

ABG-VBG Analysis

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1 Data Pre-processing

This code pulls in the master database (a STATA file) and does some initial cleaning - this will only need to be run once, and then the data can be accessed in the usual way.

```
# put this in your first R chunk
stopifnot(requireNamespace("kableExtra", quietly = TRUE))
library(kableExtra)
library(gtsummary)
library(purrr)      # functional programming

# globally tighten gtsummary/gt tables (smaller font + tighter padding)
gtsummary::theme_gtsummary_compact()

# keep figures anchored in PDF to reduce heading-only/blank pages
if (knitr::is_latex_output()) {
  knitr::opts_chunk$set(fig.pos = "H")
}

# helper: turn any gtsummary table into a PDF-safe, auto-scaling LaTeX table
to_pdf_table <- function(tbl, font_size = 8, landscape = FALSE,
                           label_col_width = NULL, longtable = FALSE) {
  tbl_ncol <- tryCatch(ncol(gtsummary::as_tibble(tbl)), error = function(e) NA_integer_)
  if (is.finite(tbl_ncol) && tbl_ncol > 6 && font_size > 6) font_size <- 6
  kbl <- gtsummary::as_kable(
    tbl,
    format    = "latex",
    booktabs  = TRUE,
    longtable = longtable
  )

  # optional: set a fixed width for the first (label) column to encourage wrapping
  if (!is.null(label_col_width)) {
    kbl <- kableExtra::column_spec(kbl, 1, width = label_col_width)
  }
}
```

```

latex_opts <- if (longtable) {
  c("repeat_header")
} else {
  c("hold_position", "scale_down")
}
kbl <- kableExtra::kable_styling(
  kbl,
  latex_options = latex_opts,
  font_size      = font_size,
  full_width     = !longtable,
  position       = "center"
)

if (landscape) kbl <- kableExtra::landscape(kbl) # needs pdflscape (enabled above)
mark_float_emitted()
kbl
}

# helper: scale generic data.frames for PDF output
kable_pdf <- function(df, caption = NULL, font_size = 7) {
  kbl <- knitr::kable(df, format = "latex", booktabs = TRUE, caption = caption)
  kbl <- kableExtra::kable_styling(
    kbl,
    latex_options = c("hold_position", "scale_down"),
    font_size      = font_size,
    full_width     = TRUE,
    position       = "center"
  )
  mark_float_emitted()
  kbl
}

# helper: pretty, relative paths for PDF output
pretty_path <- function(p) {
  p_abs <- tryCatch(fs::path_abs(p, start = getwd()), error = function(e) NA_character_)
  res_abs <- tryCatch(fs::path_abs(results_dir, start = getwd()), error = function(e) NA_character_)

```

```

if (!is.na(p_abs) && !is.na(res_abs)) {
  if (fs::path_has_parent(p_abs, res_abs) || identical(p_abs, res_abs)) {
    rel <- fs::path_rel(p_abs, res_abs)
    return(fs::path("Results", rel))
  }
}
out <- tryCatch(fs::path_rel(p, start = getwd()), error = function(e) NA_character_)
if (is.na(out) || out == "." || grepl("^\\\\.\\\\.", out)) {
  return(basename(p))
}
out
}

# helper: strip manual "Table X." prefixes in PDF to avoid double numbering
strip_manual_table_number <- function(caption) {
  if (is.null(caption)) return(caption)
  if (!knitr::is_latex_output()) return(caption)
  cap <- gsub("^\\\\s*(\\\\*\\\\*)?Table\\\\s+[0-9A-Za-z]+\\\\.\\\\.?\\\\s*:?:\\\\s*", "", caption)
  cap
}

# helper: escape LaTeX special chars in plain captions
escape_latex_text <- function(x) {
  if (is.null(x)) return(x)
  if (!knitr::is_latex_output()) return(x)
  gsub("[\\\\\\\\%$&#{}_\\\\^]", "\\\\\\\\\\\"1", x, perl = TRUE)
}

# Float barrier: emit only when a float has just been produced
float_barrier_pending <- FALSE
mark_float_emitted <- function() {
  float_barrier_pending <- TRUE
  invisible(TRUE)
}
float_barrier <- function() {
  if (!knitr::is_latex_output()) return(invisible(NULL))
}

```

```

if (!isTRUE(float_barrier_pending)) return(invisible(NULL))
float_barrier_pending <- FALSE
knitr::asis_output("\\FloatBarrier\\nopagebreak")
}

# helper: render full tables for PDF (no previews)
render_table_pdf <- function(df, caption, file_stub,
                             wide = FALSE,
                             digits = 2,
                             max_cols = 6,
                             landscape = NULL) {
  stopifnot(is.data.frame(df))
  out_csv <- results_path(paste0(file_stub, ".csv"))
  write_csv_safely(df, out_csv, row_names = FALSE)

  if (is.null(landscape)) landscape <- (wide || ncol(df) > max_cols)
  use_longtable <- nrow(df) > 40
  n_cols <- ncol(df)
  parts <- if (n_cols <= max_cols) list(df) else {
    idx <- split(seq_len(n_cols), ceiling(seq_len(n_cols) / max_cols))
    lapply(idx, function(ii) df[, ii, drop = FALSE])
  }

  build_kbl <- function(df_part, cap) {
    cap <- escape_latex_text(strip_manual_table_number(cap))
    kbl <- knitr::kable(
      df_part,
      format     = "latex",
      booktabs   = TRUE,
      longtable  = use_longtable,
      caption    = cap,
      digits     = digits
    )
    kbl <- kableExtra::kable_styling(
      kbl,
      latex_options = if (use_longtable) c("repeat_header") else c("hold_position", "scale_down"),
      ...
    )
  }
}

```

```

    font_size      = if (ncol(df_part) > max_cols || wide) 6 else 7,
    full_width    = FALSE,
    position      = "center"
)
if (landscape) kbl <- kableExtra::landscape(kbl)
kbl
}

if (length(parts) == 1L) {
  mark_float_emitted()
  return(build_kbl(parts[[1]], caption))
}

letters_part <- LETTERS[seq_along(parts)]
out <- character(0)
for (i in seq_along(parts)) {
  cap_i <- paste0(caption, " (Part ", letters_part[i], ")")
  out <- c(out, build_kbl(parts[[i]], cap_i))
}
mark_float_emitted()
knitr::asis_output(paste(out, collapse = "\n\n"))
}

render_table_pdf_maybe <- function(df, caption, file_stub,
                                    wide = FALSE,
                                    digits = 2,
                                    max_cols = 6,
                                    landscape = NULL,
                                    show = TRUE) {

tbl <- render_table_pdf(
  df,
  caption = caption,
  file_stub = file_stub,
  wide = wide,
  digits = digits,
  max_cols = max_cols,

```

```

    landscape = landscape
)
if (isTRUE(show)) {
  return(tbl)
}
invisible(NULL)
}

```

1.0.1 Package Set Up

```

# Consolidated package management -----
required_pkgs <- c(
  "WeightIt", "broom", "cobalt", "codebookr", "dplyr", "flextable", "parallel",
  "gbm", "ggplot2", "gt", "gtsummary", "haven", "labelled", "scales",
  "modelsummary", "officer", "patchwork", "rms", "survey", "tibble", "lubridate",
  "sensitivitymw", "here", "fs", "dagitty", "ggdag", "naniar", "mice", "miceadds",
  "digest"
)

# Fail fast if packages are missing (use renv to install)
missing_pkgs <- setdiff(required_pkgs, rownames(installed.packages()))
if (length(missing_pkgs)) {
  stop(
    "Missing packages: ", paste(missing_pkgs, collapse = ", "),
    ". Install with renv::install(c(...)) and then run renv::snapshot()."
  )
}

# Load (or attach) all required packages
invisible(lapply(required_pkgs, require, character.only = TRUE))

# Centralize outputs under Results/, with paths relative to project root
qmd_dir <- here::here("Code Drafts")
data_dir_param <- Sys.getenv("ABGVBG_DATA_DIR", unset = params$data_dir)

```

```

results_dir_param <- Sys.getenv("ABGVBG_RESULTS_DIR", unset = params$results_dir)
data_dir_name <- fs::path_abs(data_dir_param, start = here::here())
results_dir <- fs::path_abs(results_dir_param, start = here::here())
if (!dir.exists(data_dir_name)) {
  stop("Data directory does not exist: ", data_dir_name)
}
fs::dir_create(results_dir, recurse = TRUE)
fig_dir      <- fs::path(results_dir, "figs")
fig_path     <- paste0(fs::path_rel(fig_dir, start = qmd_dir), "/")
results_path <- function(...) fs::path(results_dir, ...)
fs::dir_create(fig_dir, recurse = TRUE)

knitr::opts_chunk$set(
  fig.path    = fig_path,
  dev         = "ragg_png",
  dpi         = 200
)
# on macOS and some setups this prevents device headaches
options(bitmapType = "cairo")

```

```

flow_png <- results_path("cohort_flow.png")
flow_pdf <- results_path("cohort_flow.pdf")
if (file.exists(flow_png) || file.exists(flow_pdf)) {
  knitr::include_graphics(if (file.exists(flow_png)) flow_png else flow_pdf)
} else {
  cat("Cohort flow diagram will be generated externally and inserted here in the final manuscript packet.\n")
}

```

Cohort flow diagram will be generated externally and inserted here in the final manuscript packet.

```

stopifnot(!is.null(params$run_mode))
stopifnot(!is.null(params$pilot_frac))
stopifnot(!is.null(params$mi_batch_threshold_pilot))
stopifnot(!is.null(params$mi_batch_threshold_full))
stopifnot(!is.null(params$sample_seed))

```

```

RUN_MODE <- match.arg(tolower(params$run_mode), c("pilot", "full"))
PILOT_FRAC <- as.numeric(params$pilot_frac)
stopifnot(is.finite(PILOT_FRAC), PILOT_FRAC > 0, PILOT_FRAC <= 1)
if (RUN_MODE == "full") PILOT_FRAC <- 1
SAMPLE_SEED <- as.integer(params$sample_seed)
stopifnot(is.finite(SAMPLE_SEED))

pilot_frac <- PILOT_FRAC
FULL_RUN <- identical(RUN_MODE, "full")
SHOW_LOW_VALUE_TABLES <- FALSE
MI_BATCH_THRESHOLD <- if (RUN_MODE == "pilot") {
  as.integer(params$mi_batch_threshold_pilot)
} else {
  as.integer(params$mi_batch_threshold_full)
}
stopifnot(is.finite(MI_BATCH_THRESHOLD), MI_BATCH_THRESHOLD > 0)
PLOT_DROP_POLICY <- "warn"
PROB_EPS <- 1e-6
MAX_SHAPE_LEVELS <- 6L
SPLINE_GRID_N <- 200L
OR_XLIM <- c(0.25, 16)
TAIL_NFINITE <- 5L
TAIL_WINDOW_ITERS <- 10L
BAL_XLIM_MAX <- 1.0
MC_ERR_RATIO_THRESH <- 0.10
SHOW_CHUNK_RUNTIME_TEXT <- FALSE
MAX_LEVELS_GBM <- 50L
GBM_MM_EST_BYTES_WARN <- 6e9
MAX_GBM_MM_COLS_WARN <- 200L
MAX_GBM_MM_COLS_STOP <- 400L
MAX_GBM_FACTOR_LEVELS_WARN <- 30L
MAX_GBM_FACTOR_LEVELS_STOP <- 60L

message(
  "CONFIG: RUN_MODE=", RUN_MODE,

```

```

  " | PILOT_FRAC=", PILOT_FRAC,
  " | SAMPLE_SEED=", SAMPLE_SEED
)

diag_run_id <- format(Sys.time(), "%Y%m%d_%H%M%S")
diag_run_ts <- as.character(Sys.time())
run_id <- diag_run_id
run_ts <- diag_run_ts
runtime_run_id <- diag_run_id
options(run_id = run_id, run_ts = run_ts)
runtime_log <- data.frame()
mi_warn_log <- data.frame(
  time = character(), stage = character(), component = character(),
  analysis_variant = character(), model_type = character(),
  group = character(), outcome = character(), imputation = integer(),
  batch = integer(), message = character(), stringsAsFactors = FALSE
)
mi_info_log <- mi_warn_log
mi_outcome_diag <- data.frame()
memory_snapshots <- data.frame()
gbm_preflight_design_dims <- data.frame()
gbm_preflight_warnings <- data.frame()
factor_diag_written <- character()
plot_drop_log_df <- data.frame(
  plot = character(), reason = character(), n_dropped = integer(),
  n_before = integer(), n_after = integer(),
  stage = character(), extra = character(),
  stringsAsFactors = FALSE
)
cleanup_diagnostics_outputs <- function() {
  diag_files <- c(
    "runtime_log.csv", "runtime_summary.csv", "runtime_summary_top15.csv",
    "warnings_log.csv", "mi_warnings_log.csv", "mi_info_log.csv",
    "diagnostics_summary.csv", "diagnostics_missingness.csv",
    "diagnostics_missingness-by-strata.csv",

```

```

"balance_target_imp_summary.csv", "balance_target_by_imp.csv",
"balance_target_worst_rows.csv", "balance_max_smd_by_imp.csv",
"balance_worst_terms.csv", "balance_worst10.csv", "balance_table.csv",
"weight_summary.csv", "ps_overlap_summary.csv",
"model_fit_diagnostics.csv", "mi_outcome_fit_diagnostics.csv",
"mi_fit_issue_summary.csv", "mi_m_stability.csv", "mi_maxit_sensitivity.csv",
"mi_obs_vs_imp_summary.csv", "mi_spline_curve_abg.csv",
"mi_spline_curve_vbg.csv", "mi_spline_coef_abg.csv",
"mi_spline_coef_vbg.csv", "diag-ps-shap-stability.csv",
"mice_smoketest.log", "mice_batches_log.csv", "mice_chain_diagnostics.csv",
"mice_pred_width_preflight.csv", "mice_logged_events_raw.csv",
"mice_logged_events_summary.csv", "mice_spec.rds",
"missingness-by-strata.csv", "missingness-drivers.csv",
"missingness-pattern.csv", "plot_drop_log.csv",
"plot_registry.csv",
"mi_logistic_ps_covariate_types.csv",
"mi_logistic_ps_abg_list.rds",
"mi_logistic_ps_vbg_list.rds"
)
diag_patterns <- c(
  "^mice_.*\\.(csv|log|rds|txt)$",
  "^diagnostics_.*\\(.csv$",
  "^runtime_.*\\(.csv$",
  "^warnings_.*\\(.csv$",
  "^balance_.*\\(.csv$",
  "^weight_summary\\(.csv$",
  "^ps_overlap_summary\\(.csv$",
  "^model_fit_diagnostics\\(.csv$",
  "^plot_drop_log\\(.csv$",
  "^diag-.*\\(.csv$",
  "^mi_logistic_ps_.*\\(.csv|rds)$"
)
files <- list.files(results_dir, full.names = TRUE)
base <- basename(files)
match_files <- base %in% diag_files
if (length(diag_patterns)) {

```

```

  match_files <- match_files | grepl(paste(diag_patterns, collapse = "|"), base)
}
to_delete <- files[match_files]
if (length(to_delete)) {
  safe_root <- normalizePath(results_dir, winslash = "/", mustWork = FALSE)
  del_paths <- normalizePath(to_delete, winslash = "/", mustWork = FALSE)
  stopifnot(all(startsWith(del_paths, safe_root)))
}
fs::file_delete(to_delete)

diag_figs <- list.files(fig_dir, full.names = TRUE)
diag_figs <- diag_figs[grep("^(diag-|or-plot|ps-)", basename(diag_figs))]
if (length(diag_figs)) {
  safe_root <- normalizePath(results_dir, winslash = "/", mustWork = FALSE)
  del_paths <- normalizePath(diag_figs, winslash = "/", mustWork = FALSE)
  stopifnot(all(startsWith(del_paths, safe_root)))
}
fs::file_delete(diag_figs)
{
  d <- fs::path(results_dir, "mice_batches")
  if (dir.exists(d)) fs::dir_delete(d)
}
{
  d <- fs::path(results_dir, "diagnostics_audit_snippets")
  if (dir.exists(d)) fs::dir_delete(d)
}
{
  f <- fs::path(results_dir, "mi_partial_mids.rds")
  if (file.exists(f)) fs::file_delete(f)
}
}

cleanup_diagnostics_outputs()
# Ensure any stale Results artifacts from prior runs are removed
stale_patterns <- c(
  "^missingness_by_strata\\.csv$",

```

```

"~missingness-drivers\\.csv$",
"~missingness_by_strata_preview\\.csv$",
"~missingness_drivers_top20\\.csv$",
"~missingness_top10\\.csv$",
"~outcome_counts_by_cohort\\.csv$",
"~weighting_diagnostics_non_mi\\.csv$",
"~mi_specification\\.csv$",
"~memory_snapshots\\.csv$",
"~gbm_preflight_design_dims\\.csv$",
"~gbm_preflight_factor_levels_.*\\.csv$",
"~mi_logistic_ps_factor_levels_.*\\.csv$",
"~mi_logistic_ps_.*\\.(csv|rds)$",
"~get_imp_usage\\.csv$",
"~diagnostics_audit\\.md$",
"~pdf_page_text_stats\\.csv$",
"~pdf_blank_pages\\.json$",
"~pdf_hygiene_scan\\.csv$"
)
stale_files <- list.files(results_dir, full.names = TRUE)
stale_base <- basename(stale_files)
stale_files <- stale_files[grepl(paste(stale_patterns, collapse = "|"), stale_base)]
if (length(stale_files)) fs::file_delete(stale_files)

```

1.1 Helper functions for model diagnostics

```

# Diagnostics helper functions for MI/IPW pipeline

assert_no_na_covars <- function(df, covars, context = "") {
  missing <- setdiff(covars, names(df))
  stopifnot(length(missing) == 0)
  na_counts <- vapply(df[, covars, drop = FALSE], function(x) sum(is.na(x)), numeric(1))
  if (any(na_counts > 0)) {
    msg <- paste0(
      "NA values found in covariates (", context, "): ",

```

```

    paste(names(na_counts)[na_counts > 0], na_counts[na_counts > 0], collapse = ", ")
)
stop(msg)
}
invisible(TRUE)
}

summarize_logged_events <- function(mids_obj) {
  ev <- mids_obj$loggedEvents
  if (is.null(ev) || nrow(ev) == 0L) {
    return(data.frame(
      variable = character(),
      method = character(),
      event = character(),
      n = integer(),
      pct = numeric(),
      stringsAsFactors = FALSE
    ))
  }
  stopifnot(all(c("dep", "meth", "out") %in% names(ev)))
  tbl <- as.data.frame(table(ev$dep, ev$meth, ev$out), stringsAsFactors = FALSE)
  names(tbl) <- c("variable", "method", "event", "n")
  tbl <-tbl[tbl$n > 0, , drop = FALSE]
  tbl <-tbl[order(-tbl$n), , drop = FALSE]
  tbl$pct <-tbl$n / sum(tbl$n)
  tbl
}

extract_weightit_ps <- function(w) {
  stopifnot(!is.null(w$ps))
  as.numeric(w$ps)
}

ess <- function(w) {
  w <- w[is.finite(w)]
  stopifnot(length(w) > 0)
}

```

```

    sum(w)^2 / sum(w^2)
}

weight_concentration <- function(w, top_p = 0.01) {
  w <- w[is.finite(w)]
  stopifnot(length(w) > 0)
  ord <- sort(w, decreasing = TRUE)
  n_top <- max(1L, floor(length(ord) * top_p))
  sum(ord[seq_len(n_top)]) / sum(ord)
}

weight_summary <- function(w, ps, ps_floor, truncated) {
  w_ok <- w[is.finite(w)]
  stopifnot(length(w_ok) > 0)
  ps_ok <- ps[is.finite(ps)]
  stopifnot(length(ps_ok) > 0)
  out <- data.frame(
    n = length(w_ok),
    mean = mean(w_ok, na.rm = TRUE),
    sd = stats::sd(w_ok, na.rm = TRUE),
    min = min(w_ok, na.rm = TRUE),
    p01 = stats::quantile(w_ok, 0.01, na.rm = TRUE),
    p05 = stats::quantile(w_ok, 0.05, na.rm = TRUE),
    p95 = stats::quantile(w_ok, 0.95, na.rm = TRUE),
    p99 = stats::quantile(w_ok, 0.99, na.rm = TRUE),
    max = max(w_ok, na.rm = TRUE),
    sum_w = sum(w_ok, na.rm = TRUE),
    ess = ess(w_ok),
    top01_weight_share = weight_concentration(w_ok, top_p = 0.01),
    ps_floor = ps_floor,
    trunc_rate = mean(truncated, na.rm = TRUE),
    ps_min = min(ps_ok, na.rm = TRUE),
    ps_p01 = stats::quantile(ps_ok, 0.01, na.rm = TRUE),
    ps_p05 = stats::quantile(ps_ok, 0.05, na.rm = TRUE),
    ps_p95 = stats::quantile(ps_ok, 0.95, na.rm = TRUE),
    ps_max = max(ps_ok, na.rm = TRUE),

```

```

    stringsAsFactors = FALSE
)
out
}

compute_ipow_weights <- function(w, treat, ps_floor_quantile = 0.01,
                                  stabilize = TRUE) {
  ps <- extract_weightit_ps(w)
  if (length(ps) != length(treat)) stop("Propensity length mismatch.")
  treat <- as.integer(treat)
  if (!all(treat %in% c(0L, 1L))) stop("Treatment indicator must be 0/1.")

  ps_obs <- ps[treat == 1L & is.finite(ps)]
  if (!length(ps_obs)) stop("No treated observations with finite propensity.")
  ps_floor <- as.numeric(stats::quantile(ps_obs, probs = ps_floor_quantile, na.rm = TRUE))
  if (!is.finite(ps_floor) || ps_floor <= 0) stop("Invalid propensity floor.")

  w_raw <- rep(NA_real_, length(ps))
  w_raw[treat == 1L] <- 1 / ps[treat == 1L]

  cap <- 1 / ps_floor
  truncated <- treat == 1L & is.finite(ps) & ps < ps_floor
  w_trunc <- w_raw
  w_trunc[truncated] <- cap

  if (stabilize) {
    w_trunc <- w_trunc / mean(w_trunc[treat == 1L], na.rm = TRUE)
  }

  list(
    weights    = w_trunc,
    ps         = ps,
    ps_floor   = ps_floor,
    cap        = cap,
    truncated  = truncated
  )
}

```

```

}

assert_finite_weights <- function(w, name = "weights") {
  if (any(!is.finite(w))) {
    stop("Non-finite values detected in ", name, ".")
  }
  invisible(TRUE)
}

runtime_logger <- function(step_name, expr, notes = NA_character_) {
  start_time <- Sys.time()
  result <- eval(expr)
  end_time <- Sys.time()
  sec <- as.numeric(difftime(end_time, start_time, units = "secs"))
  row <- data.frame(
    step_name = step_name,
    seconds = sec,
    start_time = as.character(start_time),
    end_time = as.character(end_time),
    notes = notes,
    run_id = runtime_run_id,
    run_mode = RUN_MODE,
    n_subset = subset_n,
    stringsAsFactors = FALSE
  )
  runtime_log <- dplyr::bind_rows(runtime_log, row)
  result
}

make_context <- function(stage, component,
                        analysis_variant = NA_character_,
                        model_type = NA_character_,
                        group = NA_character_,
                        outcome = NA_character_,
                        imputation = NA_integer_,
                        batch = NA_integer_) {

```

```

list(
  stage = stage,
  component = component,
  analysis_variant = analysis_variant,
  model_type = model_type,
  group = group,
  outcome = outcome,
  imputation = imputation,
  batch = batch
)
}

capture_warnings <- function(expr, context) {
  warn_rows <- list()
  stopifnot(all(c("stage", "component", "analysis_variant", "model_type",
    "group", "outcome", "imputation", "batch") %in% names(context)))
  ctx <- list(
    stage = as.character(context$stage),
    component = as.character(context$component),
    analysis_variant = as.character(context$analysis_variant),
    model_type = as.character(context$model_type),
    group = as.character(context$group),
    outcome = as.character(context$outcome),
    imputation = as.integer(context$imputation),
    batch = as.integer(context$batch)
  )
  val <- withCallingHandlers(
    expr,
    warning = function(w) {
      warn_rows <- append(warn_rows, list(data.frame(
        time = as.character(Sys.time()),
        stage = ctx$stage,
        component = ctx$component,
        analysis_variant = ctx$analysis_variant,
        model_type = ctx$model_type,
        group = ctx$group,

```

```

    outcome = ctx$outcome,
    imputation = ctx$imputation,
    batch = ctx$batch,
    message = conditionMessage(w),
    stringsAsFactors = FALSE
  )))
  invokeRestart("muffleWarning")
}
)
warnings_df <- if (length(warn_rows)) {
  dplyr::bind_rows(warn_rows)
} else {
  data.frame(
    time = character(), stage = character(), component = character(),
    analysis_variant = character(), model_type = character(),
    group = character(), outcome = character(), imputation = integer(),
    batch = integer(), message = character(), stringsAsFactors = FALSE
  )
}
list(value = val, warnings = warnings_df)
}

append_warnings <- function(wlist) {
  stopifnot(is.data.frame(wlist) || is.list(wlist))
  df <- if (is.data.frame(wlist)) wlist else dplyr::bind_rows(wlist)
  stopifnot(is.data.frame(df))
  stopifnot("message" %in% names(df))
  info_rows <- df[grep("Number of logged events", df$message), , drop = FALSE]
  if (nrow(info_rows)) {
    mi_info_log <- dplyr::bind_rows(mi_info_log, info_rows)
  }
  df <- df[!grep("Number of logged events", df$message), , drop = FALSE]
  if (nrow(df) == 0L) return(invisible(FALSE))
  mi_warn_log <- dplyr::bind_rows(mi_warn_log, df)
  invisible(TRUE)
}

```

```

collect_warnings_from_list <- function(xlist) {
  warn_list <- lapply(xlist, function(x) {
    if (is.list(x) && !is.null(x$warnings)) x$warnings else NULL
  })
  warn_list <- warn_list[!vapply(warn_list, is.null, logical(1))]
  append_warnings(warn_list)
  invisible(TRUE)
}

append_outcome_diag <- function(df) {
  stopifnot(is.data.frame(df))
  if (nrow(df) == 0L) return(invisible(FALSE))
  mi_outcome_diag <- dplyr::bind_rows(mi_outcome_diag, df)
  invisible(TRUE)
}

summarize_warnings_log <- function(path = results_path("warnings_log.csv")) {
  warn_df <- read.csv(path, stringsAsFactors = FALSE)
  if (nrow(warn_df) == 0L) return(data.frame())
  warn_df |>
    dplyr::count(stage, component, analysis_variant, model_type, message, sort = TRUE)
}

write_csv_safely <- function(df, path, row_names = FALSE, required_cols = NULL) {
  run_id <- diag_run_id
  run_ts <- diag_run_ts
  stopifnot(!is.null(df))
  df <- as.data.frame(df)
  # Normalize pillar/vctrs numeric classes to base numeric for CSV export
  df <- dplyr::mutate(
    df,
    dplyr::across(
      where(~ inherits(.x, "pillar_num")),
      ~ suppressWarnings(as.numeric(.x))
    )
}

```

```

)
if (!is.null(required_cols)) {
  missing <- setdiff(required_cols, names(df))
  stopifnot(length(missing) == 0)
}
if (nrow(df) == 0L) {
  if (!("empty" %in% names(df))) df$empty <- logical(0)
}
df$run_id <- rep(run_id, nrow(df))
df$run_ts <- rep(run_ts, nrow(df))
utils::write.csv(df, path, row.names = row_names)
invisible(TRUE)
}

write_diag_lines <- function(lines, path) {
  run_id <- diag_run_id
  run_ts <- diag_run_ts
  header <- paste0("run_id: ", run_id, " run_ts: ", run_ts)
  writeLines(c(header, lines), con = path)
  invisible(TRUE)
}

droplevels_all <- function(df, vars = NULL) {
  if (is.null(vars)) {
    vars <- names(df)[vapply(df, is.factor, logical(1))]
  } else {
    vars <- intersect(vars, names(df))
    vars <- vars[vapply(df[,vars], is.factor, logical(1))]
  }
  for (nm in vars) df[[nm]] <- droplevels(df[[nm]])
  df
}

append_mem_snapshot <- function(stage_id, context_id = NA_character_, when = "pre") {
  g <- gc()
  cn <- colnames(g)

```

```

used_col <- if ("used" %in% cn) "used" else cn[grepl("used", cn)][1]
trig_col <- if ("gc trigger" %in% cn) "gc trigger" else cn[grepl("trigger", cn)][1]
max_col <- if ("max used" %in% cn) "max used" else cn[grepl("max", cn)][1]
n_used <- as.numeric(g["Ncells", used_col])
v_used <- as.numeric(g["Vcells", used_col])
v_trig <- as.numeric(g["Vcells", trig_col])
v_max <- as.numeric(g["Vcells", max_col])
mem_max <- tryCatch(mem.maxVSize(), error = function(e) NA_real_)
row <- data.frame(
  run_id = diag_run_id,
  run_ts = diag_run_ts,
  stage_id = stage_id,
  context_id = context_id,
  when = when,
  time = as.character(Sys.time()),
  Ncells_used = n_used,
  Vcells_used = v_used,
  Vcells_gc_trigger = v_trig,
  Vcells_max_used = v_max,
  mem_max_vszie = mem_max,
  stringsAsFactors = FALSE
)
memory_snapshots <- dplyr::bind_rows(memory_snapshots, row)
invisible(TRUE)
}

write_factor_levels_diag <- function(df, vars, context_id, file_prefix = "gbm_preflight_factor_levels") {
  key <- paste0(file_prefix, "::", context_id)
  if (key %in% factor_diag_written) {
    return(invisible(FALSE))
  }
  vars <- intersect(vars, names(df))
  if (!length(vars)) {
    return(invisible(FALSE))
  }
  diag <- lapply(vars, function(v) {

```

```

x <- df[[v]]
if (!is.factor(x)) return(NULL)
tab <- table(x, useNA = "ifany")
n_unused <- sum(tab == 0)
top <- utils::head(sort(tab, decreasing = TRUE), 5)
data.frame(
  variable = v,
  class = class(x)[1],
  nlevels = nlevels(x),
  n_unused_levels = n_unused,
  top_levels = paste(names(top), as.integer(top), sep = "=", collapse = "; "),
  n_missing = sum(is.na(x)),
  context_id = context_id,
  stringsAsFactors = FALSE
)
})
diag <- dplyr::bind_rows(diag)
if (nrow(diag) == 0L) return(invisible(FALSE))
out_path <- results_path(paste0(file_prefix, "_", context_id, ".csv"))
write_csv_safely(diag, out_path, row_names = FALSE)
factor_diag_written <- c(factor_diag_written, key)
invisible(TRUE)
}

log_design_dims <- function(df, covars, context_id, sample_n = 5000L) {
  covars <- intersect(covars, names(df))
  if (!length(covars)) return(invisible(FALSE))
  n_full <- nrow(df)
  n_samp <- min(sample_n, n_full)
  set.seed(20251206)
  idx <- sample.int(n_full, n_samp)
  df_s <- df[idx, covars, drop = FALSE]
  fml <- stats::as.formula(paste("~", paste(covars, collapse = " + ")))
  mm <- stats::model.matrix(fml, data = df_s)
  n_factor <- sum(vapply(df_s, is.factor, logical(1)))
  max_nlevels <- if (n_factor > 0) max(vapply(df_s[vapply(df_s, is.factor, logical(1))], nlevels, integer(1))) else 0L
}

```

```

row <- data.frame(
  run_id = diag_run_id,
  run_ts = diag_run_ts,
  context_id = context_id,
  nrow_full = n_full,
  nrow_sample = n_samp,
  ncol_model_matrix = ncol(mm),
  n_factor_vars = n_factor,
  max_nlevels_factor = max_nlevels,
  stringsAsFactors = FALSE
)
gbm_preflight_design_dims <- dplyr::bind_rows(gbm_preflight_design_dims, row)
invisible(TRUE)
}

gbm_preflight <- function(df, covars, context_id, sample_n = 50000L) {
  df <- droplevels_all(df)
  write_factor_levels_diag(df, covars, context_id, file_prefix = "gbm_preflight_factor_levels")
  covars <- intersect(covars, names(df))
  if (!length(covars)) return(invisible(FALSE))
  n_full <- nrow(df)
  n_samp <- min(sample_n, n_full)
  set.seed(20251206)
  idx <- sample.int(n_full, n_samp)
  df_s <- df[idx, covars, drop = FALSE]
  fml <- stats::as.formula(paste("~", paste(covars, collapse = " + ")))
  mm <- stats::model.matrix(fml, data = df_s)
  n_factor <- sum(vapply(df_s, is.factor, logical(1)))
  max_nlevels <- if (n_factor > 0) {
    max(vapply(df_s[vapply(df_s, is.factor, logical(1))], nlevels, integer(1)))
  } else 0L
  est_bytes <- n_full * ncol(mm) * 8
  row <- data.frame(
    run_id = diag_run_id,
    run_ts = diag_run_ts,
    context_id = context_id,

```

```

nrow_full = n_full,
nrow_sample = n_samp,
ncol_model_matrix = ncol(mm),
n_factor_vars = n_factor,
max_nlevels_factor = max_nlevels,
est_bytes = est_bytes,
est_gb = est_bytes / 1024^3,
stringsAsFactors = FALSE
)
gbm_preflight_design_dims <- dplyr::bind_rows(gbm_preflight_design_dims, row)
warn_msgs <- character()
if (is.finite(est_bytes) && est_bytes > GBM_MM_EST_BYTES_WARN) {
  warn_msgs <- c(warn_msgs, paste0("est_dense_mm_gb>", round(GBM_MM_EST_BYTES_WARN / 1024^3, 2)))
}
if (ncol(mm) > MAX_GBM_MM_COLS_WARN) {
  warn_msgs <- c(warn_msgs, paste0("mm_cols_warn>", MAX_GBM_MM_COLS_WARN))
}
if (max_nlevels > MAX_GBM_FACTOR_LEVELS_WARN) {
  warn_msgs <- c(warn_msgs, paste0("factor_levels_warn>", MAX_GBM_FACTOR_LEVELS_WARN))
}
if (length(warn_msgs)) {
  gbm_preflight_warnings <- dplyr::bind_rows(
    gbm_preflight_warnings,
    data.frame(
      run_id = diag_run_id,
      run_ts = diag_run_ts,
      context_id = context_id,
      nrow_full = n_full,
      ncol_model_matrix = ncol(mm),
      max_nlevels_factor = max_nlevels,
      est_gb = est_bytes / 1024^3,
      warning = paste(warn_msgs, collapse = ";"),
      stringsAsFactors = FALSE
    )
  )
}

```

```

if (ncol(mm) > MAX_GBM_MM_COLS_STOP || max_nlevels > MAX_GBM_FACTOR_LEVELS_STOP) {
  stop(
    "GBM preflight stop: context=", context_id,
    "; ncol_model_matrix=", ncol(mm),
    "; max_nlevels_factor=", max_nlevels,
    ". Consider collapsing factor levels or removing high-cardinality predictors."
  )
}
invisible(TRUE)
}

print_head <- function(df, n = 10, title = NULL) {
  if (!is.null(title)) message(title)
  if (is.null(df) || nrow(df) == 0L) {
    message("No rows to display.")
    return(invisible(FALSE))
  }
  print(utils::head(df, n))
  invisible(TRUE)
}

assert_is_df <- function(x, context = "") {
  if (is.null(x)) {
    stop(context, ": object is NULL")
  }
  if (!inherits(x, "data.frame")) {
    stop(context, ": expected data.frame/tibble; got class=",
        paste(class(x), collapse = ", "), " typeof=", typeof(x))
  }
  invisible(TRUE)
}

assert_has_cols <- function(df, cols, context = "") {
  missing <- setdiff(cols, names(df))
  if (length(missing)) {
    stop(context, ": missing required columns: ", paste(missing, collapse = ", "))
  }
}

```

```

}

invisible(TRUE)
}

safe_nrow <- function(df, context = "") {
  assert_is_df(df, context)
  nr <- nrow(df)
  if (!is.numeric(nr) || length(nr) != 1L || is.na(nr)) {
    stop(context, ": nrow(df) returned invalid value: ",
         paste0(capture.output(str(nr)), collapse = " "))
  }
  as.integer(nr)
}

plot_drop_log <- function() {
  plot_drop_log_df
}

log_plot_drop <- function(plot_name, reason, n_dropped,
                           n_before = NA_integer_, n_after = NA_integer_,
                           stage = NA_character_, extra = NA_character_) {
  plot_drop_log_df <- dplyr::bind_rows(
    plot_drop_log(),
    data.frame(plot = plot_name, reason = reason, n_dropped = n_dropped,
               n_before = n_before, n_after = n_after,
               stage = stage, extra = extra,
               stringsAsFactors = FALSE)
  )
  if (identical(PLOT_DROP_POLICY, "stop")) {
    stop("Plot data dropped in ", plot_name, ":", reason)
  } else {
    warning("Plot data dropped in ", plot_name, ":", reason, call. = FALSE)
  }
}

fit_with_diagnostics <- function(fit_fun, context, prob_eps = PROB_EPS) {

```

```

stopifnot(all(c("stage", "component", "analysis_variant", "model_type",
              "group", "outcome", "imputation", "batch") %in% names(context)))
cap <- capture_warnings(
  tryCatch(fit_fun(), error = function(e) e),
  context = context
)
append_warnings(cap$warnings)
fit <- cap$value
warn_msgs <- if (is.data.frame(cap$warnings)) cap$warnings$message else character()
warning_n <- if (is.data.frame(cap$warnings)) nrow(cap$warnings) else 0L
top_warning <- if (warning_n) warn_msgs[1] else NA_character_

if (inherits(fit, "error")) {
  diag <- data.frame(
    stage = as.character(context$stage),
    component = as.character(context$component),
    analysis_variant = as.character(context$analysis_variant),
    model_type = as.character(context$model_type),
    group = as.character(context$group),
    outcome = as.character(context$outcome),
    imputation = as.integer(context$imputation),
    n_used = NA_integer_, events = NA_integer_,
    converged = NA, iter = NA_integer_,
    sep_flag = NA, nonconv_flag = NA,
    min_phat = NA_real_, max_phat = NA_real_,
    warning_n = warning_n, top_warning = top_warning,
    error_message = conditionMessage(fit),
    stringsAsFactors = FALSE
  )
  return(list(fit = NULL, diag = diag, warnings = cap$warnings))
}

phat <- tryCatch(fitted(fit), error = function(e) NA_real_)
min_phat <- if (all(is.na(phat))) NA_real_ else min(phat, na.rm = TRUE)
max_phat <- if (all(is.na(phat))) NA_real_ else max(phat, na.rm = TRUE)
sep_flag <- FALSE

```

```

if (is.finite(min_phat) && min_phat < prob_eps) sep_flag <- TRUE
if (is.finite(max_phat) && max_phat > 1 - prob_eps) sep_flag <- TRUE
if (any(grepl("fitted probabilities numerically 0 or 1", warn_msgs, fixed = TRUE))) sep_flag <- TRUE

conv_val <- if (!is.null(fit$converged)) isTRUE(fit$converged) else NA
iter_val <- if (!is.null(fit$iter)) fit$iter else NA_integer_
nonconv_flag <- isFALSE(conv_val) || any(grepl("did not converge", warn_msgs, fixed = TRUE))

mf <- tryCatch(model.frame(fit), error = function(e) NULL)
y <- if (!is.null(mf)) tryCatch(model.response(mf), error = function(e) NULL) else NULL
n_used <- if (!is.null(y)) length(y) else NA_integer_
events <- if (!is.null(y) && is.numeric(y)) sum(y == 1, na.rm = TRUE) else NA_integer_

diag <- data.frame(
  stage = as.character(context$stage),
  component = as.character(context$component),
  analysis_variant = as.character(context$analysis_variant),
  model_type = as.character(context$model_type),
  group = as.character(context$group),
  outcome = as.character(context$outcome),
  imputation = as.integer(context$imputation),
  n_used = n_used, events = events,
  converged = conv_val, iter = iter_val,
  sep_flag = sep_flag, nonconv_flag = nonconv_flag,
  min_phat = min_phat, max_phat = max_phat,
  warning_n = warning_n, top_warning = top_warning,
  error_message = NA_character_,
  stringsAsFactors = FALSE
)
list(fit = fit, diag = diag, warnings = cap$warnings)
}

pooled_mi_vcov_check <- function(pooled) {
  if (is.null(pooled$variance)) stop("MIcombine object missing variance matrix.")
  V <- pooled$variance
  if (any(!is.finite(V))) stop("Non-finite pooled variance detected.")
}

```

```

within <- attr(pooled, "within")
between <- attr(pooled, "between")
if (!is.null(within) && any(!is.finite(within))) stop("Non-finite within variance.")
if (!is.null(between) && any(!is.finite(between))) stop("Non-finite between variance.")
invisible(TRUE)
}

save_diag_plot <- function(p, file, width = 8, height = 6, dpi = 200) {
  ggplot2::ggsave(filename = file, plot = p, width = width, height = height, dpi = dpi)
  invisible(file)
}

plot_registry_path <- results_path("plot_registry.csv")

read_plot_registry <- function() {
  if (file.exists(plot_registry_path)) {
    utils::read.csv(plot_registry_path, stringsAsFactors = FALSE)
  } else {
    data.frame(
      run_id = character(), run_ts = character(),
      plot_name = character(), fig_path = character(), md5 = character(),
      stringsAsFactors = FALSE
    )
  }
}

write_plot_registry <- function(df) {
  write_csv_safely(df, plot_registry_path, row.names = FALSE)
}

register_plot_file <- function(plot_name, file, run_id = diag_run_id, run_ts = diag_run_ts) {
  md5 <- as.character(tools::md5sum(file))
  reg <- read_plot_registry()
  dup_name <- nrow(reg) > 0 &&
    any(reg$run_id == run_id & reg$plot_name == plot_name, na.rm = TRUE)
  if (dup_name) {

```

```

log_plot_drop(
  plot_name,
  "duplicate_figure",
  n_dropped = 1,
  n_before = NA_integer_,
  n_after = NA_integer_,
  stage = "plot_registry",
  extra = file
)
return(FALSE)
}
reg <- dplyr::bind_rows(
  reg,
  data.frame(run_id = run_id, run_ts = run_ts,
             plot_name = plot_name, fig_path = file, md5 = md5,
             stringsAsFactors = FALSE)
)
write_plot_registry(reg)
TRUE
}

print_plot_once <- function(p, plot_name, width = 8, height = 6, dpi = 200) {
  file <- results_path("figs", paste0(plot_name, ".png"))
  save_diag_plot(p, file, width = width, height = height, dpi = dpi)
  if (register_plot_file(plot_name, file)) {
    mark_float_emitted()
    knitr::include_graphics(file)
  } else {
    invisible(NULL)
  }
}

compute_or_axis_spec <- function(df_list, lo_col = "conf.low", hi_col = "conf.high",
                                   min_pow = -6, max_pow = 6,
                                   default_limits = c(0.25, 16)) {
  if (inherits(df_list, "data.frame")) df_list <- list(df_list)

```

```

if (!is.list(df_list)) df_list <- list(df_list)
vals <- unlist(lapply(df_list, function(df) {
  assert_is_df(df, context = "compute_or_axis_spec")
  stopifnot(all(c(lo_col, hi_col) %in% names(df)))
  lo <- df[[lo_col]]
  hi <- df[[hi_col]]
  c(lo, hi)
}), use.names = FALSE)
vals <- vals[is.finite(vals) & vals > 0]
if (!length(vals)) {
  lo_pow <- floor(log2(default_limits[1]))
  hi_pow <- ceiling(log2(default_limits[2]))
} else {
  lo_pow <- floor(log2(min(vals)))
  hi_pow <- ceiling(log2(max(vals)))
}
lo_pow <- max(lo_pow, min_pow)
hi_pow <- min(hi_pow, max_pow)
if (lo_pow > hi_pow) hi_pow <- lo_pow
limits <- 2^c(lo_pow, hi_pow)
breaks <- 2^(lo_pow:hi_pow)
list(limits = limits, breaks = breaks)
}

or_axis_scale <- function(spec) {
  list(
    ggplot2::scale_y_log10(
      breaks = spec$breaks,
      labels = scales::number_format(accuracy = 0.01)
    ),
    ggplot2::coord_cartesian(ylim = spec$limits)
  )
}

map_or_exposure <- function(df, plot_name) {
  assert_is_df(df, context = paste0("map_or_exposure(", plot_name, ")"))
}

```

```

stopifnot(nrow(df) > 0L)
stopifnot("term" %in% names(df))
df$term <- gsub("^", "", df$term)
df$exposure <- dplyr::case_when(
  grepl("^pc02_cat_abg", df$term) ~ gsub("^pc02_cat_abg", "", df$term),
  grepl("^pc02_cat_vbg", df$term) ~ gsub("^pc02_cat_vbg", "", df$term),
  grepl("^co2_cat", df$term)      ~ gsub("^co2_cat", "", df$term),
  TRUE                      ~ NA_character_
)
bad <- is.na(df$exposure) | !df$exposure %in% CO2_CAT_CONTRAST_LEVELS
if (any(bad)) {
  out_path <- results_path("or_term_mapping_failures.csv")
  bad_terms <- data.frame(term = df$term[bad], group = df$group[bad],
                           plot_name = plot_name, stringsAsFactors = FALSE)
  write_csv_safely(bad_terms, out_path, row_names = FALSE)
  stop(paste0("Unmapped OR terms in ", plot_name, ". See ", out_path))
}
df$exposure <- factor(df$exposure, levels = CO2_CAT_CONTRAST_LEVELS)
df
}

build_or_plot_df <- function(df, plot_name, expected_exposure_levels) {
  df <- tibble::as_tibble(df)
  req_cols <- c("outcome", "group", "estimate", "conf.low", "conf.high")
  req_cols <- c(req_cols, "exposure")
  assert_has_cols(df, unique(req_cols), context = paste0("build_or_plot_df(", plot_name, ")"))
  df <- dplyr::mutate(
    df,
    estimate = as.numeric(estimate),
    conf.low = as.numeric(conf.low),
    conf.high = as.numeric(conf.high)
  )
  if (safe_nrow(df, paste0("build_or_plot_df(", plot_name, ")")) == 0L) {
    stop("Empty OR plot data in ", plot_name)
  }
  drop <- !is.finite(df$estimate) | !is.finite(df$conf.low) | !is.finite(df$conf.high)
}

```

```

if (any(drop)) {
  log_plot_drop(plot_name, "non-finite estimate/conf", sum(drop),
                n_before = nrow(df), n_after = nrow(df) - sum(drop),
                stage = "build_or_plot_df")
  df <- df[!drop, , drop = FALSE]
}
drop_pos <- (df$estimate <= 0) | (df$conf.low <= 0) | (df$conf.high <= 0)
if (any(drop_pos, na.rm = TRUE)) {
  log_plot_drop(plot_name, "non-positive estimate/conf", sum(drop_pos, na.rm = TRUE),
                n_before = nrow(df), n_after = nrow(df) - sum(drop_pos, na.rm = TRUE),
                stage = "build_or_plot_df")
  df <- df[!drop_pos, , drop = FALSE]
}
exp_drop <- is.na(df$exposure) | trimws(as.character(df$exposure)) == ""
if (any(exp_drop)) {
  log_plot_drop(plot_name, "missing exposure level", sum(exp_drop),
                n_before = nrow(df), n_after = nrow(df) - sum(exp_drop),
                stage = "build_or_plot_df")
  df <- df[!exp_drop, , drop = FALSE]
}
df$exposure <- factor(df$exposure, levels = expected_exposure_levels)
bad_exp <- is.na(df$exposure)
if (any(bad_exp)) {
  bad_df <- df[bad_exp, , drop = FALSE]
  bad_path <- results_path(paste0("or_unmapped_terms_", plot_name, ".csv"))
  write_csv_safely(bad_df, bad_path, row_names = FALSE)
  stop(paste0("Unmapped exposure terms in ", plot_name, ". See ", bad_path))
}
missing_levels <- setdiff(expected_exposure_levels, unique(as.character(df$exposure)))
if (length(missing_levels)) {
  stop(paste0("Missing exposure levels in ", plot_name, ": ", paste(missing_levels, collapse = ", ")))
}
if (nrow(df) == 0L) {
  msg <- paste0("OR plot data empty after filtering in ", plot_name)
  stop(msg)
}

```

```

    df
}

plot_or_safe <- function(df, plot_name, axis_spec,
                         color_var = "group", shape_var = "exposure",
                         facet_var = NULL, title = NULL, caption = NULL) {
  df <- tibble::as_tibble(df)
  assert_is_df(df, context = paste0("plot_or_safe(", plot_name, ")"))
  nr <- safe_nrow(df, paste0("plot_or_safe(", plot_name, ")"))
  if (nr == 0L) {
    stop("plot_or_safe(", plot_name, "): no rows to plot.")
  }
  assert_has_cols(df, c("outcome", "group", "exposure", "estimate", "conf.low", "conf.high"),
                  context = paste0("plot_or_safe(", plot_name, ")"))
  if (isTRUE(getOption("ABG_VBG_DEBUG", FALSE))) {
    message("plot_or_safe(", plot_name, "): class=", paste(class(df), collapse = ", "),
           " nrow=", nr, " ncol=", ncol(df))
  }
  stopifnot(color_var %in% names(df))
  stopifnot(shape_var %in% names(df))
  stopifnot(!is.null(axis_spec))
  df[[shape_var]] <- as.factor(df[[shape_var]])
  n_shape <- dplyr::n_distinct(df[[shape_var]])
  if (n_shape > MAX_SHAPE_LEVELS) {
    message("OR plot: too many shape levels (", n_shape, ") in ", plot_name,
           ". Dropping shape and faceting by ", shape_var, ".")
    facet_var <- shape_var
    shape_var <- NULL
  }

  df$.grp <- 1L
  if (!is.null(color_var) && !is.null(shape_var)) {
    df$.grp <- interaction(df[[color_var]], df[[shape_var]], drop = TRUE)
  } else if (!is.null(color_var)) {
    df$.grp <- df[[color_var]]
  } else if (!is.null(shape_var)) {

```

```

df$.grp <- df[[shape_var]]
}

p <- ggplot2::ggplot(df, ggplot2::aes(x = outcome, y = estimate, ymin = conf.low, ymax = conf.high, group = .grp))
if (!is.null(color_var)) {
  p <- p + ggplot2::aes(color = .data[[color_var]])
}
if (!is.null(shape_var)) {
  p <- p + ggplot2::aes(shape = .data[[shape_var]])
}

p <- p +
  ggplot2::geom_pointrange(position = ggplot2::position_dodge(width = 0.7), size = 0.6) +
  ggplot2::geom_hline(yintercept = 1, linetype = "dashed", colour = "grey40") +
  or_axis_scale(axis_spec) +
  ggplot2::labs(
    title = title,
    x = "Outcome",
    y = "Odds Ratio (log scale, 95% CI)",
    color = if (!is.null(color_var)) "Blood-gas type" else NULL,
    shape = if (!is.null(shape_var)) "PC02 category" else NULL,
    caption = caption
  ) +
  ggplot2::theme_minimal(base_size = 9) +
  ggplot2::theme(
    plot.caption = ggplot2::element_text(hjust = 0),
    axis.text.x = ggplot2::element_text(angle = 15, hjust = 1),
    legend.position = "bottom",
    plot.margin = ggplot2::margin(6, 6, 6, 6)
  )
if (!is.null(color_var) || !is.null(shape_var)) {
  p <- p + ggplot2::guides(
    color = ggplot2::guide_legend(nrow = 2, byrow = TRUE),
    shape = ggplot2::guide_legend(nrow = 1, byrow = TRUE)
  )
}

```

```

if (!is.null(facet_var)) {
  p <- p + ggplot2::facet_wrap(stats::as.formula(paste("~", facet_var)))
}
p
}

library(dagitty)
library(ggdag)

# Toggle to show diagrams inline in the PDF
show_model_diagrams <- FALSE

model_diagram_dir <- fs::path(results_dir, "figs", "model-diagrams")
fs::dir_create(model_diagram_dir)

.make_safe_name <- function(x) {
  x <- gsub("[^A-Za-z0-9]+", "-", x)
  x <- gsub("(^-|-$)", "", x)
  tolower(x)
}

.extract_model_vars <- function(fml) {
  tt <- stats::terms(fml)
  response <- all.vars(stats::update(fml, . ~ 1))
  response <- if (length(response)) response[1] else NA_character_
  term_labels <- attr(tt, "term.labels")
  preds <- unique(unlist(lapply(term_labels, function(t) {
    all.vars(stats::as.formula(paste("~", t)))
  })))
  preds <- setdiff(preds, response)
  list(response = response, preds = preds)
}

.build_model_dag <- function(fml) {
  vars <- .extract_model_vars(fml)

```

```

if (is.na(vars$response) || length(vars$preds) == 0L) {
  stop("Model diagram: formula has no response or predictors: ", deparse(fml))
}
edges <- paste(sprintf("%s -> %s", vars$preds, vars$response), collapse = "\n ")
dagitty::dagitty(sprintf("dag { %s }", edges))
}

save_model_diagram <- function(name, fml, width = NULL, height = NULL) {
  dag <- .build_model_dag(fml)

  vars <- .extract_model_vars(fml)
  n_pred <- length(vars$preds)
  n_nodes <- n_pred + 1L

  label_size <- if (n_pred >= 35) 1.4 else if (n_pred >= 25) 1.8 else if (n_pred >= 15) 2.2 else 2.8
  point_size <- if (n_pred >= 25) 2.0 else if (n_pred >= 15) 2.5 else 3.0

  base_width <- if (is.null(width)) 8 else width
  base_height <- if (is.null(height)) 6 else height
  width <- max(base_width, min(24, 0.4 * n_nodes + 4))
  height <- max(base_height, min(16, 0.25 * n_nodes + 4))

  layout <- if (n_pred >= 8) "sugiyama" else "nicely"
  dag_data <- ggdag::tidy_dagitty(dag, layout = layout)$data

  p <- ggplot2::ggplot(
    dag_data,
    ggplot2::aes(x = x, y = y, xend = xend, yend = yend)
  ) +
    ggdag::geom_dag_edges() +
    ggdag::geom_dag_point(size = point_size) +
    ggdag::geom_dag_text_repel(
      ggplot2::aes(label = name),
      size = label_size,
      max.overlaps = Inf
    ) +

```

```

ggplot2::scale_x_continuous(expand = ggplot2::expansion(mult = 0.15)) +
ggplot2::scale_y_continuous(expand = ggplot2::expansion(mult = 0.15)) +
ggplot2::theme_void() +
ggplot2::labs(title = name) +
ggplot2::theme(
  plot.title = ggplot2::element_text(size = 10, hjust = 0.5),
  plot.margin = ggplot2::margin(10, 10, 10, 10)
)

file <- fs::path(model_diagram_dir, paste0(.make_safe_name(name), ".png"))
ggplot2::ggsave(file, p, width = width, height = height, dpi = 200)
if (isTRUE(show_model_diagrams)) print(p)
file
}

model_diagrams <- list()
register_model_diagram <- function(name, fml, width = 8, height = 6) {
  file <- save_model_diagram(name, fml, width = width, height = height)
  model_diagrams[[name]] <- file
  invisible(file)
}

register_model_diagrams <- function(forms, width = 8, height = 6) {
  purrr::iwalk(forms, function(fml, nm) {
    register_model_diagram(nm, fml, width = width, height = height)
  })
}

```

```

RUN_SHAP <- FALSE
if (RUN_SHAP) {
  if (!requireNamespace("shapviz", quietly = TRUE) ||
      packageVersion("shapviz") < "0.2.0") {
    stop("Package 'shapviz' (>= 0.2.0) is required. Install with renv::install(\"shapviz\") .")
  }
  if (!requireNamespace("fastshap", quietly = TRUE)) {
    stop("Package 'fastshap' is required. Install with renv::install(\"fastshap\") .")
  }
}

```

```

    }
}

# Chunk runtime annotation (printed into PDF) - disabled by default
if (isTRUE(SHOW_CHUNK_RUNTIME_TEXT)) {
  knitr::knit_hooks$set(runtimelog = local({
    starts <- list()
    escape_latex <- function(x) {
      gsub("([\\\\\\\$&{}_\\\\^~])", "\\\\\\\\\\\"1", x, perl = TRUE)
    }
    function(before, options) {
      if (before) {
        starts[[options$label]] <- proc.time()
      } else {
        st <- starts[[options$label]]
        if (is.null(st)) return(NULL)
        elapsed <- (proc.time() - st)[["elapsed"]]
        lbl <- escape_latex(options$label)
        paste0(
          "\n\n",
          "\\textit{Chunk ", lbl, " runtime: ", sprintf("%.2f", elapsed), " s}",
          "\n\n"
        )
      }
    }
  )))
  knitr::opts_chunk$set(runtimelog = TRUE)
} else {
  knitr::opts_chunk$set(runtimelog = FALSE)
}

seed_escrow <- data.frame(
  component = c(
    "Multiple imputation (mice)",
    "ABG propensity GBM (non-MI)",
    "VBG propensity GBM (non-MI)",

```

```

"MI PS (glm RCS) seeds (ABG per imputation)",
"MI PS (glm RCS) seeds (VBG per imputation)"
),
seed = c(
  "20251206",
  "42",
  "42",
  "20251206 + imputation index",
  "30251206 + imputation index"
),
stringsAsFactors = FALSE
)
render_table_pdf(
  seed_escrow,
  caption = "Seed escrow for MI and GBM runs",
  file_stub = "seed_escrow",
  digits = 0
)

```

Table 1: Seed escrow for MI and GBM runs

component	seed
Multiple imputation (mice)	20251206
ABG propensity GBM (non-MI)	42
VBG propensity GBM (non-MI)	42
MI PS (glm RCS) seeds (ABG per imputation)	20251206 + imputation index
MI PS (glm RCS) seeds (VBG per imputation)	30251206 + imputation index

```
DEBUG_SPLINE <- FALSE
```

```

# Make gt tables robust in PDF: full width, caption, small font
gt_pdf <- function(x, title = NULL, subtitle = NULL) {
  out <- x |>
    gt::tab_options(
      table.width            = gt::pct(100),
      table.align             = "left",

```

```

    table.font.size      = gt::px(9),
    data_row.padding     = gt::px(1),
    column_labels.font.size = gt::px(9),
    heading.title.font.size = gt::px(10),
    heading.subtitle.font.size = gt::px(9)
) |>
  gt::opt_align_table_header(align = "left")
if (!is.null(title))  out <- out |> gt::tab_caption(title)
if (!is.null(subtitle)) out <- out |> gt::tab_source_note(subtitle)
out
}

```

Converts the data from a STATA format to rdata if the rdata file does not exist. If it does already exist, it just loads that.

```

append_mem_snapshot("stage1", "start", "pre")

# data_dir_name resolved in setup-packages from params/env
stata_file <- file.path(data_dir_name, "full_db.dta")

stata_data <- read_dta(stata_file)
var_labels <- var_label(stata_data)
value_labels <- lapply(stata_data, function(x) if (is.labelled(x)) val_labels(x))
saveRDS(
  list(var_labels = var_labels, value_labels = value_labels),
  results_path("stata_labels.rds")
)

```

1.1.1 Configuration for the IPW models

```

drop_vars_ultra_missing <- c("bnp", "spo2")
cat_vars <- c("sex", "race_ethnicity", "location", "encounter_type")
numeric_vars <- c(
  "age_at_encounter", "curr_bmi", "temp_new", "sbp", "dbp", "hr",

```

```

"sodium", "serum_cr", "serum_hco3", "serum_cl", "serum_lac", "serum_k",
"wbc", "plt", "serum_phos", "serum_ca"
)
co2_vars <- c("paco2", "vbg_co2", "vbg_o2sat")

covars_gbm <- c(
  "age_at_encounter", "sex", "race_ethnicity", "curr_bmi",
  "copd", "asthma", "osa", "chf", "acute_nmd", "phtn", "ckd", "dm",
  "location", "encounter_type", "temp_new", "sbp", "dbp", "hr",
  "sodium", "serum_cr", "serum_hco3", "serum_cl", "serum_lac", "serum_k",
  "wbc", "plt", "serum_phos", "serum_ca"
)
covars_gbm <- setdiff(covars_gbm, drop_vars_ultra_missing)
covars_ps <- covars_gbm

# Core adjustment set for conditional prognostic models
adj_core <- c("age_at_encounter", "sex", "race_ethnicity", "location", "encounter_type")

gbm_params <- list(
  n.trees          = 800,
  interaction.depth = 3,
  shrinkage        = 0.01,
  bag.fraction     = 0.8,
  n.minobsinnode  = 10,
  cv.folds         = 0,
  stop.method      = "smd.max",
  n.cores          = 1L
)
stopifnot(gbm_params$stop.method == "smd.max")
SPLINE_BASIS <- "ns"
SPLINE_DF <- 4L
stopifnot(SPLINE_BASIS %in% c("ns", "rcs"))
get_gbm_cores <- function() {
  n_rows <- nrow(subset_data)
  if (is.finite(n_rows) && n_rows > 200000L) return(1L)
  gbm_params$n.cores
}

```

```

}

ps_trunc_quantile <- 0.01
stopifnot(ps_trunc_quantile > 0, ps_trunc_quantile < 0.5)

formula_abg      <- reformulate(covars_gbm, response = "has_abg")
formula_vbg      <- reformulate(covars_gbm, response = "has_vbg")

# Model diagrams: propensity models (GBM PS)
register_model_diagram("PS model: ABG test (GBM)", formula_abg, width = 10, height = 7)
register_model_diagram("PS model: VBG test (GBM)", formula_vbg, width = 10, height = 7)

# TODO: consider stop.method = "es.mean" (ATS version) if smd.max remains unstable on full N.

```

```

subset_data <- stata_data
if (PILOT_FRAC < 1) {
  set.seed(SAMPLE_SEED)
  subset_data <- dplyr::sample_frac(stata_data, size = PILOT_FRAC)
}
message("DATA: full_n=", nrow(stata_data), " | subset_n=", nrow(subset_data))
if (RUN_MODE == "full" && PILOT_FRAC < 1) {
  stop("RUN_MODE='full' but PILOT_FRAC < 1. Set pilot_frac=1 or run_mode='pilot'.")
}
run_rowcounts <- data.frame(
  run_id = diag_run_id,
  run_ts = diag_run_ts,
  run_mode = RUN_MODE,
  pilot_frac = PILOT_FRAC,
  full_n = nrow(stata_data),
  subset_n = nrow(subset_data),
  stringsAsFactors = FALSE
)
write_csv_safely(run_rowcounts, results_path("run_rowcounts.csv"), row_names = FALSE)

subset_data <- subset_data %>%
  filter(encounter_type != 1)

```

```

# Normalize once early and reuse everywhere

# Keep raw copy for missingness reporting
subset_data_raw <- subset_data
encounter_type_raw <- subset_data_raw$encounter_type

to01 <- function(x) {
  if (inherits(x, "haven_labelled")) x <- unclass(x)
  if (is.logical(x)) return(as.integer(x))
  if (is.factor(x)) x <- as.character(x)
  out <- rep(NA_integer_, length(x))
  xs <- suppressWarnings(as.numeric(x))
  is_num <- !is.na(xs)
  out[is_num & xs %in% c(0, 1)] <- as.integer(xs[is_num & xs %in% c(0, 1)])
  if (any(!is_num)) {
    s <- trimws(tolower(as.character(x[!is_num])))
    out[!is_num][s %in% c("0","no","false","female","f")] <- 0L
    out[!is_num][s %in% c("1","yes","true","male","m")] <- 1L
  }
  out
}

normalize_encounter_type <- function(x) {
  s_chr <- trimws(tolower(as.character(x)))
  num_from_text <- suppressWarnings(as.numeric(gsub("[^0-9]+", "", s_chr)))
  lab <- rep(NA_character_, length(s_chr))
  lab[!is.na(num_from_text) & num_from_text == 2] <- "Emergency"
  lab[!is.na(num_from_text) & num_from_text == 3] <- "Inpatient"
  is_na <- is.na(lab)
  is_em <- grepl("\bemerg(?:ency)?\b", s_chr) |
    grepl("(^|[^a-z])ed([a-z]|$)", s_chr) |
    grepl("\ba&e\b", s_chr) |
    grepl("\bemergency\s+dept\b", s_chr)
  is_ip <- grepl("\binpatient\b", s_chr) |
    grepl("\binpt\b", s_chr) |
    grepl("\binpat\b", s_chr) |

```

```

    grepl("(^|[^a-z])ip([a-z]|$)", s_chr)
  lab[is_na & is_em] <- "Emergency"
  lab[is_na & is_ip] <- "Inpatient"
  factor(lab, levels = c("Emergency", "Inpatient"))
}

coerce_num <- function(x) {
  if (inherits(x, "haven_labelled")) x <- unclass(x)
  if (is.factor(x)) x <- as.character(x)
  if (is.character(x)) x <- gsub("[^0-9.+-]", "", x)
  suppressWarnings(as.numeric(x))
}

levels_ref <- list(
  sex = c("Female", "Male"),
  race_ethnicity = levels(factor(stata_data$race_ethnicity)),
  location = levels(factor(stata_data$location)),
  encounter_type = levels(normalize_encounter_type(stata_data$encounter_type))
)

normalize_types <- function(df, levels_ref = NULL) {
  df <- df[, setdiff(names(df), drop_vars_ultra_missing), drop = FALSE]

  num_vars <- intersect(c(numeric_vars, co2_vars), names(df))
  for (nm in num_vars) df[[nm]] <- coerce_num(df[[nm]])

  stopifnot("sex" %in% names(df))
  df$sex <- factor(to01(df$sex), levels = c(0L, 1L), labels = c("Female", "Male"))

  stopifnot("encounter_type" %in% names(df))
  df$encounter_type <- normalize_encounter_type(df$encounter_type)

  for (nm in setdiff(cat_vars, c("sex", "encounter_type"))) {
    stopifnot(nm %in% names(df))
    if (!is.null(levels_ref) && !is.null(levels_ref[[nm]])) {
      df[[nm]] <- factor(df[[nm]], levels = levels_ref[[nm]])
    }
  }
}

```

```

} else {
  df[[nm]] <- factor(df[[nm]])
}
}

stopifnot(all(c("has_abg", "has_vbg") %in% names(df)))
df$has_abg <- to01(df$has_abg)
df$has_vbg <- to01(df$has_vbg)

df
}

subset_data <- normalize_types(subset_data_raw, levels_ref)
subset_data <- droplevels_all(subset_data)
subset_data$encounter_type <- droplevels(subset_data$encounter_type)
stopifnot(nlevels(subset_data$encounter_type) == 2L)
subset_n <- nrow(subset_data)

# Factor-level diagnostic (CSV + short summary)
factor_diag <- lapply(names(subset_data), function(v) {
  x <- subset_data[[v]]
  data.frame(
    variable = v,
    class = class(x)[1],
    nlevels = if (is.factor(x)) nlevels(x) else NA_integer_,
    n_missing = sum(is.na(x)),
    stringsAsFactors = FALSE
  )
})
factor_diag <- dplyr::bind_rows(factor_diag)
write_csv_safely(factor_diag, results_path("factor_levels_diagnostic.csv"), row_names = FALSE)
render_table_pdf(
  factor_diag,
  caption = "Factor level diagnostics (all variables)",
  file_stub = "factor_levels_diagnostic",
  digits = 0
)

```

)

Table 2: Factor level diagnostics (all variables)

variable	class	nlevels	n_missing
encounter_id	character	NA	0
rfs	character	NA	0
sex	factor	2	0
race	haven_labelled	NA	0
ethnicity	haven_labelled	NA	0
location	factor	4	0
age_at_encounter	numeric	NA	0
los	numeric	NA	0
curr_bmi	numeric	NA	14723
hr	numeric	NA	9418
curr_height	numeric	NA	7092
vbg_temp	numeric	NA	25852
abg_temp	numeric	NA	25852
vbg_o2sat	numeric	NA	22366
abg_o2sat	numeric	NA	20452
sao2_blood	numeric	NA	24590
value_prev_weight	numeric	NA	23428
value_prev_height	numeric	NA	22348
value_prev_bmi	numeric	NA	24178
value_highest_20198	numeric	NA	19666
value_highest_115576	numeric	NA	23340
value_highest_327718	numeric	NA	24676
vbg_co2	numeric	NA	18392
highest_vbg_co2	numeric	NA	18380
pco2_nos	numeric	NA	22937
highest_pco2_nos	numeric	NA	22936
abg_ph	numeric	NA	16397
vbg_ph	numeric	NA	17885
abg_hco3	numeric	NA	20093
vbg_hco3	numeric	NA	19107
sodium	numeric	NA	1326
serum_cr	numeric	NA	2396
hgb	numeric	NA	2824
serum_hco3	numeric	NA	1460
serum_cl	numeric	NA	1498
serum_lac	numeric	NA	15571
serum_k	numeric	NA	2021
temp_cor_oxygen	numeric	NA	25397
vbg_ph_temp_cor	numeric	NA	25398
vbg_po2	numeric	NA	19207
vbg_lactate	numeric	NA	24893
vbg_hco3_calc	numeric	NA	25092

Table 2: Factor level diagnostics (all variables) (*continued*)

variable	class	nlevels	n_missing
abg_po2	numeric	NA	19930
abg_po2_temp_cor	numeric	NA	24631
abg_ph_temp_cor	numeric	NA	24712
abg_lactate	numeric	NA	24897
ph_blood	numeric	NA	23211
po2_blood	numeric	NA	23399
wbc	numeric	NA	4542
plt	numeric	NA	2080
bnp_date	character	NA	0
serum_phos_date	character	NA	0
serum_phos	numeric	NA	13762
serum_ca_date	character	NA	0
serum_ca	numeric	NA	2627
serum_albumin_date	character	NA	0
serum_albumin	numeric	NA	9242
serum_tprot_date	character	NA	0
serum_tprot	numeric	NA	9746
has_j9612	numeric	NA	0
has_j9622	numeric	NA	0
has_j9602	numeric	NA	0
has_j9692	numeric	NA	0
ohs_code	numeric	NA	0
has_j9600	numeric	NA	0
principal_diagnosis_indicator	character	NA	0
admitting_diagnosis	character	NA	0
reason_for_visit	character	NA	0
has_j9601	numeric	NA	0
has_j9611	numeric	NA	0
has_j9610	numeric	NA	0
has_j9611	numeric	NA	0
has_j962	numeric	NA	0
has_j9620	numeric	NA	0
has_j9621	numeric	NA	0
has_j9690	numeric	NA	0
has_j9691	numeric	NA	0
other_abn_of_br	haven_labelled	NA	0
cfdo	haven_labelled	NA	0
has_i50_acute	numeric	NA	0
acute_nmd	haven_labelled	NA	0
sepsis_dx	haven_labelled	NA	0
stupor_dx	haven_labelled	NA	0
cog_signs_dx	haven_labelled	NA	0
mal_fat_dx	haven_labelled	NA	0
resp_acid_dx	haven_labelled	NA	0
sleep_hypovent_dx	haven_labelled	NA	0

Table 2: Factor level diagnostics (all variables) (*continued*)

variable	class	nlevels	n_missing
cchs_dx	haven_labelled	NA	0
other_sleep_hypovent_dx	haven_labelled	NA	0
acidosis_unspec	haven_labelled	NA	0
headache_dx	haven_labelled	NA	0
cpap	haven_labelled	NA	0
tte_proc	haven_labelled	NA	0
aero	haven_labelled	NA	0
inh_teaching	haven_labelled	NA	0
cxr1v	haven_labelled	NA	0
cxr2v	haven_labelled	NA	0
ctcnoncon	haven_labelled	NA	0
ctccon	haven_labelled	NA	0
cc_time	haven_labelled	NA	0
meas_venous_o2_proc	haven_labelled	NA	0
meas_arterial_gas_proc	haven_labelled	NA	0
blood_cx_proc	haven_labelled	NA	0
art_punct_proc	haven_labelled	NA	0
ctabdpelv	haven_labelled	NA	0
osa	haven_labelled	NA	0
asthma	haven_labelled	NA	0
copd	haven_labelled	NA	0
chf	haven_labelled	NA	0
stroke	haven_labelled	NA	0
ckd	haven_labelled	NA	0
pvd	haven_labelled	NA	0
oud	haven_labelled	NA	0
sedatives	haven_labelled	NA	0
phtn	haven_labelled	NA	0
polycy	haven_labelled	NA	0
po_steroid	haven_labelled	NA	0
narcan	haven_labelled	NA	0
inpt_inh	haven_labelled	NA	0
vasodilators	haven_labelled	NA	0
ip_diuretics	haven_labelled	NA	0
ip_abx	haven_labelled	NA	0
paralytic	haven_labelled	NA	0
op_diuretics	haven_labelled	NA	0
op_opiate	haven_labelled	NA	0
op_mat	haven_labelled	NA	0
op_nrt	haven_labelled	NA	0
copd_med	haven_labelled	NA	0
muscle_relax	haven_labelled	NA	0
pat_enc_hash	character	NA	0
ABG_rfs	numeric	NA	0
is_amb	numeric	NA	0

Table 2: Factor level diagnostics (all variables) (*continued*)

variable	class	nlevels	n_missing
encounter_date	Date	NA	0
age_by_ten	numeric	NA	0
age_decade	haven_labelled	NA	0
death_date	numeric	NA	22217
died	numeric	NA	0
months_death_or_cens	numeric	NA	0
curr_weight	numeric	NA	8264
curr_weight_date	numeric	NA	8264
prev_weight_date	numeric	NA	23428
curr_height_date	numeric	NA	7092
prev_height_date	numeric	NA	22348
curr_bmi_date	numeric	NA	14723
prev_bmi_date	numeric	NA	24177
height	numeric	NA	7062
height_date	numeric	NA	7062
weight	numeric	NA	8228
weight_date	numeric	NA	8228
calc_bmi	numeric	NA	10902
calc_bmi_date	numeric	NA	10902
working_bmi	numeric	NA	14699
working_bmi_date	numeric	NA	14699
bmi	numeric	NA	8923
bmi_date	numeric	NA	8923
bmi_int	numeric	NA	8923
bmi_by_five	numeric	NA	8923
rr	numeric	NA	14194
rr_date	numeric	NA	14147
temp_new	numeric	NA	12460
new_temp_date	numeric	NA	12460
sbp	numeric	NA	7666
sbp_date	numeric	NA	7665
dbp	numeric	NA	7738
dbp_date	numeric	NA	7708
spo2_date	numeric	NA	18248
hr_date	numeric	NA	9417
abg_ph_date	numeric	NA	20237
vbg_ph_date	numeric	NA	18528
abg_hco3_date	numeric	NA	19998
abg_hco3_int	numeric	NA	20093
vbg_hco3_date	numeric	NA	18994
sodium_date	numeric	NA	1317
serum_k_date	numeric	NA	2021
hgb_date	numeric	NA	2127
wbc_date	numeric	NA	3858
plt_date	numeric	NA	1731

Table 2: Factor level diagnostics (all variables) (*continued*)

variable	class	nlevels	n_missing
serum_hco3_date	numeric	NA	1419
any_bicarb	numeric	NA	1159
int_bicarb	numeric	NA	1159
hco3_cat	haven_labelled	NA	1460
serum_cl_date	numeric	NA	1477
serum_cr_date	numeric	NA	2209
serum_lac_date	numeric	NA	15359
vbg_co2_date	numeric	NA	18373
pco2_nos_date	numeric	NA	22936
highest_vbg_co2_date	numeric	NA	18373
highest_pco2_nos_date	numeric	NA	22936
paco2	numeric	NA	16490
paco2_date_1	numeric	NA	19665
paco2_date_2	numeric	NA	23340
paco2_date_3	numeric	NA	24676
paco2_date	numeric	NA	16478
paco2_int	numeric	NA	16490
highest_paco2	numeric	NA	16479
paco2_date_highest_1	numeric	NA	19665
paco2_date_highest_2	numeric	NA	23340
paco2_date_highest_3	numeric	NA	24676
paco2_date_highest	numeric	NA	16478
temp_cor_oxygen_date	numeric	NA	25252
temp_cor_vbg_ph_date	numeric	NA	25398
vbg_po2_date	numeric	NA	19077
vbg_lactate_date	numeric	NA	24887
vbg_hco3_calc_date	numeric	NA	25085
abg_po2_date	numeric	NA	19909
abg_po2_temp_cor_date	numeric	NA	24630
abg_ph_temp_cor_date	numeric	NA	24711
abg_lactate_date	numeric	NA	24893
ph_blood_date	numeric	NA	23209
po2_blood_date	numeric	NA	23372
vbg_temp_date	numeric	NA	25852
abg_temp_date	numeric	NA	25783
vbg_o2sat_date	numeric	NA	22315
abg_o2sat_date	numeric	NA	19781
sao2_blood_date	numeric	NA	24404
paco2_flag	haven_labelled	NA	16490
highest_paco2_flag	haven_labelled	NA	16479
paco2_52_flag	haven_labelled	NA	16490
vbg_co2_flag	haven_labelled	NA	18392
highest_vbg_co2_flag	haven_labelled	NA	18380
miss_paco2_flag	numeric	NA	0
miss_vbg_co2_flag	numeric	NA	0

Table 2: Factor level diagnostics (all variables) (*continued*)

variable	class	nlevels	n_missing
miss_vbg_or_abg_co2_flag	numeric	NA	0
hco3_flag	haven_labelled	NA	1460
not_paco2_flag	numeric	NA	16490
not_hco3_flag	numeric	NA	1460
k_cat	haven_labelled	NA	2021
acidemia	haven_labelled	NA	11444
abg_sbe	numeric	NA	20343
vbg_sbe	numeric	NA	19167
cw_simple_acute_resp_acid	haven_labelled	NA	21691
paco2_52_comp_flag	haven_labelled	NA	16498
po_steroid_date	numeric	NA	14391
narcan_date	numeric	NA	20913
inpt_inh_date	numeric	NA	14995
vasodilators_date	numeric	NA	25742
ip_diuretics_date	numeric	NA	25480
ip_abx_date	numeric	NA	25265
paralytic_date	numeric	NA	25609
inpt_inh_0	numeric	NA	0
ip_abx_0	numeric	NA	0
ip_diuretics_0	numeric	NA	0
narcan_0	numeric	NA	0
paralytic_0	numeric	NA	0
po_steroid_0	numeric	NA	0
vasodilators_0	numeric	NA	0
op_diuretics_first_date	numeric	NA	16176
op_diuretics_last_date	numeric	NA	16209
op_diuretics_365d	haven_labelled	NA	0
op_opiate_first_date	numeric	NA	9701
op_opiate_last_date	numeric	NA	9775
op_opiate_365d	haven_labelled	NA	0
op_mat_first_date	numeric	NA	24851
op_mat_last_date	numeric	NA	24856
op_mat_365d	haven_labelled	NA	0
op_nrt_first_date	numeric	NA	22742
op_nrt_last_date	numeric	NA	22752
op_nrt_365d	haven_labelled	NA	0
copd_med_first_date	numeric	NA	13261
copd_med_last_date	numeric	NA	13287
copd_med_365d	haven_labelled	NA	0
muscle_relax_first_date	numeric	NA	19799
muscle_relax_last_date	numeric	NA	19825
muscle_relax_365d	haven_labelled	NA	0
tte_proc_first_date	numeric	NA	22701
tte_proc_last_date	numeric	NA	22701
vent_proc	haven_labelled	NA	0

Table 2: Factor level diagnostics (all variables) (*continued*)

variable	class	nlevels	n_missing
niv_proc	haven_labelled	NA	0
imv_proc	haven_labelled	NA	0
cpap_first_date	numeric	NA	24312
cpap_last_date	numeric	NA	24312
niv_proc_first_date	numeric	NA	24139
niv_proc_last_date	numeric	NA	24139
imv_proc_first_date	numeric	NA	22962
imv_proc_last_date	numeric	NA	22962
vent_proc_first_date	numeric	NA	21589
vent_proc_last_date	numeric	NA	21589
aero_first_date	numeric	NA	22650
aero_last_date	numeric	NA	22650
inh_teaching_first_date	numeric	NA	25137
inh_teaching_last_date	numeric	NA	25137
cxr1v_first_date	numeric	NA	18719
cxr1v_last_date	numeric	NA	18719
cxr2v_first_date	numeric	NA	25108
cxr2v_last_date	numeric	NA	25108
ctcnnoncon_first_date	numeric	NA	25108
ctcnnoncon_last_date	numeric	NA	25108
ctcccon_first_date	numeric	NA	24774
ctcccon_last_date	numeric	NA	24774
ctabdpelv_first_date	numeric	NA	24367
ctabdpelv_last_date	numeric	NA	24367
meas_venous_o2_proc_first_date	numeric	NA	25489
meas_venous_o2_proc_last_date	numeric	NA	25489
meas_art_gas_proc_first_date	numeric	NA	25645
meas_art_gas_proc_last_date	numeric	NA	25645
blood_cx_proc_first_date	numeric	NA	22405
blood_cx_proc_last_date	numeric	NA	22405
art_punct_proc_first_date	numeric	NA	24395
art_punct_proc_last_date	numeric	NA	24395
cc_time_first_date	numeric	NA	19881
cc_time_last_date	numeric	NA	19881
aero_0	numeric	NA	0
blood_cx_proc_0	numeric	NA	0
cc_time_0	numeric	NA	0
cpap_0	numeric	NA	0
ctabdpelv_0	numeric	NA	0
ctcccon_0	numeric	NA	0
ctcnnoncon_0	numeric	NA	0
cxr1v_0	numeric	NA	0
cxr2v_0	numeric	NA	0
imv_proc_0	numeric	NA	0
inh_teaching_0	numeric	NA	0

Table 2: Factor level diagnostics (all variables) (*continued*)

variable	class	nlevels	n_missing
niv_proc_0	numeric	NA	0
tte_proc_0	numeric	NA	0
vent_proc_0	numeric	NA	0
aero_dur	numeric	NA	22650
blood_cx_proc_dur	numeric	NA	22405
cpap_dur	numeric	NA	24312
ctabdpelv_dur	numeric	NA	24367
ctccon_dur	numeric	NA	24774
ctcnoncon_dur	numeric	NA	25108
cxr1v_dur	numeric	NA	18719
cxr2v_dur	numeric	NA	25108
inv_proc_dur	numeric	NA	22962
inh_teaching_dur	numeric	NA	25137
niv_proc_dur	numeric	NA	24139
tte_proc_dur	numeric	NA	22701
hypercap_resp_failure	haven_labelled	NA	0
j9612_date	numeric	NA	25717
j9612_pcpl	haven_labelled	NA	25718
j9612_adm	haven_labelled	NA	25717
j9612_vr	haven_labelled	NA	25717
j9622_date	numeric	NA	25304
j9622_pcpl	haven_labelled	NA	25322
j9622_adm	haven_labelled	NA	25304
j9622_vr	haven_labelled	NA	25304
j9602_date	numeric	NA	25046
j9602_pcpl	haven_labelled	NA	25059
j9602_adm	haven_labelled	NA	25046
j9602_vr	haven_labelled	NA	25046
j9692_date	numeric	NA	25730
j9692_pcpl	haven_labelled	NA	25732
j9692_adm	haven_labelled	NA	25730
j9692_vr	haven_labelled	NA	25730
ohs_code_date	numeric	NA	25616
e662_pcpl	haven_labelled	NA	25617
e662_adm	haven_labelled	NA	25616
e662_vr	haven_labelled	NA	25616
hypercap_resp_failure_date	numeric	NA	24407
other_resp_failure	haven_labelled	NA	0
j9600_date	numeric	NA	24955
j9601_date	numeric	NA	21035
j961_date	numeric	NA	25852
j9610_date	numeric	NA	25702
j9611_date	numeric	NA	25217
j962_date	numeric	NA	25852
j9620_date	numeric	NA	25706

Table 2: Factor level diagnostics (all variables) (*continued*)

variable	class	nlevels	n_missing
j9621_date	numeric	NA	24576
j9690_date	numeric	NA	25274
j9691_date	numeric	NA	25499
other_resp_failure_date	numeric	NA	19074
sepsis_dx_date	numeric	NA	22837
stupor_dx_date	numeric	NA	25248
cog_signs_dx_date	numeric	NA	23346
mal_fat_dx_date	numeric	NA	23002
resp_acid_dx_date	numeric	NA	25669
sleep_hypovent_dx_date	numeric	NA	25811
cchs_dx_date	numeric	NA	25852
other_sleep_hypovent_dx_date	numeric	NA	25837
acidosis_unspec_date	numeric	NA	25036
headache_dx_date	numeric	NA	25077
dysp_dx	haven_labelled	NA	0
dysp_dx_date	numeric	NA	22196
symp_obs	haven_labelled	NA	0
symp_obs_date	numeric	NA	25636
abn_br_dx	haven_labelled	NA	0
abn_br_dx_date	numeric	NA	25827
resp_abnormality	haven_labelled	NA	0
r0689_date	numeric	NA	25404
resp_abnormality_date	numeric	NA	25360
other_abn_of_br_date	numeric	NA	25404
fast_br	haven_labelled	NA	0
fast_br_date	numeric	NA	25712
pulm_edema_dx	haven_labelled	NA	0
pulm_edema_dx_date	numeric	NA	24961
pna_dx	haven_labelled	NA	0
pna_dx_date	numeric	NA	22087
acute_chf	numeric	NA	0
acute_old	haven_labelled	NA	0
acute_old_date	numeric	NA	0
resp_dep_compl	haven_labelled	NA	0
resp_dep_compl_date	numeric	NA	24960
acute_nmd_date	numeric	NA	25813
osa_first_date	numeric	NA	21334
osa_last_date	numeric	NA	21341
asthma_first_date	numeric	NA	22325
asthma_last_date	numeric	NA	22332
copd_first_date	numeric	NA	20748
copd_last_date	numeric	NA	20758
chf_first_date	numeric	NA	20747
chf_last_date	numeric	NA	20762
stroke_first_date	numeric	NA	23962

Table 2: Factor level diagnostics (all variables) (*continued*)

variable	class	nlevels	n_missing
stroke_last_date	numeric	NA	23965
ckd_first_date	numeric	NA	21178
ckd_last_date	numeric	NA	21189
ctd	haven_labelled	NA	0
ctd_first_date	numeric	NA	24545
ctd_last_date	numeric	NA	24546
dem	haven_labelled	NA	0
dem_first_date	numeric	NA	24236
dem_last_date	numeric	NA	24237
dm	haven_labelled	NA	0
dm_first_date	numeric	NA	18216
dm_last_date	numeric	NA	18230
pvd_first_date	numeric	NA	23432
pvd_last_date	numeric	NA	23433
oud_first_date	numeric	NA	24429
oud_last_date	numeric	NA	24434
sedatives_first_date	numeric	NA	25574
sedatives_last_date	numeric	NA	25574
cfdo_first_date	numeric	NA	25806
cfdo_last_date	numeric	NA	25806
phtn_first_date	numeric	NA	23708
phtn_last_date	numeric	NA	23709
polocy_first_date	numeric	NA	25549
polocy_last_date	numeric	NA	25549
nmd	haven_labelled	NA	0
nmd_first_date	numeric	NA	24822
nmd_last_date	numeric	NA	24823
nic	haven_labelled	NA	0
nic_first_date	numeric	NA	19549
nic_last_date	numeric	NA	19554
ovs	haven_labelled	NA	0
ats_ohs_flag	numeric	NA	22851
pos_ohs_flag	numeric	NA	0
ats_copd_flag	numeric	NA	22982
guidelines	haven_labelled	NA	22982
OBESITY_rfs	numeric	NA	0
_merge_amb_obes	haven_labelled	NA	25852
PREDISPOSITION_rfs	numeric	NA	0
_merge_amb_predisp	haven_labelled	NA	25852
RESPFAIL_rfs	numeric	NA	0
_merge_amb_respfail	haven_labelled	NA	25852
VBG_rfs	numeric	NA	0
_merge_amb_vbg	haven_labelled	NA	25852
VENTSUPPORT_rfs	numeric	NA	0
_merge_amb_ventsupp	haven_labelled	NA	25852

Table 2: Factor level diagnostics (all variables) (*continued*)

variable	class	nlevels	n_missing
is_emer	numeric	NA	0
_merge_emer_obes	haven_labelled	NA	23476
_merge_emer_predisp	haven_labelled	NA	19498
_merge_emer_respfail	haven_labelled	NA	19220
_merge_emer_vbg	haven_labelled	NA	17441
_merge_emer_ventsupp	haven_labelled	NA	17342
_merge_emer	haven_labelled	NA	17342
is_inp	haven_labelled	NA	8506
_merge_inpat_obes	haven_labelled	NA	18659
_merge_inpat_predisp	haven_labelled	NA	12820
_merge_inpat_respfail	haven_labelled	NA	11256
_merge_inpat_vbg	haven_labelled	NA	9137
_merge_inpat_ventsupp	haven_labelled	NA	8506
_merge_inpat	haven_labelled	NA	0
patient_id	numeric	NA	0
rfsgroup	haven_labelled	NA	0
encounter_type	factor	2	0
first_encounter	haven_labelled	NA	0
has_abg	integer	NA	0
has_vbg	integer	NA	0
max_hco3_or_its_met_alk	numeric	NA	16490
prim_met_alk	numeric	NA	22982
max_hco3_or_its_comb_met_alk	numeric	NA	16490
combo_met_alk	numeric	NA	22982
alkalemia	numeric	NA	11444
paco2_flag_and_alk	numeric	NA	22982
paco2_50_flag	haven_labelled	NA	16490
hypercap_dx_adm_flag	numeric	NA	24407
hypercap_dx_pcpl_flag	numeric	NA	24422
hypercap_dx_vr_flag	numeric	NA	24407
hypercap_on_abg	numeric	NA	0
hypercap_on_vbg	numeric	NA	0
has_both_abg_vbg	haven_labelled	NA	0
has_neither_abg_vbg	haven_labelled	NA	0
vbg_or_abg_co2_flag	haven_labelled	NA	0
dx_hypercap_on_abg	numeric	NA	24407
sugg_hypercap_dx_on_vbg	numeric	NA	24407
dx_hypercap_on_vbg	numeric	NA	24407
vbg_o2sat_calc	numeric	NA	0
abg_o2sat_calc	numeric	NA	0
corr_vbg_co2	numeric	NA	18392
corr_vbg_co2_flag	haven_labelled	NA	18392
corr_hypercap_on_vbg	numeric	NA	0
race_ethnicity	factor	7	0
has_vbg_and_cat	haven_labelled	NA	0

Table 2: Factor level diagnostics (all variables) (*continued*)

variable	class	nlevels	n_missing
has_bmi_and_cat	haven_labelled	NA	0
has_weight_and_cat	haven_labelled	NA	0
has_height_and_cat	haven_labelled	NA	0
has_hr_and_cat	haven_labelled	NA	0
has_sbp_and_cat	haven_labelled	NA	0
has_rr_and_cat	haven_labelled	NA	0
has_temp_and_cat	haven_labelled	NA	0
has_spo2_and_cat	haven_labelled	NA	0
has_cl_and_cat	haven_labelled	NA	0
has_k_and_cat	haven_labelled	NA	0
has_hco3_and_cat	haven_labelled	NA	0
has_lactate_and_cat	haven_labelled	NA	0
has_na_and_cat	haven_labelled	NA	0
has_cr_and_cat	haven_labelled	NA	0
has_hgb_and_cat	haven_labelled	NA	0
has_wbc_and_cat	haven_labelled	NA	0
has_plt_and_cat	haven_labelled	NA	0
has_bnp_and_cat	haven_labelled	NA	0
has_phos_and_cat	haven_labelled	NA	0
has_ca_and_cat	haven_labelled	NA	0
has_alb_and_cat	haven_labelled	NA	0
has_tprot_and_cat	haven_labelled	NA	0
encounter_type_dummy1	numeric	NA	0
encounter_type_dummy2	numeric	NA	0
encounter_type_dummy3	numeric	NA	0
female	haven_labelled	NA	0
male	numeric	NA	0
white_race	numeric	NA	0
black_race	numeric	NA	0
unknown_race	numeric	NA	0
asian_race	numeric	NA	0
nat_am_race	numeric	NA	0
nhpi_race	numeric	NA	0
not_hisp_eth	numeric	NA	0
hisp_eth	numeric	NA	0
unknown_eth	numeric	NA	0
location_dummy1	numeric	NA	0
location_dummy2	numeric	NA	0
location_dummy3	numeric	NA	0
location_dummy4	numeric	NA	0
ps	numeric	NA	0
tx_pr_decile	numeric	NA	0
ps_trunc	numeric	NA	0
sumofweights	numeric	NA	0
ipw	numeric	NA	0

Table 2: Factor level diagnostics (all variables) (*continued*)

variable	class	nlevels	n_missing
stabilized_weight	numeric	NA	0
approx_ipw_fweight	numeric	NA	0
vbg_ps	numeric	NA	0
vbg_tx_pr_decile	numeric	NA	0
vbg_ps_trunc	numeric	NA	0
vbg_sumofweights	numeric	NA	0
vbg_ipw	numeric	NA	0
vbg_stabilized_weight	numeric	NA	0
vbg_approx_ipw_fweight	numeric	NA	0

```
# Factor expansion guard (logs only)
factor_guard <- factor_diag |>
  dplyr::filter(!is.na(nlevels) & nlevels > MAX_LEVELS_GBM)
write_csv_safely(factor_guard, results_path("factor_expansion_guard.csv"), row_names = FALSE)
if (nrow(factor_guard)) {
  warning("GBM factor expansion guard: factors exceeding MAX_LEVELS_GBM detected. See Results/factor_expansion_guard.csv.",
         call. = FALSE)
}

tab_enc <- table(subset_data$encounter_type, useNA = "ifany")
if (sum(!is.na(subset_data$encounter_type)) == 0) {
  message("All encounter_type values are NA after normalization. Showing top raw values:")
  s_raw <- trimws(tolower(as.character(encounter_type_raw)))
  print(utils::head(sort(table(s_raw), decreasing = TRUE), 20))
  stop("normalize_encounter_type produced all NA; extend the synonym map to your raw values.")
}

# Reference profile for conditional curves
stopifnot(all(adj_core %in% names(subset_data)))

mode_level <- function(x) {
  if (is.factor(x)) {
    tab <- table(x, useNA = "no")
    if (!length(tab)) return(factor(NA, levels = levels(x)))
    lev <- names(tab)[which.max(tab)]
```

```

    return(factor(lev, levels = levels(x)))
}
if (is.character(x)) {
  tab <- table(x, useNA = "no")
  if (!length(tab)) return(NA_character_)
  return(names(tab)[which.max(tab)])
}
stats::median(as.numeric(x), na.rm = TRUE)
}

make_ref_profile <- function(data, adj_vars) {
  out <- lapply(adj_vars, function(v) mode_level(data[[v]]))
  names(out) <- adj_vars
  as.data.frame(out, stringsAsFactors = FALSE)
}

make_co2_grid <- function(co2_var, co2_vals, ref_df) {
  grid <- data.frame(co2_vals)
  names(grid) <- co2_var
  stopifnot(!is.null(ref_df))
  stopifnot(nrow(ref_df) > 0L)
  ref_rep <- ref_df[rep(1L, nrow(grid)), , drop = FALSE]
  grid <- cbind(grid, ref_rep)
  grid
}

make_co2_grid_ref <- function(co2_var, co2_vals, ref_df, co2_ref) {
  grid_vals <- c(co2_vals, co2_ref)
  grid_vals <- grid_vals[is.finite(grid_vals)]
  grid_vals <- sort(unique(as.numeric(grid_vals)))
  if (length(grid_vals) < 2) {
    fallback_center <- NA_real_
    if (is.finite(co2_ref)) {
      fallback_center <- co2_ref
    } else if (length(co2_vals) && is.finite(co2_vals[1])) {
      fallback_center <- co2_vals[1]
    }
  }
}
```

```

}

if (is.finite(fallback_center)) {
  grid_vals <- sort(unique(c(fallback_center - 1, fallback_center, fallback_center + 1)))
  grid_vals <- grid_vals[is.finite(grid_vals)]
}
}

if (length(grid_vals) < 2) stop("CO2 grid is too small for ", co2_var, ".")
grid <- make_co2_grid(co2_var, grid_vals, ref_df)
ref_val <- if (is.finite(co2_ref)) co2_ref else stats::median(grid[[co2_var]], na.rm = TRUE)
ref_idx <- match(ref_val, grid[[co2_var]])
if (is.na(ref_idx)) {
  ref_idx <- which.min(abs(grid[[co2_var]] - ref_val))
}
if (any(diff(grid[[co2_var]]) <= 0)) {
  stop("CO2 grid is not strictly increasing for ", co2_var, ".")
}
list(grid = grid, ref_idx = ref_idx, co2_ref = grid[[co2_var]][ref_idx])
}

predict_or_curve_from_fit <- function(fit, grid_df, ref_idx, co2_var) {
  # Build a model matrix consistent with the fitted model (handles factor levels)
  tt <- stats::delete.response(stats::terms(fit))
  xlev <- stats::getXlevels(tt, stats::model.frame(fit))
  mf_new <- stats::model.frame(tt, grid_df, na.action = stats::na.pass, xlev = xlev)
  mm <- stats::model.matrix(tt, mf_new)
  beta <- stats::coef(fit)
  V <- stats::vcov(fit)

  # Align model matrix columns to coefficient names (fill missing with 0, drop extras)
  bn <- names(beta)
  if (is.null(bn) || any(!nzchar(bn))) {
    if (length(beta) == ncol(mm)) {
      bn <- colnames(mm)
      names(beta) <- bn
    } else {
      stop("predict_or_curve_from_fit: coefficient names missing and dimensions do not match.")
    }
  }
}

```

```

    }
}

if (!all(bn %in% colnames(mm))) {
  missing_cols <- setdiff(bn, colnames(mm))
  if (length(missing_cols)) {
    mm <- cbind(mm, matrix(0, nrow = nrow(mm), ncol = length(missing_cols),
                           dimnames = list(NULL, missing_cols)))
  }
}

mm <- mm[, bn, drop = FALSE]
stopifnot(ncol(mm) == length(beta))

eta <- as.numeric(mm %*% beta)
mmV <- mm %*% V
var_eta <- rowSums(mmV * mm)

mm_ref <- mm[ref_idx, , drop = FALSE]
eta_ref <- eta[ref_idx]
var_ref <- as.numeric(mm_ref %*% V %*% t(mm_ref))
cov_ref <- as.numeric(mmV %*% t(mm_ref))

logOR <- eta - eta_ref
var_logOR <- var_eta + var_ref - 2 * cov_ref
var_logOR <- pmax(var_logOR, 0)
logOR[ref_idx] <- 0
var_logOR[ref_idx] <- 0
se <- sqrt(var_logOR)

data.frame(
  grid_df,
  logOR = logOR,
  SE_logOR = se,
  var_logOR = var_logOR,
  OR = exp(logOR),
  LCL = exp(logOR - 1.96 * se),
  UCL = exp(logOR + 1.96 * se),

```

```

co2_ref = grid_df[[co2_var]][ref_idx],
ref_idx = ref_idx,
row.names = NULL
)
}

x_ref_abg <- make_ref_profile(
  subset_data |> dplyr::filter(has_abg == 1, !is.na(paco2)),
  adj_core
)
x_ref_vbg <- make_ref_profile(
  subset_data |> dplyr::filter(has_vbg == 1, !is.na(vbg_co2)),
  adj_core
)

run_meta <- tibble::tibble(
  run_id      = diag_run_id,
  run_mode    = RUN_MODE,
  pilot_frac = PILOT_FRAC,
  mi_batch_threshold = MI_BATCH_THRESHOLD,
  full_n     = nrow(stata_data),
  subset_n   = nrow(subset_data)
)
render_table_pdf(run_meta,
                 "Run metadata (pilot vs full)",
                 "run_metadata",
                 digits = 0)

```

Table 3: Run metadata (pilot vs full)

run_id	run_mode	pilot_frac	mi_batch_threshold	full_n	subset_n
20260205_110437	pilot	0	5000	833476	25852

```

# Write run config JSON for portability
json_escape <- function(x) gsub("\"", "\\\\"", x)
run_cfg <- list(
  run_id = diag_run_id,
  run_mode = RUN_MODE,
  pilot_frac = PILOT_FRAC,
  mi_batch_threshold = MI_BATCH_THRESHOLD,
  data_dir = data_dir_name,
  results_dir = results_dir,
  full_n = nrow(stata_data),
  subset_n = nrow(subset_data)
)
json_lines <- c(
  "{",
  paste0("  \"run_id\": \"", json_escape(run_cfg$run_id), "\","),
  paste0("  \"run_mode\": \"", json_escape(run_cfg$run_mode), "\","),
  paste0("  \"pilot_frac\": ", run_cfg$pilot_frac, ","),
  paste0("  \"mi_batch_threshold\": ", run_cfg$mi_batch_threshold, ","),
  paste0("  \"data_dir\": \"", json_escape(run_cfg$data_dir), "\","),
  paste0("  \"results_dir\": \"", json_escape(run_cfg$results_dir), "\","),
  paste0("  \"full_n\": ", run_cfg$full_n, ","),
  paste0("  \"subset_n\": ", run_cfg$subset_n),
  "}"
)
writeLines(json_lines, results_path("run_config.json"))

```

Codebook exported to Results/codebookr.docx.

```

study_codebook <- codebookr::codebook(
  stata_data,
  title = "Full TrinetX",
  subtitle = "Dataset Documentation",
  description = "This dataset contains patient-level records from the TrinetX database.
               It has been processed and converted from the original Stata file."
)

```

```
codebook_file <- results_path("codebookr.docx")
print(study_codebook, codebook_file)
```

