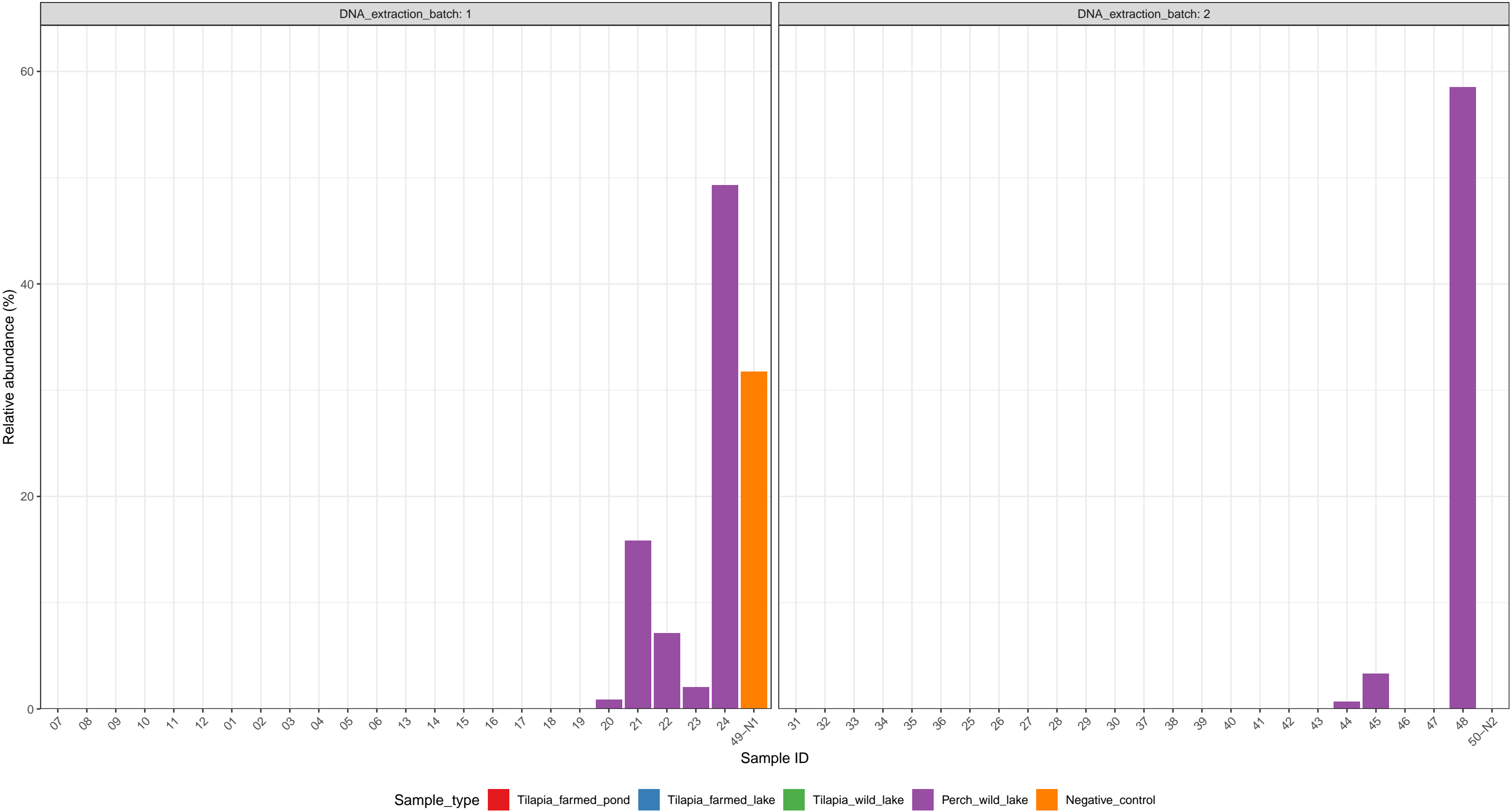


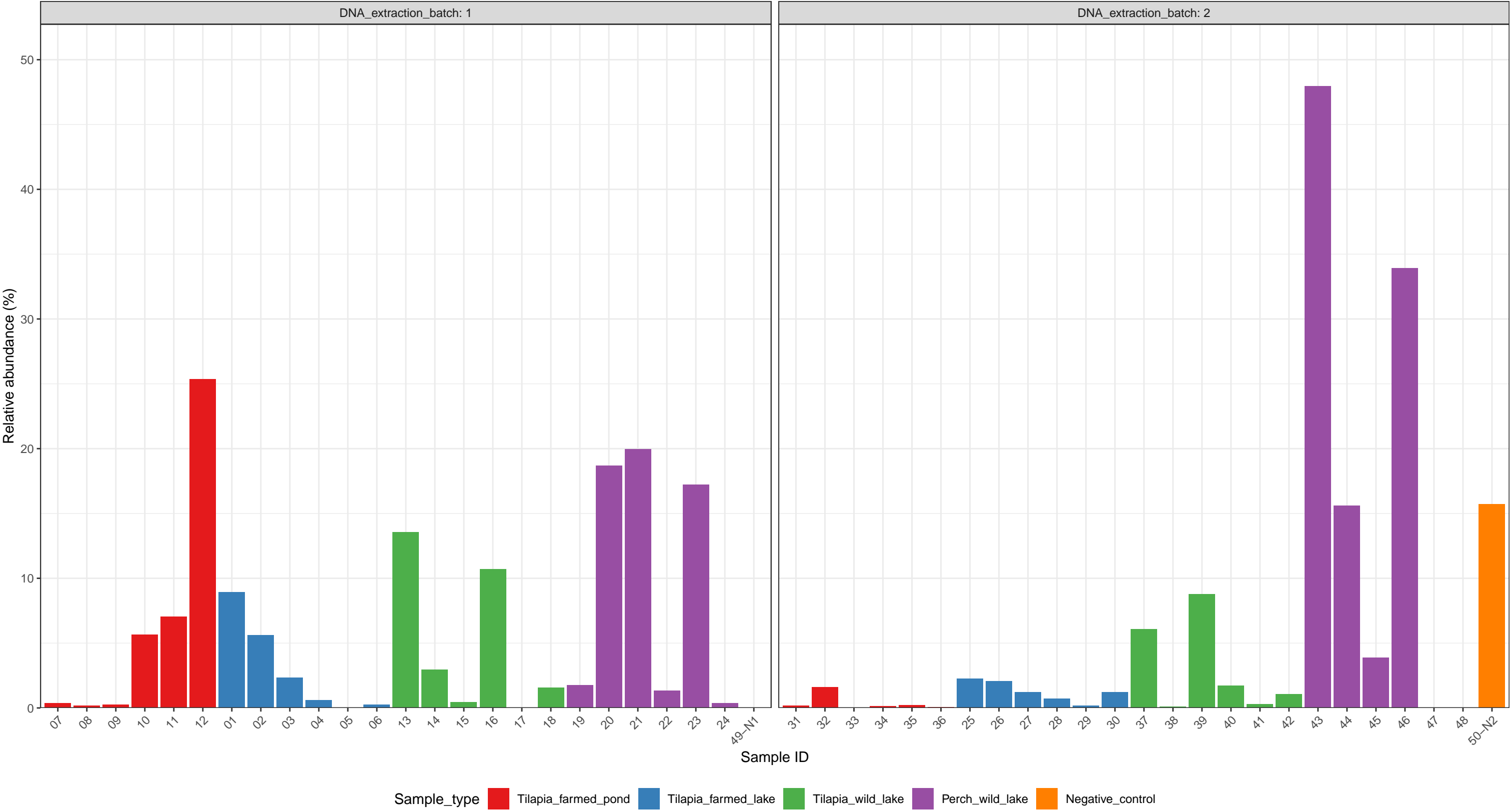
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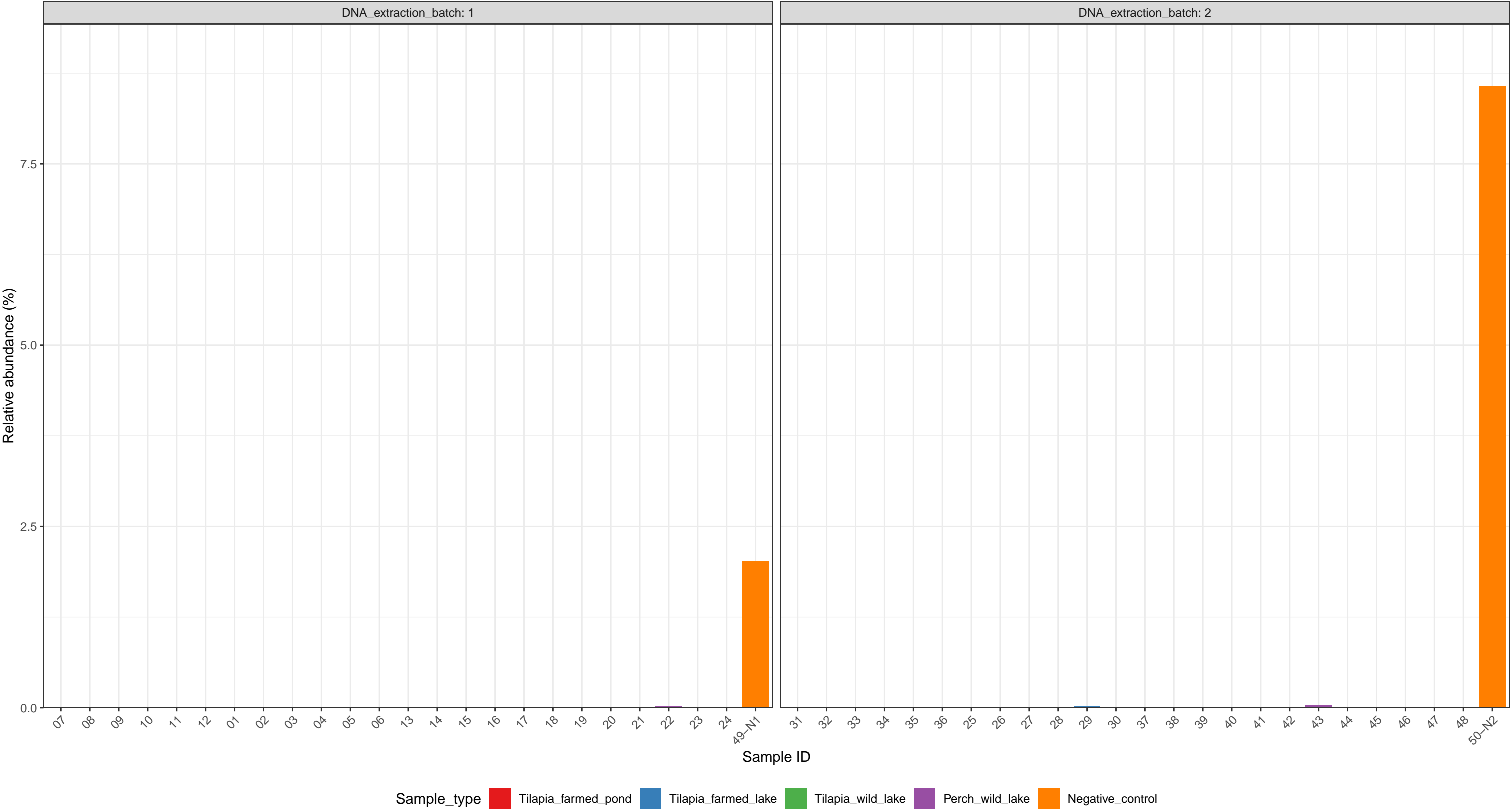
k__Bacteria; p__Fusobacteria; c__Fusobacteriia; o__Fusobacteriales; f__Fusobacteriaceae; g__Cetobacterium; NA

featureID: 9039275571577e03e38d718f59db0e1f



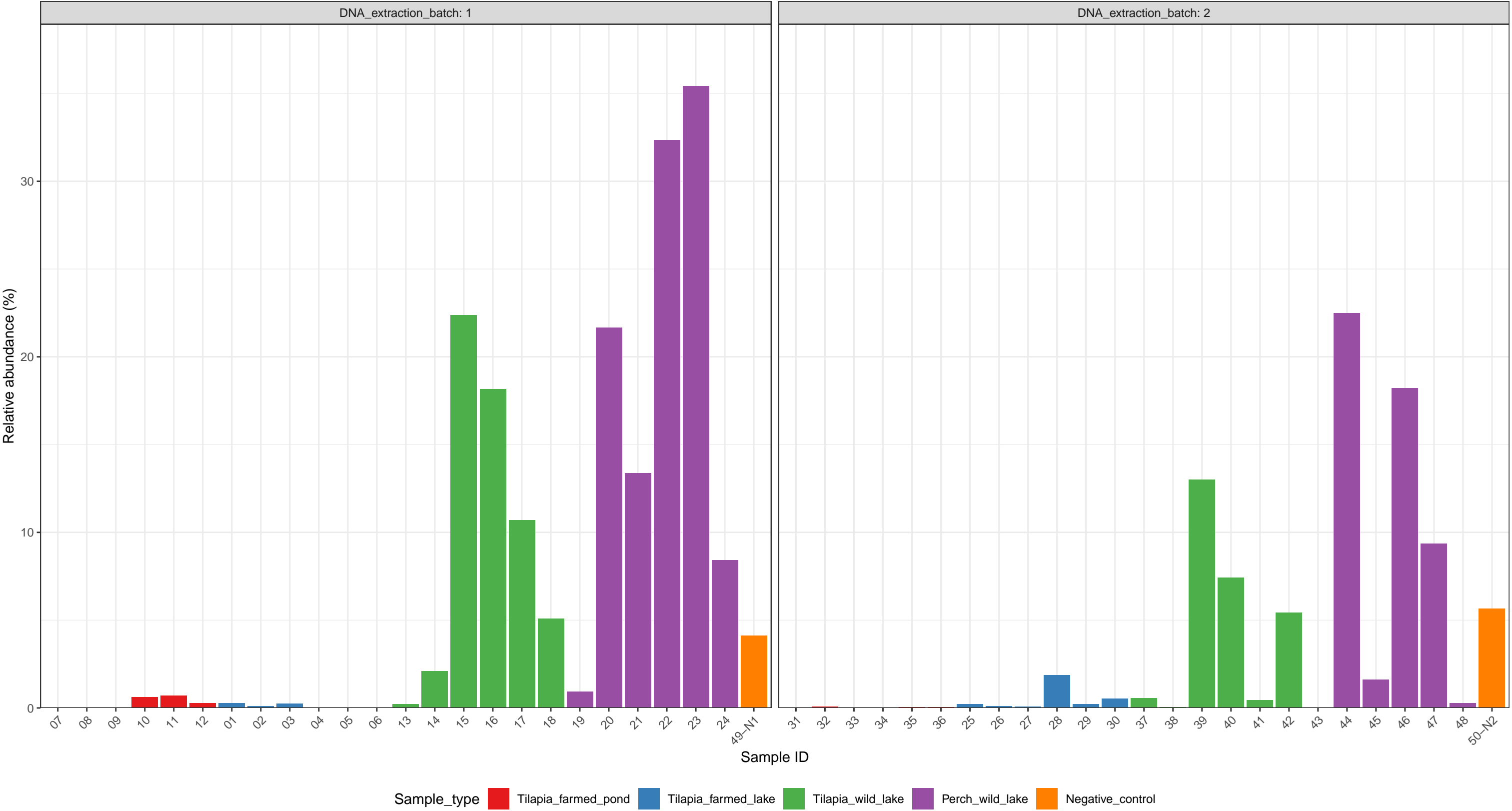
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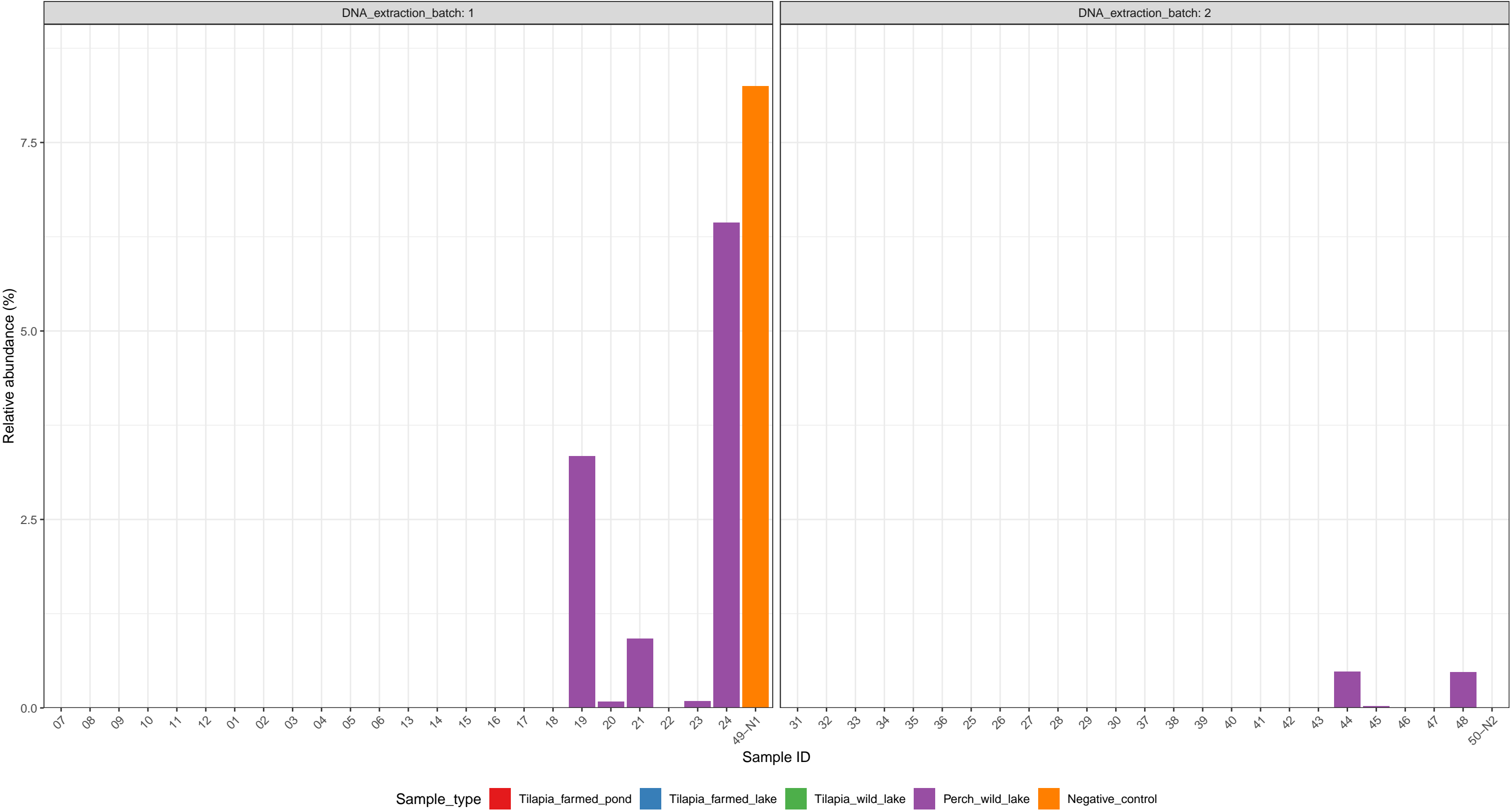
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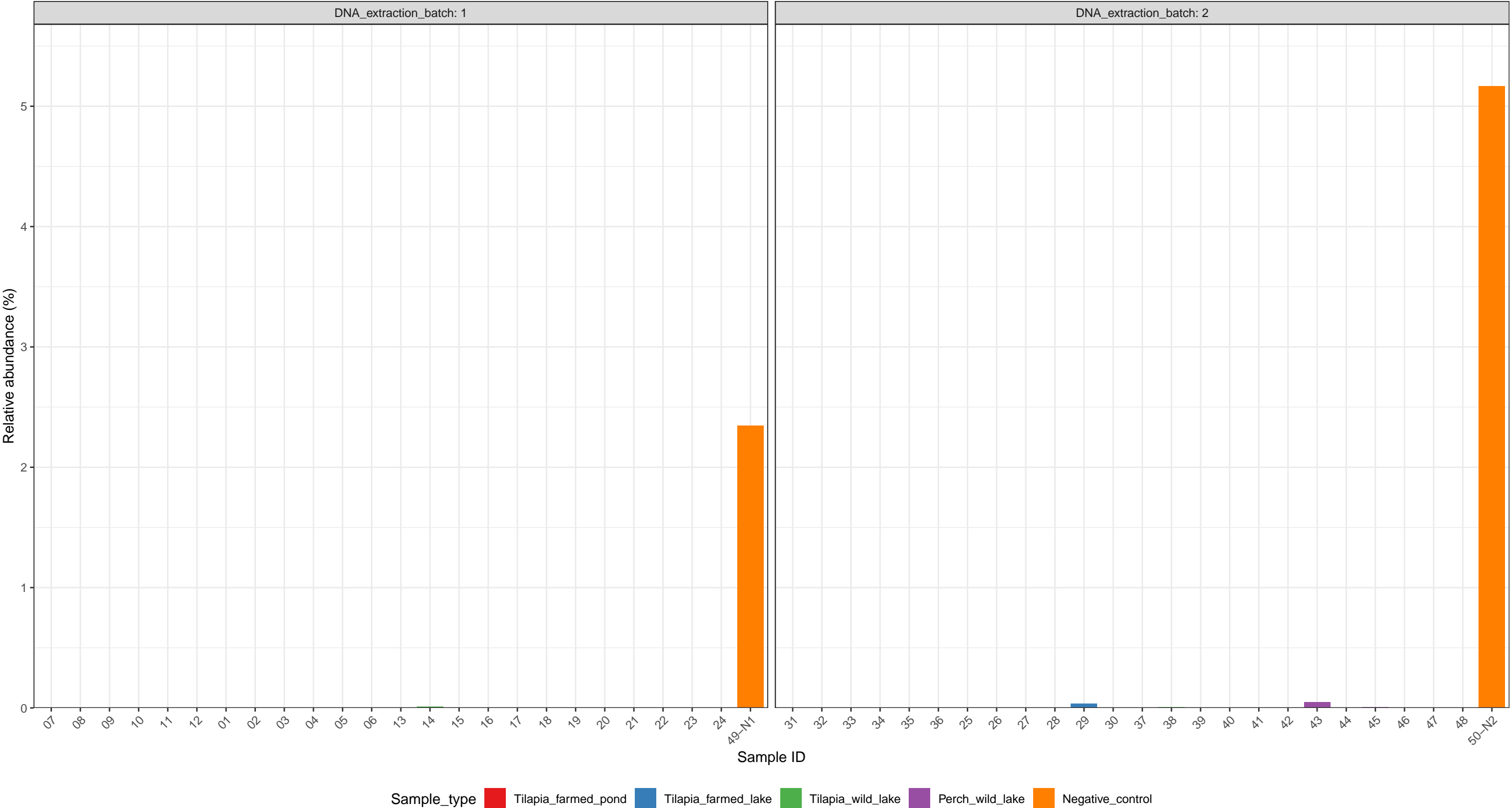
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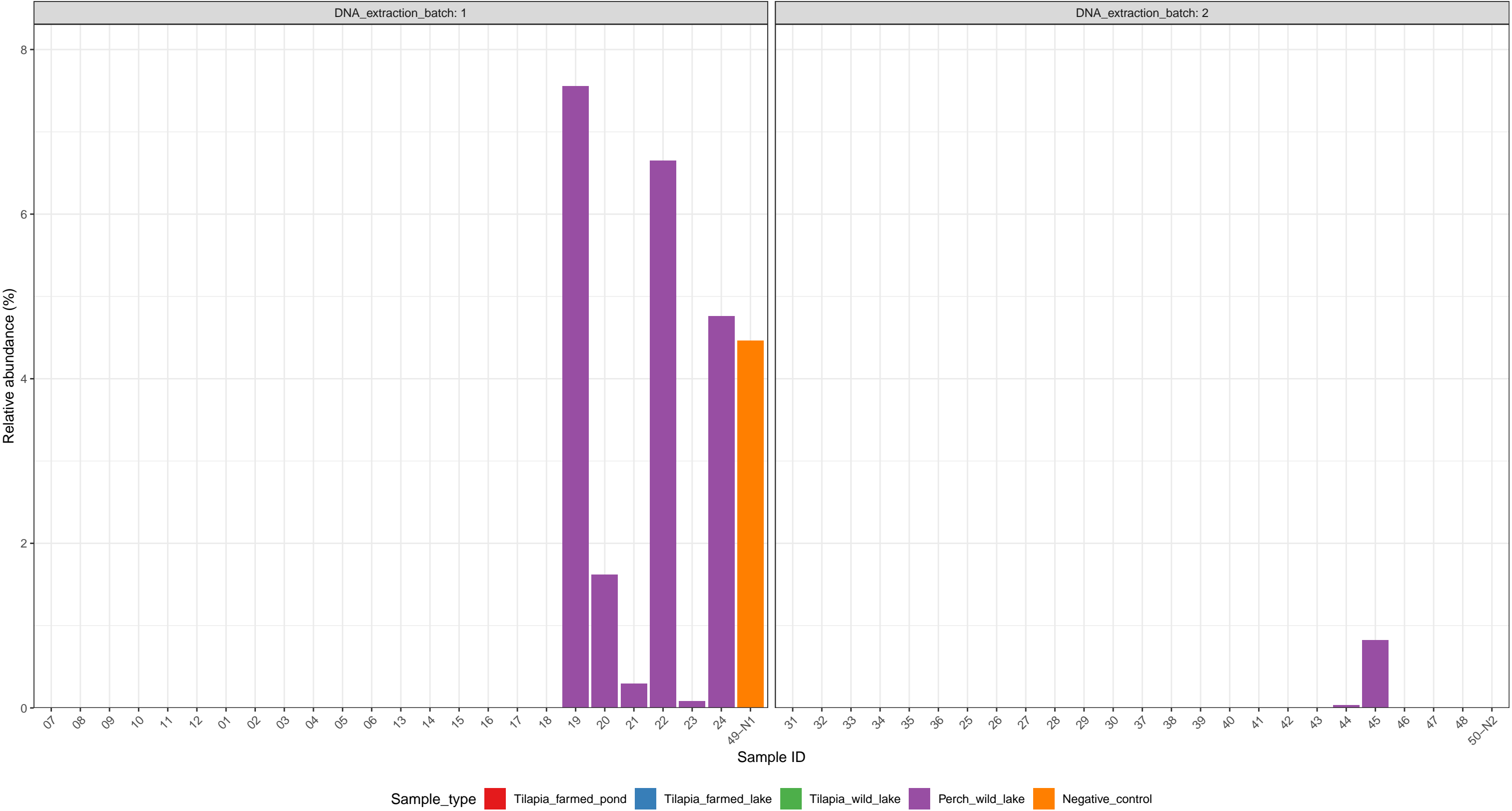
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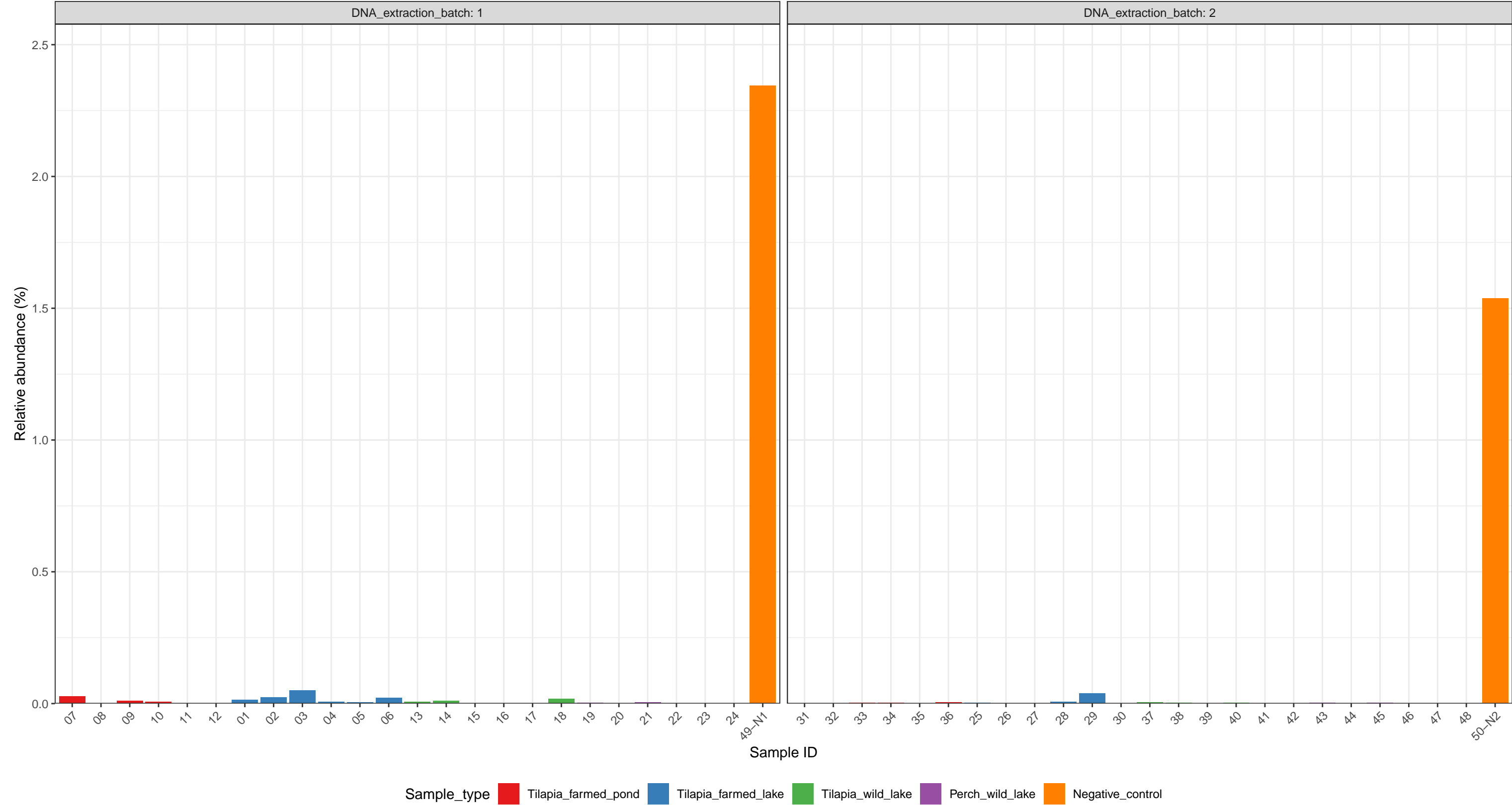
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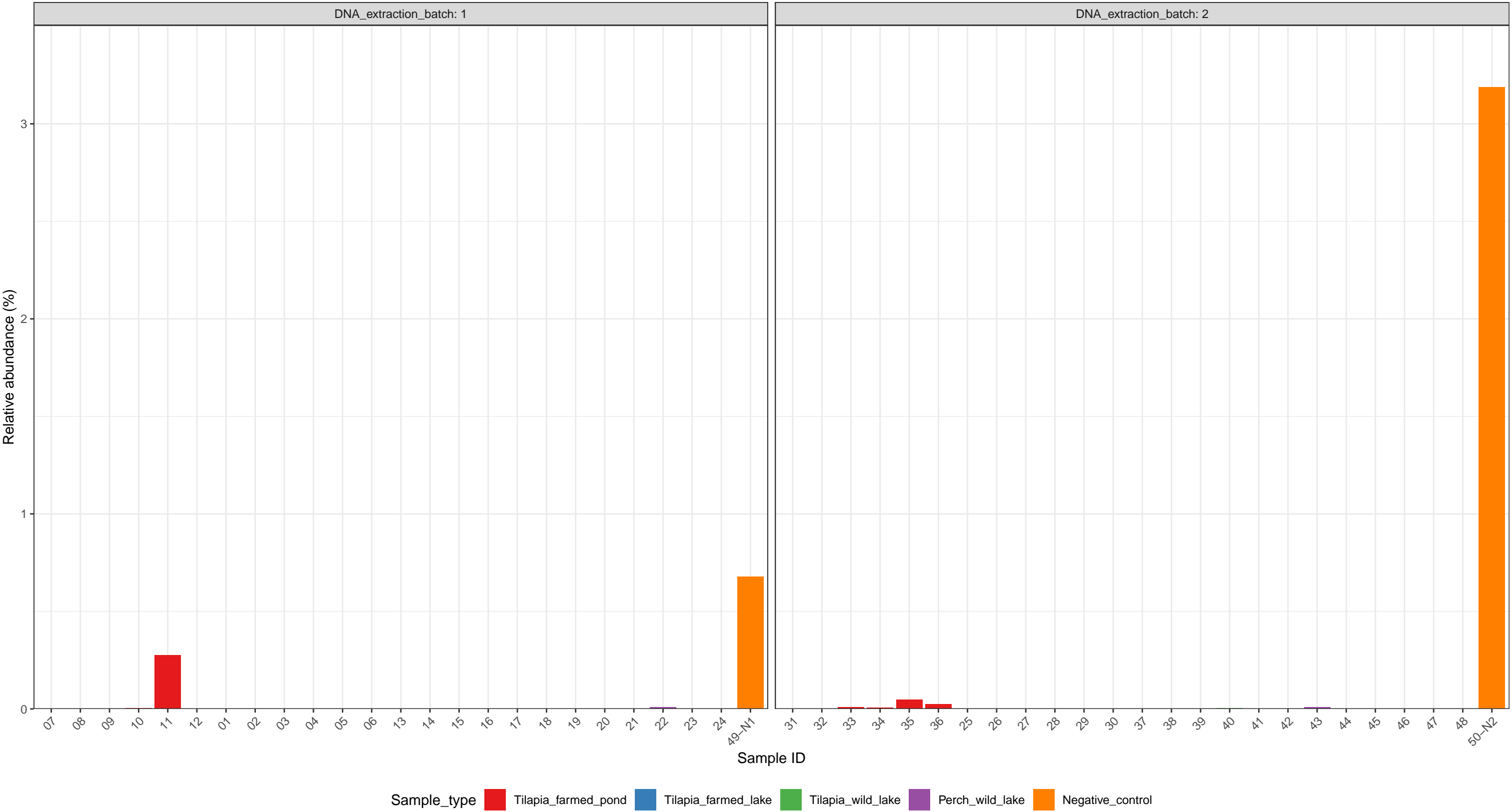
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales; f__Pseudomonadaceae; g__Pseudomonas; NA

