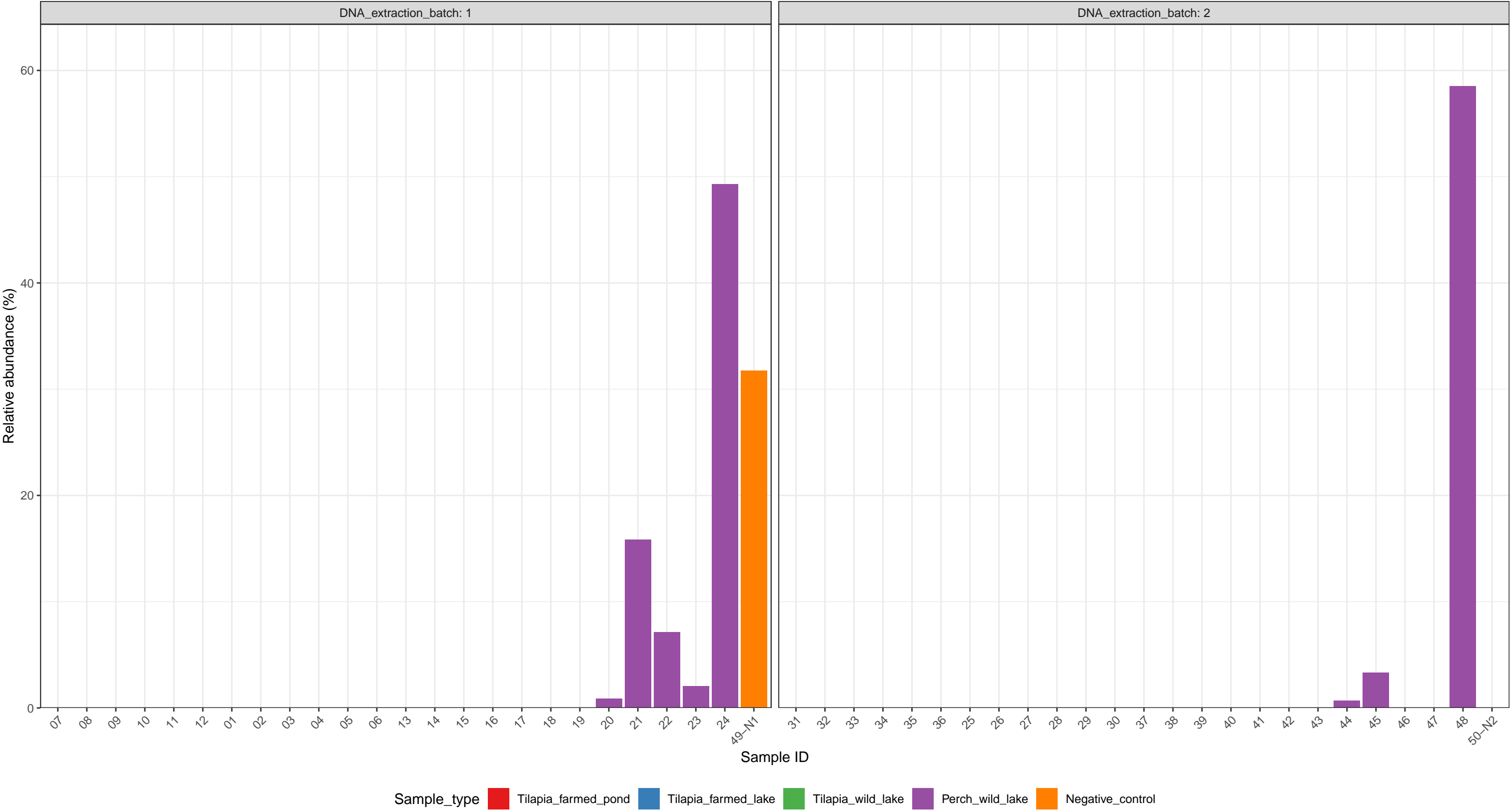


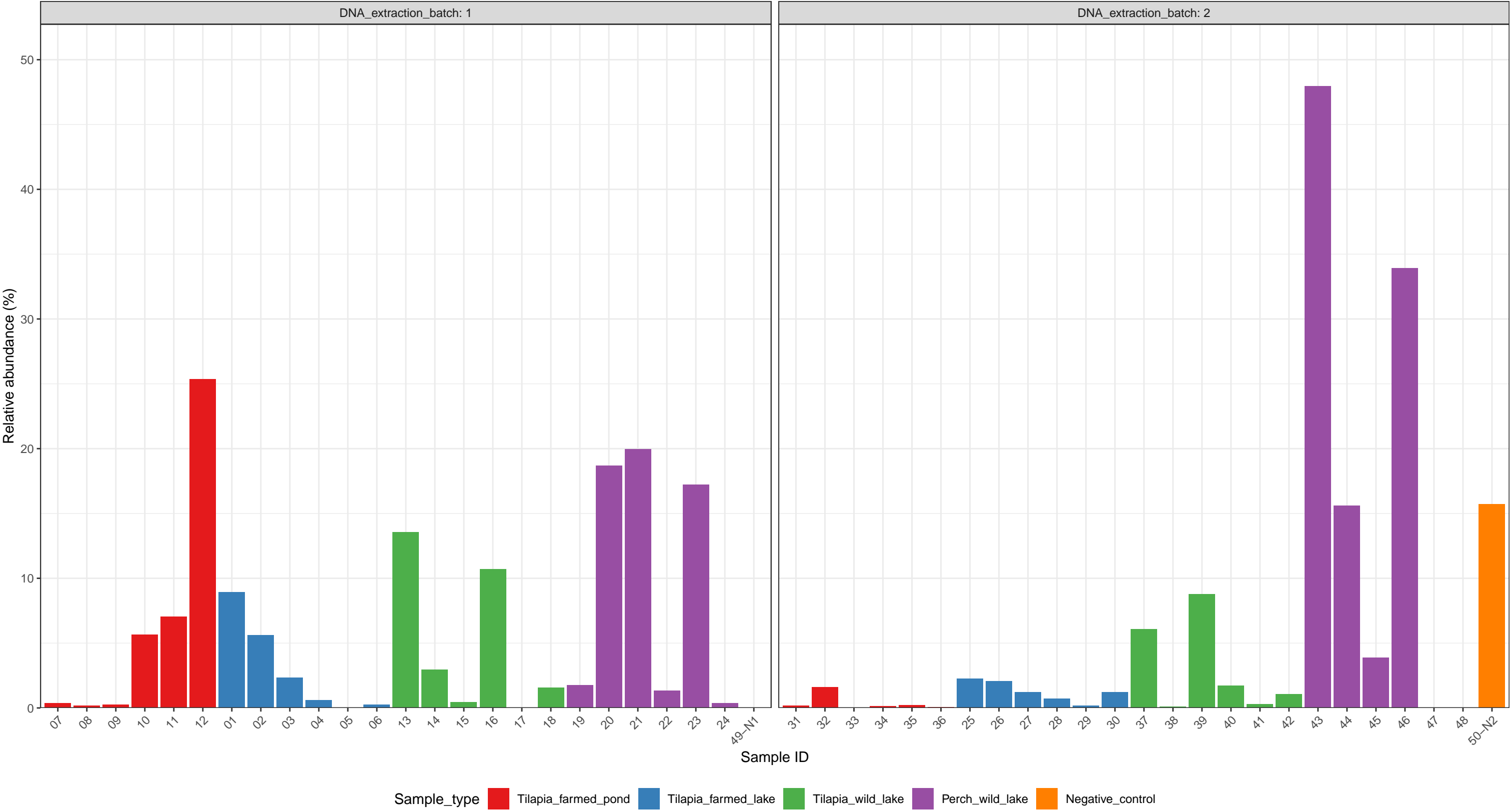
k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Clostridiaceae 1; g__Clostridium sensu stricto 1; NA

featureID: 30cd2eb39b81e92ac815ec19fd6ccdee



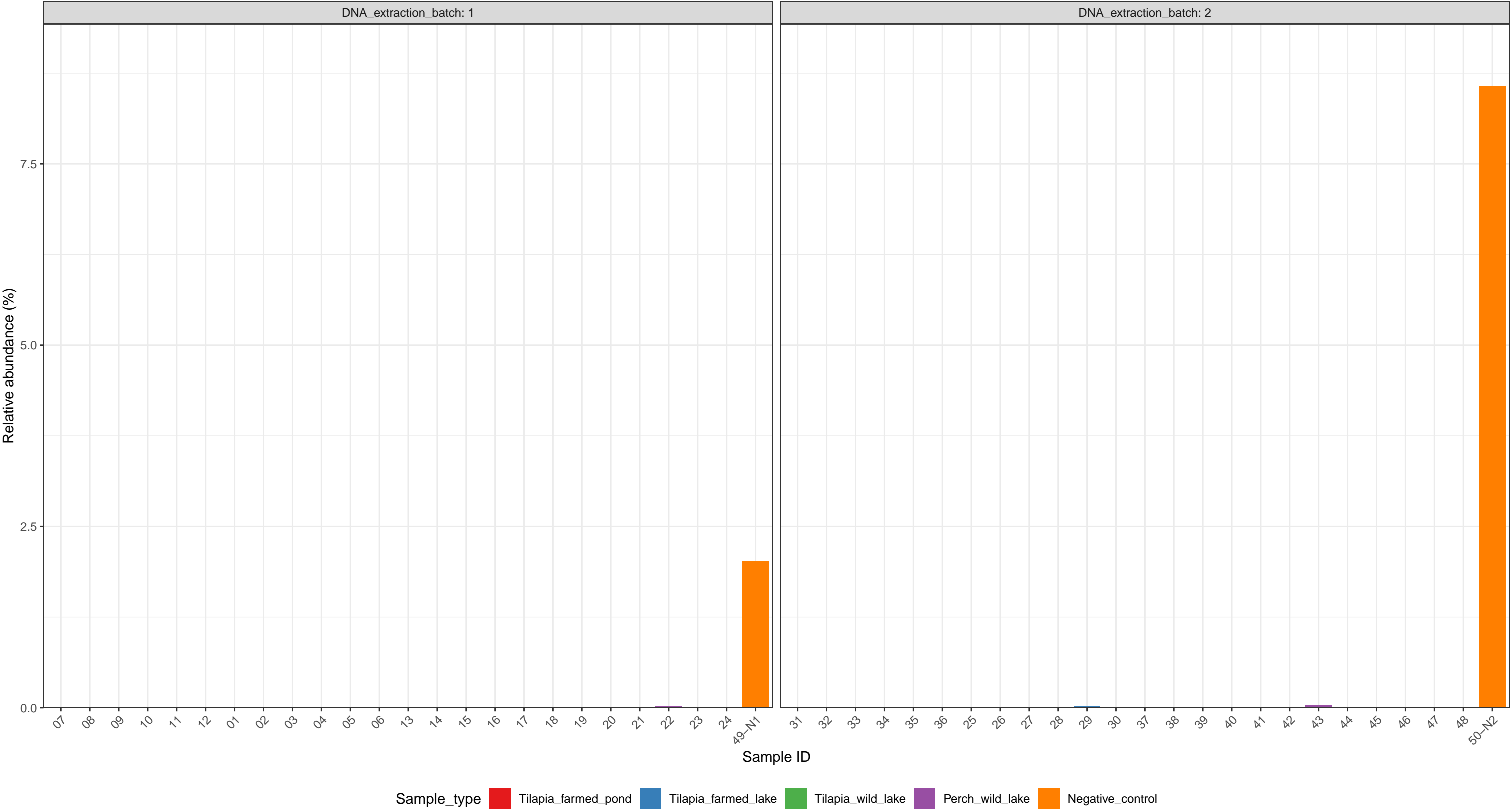
k__Bacteria; p__Fusobacteria; c__Fusobacteriia; o__Fusobacteriales; f__Fusobacteriaceae; g__Cetobacterium; NA

featureID: 9039275571577e03e38d718f59db0e1f



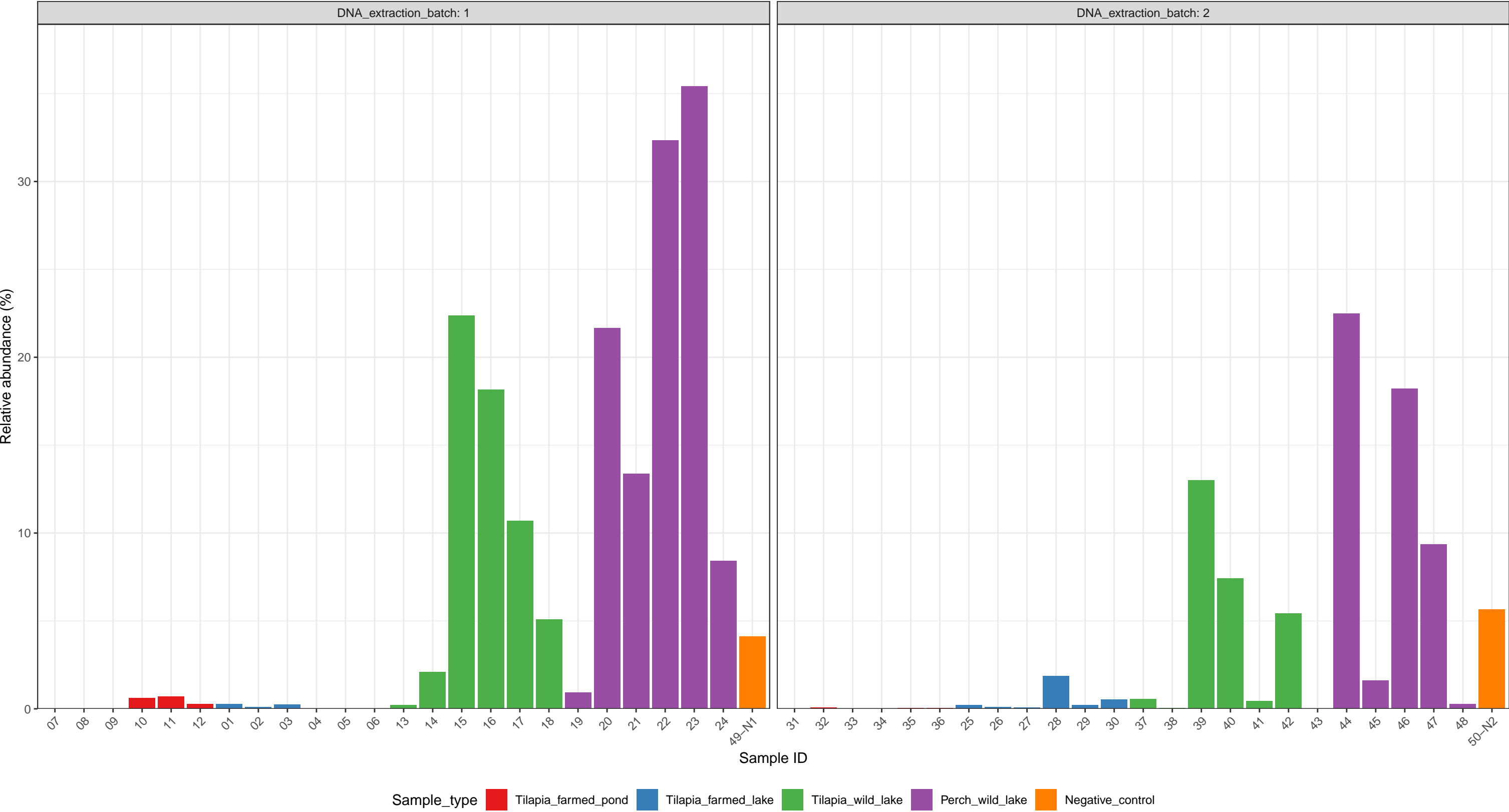
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Betaproteobacteriales; f__Burkholderiaceae; g__Curvibacter; NA

featureID: e0fcddfb9012f2ef3fe5165e818f651



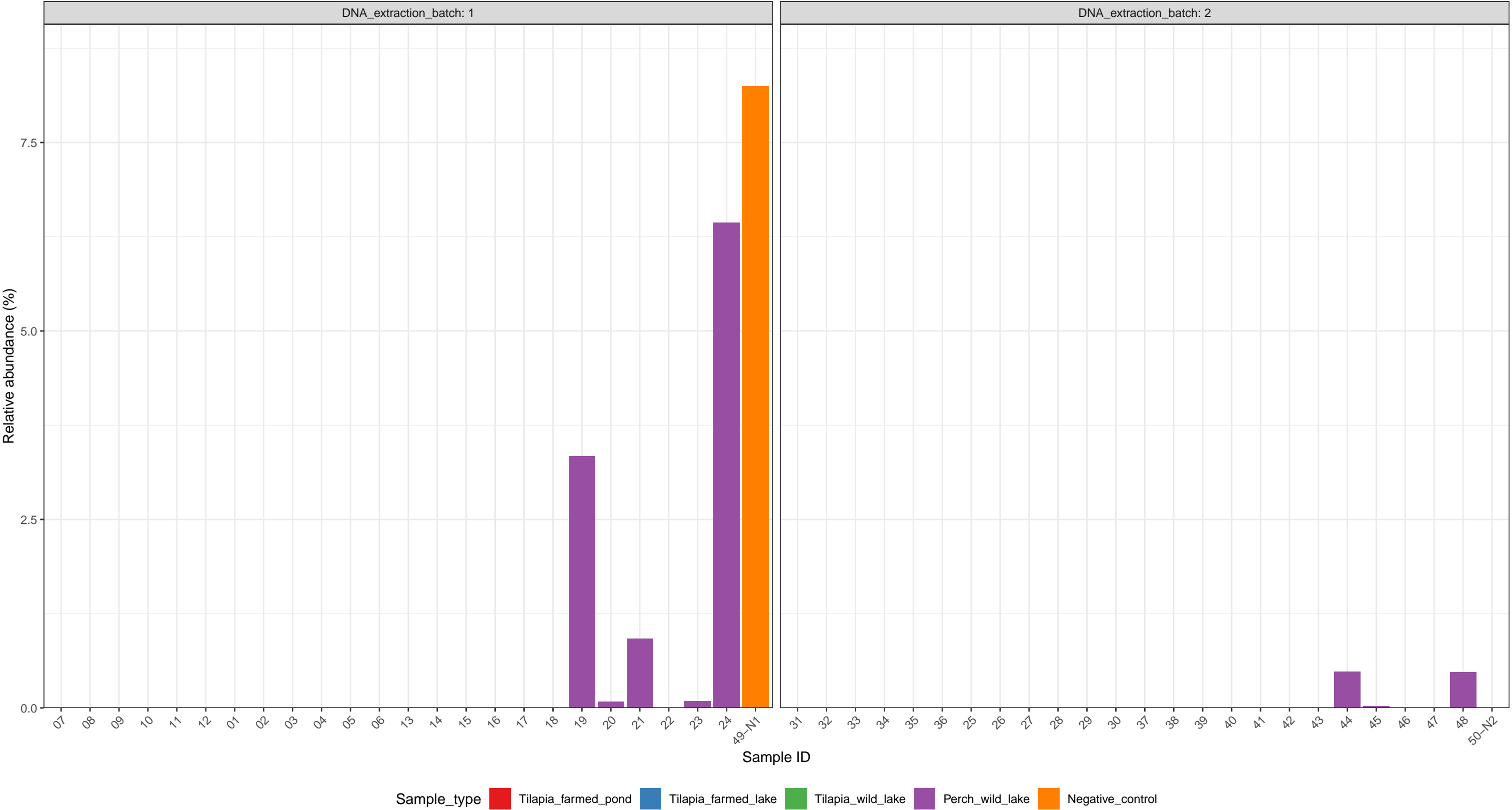
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacteriales; f__Enterobacteriaceae; g__Plesiomonas; NA

featureID: 4f52c06bab364867d8911147cbccbc38



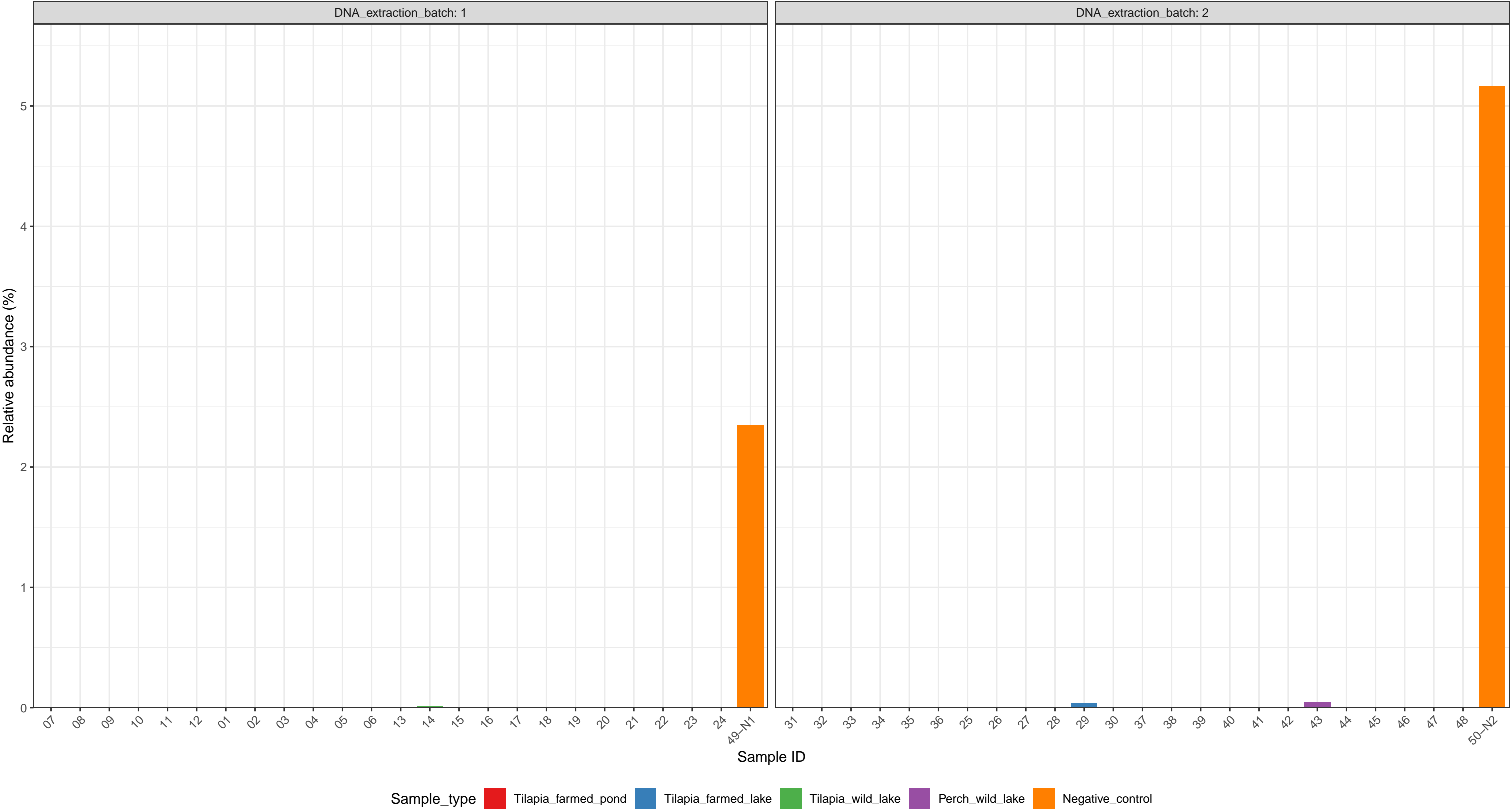
k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Clostridiaceae 1; NA; NA

featureID: 2e13ada579831ad7bc85cacea069bcb4



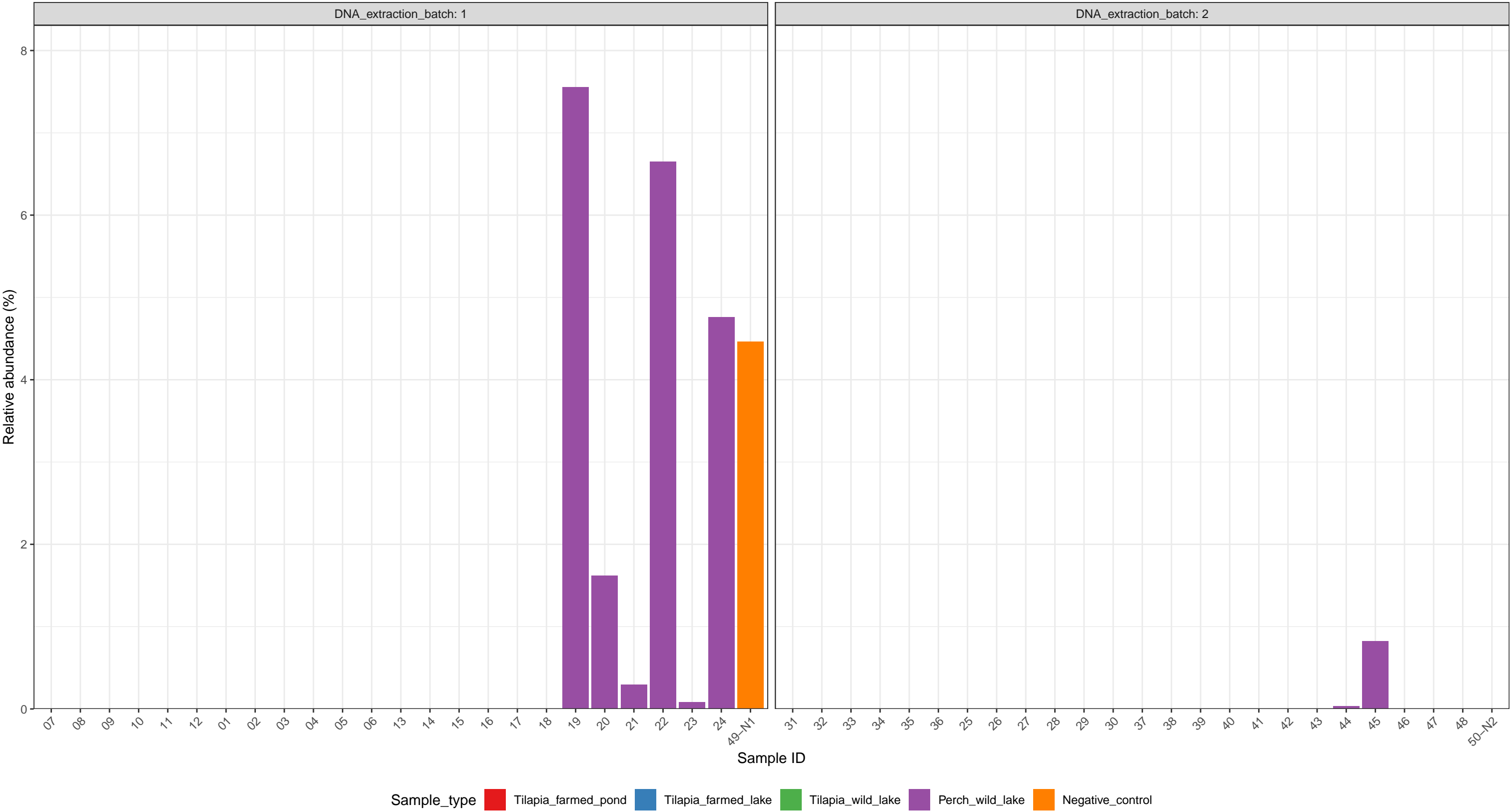
k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__Flavobacterium; NA

featureID: 11c192ca47293df7d3c26138fd796fe1



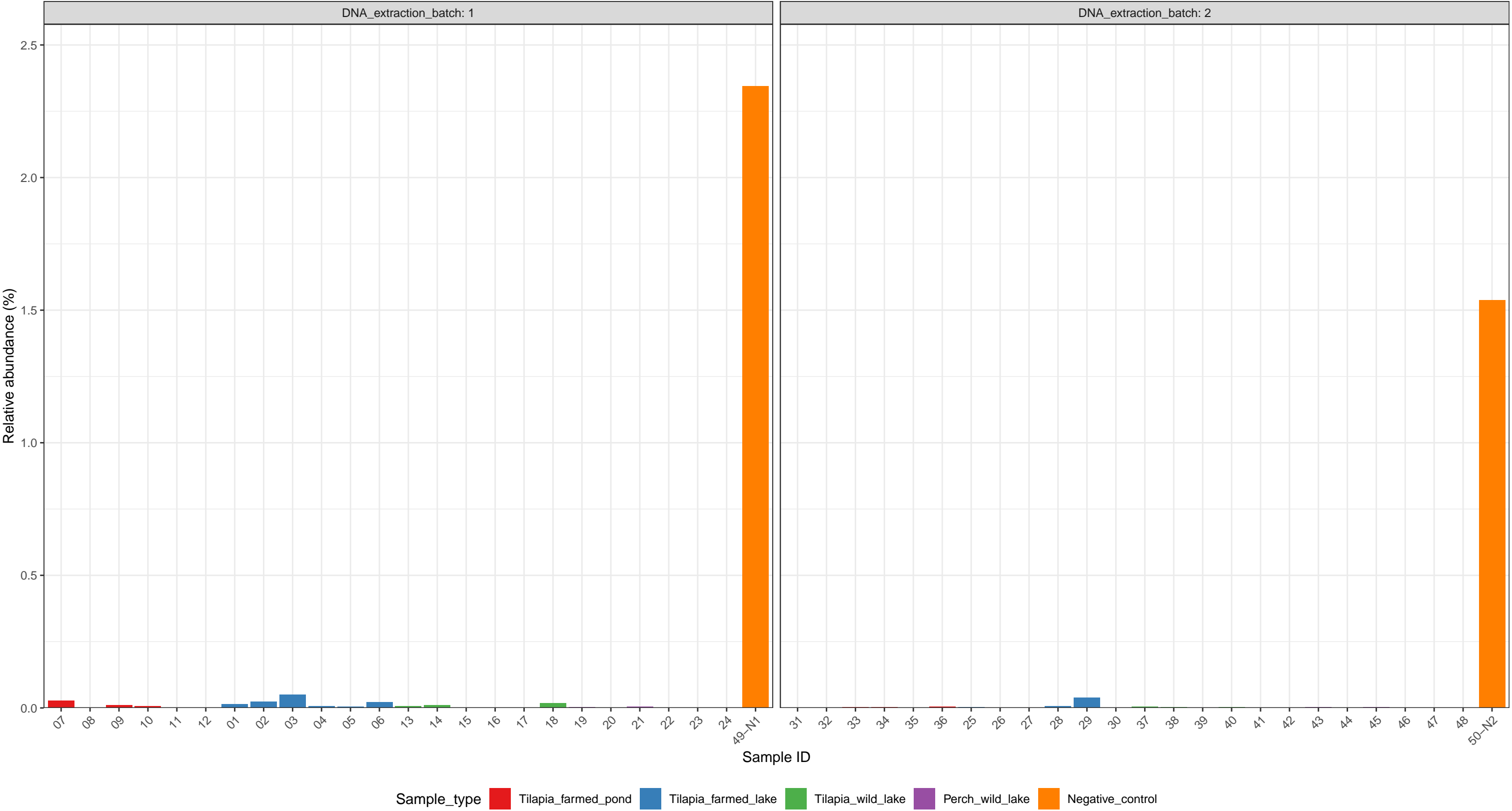
k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Clostridiaceae 1; NA; NA

