

Supplementary Table 2. Representative multiomics integration strategies and applications

Category	Representative methods	Main purpose/application	Example in KD or similar context
1. Unsupervised latent-factor models	MOFA, MOFA+	Identify shared axes of variation across omics (e.g., inflammation, metabolism)	Discover latent “inflammatory–metabolic” factors linking transcriptomic and metabolomic layers
2. Supervised multiblock models	DIABLO (mixOmics), sparse PLS	Integrate omics for biomarker discovery and outcome prediction (e.g., IVIG response)	Build composite predictor panels combining transcriptome–proteome–metabolome features
3. Pathway-centric scoring	MOPA, sample-wise multiomics pathway activity score	Map omic features to biological pathways to compute unified pathway activities	Evaluate cytokine or metabolic pathway activity per sample
4. Network construction & module detection	WGCNA, STRING, network propagation	Identify coexpression/co-abundance modules and hub nodes bridging omic layers	Reveal neutrophil degranulation or endothelial activation modules
5. Single-cell & spatial multimodal integration	Seurat/CCA, Harmony, MOFA+, paired scRNA–TCR/BCR	Integrate transcriptome, ATAC, and surface proteome at single-cell level	Localize cytokine or metabolic programs to specific immune subsets
6. Causal and colocalization analyses	Coloc, eQTL/pQTL overlap, Mendelian randomization	Link GWAS variants to gene/protein/metabolite effects for causal inference	Test genetic mediation of KD susceptibility loci via transcriptomic changes

KD, Kawasaki disease; MOFA, multiomics factor analysis; DIABLO, data integration analysis for biomarker discovery using latent variable approaches for omics studies; PLS, partial least squares; IVIG, intravenous immunoglobulin; MOPA, multiomics pathway analysis; WGCNA, weighted gene coexpression network analysis; STRING, search tool for the retrieval of interacting genes/proteins; CCA, canonical correlation analysis; TCR, T-cell receptor; BCR, B-cell receptor; ATAC, assay for transposase-accessible chromatin; Coloc, colocalization; eQTLs, expression quantitative trait loci; pQTLs, protein quantitative trait loci; GWAS, genome-wide association study.