MGA 6898 Cell Wall and Capsule / / Murein Hydrolases / D-alanyl-D-alanine carboxypeptidase (EC 3.4.16.4)

MGA 53668 Respiration / / Formate\_hydrogenase / tungsten-containing formate dehydrogenase beta subunit MGA 42996 Nucleosides and Nucleotides / Purines / Purine conversions / putative Adenosine kinase (EC 2.7.1.20)

MGA\_53665 Respiration / / Formate\_hydrogenase / tungsten-containing formate dehydrogenase beta subunit

MGA\_42235 Clustering-based subsystems / / CBSS-290633.1.peg.1906 / Mlr7403 protein

MGA 22372 Sulfur Metabolism / / Galactosylceramide and Sulfatide metabolism / probable beta-D-galactosidase

MGA\_7571 Protein Metabolism / Protein degradation / Proteolysis\_in\_bacteria,\_ATP-dependent / ATPase, AFG1 family MGA\_53305 Clustering-based subsystems / / CBSS-224911.1.peg.435 / Peptidase M23B precursor

MGA\_53666 Respiration / / Formate\_hydrogenase / tungsten-containing formate dehydrogenase beta subunit

MGA 38573 Cell Wall and Capsule / / Murein Hydrolases / D-alanyl-D-alanine carboxypeptidase (EC 3.4.16.4)

MGA 7331 Phosphorus Metabolism / / Phosphate metabolism / secreted alkaline phosphatase

MGA 6791 Carbohydrates / Central carbohydrate metabolism / Metabolism / NADPH-dependent methylglyoxal reductase (D-lactaldehyde dehydrogenase)

MGA\_6816 Carbohydrates / Fermentation / Acetyl-CoA\_fermentation\_to\_Butyrate / Probable electron transfer flavoprotein-quinone oxidoreductase FixC (EC 1.5.5.-)

MGA\_7403 Amino Acids and Derivatives / Arginine; urea cycle, polyamines / Putrescine\_utilization\_pathways / Uncharacterized protein in putrescine utilization cluster

MGA 6881 Amino Acids and Derivatives / Aromatic amino acids and derivatives / Aromatic amino acid interconversions with aryl acids / Phenylacetate-coenzyme A ligase (EC 6.2.1.30)

MGA 49990 Respiration / Electron accepting reactions / Ubiquinone Menaquinone-cytochrome\_c\_reductase\_complexes / ubiquinol cytochrome C oxidoreductase, cytochrome C1 subunit

/ Ton and Tol transport systems / tolB protein precursor, periplasmic protein involved in the tonb-independent uptake of group A colicins

MGA\_38413 Cell Wall and Capsule / Capsular and extracellular polysacchrides / Streptococcal\_Hyaluronic\_Acid\_Capsule / UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9)
MGA\_42234 Clustering-based subsystems / / CBSS-290633.1.peg.1906 / Mlr7403 protein

MGA\_49683 Virulence, Disease and Defense / Resistance to antibiotics and toxic compounds / Copper\_homeostasis / Transcriptional activator protein CopR
MGA\_7176 Amino Acids and Derivatives / Branched-chain amino acids / Branched-Chain\_Amino\_Acid\_Biosynthesis / Leucine-responsive regulatory protein, regulator for leucine (or lrp) regulon and high-affinity branched-chain amino acid transport system

MGA 28495 Virulence, Disease and Defense / Resistance to antibiotics and toxic compounds / Zinc resistance / Zinc resistance-associated protein

MGA\_38625 Cell Wall and Capsule / Gram-Negative cell wall components / Outer\_membrane / Outer membrane protein assembly factor YaeT precursor MGA\_38559 Stress Response / Periplasmic Stress / Periplasmic Stress Response / Sigma factor RpoE negative regulatory protein RseB precursor MGA\_53344 RNA Metabolism / Transcription / RNA\_polymerase\_bacterial / DNA-directed RNA polymerase alpha subunit domain

MGA 22095 Stress Response / / Bacterial hemoglobins / diguanylate cyclase/phosphodiesterase (GGDEF & EAL domains) with PAS/PAC sensor(s)

MGA 42141 Stress Response / / Bacterial hemoglobins / diguanylate cyclase/phosphodiesterase (GGDEF & EAL domains) with PAS/PAC sensor(s)