featureID: 1f1ddbae27b2e40cd4947dc079b0021e



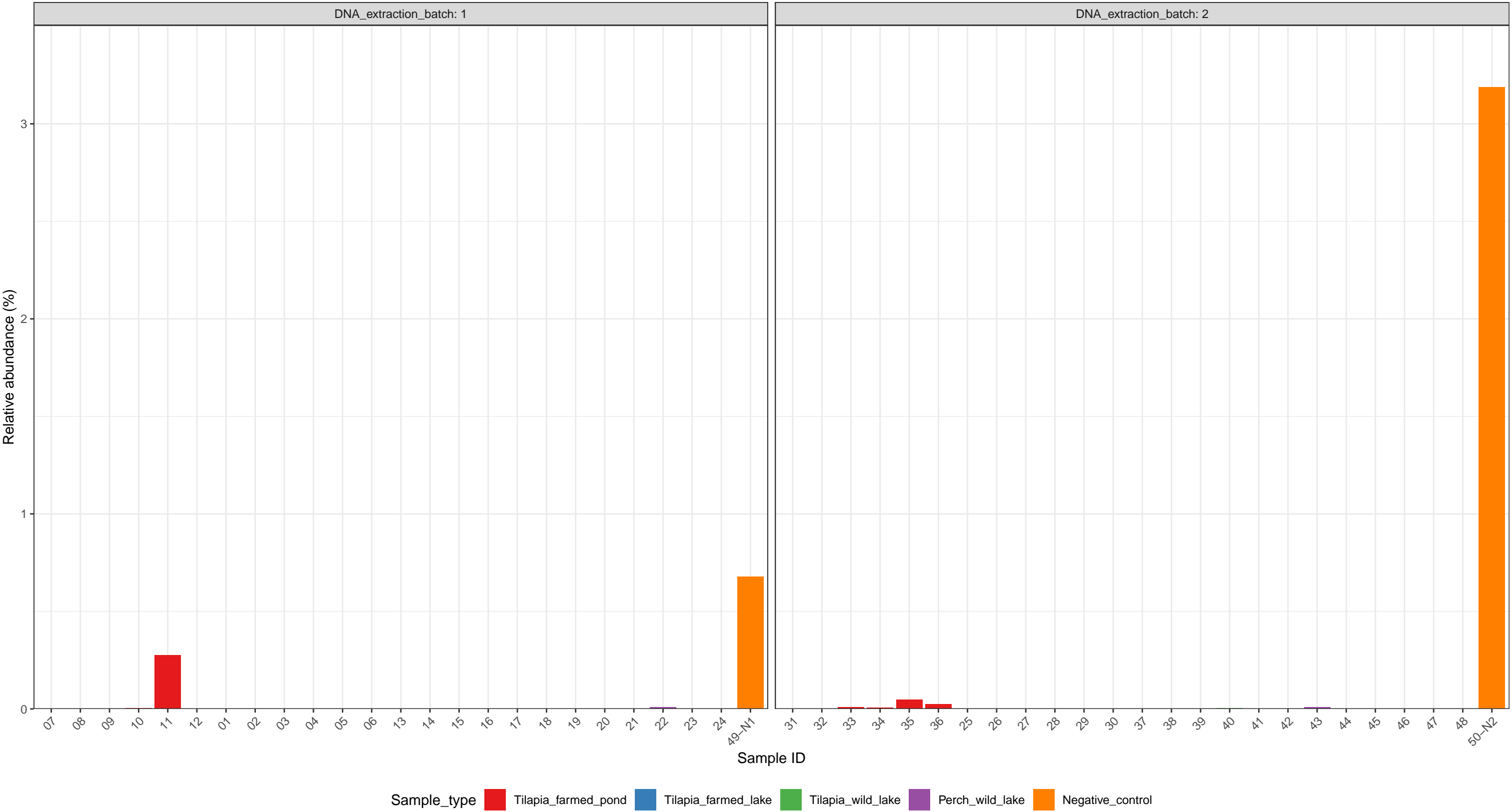
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales; f__Pseudomonadaceae; g__Pseudomonas; NA

featureID: af190b852cec0d6eb78c15eb0e8777e0



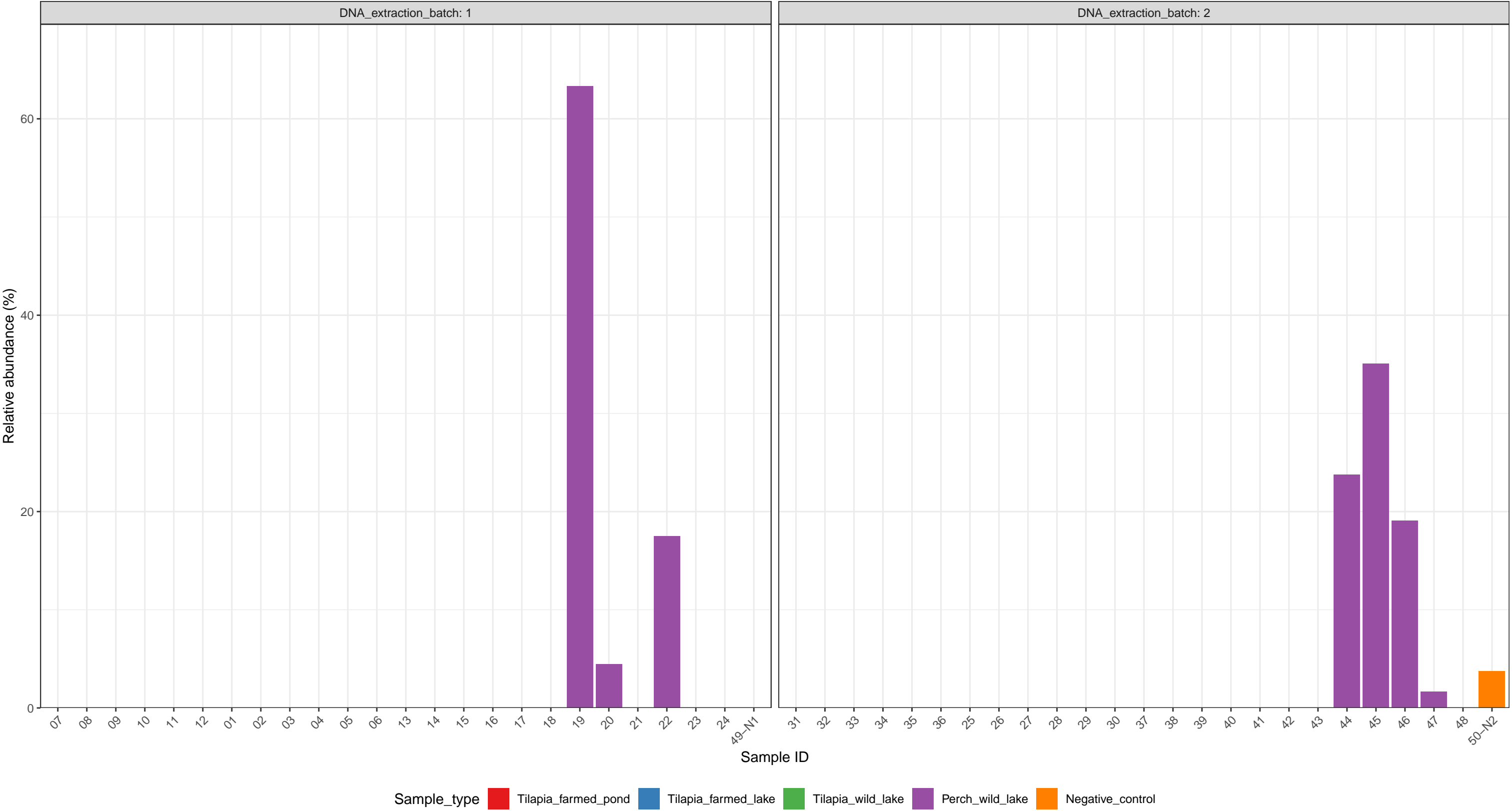
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Xanthobacteraceae; g__Bradyrhizobium; NA

featureID: 9db2817f5c42be6a7bcbca662959982d



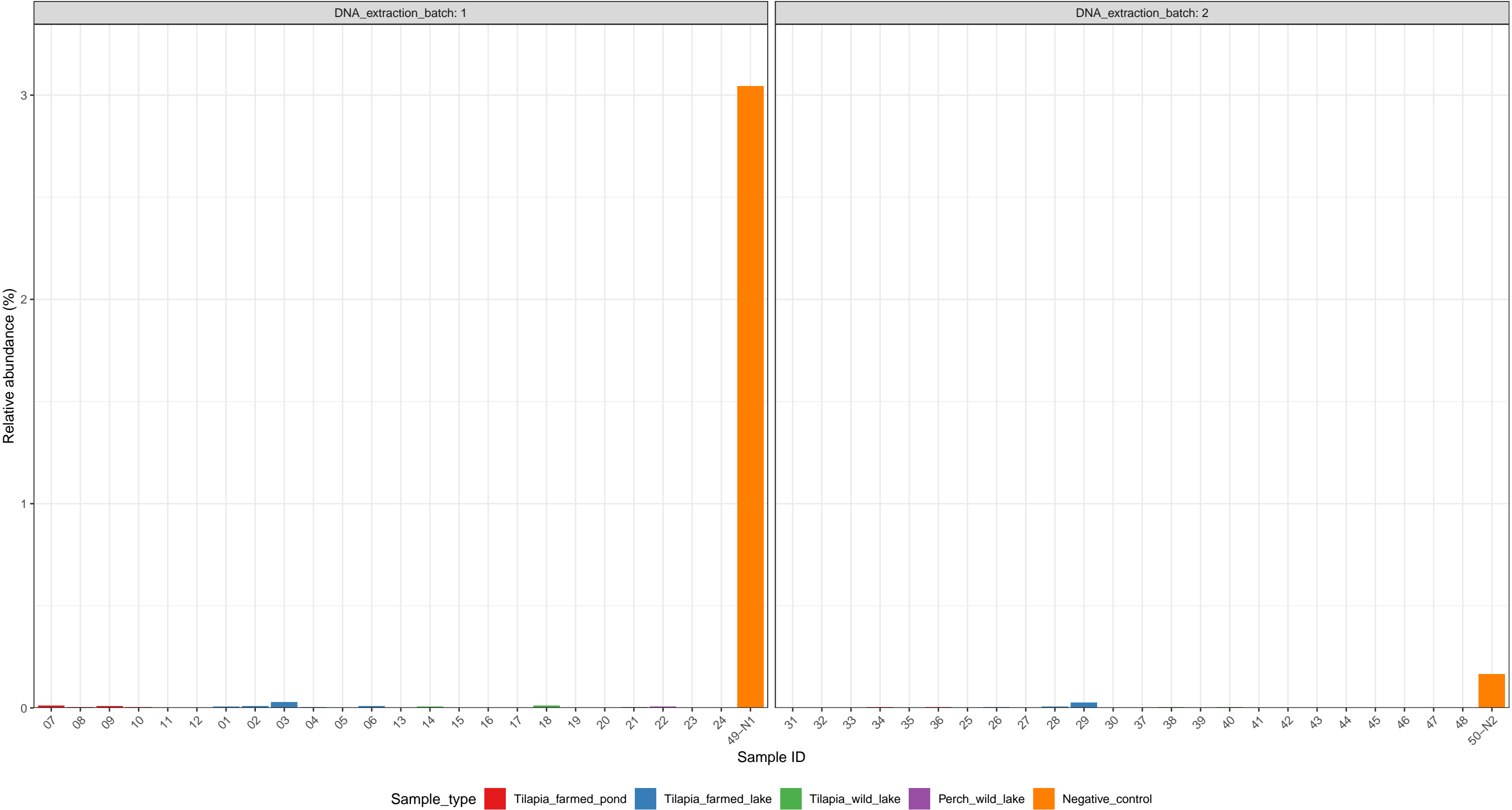
k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Clostridiaceae 1; NA; NA

featureID: 750438ef469a6a58cdf16b89f540188b



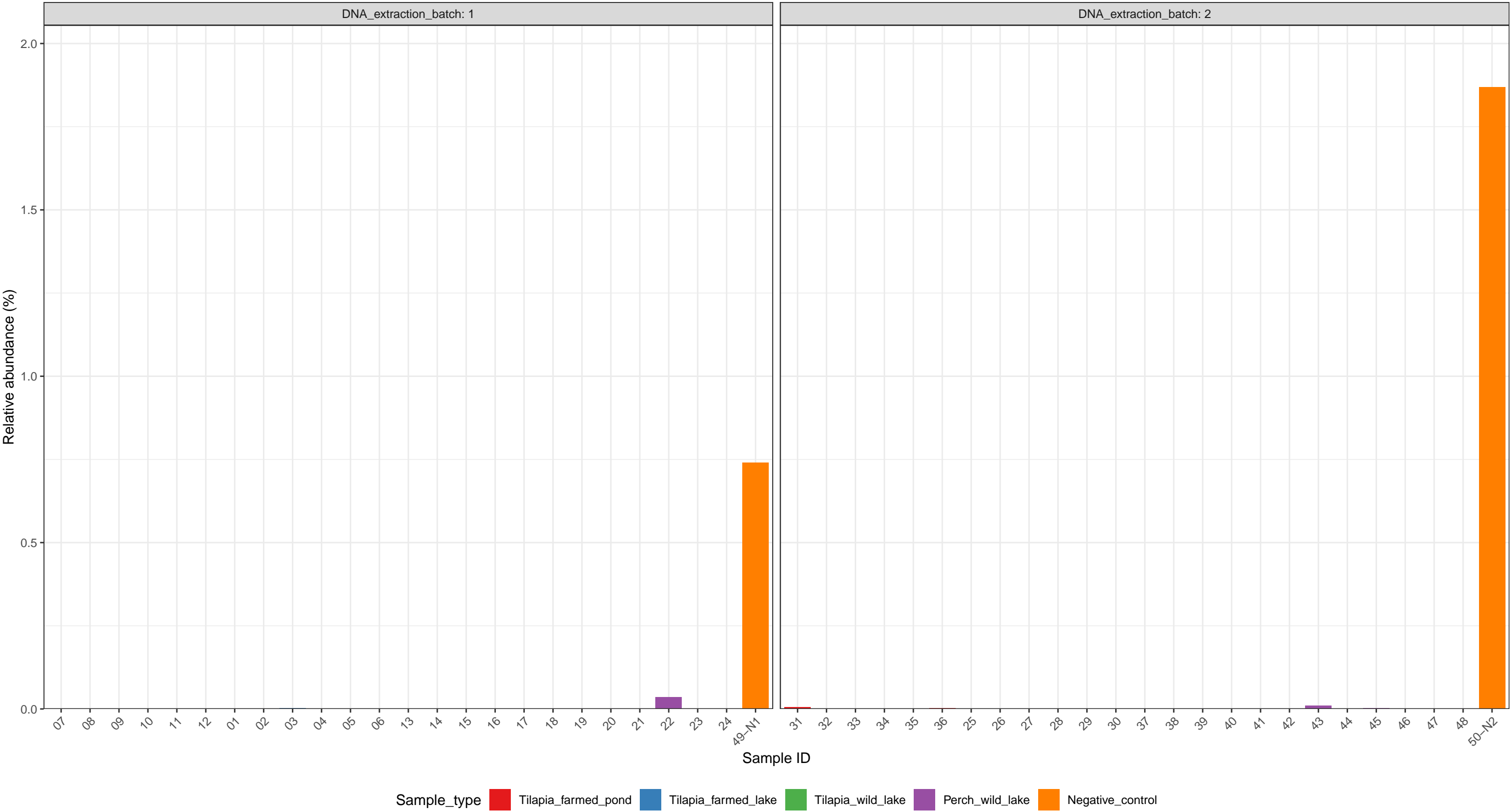
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales; f__Pseudomonadaceae; g__Pseudomonas; NA

featureID: 5a90e7ffe242256a5c625bd072bb3337



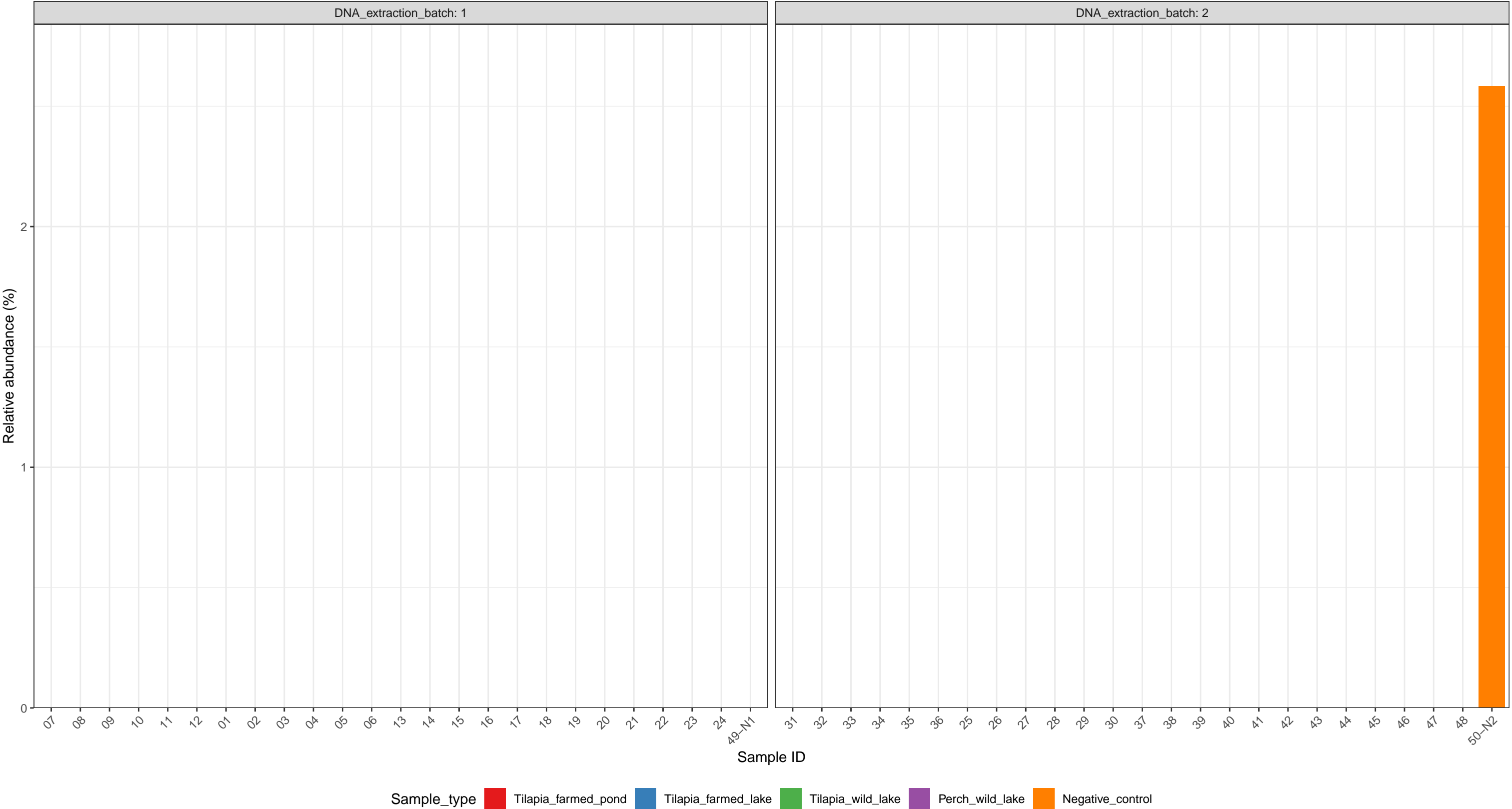
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Xanthobacteraceae; NA; NA

featureID: 8f2bbe692f7aca0f2c3959c3cf312b1d



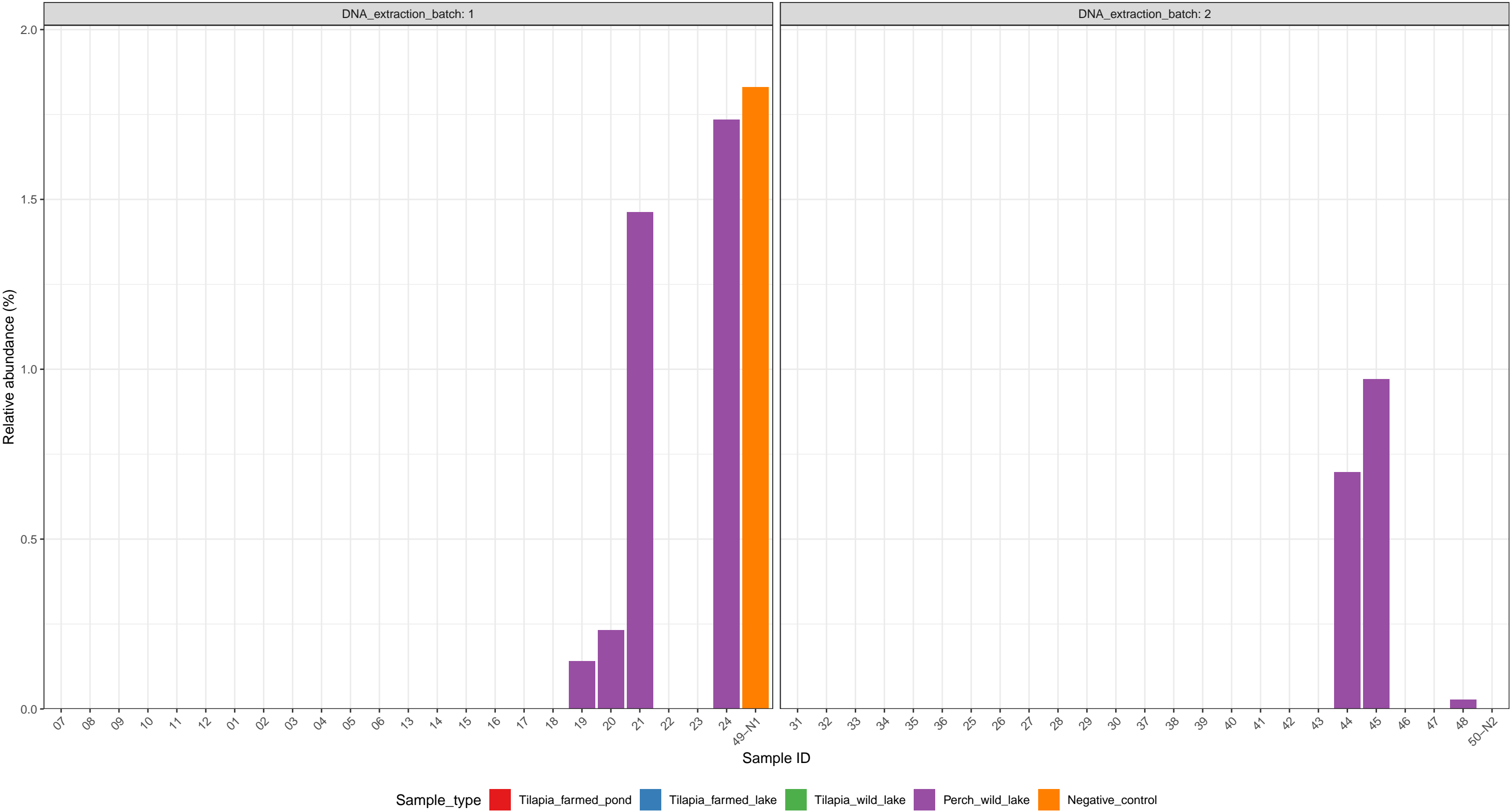
k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Corynebacteriales; f__Nocardiaceae; g__Rhodococcus; NA

featureID: 4a7f867d55034fd3b2b4b28e0b1dda36



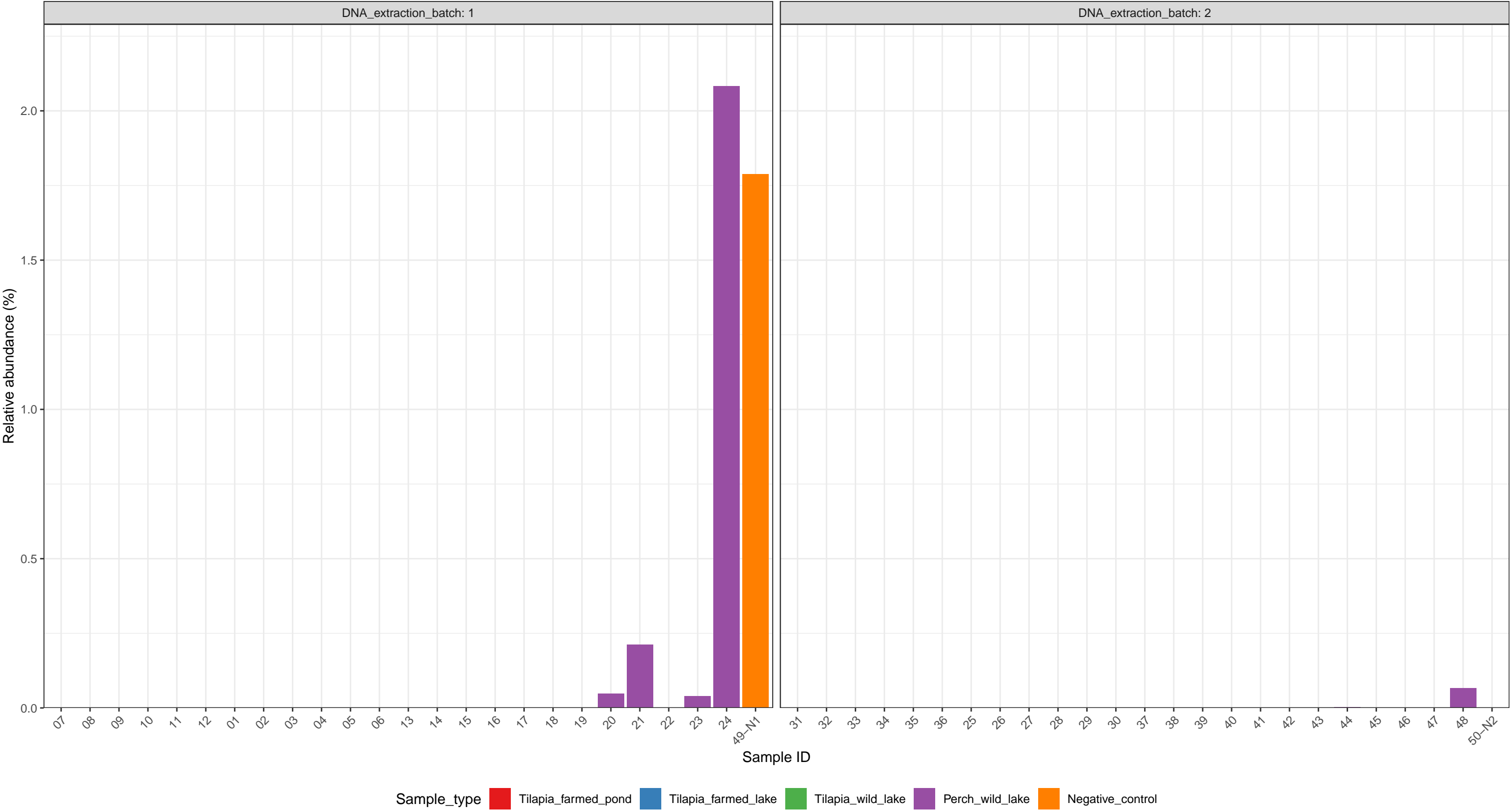
k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Clostridiaceae 1; g__Clostridium sensu stricto 1; NA

