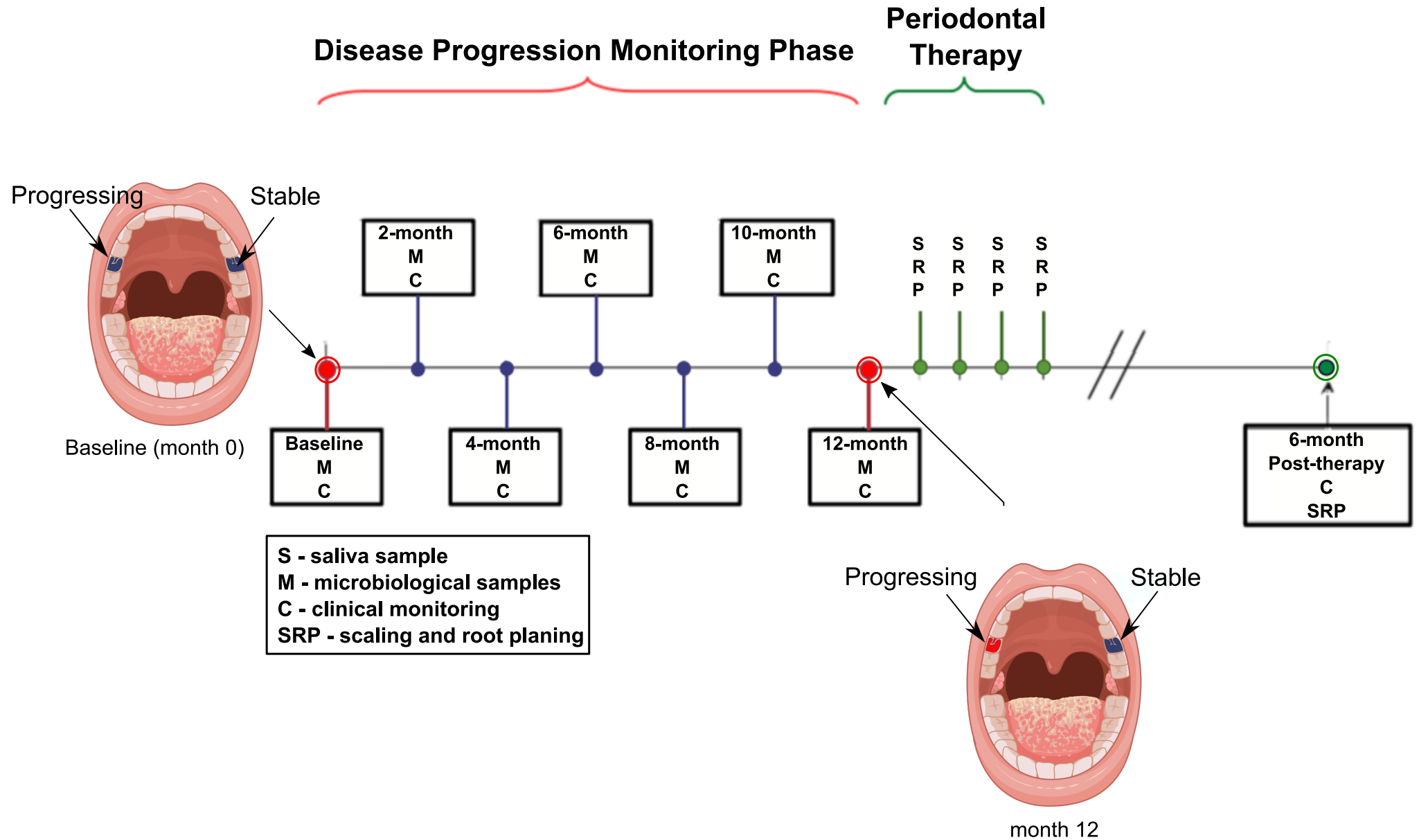
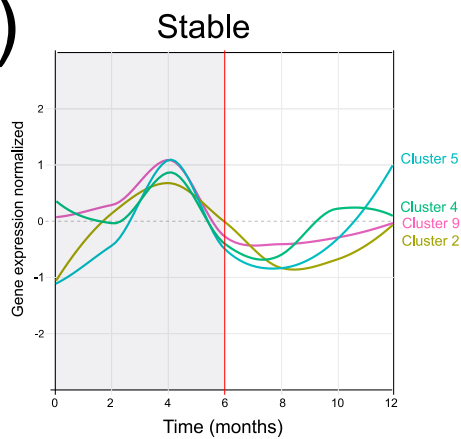


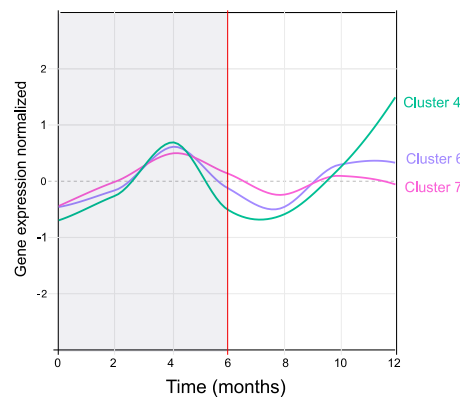
Figure S1



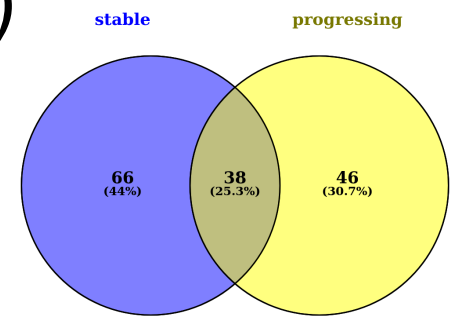
a)



Progressing



b)



c)