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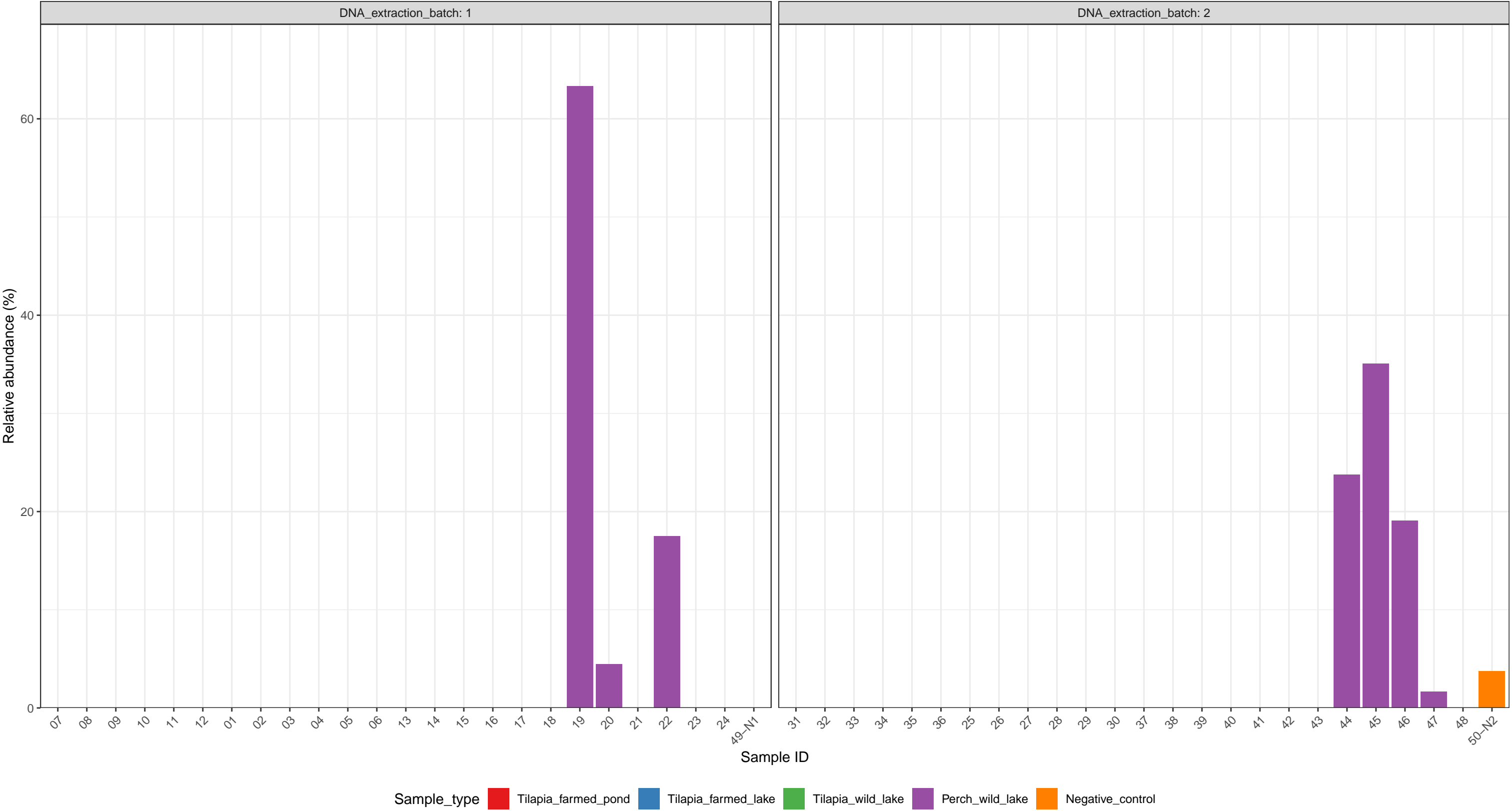
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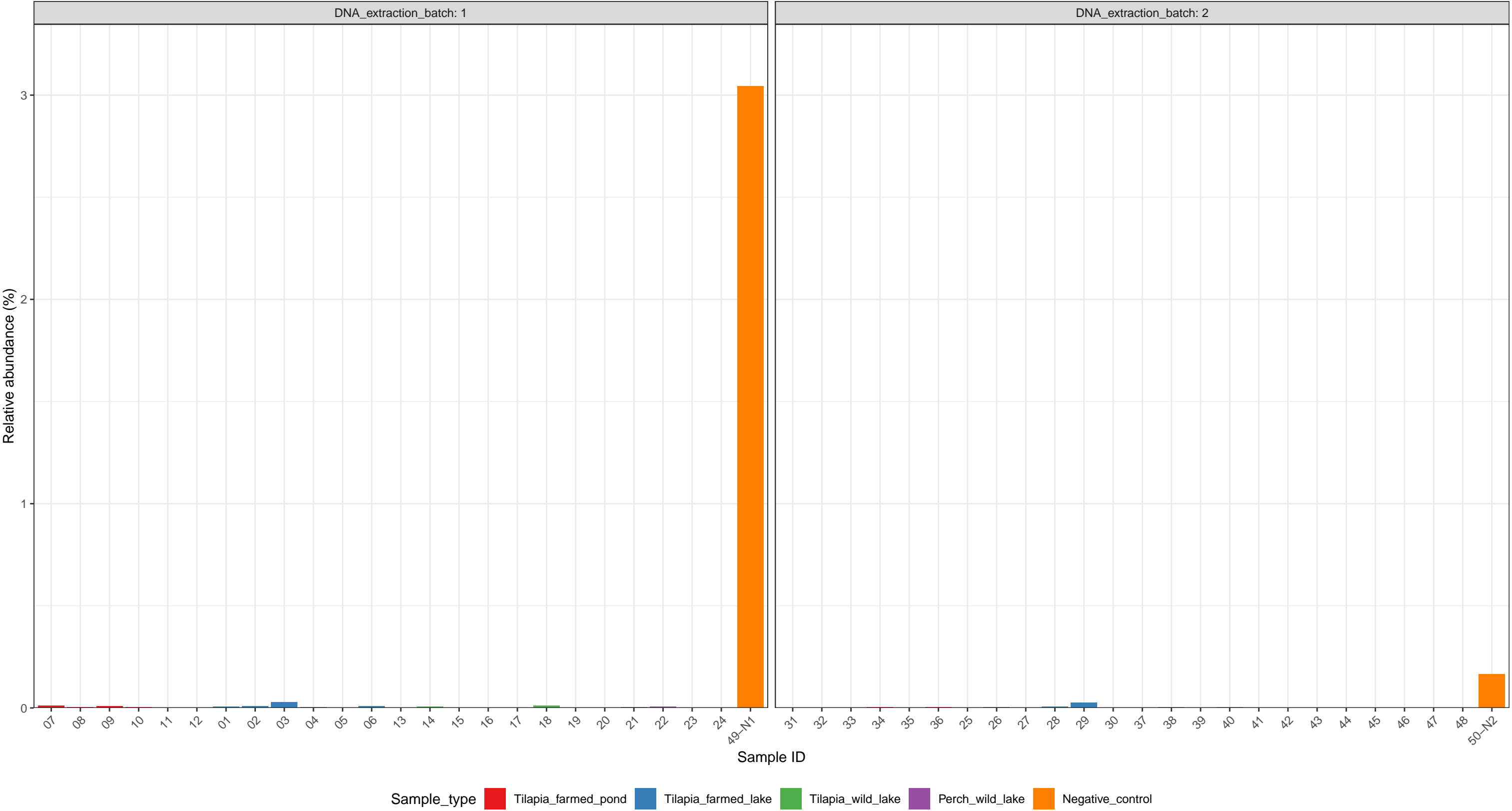
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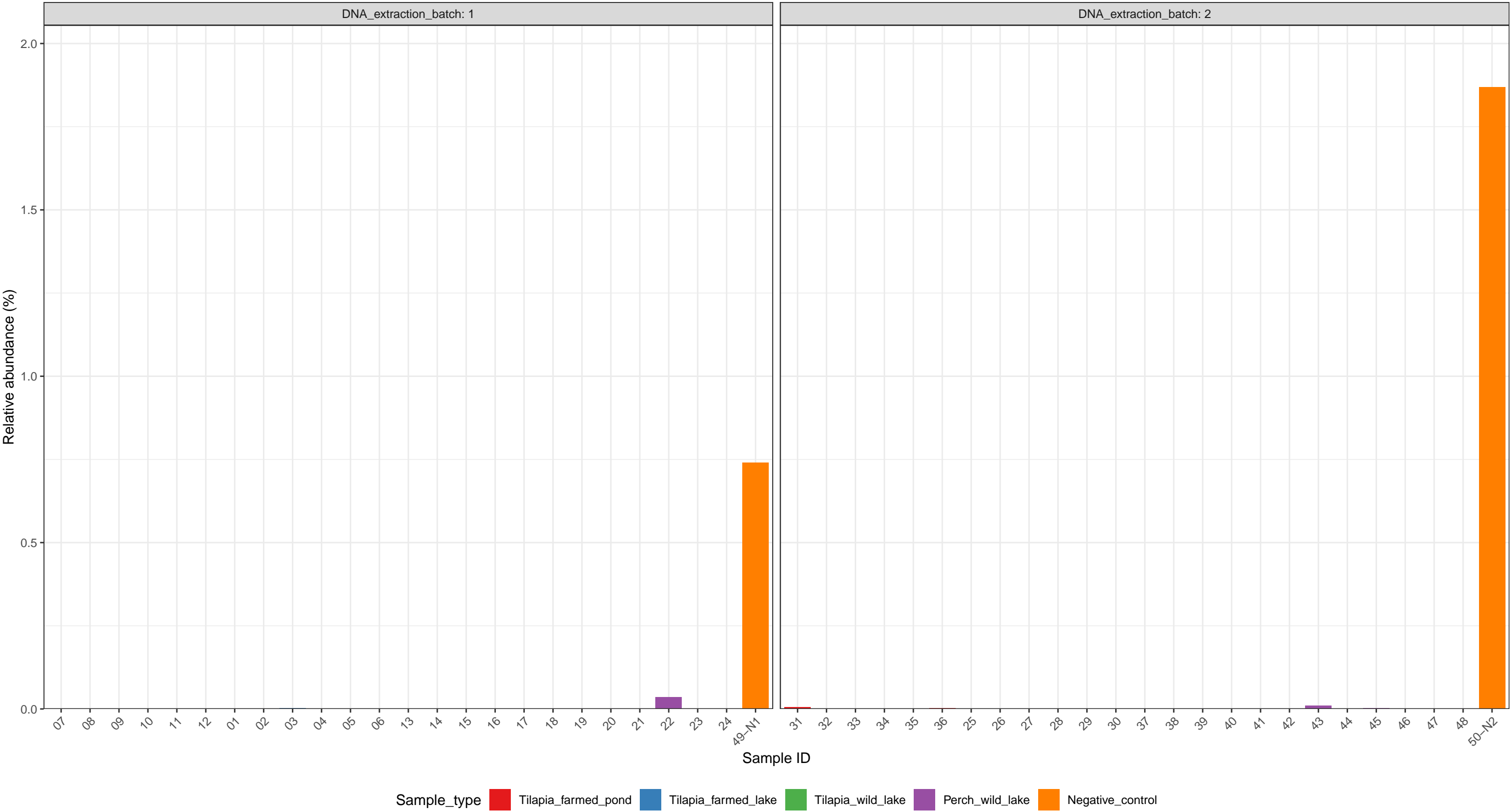
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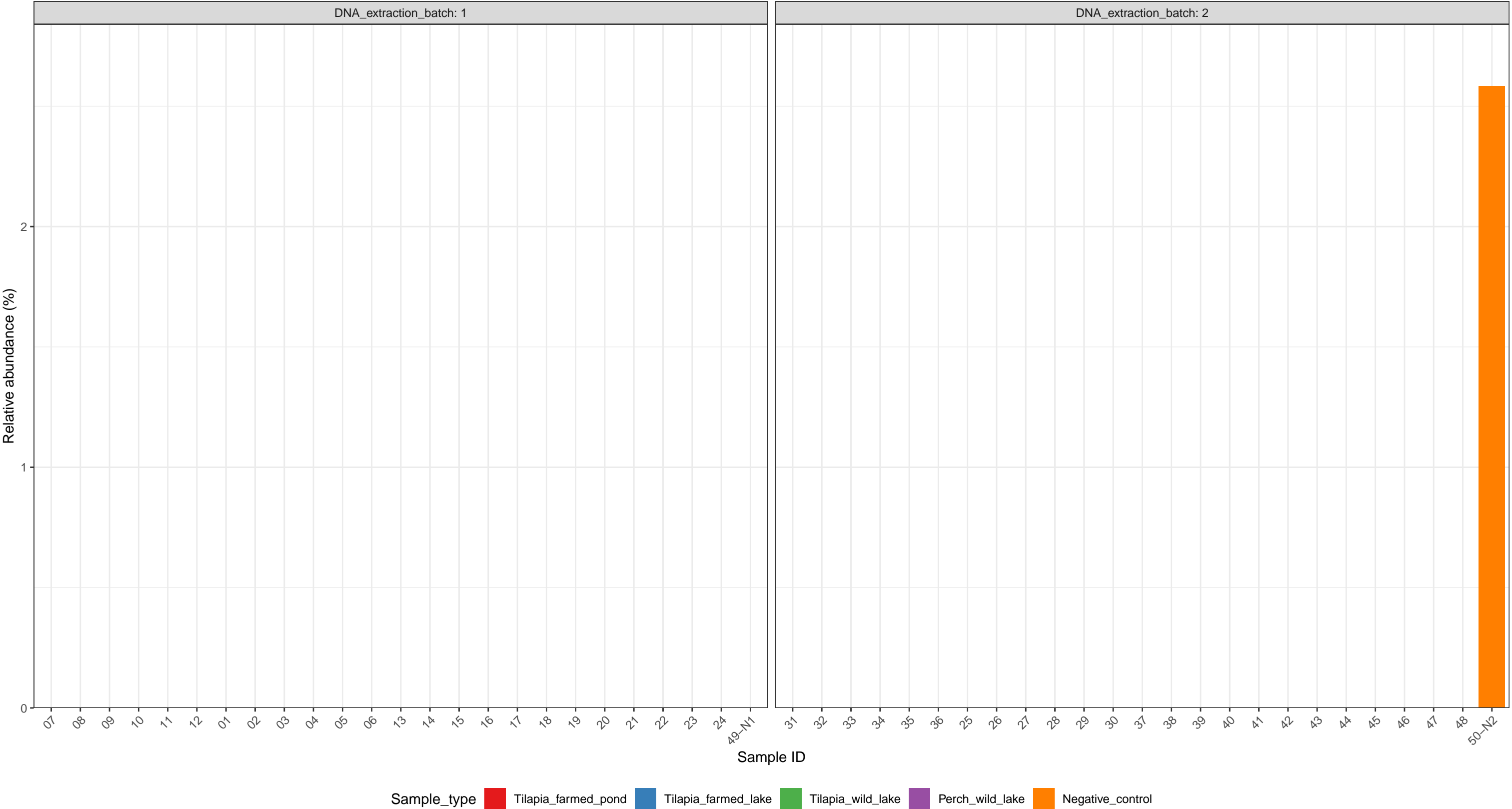
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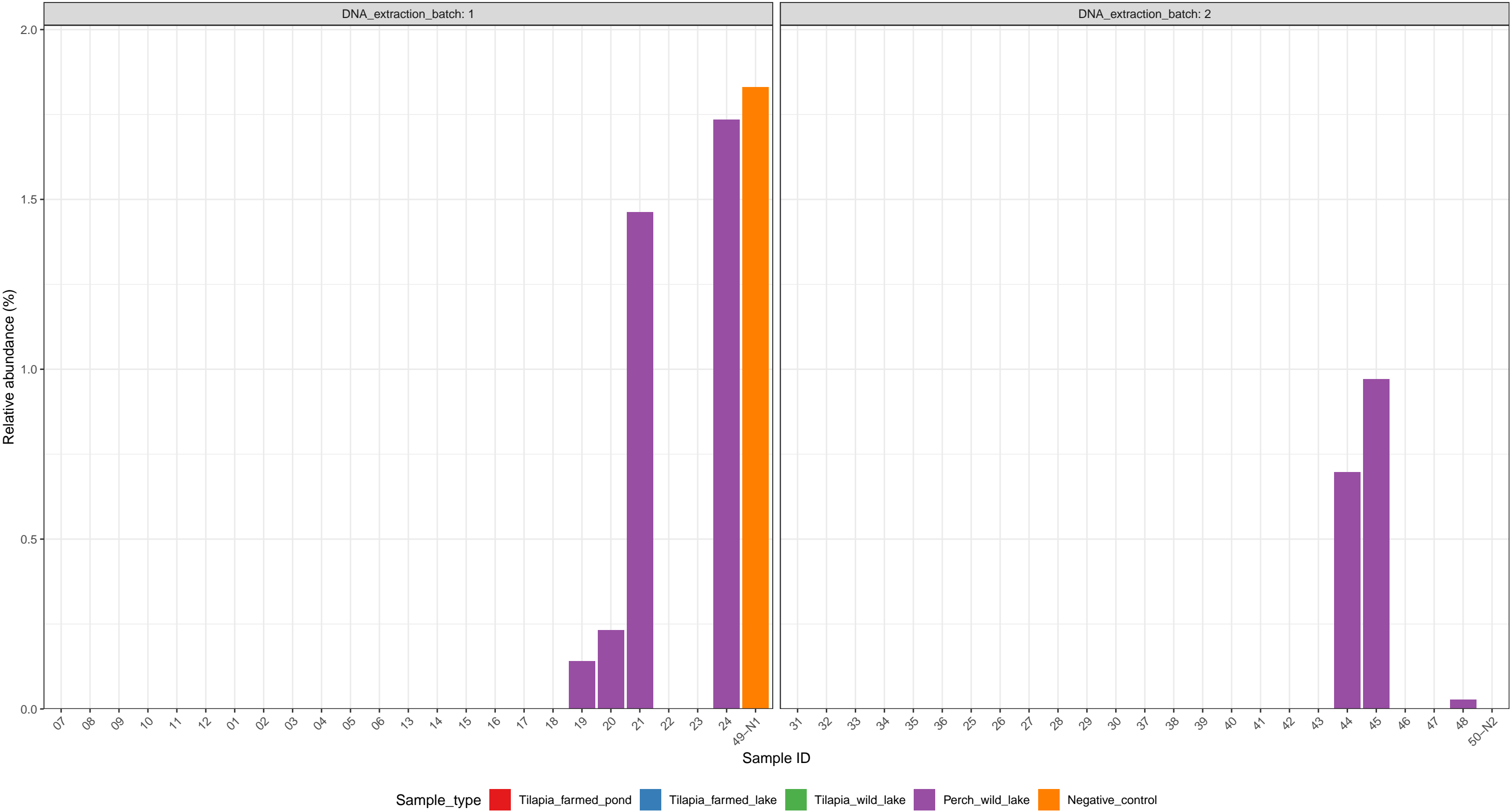
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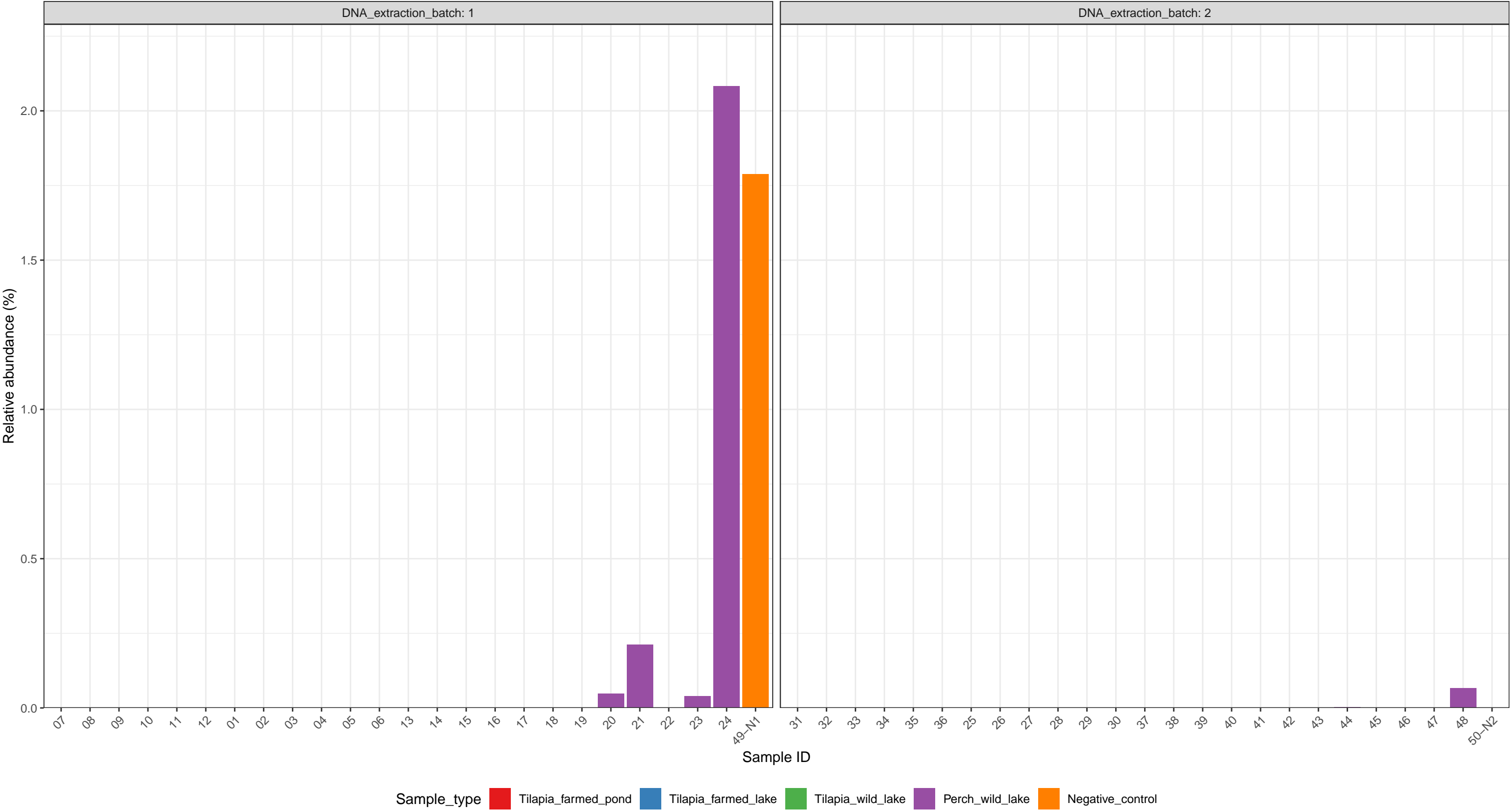
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featureID: 8f6ff8174262993339a29e403091e900