featureID: 8f6ff8174262993339a29e403091e900



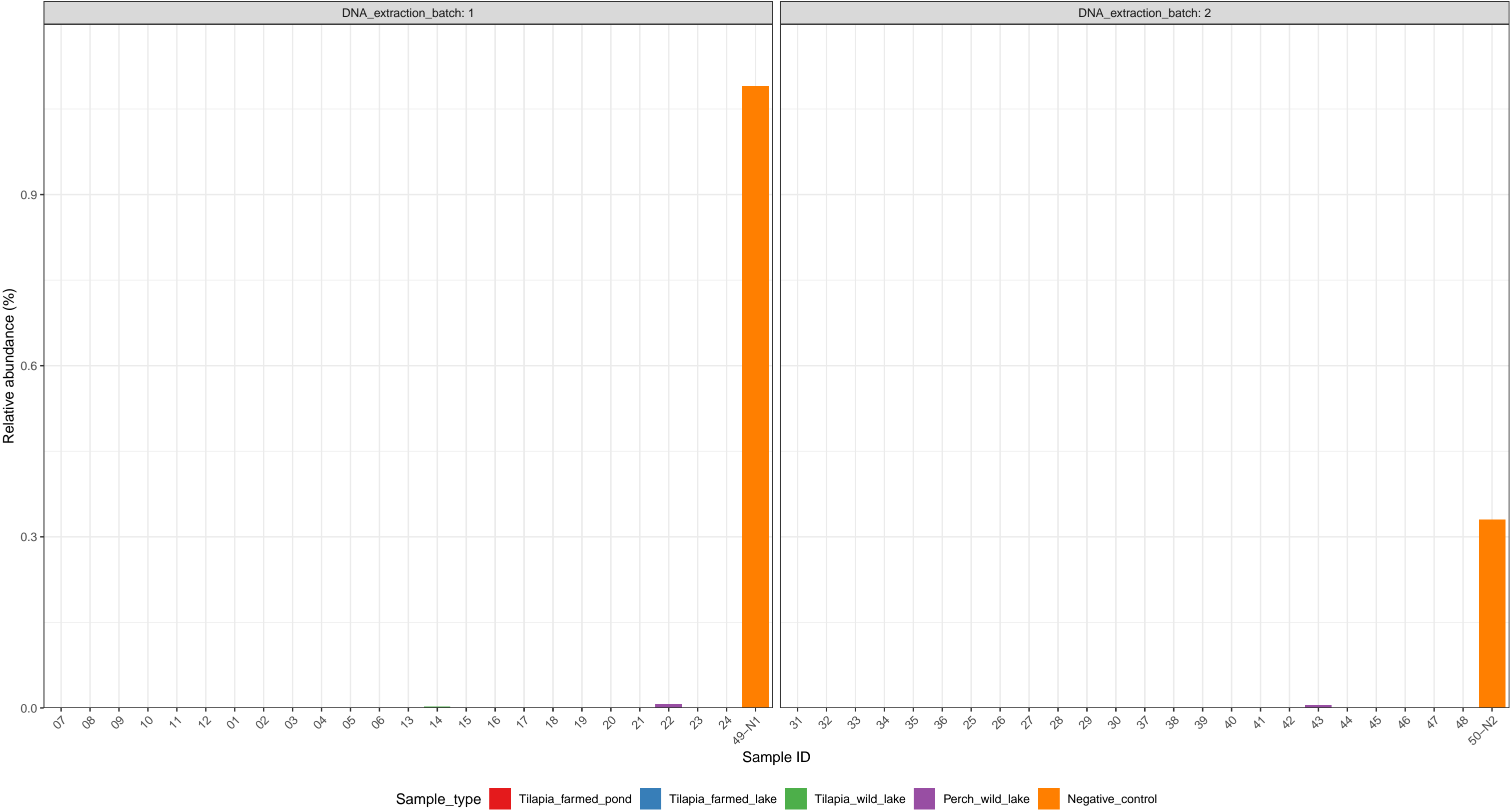
k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Clostridiaceae 1; g__Clostridium sensu stricto 1; NA

featureID: 444cb870909dcd447934e3eb70c73738



k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Micrococcales; f__Microbacteriaceae; g__Candidatus Aquiluna; NA

featureID: 10a4ba9050a60c9880edf695bd202b6e



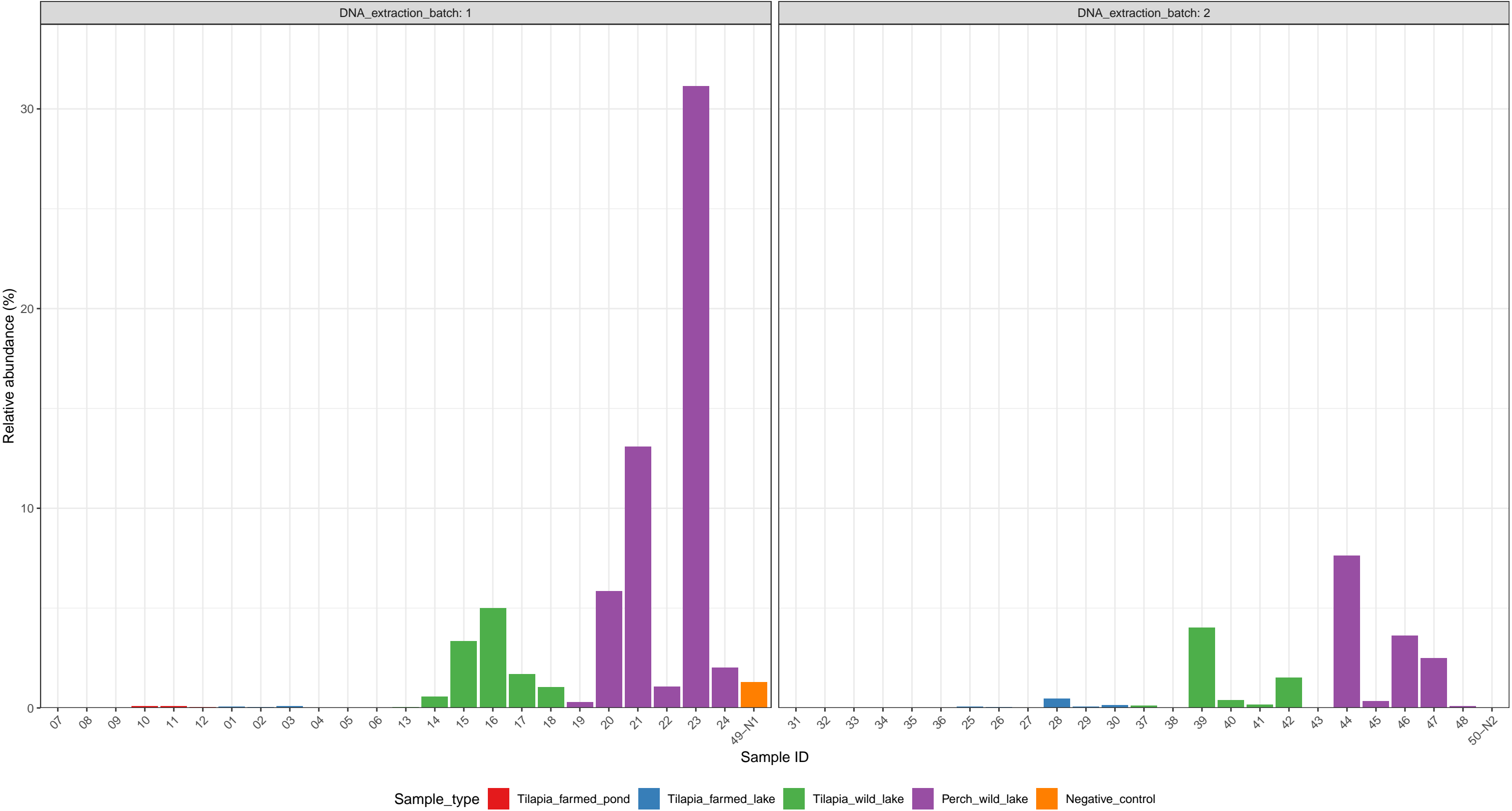
k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Micrococcales; f__Micrococcaceae; g__Kocuria; s__Kocuria marina

featureID: 19c88c43cefc0efae399898111815666



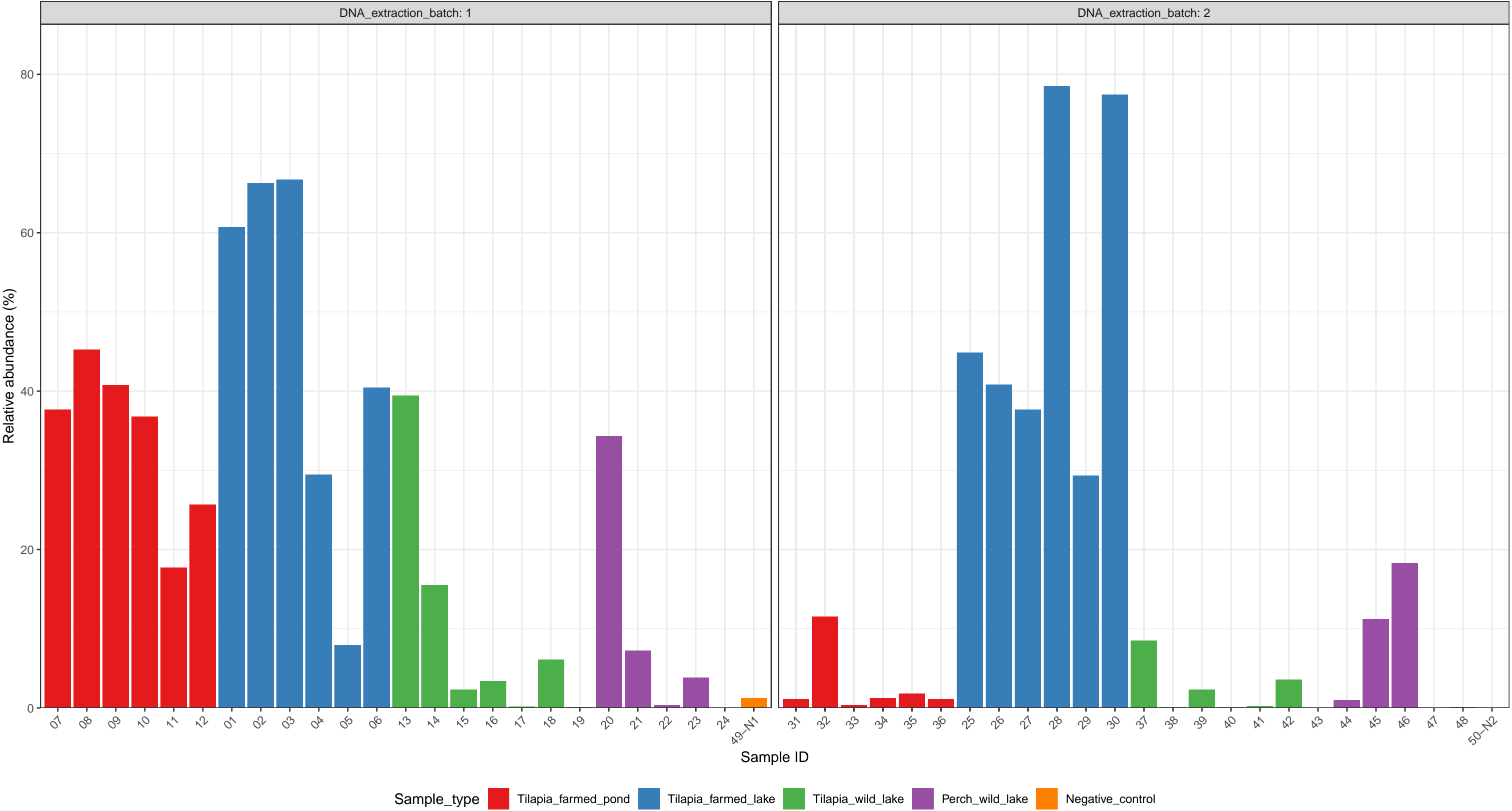
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacteriales; f__Enterobacteriaceae; g__Plesiomonas; NA

featureID: 7438db900c870a0d550a34920b927788



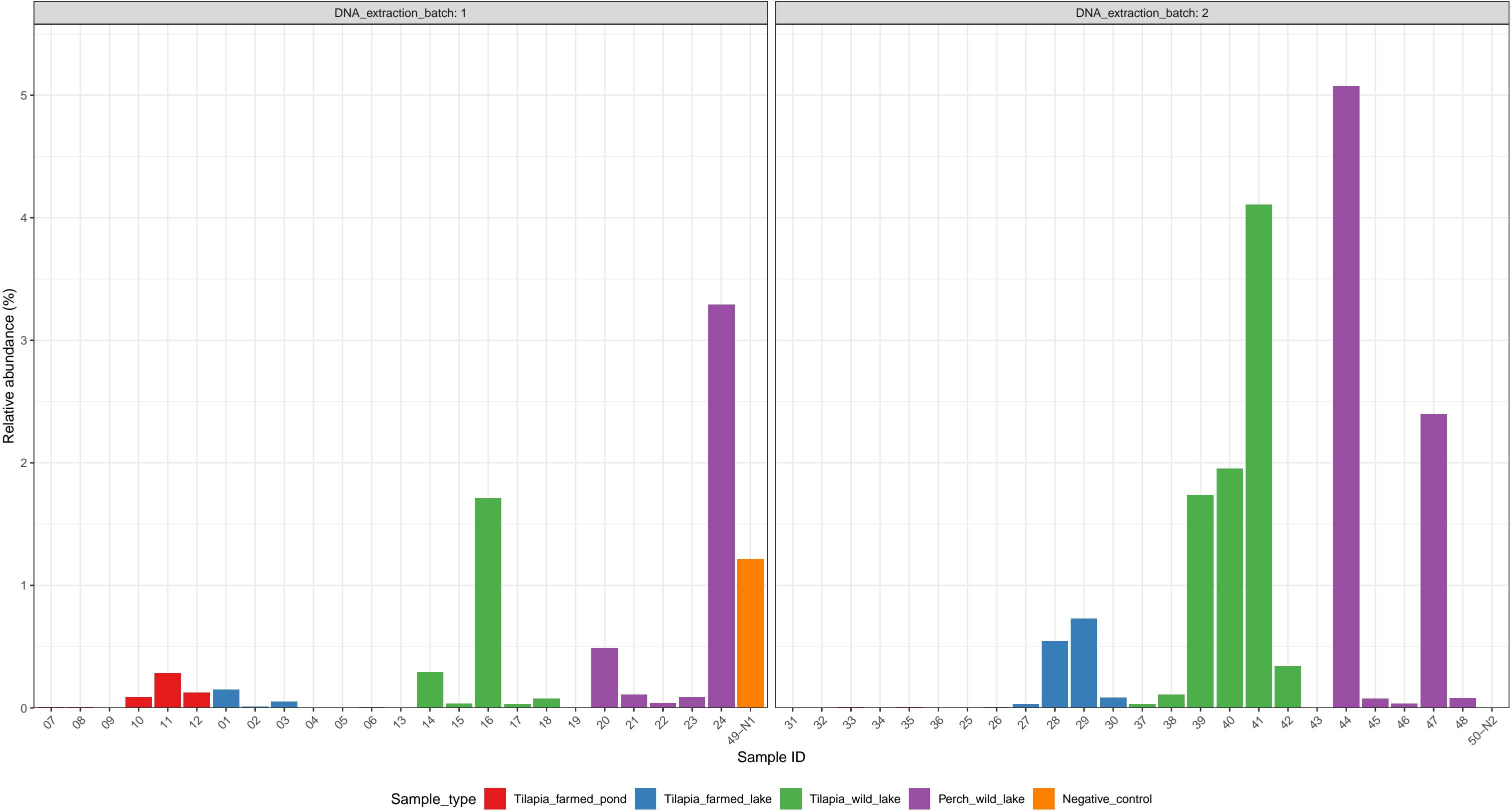
k__Bacteria; p__Fusobacteria; c__Fusobacteriia; o__Fusobacteriales; f__Fusobacteriaceae; g__Cetobacterium; NA

featureID: 03f0f9af305de66090e757aaa19b09fd



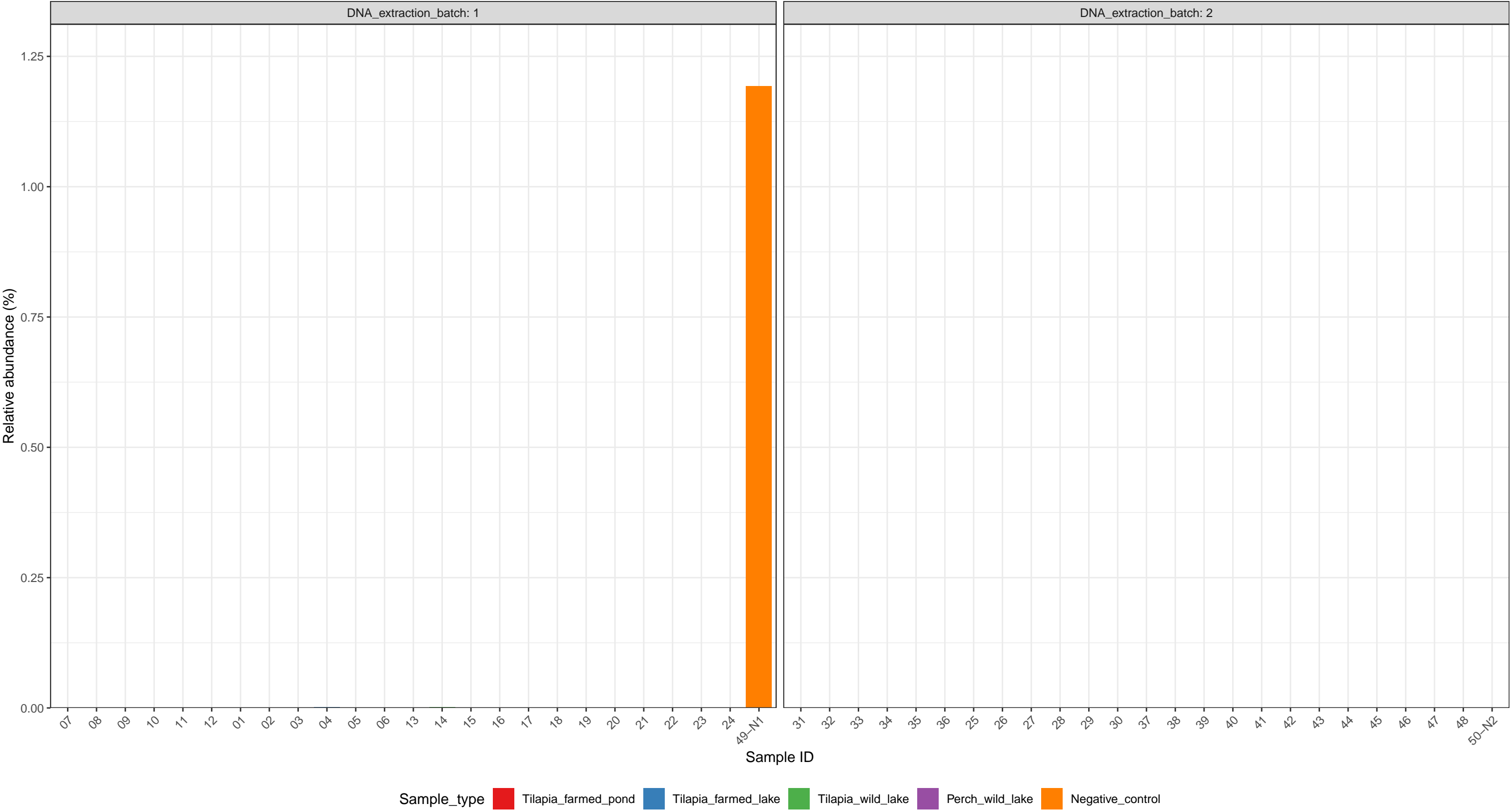
k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Peptostreptococcaceae; g__Paraclostridium; NA

featureID: f4b4dbd070c3296a6040e51b1e2aacfa



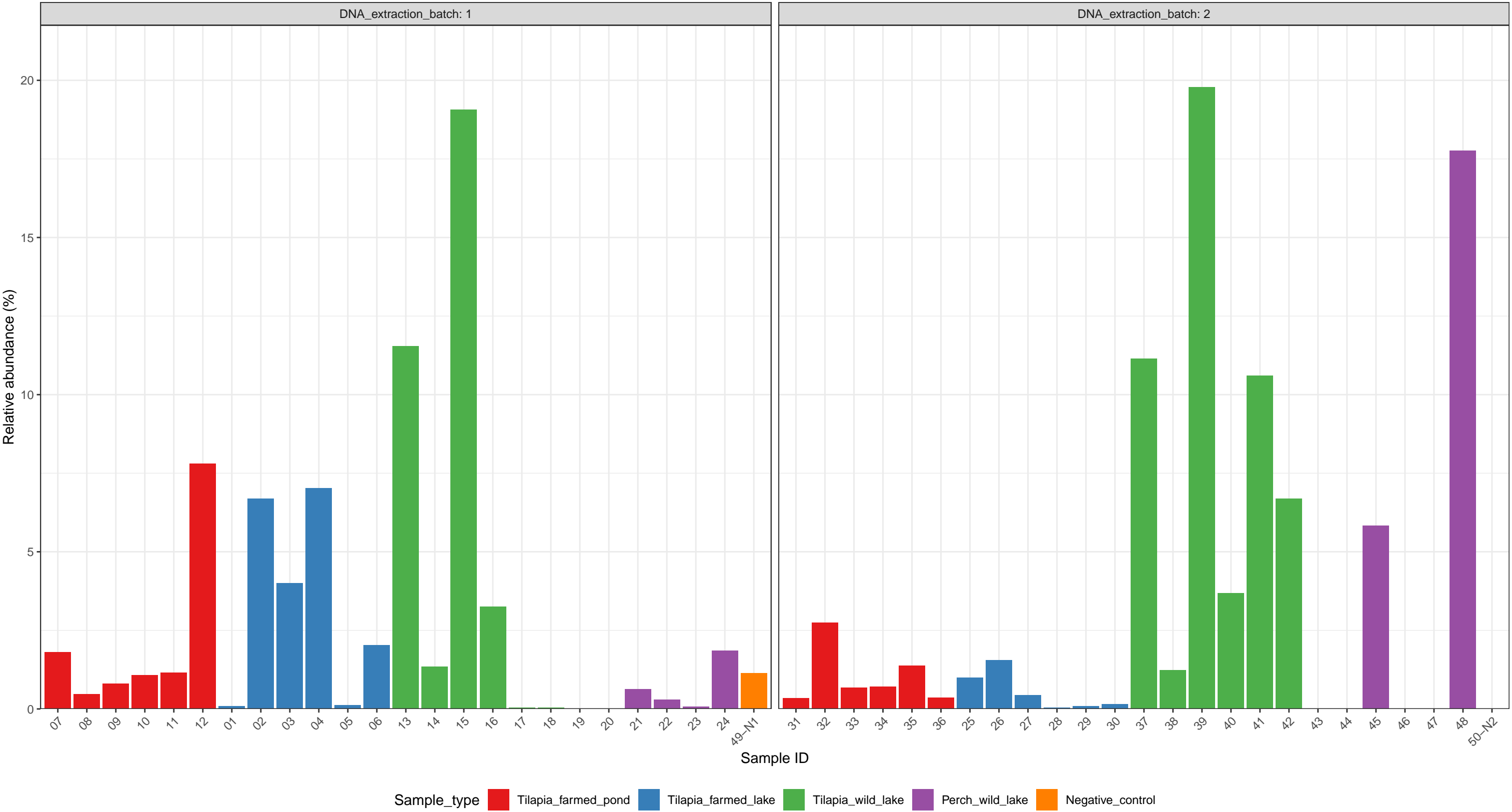
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Alteromonadales; f__Shewanellaceae; g__Shewanella; s__Shewanella algae

featureID: fadf78bc47e055f59328c8f565155ea5



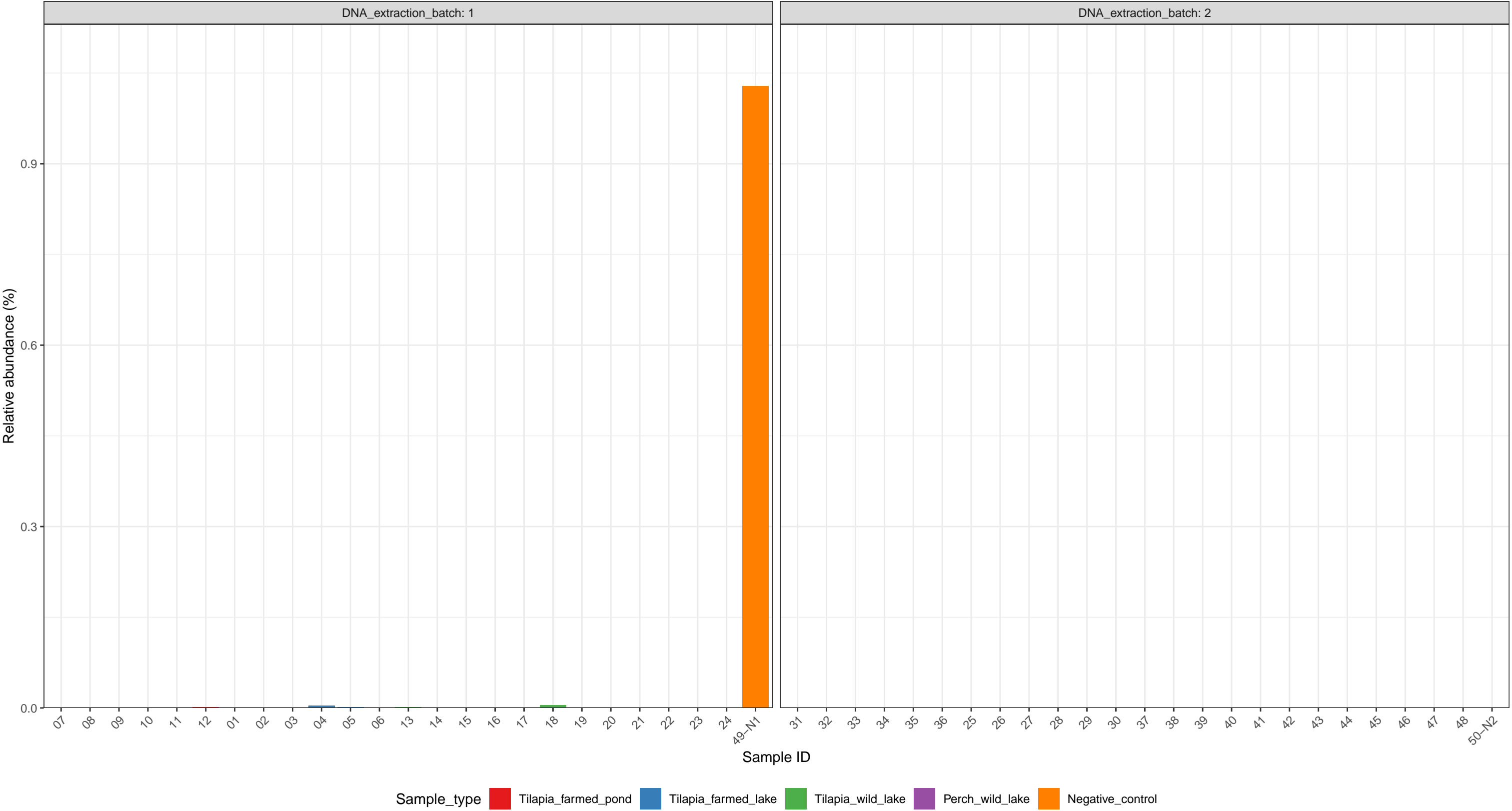
k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Peptostreptococcaceae; g__Romboutsia; NA

featureID: efa98c673cef7e11e51b27d01167c2af



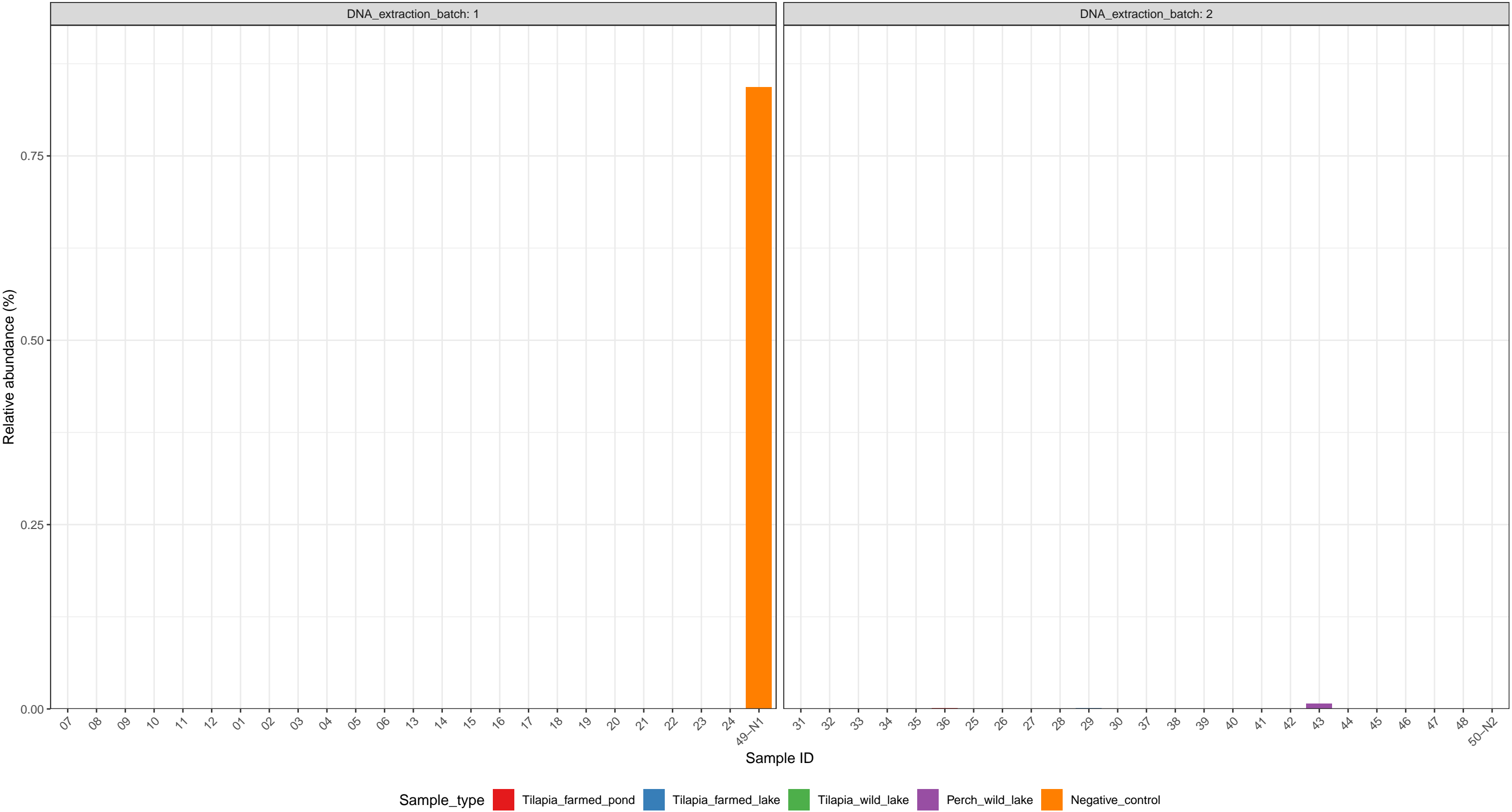
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales; f__Halomonadaceae; g__Halomonas; NA