Exclusively in stable

Actinomyces_naeslundii
Actinomyces_oris
Actinomyces_sp._oral_taxon_170
Actinomyces_sp._oral_taxon_175
Actinomyces_sp._oral_taxon_180
Actinomyces_sp._oral_taxon_414
Actinomyces_sp._oral_taxon_448
Actinomyces_timonensis
Atopobium_sp._oral_taxon_199
Campylobacter_conciscus
Campylobacter_curvus
Campylobacter_rectus
Capnocytophaga_gingivalis
Capnocytophaga_granulosa
Capnocytophaga_haemolytica
Capnocytophaga_leadbetteri
Capnocytophaga_ochracea
Capnocytophaga_sp._oral_taxon_323
Capnocytophaga_sp._oral_taxon_324
Capnocytophaga_sp._oral_taxon_335
Capnocytophaga_sp._oral_taxon_380
Capnocytophaga_sp._oral_taxon_412
Capnocytophaga_sp._oral_taxon_878
Capnocytophaga_sputigena
Cryptobacterium_curtum
Cutibacterium_acnes
Dialister_pneumosintes
Fusobacterium_periodonticum
Haemophilus_pittmaniae
Kingella_oralis
Lachnoanaerobaculum_orale
Lachnoanaerobaculum_saburreum
Leptotrichia_sp._oral_taxon_215
Leptotrichia_sp._oral_taxon_417
Leptotrichia_wadei
Mogibacterium_diversum
Mogibacterium_neglectum
Mogibacterium_timidum
Neisseria_bacilliformis
Neisseria_perflava
Neisseria_polysaccharaea
Oribacterium_asaccharolyticum
Oribacterium_sp._oral_taxon_078
Ottowia_sp._oral_taxon_894
Parvimonas_micra
Peptostreptococcaceae_bacterium_oral_taxon_113
Porphyromonas_sp._oral_taxon_275
Prevotella_jejuni
Prevotella_salivae
Prevotella_sp._oral_taxon_475
Prevotella_veroralis
Propionibacterium_acidifaciens
Pseudopropionibacterium_rubrum
Rothia_aeria
Scardovia_wiggsiae
Schaalia_meyeri
Selenomonas_sp._oral_taxon_133
Selenomonas_sp._oral_taxon_136
Selenomonas_sp._oral_taxon_478
Selenomonas_sputigena
Stomatobaculum_longum
Streptococcus_anginosus
Streptococcus_infantis
Streptococcus_peroris
Treponema_lecithinolyticum
Veillonella_sp._oral_taxon_780

Exclusively in progressing

Actinomyces_dentalis
Actinomyces_graevenitzii
Actinomyces_sp._oral_taxon_169
Actinomyces_sp._oral_taxon_171
Actinomyces_sp._oral_taxon_172
