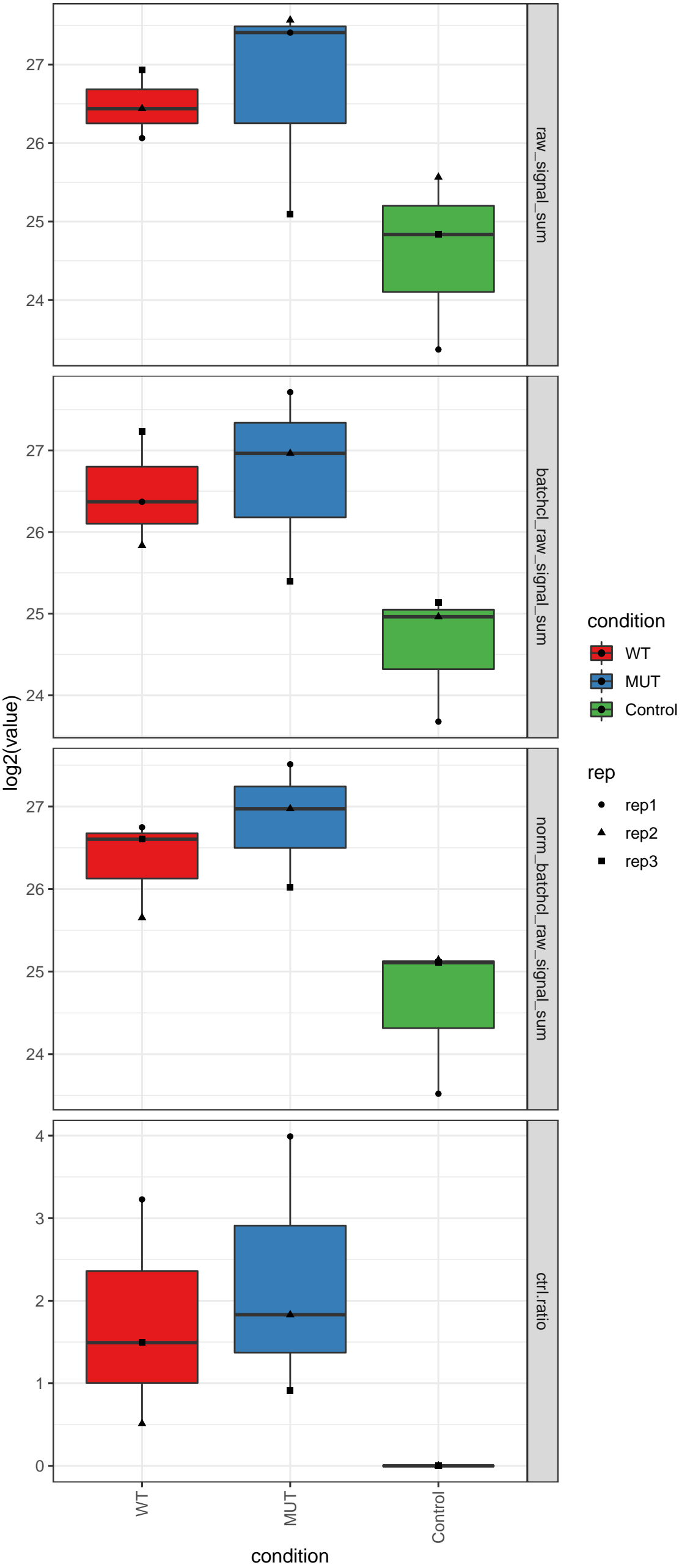
RPH1 – P39956

DNA damage–responsive transcriptional repressor RPH1 OS=Saccharomy



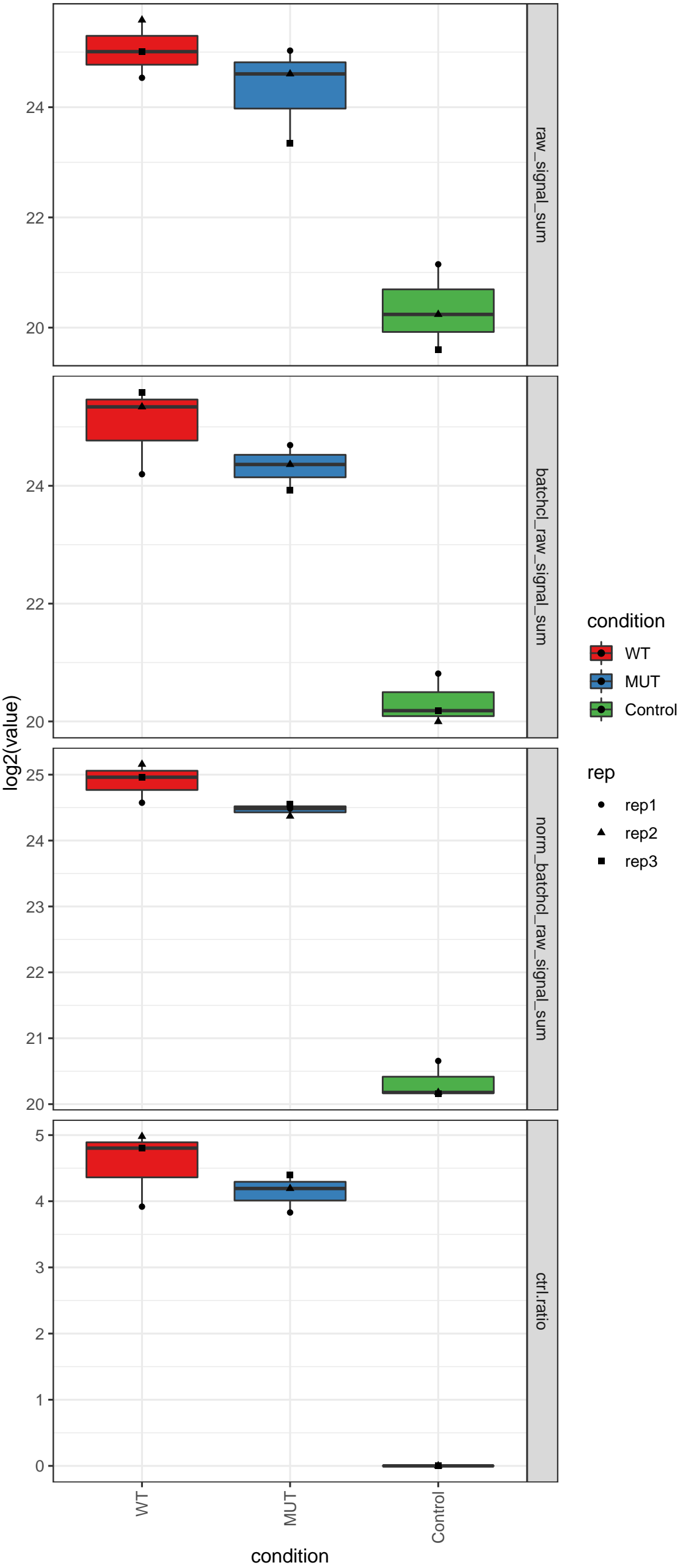
RPL10 – P41805

60S ribosomal protein L10 OS=*Saccharomyces cerevisiae* (strain ATCC 20454)



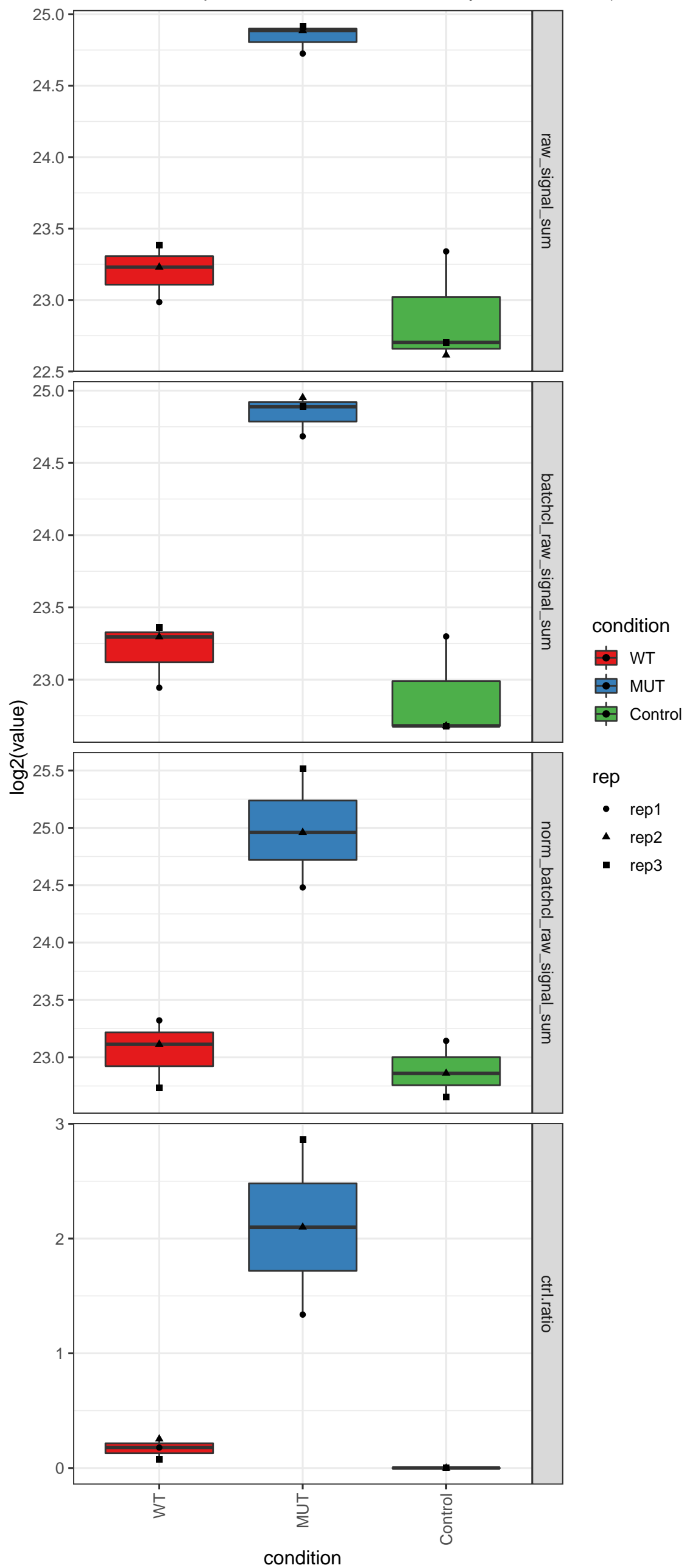
RPL11A|RPL11B – P0C0W9|Q3E757

60S ribosomal protein L11–A OS=*Saccharomyces cerevisiae* (strain ATCC

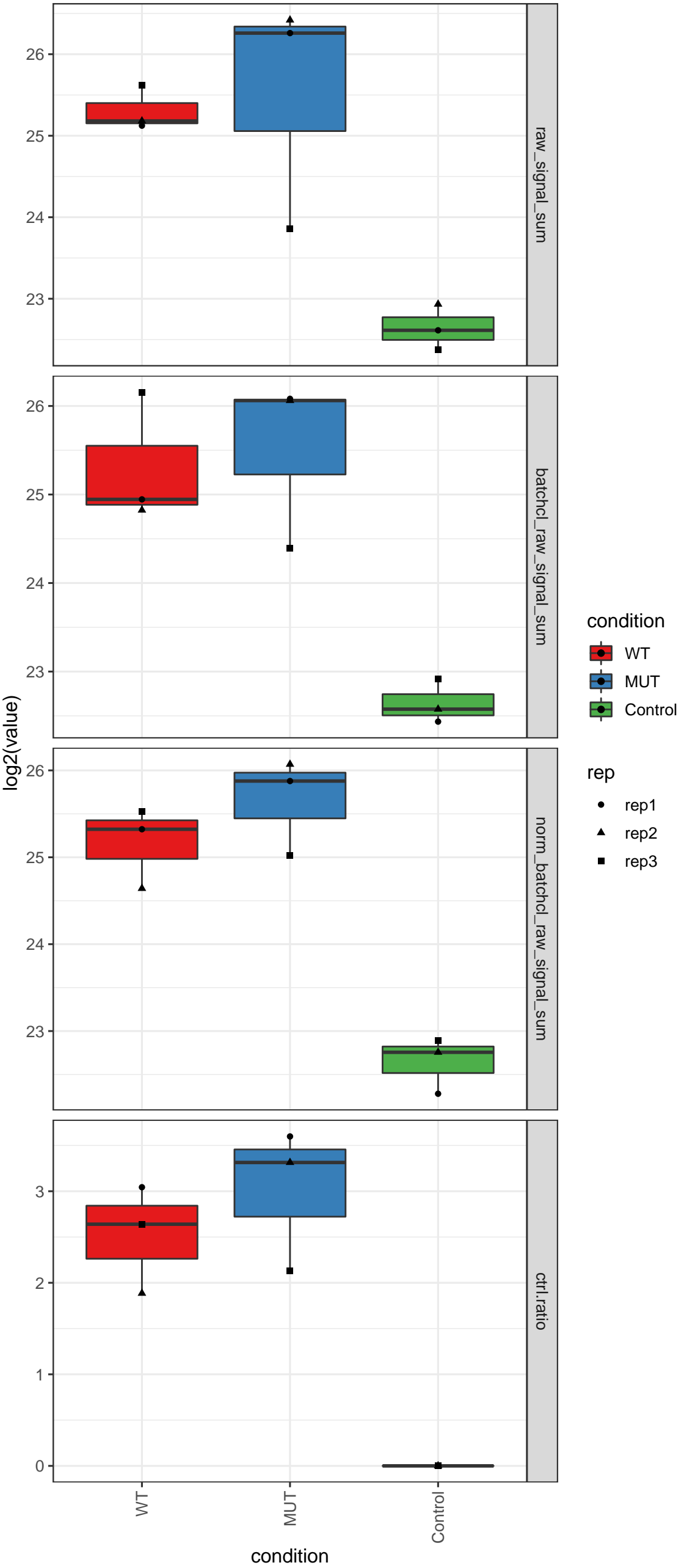


RPL12A|RPL12B – P0CX53|P0CX54

60S ribosomal protein L12–A OS=*Saccharomyces cerevisiae* (strain ATC

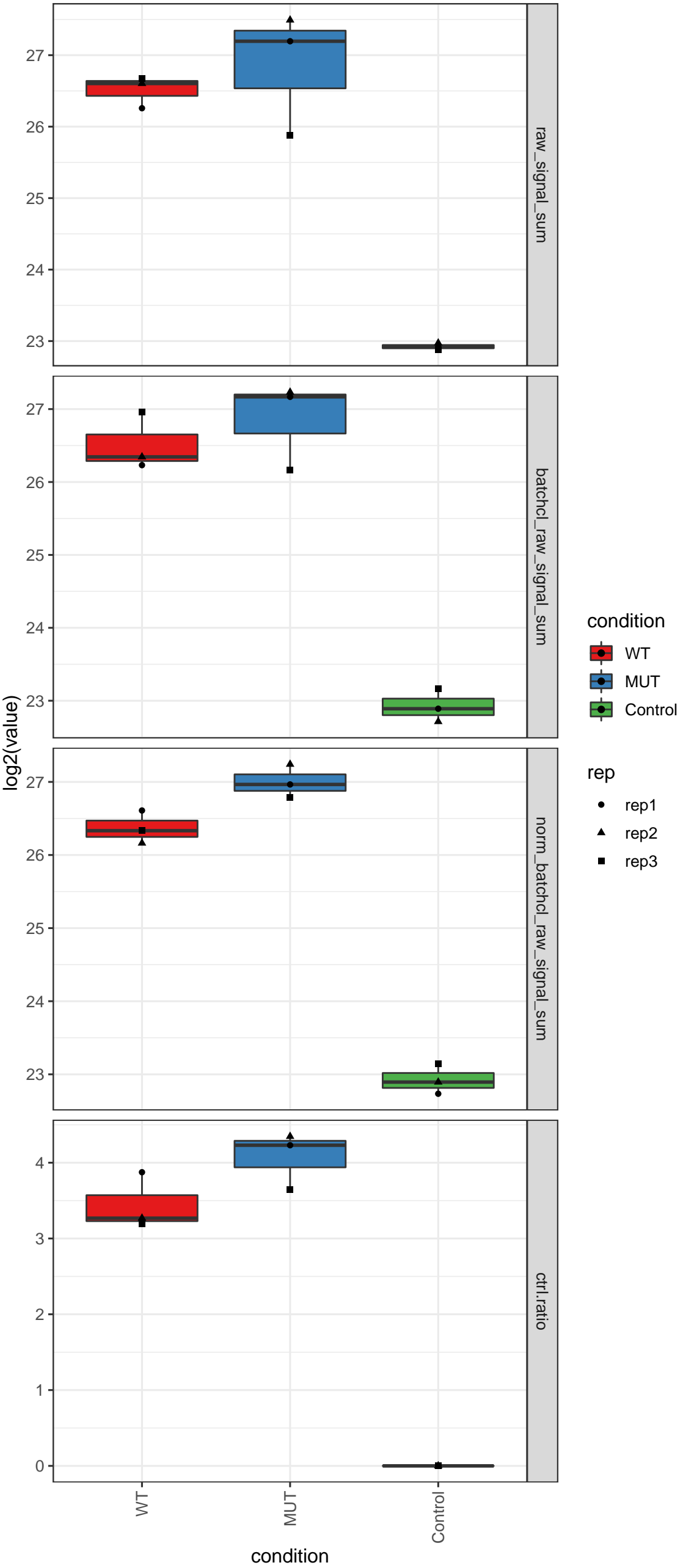


RPL13B|RPL13A – P40212|Q12690
60S ribosomal protein L13-B OS=Saccharomyces cerevisiae (strain ATCC



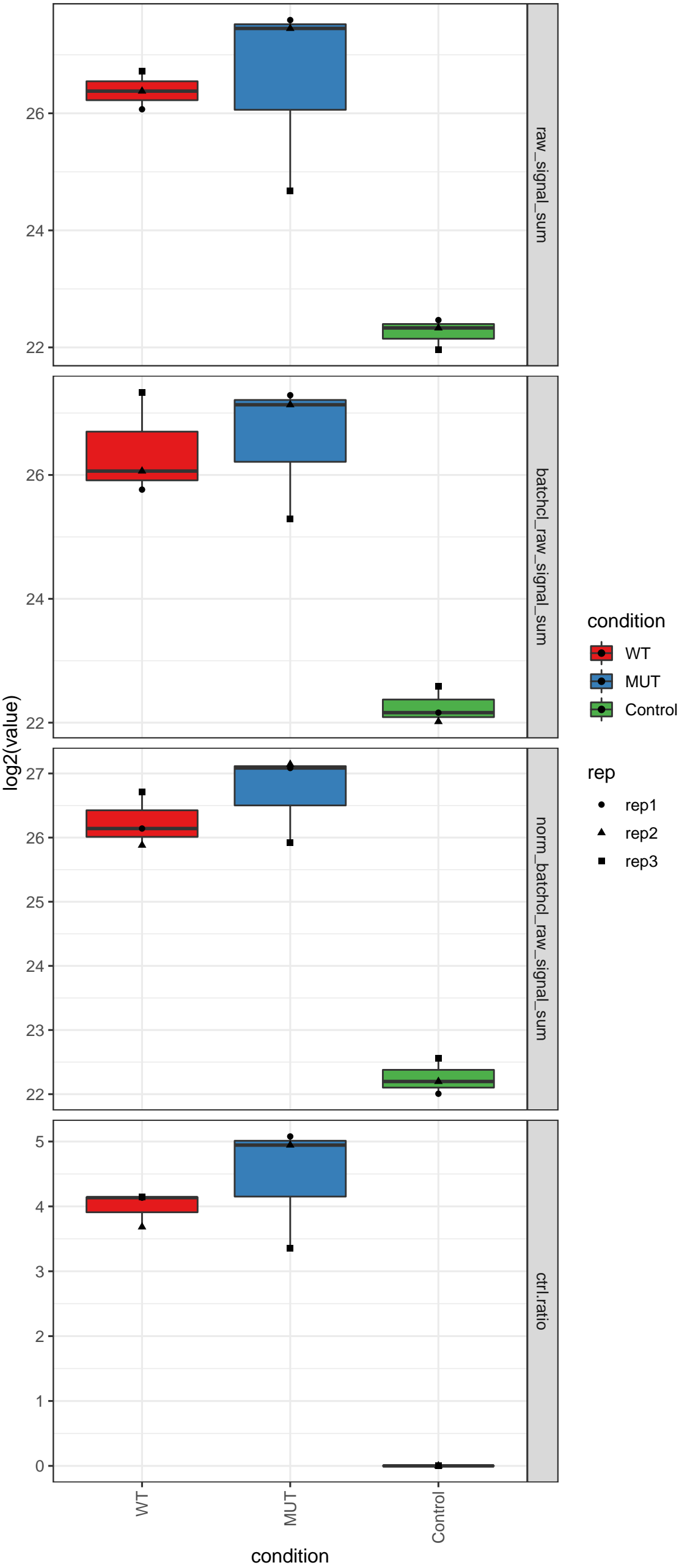
RPL14A|RPL14B – P36105|P38754

60S ribosomal protein L14–A OS=*Saccharomyces cerevisiae* (strain ATCC



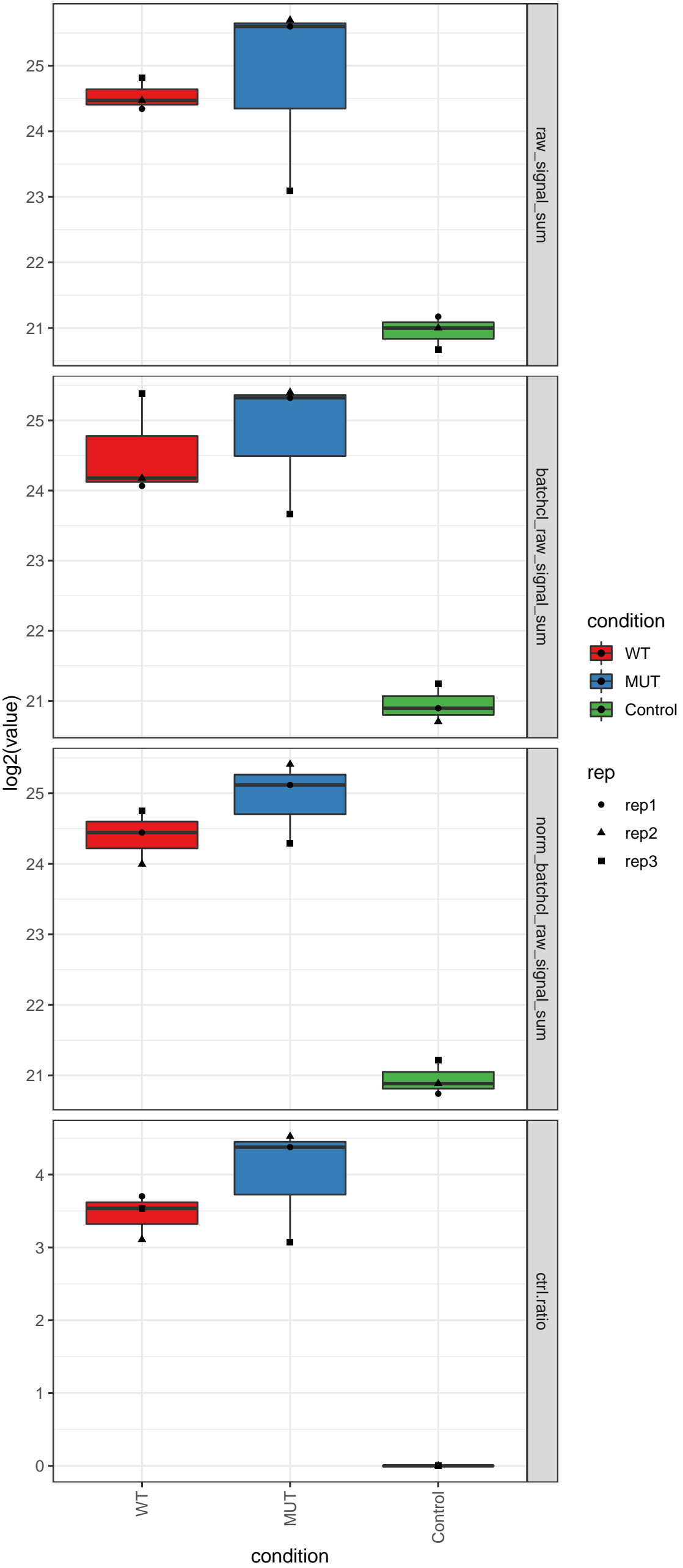
RPL15A – P05748

60S ribosomal protein L15–A OS=Saccharomyces cerevisiae (strain ATCC



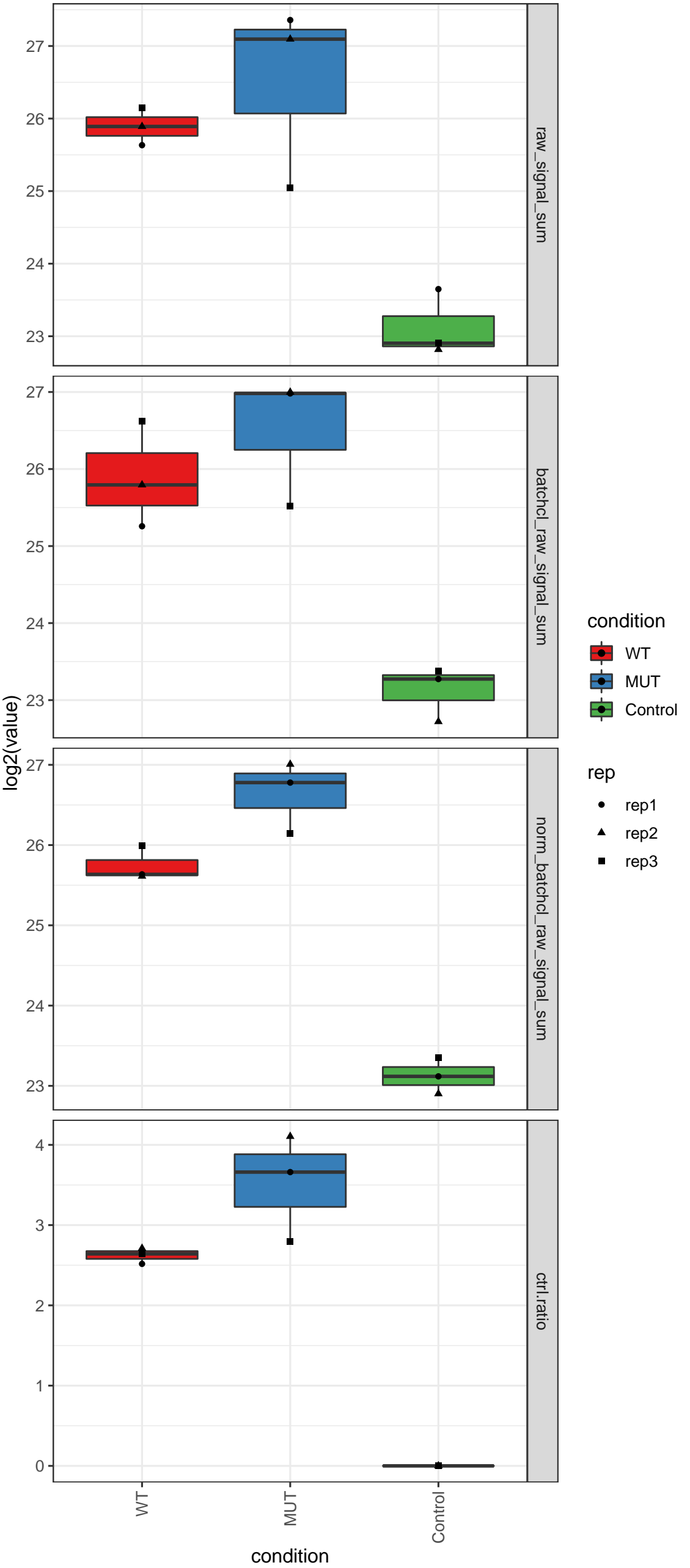
RPL16A – P26784

60S ribosomal protein L16–A OS=*Saccharomyces cerevisiae* (strain ATCC



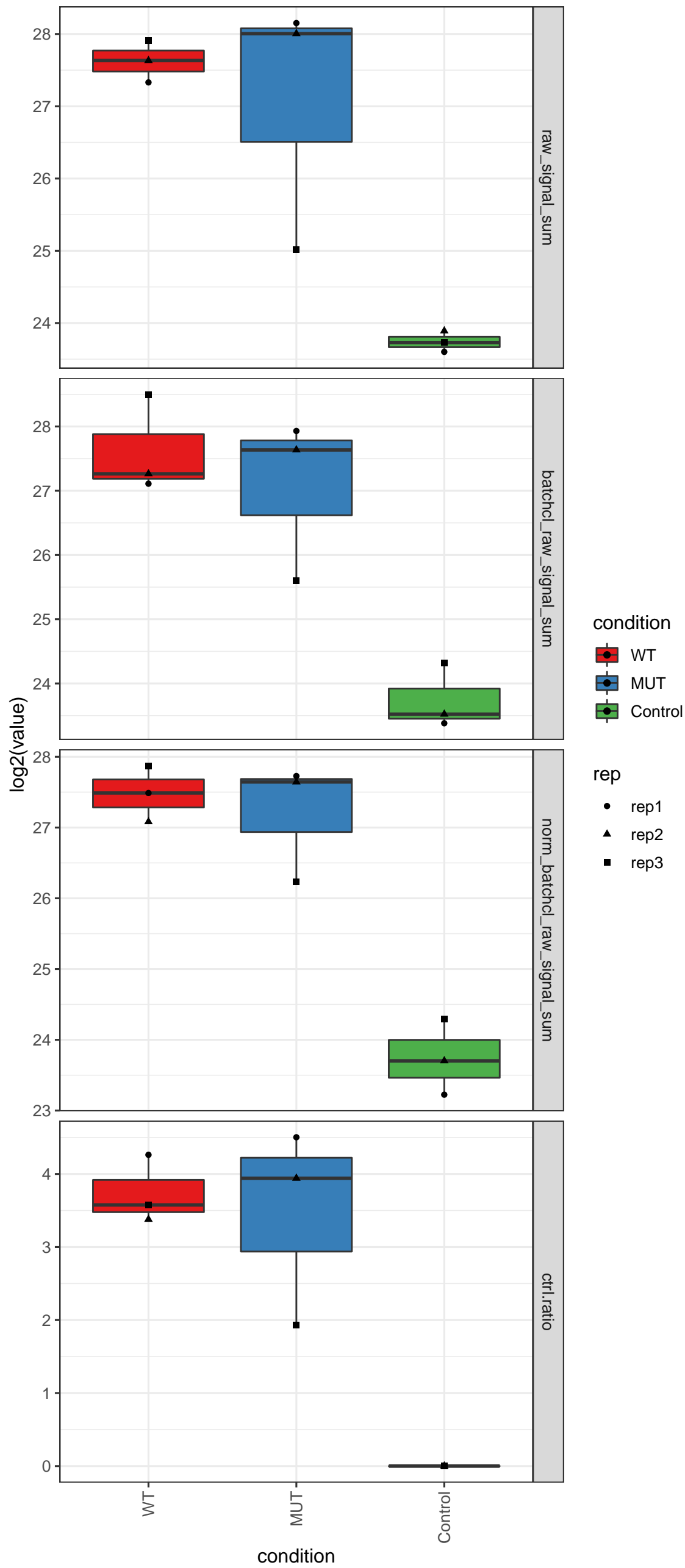
RPL16B – P26785

60S ribosomal protein L16–B OS=Saccharomyces cerevisiae (strain ATCC



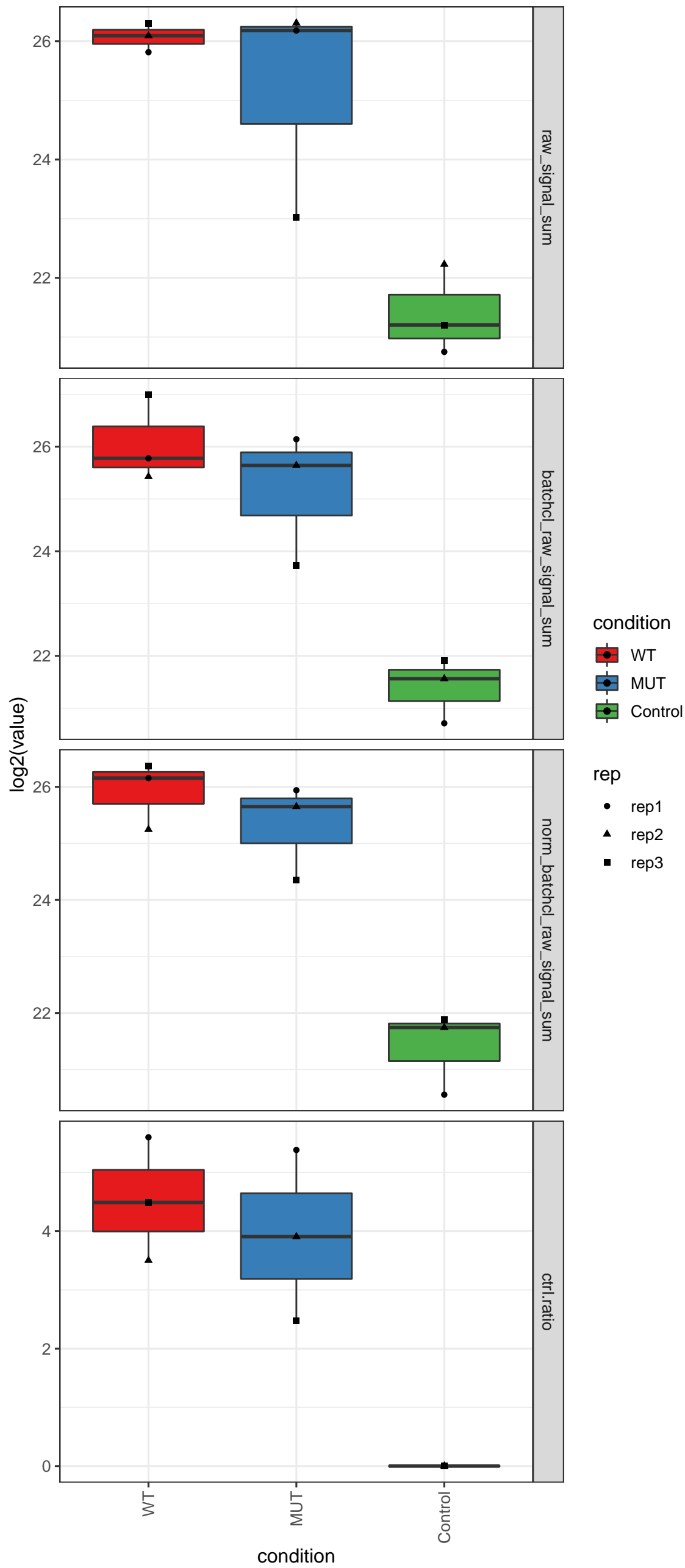
RPL18A|RPL18B – P0CX49|P0CX50

60S ribosomal protein L18-A OS=*Saccharomyces cerevisiae* (strain ATCC



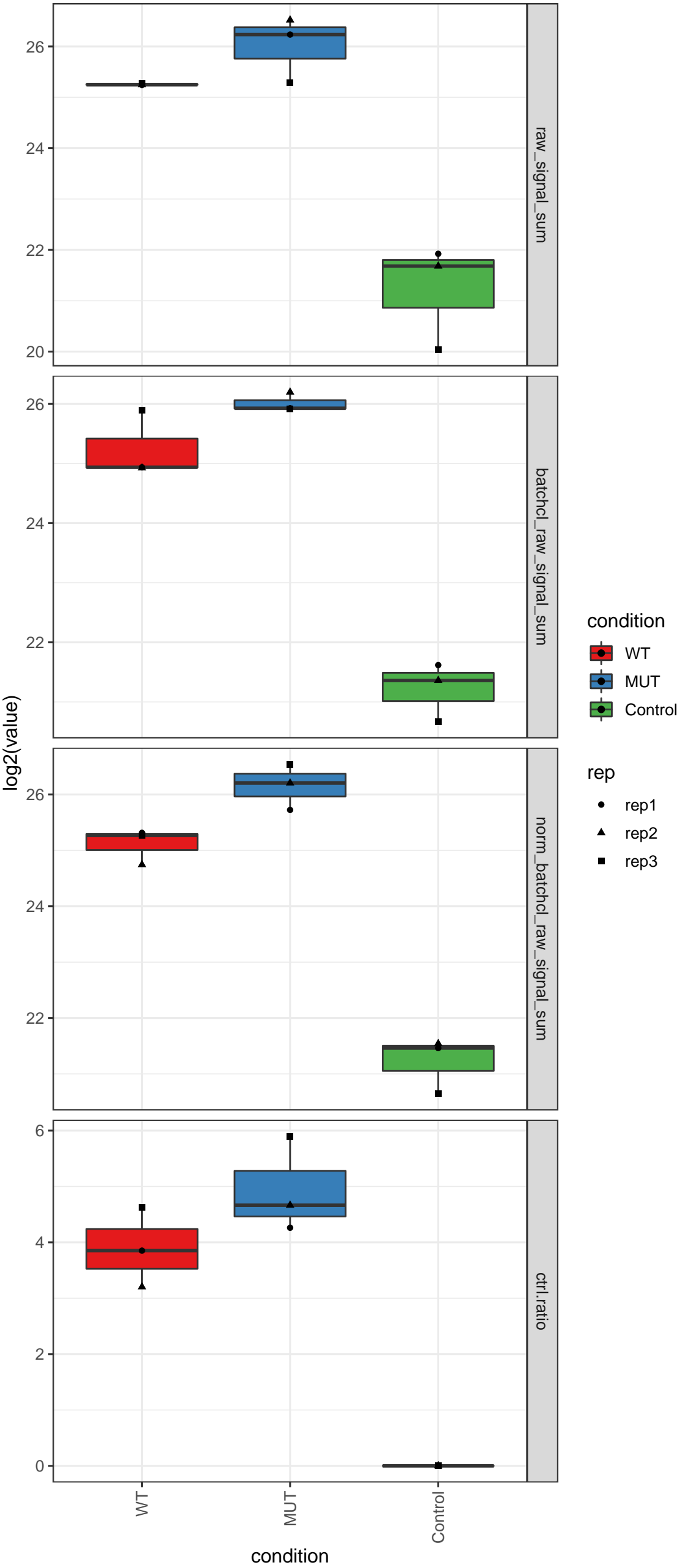
RPL19A|RPL19B – P0CX82|P0CX83

60S ribosomal protein L19–A OS=*Saccharomyces cerevisiae* (strain ATCC



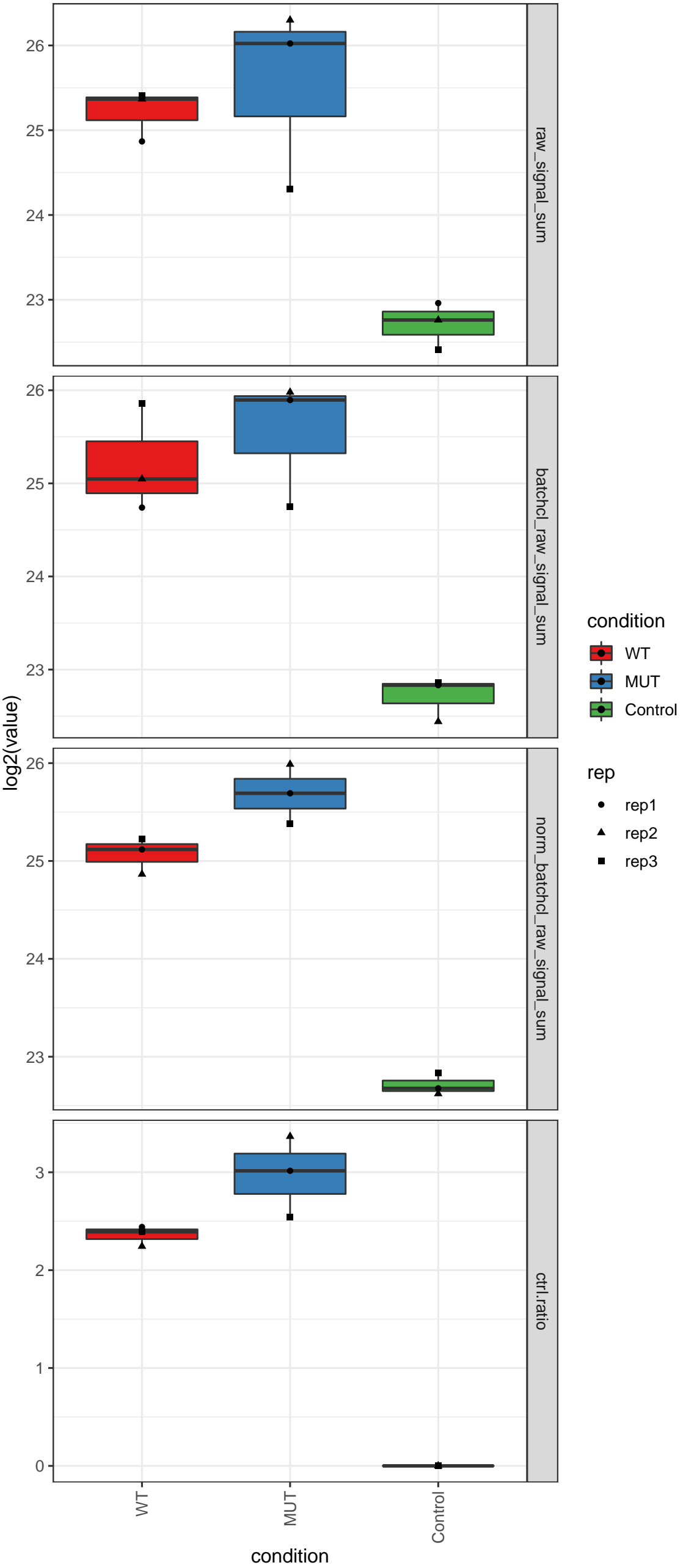
RPL1A|RPL1B – P0CX43|P0CX44

60S ribosomal protein L1–A OS=Saccharomyces cerevisiae (strain ATCC 2

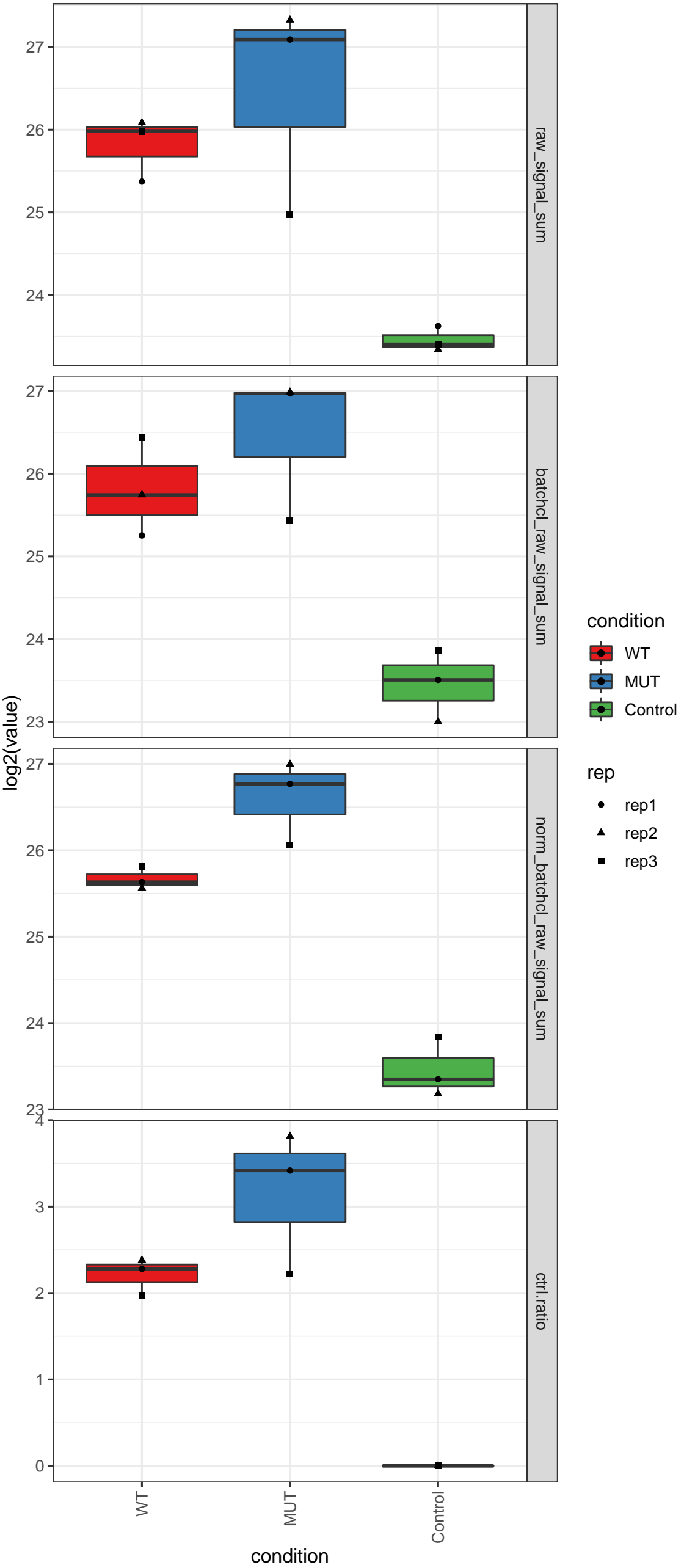


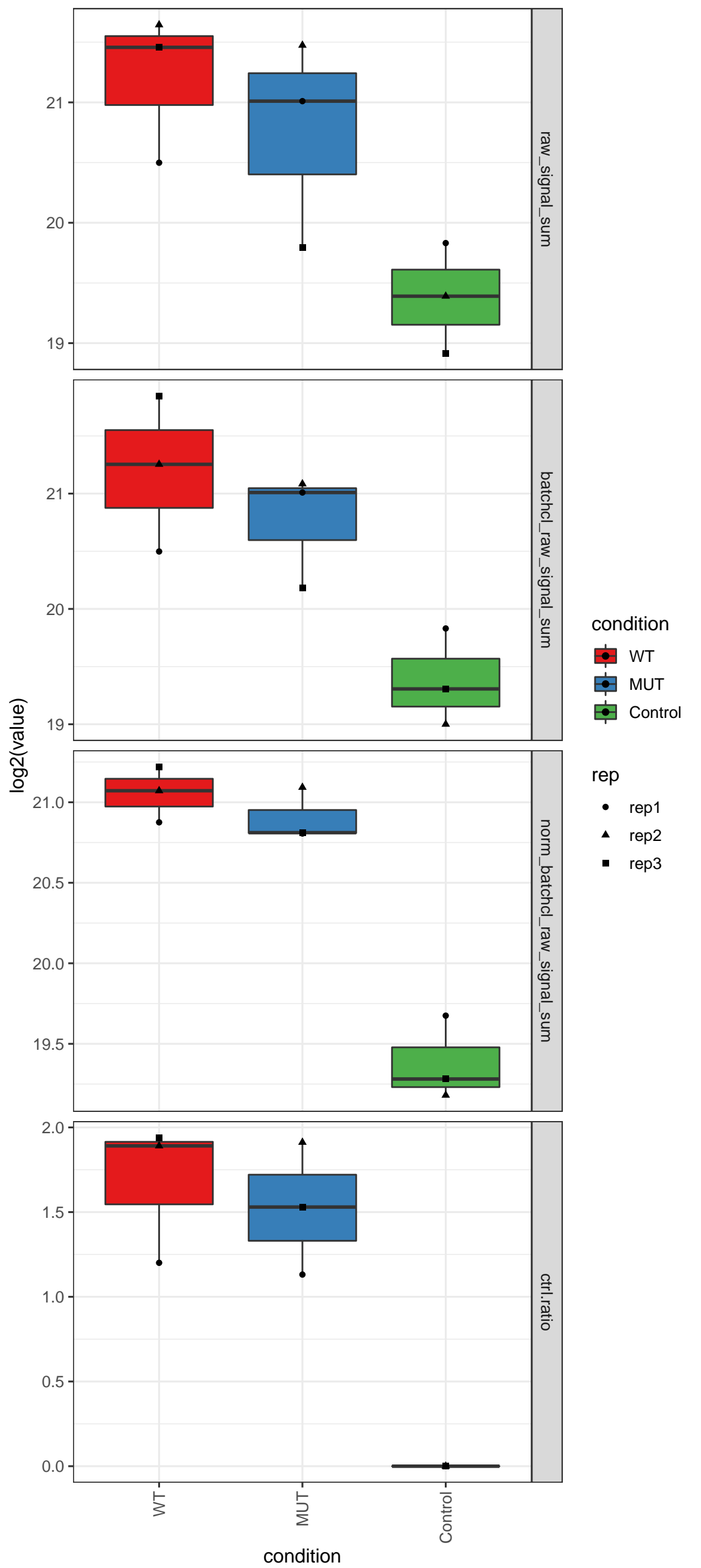
RPL20A|RPL20B – P0CX23|P0CX24

60S ribosomal protein L20–A OS=Saccharomyces cerevisiae (strain ATCC



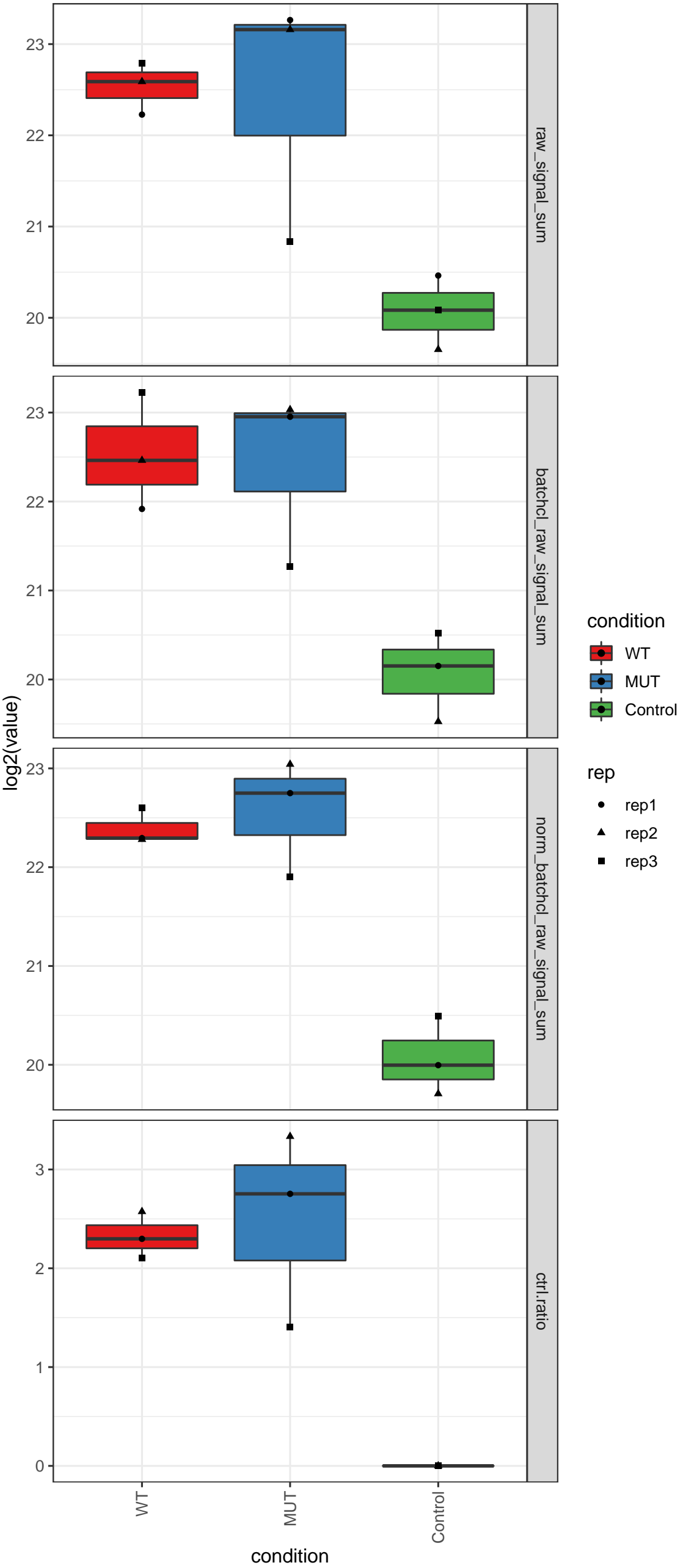
RPL21A|RPL21B – Q02753|Q12672
60S ribosomal protein L21–A OS=Saccharomyces cerevisiae (strain ATCC



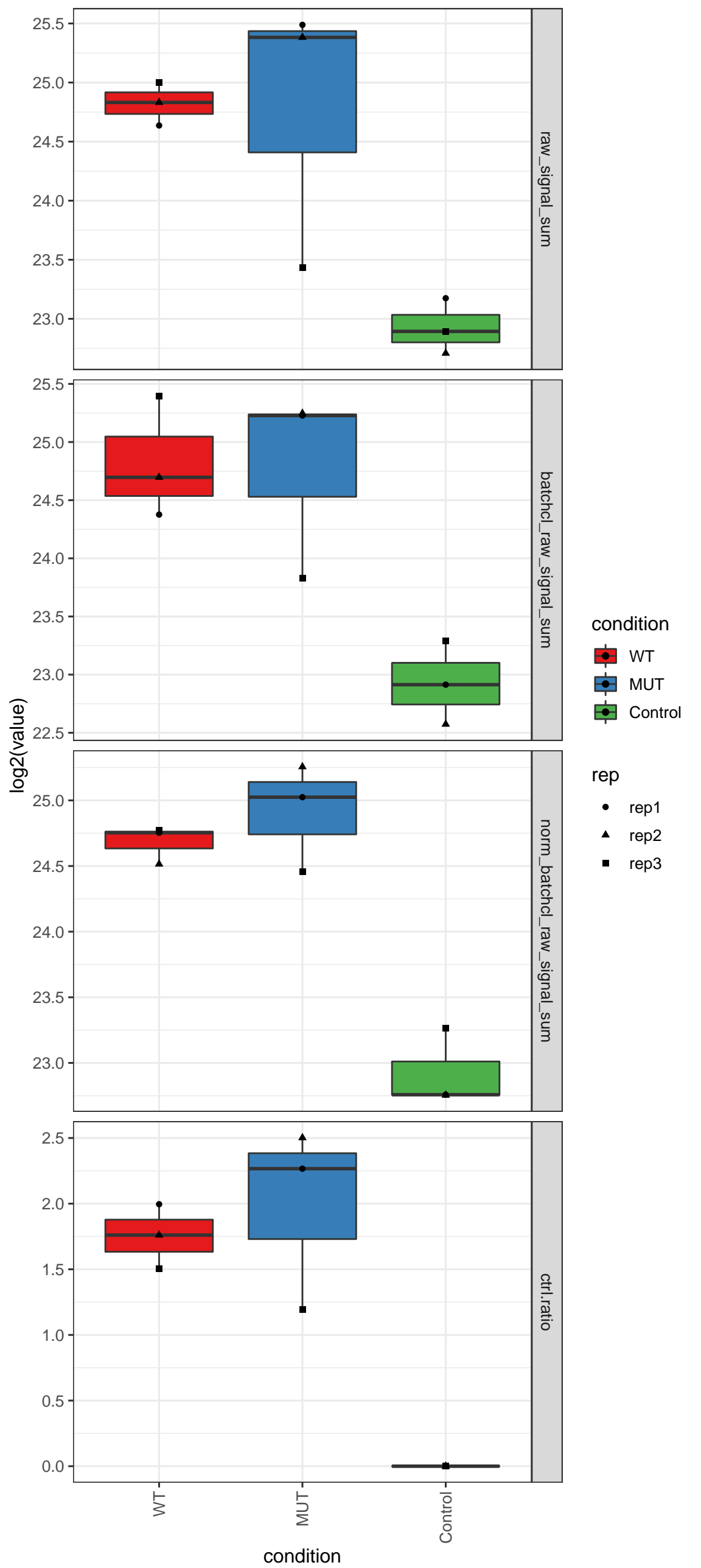
60S ribosomal protein L22-A OS=*Saccharomyces cerevisiae* (strain ATC

RPL24A – P04449

60S ribosomal protein L24-A OS=Saccharomyces cerevisiae (strain ATCC

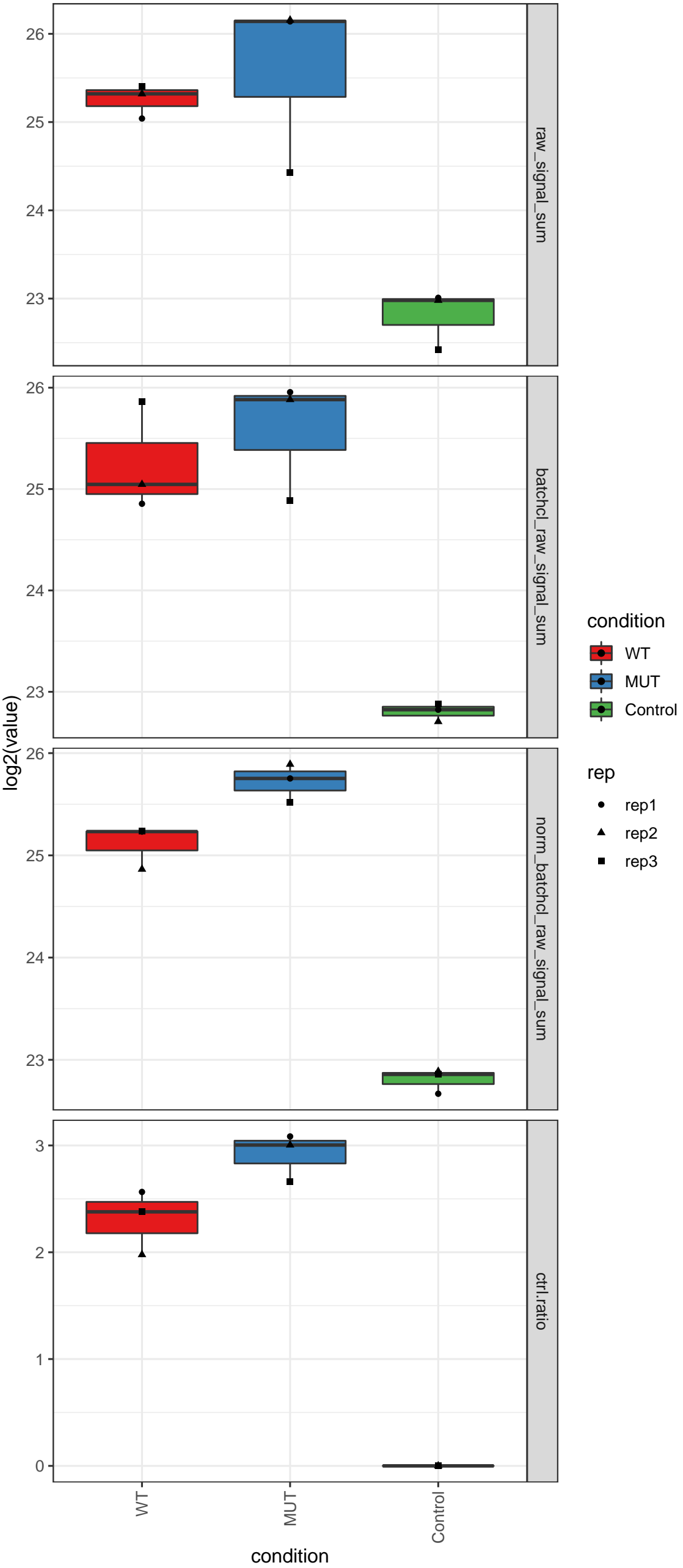


60S ribosomal protein L24-B OS=Saccharomyces cerevisiae (strain ATC



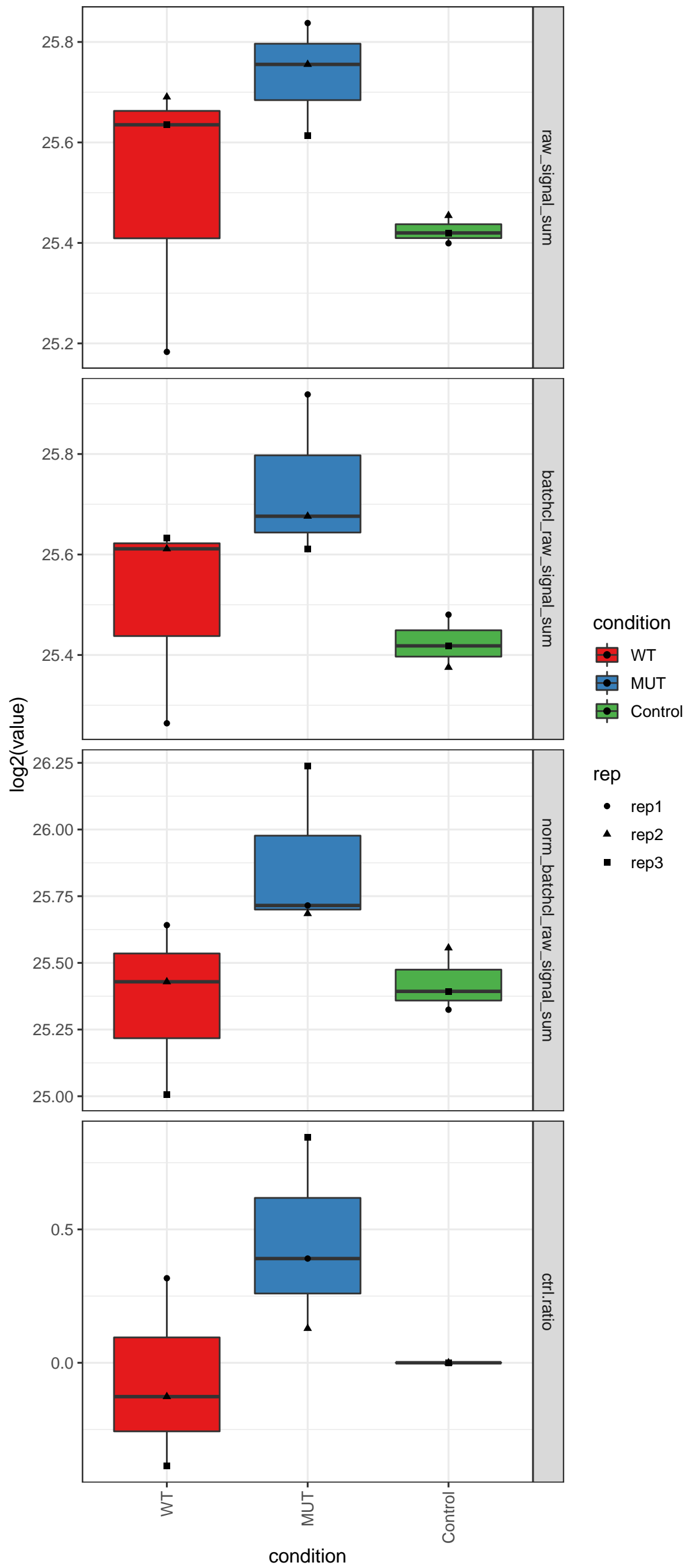
RPL25 – P04456

60S ribosomal protein L25 OS=*Saccharomyces cerevisiae* (strain ATCC 20456)

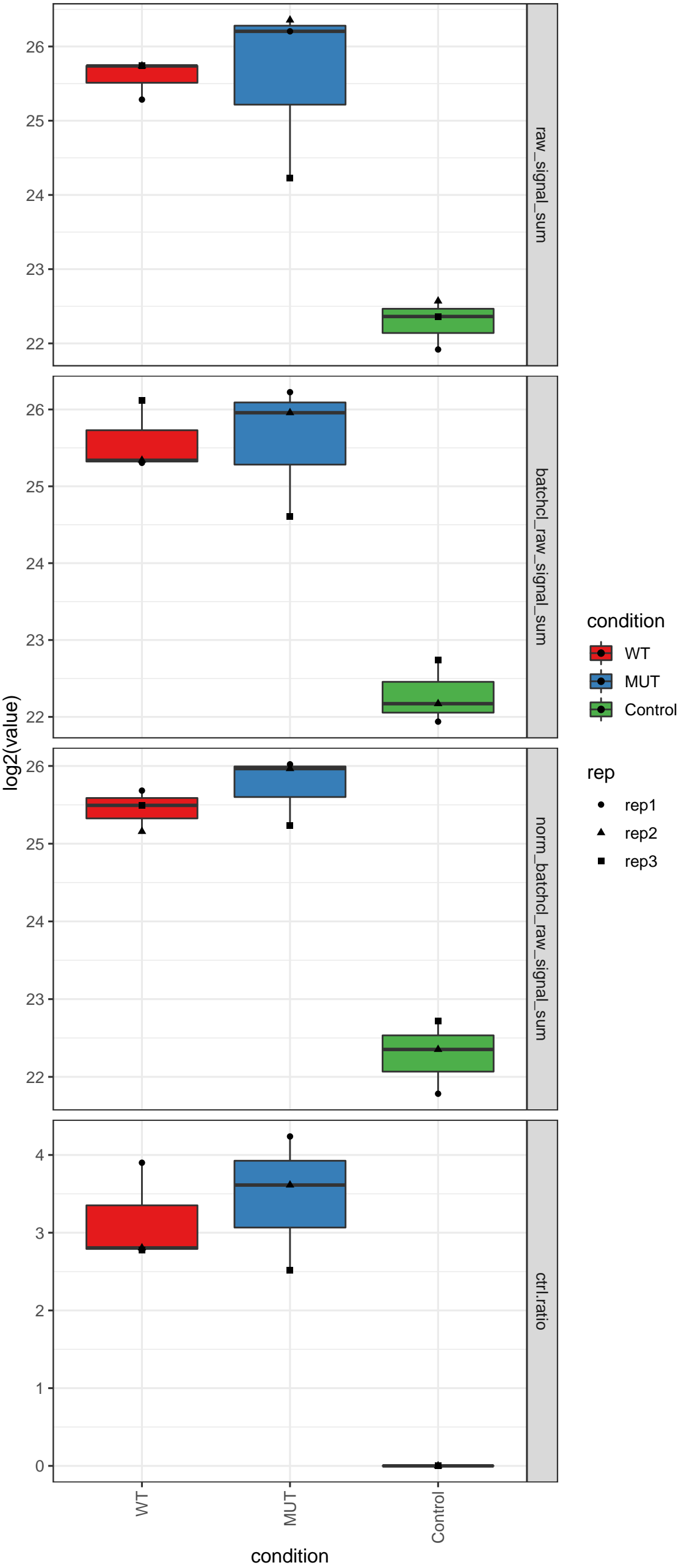


RPL26B – P53221

60S ribosomal protein L26–B OS=*Saccharomyces cerevisiae* (strain ATCC 25716)

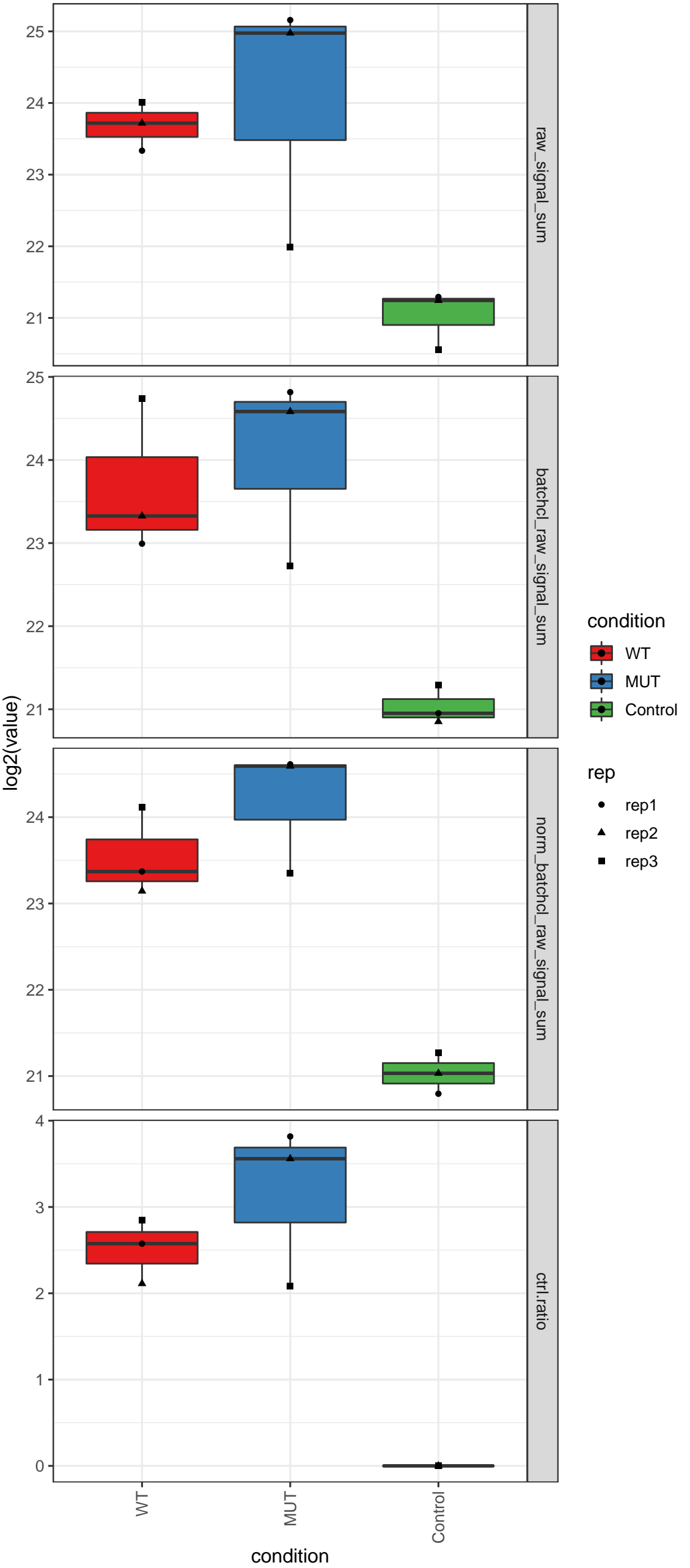


RPL27A|RPL27B – P0C2H6|P0C2H7
60S ribosomal protein L27-A OS=*Saccharomyces cerevisiae* (strain ATCC



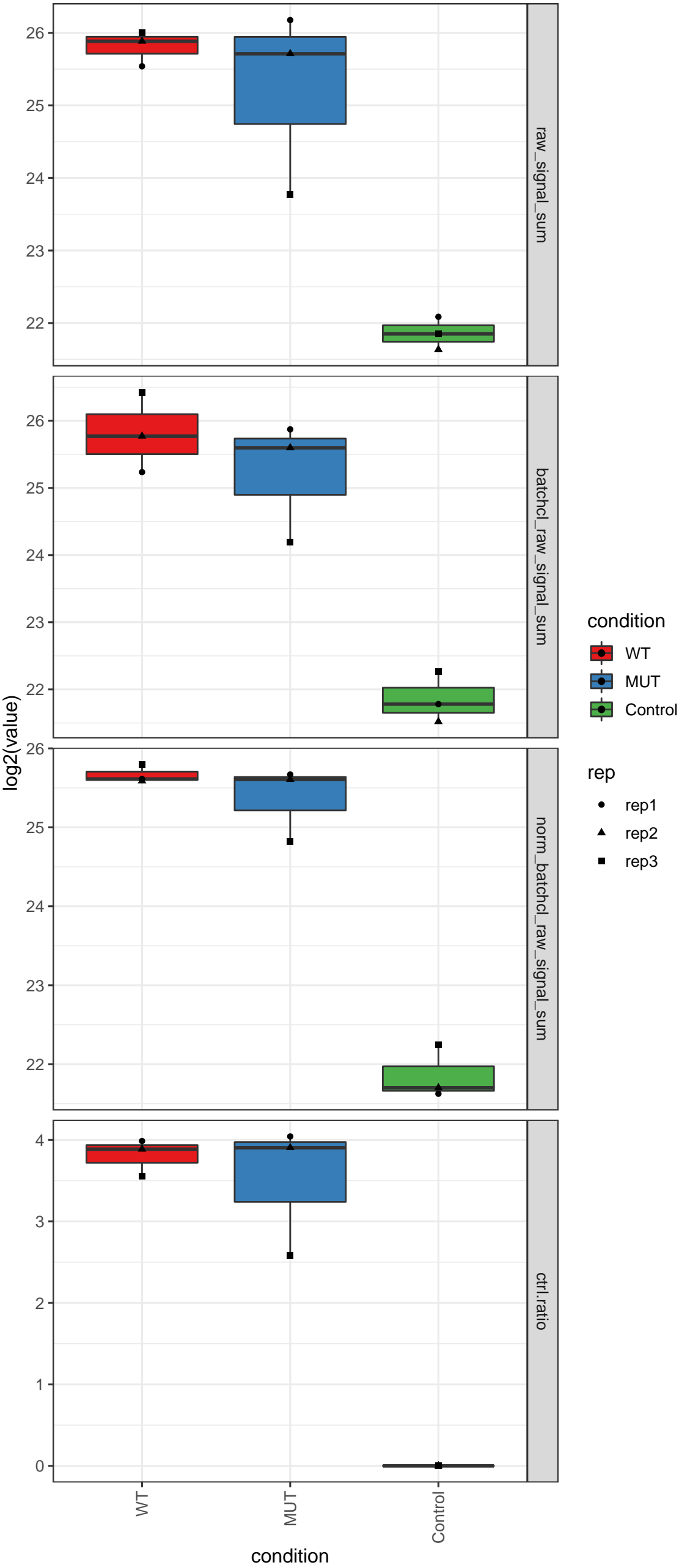
RPL28 – P02406

60S ribosomal protein L28 OS=Saccharomyces cerevisiae (strain ATCC 20



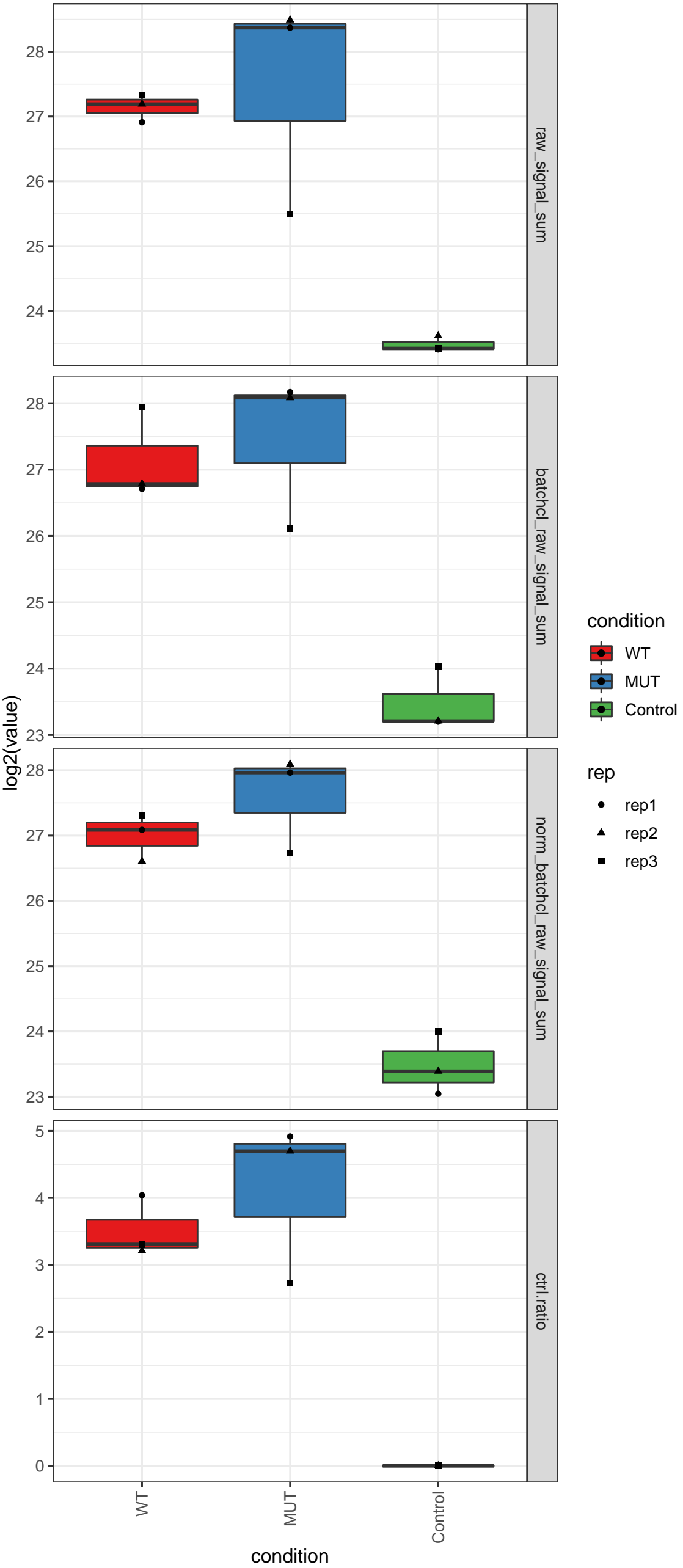
RPL29 – P05747

60S ribosomal protein L29 OS=*Saccharomyces cerevisiae* (strain ATCC 20454)



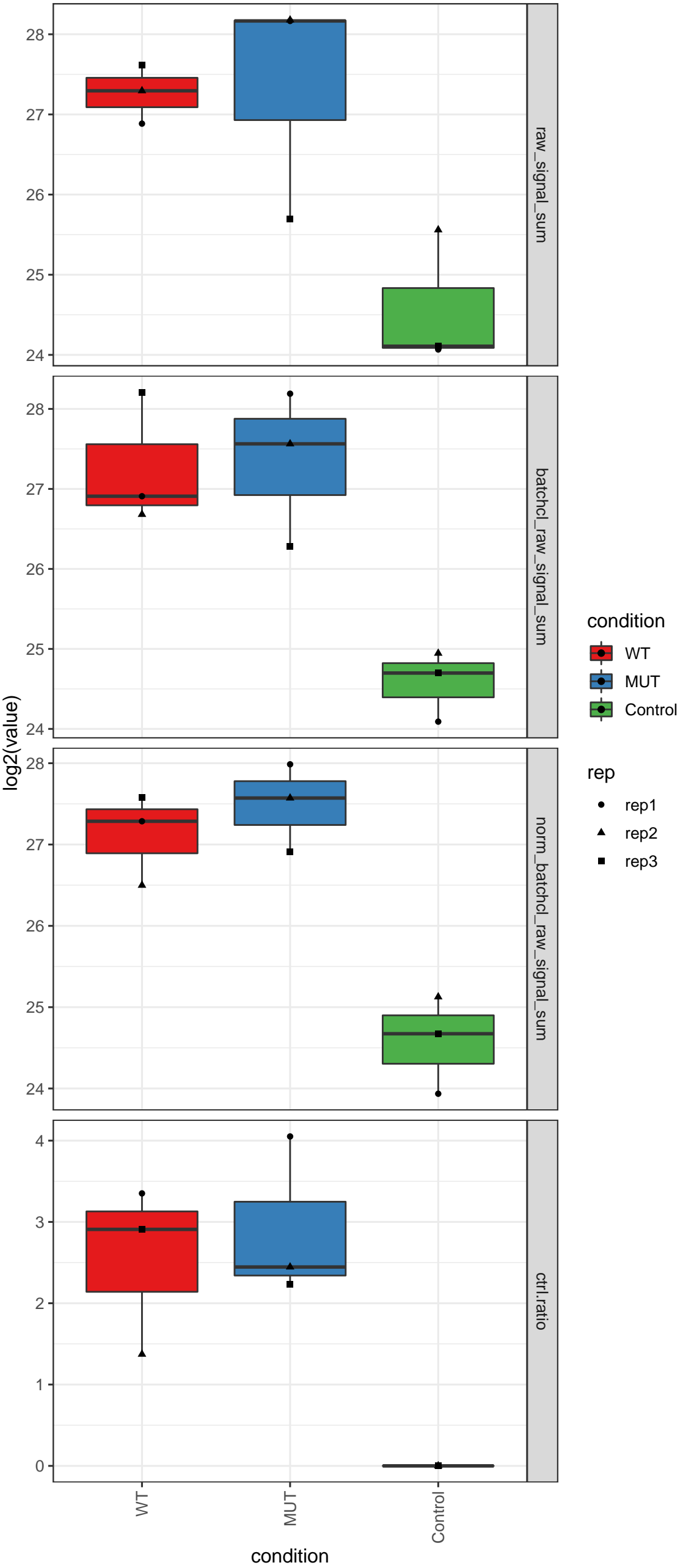
RPL2A|RPL2B – P0CX45|P0CX46

60S ribosomal protein L2–A OS=Saccharomyces cerevisiae (strain ATCC 2



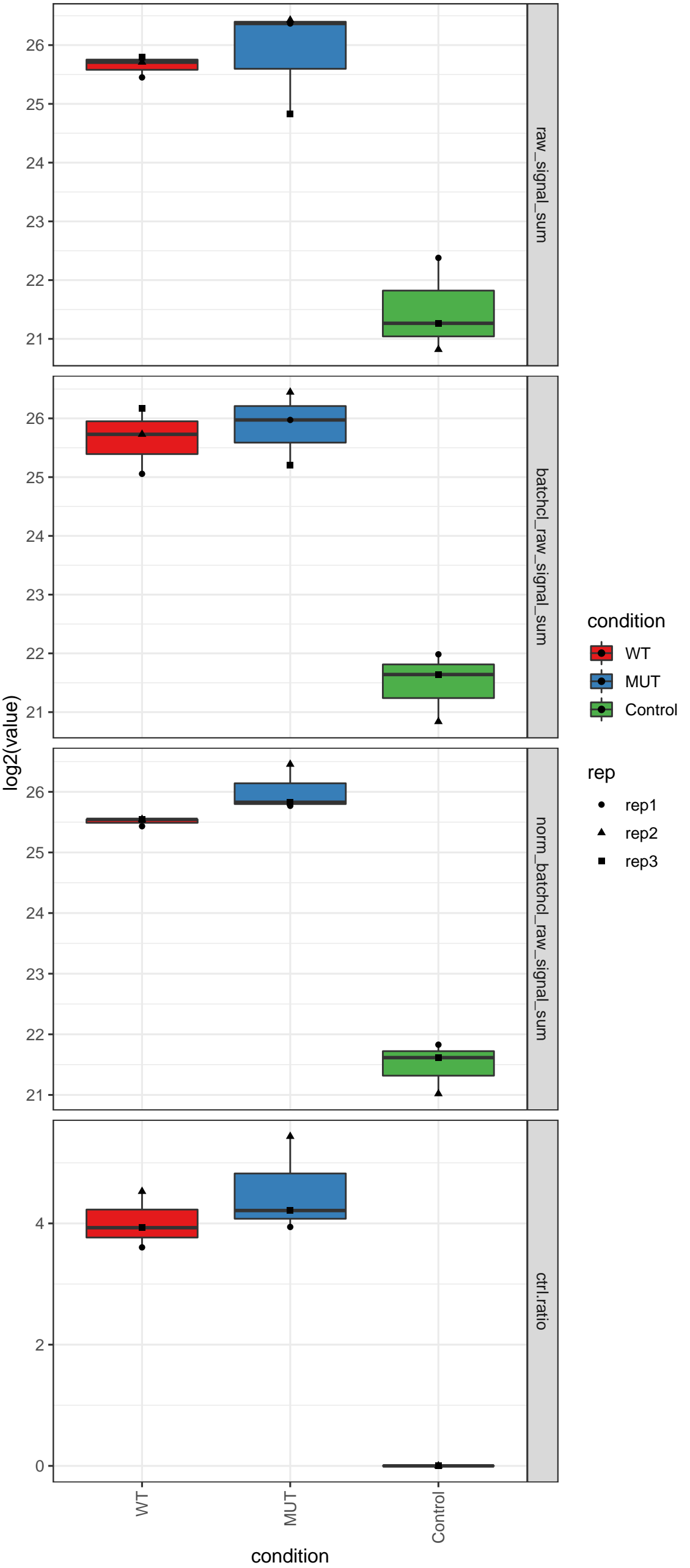
RPL3 – P14126

60S ribosomal protein L3 OS=*Saccharomyces cerevisiae* (strain ATCC 204



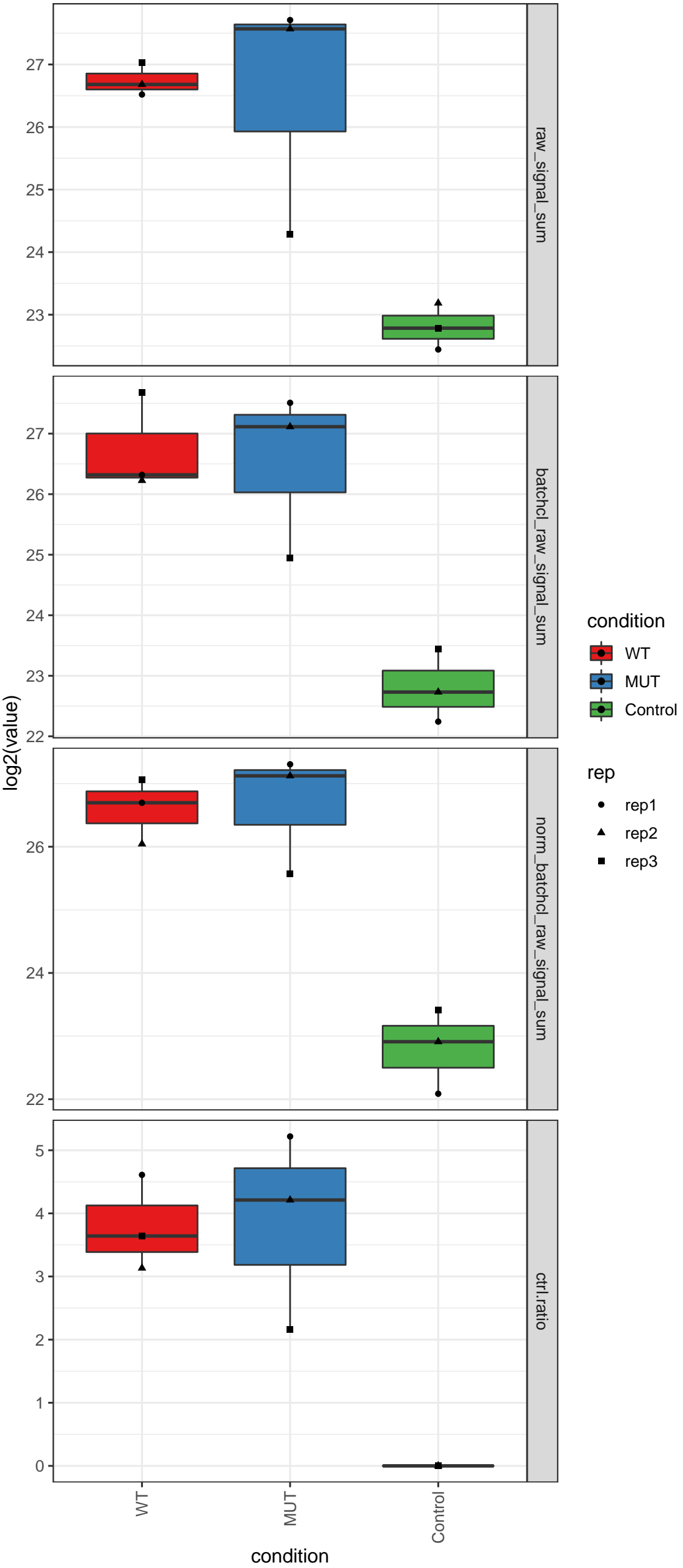
RPL30 – P14120

60S ribosomal protein L30 OS=*Saccharomyces cerevisiae* (strain ATCC 20454)



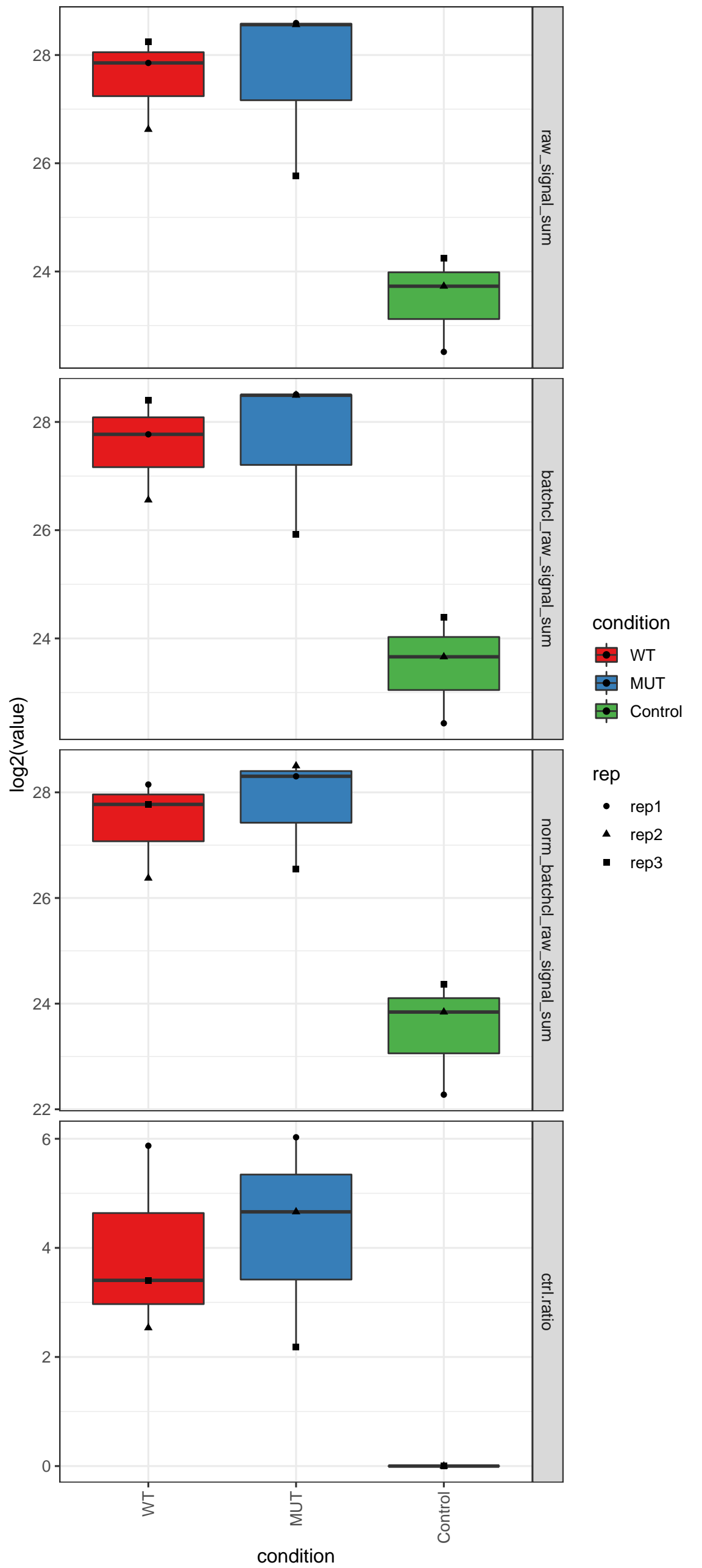
RPL32 – P38061

60S ribosomal protein L32 OS=*Saccharomyces cerevisiae* (strain ATCC 20454)



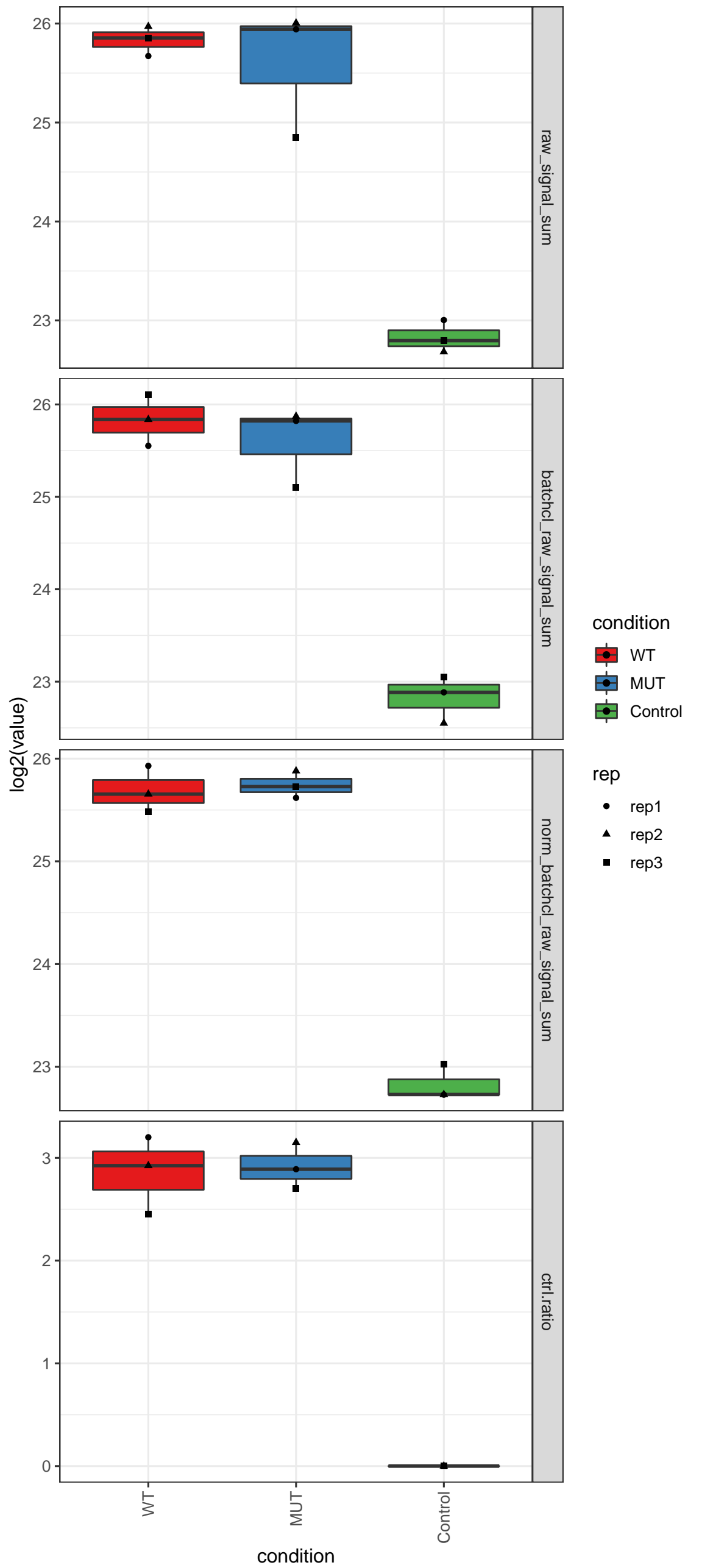
RPL34B|RPL34A – P40525|P87262

60S ribosomal protein L34–B OS=Saccharomyces cerevisiae (strain ATCC



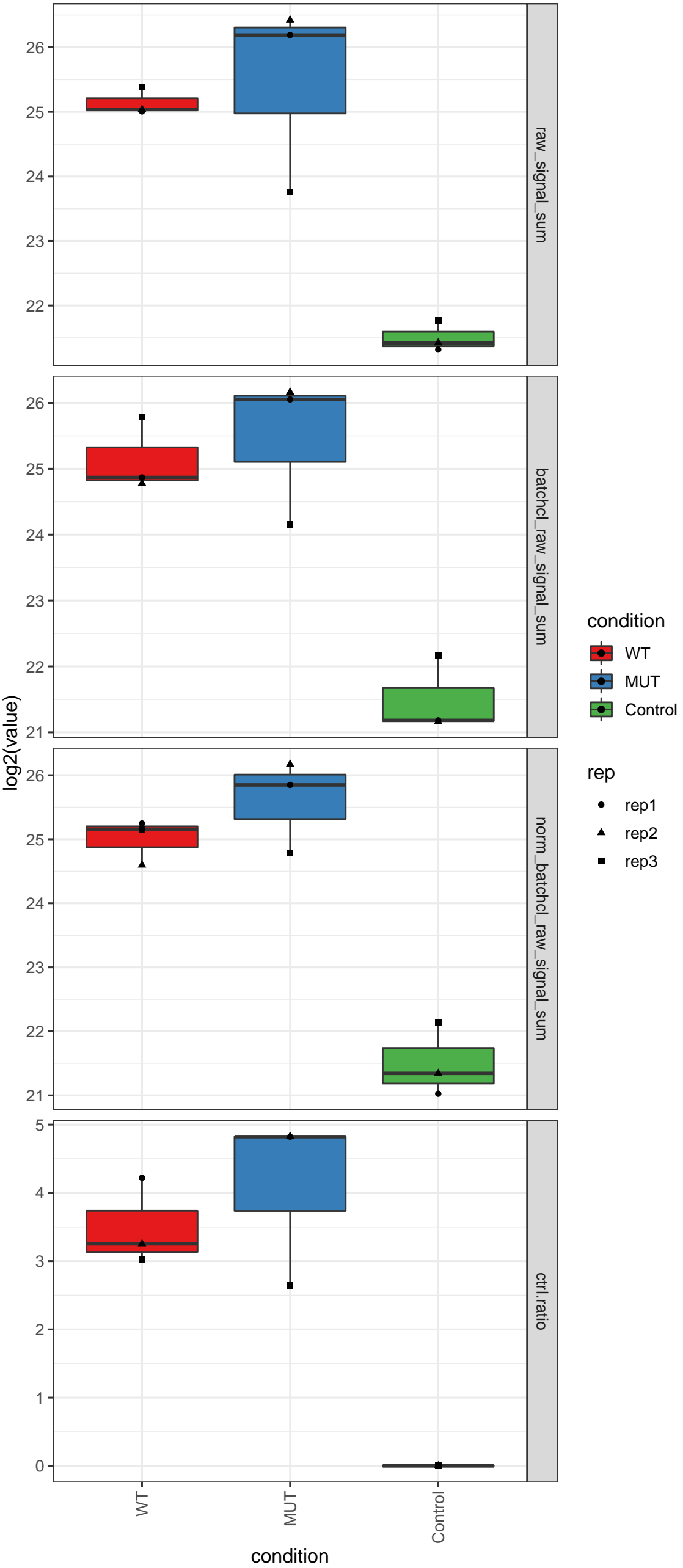
RPL35A|RPL35B – P0CX84|P0CX85

60S ribosomal protein L35–A OS=Saccharomyces cerevisiae (strain ATCC



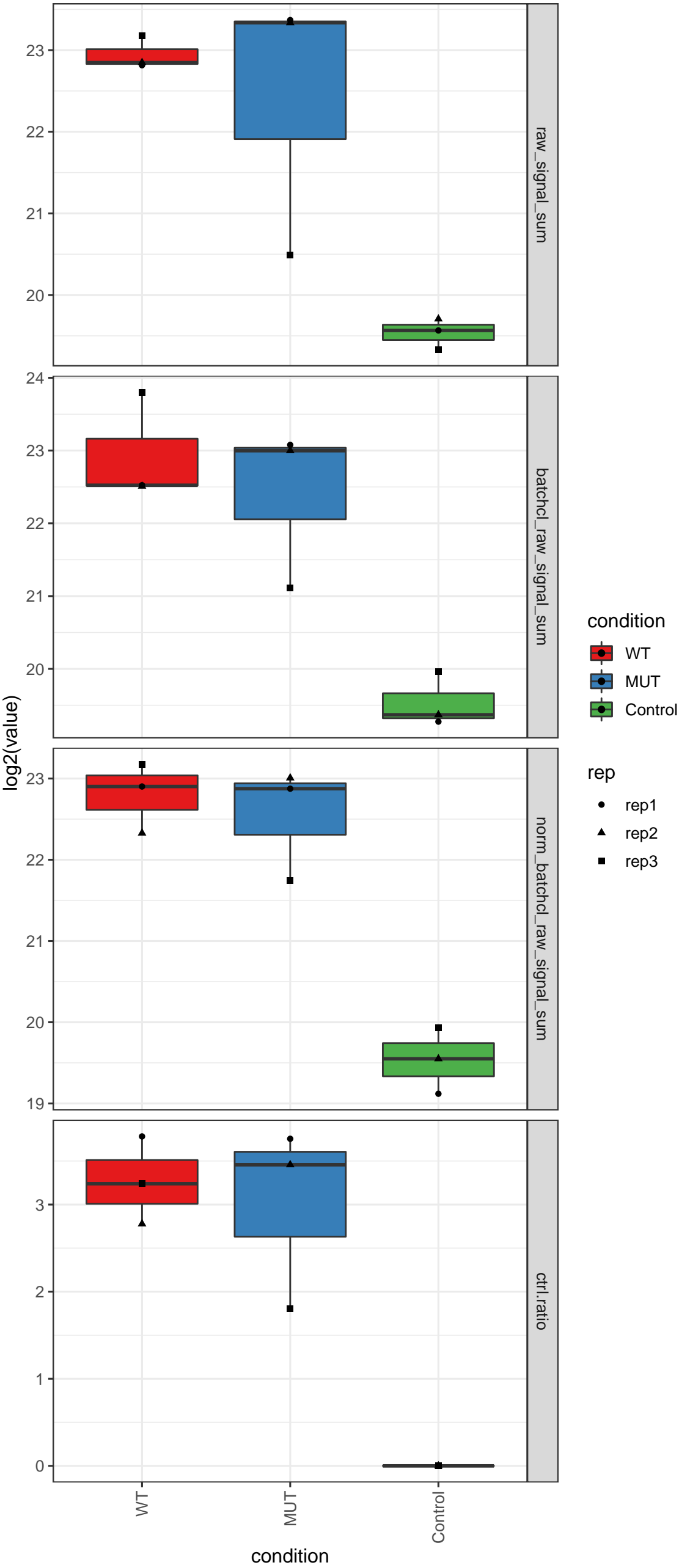
RPL36B – O14455

60S ribosomal protein L36–B OS=Saccharomyces cerevisiae (strain ATCC



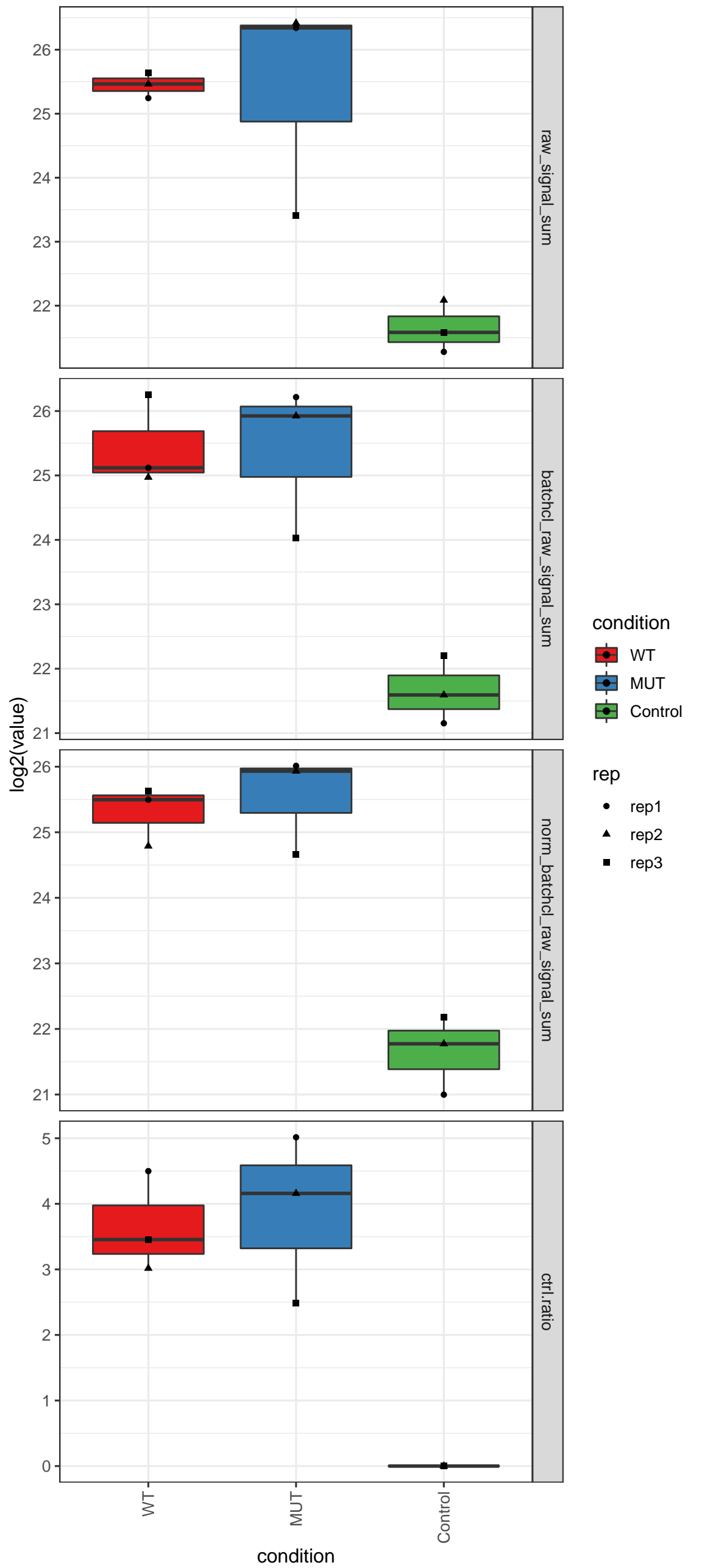
RPL37A – P49166

60S ribosomal protein L37–A OS=Saccharomyces cerevisiae (strain ATCC

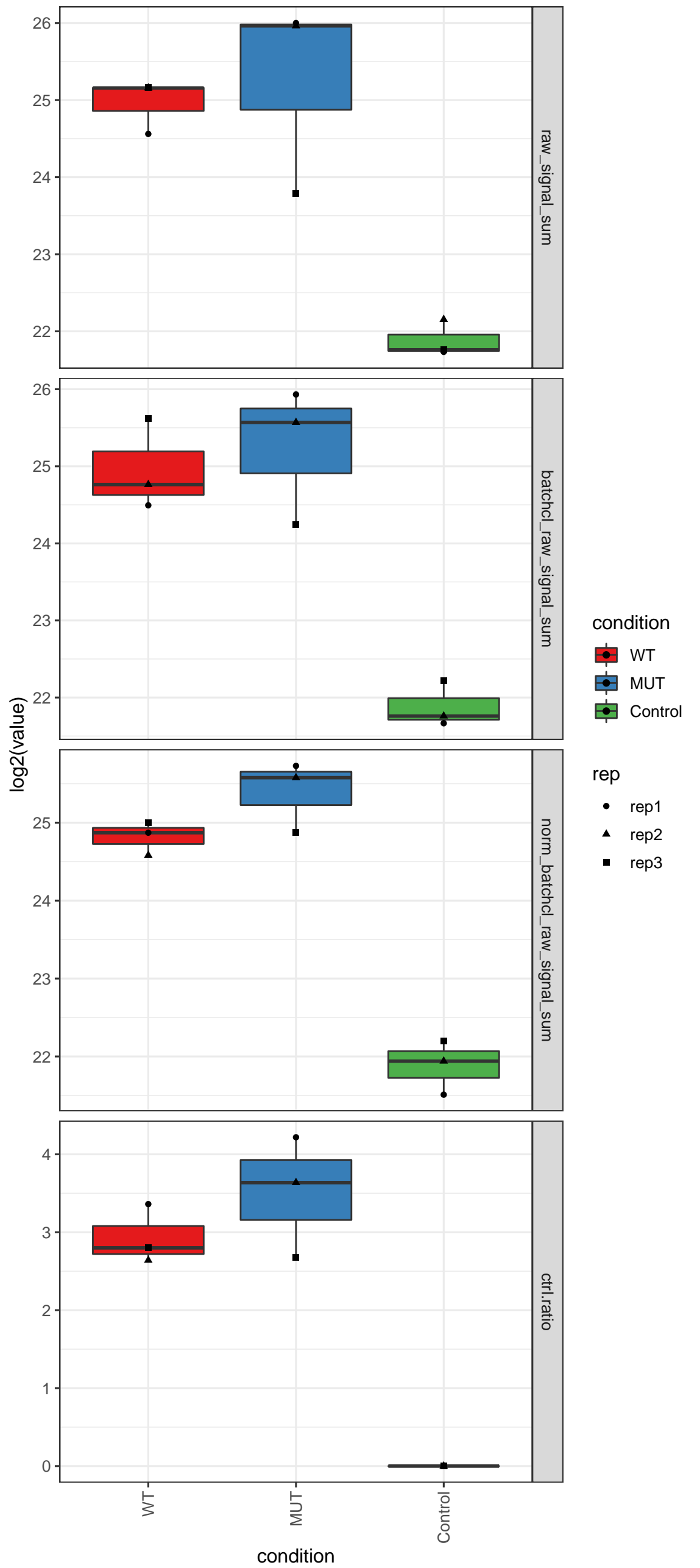


RPL42A|RPL42B – P0CX27|P0CX28

60S ribosomal protein L42–A OS=*Saccharomyces cerevisiae* (strain ATCC

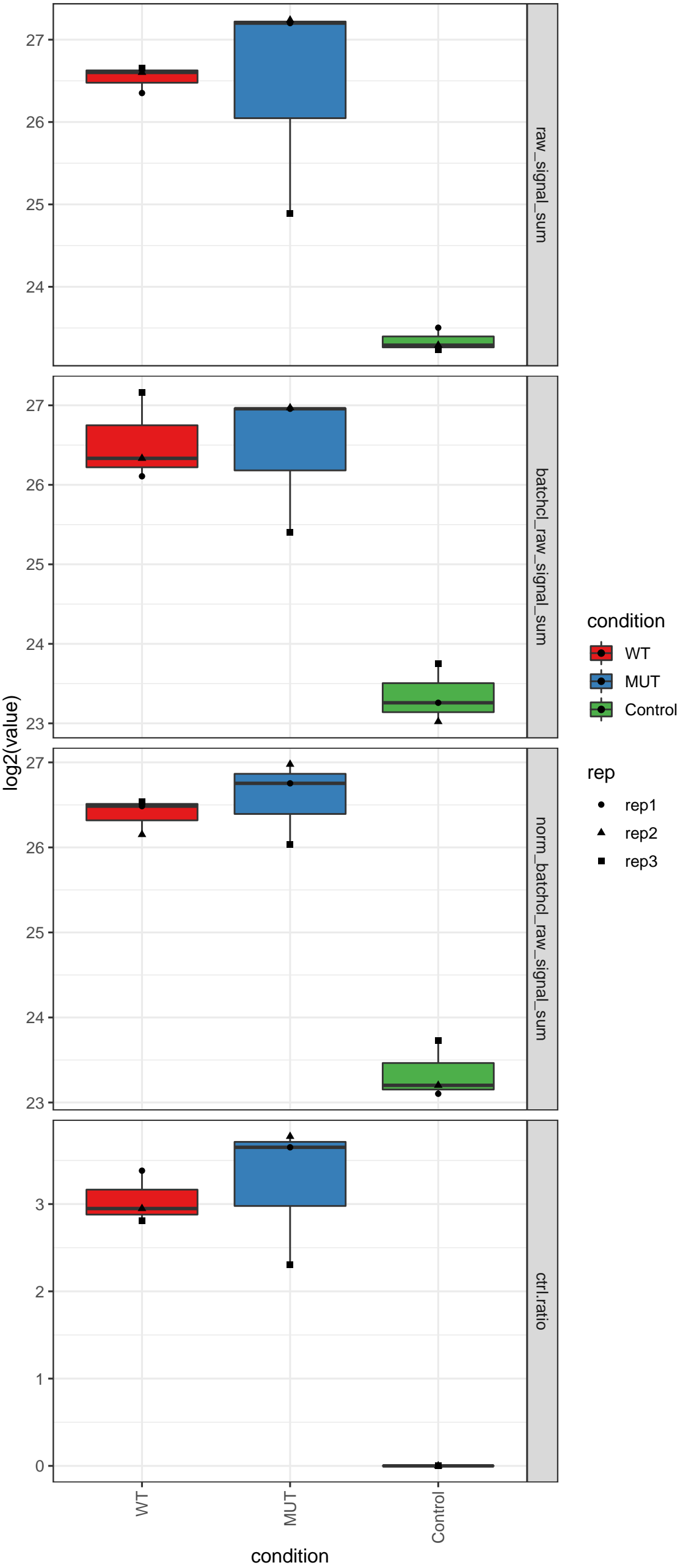


RPL43A|RPL43B – P0CX25|P0CX26
60S ribosomal protein L43–A OS=Saccharomyces cerevisiae (strain ATCC



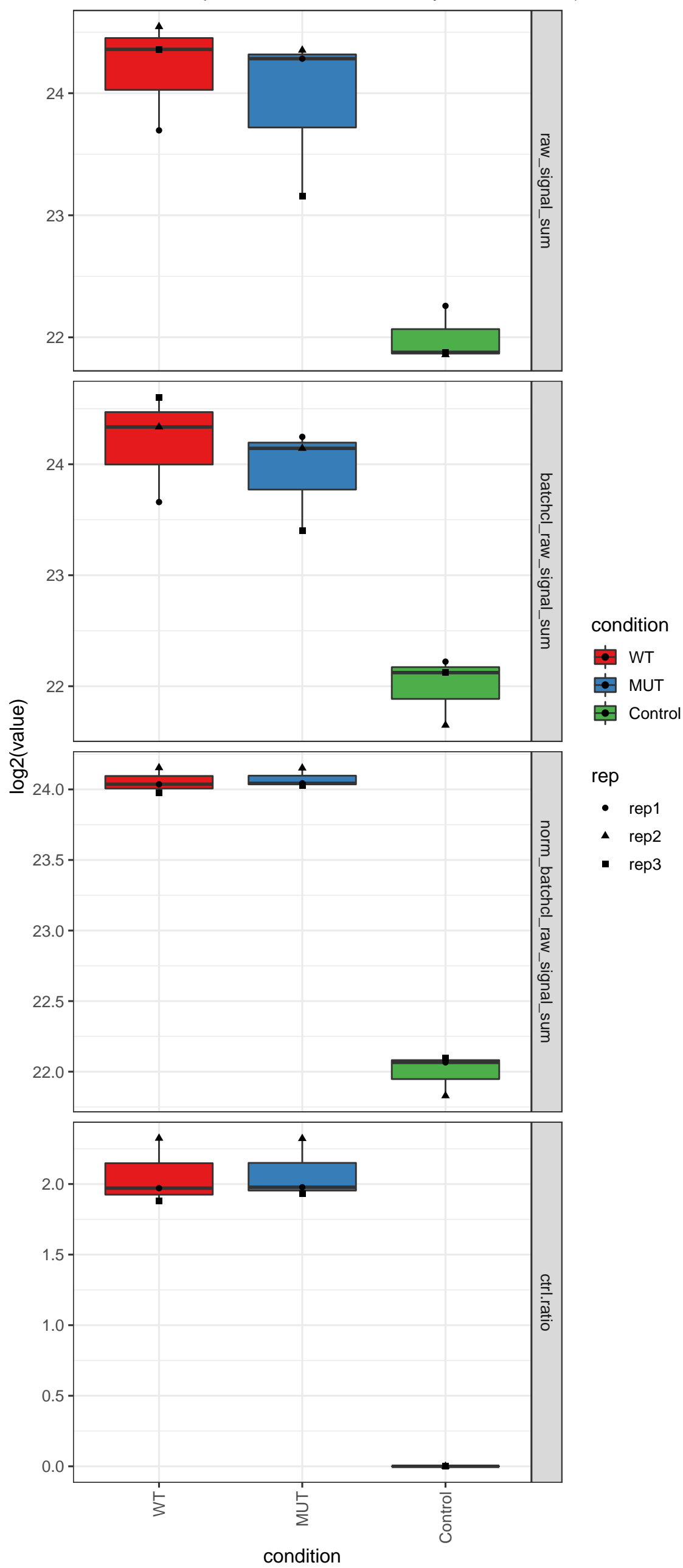
RPL4A – P10664

60S ribosomal protein L4–A OS=Saccharomyces cerevisiae (strain ATCC 2



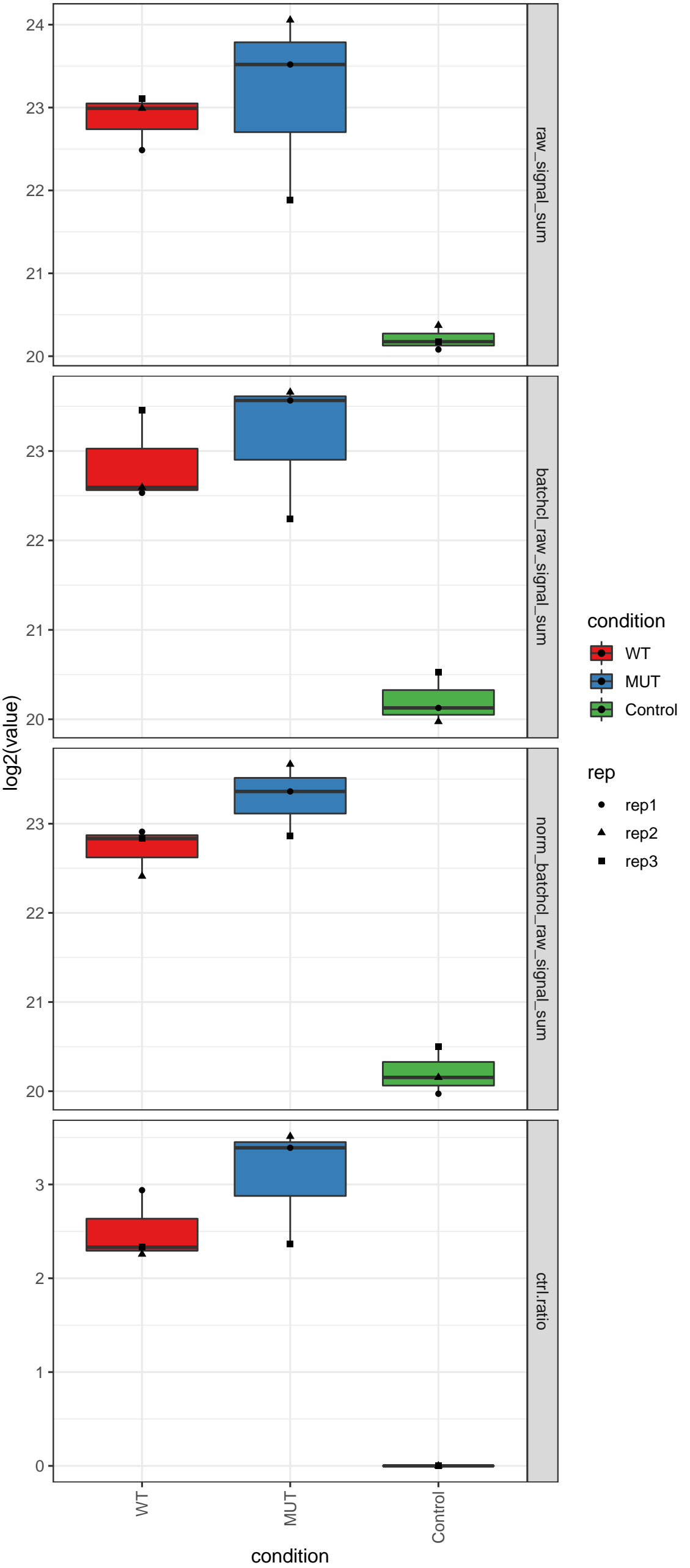
RPL5 – P26321

60S ribosomal protein L5 OS=*Saccharomyces cerevisiae* (strain ATCC 20454)