featureID: 7f46b7ea18aa6ed4244429796401c660



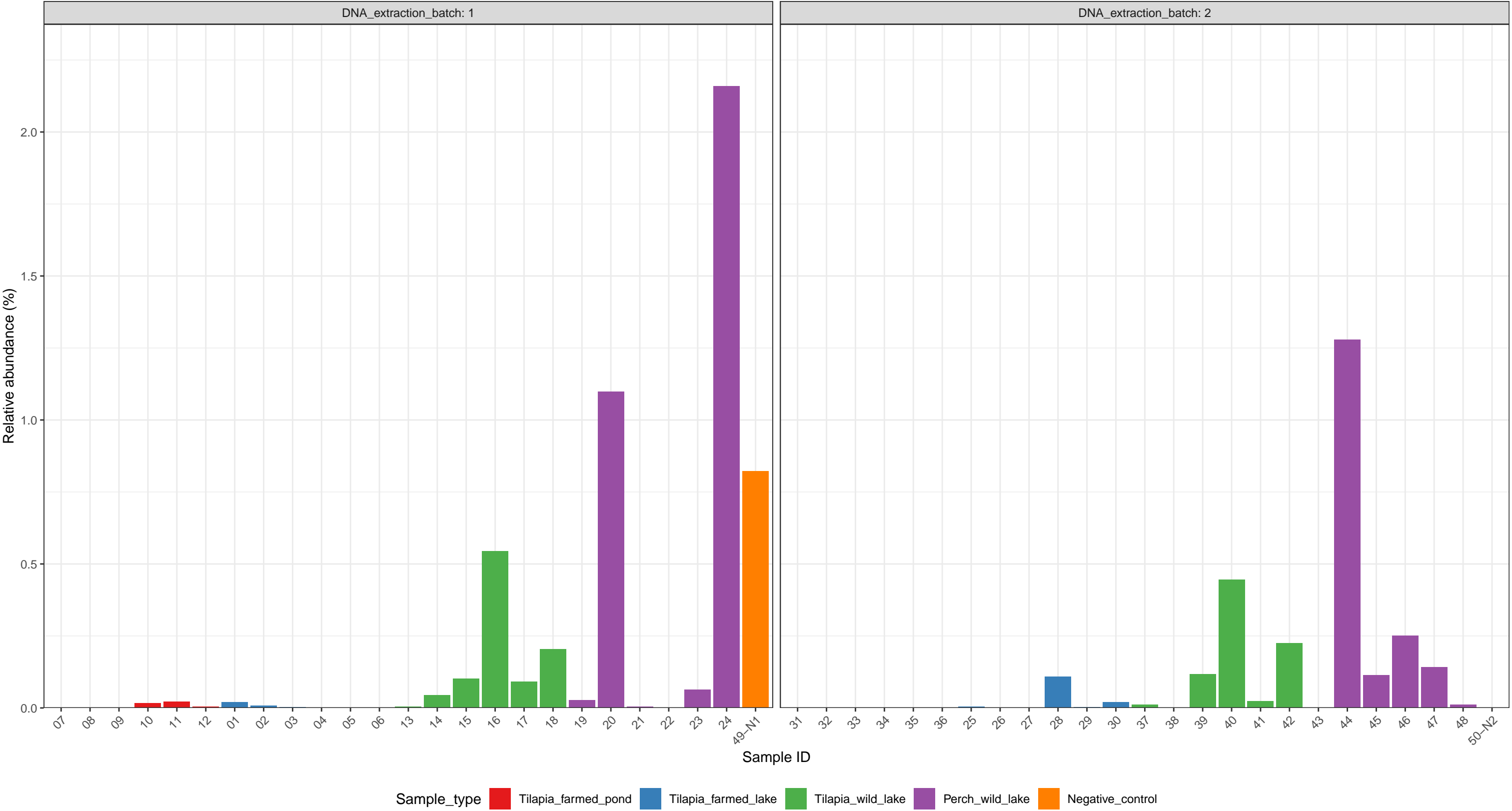
k__Bacteria; p__Patescibacteria; c__Gracilibacteria; Ambiguous_taxa; Ambiguous_taxa; Ambiguous_taxa; Ambiguous_taxa

featureID: 6bd3f3df4073826645c0bfe560765004



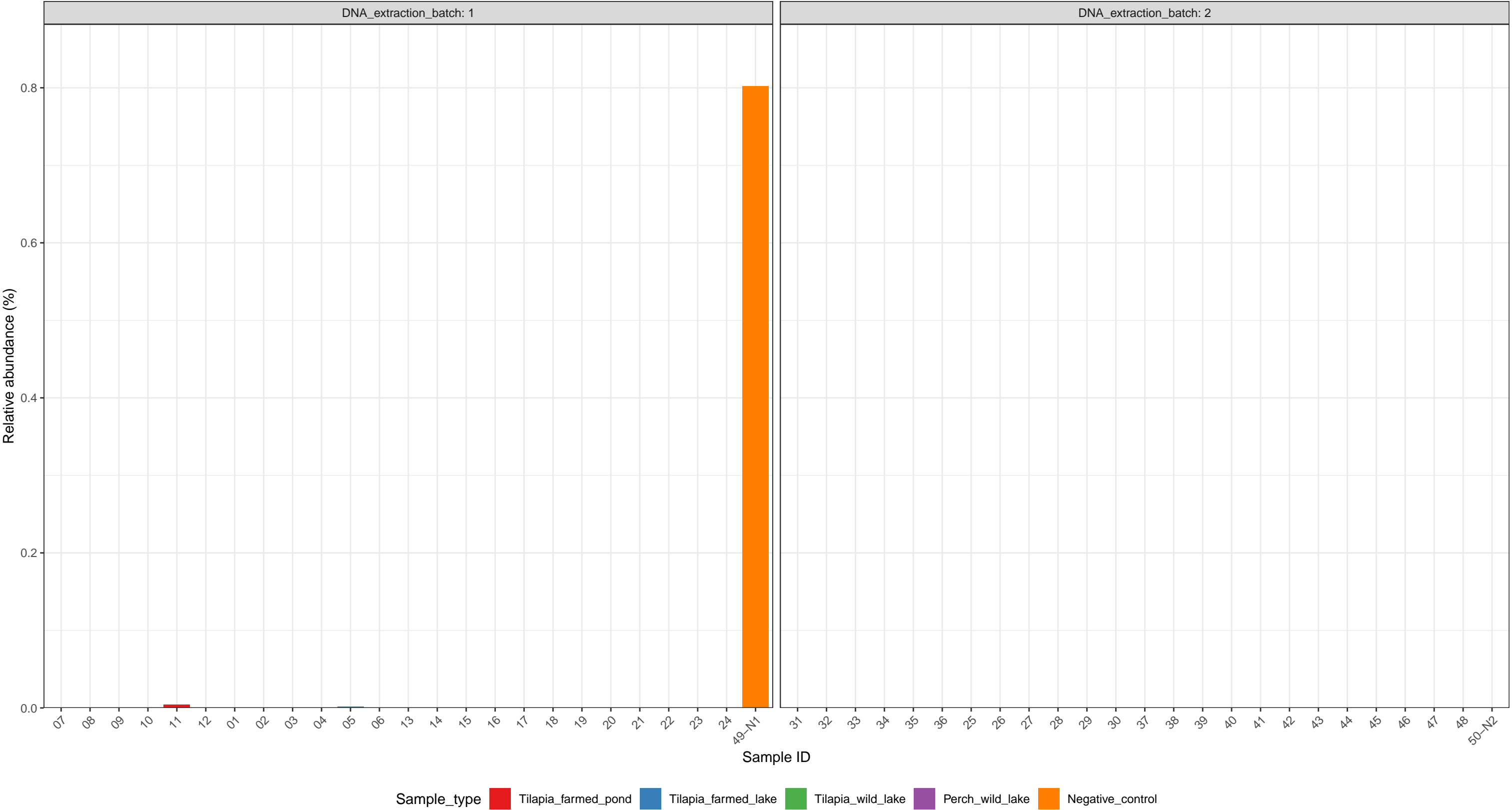
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacteriales; f__Enterobacteriaceae; g__Plesiomonas; Ambiguous_taxa

featureID: 4d951a112c225bc3bdfd2d0cfec2b2d3



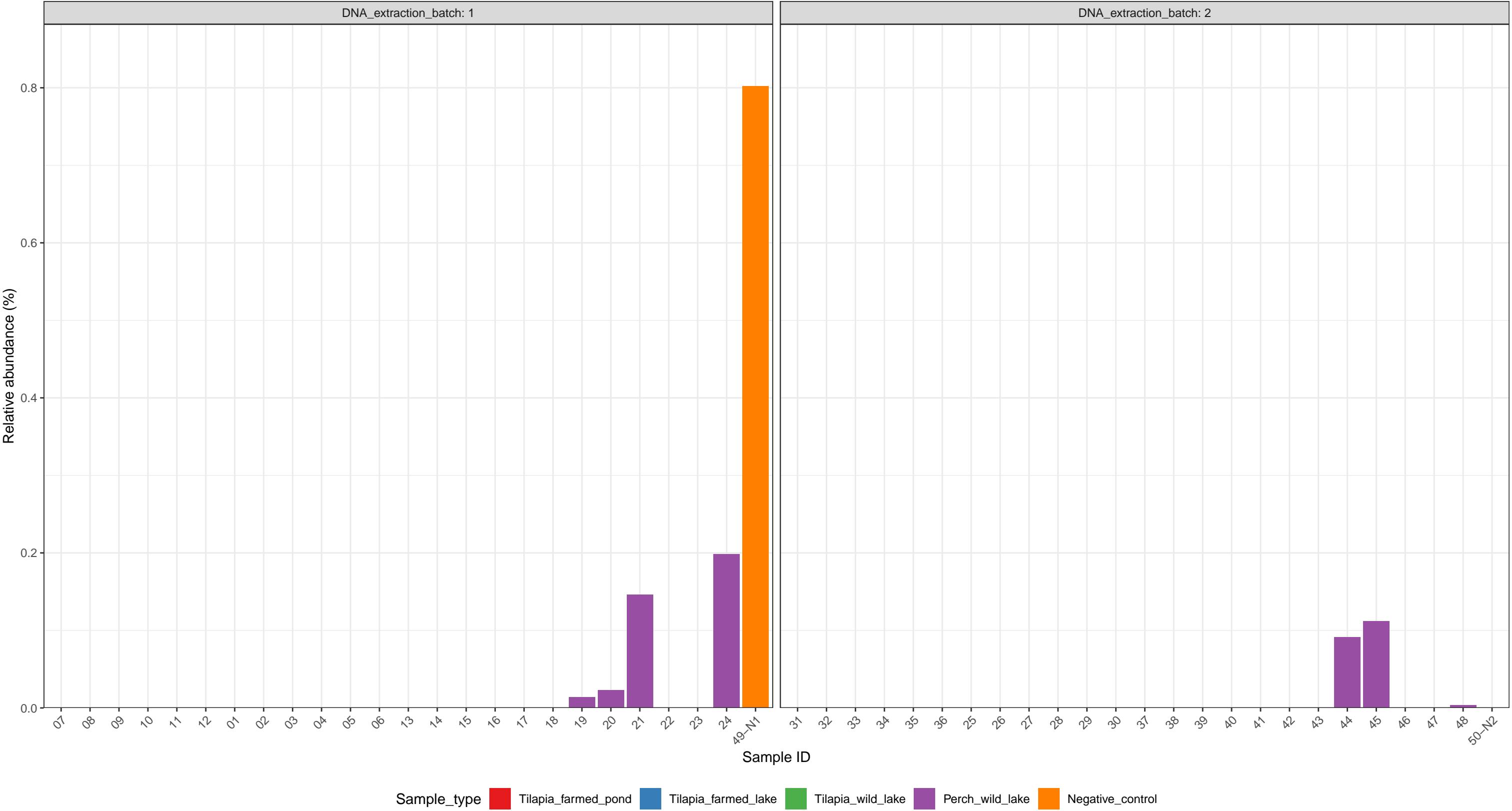
k__Bacteria; p__Acidobacteria; c__Acidobacteriia; o__Acidobacteriales; f__Acidobacteriaceae (Subgroup 1); g__Bryocella; s__uncultured bacterium

featureID: 92eda480cf7a77d3e7b6890877207fe6



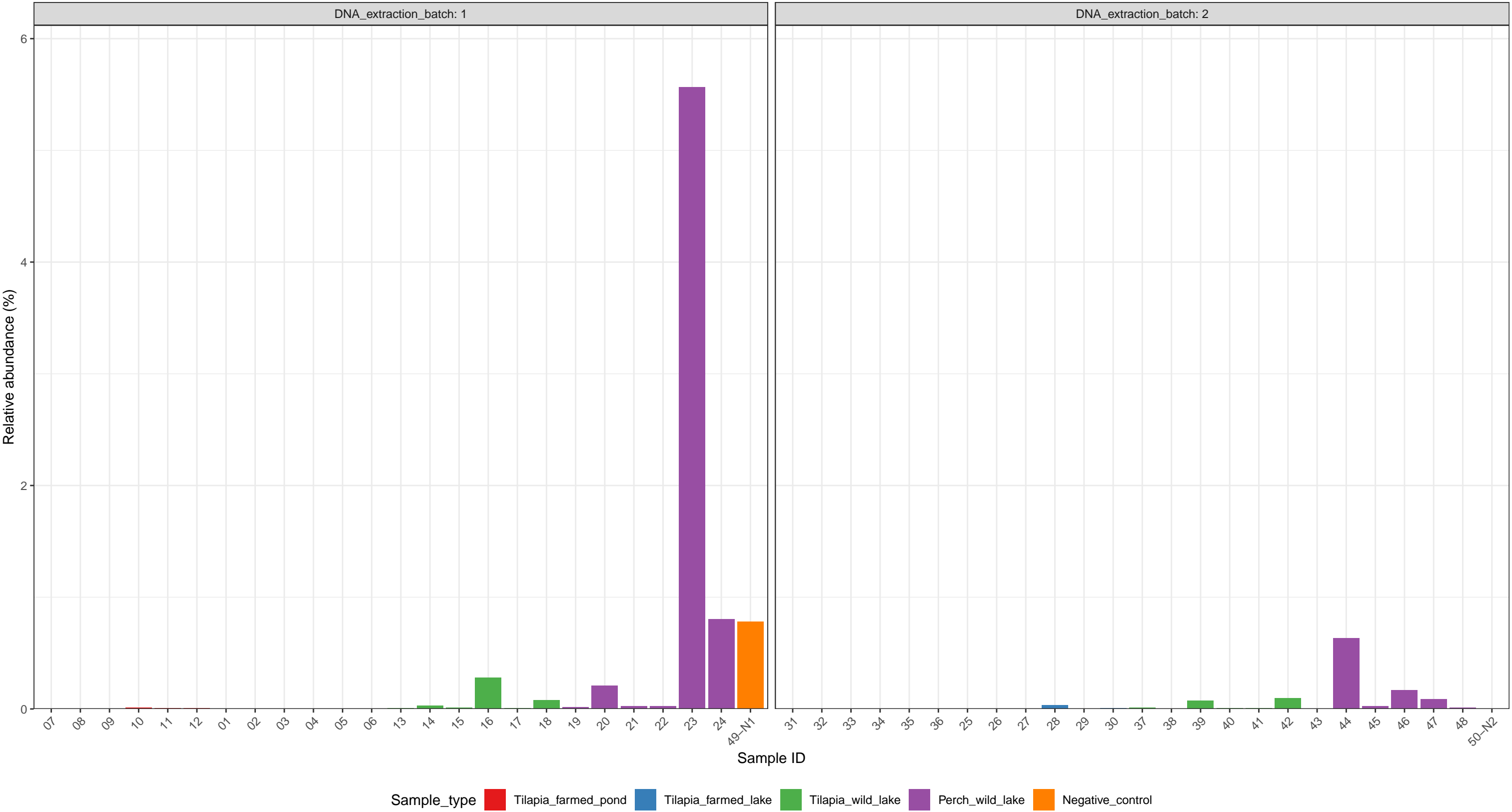
k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Clostridiaceae 1; g__Clostridium sensu stricto 1; NA

featureID: 98368b3901045189f93ca86afab6cc2b



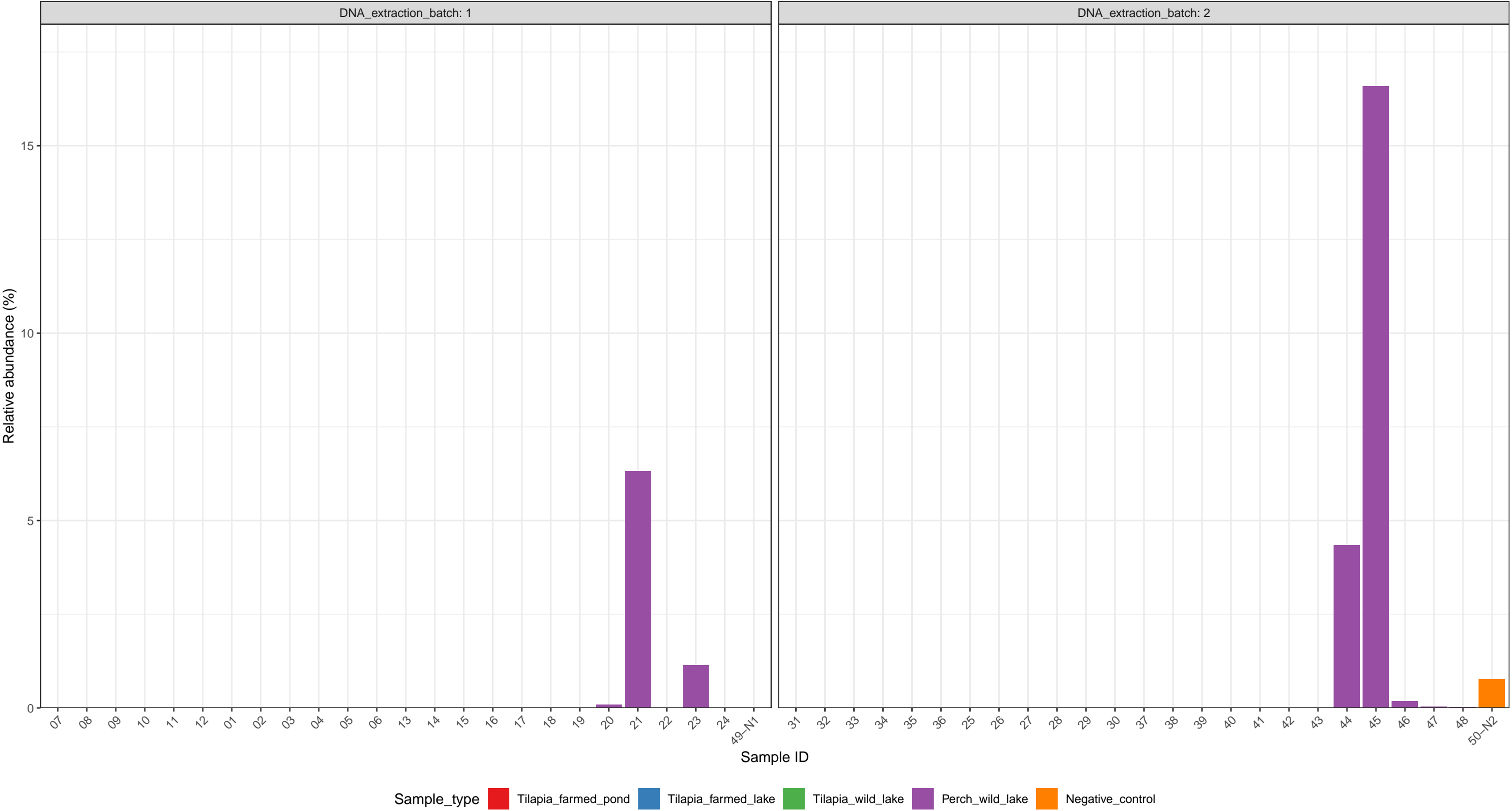
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacteriales; f__Enterobacteriaceae; g__Plesiomonas; Ambiguous_taxa

featureID: 913a3599bef09a615b00dee32ead1f48



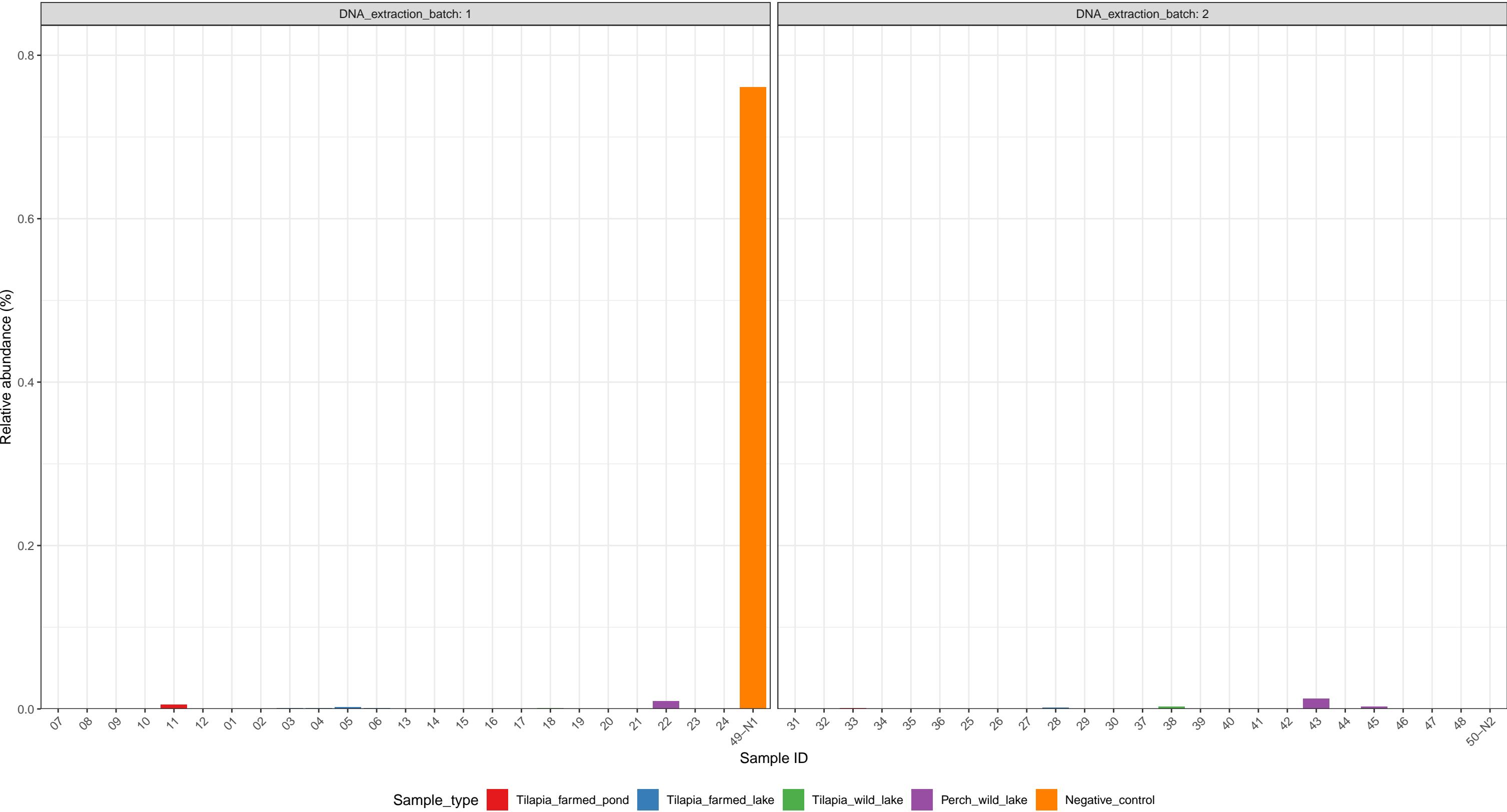
k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Clostridiaceae 1; NA; NA

featureID: d36c9dfa26099ffe57512e6dfbe0b8



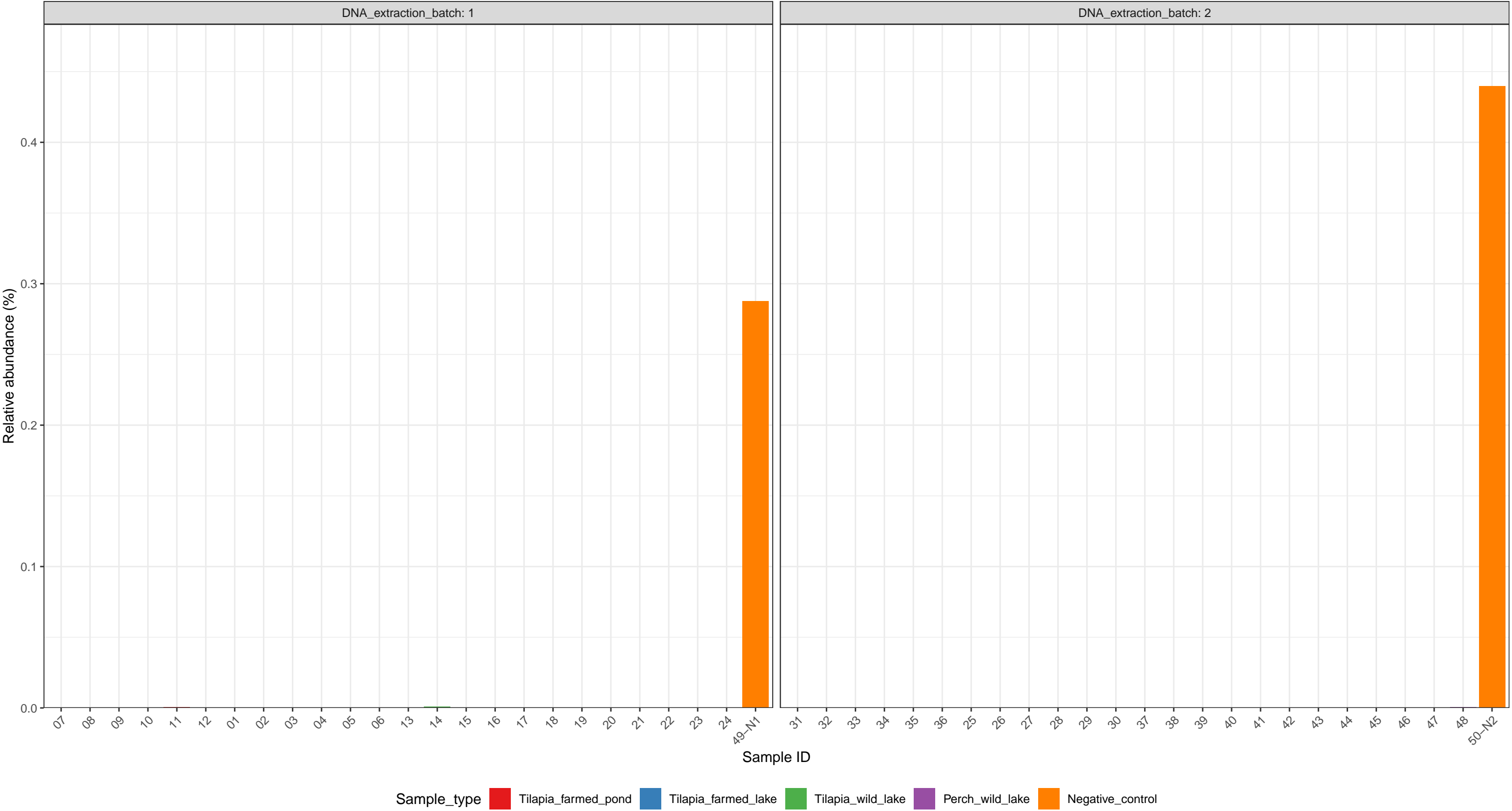
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Betaproteobacteriales; f__Burkholderiaceae; g__Ralstonia; NA

featureID: 3638f2062c305c79df283ef573a10b97



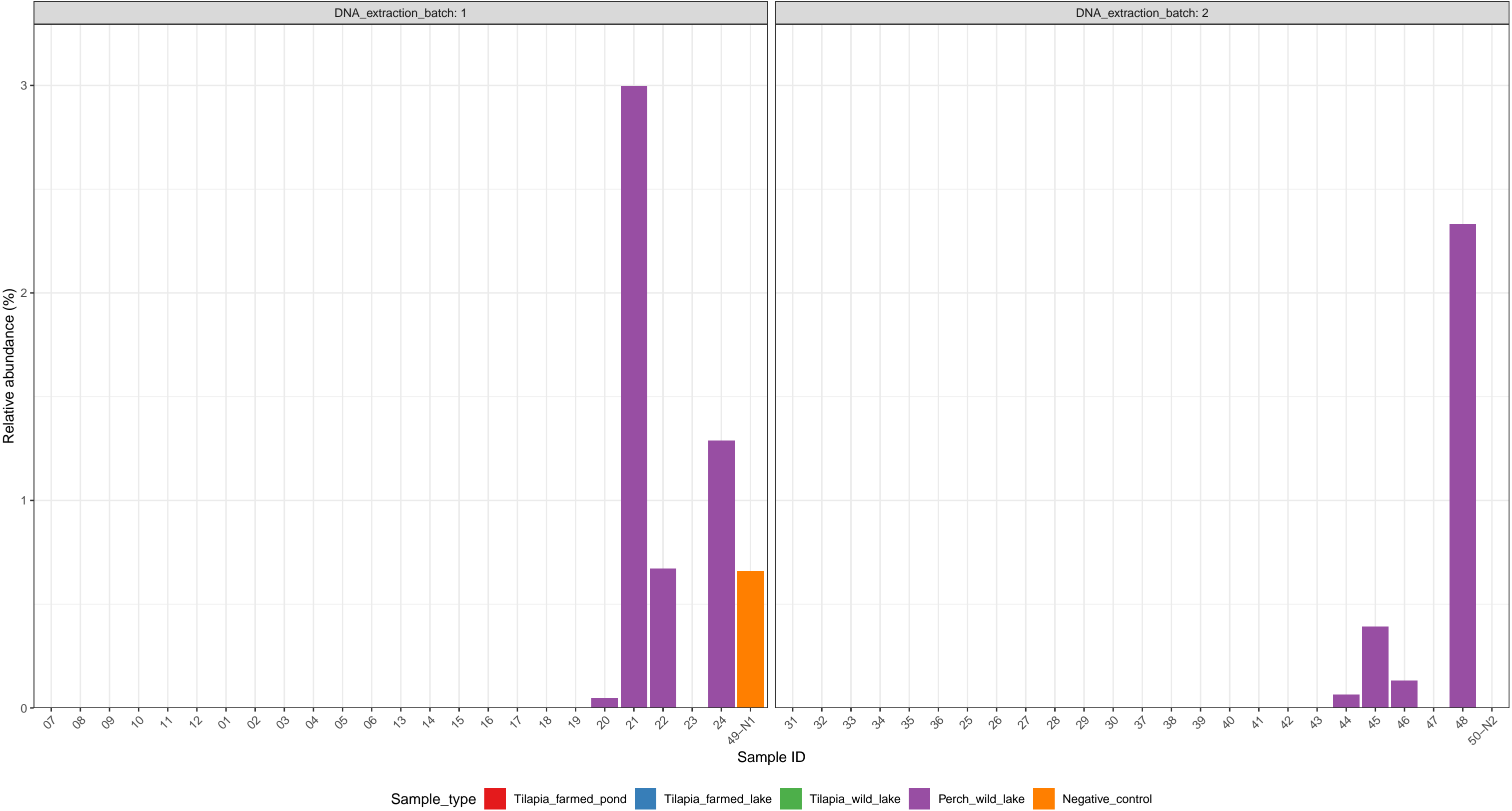
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Betaproteobacteriales; f__Burkholderiaceae; g__Comamonas; NA

