p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f_Bacteroidaceae;g_Bacteroides

p-value: 0.0078  adj. p-value 0.048
p__Firmicutes;c__Negativicutes;o__Selenomonadales;f__Veillonellaceae;g__Dialister

p-value: 0.0078  adj. p-value 0.048
p__Verrucomicrobia;c__Verrucomicrobiae;o__Verrucomicrobiales;f__Akkermansiaceae;g__Akkermansia

p-value: 0.0078  adj. p-value 0.048
p-value: 0.0078  adj. p-value 0.048
p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Lachnoclostridium

p-value: 0.0078  adj. p-value 0.048
p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Tannerellaceae;g__Parabacteroides

p−value: 0.0078  adj. p−value 0.048
p−value: 0.0078  adj. p−value 0.048
p-value: 0.0078  adj. p-value 0.048
p-value: 0.0078  adj. p-value 0.048
p-value: 0.0078  adj. p-value 0.048
p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__Ruminococcaceae_UCG−013

p−value: 0.0078   adj. p−value 0.048
p−value: 0.0078  adj. p−value 0.048
p-Firmicutes;c-Erysipelotrichia;o-Erysipelotrichales;f-Erysipelotrichaceae;g-Erysipelatoclostridium

p-value: 0.0078  adj. p-value 0.048
p-value: 0.0078  adj. p-value 0.048
p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Dorea

p−value: 0.0078  adj. p−value 0.048
p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Barnesiellaceae;g__Barnesiella

p-value: 0.0078  adj. p-value 0.048
p__Proteobacteria;c__Deltaproteobacteria;o__Desulfovibrionales;f__Desulfovibrionaceae;g__Desulfovibrio

p-value: 0.0078  adj. p-value 0.048
p-value: 0.0078  adj. p-value 0.048
p__Actinobacteria;c__Coriobacteriia;o__Coriobacteriales;f__Atopobiaceae;g__Olsenella

p-value: 0.0078  adj. p-value 0.048
p-value: 0.0078  adj. p-value 0.048
p-value: 0.0078  adj. p-value 0.048
p-value: 0.016  adj. p-value 0.052
p-value: 0.016  adj. p-value 0.052
p___Firmicutes;c___Erysipelotrichia;o___Erysipelotrichales;f___Erysipelotrichaceae;g___Holdemanella

p-value: 0.016  adj. p-value 0.052
p-value: 0.016  adj. p-value 0.052
p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__Faecalibacterium

p−value: 0.016  adj. p−value 0.052
p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__Intestimonas

p-value: 0.016  adj. p-value 0.052
p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__Ruminococcaceae_NK4A214_group

p-value: 0.016  adj. p-value 0.052
p-value: 0.016  adj. p-value 0.052
p-value: 0.016  adj. p-value 0.052
p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__UBA1819

p-value: 0.016  adj. p-value 0.052
p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__Burkholderiaceae;g__Sutterella

p−value: 0.016  adj. p−value 0.052
p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__Ruminiclostridium_5

p-value: 0.016  adj. p-value 0.052
p_Firmicutes; c_Clostridia; o_Clostridiales; f_Ruminococcaceae; g_Butyricicoccus

p-value: 0.016  adj. p-value 0.052
p__Firmicutes;c__Erysipelotrichia;o__Erysipelotrichales;f__Erysipelotrichaceae;g__Dielma

p-value: 0.016  adj. p-value 0.052
The boxplot shows the distribution of the taxonomic levels associated with the genera Oscillibacter, Clostridiales, Clostridia, and Firmicutes for the groups PQ, LG, R, C, Y, and CA. The p-value for this comparison is 0.022, and the adjusted p-value is 0.059.
p−value: 0.022  adj. p−value 0.059
p-value: 0.022  adj. p-value 0.059
p-value: 0.022 adj. p-value 0.059
p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Eisenbergiella

p-value: 0.022  adj. p-value 0.059
p\_Bacteroidetes;c\_Bacteroidia;o\_Bacteroidales;f\_Barnesiellaceae;g\_Coprobacter

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p-value: 0.022  adj. p-value 0.059
p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Barnesiellaceae;g__NA

p-value: 0.022  adj. p-value 0.059
p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__GCA-900066225

p-value: 0.022  adj. p-value 0.059
p-Value: 0.023  adj. p-value 0.059

p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__Burkholderiaceae;g__Parasutterella
p-value: 0.023  adj. p-value: 0.059
\text{p-value: 0.023 \ adj. p-value 0.059}
p-value: 0.023  adj. p-value 0.059
p-value: 0.035  adj. p-value 0.078
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_DTU089

p-value: 0.035  adj. p-value 0.078
p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__Anaerotruncus

p-value: 0.036  adj. p-value 0.078
p__Firmicutes;c__Erysipelotrichia;o__Erysipelotrichales;f__Erysipelotrichaceae;g__Holdemania

p-value: 0.036  adj. p-value 0.078
p__Firmicutes\;c__Clostridia\;o__Clostridiales\;f__Christensenellaceae\;g__NA

p−value: 0.036  adj. p−value 0.078
p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__Acetanaerobacterium

p-value: 0.036  adj. p-value 0.078
p-value: 0.036  adj. p-value 0.078
p__Actinobacteria;c__Coriobacteriia;o__Coriobacteriales;f__Coriobacteriaceae;g__Collinsella

p-value: 0.039  adj. p-value 0.082
p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Marinilaceae;g__Odoribacter

p-value: 0.039  adj. p-value: 0.082
p__Euryarchaeota;\text{c__Methanobacteria;\text{o_Methanobacteriales;\text{f__Methanobacteriaceae;\text{g_Methanobrevibacter}}}

\begin{figure}
  \centering
  \includegraphics[width=\textwidth]{figure.png}
  \caption{Graph showing the distribution of bacterial species in different groups.}
  \label{fig:bacterial_distribution}
\end{figure}

