

Supplementary Material

The gut microbiota in gallstone patients during the perioperative period

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1 Supplementary Figures and Tables

1.1 Supplementary Figures

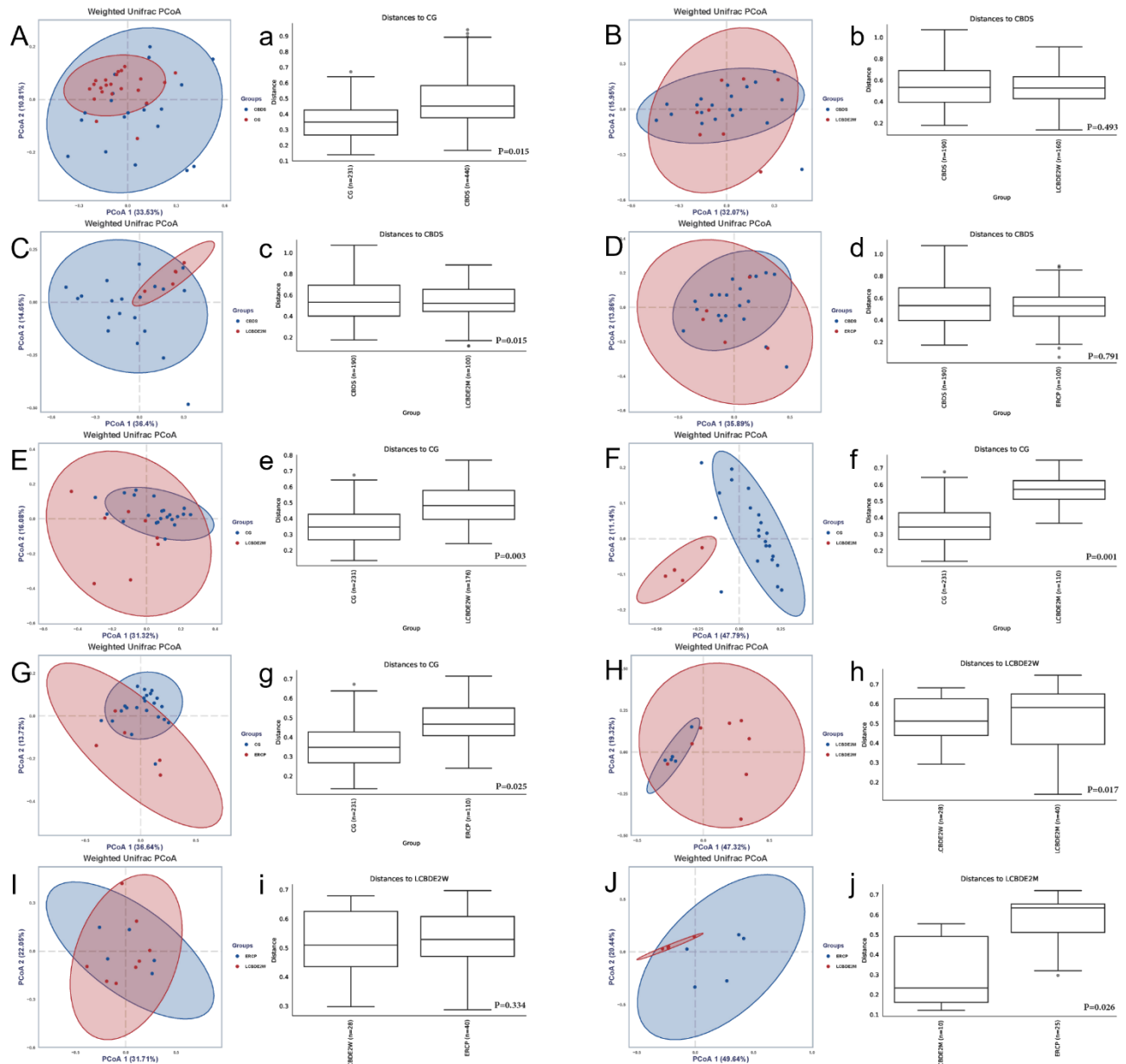


FIGURE S1 | Beta diversity of gut microbial communities in bile duct group. Principal coordinates analysis plot based on weighted UniFrac distance. Each dot represents one sample from each group. The weighted UniFrac patterns indicate that the patients and healthy individuals cluster separately, representing 33.53% and 10.81% (A), 32.07% and 15.95% (B), 36.4% and 14.65% (C), 35.89% and 13.86% (D), 31.32% and 16.08% (E), 47.79% and 11.14% (F), 36.64% and 13.72% (G), 47.32% and 19.32% (H), 31.71% and 22.05% (I), and 49.64% and 20.44% (J) of the total variance on the x-axis and y-axis, respectively. The distance between dots on the plot indicates the degree of similarity of the taxonomic composition of the samples. Charts (a-j) show the distance between groups and within

groups, $p < 0.05$, indicating that the beta diversity between groups was significant.