featureID: 8f2ddde9ccf2d7afe5abf35614fe5b43



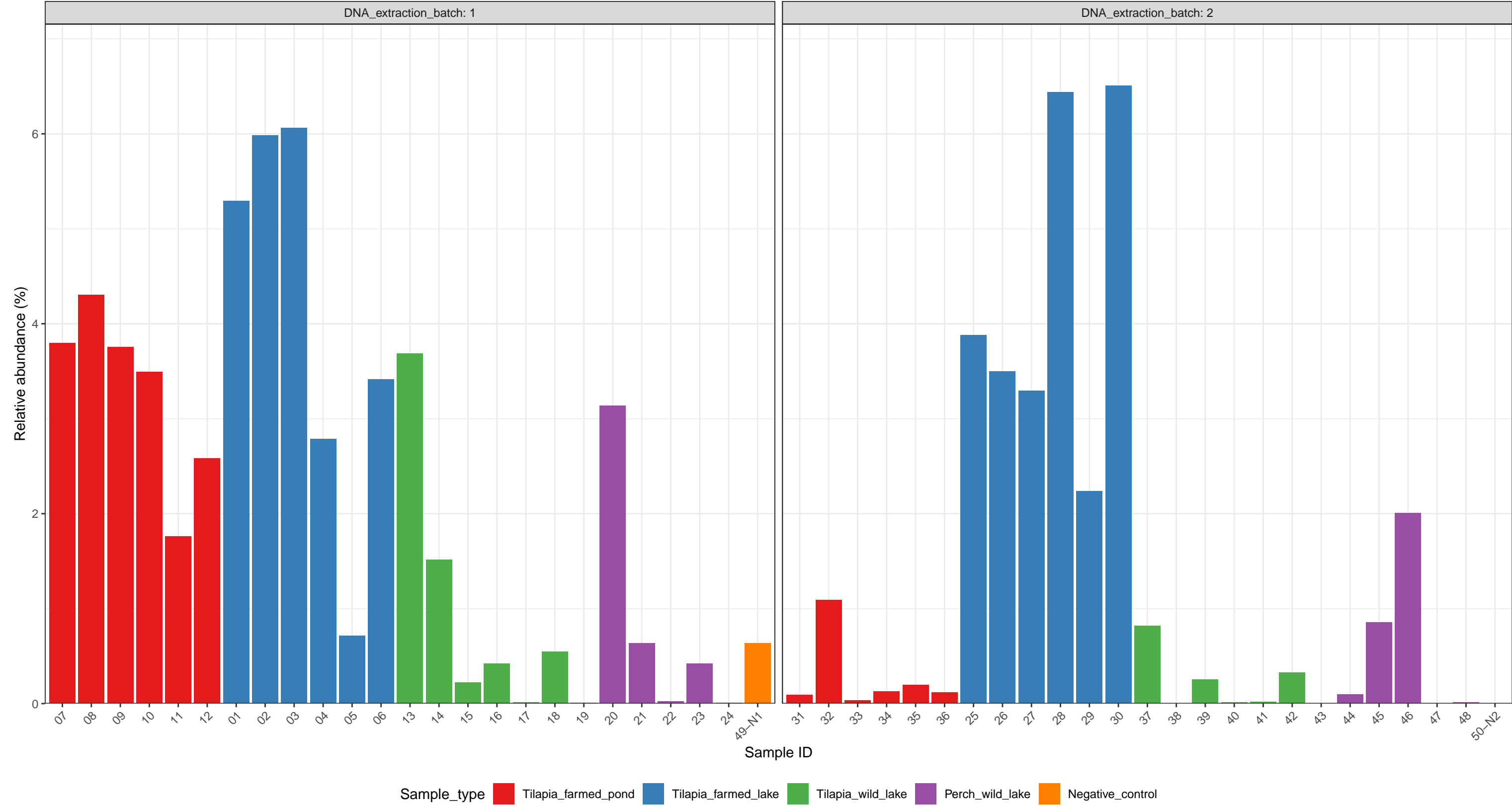
k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Clostridiaceae 1; g__Candidatus Arthromitus; NA

featureID: 249270189cd8e1c30eb0d62d77589cb8



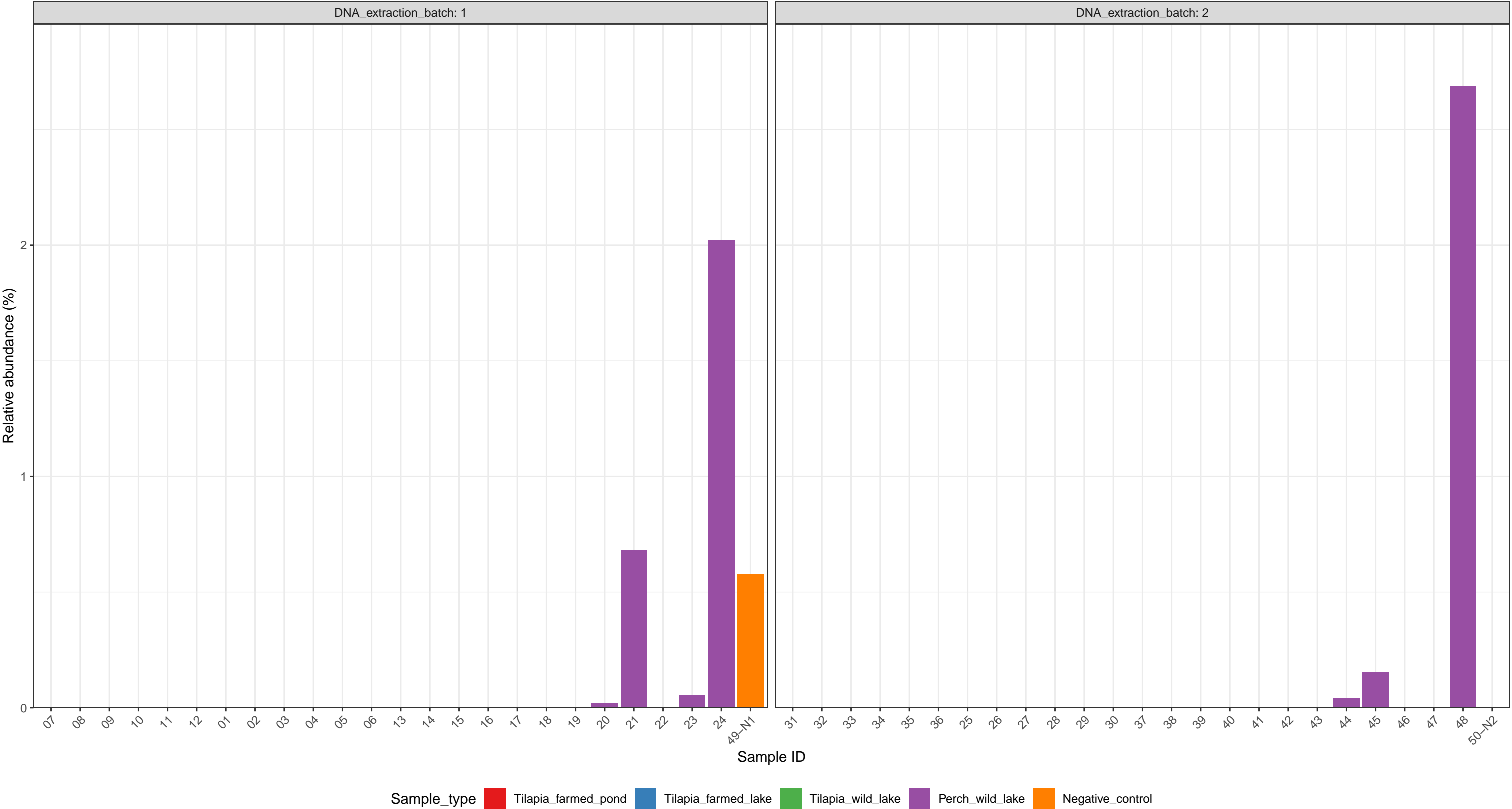
k__Bacteria; p__Fusobacteria; c__Fusobacteriia; o__Fusobacteriales; f__Fusobacteriaceae; g__Cetobacterium; s__uncultured bacterium

featureID: 7732d6712ceae4666bd66aba7880c6f1



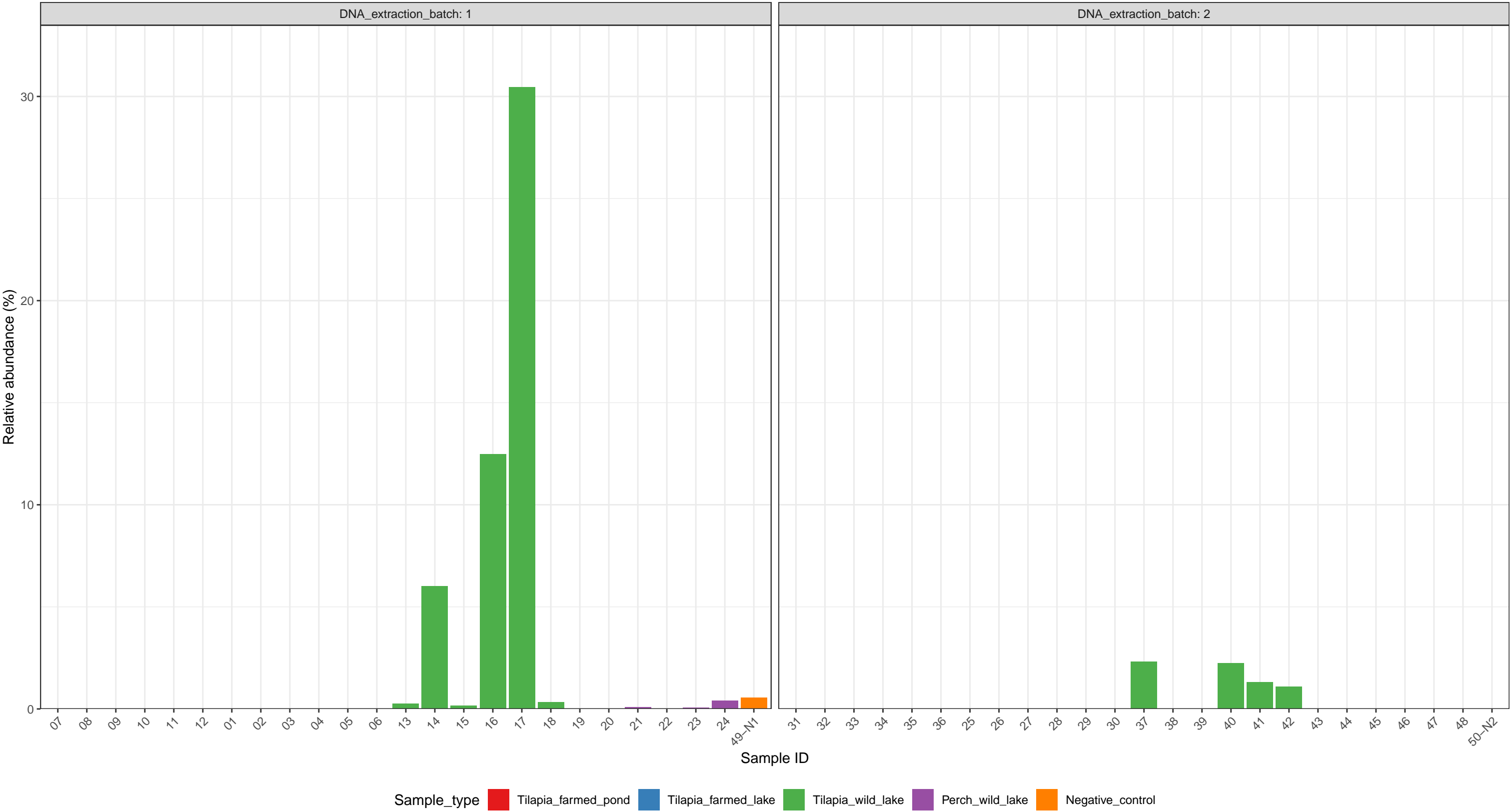
k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Clostridiaceae 1; g__Clostridium sensu stricto 1; NA

featureID: 4c5af046872782b10af8fff902cdf641



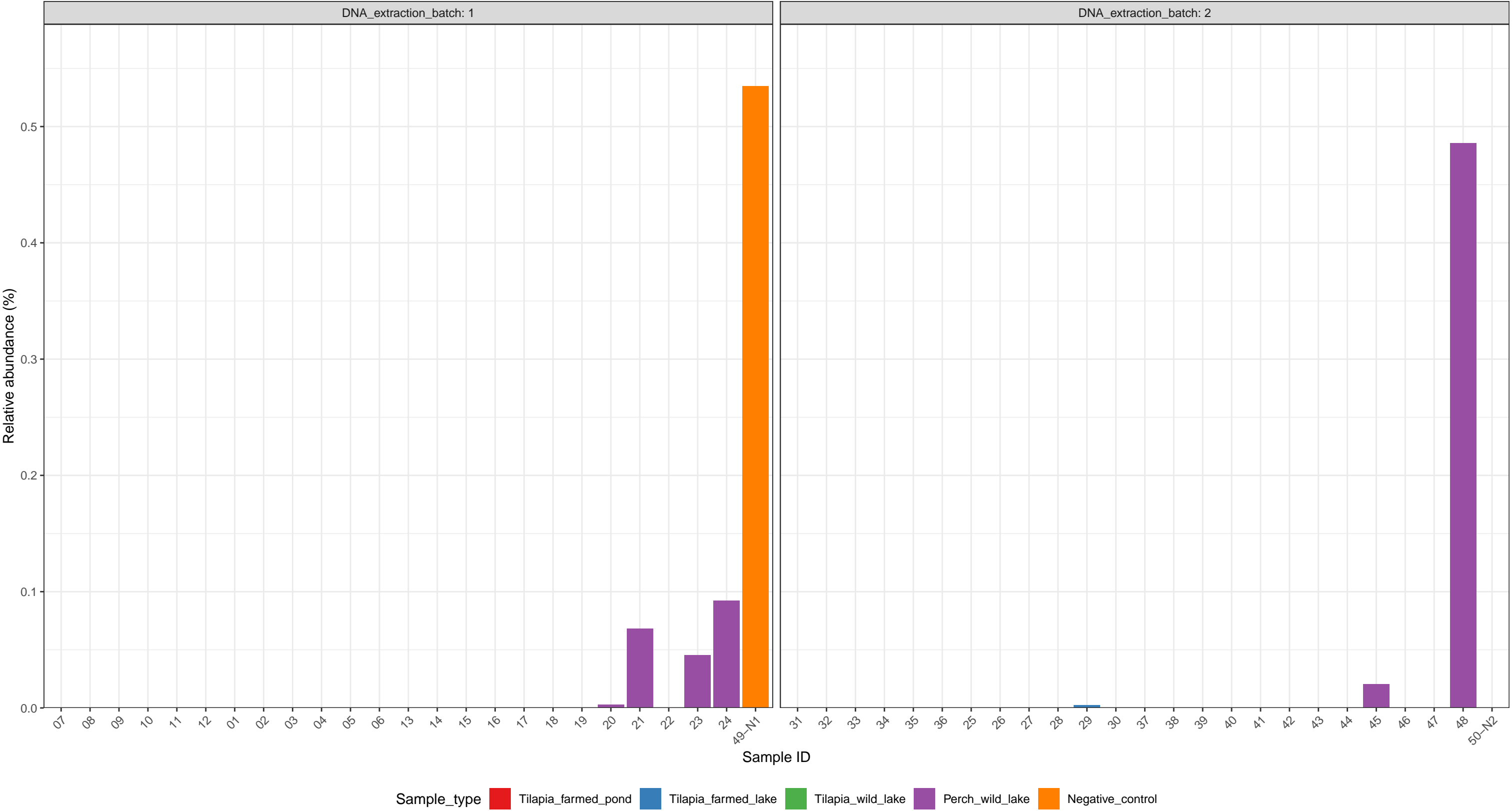
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Aeromonadales; f__Aeromonadaceae; g__Aeromonas; NA

featureID: dacf22eb1a2065568c1175d1a76c9dc7



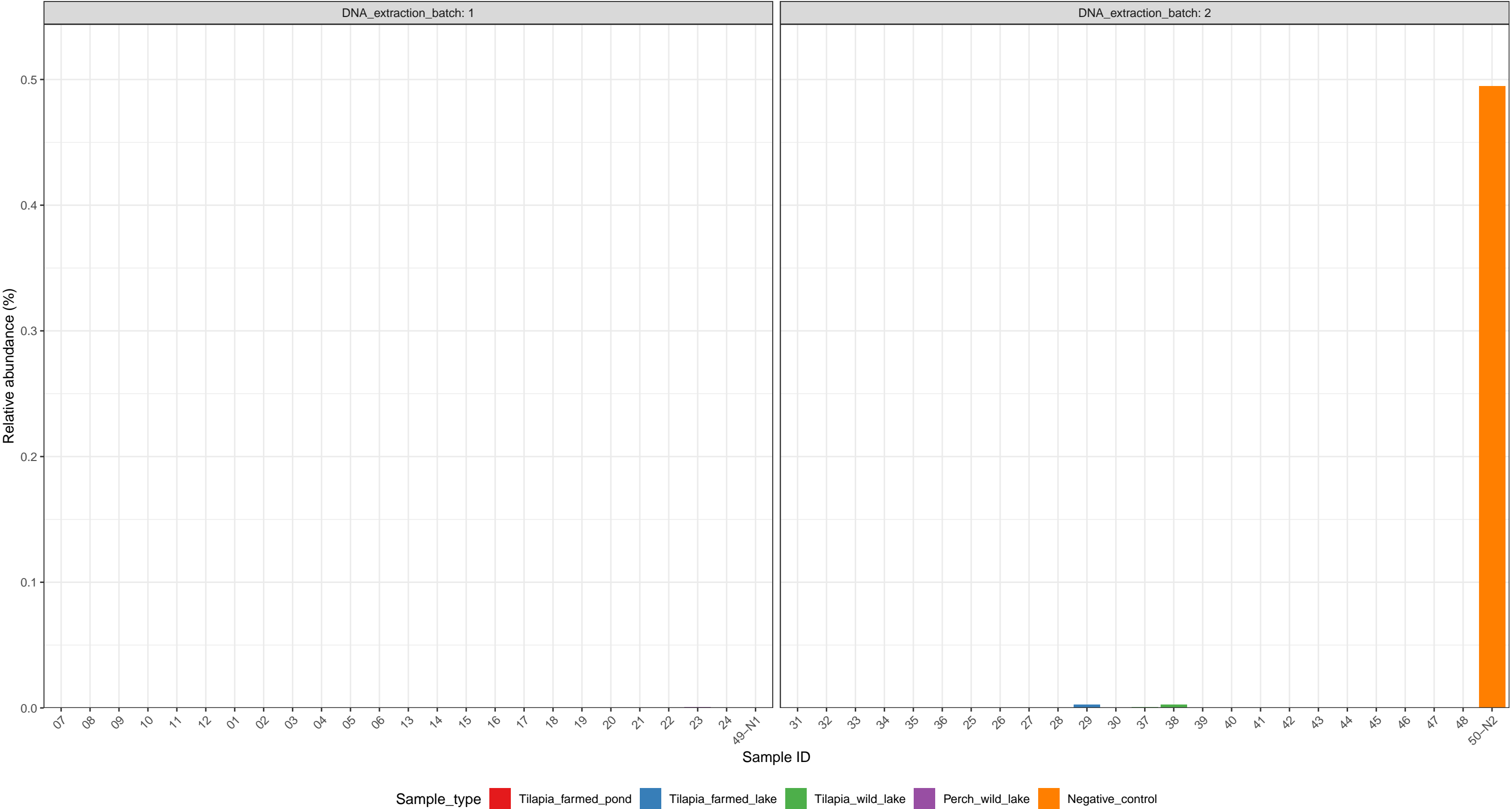
k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Clostridiaceae 1; g__Clostridium sensu stricto 1; s__uncultured bacterium

featureID: 4852811146dcf523a9ecf810088a2da5



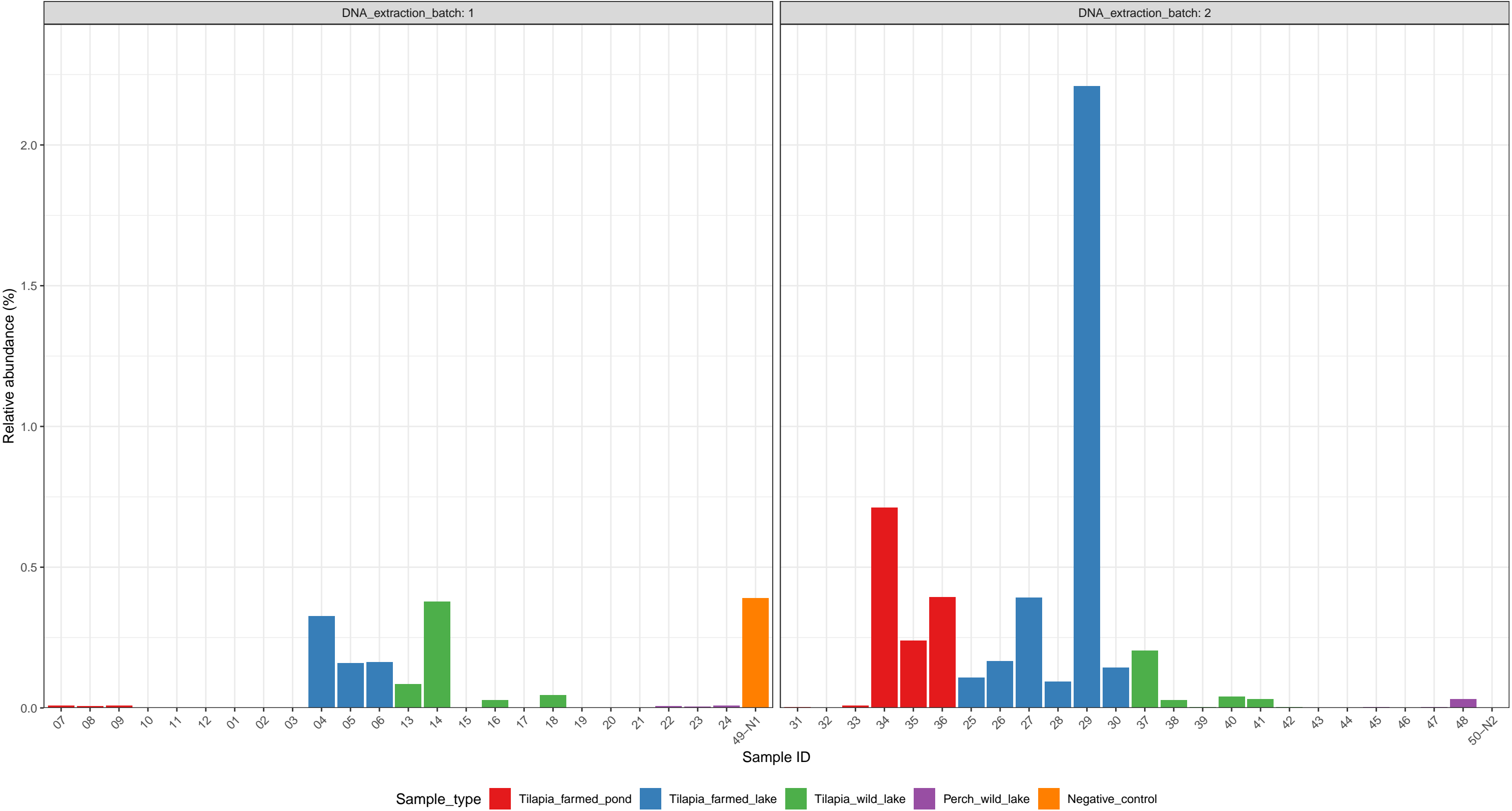
k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Staphylococcaceae; g__Staphylococcus; NA

featureID: 62611dedc42201591d0c89973f903dde



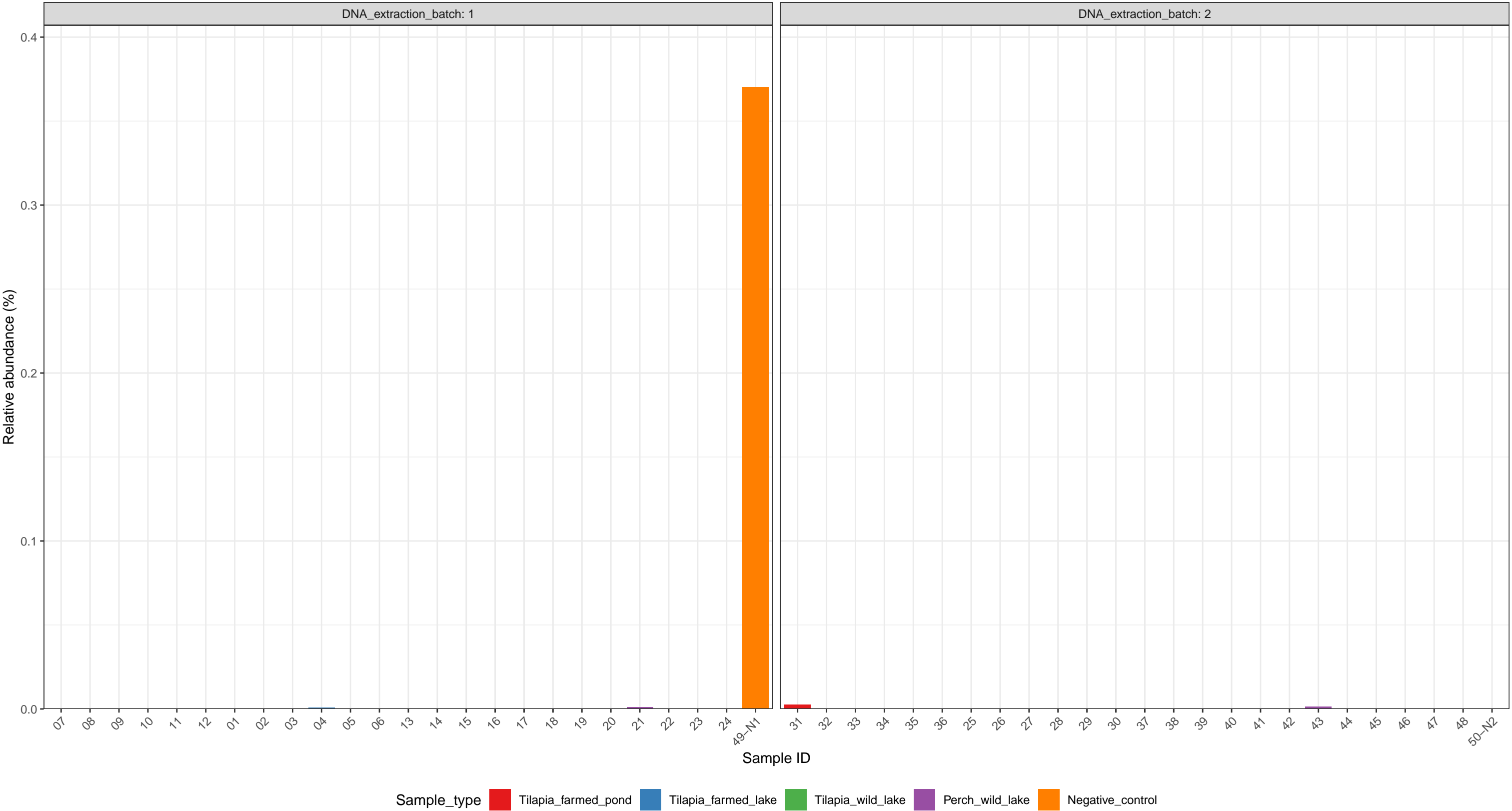
k__Bacteria; p__Verrucomicrobia; c__Verrucomicrobiae; o__Chthoniobacterales; f__Chthoniobacteraceae; g__LD29; Ambiguous_taxa