Aggregatibacter_segnis
Aggregatibacter_sp._oral_taxon_458
Alloprevotella_rava
Alloprevotella_tanneriae
Atopobium_parvulum
Bacteroidetes_oral_taxon_274
Capnocytophaga_sp._oral_taxon_338
Capnocytophaga_sp._oral_taxon_864
Catonella_morbi
Eikenella_corrodens
Fusobacterium_naviforme
Fusobacterium_nucleatum
Gemella_morbilorum
Gemella_sanguinis
Leptotrichia_buccalis
Leptotrichia_sp._oral_taxon_498
Neisseria_cinerea
Neisseria_elongata
Neisseria_macacae
Neisseria_mucosa
Neisseria_oralis
Olsenella_sp._oral_taxon_807
Peptostreptococcus_stomatis
Prevotella_fusca
Prevotella_melaninogenica
Prevotella_oralis
Prevotella_shahii
Prevotella_sp._oral_taxon_317
Pseudopropionibacterium_propionicum
Schaalia_cardiffensis
Schaalia_georgiae
Selenomonas_artemidis
Streptococcus_cristatus
Streptococcus_lactarius
Streptococcus_parasanguinis
Streptococcus_sanguinis
Tannerella_sp._oral_taxon_HOT-286
TM7_phylum_sp._oral_taxon_350
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TM7_phylum_sp._oral_taxon_957

Common elements in progressing and stable

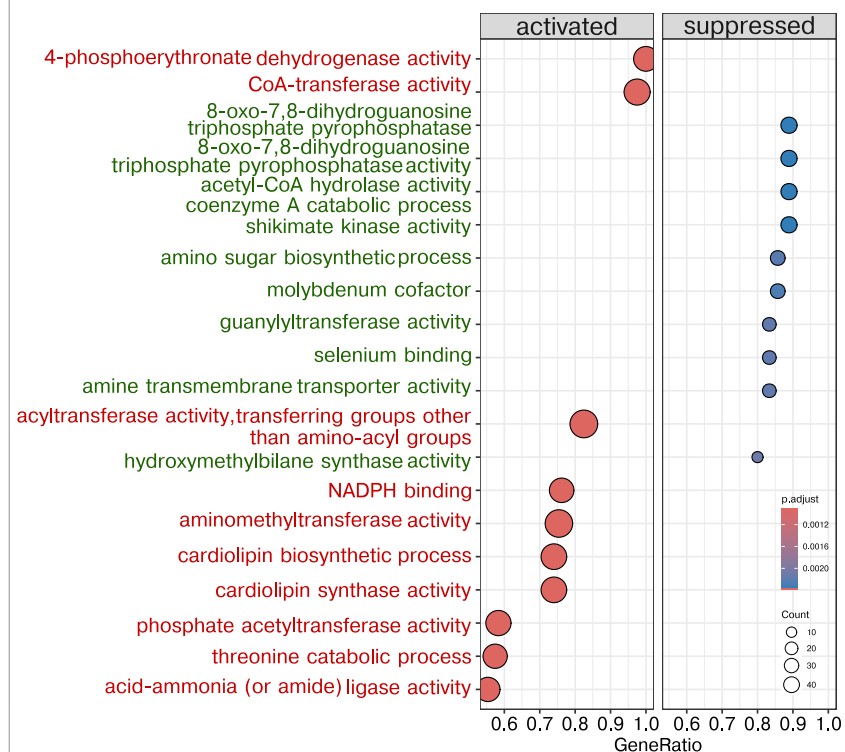
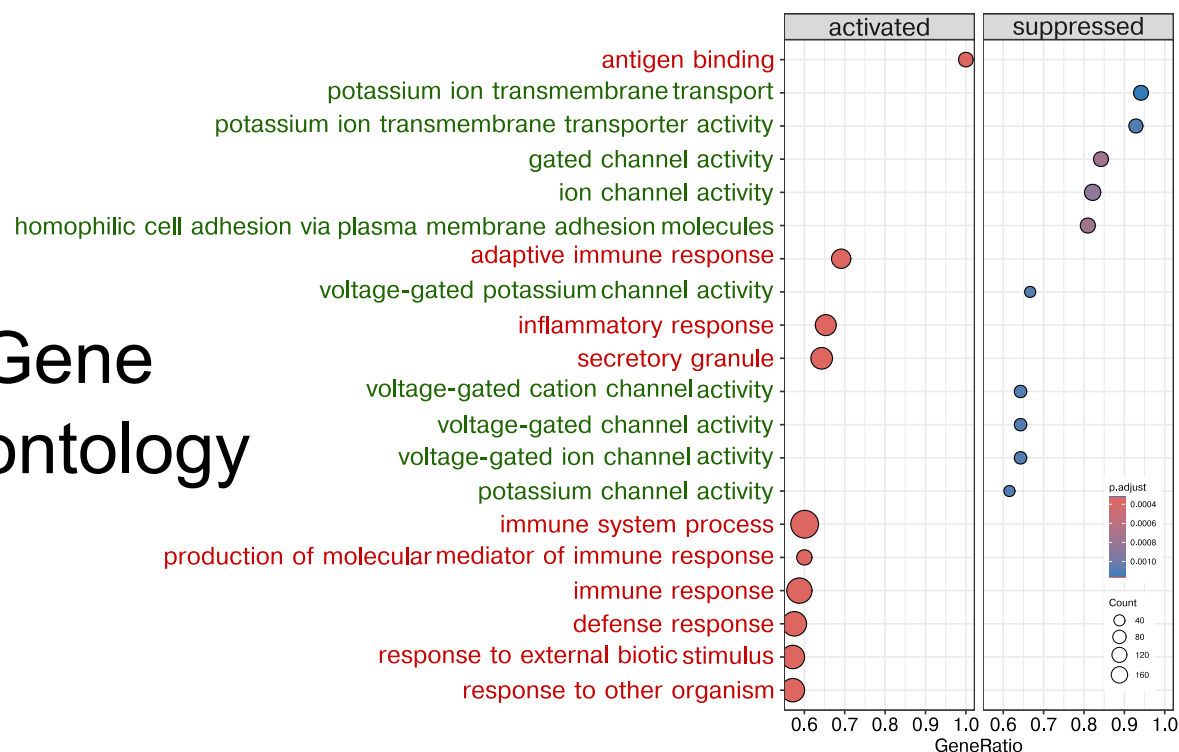
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Fusobacterium_sp._oral_taxon_370
Granulicatella_elegans
Lachnoanaerobaculum_umeaense
Leptotrichia_hofstadii
Leptotrichia_hongkongensis
Leptotrichia_showae
Leptotrichia_sp._oral_taxon_212
Leptotrichia_sp._oral_taxon_225
Neisseria_flavescens
Neisseria_subflava
Peptostreptococcus_anaerobius
Prevotella_maculosa
Prevotella_oris
Prevotella_oulorum
Prevotella_pleuritidis
Prevotella_saccharolytica
Prevotella_scopos
Rothia_dentocariosa
Schaalia_odontolytica
Selenomonas_noxia
Selenomonas_sp._oral_taxon_137
Selenomonas_sp._oral_taxon_149
Simonsiella_muelleri
Streptococcus_australis
Streptococcus_intermedius
Streptococcus_oralis
TM7_phylum_sp._oral_taxon_346
TM7_phylum_sp._oral_taxon_348
Veillonella_denticariosi
Veillonella_parvula
Veillonella_rogosae