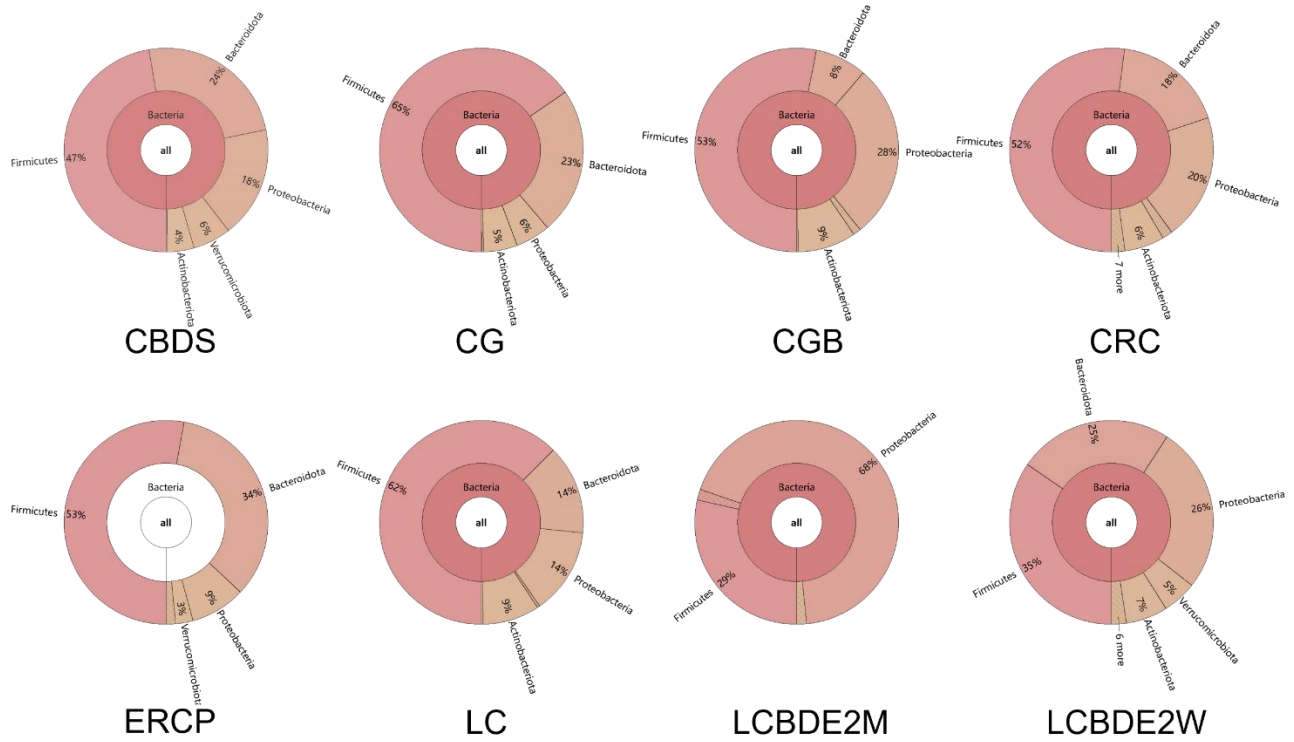


FIGURE S2 | Pie charts of gut microbiota. The major gut microbiota composition in each group at the phylum level.