MGA\_53626 Respiration / Electron donating reactions / Respiratory\_dehydrogenases\_1 / quinoprotein alcohol dehydrogenase MGA\_28531 Stress Response / / Bacterial\_hemoglobins / diguanylate cyclase/phosphodiesterase (GGDEF & EAL domains) with PAS/PAC sensor(s) MGA\_38616 Stress Response / / Bacterial\_hemoglobins / diguanylate cyclase/phosphodiesterase (GGDEF & EAL domains) with PAS/PAC sensor(s) MGA\_42203 Miscellaneous / Plant-Prokaryote DOE project / At3g21300 / Transcription regulator [contains diacylglycerol kinase catalytic domain]

MGA 7135 Stress Response / / Bacterial hemoglobins / diguanylate cyclase/phosphodiesterase (GGDEF & EAL domains) with PAS/PAC sensor(s)

MGA 29747 Metabolism of Aromatic Compounds / Metabolism of central aromatic intermediates / Salicylate and gentisate catabolism / salicylate esterase

MGA\_6875 Metabolism of Aromatic Compounds / / Phenylacetyl-CoA\_catabolic\_pathway\_(core) / Putative membrane protein, clustering with ActP PaaL

MGA\_42315 Amino Acids and Derivatives / Arginine; urea cycle, polyamines / Arginine\_Biosynthesis\_extended / Predicted arginine uptake transporter

MGA 28570 Cofactors, Vitamins, Prosthetic Groups, Pigments / Folate and pterines / Pterin metabolism 3 / Dihydropteroate synthase (EC 2.5.1.15)

MGA 29745 Cofactors, Vitamins, Prosthetic Groups, Pigments / Folate and pterines / Pterin\_metabolism 3 / Dihydropteroate synthase (EC 2.5.1.15)

MGA 70563 Respiration / Electron accepting reactions / Terminal cytochrome C oxidases / quinol oxidase polypeptide IV QoxD (EC:1.9.3.-)

MGA\_19775 Respiration / Electron accepting reactions / Anaerobic\_respiratory\_reductases / polysulfide reductase, subunit C

MGA\_53601 Carbohydrates / One-carbon Metabolism / Serine-glyoxylate\_cycle / putative isobutyryl-CoA mutase, chain B MGA\_22495 / / NOT FOUND

MGA\_50137 Nucleosides and Nucleotides / Purines / Purine\_conversions / putative Adenosine kinase (EC 2.7.1.20)

MGA\_22684 DNA Metabolism / DNA repair / DNA\_repair,\_bacterial\_UmuCD\_system / Error-prone repair protein UmuD

MGA 6889 Metabolism of Aromatic Compounds / / p-cymene degradation / HOMODA hydrolase (CmtE) (EC 3.7.1.-)

MGA\_28433 Stress Response / Heat shock / Heat\_shock\_dnaK\_gene\_cluster\_extended / tmRNA-binding protein SmpB

MGA\_28602 RNA Metabolism / Transcription / Transcription\_initiation,\_bacterial\_sigma\_factors / RNA polymerase sigma-70 factor

MGA\_53307 Protein Metabolism / Protein biosynthesis / Ribosome\_biogenesis\_bacterial / Ribonuclease E (EC 3.1.26.12)

MGA\_22707 Stress Response / Heat shock / Heat\_shock\_dnaK\_gene\_cluster\_extended / tmRNA-binding protein SmpB

MGA 7037 Protein Metabolism / Protein biosynthesis / Ribosome SSU bacterial / SSU ribosomal protein Thx

MGA 22759 Protein Metabolism / Protein biosynthesis / Ribosome LSU bacterial / LSU ribosomal protein L36p

MGA 19804 Phosphorus Metabolism / / Phosphate metabolism / secreted alkaline phosphatase

MGA 22475 Nitrogen Metabolism / / Ammonia assimilation / ammonium/methylammonium permease

MGA\_42277 DNA Metabolism / DNA repair / DNA\_repair,\_bacterial / G:T/U mismatch-specific uracil/thymine DNA-glycosylase

MGA\_50095 Protein Metabolism / Protein biosynthesis / Ribosome\_activity\_modulation / Ribosomal subunit interface protein MGA\_50094 Clustering-based subsystems / DNA polymerase III epsilon cluster / CBSS-342610.3.peg.1536 / FIG004599: Hypothetical protein MGA\_53337 Protein Metabolism / Protein folding / GroEL\_GroES / Heat shock protein 60 family co-chaperone GroES