Figure S2

Human

Microbiome

Gene ontology



KEGG pathways

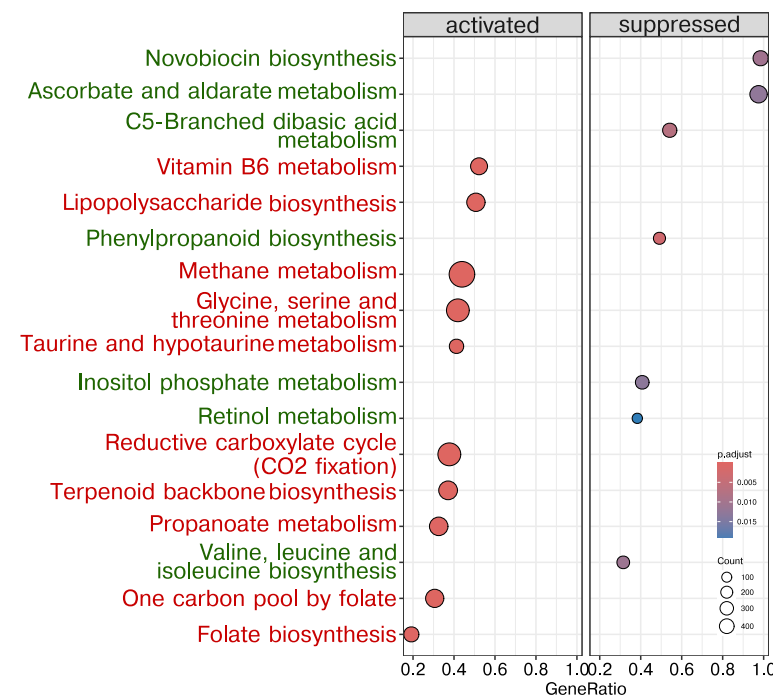
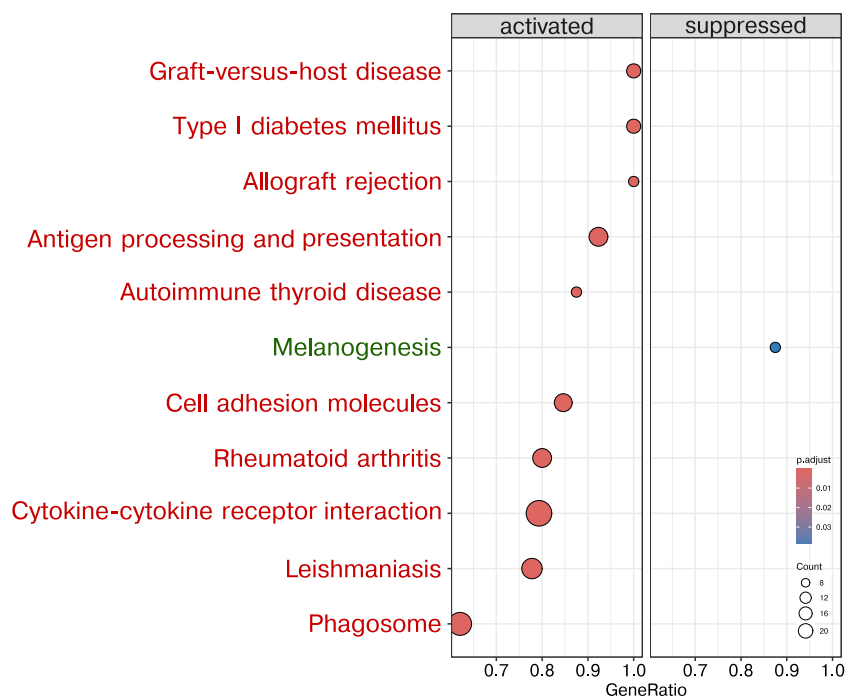
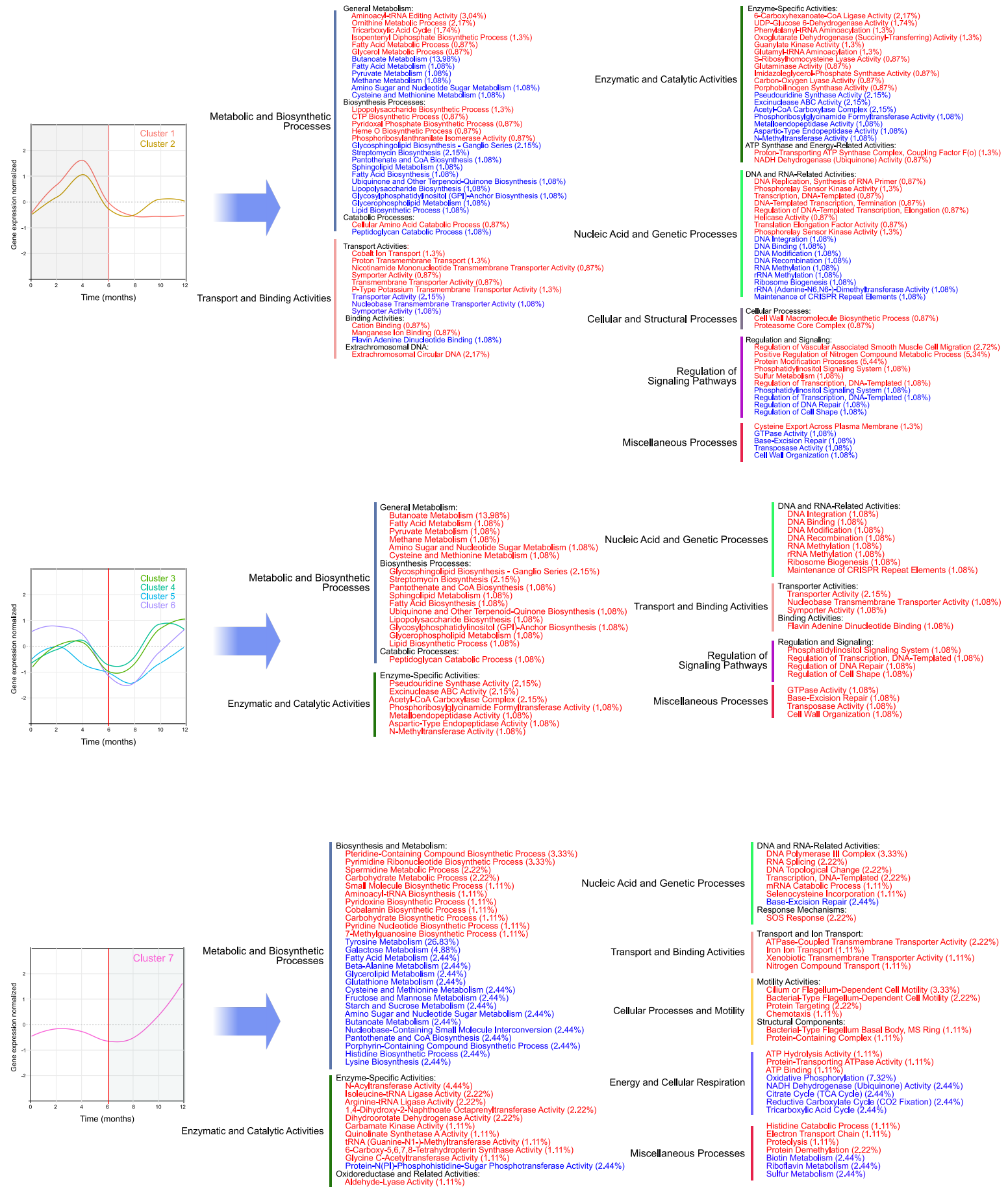
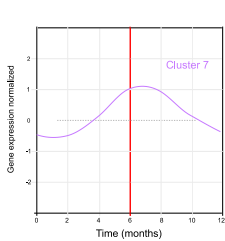
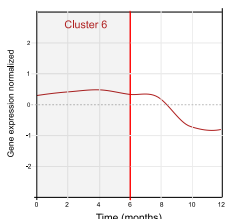
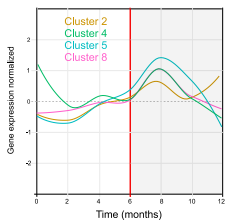
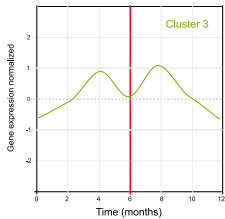