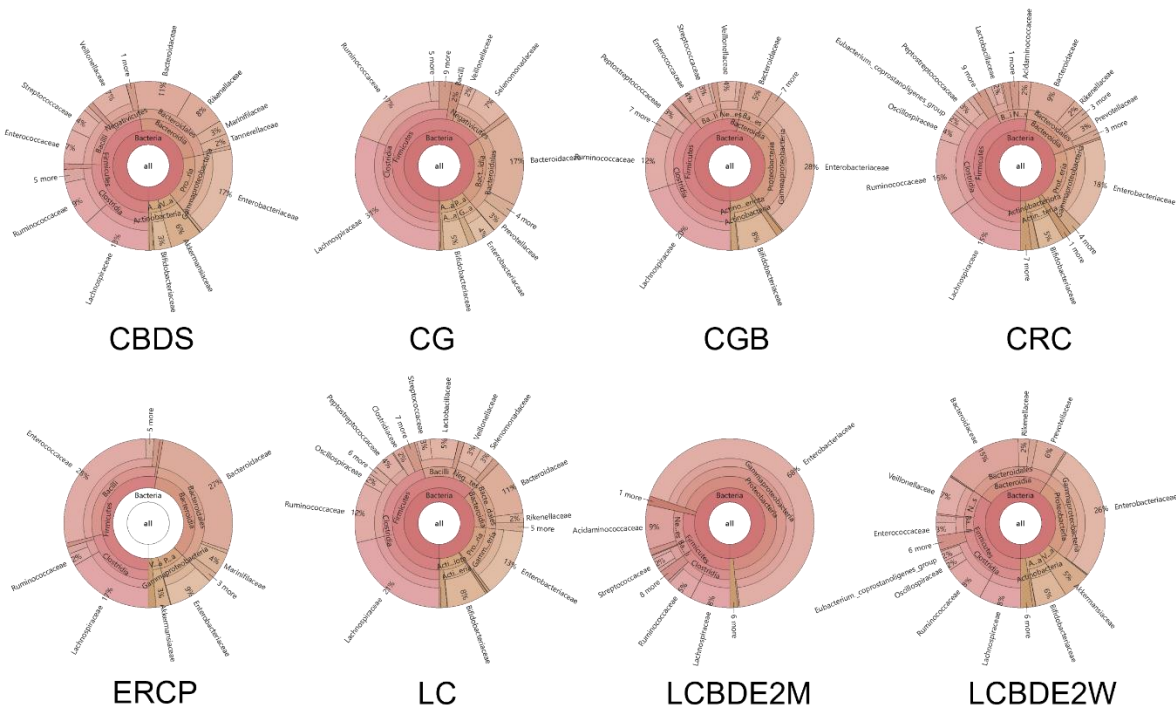


FIGURE S3 | Pie charts of gut microbiota. The major gut microbiota composition in each group at

the family level.

