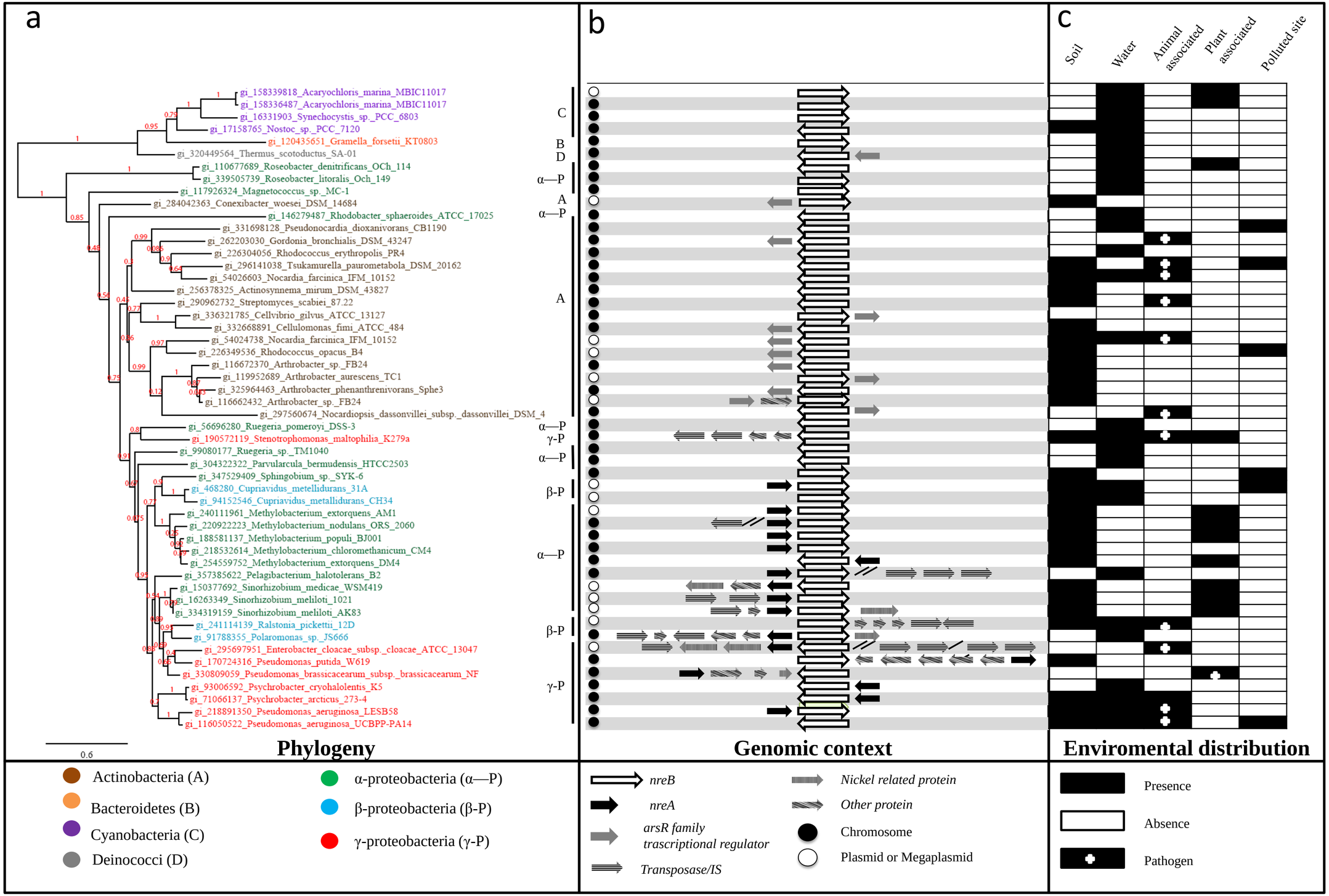
a
b
c
Soil
Water
Animal associated
Plant associated
Polluted site
gi_158339818_Acaryochloris_marina_MBIC11017
gi_158336487_Acaryochloris_marina_MBIC11017
gi_16331903_Synechocystis_sp._PCC_6803
gi_17158765_Nostoc_sp._PCC_7120
gi_120435651_Gramella_forsetii_KT0803
gi_320449564_Thermus_scotoductus_SA-01
gi_110677689_Roseobacter_denitrificans_OCh_114
gi_339505739_Roseobacter_litoralis_Och_149
gi_117926324_Magnetococcus_sp._MC-1
gi_284042363_Conexibacter_woesei_DSM_14684
gi_146279487_Rhodobacter_sphaeroides_ATCC_17025
gi_331698128_Pseudonocardia_dioxanivorans_CB1190
gi_262203030_Gordonia_bronchialis_DSM_43247
gi_226304056_Rhodococcus_erythropolis_PR4
gi_296141038_Tsukamurella_paurometabola_DSM_20162
gi_54026603_Nocardia_farcinica_IFM_10152
gi_256378325_Actinosynnema_mirum_DSM_43827
gi_290962732_Streptomyces_scabiei_87.22
gi_336321785_Cellvibrio_gilvus_ATCC_13127
gi_332668891_Cellulomonas_fimi_ATCC_484
gi_54024738_Nocardia_farcinica_IFM_10152
gi_226349536_Rhodococcus_opacus_B4
gi_116672370_Arthrobacter_sp._FB24
gi_119952689_Arthrobacter_aurescens_TC1
gi_325964463_Arthrobacter_phenanthrenivorans_Sphe3
gi_116662432_Arthrobacter_sp._FB24
gi_297560674_Nocardiopsis_dassonvillei_subsp._dassonvillei_DSM_4
gi_56696280_Ruegeria_pomeroyi_DSS-3
gi_190572119_Stenotrophomonas_maltophilia_K279a
gi_99080177_Ruegeria_sp._TM1040