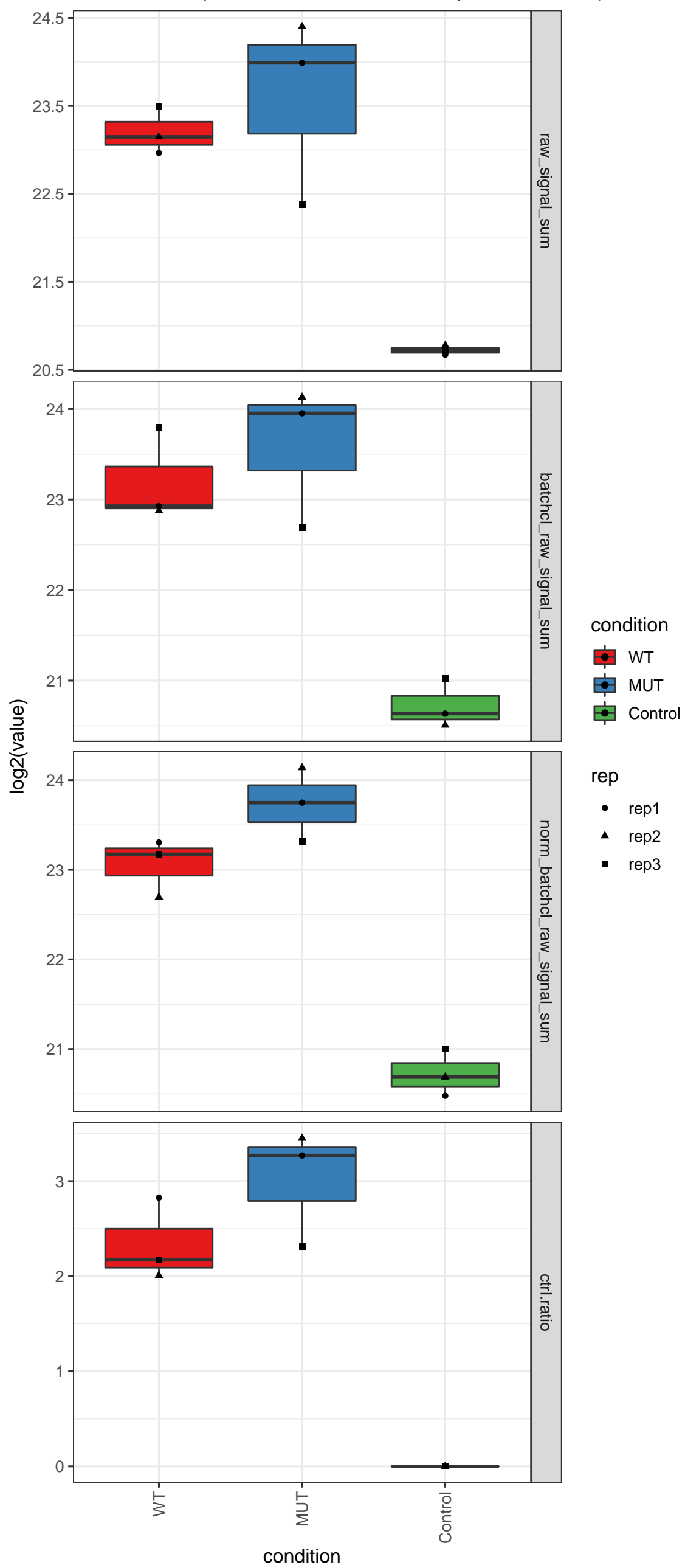
RPL6A – Q02326

60S ribosomal protein L6–A OS=Saccharomyces cerevisiae (strain ATCC 2



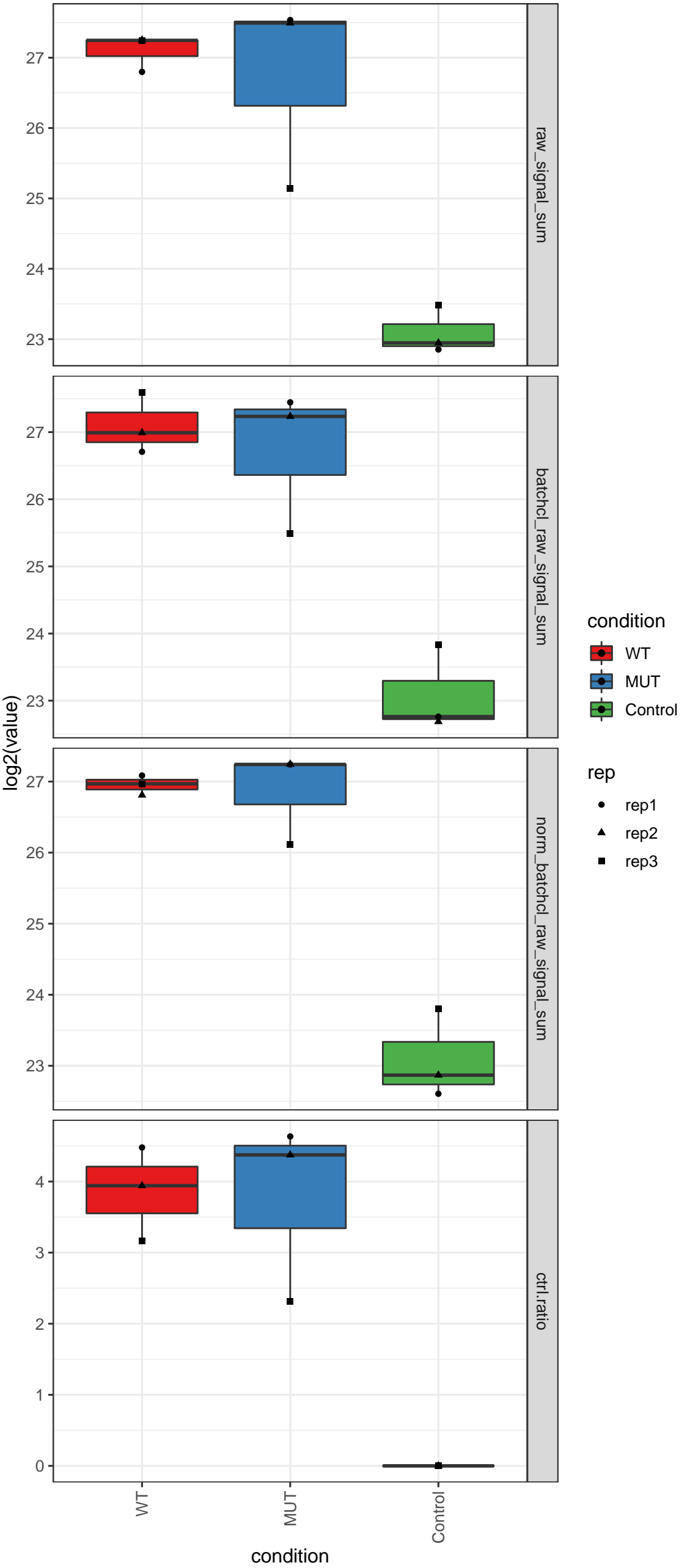
RPL6B – P05739

60S ribosomal protein L6–B OS=Saccharomyces cerevisiae (strain ATCC



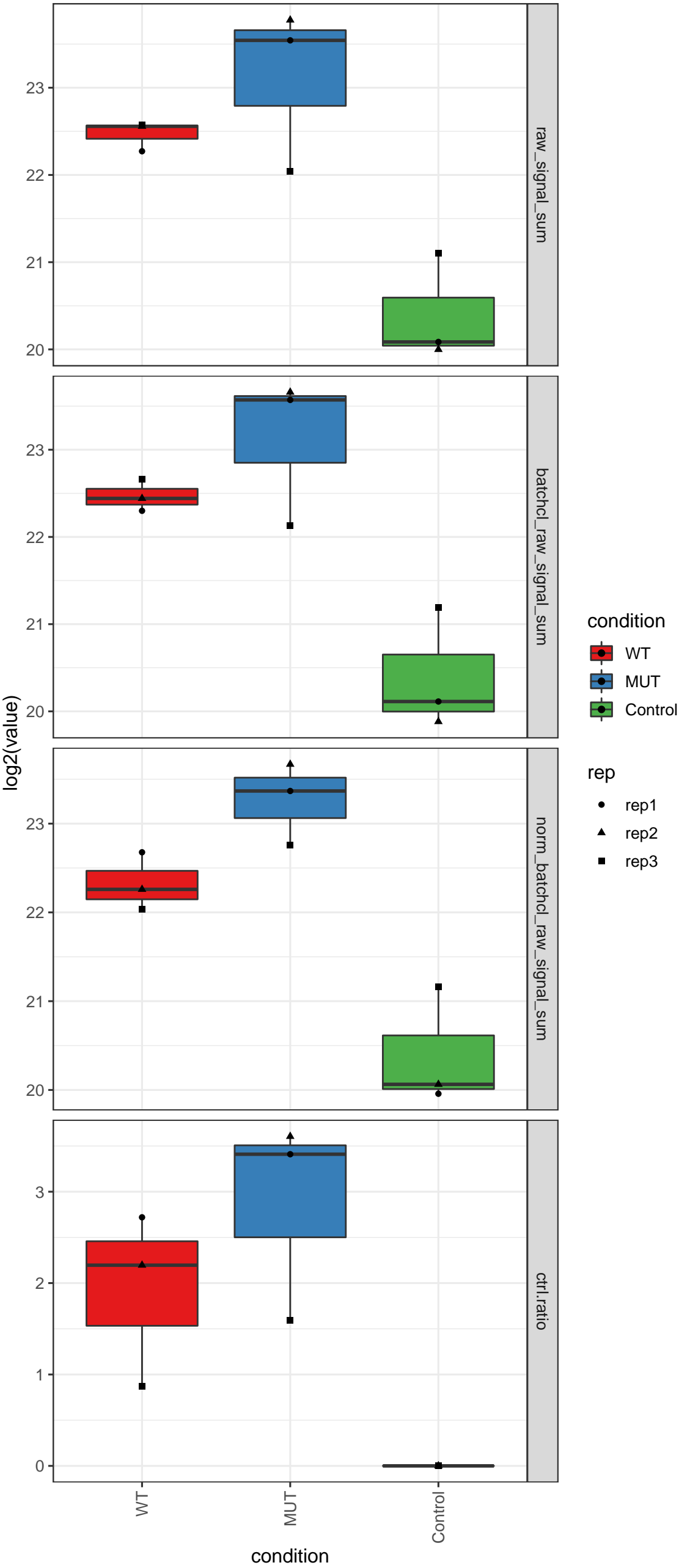
RPL7A – P05737

60S ribosomal protein L7–A OS=Saccharomyces cerevisiae (strain ATCC 2



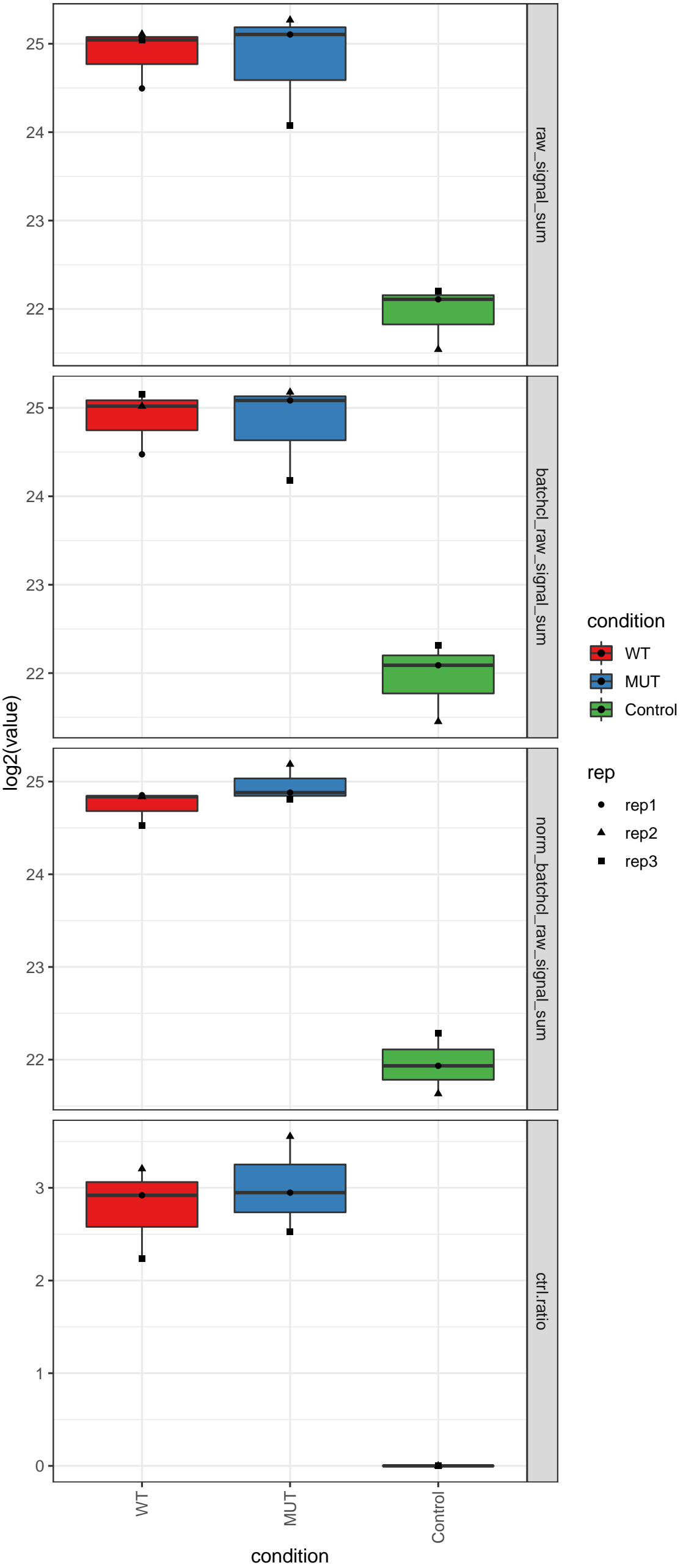
RPL8A – P17076

60S ribosomal protein L8–A OS=Saccharomyces cerevisiae (strain ATCC 2



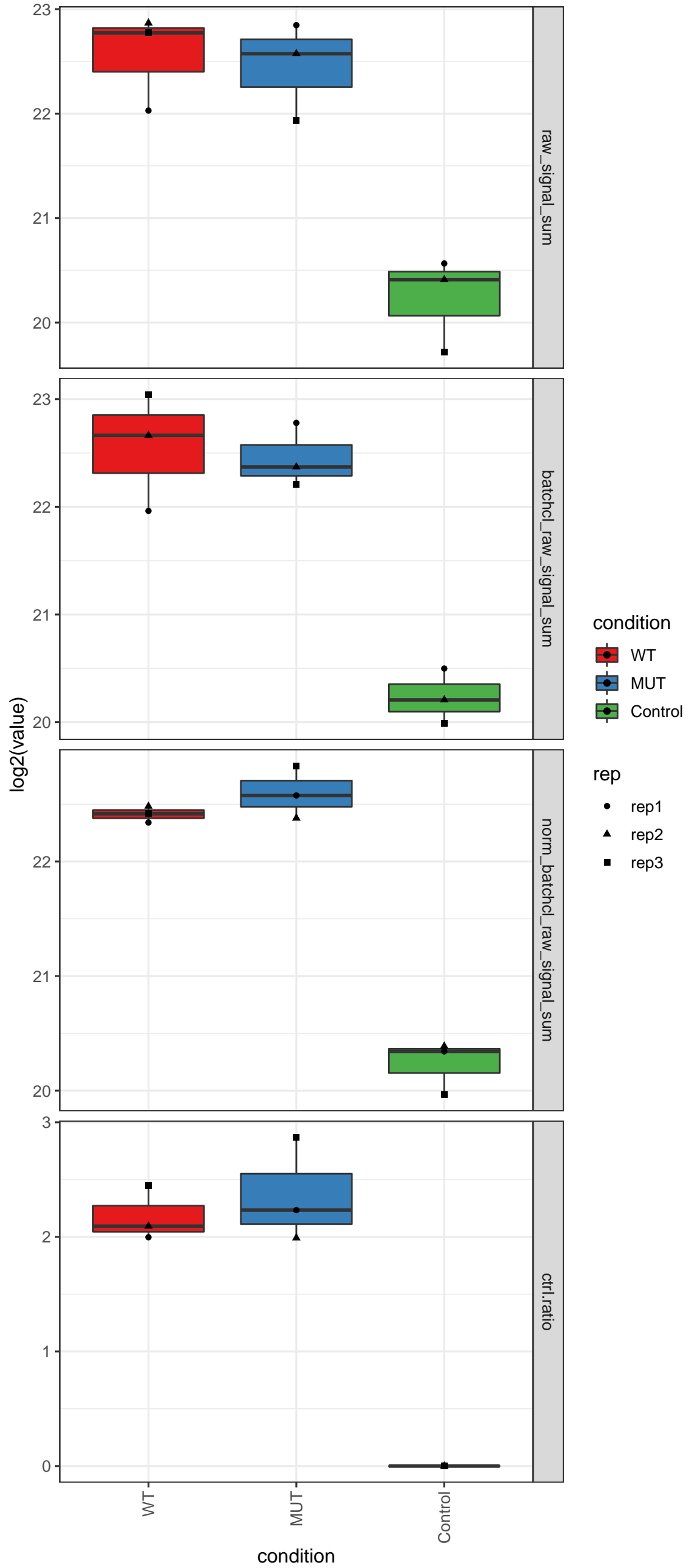
RPL9B – P51401

60S ribosomal protein L9–B OS=Saccharomyces cerevisiae (strain ATCC 2



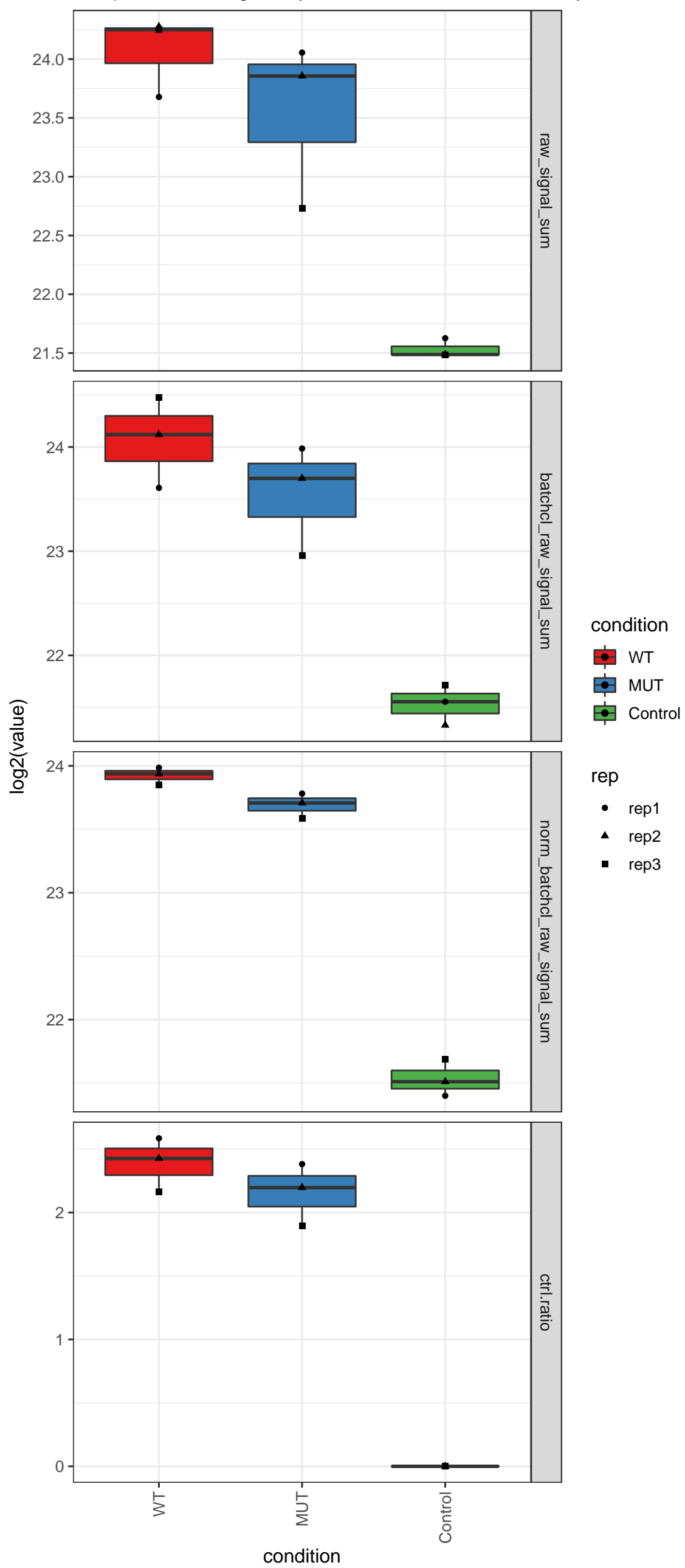
RPN1 – P38764

26S proteasome regulatory subunit RPN1 OS=*Saccharomyces cerevisiae*



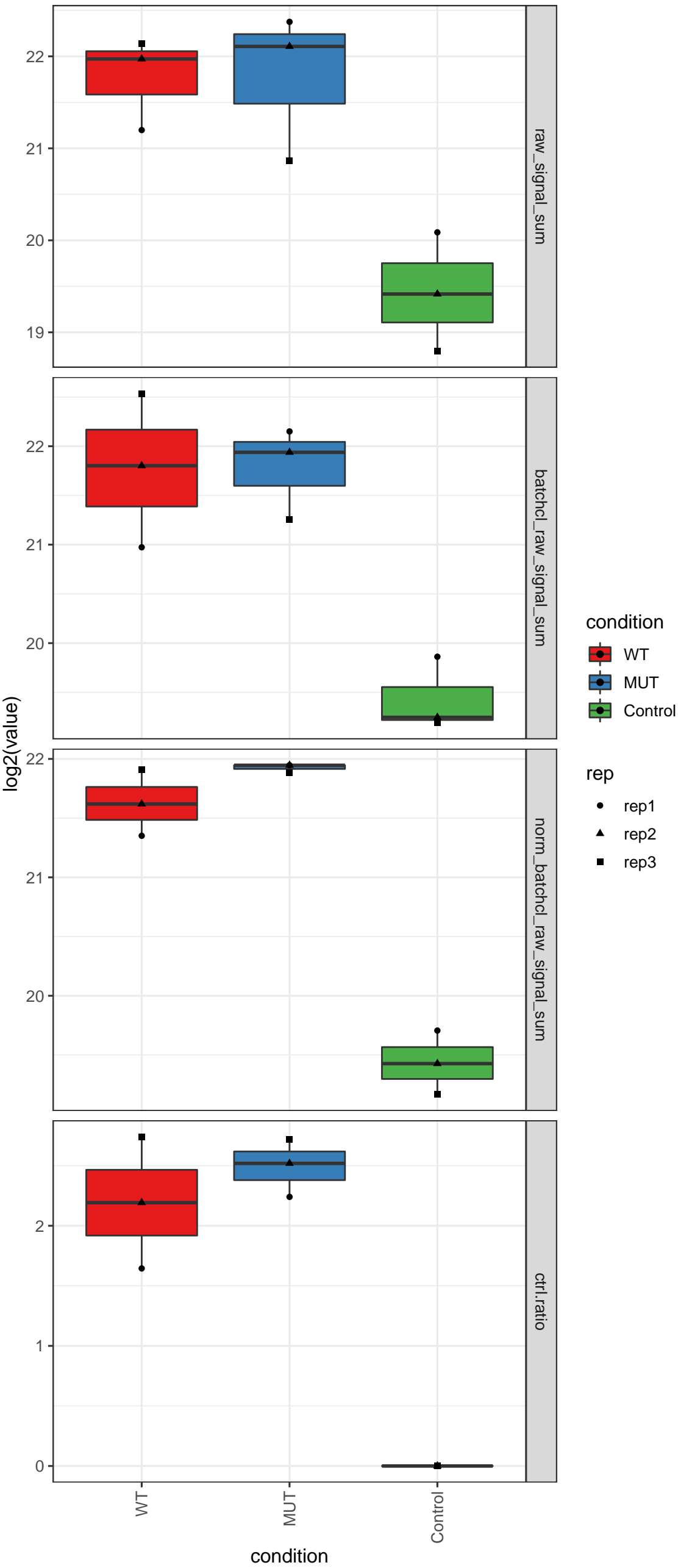
RPN2 – P32565

26S proteasome regulatory subunit RPN2 OS=*Saccharomyces cerevisiae*



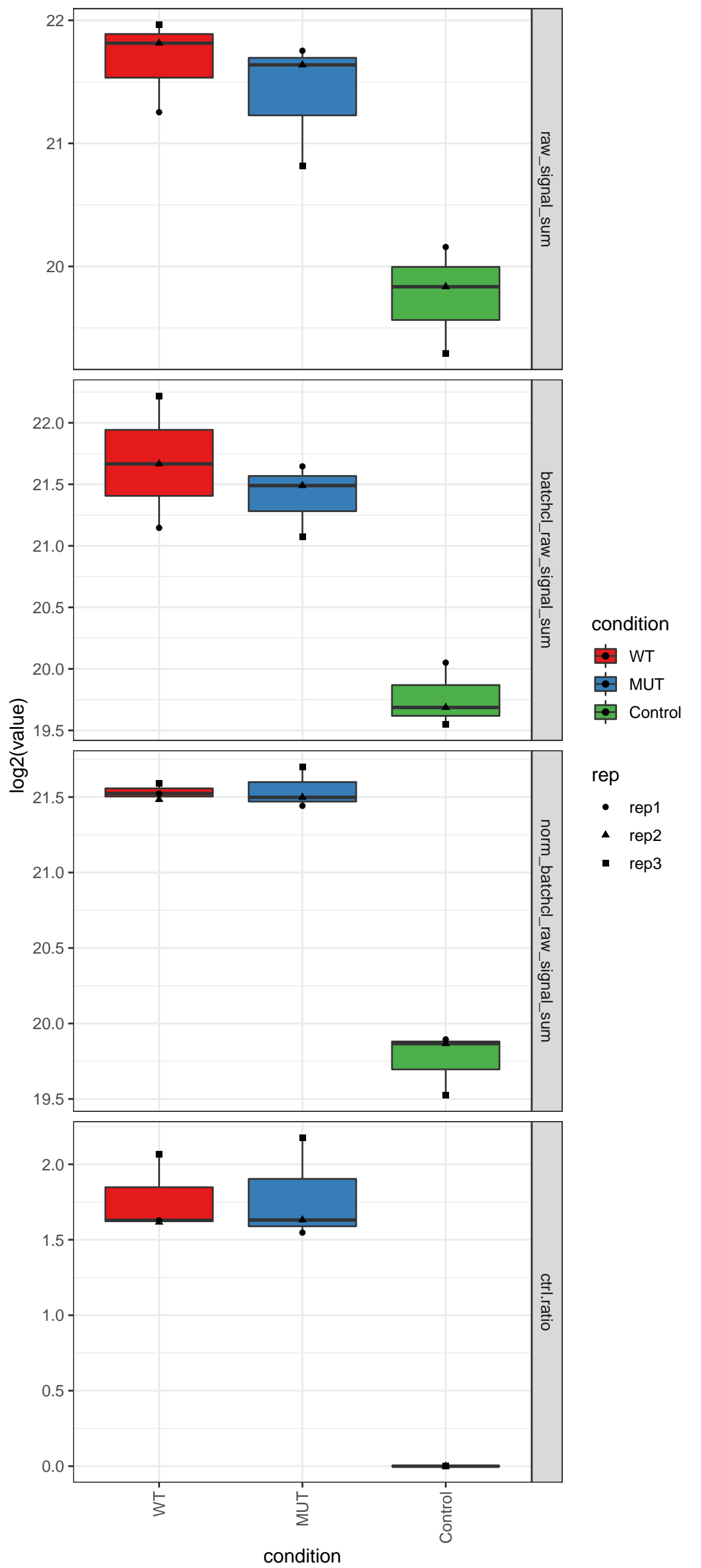
RPN3 – P40016

26S proteasome regulatory subunit RPN3 OS=*Saccharomyces cerevisiae*



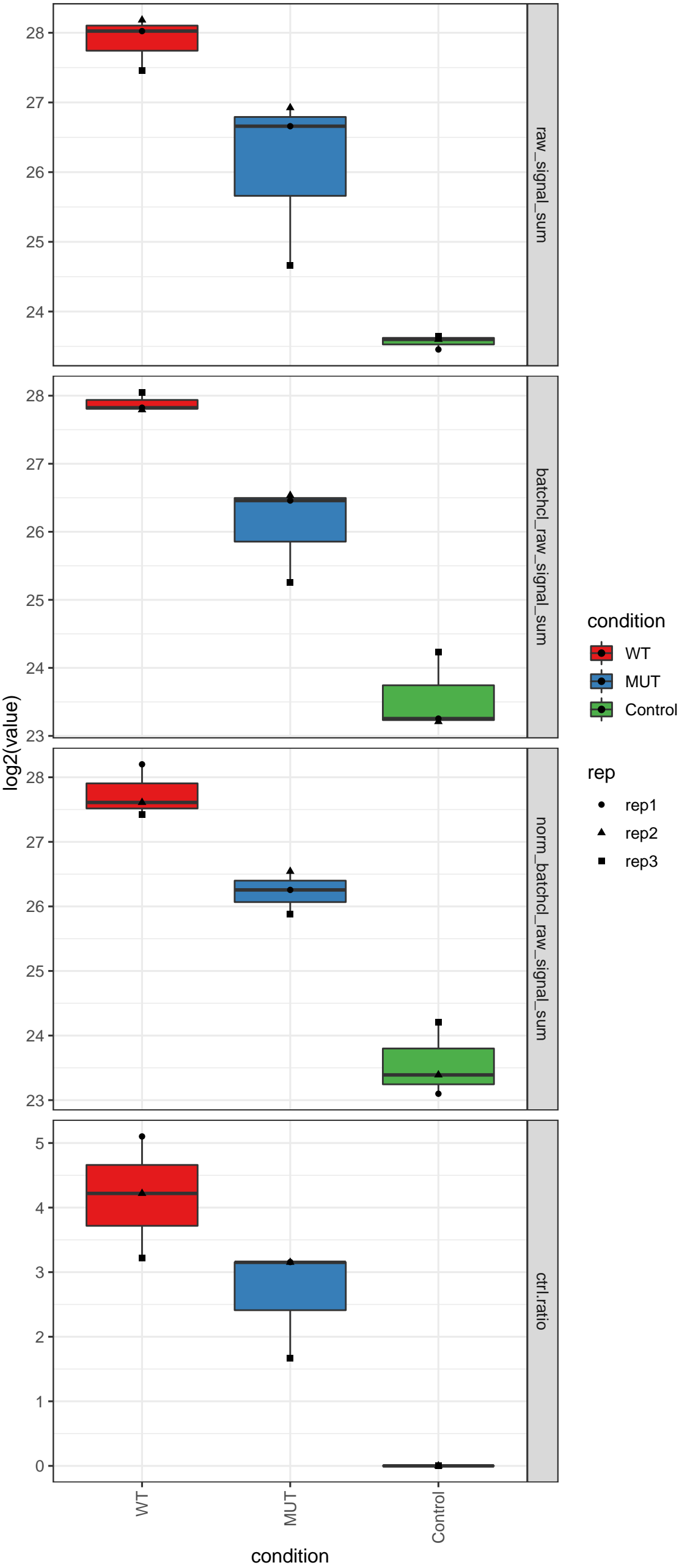
RPN6 – Q12377

26S proteasome regulatory subunit RPN6 OS=*Saccharomyces cerevisiae*



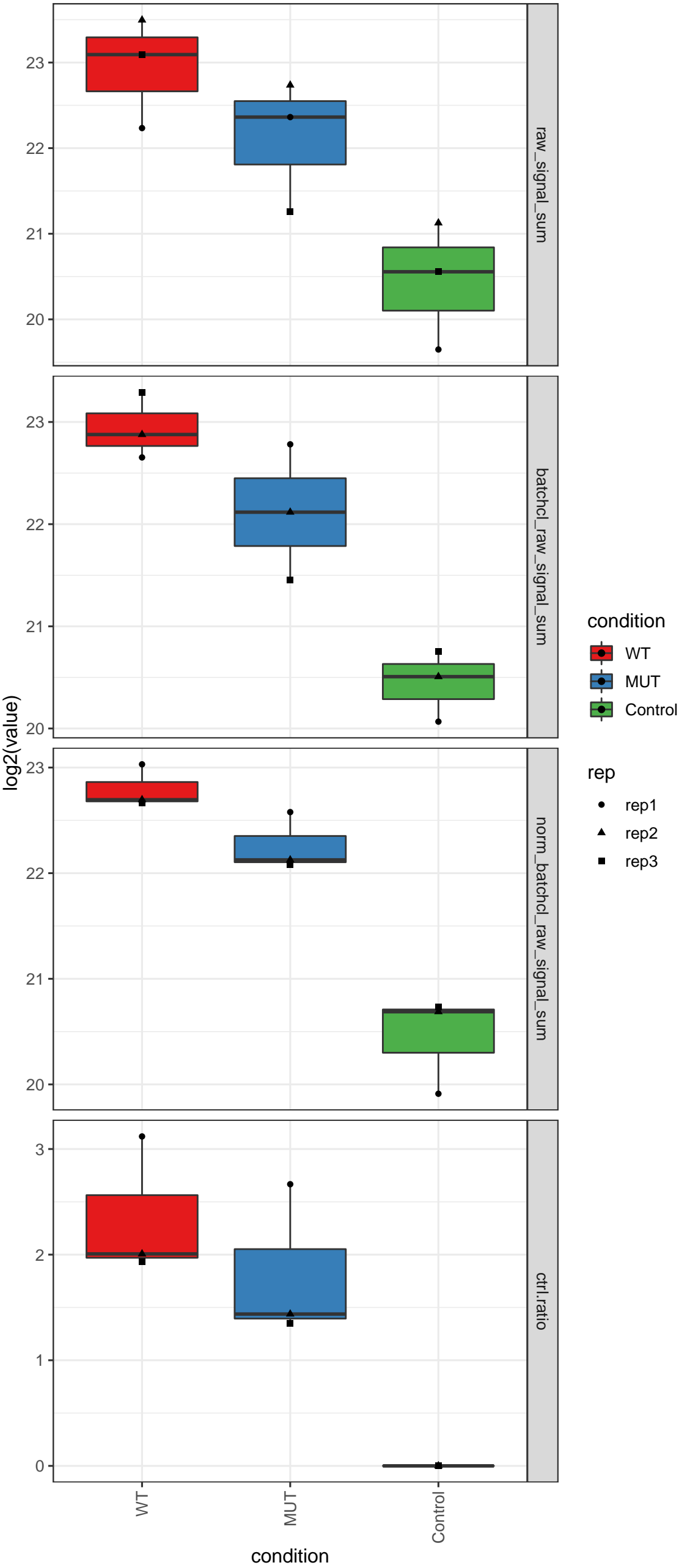
RPO21 – P04050

DNA-directed RNA polymerase II subunit RPB1 OS=*Saccharomyces cere*



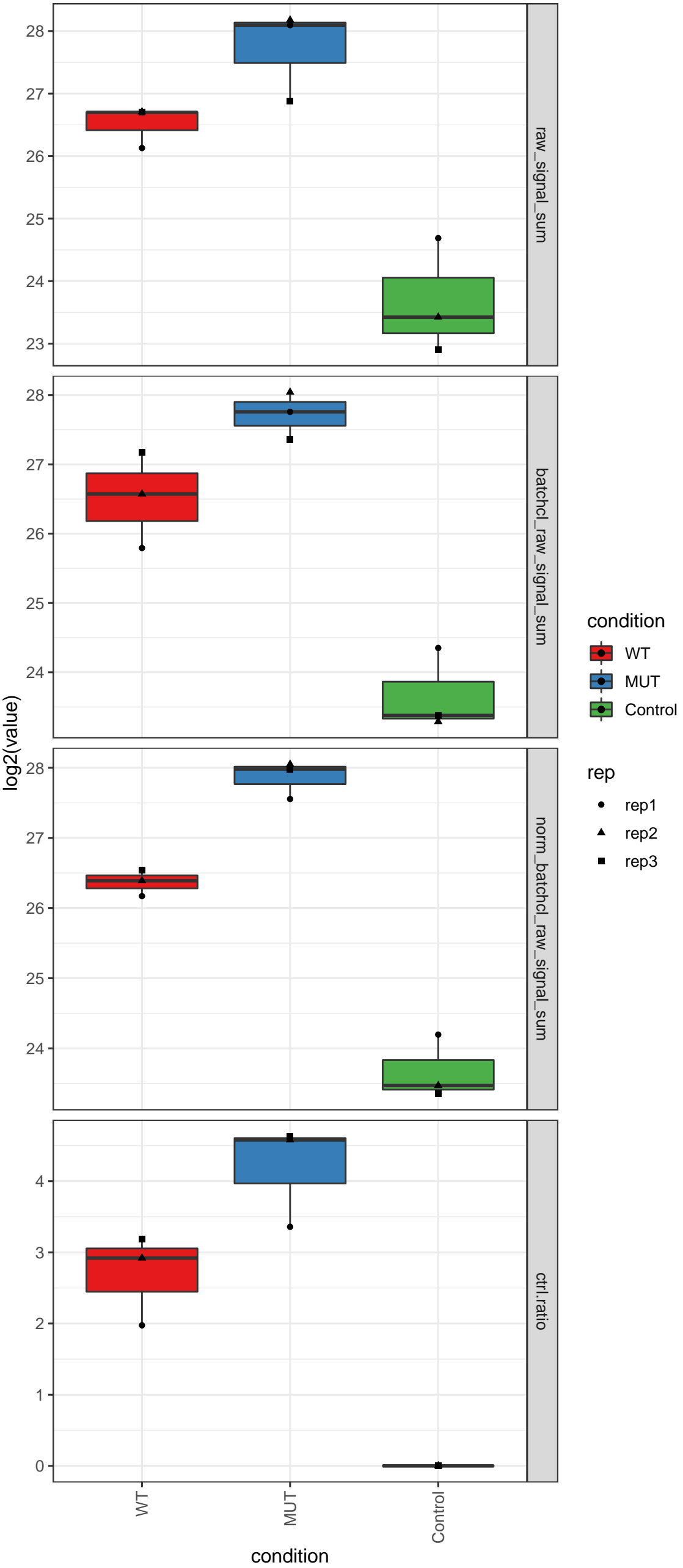
RPO31 – P04051

DNA-directed RNA polymerase III subunit RPC1 OS=*Saccharomyces cerevisiae*



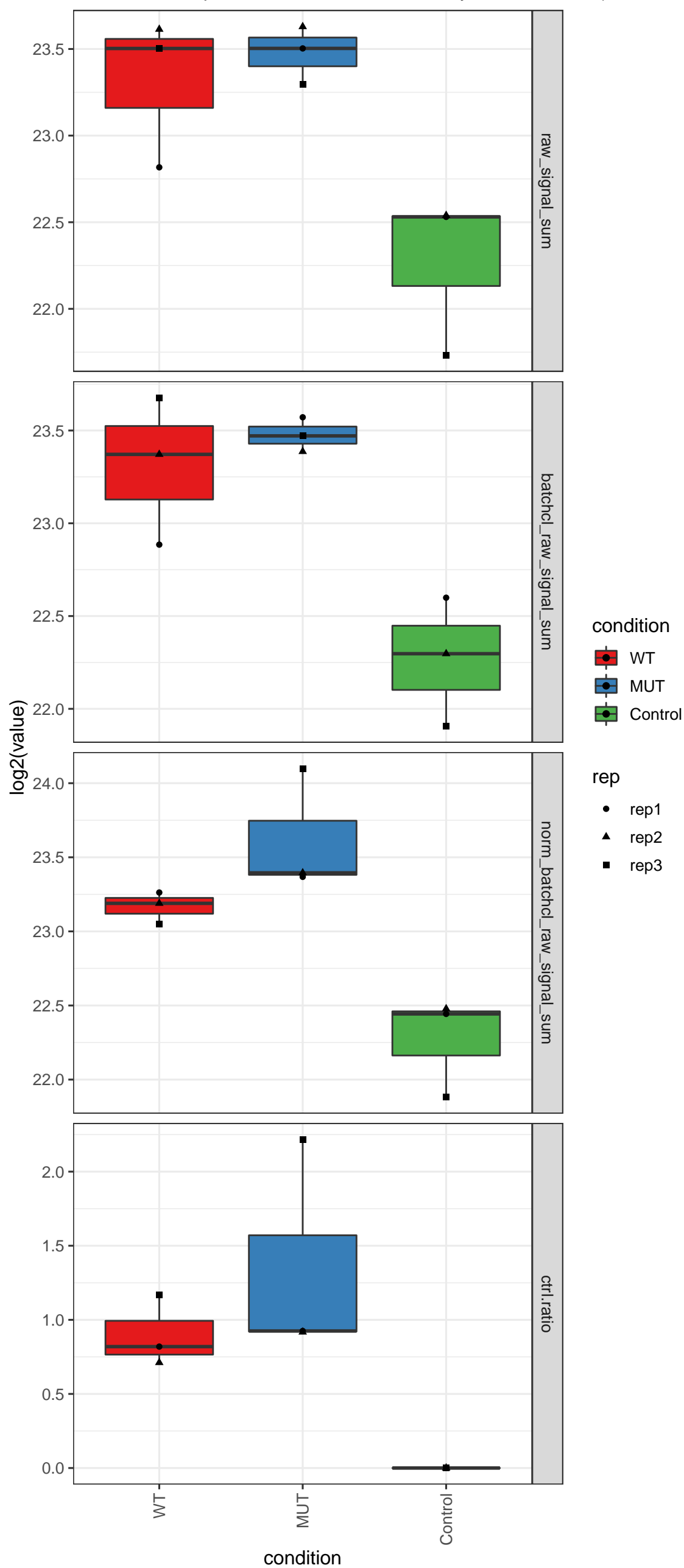
RPP0 – P05317

60S acidic ribosomal protein P0 OS=*Saccharomyces cerevisiae* (strain ATCC 25716)



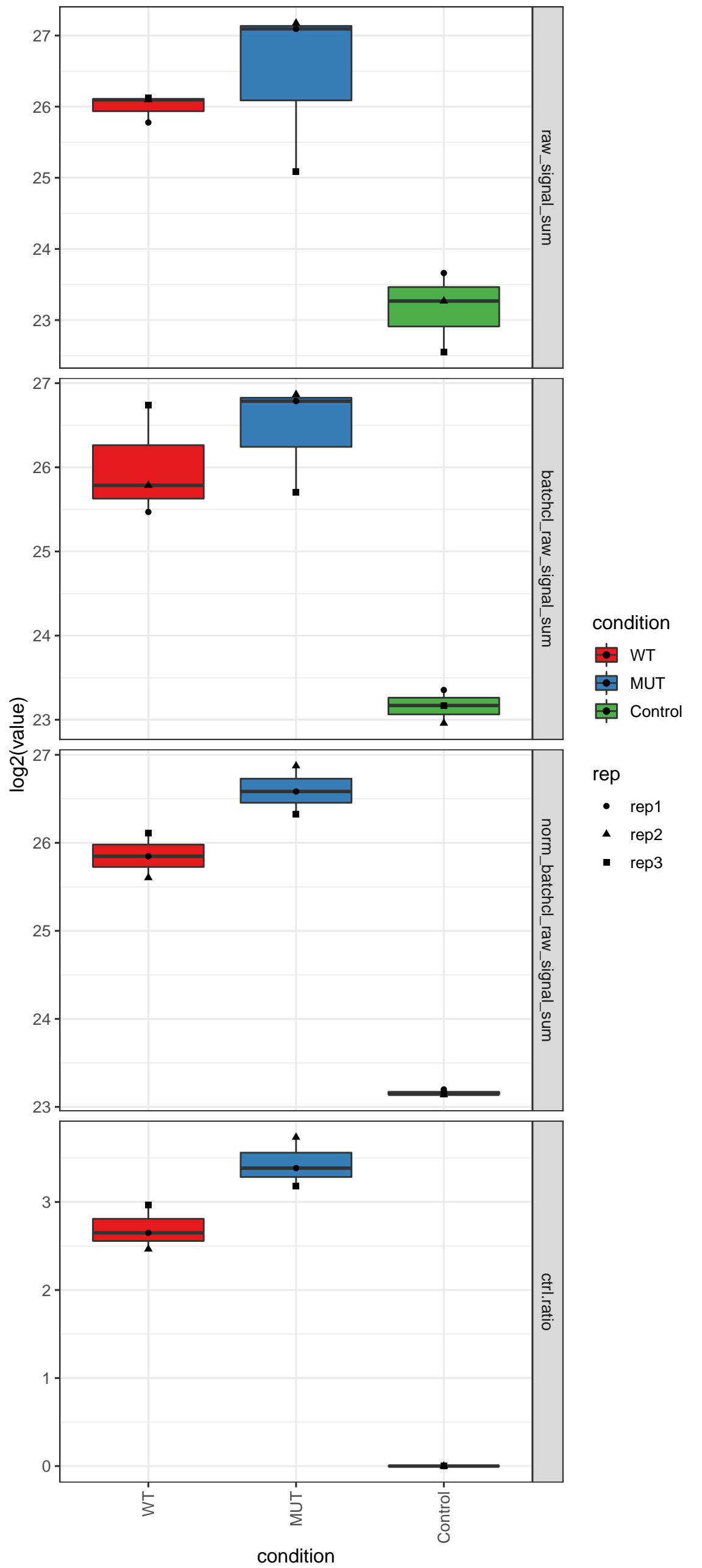
RPS0A – P32905

40S ribosomal protein S0–A OS=Saccharomyces cerevisiae (strain ATCC



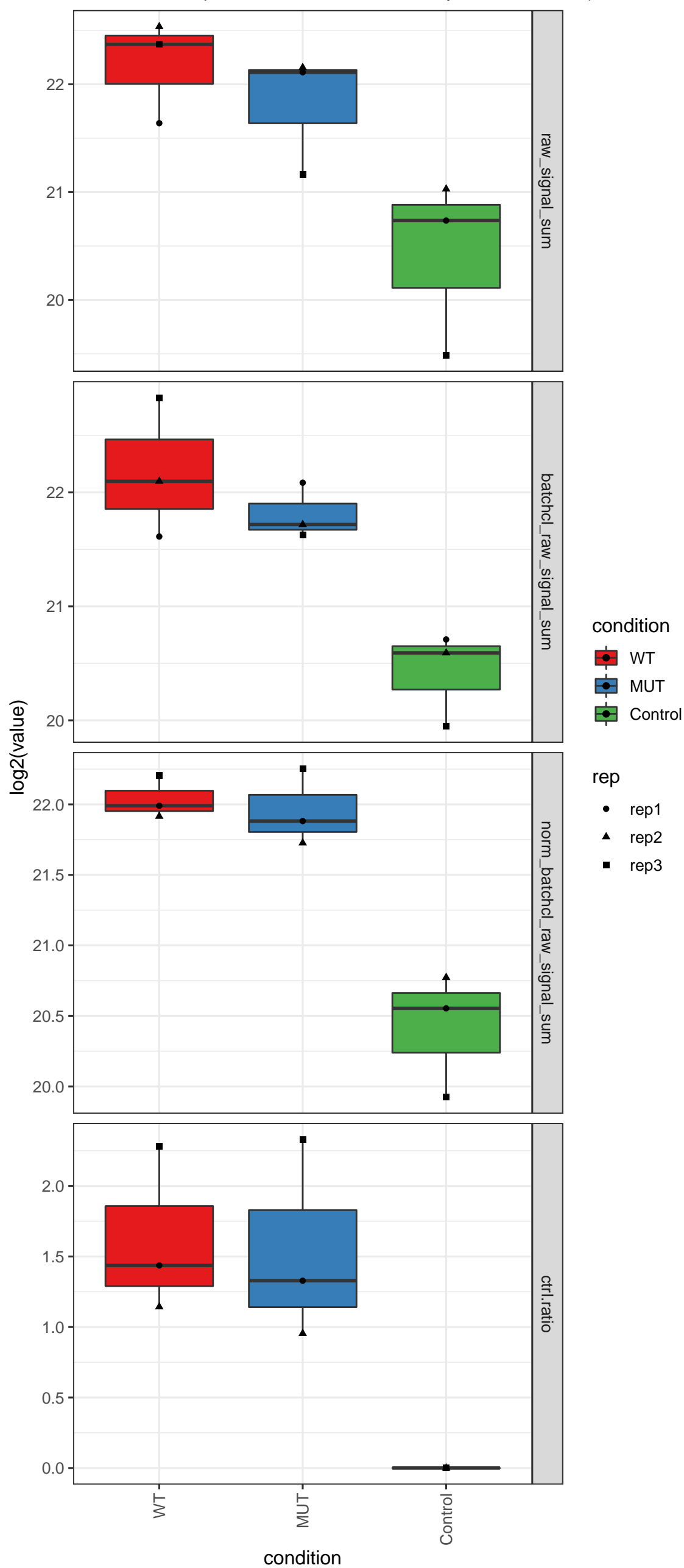
RPS11A|RPS11B – P0CX47|P0CX48

40S ribosomal protein S11–A OS=Saccharomyces cerevisiae (strain ATCC



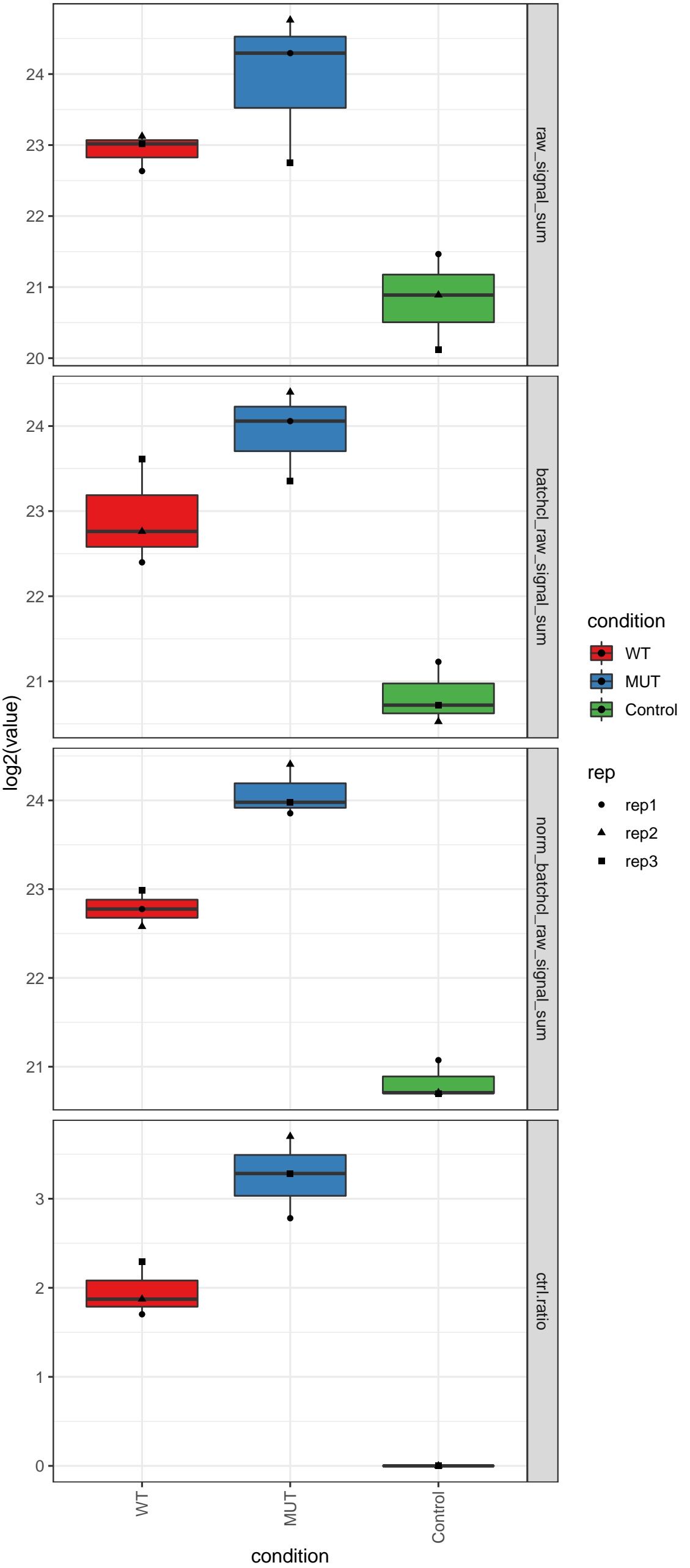
RPS12 – P48589

40S ribosomal protein S12 OS=Saccharomyces cerevisiae (strain ATCC 25814)



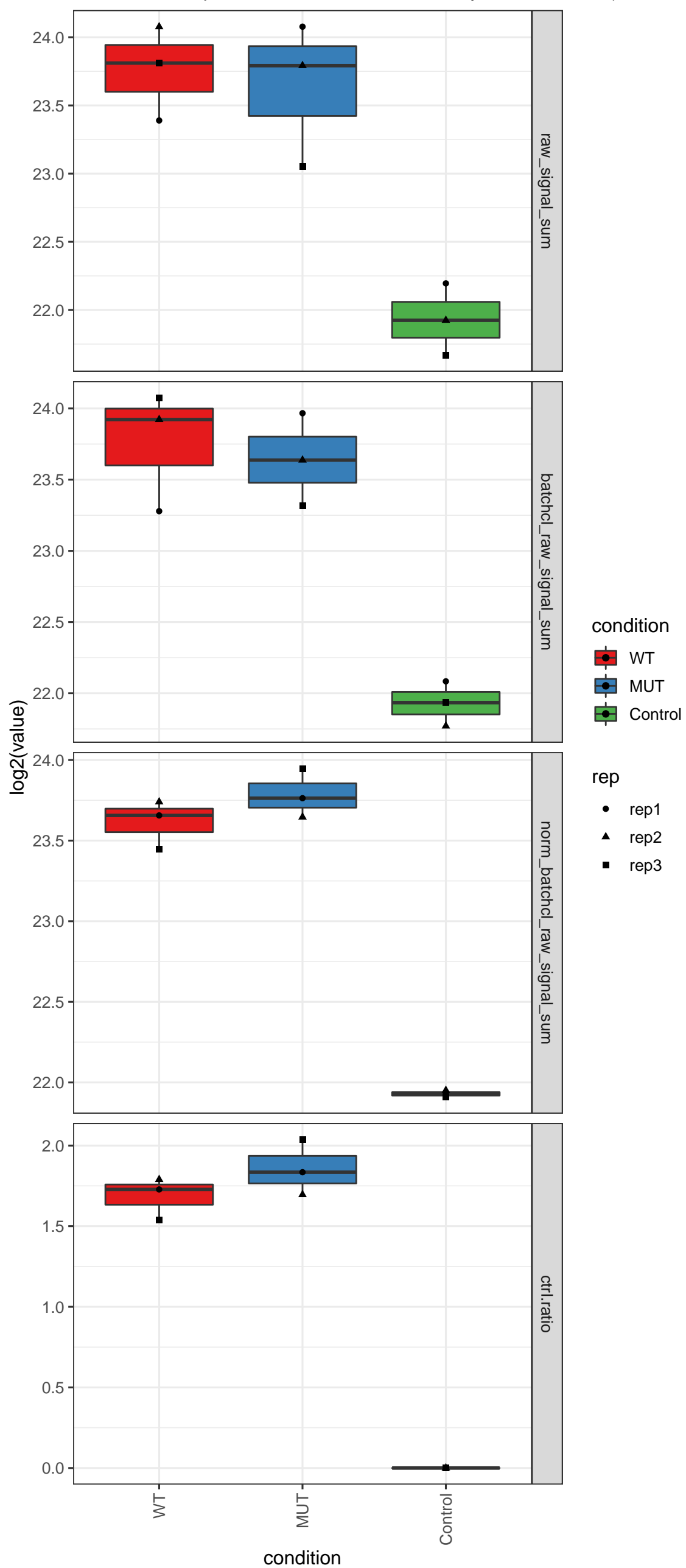
RPS13 – P05756

40S ribosomal protein S13 OS=Saccharomyces cerevisiae (strain ATCC 20



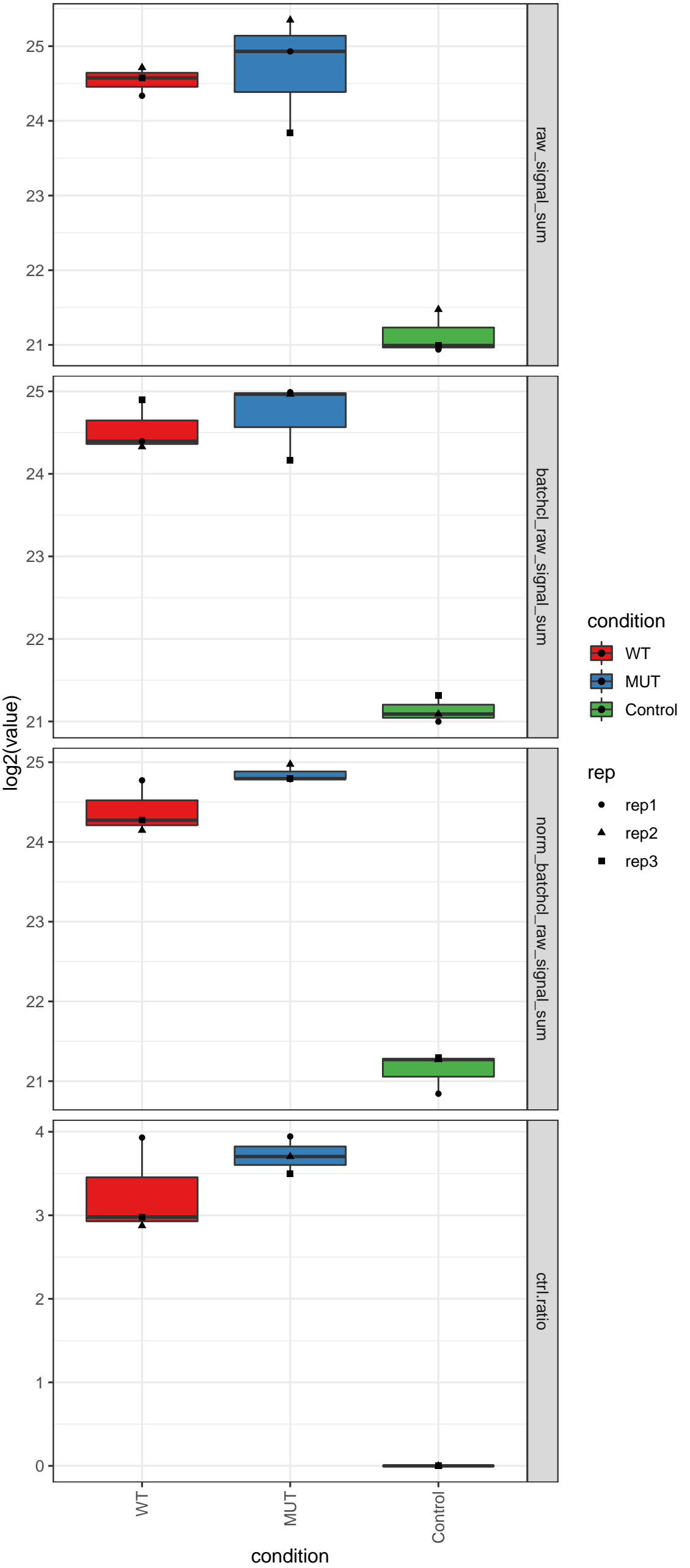
RPS14A|RPS14B – P06367|P39516

40S ribosomal protein S14–A OS=Saccharomyces cerevisiae (strain ATC



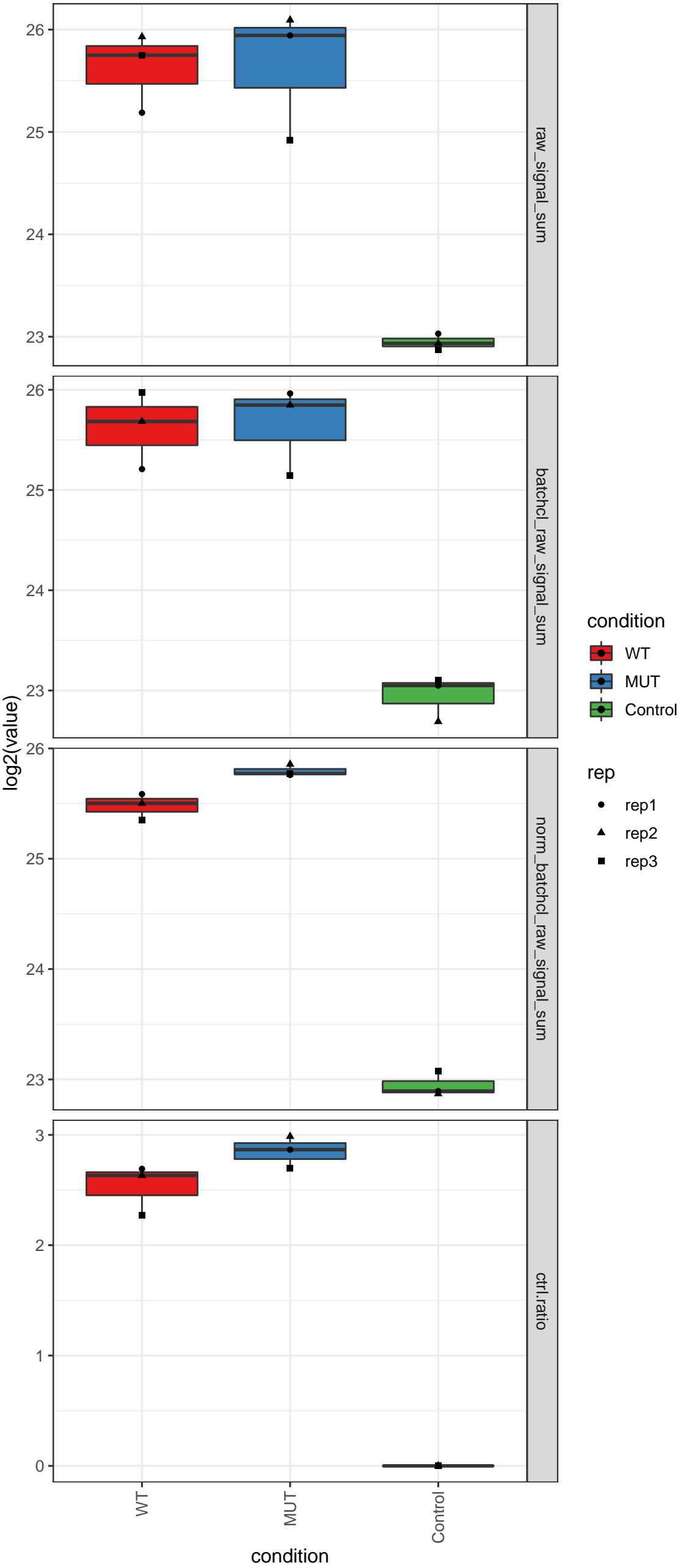
RPS15 – Q01855

40S ribosomal protein S15 OS=Saccharomyces cerevisiae (strain ATCC 20



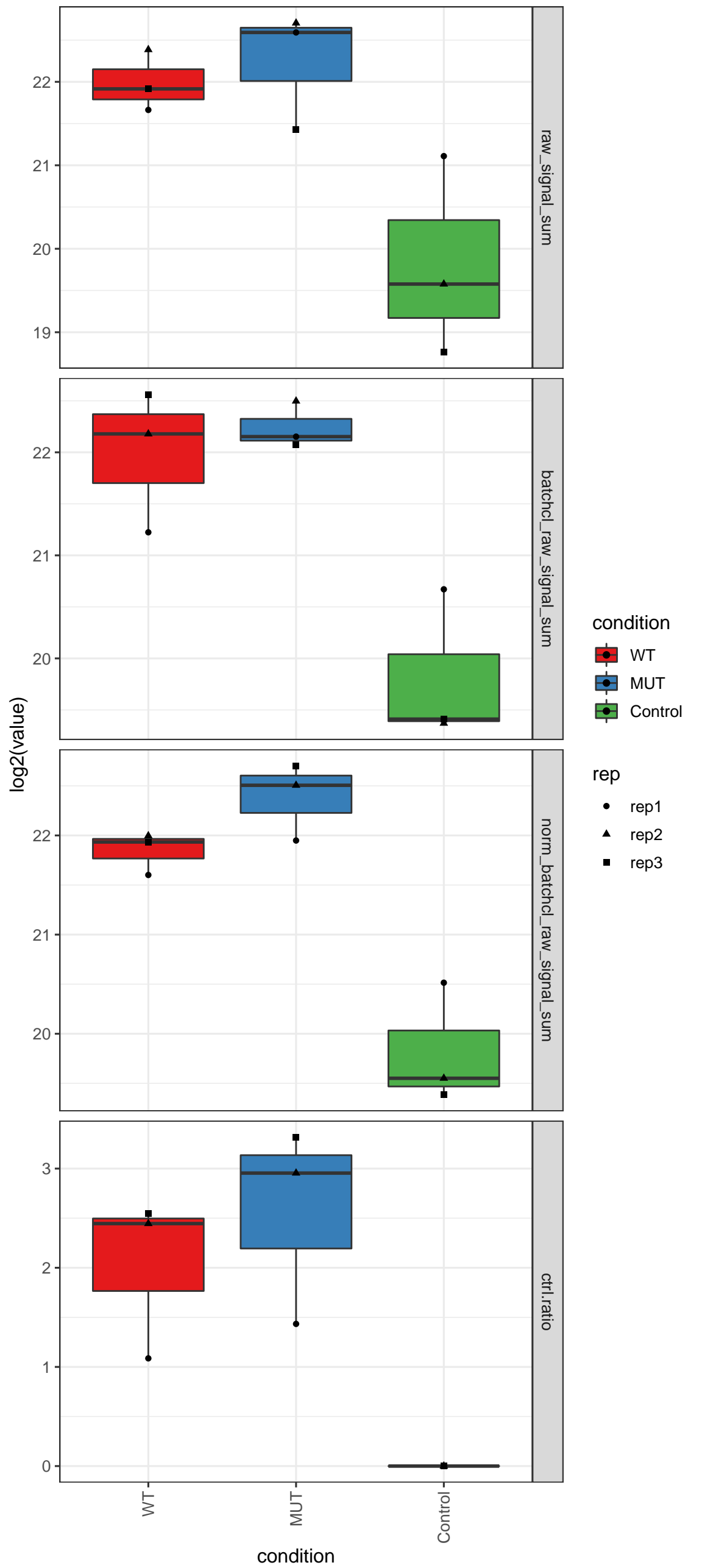
RPS16A|RPS16B – P0CX51|P0CX52

40S ribosomal protein S16–A OS=*Saccharomyces cerevisiae* (strain ATCC



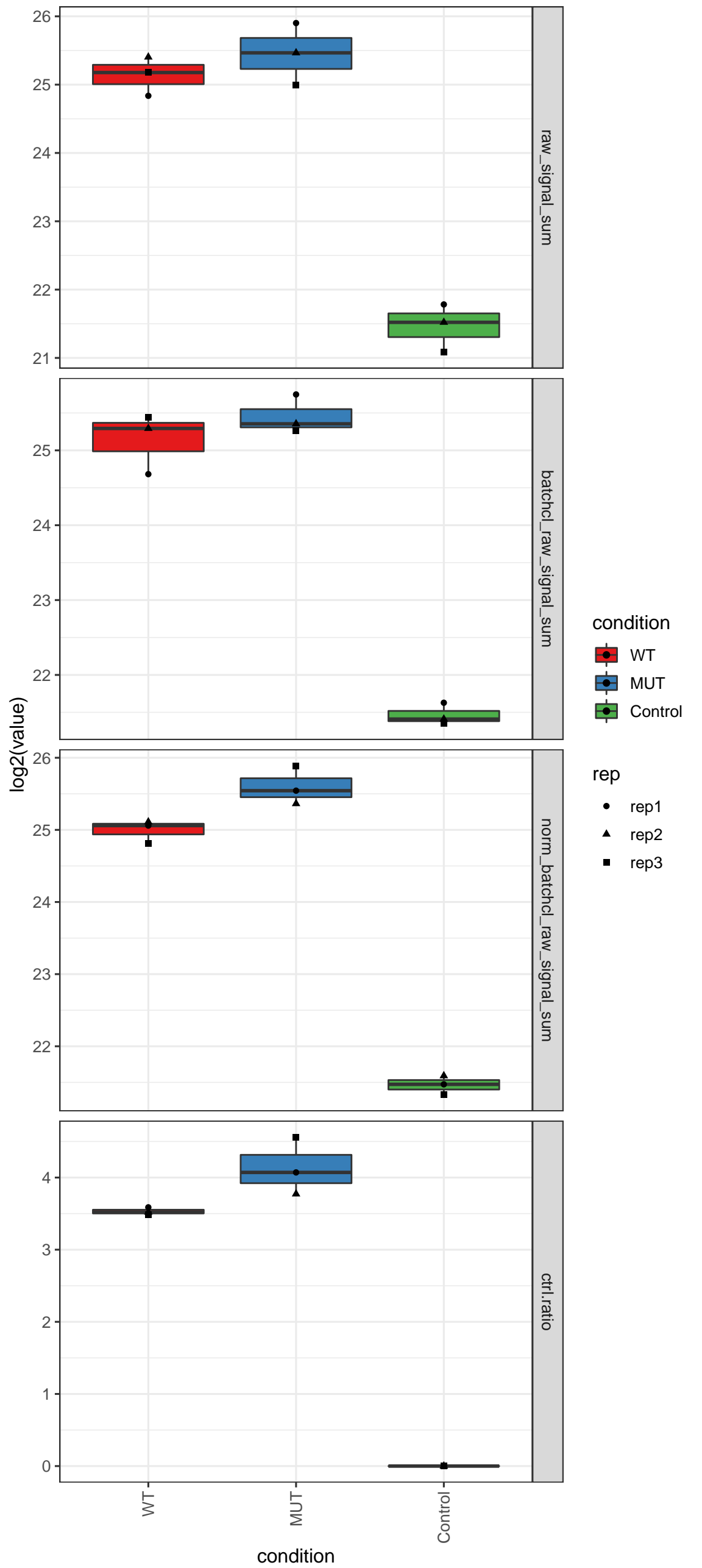
40S ribosomal protein S17-A OS=Saccharomyces cerevisiae (strain ATCC

A diagram of a horizontal beam with a central support. A downward-pointing arrow is positioned above the center of the beam, indicating a load or reaction force.



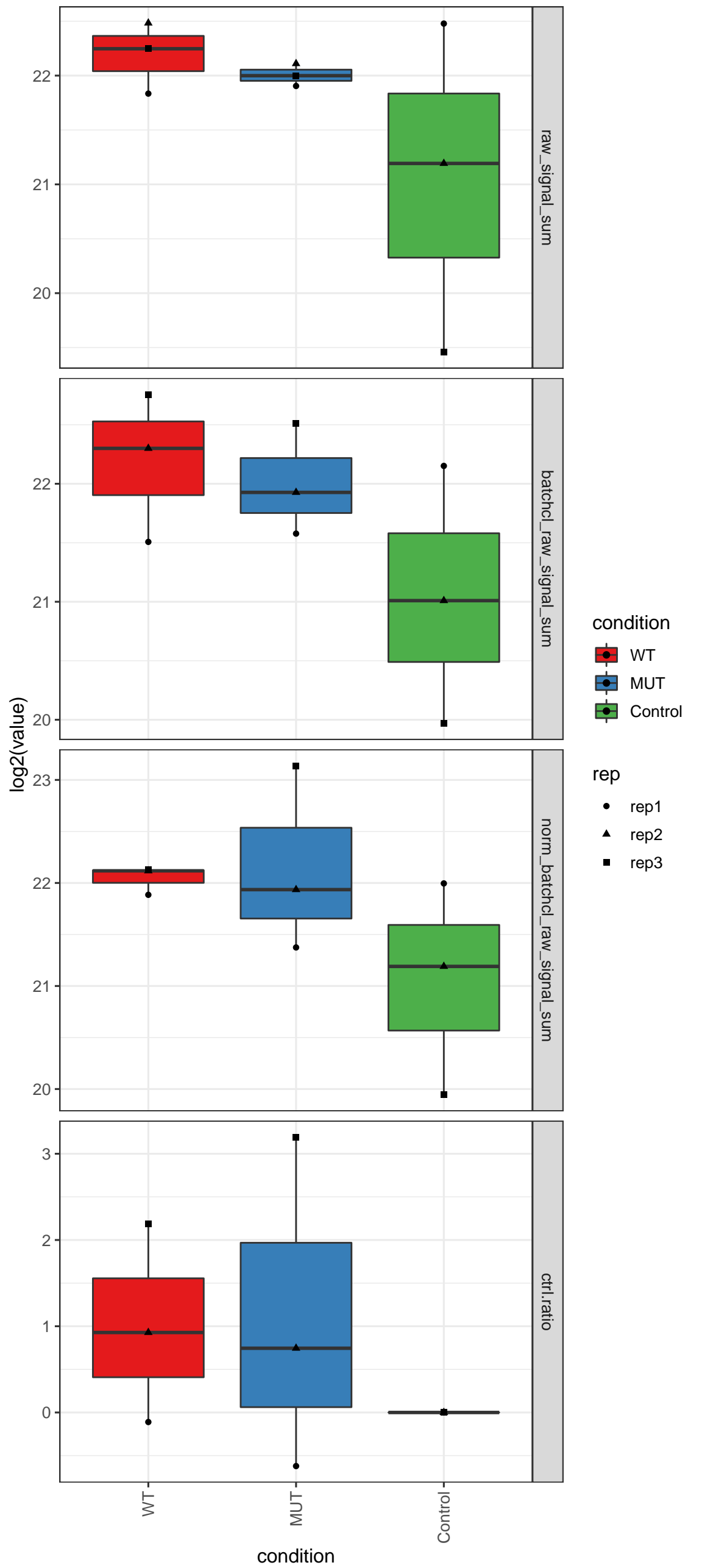
RPS18A|RPS18B – P0CX55|P0CX56

40S ribosomal protein S18-A OS=Saccharomyces cerevisiae (strain ATCC



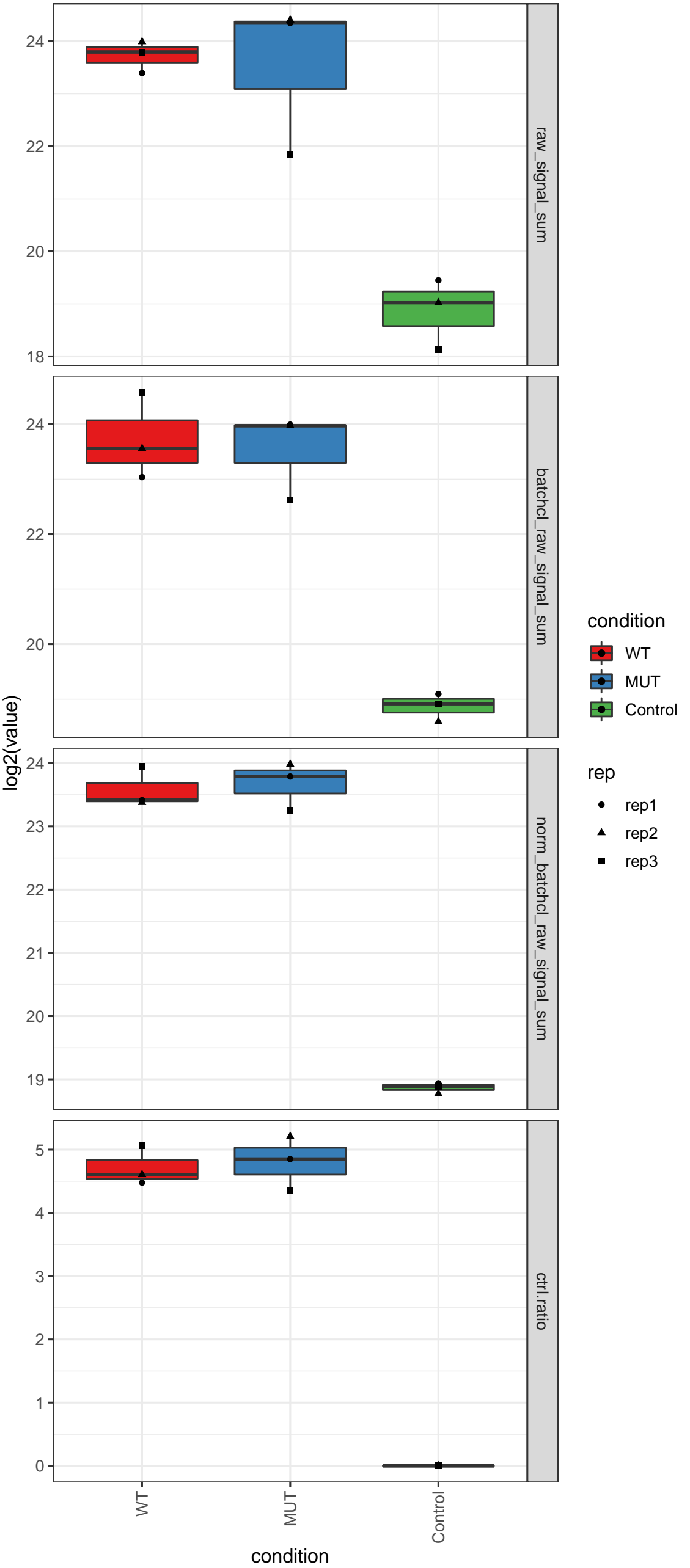
RPS19A|RPS19B – P07280|P07281

40S ribosomal protein S19–A OS=Saccharomyces cerevisiae (strain ATCC



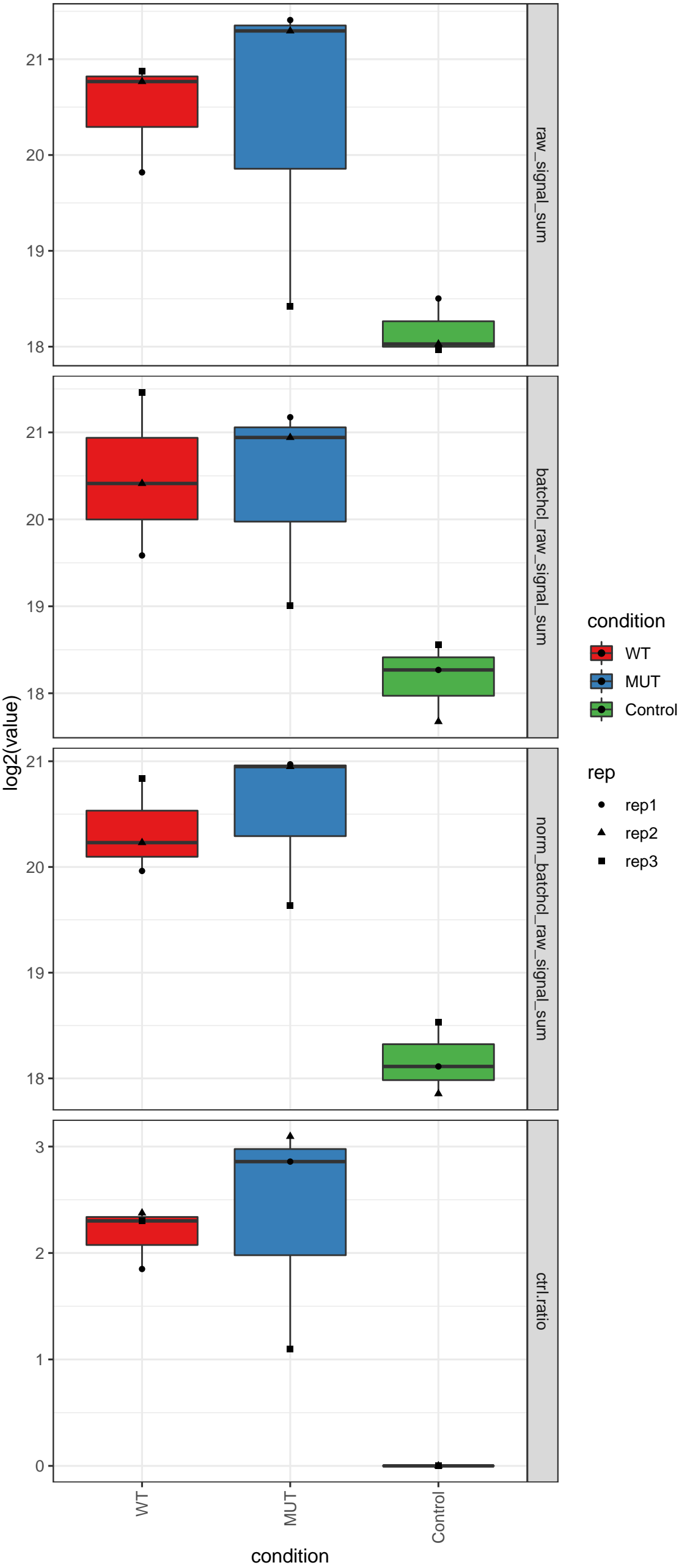
RPS1A – P33442

40S ribosomal protein S1-A OS=Saccharomyces cerevisiae (strain ATCC



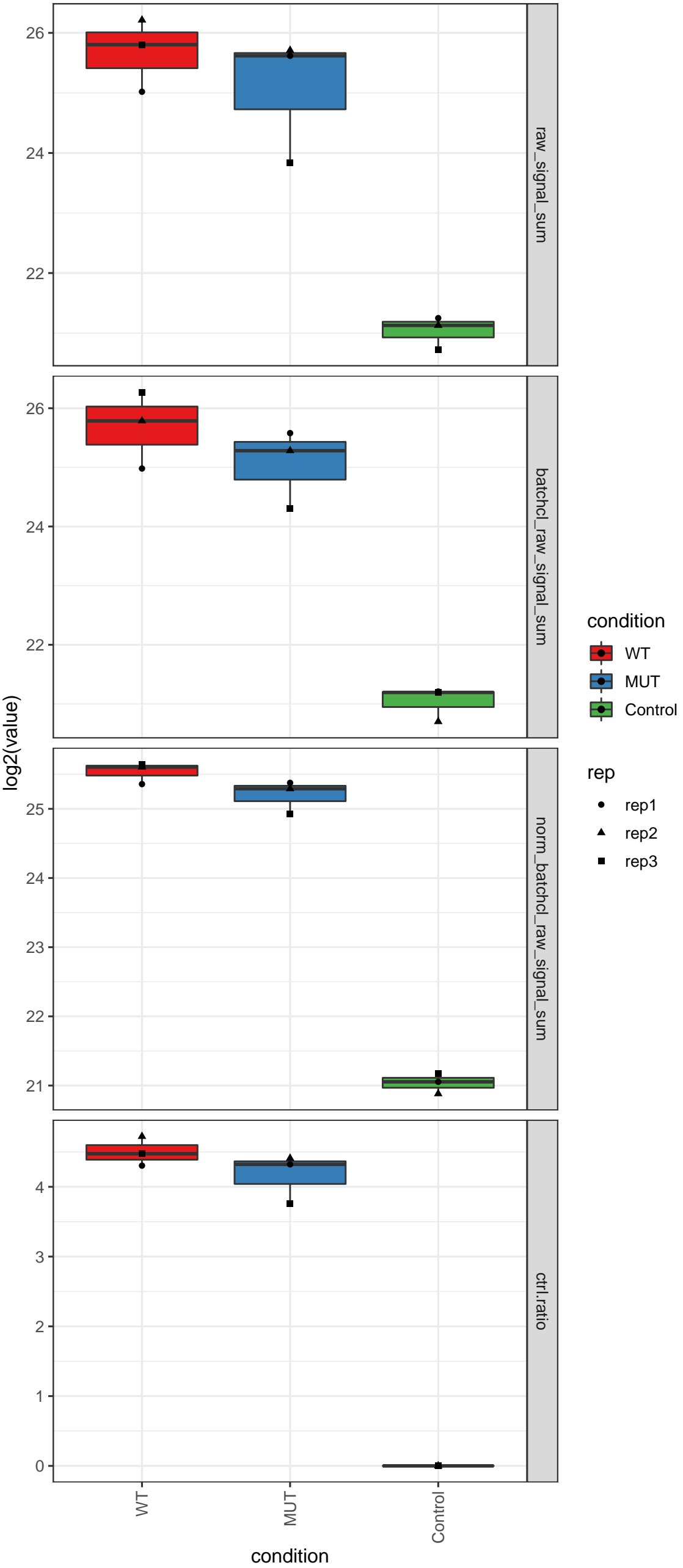
RPS1B – P23248

40S ribosomal protein S1–B OS=Saccharomyces cerevisiae (strain ATCC



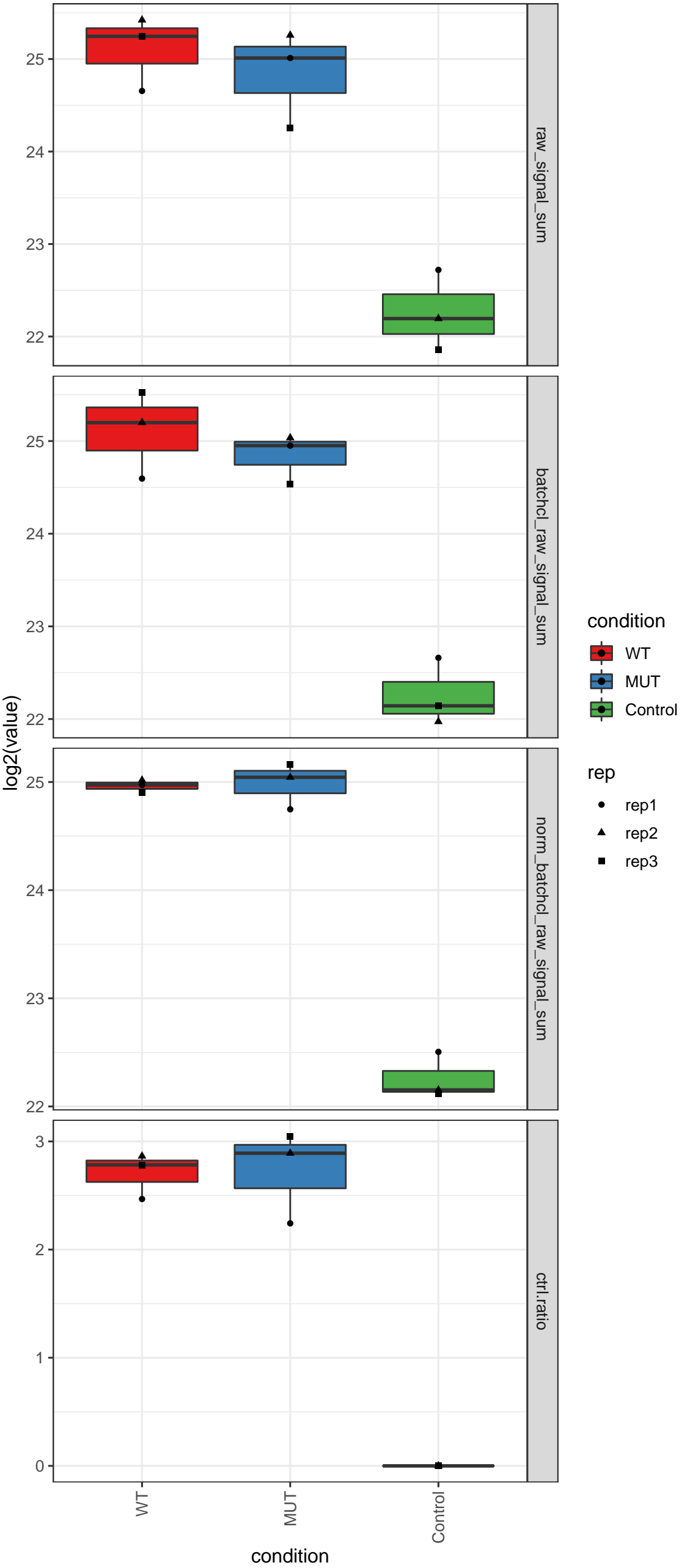
RPS2 – P25443

40S ribosomal protein S2 OS=Saccharomyces cerevisiae (strain ATCC 204



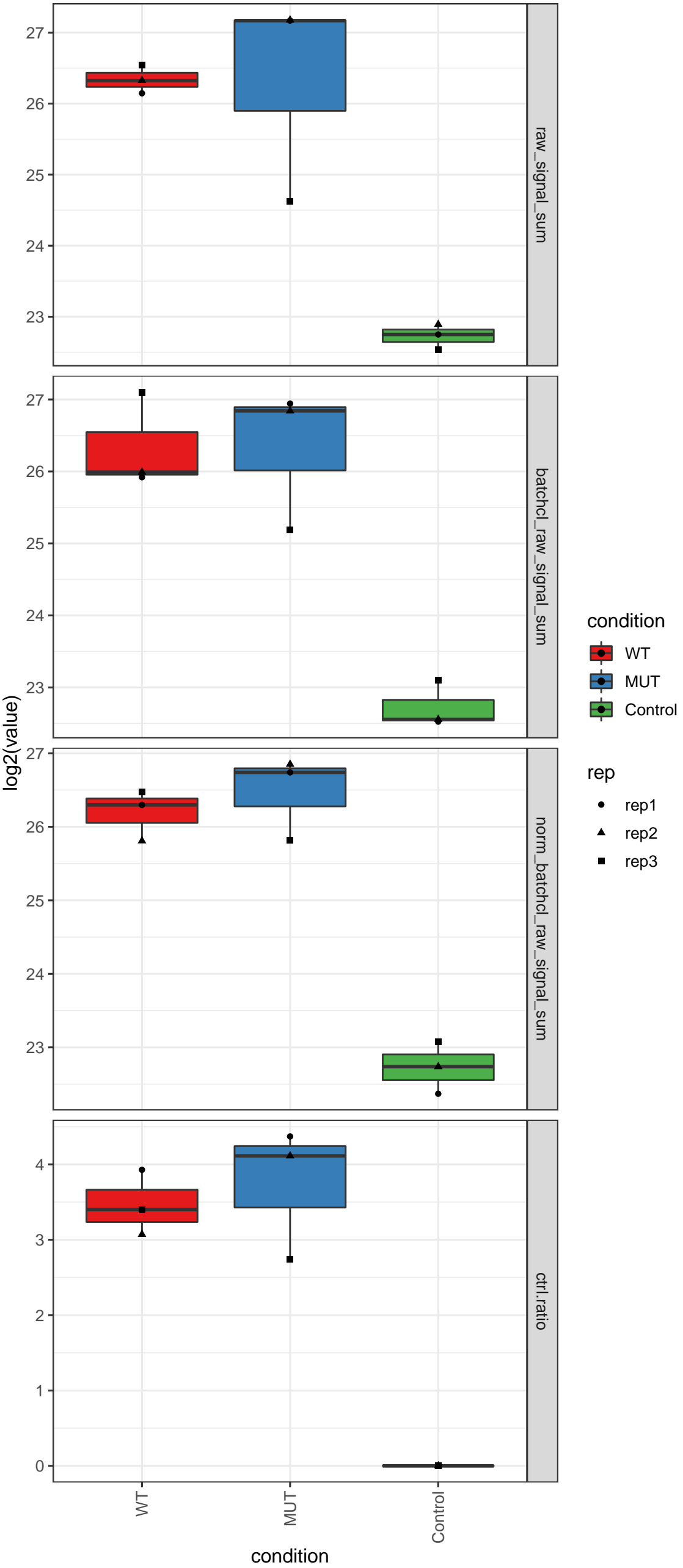
RPS20 – P38701

40S ribosomal protein S20 OS=Saccharomyces cerevisiae (strain ATCC 20



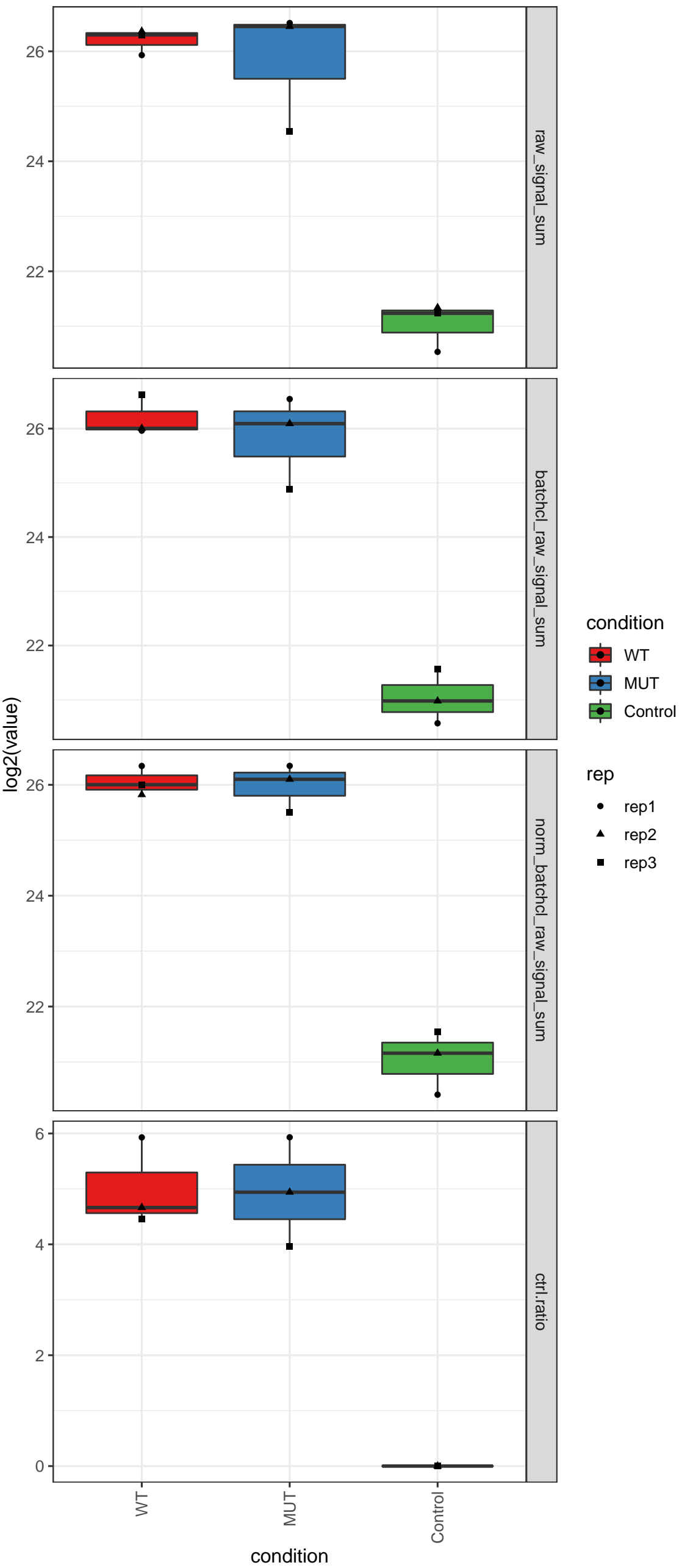
RPS23A|RPS23B – P0CX29|P0CX30

40S ribosomal protein S23–A OS=Saccharomyces cerevisiae (strain ATCC



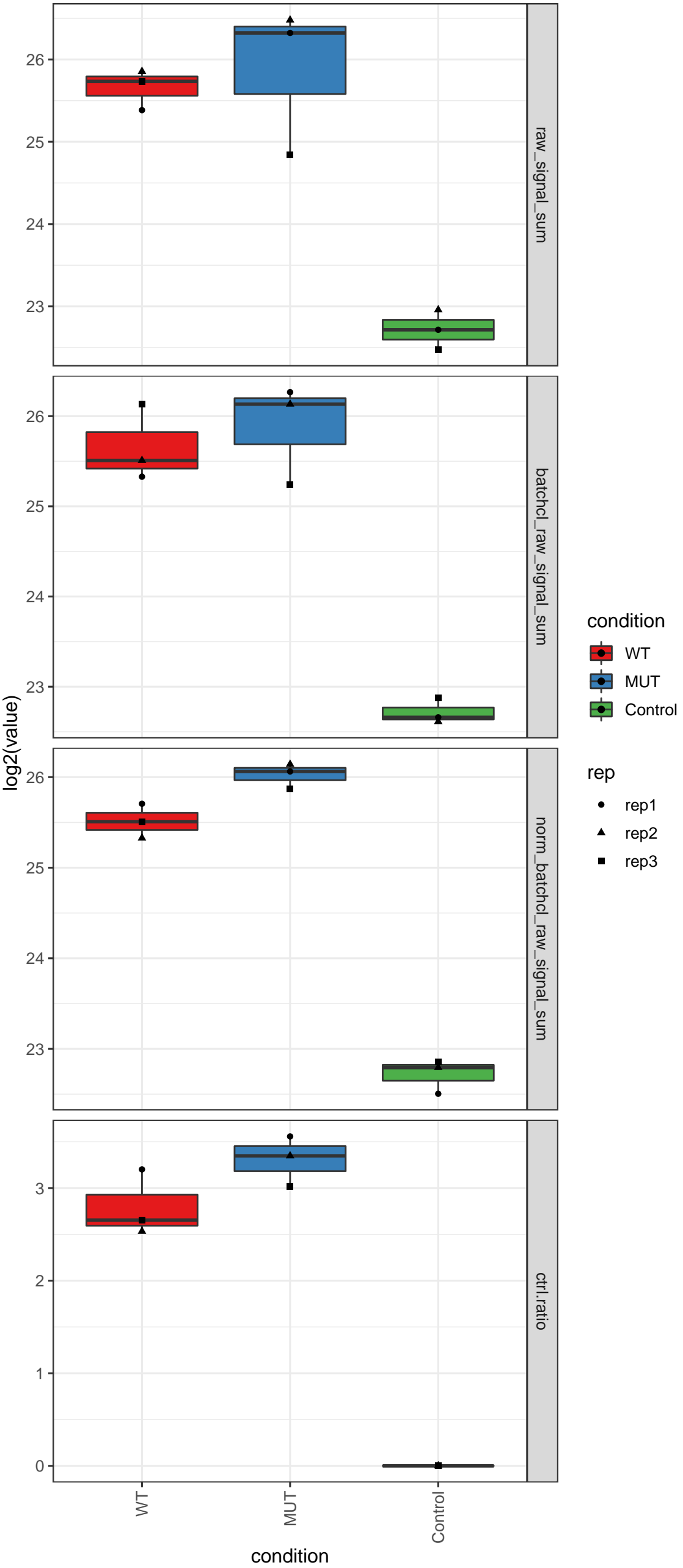
RPS24A|RPS24B – P0CX31|P0CX32

40S ribosomal protein S24-A OS=Saccharomyces cerevisiae (strain ATCC

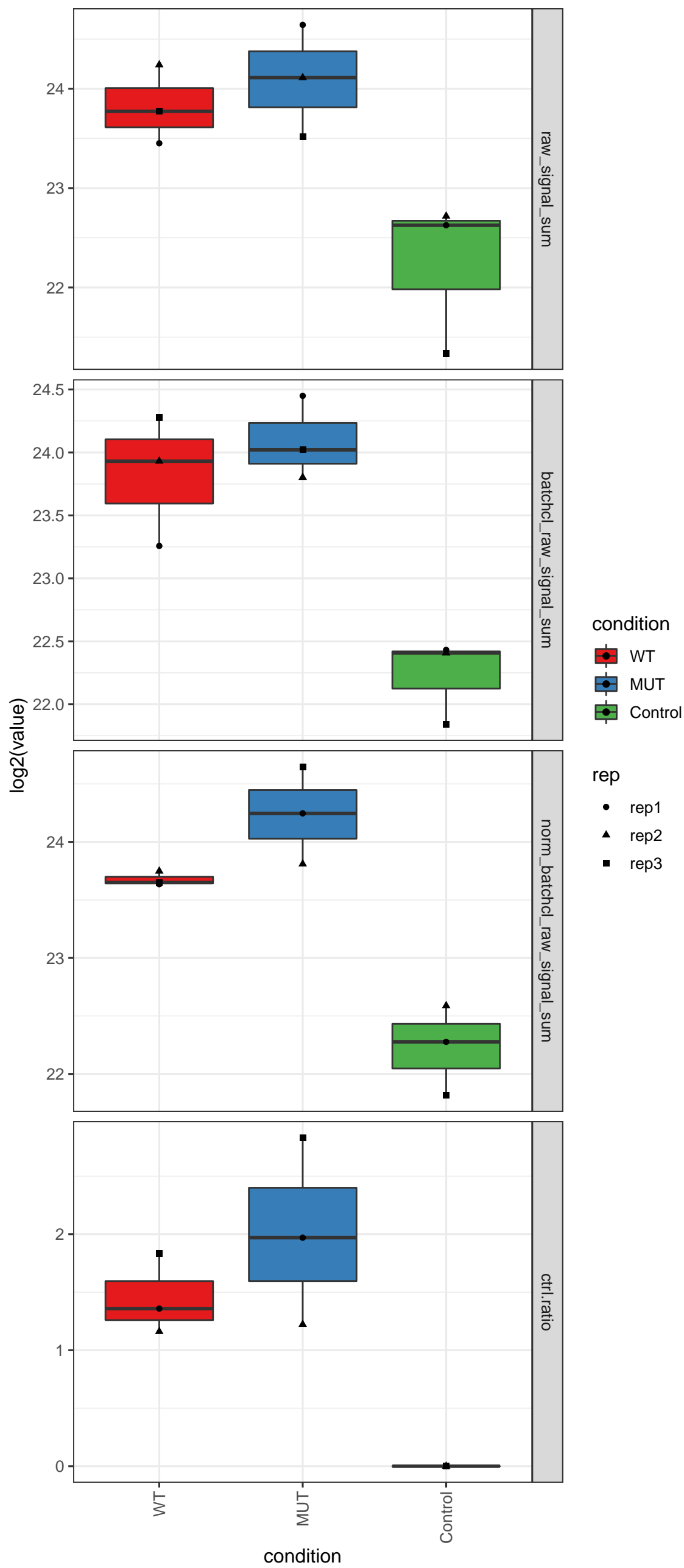


RPS25B|RPS25A – P0C0T4|Q3E792

40S ribosomal protein S25–B OS=Saccharomyces cerevisiae (strain ATCC

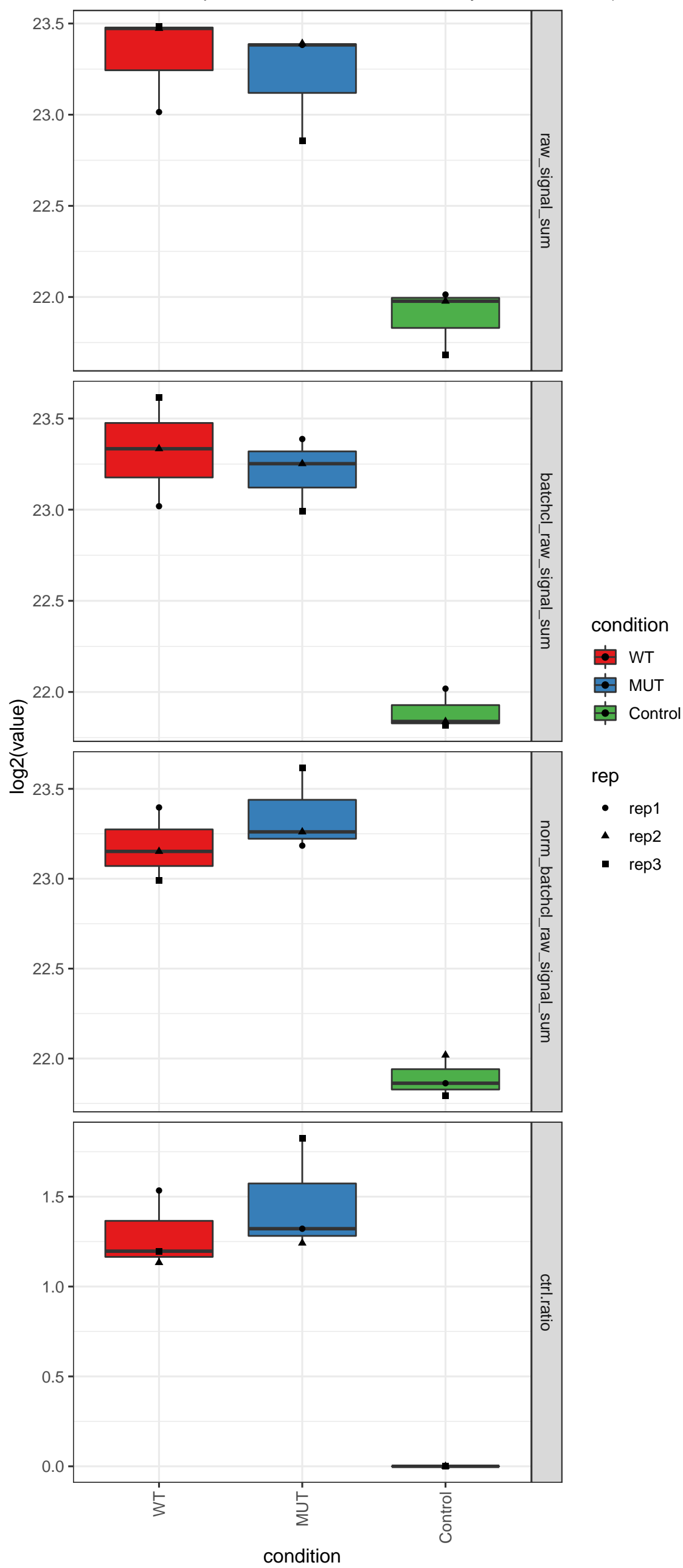


RPS27A|RPS27B – P35997|P38711
40S ribosomal protein S27–A OS=Saccharomyces cerevisiae (strain ATC



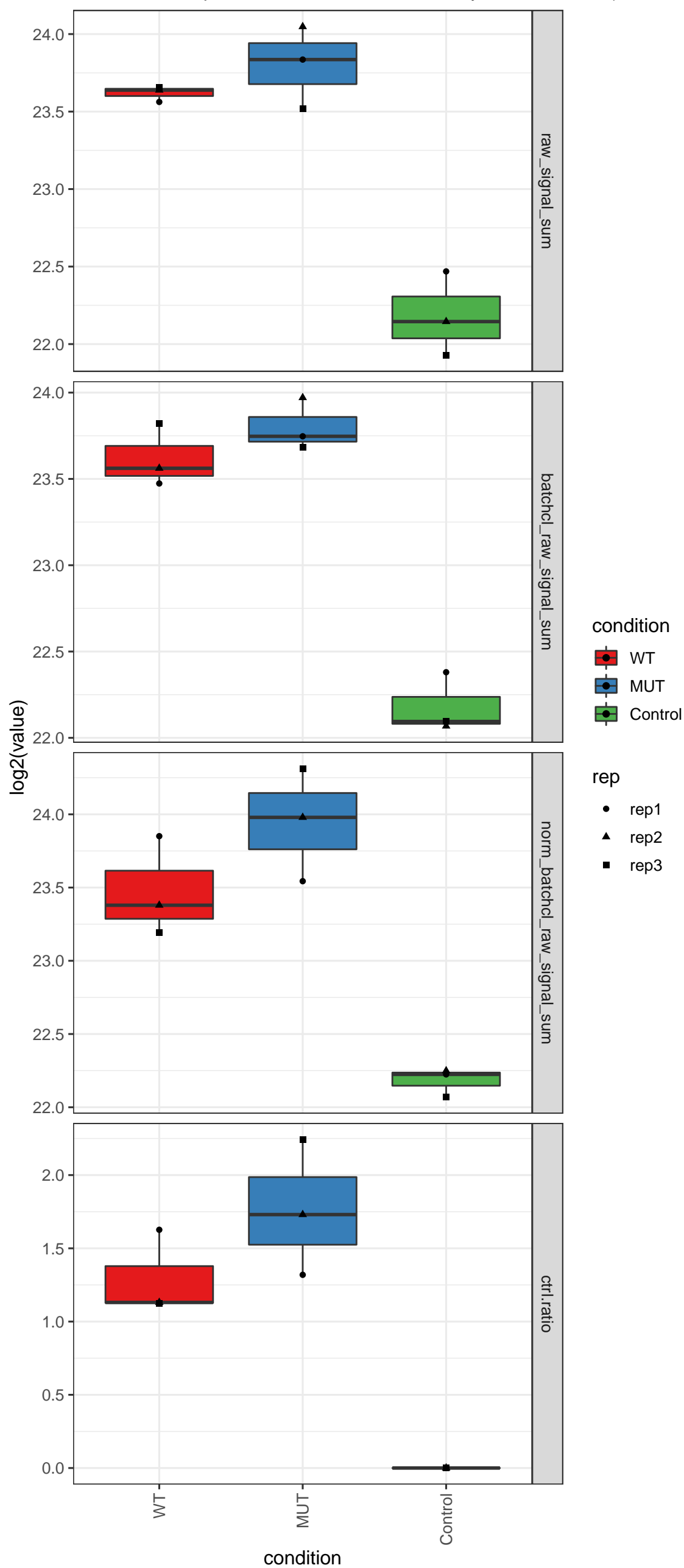
RPS28B|RPS28A – P0C0X0|Q3E7X9

40S ribosomal protein S28–B OS=Saccharomyces cerevisiae (strain ATC



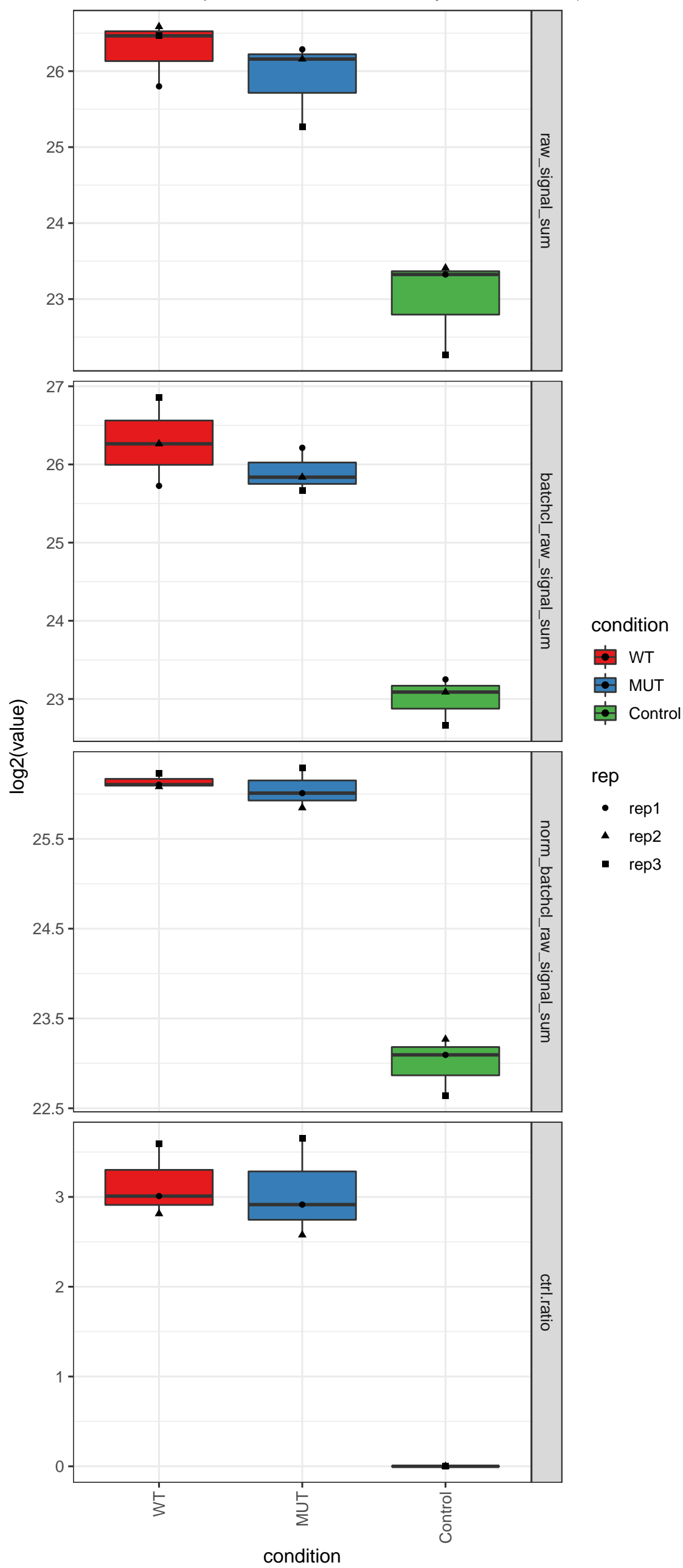
RPS29A – P41057

40S ribosomal protein S29–A OS=*Saccharomyces cerevisiae* (strain ATCC 25791)



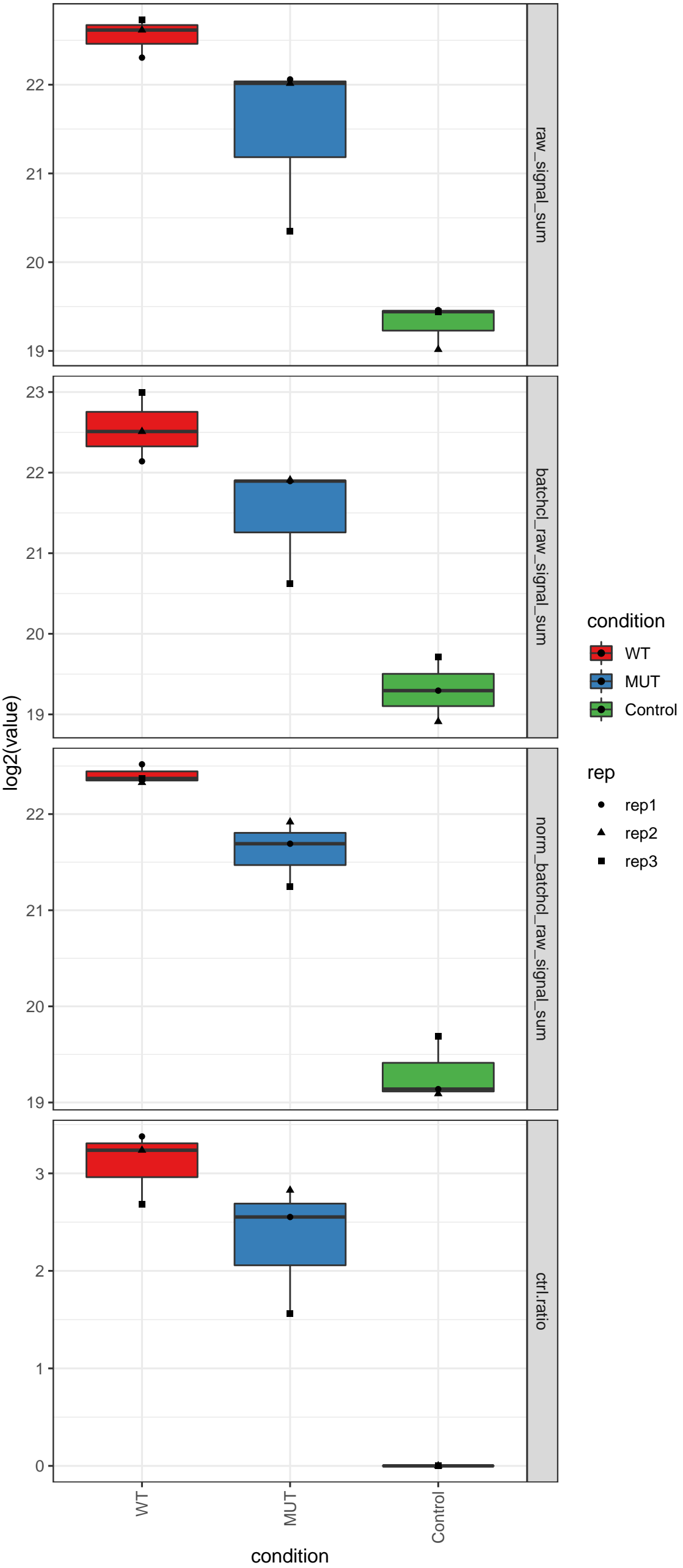
RPS3 – P05750

40S ribosomal protein S3 OS=*Saccharomyces cerevisiae* (strain ATCC 20454)



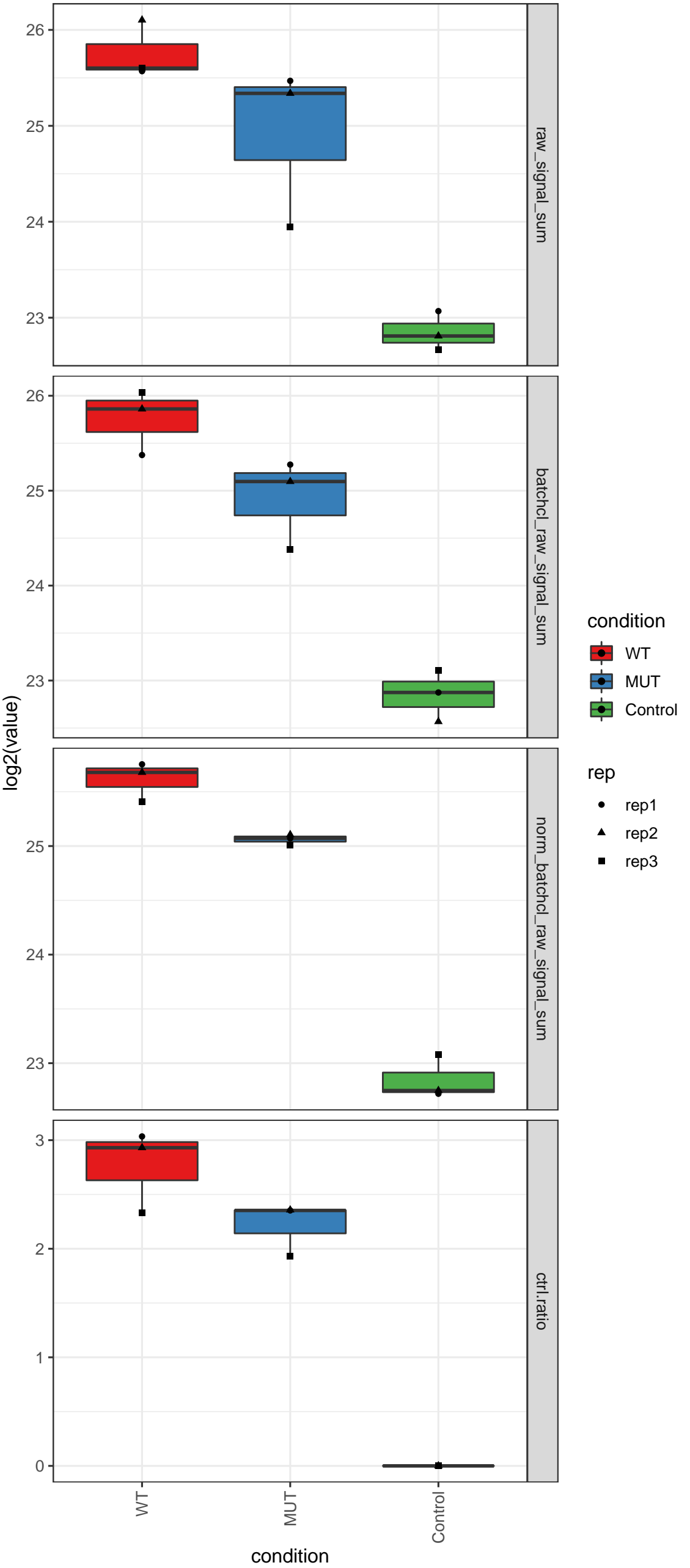
RPS30A|RPS30B – P0CX33|P0CX34

40S ribosomal protein S30–A OS=Saccharomyces cerevisiae (strain ATCC



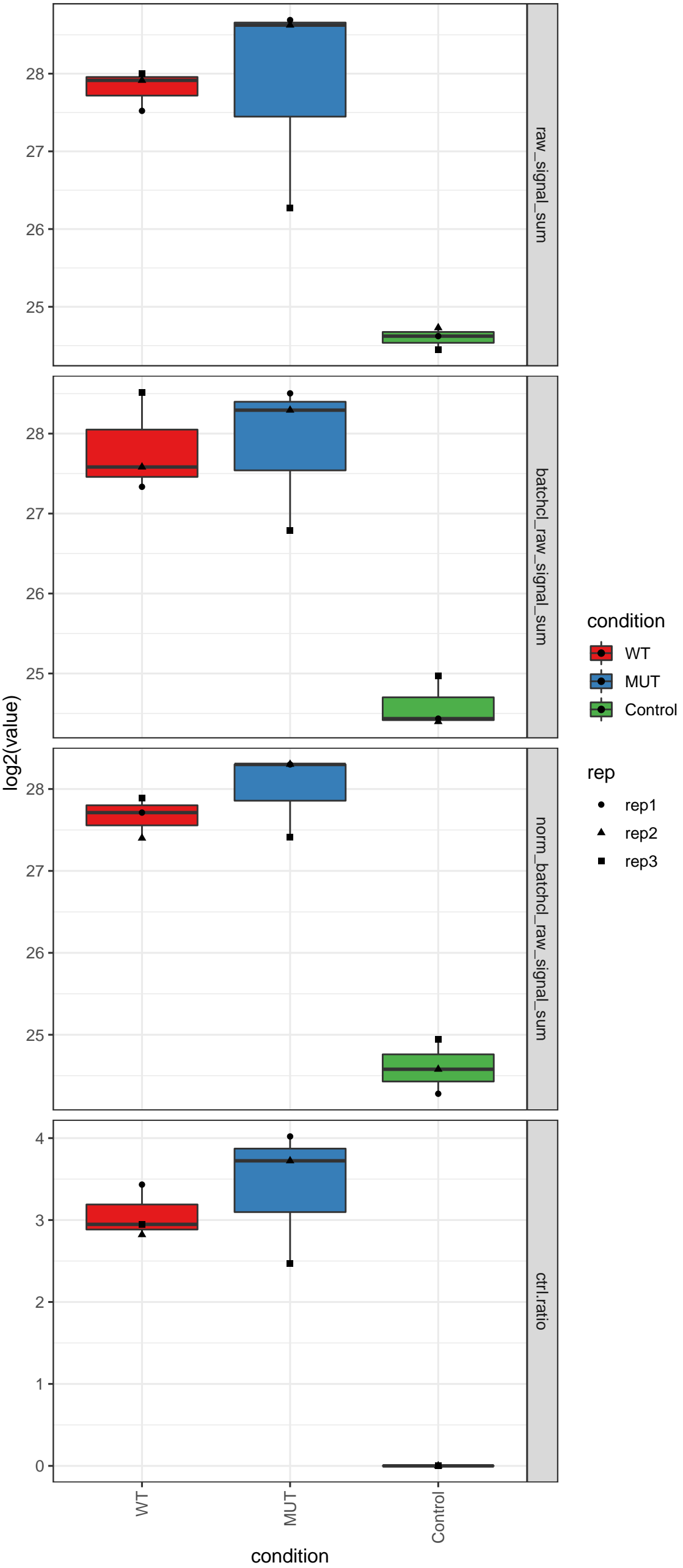
RPS31 – P05759

Ubiquitin-40S ribosomal protein S31 OS=Saccharomyces cerevisiae (strain



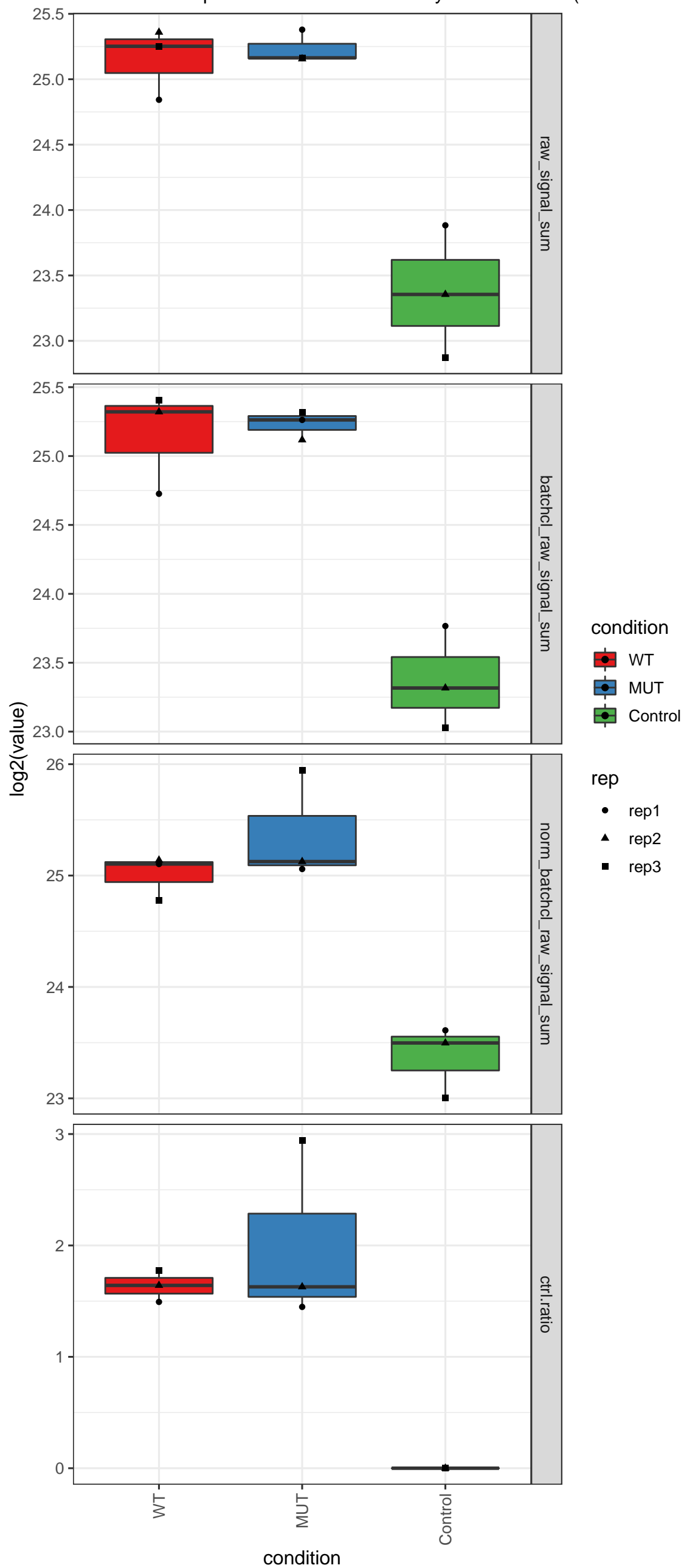
RPS4A|RPS4B – P0CX35|P0CX36

40S ribosomal protein S4-A OS=Saccharomyces cerevisiae (strain ATCC



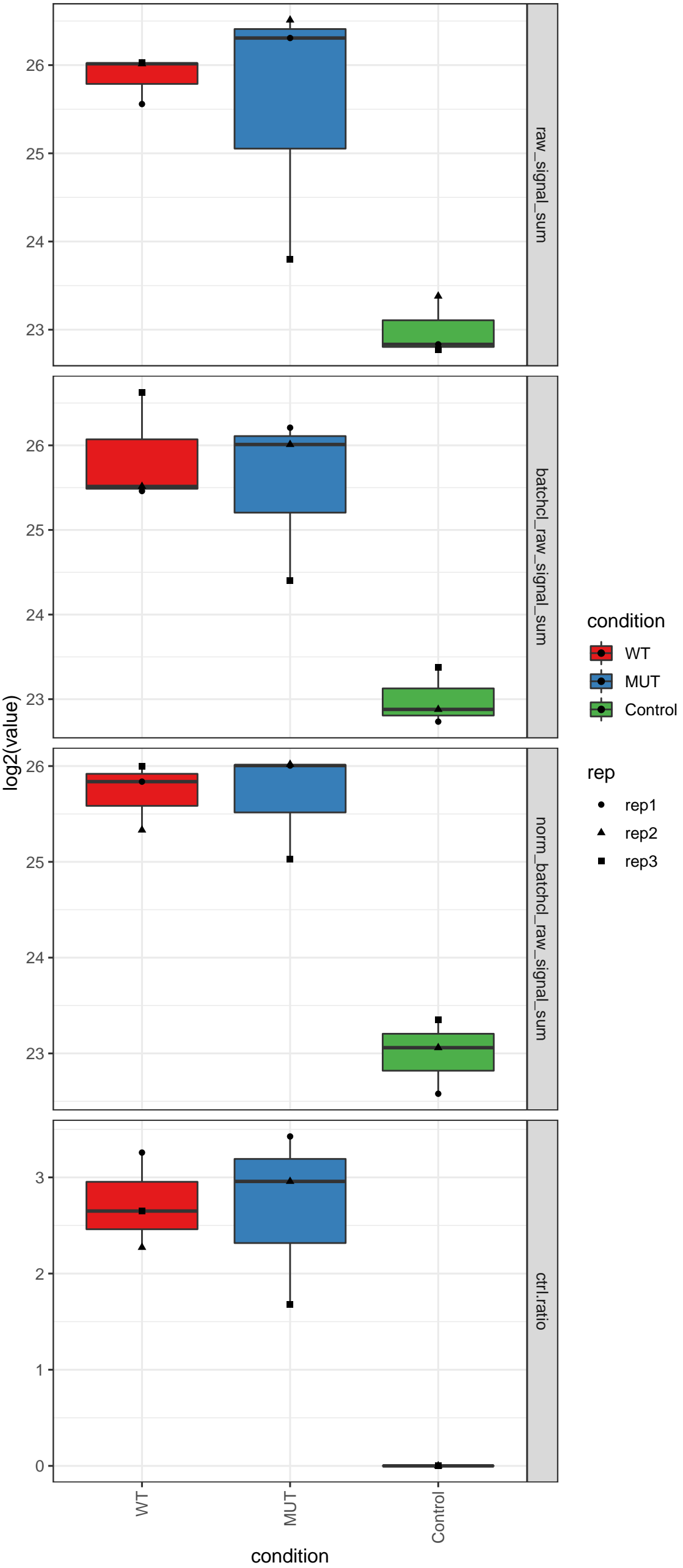
RPS5 – P26783

40S ribosomal protein S5 OS=*Saccharomyces cerevisiae* (strain ATCC 2



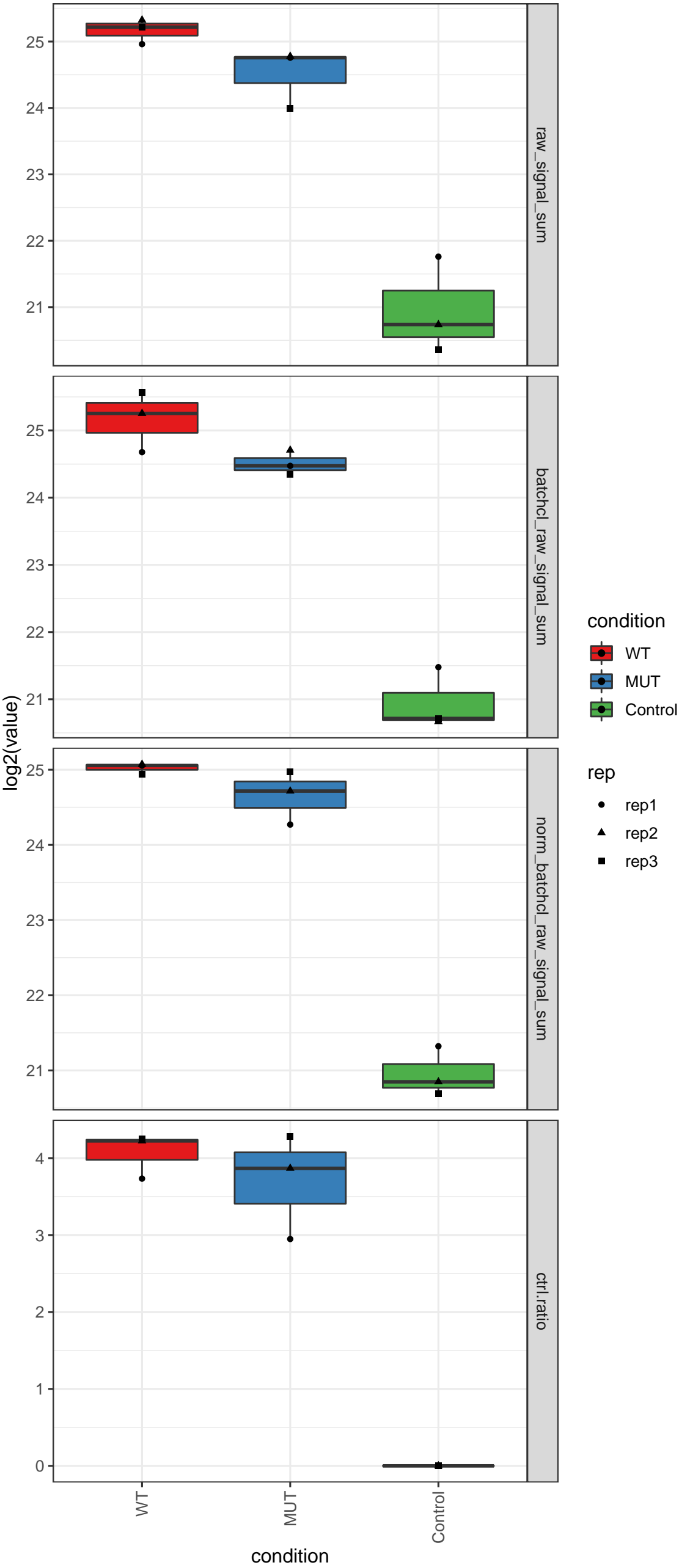
RPS6A|RPS6B – P0CX37|P0CX38

40S ribosomal protein S6–A OS=Saccharomyces cerevisiae (strain ATCC 24843)



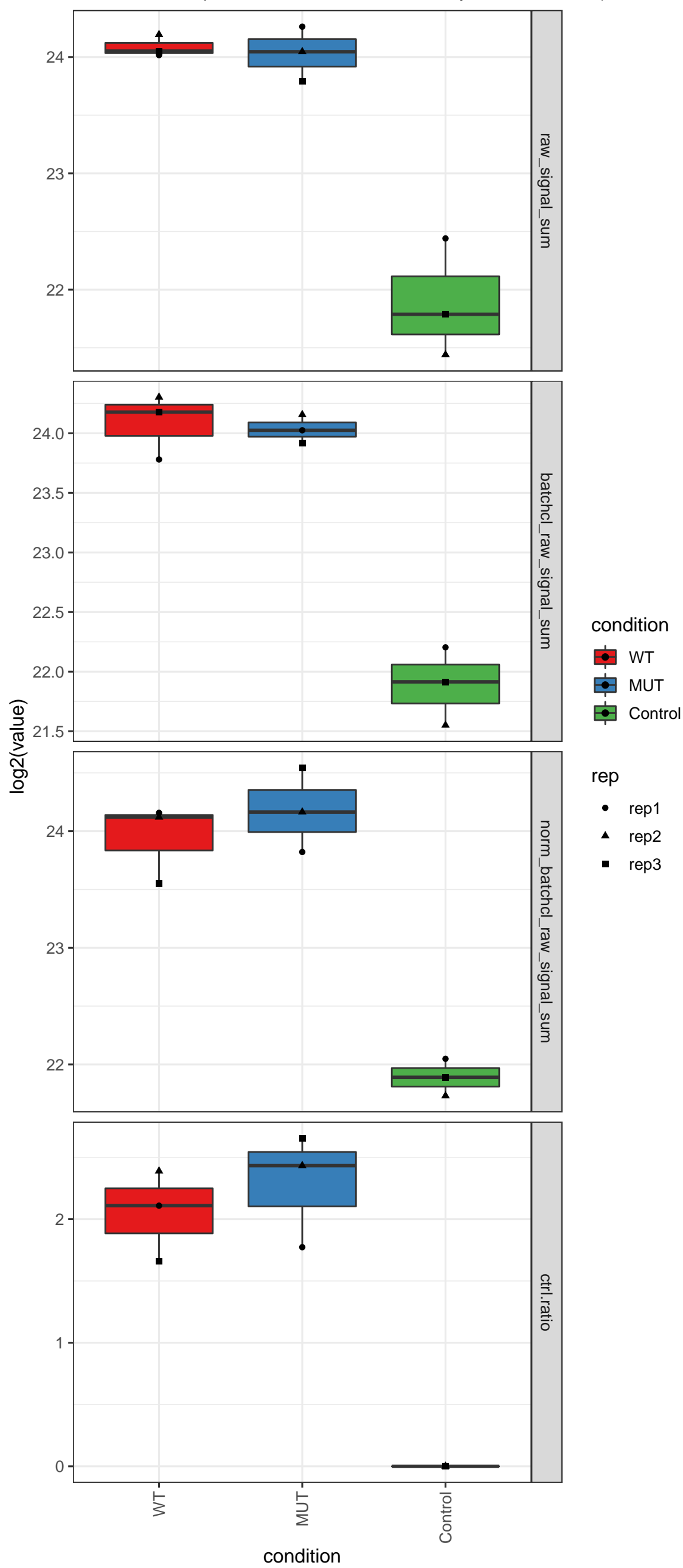
RPS7A – P26786

40S ribosomal protein S7-A OS=Saccharomyces cerevisiae (strain ATCC



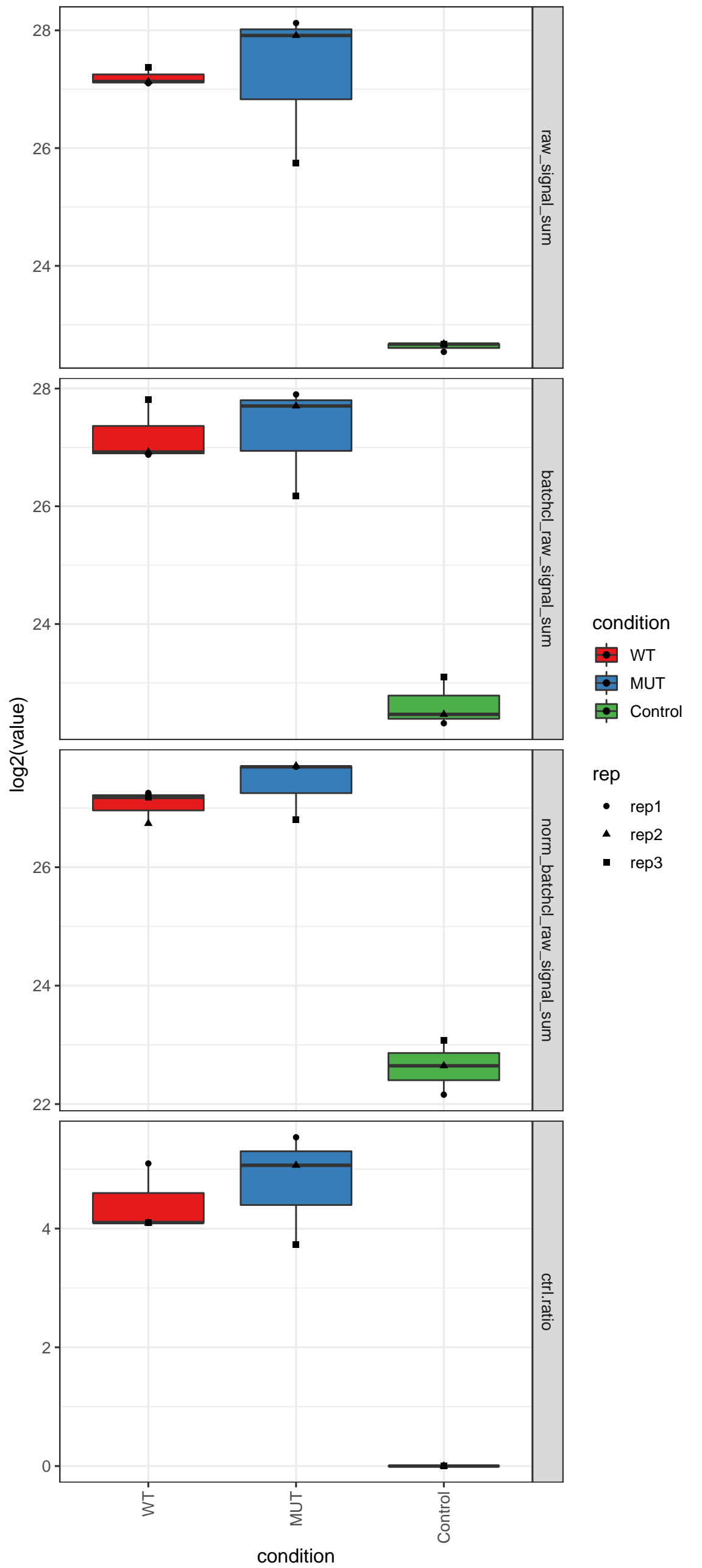
RPS7B – P48164

40S ribosomal protein S7–B OS=*Saccharomyces cerevisiae* (strain ATCC

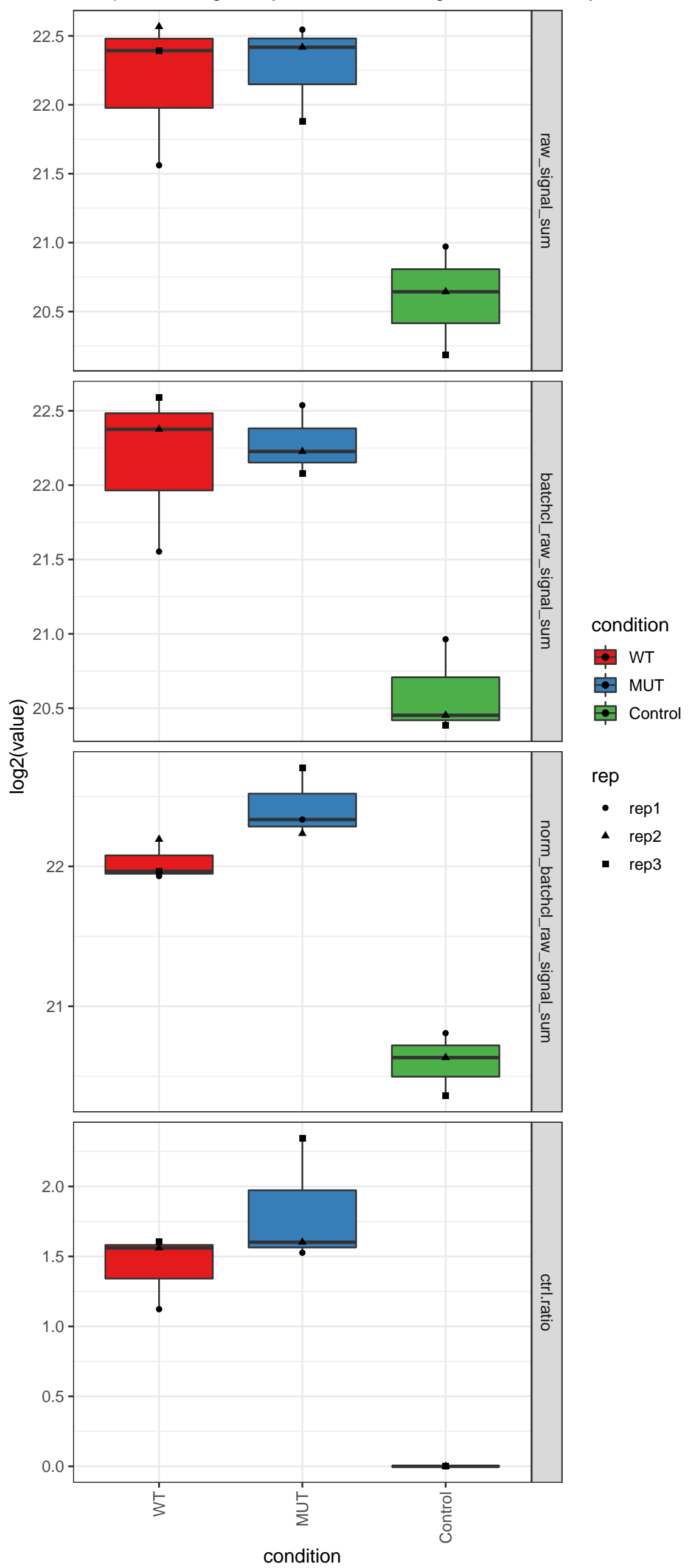


RPS8A|RPS8B – P0CX39|P0CX40

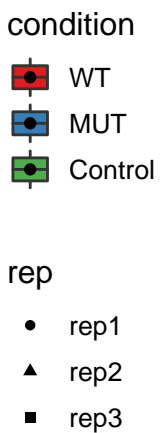
40S ribosomal protein S8–A OS=Saccharomyces cerevisiae (strain ATCC



