

Supplementary Table 1. Summary of microbial taxa reported to be associated with Kawasaki disease (KD)

Body site	Taxon (genus or higher)	Direction in acute KD	Associated findings	Interpretation / notes	Ref.
Gut	<i>Akkermansia</i>	↓ Decreased	Reduced abundance during acute KD; partial recovery after IVIG	Anti-inflammatory mucin-degrading genus; association only, causality unproven	59, 97
	<i>Faecalibacterium</i>	↓ Decreased	Lower levels correlated with inflammatory state	SCFA-producing genus; common finding across inflammatory conditions	59, 97
	<i>Bacteroides</i>	Variable	Inconsistent changes across cohorts	Population- and method-dependent findings	97
	Proteobacteria (phylum)	↑ Increased (subset)	Enrichment in some acute KD cohorts	Broad inflammatory signature, not KD-specific	97
Nasopharynx	<i>Corynebacterium</i>	↑ Increased	Higher relative abundance in acute KD	Possible association with airway immune triggering; correlative	98
	<i>Streptococcus</i>	Variable	Inconsistent across studies	Likely reflects background respiratory flora	98
Oral cavity	Mixed oral taxa	Variable	Differences vs febrile controls	Small cohorts, high interindividual variability	99
Animal model (LCWE)	<i>Akkermansia</i>	↓ Reduced (experimental)	Reduction associated with worsened vasculitis severity	Functional relevance shown in mouse model; extrapolation to humans limited	23, 100
	<i>Faecalibacterium</i> -like taxa	↓ Reduced (experimental)	Associated with enhanced IL-1–driven inflammation	Proof-of-principle in KD-like vasculitis	100

IVIG, intravenous immunoglobulin; IL, interleukin; SCFA, short-chain fatty acid; LCWE, *Lactobacillus casei* cell wall extract.