featureID: 550884702aea7eaa9461b76e8ef9da16



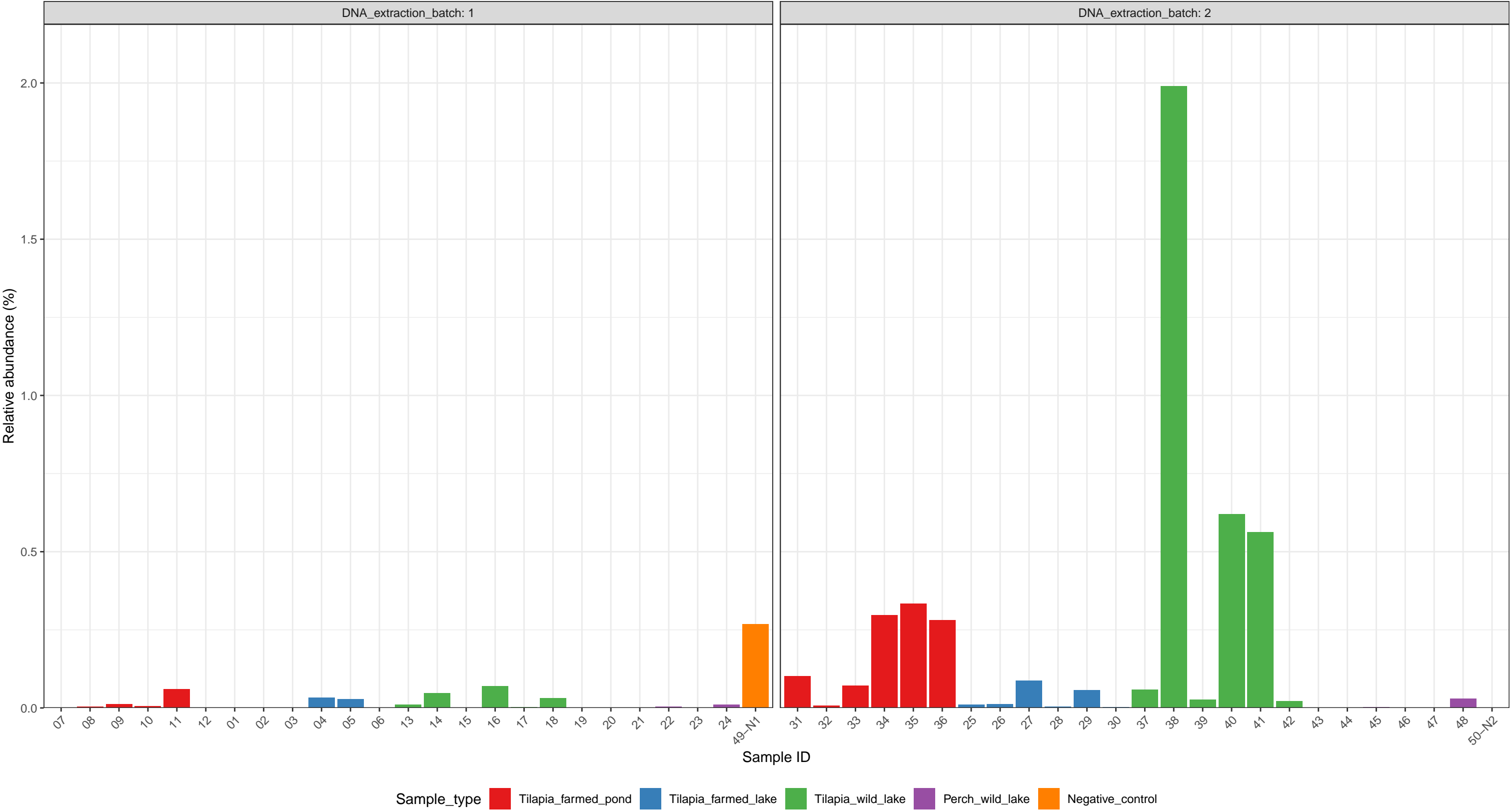
k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Staphylococcaceae; g__Staphylococcus; NA

featureID: 43a54829cc0d7a58a61ad7f833cc2b22



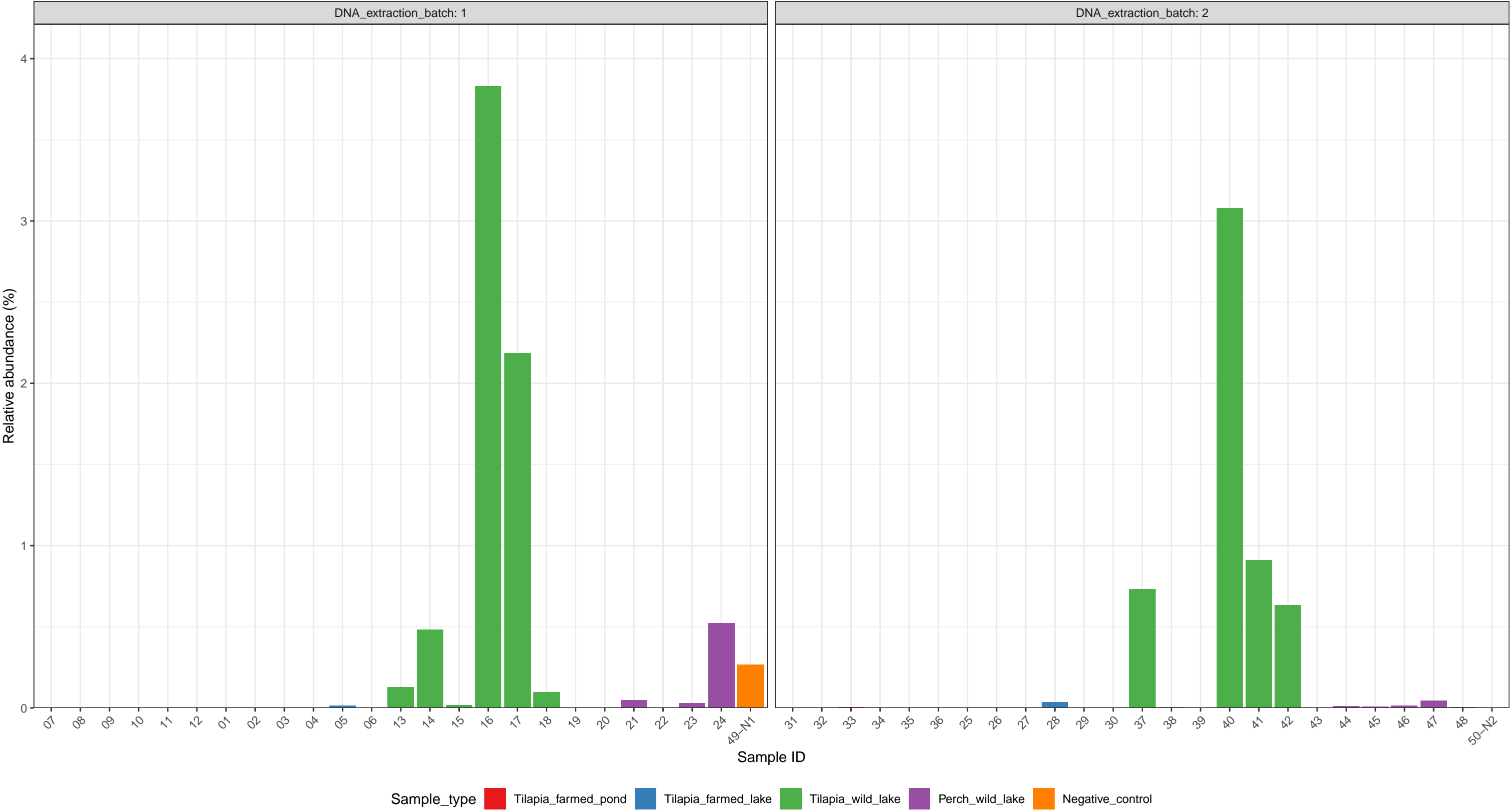
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Beijerinckiaceae; g__Methylocystis; NA

featureID: 675f287d70a622c1c4cd8e1b634e8aed



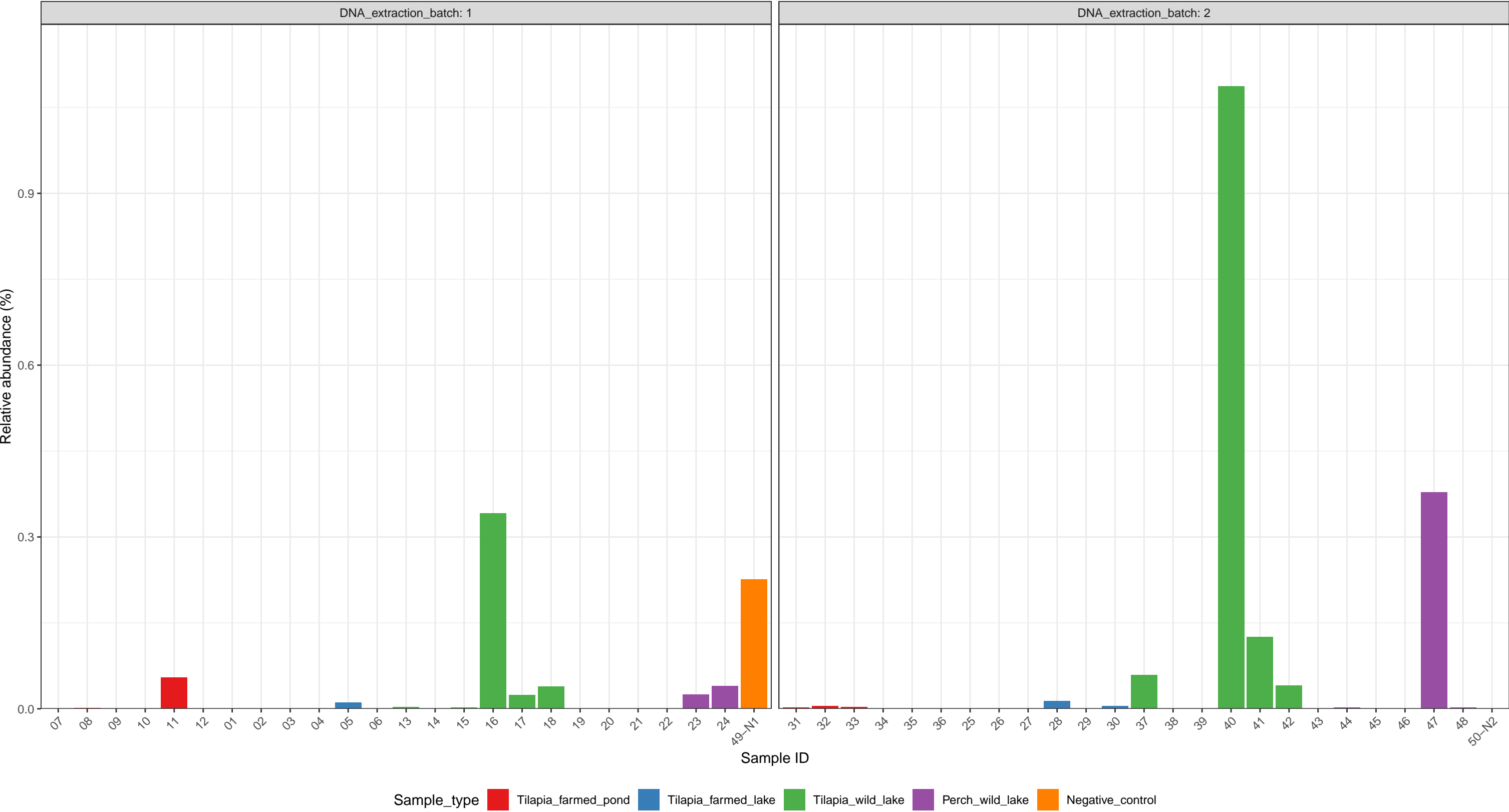
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Aeromonadales; f__Aeromonadaceae; g__Aeromonas; NA

featureID: f4ddba285154bdd47f4dc510c2038305



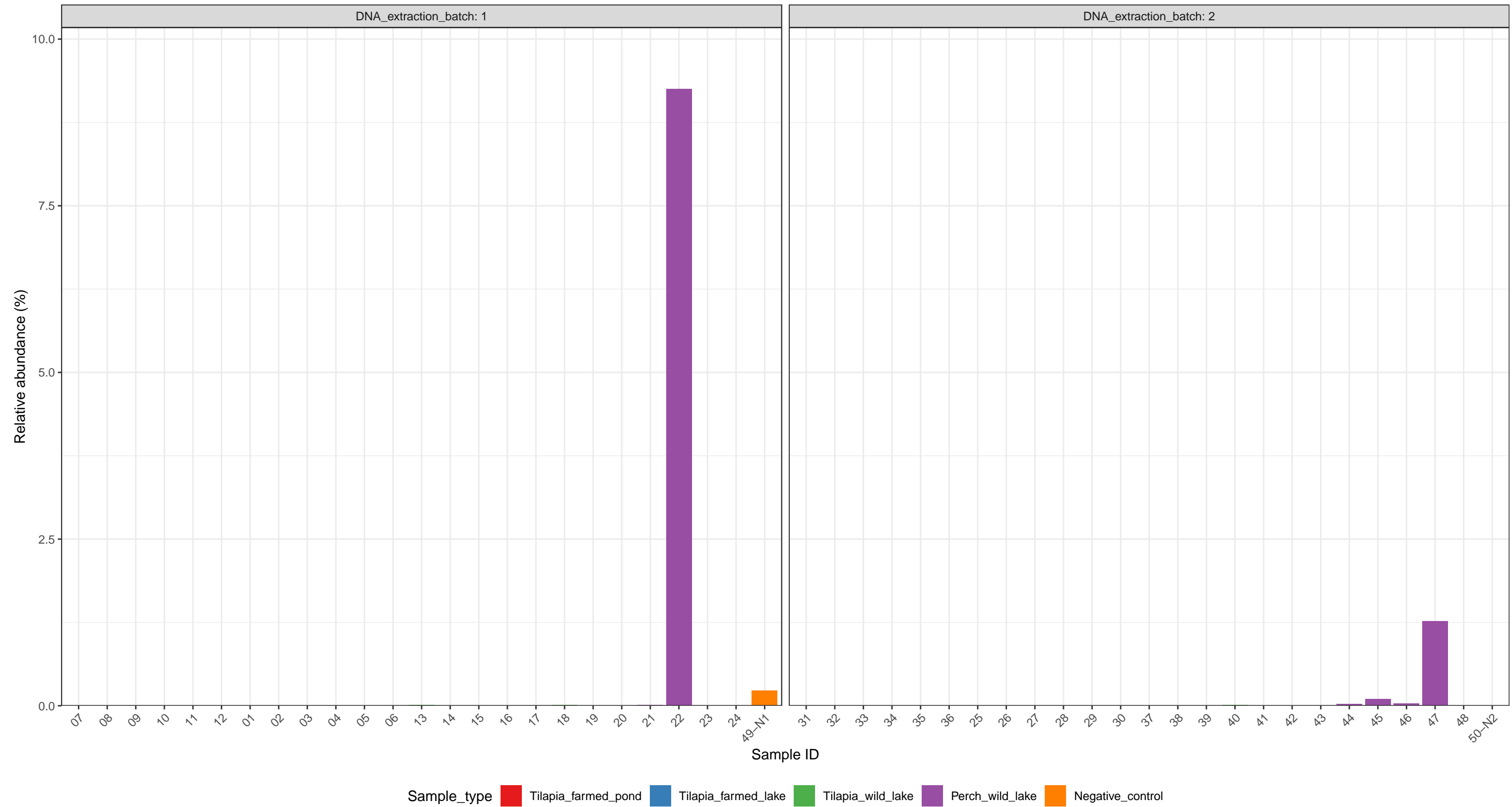
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Aeromonadales; f__Aeromonadaceae; g__Aeromonas; NA

featureID: 2e119ce67894fe00027176e52f17a225



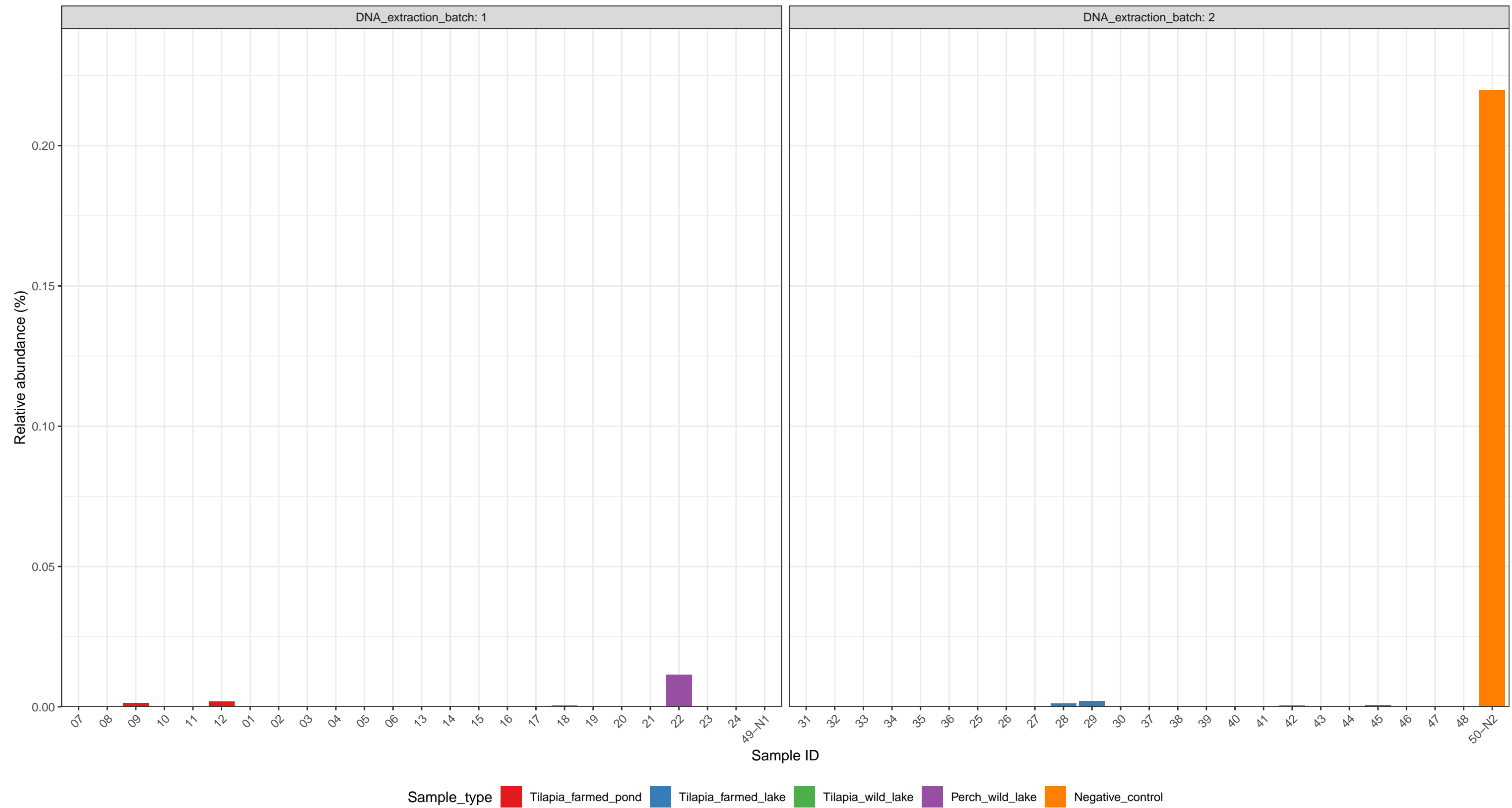
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacteriales; f__Enterobacteriaceae; g__Plesiomonas; NA

featureID: 8cc0e176d680aac1a413121d8633c30d



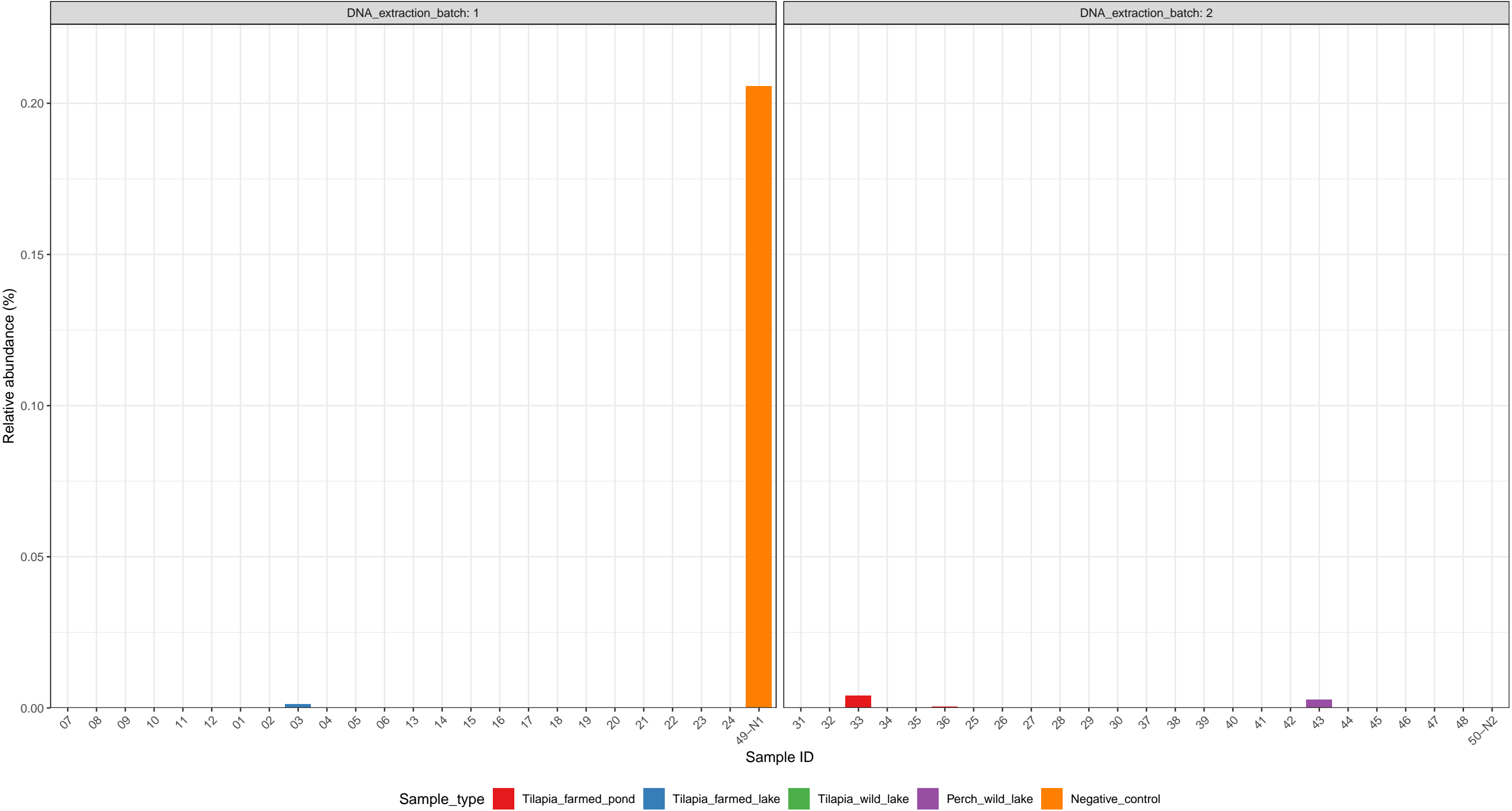
k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Micrococcales; f__Micrococcaceae; g__Micrococcus; NA

featureID: 09403870435de24e0d1079059a287957



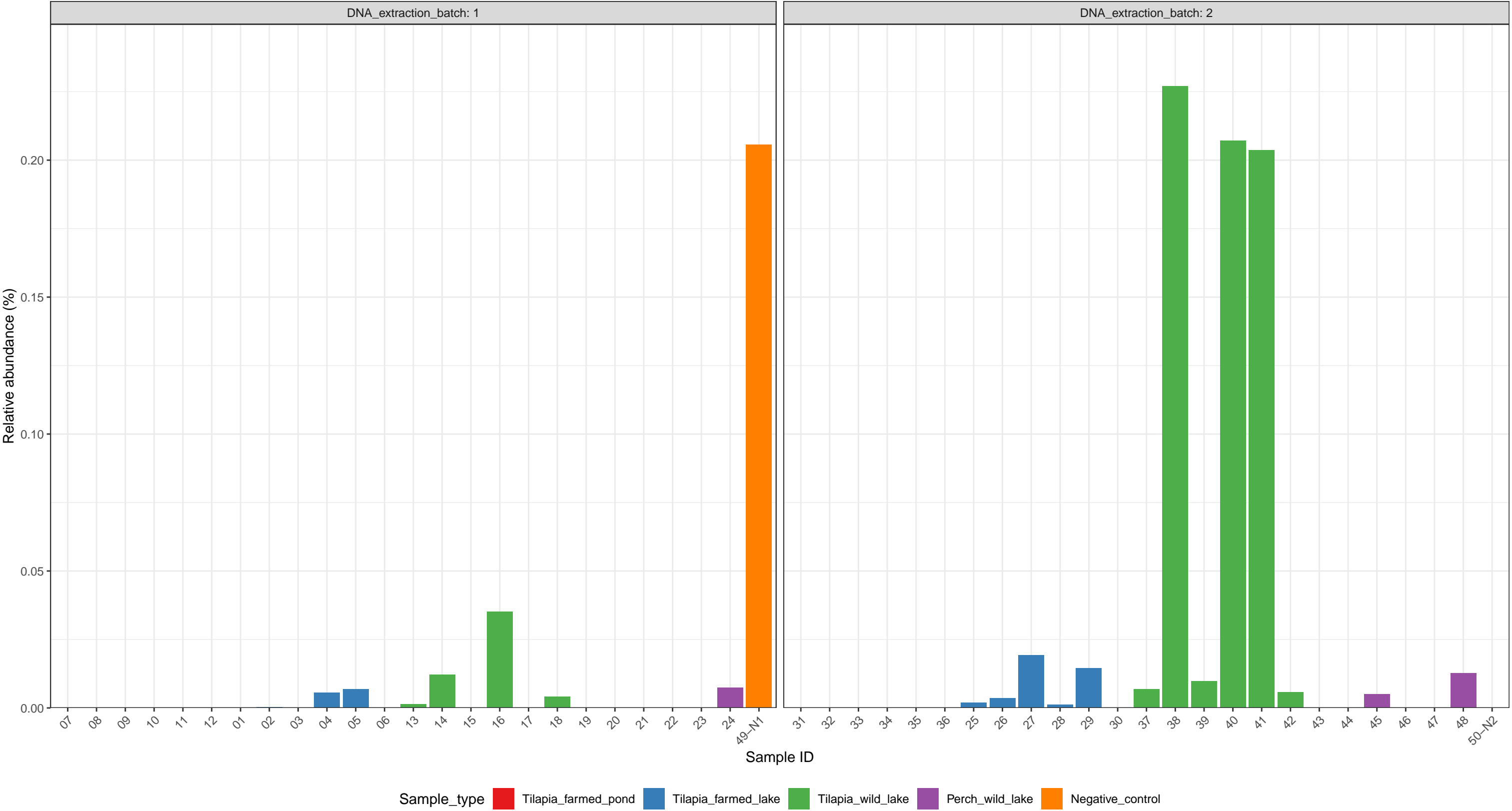
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Betaproteobacteriales; f__Burkholderiaceae; g__Ralstonia; NA

featureID: 07c3160551922faa7be5740ea3adc189



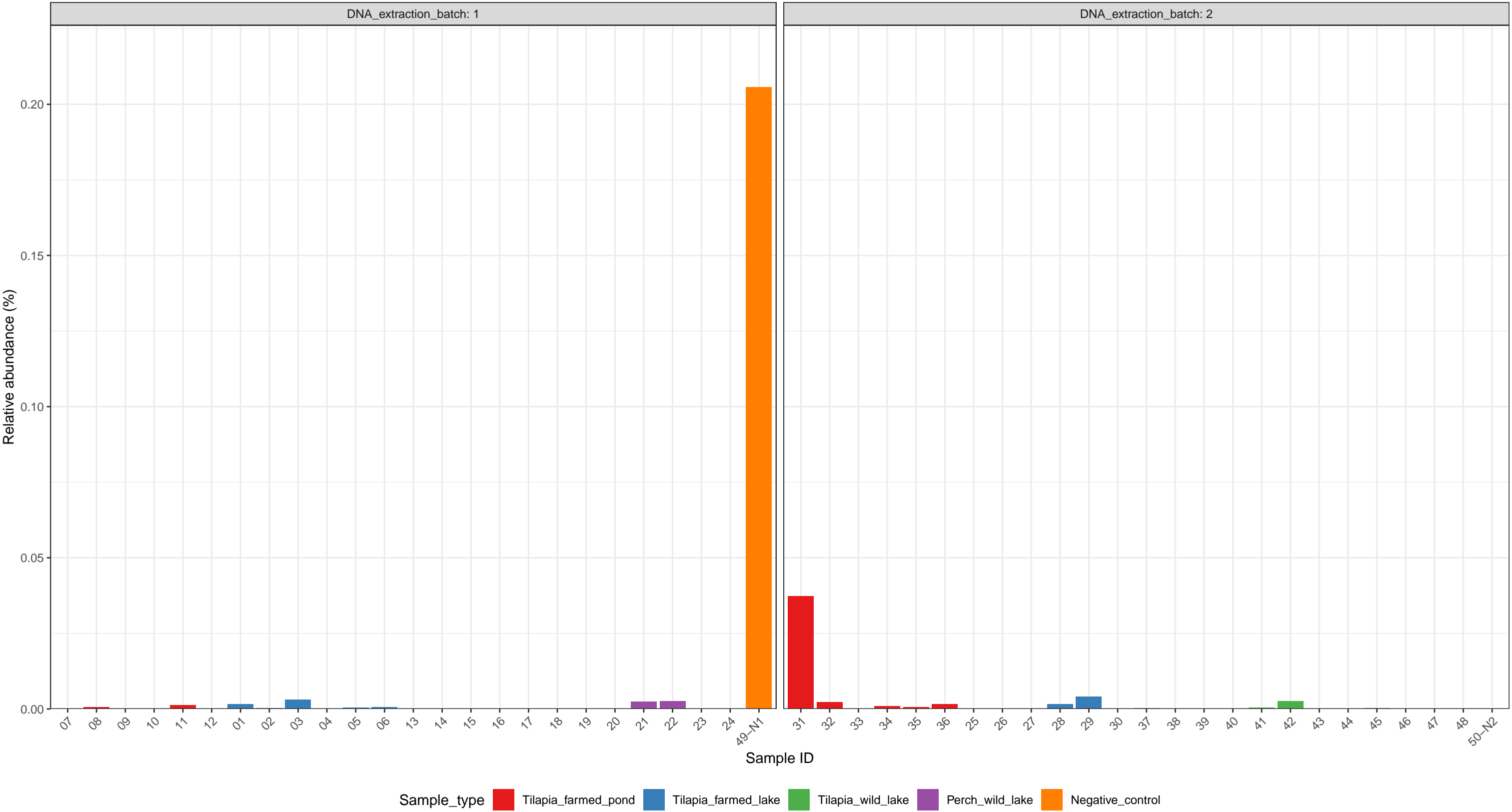
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Methylococcales; f__Methylococcaceae; g__Methylocaldum; s__uncultured bacterium