26S protease regulatory subunit 7 homolog OS=Saccharomyces cerevisiae

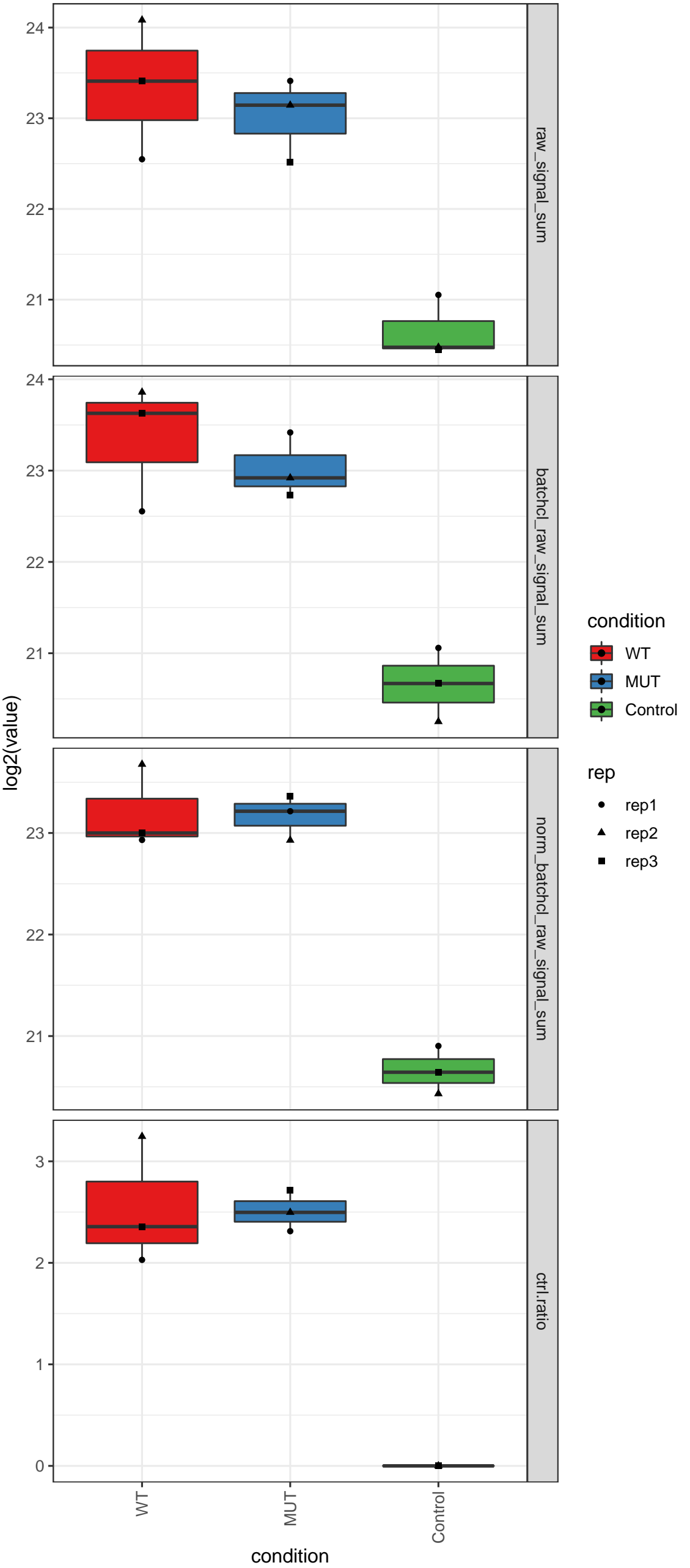


26S protease regulatory subunit 4 homolog OS=Saccharomyces cerevisiae



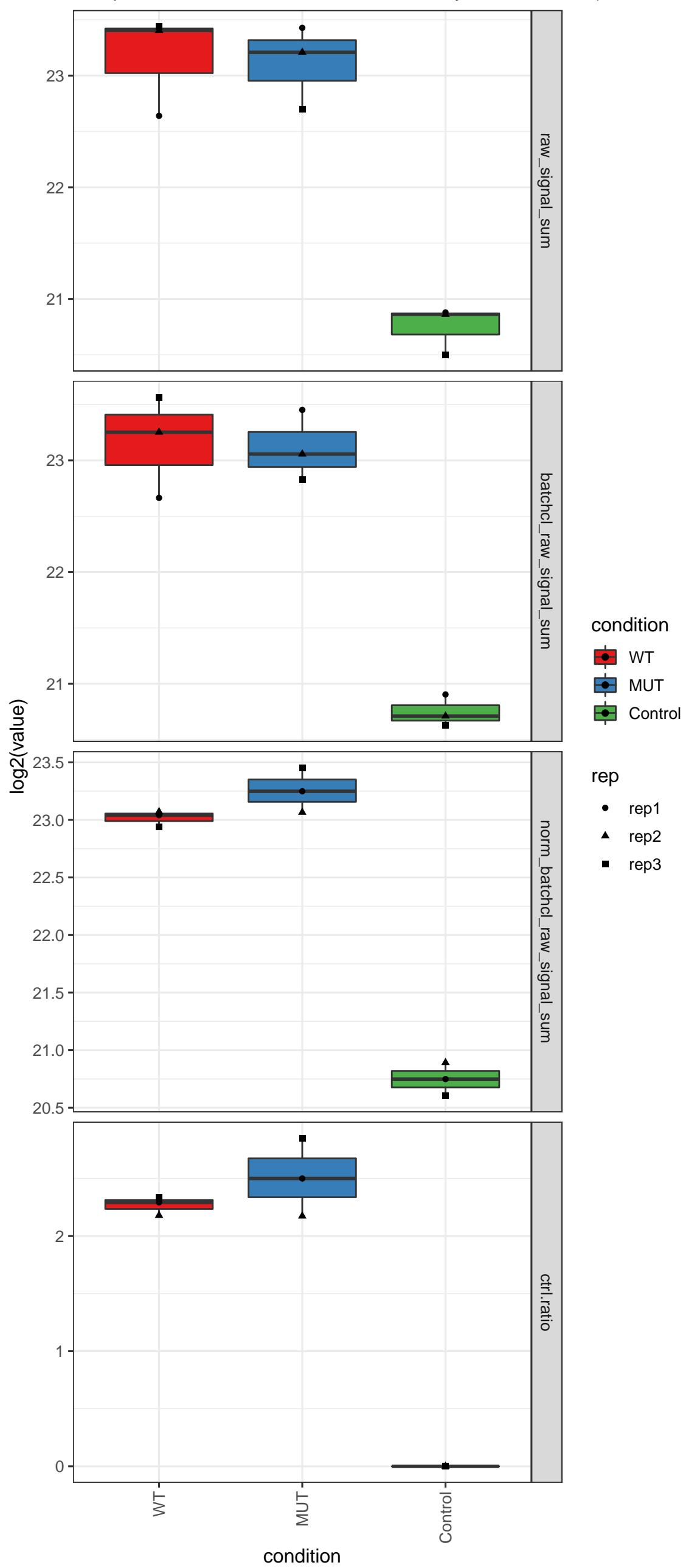
RPT3 – P33298

26S protease regulatory subunit 6B homolog OS=*Saccharomyces cerevisiae*



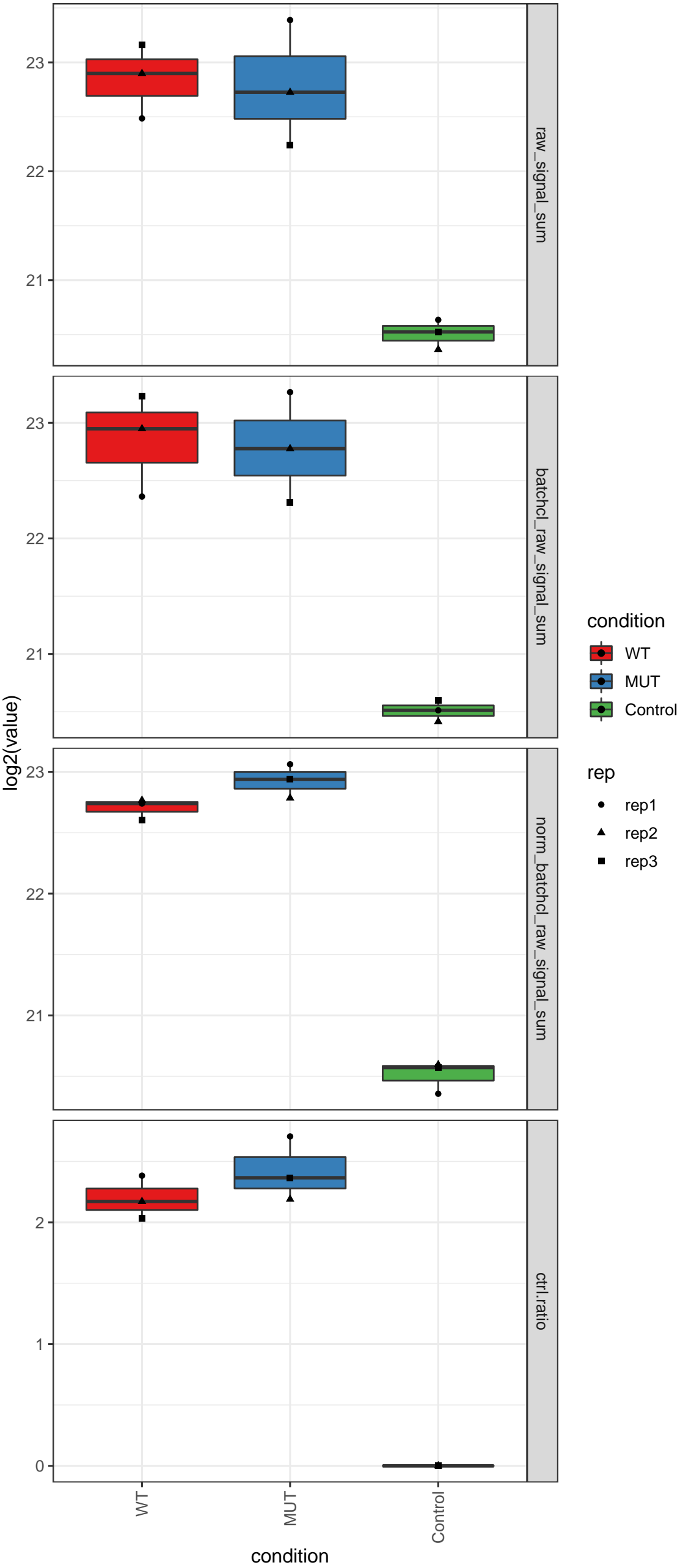
RPT4 – P53549

26S protease subunit RPT4 OS=*Saccharomyces cerevisiae* (strain ATCC 25716)



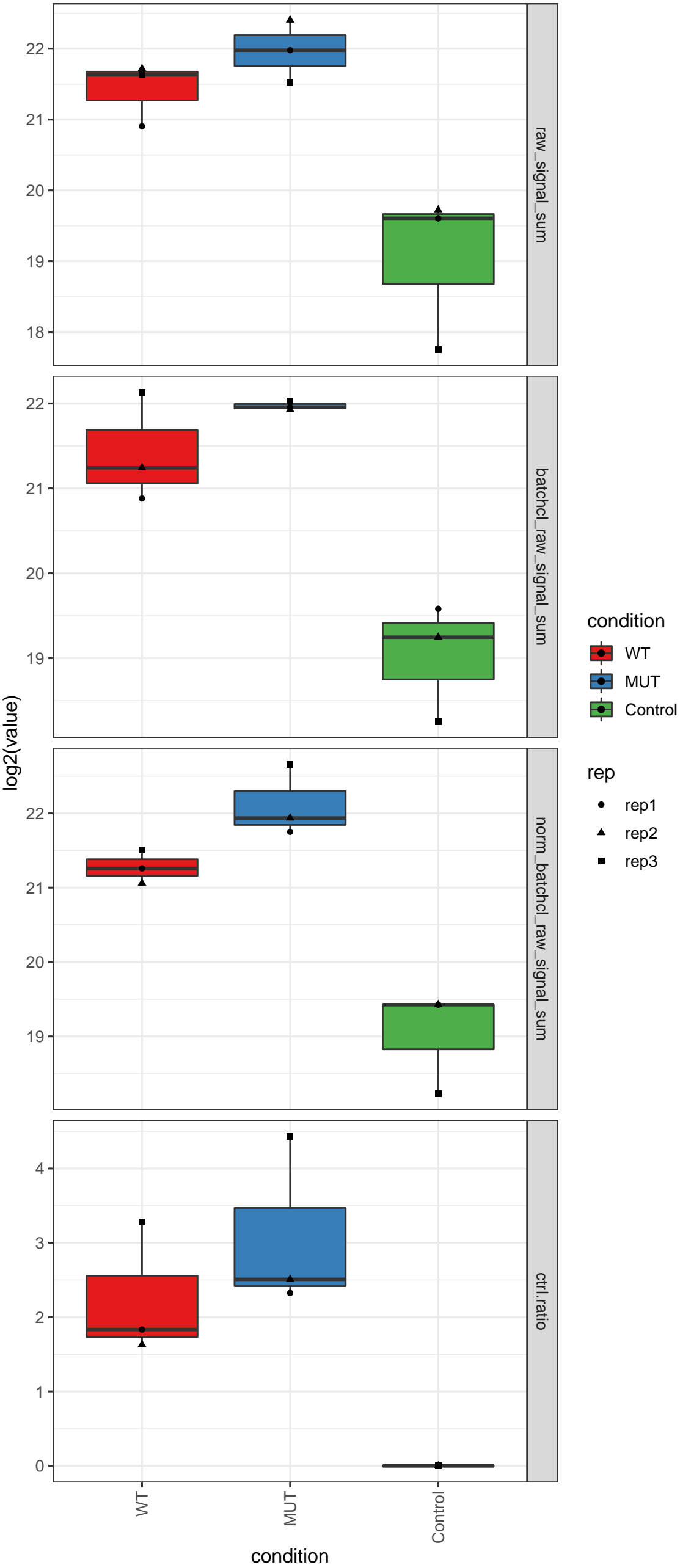
RPT6 – Q01939

26S protease regulatory subunit 8 homolog OS=*Saccharomyces cerevisiae*



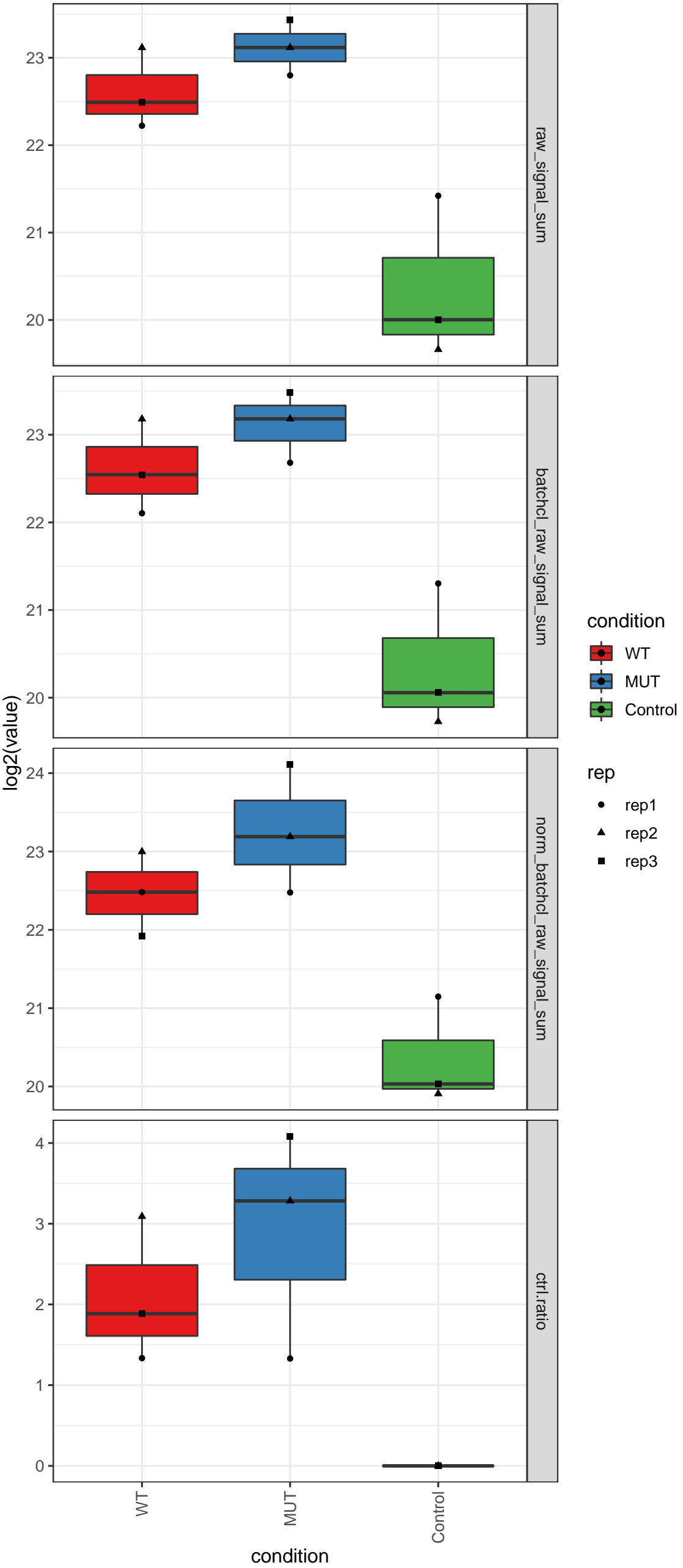
RQC2 – Q12532

Ribosome quality control complex subunit 2 OS=*Saccharomyces cerevisiae*



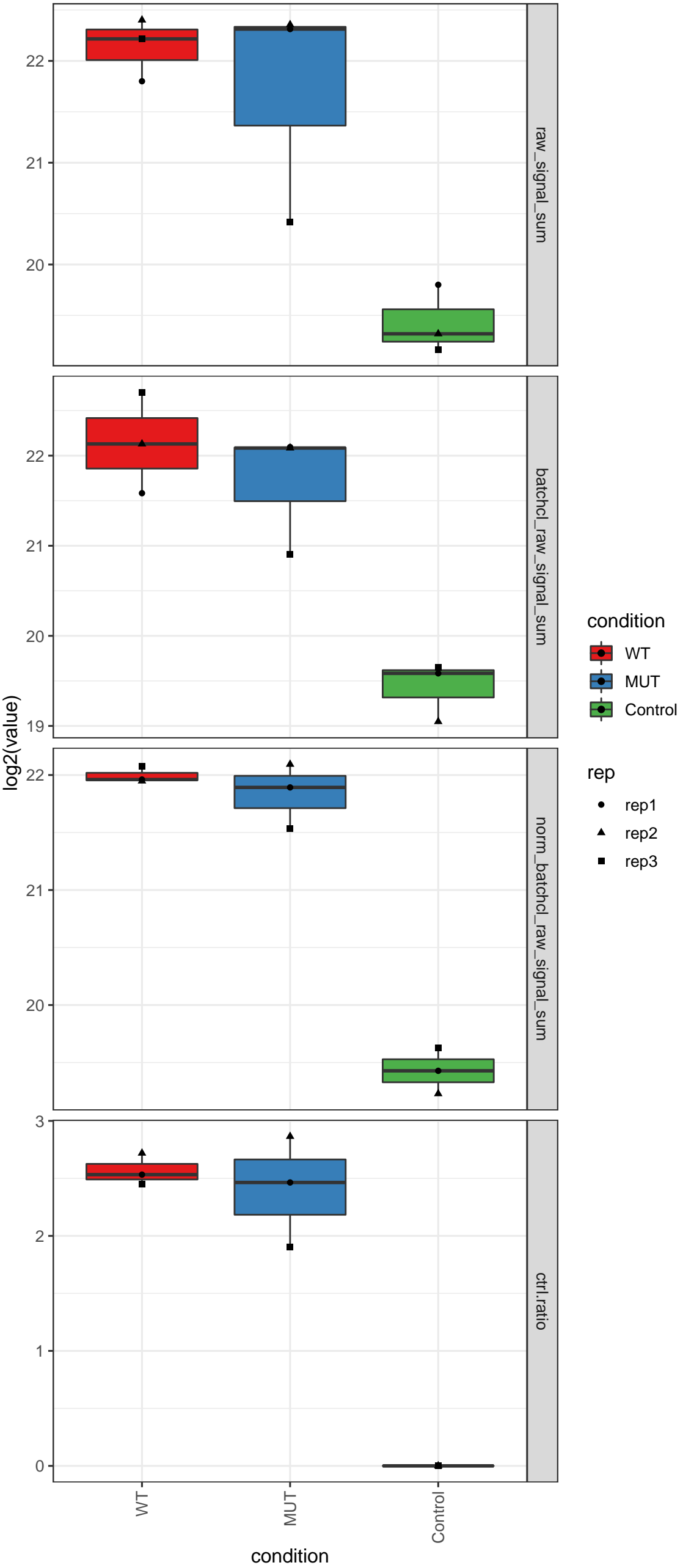
RRF1 – P38771

Ribosome–recycling factor, mitochondrial OS=*Saccharomyces cerevisiae* (



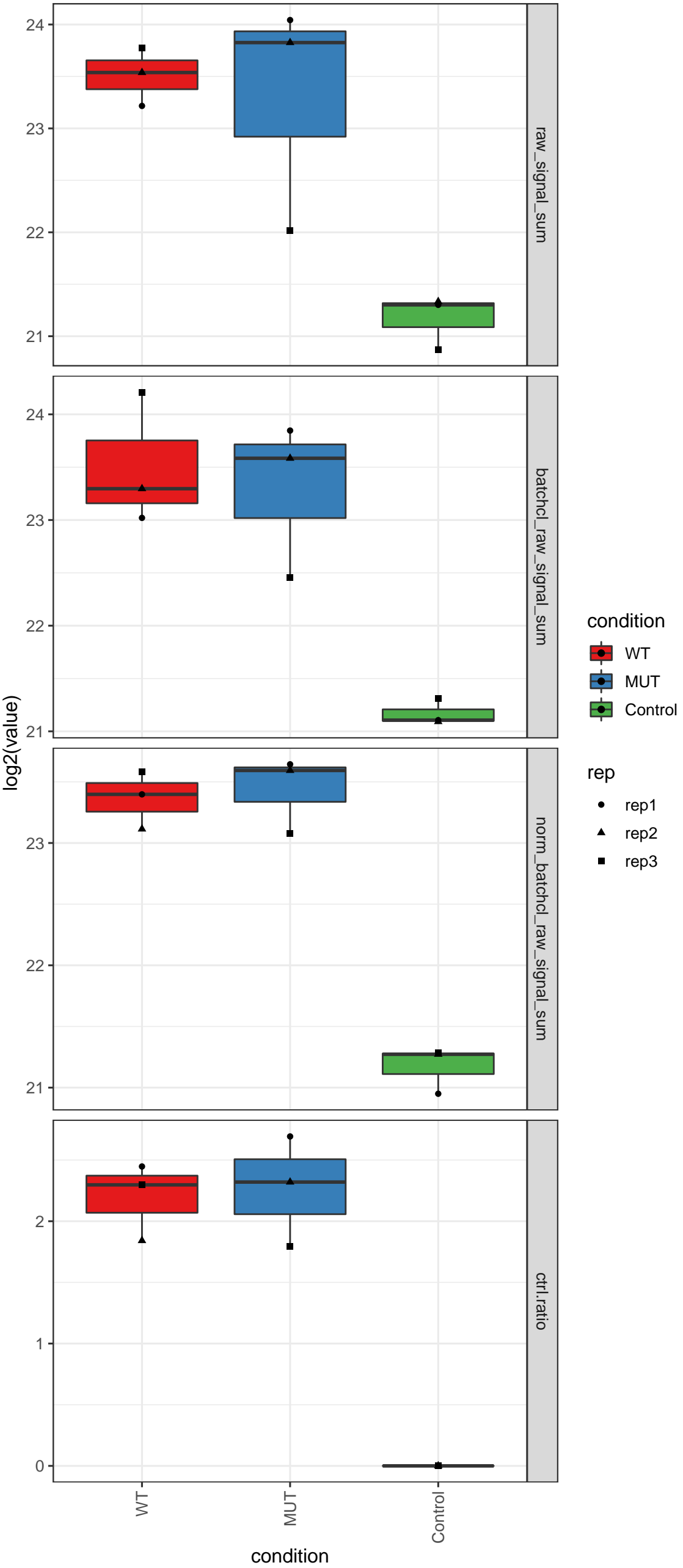
RRN5 – Q02983

RNA polymerase I–specific transcription initiation factor RRN5 OS=Saccha



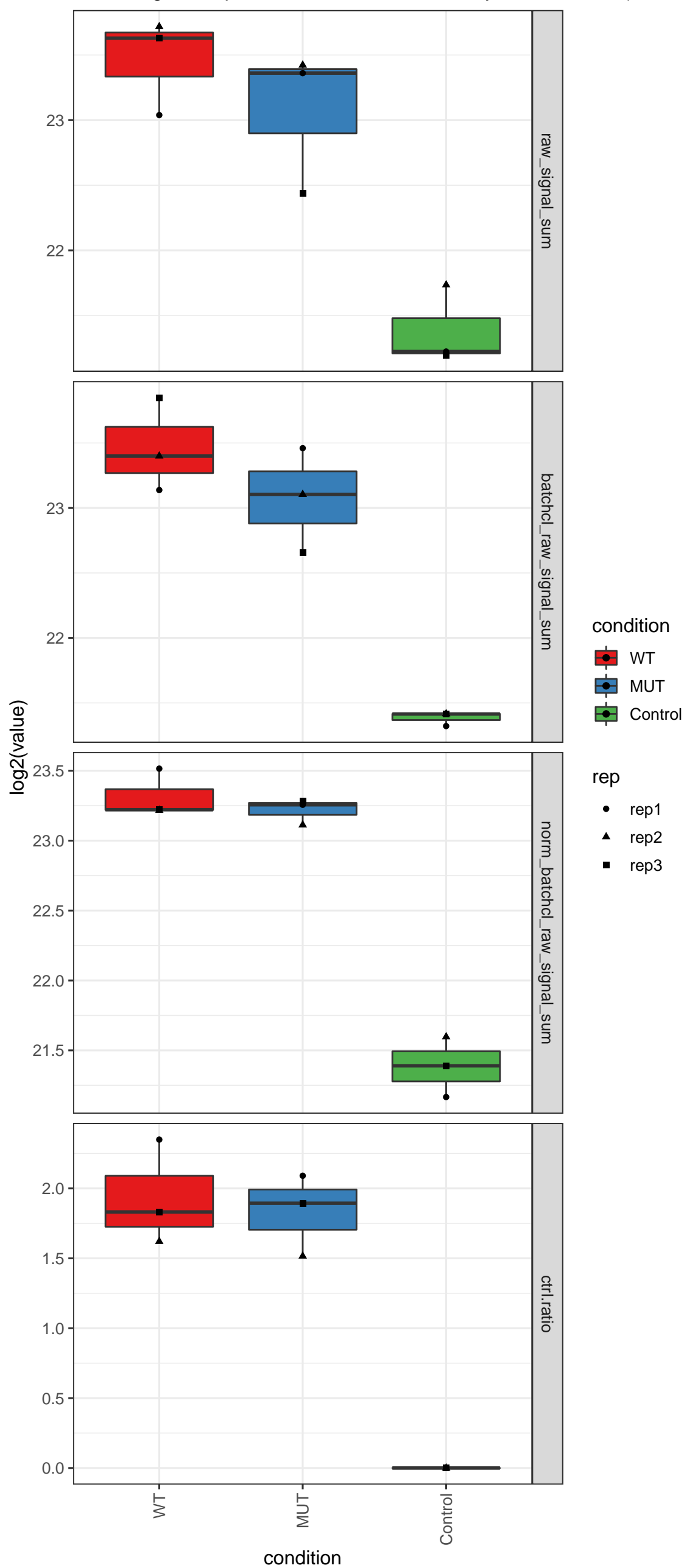
RRP14 – P36080

Ribosomal RNA–processing protein 14 OS=*Saccharomyces cerevisiae* (str



RRP5 – Q05022

rRNA biogenesis protein RRP5 OS=*Saccharomyces cerevisiae* (strain ATCC 22016 / S288c)

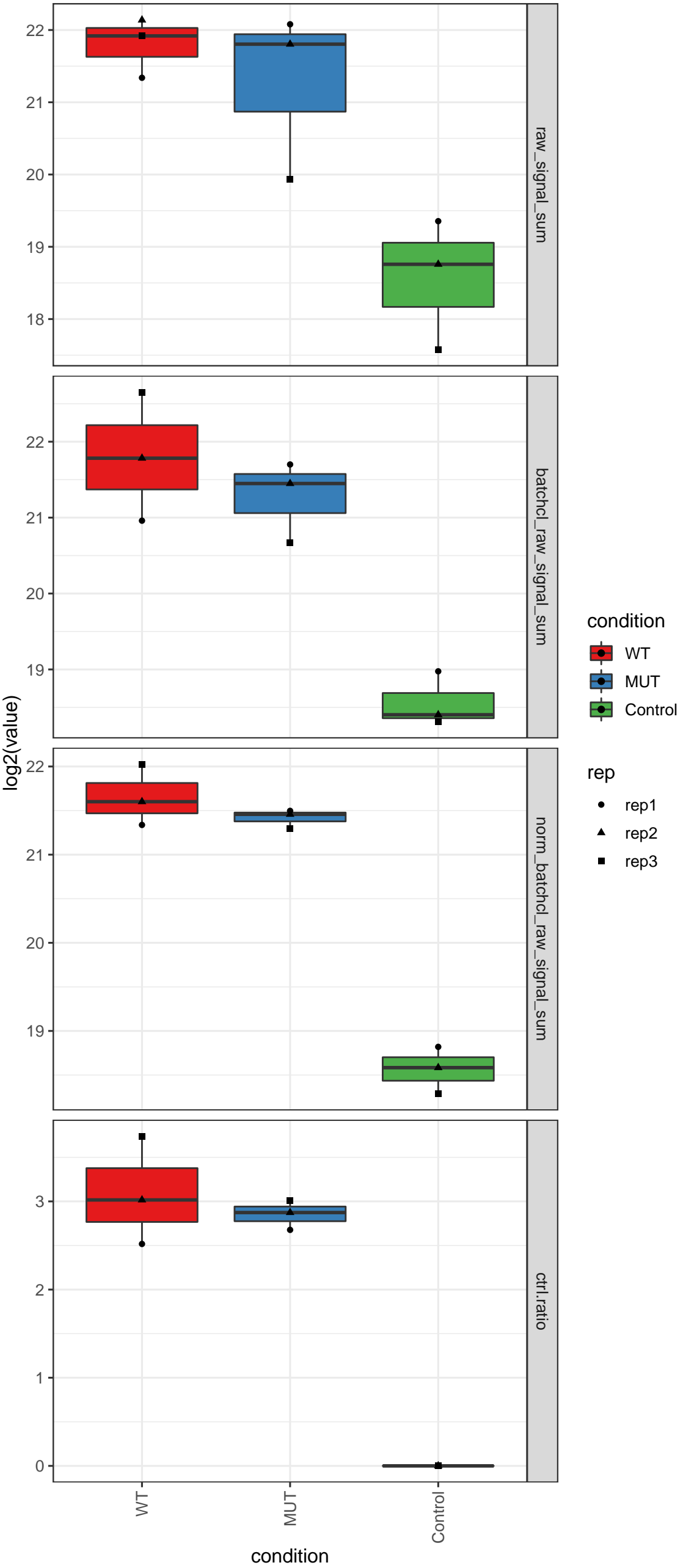


Ribosome assembly protein 4 OS=Saccharomyces cerevisiae (strain ATCC



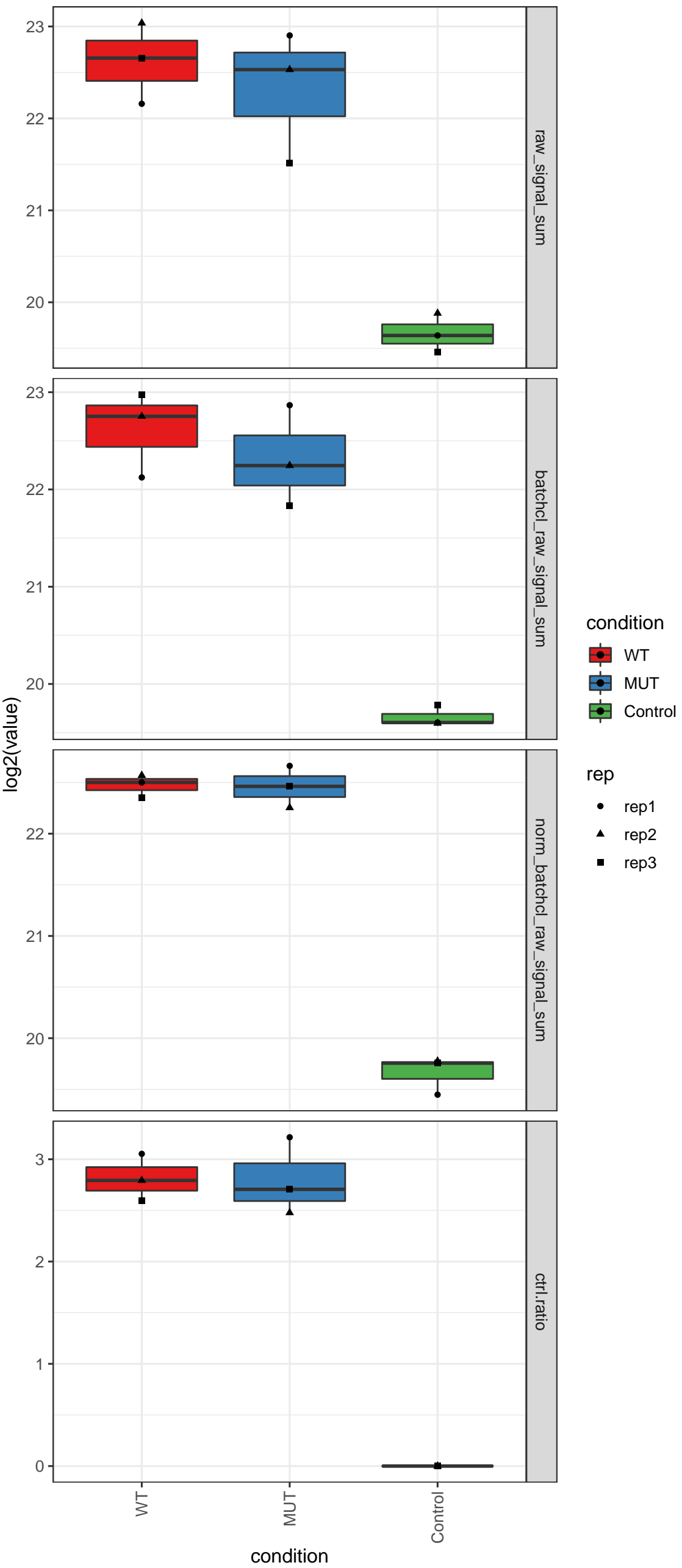
RSC2 – Q06488

Chromatin structure–remodeling complex subunit RSC2 OS=*Saccharomyces cerevisiae*



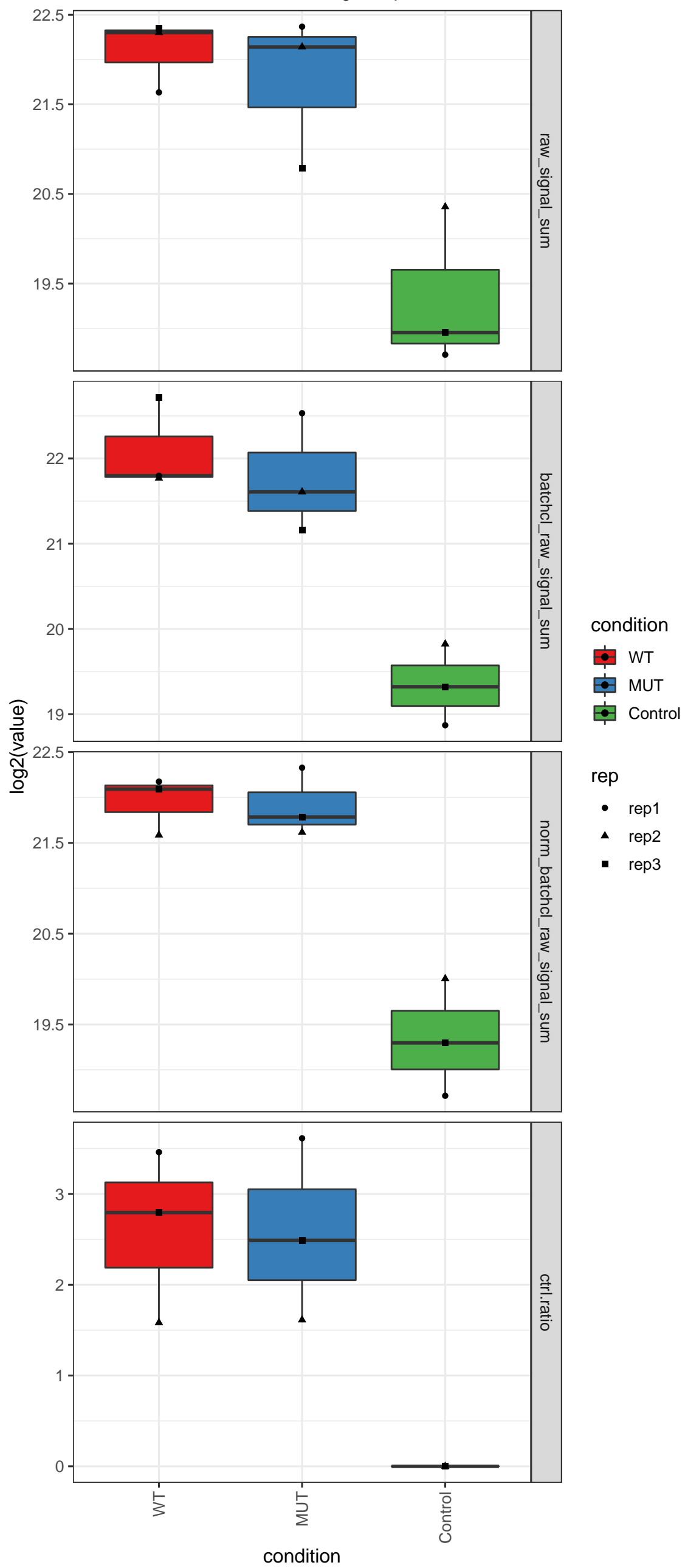
RSC8 – P43609

Chromatin structure–remodeling complex protein RSC8 OS=*Saccharomyces cerevisiae*



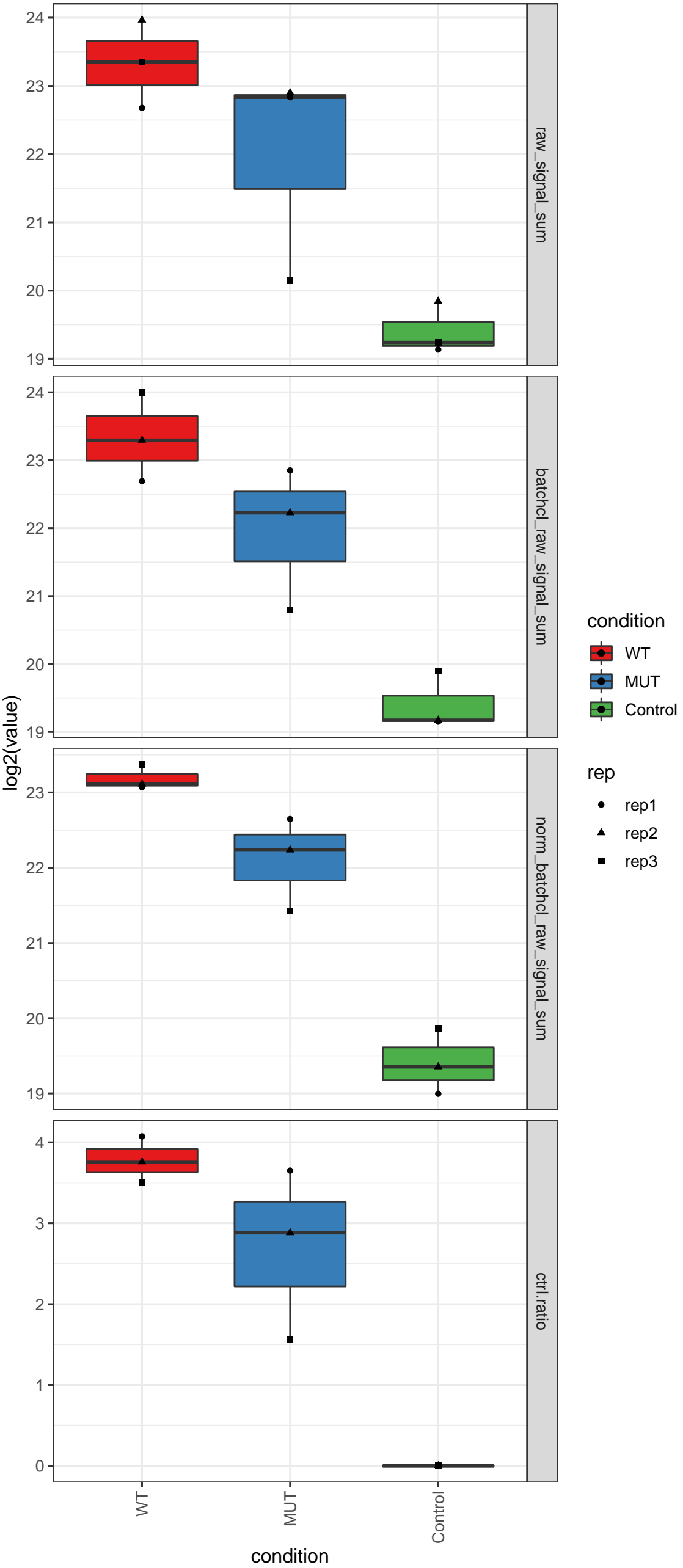
RSC9 – Q03124

Chromatin structure–remodeling complex subunit RSC9 OS=Saccharomy



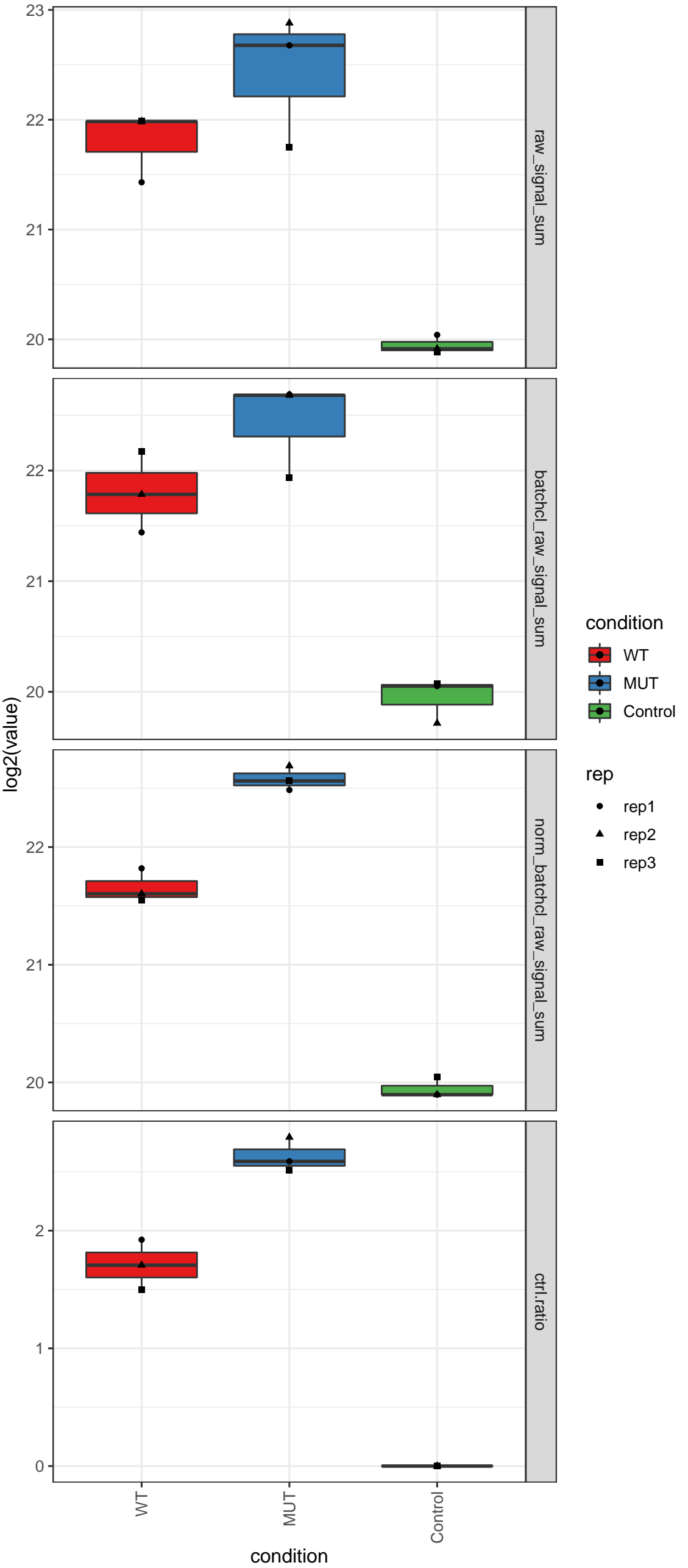
RSF1 – Q05043

Respiration factor 1 OS=*Saccharomyces cerevisiae* (strain ATCC 204508 /



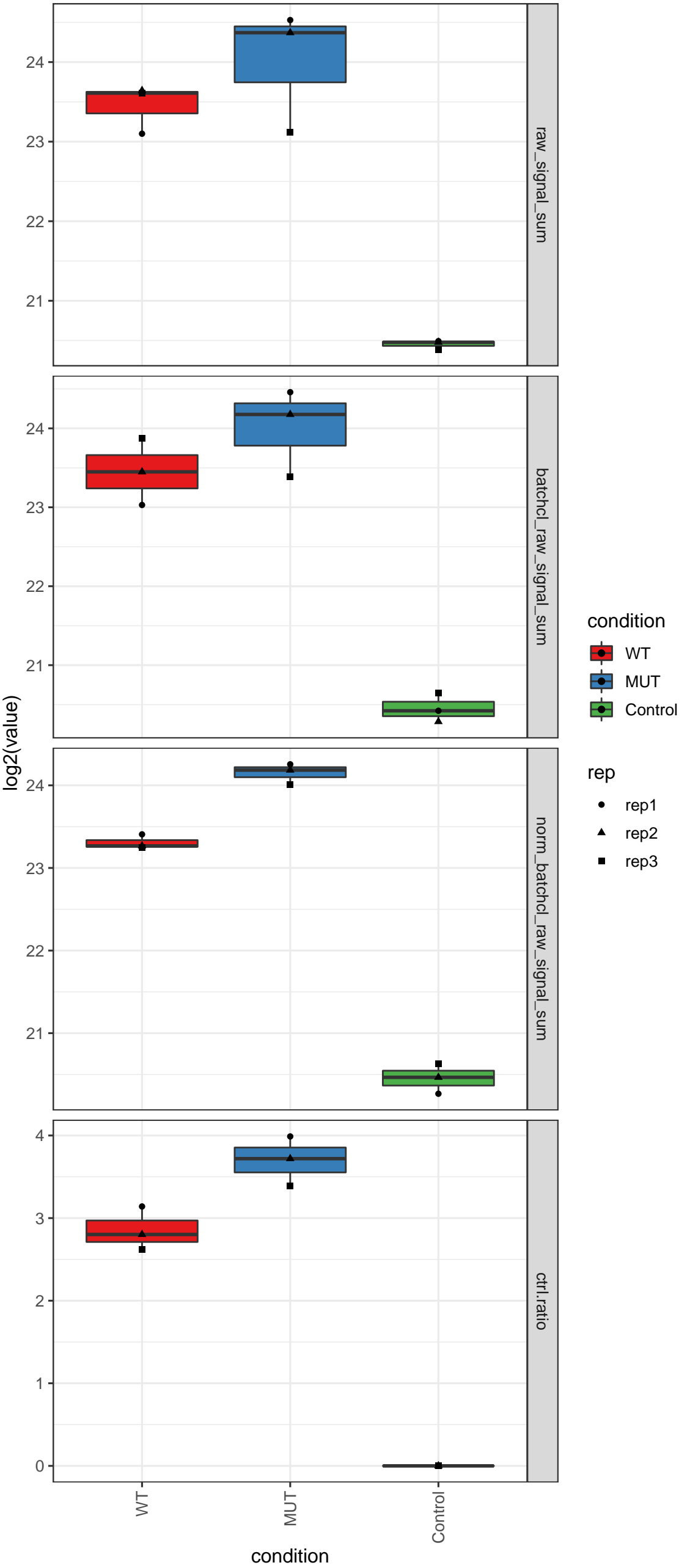
RSM18 – P40033

37S ribosomal protein RSM18, mitochondrial OS=*Saccharomyces cerevisiae*



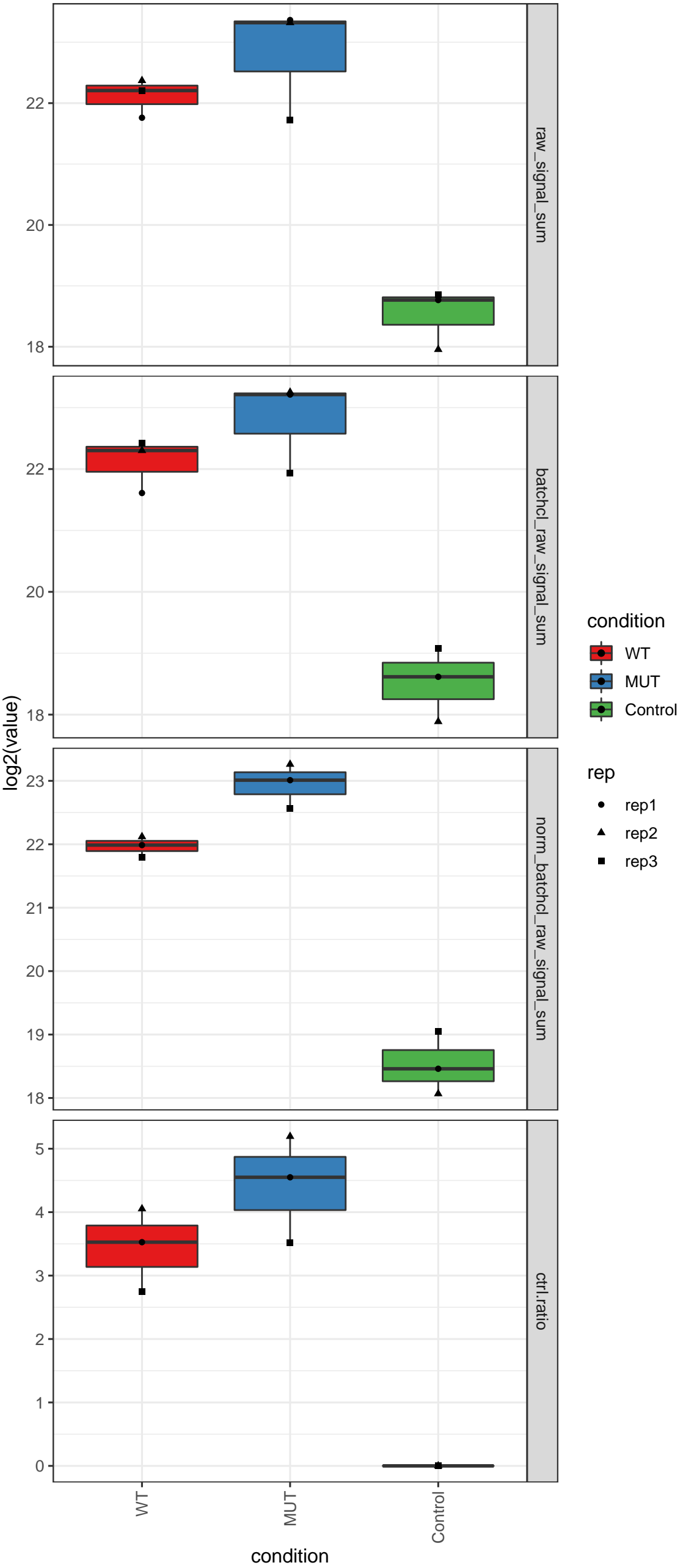
RSM23 – Q01163

37S ribosomal protein S23, mitochondrial OS=Saccharomyces cerevisiae (



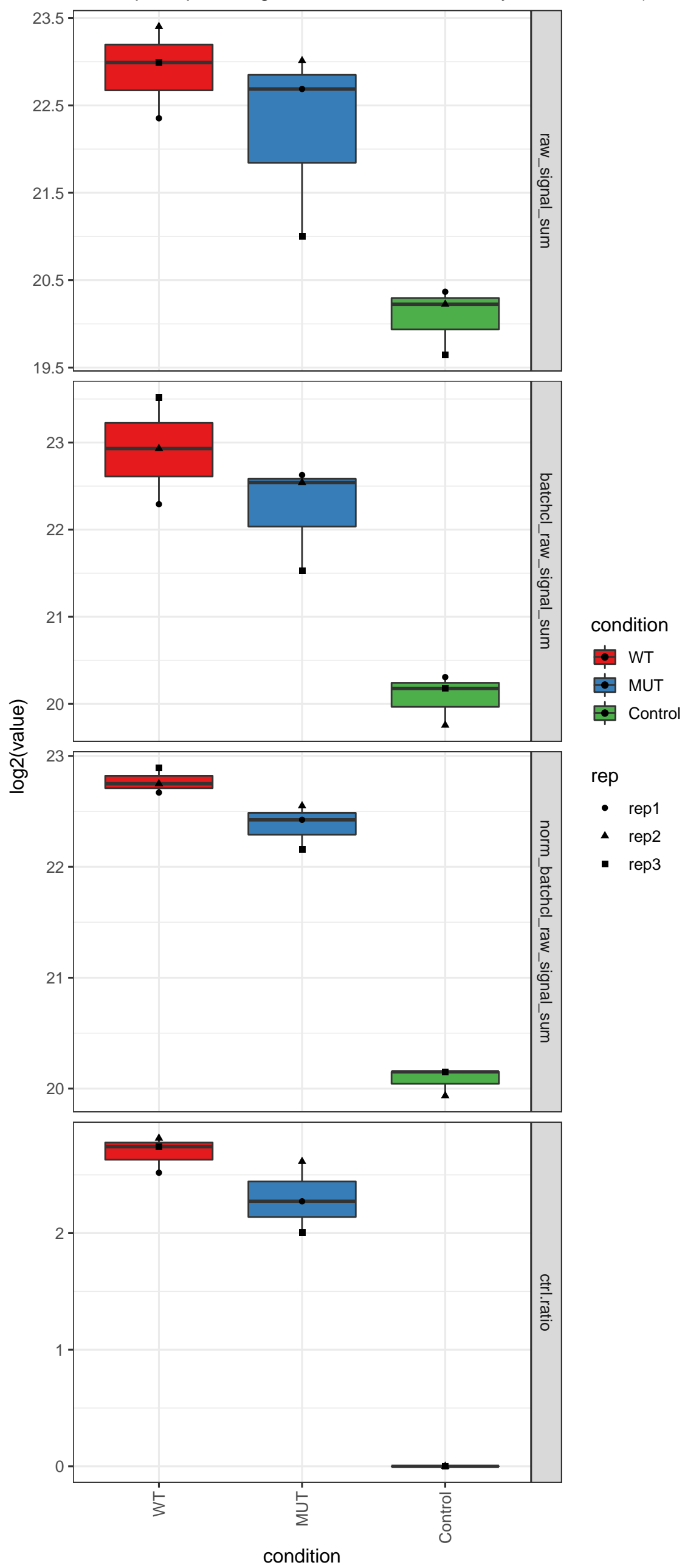
RSM24 – Q03976

37S ribosomal protein S24, mitochondrial OS=Saccharomyces cerevisiae (



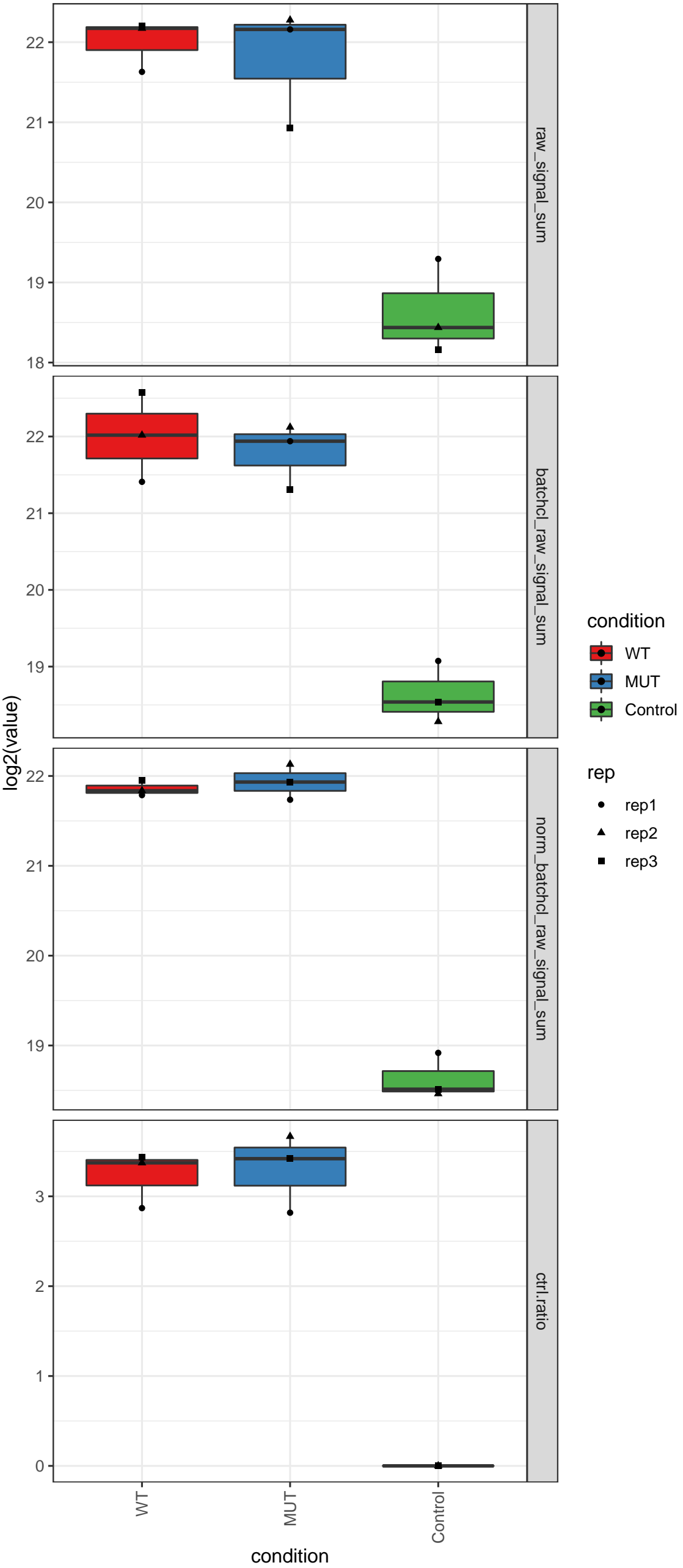
RSP5 – P39940

E3 ubiquitin–protein ligase RSP5 OS=*Saccharomyces cerevisiae* (strain)



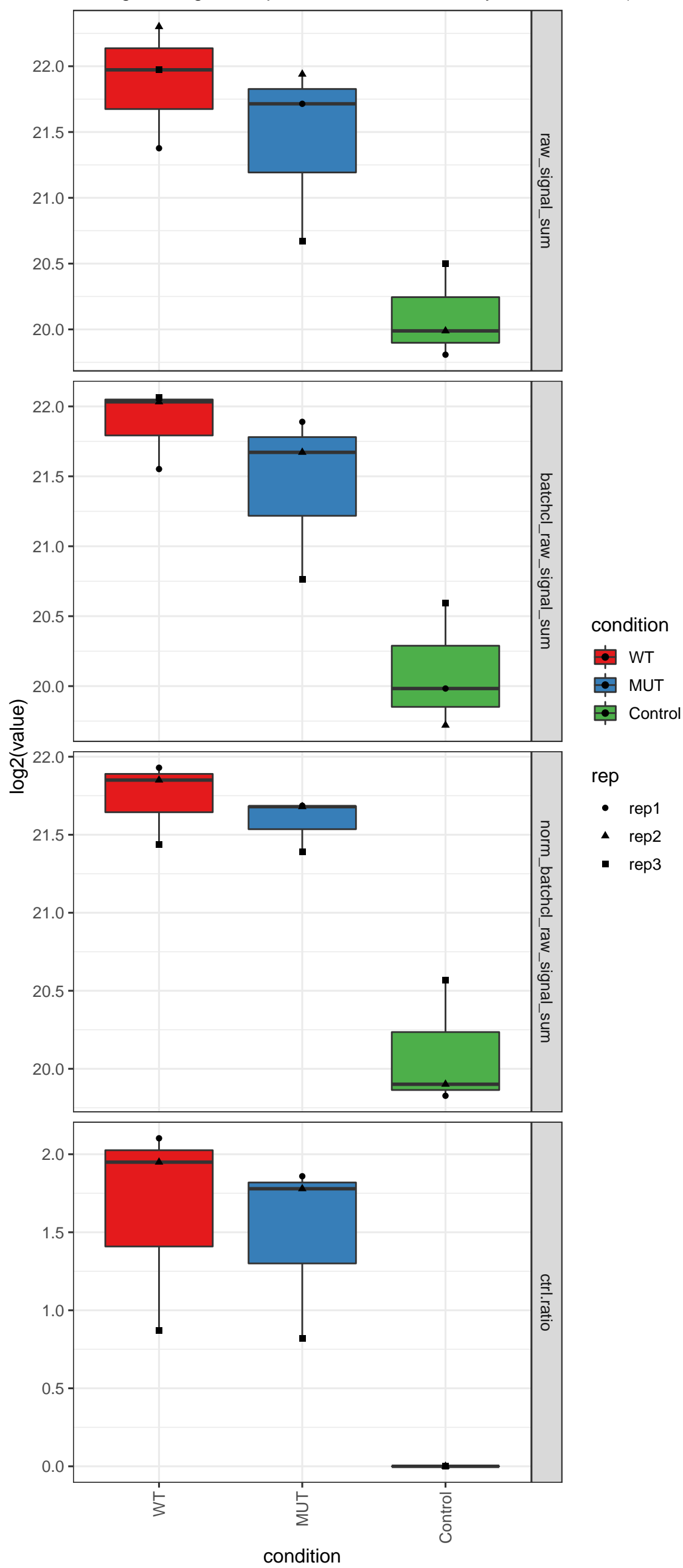
RSR1 – P13856

Ras-related protein RSR1 OS=*Saccharomyces cerevisiae* (strain ATCC 20



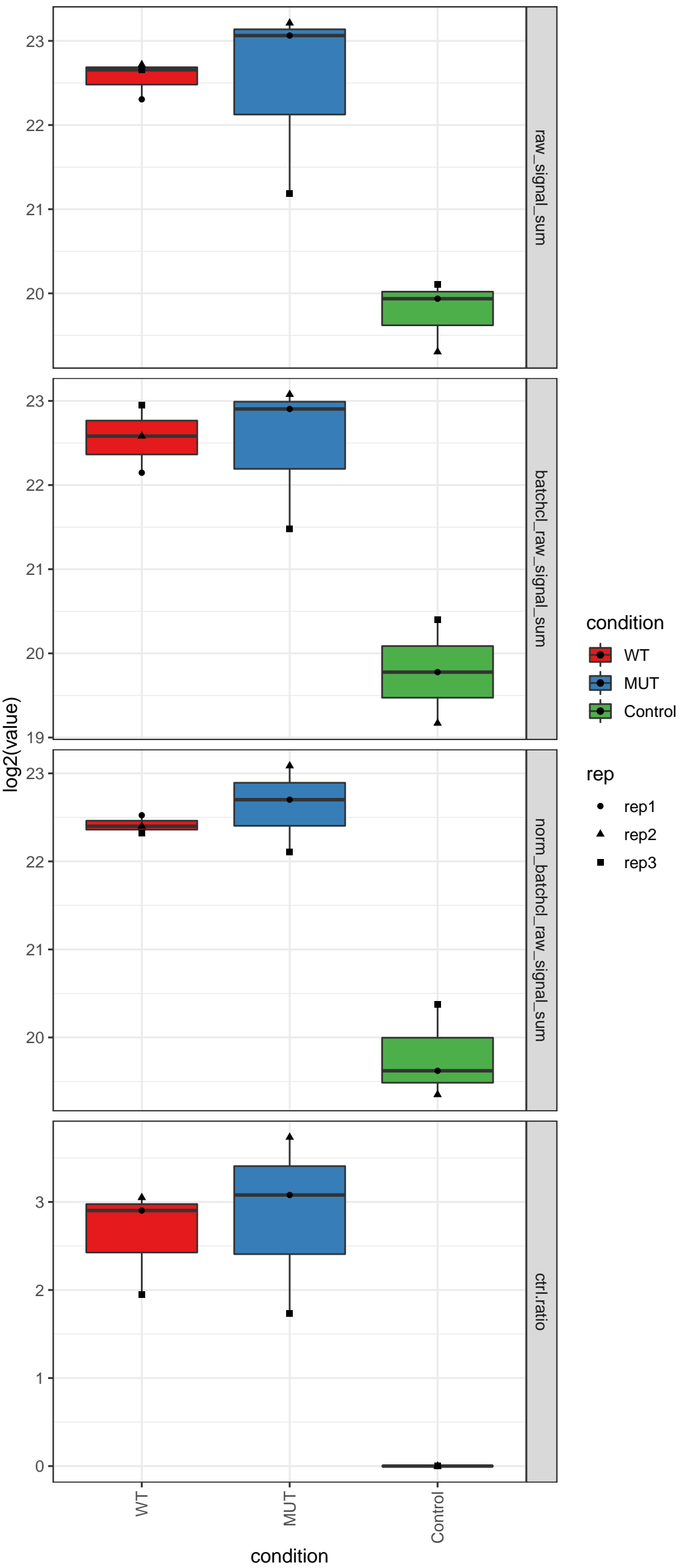
RTG2 – P32608

Retrograde regulation protein 2 OS=*Saccharomyces cerevisiae* (strain ATCC 25716)



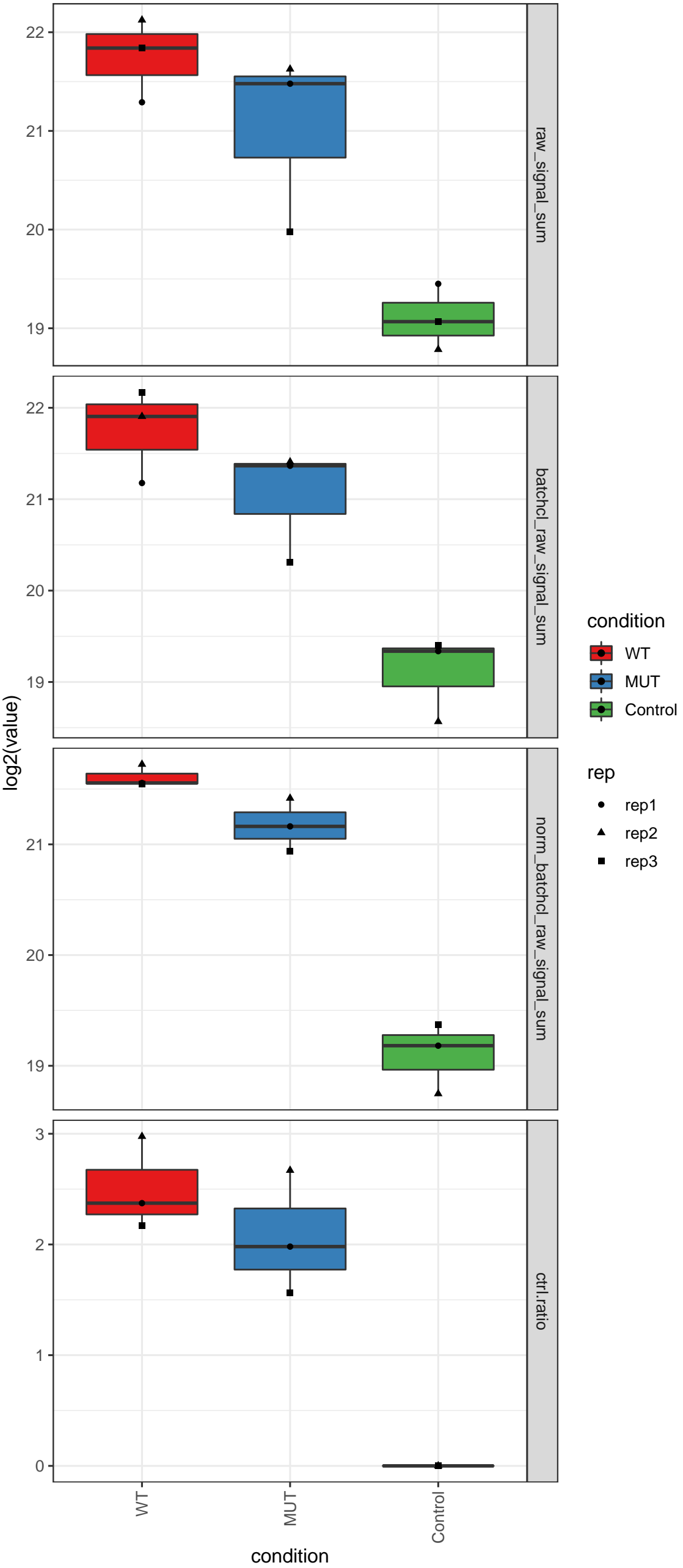
RTS1 – P38903

Serine/threonine–protein phosphatase 2A 56 kDa regulatory subunit delta



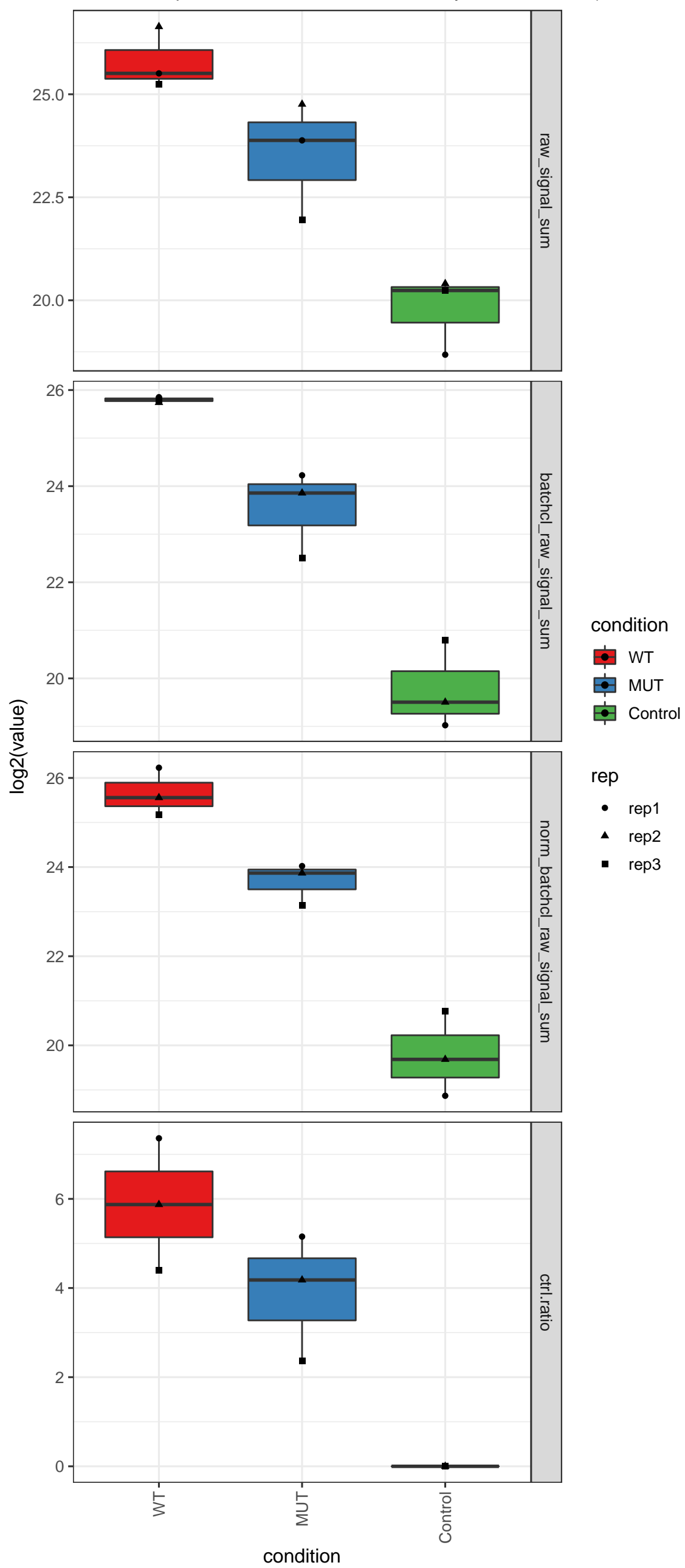
RTS2 – P40962

Zinc finger protein RTS2 OS=*Saccharomyces cerevisiae* (strain ATCC 204



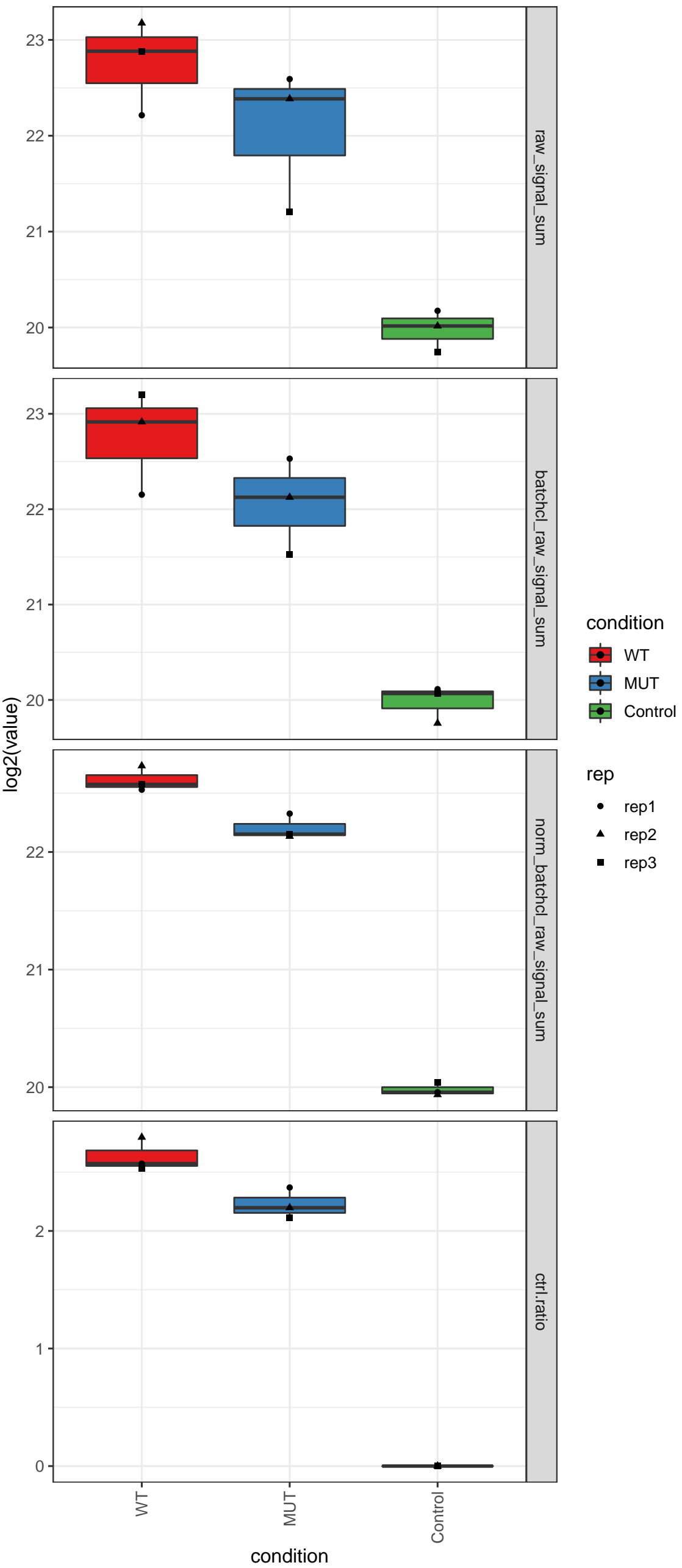
RTT106 – P40161

Histone chaperone RTT106 OS=*Saccharomyces cerevisiae* (strain ATCC



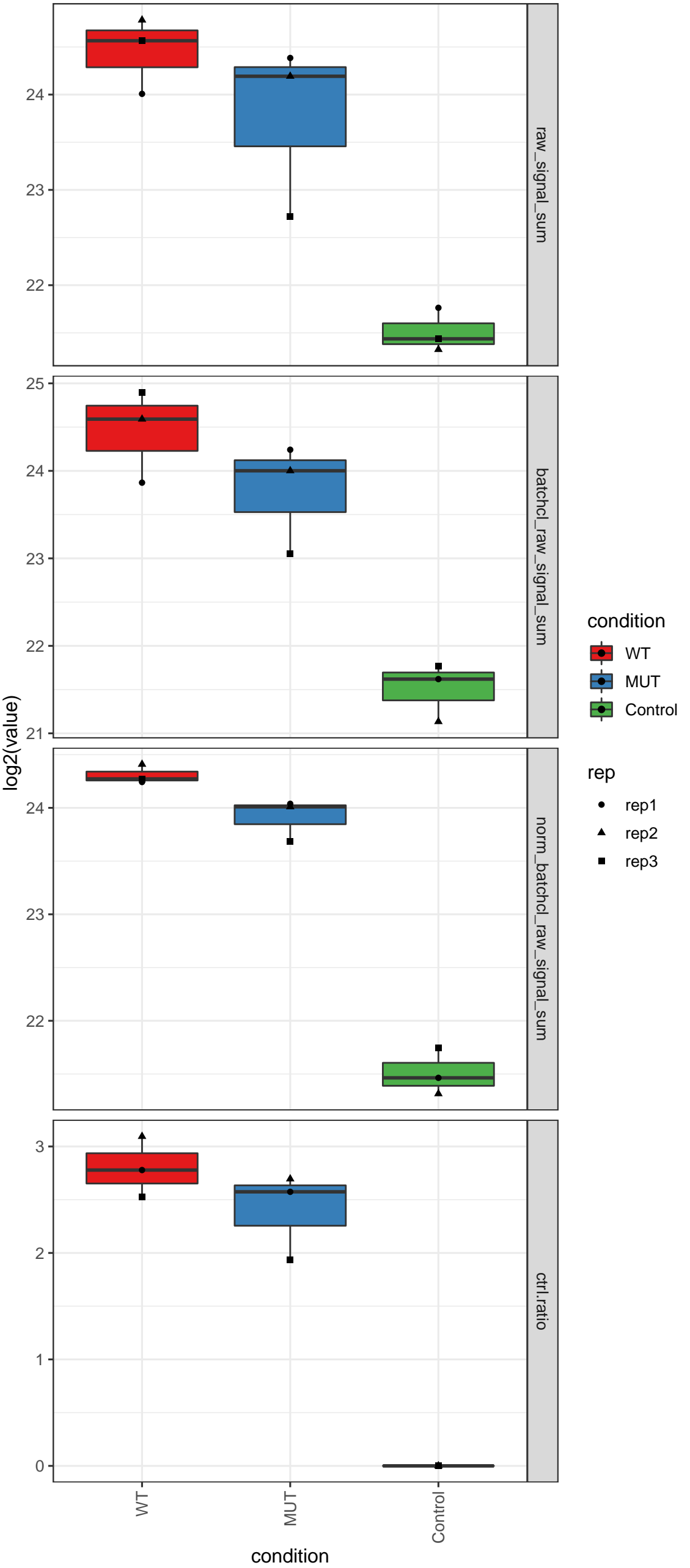
RVB1 – Q03940

RuvB-like protein 1 OS=*Saccharomyces cerevisiae* (strain ATCC 204508 /



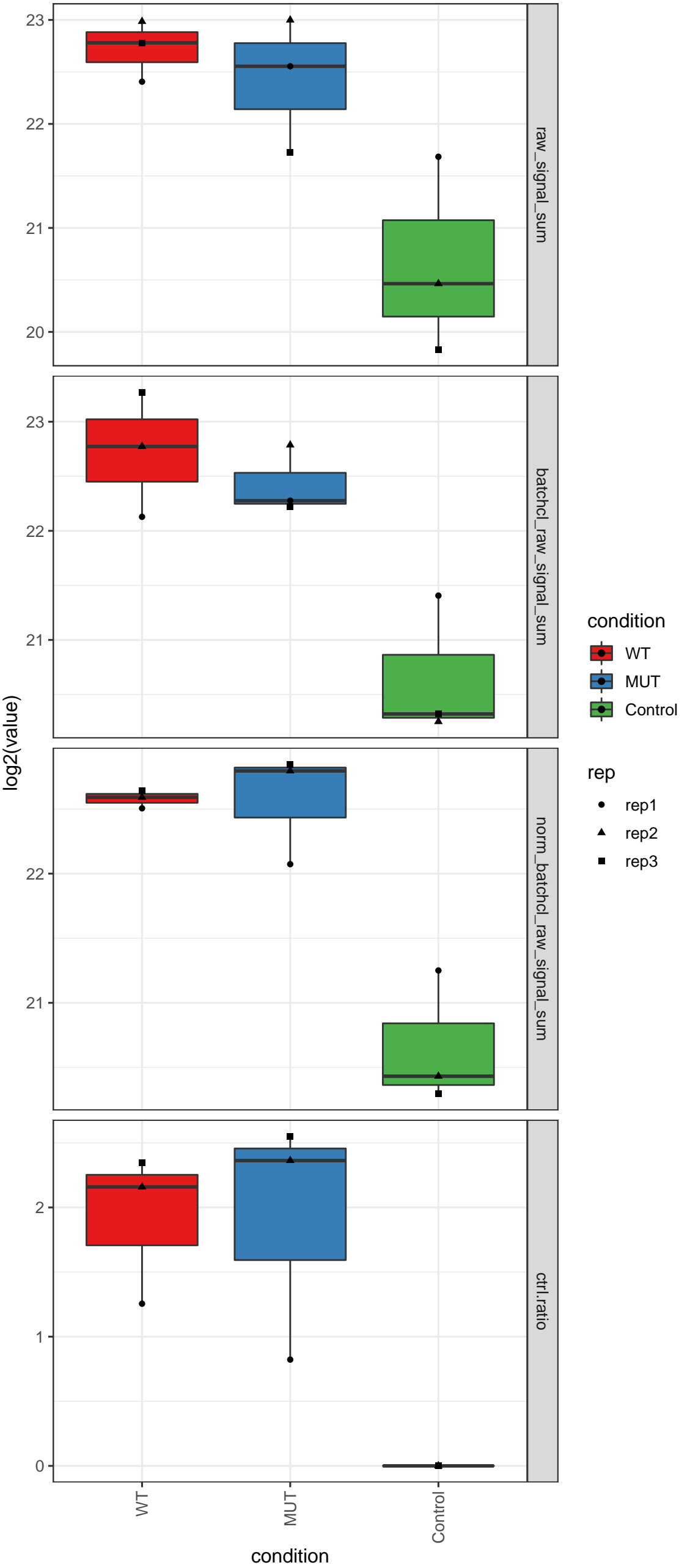
RVB2 – Q12464

RuvB-like protein 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 /



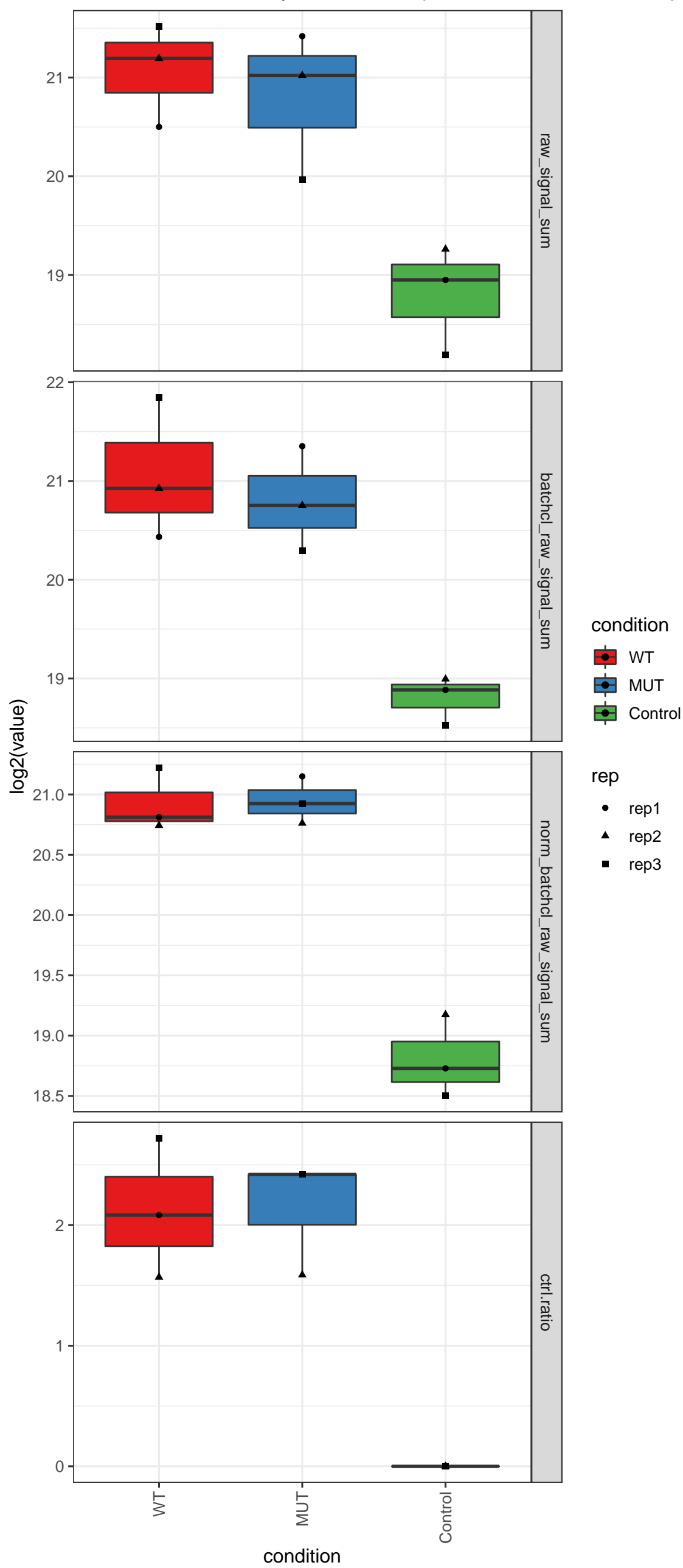
RVS161 – P25343

Reduced viability upon starvation protein 161 OS=*Saccharomyces cerevisiae*



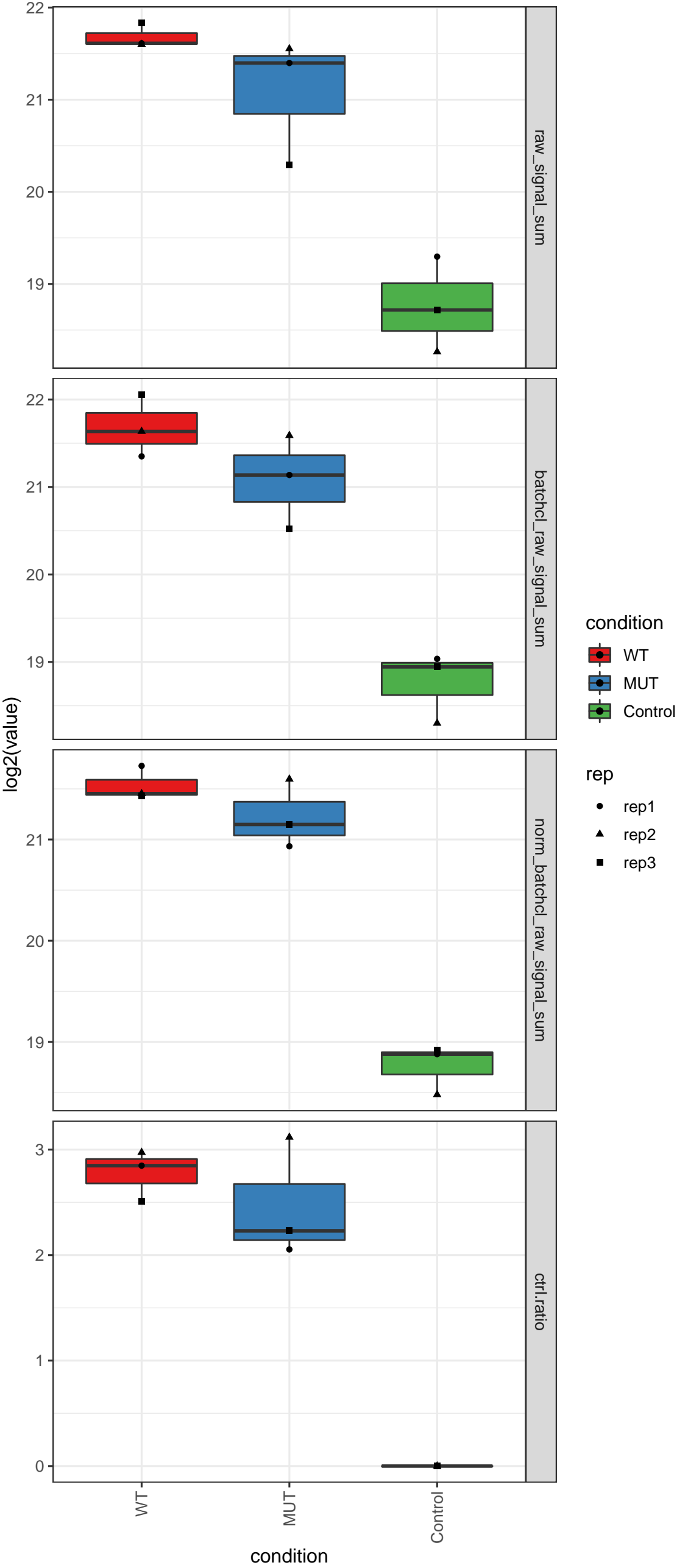
SAC6 – P32599

Fimbrin OS=*Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) G



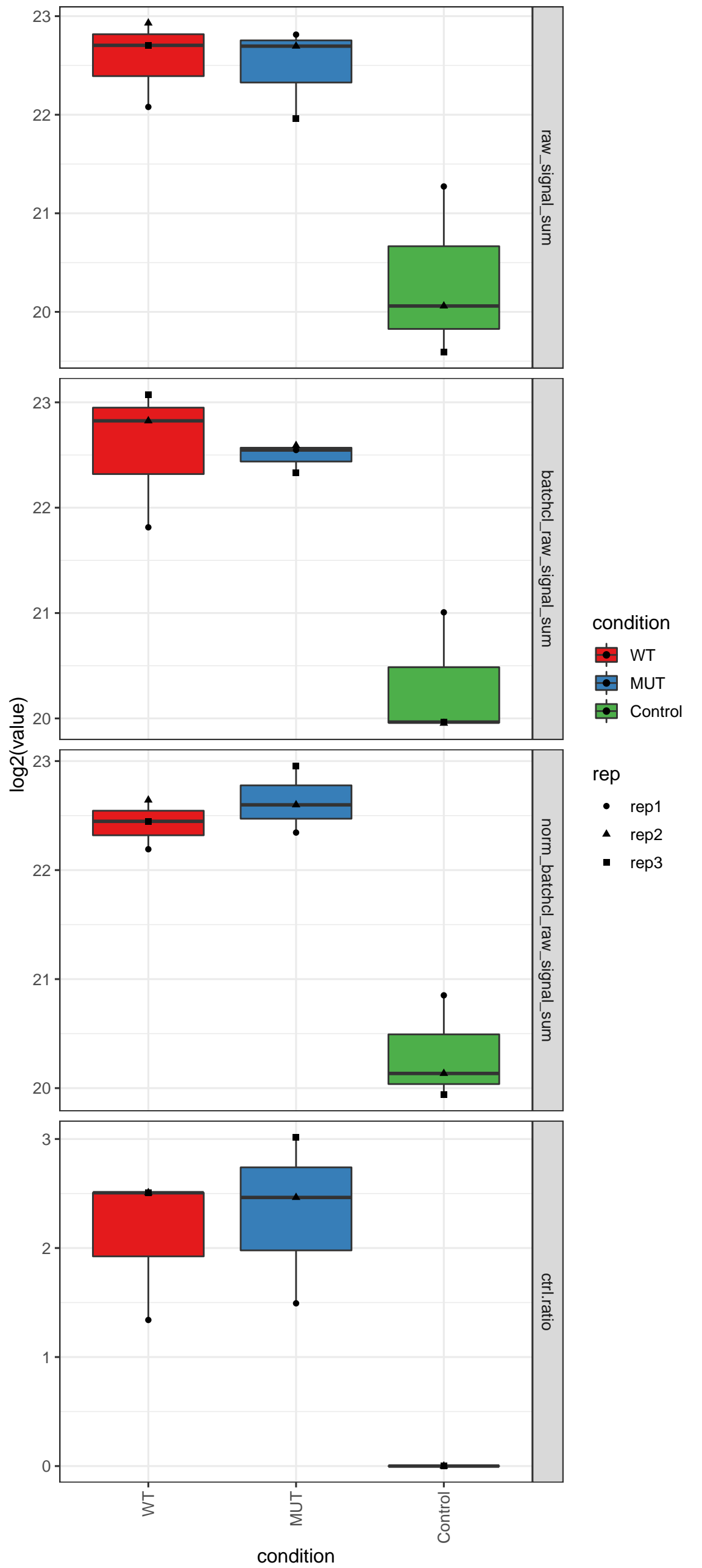
SAH1 – P39954

Adenosylhomocysteinase OS=*Saccharomyces cerevisiae* (strain ATCC 20454)



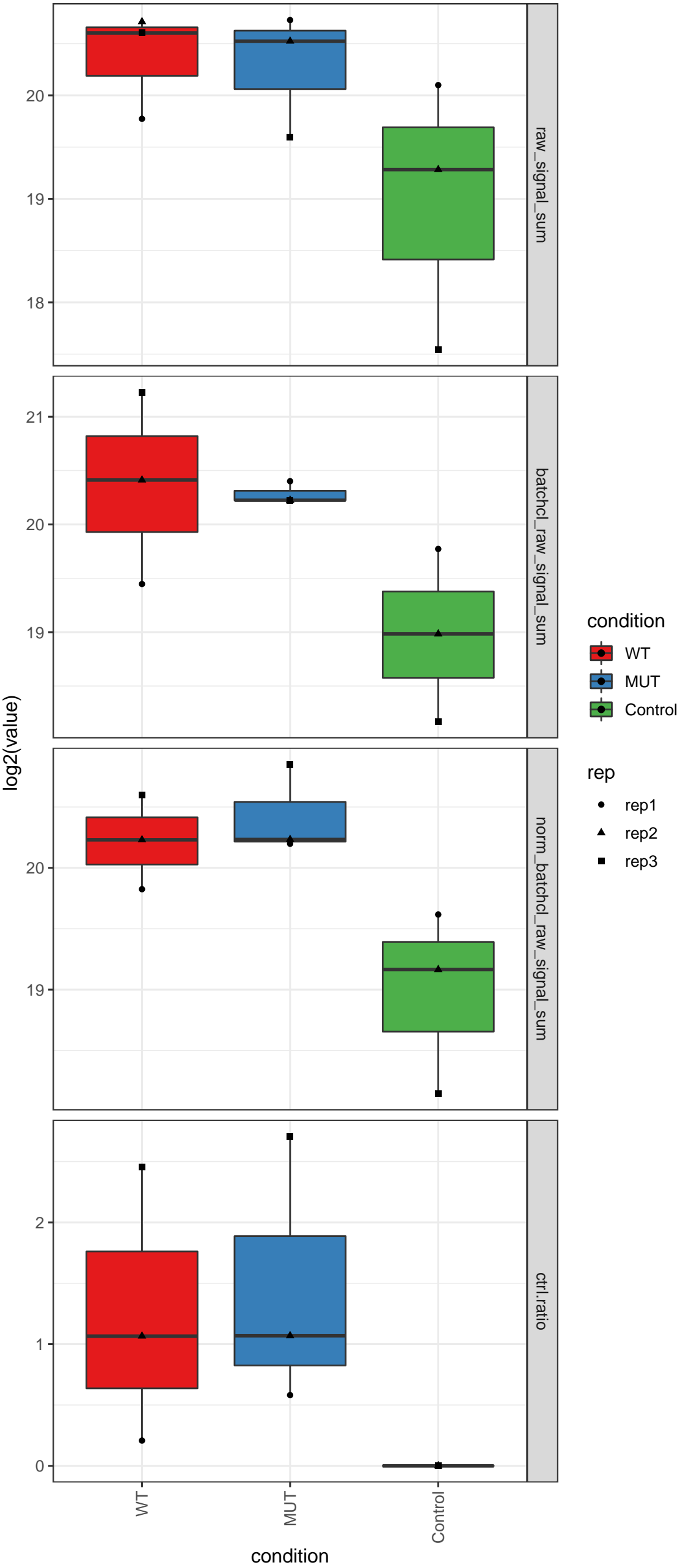
SAM1 – P10659

S-adenosylmethionine synthase 1 OS=*Saccharomyces cerevisiae* (strain /



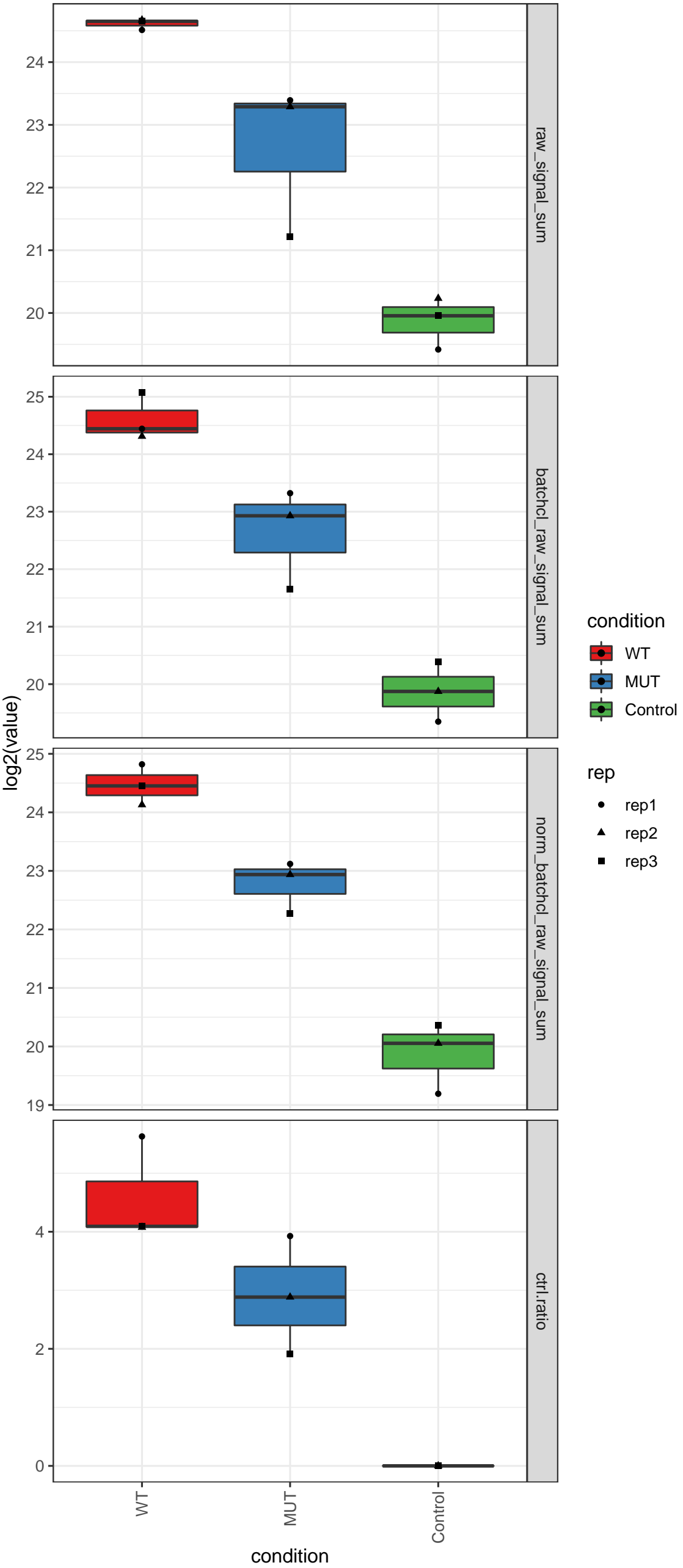
SAM2 – P19358

S-adenosylmethionine synthase 2 OS=Saccharomyces cerevisiae (strain /



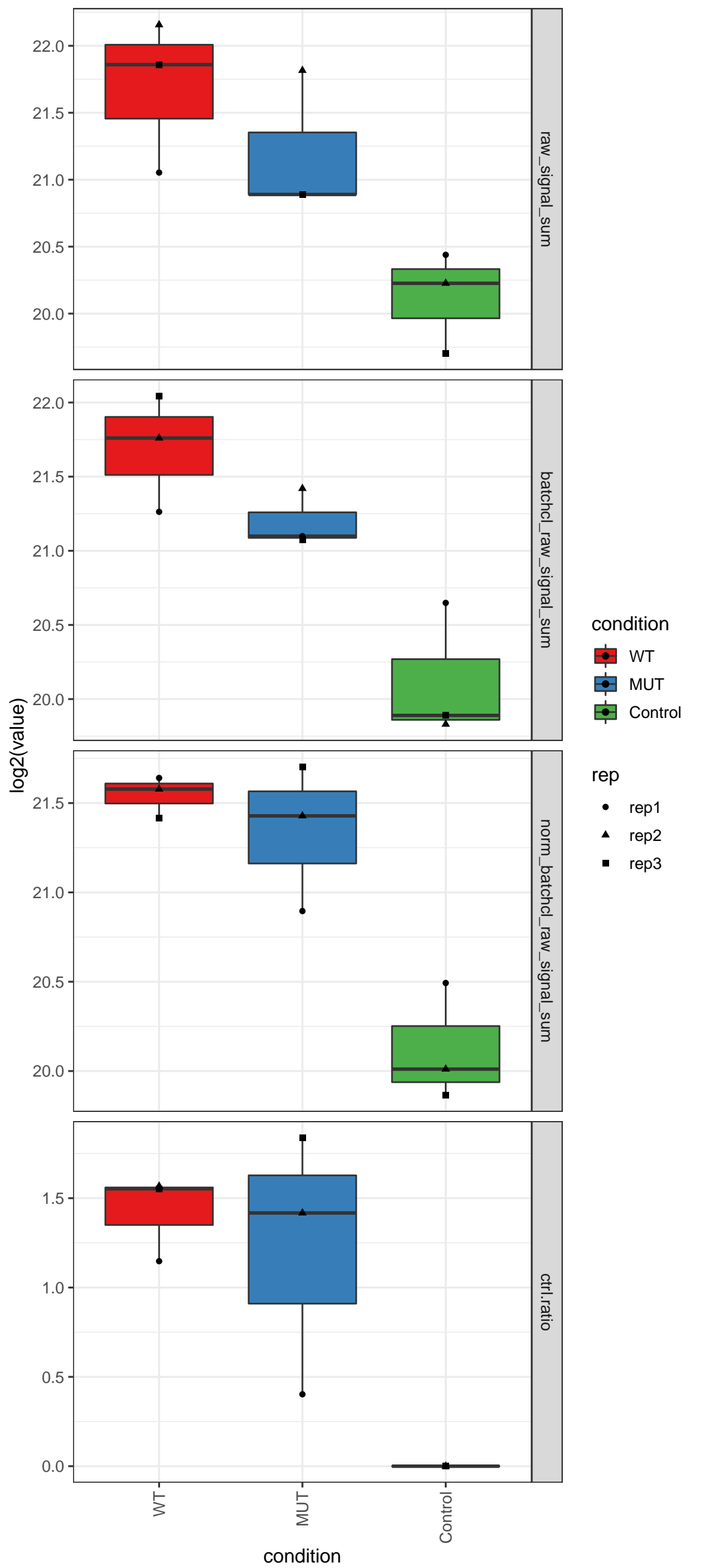
SAS3 – P34218

Histone acetyltransferase SAS3 OS=*Saccharomyces cerevisiae* (strain ATCC 22016 /



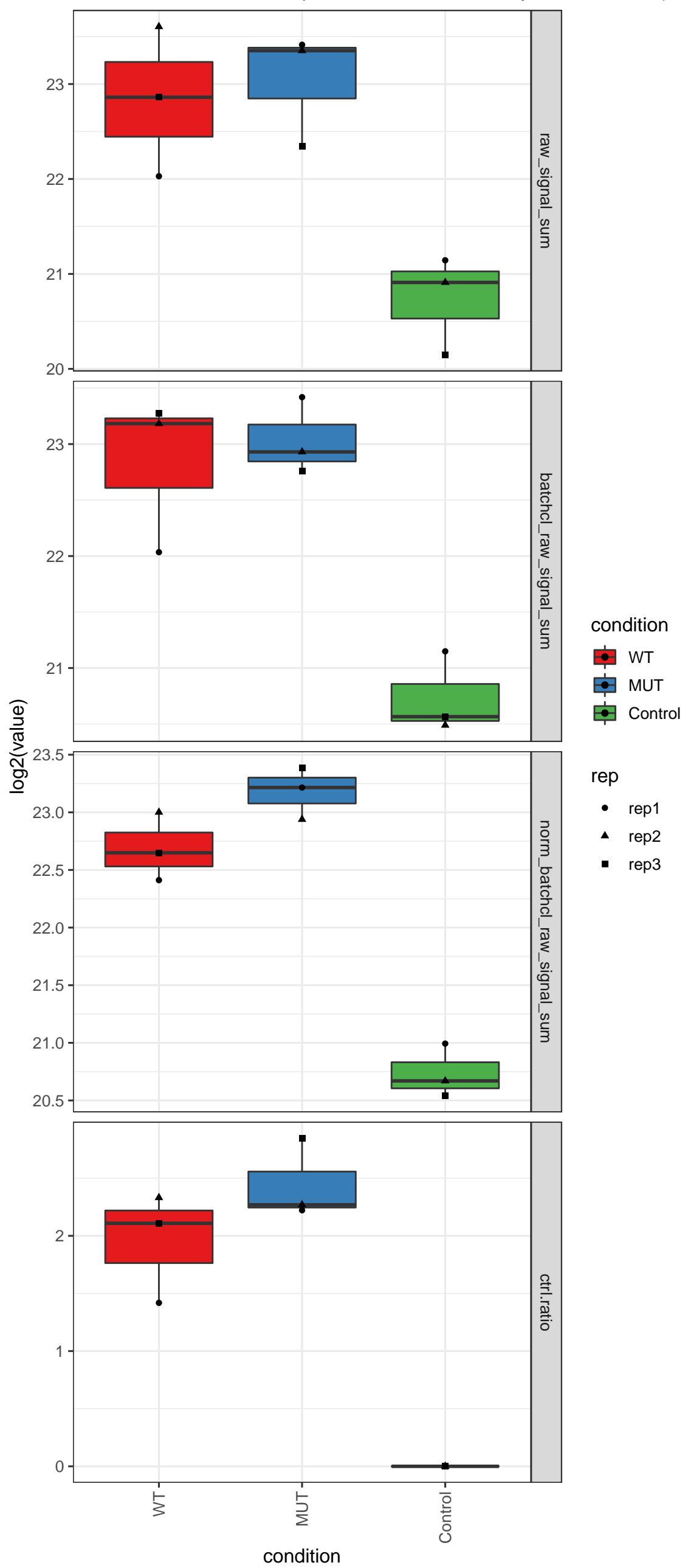
SBP1 – P10080

Single-stranded nucleic acid-binding protein OS=*Saccharomyces cerevisiae*



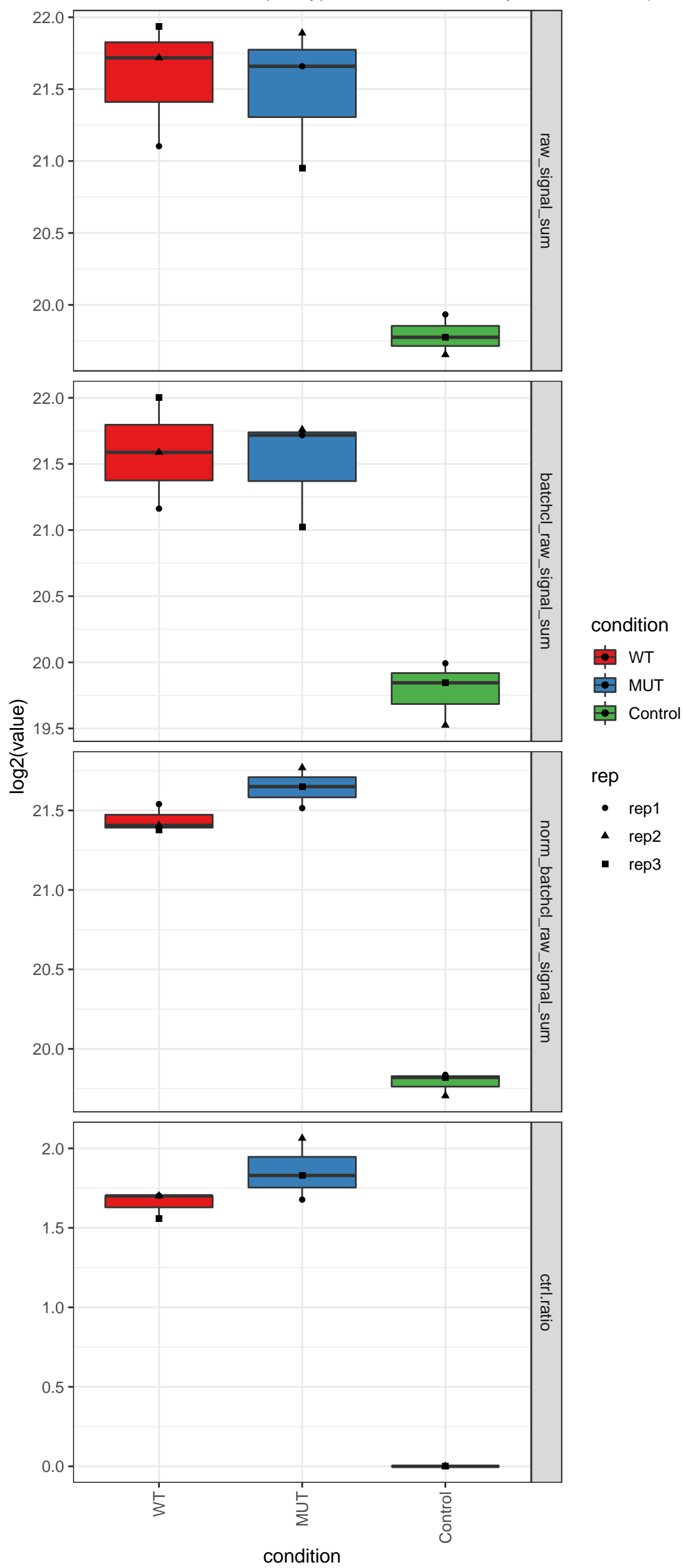
SCC2 – Q04002

Sister chromatid cohesion protein 2 OS=*Saccharomyces cerevisiae* (strain



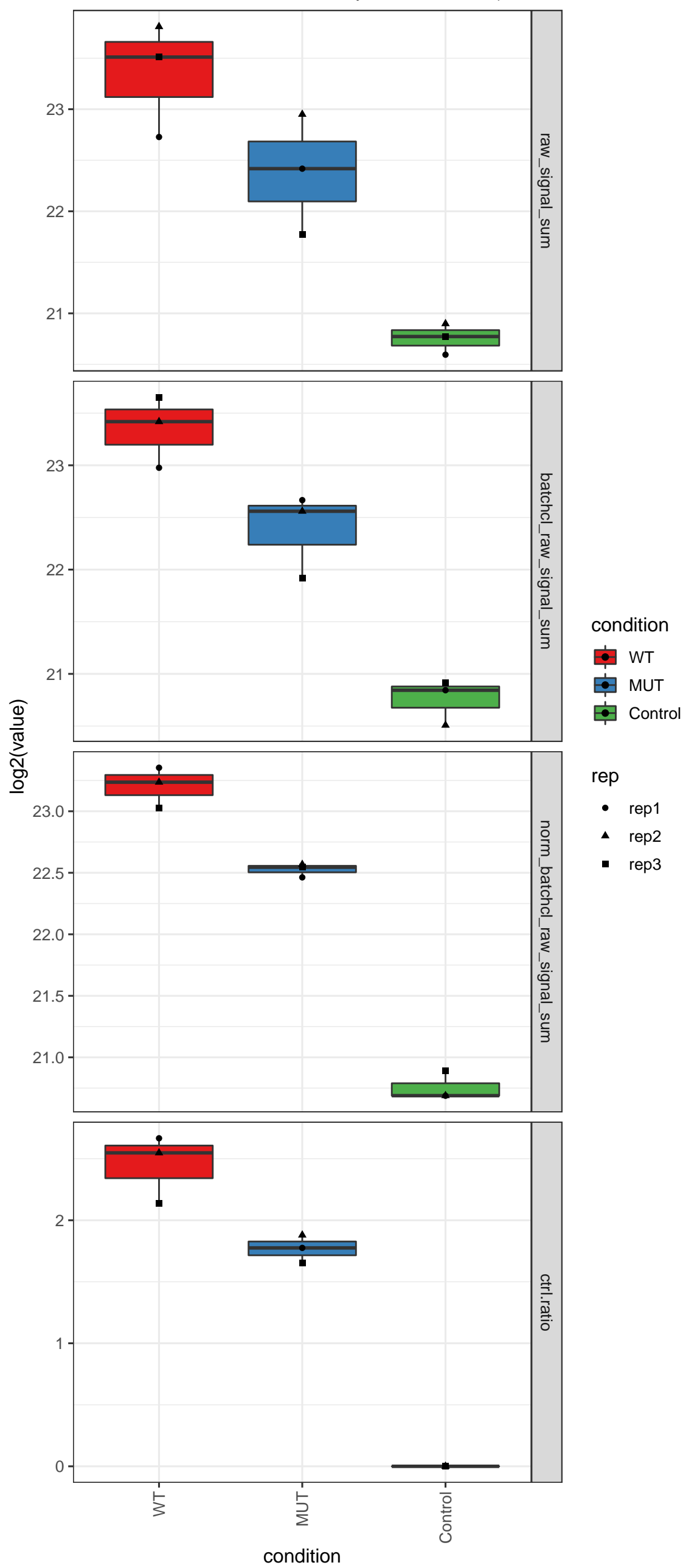
SCL1 – P21243

Proteasome subunit alpha type-1 OS=*Saccharomyces cerevisiae* (strain



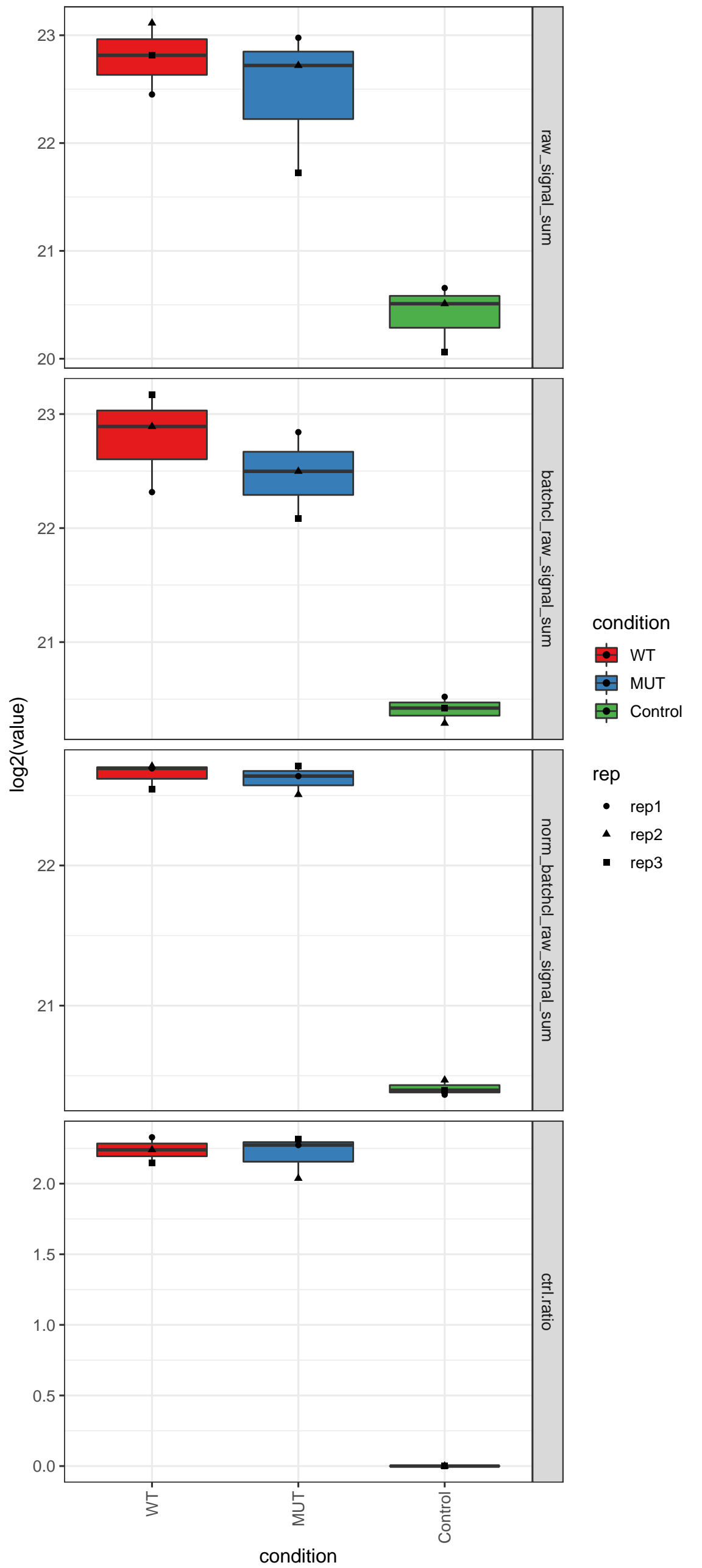
SCP160 – P06105

Protein SCP160 OS=*Saccharomyces cerevisiae* (strain ATCC 204508 / S



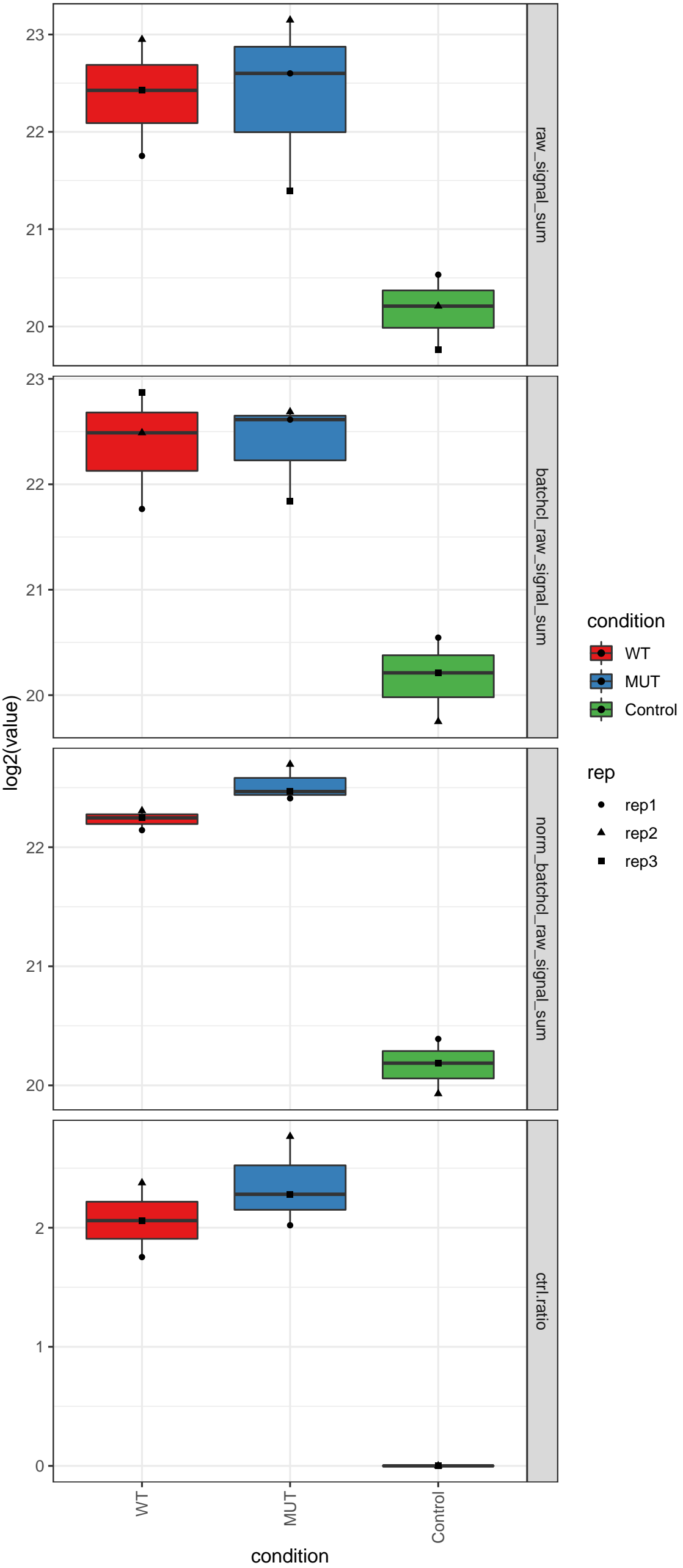
SCS2 – P40075

Vesicle-associated membrane protein-associated protein SCS2 OS=Sac



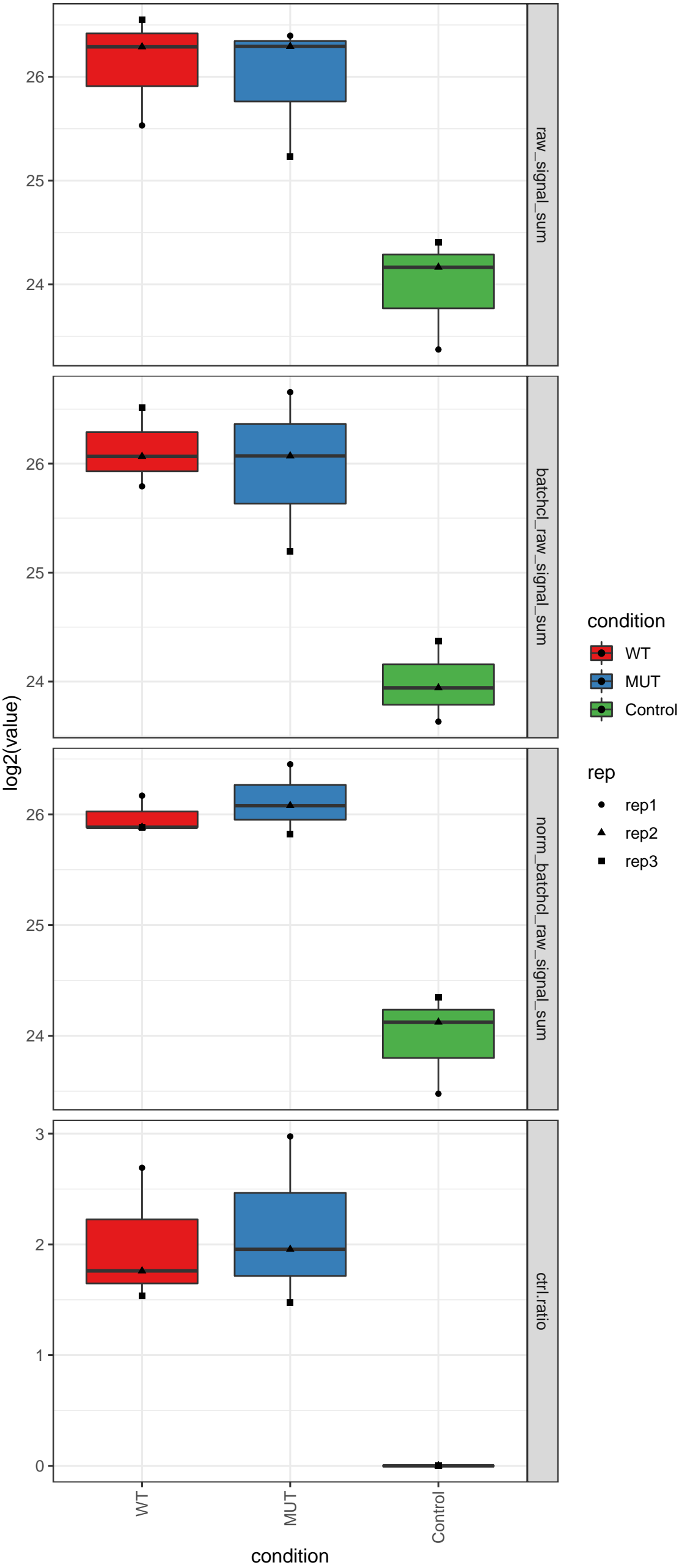
SCY1 – P53009

Protein kinase–like protein SCY1 OS=*Saccharomyces cerevisiae* (strain ATCC 25716)



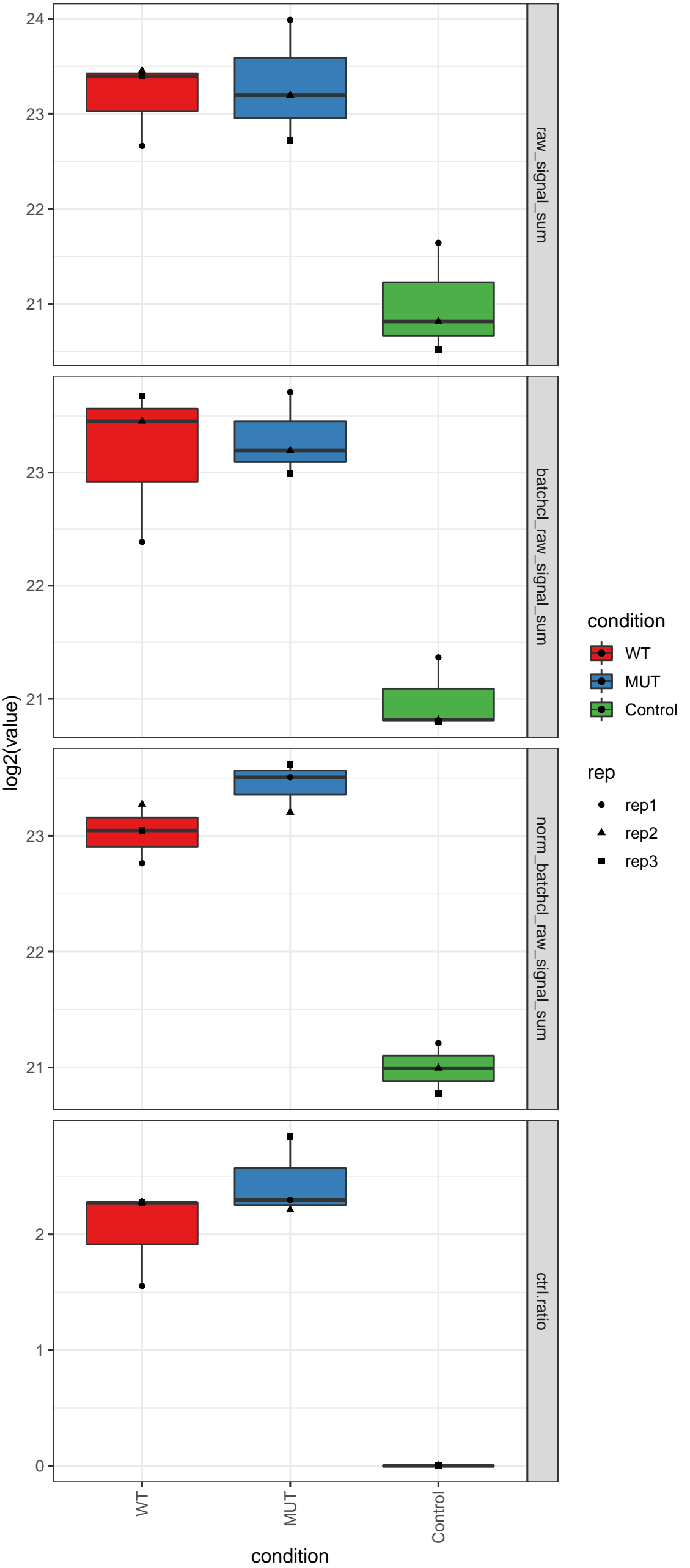
SDH1 – Q00711

Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial



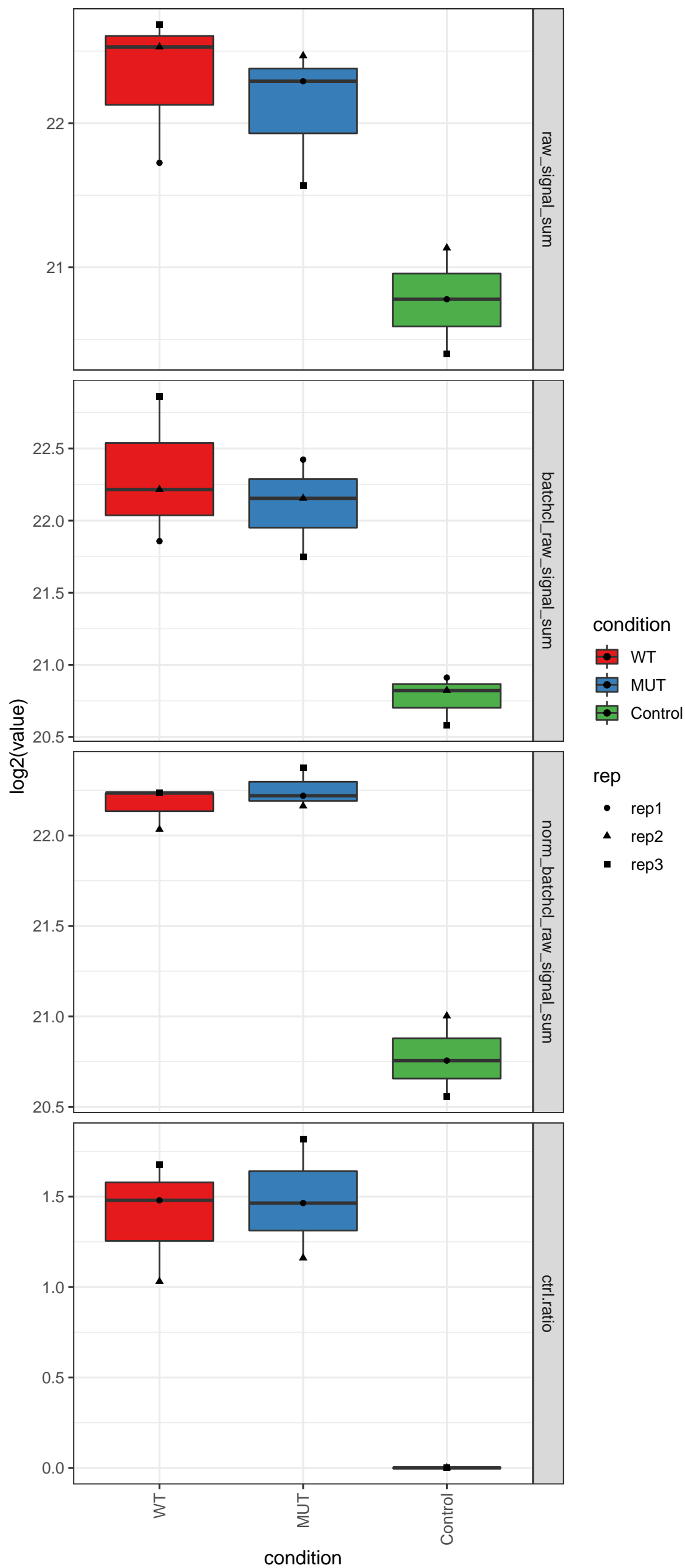
SDH2 – P21801

Succinate dehydrogenase [ubiquinone] iron–sulfur subunit, mitochondrial C



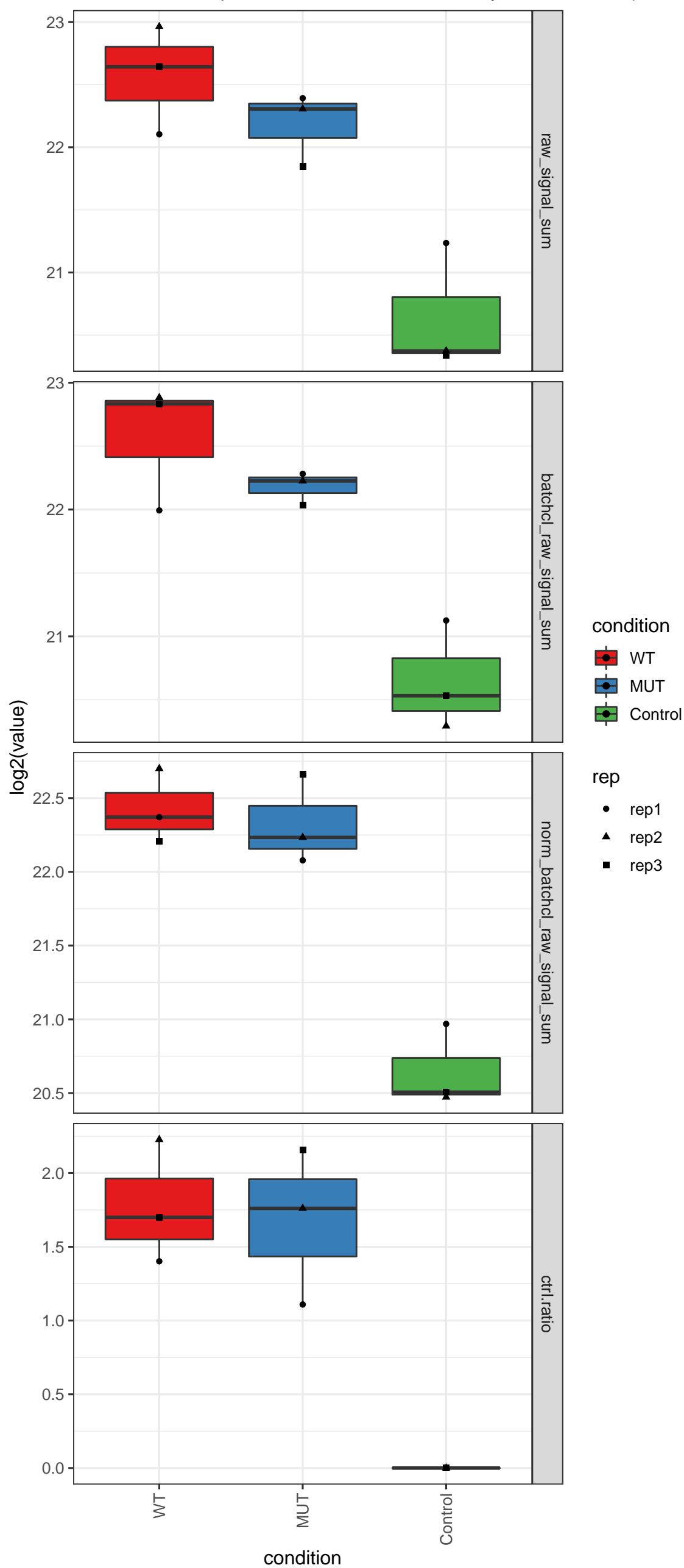
SDS24 – P38314

Protein SDS24 OS=*Saccharomyces cerevisiae* (strain ATCC 204508 / S288c)