1.1.2 Outcome Variable Creation

```
subset_data <- subset_data %>%
  mutate(
    ## 1. Did the patient die?
    died = if_else(!is.na(death_date), 1L, 0L),

    ## 2. Absolute death date (if death_date is an offset)
    death_abs = if_else(!is.na(death_date),
                        encounter_date + death_date,
                        as.Date(NA)),

    ## 3. Year month (YM) for encounter and death
    enc_ym   = floor_date(encounter_date, unit = "month"),
    death_ym = floor_date(death_abs      , unit = "month"),

    ## 4. Reference censoring date: 1 Jun 2024
    ref_ym = ymd("2024-06-01"),

    ## 5. Months from encounter to death or censoring
    months_death_or_cens = case_when(
      !is.na(death_ym) ~ interval(enc_ym, death_ym) %/% months(1),
      TRUE           ~ interval(enc_ym, ref_ym)    %/% months(1)
    ),

    ## 6. Remove impossible values
    months_death_or_cens = if_else(
      months_death_or_cens < 0 | months_death_or_cens > 16,
      NA_integer_, months_death_or_cens
    ),
```

```

## 7. Death within one or two months
died_1mo = if_else(died == 1 & months_death_or_cens < 1, 1L, 0L),
died_2mo = if_else(died == 1 & months_death_or_cens <= 1, 1L, 0L),

## 8. Month of death (missing if censored)
death_time = if_else(died == 1, months_death_or_cens, NA_integer_),

## 9. Death within 60 days (new variable)
death_60d = if_else(died == 1 & death_abs <= (encounter_date + days(60)), 1L, 0L)
) %>%
select(-enc_ym, -death_ym)

subset_data <- subset_data %>%
  mutate(
    death_60d = if_else(died == 1 & death_abs <= (encounter_date + days(60)), 1L, 0L)
  )

table(subset_data$death_60d, useNA = "ifany")

```

0	1
23166	2686

```
prop.table(table(subset_data$death_60d, useNA = "ifany"))
```

0	1
0.8961009	0.1038991

```
summary(subset_data$death_60d)
```

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
0.0000	0.0000	0.0000	0.1039	0.0000	1.0000

1.2 2) Baseline tables

```
# Robust derivation of analysis variables + helper for Table 1 production
# -----
#
# helper: label binary 0/1 → "No"/"Yes"
bin_lab <- function(x) {
  y <- to01(x)
  if (all(is.na(y))) {
    return(factor(y, levels = c(0, 1), labels = c("No", "Yes")))
  }
  factor(y, levels = c(0, 1), labels = c("No", "Yes"))
}

# helper: preserve labeled factors if already present; otherwise map numeric codes
label_from_codes <- function(x, codes, labels) {
  if (is.factor(x)) {
    lev <- levels(x)
    if (all(lev %in% labels)) {
      return(factor(x, levels = labels))
    }
    lev_num <- suppressWarnings(as.numeric(lev))
    if (all(!is.na(lev_num)) && all(lev_num %in% codes)) {
      return(factor(as.numeric(as.character(x)), levels = codes, labels = labels))
    }
    return(x)
  }
  x_num <- suppressWarnings(as.numeric(as.character(x)))
  if (all(is.na(x_num))) return(factor(x, levels = labels))
  if (all(x_num %in% codes, na.rm = TRUE)) {
    return(factor(x_num, levels = codes, labels = labels))
  }
  factor(x)
}
```

```

subset_data <- subset_data %>%
  mutate(
    ## ensure 0/1 numerics (avoids factor-level coercion)
    across(c(has_abg, has_vbg),
           ~ to01(.)),

    ## derive ABG / VBG status groups (binary test status only)
    abg_group = case_when(
      has_abg == 0 ~ "No ABG",
      has_abg == 1 ~ "ABG",
      TRUE          ~ "Missing"
    ),
    vbg_group = case_when(
      has_vbg == 0 ~ "No VBG",
      has_vbg == 1 ~ "VBG",
      TRUE          ~ "Missing"
    ),

    ## factorise groups with explicit NA/Missing level
    abg_group = factor(
      abg_group,
      levels = c("No ABG", "ABG", "Missing")
    ),
    vbg_group = factor(
      vbg_group,
      levels = c("No VBG", "VBG", "Missing")
    ),

    ## labelled covariates (robust to factor or numeric codes)
    sex_label = label_from_codes(sex, c(0, 1), c("Female", "Male")),
    race_ethnicity_label = label_from_codes(
      race_ethnicity,
      0:6,
      c("White", "Black or African American", "Hispanic",
        "Asian", "American Indian", "Pacific Islander", "Unknown")
    ),
  )

```

```

location_label = label_from_codes(
  location,
  0:3,
  c("South", "Northeast", "Midwest", "West")
),
encounter_type_label = label_from_codes(
  encounter_type,
  c(2, 3),
  c("Emergency", "Inpatient")
),
osa_label      = bin_lab(osa),
asthma_label   = bin_lab(asthma),
copd_label     = bin_lab(copd),
chf_label      = bin_lab(chf),
nmd_label      = bin_lab(nmd),
phtn_label     = bin_lab(phtn),
ckd_label      = bin_lab(ckd),
diabetes_label = bin_lab(dm)
)

# variables to summarise
vars <- c(
  "age_at_encounter", "curr_bmi", "sex_label", "race_ethnicity_label", "location_label",
  "osa_label", "asthma_label", "copd_label", "chf_label", "nmd_label",
  "phtn_label", "ckd_label", "diabetes_label", "encounter_type_label", "vbg_co2", "paco2"
)
vars_baseline <- setdiff(vars, c("vbg_co2", "paco2"))
vars_abg <- c(vars_baseline, "paco2")
vars_vbg <- c(vars_baseline, "vbg_co2")

# Table 1 constructor
make_table1 <- function(data, group_var, caption = "") {
  group_sym <- rlang::sym(group_var)

  df <- data %>%
    filter(!is.na (!!group_sym), # drop explicit NA

```

```

  !!group_sym != "Missing") %>%          # drop "Missing" cohort
  mutate (!!group_sym := droplevels (!!group_sym)) %>%  # only drop group levels
  select(all_of(c(group_var, vars_baseline)))

empty_fac <- names(which(vapply(df, function(z) is.factor(z) && length(levels(z)) == 0L, logical(1))))
if (length(empty_fac) > 0) {
  warning("0-level factor columns detected: ", paste(empty_fac, collapse = ", "),
         ". Converting to character to prevent gtsummary failure.", call. = FALSE)
  df[empty_fac] <- lapply(df[empty_fac], as.character)
}

df %>%
  gtsummary::tbl_summary(
    by     = !!group_sym,
    type   = list(sex_label ~ "categorical"),
    statistic = list(
      gtsummary::all_continuous() ~ "{mean} ± {sd}; {N_miss}/{N_obs} missing ({p_miss}%)",
      gtsummary::all_categorical() ~ "{n} ({p}%)"
    ),
    digits  = list(gtsummary::all_continuous() ~ 1),
    missing  = "no"                                # no gtsummary missing column/row
  ) %>%
  gtsummary::modify_header(label = "***Variable***") %>%
  gtsummary::modify_caption(strip_manual_table_number(caption))
}

if (sum(!is.na(subset_data$sex_label)) == 0L || length(levels(subset_data$sex_label)) == 0L) {
  warning("sex_label is all NA or has zero levels; check sex normalization/mapping.", call. = FALSE)
  stopifnot("sex" %in% names(subset_data))
}

# build tables
table1A <- make_table1(subset_data, "abg_group", caption = "Table 1A: ABG cohorts")
table1B <- make_table1(subset_data, "vbg_group", caption = "Table 1B: VBG cohorts")

tbl1a_pdf <- to_pdf_table(table1A, font_size = 7, landscape = FALSE, label_col_width = "2.0in",

```

```

    longtable = TRUE)
tbl1b_pdf <- to_pdf_table(table1B, font_size = 7, landscape = FALSE, label_col_width = "2.0in",
                           longtable = TRUE)
tbl1a_pdf

```

Table 4: ABG cohorts

Variable	**No ABG** N = 16,490	**ABG** N = 9,362
age_at_encounter	58.2 ± 18.1; 0.0/16,490.0 missing (0.0%)	61.1 ± 16.9; 0.0/9,362.0 missing (0.0%)
curr_bmi	32.5 ± 8.7; 9,223.0/16,490.0 missing (55.9%)	29.0 ± 7.1; 5,500.0/9,362.0 missing (58.7%)
sex_label		
Female	8,598 (52%)	4,218 (45%)
Male	7,892 (48%)	5,144 (55%)
race_ethnicity_label		
White	10,061 (61%)	6,090 (65%)
Black or African American	3,149 (19%)	1,387 (15%)
Hispanic	1,168 (7.1%)	500 (5.3%)
Asian	252 (1.5%)	179 (1.9%)
American Indian	88 (0.5%)	101 (1.1%)
Pacific Islander	25 (0.2%)	14 (0.1%)
Unknown	1,747 (11%)	1,091 (12%)
location_label		
South	6,962 (42%)	5,171 (55%)
Northeast	4,707 (29%)	1,831 (20%)
Midwest	1,143 (6.9%)	783 (8.4%)
West	3,678 (22%)	1,577 (17%)
osa_label	3,047 (18%)	1,455 (16%)
asthma_label	2,439 (15%)	1,086 (12%)
copd_label	3,037 (18%)	2,052 (22%)
chf_label	2,964 (18%)	2,104 (22%)
nmd_label	599 (3.6%)	428 (4.6%)
phtn_label	1,231 (7.5%)	897 (9.6%)
ckd_label	2,825 (17%)	1,837 (20%)
diabetes_label	4,838 (29%)	2,776 (30%)
encounter_type_label		
Emergency	7,055 (43%)	1,451 (15%)
Inpatient	9,435 (57%)	7,911 (85%)

```
tbl1b_pdf
```

Table 5: VBG cohorts

Variable	**No VBG** N = 18,392	**VBG** N = 7,460
age_at_encounter	59.4 ± 17.7; 0.0/18,392.0 missing (0.0%)	58.9 ± 17.7; 0.0/7,460.0 missing (0.0%)
curr_bmi	31.9 ± 8.5; 9,691.0/18,392.0 missing (52.7%)	29.0 ± 7.5; 5,032.0/7,460.0 missing (67.5%)
sex_label		
Female	9,331 (51%)	3,485 (47%)
Male	9,061 (49%)	3,975 (53%)
race_ethnicity_label		
White	12,190 (66%)	3,961 (53%)
Black or African American	3,109 (17%)	1,427 (19%)
Hispanic	1,149 (6.2%)	519 (7.0%)
Asian	279 (1.5%)	152 (2.0%)
American Indian	91 (0.5%)	98 (1.3%)
Pacific Islander	33 (0.2%)	6 (<0.1%)
Unknown	1,541 (8.4%)	1,297 (17%)
location_label		
South	9,882 (54%)	2,251 (30%)
Northeast	3,358 (18%)	3,180 (43%)
Midwest	1,241 (6.7%)	685 (9.2%)
West	3,911 (21%)	1,344 (18%)
osa_label	3,273 (18%)	1,229 (16%)
asthma_label	2,520 (14%)	1,005 (13%)
copd_label	3,596 (20%)	1,493 (20%)
chf_label	3,495 (19%)	1,573 (21%)
nmd_label	757 (4.1%)	270 (3.6%)
phtn_label	1,405 (7.6%)	723 (9.7%)
ckd_label	3,119 (17%)	1,543 (21%)
diabetes_label	5,137 (28%)	2,477 (33%)
encounter_type_label		
Emergency	6,183 (34%)	2,323 (31%)
Inpatient	12,209 (66%)	5,137 (69%)

```

ft_table1A <- as_flex_table(table1A)
ft_table1B <- as_flex_table(table1B)

doc <- read_docx() %>%
  body_add_par("Table 1A. Baseline Characteristics by ABG Group", style = "heading 1") %>%
  body_add_flextable(ft_table1A) %>%
  body_add_par("Table 1B. Baseline Characteristics by VBG Group", style = "heading 1") %>%
  body_add_flextable(ft_table1B)

print(doc, target = results_path("Table1_ABG_VBG.docx"))

```

```

# Status factors (column labels are taken from factor levels)
subset_data <- subset_data %>%
  mutate(
    abg_status = factor(has_abg, levels = c(0, 1),
                         labels = c("Did not get ABG", "Did get ABG")),
    vbg_status = factor(has_vbg, levels = c(0, 1),
                         labels = c("Did not get VBG", "Did get VBG"))
  )

# ABG table with "Everyone" column first
tbl1_abg <- subset_data %>%
  select(all_of(vars_baseline), abg_status) %>%
  gtsummary::tbl_summary(
    by = abg_status,
    type = list(sex_label ~ "categorical"),
    statistic = list(
      gtsummary::all_continuous() ~ "{mean} ± {sd}; {N_miss}/{N_obs} missing ({p_miss}%)",
      gtsummary::all_categorical() ~ "{n} ({p}%)"
    ),
    digits = list(gtsummary::all_continuous() ~ 1),
    missing = "no"
  ) %>%
  gtsummary::add_overall(last = FALSE, col_label = "Everyone") %>%
  gtsummary::modify_header(label = "***Variable***")

# VBG table with "Everyone" column first
tbl1_vbg <- subset_data %>%
  select(all_of(vars_baseline), vbg_status) %>%
  gtsummary::tbl_summary(
    by = vbg_status,
    type = list(sex_label ~ "categorical"),
    statistic = list(
      gtsummary::all_continuous() ~ "{mean} ± {sd}; {N_miss}/{N_obs} missing ({p_miss}%)",
      gtsummary::all_categorical() ~ "{n} ({p}%)"
    ),
    digits = list(gtsummary::all_continuous() ~ 1),

```

```

missing = "no"
) %>%
gtsummary::add_overall(last = FALSE, col_label = "Everyone") %>%
gtsummary::modify_header(label = "**Variable**")

tbl1_abg <- tbl1_abg %>%
  modify_caption(strip_manual_table_number("**Table 1A. Baseline summary: Everyone and ABG status**"))
tbl1_vbg <- tbl1_vbg %>%
  modify_caption(strip_manual_table_number("**Table 1B. Baseline summary: Everyone and VBG status**"))

# merged table for Word export (Table 1: Everyone + ABG/VBG status)
tbl1 <- gtsummary::tbl_merge(
  list(tbl1_abg, tbl1_vbg),
  tab_spanner = c("**ABG status**", "**VBG status**")
)

tbl1_abg_pdf <- to_pdf_table(tbl1_abg, font_size = 7, landscape = FALSE, label_col_width = "2.0in",
                               longtable = TRUE)
tbl1_vbg_pdf <- to_pdf_table(tbl1_vbg, font_size = 7, landscape = FALSE, label_col_width = "2.0in",
                               longtable = TRUE)
tbl1_abg_pdf

```

Table 6: Baseline summary: Everyone and ABG status**

Variable	Everyone	**Did not get ABG** N = 16,490	**Did get ABG** N = 9,362
age_at_encounter	59.2 ± 17.7; 0/25,852.0 missing (0.0%)	58.2 ± 18.1; 0/16,490.0 missing (0.0%)	61.1 ± 16.9; 0/9,362.0 missing (0.0%)
curr_bmi	31.3 ± 8.4; 14,723.0/25,852.0 missing (57.0%)	32.5 ± 8.7; 9,223.0/16,490.0 missing (55.9%)	29.0 ± 7.1; 5,500.0/9,362.0 missing (58.7%)
sex_label			
Female	12,816 (50%)	8,598 (52%)	4,218 (45%)
Male	13,036 (50%)	7,892 (48%)	5,144 (55%)
race_ethnicity_label			
White	16,151 (62%)	10,061 (61%)	6,090 (65%)
Black or African American	4,536 (18%)	3,149 (19%)	1,387 (15%)
Hispanic	1,668 (6.5%)	1,168 (7.1%)	500 (5.3%)
Asian	431 (1.7%)	252 (1.5%)	179 (1.9%)
American Indian	189 (0.7%)	88 (0.5%)	101 (1.1%)
Pacific Islander	39 (0.2%)	25 (0.2%)	14 (0.1%)
Unknown	2,838 (11%)	1,747 (11%)	1,091 (12%)
location_label			
South	12,133 (47%)	6,962 (42%)	5,171 (55%)

Table 6: Baseline summary: Everyone and ABG status** (*continued*)

Variable	Everyone	**Did not get ABG** N = 16,490	**Did get ABG** N = 9,362
Northeast	6,538 (25%)	4,707 (29%)	1,831 (20%)
Midwest	1,926 (7.5%)	1,143 (6.9%)	783 (8.4%)
West	5,255 (20%)	3,678 (22%)	1,577 (17%)
osa_label	4,502 (17%)	3,047 (18%)	1,455 (16%)
asthma_label	3,525 (14%)	2,439 (15%)	1,086 (12%)
copd_label	5,089 (20%)	3,037 (18%)	2,052 (22%)
chf_label	5,068 (20%)	2,964 (18%)	2,104 (22%)
nmd_label	1,027 (4.0%)	599 (3.6%)	428 (4.6%)
phtn_label	2,128 (8.2%)	1,231 (7.5%)	897 (9.6%)
ckd_label	4,662 (18%)	2,825 (17%)	1,837 (20%)
diabetes_label	7,614 (29%)	4,838 (29%)	2,776 (30%)
encounter_type_label			
Emergency	8,506 (33%)	7,055 (43%)	1,451 (15%)
Inpatient	17,346 (67%)	9,435 (57%)	7,911 (85%)

tbl1_vbg_pdf

Table 7: Baseline summary: Everyone and VBG status**

Variable	Everyone	**Did not get VBG** N = 18,392	**Did get VBG** N = 7,460
age_at_encounter	59.2 ± 17.7; 0.0/25,852.0 missing (0.0%)	59.4 ± 17.7; 0.0/18,392.0 missing (0.0%)	58.9 ± 17.7; 0.0/7,460.0 missing (0.0%)
curr_bmi	31.3 ± 8.4; 14,723.0/25,852.0 missing (57.0%)	31.9 ± 8.5; 9,691.0/18,392.0 missing (52.7%)	29.0 ± 7.5; 5,032.0/7,460.0 missing (67.5%)
sex_label			
Female	12,816 (50%)	9,331 (51%)	3,485 (47%)
Male	13,036 (50%)	9,061 (49%)	3,975 (53%)
race_ethnicity_label			
White	16,151 (62%)	12,190 (66%)	3,961 (53%)
Black or African American	4,536 (18%)	3,109 (17%)	1,427 (19%)
Hispanic	1,668 (6.5%)	1,149 (6.2%)	519 (7.0%)
Asian	431 (1.7%)	279 (1.5%)	152 (2.0%)
American Indian	189 (0.7%)	91 (0.5%)	98 (1.3%)
Pacific Islander	39 (0.2%)	33 (0.2%)	6 (<0.1%)
Unknown	2,838 (11%)	1,541 (8.4%)	1,297 (17%)
location_label			
South	12,133 (47%)	9,882 (54%)	2,251 (30%)
Northeast	6,538 (25%)	3,358 (18%)	3,180 (43%)
Midwest	1,926 (7.5%)	1,241 (6.7%)	685 (9.2%)
West	5,255 (20%)	3,911 (21%)	1,344 (18%)
osa_label	4,502 (17%)	3,273 (18%)	1,229 (16%)
asthma_label	3,525 (14%)	2,520 (14%)	1,005 (13%)
copd_label	5,089 (20%)	3,596 (20%)	1,493 (20%)
chf_label	5,068 (20%)	3,495 (19%)	1,573 (21%)

Table 7: Baseline summary: Everyone and VBG status** (*continued*)

Variable	Everyone	**Did not get VBG** N = 18,392	**Did get VBG** N = 7,460
nmd_label	1,027 (4.0%)	757 (4.1%)	270 (3.6%)
phtn_label	2,128 (8.2%)	1,405 (7.6%)	723 (9.7%)
ckd_label	4,662 (18%)	3,119 (17%)	1,543 (21%)
diabetes_label	7,614 (29%)	5,137 (28%)	2,477 (33%)
encounter_type_label			
Emergency	8,506 (33%)	6,183 (34%)	2,323 (31%)
Inpatient	17,346 (67%)	12,209 (66%)	5,137 (69%)

```

ABG_CO2_VAR <- "paco2"
VBG_CO2_VAR <- "vbg_co2"
ABG_CO2_LOW <- 35
ABG_CO2_HIGH <- 45
VBG_CO2_LOW <- 40
VBG_CO2_HIGH <- 50
CO2_SPEC <- list(
  ABG = list(var = ABG_CO2_VAR, normal_lo = ABG_CO2_LOW, normal_hi = ABG_CO2_HIGH),
  VBG = list(var = VBG_CO2_VAR, normal_lo = VBG_CO2_LOW, normal_hi = VBG_CO2_HIGH)
)
CO2_SPEC$ABG$ref <- (CO2_SPEC$ABG$normal_lo + CO2_SPEC$ABG$normal_hi) / 2
CO2_SPEC$VBG$ref <- (CO2_SPEC$VBG$normal_lo + CO2_SPEC$VBG$normal_hi) / 2
# Reference values for spline OR curves (midpoint of normal range)
ABG_CO2_REF <- CO2_SPEC$ABG$ref
VBG_CO2_REF <- CO2_SPEC$VBG$ref
CO2_CAT_LEVELS <- c("Normal", "Low", "High")
CO2_CAT_CONTRAST_LEVELS <- setdiff(CO2_CAT_LEVELS, "Normal")

make_co2_cat3 <- function(x, low_cut, high_cut) {
  x <- suppressWarnings(as.numeric(x))
  out <- dplyr::case_when(
    is.na(x)      ~ NA_character_,
    x < low_cut   ~ "Low",
    x > high_cut  ~ "High",
    TRUE          ~ "Normal"
  )
  factor(out, levels = CO2_CAT_LEVELS)
}

```

```

}

subset_data <- subset_data %>%
  mutate(
    pco2_cat_abg = make_co2_cat3(.data[[ABG_CO2_VAR]], ABG_CO2_LOW, ABG_CO2_HIGH),
    pco2_cat_vbg = make_co2_cat3(.data[[V ро_2_VAR]], VBG_CO2_LOW, VBG_CO2_HIGH)
  )

stopifnot("Normal" %in% levels(subset_data$pco2_cat_abg),
          "Normal" %in% levels(subset_data$pco2_cat_vbg))

warn_low_counts <- function(cat, label) {
  tab <- table(cat, useNA = "no")
  if (length(tab) && any(tab < 10)) {
    warning(label, ": low counts in CO2 categories: ",
            paste(names(tab), tab, collapse = ", "), call. = FALSE)
  }
}
warn_low_counts(subset_data$pco2_cat_abg[subset_data$has_abg == 1 & !is.na(subset_data$paco2)],
                "ABG")
warn_low_counts(subset_data$pco2_cat_vbg[subset_data$has_vbg == 1 & !is.na(subset_data$vbg_co2)],
                "V ро_2")

# Fail-fast if any binary CO2 indicator references remain in this QMD
qmd_path <- knitr::current_input()
stopifnot(!is.null(qmd_path), file.exists(qmd_path))
txt <- readLines(qmd_path, warn = FALSE)
pat_var <- paste0("hypercap", "_on_")
pat_txt <- paste0("binary", " hypercapnia")
if (any(grepl(pat_var, txt))) {
  stop("Binary CO2 indicator variable references remain in the QMD.")
}
if (any(grepl(pat_txt, txt, ignore.case = TRUE))) {
  stop("Binary CO2 indicator text remains in the QMD.")
}

```

```

# ABG cohort (has_abg == 1)
tbl2_abg <- subset_data %>%
  filter(has_abg == 1) %>%
  select(all_of(vars_abg), pco2_cat_abg) %>%
  gtsummary::tbl_summary(
    by = pco2_cat_abg,
    type = list(sex_label ~ "categorical"),
    statistic = list(
      gtsummary::all_continuous() ~ "{mean} ± {sd}; {N_miss}/{N_obs} missing ({p_miss}%)",
      gtsummary::all_categorical() ~ "{n} ({p}%)"
    ),
    digits = list(gtsummary::all_continuous() ~ 1),
    missing = "no"
  ) %>%
  gtsummary::modify_header(
    label = "***Variable***",
    stat_1 = "***Normal***",
    stat_2 = "***Low***",
    stat_3 = "***High***"
  )

# VBG cohort (has_vbg == 1)
tbl2_vbg <- subset_data %>%
  filter(has_vbg == 1) %>%
  select(all_of(vars_vbg), pco2_cat_vbg) %>%
  gtsummary::tbl_summary(
    by = pco2_cat_vbg,
    type = list(sex_label ~ "categorical"),
    statistic = list(
      gtsummary::all_continuous() ~ "{mean} ± {sd}; {N_miss}/{N_obs} missing ({p_miss}%)",
      gtsummary::all_categorical() ~ "{n} ({p}%)"
    ),
    digits = list(gtsummary::all_continuous() ~ 1),
    missing = "no"
  ) %>%
  gtsummary::modify_header()

```

```

label  = "##Variable**",
stat_1 = "##Normal**",
stat_2 = "##Low**",
stat_3 = "##High**"
)

tbl2 <- gtsummary::tbl_merge(
  tbls = list(tbl2_abg, tbl2_vbg),
  tab_spanner = c("##ABG (PaCO2)**", "##VBG (PvCO2)**")
) %>%
  gtsummary::modify_caption(strip_manual_table_number("##Table 2. Baseline summary by CO2 category within ABG and VBG cohorts##"))

tbl2_pdf <- to_pdf_table(tbl2, font_size = 7, landscape = FALSE, label_col_width = "2.0in",
                           longtable = TRUE)
tbl2_pdf

```

Table 8: Baseline summary by CO2 category within ABG and VBG cohorts**

##Variable##	##Normal##	##Low##	##High##	##Normal##
age_at_encounter	60.9 ± 16.9; 0.0/4,229.0 missing (0.0%)	60.4 ± 17.4; 0.0/2,488.0 missing (0.0%)	62.0 ± 16.3; 0.0/2,645.0 missing (0.0%)	58.0 ± 18.0; 0.0/3,427.0 missing (0.0%)
curr_bmi	29.0 ± 6.9; 2,440.0/4,229.0 missing (57.7%)	28.3 ± 6.8; 1,493.0/2,488.0 missing (60.0%)	29.8 ± 7.6; 1,567.0/2,645.0 missing (59.2%)	29.1 ± 7.3; 2,398.0/3,427.0 missing (59.2%)
sex_label				
Female	1,878 (44%)	1,123 (45%)	1,217 (46%)	1,627 (47%)
Male	2,351 (56%)	1,365 (55%)	1,428 (54%)	1,800 (53%)
race_ethnicity_label				
White	2,742 (65%)	1,510 (61%)	1,838 (69%)	1,825 (53%)
Black or African American	609 (14%)	400 (16%)	378 (14%)	648 (19%)
Hispanic	229 (5.4%)	144 (5.8%)	127 (4.8%)	243 (7.1%)
Asian	82 (1.9%)	59 (2.4%)	38 (1.4%)	71 (2.1%)
American Indian	58 (1.4%)	32 (1.3%)	11 (0.4%)	34 (1.0%)
Pacific Islander	8 (0.2%)	5 (0.2%)	1 (<0.1%)	3 (<0.1%)
Unknown	501 (12%)	338 (14%)	252 (9.5%)	603 (18%)
location_label				
South	2,334 (55%)	1,399 (56%)	1,438 (54%)	1,106 (32%)
Northeast	795 (19%)	405 (16%)	631 (24%)	1,510 (44%)
Midwest	373 (8.8%)	184 (7.4%)	226 (8.5%)	312 (9.1%)
West	727 (17%)	500 (20%)	350 (13%)	499 (15%)
osa_label	602 (14%)	291 (12%)	562 (21%)	528 (15%)
asthma_label	474 (11%)	245 (9.8%)	367 (14%)	433 (13%)
copd_label	779 (18%)	374 (15%)	899 (34%)	548 (16%)
chf_label	834 (20%)	503 (20%)	767 (29%)	639 (19%)
nmd_label	210 (5.0%)	105 (4.2%)	113 (4.3%)	114 (3.3%)
phtn_label	346 (8.2%)	207 (8.3%)	344 (13%)	286 (8.3%)
ckd_label	799 (19%)	497 (20%)	541 (20%)	650 (19%)

Table 8: Baseline summary by CO2 category within ABG and VBG cohorts** (*continu*

Variable	**Normal**	**Low**	**High**	**Normal**
diabetes_label	1,211 (29%)	750 (30%)	815 (31%)	1,070 (31%)
encounter_type_label				
Emergency	627 (15%)	345 (14%)	479 (18%)	1,173 (34%)
Inpatient	3,602 (85%)	2,143 (86%)	2,166 (82%)	2,254 (66%)
paco2	39.7 ± 3.0; 0.0/4,229.0 missing (0.0%)	29.4 ± 4.4; 0.0/2,488.0 missing (0.0%)	59.6 ± 20.6; 0.0/2,645.0 missing (0.0%)	
vbg_co2				44.6 ± 3.0; 0.0/3,427.0 missing (0.0%)

Table 9: Table 2a. Crude outcomes by CO2 category

Cohort	Outcome	Normal	Low	High
ABG	IMV	979/4229 (23.1%)	691/2488 (27.8%)	721/2645 (27.3%)
ABG	NIV	288/4229 (6.8%)	187/2488 (7.5%)	421/2645 (15.9%)
ABG	Death (60d)	604/4229 (14.3%)	537/2488 (21.6%)	504/2645 (19.1%)
ABG	Hypercapnic RF	207/4229 (4.9%)	119/2488 (4.8%)	666/2645 (25.2%)
VBG	IMV	432/3427 (12.6%)	357/2058 (17.3%)	373/1975 (18.9%)
VBG	NIV	175/3427 (5.1%)	122/2058 (5.9%)	257/1975 (13.0%)
VBG	Death (60d)	378/3427 (11.0%)	356/2058 (17.3%)	310/1975 (15.7%)
VBG	Hypercapnic RF	146/3427 (4.3%)	70/2058 (3.4%)	476/1975 (24.1%)

```

library(gtsummary)
library(flextable)
library(officer)

# gtsummary objects (example: tbl1, tbl2)
ft1 <- as_flex_table(tbl1)
ft2 <- as_flex_table(tbl2)

doc1 <- read_docx() %>%
  body_add_par("Table 1. Baseline summary: Everyone, ABG status, and VBG status",
               style = "heading 1") %>%
  body_add_flextable(ft1)
print(doc1, target = results_path("Table1.docx"))

doc2 <- read_docx() %>%
  body_add_par("Table 2. Baseline summary by CO2 category within ABG and VBG cohorts",
               style = "heading 1") %>%

```

```

  body_add_flextable(ft2)
print(doc2, target = results_path("Table2.docx"))

```

1.3 3) Three-level PCO2 categories (unweighted)

Three groups using low/normal/high CO2 categories

```

stopifnot(all(c("pco2_cat_abg", "pco2_cat_vbg") %in% names(subset_data)))

library(broom)
library(tidyr)
library(dplyr)

run_logit <- function(data, outcome, exposure, group_name, adj_vars = NULL, model_type = "Crude") {
  f <- if (length(adj_vars)) {
    reformulate(c(exposure, adj_vars), response = outcome)
  } else {
    as.formula(paste(outcome, "~", exposure))
  }
  fit_res <- fit_with_diagnostics(
    function() glm(f, data = data, family = binomial, control = glm.control(maxit = 50)),
    context = make_context(
      stage = "outcome",
      component = "cat3",
      analysis_variant = "unweighted",
      model_type = "cat3",
      group = group_name,
      outcome = outcome,
      imputation = NA_integer_,
      batch = NA_integer_
    )
  )
  append_outcome_diag(fit_res$diag)
  if (is.null(fit_res$fit)) {
    stop("run_logit: model fit failed for outcome=", outcome,

```

```

    " exposure=", exposure, " group=", group_name)
}

tidy(fit_res$fit, exponentiate = TRUE, conf.int = TRUE) %>%
  filter(term != "(Intercept)", startsWith(term, exposure)) %>%
  mutate(
    outcome = outcome,
    group   = group_name,
    model   = model_type
  )
}

outcomes_unw <- c("imv_proc", "niv_proc", "death_60d", "hypercap_resp_failure")

unw_three_level_forms <- list(
  "ABG 3-level: IMV ~ CO2 category + X"      = reformulate(c("pc02_cat_abg", adj_core), response = "imv_proc"),
  "ABG 3-level: NIV ~ CO2 category + X"        = reformulate(c("pc02_cat_abg", adj_core), response = "niv_proc"),
  "ABG 3-level: Death60d ~ CO2 category + X"   = reformulate(c("pc02_cat_abg", adj_core), response = "death_60d"),
  "ABG 3-level: HCRF ~ CO2 category + X"        = reformulate(c("pc02_cat_abg", adj_core), response = "hypercap_resp_failure"),
  "VBG 3-level: IMV ~ CO2 category + X"         = reformulate(c("pc02_cat_vbg", adj_core), response = "imv_proc"),
  "VBG 3-level: NIV ~ CO2 category + X"         = reformulate(c("pc02_cat_vbg", adj_core), response = "niv_proc"),
  "VBG 3-level: Death60d ~ CO2 category + X"    = reformulate(c("pc02_cat_vbg", adj_core), response = "death_60d"),
  "VBG 3-level: HCRF ~ CO2 category + X"        = reformulate(c("pc02_cat_vbg", adj_core), response = "hypercap_resp_failure")
)
register_model_diagrams(unw_three_level_forms)

unw_results_crude <- bind_rows(
  lapply(outcomes_unw, function(o) run_logit(subset_data, o, "pc02_cat_abg", "ABG")),
  lapply(outcomes_unw, function(o) run_logit(subset_data, o, "pc02_cat_vbg", "VBG"))
)
unw_results_adj <- bind_rows(
  lapply(outcomes_unw, function(o) run_logit(subset_data, o, "pc02_cat_abg", "ABG", adj_core, "Adjusted")),
  lapply(outcomes_unw, function(o) run_logit(subset_data, o, "pc02_cat_vbg", "VBG", adj_core, "Adjusted"))
)

unw_threellevel_results <- unw_results_adj %>%
  mutate(method = "Unweighted adjusted")

```

```

unw_combined_or_df <- unw_results_adj %>%
  mutate(
    outcome = recode(outcome,
      imv_proc = "Intubation",
      niv_proc = "NIV",
      death_60d = "Death (60d)",
      hypercap_resp_failure = "Hypercapnic RF")
  )
unw_combined_or_df <- map_or_exposure(unw_combined_or_df, "or-plot-three-level-unweighted") |>
  select(outcome, group, exposure, estimate, conf.low, conf.high)

```

```

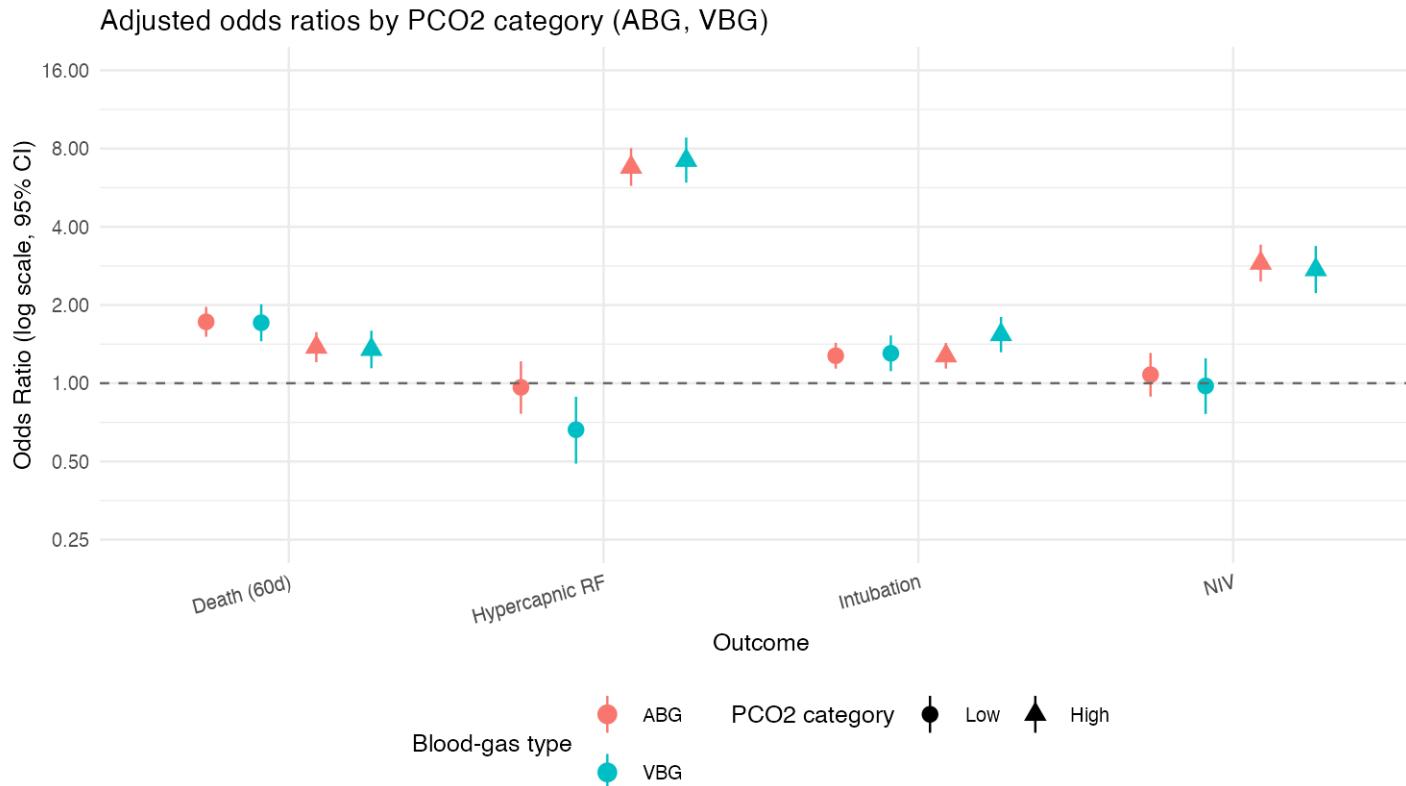
library(scales)

unw_combined_or_df$group <- factor(
  unw_combined_or_df$group,
  levels = c("ABG", "VBG")
)

unw_plot_df <- build_or_plot_df(unw_combined_or_df, "or-plot-three-level-unweighted",
  expected_exposure_levels = CO2_CAT_CONTRAST_LEVELS)
stopifnot(is.data.frame(unw_plot_df))
unw_axis_spec <- compute_or_axis_spec(unw_plot_df, lo_col = "conf.low", hi_col = "conf.high",
  default_limits = OR_XLIM)
unw_p_or <- plot_or_safe(
  unw_plot_df,
  plot_name = "or-plot-three-level-unweighted",
  axis_spec = unw_axis_spec,
  title = "Adjusted odds ratios by PCO2 category (ABG, VBG)",
  caption = paste(
    "Adjusted for age, sex, race/ethnicity, location, and encounter type.",
    "Reference = patients in the normal PCO2 range.",
    "Low: <35 mmHg (ABG) or <40 mmHg (VBG); High: >45 mmHg (ABG) or >50 mmHg (VBG).",
    "Because the underlying cohorts differ (ABG, VBG), denominators are not identical across groups.",
    sep = "\n"
)

```

```
)
print_plot_once(unw_p_or, "or-plot-three-level-unweighted", width = 7.5, height = 4.8)
```



1.4 4) Restricted cubic spline regressions (unweighted)

Spline curves are shown as odds ratios relative to CO₂_ref (midpoint of the normal range), holding covariates at the reference profile.

```
# ABG spline dataset
subset_data_abg <- subset_data %>%
  filter(has_abg == 1, !is.na(paco2)) %>%
  select(paco2, imv_proc, niv_proc, death_60d, hypercap_resp_failure, all_of(adj_core)) %>%
  filter(complete.cases(.))
```

1.4.1 4.1 Unweighted, Restricted Cubic Spline Regression - ABG by PaCO2

```
make_spline_fml <- function(outcome, co2_var, adj_vars) {
  spline_term <- if (SPLINE_BASIS == "rcs") {
    sprintf("rms::rcs(%s, %d)", co2_var, SPLINE_DF)
  } else {
    sprintf("splines::ns(%s, %d)", co2_var, SPLINE_DF)
  }
  stats::as.formula(
    paste0(outcome, " ~ ", spline_term,
           if (length(adj_vars)) paste0(" + ", paste(adj_vars, collapse = " + ")) else ""))
}
}

#| code-block-title: "Unweighted ABG spline models (adjusted)"
abg_spline_forms <- list(
  "ABG spline (adjusted): IMV ~ CO2 spline + X"      = make_spline_fml("imv_proc", "paco2", adj_core),
  "ABG spline (adjusted): NIV ~ CO2 spline + X"      = make_spline_fml("niv_proc", "paco2", adj_core),
  "ABG spline (adjusted): Death60d ~ CO2 spline + X" = make_spline_fml("death_60d", "paco2", adj_core),
  "ABG spline (adjusted): HCRF ~ CO2 spline + X"     = make_spline_fml("hypercap_resp_failure", "paco2", adj_core)
)
register_model_diagrams(abg_spline_forms)

co2_seq_abg <- stats::quantile(subset_data_abg$paco2, probs = c(0.02, 0.98), na.rm = TRUE)
grid_abg_info_unw <- make_co2_grid_ref(
  "paco2",
  seq(co2_seq_abg[1], co2_seq_abg[2], length.out = SPLINE_GRID_N),
  x_ref_abg,
```

```

    ABG_CO2_REF
)
grid_abg_unw <- grid_abg_info_unw$grid
ref_idx_abg_unw <- grid_abg_info_unw$ref_idx
co2_ref_abg_unw <- grid_abg_info_unw$co2_ref

fit_spline_glm <- function(outcome, co2_var, data, group_label) {
  fit_res <- fit_with_diagnostics(
    function() glm(make_spline_fml(outcome, co2_var, adj_core),
                  data = data, family = binomial,
                  control = glm.control(maxit = 50)),
    context = make_context(
      stage = "outcome",
      component = "spline",
      analysis_variant = "unweighted",
      model_type = "spline",
      group = group_label,
      outcome = outcome,
      imputation = NA_integer_,
      batch = NA_integer_
    )
  )
  append_outcome_diag(fit_res$diag)
  fit_res$fit
}

fit_imv <- fit_spline_glm("imv_proc", "paco2", subset_data_abg, "ABG")
fit_niv <- fit_spline_glm("niv_proc", "paco2", subset_data_abg, "ABG")
fit_death <- fit_spline_glm("death_60d", "paco2", subset_data_abg, "ABG")
fit_hcrcf <- fit_spline_glm("hypercap_resp_failure", "paco2", subset_data_abg, "ABG")
if (any(vapply(list(fit_imv, fit_niv, fit_death, fit_hcrcf), is.null, logical(1)))) {
  stop("Unweighted ABG spline fits failed; see model_fit_diagnostics.csv.")
}

pred_imv <- predict_or_curve_from_fit(fit_imv, grid_abg_unw, ref_idx_abg_unw, "paco2")
pred_niv <- predict_or_curve_from_fit(fit_niv, grid_abg_unw, ref_idx_abg_unw, "paco2")

```

```

pred_death <- predict_or_curve_from_fit(fit_death, grid_abg_unw, ref_idx_abg_unw, "paco2")
pred_hcrf <- predict_or_curve_from_fit(fit_hcrf, grid_abg_unw, ref_idx_abg_unw, "paco2")
## Plotting deferred until VBG curves are computed so axes can be shared.

```

1.4.2 4.2 Unweighted, Restricted Cubic Spline - VBG

```

# --- VBG dataset ---
subset_data_vbg <- subset_data %>%
  dplyr::filter(has_vbg == 1, !is.na(vbg_co2)) %>%
  dplyr::select(vbg_co2, imv_proc, niv_proc, death_60d, hypercap_resp_failure, all_of(adj_core)) %>%
  dplyr::filter(complete.cases(.))

vbg_spline_forms <- list(
  "VBG spline (adjusted): IMV ~ CO2 spline + X"      = make_spline_fml("imv_proc", "vbg_co2", adj_core),
  "VBG spline (adjusted): NIV ~ CO2 spline + X"      = make_spline_fml("niv_proc", "vbg_co2", adj_core),
  "VBG spline (adjusted): Death60d ~ CO2 spline + X" = make_spline_fml("death_60d", "vbg_co2", adj_core),
  "VBG spline (adjusted): HCRF ~ CO2 spline + X"     = make_spline_fml("hypercap_resp_failure", "vbg_co2", adj_core)
)
register_model_diagrams(vbg_spline_forms)

co2_seq_vbg <- stats::quantile(subset_data_vbg$vbg_co2, probs = c(0.02, 0.98), na.rm = TRUE)
grid_vbg_info_unw <- make_co2_grid_ref(
  "vbg_co2",
  seq(co2_seq_vbg[1], co2_seq_vbg[2], length.out = SPLINE_GRID_N),
  x_ref_vbg,
  VBG_CO2_REF
)
grid_vbg_unw <- grid_vbg_info_unw$grid
ref_idx_vbg_unw <- grid_vbg_info_unw$ref_idx
co2_ref_vbg_unw <- grid_vbg_info_unw$co2_ref

fit_imv_vbg <- fit_spline_glm("imv_proc", "vbg_co2", subset_data_vbg, "VBG")
fit_niv_vbg <- fit_spline_glm("niv_proc", "vbg_co2", subset_data_vbg, "VBG")
fit_death_vbg <- fit_spline_glm("death_60d", "vbg_co2", subset_data_vbg, "VBG")

```

```

fit_hcrf_vbg <- fit_spline_glm("hypercap_resp_failure", "vbg_co2", subset_data_vbg, "VBG")
if (any(vapply(list(fit_imv_vbg, fit_niv_vbg, fit_death_vbg, fit_hcrf_vbg), is.null, logical(1)))) {
  stop("Unweighted VBG spline fits failed; see model_fit_diagnostics.csv.")
}

pred_imv_vbg <- predict_or_curve_from_fit(fit_imv_vbg, grid_vbg_unw, ref_idx_vbg_unw, "vbg_co2")
pred_niv_vbg <- predict_or_curve_from_fit(fit_niv_vbg, grid_vbg_unw, ref_idx_vbg_unw, "vbg_co2")
pred_death_vbg <- predict_or_curve_from_fit(fit_death_vbg, grid_vbg_unw, ref_idx_vbg_unw, "vbg_co2")
pred_hcrf_vbg <- predict_or_curve_from_fit(fit_hcrf_vbg, grid_vbg_unw, ref_idx_vbg_unw, "vbg_co2")
axis_unw_common <- compute_or_axis_spec(
  list(pred_imv, pred_niv, pred_death, pred_hcrf,
    pred_imv_vbg, pred_niv_vbg, pred_death_vbg, pred_hcrf_vbg),
  lo_col = "LCL", hi_col = "UCL"
)

plot_imv <- ggplot(pred_imv, aes(x = paco2, y = OR)) +
  geom_line(color = "blue", linewidth = 1.2) +
  geom_ribbon(aes(ymin = LCL, ymax = UCL), fill = "blue", alpha = 0.2) +
  geom_hline(yintercept = 1, linetype = "dashed", color = "grey40") +
  or_axis_scale(axis_unw_common) +
  labs(title = "Intubation (adjusted)", x = "PaCO2 (mmHg)",
       y = paste0("Odds ratio (ref PaCO2 = ", co2_ref_abg_unw, "; log scale)")) +
  theme_minimal()

plot_niv <- ggplot(pred_niv, aes(x = paco2, y = OR)) +
  geom_line(color = "green", linewidth = 1.2) +
  geom_ribbon(aes(ymin = LCL, ymax = UCL), fill = "green", alpha = 0.2) +
  geom_hline(yintercept = 1, linetype = "dashed", color = "grey40") +
  or_axis_scale(axis_unw_common) +
  labs(title = "NIV (adjusted)", x = "PaCO2 (mmHg)",
       y = paste0("Odds ratio (ref PaCO2 = ", co2_ref_abg_unw, "; log scale)")) +
  theme_minimal()

plot_death <- ggplot(pred_death, aes(x = paco2, y = OR)) +
  geom_line(color = "red", linewidth = 1.2) +
  geom_ribbon(aes(ymin = LCL, ymax = UCL), fill = "red", alpha = 0.2) +

```

```

geom_hline(yintercept = 1, linetype = "dashed", color = "grey40") +
or_axis_scale(axis_unw_common) +
labs(title = "Death (60d, adjusted)", x = "PaCO2 (mmHg)",
y = paste0("Odds ratio (ref PaCO2 = ", co2_ref_abg_unw, "; log scale)")) +
theme_minimal()

plot_hcrcf <- ggplot(pred_hcrcf, aes(x = paco2, y = OR)) +
geom_line(color = "purple", linewidth = 1.2) +
geom_ribbon(aes(ymin = LCL, ymax = UCL), fill = "purple", alpha = 0.2) +
geom_hline(yintercept = 1, linetype = "dashed", color = "grey40") +
or_axis_scale(axis_unw_common) +
labs(title = "Hypercapnic RF (adjusted)", x = "PaCO2 (mmHg)",
y = paste0("Odds ratio (ref PaCO2 = ", co2_ref_abg_unw, "; log scale)")) +
theme_minimal()

plot_imv_vbg <- ggplot(pred_imv_vbg, aes(x = vbg_co2, y = OR)) +
geom_line(color = "blue") +
geom_ribbon(aes(ymin = LCL, ymax = UCL), fill = "blue", alpha = 0.2) +
geom_hline(yintercept = 1, linetype = "dashed", color = "grey40") +
or_axis_scale(axis_unw_common) +
labs(title = "IMV (adjusted)", x = "VBG CO2 (mmHg)",
y = paste0("Odds ratio (ref VBG CO2 = ", co2_ref_vbg_unw, "; log scale)")) +
theme_minimal()

plot_niv_vbg <- ggplot(pred_niv_vbg, aes(x = vbg_co2, y = OR)) +
geom_line(color = "green") +
geom_ribbon(aes(ymin = LCL, ymax = UCL), fill = "green", alpha = 0.2) +
geom_hline(yintercept = 1, linetype = "dashed", color = "grey40") +
or_axis_scale(axis_unw_common) +
labs(title = "NIV (adjusted)", x = "VBG CO2 (mmHg)",
y = paste0("Odds ratio (ref VBG CO2 = ", co2_ref_vbg_unw, "; log scale)")) +
theme_minimal()

plot_death_vbg <- ggplot(pred_death_vbg, aes(x = vbg_co2, y = OR)) +
geom_line(color = "red") +
geom_ribbon(aes(ymin = LCL, ymax = UCL), fill = "red", alpha = 0.2) +

```

```

geom_hline(yintercept = 1, linetype = "dashed", color = "grey40") +
or_axis_scale(axis_unw_common) +
labs(title = "Death (60d, adjusted)", x = "VBG CO2 (mmHg)",
y = paste0("Odds ratio (ref VBG CO2 = ", co2_ref_vbg_unw, "; log scale)")) +
theme_minimal()

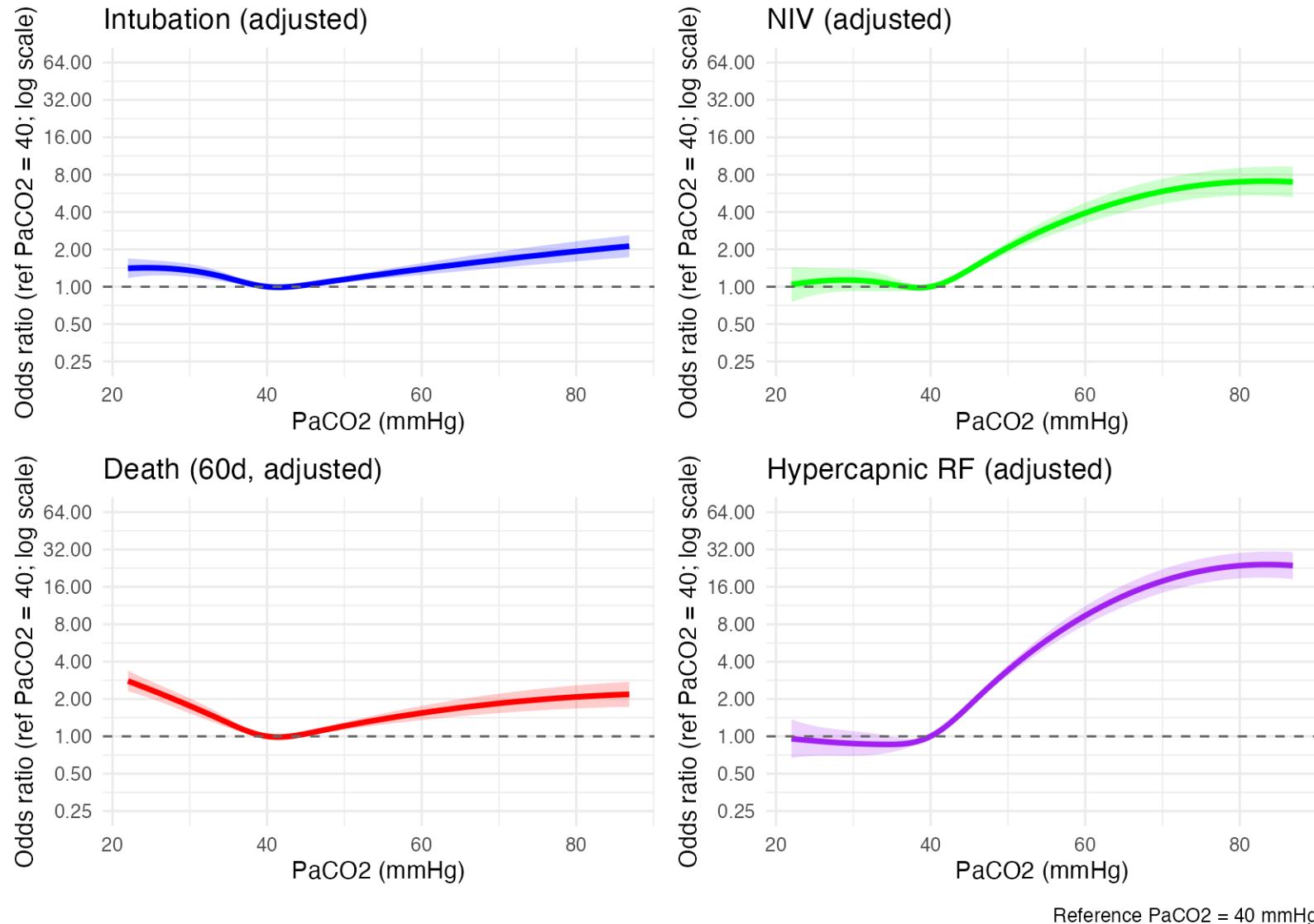
plot_hcrf_vbg <- ggplot(pred_hcrf_vbg, aes(x = vbg_co2, y = OR)) +
geom_line(color = "purple") +
geom_ribbon(aes(ymin = LCL, ymax = UCL), fill = "purple", alpha = 0.2) +
geom_hline(yintercept = 1, linetype = "dashed", color = "grey40") +
or_axis_scale(axis_unw_common) +
labs(title = "Hypercapnic RF (adjusted)", x = "VBG CO2 (mmHg)",
y = paste0("Odds ratio (ref VBG CO2 = ", co2_ref_vbg_unw, "; log scale)")) +
theme_minimal()

unw_abg_panel <- (plot_imv | plot_niv) / (plot_death | plot_hcrf) +
plot_annotation(caption = paste0("Reference PaCO2 = ", co2_ref_abg_unw, " mmHg"))

unw_vbg_panel <- ((plot_imv_vbg | plot_niv_vbg) /
(plot_death_vbg | plot_hcrf_vbg)) +
plot_annotation(
  title = paste0("Adjusted odds ratios by VBG CO2 (ref = ", co2_ref_vbg_unw, ")"),
  caption = paste0("Reference VBG CO2 = ", co2_ref_vbg_unw, " mmHg")
)

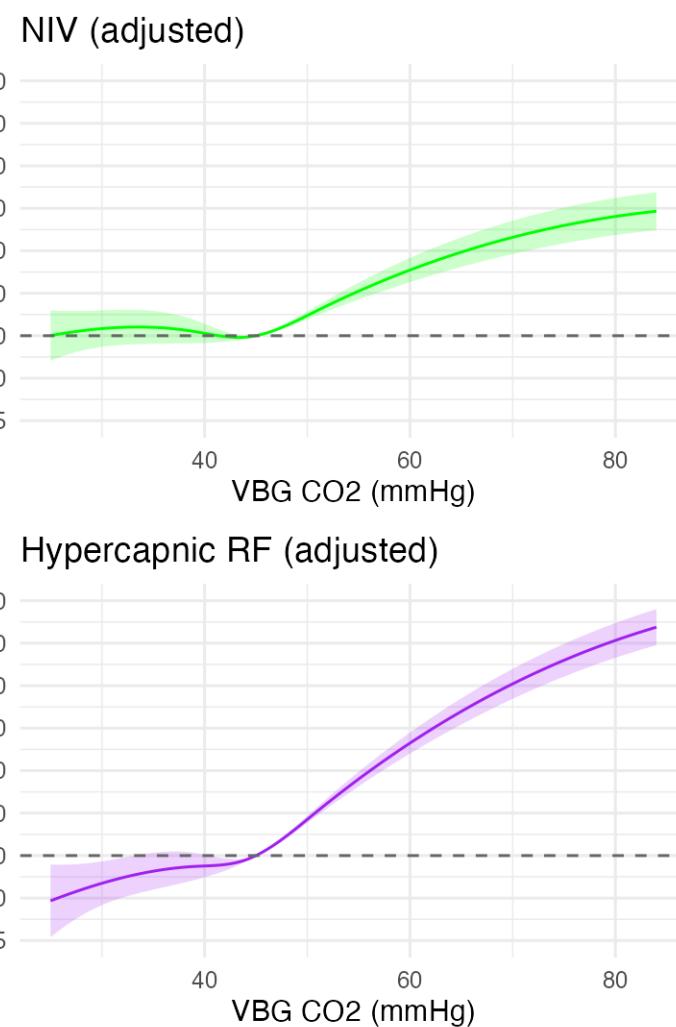
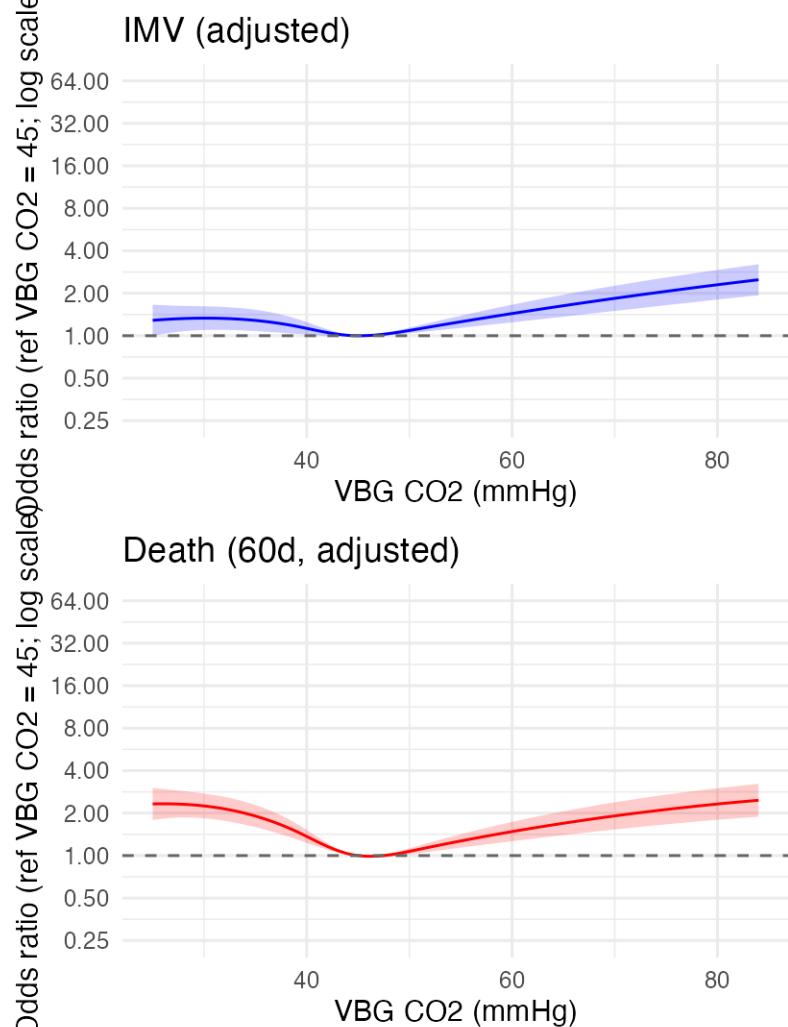
print_plot_once(unw_abg_panel, "spline-unweighted-abg", width = 8.5, height = 6)

```



```
print_plot_once(unw_vbg_panel, "spline-unweighted-vbg", width = 8.5, height = 6)
```

Adjusted odds ratios by VBG CO₂ (ref = 45)



Reference VBG CO₂ = 45 mmHg

2 Inverse Propensity Weighting

IPW done using Gradient Boosting Methods (GBM) - a type of decision-tree based machine learning. “***Random forests and GBM are designed to automatically include relevant interactions for variables included in the model.*** As such, using a GBM to estimate the PS model, can reduce model misspecification, since ***the analyst is not required to identify relevant interactions or nonlinearities.***” from this citation: PMID: 39947224<https://pmc.ncbi.nlm.nih.gov/articles/PMC11825193/>

Current propensity score uses `covars_gbm` (demographics, comorbidities, encounter type, vitals, labs) as defined above; in this block only `encounter_type` is explicitly factored before weighting.

Note: for all these, I suggested new GBM adjustments that accomplish the following:

1. Smaller GBM & balance-based stopping (`stop.method = “smd.max”`) → faster fit, avoids over-fitting, lighter tails (which lead to extreme weights that are problematic).
2. Target balance compares weighted treated cohort to the full sample; aim for $|SMD| < 0.1$.
3. Weight stabilization (divide by mean) mitigates a few huge weights. We use one-sided truncation at very small propensities (caps large weights only).
4. Uses robust variance estimation (e.g. allows the variances to change by PaCO2) for IP-weighted GLM; works with splines via `rcs()`. This is a bit nuanced but I think good to change even though it adds complexity
5. Deterministic seed ensures result replication.

2.0.1 5.1 ABG IPW weighting and diagnostics

```
# Already normalized globally; just drop unused levels
subset_data$encounter_type <- droplevels(subset_data$encounter_type)
```

GBM tuning is shared across ABG and VBG via `gbm_params` to keep symmetry; update there if needed.

```
#   1. fit GBM propensity model, ABG
set.seed(42)
gbm_df_abg <- subset_data[, c("has_abg", "has_vbg", covars_gbm), drop = FALSE]
gbm_df_abg <- normalize_types(gbm_df_abg, levels_ref)
gbm_df_abg <- droplevels_all(gbm_df_abg)
```

```

gbm_preflight(gbm_df_abg, covars_gbm, "unimp_abg")
append_mem_snapshot("gbm_unimp", "unimp_abg", "pre")

weight_model <- do.call(
  weightit,
  c(
    list(
      formula_abg,
      data      = gbm_df_abg,
      method    = "gbm",
      estimand  = "ATE",
      missing   = "ind",
      include.obj = FALSE
    ),
    gbm_params
  )
)
append_mem_snapshot("gbm_unimp", "unimp_abg", "post")

# 2. One-sided IPSW (ABG observed only) + truncation of small propensities
ipow_abg <- compute_ipow_weights(
  weight_model,
  treat = gbm_df_abg$has_abg,
  ps_floor_quantile = ps_trunc_quantile,
  stabilize = TRUE
)
w_abg <- ipow_abg$weights
ps_floor_abg <- ipow_abg$ps_floor
subset_data$trunc_abg <- ipow_abg$truncated
subset_data$ps_abg <- ipow_abg$ps
subset_data$w_abg <- w_abg
assert_finite_weights(w_abg[subset_data$has_abg == 1], "w_abg")
rm(weight_model, gbm_df_abg)
invisible(gc())

# Balance diagnostics and treated-only outcome models are handled later.

```

Inverse Propensity-Weighted Logistic Regressions with CO2 predictor represented as a restricted cubic spline.

These are covariate-adjusted outcome models ($\text{outcome} \sim \text{spline}(\text{CO2}) + \text{X}$), fit separately for ABG and VBG cohorts using `survey::svyglm` with robust (design-based) SEs. Spline curves are shown as odds ratios relative to `CO2_ref` (midpoint of the normal range).

2.0.2 5.2 ABG IPW spline models

```
# set.seed(42) # reproducible GBM fit
#
# # 1. inverse-probability weights for receiving an ABG
#
# # done in the last block, so not needed
#
#
# Model diagrams: IPW ABG spline models
ipw_abg_rcs_forms <- list(
  "ABG IPW spline (adjusted): IMV ~ CO2 spline + X"      = make_spline_fml("imv_proc", "paco2", adj_core),
  "ABG IPW spline (adjusted): NIV ~ CO2 spline + X"      = make_spline_fml("niv_proc", "paco2", adj_core),
  "ABG IPW spline (adjusted): Death60d ~ CO2 spline + X" = make_spline_fml("death_60d", "paco2", adj_core),
  "ABG IPW spline (adjusted): HCRF ~ CO2 spline + X"     = make_spline_fml("hypercap_resp_failure", "paco2", adj_core)
)
register_model_diagrams(ipw_abg_rcs_forms)

# 2. analysis sample: rows with a measured PaCO2
subset_data_abg <- subset_data %>%
  filter(!is.na(paco2)) %>% # implies has_abg == 1
  select(paco2, imv_proc, niv_proc, death_60d,
         hypercap_resp_failure, w_abg, all_of(adj_core)) %>%
  filter(complete.cases(.))

#
# 3. weighted logistic spline models with robust SEs
fitfun <- function(formula, outcome) {
  fit_res <- fit_with_diagnostics(
    function() svyglm(
```

```

formula,
design = svydesign(ids = ~1, weights = ~w_abg, data = subset_data_abg),
family = quasibinomial(),
control = glm.control(maxit = 50)
),
context = make_context(
  stage = "outcome",
  component = "spline",
  analysis_variant = "ipw",
  model_type = "spline",
  group = "ABG",
  outcome = outcome,
  imputation = NA_integer_,
  batch = NA_integer_
)
)
append_outcome_diag(fit_res$diag)
fit_res$fit
}

fit_imv_abg  <- fitfun(make_spline_fml("imv_proc", "paco2", adj_core), "imv_proc")
fit_niv_abg  <- fitfun(make_spline_fml("niv_proc", "paco2", adj_core), "niv_proc")
fit_death_abg <- fitfun(make_spline_fml("death_60d", "paco2", adj_core), "death_60d")
fit_hcrcf_abg <- fitfun(make_spline_fml("hypercap_resp_failure", "paco2", adj_core),
                           "hypercap_resp_failure")
if (any(vapply(list(fit_imv_abg, fit_niv_abg, fit_death_abg, fit_hcrcf_abg), is.null, logical(1)))) {
  stop("IPW ABG spline fits failed; see model_fit_diagnostics.csv.")
}

# 4. prediction helper
mkpred <- function(fit, data_ref, co2_var, ref_df, co2_ref) {
  co2_seq <- stats::quantile(data_ref[[co2_var]], probs = c(0.02, 0.98), na.rm = TRUE)
  grid_info <- make_co2_grid_ref(
    co2_var,
    seq(co2_seq[1], co2_seq[2], length.out = SPLINE_GRID_N),
    ref_df,

```

```

    co2_ref
  )
  predict_or_curve_from_fit(fit, grid_info$grid, grid_info$ref_idx, co2_var)
}

pred_imv_abg  <- mkpred(fit_imv_abg, subset_data_abg, "paco2", x_ref_abg, ABG_CO2_REF)
pred_niv_abg  <- mkpred(fit_niv_abg, subset_data_abg, "paco2", x_ref_abg, ABG_CO2_REF)
pred_death_abg <- mkpred(fit_death_abg, subset_data_abg, "paco2", x_ref_abg, ABG_CO2_REF)
pred_hcrf_abg <- mkpred(fit_hcrf_abg, subset_data_abg, "paco2", x_ref_abg, ABG_CO2_REF)
axis_abg_ipw_trim <- compute_or_axis_spec(
  list(pred_imv_abg, pred_niv_abg, pred_death_abg, pred_hcrf_abg),
  lo_col = "LCL", hi_col = "UCL"
)
# 5. plotting
# Plotting deferred until VBG curves are computed so axes can be shared.

```

Restricting plots bewtween 0.02 and 0.98

2.0.3 5.3 ABG IPW spline models (2–98th percentile)

```

subset_data_abg <- subset_data %>%
  filter(!is.na(paco2)) %>%                                # implies has_abg == 1
  select(paco2, imv_proc, niv_proc, death_60d,
         hypercap_resp_failure, w_abg, all_of(adj_core)) %>%
  filter(complete.cases(.))

fitfun <- function(formula, outcome) {
  fit_res <- fit_with_diagnostics(
    function() svyglm(
      formula,
      design = svydesign(ids = ~1, weights = ~w_abg, data = subset_data_abg),
      family = quasibinomial(),
      control = glm.control(maxit = 50)
    ),

```

```

context = make_context(
  stage = "outcome",
  component = "spline",
  analysis_variant = "ipw",
  model_type = "spline",
  group = "ABG",
  outcome = outcome,
  imputation = NA_integer_,
  batch = NA_integer_
)
)
append_outcome_diag(fit_res$diag)
fit_res$fit
}

fit_imv_abg <- fitfun(make_spline_fml("imv_proc", "paco2", adj_core), "imv_proc")
fit_niv_abg <- fitfun(make_spline_fml("niv_proc", "paco2", adj_core), "niv_proc")
fit_death_abg <- fitfun(make_spline_fml("death_60d", "paco2", adj_core), "death_60d")
fit_hcrcf_abg <- fitfun(make_spline_fml("hypercap_resp_failure", "paco2", adj_core),
                           "hypercap_resp_failure")
if (any(vapply(list(fit_imv_abg, fit_niv_abg, fit_death_abg, fit_hcrcf_abg), is.null, logical(1)))) {
  stop("IPW ABG spline fits (trimmed) failed; see model_fit_diagnostics.csv.")
}

# 4. prediction helper
mkpred <- function(fit, data_ref, co2_var, ref_df, co2_ref) {
  q <- stats::quantile(data_ref[[co2_var]], probs = c(0.02, 0.98), na.rm = TRUE)
  grid_info <- make_co2_grid_ref(
    co2_var,
    seq(q[1], q[2], length.out = SPLINE_GRID_N),
    ref_df,
    co2_ref
  )
  predict_or_curve_from_fit(fit, grid_info$grid, grid_info$ref_idx, co2_var)
}

```

```

pred_imv_abg   <- mkpred(fit_imv_abg,   subset_data_abg, "paco2", x_ref_abg, ABG_CO2_REF)
pred_niv_abg   <- mkpred(fit_niv_abg,   subset_data_abg, "paco2", x_ref_abg, ABG_CO2_REF)
pred_death_abg <- mkpred(fit_death_abg, subset_data_abg, "paco2", x_ref_abg, ABG_CO2_REF)
pred_hcrcf_abg <- mkpred(fit_hcrcf_abg, subset_data_abg, "paco2", x_ref_abg, ABG_CO2_REF)

# 5. plotting
xlab <- expression(paste("ABG CO" [2], " (mmHg)"))

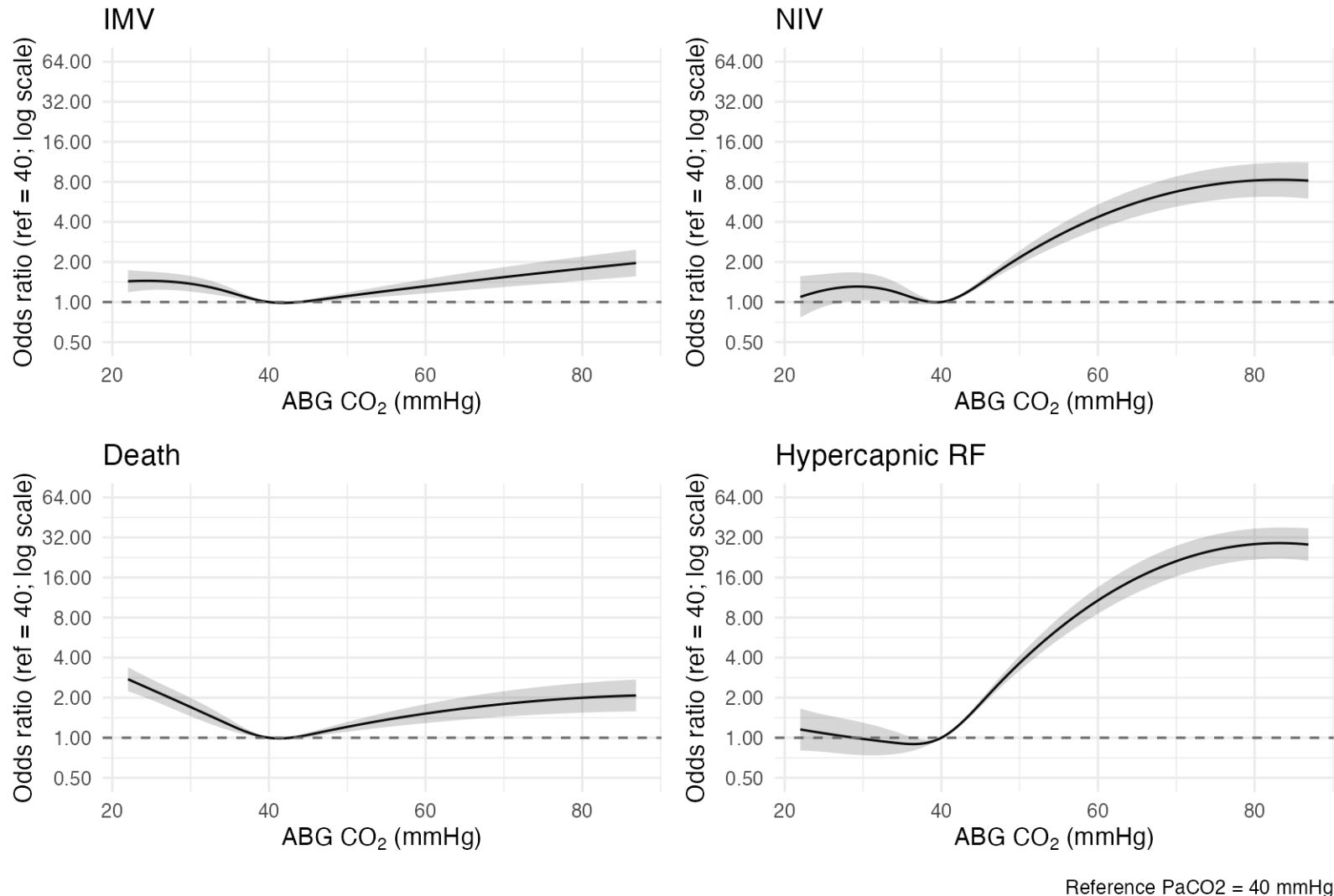
plt <- function(dat, title)
  ggplot(dat, aes(paco2, OR)) +
    geom_line() +
    geom_ribbon(aes(ymin = LCL, ymax = UCL), alpha = 0.2) +
    geom_hline(yintercept = 1, linetype = "dashed", color = "grey40") +
    or_axis_scale(axis_abg_ipw_trim) +
    labs(title = title, x = xlab,
         y = paste0("Odds ratio (ref = ", ABG_CO2_REF, "; log scale)")) +
    theme_minimal()

ipw_abg_panel <- (patchwork::wrap_plots(
  plt(pred_imv_abg,    "IMV"),
  plt(pred_niv_abg,    "NIV"),
  plt(pred_death_abg,  "Death"),
  plt(pred_hcrcf_abg,  "Hypercapnic RF"),
  ncol = 2
)) +
  plot_annotation(
    title = paste0("Propensity-weighted adjusted odds ratios by ABG CO2 (ref = ",
                  ABG_CO2_REF, "; conditional on X; 2-98% range)"),
    caption = paste0("Reference PaCO2 = ", ABG_CO2_REF, " mmHg")
  )

print_plot_once(ipw_abg_panel, "spline-ipw-abg-trimmed", width = 8.5, height = 6)

```

Propensity-weighted adjusted odds ratios by ABG CO₂ (ref = 40; conditional on X; 2–98% range)



VBG uses the same GBM tuning as ABG (shared `gbm_params`).

2.0.4 5.4 VBG IPW weighting and spline models

```
# Inverse-propensity weighting & outcome modelling for **VBG** cohort
#   - mirrored 1-to-1 to the validated ABG workflow

set.seed(42)

# 1. IPW for VBG -----
set.seed(42)
gbm_df_vbg <- subset_data[, c("has_abg", "has_vbg", covars_gbm), drop = FALSE]
gbm_df_vbg <- normalize_types(gbm_df_vbg, levels_ref)
gbm_df_vbg <- droplevels_all(gbm_df_vbg)
gbm_preflight(gbm_df_vbg, covars_gbm, "unimp_vbg")
append_mem_snapshot("gbm_unimp", "unimp_vbg", "pre")
w_vbg <- do.call(
  weightit,
  c(
    list(
      formula_vbg,
      data      = gbm_df_vbg,
      method    = "gbm",
      estimand  = "ATE",
      missing   = "ind",
      include.obj = FALSE
    ),
    gbm_params
  )
)
append_mem_snapshot("gbm_unimp", "unimp_vbg", "post")

# One-sided IPSW (VBG observed only) + truncation of small propensities
ipow_vbg <- compute_ipow_weights(
  w_vbg,
  treat = gbm_df_vbg$has_vbg,
  ps_floor_quantile = ps_trunc_quantile,
```

```

    stabilize = TRUE
)
w_vbg_ipow <- ipow_vbg$weights
ps_floor_vbg <- ipow_vbg$ps_floor
subset_data$trunc_vbg <- ipow_vbg$truncated
subset_data$ps_vbg <- ipow_vbg$ps
subset_data$w_vbg <- w_vbg_ipow
assert_finite_weights(w_vbg_ipow[subset_data$has_vbg == 1], "w_vbg")
rm(w_vbg, gbm_df_vbg)
invisible(gc())

# Balance diagnostics are handled later.

# 2. Analysis set (VBG only) -----
subset_data_vbg <- subset_data %>%
  filter(!is.na(vbg_co2)) %>%
  select(vbg_co2, imv_proc, niv_proc, death_60d,
         hypercap_resp_failure, w_vbg, all_of(adj_core)) %>%
  filter(complete.cases(.))

fitfun <- function(formula, outcome) {
  fit_res <- fit_with_diagnostics(
    function() svyglm(
      formula,
      design = svydesign(ids = ~1, weights = ~w_vbg, data = subset_data_vbg),
      family = quasibinomial(),
      control = glm.control(maxit = 50)
    ),
    context = make_context(
      stage = "outcome",
      component = "spline",
      analysis_variant = "ipw",
      model_type = "spline",
      group = "VBG",
      outcome = outcome,
      imputation = NA_integer_
    )
  )
}
```

```

    batch = NA_integer_
  )
)
append_outcome_diag(fit_res$diag)
fit_res$fit
}

# Model diagrams: IPW VBG spline models
ipw_vbg_rcs_forms <- list(
  "VBG IPW spline (adjusted): IMV ~ CO2 spline + X"      = make_spline_fml("imv_proc", "vbg_co2", adj_core),
  "VBG IPW spline (adjusted): NIV ~ CO2 spline + X"      = make_spline_fml("niv_proc", "vbg_co2", adj_core),
  "VBG IPW spline (adjusted): Death60d ~ CO2 spline + X" = make_spline_fml("death_60d", "vbg_co2", adj_core),
  "VBG IPW spline (adjusted): HCRF ~ CO2 spline + X"      = make_spline_fml("hypercap_resp_failure", "vbg_co2", adj_core)
)
register_model_diagrams(ipw_vbg_rcs_forms)

fit_imv_vbg   <- fitfun(make_spline_fml("imv_proc", "vbg_co2", adj_core), "imv_proc")
fit_niv_vbg   <- fitfun(make_spline_fml("niv_proc", "vbg_co2", adj_core), "niv_proc")
fit_death_vbg <- fitfun(make_spline_fml("death_60d", "vbg_co2", adj_core), "death_60d")
fit_hcrf_vbg  <- fitfun(make_spline_fml("hypercap_resp_failure", "vbg_co2", adj_core),
                           "hypercap_resp_failure")
if (any(vapply(list(fit_imv_vbg, fit_niv_vbg, fit_death_vbg, fit_hcrf_vbg), is.null, logical(1)))) {
  stop("IPW VBG spline fits failed; see model_fit_diagnostics.csv.")
}

# 4. Prediction helper -----
mkpred <- function(fit, data_ref, co2_var, ref_df, co2_ref) {
  co2_seq <- stats::quantile(data_ref[[co2_var]], probs = c(0.02, 0.98), na.rm = TRUE)
  grid_info <- make_co2_grid_ref(
    co2_var,
    seq(co2_seq[1], co2_seq[2], length.out = SPLINE_GRID_N),
    ref_df,
    co2_ref
  )
  predict_or_curve_from_fit(fit, grid_info$grid, grid_info$ref_idx, co2_var)
}

```

```

pred_imv_vbg   <- mkpred(fit_imv_vbg,   subset_data_vbg, "vbg_co2", x_ref_vbg, VBG_CO2_REF)
pred_niv_vbg   <- mkpred(fit_niv_vbg,   subset_data_vbg, "vbg_co2", x_ref_vbg, VBG_CO2_REF)
pred_death_vbg <- mkpred(fit_death_vbg, subset_data_vbg, "vbg_co2", x_ref_vbg, VBG_CO2_REF)
pred_hcrf_vbg  <- mkpred(fit_hcrf_vbg,  subset_data_vbg, "vbg_co2", x_ref_vbg, VBG_CO2_REF)
axis_ipw_common <- compute_or_axis_spec(
  list(pred_imv_abg, pred_niv_abg, pred_death_abg, pred_hcrf_abg,
       pred_imv_vbg, pred_niv_vbg, pred_death_vbg, pred_hcrf_vbg),
  lo_col = "LCL", hi_col = "UCL"
)

# 5. Plotting (gray scheme) -----
xlab <- expression(paste("VBG CO" [2], " (mmHg)"))

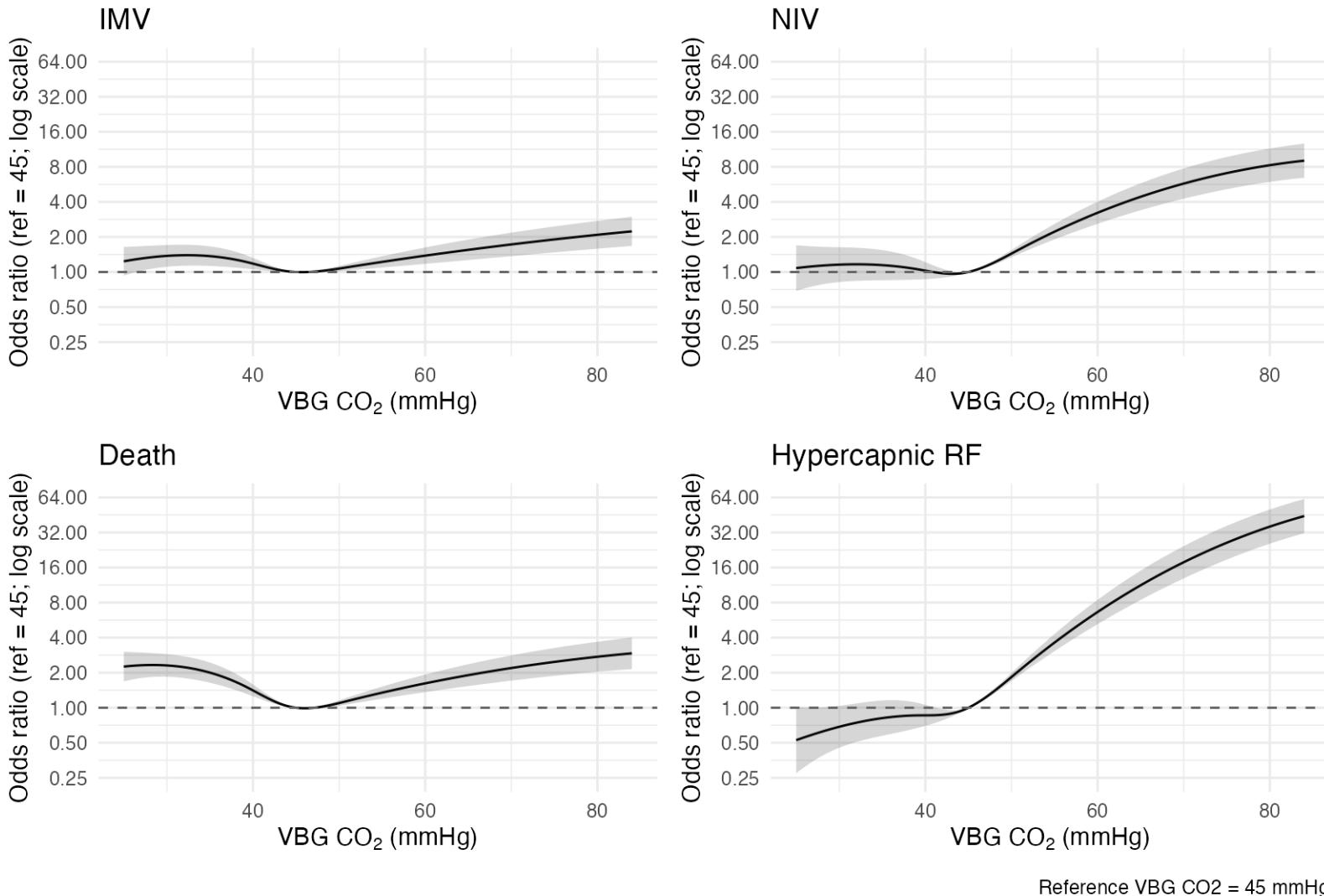
plt <- function(dat, title)
  ggplot(dat, aes(vbg_co2, OR)) +
    geom_line() +
    geom_ribbon(aes(ymin = LCL, ymax = UCL), alpha = 0.2) +
    geom_hline(yintercept = 1, linetype = "dashed", color = "grey40") +
    or_axis_scale(axis_ipw_common) +
    labs(title = title, x = xlab,
         y = paste0("Odds ratio (ref = ", VBG_CO2_REF, "; log scale)")) +
    theme_minimal()

ipw_vbg_panel <- (patchwork::wrap_plots(
  plt(pred_imv_vbg,    "IMV"),
  plt(pred_niv_vbg,    "NIV"),
  plt(pred_death_vbg,  "Death"),
  plt(pred_hcrf_vbg,   "Hypercapnic RF"),
  ncol = 2
)) +
  plot_annotation(
    title = paste0("Propensity-weighted adjusted odds ratios by VBG CO2 (ref = ",
                  VBG_CO2_REF, "; conditional on X)"),
    caption = paste0("Reference VBG CO2 = ", VBG_CO2_REF, " mmHg")
)

```

```
print_plot_once(ipw_vbg_panel, "spline-ipw-vbg", width = 8.5, height = 6)
```

Propensity-weighted adjusted odds ratios by VBG CO₂ (ref = 45; conditional on X)



```

# ABG plots with the same axis (shared with VBG)
xlab_abg <- expression(paste("ABG CO"[2], " (mmHg)"))

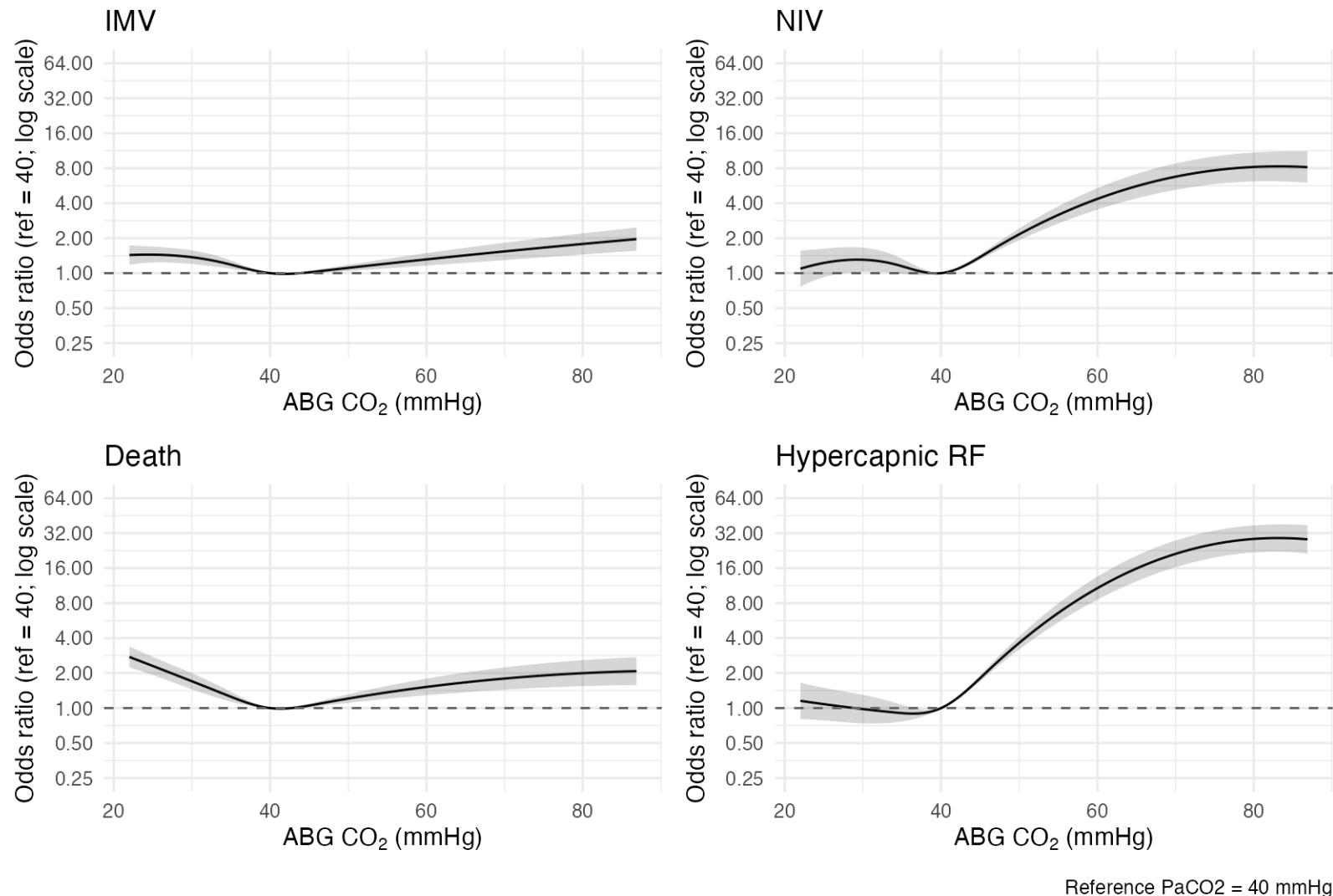
plt_abg <- function(dat, title)
  ggplot(dat, aes(paco2, OR)) +
    geom_line() +
    geom_ribbon(aes(ymin = LCL, ymax = UCL), alpha = 0.2) +
    geom_hline(yintercept = 1, linetype = "dashed", color = "grey40") +
    or_axis_scale(axis_ipw_common) +
    labs(title = title, x = xlab_abg,
         y = paste0("Odds ratio (ref = ", ABG_CO2_REF, "; log scale)")) +
    theme_minimal()

ipw_abg_shared_panel <- (patchwork::wrap_plots(
  plt_abg(pred_imv_abg,    "IMV"),
  plt_abg(pred_niv_abg,    "NIV"),
  plt_abg(pred_death_abg, "Death"),
  plt_abg(pred_hcrf_abg,   "Hypercapnic RF"),
  ncol = 2
)) +
  plot_annotation(
    title = paste0("Propensity-weighted adjusted odds ratios by ABG CO2 (ref = ",
                  ABG_CO2_REF, "; conditional on X)"),
    caption = paste0("Reference PaCO2 = ", ABG_CO2_REF, " mmHg")
  )

print_plot_once(ipw_abg_shared_panel, "spline-ipw-abg-shared", width = 8.5, height = 6)

```

Propensity-weighted adjusted odds ratios by ABG CO₂ (ref = 40; conditional on X)



2.0.5 5.5 Three-level PCO₂ categories (weighted; ABG, VBG)

Three groups with weights and covariate adjustment

```

library(dplyr)
library(survey)
library(broom)
library(ggplot2)
library(scales)

# 1. Ensure PCO2 categories are present
stopifnot(all(c("pc02_cat_abg", "pc02_cat_vbg") %in% names(subset_data)))

# 2. Function: weighted logistic regression & OR extraction
run_weighted_or <- function(data, outcome, cat_var, weight_var, group_name,
                           treat_var, adj_vars) {
  stopifnot(!is.null(treat_var))
  stopifnot(!is.null(adj_vars))
  dat <- data %>%
    filter(
      .data[[treat_var]] == 1,
      !is.na(.data[[cat_var]]),
      !is.na(.data[[outcome]]),
      !is.na(.data[[weight_var]]),
      .data[[weight_var]] > 0
    ) %>%
    mutate(
      !!cat_var := factor(.data[[cat_var]],
                           levels = CO2_CAT_LEVELS)
    ) %>%
    droplevels()

  design <- svydesign(
    ids = ~1,
    weights = as.formula(paste0("~", weight_var)),
    data = dat
  )

  rhs_terms <- c(cat_var, adj_vars)
  fml <- stats::reformulate(rhs_terms, response = outcome)
}

```

```

fit_res <- fit_with_diagnostics(
  function() svyglm(fml, design = design, family = quasibinomial(),
    control = glm.control(maxit = 50)),
  context = make_context(
    stage = "outcome",
    component = "cat3",
    analysis_variant = "ipw",
    model_type = "cat3",
    group = group_name,
    outcome = outcome,
    imputation = NA_integer_,
    batch = NA_integer_
  )
)
append_outcome_diag(fit_res$diag)
if (is.null(fit_res$fit)) {
  stop("run_weighted_or: model fit failed for outcome=", outcome,
    " cat_var=", cat_var, " group=", group_name)
}

tidy(fit_res$fit, exponentiate = TRUE, conf.int = TRUE) %>%
  filter(term != "(Intercept)", startsWith(term, cat_var)) %>%
  mutate(
    group    = group_name,
    outcome   = outcome
  )
}

# 3. Run across outcomes & cohorts
outcomes_ipw <- c("imv_proc", "niv_proc", "death_60d", "hypercap_resp_failure")

ipw_three_level_forms <- list(
  "ABG IPW 3-level: IMV ~ CO2 category + X"      = reformulate(c("pc02_cat_abg", adj_core), response = "imv_proc"),
  "ABG IPW 3-level: NIV ~ CO2 category + X"      = reformulate(c("pc02_cat_abg", adj_core), response = "niv_proc"),
  "ABG IPW 3-level: Death60d ~ CO2 category + X" = reformulate(c("pc02_cat_abg", adj_core), response = "death_60d"),
  "ABG IPW 3-level: HCRF ~ CO2 category + X"     = reformulate(c("pc02_cat_abg", adj_core), response = "hypercap_resp_failure"),
)

```

```

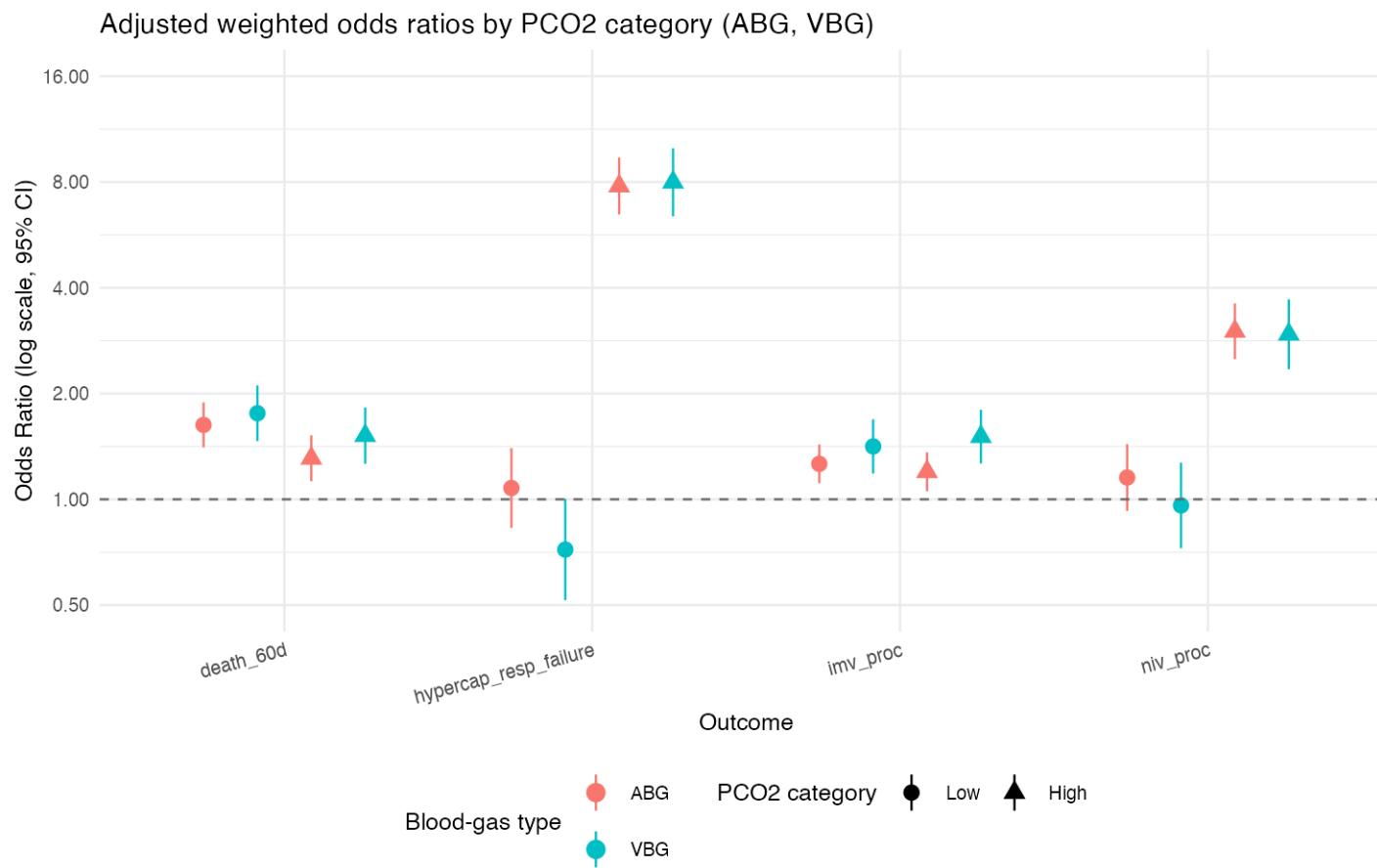
"VBG IPW 3-level: IMV ~ CO2 category + X"      = reformulate(c("pco2_cat_vbg", adj_core), response = "imv_proc"),
"VBG IPW 3-level: NIV ~ CO2 category + X"      = reformulate(c("pco2_cat_vbg", adj_core), response = "niv_proc"),
"VBG IPW 3-level: Death60d ~ CO2 category + X" = reformulate(c("pco2_cat_vbg", adj_core), response = "death_60d"),
"VBG IPW 3-level: HCRF ~ CO2 category + X"      = reformulate(c("pco2_cat_vbg", adj_core), response = "hypercap_resp_failure")
)
register_model_diagrams(ipw_three_level_forms)

ipw_combined_or_df <- bind_rows(
  lapply(outcomes_ipw, function(out)
    run_weighted_or(subset_data, out, "pco2_cat_abg", "w_abg",       "ABG",
                     treat_var = "has_abg", adj_vars = adj_core)),
  lapply(outcomes_ipw, function(out)
    run_weighted_or(subset_data, out, "pco2_cat_vbg", "w_vbg",       "VBG",
                     treat_var = "has_vbg", adj_vars = adj_core))
)
ipw_threellevel_results <- ipw_combined_or_df %>%
  mutate(method = "IPW adjusted")

ipw_combined_or_df <- map_or_exposure(ipw_combined_or_df, "or-plot-three-level-weighted")
ipw_combined_or_df$group <- factor(ipw_combined_or_df$group, levels = c("ABG", "VBG"))

# 4. Plot weighted odds ratios
ipw_plot_df <- build_or_plot_df(ipw_combined_or_df, "or-plot-three-level-weighted",
                                  expected_exposure_levels = CO2_CAT_CONTRAST_LEVELS)
ipw_axis_spec <- compute_or_axis_spec(ipw_plot_df, lo_col = "conf.low", hi_col = "conf.high",
                                       default_limits = OR_XLIM)
ipw_p_or <- plot_or_safe(
  ipw_plot_df,
  plot_name = "or-plot-three-level-weighted",
  axis_spec = ipw_axis_spec,
  title   = "Adjusted weighted odds ratios by PCO2 category (ABG, VBG)"
)
print_plot_once(ipw_p_or, "or-plot-three-level-weighted", width = 7.5, height = 4.8)