MGA\_29700 Protein Metabolism / Protein biosynthesis / Translation\_initiation\_factors\_bacterial / Translation initiation factor SUI1-related protein
MGA\_49682 Virulence, Disease and Defense / Resistance to antibiotics and toxic compounds / Copper\_homeostasis / Transcriptional activator protein CopR
MGA\_19989 Cell Wall and Capsule / / Peptidoglycan\_Crosslinking\_of\_Peptide\_Stems / L,D-transpeptidase YhG
MGA\_28513 Fatty Acids, Lipidos, Lipidos,

MGA 7624 Cell Wall and Capsule / Gram-Negative cell wall components / Lipoprotein sorting system / Outer membrane lipoprotein LolB precursor

MGA 49678 Virulence, Disease and Defense / Resistance to antibiotics and toxic compounds / Copper homeostasis / Transcriptional activator protein CopR MGA\_20073 Carbohydrates / Central carbohydrate metabolism / Pyruvate\_Alanine\_Serine\_Interconversions / Valine--pyruvate aminotransferase (EC 2.6.1.66)

MGA\_42198 Cell Wall and Capsule / Capsular and extracellular polysacchrides / Sialic\_Acid\_Metabolism / UDP-N-acetylglucosamine 2-epimerase (EC 5.1.3.14)

MGA\_20238 Cofactors, Vitamins, Prosthetic Groups, Pigments / Quinone cofactors / Pyrroloquinoline\_Quinone\_biosynthesis / Microsomal dipeptidase (EC 3.4.13.19)
MGA\_42290 Regulation and Cell signaling / / The\_Chv\_regulatory\_system\_of\_Alphaproteobacteria / Phosphocarrier protein, nitrogen regulation associated
MGA\_42289 Regulation and Cell signaling / / The\_Chv\_regulatory\_system\_of\_Alphaproteobacteria / Phosphocarrier protein, nitrogen regulation associated

MGA 6975 Amino Acids and Derivatives / Histidine Metabolism / Histidine Degradation / Conserved hypothetical protein (perhaps related to histidine degradation)

MGA 7337 Membrane Transport / / Ton\_and\_Tol\_transport\_systems / tolB protein precursor, periplasmic protein involved in the tonb-independent uptake of group A colicins

MGA 7294 Amino Acids and Derivatives / Branched-chain amino acids / Valine degradation / Predicted transcriptional regulator of leucine degradation pathway, MerR family

MGA-42350 Phages, Prophages, Transposable elements, Plasmids / Phages, Prophages / Phage packaging machinery / Phage terminase, small subunit

MGA 38400 Cell Wall and Capsule / Gram-Negative cell wall components / Major Outer Membrane Proteins / Integral membrane protein YfiB

MGA\_28511 Carbohydrates / Fermentation / Acetyl-CoA\_fermentation\_to\_Butyrate / Probable electron transfer flavoprotein-quinone oxidoreductase FixC (EC 1.5.5.-) MGA\_7459 Carbohydrates / Central carbohydrate metabolism / Methylglyoxal\_Metabolism / NADPH-dependent methylglyoxal reductase (D-lactaldehyde dehydrogenase)
MGA\_28512 NA / NA / NA

MGA\_20078 Carbohydrates / Central carbohydrate metabolism / Dehydrogenase\_complexes / Enoyl-CoA hydratase [branched-chain amino acid degradation] (EC 4.2.1.17)

MGA\_20077 Carbohydrates / Central carbohydrate metabolism / Dehydrogenase\_complexes / Enoyl-CoA hydratase [branched-chain amino acid degradation] (EC 4.2.1.17)

MGA\_7321 Membrane Transport / Protein secretion system, Type II / Widespread\_colonization\_island / Von Willebrand factor type A domain protein, associated with Flp pilus assembly

MGA\_7398 Metabolism of Aromatic Compounds / Metabolism of central aromatic intermediates / N-heterocyclic\_aromatic\_compound\_degradation / Isoquinoline 1-oxidoreductase beta subunit (EC 1.3.99.16)

MGA 53308 Miscellaneous / Plant-Prokaryote DOE project / Iojap / Nicotinamidase (EC 3.5.1.19)

MGA\_7189 Stress Response / / Phage\_shock\_protein\_(psp)\_operon / Phage shock protein E

MGA 42855 RNA Metabolism / RNA processing and modification / Queuosine-Archaeosine Biosynthesis / tRNA-guanine transglycosylase (EC 2.4.2.29)