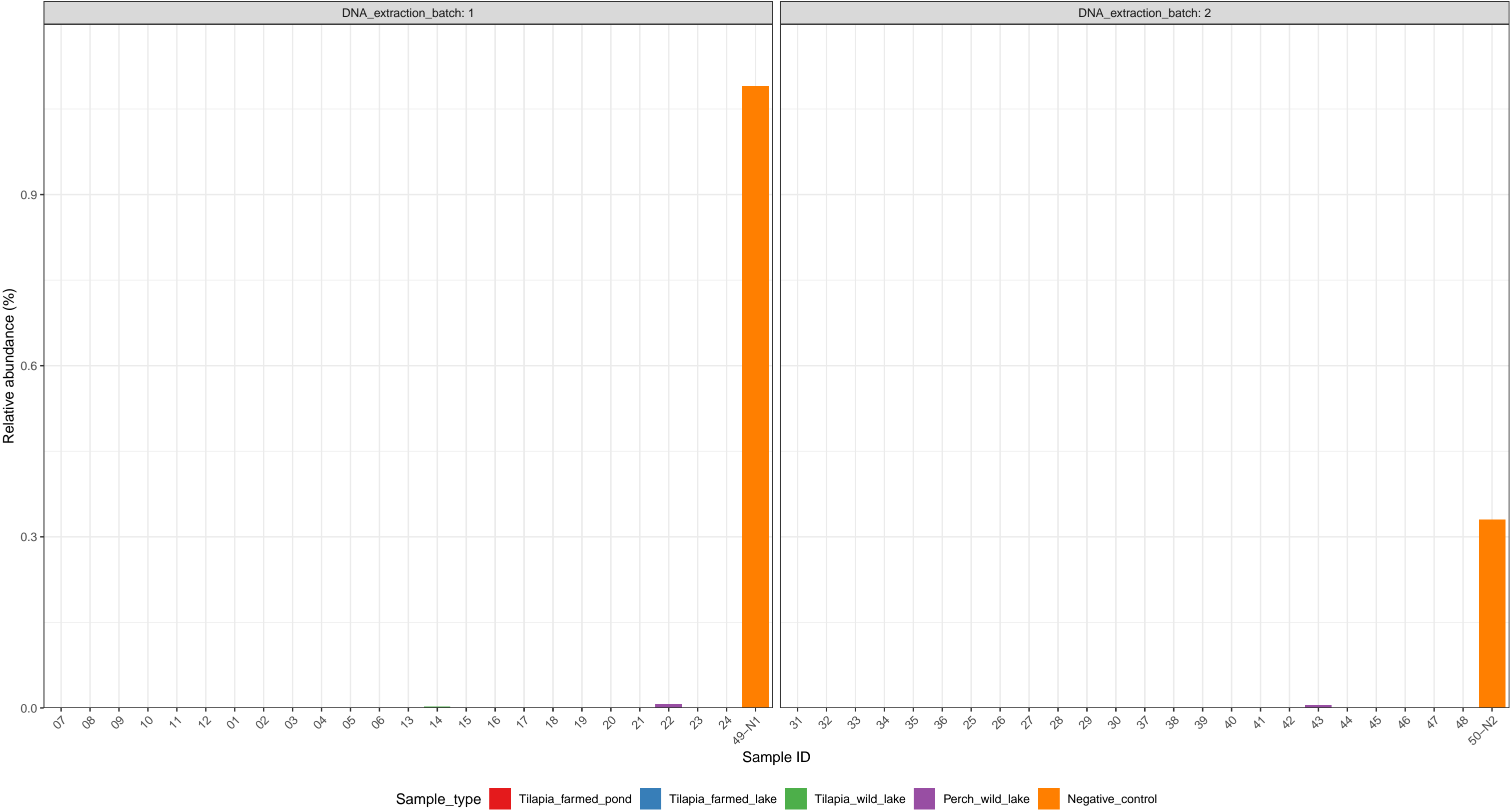
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featureID: 444cb870909dcd447934e3eb70c73738



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

featureID: 10a4ba9050a60c9880edf695bd202b6e



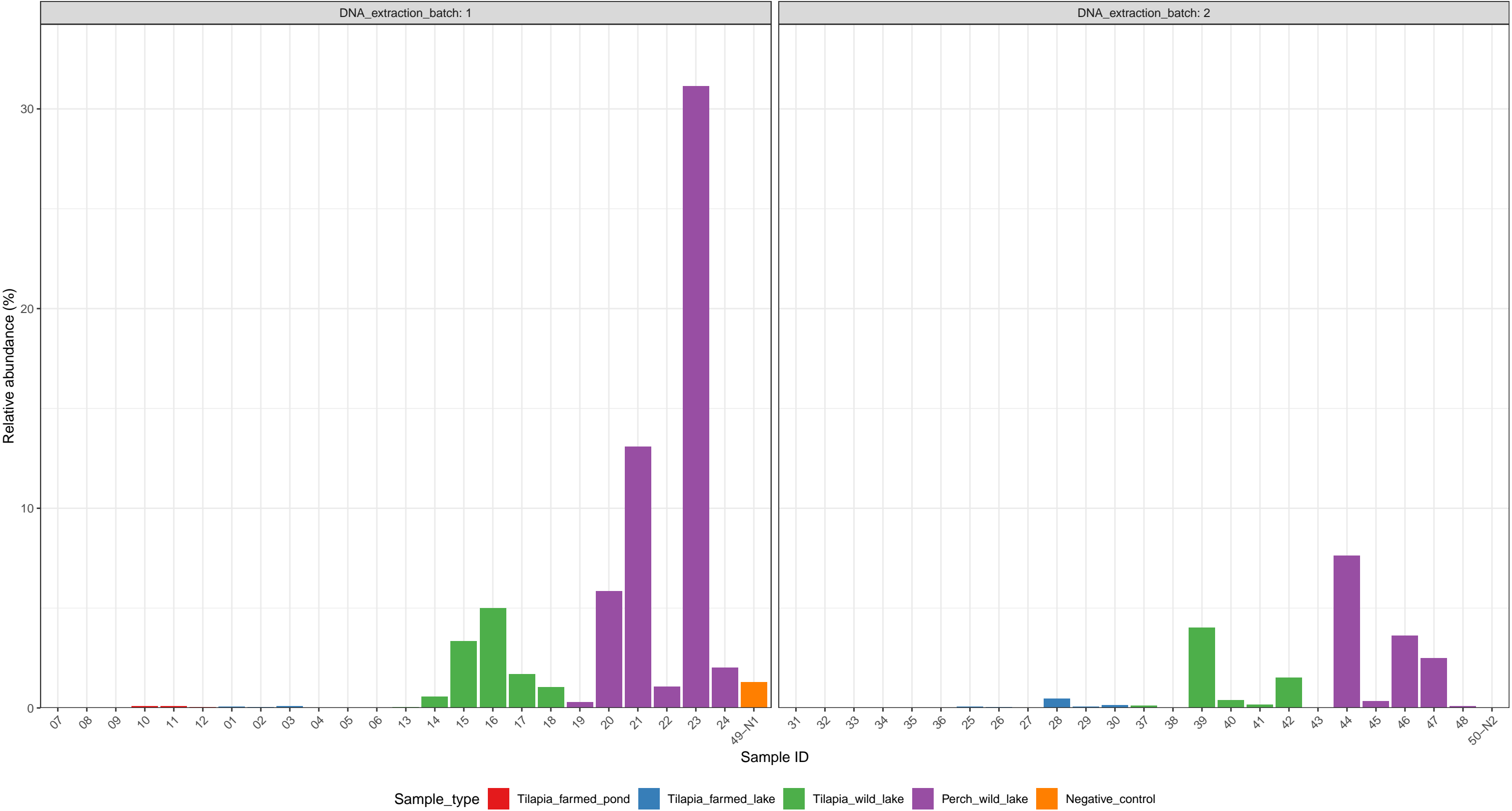
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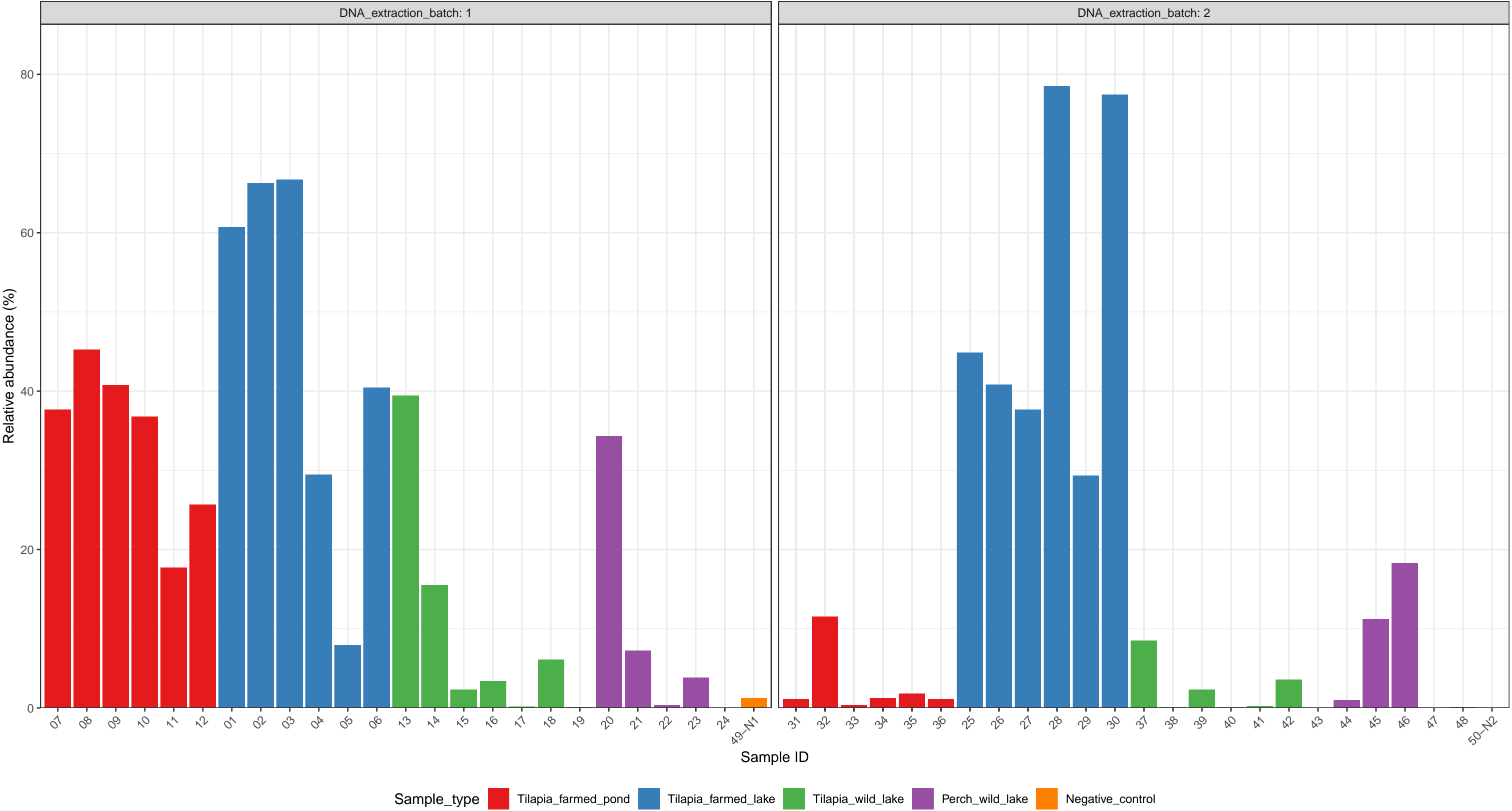
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacteriales; f__Enterobacteriaceae; g__Plesiomonas; NA

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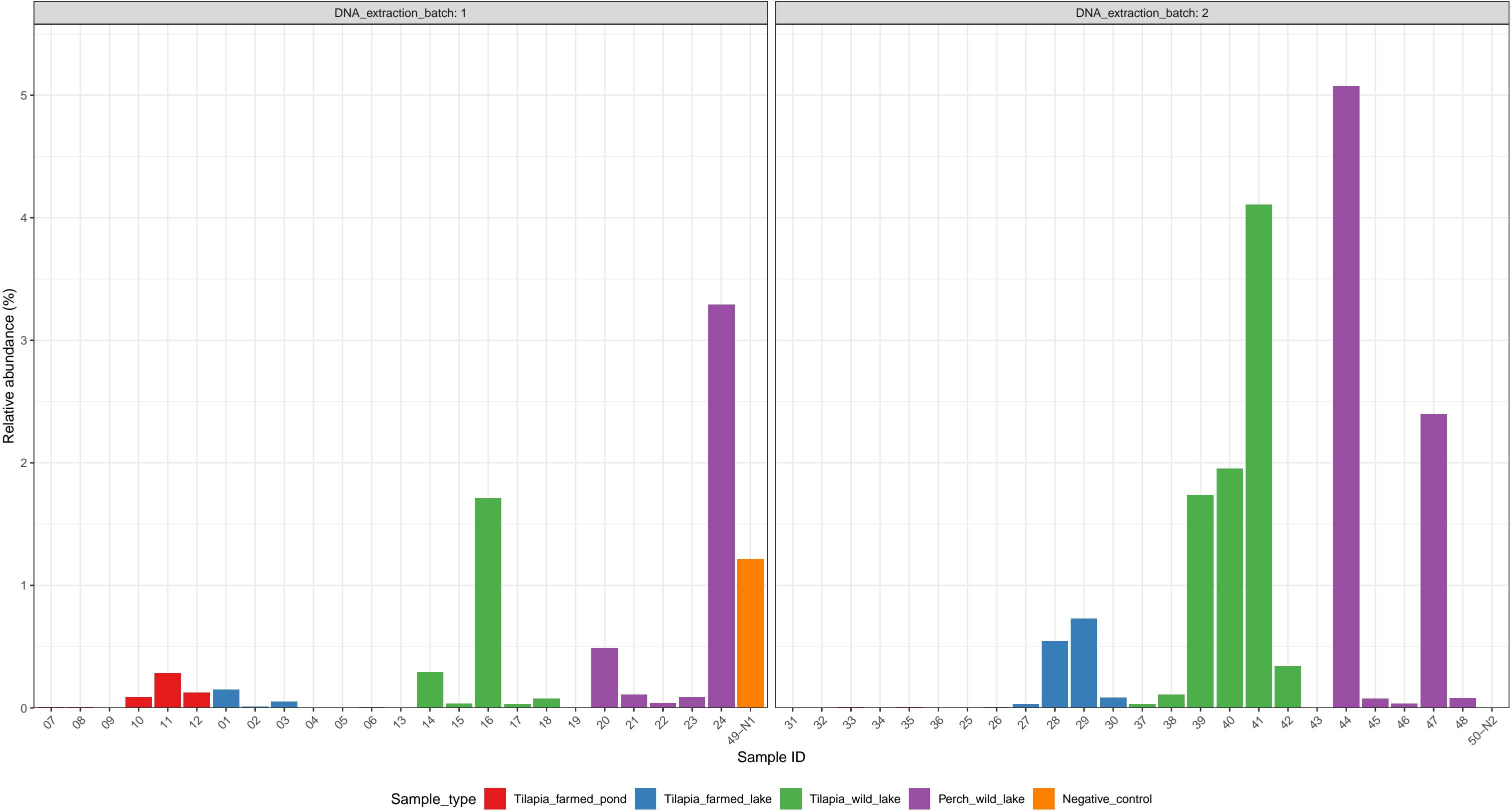
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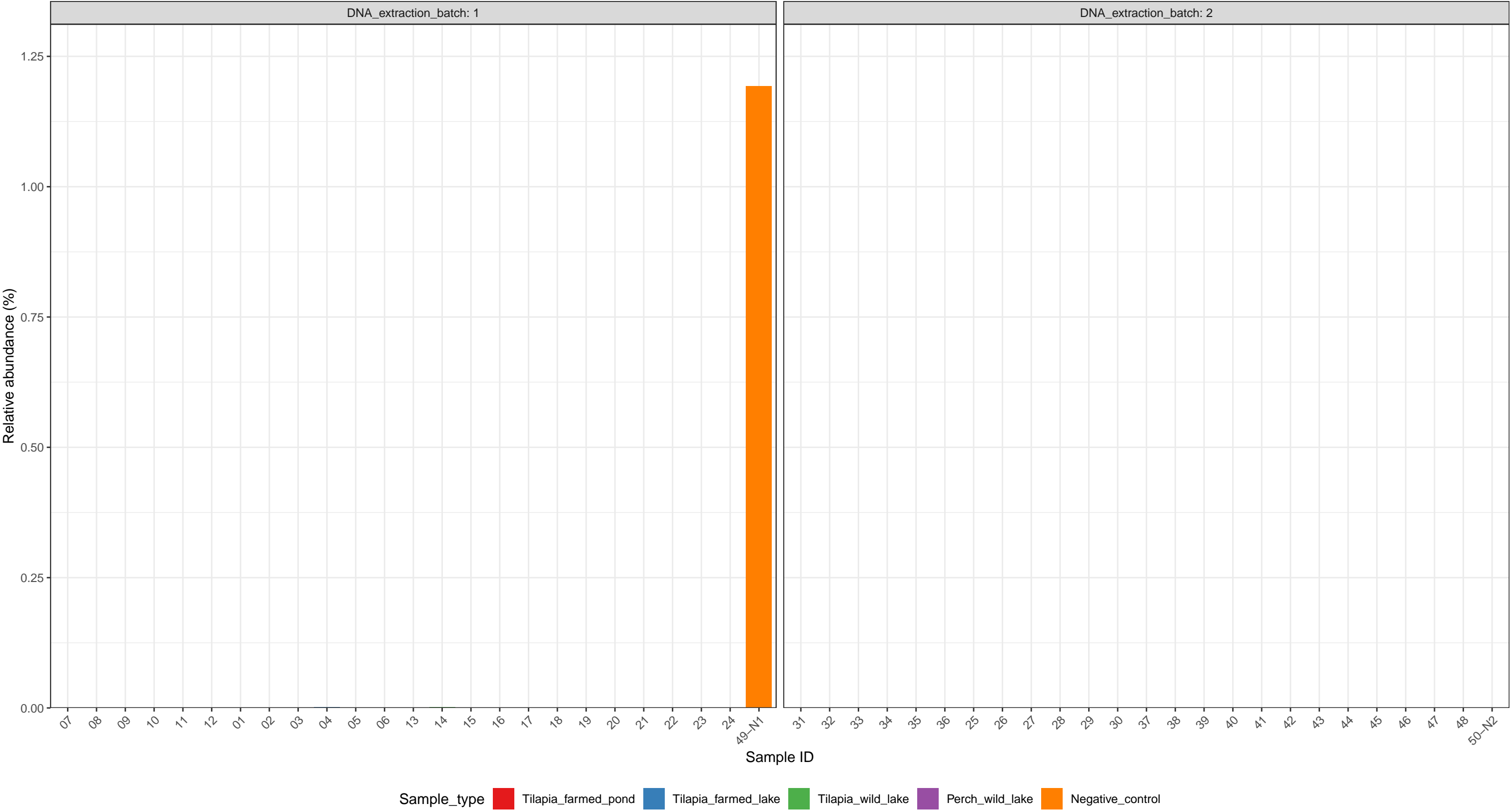
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featureID: f4b4dbd070c3296a6040e51b1e2aacfa



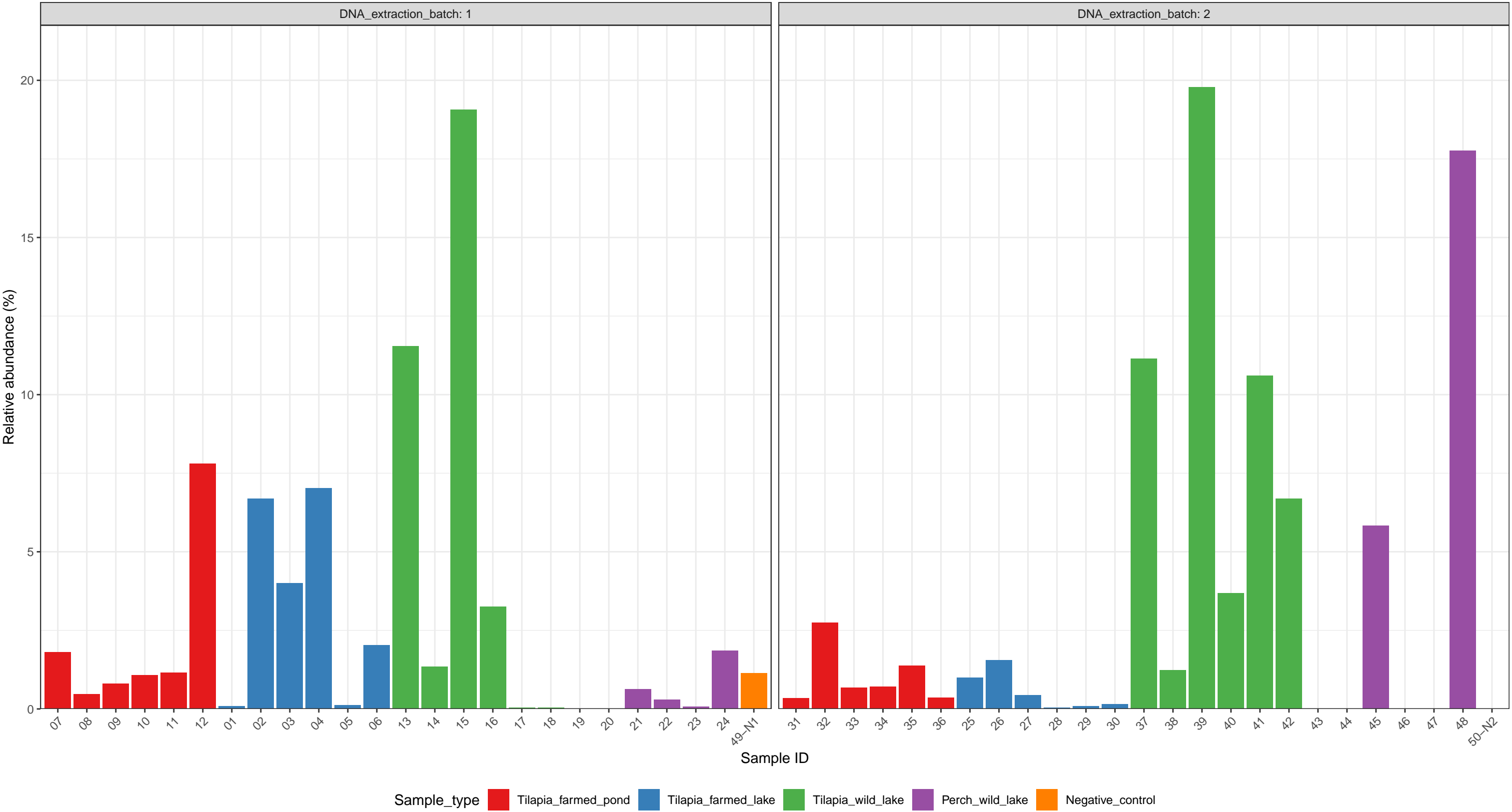
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Alteromonadales; f__Shewanellaceae; g__Shewanella; s__Shewanella algae

featureID: fadf78bc47e055f59328c8f565155ea5



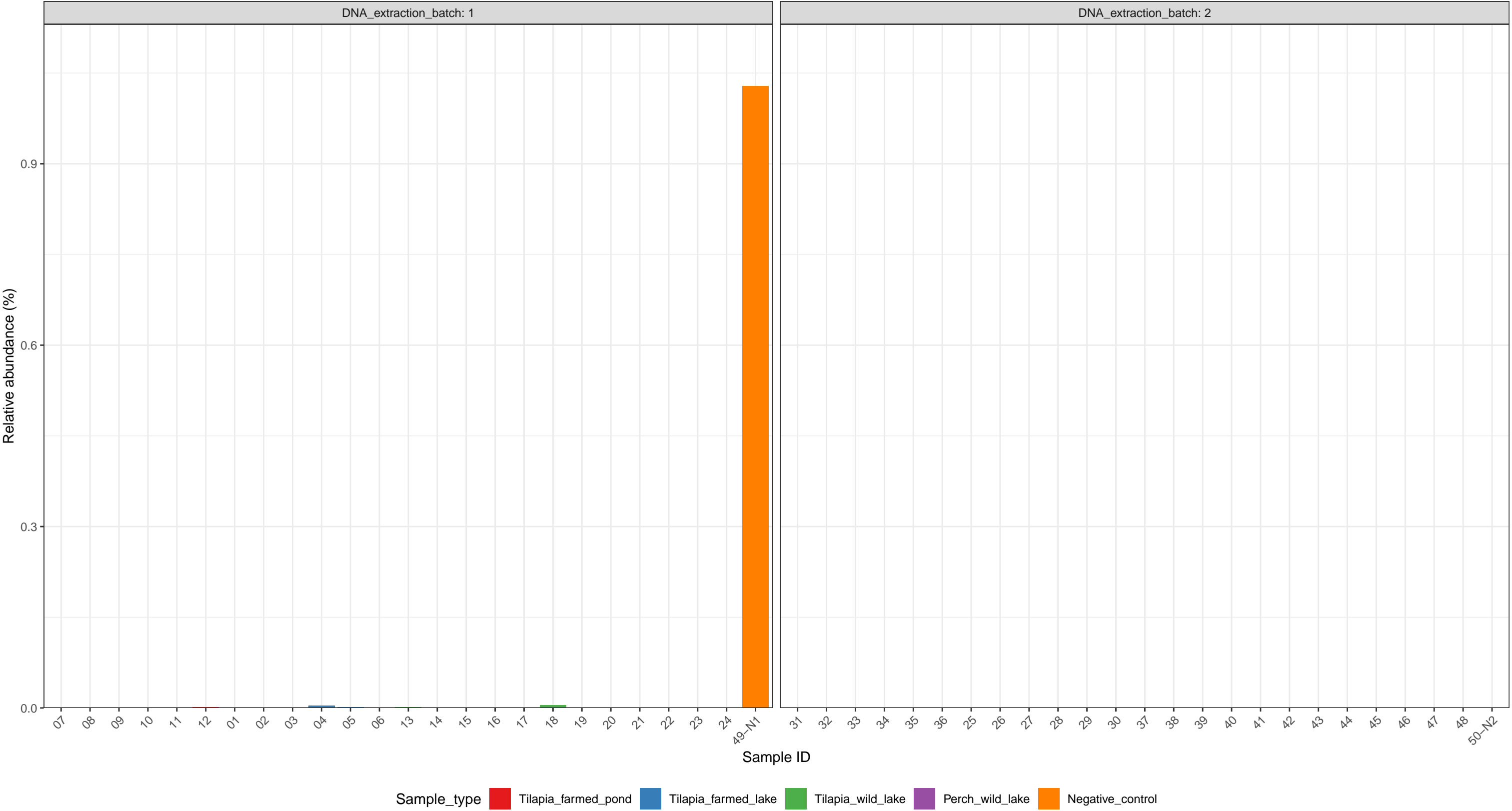
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featureID: efa98c673cef7e11e51b27d01167c2af



