

uvr genes

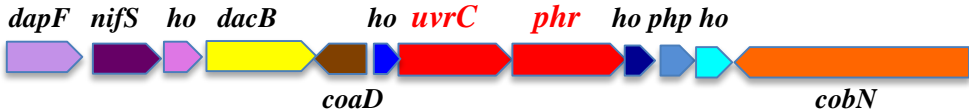
Cluster a



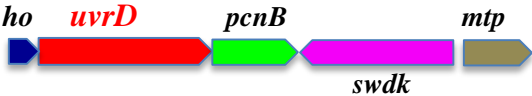
Cluster b



Cluster c

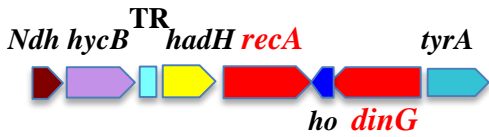


Cluster d

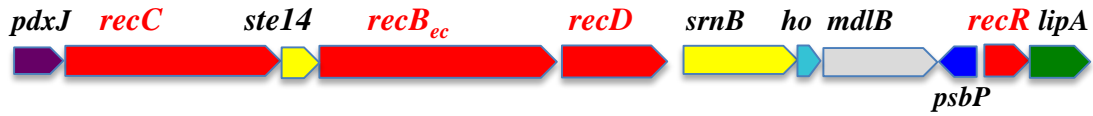


rec genes

Cluster e



Cluster f



Cluster g

Nuc-like



Cluster h



Cluster i



Cluster j

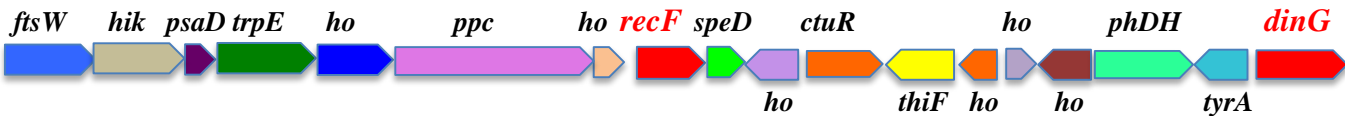
recD



Cluster k



Cluster l



Cluster m



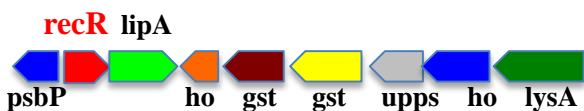
Cluster m'



Cluster n



Cluster q



Cluster j

recD_{cy}



Cluster k

had

recF



Cluster l

ftsW

hik

psaD

trpE

ho

ppc

ho

recF

speD

ctuR

ho

phDH

dinG



Cluster m

dcm

deoC

recO

mjf

rfaG



Cluster m''

lrtA

deoC

recO

mjf

rfaG



Cluster n

mutY

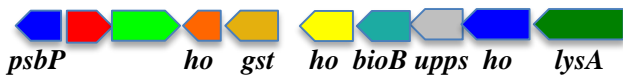
recR



Cluster q

recR

lipA



Cluster r

glf

rpsB

tsf

ho

recG



Cluster s

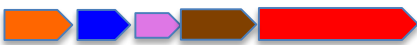
glf

rpsB

tsf

adcY

recG



Cluster t

recJ_{ec}

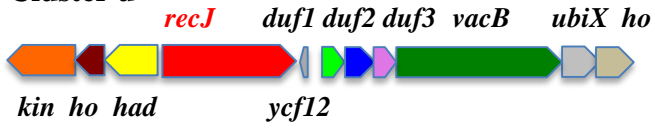
dufI

dufII

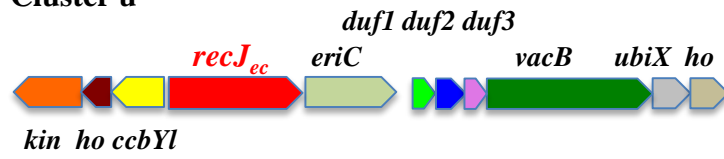
dufIII



Cluster u



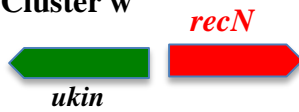
Cluster u'