\textit{p-value: 0.052  \text{adj. p-value: 0.11}}
p−value: 0.055  adj. p−value 0.11
p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__Ruminococcaceae_UCG−005

p−value: 0.055  adj. p−value 0.11
p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__Ruminococcaceae_UCG-014

p-value: 0.055  adj. p-value 0.11
p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Tyzzerella_4

p–value: 0.059    adj. p–value 0.11
p-value: 0.059  adj. p-value 0.11
p-value: 0.059  adj. p-value: 0.11
p-value: 0.078  adj. p-value 0.14
p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Citrobacter

p-value: 0.093  adj. p-value 0.16
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p-value: 0.1  adj. p-value 0.16
p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella
p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Anaerostipes

p-value: 0.1  adj. p-value 0.16
p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__Candidatus_Soleaferrea

p−value: 0.1  adj. p−value 0.16
p-value: 0.1  adj. p-value 0.16
p__Firmicutes; c__Clostridia; o__Clostridiales; f__Ruminococcaceae; g__Subdoligranulum

p−value: 0.11  adj. p−value 0.17
p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Agathobacter

p–value: 0.11  adj. p–value 0.17
p-value: 0.15  adj. p-value 0.22
p-value: 0.15  adj. p-value 0.22
p__Firmicutes;c__Erysipelotrichia;o__Erysipelotrichales;f__Erysipelotrichaceae;g__Merdibacter

p-value: 0.18  adj. p-value 0.25
p__Actinobacteria;c__Coriobacteriia;o__Coriobacteriales;f__NA;g__NA

p-value: 0.18  adj. p-value 0.25
p__Firmicutes;c__Clostridia;o__Clostridiales;f__Peptococcaceae;g__Peptococcus

p−value: 0.18  
adj. p−value 0.25

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p−value: 0.18  adj. p−value 0.25
p__Proteobacteria; c__Gammaproteobacteria; o__Betaproteobacteriales; f__Burkholderiaceae; g__Oxalobacter

p−value: 0.18  adj. p−value 0.25

p_Proteobacteria,c_Gammaproteobacteria,o_Betaproteobacteriales,f_Burkholderiaceae,g_Oxalobacter
p__Firmicutes;c__Clostridia;o__Clostridiales;f__Peptostreptococcaceae;g__Romboutsia

p-value: 0.29  adj. p-value 0.4
p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus

p-value: 0.31  adj. p-value 0.41
p-value: 0.31  adj. p-value 0.41
p__Bacteroidetes;c__Bacteroidia;o__Flavobacteriales;f__NA;g__NA

p-value: 0.31  adj. p-value 0.41
p-value: 0.36  adj. p-value 0.46
p__Actinobacteria;c__Coriobacteriia;o__Coriobacteriales;f__Eggerthellaceae;g__Adlercreutzia

p-value: 0.37  adj. p-value 0.46
p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Lachnospiraceae_UCG-001

p-value: 0.37  adj. p-value 0.46
p__Firmicutes;c__Erysipelotrichia;o__Erysipelotrichales;f__Erysipelotrichaceae;g__Coprobacillus

p-value: 0.37  adj. p-value 0.46
p__Actinobacteria;c__Coriobacteriia;o__Coriobacteriales;f__Eggerthellaceae;g__Slackia

p−value: 0.37  adj. p−value 0.46
p-value: 0.37  adj. p-value 0.46
p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Prevotellaceae;g__Paraprevotella

p-value: 0.38  adj. p-value 0.46
p-value: 0.4  adj. p-value 0.48
p-value: 0.42  adj. p-value 0.49
p__Actinobacteria;c__Coriobacteriia;o__Coriobacteriales;f__Atopobiaceae;g__Coriobacteriaceae_UCG-002
p__Firmicutes;c__Clostridia;o__Clostridiales;f__Peptostreptococcaceae;g__Intestinibacter

p-value: 0.55  adj. p-value 0.64
p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus

p−value: 0.58  adj. p−value 0.67
p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Carnobacteriaceae;g__Granulicatella
p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Roseburia

p−value: 0.59  adj. p−value 0.67
p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Lachnospiraceae_NK4A136_group

p−value: 0.67  adj. p−value 0.76
p__Firmicutes; c__Clostridia; o__Clostridiales; f__Lachnospiraceae; g__Tyzzerella_3

p-value: 0.86  adj. p-value 0.94
p__Firmicutes;c__Negativicutes;o__Selenomonadales;f__Veillonellaceae;g__NA

p-value: 1  adj. p-value 1
p__Firmicutes;c__Clostridia;o__Clostridiales;f__Eubacteriaceae;g__Eubacterium

p-value: 1  adj. p-value 1
p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__Pseudoflavonifractor

p-value: 1  adj. p-value 1
p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Aerococcaceae;g__Abiotrophia

p−value: 1  adj. p−value 1