STATISTICAL ANALYSIS PLAN

Analysis populations. The primary analysis population includes all eligible participants with prealbumin measured on Day 1 and Day 7. A safety population includes all participants in whom nasojejunal placement was attempted.

Primary endpoint analysis. The outcome is change in prealbumin from Day 1 to Day 7. The primary comparison is exposure to nasojejunal short-peptide feeding versus conventional care. Because exposure is not randomised, confounding will be addressed using propensity score methods. A propensity score for receiving nasojejunal short-peptide feeding within 24 hours is estimated with logistic regression including baseline covariates such as age, sex, site, ARDS severity (PaO_2/FiO_2, PEEP), haemodynamic status, recent transfusion, renal function, baseline albumin and prealbumin, contraindications to gastric feeding, and clinician preference proxies. The primary model is a weighted linear regression of change in prealbumin on exposure using stabilised inverse probability of treatment weights with robust standard errors clustered by site. A covariate-adjusted linear regression without weights serves as a co-primary model.

Secondary endpoints. Continuous secondary endpoints (albumin, nitrogen balance, caloric/protein intake) are analysed similarly using weighted or adjusted linear models. Biomarkers measured at multiple time points (C-reactive protein, interleukin-6) are analysed with weighted linear mixed-effects models including fixed effects for time and exposure×time interaction and random intercepts at the patient level. Binary endpoints (any feeding intolerance, aspiration, rebleeding, ICU-acquired infection) use weighted log-binomial or Poisson models with robust variance to estimate risk ratios. Time-to-event endpoints (time to first infection; ICU discharge) use weighted Cox models. Ventilator-free days to Day 14 are analysed as a zero-inflated count using a two-part model or as ordinal categories in a proportional odds model, with death assigned the worst outcome.

Missing data. If missingness in baseline covariates exceeds trivial levels, multiple imputation by chained equations will be used under missing at random assumptions; imputations will be performed within sites and combined using Rubin's rules. For outcomes missing due to early discharge before Day 7 labs, pattern-mixture sensitivity analyses will be performed, including best-case and worst-case bounds and inverse probability of censoring weights.

Subgroups and interactions. Prespecified subgroups include site, age (<65 vs ≥65), ARDS severity (PaO_2/FiO_2 ≤100 vs 101–200), and presence of shock at baseline. Interaction terms will be tested cautiously and interpreted as exploratory.

Sensitivity analyses. Analyses will be repeated with 1:1 nearest-neighbour propensity-score matching with caliper and with overlap-weights targeting the population with clinical equipoise. Exposure redefinition windows (12 and 48 hours) will be evaluated to assess misclassification. A falsification endpoint not biologically related to nutrition will be analysed to probe residual confounding.

Multiplicity and inference. The primary endpoint will be tested at a two-sided alpha of 0.05. Secondary endpoints will be considered exploratory with false discovery rate control where appropriate. Effect estimates will be presented with 95% confidence intervals.

Software and reporting. Analyses will be performed in R or Python using validated packages. A reproducible code repository and analysis log will be archived with the final manuscript.