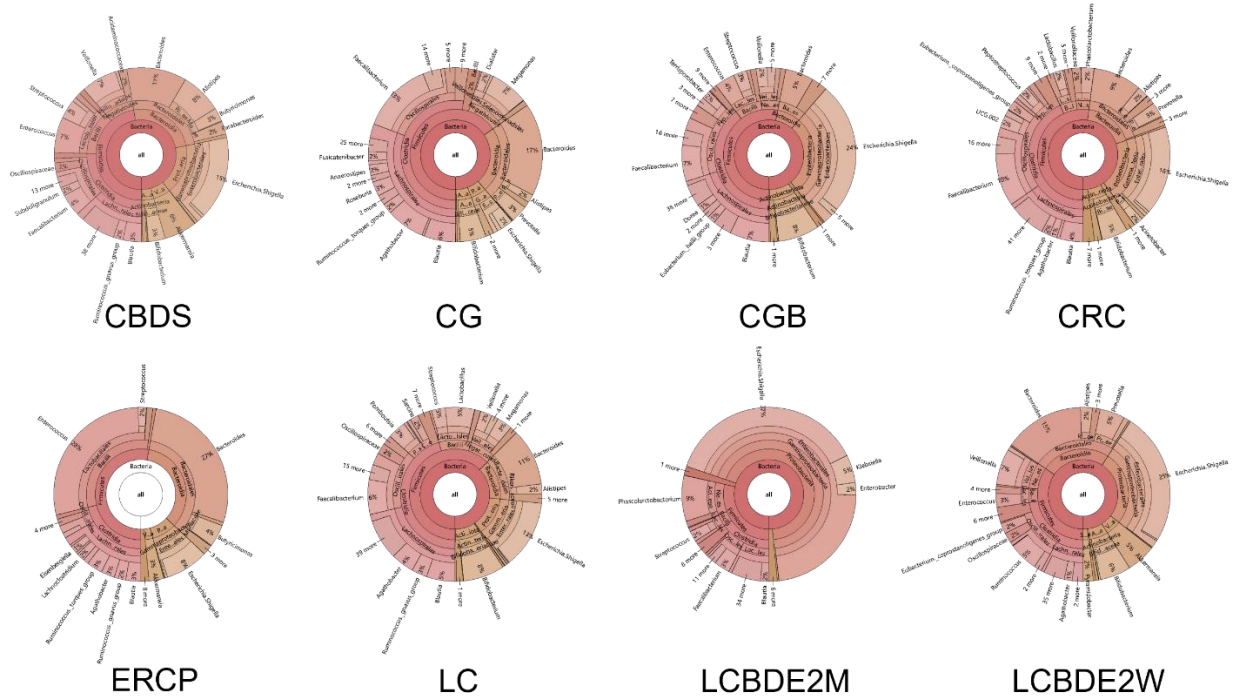


FIGURE S4 | Pie charts of gut microbiota. The major gut microbiota composition in each group at the genus level.

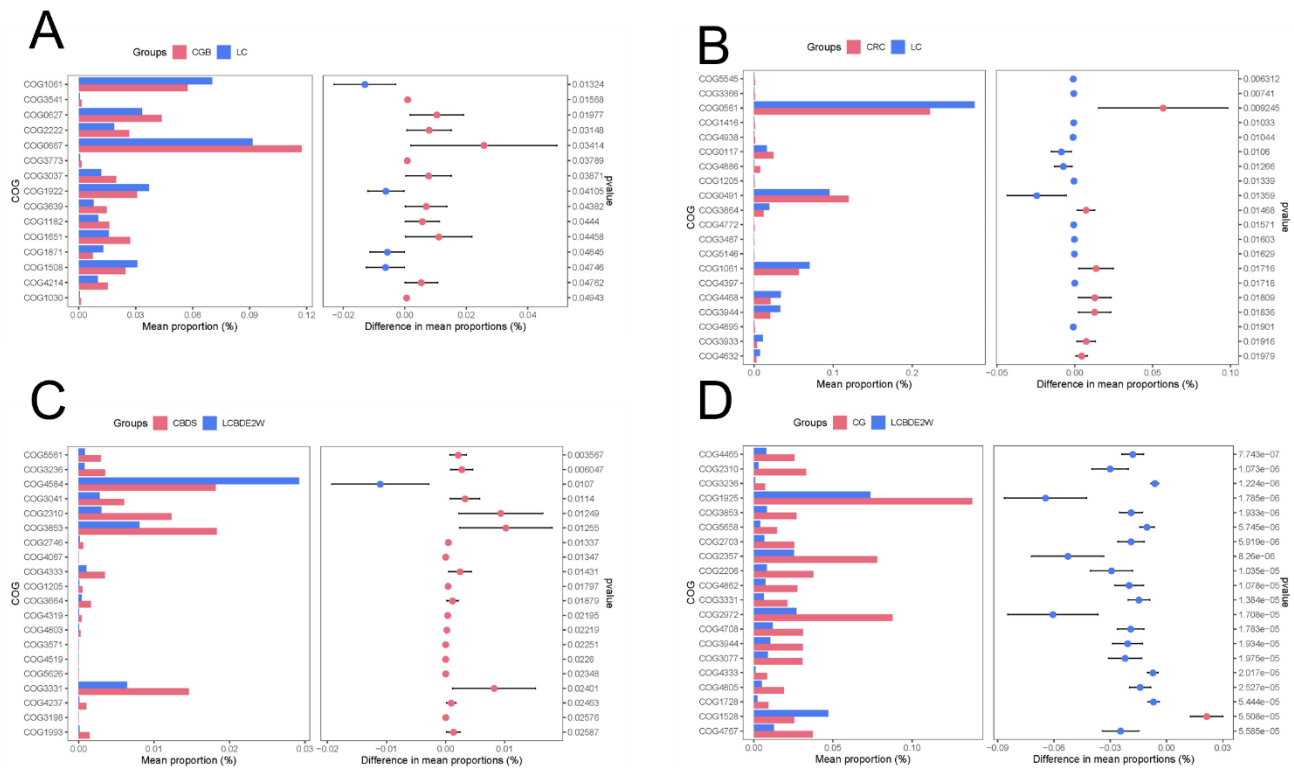


FIGURE S5 | The COG profiles and the components of functional genomics in COG pathways. (A): CGB vs. LC; (B): CRC vs. LC; (C): CBDS vs. LCBDE2W; (D): LCBDE2W vs. CG.