MGA 7431 Carbohydrates / Monosaccharides / L-fucose\_utilization\_temp / dehydrogenase clustered with L-fuconate utilization genes

MGA\_22451 Carbohydrates / Di- and oligosaccharides / Maltose\_and\_Maltodextrin\_Utilization / Maltodextrin glycosyltransferase MmtA\_MGA\_7545 Carbohydrates / Central carbohydrate metabolism / Glyoxylate\_bypass / Malate synthase G (EC 2.3.3.9)

MGA 7401 Amino Acids and Derivatives / Arginine; urea cycle, polyamines / Putrescine utilization pathways / Uncharacterized protein in putrescine utilization cluster

MGA\_50043 Regulation and Cell signaling / / Orphan\_regulatory\_proteins / Two-component system response regulator QseB
MGA\_20079 Carbohydrates / Central carbohydrate metabolism / Dehydrogenase\_complexes / Enoyl-CoA hydratase [branched-chain amino acid degradation] (EC 4.2.1.17)

MGA\_53653 Cell Wall and Capsule / Capsular and extracellular polysacchrides / Streptococcal\_Hyaluronic\_Acid\_Capsule / UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9)

MGA\_20026 Membrane Transport / / Ton\_and\_Tol\_transport\_systems / tolB protein precursor, periplasmic protein involved in the tonb-independent uptake of group A colicins MGA\_28514 Cofactors, Vitamins, Prosthetic Groups, Pigments / Biotin / Biotin\_biosynthesis / predicted biotin regulatory protein BioR (GntR family)

MGA\_28510 Carbohydrates / Fermentation / Acetyl-CoA\_fermentation\_to\_Butyrate / Probable electron transfer flavoprotein-quinone oxidoreductase FixC (EC 1.5.5.-)

MGA\_7456 / / NOT FOUND

MGA\_703747 Matter Street Company (April 1997) Acetyl-CoA\_fermentation\_to\_Butyrate / Probable electron transfer flavoprotein-quinone oxidoreductase FixC (EC 1.5.5.-)

MGA 28439 Amino Acids and Derivatives / Branched-chain amino acids / Valine degradation / Predicted transcriptional regulator of leucine degradation pathway, MerR family

MGA\_22327 Membrane Transport / / Ton\_and\_Tol\_transport\_systems / tolB protein precursor, periplasmic protein involved in the tonb-independent uptake of group A colicins

MGA\_53322 DNA Metabolism / / DNA\_structural\_proteins,\_bacterial / Chromosome partition protein MukF
MGA\_53380 Membrane Transport / / Ton\_and\_Tol\_transport\_systems / tolB protein precursor, periplasmic protein involved in the tonb-independent uptake of group A colicins

MGA\_20106 Miscellaneous / / ZZ\_gjo\_need\_homes / Virulence factor MviM MGA\_22754 Carbohydrates / Central carbohydrate metabolism / Pyruvate\_metabolism\_I:\_anaplerotic\_reactions,\_PEP / Two-component sensor histidine kinase, malate (EC 2.7.3.-)

MGA\_50116 Membrane Transport / / Ton\_and\_Tol\_transport\_systems / tolB protein precursor, periplasmic protein involved in the tonb-independent uptake of group A colicins

MGA\_29581 Phages, Prophages, Transposable elements / Bacteriophage integration/excision/lysogeny / Phage\_integration\_and\_excision / Phage inihibitor of recBCD nuclease MGA\_6883 Metabolism of Aromatic Compounds / / Aromatic\_Amin\_Catabolism / Phenylacetaldehyde dehydrogenase (EC 1.2.1.39)

MGA\_50133 Protein Metabolism / Protein degradation / Proteolysis\_in\_bacteria,\_ATP-dependent / ATPase, AFG1 family
MGA\_22437 Membrane Transport / Protein secretion system, Type II / Widespread\_colonization\_island / Von Willebrand factor type A domain protein, associated with Flp pilus assembly

MGA\_22510 Cofactors, Vitamins, Prosthetic Groups, Pigments / Tetrapyrroles / Heme\_and\_Siroheme\_Biosynthesis / Uroporphyrinogen-III synthase, divergent, Francisella type (EC 4.2.1.75) MGA\_29622 Clustering-based subsystems / Biosynthesis of galactoglycans and related lipopolysacharides / CBSS-258594.1.peg.3339 / putative glycosyltransferase protein MGA\_22260 Membrane Transport / / Ton\_and\_Tol\_transport\_systems / tolB protein precursor, periplasmic protein involved in the tonb-independent uptake of group A colicins