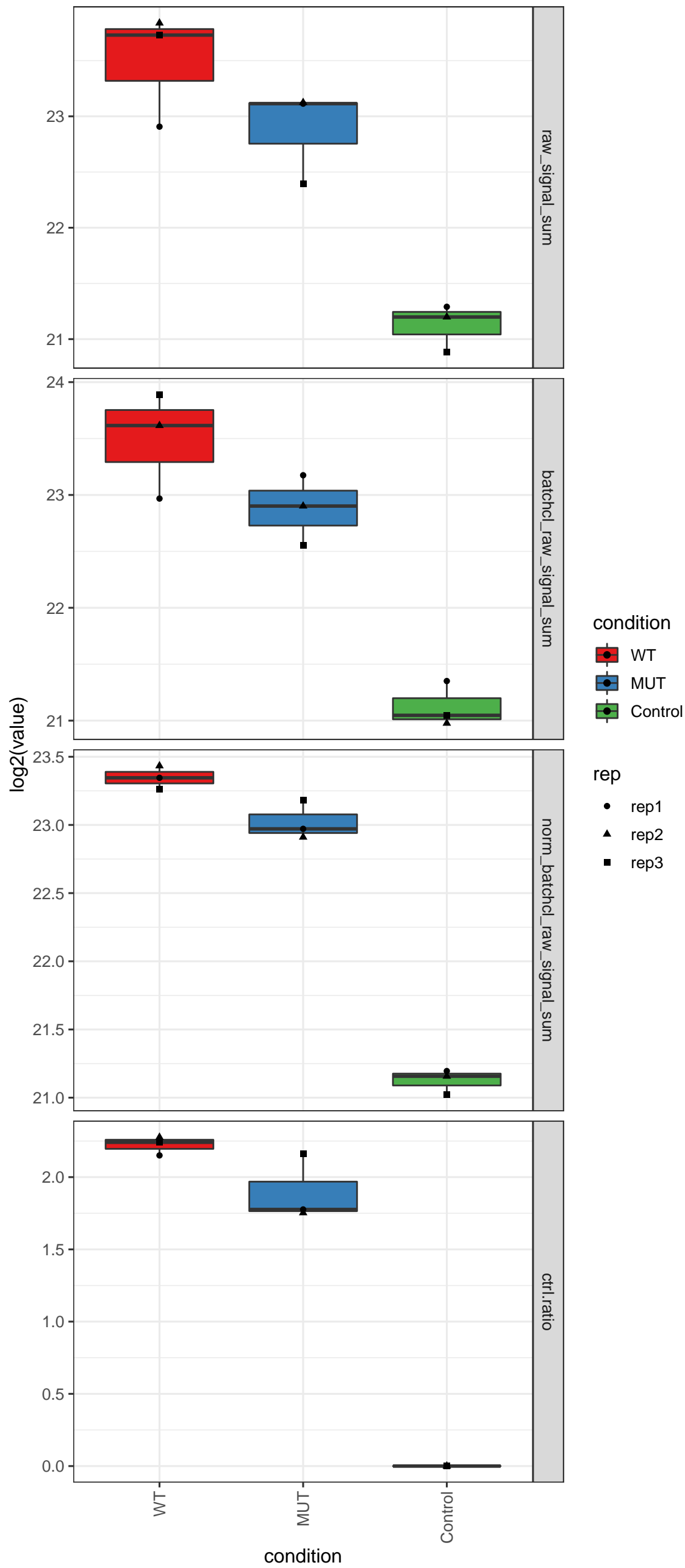
SEC18 – P18759

Vesicular-fusion protein SEC18 OS=*Saccharomyces cerevisiae* (strain ATCC 22016 / DSM 5780 / S288c)



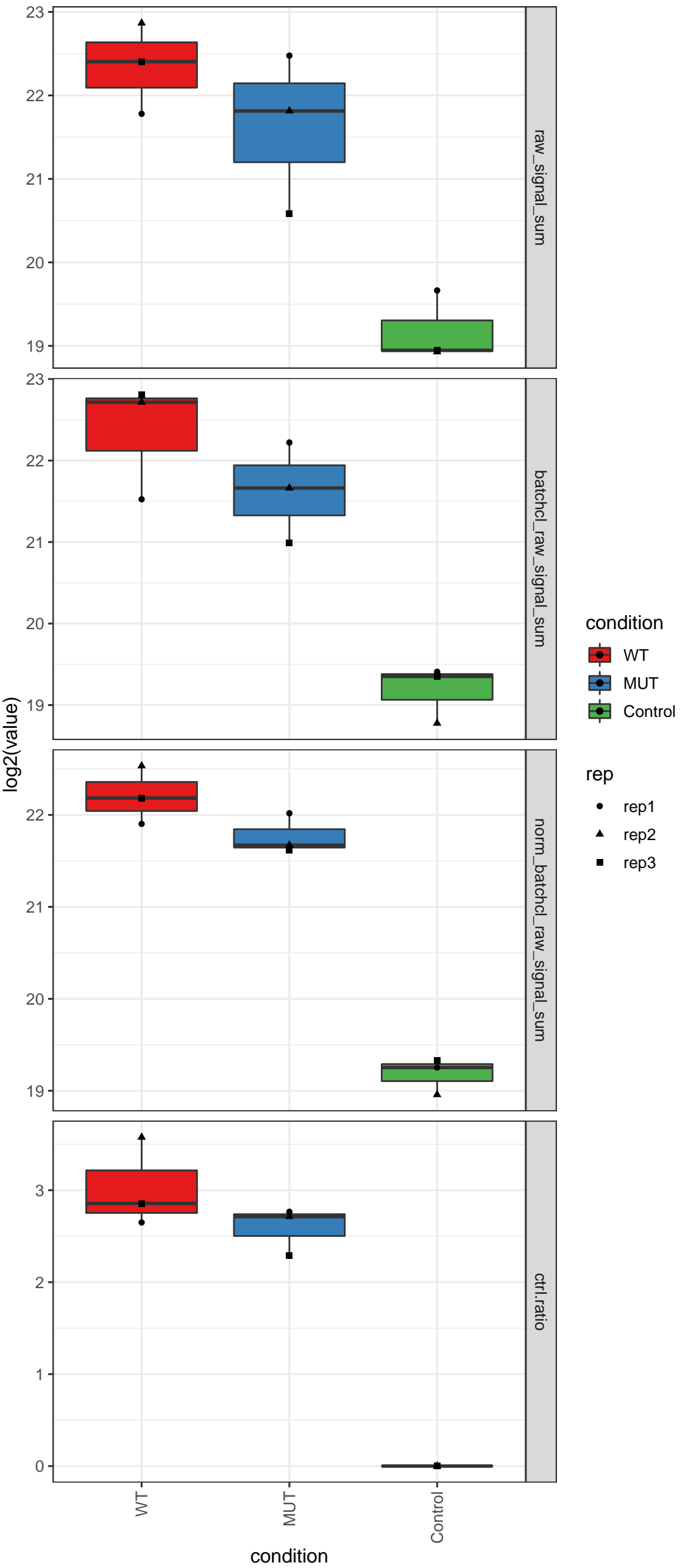
SEC23 – P15303

Protein transport protein SEC23 OS=*Saccharomyces cerevisiae* (strain A



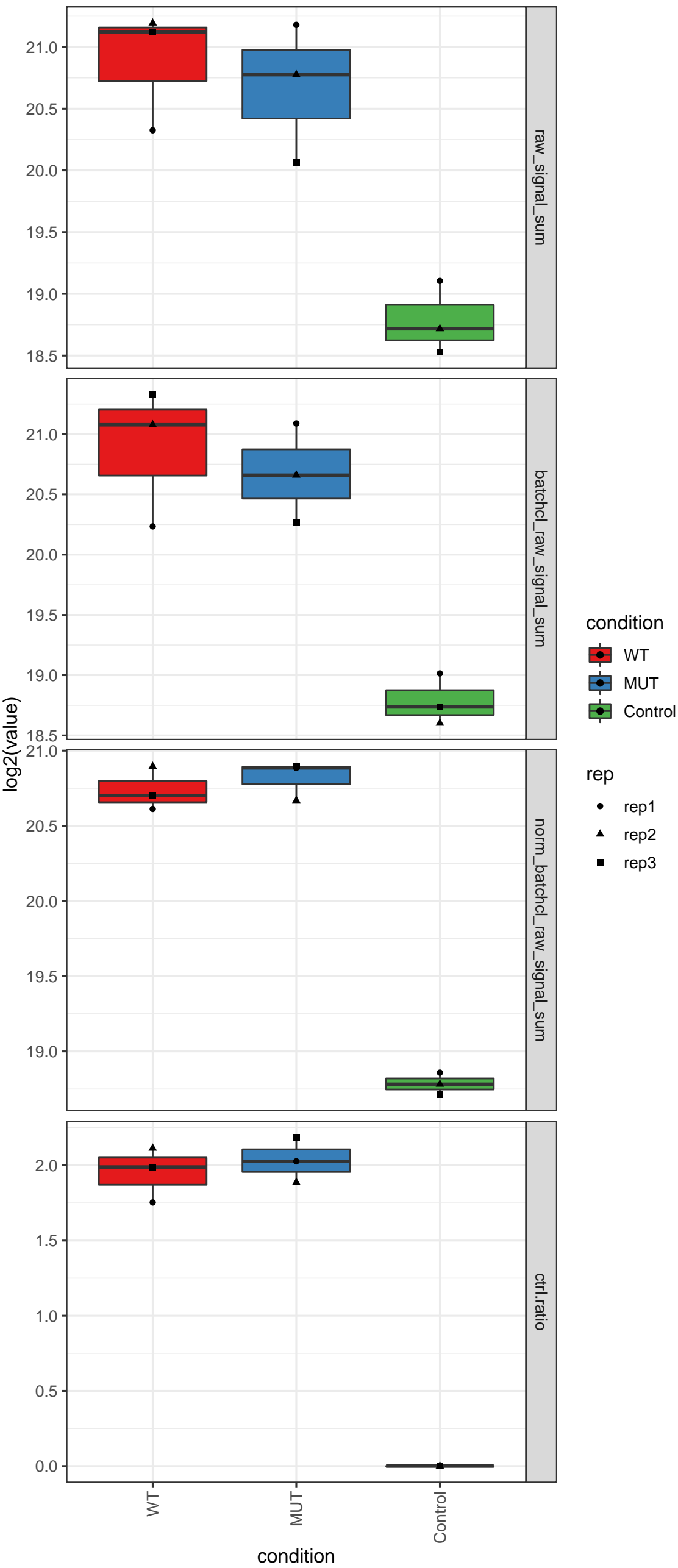
SEC24 – P40482

Protein transport protein SEC24 OS=*Saccharomyces cerevisiae* (strain ATCC 25716)



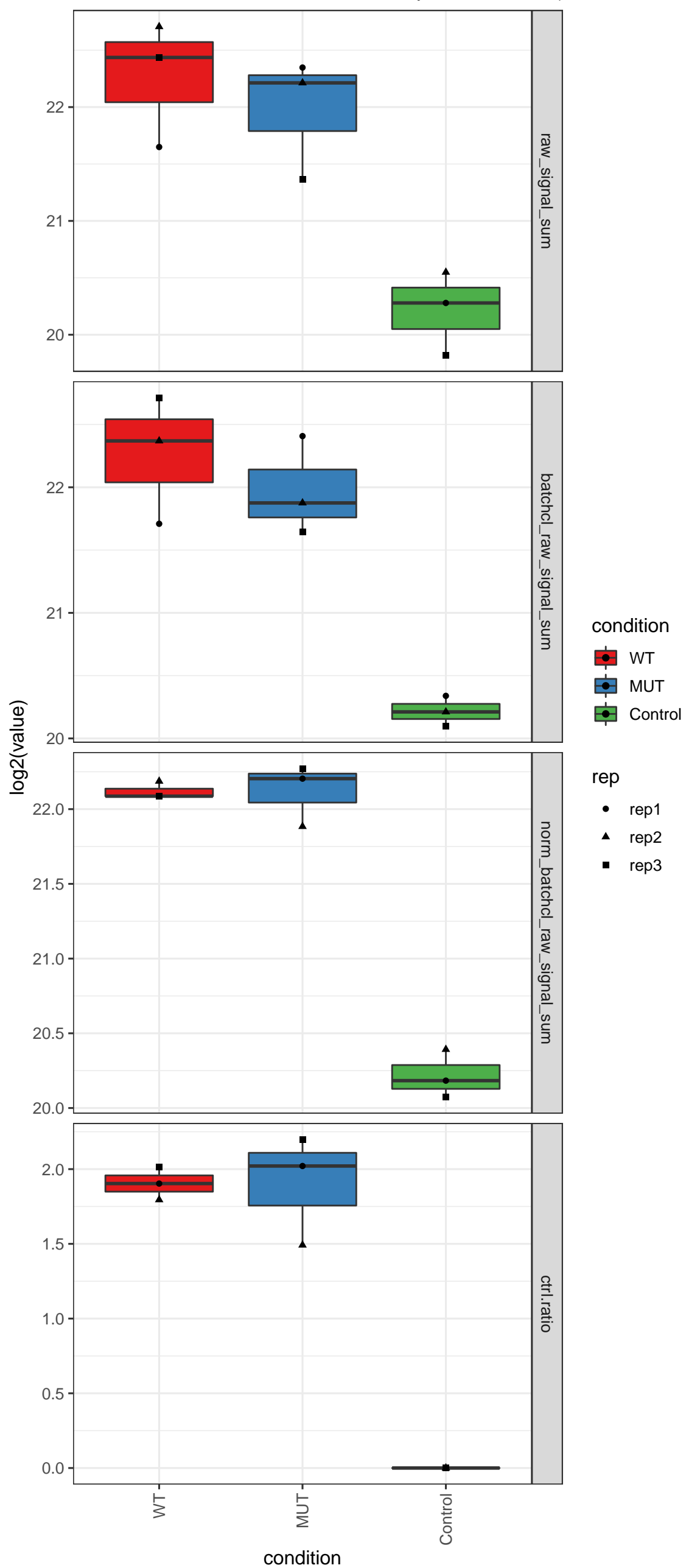
SEC26 – P41810

Coatomer subunit beta OS=*Saccharomyces cerevisiae* (strain ATCC 204



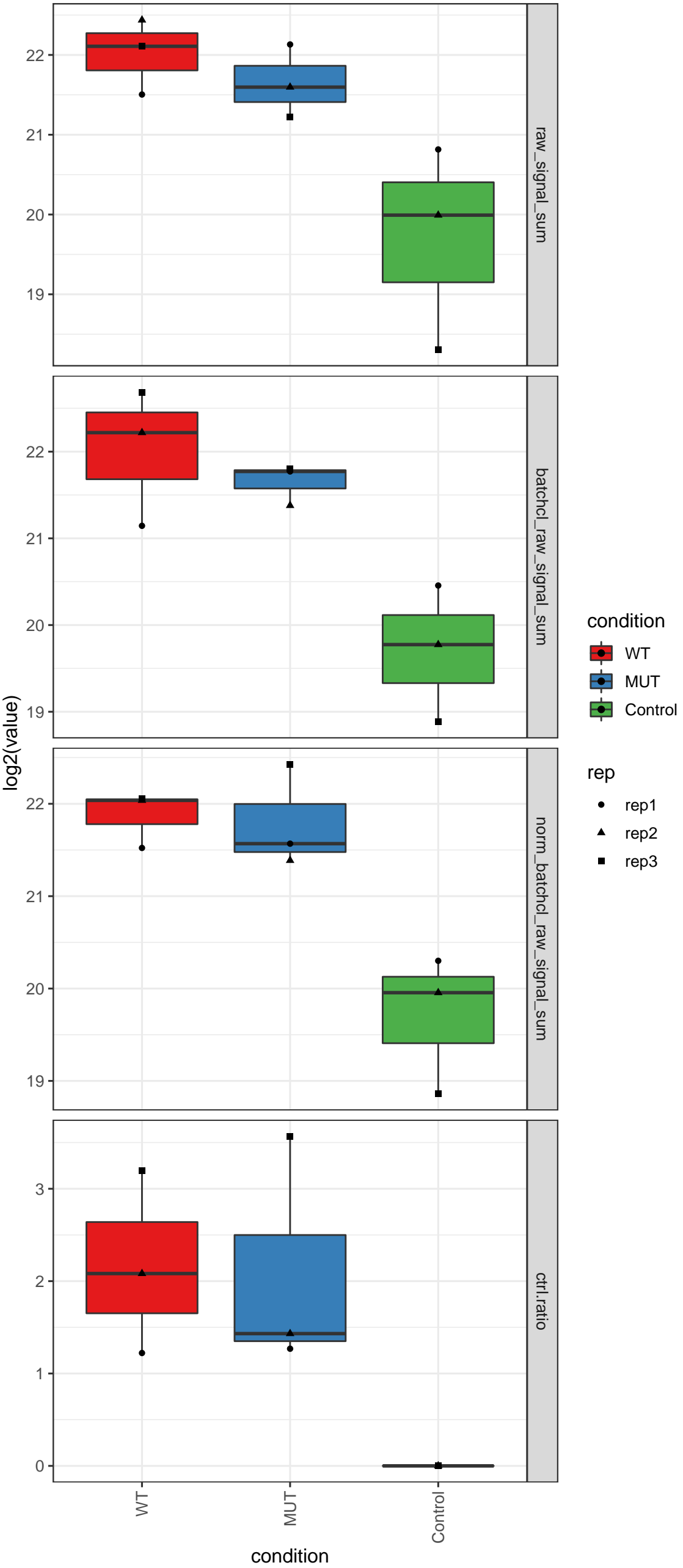
SEC27 – P41811

Coatomer subunit beta' OS=*Saccharomyces cerevisiae* (strain ATCC 204



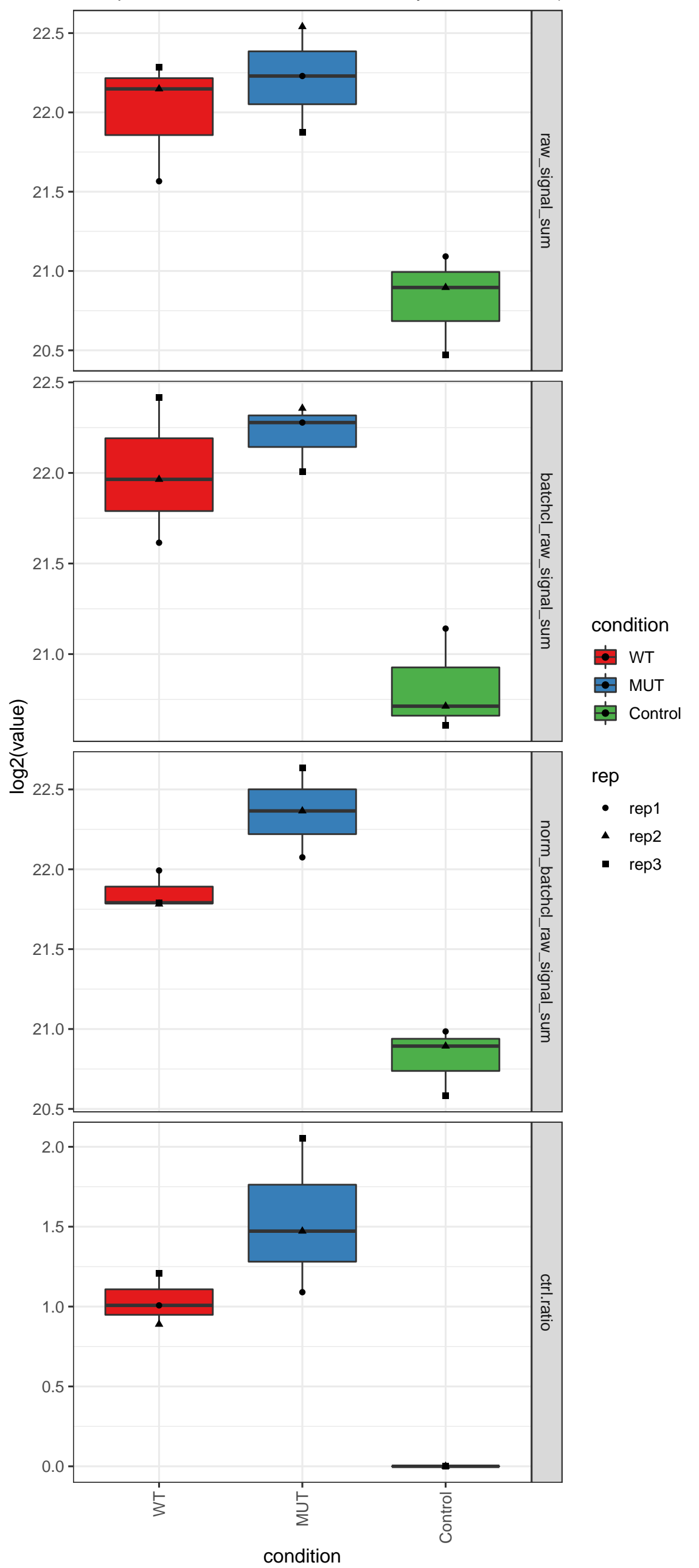
SEC4 – P07560

Ras-related protein SEC4 OS=Saccharomyces cerevisiae (strain ATCC 20



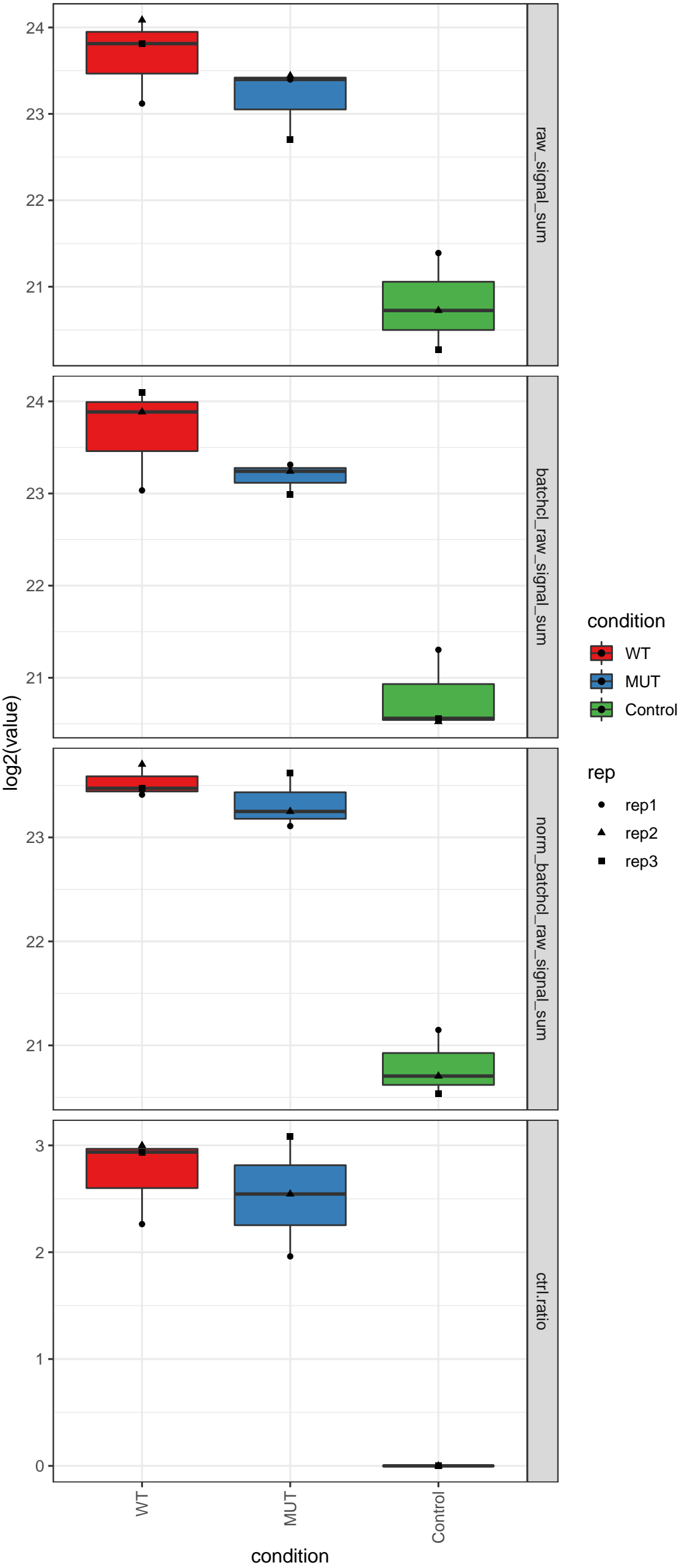
SEC53 – P07283

Phosphomannomutase OS=*Saccharomyces cerevisiae* (strain ATCC 204



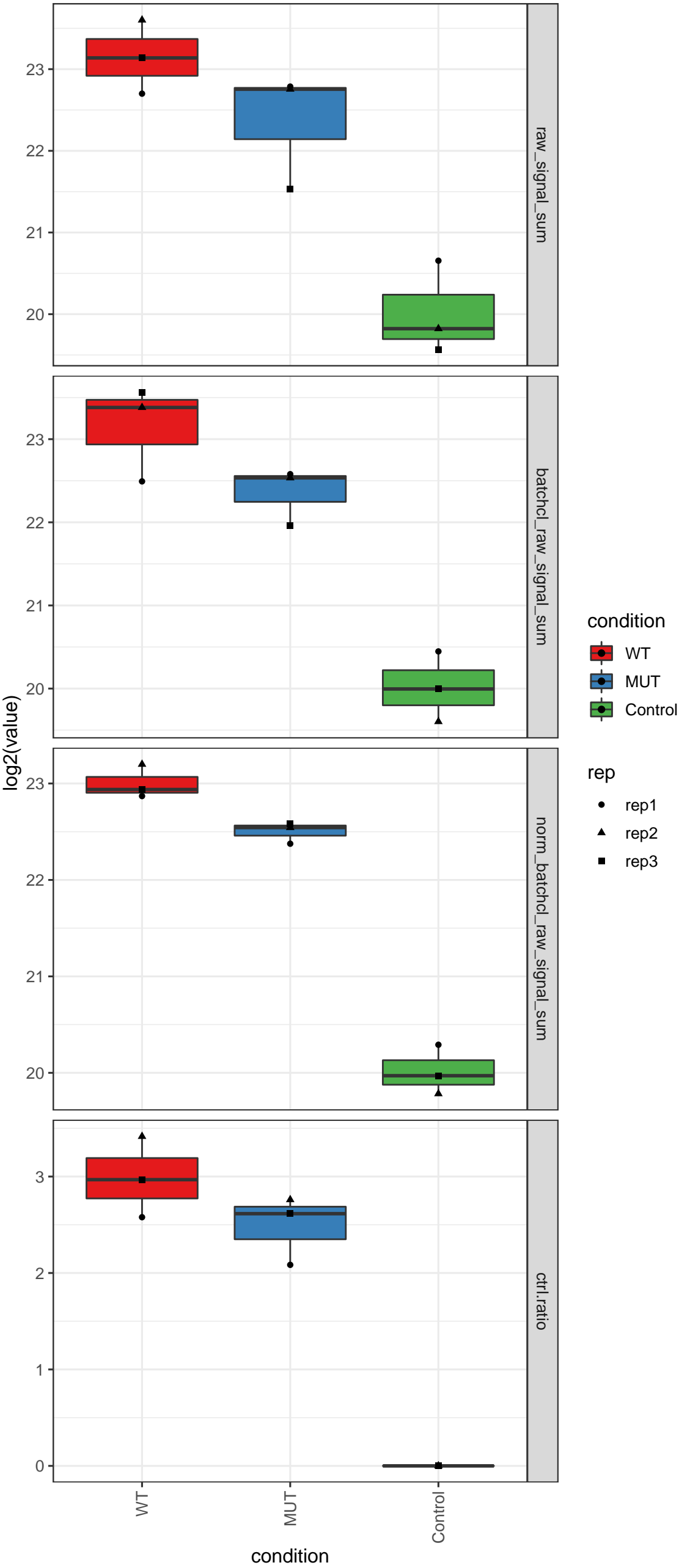
SEC61 – P32915

Protein transport protein SEC61 OS=*Saccharomyces cerevisiae* (strain ATCC 22016 /



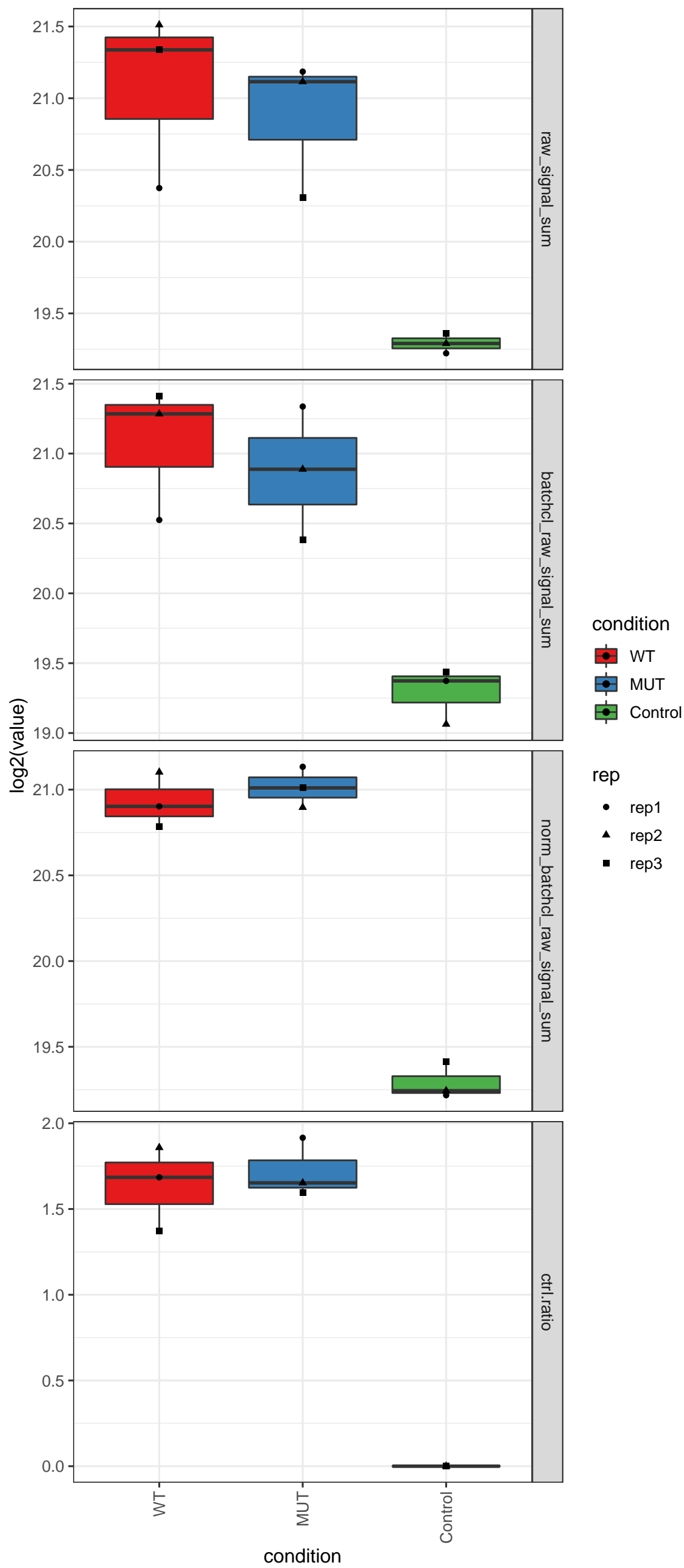
SEC63 – P14906

Protein translocation protein SEC63 OS=*Saccharomyces cerevisiae* (strain



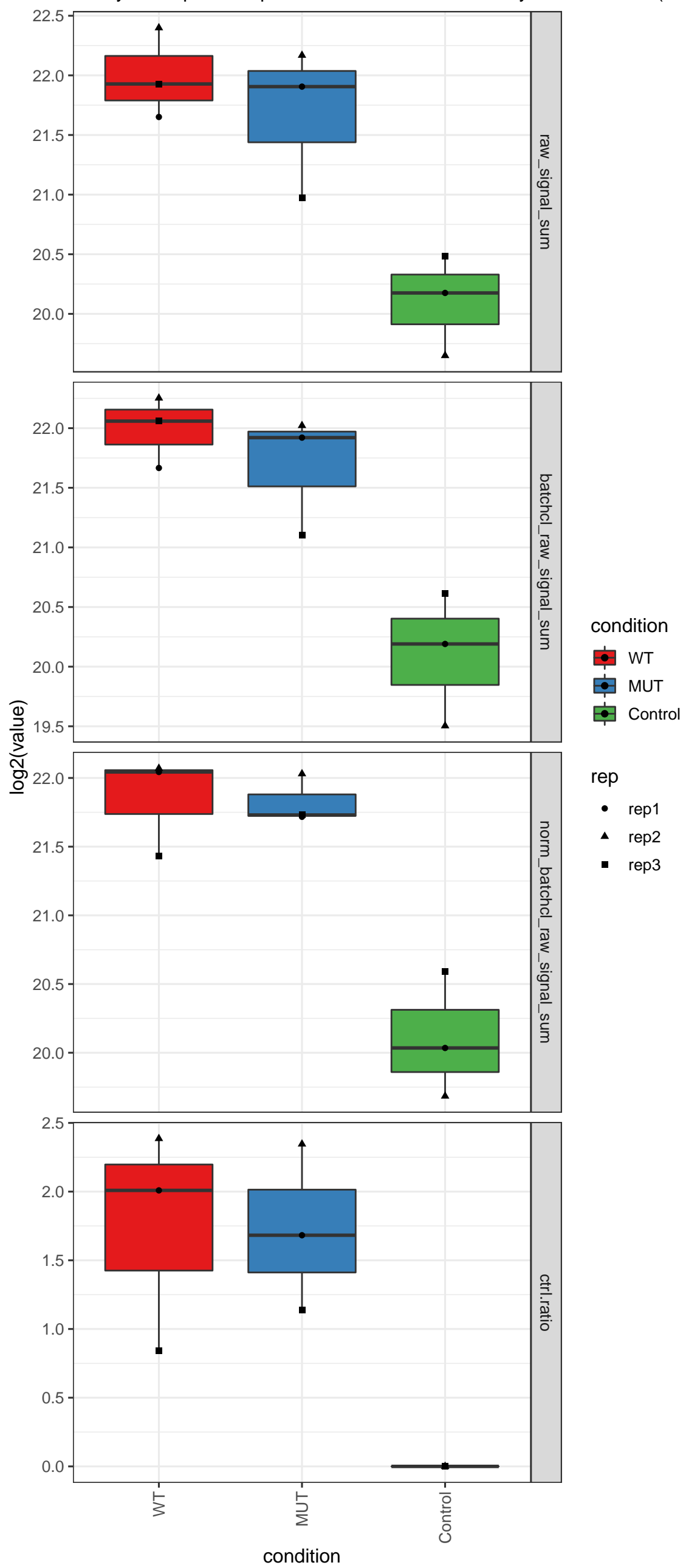
SEC7 – P11075

Protein transport protein SEC7 OS=*Saccharomyces cerevisiae* (strain ATCC 22016 / S288c)



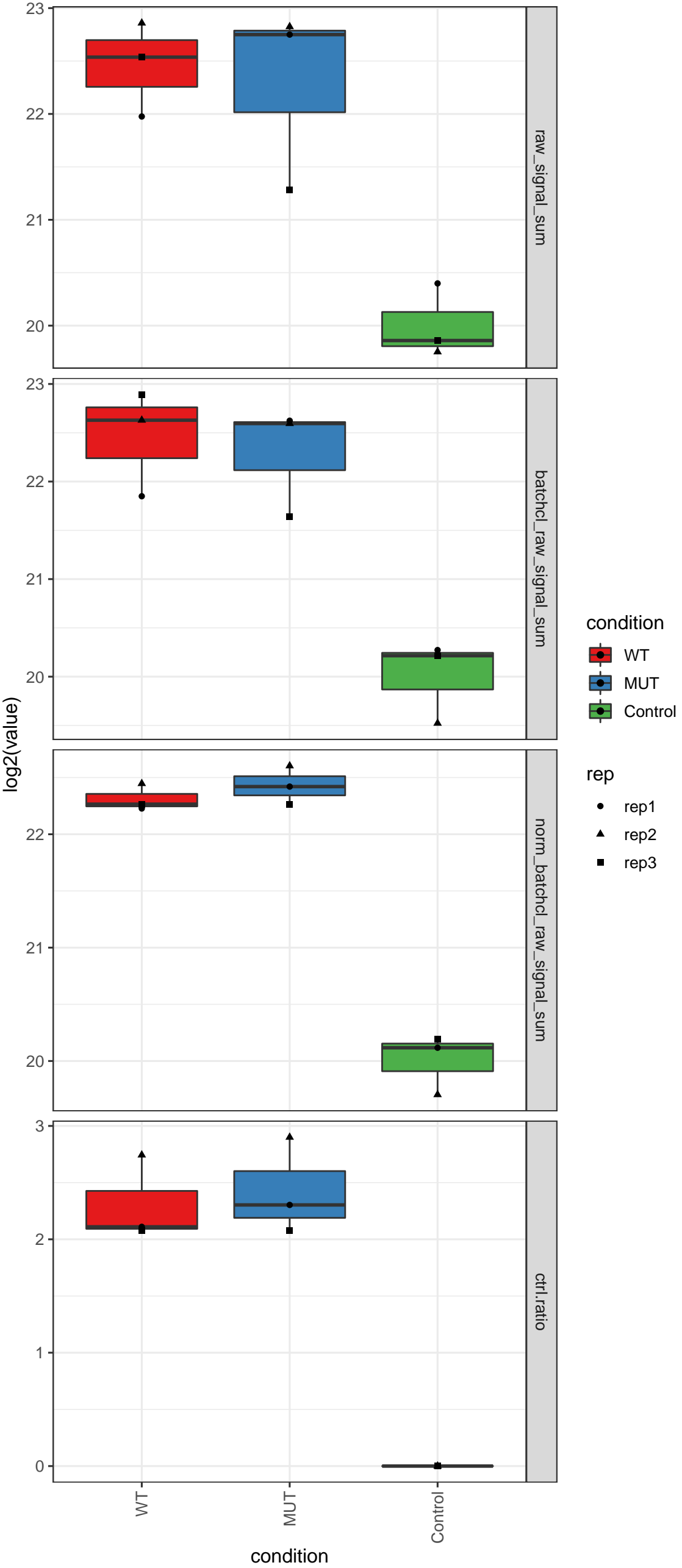
SEC8 – P32855

Exocyst complex component SEC8 OS=*Saccharomyces cerevisiae* (strain



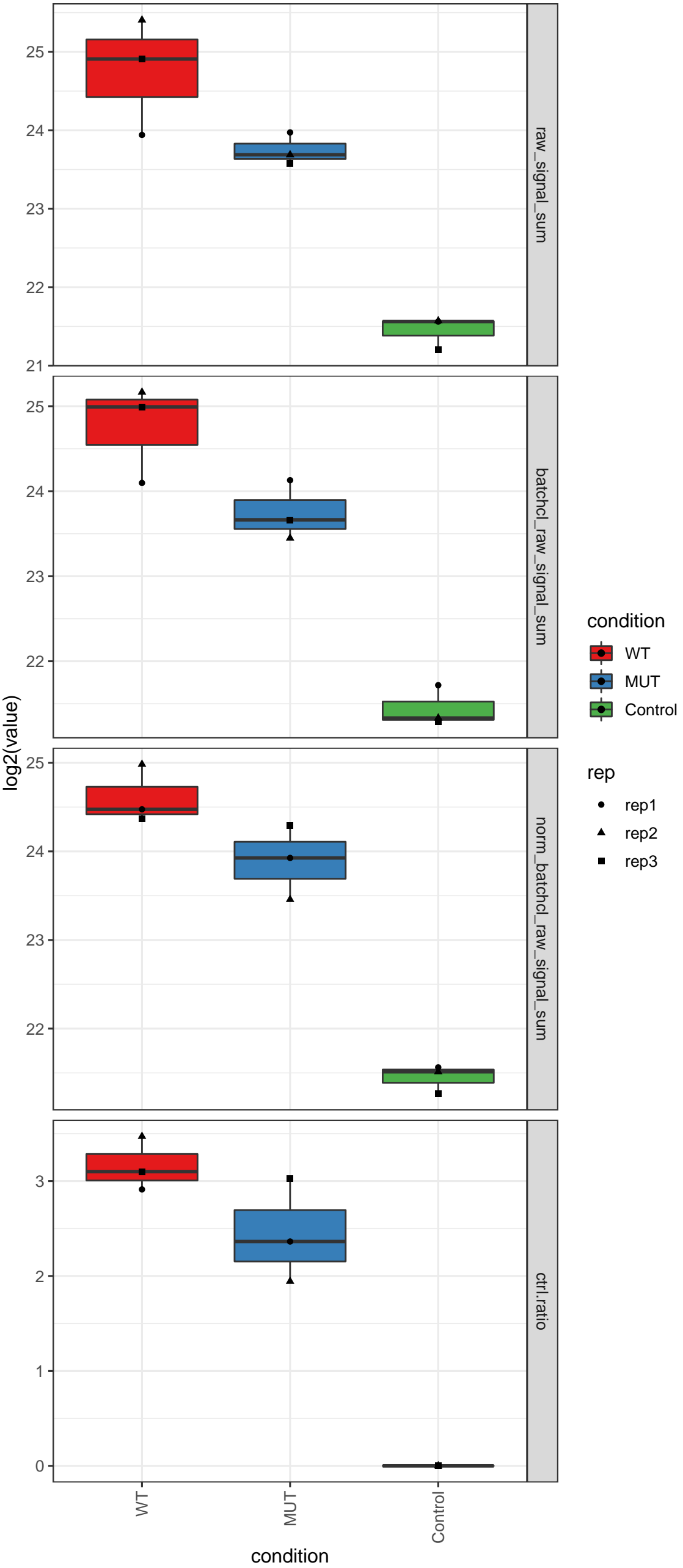
SEG1 – Q04279

Eisosome protein SEG1 OS=*Saccharomyces cerevisiae* (strain ATCC 20454)



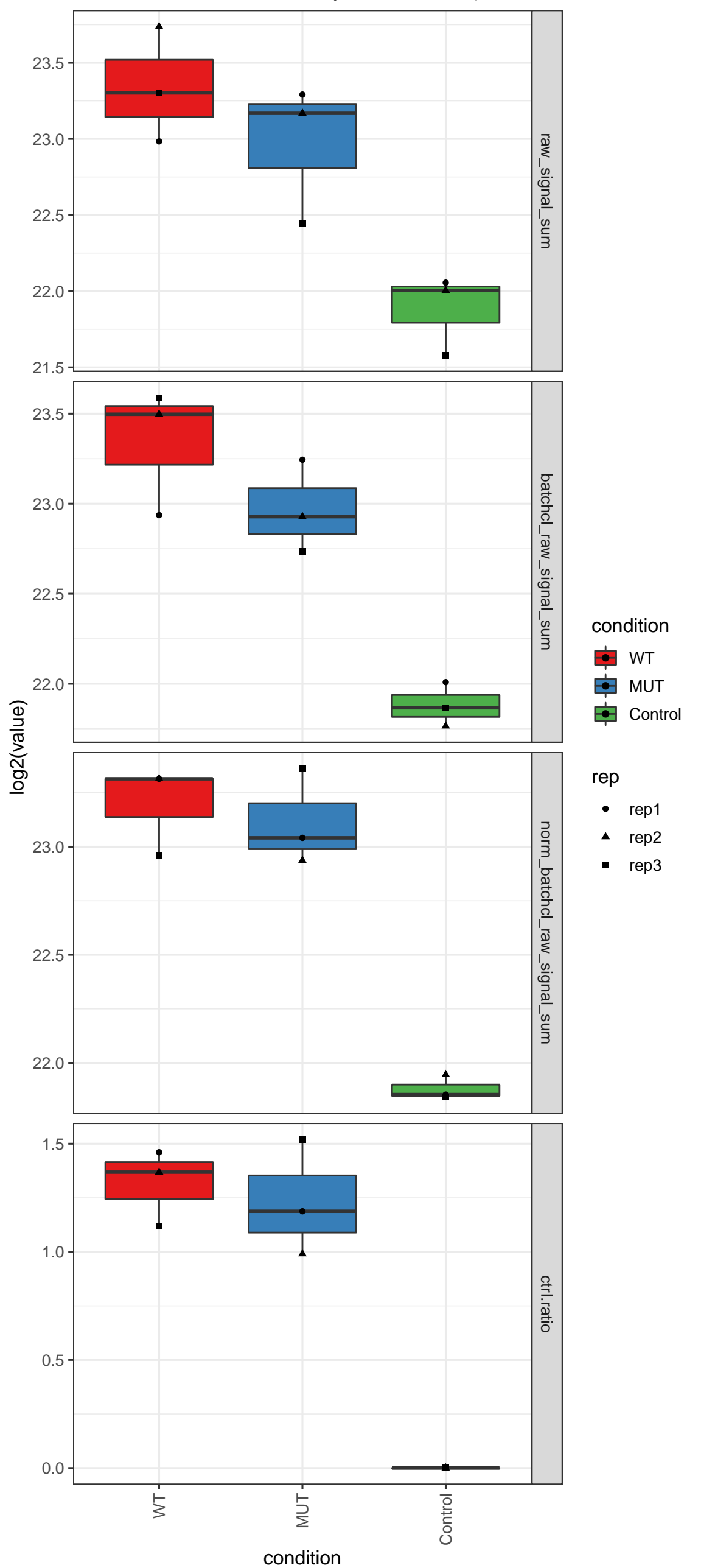
SES1 – P07284

Serine--tRNA ligase, cytoplasmic OS=*Saccharomyces cerevisiae* (strain A



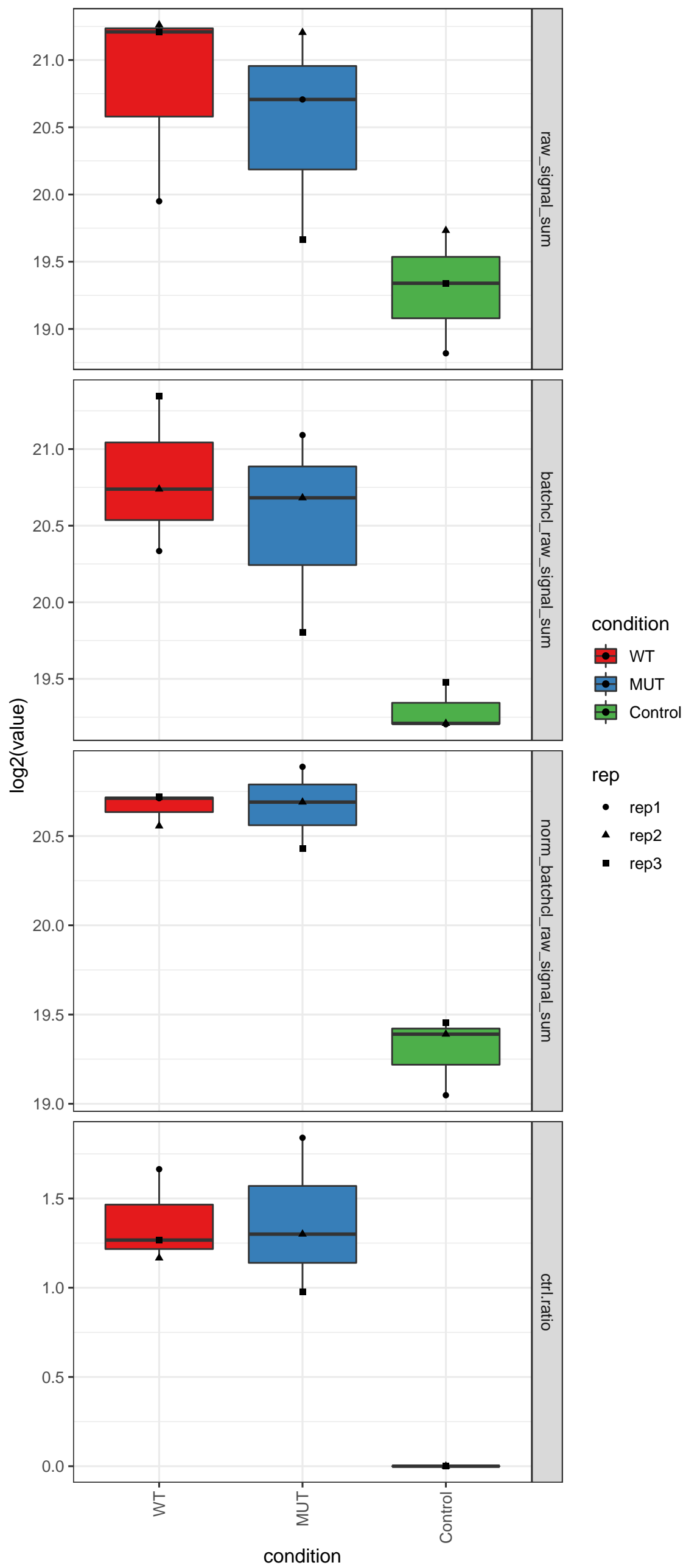
SEY1 – Q99287

Protein SEY1 OS=*Saccharomyces cerevisiae* (strain ATCC 204508 / S28)



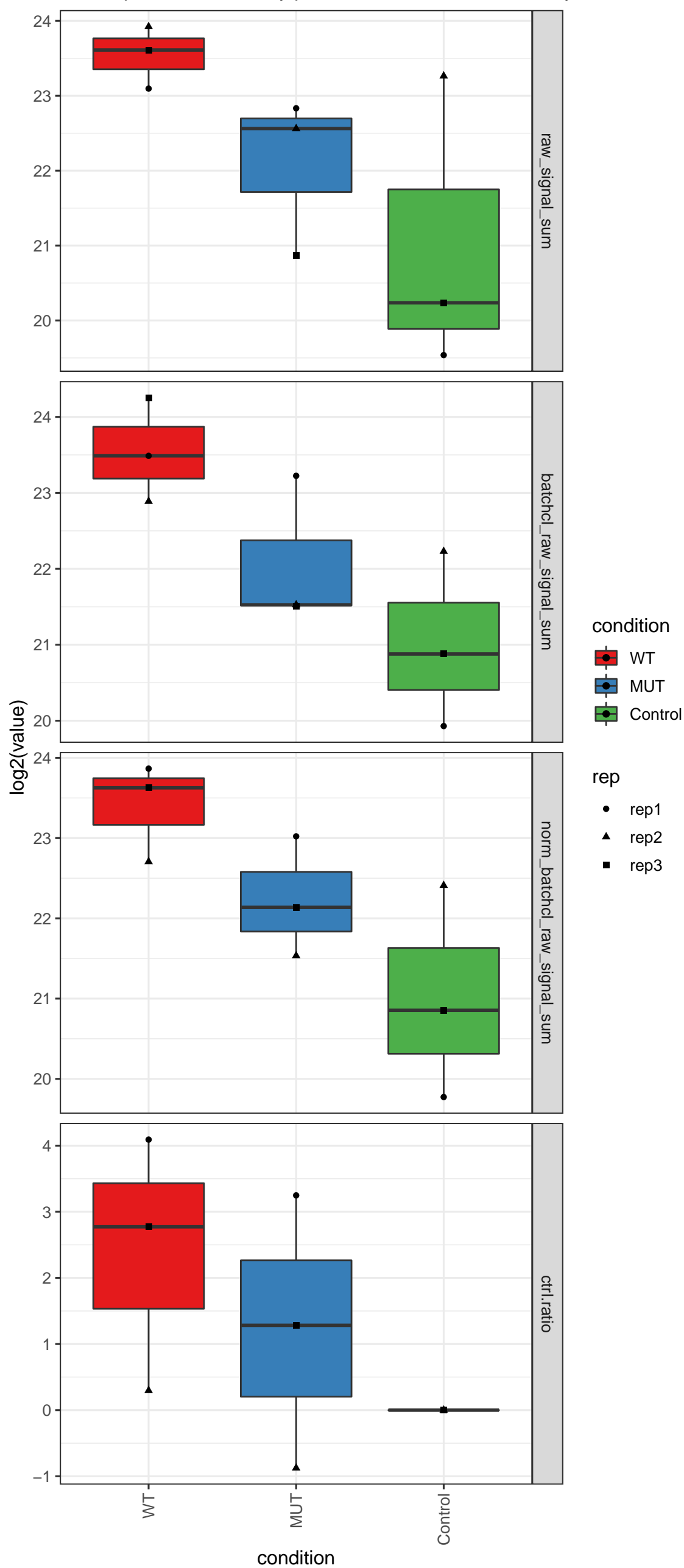
SGV1 – P23293

Serine/threonine–protein kinase BUR1 OS=*Saccharomyces cerevisiae* (s



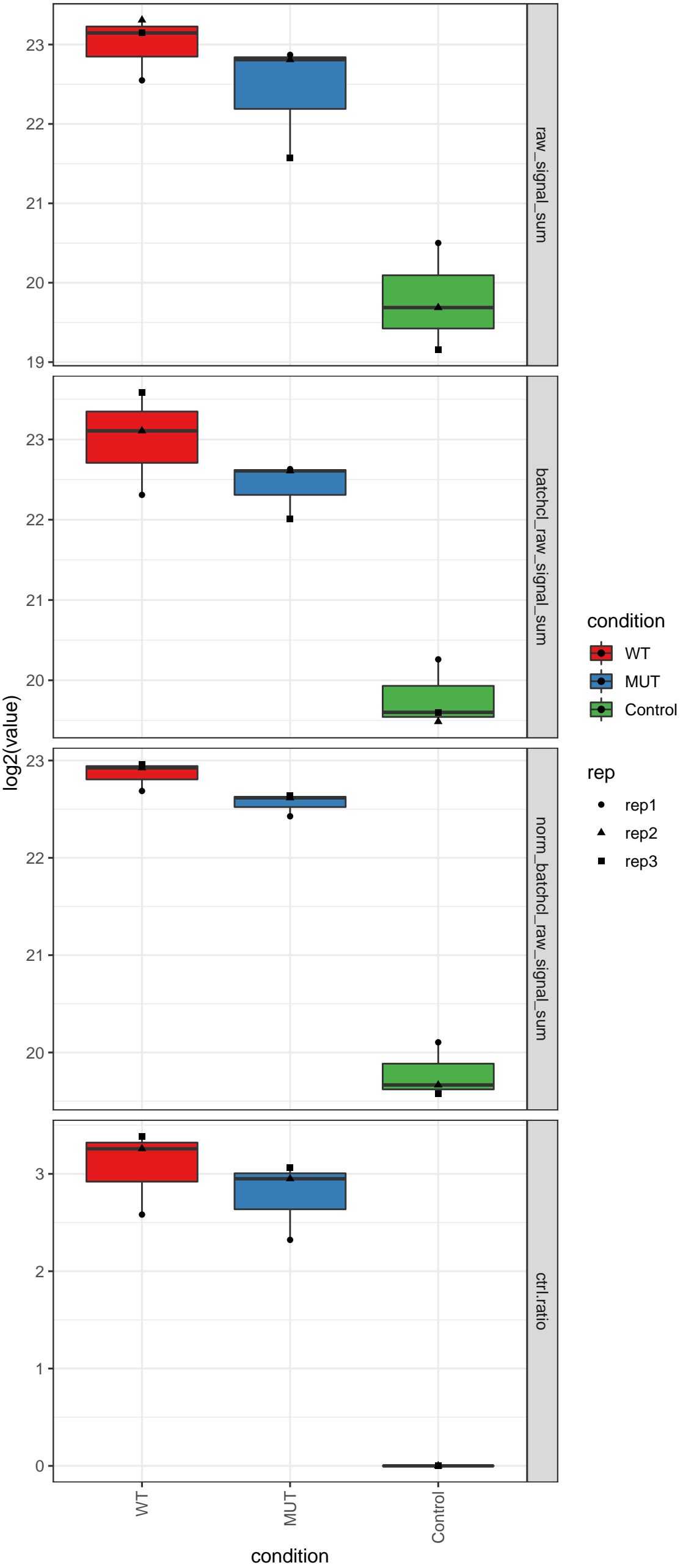
SHE10 – P53075

Outer spore wall assembly protein SHE10 OS=*Saccharomyces cerevisiae*



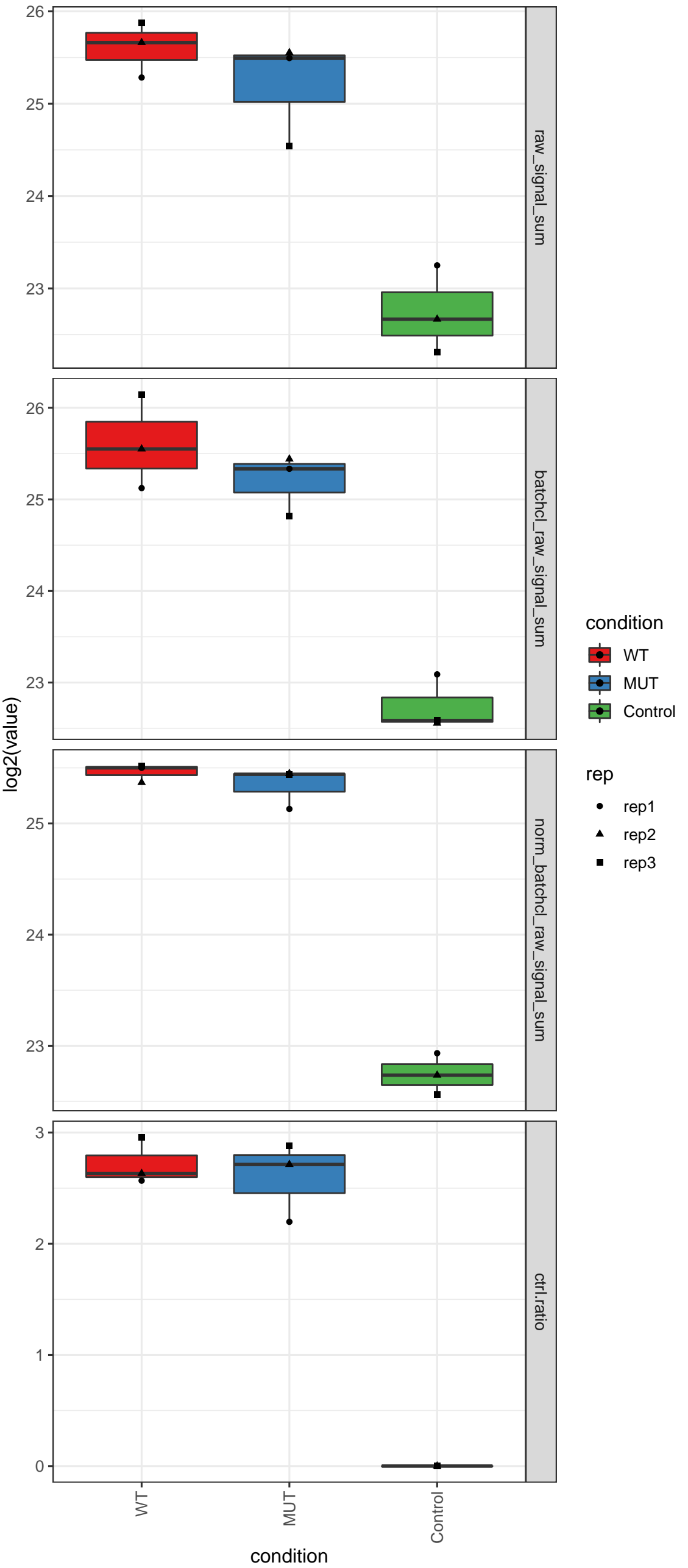
SHM1 – P37292

Serine hydroxymethyltransferase, mitochondrial OS=Saccharomyces cerevisiae



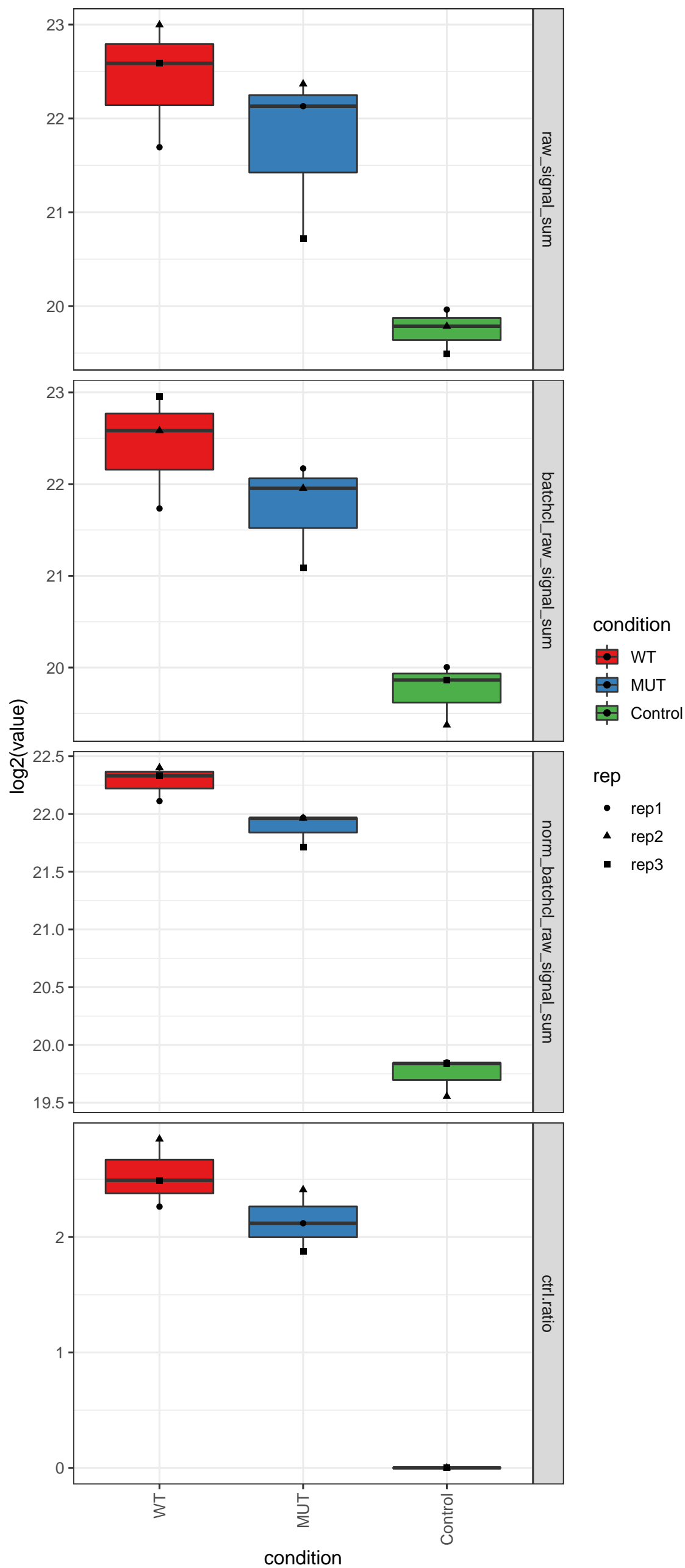
SHM2 – P37291

Serine hydroxymethyltransferase, cytosolic OS=*Saccharomyces cerevisiae*



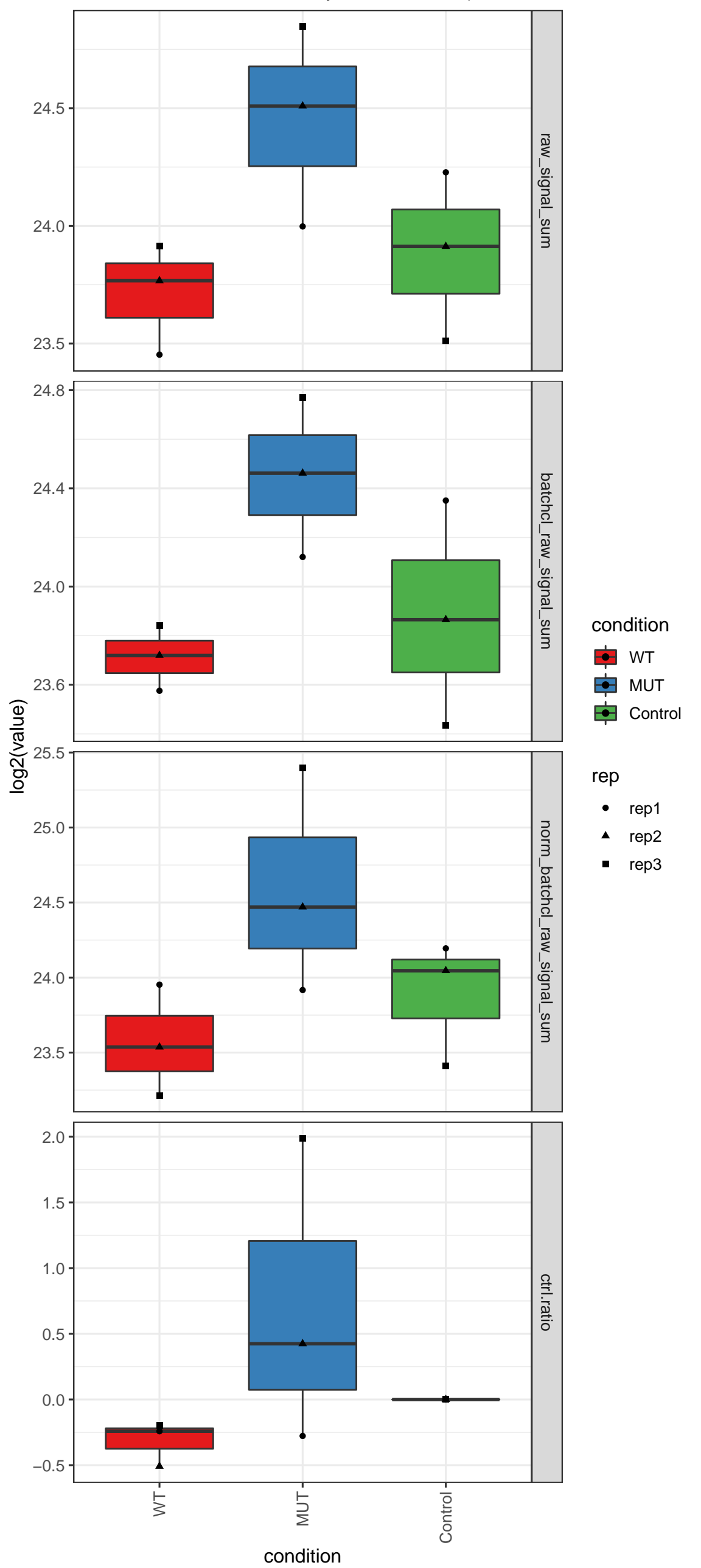
SHS1 – Q07657

Seventh homolog of septin 1 OS=*Saccharomyces cerevisiae* (strain ATCC 25794)



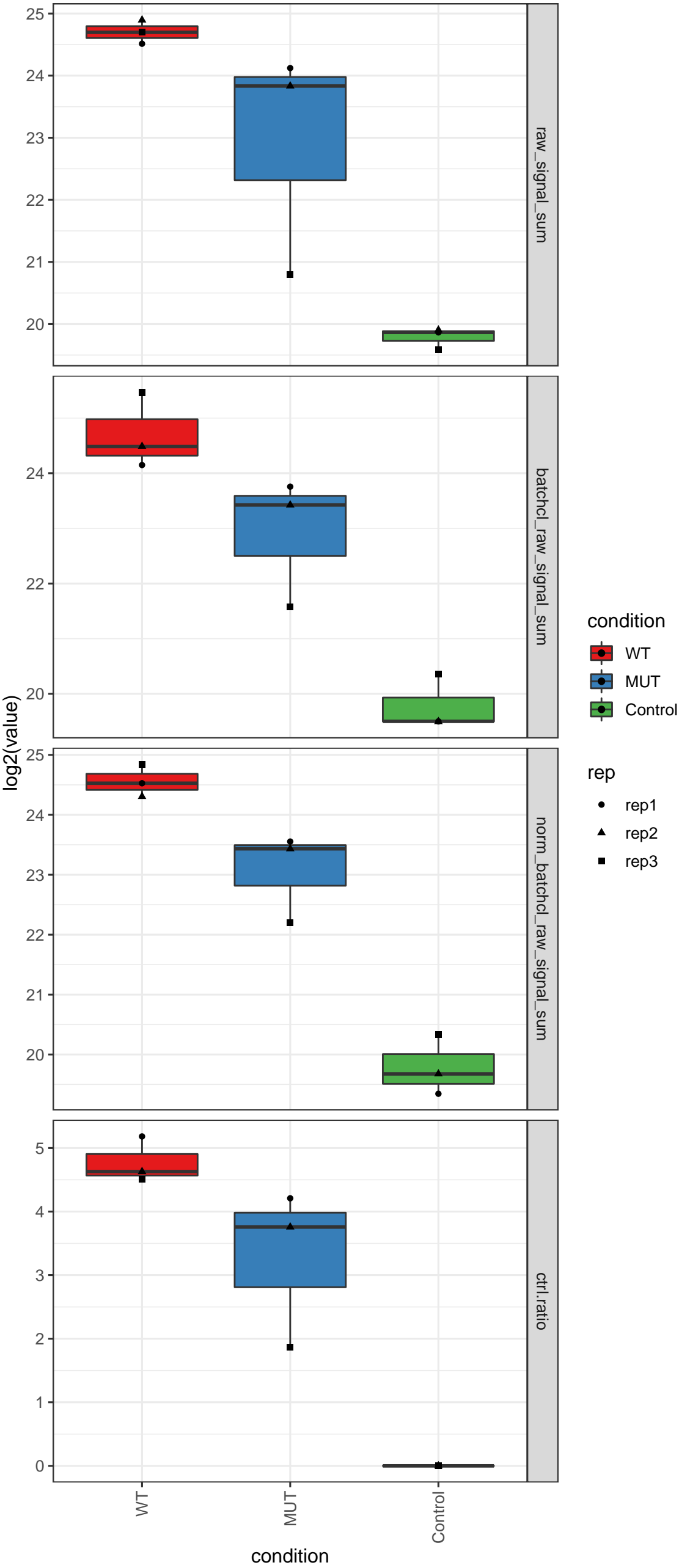
SIS1 – P25294

Protein SIS1 OS=*Saccharomyces cerevisiae* (strain ATCC 204508 / S288c)



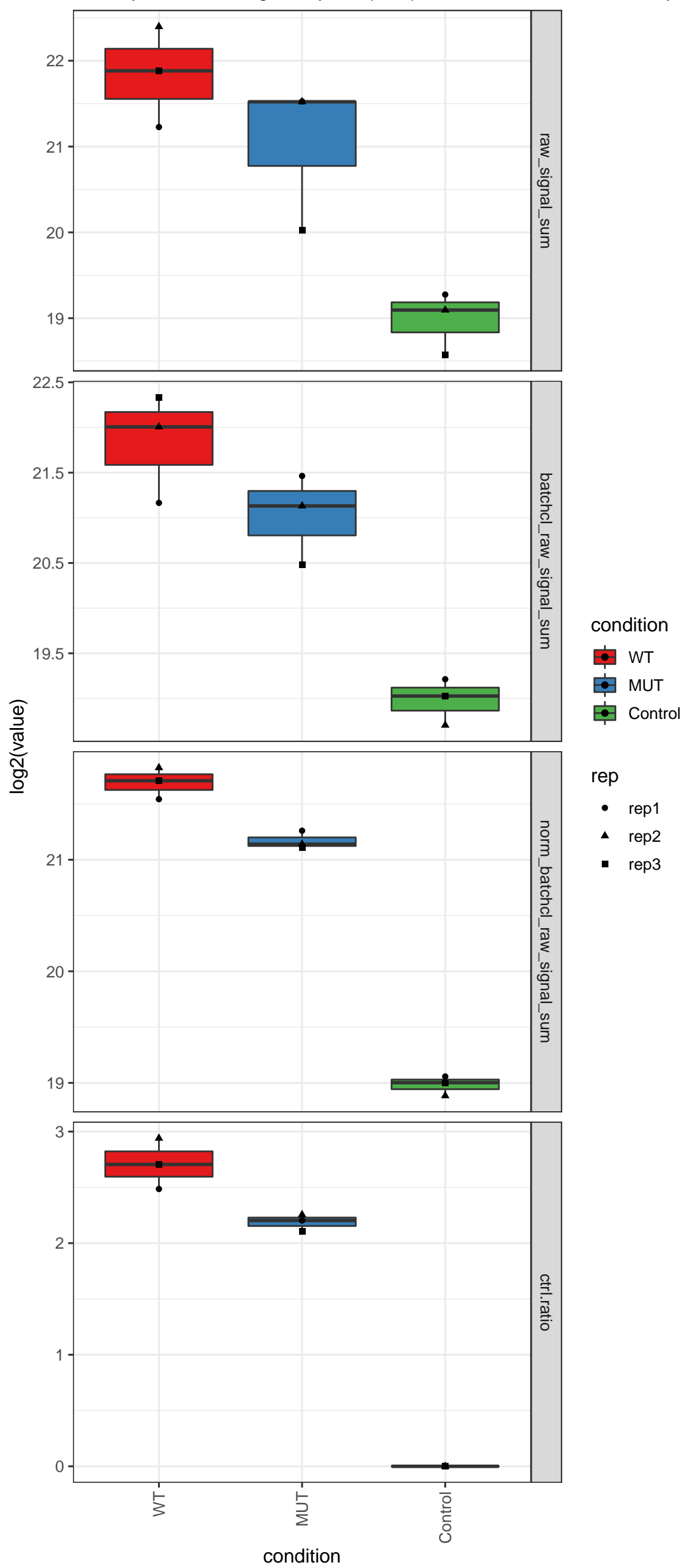
SKO1 – Q02100

CRE-binding bZIP protein SKO1 OS=*Saccharomyces cerevisiae* (strain ATCC 22016 /



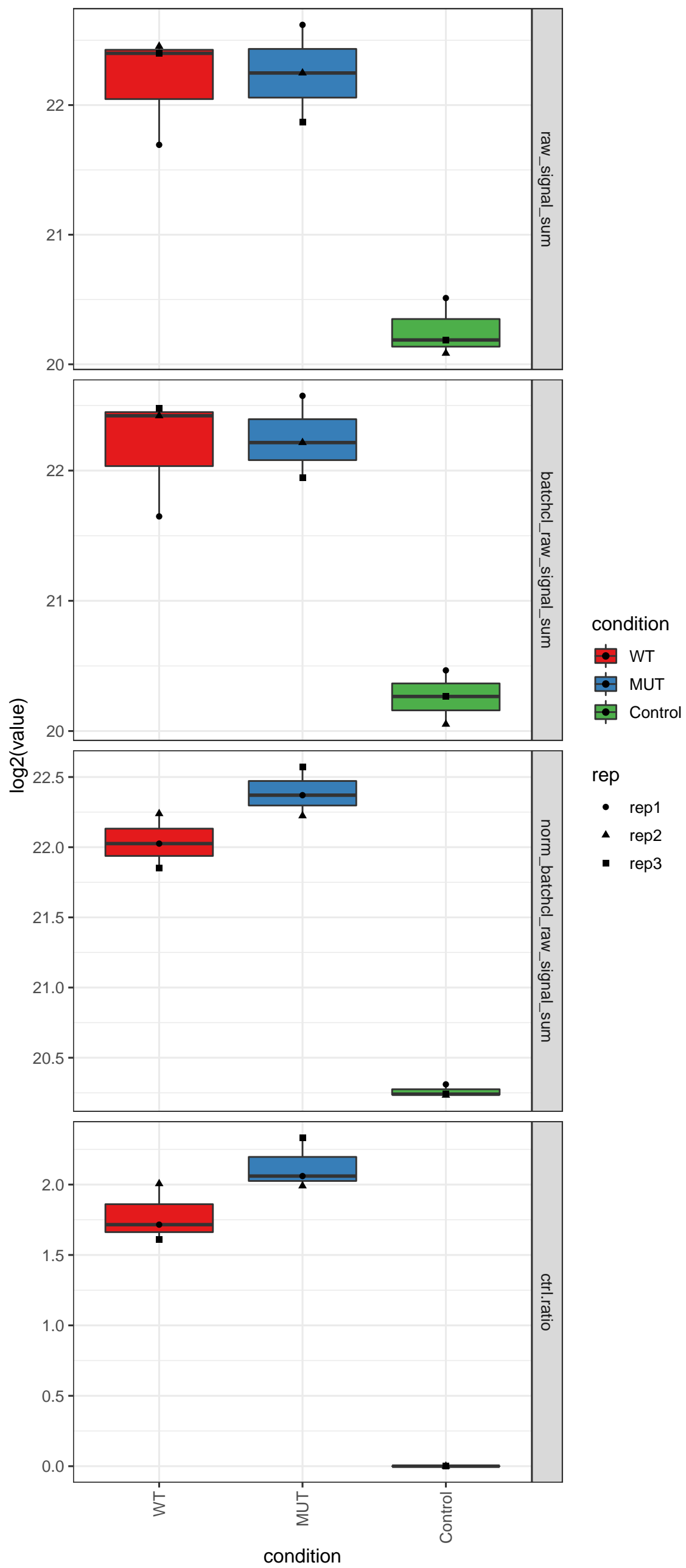
SLA1 – P32790

Actin cytoskeleton–regulatory complex protein SLA1 OS=Saccharomyces



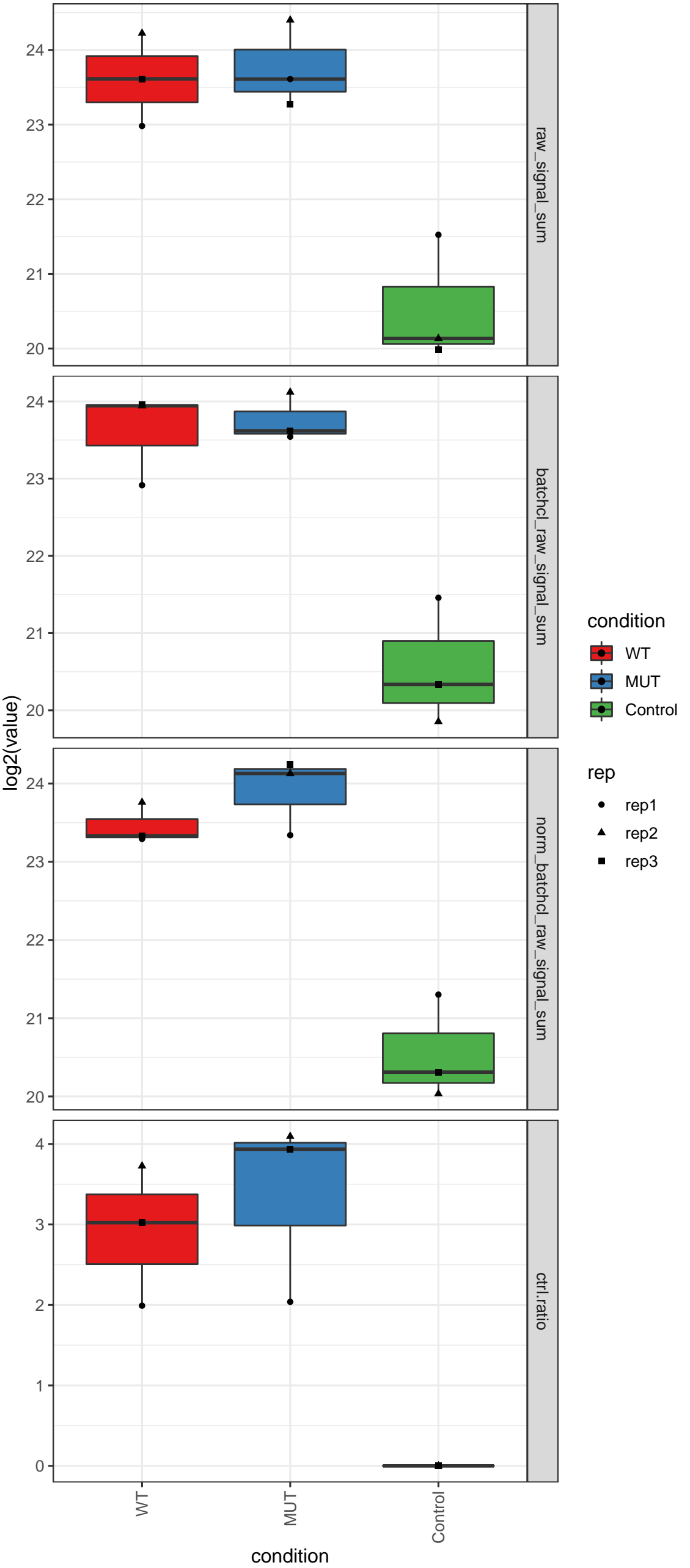
SLI15 – P38283

Inner centromere protein–related protein SLI15 OS=*Saccharomyces cerevisiae*



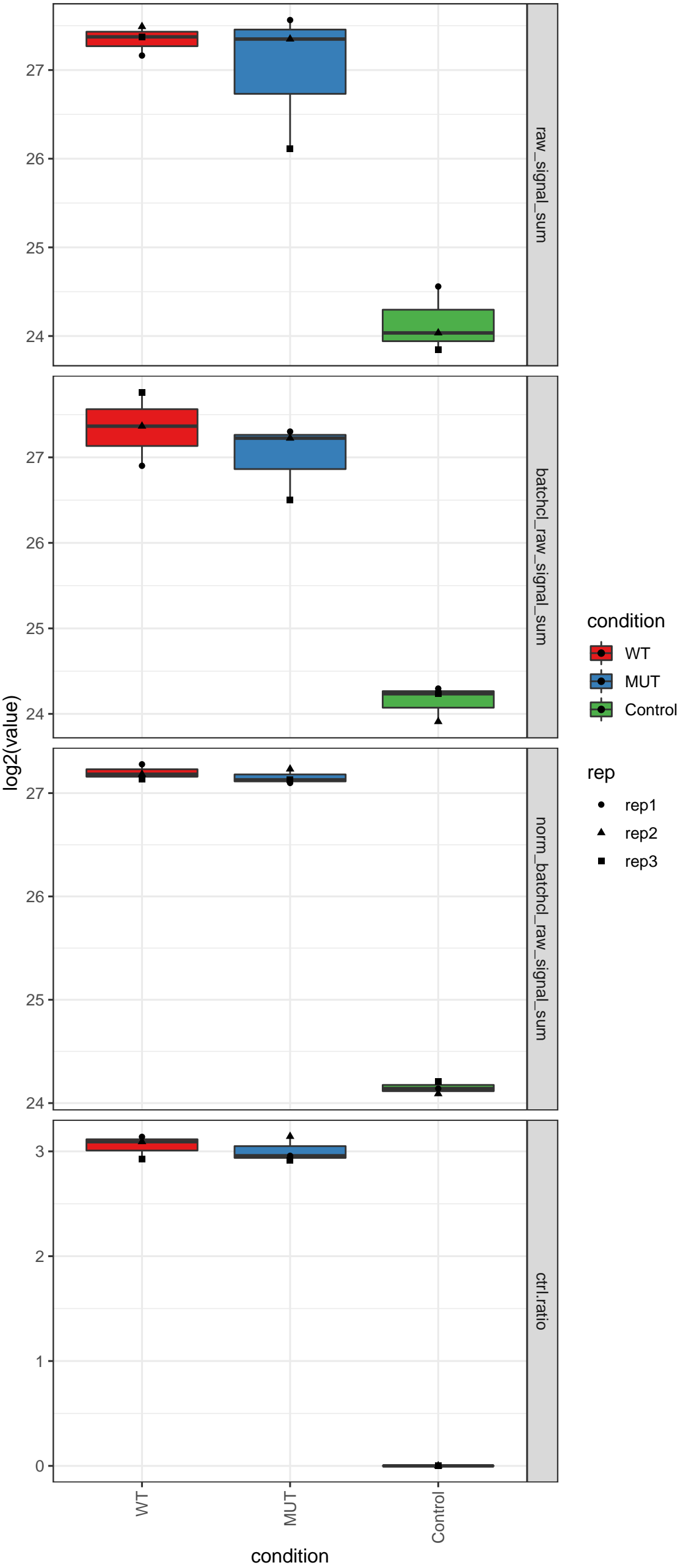
SLM1 – P40485

Phosphatidylinositol 4,5-bisphosphate-binding protein SLM1 OS=Sacchar



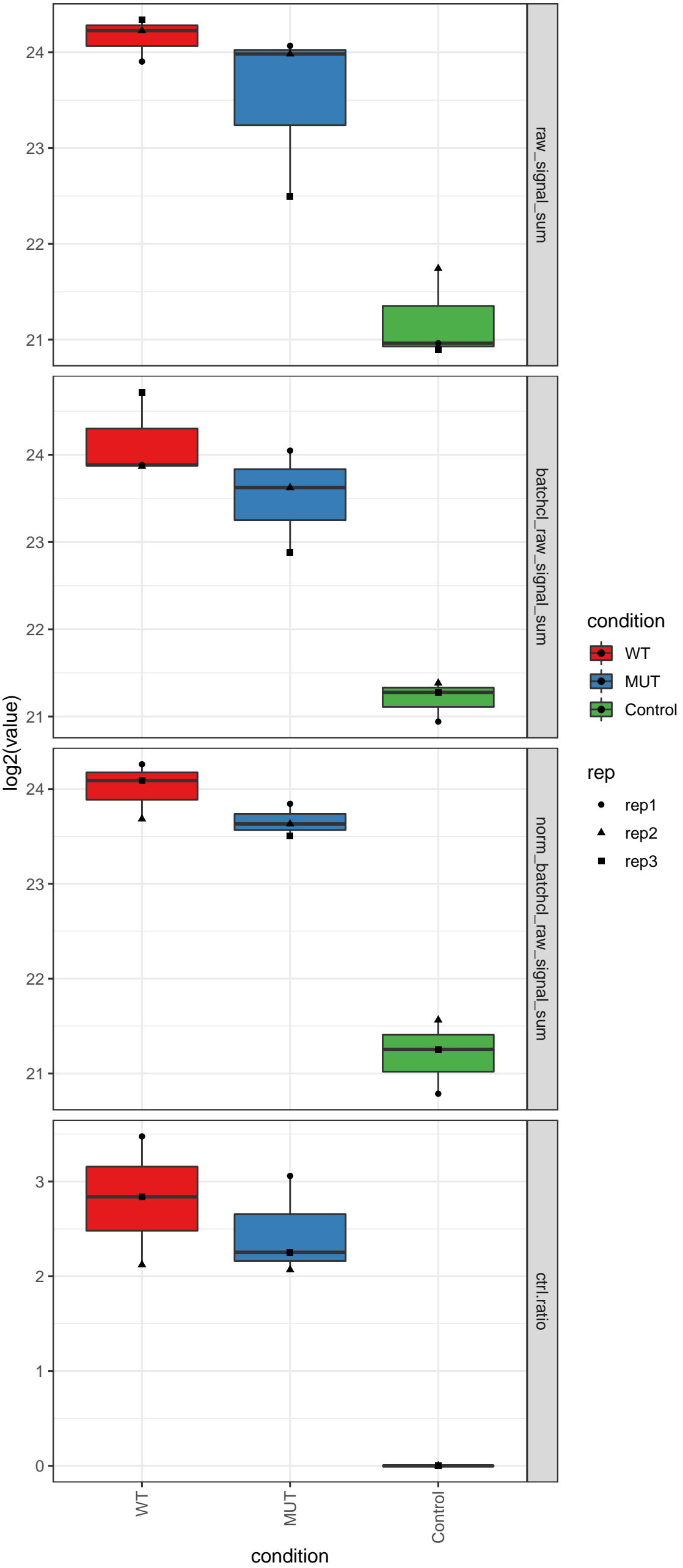
SMC1 – P32908

Structural maintenance of chromosomes protein 1 OS=Saccharomyces ce



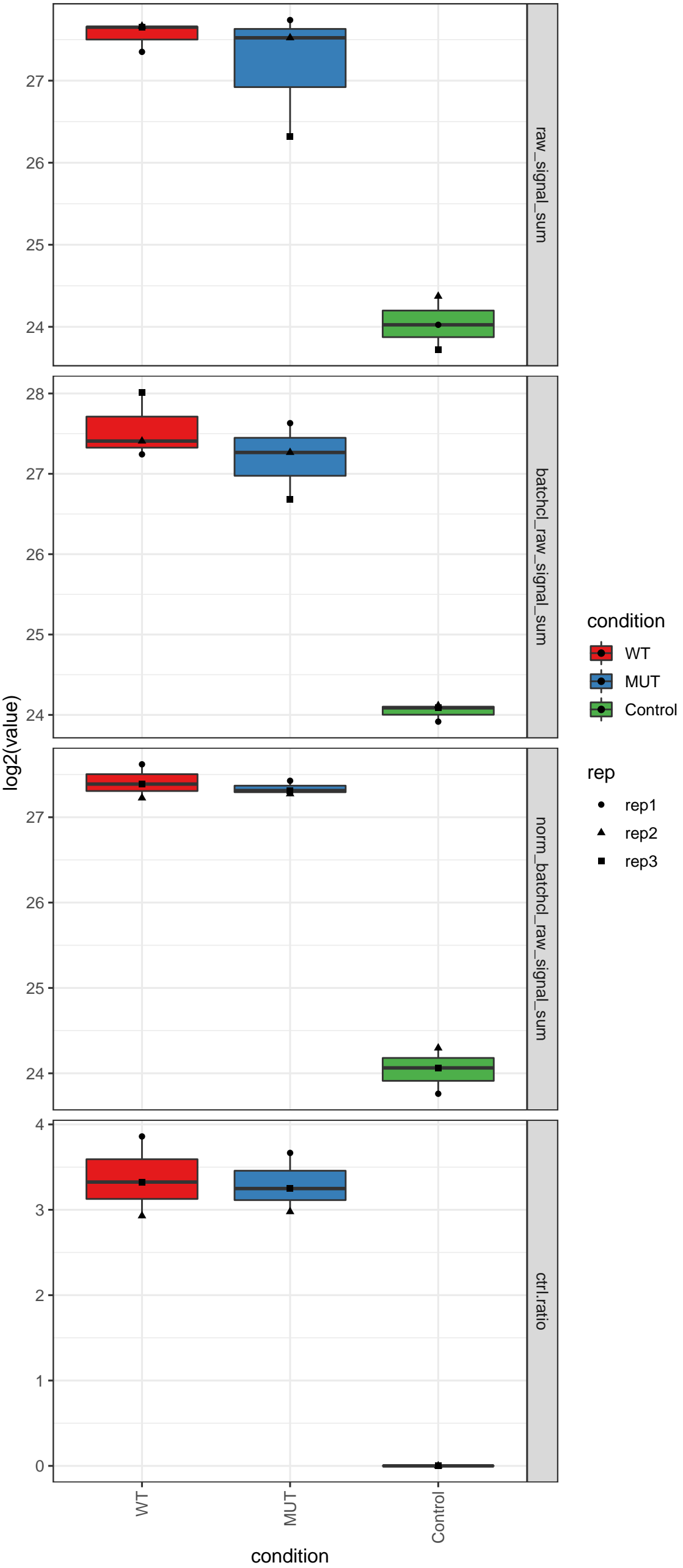
SMC2 – P38989

Structural maintenance of chromosomes protein 2 OS=Saccharomyces ce



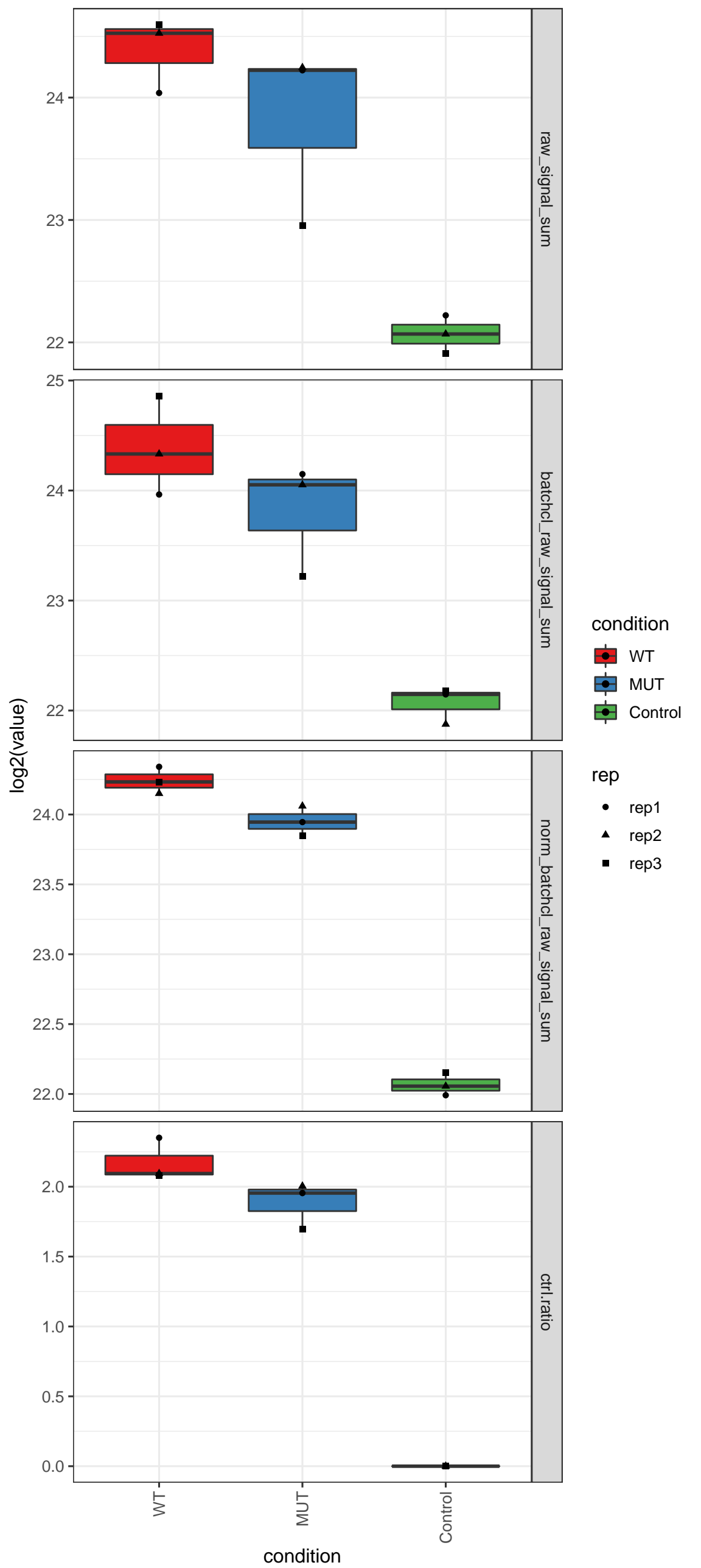
SMC3 – P47037

Structural maintenance of chromosomes protein 3 OS=Saccharomyces ce



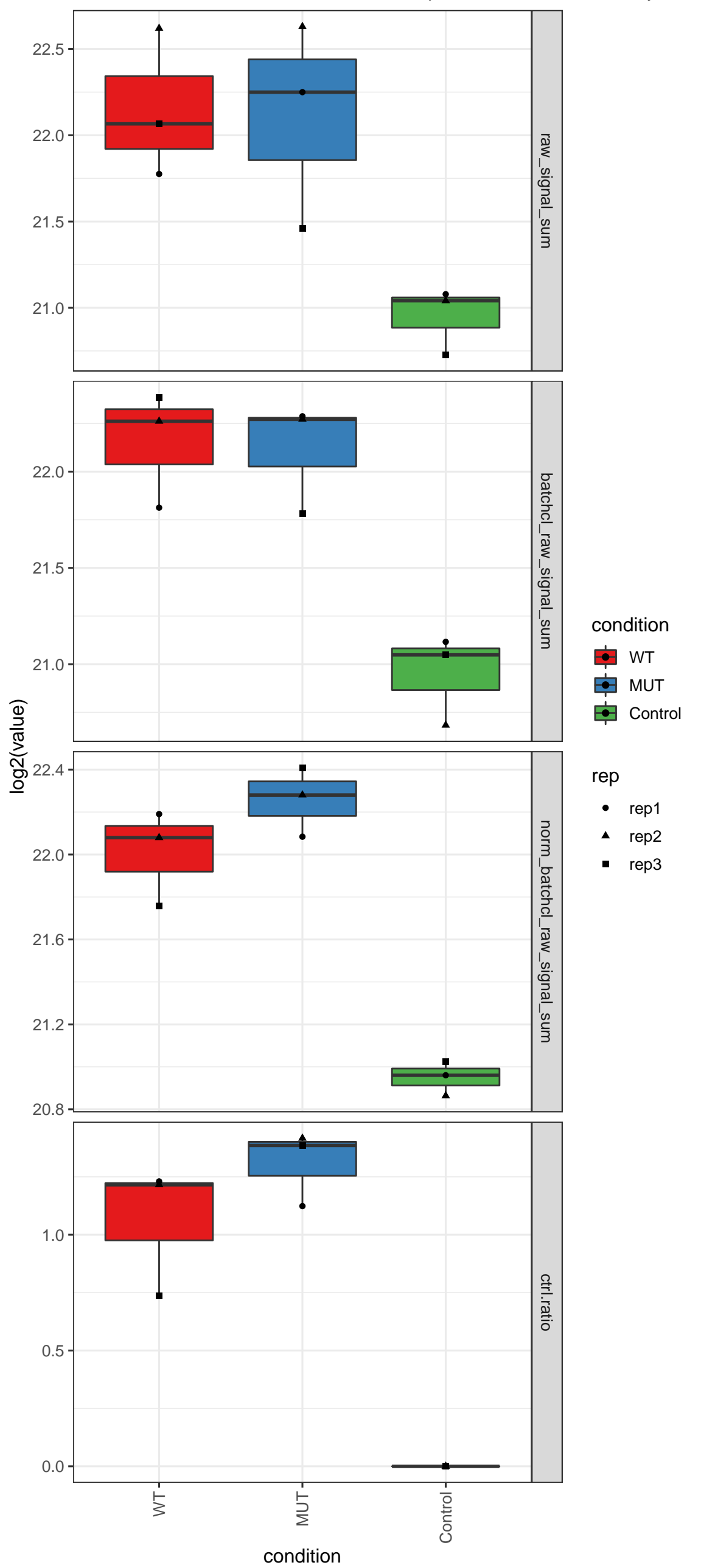
SMC4 – Q12267

Structural maintenance of chromosomes protein 4 OS=Saccharomyces cerevisiae



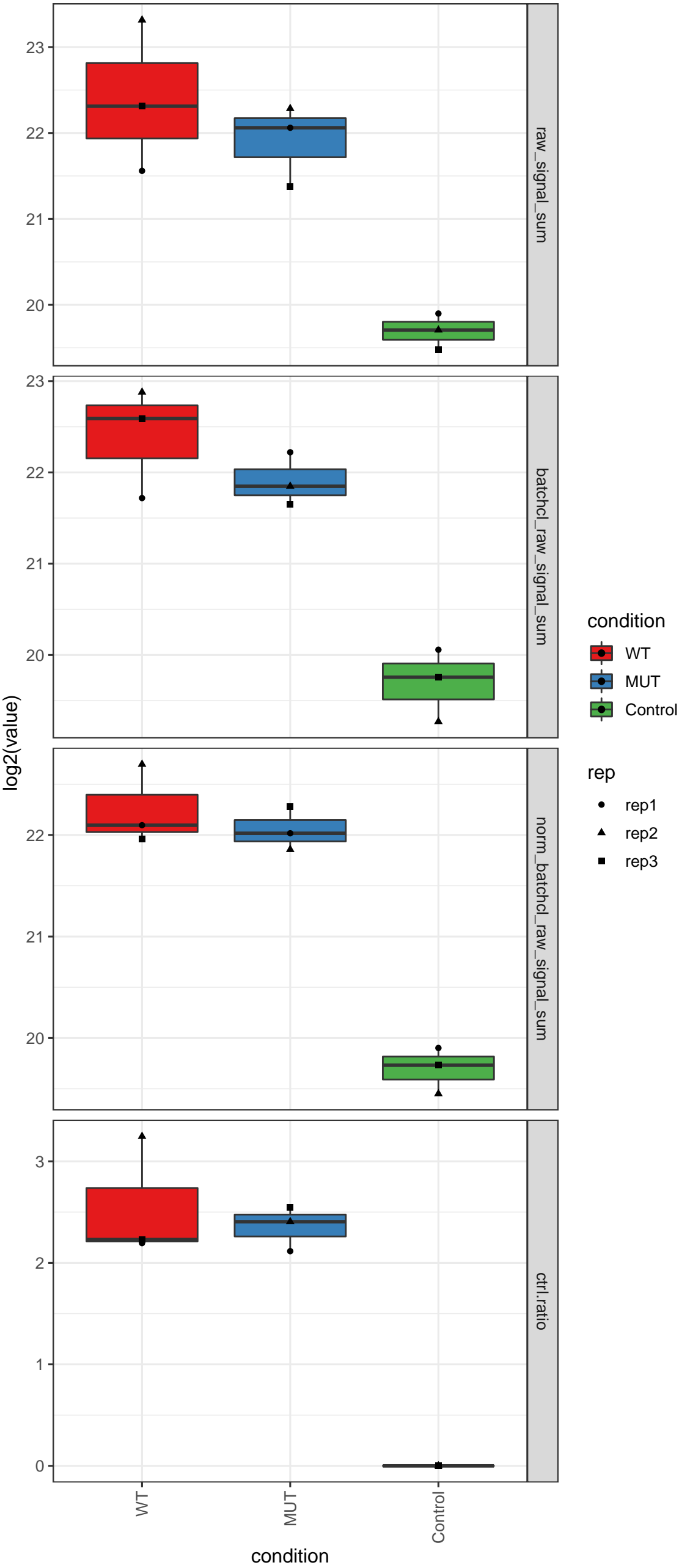
SMC5 – Q08204

Structural maintenance of chromosomes protein 5 OS=Saccharomyces cerevisiae



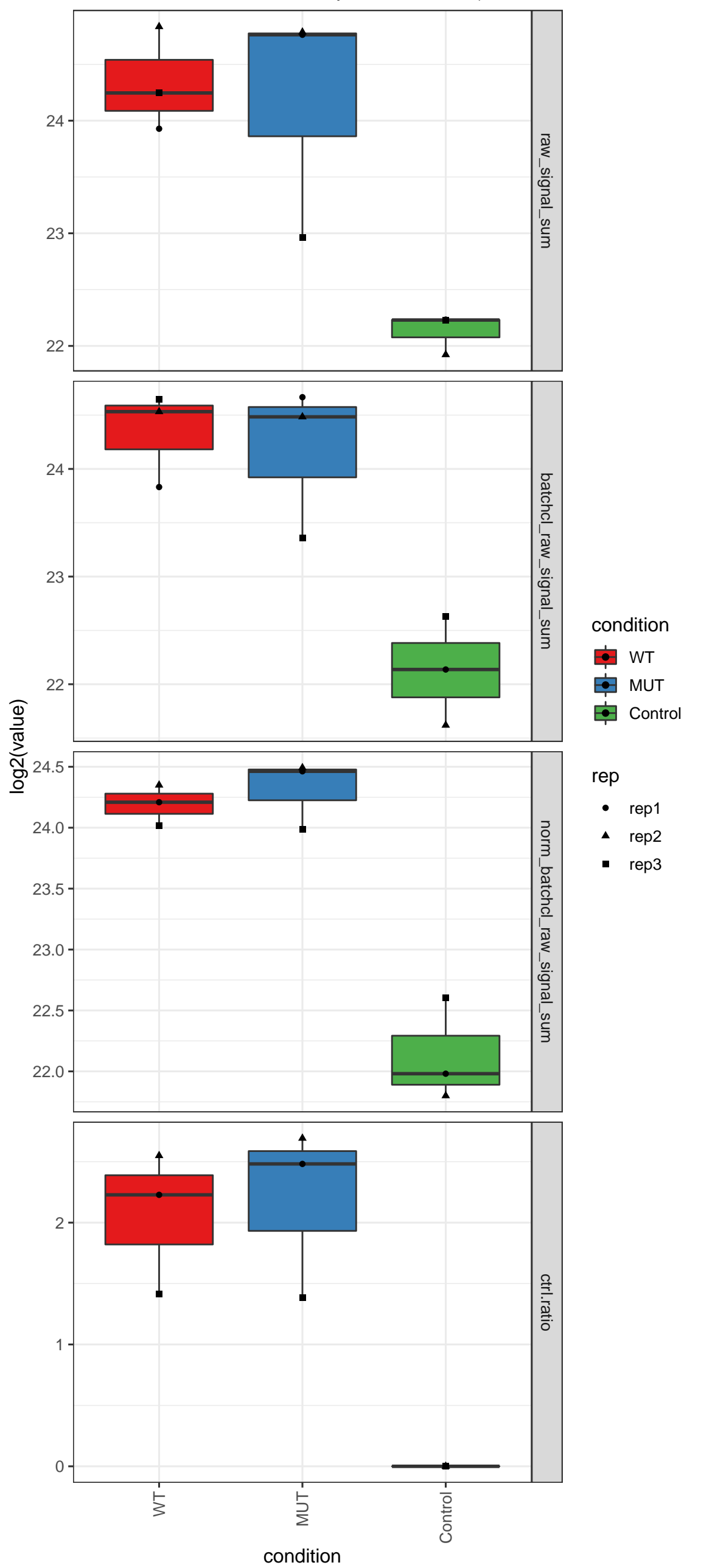
SMC6 – Q12749

Structural maintenance of chromosomes protein 6 OS=Saccharomyces ce



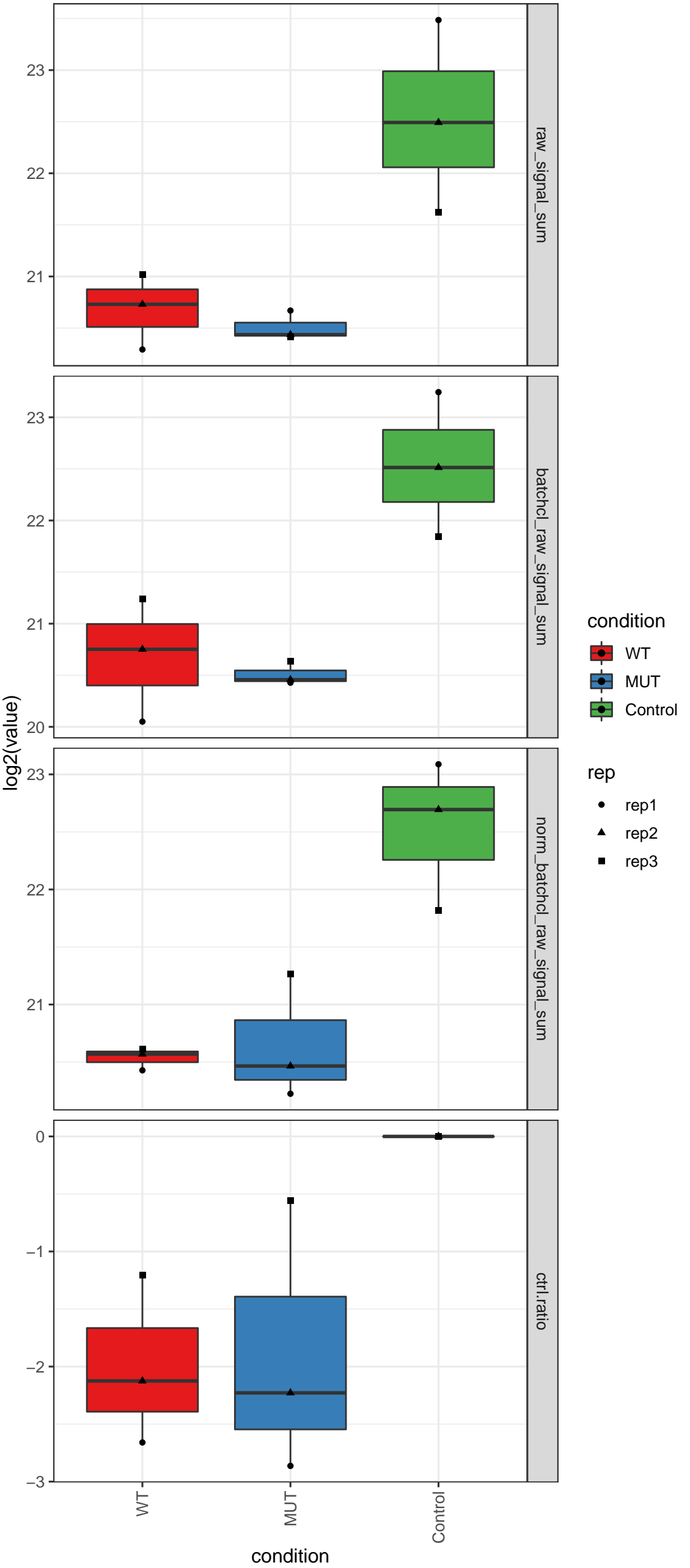
SMY2 – P32909

Protein SMY2 OS=*Saccharomyces cerevisiae* (strain ATCC 204508 / S288c)



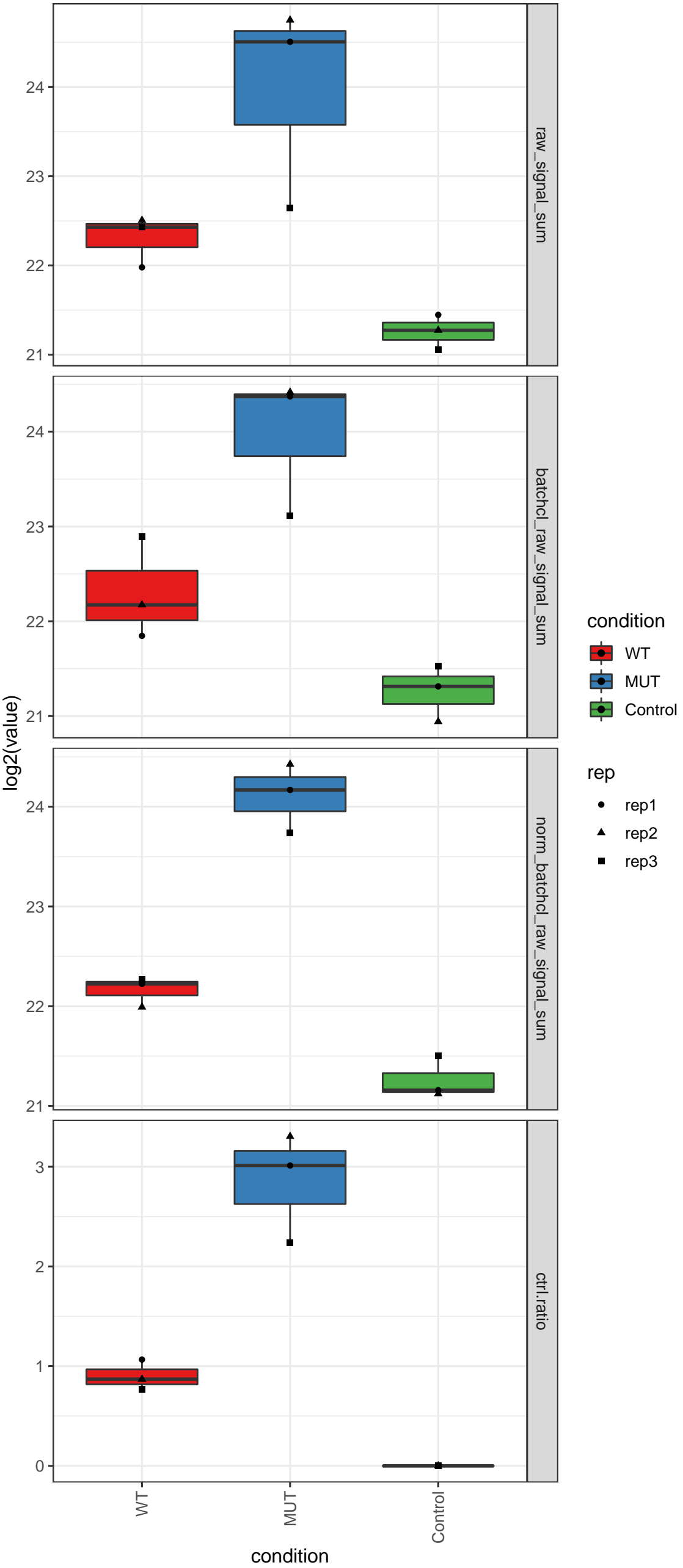
SNC2 – P33328

Synaptobrevin homolog 2 OS=*Saccharomyces cerevisiae* (strain ATCC 20457)



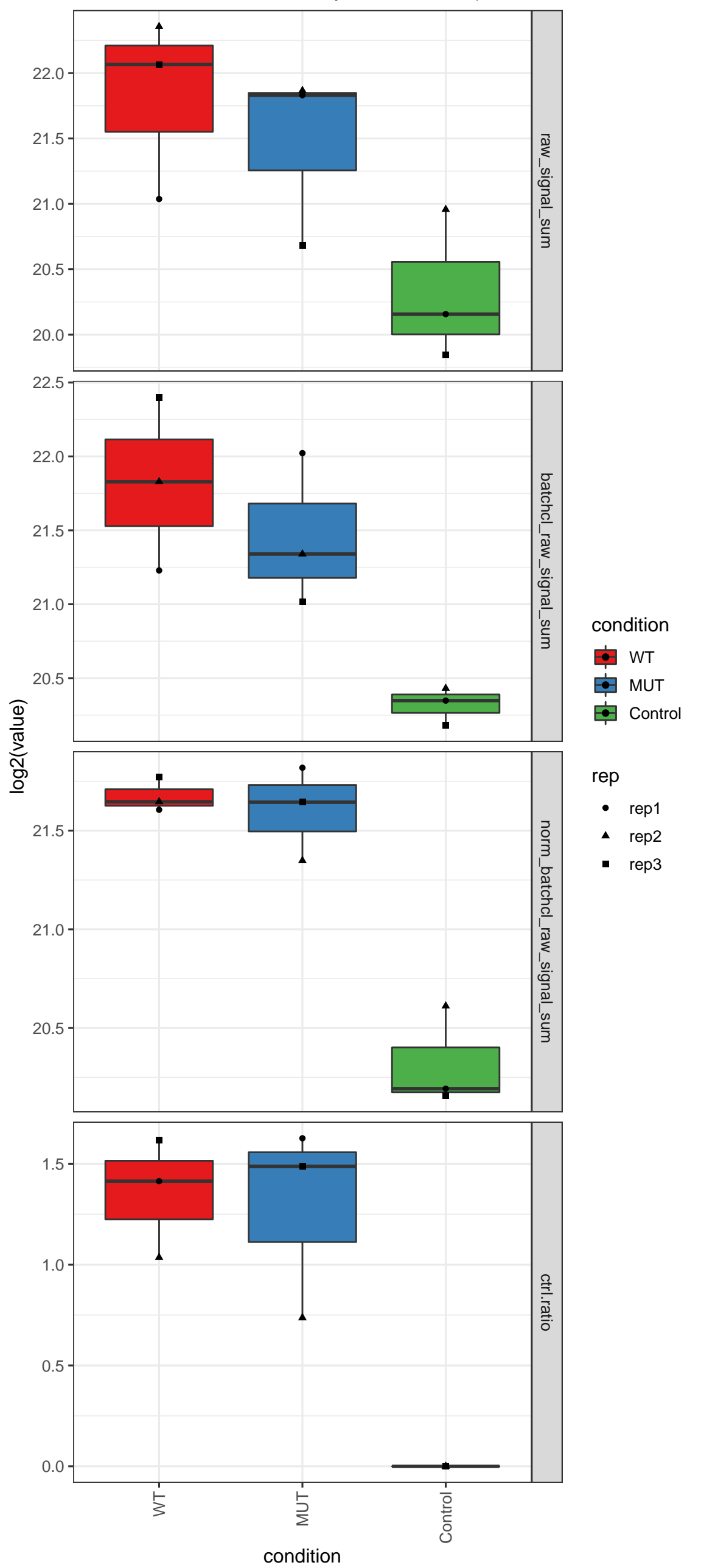
SNF1 – P06782

Carbon catabolite–derepressing protein kinase OS=*Saccharomyces cerevisiae*



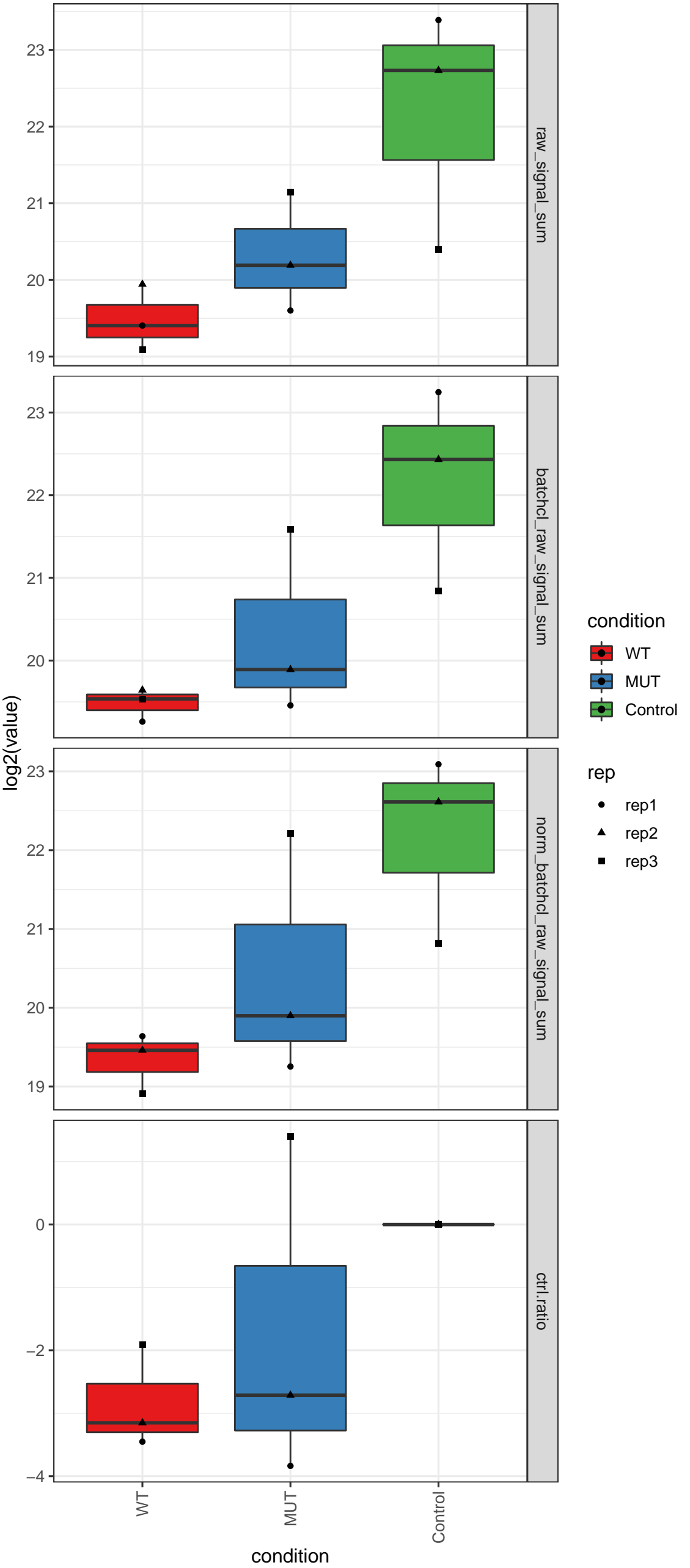
SOF1 – P33750

Protein SOF1 OS=*Saccharomyces cerevisiae* (strain ATCC 204508 / S28)



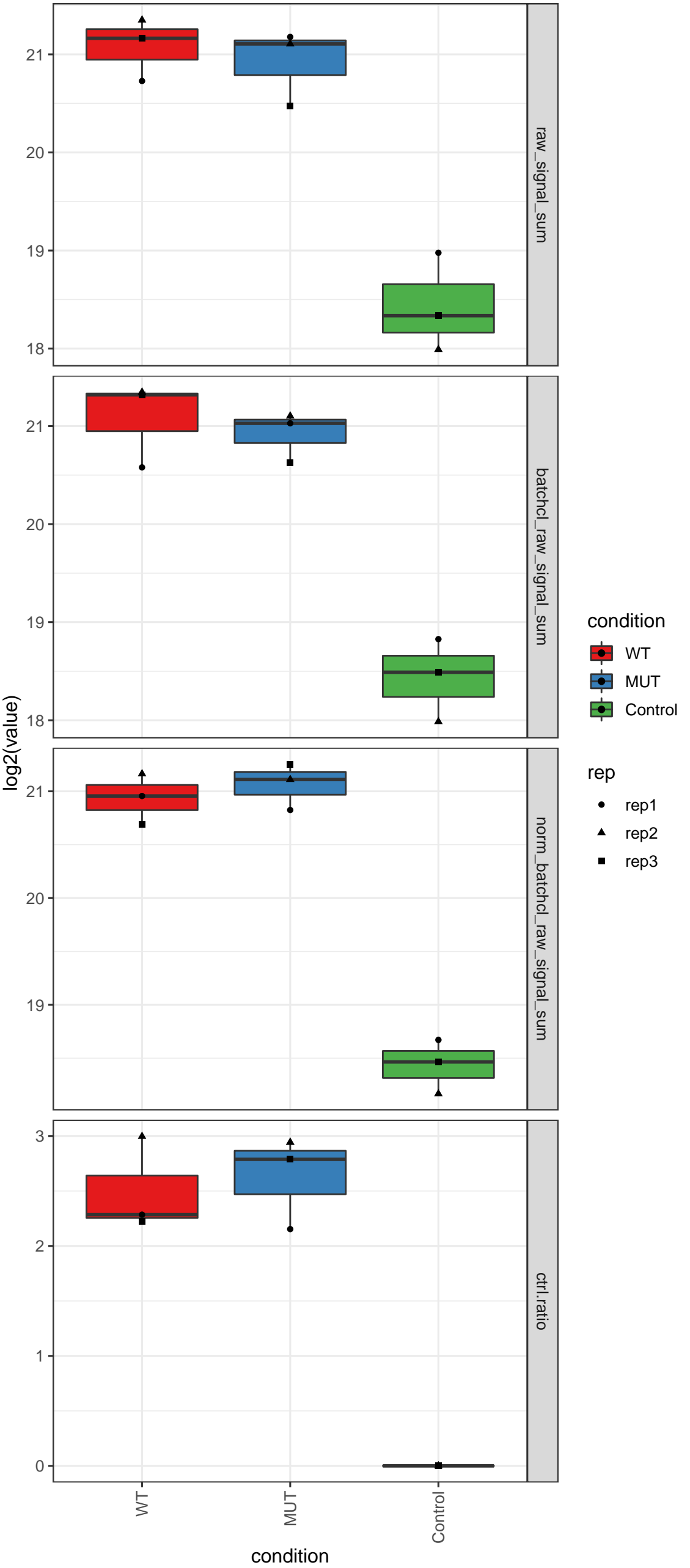
SPA2 – P23201

Protein SPA2 OS=*Saccharomyces cerevisiae* (strain ATCC 204508 / S288c)