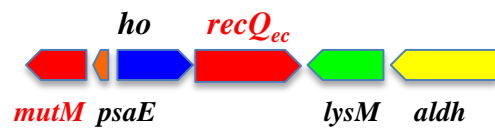
Cluster v



Cluster w



Cluster x

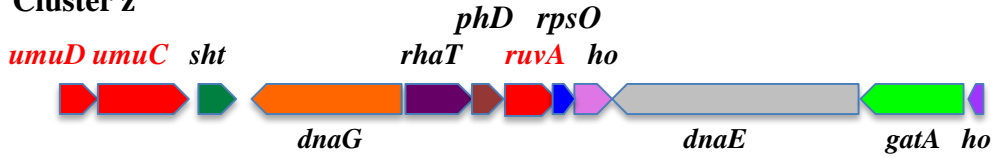


Cluster y

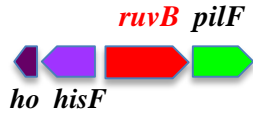
spp ruvA aos



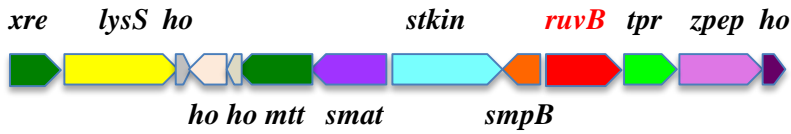
Cluster z



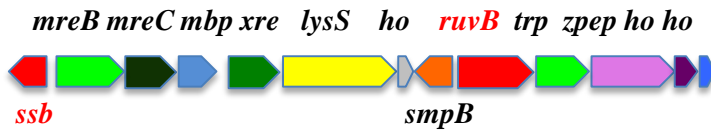
Cluster ab



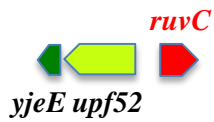
Cluster ac



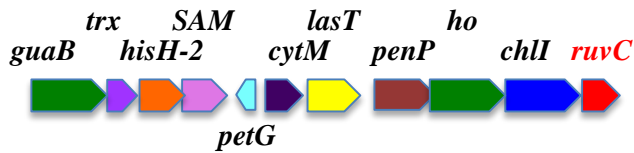
Cluster ad



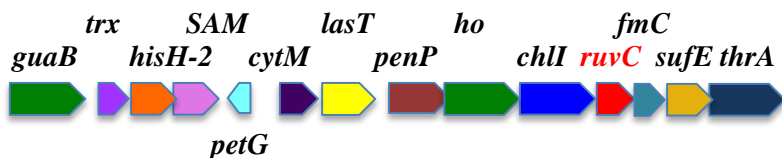
Cluster ae



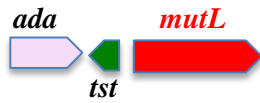
Cluster af



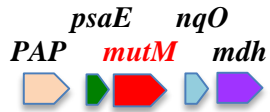
Cluster af^s



Cluster ag



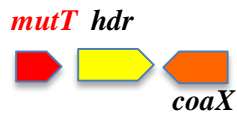
Cluster ah



Cluster ai et ai'