MGA\_20011 Cell Division and Cell Cycle / / Bacterial\_Cytoskeleton / Cell-shape determining protein MreBH
MGA\_42827 Cofactors, Vitamins, Prosthetic Groups, Pigments / Folate and pterines / Molybdenum\_cofactor\_biosynthesis / Protein co-occurring with molybdenum cofactor biosynthesis protein B

MGA\_7034 Protein Metabolism / Protein biosynthesis / Translation\_elongation\_factors\_bacterial / Translation elongation factor LepA
MGA\_7156 DNA Metabolism / DNA repair / DNA\_repair, \_UvrABC\_system / Excinuclease ABC subunit A paralog of unknown function
MGA\_28432 Protein Metabolism / Protein biosynthesis / Ribosome\_biogenesis\_bacterial / Ribonuclease E (EC 3.1.26.12)
MGA\_38407 Stress Response / Cold shock / Cold\_shock, \_CspA\_family\_of\_proteins / Cold shock protein CspI
MGA\_42165 Clustering-based subsystems / Isographics is / Translation initiation footage of the protein initiat

MGA\_19986 Membrane Transport / Protein and nucleoprotein secretion system, Type IV / pVir\_Plasmid\_of\_Campylobacter / Type IV secretion/competence protein (VirB9)

MGA\_95529 Carbohydrates / Fermentation / Acetyl-CoA\_fermentation\_to\_Butyrate / Probable electron transfer flavoprotein-quinone oxidoreductase FixC (EC 1.5.5.-) MGA 95530 Carbohýdrates / Fermentation / Acetýl-CoA fermentation to Butýrate / Probable electron transfer flavoprotein-quinone oxidoreductase FixC (EC 1.5.5.-)

MGA\_7607 Clustering-based subsystems / Putative asociate of RNA polymerase sigma-54 factor rpoN / CBSS-316057.3.peg.1308 / RNA polymerase sigma-70 factor MGA\_19774 Carbohydrates / Fermentation / Acetyl-CoA\_fermentation\_to\_Butyrate / Probable electron transfer flavoprotein-quinone oxidoreductase FixC (EC 1.5.5.-)

MGA\_7320 Membrane Transport / Protein secretion system, Type II / Widespread\_colonization\_island / Von Willebrand factor type A domain protein, associated with Flp pilus assembly MGA\_22458 Membrane Transport / Protein secretion system, Type II / Widespread\_colonization\_island / Von Willebrand factor type A domain protein, associated with Flp pilus assembly MGA\_53304 Protein Metabolism / Protein folding / Periplasmic\_disulfide\_interchange / Thiol:disulfide interchange protein DsbG precursor

MGA 22238 Stress Response / Oxidative stress / Glutathione: Non-redox reactions / Uncharacterized glutathione S-transferase-like protein

MGA\_50057 Miscellaneous / / ZZ\_gjo\_need\_homes / Virulence factor MviM
MGA\_28711 RNA Metabolism / Transcription / Transcription\_factors\_bacterial / Rho-specific inhibitor of transcription termination (YaeO)

MGA\_28529 Regulation and Cell signaling / / Orphan\_regulatory\_proteins / Two-component system response regulator QseB
MGA\_22659 Amino Acids and Derivatives / Lysine, threonine, methionine, and cysteine / Methionine\_Biosynthesis / Predicted regulator of methionine metabolism, ArsR family
MGA\_70564 Respiration / Electron accepting reactions / Terminal\_cytochrome\_C\_oxidases / quinol oxidase polypeptide IV QoxD (EC:1.9.3.-)

MGA 20197 NA / NA / NA / NA

MGA 7199 / / NOT FOUND MGA\_22825 NA / NA / NA / NA MGA\_7628 NA / NA / NA / NA

MGA\_53335 NA / NA / NA / NA

MGA\_22692 NA / NA / NA / NA MGA<sup>-</sup>7583 NA / NA / NA / NA

MGA\_28595 NA / NA / NA / NA

MGA<sup>-</sup>7466 NA / NA <sup>-</sup>/ NA / NA

MGA\_71050 / / NOT FOUND MGA 7582 NA / NA / NA / NA

MGA\_19800 NA / NA / NA / NA MGA\_7336 NA / NA / NA / NA MGA 7615 / / NOT FOUND

MGA\_20260 NA '/ NA / NA / NA

MGA<sup>-</sup>42204 NA / NA / NA / NA

MGA\_42227 NA / NA / NA / NA

MGA\_22729 NA / NA / NA / NA / NA / NA MGA\_22862 NA / NA / NA / NA / NA MGA\_29480 NA / NA / NA / NA / NA MGA\_28603 NA / NA / NA / NA MGA\_42929 / / / NOT FOUND