Figure S3

Figure S4





Enzymatic and Catalytic Activities

Protein and Ribosomal Processes

Metabolic and Biosynthetic

Protein and Ribosomal Processes

Metabolic and Biosynthetic

Protein and Ribosomal Processes

Metabolic and Biosynthetic

General Metabolism:	
Fucose Catabolic Process (4.59%)	
Glycerate-3P + CoA Metabolic Process (3.03%)	
Cycohydrate Metabolic Process (1.52%)	
Aspartate Family Amino Acid Biosynthetic Process (1.52%)	
Small Molecule Biosynthetic Process (1.52%)	
Nucleic Large Ribosomal Subunit (1.52%)	
Carbohydrate Biosynthetic Process (1.52%)	
Asparagine Biosynthetic Process (1.52%)	
Steroid Biosynthesis	
Tyrosine Metabolism (27.77%)	
Oxidative Phosphorylation (13.64%)	
Chinupridil Metabolic Process (2.33%)	
Glycerolipid Metabolism (4.55%)	
Pyruvate Metabolism (4.55%)	
Histidine Biosynthesis (4.55%)	
Arginine and Proline Metabolism (4.55%)	
Starch and Sucrose Metabolism (4.55%)	
Enzyme-Specific Activities:	
Serine-Type D-Allo-Di-Aldo Carboxypeptidase Activity (3.03%)	
Methylmalonyl-CoA Mutase Activity (3.03%)	
N-Acetylornithine Carbamoyltransferase Activity (1.52%)	
Ribonucleotide-Triphosphate Reductase Activity (1.52%)	
Nucleoside Synthesis (1.52%)	
3-Oxoacyl-(Acyl-Carrier-Protein) Synthase Activity (1.52%)	
Glycine C-Acetyltransferase Activity (3.03%)	
Translation and Ribosome-Related Processes:	
Translation (5.06%)	
Translation Release Factor Activity (3.03%)	
Translation Elongation Factor Activity, Codon Specific (1.52%)	
Protein-Containing Complex Assembly (3.03%)	
Regulator Small Ribosomal Subunit (3.03%)	
Plasid Large Ribosomal Subunit (1.52%)	
Large Ribosomal Subunit (1.52%)	
5S rRNA Binding (1.52%)	
General Metabolism:	
Ticarboxylic Acid Cycle (5.38%)	
Tyroxine Biosynthetic Process (5.38%)	
Anaerobic Respiration (3.23%)	
Histidine Catabolic Process (2.15%)	
Bimafalant Metabolic Process (2.15%)	
Cobalam Biosynthetic Process (1.08%)	
Glycogen Catabolic Process (1.08%)	
Lysate Biosynthesis (1.08%)	
CoA-H Macromolecule Biosynthetic Process (2.15%)	
Biosynthesis of Type II Polyketide Products (25.0%)	
Selective Metabolism (8.33%)	
Macrophophor Metabolism (8.33%)	
Pyruvate Metabolism (4.17%)	
Amino Sugar and Nucleotide Sugar Metabolism (4.17%)	
Lactate and Nicotinate Metabolism (4.17%)	
Nicotinate and Nicotinamide Metabolism (4.17%)	
Butanote Metabolism (4.17%)	
Quilic Metabolism (4.17%)	
Fatty Acid Metabolism (4.17%)	
Tryptophan Biosynthetic Process (4.17%)	
Antiotherone and CoA Biosynthesis (4.17%)	
Ribosome and Protein Activities:	
Structural Constituent of Ribosome (2.15%)	
Ribosome (1.08%)	
Translation Release Factor Activity, Codon Specific (1.08%)	
Translation Elongation Factor Activity, Codon Specific (1.08%)	
Cysteine-RNA Ligase Activity (2.15%)	
Phenylalanine-RNA Aminocyclization (3.23%)	
RNA Processing (3.23%)	
rRNA 2'-O-Methylation (2.15%)	
Polynucleotide Nucleotidyltransferase Activity (2.15%)	
Nascent Polypeptide-Associated Complex (2.15%)	
General Metabolism:	
Methionine Catabolic Process (1.15%)	
Ornithine Metabolic Process (0.77%)	
L-Lysine Metabolic Process (0.77%)	
Fatty Acid Metabolic Metabolism (0.77%)	
Glycerol Metabolic Process (0.77%)	
Nucleobase-Containing Compound Metabolic Process (0.77%)	
Butanote Metabolism (10.62%)	
Fatty Acid Metabolism (2.5%)	
Fructose and Mannose Metabolism (0.62%)	
Glycerolipid Metabolism (0.62%)	
Amino Sugar and Nucleotide Sugar Metabolism (0.62%)	
Thiamine Metabolism (0.62%)	
Arginine and Nicotinate Metabolism (0.62%)	
Arginine and Proline Metabolism (0.62%)	
Thiamine Metabolism (0.62%)	
Glutathione Metabolism (0.62%)	
Synase Degradation (0.62%)	
Purine Metabolism (0.62%)	
Starch and Sucrose Metabolism (0.62%)	
Positio Phosphate Metabolism (0.62%)	
Biosynthesis and Biosynthetic Pathways:	
Pyrimidine Ribonucleotide Biosynthetic Process (1.54%)	
Uridide Biosynthesis (0.77%)	
Isoentenyldiphosphate Biosynthetic Process, Methylerythritol CTP Biosynthetic Process (0.77%)	
Quinolone Glyoxylate Synthase (0.77%)	
Pantothenate and CoA Biosynthesis (1.25%)	
Inositol AcAlkoal Biosynthesis (5.62%)	
Biosynthesis of Androstane Steroids (1.25%)	
Novobiose Biosynthesis (0.62%)	
Lipopolysaccharide Biosynthesis (0.62%)	
Zellulin Biosynthesis (0.62%)	
Mo-Molybdopterin Cofactor Biosynthetic Process (0.62%)	
Catabolic Processes:	
Brain Amino Acid Catabolic Process (0.77%)	
Proteosomal Protein Catabolic Process (1.25%)	
Peptidoglycan Catabolic Process (0.62%)	
Branching-Chain Amino Acid Catabolic Process (0.62%)	
Enzyme-Specific Activities:	
4-Phosphopyruvate Dehydrogenase Activity (1.15%)	
Glutamate-RNA Ligase Activity (1.15%)	
Hydroxyglutamate Synthase Activity (1.92%)	
Glylate Lyase Activity (1.15%)	
Nitrate Reductase Complex (1.15%)	
Nucleoside ABC Activity (1.15%)	
Malto-(Acyl-Carrier-Protein) Synthase Activity (1.08%)	
Oxododecarboxylate Activity, Acting on the Aldehyde or Oxo Group (1.08%)	
Shikimate 3-Dehydrogenase (NADP+) Activity (0.62%)	
Nucleoside Diphosphate Kinase Activity (0.62%)	
Cydidylate Kinase Activity (0.62%)	
Ribosome Structure and Activity:	
Structural Constituent of Ribosome (8.0%)	
Cytosolic Small Ribosomal Subunit (4.0%)	
Plasid Large Ribosomal Subunit (2.0%)	
Ribosome (2.0%)	
Translation and RNA Processes:	
Translation Elongation Factor Activity (4.0%)	
Translation Initiation Factor Activity (4.0%)	
DNA-Directed 5'-3' RNA Polymerase Activity (4.0%)	
Protein Modification and Transport:	
Post-Translational Protein Folding (2.0%)	
Post-Translational Protein Modification (2.0%)	
Protein Insertion Into Membrane (2.0%)	
Protein Binding (2.0%)	
Peptide and Enzymatic Activities:	
Serine-Type D-Allo-Di-Aldo Carboxypeptidase Activity (4.0%)	
Proteolysis (4.0%)	
Peptidase Activity (2.0%)	
Endonuclease Activity (2.0%)	
Other Substituted Phosphate	
Metabolic Pathways:	
Tetrahydrofolate Interconversion (2.0%)	
Rhamnose Metabolic Process (4.0%)	
aconic Catabolic Process (4.0%)	
Mannagone Biosynthetic Process (2.0%)	
AMP Salvage (4.0%)	
Cyclic Nucleotide Biosynthetic Process (4.0%)	
Nitrogen and Carbon Metabolism:	
Nitrogen Metabolism (11.11%)	
Formate Carboxylation (CO ₂ Fixation) (11.11%)	
Citrate Cycle (TCA Cycle) (11.11%)	
Sugar and Carbohydrate Metabolism:	
Arabinose and Nucleotide Sugar Metabolism (11.11%)	
Galactose Metabolism (11.11%)	