Cluster aj



Cluster ak



Cluster al



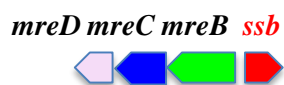
Cluster am



Cluster an

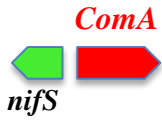


Cluster ao



Com genes

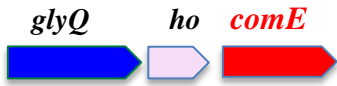
Cluster aq



Cluster ar



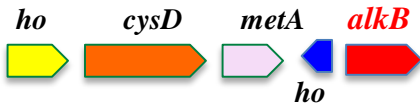
Cluster as



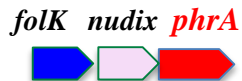
Cluster at



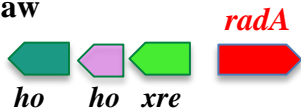
Cluster au



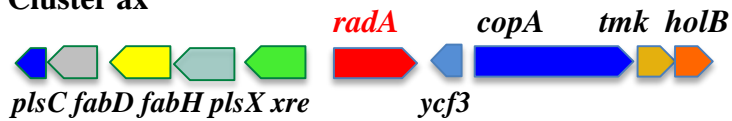
Cluster av



Cluster aw



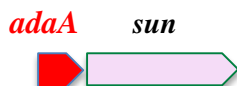
Cluster ax



Cluster ay



Cluster az



- **Supplemental Fig.1: Conserved genomic organization around the DNA repair genes in cyanobacterial genomes.**
- Genes are represented by boxes pointing in the direction of their transcription. DNA repair genes are colored in red. Genes encoding hypothetical proteins are indicated as “ho”.
- **Cluster a:** thrC: threonine synthase; ump: uncharacterized membrane protein; aarF: protein kinase; recN; uvrB; elp: esterase-lipase protein; sps: sucrose phosphate synthase. **Cluster b:** asd: aspartate semialdehyde dehydrogenase; dapA: dihydrodipicolinate synthase; hyd: metallo-beta-lactamase hydrolase; mesJ: ATPase; uvrB; lysC: aspartate kinase; holA: DNA polymerase III subunit; CobH: precorrin-8X methylmutase; mutS. **Cluster c:** dapF: diaminopimelate epimerase; nifS: cysteine desulfurase; ho; dacB: D-alanyl-D-alanine carboxypeptidase; coaD phosphopantetheine adenylyltransferase; uvrC; phr; PHP metal-dependent phosphoesterase; cobN: cobalamin biosynthesis protein. **Cluster c’:** cluster c without phr. **Cluster d:** uvrD; pcnB: tRNA nucleotidyltransferase/poly(A) polymerase; swdk: selenide water dikinase; mtp : methylthioadenosine phosphorylase. **Cluster e:** Ndh: NAD(P)H-quinone oxidoreductase; hycB: Fe-S-hydrogenase; TR tRNA-Gln; hadh: haloacid dehalogenase; recA; dinG: DNA helicase; tyrA: arogenate dehydrogenase.
- **Cluster f:** pdxJ: pyridoxine 5'-phosphate synthase; recC; ste14: S-isoprenylcysteine methyltransferase; recBec; recD; srnB: RNA helicase; mdlB: ABC-type transport; psbP: photosystem II protein; recR; lipA: lipoate synthase. **Cluster g:** nuc-like: ATP dependant nuclease; recBec. **Cluster h:** nifS: L-cysteine/cystine lyase; recB_{cy}. **Cluster i:** rgd: deoxyribonucleotide pyrophosphatase; manB: phospho-mannomutase; gcvT: aminomethyl