

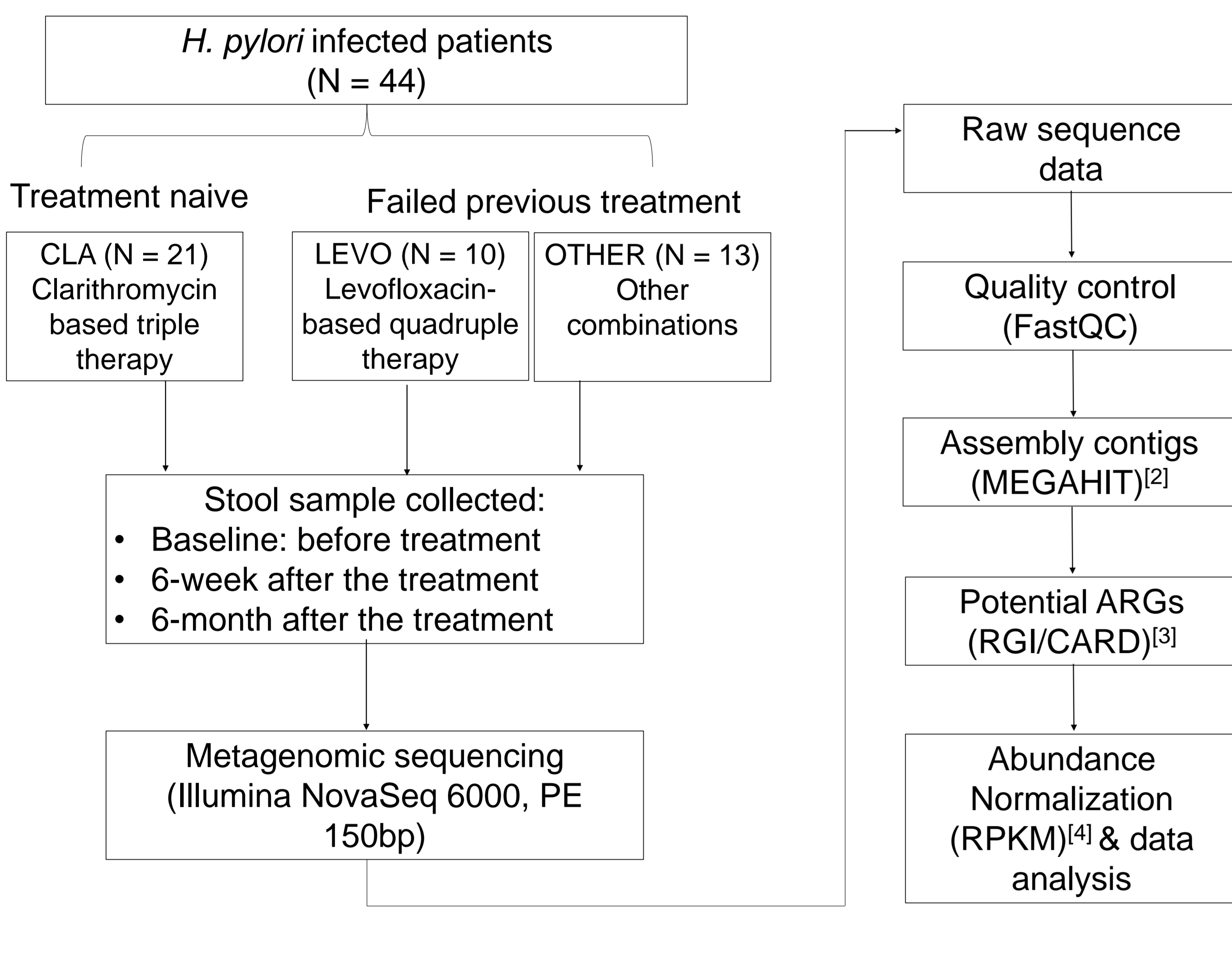
Shifts in gut antibiotics resistance genes (ARGs) after the exposure to different *H. pylori* eradication therapies

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Introduction

Antibiotics used in *H. pylori* eradication therapies could alter the gut microbiota^[1] as well as ARGs, thus increasing the risk of antibiotics resistance. We aimed to investigate the relationship between antibiotics use and subsequent gut ARGs patterns after *H. pylori* eradication therapy.