- Transport and Binding Activities
- Enzymatic Activities
- Cellular Acid and Genetic Processes
- Cellular and Structural Processes
- Cellular and Motility Processes
- Oxidative and Stress Responses

Miscellaneous Processes

Transport and Binding Activities

Cellular and Motility Processes

Enzymatic and Catalytic Activities

Miscellaneous Processes

Nucleic Acid and Ge

Transport and

Cellular and Stru

Miscellaneous

o of Donors, NAD or NADP as Ac

Transport and E

Cellular and M
Groups (2.0%)
Energy and

Nucleic A

Protein and Ribosom

Transport and B

Nucleic Acid and Gene

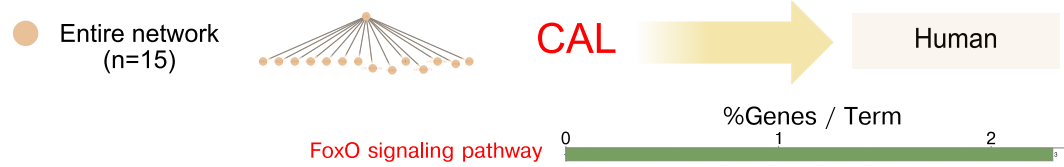
Enzymatic and Ca

Cellular and Molecular Biology

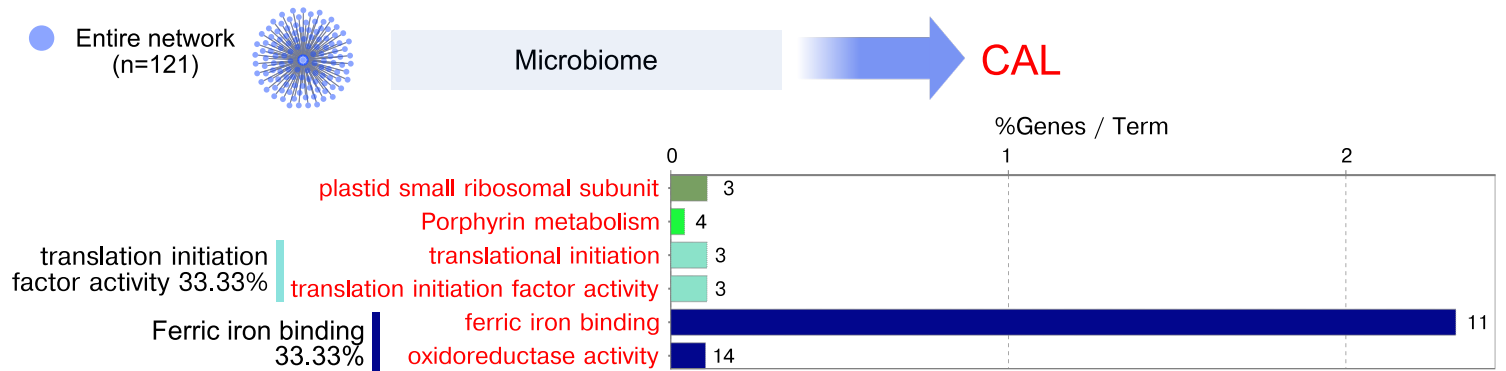
Miscellaneous

Transport and Symporter Activities:	Sodium Symporter Activity (3,03%)		
	Cobalt Ion Transmembrane Transporter Activity (1,52%)		
	Sugar Transport and Processing:		
	Phosphoenolpyruvate-Dependent Sugar Phosphotransferase System (4,55%)		
	Binding Activities:	NAD Binding (1,52%)	
		S-Adenosyl-L-Methionine Binding (1,52%)	
		Carbohydrate Binding (1,52%)	
	DNA and RNA-Related Activities:	DNA-Templated Transcription, Termination (3,03%)	
		mRNA Catabolic Process (1,52%)	
DNA Binding (4,55%)			
Regulation of Transcription, DNA-Templated (4,55%)			
Ribosome Biogenesis (4,55%)			
Cellular Processes and Structures:	Cell Outer Membrane (3,03%)		
	FtsZ-Dependent Cytokinesis (1,52%)		
Motility Activities:	Bacterial-Type Flagellum-Dependent Cell Motility (1,52%)		
Oxidative Processes:	Oxidoreductase Activity, Acting on the Aldehyde or Oxo Group of Donors (4,55%)		
	Response to Oxidative Stress (1,52%)		
Molecular Function (4,55%)	Novobiocin Biosynthesis (4,55%)		
Binding Activities:	NAD Binding (5,38%)		
	Pyridoxal Phosphate Binding (1,08%)		
	Copper Ion Binding (1,08%)		
	TP Binding (1,08%)		
	Adenyl Nucleotide Binding (1,08%)		
	Transport Activities:	Transmembrane Transport (1,08%)	
	Motility Activities:	Cilium or Flagellum-Dependent Cell Motility (1,08%)	
		Bacterial-Type Flagellum (1,08%)	
Enzyme-Specific Activities:	4-Phosphorylthionate Dehydrogenase Activity (4,3%)		
	Oxoglutarate Dehydrogenase (Succinyl-Transferring) Activity (3,23%)		
	Carbon-Nitrogen Ligase Activity, with Glutamine as Amido-N-Donor (3,23%)		
	Holo-Acyl Carrier-Protein Synthase Activity (1,08%)		
	6-Carboxy-5,6,7,8-Tetrahydropterin Synthase Activity (1,08%)		
	Methylmalonyl-CoA Mutase Activity (1,08%)		
	6-Phospho-beta-D-Glucosidase Activity (1,08%)		
	UDP-Glucose 6-Dehydrogenase Activity (1,08%)		
	Regulation and DNA Processes:	Regulation of DNA Replication (3,23%)	
Site-Specific Recombinase Activity (1,08%)			
Regulation of Transcription, DNA-Templated (4,17%)			
DNA Binding (4,17%)			
Maintenance of CRISPR Repeat Elements (4,17%)			
Signal Transduction (1,08%)	Glycine Decarboxylation via Glycine Cleavage System (1,08%)		
	Nucleoside-Containing Compound Kinase Activity (2,15%)		
	Oxidoreductase Activity, Acting on NAD(P)H, Quinone or Similar Compound as Acceptor (2,15%)		
	Nucleoside Metabolic Process (4,17%)		
	Transposase Activity (4,17%)		
DNA and RNA-Related Activities:	DNA Topological Change (1,54%)		
	DNA Polymerase III complex (1,15%)		
	Regulation of DNA-Templated Transcription, Elongation (0,77%)		
	DNA Repair (0,77%)		
	DNA Binding (0,62%)		
	DNA Strand Exchange Activity (0,62%)		
	DNA Integration (0,62%)		
	DNA Methylation (0,62%)		
	Base-Excision Repair (0,62%)		
	Double-Strand Break Repair via Homologous Recombination (0,62%)		
Regulation of DNA Repair (0,62%)	Regulation of DNA Repair (0,62%)		
	DNA Modification (0,62%)		