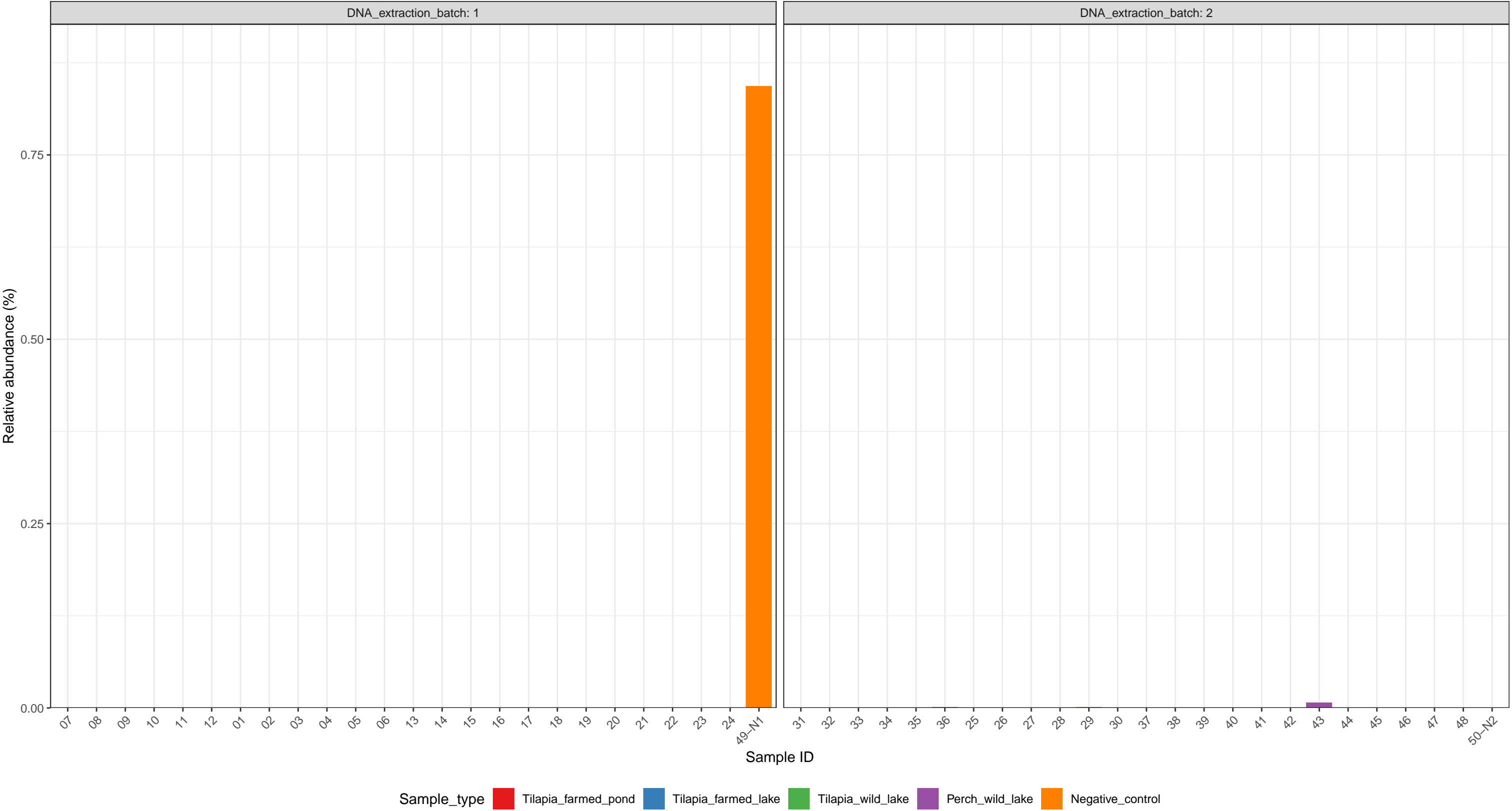
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales; f__Halomonadaceae; g__Halomonas; NA

featureID: 7f46b7ea18aa6ed4244429796401c660



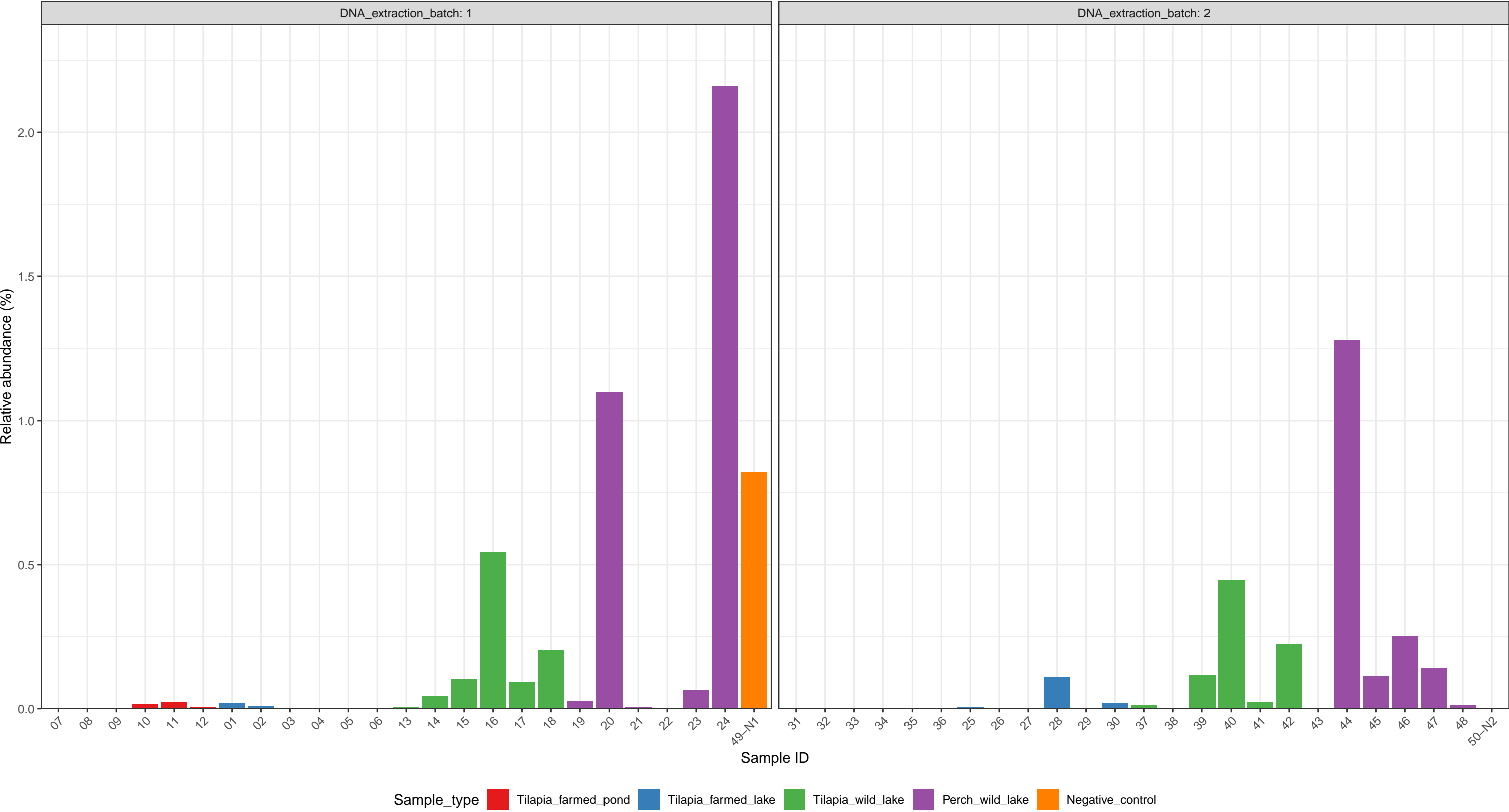
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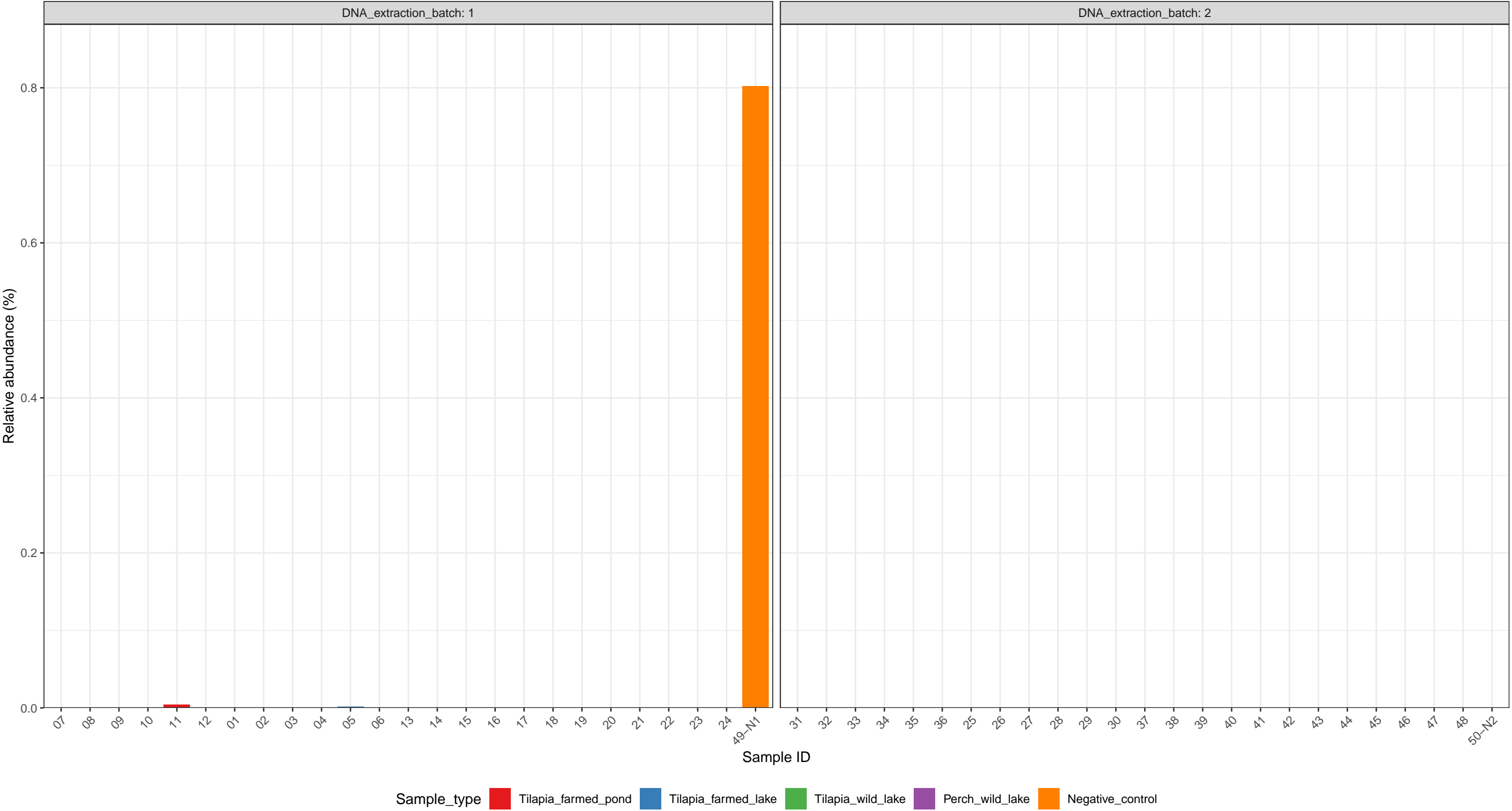
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacteriales; f__Enterobacteriaceae; g__Plesiomonas; Ambiguous_taxa

featureID: 4d951a112c225bc3bdfd2d0cfec2b2d3



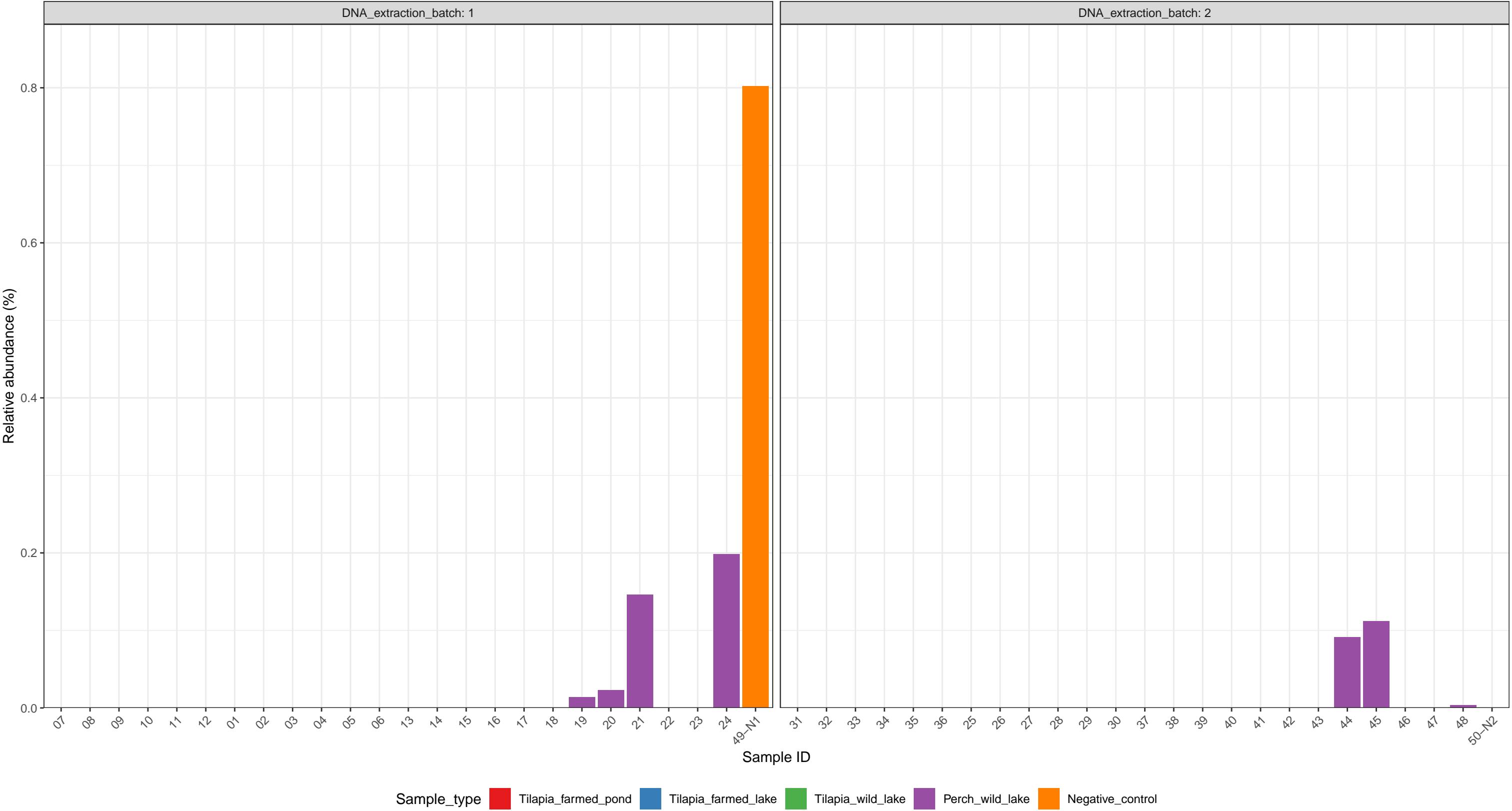
k__Bacteria; p__Acidobacteria; c__Acidobacteriia; o__Acidobacteriales; f__Acidobacteriaceae (Subgroup 1); g__Bryocella; s__uncultured bacterium

featureID: 92eda480cf7a77d3e7b6890877207fe6



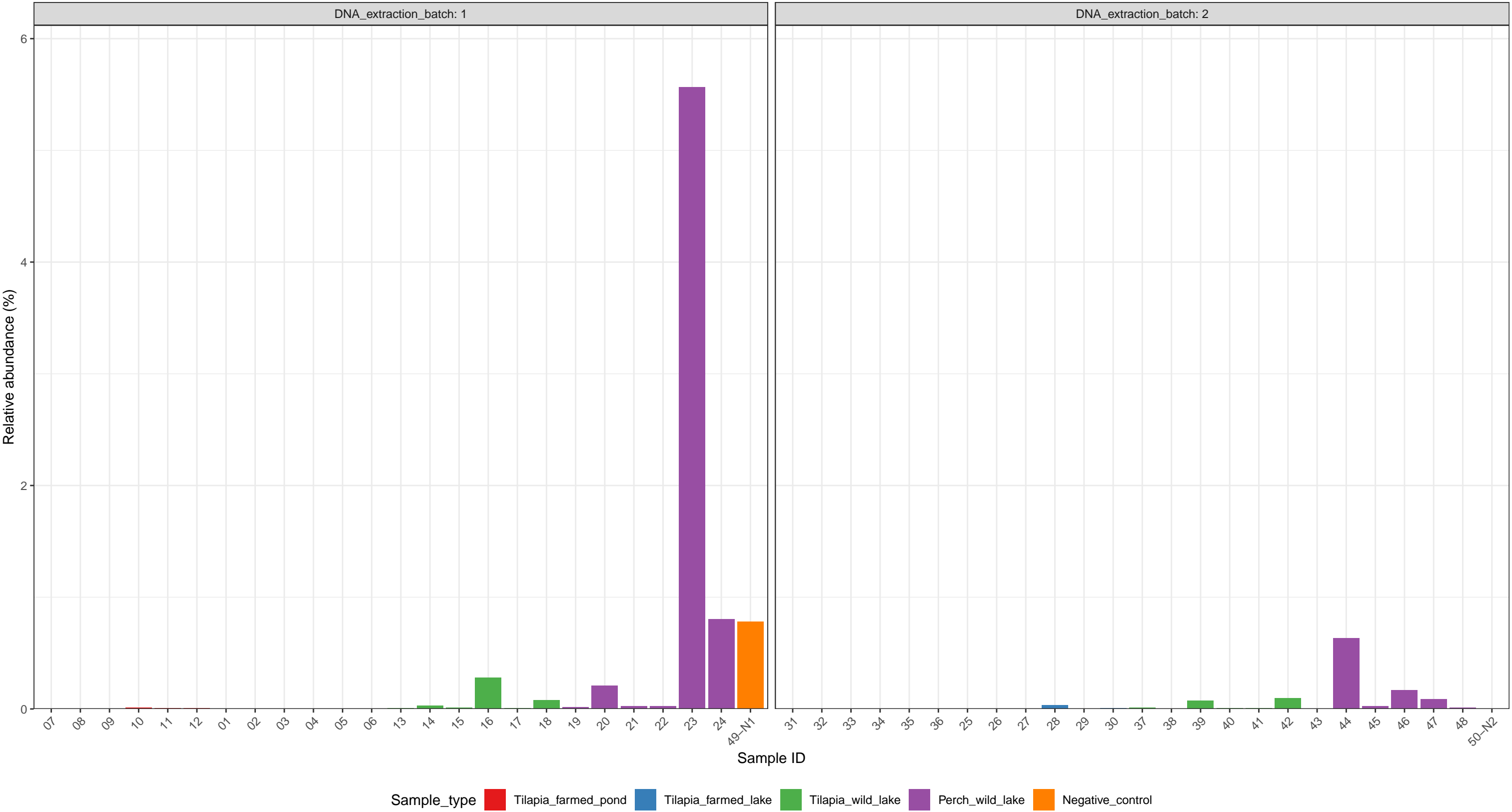
k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Clostridiaceae 1; g__Clostridium sensu stricto 1; NA

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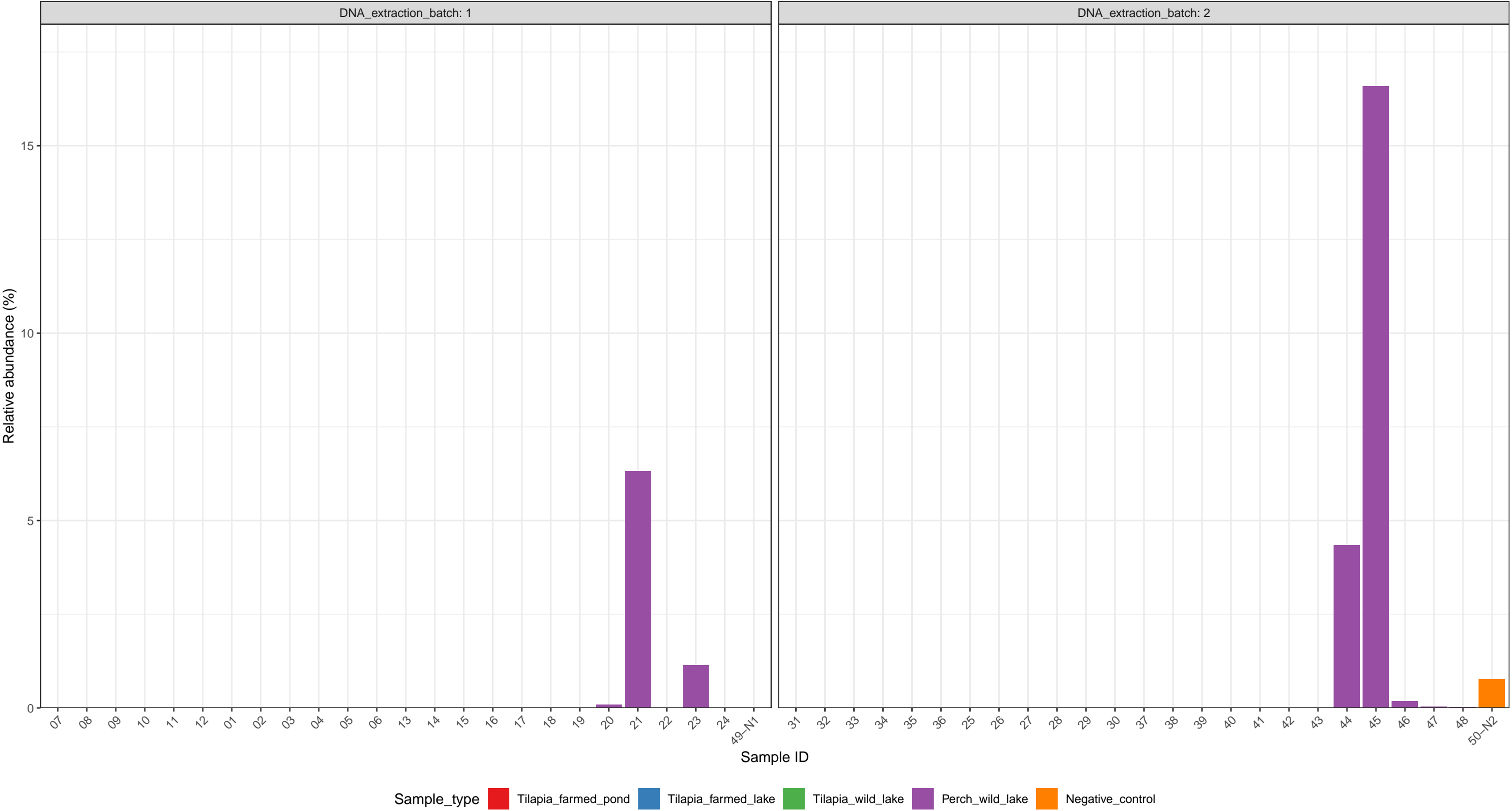
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacteriales; f__Enterobacteriaceae; g__Plesiomonas; Ambiguous_taxa

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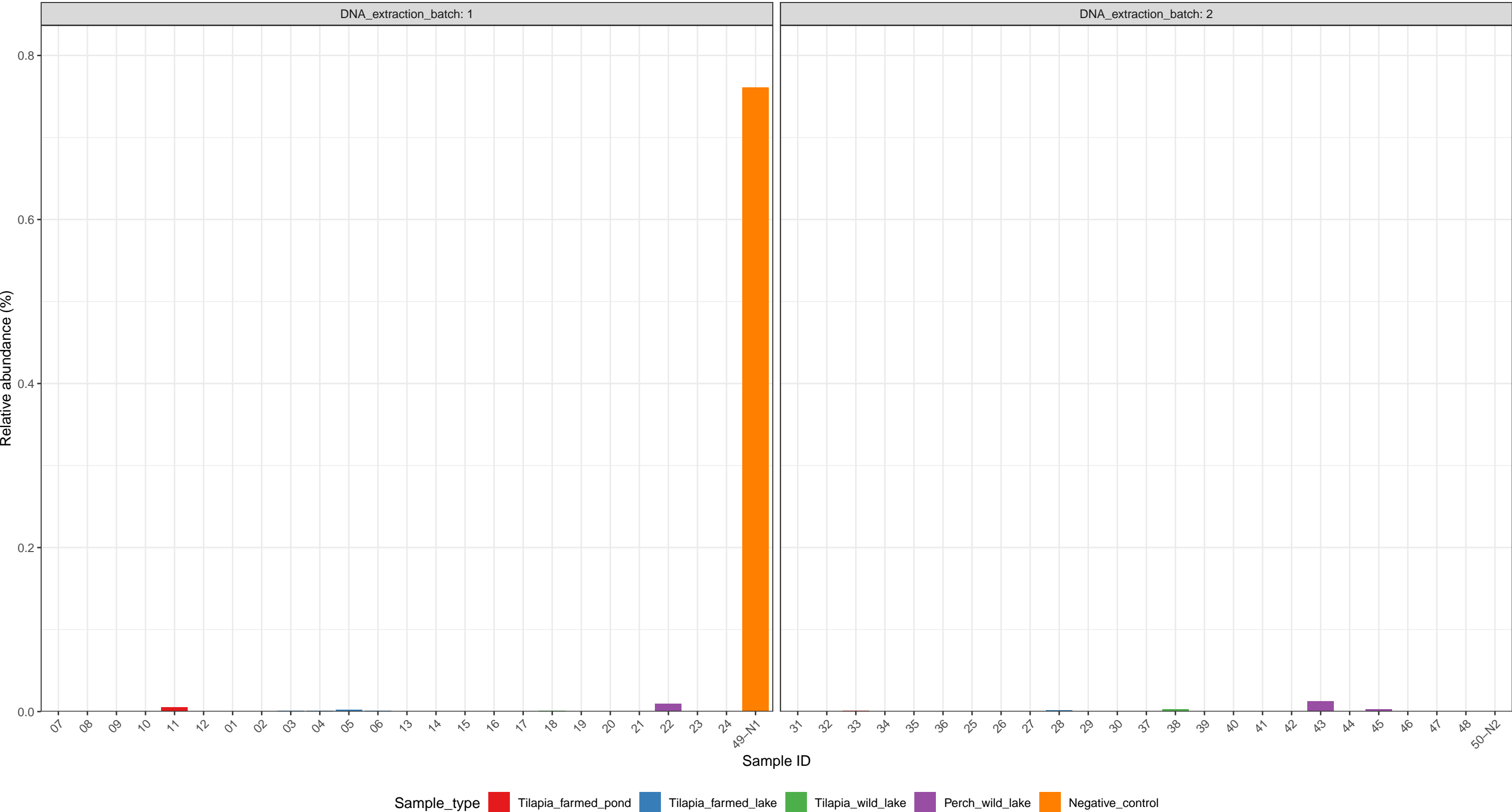
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featureID: d36c9dfa26099ffe57512e6dfbe0b8



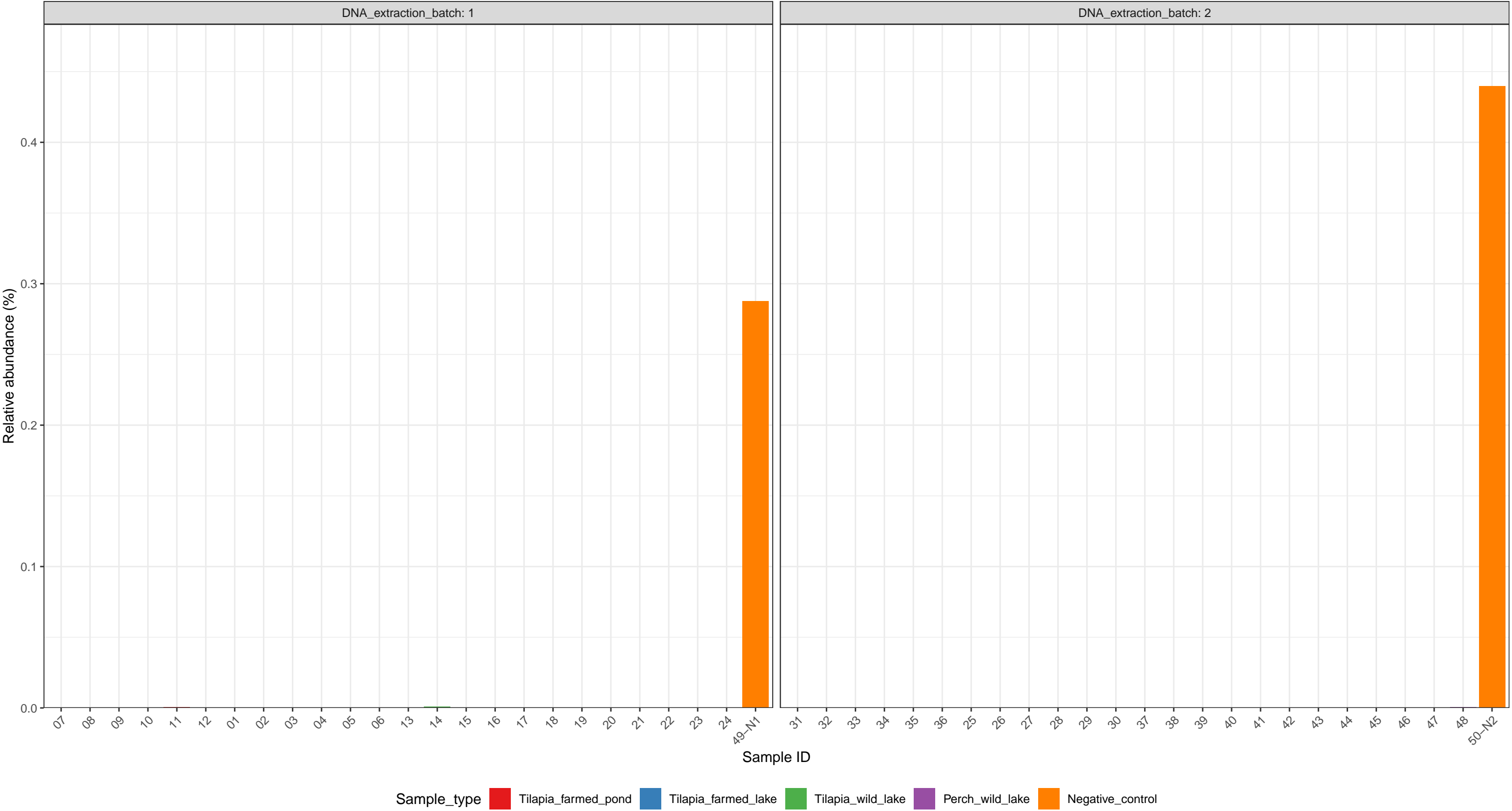
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Betaproteobacteriales; f__Burkholderiaceae; g__Ralstonia; NA

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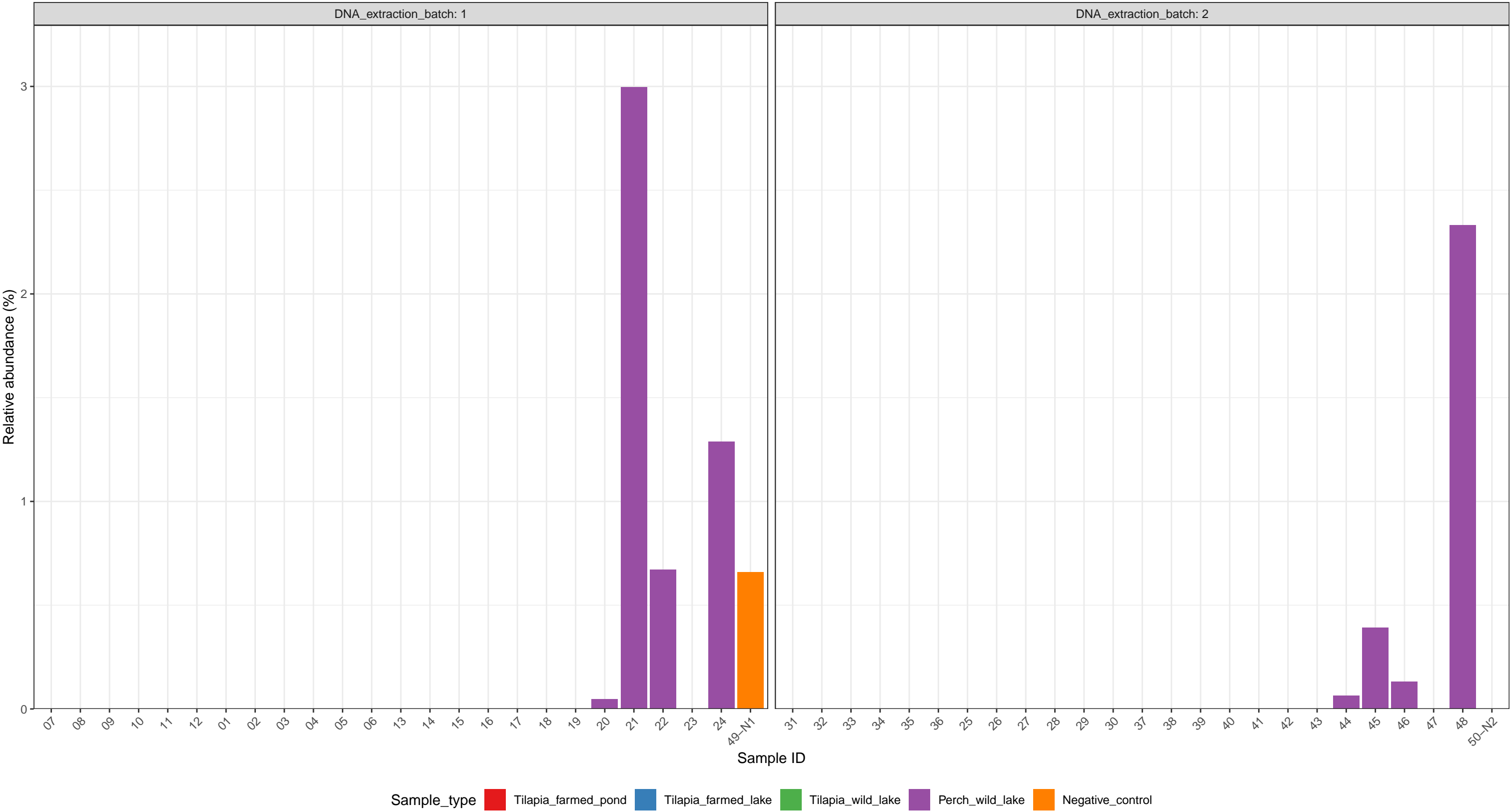
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featureID: 8f2ddde9ccf2d7afe5abf35614fe5b43