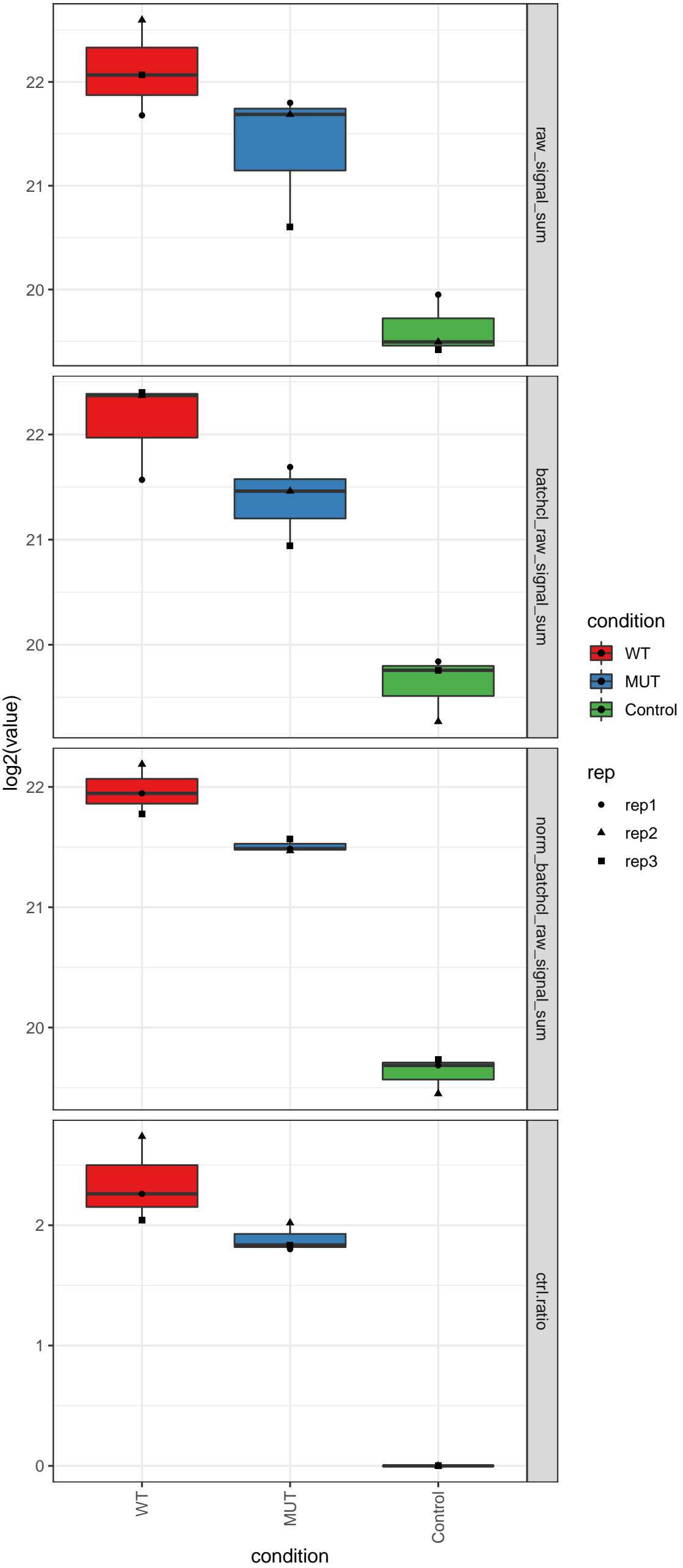
SPB4 – P25808

ATP-dependent rRNA helicase SPB4 OS=*Saccharomyces cerevisiae* (strain



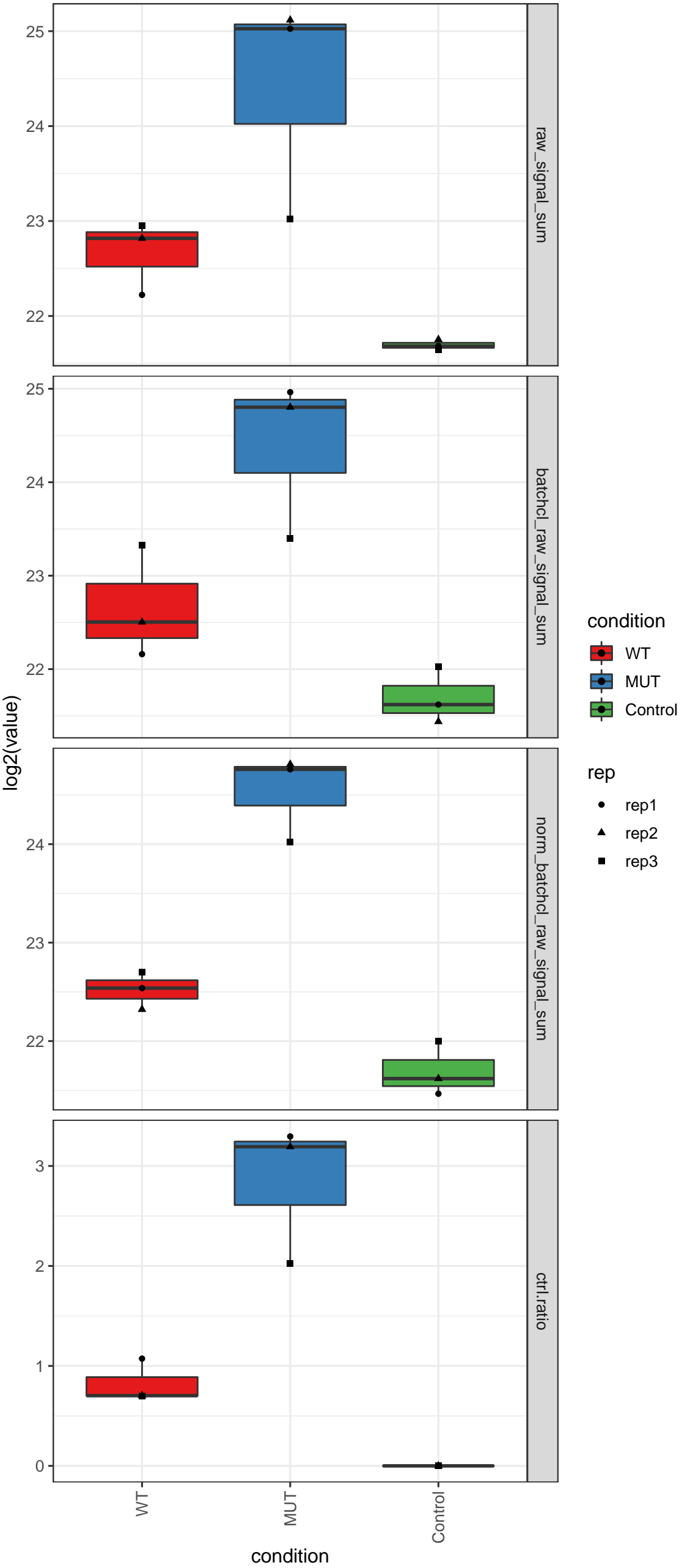
SPF1 – P39986

Manganese-transporting ATPase 1 OS=*Saccharomyces cerevisiae* (strain



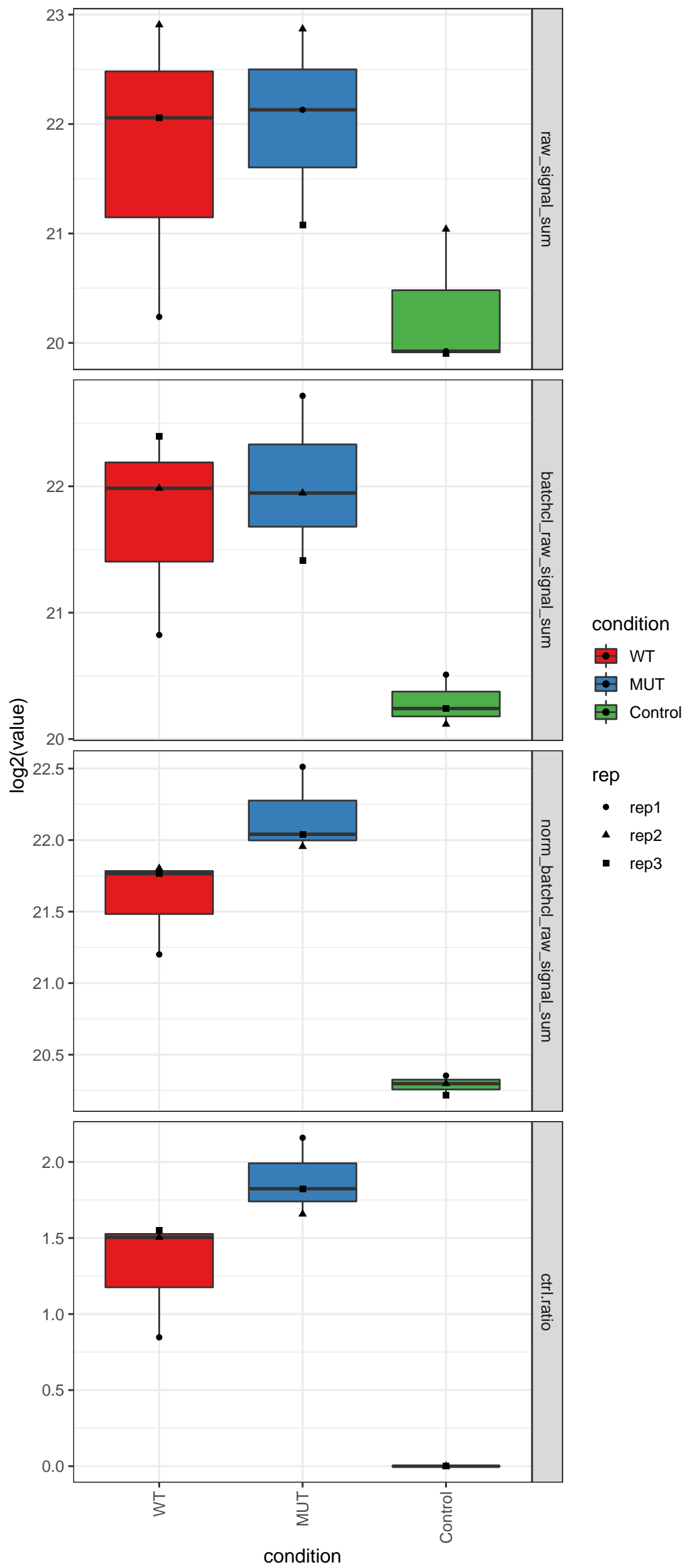
SPO14 – P36126

Phospholipase D1 OS=*Saccharomyces cerevisiae* (strain ATCC 204508 / S



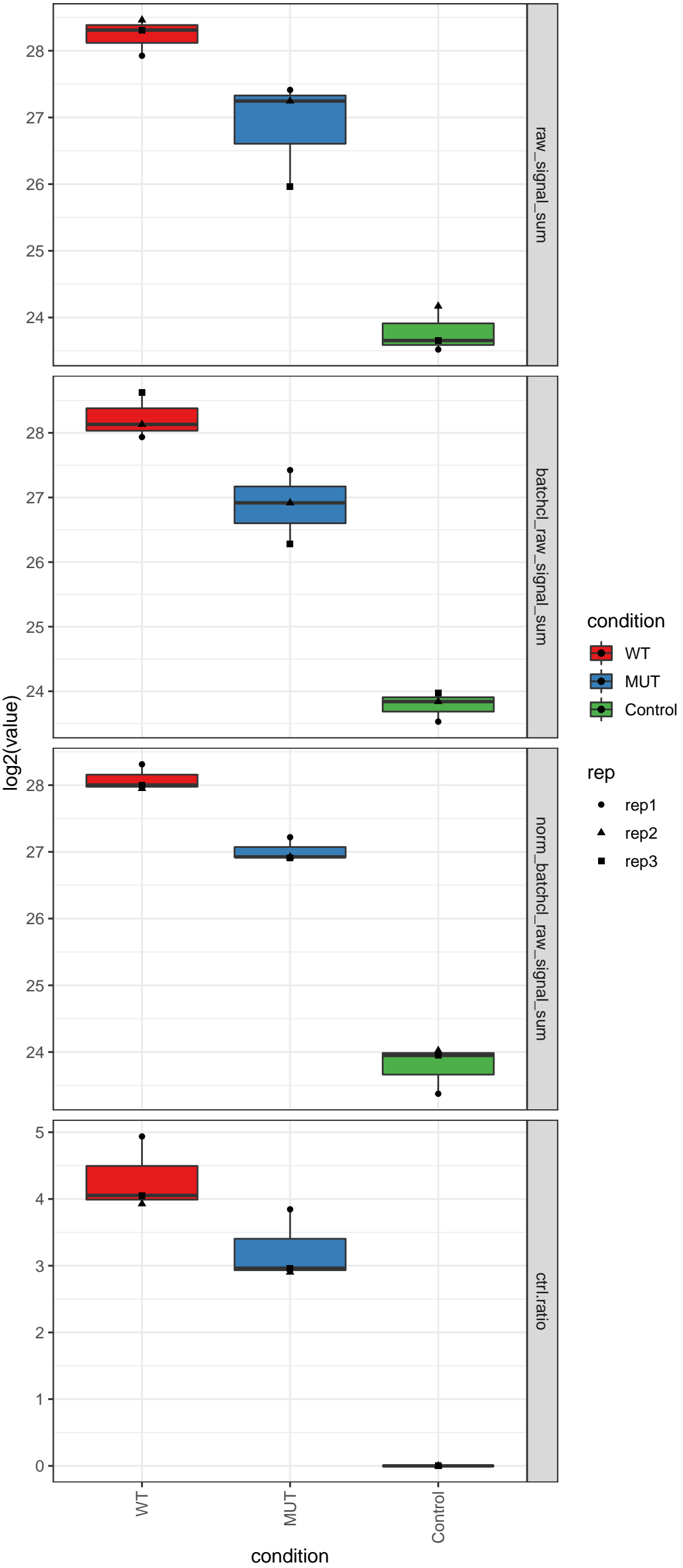
SPO22 – P40511

Sporulation-specific protein 22 OS=*Saccharomyces cerevisiae* (strain ATCC 25716)



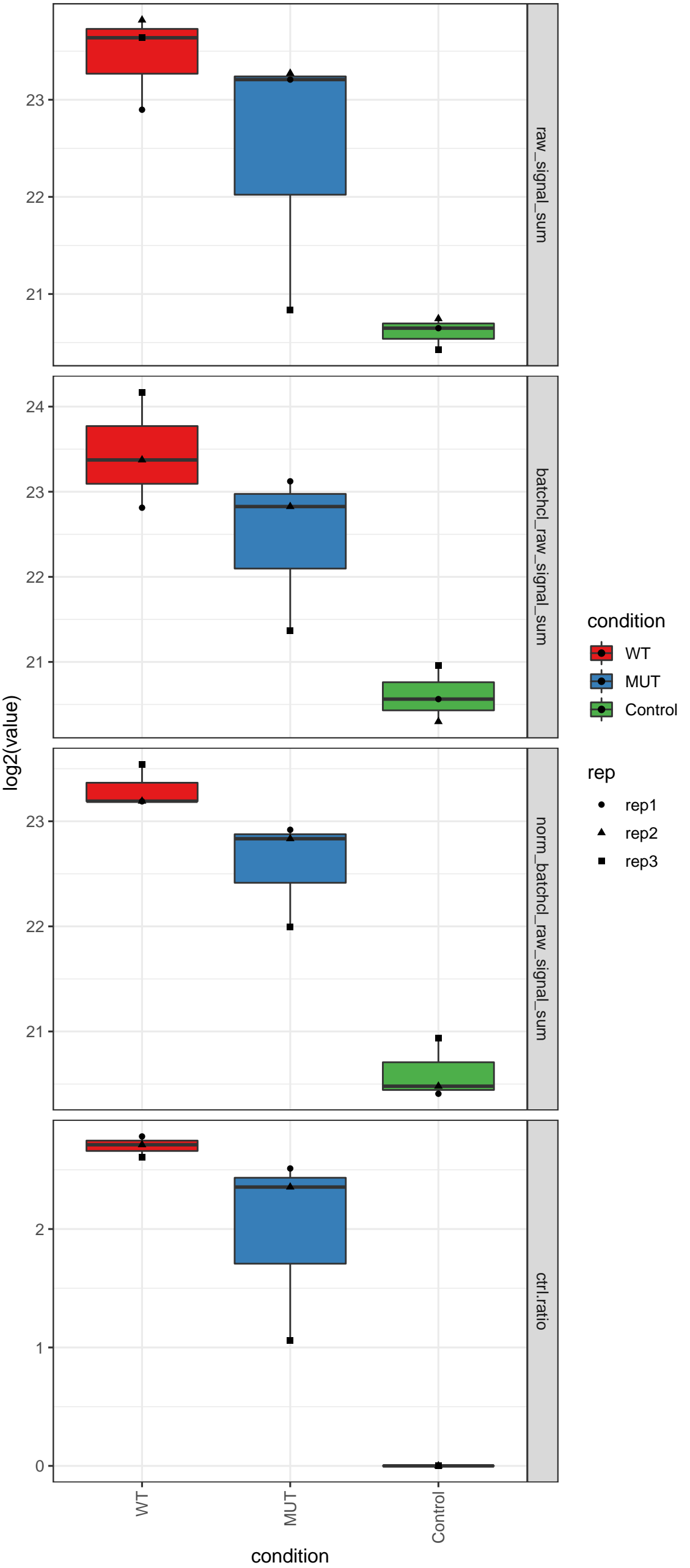
SPP1 – Q03012

COMPASS component SPP1 OS=*Saccharomyces cerevisiae* (strain ATCC



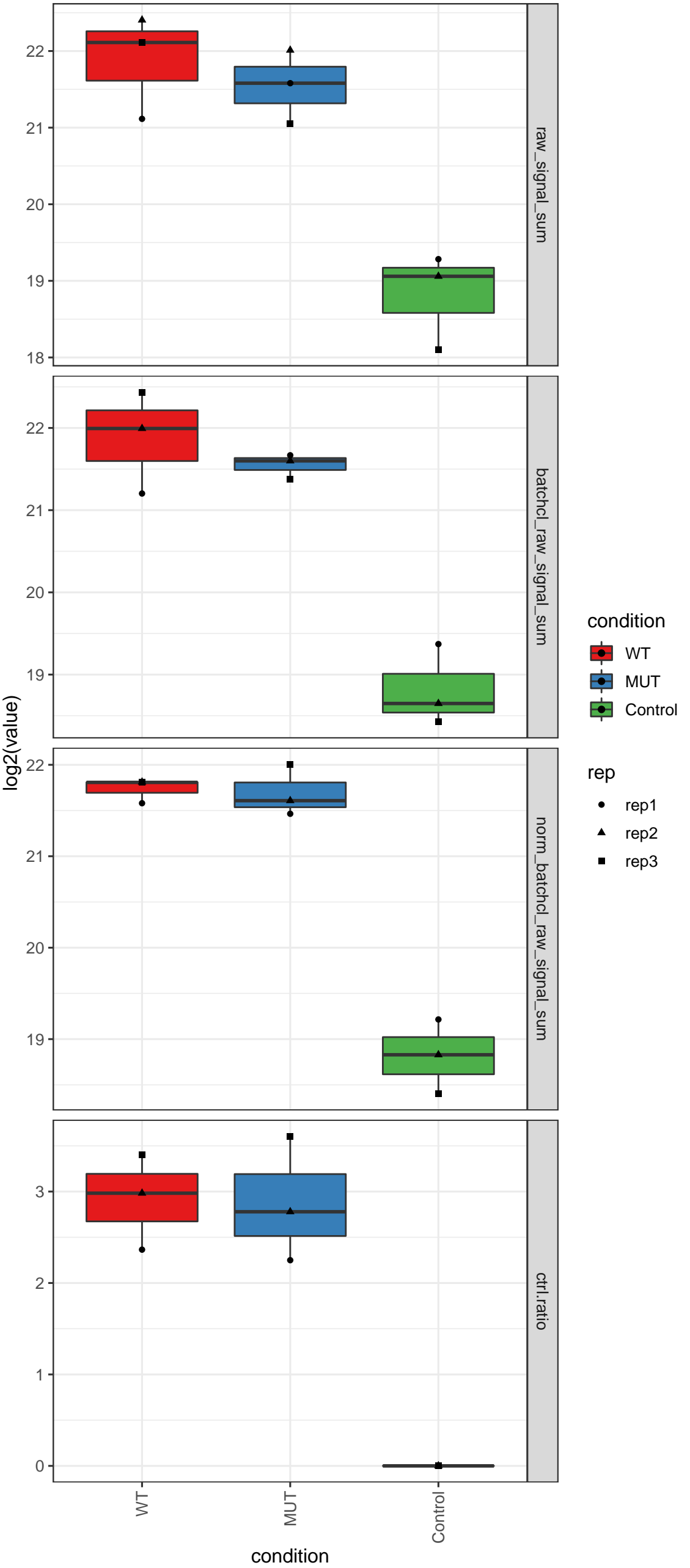
SPP41 – P38904

Protein SPP41 OS=*Saccharomyces cerevisiae* (strain ATCC 204508 / S28



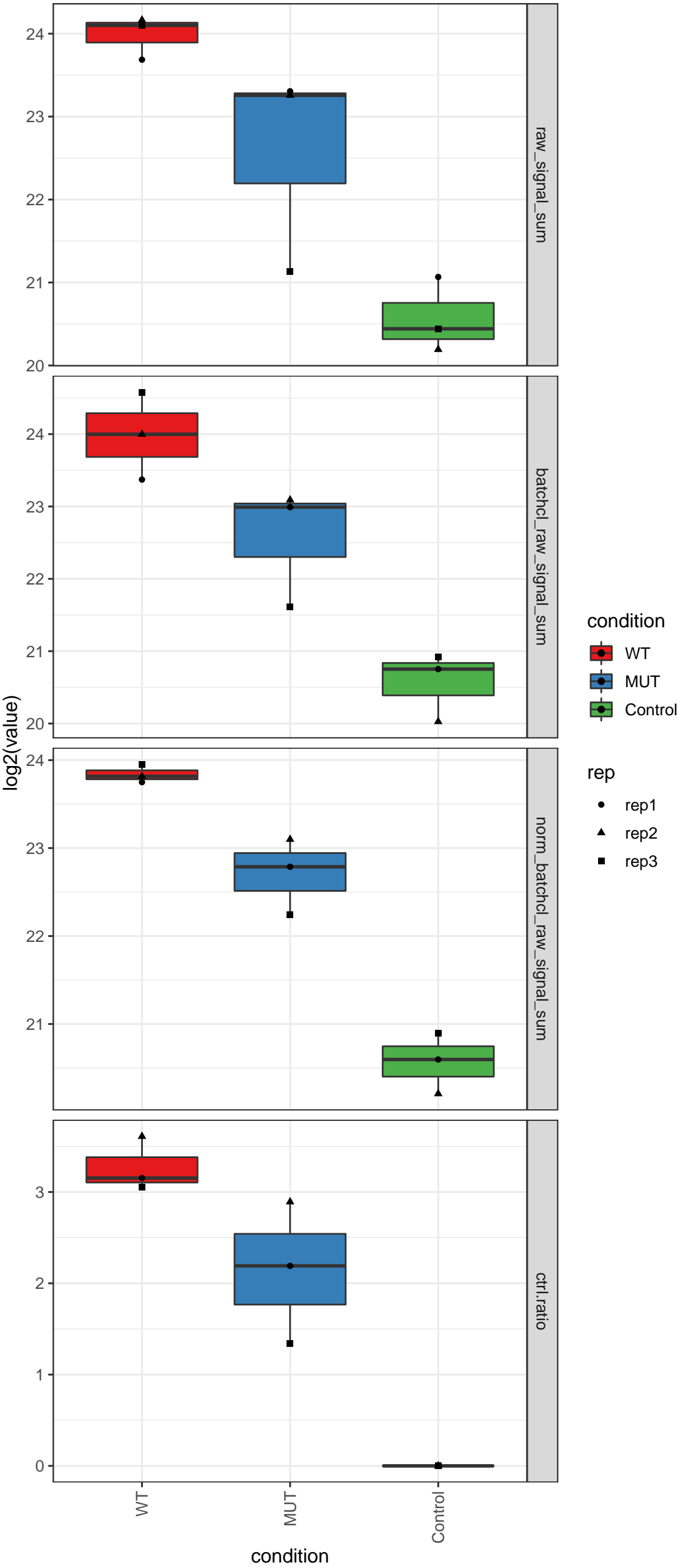
SPS19 – P32573

Peroxisomal 2,4–dienoyl–CoA reductase SPS19 OS=*Saccharomyces cere*



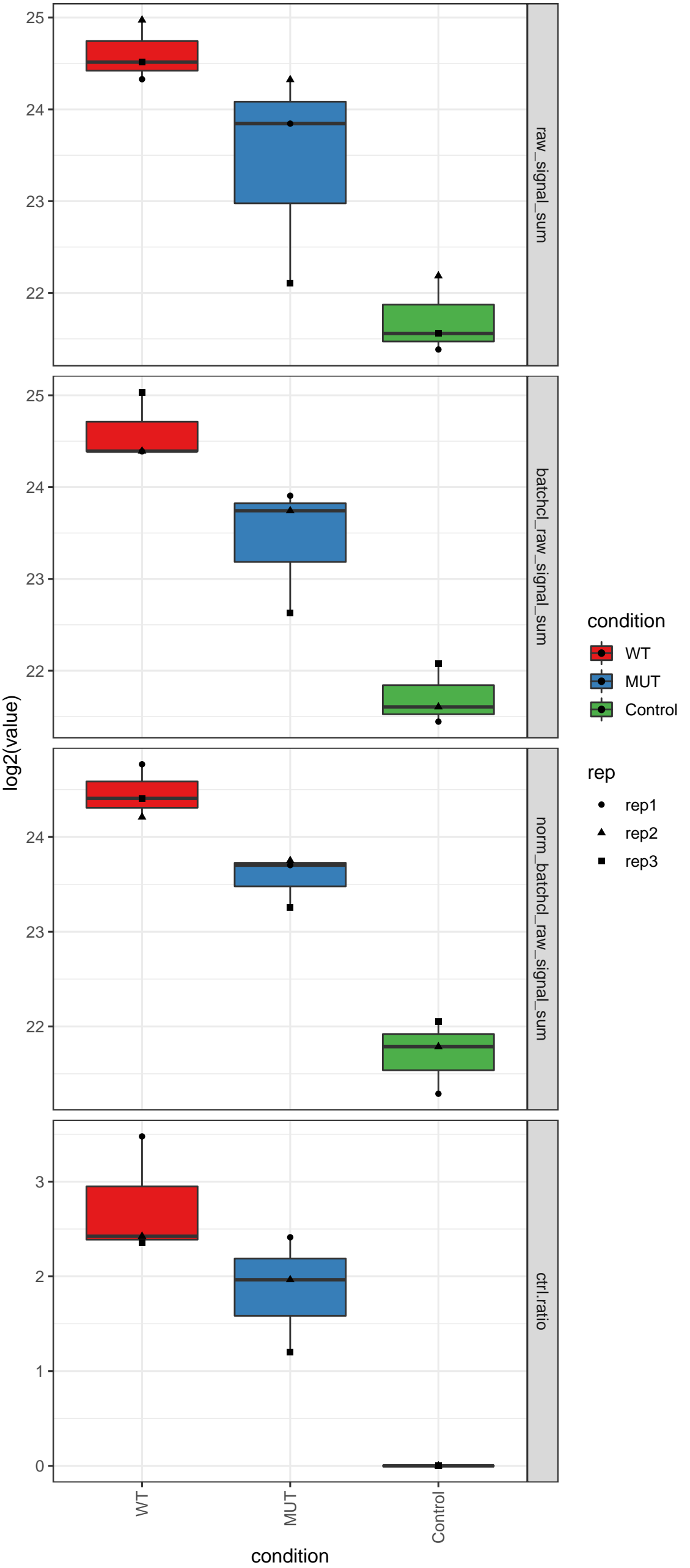
SPT15 – P13393

TATA-box-binding protein OS=*Saccharomyces cerevisiae* (strain ATCC 20



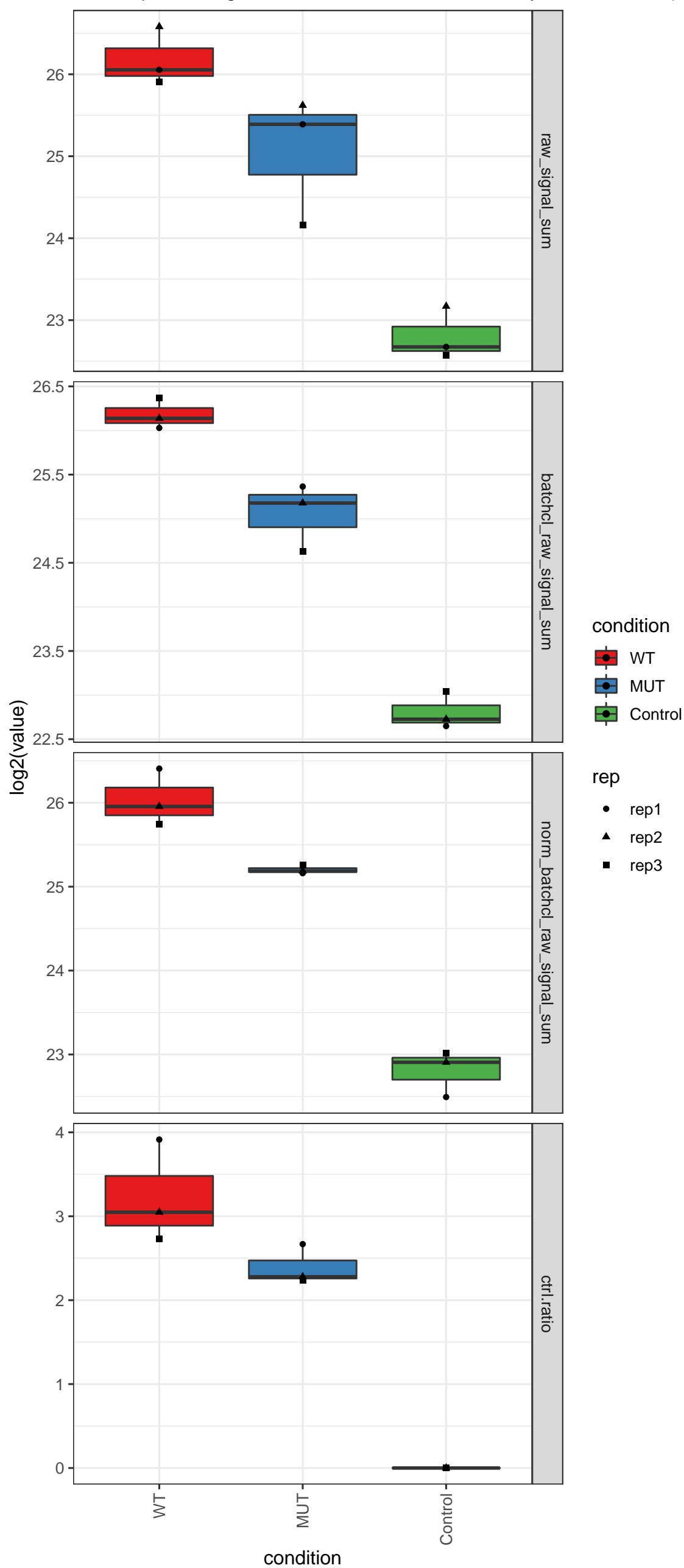
SPT16 – P32558

FACT complex subunit SPT16 OS=*Saccharomyces cerevisiae* (strain ATCC 24843)



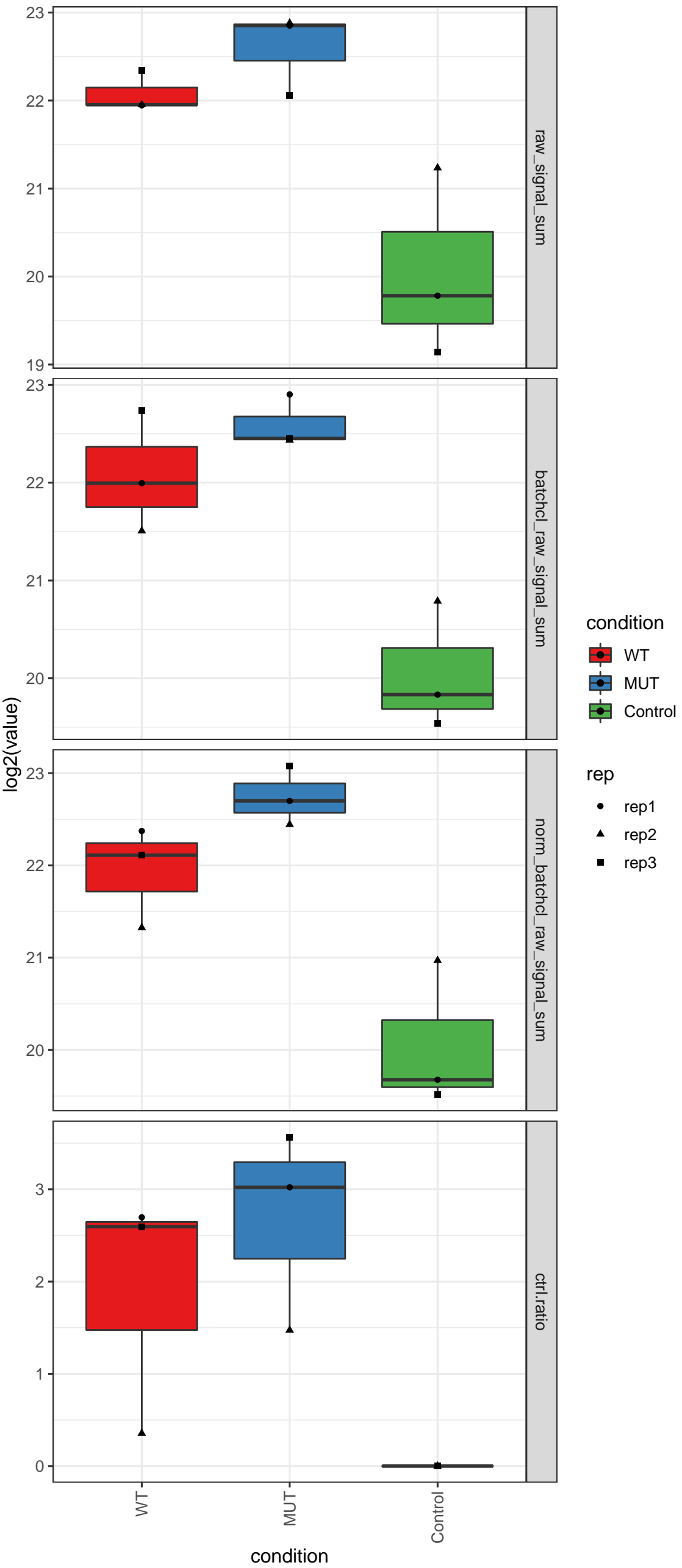
SPT5 – P27692

Transcription elongation factor SPT5 OS=*Saccharomyces cerevisiae* (strain



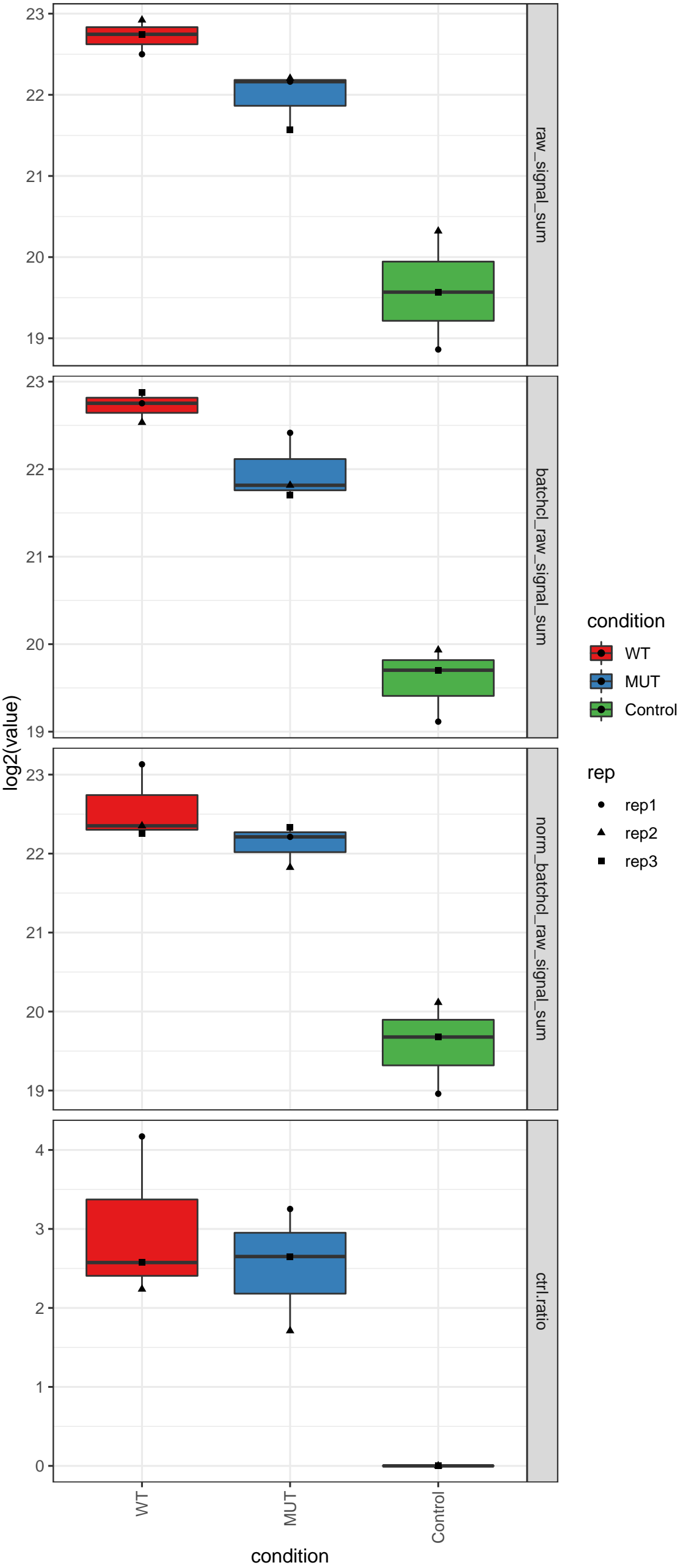
SPT6 – P23615

Transcription elongation factor SPT6 OS=*Saccharomyces cerevisiae* (strain



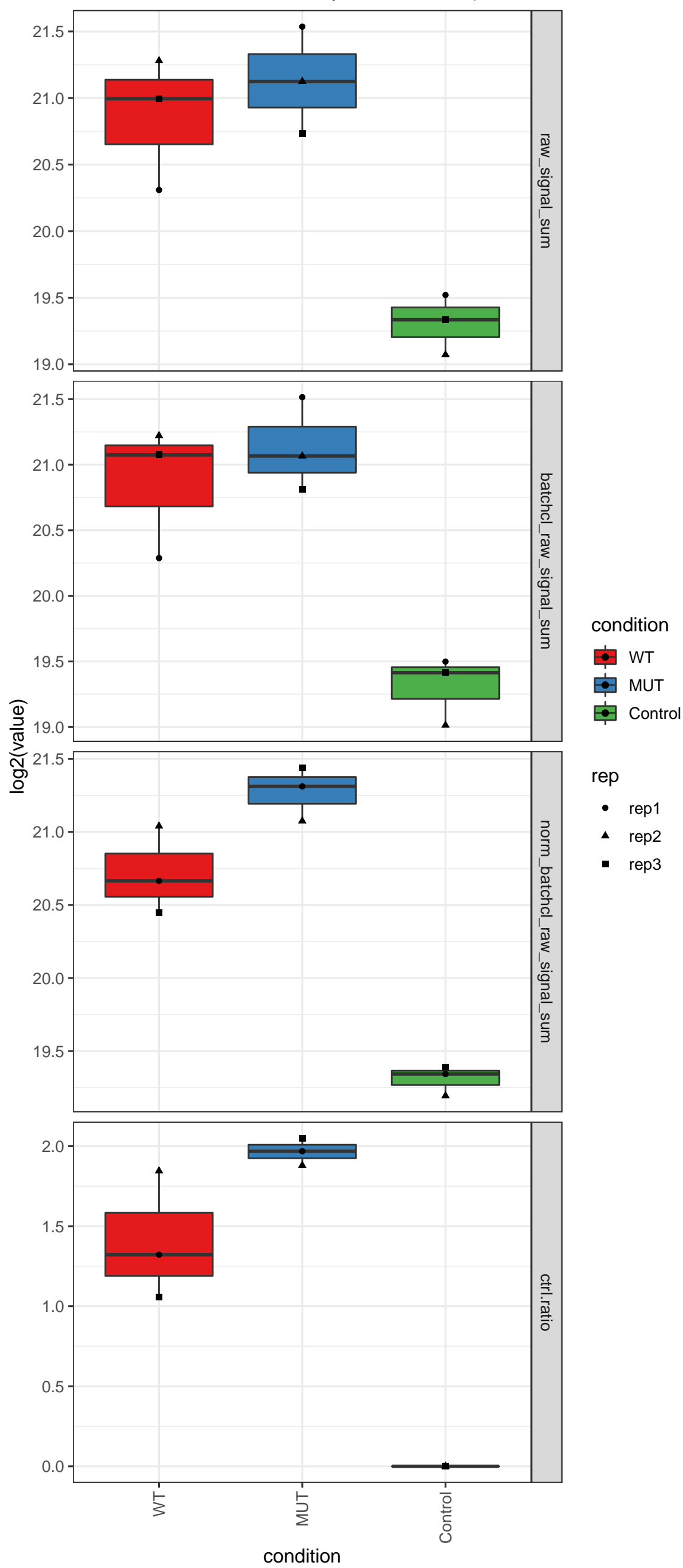
SPT7 – P35177

Transcriptional activator SPT7 OS=*Saccharomyces cerevisiae* (strain ATCC



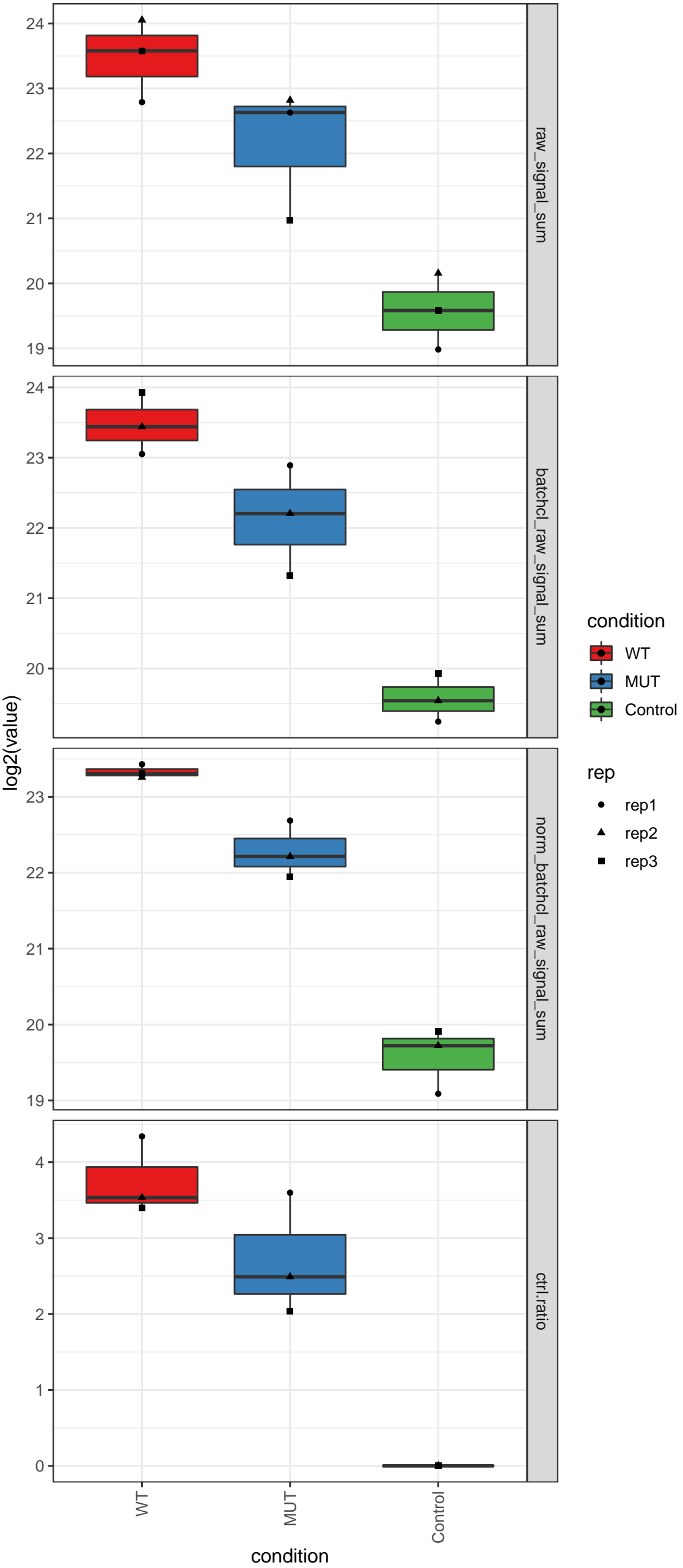
SRL2 – Q12020

Protein SRL2 OS=*Saccharomyces cerevisiae* (strain ATCC 204508 / S28)



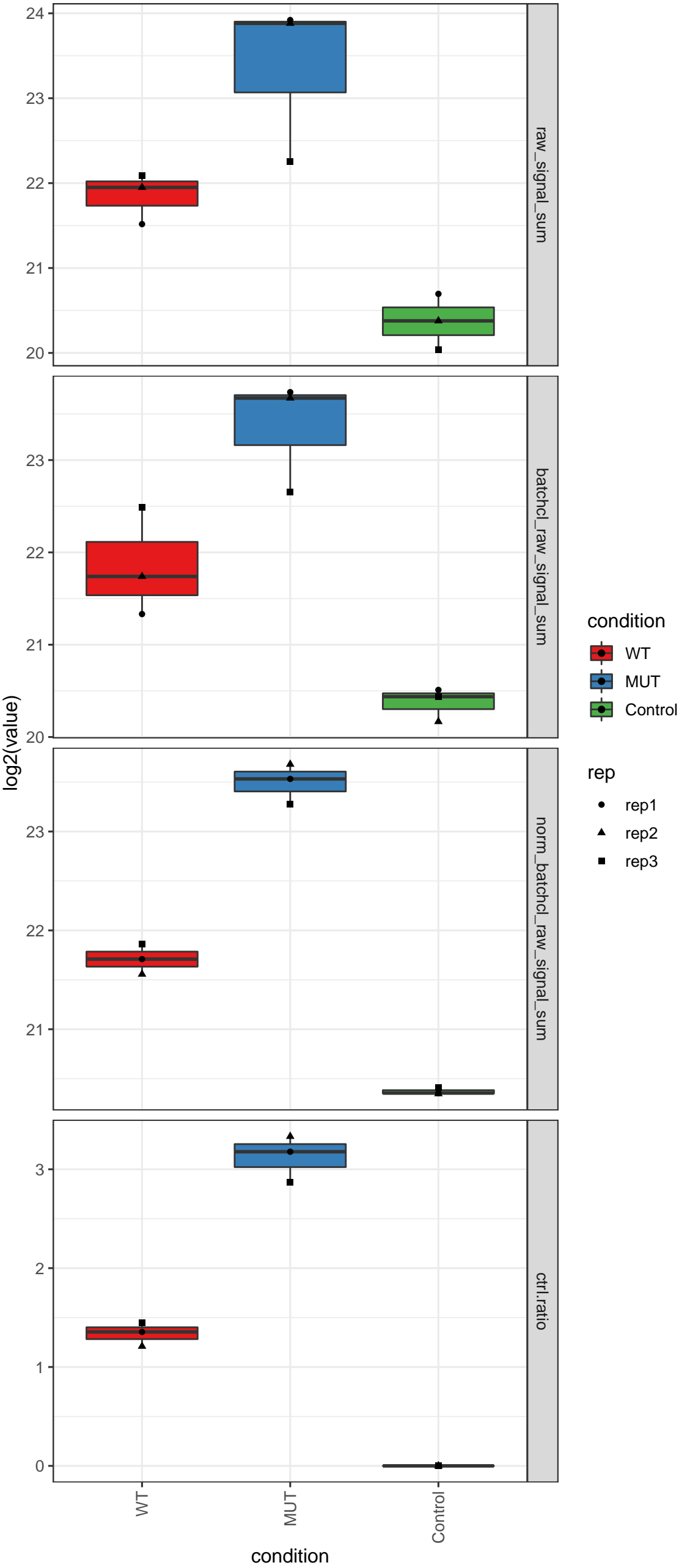
SRM1 – P21827

Guanine nucleotide exchange factor SRM1 OS=*Saccharomyces cerevisiae*



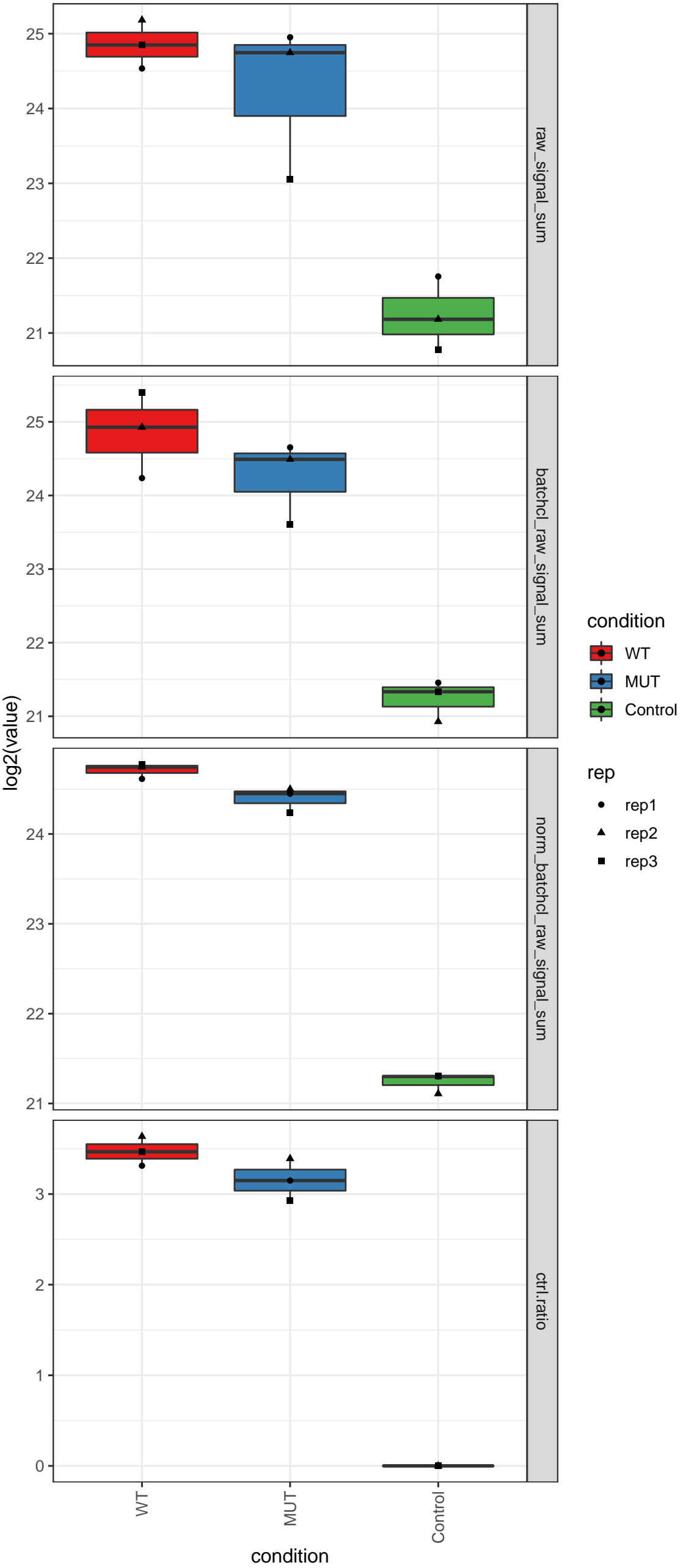
SRO9 – P25567

RNA-binding protein SRO9 OS=*Saccharomyces cerevisiae* (strain ATCC 2



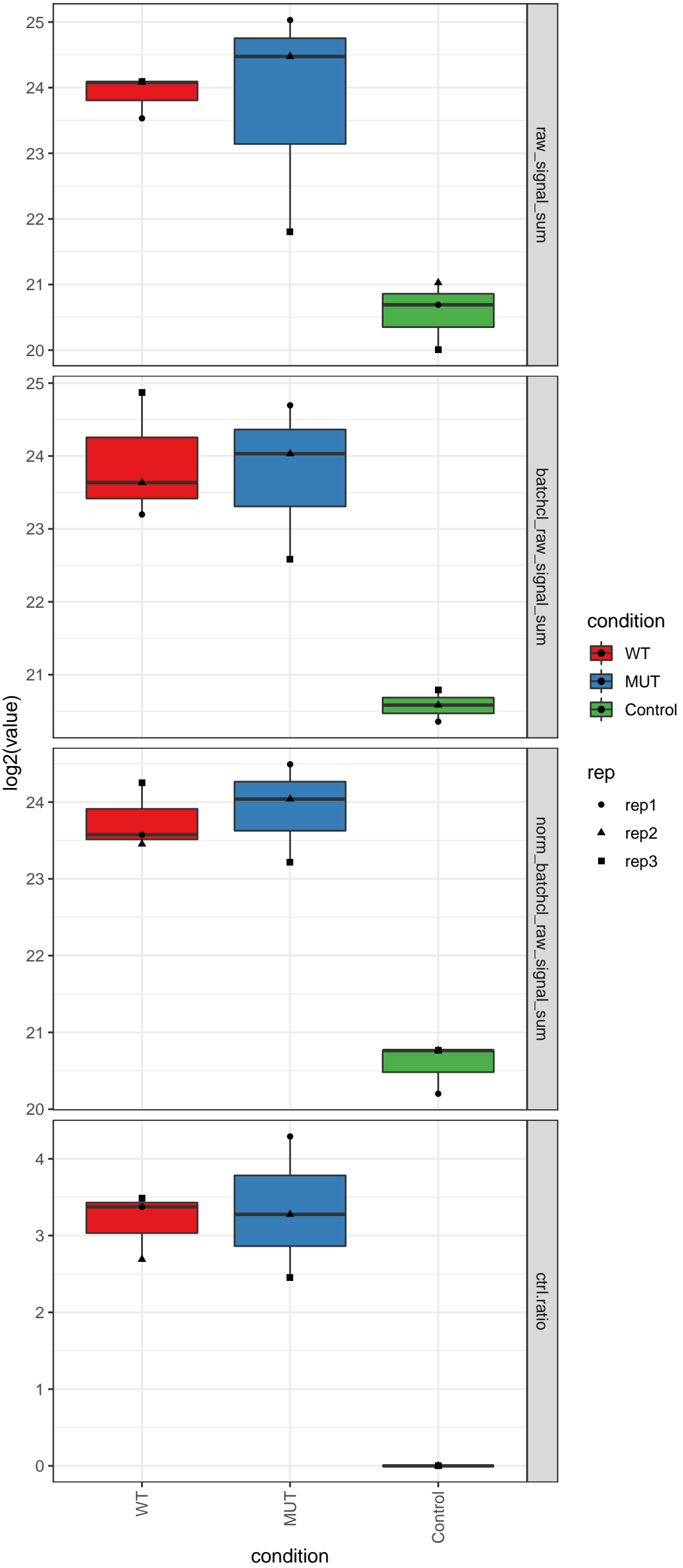
SRP1 – Q02821

Importin subunit alpha OS=Saccharomyces cerevisiae (strain ATCC 20450)



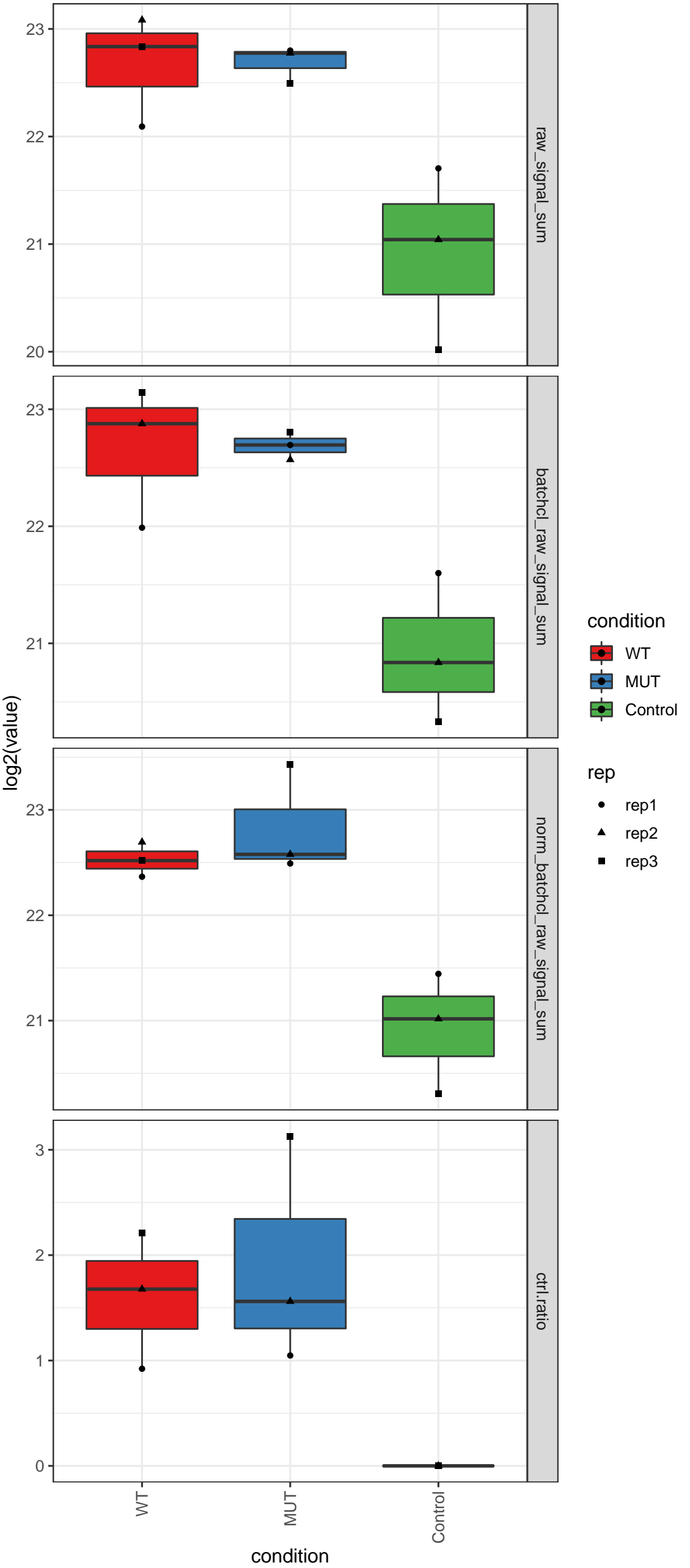
SRP40 – P32583

Suppressor protein SRP40 OS=*Saccharomyces cerevisiae* (strain ATCC 20464)



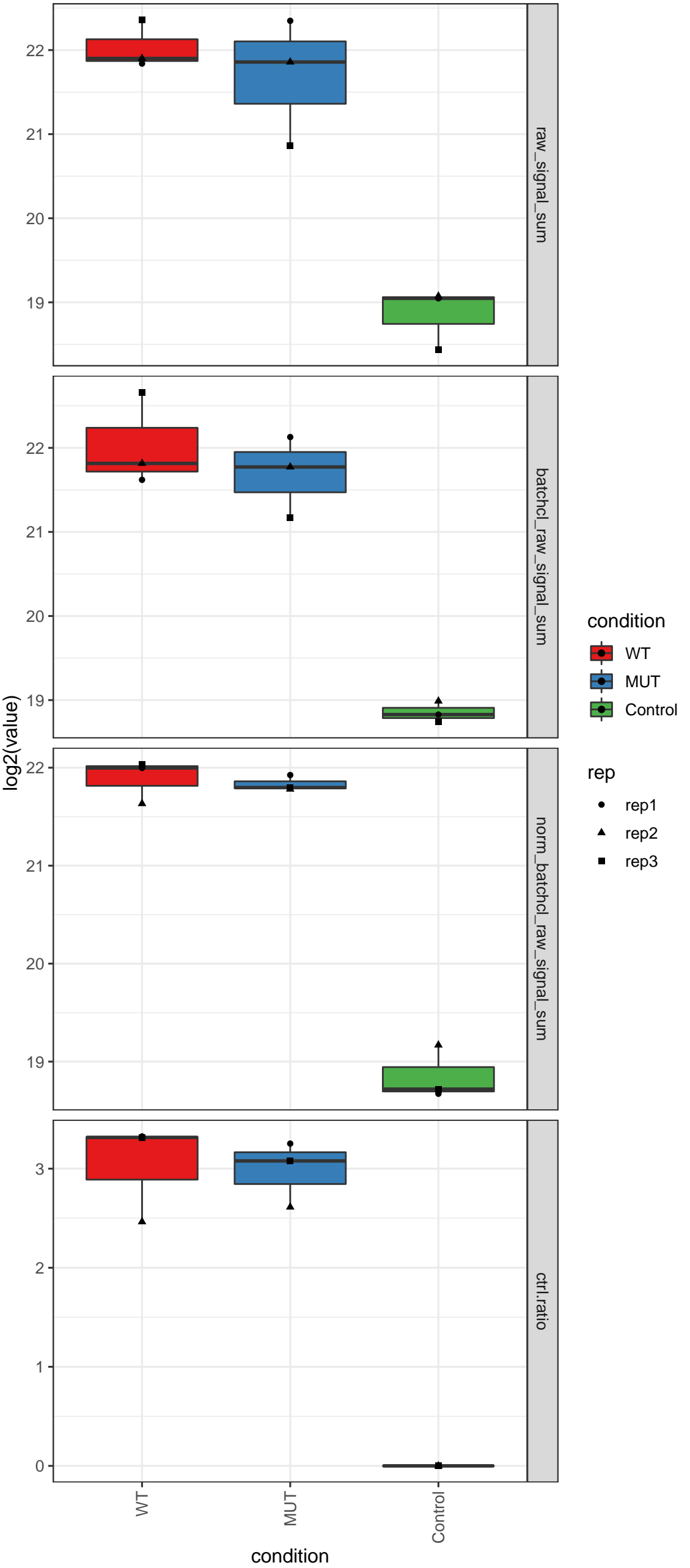
SRP54 – P20424

Signal recognition particle subunit SRP54 OS=*Saccharomyces cerevisiae*



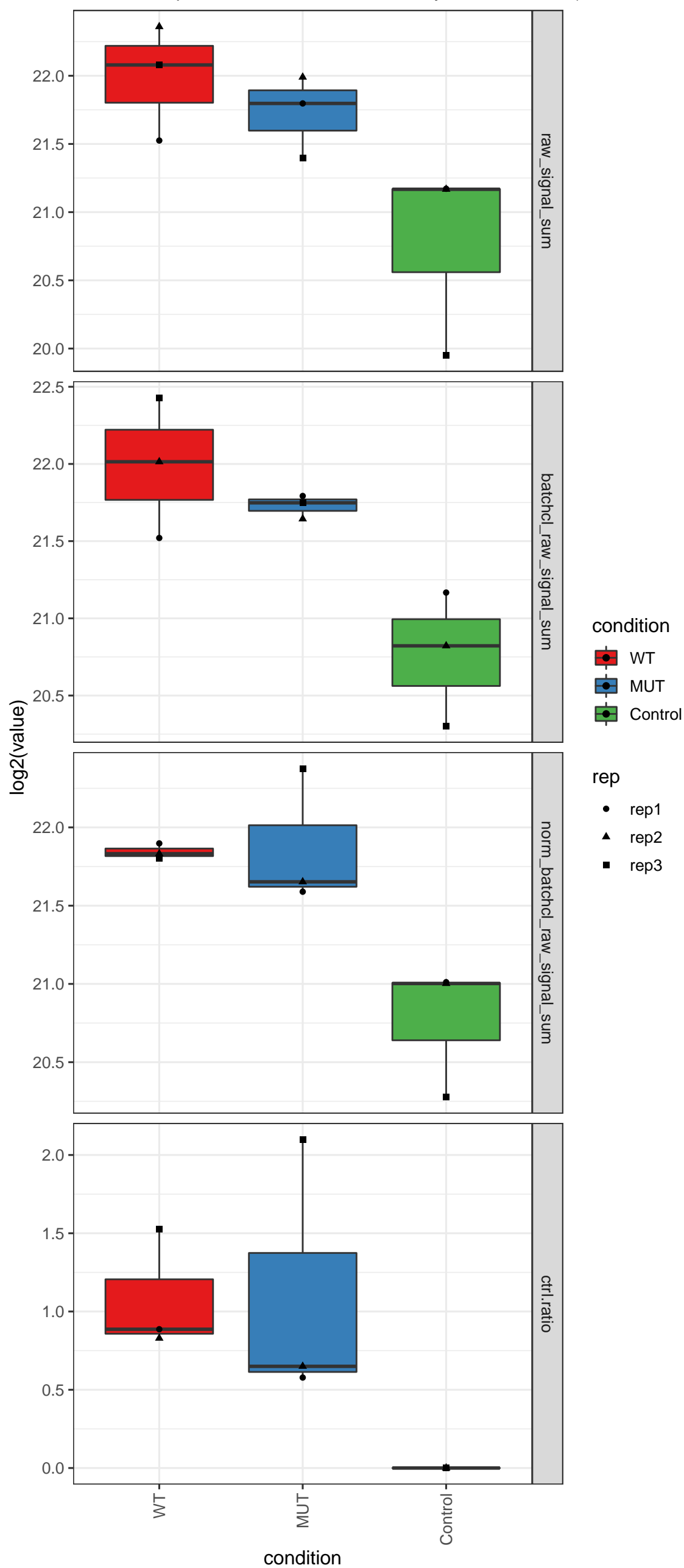
SRP72 – P38688

Signal recognition particle subunit SRP72 OS=*Saccharomyces cerevisiae*



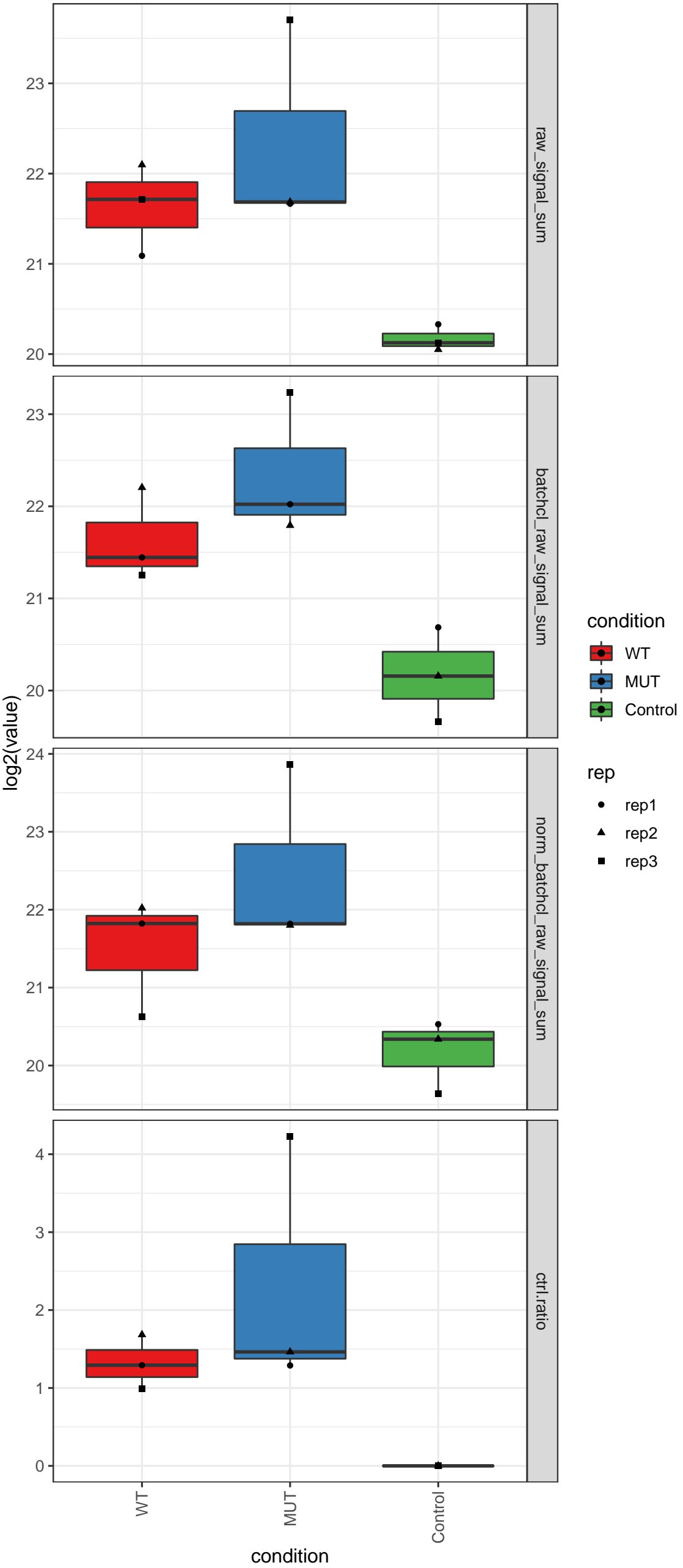
SSA1 – P10591

Heat shock protein SSA1 OS=Saccharomyces cerevisiae (strain ATCC 20454) [Fungi]



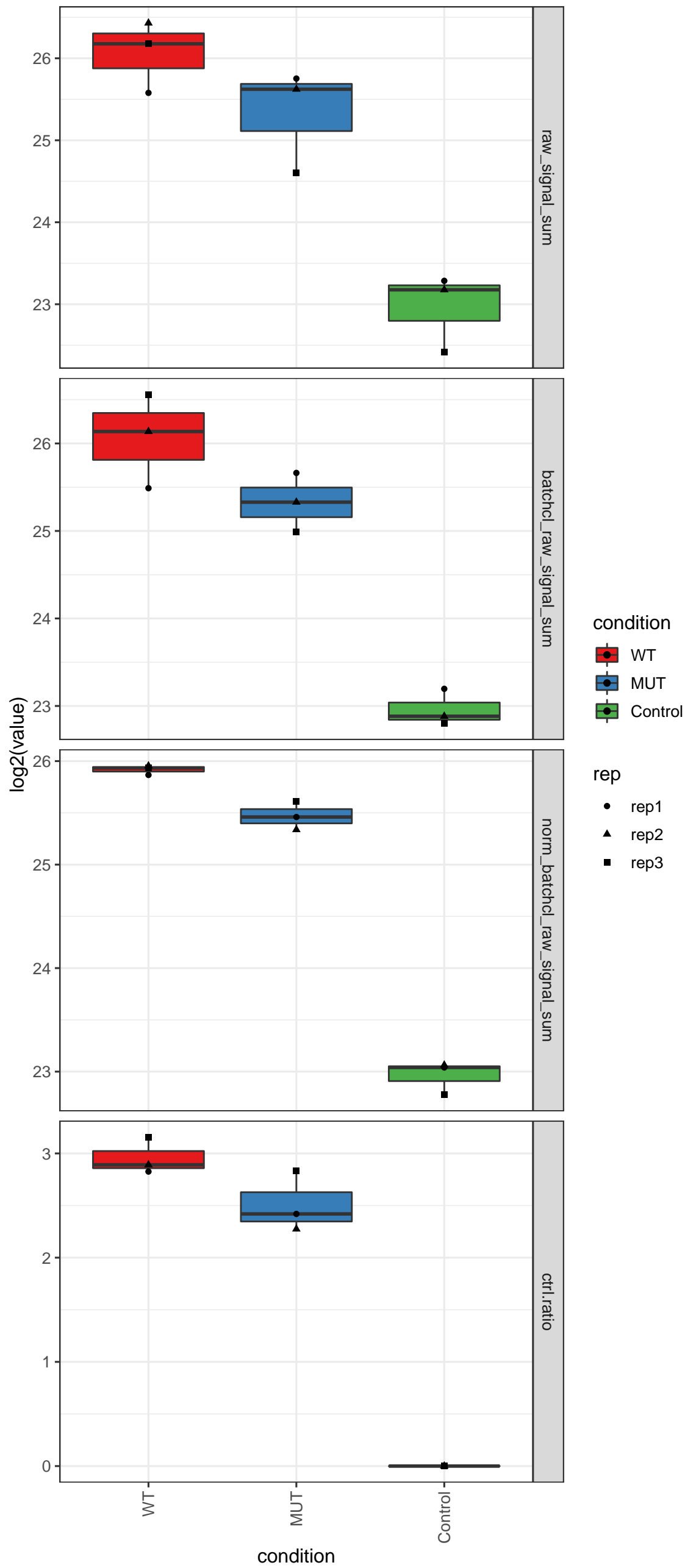
SSA3 – P09435

Heat shock protein SSA3 OS=*Saccharomyces cerevisiae* (strain ATCC 204



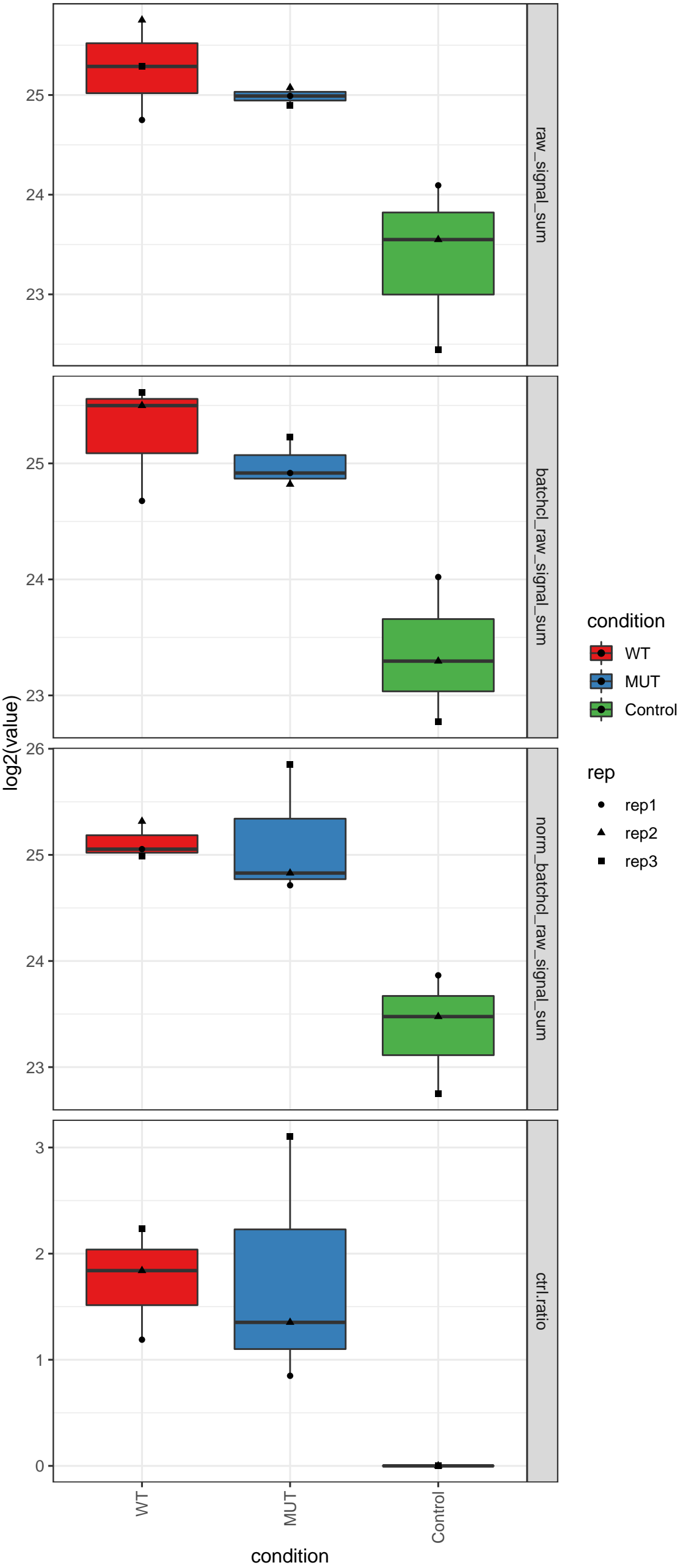
SSB1|SSB2 – P11484|P40150

Heat shock protein SSB1 OS=*Saccharomyces cerevisiae* (strain ATCC 204



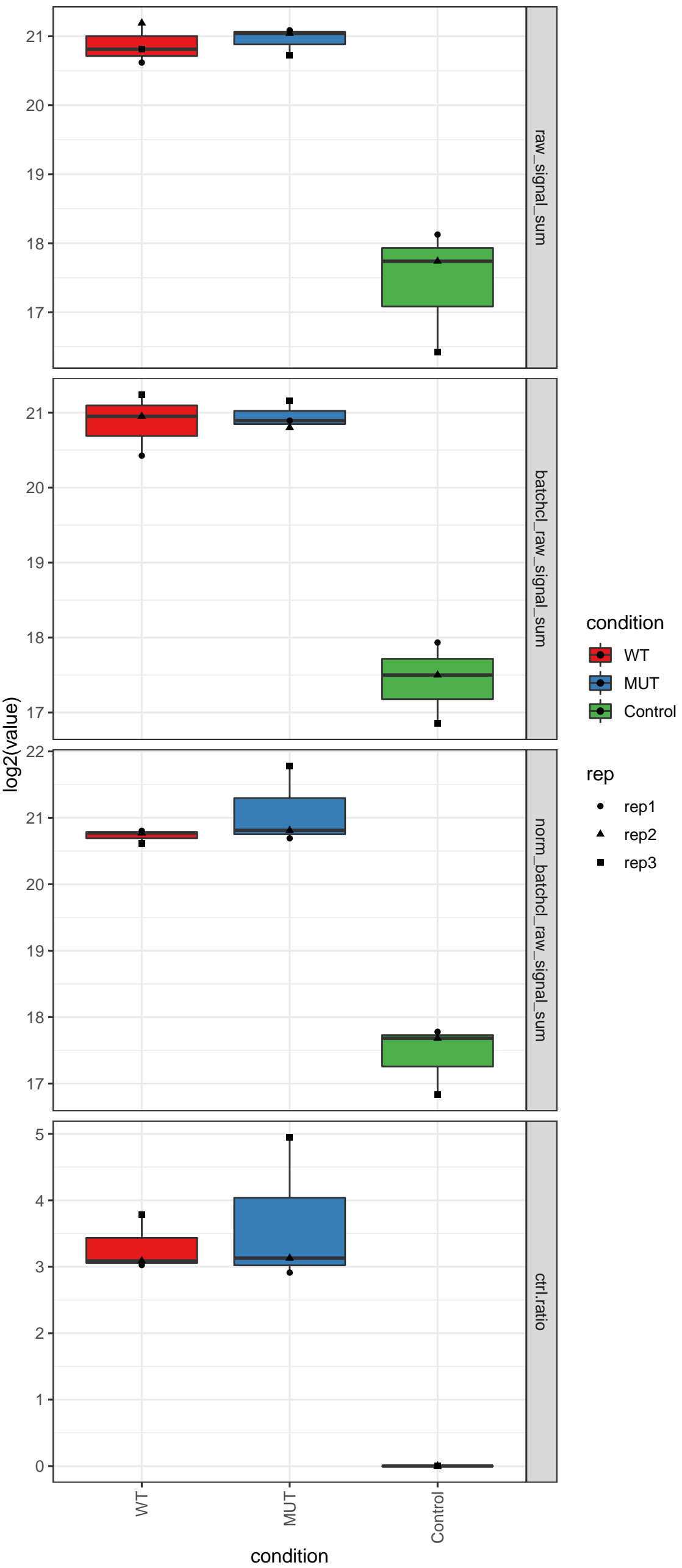
SSC1 – P0CS90

Heat shock protein SSC1, mitochondrial OS=*Saccharomyces cerevisiae* (s



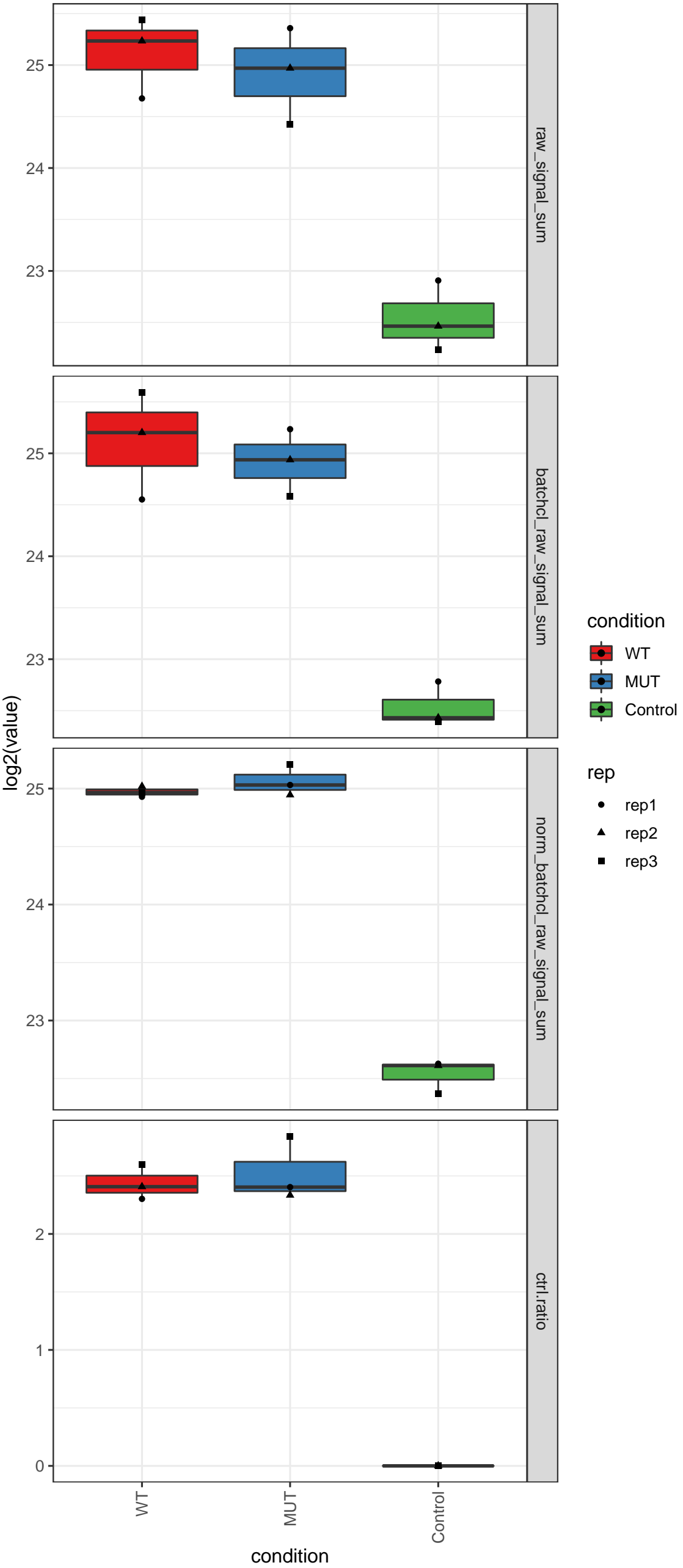
SSD1 – P24276

Protein SSD1 OS=*Saccharomyces cerevisiae* (strain ATCC 204508 / S288



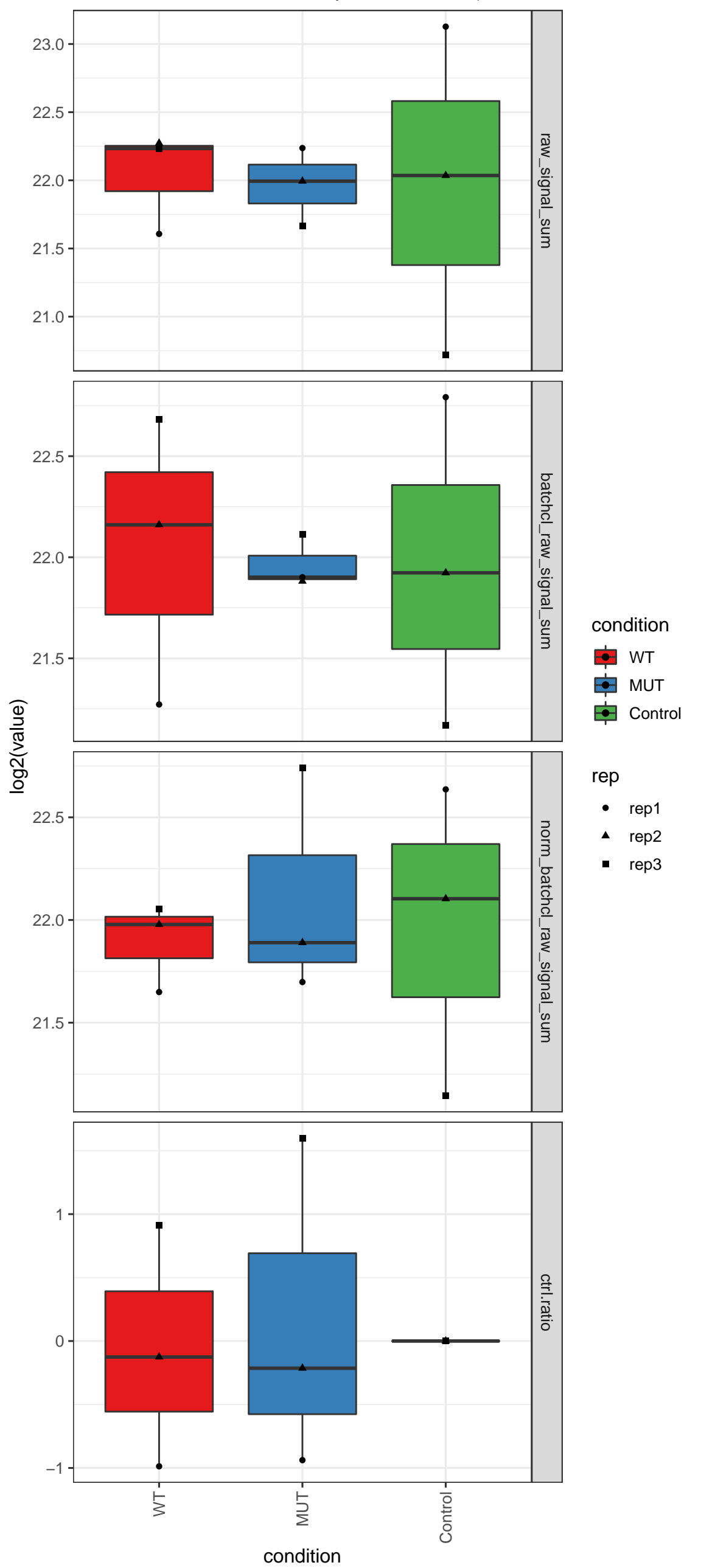
SSE1 – P32589

Heat shock protein homolog SSE1 OS=*Saccharomyces cerevisiae* (strain /



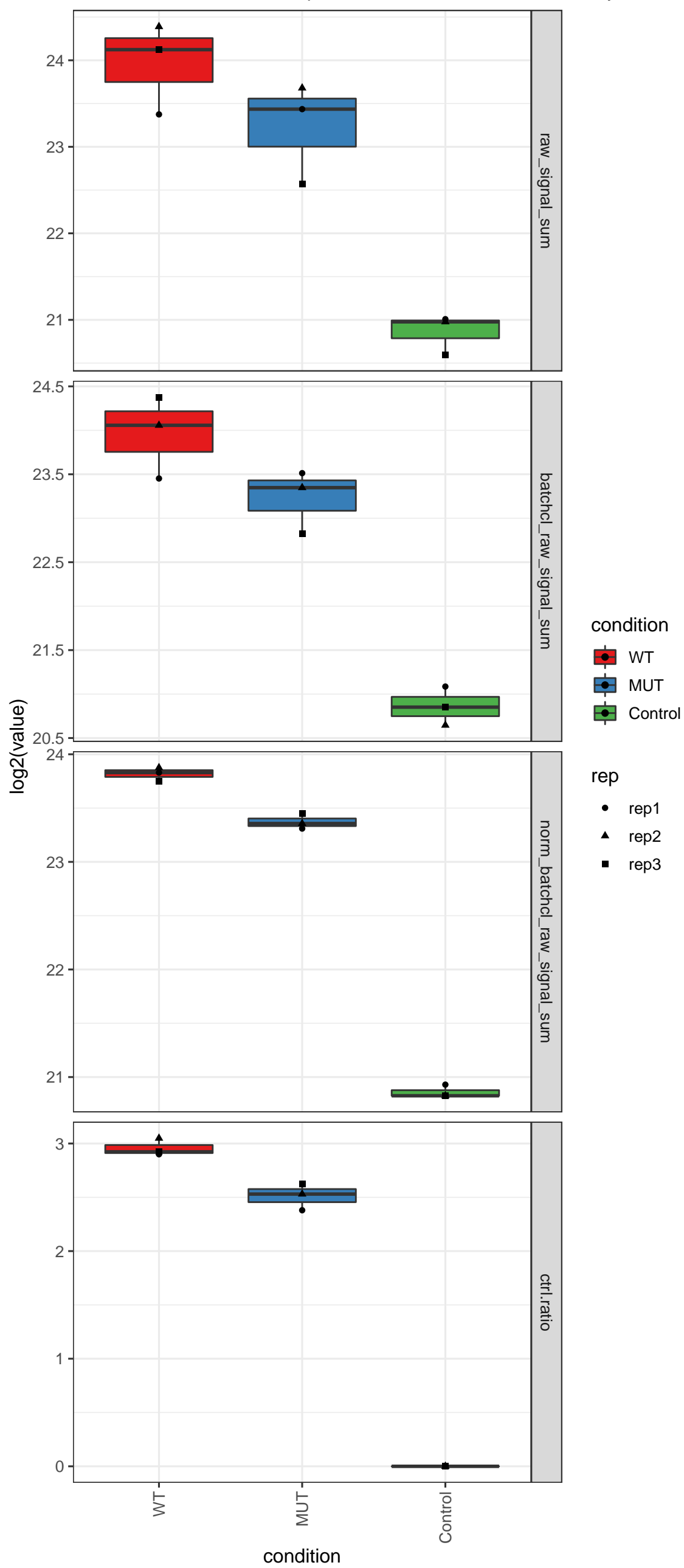
SSO1 – P32867

Protein SSO1 OS=*Saccharomyces cerevisiae* (strain ATCC 204508 / S28)



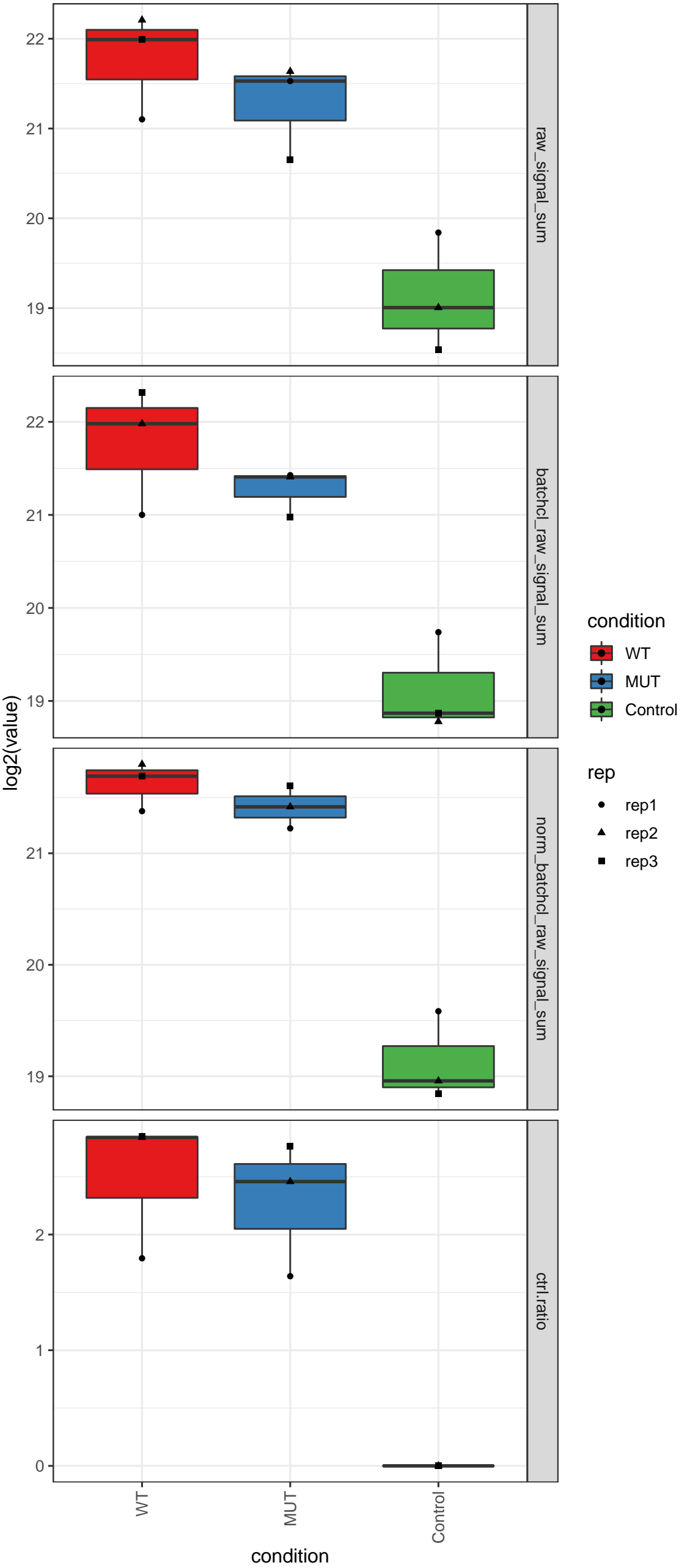
SSZ1 – P38788

Ribosome-associated complex subunit SSZ1 OS=Saccharomyces cerevisiae



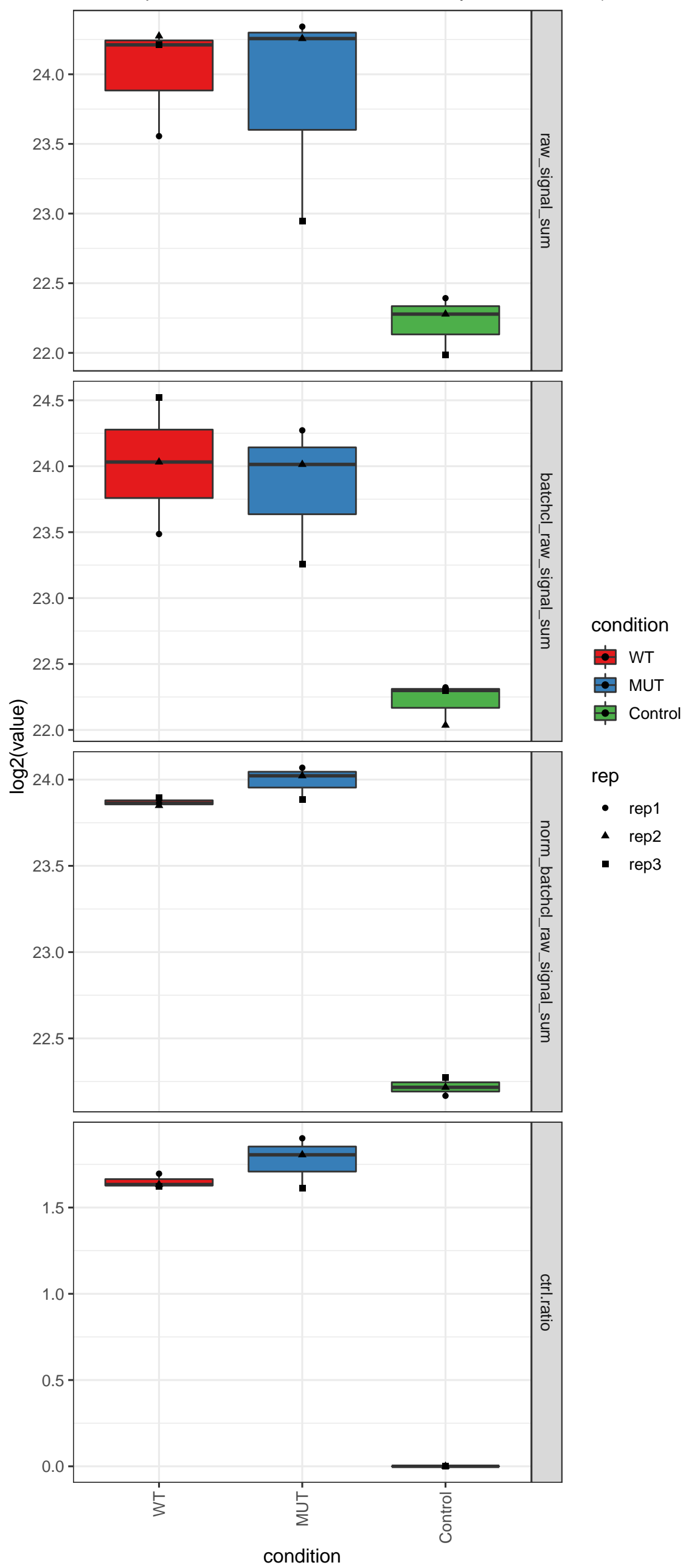
STE24 – P47154

CAAX prenyl protease 1 OS=*Saccharomyces cerevisiae* (strain ATCC 20454)



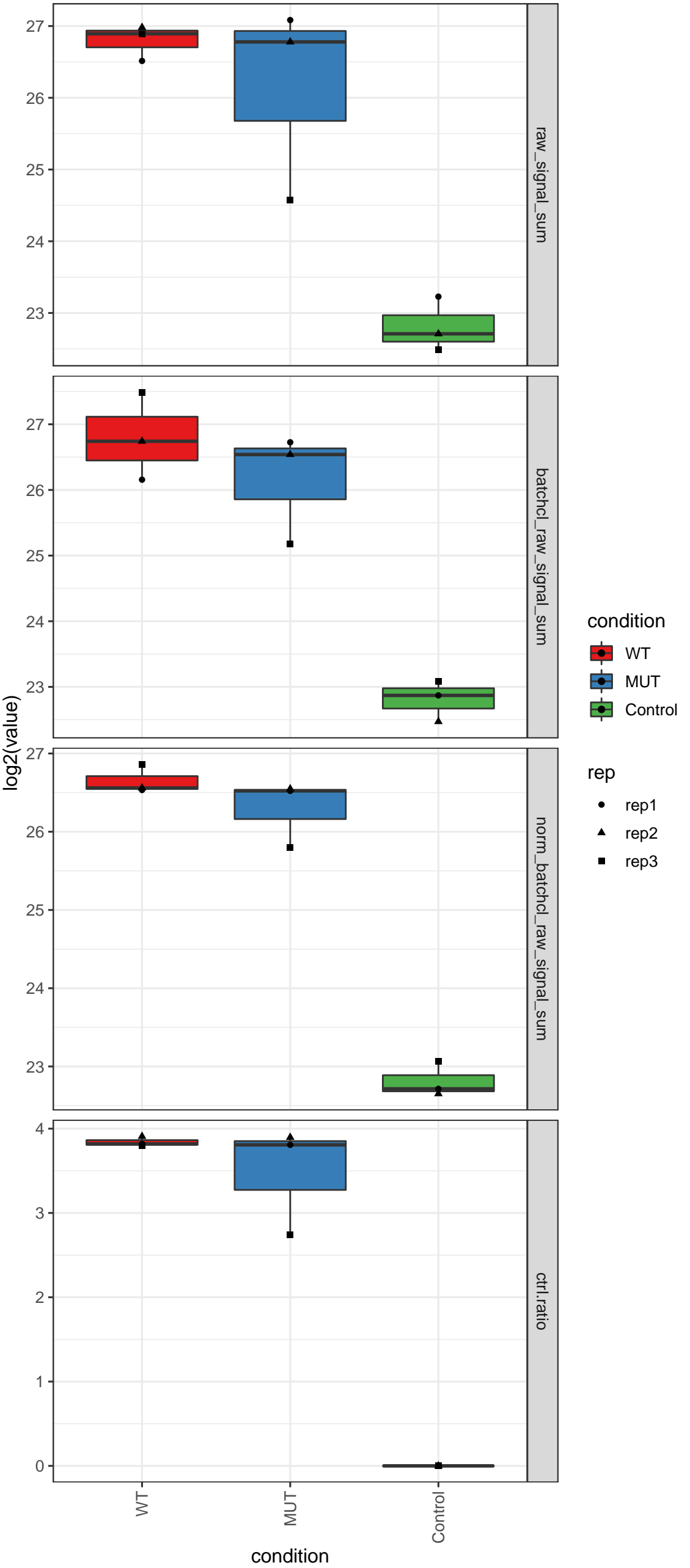
STH1 – P32597

Nuclear protein STH1/NPS1 OS=*Saccharomyces cerevisiae* (strain ATCC



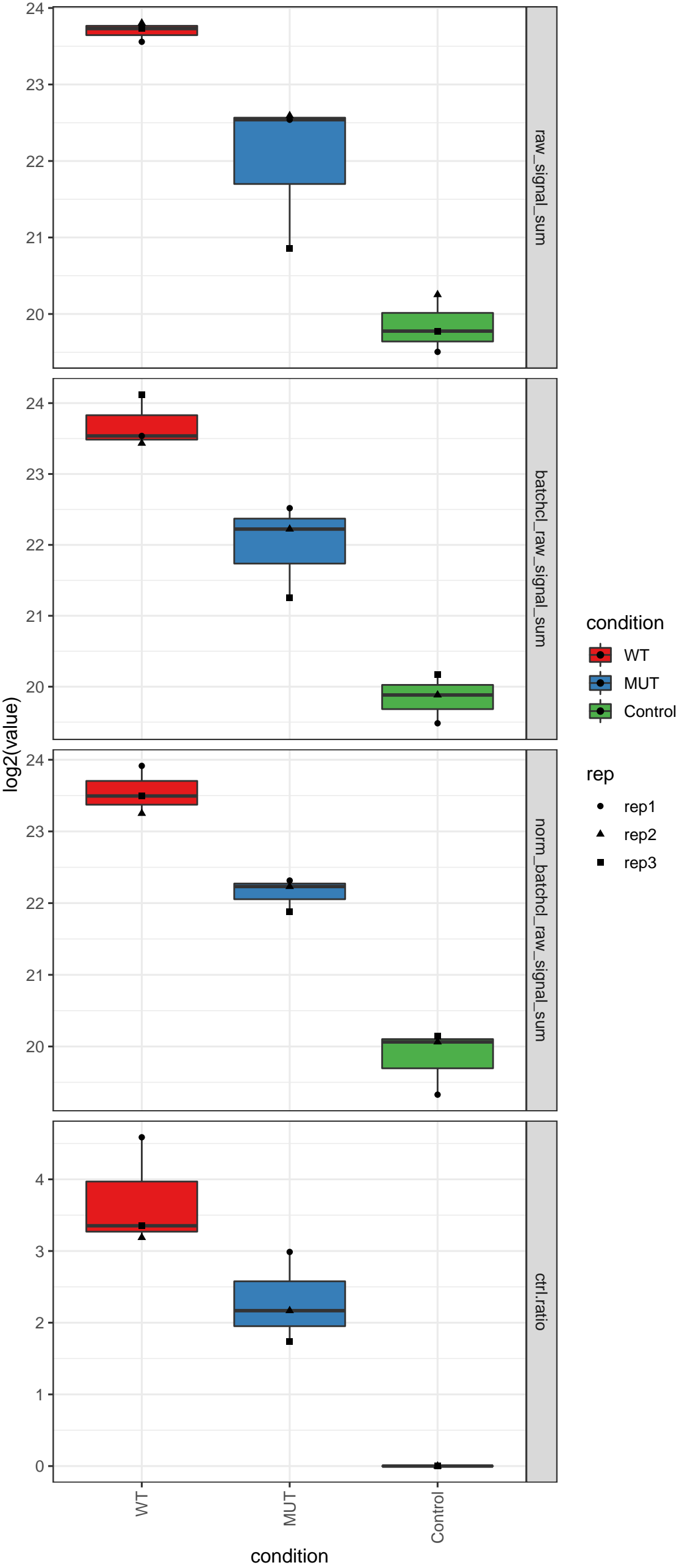
STM1 – P39015

Suppressor protein STM1 OS=*Saccharomyces cerevisiae* (strain ATCC 20490)



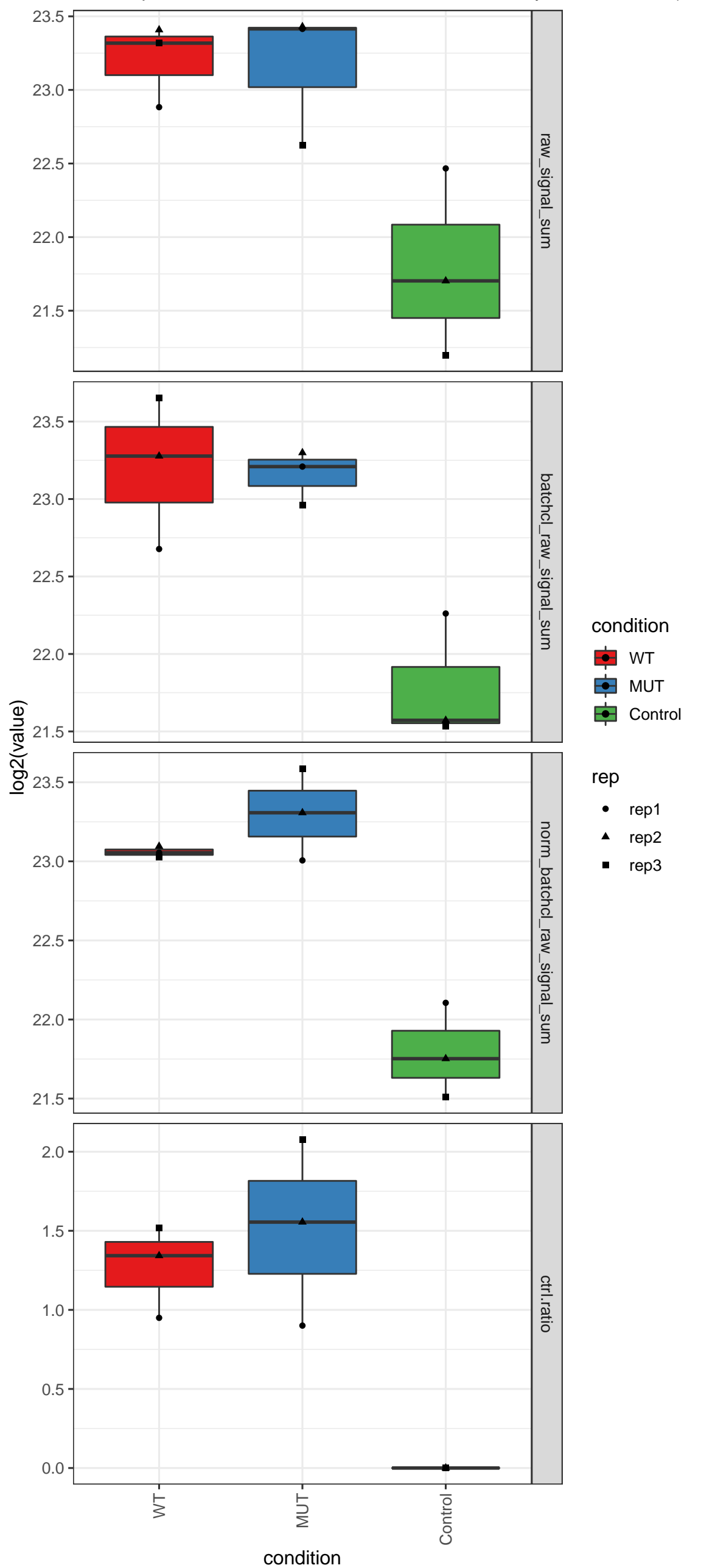
SUB1 – P54000

RNA polymerase II transcriptional coactivator SUB1 OS=Saccharomyces cerevisiae



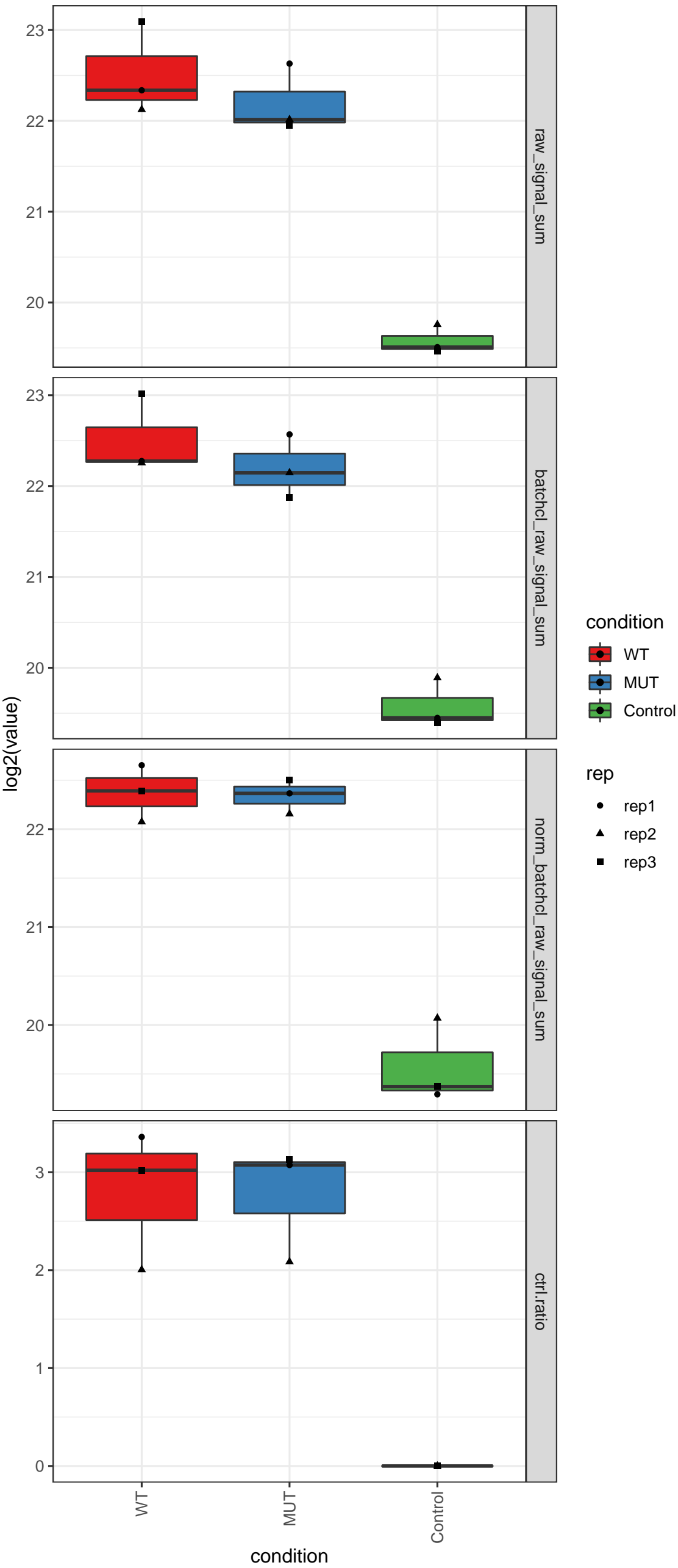
SUB2 – Q07478

ATP-dependent RNA helicase SUB2 OS=Saccharomyces cerevisiae (str



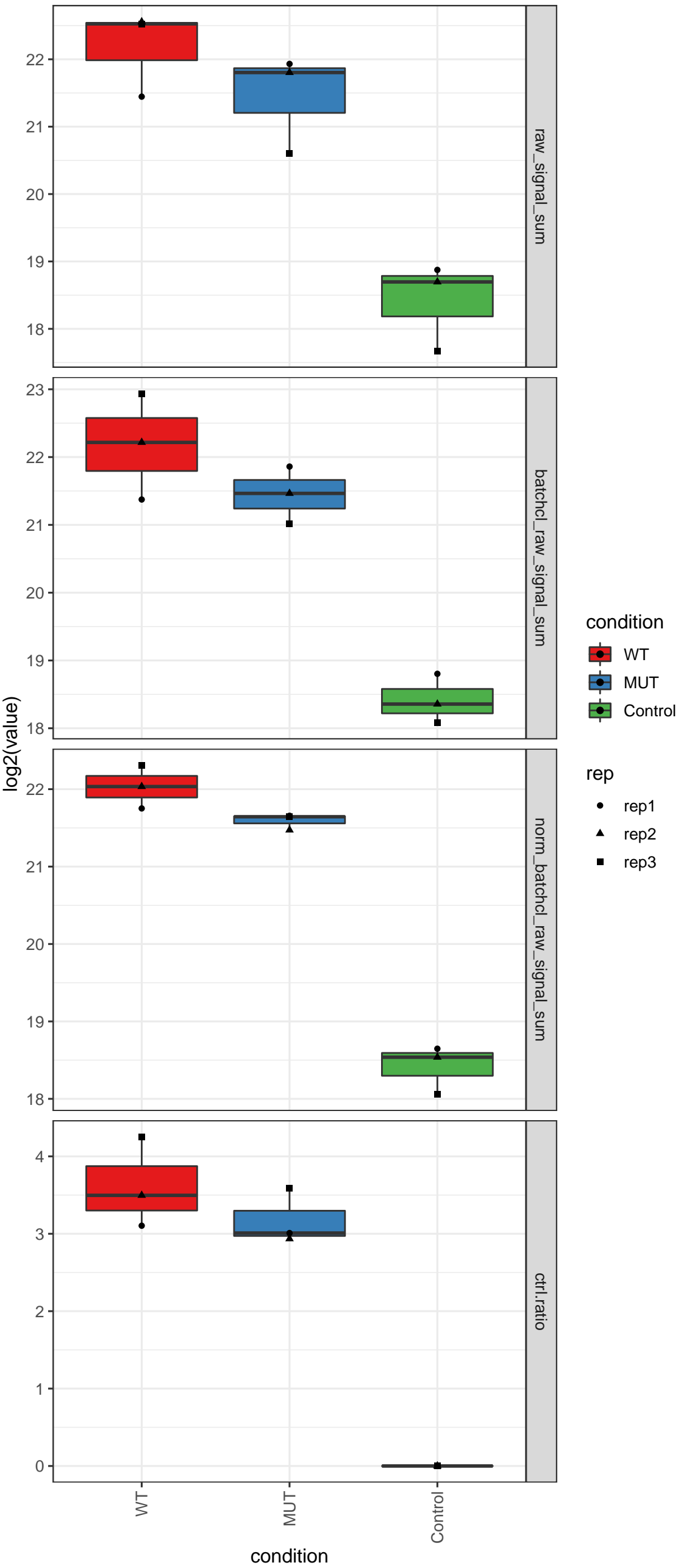
SUC2 – P00724|P00724–2

Invertase 2 OS=*Saccharomyces cerevisiae* (strain ATCC 204508 / S288c)



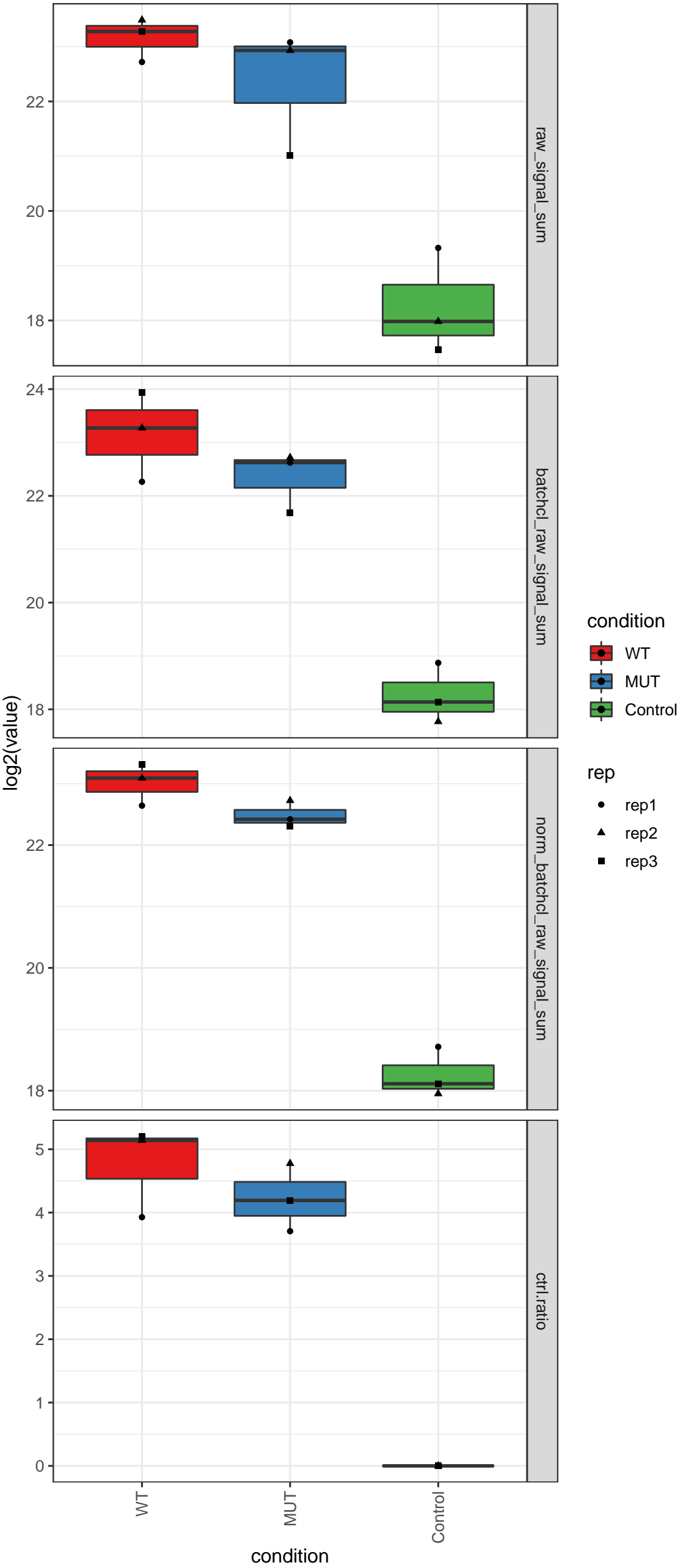
SUI2 – P20459

Eukaryotic translation initiation factor 2 subunit alpha OS=Saccharomyces



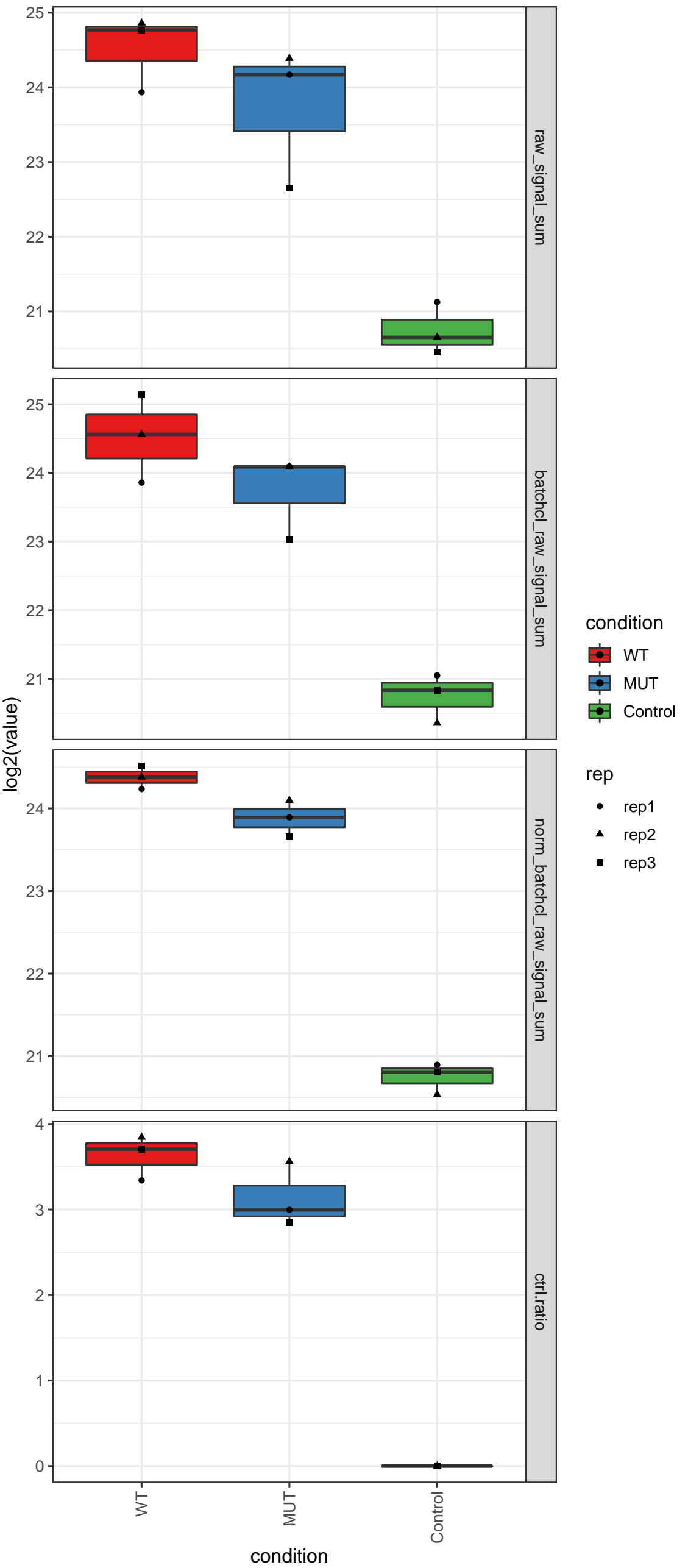
SUI3 – P09064

Eukaryotic translation initiation factor 2 subunit beta OS=Saccharomyces c



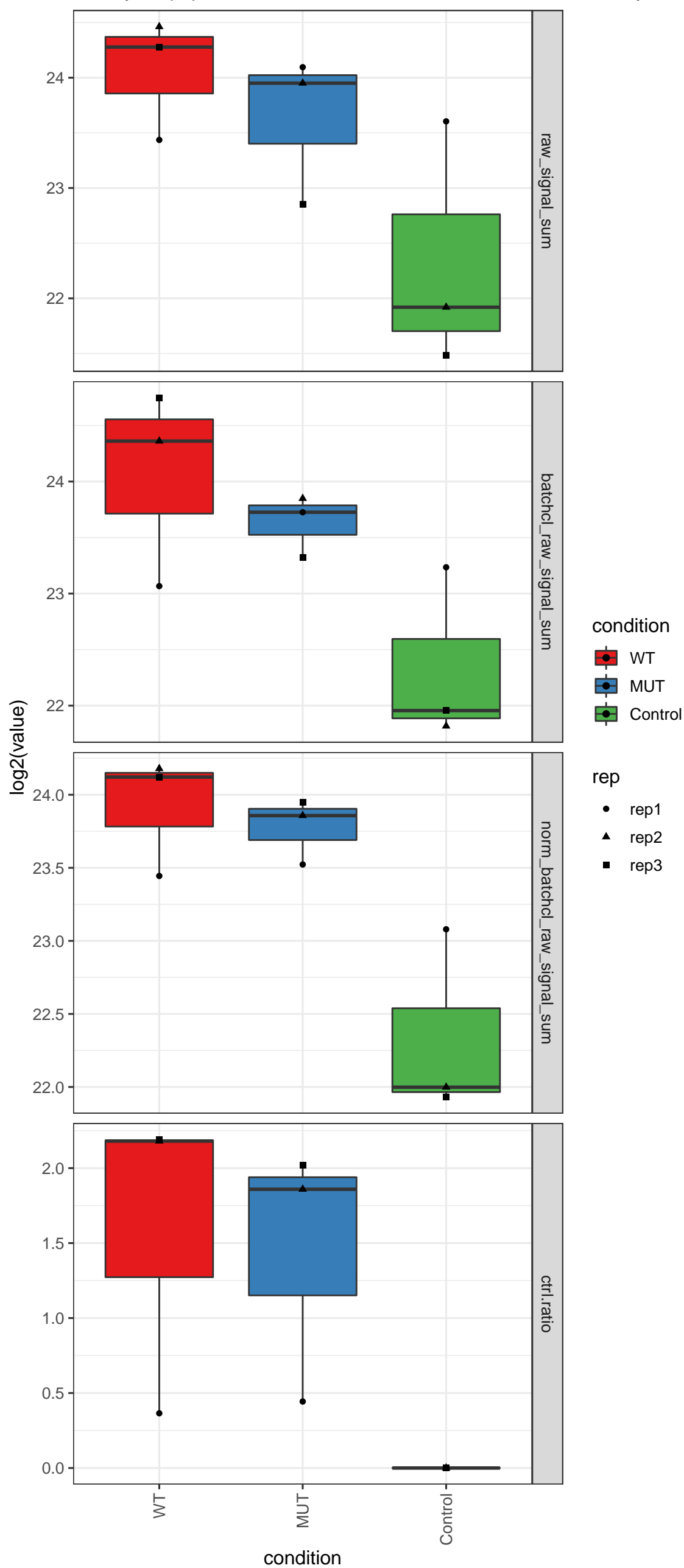
SUP35 – P05453

Eukaryotic peptide chain release factor GTP-binding subunit OS=Sacchar



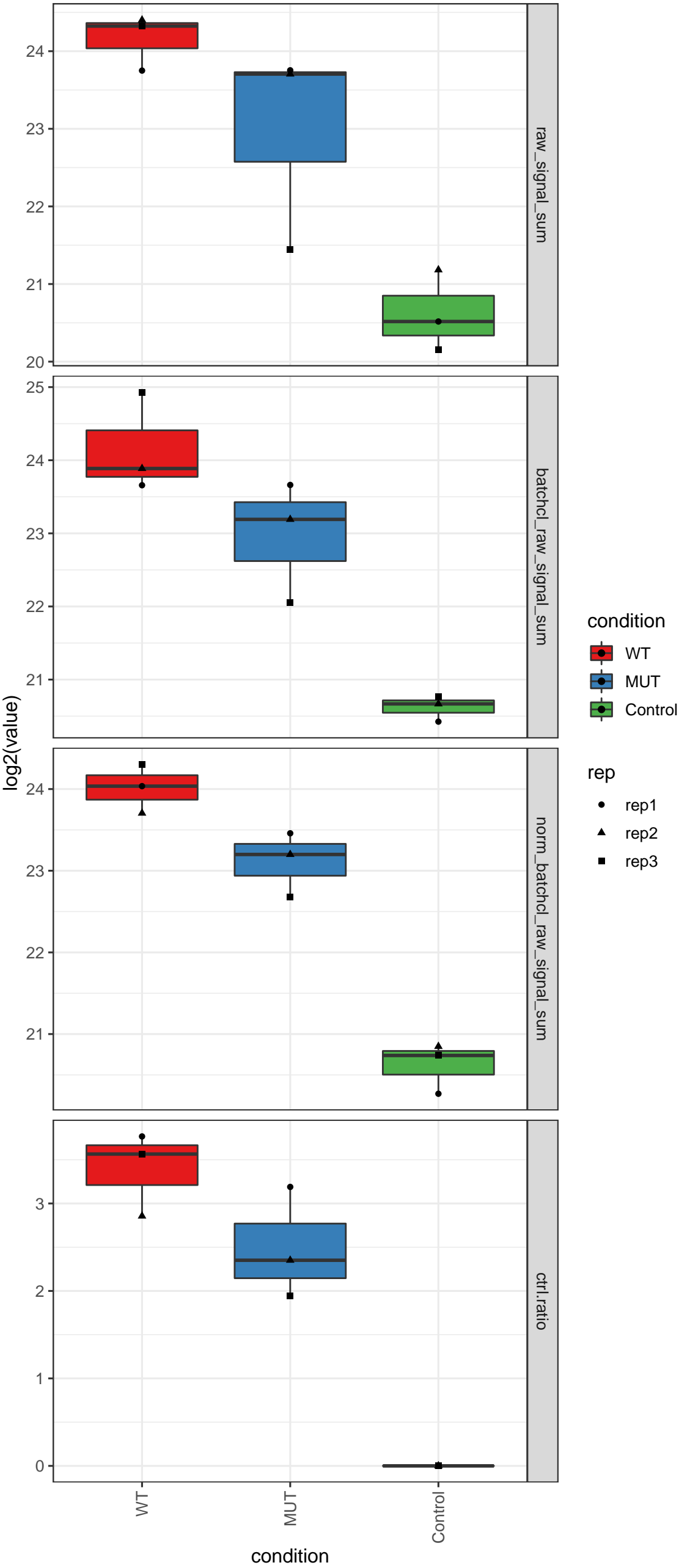
SUP45 – P12385

Eukaryotic peptide chain release factor subunit 1 OS=Saccharomyces cerevisiae



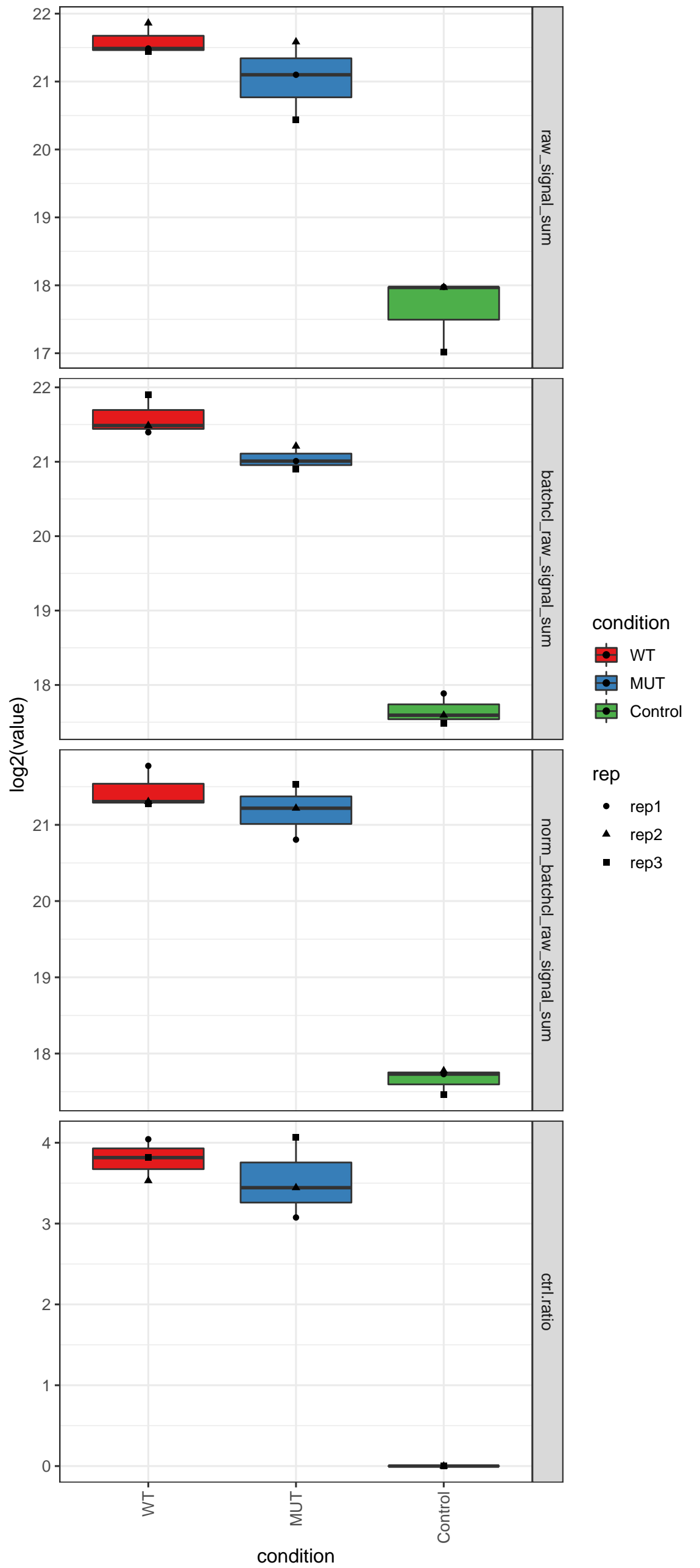
SWC3 – P31376

SWR1-complex protein 3 OS=*Saccharomyces cerevisiae* (strain ATCC 20454)



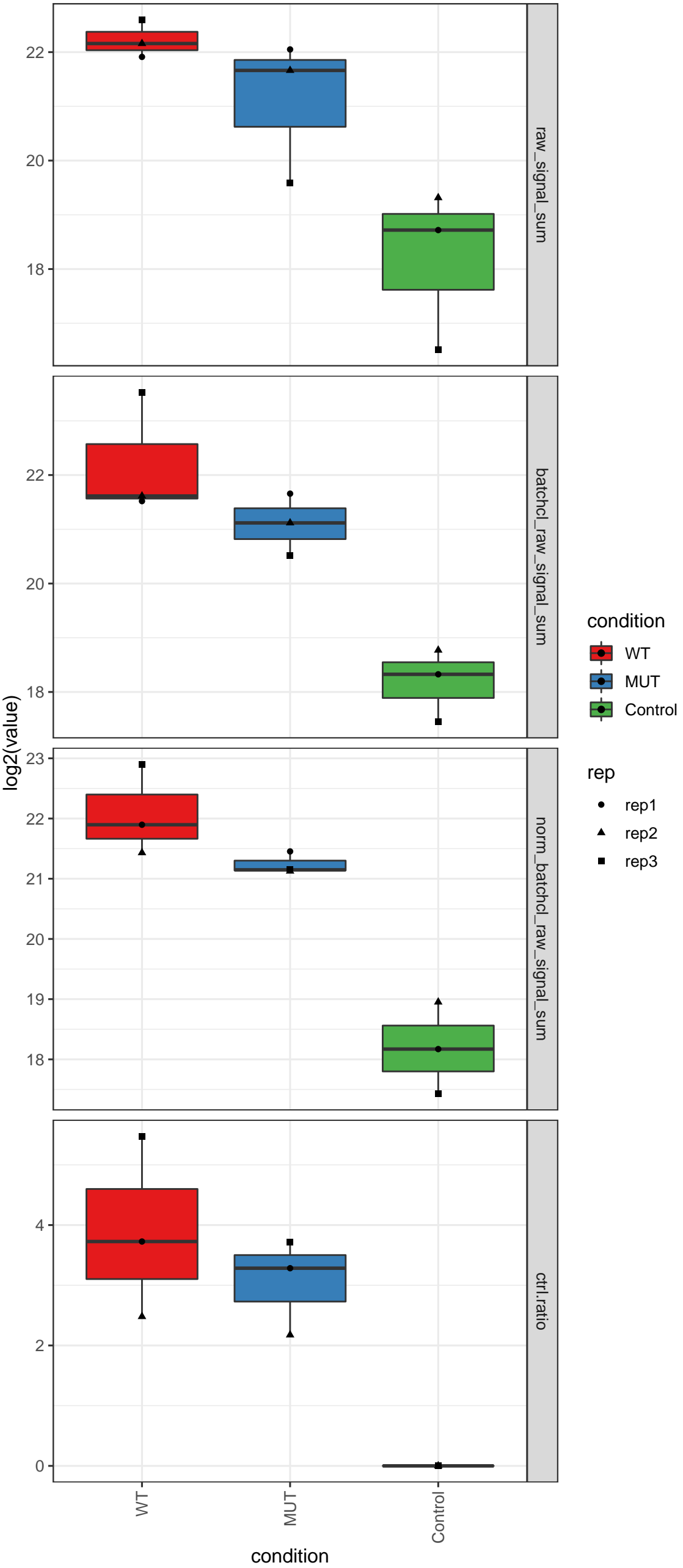
SWC4 – P53201

SWR1-complex protein 4 OS=*Saccharomyces cerevisiae* (strain ATCC 20456)