1.2 Supplementary Table

TABLE S1 | The COG of CBDS vs. CG.

ID	<i>p</i> -value	Functional description
COG1115	3.64283E-07	Na ⁺ /alanine symporter
COG0822	1.94684E-06	NifU homolog involved in Fe-S cluster formation
COG1699	2.74172E-06	Uncharacterized protein conserved in bacteria
COG0860	2.87565E-06	N-acetylmuramoyl-L-alanine amidase
COG1728	4.74429E-06	Uncharacterized protein conserved in bacteria
COG1387	9.02915E-06	Histidinol phosphatase and related hydrolases of the PHP family
COG0370	1.00241E-05	Fe ²⁺ transport system protein B
COG1797	1.02215E-05	Cobyrinic acid a,c-diamide synthase
COG1249	1.03553E-05	Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide dehydrogenase (E3) component, and related enzymes
COG2607	1.43975E-05	Predicted ATPase (AAA+ superfamily)
COG2257	1.55718E-05	Uncharacterized homolog of the cytoplasmic domain of flagellar protein FliB
COG1313	1.58831E-05	Uncharacterized Fe-S protein PflX, homolog of pyruvate formate lyase activating proteins
COG4823	1.97105E-05	Abortive infection bacteriophage resistance protein
COG0037	2.12229E-05	Predicted ATPase of the PP-loop superfamily implicated in cell cycle control
COG2206	2.12263E-05	HD-GYP domain
COG1366	2.19128E-05	Anti-anti-sigma regulatory factor (antagonist of anti-sigma factor)
COG2129	2.21863E-05	Predicted phosphoesterases, related to the Icc protein
COG2013	2.38115E-05	Uncharacterized conserved protein
COG2426	2.84093E-05	Predicted membrane protein
COG0726	2.99047E-05	Predicted xylanase/chitin deacetylase

TABLE S2 | The COG of LCBDE2M vs. LCBDE2W.

ID	<i>p</i> -value	Functional description
COG3426	4.88304E-04	Butyrate kinase
COG0612	6.93239E-04	Predicted Zn-dependent peptidases
COG5523	1.40360E-03	Predicted integral membrane protein
COG0266	1.66233E-03	Formamidopyrimidine-DNA glycosylase
COG3290	1.84166E-03	Signal transduction histidine kinase regulating citrate/malate metabolism
COG3408	2.00285E-03	Glycogen debranching enzyme
COG1694	2.08416E-03	Predicted pyrophosphatase
COG1480	2.29709E-03	Predicted membrane-associated HD superfamily hydrolase
COG0149	2.39555E-03	Triosephosphate isomerase
COG5495	2.43548E-03	Uncharacterized conserved protein
COG0438	2.60316E-03	Glycosyltransferase
COG0684	2.70966E-03	Demethylmenaquinone methyltransferase
COG2030	3.33444E-03	Acyl dehydratase
COG0494	3.41209E-03	NTP pyrophosphohydrolases including oxidative damage repair enzymes
COG1629	3.44635E-03	Outer membrane receptor proteins, mostly Fe transport
COG3878	3.62313E-03	Uncharacterized protein conserved in bacteria

COG0589	3.65146E-03	Universal stress protein UspA and related nucleotide-binding proteins
COG3884	3.68718E-03	Acyl-ACP thioesterase
COG0722	3.70642E-03	3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase
COG4565	3.72583E-03	Response regulator of citrate/malate metabolism

TABLE S3| The COG of CBDS vs. ERCP.