MGA\_22689 NA / NA / NA / NA MGA 7629 NA / NA / NA / NA MGA<sup>22513</sup> Membrane Transport /

MGA\_53604 NA / NA / NA / NA MGA<sup>-</sup>7162 NA / NA / NA / NA MGA<sup>-</sup>66867 NA / NA / NA / NA MGA\_19987 NA / NA / NA / NA MGA 42930 / / NOT FOUND

MGA 53603 NA / NA / NA / NA

MGA\_19978 NA / NA / NA / NA MGA<sup>-</sup>42830 NA / NA / NA / NA MGA<sup>2</sup>9723 NA / NA / NA / NA

MGA<sup>-</sup>6908 NA / NA / NA / NA

MGA<sup>-</sup>49633 NA <sup>'</sup>/ NA / NA / NA MGA\_49999 NA / NA / NA / NA

MGA<sup>22539</sup> / / NOT FOUND

MGA 19988 NA / NA / NA / NA

MGA\_38505 / / / NOT FOUND MGA\_22664 NA / NA / NA / NA MGA\_38380 NA / NA / NA / NA MGA\_42316 / / NOT FOUND

MGA 53725 NA / NA / NA / NA MGA<sup>-</sup>76905 NA / NA / NA / NA

MGA 72835 NA / NA / NA / NA MGA\_7334 NA / NA / NA / NA

MGA\_6958 / / / NOT FOUND MGA 43272 NA / NA / NA / NA

MGA\_29482 NA / NA / NA / NA MGA 28509 / / NOT FOUND MGA<sup>2</sup>9746 / / NOT FOUND

MGA\_7465 / / / NOT FOUND MGA\_22320 / / / NOT FOUND MGA 7589 NA / NA / NA / NA

MGA\_80647 / / 1/ NOT FOUND MGA\_53302 NA / NA / NA / NA MGA\_75221 NA / NA / NA / NA

MGA\_38612 NA / NA / NA / NA MGA 71047 / / / NOT FOUND

MGA\_20164 NA / NA / NA / NA MGA\_20165 NA / NA / NA / NA MGA\_42137 NA / NA / NA / NA

MGA\_7267 NA / NA / NA / NA MGA<sup>-</sup>10415 NA / NA / NA / NA

MGA\_42113 NA / NA / NA / NA

MGA\_6884 NA / NA / NA / NA MGA 20146 / / NOT FOUND

MGA 6890 NA / NA / NA / NA

MGA\_29491 NA / NA / NA / NA MGA\_38620 NA / NA / NA / NA MGA\_42344 NA / NA / NA / NA

MGA<sup>-</sup>22822 NA / NA / NA / NA

MGA 22542 NA / NA / NA / NA

MGA\_7137 NA / NA / NA / NA MGA 6891 / / / NOT FOUND MGA\_19808 NA / NA / NA / NA MGA<sup>-</sup>19803 NA / NA / NA / NA MGA<sup>2</sup>0166 NA / NA / NA / NA MGA\_66850 NA / NA / NA / NA

|MGA<sup>-</sup>7099 NA / NA / NA / NA

MGA<sup>-</sup>50031 NA / NA / NA / NA

MGA 7470 NA / NA / NA / NA

MGA 7089 NA / NA / NA / NA

MGA<sup>-</sup>19985 NA / NA / NA / NA

SUC73\_c\_vs\_SUC.57\_mean\_log2F0 SUC73\_a\_vs\_SUC.57\_mean\_log2F0 SUC57\_c\_vs\_SUC.57\_mean\_log2F0 SUC57\_a\_vs\_SUC.57\_mean\_log2F0 SUC57\_b\_vs\_SUC.57\_mean\_log2F0 SUC109\_b\_vs\_SUC.57\_mean\_log2F0 SUC109\_a\_vs\_SUC.57\_mean\_log2F0 SUC109\_c\_vs\_SUC.57\_mean\_log2F0 SUC109\_c\_vs\_SUC.57\_mean\_log2F0

10

-10

-15