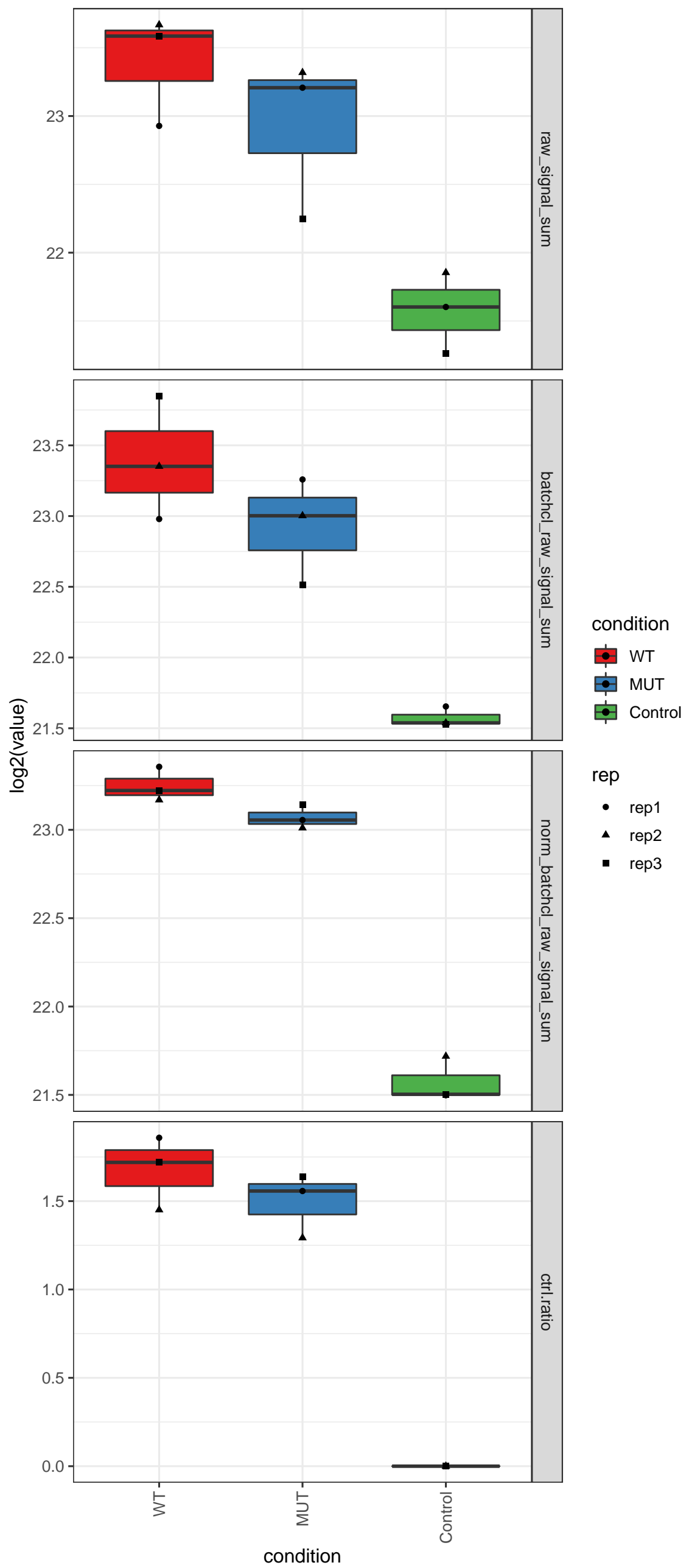
SWR1 – Q05471

Helicase SWR1 OS=*Saccharomyces cerevisiae* (strain ATCC 204508 / S288c)



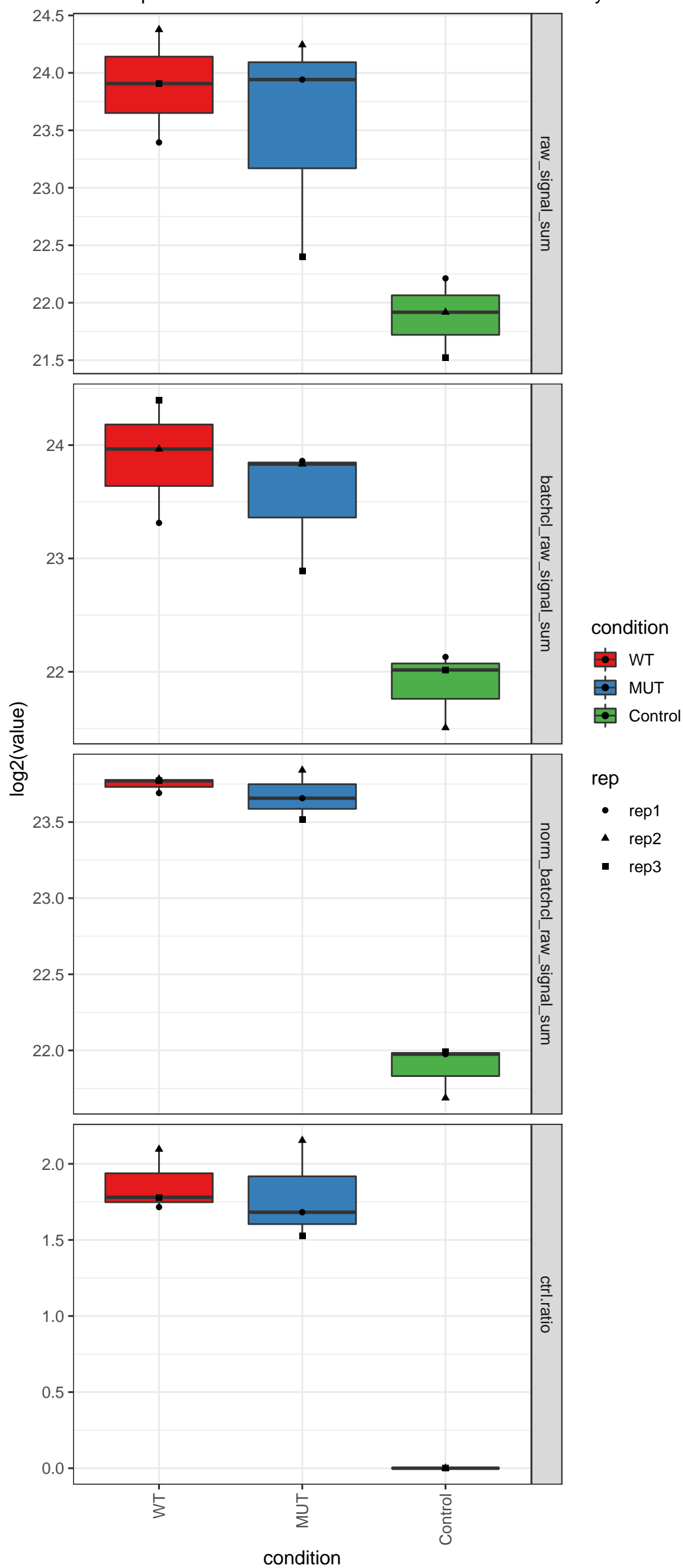
SYP1 – P25623

Suppressor of yeast profilin deletion OS=*Saccharomyces cerevisiae* (stra



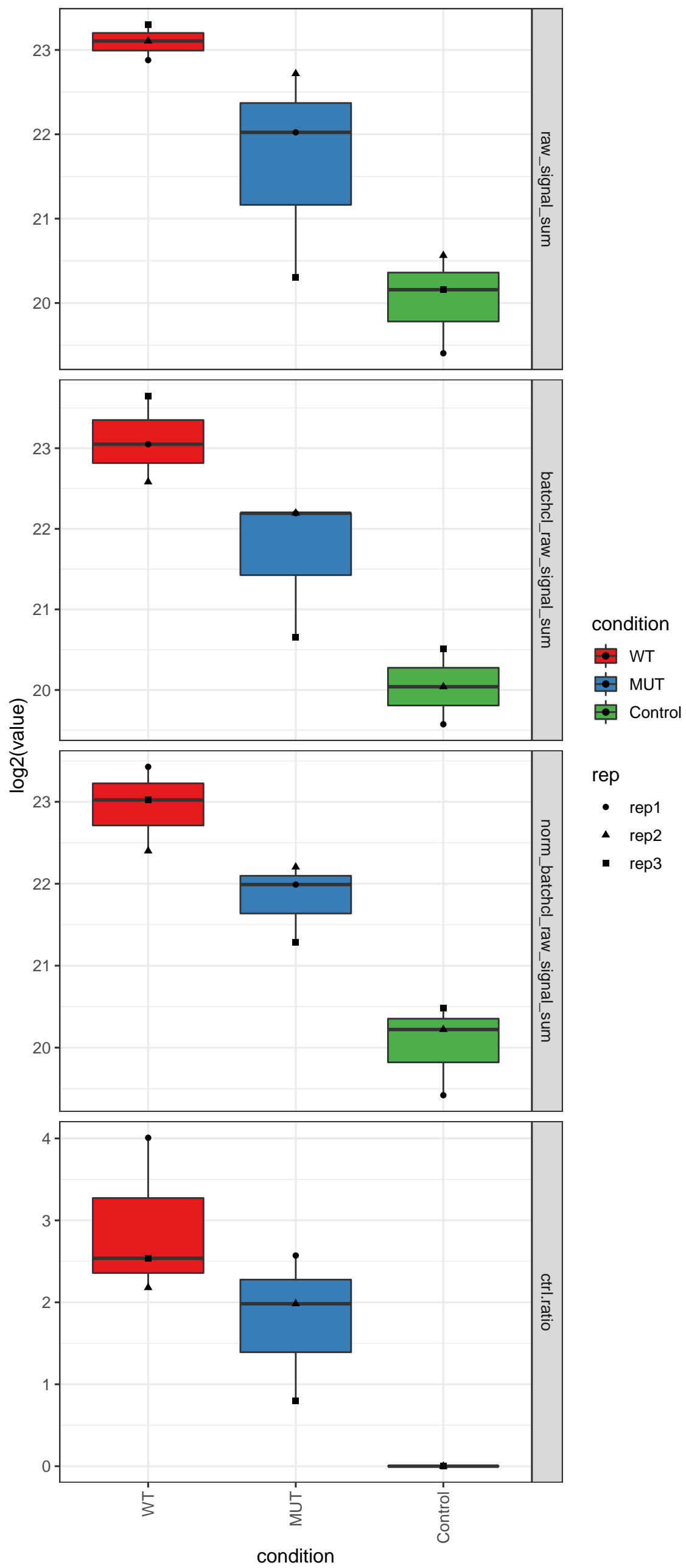
TAF1 – P46677

Transcription initiation factor TFIID subunit 1 OS=*Saccharomyces cerevisiae*



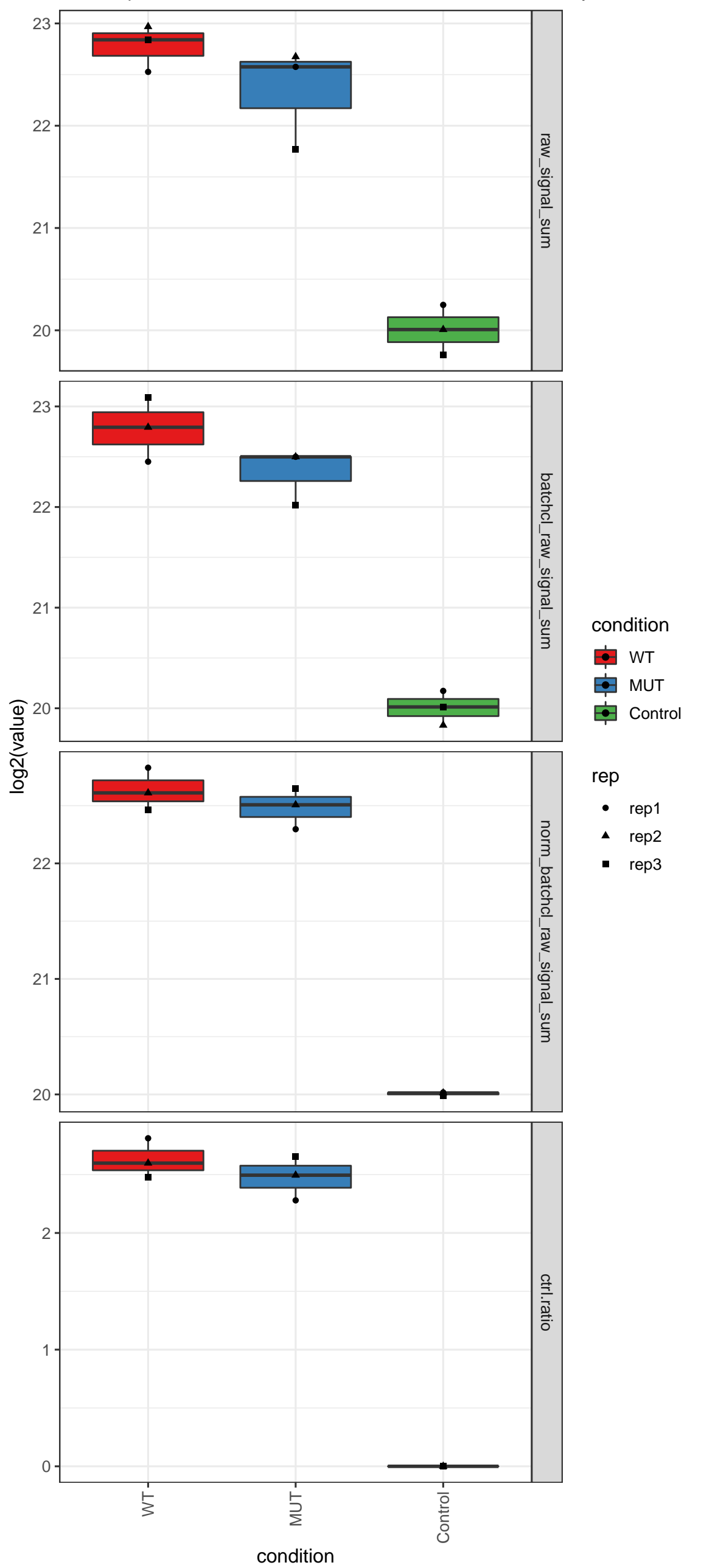
TAF14 – P35189

Transcription initiation factor TFIID subunit 14 OS=*Saccharomyces cerevisiae*



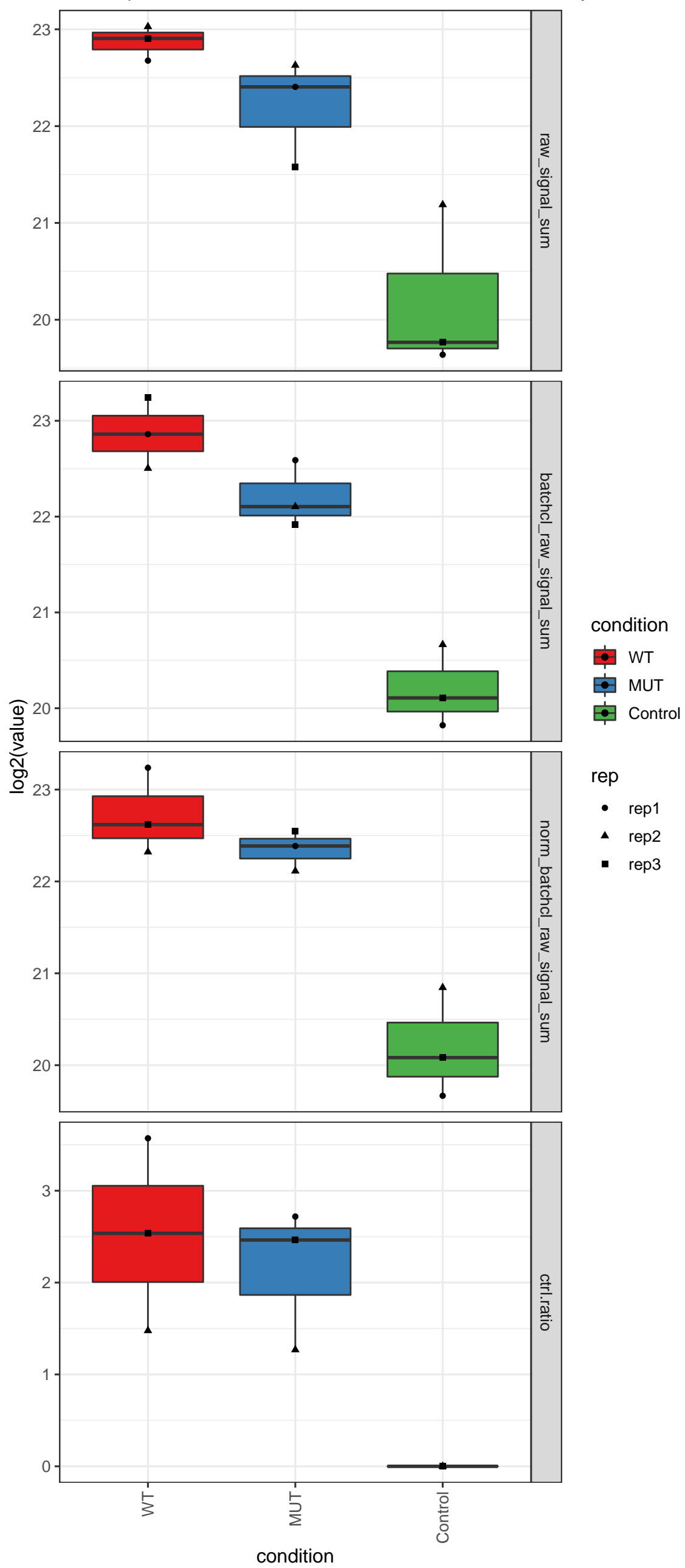
TAF5 – P38129

Transcription initiation factor TFIID subunit 5 OS=*Saccharomyces cerevisiae*



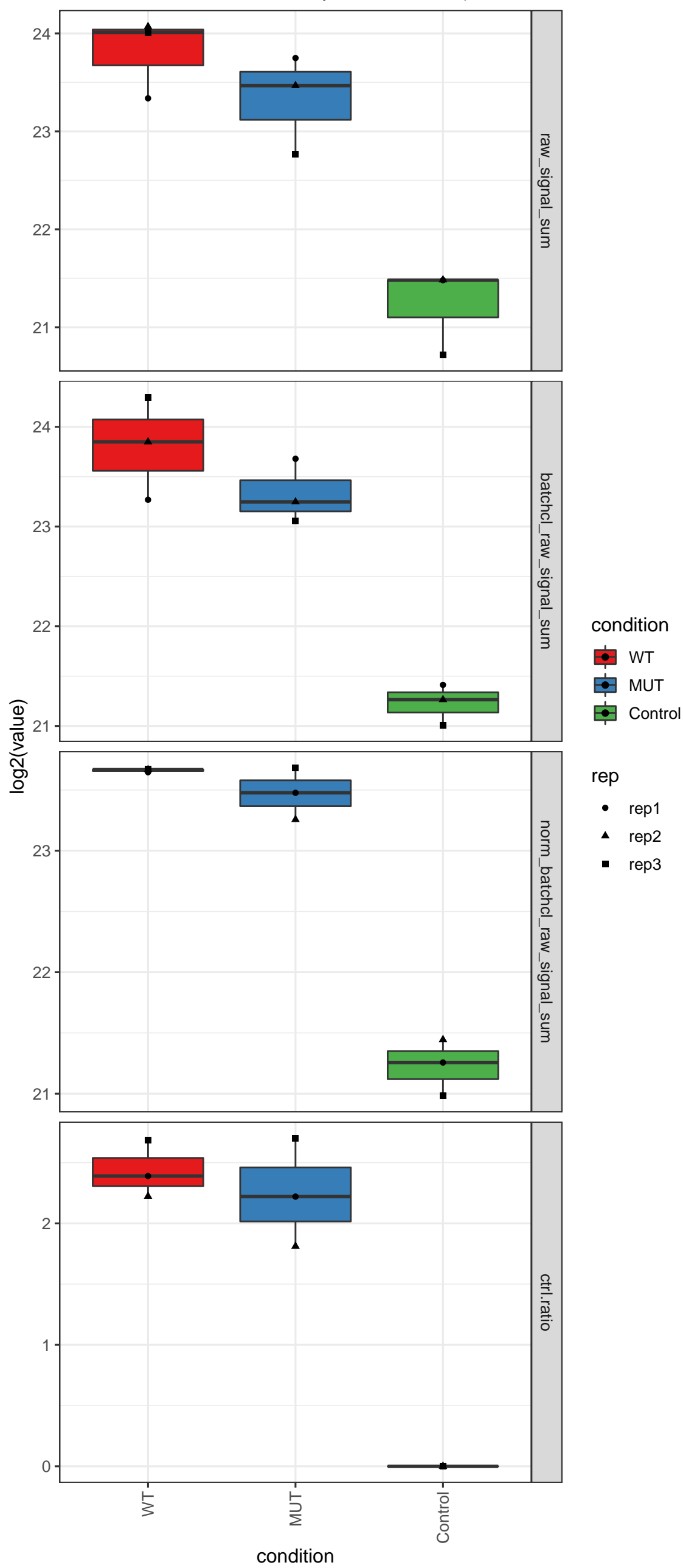
TAF6 – P53040

Transcription initiation factor TFIIID subunit 6 OS=Saccharomyces cerevisiae



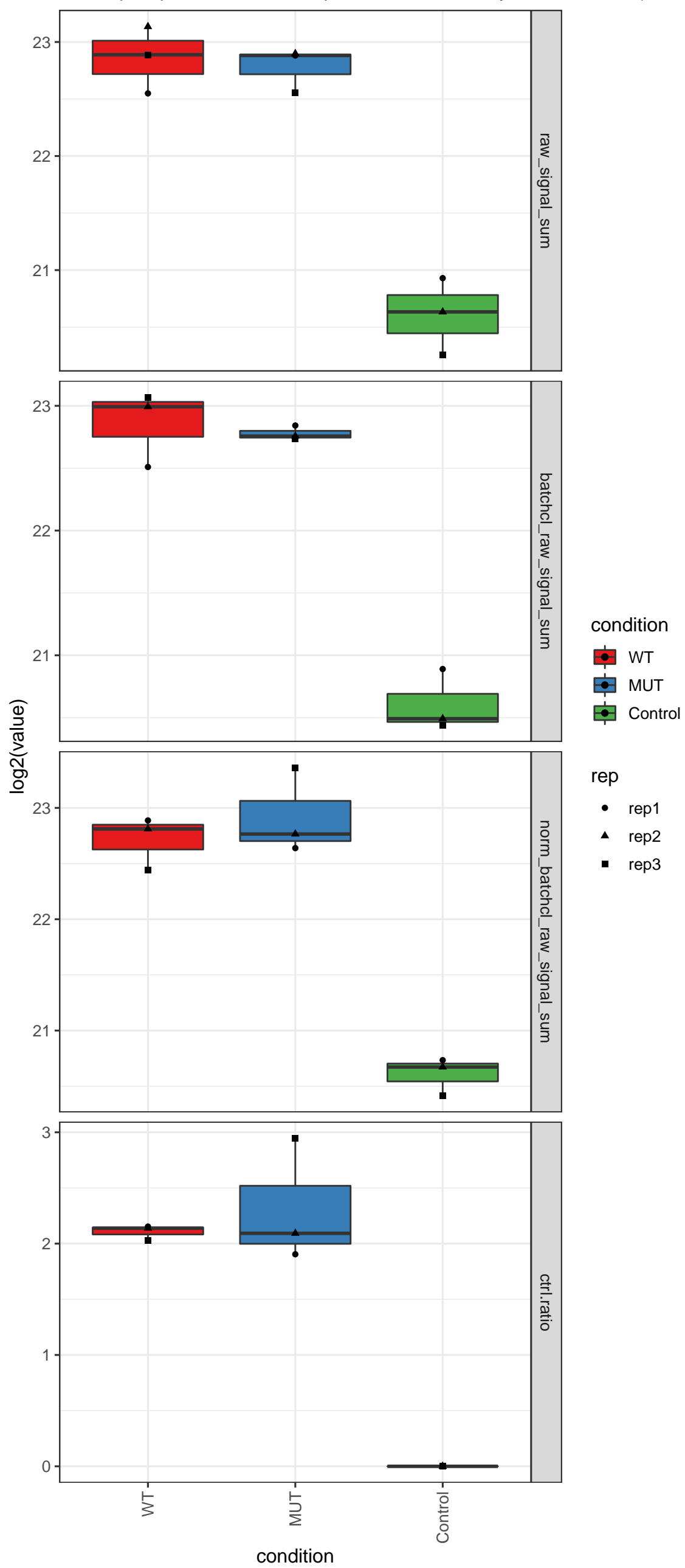
TAL1 – P15019

Transaldolase OS=*Saccharomyces cerevisiae* (strain ATCC 204508 / S288



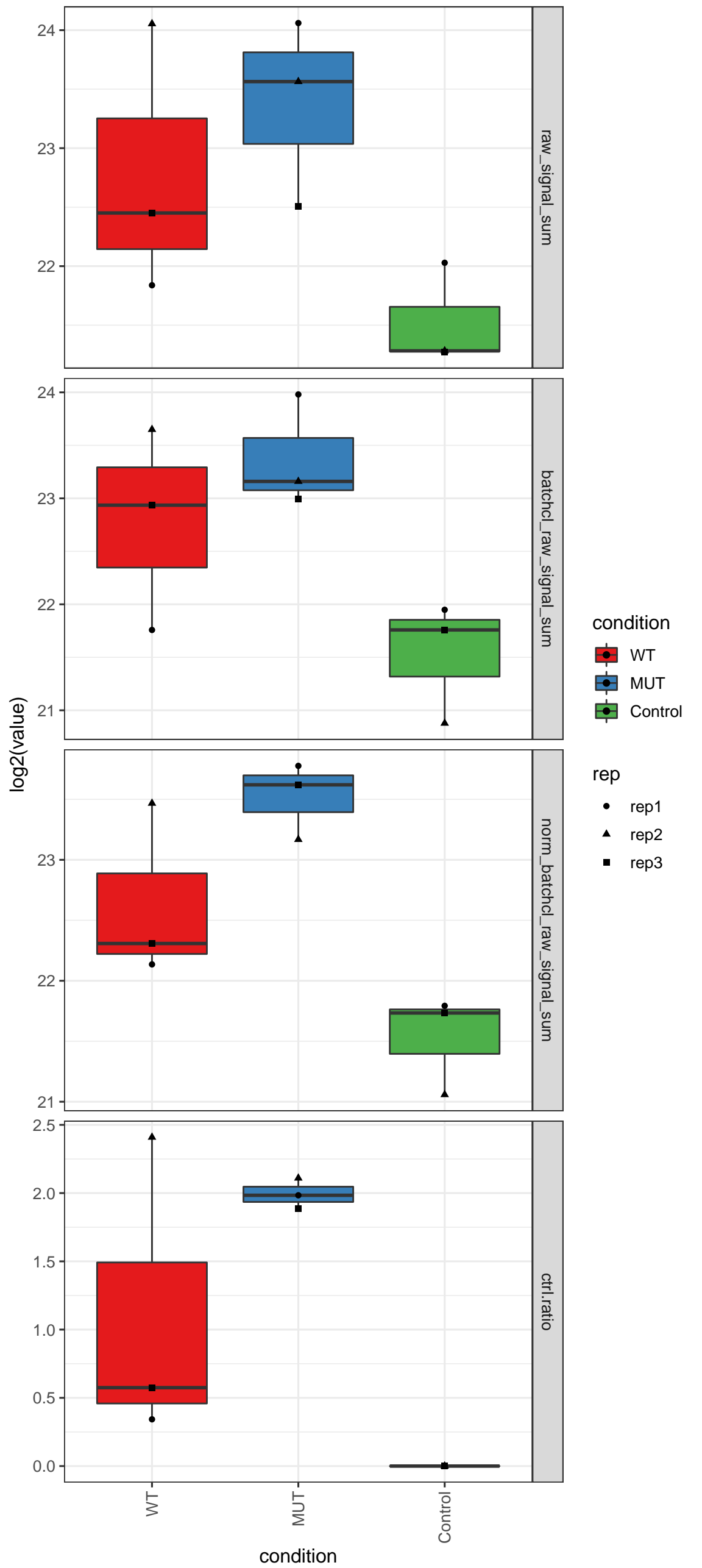
TCP1 – P12612

T-complex protein 1 subunit alpha OS=*Saccharomyces cerevisiae* (strain A



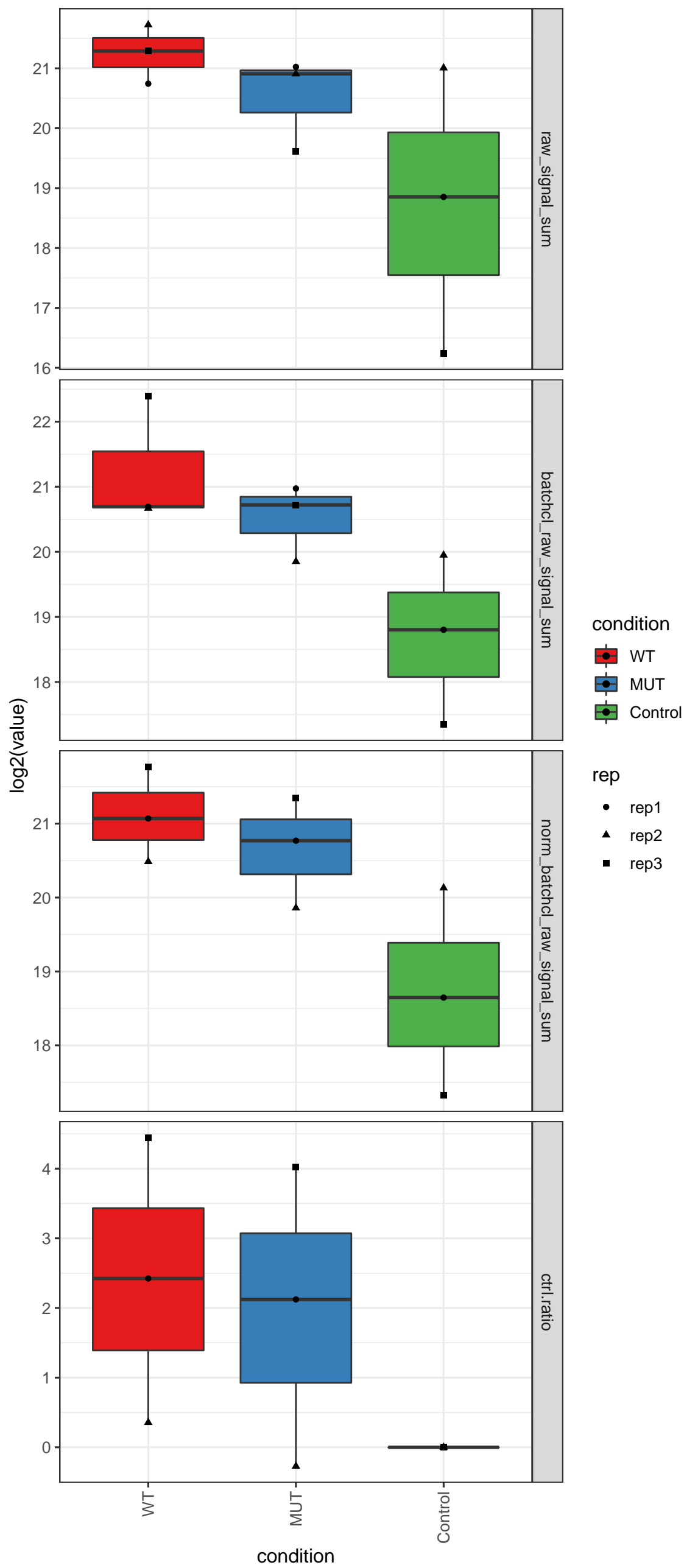
TDH1 – P00360

Glyceraldehyde-3-phosphate dehydrogenase 1 OS=Saccharomyces cere



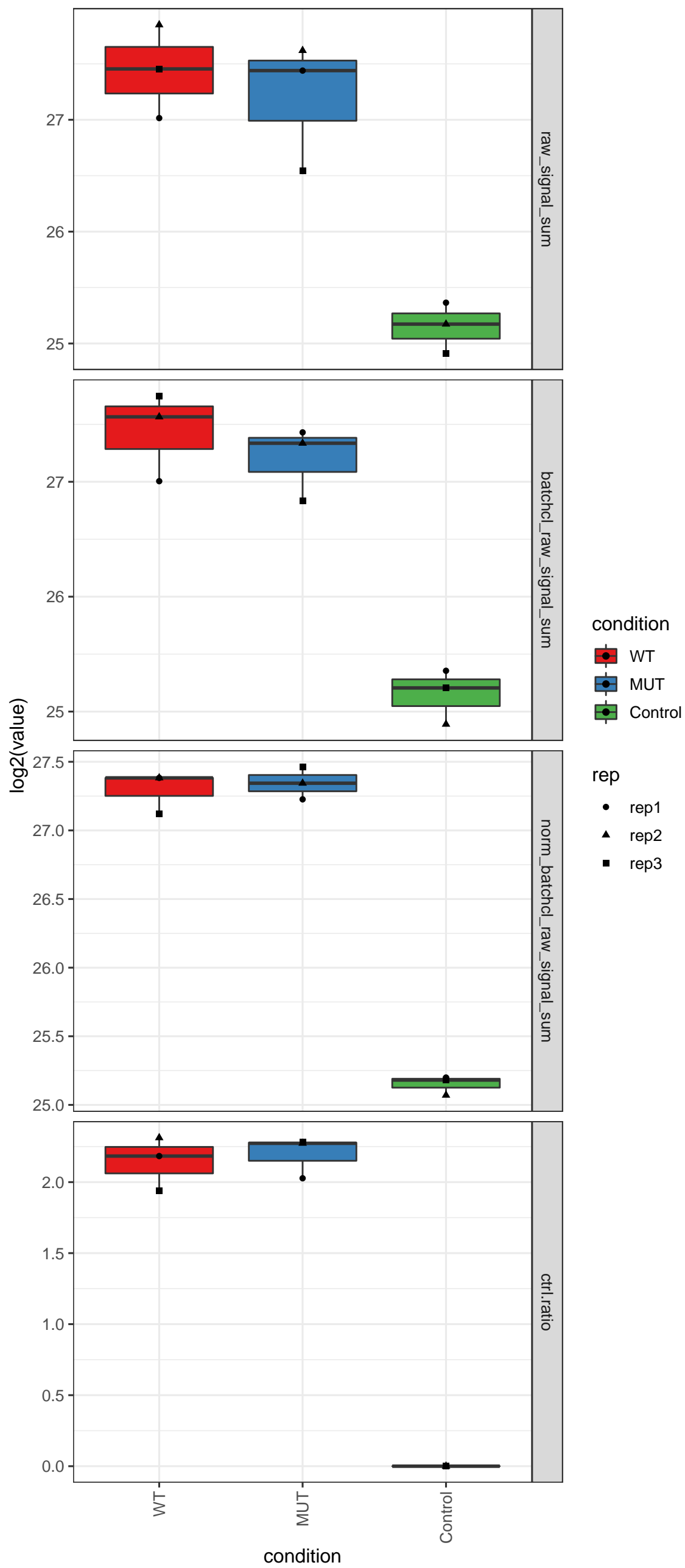
TED1 – P40533

Protein TED1 OS=*Saccharomyces cerevisiae* (strain ATCC 204508 / S288)



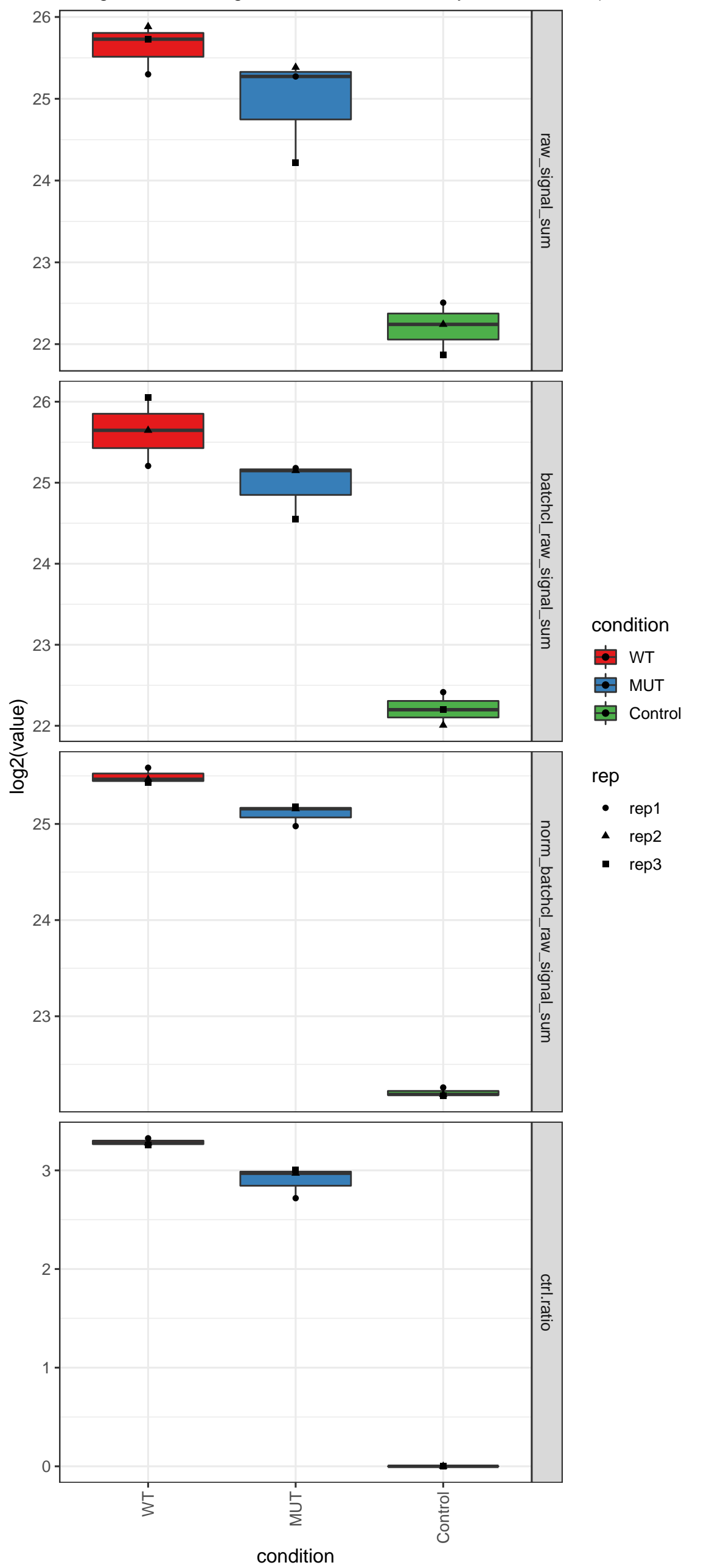
TEF1 – P02994

Elongation factor 1- α OS=*Saccharomyces cerevisiae* (strain ATCC 2



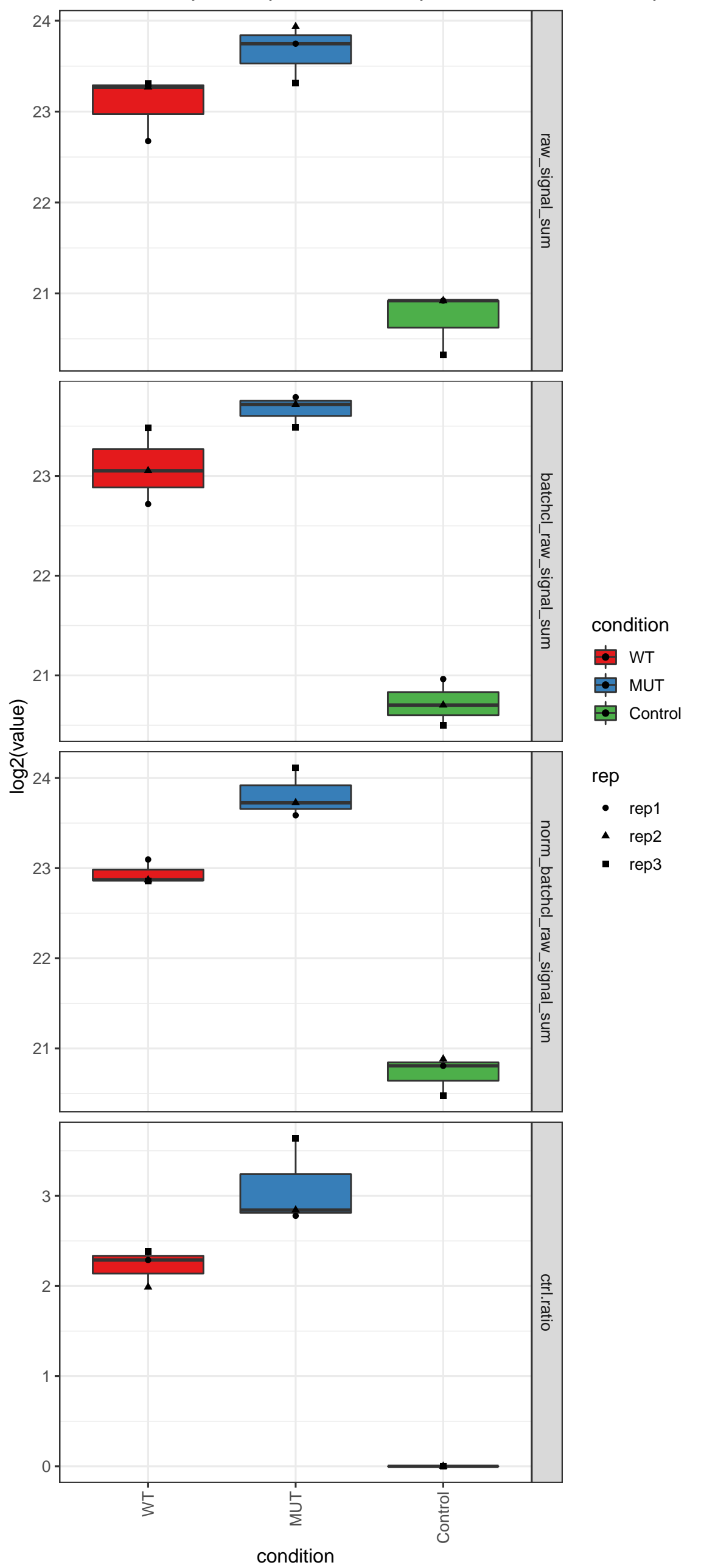
TEF4 – P36008

Elongation factor 1–gamma 2 OS=*Saccharomyces cerevisiae* (strain ATCC



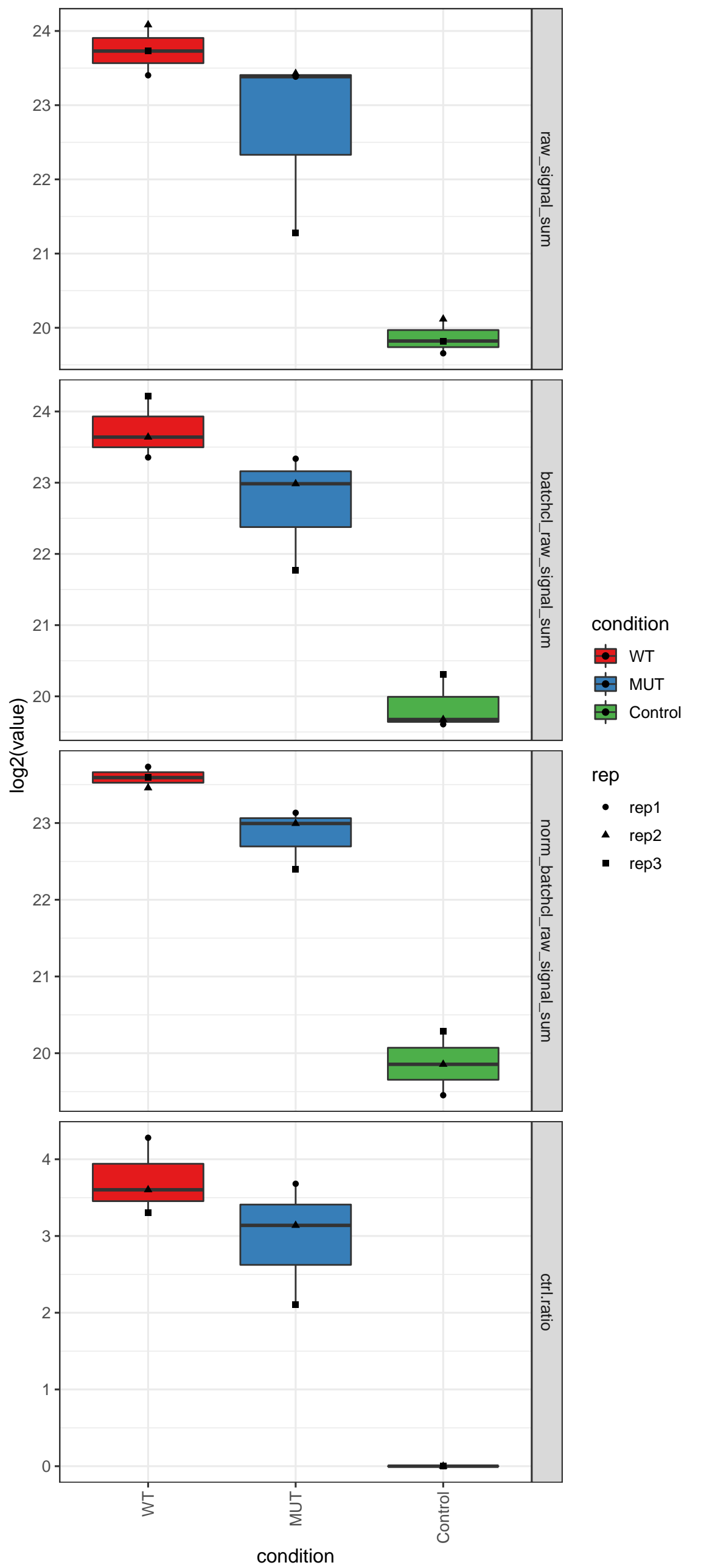
TES1 – P41903

Peroxisomal acyl-coenzyme A thioester hydrolase 1 OS=Saccharomyces cerevisiae



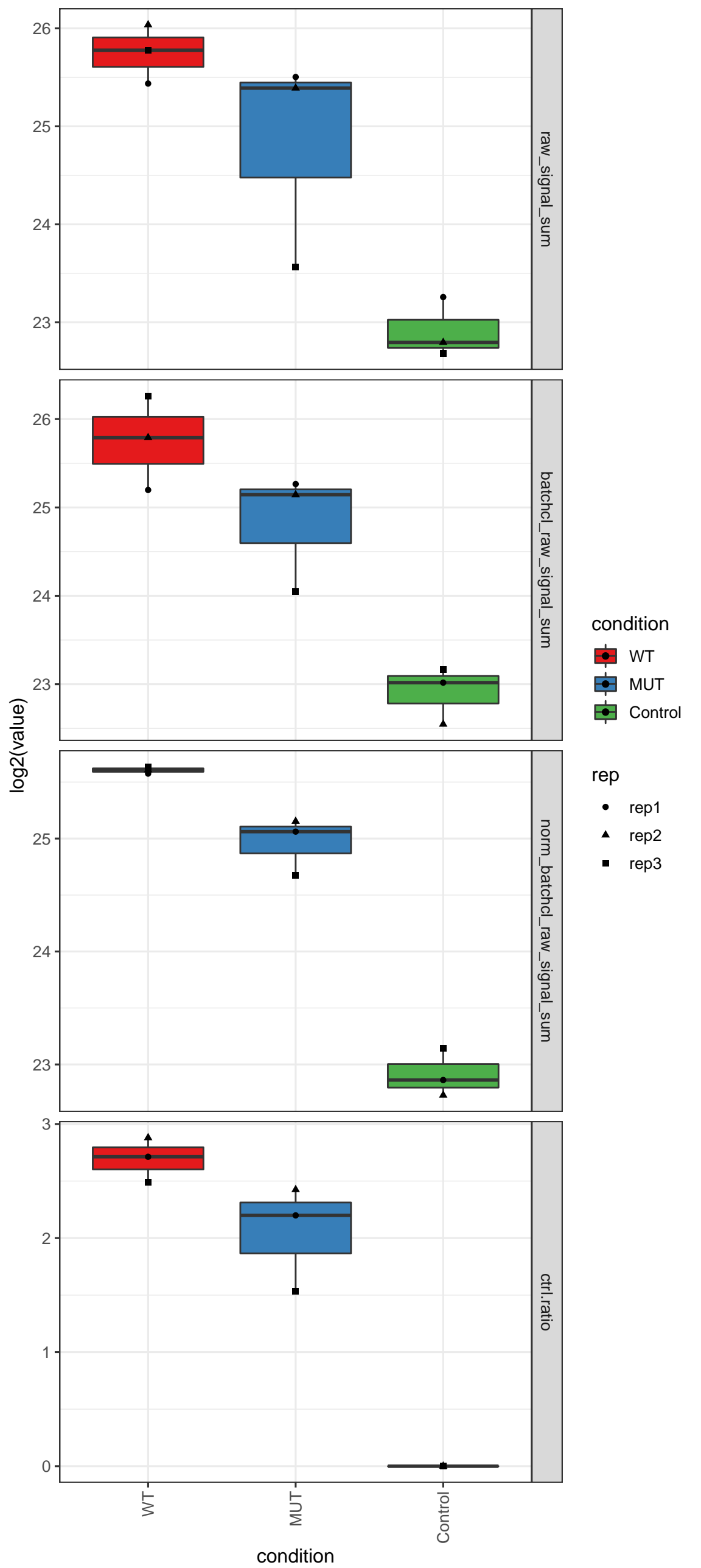
TFC1 – P32367

Transcription factor tau 95 kDa subunit OS=Saccharomyces cerevisiae (str



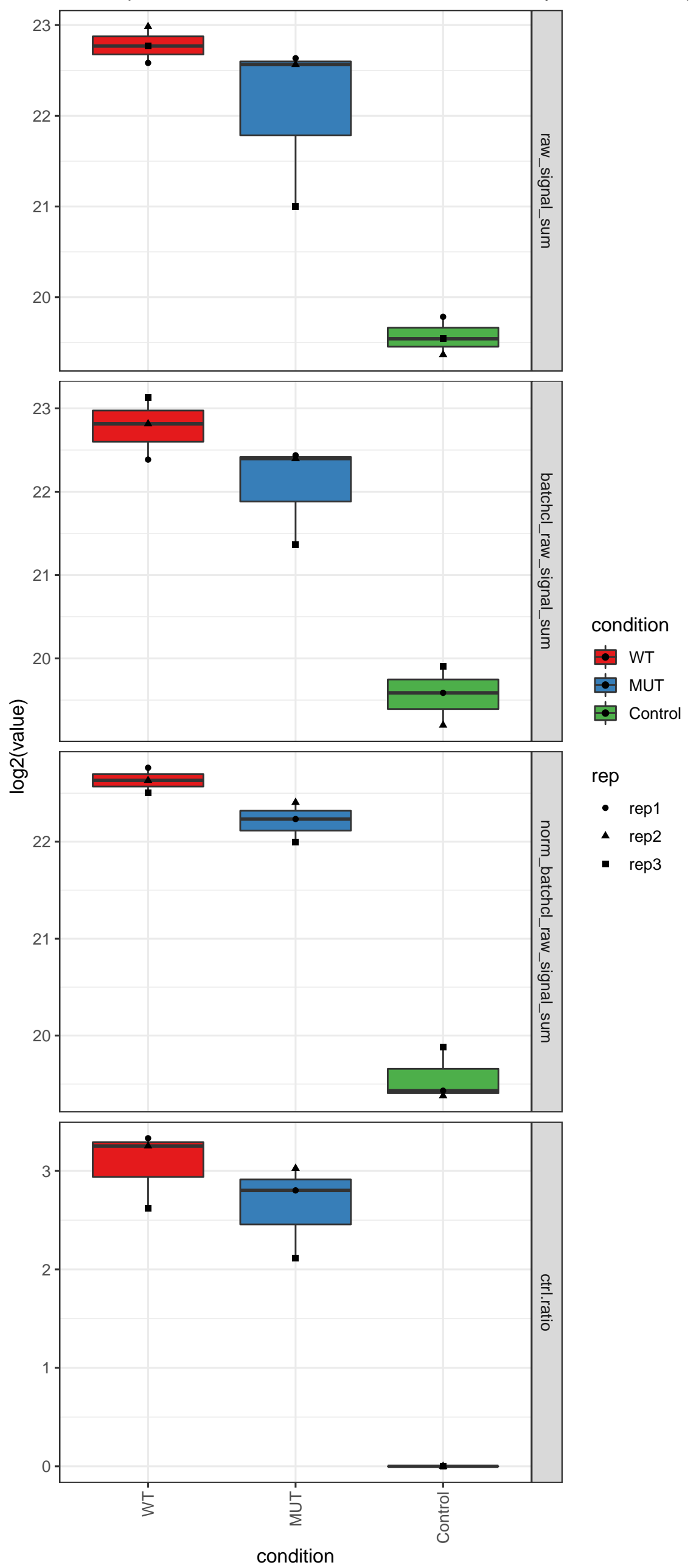
TFC3 – P34111

Transcription factor tau 138 kDa subunit OS=Saccharomyces cerevisiae (strain



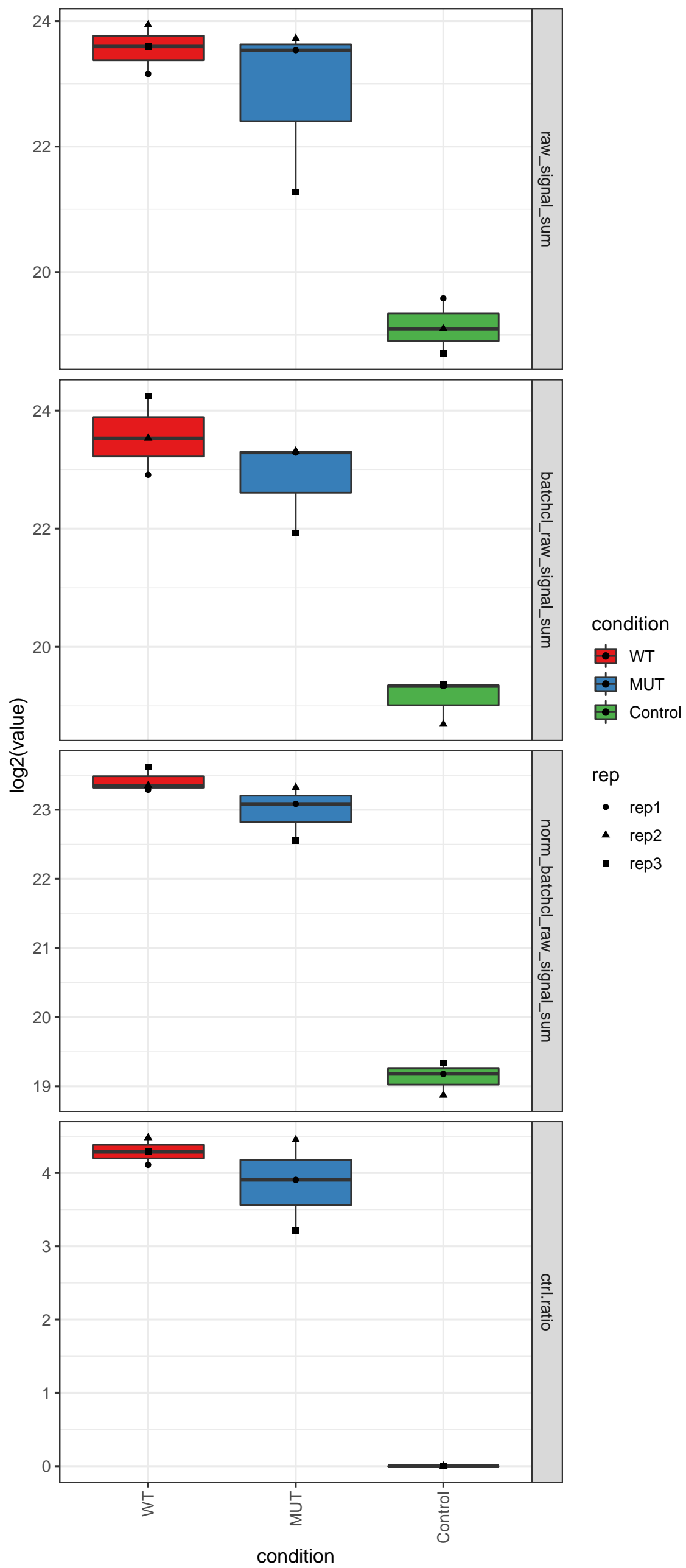
TFC4 – P33339

Transcription factor tau 131 kDa subunit OS=Saccharomyces cerevisiae (s



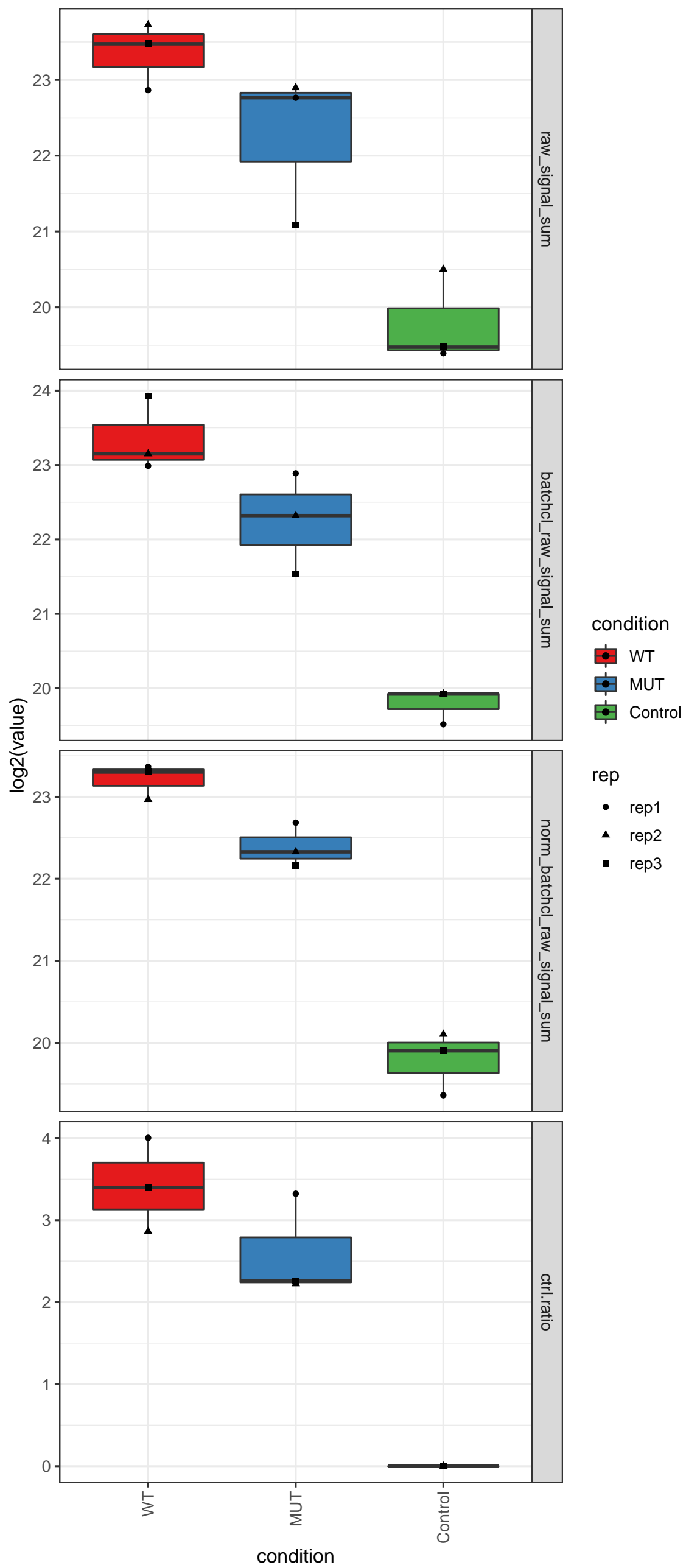
TFC6 – Q06339

Transcription factor tau 91 kDa subunit OS=Saccharomyces cerevisiae (str



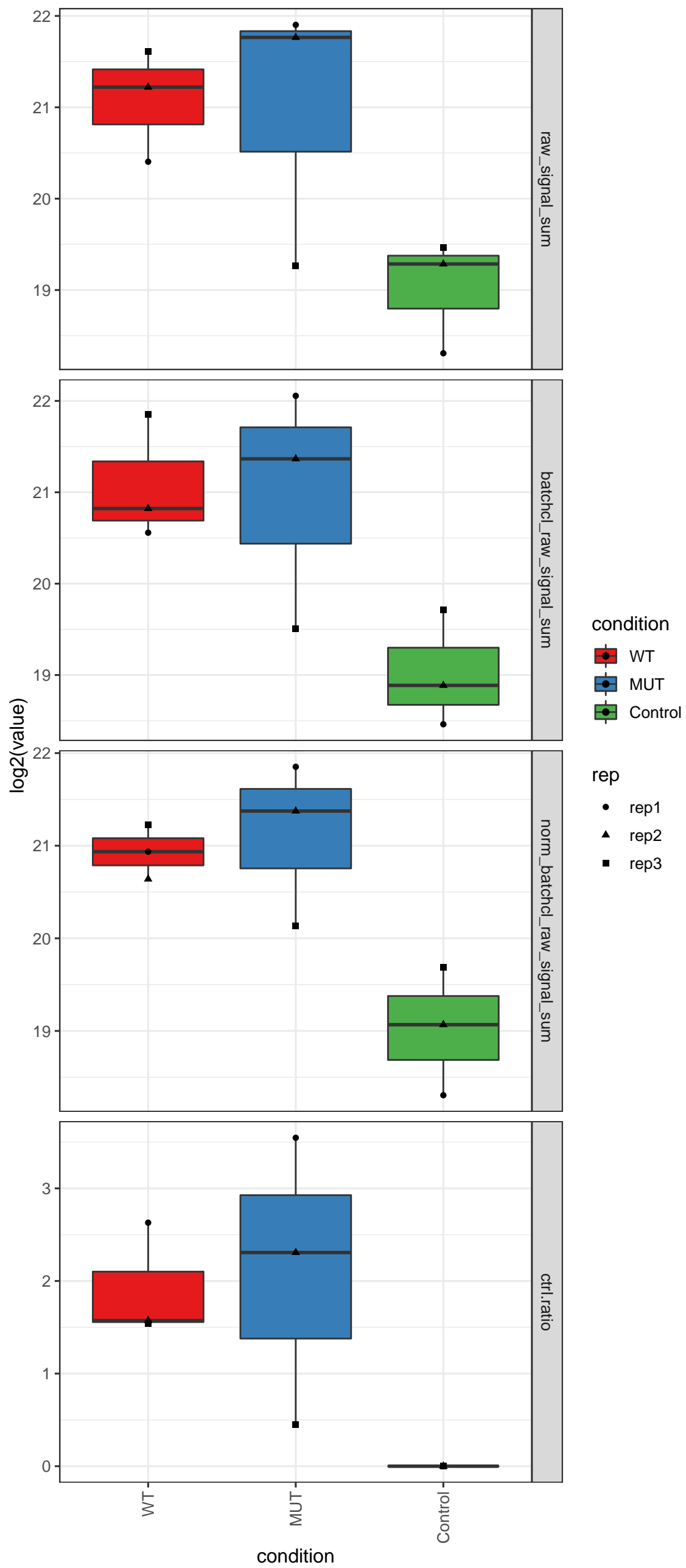
TFC8 – Q12308

Transcription factor tau 60 kDa subunit OS=Saccharomyces cerevisiae (str



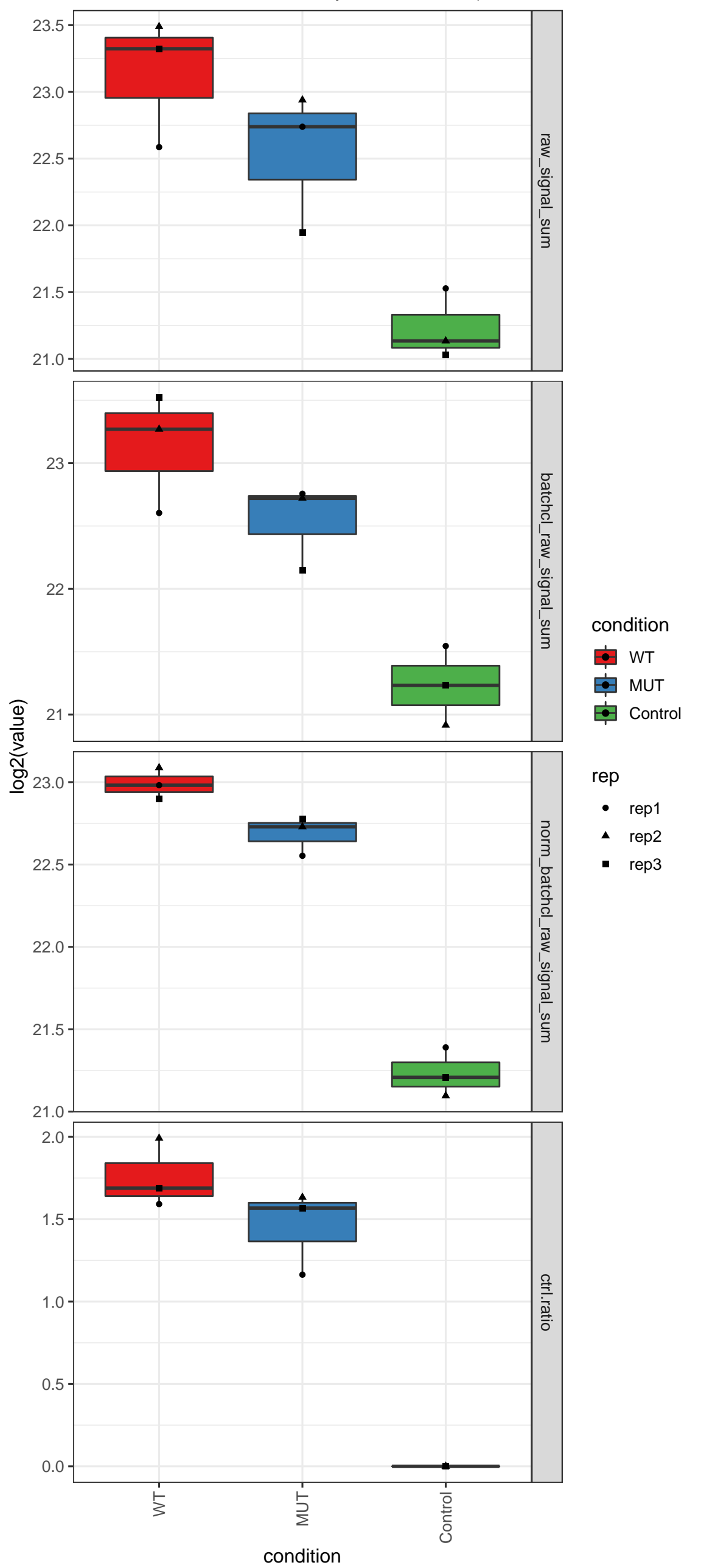
TGS1 – Q12052

Trimethylguanosine synthase OS=*Saccharomyces cerevisiae* (strain ATCC



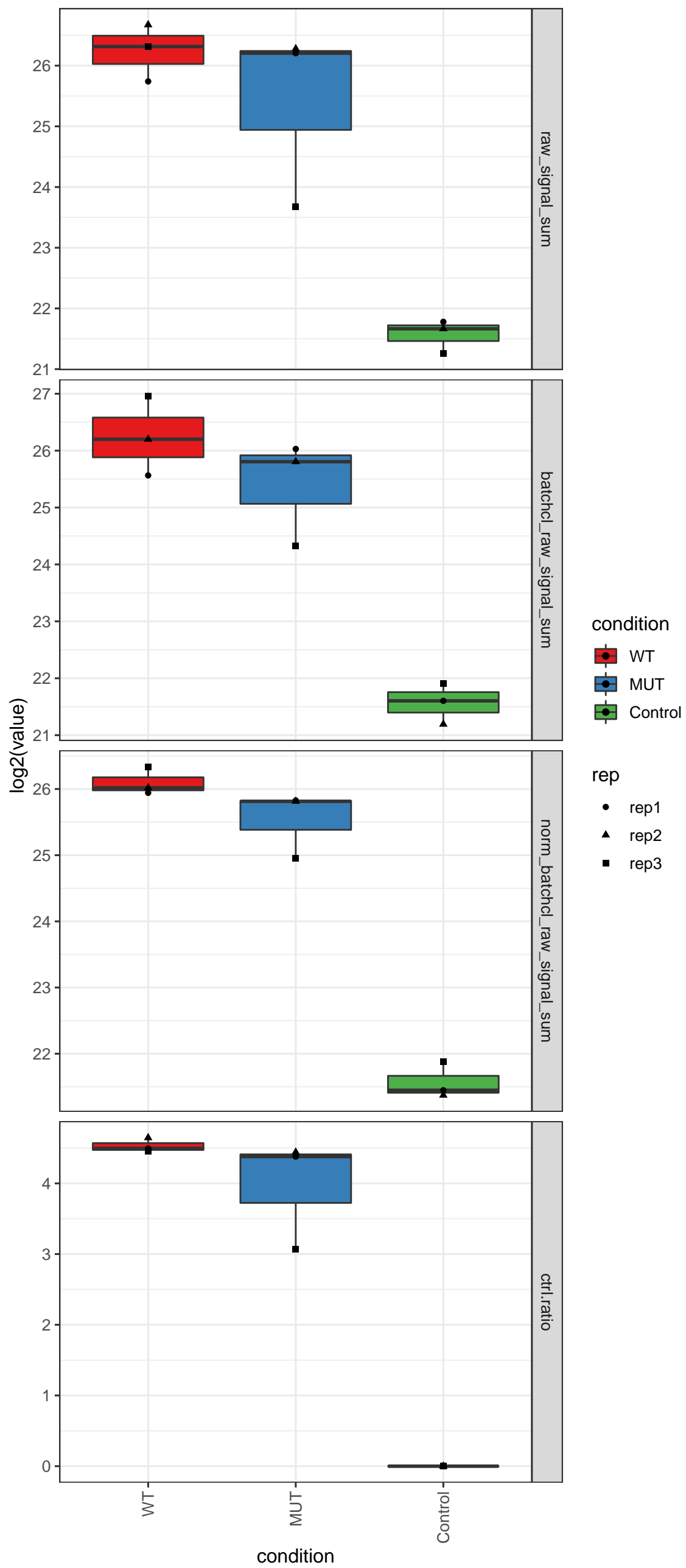
THO1 – P40040

Protein THO1 OS=*Saccharomyces cerevisiae* (strain ATCC 204508 / S28)



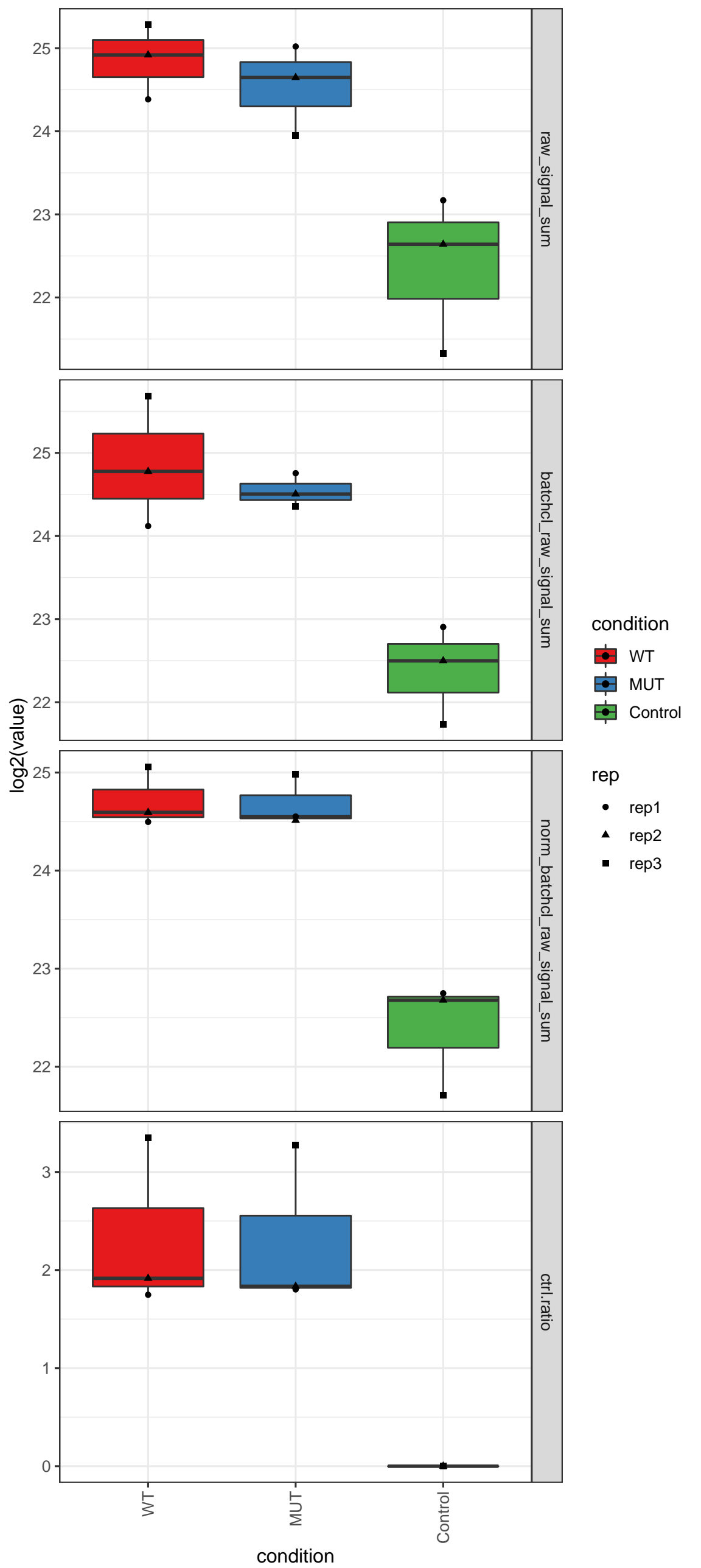
THS1 – P04801

Threonine--tRNA ligase, cytoplasmic OS=*Saccharomyces cerevisiae* (strain



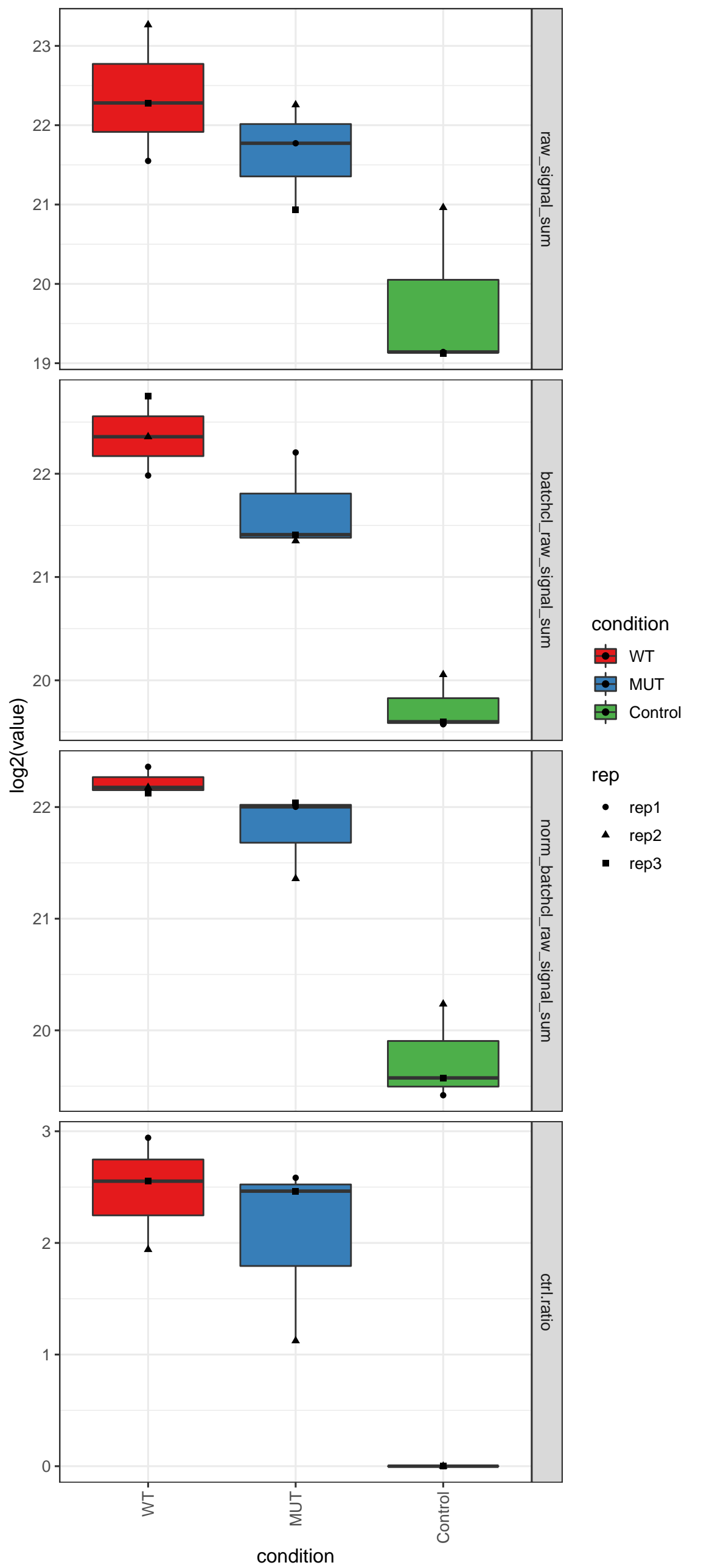
TIF1 – P10081

ATP-dependent RNA helicase eIF4A OS=Saccharomyces cerevisiae (strain



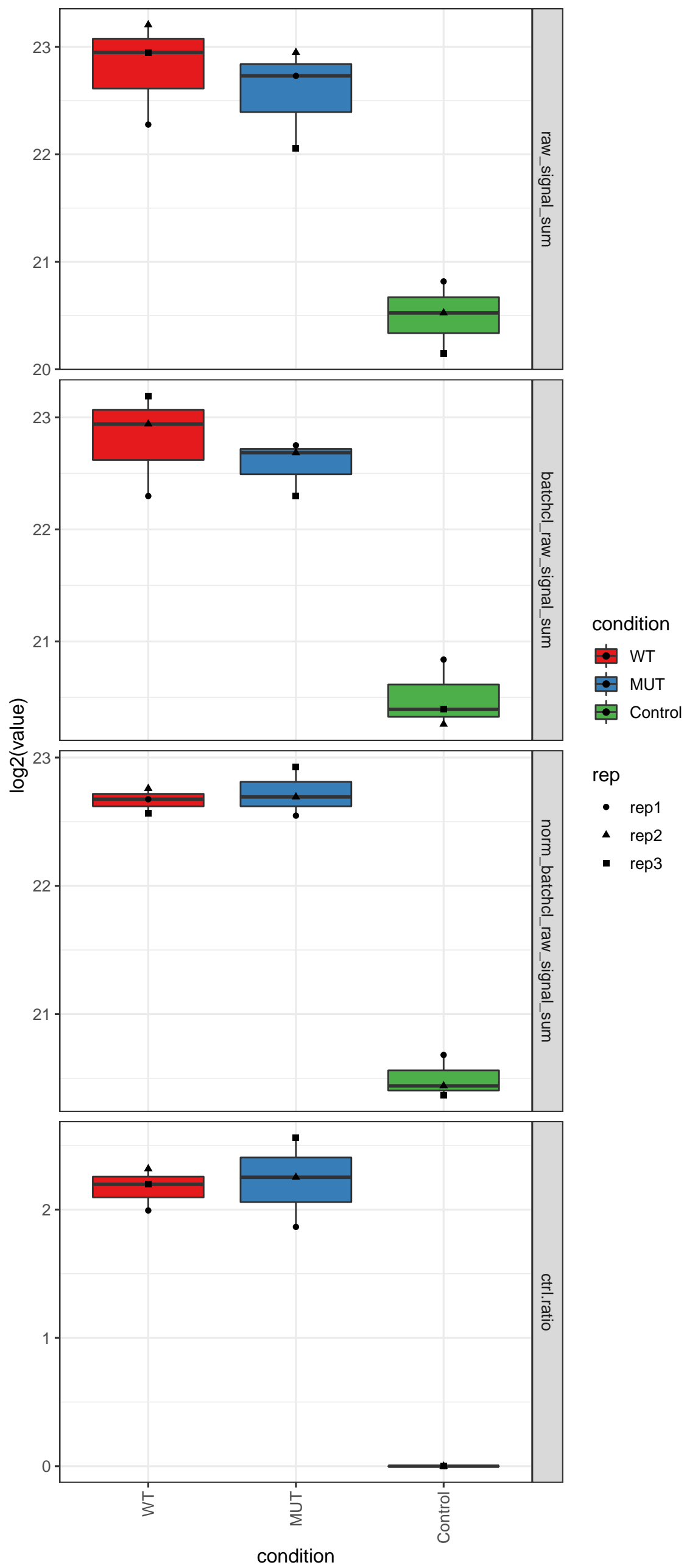
TIF34 – P40217

Eukaryotic translation initiation factor 3 subunit I OS=*Saccharomyces cerevisiae*



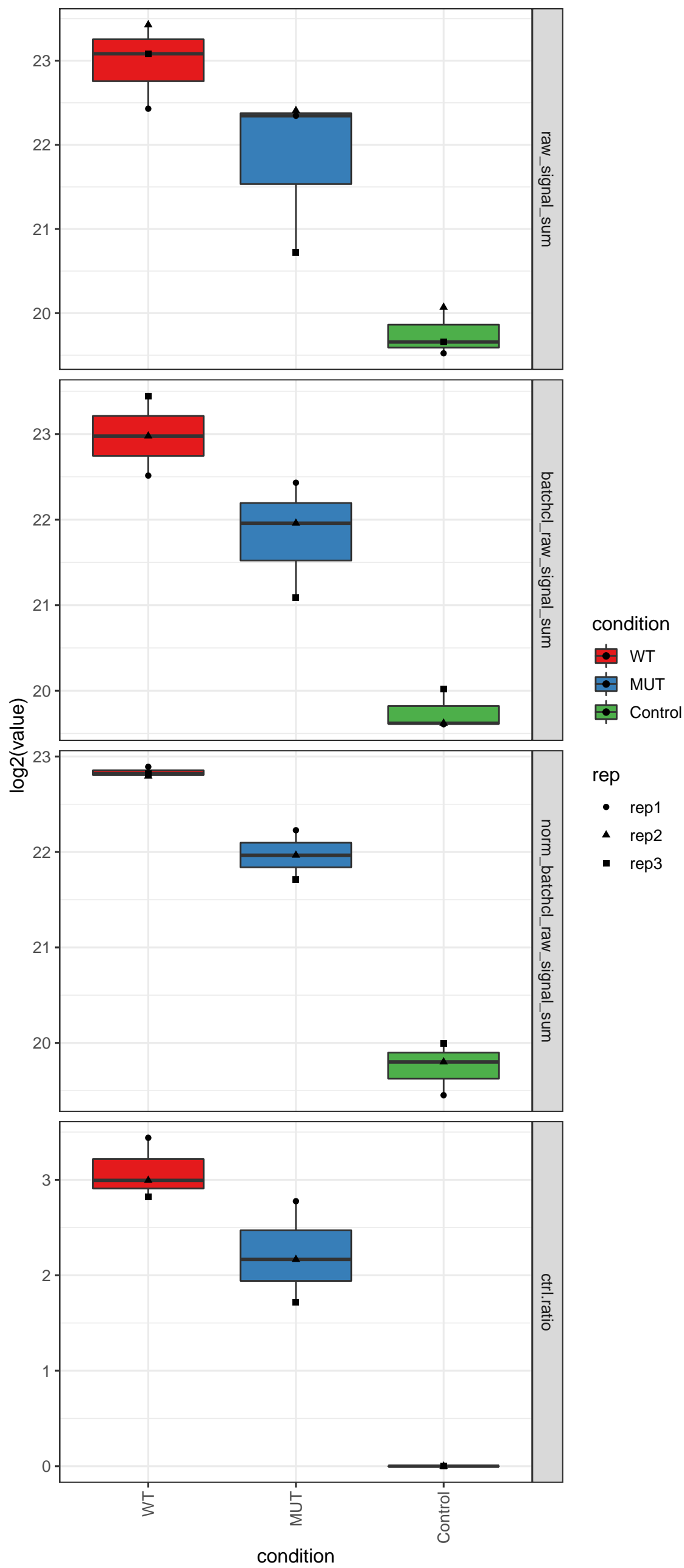
TIF35 – Q04067

Eukaryotic translation initiation factor 3 subunit G OS=*Saccharomyces cerevisiae*



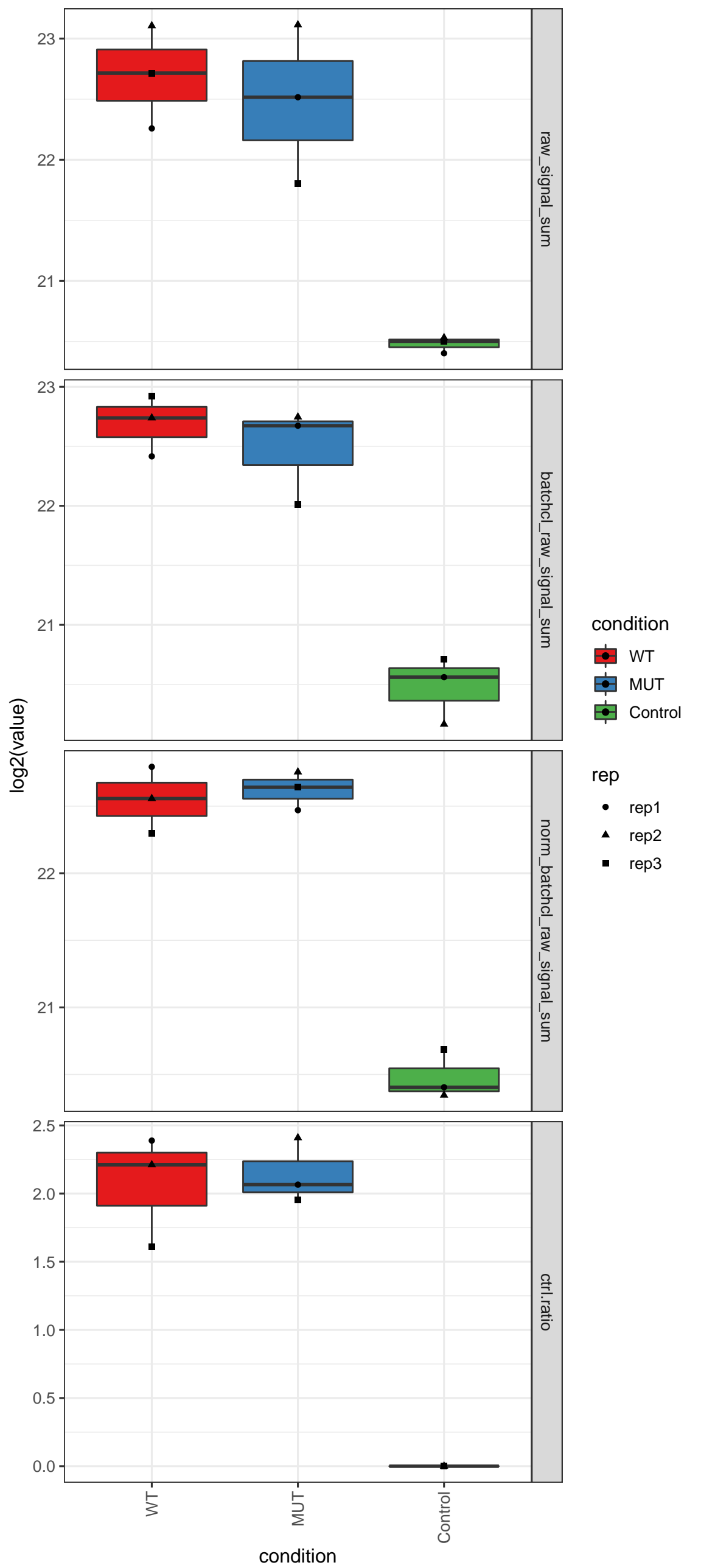
TIF4631 – P39935

Eukaryotic initiation factor 4F subunit p150 OS=*Saccharomyces cerevisiae*



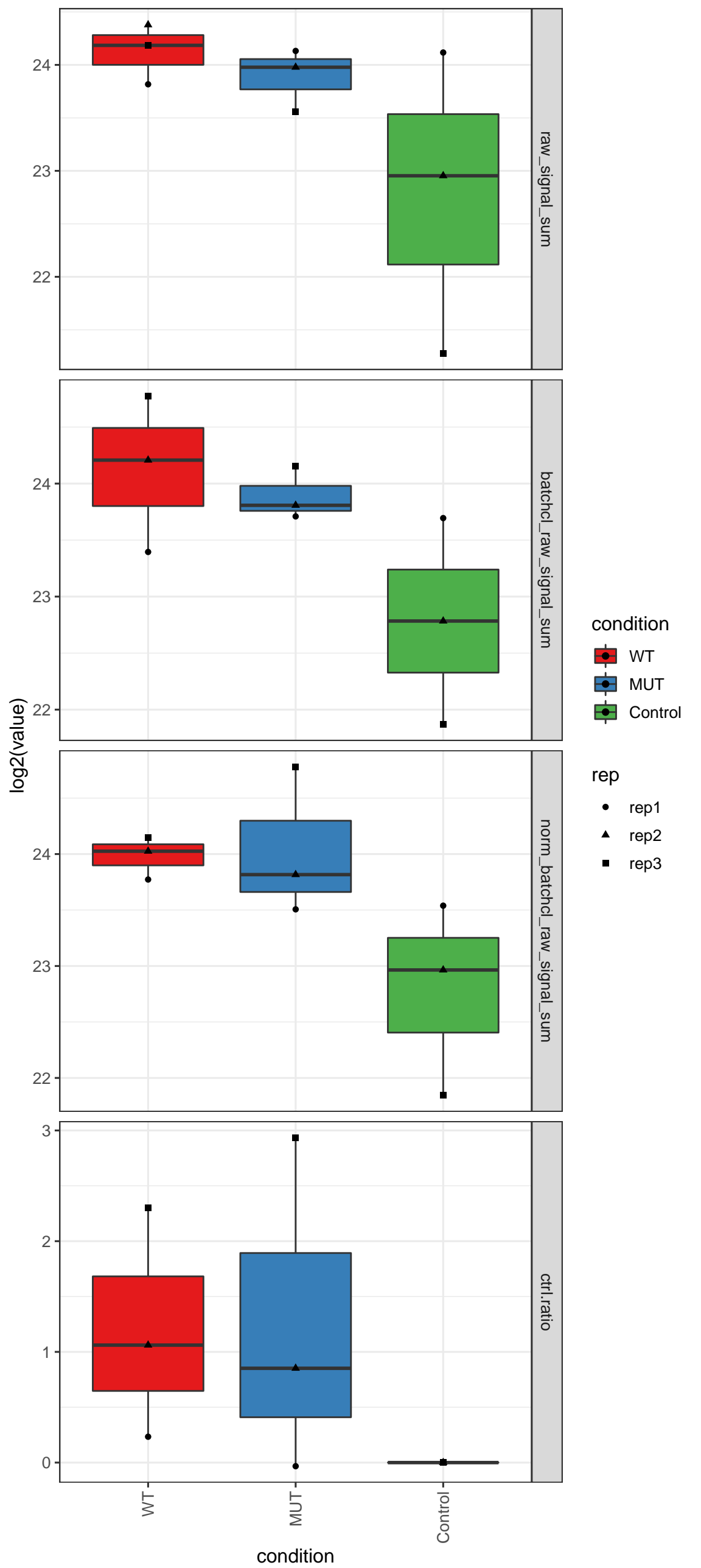
TIF5 – P38431|P38431–2

Eukaryotic translation initiation factor 5 OS=*Saccharomyces cerevisiae* (str. *S. cerevisiae*)

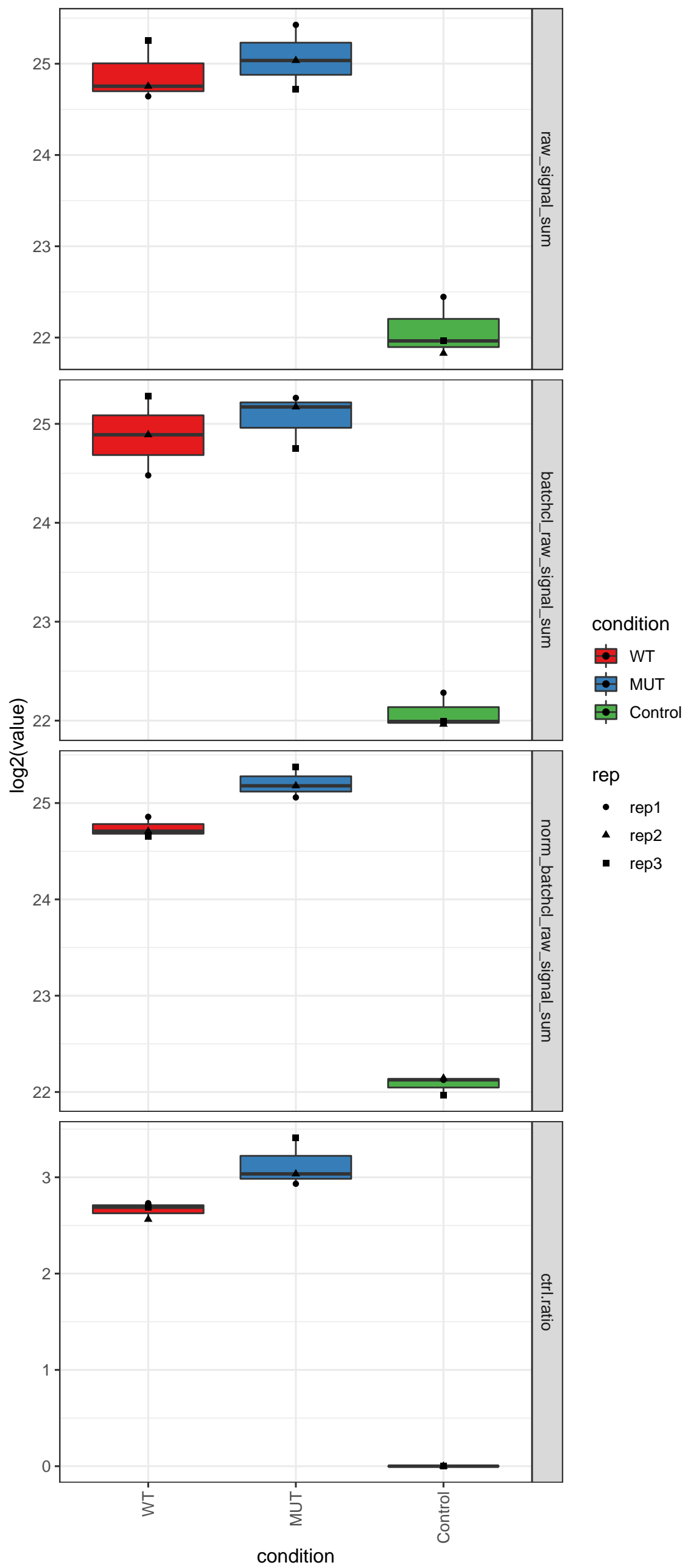


TIM44 – Q01852

Mitochondrial import inner membrane translocase subunit TIM44 OS=Saccharomyces cerevisiae

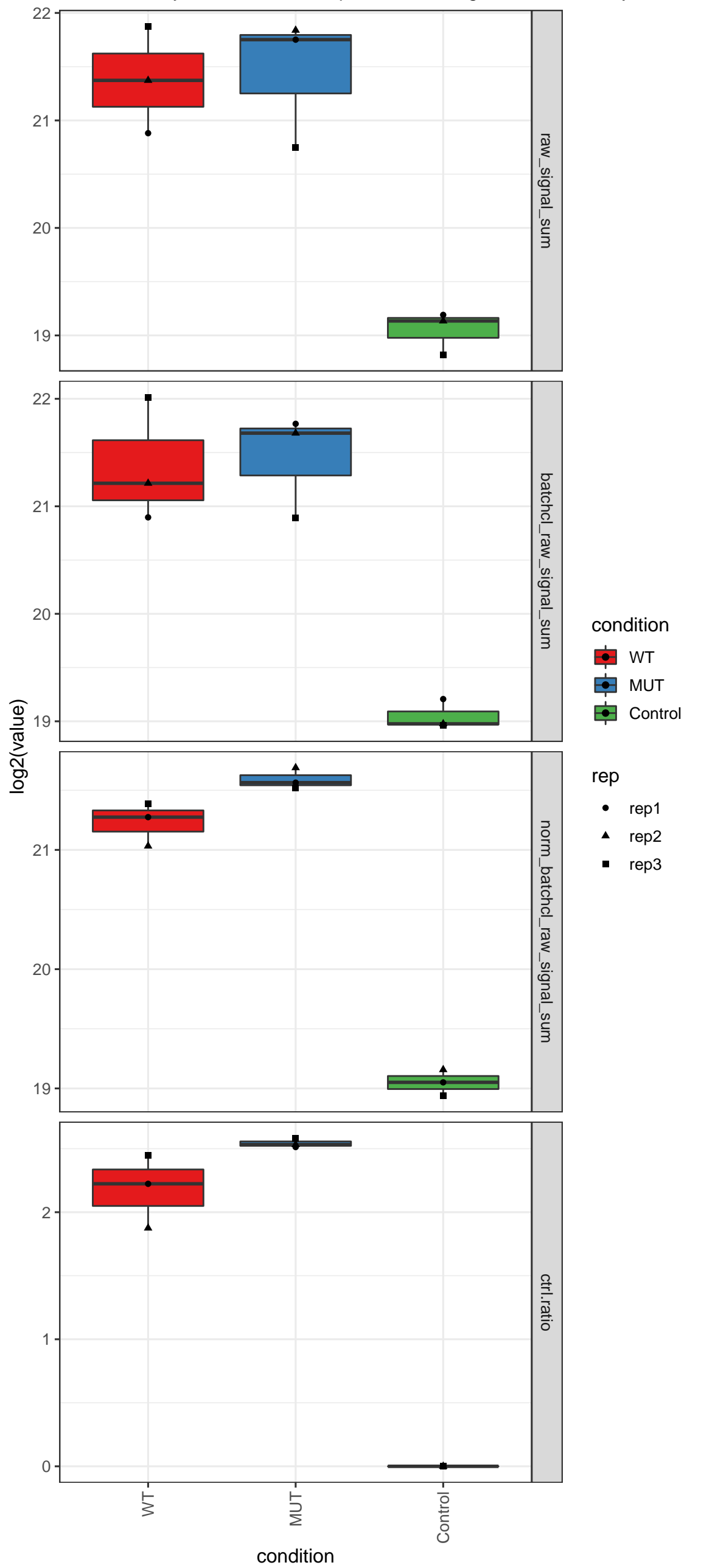


TKL1 – P23254

Transketolase 1 OS=*Saccharomyces cerevisiae* (strain ATCC 204508 / S288c)

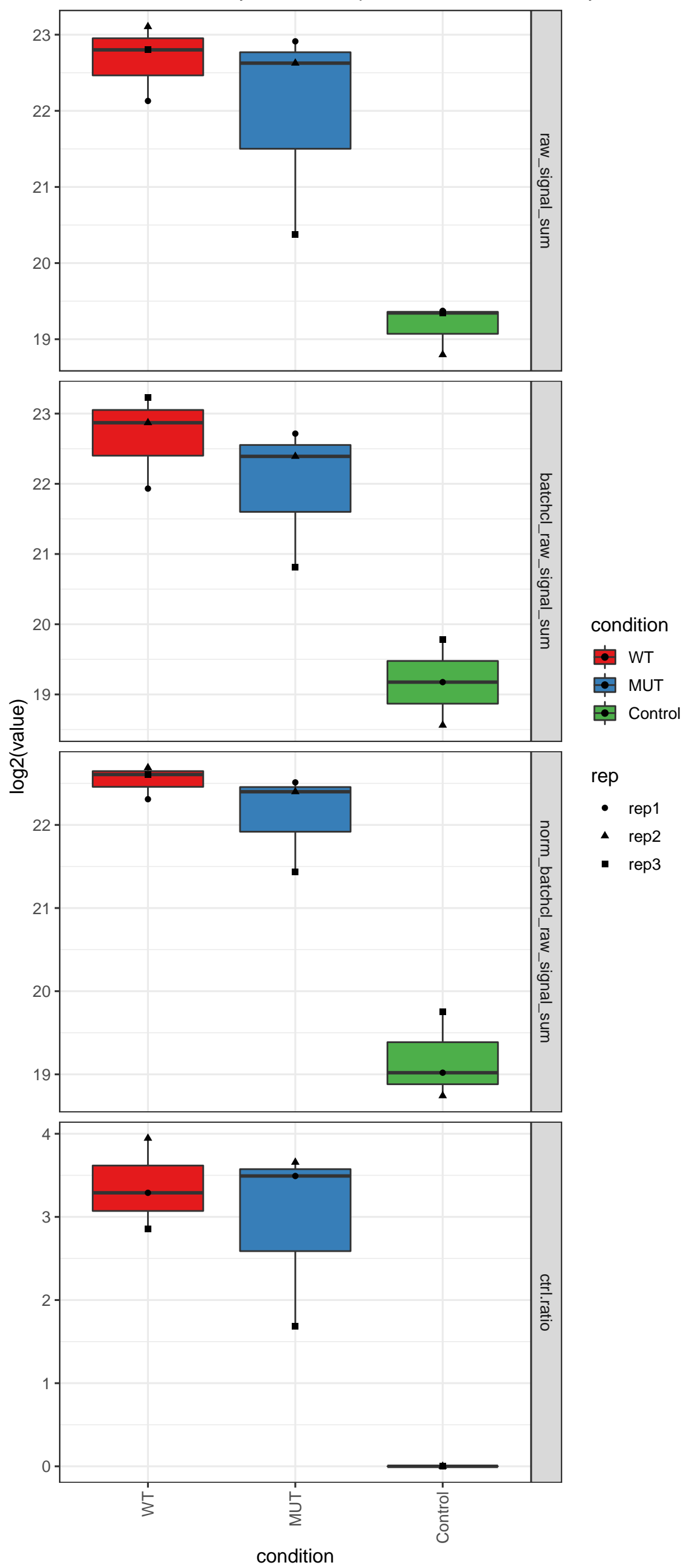
TMA19 – P35691

Translationally-controlled tumor protein homolog OS=*Saccharomyces cerevisiae*



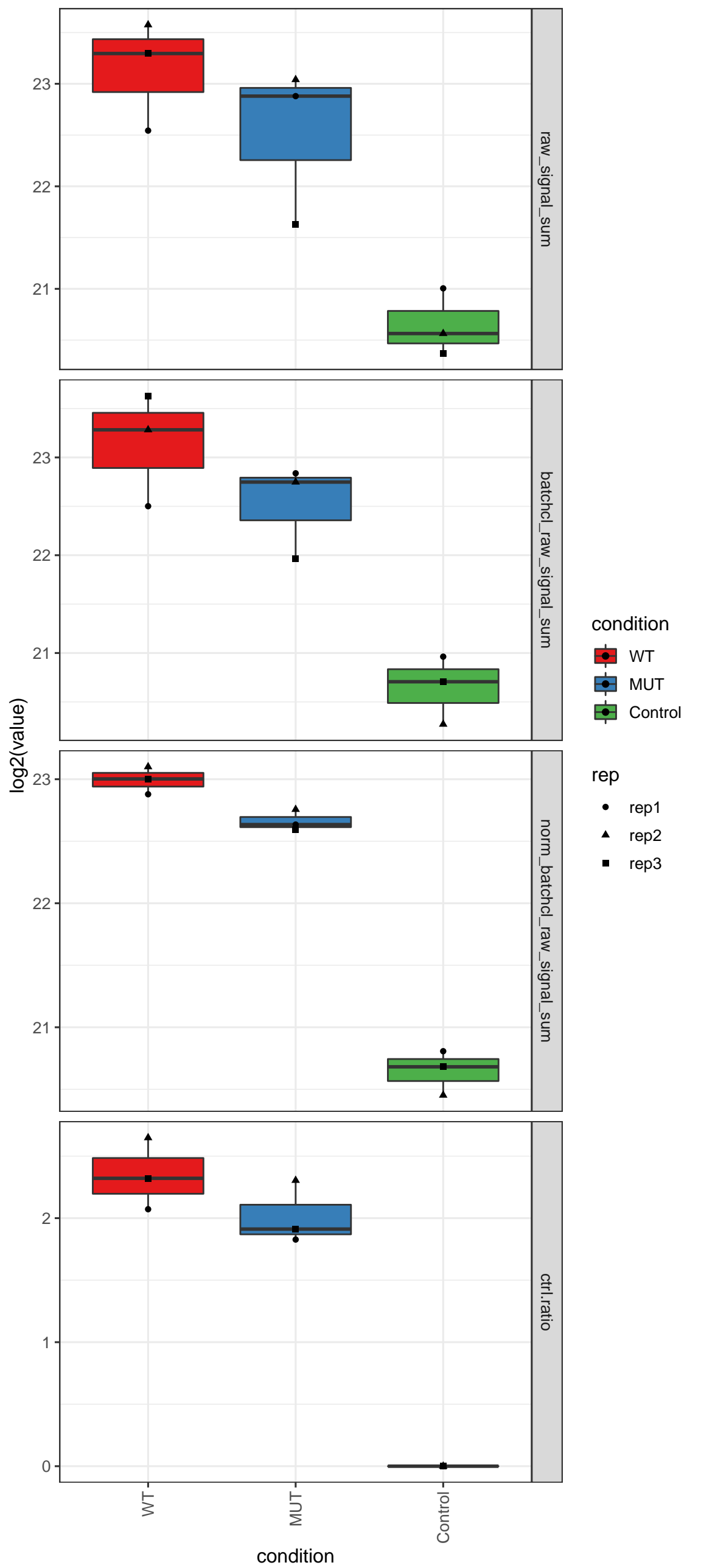
TMA22 – P47089

Translation machinery–associated protein 22 OS=*Saccharomyces cerevisiae*



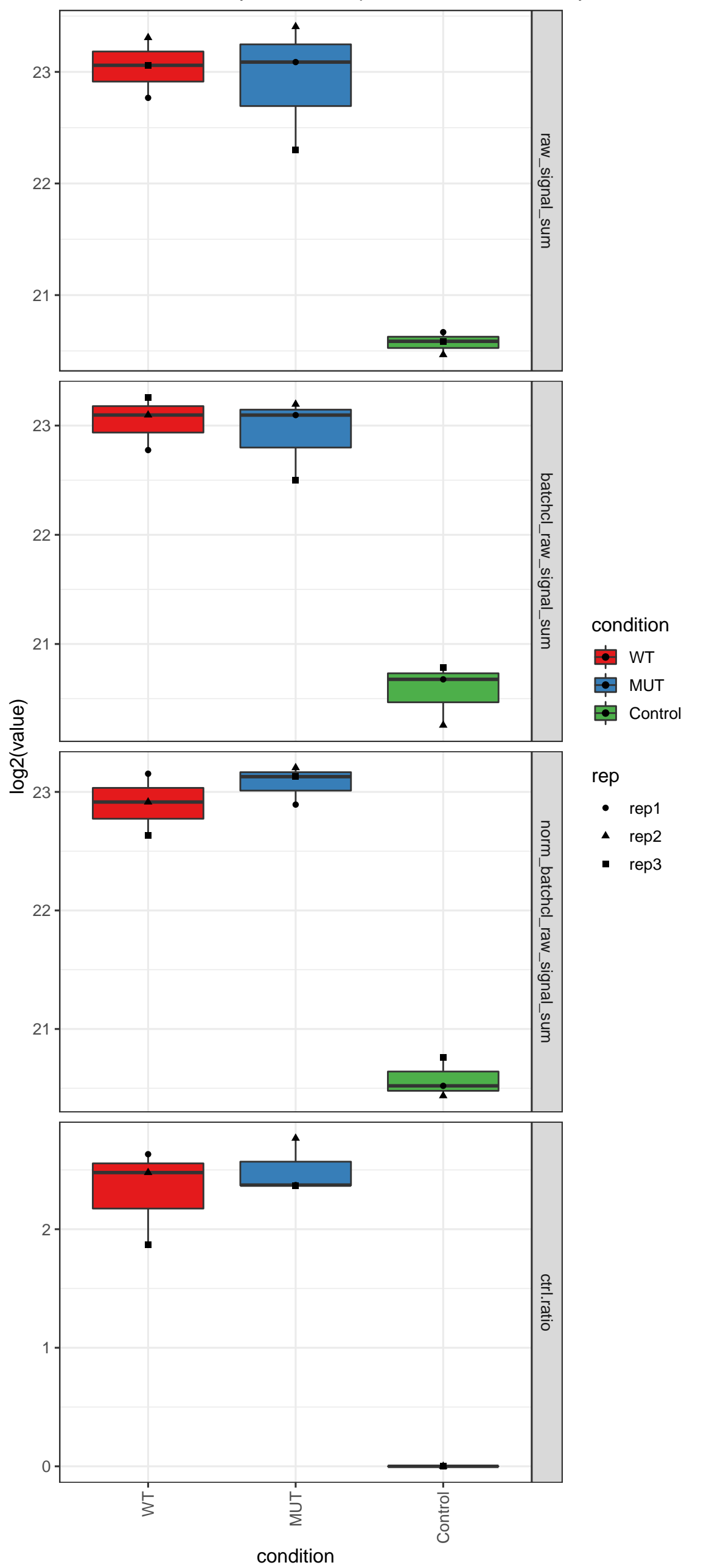
TMA64 – Q04600

Translation machinery–associated protein 64 OS=*Saccharomyces cerevisiae*



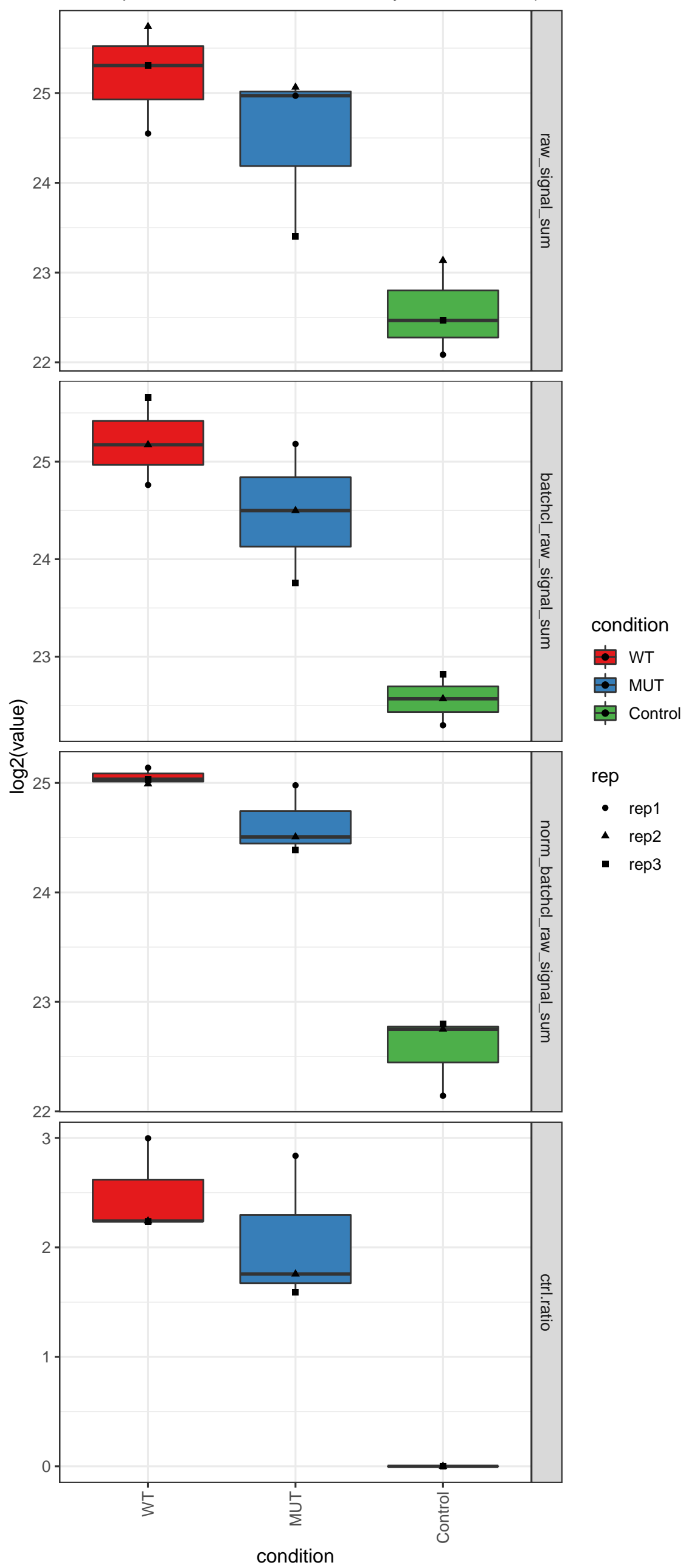
TMA7 – Q3E764

Translation machinery–associated protein 7 OS=*Saccharomyces cerevisiae*



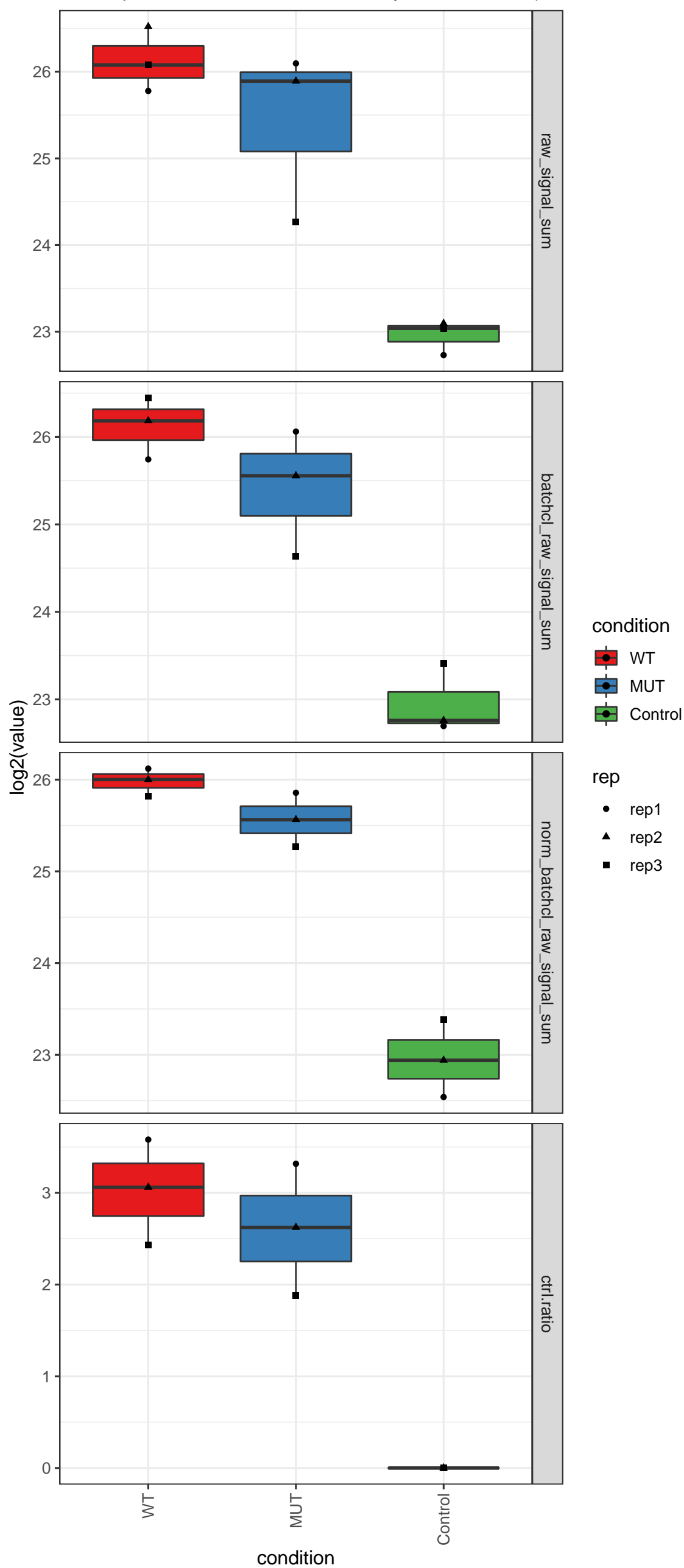
TOP1 – P04786

DNA topoisomerase 1 OS=Saccharomyces cerevisiae (strain ATCC 20450)



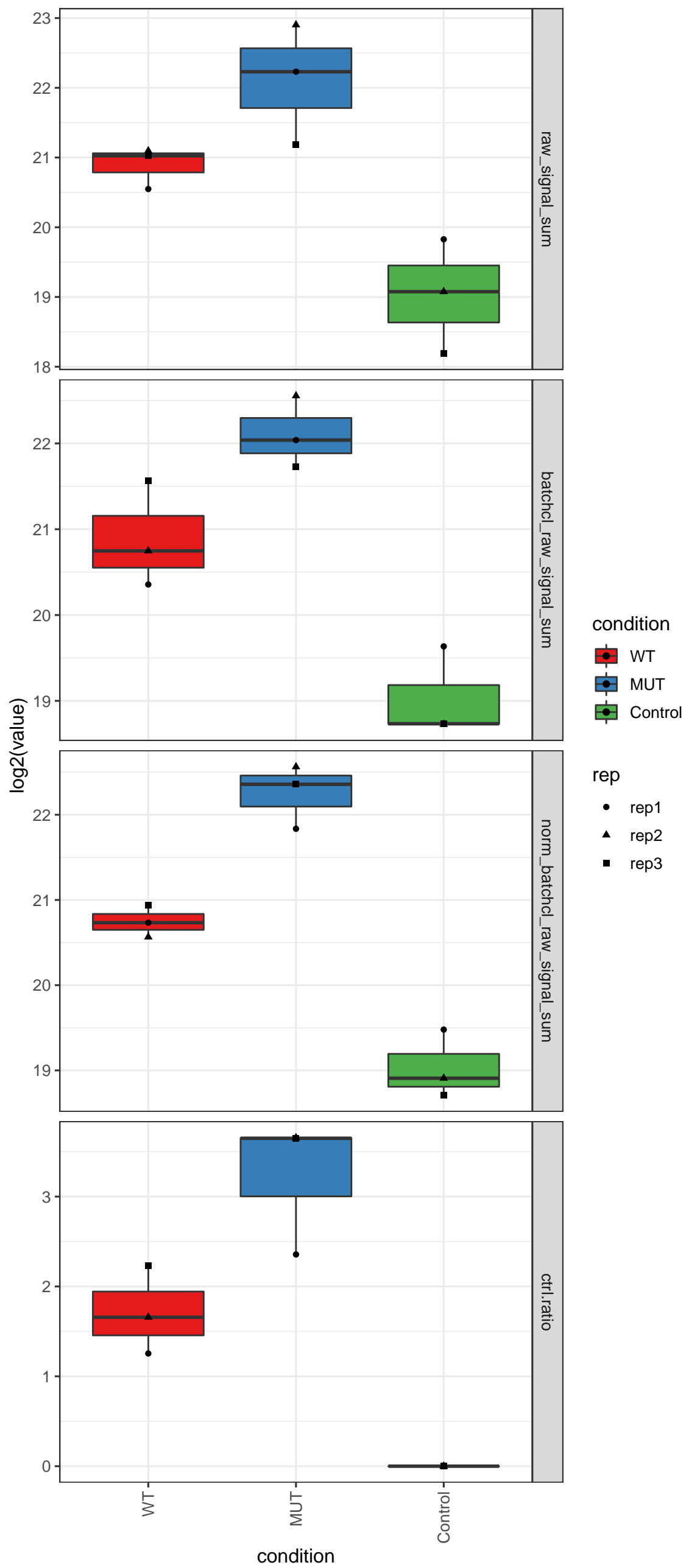
TOP2 – P06786

DNA topoisomerase 2 OS=Saccharomyces cerevisiae (strain ATCC 20450)



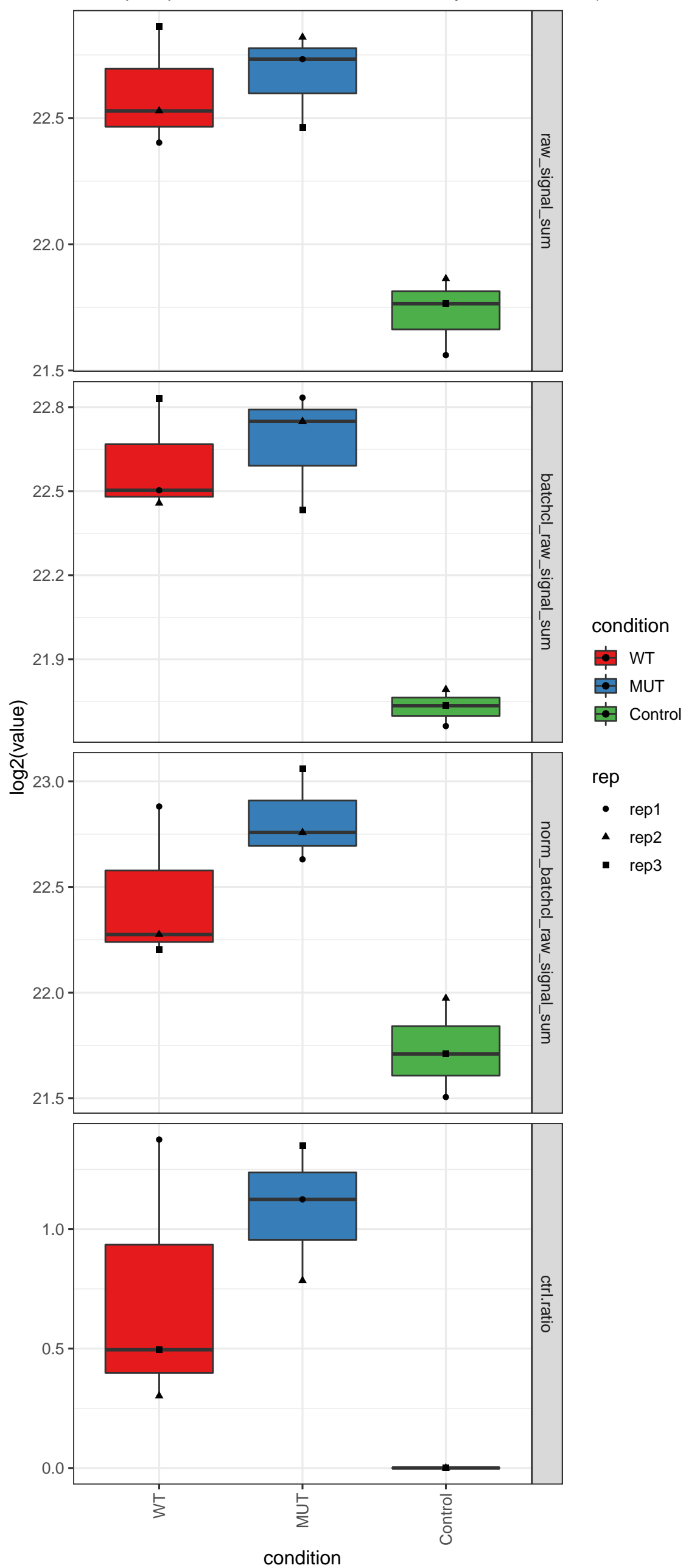
TOR2 – P32600

Serine/threonine–protein kinase TOR2 OS=*Saccharomyces cerevisiae* (str



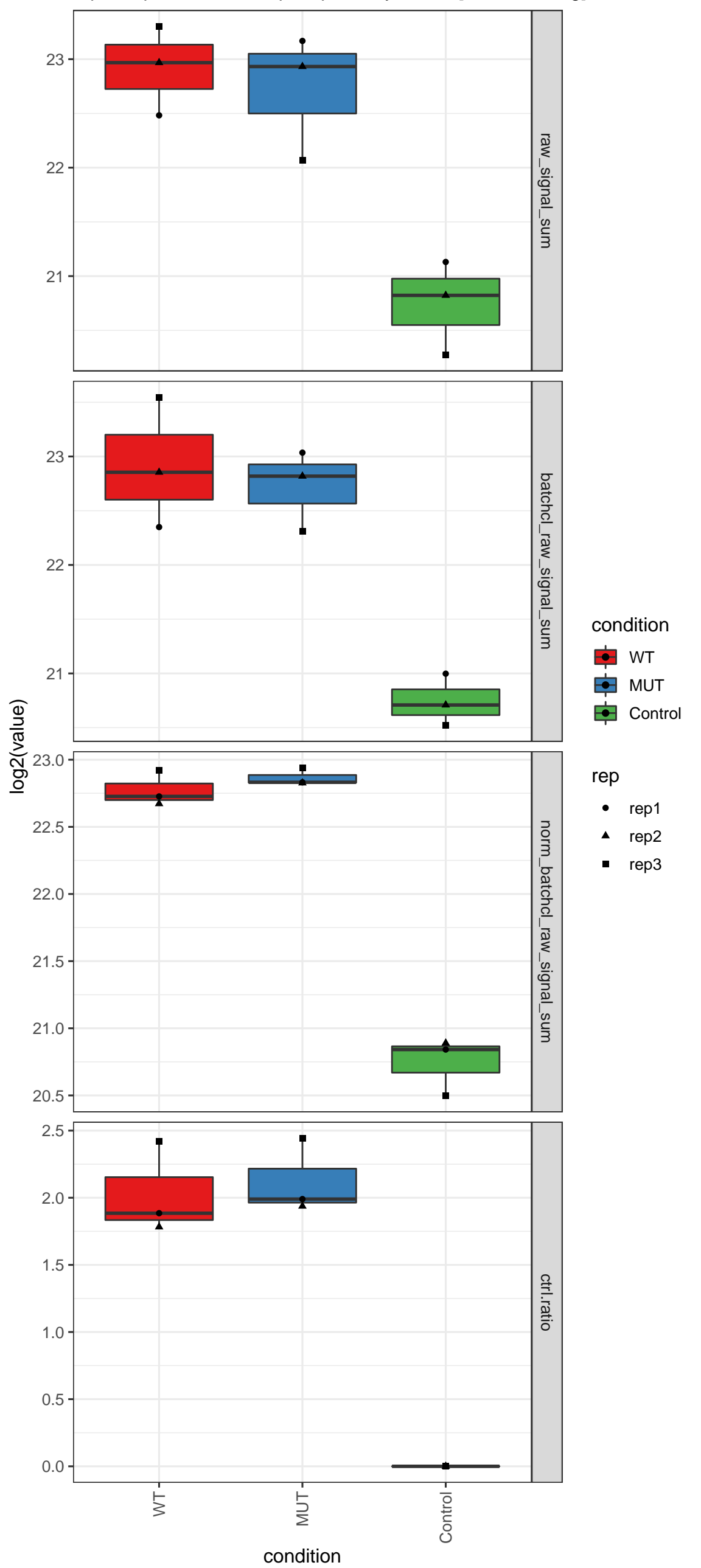
TPI1 – P00942

Triosephosphate isomerase OS=*Saccharomyces cerevisiae* (strain ATCC



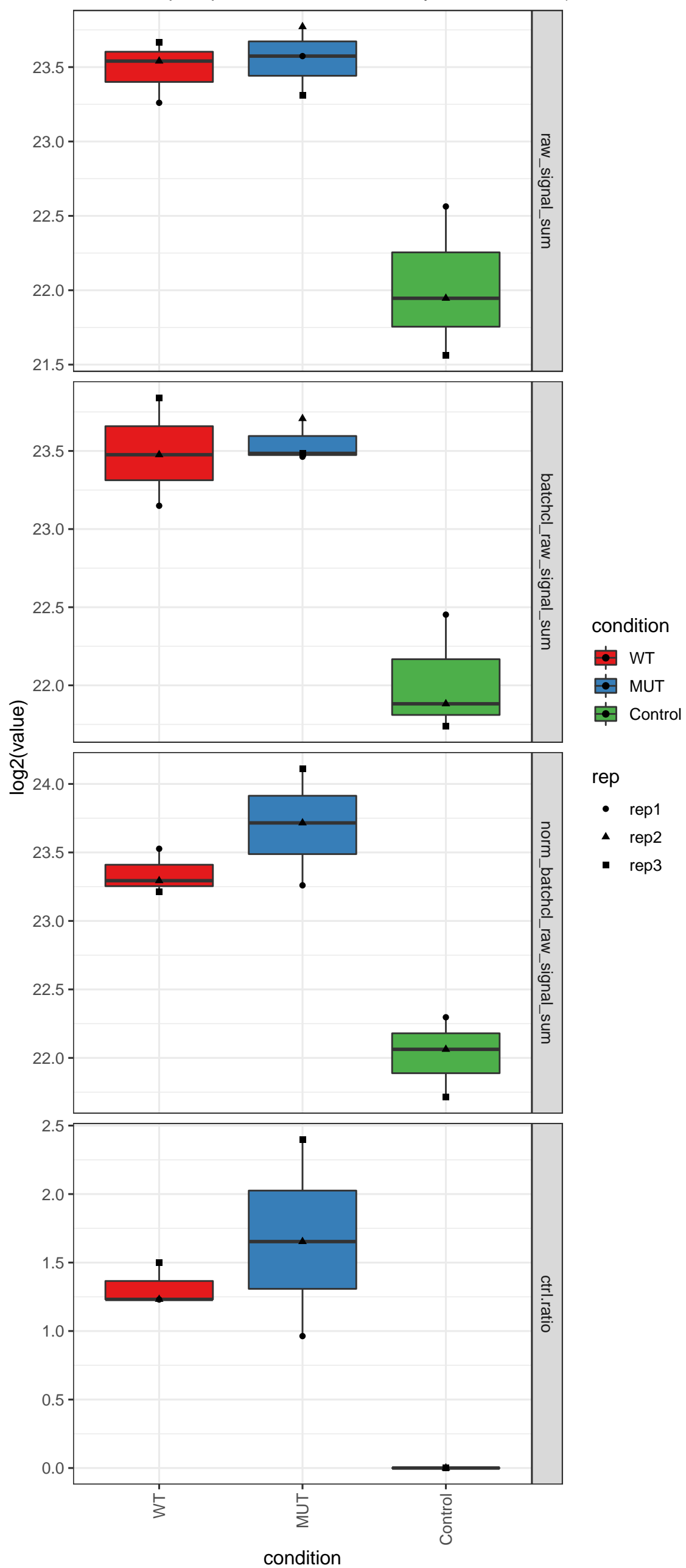
TPS1 – Q00764

Alpha,alpha-trehalose-phosphate synthase [UDP-forming] 56 kDa subu



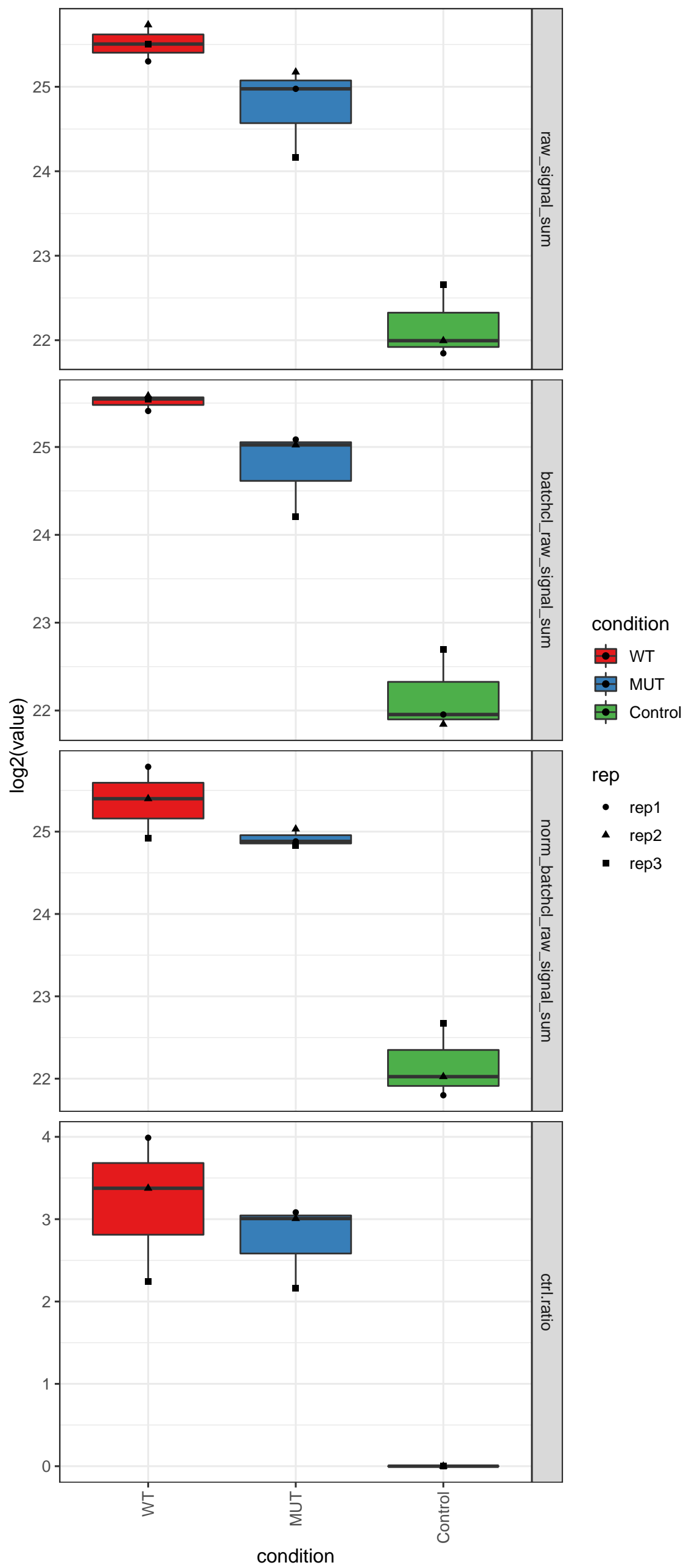
TPS2 – P31688

Trehalose-phosphatase OS=*Saccharomyces cerevisiae* (strain ATCC 20457)