gi_304322322_Parvularcula_bermudensis_HTCC2503
gi_347529409_Sphingobium_sp._SYK-6
gi_468280_Cupriavidus_metellidurans_31A
gi_94152546_Cupriavidus_metallidurans_CH34
gi_240111961_Methylobacterium_extorquens_AM1
gi_220922223_Methylobacterium_nodulans_ORS_2060
gi_188581137_Methylobacterium_populi_BJ001
gi_218532614_Methylobacterium_chloromethanicum_CM4
gi_254559752_Methylobacterium_extorquens_DM4
gi_357385622_Pelagibacterium_halotolerans_B2
gi_150377692_Sinorhizobium_medicae_WSM419
gi_16263349_Sinorhizobium_meliloti_1021
gi_334319159_Sinorhizobium_meliloti_AK83
gi_241114139_Ralstonia_pickettii_12D
gi_91788355_Polaromonas_sp._JS666
gi_295697951_Enterobacter_cloacae_subsp._cloacae_ATCC_13047
gi_170724316_Pseudomonas_putida_W619
gi_330809059_Pseudomonas_brassicacearum_subsp._brassicacearum_NF
gi_93006592_Psychrobacter_cryohalolentis_K5
gi_71066137_Psychrobacter_arcticus_273-4
gi_218891350_Pseudomonas_aeruginosa_LESB58
gi_116050522_Pseudomonas_aeruginosa_UCBPP-PA14
C
B
D
α—P
A
α—P
A
α—P
γ-P
α—P
β-P
α—P
β-P
γ-P
0.6
Phylogeny
Genomic context
Enviromental distribution
Actinobacteria (A)
Bacteroidetes (B)
Cyanobacteria (C)
Deinococci (D)
α-proteobacteria (α—P)
β-proteobacteria (β-P)
γ-proteobacteria (γ-P)
nreB
nreA
arsR family trascriptional regulator
Transposase/IS
Nickel related protein
Other protein
Chromosome
Plasmid or Megaplasmid
Presence
Absence
Pathogen