transferase; pyrE: orotate phosphoribosyl-transferase; tlyC: hemolysin; mviN: oxidoreductase. **Cluster j:** recD-like protein. \$: recD behind recA. **Cluster k:** had: haloacid dehalogenase; recF. **Cluster l:** ftsW: cell division protein; hik: histidine kinase; psaD: photosystem I protein; trpE: anthranilate synthase; ppc: phosphoenol-pyruvate carboxylase; recF; speD: S-adenosylmethionine decarboxylase; ctuR: corrinoid adenosyltransferase; thiF: molybdopterin biosynthesis; phdh: phytoene dehydrogenase; tyrA : arogenate dehydrogenase; dinG : Rad3-related helicase. **Cluster m:** dcm: cytosine methyltransferase; deoC: deoxyribose-phosphate aldolase; recO; mjf: facilitator transporter; rfaG: glycosyltransferase. **Cluster m’:** cluster m without dcm. **Cluster m’*:** cluster m’ without rfaG. **Cluster m’*’:** cluster m where dcm replaces lrtA: light-repressed protein. **Cluster m’*’*:** cluster m without dcm and deoC. **Cluster m’*’*’:** cluster m’*’ without rfaG. **Cluster m’*’*’*:** only deoC upstream recO. **Cluster m’*’*’*’:** Cluster m’*’*’ without mjf. **Cluster n:** mutY; recR. **Cluster q:** shares genes with cluster f. psbP; recR; lipA: lipoate synthase; gst: glutathione S-transferase; bioB: biotin synthase; upps: UDP pyrophosphate synthase; lysA: diaminopimelate decarboxylase. **Cluster q’:** cluster q without gst. **Cluster q’*:** cluster q without ho between psbP and recR. **Cluster r:** gltf: glycosyl transferase; rspB: 30S ribosomal protein; tsf: elongation factor. **Cluster r*:** cluster r with insertion between gltf and rpsB. **Cluster r’:** cluster r without gltf. **Cluster r’*:** cluster r without gltf, rpsB, tsf. **Cluster s:** cluster r where recG is replaced by adcy: adenylate cyclase. **Cluster t:** recJ_{cc}; ycf12: photosystem II protein; duf1: UPF0153 Fe-S protein; duf2: UPF0016 protein; duf3: conserved domain protein. **Cluster t’:** cluster t with insertion between duf1 and duf2. **Cluster t*:** cluster t without ycf12. **Cluster u:** cluster t harboring kin (kinase) and had (putative haloacid dehalogenase) upstream of recJ and ubiX and ho downstream duf3; UbiX: amino acid decarboxylase. had; vacB: acetazolamide resistance Zam/organic solvent ABC permease. **Cluster u’:** cluster u with eriC (chloride channel) replacing ycf12. **Cluster u’*:** cluster u without kin.