```



2.1 6) Propensity score diagnostics

Plotting propensity scores

```
# --- Propensity score histograms (ABG / VBG) -----
# ABG = arterial blood gas; VBG = venous blood gas

library(dplyr)
library(ggplot2)
```

```

library(scales)

stopifnot("has_abg" %in% names(subset_data))
stopifnot("has_vbg" %in% names(subset_data))
stopifnot(all(c("ps_abg", "ps_vbg") %in% names(subset_data)))

# Build list of per-cohort PS data frames conditionally (so missing cohorts don't error)
ps_dfs_cond <- list(
  ABG = data.frame(
    ps      = subset_data$ps_abg,
    treat   = subset_data$has_abg,
    ScoreType = "ABG"
  ),
  VBG = data.frame(
    ps      = subset_data$ps_vbg,
    treat   = subset_data$has_vbg,
    ScoreType = "VBG"
  )
)

# Bind, clean, and factorize for plotting
df_ps_cond <- bind_rows(ps_dfs_cond) %>%
  filter(!is.na(ps), !is.na(treat)) %>%
  mutate(
    treat   = factor(treat, levels = c(0, 1), labels = c("No Test", "Test")),
    ScoreType = factor(ScoreType, levels = c("ABG", "VBG"))
  )

# Plot
p_ps_cond <- ggplot(df_ps_cond, aes(x = ps, fill = treat)) +
  geom_histogram(aes(y = after_stat(density)), alpha = 0.5,
                 position = "identity", bins = 30) +
  scale_fill_manual(values = c("No Test" = "steelblue", "Test" = "tomato")) +
  facet_wrap(~ScoreType, scales = "free_y") +
  coord_cartesian(xlim = c(0, 1)) +
  labs(

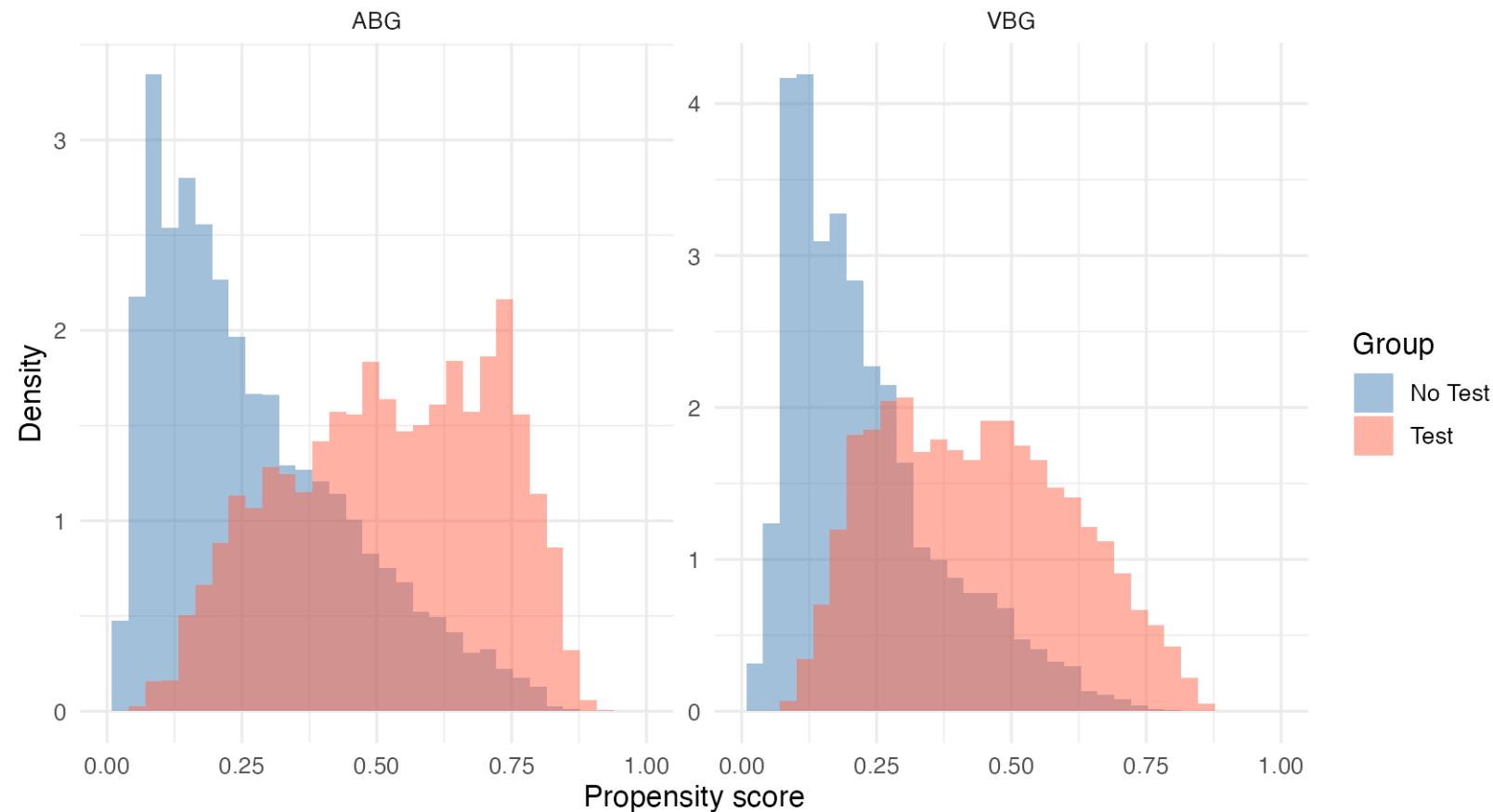
```

```

title = "Propensity Score Distributions",
x      = "Propensity score",
y      = "Density",
fill   = "Group"
) +
theme_minimal(base_size = 12)
print_plot_once(p_ps_cond, "propensity-histograms-conditional", width = 8.5, height = 5)

```

Propensity Score Distributions



```

stopifnot(all(c("ps_abg", "ps_vbg") %in% names(subset_data)))

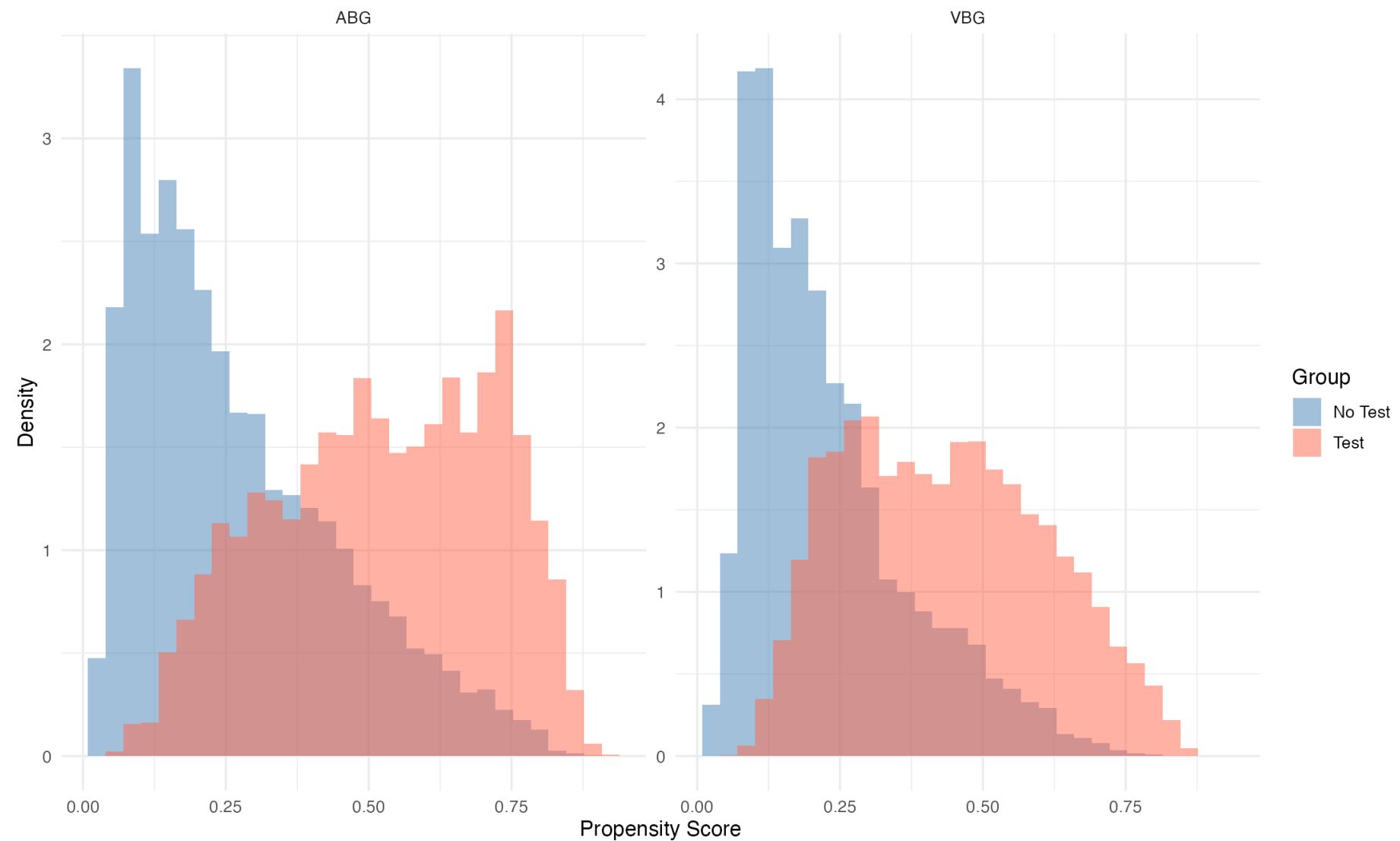
ps_dfs_all <- list(
  ABG = data.frame(
    ps      = subset_data$ps_abg,
    treat   = subset_data$has_abg,
    ScoreType = "ABG"
  ),
  VBG = data.frame(
    ps      = subset_data$ps_vbg,
    treat   = subset_data$has_vbg,
    ScoreType = "VBG"
  )
)

df_ps_all <- bind_rows(ps_dfs_all) %>%
  mutate(
    treat     = factor(treat, levels = c(0,1), labels = c("No Test", "Test")),
    ScoreType = factor(ScoreType, levels = c("ABG", "VBG"))
  )

ggplot(df_ps_all, aes(x = ps, fill = treat)) +
  geom_histogram(aes(y = after_stat(density)), alpha = 0.5,
                 position = "identity", bins = 30) +
  scale_fill_manual(values = c("No Test" = "steelblue", "Test" = "tomato")) +
  facet_wrap(~ScoreType, scales = "free_y") +
  labs(
    title = "Propensity Score Distributions",
    x = "Propensity Score",
    y = "Density",
    fill = "Group"
  ) +
  theme_minimal(base_size = 12)

```

Propensity Score Distributions



```
append_mem_snapshot("stage2", "end", "post")
stage2_rm <- c(
  "ipow_abg", "ipow_vbg", "w_abg", "w_vbg_ipow",
```

```

"subset_data_abg", "subset_data_vbg",
"fit_imv_abg", "fit_niv_abg", "fit_death_abg", "fit_hcrf_abg",
"pred_imv_abg", "pred_niv_abg", "pred_death_abg", "pred_hcrf_abg",
"fit_imv_vbg", "fit_niv_vbg", "fit_death_vbg", "fit_hcrf_vbg",
"pred_imv_vbg", "pred_niv_vbg", "pred_death_vbg", "pred_hcrf_vbg",
"plt", "mkpred",
"ipw_combined_or_df", "ipw_plot_df", "ipw_p_or", "ipw_axis_spec", "outcomes_ipw",
"df_ps_cond", "ps_dfs_cond", "p_ps_cond",
"df_ps_all", "ps_dfs_all"
)
missing_stage2 <- setdiff(stage2_rm, ls())
stopifnot(length(missing_stage2) == 0)
rm(list = stage2_rm)
invisible(gc())
append_mem_snapshot("stage2", "cleanup", "post")

```

3 Multiple Imputation Analysis

added 12/6/2025

```

# Core MI + diagnostics
library(mice)          # chained equations (MICE)
library(miceadds)       # pooling helpers & utilities
library(naniar)         # missingness summaries/plots
library(visdat)         # quick type/missingness viz
library(skimr)          # data skim for large frames

# Modeling
library(WeightIt)       # GBM propensity with weights
library(gbm)             # underlying GBM engine
library(survey)          # svyglm outcome models
library(cobalt)          # balance diagnostics
library(broom)            # tidy model outputs
library(dplyr)           # data manipulation

```

```

library(ggplot2)

# Pooling and MI bookkeeping
library(mitoools)      # MIcombine for pooling (generic)
library(parallel)       # basic parallel where helpful

# Parallel + progress setup
library(future)

# setup
library(future.apply)
library(progressr)

mi_mids_file    <- results_path("mi_abg_vbg_mids.rds")
mi_logistic_ps_abg_file   <- results_path("mi_logistic_ps_abg_list.rds")
mi_logistic_ps_vbg_file   <- results_path("mi_logistic_ps_vbg_list.rds")
mi_pooled_file   <- results_path("mi_pooled_results.rds")

# Use sequential futures to avoid PSOCK cluster startup failures during render
future::plan(sequential)

# choose a handler, but DO NOT make it global inside a knitted document
progressr::handlers(progressr::handler_rstudio)  # or handler_txtprogressbar
options(future.rng.onMisuse = "error")           # safer RNG with futures

set.seed(20251206)

# ensure a writable figure dir + stable device on macOS
fs::dir_create(fig_dir, recurse = TRUE)
knitr::opts_chunk$set(fig.path = fig_path, dev = "png", dpi = 144)
options(bitmapType = "cairo")  # prevents device issues on macOS

```

```

M_IMP    <- 80
MAXIT_MI <- 20
MI_SEED   <- 20251206
DEBUG_SPLINE <- FALSE

```

```

M_IMP_TARGET <- 80
M_IMP_MIN <- 20
M_IMP_STEP <- 10
MCERR_RATIO_TARGET <- 0.10
ALLOW_M_IMP_EARLY_STOP <- FALSE

# MI propensity model (MI-only)
MI_PS_METHOD      <- "glm_rcs4"
MI_PS_SPLINE_K    <- 4L
MI_GLM_MAXIT      <- 25L

MINCOR_QUICKPRED <- 0.05
MINPUC_QUICKPRED <- 0.25
MAX_PRED_PER_VAR <- 40L
MAX_MM_COLS <- 300L
MAX_LEVELS_PRED <- 100L
COR_SAMPLE_N <- 50000L
MI_MAX_BYTES <- 8e9

MI_RAM_GB <- 16L
MI_BATCH_START <- ifelse(MI_RAM_GB <= 16, 2L, 5L)
MI_BATCH_MIN <- 1L
MI_BATCH_SEED_STRIDE <- 100000L
MI_GC_EVERY_BATCH <- TRUE
MI_PREEMPTIVE_BATCH_REDUCE <- TRUE
MI_VCELLS_FRAC_THRESHOLD <- 0.80
MI_SMOKE_TEST <- TRUE
MI_DEBUG_PRINTFLAG <- FALSE
MI_MEMORY_HYGIENE <- TRUE
FORCE_MI_BATCHED <- FALSE

stopifnot(exists("RUN_MODE"), exists("FULL_RUN"))

M_IMP <- M_IMP_TARGET
M_IMP_MIN <- max(M_IMP_MIN, 50L)
if (isTRUE(DEBUG_SPLINE)) {

```

```

    stop("DEBUG_SPLINE must be FALSE; pilot and full runs must use the same model workflow.")
}
stopifnot(M_IMP >= M_IMP_MIN, M_IMP <= 100)
stopifnot(MI_PS_METHOD %in% c("glm_rcs4"))

# Key covariates + outcomes used in MI (plus report-only BNP/Spo2)
extra_miss_vars <- intersect(c("bpn", "spo2"), names(subset_data_raw))
miss_vars <- unique(c(
  covars_ps,
  extra_miss_vars,
  "paco2", "vbg_co2", "vbg_o2sat",
  "has_abg", "has_vbg",
  "imv_proc", "niv_proc", "death_60d", "hypercap_resp_failure"
))
miss_vars <- intersect(miss_vars, names(subset_data_raw))

miss_tbl <- subset_data_raw |>
  dplyr::select(dplyr::all_of(miss_vars)) |>
  dplyr::summarise(dplyr::across(dplyr::everything(), ~ sum(is.na(.)))) |>
  tidyr::pivot_longer(dplyr::everything(), names_to = "variable", values_to = "n_missing") |>
  dplyr::mutate(
    total_n      = nrow(subset_data_raw),
    pct_missing = 100 * n_missing / total_n
  ) |>
  dplyr::arrange(dplyr::desc(pct_missing))

miss_tbl_disp <- miss_tbl |>
  dplyr::mutate(
    n_missing    = scales::comma(n_missing),
    pct_missing = sprintf("%.1f%%", pct_missing)
  ) |>
  dplyr::select(variable, n_missing, pct_missing)

gt::gt(miss_tbl_disp) |>
  gt::tab_header(title = "Pre-imputation missingness") |>
  gt::cols_label(

```

```

variable      = "Variable",
n_missing    = "Missing (n)",
pct_missing  = "Missing (%)"
) |>
gt::tab_source_note(
  paste0(
    "n = ", nrow(subset_data_raw),
    "; MI plan: m = ", M_IMP, " imputations (seed ", MI_SEED,
    "); methods: logreg (binary), polyreg (categorical), pmm (numeric).",
    if (length(extra_miss_vars)) " BNP and Sp02 are reported here but excluded from MI/weighting models." else ""
  )
)

```

```

# MI propensity model helpers (glm with RCS on continuous covariates)
ps_is_continuous <- function(v, df) {
  x <- df[[v]]
  if (!is.numeric(x)) return(FALSE)
  x <- x[is.finite(x)]
  if (length(x) < 10) return(FALSE)
  if (length(unique(x)) < 10) return(FALSE)
  TRUE
}

build_mi_ps_formula <- function(treat, covars, df, k = 4L, basis = "rcs") {
  cont <- covars[vapply(covars, ps_is_continuous, logical(1), df = df)]
  catv <- setdiff(covars, cont)
  term_cont <- character()
  if (length(cont)) {
    term_cont <- if (basis == "rcs") {
      paste0("rms::rcs(`", cont, "`", ", k, `")")
    } else {
      paste0("splines::ns(`", cont, "`", ", k, `")")
    }
  }
  term_cat <- if (length(catv)) paste0("`", catv, "`") else character()

```

Pre-imputation missingness

Variable	Missing (n)	Missing (%)
vbg_o2sat	22,366	86.5%
bnp	21,181	81.9%
vbg_co2	18,392	71.1%
spo2	18,319	70.9%
paco2	16,490	63.8%
serum_lac	15,571	60.2%
curr_bmi	14,723	57.0%
serum_phos	13,762	53.2%
temp_new	12,460	48.2%
hr	9,418	36.4%
dbp	7,738	29.9%
sbp	7,666	29.7%
wbc	4,542	17.6%
serum_ca	2,627	10.2%
serum_cr	2,396	9.3%
plt	2,080	8.0%
serum_k	2,021	7.8%
serum_cl	1,498	5.8%
serum_hco3	1,460	5.6%
sodium	1,326	5.1%
age_at_encounter	0	0.0%
sex	0	0.0%
race_ethnicity	0	0.0%
copd	0	0.0%
asthma	0	0.0%
osa	0	0.0%
chf	0	0.0%
acute_nmd	0	0.0%
phtn	0	0.0%
ckd	0	0.0%
dm	0	0.0%
location	0	0.0%
encounter_type	0	0.0%
has_abg	0	0.0%
has_vbg	0	0.0%
imv_proc	0	0.0%
	123	0.0%

```

rhs <- c(term_cont, term_cat)
if (!length(rhs)) stop("No covariates available for MI PS model.")
stats::as.formula(paste0(``, treat, `` ~ ``, paste(rhs, collapse = " + ")))
}

fit_mi_ps_glm <- function(df, treat, covars, k = 4L, maxit = 25L, context = NULL) {
  stopifnot(all(c(treat, covars) %in% names(df)))
  df <- droplevels_all(df)
  basis <- if (requireNamespace("rms", quietly = TRUE)) "rcs" else "ns"
  if (is.null(context)) {
    context <- make_context(
      stage = "MI", component = "mi_ps_glm",
      analysis_variant = "weighted_imputed",
      model_type = "ps",
      group = NA_character_,
      outcome = NA_character_,
      imputation = NA_integer_,
      batch = NA_integer_
    )
  }

  fit_once <- function(basis_type) {
    if (basis_type == "rcs") {
      dd <- rms::datadist(df)
      old_opt <- options(datadist = ".__dd_ps__")
      assign(".__dd_ps__", dd, envir = .GlobalEnv)
      on.exit({
        options(old_opt)
        rm(list = ".__dd_ps__", envir = .GlobalEnv)
      }, add = TRUE)
    }
    form <- build_mi_ps_formula(treat, covars, df, k = k, basis = basis_type)
    cap <- capture_warnings(
      tryCatch(
        stats::glm(form, data = df, family = stats::binomial(),
                  control = stats::glm.control(maxit = maxit),

```

```

        model = FALSE, x = FALSE, y = FALSE),
    error = function(e) e
  ),
  context = context
)
append_warnings(cap$warnings)
list(fit = cap$value, formula = form, basis = basis_type)
}

res <- fit_once(basis)
if (inherits(res$fit, "error") && basis == "rcs") {
  res <- fit_once("ns")
}
if (inherits(res$fit, "error")) {
  return(list(error = conditionMessage(res$fit), method = paste0("glm_", res$basis)))
}

ps <- as.numeric(res$fit$fitted.values)
ps <- pmin(pmax(ps, 1e-8), 1 - 1e-8)
list(
  ps = ps,
  fit_ok = TRUE,
  converged = if (!is.null(res$fit$converged)) isTRUE(res$fit$converged) else NA,
  formula = as.character(res$formula),
  n = nrow(df),
  p = length(res$fit$coefficients),
  method = paste0("glm_", res$basis)
)
}

```

3.0.1 7.2 Missingness structure and drivers

```

library(dplyr)
library(tidyr)

```

```

library(rlang)

# Use raw data for missingness rates; normalized data for model-based drivers
miss_data <- subset_data_raw
model_data <- subset_data

# Focus on key variables (same as MI set) for consistency
extra_miss_vars <- intersect(c("bnp", "spo2"), names(miss_data))
miss_vars <- unique(c(
  covars_ps,
  extra_miss_vars,
  "paco2", "vbg_co2", "vbg_o2sat",
  "has_abg", "has_vbg",
  "imv_proc", "niv_proc", "death_60d", "hypercap_resp_failure"
))
miss_vars <- intersect(miss_vars, names(miss_data))
stopifnot(length(miss_vars) > 0)

# Strata to compare missingness across
strata_vars <- c("has_abg", "has_vbg",
                 "imv_proc", "death_60d", "encounter_type", "location")
strata_vars <- intersect(strata_vars, names(miss_data))

# Overall missingness %
miss_overall <- miss_data |>
  summarise(across(all_of(miss_vars), ~ mean(is.na(.)) * 100)) |>
  pivot_longer(everything(), names_to = "variable", values_to = "pct_missing_overall")

# Missingness % on model_data (used for driver models)
miss_overall_model <- model_data |>
  summarise(across(all_of(intersect(miss_vars, names(model_data)))), ~ mean(is.na(.)) * 100)) |>
  pivot_longer(everything(), names_to = "variable", values_to = "pct_missing_overall_model")

# Missingness by strata (percent within each level)
miss_by_strata <- purrr::map_dfr(strata_vars, function(sv) {
  # drop the current grouping variable from targets

```

```

vars_here <- setdiff(intersect(miss_vars, names(miss_data)), sv)
stopifnot(length(vars_here) > 0L)
stopifnot(sv %in% names(miss_data))

miss_data |>
  group_by(.data[[sv]]) |>
  summarise(across(all_of(vars_here), ~ mean(is.na(.)) * 100), .groups = "drop") |>
  pivot_longer(-all_of(sv), names_to = "variable", values_to = "pct_missing") |>
  rename(level = !!sym(sv)) |>
  mutate(
    stratum = sv,
    level   = as.character(level)
  )
}

# Combine overall + strata (save full table; display full table in PDF)
miss_panel_full <- miss_by_strata |>
  left_join(miss_overall, by = "variable") |>
  arrange(desc(pct_missing_overall), stratum, level)

miss_panel_file <- results_path("missingness-by-strata.csv")
write_csv_safely(miss_panel_full, miss_panel_file, row_names = FALSE)

render_table_pdf(
  miss_panel_full,
  caption = "Missingness by key strata (pre-imputation).",
  file_stub = "missingness_by_strata",
  digits = 1
)

```

Table 10: Missingness by key strata (pre-imputation).

level	variable	pct_missing	stratum	pct_missing_overall
2	vbg_o2sat	90.5	encounter_type	86.5
3	vbg_o2sat	84.5	encounter_type	86.5
0	vbg_o2sat	86.4	has_abg	86.5
1	vbg_o2sat	86.7	has_abg	86.5

Table 10: Missingness by key strata (pre-imputation). (*continued*)

level	variable	pct_missing	stratum	pct_missing_overall
0	vbg_o2sat	99.2	has_vbg	86.5
1	vbg_o2sat	55.3	has_vbg	86.5
0	vbg_o2sat	87.1	imv_proc	86.5
1	vbg_o2sat	82.1	imv_proc	86.5
0	vbg_o2sat	85.4	location	86.5
1	vbg_o2sat	84.6	location	86.5
2	vbg_o2sat	70.4	location	86.5
3	vbg_o2sat	97.5	location	86.5
2	bnp	86.2	encounter_type	81.9
3	bnp	79.9	encounter_type	81.9
0	bnp	84.4	has_abg	81.9
1	bnp	77.7	has_abg	81.9
0	bnp	82.8	has_vbg	81.9
1	bnp	79.8	has_vbg	81.9
0	bnp	82.4	imv_proc	81.9
1	bnp	78.5	imv_proc	81.9
0	bnp	77.6	location	81.9
1	bnp	87.7	location	81.9
2	bnp	77.3	location	81.9
3	bnp	86.3	location	81.9
2	vbg_co2	72.7	encounter_type	71.1
3	vbg_co2	70.4	encounter_type	71.1
0	vbg_co2	71.5	has_abg	71.1
1	vbg_co2	70.5	has_abg	71.1
0	vbg_co2	100.0	has_vbg	71.1
1	vbg_co2	0.0	has_vbg	71.1
0	vbg_co2	72.6	imv_proc	71.1
1	vbg_co2	59.8	imv_proc	71.1
0	vbg_co2	81.4	location	71.1
1	vbg_co2	51.4	location	71.1
2	vbg_co2	64.4	location	71.1
3	vbg_co2	74.4	location	71.1
2	spo2	81.8	encounter_type	70.9
3	spo2	65.5	encounter_type	70.9
0	spo2	69.6	has_abg	70.9
1	spo2	73.1	has_abg	70.9
0	spo2	71.4	has_vbg	70.9
1	spo2	69.7	has_vbg	70.9
0	spo2	71.4	imv_proc	70.9
1	spo2	66.6	imv_proc	70.9
0	spo2	70.9	location	70.9
1	spo2	63.7	location	70.9
2	spo2	99.4	location	70.9
3	spo2	69.2	location	70.9
2	paco2	82.9	encounter_type	63.8

Table 10: Missingness by key strata (pre-imputation). (*continued*)

level	variable	pct_missing	stratum	pct_missing_overall
3	paco2	54.4	encounter_type	63.8
0	paco2	100.0	has_abg	63.8
1	paco2	0.0	has_abg	63.8
0	paco2	64.1	has_vbg	63.8
1	paco2	63.0	has_vbg	63.8
0	paco2	69.6	imv_proc	63.8
1	paco2	17.3	imv_proc	63.8
0	paco2	57.4	location	63.8
1	paco2	72.0	location	63.8
2	paco2	59.3	location	63.8
3	paco2	70.0	location	63.8
2	serum_lac	72.6	encounter_type	60.2
3	serum_lac	54.2	encounter_type	60.2
0	serum_lac	72.2	has_abg	60.2
1	serum_lac	39.2	has_abg	60.2
0	serum_lac	64.9	has_vbg	60.2
1	serum_lac	48.6	has_vbg	60.2
0	serum_lac	63.6	imv_proc	60.2
1	serum_lac	33.8	imv_proc	60.2
0	serum_lac	56.6	location	60.2
1	serum_lac	56.7	location	60.2
2	serum_lac	52.8	location	60.2
3	serum_lac	75.8	location	60.2
2	curr_bmi	41.4	encounter_type	57.0
3	curr_bmi	64.6	encounter_type	57.0
0	curr_bmi	55.9	has_abg	57.0
1	curr_bmi	58.7	has_abg	57.0
0	curr_bmi	52.7	has_vbg	57.0
1	curr_bmi	67.5	has_vbg	57.0
0	curr_bmi	55.8	imv_proc	57.0
1	curr_bmi	66.4	imv_proc	57.0
0	curr_bmi	66.3	location	57.0
1	curr_bmi	64.8	location	57.0
2	curr_bmi	50.6	location	57.0
3	curr_bmi	27.9	location	57.0
2	serum_phos	84.5	encounter_type	53.2
3	serum_phos	37.9	encounter_type	53.2
0	serum_phos	64.8	has_abg	53.2
1	serum_phos	32.9	has_abg	53.2
0	serum_phos	58.5	has_vbg	53.2
1	serum_phos	40.2	has_vbg	53.2
0	serum_phos	57.3	imv_proc	53.2
1	serum_phos	20.7	imv_proc	53.2
0	serum_phos	54.7	location	53.2
1	serum_phos	47.8	location	53.2

Table 10: Missingness by key strata (pre-imputation). (*continued*)

level	variable	pct_missing	stratum	pct_missing_overall
2	serum_phos	58.1	location	53.2
3	serum_phos	54.8	location	53.2
2	temp_new	57.4	encounter_type	48.2
3	temp_new	43.7	encounter_type	48.2
0	temp_new	51.9	has_abg	48.2
1	temp_new	41.7	has_abg	48.2
0	temp_new	48.0	has_vbg	48.2
1	temp_new	48.7	has_vbg	48.2
0	temp_new	48.1	imv_proc	48.2
1	temp_new	49.2	imv_proc	48.2
0	temp_new	36.0	location	48.2
1	temp_new	56.8	location	48.2
2	temp_new	39.6	location	48.2
3	temp_new	68.8	location	48.2
2	hr	34.1	encounter_type	36.4
3	hr	37.6	encounter_type	36.4
0	hr	35.1	has_abg	36.4
1	hr	38.8	has_abg	36.4
0	hr	33.2	has_vbg	36.4
1	hr	44.4	has_vbg	36.4
0	hr	36.1	imv_proc	36.4
1	hr	38.9	imv_proc	36.4
0	hr	35.7	location	36.4
1	hr	53.4	location	36.4
2	hr	49.0	location	36.4
3	hr	12.4	location	36.4
2	dbp	35.1	encounter_type	29.9
3	dbp	27.4	encounter_type	29.9
0	dbp	31.7	has_abg	29.9
1	dbp	26.9	has_abg	29.9
0	dbp	24.8	has_vbg	29.9
1	dbp	42.5	has_vbg	29.9
0	dbp	29.5	imv_proc	29.9
1	dbp	33.4	imv_proc	29.9
0	dbp	10.4	location	29.9
1	dbp	39.0	location	29.9
2	dbp	43.7	location	29.9
3	dbp	58.7	location	29.9
2	sbp	34.7	encounter_type	29.7
3	sbp	27.2	encounter_type	29.7
0	sbp	31.4	has_abg	29.7
1	sbp	26.6	has_abg	29.7
0	sbp	24.6	has_vbg	29.7
1	sbp	42.1	has_vbg	29.7
0	sbp	29.2	imv_proc	29.7

Table 10: Missingness by key strata (pre-imputation). (*continued*)

level	variable	pct_missing	stratum	pct_missing_overall
1	sbp	33.0	imv_proc	29.7
0	sbp	10.0	location	29.7
1	sbp	39.0	location	29.7
2	sbp	43.6	location	29.7
3	sbp	58.3	location	29.7
2	wbc	18.4	encounter_type	17.6
3	wbc	17.2	encounter_type	17.6
0	wbc	20.6	has_abg	17.6
1	wbc	12.2	has_abg	17.6
0	wbc	21.4	has_vbg	17.6
1	wbc	8.2	has_vbg	17.6
0	wbc	17.9	imv_proc	17.6
1	wbc	15.1	imv_proc	17.6
0	wbc	20.5	location	17.6
1	wbc	11.3	location	17.6
2	wbc	14.4	location	17.6
3	wbc	19.6	location	17.6
2	serum_ca	15.9	encounter_type	10.2
3	serum_ca	7.3	encounter_type	10.2
0	serum_ca	13.0	has_abg	10.2
1	serum_ca	5.1	has_abg	10.2
0	serum_ca	11.3	has_vbg	10.2
1	serum_ca	7.3	has_vbg	10.2
0	serum_ca	10.7	imv_proc	10.2
1	serum_ca	6.3	imv_proc	10.2
0	serum_ca	13.6	location	10.2
1	serum_ca	4.3	location	10.2
2	serum_ca	9.5	location	10.2
3	serum_ca	9.8	location	10.2
2	serum_cr	13.0	encounter_type	9.3
3	serum_cr	7.4	encounter_type	9.3
0	serum_cr	11.4	has_abg	9.3
1	serum_cr	5.6	has_abg	9.3
0	serum_cr	10.7	has_vbg	9.3
1	serum_cr	5.8	has_vbg	9.3
0	serum_cr	9.8	imv_proc	9.3
1	serum_cr	5.2	imv_proc	9.3
0	serum_cr	13.5	location	9.3
1	serum_cr	3.5	location	9.3
2	serum_cr	9.3	location	9.3
3	serum_cr	6.6	location	9.3
2	plt	12.2	encounter_type	8.0
3	plt	6.0	encounter_type	8.0
0	plt	9.0	has_abg	8.0
1	plt	6.3	has_abg	8.0

Table 10: Missingness by key strata (pre-imputation). (*continued*)

level	variable	pct_missing	stratum	pct_missing_overall
0	plt	9.4	has_vbg	8.0
1	plt	4.6	has_vbg	8.0
0	plt	8.1	imv_proc	8.0
1	plt	7.8	imv_proc	8.0
0	plt	9.7	location	8.0
1	plt	5.6	location	8.0
2	plt	8.8	location	8.0
3	plt	6.9	location	8.0
2	serum_k	11.7	encounter_type	7.8
3	serum_k	5.9	encounter_type	7.8
0	serum_k	10.1	has_abg	7.8
1	serum_k	3.9	has_abg	7.8
0	serum_k	9.0	has_vbg	7.8
1	serum_k	5.0	has_vbg	7.8
0	serum_k	8.2	imv_proc	7.8
1	serum_k	4.5	imv_proc	7.8
0	serum_k	10.6	location	7.8
1	serum_k	3.6	location	7.8
2	serum_k	7.5	location	7.8
3	serum_k	6.8	location	7.8
2	serum_cl	10.2	encounter_type	5.8
3	serum_cl	3.7	encounter_type	5.8
0	serum_cl	7.8	has_abg	5.8
1	serum_cl	2.3	has_abg	5.8
0	serum_cl	7.4	has_vbg	5.8
1	serum_cl	1.8	has_vbg	5.8
0	serum_cl	6.1	imv_proc	5.8
1	serum_cl	3.0	imv_proc	5.8
0	serum_cl	6.4	location	5.8
1	serum_cl	3.4	location	5.8
2	serum_cl	7.5	location	5.8
3	serum_cl	6.9	location	5.8
2	serum_hco3	10.3	encounter_type	5.6
3	serum_hco3	3.4	encounter_type	5.6
0	serum_hco3	7.8	has_abg	5.6
1	serum_hco3	1.9	has_abg	5.6
0	serum_hco3	7.2	has_vbg	5.6
1	serum_hco3	1.9	has_vbg	5.6
0	serum_hco3	6.0	imv_proc	5.6
1	serum_hco3	2.9	imv_proc	5.6
0	serum_hco3	6.1	location	5.6
1	serum_hco3	3.6	location	5.6
2	serum_hco3	7.6	location	5.6
3	serum_hco3	6.5	location	5.6
2	sodium	10.1	encounter_type	5.1

Table 10: Missingness by key strata (pre-imputation). (*continued*)

level	variable	pct_missing	stratum	pct_missing_overall
3	sodium	2.7	encounter_type	5.1
0	sodium	6.9	has_abg	5.1
1	sodium	2.0	has_abg	5.1
0	sodium	6.6	has_vbg	5.1
1	sodium	1.5	has_vbg	5.1
0	sodium	5.6	imv_proc	5.1
1	sodium	1.7	imv_proc	5.1
0	sodium	5.1	location	5.1
1	sodium	3.2	location	5.1
2	sodium	7.5	location	5.1
3	sodium	6.8	location	5.1
2	age_at_encounter	0.0	encounter_type	0.0
2	sex	0.0	encounter_type	0.0
2	race_ethnicity	0.0	encounter_type	0.0
2	copd	0.0	encounter_type	0.0
2	asthma	0.0	encounter_type	0.0
2	osa	0.0	encounter_type	0.0
2	chf	0.0	encounter_type	0.0
2	acute_nmd	0.0	encounter_type	0.0
2	phtn	0.0	encounter_type	0.0
2	ckd	0.0	encounter_type	0.0
2	dm	0.0	encounter_type	0.0
2	location	0.0	encounter_type	0.0
2	has_abg	0.0	encounter_type	0.0
2	has_vbg	0.0	encounter_type	0.0
2	imv_proc	0.0	encounter_type	0.0
2	niv_proc	0.0	encounter_type	0.0
2	hypercap_resp_failure	0.0	encounter_type	0.0
3	age_at_encounter	0.0	encounter_type	0.0
3	sex	0.0	encounter_type	0.0
3	race_ethnicity	0.0	encounter_type	0.0
3	copd	0.0	encounter_type	0.0
3	asthma	0.0	encounter_type	0.0
3	osa	0.0	encounter_type	0.0
3	chf	0.0	encounter_type	0.0
3	acute_nmd	0.0	encounter_type	0.0
3	phtn	0.0	encounter_type	0.0
3	ckd	0.0	encounter_type	0.0
3	dm	0.0	encounter_type	0.0
3	location	0.0	encounter_type	0.0
3	has_abg	0.0	encounter_type	0.0
3	has_vbg	0.0	encounter_type	0.0
3	imv_proc	0.0	encounter_type	0.0
3	niv_proc	0.0	encounter_type	0.0
3	hypercap_resp_failure	0.0	encounter_type	0.0

Table 10: Missingness by key strata (pre-imputation). (*continued*)

level	variable	pct_missing	stratum	pct_missing_overall
0	age_at_encounter	0.0	has_abg	0.0
0	sex	0.0	has_abg	0.0
0	race_ethnicity	0.0	has_abg	0.0
0	copd	0.0	has_abg	0.0
0	asthma	0.0	has_abg	0.0
0	osa	0.0	has_abg	0.0
0	chf	0.0	has_abg	0.0
0	acute_nmd	0.0	has_abg	0.0
0	phtn	0.0	has_abg	0.0
0	ckd	0.0	has_abg	0.0
0	dm	0.0	has_abg	0.0
0	location	0.0	has_abg	0.0
0	encounter_type	0.0	has_abg	0.0
0	has_vbg	0.0	has_abg	0.0
0	imv_proc	0.0	has_abg	0.0
0	niv_proc	0.0	has_abg	0.0
0	hypercap_resp_failure	0.0	has_abg	0.0
1	age_at_encounter	0.0	has_abg	0.0
1	sex	0.0	has_abg	0.0
1	race_ethnicity	0.0	has_abg	0.0
1	copd	0.0	has_abg	0.0
1	asthma	0.0	has_abg	0.0
1	osa	0.0	has_abg	0.0
1	chf	0.0	has_abg	0.0
1	acute_nmd	0.0	has_abg	0.0
1	phtn	0.0	has_abg	0.0
1	ckd	0.0	has_abg	0.0
1	dm	0.0	has_abg	0.0
1	location	0.0	has_abg	0.0
1	encounter_type	0.0	has_abg	0.0
1	has_vbg	0.0	has_abg	0.0
1	imv_proc	0.0	has_abg	0.0
1	niv_proc	0.0	has_abg	0.0
1	hypercap_resp_failure	0.0	has_abg	0.0
0	age_at_encounter	0.0	has_vbg	0.0
0	sex	0.0	has_vbg	0.0
0	race_ethnicity	0.0	has_vbg	0.0
0	copd	0.0	has_vbg	0.0
0	asthma	0.0	has_vbg	0.0
0	osa	0.0	has_vbg	0.0
0	chf	0.0	has_vbg	0.0
0	acute_nmd	0.0	has_vbg	0.0
0	phtn	0.0	has_vbg	0.0
0	ckd	0.0	has_vbg	0.0
0	dm	0.0	has_vbg	0.0

Table 10: Missingness by key strata (pre-imputation). (*continued*)

level	variable	pct_missing	stratum	pct_missing_overall
0	location	0.0	has_vbg	0.0
0	encounter_type	0.0	has_vbg	0.0
0	has_abg	0.0	has_vbg	0.0
0	imv_proc	0.0	has_vbg	0.0
0	niv_proc	0.0	has_vbg	0.0
0	hypercap_resp_failure	0.0	has_vbg	0.0
1	age_at_encounter	0.0	has_vbg	0.0
1	sex	0.0	has_vbg	0.0
1	race_ethnicity	0.0	has_vbg	0.0
1	copd	0.0	has_vbg	0.0
1	asthma	0.0	has_vbg	0.0
1	osa	0.0	has_vbg	0.0
1	chf	0.0	has_vbg	0.0
1	acute_nmd	0.0	has_vbg	0.0
1	phtn	0.0	has_vbg	0.0
1	ckd	0.0	has_vbg	0.0
1	dm	0.0	has_vbg	0.0
1	location	0.0	has_vbg	0.0
1	encounter_type	0.0	has_vbg	0.0
1	has_abg	0.0	has_vbg	0.0
1	imv_proc	0.0	has_vbg	0.0
1	niv_proc	0.0	has_vbg	0.0
1	hypercap_resp_failure	0.0	has_vbg	0.0
0	age_at_encounter	0.0	imv_proc	0.0
0	sex	0.0	imv_proc	0.0
0	race_ethnicity	0.0	imv_proc	0.0
0	copd	0.0	imv_proc	0.0
0	asthma	0.0	imv_proc	0.0
0	osa	0.0	imv_proc	0.0
0	chf	0.0	imv_proc	0.0
0	acute_nmd	0.0	imv_proc	0.0
0	phtn	0.0	imv_proc	0.0
0	ckd	0.0	imv_proc	0.0
0	dm	0.0	imv_proc	0.0
0	location	0.0	imv_proc	0.0
0	encounter_type	0.0	imv_proc	0.0
0	has_abg	0.0	imv_proc	0.0
0	has_vbg	0.0	imv_proc	0.0
0	niv_proc	0.0	imv_proc	0.0
0	hypercap_resp_failure	0.0	imv_proc	0.0
1	age_at_encounter	0.0	imv_proc	0.0
1	sex	0.0	imv_proc	0.0
1	race_ethnicity	0.0	imv_proc	0.0
1	copd	0.0	imv_proc	0.0
1	asthma	0.0	imv_proc	0.0

Table 10: Missingness by key strata (pre-imputation). (*continued*)

level	variable	pct_missing	stratum	pct_missing_overall
1	osa	0.0	imv_proc	0.0
1	chf	0.0	imv_proc	0.0
1	acute_nmd	0.0	imv_proc	0.0
1	phtn	0.0	imv_proc	0.0
1	ckd	0.0	imv_proc	0.0
1	dm	0.0	imv_proc	0.0
1	location	0.0	imv_proc	0.0
1	encounter_type	0.0	imv_proc	0.0
1	has_abg	0.0	imv_proc	0.0
1	has_vbg	0.0	imv_proc	0.0
1	niv_proc	0.0	imv_proc	0.0
1	hypercap_resp_failure	0.0	imv_proc	0.0
0	age_at_encounter	0.0	location	0.0
0	sex	0.0	location	0.0
0	race_ethnicity	0.0	location	0.0
0	copd	0.0	location	0.0
0	asthma	0.0	location	0.0
0	osa	0.0	location	0.0
0	chf	0.0	location	0.0
0	acute_nmd	0.0	location	0.0
0	phtn	0.0	location	0.0
0	ckd	0.0	location	0.0
0	dm	0.0	location	0.0
0	encounter_type	0.0	location	0.0
0	has_abg	0.0	location	0.0
0	has_vbg	0.0	location	0.0
0	imv_proc	0.0	location	0.0
0	niv_proc	0.0	location	0.0
0	hypercap_resp_failure	0.0	location	0.0
1	age_at_encounter	0.0	location	0.0
1	sex	0.0	location	0.0
1	race_ethnicity	0.0	location	0.0
1	copd	0.0	location	0.0
1	asthma	0.0	location	0.0
1	osa	0.0	location	0.0
1	chf	0.0	location	0.0
1	acute_nmd	0.0	location	0.0
1	phtn	0.0	location	0.0
1	ckd	0.0	location	0.0
1	dm	0.0	location	0.0
1	encounter_type	0.0	location	0.0
1	has_abg	0.0	location	0.0
1	has_vbg	0.0	location	0.0
1	imv_proc	0.0	location	0.0
1	niv_proc	0.0	location	0.0

Table 10: Missingness by key strata (pre-imputation). (*continued*)

level	variable	pct_missing	stratum	pct_missing_overall
1	hypercap_resp_failure	0.0	location	0.0
2	age_at_encounter	0.0	location	0.0
2	sex	0.0	location	0.0
2	race_ethnicity	0.0	location	0.0
2	copd	0.0	location	0.0
2	asthma	0.0	location	0.0
2	osa	0.0	location	0.0
2	chf	0.0	location	0.0
2	acute_nmd	0.0	location	0.0
2	phtn	0.0	location	0.0
2	ckd	0.0	location	0.0
2	dm	0.0	location	0.0
2	encounter_type	0.0	location	0.0
2	has_abg	0.0	location	0.0
2	has_vbg	0.0	location	0.0
2	imv_proc	0.0	location	0.0
2	niv_proc	0.0	location	0.0
2	hypercap_resp_failure	0.0	location	0.0
3	age_at_encounter	0.0	location	0.0
3	sex	0.0	location	0.0
3	race_ethnicity	0.0	location	0.0
3	copd	0.0	location	0.0
3	asthma	0.0	location	0.0
3	osa	0.0	location	0.0
3	chf	0.0	location	0.0
3	acute_nmd	0.0	location	0.0
3	phtn	0.0	location	0.0
3	ckd	0.0	location	0.0
3	dm	0.0	location	0.0
3	encounter_type	0.0	location	0.0
3	has_abg	0.0	location	0.0
3	has_vbg	0.0	location	0.0
3	imv_proc	0.0	location	0.0
3	niv_proc	0.0	location	0.0
3	hypercap_resp_failure	0.0	location	0.0

```
float_barrier()
```

```
# --- Drivers of missingness (logit I(NA) on observed covariates) -----
# Candidate predictors (observed covariates only)
driver_covars <- intersect(
```

```

c("age_at_encounter", "sex", "encounter_type", "location", "curr_bmi",
  "has_abg", "has_vbg", "imv_proc", "death_60d"),
  names(model_data)
)

# Fit models for variables with any missingness
vars_to_model <- miss_overall_model |>
  filter(pct_missing_overall_model > 0) |>
  pull(variable)
vars_to_model <- intersect(vars_to_model, names(model_data))

skip_log <- list()

model_results <- purrr::map_dfr(vars_to_model, function(v) {
  df <- model_data |>
    select(all_of(c(v, driver_covars))) |>
    mutate(miss = as.integer(is.na(.data[[v]])))

  # use only rows with observed predictors and varying miss indicator
  df <- df[stats::complete.cases(df[driver_covars]), , drop = FALSE]
  if (nrow(df) == 0L) {
    skip_log[[length(skip_log) + 1L]] <- data.frame(
      variable = v,
      reason = "no_complete_cases",
      stringsAsFactors = FALSE
    )
    return(tibble::tibble())
  }
  if (dplyr::n_distinct(df$miss) < 2L) {
    skip_log[[length(skip_log) + 1L]] <- data.frame(
      variable = v,
      reason = "miss_indicator_constant",
      stringsAsFactors = FALSE
    )
    return(tibble::tibble())
  }
})

```

```

fml <- as.formula(paste0("miss ~ ", paste(driver_covars, collapse = " + ")))
if (length(driver_covars) > 0L) {
  diag_outcome <- paste0("missing_", make.names(v))
  diag_terms <- paste0("~", driver_covars, "~", collapse = " + ")
  diag_fml <- stats::as.formula(paste0(diag_outcome, " ~ ", diag_terms))
  register_model_diagram(paste("Missingness model:", v), diag_fml, width = 10, height = 6)
}
fit <- tryCatch(
  suppressWarnings(glm(fml, data = df, family = binomial())),
  error = function(e) e
)
if (inherits(fit, "error")) {
  stop("Missingness driver: glm failed for variable ", v)
}

broom::tidy(fit, conf.int = FALSE, exponentiate = FALSE) |>
  filter(term != "(Intercept)") |>
  mutate(
    OR = exp(estimate),
    LCL = exp(estimate - 1.96 * std.error),
    UCL = exp(estimate + 1.96 * std.error)
  ) |>
  transmute(
    variable = v,
    term,
    OR,
    LCL,
    UCL,
    p.value
  )
)

skip_tbl <- dplyr::bind_rows(skip_log)
write_csv_safely(skip_tbl, results_path("missingness_driver_skips.csv"), row_names = FALSE)

```

```

if (nrow(model_results) > 0) {
  model_results_file <- results_path("missingness-drivers.csv")
  model_results_out <- model_results |>
    dplyr::mutate(run_id = diag_run_id)
  write_csv_safely(model_results_out, model_results_file, row_names = FALSE)

  model_results_disp <- model_results_out |>
    dplyr::select(-run_id) |>
    arrange(p.value) |>
    mutate(
      OR = round(OR, 2),
      LCL = round(LCL, 2),
      UCL = round(UCL, 2),
      p.value = signif(p.value, 3)
    )
}

render_table_pdf(
  model_results_disp,
  caption = "Predictors of missingness (logit OR).",
  file_stub = "missingness-drivers",
  digits = 2
)
} else {
  model_results_stub <- data.frame(
    variable = character(),
    term = character(),
    OR = numeric(),
    LCL = numeric(),
    UCL = numeric(),
    p.value = numeric(),
    stringsAsFactors = FALSE
  )
  write_csv_safely(model_results_stub, results_path("missingness-drivers.csv"), row_names = FALSE)
  message("No modelable missingness signals (all complete or no variation).")
}

```

Table 11: Predictors of missingness (logit OR).

variable	term	OR	LCL	UCL	p.value
temp_new	location1	18.41	15.92	2.129000e+01	0.00
temp_new	location3	21.44	18.95	2.426000e+01	0.00
serum_phos	encounter_typeInpatient	0.12	0.11	1.400000e-01	0.00
hr	location1	11.68	10.14	1.346000e+01	0.00
sbp	encounter_typeInpatient	0.04	0.04	5.000000e-02	0.00
dbp	encounter_typeInpatient	0.05	0.04	6.000000e-02	0.00
serum_lac	has_abg	0.24	0.22	2.600000e-01	0.00
vbg_o2sat	has_vbg	0.00	0.00	0.000000e+00	0.00
dbp	location3	1607.67	847.74	3.048810e+03	0.00
serum_lac	location3	3.24	2.89	3.620000e+00	0.00
serum_phos	has_abg	0.34	0.31	3.800000e-01	0.00
sbp	location3	3373.24	1382.62	8.229860e+03	0.00
hr	location2	4.34	3.68	5.130000e+00	0.00
wbc	location3	3.13	2.72	3.610000e+00	0.00
temp_new	location2	3.76	3.17	4.450000e+00	0.00
serum_cl	age_at_encounter	0.96	0.96	9.700000e-01	0.00
sodium	age_at_encounter	0.96	0.96	9.700000e-01	0.00
serum_ca	age_at_encounter	0.97	0.97	9.700000e-01	0.00
serum_hco3	age_at_encounter	0.97	0.96	9.700000e-01	0.00
serum_phos	has_vbg	0.38	0.33	4.300000e-01	0.00
serum_cr	age_at_encounter	0.97	0.96	9.700000e-01	0.00
serum_k	age_at_encounter	0.97	0.96	9.700000e-01	0.00
vbg_o2sat	encounter_typeInpatient	0.22	0.17	2.800000e-01	0.00
temp_new	has_abg	0.49	0.43	5.400000e-01	0.00
wbc	age_at_encounter	0.98	0.98	9.800000e-01	0.00
serum_phos	location3	0.48	0.43	5.400000e-01	0.00
wbc	location2	3.39	2.78	4.130000e+00	0.00
serum_lac	has_vbg	0.49	0.44	5.600000e-01	0.00
wbc	location1	2.80	2.36	3.320000e+00	0.00
vbg_o2sat	location3	11.26	7.52	1.686000e+01	0.00
serum_k	has_abg	0.12	0.08	1.700000e-01	0.00
serum_ca	has_abg	0.18	0.14	2.500000e-01	0.00
vbg_o2sat	location2	0.06	0.04	1.000000e-01	0.00
plt	age_at_encounter	0.97	0.97	9.800000e-01	0.00
hr	has_abg	0.49	0.43	5.500000e-01	0.00
sodium	has_abg	0.12	0.08	1.700000e-01	0.00
serum_hco3	has_abg	0.15	0.11	2.100000e-01	0.00
serum_cl	has_abg	0.14	0.09	1.900000e-01	0.00
serum_cr	has_abg	0.22	0.17	2.900000e-01	0.00
temp_new	encounter_typeInpatient	0.58	0.52	6.400000e-01	0.00
plt	has_abg	0.22	0.17	3.000000e-01	0.00
plt	encounter_typeInpatient	0.39	0.32	4.700000e-01	0.00
serum_phos	imv_proc	0.38	0.31	4.600000e-01	0.00
serum_ca	encounter_typeInpatient	0.44	0.37	5.100000e-01	0.00
serum_k	has_vbg	0.10	0.07	1.600000e-01	0.00

Table 11: Predictors of missingness (logit OR). (*continued*)

variable	term	OR	LCL	UCL	p.value
hr	imv_proc	2.41	2.01	2.890000e+00	0.00
serum_hco3	has_vbg	0.15	0.10	2.200000e-01	0.00
serum_cl	has_vbg	0.11	0.07	1.700000e-01	0.00
sodium	has_vbg	0.10	0.06	1.700000e-01	0.00
plt	has_vbg	0.20	0.14	2.800000e-01	0.00
wbc	has_vbg	0.48	0.41	5.600000e-01	0.00
serum_cr	has_vbg	0.19	0.13	2.700000e-01	0.00
hr	age_at_encounter	0.99	0.98	9.900000e-01	0.00
sbp	age_at_encounter	1.02	1.01	1.020000e+00	0.00
serum_lac	curr_bmi	1.02	1.02	1.030000e+00	0.00
vbg_o2sat	imv_proc	0.28	0.19	3.900000e-01	0.00
serum_lac	location1	1.60	1.40	1.820000e+00	0.00
serum_hco3	encounter_typeInpatient	0.52	0.44	6.300000e-01	0.00
dbp	age_at_encounter	1.02	1.01	1.020000e+00	0.00
sodium	encounter_typeInpatient	0.53	0.44	6.400000e-01	0.00
serum_cl	encounter_typeInpatient	0.54	0.45	6.400000e-01	0.00
serum_cr	encounter_typeInpatient	0.55	0.46	6.600000e-01	0.00
serum_k	encounter_typeInpatient	0.55	0.46	6.600000e-01	0.00
serum_lac	age_at_encounter	0.99	0.99	9.900000e-01	0.00
serum_phos	location1	0.63	0.54	7.200000e-01	0.00
temp_new	age_at_encounter	1.01	1.01	1.010000e+00	0.00
serum_phos	curr_bmi	1.02	1.01	1.030000e+00	0.00
serum_cr	location3	0.56	0.47	6.800000e-01	0.00
vbg_o2sat	has_abg	2.18	1.69	2.810000e+00	0.00
serum_k	location3	0.57	0.47	6.900000e-01	0.00
serum_ca	has_vbg	0.52	0.41	6.500000e-01	0.00
serum_lac	imv_proc	0.64	0.54	7.500000e-01	0.00
serum_ca	curr_bmi	1.02	1.02	1.030000e+00	0.00
serum_lac	death_60d	0.65	0.56	7.600000e-01	0.00
plt	location3	0.60	0.50	7.200000e-01	0.00
serum_hco3	location3	0.61	0.51	7.400000e-01	0.00
temp_new	imv_proc	1.60	1.34	1.910000e+00	0.00
hr	encounter_typeInpatient	1.33	1.19	1.480000e+00	0.00
sodium	location3	0.62	0.51	7.400000e-01	0.00
serum_cl	location3	0.62	0.51	7.500000e-01	0.00
serum_k	curr_bmi	1.02	1.01	1.030000e+00	0.00
plt	curr_bmi	1.02	1.01	1.030000e+00	0.00
sbp	curr_bmi	1.03	1.01	1.040000e+00	0.00
serum_lac	location2	1.45	1.23	1.710000e+00	0.00
sodium	curr_bmi	1.02	1.01	1.030000e+00	0.00
temp_new	death_60d	1.46	1.23	1.730000e+00	0.00
serum_cl	curr_bmi	1.02	1.01	1.030000e+00	0.00
serum_cr	curr_bmi	1.02	1.01	1.030000e+00	0.00
dbp	curr_bmi	1.02	1.01	1.030000e+00	0.00
hr	death_60d	1.44	1.21	1.710000e+00	0.00

Table 11: Predictors of missingness (logit OR). (*continued*)

variable	term	OR	LCL	UCL	p.value
serum_phos	age_at_encounter	0.99	0.99	1.000000e+00	0.00
serum_hco3	curr_bmi	1.02	1.01	1.030000e+00	0.00
wbc	curr_bmi	1.01	1.01	1.020000e+00	0.00
serum_phos	sexMale	0.84	0.77	9.200000e-01	0.00
serum_cr	location2	1.58	1.23	2.020000e+00	0.00
wbc	has_abg	0.78	0.67	8.900000e-01	0.00
sbp	location2	6.06	1.91	1.923000e+01	0.00
serum_cr	location1	0.70	0.56	8.900000e-01	0.00
sbp	has_vbg	0.72	0.58	9.000000e-01	0.00
serum_phos	death_60d	0.78	0.65	9.200000e-01	0.00
serum_ca	location1	0.72	0.58	9.000000e-01	0.00
vbg_o2sat	age_at_encounter	1.01	1.00	1.010000e+00	0.00
dbp	has_vbg	0.74	0.60	9.100000e-01	0.01
sbp	death_60d	0.65	0.48	8.800000e-01	0.01
serum_cl	inv_proc	0.25	0.09	6.700000e-01	0.01
plt	location2	1.42	1.10	1.840000e+00	0.01
sodium	location1	0.72	0.56	9.200000e-01	0.01
serum_cl	location1	0.73	0.57	9.300000e-01	0.01
dbp	location2	3.45	1.35	8.820000e+00	0.01
wbc	inv_proc	1.32	1.07	1.630000e+00	0.01
temp_new	has_vbg	0.86	0.76	9.600000e-01	0.01
serum_k	location1	0.74	0.59	9.400000e-01	0.01
serum_lac	sexMale	0.90	0.82	9.800000e-01	0.02
serum_hco3	inv_proc	0.37	0.16	8.500000e-01	0.02
sbp	has_abg	1.28	1.04	1.560000e+00	0.02
sodium	inv_proc	0.34	0.14	8.500000e-01	0.02
dbp	has_abg	1.26	1.03	1.550000e+00	0.02
serum_ca	inv_proc	0.51	0.27	9.500000e-01	0.03
serum_hco3	location1	0.78	0.62	9.900000e-01	0.04
serum_ca	death_60d	0.58	0.34	1.000000e+00	0.05
serum_cr	inv_proc	0.54	0.29	1.010000e+00	0.05
wbc	death_60d	0.80	0.64	1.010000e+00	0.06
dbp	inv_proc	1.30	0.99	1.720000e+00	0.06
hr	has_vbg	1.12	0.99	1.270000e+00	0.07
vbg_o2sat	location1	1.33	0.96	1.850000e+00	0.09
sbp	inv_proc	1.27	0.96	1.680000e+00	0.09
temp_new	curr_bmi	1.01	1.00	1.010000e+00	0.10
dbp	death_60d	0.78	0.58	1.050000e+00	0.10
serum_cr	death_60d	0.63	0.35	1.110000e+00	0.11
serum_k	death_60d	0.60	0.32	1.130000e+00	0.11
sodium	sexMale	0.88	0.74	1.030000e+00	0.12
serum_ca	sexMale	0.89	0.77	1.030000e+00	0.13
sodium	location2	1.23	0.94	1.620000e+00	0.13
serum_cl	sexMale	0.88	0.75	1.040000e+00	0.13
serum_phos	location2	1.15	0.95	1.390000e+00	0.14

Table 11: Predictors of missingness (logit OR). (*continued*)

variable	term	OR	LCL	UCL	p.value
sbp	sexMale	0.89	0.75	1.050000e+00	0.15
serum_k	sexMale	0.89	0.76	1.050000e+00	0.15
serum_hco3	death_60d	0.64	0.34	1.190000e+00	0.16
serum_cr	sexMale	0.90	0.77	1.050000e+00	0.19
dbp	sexMale	0.90	0.76	1.060000e+00	0.21
hr	curr_bmi	1.00	0.99	1.000000e+00	0.22
serum_hco3	sexMale	0.91	0.77	1.070000e+00	0.24
serum_ca	location3	0.91	0.77	1.070000e+00	0.24
serum_cl	location2	1.17	0.89	1.540000e+00	0.25
serum_k	imv_proc	0.69	0.35	1.340000e+00	0.27
sbp	location1	2.00	0.58	6.970000e+00	0.28
sodium	death_60d	0.71	0.38	1.330000e+00	0.28
serum_ca	location2	1.15	0.89	1.480000e+00	0.28
plt	location1	0.88	0.70	1.110000e+00	0.29
serum_hco3	location2	1.16	0.88	1.510000e+00	0.29
temp_new	sexMale	1.04	0.95	1.150000e+00	0.39
plt	imv_proc	0.79	0.45	1.390000e+00	0.42
vbg_o2sat	curr_bmi	0.99	0.98	1.010000e+00	0.42
wbc	encounter_typeInpatient	1.05	0.93	1.180000e+00	0.43
vbg_o2sat	death_60d	0.90	0.67	1.200000e+00	0.48
serum_k	location2	1.09	0.84	1.430000e+00	0.51
vbg_o2sat	sexMale	1.06	0.87	1.300000e+00	0.56
serum_cl	death_60d	0.86	0.48	1.520000e+00	0.60
wbc	sexMale	0.98	0.88	1.090000e+00	0.74
plt	death_60d	1.08	0.68	1.710000e+00	0.74
plt	sexMale	1.02	0.87	1.200000e+00	0.77
hr	location3	0.98	0.86	1.130000e+00	0.81
hr	sexMale	0.99	0.90	1.100000e+00	0.90
serum_lac	encounter_typeInpatient	1.00	0.90	1.100000e+00	0.94
dbp	location1	0.99	0.34	2.920000e+00	0.99
paco2	has_abg	0.00	0.00	Inf	1.00
vbg_co2	has_vbg	0.00	0.00	Inf	1.00
vbg_co2	location3	1.00	0.00	Inf	1.00
vbg_co2	location1	1.00	0.00	Inf	1.00
vbg_co2	location2	1.00	0.00	Inf	1.00
vbg_co2	curr_bmi	1.00	0.00	Inf	1.00
vbg_co2	has_abg	1.00	0.00	Inf	1.00
vbg_co2	inv_proc	1.00	0.00	Inf	1.00
vbg_co2	encounter_typeInpatient	1.00	0.00	Inf	1.00
vbg_co2	age_at_encounter	1.00	0.00	1.856707e+167	1.00
vbg_co2	death_60d	1.00	0.00	Inf	1.00
vbg_co2	sexMale	1.00	0.00	Inf	1.00
paco2	encounter_typeInpatient	1.00	0.00	Inf	1.00
paco2	curr_bmi	1.00	0.00	Inf	1.00
paco2	location1	1.00	0.00	Inf	1.00

Table 11: Predictors of missingness (logit OR). (*continued*)

variable	term	OR	LCL	UCL	p.value
paco2	location3	1.00	0.00	Inf	1.00
paco2	age_at_encounter	1.00	0.00	1.856981e+167	1.00
paco2	death_60d	1.00	0.00	Inf	1.00
paco2	has_vbg	1.00	0.00	Inf	1.00
paco2	location2	1.00	0.00	Inf	1.00
paco2	sexMale	1.00	0.00	Inf	1.00
paco2	imv_proc	1.00	0.00	Inf	1.00

3.0.2 7.3 Monte Carlo error check after MI

3.1 8) Pre-imputation data prep (consistent types & predictors)

Why: MI models need coherent types; using exactly the same covariates as the propensity score models avoids model drift.

```
# Types are normalized in the schema-normalize block.
```

3.2 9) Imputation model specification (MICE)

3.2.1 9.1 Predictor matrix & methods. Run MICE (moderate settings for scale)

```
# --- variables for propensity score model (kept identical to main analysis) ---
# ----- MICE setup: include PaCO2/VBG CO2 as predictors but do not impute -----
library(mice)
library(dplyr)

# --- add analysis targets and CO2 measures explicitly -----
mi_vars <- setdiff(unique(c(
  covars_ps,
  "has_abg", "has_vbg", # treatments (NOT imputed)
  "imv_proc", "niv_proc", "death_60d", "hypercap_resp_failure", # outcomes (NOT imputed)
  co2_vars
)), drop_vars_ultra_missing)
```

```

mi_df <- subset_data[, mi_vars, drop = FALSE]
mi_df <- normalize_types(mi_df, levels_ref)

mi_df_size <- utils::object.size(mi_df)
message("MI data size (bytes): ", format(mi_df_size, units = "auto"))

# Rough memory preflight based on total missing cells (imputed values only).
miss_counts <- vapply(mi_df, function(x) sum(is.na(x)), numeric(1))
miss_total <- sum(miss_counts)
if (is.finite(miss_total) && miss_total > 0) {
  est_bytes <- miss_total * M_IMP * 8
  message("MI imputation storage estimate: ", format(structure(est_bytes, class = "object_size"), units = "auto"))
  if (est_bytes > MI_MAX_BYTES) {
    m_max <- floor(MI_MAX_BYTES / (miss_total * 8))
    m_target <- max(50L, m_max)
    if (m_target < 50L) {
      stop("Estimated MI storage exceeds memory (m=", M_IMP,
           ", estimated=", format(structure(est_bytes, class = "object_size"), units = "auto"),
           "). Reduce missingness or MI scope, or increase available memory.")
    }
    if (m_target < M_IMP) {
      message("Reducing M_IMP from ", M_IMP, " to ", m_target,
              " to stay within MI_MAX_BYTES.")
      M_IMP <- m_target
    }
  }
}

# Make binary comorbid factors so "logreg" is used (and stays binary)
bin_covars <- c("copd", "asthma", "osa", "chf", "acute_nmd", "phtn", "ckd", "dm")
missing_bin <- setdiff(bin_covars, names(mi_df))
stopifnot(length(missing_bin) == 0)
mi_df[bin_covars] <- lapply(mi_df[bin_covars], function(z) {
  if (is.factor(z)) return(droplevels(z))
  zz <- suppressWarnings(as.integer(z))
  })

```

```

    factor(zz, levels = c(0L,1L), labels = c("0","1"))
  })

# For MICE: convert any remaining characters → factors
mi_df <- dplyr::mutate(mi_df, across(where(is.character), ~ factor(.x)))

# Guardrail: high-cardinality factors can blow up MICE model matrices.
# Exclude them from predictorMatrix and (if missing) make "Missing" explicit.
high_card <- names(which(vapply(mi_df, function(x) is.factor(x) && nlevels(x) > MAX_LEVELS_PRED, logical(1))))
if (length(high_card)) {
  message("MICE: high-cardinality factors detected (nlevels > ", MAX_LEVELS_PRED, "): ",
         paste(high_card, collapse = ", "))
  for (v in high_card) {
    if (any(is.na(mi_df[[v]]))) {
      lv <- levels(mi_df[[v]])
      tmp <- as.character(mi_df[[v]])
      tmp[is.na(tmp)] <- "Missing"
      mi_df[[v]] <- factor(tmp, levels = unique(c(lv, "Missing")))
      if (!is.null(levels_ref) && !is.null(levels_ref[[v]]) &&
          !"Missing" %in% levels_ref[[v]]) {
        levels_ref[[v]] <- c(levels_ref[[v]], "Missing")
      }
    }
  }
}

# --- methods & predictor matrix aligned to *mi_df* -----
meth <- mice::make.method(mi_df)

is_fac     <- vapply(mi_df, is.factor, logical(1))
is_num     <- vapply(mi_df, is.numeric, logical(1))
is_bin_fac <- vapply(mi_df, function(x) is.factor(x) && nlevels(x) == 2, logical(1))
is_multicat <- vapply(mi_df, function(x) is.factor(x) && nlevels(x) > 2, logical(1))

# robust defaults
meth[is_num]     <- "pmm"      # numerics: predictive mean matching

```

```

meth[is_multicat] <- "polyreg" # unordered multicategory
meth[is_bin_fac]  <- "logreg"  # binary factors: logistic regression

# never impute treatments, outcomes, or CO2 exposures
no_imp <- c("has_abg", "has_vbg", "imv_proc", "niv_proc", "death_60d", "hypercap_resp_failure",
           "paco2", "vbg_co2")
if (length(high_card)) no_imp <- unique(c(no_imp, high_card))
meth[intersect(names(meth), no_imp)] <- ""

# predictor matrix; force has_abg/has_vbg as predictors, but do not impute no_imp
pred <- mice:::quickpred(mi_df, mincor = MINCOR_QUICKPRED, minpuc = MINPUC_QUICKPRED)
for (nm in intersect(c("has_abg", "has_vbg"), colnames(pred))) {
  pred[, nm] <- 1
}
pred[intersect(rownames(pred), no_imp), ] <- 0

if (length(high_card)) {
  pred[, intersect(high_card, colnames(pred))] <- 0
  pred[intersect(high_card, rownames(pred)), ] <- 0
}

# Ensure dropped covariates do not appear as predictors
drop_covars <- intersect(drop_vars_ultra_missing, colnames(pred))
if (length(drop_covars)) {
  pred[, drop_covars] <- 0
}

# Non-imputed variables with missingness should NOT be predictors
no_imp_with_missing <- intersect(no_imp, names(mi_df))
no_imp_with_missing <- no_imp_with_missing[
  vapply(mi_df[no_imp_with_missing], function(x) any(is.na(x)), logical(1))
]
no_imp_with_missing <- setdiff(no_imp_with_missing, c("has_abg", "has_vbg"))

pred_cols_check <- intersect(c("paco2", "vbg_co2"), colnames(pred))
if (length(pred_cols_check)) {

```

```

message(
  "MICE: predictor column sums (pre-exclude) for ",
  paste(pred_cols_check, collapse = ", "),
  ": ",
  paste(colSums(pred[, pred_cols_check, drop = FALSE]), collapse = ", ")
)
}

if (length(no_imp_with_missing)) {
  pred[, intersect(no_imp_with_missing, colnames(pred))] <- 0
  message("MICE: excluded non-imputed missing predictors: ",
    paste(no_imp_with_missing, collapse = ", "))
}

if (length(pred_cols_check)) {
  message(
    "MICE: predictor column sums (post-exclude) for ",
    paste(pred_cols_check, collapse = ", "),
    ": ",
    paste(colSums(pred[, pred_cols_check, drop = FALSE]), collapse = ", "))
}

# Ensure key covariates with missingness have predictors (avoid zero-row pred)
core_preds <- intersect(
  c("age_at_encounter", "sex", "race_ethnicity", "location", "encounter_type",
    "has_abg", "has_vbg", "imv_proc", "niv_proc", "death_60d",
    "hypercap_resp_failure", "paco2", "vbg_co2"),
  colnames(pred)
)
core_preds <- setdiff(core_preds, no_imp_with_missing)
vars_need_pred <- intersect(covars_ps, rownames(pred))
vars_need_pred <- setdiff(vars_need_pred, no_imp)
vars_need_pred <- vars_need_pred[vapply(mi_df[vars_need_pred], function(x) any(is.na(x)), logical(1))]
zero_pred <- vars_need_pred[rowSums(pred[vars_need_pred, , drop = FALSE] != 0, na.rm = TRUE) == 0]
if (length(zero_pred)) {
  message("MICE predictor rows empty for: ", paste(zero_pred, collapse = ", "),
    ". Adding core predictors.")
}

```

```

    pred[zero_pred, core_preds] <- 1
}
pred[intersect(rownames(pred), no_imp), ] <- 0
pred[c(zero_pred), c(zero_pred)] <- 0

# --- Preflight and cap predictor rows to avoid huge model matrices ----

n_mm_cols <- function(pred_row, df) {
  preds <- names(which(pred_row != 0))
  cols <- 1L
  for (p in preds) {
    x <- df[[p]]
    if (is.factor(x)) {
      lv <- nlevels(x)
      cols <- cols + max(1L, lv - 1L)
    } else {
      cols <- cols + 1L
    }
  }
  cols
}

pred_width_preflight <- function(pred, df, meth) {
  vars <- names(meth)[meth != ""]
  vars <- vars[vapply(df[vars], function(x) any(is.na(x)), logical(1))]
  rows <- lapply(vars, function(v) {
    pred_row <- pred[v, ]
    n_pred <- sum(pred_row != 0, na.rm = TRUE)
    mm_cols <- n_mm_cols(pred_row, df)
    x <- df[[v]]
    nlevels_v <- if (is.factor(x)) nlevels(x) else NA_integer_
    miss_n <- sum(is.na(x))
    data.frame(
      variable = v,
      method = meth[[v]],
      n_pred = n_pred,

```

```

    mm_cols = mm_cols,
    nlevels_v = nlevels_v,
    miss_n = miss_n,
    stringsAsFactors = FALSE
)
})
if (!length(rows)) {
  return(data.frame(variable = character(), method = character(), n_pred = integer(),
                    mm_cols = integer(), nlevels_v = integer(), miss_n = integer()))
}
dplyr::bind_rows(rows)
}

preflight_pre <- pred_width_preflight(pred, mi_df, meth) |>
  dplyr::mutate(stage = "pre")

core_preds <- intersect(
  c("age_at_encounter", "sex", "race_ethnicity", "location", "encounter_type",
    "has_abg", "has_vbg", "imv_proc", "niv_proc", "death_60d",
    "hypercap_resp_failure", "paco2", "vbg_co2"),
  colnames(pred))
)
core_preds <- setdiff(core_preds, no_imp_with_missing)

set.seed(MI_SEED + 100)
idx <- sample.int(nrow(mi_df), min(COR_SAMPLE_N, nrow(mi_df)))

vars_cap <- names(meth)[meth != ""]
vars_cap <- vars_cap[vapply(mi_df[vars_cap], function(x) any(is.na(x))), logical(1)]]

pred_nlevels <- function(x) {
  if (is.factor(x)) nlevels(x) else 1L
}

for (v in vars_cap) {
  cand <- names(which(pred[, ] != 0))

```

```

if (!length(cand)) next
keep <- intersect(core_preds, cand)
rem  <- setdiff(cand, keep)

if (length(rem)) {
  y_raw <- mi_df[[v]][idx]
  y <- if (is.factor(y_raw)) as.integer(y_raw) else suppressWarnings(as.numeric(y_raw))
  scores <- vapply(rem, function(r) {
    x_raw <- mi_df[[r]][idx]
    x <- if (is.factor(x_raw)) as.integer(x_raw) else suppressWarnings(as.numeric(x_raw))
    suppressWarnings(abs(stats::cor(y, x, use = "pairwise.complete.obs")))
  }, numeric(1))
  ord <- order(is.na(scores), -scores)
  rem_keep <- rem[ord]
  rem_keep <- rem_keep[seq_len(min(length(rem_keep), max(0L, MAX_PRED_PER_VAR - length(keep))))]
} else {
  rem_keep <- character()
}

keep_all <- unique(c(keep, rem_keep))
pred[v, ] <- 0
pred[v, keep_all] <- 1
pred[v, v] <- 0

mm_cols <- n_mm_cols(pred[v, ], mi_df)
if (mm_cols > MAX_MM_COLS) {
  drop_pool <- setdiff(keep_all, keep)
  if (!length(drop_pool)) drop_pool <- keep
  drop_order <- drop_pool[order(vapply(drop_pool, function(p) pred_nlevels(mi_df[[p]]), integer(1)),
                                 decreasing = TRUE)]}
  for (p in drop_order) {
    if (p %in% keep && length(keep) == 1) break
    pred[v, p] <- 0
    mm_cols <- n_mm_cols(pred[v, ], mi_df)
    if (mm_cols <= MAX_MM_COLS) break
  }
}

```

```

    }

preflight_post <- pred_width_preflight(pred, mi_df, meth) |>
  dplyr::mutate(stage = "post")
preflight_all <- dplyr::bind_rows(preflight_pre, preflight_post)
write_csv_safely(preflight_all, results_path("mice_pred_width_preflight.csv"), row_names = FALSE)

# MI integrity: treatments/outcomes excluded; binaries use logreg
stopifnot(all(meth[no_imp] == ""))
stopifnot(all(rowSums(pred[intersect(rownames(pred), no_imp), , drop = FALSE]) == 0))
bin_fac <- names(which(vapply(mi_df, function(x) is.factor(x) && nlevels(x) == 2, logical(1))))
bin_fac <- setdiff(bin_fac, no_imp)
stopifnot(all(meth[bin_fac] == "logreg"))

# integrity checks
stopifnot(
  ncol(pred) == ncol(mi_df),
  nrow(pred) == ncol(mi_df),
  length(meth) == ncol(mi_df),
  identical(names(meth), colnames(mi_df)))
)

# --- run MICE -----
mi_df_run <- mi_df
M_IMP_RUN <- M_IMP
MAXIT_RUN <- MAXIT_MI
FORCE_MI_BATCHED <- nrow(mi_df_run) > MI_BATCH_THRESHOLD

if (!requireNamespace("digest", quietly = TRUE)) {
  stop("Package 'digest' is required for MI checkpoint signatures.")
}

make_mi_signature <- function(df) {
  classes <- vapply(df, function(x) class(x)[1], character(1))
  na_counts <- vapply(df, function(x) sum(is.na(x)), integer(1))
}

```

```

nlevels <- vapply(df, function(x) if (is.factor(x)) nlevels(x) else NA_integer_, integer(1))
lvl_hash <- vapply(df, function(x) {
  if (!is.factor(x)) return(NA_character_)
  digest::digest(levels(x), algo = "xxhash64")
}, character(1))
col_sig <- data.frame(
  name = names(df),
  class = classes,
  na = na_counts,
  nlevels = nlevels,
  lvl_hash = lvl_hash,
  stringsAsFactors = FALSE
)
hash <- digest::digest(
  list(dim = dim(df), col_sig = col_sig),
  algo = "xxhash64"
)
list(
  hash = hash,
  nrow = nrow(df),
  ncol = ncol(df),
  run_mode = RUN_MODE,
  pilot_frac = PILOT_FRAC,
  mi_pilot_mode = RUN_MODE,
  sample_seed = SAMPLE_SEED,
  mi_seed = MI_SEED,
  col_sig = col_sig
)
}

mi_smoke_log_path <- results_path("mice_smoketest.log")
write_smoke_log <- function(lines) {
  write_diag_lines(lines, mi_smoke_log_path)
}

mem_max <- tryCatch(mem.maxVSize(), error = function(e) NA_real_)
```

```

mem_env <- Sys.getenv("R_MAX_VSIZE", unset = NA_character_)
gc_pre <- utils::capture.output(gc())
write_smoke_log(c(
  paste0("MI smoke test log: ", Sys.time()),
  paste0("mem.maxVSize: ", ifelse(is.na(mem_max), "NA", format(mem_max, scientific = FALSE))),
  paste0("R_MAX_VSIZE env: ", ifelse(nchar(mem_env), mem_env, "NA")),
  paste0("mi_df size: ", format(utils::object.size(mi_df), units = "auto")),
  paste0("mi_df_run size: ", format(utils::object.size(mi_df_run), units = "auto")),
  "gc() pre:",
  gc_pre
))
if (RUN_MODE == "full" && is.finite(mem_max) && mem_max < 2.2e10) {
  message("Full run on ~16GB memory: consider running MI/weights on a >32GB machine for speed.")
}

subset_data_saved <- FALSE
subset_data_path <- results_path("subset_data_pre_mi.rds")
if (MI_MEMORY_HYGIENE) {
  saveRDS(subset_data, subset_data_path)
  rm(subset_data)
  subset_data_saved <- TRUE
  invisible(gc())
}

run_mice_call <- function(m_val, maxit, seed_val, print_flag = FALSE) {
  mice::mice(
    data      = mi_df_run,
    m         = m_val,
    maxit     = maxit,
    predictorMatrix = pred,
    method    = meth,
    printFlag = print_flag,
    seed      = seed_val
  )
}

```

```

if (MI_SMOKE_TEST) {
  smoke_con <- file(mi_smoke_log_path, open = "at")
  sink(smoke_con, type = "output")

  cap_smoke <- capture_warnings(
    tryCatch(
      run_mice_call(m_val = 1L, maxit = 1L, seed_val = MI_SEED, print_flag = TRUE),
      error = function(e) e
    ),
    context = make_context(
      stage = "MI",
      component = "mice_smoketest",
      analysis_variant = "mi",
      model_type = "mice",
      group = NA_character_,
      outcome = NA_character_,
      imputation = NA_integer_,
      batch = NA_integer_
    )
  )
  append_warnings(cap_smoke$warnings)
  sink(type = "output")
  close(smoke_con)

  if (inherits(cap_smoke$value, "error")) {
    smoke_msg <- conditionMessage(cap_smoke$value)
    message("MICE smoke test failed: ", smoke_msg)
    write_smoke_log(c(
      "Smoke test failed.",
      paste0("Error: ", smoke_msg)
    ))
    if (grepl("vector memory limit", smoke_msg, fixed = TRUE)) {
      MI_DEBUG_PRINTFAG <- TRUE
    }
    if (subset_data_saved) {
      subset_data <- readRDS(subset_data_path)
    }
  }
}

```

```

}

if (MI_DEBUG_PRINTFLAG) {
  debug_path <- results_path("mice_debug_print.txt")
  dbg_con <- file(debug_path, open = "wt")
  sink(dbg_con, type = "output")
  message("Debug MI: running m=1, maxit=1 with printFlag=TRUE.")
  tryCatch(
    run_mice_call(m_val = 1L, maxit = 1L, seed_val = MI_SEED, print_flag = TRUE),
    error = function(e) e
  )
  sink(type = "output")
  close(dbg_con)
}
stop("MICE smoke test failed; see ", mi_smoke_log_path, " and Results/mice_debug_print.txt.")
} else {
  message("MICE smoke test succeeded (m=1, maxit=1).")
}
}

get_vcells_stats <- function() {
  g <- gc()
  cn <- colnames(g)
  mb_cols <- cn[grep("\\\\(Mb\\\\)", cn)]
  used_mb_col <- if (length(mb_cols)) mb_cols[1] else NA_character_
  limit_col <- cn[grep("limit", cn, ignore.case = TRUE)]
  limit_col <- if (length(limit_col)) limit_col[1] else NA_character_
  trig_col <- cn[grep("trigger", cn, ignore.case = TRUE)]
  trig_col <- if (length(trig_col)) trig_col[1] else NA_character_
  max_col <- cn[grep("max", cn, ignore.case = TRUE)]
  max_col <- if (length(max_col)) max_col[1] else NA_character_

  used_mb <- if (!is.na(used_mb_col)) as.numeric(g["Vcells", used_mb_col]) else NA_real_
  limit_mb <- if (!is.na(limit_col)) as.numeric(g["Vcells", limit_col]) else NA_real_
  trig_mb <- if (!is.na(trig_col)) as.numeric(g["Vcells", trig_col]) else NA_real_
  max_mb <- if (!is.na(max_col)) as.numeric(g["Vcells", max_col]) else NA_real_
}

```

```

if (!is.finite(limit_mb) || limit_mb <= 0) {
  mem_lim <- tryCatch(mem.maxVSize(), error = function(e) NA_real_)
  if (is.finite(mem_lim) && mem_lim > 0) {
    limit_mb <- if (mem_lim < 1e8) mem_lim else mem_lim / 1024^2
  }
}

data.frame(
  gc_vcells_used_mb = used_mb,
  gc_vcells_limit_mb = limit_mb,
  gc_vcells_frac = ifelse(is.finite(limit_mb) && limit_mb > 0, used_mb / limit_mb, NA_real_),
  gc_vcells_trigger_mb = trig_mb,
  gc_vcells_max_used_mb = max_mb,
  stringsAsFactors = FALSE
)
}

set.seed(MI_SEED)
run_mice_single <- function(m_val) {
  runtime_logger(
    "mice_imputation",
    run_mice_call(m_val = m_val, maxit = MAXIT_RUN, seed_val = MI_SEED, print_flag = FALSE),
    notes = paste0("m=", m_val, "; maxit=", MAXIT_RUN)
  )
}

mc_progress <- list()
sentinel_specs <- list(
  list(name = "abg_imv", outcome = "imv_proc", treat = "has_abg", co2_var = "paco2",
       low = ABG_CO2_LOW, high = ABG_CO2_HIGH),
  list(name = "vbg_imv", outcome = "imv_proc", treat = "has_vbg", co2_var = "vbg_co2",
       low = VBG_CO2_LOW, high = VBG_CO2_HIGH)
)

mcerr_ratio_for_spec <- function(imp_obj, spec) {
  fits <- lapply(seq_len(imp_obj$m), function(i) {

```

```

d <- mice::complete(imp_obj, action = i)
d <- d[, c(spec$outcome, spec$treat, spec$co2_var), drop = FALSE]
d <- d[d[[spec$treat]] == 1 & is.finite(d[[spec$co2_var]]), , drop = FALSE]
if (nrow(d) == 0L) return(NULL)
d$co2_cat <- make_co2_cat3(d[[spec$co2_var]], spec$low, spec$high)
d$co2_cat <- stats::relevel(base::droplevels(d$co2_cat), ref = "Normal")
if (dplyr::n_distinct(d[[spec$outcome]]) < 2L) return(NULL)
fit <- tryCatch(
  stats::glm(stats::reformulate("co2_cat", response = spec$outcome),
             data = d, family = binomial(), x = FALSE, y = FALSE, model = FALSE),
  error = function(e) NULL
)
if (is.null(fit)) return(NULL)
list(coef = stats::coef(fit), vcov = stats::vcov(fit))
})
fits <- fits[!vapply(fits, is.null, logical(1))]
if (length(fits) < 2L) return(NA_real_)
results <- lapply(fits, `[[`, "coef")
variances <- lapply(fits, `[[`, "vcov")
pooled <- mitools::MIcombine(results = results, variances = variances)
est <- as.numeric(stats::coef(pooled))
names(est) <- names(stats::coef(pooled))
se <- sqrt(diag(pooled$variance))
names(se) <- names(stats::coef(pooled))
coef_mat <- do.call(cbind, lapply(results, function(v) v[names(est)]))
B <- apply(coef_mat, 1, stats::var, na.rm = TRUE)
mcerr <- sqrt(B / length(results))
ratio <- mcerr / se
idx <- grep("co2_cat", names(ratio))
if (!any(idx)) return(max(ratio, na.rm = TRUE))
max(ratio[idx], na.rm = TRUE)
}

run_mice_batched <- function(m_total, m_batch_start, maxit, base_seed) {
  imp_acc <- NULL
  m_done <- 0L
}

```

```

batch_attempt_idx <- 0L
m_batch <- m_batch_start
batch_log <- list()
logged_events_acc <- list()

while (m_done < m_total) {
  if (MI_GC_EVERY_BATCH) invisible(gc())
  mem_stats <- get_vcells_stats()
  if (MI_PREEMPTIVE_BATCH_REDUCE &&
      is.finite(mem_stats$gc_vcells_frac) &&
      mem_stats$gc_vcells_frac > MI_VCELLS_FRAC_THRESHOLD &&
      m_batch > MI_BATCH_MIN) {
    m_batch <- max(MI_BATCH_MIN, floor(m_batch / 2))
    message("Preemptively reducing MI batch size to ", m_batch,
           " (Vcells pressure: ", round(mem_stats$gc_vcells_frac, 2), ".)")
  }

  m_b <- min(m_batch, m_total - m_done)
  batch_attempt_idx <- batch_attempt_idx + 1L
  seed_b <- base_seed + batch_attempt_idx * MI_BATCH_SEED_STRIDE
  message("MICE batch ", batch_attempt_idx, " (m=", m_b, ", seed=", seed_b, ")")

  t0 <- Sys.time()
  mem_pre <- get_vcells_stats()
  cap <- capture_warnings(
    tryCatch(
      runtime_logger(
        paste0("mice_batch_", batch_attempt_idx),
        mice::mice(
          data = mi_df_run,
          m = m_b,
          maxit = maxit,
          predictorMatrix = pred,
          method = meth,
          printFlag = FALSE,
          seed = seed_b

```

```

),
notes = paste0("batch=", batch_attempt_idx, "; m=", m_b, "; maxit=", maxit)
),
error = function(e) e
),
context = make_context(
  stage = "MI",
  component = "mice_batch",
  analysis_variant = "mi",
  model_type = "mice",
  group = NA_character_,
  outcome = NA_character_,
  imputation = NA_integer_,
  batch = batch_attempt_idx
)
)
append_warnings(cap$warnings)

imp_b <- cap$value
if (inherits(imp_b, "error")) {
  err_msg <- conditionMessage(imp_b)
  message("MICE batch ", batch_attempt_idx, " failed: ", err_msg)
  mem_stats <- get_vcells_stats()
  batch_log[[batch_attempt_idx]] <- data.frame(
    batch = batch_attempt_idx,
    m_batch = m_b,
    seed = seed_b,
    ok = FALSE,
    error_message = err_msg,
    seconds = as.numeric(difftime(Sys.time(), t0, units = "secs")),
    gc_vcells_used_mb_pre = mem_pre$gc_vcells_used_mb,
    gc_vcells_limit_mb_pre = mem_pre$gc_vcells_limit_mb,
    gc_vcells_frac_pre = mem_pre$gc_vcells_frac,
    gc_vcells_used_mb_post = mem_stats$gc_vcells_used_mb,
    gc_vcells_limit_mb_post = mem_stats$gc_vcells_limit_mb,
    gc_vcells_frac_post = mem_stats$gc_vcells_frac,

```

```

    stringsAsFactors = FALSE
)
if (grepl("vector memory limit", err_msg, fixed = TRUE) && m_batch > MI_BATCH_MIN) {
  m_batch <- max(MI_BATCH_MIN, floor(m_batch / 2))
  message("Reducing MI batch size to ", m_batch, " and retrying.")
  invisible(gc())
  next
}
write_csv_safely(dplyr::bind_rows(batch_log), results_path("mice_batches_log.csv"), row_names = FALSE)
stop("MICE batch ", batch_attempt_idx, " failed; see log: ", results_path("mice_batches_log.csv"))
}

if (is.null(imp_acc)) {
  imp_acc <- imp_b
} else {
  imp_acc <- mice::ibind(imp_acc, imp_b)
}

le_b <- imp_b$loggedEvents
le_b <- if (is.null(le_b)) data.frame() else as.data.frame(le_b)
if (NROW(le_b) > 0) {
  le_b <- le_b |>
    dplyr::mutate(
      batch = batch_attempt_idx,
      seed = seed_b,
      m_global_start = m_done + 1L
    )
  logged_events_acc[[length(logged_events_acc) + 1L]] <- le_b
}

m_done <- imp_acc$m
mem_stats <- get_vcells_stats()
batch_log[[batch_attempt_idx]] <- data.frame(
  batch = batch_attempt_idx,
  m_batch = m_b,
  seed = seed_b,

```

```

ok = TRUE,
error_message = NA_character_,
seconds = as.numeric(difftime(Sys.time(), t0, units = "secs")),
gc_vcells_used_mb_pre = mem_pre$gc_vcells_used_mb,
gc_vcells_limit_mb_pre = mem_pre$gc_vcells_limit_mb,
gc_vcells_frac_pre = mem_pre$gc_vcells_frac,
gc_vcells_used_mb_post = mem_stats$gc_vcells_used_mb,
gc_vcells_limit_mb_post = mem_stats$gc_vcells_limit_mb,
gc_vcells_frac_post = mem_stats$gc_vcells_frac,
stringsAsFactors = FALSE
)
rm(imp_b)
if (MI_GC_EVERY_BATCH) invisible(gc())

if (ALLOW_M_IMP_EARLY_STOP &&
  m_done >= M_IMP_MIN &&
  (m_done %% M_IMP_STEP == 0 || m_done == m_total)) {
  ratios <- vapply(sentinel_specs, function(s) mcerr_ratio_for_spec(imp_acc, s), numeric(1))
  mc_progress[[length(mc_progress) + 1L]] <- data.frame(
    m = m_done,
    abg_ratio = ratios[["abg_imv"]],
    vbg_ratio = ratios[["vbg_imv"]],
    max_ratio = max(ratios, na.rm = TRUE),
    stringsAsFactors = FALSE
  )
  write_csv_safely(dplyr::bind_rows(mc_progress),
                  results_path("mi_mcerr_progress.csv"),
                  row_names = FALSE)
  if (all(is.finite(ratios)) && max(ratios, na.rm = TRUE) <= MCERR_RATIO_TARGET) {
    message("MC error criterion met at m=", m_done,
           " (max MCerr/SE=", round(max(ratios, na.rm = TRUE), 3), "). Stopping early.")
    break
  }
}
}

```

```

write_csv_safely(dplyr::bind_rows(batch_log), results_path("mice_batches_log.csv"), row_names = FALSE)
log_events_raw_batched <- dplyr::bind_rows(logged_events_acc)
attr(imp_acc, "logged_events_batched") <- log_events_raw_batched
imp_acc
}

imp <- NULL
use_batched <- isTRUE(FORCE_MI_BATCHED)
if (!use_batched) {
  cap_mice <- capture_warnings(
    tryCatch(run_mice_single(M_IMP_RUN), error = function(e) e),
    context = make_context(
      stage = "MI",
      component = "mice",
      analysis_variant = "mi",
      model_type = "mice",
      group = NA_character_,
      outcome = NA_character_,
      imputation = NA_integer_,
      batch = NA_integer_
    )
  )
  append_warnings(cap_mice$warnings)
  imp <- cap_mice$value
  if (inherits(imp, "error") && grepl("vector memory limit", conditionMessage(imp), fixed = TRUE)) {
    message("MICE memory limit hit; switching to batched mode.")
    use_batched <- TRUE
  }
}
if (use_batched) {
  message("MICE: running in batches (start=", MI_BATCH_START, ").")
  imp <- run_mice_batched(M_IMP_RUN, MI_BATCH_START, MAXIT_RUN, MI_SEED)
} else {
  write_csv_safely(data.frame(), results_path("mice_batches_log.csv"), row_names = FALSE)
}

```

```

if (inherits(imp, "error")) stop(imp)
stopifnot(inherits(imp, "mids"))
if (ALLOW_M_IMP_EARLY_STOP && imp$m < M_IMP_RUN) {
  message("Early stop: stopping at m=", imp$m, " (target ", M_IMP_RUN, ").")
  M_IMP_RUN <- imp$m
} else {
  stopifnot(imp$m == M_IMP_RUN)
}
if (M_IMP != M_IMP_RUN) M_IMP <- M_IMP_RUN
if (MAXIT_MI != MAXIT_RUN) MAXIT_MI <- MAXIT_RUN
write_csv_safely(dplyr::bind_rows(mc_progress), results_path("mi_mcerr_progress.csv"), row_names = FALSE)
saveRDS(imp, file = mi_mids_file)

# Save MICE spec for reproducibility
saveRDS(
  list(method = imp$method, predictorMatrix = imp$predictorMatrix),
  results_path("mice_spec.rds")
)
if (use_batched) {
  message("Multiple imputation was run in batches and combined via mice::ibind().")
}
if (subset_data_saved) {
  subset_data <- readRDS(subset_data_path)
}

# Logged events: raw + summary (by dep/out/meth)
log_events_raw <- as.data.frame(imp$loggedEvents)
log_events_batched <- as.data.frame(attr(imp, "logged_events_batched"))
log_events_raw <- dplyr::bind_rows(log_events_raw, log_events_batched)

if (nrow(log_events_raw)) {
  write_csv_safely(log_events_raw, results_path("mice_logged_events_raw.csv"), row_names = FALSE,
                  required_cols = c("dep", "out", "meth"))
  log_events_summary <- log_events_raw |>
    dplyr::count(dep, out, meth, name = "n") |>
    dplyr::mutate(variable = dep) |>

```

```

dplyr::arrange(dplyr::desc(n)) |>
  dplyr::mutate(pct = n / sum(n))
  write_csv_safely(log_events_summary, results_path("mice_logged_events_summary.csv"), row_names = FALSE,
                  required_cols = c("variable", "n", "pct"))
} else {
  log_events_raw_empty <- data.frame(
    dep = character(), out = character(), meth = character(),
    stringsAsFactors = FALSE
  )
  log_events_summary_empty <- data.frame(
    variable = character(), n = integer(), pct = numeric(),
    stringsAsFactors = FALSE
  )
  write_csv_safely(log_events_raw_empty, results_path("mice_logged_events_raw.csv"), row_names = FALSE,
                  required_cols = c("dep", "out", "meth"))
  write_csv_safely(log_events_summary_empty, results_path("mice_logged_events_summary.csv"), row_names = FALSE,
                  required_cols = c("variable", "n", "pct"))
  log_events_summary <- log_events_summary_empty
}
if (nrow(mi_info_log)) {
  warns_events <- mi_info_log |>
    dplyr::filter(stage == "MI", component %in% c("mice", "mice_batch"))
  if (nrow(warns_events) && nrow(log_events_raw) == 0L) {
    warning("Mismatch: main MI run reported logged events but loggedEvents table is empty; ",
            "check batch capture and loggedEvents exports.", call. = FALSE)
  }
}

# Chain diagnostics (lightweight; no complete("long"))
chain_diag <- data.frame()
chain_diag_stats <- list(
  n_imputed_vars = 0L,
  n_with_chainMean = 0L,
  n_with_drift_tail = 0L,
  drift_tail_na_frac = NA_real_,
  tail_window_na_mean = NA_real_

```

```

)
stopifnot(!is.null(imp$method))
impute_vars <- names(imp$method)[imp$method != ""]
impute_vars <- intersect(impute_vars, names(imp$data))
if (length(impute_vars)) {
  impute_vars <- impute_vars[vapply(imp$data[impute_vars], function(x) any(is.na(x)), logical(1))]
}
stopifnot(!is.null(imp$chainMean))
{
  cm <- imp$chainMean
  dims <- dim(cm)
  dn <- dimnames(cm)
  iter_candidates <- unique(c(imp$iteration, MAXIT_MI, MAXIT_MI + 1L))
  iter_candidates <- iter_candidates[is.finite(iter_candidates) & iter_candidates > 0]
  imp_m <- imp$m

  extract_chain_mean <- function(cm_obj, dims_obj, dn_obj, imp_m_val, iter_cand) {
    mean_chain <- NULL
    var_names <- NULL
    iter_dim <- NA_integer_
    var_dim <- NA_integer_
    m_dim <- NA_integer_
    if (!is.null(dims_obj) && length(dims_obj) == 2) {
      iter_dim <- which(dims_obj %in% iter_cand)[1]
      if (length(iter_dim) == 0) iter_dim <- 1L
      var_dim <- setdiff(seq_along(dims_obj), iter_dim)[1]
      mean_chain <- cm_obj
      if (iter_dim == 2L) mean_chain <- t(mean_chain)
    } else if (!is.null(dims_obj) && length(dims_obj) == 3) {
      m_dim <- which(dims_obj == imp_m_val)
      if (length(m_dim)) {
        m_dim <- m_dim[1]
      } else {
        m_dim <- 3L
      }
      iter_dim <- setdiff(which(dims_obj %in% iter_cand), m_dim)[1]
    }
  }
}

```

```

if (length(iter_dim) == 0) iter_dim <- setdiff(1:3, c(m_dim, NA_integer_))[1]
var_dim <- setdiff(1:3, c(iter_dim, m_dim))[1]
if (all(is.finite(c(iter_dim, var_dim, m_dim)))) {
  cm_std <- aperm(cm_obj, c(iter_dim, var_dim, m_dim))
  mean_chain <- apply(cm_std, c(1, 2), mean, na.rm = TRUE)
  if (!is.null(dimnames(cm_std))) {
    if (!is.null(dimnames(cm_std)[[2]])) {
      var_names <- dimnames(cm_std)[[2]]
    }
    if (!is.null(dimnames(cm_std)[[1]])) {
      rownames(mean_chain) <- dimnames(cm_std)[[1]]
    }
  }
}
if (is.null(mean_chain)) {
  return(list(mean_chain = NULL, var_names = NULL, iter_dim = iter_dim, var_dim = var_dim, m_dim = m_dim))
}
if (is.null(var_names) && !is.null(dn_obj) && length(dn_obj) >= var_dim) {
  var_names <- dn_obj[[var_dim]]
}
if (is.null(var_names)) {
  var_names <- colnames(mean_chain)
}
list(mean_chain = mean_chain, var_names = var_names, iter_dim = iter_dim, var_dim = var_dim, m_dim = m_dim)
}

res_chain <- extract_chain_mean(cm, dims, dn, imp_m, iter_candidates)
mean_chain <- res_chain$mean_chain
var_names <- res_chain$var_names
if (is.null(mean_chain)) {
  stop("Chain diagnostics: unable to construct mean_chain from imp$chainMean.")
}
{
  iter_idx <- seq_len(nrow(mean_chain))