	RNA Methylation (0,62%)		
	RNA Processing and Splicing:		
	RNA Modification (0,77%)		
	Translation Initiation Factor Activity (0,77%)		
	Translation Release Factor Activity (0,77%)		
	Translational Elongation (0,77%)		
Transport Activities:	P-Type Potassium Transmembrane Transporter Activity (1,15%)		
	Sodium Ion Transport (0,77%)		
	Xenobiotic Transmembrane Transport (1,15%)		
	Nicotinate and Nicotinamide Transporter Activity (0,62%)		
	Sodium Ion Transport (0,77%)		
	Binding Activities:	Nucleotide Binding (2,69%)	
		4Fe-4S Binding (0,77%)	
		NAD Binding (0,62%)	
		FMN Binding (0,62%)	
	Cellular Processes:	Bacterial-Type Flagellum-Dependent Cell Motility (1,54%)	
Protein Targeting (0,77%)			
Stringent Response (0,77%)			
Cytokinesis (0,62%)			
Structural Components:		Structural Constituent of Ribosome (1,54%)	
		Cell Wall Organization (1,25%)	
ATPase-Coupled Transmembrane Transporter Activity (0,77%)	Transketolase Activity (0,77%)		
	4-Cytidine 5-Diphosphate-2-C-Methyl-D-Erythritol Kinase Activity (0,77%)		
	Maintenance of Dehydrophosphorylation (0,62%)		
	Transposase Activity (0,62%)		
	Maintenance of CRISPR Repeat Elements (0,62%)		
Transport Activities:	Organic Substance Transport (2,0%)		
	Inorganic Cation Transmembrane Transport (2,0%)		
	Efflux Transmembrane Transporter Activity (2,0%)		
	Electron Transfer and Chain:	Electron Transfer Activity (2,0%)	
		Electron Transport Chain (2,0%)	
	Phosphotransferase Systems:	Phosphoenolpyruvate-Dependent Sugar Phosphotransferase System (11,11%)	
	Cellular Components:	Cell Outer Membrane (2,0%)	
		Extracellular Region (2,0%)	
		Motility and Channels:	Bacterial-Type Flagellum-Dependent Cell Motility (2,0%)
Channel Activity (2,0%)			
Energy Generation:	Oxidative Phosphorylation (11,11%)		
	Proton-Transporting ATP Synthase Activity, Rotational Mechanism (11,11%)		
Transcriptional Regulation:	Regulation of Transcription, DNA-Templated (11,11%)		
Ribosomal Activities:	Ribosomal Constituent of Ribosome (3,88%)		
	Cytosolic Small Ribosomal Subunit (2,33%)		
	Small Ribosomal Subunit (1,55%)		
	Translational Elongation (1,55%)		
	Protein and Peptide Processes:	Signal Peptide Processing (3,1%)	
		Aminopeptidase Activity (1,55%)	
	Transport Activities:	Cobalt Ion Transmembrane Transporter Activity (2,33%)	
		Ferrous Iron Transmembrane Transporter Activity (1,55%)	
		Potassium Ion Transmembrane Transporter Activity (1,55%)	
		Transport Systems:	ATP-Binding Cassette (ABC) Transporter Complex (2,86%)
Protein-Nucleoside/Nucleotide-Sugar Phosphotransferase System (1,43%)			
Binding Activities:	Ribonucleoside Binding (2,33%)		
	NADP Binding (1,43%)		
	DNA and RNA-Related Activities:	DNA-Templated Transcription, Termination (2,33%)	
		mRNA Catabolic Process (1,55%)	
		DNA Modification (1,43%)	
Base-Excision Repair (1,43%)			
Exonuclease ABC Activity (1,43%)			
Maintenance of CRISPR Repeat Elements (1,43%)	Maintenance of CRISPR Repeat Elements (1,43%)		
	DNA-Templated Transcription Regulation (1,43%)		
	RNA Processing and Synthesis:	RNA Processing (2,86%)	
		Pseudouridine Synthase Activity (1,43%)	
	Enzyme-Specific Activities:	Exodeoxyribonuclease III Complex (2,33%)	
Transposase Activity (1,43%)			
Methyltransferase Activity (1,43%)			
Phosphoenolpyruvate-Dependent Sugar Phosphotransferase System (1,43%)			
Exonuclease and Endonuclease Activities (1,43%)			
Motility Activities:	Cilium or Flagellum-Dependent Cell Motility (1,55%)		
Electron Transport Chain (2,33%)	Histidine Biosynthetic Process (1,43%)		
	Tryptophan Biosynthetic Process (1,43%)		
	Nucleoside-Containing Small Molecule Interconversion (1,43%)		