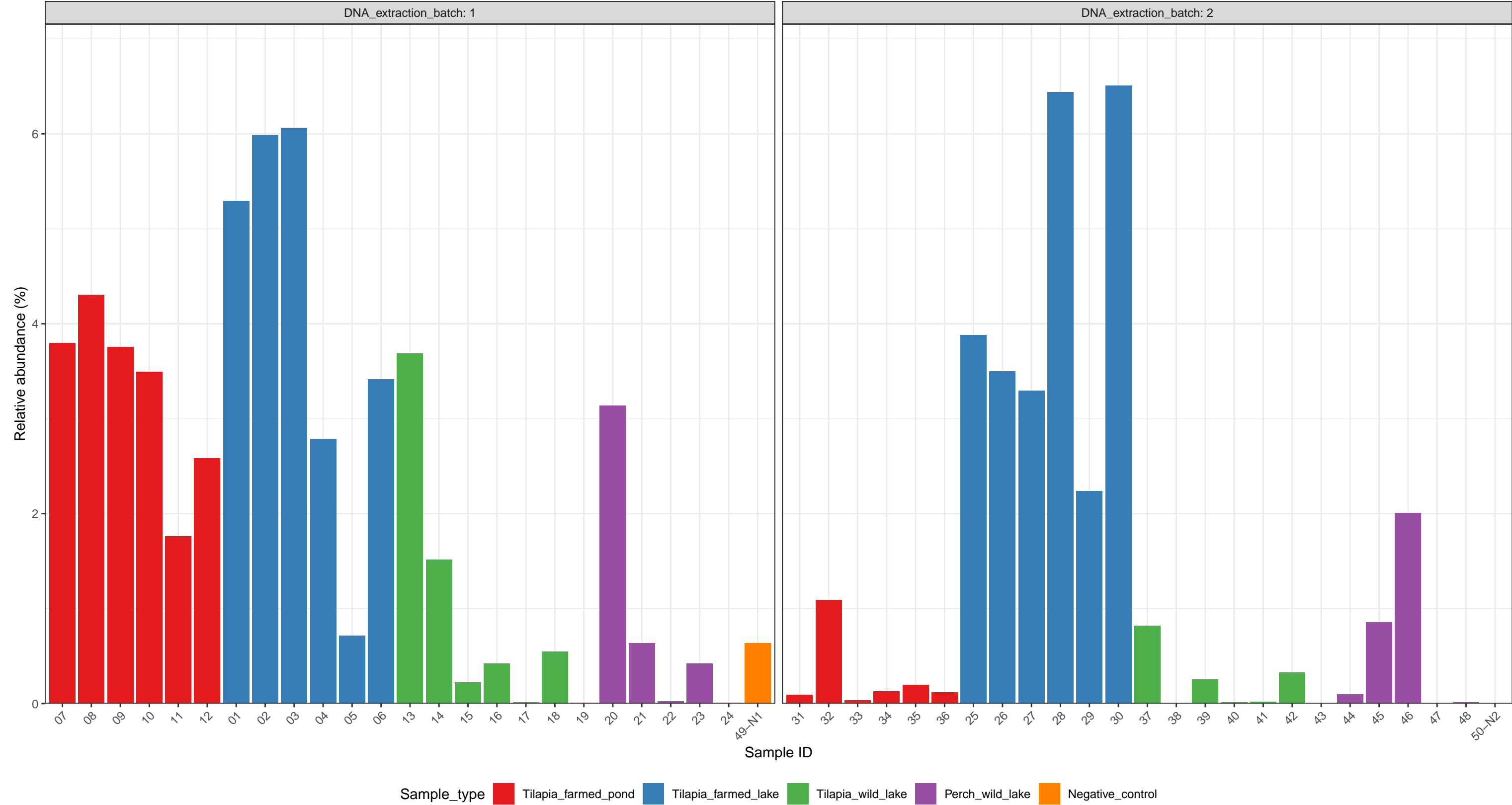
k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Clostridiaceae 1; g__Candidatus Arthromitus; NA

featureID: 249270189cd8e1c30eb0d62d77589cb8



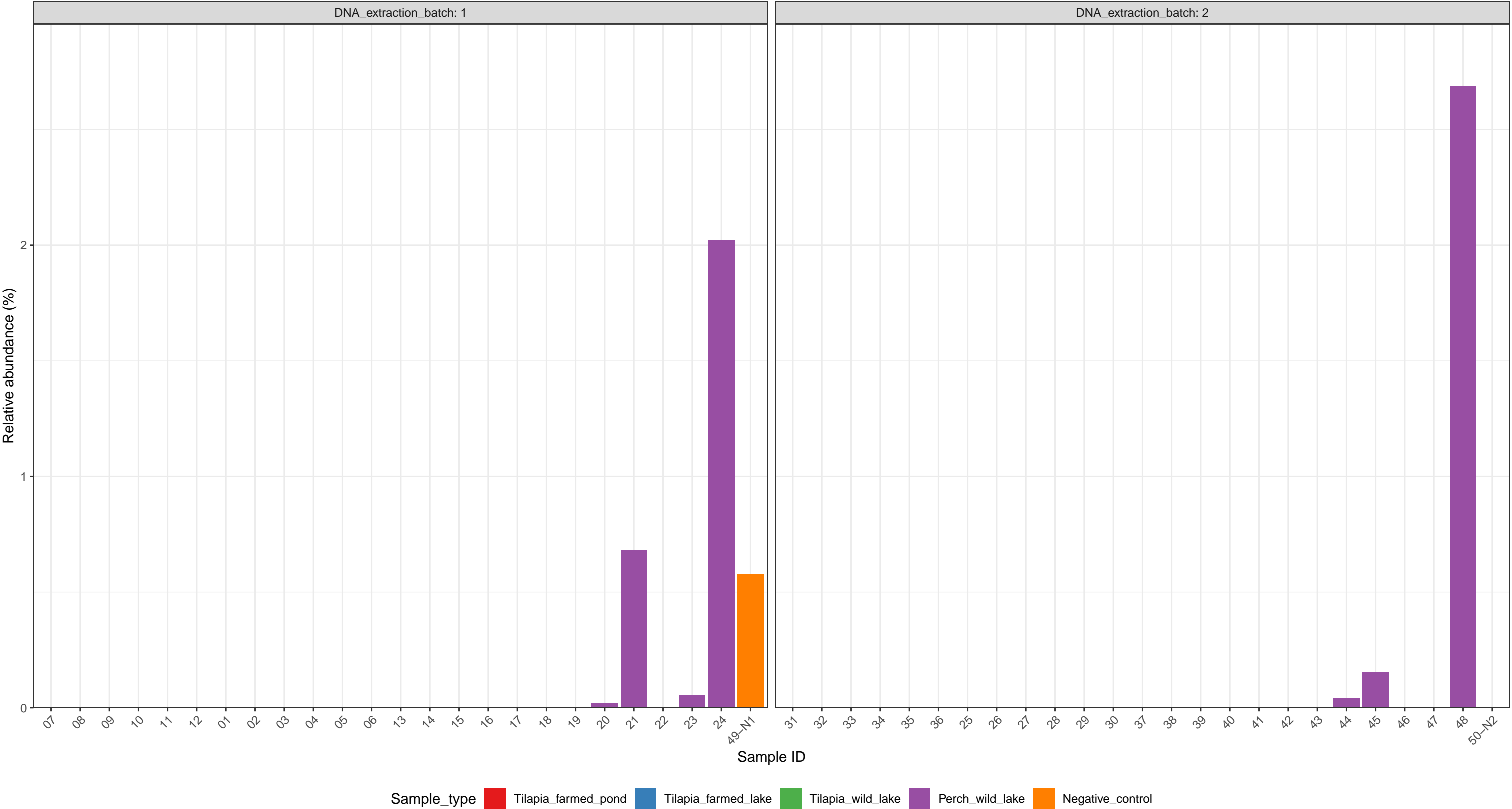
k__Bacteria; p__Fusobacteria; c__Fusobacteriia; o__Fusobacteriales; f__Fusobacteriaceae; g__Cetobacterium; s__uncultured bacterium

featureID: 7732d6712ceae4666bd66aba7880c6f1



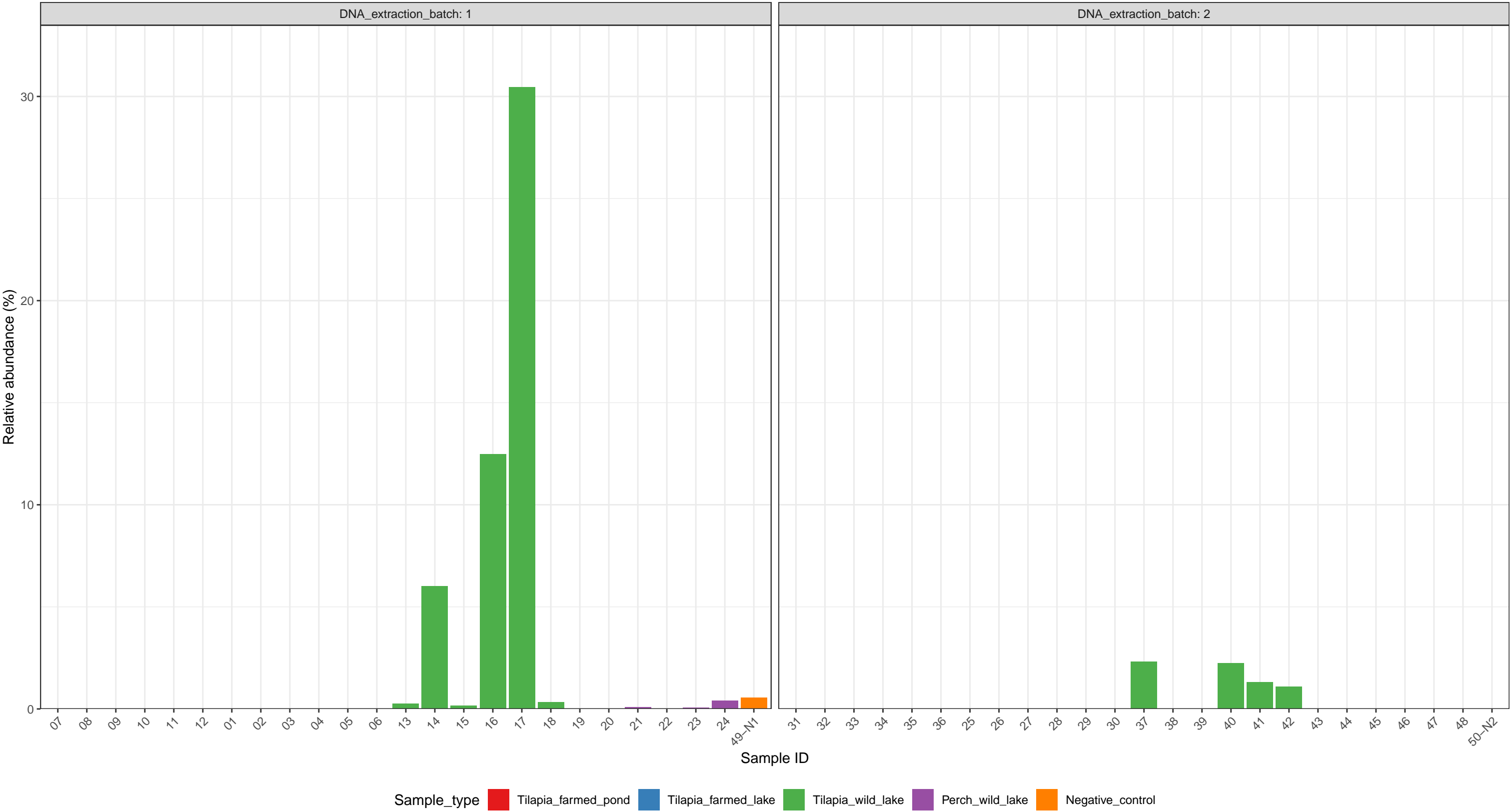
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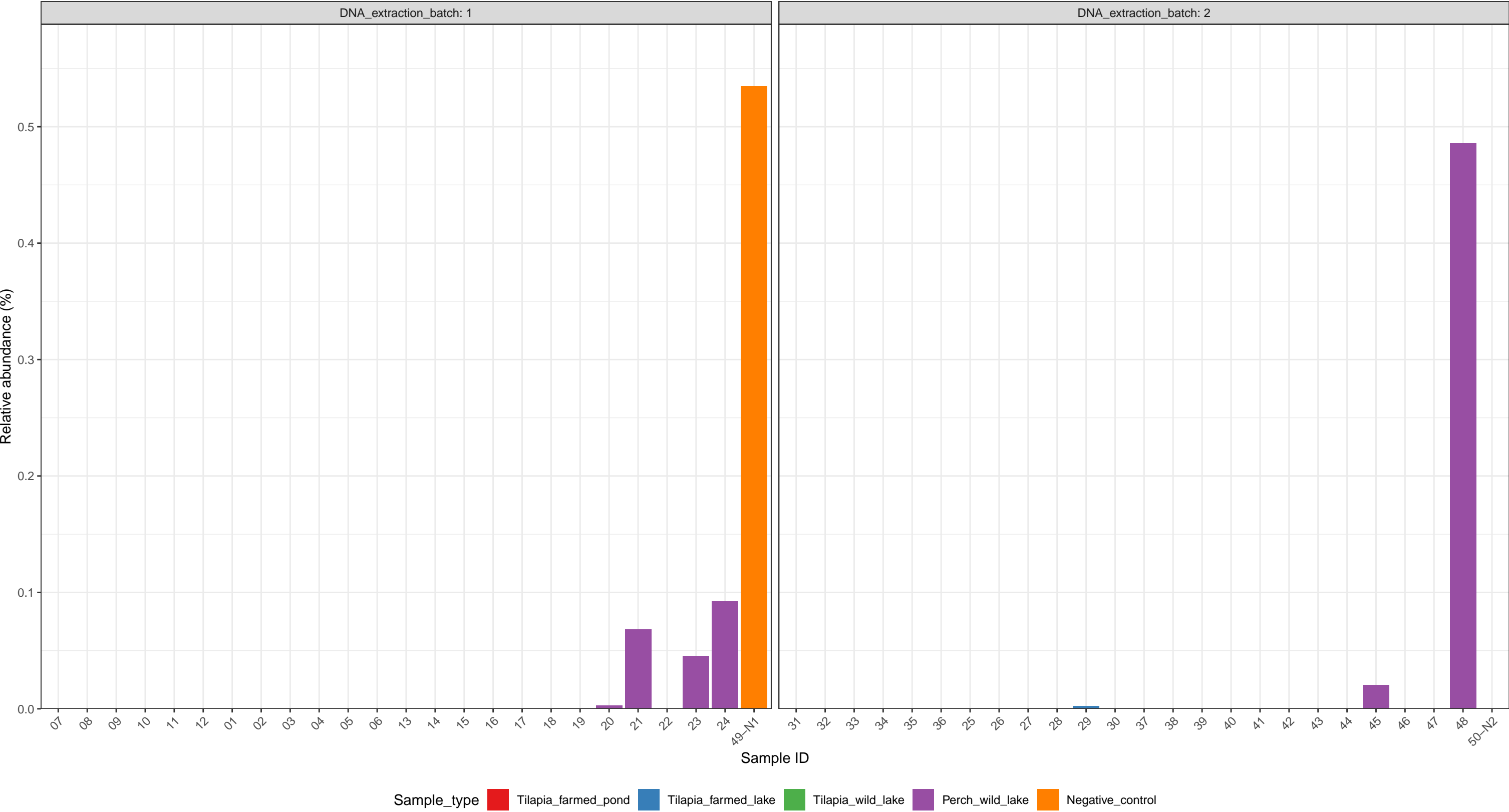
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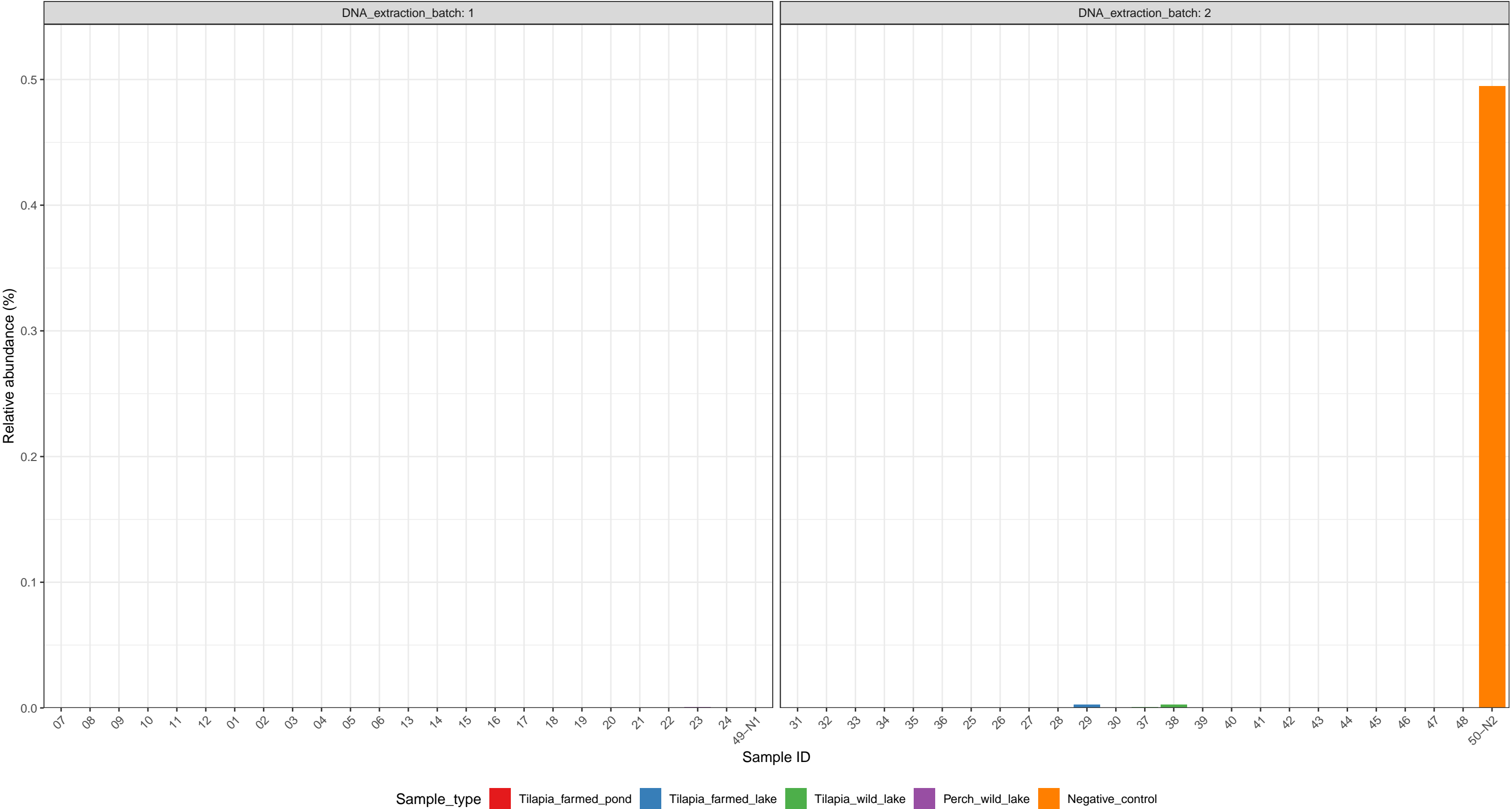
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featureID: 4852811146dcf523a9ecf810088a2da5



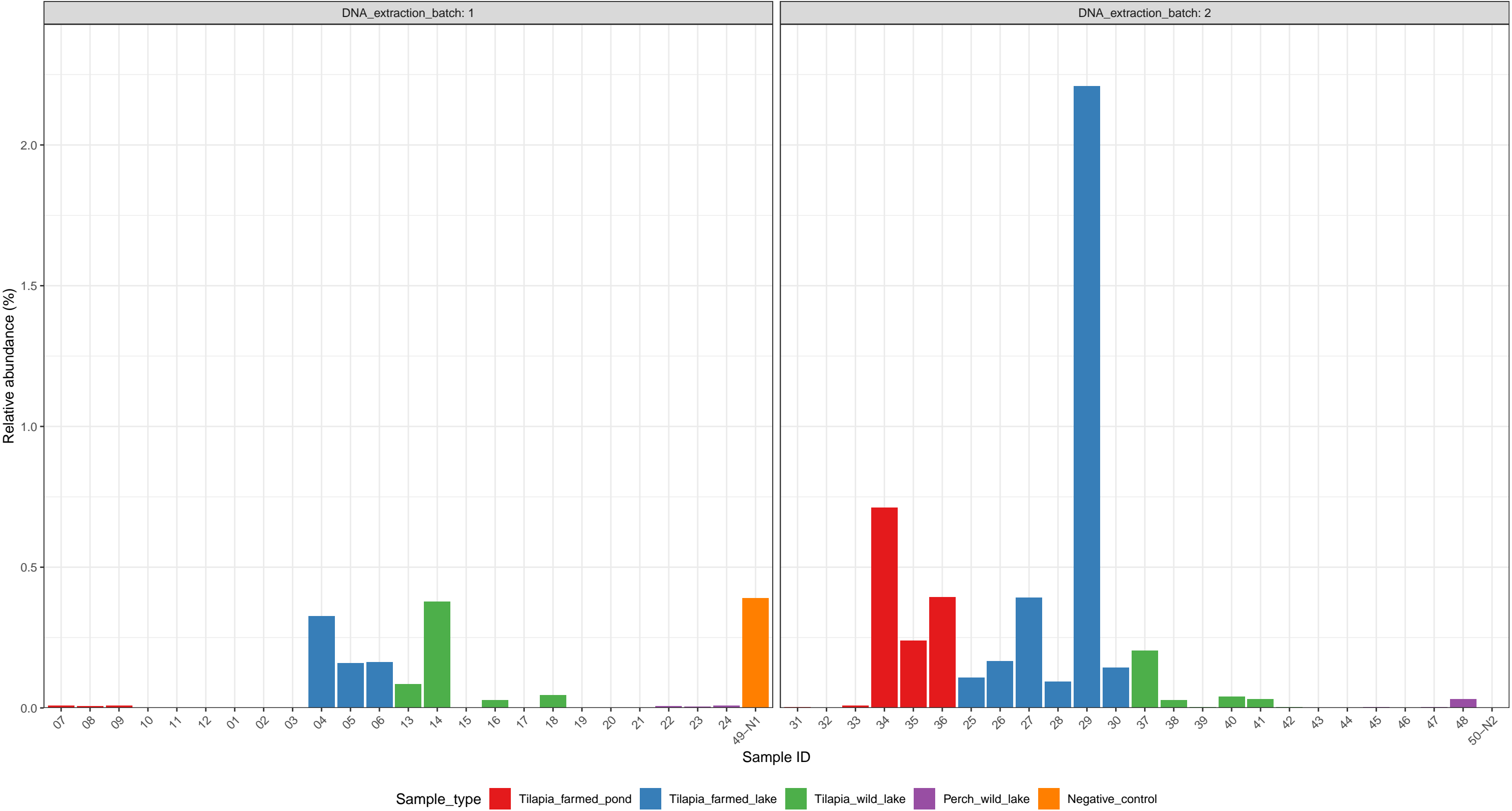
k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Staphylococcaceae; g__Staphylococcus; NA

featureID: 62611dedc42201591d0c89973f903dde



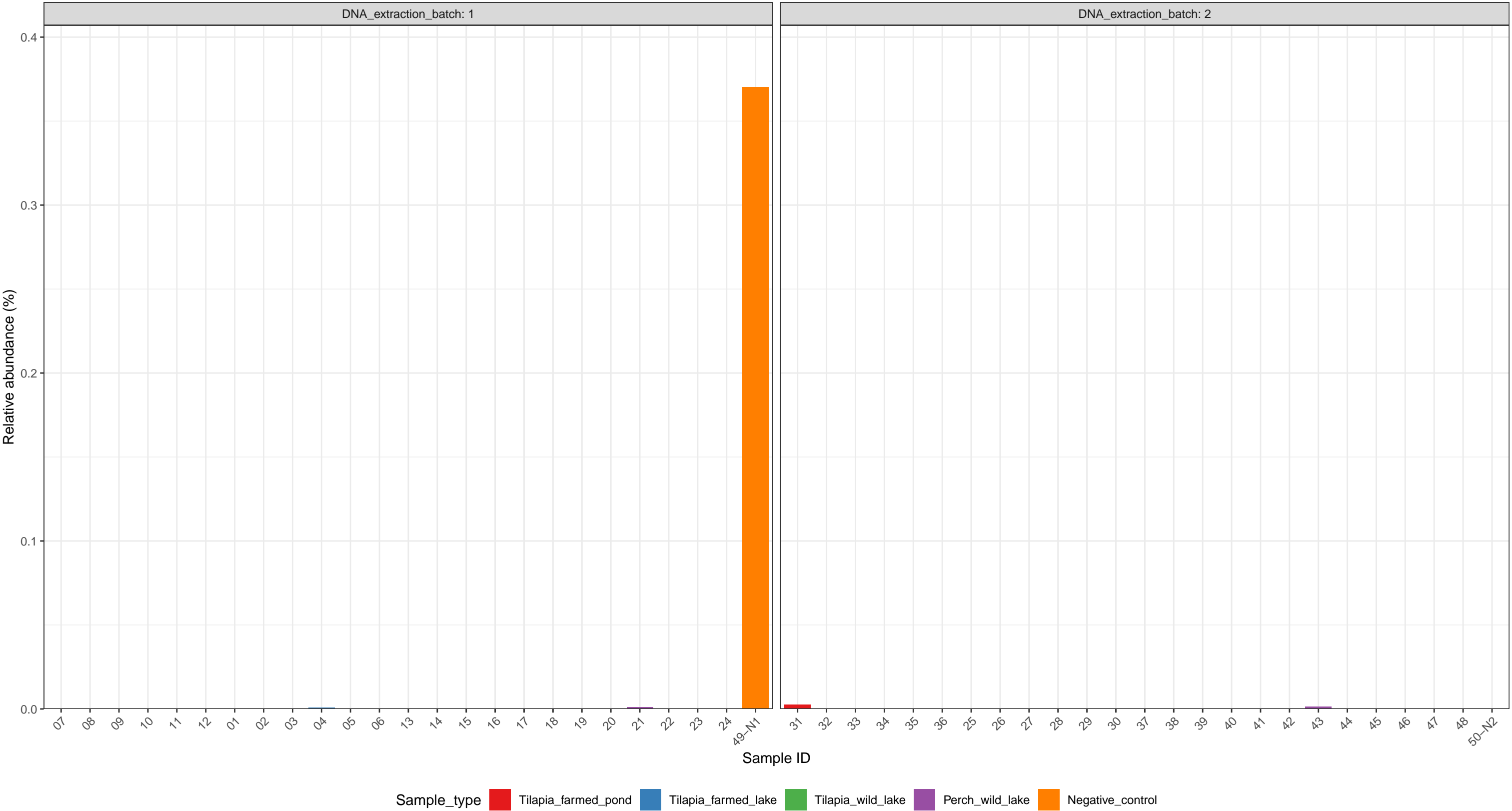
k__Bacteria; p__Verrucomicrobia; c__Verrucomicrobiae; o__Chthoniobacterales; f__Chthoniobacteraceae; g__LD29; Ambiguous_taxa