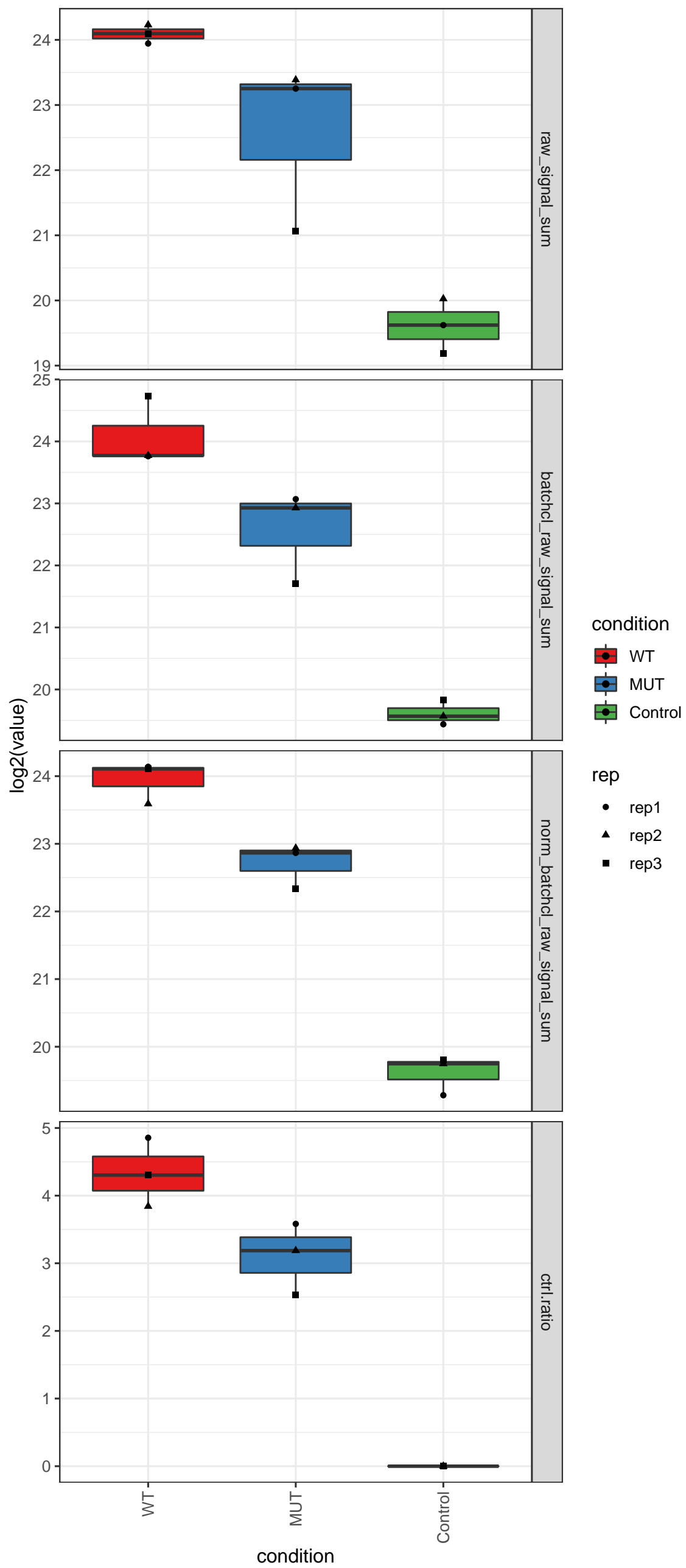
TRA1 – P38811

Transcription-associated protein 1 OS=*Saccharomyces cerevisiae* (strain A



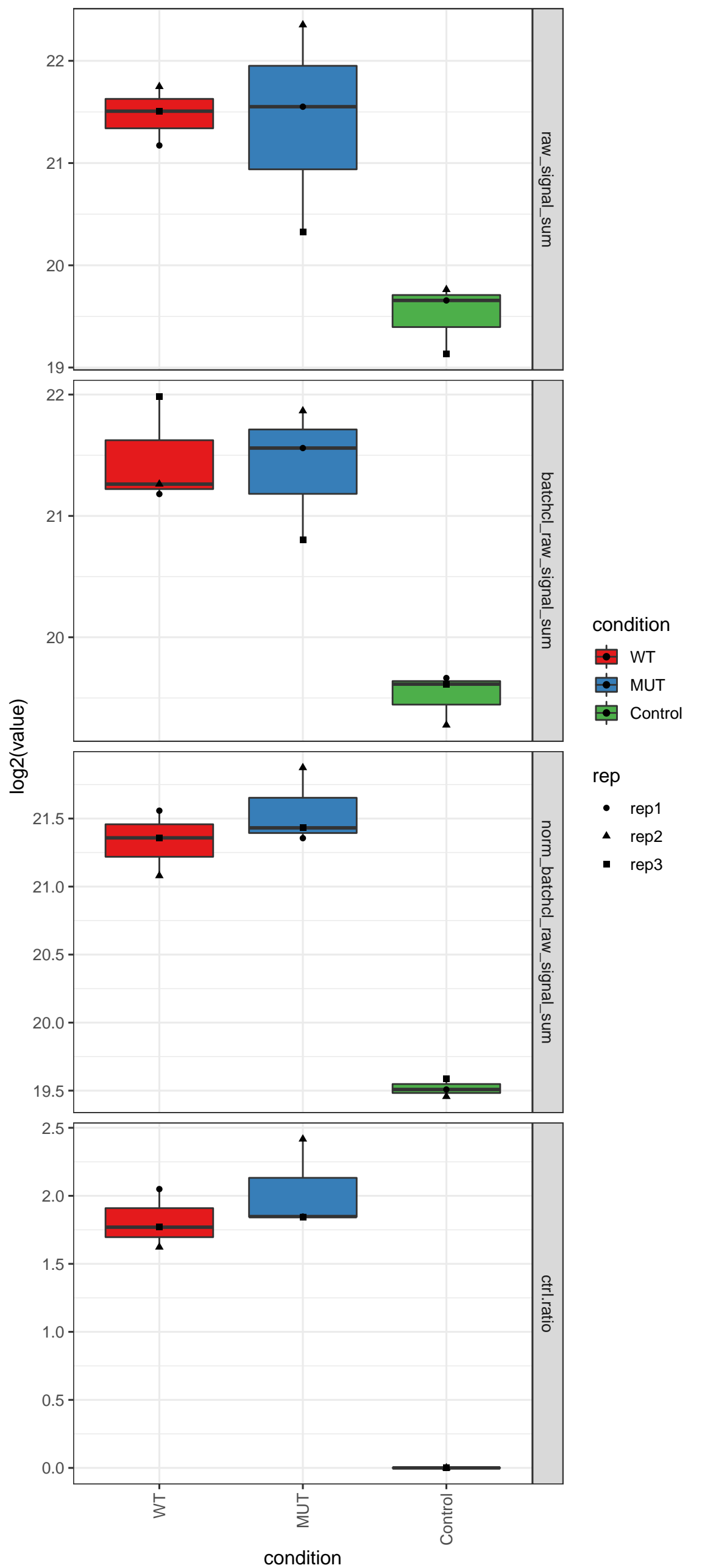
TRI1 – Q05024

Protein TRI1 OS=*Saccharomyces cerevisiae* (strain ATCC 204508 / S288c)



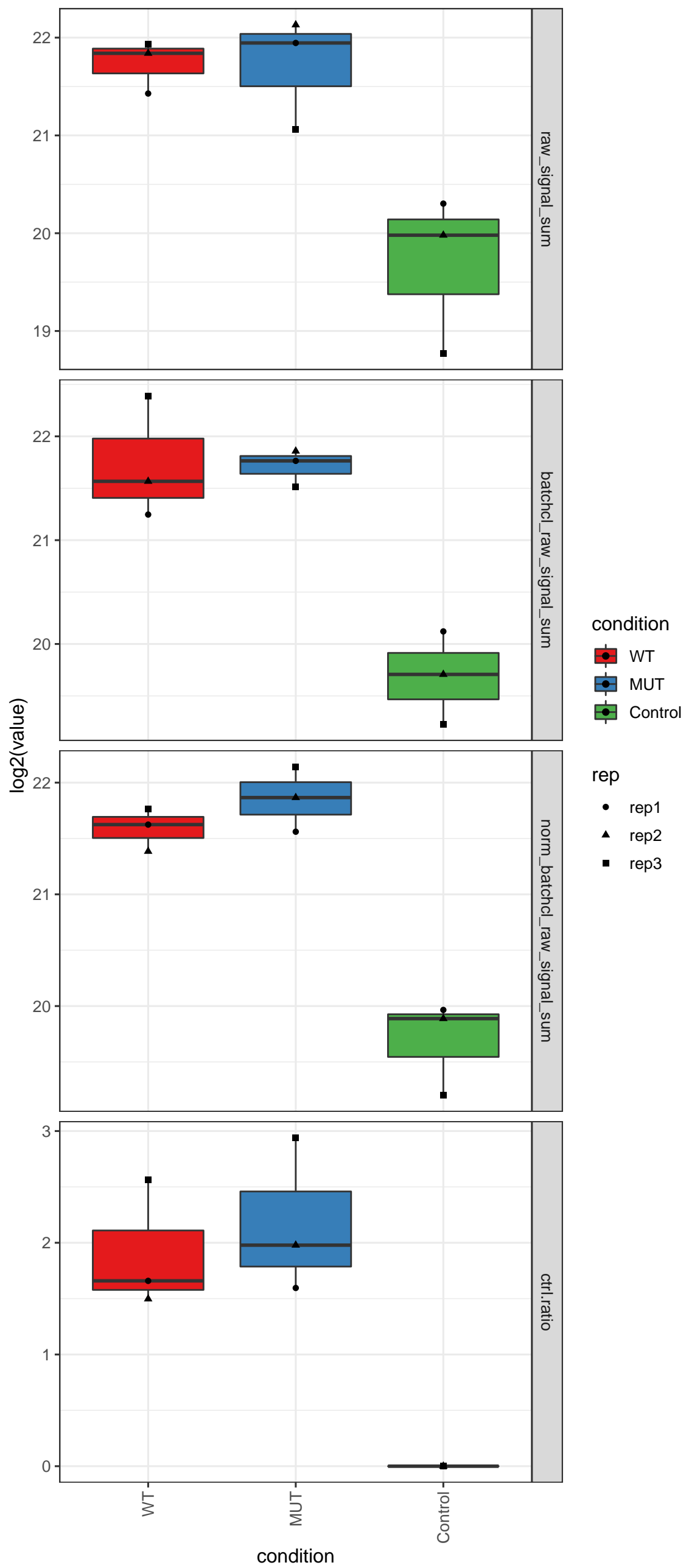
TRM1 – P15565|P15565–2

tRNA (guanine(26)–N(2))–dimethyltransferase, mitochondrial OS=Saccha



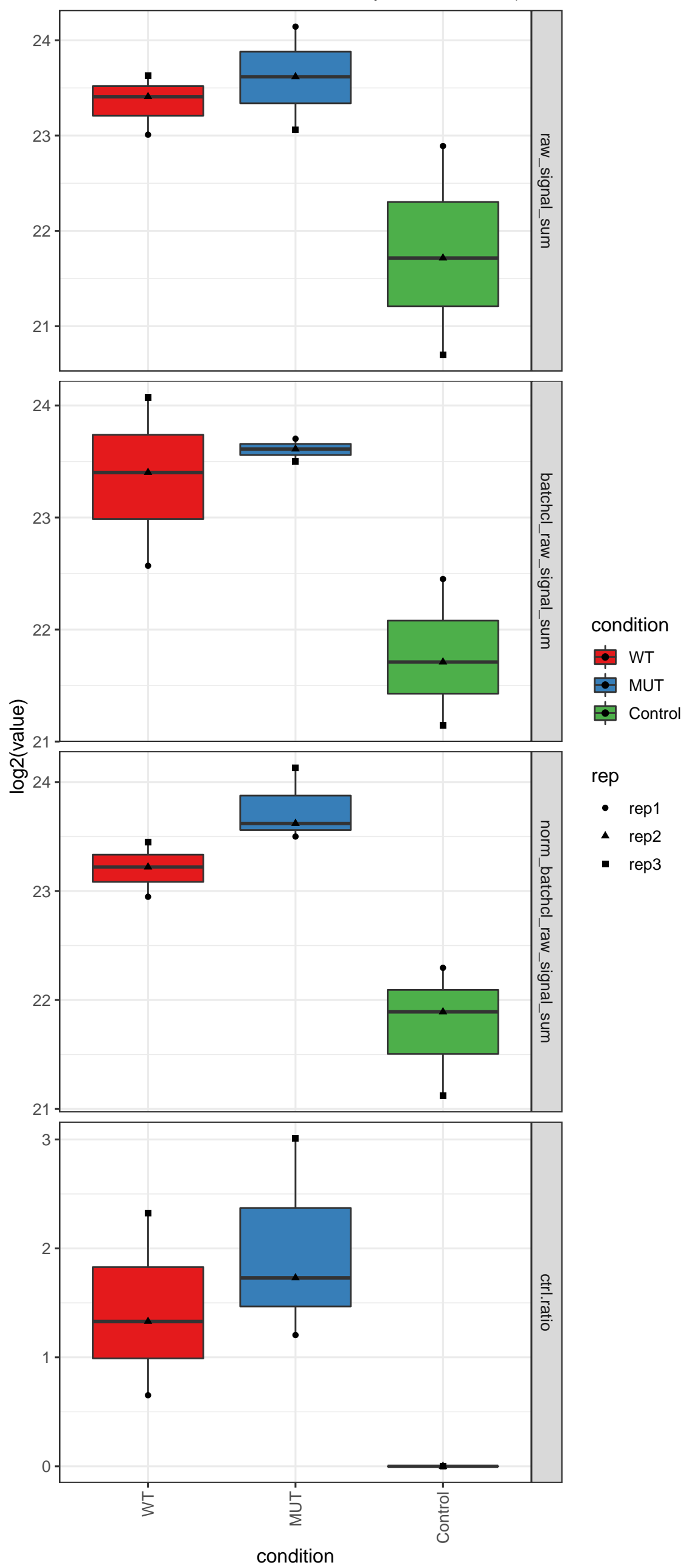
TRP3 – P00937

Multifunctional tryptophan biosynthesis protein OS=*Saccharomyces cerevisiae*



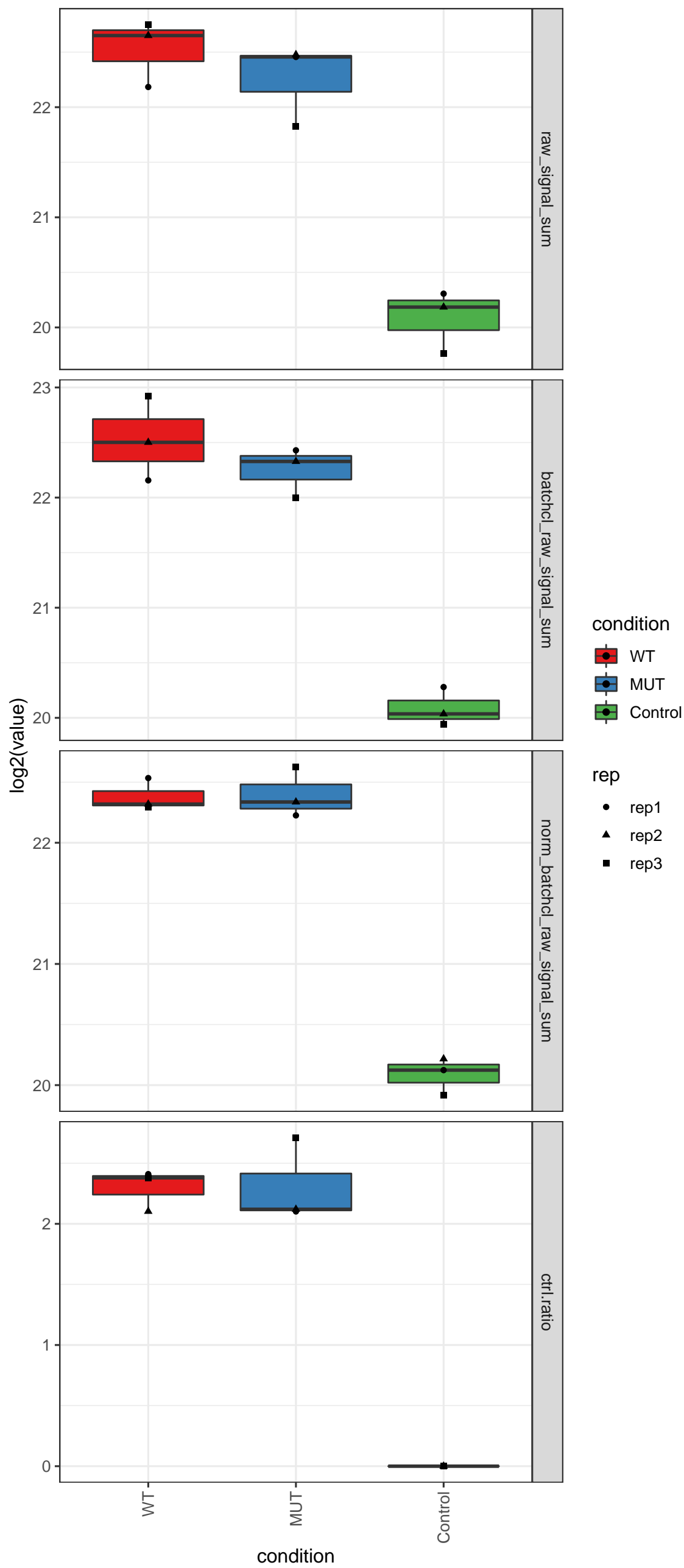
TSA1 – P34760

Peroxisredoxin TSA1 OS=Saccharomyces cerevisiae (strain ATCC 204508 /



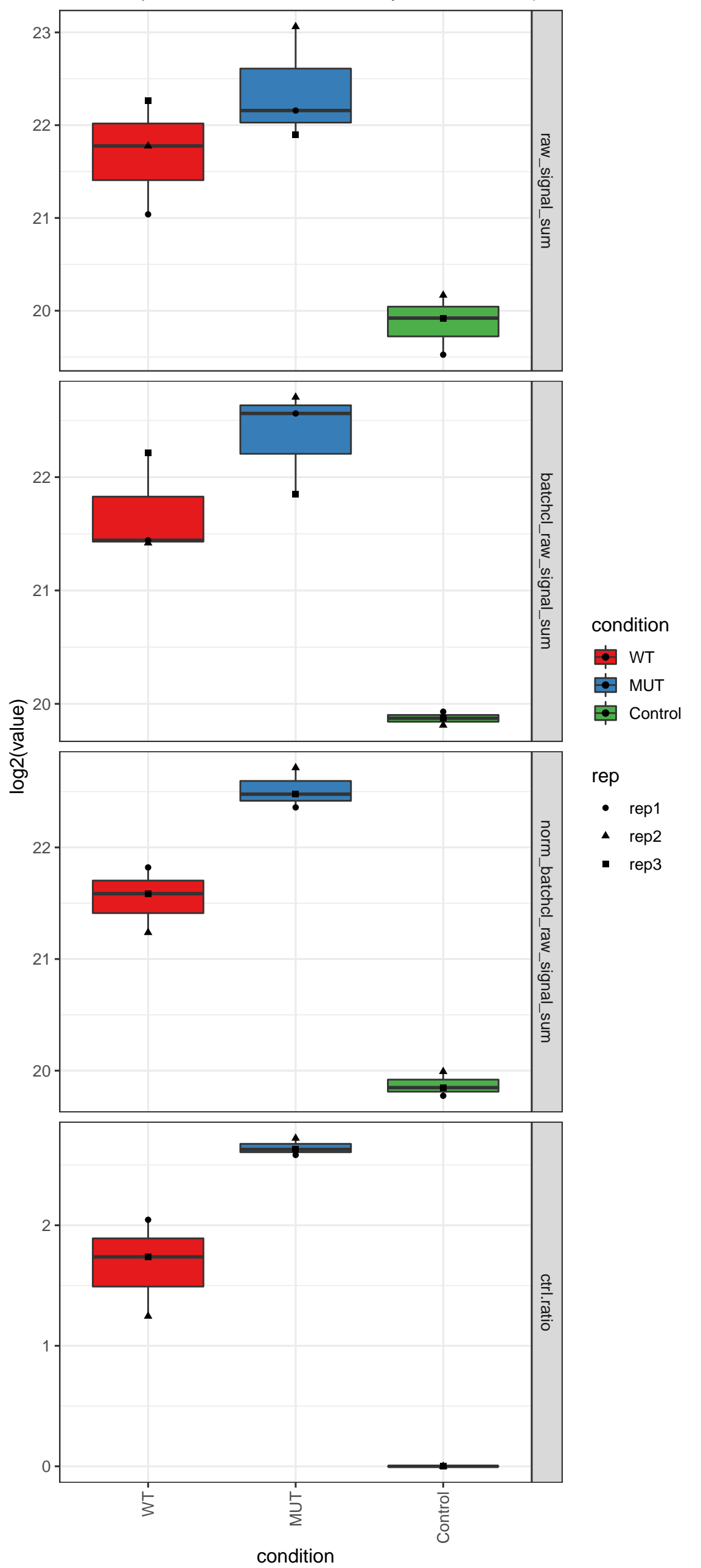
TSL1 – P38427

Trehalose synthase complex regulatory subunit TSL1 OS=Saccharomyces



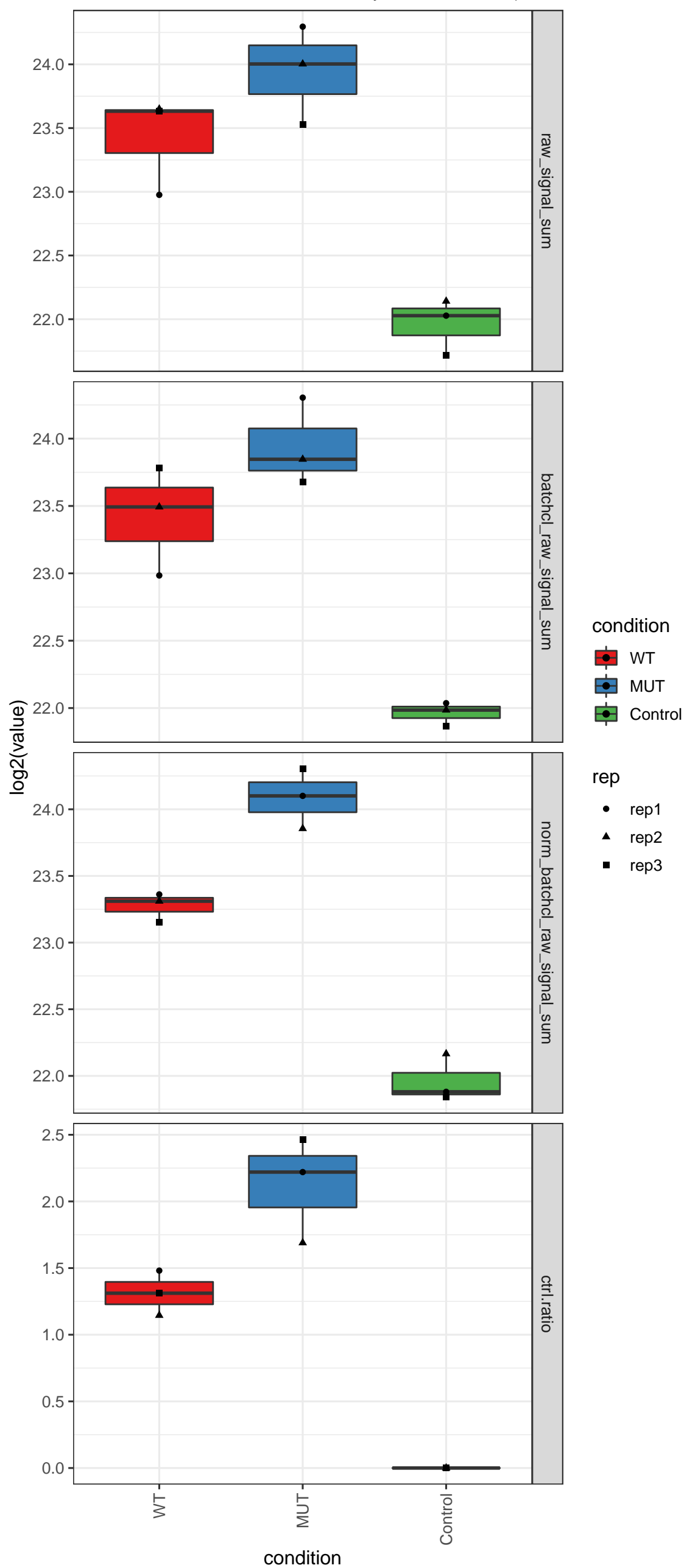
TUB1|TUB3 – P09733|P09734

Tubulin alpha-1 chain OS=*Saccharomyces cerevisiae* (strain ATCC 20450)



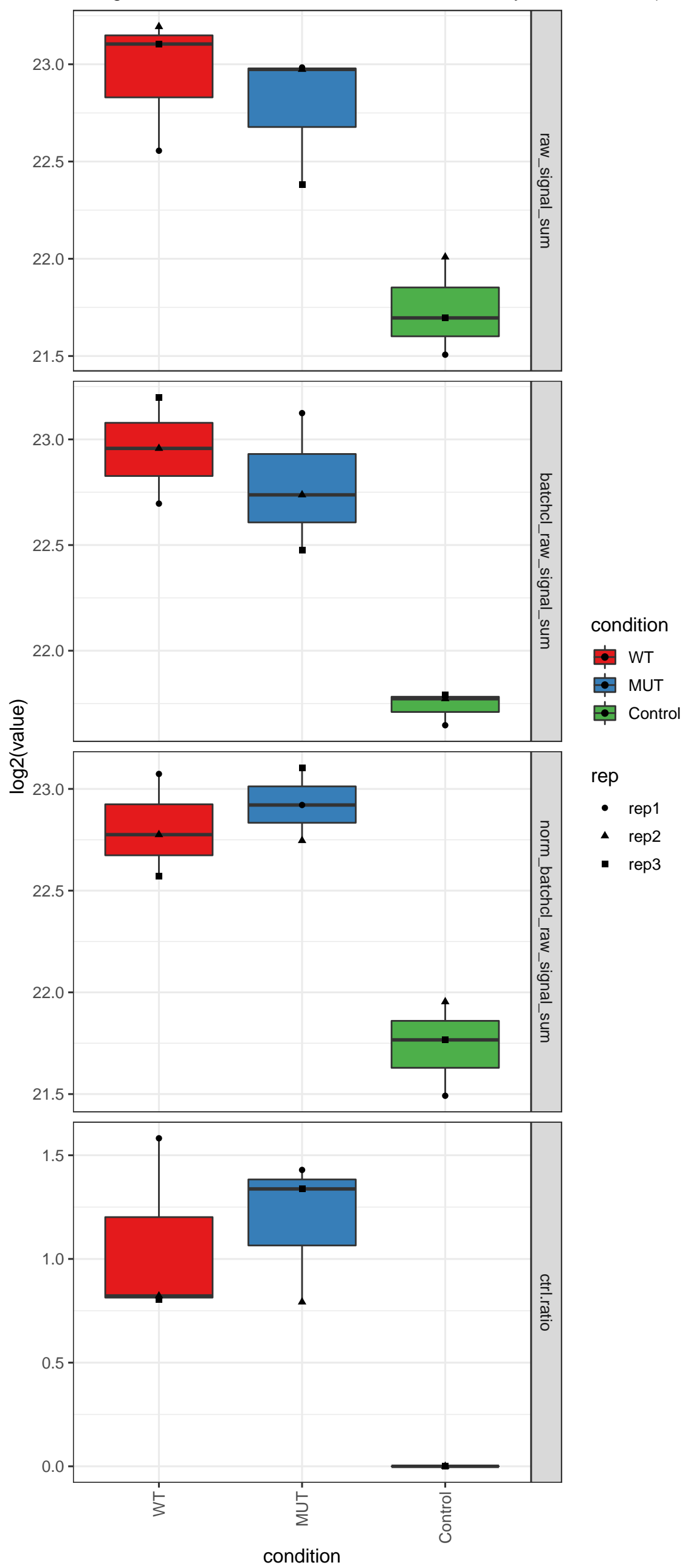
TUB2 – P02557

Tubulin beta chain OS=*Saccharomyces cerevisiae* (strain ATCC 204508 /



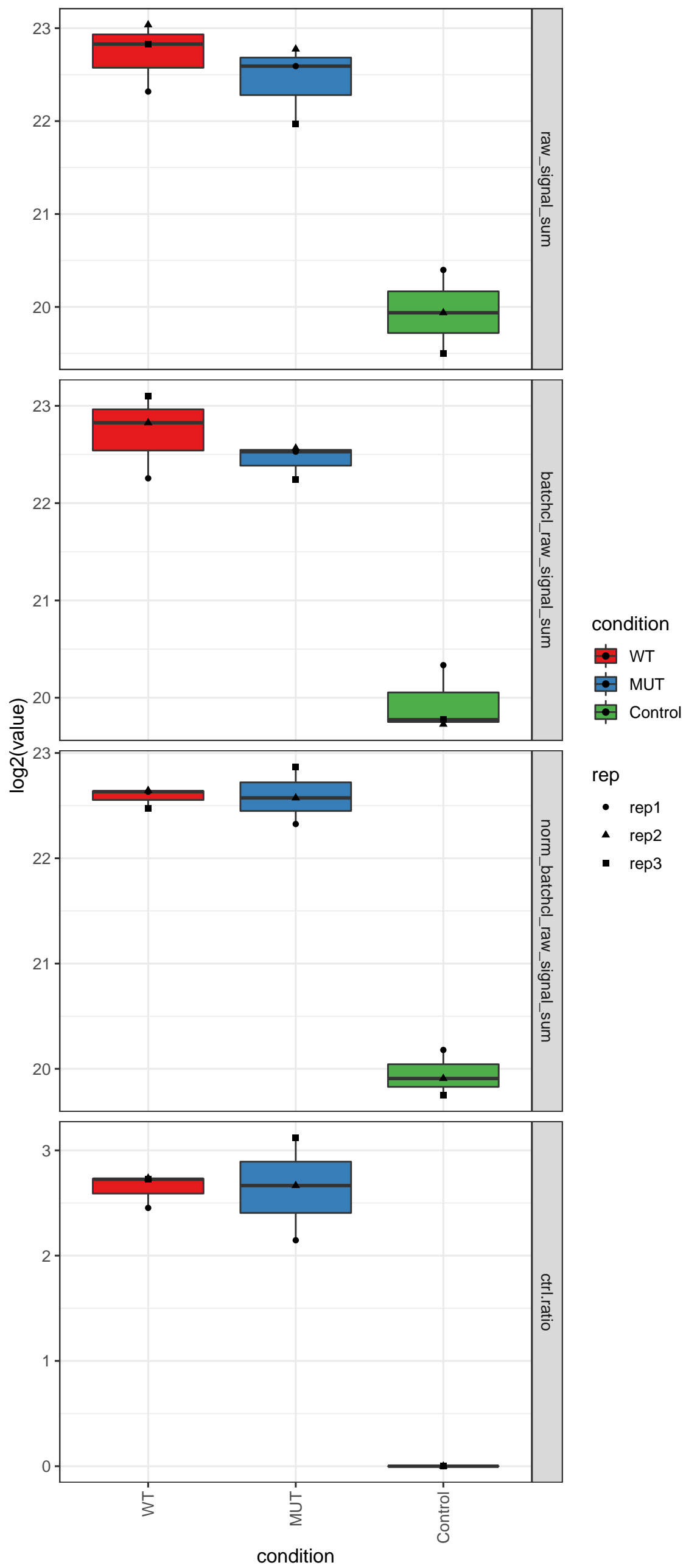
TUF1 – P02992

Elongation factor Tu, mitochondrial OS=*Saccharomyces cerevisiae* (strain



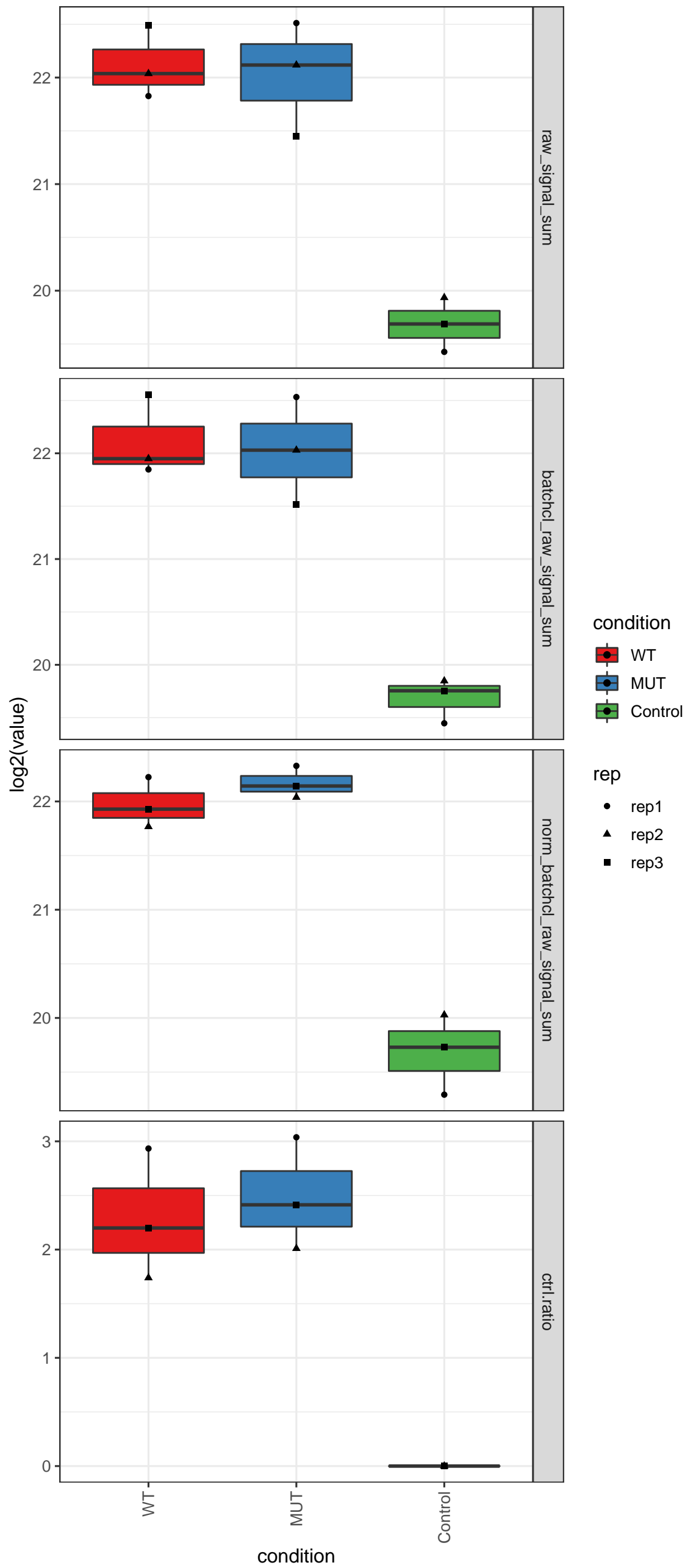
TYS1 – P36421

Tyrosine--tRNA ligase, cytoplasmic OS=*Saccharomyces cerevisiae* (strain



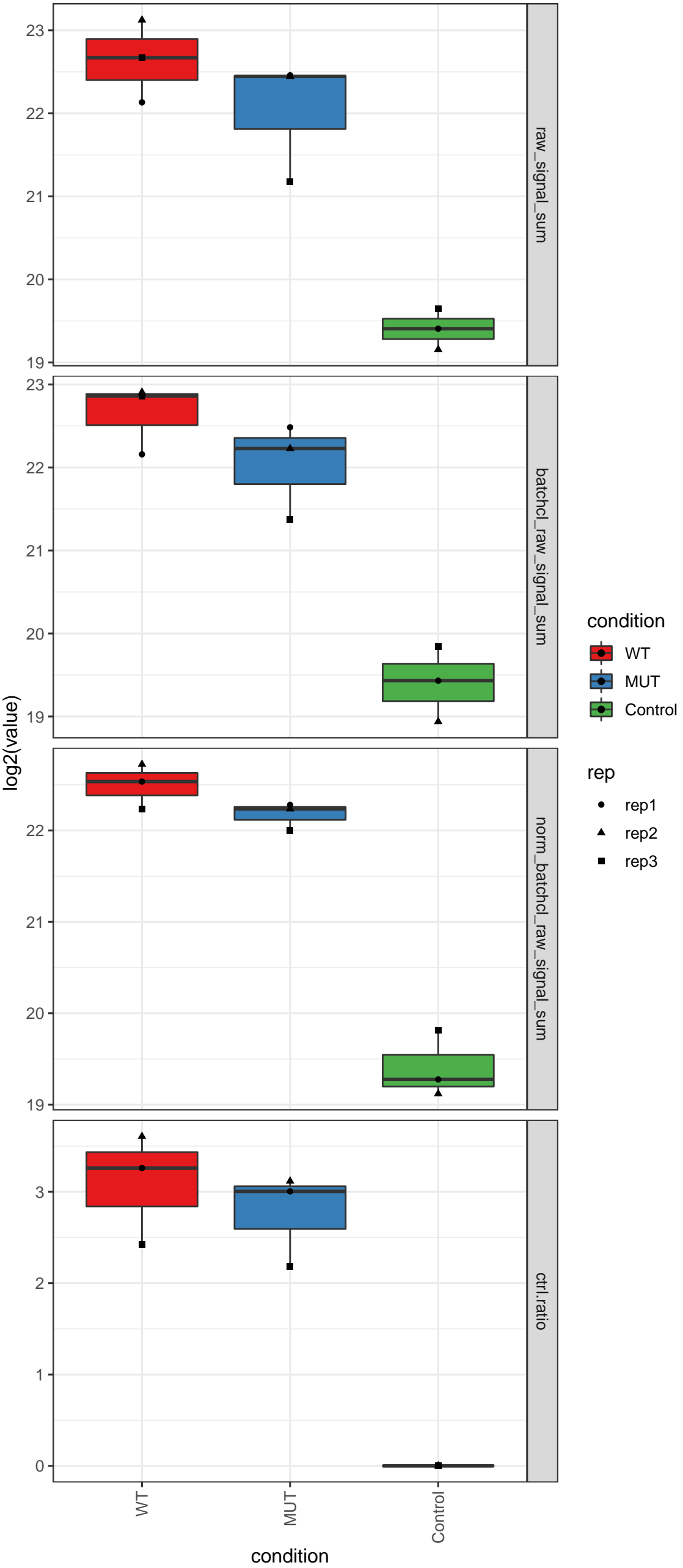
UBA1 – P22515

Ubiquitin-activating enzyme E1 1 OS=Saccharomyces cerevisiae (strain A



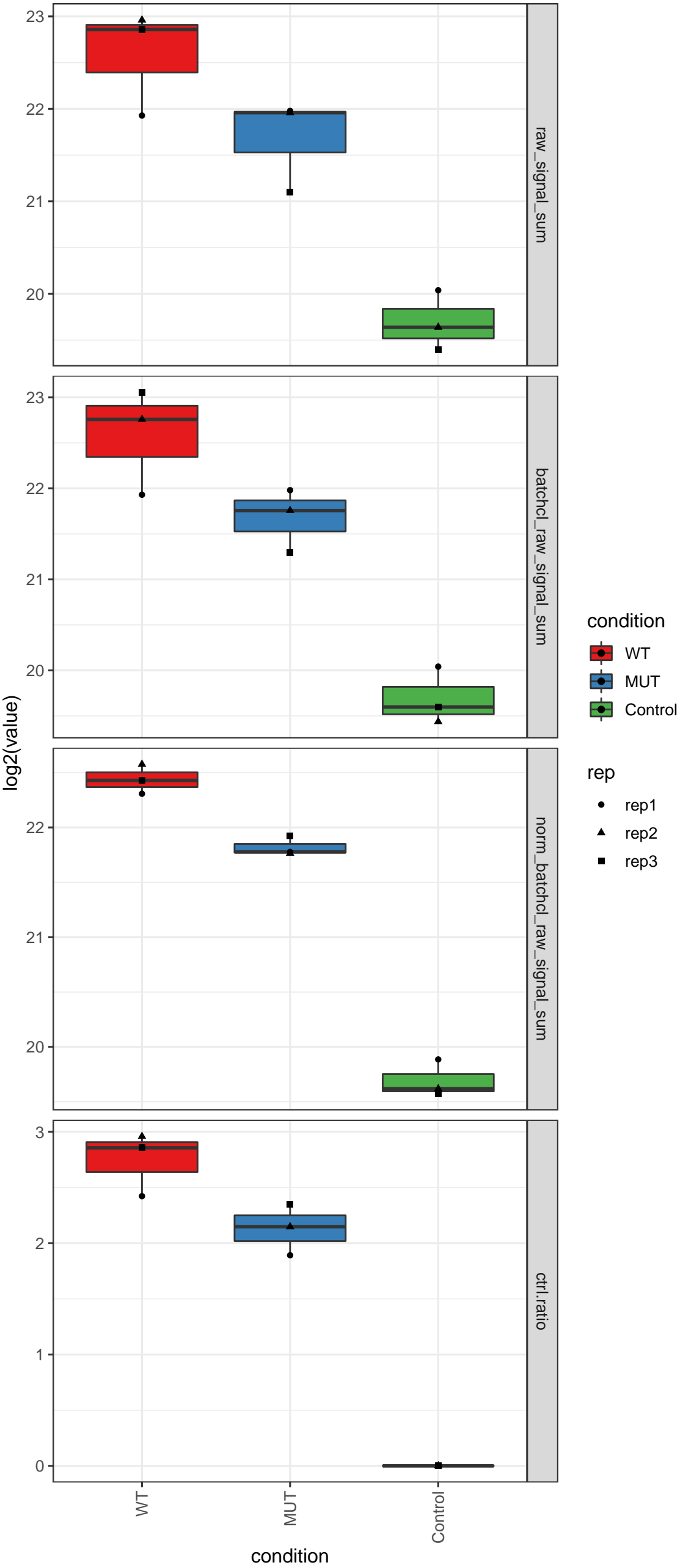
UBP3 – Q01477

Ubiquitin carboxyl-terminal hydrolase 3 OS=Saccharomyces cerevisiae (strain



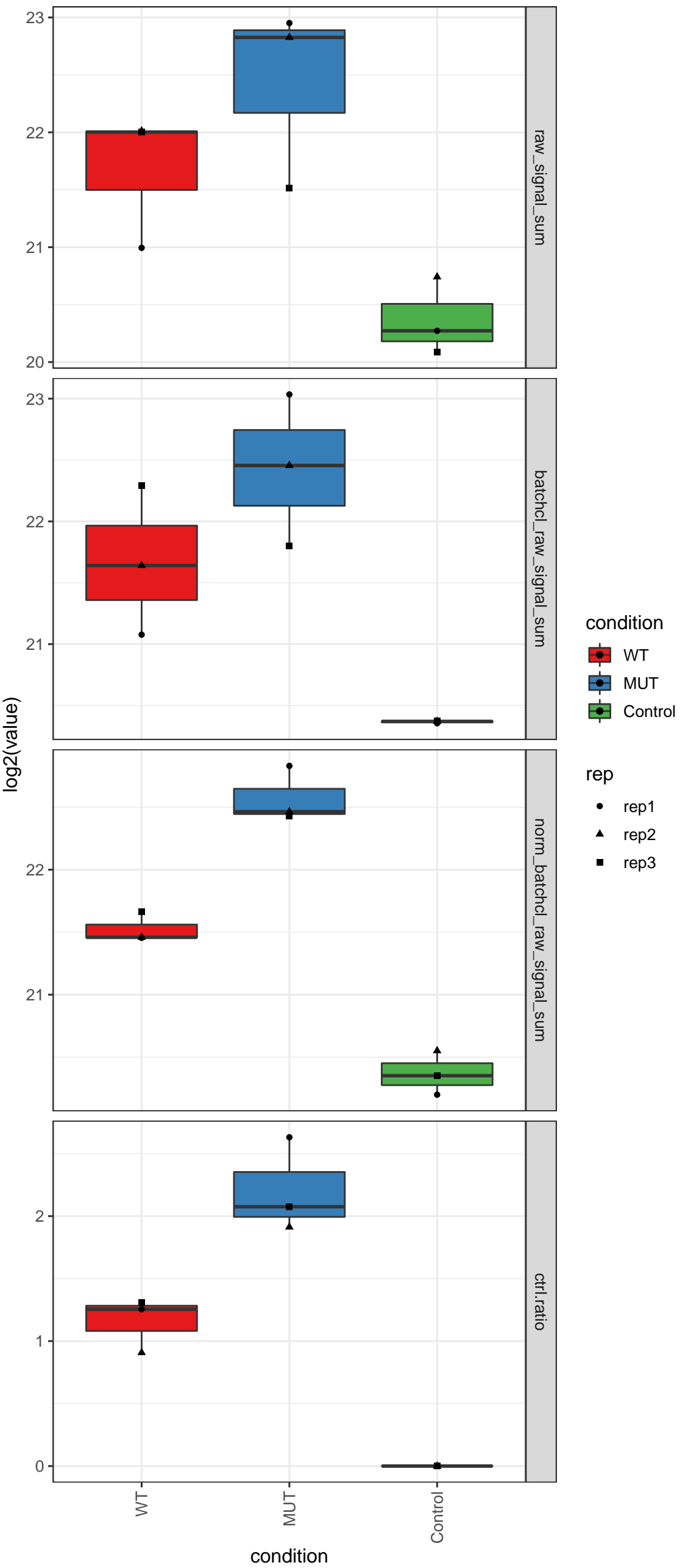
UBP6 – P43593

Ubiquitin carboxyl-terminal hydrolase 6 OS=Saccharomyces cerevisiae (str. *S. cerevisiae*)



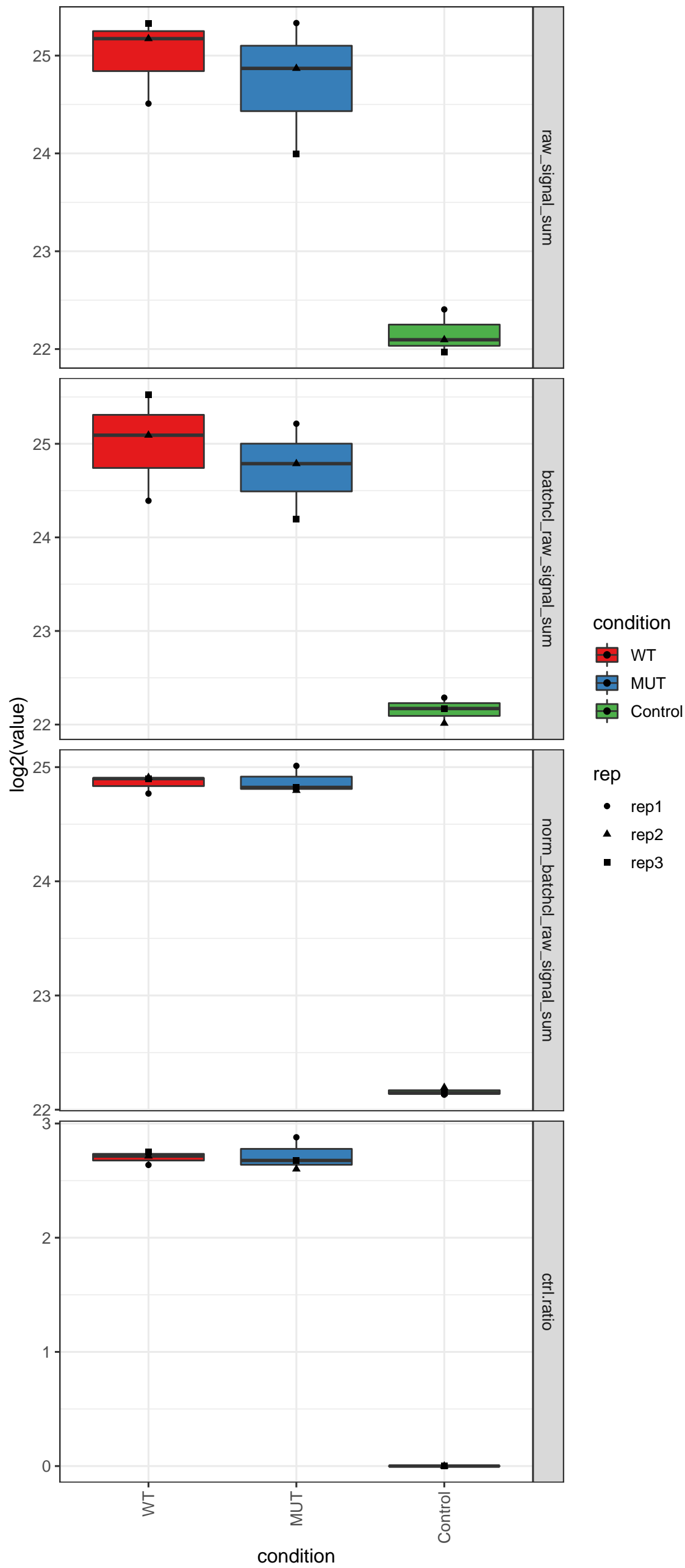
UBP7 – P40453

Ubiquitin carboxyl-terminal hydrolase 7 OS=Saccharomyces cerevisiae (st



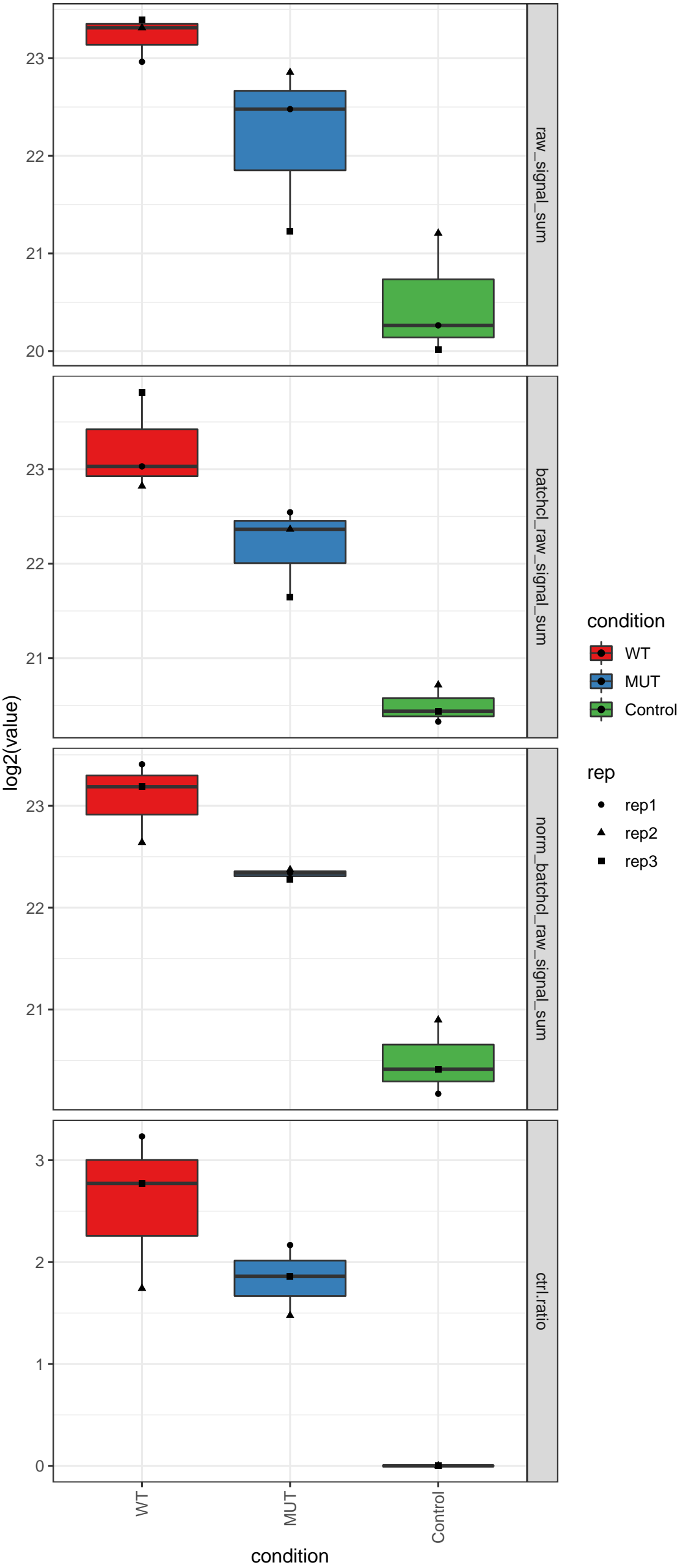
UGP1 – P32861

UTP--glucose-1-phosphate uridylyltransferase OS=Saccharomyces cere



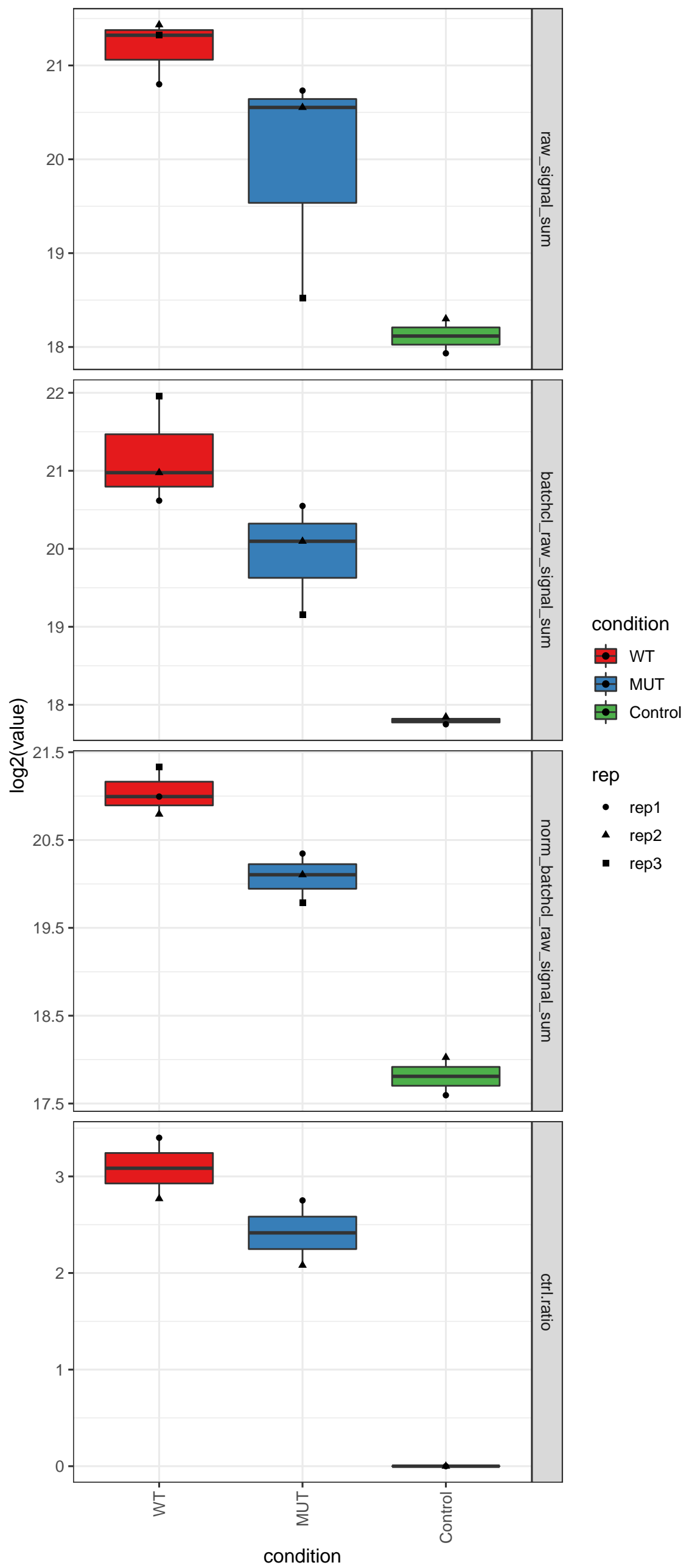
ULS1 – Q08562

ATP-dependent helicase ULS1 OS=*Saccharomyces cerevisiae* (strain ATCC 25716)



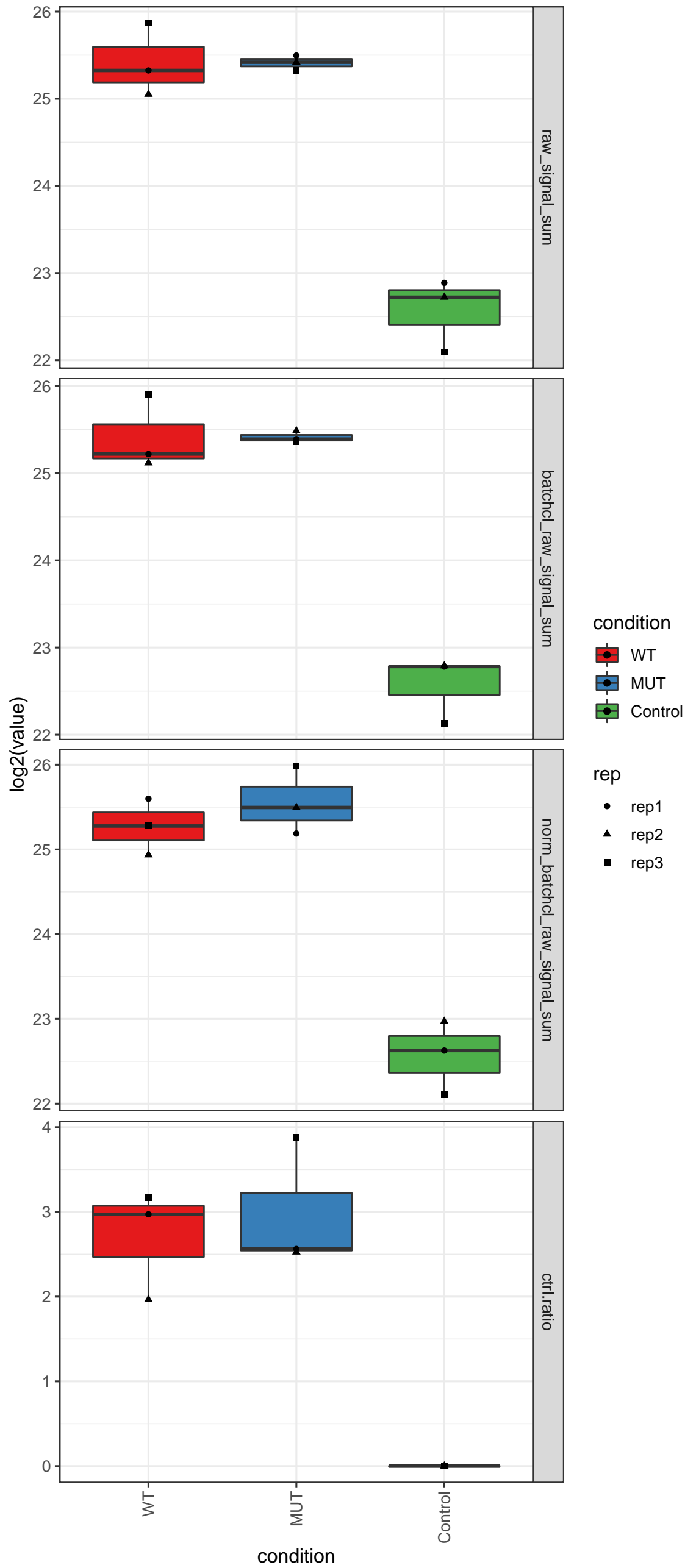
UME6 – P39001

Transcriptional regulatory protein UME6 OS=*Saccharomyces cerevisiae* (



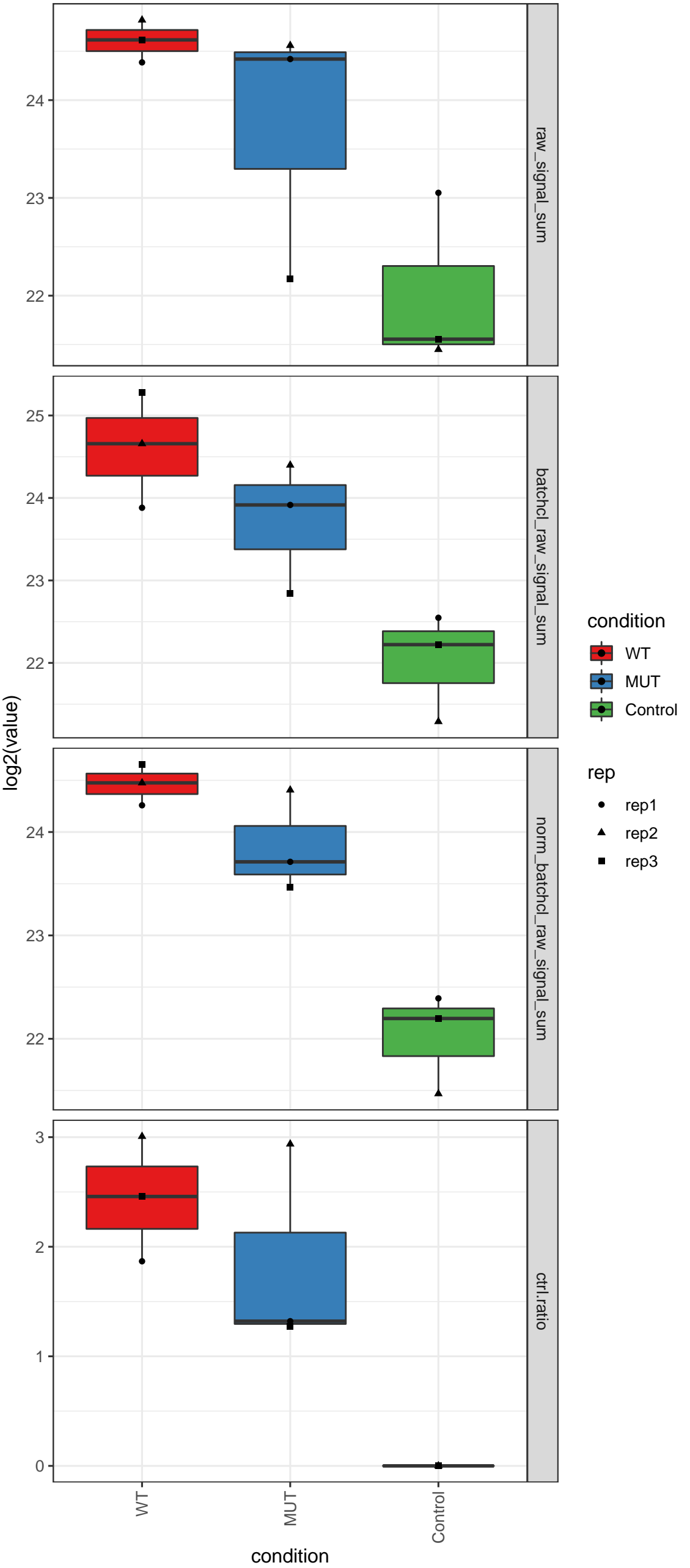
URA2 – P07259

Protein URA2 OS=*Saccharomyces cerevisiae* (strain ATCC 204508 / S288

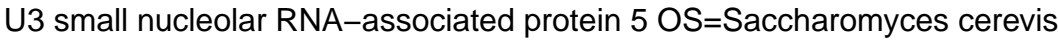


UTP23 – Q12339

rRNA-processing protein UTP23 OS=*Saccharomyces cerevisiae* (strain ATCC 22016 / S288c)

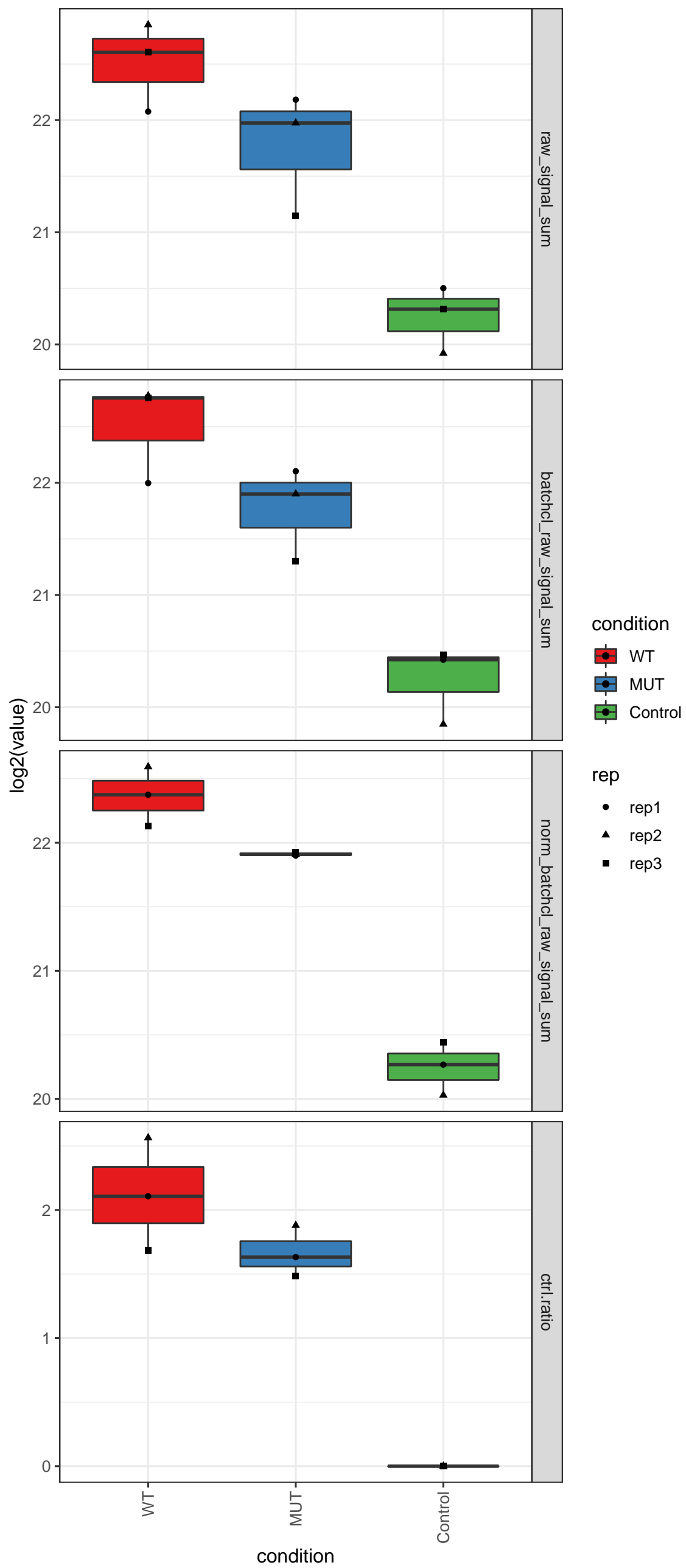


U3 small nucleolar RNA-associated protein 5 OS=Saccharomyces cerevis



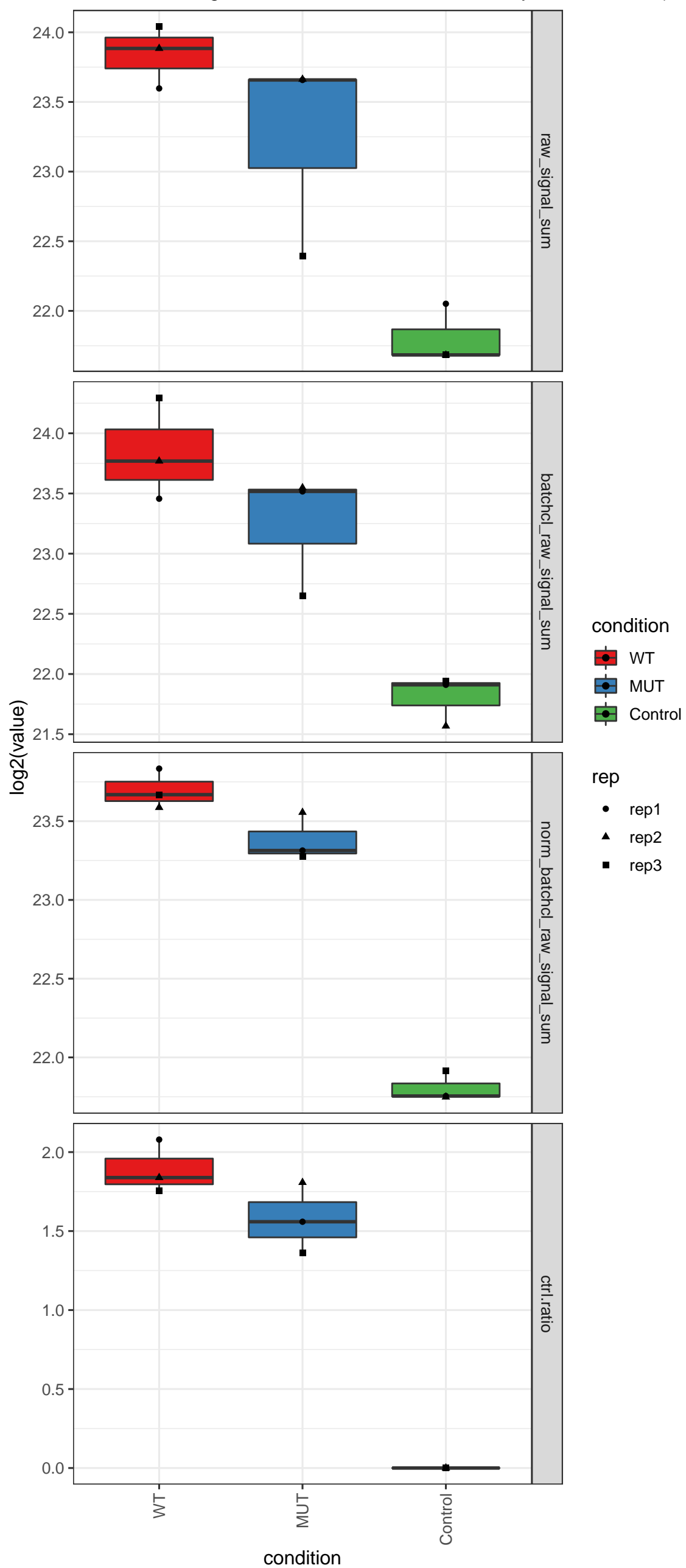
VAC8 – P39968

Vacuolar protein 8 OS=*Saccharomyces cerevisiae* (strain ATCC 204508 / S



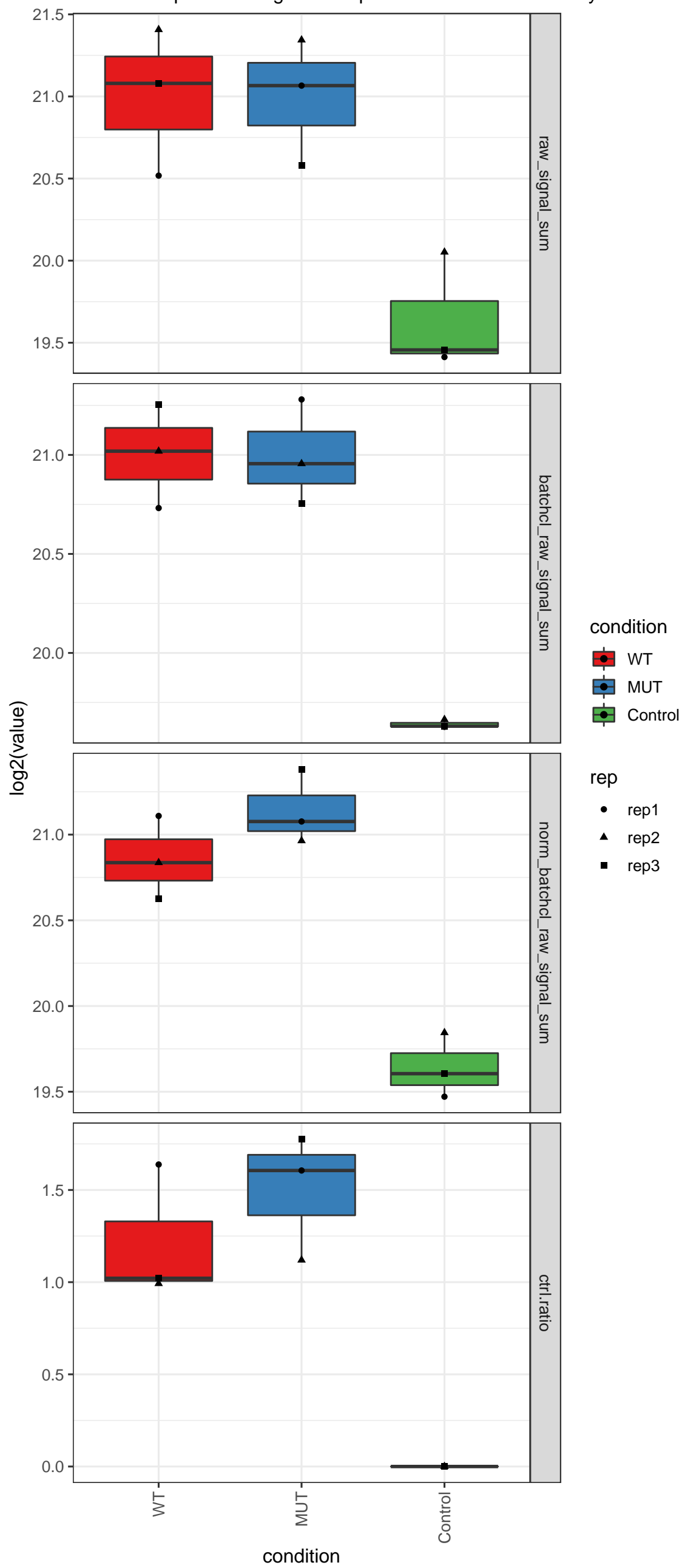
VAS1 – P07806|P07806–2

Valine--tRNA ligase, mitochondrial OS=*Saccharomyces cerevisiae* (strain



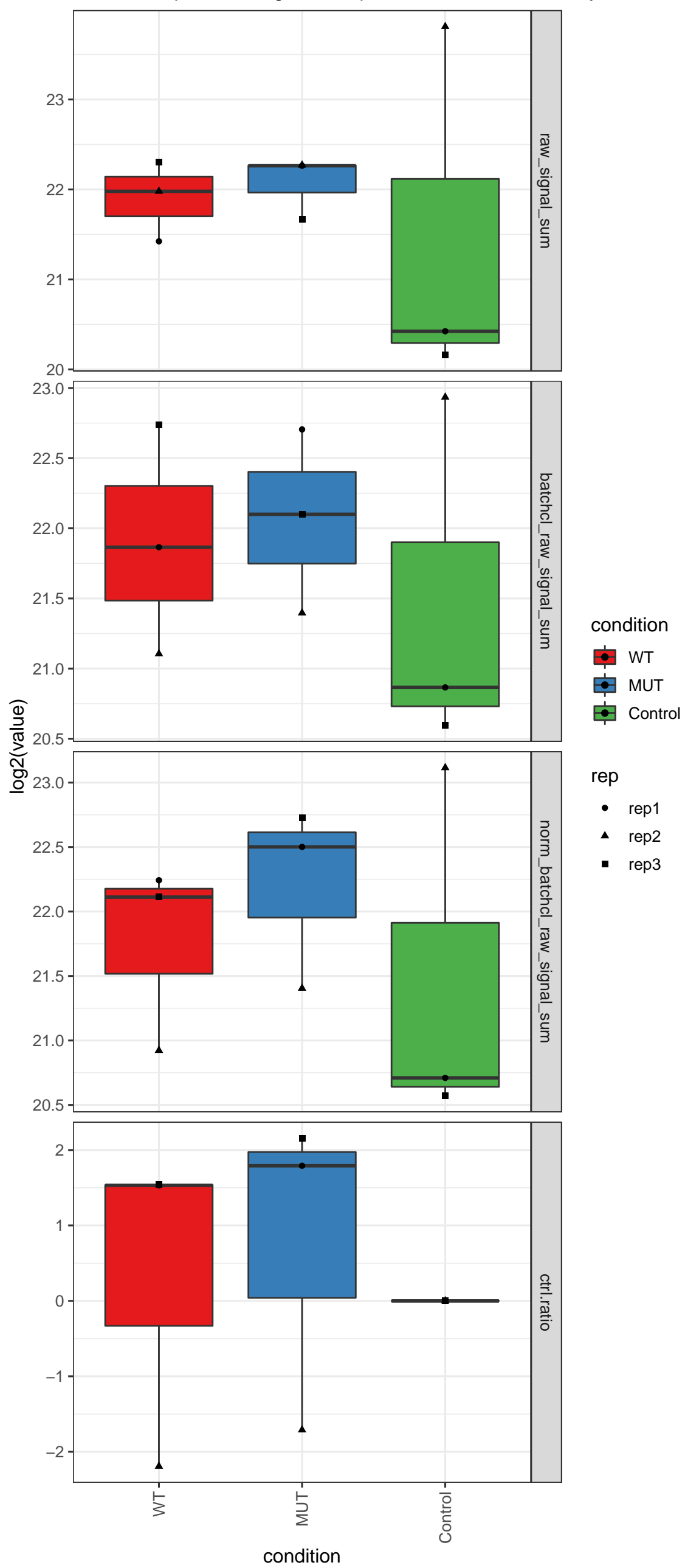
VID27 – P40157

Vacuolar import and degradation protein 27 OS=*Saccharomyces cerevisiae*



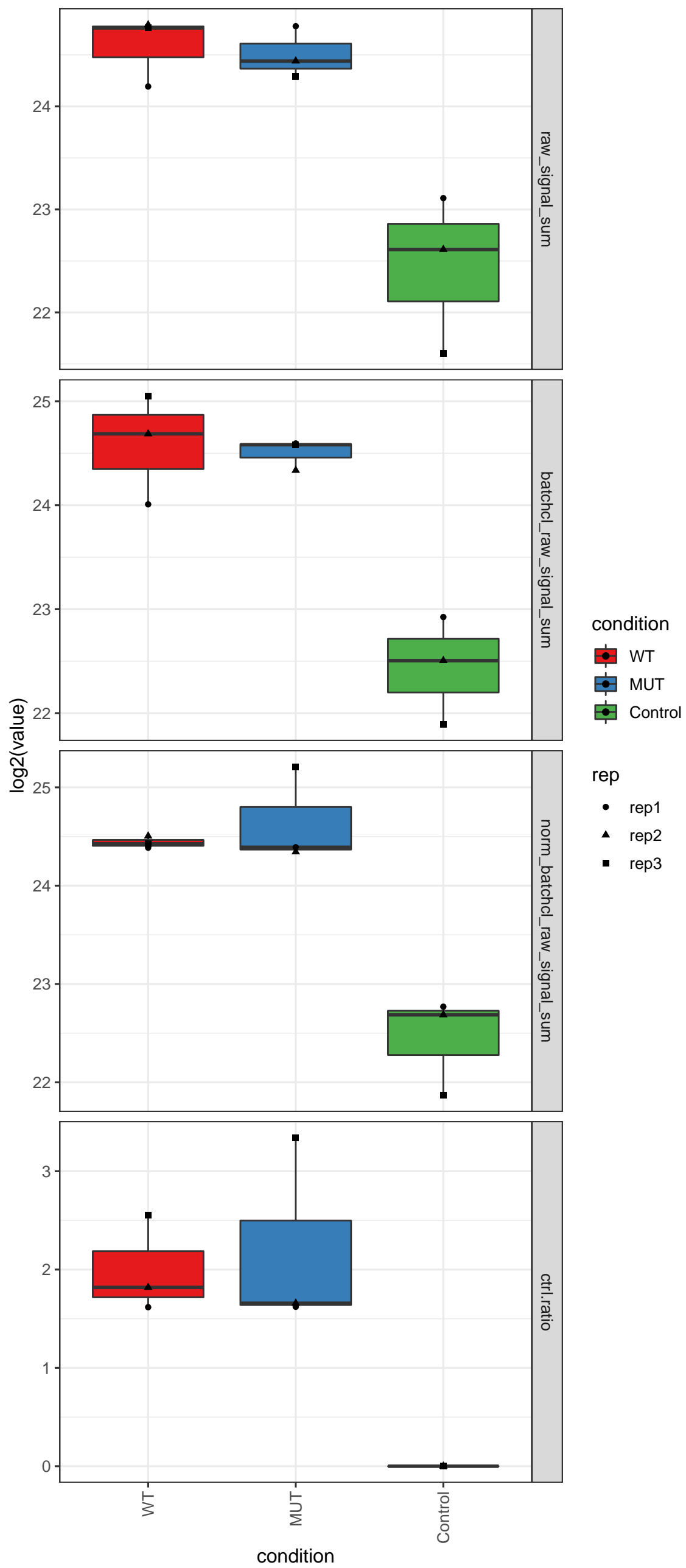
VID30 – P53076

Vacuolar import and degradation protein 30 OS=*Saccharomyces cerevisiae*



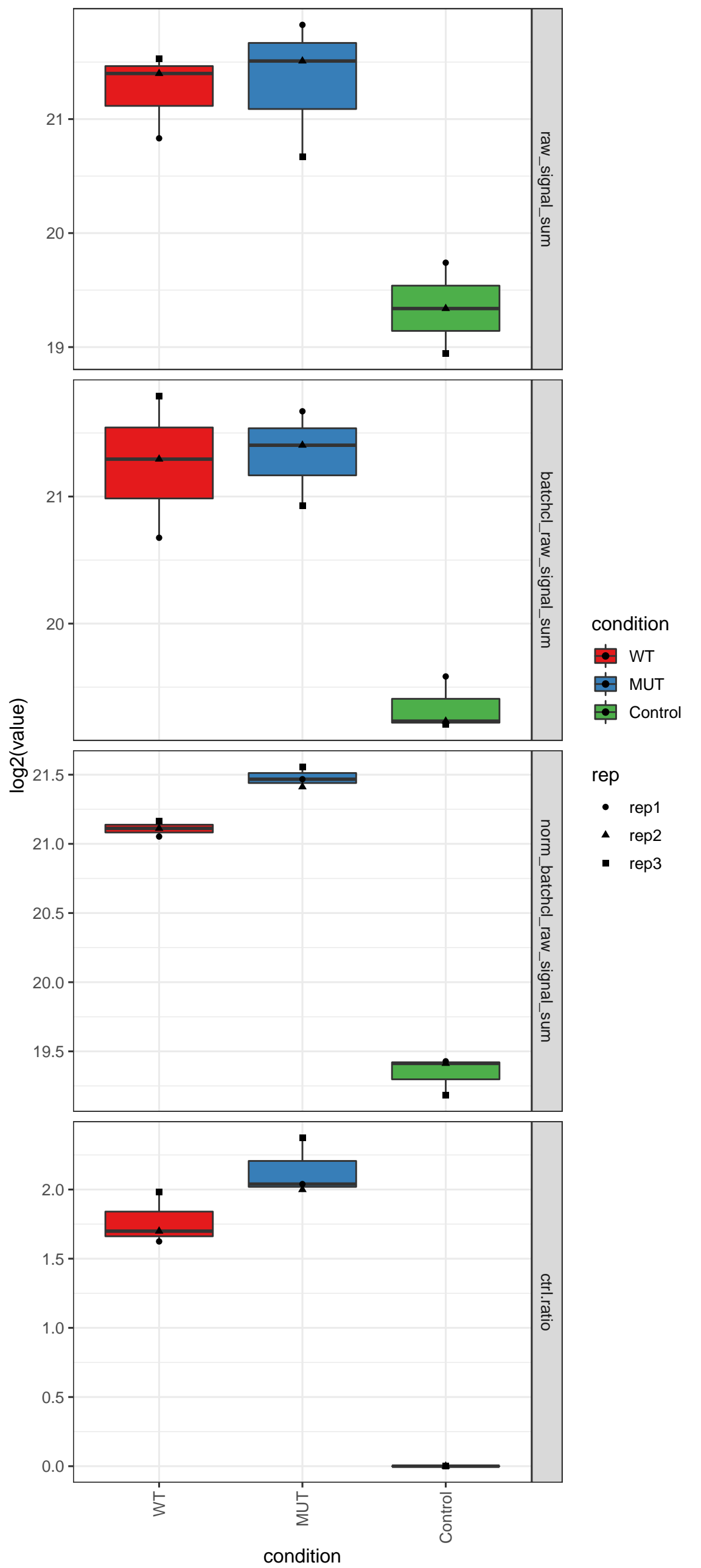
VMA1 – P17255

V-type proton ATPase catalytic subunit A OS=*Saccharomyces cerevisiae* (



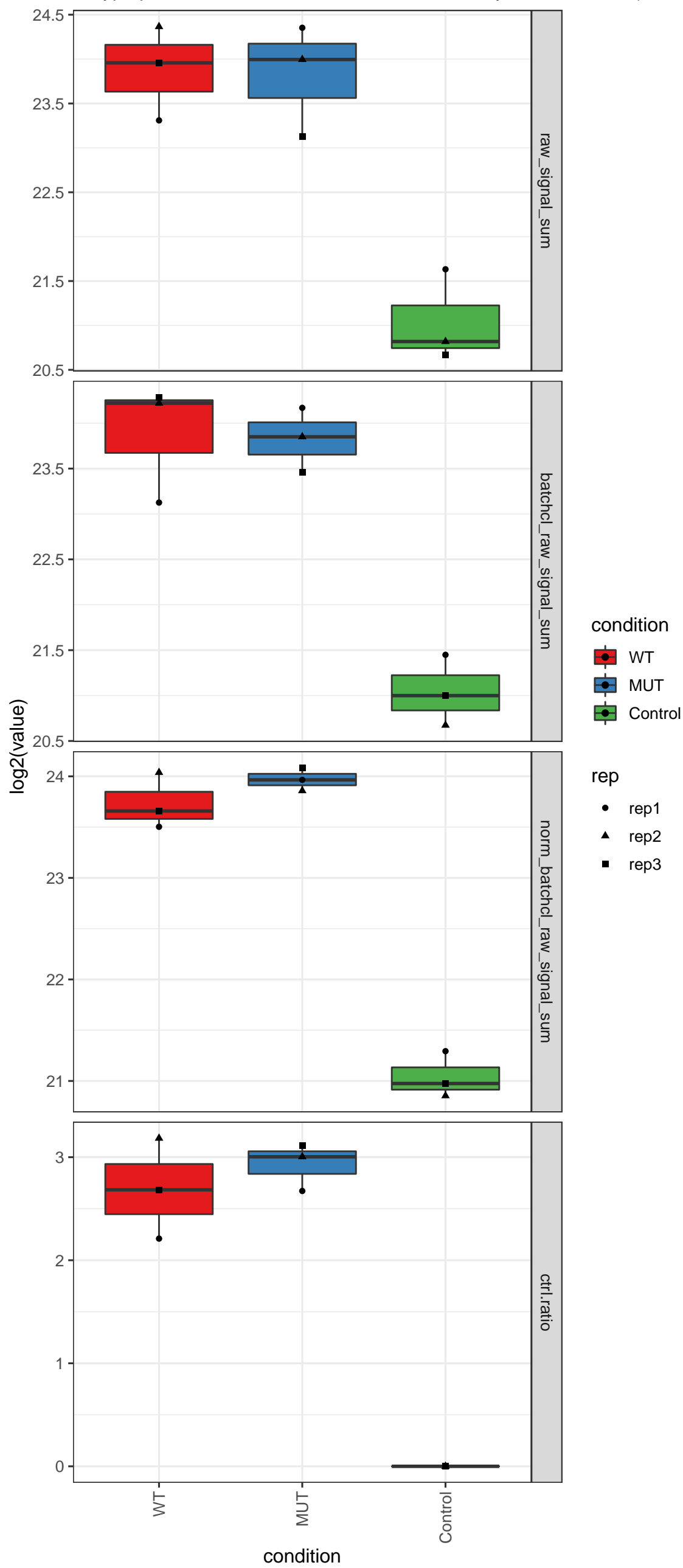
VMA13 – P41807

V-type proton ATPase subunit H OS=*Saccharomyces cerevisiae* (strain *A*)



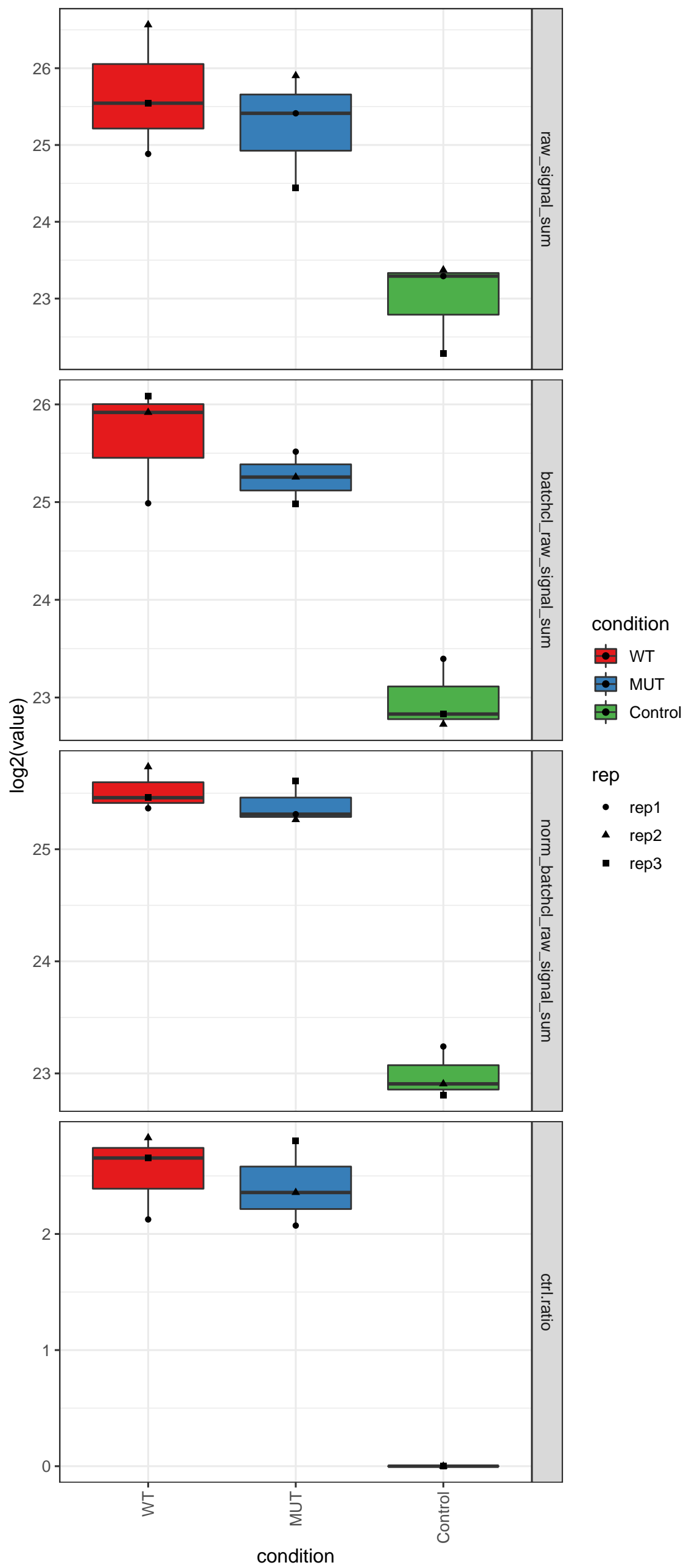
VMA2 – P16140

V-type proton ATPase subunit B OS=Saccharomyces cerevisiae (strain A)



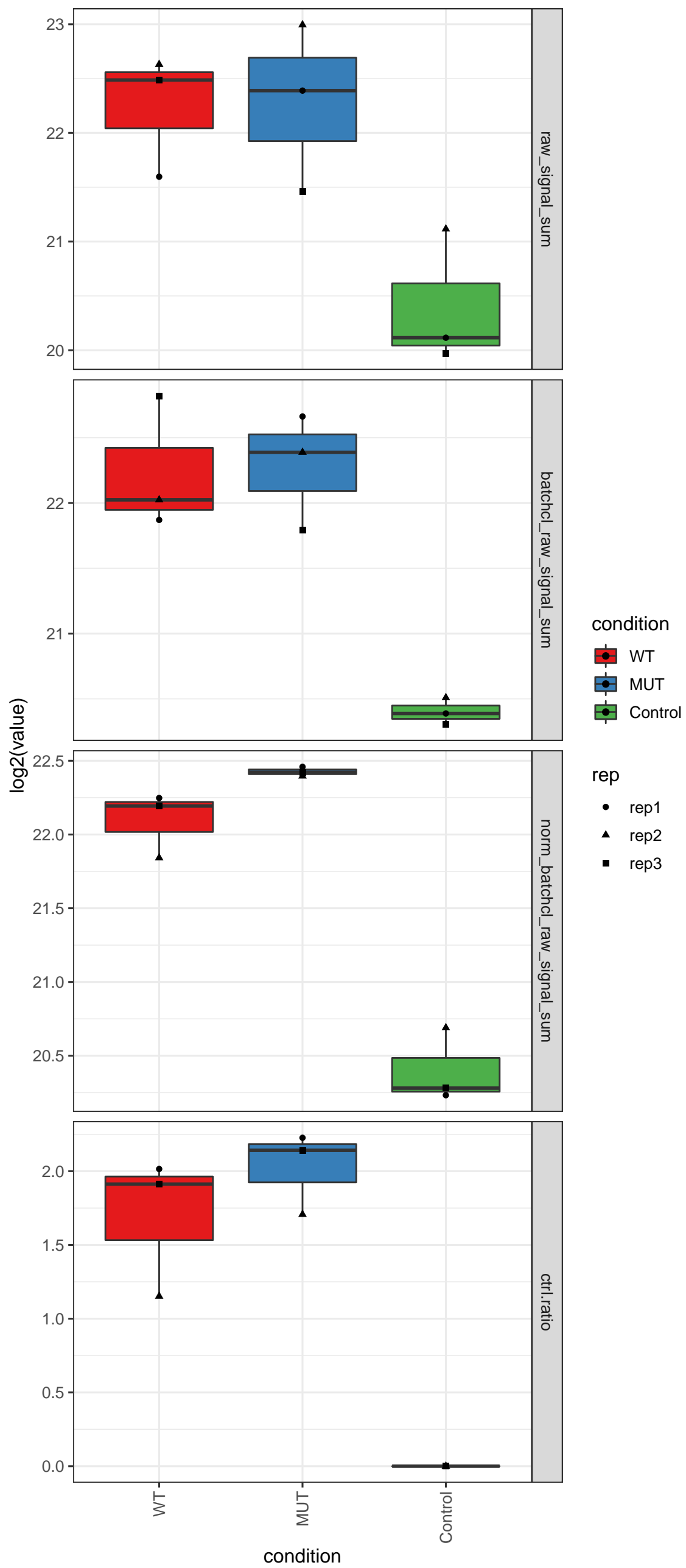
VPS1 – P21576

Vacuolar protein sorting–associated protein 1 OS=*Saccharomyces cerevisiae*



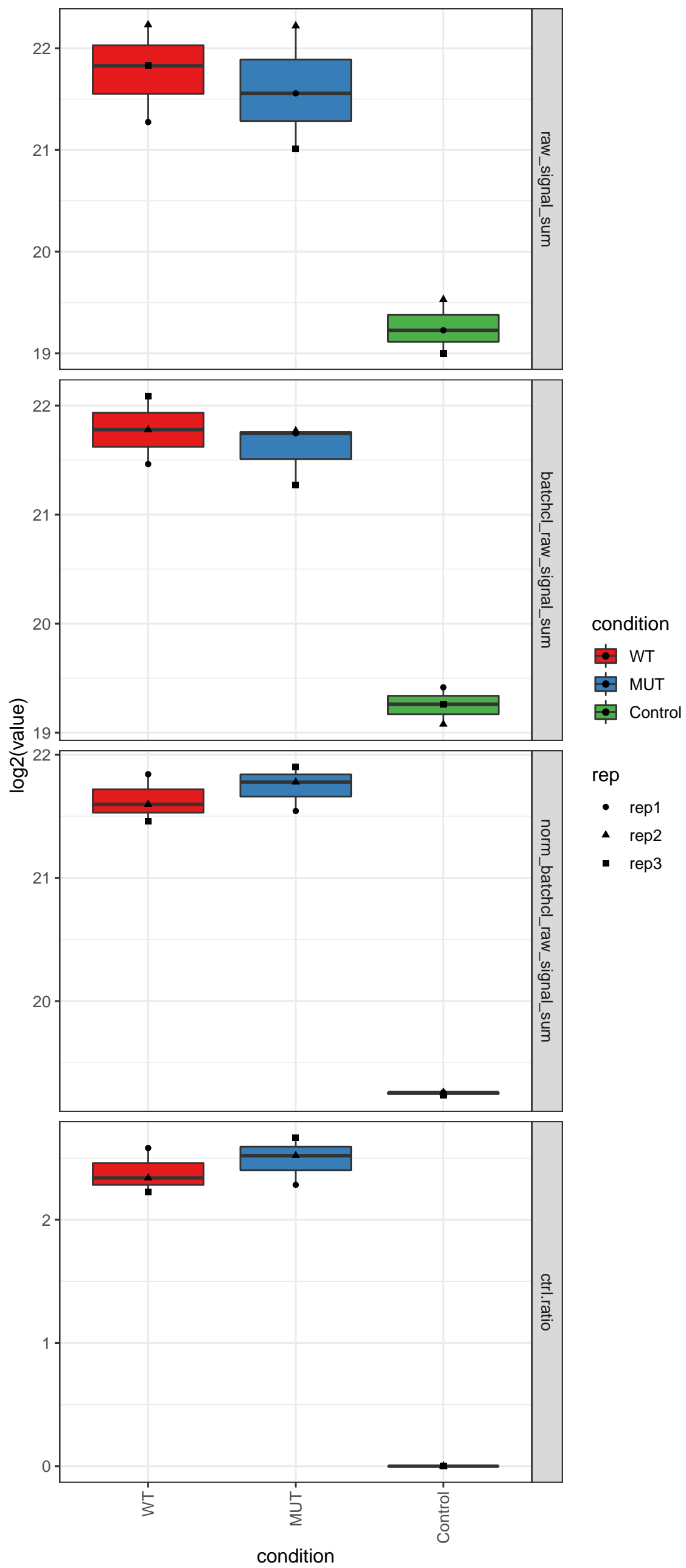
VPS17 – P32913

Vacuolar protein sorting–associated protein 17 OS=*Saccharomyces cerevisiae*



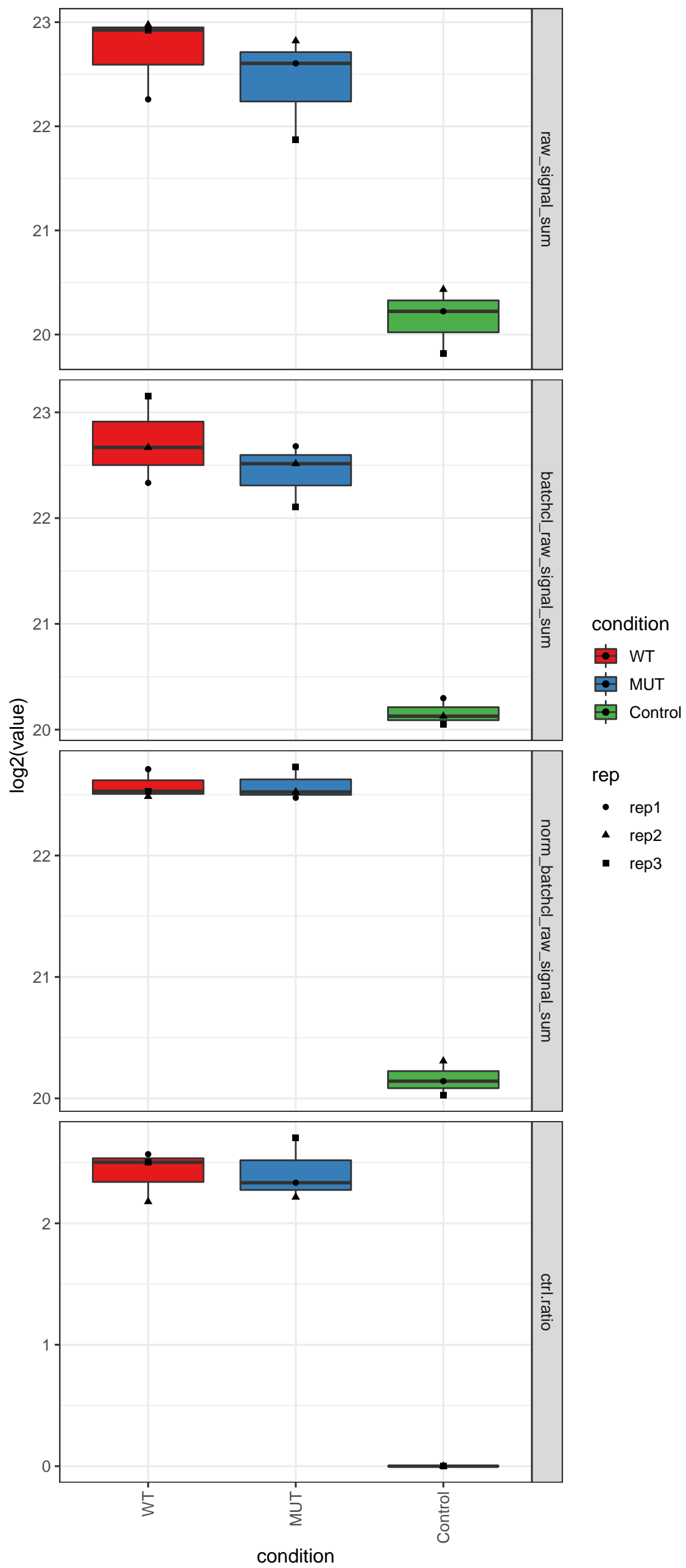
VPS33 – P20795

Vacuolar protein sorting–associated protein 33 OS=Saccharomyces cerevisiae



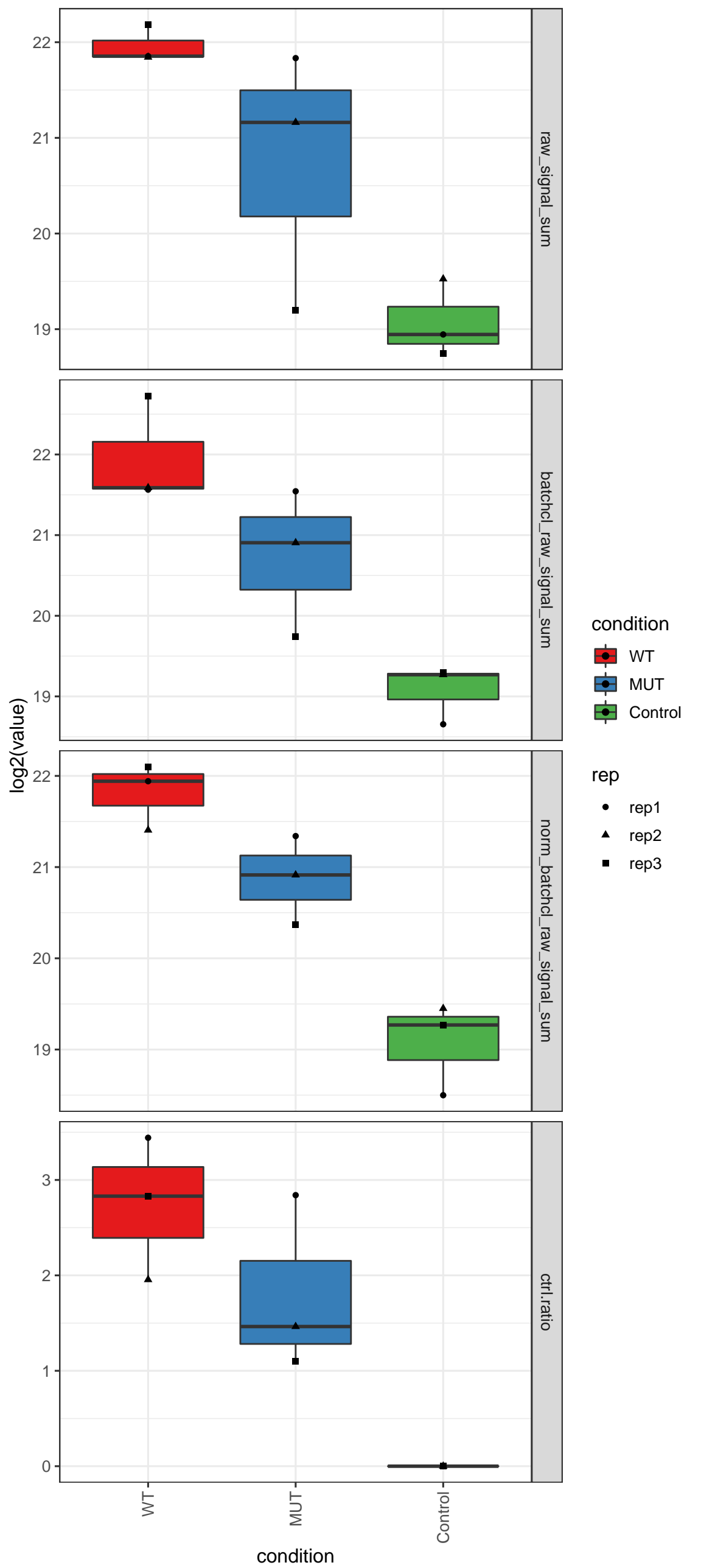
VPS5 – Q92331

Vacuolar protein sorting–associated protein 5 OS=Saccharomyces cerevis



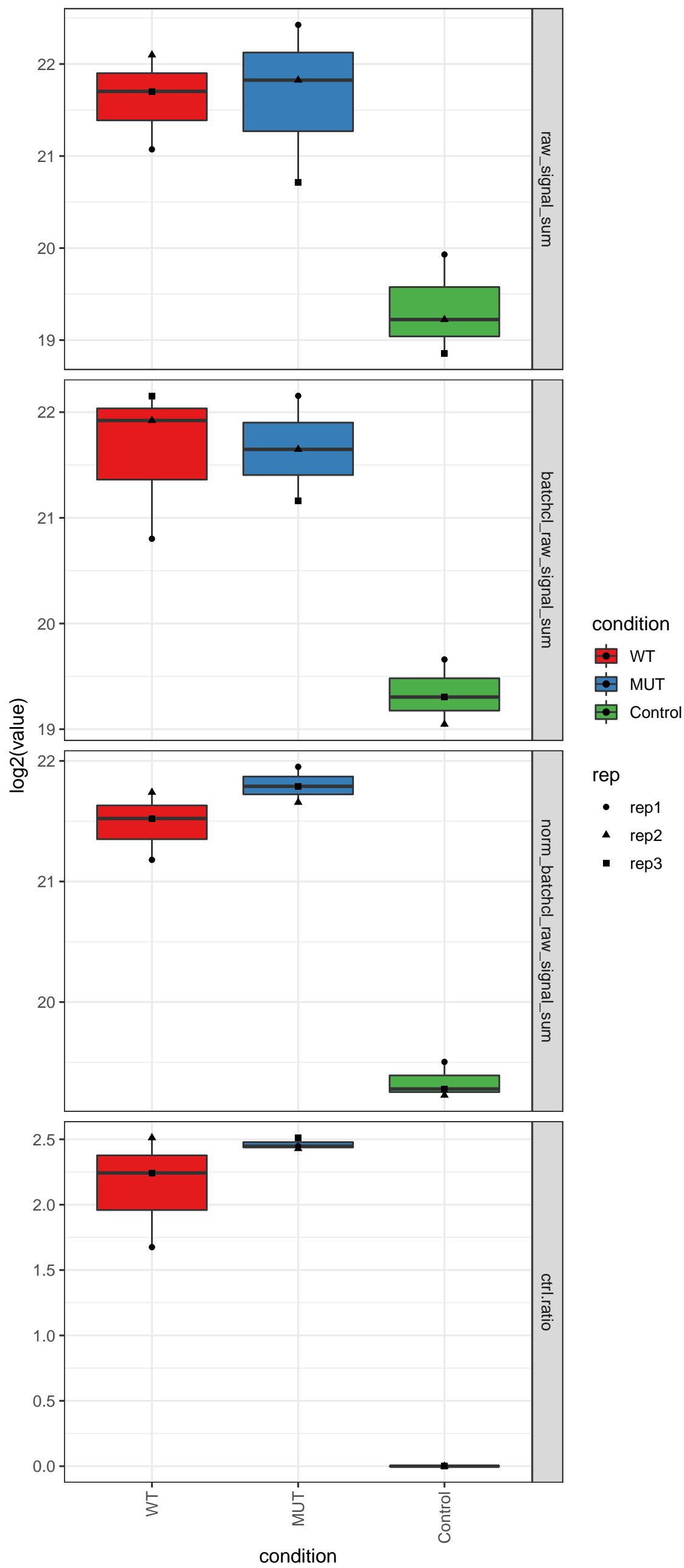
VPS72 – Q03388

Vacuolar protein sorting–associated protein 72 OS=*Saccharomyces cerevisiae*



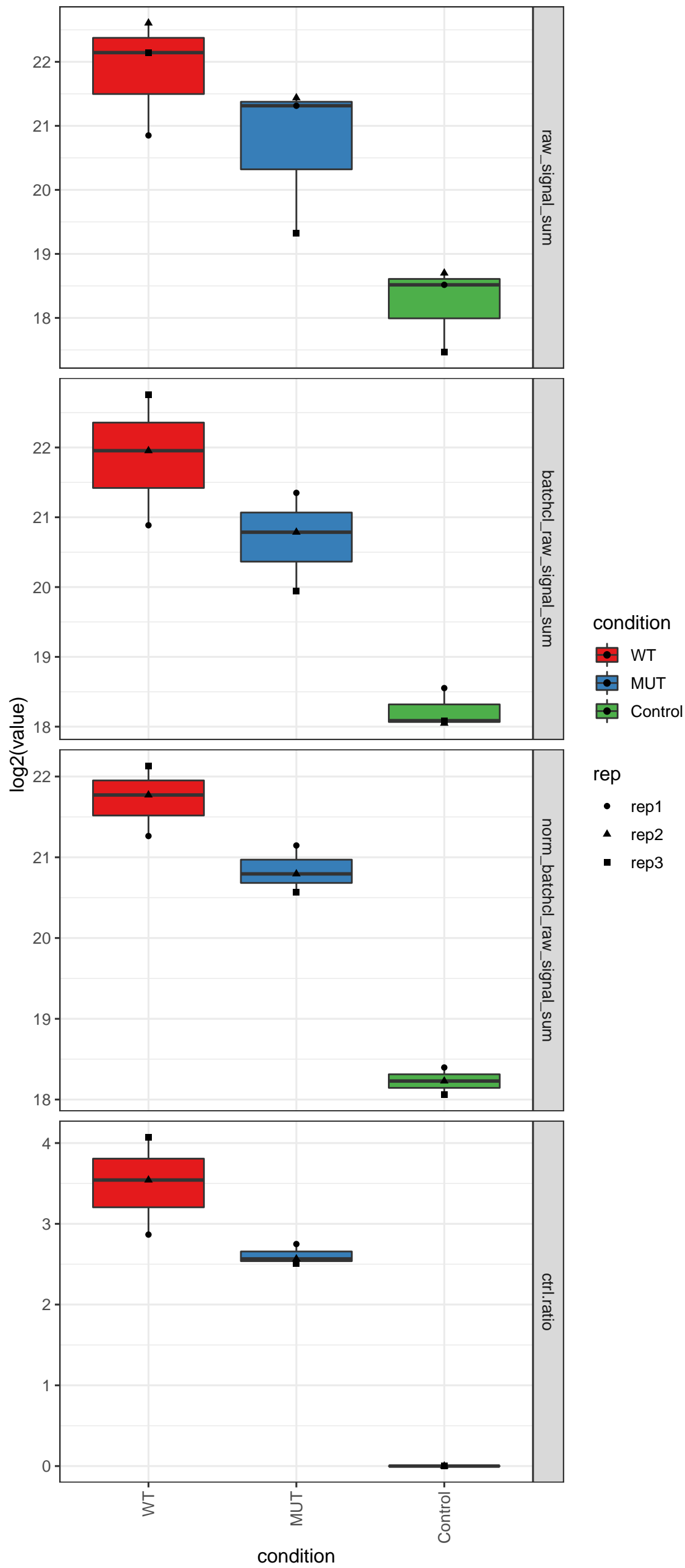
VTC4 – P47075

Vacuolar transporter chaperone 4 OS=*Saccharomyces cerevisiae* (strain *A*)



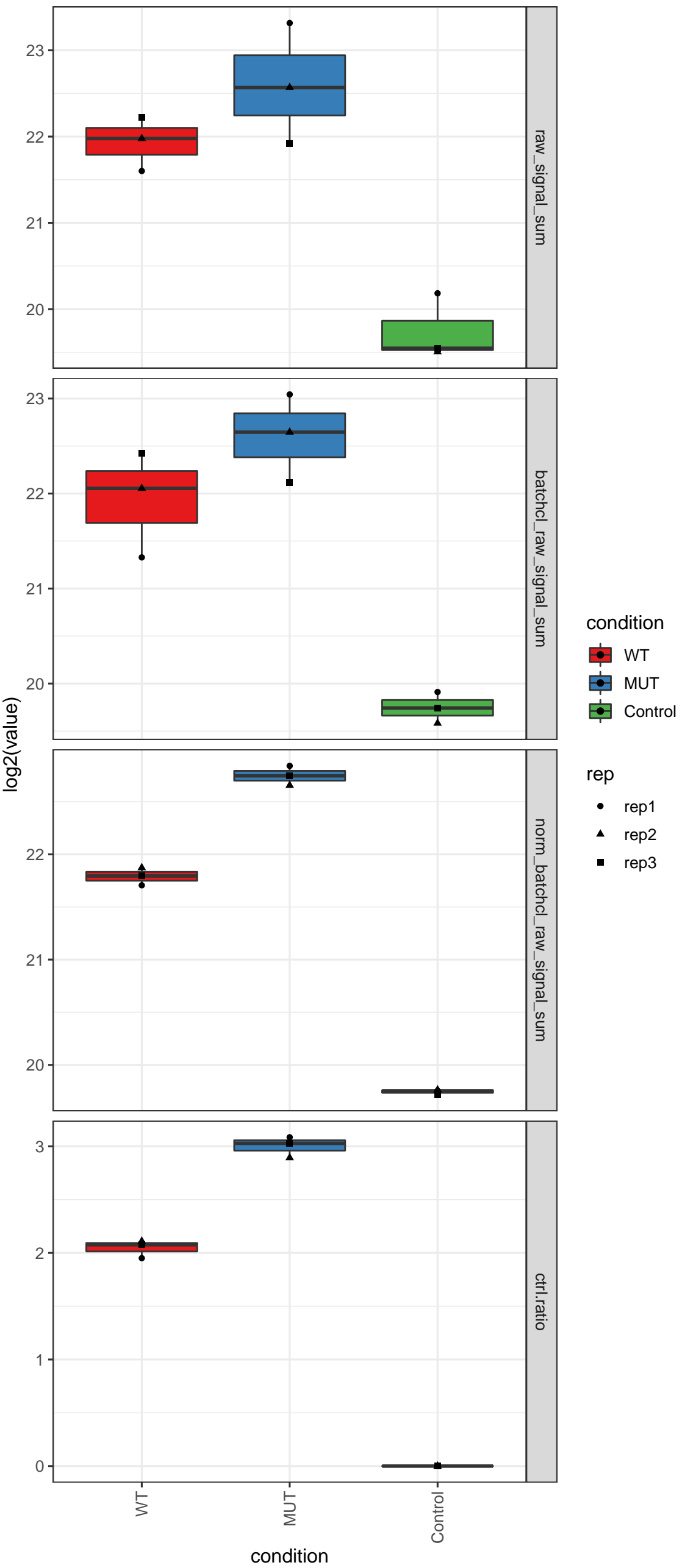
WRS1 – Q12109

Tryptophan--tRNA ligase, cytoplasmic OS=*Saccharomyces cerevisiae* (str)



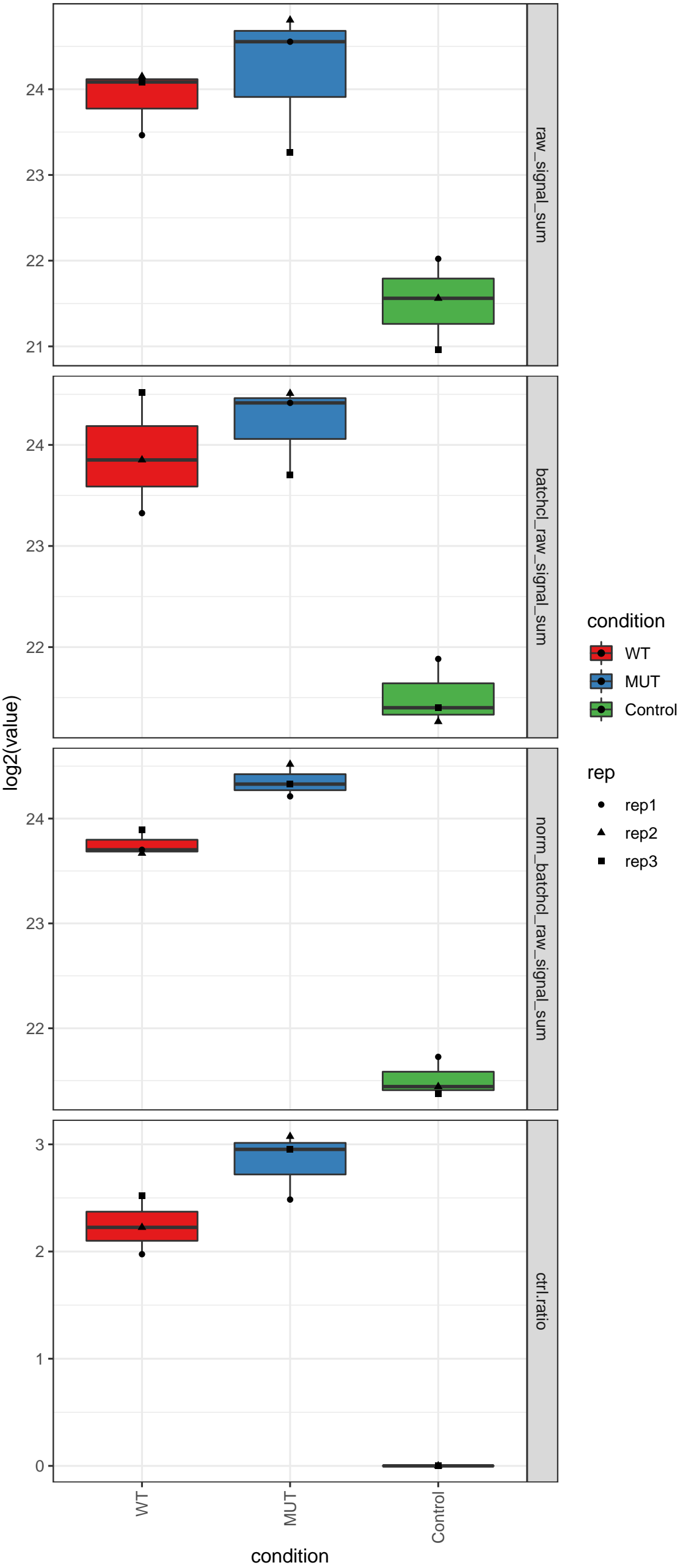
WTM1 – Q12363

Transcriptional modulator WTM1 OS=*Saccharomyces cerevisiae* (strain ATCC 25716)



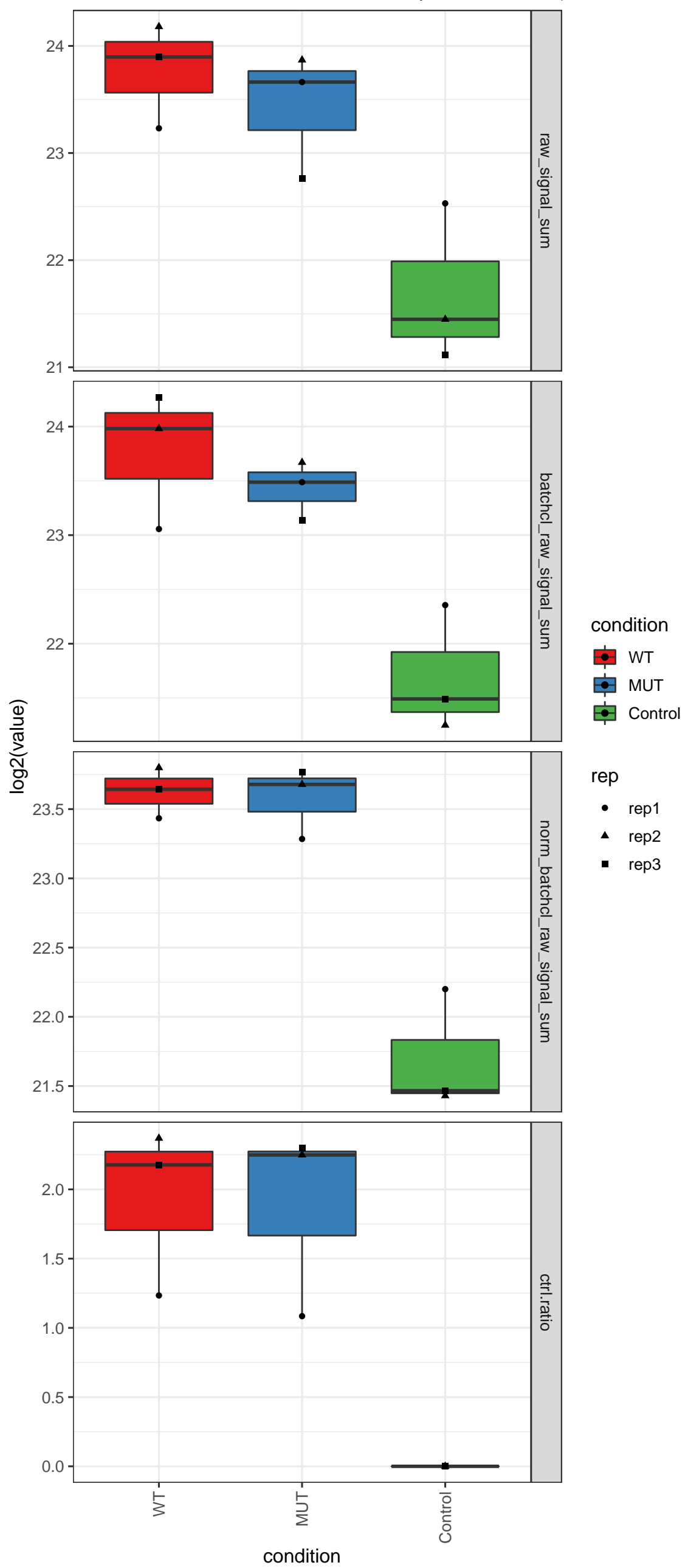
XDJ1 – P39102

DnaJ protein homolog XDJ1 OS=*Saccharomyces cerevisiae* (strain ATCC 25716)



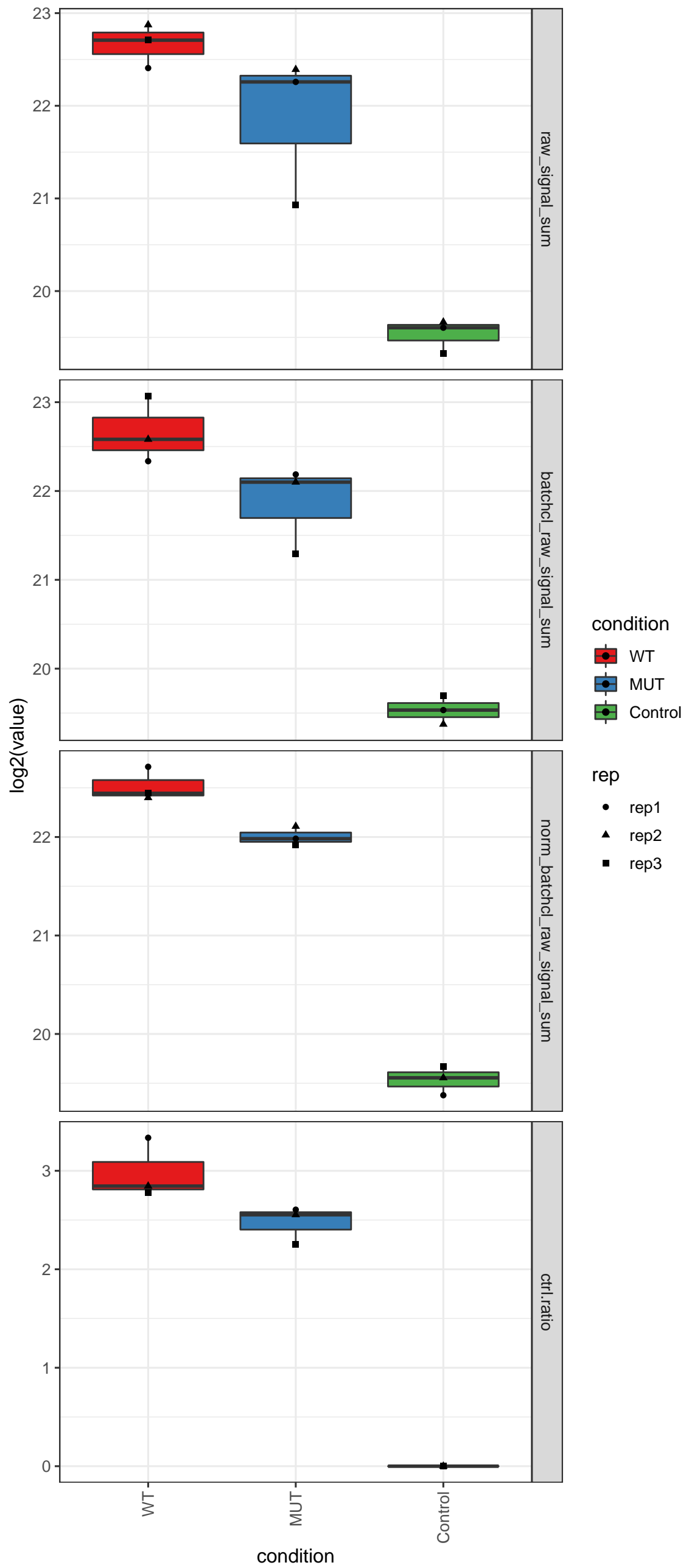
XRN1 – P22147

5'-3' exoribonuclease 1 OS=*Saccharomyces cerevisiae* (strain ATCC 204



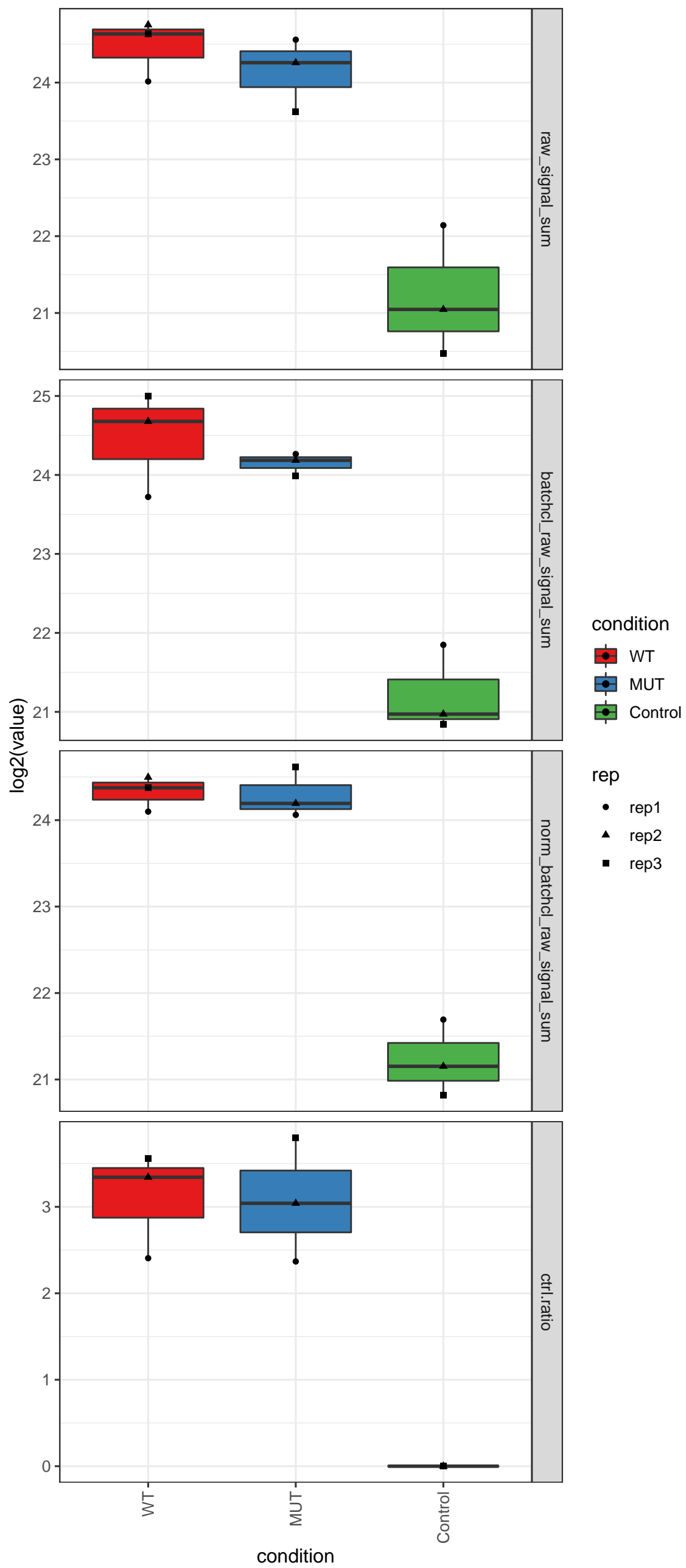
YAF9 – P53930

Protein AF-9 homolog OS=*Saccharomyces cerevisiae* (strain ATCC 20450)