ID	<i>p-value</i>	Functional description
COG0223	1.21925E-03	Methionyl-tRNA formyltransferase
COG1834	2.74611E-03	N-Dimethylarginine dimethylaminohydrolase
COG2890	2.87368E-03	Methylase of polypeptide chain release factors
COG1990	5.10106E-03	Uncharacterized conserved protein
COG0231	5.38104E-03	Translation elongation factor P (EF-P)/translation initiation factor 5A (eIF-5A)
COG0136	5.58878E-03	Aspartate-semialdehyde dehydrogenase
COG4333	5.80422E-03	Uncharacterized protein conserved in bacteria
COG0254	5.95216E-03	Ribosomal protein L31
COG2359	6.64606E-03	Uncharacterized protein conserved in bacteria
COG1994	6.88359E-03	Zn-dependent proteases
COG0617	7.26385E-03	tRNA nucleotidyltransferase/poly(A) polymerase
COG2310	8.28664E-03	Uncharacterized proteins involved in stress response, homologs of TerZ and putative cAMP-binding protein CABP1
COG1768	8.36619E-03	Predicted phosphohydrolase
COG1544	9.54135E-03	Ribosome-associated protein Y (PSrp-1)
COG3184	1.00728E-02	Uncharacterized protein conserved in bacteria
COG3707	1.14999E-02	Response regulator with putative antiterminator output domain
COG2052	1.49265E-02	Uncharacterized protein conserved in bacteria
COG1502	1.51412E-02	Phosphatidylserine/phosphatidylglycerophosphate/cardioplin synthases and related enzymes
COG1993	1.60853E-02	Uncharacterized conserved protein
COG1295	1.63912E-02	Predicted membrane protein

TABLE S4 | The COG of ERCP vs. LCBDE2W.

ID	<i>p-value</i>	Functional description
COG2972	2.95503E-03	Predicted signal transduction protein with a C-terminal ATPase domain
COG4753	4.65547E-03	Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain
COG0693	5.06093E-03	Putative intracellular protease/amidase
COG0554	5.97155E-03	Glycerol kinase
COG0424	6.32738E-03	Nucleotide-binding protein implicated in inhibition of septum formation
COG0341	7.12601E-03	Preprotein translocase subunit SecF
COG0254	7.89056E-03	Ribosomal protein L31
COG0231	8.69467E-03	Translation elongation factor P (EF-P)/translation initiation factor 5A (eIF-5A)
COG0136	8.75074E-03	Aspartate-semialdehyde dehydrogenase
COG0469	9.20475E-03	Pyruvate kinase
COG0223	9.68403E-03	Methionyl-tRNA formyltransferase
COG0548	1.01803E-02	Acetylglutamate kinase
COG0773	1.04557E-02	UDP-N-acetylmuramate-alanine ligase
COG1803	1.10888E-02	Methylglyoxal synthase

COG2890	1.10923E-02	Methylase of polypeptide chain release factors
COG0617	1.16877E-02	tRNA nucleotidyltransferase/poly(A) polymerase
COG4584	1.31758E-02	Transposase and inactivated derivatives
COG1190	1.61309E-02	Lysyl-tRNA synthetase (class II)
COG0033	1.70387E-02	Phosphoglucomutase
COG0828	1.75703E-02	Ribosomal protein S21

TABLE S5 | The COG of CGB vs. LC.

ID	<i>p</i> -value	Functional description
COG1061	1.32380E-02	DNA or RNA helicases of superfamily II
COG3541	1.56785E-02	Predicted nucleotidyltransferase
COG0627	1.97735E-02	Predicted esterase
COG2222	3.14813E-02	Predicted phosphosugar isomerases
COG0667	3.41406E-02	Predicted oxidoreductases (related to aryl-alcohol dehydrogenases)
COG3773	3.78945E-02	Cell wall hydrolyses involved in spore germination
COG3037	3.87069E-02	Uncharacterized protein conserved in bacteria
COG1922	4.10523E-02	Teichoic acid biosynthesis proteins
COG3639	4.38241E-02	ABC-type phosphate/phosphonate transport system, permease component
COG1182	4.43964E-02	Acyl carrier protein phosphodiesterase
COG1651	4.45802E-02	Protein-disulfide isomerase
COG1871	4.64527E-02	Chemotaxis protein; stimulates methylation of MCP proteins
COG1508	4.74582E-02	DNA-directed RNA polymerase specialized sigma subunit, sigma54 homolog
COG4214	4.76155E-02	ABC-type xylose transport system, permease component
COG1030	4.94307E-02	Membrane-bound serine protease (ClpP class)

TABLE S6 | The COG of CRC vs. LC.