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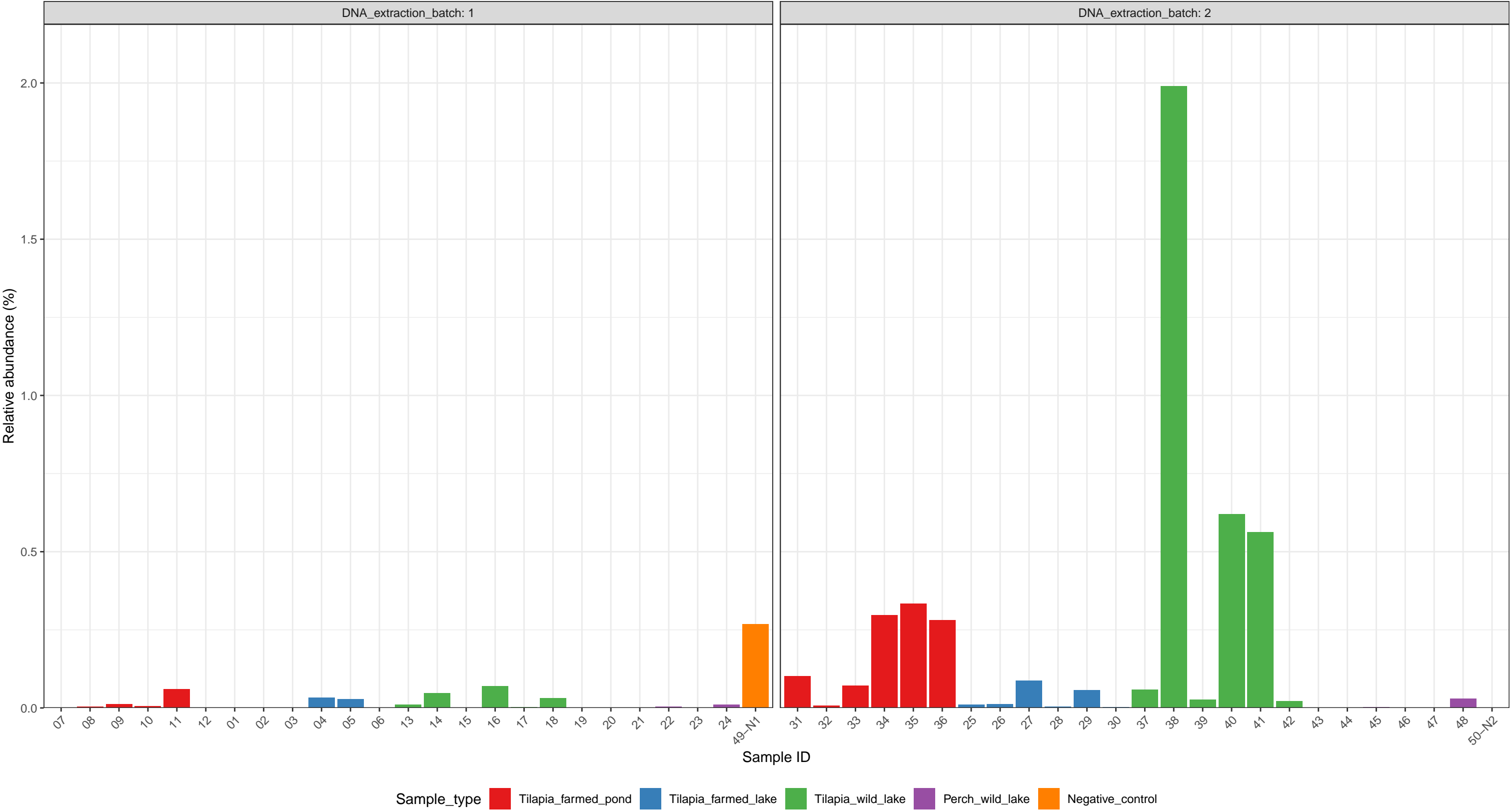
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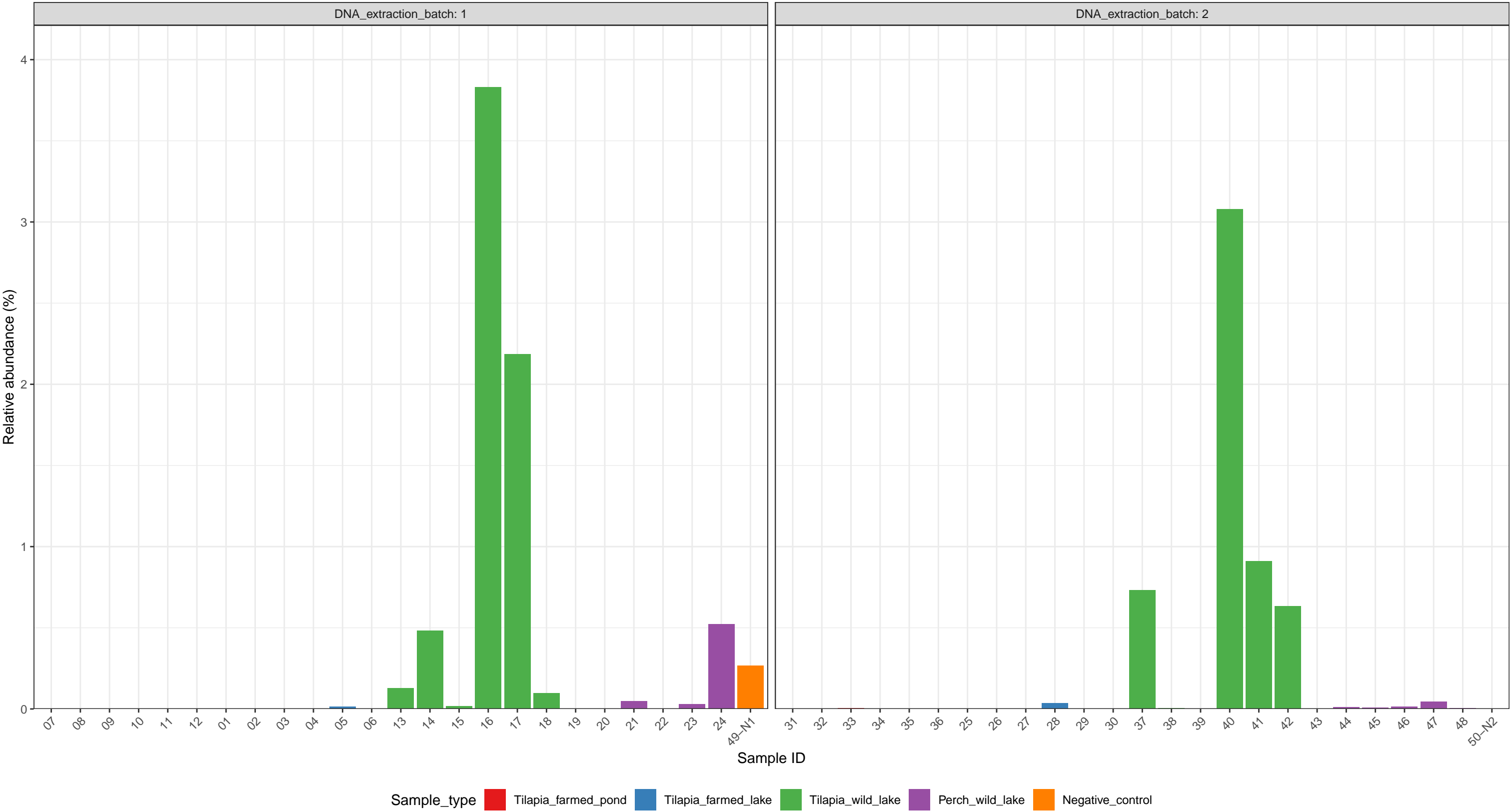
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Beijerinckiaceae; g__Methylocystis; NA

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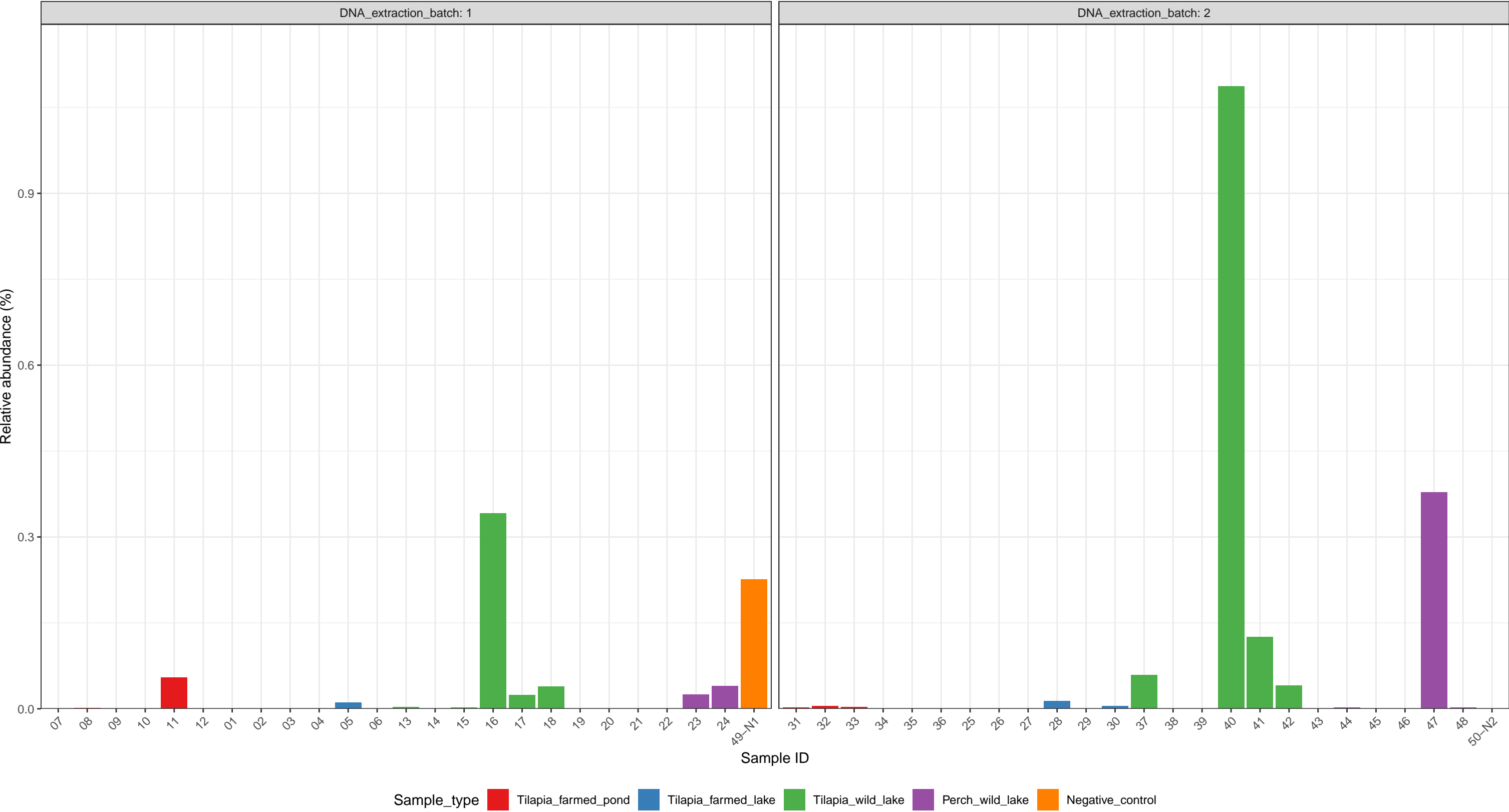
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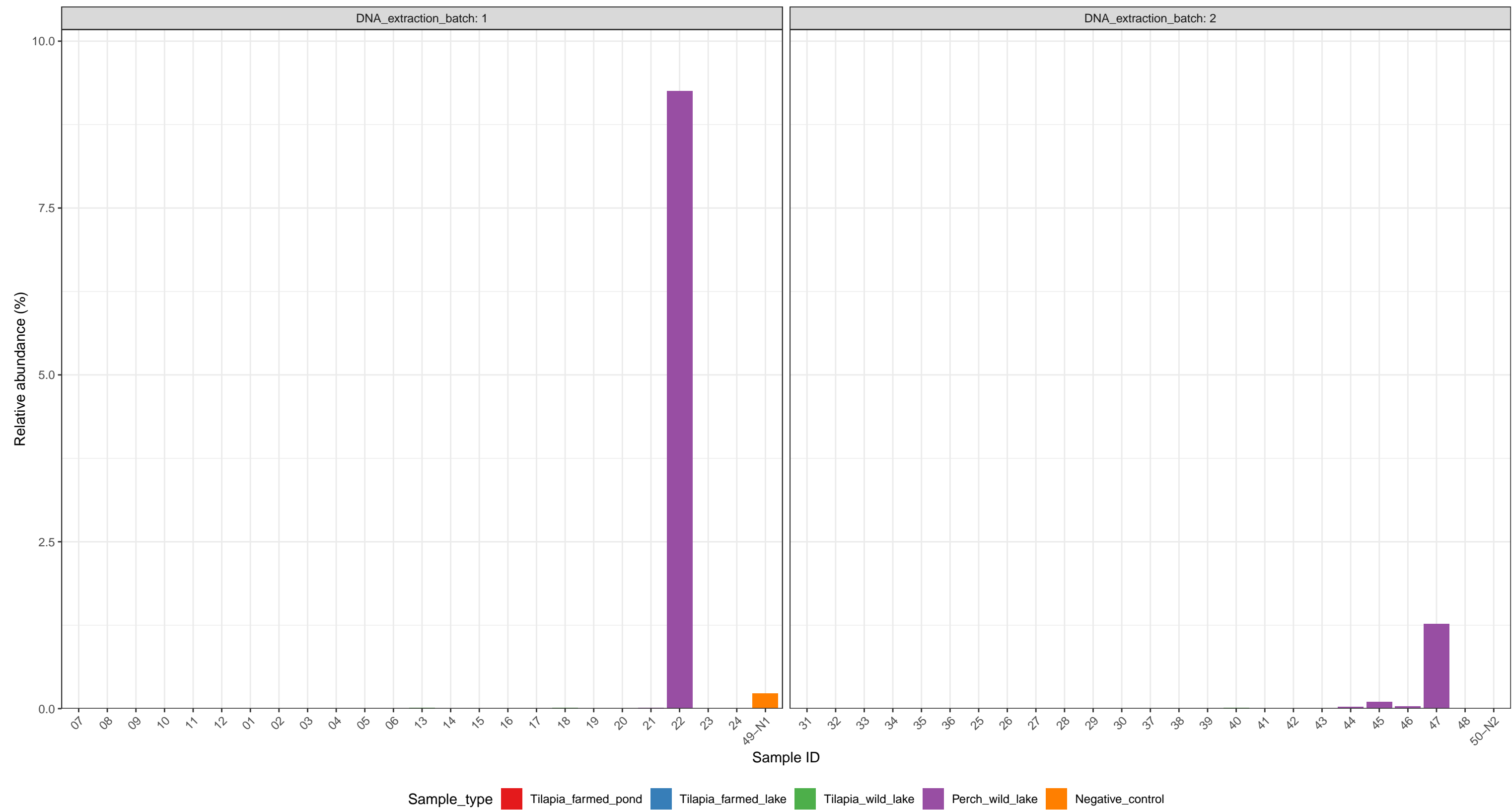
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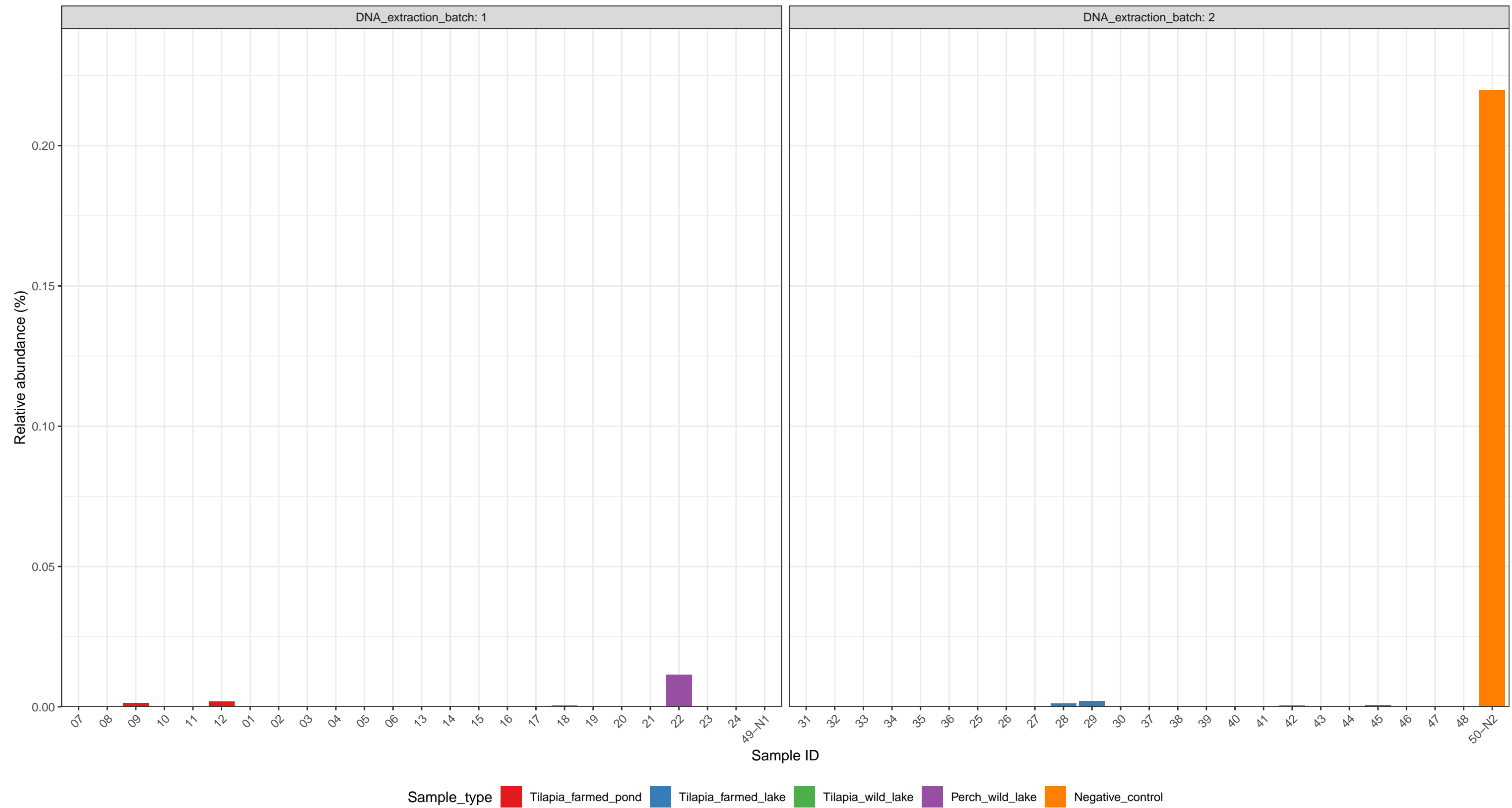
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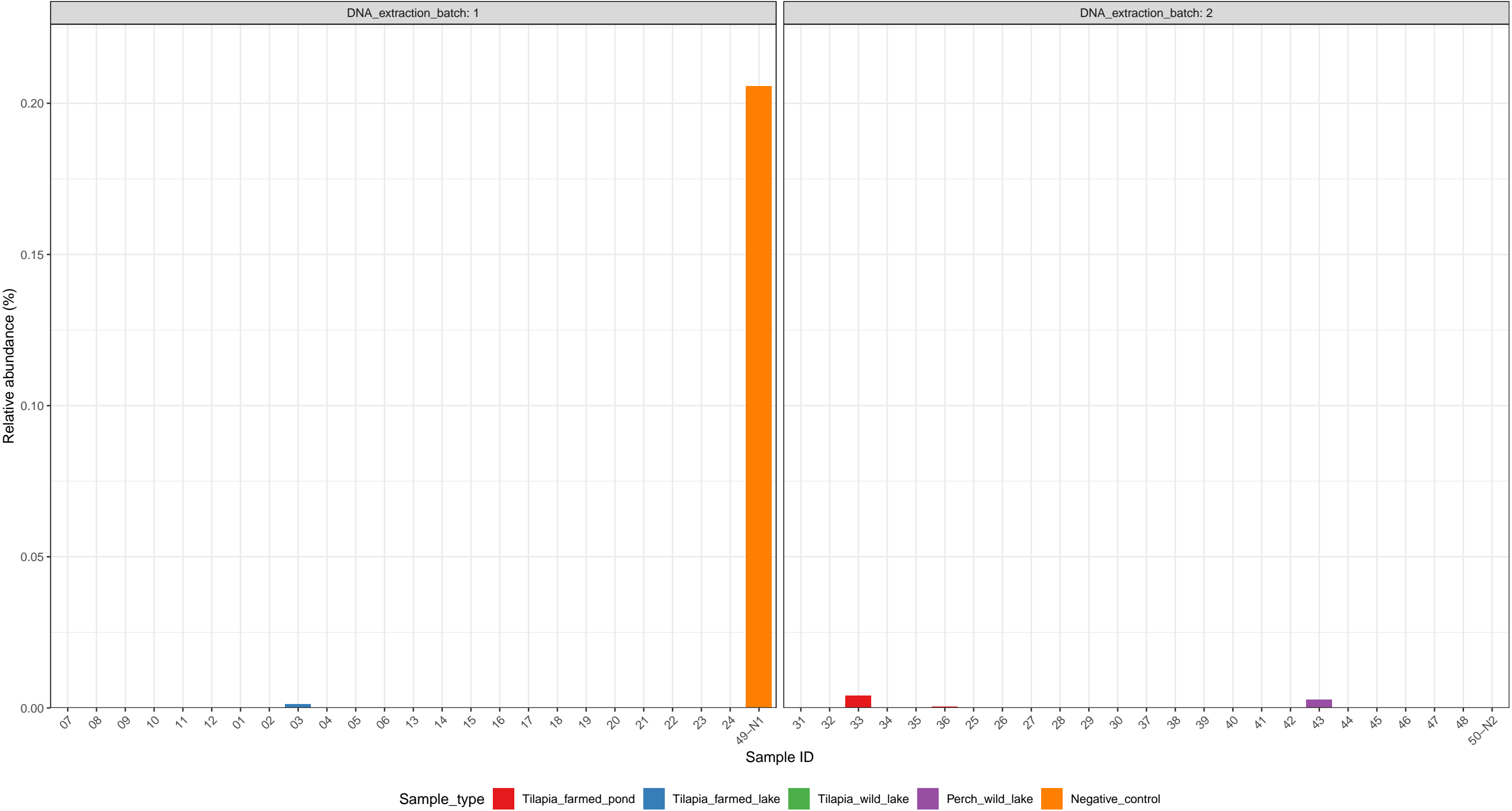
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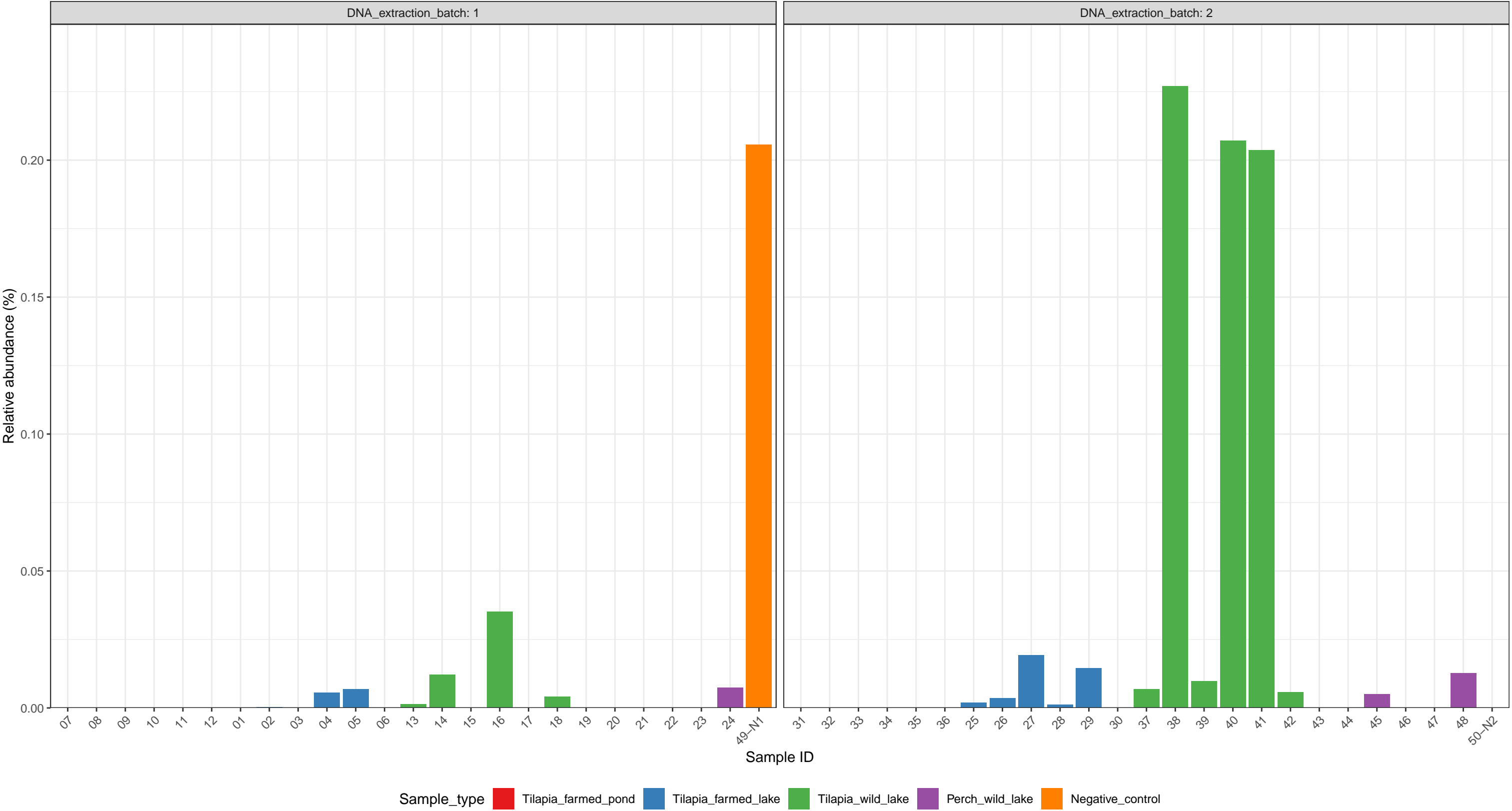
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Betaproteobacteriales; f__Burkholderiaceae; g__Ralstonia; NA

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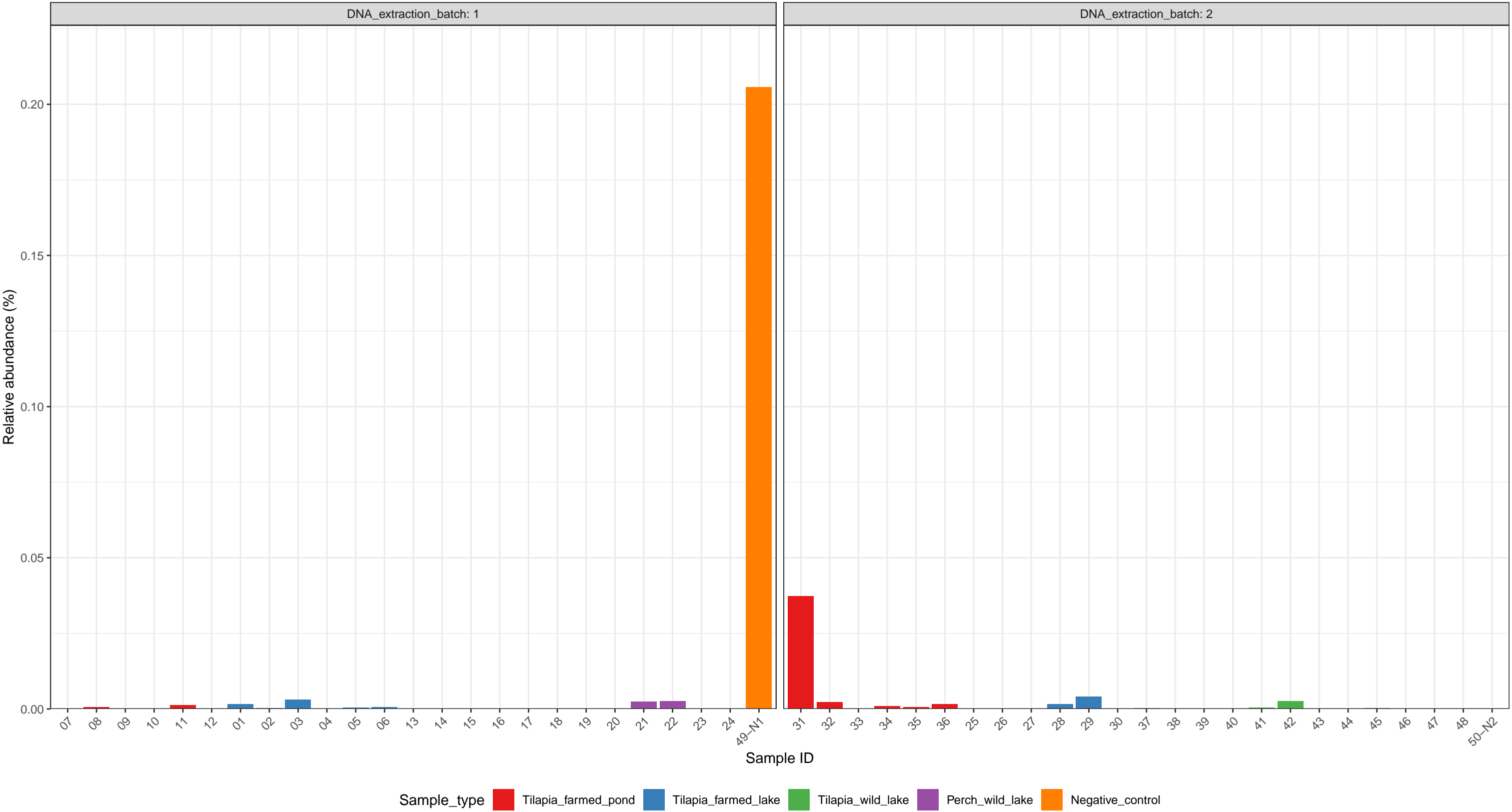
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Methylococcales; f__Methylococcaceae; g__Methylocaldum; s__uncultured bacterium