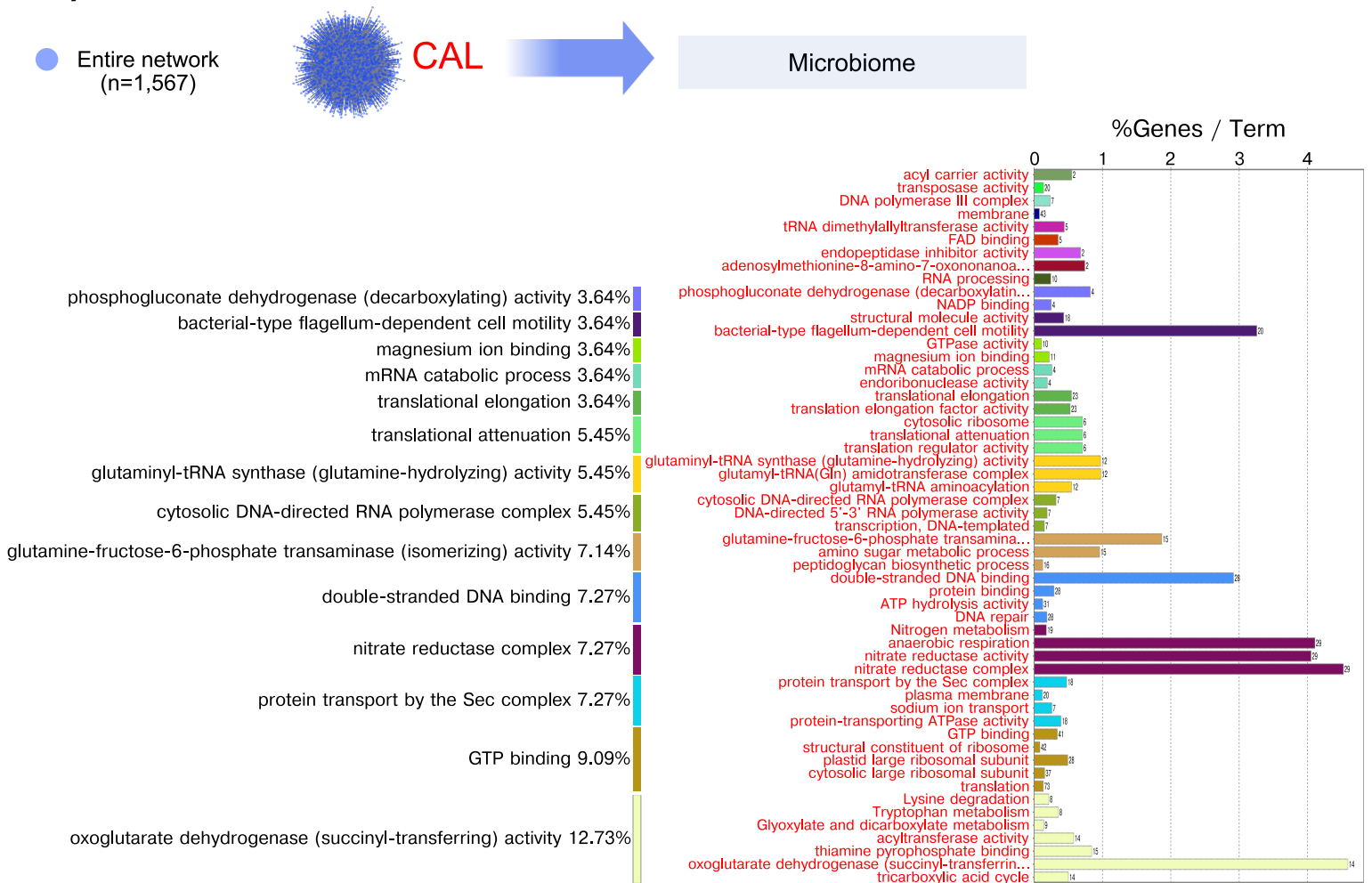
a) stable



b)



c) stable



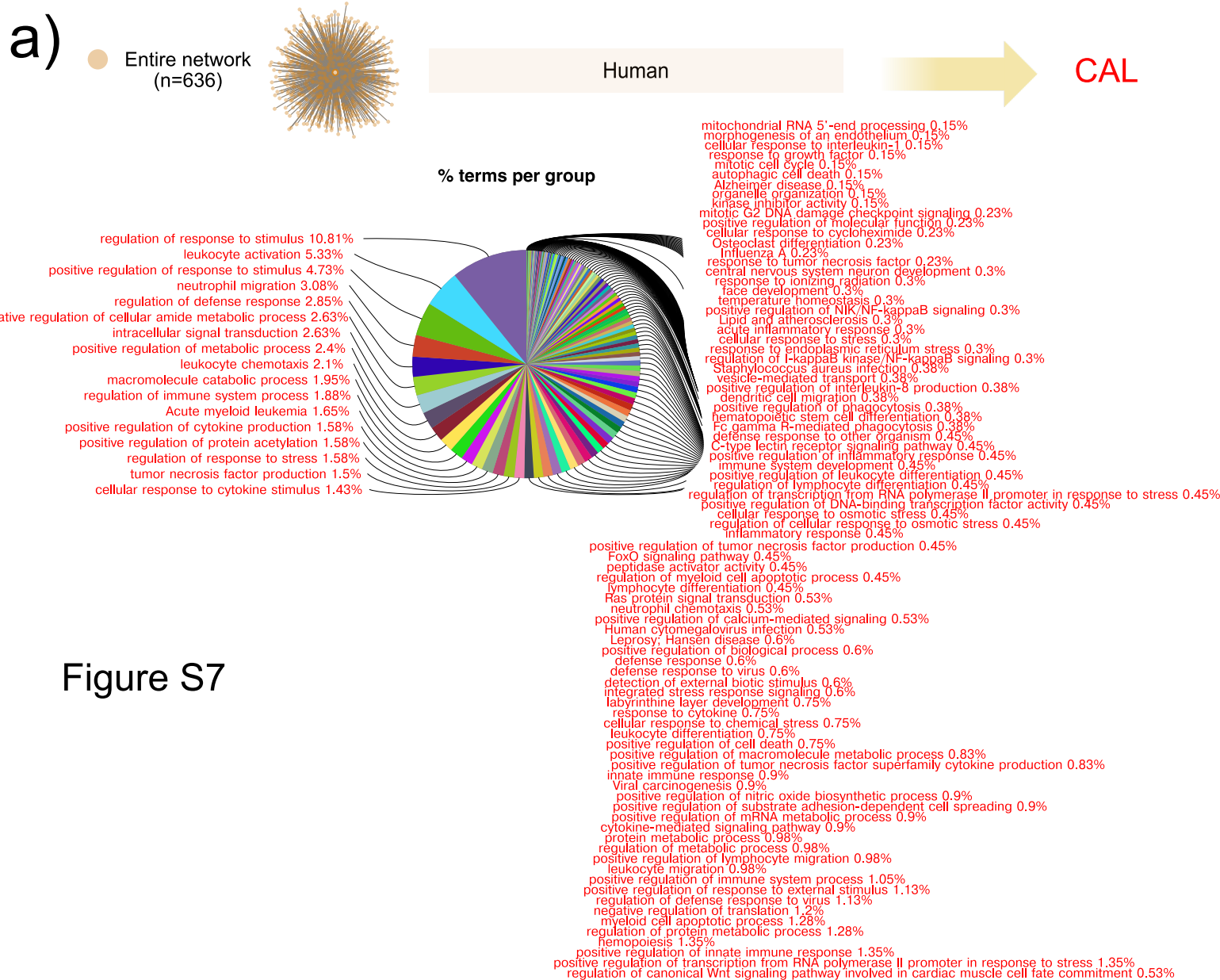


Figure S7