ID	<i>p</i> -value	Functional description
COG5545	0.0063123	Predicted P-loop ATPase and inactivated derivatives
COG3366	0.0074101	Uncharacterized protein conserved in archaea
COG0561	0.0092451	Predicted hydrolases of the HAD superfamily
COG1416	0.0103323	Uncharacterized conserved protein
COG4938	0.0104369	Uncharacterized conserved protein
COG0117	0.0106009	Pyrimidine deaminase
COG4886	0.0126559	Leucine-rich repeat (LRR) protein
COG1205	0.0133859	Distinct helicase family with a unique C-terminal domain including a metal-binding cysteine cluster
COG0491	0.0135874	Zn-dependent hydrolases, including glyoxylases
COG3864	0.0146816	Uncharacterized protein conserved in bacteria
COG4772	0.0157137	Outer membrane receptor for Fe ³⁺ -dicitrate
COG3487	0.0160266	Uncharacterized iron-regulated protein
COG5146	0.0162914	Pantothenate kinase, acetyl-CoA regulated
COG1061	0.0171639	DNA or RNA helicases of superfamily II
COG4397	0.0171817	Mu-like prophage major head subunit gpT
COG4468	0.0180898	Galactose-1-phosphate uridylyltransferase
COG3944	0.0183625	Capsular polysaccharide biosynthesis protein
COG4895	0.0190061	Uncharacterized conserved protein

COG3933	0.0191637	Transcriptional antiterminator
COG4632	0.0197925	Exopolysaccharide biosynthesis protein related to N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase

TABLE S7 | The COG of CBDS vs. LCBDE2W.

ID	p-value	Functional description
COG5561	3.56675E-03	Predicted metal-binding protein
COG3236	6.04712E-03	Uncharacterized protein conserved in bacteria
COG4584	1.06987E-02	Transposase and inactivated derivatives
COG3041	1.14042E-02	Uncharacterized protein conserved in bacteria
COG2310	1.24901E-02	Uncharacterized proteins involved in stress response, homologs of TerZ and putative cAMP-binding protein CABP1
COG3853	1.25519E-02	Uncharacterized protein involved in tellurite resistance
COG2746	1.33724E-02	Aminoglycoside N3'-acetyltransferase
COG4067	1.34706E-02	Uncharacterized protein conserved in archaea
COG4333	1.43091E-02	Uncharacterized protein conserved in bacteria
COG1205	1.79695E-02	Distinct helicase family with a unique C-terminal domain including a metal-binding cysteine cluster
COG3664	1.87901E-02	Beta-xylosidase
COG4319	2.19528E-02	Ketosteroid isomerase homolog
COG4803	2.21881E-02	Predicted membrane protein
COG3571	2.25100E-02	Predicted hydrolase of the alpha/beta-hydrolase fold
COG4519	2.25978E-02	Uncharacterized protein conserved in bacteria
COG5626	2.34841E-02	Uncharacterized conserved small protein
COG3331	2.40147E-02	Penicillin-binding protein-related factor A, putative recombinase
COG4237	2.46336E-02	Hydrogenase 4 membrane component (E)
COG3198	2.57574E-02	Uncharacterized protein conserved in bacteria
COG1993	2.58666E-02	Uncharacterized conserved protein

TABLE S8 | The COG of CG vs. LCBDE2W.

ID	p-value	Functional description
COG4465	7.74327E-07	Pleiotropic transcriptional repressor
COG2310	1.07302E-06	Uncharacterized proteins involved in stress response, homologs of TerZ and putative cAMP-binding protein CABP1
COG3236	1.22426E-06	Uncharacterized protein conserved in bacteria
COG1925	1.78525E-06	Phosphotransferase system, HPr-related proteins
COG3853	1.93292E-06	Uncharacterized protein involved in tellurite resistance
COG5658	5.74464E-06	Predicted integral membrane protein
COG2703	5.91875E-06	Hemerythrin
COG2357	8.26042E-06	Uncharacterized protein conserved in bacteria
COG2206	1.03550E-05	HD-GYP domain
COG4862	1.07818E-05	Negative regulator of genetic competence, sporulation and motility
COG3331	1.38438E-05	Penicillin-binding protein-related factor A, putative recombinase
COG2972	1.70832E-05	Predicted signal transduction protein with a C-terminal ATPase domain
COG4708	1.78282E-05	Predicted membrane protein
COG3944	1.93385E-05	Capsular polysaccharide biosynthesis protein
COG3077	1.97501E-05	DNA-damage-inducible protein J
COG4333	2.01691E-05	Uncharacterized protein conserved in bacteria

COG4805	2.52653E-05	Uncharacterized protein conserved in bacteria
COG1728	5.44353E-05	Uncharacterized protein conserved in bacteria
COG1528	5.50838E-05	Ferritin-like protein
COG4767	5.58495E-05	Glycopeptide antibiotics resistance protein