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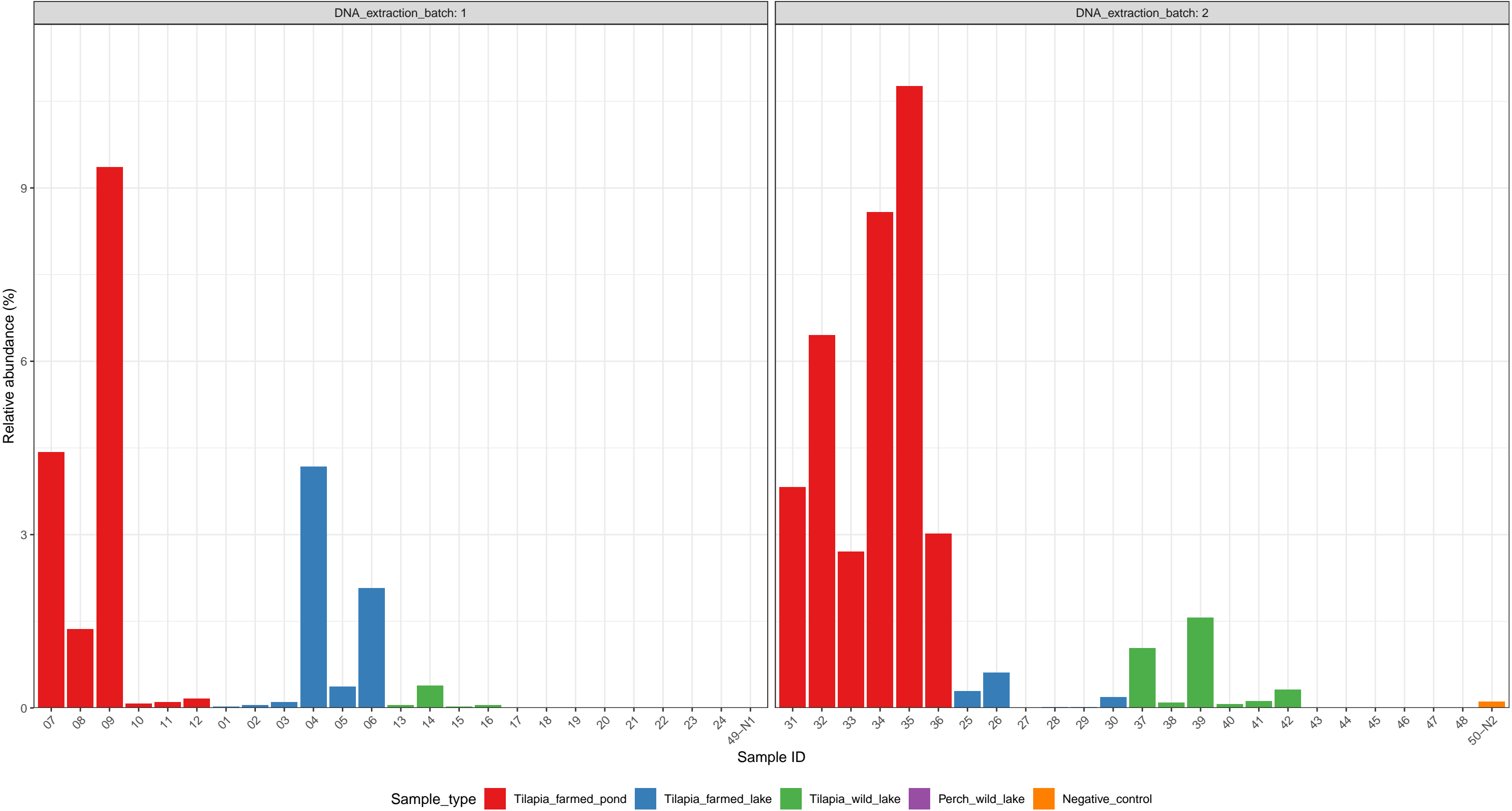
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featureID: b02a8d33d018119dedb2db15db887bfd



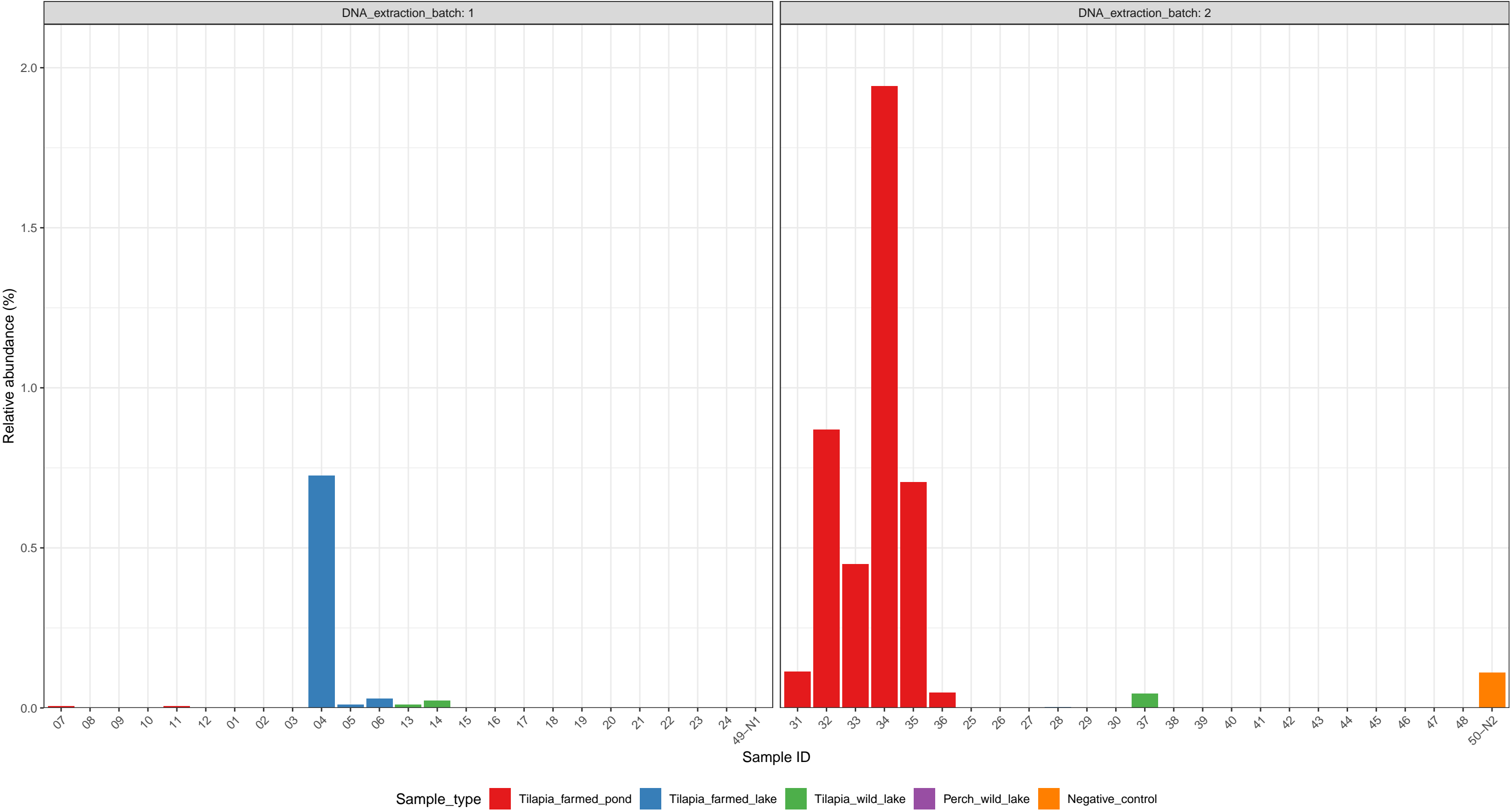
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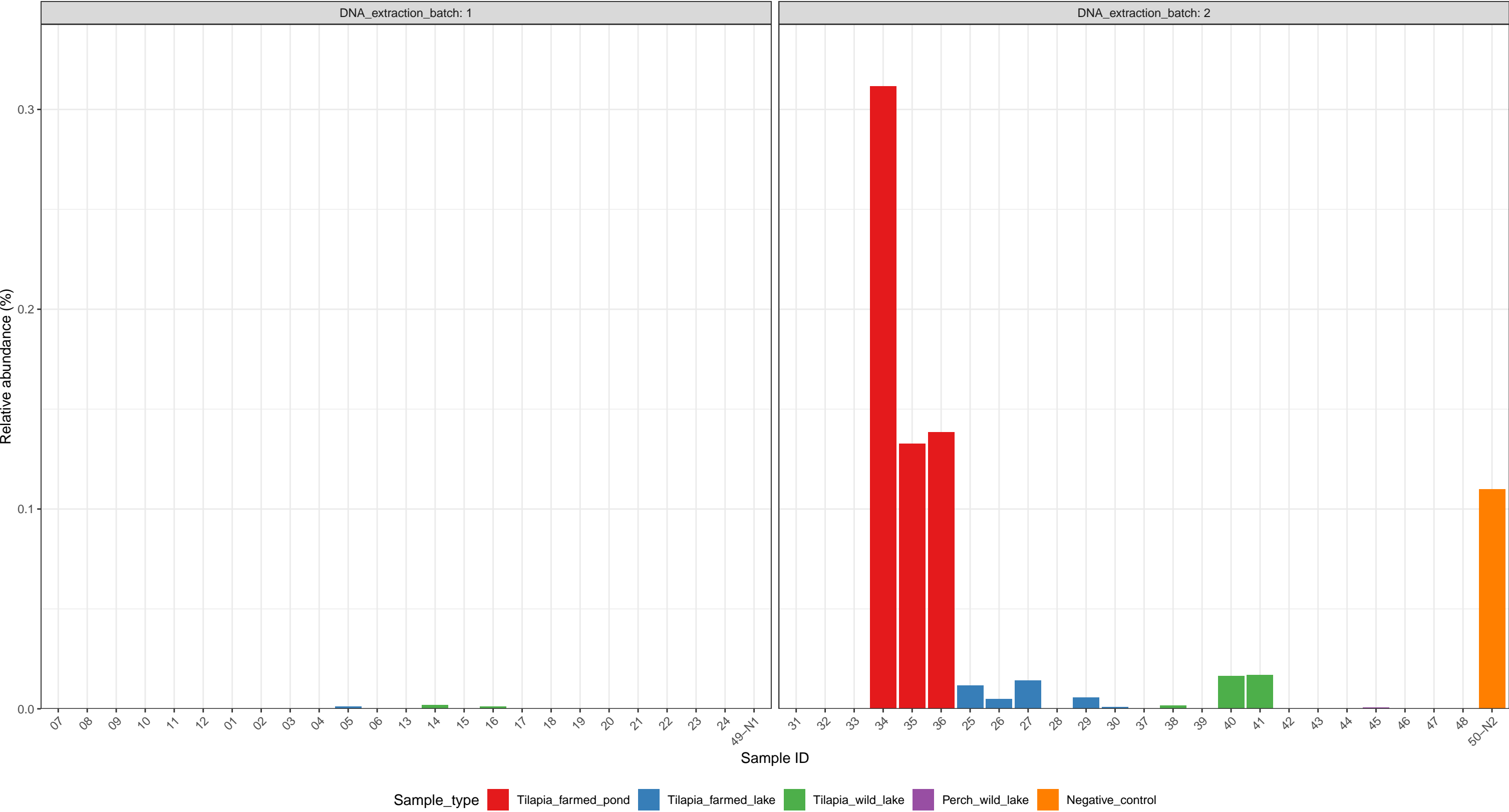
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featureID: 1b00cdeda74eca68518123e3b3036f1f



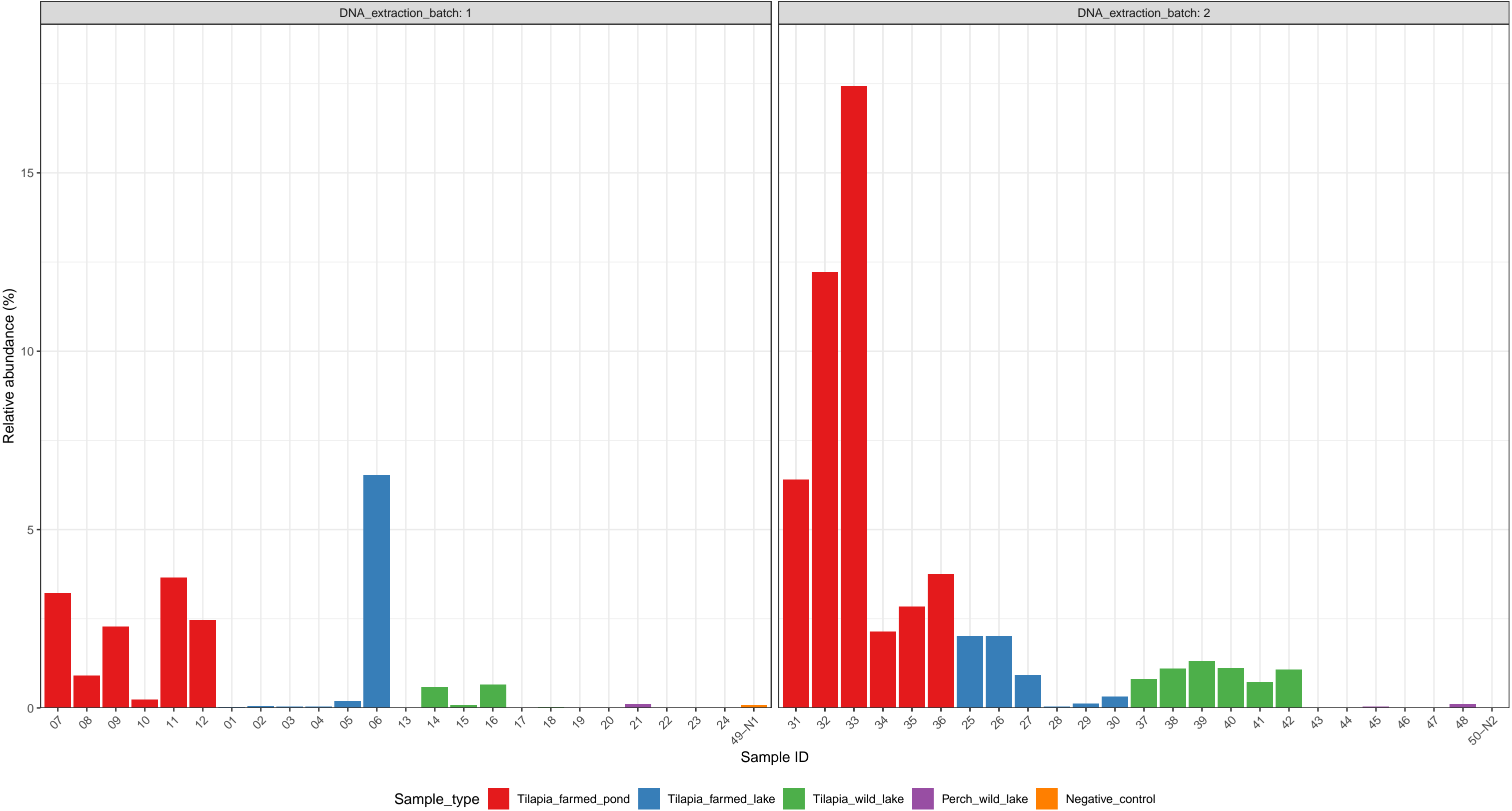
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featureID: e7ce2cd99fee0bb346892bd41d5aae49



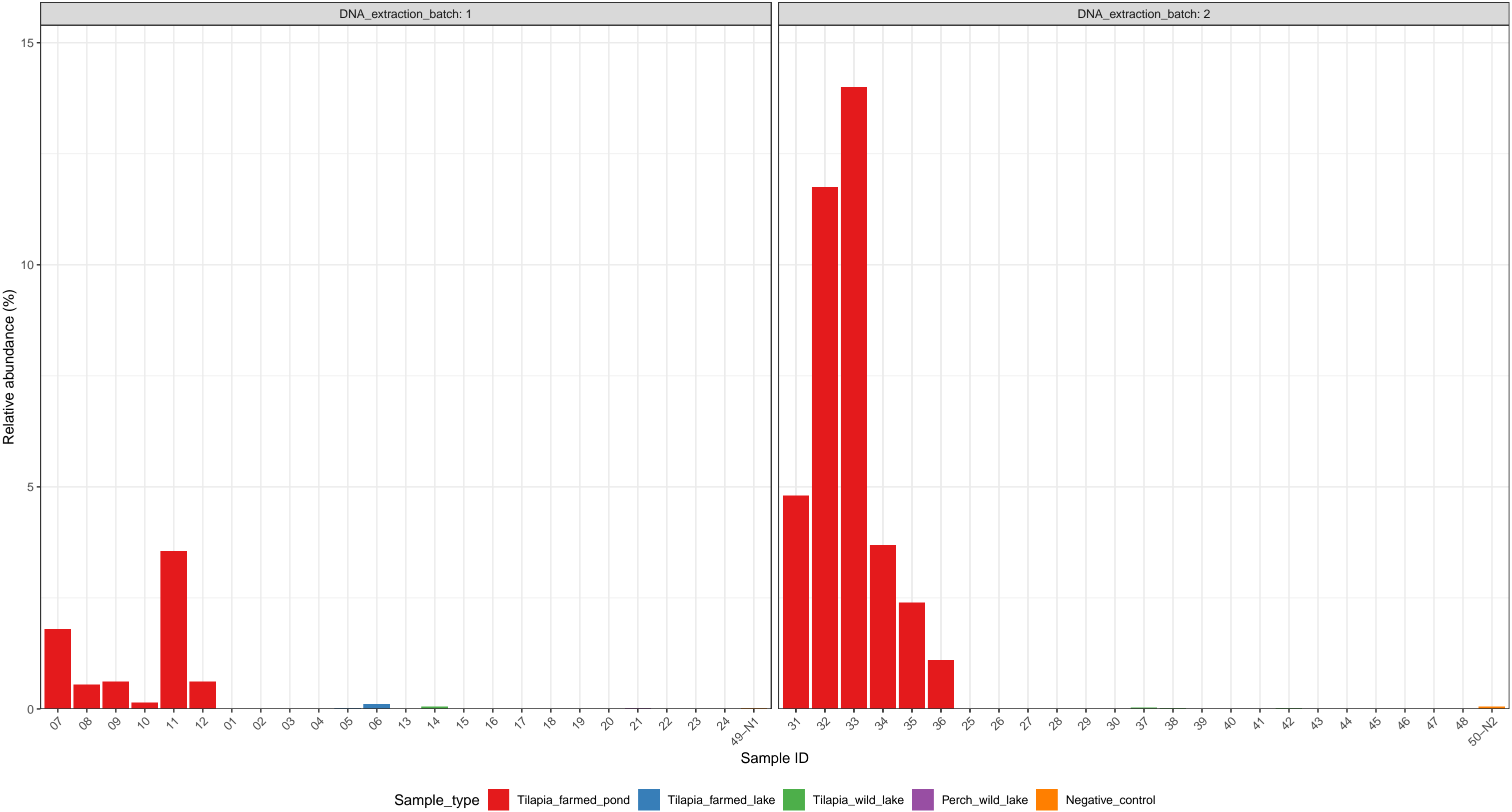
k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Clostridiaceae 1; g__Clostridium sensu stricto 1; NA

featureID: b7d96ace8aeb2c69a218149ac26a6ce9



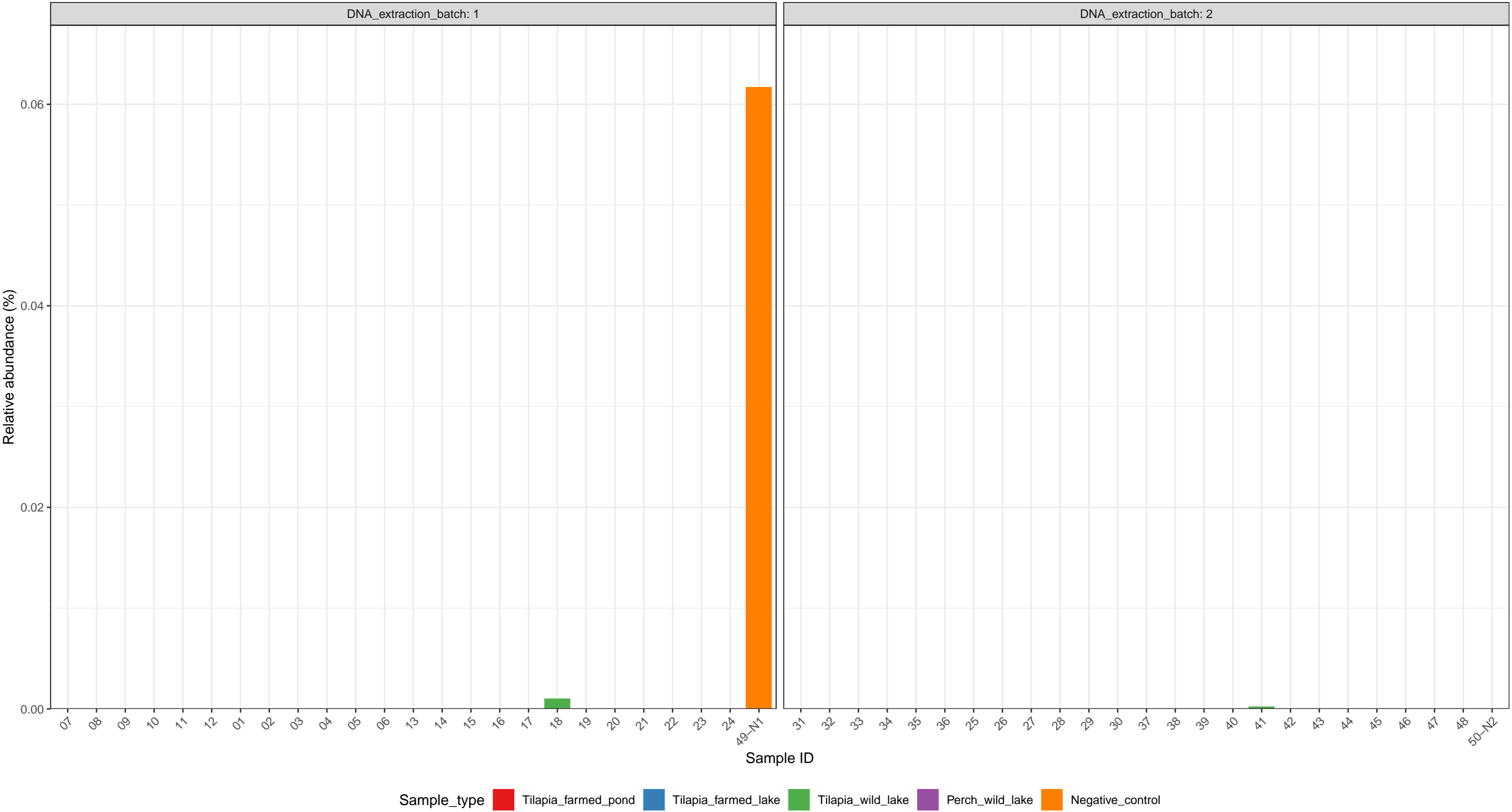
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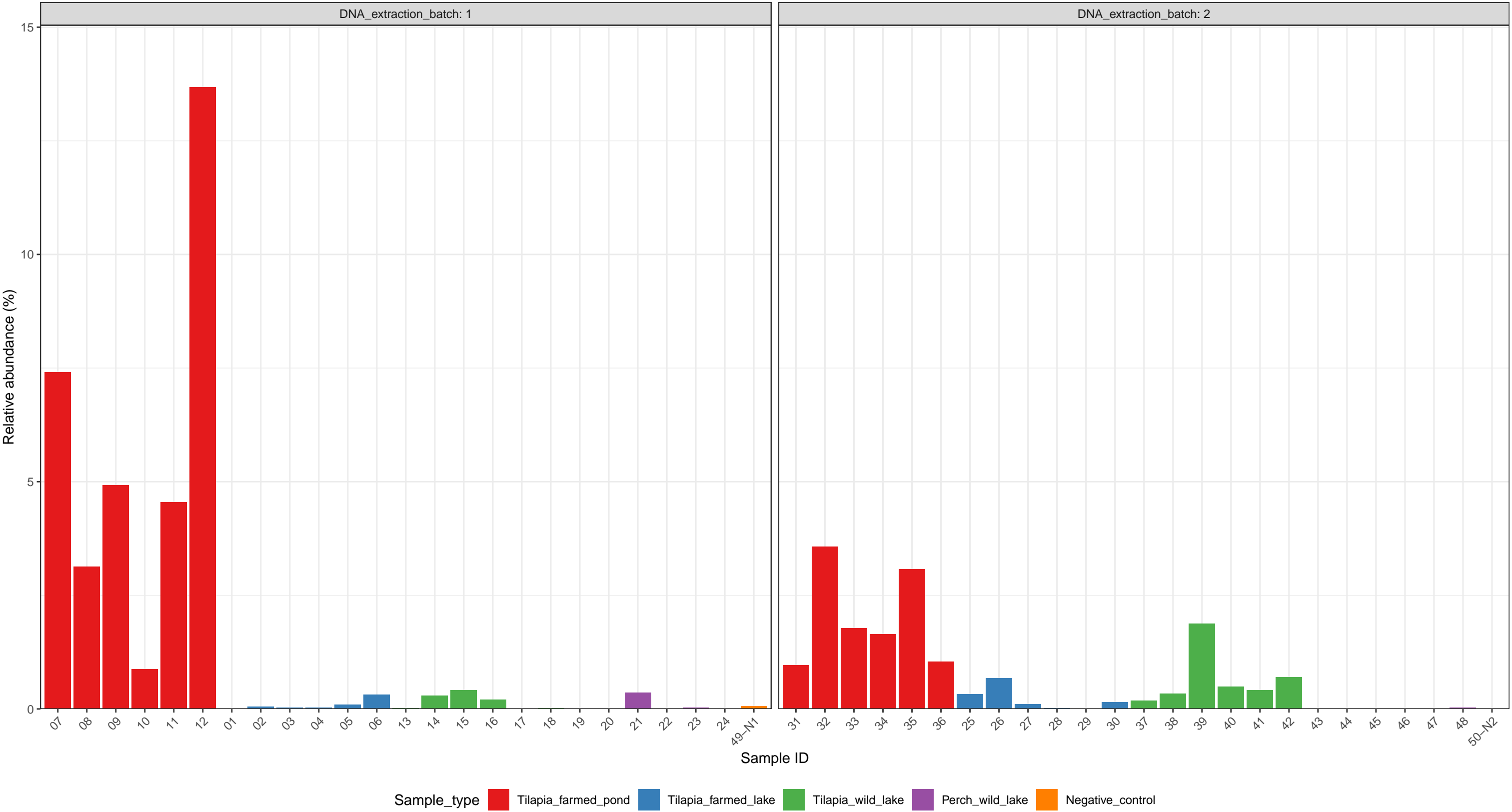
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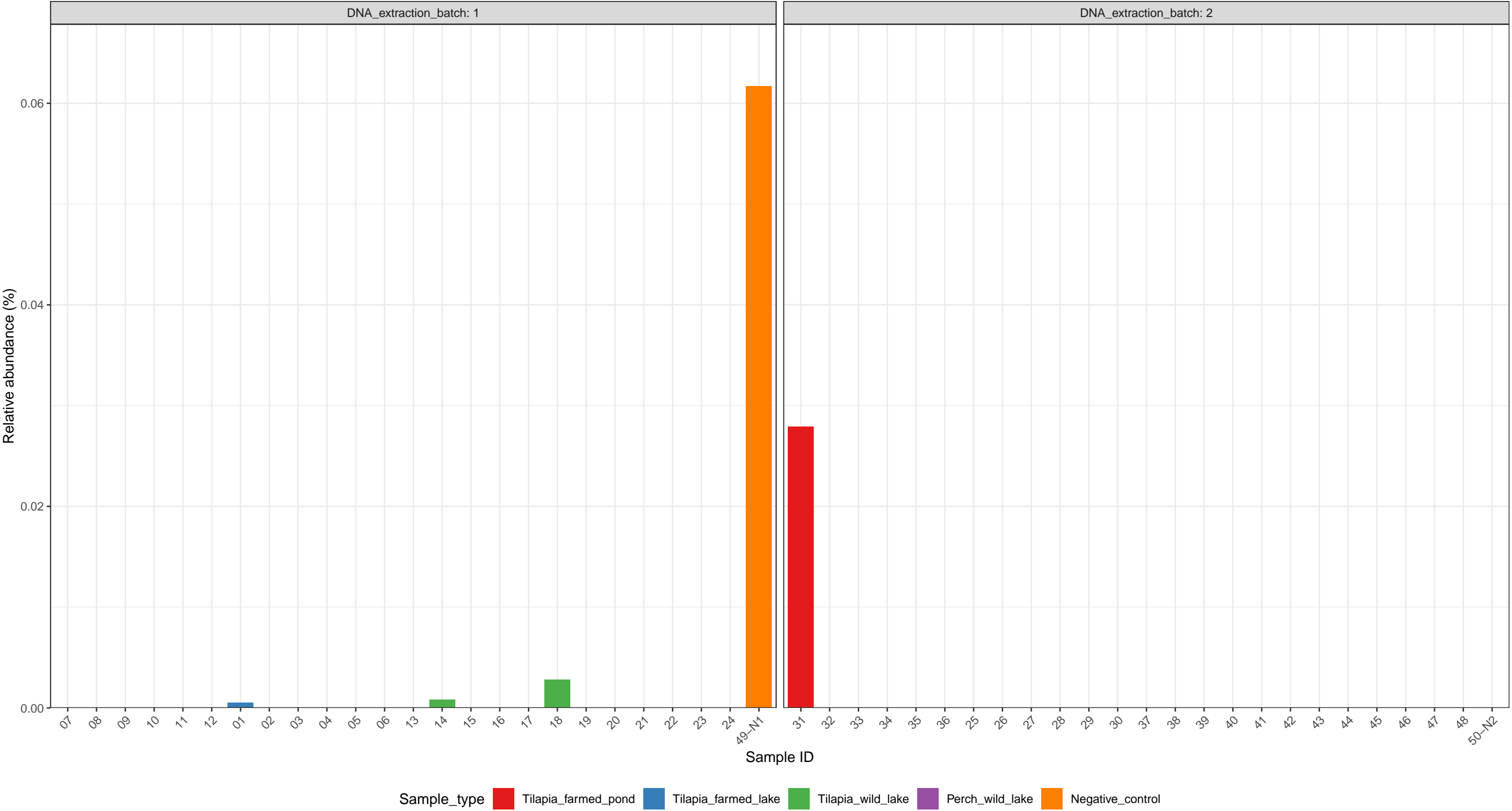
k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Clostridiaceae 1; g__Clostridium sensu stricto 1; NA