```

```

numeric_names <- !is.null(var_names) && all(grepl("^\\d+$", var_names))
if (is.null(var_names) || numeric_names) {
  if (length(impute_vars) && length(impute_vars) == ncol(mean_chain)) {
    var_names <- impute_vars
    numeric_names <- FALSE
  }
}
if (is.null(var_names)) {
  stop("Chain diagnostics: variable names missing and could not be matched to imp$method.")
}
colnames(mean_chain) <- var_names

if (numeric_names) {
  warn_df <- data.frame(
    time = as.character(Sys.time()),
    stage = "MI",
    component = "chain_diagnostics",
    analysis_variant = NA_character_,
    model_type = NA_character_,
    group = NA_character_,
    outcome = NA_character_,
    imputation = NA_integer_,
    batch = NA_integer_,
    message = "Chain diagnostics variable name mapping failed; using numeric/fallback names.",
    stringsAsFactors = FALSE
  )
  append_warnings(warn_df)
}

vars_imputed <- impute_vars
chain_diag_stats$n_imputed_vars <- length(vars_imputed)
keep_vars <- intersect(vars_imputed, var_names)
missing_in_chain <- setdiff(vars_imputed, var_names)
if (length(missing_in_chain)) {
  missing_df <- data.frame(
    variable = missing_in_chain,

```

```

        stringsAsFactors = FALSE
    )
    write_csv_safely(missing_df, results_path("mice_chain_diagnostics_missing_vars.csv"), row_names = FALSE)
}
if (length(vars_imputed) && length(keep_vars) == 0L) {
  warn_df <- data.frame(
    time = as.character(Sys.time()),
    stage = "MI",
    component = "chain_diagnostics",
    analysis_variant = NA_character_,
    model_type = NA_character_,
    group = NA_character_,
    outcome = NA_character_,
    imputation = NA_integer_,
    batch = NA_integer_,
    message = "Chain diagnostics: no imputed variables matched chainMean names; skipping drift metrics.",
    stringsAsFactors = FALSE
  )
  append_warnings(warn_df)
  mean_chain <- mean_chain[, 0, drop = FALSE]
  var_names <- character()
} else if (length(keep_vars)) {
  mean_chain <- mean_chain[, keep_vars, drop = FALSE]
  var_names <- keep_vars
}

safe_sd <- function(x) if (sum(is.finite(x)) < 2) NA_real_ else stats::sd(x, na.rm = TRUE)
safe_maxdiff <- function(x) {
  x <- x[is.finite(x)]
  if (length(x) < 2) return(NA_real_)
  max(abs(diff(x)))
}
safe_slope <- function(x, iter) {
  ok <- is.finite(x)
  if (sum(ok) < 2) return(NA_real_)
  coef(stats::lm(x[ok] ~ iter[ok]))[2]
}

```

```

}

tail_finite <- function(x, k) tail(x[is.finite(x)], k)
safe_maxdiff_tail <- function(x, k) {
  xf <- tail_finite(x, k)
  if (length(xf) < 2) return(NA_real_)
  max(abs(diff(xf)))
}

n_vars <- ncol(mean_chain)
n_finite <- integer(n_vars)
drift_all <- numeric(n_vars)
drift_tail <- numeric(n_vars)
tail_n_finite <- integer(n_vars)
tail_window_na_frac <- numeric(n_vars)
slope <- numeric(n_vars)
sd_chain <- numeric(n_vars)
overall_reason <- character(n_vars)
tail_reason <- character(n_vars)
flag_reason <- character(n_vars)
flag <- logical(n_vars)
diagnostic_available <- logical(n_vars)
sd_obs <- rep(NA_real_, n_vars)

chain_src_df <- mi_df_run
stopifnot(is.data.frame(chain_src_df))
sd_obs <- vapply(var_names, function(v) {
  stopifnot(v %in% names(chain_src_df))
  x <- chain_src_df[[v]]
  if (inherits(x, "haven_labelled")) x <- suppressWarnings(as.numeric(x))
  if (!is.numeric(x)) return(NA_real_)
  safe_sd(x)
}, numeric(1))

for (j in seq_len(n_vars)) {
  x <- mean_chain[, j]
  n_finite[j] <- sum(is.finite(x))
}

```

```

drift_all[j] <- safe_maxdiff(x)
slope[j] <- safe_slope(x, iter_idx)
sd_chain[j] <- safe_sd(x)
tail_vals <- tail_finite(x, TAIL_NFINITE)
tail_n_finite[j] <- length(tail_vals)
drift_tail[j] <- safe_maxdiff_tail(x, TAIL_NFINITE)
tail_window <- tail(x, min(TAIL_WINDOW_ITERS, length(x)))
tail_window_na_frac[j] <- mean(!is.finite(tail_window))
overall_reason[j] <- if (n_finite[j] >= 2) "ok" else "insufficient_finite_overall"
tail_reason[j] <- if (tail_n_finite[j] >= 2) "ok" else "insufficient_finite_tail"
}

drift_all_scaled <- drift_all / sd_obs
drift_tail_scaled <- drift_tail / sd_obs
slope_scaled <- slope / sd_obs

for (j in seq_len(n_vars)) {
  if (!is.finite(sd_obs[j]) || sd_obs[j] <= 0) {
    flag[j] <- NA
    flag_reason[j] <- "missing_scale"
    diagnostic_available[j] <- FALSE
    next
  }
  if (tail_n_finite[j] < 2) {
    flag[j] <- NA
    flag_reason[j] <- "tail_insufficient"
    diagnostic_available[j] <- FALSE
    next
  }
  if (!is.finite(drift_tail_scaled[j]) || !is.finite(slope_scaled[j])) {
    flag[j] <- NA
    flag_reason[j] <- "insufficient_data"
    diagnostic_available[j] <- FALSE
    next
  }
  flag_tail <- drift_tail_scaled[j] > 0.01
}

```

```

flag_slope <- abs(slope_scaled[j]) > 0.001
flag[j] <- flag_tail | flag_slope
flag_reason[j] <- if (flag_tail & flag_slope) {
  "both"
} else if (flag_tail) {
  "tail_drift"
} else if (flag_slope) {
  "slope"
} else {
  "none"
}
diagnostic_available[j] <- TRUE
}

chain_diag <- data.frame(
  variable = var_names,
  method = imp$method[var_names],
  n_finite = n_finite,
  drift_all = drift_all,
  drift_tail = drift_tail,
  drift_all_scaled = drift_all_scaled,
  drift_tail_scaled = drift_tail_scaled,
  tail_n_finite = tail_n_finite,
  tail_window_na_frac = tail_window_na_frac,
  slope = slope,
  slope_scaled = slope_scaled,
  sd_chain = sd_chain,
  sd_obs = sd_obs,
  overall_reason = overall_reason,
  tail_reason = tail_reason,
  flag_reason = flag_reason,
  diagnostic_available = diagnostic_available,
  flag = flag,
  stringsAsFactors = FALSE
)

```

```

chain_diag_stats$n_with_chainMean <- nrow(chain_diag)
chain_diag_stats$n_with_drift_tail <- sum(is.finite(chain_diag$drift_tail))
if (chain_diag_stats$n_with_chainMean > 0) {
  chain_diag_stats$drift_tail_na_frac <- 1 - (chain_diag_stats$n_with_drift_tail /
                                                 chain_diag_stats$n_with_chainMean)
  chain_diag_stats$tail_window_na_mean <- mean(chain_diag$tail_window_na_frac, na.rm = TRUE)
}
write_csv_safely(chain_diag, results_path("mice_chain_diagnostics.csv"), row.names = FALSE)
if (any(isTRUE(chain_diag$flag), na.rm = TRUE)) {
  frac_flag <- mean(chain_diag$flag, na.rm = TRUE)
  if (is.finite(frac_flag) && frac_flag < 0.05) {
    message("Chain diagnostics: low drift flags (", round(frac_flag * 100, 1),
           "%). MAXIT_MI may be reduced safely (consider 10 or 5).")
  }
}
}

# quick sanity: these must exist and be numeric in completed data
imp_n <- imp$m
get_imp_stats <- list(count = 0L, seconds = 0)
get_imp <- function(i, imp_obj = imp) {
  t0 <- Sys.time()
  d <- normalize_types(mice:::complete(imp_obj, action = i), levels_ref)
  get_imp_stats$count <-> get_imp_stats$count + 1L
  get_imp_stats$seconds <-> get_imp_stats$seconds +
    as.numeric(difftime(Sys.time(), t0, units = "secs"))
  d
}
d1 <- get_imp(1)
stopifnot(all(c("paco2", "vbg_co2") %in% names(d1)))
stopifnot(is.numeric(d1$paco2), is.numeric(d1$vbg_co2))

# post-MICE sanity: no remaining NA in covars_ps
covars_check <- intersect(covars_ps, names(d1))
na_counts <- vapply(d1[, covars_check, drop = FALSE], function(x) sum(is.na(x)), numeric(1))

```

```

na_counts <- na_counts[na_counts > 0]
if (length(na_counts)) {
  message("Post-MICE NA counts (covars_ps): ",
         paste(names(na_counts), na_counts, collapse = ", "))
  ev_sum <- summarize_logged_events(imp)
  if (nrow(ev_sum)) {
    ev_sub <- ev_sum[ev_sum$variable %in% names(na_counts), , drop = FALSE]
    if (nrow(ev_sub)) {
      print(utils::head(ev_sub, 10))
    } else {
      message("No loggedEvents entries for covars_ps with NA.")
    }
  } else {
    message("No loggedEvents recorded.")
  }
  stop("Post-MICE check failed: remaining NA in covars_ps. See loggedEvents summary above.")
}

```

```

stopifnot(exists("imp"))

# Representative logistic model (unweighted) to assess Monte Carlo error
mc_diag_fml <- imv_proc ~ has_abg + age_at_encounter + curr_bmi + sex + encounter_type
register_model_diagram("MI MC error: IMV ~ ABG + covariates", mc_diag_fml, width = 10, height = 6)
cap_mc <- capture_warnings(
  tryCatch(
    with(
      imp,
      glm(imv_proc ~ has_abg + age_at_encounter + curr_bmi + sex + encounter_type,
           family = binomial(), x = FALSE, y = FALSE, model = FALSE)
    ),
    error = function(e) e
  ),
  context = make_context(
    stage = "diagnostics",
    component = "mi_mcerror_glm",
    analysis_variant = "mi",
  )
)

```

```

model_type = "glm",
group = NA_character_,
outcome = "imv_proc",
imputation = NA_integer_,
batch = NA_integer_
)
)
append_warnings(cap_mc$warnings)
mc_fit <- cap_mc$value

use_compact <- inherits(mc_fit, "error")
if (use_compact) {
  message("MC error: fallback to compact per-imputation fits (", conditionMessage(mc_fit), ".)")
}

mc_pool <- NULL
mc_sum <- NULL
mc_results <- NULL
mc_variances <- NULL
if (!use_compact) {
  mc_pool <- pool(mc_fit)
  mc_sum <- summary(mc_pool, conf.int = TRUE)
}

compute_mc_error <- function(mc_pool, mc_fit, m) {
  stopifnot(!is.null(mc_fit$analyses), length(mc_fit$analyses) >= 2)
  coefs <- lapply(mc_fit$analyses, coef)
  common_terms <- Reduce(intersect, lapply(coefs, names))
  stopifnot(length(common_terms) > 0)
  Q <- do.call(cbind, lapply(coefs, function(v) v[common_terms]))
  B <- apply(Q, 1, stats::var, na.rm = TRUE)
  out <- sqrt(B / ncol(Q))
  names(out) <- common_terms
  out
}

```

```

compute_mc_error_from_results <- function(results_list) {
  coefs <- results_list
  common_terms <- Reduce(intersect, lapply(coefs, names))
  if (!length(common_terms)) return(NA_real_)
  Q <- do.call(cbind, lapply(coefs, function(v) v[common_terms]))
  B <- apply(Q, 1, stats::var, na.rm = TRUE)
  out <- sqrt(B / ncol(Q))
  names(out) <- common_terms
  out
}

if (use_compact) {
  mc_terms <- all.vars(mc_diag_fml)
  mc_fit_list <- lapply(seq_len(imp$m), function(i) {
    d <- mice::complete(imp, action = i)
    d <- d[, mc_terms, drop = FALSE]
    cap_i <- capture_warnings(
      tryCatch(
        glm(mc_diag_fml, data = d, family = binomial(), x = FALSE, y = FALSE, model = FALSE),
        error = function(e) e
      ),
      context = make_context(
        stage = "diagnostics",
        component = "mi_mcerror_glm",
        analysis_variant = "mi",
        model_type = "glm",
        group = NA_character_,
        outcome = "imv_proc",
        imputation = i,
        batch = NA_integer_
      )
    )
    append_warnings(cap_i$warnings)
    fit_i <- cap_i$value
    if (inherits(fit_i, "error")) return(list(error = conditionMessage(fit_i)))
    list(coef = coef(fit_i), vcov = vcov(fit_i))
  })
}

```

```

})

ok <- vapply(mc_fit_list, function(x) is.list(x) && is.null(x$error), logical(1))
mc_fit_list <- mc_fit_list[ok]
if (!length(mc_fit_list)) stop("MC error fallback failed: no successful fits.")

mc_results <- lapply(mc_fit_list, function(x) x$coef)
mc_variances <- lapply(mc_fit_list, function(x) x$vcov)

mc_pool <- mitools::MIcombine(results = mc_results, variances = mc_variances)
est <- as.numeric(coef(mc_pool))
se <- sqrt(diag(mc_pool$variance))
mc_sum <- data.frame(
  term = names(coef(mc_pool)),
  estimate = est,
  std.error = se,
  conf.low = est - 1.96 * se,
  conf.high = est + 1.96 * se,
  stringsAsFactors = FALSE
)
}

m_mc <- if (!use_compact && !is.null(mc_fit$analyses)) length(mc_fit$analyses) else imp$m
mc_err_vec <- if (!use_compact) {
  compute_mc_error(mc_pool, mc_fit, m_mc)
} else {
  compute_mc_error_from_results(mc_results)
}

if (is.null(names(mc_err_vec)) || all(names(mc_err_vec) == "")) {
  names(mc_err_vec) <- mc_sum$term[seq_len(min(length(mc_err_vec), nrow(mc_sum)))]
}
mc_err_aligned <- mc_err_vec[mc_sum$term]
if (all(is.na(mc_err_aligned))) {
  message("MC error not computed (all NA). mice version: ", as.character(packageVersion("mice")))
  if (!is.null(mc_pool$pooled)) {

```

```

    message("mc_pool$pooled columns: ", paste(names(mc_pool$pooled), collapse = ", "))
}

stopifnot(all(c("conf.low", "conf.high") %in% names(mc_sum)))

mc_tab <- mc_sum |>
  mutate(
    mc_error = mc_err_aligned,
    mc_err_over_se = mc_error / std.error
  ) |>
  select(term, estimate, std.error, mc_error, mc_err_over_se, conf.low, conf.high)

mc_model_desc <- "Diagnostic model: imv_proc ~ has_abg + age_at_encounter + curr_bmi + sex + encounter_type (unweighted)."
knitr::asis_output(paste0("**MC error diagnostic model:** ", mc_model_desc, "\n"))

```

MC error diagnostic model: Diagnostic model: imv_proc ~ has_abg + age_at_encounter + curr_bmi + sex + encounter_type (unweighted).

```

gt:::gt(mc_tab) |>
  gt:::tab_header(title = "Monte Carlo error vs SE (diagnostic only)") |>
  gt:::cols_label(
    term      = "Term",
    estimate   = "Estimate",
    std.error   = "SE",
    mc_error    = "MC error",
    mc_err_over_se = "MC error / SE",
    conf.low     = "2.5%",
    conf.high    = "97.5%"
  ) |>
  gt:::fmt_number(columns = c(estimate, std.error, mc_error, mc_err_over_se), decimals = 3) |>
  gt:::fmt_missing(columns = gt:::everything(), missing_text = "-")

```

Monte Carlo error vs SE (diagnostic only)

Term	Estimate	SE	MC error	MC error / SE	2.5%	97.5%
(Intercept)	-3.821	0.189	0.014	0.074	-4.19136254	-3.4497745159
has_abg	2.166	0.053	0.001	0.016	2.06223732	2.2704301035
age_at_encounter	-0.003	0.001	0.000	0.014	-0.00596037	-0.0009504728
curr_bmi	-0.009	0.005	0.000	0.086	-0.01787779	0.0001613787
sexMale	0.236	0.043	0.001	0.014	0.15097989	0.3212478672
encounter_typeInpatient	1.044	0.068	0.000	0.005	0.91072250	1.1766322121

```
# QC flag for key estimands only (diagnostic, not pass/fail for all coefficients)
mc_key_terms <- intersect(c("has_abg"), mc_tab$term)
if (length(mc_key_terms)) {
  mc_key <- mc_tab |>
    dplyr::filter(term %in% mc_key_terms) |>
    dplyr::mutate(qc_flag = mc_err_over_se > MC_ERR_RATIO_THRESH)
  render_table_pdf(
    mc_key,
    caption = paste0("MC error QC (key terms only; threshold = ", MC_ERR_RATIO_THRESH, ")"),
    file_stub = "mc_error_qc_key_terms",
    digits = 3
  )
  if (any(mc_key$qc_flag, na.rm = TRUE)) {
    knitr::asis_output(
      paste0(
        "***QC note:** MC error/SE exceeds ",
        MC_ERR_RATIO_THRESH,
        " for at least one key term; consider larger m or report as a limitation."
      )
    )
  }
}
```

```

stopifnot(exists("imp"))
imp_n <- imp$m
get_imp <- function(i, imp_obj = imp) {
  normalize_types(mice::complete(imp_obj, action = i), levels_ref)
}

# Guard against memory blow-up from complete("long")
N <- nrow(imp$data)
M <- imp$m
long_rows <- (M + 1L) * N
LONG_ROWS_MAX <- 2e6
imp_size <- as.numeric(utils::object.size(imp))
if (long_rows > LONG_ROWS_MAX || imp_size > 1e9) {
  message("Skipping mice::densityplot/striplot (mids -> complete('long')) due to size; using memory-safe diagnostics.")
}

get_obs_imp_vectors <- function(imp_obj, var) {
  obs <- imp_obj$data[[var]]
  obs <- obs[!is.na(obs)]
  impv <- imp_obj$imp[[var]]
  stopifnot(!is.null(impv))
  imp_vals <- unlist(impv, use.names = FALSE)
  if (is.numeric(obs)) obs <- obs[is.finite(obs)]
  if (is.numeric(imp_vals)) imp_vals <- imp_vals[is.finite(imp_vals)]
  list(obs = obs, imp = imp_vals)
}

plot_obs_imp <- function(imp_obj, var, fig_dir, n_obs = 50000, n_imp = 50000) {
  vecs <- get_obs_imp_vectors(imp_obj, var)
  obs <- vecs$obs
  imp_vals <- vecs$imp
  stopifnot(length(obs) + length(imp_vals) > 0)

  is_cat <- is.factor(obs) || is.character(obs) ||
    (is.numeric(obs) && length(unique(obs[!is.na(obs)])) <= 5)
}

```

```

if (!is_cat) {
  set.seed(MI_SEED)
  if (length(obs) > n_obs) obs <- sample(obs, n_obs)
  if (length(imp_vals) > n_imp) imp_vals <- sample(imp_vals, n_imp)

  df <- dplyr::tibble(
    value = c(obs, imp_vals),
    status = c(rep("Observed", length(obs)), rep("Imputed", length(imp_vals)))
  )
  p <- ggplot2::ggplot(df, ggplot2::aes(x = value, color = status, fill = status)) +
    ggplot2::geom_density(alpha = 0.2, na.rm = TRUE) +
    ggplot2::theme_minimal(base_size = 10) +
    ggplot2::labs(title = paste("Observed vs imputed:", var), x = NULL, y = "Density")
  out_file <- fs::path(fig_dir, paste0("diag-mi-density-", .make_safe_name(var), ".png"))
  ggplot2::ggsave(out_file, p, width = 7, height = 5, dpi = 200)

  stat_names <- c("mean", "sd", "p10", "p50", "p90", "n")
  obs_stats <- c(
    mean = mean(obs, na.rm = TRUE),
    sd = stats::sd(obs, na.rm = TRUE),
    p10 = stats::quantile(obs, 0.10, na.rm = TRUE),
    p50 = stats::quantile(obs, 0.50, na.rm = TRUE),
    p90 = stats::quantile(obs, 0.90, na.rm = TRUE),
    n = length(obs)
  )
  imp_stats <- c(
    mean = if (length(imp_vals)) mean(imp_vals, na.rm = TRUE) else NA_real_,
    sd = if (length(imp_vals)) stats::sd(imp_vals, na.rm = TRUE) else NA_real_,
    p10 = if (length(imp_vals)) stats::quantile(imp_vals, 0.10, na.rm = TRUE) else NA_real_,
    p50 = if (length(imp_vals)) stats::quantile(imp_vals, 0.50, na.rm = TRUE) else NA_real_,
    p90 = if (length(imp_vals)) stats::quantile(imp_vals, 0.90, na.rm = TRUE) else NA_real_,
    n = length(imp_vals)
  )
  return(dplyr::tibble(
    variable = var,
    type = "numeric",

```

```

    stat = stat_names,
    observed = unname(obs_stats),
    imputed = unname(imp_stats)
  )))
}

obs_chr <- as.character(obs)
imp_chr <- as.character(imp_vals)
levels_all <- sort(unique(c(obs_chr, imp_chr)))
prop_obs <- if (length(obs_chr)) {
  as.numeric(table(factor(obs_chr, levels = levels_all))) / length(obs_chr)
} else {
  rep(0, length(levels_all))
}
prop_imp <- if (length(imp_chr)) {
  as.numeric(table(factor(imp_chr, levels = levels_all))) / length(imp_chr)
} else {
  rep(0, length(levels_all))
}
prop_df <- dplyr::tibble(
  level = levels_all,
  observed = prop_obs,
  imputed = prop_imp
)
miss_plot_df <- tidyr::pivot_longer(prop_df, c(observed, imputed),
                                      names_to = "status", values_to = "prop")
p <- ggplot2::ggplot(miss_plot_df, ggplot2::aes(x = level, y = prop, fill = status)) +
  ggplot2::geom_col(position = "dodge", width = 0.7) +
  ggplot2::theme_minimal(base_size = 10) +
  ggplot2::theme(axis.text.x = ggplot2::element_text(angle = 20, hjust = 1)) +
  ggplot2::labs(title = paste("Observed vs imputed:", var), x = NULL, y = "Proportion")
out_file <- fs::path(fig_dir, paste0("diag-mi-bar-", .make_safe_name(var), ".png"))
ggplot2::ggsave(out_file, p, width = 7, height = 5, dpi = 200)

return(prop_df |>
  tidyr::pivot_longer(c(observed, imputed), names_to = "status", values_to = "prop") |>

```

```

        dplyr::mutate(variable = var, type = "categorical", stat = "prop"))
}

# Throttle diagnostics to avoid memory blow-up
trace_vars <- intersect(c("curr_bmi", "serum_hco3", "hr"), names(imp$imp))
if (length(trace_vars)) {
  trace_list <- lapply(trace_vars, function(v) {
    imp_mat <- imp$imp[[v]]
    stopifnot(!is.null(imp_mat))
    means <- colMeans(imp_mat, na.rm = TRUE)
    dplyr::tibble(variable = v, imputation = seq_along(means), mean_imputed = means)
  })
  trace_df <- dplyr::bind_rows(trace_list)
  if (nrow(trace_df)) {
    p_trace <- ggplot2::ggplot(trace_df, ggplot2::aes(x = imputation, y = mean_imputed)) +
      ggplot2::geom_line() +
      ggplot2::geom_point(size = 0.6) +
      ggplot2::facet_wrap(~variable, scales = "free_y") +
      ggplot2::theme_minimal(base_size = 10) +
      ggplot2::labs(title = "Mean imputed value by imputation", x = "Imputation", y = "Mean")
    print(p_trace)
  }

  vars_show <- trace_vars[seq_len(min(2, length(trace_vars)))]
  dens_list <- lapply(vars_show, function(v) {
    obs <- imp$data[[v]]
    imp1 <- get_imp(1)[[v]]
    obs_vals <- obs[!is.na(obs)]
    imp_vals <- imp1[is.na(obs)]
    if (length(obs_vals) > 5000) obs_vals <- sample(obs_vals, 5000)
    if (length(imp_vals) > 5000) imp_vals <- sample(imp_vals, 5000)
    dplyr::tibble(
      variable = v,
      value = c(obs_vals, imp_vals),
      status = c(rep("Observed", length(obs_vals)),
                rep("Imputed (imp1)", length(imp_vals)))
  })
}

```

```

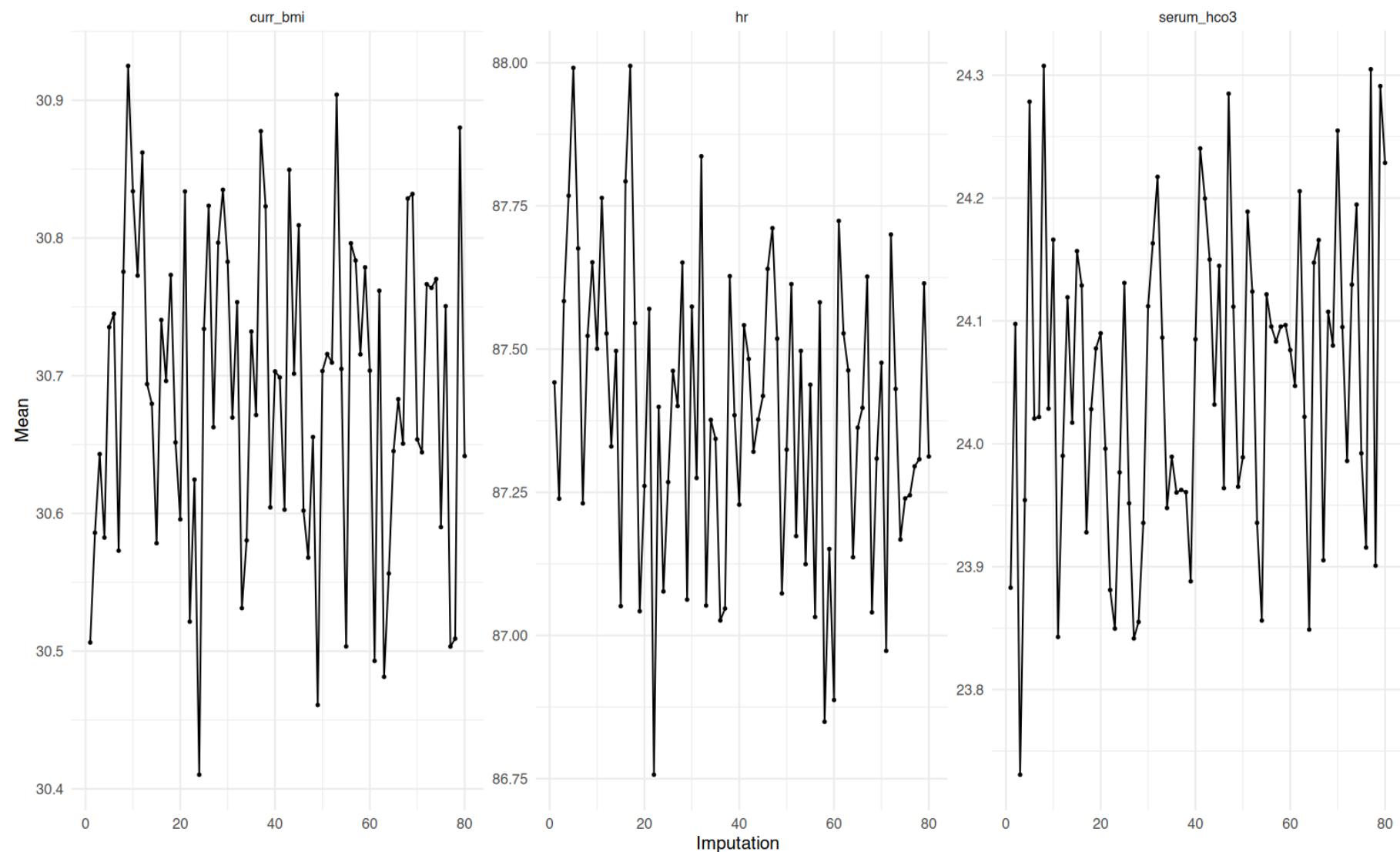
)
})

dens_df <- dplyr::bind_rows(dens_list)
p_dens <- ggplot2::ggplot(dens_df, ggplot2::aes(x = value, color = status, fill = status)) +
  ggplot2::geom_density(alpha = 0.2, na.rm = TRUE) +
  ggplot2::facet_wrap(~variable, scales = "free") +
  ggplot2::theme_minimal(base_size = 10) +
  ggplot2::labs(title = "Observed vs imputed distributions (imp1)", x = NULL, y = "Density")
print(p_dens)

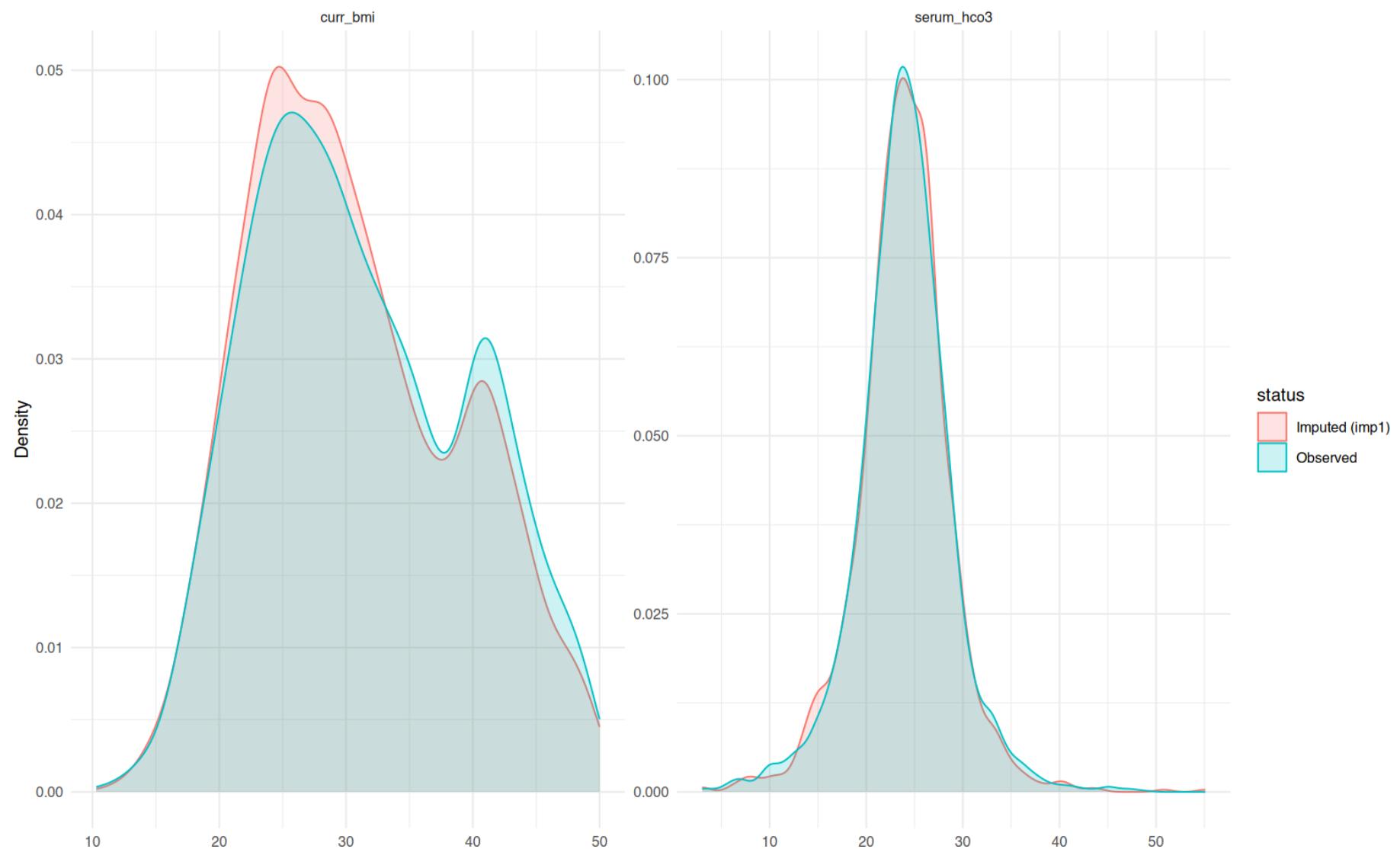
p_box <- ggplot2::ggplot(dens_df, ggplot2::aes(x = status, y = value, fill = status)) +
  ggplot2::geom_boxplot(outlier.size = 0.5, na.rm = TRUE) +
  ggplot2::facet_wrap(~variable, scales = "free") +
  ggplot2::theme_minimal(base_size = 10) +
  ggplot2::theme(axis.text.x = ggplot2::element_text(angle = 20, hjust = 1)) +
  ggplot2::labs(title = "Observed vs imputed (imp1)", x = NULL, y = NULL)
print(p_box)
}

```

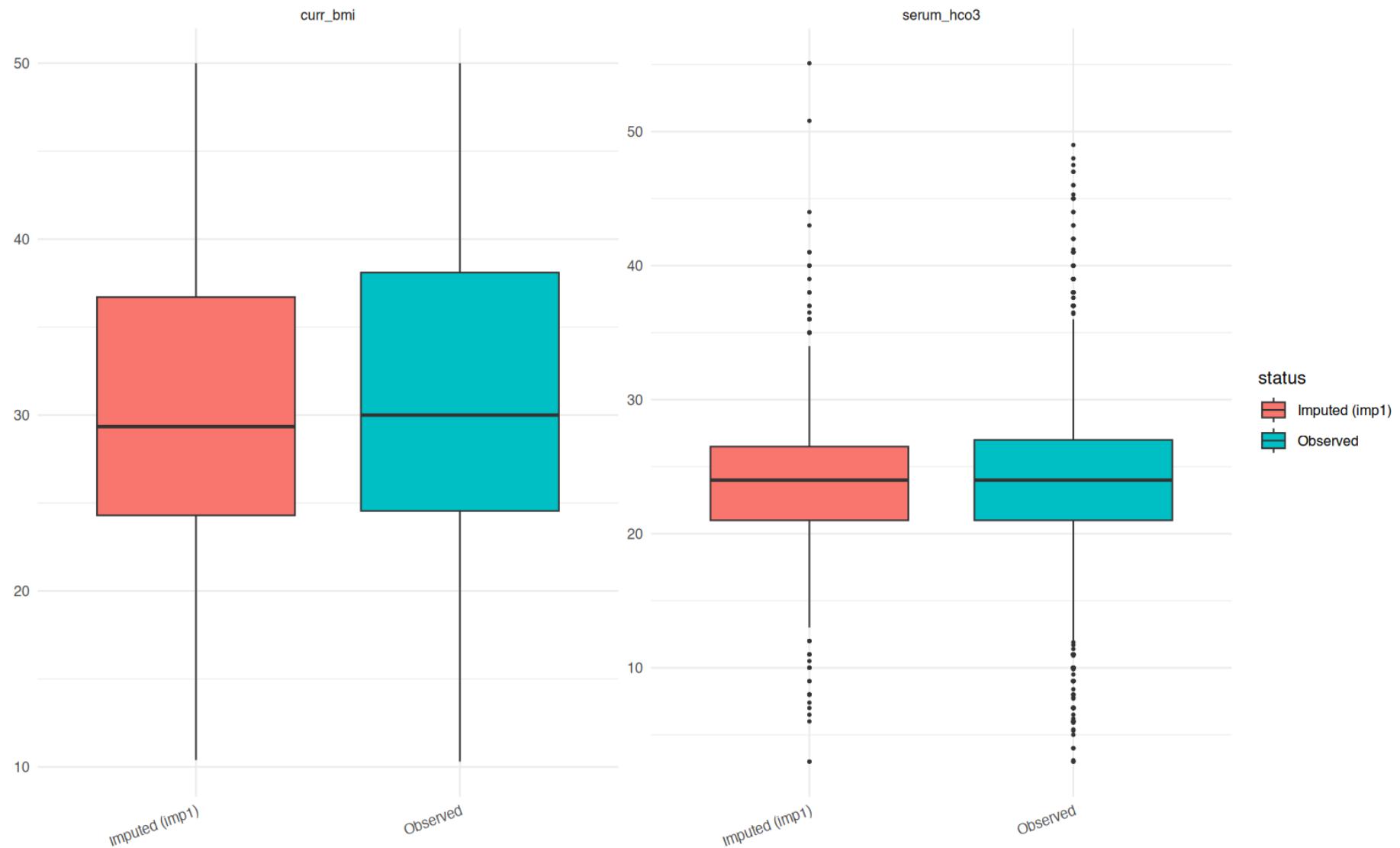
Mean imputed value by imputation



Observed vs imputed distributions (imp1)



Observed vs imputed (imp1)



```
# Observed vs imputed summaries (memory-safe)
diag_vars <- intersect(
  c("age_at_encounter", "curr_bmi", "temp_new", "sbp", "dbp", "hr",
    "sodium", "serum_cr", "serum_hco3", "serum_lac", "wbc", "plt",
```

```

"sex", "race_ethnicity", "location", "encounter_type",
"copd", "asthma", "chf", "dm"),
names(imp$data)
)
diag_vars <- intersect(diag_vars, names(imp$imp))
if (length(diag_vars)) {
  miss_counts <- colSums(is.na(imp$data[diag_vars]))
  diag_vars <- diag_vars[miss_counts > 0]
}

mi_obs_imp_summary <- dplyr::bind_rows(lapply(diag_vars, function(v) {
  out <- plot_obs_imp(imp, v, results_path("figs"))
  invisible(gc())
  out
}))

mi_obs_imp_summary_file <- results_path("mi_obs_vs_imp_summary.csv")
if (nrow(mi_obs_imp_summary)) {
  write_csv_safely(mi_obs_imp_summary, mi_obs_imp_summary_file, row_names = FALSE)
  render_table_pdf(
    mi_obs_imp_summary,
    caption = "Observed vs imputed summaries",
    file_stub = "mi_obs_vs_imp_summary",
    digits = 3
  )
} else {
  mi_obs_imp_stub <- data.frame(
    variable = character(),
    n_obs = numeric(),
    mean_obs = numeric(),
    sd_obs = numeric(),
    mean_imp = numeric(),
    sd_imp = numeric(),
    stringsAsFactors = FALSE
  )
  write_csv_safely(mi_obs_imp_stub, mi_obs_imp_summary_file, row_names = FALSE)
  message("No variables with missingness available for observed vs imputed summaries.")
}

```

{}

Table 12: Observed vs imputed summaries

variable	type	stat	observed	imputed
curr_bmi	numeric	mean	31.286	30.689
curr_bmi	numeric	sd	8.363	8.170
curr_bmi	numeric	p10	21.046	20.810
curr_bmi	numeric	p50	30.000	29.400
curr_bmi	numeric	p90	43.300	42.620
curr_bmi	numeric	n	11129.000	50000.000
temp_new	numeric	mean	97.911	97.951
temp_new	numeric	sd	1.328	1.239
temp_new	numeric	p10	96.812	97.000
temp_new	numeric	p50	98.000	98.000
temp_new	numeric	p90	99.000	99.000
temp_new	numeric	n	13392.000	50000.000
sbp	numeric	mean	128.091	127.246
sbp	numeric	sd	26.449	25.998
sbp	numeric	p10	97.000	97.000
sbp	numeric	p50	127.000	126.000
sbp	numeric	p90	160.500	159.000
sbp	numeric	n	18186.000	50000.000
dbp	numeric	mean	72.568	72.705
dbp	numeric	sd	16.273	15.980
dbp	numeric	p10	53.000	54.000
dbp	numeric	p50	72.000	72.000
dbp	numeric	p90	93.000	92.000
dbp	numeric	n	18114.000	50000.000
hr	numeric	mean	85.773	87.539
hr	numeric	sd	20.436	20.629
hr	numeric	p10	62.000	63.000
hr	numeric	p50	84.000	86.000
hr	numeric	p90	112.000	115.000
hr	numeric	n	16434.000	50000.000
sodium	numeric	mean	137.050	137.511
sodium	numeric	sd	4.721	4.383
sodium	numeric	p10	131.000	132.000
sodium	numeric	p50	138.000	138.000
sodium	numeric	p90	142.000	142.000
sodium	numeric	n	24526.000	50000.000
serum_cr	numeric	mean	1.429	1.321
serum_cr	numeric	sd	1.679	1.513
serum_cr	numeric	p10	0.600	0.600
serum_cr	numeric	p50	0.970	0.930
serum_cr	numeric	p90	2.335	2.080
serum_cr	numeric	n	23456.000	50000.000

Table 12: Observed vs imputed summaries (*continued*)

variable	type	stat	observed	imputed
serum_hco3	numeric	mean	23.979	24.048
serum_hco3	numeric	sd	4.910	4.643
serum_hco3	numeric	p10	18.000	19.000
serum_hco3	numeric	p50	24.000	24.000
serum_hco3	numeric	p90	29.000	29.000
serum_hco3	numeric	n	24392.000	50000.000
serum_lac	numeric	mean	2.216	1.906
serum_lac	numeric	sd	2.282	1.707
serum_lac	numeric	p10	0.800	0.800
serum_lac	numeric	p50	1.600	1.500
serum_lac	numeric	p90	4.000	3.300
serum_lac	numeric	n	10281.000	50000.000
wbc	numeric	mean	10.575	10.478
wbc	numeric	sd	9.149	9.014
wbc	numeric	p10	5.150	5.100
wbc	numeric	p50	9.190	9.100
wbc	numeric	p90	17.000	16.800
wbc	numeric	n	21310.000	50000.000
plt	numeric	mean	243.623	251.437
plt	numeric	sd	104.245	107.621
plt	numeric	p10	129.000	135.000
plt	numeric	p50	231.000	239.000
plt	numeric	p90	367.000	378.000
plt	numeric	n	23772.000	50000.000

```

md_pat <- NULL
invisible(utils::capture.output(
  md_pat <- mice:::md.pattern(imp$data, plot = FALSE)
))

md_pat_file <- results_path("missingness-pattern.csv")
write_csv_safely(md_pat, md_pat_file, row_names = TRUE)

md_fig_file <- results_path("figs", "missingness-pattern.png")
grDevices::png(md_fig_file, width = 1800, height = 1200, res = 200)
mice:::md.pattern(imp$data, plot = TRUE)
grDevices::dev.off()

```

```

stopifnot(exists("imp"))
imp_n <- imp$m
get_imp <- function(i, imp_obj = imp) { normalize_types(mice::complete(imp_obj, action = i), levels_ref) }

# Choose a manageable set of incomplete variables
miss_overall <- naniar::miss_var_summary(subset_data) %>% arrange(desc(pct_miss))
vars_incomplete <- miss_overall$variable[miss_overall$n_miss > 0]
per_imp_n <- min(500, nrow(imp$data))
dat_obs <- imp$data %>%
  dplyr::slice_sample(n = min(per_imp_n, nrow(imp$data))) %>%
  dplyr::mutate(.imp = 0L, .imp_label = "Observed")
dat_imp <- purrr::map_dfr(seq_len(imp_n), function(i) {
  di <- get_imp(i)
  di <- dplyr::slice_sample(di, n = min(per_imp_n, nrow(di)))
  di$.imp <- i
  di$.imp_label <- "Imputed"
  di
})
dat_long <- dplyr::bind_rows(dat_obs, dat_imp)
vars_show <- head(intersect(vars_incomplete, names(dat_long)), 6) # limit for plotting & ensure present in imp

# Density plots by imputation status
if (length(vars_show)) {
  strata_candidates <- intersect(c("has_abg", "has_vbg", "imv_proc", "death_60d"), names(dat_long))
  printed_counts <- FALSE

  for (v in vars_show) {
    if (is.numeric(dat_long[[v]])) {
      df_plot <- dat_long |>
        dplyr::filter(is.finite(.data[[v]]))
      p <- ggplot(df_plot, aes(x = .data[[v]], fill = .imp_label)) +
        geom_density(alpha = 0.4, adjust = 1, na.rm = TRUE) +
        labs(title = paste("Observed vs imputed density:", v), x = v, fill = "Source") +
        theme_minimal()
    } else {
      df_plot <- dat_long |>
    }
  }
}

```

```

dplyr::filter(!is.na(.data[[v]]))
p <- ggplot(df_plot, aes(x = .data[[v]], fill = .imp_label)) +
  geom_bar(position = "fill", na.rm = TRUE) +
  labs(title = paste("Observed vs imputed proportions:", v), x = v, y = "Proportion", fill = "Source") +
  theme_minimal() +
  coord_flip()
}
print(p)
}

# Box/violin plots by strata (numeric vars only)
if (length(strata_candidates)) {
  pd <- position_dodge(width = 0.8)
  for (sv in strata_candidates) {
    for (v in vars_show) {
      if (!is.numeric(dat_long[[v]])) next
      df_plot <- dat_long |>
        dplyr::filter(!is.na(.data[[sv]]), is.finite(.data[[v]])) |>
        dplyr::mutate(strata = factor(.data[[sv]]))
      if (nrow(df_plot) == 0L) next

      if (!printed_counts) {
        invisible(table(strata = df_plot$strata, source = df_plot$imp_label))
        printed_counts <- TRUE
      }

      if (all(levels(df_plot$strata) %in% c("0", "1"))) {
        x_scale <- ggplot2::scale_x_discrete(labels = c("0" = "No", "1" = "Yes"))
      } else {
        x_scale <- ggplot2::scale_x_discrete(drop = FALSE)
      }

      p <- ggplot(df_plot, aes(
        x = .strata,
        y = .data[[v]],
        fill = .imp_label,

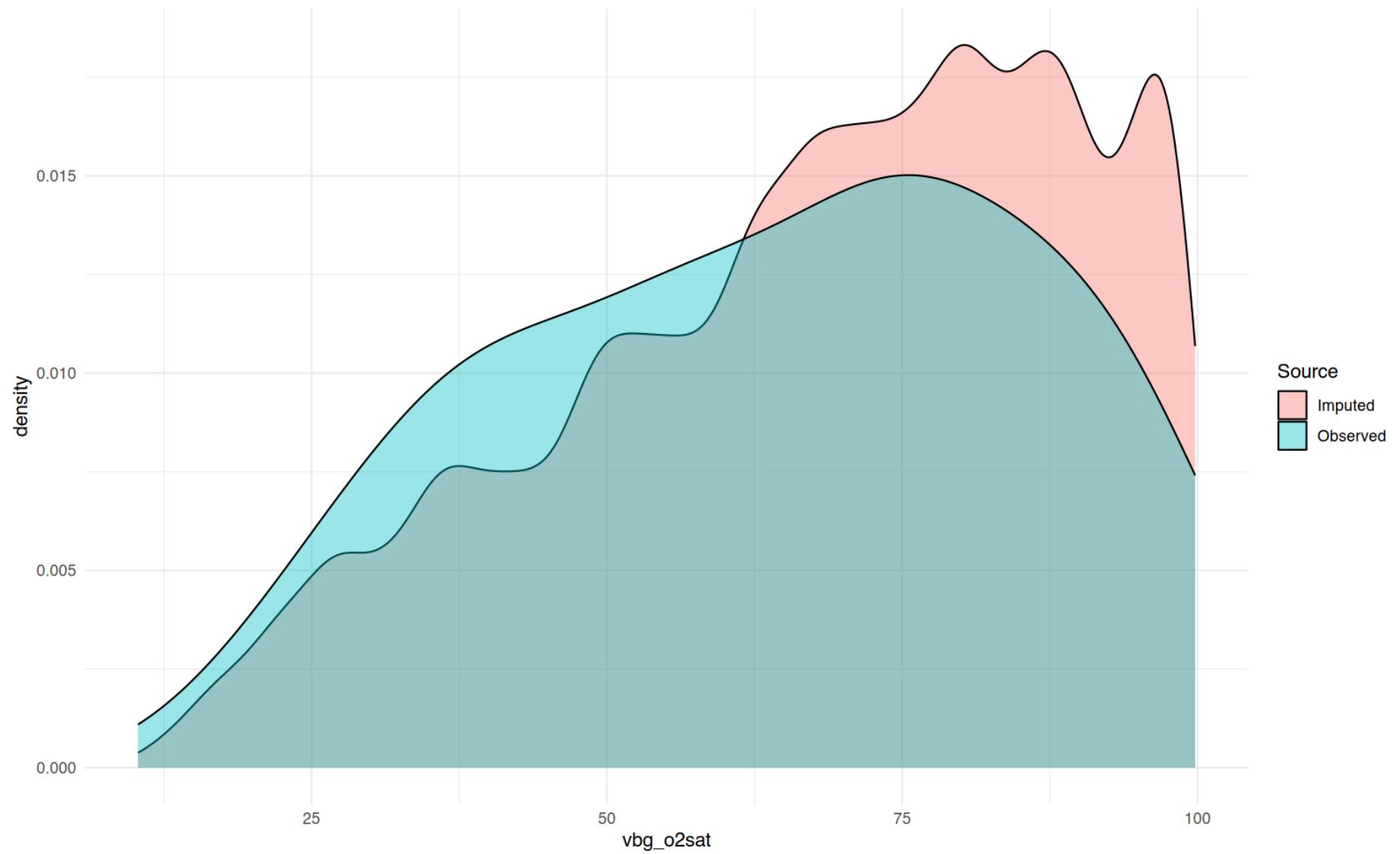
```

```

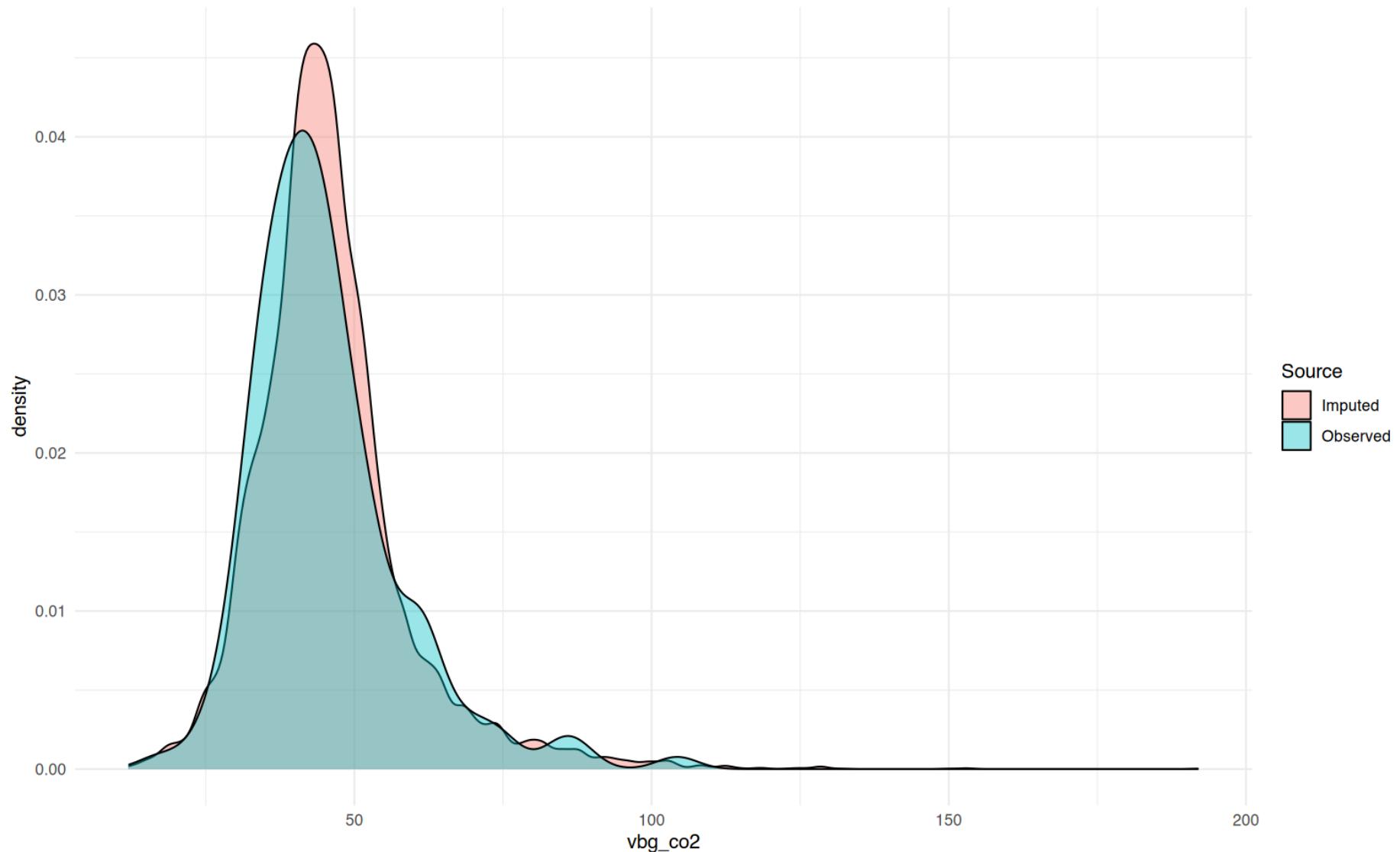
    group = interaction(.imp_label, .strata)
)) +
  geom_violin(alpha = 0.5, scale = "width", trim = TRUE, position = pd, na.rm = TRUE) +
  geom_boxplot(width = 0.2, outlier.size = 0.6, position = pd, na.rm = TRUE) +
  x_scale +
  labs(title = paste("Observed vs imputed:", v, "by", sv),
       x = sv, y = v, fill = "Source") +
  theme_minimal()
print(p)
out_file <- results_path(
  "figs",
  paste0("diag-mi-obs-imp-by-", .make_safe_name(sv), "-", .make_safe_name(v), ".png")
)
save_diag_plot(p, out_file, width = 7, height = 5)
}
}
}
}

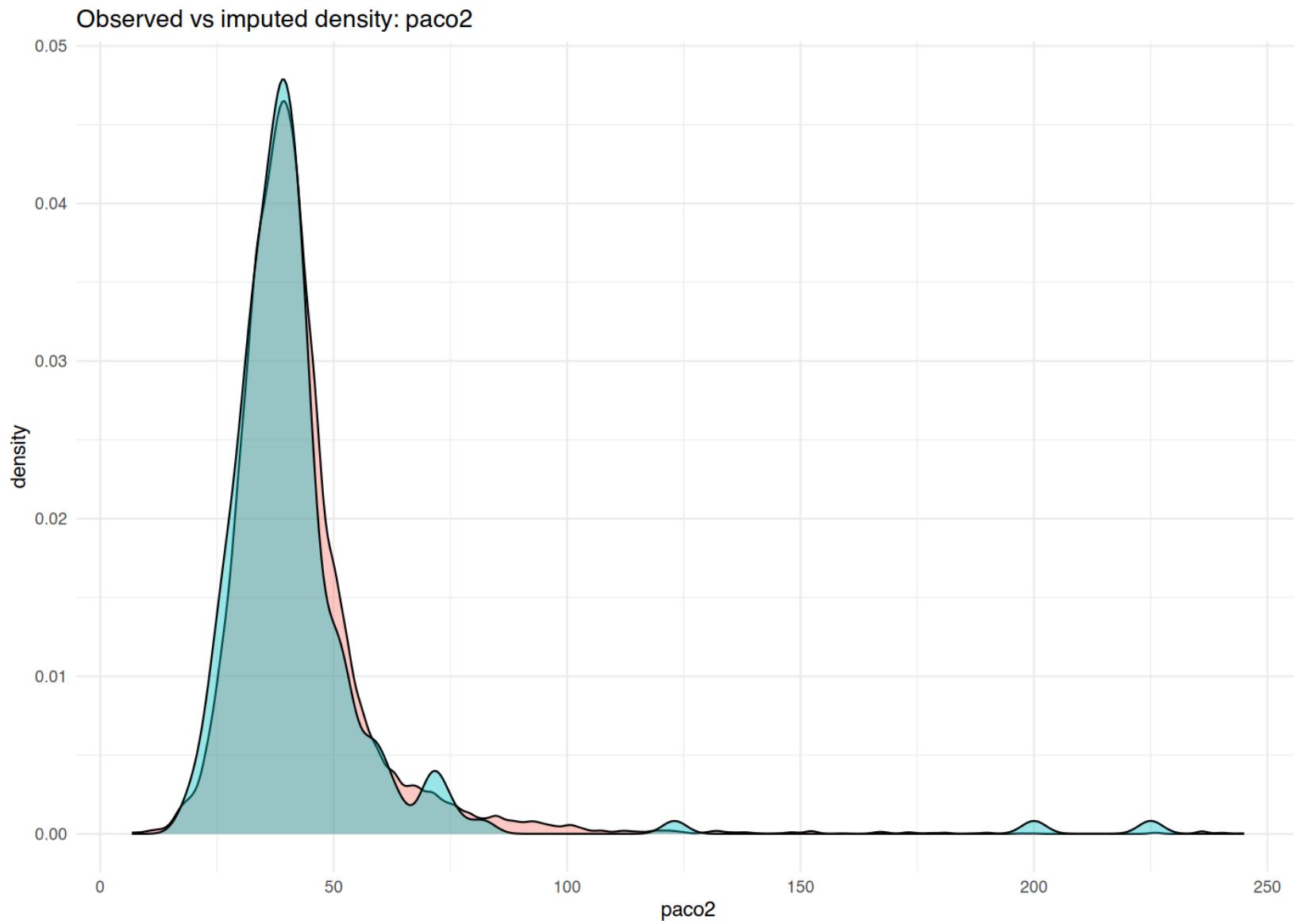
```

Observed vs imputed density: vbg_o2sat

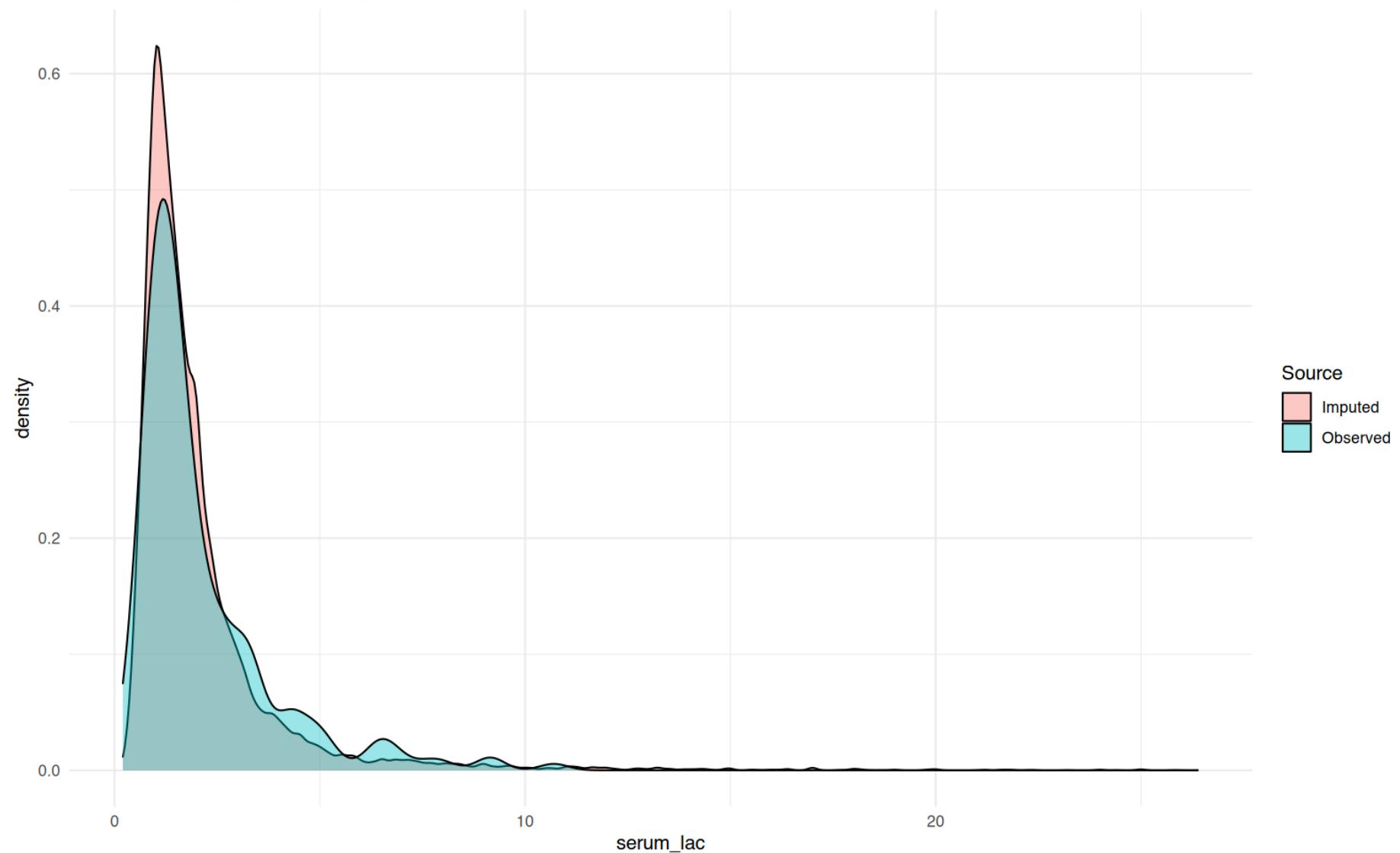


Observed vs imputed density: vbg_co2

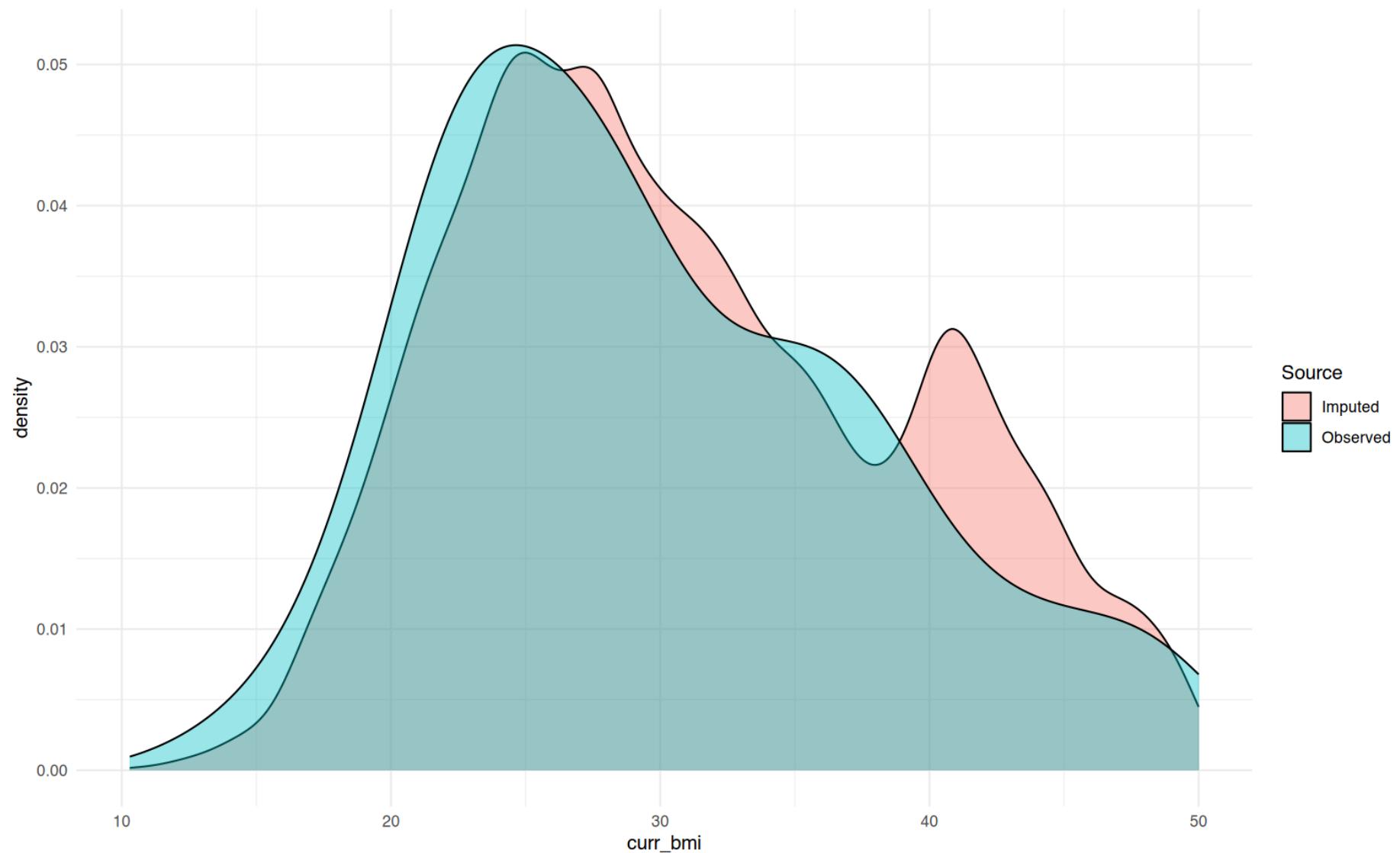




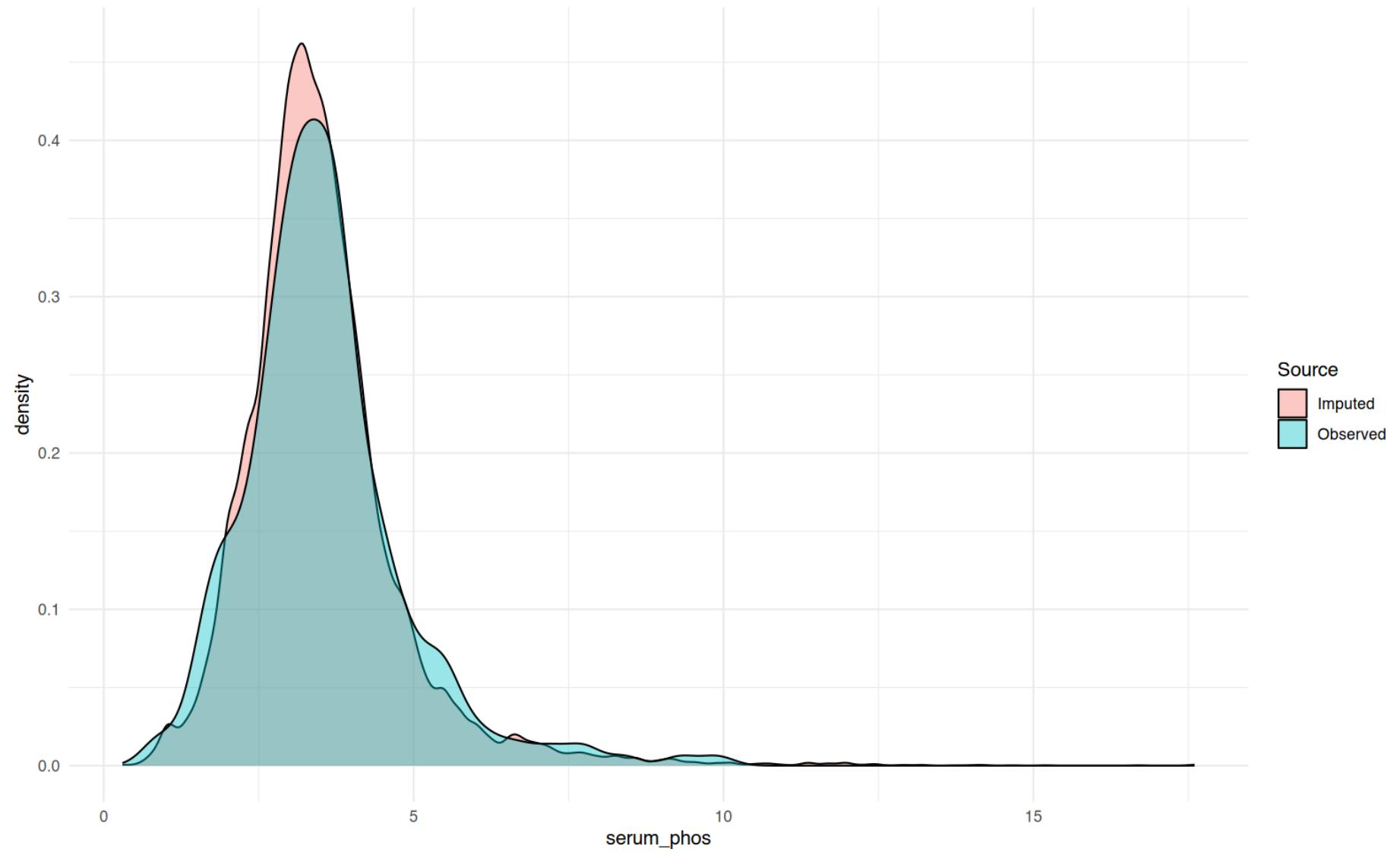
Observed vs imputed density: serum_lac



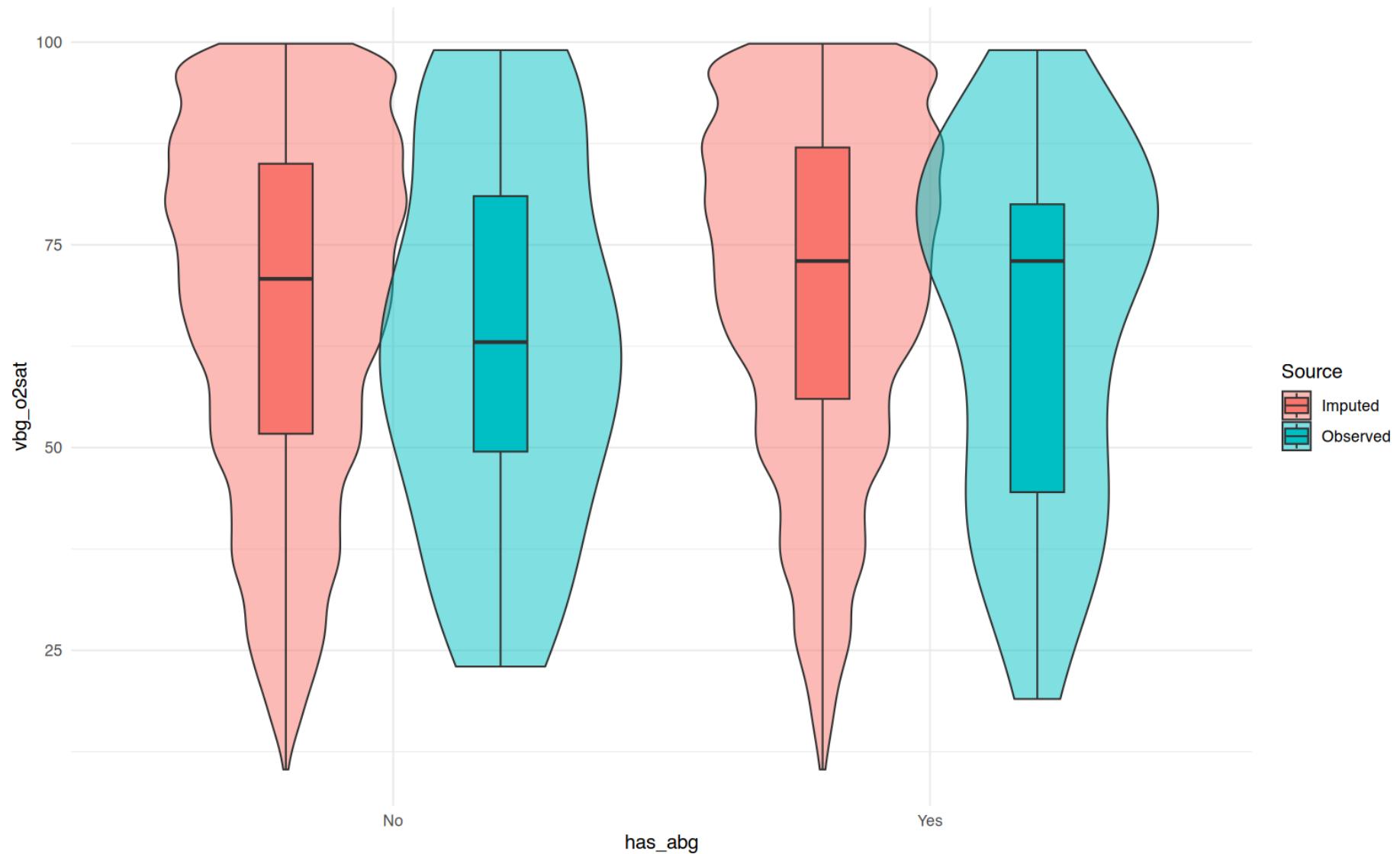
Observed vs imputed density: curr_bmi



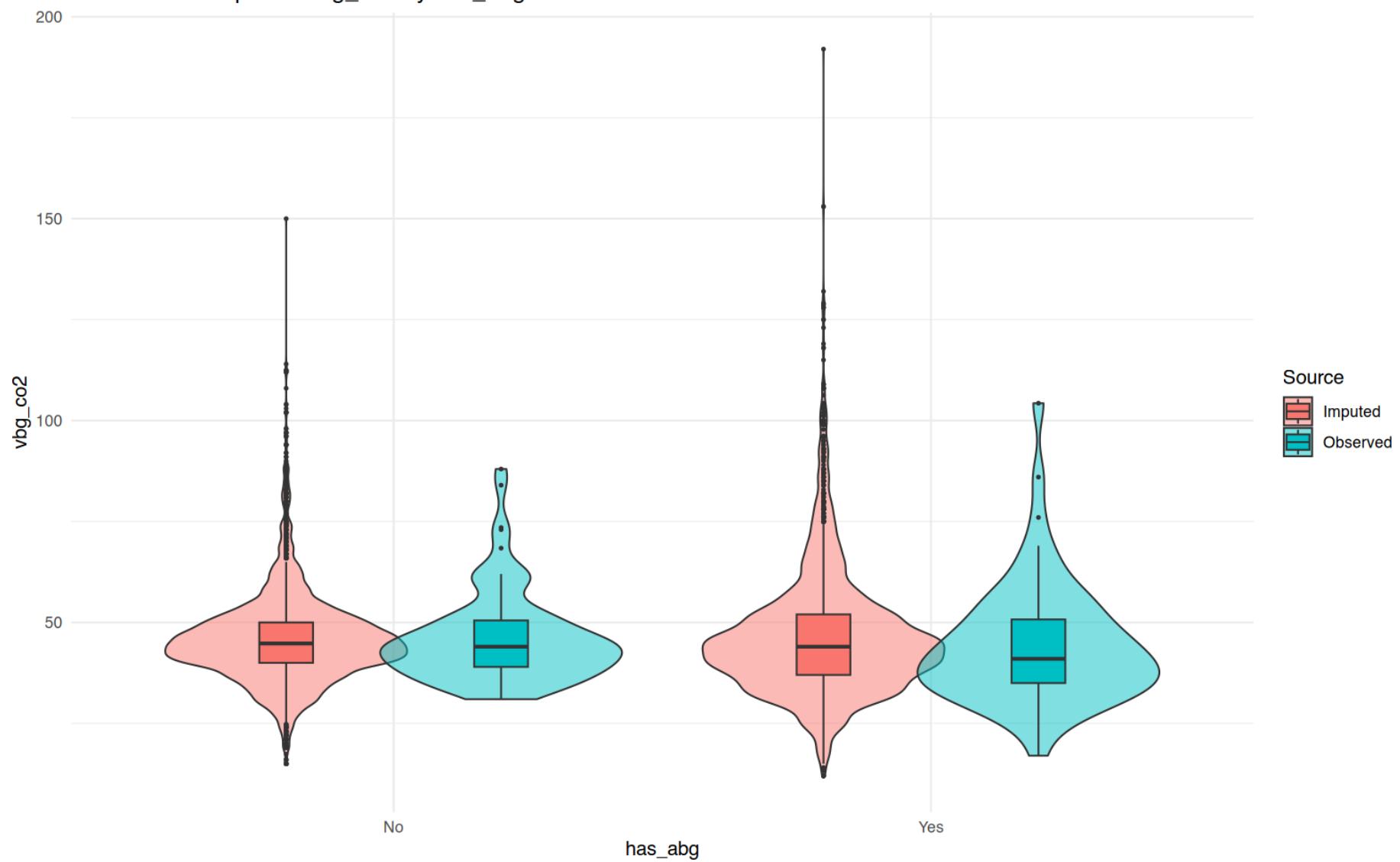
Observed vs imputed density: serum_phos



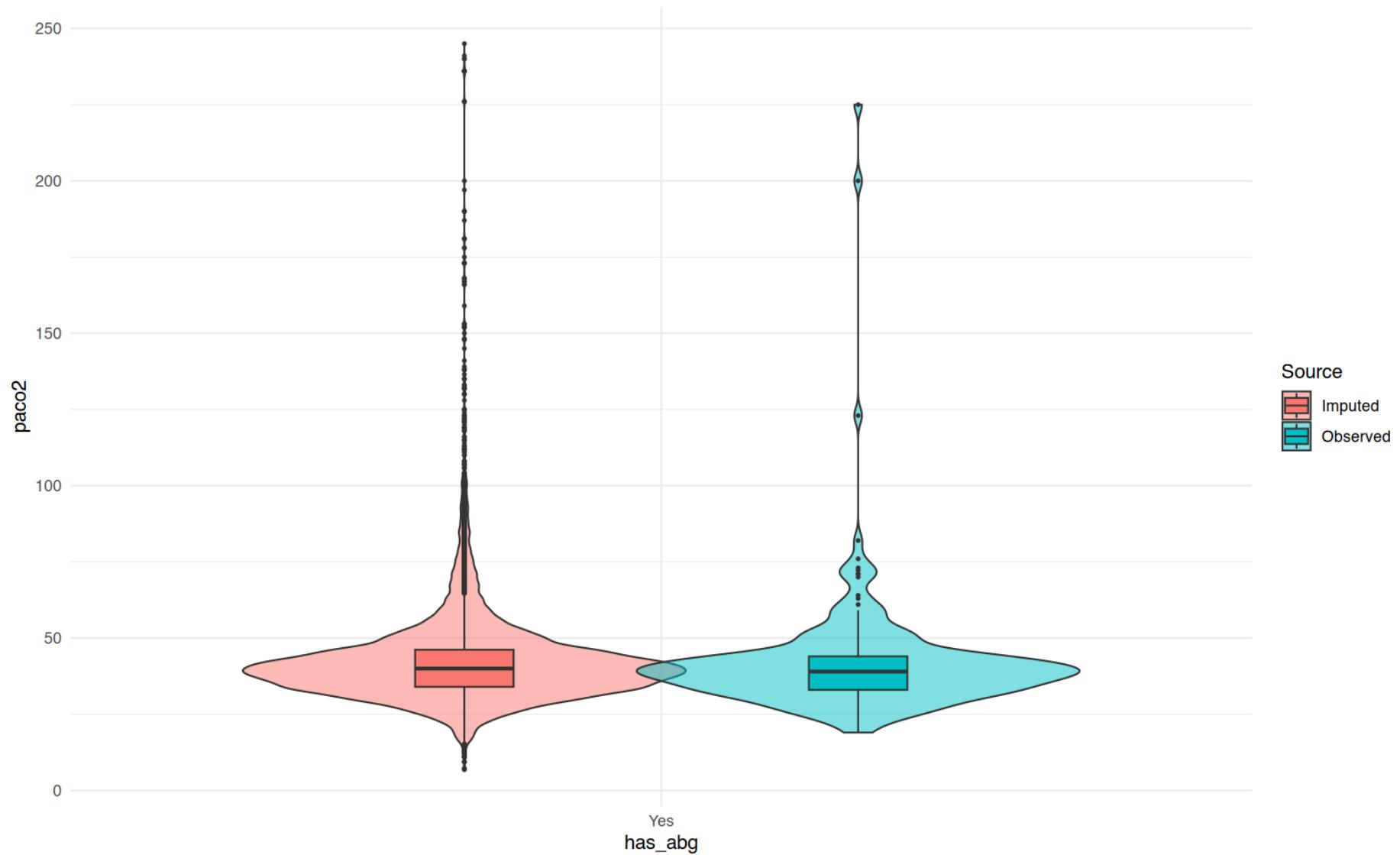
Observed vs imputed: vbg_o2sat by has_abg



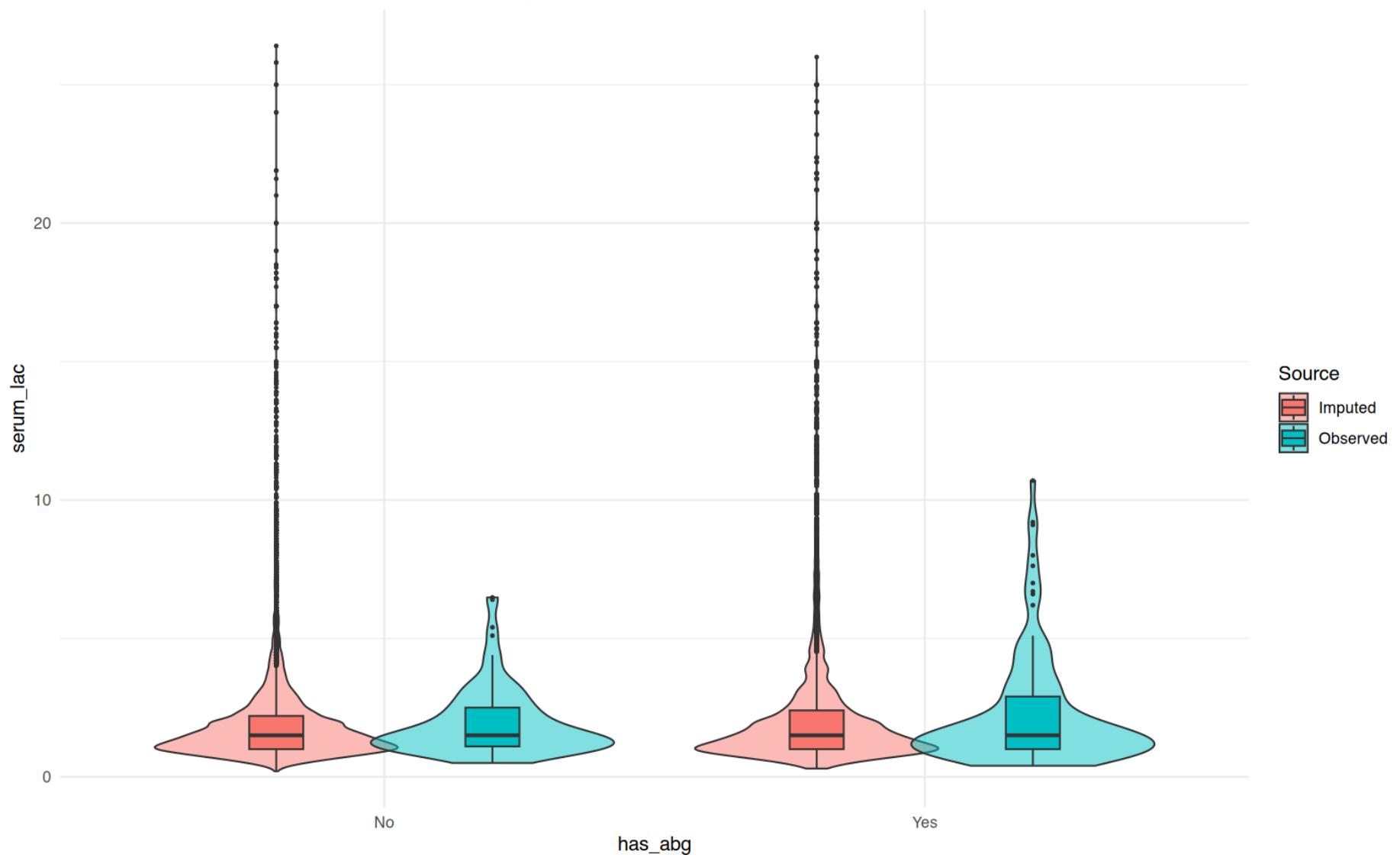
Observed vs imputed: vbg_co2 by has_abg



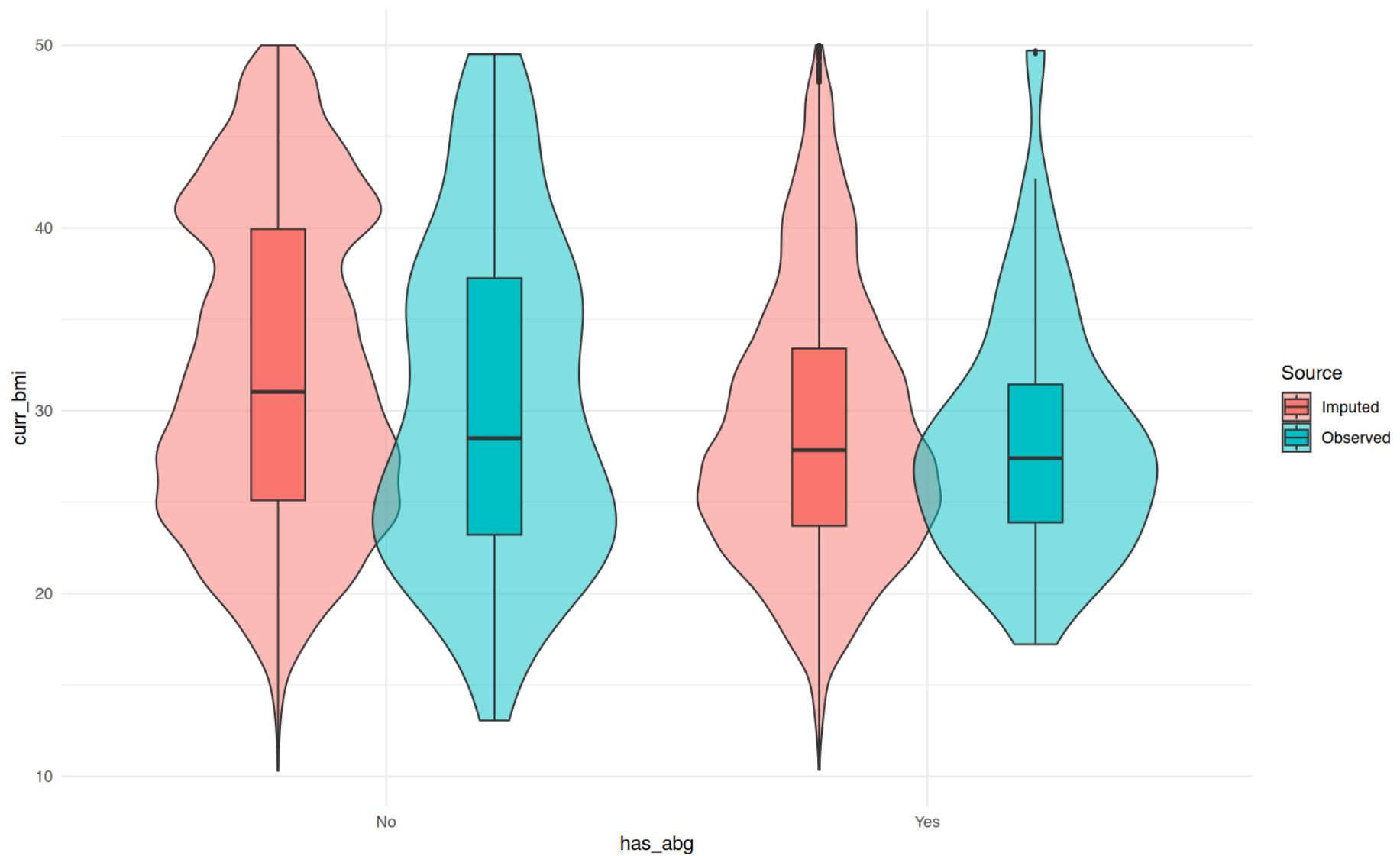
Observed vs imputed: paco2 by has_abg



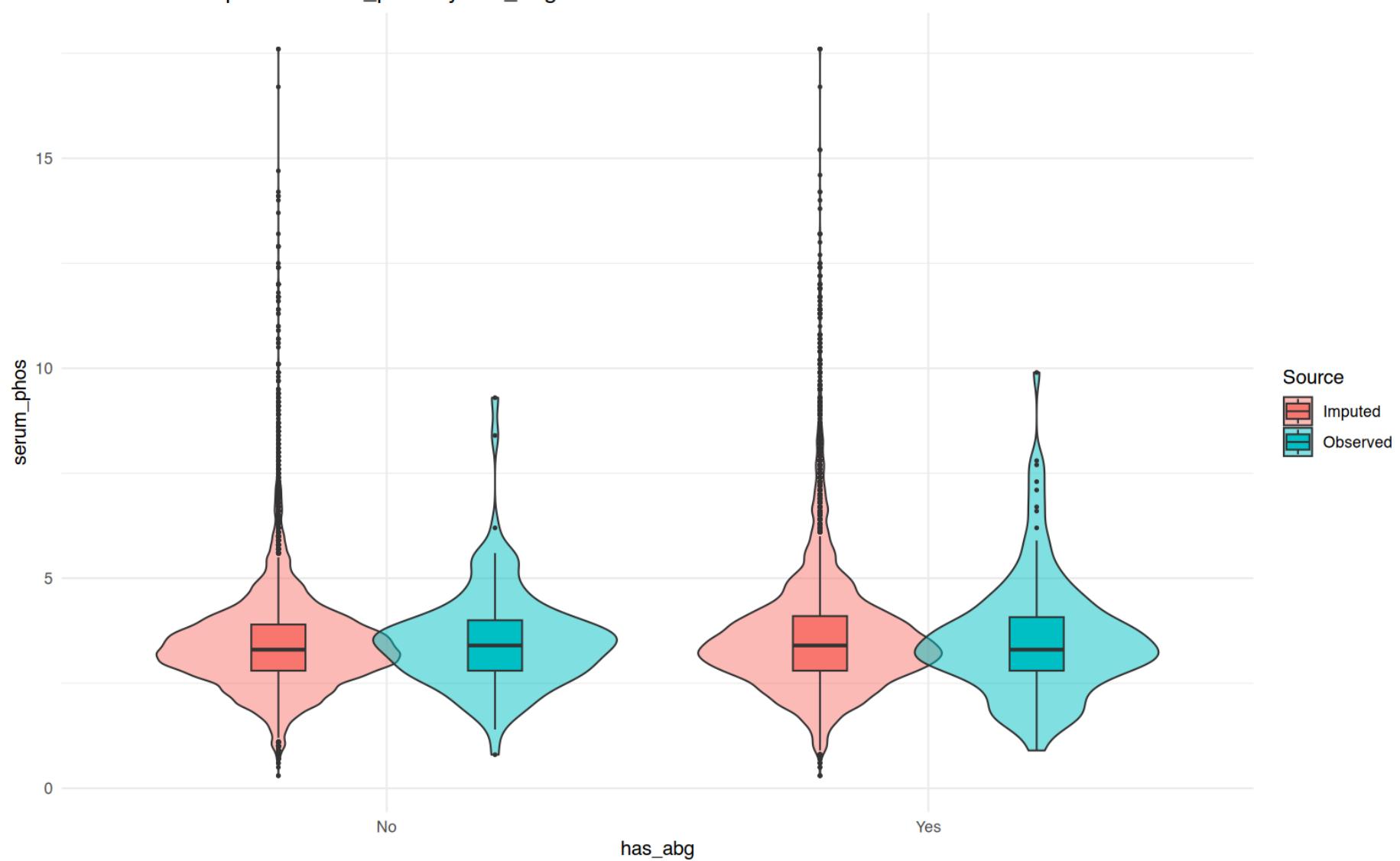
Observed vs imputed: serum_lac by has_abg



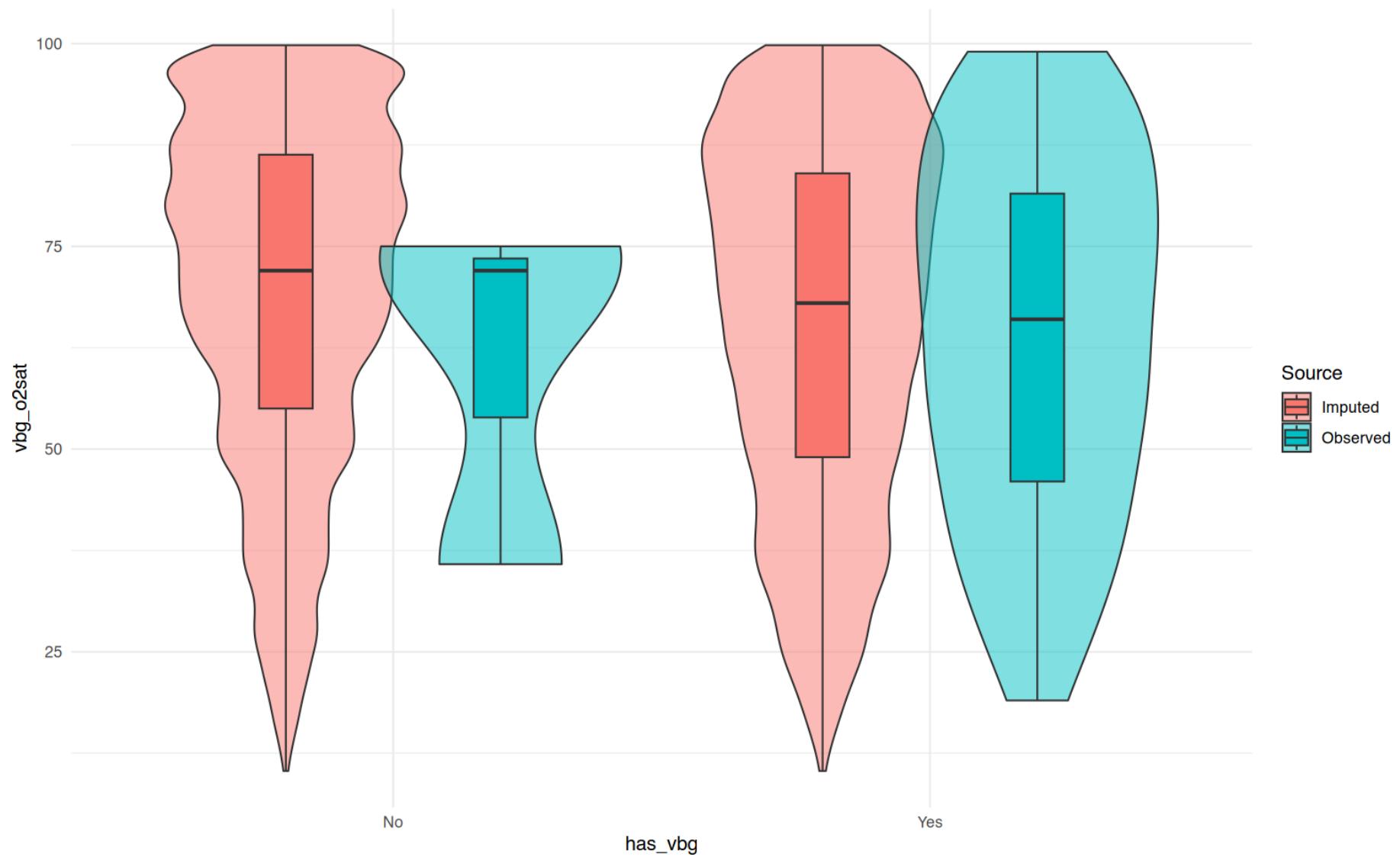
Observed vs imputed: curr_bmi by has_abg



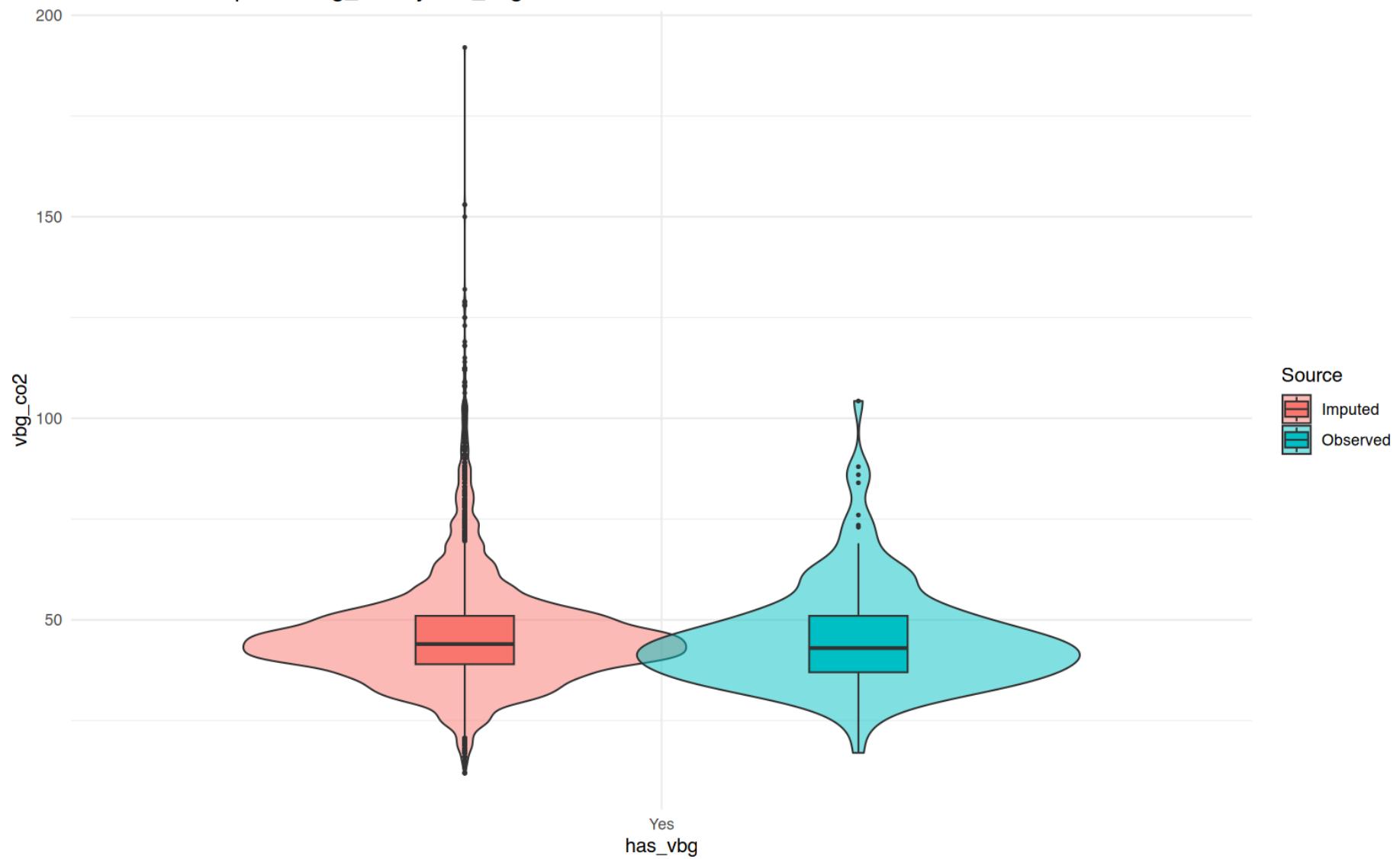
Observed vs imputed: serum_phos by has_abg



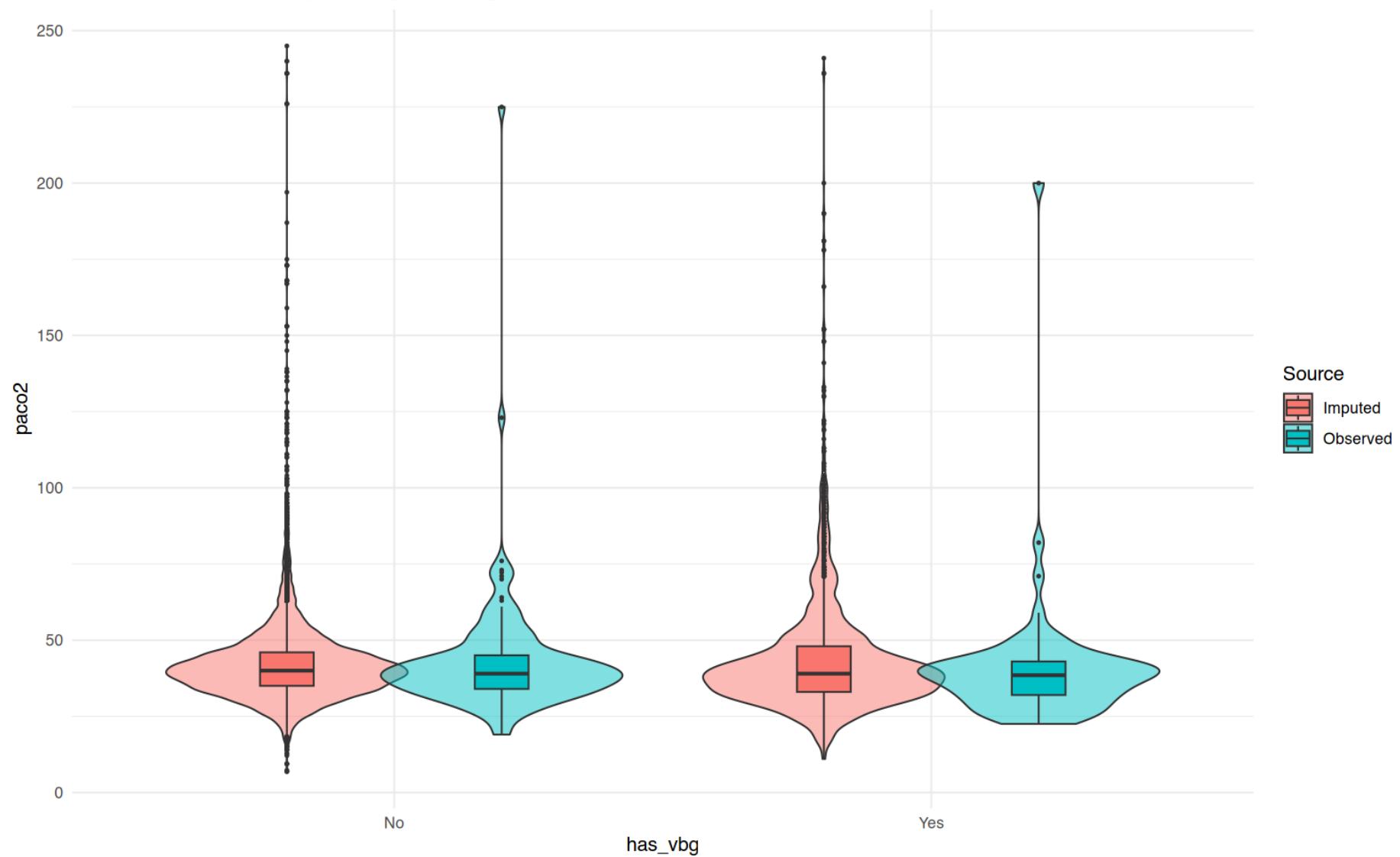
Observed vs imputed: vbg_o2sat by has_vbg