featureID: 572e092b99869f99a6ae2c111893fbc5



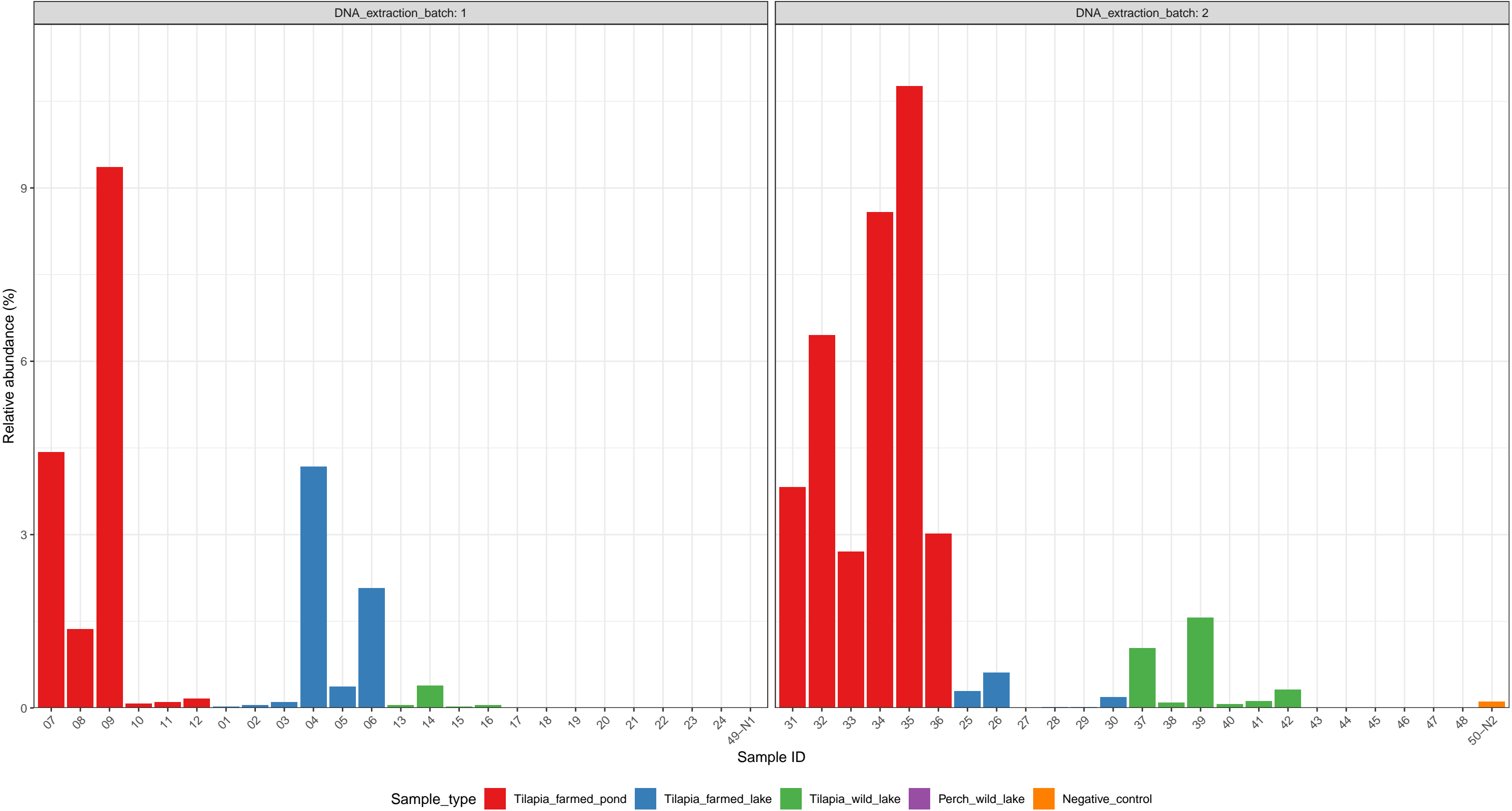
k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Propionibacteriales; f__Propionibacteriaceae; g__Cutibacterium; NA

featureID: b02a8d33d018119dedb2db15db887bfd



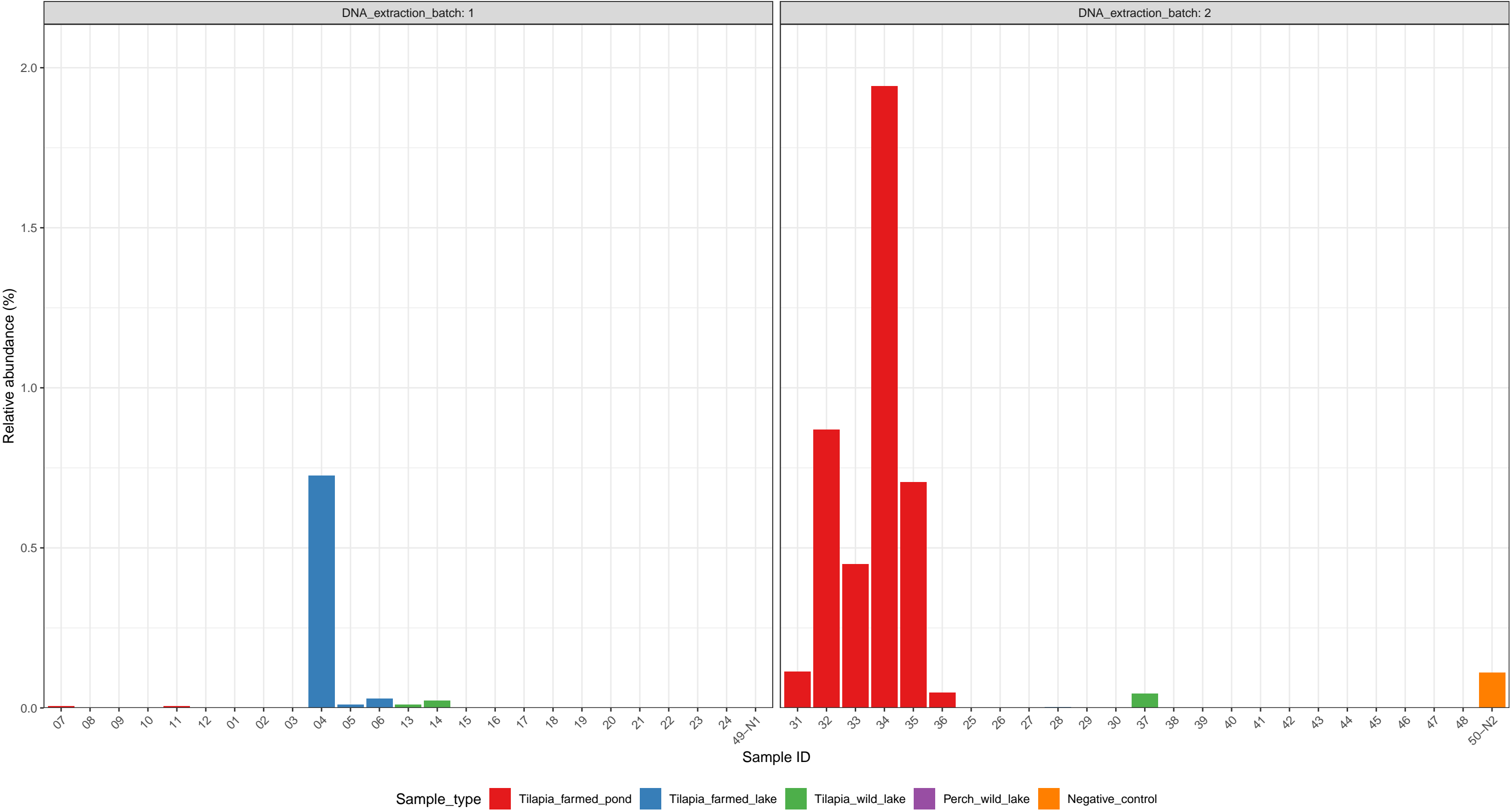
k__Bacteria; p__Fusobacteria; c__Fusobacteriia; o__Fusobacteriales; f__Fusobacteriaceae; g__Cetobacterium; s__uncultured bacterium

featureID: 17d5a49452a6ccbe4473c55b3f818efc



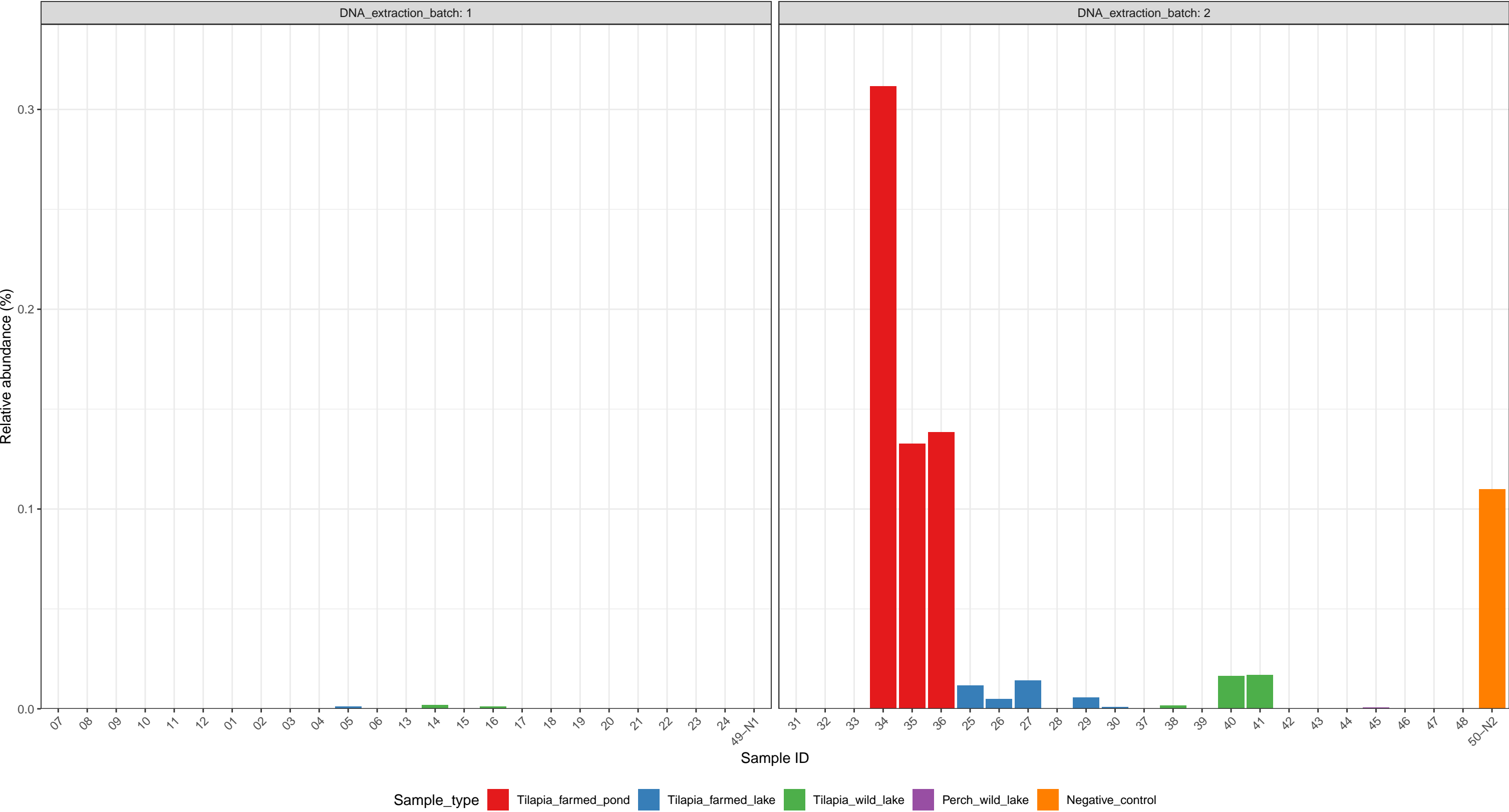
k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Peptostreptococcaceae; g__Paeniclostridium; s__uncultured bacterium

featureID: 1b00cdeda74eca68518123e3b3036f1f



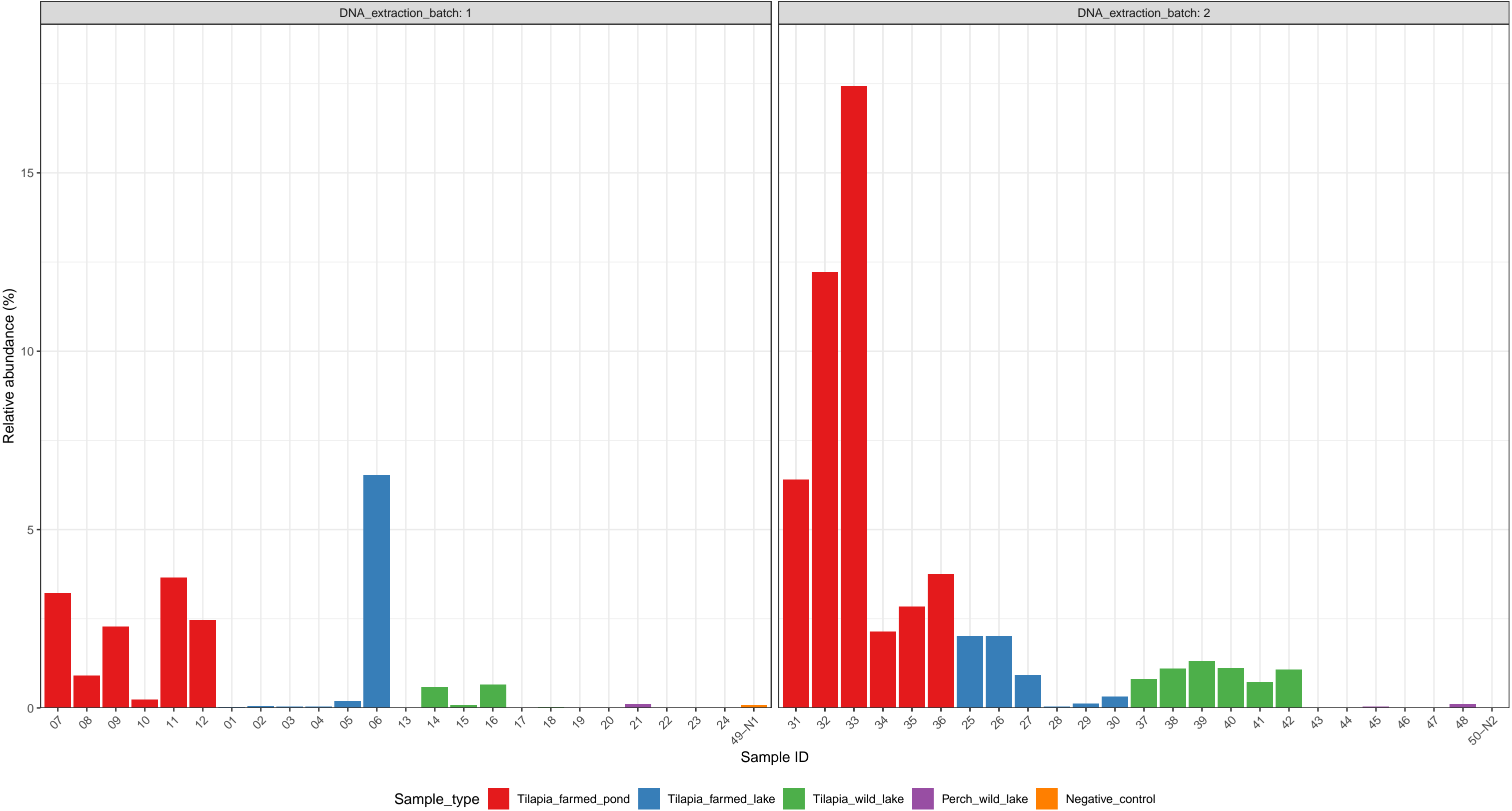
k__Bacteria; p__Cyanobacteria; c__Oxyphotobacteria; o__Synechococcales; f__Cyanobiaceae; g__Cyanobium PCC-6307; NA

featureID: e7ce2cd99fee0bb346892bd41d5aae49



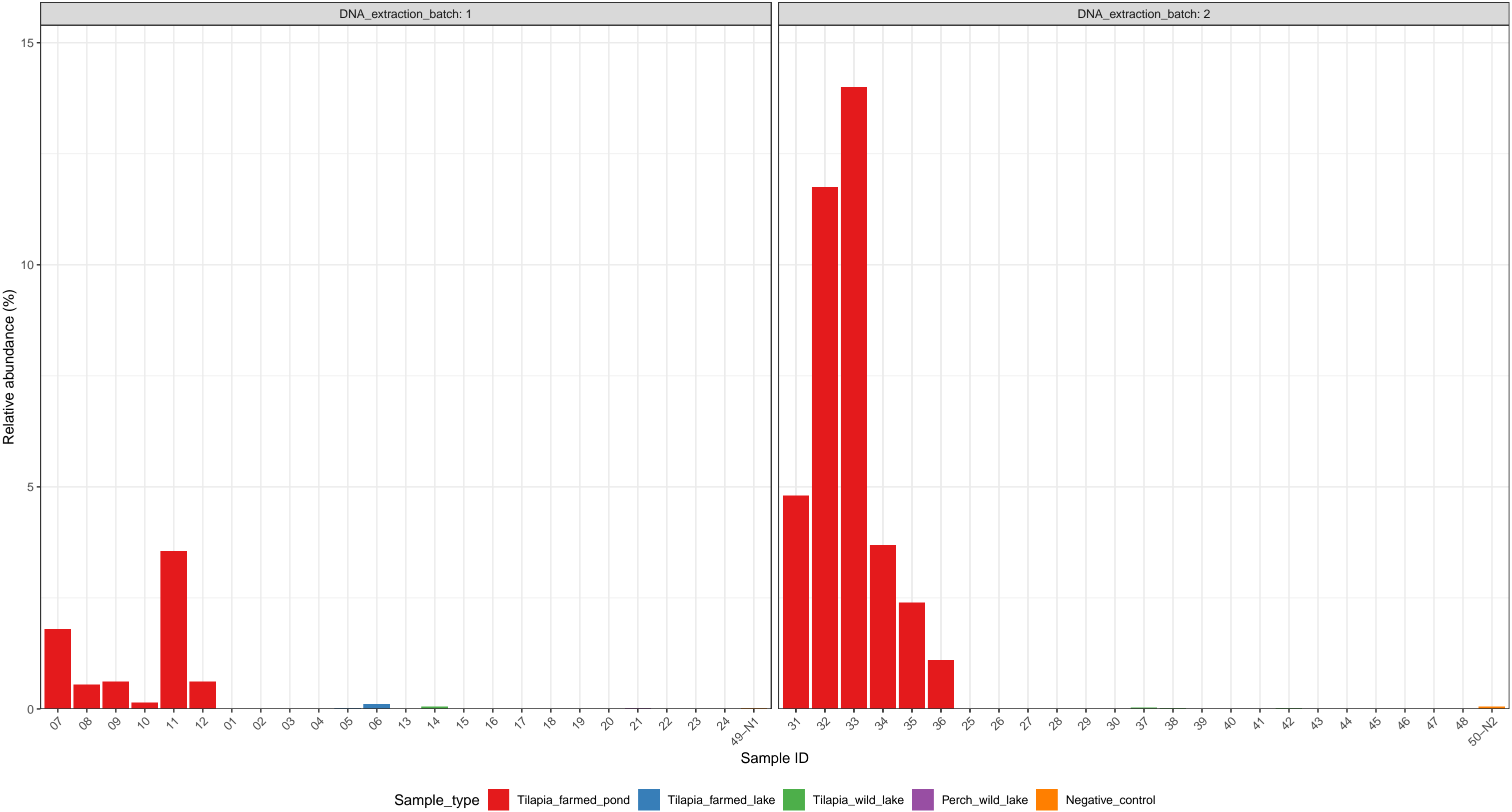
k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Clostridiaceae 1; g__Clostridium sensu stricto 1; NA

featureID: b7d96ace8aeb2c69a218149ac26a6ce9



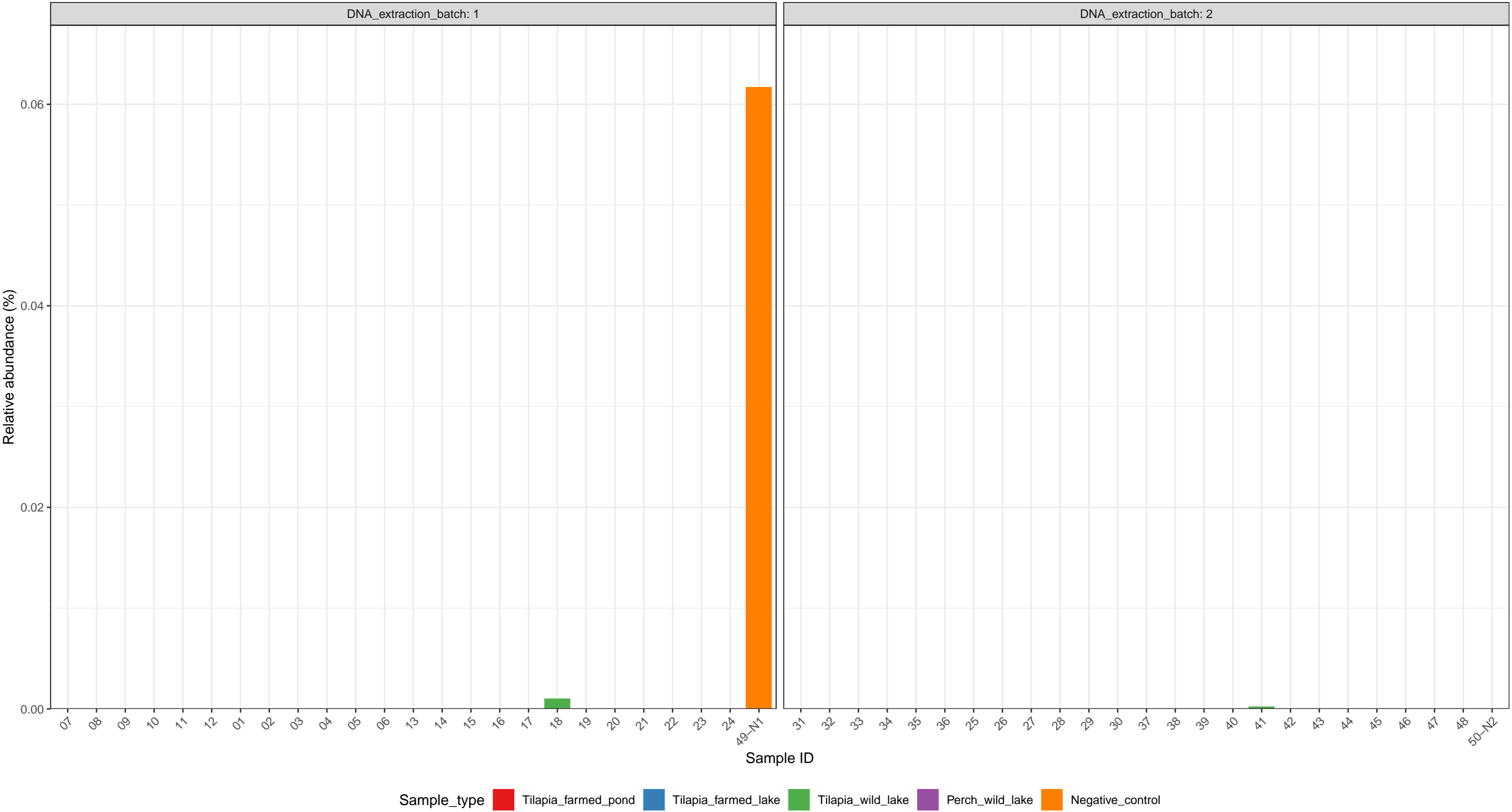
k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Clostridiaceae 1; NA; NA

featureID: eeb27bcd7d7aaa8b5bd04631b5bea486



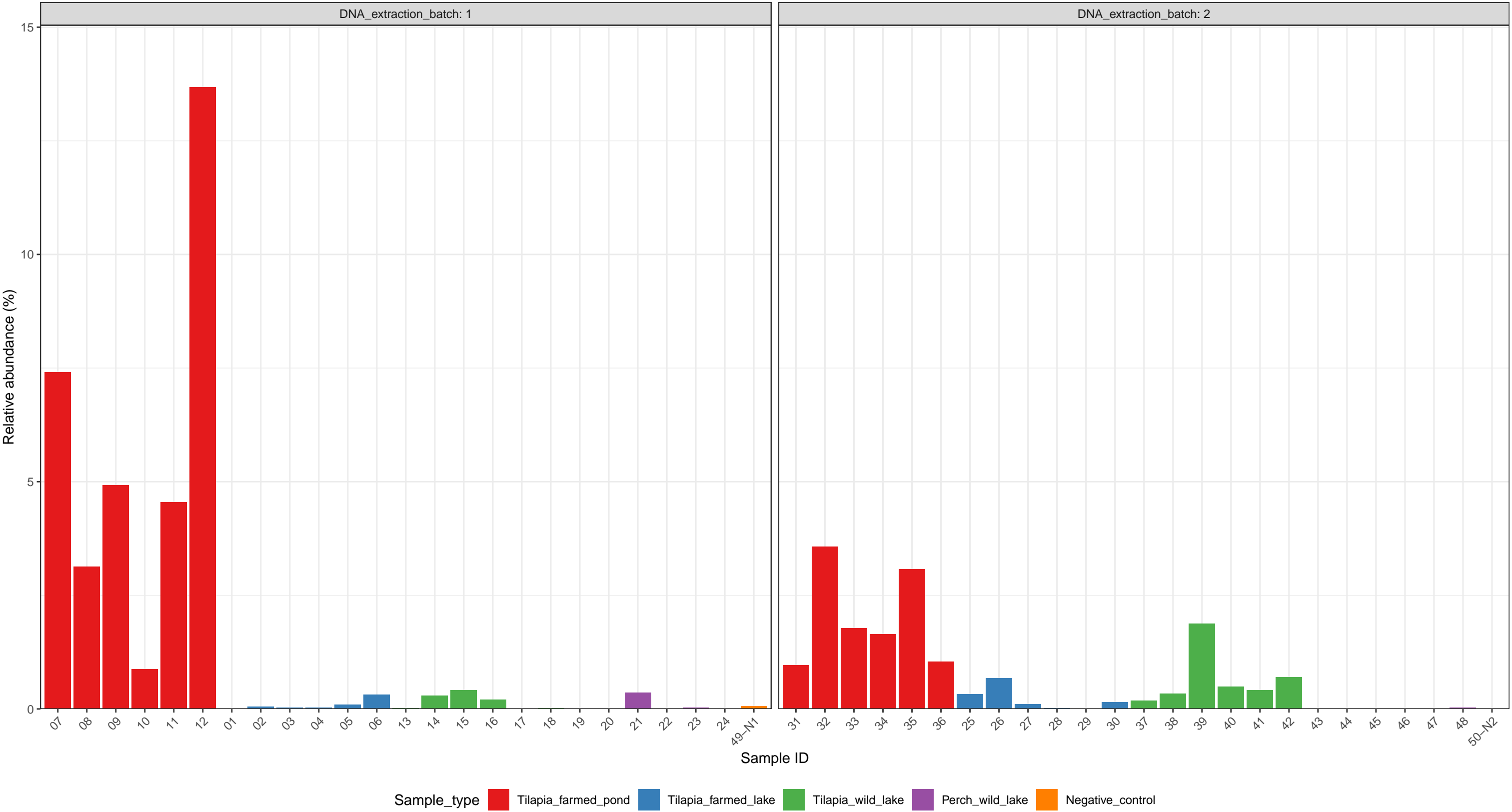
k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Streptococcaceae; g__Streptococcus; NA

featureID: ba4ab8dea6b4223dbc9ed5bbf3ea60ea



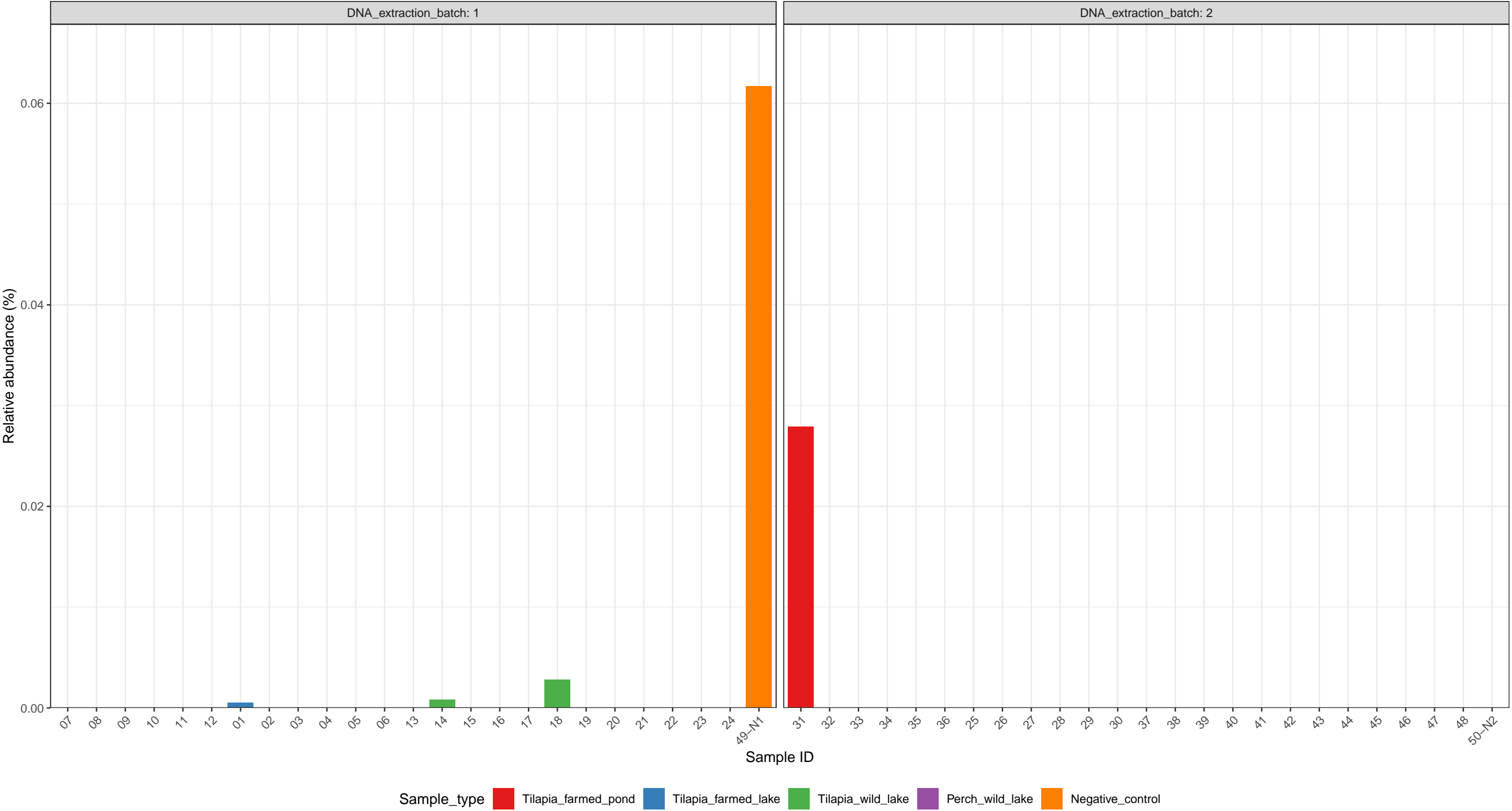
k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Clostridiaceae 1; g__Clostridium sensu stricto 1; NA