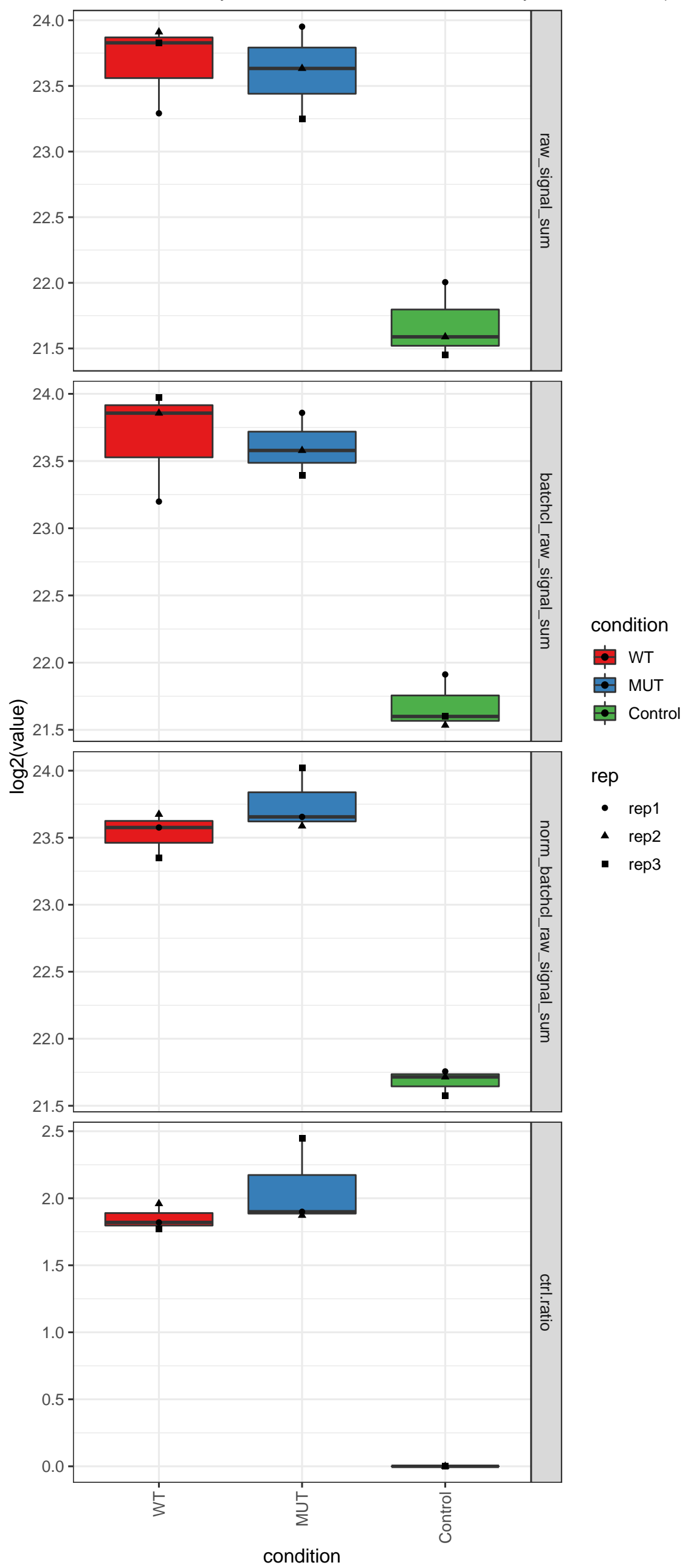
YAT1 – P80235

Putative mitochondrial carnitine O-acetyltransferase OS=Saccharomyces cerevisiae



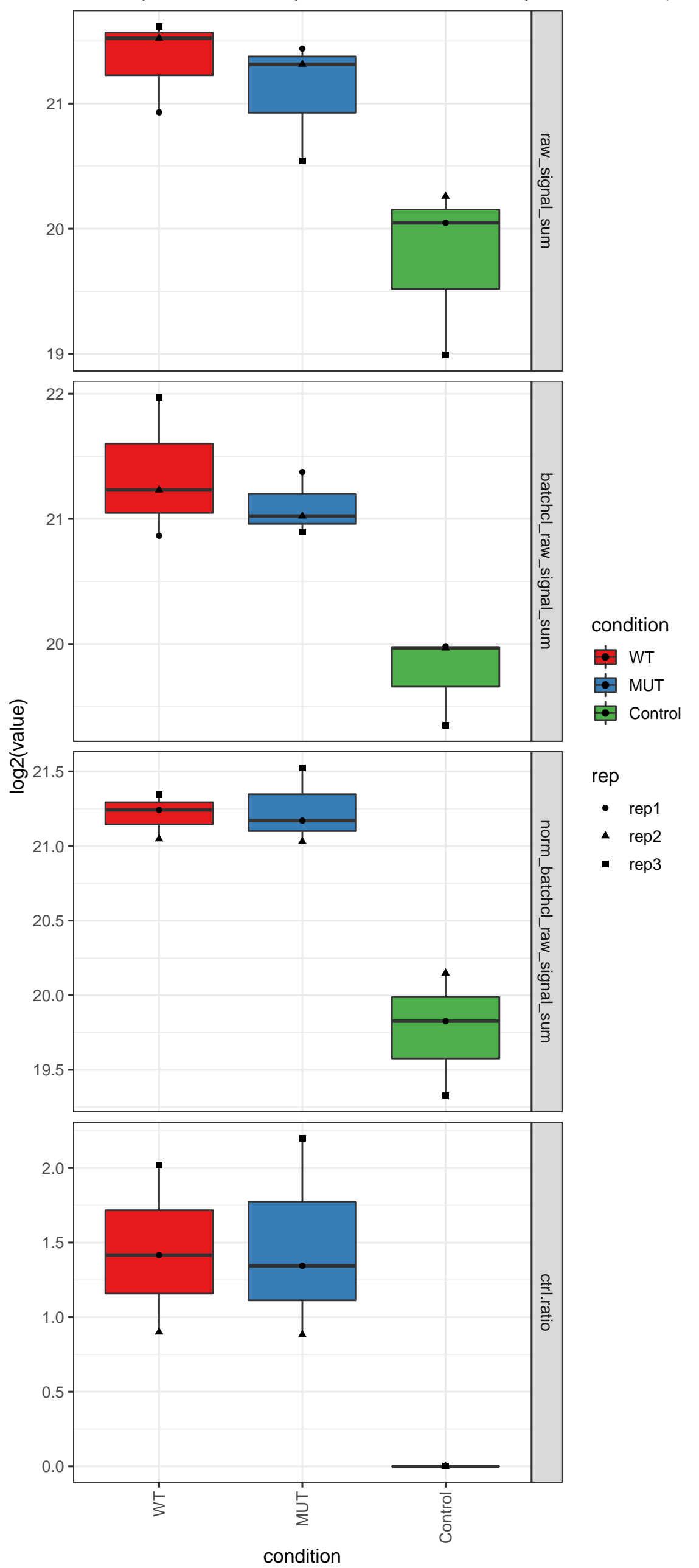
YAT2 – P40017

Carnitine O–acetyltransferase YAT2 OS=*Saccharomyces cerevisiae* (stra



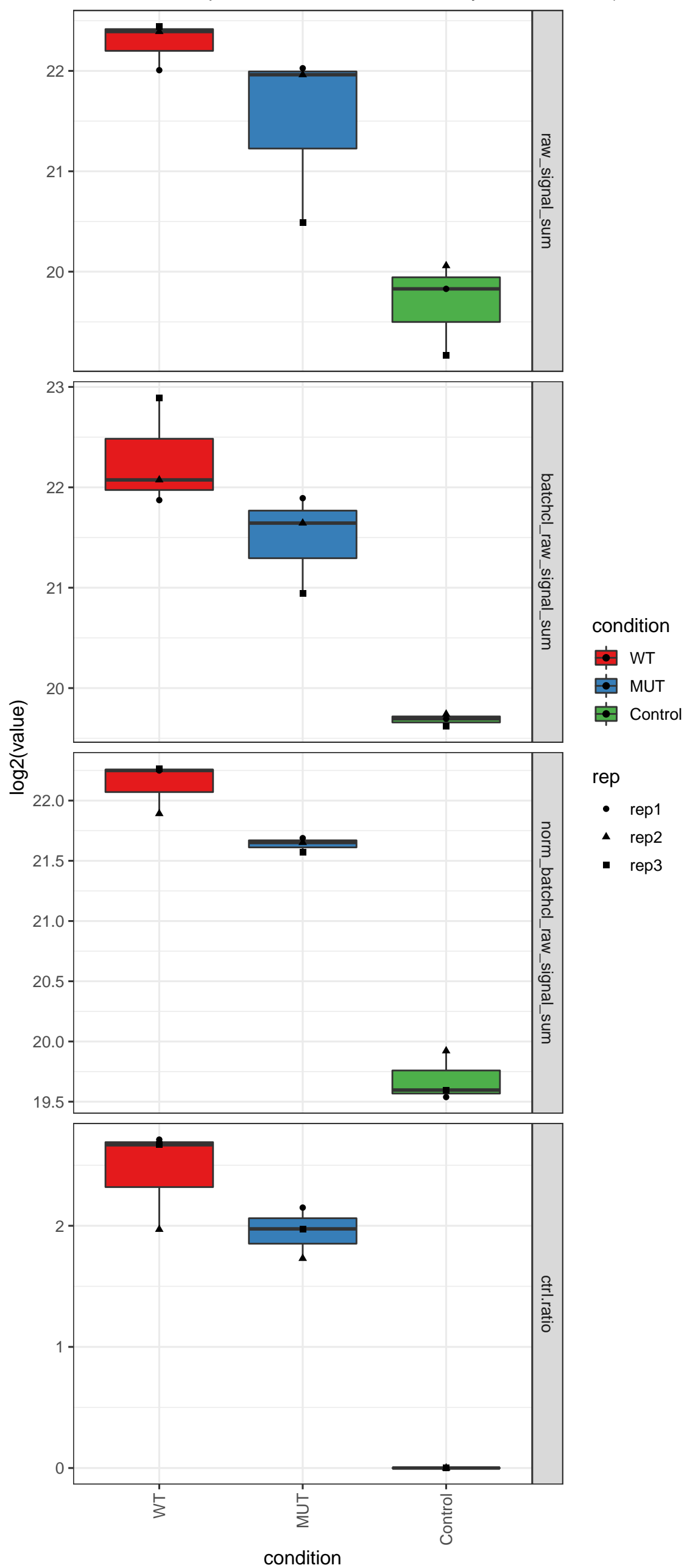
YBT1 – P32386

ATP-dependent bile acid permease OS=*Saccharomyces cerevisiae* (stra



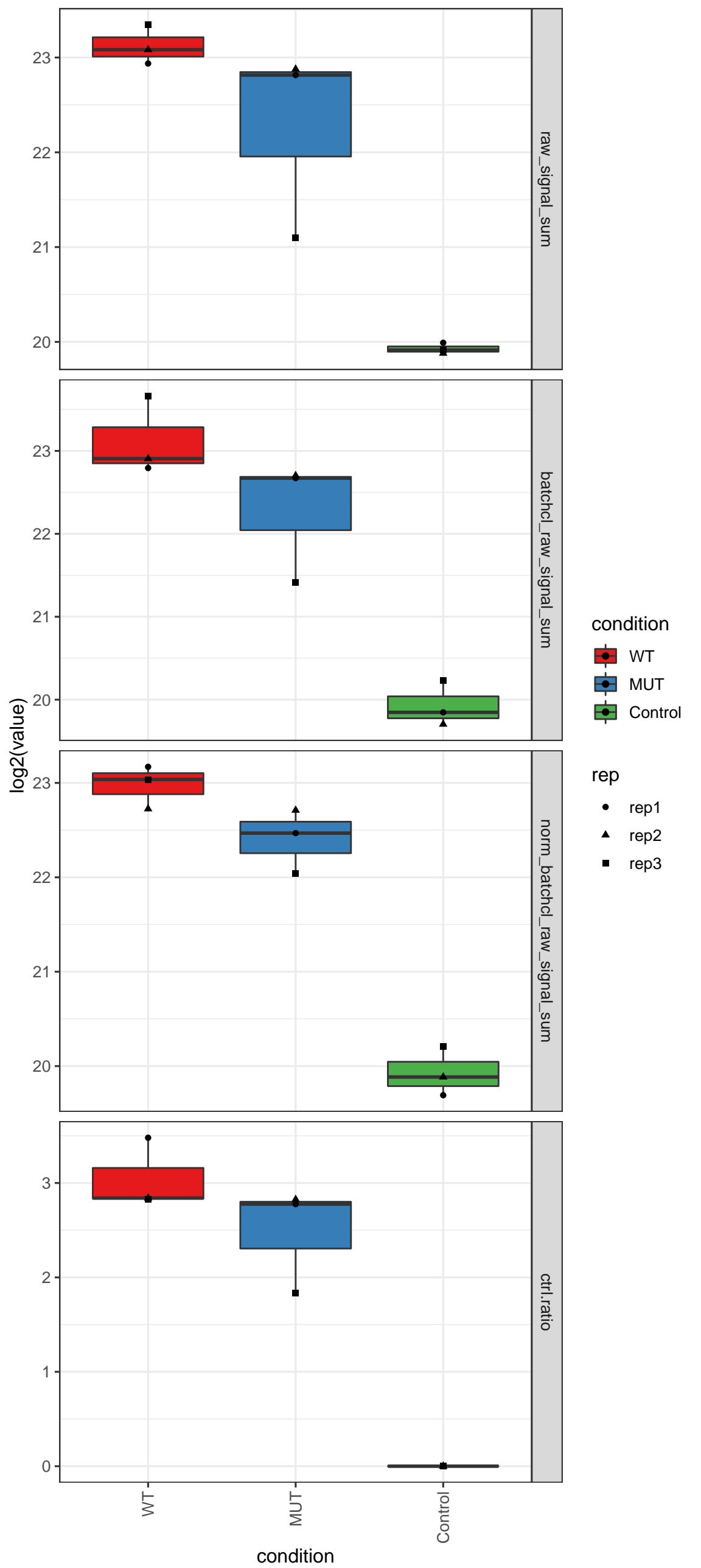
YCG1 – Q06680

Condensin complex subunit 3 OS=*Saccharomyces cerevisiae* (strain ATCC 25791)



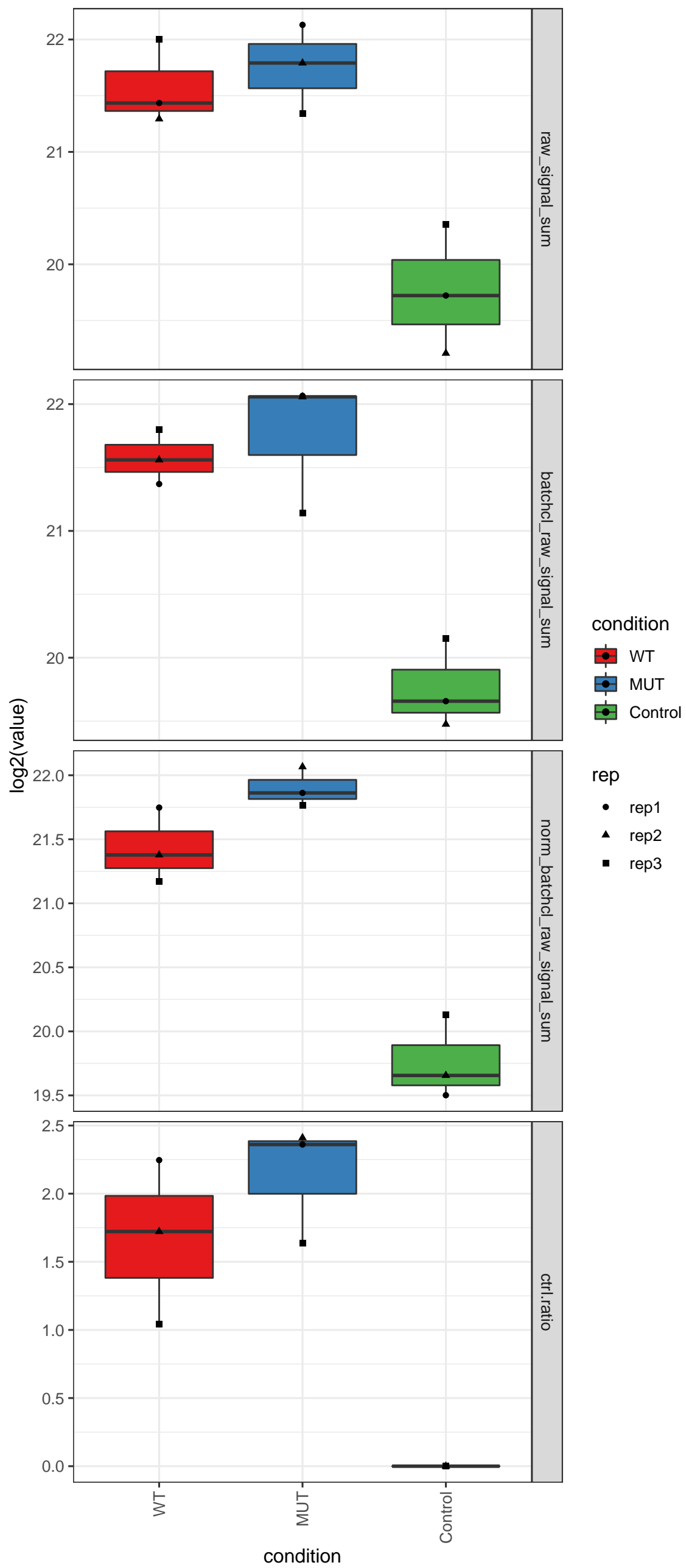
YCS4 – Q06156

Condensin complex subunit 1 OS=*Saccharomyces cerevisiae* (strain ATCC 25716)



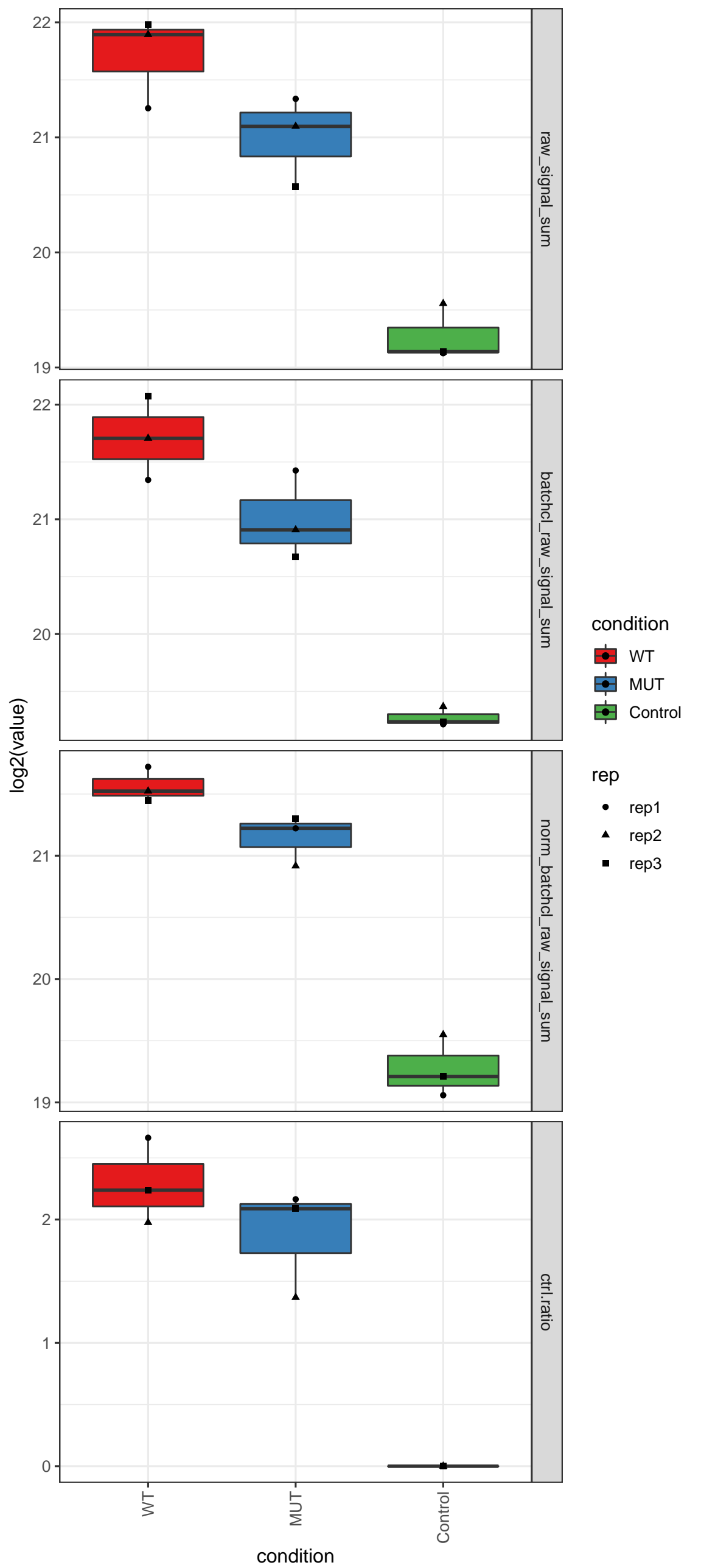
YDR115W – Q04598

54S ribosomal protein L34, mitochondrial OS=Saccharomyces cerevisiae

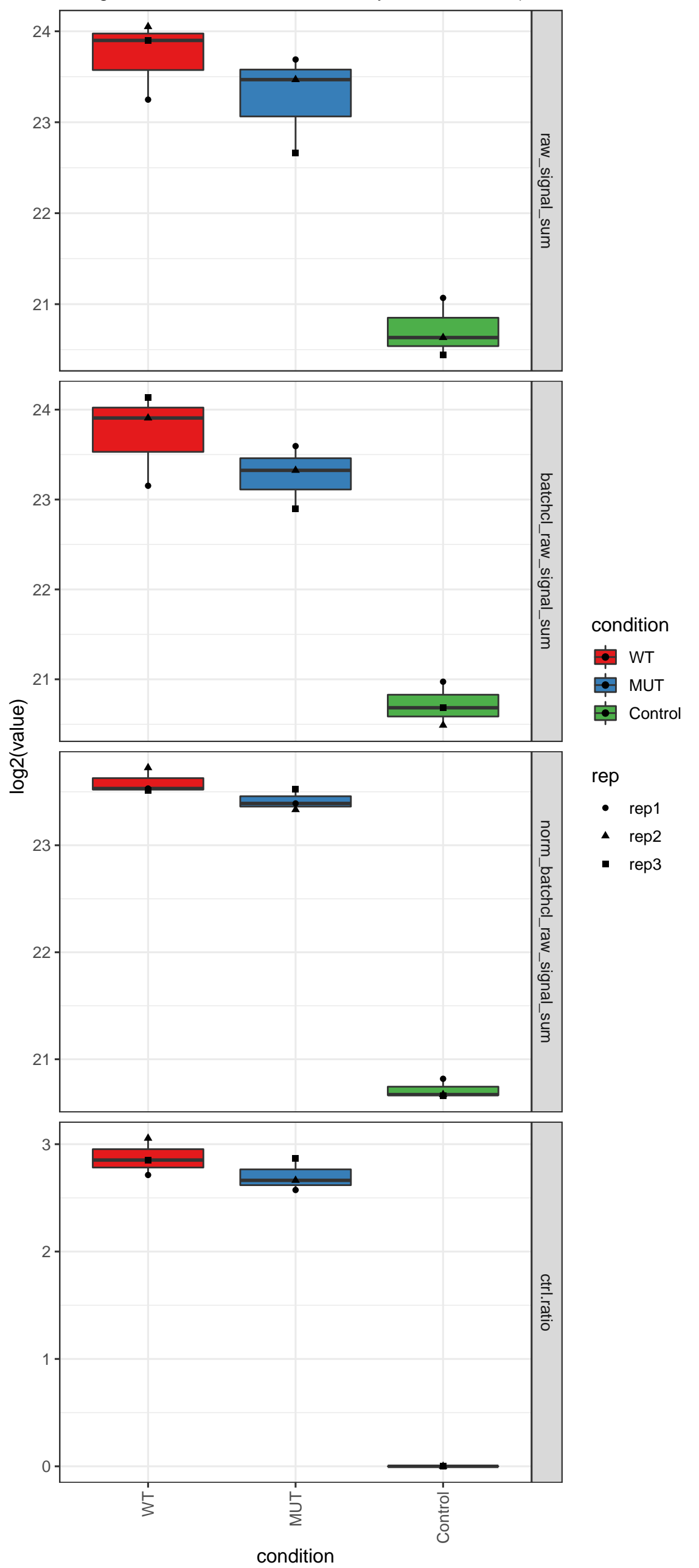


YDR341C - Q05506

Arginine--tRNA ligase, cytoplasmic OS=*Saccharomyces cerevisiae* (strain

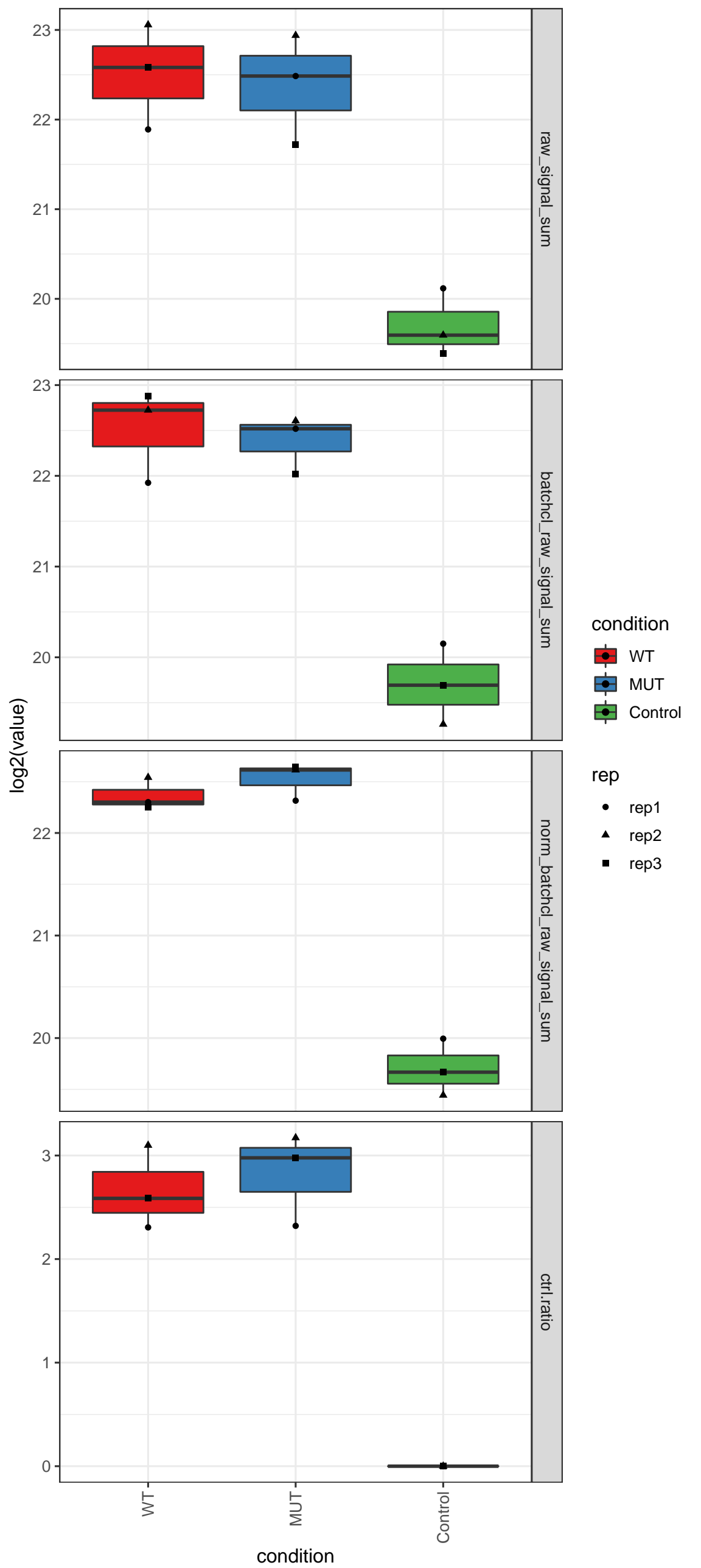


Elongation factor 3A OS=Saccharomyces cerevisiae (strain ATCC 204508



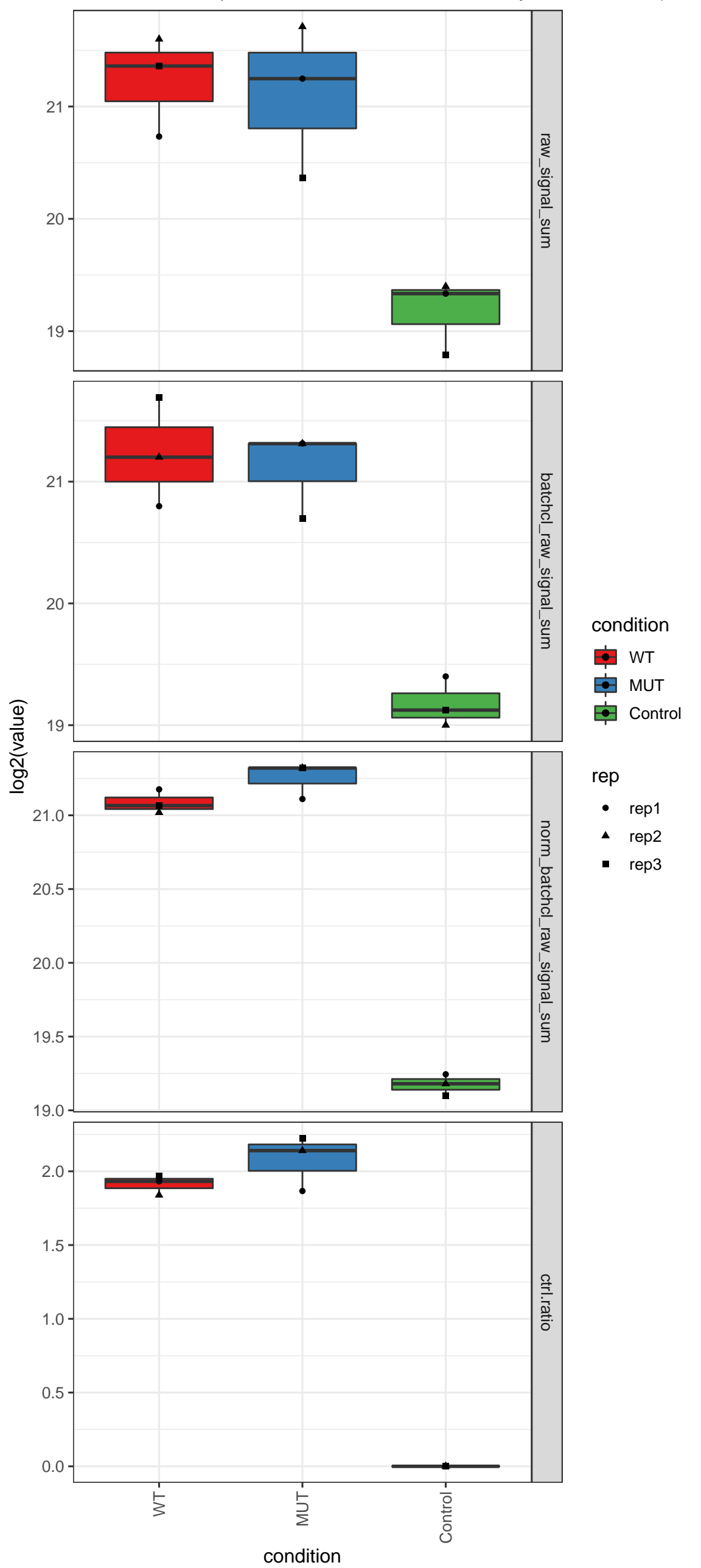
YEL020C – P39994

Putative 2-hydroxyacyl-CoA lyase OS=*Saccharomyces cerevisiae* (strain /



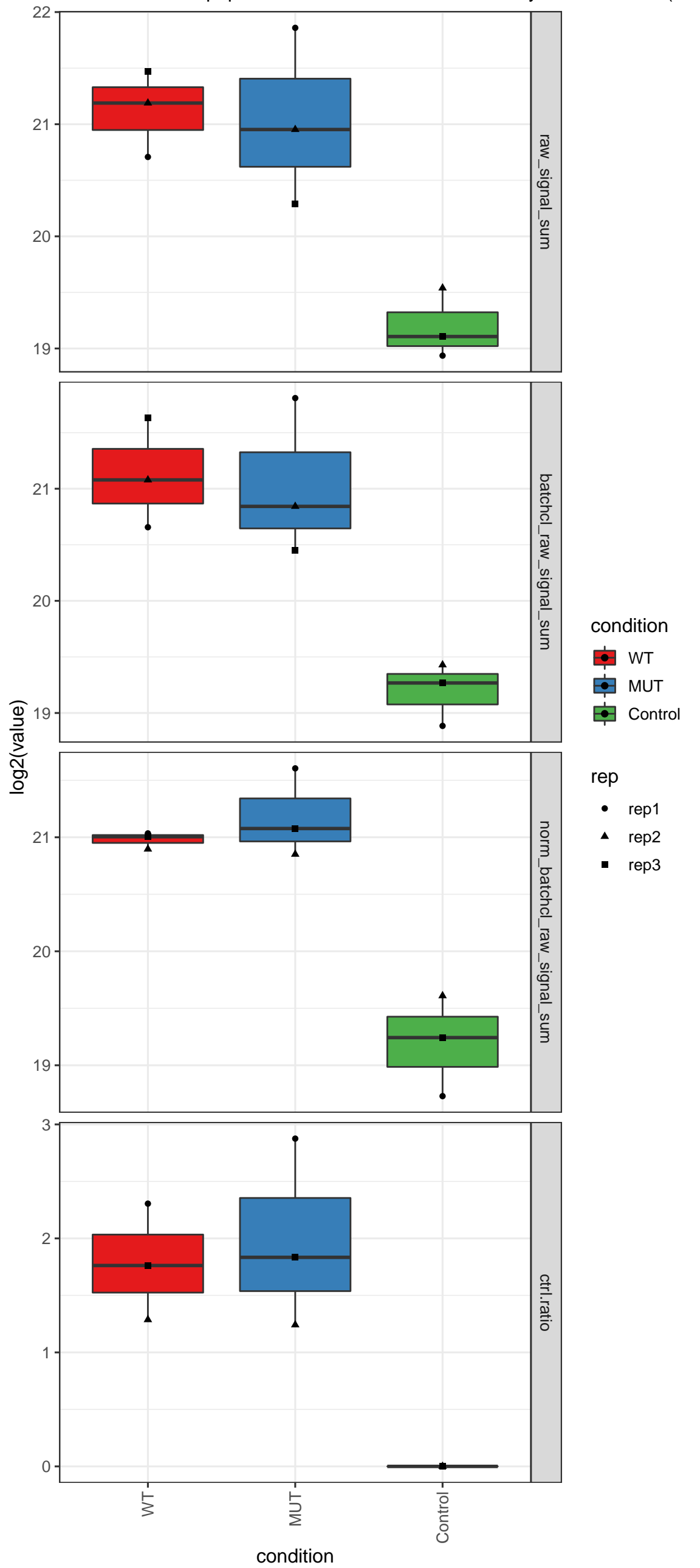
YER079W - P40052

Uncharacterized protein YER079W OS=*Saccharomyces cerevisiae* (strain



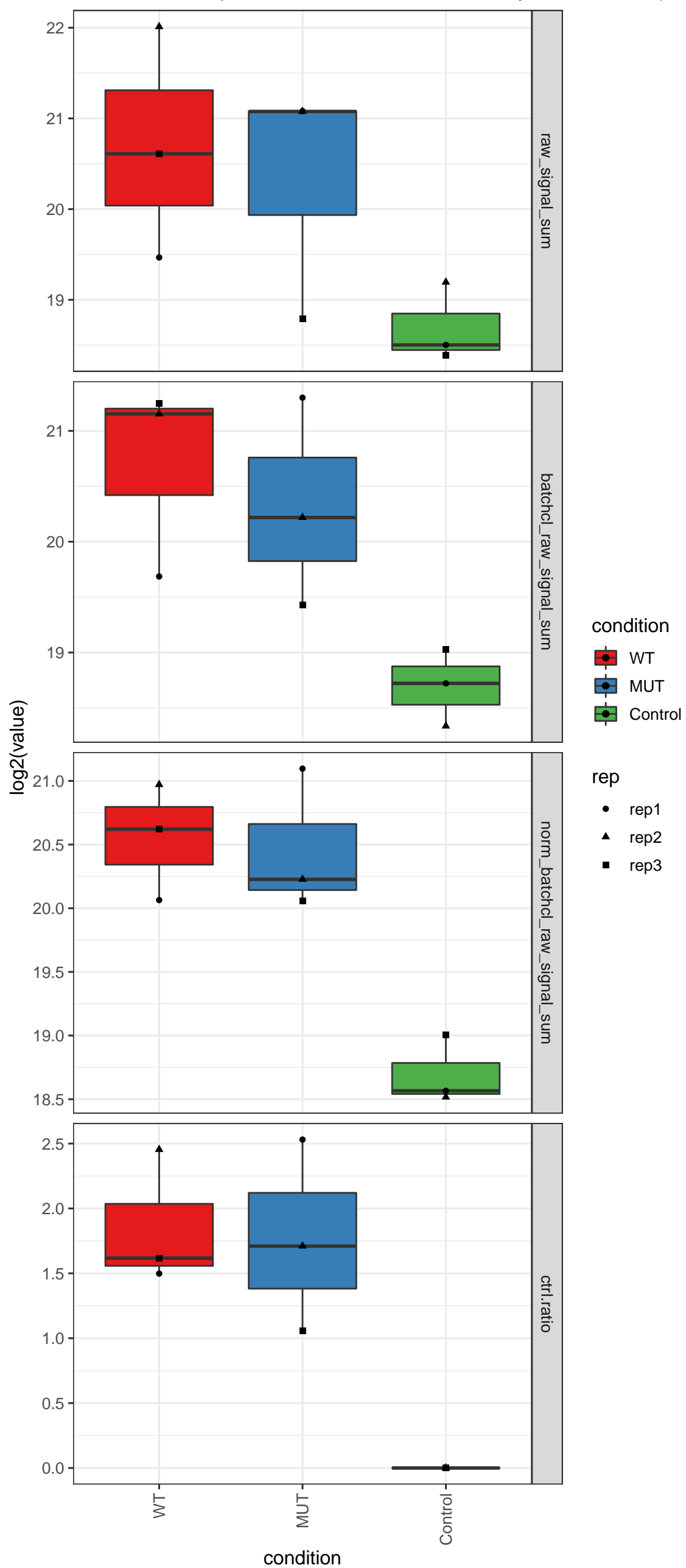
YFR006W – P43590

Uncharacterized peptidase YFR006W OS=*Saccharomyces cerevisiae* (strain



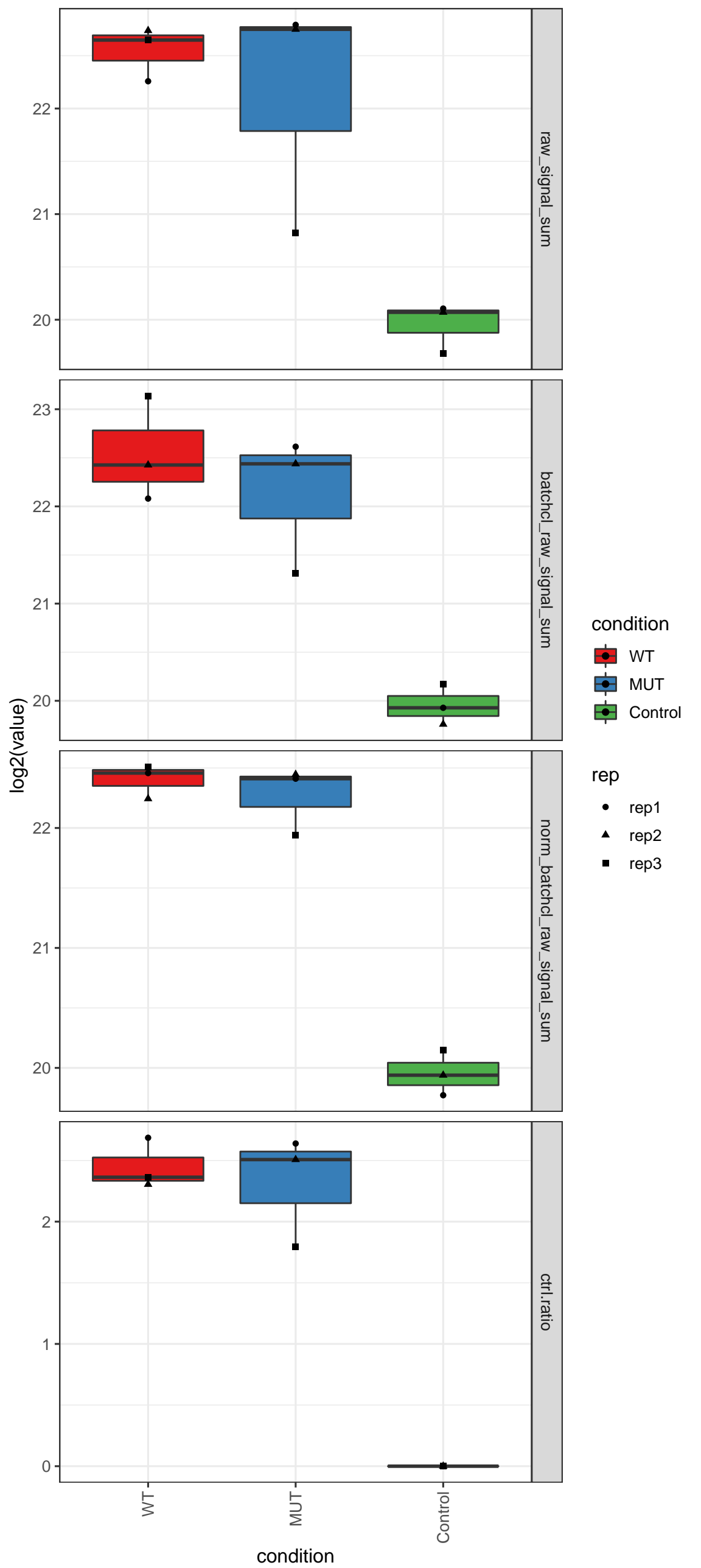
YGL081W – P53156

Uncharacterized protein YGL081W OS=*Saccharomyces cerevisiae* (strain



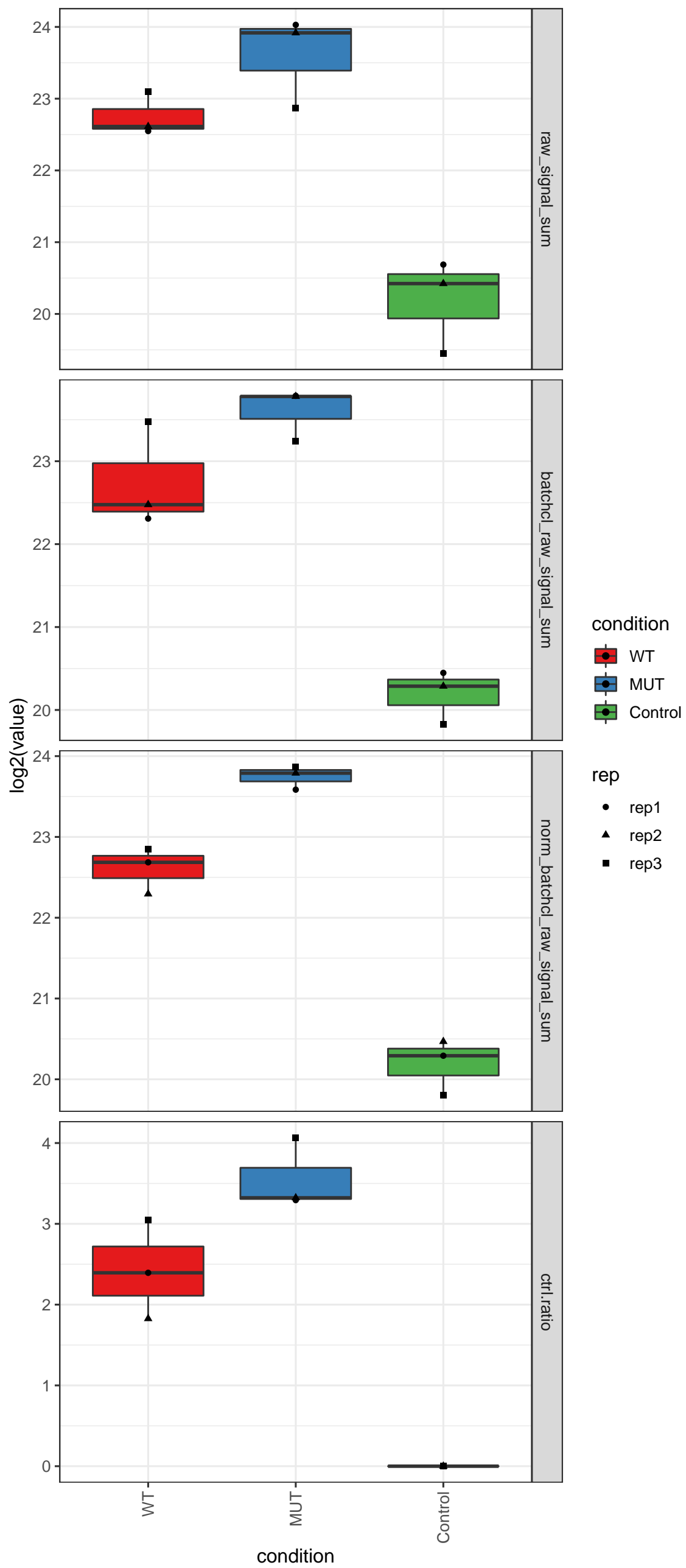
YGL108C – P53139

Uncharacterized protein YGL108C OS=*Saccharomyces cerevisiae* (strain /



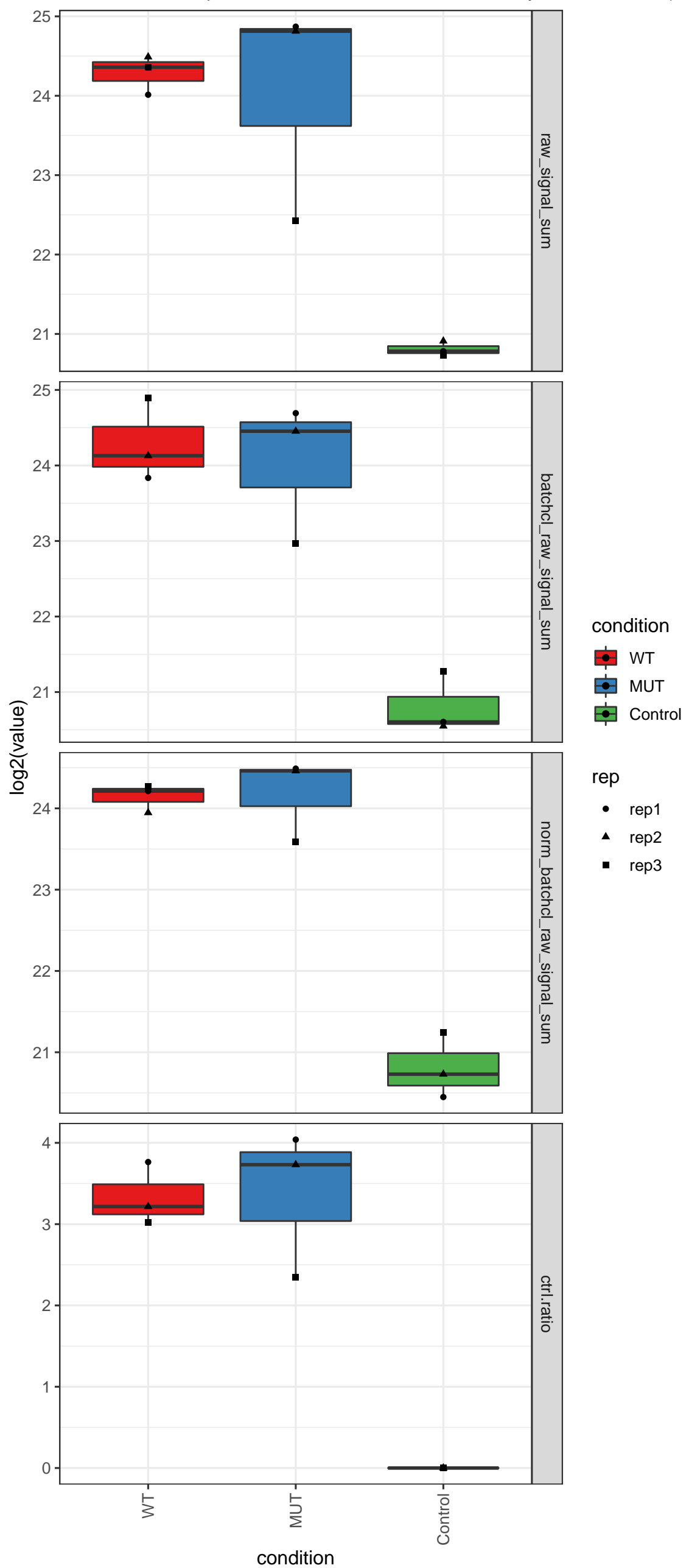
YGR130C – P53278

Uncharacterized protein YGR130C OS=*Saccharomyces cerevisiae* (strain



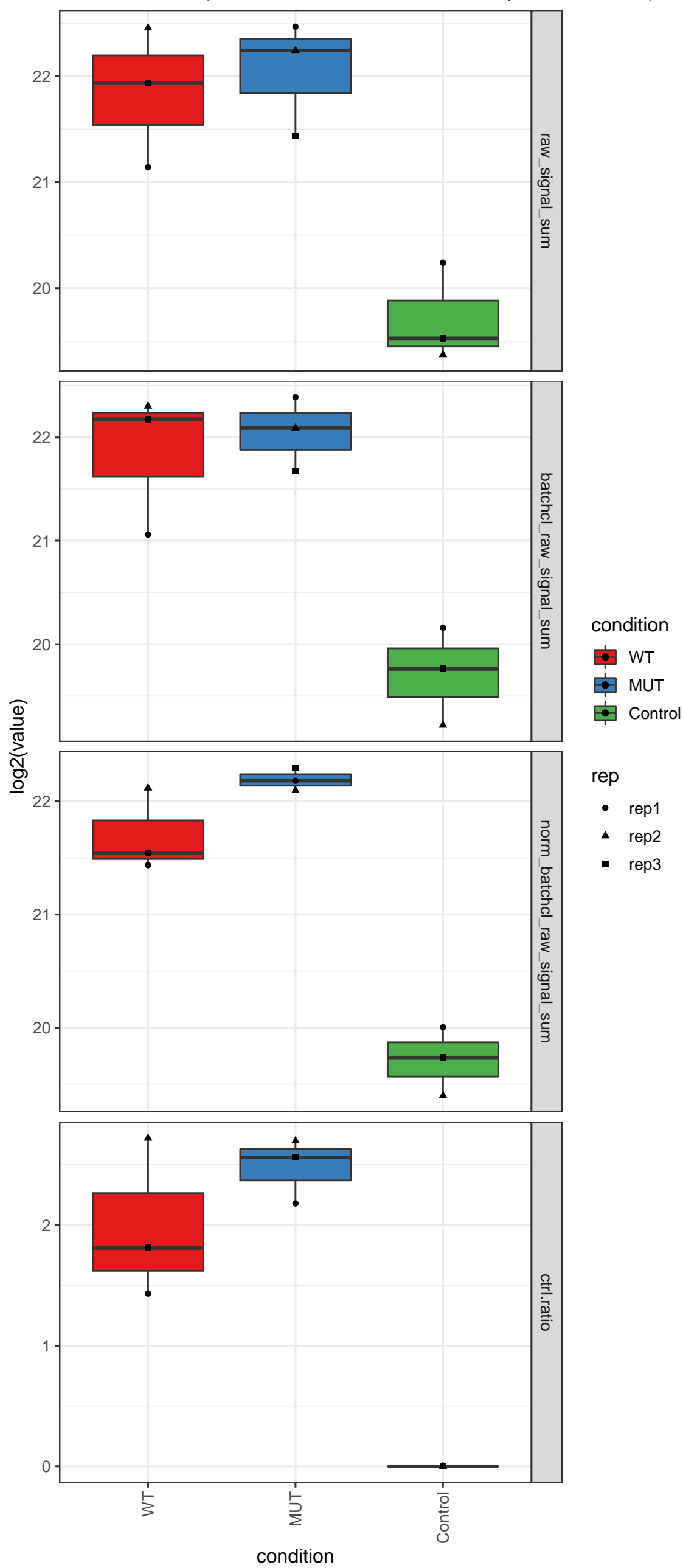
YGR169C-A – Q3E772

Uncharacterized protein YGR169C-A OS=Saccharomyces cerevisiae (stra



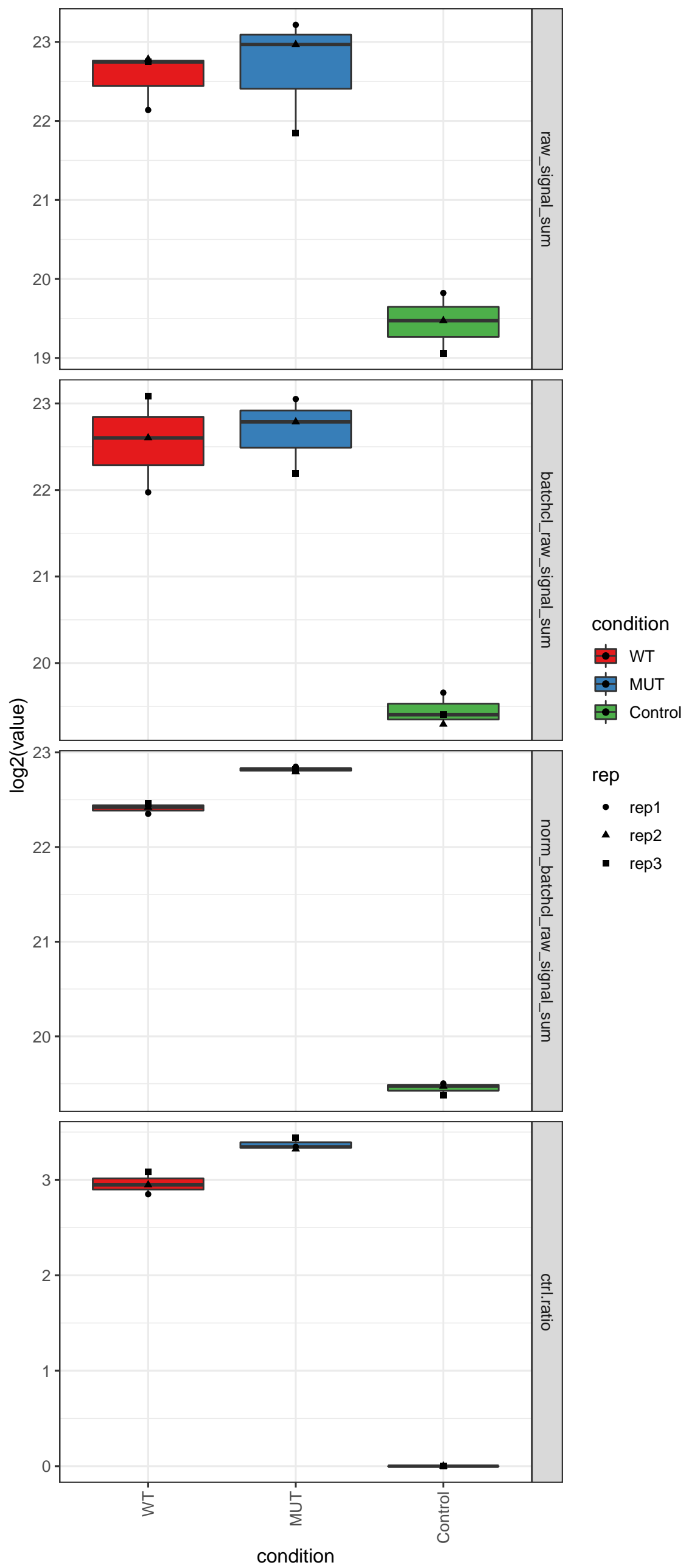
YGR266W – P53326

Uncharacterized protein YGR266W OS=*Saccharomyces cerevisiae* (strain



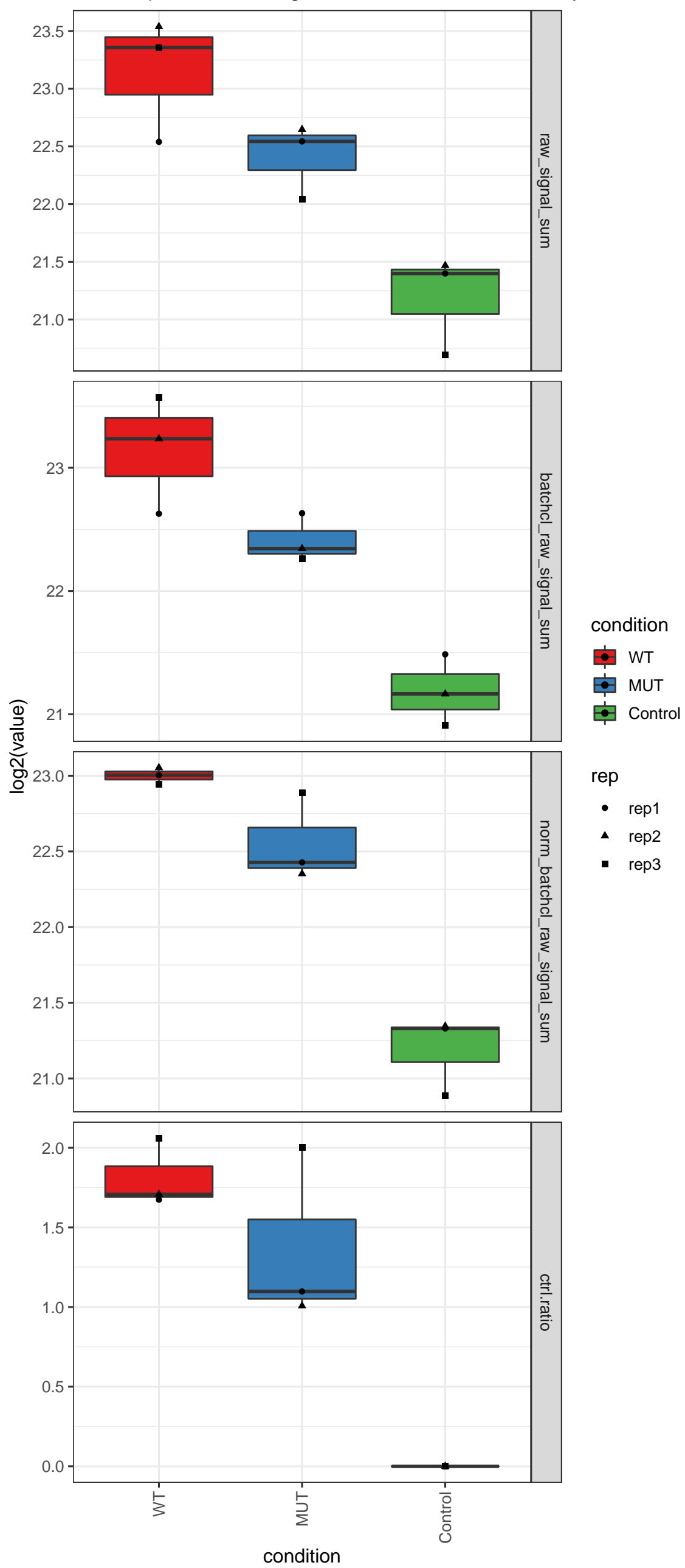
YHM2 – Q04013

Citrate/oxoglutarate carrier protein OS=*Saccharomyces cerevisiae* (strain A



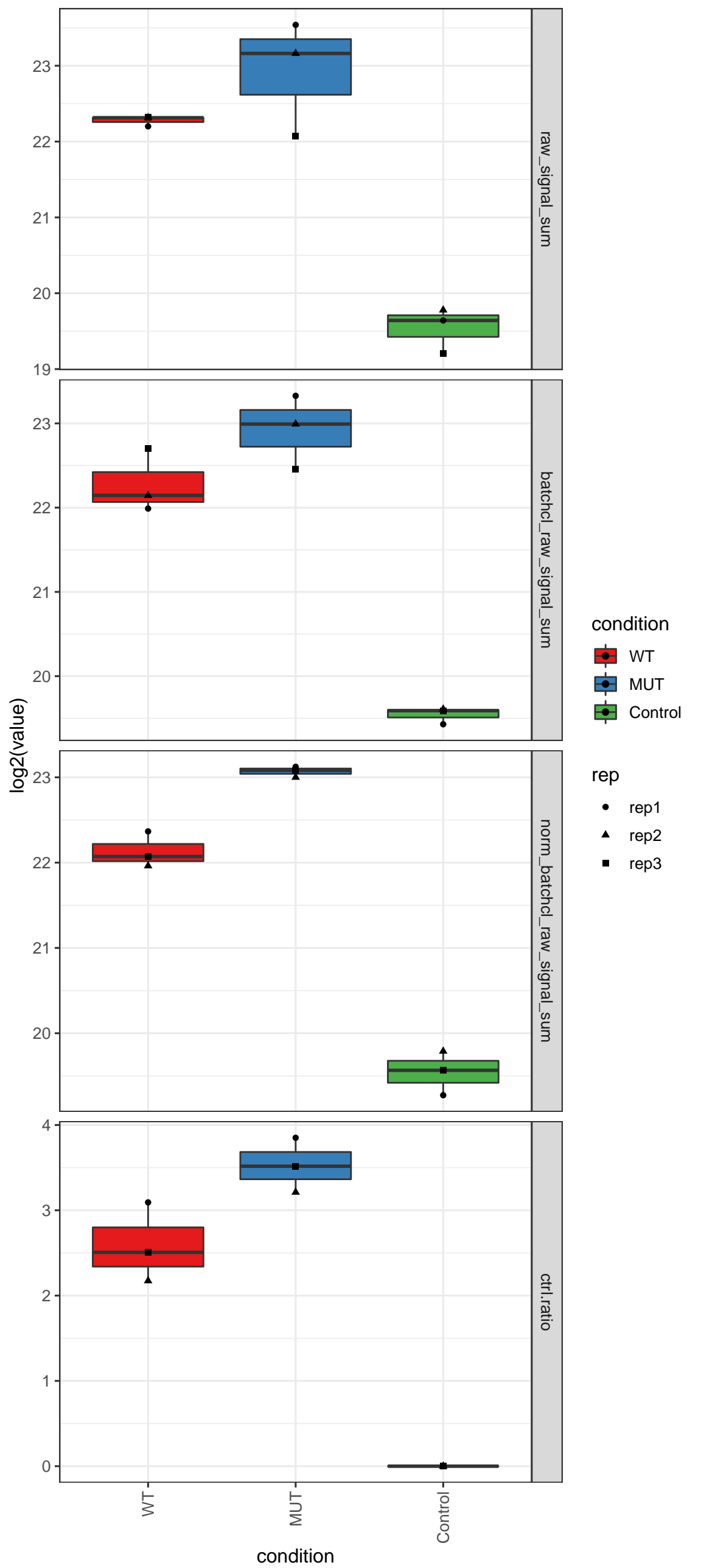
YHR020W – P38708

Putative proline--tRNA ligase YHR020W OS=*Saccharomyces cerevisiae*



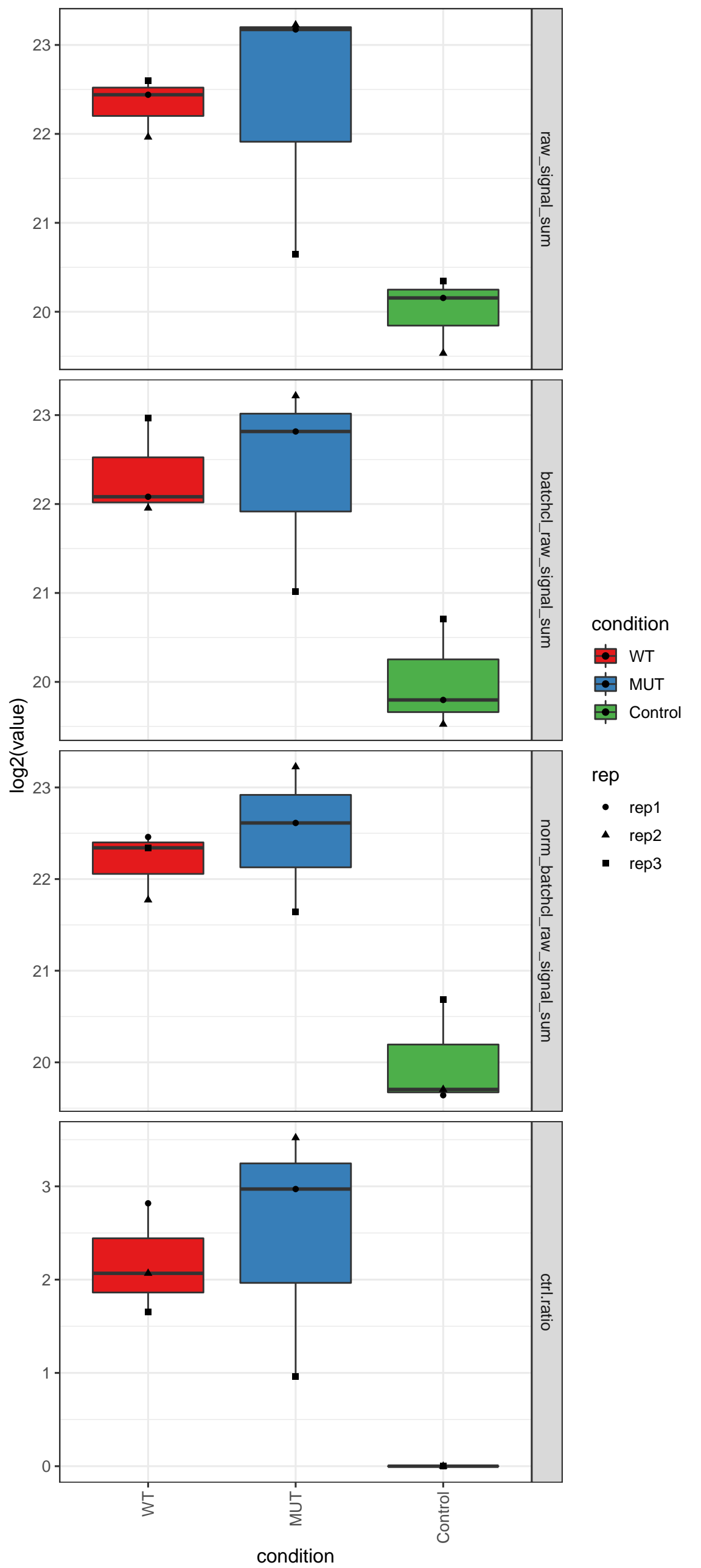
YHR097C - P38809

Uncharacterized protein YHR097C OS=*Saccharomyces cerevisiae* (strain



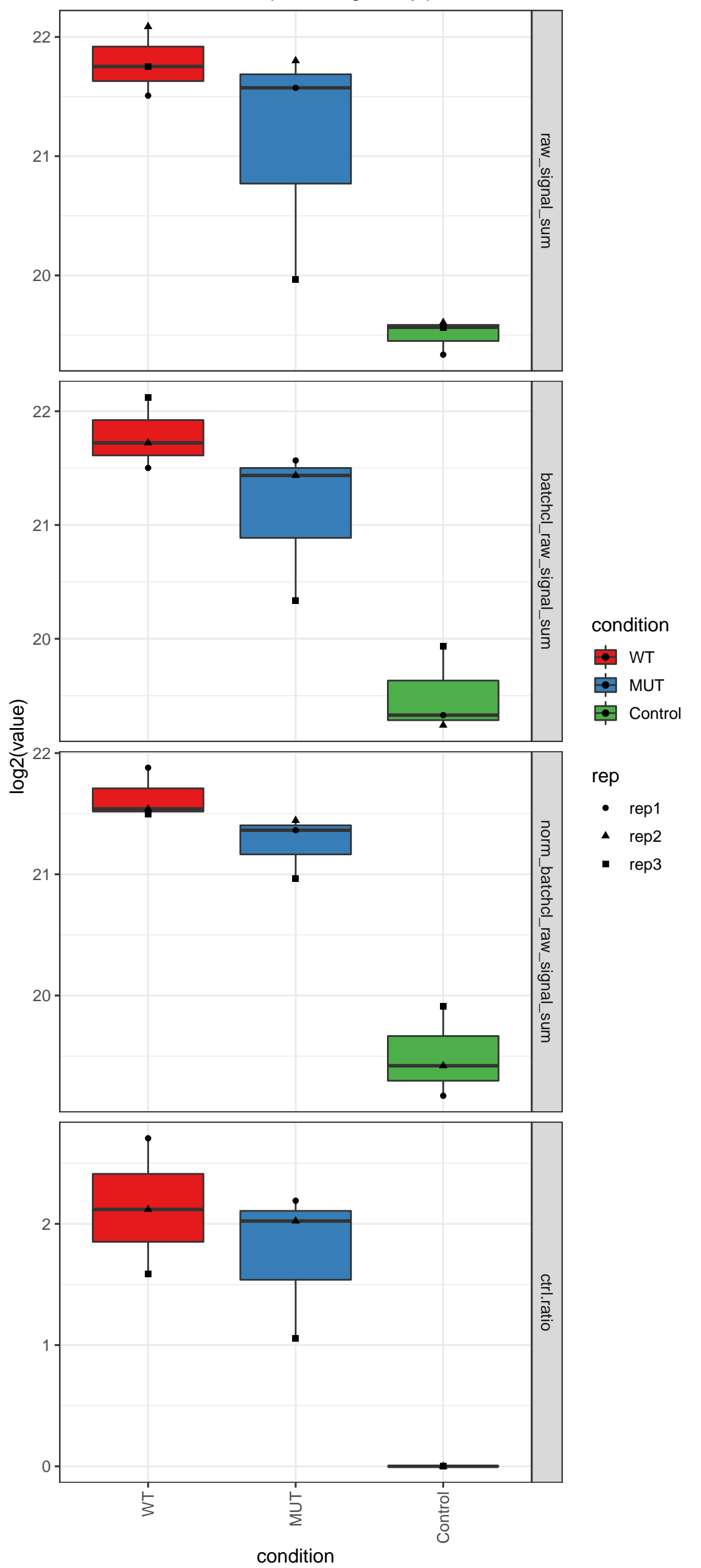
YJR005C-A – Q3E827

Uncharacterized protein YJR005C-A OS=*Saccharomyces cerevisiae* (strain



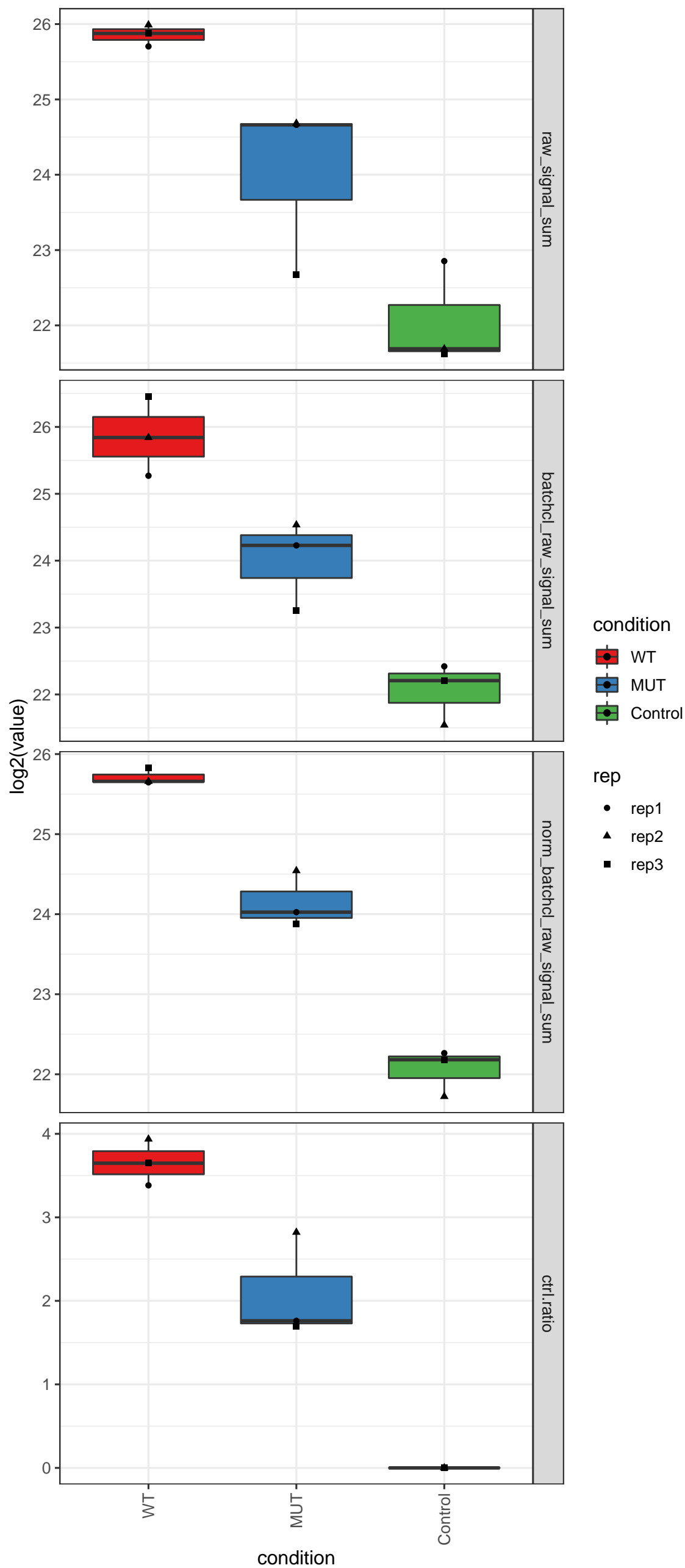
YLR278C – Q05854

Uncharacterized transcriptional regulatory protein YLR278C OS=Saccharomyces cerevisiae



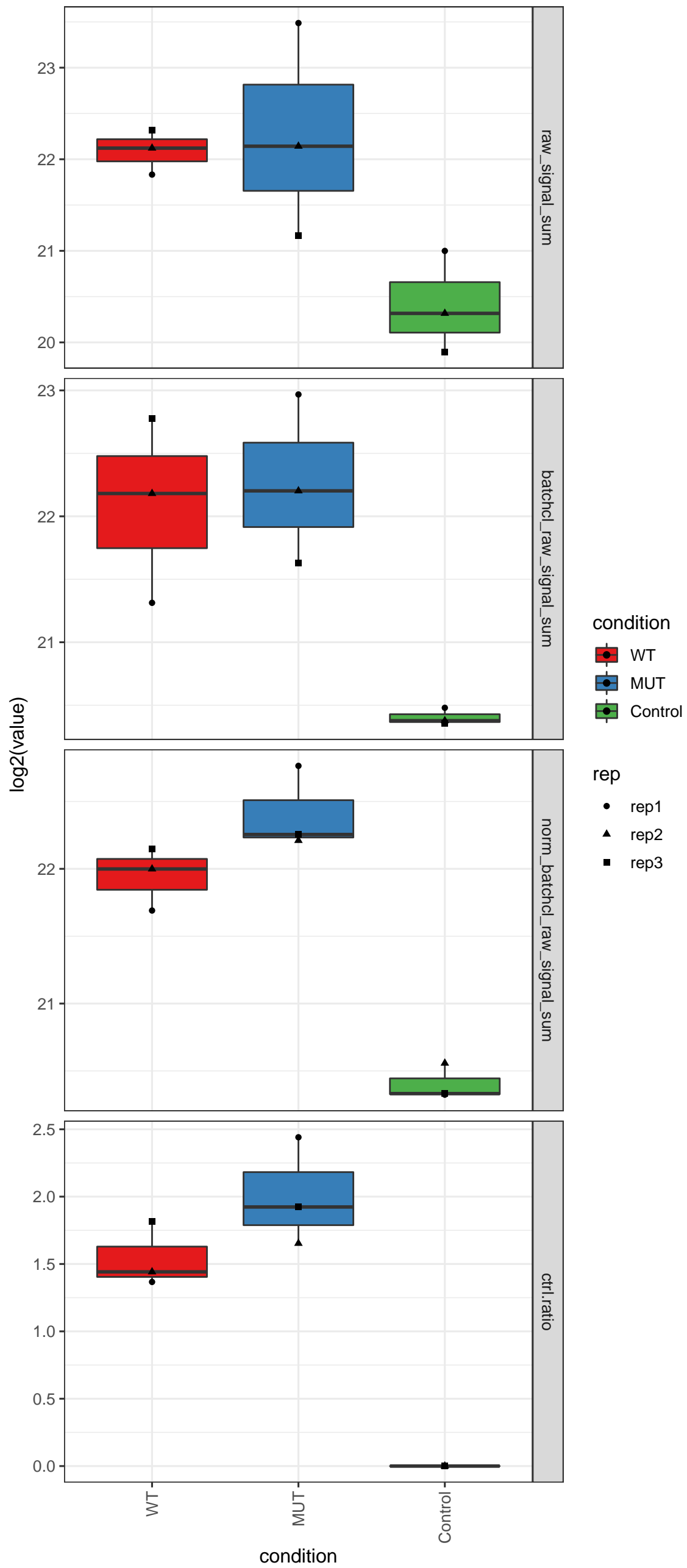
YLR455W – Q06188

PWWP domain-containing protein YLR455W OS=*Saccharomyces cerevisiae*



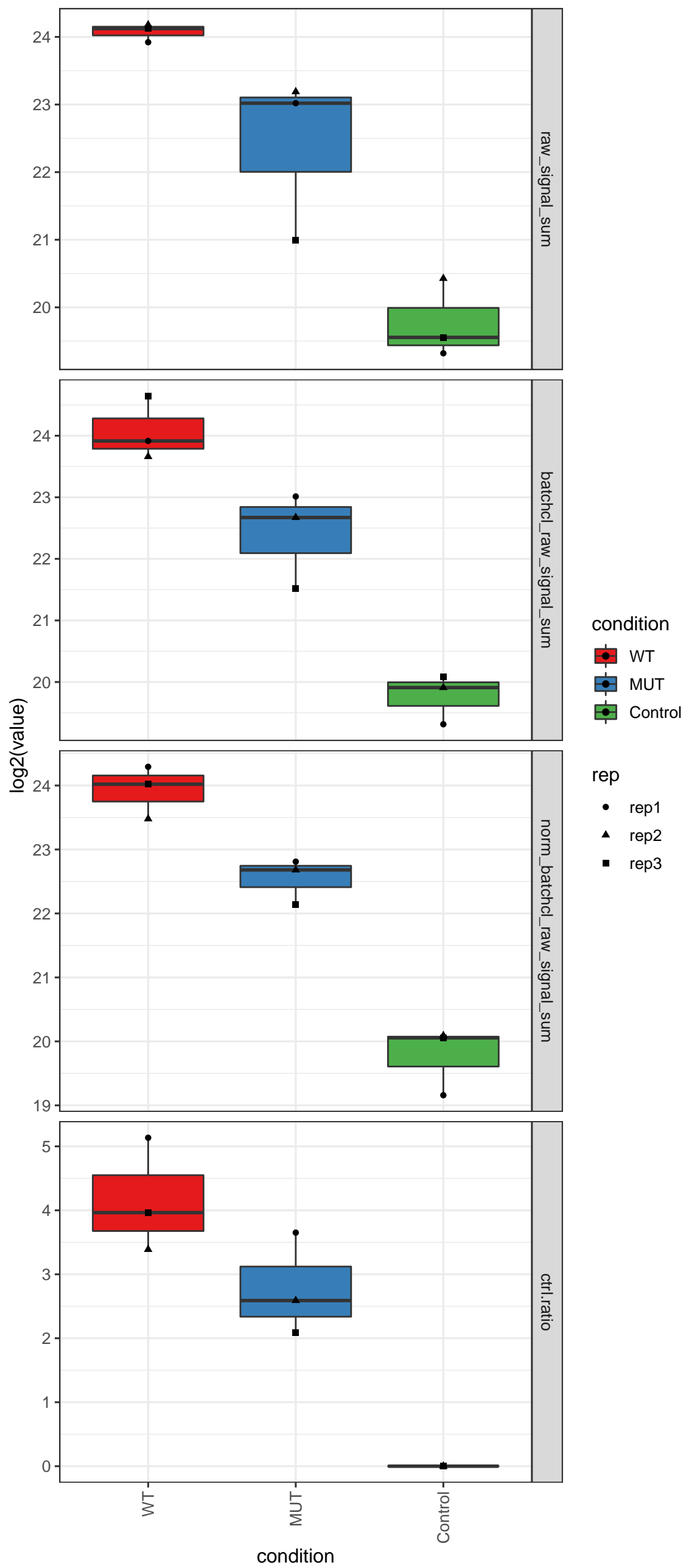
YMR027W – Q04371

Protein-glutamate O-methyltransferase OS=*Saccharomyces cerevisiae* (S)



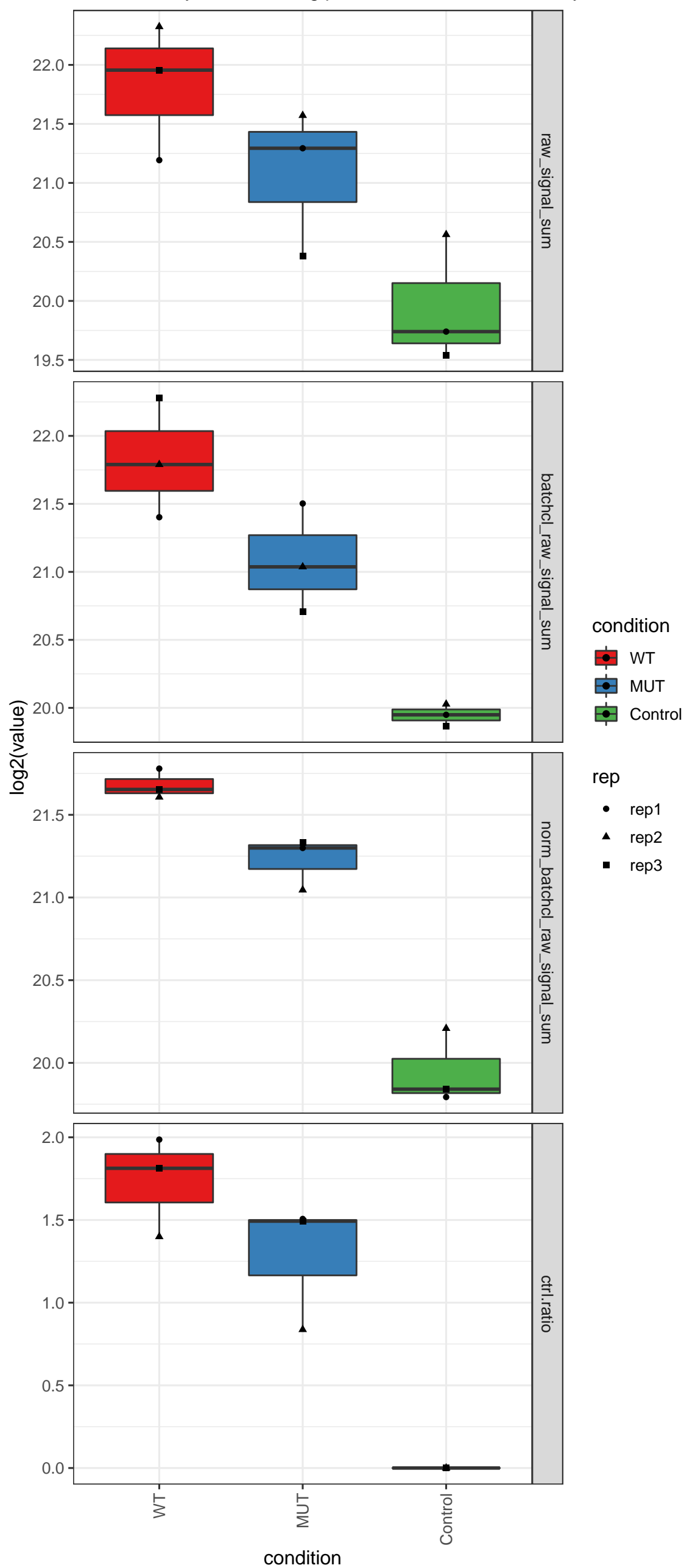
YNG1 – Q08465

Protein YNG1 OS=*Saccharomyces cerevisiae* (strain ATCC 204508 / S288



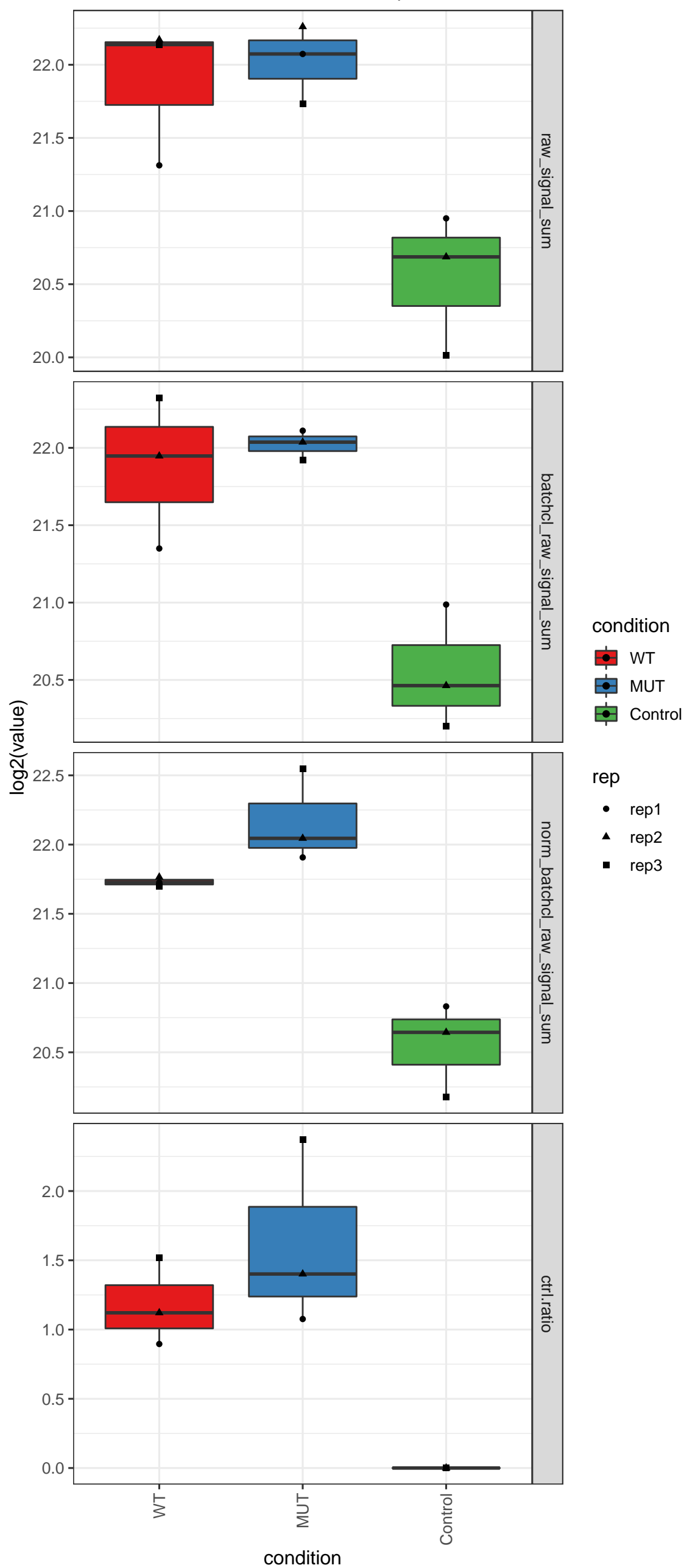
YNL040W – P53960

Putative alanyl–tRNA editing protein alaX OS=*Saccharomyces cerevisiae*

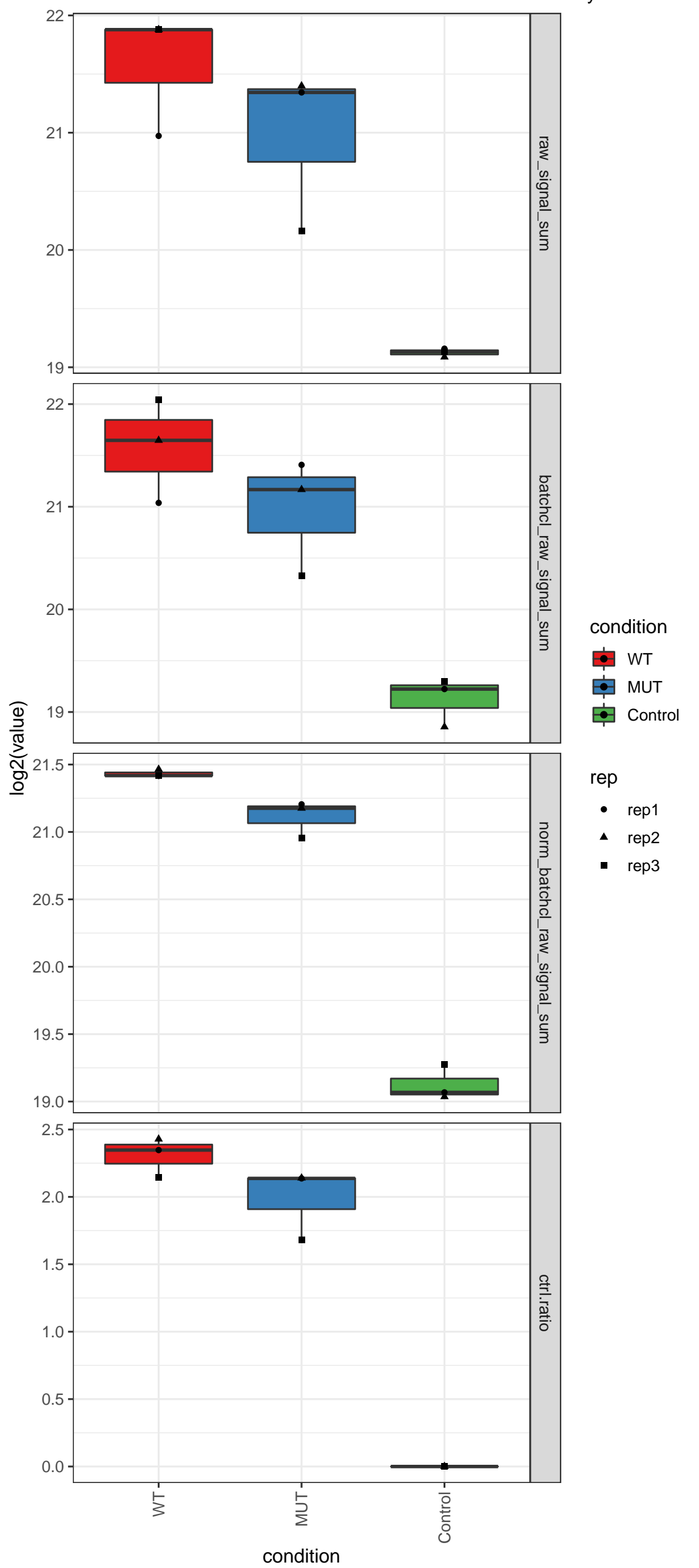


YNL115C – P53925

Uncharacterized vacuolar membrane protein YNL115C OS=Saccharomy

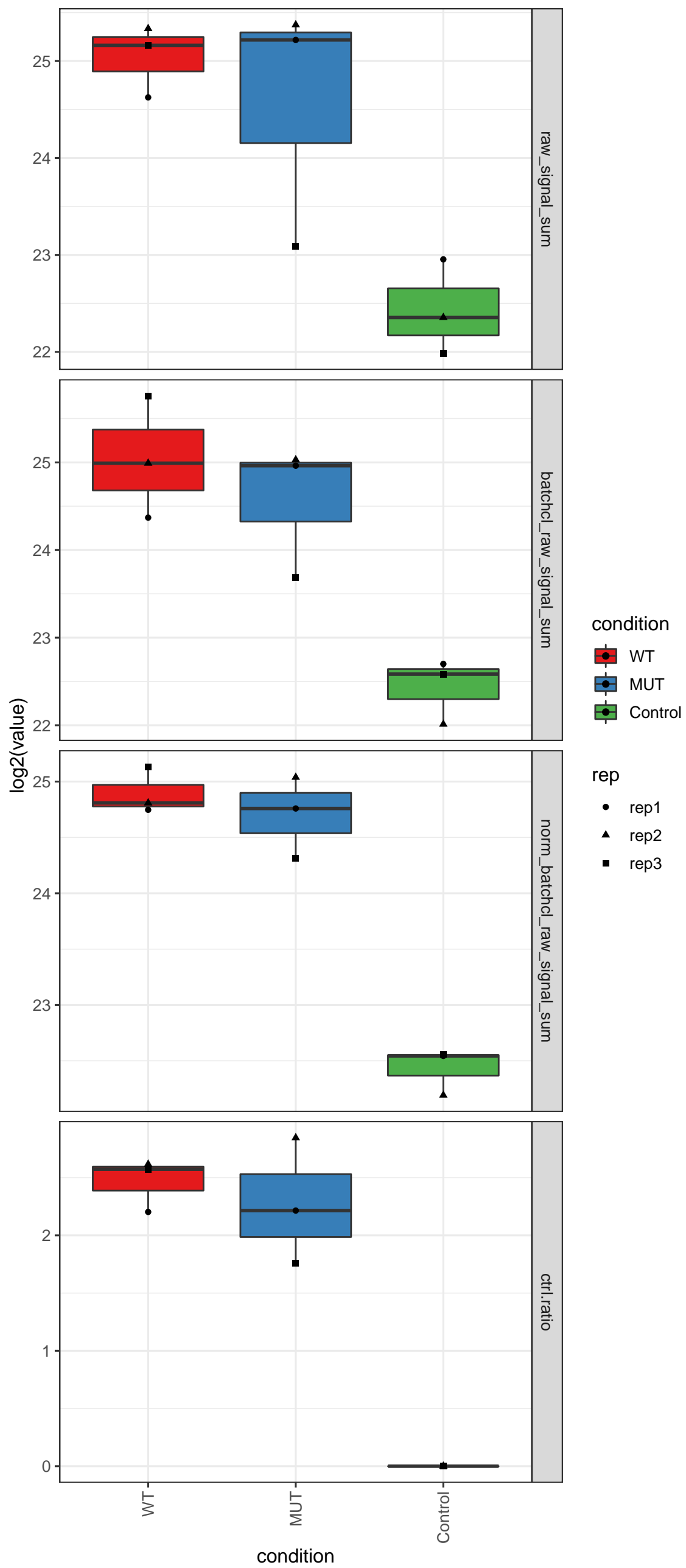


Uncharacterized oxidoreductase YNL181W OS=Saccharomyces cerevisiae



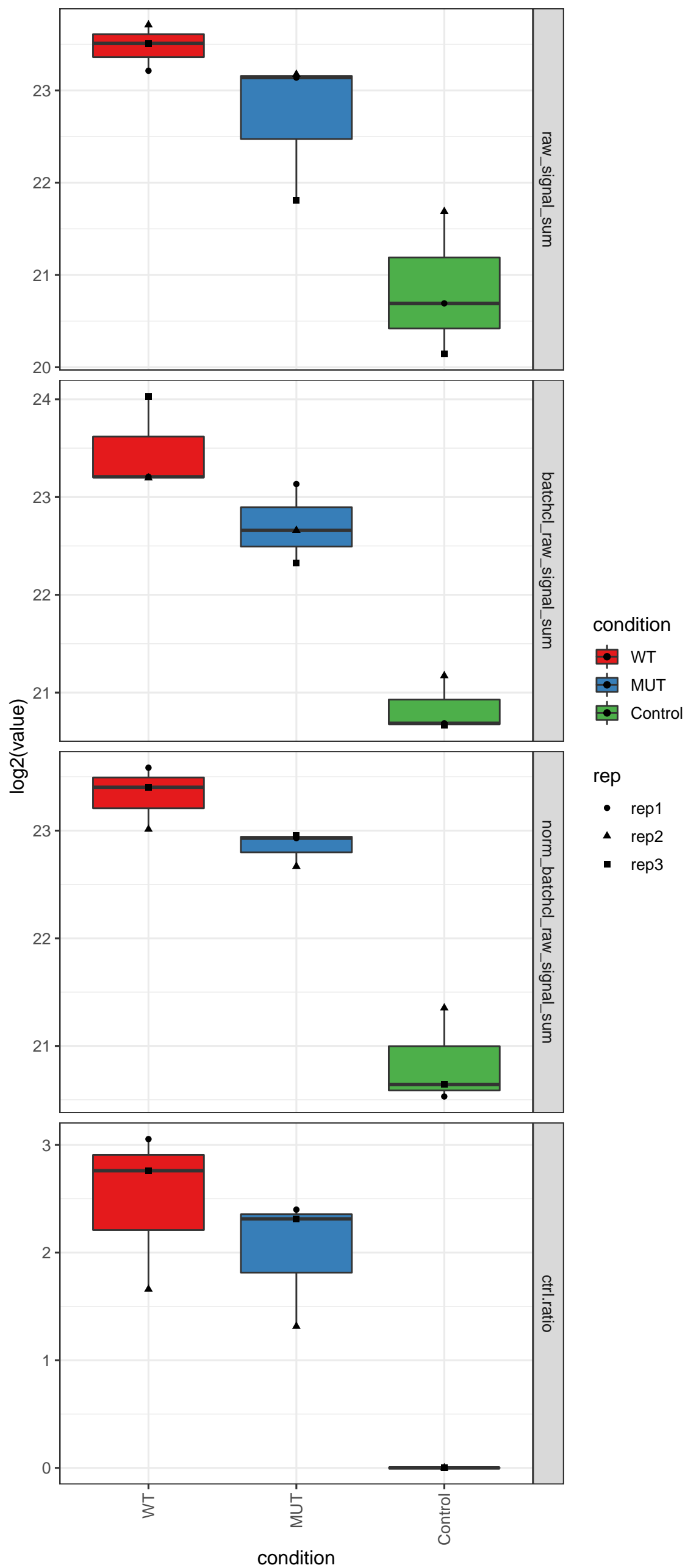
YNL247W – P53852

Cysteine--tRNA ligase OS=*Saccharomyces cerevisiae* (strain ATCC 2045



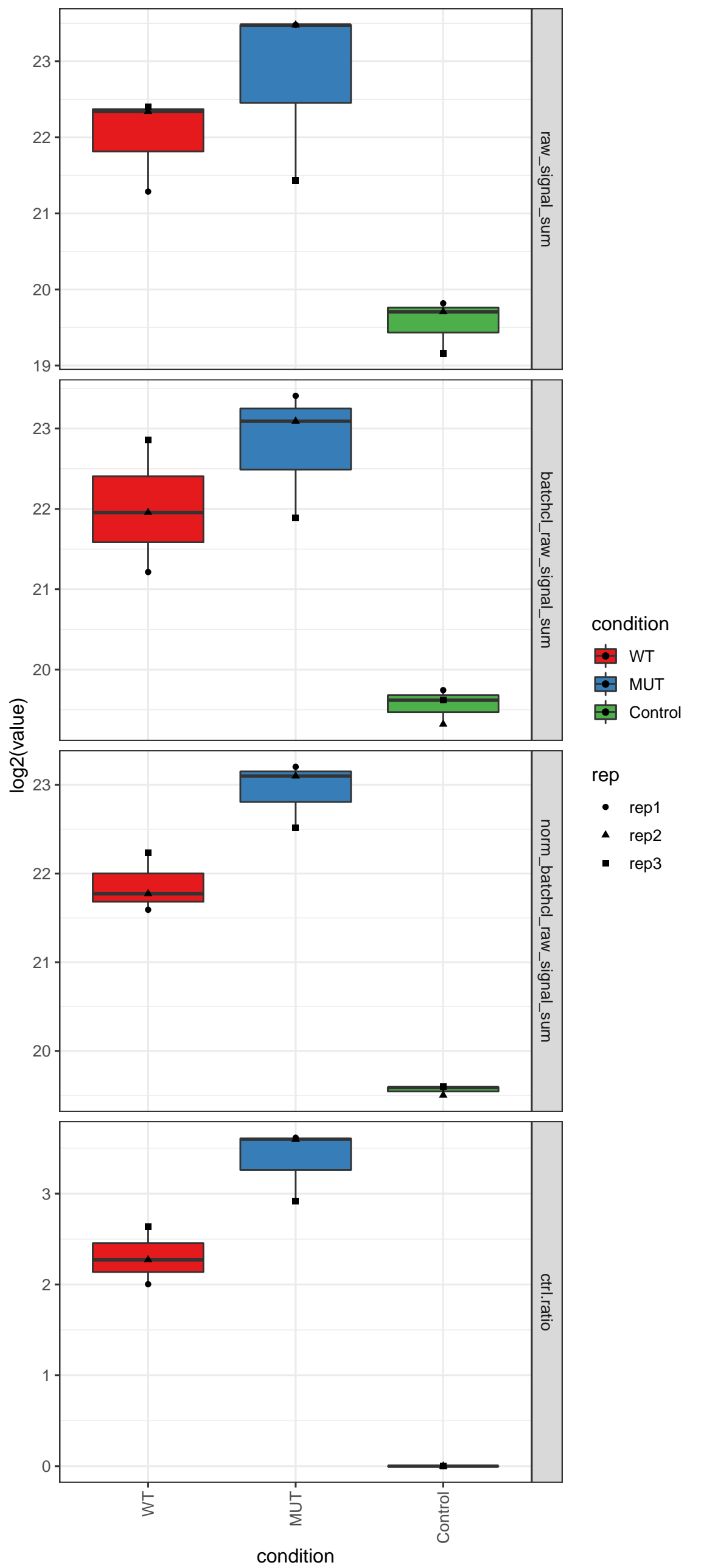
YNR021W – P53723

UPF0674 endoplasmic reticulum membrane protein YNR021W OS=Saccharomyces cerevisiae



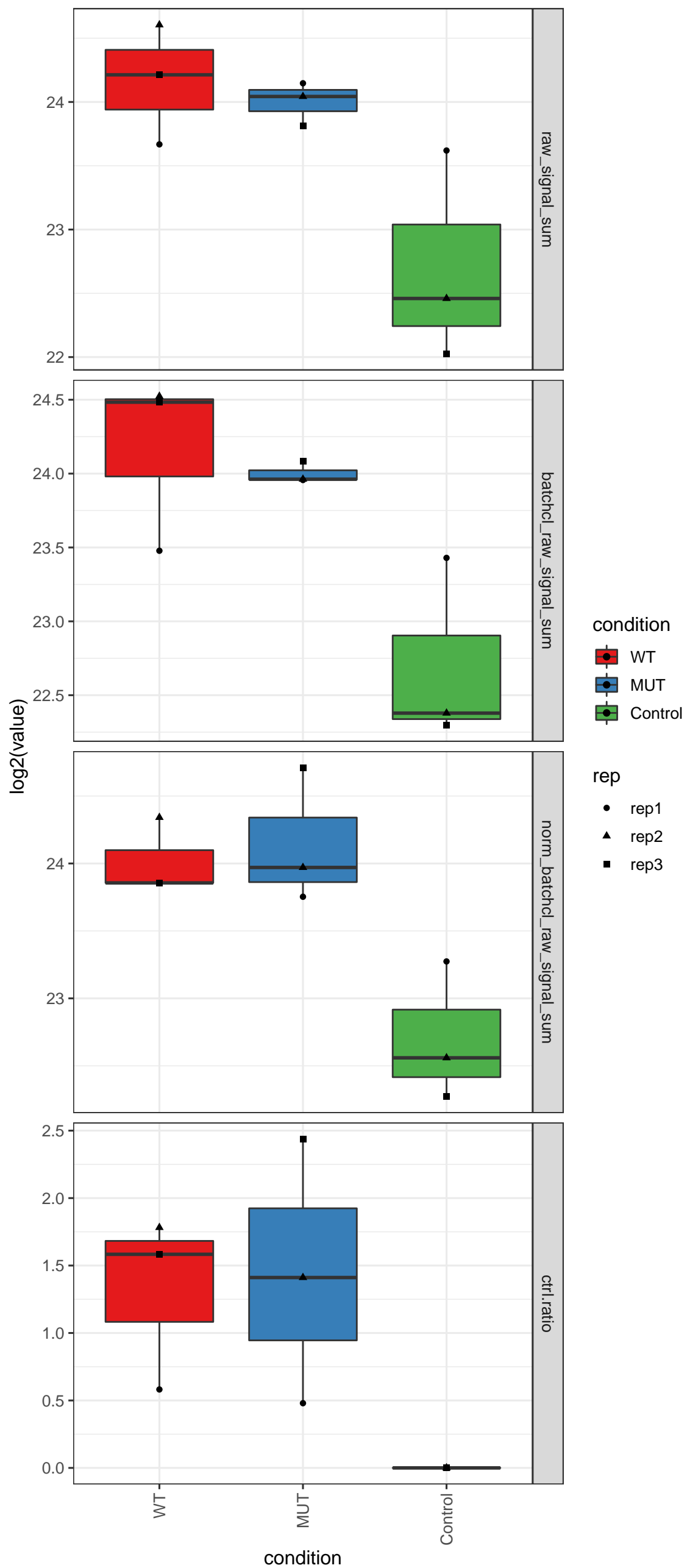
YPK2 – P18961

Serine/threonine–protein kinase YPK2/YKR2 OS=*Saccharomyces cerevisiae*



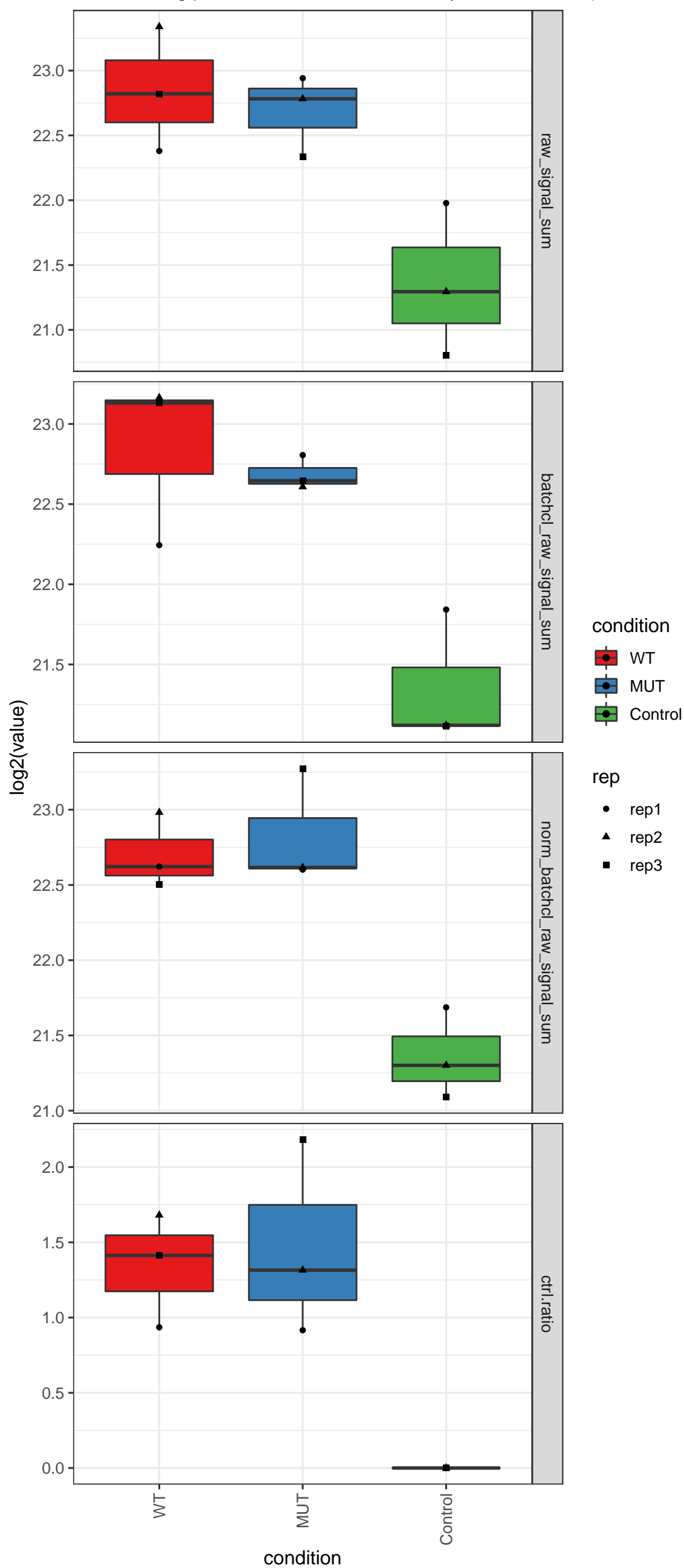
YPT1 – P01123

GTP-binding protein YPT1 OS=*Saccharomyces cerevisiae* (strain ATCC



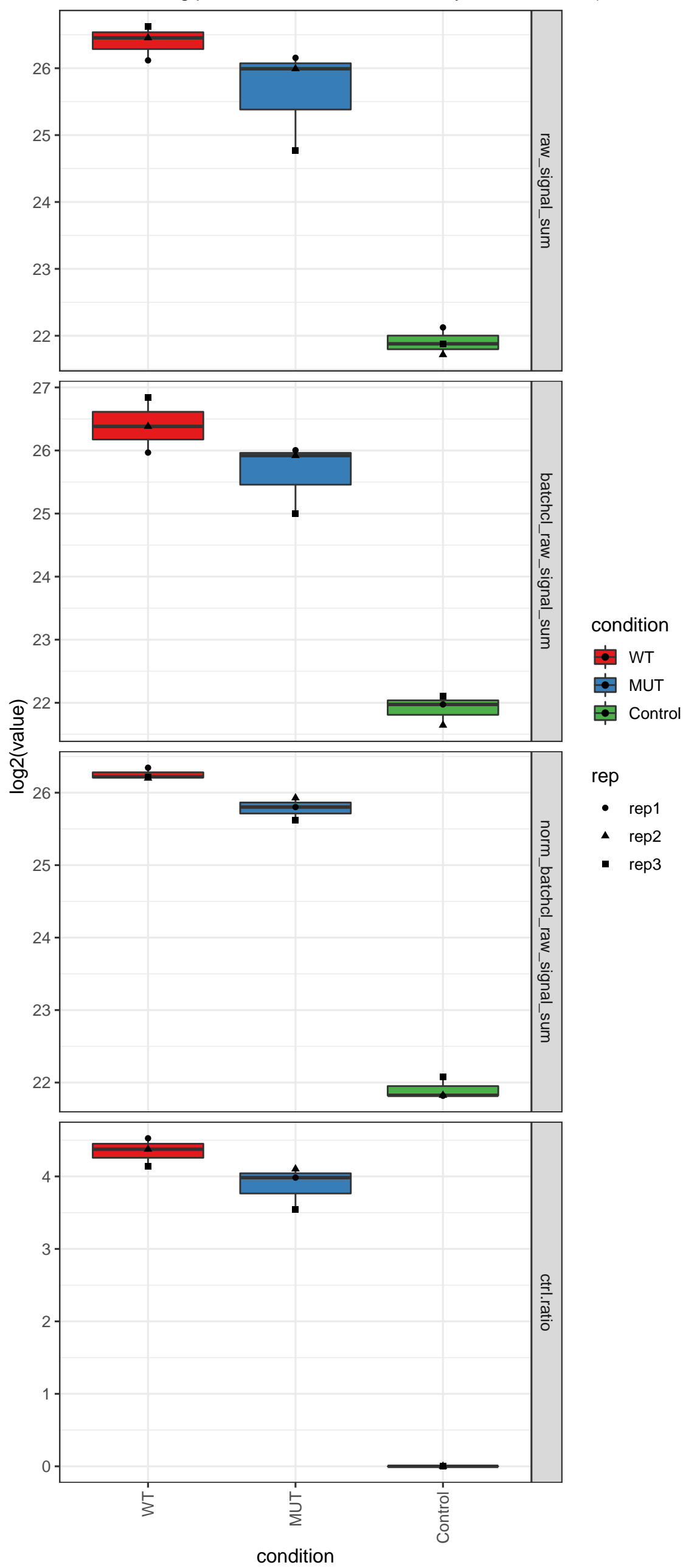
YPT7 – P32939

GTP-binding protein YPT7 OS=*Saccharomyces cerevisiae* (strain ATCC



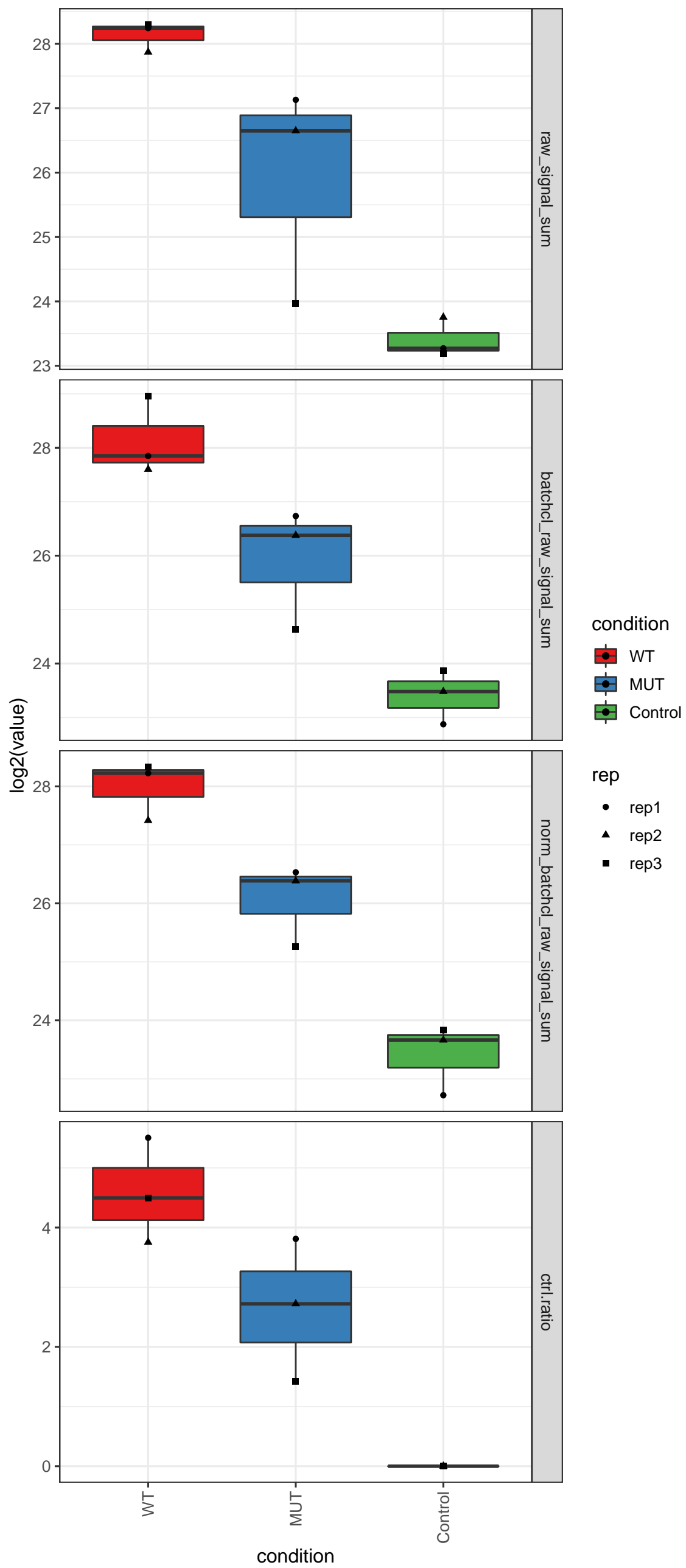
YRA1 – Q12159

RNA annealing protein YRA1 OS=*Saccharomyces cerevisiae* (strain ATCC 25796)



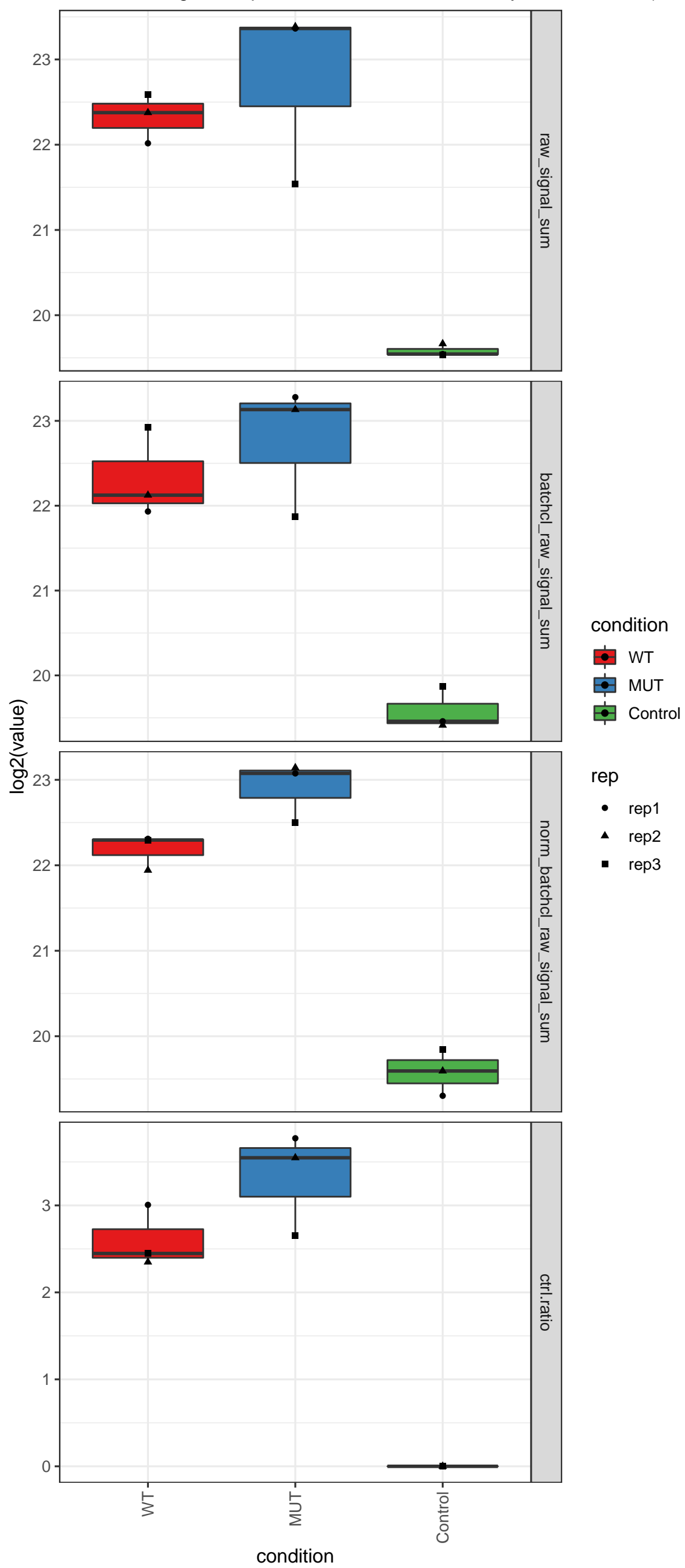
YTA7 – P40340

Tat-binding homolog 7 OS=*Saccharomyces cerevisiae* (strain ATCC 20450)



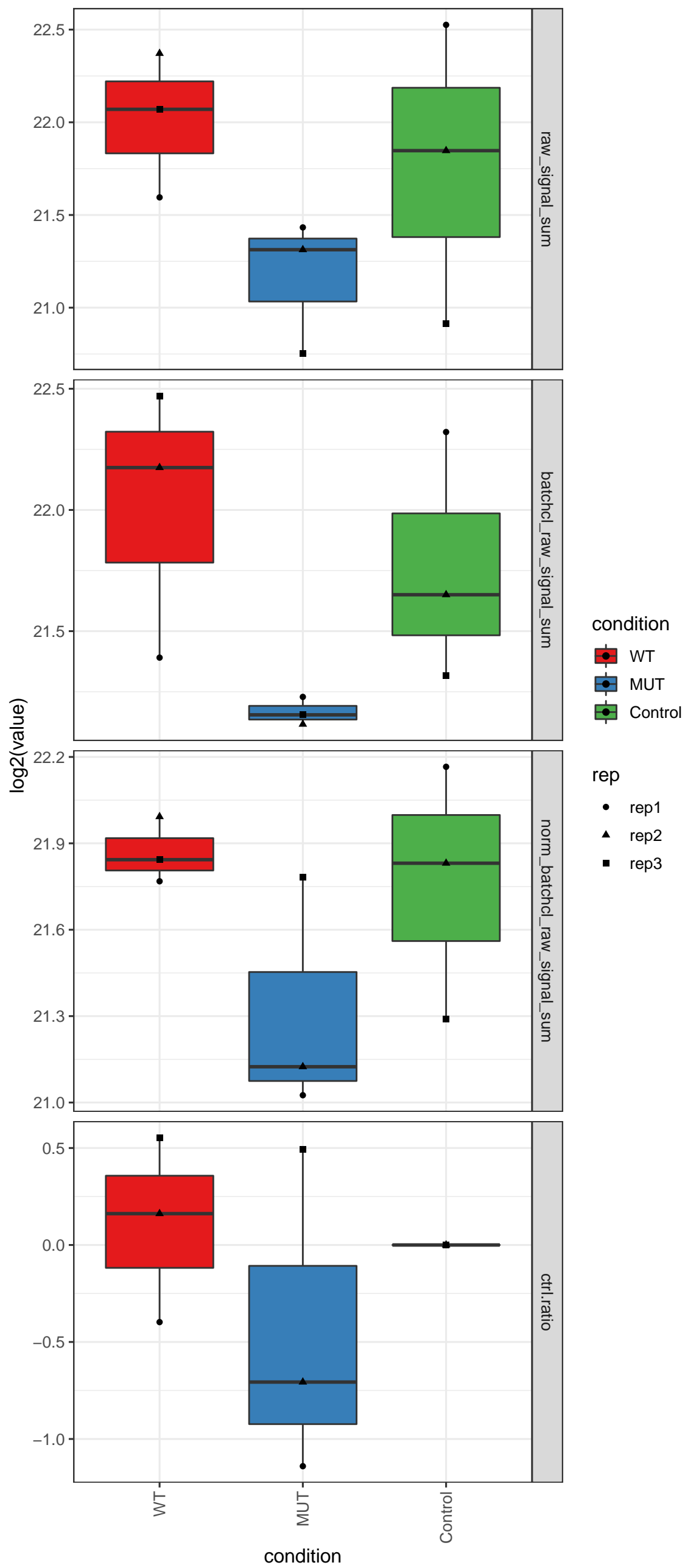
YTM1 – Q12024

Ribosome biogenesis protein YTM1 OS=*Saccharomyces cerevisiae* (strain



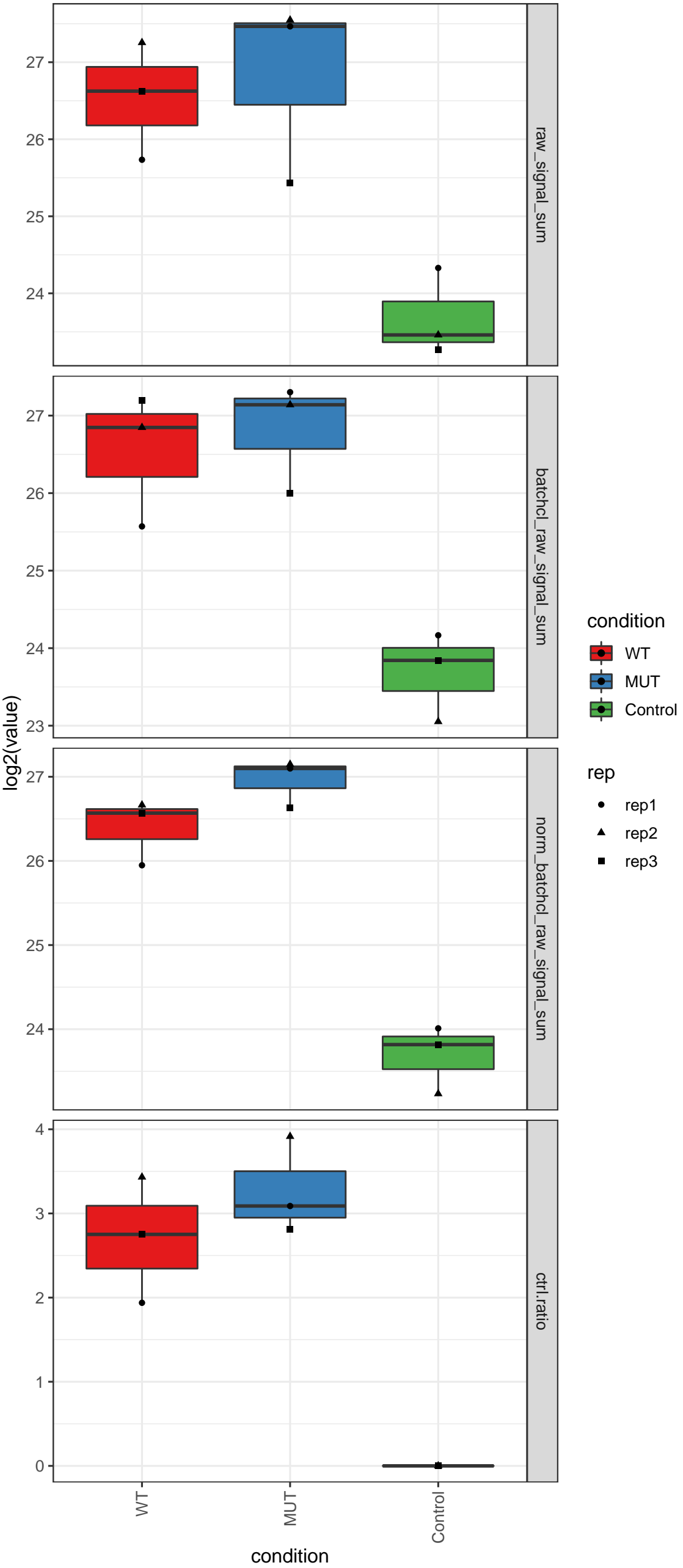
ZEO1 – Q08245

Protein ZEO1 OS=*Saccharomyces cerevisiae* (strain ATCC 204508 / S28)



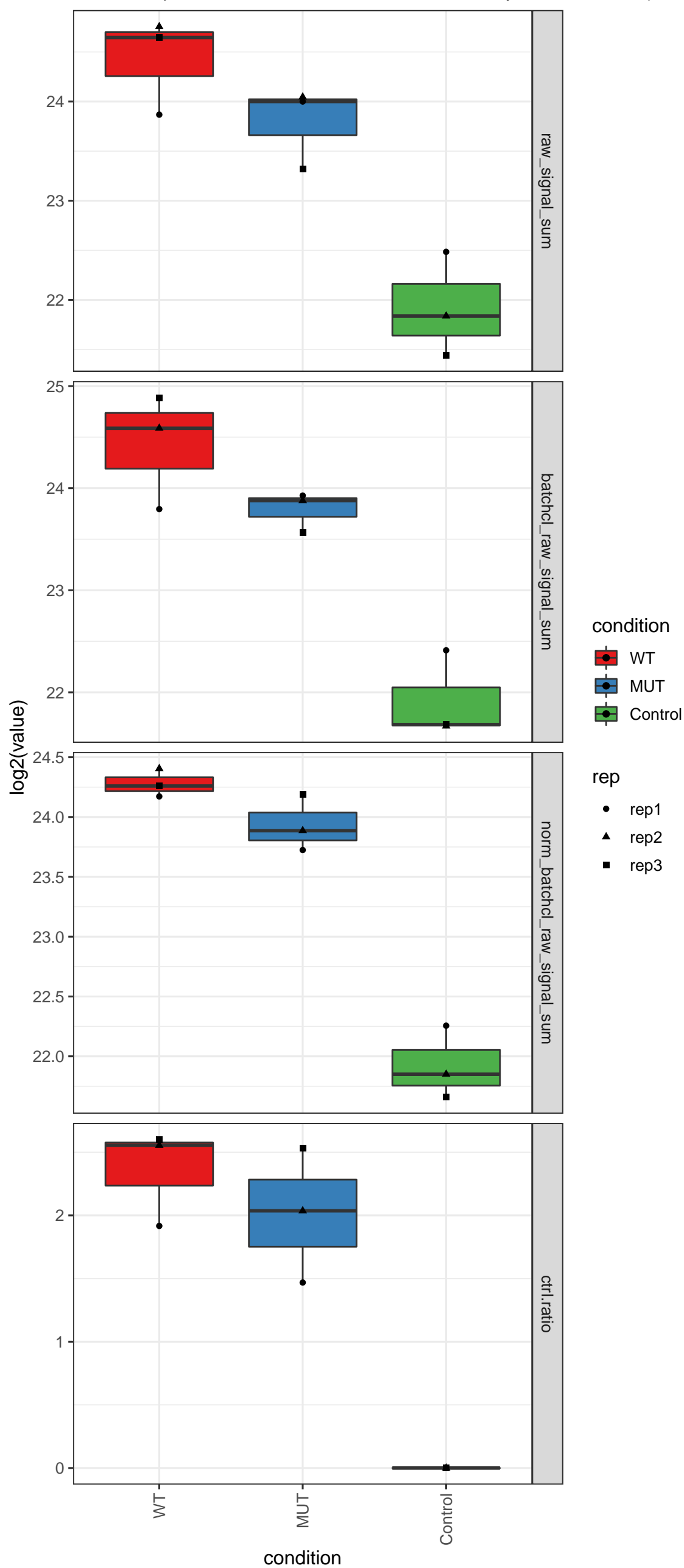
ZIP1 – P31111

Synaptonemal complex protein ZIP1 OS=*Saccharomyces cerevisiae* (strain



Probable quinone oxidoreductase OS=Saccharomyces cerevisiae (strain

Probable quinone oxidoreductase OS=Saccharomyces cerevisiae (strain



ZUO1 – P32527

Zuotin OS=*Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN=