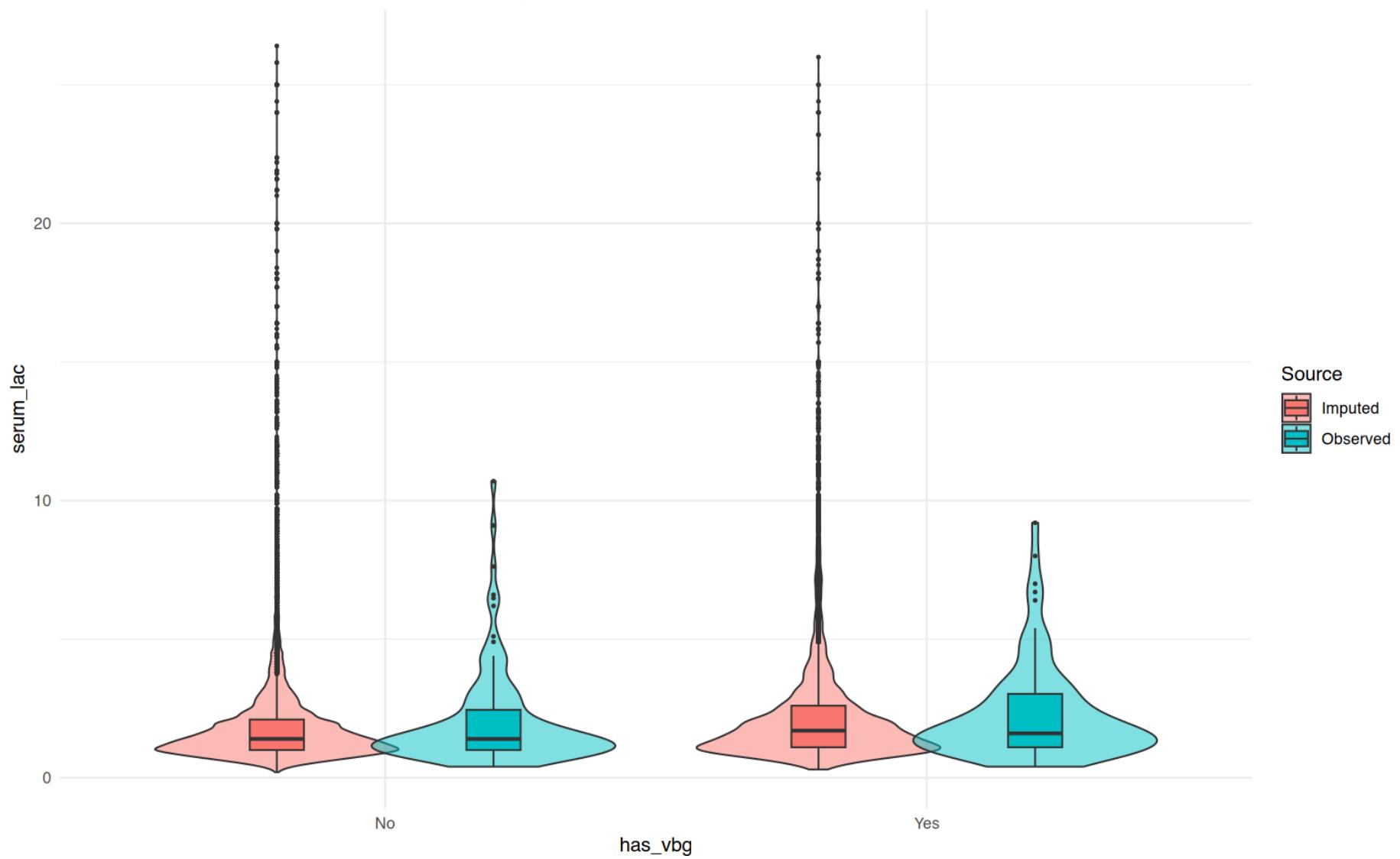
Observed vs imputed: vbg_co2 by has_vbg



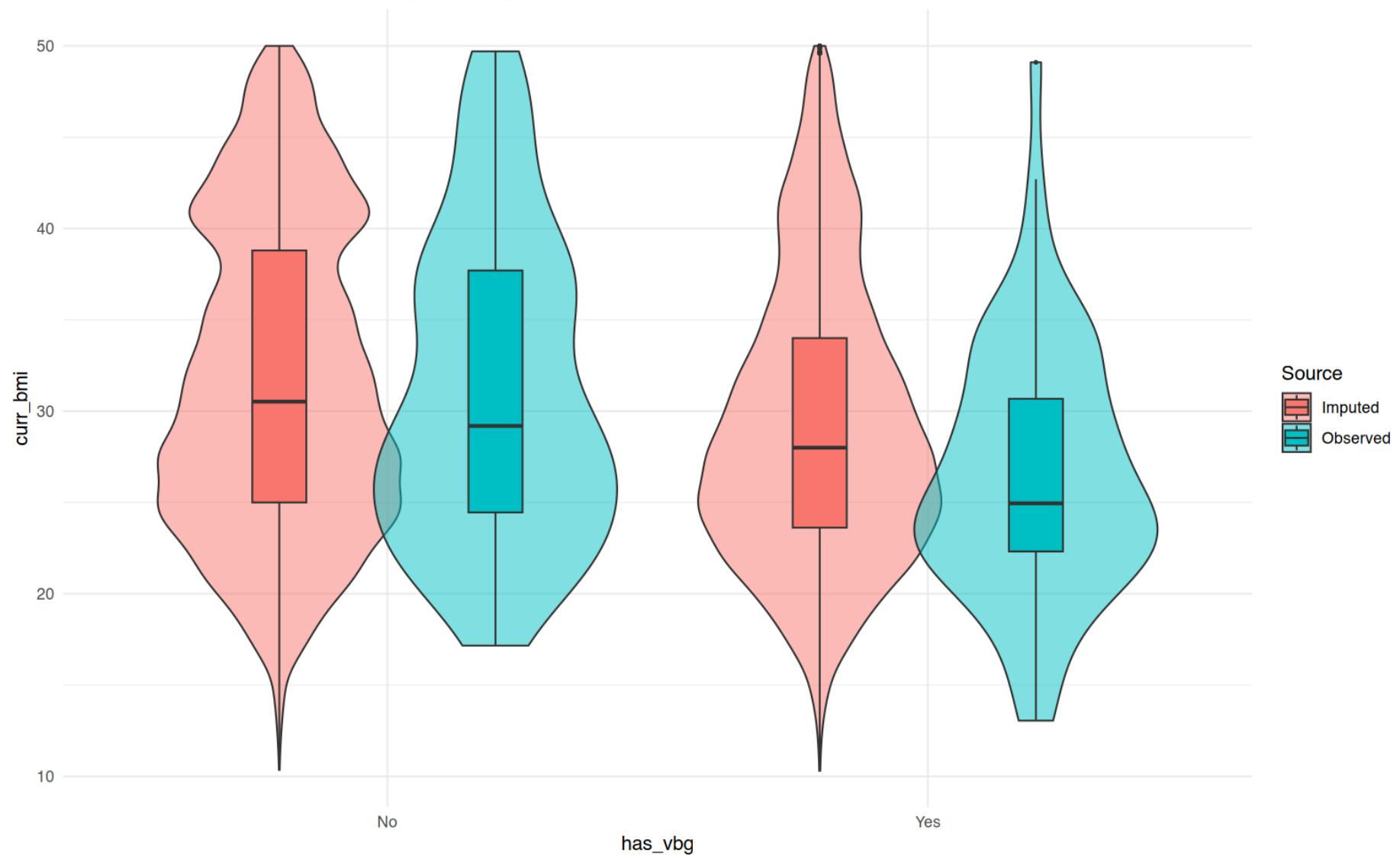
Observed vs imputed: paco2 by has_vbg



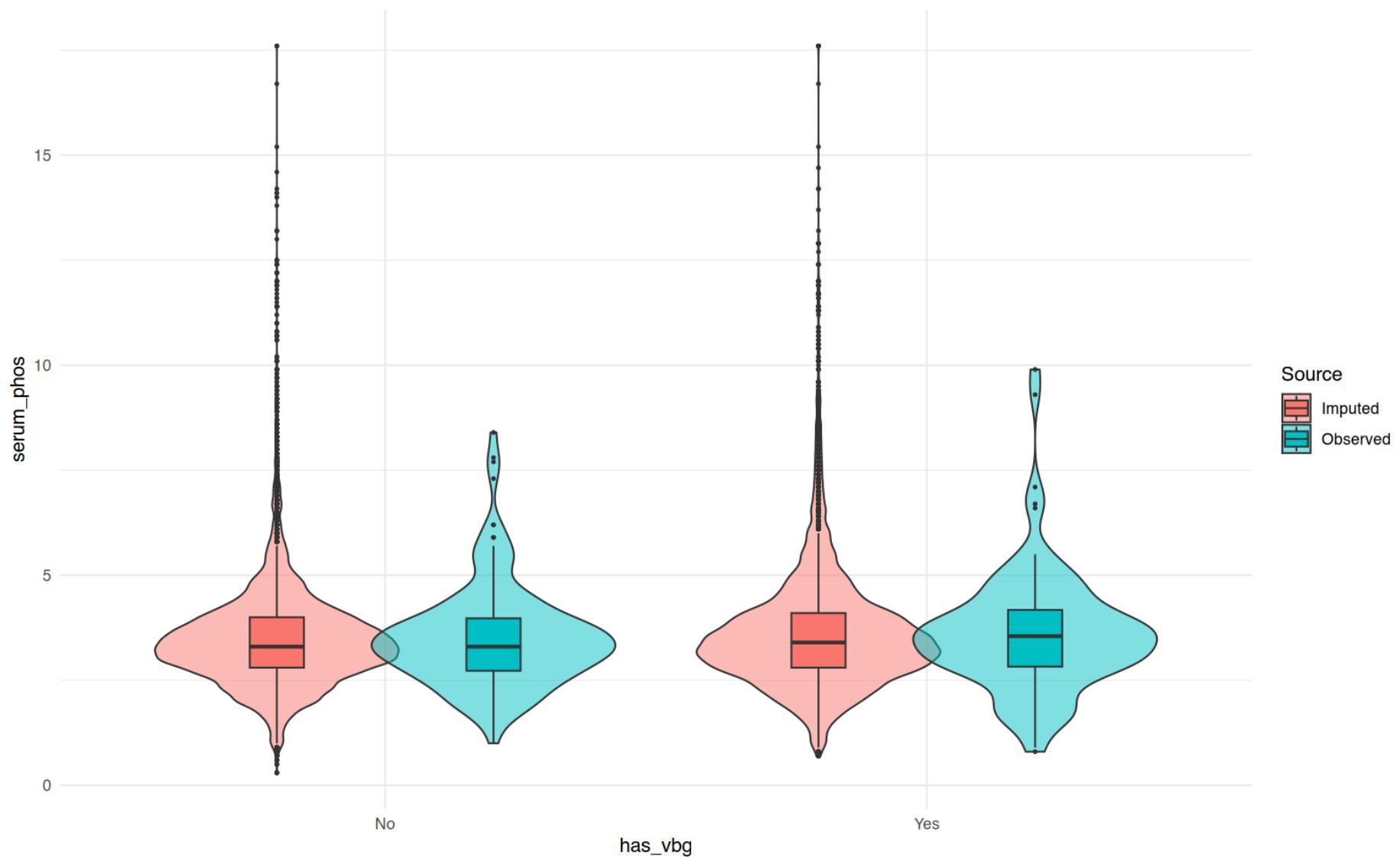
Observed vs imputed: serum_lac by has_vbg



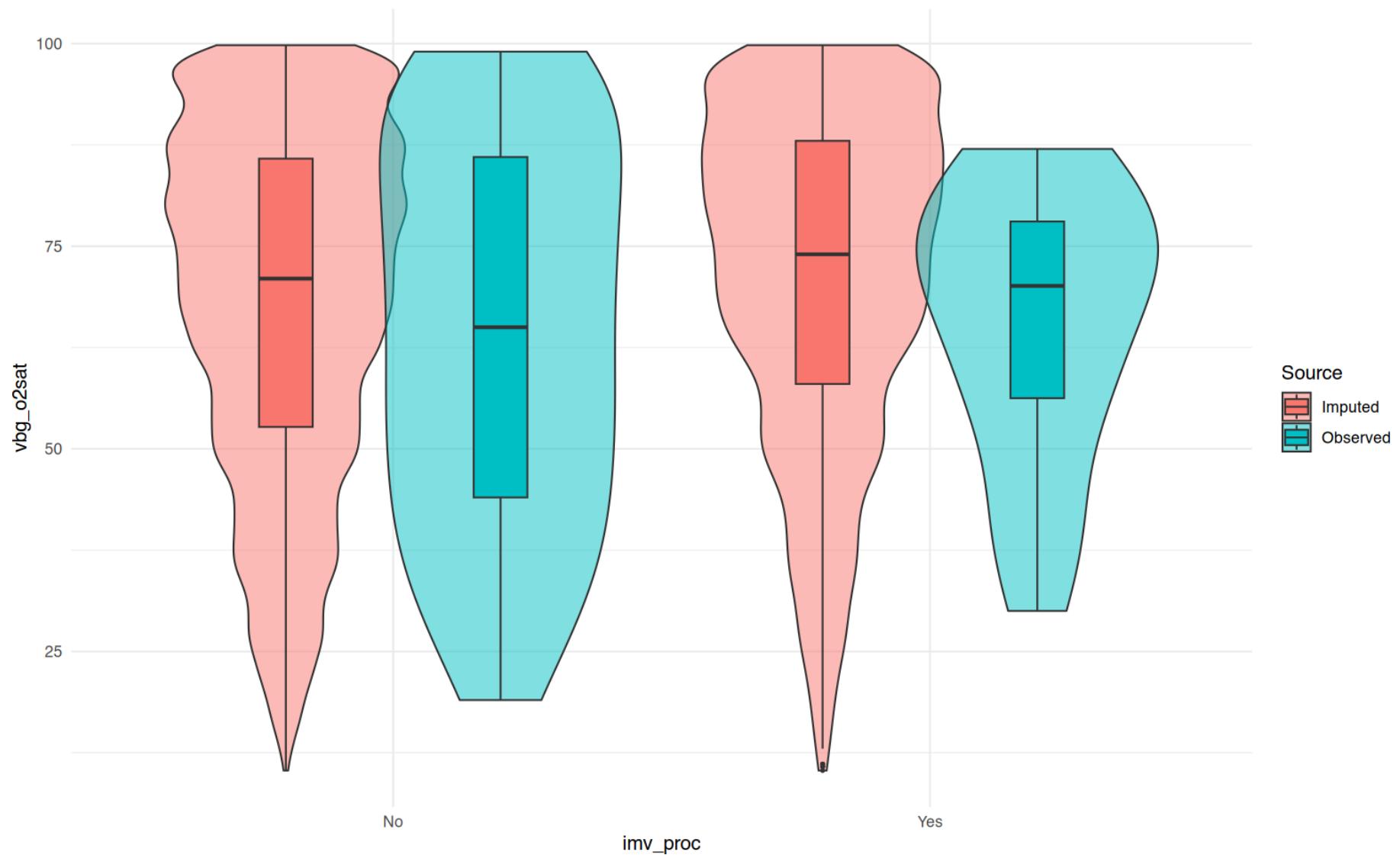
Observed vs imputed: curr_bmi by has_vbg



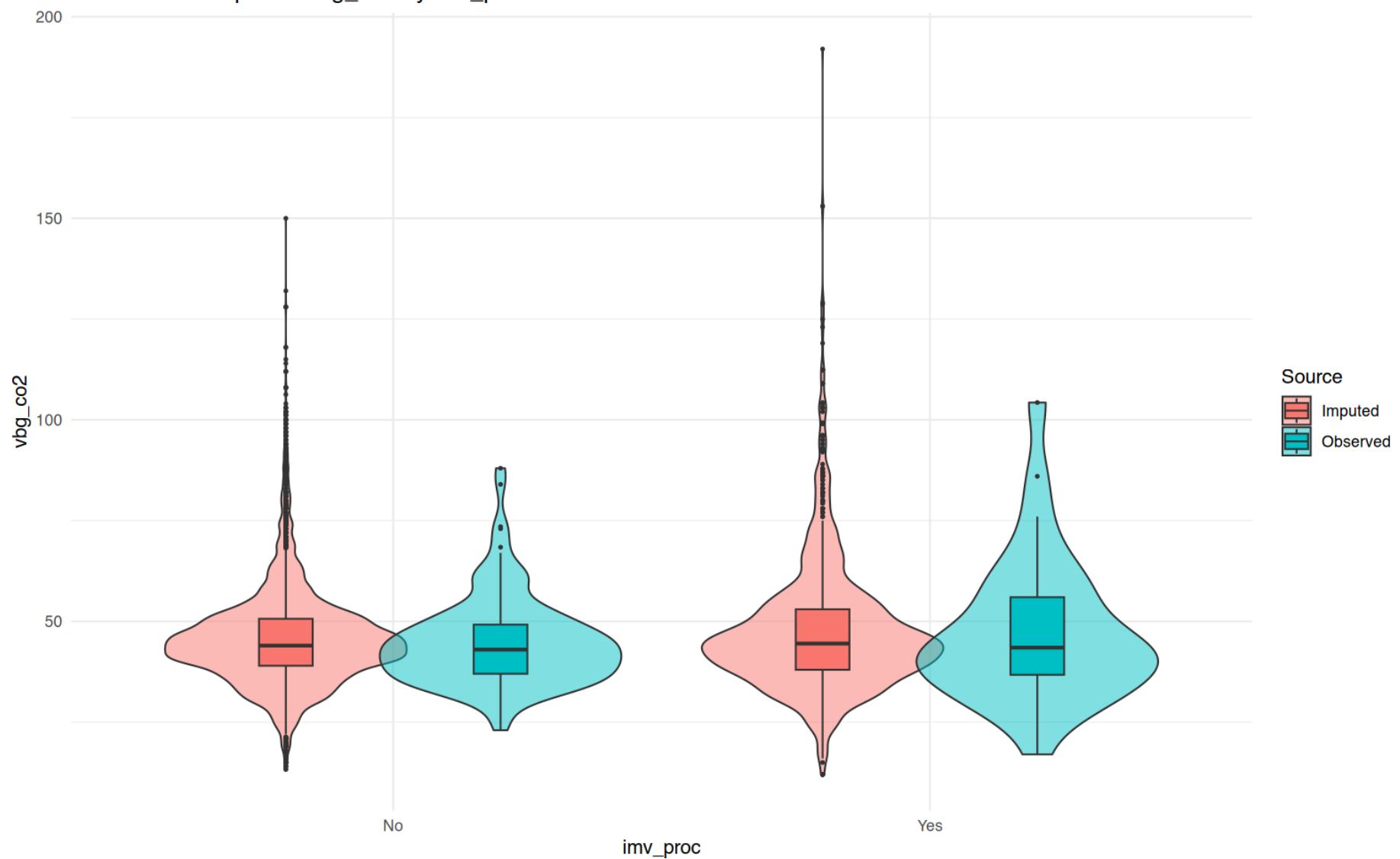
Observed vs imputed: serum_phos by has_vbg



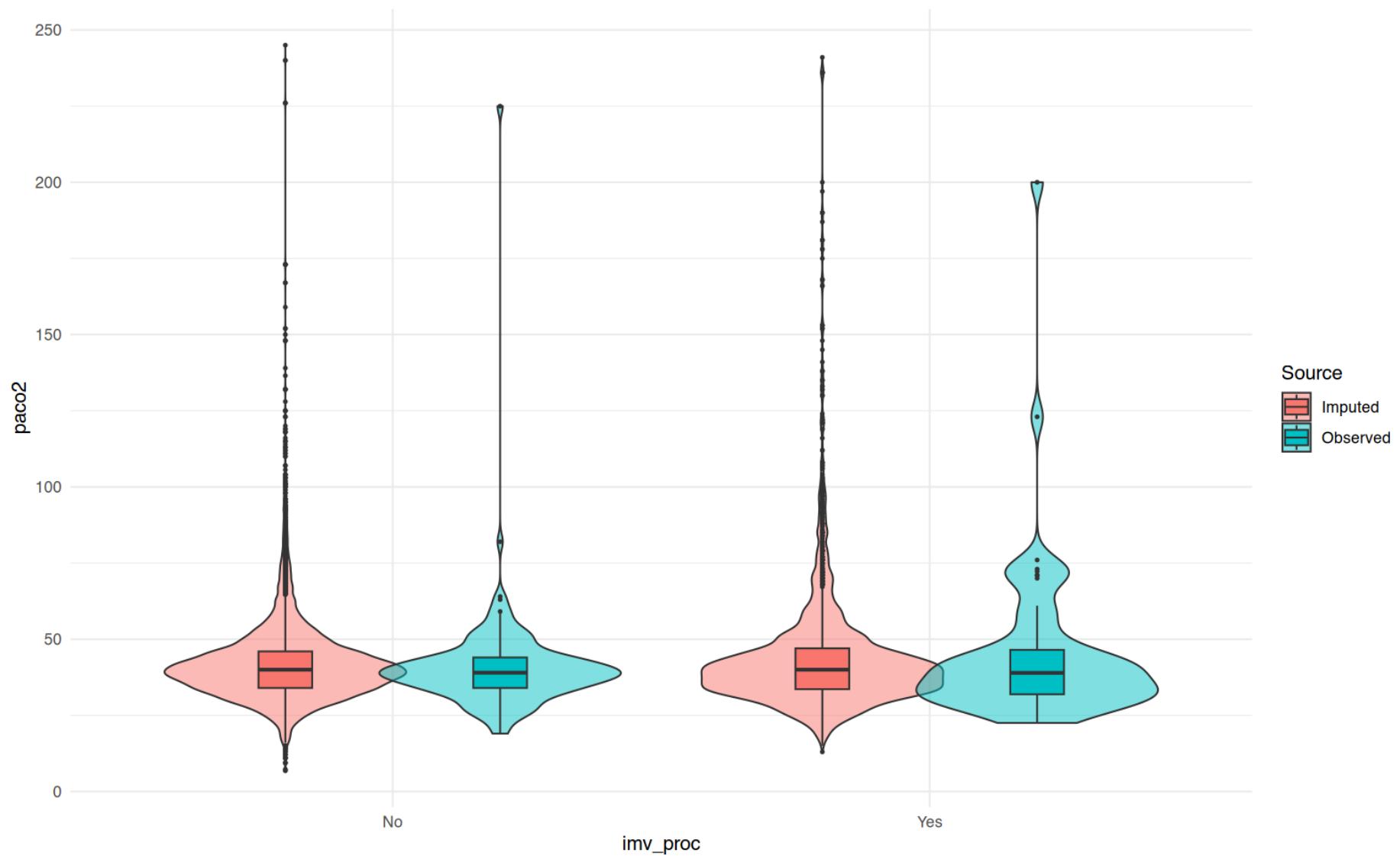
Observed vs imputed: vbg_o2sat by imv_proc



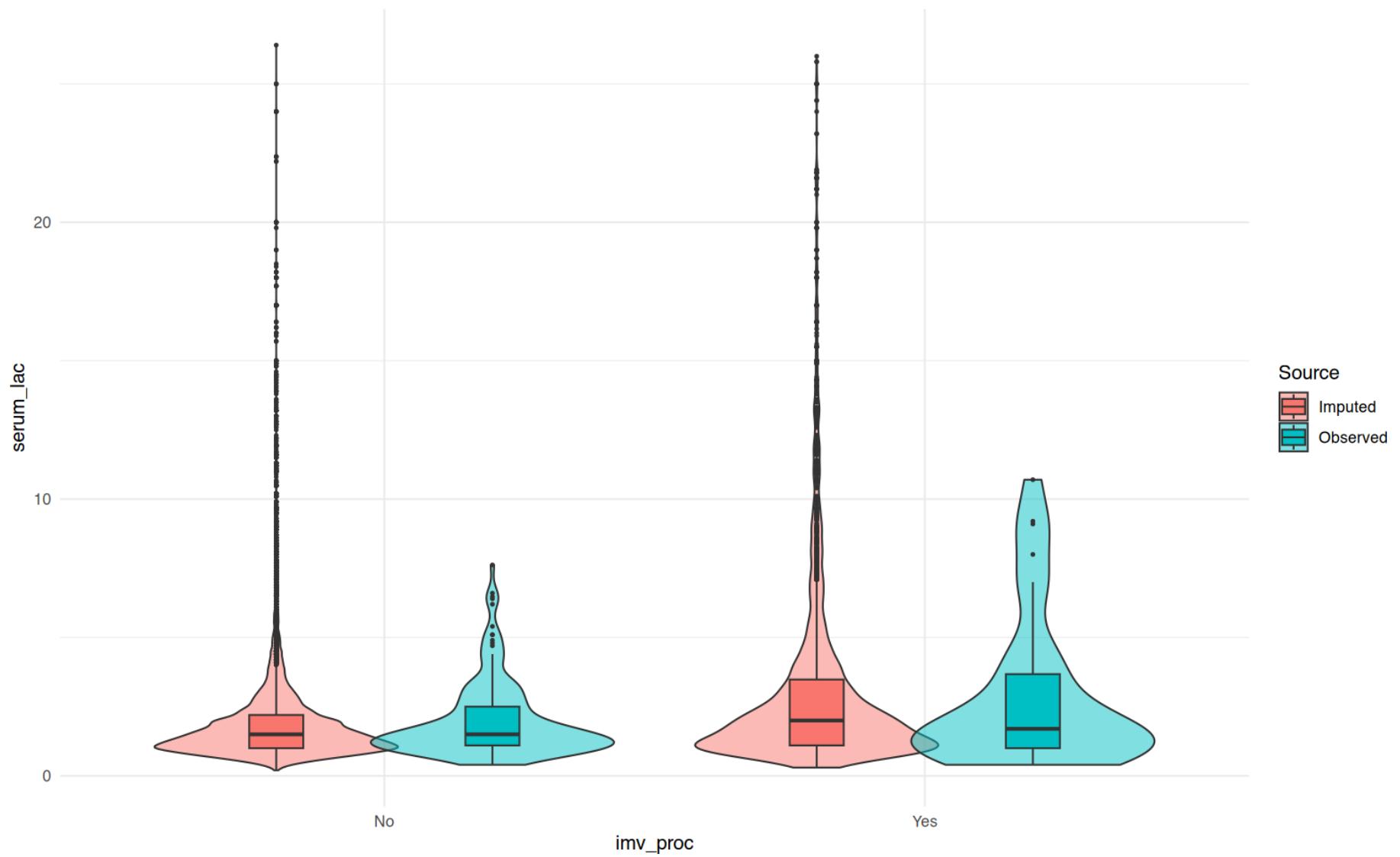
Observed vs imputed: vbg_co2 by imv_proc



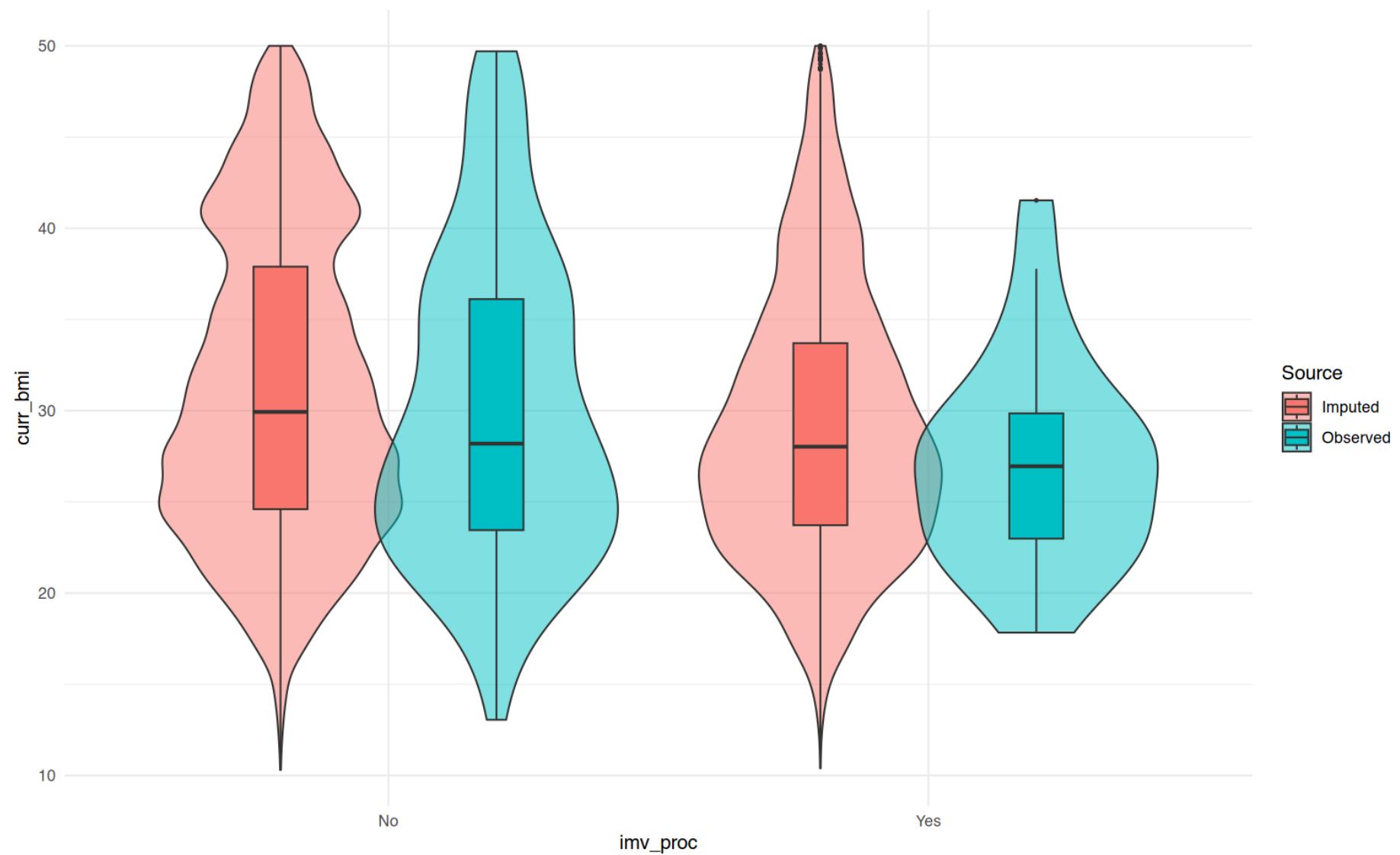
Observed vs imputed: paco2 by imv_proc



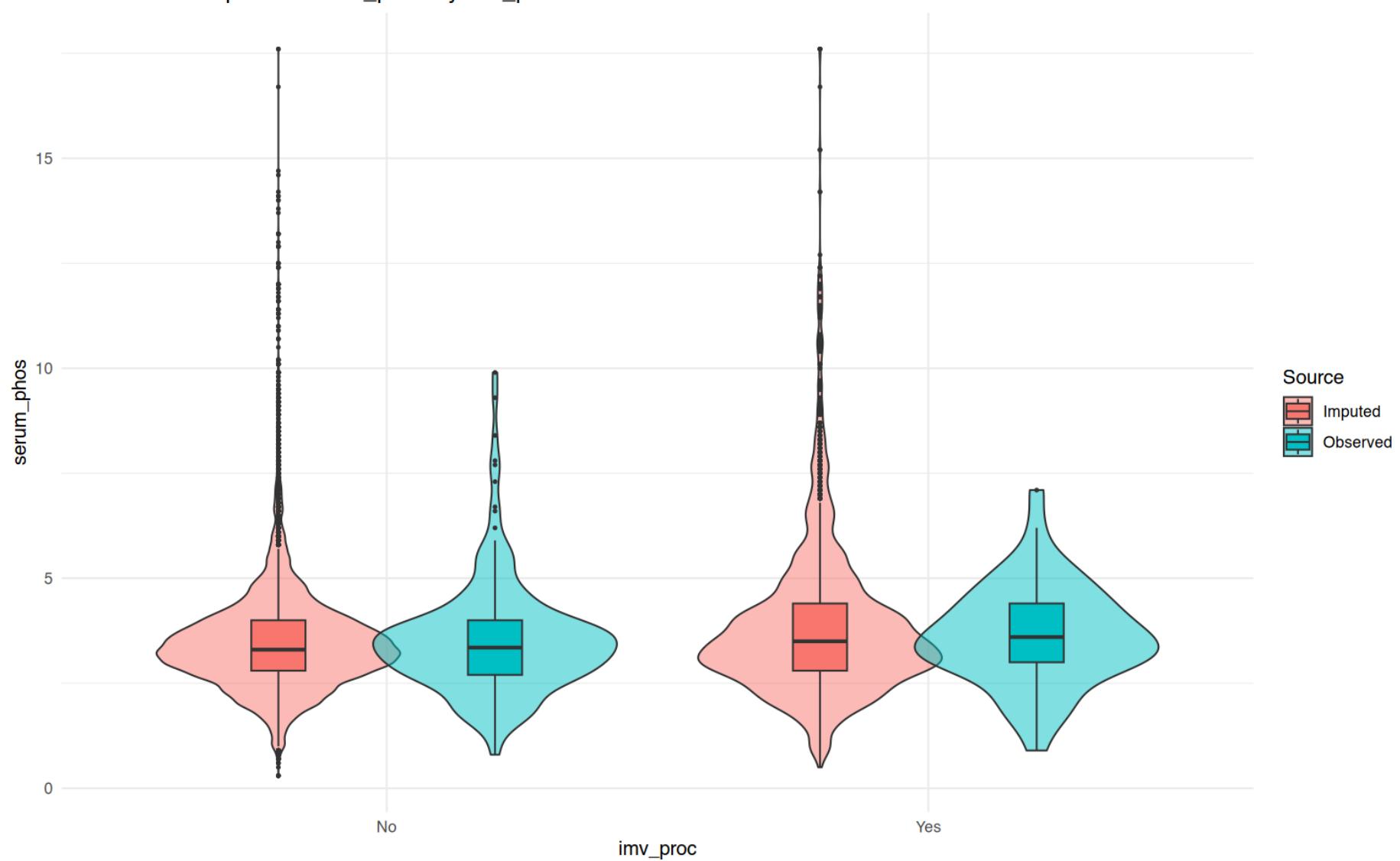
Observed vs imputed: serum_lac by imv_proc



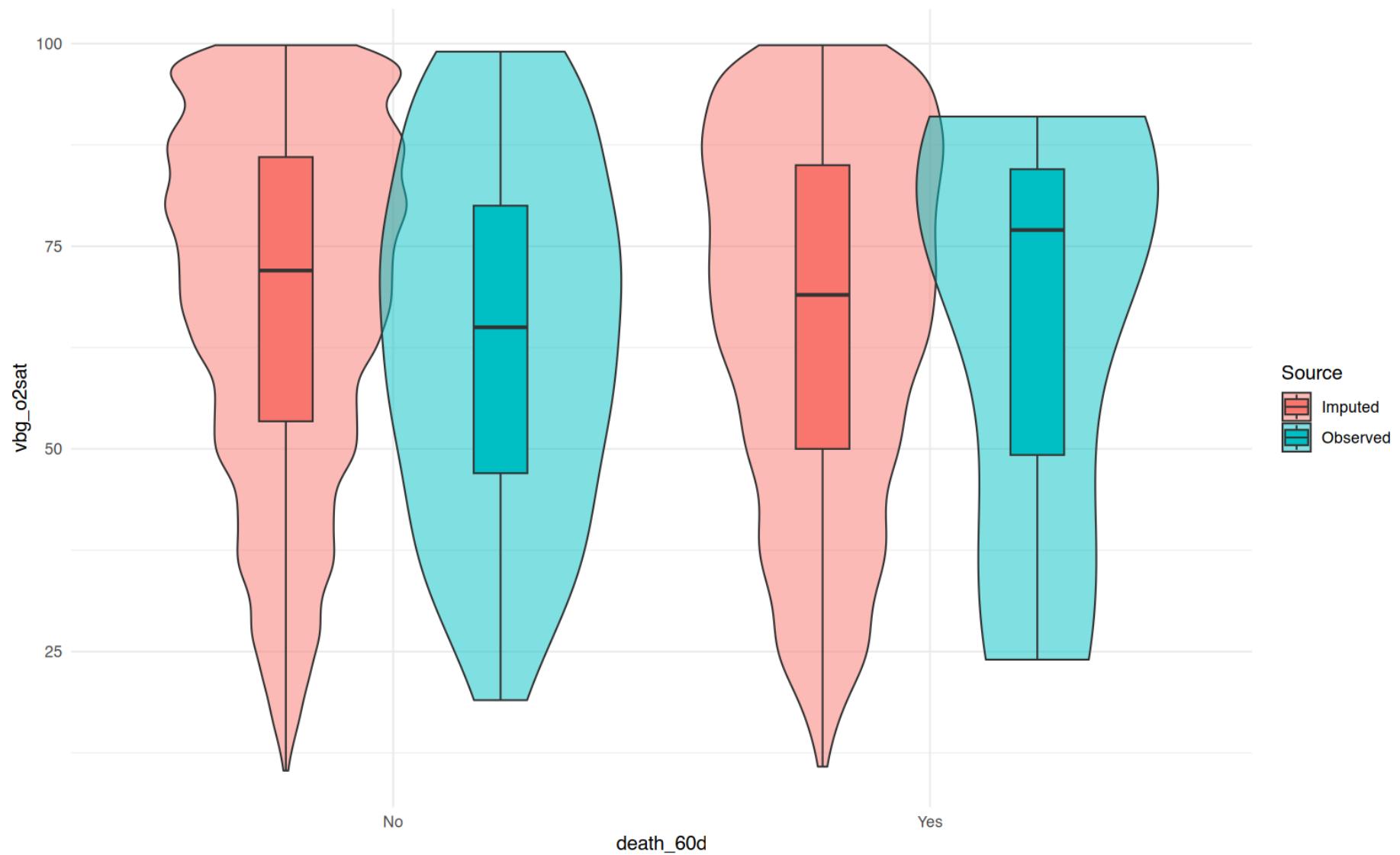
Observed vs imputed: curr_bmi by imv_proc



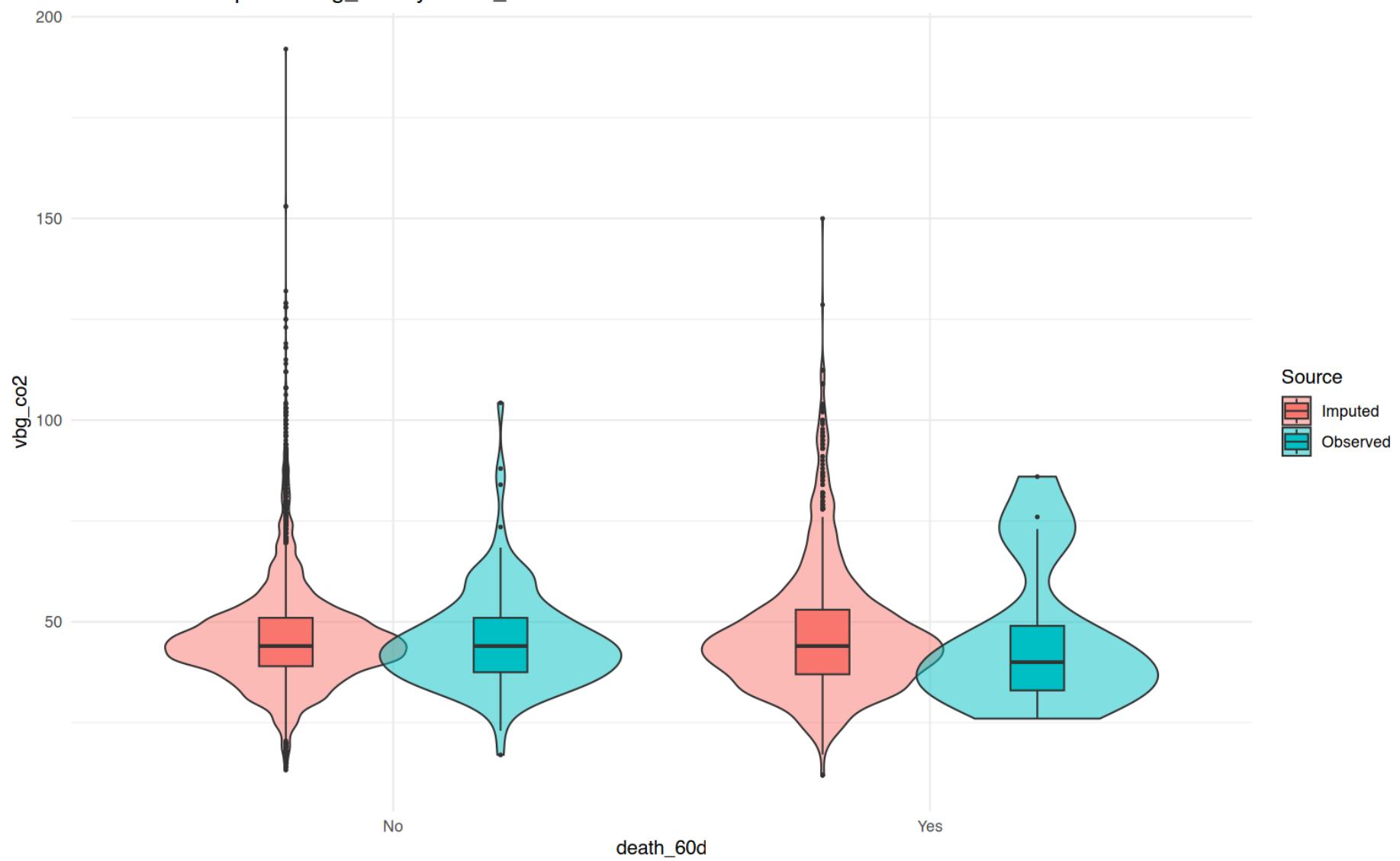
Observed vs imputed: serum_phos by imv_proc



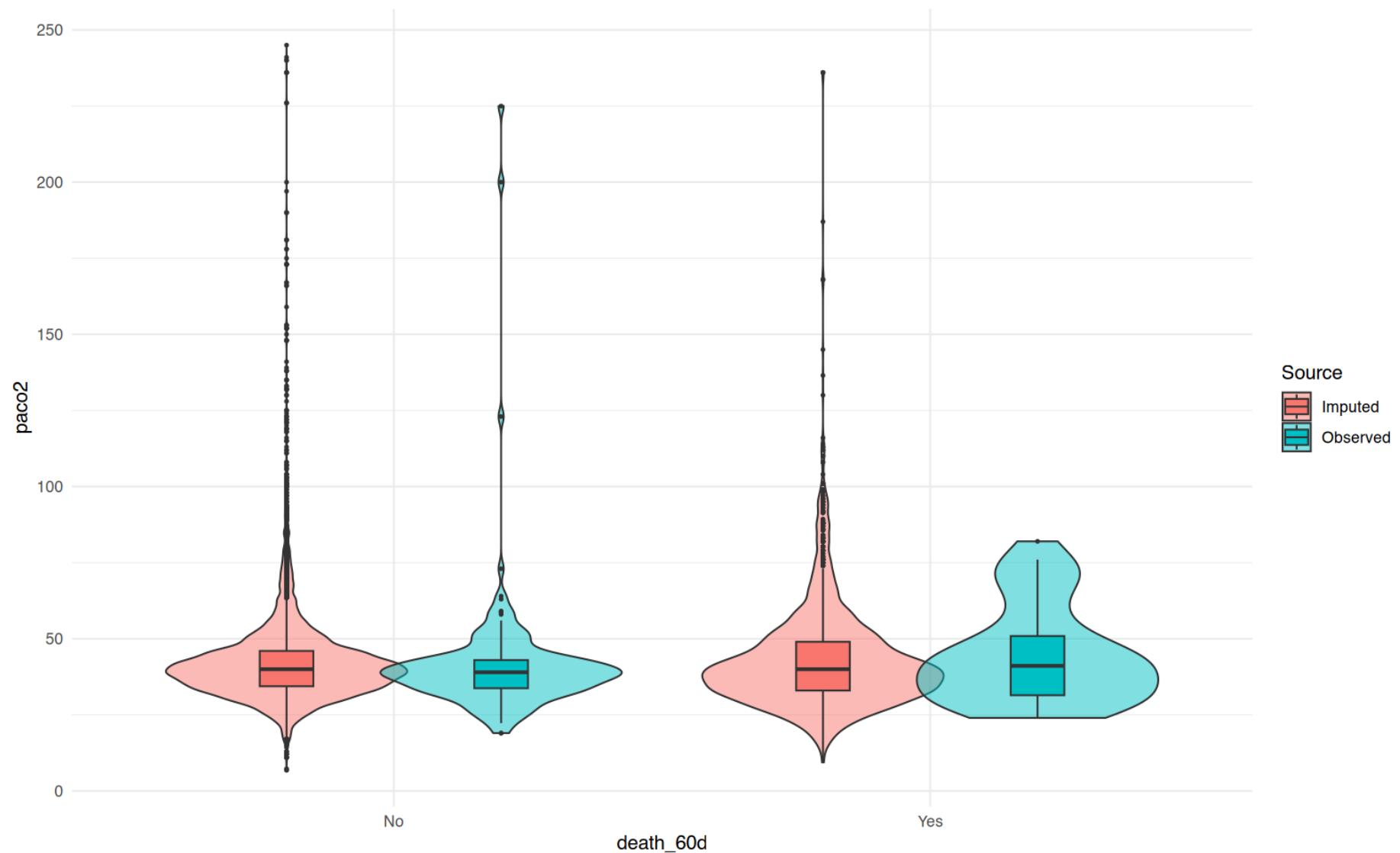
Observed vs imputed: vbg_o2sat by death_60d



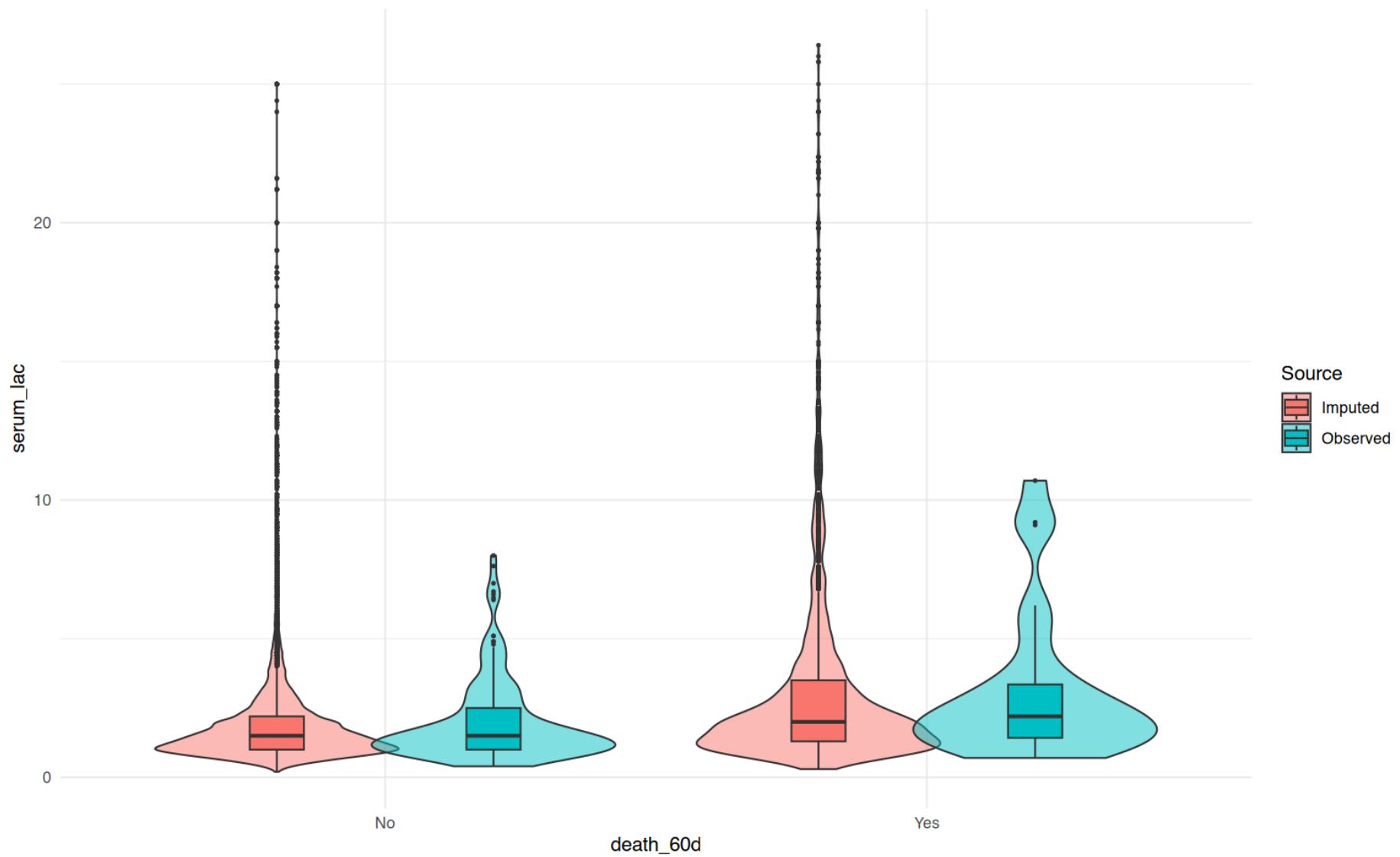
Observed vs imputed: vbg_co2 by death_60d



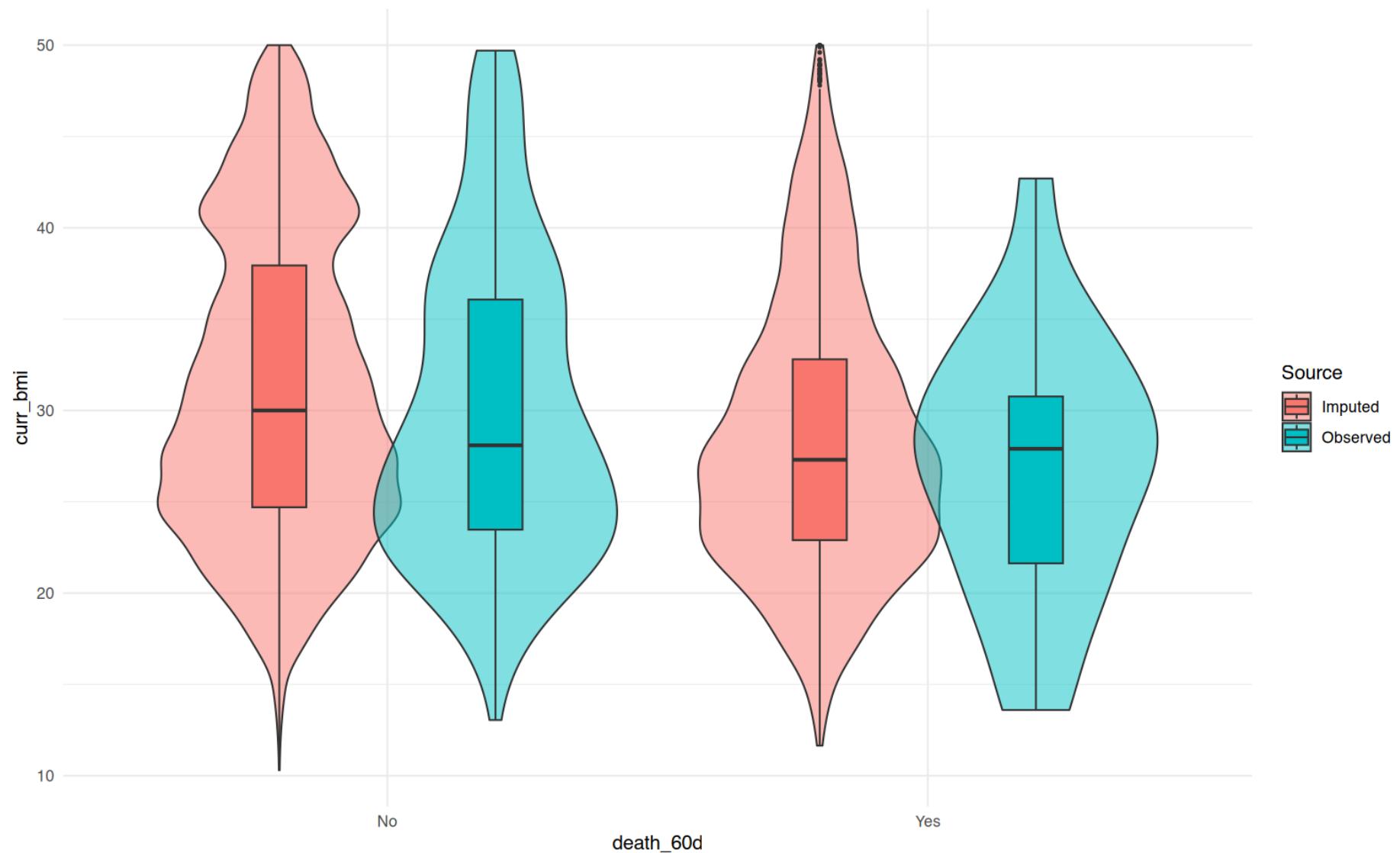
Observed vs imputed: paco2 by death_60d



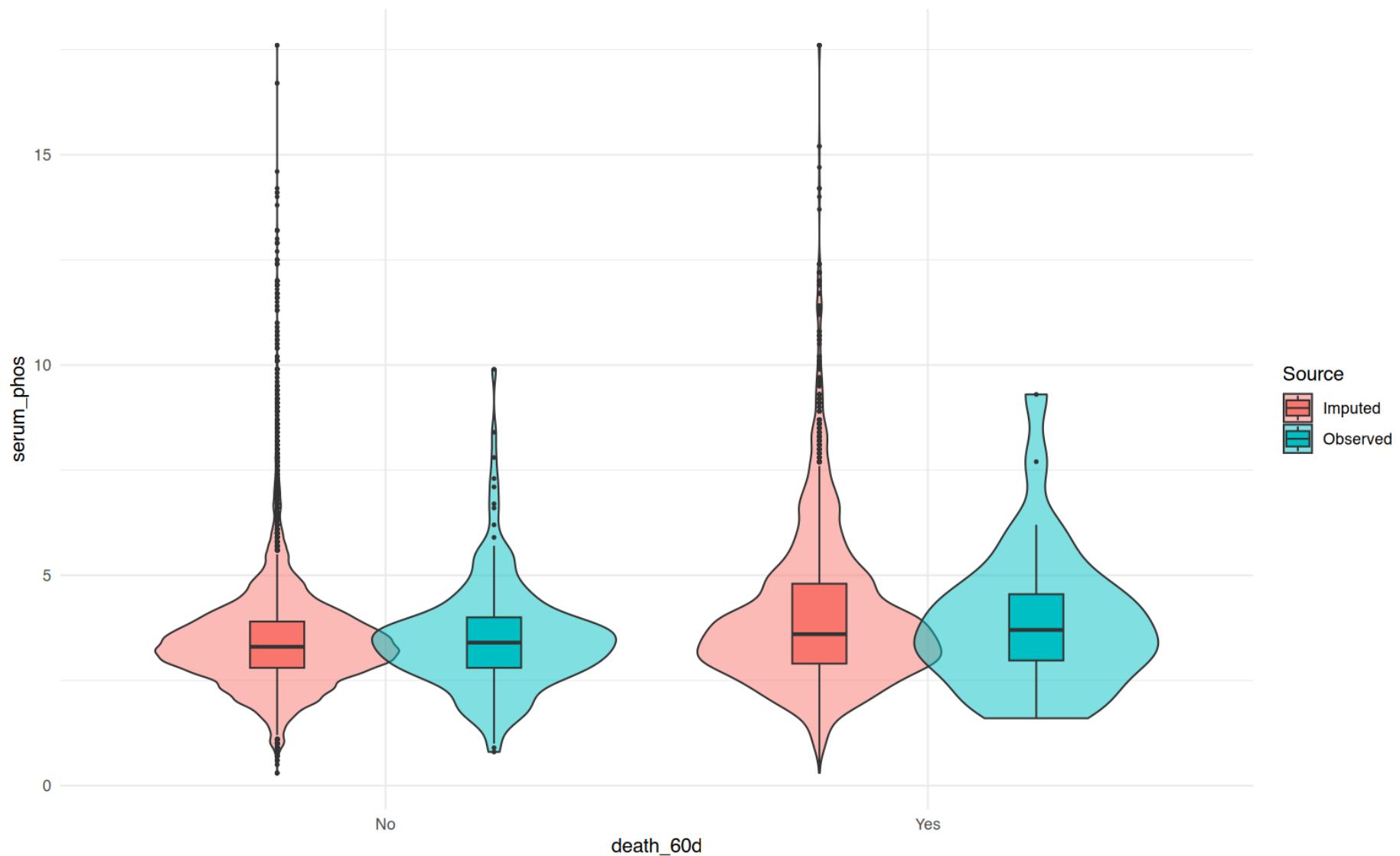
Observed vs imputed: serum_lac by death_60d



Observed vs imputed: curr_bmi by death_60d



Observed vs imputed: serum_phos by death_60d



```
mc_file <- results_path("mi_mcerr_progress.csv")
stopifnot(file.exists(mc_file))
mc_prog <- utils:::read.csv(mc_file)
render_table_pdf(
```

```

mc_prog,
caption = "MC error progress by m (early-stop diagnostic)",
file_stub = "mi_mcerr_progress",
digits = 3
)

```

Table 13: MC error progress by m (early-stop diagnostic)

empty	run_id	run_ts
-------	--------	--------

```

# --- Lean missingness audit (memory-safe) -----
library(dplyr)
library(ggplot2)
library(naniar)

stopifnot(exists("imp"))

dat_imp <- mice::complete(imp, action = 1, include = FALSE)

# 1) Tabular summary on completed data (should be near 0% by design)
miss_tbl <- naniar::miss_var_summary(dat_imp) %>% arrange(desc(pct_miss))
render_table_pdf(
  miss_tbl,
  caption = "Missingness after MI (completed data)",
  file_stub = "missingness_after_mi",
  digits = 2
)

```

```

# 2) Bar plot of top-K (mostly zeros after imputation)
K <- 40
top_vars <- miss_tbl$variable[seq_len(min(K, nrow(miss_tbl)))]
p_top <- ggplot(miss_tbl[miss_tbl$variable %in% top_vars, ],
                 aes(x = reorder(variable, pct_miss), y = pct_miss)) +
  geom_col() +
  coord_flip() +

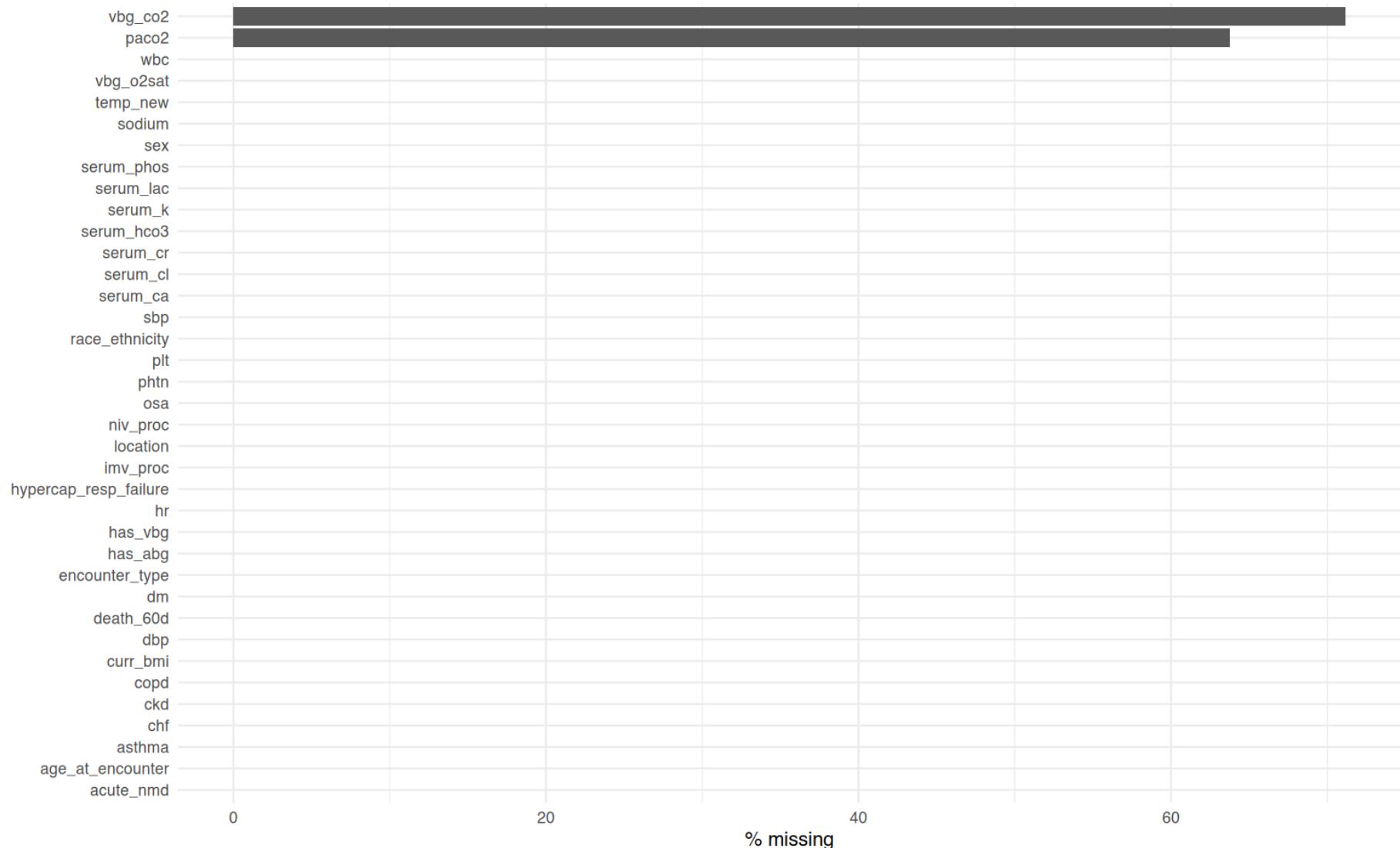
```

Table 14: Missingness after MI (completed data)

variable	n_miss	pct_miss
vbg_co2	18392	71.1
paco2	16490	63.8
age_at_encounter	0	0
sex	0	0
race_ethnicity	0	0
curr_bmi	0	0
copd	0	0
asthma	0	0
osa	0	0
chf	0	0
acute_nmd	0	0
phtn	0	0
ckd	0	0
dm	0	0
location	0	0
encounter_type	0	0
temp_new	0	0
sbp	0	0
dbp	0	0
hr	0	0
sodium	0	0
serum_cr	0	0
serum_hco3	0	0
serum_cl	0	0
serum_lac	0	0
serum_k	0	0
wbc	0	0
plt	0	0
serum_phos	0	0
serum_ca	0	0
has_abg	0	0
has_vbg	0	0
imv_proc	0	0
niv_proc	0	0
death_60d	0	0
hypercap_resp_failure	0	0
vbg_o2sat	0	0

```
labs(title = "Top missing variables (after MI)", x = NULL, y = "% missing") +
  theme_minimal()
print(p_top)
```

Top missing variables (after MI)

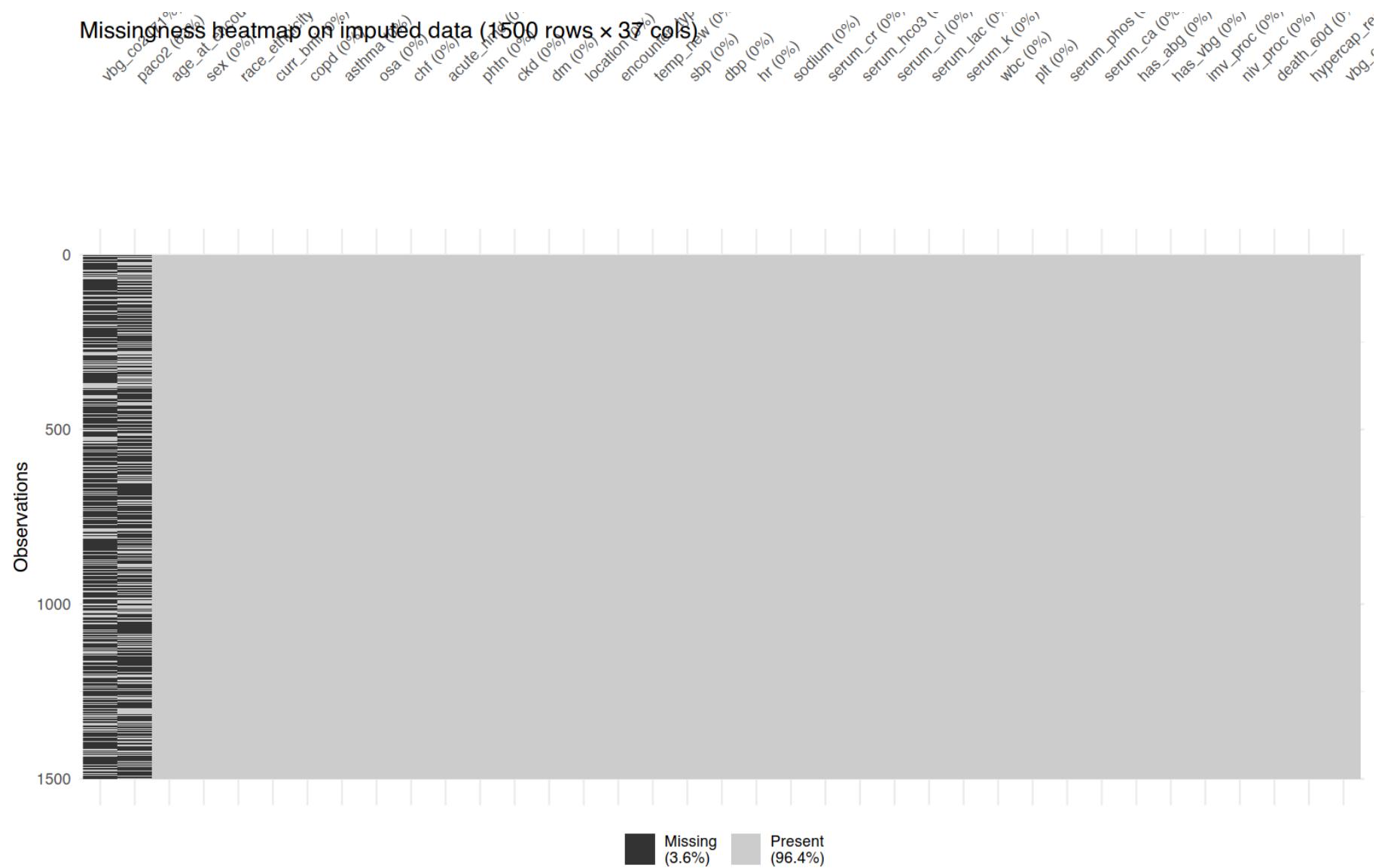


```
# 3) Small heatmap on imputed data (rows/cols sampled)
M <- 60
R <- min(1500, nrow(dat_imp))
cols_heat <- head(top_vars, M)
```

```
rows_heat <- dplyr::slice_sample(dat_imp, n = R)

p_heat <- naniar::vis_miss(rows_heat[, cols_heat, drop = FALSE]) +
  labs(title = sprintf("Missingness heatmap on imputed data (%d rows × %d cols)", R, length(cols_heat)))
print(p_heat)
```

Missingness heatmap on imputed data (1500 rows x 37 cols)



```
# 4) Optional, but often heavy: UpSet of co-missingness - skip by default.  
# If you really want it, do it for top 6-10 variables only:  
# naniar::gg_miss_upset(dat_imp[, head(top_vars, 8), drop = FALSE])
```

3.3 10) Refit propensity models within each imputation

MI propensity scores use logistic regression with restricted cubic splines (`rms::rcs`, 4 knots by default) for continuous covariates; the same covariate set used in non-MI models is reused here (`covars_ps`). IPSW truncation rules are unchanged.

Note: the MI computations below run in a single pass per imputation (weights, balance, cat3, spline). Subsequent MI sections reuse those outputs and will stop if they are missing.

3.3.1 FAIL-FAST CHECKS

```
if (M_IMP < 50) {
  stop("M_IMP must be >= 50. Current M_IMP = ", M_IMP)
}

stopifnot(exists("imp"))

if (imp$m < 50) {
  stop("imp$m must be >= 50. Current imp$m = ", imp$m)
}

# Ensure no missing covariates in each imputation for WeightIt
for (i in seq_len(imp$m)) {
  di <- get_imp(i)
  assert_no_na_covars(di, covars_ps, context = paste0("imputation ", i))
}

# This single-pass loop computes MI weights, target balance, 3-level outcomes,
# and spline outcomes in one traversal of imputations to avoid repeated
# mice::complete() calls and re-normalization.

stopifnot(exists("imp"))
imp_n <- imp$m
mi_single_pass_t0 <- Sys.time()

# --- Helper: fit ABG/VBG weights for a single imputation -----
```

```

fit_abg_one <- function(d, imp_index) {
  d <- normalize_types(d, levels_ref)
  d_ps <- d[, c("has_abg", "has_vbg", covars_ps), drop = FALSE]
  d_ps <- droplevels_all(d_ps)
  write_factor_levels_diag(d_ps, covars_ps, "abg", file_prefix = "mi_logistic_ps_factor_levels")
  assert_no_na_covars(d_ps, covars_ps, context = "ABG MI PS (glm)")
  ps_fit <- fit_mi_ps_glm(
    d_ps, "has_abg", covars_ps,
    k = MI_PS_SPLINE_K, maxit = MI_GLM_MAXIT,
    context = make_context(
      stage = "MI", component = "mi_ps_glm",
      analysis_variant = "weighted_imputed",
      model_type = "ps",
      group = "ABG",
      outcome = NA_character_,
      imputation = imp_index,
      batch = NA_integer_
    )
  )
  if (!is.null(ps_fit$error)) {
    stop("MI PS model failed (ABG, imp ", imp_index, "): ", ps_fit$error)
  }
  ipow <- compute_ipow_weights(
    ps_fit,
    treat = to01(d_ps$has_abg),
    ps_floor_quantile = ps_trunc_quantile,
    stabilize = TRUE
  )
  assert_finite_weights(ipow$weights[d_ps$has_abg == 1], "w_abg")
  ps_fit$weights <- ipow$weights
  ps_fit$ipow_info <- list(
    ps_floor = ipow$ps_floor,
    cap = ipow$cap,
    trunc_rate = mean(ipow$truncated, na.rm = TRUE)
  )
  ps_fit
}

```

```

}

fit_vbg_one <- function(d, imp_index) {
  d <- normalize_types(d, levels_ref)
  d_ps <- d[, c("has_abg", "has_vbg", covars_ps), drop = FALSE]
  d_ps <- droplevels_all(d_ps)
  write_factor_levels_diag(d_ps, covars_ps, "vbg", file_prefix = "mi_logistic_ps_factor_levels")
  assert_no_na_covars(d_ps, covars_ps, context = "VBG MI PS (glm)")
  ps_fit <- fit_mi_ps_glm(
    d_ps, "has_vbg", covars_ps,
    k = MI_PS_SPLINE_K, maxit = MI_GLM_MAXIT,
    context = make_context(
      stage = "MI", component = "mi_ps_glm",
      analysis_variant = "weighted_imputed",
      model_type = "ps",
      group = "VBG",
      outcome = NA_character_,
      imputation = imp_index,
      batch = NA_integer_
    )
  )
  if (!is.null(ps_fit$error)) {
    stop("MI PS model failed (VBG, imp ", imp_index, "): ", ps_fit$error)
  }
  ipow <- compute_ipow_weights(
    ps_fit,
    treat = to01(d_ps$has_vbg),
    ps_floor_quantile = ps_trunc_quantile,
    stabilize = TRUE
  )
  assert_finite_weights(ipow$weights[d_ps$has_vbg == 1], "w_vbg")
  ps_fit$weights <- ipow$weights
  ps_fit$ipow_info <- list(
    ps_floor = ipow$ps_floor,
    cap = ipow$cap,
    trunc_rate = mean(ipow$truncated, na.rm = TRUE)
  )
}

```

```

)
ps_fit
}

# --- Helper: target balance (treated vs target) -----
target_balance_table <- function(data, treat_var, weights, covars, levels_ref = NULL) {
  stopifnot(length(weights) == nrow(data))
  treat <- to01(data[[treat_var]]) == 1L
  treat[is.na(treat)] <- FALSE
  w <- as.numeric(weights)

  w_mean <- function(x, wts) {
    ok <- is.finite(x) & is.finite(wts)
    if (!any(ok)) return(NA_real_)
    sum(wts[ok] * x[ok]) / sum(wts[ok])
  }

  out <- lapply(covars, function(v) {
    x <- data[[v]]
    if (is.character(x)) {
      if (!is.null(levels_ref) && !is.null(levels_ref[[v]])) {
        x <- factor(x, levels = levels_ref[[v]])
      } else {
        x <- factor(x)
      }
    }

    if (is.factor(x)) {
      levs <- levels(x)
      lapply(levs, function(lv) {
        ind <- as.integer(x == lv)
        p_target <- mean(ind, na.rm = TRUE)
        sd_target <- sqrt(p_target * (1 - p_target))
        ind_treat <- ind[treat]
        w_treat <- w[treat]
        pre <- mean(ind_treat, na.rm = TRUE)
      })
    }
  })
}

```

```

post <- w_mean(ind_treat, w_treat)
smd_pre <- if (is.finite(sd_target) && sd_target > 0) (pre - p_target) / sd_target else NA_real_
smd_post <- if (is.finite(sd_target) && sd_target > 0) (post - p_target) / sd_target else NA_real_
data.frame(
  variable = v,
  level = lv,
  type = "factor",
  smd_pre = smd_pre,
  smd_post = smd_post,
  stringsAsFactors = FALSE
)
}) |> dplyr::bind_rows()
} else {
  x_num <- suppressWarnings(as.numeric(x))
  mean_target <- mean(x_num, na.rm = TRUE)
  sd_target <- stats::sd(x_num, na.rm = TRUE)
  x_treat <- x_num[treat]
  w_treat <- w[treat]
  mean_pre <- mean(x_treat, na.rm = TRUE)
  mean_post <- w_mean(x_treat, w_treat)
  smd_pre <- if (is.finite(sd_target) && sd_target > 0) (mean_pre - mean_target) / sd_target else NA_real_
  smd_post <- if (is.finite(sd_target) && sd_target > 0) (mean_post - mean_target) / sd_target else NA_real_
  data.frame(
    variable = v,
    level = NA_character_,
    type = "numeric",
    smd_pre = smd_pre,
    smd_post = smd_post,
    stringsAsFactors = FALSE
  )
}
})
dplyr::bind_rows(out)
}

# --- Helper: fit 3-level outcome per imputation -----

```

```

fit_cat3_imp <- function(d, weights, outcome_var, co2_var, treat_var,
                           low_cut, high_cut, group_label, imp_index) {
  stopifnot(co2_var %in% names(d))
  d[[co2_var]] <- coerce_num(d[[co2_var]])
  g <- d[[treat_var]] == 1 & is.finite(d[[co2_var]])
  if (!any(g)) {
    return(list(error = "No treated rows with finite CO2"))
  }

  d2 <- d[g, , drop = FALSE]
  w <- weights[g]
  w[!is.finite(w)] <- NA_real_
  ok <- is.finite(w)
  if (!all(ok)) {
    d2 <- d2[ok, , drop = FALSE]
    w <- w[ok]
    if (nrow(d2) == 0L) return(list(error = "All weights non-finite"))
  }

  d2$co2_cat <- make_co2_cat3(d2[[co2_var]], low_cut, high_cut)
  d2$co2_cat <- stats::relevel(base::droplevels(d2$co2_cat), ref = "Normal")
  if (nlevels(d2$co2_cat) < 2) {
    return(list(error = "co2_cat has <2 levels"))
  }

  d2[[outcome_var]] <- to01(d2[[outcome_var]])
  des <- survey::svydesign(ids = ~1, weights = ~w, data = d2)
  fml <- stats::reformulate(c("co2_cat", adj_core), response = outcome_var)
  fit_res <- fit_with_diagnostics(
    function() survey::svyglm(fml, design = des, family = quasibinomial(),
                               control = stats::glm.control(maxit = 50)),
    context = make_context(
      stage = "outcome",
      component = "cat3",
      analysis_variant = "mi_ipw",
      model_type = "cat3",

```

```

group = group_label,
outcome = outcome_var,
imputation = imp_index,
batch = NA_integer_
)
)
diag <- fit_res$diag
if (!is.null(diag) && nrow(diag)) {
  diag$n_used <- nrow(d2)
  diag$events <- sum(d2[[outcome_var]] == 1, na.rm = TRUE)
}
list(fit = fit_res$fit, diag = diag, warnings = fit_res$warnings)
}

# --- Pool terms across imputations (robust svyglm) -----
pool_terms <- function(fits, term_prefix = NULL, term_pattern = NULL, min_ok_frac = 0.9) {
  ok <- vapply(fits, function(x) inherits(x, "svyglm"), logical(1))
  fits <- fits[ok]
  m_tot <- length(ok)
  m_ok <- length(fits)
  if (m_ok == 0L) {
    stop("pool_terms: no successful svyglm fits; check per-imputation diagnostics.")
  }
  if (m_ok < ceiling(min_ok_frac * m_tot)) {
    warning("pool_terms: only ", m_ok, " / ", m_tot,
           " fits succeeded (below min_ok_frac).", call. = FALSE)
  }
  if (!all(vapply(fits, inherits, logical(1), "svyglm"))) {
    stop("pool_terms expects svyglm fits so pooled vcov is robust.")
  }
  results <- lapply(fits, coef)
  variances <- lapply(fits, vcov)
  pooled <- mitools::MIcombine(results = results, variances = variances)
  pooled_mi_vcov_check(pooled)
  est <- as.numeric(coef(pooled))
  se <- sqrt(diag(pooled$variance))
}

```

```

term <- names(coef(pooled))
out <- data.frame(
  term = term,
  logOR = est,
  estimate = exp(est),
  SE = se,
  LCL = exp(est - 1.96 * se),
  UCL = exp(est + 1.96 * se),
  stringsAsFactors = FALSE
)
if (!is.null(term_prefix)) {
  out <- out[grep0("^", term_prefix), out$term], , drop = FALSE]
}
if (!is.null(term_pattern)) {
  out <- out[grep0(term_pattern, out$term), , drop = FALSE]
}
out
}

# --- Fit spline model on treated cohort only (IPSW) -----
fit_spline_imp <- function(data, weights, outcome, co2_var, treat_var,
                            adj_vars = NULL,
                            spline_df = SPLINE_DF,
                            spline_basis = SPLINE_BASIS,
                            grid_df = NULL,
                            ref_idx = NULL,
                            imp_index = NA_integer_) {
  spline_basis <- match.arg(spline_basis, c("ns", "rcs"))
  stopifnot(is.data.frame(data))
  stopifnot(length(weights) == nrow(data))
  stopifnot(all(c(outcome, co2_var, treat_var) %in% names(data)))
  if (!is.null(adj_vars) && length(adj_vars)) {
    missing_adj <- setdiff(adj_vars, names(data))
    if (length(missing_adj)) {
      return(list(error = paste0("Missing adj_core vars: ", paste(missing_adj, collapse = ", "))))
    }
  }
}

```

```
}
```

```
data[[treat_var]] <- to01(data[[treat_var]])
data[[outcome]]   <- to01(data[[outcome]])
data[[co2_var]]   <- coerce_num(data[[co2_var]])
w <- suppressWarnings(as.numeric(weights))

keep <- (data[[treat_var]] == 1L) &
  is.finite(data[[co2_var]]) &
  !is.na(data[[outcome]]) &
  is.finite(w) & (w > 0)

if (!any(keep)) {
  return(list(error = "No eligible treated rows after filtering (treated==1, finite CO2, non-missing outcome, finite positive weight)"))
}

d2 <- data[keep, , drop = FALSE]
w2 <- w[keep]
d2$w <- w2

if (length(unique(d2[[outcome]])) < 2L) {
  return(list(error = paste0("Outcome has one level in treated sample after filtering: outcome=", outcome, ", n=", nrow(d2),
                             ", events=", sum(d2[[outcome]] == 1, na.rm = TRUE))))
}

des <- survey::svydesign(ids = ~1, weights = ~w, data = d2)
if (spline_basis == "ns") {
  rhs_terms <- c(sprintf("splines::ns(%s, %d)", co2_var, spline_df), adj_vars)
  fml <- stats::as.formula(paste(outcome, "~", paste(rhs_terms, collapse = " + ")))
} else {
  dd <- rms::datadist(d2)
  old_opt <- options(datadist = ".__dd_tmp__")
  assign(".__dd_tmp__", dd, envir = .GlobalEnv)
  on.exit({
    options(old_opt)
  })
}
```

```

    rm(list = ".__dd_tmp__", envir = .GlobalEnv)
}, add = TRUE)
rhs_terms <- c(sprintf("rms::rcs(%s, %d)", co2_var, spline_df), adj_vars)
fml <- stats::as.formula(paste(outcome, "~", paste(rhs_terms, collapse = " + ")))
}

group_label <- if (identical(treat_var, "has_abg")) "ABG" else if (identical(treat_var, "has_vbg")) "VBG" else treat_var
fit_res <- fit_with_diagnostics(
  function() survey::svyglm(fml, design = des, family = quasibinomial(),
                            control = stats::glm.control(maxit = 50)),
  context = make_context(
    stage = "outcome",
    component = "spline",
    analysis_variant = "mi_ipw",
    model_type = "spline",
    group = group_label,
    outcome = outcome,
    imputation = imp_index,
    batch = NA_integer_
  )
)
fit <- fit_res$fit
warns <- fit_res$warnings
diag <- fit_res$diag
if (!is.null(diag) && nrow(diag)) {
  diag$n_used <- nrow(d2)
  diag$events <- sum(d2[[outcome]] == 1, na.rm = TRUE)
}
if (is.null(fit)) {
  err_msg <- if (!is.null(diag$error_message) && is.finite(nchar(diag$error_message))) diag$error_message else "svyglm error"
  return(list(error = err_msg,
             warnings = warns,
             diag = diag,
             n_used = nrow(d2),
             events = sum(d2[[outcome]] == 1, na.rm = TRUE)))
}

```

```

if (!is.null(grid_df)) {
  if (is.null(ref_idx)) {
    return(list(error = "ref_idx is required when grid_df is provided.",
               warnings = warns, diag = diag))
  }
  pr <- tryCatch(
    predict_or_curve_from_fit(fit, grid_df, ref_idx, co2_var),
    error = function(e) list(error = paste0("predict error: ", conditionMessage(e)))
  )
  if (!is.null(pr$error)) return(list(error = pr$error,
                                         warnings = warns,
                                         diag = diag,
                                         n_used = nrow(d2),
                                         events = sum(d2[[outcome]] == 1, na.rm = TRUE)))
  return(list(
    fit = fit,
    logOR = pr$logOR,
    var_logOR = pr$var_logOR,
    warnings = warns,
    diag = diag,
    n_used = nrow(d2),
    events = sum(d2[[outcome]] == 1, na.rm = TRUE)
  ))
}

list(fit = fit, warnings = warns, diag = diag,
      n_used = nrow(d2),
      events = sum(d2[[outcome]] == 1, na.rm = TRUE))
}

# --- Pool spline coefficients across imputations -----
pool_spline_coefs <- function(fit_list, min_ok_frac = 0.9) {
  fits <- lapply(fit_list, function(x) if (is.list(x) && !is.null(x$fit)) x$fit else if (inherits(x, "svyglm")) x else NULL)
  ok <- !vapply(fits, is.null, logical(1))
  m_tot <- length(ok)
}

```

```

m_ok <- sum(ok)
if (m_ok < ceiling(min_ok_frac * m_tot)) {
  stop("Too many failed spline fits: m_ok=", m_ok, " / m_total=", m_tot)
}
fits <- fits[ok]
results <- lapply(fits, coef)
variances <- lapply(fits, vcov)
pooled <- mitools::MIcombine(results = results, variances = variances)
pooled_mi_vcov_check(pooled)
est <- as.numeric(coef(pooled))
se <- sqrt(diag(pooled$variance))
data.frame(
  term = names(coef(pooled)),
  estimate = est,
  SE = se,
  LCL = est - 1.96 * se,
  UCL = est + 1.96 * se,
  m_used = m_ok,
  m_total = m_tot,
  row.names = NULL
)
}

# --- Pool spline curves (pointwise Rubin pooling on log-OR scale) -----
pool_spline_curve <- function(fit_list, grid_df, ref_idx, co2_ref, min_ok_frac = 0.9) {
  n_grid <- nrow(grid_df)
  ok <- vapply(fit_list, function(x) {
    is.list(x) && is.null(x$error) &&
      !is.null(x$logOR) && !is.null(x$var_logOR) &&
      length(x$logOR) == n_grid && length(x$var_logOR) == n_grid
  }, logical(1))
  m_tot <- length(ok)
  m_ok <- sum(ok)
  if (m_ok < ceiling(min_ok_frac * m_tot)) {
    stop("Too many failed spline fits: m_ok=", m_ok, " / m_total=", m_tot)
  }
}

```

```

logOR_mat <- matrix(NA_real_, nrow = n_grid, ncol = m_ok)
var_mat <- matrix(NA_real_, nrow = n_grid, ncol = m_ok)
ok_idx <- which(ok)
for (i in seq_along(ok_idx)) {
  fit_i <- fit_list[[ok_idx[i]]]
  logOR_mat[, i] <- fit_i$logOR
  var_mat[, i] <- fit_i$var_logOR
}
Qbar <- rowMeans(logOR_mat, na.rm = TRUE)
Ubar <- rowMeans(var_mat, na.rm = TRUE)
B <- apply(logOR_mat, 1, stats::var, na.rm = TRUE)
Tvar <- Ubar + (1 + 1 / m_ok) * B
se <- sqrt(Tvar)
if (!is.na(ref_idx) && is.finite(ref_idx)) {
  if (abs(exp(Qbar[ref_idx]) - 1) > 1e-6) {
    warning("Pooled spline OR at reference differs from 1 (check ref_idx/co2_ref).", call. = FALSE)
  }
}
data.frame(
  grid_df,
  logOR = Qbar,
  SE_logOR = se,
  OR = exp(Qbar),
  LCL = exp(Qbar - 1.96 * se),
  UCL = exp(Qbar + 1.96 * se),
  co2_ref = co2_ref,
  m_used = m_ok,
  m_total = m_tot,
  row.names = NULL
)
# --- Single-pass loop -----
cat3_outcomes <- c("imv_proc", "niv_proc", "death_60d", "hypercap_resp_failure")
cat3_labels <- c(

```

```

imv_proc = "IMV",
niv_proc = "NIV",
death_60d = "Death60d",
hypercap_resp_failure = "HCRF"
)

abg_co2_obs <- subset_data$paco2[subset_data$has_abg == 1 & !is.na(subset_data$paco2)]
if (length(abg_co2_obs) < 10) stop("ABG spline: not enough observed PaCO2 values.")
q_abg <- stats::quantile(abg_co2_obs, probs = c(0.02, 0.98), na.rm = TRUE)
grid_abg_info_mi <- make_co2_grid_ref(
  "paco2",
  seq(q_abg[1], q_abg[2], length.out = SPLINE_GRID_N),
  x_ref_abg,
  ABG_CO2_REF
)
grid_abg_mi <- grid_abg_info_mi$grid
ref_idx_abg_mi <- grid_abg_info_mi$ref_idx
co2_ref_abg_mi <- grid_abg_info_mi$co2_ref

vbg_co2_obs <- subset_data$vbg_co2[subset_data$has_vbg == 1 & !is.na(subset_data$vbg_co2)]
if (length(vbg_co2_obs) < 10) stop("VBG spline: not enough observed VBG CO2 values.")
q_vbg <- stats::quantile(vbg_co2_obs, probs = c(0.02, 0.98), na.rm = TRUE)
grid_vbg_info_mi <- make_co2_grid_ref(
  "vbg_co2",
  seq(q_vbg[1], q_vbg[2], length.out = SPLINE_GRID_N),
  x_ref_vbg,
  VBG_CO2_REF
)
grid_vbg_mi <- grid_vbg_info_mi$grid
ref_idx_vbg_mi <- grid_vbg_info_mi$ref_idx
co2_ref_vbg_mi <- grid_vbg_info_mi$co2_ref

covars_use <- intersect(covars_ps, names(subset_data))
covars_use_abg <- covars_use
covars_use_vbg <- covars_use

```

```

# MI PS covariate typing (continuous vs categorical) for transparency
mi_logistic_ps_type_file <- results_path("mi_logistic_ps_covariate_types.csv")
d_ps_tmp <- get_imp(1)
d_ps_tmp <- normalize_types(d_ps_tmp, levels_ref)
d_ps_tmp <- d_ps_tmp[, c("has_abg", "has_vbg", covars_ps), drop = FALSE]
d_ps_tmp <- droplevels_all(d_ps_tmp)
cont_vars <- covars_ps[vapply(covars_ps, ps_is_continuous, logical(1), df = d_ps_tmp)]
cat_vars_ps <- setdiff(covars_ps, cont_vars)
mi_logistic_ps_types <- dplyr::bind_rows(
  data.frame(variable = cont_vars, type = "continuous", stringsAsFactors = FALSE),
  data.frame(variable = cat_vars_ps, type = "categorical", stringsAsFactors = FALSE)
)
write_csv_safely(mi_logistic_ps_types, mi_logistic_ps_type_file, row_names = FALSE)
rm(d_ps_tmp, cont_vars, cat_vars_ps, mi_logistic_ps_types)
gc()

```

	used (Mb)	gc trigger (Mb)	limit (Mb)	max used (Mb)
Ncells	6608979	353.0	11762510	628.2 NA 9528452 508.9
Vcells	610420413	4657.2	1054093700	8042.1 16384 1054093700 8042.1

```

mi_logistic_ps_abg_list <- vector("list", imp_n)
mi_logistic_ps_vbg_list <- vector("list", imp_n)
bal_rows_abg <- vector("list", imp_n)
bal_rows_vbg <- vector("list", imp_n)
cat3_fits_abg <- setNames(lapply(cat3_outcomes, function(x) vector("list", imp_n)), cat3_outcomes)
cat3_fits_vbg <- setNames(lapply(cat3_outcomes, function(x) vector("list", imp_n)), cat3_outcomes)
spline_fits_abg <- setNames(lapply(cat3_outcomes, function(x) vector("list", imp_n)), cat3_outcomes)
spline_fits_vbg <- setNames(lapply(cat3_outcomes, function(x) vector("list", imp_n)), cat3_outcomes)

cat3_diag_rows <- list()
spline_diag_rows <- list()
weight_diag_abg <- vector("list", imp_n)
weight_diag_vbg <- vector("list", imp_n)

message("MI single-pass: running ", imp_n, " imputations sequentially.")