Methods



Results

1. The impact of antibiotics to ARG abundance varies in different treatment groups

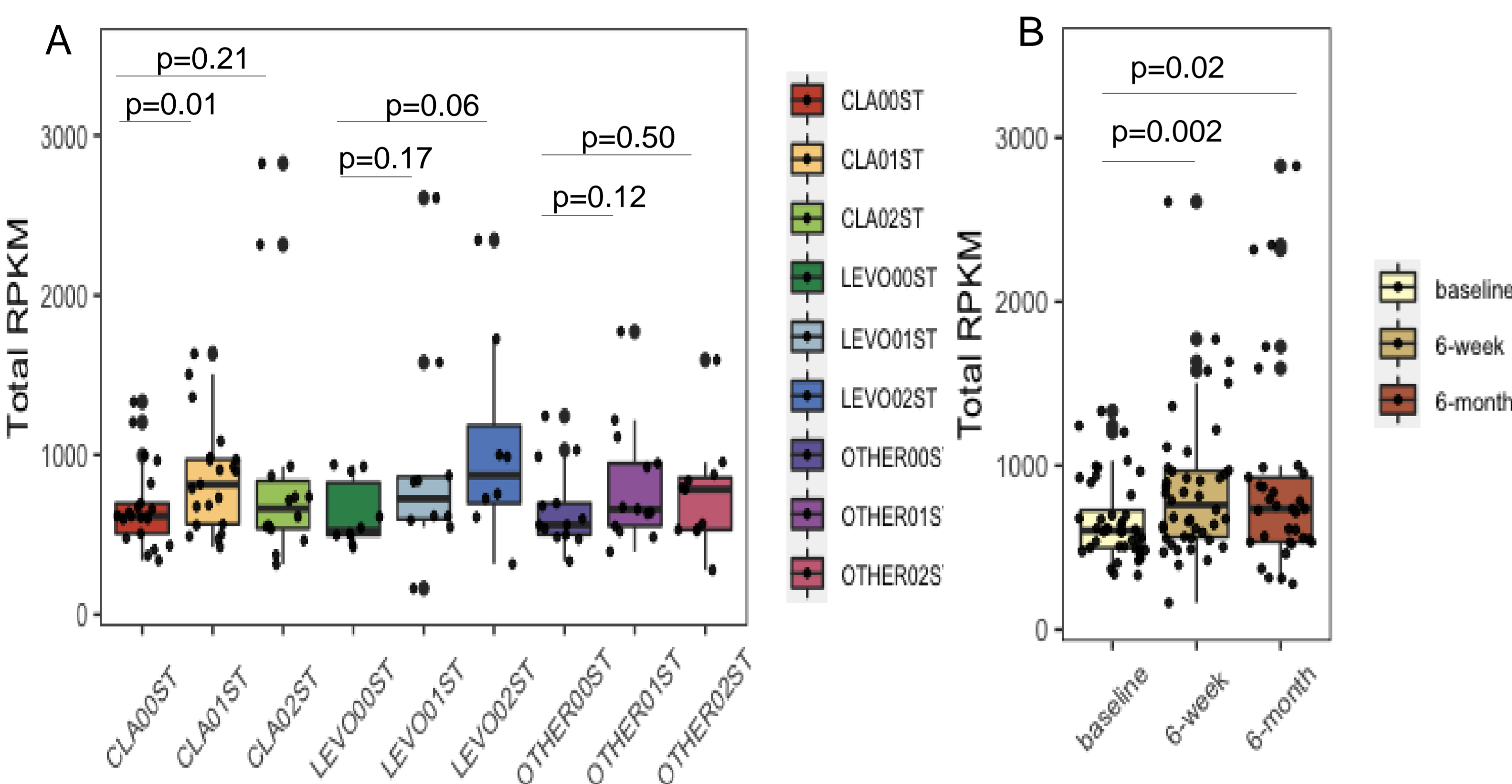
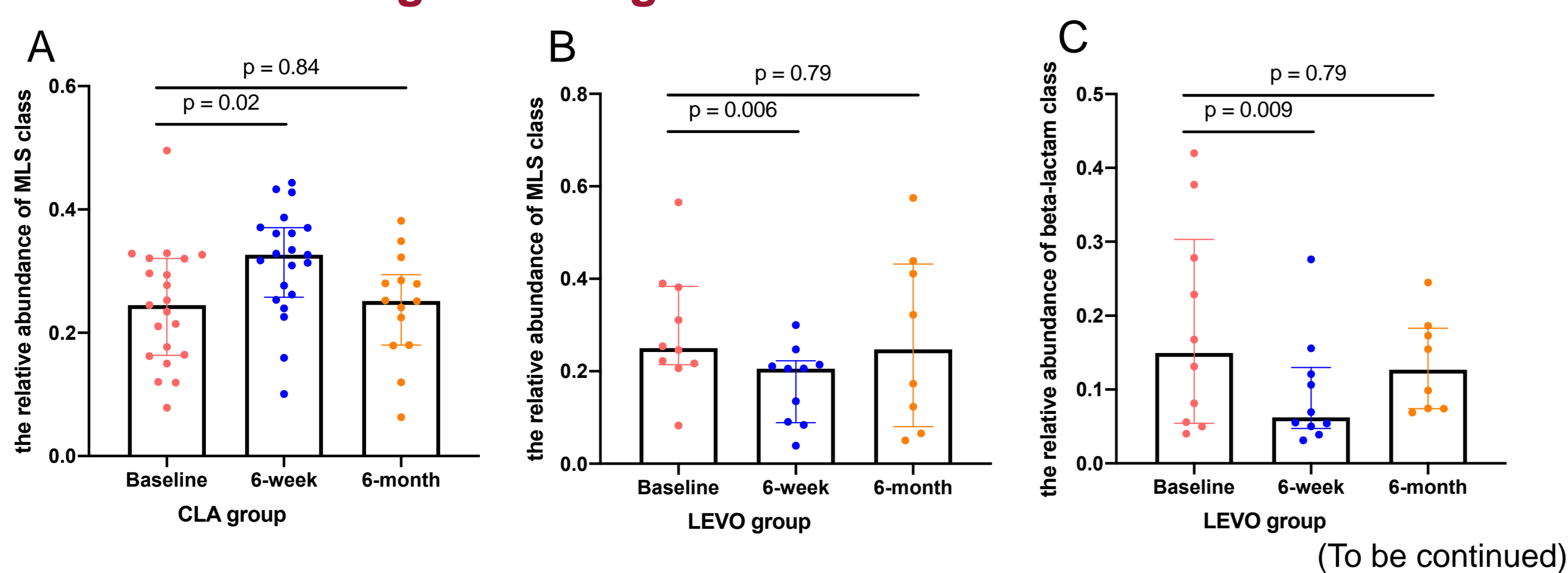