featureID: d112db53cc44b1be8395e16355a2109d



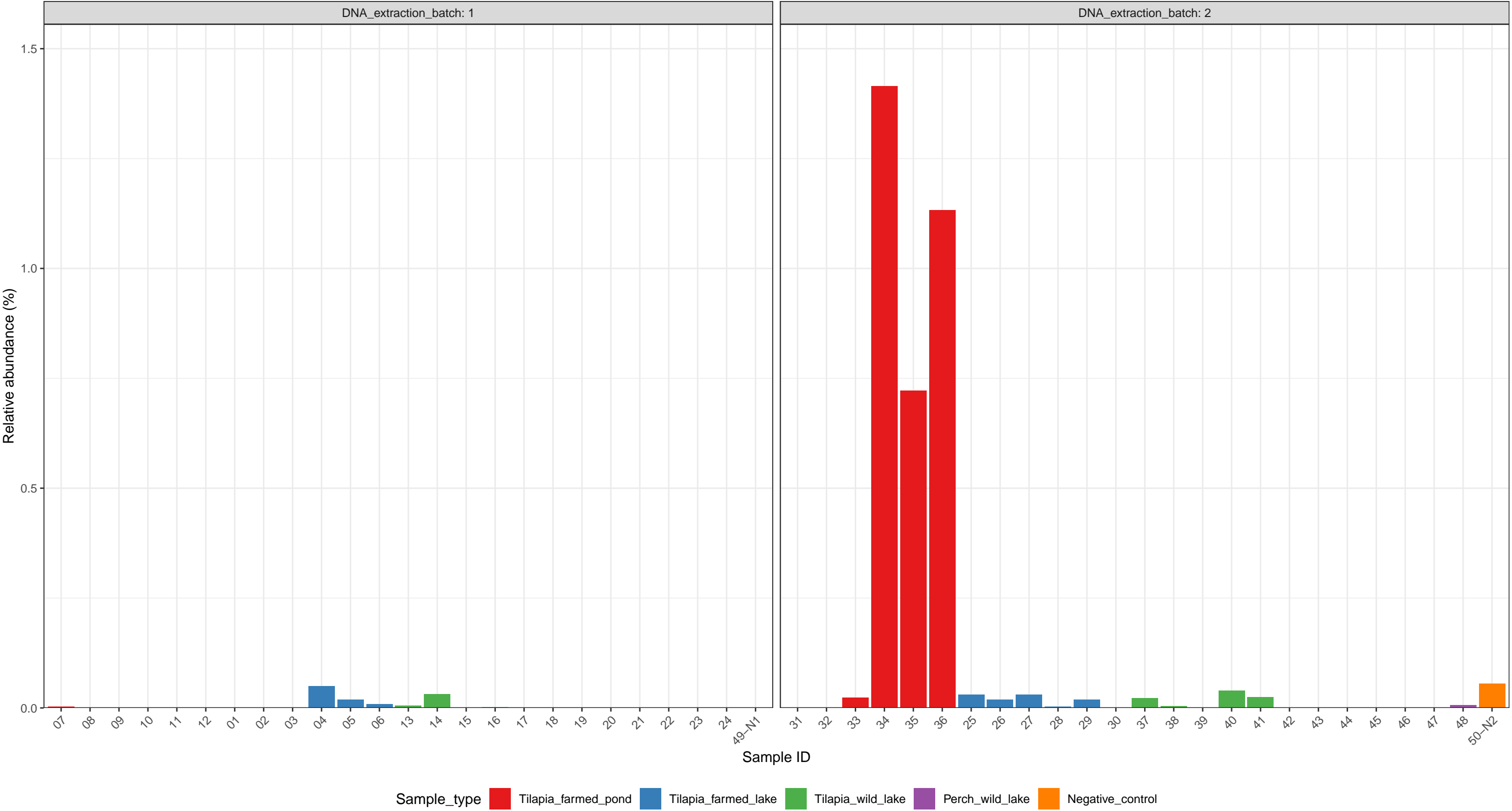
k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Corynebacteriales; f__Corynebacteriaceae; g__Corynebacterium 1; NA

featureID: d4e740bc5c2587cbbb188e8e30026611



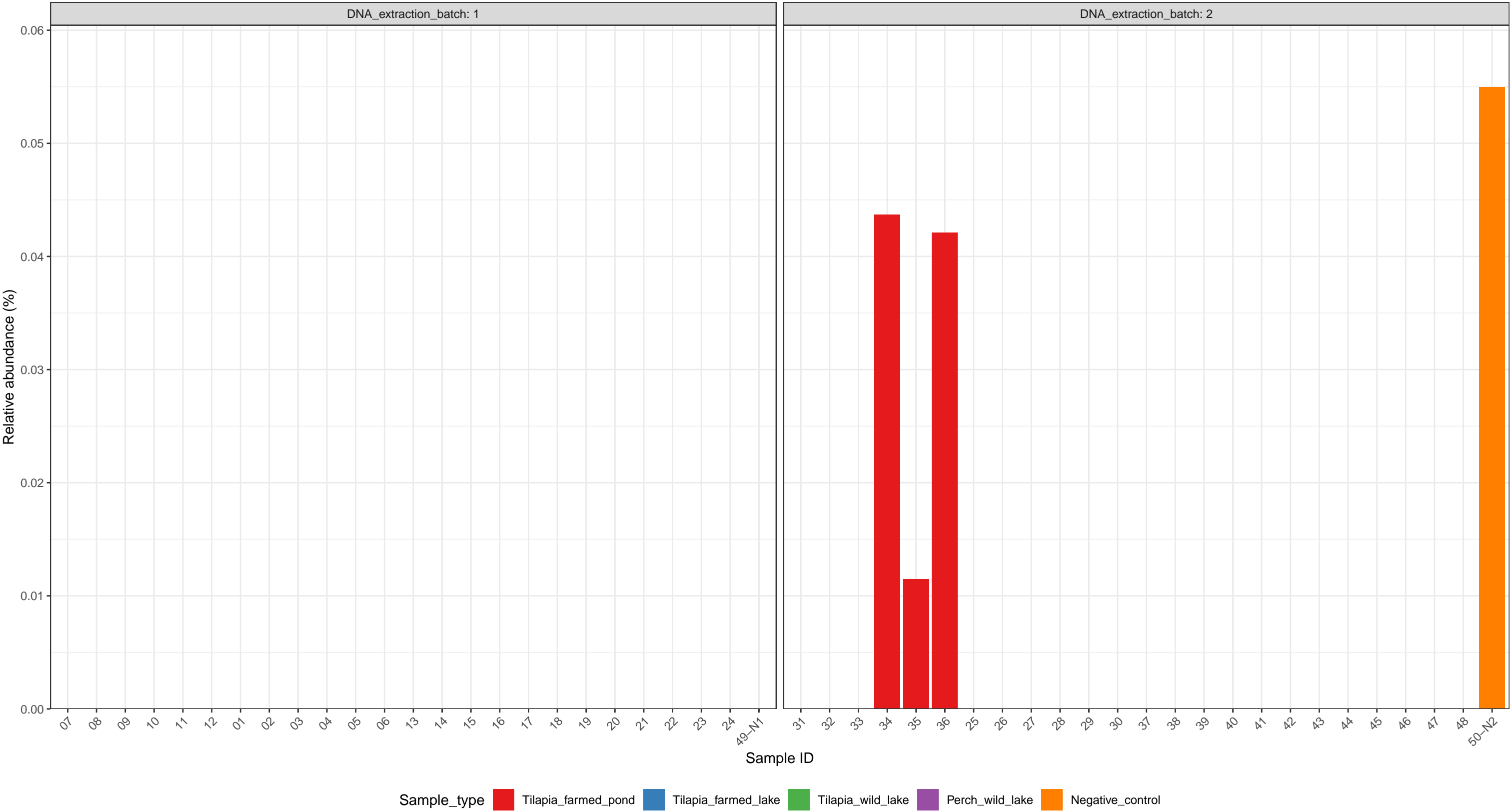
k__Bacteria; p__Cyanobacteria; c__Oxyphotobacteria; o__Synechococcales; f__Cyanobiaceae; g__Cyanobium PCC-6307; NA

featureID: 12e90f65e34a30ad48d9e3f3b842b30d



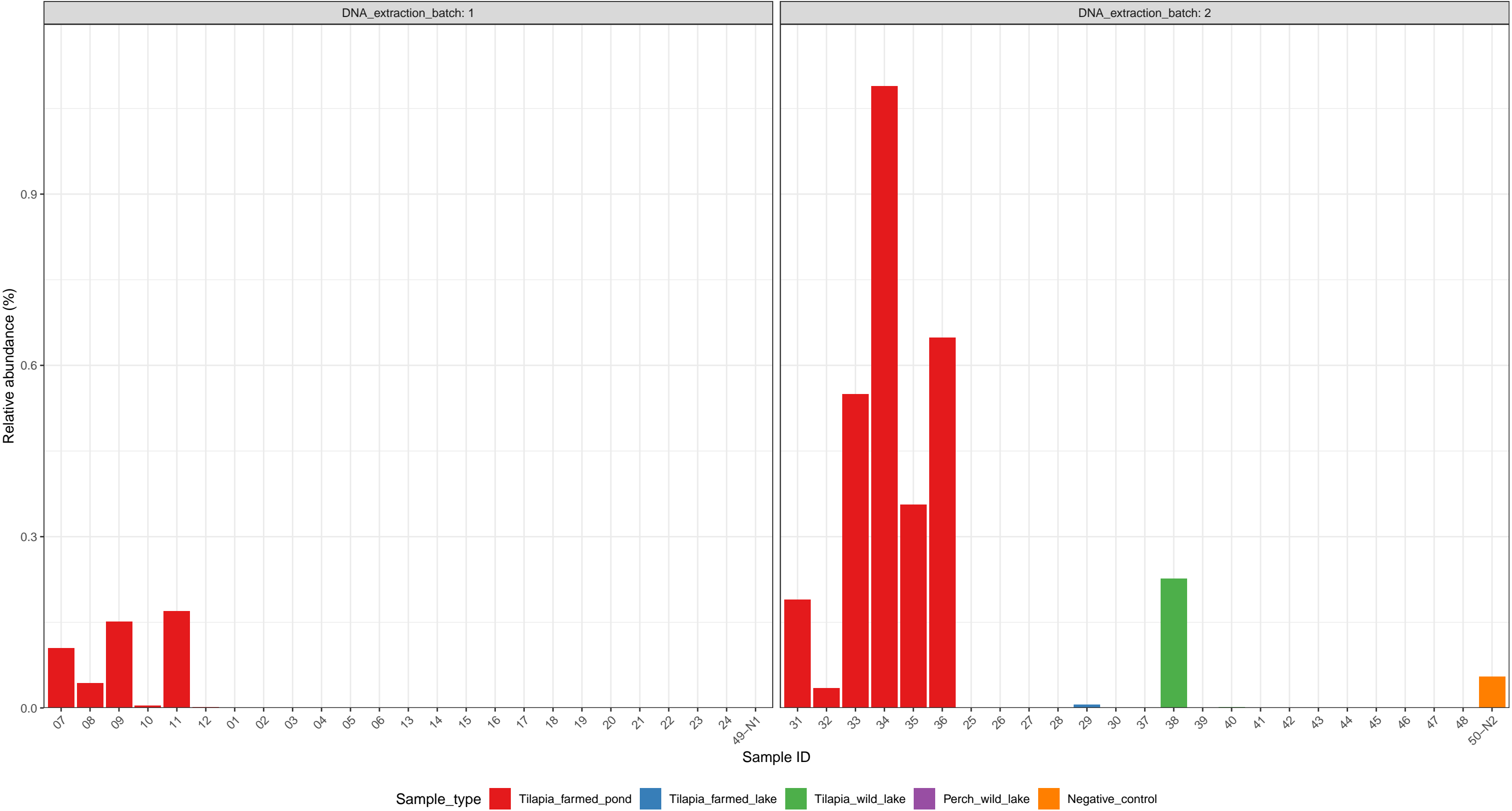
k__Bacteria; p__Chlamydiae; c__Chlamydiae; o__Chlamydiales; f__Parachlamydiaceae; g__Neochlamydia; NA

featureID: 35e38ee9b5dff68dbd41115b73741414



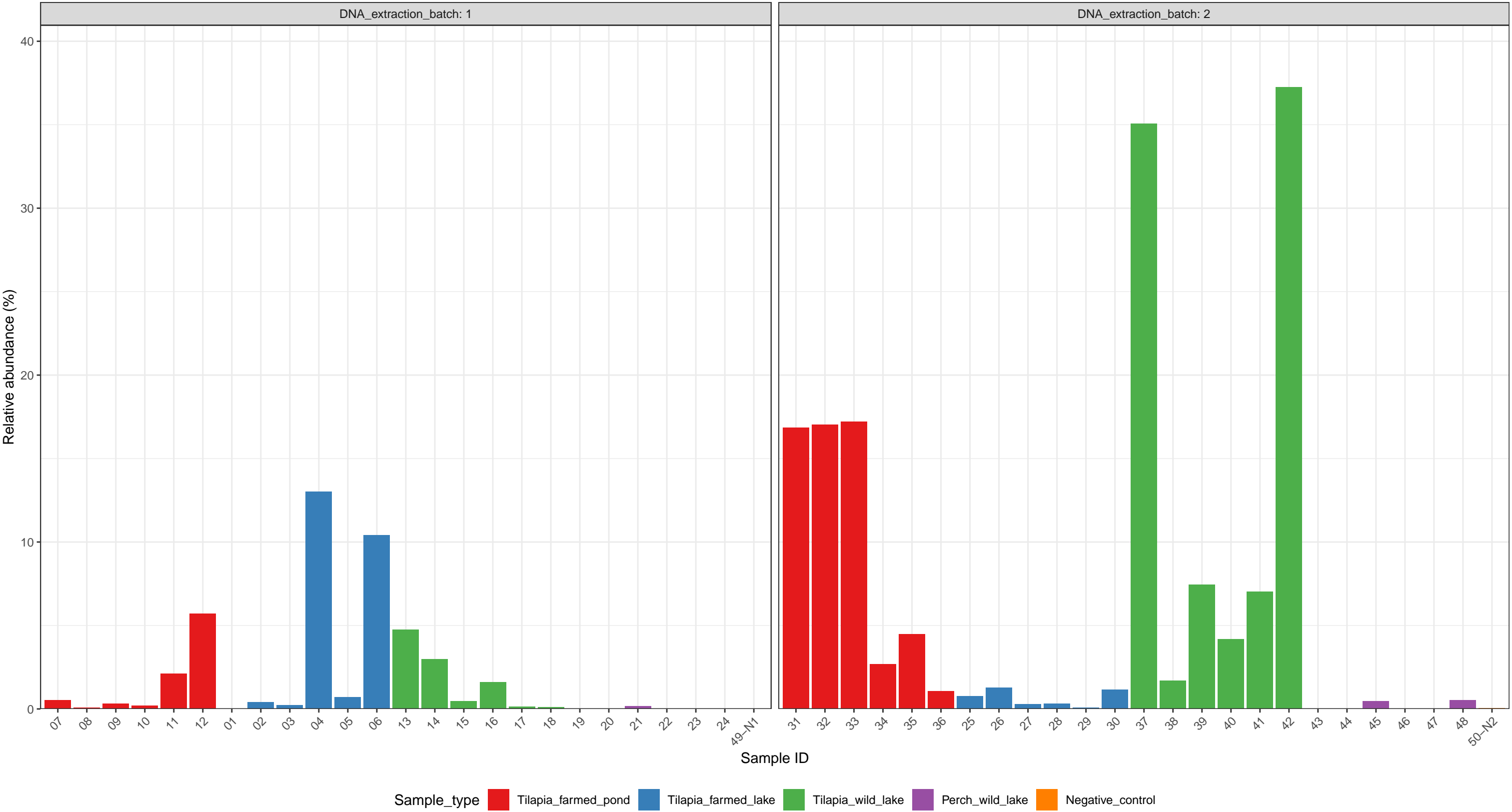
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Methylococcales; f__Methylococcaceae; g__Methyloparacoccus; s__uncultured bacterium

featureID: 66c3e0b10570a19d613f692d701da8d0



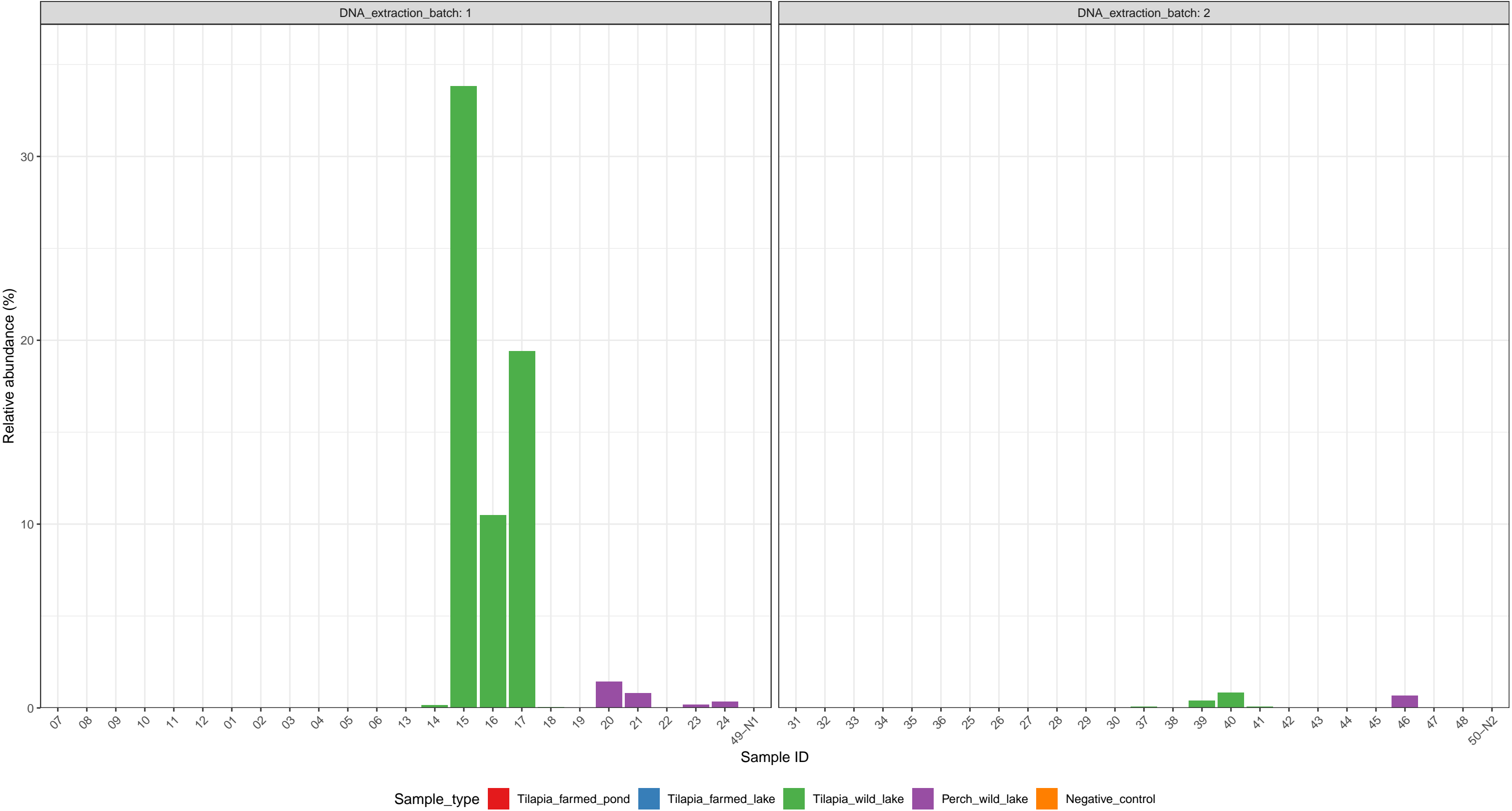
k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Peptostreptococcaceae; NA; NA

featureID: 8ebe63f7e7dd6bd4ca4dca5a66df57c2



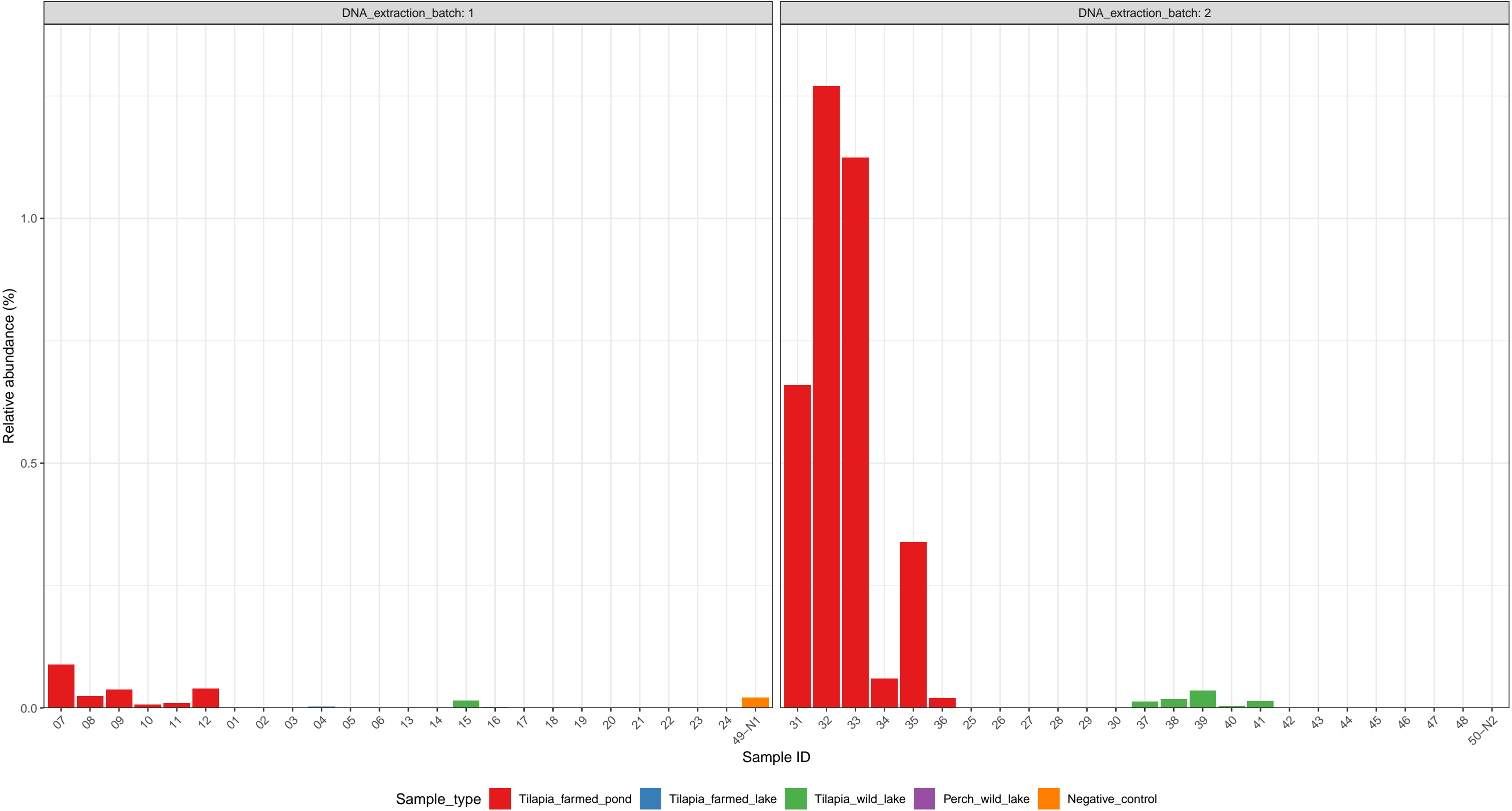
k__Bacteria; p__Fusobacteria; c__Fusobacteriia; o__Fusobacteriales; f__Fusobacteriaceae; g__Cetobacterium; NA

featureID: 50b18b94311c09ff882fda744bc15200



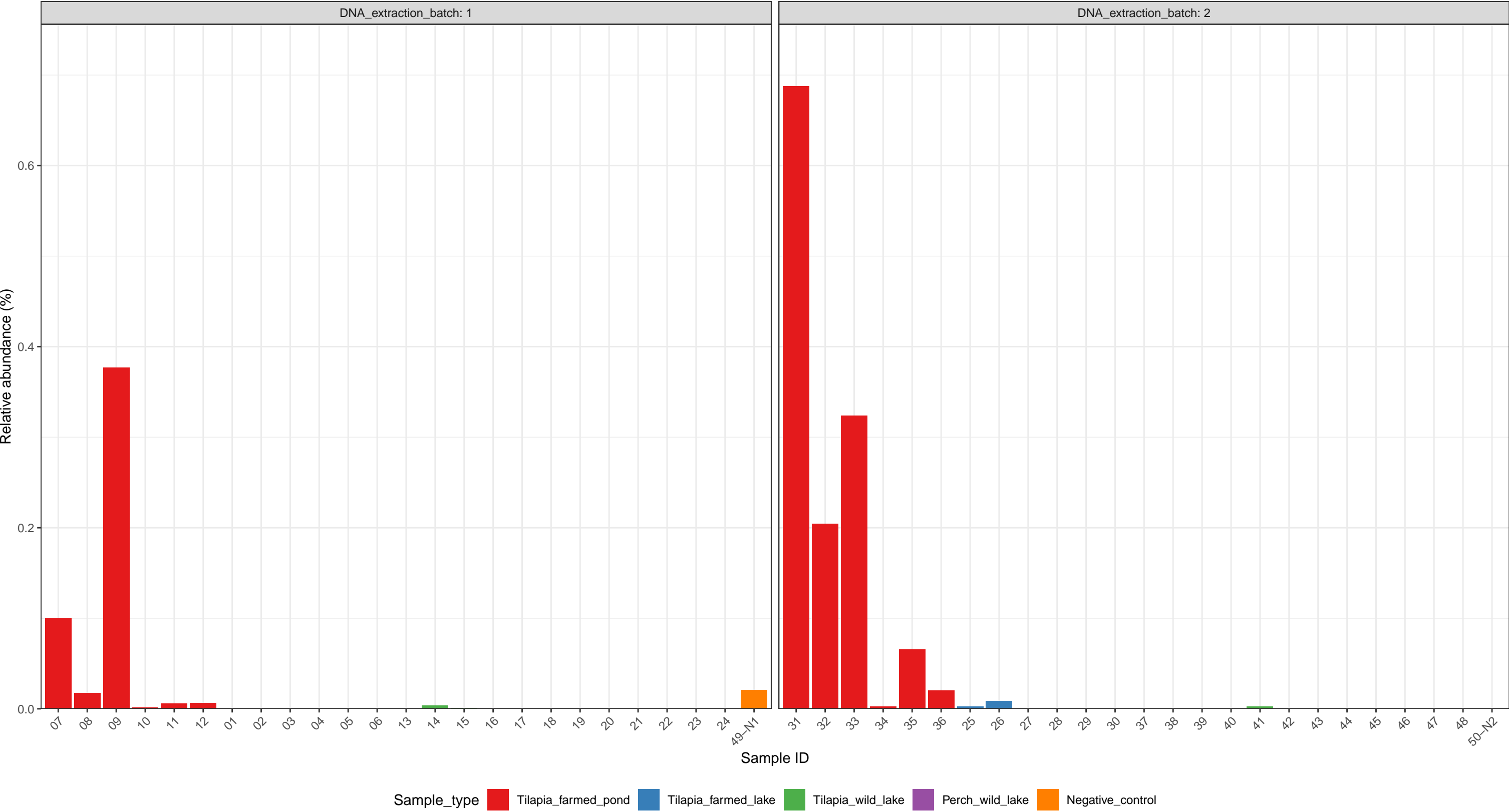
k__Bacteria; p__Firmicutes; c__Erysipelotrichia; o__Erysipelotrichales; f__Erysipelotrichaceae; g__Turicibacter; s__uncultured bacterium

featureID: 8440d53055be17f665533f3bf79970b8



k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__uncultured; Ambiguous_taxa; Ambiguous_taxa

featureID: c63bd7419c3dcdbff038ae017cba123c



k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Clostridiaceae 1; g__Clostridium sensu stricto 1; NA

featureID: e576356609fe0b38ceff9ad3b12816a