```

```

for (i in seq_len(imp_n)) {
  d <- get_imp(i)

  set.seed(20251206 + i)
  mi_logistic_ps_abg_list[[i]] <- fit_abg_one(d, i)
  set.seed(30251206 + i)
  mi_logistic_ps_vbg_list[[i]] <- fit_vbg_one(d, i)

  bal_rows_abg[[i]] <- target_balance_table(
    d, "has_abg", mi_logistic_ps_abg_list[[i]]$weights, covars_use_abg, levels_ref
  ) |>
    dplyr::mutate(group = "ABG", imp = i)
  bal_rows_vbg[[i]] <- target_balance_table(
    d, "has_vbg", mi_logistic_ps_vbg_list[[i]]$weights, covars_use_vbg, levels_ref
  ) |>
    dplyr::mutate(group = "VBG", imp = i)

  for (outcome_var in cat3_outcomes) {
    fit_abg_cat <- fit_cat3_imp(
      d, mi_logistic_ps_abg_list[[i]]$weights, outcome_var, "paco2", "has_abg",
      ABG_CO2_LOW, ABG_CO2_HIGH, "ABG", i
    )
    cat3_fits_abg[[outcome_var]][[i]] <- fit_abg_cat$fit
    if (!is.null(fit_abg_cat$diag)) cat3_diag_rows[[length(cat3_diag_rows) + 1L]] <- fit_abg_cat$diag

    fit_vbg_cat <- fit_cat3_imp(
      d, mi_logistic_ps_vbg_list[[i]]$weights, outcome_var, "vbg_co2", "has_vbg",
      VBG_CO2_LOW, VBG_CO2_HIGH, "V ро", i
    )
    cat3_fits_vbg[[outcome_var]][[i]] <- fit_vbg_cat$fit
    if (!is.null(fit_vbg_cat$diag)) cat3_diag_rows[[length(cat3_diag_rows) + 1L]] <- fit_vbg_cat$diag
  }

  for (outcome_var in cat3_outcomes) {
    spline_abg <- fit_spline_imp(
      d, mi_logistic_ps_abg_list[[i]]$weights, outcome_var, "paco2", "has_abg",

```

```

adj_vars = adj_core, spline_df = SPLINE_DF, spline_basis = SPLINE_BASIS,
grid_df = grid_abg_mi, ref_idx = ref_idx_abg_mi, imp_index = i
)
spline_fits_abg[[outcome_var]][[i]] <- spline_abg
if (!is.null(spline_abg$diag)) spline_diag_rows[[length(spline_diag_rows) + 1L]] <- spline_abg$diag

spline_vbg <- fit_spline_imp(
  d, mi_logistic_ps_vbg_list[[i]]$weights, outcome_var, "vbg_co2", "has_vbg",
  adj_vars = adj_core, spline_df = SPLINE_DF, spline_basis = SPLINE_BASIS,
  grid_df = grid_vbg_mi, ref_idx = ref_idx_vbg_mi, imp_index = i
)
spline_fits_vbg[[outcome_var]][[i]] <- spline_vbg
if (!is.null(spline_vbg$diag)) spline_diag_rows[[length(spline_diag_rows) + 1L]] <- spline_vbg$diag
}

weight_diag_abg[[i]] <- {
  w <- mi_logistic_ps_abg_list[[i]]$weights
  t <- d$has_abg
  w <- w[t == 1]
  c(
    n = length(w),
    min = min(w, na.rm = TRUE),
    p99 = stats::quantile(w, 0.99, na.rm = TRUE),
    max = max(w, na.rm = TRUE),
    ess = sum(w^2) / sum(w^2)
  )
}
weight_diag_vbg[[i]] <- {
  w <- mi_logistic_ps_vbg_list[[i]]$weights
  t <- d$has_vbg
  w <- w[t == 1]
  c(
    n = length(w),
    min = min(w, na.rm = TRUE),
    p99 = stats::quantile(w, 0.99, na.rm = TRUE),
    max = max(w, na.rm = TRUE),
    ess = sum(w^2) / sum(w^2)
  )
}

```

```

    ess = sum(w)^2 / sum(w^2)
  )
}

rm(d)
invisible(gc())
}

append_outcome_diag(dplyr::bind_rows(cat3_diag_rows, spline_diag_rows))

bal_imp_abg <- list(
  bal_long = dplyr::bind_rows(bal_rows_abg)
)
bal_imp_abg$bal_imp_summary <- bal_imp_abg$bal_long |>
  dplyr::group_by(group, imp) |>
  dplyr::summarise(
    max_abs_post = max(abs(smd_post), na.rm = TRUE),
    mean_abs_post = mean(abs(smd_post), na.rm = TRUE),
    .groups = "drop"
  )
bal_imp_abg$worst_rows_overall <- bal_imp_abg$bal_long |>
  dplyr::mutate(abs_post = abs(smd_post)) |>
  dplyr::arrange(desc(abs_post)) |>
  dplyr::ungroup()
bal_imp_abg$worst_by_imp <- bal_imp_abg$bal_long |>
  dplyr::mutate(term = ifelse(is.na(level), variable, paste0(variable, ":", level)),
    abs_post = abs(smd_post)) |>
  dplyr::group_by(group, imp) |>
  dplyr::slice_max(abs_post, n = 1, with_ties = FALSE) |>
  dplyr::ungroup() |>
  dplyr::select(group, imp, term, smd_pre, smd_post, abs_post)
bal_imp_abg$worst_terms_by_imp <- bal_imp_abg$bal_long |>
  dplyr::mutate(term = ifelse(is.na(level), variable, paste0(variable, ":", level)),
    abs_post = abs(smd_post)) |>
  dplyr::group_by(group, imp) |>
  dplyr::slice_max(abs_post, n = 10, with_ties = FALSE) |>

```

```

dplyr::ungroup() |>
dplyr::select(group, imp, term, smd_pre, smd_post, abs_post)

bal_imp_vbg <- list(
  bal_long = dplyr::bind_rows(bal_rows_vbg)
)
bal_imp_vbg$bal_imp_summary <- bal_imp_vbg$bal_long |>
  dplyr::group_by(group, imp) |>
  dplyr::summarise(
    max_abs_post = max(abs(smd_post), na.rm = TRUE),
    mean_abs_post = mean(abs(smd_post), na.rm = TRUE),
    .groups = "drop"
  )
bal_imp_vbg$worst_rows_overall <- bal_imp_vbg$bal_long |>
  dplyr::mutate(abs_post = abs(smd_post)) |>
  dplyr::arrange(desc(abs_post)) |>
  dplyr::ungroup()
bal_imp_vbg$worst_by_imp <- bal_imp_vbg$bal_long |>
  dplyr::mutate(term = ifelse(is.na(level), variable, paste0(variable, ":", level)),
                abs_post = abs(smd_post)) |>
  dplyr::group_by(group, imp) |>
  dplyr::slice_max(abs_post, n = 1, with_ties = FALSE) |>
  dplyr::ungroup() |>
  dplyr::select(group, imp, term, smd_pre, smd_post, abs_post)
bal_imp_vbg$worst_terms_by_imp <- bal_imp_vbg$bal_long |>
  dplyr::mutate(term = ifelse(is.na(level), variable, paste0(variable, ":", level)),
                abs_post = abs(smd_post)) |>
  dplyr::group_by(group, imp) |>
  dplyr::slice_max(abs_post, n = 10, with_ties = FALSE) |>
  dplyr::ungroup() |>
  dplyr::select(group, imp, term, smd_pre, smd_post, abs_post)

mi_weight_diag_abg <- dplyr::bind_rows(lapply(weight_diag_abg, function(x) {
  as.data.frame(as.list(x), stringsAsFactors = FALSE)
}()))
mi_weight_diag_vbg <- dplyr::bind_rows(lapply(weight_diag_vbg, function(x) {

```

```

    as.data.frame(as.list(x), stringsAsFactors = FALSE)
}))

abg_cat_results <- dplyr::bind_rows(lapply(cat3_outcomes, function(outcome_var) {
  pool_terms(cat3_fits_abg[[outcome_var]], term_prefix = "co2_cat") |>
    dplyr::mutate(
      outcome = cat3_labels[[outcome_var]],
      group = "ABG",
      OR = estimate
    )
}))

vbg_cat_results <- dplyr::bind_rows(lapply(cat3_outcomes, function(outcome_var) {
  pool_terms(cat3_fits_vbg[[outcome_var]], term_prefix = "co2_cat") |>
    dplyr::mutate(
      outcome = cat3_labels[[outcome_var]],
      group = "VBG",
      OR = estimate
    )
}))

abg_spline <- list(
  curves = dplyr::bind_rows(lapply(cat3_outcomes, function(outcome_var) {
    pool_spline_curve(spline_fits_abg[[outcome_var]], grid_abg_mi, ref_idx_abg_mi, co2_ref_abg_mi) |>
      dplyr::mutate(outcome = outcome_var, group = "ABG")
  })),
  coefs = dplyr::bind_rows(lapply(cat3_outcomes, function(outcome_var) {
    pool_spline_coefs(spline_fits_abg[[outcome_var]]) |>
      dplyr::mutate(outcome = outcome_var, group = "ABG")
  }))
)

vbg_spline <- list(
  curves = dplyr::bind_rows(lapply(cat3_outcomes, function(outcome_var) {
    pool_spline_curve(spline_fits_vbg[[outcome_var]], grid_vbg_mi, ref_idx_vbg_mi, co2_ref_vbg_mi) |>
      dplyr::mutate(outcome = outcome_var, group = "VBG")
  })),
  coefs = dplyr::bind_rows(lapply(cat3_outcomes, function(outcome_var) {

```

```

    pool_spline_coefs(spline_fits_vbg[[outcome_var]]) |>
      dplyr::mutate(outcome = outcome_var, group = "VBG")
  }))

abg_curves <- abg_spline$curves
abg_coefs  <- abg_spline$coefs
vbg_curves <- vbg_spline$curves
vbg_coefs  <- vbg_spline$coefs

write_csv_safely(abg_curves, results_path("mi_spline_curve_abg.csv"), row_names = FALSE)
write_csv_safely(abg_coefs,  results_path("mi_spline_coef_abg.csv"), row_names = FALSE)
write_csv_safely(vbg_curves, results_path("mi_spline_curve_vbg.csv"), row_names = FALSE)
write_csv_safely(vbg_coefs,  results_path("mi_spline_coef_vbg.csv"), row_names = FALSE)

mi_single_pass_t1 <- Sys.time()
stopifnot(exists("runtime_log"))
runtime_log <- dplyr::bind_rows(
  runtime_log,
  data.frame(
    step_name = "mi_single_pass",
    seconds = as.numeric(difftime(mi_single_pass_t1, mi_single_pass_t0, units = "secs")),
    start_time = as.character(mi_single_pass_t0),
    end_time = as.character(mi_single_pass_t1),
    notes = paste0("m=", imp_n),
    run_id = runtime_run_id,
    run_mode = RUN_MODE,
    n_subset = nrow(subset_data),
    stringsAsFactors = FALSE
  )
)

mi_single_pass_done <- TRUE

```

3.3.2 10.1 ABG propensity (has_abg)

```
stopifnot(exists("mi_single_pass_done"), isTRUE(mi_single_pass_done))
stopifnot(exists("mi_logistic_ps_abg_list"))
message("ABG MI weights were computed in the single-pass MI loop above.")
```

Table 15: ABG weight diagnostics (MI; median across imputations)

n	min	p99.99.	max	ess
9362	0.384	3.819	3.821	6847.997

3.3.3 10.2 Balance diagnostics across imputations

```
stopifnot(exists("target_balance_table"))

# Use a fixed x-axis max so ABG/VBG balance plots are directly comparable.

stopifnot(exists("bal_imp_abg"))

bal_abg_pooled <- bal_imp_abg$bal_long |>
  mutate(label = ifelse(is.na(level), variable, paste0(variable, ":", level))) |>
  group_by(label) |>
  summarise(
    pre_med = median(abs(smd_pre), na.rm = TRUE),
    post_med = median(abs(smd_post), na.rm = TRUE),
    pre_mean = mean(abs(smd_pre), na.rm = TRUE),
    post_mean = mean(abs(smd_post), na.rm = TRUE),
    post_max = max(abs(smd_post), na.rm = TRUE),
    .groups = "drop"
  )
  bal_abg_plot <- bal_abg_pooled |>
```

```

mutate(label = factor(label, levels = label[order(post_med, decreasing = TRUE)])) |>
pivot_longer(c(pre_med, post_med), names_to = "type", values_to = "smd") |>
mutate(type = recode(type, pre_med = "Pre", post_med = "Post"))

p_abg <- ggplot(bal_abg_plot, aes(x = smd, y = label, shape = type)) +
  geom_vline(xintercept = 0.1, linetype = 2, linewidth = 0.3) +
  geom_point(size = 1.2) +
  labs(title = "MI target balance (ABG): pooled |SMD|", x = "|Target SMD|", y = NULL, shape = "Stage") +
  scale_x_continuous(limits = c(0, BAL_XLIM_MAX),
                     expand = expansion(mult = c(0, 0.02))) +
  theme_minimal(base_size = 10)
save_diag_plot(p_abg, results_path("figs", "diag-mi-balance-pooled-abg.png"), width = 7, height = 6)

render_table_pdf(
  bal_imp_abg$worst_rows_overall,
  caption = "ABG: target SMD rows across imputations (sorted by |SMD|)",
  file_stub = "abg_worst_target_smd_rows",
  digits = 3
)

```

Table 16: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part A)

variable	level	type	smd_pre	smd_post	group
encounter_type	Inpatient	factor	0.370	0.100	ABG
encounter_type	Emergency	factor	-0.370	-0.100	ABG
encounter_type	Inpatient	factor	0.370	0.098	ABG
encounter_type	Emergency	factor	-0.370	-0.098	ABG
encounter_type	Inpatient	factor	0.370	0.096	ABG
encounter_type	Emergency	factor	-0.370	-0.096	ABG
encounter_type	Emergency	factor	-0.370	-0.095	ABG
encounter_type	Inpatient	factor	0.370	0.095	ABG
encounter_type	Emergency	factor	-0.370	-0.095	ABG
encounter_type	Inpatient	factor	0.370	0.095	ABG
encounter_type	Emergency	factor	-0.370	-0.095	ABG
encounter_type	Inpatient	factor	0.370	0.095	ABG
encounter_type	Emergency	factor	-0.370	-0.094	ABG
encounter_type	Inpatient	factor	0.370	0.094	ABG
encounter_type	Emergency	factor	-0.370	-0.094	ABG
encounter_type	Inpatient	factor	0.370	0.094	ABG
encounter_type	Emergency	factor	-0.370	-0.094	ABG
encounter_type	Inpatient	factor	0.370	0.094	ABG
encounter_type	Emergency	factor	-0.370	-0.094	ABG
location	0	factor	0.166	0.094	ABG
location	0	factor	0.166	0.094	ABG
encounter_type	Emergency	factor	-0.370	-0.093	ABG
encounter_type	Inpatient	factor	0.370	0.093	ABG
location	0	factor	0.166	0.093	ABG
encounter_type	Inpatient	factor	0.370	0.093	ABG
encounter_type	Emergency	factor	-0.370	-0.093	ABG
encounter_type	Inpatient	factor	0.370	0.093	ABG
encounter_type	Emergency	factor	-0.370	-0.093	ABG
location	0	factor	0.166	0.093	ABG
encounter_type	Inpatient	factor	0.370	0.093	ABG
encounter_type	Emergency	factor	-0.370	-0.093	ABG
encounter_type	Inpatient	factor	0.370	0.093	ABG
encounter_type	Emergency	factor	-0.370	-0.093	ABG
encounter_type	Inpatient	factor	0.370	0.093	ABG
encounter_type	Emergency	factor	-0.370	-0.093	ABG
encounter_type	Inpatient	factor	0.370	0.093	ABG
encounter_type	Emergency	factor	-0.370	-0.093	ABG
location	0	factor	0.166	0.093	ABG
encounter_type	Emergency	factor	-0.370	-0.093	ABG
encounter_type	Inpatient	factor	0.370	0.092	ABG
encounter_type	Emergency	factor	-0.370	-0.092	ABG
location	0	factor	0.166	0.092	ABG
encounter_type	Inpatient	factor	0.370	0.092	ABG
encounter_type	Emergency	factor	-0.370	-0.092	ABG
location	0	factor	0.166	0.092	ABG
encounter_type	Emergency	factor	-0.370	-0.092	ABG
encounter_type	Inpatient	factor	0.370	0.091	ABG

Table 16: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
location	0	factor	0.166	0.091	ABG
location	0	factor	0.166	0.091	ABG
location	0	factor	0.166	0.091	ABG
encounter_type	Emergency	factor	-0.370	-0.091	ABG
encounter_type	Inpatient	factor	0.370	0.091	ABG
location	0	factor	0.166	0.091	ABG
location	0	factor	0.166	0.091	ABG
encounter_type	Inpatient	factor	0.370	0.091	ABG
encounter_type	Emergency	factor	-0.370	-0.091	ABG
encounter_type	Emergency	factor	-0.370	-0.091	ABG
encounter_type	Inpatient	factor	0.370	0.091	ABG
location	0	factor	0.166	0.091	ABG
location	0	factor	0.166	0.091	ABG
location	0	factor	0.166	0.091	ABG
location	0	factor	0.166	0.090	ABG
encounter_type	Emergency	factor	-0.370	-0.090	ABG
encounter_type	Inpatient	factor	0.370	0.090	ABG
encounter_type	Inpatient	factor	0.370	0.090	ABG
encounter_type	Emergency	factor	-0.370	-0.090	ABG
location	0	factor	0.166	0.090	ABG
location	0	factor	0.166	0.090	ABG
encounter_type	Emergency	factor	-0.370	-0.090	ABG
encounter_type	Inpatient	factor	0.370	0.090	ABG
encounter_type	Inpatient	factor	0.370	0.090	ABG
encounter_type	Emergency	factor	-0.370	-0.090	ABG
location	0	factor	0.166	0.090	ABG
encounter_type	Emergency	factor	-0.370	-0.090	ABG
encounter_type	Inpatient	factor	0.370	0.090	ABG
encounter_type	Inpatient	factor	0.370	0.090	ABG
encounter_type	Emergency	factor	-0.370	-0.090	ABG
location	0	factor	0.166	0.090	ABG
encounter_type	Emergency	factor	-0.370	-0.090	ABG
encounter_type	Inpatient	factor	0.370	0.090	ABG
encounter_type	Emergency	factor	-0.370	-0.090	ABG
encounter_type	Inpatient	factor	0.370	0.090	ABG
encounter_type	Emergency	factor	-0.370	-0.090	ABG
location	0	factor	0.166	0.090	ABG
encounter_type	Emergency	factor	-0.370	-0.090	ABG
encounter_type	Inpatient	factor	0.370	0.090	ABG
encounter_type	Emergency	factor	-0.370	-0.090	ABG
encounter_type	Inpatient	factor	0.370	0.090	ABG
encounter_type	Emergency	factor	-0.370	-0.090	ABG
location	0	factor	0.166	0.090	ABG
encounter_type	Inpatient	factor	0.370	0.090	ABG
encounter_type	Emergency	factor	-0.370	-0.090	ABG
encounter_type	Emergency	factor	-0.370	-0.090	ABG
encounter_type	Inpatient	factor	0.370	0.090	ABG
encounter_type	Emergency	factor	-0.370	-0.090	ABG
location	0	factor	0.166	0.090	ABG
encounter_type	Inpatient	factor	0.370	0.089	ABG
encounter_type	Emergency	factor	-0.370	-0.089	ABG
location	0	factor	0.166	0.089	ABG
location	0	factor	0.166	0.089	ABG
encounter_type	Emergency	factor	-0.370	-0.089	ABG
encounter_type	Inpatient	factor	0.370	0.089	ABG
encounter_type	Inpatient	factor	0.370	0.089	ABG
encounter_type	Emergency	factor	-0.370	-0.089	ABG
location	0	factor	0.166	0.089	ABG
location	0	factor	0.166	0.089	ABG

Table 16: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

Table 16: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

Table 16: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
location	1	factor	-0.132	-0.079	ABG
location	1	factor	-0.132	-0.079	ABG
location	1	factor	-0.132	-0.078	ABG
location	1	factor	-0.132	-0.078	ABG
location	1	factor	-0.132	-0.078	ABG
location	1	factor	-0.132	-0.078	ABG
location	1	factor	-0.132	-0.078	ABG
location	1	factor	-0.132	-0.078	ABG
location	1	factor	-0.132	-0.078	ABG
location	1	factor	-0.132	-0.078	ABG
location	1	factor	-0.132	-0.077	ABG
location	1	factor	-0.132	-0.077	ABG
location	1	factor	-0.132	-0.077	ABG
location	1	factor	-0.132	-0.077	ABG
location	1	factor	-0.132	-0.077	ABG
location	1	factor	-0.132	-0.077	ABG
location	1	factor	-0.132	-0.077	ABG
location	1	factor	-0.132	-0.077	ABG
location	1	factor	-0.132	-0.077	ABG
location	1	factor	-0.132	-0.077	ABG
location	1	factor	-0.132	-0.076	ABG
location	1	factor	-0.132	-0.076	ABG
location	1	factor	-0.132	-0.076	ABG
location	1	factor	-0.132	-0.076	ABG
location	1	factor	-0.132	-0.076	ABG
location	1	factor	-0.132	-0.076	ABG
location	1	factor	-0.132	-0.076	ABG
location	1	factor	-0.132	-0.076	ABG
location	1	factor	-0.132	-0.075	ABG
location	1	factor	-0.132	-0.075	ABG
location	1	factor	-0.132	-0.075	ABG
location	1	factor	-0.132	-0.075	ABG
location	1	factor	-0.132	-0.075	ABG
location	1	factor	-0.132	-0.074	ABG
location	1	factor	-0.132	-0.074	ABG
location	1	factor	-0.132	-0.074	ABG
location	1	factor	-0.132	-0.074	ABG
location	1	factor	-0.132	-0.074	ABG
location	1	factor	-0.132	-0.073	ABG
location	1	factor	-0.132	-0.073	ABG
location	1	factor	-0.132	-0.073	ABG

Table 16: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
location	1	factor	-0.132	-0.072	ABG
location	1	factor	-0.132	-0.071	ABG
location	1	factor	-0.132	-0.071	ABG
curr_bmi	NA	numeric	-0.248	-0.071	ABG
location	1	factor	-0.132	-0.070	ABG
curr_bmi	NA	numeric	-0.254	-0.069	ABG
curr_bmi	NA	numeric	-0.250	-0.069	ABG
curr_bmi	NA	numeric	-0.239	-0.068	ABG
curr_bmi	NA	numeric	-0.229	-0.068	ABG
curr_bmi	NA	numeric	-0.238	-0.068	ABG
curr_bmi	NA	numeric	-0.238	-0.068	ABG
curr_bmi	NA	numeric	-0.261	-0.067	ABG
curr_bmi	NA	numeric	-0.241	-0.067	ABG
curr_bmi	NA	numeric	-0.242	-0.067	ABG
curr_bmi	NA	numeric	-0.260	-0.067	ABG
curr_bmi	NA	numeric	-0.245	-0.067	ABG
curr_bmi	NA	numeric	-0.240	-0.067	ABG
curr_bmi	NA	numeric	-0.242	-0.067	ABG
curr_bmi	NA	numeric	-0.247	-0.066	ABG
curr_bmi	NA	numeric	-0.240	-0.066	ABG
curr_bmi	NA	numeric	-0.238	-0.065	ABG
curr_bmi	NA	numeric	-0.241	-0.065	ABG
curr_bmi	NA	numeric	-0.236	-0.065	ABG
curr_bmi	NA	numeric	-0.237	-0.064	ABG
curr_bmi	NA	numeric	-0.255	-0.064	ABG
curr_bmi	NA	numeric	-0.238	-0.064	ABG
curr_bmi	NA	numeric	-0.249	-0.064	ABG
curr_bmi	NA	numeric	-0.237	-0.064	ABG
curr_bmi	NA	numeric	-0.241	-0.064	ABG
curr_bmi	NA	numeric	-0.234	-0.064	ABG
curr_bmi	NA	numeric	-0.232	-0.063	ABG
curr_bmi	NA	numeric	-0.238	-0.063	ABG
curr_bmi	NA	numeric	-0.244	-0.063	ABG
curr_bmi	NA	numeric	-0.245	-0.063	ABG
curr_bmi	NA	numeric	-0.239	-0.063	ABG
curr_bmi	NA	numeric	-0.250	-0.062	ABG
curr_bmi	NA	numeric	-0.259	-0.062	ABG
curr_bmi	NA	numeric	-0.239	-0.062	ABG
curr_bmi	NA	numeric	-0.233	-0.062	ABG
curr_bmi	NA	numeric	-0.238	-0.062	ABG
curr_bmi	NA	numeric	-0.239	-0.062	ABG
curr_bmi	NA	numeric	-0.227	-0.061	ABG
curr_bmi	NA	numeric	-0.224	-0.061	ABG
curr_bmi	NA	numeric	-0.243	-0.061	ABG
curr_bmi	NA	numeric	-0.253	-0.061	ABG
curr_bmi	NA	numeric	-0.235	-0.061	ABG
curr_bmi	NA	numeric	-0.242	-0.061	ABG
curr_bmi	NA	numeric	-0.235	-0.061	ABG
curr_bmi	NA	numeric	-0.235	-0.061	ABG
curr_bmi	NA	numeric	-0.249	-0.061	ABG
curr_bmi	NA	numeric	-0.242	-0.060	ABG
curr_bmi	NA	numeric	-0.246	-0.060	ABG
curr_bmi	NA	numeric	-0.237	-0.060	ABG
curr_bmi	NA	numeric	-0.240	-0.060	ABG
curr_bmi	NA	numeric	-0.243	-0.060	ABG
curr_bmi	NA	numeric	-0.251	-0.060	ABG
curr_bmi	NA	numeric	-0.259	-0.060	ABG
curr_bmi	NA	numeric	-0.238	-0.060	ABG
curr_bmi	NA	numeric	-0.249	-0.060	ABG
curr_bmi	NA	numeric	-0.238	-0.060	ABG
age_at_encounter	NA	numeric	0.106	0.059	ABG
age_at_encounter	NA	numeric	0.106	0.059	ABG
curr_bmi	NA	numeric	-0.252	-0.059	ABG
age_at_encounter	NA	numeric	0.106	0.059	ABG

Table 16: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

Table 16: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
age_at_encounter	NA	numeric	0.106	0.054	ABG
age_at_encounter	NA	numeric	0.106	0.054	ABG
age_at_encounter	NA	numeric	0.106	0.054	ABG
age_at_encounter	NA	numeric	0.106	0.054	ABG
age_at_encounter	NA	numeric	0.106	0.054	ABG
curr_bmi	NA	numeric	-0.244	-0.053	ABG
age_at_encounter	NA	numeric	0.106	0.053	ABG
age_at_encounter	NA	numeric	0.106	0.053	ABG
age_at_encounter	NA	numeric	0.106	0.053	ABG
age_at_encounter	NA	numeric	0.106	0.053	ABG
age_at_encounter	NA	numeric	0.106	0.053	ABG
age_at_encounter	NA	numeric	0.106	0.053	ABG
age_at_encounter	NA	numeric	0.106	0.053	ABG
age_at_encounter	NA	numeric	0.106	0.053	ABG
age_at_encounter	NA	numeric	0.106	0.052	ABG
age_at_encounter	NA	numeric	0.106	0.052	ABG
age_at_encounter	NA	numeric	0.106	0.052	ABG
age_at_encounter	NA	numeric	0.106	0.052	ABG
age_at_encounter	NA	numeric	0.106	0.052	ABG
age_at_encounter	NA	numeric	0.106	0.052	ABG
age_at_encounter	NA	numeric	0.106	0.052	ABG
age_at_encounter	NA	numeric	0.106	0.051	ABG
age_at_encounter	NA	numeric	0.106	0.051	ABG
age_at_encounter	NA	numeric	0.106	0.051	ABG
age_at_encounter	NA	numeric	0.106	0.051	ABG
age_at_encounter	NA	numeric	0.106	0.051	ABG
age_at_encounter	NA	numeric	0.106	0.051	ABG
age_at_encounter	NA	numeric	0.106	0.050	ABG
age_at_encounter	NA	numeric	0.106	0.050	ABG
curr_bmi	NA	numeric	-0.229	-0.048	ABG
chf	1	factor	0.072	0.047	ABG
chf	0	factor	-0.072	-0.047	ABG
chf	0	factor	-0.072	-0.047	ABG
chf	1	factor	0.072	0.047	ABG
chf	0	factor	-0.072	-0.047	ABG
chf	1	factor	0.072	0.047	ABG
chf	1	factor	0.072	0.046	ABG
chf	0	factor	-0.072	-0.046	ABG
chf	1	factor	0.072	0.046	ABG
chf	0	factor	-0.072	-0.046	ABG
chf	1	factor	0.072	0.046	ABG
chf	0	factor	-0.072	-0.046	ABG
chf	0	factor	-0.072	-0.046	ABG
chf	0	factor	-0.072	-0.046	ABG
chf	1	factor	0.072	0.046	ABG
chf	0	factor	-0.072	-0.046	ABG
chf	0	factor	-0.072	-0.046	ABG
chf	1	factor	0.072	0.046	ABG
serum_cr	NA	numeric	0.052	0.046	ABG
serum_cr	NA	numeric	0.052	0.046	ABG
ckd	1	factor	0.041	0.046	ABG
ckd	0	factor	-0.041	-0.046	ABG
chf	1	factor	0.072	0.046	ABG
chf	0	factor	-0.072	-0.046	ABG
chf	0	factor	-0.072	-0.046	ABG
chf	1	factor	0.072	0.046	ABG
ckd	0	factor	-0.041	-0.046	ABG
ckd	1	factor	0.041	0.046	ABG
chf	0	factor	-0.072	-0.046	ABG
chf	1	factor	0.072	0.046	ABG

Table 16: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
chf	1	factor	0.072	0.045	ABG
chf	0	factor	-0.072	-0.045	ABG
chf	0	factor	-0.072	-0.045	ABG
chf	1	factor	0.072	0.045	ABG
serum_cr	NA	numeric	0.045	0.045	ABG
chf	0	factor	-0.072	-0.045	ABG
chf	1	factor	0.072	0.045	ABG
chf	1	factor	0.072	0.045	ABG
chf	0	factor	-0.072	-0.045	ABG
ckd	0	factor	-0.041	-0.045	ABG
ckd	1	factor	0.041	0.045	ABG
chf	1	factor	0.072	0.045	ABG
chf	0	factor	-0.072	-0.045	ABG
serum_cr	NA	numeric	0.047	0.045	ABG
serum_cr	NA	numeric	0.048	0.045	ABG
chf	0	factor	-0.072	-0.045	ABG
chf	1	factor	0.072	0.045	ABG
chf	1	factor	0.072	0.045	ABG
chf	0	factor	-0.072	-0.045	ABG
chf	0	factor	-0.072	-0.045	ABG
chf	1	factor	0.072	0.045	ABG
chf	0	factor	-0.072	-0.044	ABG
ckd	1	factor	0.041	0.044	ABG
ckd	0	factor	-0.041	-0.044	ABG
ckd	1	factor	0.041	0.044	ABG
ckd	0	factor	-0.041	-0.044	ABG
dbp	NA	numeric	-0.156	-0.044	ABG
chf	0	factor	-0.072	-0.044	ABG
chf	1	factor	0.072	0.044	ABG
ckd	1	factor	0.041	0.044	ABG
ckd	0	factor	-0.041	-0.044	ABG
chf	1	factor	0.072	0.044	ABG
chf	0	factor	-0.072	-0.044	ABG
chf	1	factor	0.072	0.044	ABG
chf	0	factor	-0.072	-0.044	ABG
serum_cr	NA	numeric	0.048	0.043	ABG
serum_cr	NA	numeric	0.048	0.043	ABG
ckd	0	factor	-0.041	-0.043	ABG
ckd	1	factor	0.041	0.043	ABG
ckd	1	factor	0.041	0.043	ABG
ckd	0	factor	-0.041	-0.043	ABG
ckd	0	factor	-0.041	-0.043	ABG
ckd	1	factor	0.041	0.043	ABG
dbp	NA	numeric	-0.156	-0.043	ABG
serum_cr	NA	numeric	0.045	0.043	ABG
ckd	1	factor	0.041	0.043	ABG
ckd	0	factor	-0.041	-0.043	ABG
chf	1	factor	0.072	0.043	ABG
chf	0	factor	-0.072	-0.043	ABG
chf	1	factor	0.072	0.043	ABG
chf	0	factor	-0.072	-0.043	ABG
chf	1	factor	0.072	0.043	ABG
chf	0	factor	-0.072	-0.043	ABG
chf	1	factor	0.072	0.043	ABG
chf	0	factor	-0.072	-0.043	ABG
chf	1	factor	0.072	0.043	ABG
chf	0	factor	-0.072	-0.043	ABG
ckd	0	factor	-0.041	-0.043	ABG

Table 16: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
ckd	1	factor	0.041	0.043	ABG
ckd	1	factor	0.041	0.043	ABG
ckd	0	factor	-0.041	-0.043	ABG
chf	1	factor	0.072	0.043	ABG
chf	0	factor	-0.072	-0.043	ABG
chf	0	factor	-0.072	-0.043	ABG
chf	1	factor	0.072	0.043	ABG
ckd	0	factor	-0.041	-0.043	ABG
ckd	1	factor	0.041	0.043	ABG
chf	1	factor	0.072	0.043	ABG
chf	0	factor	-0.072	-0.043	ABG
ckd	0	factor	-0.041	-0.043	ABG
ckd	1	factor	0.041	0.043	ABG
ckd	0	factor	-0.041	-0.042	ABG
ckd	1	factor	0.041	0.042	ABG
chf	0	factor	-0.072	-0.042	ABG
chf	1	factor	0.072	0.042	ABG
serum_cr	NA	numeric	0.047	0.042	ABG
ckd	1	factor	0.041	0.042	ABG
ckd	0	factor	-0.041	-0.042	ABG
chf	1	factor	0.072	0.042	ABG
chf	0	factor	-0.072	-0.042	ABG
chf	0	factor	-0.072	-0.042	ABG
chf	1	factor	0.072	0.042	ABG
chf	0	factor	-0.072	-0.042	ABG
sbp	NA	numeric	-0.169	-0.042	ABG
chf	1	factor	0.072	0.042	ABG
chf	0	factor	-0.072	-0.042	ABG
dbp	NA	numeric	-0.162	-0.042	ABG
chf	0	factor	-0.072	-0.042	ABG
chf	1	factor	0.072	0.042	ABG
ckd	0	factor	-0.041	-0.042	ABG
ckd	1	factor	0.041	0.042	ABG
chf	0	factor	-0.072	-0.042	ABG
chf	1	factor	0.072	0.042	ABG
chf	0	factor	-0.072	-0.042	ABG
chf	1	factor	0.072	0.042	ABG
chf	0	factor	-0.072	-0.042	ABG
chf	0	factor	-0.072	-0.042	ABG
chf	1	factor	0.072	0.042	ABG
chf	0	factor	-0.072	-0.042	ABG
chf	1	factor	0.072	0.042	ABG
chf	0	factor	-0.072	-0.042	ABG
chf	1	factor	0.072	0.042	ABG
chf	0	factor	-0.072	-0.042	ABG
chf	1	factor	0.072	0.042	ABG
chf	0	factor	-0.072	-0.042	ABG
chf	1	factor	0.072	0.042	ABG
chf	0	factor	-0.072	-0.042	ABG
ckd	0	factor	-0.041	-0.042	ABG
ckd	1	factor	0.041	0.042	ABG
ckd	0	factor	-0.041	-0.042	ABG
ckd	1	factor	0.041	0.042	ABG
ckd	0	factor	-0.041	-0.042	ABG
ckd	1	factor	0.041	0.042	ABG
ckd	0	factor	-0.041	-0.042	ABG
ckd	1	factor	0.041	0.042	ABG
ckd	0	factor	-0.041	-0.042	ABG
ckd	1	factor	0.041	0.042	ABG
ckd	0	factor	-0.041	-0.042	ABG
ckd	1	factor	0.041	0.042	ABG
chf	0	factor	-0.072	-0.042	ABG

Table 16: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
chf	1	factor	0.072	0.042	ABG
ckd	1	factor	0.041	0.042	ABG
ckd	0	factor	-0.041	-0.042	ABG
dbp	NA	numeric	-0.162	-0.042	ABG
ckd	1	factor	0.041	0.042	ABG
ckd	0	factor	-0.041	-0.042	ABG
ckd	0	factor	-0.041	-0.042	ABG
ckd	1	factor	0.041	0.042	ABG
serum_cr	NA	numeric	0.047	0.042	ABG
serum_cr	NA	numeric	0.047	0.042	ABG
ckd	1	factor	0.041	0.042	ABG
ckd	0	factor	-0.041	-0.042	ABG
chf	0	factor	-0.072	-0.042	ABG
chf	1	factor	0.072	0.042	ABG
dbp	NA	numeric	-0.160	-0.042	ABG
chf	1	factor	0.072	0.042	ABG
chf	0	factor	-0.072	-0.042	ABG
serum_cr	NA	numeric	0.046	0.042	ABG
ckd	0	factor	-0.041	-0.042	ABG
ckd	1	factor	0.041	0.042	ABG
ckd	1	factor	0.041	0.042	ABG
ckd	0	factor	-0.041	-0.042	ABG
chf	0	factor	-0.072	-0.042	ABG
chf	1	factor	0.072	0.042	ABG
serum_cr	NA	numeric	0.044	0.042	ABG
serum_cr	NA	numeric	0.048	0.042	ABG
chf	1	factor	0.072	0.042	ABG
chf	0	factor	-0.072	-0.042	ABG
chf	0	factor	-0.072	-0.042	ABG
chf	1	factor	0.072	0.042	ABG
chf	1	factor	0.072	0.041	ABG
chf	0	factor	-0.072	-0.041	ABG
serum_cr	NA	numeric	0.046	0.041	ABG
ckd	0	factor	-0.041	-0.041	ABG
ckd	1	factor	0.041	0.041	ABG
serum_cr	NA	numeric	0.051	0.041	ABG
ckd	1	factor	0.041	0.041	ABG
ckd	0	factor	-0.041	-0.041	ABG
dbp	NA	numeric	-0.164	-0.041	ABG
serum_cr	NA	numeric	0.048	0.041	ABG
chf	1	factor	0.072	0.041	ABG
chf	0	factor	-0.072	-0.041	ABG
serum_cr	NA	numeric	0.049	0.041	ABG
serum_cr	NA	numeric	0.049	0.041	ABG
ckd	0	factor	-0.041	-0.041	ABG
ckd	1	factor	0.041	0.041	ABG
ckd	1	factor	0.041	0.041	ABG
ckd	0	factor	-0.041	-0.041	ABG
chf	1	factor	0.072	0.041	ABG
chf	0	factor	-0.072	-0.041	ABG
serum_cr	NA	numeric	0.048	0.041	ABG
chf	1	factor	0.072	0.041	ABG
chf	0	factor	-0.072	-0.041	ABG
ckd	1	factor	0.041	0.041	ABG
ckd	0	factor	-0.041	-0.041	ABG
ckd	0	factor	-0.041	-0.041	ABG
ckd	1	factor	0.041	0.041	ABG
chf	0	factor	-0.072	-0.041	ABG
chf	1	factor	0.072	0.041	ABG
chf	1	factor	0.072	0.041	ABG
chf	0	factor	-0.072	-0.041	ABG

Table 16: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
chf	1	factor	0.072	0.041	ABG
chf	0	factor	-0.072	-0.041	ABG
chf	0	factor	-0.072	-0.041	ABG
chf	1	factor	0.072	0.041	ABG
ckd	0	factor	-0.041	-0.041	ABG
ckd	1	factor	0.041	0.041	ABG
chf	1	factor	0.072	0.041	ABG
chf	0	factor	-0.072	-0.041	ABG
ckd	0	factor	-0.041	-0.041	ABG
ckd	1	factor	0.041	0.041	ABG
chf	1	factor	0.072	0.041	ABG
chf	0	factor	-0.072	-0.041	ABG
ckd	1	factor	0.041	0.041	ABG
ckd	0	factor	-0.041	-0.041	ABG
chf	0	factor	-0.072	-0.041	ABG
chf	1	factor	0.072	0.041	ABG
chf	1	factor	0.072	0.041	ABG
chf	0	factor	-0.072	-0.041	ABG
ckd	0	factor	-0.041	-0.041	ABG
ckd	1	factor	0.041	0.041	ABG
ckd	0	factor	-0.041	-0.041	ABG
chf	0	factor	-0.072	-0.041	ABG
chf	1	factor	0.072	0.041	ABG
chf	1	factor	0.072	0.041	ABG
chf	0	factor	-0.072	-0.041	ABG
ckd	0	factor	-0.041	-0.041	ABG
ckd	1	factor	0.041	0.041	ABG
ckd	0	factor	-0.041	-0.041	ABG
dbp	NA	numeric	-0.156	-0.041	ABG
ckd	0	factor	-0.041	-0.041	ABG
ckd	1	factor	0.041	0.041	ABG
ckd	0	factor	-0.041	-0.041	ABG
ckd	1	factor	0.041	0.041	ABG
ckd	0	factor	-0.041	-0.041	ABG
ckd	1	factor	0.041	0.041	ABG
ckd	0	factor	-0.041	-0.041	ABG
ckd	1	factor	0.041	0.041	ABG
serum_cr	NA	numeric	0.044	0.041	ABG
ckd	0	factor	-0.041	-0.041	ABG
ckd	1	factor	0.041	0.041	ABG
ckd	0	factor	-0.041	-0.041	ABG
ckd	1	factor	0.041	0.041	ABG
serum_cr	NA	numeric	0.049	0.041	ABG
serum_cr	NA	numeric	0.050	0.041	ABG
sbp	NA	numeric	-0.169	-0.041	ABG
serum_cr	NA	numeric	0.049	0.041	ABG
ckd	1	factor	0.041	0.040	ABG
ckd	0	factor	-0.041	-0.040	ABG
ckd	NA	numeric	-0.166	-0.040	ABG
chf	0	factor	-0.072	-0.040	ABG
chf	1	factor	0.072	0.040	ABG
ckd	0	factor	-0.041	-0.040	ABG
ckd	1	factor	0.041	0.040	ABG
ckd	0	factor	-0.041	-0.040	ABG
chf	0	factor	-0.072	-0.040	ABG
chf	1	factor	0.072	0.040	ABG
ckd	0	factor	-0.041	-0.040	ABG
ckd	1	factor	0.041	0.040	ABG
ckd	0	factor	-0.041	-0.040	ABG
ckd	1	factor	0.041	0.040	ABG
serum_cr	NA	numeric	0.045	0.040	ABG
ckd	0	factor	-0.041	-0.040	ABG
ckd	1	factor	0.041	0.040	ABG
sbp	NA	numeric	-0.172	-0.040	ABG
chf	0	factor	-0.072	-0.040	ABG
chf	1	factor	0.072	0.040	ABG
dbp	NA	numeric	-0.157	-0.040	ABG
ckd	0	factor	-0.041	-0.040	ABG
ckd	1	factor	0.041	0.040	ABG
sbp	NA	numeric	-0.174	-0.040	ABG
ckd	1	factor	0.041	0.040	ABG
ckd	0	factor	-0.041	-0.040	ABG
chf	1	factor	0.072	0.040	ABG

Table 16: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
chf	0	factor	-0.072	-0.040	ABG
ckd	1	factor	0.041	0.040	ABG
ckd	0	factor	-0.041	-0.040	ABG
chf	1	factor	0.072	0.040	ABG
chf	0	factor	-0.072	-0.040	ABG
chf	1	factor	0.072	0.040	ABG
chf	0	factor	-0.072	-0.040	ABG
sbp	NA	numeric	-0.168	-0.040	ABG
chf	1	factor	0.072	0.040	ABG
chf	0	factor	-0.072	-0.040	ABG
serum_cr	NA	numeric	0.044	0.040	ABG
ckd	0	factor	-0.041	-0.040	ABG
ckd	1	factor	0.041	0.040	ABG
ckd	1	factor	0.041	0.040	ABG
ckd	0	factor	-0.041	-0.040	ABG
ckd	1	factor	0.041	0.040	ABG
ckd	0	factor	-0.041	-0.040	ABG
serum_cr	NA	numeric	0.049	0.040	ABG
chf	0	factor	-0.072	-0.040	ABG
chf	1	factor	0.072	0.040	ABG
dbp	NA	numeric	-0.163	-0.040	ABG
dbp	NA	numeric	-0.163	-0.040	ABG
ckd	1	factor	0.041	0.040	ABG
ckd	0	factor	-0.041	-0.040	ABG
serum_cr	NA	numeric	0.049	0.040	ABG
chf	1	factor	0.072	0.040	ABG
chf	0	factor	-0.072	-0.040	ABG
serum_cr	NA	numeric	0.048	0.040	ABG
serum_cr	NA	numeric	0.049	0.040	ABG
dbp	NA	numeric	-0.155	-0.040	ABG
chf	1	factor	0.072	0.040	ABG
chf	0	factor	-0.072	-0.040	ABG
dbp	NA	numeric	-0.161	-0.040	ABG
chf	1	factor	0.072	0.040	ABG
chf	0	factor	-0.072	-0.040	ABG
serum_cr	NA	numeric	0.052	0.040	ABG
dbp	NA	numeric	-0.165	-0.040	ABG
sbp	NA	numeric	-0.164	-0.040	ABG
chf	1	factor	0.072	0.040	ABG
chf	0	factor	-0.072	-0.040	ABG
sbp	NA	numeric	-0.168	-0.040	ABG
sbp	NA	numeric	-0.168	-0.039	ABG
dbp	NA	numeric	-0.156	-0.039	ABG
dbp	NA	numeric	-0.172	-0.039	ABG
ckd	1	factor	0.041	0.039	ABG
ckd	0	factor	-0.041	-0.039	ABG
ckd	1	factor	0.041	0.039	ABG
ckd	0	factor	-0.041	-0.039	ABG
ckd	0	factor	-0.041	-0.039	ABG
ckd	1	factor	0.041	0.039	ABG
ckd	0	factor	-0.041	-0.039	ABG
serum_cr	NA	numeric	0.050	0.039	ABG
serum_cr	NA	numeric	0.048	0.039	ABG
serum_cr	NA	numeric	0.049	0.039	ABG
ckd	1	factor	0.041	0.039	ABG
ckd	0	factor	-0.041	-0.039	ABG
ckd	1	factor	0.041	0.039	ABG
ckd	0	factor	-0.041	-0.039	ABG
serum_cr	NA	numeric	0.050	0.039	ABG
chf	0	factor	-0.072	-0.039	ABG
chf	1	factor	0.072	0.039	ABG
sbp	NA	numeric	-0.167	-0.039	ABG

Table 16: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
serum_cr	NA	numeric	0.047	0.039	ABG
serum_cr	NA	numeric	0.049	0.039	ABG
ckd	0	factor	-0.041	-0.039	ABG
ckd	1	factor	0.041	0.039	ABG
dbp	NA	numeric	-0.153	-0.039	ABG
sbp	NA	numeric	-0.168	-0.039	ABG
chf	0	factor	-0.072	-0.039	ABG
chf	1	factor	0.072	0.039	ABG
serum_cr	NA	numeric	0.046	0.039	ABG
serum_cr	NA	numeric	0.050	0.039	ABG
serum_cr	NA	numeric	0.050	0.039	ABG
sbp	NA	numeric	-0.180	-0.039	ABG
serum_cr	NA	numeric	0.046	0.039	ABG
serum_cr	NA	numeric	0.051	0.039	ABG
ckd	0	factor	-0.041	-0.039	ABG
ckd	1	factor	0.041	0.039	ABG
ckd	1	factor	0.041	0.039	ABG
ckd	0	factor	-0.041	-0.039	ABG
dbp	NA	numeric	-0.155	-0.039	ABG
serum_cr	NA	numeric	0.048	0.039	ABG
sbp	NA	numeric	-0.158	-0.039	ABG
ckd	0	factor	-0.041	-0.039	ABG
ckd	1	factor	0.041	0.039	ABG
ckd	0	factor	-0.041	-0.039	ABG
ckd	1	factor	0.041	0.039	ABG
ckd	0	factor	-0.041	-0.039	ABG
ckd	0	factor	-0.041	-0.038	ABG
ckd	1	factor	0.041	0.038	ABG
serum_cr	NA	numeric	0.046	0.038	ABG
ckd	1	factor	0.041	0.038	ABG
ckd	0	factor	-0.041	-0.038	ABG
ckd	1	factor	0.041	0.038	ABG
ckd	0	factor	-0.041	-0.038	ABG
serum_cr	NA	numeric	0.048	0.038	ABG
ckd	1	factor	0.041	0.038	ABG
ckd	0	factor	-0.041	-0.038	ABG
chf	0	factor	-0.072	-0.038	ABG
chf	1	factor	0.072	0.038	ABG
serum_cr	NA	numeric	0.048	0.038	ABG
serum_cr	NA	numeric	0.050	0.038	ABG
ckd	0	factor	-0.041	-0.038	ABG
ckd	1	factor	0.041	0.038	ABG
serum_cr	NA	numeric	0.048	0.038	ABG
ckd	0	factor	-0.041	-0.038	ABG
ckd	1	factor	0.041	0.038	ABG
ckd	0	factor	-0.041	-0.038	ABG
dbp	NA	numeric	-0.154	-0.038	ABG
serum_cr	NA	numeric	0.049	0.038	ABG
ckd	0	factor	-0.041	-0.038	ABG
ckd	1	factor	0.041	0.038	ABG
ckd	0	factor	-0.041	-0.038	ABG
ckd	1	factor	0.041	0.038	ABG
ckd	0	factor	-0.041	-0.038	ABG
ckd	1	factor	0.041	0.038	ABG
ckd	0	factor	-0.041	-0.038	ABG
dbp	NA	numeric	-0.171	-0.038	ABG
serum_cr	NA	numeric	0.046	0.038	ABG
dbp	NA	numeric	-0.152	-0.038	ABG
dbp	NA	numeric	-0.148	-0.038	ABG
sbp	NA	numeric	-0.172	-0.038	ABG
dbp	NA	numeric	-0.152	-0.038	ABG
serum_cr	NA	numeric	0.053	0.038	ABG
serum_cr	NA	numeric	0.050	0.038	ABG
chf	0	factor	-0.072	-0.038	ABG

Table 16: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
chf	1	factor	0.072	0.038	ABG
dbp	NA	numeric	-0.166	-0.038	ABG
serum_cr	NA	numeric	0.049	0.038	ABG
ckd	1	factor	0.041	0.038	ABG
ckd	0	factor	-0.041	-0.038	ABG
serum_cr	NA	numeric	0.050	0.038	ABG
dbp	NA	numeric	-0.152	-0.038	ABG
dbp	NA	numeric	-0.155	-0.038	ABG
ckd	1	factor	0.041	0.038	ABG
ckd	0	factor	-0.041	-0.038	ABG
serum_cr	NA	numeric	0.046	0.037	ABG
serum_cr	NA	numeric	0.052	0.037	ABG
sbp	NA	numeric	-0.166	-0.037	ABG
dbp	NA	numeric	-0.159	-0.037	ABG
serum_cr	NA	numeric	0.048	0.037	ABG
ckd	1	factor	0.041	0.037	ABG
ckd	0	factor	-0.041	-0.037	ABG
dbp	NA	numeric	-0.152	-0.037	ABG
ckd	1	factor	0.041	0.037	ABG
ckd	0	factor	-0.041	-0.037	ABG
sbp	NA	numeric	-0.177	-0.037	ABG
sbp	NA	numeric	-0.167	-0.037	ABG
sbp	NA	numeric	-0.171	-0.037	ABG
ckd	0	factor	-0.041	-0.037	ABG
ckd	1	factor	0.041	0.037	ABG
sbp	NA	numeric	-0.172	-0.037	ABG
dbp	NA	numeric	-0.154	-0.037	ABG
dbp	NA	numeric	-0.160	-0.037	ABG
sbp	NA	numeric	-0.166	-0.037	ABG
sbp	NA	numeric	-0.164	-0.037	ABG
serum_cr	NA	numeric	0.050	0.037	ABG
dbp	NA	numeric	-0.160	-0.037	ABG
serum_cr	NA	numeric	0.050	0.037	ABG
serum_cr	NA	numeric	0.049	0.037	ABG
dbp	NA	numeric	-0.149	-0.037	ABG
dbp	NA	numeric	-0.155	-0.037	ABG
sbp	NA	numeric	-0.168	-0.037	ABG
serum_cr	NA	numeric	0.051	0.037	ABG
dbp	NA	numeric	-0.156	-0.037	ABG
dbp	NA	numeric	-0.155	-0.036	ABG
sbp	NA	numeric	-0.172	-0.036	ABG
dbp	NA	numeric	-0.149	-0.036	ABG
sbp	NA	numeric	-0.174	-0.036	ABG
serum_cr	NA	numeric	0.048	0.036	ABG
dbp	NA	numeric	-0.166	-0.036	ABG
sbp	NA	numeric	-0.165	-0.036	ABG
sbp	NA	numeric	-0.170	-0.036	ABG
dbp	NA	numeric	-0.160	-0.036	ABG
dbp	NA	numeric	-0.156	-0.036	ABG
sbp	NA	numeric	-0.168	-0.036	ABG
serum_cr	NA	numeric	0.049	0.036	ABG
dbp	NA	numeric	-0.164	-0.036	ABG
sbp	NA	numeric	-0.170	-0.036	ABG
dbp	NA	numeric	-0.167	-0.036	ABG
sbp	NA	numeric	-0.173	-0.036	ABG
dbp	NA	numeric	-0.162	-0.036	ABG
dbp	NA	numeric	-0.156	-0.036	ABG
dbp	NA	numeric	-0.160	-0.036	ABG
dbp	NA	numeric	-0.153	-0.035	ABG
sbp	NA	numeric	-0.172	-0.035	ABG
sbp	NA	numeric	-0.162	-0.035	ABG
serum_cr	NA	numeric	0.046	0.035	ABG
hr	NA	numeric	-0.068	-0.035	ABG
dbp	NA	numeric	-0.161	-0.035	ABG

Table 16: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
serum_cr	NA	numeric	0.047	0.035	ABG
dbp	NA	numeric	-0.150	-0.035	ABG
sbp	NA	numeric	-0.170	-0.035	ABG
dbp	NA	numeric	-0.169	-0.035	ABG
sbp	NA	numeric	-0.167	-0.035	ABG
serum_cr	NA	numeric	0.045	0.035	ABG
sbp	NA	numeric	-0.161	-0.035	ABG
serum_cr	NA	numeric	0.048	0.035	ABG
dbp	NA	numeric	-0.153	-0.035	ABG
dbp	NA	numeric	-0.162	-0.035	ABG
sbp	NA	numeric	-0.155	-0.035	ABG
sbp	NA	numeric	-0.164	-0.035	ABG
serum_cr	NA	numeric	0.047	0.035	ABG
dbp	NA	numeric	-0.157	-0.035	ABG
serum_cr	NA	numeric	0.051	0.035	ABG
sbp	NA	numeric	-0.170	-0.035	ABG
serum_cr	NA	numeric	0.045	0.035	ABG
serum_cr	NA	numeric	0.049	0.035	ABG
sbp	NA	numeric	-0.175	-0.034	ABG
serum_cr	NA	numeric	0.050	0.034	ABG
sbp	NA	numeric	-0.172	-0.034	ABG
serum_cr	NA	numeric	0.046	0.034	ABG
sbp	NA	numeric	-0.163	-0.034	ABG
dbp	NA	numeric	-0.159	-0.034	ABG
sbp	NA	numeric	-0.161	-0.034	ABG
sbp	NA	numeric	-0.166	-0.034	ABG
dbp	NA	numeric	-0.144	-0.034	ABG
sbp	NA	numeric	-0.163	-0.034	ABG
sbp	NA	numeric	-0.163	-0.034	ABG
dbp	NA	numeric	-0.160	-0.034	ABG
sbp	NA	numeric	-0.175	-0.034	ABG
sbp	NA	numeric	-0.168	-0.034	ABG
hr	NA	numeric	-0.073	-0.034	ABG
sbp	NA	numeric	-0.163	-0.034	ABG
dbp	NA	numeric	-0.157	-0.034	ABG
serum_cr	NA	numeric	0.048	0.034	ABG
sbp	NA	numeric	-0.169	-0.034	ABG
dbp	NA	numeric	-0.152	-0.034	ABG
dbp	NA	numeric	-0.153	-0.034	ABG
dbp	NA	numeric	-0.159	-0.033	ABG
sbp	NA	numeric	-0.166	-0.033	ABG
dbp	NA	numeric	-0.152	-0.033	ABG
hr	NA	numeric	-0.074	-0.033	ABG
sbp	NA	numeric	-0.175	-0.033	ABG
serum_cr	NA	numeric	0.047	0.033	ABG
dbp	NA	numeric	-0.149	-0.033	ABG
serum_ca	NA	numeric	-0.236	-0.033	ABG
serum_cr	NA	numeric	0.047	0.033	ABG
dbp	NA	numeric	-0.153	-0.033	ABG
dbp	NA	numeric	-0.160	-0.033	ABG
sbp	NA	numeric	-0.164	-0.033	ABG
sbp	NA	numeric	-0.162	-0.033	ABG
dbp	NA	numeric	-0.148	-0.033	ABG
dbp	NA	numeric	-0.158	-0.033	ABG
sbp	NA	numeric	-0.168	-0.033	ABG
sbp	NA	numeric	-0.163	-0.033	ABG
sbp	NA	numeric	-0.162	-0.033	ABG
sbp	NA	numeric	-0.166	-0.033	ABG
sbp	NA	numeric	-0.170	-0.033	ABG
hr	NA	numeric	-0.062	-0.033	ABG
dbp	NA	numeric	-0.156	-0.032	ABG
dbp	NA	numeric	-0.157	-0.032	ABG
copd	0	factor	-0.056	-0.032	ABG

Table 16: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
copd	1	factor	0.056	0.032	ABG
dbp	NA	numeric	-0.149	-0.032	ABG
sbp	NA	numeric	-0.171	-0.032	ABG
hr	NA	numeric	-0.081	-0.032	ABG
dbp	NA	numeric	-0.153	-0.032	ABG
hr	NA	numeric	-0.085	-0.032	ABG
copd	0	factor	-0.056	-0.032	ABG
copd	1	factor	0.056	0.032	ABG
copd	0	factor	-0.056	-0.032	ABG
copd	1	factor	0.056	0.032	ABG
sbp	NA	numeric	-0.167	-0.032	ABG
hr	NA	numeric	-0.067	-0.032	ABG
copd	1	factor	0.056	0.032	ABG
copd	0	factor	-0.056	-0.032	ABG
sbp	NA	numeric	-0.167	-0.032	ABG
dbp	NA	numeric	-0.159	-0.032	ABG
sbp	NA	numeric	-0.173	-0.032	ABG
dbp	NA	numeric	-0.161	-0.032	ABG
sbp	NA	numeric	-0.169	-0.032	ABG
dbp	NA	numeric	-0.159	-0.031	ABG
sbp	NA	numeric	-0.162	-0.031	ABG
dbp	NA	numeric	-0.156	-0.031	ABG
sbp	NA	numeric	-0.165	-0.031	ABG
dbp	NA	numeric	-0.158	-0.031	ABG
sbp	NA	numeric	-0.164	-0.031	ABG
location	2	factor	0.035	-0.031	ABG
hr	NA	numeric	-0.073	-0.031	ABG
sbp	NA	numeric	-0.165	-0.031	ABG
sbp	NA	numeric	-0.166	-0.031	ABG
copd	1	factor	0.056	0.031	ABG
copd	0	factor	-0.056	-0.031	ABG
hr	NA	numeric	-0.070	-0.031	ABG
hr	NA	numeric	-0.078	-0.031	ABG
hr	NA	numeric	-0.060	-0.031	ABG
hr	NA	numeric	-0.079	-0.031	ABG
serum_cr	NA	numeric	0.048	0.031	ABG
dbp	NA	numeric	-0.150	-0.031	ABG
location	2	factor	0.035	-0.031	ABG
sbp	NA	numeric	-0.167	-0.031	ABG
sbp	NA	numeric	-0.164	-0.031	ABG
dbp	NA	numeric	-0.149	-0.031	ABG
copd	0	factor	-0.056	-0.031	ABG
copd	1	factor	0.056	0.031	ABG
hr	NA	numeric	-0.068	-0.030	ABG
sbp	NA	numeric	-0.168	-0.030	ABG
copd	1	factor	0.056	0.030	ABG
copd	0	factor	-0.056	-0.030	ABG
copd	1	factor	0.056	0.030	ABG
copd	0	factor	-0.056	-0.030	ABG
sbp	NA	numeric	-0.163	-0.030	ABG
copd	1	factor	0.056	0.030	ABG
copd	0	factor	-0.056	-0.030	ABG
copd	0	factor	-0.056	-0.030	ABG
copd	1	factor	0.056	0.030	ABG
sbp	NA	numeric	-0.164	-0.030	ABG
hr	NA	numeric	-0.077	-0.030	ABG
dbp	NA	numeric	-0.154	-0.030	ABG
copd	0	factor	-0.056	-0.030	ABG
copd	1	factor	0.056	0.030	ABG
dm	1	factor	0.004	0.030	ABG
dm	0	factor	-0.004	-0.030	ABG
dbp	NA	numeric	-0.151	-0.030	ABG
hr	NA	numeric	-0.070	-0.030	ABG

Table 16: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
hr	NA	numeric	-0.084	-0.030	ABG
sbp	NA	numeric	-0.158	-0.030	ABG
location	2	factor	0.035	-0.030	ABG
dm	0	factor	-0.004	-0.030	ABG
dm	1	factor	0.004	0.030	ABG
copd	0	factor	-0.056	-0.030	ABG
copd	1	factor	0.056	0.030	ABG
copd	1	factor	0.056	0.030	ABG
copd	0	factor	-0.056	-0.030	ABG
serum_ca	NA	numeric	-0.236	-0.030	ABG
copd	0	factor	-0.056	-0.030	ABG
copd	1	factor	0.056	0.030	ABG
location	2	factor	0.035	-0.030	ABG
dm	0	factor	-0.004	-0.030	ABG
dm	1	factor	0.004	0.030	ABG
location	2	factor	0.035	-0.030	ABG
location	2	factor	0.035	-0.030	ABG
dm	1	factor	0.004	0.030	ABG
dm	0	factor	-0.004	-0.030	ABG
location	2	factor	0.035	-0.030	ABG
hr	NA	numeric	-0.065	-0.030	ABG
copd	1	factor	0.056	0.030	ABG
copd	0	factor	-0.056	-0.030	ABG
copd	1	factor	0.056	0.030	ABG
copd	0	factor	-0.056	-0.030	ABG
dm	1	factor	0.004	0.030	ABG
dm	0	factor	-0.004	-0.030	ABG
dm	1	factor	0.004	0.030	ABG
dm	1	factor	0.004	0.030	ABG
dm	0	factor	-0.004	-0.030	ABG
dm	0	factor	-0.004	-0.030	ABG
dm	1	factor	0.004	0.030	ABG
location	2	factor	0.035	-0.029	ABG
hr	NA	numeric	-0.069	-0.029	ABG
dm	0	factor	-0.004	-0.029	ABG
dm	1	factor	0.004	0.029	ABG
dm	1	factor	0.004	0.029	ABG
dm	0	factor	-0.004	-0.029	ABG
location	2	factor	0.035	-0.029	ABG
copd	0	factor	-0.056	-0.029	ABG
copd	1	factor	0.056	0.029	ABG
serum_k	NA	numeric	0.019	0.029	ABG
hr	NA	numeric	-0.080	-0.029	ABG
hr	NA	numeric	-0.076	-0.029	ABG
serum_phos	NA	numeric	0.105	0.029	ABG
location	2	factor	0.035	-0.029	ABG
copd	1	factor	0.056	0.029	ABG
copd	0	factor	-0.056	-0.029	ABG
serum_ca	NA	numeric	-0.233	-0.029	ABG
dm	1	factor	0.004	0.029	ABG
dm	0	factor	-0.004	-0.029	ABG
location	2	factor	0.035	-0.029	ABG
serum_k	NA	numeric	0.021	0.029	ABG
copd	0	factor	-0.056	-0.029	ABG
copd	1	factor	0.056	0.029	ABG
dm	1	factor	0.004	0.029	ABG
dm	0	factor	-0.004	-0.029	ABG
location	2	factor	0.035	-0.029	ABG
dm	0	factor	-0.004	-0.029	ABG
dm	1	factor	0.004	0.029	ABG
dm	0	factor	-0.004	-0.029	ABG
dm	1	factor	0.004	0.029	ABG
copd	0	factor	-0.056	-0.029	ABG
copd	1	factor	0.056	0.029	ABG

Table 16: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
dm	0	factor	-0.004	-0.029	ABG
dm	1	factor	0.004	0.029	ABG
copd	1	factor	0.056	0.029	ABG
copd	0	factor	-0.056	-0.029	ABG
hr	NA	numeric	-0.067	-0.029	ABG
serum_k	NA	numeric	0.020	0.029	ABG
dm	0	factor	-0.004	-0.029	ABG
dm	1	factor	0.004	0.029	ABG
dm	1	factor	0.004	0.029	ABG
dm	0	factor	-0.004	-0.029	ABG
copd	0	factor	-0.056	-0.029	ABG
copd	1	factor	0.056	0.029	ABG
location	2	factor	0.035	-0.029	ABG
dm	0	factor	-0.004	-0.029	ABG
dm	1	factor	0.004	0.029	ABG
dm	1	factor	0.004	0.029	ABG
dm	0	factor	-0.004	-0.029	ABG
copd	0	factor	-0.056	-0.029	ABG
copd	1	factor	0.056	0.029	ABG
location	2	factor	0.035	-0.029	ABG
copd	0	factor	-0.056	-0.029	ABG
copd	1	factor	0.056	0.029	ABG
serum_k	NA	numeric	0.016	0.029	ABG
location	2	factor	0.035	-0.029	ABG
serum_ca	NA	numeric	-0.239	-0.029	ABG
location	2	factor	0.035	-0.029	ABG
copd	1	factor	0.056	0.029	ABG
copd	0	factor	-0.056	-0.029	ABG
copd	0	factor	-0.056	-0.029	ABG
copd	1	factor	0.056	0.029	ABG
hr	NA	numeric	-0.069	-0.029	ABG
copd	1	factor	0.056	0.029	ABG
copd	0	factor	-0.056	-0.029	ABG
location	2	factor	0.035	-0.029	ABG
location	2	factor	0.035	-0.029	ABG
copd	1	factor	0.056	0.029	ABG
copd	0	factor	-0.056	-0.029	ABG
location	2	factor	0.035	-0.029	ABG
sbp	NA	numeric	-0.166	-0.029	ABG
dm	0	factor	-0.004	-0.029	ABG
dm	1	factor	0.004	0.029	ABG
dm	1	factor	0.004	0.029	ABG
dm	0	factor	-0.004	-0.029	ABG
location	2	factor	0.035	-0.029	ABG
dm	0	factor	-0.004	-0.028	ABG
dm	1	factor	0.004	0.028	ABG
dbp	NA	numeric	-0.161	-0.028	ABG
serum_ca	NA	numeric	-0.236	-0.028	ABG
location	2	factor	0.035	-0.028	ABG
serum_ca	NA	numeric	-0.238	-0.028	ABG
copd	0	factor	-0.056	-0.028	ABG
copd	1	factor	0.056	0.028	ABG
hr	NA	numeric	-0.075	-0.028	ABG
location	2	factor	0.035	-0.028	ABG
serum_ca	NA	numeric	-0.238	-0.028	ABG
hr	NA	numeric	-0.073	-0.028	ABG
dm	0	factor	-0.004	-0.028	ABG
dm	1	factor	0.004	0.028	ABG
copd	1	factor	0.056	0.028	ABG
copd	0	factor	-0.056	-0.028	ABG
dm	1	factor	0.004	0.028	ABG
dm	0	factor	-0.004	-0.028	ABG
dm	0	factor	-0.004	-0.028	ABG

Table 16: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
dm	1	factor	0.004	0.028	ABG
hr	NA	numeric	-0.070	-0.028	ABG
hr	NA	numeric	-0.072	-0.028	ABG
dm	1	factor	0.004	0.028	ABG
dm	0	factor	-0.004	-0.028	ABG
location	2	factor	0.035	-0.028	ABG
copd	0	factor	-0.056	-0.028	ABG
copd	1	factor	0.056	0.028	ABG
dm	1	factor	0.004	0.028	ABG
dm	0	factor	-0.004	-0.028	ABG
dm	1	factor	0.004	0.028	ABG
dm	0	factor	-0.004	-0.028	ABG
dm	1	factor	0.004	0.028	ABG
dm	0	factor	-0.004	-0.028	ABG
location	2	factor	0.035	-0.028	ABG
location	2	factor	0.035	-0.028	ABG
serum_ca	NA	numeric	-0.237	-0.028	ABG
location	2	factor	0.035	-0.028	ABG
hr	NA	numeric	-0.079	-0.028	ABG
copd	1	factor	0.056	0.028	ABG
copd	0	factor	-0.056	-0.028	ABG
location	2	factor	0.035	-0.028	ABG
serum_ca	NA	numeric	-0.239	-0.028	ABG
serum_k	NA	numeric	0.019	0.028	ABG
copd	0	factor	-0.056	-0.028	ABG
copd	1	factor	0.056	0.028	ABG
copd	1	factor	0.056	0.028	ABG
copd	0	factor	-0.056	-0.028	ABG
hr	NA	numeric	-0.076	-0.028	ABG
hr	NA	numeric	-0.073	-0.028	ABG
serum_k	NA	numeric	0.019	0.028	ABG
location	2	factor	0.035	-0.028	ABG
dm	0	factor	-0.004	-0.028	ABG
dm	1	factor	0.004	0.028	ABG
dm	1	factor	0.004	0.028	ABG
dm	0	factor	-0.004	-0.028	ABG
copd	1	factor	0.056	0.028	ABG
copd	0	factor	-0.056	-0.028	ABG
location	2	factor	0.035	-0.028	ABG
dm	1	factor	0.004	0.028	ABG
dm	0	factor	-0.004	-0.028	ABG
copd	0	factor	-0.056	-0.028	ABG
copd	1	factor	0.056	0.028	ABG
copd	0	factor	-0.056	-0.028	ABG
copd	1	factor	0.056	0.028	ABG
location	2	factor	0.035	-0.028	ABG
copd	0	factor	-0.056	-0.028	ABG
copd	1	factor	0.056	0.028	ABG
hr	NA	numeric	-0.069	-0.028	ABG
location	2	factor	0.035	-0.028	ABG
copd	1	factor	0.056	0.028	ABG
copd	0	factor	-0.056	-0.028	ABG
hr	NA	numeric	-0.071	-0.028	ABG
dm	1	factor	0.004	0.028	ABG
dm	0	factor	-0.004	-0.028	ABG
dm	0	factor	-0.004	-0.028	ABG
dm	1	factor	0.004	0.028	ABG
location	2	factor	0.035	-0.028	ABG
hr	NA	numeric	-0.075	-0.028	ABG
copd	0	factor	-0.056	-0.028	ABG
copd	1	factor	0.056	0.028	ABG
hr	NA	numeric	-0.065	-0.028	ABG
serum_ca	NA	numeric	-0.238	-0.028	ABG

Table 16: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
dbp	NA	numeric	-0.152	-0.028	ABG
hr	NA	numeric	-0.080	-0.028	ABG
hr	NA	numeric	-0.076	-0.028	ABG
serum_ca	NA	numeric	-0.234	-0.028	ABG
copd	0	factor	-0.056	-0.028	ABG
copd	1	factor	0.056	0.028	ABG
location	2	factor	0.035	-0.028	ABG
location	2	factor	0.035	-0.028	ABG
location	2	factor	0.035	-0.028	ABG
sbp	NA	numeric	-0.173	-0.028	ABG
hr	NA	numeric	-0.060	-0.028	ABG
location	2	factor	0.035	-0.028	ABG
serum_ca	NA	numeric	-0.238	-0.028	ABG
dm	1	factor	0.004	0.028	ABG
dm	0	factor	-0.004	-0.028	ABG
location	2	factor	0.035	-0.028	ABG
copd	0	factor	-0.056	-0.028	ABG
copd	1	factor	0.056	0.028	ABG
copd	1	factor	0.056	0.028	ABG
copd	0	factor	-0.056	-0.028	ABG
location	2	factor	0.035	-0.028	ABG
serum_ca	NA	numeric	-0.240	-0.028	ABG
copd	0	factor	-0.056	-0.028	ABG
copd	1	factor	0.056	0.028	ABG
hr	NA	numeric	-0.080	-0.027	ABG
copd	1	factor	0.056	0.027	ABG
copd	0	factor	-0.056	-0.027	ABG
serum_k	NA	numeric	0.018	0.027	ABG
location	2	factor	0.035	-0.027	ABG
location	2	factor	0.035	-0.027	ABG
location	2	factor	0.035	-0.027	ABG
serum_k	NA	numeric	0.020	0.027	ABG
hr	NA	numeric	-0.070	-0.027	ABG
location	2	factor	0.035	-0.027	ABG
serum_ca	NA	numeric	-0.234	-0.027	ABG
location	2	factor	0.035	-0.027	ABG
serum_ca	NA	numeric	-0.240	-0.027	ABG
location	2	factor	0.035	-0.027	ABG
location	2	factor	0.035	-0.027	ABG
location	2	factor	0.035	-0.027	ABG
serum_ca	NA	numeric	-0.235	-0.027	ABG
serum_k	NA	numeric	0.017	0.027	ABG
location	2	factor	0.035	-0.027	ABG
dm	1	factor	0.004	0.027	ABG
dm	0	factor	-0.004	-0.027	ABG
dm	1	factor	0.004	0.027	ABG
copd	1	factor	0.056	0.027	ABG
copd	0	factor	-0.056	-0.027	ABG
serum_ca	NA	numeric	-0.238	-0.027	ABG
serum_phos	NA	numeric	0.101	0.027	ABG
serum_k	NA	numeric	0.021	0.027	ABG
hr	NA	numeric	-0.081	-0.027	ABG
copd	0	factor	-0.056	-0.027	ABG
copd	1	factor	0.056	0.027	ABG
dm	1	factor	0.004	0.027	ABG
dm	0	factor	-0.004	-0.027	ABG
dm	1	factor	0.004	0.027	ABG
serum_ca	NA	numeric	-0.235	-0.027	ABG
dm	1	factor	0.004	0.027	ABG
dm	0	factor	-0.004	-0.027	ABG
dm	0	factor	-0.004	-0.027	ABG
dm	1	factor	0.004	0.027	ABG

Table 16: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
serum_ca	NA	numeric	-0.236	-0.027	ABG
serum_ca	NA	numeric	-0.235	-0.027	ABG
dm	1	factor	0.004	0.027	ABG
dm	0	factor	-0.004	-0.027	ABG
dm	0	factor	-0.004	-0.027	ABG
dm	1	factor	0.004	0.027	ABG
dm	1	factor	0.004	0.027	ABG
dm	0	factor	-0.004	-0.027	ABG
copd	1	factor	0.056	0.027	ABG
copd	0	factor	-0.056	-0.027	ABG
copd	0	factor	-0.056	-0.027	ABG
copd	1	factor	0.056	0.027	ABG
dm	1	factor	0.004	0.027	ABG
dm	0	factor	-0.004	-0.027	ABG
hr	NA	numeric	-0.072	-0.027	ABG
serum_phos	NA	numeric	0.107	0.027	ABG
dm	0	factor	-0.004	-0.027	ABG
dm	1	factor	0.004	0.027	ABG
location	2	factor	0.035	-0.027	ABG
location	2	factor	0.035	-0.027	ABG
dm	1	factor	0.004	0.027	ABG
dm	0	factor	-0.004	-0.027	ABG
location	2	factor	0.035	-0.027	ABG
serum_ca	NA	numeric	-0.235	-0.027	ABG
serum_ca	NA	numeric	-0.238	-0.027	ABG
dm	1	factor	0.004	0.027	ABG
dm	0	factor	-0.004	-0.027	ABG
location	2	factor	0.035	-0.027	ABG
location	2	factor	0.035	-0.027	ABG
serum_ca	NA	numeric	-0.239	-0.027	ABG
serum_k	NA	numeric	0.020	0.027	ABG
serum_ca	NA	numeric	-0.238	-0.027	ABG
dm	0	factor	-0.004	-0.027	ABG
dm	1	factor	0.004	0.027	ABG
hr	NA	numeric	-0.078	-0.027	ABG
dm	1	factor	0.004	0.026	ABG
dm	0	factor	-0.004	-0.026	ABG
dm	1	factor	0.004	0.026	ABG
dm	0	factor	-0.004	-0.026	ABG
copd	0	factor	-0.056	-0.026	ABG
copd	1	factor	0.056	0.026	ABG
location	2	factor	0.035	-0.026	ABG
location	2	factor	0.035	-0.026	ABG
location	2	factor	0.035	-0.026	ABG
location	2	factor	0.035	-0.026	ABG
dm	1	factor	0.004	0.026	ABG
dm	0	factor	-0.004	-0.026	ABG
location	2	factor	0.035	-0.026	ABG
dm	0	factor	-0.004	-0.026	ABG
dm	1	factor	0.004	0.026	ABG
serum_ca	NA	numeric	-0.236	-0.026	ABG
hr	NA	numeric	-0.068	-0.026	ABG
dm	0	factor	-0.004	-0.026	ABG
dm	1	factor	0.004	0.026	ABG
serum_k	NA	numeric	0.020	0.026	ABG
copd	1	factor	0.056	0.026	ABG
copd	0	factor	-0.056	-0.026	ABG
copd	1	factor	0.056	0.026	ABG
copd	0	factor	-0.056	-0.026	ABG
copd	1	factor	0.056	0.026	ABG
copd	0	factor	-0.056	-0.026	ABG
serum_ca	NA	numeric	-0.240	-0.026	ABG
hr	NA	numeric	-0.076	-0.026	ABG

Table 16: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
serum_ca	NA	numeric	-0.238	-0.026	ABG
serum_ca	NA	numeric	-0.236	-0.026	ABG
location	2	factor	0.035	-0.026	ABG
dm	1	factor	0.004	0.026	ABG
dm	0	factor	-0.004	-0.026	ABG
serum_phos	NA	numeric	0.106	0.026	ABG
copd	1	factor	0.056	0.026	ABG
copd	0	factor	-0.056	-0.026	ABG
location	2	factor	0.035	-0.026	ABG
serum_k	NA	numeric	0.020	0.026	ABG
location	2	factor	0.035	-0.026	ABG
location	2	factor	0.035	-0.026	ABG
serum_k	NA	numeric	0.020	0.026	ABG
serum_k	NA	numeric	0.020	0.026	ABG
location	2	factor	0.035	-0.026	ABG
serum_ca	NA	numeric	-0.236	-0.026	ABG
serum_k	NA	numeric	0.017	0.026	ABG
sex	Male	factor	0.090	0.026	ABG
sex	Female	factor	-0.090	-0.026	ABG
copd	0	factor	-0.056	-0.026	ABG
copd	1	factor	0.056	0.026	ABG
copd	1	factor	0.056	0.026	ABG
copd	0	factor	-0.056	-0.026	ABG
serum_ca	NA	numeric	-0.237	-0.026	ABG
serum_k	NA	numeric	0.021	0.026	ABG
hr	NA	numeric	-0.066	-0.026	ABG
location	2	factor	0.035	-0.026	ABG
hr	NA	numeric	-0.077	-0.026	ABG
location	2	factor	0.035	-0.026	ABG
serum_ca	NA	numeric	-0.235	-0.026	ABG
dm	1	factor	0.004	0.026	ABG
dm	0	factor	-0.004	-0.026	ABG
location	2	factor	0.035	-0.026	ABG
serum_ca	NA	numeric	-0.235	-0.026	ABG
copd	0	factor	-0.056	-0.026	ABG
copd	1	factor	0.056	0.026	ABG
dm	0	factor	-0.004	-0.026	ABG
dm	1	factor	0.004	0.026	ABG
location	2	factor	0.035	-0.026	ABG
location	2	factor	0.035	-0.026	ABG
dm	1	factor	0.004	0.026	ABG
dm	0	factor	-0.004	-0.026	ABG
copd	0	factor	-0.056	-0.026	ABG
location	2	factor	0.035	-0.026	ABG
location	2	factor	0.035	-0.026	ABG
dm	1	factor	0.004	0.026	ABG
dm	0	factor	-0.004	-0.026	ABG
copd	0	factor	-0.056	-0.026	ABG
copd	1	factor	0.056	0.026	ABG
serum_k	NA	numeric	0.022	0.026	ABG
dm	1	factor	0.004	0.026	ABG
dm	0	factor	-0.004	-0.026	ABG
hr	NA	numeric	-0.082	-0.026	ABG
copd	1	factor	0.056	0.026	ABG
copd	0	factor	-0.056	-0.026	ABG
copd	0	factor	-0.056	-0.026	ABG
copd	1	factor	0.056	0.026	ABG
copd	1	factor	0.056	0.026	ABG
copd	0	factor	-0.056	-0.026	ABG
hr	NA	numeric	-0.071	-0.026	ABG
serum_ca	NA	numeric	-0.235	-0.026	ABG
hr	NA	numeric	-0.075	-0.026	ABG
serum_ca	NA	numeric	-0.234	-0.026	ABG
copd	1	factor	0.056	0.026	ABG

Table 16: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
copd	0	factor	-0.056	-0.026	ABG
hr	NA	numeric	-0.071	-0.026	ABG
location	2	factor	0.035	-0.026	ABG
serum_ca	NA	numeric	-0.238	-0.026	ABG
copd	1	factor	0.056	0.026	ABG
copd	0	factor	-0.056	-0.026	ABG
dm	0	factor	-0.004	-0.026	ABG
dm	1	factor	0.004	0.026	ABG
dm	0	factor	-0.004	-0.026	ABG
dm	1	factor	0.004	0.026	ABG
dm	1	factor	0.004	0.026	ABG
dm	1	factor	0.004	0.026	ABG
dm	0	factor	-0.004	-0.026	ABG
dm	0	factor	-0.004	-0.026	ABG
dm	1	factor	0.004	0.026	ABG
copd	1	factor	0.056	0.026	ABG
copd	0	factor	-0.056	-0.026	ABG
location	2	factor	0.035	-0.026	ABG
copd	1	factor	0.056	0.026	ABG
copd	0	factor	-0.056	-0.026	ABG
serum_ca	NA	numeric	-0.236	-0.026	ABG
dm	1	factor	0.004	0.026	ABG
dm	0	factor	-0.004	-0.026	ABG
serum_phos	NA	numeric	0.106	0.026	ABG
serum_phos	NA	numeric	0.092	0.026	ABG
dm	1	factor	0.004	0.025	ABG
dm	0	factor	-0.004	-0.025	ABG
serum_k	NA	numeric	0.020	0.025	ABG
serum_ca	NA	numeric	-0.237	-0.025	ABG
serum_ca	NA	numeric	-0.236	-0.025	ABG
race_ethnicity	2	factor	-0.045	-0.025	ABG
serum_ca	NA	numeric	-0.237	-0.025	ABG
serum_k	NA	numeric	0.019	0.025	ABG
dm	0	factor	-0.004	-0.025	ABG
dm	1	factor	0.004	0.025	ABG
serum_k	NA	numeric	0.020	0.025	ABG
copd	0	factor	-0.056	-0.025	ABG
copd	1	factor	0.056	0.025	ABG
hr	NA	numeric	-0.078	-0.025	ABG
serum_ca	NA	numeric	-0.238	-0.025	ABG
hr	NA	numeric	-0.064	-0.025	ABG
copd	0	factor	-0.056	-0.025	ABG
copd	1	factor	0.056	0.025	ABG
serum_ca	NA	numeric	-0.234	-0.025	ABG
sex	Male	factor	0.090	0.025	ABG
sex	Female	factor	-0.090	-0.025	ABG
serum_k	NA	numeric	0.020	0.025	ABG
location	2	factor	0.035	-0.025	ABG
serum_k	NA	numeric	0.020	0.025	ABG
serum_ca	NA	numeric	-0.234	-0.025	ABG
hr	NA	numeric	-0.073	-0.025	ABG
location	2	factor	0.035	-0.025	ABG
copd	1	factor	0.056	0.025	ABG
copd	0	factor	-0.056	-0.025	ABG
hr	NA	numeric	-0.074	-0.025	ABG
location	2	factor	0.035	-0.025	ABG
copd	1	factor	0.056	0.025	ABG
copd	0	factor	-0.056	-0.025	ABG
serum_ca	NA	numeric	-0.236	-0.025	ABG
serum_phos	NA	numeric	0.101	0.025	ABG
sex	Female	factor	-0.090	-0.025	ABG
sex	Male	factor	0.090	0.025	ABG
serum_ca	NA	numeric	-0.236	-0.025	ABG
serum_ca	NA	numeric	-0.237	-0.025	ABG
serum_k	NA	numeric	0.020	0.025	ABG

Table 16: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
serum_ca	NA	numeric	-0.243	-0.025	ABG
serum_k	NA	numeric	0.017	0.025	ABG
serum_k	NA	numeric	0.017	0.025	ABG
dm	0	factor	-0.004	-0.025	ABG
dm	1	factor	0.004	0.025	ABG
serum_ca	NA	numeric	-0.235	-0.025	ABG
serum_k	NA	numeric	0.018	0.025	ABG
dm	0	factor	-0.004	-0.025	ABG
dm	1	factor	0.004	0.025	ABG
dm	0	factor	-0.004	-0.025	ABG
dm	1	factor	0.004	0.025	ABG
serum_k	NA	numeric	0.020	0.025	ABG
serum_k	NA	numeric	0.022	0.025	ABG
serum_phos	NA	numeric	0.100	0.025	ABG
race_ethnicity	4	factor	0.041	0.025	ABG
hr	NA	numeric	-0.081	-0.025	ABG
copd	0	factor	-0.056	-0.025	ABG
copd	1	factor	0.056	0.025	ABG
sex	Female	factor	-0.090	-0.025	ABG
sex	Male	factor	0.090	0.025	ABG
copd	0	factor	-0.056	-0.025	ABG
copd	1	factor	0.056	0.025	ABG
race_ethnicity	2	factor	-0.045	-0.025	ABG
dm	0	factor	-0.004	-0.025	ABG
dm	1	factor	0.004	0.025	ABG
serum_k	NA	numeric	0.020	0.025	ABG
serum_ca	NA	numeric	-0.236	-0.025	ABG
dm	0	factor	-0.004	-0.025	ABG
dm	1	factor	0.004	0.025	ABG
serum_k	NA	numeric	0.024	0.025	ABG
location	2	factor	0.035	-0.025	ABG
serum_phos	NA	numeric	0.103	0.025	ABG
serum_phos	NA	numeric	0.093	0.025	ABG
sex	Male	factor	0.090	0.025	ABG
sex	Female	factor	-0.090	-0.025	ABG
sex	Female	factor	-0.090	-0.025	ABG
sex	Male	factor	0.090	0.025	ABG
serum_k	NA	numeric	0.021	0.025	ABG
serum_ca	NA	numeric	-0.235	-0.025	ABG
serum_ca	NA	numeric	-0.234	-0.025	ABG
hr	NA	numeric	-0.064	-0.025	ABG
serum_phos	NA	numeric	0.109	0.025	ABG
serum_ca	NA	numeric	-0.234	-0.025	ABG
serum_k	NA	numeric	0.017	0.025	ABG
serum_ca	NA	numeric	-0.238	-0.025	ABG
serum_ca	NA	numeric	-0.235	-0.025	ABG
serum_k	NA	numeric	0.017	0.025	ABG
serum_k	NA	numeric	0.022	0.025	ABG
sex	Male	factor	0.090	0.025	ABG
sex	Female	factor	-0.090	-0.025	ABG
location	2	factor	0.035	-0.025	ABG
serum_phos	NA	numeric	0.100	0.024	ABG
hr	NA	numeric	-0.075	-0.024	ABG
serum_ca	NA	numeric	-0.236	-0.024	ABG
hr	NA	numeric	-0.066	-0.024	ABG
sex	Male	factor	0.090	0.024	ABG
sex	Female	factor	-0.090	-0.024	ABG
serum_ca	NA	numeric	-0.241	-0.024	ABG
race_ethnicity	2	factor	-0.045	-0.024	ABG
copd	1	factor	0.056	0.024	ABG
copd	0	factor	-0.056	-0.024	ABG
serum_k	NA	numeric	0.024	0.024	ABG
serum_k	NA	numeric	0.022	0.024	ABG

Table 16: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
dm	1	factor	0.004	0.024	ABG
dm	0	factor	-0.004	-0.024	ABG
location	2	factor	0.035	-0.024	ABG
hr	NA	numeric	-0.076	-0.024	ABG
hr	NA	numeric	-0.061	-0.024	ABG
serum_phos	NA	numeric	0.104	0.024	ABG
serum_ca	NA	numeric	-0.241	-0.024	ABG
serum_ca	NA	numeric	-0.236	-0.024	ABG
serum_ca	NA	numeric	-0.237	-0.024	ABG
hr	NA	numeric	-0.066	-0.024	ABG
location	2	factor	0.035	-0.024	ABG
copd	0	factor	-0.056	-0.024	ABG
copd	1	factor	0.056	0.024	ABG
race_ethnicity	2	factor	-0.045	-0.024	ABG
hr	NA	numeric	-0.068	-0.024	ABG
copd	1	factor	0.056	0.024	ABG
copd	0	factor	-0.056	-0.024	ABG
serum_ca	NA	numeric	-0.235	-0.024	ABG
serum_ca	NA	numeric	-0.240	-0.024	ABG
serum_k	NA	numeric	0.019	0.024	ABG
serum_phos	NA	numeric	0.104	0.024	ABG
serum_k	NA	numeric	0.018	0.024	ABG
serum_k	NA	numeric	0.022	0.024	ABG
serum_ca	NA	numeric	-0.233	-0.024	ABG
sex	Female	factor	-0.090	-0.024	ABG
sex	Male	factor	0.090	0.024	ABG
dm	0	factor	-0.004	-0.024	ABG
dm	1	factor	0.004	0.024	ABG
serum_phos	NA	numeric	0.098	0.024	ABG
serum_k	NA	numeric	0.018	0.024	ABG
copd	1	factor	0.056	0.024	ABG
copd	0	factor	-0.056	-0.024	ABG
hr	NA	numeric	-0.074	-0.024	ABG
serum_ca	NA	numeric	-0.237	-0.024	ABG
serum_k	NA	numeric	0.021	0.024	ABG
sex	Female	factor	-0.090	-0.024	ABG
sex	Male	factor	0.090	0.024	ABG
race_ethnicity	2	factor	-0.045	-0.024	ABG
dm	0	factor	-0.004	-0.024	ABG
dm	1	factor	0.004	0.024	ABG
dm	0	factor	-0.004	-0.024	ABG
dm	1	factor	0.004	0.024	ABG
serum_k	NA	numeric	0.020	0.024	ABG
serum_k	NA	numeric	0.021	0.024	ABG
hr	NA	numeric	-0.080	-0.024	ABG
hr	NA	numeric	-0.071	-0.024	ABG
race_ethnicity	2	factor	-0.045	-0.024	ABG
location	2	factor	0.035	-0.024	ABG
sex	Female	factor	-0.090	-0.024	ABG
sex	Male	factor	0.090	0.024	ABG
sex	Female	factor	-0.090	-0.024	ABG
sex	Male	factor	0.090	0.024	ABG
race_ethnicity	2	factor	-0.045	-0.024	ABG
serum_k	NA	numeric	0.019	0.024	ABG
serum_k	NA	numeric	0.020	0.024	ABG
sex	Female	factor	-0.090	-0.024	ABG
sex	Male	factor	0.090	0.024	ABG
sex	Male	factor	0.090	0.024	ABG
sex	Female	factor	-0.090	-0.024	ABG
serum_k	NA	numeric	0.020	0.023	ABG
phtn	0	factor	-0.049	-0.023	ABG
phtn	1	factor	0.049	0.023	ABG
temp_new	NA	numeric	-0.084	-0.023	ABG

Table 16: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
serum_k	NA	numeric	0.018	0.023	ABG
serum_ca	NA	numeric	-0.240	-0.023	ABG
serum_ca	NA	numeric	-0.238	-0.023	ABG
hr	NA	numeric	-0.071	-0.023	ABG
location	2	factor	0.035	-0.023	ABG
serum_k	NA	numeric	0.021	0.023	ABG
serum_k	NA	numeric	0.015	0.023	ABG
serum_phos	NA	numeric	0.107	0.023	ABG
serum_k	NA	numeric	0.022	0.023	ABG
hr	NA	numeric	-0.077	-0.023	ABG
hr	NA	numeric	-0.067	-0.023	ABG
hr	NA	numeric	-0.082	-0.023	ABG
sex	Male	factor	0.090	0.023	ABG
sex	Female	factor	-0.090	-0.023	ABG
dm	0	factor	-0.004	-0.023	ABG
dm	1	factor	0.004	0.023	ABG
serum_phos	NA	numeric	0.098	0.023	ABG
serum_phos	NA	numeric	0.099	0.023	ABG
sex	Male	factor	0.090	0.023	ABG
sex	Female	factor	-0.090	-0.023	ABG
serum_phos	NA	numeric	0.109	0.023	ABG
copd	1	factor	0.056	0.023	ABG
copd	0	factor	-0.056	-0.023	ABG
serum_ca	NA	numeric	-0.237	-0.023	ABG
serum_k	NA	numeric	0.024	0.023	ABG
copd	0	factor	-0.056	-0.023	ABG
copd	1	factor	0.056	0.023	ABG
serum_phos	NA	numeric	0.105	0.023	ABG
serum_k	NA	numeric	0.021	0.023	ABG
race_ethnicity	2	factor	-0.045	-0.023	ABG
location	2	factor	0.035	-0.023	ABG
sex	Male	factor	0.090	0.023	ABG
sex	Female	factor	-0.090	-0.023	ABG
serum_ca	NA	numeric	-0.238	-0.023	ABG
serum_ca	NA	numeric	-0.236	-0.023	ABG
serum_ca	NA	numeric	-0.240	-0.023	ABG
serum_ca	NA	numeric	-0.238	-0.023	ABG
dm	1	factor	0.004	0.023	ABG
dm	0	factor	-0.004	-0.023	ABG
sex	Male	factor	0.090	0.023	ABG
sex	Female	factor	-0.090	-0.023	ABG
serum_ca	NA	numeric	-0.239	-0.023	ABG
serum_k	NA	numeric	0.020	0.023	ABG
phtn	1	factor	0.049	0.023	ABG
phtn	0	factor	-0.049	-0.023	ABG
sex	Male	factor	0.090	0.023	ABG
sex	Female	factor	-0.090	-0.023	ABG
hr	NA	numeric	-0.072	-0.023	ABG
dm	1	factor	0.004	0.023	ABG
dm	0	factor	-0.004	-0.023	ABG
sex	Male	factor	0.090	0.023	ABG
sex	Female	factor	-0.090	-0.023	ABG
serum_k	NA	numeric	0.023	0.023	ABG
serum_ca	NA	numeric	-0.236	-0.023	ABG
race_ethnicity	2	factor	-0.045	-0.023	ABG
copd	1	factor	0.056	0.023	ABG
copd	0	factor	-0.056	-0.023	ABG
dm	1	factor	0.004	0.023	ABG
dm	0	factor	-0.004	-0.023	ABG
race_ethnicity	2	factor	-0.045	-0.023	ABG
serum_k	NA	numeric	0.018	0.023	ABG
phtn	1	factor	0.049	0.023	ABG
phtn	0	factor	-0.049	-0.023	ABG
serum_k	NA	numeric	0.018	0.023	ABG

Table 16: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
copd	1	factor	0.056	0.023	ABG
copd	0	factor	-0.056	-0.023	ABG
serum_k	NA	numeric	0.021	0.023	ABG
serum_k	NA	numeric	0.025	0.023	ABG
race_ethnicity	2	factor	-0.045	-0.023	ABG
race_ethnicity	2	factor	-0.045	-0.023	ABG
dm	1	factor	0.004	0.023	ABG
dm	0	factor	-0.004	-0.023	ABG
race_ethnicity	2	factor	-0.045	-0.023	ABG
phtn	0	factor	-0.049	-0.023	ABG
phtn	1	factor	0.049	0.023	ABG
hr	NA	numeric	-0.070	-0.023	ABG
sex	Female	factor	-0.090	-0.023	ABG
sex	Male	factor	0.090	0.023	ABG
serum_k	NA	numeric	0.020	0.023	ABG
race_ethnicity	2	factor	-0.045	-0.023	ABG
serum_k	NA	numeric	0.023	0.022	ABG
hr	NA	numeric	-0.072	-0.022	ABG
race_ethnicity	2	factor	-0.045	-0.022	ABG
serum_phos	NA	numeric	0.091	0.022	ABG
serum_ca	NA	numeric	-0.240	-0.022	ABG
serum_k	NA	numeric	0.020	0.022	ABG
plt	NA	numeric	-0.117	-0.022	ABG
race_ethnicity	2	factor	-0.045	-0.022	ABG
sex	Male	factor	0.090	0.022	ABG
sex	Female	factor	-0.090	-0.022	ABG
race_ethnicity	4	factor	0.041	0.022	ABG
sex	Male	factor	0.090	0.022	ABG
sex	Female	factor	-0.090	-0.022	ABG
serum_k	NA	numeric	0.020	0.022	ABG
serum_phos	NA	numeric	0.109	0.022	ABG
sex	Male	factor	0.090	0.022	ABG
sex	Female	factor	-0.090	-0.022	ABG
phtn	0	factor	-0.049	-0.022	ABG
phtn	1	factor	0.049	0.022	ABG
race_ethnicity	2	factor	-0.045	-0.022	ABG
sex	Female	factor	-0.090	-0.022	ABG
sex	Male	factor	0.090	0.022	ABG
race_ethnicity	2	factor	-0.045	-0.022	ABG
serum_ca	NA	numeric	-0.236	-0.022	ABG
sex	Female	factor	-0.090	-0.022	ABG
sex	Male	factor	0.090	0.022	ABG
serum_k	NA	numeric	0.015	0.022	ABG
hr	NA	numeric	-0.067	-0.022	ABG
sex	Female	factor	-0.090	-0.022	ABG
sex	Male	factor	0.090	0.022	ABG
serum_ca	NA	numeric	-0.238	-0.022	ABG
serum_k	NA	numeric	0.019	0.022	ABG
hr	NA	numeric	-0.060	-0.022	ABG
serum_k	NA	numeric	0.021	0.022	ABG
serum_k	NA	numeric	0.018	0.022	ABG
serum_phos	NA	numeric	0.105	0.022	ABG
sex	Female	factor	-0.090	-0.022	ABG
sex	Male	factor	0.090	0.022	ABG
race_ethnicity	2	factor	-0.045	-0.022	ABG
phtn	0	factor	-0.049	-0.022	ABG
phtn	1	factor	0.049	0.022	ABG
sex	Male	factor	0.090	0.022	ABG
sex	Female	factor	-0.090	-0.022	ABG
sex	Female	factor	-0.090	-0.022	ABG
sex	Male	factor	0.090	0.022	ABG
sex	Male	factor	0.090	0.022	ABG
sex	Female	factor	-0.090	-0.022	ABG

Table 16: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
race_ethnicity	2	factor	-0.045	-0.022	ABG
serum_k	NA	numeric	0.019	0.022	ABG
serum_k	NA	numeric	0.017	0.022	ABG
race_ethnicity	2	factor	-0.045	-0.022	ABG
serum_phos	NA	numeric	0.099	0.022	ABG
serum_phos	NA	numeric	0.090	0.022	ABG
race_ethnicity	2	factor	-0.045	-0.022	ABG
serum_ca	NA	numeric	-0.238	-0.022	ABG
plt	NA	numeric	-0.118	-0.022	ABG
serum_k	NA	numeric	0.019	0.022	ABG
serum_ca	NA	numeric	-0.238	-0.022	ABG
serum_ca	NA	numeric	-0.236	-0.022	ABG
serum_k	NA	numeric	0.021	0.022	ABG
race_ethnicity	2	factor	-0.045	-0.022	ABG
hr	NA	numeric	-0.064	-0.022	ABG
serum_k	NA	numeric	0.020	0.022	ABG
serum_k	NA	numeric	0.026	0.022	ABG
serum_phos	NA	numeric	0.098	0.022	ABG
serum_cl	NA	numeric	0.026	-0.022	ABG
serum_k	NA	numeric	0.019	0.022	ABG
race_ethnicity	2	factor	-0.045	-0.022	ABG
sex	Female	factor	-0.090	-0.022	ABG
sex	Male	factor	0.090	0.022	ABG
sex	Female	factor	-0.090	-0.022	ABG
sex	Male	factor	0.090	0.022	ABG
temp_new	NA	numeric	-0.103	-0.021	ABG
sodium	NA	numeric	-0.033	-0.021	ABG
sex	Female	factor	-0.090	-0.021	ABG
sex	Male	factor	0.090	0.021	ABG
race_ethnicity	2	factor	-0.045	-0.021	ABG
serum_phos	NA	numeric	0.092	0.021	ABG
sex	Female	factor	-0.090	-0.021	ABG
sex	Male	factor	0.090	0.021	ABG
serum_lac	NA	numeric	0.123	0.021	ABG
race_ethnicity	2	factor	-0.045	-0.021	ABG
serum_cl	NA	numeric	0.030	-0.021	ABG
serum_lac	NA	numeric	0.111	0.021	ABG
race_ethnicity	2	factor	-0.045	-0.021	ABG
sex	Male	factor	0.090	0.021	ABG
sex	Female	factor	-0.090	-0.021	ABG
serum_ca	NA	numeric	-0.235	-0.021	ABG
sex	Male	factor	0.090	0.021	ABG
sex	Female	factor	-0.090	-0.021	ABG
sex	Male	factor	0.090	0.021	ABG
sex	Female	factor	-0.090	-0.021	ABG
race_ethnicity	2	factor	-0.045	-0.021	ABG
phtn	1	factor	0.049	0.021	ABG
phtn	0	factor	-0.049	-0.021	ABG
plt	NA	numeric	-0.117	-0.021	ABG
race_ethnicity	4	factor	0.041	0.021	ABG
hr	NA	numeric	-0.070	-0.021	ABG
race_ethnicity	2	factor	-0.045	-0.021	ABG
temp_new	NA	numeric	-0.102	-0.021	ABG
phtn	0	factor	-0.049	-0.021	ABG
phtn	1	factor	0.049	0.021	ABG
sex	Female	factor	-0.090	-0.021	ABG
sex	Male	factor	0.090	0.021	ABG
sex	Male	factor	0.090	0.021	ABG
sex	Female	factor	-0.090	-0.021	ABG
race_ethnicity	4	factor	0.041	0.021	ABG

Table 16: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
serum_ca	NA	numeric	-0.238	-0.021	ABG
race_ethnicity	2	factor	-0.045	-0.021	ABG
sex	Female	factor	-0.090	-0.021	ABG
sex	Male	factor	0.090	0.021	ABG
race_ethnicity	2	factor	-0.045	-0.021	ABG
serum_k	NA	numeric	0.020	0.021	ABG
serum_k	NA	numeric	0.023	0.021	ABG
serum_ca	NA	numeric	-0.240	-0.021	ABG
phtn	1	factor	0.049	0.021	ABG
phtn	0	factor	-0.049	-0.021	ABG
serum_k	NA	numeric	0.020	0.021	ABG
race_ethnicity	4	factor	0.041	0.021	ABG
race_ethnicity	2	factor	-0.045	-0.021	ABG
phtn	0	factor	-0.049	-0.021	ABG
phtn	1	factor	0.049	0.021	ABG
sex	Male	factor	0.090	0.021	ABG
sex	Female	factor	-0.090	-0.021	ABG
sex	Female	factor	-0.090	-0.021	ABG
sex	Male	factor	0.090	0.021	ABG
serum_phos	NA	numeric	0.101	0.021	ABG
sex	Male	factor	0.090	0.021	ABG
sex	Female	factor	-0.090	-0.021	ABG
hr	NA	numeric	-0.064	-0.021	ABG
phtn	0	factor	-0.049	-0.021	ABG
phtn	1	factor	0.049	0.021	ABG
sex	Male	factor	0.090	0.021	ABG
sex	Female	factor	-0.090	-0.021	ABG
temp_new	NA	numeric	-0.099	-0.021	ABG
serum_phos	NA	numeric	0.103	0.021	ABG
serum_phos	NA	numeric	0.101	0.021	ABG
race_ethnicity	2	factor	-0.045	-0.021	ABG
hr	NA	numeric	-0.063	-0.021	ABG
sex	Male	factor	0.090	0.021	ABG
sex	Female	factor	-0.090	-0.021	ABG
serum_phos	NA	numeric	0.102	0.021	ABG
sex	Female	factor	-0.090	-0.021	ABG
sex	Male	factor	0.090	0.021	ABG
race_ethnicity	2	factor	-0.045	-0.021	ABG
race_ethnicity	2	factor	-0.045	-0.021	ABG
race_ethnicity	2	factor	-0.045	-0.021	ABG
sex	Male	factor	0.090	0.021	ABG
sex	Female	factor	-0.090	-0.021	ABG
race_ethnicity	2	factor	-0.045	-0.021	ABG
race_ethnicity	2	factor	-0.045	-0.021	ABG
race_ethnicity	2	factor	-0.045	-0.021	ABG
sex	Female	factor	-0.090	-0.021	ABG
sex	Male	factor	0.090	0.021	ABG
phtn	0	factor	-0.049	-0.021	ABG
phtn	1	factor	0.049	0.021	ABG
plt	NA	numeric	-0.114	-0.021	ABG
phtn	0	factor	-0.049	-0.021	ABG
phtn	1	factor	0.049	0.021	ABG
plt	NA	numeric	-0.116	-0.021	ABG
race_ethnicity	2	factor	-0.045	-0.021	ABG
race_ethnicity	2	factor	-0.045	-0.021	ABG
race_ethnicity	2	factor	-0.045	-0.021	ABG
race_ethnicity	4	factor	0.041	0.021	ABG
sodium	NA	numeric	-0.031	-0.021	ABG
sex	Female	factor	-0.090	-0.021	ABG
sex	Male	factor	0.090	0.021	ABG
sex	Female	factor	-0.090	-0.021	ABG
sex	Male	factor	0.090	0.021	ABG
serum_phos	NA	numeric	0.116	0.021	ABG
phtn	0	factor	-0.049	-0.021	ABG
phtn	1	factor	0.049	0.021	ABG
plt	NA	numeric	-0.115	-0.021	ABG
sex	Female	factor	-0.090	-0.021	ABG

Table 16: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
sex	Male	factor	0.090	0.021	ABG
sex	Female	factor	-0.090	-0.020	ABG
sex	Male	factor	0.090	0.020	ABG
dm	1	factor	0.004	0.020	ABG
dm	0	factor	-0.004	-0.020	ABG
race_ethnicity	2	factor	-0.045	-0.020	ABG
osa	0	factor	0.049	-0.020	ABG
osa	1	factor	-0.049	0.020	ABG
plt	NA	numeric	-0.121	-0.020	ABG
phtn	1	factor	0.049	0.020	ABG
phtn	0	factor	-0.049	-0.020	ABG
serum_k	NA	numeric	0.022	0.020	ABG
serum_phos	NA	numeric	0.099	0.020	ABG
sex	Male	factor	0.090	0.020	ABG
sex	Female	factor	-0.090	-0.020	ABG
serum_phos	NA	numeric	0.092	0.020	ABG
serum_phos	NA	numeric	0.102	0.020	ABG
phtn	0	factor	-0.049	-0.020	ABG
phtn	1	factor	0.049	0.020	ABG
sex	Male	factor	0.090	0.020	ABG
sex	Female	factor	-0.090	-0.020	ABG
race_ethnicity	4	factor	0.041	0.020	ABG
temp_new	NA	numeric	-0.104	-0.020	ABG
serum_phos	NA	numeric	0.098	0.020	ABG
phtn	1	factor	0.049	0.020	ABG
phtn	0	factor	-0.049	-0.020	ABG
sodium	NA	numeric	-0.028	-0.020	ABG
osa	0	factor	0.049	-0.020	ABG
osa	1	factor	-0.049	0.020	ABG
phtn	0	factor	-0.049	-0.020	ABG
phtn	1	factor	0.049	0.020	ABG
sodium	NA	numeric	-0.027	-0.020	ABG
sex	Male	factor	0.090	0.020	ABG
sex	Female	factor	-0.090	-0.020	ABG
race_ethnicity	4	factor	0.041	0.020	ABG
temp_new	NA	numeric	-0.094	-0.020	ABG
sex	Female	factor	-0.090	-0.020	ABG
sex	Male	factor	0.090	0.020	ABG
plt	NA	numeric	-0.111	-0.020	ABG
serum_lac	NA	numeric	0.114	0.020	ABG
sex	Female	factor	-0.090	-0.020	ABG
sex	Male	factor	0.090	0.020	ABG
race_ethnicity	4	factor	0.041	0.020	ABG
race_ethnicity	2	factor	-0.045	-0.020	ABG
race_ethnicity	2	factor	-0.045	-0.020	ABG
phtn	1	factor	0.049	0.020	ABG
phtn	0	factor	-0.049	-0.020	ABG
sodium	NA	numeric	-0.029	-0.020	ABG
sex	Female	factor	-0.090	-0.020	ABG
sex	Male	factor	0.090	0.020	ABG
serum_lac	NA	numeric	0.122	0.020	ABG
serum_lac	NA	numeric	0.119	0.020	ABG
serum_lac	NA	numeric	0.109	0.020	ABG
serum_cl	NA	numeric	0.029	-0.020	ABG
race_ethnicity	2	factor	-0.045	-0.020	ABG
serum_phos	NA	numeric	0.101	0.020	ABG
serum_cl	NA	numeric	0.028	-0.020	ABG
race_ethnicity	4	factor	0.041	0.020	ABG
race_ethnicity	2	factor	-0.045	-0.020	ABG
race_ethnicity	2	factor	-0.045	-0.020	ABG
phtn	0	factor	-0.049	-0.020	ABG
phtn	1	factor	0.049	0.020	ABG
race_ethnicity	2	factor	-0.045	-0.020	ABG