Fig. 1 the total ARG abundance (RPKM)

In CLA group, the ARG abundance increased at 6-week and returned to baseline level at 6-month (Figure 1A); in LEVO group, there was no significant increase at 6-week, but had an increase trend after 6-month (Figure 1A); In OTHER group, no significant difference was observed at 6-week or 6-month (Figure 1A); Regardless treatment difference, the total ARG abundance increased at 6-week and persist high level at 6-month (Figure 1B);

2. The ARG changes at drug class level



Results

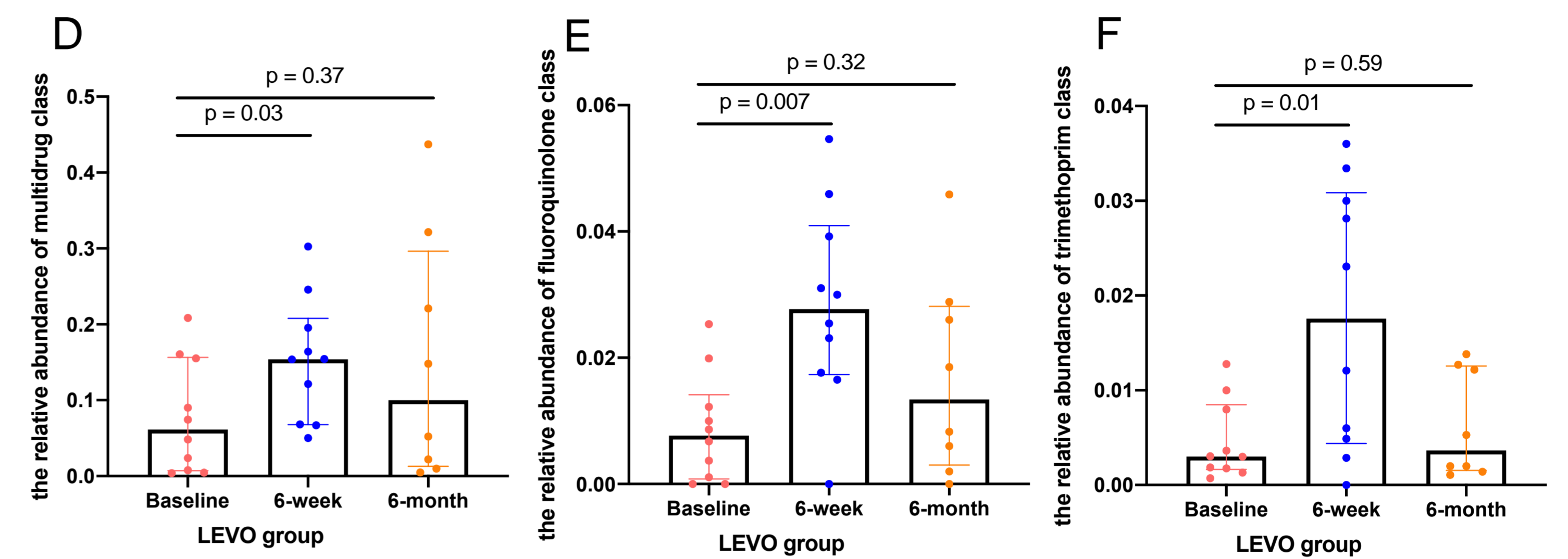


Fig. 2

In CLA group, the relative abundance of ARGs in macrolide-lincosamide-streptogramin (MLS) class increased at 6-week, and returned to baseline level at 6-month; In LEVO group, MLS and beta-lactam class decreased, while multidrug, fluoroquinolone and trimethoprim class increased at 6-week, and all returned to near baseline level at 6-month; No significant difference was found in OTHER group.

3. LEVO group have the highest number of significantly changed unique ARGs at 6-week

	CLA	LEVO	OTHER
ARGs with increased relative abundance	APH(3')-IIIa, aad(6), cepA, ErmF	mdtA, E. coli gyrA, aadA5, E. coli ampC, kdp, mphA, AcrS, E. coli GlpT mutation, E. coli soxS mutation, emrA, E. coli ampH, E. coli acrA, E. coli emrE, mdtH, E. coli ampC1, gadX, TEM-1, qacEdelta1, evgA, E. coli acrR mutation, emrK, YojI, mdtN, mdtF, baeS, mdtP, PmrF, mdtM, mdtG, E. coli mdfA, TolC, eptA, E. coli marR mutation, AcrF, Ugd, E. coli soxR mutation, emrY, mdtO, E. coli EF-Tu mutants, mdtE, sul1, evgS,	AAC(6')-Im, acrD, tet(A), vanSD, floR
ARGs with decreased relative abundance	Mef(En2), pmrA, tetA(46)	OXA-347, ErmF	ErmB, Bifidobacterium bifidum ileS, tetW

Table. 1 unique ARGs changed at 6-week

In CLA group, 7 unique ARGs altered at 6-week (including 4 increased; 3 decrease); In LEVO group, 45 unique ARGs significantly changed at 6-week, 43 of them had an increased abundance; In OTHER group, 8 unique ARGs significantly changed (5 increased and 3 decreased);

Conclusion

Antibiotic used in various *H. pylori* eradication therapies had a significant impact on the total gut ARGs abundance, which last for at least 6 months.

However, short-term changes in specific ARGs are more prevalent after treatment with levofloxacin-based therapy.

Reference

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