featureID: d112db53cc44b1be8395e16355a2109d



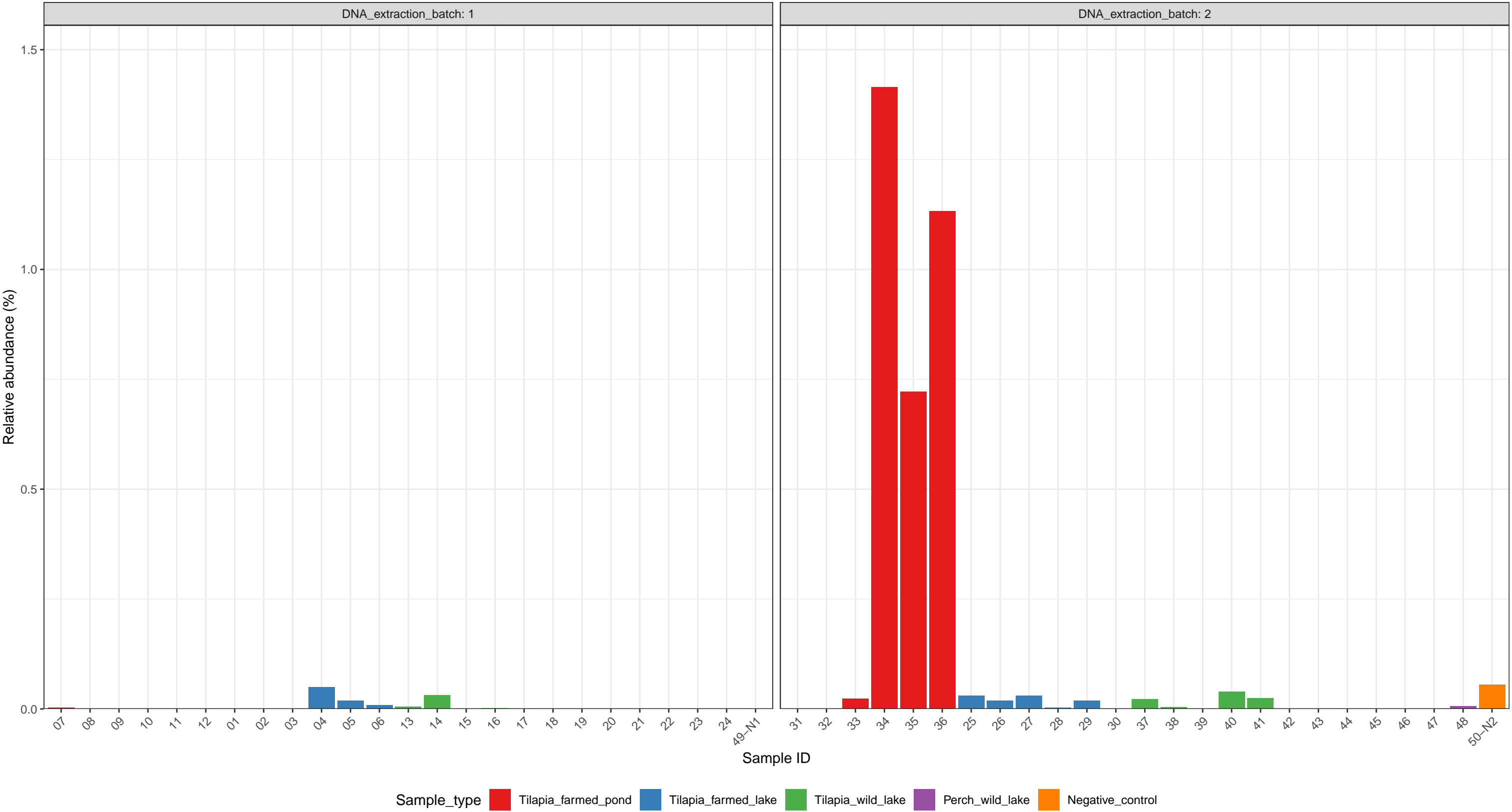
k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Corynebacteriales; f__Corynebacteriaceae; g__Corynebacterium 1; NA

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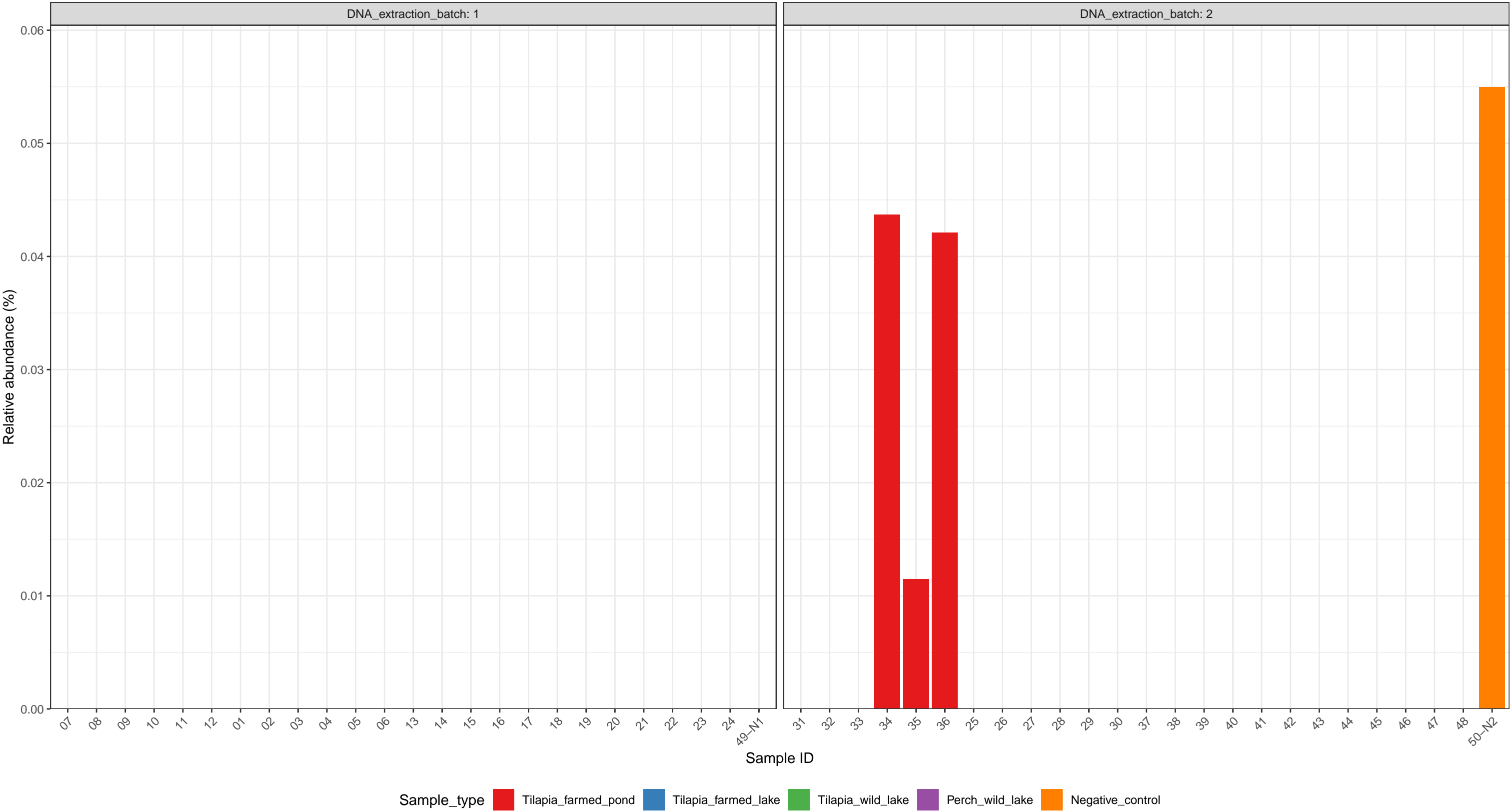
k__Bacteria; p__Cyanobacteria; c__Oxyphotobacteria; o__Synechococcales; f__Cyanobiaceae; g__Cyanobium PCC-6307; NA

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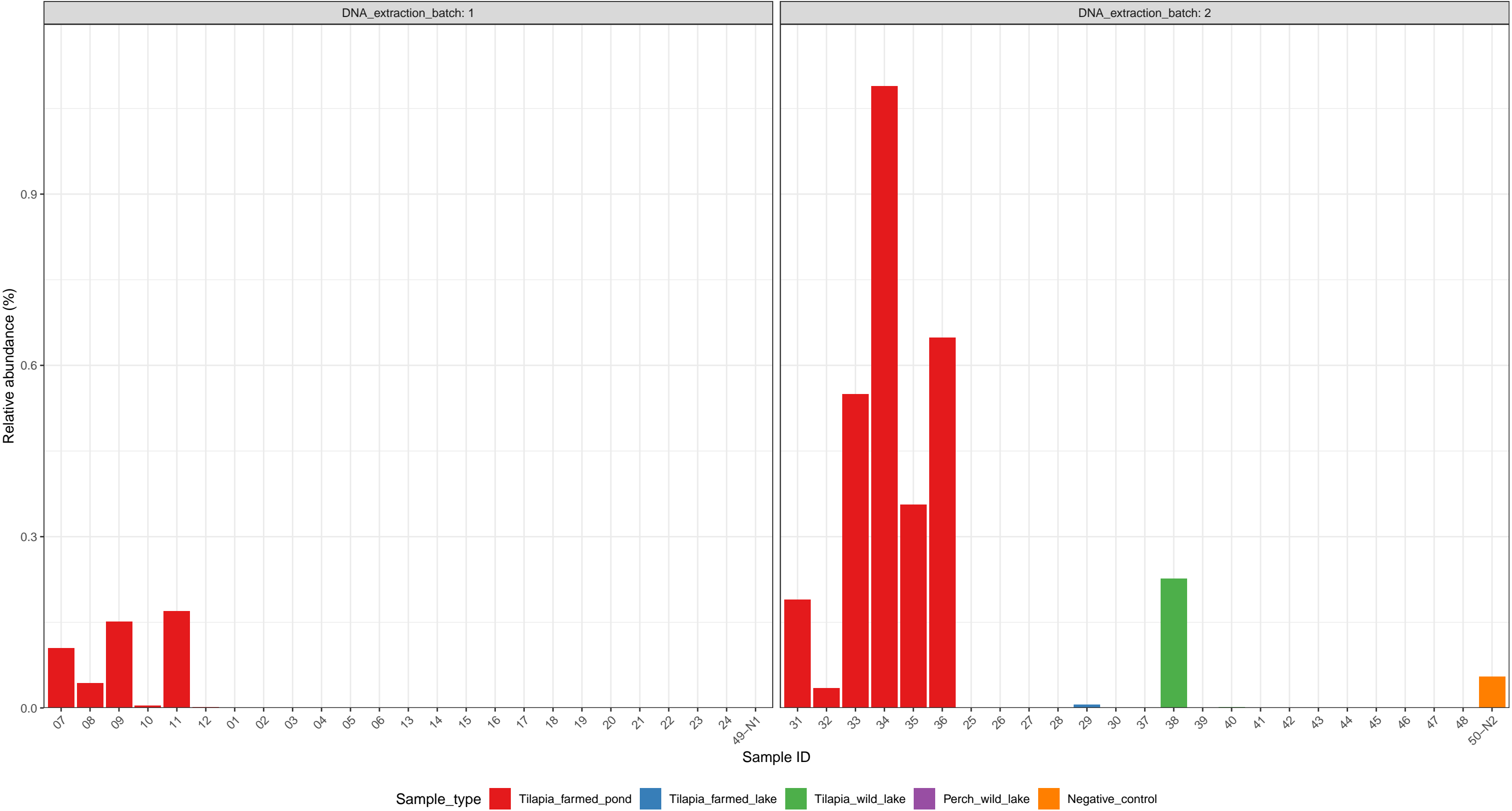
k__Bacteria; p__Chlamydiae; c__Chlamydiae; o__Chlamydiales; f__Parachlamydiaceae; g__Neochlamydia; NA

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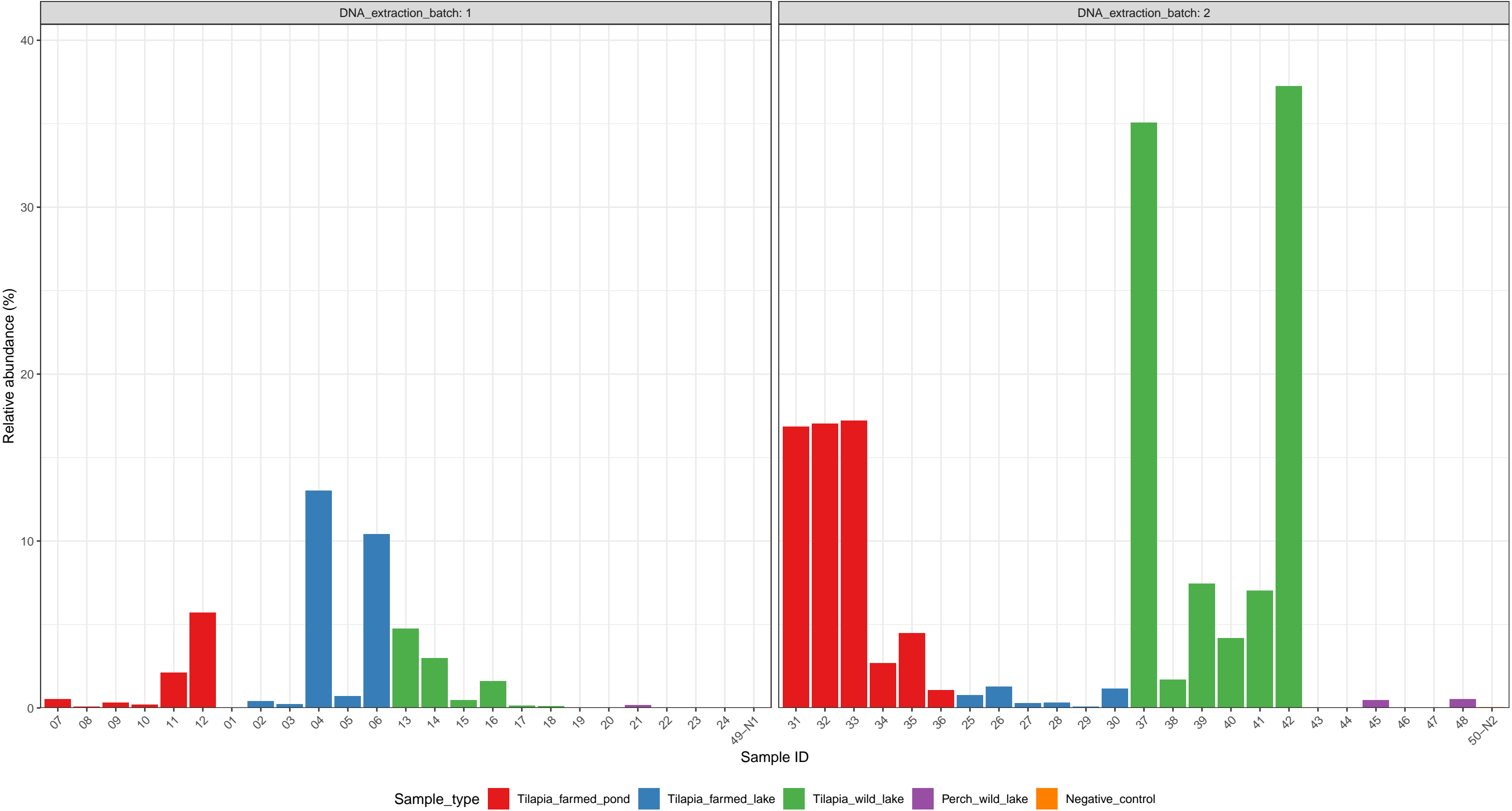
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Methylococcales; f__Methylococcaceae; g__Methyloparacoccus; s__uncultured bacterium

featureID: 66c3e0b10570a19d613f692d701da8d0



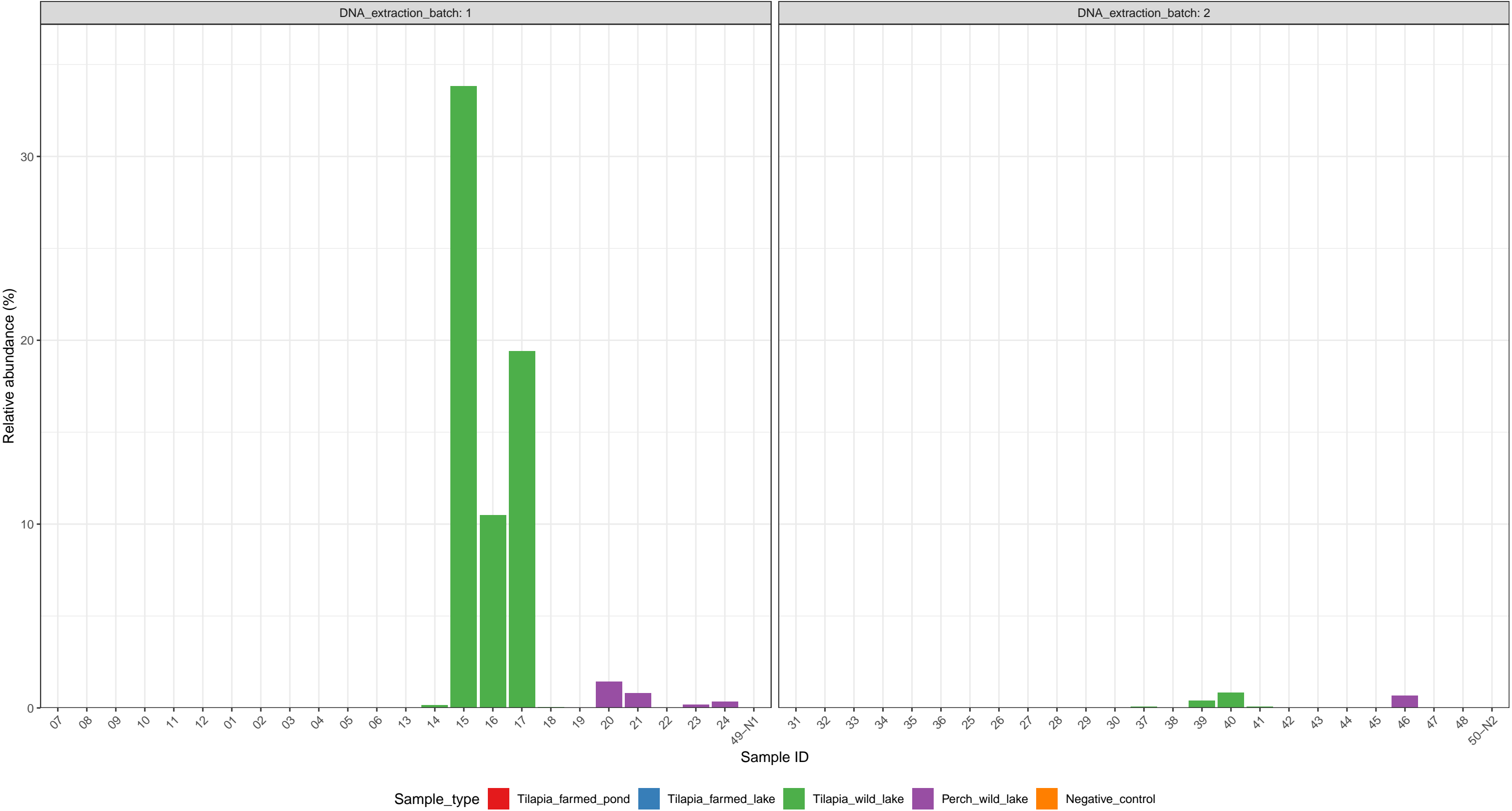
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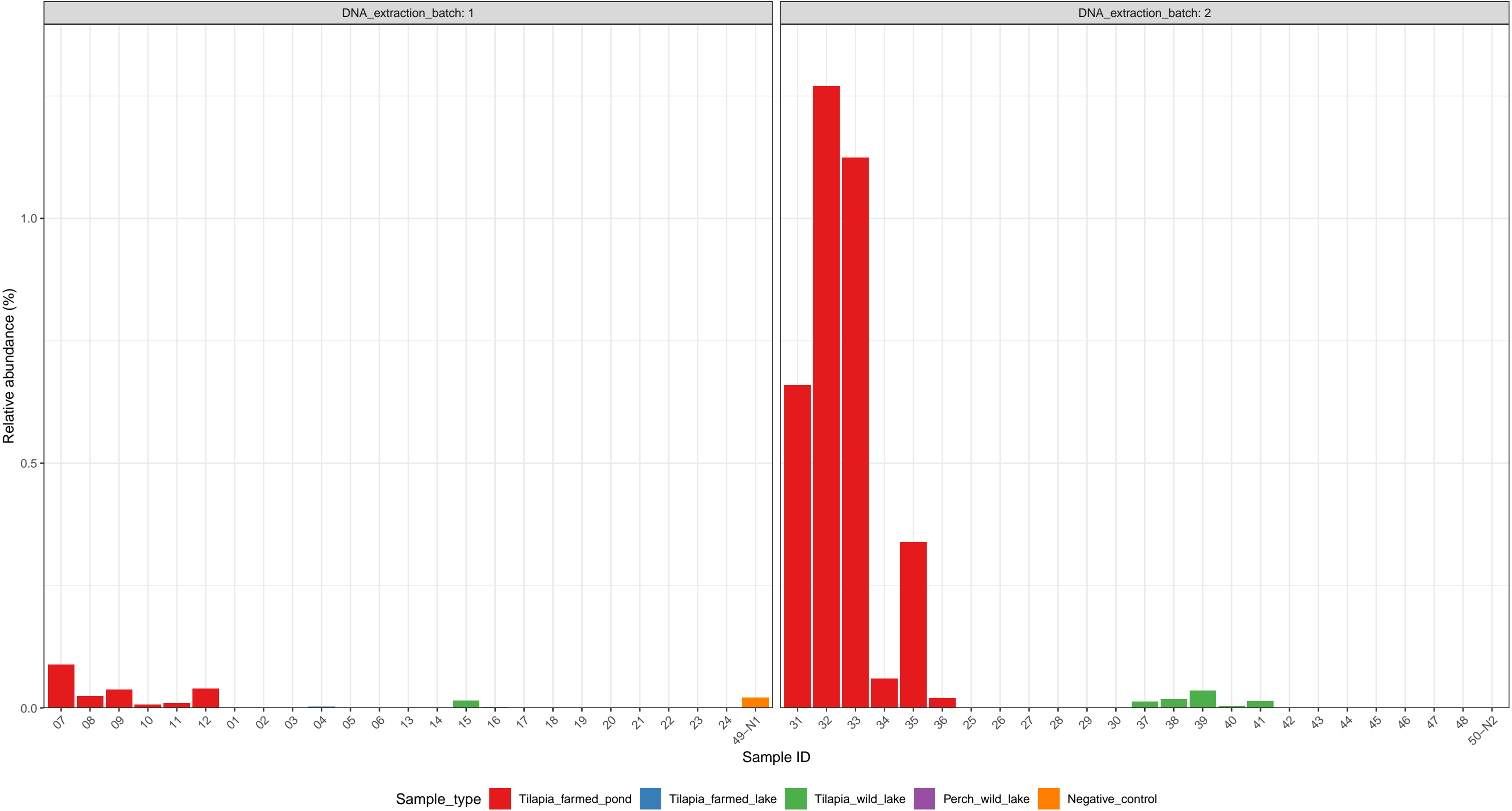
k__Bacteria; p__Fusobacteria; c__Fusobacteriia; o__Fusobacteriales; f__Fusobacteriaceae; g__Cetobacterium; NA

featureID: 50b18b94311c09ff882fda744bc15200



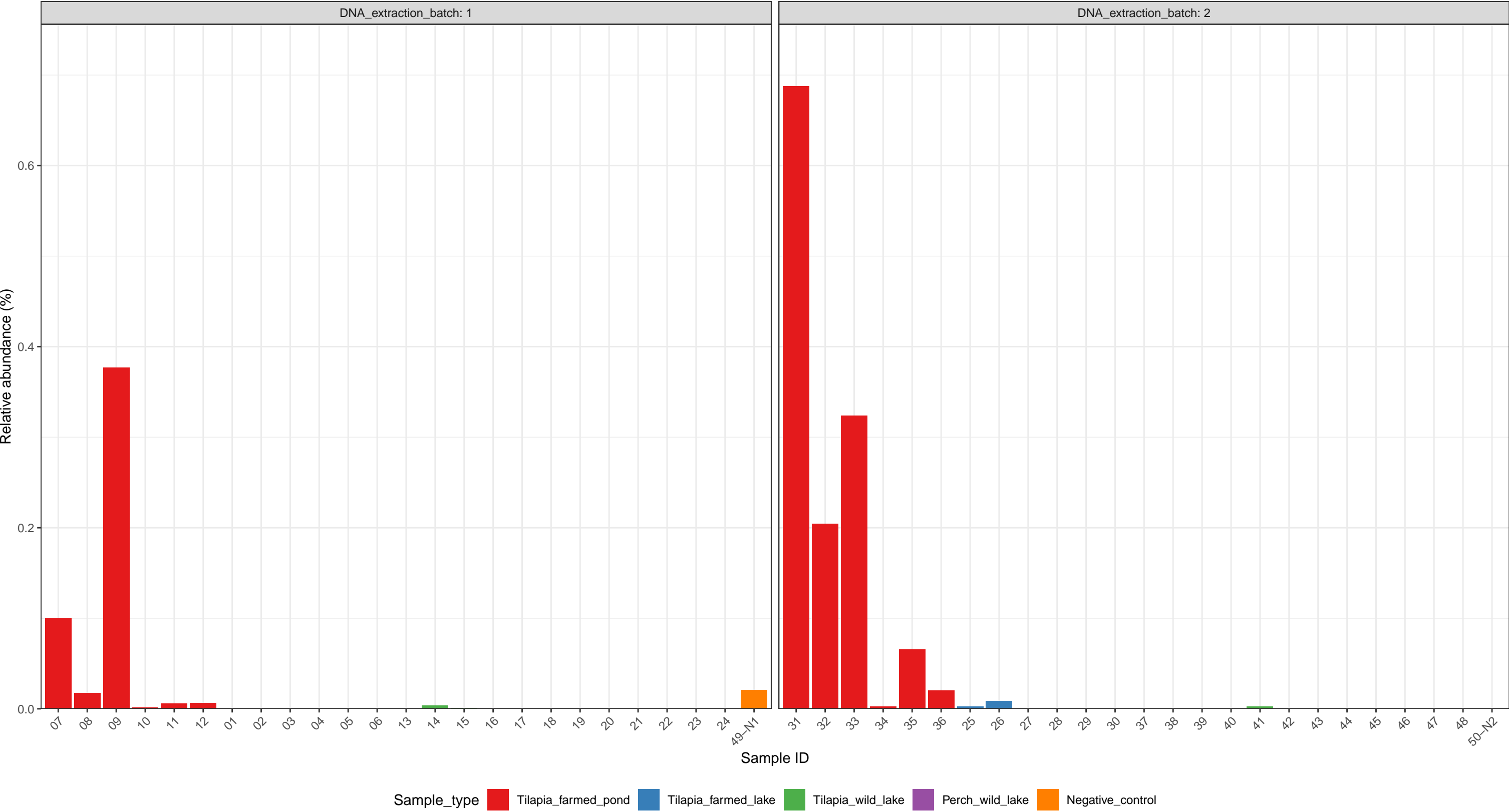
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featureID: 8440d53055be17f665533f3bf79970b8



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

featureID: c63bd7419c3dcdcff038ae017cba123c



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

featureID: e576356609fe0b38ceff9ad3b12816a