Table 16: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
plt	NA	numeric	-0.116	-0.020	ABG
serum_phos	NA	numeric	0.090	0.020	ABG
phtn	1	factor	0.049	0.020	ABG
phtn	0	factor	-0.049	-0.020	ABG
temp_new	NA	numeric	-0.094	-0.020	ABG
phtn	1	factor	0.049	0.020	ABG
phtn	0	factor	-0.049	-0.020	ABG
serum_phos	NA	numeric	0.099	0.020	ABG
sex	Female	factor	-0.090	-0.020	ABG
sex	Male	factor	0.090	0.020	ABG
phtn	0	factor	-0.049	-0.020	ABG
phtn	1	factor	0.049	0.020	ABG
serum_phos	NA	numeric	0.094	0.020	ABG
phtn	0	factor	-0.049	-0.020	ABG
phtn	1	factor	0.049	0.020	ABG
race_ethnicity	4	factor	0.041	0.020	ABG
sex	Female	factor	-0.090	-0.020	ABG
sex	Male	factor	0.090	0.020	ABG
serum_cl	NA	numeric	0.031	-0.020	ABG
race_ethnicity	4	factor	0.041	0.020	ABG
race_ethnicity	2	factor	-0.045	-0.020	ABG
race_ethnicity	4	factor	0.041	0.020	ABG
sex	Male	factor	0.090	0.020	ABG
sex	Female	factor	-0.090	-0.020	ABG
phtn	0	factor	-0.049	-0.020	ABG
phtn	1	factor	0.049	0.020	ABG
sex	Male	factor	0.090	0.020	ABG
sex	Female	factor	-0.090	-0.020	ABG
serum_lac	NA	numeric	0.121	0.020	ABG
race_ethnicity	2	factor	-0.045	-0.020	ABG
phtn	1	factor	0.049	0.020	ABG
phtn	0	factor	-0.049	-0.020	ABG
race_ethnicity	2	factor	-0.045	-0.020	ABG
sex	Female	factor	-0.090	-0.020	ABG
plt	NA	numeric	-0.119	-0.020	ABG
serum_phos	NA	numeric	0.101	0.020	ABG
serum_cl	NA	numeric	0.028	-0.020	ABG
sex	Male	factor	0.090	0.020	ABG
sex	Female	factor	-0.090	-0.020	ABG
plt	NA	numeric	-0.118	-0.019	ABG
race_ethnicity	2	factor	-0.045	-0.019	ABG
plt	NA	numeric	-0.116	-0.019	ABG
sex	Female	factor	-0.090	-0.019	ABG
sex	Male	factor	0.090	0.019	ABG
sex	Male	factor	0.090	0.019	ABG
sex	Female	factor	-0.090	-0.019	ABG
serum_phos	NA	numeric	0.100	0.019	ABG
phtn	1	factor	0.049	0.019	ABG
phtn	0	factor	-0.049	-0.019	ABG
race_ethnicity	2	factor	-0.045	-0.019	ABG
osa	0	factor	0.049	-0.019	ABG
osa	1	factor	-0.049	0.019	ABG
serum_cl	NA	numeric	0.028	-0.019	ABG
wbc	NA	numeric	0.108	0.019	ABG
phtn	0	factor	-0.049	-0.019	ABG
phtn	1	factor	0.049	0.019	ABG
phtn	0	factor	-0.049	-0.019	ABG
phtn	1	factor	0.049	0.019	ABG
race_ethnicity	4	factor	0.041	0.019	ABG
race_ethnicity	2	factor	-0.045	-0.019	ABG
osa	0	factor	0.049	-0.019	ABG
osa	1	factor	-0.049	0.019	ABG

Table 16: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
serum_phos	NA	numeric	0.088	0.019	ABG
race_ethnicity	2	factor	-0.045	-0.019	ABG
race_ethnicity	2	factor	-0.045	-0.019	ABG
sodium	NA	numeric	-0.026	-0.019	ABG
sodium	NA	numeric	-0.029	-0.019	ABG
serum_phos	NA	numeric	0.098	0.019	ABG
plt	NA	numeric	-0.116	-0.019	ABG
serum_phos	NA	numeric	0.103	0.019	ABG
sex	Male	factor	0.090	0.019	ABG
sex	Female	factor	-0.090	-0.019	ABG
race_ethnicity	2	factor	-0.045	-0.019	ABG
race_ethnicity	2	factor	-0.045	-0.019	ABG
race_ethnicity	2	factor	-0.045	-0.019	ABG
race_ethnicity	2	factor	-0.045	-0.019	ABG
phtn	1	factor	0.049	0.019	ABG
phtn	0	factor	-0.049	-0.019	ABG
phtn	0	factor	-0.049	-0.019	ABG
phtn	1	factor	0.049	0.019	ABG
sodium	NA	numeric	-0.027	-0.019	ABG
sex	Female	factor	-0.090	-0.019	ABG
sex	Male	factor	0.090	0.019	ABG
sodium	NA	numeric	-0.028	-0.019	ABG
race_ethnicity	4	factor	0.041	0.019	ABG
temp_new	NA	numeric	-0.099	-0.019	ABG
serum_k	NA	numeric	0.022	0.019	ABG
serum_lac	NA	numeric	0.114	0.019	ABG
serum_cl	NA	numeric	0.026	-0.019	ABG
phtn	1	factor	0.049	0.019	ABG
phtn	0	factor	-0.049	-0.019	ABG
sodium	NA	numeric	-0.029	-0.019	ABG
phtn	0	factor	-0.049	-0.019	ABG
phtn	1	factor	0.049	0.019	ABG
phtn	0	factor	-0.049	-0.019	ABG
phtn	1	factor	0.049	0.019	ABG
serum_phos	NA	numeric	0.097	0.019	ABG
sodium	NA	numeric	-0.028	-0.019	ABG
phtn	0	factor	-0.049	-0.019	ABG
phtn	1	factor	0.049	0.019	ABG
serum_phos	NA	numeric	0.101	0.019	ABG
serum_cl	NA	numeric	0.029	-0.019	ABG
sex	Female	factor	-0.090	-0.019	ABG
sex	Male	factor	0.090	0.019	ABG
phtn	1	factor	0.049	0.019	ABG
phtn	0	factor	-0.049	-0.019	ABG
plt	NA	numeric	-0.118	-0.019	ABG
serum_cl	NA	numeric	0.029	-0.019	ABG
serum_phos	NA	numeric	0.090	0.019	ABG
phtn	1	factor	0.049	0.019	ABG
phtn	0	factor	-0.049	-0.019	ABG
serum_cl	NA	numeric	0.026	-0.019	ABG
race_ethnicity	2	factor	-0.045	-0.019	ABG
wbc	NA	numeric	0.107	0.019	ABG
asthma	1	factor	-0.059	-0.019	ABG
asthma	0	factor	0.059	0.019	ABG
sodium	NA	numeric	-0.027	-0.019	ABG
race_ethnicity	4	factor	0.041	0.019	ABG
wbc	NA	numeric	0.108	0.019	ABG
phtn	1	factor	0.049	0.019	ABG
phtn	0	factor	-0.049	-0.019	ABG
plt	NA	numeric	-0.120	-0.019	ABG
osa	0	factor	0.049	-0.019	ABG
osa	1	factor	-0.049	0.019	ABG
phtn	0	factor	-0.049	-0.019	ABG
phtn	1	factor	0.049	0.019	ABG

Table 16: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
race_ethnicity	2	factor	-0.045	-0.019	ABG
serum_cl	NA	numeric	0.028	-0.019	ABG
race_ethnicity	4	factor	0.041	0.019	ABG
race_ethnicity	2	factor	-0.045	-0.019	ABG
phtn	0	factor	-0.049	-0.019	ABG
phtn	1	factor	0.049	0.019	ABG
temp_new	NA	numeric	-0.098	-0.019	ABG
serum_phos	NA	numeric	0.099	0.019	ABG
serum_lac	NA	numeric	0.104	0.019	ABG
race_ethnicity	4	factor	0.041	0.019	ABG
serum_lac	NA	numeric	0.114	0.019	ABG
race_ethnicity	4	factor	0.041	0.019	ABG
temp_new	NA	numeric	-0.103	-0.019	ABG
sex	Male	factor	0.090	0.019	ABG
sex	Female	factor	-0.090	-0.019	ABG
serum_cl	NA	numeric	0.032	-0.018	ABG
temp_new	NA	numeric	-0.095	-0.018	ABG
sodium	NA	numeric	-0.027	-0.018	ABG
plt	NA	numeric	-0.114	-0.018	ABG
race_ethnicity	2	factor	-0.045	-0.018	ABG
serum_lac	NA	numeric	0.119	0.018	ABG
serum_phos	NA	numeric	0.087	0.018	ABG
serum_phos	NA	numeric	0.095	0.018	ABG
serum_cl	NA	numeric	0.028	-0.018	ABG
serum_phos	NA	numeric	0.096	0.018	ABG
sodium	NA	numeric	-0.027	-0.018	ABG
race_ethnicity	4	factor	0.041	0.018	ABG
serum_lac	NA	numeric	0.112	0.018	ABG
plt	NA	numeric	-0.117	-0.018	ABG
sodium	NA	numeric	-0.029	-0.018	ABG
race_ethnicity	2	factor	-0.045	-0.018	ABG
phtn	1	factor	0.049	0.018	ABG
phtn	0	factor	-0.049	-0.018	ABG
race_ethnicity	2	factor	-0.045	-0.018	ABG
sodium	NA	numeric	-0.029	-0.018	ABG
phtn	0	factor	-0.049	-0.018	ABG
phtn	1	factor	0.049	0.018	ABG
serum_phos	NA	numeric	0.098	0.018	ABG
serum_phos	NA	numeric	0.092	0.018	ABG
plt	NA	numeric	-0.113	-0.018	ABG
phtn	0	factor	-0.049	-0.018	ABG
phtn	1	factor	0.049	0.018	ABG
phtn	0	factor	-0.049	-0.018	ABG
phtn	1	factor	0.049	0.018	ABG
serum_cl	NA	numeric	0.028	-0.018	ABG
serum_cl	NA	numeric	0.027	-0.018	ABG
sodium	NA	numeric	-0.028	-0.018	ABG
phtn	1	factor	0.049	0.018	ABG
phtn	0	factor	-0.049	-0.018	ABG
plt	NA	numeric	-0.116	-0.018	ABG
serum_cl	NA	numeric	0.028	-0.018	ABG
plt	NA	numeric	-0.116	-0.018	ABG
race_ethnicity	4	factor	0.041	0.018	ABG
race_ethnicity	4	factor	0.041	0.018	ABG
sodium	NA	numeric	-0.030	-0.018	ABG
sex	Male	factor	0.090	0.018	ABG
sex	Female	factor	-0.090	-0.018	ABG
sodium	NA	numeric	-0.030	-0.018	ABG
serum_cl	NA	numeric	0.028	-0.018	ABG
race_ethnicity	2	factor	-0.045	-0.018	ABG
serum_phos	NA	numeric	0.103	0.018	ABG
plt	NA	numeric	-0.115	-0.018	ABG

Table 16: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
race_ethnicity	4	factor	0.041	0.018	ABG
wbc	NA	numeric	0.109	0.018	ABG
race_ethnicity	2	factor	-0.045	-0.018	ABG
sex	Female	factor	-0.090	-0.018	ABG
sex	Male	factor	0.090	0.018	ABG
serum_lac	NA	numeric	0.107	0.018	ABG
plt	NA	numeric	-0.113	-0.018	ABG
serum_phos	NA	numeric	0.092	0.018	ABG
serum_cl	NA	numeric	0.030	-0.018	ABG
phtn	1	factor	0.049	0.018	ABG
phtn	0	factor	-0.049	-0.018	ABG
phtn	0	factor	-0.049	-0.018	ABG
phtn	1	factor	0.049	0.018	ABG
serum_cl	NA	numeric	0.025	-0.018	ABG
phtn	1	factor	0.049	0.018	ABG
phtn	0	factor	-0.049	-0.018	ABG
sex	Female	factor	-0.090	-0.018	ABG
sex	Male	factor	0.090	0.018	ABG
serum_phos	NA	numeric	0.105	0.018	ABG
plt	NA	numeric	-0.117	-0.018	ABG
serum_lac	NA	numeric	0.114	0.018	ABG
sex	Female	factor	-0.090	-0.018	ABG
sex	Male	factor	0.090	0.018	ABG
phtn	0	factor	-0.049	-0.018	ABG
phtn	1	factor	0.049	0.018	ABG
sodium	NA	numeric	-0.030	-0.018	ABG
sex	Male	factor	0.090	0.018	ABG
sex	Female	factor	-0.090	-0.018	ABG
phtn	1	factor	0.049	0.018	ABG
phtn	0	factor	-0.049	-0.018	ABG
serum_cl	NA	numeric	0.030	-0.018	ABG
sodium	NA	numeric	-0.028	-0.018	ABG
plt	NA	numeric	-0.114	-0.018	ABG
race_ethnicity	2	factor	-0.045	-0.018	ABG
sex	Male	factor	0.090	0.018	ABG
sex	Female	factor	-0.090	-0.018	ABG
serum_lac	NA	numeric	0.109	0.018	ABG
race_ethnicity	4	factor	0.041	0.018	ABG
sodium	NA	numeric	-0.026	-0.018	ABG
phtn	0	factor	-0.049	-0.018	ABG
phtn	1	factor	0.049	0.018	ABG
sodium	NA	numeric	-0.031	-0.018	ABG
phtn	0	factor	-0.049	-0.018	ABG
phtn	1	factor	0.049	0.018	ABG
race_ethnicity	2	factor	-0.045	-0.018	ABG
race_ethnicity	2	factor	-0.045	-0.018	ABG
race_ethnicity	4	factor	0.041	0.018	ABG
hr	NA	numeric	-0.060	-0.018	ABG
wbc	NA	numeric	0.107	0.018	ABG
phtn	0	factor	-0.049	-0.018	ABG
phtn	1	factor	0.049	0.018	ABG
plt	NA	numeric	-0.115	-0.018	ABG
phtn	0	factor	-0.049	-0.018	ABG
phtn	1	factor	0.049	0.018	ABG
race_ethnicity	4	factor	0.041	0.018	ABG
serum_phos	NA	numeric	0.089	0.018	ABG
sodium	NA	numeric	-0.029	-0.018	ABG
plt	NA	numeric	-0.112	-0.018	ABG
serum_cl	NA	numeric	0.032	-0.018	ABG
phtn	0	factor	-0.049	-0.018	ABG
phtn	1	factor	0.049	0.018	ABG
serum_lac	NA	numeric	0.105	0.018	ABG
serum_cl	NA	numeric	0.029	-0.018	ABG

Table 16: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
phtn	0	factor	-0.049	-0.018	ABG
phtn	1	factor	0.049	0.018	ABG
serum_phos	NA	numeric	0.093	0.018	ABG
race_ethnicity	4	factor	0.041	0.018	ABG
serum_cl	NA	numeric	0.026	-0.018	ABG
wbc	NA	numeric	0.106	0.018	ABG
wbc	NA	numeric	0.100	0.018	ABG
sodium	NA	numeric	-0.030	-0.018	ABG
race_ethnicity	4	factor	0.041	0.018	ABG
race_ethnicity	4	factor	0.041	0.018	ABG
phtn	0	factor	-0.049	-0.018	ABG
phtn	1	factor	0.049	0.018	ABG
race_ethnicity	4	factor	0.041	0.018	ABG
serum_cl	NA	numeric	0.028	-0.018	ABG
phtn	1	factor	0.049	0.018	ABG
phtn	0	factor	-0.049	-0.018	ABG
serum_cl	NA	numeric	0.030	-0.018	ABG
sodium	NA	numeric	-0.029	-0.018	ABG
phtn	1	factor	0.049	0.018	ABG
phtn	0	factor	-0.049	-0.018	ABG
plt	NA	numeric	-0.118	-0.018	ABG
wbc	NA	numeric	0.112	0.018	ABG
sodium	NA	numeric	-0.029	-0.017	ABG
sodium	NA	numeric	-0.029	-0.017	ABG
plt	NA	numeric	-0.118	-0.017	ABG
race_ethnicity	2	factor	-0.045	-0.017	ABG
serum_lac	NA	numeric	0.109	0.017	ABG
sodium	NA	numeric	-0.029	-0.017	ABG
serum_phos	NA	numeric	0.101	0.017	ABG
phtn	1	factor	0.049	0.017	ABG
phtn	0	factor	-0.049	-0.017	ABG
serum_lac	NA	numeric	0.116	0.017	ABG
phtn	0	factor	-0.049	-0.017	ABG
phtn	1	factor	0.049	0.017	ABG
phtn	0	factor	-0.049	-0.017	ABG
wbc	NA	numeric	0.102	0.017	ABG
sodium	NA	numeric	-0.030	-0.017	ABG
plt	NA	numeric	-0.116	-0.017	ABG
osa	1	factor	-0.049	0.017	ABG
osa	0	factor	0.049	-0.017	ABG
serum_cl	NA	numeric	0.027	-0.017	ABG
osa	1	factor	-0.049	0.017	ABG
osa	0	factor	0.049	-0.017	ABG
sodium	NA	numeric	-0.031	-0.017	ABG
osa	0	factor	0.049	-0.017	ABG
osa	1	factor	-0.049	0.017	ABG
sodium	NA	numeric	-0.029	-0.017	ABG
temp_new	NA	numeric	-0.092	-0.017	ABG
race_ethnicity	4	factor	0.041	0.017	ABG
serum_lac	NA	numeric	0.117	0.017	ABG
phtn	0	factor	-0.049	-0.017	ABG
phtn	1	factor	0.049	0.017	ABG
serum_phos	NA	numeric	0.101	0.017	ABG
osa	1	factor	-0.049	0.017	ABG
osa	0	factor	0.049	-0.017	ABG
race_ethnicity	2	factor	-0.045	-0.017	ABG
serum_cl	NA	numeric	0.029	-0.017	ABG
wbc	NA	numeric	0.107	0.017	ABG
race_ethnicity	2	factor	-0.045	-0.017	ABG
sodium	NA	numeric	-0.030	-0.017	ABG

Table 16: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
wbc	NA	numeric	0.110	0.017	ABG
temp_new	NA	numeric	-0.108	-0.017	ABG
asthma	1	factor	-0.059	-0.017	ABG
asthma	0	factor	0.059	0.017	ABG
osa	1	factor	-0.049	0.017	ABG
osa	0	factor	0.049	-0.017	ABG
sodium	NA	numeric	-0.030	-0.017	ABG
serum_lac	NA	numeric	0.105	0.017	ABG
sodium	NA	numeric	-0.029	-0.017	ABG
serum_cl	NA	numeric	0.026	-0.017	ABG
osa	0	factor	0.049	-0.017	ABG
osa	1	factor	-0.049	0.017	ABG
plt	NA	numeric	-0.113	-0.017	ABG
sodium	NA	numeric	-0.029	-0.017	ABG
wbc	NA	numeric	0.111	0.017	ABG
osa	1	factor	-0.049	0.017	ABG
osa	0	factor	0.049	-0.017	ABG
asthma	0	factor	0.059	0.017	ABG
asthma	1	factor	-0.059	-0.017	ABG
race_ethnicity	2	factor	-0.045	-0.017	ABG
serum_cl	NA	numeric	0.029	-0.017	ABG
sex	Female	factor	-0.090	-0.017	ABG
sex	Male	factor	0.090	0.017	ABG
wbc	NA	numeric	0.111	0.017	ABG
serum_cl	NA	numeric	0.030	-0.017	ABG
phtn	1	factor	0.049	0.017	ABG
phtn	0	factor	-0.049	-0.017	ABG
serum_phos	NA	numeric	0.092	0.017	ABG
asthma	0	factor	0.059	0.017	ABG
asthma	1	factor	-0.059	-0.017	ABG
race_ethnicity	4	factor	0.041	0.017	ABG
sodium	NA	numeric	-0.032	-0.017	ABG
serum_cl	NA	numeric	0.028	-0.017	ABG
plt	NA	numeric	-0.116	-0.017	ABG
race_ethnicity	4	factor	0.041	0.017	ABG
plt	NA	numeric	-0.115	-0.017	ABG
phtn	0	factor	-0.049	-0.017	ABG
phtn	1	factor	0.049	0.017	ABG
serum_cl	NA	numeric	0.025	-0.017	ABG
serum_lac	NA	numeric	0.115	0.017	ABG
sodium	NA	numeric	-0.028	-0.017	ABG
race_ethnicity	4	factor	0.041	0.017	ABG
osa	1	factor	-0.049	0.017	ABG
osa	0	factor	0.049	-0.017	ABG
phtn	0	factor	-0.049	-0.017	ABG
phtn	1	factor	0.049	0.017	ABG
sodium	NA	numeric	-0.028	-0.017	ABG
sodium	NA	numeric	-0.030	-0.017	ABG
serum_cl	NA	numeric	0.028	-0.017	ABG
wbc	NA	numeric	0.109	0.017	ABG
plt	NA	numeric	-0.117	-0.017	ABG
serum_cl	NA	numeric	0.026	-0.017	ABG
sodium	NA	numeric	-0.027	-0.017	ABG
race_ethnicity	2	factor	-0.045	-0.017	ABG
wbc	NA	numeric	0.113	0.017	ABG
phtn	1	factor	0.049	0.017	ABG
phtn	0	factor	-0.049	-0.017	ABG
plt	NA	numeric	-0.118	-0.017	ABG
plt	NA	numeric	-0.116	-0.017	ABG
osa	1	factor	-0.049	0.017	ABG
osa	0	factor	0.049	-0.017	ABG
plt	NA	numeric	-0.116	-0.017	ABG
wbc	NA	numeric	0.104	0.017	ABG

Table 16: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
wbc	NA	numeric	0.107	0.017	ABG
serum_cl	NA	numeric	0.026	-0.017	ABG
osa	1	factor	-0.049	0.017	ABG
osa	0	factor	0.049	-0.017	ABG
serum_cl	NA	numeric	0.026	-0.017	ABG
sodium	NA	numeric	-0.028	-0.017	ABG
sodium	NA	numeric	-0.031	-0.017	ABG
race_ethnicity	4	factor	0.041	0.017	ABG
serum_lac	NA	numeric	0.113	0.017	ABG
sodium	NA	numeric	-0.028	-0.017	ABG
sodium	NA	numeric	-0.028	-0.017	ABG
plt	NA	numeric	-0.115	-0.017	ABG
asthma	0	factor	0.059	0.017	ABG
asthma	1	factor	-0.059	-0.017	ABG
plt	NA	numeric	-0.117	-0.017	ABG
plt	NA	numeric	-0.114	-0.017	ABG
phtn	1	factor	0.049	0.017	ABG
phtn	0	factor	-0.049	-0.017	ABG
plt	NA	numeric	-0.113	-0.017	ABG
serum_phos	NA	numeric	0.097	0.017	ABG
serum_cl	NA	numeric	0.030	-0.017	ABG
race_ethnicity	4	factor	0.041	0.017	ABG
race_ethnicity	2	factor	-0.045	-0.017	ABG
wbc	NA	numeric	0.100	0.017	ABG
plt	NA	numeric	-0.115	-0.017	ABG
race_ethnicity	4	factor	0.041	0.017	ABG
temp_new	NA	numeric	-0.101	-0.017	ABG
serum_lac	NA	numeric	0.102	0.017	ABG
plt	NA	numeric	-0.115	-0.017	ABG
plt	NA	numeric	-0.113	-0.017	ABG
sodium	NA	numeric	-0.029	-0.017	ABG
wbc	NA	numeric	0.109	0.017	ABG
sodium	NA	numeric	-0.028	-0.017	ABG
sodium	NA	numeric	-0.027	-0.017	ABG
wbc	NA	numeric	0.105	0.017	ABG
osa	0	factor	0.049	-0.017	ABG
osa	1	factor	-0.049	0.017	ABG
race_ethnicity	4	factor	0.041	0.016	ABG
plt	NA	numeric	-0.120	-0.016	ABG
osa	1	factor	-0.049	0.016	ABG
osa	0	factor	0.049	-0.016	ABG
sodium	NA	numeric	-0.027	-0.016	ABG
serum_lac	NA	numeric	0.112	0.016	ABG
sex	Male	factor	0.090	0.016	ABG
sex	Female	factor	-0.090	-0.016	ABG
wbc	NA	numeric	0.103	0.016	ABG
plt	NA	numeric	-0.116	-0.016	ABG
asthma	1	factor	-0.059	-0.016	ABG
asthma	0	factor	0.059	0.016	ABG
sodium	NA	numeric	-0.028	-0.016	ABG
serum_cl	NA	numeric	0.029	-0.016	ABG
wbc	NA	numeric	0.108	0.016	ABG
asthma	1	factor	-0.059	-0.016	ABG
asthma	0	factor	0.059	0.016	ABG
phtn	1	factor	0.049	0.016	ABG
phtn	0	factor	-0.049	-0.016	ABG
wbc	NA	numeric	0.110	0.016	ABG
plt	NA	numeric	-0.114	-0.016	ABG
serum_lac	NA	numeric	0.102	0.016	ABG
serum_lac	NA	numeric	0.114	0.016	ABG
serum_lac	NA	numeric	0.111	0.016	ABG
serum_cl	NA	numeric	0.026	-0.016	ABG
sodium	NA	numeric	-0.027	-0.016	ABG

Table 16: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
race_ethnicity	4	factor	0.041	0.016	ABG
serum_cl	NA	numeric	0.028	-0.016	ABG
phtn	0	factor	-0.049	-0.016	ABG
phtn	1	factor	0.049	0.016	ABG
race_ethnicity	2	factor	-0.045	-0.016	ABG
sodium	NA	numeric	-0.030	-0.016	ABG
sodium	NA	numeric	-0.032	-0.016	ABG
plt	NA	numeric	-0.118	-0.016	ABG
race_ethnicity	4	factor	0.041	0.016	ABG
sodium	NA	numeric	-0.028	-0.016	ABG
race_ethnicity	4	factor	0.041	0.016	ABG
plt	NA	numeric	-0.114	-0.016	ABG
temp_new	NA	numeric	-0.101	-0.016	ABG
race_ethnicity	4	factor	0.041	0.016	ABG
sodium	NA	numeric	-0.031	-0.016	ABG
osa	0	factor	0.049	-0.016	ABG
osa	1	factor	-0.049	0.016	ABG
osa	0	factor	0.049	-0.016	ABG
osa	1	factor	-0.049	0.016	ABG
serum_lac	NA	numeric	0.117	0.016	ABG
serum_phos	NA	numeric	0.092	0.016	ABG
sodium	NA	numeric	-0.029	-0.016	ABG
osa	0	factor	0.049	-0.016	ABG
osa	1	factor	-0.049	0.016	ABG
serum_cl	NA	numeric	0.029	-0.016	ABG
serum_lac	NA	numeric	0.103	0.016	ABG
plt	NA	numeric	-0.118	-0.016	ABG
race_ethnicity	4	factor	0.041	0.016	ABG
sodium	NA	numeric	-0.027	-0.016	ABG
serum_cl	NA	numeric	0.029	-0.016	ABG
serum_phos	NA	numeric	0.103	0.016	ABG
sodium	NA	numeric	-0.029	-0.016	ABG
serum_cl	NA	numeric	0.026	-0.016	ABG
osa	0	factor	0.049	-0.016	ABG
osa	1	factor	-0.049	0.016	ABG
wbc	NA	numeric	0.098	0.016	ABG
osa	0	factor	0.049	-0.016	ABG
osa	1	factor	-0.049	0.016	ABG
asthma	0	factor	0.059	0.016	ABG
asthma	1	factor	-0.059	-0.016	ABG
sodium	NA	numeric	-0.031	-0.016	ABG
serum_lac	NA	numeric	0.113	0.016	ABG
serum_lac	NA	numeric	0.112	0.016	ABG
sex	Female	factor	-0.090	-0.016	ABG
sex	Male	factor	0.090	0.016	ABG
wbc	NA	numeric	0.105	0.016	ABG
phtn	0	factor	-0.049	-0.016	ABG
phtn	1	factor	0.049	0.016	ABG
osa	0	factor	0.049	-0.016	ABG
osa	1	factor	-0.049	0.016	ABG
wbc	NA	numeric	0.095	0.016	ABG
race_ethnicity	4	factor	0.041	0.016	ABG
serum_lac	NA	numeric	0.107	0.016	ABG
wbc	NA	numeric	0.114	0.016	ABG
serum_cl	NA	numeric	0.027	-0.016	ABG
osa	0	factor	0.049	-0.016	ABG
osa	1	factor	-0.049	0.016	ABG
serum_lac	NA	numeric	0.100	0.016	ABG
race_ethnicity	4	factor	0.041	0.016	ABG
plt	NA	numeric	-0.117	-0.016	ABG
wbc	NA	numeric	0.104	0.016	ABG
plt	NA	numeric	-0.115	-0.016	ABG
serum_cl	NA	numeric	0.028	-0.016	ABG
wbc	NA	numeric	0.096	0.016	ABG

Table 16: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
serum_cl	NA	numeric	0.030	-0.016	ABG
serum_lac	NA	numeric	0.119	0.016	ABG
plt	NA	numeric	-0.117	-0.016	ABG
sodium	NA	numeric	-0.027	-0.016	ABG
plt	NA	numeric	-0.116	-0.016	ABG
plt	NA	numeric	-0.115	-0.016	ABG
serum_phos	NA	numeric	0.093	0.016	ABG
serum_cl	NA	numeric	0.027	-0.016	ABG
phtn	1	factor	0.049	0.016	ABG
phtn	0	factor	-0.049	-0.016	ABG
serum_lac	NA	numeric	0.109	0.016	ABG
race_ethnicity	4	factor	0.041	0.016	ABG
temp_new	NA	numeric	-0.099	-0.016	ABG
osa	0	factor	0.049	-0.016	ABG
osa	1	factor	-0.049	0.016	ABG
serum_lac	NA	numeric	0.107	0.016	ABG
plt	NA	numeric	-0.117	-0.016	ABG
plt	NA	numeric	-0.113	-0.016	ABG
serum_cl	NA	numeric	0.029	-0.016	ABG
plt	NA	numeric	-0.116	-0.016	ABG
osa	0	factor	0.049	-0.016	ABG
osa	1	factor	-0.049	0.016	ABG
serum_cl	NA	numeric	0.026	-0.016	ABG
serum_lac	NA	numeric	0.101	0.016	ABG
serum_lac	NA	numeric	0.117	0.016	ABG
serum_phos	NA	numeric	0.101	0.016	ABG
race_ethnicity	4	factor	0.041	0.016	ABG
asthma	1	factor	-0.059	-0.016	ABG
asthma	0	factor	0.059	0.016	ABG
sodium	NA	numeric	-0.026	-0.016	ABG
plt	NA	numeric	-0.119	-0.016	ABG
serum_lac	NA	numeric	0.117	0.016	ABG
phtn	1	factor	0.049	0.016	ABG
phtn	0	factor	-0.049	-0.016	ABG
osa	1	factor	-0.049	0.016	ABG
osa	0	factor	0.049	-0.016	ABG
race_ethnicity	4	factor	0.041	0.016	ABG
race_ethnicity	4	factor	0.041	0.016	ABG
serum_cl	NA	numeric	0.031	-0.016	ABG
race_ethnicity	4	factor	0.041	0.016	ABG
race_ethnicity	4	factor	0.041	0.016	ABG
plt	NA	numeric	-0.117	-0.016	ABG
race_ethnicity	4	factor	0.041	0.016	ABG
serum_cl	NA	numeric	0.027	-0.016	ABG
sodium	NA	numeric	-0.030	-0.016	ABG
serum_lac	NA	numeric	0.125	0.016	ABG
temp_new	NA	numeric	-0.095	-0.016	ABG
sodium	NA	numeric	-0.028	-0.016	ABG
temp_new	NA	numeric	-0.105	-0.016	ABG
temp_new	NA	numeric	-0.103	-0.016	ABG
serum_lac	NA	numeric	0.110	0.016	ABG
osa	0	factor	0.049	-0.016	ABG
osa	1	factor	-0.049	0.016	ABG
asthma	1	factor	-0.059	-0.015	ABG
asthma	0	factor	0.059	0.015	ABG
wbc	NA	numeric	0.106	0.015	ABG
asthma	0	factor	0.059	0.015	ABG
asthma	1	factor	-0.059	-0.015	ABG
serum_lac	NA	numeric	0.116	0.015	ABG
phtn	1	factor	0.049	0.015	ABG
phtn	0	factor	-0.049	-0.015	ABG
serum_cl	NA	numeric	0.028	-0.015	ABG
serum_cl	NA	numeric	0.029	-0.015	ABG

Table 16: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
osa	1	factor	-0.049	0.015	ABG
osa	0	factor	0.049	-0.015	ABG
osa	0	factor	0.049	-0.015	ABG
osa	1	factor	-0.049	0.015	ABG
race_ethnicity	4	factor	0.041	0.015	ABG
race_ethnicity	4	factor	0.041	0.015	ABG
wbc	NA	numeric	0.106	0.015	ABG
race_ethnicity	4	factor	0.041	0.015	ABG
serum_phos	NA	numeric	0.086	0.015	ABG
temp_new	NA	numeric	-0.098	-0.015	ABG
asthma	0	factor	0.059	0.015	ABG
asthma	1	factor	-0.059	-0.015	ABG
osa	1	factor	-0.049	0.015	ABG
osa	0	factor	0.049	-0.015	ABG
wbc	NA	numeric	0.111	0.015	ABG
asthma	1	factor	-0.059	-0.015	ABG
asthma	0	factor	0.059	0.015	ABG
race_ethnicity	4	factor	0.041	0.015	ABG
serum_cl	NA	numeric	0.030	-0.015	ABG
osa	0	factor	0.049	-0.015	ABG
osa	1	factor	-0.049	0.015	ABG
plt	NA	numeric	-0.121	-0.015	ABG
plt	NA	numeric	-0.114	-0.015	ABG
wbc	NA	numeric	0.109	0.015	ABG
temp_new	NA	numeric	-0.100	-0.015	ABG
temp_new	NA	numeric	-0.093	-0.015	ABG
asthma	0	factor	0.059	0.015	ABG
asthma	1	factor	-0.059	-0.015	ABG
serum_cl	NA	numeric	0.030	-0.015	ABG
race_ethnicity	4	factor	0.041	0.015	ABG
serum_phos	NA	numeric	0.094	0.015	ABG
wbc	NA	numeric	0.113	0.015	ABG
serum_cl	NA	numeric	0.029	-0.015	ABG
temp_new	NA	numeric	-0.084	-0.015	ABG
osa	0	factor	0.049	-0.015	ABG
osa	1	factor	-0.049	0.015	ABG
wbc	NA	numeric	0.110	0.015	ABG
serum_cl	NA	numeric	0.027	-0.015	ABG
hr	NA	numeric	-0.084	-0.015	ABG
wbc	NA	numeric	0.103	0.015	ABG
wbc	NA	numeric	0.107	0.015	ABG
temp_new	NA	numeric	-0.106	-0.015	ABG
plt	NA	numeric	-0.117	-0.015	ABG
wbc	NA	numeric	0.108	0.015	ABG
plt	NA	numeric	-0.117	-0.015	ABG
serum_lac	NA	numeric	0.105	0.015	ABG
sodium	NA	numeric	-0.027	-0.015	ABG
wbc	NA	numeric	0.109	0.015	ABG
wbc	NA	numeric	0.111	0.015	ABG
wbc	NA	numeric	0.109	0.015	ABG
osa	0	factor	0.049	-0.015	ABG
osa	1	factor	-0.049	0.015	ABG
serum_cl	NA	numeric	0.030	-0.015	ABG
serum_lac	NA	numeric	0.114	0.015	ABG
wbc	NA	numeric	0.112	0.015	ABG
serum_cl	NA	numeric	0.029	-0.015	ABG
sodium	NA	numeric	-0.025	-0.015	ABG
serum_phos	NA	numeric	0.097	0.015	ABG
temp_new	NA	numeric	-0.103	-0.015	ABG
sodium	NA	numeric	-0.031	-0.015	ABG
serum_lac	NA	numeric	0.115	0.015	ABG
asthma	0	factor	0.059	0.015	ABG
asthma	1	factor	-0.059	-0.015	ABG

Table 16: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
sodium	NA	numeric	-0.024	-0.015	ABG
osa	1	factor	-0.049	0.015	ABG
osa	0	factor	0.049	-0.015	ABG
asthma	0	factor	0.059	0.015	ABG
asthma	1	factor	-0.059	-0.015	ABG
serum_cl	NA	numeric	0.030	-0.015	ABG
osa	1	factor	-0.049	0.015	ABG
osa	0	factor	0.049	-0.015	ABG
wbc	NA	numeric	0.106	0.015	ABG
osa	1	factor	-0.049	0.015	ABG
osa	0	factor	0.049	-0.015	ABG
temp_new	NA	numeric	-0.099	-0.015	ABG
osa	0	factor	0.049	-0.015	ABG
osa	1	factor	-0.049	0.015	ABG
serum_lac	NA	numeric	0.125	0.015	ABG
plt	NA	numeric	-0.115	-0.015	ABG
wbc	NA	numeric	0.111	0.015	ABG
plt	NA	numeric	-0.116	-0.015	ABG
serum_phos	NA	numeric	0.092	0.015	ABG
race_ethnicity	4	factor	0.041	0.015	ABG
sodium	NA	numeric	-0.030	-0.015	ABG
temp_new	NA	numeric	-0.097	-0.015	ABG
wbc	NA	numeric	0.110	0.015	ABG
wbc	NA	numeric	0.101	0.015	ABG
asthma	0	factor	0.059	0.015	ABG
asthma	1	factor	-0.059	-0.015	ABG
phtn	0	factor	-0.049	-0.015	ABG
phtn	1	factor	0.049	0.015	ABG
plt	NA	numeric	-0.113	-0.015	ABG
asthma	1	factor	-0.059	-0.015	ABG
asthma	0	factor	0.059	0.015	ABG
phtn	1	factor	0.049	0.015	ABG
phtn	0	factor	-0.049	-0.015	ABG
osa	0	factor	0.049	-0.015	ABG
osa	1	factor	-0.049	0.015	ABG
wbc	NA	numeric	0.106	0.015	ABG
osa	0	factor	0.049	-0.015	ABG
osa	1	factor	-0.049	0.015	ABG
serum_lac	NA	numeric	0.108	0.015	ABG
plt	NA	numeric	-0.112	-0.015	ABG
serum_cl	NA	numeric	0.031	-0.015	ABG
serum_lac	NA	numeric	0.106	0.015	ABG
wbc	NA	numeric	0.103	0.015	ABG
plt	NA	numeric	-0.114	-0.015	ABG
race_ethnicity	4	factor	0.041	0.015	ABG
serum_cl	NA	numeric	0.029	-0.015	ABG
wbc	NA	numeric	0.109	0.015	ABG
asthma	1	factor	-0.059	-0.015	ABG
asthma	0	factor	0.059	0.015	ABG
osa	1	factor	-0.049	0.015	ABG
osa	0	factor	0.049	-0.015	ABG
asthma	0	factor	0.059	0.015	ABG
asthma	1	factor	-0.059	-0.015	ABG
serum_cl	NA	numeric	0.028	-0.015	ABG
sodium	NA	numeric	-0.031	-0.015	ABG
serum_lac	NA	numeric	0.098	0.015	ABG
asthma	1	factor	-0.059	-0.015	ABG
asthma	0	factor	0.059	0.015	ABG
osa	1	factor	-0.049	0.015	ABG
osa	0	factor	0.049	-0.015	ABG
asthma	0	factor	0.059	0.015	ABG
asthma	1	factor	-0.059	-0.015	ABG
wbc	NA	numeric	0.099	0.015	ABG

Table 16: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
osa	1	factor	-0.049	0.014	ABG
osa	0	factor	0.049	-0.014	ABG
race_ethnicity	4	factor	0.041	0.014	ABG
sodium	NA	numeric	-0.027	-0.014	ABG
asthma	0	factor	0.059	0.014	ABG
asthma	1	factor	-0.059	-0.014	ABG
race_ethnicity	4	factor	0.041	0.014	ABG
serum_cl	NA	numeric	0.028	-0.014	ABG
race_ethnicity	4	factor	0.041	0.014	ABG
asthma	0	factor	0.059	0.014	ABG
asthma	1	factor	-0.059	-0.014	ABG
osa	1	factor	-0.049	0.014	ABG
osa	0	factor	0.049	-0.014	ABG
asthma	1	factor	-0.059	-0.014	ABG
asthma	0	factor	0.059	0.014	ABG
wbc	NA	numeric	0.110	0.014	ABG
osa	1	factor	-0.049	0.014	ABG
osa	0	factor	0.049	-0.014	ABG
race_ethnicity	4	factor	0.041	0.014	ABG
osa	1	factor	-0.049	0.014	ABG
osa	0	factor	0.049	-0.014	ABG
race_ethnicity	4	factor	0.041	0.014	ABG
wbc	NA	numeric	0.108	0.014	ABG
phtn	0	factor	-0.049	-0.014	ABG
phtn	1	factor	0.049	0.014	ABG
sodium	NA	numeric	-0.029	-0.014	ABG
race_ethnicity	4	factor	0.041	0.014	ABG
serum_lac	NA	numeric	0.103	0.014	ABG
osa	1	factor	-0.049	0.014	ABG
osa	0	factor	0.049	-0.014	ABG
serum_lac	NA	numeric	0.104	0.014	ABG
plt	NA	numeric	-0.118	-0.014	ABG
serum_cl	NA	numeric	0.029	-0.014	ABG
race_ethnicity	2	factor	-0.045	-0.014	ABG
sodium	NA	numeric	-0.028	-0.014	ABG
plt	NA	numeric	-0.115	-0.014	ABG
temp_new	NA	numeric	-0.101	-0.014	ABG
serum_phos	NA	numeric	0.097	0.014	ABG
serum_lac	NA	numeric	0.115	0.014	ABG
serum_lac	NA	numeric	0.116	0.014	ABG
plt	NA	numeric	-0.118	-0.014	ABG
wbc	NA	numeric	0.111	0.014	ABG
osa	1	factor	-0.049	0.014	ABG
osa	0	factor	0.049	-0.014	ABG
wbc	NA	numeric	0.109	0.014	ABG
race_ethnicity	4	factor	0.041	0.014	ABG
serum_cl	NA	numeric	0.029	-0.014	ABG
serum_cl	NA	numeric	0.027	-0.014	ABG
osa	0	factor	0.049	-0.014	ABG
osa	1	factor	-0.049	0.014	ABG
osa	0	factor	0.049	-0.014	ABG
osa	1	factor	-0.049	0.014	ABG
temp_new	NA	numeric	-0.104	-0.014	ABG
race_ethnicity	4	factor	0.041	0.014	ABG
serum_phos	NA	numeric	0.092	0.014	ABG
location	3	factor	-0.087	-0.014	ABG
serum_phos	NA	numeric	0.098	0.014	ABG
race_ethnicity	4	factor	0.041	0.014	ABG
asthma	0	factor	0.059	0.014	ABG
asthma	1	factor	-0.059	-0.014	ABG
serum_lac	NA	numeric	0.109	0.014	ABG
serum_cl	NA	numeric	0.029	-0.014	ABG
wbc	NA	numeric	0.102	0.014	ABG

Table 16: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
asthma	1	factor	-0.059	-0.014	ABG
asthma	0	factor	0.059	0.014	ABG
plt	NA	numeric	-0.113	-0.014	ABG
serum_lac	NA	numeric	0.112	0.014	ABG
serum_lac	NA	numeric	0.102	0.014	ABG
wbc	NA	numeric	0.105	0.014	ABG
location	3	factor	-0.087	-0.014	ABG
osa	0	factor	0.049	-0.014	ABG
osa	1	factor	-0.049	0.014	ABG
race_ethnicity	4	factor	0.041	0.014	ABG
phtn	0	factor	-0.049	-0.014	ABG
phtn	1	factor	0.049	0.014	ABG
wbc	NA	numeric	0.101	0.014	ABG
temp_new	NA	numeric	-0.094	-0.014	ABG
serum_phos	NA	numeric	0.095	0.014	ABG
wbc	NA	numeric	0.099	0.014	ABG
temp_new	NA	numeric	-0.087	-0.014	ABG
plt	NA	numeric	-0.118	-0.014	ABG
serum_lac	NA	numeric	0.107	0.014	ABG
plt	NA	numeric	-0.115	-0.014	ABG
serum_lac	NA	numeric	0.111	0.014	ABG
plt	NA	numeric	-0.115	-0.014	ABG
serum_lac	NA	numeric	0.113	0.014	ABG
serum_lac	NA	numeric	0.111	0.014	ABG
sodium	NA	numeric	-0.028	-0.014	ABG
race_ethnicity	4	factor	0.041	0.014	ABG
asthma	0	factor	0.059	0.014	ABG
asthma	1	factor	-0.059	-0.014	ABG
sodium	NA	numeric	-0.028	-0.014	ABG
wbc	NA	numeric	0.094	0.014	ABG
serum_cl	NA	numeric	0.029	-0.014	ABG
race_ethnicity	4	factor	0.041	0.014	ABG
osa	1	factor	-0.049	0.014	ABG
osa	0	factor	0.049	-0.014	ABG
serum_lac	NA	numeric	0.108	0.014	ABG
serum_lac	NA	numeric	0.104	0.014	ABG
osa	0	factor	0.049	-0.014	ABG
osa	1	factor	-0.049	0.014	ABG
serum_cl	NA	numeric	0.027	-0.014	ABG
race_ethnicity	4	factor	0.041	0.014	ABG
sodium	NA	numeric	-0.027	-0.014	ABG
location	3	factor	-0.087	-0.014	ABG
wbc	NA	numeric	0.093	0.014	ABG
serum_lac	NA	numeric	0.109	0.014	ABG
race_ethnicity	6	factor	0.022	0.014	ABG
asthma	0	factor	0.059	0.014	ABG
asthma	1	factor	-0.059	-0.014	ABG
osa	0	factor	0.049	-0.014	ABG
osa	1	factor	-0.049	0.014	ABG
serum_lac	NA	numeric	0.093	0.014	ABG
temp_new	NA	numeric	-0.099	-0.013	ABG
osa	1	factor	-0.049	0.013	ABG
osa	0	factor	0.049	-0.013	ABG
race_ethnicity	4	factor	0.041	0.013	ABG
temp_new	NA	numeric	-0.090	-0.013	ABG
serum_lac	NA	numeric	0.122	0.013	ABG
asthma	1	factor	-0.059	-0.013	ABG
asthma	0	factor	0.059	0.013	ABG
wbc	NA	numeric	0.113	0.013	ABG
wbc	NA	numeric	0.113	0.013	ABG
temp_new	NA	numeric	-0.090	-0.013	ABG
asthma	1	factor	-0.059	-0.013	ABG
asthma	0	factor	0.059	0.013	ABG

Table 16: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
osa	1	factor	-0.049	0.013	ABG
osa	0	factor	0.049	-0.013	ABG
temp_new	NA	numeric	-0.098	-0.013	ABG
asthma	0	factor	0.059	0.013	ABG
asthma	1	factor	-0.059	-0.013	ABG
phtn	1	factor	0.049	0.013	ABG
phtn	0	factor	-0.049	-0.013	ABG
temp_new	NA	numeric	-0.091	-0.013	ABG
temp_new	NA	numeric	-0.083	-0.013	ABG
location	3	factor	-0.087	-0.013	ABG
osa	0	factor	0.049	-0.013	ABG
osa	1	factor	-0.049	0.013	ABG
asthma	0	factor	0.059	0.013	ABG
asthma	1	factor	-0.059	-0.013	ABG
wbc	NA	numeric	0.110	0.013	ABG
asthma	1	factor	-0.059	-0.013	ABG
asthma	0	factor	0.059	0.013	ABG
temp_new	NA	numeric	-0.086	-0.013	ABG
serum_phos	NA	numeric	0.092	0.013	ABG
race_ethnicity	4	factor	0.041	0.013	ABG
race_ethnicity	4	factor	0.041	0.013	ABG
serum_cl	NA	numeric	0.030	-0.013	ABG
location	3	factor	-0.087	-0.013	ABG
temp_new	NA	numeric	-0.085	-0.013	ABG
asthma	0	factor	0.059	0.013	ABG
asthma	1	factor	-0.059	-0.013	ABG
race_ethnicity	4	factor	0.041	0.013	ABG
location	3	factor	-0.087	-0.013	ABG
osa	1	factor	-0.049	0.013	ABG
osa	0	factor	0.049	-0.013	ABG
wbc	NA	numeric	0.108	0.013	ABG
temp_new	NA	numeric	-0.098	-0.013	ABG
serum_lac	NA	numeric	0.112	0.013	ABG
race_ethnicity	6	factor	0.022	0.013	ABG
temp_new	NA	numeric	-0.082	-0.013	ABG
osa	1	factor	-0.049	0.013	ABG
osa	0	factor	0.049	-0.013	ABG
serum_cl	NA	numeric	0.029	-0.013	ABG
serum_cl	NA	numeric	0.029	-0.013	ABG
temp_new	NA	numeric	-0.101	-0.013	ABG
asthma	0	factor	0.059	0.013	ABG
asthma	1	factor	-0.059	-0.013	ABG
location	3	factor	-0.087	-0.013	ABG
temp_new	NA	numeric	-0.107	-0.013	ABG
wbc	NA	numeric	0.101	0.013	ABG
wbc	NA	numeric	0.104	0.013	ABG
wbc	NA	numeric	0.100	0.013	ABG
location	3	factor	-0.087	-0.013	ABG
sodium	NA	numeric	-0.030	-0.013	ABG
plt	NA	numeric	-0.116	-0.013	ABG
race_ethnicity	6	factor	0.022	0.013	ABG
temp_new	NA	numeric	-0.100	-0.013	ABG
asthma	1	factor	-0.059	-0.013	ABG
asthma	0	factor	0.059	0.013	ABG
temp_new	NA	numeric	-0.095	-0.013	ABG
osa	1	factor	-0.049	0.013	ABG
osa	0	factor	0.049	-0.013	ABG
plt	NA	numeric	-0.117	-0.013	ABG
wbc	NA	numeric	0.097	0.013	ABG
osa	0	factor	0.049	-0.013	ABG
osa	1	factor	-0.049	0.013	ABG
plt	NA	numeric	-0.114	-0.013	ABG
wbc	NA	numeric	0.105	0.013	ABG
serum_cl	NA	numeric	0.029	-0.013	ABG

Table 16: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
race_ethnicity	2	factor	-0.045	-0.013	ABG
location	3	factor	-0.087	-0.013	ABG
osa	0	factor	0.049	-0.013	ABG
osa	1	factor	-0.049	0.013	ABG
sodium	NA	numeric	-0.027	-0.013	ABG
location	3	factor	-0.087	-0.013	ABG
asthma	1	factor	-0.059	-0.013	ABG
asthma	0	factor	0.059	0.013	ABG
temp_new	NA	numeric	-0.100	-0.013	ABG
serum_lac	NA	numeric	0.113	0.013	ABG
asthma	1	factor	-0.059	-0.013	ABG
asthma	0	factor	0.059	0.013	ABG
asthma	0	factor	0.059	0.013	ABG
asthma	1	factor	-0.059	-0.013	ABG
race_ethnicity	4	factor	0.041	0.013	ABG
asthma	1	factor	-0.059	-0.013	ABG
asthma	0	factor	0.059	0.013	ABG
serum_lac	NA	numeric	0.110	0.013	ABG
serum_cl	NA	numeric	0.031	-0.013	ABG
osa	0	factor	0.049	-0.013	ABG
osa	1	factor	-0.049	0.013	ABG
race_ethnicity	4	factor	0.041	0.013	ABG
serum_phos	NA	numeric	0.089	0.013	ABG
asthma	1	factor	-0.059	-0.013	ABG
asthma	0	factor	0.059	0.013	ABG
asthma	1	factor	-0.059	-0.013	ABG
asthma	0	factor	0.059	0.013	ABG
race_ethnicity	4	factor	0.041	0.013	ABG
plt	NA	numeric	-0.113	-0.013	ABG
location	3	factor	-0.087	-0.013	ABG
location	3	factor	-0.087	-0.012	ABG
location	3	factor	-0.087	-0.012	ABG
asthma	0	factor	0.059	0.012	ABG
asthma	1	factor	-0.059	-0.012	ABG
race_ethnicity	4	factor	0.041	0.012	ABG
wbc	NA	numeric	0.094	0.012	ABG
serum_cl	NA	numeric	0.026	-0.012	ABG
asthma	1	factor	-0.059	-0.012	ABG
asthma	0	factor	0.059	0.012	ABG
location	3	factor	-0.087	-0.012	ABG
serum_lac	NA	numeric	0.104	0.012	ABG
serum_hco3	NA	numeric	-0.123	0.012	ABG
temp_new	NA	numeric	-0.102	-0.012	ABG
wbc	NA	numeric	0.099	0.012	ABG
wbc	NA	numeric	0.106	0.012	ABG
location	3	factor	-0.087	-0.012	ABG
temp_new	NA	numeric	-0.094	-0.012	ABG
temp_new	NA	numeric	-0.099	-0.012	ABG
osa	1	factor	-0.049	0.012	ABG
osa	0	factor	0.049	-0.012	ABG
location	3	factor	-0.087	-0.012	ABG
asthma	0	factor	0.059	0.012	ABG
asthma	1	factor	-0.059	-0.012	ABG
temp_new	NA	numeric	-0.104	-0.012	ABG
osa	1	factor	-0.049	0.012	ABG
osa	0	factor	0.049	-0.012	ABG
asthma	1	factor	-0.059	-0.012	ABG
asthma	0	factor	0.059	0.012	ABG
serum_lac	NA	numeric	0.116	0.012	ABG
serum_lac	NA	numeric	0.115	0.012	ABG
location	3	factor	-0.087	-0.012	ABG
serum_lac	NA	numeric	0.104	0.012	ABG

Table 16: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
asthma	0	factor	0.059	0.012	ABG
asthma	1	factor	-0.059	-0.012	ABG
asthma	0	factor	0.059	0.012	ABG
asthma	1	factor	-0.059	-0.012	ABG
wbc	NA	numeric	0.088	0.012	ABG
temp_new	NA	numeric	-0.080	-0.012	ABG
asthma	1	factor	-0.059	-0.012	ABG
asthma	0	factor	0.059	0.012	ABG
serum_cl	NA	numeric	0.034	-0.012	ABG
serum_lac	NA	numeric	0.109	0.012	ABG
asthma	0	factor	0.059	0.012	ABG
asthma	1	factor	-0.059	-0.012	ABG
osa	1	factor	-0.049	0.012	ABG
osa	0	factor	0.049	-0.012	ABG
location	3	factor	-0.087	-0.012	ABG
serum_lac	NA	numeric	0.105	0.012	ABG
temp_new	NA	numeric	-0.104	-0.012	ABG
asthma	1	factor	-0.059	-0.012	ABG
asthma	0	factor	0.059	0.012	ABG
osa	0	factor	0.049	-0.012	ABG
osa	1	factor	-0.049	0.012	ABG
location	3	factor	-0.087	-0.012	ABG
asthma	0	factor	0.059	0.012	ABG
asthma	1	factor	-0.059	-0.012	ABG
temp_new	NA	numeric	-0.084	-0.012	ABG
serum_phos	NA	numeric	0.084	0.012	ABG
race_ethnicity	6	factor	0.022	0.012	ABG
wbc	NA	numeric	0.110	0.012	ABG
osa	0	factor	0.049	-0.012	ABG
osa	1	factor	-0.049	0.012	ABG
location	3	factor	-0.087	-0.012	ABG
temp_new	NA	numeric	-0.089	-0.012	ABG
asthma	1	factor	-0.059	-0.012	ABG
asthma	0	factor	0.059	0.012	ABG
sodium	NA	numeric	-0.028	-0.012	ABG
serum_lac	NA	numeric	0.103	0.012	ABG
wbc	NA	numeric	0.109	0.011	ABG
race_ethnicity	6	factor	0.022	0.011	ABG
asthma	1	factor	-0.059	-0.011	ABG
asthma	0	factor	0.059	0.011	ABG
location	3	factor	-0.087	-0.011	ABG
asthma	0	factor	0.059	0.011	ABG
asthma	1	factor	-0.059	-0.011	ABG
osa	1	factor	-0.049	0.011	ABG
osa	0	factor	0.049	-0.011	ABG
osa	0	factor	0.049	-0.011	ABG
osa	1	factor	-0.049	0.011	ABG
asthma	0	factor	0.059	0.011	ABG
asthma	1	factor	-0.059	-0.011	ABG
serum_hco3	NA	numeric	-0.123	0.011	ABG
asthma	0	factor	0.059	0.011	ABG
asthma	1	factor	-0.059	-0.011	ABG
temp_new	NA	numeric	-0.093	-0.011	ABG
serum_hco3	NA	numeric	-0.126	0.011	ABG
location	3	factor	-0.087	-0.011	ABG
location	3	factor	-0.087	-0.011	ABG
location	3	factor	-0.087	-0.011	ABG
race_ethnicity	0	factor	0.053	0.011	ABG
race_ethnicity	0	factor	0.053	0.011	ABG
race_ethnicity	6	factor	0.022	0.011	ABG

Table 16: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
temp_new	NA	numeric	-0.104	-0.011	ABG
temp_new	NA	numeric	-0.089	-0.011	ABG
location	3	factor	-0.087	-0.011	ABG
asthma	1	factor	-0.059	-0.011	ABG
asthma	0	factor	0.059	0.011	ABG
serum_lac	NA	numeric	0.112	0.011	ABG
asthma	1	factor	-0.059	-0.011	ABG
asthma	0	factor	0.059	0.011	ABG
serum_hco3	NA	numeric	-0.125	0.011	ABG
race_ethnicity	6	factor	0.022	0.011	ABG
location	3	factor	-0.087	-0.011	ABG
wbc	NA	numeric	0.090	0.011	ABG
asthma	0	factor	0.059	0.011	ABG
asthma	1	factor	-0.059	-0.011	ABG
serum_hco3	NA	numeric	-0.125	0.011	ABG
osa	0	factor	0.049	-0.011	ABG
osa	1	factor	-0.049	0.011	ABG
location	3	factor	-0.087	-0.011	ABG
asthma	1	factor	-0.059	-0.011	ABG
asthma	0	factor	0.059	0.011	ABG
asthma	0	factor	0.059	0.011	ABG
asthma	1	factor	-0.059	-0.011	ABG
location	3	factor	-0.087	-0.011	ABG
wbc	NA	numeric	0.105	0.011	ABG
temp_new	NA	numeric	-0.099	-0.011	ABG
race_ethnicity	6	factor	0.022	0.011	ABG
location	3	factor	-0.087	-0.011	ABG
osa	1	factor	-0.049	0.011	ABG
osa	0	factor	0.049	-0.011	ABG
asthma	1	factor	-0.059	-0.011	ABG
asthma	0	factor	0.059	0.011	ABG
serum_lac	NA	numeric	0.103	0.011	ABG
location	3	factor	-0.087	-0.011	ABG
osa	0	factor	0.049	-0.011	ABG
osa	1	factor	-0.049	0.011	ABG
asthma	0	factor	0.059	0.011	ABG
asthma	1	factor	-0.059	-0.011	ABG
race_ethnicity	6	factor	0.022	0.011	ABG
location	3	factor	-0.087	-0.011	ABG
temp_new	NA	numeric	-0.093	-0.011	ABG
osa	0	factor	0.049	-0.011	ABG
osa	1	factor	-0.049	0.011	ABG
race_ethnicity	0	factor	0.053	0.011	ABG
serum_hco3	NA	numeric	-0.124	0.011	ABG
location	3	factor	-0.087	-0.011	ABG
location	3	factor	-0.087	-0.011	ABG
serum_hco3	NA	numeric	-0.126	0.010	ABG
location	3	factor	-0.087	-0.010	ABG
serum_hco3	NA	numeric	-0.127	0.010	ABG
location	3	factor	-0.087	-0.010	ABG
location	3	factor	-0.087	-0.010	ABG
serum_hco3	NA	numeric	-0.123	0.010	ABG
osa	1	factor	-0.049	0.010	ABG
osa	0	factor	0.049	-0.010	ABG
serum_hco3	NA	numeric	-0.123	0.010	ABG
location	3	factor	-0.087	-0.010	ABG
race_ethnicity	6	factor	0.022	0.010	ABG
temp_new	NA	numeric	-0.106	-0.010	ABG
serum_hco3	NA	numeric	-0.126	0.010	ABG
serum_hco3	NA	numeric	-0.122	0.010	ABG
temp_new	NA	numeric	-0.103	-0.010	ABG

Table 16: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
race_ethnicity	0	factor	0.053	0.010	ABG
serum_cl	NA	numeric	0.030	-0.010	ABG
location	3	factor	-0.087	-0.010	ABG
location	3	factor	-0.087	-0.010	ABG
location	3	factor	-0.087	-0.010	ABG
location	3	factor	-0.087	-0.010	ABG
serum_hco3	NA	numeric	-0.124	0.010	ABG
osa	1	factor	-0.049	0.010	ABG
osa	0	factor	0.049	-0.010	ABG
asthma	0	factor	0.059	0.010	ABG
asthma	1	factor	-0.059	-0.010	ABG
serum_hco3	NA	numeric	-0.125	0.010	ABG
location	3	factor	-0.087	-0.010	ABG
serum_hco3	NA	numeric	-0.122	0.010	ABG
asthma	1	factor	-0.059	-0.010	ABG
asthma	0	factor	0.059	0.010	ABG
osa	0	factor	0.049	-0.010	ABG
osa	1	factor	-0.049	0.010	ABG
serum_hco3	NA	numeric	-0.125	0.010	ABG
temp_new	NA	numeric	-0.094	-0.010	ABG
location	3	factor	-0.087	-0.010	ABG
asthma	0	factor	0.059	0.010	ABG
asthma	1	factor	-0.059	-0.010	ABG
asthma	0	factor	0.059	0.010	ABG
asthma	1	factor	-0.059	-0.010	ABG
temp_new	NA	numeric	-0.096	-0.010	ABG
temp_new	NA	numeric	-0.085	-0.010	ABG
race_ethnicity	6	factor	0.022	0.010	ABG
asthma	1	factor	-0.059	-0.010	ABG
asthma	0	factor	0.059	0.010	ABG
location	3	factor	-0.087	-0.010	ABG
location	3	factor	-0.087	-0.010	ABG
serum_hco3	NA	numeric	-0.123	0.010	ABG
race_ethnicity	6	factor	0.022	0.010	ABG
osa	1	factor	-0.049	0.010	ABG
osa	0	factor	0.049	-0.010	ABG
location	3	factor	-0.087	-0.010	ABG
location	3	factor	-0.087	-0.010	ABG
serum_hco3	NA	numeric	-0.125	0.010	ABG
location	3	factor	-0.087	-0.010	ABG
race_ethnicity	6	factor	0.022	0.010	ABG
location	3	factor	-0.087	-0.010	ABG
asthma	1	factor	-0.059	-0.010	ABG
asthma	0	factor	0.059	0.010	ABG
serum_hco3	NA	numeric	-0.123	0.010	ABG
wbc	NA	numeric	0.099	0.010	ABG
asthma	1	factor	-0.059	-0.010	ABG
asthma	0	factor	0.059	0.010	ABG
temp_new	NA	numeric	-0.097	-0.010	ABG
race_ethnicity	6	factor	0.022	0.010	ABG
race_ethnicity	6	factor	0.022	0.009	ABG
temp_new	NA	numeric	-0.096	-0.009	ABG
location	3	factor	-0.087	-0.009	ABG
serum_hco3	NA	numeric	-0.125	0.009	ABG
race_ethnicity	1	factor	-0.072	-0.009	ABG
race_ethnicity	6	factor	0.022	0.009	ABG
race_ethnicity	6	factor	0.022	0.009	ABG
location	3	factor	-0.087	-0.009	ABG
serum_hco3	NA	numeric	-0.127	0.009	ABG
serum_hco3	NA	numeric	-0.126	0.009	ABG

Table 16: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
temp_new	NA	numeric	-0.099	-0.009	ABG
serum_hco3	NA	numeric	-0.127	0.009	ABG
serum_hco3	NA	numeric	-0.124	0.009	ABG
location	3	factor	-0.087	-0.009	ABG
location	3	factor	-0.087	-0.009	ABG
race_ethnicity	6	factor	0.022	0.009	ABG
osa	0	factor	0.049	-0.009	ABG
osa	1	factor	-0.049	0.009	ABG
osa	0	factor	0.049	-0.009	ABG
osa	1	factor	-0.049	0.009	ABG
race_ethnicity	6	factor	0.022	0.009	ABG
serum_hco3	NA	numeric	-0.127	0.009	ABG
race_ethnicity	6	factor	0.022	0.009	ABG
race_ethnicity	0	factor	0.053	0.009	ABG
race_ethnicity	6	factor	0.022	0.009	ABG
serum_hco3	NA	numeric	-0.125	0.009	ABG
serum_hco3	NA	numeric	-0.124	0.009	ABG
plt	NA	numeric	-0.114	-0.009	ABG
location	3	factor	-0.087	-0.009	ABG
serum_lac	NA	numeric	0.106	0.009	ABG
serum_hco3	NA	numeric	-0.124	0.009	ABG
race_ethnicity	6	factor	0.022	0.009	ABG
temp_new	NA	numeric	-0.091	-0.009	ABG
serum_hco3	NA	numeric	-0.123	0.009	ABG
location	3	factor	-0.087	-0.009	ABG
serum_lac	NA	numeric	0.103	0.009	ABG
serum_hco3	NA	numeric	-0.122	0.009	ABG
asthma	0	factor	0.059	0.009	ABG
asthma	1	factor	-0.059	-0.009	ABG
race_ethnicity	1	factor	-0.072	-0.009	ABG
serum_hco3	NA	numeric	-0.127	0.009	ABG
temp_new	NA	numeric	-0.094	-0.009	ABG
serum_hco3	NA	numeric	-0.125	0.009	ABG
location	3	factor	-0.087	-0.009	ABG
race_ethnicity	6	factor	0.022	0.009	ABG
race_ethnicity	6	factor	0.022	0.009	ABG
serum_hco3	NA	numeric	-0.122	0.009	ABG
race_ethnicity	6	factor	0.022	0.009	ABG
serum_hco3	NA	numeric	-0.123	0.009	ABG
serum_hco3	NA	numeric	-0.129	0.009	ABG
temp_new	NA	numeric	-0.088	-0.009	ABG
location	3	factor	-0.087	-0.009	ABG
race_ethnicity	6	factor	0.022	0.009	ABG
race_ethnicity	6	factor	0.022	0.009	ABG
location	3	factor	-0.087	-0.009	ABG
race_ethnicity	6	factor	0.022	0.009	ABG
race_ethnicity	0	factor	0.053	0.008	ABG
asthma	1	factor	-0.059	-0.008	ABG
asthma	0	factor	0.059	0.008	ABG
serum_hco3	NA	numeric	-0.124	0.008	ABG
serum_hco3	NA	numeric	-0.125	0.008	ABG
serum_hco3	NA	numeric	-0.126	0.008	ABG
temp_new	NA	numeric	-0.103	-0.008	ABG
location	3	factor	-0.087	-0.008	ABG
location	3	factor	-0.087	-0.008	ABG
asthma	1	factor	-0.059	-0.008	ABG
asthma	0	factor	0.059	0.008	ABG
serum_hco3	NA	numeric	-0.126	0.008	ABG
serum_hco3	NA	numeric	-0.121	0.008	ABG
asthma	1	factor	-0.059	-0.008	ABG
asthma	0	factor	0.059	0.008	ABG
location	3	factor	-0.087	-0.008	ABG

Table 16: ABG: target SMD rows across imputations (sorted by |SMD|) (Part A) (*continued*)

variable	level	type	smd_pre	smd_post	group
race_ethnicity	0	factor	0.053	0.008	ABG
race_ethnicity	0	factor	0.053	0.008	ABG
race_ethnicity	6	factor	0.022	0.008	ABG
race_ethnicity	6	factor	0.022	0.008	ABG
serum_hco3	NA	numeric	-0.127	0.008	ABG
location	3	factor	-0.087	-0.008	ABG
race_ethnicity	6	factor	0.022	0.008	ABG
race_ethnicity	6	factor	0.022	0.008	ABG
location	3	factor	-0.087	-0.008	ABG
race_ethnicity	1	factor	-0.072	-0.008	ABG
race_ethnicity	6	factor	0.022	0.008	ABG
serum_hco3	NA	numeric	-0.124	0.008	ABG
race_ethnicity	6	factor	0.022	0.008	ABG
race_ethnicity	0	factor	0.053	0.008	ABG
race_ethnicity	6	factor	0.022	0.008	ABG
race_ethnicity	0	factor	0.053	0.008	ABG
serum_hco3	NA	numeric	-0.122	0.008	ABG
location	3	factor	-0.087	-0.008	ABG
race_ethnicity	6	factor	0.022	0.008	ABG
race_ethnicity	6	factor	0.022	0.008	ABG
temp_new	NA	numeric	-0.078	-0.008	ABG
serum_hco3	NA	numeric	-0.126	0.008	ABG
race_ethnicity	6	factor	0.022	0.008	ABG
location	3	factor	-0.087	-0.008	ABG
asthma	1	factor	-0.059	-0.008	ABG
asthma	0	factor	0.059	0.008	ABG
serum_hco3	NA	numeric	-0.122	0.008	ABG
race_ethnicity	1	factor	-0.072	-0.008	ABG
race_ethnicity	1	factor	-0.072	-0.008	ABG
location	3	factor	-0.087	-0.008	ABG
serum_hco3	NA	numeric	-0.125	0.008	ABG
race_ethnicity	1	factor	-0.072	-0.008	ABG
race_ethnicity	6	factor	0.022	0.008	ABG
serum_phos	NA	numeric	0.093	0.008	ABG
serum_hco3	NA	numeric	-0.125	0.008	ABG
race_ethnicity	6	factor	0.022	0.008	ABG
serum_hco3	NA	numeric	-0.120	0.008	ABG
serum_hco3	NA	numeric	-0.122	0.008	ABG
race_ethnicity	6	factor	0.022	0.008	ABG
race_ethnicity	0	factor	0.053	0.008	ABG
temp_new	NA	numeric	-0.089	-0.008	ABG
race_ethnicity	6	factor	0.022	0.007	ABG
race_ethnicity	0	factor	0.053	0.007	ABG
race_ethnicity	1	factor	-0.072	-0.007	ABG
serum_hco3	NA	numeric	-0.126	0.007	ABG
serum_hco3	NA	numeric	-0.124	0.007	ABG
race_ethnicity	6	factor	0.022	0.007	ABG
location	3	factor	-0.087	-0.007	ABG
asthma	0	factor	0.059	0.007	ABG
asthma	1	factor	-0.059	-0.007	ABG
race_ethnicity	1	factor	-0.072	-0.007	ABG
race_ethnicity	6	factor	0.022	0.007	ABG
race_ethnicity	6	factor	0.022	0.007	ABG
serum_hco3	NA	numeric	-0.130	0.007	ABG
race_ethnicity	0	factor	0.053	0.007	ABG
race_ethnicity	6	factor	0.022	0.007	ABG
race_ethnicity	0	factor	0.053	0.007	ABG
serum_hco3	NA	numeric	-0.122	0.007	ABG
serum_lac	NA	numeric	0.107	0.007	ABG
race_ethnicity	6	factor	0.022	0.007	ABG

Table 16: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
race_ethnicity	0	factor	0.053	0.007	ABG
race_ethnicity	0	factor	0.053	0.007	ABG
race_ethnicity	0	factor	0.053	0.007	ABG
race_ethnicity	6	factor	0.022	0.007	ABG
race_ethnicity	0	factor	0.053	0.007	ABG
temp_new	NA	numeric	-0.098	-0.007	ABG
race_ethnicity	6	factor	0.022	0.007	ABG
race_ethnicity	1	factor	-0.072	-0.007	ABG
race_ethnicity	5	factor	0.000	-0.007	ABG
race_ethnicity	5	factor	0.000	-0.007	ABG
temp_new	NA	numeric	-0.100	-0.007	ABG
race_ethnicity	6	factor	0.022	0.007	ABG
race_ethnicity	6	factor	0.022	0.007	ABG
serum_hco3	NA	numeric	-0.123	0.007	ABG
location	3	factor	-0.087	-0.007	ABG
serum_hco3	NA	numeric	-0.124	0.007	ABG
race_ethnicity	0	factor	0.053	0.007	ABG
serum_hco3	NA	numeric	-0.124	0.007	ABG
temp_new	NA	numeric	-0.094	-0.007	ABG
temp_new	NA	numeric	-0.095	-0.007	ABG
serum_phos	NA	numeric	0.088	0.007	ABG
race_ethnicity	0	factor	0.053	0.007	ABG
race_ethnicity	6	factor	0.022	0.007	ABG
race_ethnicity	5	factor	0.000	-0.007	ABG
race_ethnicity	5	factor	0.000	-0.007	ABG
location	3	factor	-0.087	-0.007	ABG
race_ethnicity	6	factor	0.022	0.007	ABG
race_ethnicity	6	factor	0.022	0.007	ABG
race_ethnicity	0	factor	0.053	0.006	ABG
race_ethnicity	5	factor	0.000	-0.006	ABG
race_ethnicity	6	factor	0.022	0.006	ABG
race_ethnicity	6	factor	0.022	0.006	ABG
temp_new	NA	numeric	-0.091	-0.006	ABG
race_ethnicity	5	factor	0.000	-0.006	ABG
serum_hco3	NA	numeric	-0.123	0.006	ABG
race_ethnicity	5	factor	0.000	-0.006	ABG
race_ethnicity	0	factor	0.053	0.006	ABG
race_ethnicity	0	factor	0.053	0.006	ABG
race_ethnicity	5	factor	0.000	-0.006	ABG
race_ethnicity	1	factor	-0.072	-0.006	ABG
serum_hco3	NA	numeric	-0.127	0.006	ABG
acute_nmd	1	factor	0.002	-0.006	ABG
acute_nmd	0	factor	-0.002	0.006	ABG
serum_hco3	NA	numeric	-0.126	0.006	ABG
serum_hco3	NA	numeric	-0.127	0.006	ABG
serum_hco3	NA	numeric	-0.123	0.006	ABG
race_ethnicity	6	factor	0.022	0.006	ABG
race_ethnicity	6	factor	0.022	0.006	ABG
race_ethnicity	5	factor	0.000	-0.006	ABG
race_ethnicity	5	factor	0.000	-0.006	ABG
race_ethnicity	6	factor	0.022	0.006	ABG
race_ethnicity	6	factor	0.022	0.006	ABG
serum_hco3	NA	numeric	-0.124	0.006	ABG
temp_new	NA	numeric	-0.080	-0.006	ABG
location	3	factor	-0.087	-0.006	ABG
race_ethnicity	6	factor	0.022	0.006	ABG
race_ethnicity	0	factor	0.053	0.006	ABG
race_ethnicity	5	factor	0.000	-0.006	ABG
race_ethnicity	6	factor	0.022	0.006	ABG
race_ethnicity	6	factor	0.022	0.006	ABG
race_ethnicity	0	factor	0.053	0.006	ABG
race_ethnicity	6	factor	0.022	0.006	ABG

Table 16: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
race_ethnicity	5	factor	0.000	-0.006	ABG
serum_hco3	NA	numeric	-0.126	0.006	ABG
serum_hco3	NA	numeric	-0.127	0.006	ABG
race_ethnicity	0	factor	0.053	0.006	ABG
race_ethnicity	1	factor	-0.072	-0.006	ABG
race_ethnicity	5	factor	0.000	-0.006	ABG
race_ethnicity	0	factor	0.053	0.006	ABG
race_ethnicity	1	factor	-0.072	-0.006	ABG
race_ethnicity	0	factor	0.053	0.006	ABG
serum_hco3	NA	numeric	-0.125	0.006	ABG
race_ethnicity	6	factor	0.022	0.006	ABG
race_ethnicity	6	factor	0.022	0.006	ABG
race_ethnicity	5	factor	0.000	-0.006	ABG
location	3	factor	-0.087	-0.006	ABG
race_ethnicity	0	factor	0.053	0.006	ABG
race_ethnicity	5	factor	0.000	-0.006	ABG
race_ethnicity	3	factor	0.019	0.006	ABG
race_ethnicity	5	factor	0.000	-0.006	ABG
race_ethnicity	6	factor	0.022	0.006	ABG
serum_hco3	NA	numeric	-0.126	0.006	ABG
temp_new	NA	numeric	-0.095	-0.006	ABG
race_ethnicity	5	factor	0.000	-0.006	ABG
race_ethnicity	6	factor	0.022	0.006	ABG
race_ethnicity	6	factor	0.022	0.006	ABG
serum_hco3	NA	numeric	-0.125	0.006	ABG
acute_nmd	1	factor	0.002	-0.006	ABG
acute_nmd	0	factor	-0.002	0.006	ABG
race_ethnicity	0	factor	0.053	0.006	ABG
serum_hco3	NA	numeric	-0.124	0.006	ABG
acute_nmd	0	factor	-0.002	0.006	ABG
acute_nmd	1	factor	0.002	-0.006	ABG
race_ethnicity	5	factor	0.000	-0.006	ABG
race_ethnicity	6	factor	0.022	0.006	ABG
race_ethnicity	5	factor	0.000	-0.005	ABG
race_ethnicity	1	factor	-0.072	-0.005	ABG
race_ethnicity	1	factor	-0.072	-0.005	ABG
race_ethnicity	5	factor	0.000	-0.005	ABG
race_ethnicity	0	factor	0.053	0.005	ABG
race_ethnicity	6	factor	0.022	0.005	ABG
acute_nmd	1	factor	0.002	-0.005	ABG
acute_nmd	0	factor	-0.002	0.005	ABG
race_ethnicity	0	factor	0.053	0.005	ABG
race_ethnicity	0	factor	0.053	0.005	ABG
race_ethnicity	1	factor	-0.072	-0.005	ABG
race_ethnicity	5	factor	0.000	-0.005	ABG
race_ethnicity	5	factor	0.000	-0.005	ABG
location	3	factor	-0.087	-0.005	ABG
race_ethnicity	5	factor	0.000	-0.005	ABG
race_ethnicity	5	factor	0.000	-0.005	ABG
serum_hco3	NA	numeric	-0.121	0.005	ABG
location	3	factor	-0.087	-0.005	ABG
race_ethnicity	5	factor	0.000	-0.005	ABG
race_ethnicity	5	factor	0.000	-0.005	ABG
acute_nmd	0	factor	-0.002	0.005	ABG
acute_nmd	1	factor	0.002	-0.005	ABG
race_ethnicity	6	factor	0.022	0.005	ABG
location	3	factor	-0.087	-0.005	ABG
race_ethnicity	5	factor	0.000	-0.005	ABG
race_ethnicity	0	factor	0.053	0.005	ABG
acute_nmd	1	factor	0.002	-0.005	ABG
acute_nmd	0	factor	-0.002	0.005	ABG
race_ethnicity	6	factor	0.022	0.005	ABG

Table 16: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
race_ethnicity	5	factor	0.000	-0.005	ABG
race_ethnicity	0	factor	0.053	0.005	ABG
acute_nmd	1	factor	0.002	-0.005	ABG
acute_nmd	0	factor	-0.002	0.005	ABG
race_ethnicity	5	factor	0.000	-0.005	ABG
race_ethnicity	0	factor	0.053	0.005	ABG
race_ethnicity	5	factor	0.000	-0.005	ABG
acute_nmd	1	factor	0.002	-0.005	ABG
acute_nmd	0	factor	-0.002	0.005	ABG
race_ethnicity	0	factor	0.053	0.005	ABG
race_ethnicity	6	factor	0.022	0.005	ABG
location	3	factor	-0.087	-0.005	ABG
acute_nmd	1	factor	0.002	-0.005	ABG
acute_nmd	0	factor	-0.002	0.005	ABG
acute_nmd	1	factor	0.002	-0.005	ABG
acute_nmd	0	factor	-0.002	0.005	ABG
race_ethnicity	3	factor	0.019	0.005	ABG
serum_hco3	NA	numeric	-0.122	0.005	ABG
race_ethnicity	0	factor	0.053	0.005	ABG
acute_nmd	1	factor	0.002	-0.005	ABG
acute_nmd	0	factor	-0.002	0.005	ABG
race_ethnicity	5	factor	0.000	-0.005	ABG
race_ethnicity	0	factor	0.053	0.005	ABG
race_ethnicity	6	factor	0.022	0.005	ABG
race_ethnicity	5	factor	0.000	-0.005	ABG
race_ethnicity	1	factor	-0.072	-0.005	ABG
acute_nmd	0	factor	-0.002	0.005	ABG
acute_nmd	1	factor	0.002	-0.005	ABG
serum_hco3	NA	numeric	-0.125	0.005	ABG
race_ethnicity	6	factor	0.022	0.005	ABG
race_ethnicity	3	factor	0.019	-0.005	ABG
race_ethnicity	5	factor	0.000	-0.005	ABG
race_ethnicity	6	factor	0.022	0.005	ABG
race_ethnicity	0	factor	0.053	0.005	ABG
race_ethnicity	0	factor	0.053	0.005	ABG
acute_nmd	1	factor	0.002	-0.005	ABG
acute_nmd	0	factor	-0.002	0.005	ABG
acute_nmd	0	factor	-0.002	0.005	ABG
acute_nmd	1	factor	0.002	-0.005	ABG
acute_nmd	0	factor	-0.002	0.005	ABG
acute_nmd	1	factor	0.002	-0.005	ABG
acute_nmd	1	factor	0.002	-0.005	ABG
acute_nmd	1	factor	0.002	-0.005	ABG
acute_nmd	0	factor	-0.002	0.005	ABG
serum_hco3	NA	numeric	-0.125	0.005	ABG
serum_hco3	NA	numeric	-0.124	0.005	ABG
race_ethnicity	5	factor	0.000	-0.005	ABG
race_ethnicity	1	factor	-0.072	0.004	ABG
race_ethnicity	0	factor	0.053	0.004	ABG
race_ethnicity	1	factor	-0.072	-0.004	ABG
acute_nmd	1	factor	0.002	-0.004	ABG
acute_nmd	0	factor	-0.002	0.004	ABG
acute_nmd	1	factor	0.002	-0.004	ABG
acute_nmd	0	factor	-0.002	0.004	ABG
race_ethnicity	1	factor	-0.072	-0.004	ABG
race_ethnicity	5	factor	0.000	-0.004	ABG
race_ethnicity	5	factor	0.000	-0.004	ABG
acute_nmd	0	factor	-0.002	0.004	ABG
acute_nmd	1	factor	0.002	-0.004	ABG
race_ethnicity	1	factor	-0.072	-0.004	ABG
race_ethnicity	5	factor	0.000	-0.004	ABG
race_ethnicity	0	factor	0.053	0.004	ABG
race_ethnicity	3	factor	0.019	0.004	ABG
race_ethnicity	1	factor	-0.072	-0.004	ABG
race_ethnicity	0	factor	0.053	0.004	ABG

Table 16: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

Table 16: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

Table 16: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
race_ethnicity	0	factor	0.053	0.003	ABG
race_ethnicity	3	factor	0.019	0.003	ABG
race_ethnicity	0	factor	0.053	0.003	ABG
acute_nmd	0	factor	-0.002	0.003	ABG
acute_nmd	1	factor	0.002	-0.003	ABG
race_ethnicity	3	factor	0.019	0.003	ABG
race_ethnicity	5	factor	0.000	-0.003	ABG
race_ethnicity	5	factor	0.000	-0.003	ABG
race_ethnicity	1	factor	-0.072	-0.003	ABG
acute_nmd	0	factor	-0.002	0.003	ABG
acute_nmd	1	factor	0.002	-0.003	ABG
acute_nmd	1	factor	0.002	-0.003	ABG
acute_nmd	0	factor	-0.002	0.003	ABG
serum_hco3	NA	numeric	-0.125	0.003	ABG
race_ethnicity	0	factor	0.053	0.003	ABG
race_ethnicity	3	factor	0.019	0.003	ABG
race_ethnicity	1	factor	-0.072	-0.003	ABG
race_ethnicity	5	factor	0.000	-0.003	ABG
acute_nmd	0	factor	-0.002	0.003	ABG
acute_nmd	1	factor	0.002	-0.003	ABG
acute_nmd	1	factor	0.002	-0.003	ABG
acute_nmd	0	factor	-0.002	0.003	ABG
acute_nmd	0	factor	-0.002	0.003	ABG
race_ethnicity	1	factor	-0.072	-0.003	ABG
race_ethnicity	3	factor	0.019	0.003	ABG
race_ethnicity	5	factor	0.000	-0.003	ABG
race_ethnicity	0	factor	0.053	0.003	ABG
race_ethnicity	3	factor	0.019	-0.003	ABG
race_ethnicity	5	factor	0.000	-0.003	ABG
race_ethnicity	1	factor	-0.072	-0.003	ABG
race_ethnicity	5	factor	0.000	-0.003	ABG
race_ethnicity	1	factor	0.000	-0.003	ABG
race_ethnicity	5	factor	0.000	-0.003	ABG
race_ethnicity	0	factor	0.053	0.002	ABG
acute_nmd	0	factor	-0.002	0.002	ABG
acute_nmd	1	factor	0.002	-0.002	ABG
race_ethnicity	1	factor	-0.072	-0.002	ABG
race_ethnicity	0	factor	0.053	0.002	ABG
race_ethnicity	1	factor	-0.072	-0.002	ABG
race_ethnicity	1	factor	-0.072	-0.002	ABG
race_ethnicity	0	factor	0.053	0.002	ABG
acute_nmd	0	factor	-0.002	0.002	ABG
acute_nmd	1	factor	0.002	-0.002	ABG
race_ethnicity	0	factor	0.053	0.002	ABG
race_ethnicity	1	factor	-0.072	-0.002	ABG
race_ethnicity	1	factor	-0.072	-0.002	ABG
race_ethnicity	0	factor	0.053	0.002	ABG
race_ethnicity	3	factor	0.019	0.002	ABG
race_ethnicity	0	factor	0.053	0.002	ABG
acute_nmd	0	factor	-0.002	0.002	ABG
acute_nmd	1	factor	0.002	-0.002	ABG
race_ethnicity	1	factor	-0.072	-0.002	ABG
race_ethnicity	3	factor	0.019	-0.002	ABG
race_ethnicity	3	factor	0.019	-0.002	ABG
race_ethnicity	0	factor	0.053	0.002	ABG
race_ethnicity	3	factor	0.019	0.002	ABG

Table 16: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
acute_nmd	0	factor	-0.002	0.002	ABG
acute_nmd	1	factor	0.002	-0.002	ABG
race_ethnicity	1	factor	-0.072	-0.002	ABG
race_ethnicity	0	factor	0.053	-0.002	ABG
race_ethnicity	3	factor	0.019	-0.002	ABG
race_ethnicity	1	factor	-0.072	-0.002	ABG
race_ethnicity	3	factor	0.019	-0.002	ABG
race_ethnicity	0	factor	0.053	0.002	ABG
race_ethnicity	3	factor	0.019	0.002	ABG
race_ethnicity	3	factor	0.019	-0.002	ABG
race_ethnicity	1	factor	-0.072	-0.002	ABG
acute_nmd	1	factor	0.002	-0.002	ABG
acute_nmd	0	factor	-0.002	0.002	ABG
race_ethnicity	3	factor	0.019	0.002	ABG
race_ethnicity	1	factor	-0.072	-0.002	ABG
race_ethnicity	3	factor	0.019	0.002	ABG
acute_nmd	1	factor	0.002	-0.002	ABG
acute_nmd	0	factor	-0.002	0.002	ABG
race_ethnicity	3	factor	0.019	-0.002	ABG
race_ethnicity	1	factor	-0.072	-0.002	ABG
race_ethnicity	3	factor	0.019	0.002	ABG
race_ethnicity	3	factor	0.019	-0.002	ABG
race_ethnicity	1	factor	-0.072	-0.002	ABG
race_ethnicity	1	factor	-0.072	-0.002	ABG
acute_nmd	0	factor	-0.002	0.002	ABG
acute_nmd	0	factor	-0.002	0.002	ABG
race_ethnicity	3	factor	0.019	-0.002	ABG
acute_nmd	3	factor	0.019	-0.002	ABG
acute_nmd	3	factor	0.019	-0.002	ABG
race_ethnicity	3	factor	0.019	-0.002	ABG
race_ethnicity	1	factor	-0.072	-0.002	ABG
race_ethnicity	1	factor	-0.072	0.001	ABG
race_ethnicity	1	factor	-0.072	-0.001	ABG
race_ethnicity	3	factor	0.019	-0.001	ABG
acute_nmd	0	factor	-0.002	-0.001	ABG
acute_nmd	1	factor	0.002	0.001	ABG
race_ethnicity	3	factor	0.019	-0.001	ABG
acute_nmd	0	factor	-0.002	0.001	ABG
acute_nmd	1	factor	0.002	-0.001	ABG
race_ethnicity	0	factor	0.053	0.001	ABG
acute_nmd	0	factor	-0.002	0.001	ABG
acute_nmd	1	factor	0.002	-0.001	ABG
acute_nmd	1	factor	0.002	-0.001	ABG
acute_nmd	0	factor	-0.002	0.001	ABG
race_ethnicity	3	factor	0.019	-0.001	ABG
race_ethnicity	3	factor	0.019	-0.001	ABG
race_ethnicity	3	factor	0.019	-0.001	ABG
race_ethnicity	3	factor	0.019	0.001	ABG
race_ethnicity	3	factor	0.019	0.001	ABG
race_ethnicity	3	factor	0.019	-0.001	ABG
race_ethnicity	1	factor	-0.072	0.001	ABG
race_ethnicity	5	factor	0.000	-0.001	ABG

Table 16: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (*continued*)

variable	level	type	smd_pre	smd_post	group
acute_nmd	1	factor	0.002	-0.001	ABG
acute_nmd	0	factor	-0.002	0.001	ABG
acute_nmd	1	factor	0.002	-0.001	ABG
acute_nmd	0	factor	-0.002	0.001	ABG
race_ethnicity	1	factor	-0.072	0.001	ABG
acute_nmd	1	factor	0.002	0.001	ABG
acute_nmd	0	factor	-0.002	-0.001	ABG
race_ethnicity	0	factor	0.053	0.001	ABG
race_ethnicity	3	factor	0.019	-0.001	ABG
race_ethnicity	3	factor	0.019	-0.001	ABG
race_ethnicity	3	factor	0.019	-0.001	ABG
race_ethnicity	1	factor	-0.072	-0.001	ABG
race_ethnicity	1	factor	-0.072	-0.001	ABG
acute_nmd	0	factor	-0.002	0.001	ABG
acute_nmd	1	factor	0.002	-0.001	ABG
acute_nmd	1	factor	0.002	-0.001	ABG
acute_nmd	0	factor	-0.002	0.001	ABG
race_ethnicity	3	factor	0.019	0.001	ABG
race_ethnicity	0	factor	0.053	0.001	ABG
race_ethnicity	0	factor	0.053	0.001	ABG
race_ethnicity	3	factor	0.019	-0.001	ABG
race_ethnicity	1	factor	-0.072	0.001	ABG
acute_nmd	0	factor	-0.002	0.001	ABG
acute_nmd	1	factor	0.002	-0.001	ABG
acute_nmd	1	factor	0.002	-0.001	ABG
acute_nmd	0	factor	-0.002	0.001	ABG
acute_nmd	0	factor	-0.002	0.001	ABG
acute_nmd	1	factor	0.002	-0.001	ABG
acute_nmd	3	factor	0.019	-0.001	ABG
acute_nmd	0	factor	-0.002	0.001	ABG
acute_nmd	1	factor	0.002	-0.001	ABG
race_ethnicity	3	factor	0.019	0.001	ABG
race_ethnicity	3	factor	0.019	-0.001	ABG
race_ethnicity	1	factor	-0.072	-0.001	ABG
race_ethnicity	3	factor	0.019	0.001	ABG
acute_nmd	1	factor	0.002	-0.001	ABG
acute_nmd	0	factor	-0.002	0.001	ABG
race_ethnicity	3	factor	0.019	0.001	ABG
race_ethnicity	3	factor	0.019	-0.001	ABG
race_ethnicity	3	factor	0.019	0.000	ABG
race_ethnicity	1	factor	-0.072	0.000	ABG
race_ethnicity	3	factor	0.019	0.000	ABG
race_ethnicity	1	factor	-0.072	0.000	ABG
race_ethnicity	3	factor	0.019	0.000	ABG
race_ethnicity	3	factor	0.019	0.000	ABG
race_ethnicity	5	factor	0.000	0.000	ABG
acute_nmd	0	factor	-0.002	0.000	ABG
acute_nmd	1	factor	0.002	0.000	ABG
race_ethnicity	3	factor	0.019	0.000	ABG

Table 16: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (*continued*)

variable	level	type	smd_pre	smd_post	group
acute_nmd	0	factor	-0.002	0.000	ABG
acute_nmd	1	factor	0.002	0.000	ABG
acute_nmd	0	factor	-0.002	0.000	ABG
acute_nmd	1	factor	0.002	0.000	ABG
race_ethnicity	1	factor	-0.072	0.000	ABG
race_ethnicity	3	factor	0.019	0.000	ABG
race_ethnicity	1	factor	-0.072	0.000	ABG
race_ethnicity	1	factor	-0.072	0.000	ABG
race_ethnicity	3	factor	0.019	0.000	ABG
race_ethnicity	3	factor	0.019	0.000	ABG
race_ethnicity	1	factor	-0.072	0.000	ABG
race_ethnicity	1	factor	-0.072	0.000	ABG
acute_nmd	0	factor	-0.002	0.000	ABG
acute_nmd	1	factor	0.002	0.000	ABG
race_ethnicity	1	factor	-0.072	0.000	ABG
race_ethnicity	1	factor	-0.072	0.000	ABG
race_ethnicity	3	factor	0.019	0.000	ABG
race_ethnicity	3	factor	0.019	0.000	ABG
race_ethnicity	1	factor	-0.072	0.000	ABG
race_ethnicity	5	factor	0.000	0.000	ABG
race_ethnicity	1	factor	-0.072	0.000	ABG
race_ethnicity	5	factor	0.000	0.000	ABG
race_ethnicity	3	factor	0.019	0.000	ABG

Table 17: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part B)

imp	abs_post
45	0.100
45	0.100
40	0.098
40	0.098
38	0.096
38	0.096
51	0.095
51	0.095
8	0.095
8	0.095
34	0.095
34	0.095
69	0.094
69	0.094
22	0.094
22	0.094
70	0.094
70	0.094
54	0.094
54	0.094
5	0.094
5	0.094
59	0.094
20	0.094
57	0.093
57	0.093
24	0.093
19	0.093
19	0.093
9	0.093
9	0.093
68	0.093
28	0.093
31	0.093
31	0.093
76	0.093
76	0.093
2	0.093
2	0.093
12	0.093
12	0.093
6	0.093
6	0.093
15	0.093
61	0.093
61	0.093
74	0.093
74	0.093
52	0.092
52	0.092
47	0.092
63	0.092
63	0.092
28	0.092
28	0.092
55	0.092
30	0.092
30	0.092
4	0.092
16	0.092
2	0.092
7	0.091
7	0.091

Table 17: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
36	0.091
77	0.091
50	0.091
13	0.091
13	0.091
26	0.091
25	0.091
25	0.091
26	0.091
26	0.091
11	0.091
49	0.091
17	0.091
78	0.091
63	0.090
4	0.090
4	0.090
79	0.090
79	0.090
70	0.090
71	0.090
29	0.090
29	0.090
65	0.090
65	0.090
72	0.090
73	0.090
73	0.090
47	0.090
47	0.090
18	0.090
64	0.090
64	0.090
32	0.090
32	0.090
20	0.090
20	0.090
29	0.090
41	0.090
41	0.090
77	0.090
77	0.090
75	0.090
75	0.090
39	0.090
39	0.090
12	0.090
62	0.090
62	0.090
36	0.090
36	0.090
52	0.090
55	0.089
55	0.089
14	0.089
10	0.089
68	0.089
68	0.089
15	0.089
15	0.089
32	0.089
1	0.089

Table 17: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
38	0.089
44	0.089
66	0.089
66	0.089
46	0.089
67	0.089
67	0.089
67	0.089
6	0.089
43	0.089
33	0.089
10	0.089
10	0.089
49	0.089
49	0.089
80	0.089
33	0.089
33	0.089
11	0.089
11	0.089
50	0.089
50	0.089
53	0.089
53	0.089
72	0.089
72	0.089
46	0.089
46	0.089
48	0.089
48	0.089
37	0.089
37	0.089
65	0.089
57	0.089
74	0.089
18	0.089
18	0.089
1	0.089
1	0.089
69	0.089
60	0.088
60	0.088
13	0.088
45	0.088
22	0.088
5	0.088
62	0.088
79	0.088
40	0.088
42	0.088
42	0.088
39	0.088
56	0.088
66	0.087
60	0.087
35	0.087
71	0.087
71	0.087
9	0.087
80	0.087
80	0.087
48	0.087
44	0.087
44	0.087

Table 17: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
61	0.087
16	0.087
16	0.087
21	0.087
19	0.087
3	0.087
43	0.087
43	0.087
24	0.087
24	0.087
14	0.087
14	0.087
8	0.087
27	0.087
58	0.087
58	0.087
17	0.087
17	0.087
3	0.087
3	0.087
41	0.087
64	0.087
53	0.086
21	0.086
21	0.086
42	0.086
23	0.086
58	0.086
7	0.086
51	0.086
23	0.086
23	0.086
78	0.086
78	0.086
76	0.085
30	0.085
31	0.085
56	0.085
56	0.085
27	0.085
27	0.085
73	0.085
54	0.085
59	0.085
59	0.085
35	0.084
35	0.084
37	0.084
34	0.083
75	0.083
59	0.082
77	0.080
43	0.080
20	0.080
26	0.080
68	0.079
47	0.079
35	0.079
11	0.079
49	0.079
44	0.079
36	0.079
72	0.079

Table 17: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
71	0.079
28	0.079
24	0.078
16	0.078
4	0.078
55	0.078
74	0.078
56	0.078
17	0.078
52	0.077
63	0.077
62	0.077
29	0.077
78	0.077
39	0.077
50	0.077
3	0.077
2	0.077
21	0.077
14	0.077
1	0.077
76	0.077
38	0.076
6	0.076
25	0.076
15	0.076
12	0.076
58	0.076
46	0.076
7	0.076
48	0.076
60	0.076
41	0.076
70	0.076
5	0.076
53	0.076
66	0.075
69	0.075
23	0.075
64	0.075
18	0.075
40	0.075
80	0.075
22	0.075
79	0.075
27	0.075
8	0.074
73	0.074
32	0.074
67	0.074
42	0.074
19	0.074
51	0.074
13	0.074
33	0.074
45	0.073
9	0.073
10	0.073
30	0.073
57	0.073
61	0.073
65	0.073
75	0.073

Table 17: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
37	0.072
54	0.071
34	0.071
40	0.071
31	0.070
54	0.069
8	0.069
28	0.068
67	0.068
39	0.068
49	0.068
45	0.067
11	0.067
68	0.067
38	0.067
15	0.067
12	0.067
20	0.067
55	0.066
24	0.066
26	0.065
76	0.065
52	0.065
30	0.064
77	0.064
22	0.064
70	0.064
5	0.064
25	0.064
29	0.064
36	0.063
64	0.063
61	0.063
44	0.063
7	0.063
62	0.062
57	0.062
6	0.062
17	0.062
47	0.062
53	0.062
14	0.061
48	0.061
32	0.061
34	0.061
42	0.061
10	0.061
73	0.061
74	0.061
69	0.061
3	0.060
19	0.060
58	0.060
51	0.060
50	0.060
21	0.060
9	0.060
41	0.060
31	0.060
2	0.060
40	0.059
8	0.059
43	0.059
70	0.059

Table 17: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
13	0.059
33	0.059
18	0.059
78	0.059
79	0.059
9	0.058
76	0.058
63	0.058
65	0.058
54	0.058
79	0.058
31	0.057
73	0.057
35	0.057
46	0.057
75	0.057
38	0.057
12	0.057
45	0.057
51	0.057
69	0.057
72	0.057
65	0.056
80	0.056
39	0.056
60	0.056
4	0.056
1	0.056
16	0.056
37	0.056
68	0.056
71	0.056
33	0.056
66	0.056
50	0.056
5	0.056
11	0.056
34	0.056
60	0.056
20	0.056
78	0.056
14	0.056
62	0.056
27	0.055
53	0.055
25	0.055
13	0.055
29	0.055
59	0.055
58	0.055
37	0.055
23	0.055
61	0.054
57	0.054
26	0.054
15	0.054
64	0.054
18	0.054
6	0.054
77	0.054
28	0.054
30	0.054
19	0.054

Table 17: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
7	0.054
17	0.054
49	0.054
10	0.054
23	0.054
55	0.053
1	0.053
47	0.053
52	0.053
24	0.053
48	0.053
44	0.053
2	0.053
74	0.053
3	0.053
21	0.053
67	0.052
36	0.052
46	0.052
22	0.052
80	0.052
16	0.052
35	0.052
75	0.052
63	0.051
71	0.051
41	0.051
27	0.051
4	0.051
72	0.051
42	0.051
66	0.051
32	0.051
59	0.050
56	0.050
43	0.049
56	0.048
79	0.047
79	0.047
70	0.047
70	0.047
69	0.047
69	0.047
37	0.046
37	0.046
78	0.046
78	0.046
62	0.046
62	0.046
20	0.046
20	0.046
69	0.046
41	0.046
79	0.046
79	0.046
41	0.046
41	0.046
8	0.046
8	0.046
70	0.046
70	0.046
63	0.046
63	0.046

Table 17: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
43	0.045
43	0.045
34	0.045
34	0.045
66	0.045
64	0.045
64	0.045
65	0.045
65	0.045
16	0.045
16	0.045
38	0.045
38	0.045
72	0.045
49	0.045
73	0.045
73	0.045
2	0.045
2	0.045
7	0.045
7	0.045
21	0.045
21	0.045
60	0.044
60	0.044
54	0.044
54	0.044
15	0.044
15	0.044
19	0.044
4	0.044
4	0.044
2	0.044
2	0.044
19	0.044
19	0.044
16	0.044
16	0.044
72	0.044
72	0.044
79	0.043
15	0.043
8	0.043
8	0.043
78	0.043
78	0.043
12	0.043
12	0.043
20	0.043
47	0.043
28	0.043
28	0.043
46	0.043
46	0.043
50	0.043
50	0.043
76	0.043
54	0.043
54	0.043
25	0.043
25	0.043
53	0.043
53	0.043
20	0.043

Table 17: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
20	0.043
66	0.043
66	0.043
55	0.043
55	0.043
51	0.043
51	0.043
56	0.043
56	0.043
64	0.043
64	0.043
15	0.043
15	0.043
51	0.043
51	0.043
58	0.042
58	0.042
18	0.042
18	0.042
38	0.042
60	0.042
60	0.042
14	0.042
14	0.042
23	0.042
23	0.042
80	0.042
80	0.042
71	0.042
71	0.042
11	0.042
26	0.042
26	0.042
45	0.042
32	0.042
32	0.042
63	0.042
63	0.042
17	0.042
17	0.042
5	0.042
5	0.042
27	0.042
27	0.042
10	0.042
10	0.042
29	0.042
29	0.042
26	0.042
9	0.042
9	0.042
73	0.042
73	0.042
68	0.042
68	0.042
41	0.042
41	0.042
53	0.042
69	0.042
69	0.042
72	0.042
72	0.042
52	0.042