- Cluster v:** def: peptide deformylase; gcn5: N-acetyltransferase. **Cluster v*:** cluster v with an insertion between the two ho. **Cluster v':** cluster v without def and ho. **Cluster v'':** cluster v without gcn5. **Cluster w:** ukin: unusual protein kinase &: cluster w with mutL downstream recN. **Cluster a:** see uvrA. **Cluster x:** psaE: photosystem I centre. mut M; recQ; LysM; peptidoglycan-binding; aldH; aldehyde dehydrogenase. **Cluster y:** spp: sucrose-phosphate phosphatase; ruvA; aos: 8-amino-7-oxononanoate synthase. **Cluster y':** cluster y without aos. **Cluster y'':** cluster y without spp. **Cluster z:** umuD; umuC; sht: serine hydroxymethyltransferase; dnaG: DNA primase; rahT: putative transporter; phD: cAMP phosphodiesterase; ruvA; rpsO: ribosomal protein S15; dnaE: DNA polymerase III; gatA: glutamyl-tRNA(Gln) amidotransferase. ho. **Cluster z':** cluster z without umuCD and sht. **Cluster z'':** cluster z with only rpsO and ho downstream ruvA. **Cluster z*:** cluster z with various genes upstream of dnaG and RuvA. **Cluster ab:** hisF: imidazole glycerol phosphate synthase; ruvB; pilF: pilus assembly. **Cluster ab':** cluster ab without pilF. **Cluster ab'':** cluster ab without hisF. **Cluster ac:** xre: transcriptional regulator; lysS; lysine-tRNA ligase; 3 ho; mtt: methyltransferase; Smat: sulfatase maturase ; stkin : serine/threonine kinase ; smpB: SsrA-binding; ruvB; tpr: TPR repeat-containing protein; zpep: zinc metallopeptidase; ho. **Cluster ad:** cluster ac where genes are replaced by ad: ssb; mreB: rod shape; mreC: rod shape MreB; mbp: membrane protein. **Cluster ae:** yjeE: UPF0079 protein; upf52: UPF0052 protein; ruvC. **Cluster af:** guaB: inosine-5-monophosphate dehydrogenase; trx: thioredoxin; hisH-2: glutamine amidotransferase; SAM: methyltransferase; petG: cytochrome b6-f; cytM: cytochrome C; lasT: rRNA methyltransferase; penP: serine hydrolase; Ho; clhI: Mg-protoporphyrin chelatase; ruvC. **Cluster af':** cluster af without petG. **Cluster af⁶:** cluster af with genes downstream of ruvC. fmC; 5-formyltetrahydrofolate ligase; sufE: cysteine desulfurase and thrA: homoserine dehydrogenase. **Cluster ag:** ada: adenosine deaminase; tst: rhodanese protein; mutL. **Cluster ag':** cluster ag without ada. **Cluster ag*:** cluster ag genes inserted between ada and tst. **Cluster ah:** PAP: PAP fibrillin; psaE: photosystem I; *mutM*; nqO: NAD(P)H-quinone oxidoreductase; mdh: malate dehydrogenase. **Cluster ai:** dnaJ: chaperone; hemN: delta-aminolevulinic dehydratase; glo: lactoylglutathione lyase ; mutS; malK: sugar transporter. cgtA: GTPase. **Cluster ai':** cluster ai without dnaJ. **Cluster ai'':** cluster ai without glo1. **Cluster ai*:** cluster ai without malK. **Cluster ai'':** cluster ai without both dnaJ and malK. **Cluster aj:** mutT; hdr: alpha/beta hydrolase; coaX: pantothenate kinase. **Cluster aj':** cluster aj without coaX. **Cluster aj'':** cluster aj without hdr. **Cluster ak:** mutY; cscK: sugar kinase. **Cluster al:** umuC; umuD. **Cluster am:** argF: ornithine carbamoyltransferase; lexA; resIII: DNA phosphorothioation. **Cluster an:** ftsH: cell division; argF: ornithine carbamoyltransferase; lexA. **Cluster an*:** similar to cluster an with genes inserted between argF and lexA. **Cluster ao:** mreD; mreC; mreB; ssb. **Cluster ao'** cluster ao without mreD mreC. **Cluster aq:** nifS; comA. **Cluster aq':** cluster aq with ho between nifS and comA. **Cluster ar:** rhoT: rho termination protein; homb hypothetical protein; comA. **Cluster ar*:** comA triplicated. **Cluster as:** glyQ: glycyl-tRNA synthetase; ho; comE. **Cluster as':** Cluster as without ho. **Cluster as'':** Cluster as without glyQ. **Cluster at:** gcn5: GCN5-N-acetyltransferase peptidase; comFC: pep: peptidase. **Cluster au:** cysD: O-acetylhomoserine aminocarboxypropyltransferase; metA : homoserine O-succinyltransferase; ho; alkB: oxidative demethylase. **Cluster av:** folK: 2-amino-4-hydroxy-6- hydroxymethylidihydropteridine pyrophosphokinase; nudix: NTP pyrophosphohydrolase; phrA. **Cluster av':** Cluster av harboring ho between nudix and phrA. **Cluster av'':** Cluster av without folK. **Cluster aw:** ho; ho; xre: transcriptional regulator; radA. **Cluster aw':** cluster aw with one ho gene.

- **Cluster aw**”: cluster aw with no ho. **Cluster ax**: plsC: glycerol 3-phosphate transferase; fabD: malonyl CoA transacylase; fabH:3-oxoacyl-ACP synthase; plsX: glycerol-3-phosphate acyl-transferase; xre: transcriptional regulator; radA; ycf3: photosystem I; copA: heavy metal transport; tmk : thymidylate kinase; holB : DNA polymerase III. **Cluster ay**: ada: transcriptional activator: methylated-DNA-cysteine S-methyltransferase. In some cases Ada is fused to AdaA. **Cluster az**: adaA; sun: 16S rRNA methyltransferase.