Table 17: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
52	0.042
80	0.042
80	0.042
78	0.042
19	0.042
19	0.042
22	0.042
22	0.042
20	0.042
58	0.042
62	0.042
62	0.042
22	0.042
22	0.042
8	0.042
28	0.042
28	0.042
59	0.042
34	0.042
34	0.042
38	0.042
38	0.042
3	0.042
3	0.042
76	0.042
37	0.042
11	0.042
11	0.042
9	0.042
9	0.042
35	0.041
35	0.041
55	0.041
4	0.041
4	0.041
4	0.041
59	0.041
59	0.041
37	0.041
12	0.041
24	0.041
24	0.041
54	0.041
68	0.041
47	0.041
47	0.041
45	0.041
45	0.041
30	0.041
30	0.041
50	0.041
76	0.041
76	0.041
30	0.041
30	0.041
37	0.041
37	0.041
65	0.041
65	0.041
49	0.041
49	0.041
45	0.041
45	0.041

Table 17: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
77	0.041
77	0.041
68	0.041
68	0.041
49	0.041
49	0.041
57	0.041
57	0.041
43	0.041
43	0.041
12	0.041
12	0.041
71	0.041
71	0.041
44	0.041
44	0.041
67	0.041
67	0.041
61	0.041
61	0.041
75	0.041
75	0.041
21	0.041
17	0.041
17	0.041
27	0.041
27	0.041
13	0.041
13	0.041
62	0.041
56	0.041
56	0.041
11	0.041
11	0.041
51	0.041
73	0.041
6	0.041
46	0.041
40	0.040
40	0.040
54	0.040
31	0.040
31	0.040
6	0.040
6	0.040
47	0.040
47	0.040
18	0.040
18	0.040
7	0.040
7	0.040
2	0.040
36	0.040
36	0.040
28	0.040
58	0.040
58	0.040
53	0.040
3	0.040
3	0.040
45	0.040
48	0.040
48	0.040
59	0.040

Table 17: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
59	0.040
50	0.040
50	0.040
48	0.040
48	0.040
74	0.040
74	0.040
18	0.040
39	0.040
39	0.040
70	0.040
26	0.040
26	0.040
53	0.040
53	0.040
25	0.040
25	0.040
21	0.040
75	0.040
75	0.040
18	0.040
52	0.040
57	0.040
57	0.040
67	0.040
66	0.040
66	0.040
64	0.040
19	0.040
31	0.040
33	0.040
33	0.040
62	0.040
40	0.040
40	0.040
29	0.040
34	0.040
52	0.040
44	0.040
44	0.040
32	0.040
10	0.039
74	0.039
3	0.039
23	0.039
23	0.039
61	0.039
61	0.039
68	0.039
42	0.039
21	0.039
21	0.039
1	0.039
1	0.039
63	0.039
57	0.039
18	0.039
76	0.039
76	0.039
13	0.039
42	0.039
42	0.039
30	0.039

Table 17: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
65	0.039
25	0.039
31	0.039
31	0.039
54	0.039
65	0.039
36	0.039
36	0.039
31	0.039
34	0.039
43	0.039
37	0.039
7	0.039
45	0.039
52	0.039
52	0.039
24	0.039
24	0.039
29	0.039
8	0.039
61	0.039
13	0.039
13	0.039
42	0.039
42	0.039
52	0.039
28	0.039
30	0.038
55	0.038
55	0.038
35	0.038
35	0.038
6	0.038
33	0.038
33	0.038
1	0.038
1	0.038
75	0.038
33	0.038
5	0.038
5	0.038
9	0.038
67	0.038
67	0.038
26	0.038
23	0.038
32	0.038
32	0.038
51	0.038
78	0.038
29	0.038
29	0.038
14	0.038
14	0.038
29	0.038
32	0.038
73	0.038
30	0.038
22	0.038
5	0.038
11	0.038
13	0.038
6	0.038

Table 17: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
6	0.038
55	0.038
24	0.038
77	0.038
77	0.038
61	0.038
80	0.038
35	0.038
74	0.038
74	0.038
14	0.037
60	0.037
42	0.037
61	0.037
36	0.037
39	0.037
39	0.037
67	0.037
46	0.037
46	0.037
51	0.037
73	0.037
56	0.037
10	0.037
10	0.037
76	0.037
50	0.037
79	0.037
55	0.037
12	0.037
16	0.037
71	0.037
80	0.037
44	0.037
40	0.037
32	0.037
5	0.037
40	0.037
12	0.037
70	0.036
16	0.036
33	0.036
69	0.036
22	0.036
25	0.036
78	0.036
44	0.036
14	0.036
49	0.036
49	0.036
3	0.036
66	0.036
19	0.036
10	0.036
80	0.036
42	0.036
16	0.036
11	0.036
39	0.035
46	0.035
66	0.035
53	0.035
32	0.035
17	0.035

Table 17: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
35	0.035
7	0.035
77	0.035
36	0.035
34	0.035
10	0.035
7	0.035
56	0.035
43	0.035
38	0.035
3	0.035
70	0.035
74	0.035
72	0.035
17	0.035
62	0.035
26	0.035
48	0.035
8	0.034
39	0.034
57	0.034
5	0.034
1	0.034
2	0.034
39	0.034
79	0.034
64	0.034
35	0.034
38	0.034
4	0.034
25	0.034
47	0.034
50	0.034
21	0.034
69	0.034
1	0.034
20	0.034
47	0.034
48	0.034
63	0.033
24	0.033
58	0.033
6	0.033
2	0.033
71	0.033
28	0.033
45	0.033
27	0.033
6	0.033
22	0.033
31	0.033
67	0.033
24	0.033
44	0.033
64	0.033
58	0.033
50	0.033
68	0.033
27	0.033
30	0.033
41	0.032
59	0.032
34	0.032

Table 17: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
34	0.032
13	0.032
72	0.032
29	0.032
9	0.032
78	0.032
8	0.032
8	0.032
1	0.032
1	0.032
23	0.032
37	0.032
26	0.032
26	0.032
33	0.032
57	0.032
9	0.032
15	0.032
17	0.032
65	0.031
75	0.031
27	0.031
74	0.031
60	0.031
59	0.031
53	0.031
48	0.031
60	0.031
4	0.031
78	0.031
78	0.031
74	0.031
64	0.031
39	0.031
14	0.031
77	0.031
46	0.031
32	0.031
15	0.031
63	0.031
75	0.031
10	0.031
10	0.031
80	0.030
71	0.030
79	0.030
79	0.030
25	0.030
25	0.030
14	0.030
38	0.030
38	0.030
70	0.030
70	0.030
36	0.030
20	0.030
77	0.030
64	0.030
64	0.030
14	0.030
14	0.030
1	0.030
67	0.030

Table 17: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
69	0.030
43	0.030
71	0.030
70	0.030
70	0.030
11	0.030
11	0.030
80	0.030
80	0.030
69	0.030
41	0.030
41	0.030
57	0.030
3	0.030
3	0.030
36	0.030
22	0.030
37	0.030
37	0.030
80	0.030
76	0.030
35	0.030
35	0.030
62	0.030
62	0.030
24	0.030
24	0.030
40	0.030
8	0.030
8	0.030
33	0.030
33	0.030
45	0.029
72	0.029
41	0.029
41	0.029
2	0.029
2	0.029
4	0.029
23	0.029
23	0.029
58	0.029
44	0.029
12	0.029
79	0.029
43	0.029
55	0.029
55	0.029
28	0.029
69	0.029
69	0.029
52	0.029
62	0.029
13	0.029
13	0.029
44	0.029
44	0.029
73	0.029
51	0.029
51	0.029
7	0.029
7	0.029
7	0.029

Table 17: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
25	0.029
25	0.029
15	0.029
15	0.029
33	0.029
8	0.029
63	0.029
63	0.029
26	0.029
26	0.029
9	0.029
9	0.029
78	0.029
12	0.029
12	0.029
54	0.029
54	0.029
6	0.029
6	0.029
18	0.029
4	0.029
4	0.029
69	0.029
55	0.029
32	0.029
77	0.029
54	0.029
54	0.029
63	0.029
63	0.029
28	0.029
33	0.029
33	0.029
49	0.029
56	0.029
2	0.029
2	0.029
15	0.029
48	0.029
16	0.029
16	0.029
79	0.029
79	0.029
72	0.029
57	0.028
57	0.028
23	0.028
12	0.028
6	0.028
7	0.028
68	0.028
68	0.028
10	0.028
11	0.028
77	0.028
71	0.028
75	0.028
75	0.028
24	0.028
24	0.028
45	0.028
45	0.028
13	0.028

Table 17: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
13	0.028
21	0.028
18	0.028
19	0.028
19	0.028
61	0.028
3	0.028
3	0.028
78	0.028
78	0.028
74	0.028
74	0.028
28	0.028
28	0.028
37	0.028
46	0.028
44	0.028
65	0.028
61	0.028
69	0.028
69	0.028
33	0.028
42	0.028
38	0.028
58	0.028
58	0.028
30	0.028
30	0.028
53	0.028
79	0.028
18	0.028
19	0.028
73	0.028
73	0.028
64	0.028
64	0.028
28	0.028
28	0.028
27	0.028
40	0.028
40	0.028
52	0.028
52	0.028
67	0.028
67	0.028
38	0.028
17	0.028
17	0.028
42	0.028
3	0.028
19	0.028
19	0.028
73	0.028
66	0.028
66	0.028
29	0.028
29	0.028
40	0.028
70	0.028
49	0.028
49	0.028
5	0.028
26	0.028

Table 17: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
56	0.028
23	0.028
35	0.028
31	0.028
75	0.028
75	0.028
63	0.028
76	0.028
69	0.028
41	0.028
55	0.028
67	0.028
22	0.028
80	0.028
80	0.028
59	0.028
31	0.028
31	0.028
50	0.028
50	0.028
24	0.028
30	0.028
51	0.028
51	0.028
11	0.027
61	0.027
61	0.027
79	0.027
35	0.027
54	0.027
10	0.027
43	0.027
46	0.027
58	0.027
63	0.027
28	0.027
70	0.027
31	0.027
16	0.027
48	0.027
8	0.027
4	0.027
62	0.027
23	0.027
23	0.027
48	0.027
48	0.027
29	0.027
29	0.027
37	0.027
32	0.027
68	0.027
7	0.027
18	0.027
18	0.027
76	0.027
76	0.027
67	0.027
67	0.027
54	0.027
6	0.027
6	0.027
4	0.027
4	0.027

Table 17: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
6	0.027
73	0.027
53	0.027
53	0.027
17	0.027
17	0.027
35	0.027
35	0.027
40	0.027
40	0.027
16	0.027
16	0.027
20	0.027
20	0.027
65	0.027
58	0.027
11	0.027
11	0.027
1	0.027
20	0.027
43	0.027
43	0.027
25	0.027
52	0.027
49	0.027
50	0.027
50	0.027
70	0.027
60	0.027
53	0.027
1	0.027
23	0.027
18	0.027
18	0.027
36	0.027
60	0.026
60	0.026
5	0.026
5	0.026
22	0.026
22	0.026
79	0.026
39	0.026
66	0.026
44	0.026
59	0.026
59	0.026
2	0.026
56	0.026
56	0.026
15	0.026
9	0.026
21	0.026
21	0.026
42	0.026
60	0.026
60	0.026
37	0.026
37	0.026
57	0.026
57	0.026
78	0.026
62	0.026

Table 17: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
51	0.026
40	0.026
13	0.026
58	0.026
58	0.026
47	0.026
14	0.026
14	0.026
26	0.026
57	0.026
75	0.026
42	0.026
70	0.026
34	0.026
5	0.026
62	0.026
12	0.026
9	0.026
9	0.026
73	0.026
73	0.026
71	0.026
71	0.026
76	0.026
56	0.026
66	0.026
50	0.026
34	0.026
7	0.026
33	0.026
65	0.026
65	0.026
29	0.026
34	0.026
56	0.026
56	0.026
42	0.026
42	0.026
23	0.026
44	0.026
44	0.026
54	0.026
14	0.026
8	0.026
49	0.026
49	0.026
32	0.026
32	0.026
44	0.026
62	0.026
62	0.026
63	0.026
59	0.026
59	0.026
72	0.026
72	0.026
20	0.026
20	0.026
43	0.026
20	0.026
1	0.026
74	0.026
21	0.026

Table 17: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
21	0.026
4	0.026
47	0.026
9	0.026
77	0.026
77	0.026
47	0.026
47	0.026
72	0.026
72	0.026
15	0.026
15	0.026
27	0.026
27	0.026
5	0.026
5	0.026
30	0.026
65	0.026
65	0.026
75	0.026
30	0.026
30	0.026
62	0.026
7	0.026
38	0.025
38	0.025
29	0.025
48	0.025
66	0.025
50	0.025
61	0.025
41	0.025
34	0.025
34	0.025
47	0.025
36	0.025
36	0.025
27	0.025
39	0.025
24	0.025
47	0.025
47	0.025
24	0.025
39	0.025
39	0.025
19	0.025
9	0.025
33	0.025
50	0.025
19	0.025
17	0.025
53	0.025
53	0.025
68	0.025
51	0.025
76	0.025
76	0.025
18	0.025
49	0.025
43	0.025
43	0.025
4	0.025
21	0.025
7	0.025

Table 17: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
5	0.025
21	0.025
67	0.025
22	0.025
22	0.025
59	0.025
51	0.025
52	0.025
52	0.025
68	0.025
68	0.025
23	0.025
72	0.025
28	0.025
6	0.025
58	0.025
27	0.025
27	0.025
52	0.025
52	0.025
12	0.025
12	0.025
13	0.025
1	0.025
1	0.025
73	0.025
38	0.025
10	0.025
10	0.025
16	0.025
34	0.025
78	0.025
6	0.025
62	0.025
62	0.025
13	0.025
13	0.025
30	0.025
68	0.025
46	0.025
40	0.025
40	0.025
35	0.025
65	0.025
25	0.025
56	0.025
53	0.025
75	0.025
76	0.025
76	0.025
68	0.025
34	0.024
47	0.024
2	0.024
41	0.024
26	0.024
26	0.024
57	0.024
10	0.024
46	0.024
46	0.024
28	0.024
50	0.024

Table 17: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
55	0.024
55	0.024
21	0.024
22	0.024
15	0.024
19	0.024
11	0.024
14	0.024
58	0.024
3	0.024
41	0.024
48	0.024
48	0.024
6	0.024
60	0.024
39	0.024
39	0.024
72	0.024
64	0.024
76	0.024
52	0.024
40	0.024
78	0.024
10	0.024
61	0.024
61	0.024
36	0.024
36	0.024
43	0.024
52	0.024
43	0.024
43	0.024
26	0.024
29	0.024
59	0.024
10	0.024
10	0.024
42	0.024
32	0.024
32	0.024
31	0.024
31	0.024
37	0.024
80	0.024
51	0.024
38	0.024
51	0.024
74	0.024
66	0.024
66	0.024
75	0.024
75	0.024
68	0.024
64	0.024
24	0.024
32	0.024
32	0.024
38	0.024
38	0.024
49	0.023
23	0.023
23	0.023
55	0.023

Table 17: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
45	0.023
55	0.023
3	0.023
52	0.023
12	0.023
74	0.023
60	0.023
29	0.023
9	0.023
57	0.023
13	0.023
16	0.023
57	0.023
57	0.023
61	0.023
61	0.023
70	0.023
76	0.023
67	0.023
67	0.023
41	0.023
45	0.023
45	0.023
71	0.023
54	0.023
42	0.023
42	0.023
55	0.023
13	0.023
53	0.023
64	0.023
37	0.023
37	0.023
47	0.023
60	0.023
13	0.023
41	0.023
39	0.023
39	0.023
55	0.023
55	0.023
43	0.023
66	0.023
38	0.023
38	0.023
69	0.023
69	0.023
25	0.023
77	0.023
77	0.023
74	0.023
74	0.023
32	0.023
67	0.023
69	0.023
66	0.023
66	0.023
46	0.023
46	0.023
79	0.023
39	0.023
79	0.023
79	0.023
31	0.023

Table 17: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
74	0.023
74	0.023
11	0.023
6	0.023
34	0.023
25	0.023
9	0.023
9	0.023
77	0.023
73	0.023
73	0.023
8	0.023
68	0.023
68	0.023
25	0.023
9	0.023
55	0.022
45	0.022
40	0.022
38	0.022
65	0.022
2	0.022
54	0.022
26	0.022
6	0.022
6	0.022
49	0.022
30	0.022
30	0.022
71	0.022
74	0.022
77	0.022
77	0.022
3	0.022
3	0.022
31	0.022
25	0.022
25	0.022
67	0.022
80	0.022
12	0.022
12	0.022
14	0.022
75	0.022
3	0.022
3	0.022
16	0.022
15	0.022
2	0.022
46	0.022
20	0.022
12	0.022
72	0.022
72	0.022
27	0.022
70	0.022
70	0.022
53	0.022
53	0.022
58	0.022
58	0.022
79	0.022
79	0.022

Table 17: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
17	0.022
63	0.022
26	0.022
7	0.022
39	0.022
72	0.022
45	0.022
19	0.022
58	0.022
3	0.022
36	0.022
17	0.022
35	0.022
1	0.022
49	0.022
10	0.022
77	0.022
75	0.022
79	0.022
48	0.022
20	0.022
8	0.022
8	0.022
27	0.022
27	0.022
5	0.022
50	0.021
50	0.021
72	0.021
77	0.021
18	0.021
18	0.021
47	0.021
65	0.021
63	0.021
63	0.021
14	0.021
65	0.021
15	0.021
47	0.021
32	0.021
33	0.021
33	0.021
27	0.021
65	0.021
65	0.021
54	0.021
54	0.021
60	0.021
62	0.021
62	0.021
78	0.021
17	0.021
77	0.021
28	0.021
33	0.021
22	0.021
22	0.021
42	0.021
42	0.021
15	0.021
15	0.021
71	0.021

Table 17: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
1	0.021
24	0.021
5	0.021
5	0.021
59	0.021
36	0.021
17	0.021
79	0.021
71	0.021
71	0.021
27	0.021
37	0.021
54	0.021
29	0.021
29	0.021
71	0.021
71	0.021
36	0.021
36	0.021
18	0.021
40	0.021
40	0.021
31	0.021
75	0.021
75	0.021
14	0.021
14	0.021
19	0.021
68	0.021
53	0.021
38	0.021
17	0.021
19	0.021
19	0.021
42	0.021
22	0.021
22	0.021
55	0.021
11	0.021
29	0.021
24	0.021
24	0.021
64	0.021
8	0.021
53	0.021
53	0.021
57	0.021
8	0.021
8	0.021
47	0.021
46	0.021
30	0.021
21	0.021
62	0.021
75	0.021
4	0.021
4	0.021
51	0.021
51	0.021
69	0.021
65	0.021
65	0.021
45	0.021
31	0.021

Table 17: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
31	0.021
20	0.020
20	0.020
71	0.020
71	0.020
16	0.020
1	0.020
1	0.020
18	0.020
12	0.020
12	0.020
61	0.020
5	0.020
11	0.020
11	0.020
30	0.020
9	0.020
80	0.020
80	0.020
44	0.020
44	0.020
56	0.020
32	0.020
51	0.020
33	0.020
33	0.020
79	0.020
3	0.020
3	0.020
4	0.020
4	0.020
18	0.020
80	0.020
80	0.020
60	0.020
7	0.020
49	0.020
49	0.020
53	0.020
11	0.020
70	0.020
70	0.020
3	0.020
49	0.020
5	0.020
57	0.020
57	0.020
45	0.020
47	0.020
47	0.020
40	0.020
44	0.020
38	0.020
57	0.020
12	0.020
46	0.020
70	0.020
66	0.020
37	0.020
36	0.020
21	0.020
21	0.020
3	0.020

Table 17: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
38	0.020
44	0.020
9	0.020
9	0.020
30	0.020
48	0.020
48	0.020
21	0.020
1	0.020
1	0.020
63	0.020
63	0.020
16	0.020
27	0.020
27	0.020
23	0.020
34	0.020
34	0.020
9	0.020
36	0.020
76	0.020
40	0.020
23	0.020
23	0.020
31	0.020
31	0.020
48	0.020
48	0.020
60	0.020
74	0.020
60	0.020
60	0.020
43	0.020
17	0.020
17	0.020
74	0.020
50	0.020
2	0.020
45	0.020
45	0.020
12	0.019
35	0.019
70	0.019
56	0.019
56	0.019
2	0.019
2	0.019
26	0.019
54	0.019
54	0.019
56	0.019
22	0.019
22	0.019
4	0.019
11	0.019
78	0.019
78	0.019
10	0.019
10	0.019
39	0.019
18	0.019
63	0.019
63	0.019

Table 17: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
20	0.019
71	0.019
2	0.019
4	0.019
32	0.019
71	0.019
59	0.019
3	0.019
78	0.019
78	0.019
44	0.019
63	0.019
66	0.019
61	0.019
19	0.019
19	0.019
6	0.019
6	0.019
57	0.019
64	0.019
64	0.019
39	0.019
45	0.019
68	0.019
22	0.019
49	0.019
62	0.019
44	0.019
44	0.019
69	0.019
16	0.019
16	0.019
34	0.019
34	0.019
60	0.019
24	0.019
49	0.019
49	0.019
33	0.019
76	0.019
35	0.019
35	0.019
25	0.019
25	0.019
25	0.019
41	0.019
25	0.019
66	0.019
66	0.019
38	0.019
80	0.019
14	0.019
36	0.019
36	0.019
38	0.019
7	0.019
51	0.019
2	0.019
2	0.019
37	0.019
70	0.019
70	0.019
41	0.019
41	0.019

Table 17: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
39	0.019
63	0.019
26	0.019
58	0.019
47	0.019
47	0.019
69	0.019
24	0.019
32	0.019
52	0.019
26	0.019
42	0.019
50	0.019
46	0.019
46	0.019
29	0.018
28	0.018
17	0.018
6	0.018
23	0.018
13	0.018
56	0.018
54	0.018
25	0.018
77	0.018
74	0.018
13	0.018
34	0.018
40	0.018
9	0.018
75	0.018
15	0.018
15	0.018
70	0.018
76	0.018
35	0.018
35	0.018
15	0.018
63	0.018
67	0.018
32	0.018
32	0.018
1	0.018
1	0.018
11	0.018
47	0.018
49	0.018
43	0.018
24	0.018
24	0.018
63	0.018
73	0.018
60	0.018
64	0.018
55	0.018
52	0.018
60	0.018
60	0.018
36	0.018
40	0.018
78	0.018
31	0.018
28	0.018

Table 17: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
76	0.018
25	0.018
41	0.018
7	0.018
7	0.018
74	0.018
30	0.018
14	0.018
75	0.018
7	0.018
7	0.018
20	0.018
20	0.018
74	0.018
5	0.018
5	0.018
73	0.018
73	0.018
61	0.018
68	0.018
16	0.018
29	0.018
29	0.018
51	0.018
51	0.018
71	0.018
21	0.018
21	0.018
76	0.018
76	0.018
61	0.018
63	0.018
10	0.018
57	0.018
28	0.018
28	0.018
71	0.018
16	0.018
11	0.018
69	0.018
69	0.018
3	0.018
42	0.018
42	0.018
14	0.018
19	0.018
48	0.018
59	0.018
67	0.018
43	0.018
43	0.018
8	0.018
64	0.018
64	0.018
19	0.018
66	0.018
15	0.018
44	0.018
34	0.018
28	0.018
28	0.018
55	0.018
58	0.018

Table 17: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
52	0.018
52	0.018
8	0.018
43	0.018
69	0.018
19	0.018
57	0.018
28	0.018
63	0.018
46	0.018
58	0.018
58	0.018
75	0.018
68	0.018
68	0.018
68	0.018
39	0.018
67	0.018
26	0.018
26	0.018
47	0.018
55	0.018
55	0.018
46	0.018
26	0.018
59	0.017
70	0.017
13	0.017
4	0.017
77	0.017
46	0.017
11	0.017
46	0.017
46	0.017
27	0.017
11	0.017
11	0.017
37	0.017
37	0.017
7	0.017
66	0.017
71	0.017
37	0.017
37	0.017
64	0.017
43	0.017
43	0.017
42	0.017
41	0.017
41	0.017
73	0.017
39	0.017
34	0.017
18	0.017
45	0.017
45	0.017
37	0.017
80	0.017
80	0.017
52	0.017
45	0.017
62	0.017
73	0.017
2	0.017

Table 17: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
31	0.017
5	0.017
65	0.017
65	0.017
78	0.017
78	0.017
44	0.017
37	0.017
13	0.017
67	0.017
64	0.017
64	0.017
50	0.017
68	0.017
76	0.017
69	0.017
69	0.017
57	0.017
57	0.017
22	0.017
17	0.017
16	0.017
16	0.017
77	0.017
77	0.017
40	0.017
40	0.017
59	0.017
39	0.017
39	0.017
27	0.017
21	0.017
66	0.017
7	0.017
68	0.017
39	0.017
36	0.017
36	0.017
10	0.017
39	0.017
34	0.017
30	0.017
38	0.017
38	0.017
72	0.017
72	0.017
40	0.017
56	0.017
18	0.017
69	0.017
26	0.017
59	0.017
64	0.017
15	0.017
71	0.017
59	0.017
59	0.017
73	0.017
64	0.017
28	0.017
28	0.017
17	0.017
66	0.017

Table 17: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
74	0.017
1	0.017
25	0.017
25	0.017
43	0.017
29	0.017
25	0.017
20	0.017
45	0.017
62	0.017
7	0.017
79	0.017
14	0.017
14	0.017
20	0.017
24	0.017
39	0.017
39	0.017
76	0.017
17	0.017
71	0.017
57	0.017
72	0.017
43	0.017
80	0.017
31	0.017
60	0.017
35	0.017
72	0.017
32	0.017
61	0.017
58	0.017
33	0.017
80	0.017
45	0.017
20	0.017
20	0.017
28	0.016
29	0.016
2	0.016
2	0.016
10	0.016
28	0.016
59	0.016
59	0.016
63	0.016
41	0.016
67	0.016
67	0.016
16	0.016
33	0.016
8	0.016
73	0.016
73	0.016
61	0.016
61	0.016
9	0.016
14	0.016
63	0.016
42	0.016
54	0.016
19	0.016
50	0.016

Table 17: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
58	0.016
28	0.016
17	0.016
17	0.016
62	0.016
23	0.016
30	0.016
3	0.016
32	0.016
14	0.016
14	0.016
51	0.016
6	0.016
51	0.016
20	0.016
8	0.016
8	0.016
21	0.016
21	0.016
5	0.016
45	0.016
72	0.016
29	0.016
29	0.016
52	0.016
72	0.016
77	0.016
8	0.016
55	0.016
55	0.016
64	0.016
53	0.016
72	0.016
16	0.016
16	0.016
72	0.016
13	0.016
13	0.016
77	0.016
77	0.016
22	0.016
31	0.016
7	0.016
41	0.016
41	0.016
68	0.016
18	0.016
18	0.016
34	0.016
34	0.016
40	0.016
50	0.016
79	0.016
38	0.016
54	0.016
23	0.016
23	0.016
19	0.016
72	0.016
22	0.016
73	0.016
1	0.016
65	0.016
6	0.016

Table 17: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
16	0.016
58	0.016
75	0.016
78	0.016
52	0.016
5	0.016
1	0.016
24	0.016
30	0.016
30	0.016
43	0.016
4	0.016
67	0.016
17	0.016
17	0.016
73	0.016
2	0.016
11	0.016
3	0.016
49	0.016
72	0.016
72	0.016
32	0.016
6	0.016
41	0.016
48	0.016
12	0.016
11	0.016
11	0.016
58	0.016
35	0.016
65	0.016
77	0.016
77	0.016
79	0.016
79	0.016
69	0.016
67	0.016
37	0.016
70	0.016
79	0.016
42	0.016
54	0.016
42	0.016
37	0.016
67	0.016
70	0.016
65	0.016
10	0.016
24	0.016
3	0.016
65	0.016
65	0.016
52	0.015
52	0.015
78	0.015
21	0.015
21	0.015
25	0.015
50	0.015
50	0.015
7	0.015
22	0.015

Table 17: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
57	0.015
57	0.015
7	0.015
7	0.015
73	0.015
78	0.015
34	0.015
80	0.015
73	0.015
13	0.015
45	0.015
45	0.015
60	0.015
60	0.015
47	0.015
58	0.015
58	0.015
47	0.015
36	0.015
11	0.015
11	0.015
23	0.015
61	0.015
65	0.015
23	0.015
66	0.015
33	0.015
33	0.015
14	0.015
33	0.015
23	0.015
54	0.015
80	0.015
29	0.015
58	0.015
58	0.015
13	0.015
35	0.015
56	0.015
28	0.015
61	0.015
80	0.015
9	0.015
29	0.015
34	0.015
53	0.015
31	0.015
37	0.015
5	0.015
16	0.015
56	0.015
56	0.015
23	0.015
62	0.015
59	0.015
21	0.015
12	0.015
36	0.015
56	0.015
27	0.015
46	0.015
66	0.015
66	0.015

Table 17: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
54	0.015
33	0.015
33	0.015
54	0.015
54	0.015
13	0.015
46	0.015
46	0.015
22	0.015
62	0.015
62	0.015
16	0.015
51	0.015
51	0.015
10	0.015
55	0.015
50	0.015
56	0.015
2	0.015
9	0.015
51	0.015
22	0.015
70	0.015
20	0.015
74	0.015
74	0.015
67	0.015
67	0.015
27	0.015
51	0.015
51	0.015
74	0.015
74	0.015
27	0.015
27	0.015
18	0.015
10	0.015
10	0.015
15	0.015
48	0.015
51	0.015
4	0.015
79	0.015
66	0.015
74	0.015
31	0.015
27	0.015
47	0.015
47	0.015
74	0.015
74	0.015
61	0.015
61	0.015
44	0.015
19	0.015
66	0.015
42	0.015
42	0.015
6	0.015
6	0.015
15	0.015
60	0.015
60	0.015
39	0.015

Table 17: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
12	0.014
12	0.014
44	0.014
49	0.014
55	0.014
55	0.014
22	0.014
20	0.014
41	0.014
44	0.014
44	0.014
66	0.014
66	0.014
68	0.014
68	0.014
75	0.014
50	0.014
50	0.014
65	0.014
19	0.014
19	0.014
15	0.014
46	0.014
56	0.014
56	0.014
1	0.014
1	0.014
30	0.014
54	0.014
54	0.014
24	0.014
4	0.014
12	0.014
48	0.014
26	0.014
19	0.014
53	0.014
35	0.014
68	0.014
1	0.014
65	0.014
41	0.014
76	0.014
76	0.014
10	0.014
38	0.014
50	0.014
27	0.014
32	0.014
32	0.014
31	0.014
31	0.014
63	0.014
61	0.014
57	0.014
15	0.014
13	0.014
35	0.014
48	0.014
48	0.014
20	0.014
53	0.014
42	0.014

Table 17: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
56	0.014
56	0.014
21	0.014
23	0.014
75	0.014
30	0.014
12	0.014
9	0.014
9	0.014
29	0.014
13	0.014
13	0.014
24	0.014
47	0.014
10	0.014
64	0.014
54	0.014
16	0.014
78	0.014
43	0.014
76	0.014
69	0.014
61	0.014
8	0.014
8	0.014
25	0.014
80	0.014
80	0.014
6	0.014
32	0.014
30	0.014
5	0.014
35	0.014
35	0.014
70	0.014
59	0.014
75	0.014
75	0.014
46	0.014
77	0.014
41	0.014
10	0.014
55	0.014
22	0.014
19	0.014
2	0.014
2	0.014
53	0.014
53	0.014
12	0.014
15	0.013
59	0.013
59	0.013
18	0.013
65	0.013
50	0.013
72	0.013
72	0.013
53	0.013
12	0.013
62	0.013
7	0.013
7	0.013

Table 17: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
61	0.013
61	0.013
45	0.013
15	0.013
15	0.013
14	0.013
14	0.013
1	0.013
31	0.013
68	0.013
67	0.013
67	0.013
26	0.013
26	0.013
80	0.013
31	0.013
31	0.013
12	0.013
4	0.013
11	0.013
24	0.013
6	0.013
25	0.013
71	0.013
24	0.013
24	0.013
21	0.013
2	0.013
55	0.013
55	0.013
23	0.013
21	0.013
48	0.013
53	0.013
74	0.013
26	0.013
26	0.013
60	0.013
78	0.013
42	0.013
5	0.013
5	0.013
50	0.013
46	0.013
17	0.013
3	0.013
2	0.013
65	0.013
48	0.013
36	0.013
42	0.013
4	0.013
32	0.013
32	0.013
57	0.013
30	0.013
30	0.013
31	0.013
33	0.013
52	0.013
52	0.013
62	0.013
48	0.013
26	0.013

Table 17: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
33	0.013
13	0.013
49	0.013
49	0.013
5	0.013
70	0.013
63	0.013
63	0.013
78	0.013
17	0.013
27	0.013
27	0.013
40	0.013
40	0.013
2	0.013
34	0.013
34	0.013
57	0.013
8	0.013
18	0.013
18	0.013
59	0.013
22	0.013
13	0.013
13	0.013
20	0.013
20	0.013
10	0.013
33	0.013
20	0.013
24	0.013
9	0.012
67	0.012
71	0.012
71	0.012
53	0.012
52	0.012
48	0.012
18	0.012
18	0.012
33	0.012
80	0.012
21	0.012
52	0.012
1	0.012
44	0.012
28	0.012
41	0.012
37	0.012
71	0.012
71	0.012
18	0.012
38	0.012
38	0.012
43	0.012
5	0.012
5	0.012
9	0.012
9	0.012
2	0.012
36	0.012
17	0.012
64	0.012

Table 17: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
76	0.012
76	0.012
12	0.012
12	0.012
36	0.012
3	0.012
4	0.012
4	0.012
5	0.012
52	0.012
19	0.012
19	0.012
15	0.012
15	0.012
31	0.012
56	0.012
64	0.012
75	0.012
75	0.012
48	0.012
48	0.012
47	0.012
59	0.012
59	0.012
56	0.012
49	0.012
49	0.012
8	0.012
67	0.012
44	0.012
49	0.012
73	0.012
73	0.012
16	0.012
77	0.012
23	0.012
23	0.012
60	0.012
51	0.012
60	0.011
27	0.011
6	0.011
6	0.011
29	0.011
62	0.011
62	0.011
39	0.011
39	0.011
4	0.011
4	0.011
28	0.011
28	0.011
64	0.011
69	0.011
69	0.011
11	0.011
71	0.011
64	0.011
57	0.011
79	0.011
31	0.011
54	0.011
37	0.011

Table 17: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
34	0.011
49	0.011
55	0.011
16	0.011
16	0.011
33	0.011
3	0.011
3	0.011
31	0.011
48	0.011
14	0.011
4	0.011
43	0.011
43	0.011
40	0.011
36	0.011
36	0.011
61	0.011
8	0.011
8	0.011
46	0.011
46	0.011
45	0.011
21	0.011
9	0.011
56	0.011
32	0.011
40	0.011
40	0.011
79	0.011
79	0.011
29	0.011
34	0.011
47	0.011
47	0.011
37	0.011
37	0.011
35	0.011
5	0.011
75	0.011
14	0.011
14	0.011
9	0.011
60	0.011
1	0.011
63	0.011
13	0.010
74	0.010
70	0.010
69	0.010
68	0.010
35	0.010
8	0.010
4	0.010
1	0.010
45	0.010
45	0.010
39	0.010
54	0.010
30	0.010
17	0.010
9	0.010
22	0.010
36	0.010

Table 17: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
14	0.010
56	0.010
46	0.010
78	0.010
40	0.010
51	0.010
35	0.010
44	0.010
44	0.010
53	0.010
53	0.010
51	0.010
80	0.010
27	0.010
35	0.010
35	0.010
24	0.010
24	0.010
30	0.010
25	0.010
26	0.010
50	0.010
50	0.010
78	0.010
78	0.010
76	0.010
27	0.010
66	0.010
29	0.010
29	0.010
19	0.010
70	0.010
70	0.010
59	0.010
38	0.010
11	0.010
7	0.010
77	0.010
77	0.010
41	0.010
66	0.010
33	0.010
42	0.010
59	0.010
30	0.010
17	0.010
17	0.010
65	0.010
35	0.010
30	0.010
30	0.010
18	0.010
45	0.010
13	0.009
79	0.009
6	0.009
43	0.009
19	0.009
43	0.009
62	0.009
22	0.009
15	0.009
59	0.009

Table 17: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
20	0.009
74	0.009
10	0.009
60	0.009
21	0.009
50	0.009
42	0.009
42	0.009
68	0.009
68	0.009
11	0.009
62	0.009
6	0.009
26	0.009
58	0.009
45	0.009
75	0.009
15	0.009
36	0.009
69	0.009
26	0.009
16	0.009
61	0.009
23	0.009
27	0.009
9	0.009
57	0.009
25	0.009
25	0.009
57	0.009
42	0.009
48	0.009
17	0.009
11	0.009
55	0.009
29	0.009
29	0.009
24	0.009
4	0.009
77	0.009
73	0.009
48	0.009
74	0.009
23	0.009
12	0.009
49	0.009
34	0.009
67	0.008
22	0.008
22	0.008
69	0.008
73	0.008
41	0.008
40	0.008
39	0.008
52	0.008
1	0.008
1	0.008
18	0.008
46	0.008
10	0.008
10	0.008
44	0.008

Table 17: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
71	0.008
50	0.008
57	0.008
76	0.008
79	0.008
72	0.008
40	0.008
73	0.008
62	0.008
22	0.008
8	0.008
61	0.008
36	0.008
34	0.008
64	0.008
57	0.008
50	0.008
37	0.008
12	0.008
77	0.008
59	0.008
20	0.008
39	0.008
77	0.008
41	0.008
41	0.008
28	0.008
31	0.008
14	0.008
75	0.008
10	0.008
21	0.008
38	0.008
7	0.008
16	0.008
71	0.008
22	0.008
27	0.008
72	0.008
61	0.008
49	0.008
3	0.008
75	0.008
38	0.008
26	0.008
63	0.007
22	0.007
48	0.007
2	0.007
44	0.007
17	0.007
71	0.007
64	0.007
64	0.007
42	0.007
33	0.007
47	0.007
52	0.007
63	0.007
80	0.007
78	0.007
37	0.007
21	0.007
68	0.007

Table 17: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
32	0.007
20	0.007
3	0.007
26	0.007
28	0.007
35	0.007
71	0.007
9	0.007
5	0.007
8	0.007
44	0.007
51	0.007
4	0.007
36	0.007
58	0.007
58	0.007
18	0.007
56	0.007
14	0.007
58	0.007
80	0.007
5	0.007
65	0.007
16	0.007
37	0.007
3	0.007
2	0.007
23	0.007
1	0.006
7	0.006
1	0.006
32	0.006
51	0.006
68	0.006
53	0.006
21	0.006
49	0.006
60	0.006
65	0.006
10	0.006
32	0.006
34	0.006
8	0.006
74	0.006
74	0.006
63	0.006
47	0.006
14	0.006
52	0.006
25	0.006
47	0.006
63	0.006
3	0.006
25	0.006
38	0.006
56	0.006
41	0.006
74	0.006
77	0.006
46	0.006
69	0.006
77	0.006
79	0.006

Table 17: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
71	0.006
55	0.006
32	0.006
61	0.006
26	0.006
30	0.006
25	0.006
33	0.006
42	0.006
80	0.006
60	0.006
72	0.006
14	0.006
73	0.006
23	0.006
18	0.006
72	0.006
70	0.006
5	0.006
6	0.006
2	0.006
67	0.006
70	0.006
15	0.006
48	0.006
7	0.006
7	0.006
39	0.006
19	0.006
53	0.006
53	0.006
51	0.006
31	0.006
58	0.005
63	0.005
37	0.005
48	0.005
46	0.005
9	0.005
58	0.005
58	0.005
70	0.005
68	0.005
54	0.005
27	0.005
54	0.005
1	0.005
53	0.005
69	0.005
40	0.005
76	0.005
43	0.005
4	0.005
39	0.005
46	0.005
46	0.005
49	0.005
35	0.005
49	0.005
11	0.005
65	0.005
65	0.005
20	0.005

Table 17: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
45	0.005
64	0.005
2	0.005
2	0.005
24	0.005
58	0.005
22	0.005
14	0.005
14	0.005
24	0.005
38	0.005
76	0.005
40	0.005
40	0.005
20	0.005
20	0.005
21	0.005
78	0.005
51	0.005
37	0.005
37	0.005
78	0.005
73	0.005
14	0.005
62	0.005
49	0.005
21	0.005
21	0.005
24	0.005
78	0.005
55	0.005
28	0.005
28	0.005
8	0.005
69	0.005
67	0.005
67	0.005
34	0.005
34	0.005
44	0.005
44	0.005
42	0.005
42	0.005
7	0.005
66	0.005
64	0.005
4	0.004
19	0.004
64	0.004
29	0.004
29	0.004
56	0.004
56	0.004
23	0.004
35	0.004
23	0.004
3	0.004
3	0.004
61	0.004
75	0.004
52	0.004
41	0.004
39	0.004
7	0.004

Table 17: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
52	0.004
80	0.004
41	0.004
50	0.004
50	0.004
63	0.004
63	0.004
16	0.004
73	0.004
34	0.004
60	0.004
79	0.004
74	0.004
44	0.004
55	0.004
58	0.004
33	0.004
3	0.004
56	0.004
76	0.004
76	0.004
8	0.004
8	0.004
3	0.004
76	0.004
59	0.004
5	0.004
18	0.004
18	0.004
43	0.004
67	0.004
64	0.004
10	0.004
48	0.004
48	0.004
34	0.004
50	0.004
50	0.004
16	0.004
16	0.004
33	0.004
33	0.004
25	0.004
25	0.004
48	0.004
37	0.004
66	0.004
66	0.004
20	0.004
47	0.004
21	0.004
59	0.004
45	0.004
45	0.004
30	0.004
30	0.004
62	0.004
39	0.004
39	0.004
72	0.004
67	0.004
78	0.004
32	0.004

Table 17: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
42	0.004
2	0.004
25	0.004
33	0.004
2	0.004
38	0.004
11	0.004
79	0.004
79	0.004
9	0.004
13	0.004
22	0.004
22	0.004
66	0.004
66	0.004
78	0.004
78	0.004
24	0.004
24	0.004
45	0.004
57	0.003
55	0.003
74	0.003
27	0.003
5	0.003
65	0.003
49	0.003
75	0.003
75	0.003
31	0.003
31	0.003
41	0.003
41	0.003
18	0.003
31	0.003
10	0.003
10	0.003
1	0.003
1	0.003
80	0.003
80	0.003
3	0.003
28	0.003
28	0.003
72	0.003
11	0.003
27	0.003
17	0.003
6	0.003
75	0.003
39	0.003
61	0.003
40	0.003
77	0.003
77	0.003
18	0.003
15	0.003
15	0.003
73	0.003
15	0.003
4	0.003
4	0.003
7	0.003

Table 17: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
66	0.003
43	0.003
35	0.003
61	0.003
61	0.003
15	0.003
6	0.003
46	0.003
44	0.003
11	0.003
11	0.003
5	0.003
5	0.003
54	0.003
59	0.003
69	0.003
70	0.003
13	0.003
60	0.003
60	0.003
54	0.003
54	0.003
70	0.003
70	0.003
20	0.003
5	0.003
29	0.003
76	0.003
26	0.003
38	0.003
67	0.003
79	0.003
54	0.003
36	0.003
45	0.003
42	0.003
44	0.002
56	0.002
24	0.002
12	0.002
35	0.002
35	0.002
16	0.002
62	0.002
32	0.002
32	0.002
36	0.002
18	0.002
80	0.002
1	0.002
17	0.002
63	0.002
53	0.002
26	0.002
53	0.002
9	0.002
29	0.002
73	0.002
73	0.002
65	0.002
14	0.002
48	0.002
30	0.002
52	0.002

Table 17: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
47	0.002
47	0.002
77	0.002
4	0.002
73	0.002
46	0.002
62	0.002
79	0.002
4	0.002
35	0.002
35	0.002
43	0.002
43	0.002
38	0.002
11	0.002
56	0.002
22	0.002
58	0.002
13	0.002
13	0.002
28	0.002
21	0.002
45	0.002
50	0.002
8	0.002
28	0.002
64	0.002
64	0.002
51	0.002
36	0.002
75	0.002
60	0.002
52	0.002
52	0.002
53	0.002
25	0.001
6	0.001
41	0.001
75	0.001
17	0.001
6	0.001
6	0.001
78	0.001
72	0.001
72	0.001
47	0.001
69	0.001
69	0.001
16	0.001
76	0.001
15	0.001
27	0.001
27	0.001
68	0.001
68	0.001
54	0.001
71	0.001
8	0.001
27	0.001
24	0.001
44	0.001
59	0.001
12	0.001

Table 17: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
57	0.001
57	0.001
17	0.001
17	0.001
29	0.001
59	0.001
59	0.001
43	0.001
47	0.001
65	0.001
23	0.001
10	0.001
43	0.001
30	0.001
9	0.001
9	0.001
62	0.001
62	0.001
6	0.001
41	0.001
80	0.001
40	0.001
15	0.001
26	0.001
26	0.001
19	0.001
56	0.001
37	0.001
71	0.001
71	0.001
12	0.001
12	0.001
2	0.001
38	0.001
38	0.001
19	0.001
31	0.001
32	0.001
29	0.001
53	0.001
70	0.001
36	0.001
36	0.001
20	0.001
49	0.001
49	0.001
76	0.001
33	0.001
66	0.001
12	0.000
68	0.000
61	0.000
36	0.000
46	0.000
80	0.000
34	0.000
60	0.000
67	0.000
77	0.000
74	0.000
19	0.000
19	0.000
13	0.000

Table 17: ABG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
51	0.000
51	0.000
55	0.000
55	0.000
55	0.000
68	0.000
40	0.000
13	0.000
57	0.000
30	0.000
10	0.000
2	0.000
17	0.000
23	0.000
23	0.000
25	0.000
69	0.000
7	0.000
1	0.000
12	0.000
72	0.000
51	0.000
52	0.000
79	0.000

```

abg_imp_summary <- bal_imp_abg$bal_imp_summary |>
  summarise(
    med = median(max_abs_post, na.rm = TRUE),
    p90 = quantile(max_abs_post, 0.9, na.rm = TRUE),
    max = max(max_abs_post, na.rm = TRUE)
  )
render_table_pdf(
  abg_imp_summary,
  caption = "ABG: max |Target SMD| summary across imputations",
  file_stub = "abg_target_smd_summary",
  digits = 3
)

```

Table 18: ABG: max |Target SMD| summary across imputations

med	p90	max
0.091	0.094	0.1

3.3.4 10.3 VBG propensity (has_vbg)

```

stopifnot(exists("mi_single_pass_done"), isTRUE(mi_single_pass_done))
stopifnot(exists("mi_logistic_ps_vbg_list"))
message("VBG MI weights were computed in the single-pass MI loop above.")

```

Table 19: VBG weight diagnostics (MI; median across imputations)

n	min	p99.99.	max	ess
7460	0.308	3.892	3.895	5076.89

3.3.5 10.4 VBG balance

```

stopifnot(exists("bal_imp_vbg"))

bal_vbg_pooled <- bal_imp_vbg$bal_long |>
  mutate(label = ifelse(is.na(level), variable, paste0(variable, ":", level))) |>
  group_by(label) |>
  summarise(
    pre_med = median(abs(smd_pre), na.rm = TRUE),
    post_med = median(abs(smd_post), na.rm = TRUE),
    pre_mean = mean(abs(smd_pre), na.rm = TRUE),
    post_mean = mean(abs(smd_post), na.rm = TRUE),
    post_max = max(abs(smd_post), na.rm = TRUE),
    .groups = "drop"
  )

bal_vbg_plot <- bal_vbg_pooled |>
  mutate(label = factor(label, levels = label[order(post_med, decreasing = TRUE)])) |>
  pivot_longer(c(pre_med, post_med), names_to = "type", values_to = "smd") |>
  mutate(type = recode(type, pre_med = "Pre", post_med = "Post"))

p_vbg <- ggplot(bal_vbg_plot, aes(x = smd, y = label, shape = type)) +
  geom_vline(xintercept = 0.1, linetype = 2, linewidth = 0.3) +
  geom_point(size = 1.2) +
  labs(title = "MI target balance (VBG): pooled |SMD|", x = "|Target SMD|", y = NULL, shape = "Stage") +
  scale_x_continuous(limits = c(0, BAL_XLIM_MAX),
                     expand = expansion(mult = c(0, 0.02))) +
  theme_minimal(base_size = 10)
save_diag_plot(p_vbg, results_path("figs", "diag-mi-balance-pooled-vbg.png"), width = 7, height = 6)

render_table_pdf(
  bal_imp_vbg$worst_rows_overall,
  caption = "VBG: target SMD rows across imputations (sorted by |SMD|)",
  file_stub = "vbg_worst_target_smd_rows",
  digits = 3
)

```

Table 20: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part A)

Table 20: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

Table 20: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

Table 20: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
serum_ca	NA	numeric	-0.037	-0.040	VBG
age_at_encounter	NA	numeric	-0.018	0.040	VBG
encounter_type	Emergency	factor	-0.038	-0.040	VBG
encounter_type	Inpatient	factor	0.038	0.040	VBG
age_at_encounter	NA	numeric	-0.018	0.040	VBG
age_at_encounter	NA	numeric	-0.018	0.040	VBG
encounter_type	Emergency	factor	-0.038	-0.040	VBG
encounter_type	Inpatient	factor	0.038	0.040	VBG
age_at_encounter	NA	numeric	-0.018	0.040	VBG
age_at_encounter	NA	numeric	-0.018	0.040	VBG
age_at_encounter	NA	numeric	-0.018	0.040	VBG
encounter_type	Emergency	factor	-0.038	-0.040	VBG
encounter_type	Inpatient	factor	0.038	0.040	VBG
age_at_encounter	NA	numeric	-0.018	0.040	VBG
encounter_type	Emergency	factor	-0.038	-0.040	VBG
encounter_type	Inpatient	factor	0.038	0.040	VBG
serum_ca	NA	numeric	-0.037	-0.039	VBG
serum_ca	NA	numeric	-0.035	-0.039	VBG
encounter_type	Emergency	factor	-0.038	-0.039	VBG
encounter_type	Inpatient	factor	0.038	0.039	VBG
age_at_encounter	NA	numeric	-0.018	0.039	VBG
encounter_type	Emergency	factor	-0.038	-0.039	VBG
encounter_type	Inpatient	factor	0.038	0.039	VBG
age_at_encounter	NA	numeric	-0.018	0.038	VBG
age_at_encounter	NA	numeric	-0.018	0.038	VBG
age_at_encounter	NA	numeric	-0.018	0.038	VBG
serum_ca	NA	numeric	-0.032	-0.038	VBG
age_at_encounter	NA	numeric	-0.018	0.038	VBG
encounter_type	Emergency	factor	-0.038	-0.038	VBG
encounter_type	Inpatient	factor	0.038	0.038	VBG
age_at_encounter	NA	numeric	-0.018	0.038	VBG
encounter_type	Emergency	factor	-0.038	-0.038	VBG
encounter_type	Inpatient	factor	0.038	0.038	VBG
age_at_encounter	NA	numeric	-0.018	0.038	VBG
age_at_encounter	NA	numeric	-0.018	0.038	VBG
age_at_encounter	NA	numeric	-0.018	0.038	VBG
encounter_type	Emergency	factor	-0.038	-0.038	VBG
encounter_type	Inpatient	factor	0.038	0.038	VBG
serum_ca	NA	numeric	-0.034	-0.038	VBG
age_at_encounter	NA	numeric	-0.018	0.038	VBG
serum_ca	NA	numeric	-0.035	-0.038	VBG
age_at_encounter	NA	numeric	-0.018	0.037	VBG
serum_ca	NA	numeric	-0.029	-0.037	VBG
serum_ca	NA	numeric	-0.037	-0.037	VBG
serum_ca	NA	numeric	-0.039	-0.037	VBG
serum_ca	NA	numeric	-0.032	-0.037	VBG
age_at_encounter	NA	numeric	-0.018	0.037	VBG
age_at_encounter	NA	numeric	-0.018	0.037	VBG
age_at_encounter	NA	numeric	-0.018	0.037	VBG
encounter_type	Emergency	factor	-0.038	-0.036	VBG
encounter_type	Inpatient	factor	0.038	0.036	VBG
age_at_encounter	NA	numeric	-0.018	0.036	VBG
serum_ca	NA	numeric	-0.036	-0.036	VBG
serum_ca	NA	numeric	-0.035	-0.036	VBG
temp_new	NA	numeric	-0.004	0.036	VBG
age_at_encounter	NA	numeric	-0.018	0.036	VBG
serum_ca	NA	numeric	-0.032	-0.036	VBG
serum_ca	NA	numeric	-0.040	-0.036	VBG
serum_ca	NA	numeric	-0.034	-0.036	VBG

Table 20: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
serum_ca	NA	numeric	-0.037	-0.036	VBG
serum_ca	NA	numeric	-0.032	-0.035	VBG
serum_ca	NA	numeric	-0.039	-0.035	VBG
serum_ca	NA	numeric	-0.038	-0.035	VBG
serum_ca	NA	numeric	-0.031	-0.035	VBG
serum_ca	NA	numeric	-0.036	-0.035	VBG
age_at_encounter	NA	numeric	-0.018	0.035	VBG
serum_ca	NA	numeric	-0.032	-0.035	VBG
age_at_encounter	NA	numeric	-0.018	0.035	VBG
serum_ca	NA	numeric	-0.032	-0.035	VBG
serum_ca	NA	numeric	-0.034	-0.035	VBG
serum_ca	NA	numeric	-0.039	-0.035	VBG
serum_ca	NA	numeric	-0.033	-0.035	VBG
serum_ca	NA	numeric	-0.037	-0.035	VBG
age_at_encounter	NA	numeric	-0.018	0.035	VBG
serum_ca	NA	numeric	-0.034	-0.035	VBG
serum_ca	NA	numeric	-0.039	-0.035	VBG
serum_ca	NA	numeric	-0.033	-0.035	VBG
serum_ca	NA	numeric	-0.037	-0.035	VBG
serum_ca	NA	numeric	-0.032	-0.034	VBG
serum_ca	NA	numeric	-0.033	-0.034	VBG
serum_ca	NA	numeric	-0.035	-0.034	VBG
serum_ca	NA	numeric	-0.032	-0.034	VBG
serum_ca	NA	numeric	-0.036	-0.033	VBG
serum_ca	NA	numeric	-0.033	-0.033	VBG
serum_ca	NA	numeric	-0.032	-0.033	VBG
serum_ca	NA	numeric	-0.038	-0.033	VBG
serum_ca	NA	numeric	-0.035	-0.033	VBG
serum_ca	NA	numeric	-0.032	-0.034	VBG
serum_ca	NA	numeric	-0.033	-0.033	VBG
serum_ca	NA	numeric	-0.030	-0.033	VBG
serum_ca	NA	numeric	-0.034	-0.033	VBG
serum_ca	NA	numeric	-0.035	-0.033	VBG
serum_ca	NA	numeric	-0.037	-0.033	VBG
location	3	factor	-0.057	-0.033	VBG
location	3	factor	-0.057	-0.033	VBG
age_at_encounter	NA	numeric	-0.018	0.033	VBG
serum_ca	NA	numeric	-0.035	-0.033	VBG
curr_bmi	NA	numeric	-0.216	-0.033	VBG
serum_ca	NA	numeric	-0.030	-0.033	VBG
serum_ca	NA	numeric	-0.028	-0.033	VBG
location	3	factor	-0.057	-0.033	VBG
serum_ca	NA	numeric	-0.031	-0.032	VBG
serum_ca	NA	numeric	-0.030	-0.032	VBG
serum_ca	NA	numeric	-0.030	-0.032	VBG
temp_new	NA	numeric	-0.002	0.032	VBG
temp_new	NA	numeric	0.008	0.032	VBG
serum_ca	NA	numeric	-0.030	-0.032	VBG
serum_ca	NA	numeric	-0.029	-0.032	VBG
serum_ca	NA	numeric	-0.032	-0.032	VBG
temp_new	NA	numeric	0.025	0.032	VBG
serum_ca	NA	numeric	-0.036	-0.032	VBG
serum_ca	NA	numeric	-0.037	-0.032	VBG
location	3	factor	-0.057	-0.032	VBG
age_at_encounter	NA	numeric	-0.018	0.032	VBG
location	3	factor	-0.057	-0.032	VBG
curr_bmi	NA	numeric	-0.212	-0.032	VBG
serum_ca	NA	numeric	-0.028	-0.032	VBG
serum_ca	NA	numeric	-0.033	-0.032	VBG
location	3	factor	-0.057	-0.031	VBG
serum_ca	NA	numeric	-0.031	-0.031	VBG
serum_ca	NA	numeric	-0.035	-0.031	VBG
serum_phos	NA	numeric	0.077	0.031	VBG
serum_ca	NA	numeric	-0.031	-0.031	VBG
location	3	factor	-0.057	-0.031	VBG

Table 20: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
location	3	factor	-0.057	-0.031	VBG
serum_ca	NA	numeric	-0.037	-0.031	VBG
serum_ca	NA	numeric	-0.035	-0.031	VBG
location	3	factor	-0.057	-0.031	VBG
serum_ca	NA	numeric	-0.036	-0.031	VBG
location	3	factor	-0.057	-0.031	VBG
serum_phos	NA	numeric	0.090	0.031	VBG
location	3	factor	-0.057	-0.031	VBG
serum_ca	NA	numeric	-0.036	-0.030	VBG
serum_ca	NA	numeric	-0.035	-0.030	VBG
location	3	factor	-0.057	-0.030	VBG
serum_ca	NA	numeric	-0.036	-0.030	VBG
serum_lac	NA	numeric	0.128	0.030	VBG
location	3	factor	-0.057	-0.030	VBG
location	3	factor	-0.057	-0.030	VBG
serum_phos	NA	numeric	0.079	0.030	VBG
location	3	factor	-0.057	-0.030	VBG
serum_ca	NA	numeric	-0.029	-0.030	VBG
location	3	factor	-0.057	-0.030	VBG
location	3	factor	-0.057	-0.029	VBG
location	3	factor	-0.057	-0.029	VBG
location	3	factor	-0.057	-0.029	VBG
location	3	factor	-0.057	-0.029	VBG
location	3	factor	-0.057	-0.029	VBG
location	3	factor	-0.057	-0.029	VBG
location	3	factor	-0.057	-0.029	VBG
serum_phos	NA	numeric	0.082	0.029	VBG
location	3	factor	-0.057	-0.029	VBG
location	3	factor	-0.057	-0.029	VBG
location	3	factor	-0.057	-0.029	VBG
serum_ca	NA	numeric	-0.032	-0.029	VBG
location	3	factor	-0.057	-0.029	VBG
location	3	factor	-0.057	-0.028	VBG
temp_new	NA	numeric	-0.006	0.028	VBG
location	3	factor	-0.057	-0.028	VBG
plt	NA	numeric	-0.032	-0.028	VBG
location	3	factor	-0.057	-0.028	VBG
location	3	factor	-0.057	-0.028	VBG
serum_cr	NA	numeric	0.093	0.028	VBG
location	3	factor	-0.057	-0.028	VBG
dbp	NA	numeric	-0.062	-0.028	VBG
location	3	factor	-0.057	-0.028	VBG
temp_new	NA	numeric	0.005	0.028	VBG
serum_ca	NA	numeric	-0.030	-0.028	VBG
location	3	factor	-0.057	-0.028	VBG
serum_cr	NA	numeric	0.095	0.028	VBG
location	0	factor	-0.336	0.028	VBG
serum_ca	NA	numeric	-0.027	-0.028	VBG
temp_new	NA	numeric	0.006	0.028	VBG
serum_ca	NA	numeric	-0.031	-0.028	VBG
serum_phos	NA	numeric	0.074	0.028	VBG
temp_new	NA	numeric	-0.001	0.027	VBG
temp_new	NA	numeric	0.011	0.027	VBG
serum_phos	NA	numeric	0.077	0.027	VBG
location	3	factor	-0.057	-0.027	VBG
location	3	factor	-0.057	-0.027	VBG

Table 20: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
location	3	factor	-0.057	-0.027	VBG
serum_ca	NA	numeric	-0.032	-0.027	VBG
location	3	factor	-0.057	-0.027	VBG
location	0	factor	-0.336	0.027	VBG
location	3	factor	-0.057	-0.027	VBG
asthma	1	factor	-0.005	-0.027	VBG
asthma	0	factor	0.005	0.027	VBG
dbp	NA	numeric	-0.062	-0.027	VBG
dbp	NA	numeric	-0.070	-0.027	VBG
location	3	factor	-0.057	-0.027	VBG
location	3	factor	-0.057	-0.027	VBG
location	3	factor	-0.057	-0.027	VBG
serum_ca	NA	numeric	-0.035	-0.027	VBG
serum_lac	NA	numeric	0.131	0.027	VBG
location	3	factor	-0.057	-0.027	VBG
serum_ca	NA	numeric	-0.033	-0.027	VBG
dbp	NA	numeric	-0.067	-0.027	VBG
hr	NA	numeric	0.145	0.027	VBG
location	3	factor	-0.057	-0.027	VBG
location	3	factor	-0.057	-0.026	VBG
serum_phos	NA	numeric	0.091	0.026	VBG
serum_lac	NA	numeric	0.139	0.026	VBG
temp_new	NA	numeric	0.002	0.026	VBG
serum_phos	NA	numeric	0.093	0.026	VBG
curr_bmi	NA	numeric	-0.214	-0.026	VBG
serum_cl	NA	numeric	-0.153	-0.026	VBG
temp_new	NA	numeric	-0.003	0.026	VBG
serum_phos	NA	numeric	0.083	0.026	VBG
temp_new	NA	numeric	-0.001	0.026	VBG
serum_phos	NA	numeric	0.078	0.026	VBG
location	3	factor	-0.057	-0.026	VBG
location	3	factor	-0.057	-0.026	VBG
serum_phos	NA	numeric	0.079	0.026	VBG
location	3	factor	-0.057	-0.026	VBG
location	3	factor	-0.057	-0.026	VBG
location	3	factor	-0.057	-0.026	VBG
serum_cl	NA	numeric	-0.156	-0.026	VBG
serum_ca	NA	numeric	-0.033	-0.026	VBG
serum_cr	NA	numeric	0.095	0.026	VBG
location	3	factor	-0.057	-0.026	VBG
location	3	factor	-0.057	-0.026	VBG
serum_phos	NA	numeric	0.081	0.026	VBG
serum_lac	NA	numeric	0.125	0.026	VBG
location	3	factor	-0.057	-0.026	VBG
location	0	factor	-0.336	0.026	VBG
curr_bmi	NA	numeric	-0.232	-0.026	VBG
serum_ca	NA	numeric	-0.036	-0.026	VBG
temp_new	NA	numeric	0.010	0.025	VBG
serum_cl	NA	numeric	-0.152	-0.025	VBG
race_ethnicity	6	factor	0.205	-0.025	VBG
location	3	factor	-0.057	-0.025	VBG
race_ethnicity	6	factor	0.205	-0.025	VBG
serum_cl	NA	numeric	-0.150	-0.025	VBG
serum_cr	NA	numeric	0.096	0.025	VBG
temp_new	NA	numeric	-0.002	0.025	VBG
temp_new	NA	numeric	0.011	0.025	VBG
serum_cr	NA	numeric	0.095	0.025	VBG
temp_new	NA	numeric	0.006	0.025	VBG
temp_new	NA	numeric	-0.005	0.025	VBG
location	3	factor	-0.057	-0.025	VBG
location	3	factor	-0.057	-0.025	VBG
temp_new	NA	numeric	0.004	0.025	VBG

Table 20: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
location	0	factor	-0.336	0.025	VBG
plt	NA	numeric	-0.030	-0.025	VBG
location	3	factor	-0.057	-0.025	VBG
serum_cr	NA	numeric	0.097	0.025	VBG
serum_phos	NA	numeric	0.075	0.025	VBG
serum_phos	NA	numeric	0.089	0.025	VBG
serum_cl	NA	numeric	-0.154	-0.025	VBG
race_ethnicity	6	factor	0.205	-0.025	VBG
serum_phos	NA	numeric	0.088	0.025	VBG
location	0	factor	-0.336	0.025	VBG
serum_cr	NA	numeric	0.090	0.025	VBG
serum_phos	NA	numeric	0.080	0.025	VBG
serum_lac	NA	numeric	0.126	0.025	VBG
location	3	factor	-0.057	-0.025	VBG
temp_new	NA	numeric	-0.001	0.025	VBG
serum_lac	NA	numeric	0.124	0.025	VBG
race_ethnicity	6	factor	0.205	-0.025	VBG
location	0	factor	-0.336	0.025	VBG
serum_cl	NA	numeric	-0.151	-0.025	VBG
dbp	NA	numeric	-0.062	-0.025	VBG
serum_lac	NA	numeric	0.145	0.025	VBG
serum_phos	NA	numeric	0.065	0.025	VBG
serum_ca	NA	numeric	-0.032	-0.024	VBG
location	0	factor	-0.336	0.024	VBG
temp_new	NA	numeric	-0.003	0.024	VBG
location	3	factor	-0.057	-0.024	VBG
location	3	factor	-0.057	-0.024	VBG
serum_cr	NA	numeric	0.093	0.024	VBG
serum_lac	NA	numeric	0.133	0.024	VBG
location	3	factor	-0.057	-0.024	VBG
hr	NA	numeric	0.144	0.024	VBG
race_ethnicity	6	factor	0.205	-0.024	VBG
curr_bmi	NA	numeric	-0.215	-0.024	VBG
serum_phos	NA	numeric	0.076	0.024	VBG
location	3	factor	-0.057	-0.024	VBG
serum_cr	NA	numeric	0.097	0.024	VBG
location	0	factor	-0.336	0.024	VBG
serum_phos	NA	numeric	0.077	0.024	VBG
location	0	factor	-0.336	0.024	VBG
temp_new	NA	numeric	-0.009	0.024	VBG
serum_cl	NA	numeric	-0.155	-0.024	VBG
hr	NA	numeric	0.132	0.024	VBG
temp_new	NA	numeric	-0.002	0.024	VBG
serum_phos	NA	numeric	0.081	0.024	VBG
sbp	NA	numeric	-0.090	-0.024	VBG
dbp	NA	numeric	-0.062	-0.024	VBG
location	0	factor	-0.336	0.024	VBG
location	3	factor	-0.057	-0.024	VBG
plt	NA	numeric	-0.032	-0.024	VBG
serum_lac	NA	numeric	0.127	0.024	VBG
hr	NA	numeric	0.148	0.024	VBG
location	0	factor	-0.336	0.024	VBG
location	3	factor	-0.057	-0.024	VBG
location	3	factor	-0.057	-0.024	VBG
serum_cr	NA	numeric	0.096	0.024	VBG
serum_lac	NA	numeric	0.143	0.024	VBG
race_ethnicity	6	factor	0.205	-0.024	VBG
dbp	NA	numeric	-0.065	-0.024	VBG
serum_phos	NA	numeric	0.074	0.024	VBG
location	0	factor	-0.336	0.024	VBG
temp_new	NA	numeric	-0.004	0.024	VBG
asthma	1	factor	-0.005	-0.024	VBG

Table 20: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
asthma	0	factor	0.005	0.024	VBG
race_ethnicity	6	factor	0.205	-0.024	VBG
serum_phos	NA	numeric	0.082	0.024	VBG
location	3	factor	-0.057	-0.024	VBG
race_ethnicity	6	factor	0.205	-0.023	VBG
temp_new	NA	numeric	-0.013	0.023	VBG
location	0	factor	-0.336	0.023	VBG
temp_new	NA	numeric	0.004	0.023	VBG
location	0	factor	-0.336	0.023	VBG
serum_lac	NA	numeric	0.136	0.023	VBG
race_ethnicity	6	factor	0.205	-0.023	VBG
hr	NA	numeric	0.142	0.023	VBG
serum_lac	NA	numeric	0.133	0.023	VBG
asthma	1	factor	-0.005	-0.023	VBG
asthma	0	factor	0.005	0.023	VBG
temp_new	NA	numeric	-0.002	0.023	VBG
location	0	factor	-0.336	0.023	VBG
serum_cr	NA	numeric	0.100	0.023	VBG
serum_cl	NA	numeric	-0.152	-0.023	VBG
race_ethnicity	6	factor	0.205	-0.023	VBG
asthma	1	factor	-0.005	-0.023	VBG
asthma	0	factor	0.005	0.023	VBG
hr	NA	numeric	0.132	0.023	VBG
race_ethnicity	6	factor	0.205	-0.023	VBG
serum_cl	NA	numeric	-0.151	-0.023	VBG
serum_cl	NA	numeric	-0.155	-0.023	VBG
temp_new	NA	numeric	0.002	0.023	VBG
race_ethnicity	6	factor	0.205	-0.023	VBG
dbp	NA	numeric	-0.060	-0.023	VBG
serum_lac	NA	numeric	0.126	0.023	VBG
location	0	factor	-0.336	0.023	VBG
location	0	factor	-0.336	0.023	VBG
serum_lac	NA	numeric	0.145	0.023	VBG
temp_new	NA	numeric	-0.008	0.023	VBG
hr	NA	numeric	0.131	0.023	VBG
dbp	NA	numeric	-0.060	-0.023	VBG
temp_new	NA	numeric	0.005	0.023	VBG
curr_bmi	NA	numeric	-0.213	-0.023	VBG
serum_cl	NA	numeric	-0.156	-0.023	VBG
location	0	factor	-0.336	0.023	VBG
serum_phos	NA	numeric	0.075	0.023	VBG
serum_lac	NA	numeric	0.129	0.023	VBG
serum_phos	NA	numeric	0.074	0.023	VBG
hr	NA	numeric	0.127	0.023	VBG
location	3	factor	-0.057	-0.023	VBG
hr	NA	numeric	0.136	0.023	VBG
serum_lac	NA	numeric	0.128	0.023	VBG
serum_cr	NA	numeric	0.094	0.023	VBG
serum_cr	NA	numeric	0.095	0.023	VBG
serum_phos	NA	numeric	0.078	0.023	VBG
asthma	1	factor	-0.005	-0.023	VBG
asthma	0	factor	0.005	0.023	VBG
serum_cl	NA	numeric	-0.153	-0.023	VBG
serum_phos	NA	numeric	0.078	0.023	VBG
plt	NA	numeric	-0.024	-0.023	VBG
serum_phos	NA	numeric	0.093	0.023	VBG
serum_lac	NA	numeric	0.123	0.023	VBG
serum_cr	NA	numeric	0.094	0.023	VBG
temp_new	NA	numeric	-0.011	0.023	VBG
curr_bmi	NA	numeric	-0.247	-0.023	VBG
serum_cl	NA	numeric	-0.152	-0.023	VBG

Table 20: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
race_ethnicity	6	factor	0.205	-0.023	VBG
serum_phos	NA	numeric	0.077	0.023	VBG
serum_phos	NA	numeric	0.084	0.023	VBG
hr	NA	numeric	0.133	0.023	VBG
hr	NA	numeric	0.149	0.023	VBG
race_ethnicity	6	factor	0.205	-0.023	VBG
temp_new	NA	numeric	0.018	0.023	VBG
temp_new	NA	numeric	-0.001	0.023	VBG
serum_cl	NA	numeric	-0.155	-0.023	VBG
serum_phos	NA	numeric	0.066	0.023	VBG
race_ethnicity	6	factor	0.205	-0.023	VBG
serum_phos	NA	numeric	0.084	0.023	VBG
serum_cr	NA	numeric	0.093	0.023	VBG
curr_bmi	NA	numeric	-0.201	-0.023	VBG
temp_new	NA	numeric	-0.005	0.023	VBG
serum_cr	NA	numeric	0.097	0.023	VBG
serum_phos	NA	numeric	0.081	0.023	VBG
serum_lac	NA	numeric	0.135	0.023	VBG
serum_cl	NA	numeric	-0.152	-0.023	VBG
serum_cr	NA	numeric	0.094	0.023	VBG
serum_phos	NA	numeric	0.086	0.023	VBG
race_ethnicity	6	factor	0.205	-0.022	VBG
temp_new	NA	numeric	0.005	0.022	VBG
temp_new	NA	numeric	0.001	0.022	VBG
serum_cr	NA	numeric	0.096	0.022	VBG
curr_bmi	NA	numeric	-0.211	-0.022	VBG
location	0	factor	-0.336	0.022	VBG
serum_phos	NA	numeric	0.072	0.022	VBG
serum_cl	NA	numeric	-0.157	-0.022	VBG
serum_cl	NA	numeric	-0.157	-0.022	VBG
serum_cl	NA	numeric	-0.150	-0.022	VBG
dbp	NA	numeric	-0.070	-0.022	VBG
serum_lac	NA	numeric	0.121	0.022	VBG
curr_bmi	NA	numeric	-0.204	-0.022	VBG
race_ethnicity	6	factor	0.205	-0.022	VBG
dbp	NA	numeric	-0.060	-0.022	VBG
serum_phos	NA	numeric	0.093	0.022	VBG
race_ethnicity	6	factor	0.205	-0.022	VBG
location	3	factor	-0.057	-0.022	VBG
curr_bmi	NA	numeric	-0.218	-0.022	VBG
serum_cl	NA	numeric	-0.154	-0.022	VBG
plt	NA	numeric	-0.028	-0.022	VBG
serum_cl	NA	numeric	-0.153	-0.022	VBG
serum_cl	NA	numeric	-0.154	-0.022	VBG
serum_cl	NA	numeric	-0.151	-0.022	VBG
serum_phos	NA	numeric	0.086	0.022	VBG
serum_phos	NA	numeric	0.078	0.022	VBG
serum_phos	NA	numeric	0.082	0.022	VBG
wbc	NA	numeric	0.023	0.022	VBG
race_ethnicity	6	factor	0.205	-0.022	VBG
race_ethnicity	6	factor	0.205	-0.022	VBG
serum_lac	NA	numeric	0.146	0.022	VBG
race_ethnicity	6	factor	0.205	-0.022	VBG
serum_cr	NA	numeric	0.094	0.022	VBG
temp_new	NA	numeric	-0.011	0.022	VBG
curr_bmi	NA	numeric	-0.212	-0.022	VBG
serum_cr	NA	numeric	0.098	0.022	VBG
serum_cl	NA	numeric	-0.153	-0.022	VBG
location	0	factor	-0.336	0.022	VBG
location	0	factor	-0.336	0.022	VBG
serum_cr	NA	numeric	0.095	0.022	VBG
serum_cr	NA	numeric	0.095	0.022	VBG
race_ethnicity	6	factor	0.205	-0.022	VBG

Table 20: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
race_ethnicity	6	factor	0.205	-0.022	VBG
race_ethnicity	6	factor	0.205	-0.022	VBG
serum_cr	NA	numeric	0.098	0.022	VBG
serum_lac	NA	numeric	0.116	0.022	VBG
hr	NA	numeric	0.125	0.022	VBG
serum_cr	NA	numeric	0.096	0.022	VBG
curr_bmi	NA	numeric	-0.214	-0.022	VBG
serum_cr	NA	numeric	0.094	0.022	VBG
serum_phos	NA	numeric	0.069	0.022	VBG
serum_cl	NA	numeric	-0.154	-0.022	VBG
serum_cl	NA	numeric	-0.152	-0.022	VBG
race_ethnicity	6	factor	0.205	-0.022	VBG
serum_lac	NA	numeric	0.134	0.022	VBG
location	0	factor	-0.336	0.022	VBG
hr	NA	numeric	0.139	0.022	VBG
location	3	factor	-0.057	-0.022	VBG
race_ethnicity	6	factor	0.205	-0.022	VBG
race_ethnicity	6	factor	0.205	-0.022	VBG
location	3	factor	-0.057	-0.022	VBG
serum_phos	NA	numeric	0.074	0.022	VBG
serum_phos	NA	numeric	0.061	0.022	VBG
serum_cl	NA	numeric	-0.155	-0.022	VBG
curr_bmi	NA	numeric	-0.206	-0.022	VBG
race_ethnicity	6	factor	0.205	-0.022	VBG
serum_lac	NA	numeric	0.120	0.022	VBG
location	0	factor	-0.336	0.022	VBG
ckd	1	factor	0.069	0.022	VBG
ckd	0	factor	-0.069	-0.022	VBG
temp_new	NA	numeric	0.010	0.022	VBG
curr_bmi	NA	numeric	-0.212	-0.022	VBG
serum_cr	NA	numeric	0.092	0.022	VBG
serum_cr	NA	numeric	0.097	0.022	VBG
location	0	factor	-0.336	0.022	VBG
serum_phos	NA	numeric	0.084	0.022	VBG
location	0	factor	-0.336	0.022	VBG
serum_lac	NA	numeric	0.131	0.022	VBG
serum_cr	NA	numeric	0.091	0.022	VBG
race_ethnicity	6	factor	0.205	-0.022	VBG
temp_new	NA	numeric	-0.001	0.022	VBG
plt	NA	numeric	-0.028	-0.022	VBG
hr	NA	numeric	0.142	0.022	VBG
location	3	factor	-0.057	-0.022	VBG
race_ethnicity	6	factor	0.205	-0.022	VBG
race_ethnicity	6	factor	0.205	-0.022	VBG
hr	NA	numeric	0.143	0.022	VBG
curr_bmi	NA	numeric	-0.217	-0.022	VBG
serum_cr	NA	numeric	0.097	0.022	VBG
race_ethnicity	6	factor	0.205	-0.022	VBG
wbc	NA	numeric	0.021	0.022	VBG
location	0	factor	-0.336	0.021	VBG
dbp	NA	numeric	-0.068	-0.021	VBG
serum_cl	NA	numeric	-0.153	-0.021	VBG
race_ethnicity	6	factor	0.205	-0.021	VBG
serum_phos	NA	numeric	0.073	0.021	VBG
serum_phos	NA	numeric	0.085	0.021	VBG
dbp	NA	numeric	-0.063	-0.021	VBG
serum_cl	NA	numeric	-0.153	-0.021	VBG
serum_phos	NA	numeric	0.080	0.021	VBG
wbc	NA	numeric	0.023	0.021	VBG
serum_cr	NA	numeric	0.099	0.021	VBG
location	0	factor	-0.336	0.021	VBG
race_ethnicity	6	factor	0.205	-0.021	VBG
serum_cl	NA	numeric	-0.154	-0.021	VBG

Table 20: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
hr	NA	numeric	0.139	0.021	VBG
hr	NA	numeric	0.117	0.021	VBG
race_ethnicity	6	factor	0.205	-0.021	VBG
race_ethnicity	6	factor	0.205	-0.021	VBG
serum_phos	NA	numeric	0.077	0.021	VBG
wbc	NA	numeric	0.025	0.021	VBG
hr	NA	numeric	0.126	0.021	VBG
serum_cl	NA	numeric	-0.150	-0.021	VBG
serum_lac	NA	numeric	0.129	0.021	VBG
plt	NA	numeric	-0.022	-0.021	VBG
race_ethnicity	6	factor	0.205	-0.021	VBG
serum_cr	NA	numeric	0.093	0.021	VBG
serum_cl	NA	numeric	-0.152	-0.021	VBG
race_ethnicity	6	factor	0.205	-0.021	VBG
serum_lac	NA	numeric	0.119	0.021	VBG
serum_cl	NA	numeric	-0.152	-0.021	VBG
serum_phos	NA	numeric	0.081	0.021	VBG
dbp	NA	numeric	-0.062	-0.021	VBG
serum_cl	NA	numeric	-0.155	-0.021	VBG
temp_new	NA	numeric	-0.008	0.021	VBG
serum_cr	NA	numeric	0.093	0.021	VBG
serum_hco3	NA	numeric	-0.068	0.021	VBG
dbp	NA	numeric	-0.065	-0.021	VBG
asthma	1	factor	-0.005	-0.021	VBG
asthma	0	factor	0.005	0.021	VBG
asthma	0	factor	0.005	0.021	VBG
asthma	1	factor	-0.005	-0.021	VBG
location	0	factor	-0.336	0.021	VBG
race_ethnicity	6	factor	0.205	-0.021	VBG
serum_lac	NA	numeric	0.137	0.021	VBG
serum_cl	NA	numeric	-0.155	-0.021	VBG
serum_cr	NA	numeric	0.097	0.021	VBG
location	0	factor	-0.336	0.021	VBG
wbc	NA	numeric	0.024	0.021	VBG
plt	NA	numeric	-0.029	-0.021	VBG
serum_cr	NA	numeric	0.094	0.021	VBG
race_ethnicity	6	factor	0.205	-0.021	VBG
serum_cl	NA	numeric	-0.153	-0.021	VBG
asthma	1	factor	-0.005	-0.021	VBG
asthma	0	factor	0.005	0.021	VBG
phtn	1	factor	0.053	0.021	VBG
phtn	0	factor	-0.053	-0.021	VBG
race_ethnicity	6	factor	0.205	-0.021	VBG
location	0	factor	-0.336	0.021	VBG
curr_bmi	NA	numeric	-0.211	-0.021	VBG
serum_cl	NA	numeric	-0.150	-0.021	VBG
asthma	0	factor	0.005	0.021	VBG
asthma	1	factor	-0.005	-0.021	VBG
temp_new	NA	numeric	0.007	0.021	VBG
temp_new	NA	numeric	0.002	0.021	VBG
race_ethnicity	6	factor	0.205	-0.021	VBG
curr_bmi	NA	numeric	-0.235	-0.021	VBG
asthma	1	factor	-0.005	-0.021	VBG
asthma	0	factor	0.005	0.021	VBG
hr	NA	numeric	0.159	0.021	VBG
race_ethnicity	6	factor	0.205	-0.021	VBG
race_ethnicity	6	factor	0.205	-0.021	VBG
serum_cl	NA	numeric	-0.154	-0.021	VBG
temp_new	NA	numeric	-0.010	0.021	VBG
temp_new	NA	numeric	-0.019	0.021	VBG
location	0	factor	-0.336	0.021	VBG
serum_cl	NA	numeric	-0.153	-0.021	VBG
wbc	NA	numeric	0.023	0.021	VBG
serum_cr	NA	numeric	0.094	0.021	VBG

Table 20: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
wbc	NA	numeric	0.022	0.021	VBG
plt	NA	numeric	-0.024	-0.021	VBG
race_ethnicity	6	factor	0.205	-0.021	VBG
dbp	NA	numeric	-0.058	-0.021	VBG
race_ethnicity	6	factor	0.205	-0.021	VBG
serum_cl	NA	numeric	-0.152	-0.021	VBG
race_ethnicity	6	factor	0.205	-0.021	VBG
serum_cl	NA	numeric	-0.152	-0.021	VBG
serum_cl	NA	numeric	-0.155	-0.021	VBG
temp_new	NA	numeric	-0.013	0.021	VBG
race_ethnicity	6	factor	0.205	-0.021	VBG
location	3	factor	-0.057	-0.021	VBG
location	0	factor	-0.336	0.021	VBG
serum_cl	NA	numeric	-0.151	-0.021	VBG
location	0	factor	-0.336	0.021	VBG
sex	Female	factor	-0.057	-0.021	VBG
sex	Male	factor	0.057	0.021	VBG
serum_lac	NA	numeric	0.131	0.021	VBG
location	0	factor	-0.336	0.020	VBG
serum_lac	NA	numeric	0.129	0.020	VBG
plt	NA	numeric	-0.028	-0.020	VBG
hr	NA	numeric	0.126	0.020	VBG
asthma	1	factor	-0.005	-0.020	VBG
asthma	0	factor	0.005	0.020	VBG
location	0	factor	-0.336	0.020	VBG
sex	Female	factor	-0.057	-0.020	VBG
sex	Male	factor	0.057	0.020	VBG
race_ethnicity	6	factor	0.205	-0.020	VBG
race_ethnicity	6	factor	0.205	-0.020	VBG
curr_bmi	NA	numeric	-0.213	-0.020	VBG
serum_lac	NA	numeric	0.131	0.020	VBG
serum_cl	NA	numeric	-0.153	-0.020	VBG
wbc	NA	numeric	0.020	0.020	VBG
race_ethnicity	6	factor	0.205	-0.020	VBG
race_ethnicity	6	factor	0.205	-0.020	VBG
serum_lac	NA	numeric	0.142	0.020	VBG
serum_cr	NA	numeric	0.094	0.020	VBG
serum_lac	NA	numeric	0.137	0.020	VBG
location	3	factor	-0.057	-0.020	VBG
temp_new	NA	numeric	-0.005	0.020	VBG
serum_cr	NA	numeric	0.100	0.020	VBG
dbp	NA	numeric	-0.075	-0.020	VBG
curr_bmi	NA	numeric	-0.215	-0.020	VBG
dbp	NA	numeric	-0.057	-0.020	VBG
serum_cl	NA	numeric	-0.151	-0.020	VBG
serum_phos	NA	numeric	0.079	0.020	VBG
serum_lac	NA	numeric	0.126	0.020	VBG
dbp	NA	numeric	-0.062	-0.020	VBG
serum_hco3	NA	numeric	-0.070	0.020	VBG
serum_phos	NA	numeric	0.079	0.020	VBG
serum_lac	NA	numeric	0.129	0.020	VBG
serum_phos	NA	numeric	0.067	0.020	VBG
dbp	NA	numeric	-0.062	-0.020	VBG
race_ethnicity	6	factor	0.205	-0.020	VBG
serum_phos	NA	numeric	0.085	0.020	VBG
dbp	NA	numeric	-0.061	-0.020	VBG
serum_phos	NA	numeric	0.062	0.020	VBG
serum_lac	NA	numeric	0.131	0.020	VBG
location	0	factor	-0.336	0.020	VBG
dbp	NA	numeric	-0.068	-0.020	VBG
wbc	NA	numeric	0.015	0.020	VBG
serum_cl	NA	numeric	-0.151	-0.020	VBG
race_ethnicity	6	factor	0.205	-0.020	VBG

Table 20: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
serum_cr	NA	numeric	0.094	0.020	VBG
serum_lac	NA	numeric	0.143	0.020	VBG
serum_cl	NA	numeric	-0.153	-0.020	VBG
wbc	NA	numeric	0.021	0.020	VBG
temp_new	NA	numeric	0.011	0.020	VBG
temp_new	NA	numeric	0.012	0.020	VBG
serum_lac	NA	numeric	0.126	0.020	VBG
serum_cr	NA	numeric	0.095	0.020	VBG
race_ethnicity	6	factor	0.205	-0.020	VBG
serum_cl	NA	numeric	-0.155	-0.020	VBG
sex	Male	factor	0.057	0.020	VBG
sex	Female	factor	-0.057	-0.020	VBG
serum_cl	NA	numeric	-0.149	-0.020	VBG
serum_cl	NA	numeric	-0.154	-0.020	VBG
location	0	factor	-0.336	0.020	VBG
sex	Female	factor	-0.057	-0.020	VBG
sex	Male	factor	0.057	0.020	VBG
race_ethnicity	6	factor	0.205	-0.020	VBG
location	0	factor	-0.336	0.020	VBG
asthma	1	factor	-0.005	-0.020	VBG
asthma	0	factor	0.005	0.020	VBG
serum_cr	NA	numeric	0.092	0.020	VBG
temp_new	NA	numeric	-0.004	0.020	VBG
curr_bmi	NA	numeric	-0.211	-0.020	VBG
dbp	NA	numeric	-0.068	-0.020	VBG
serum_cr	NA	numeric	0.092	0.020	VBG
plt	NA	numeric	-0.026	-0.020	VBG
serum_cr	NA	numeric	0.096	0.020	VBG
dbp	NA	numeric	-0.064	-0.020	VBG
temp_new	NA	numeric	0.004	0.020	VBG
hr	NA	numeric	0.143	0.020	VBG
serum_lac	NA	numeric	0.136	0.020	VBG
dbp	NA	numeric	-0.071	-0.020	VBG
curr_bmi	NA	numeric	-0.192	-0.020	VBG
location	0	factor	-0.336	0.020	VBG
sbp	NA	numeric	-0.081	-0.020	VBG
dbp	NA	numeric	-0.068	-0.020	VBG
serum_lac	NA	numeric	0.128	0.020	VBG
dbp	NA	numeric	-0.065	-0.020	VBG
ckd	1	factor	0.069	0.020	VBG
ckd	0	factor	-0.069	-0.020	VBG
wbc	NA	numeric	0.022	0.020	VBG
serum_lac	NA	numeric	0.133	0.020	VBG
location	0	factor	-0.336	0.020	VBG
serum_lac	NA	numeric	0.130	0.020	VBG
wbc	NA	numeric	0.018	0.020	VBG
plt	NA	numeric	-0.021	-0.020	VBG
race_ethnicity	1	factor	0.042	0.019	VBG
ckd	0	factor	-0.069	-0.019	VBG
ckd	1	factor	0.069	0.019	VBG
serum_cr	NA	numeric	0.095	0.019	VBG
plt	NA	numeric	-0.022	-0.019	VBG
serum_phos	NA	numeric	0.066	0.019	VBG
serum_phos	NA	numeric	0.085	0.019	VBG
serum_cl	NA	numeric	-0.154	-0.019	VBG
asthma	1	factor	-0.005	-0.019	VBG
asthma	0	factor	0.005	0.019	VBG
wbc	NA	numeric	0.016	0.019	VBG
serum_lac	NA	numeric	0.135	0.019	VBG
serum_cl	NA	numeric	-0.154	-0.019	VBG
serum_cr	NA	numeric	0.097	0.019	VBG
race_ethnicity	6	factor	0.205	-0.019	VBG
race_ethnicity	6	factor	0.205	-0.019	VBG

Table 20: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
curr_bmi	NA	numeric	-0.208	-0.019	VBG
serum_cr	NA	numeric	0.092	0.019	VBG
serum_lac	NA	numeric	0.116	0.019	VBG
serum_cl	NA	numeric	-0.149	-0.019	VBG
asthma	0	factor	0.005	0.019	VBG
asthma	1	factor	-0.005	-0.019	VBG
serum_lac	NA	numeric	0.132	0.019	VBG
race_ethnicity	6	factor	0.205	-0.019	VBG
temp_new	NA	numeric	-0.011	0.019	VBG
hr	NA	numeric	0.147	0.019	VBG
serum_cr	NA	numeric	0.097	0.019	VBG
serum_cl	NA	numeric	-0.153	-0.019	VBG
curr_bmi	NA	numeric	-0.224	-0.019	VBG
asthma	0	factor	0.005	0.019	VBG
asthma	1	factor	-0.005	-0.019	VBG
asthma	1	factor	-0.005	-0.019	VBG
asthma	0	factor	0.005	0.019	VBG
race_ethnicity	6	factor	0.205	-0.019	VBG
wbc	NA	numeric	0.014	0.019	VBG
serum_lac	NA	numeric	0.139	0.019	VBG
serum_lac	NA	numeric	0.130	0.019	VBG
sex	Female	factor	-0.057	-0.019	VBG
sex	Male	factor	0.057	0.019	VBG
serum_cr	NA	numeric	0.096	0.019	VBG
asthma	1	factor	-0.005	-0.019	VBG
asthma	0	factor	0.005	0.019	VBG
asthma	1	factor	-0.005	-0.019	VBG
asthma	0	factor	0.005	0.019	VBG
race_ethnicity	6	factor	0.205	-0.019	VBG
hr	NA	numeric	0.144	0.019	VBG
serum_cl	NA	numeric	-0.152	-0.019	VBG
serum_lac	NA	numeric	0.139	0.019	VBG
serum_cl	NA	numeric	-0.151	-0.019	VBG
curr_bmi	NA	numeric	-0.230	-0.019	VBG
race_ethnicity	6	factor	0.205	-0.019	VBG
curr_bmi	NA	numeric	-0.216	-0.019	VBG
hr	NA	numeric	0.143	0.019	VBG
location	0	factor	-0.336	0.019	VBG
asthma	0	factor	0.005	0.019	VBG
asthma	1	factor	-0.005	-0.019	VBG
hr	NA	numeric	0.131	0.019	VBG
asthma	1	factor	-0.005	-0.019	VBG
asthma	0	factor	0.005	0.019	VBG
serum_phos	NA	numeric	0.081	0.019	VBG
wbc	NA	numeric	0.022	0.019	VBG
serum_cr	NA	numeric	0.093	0.019	VBG
race_ethnicity	6	factor	0.205	-0.019	VBG
temp_new	NA	numeric	-0.001	0.019	VBG
sex	Female	factor	-0.057	-0.019	VBG
sex	Male	factor	0.057	0.019	VBG
serum_cl	NA	numeric	-0.154	-0.019	VBG
race_ethnicity	6	factor	0.205	-0.019	VBG
asthma	0	factor	0.005	0.019	VBG
asthma	1	factor	-0.005	-0.019	VBG
location	0	factor	-0.336	0.019	VBG
serum_hco3	NA	numeric	-0.070	0.019	VBG
serum_lac	NA	numeric	0.132	0.019	VBG
serum_lac	NA	numeric	0.132	0.019	VBG
serum_cr	NA	numeric	0.096	0.019	VBG
location	0	factor	-0.336	0.019	VBG
asthma	0	factor	0.005	0.019	VBG
asthma	1	factor	-0.005	-0.019	VBG
serum_cl	NA	numeric	-0.148	-0.019	VBG
temp_new	NA	numeric	0.011	0.019	VBG

Table 20: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
serum_cr	NA	numeric	0.094	0.019	VBG
serum_cl	NA	numeric	-0.154	-0.019	VBG
serum_cl	NA	numeric	-0.151	-0.019	VBG
serum_phos	NA	numeric	0.077	0.019	VBG
serum_cr	NA	numeric	0.098	0.019	VBG
temp_new	NA	numeric	0.006	0.019	VBG
curr_bmi	NA	numeric	-0.220	-0.019	VBG
temp_new	NA	numeric	0.000	0.019	VBG
dbp	NA	numeric	-0.067	-0.019	VBG
hr	NA	numeric	0.135	0.019	VBG
serum_cr	NA	numeric	0.093	0.019	VBG
curr_bmi	NA	numeric	-0.217	-0.019	VBG
race_ethnicity	6	factor	0.205	-0.019	VBG
serum_phos	NA	numeric	0.083	0.019	VBG
hr	NA	numeric	0.129	0.019	VBG
dbp	NA	numeric	-0.078	-0.019	VBG
asthma	0	factor	0.005	0.019	VBG
asthma	1	factor	-0.005	-0.019	VBG
serum_lac	NA	numeric	0.120	0.019	VBG
location	0	factor	-0.336	0.019	VBG
wbc	NA	numeric	0.022	0.019	VBG
temp_new	NA	numeric	0.001	0.019	VBG
serum_cl	NA	numeric	-0.155	-0.019	VBG
dbp	NA	numeric	-0.067	-0.019	VBG
serum_cr	NA	numeric	0.092	0.019	VBG
phtn	0	factor	-0.053	-0.019	VBG
phtn	1	factor	0.053	0.019	VBG
asthma	1	factor	-0.005	-0.019	VBG
asthma	0	factor	0.005	0.019	VBG
race_ethnicity	6	factor	0.205	-0.019	VBG
serum_lac	NA	numeric	0.136	0.019	VBG
dbp	NA	numeric	-0.064	-0.019	VBG
serum_cl	NA	numeric	-0.151	-0.019	VBG
wbc	NA	numeric	0.013	0.019	VBG
race_ethnicity	6	factor	0.205	-0.019	VBG
serum_lac	NA	numeric	0.131	0.019	VBG
hr	NA	numeric	0.142	0.019	VBG
plt	NA	numeric	-0.024	-0.019	VBG
serum_lac	NA	numeric	0.121	0.019	VBG
wbc	NA	numeric	0.015	0.019	VBG
serum_phos	NA	numeric	0.071	0.019	VBG
serum_phos	NA	numeric	0.075	0.019	VBG
serum_phos	NA	numeric	0.077	0.018	VBG
sbp	NA	numeric	-0.088	-0.018	VBG
sbp	NA	numeric	-0.095	-0.018	VBG
serum_cr	NA	numeric	0.097	0.018	VBG
asthma	0	factor	0.005	0.018	VBG
asthma	1	factor	-0.005	-0.018	VBG
temp_new	NA	numeric	0.006	0.018	VBG
serum_lac	NA	numeric	0.128	0.018	VBG
serum_cl	NA	numeric	-0.152	-0.018	VBG
serum_phos	NA	numeric	0.075	0.018	VBG
serum_phos	NA	numeric	0.075	0.018	VBG
serum_cr	NA	numeric	0.095	0.018	VBG
serum_cl	NA	numeric	-0.151	-0.018	VBG
race_ethnicity	6	factor	0.205	-0.018	VBG
asthma	1	factor	-0.005	-0.018	VBG
asthma	0	factor	0.005	0.018	VBG
serum_cr	NA	numeric	0.097	0.018	VBG
serum_phos	NA	numeric	0.088	0.018	VBG
dbp	NA	numeric	-0.080	-0.018	VBG
temp_new	NA	numeric	-0.009	0.018	VBG
location	0	factor	-0.336	0.018	VBG

Table 20: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
asthma	1	factor	-0.005	-0.018	VBG
asthma	0	factor	0.005	0.018	VBG
race_ethnicity	6	factor	0.205	-0.018	VBG
phtn	0	factor	-0.053	-0.018	VBG
phtn	1	factor	0.053	0.018	VBG
sex	Male	factor	0.057	0.018	VBG
sex	Female	factor	-0.057	-0.018	VBG
hr	NA	numeric	0.142	0.018	VBG
dbp	NA	numeric	-0.054	-0.018	VBG
temp_new	NA	numeric	-0.006	0.018	VBG
curr_bmi	NA	numeric	-0.207	-0.018	VBG
wbc	NA	numeric	0.018	0.018	VBG
asthma	1	factor	-0.005	-0.018	VBG
asthma	0	factor	0.005	0.018	VBG
sex	Male	factor	0.057	0.018	VBG
sex	Female	factor	-0.057	-0.018	VBG
dbp	NA	numeric	-0.056	-0.018	VBG
dbp	NA	numeric	-0.073	-0.018	VBG
serum_cr	NA	numeric	0.099	0.018	VBG
serum_phos	NA	numeric	0.075	0.018	VBG
location	0	factor	-0.336	0.018	VBG
plt	NA	numeric	-0.024	-0.018	VBG
temp_new	NA	numeric	-0.010	0.018	VBG
hr	NA	numeric	0.133	0.018	VBG
race_ethnicity	6	factor	0.205	-0.018	VBG
sex	Male	factor	0.057	0.018	VBG
sex	Female	factor	-0.057	-0.018	VBG
location	0	factor	-0.336	0.018	VBG
temp_new	NA	numeric	-0.019	0.018	VBG
serum_cl	NA	numeric	-0.152	-0.018	VBG
serum_cl	NA	numeric	-0.151	-0.018	VBG
sex	Female	factor	-0.057	-0.018	VBG
sex	Male	factor	0.057	0.018	VBG
location	0	factor	-0.336	0.018	VBG
serum_cr	NA	numeric	0.094	0.018	VBG
dbp	NA	numeric	-0.066	-0.018	VBG
ckd	1	factor	0.069	0.018	VBG
ckd	0	factor	-0.069	-0.018	VBG
serum_lac	NA	numeric	0.138	0.018	VBG
race_ethnicity	1	factor	0.042	0.018	VBG
location	0	factor	-0.336	0.018	VBG
serum_hco3	NA	numeric	-0.068	0.018	VBG
dbp	NA	numeric	-0.076	-0.018	VBG
curr_bmi	NA	numeric	-0.225	-0.018	VBG
asthma	1	factor	-0.005	-0.018	VBG
asthma	0	factor	0.005	0.018	VBG
dbp	NA	numeric	-0.061	-0.018	VBG
wbc	NA	numeric	0.022	0.018	VBG
temp_new	NA	numeric	-0.003	0.018	VBG
temp_new	NA	numeric	0.004	0.018	VBG
serum_cr	NA	numeric	0.097	0.018	VBG
plt	NA	numeric	-0.026	-0.018	VBG
temp_new	NA	numeric	-0.003	0.018	VBG
serum_hco3	NA	numeric	-0.073	0.018	VBG
temp_new	NA	numeric	-0.015	0.018	VBG
serum_cr	NA	numeric	0.099	0.018	VBG
serum_cr	NA	numeric	0.092	0.018	VBG
serum_lac	NA	numeric	0.138	0.018	VBG
plt	NA	numeric	-0.025	-0.018	VBG
wbc	NA	numeric	0.013	0.018	VBG
serum_cr	NA	numeric	0.094	0.018	VBG
asthma	0	factor	0.005	0.018	VBG
asthma	1	factor	-0.005	-0.018	VBG

Table 20: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
hr	NA	numeric	0.141	0.018	VBG
asthma	1	factor	-0.005	-0.018	VBG
asthma	0	factor	0.005	0.018	VBG
phtn	1	factor	0.053	0.018	VBG
phtn	0	factor	-0.053	-0.018	VBG
sex	Male	factor	0.057	0.018	VBG
sex	Female	factor	-0.057	-0.018	VBG
plt	NA	numeric	-0.028	-0.018	VBG
asthma	1	factor	-0.005	-0.018	VBG
asthma	0	factor	0.005	0.018	VBG
serum_hco3	NA	numeric	-0.073	0.018	VBG
race_ethnicity	1	factor	0.042	0.018	VBG
location	0	factor	-0.336	0.018	VBG
temp_new	NA	numeric	0.012	0.018	VBG
dbp	NA	numeric	-0.079	-0.018	VBG
curr_bmi	NA	numeric	-0.211	-0.018	VBG
curr_bmi	NA	numeric	-0.213	-0.018	VBG
plt	NA	numeric	-0.030	-0.018	VBG
hr	NA	numeric	0.137	0.018	VBG
sex	Female	factor	-0.057	-0.017	VBG
sex	Male	factor	0.057	0.017	VBG
sex	Male	factor	0.057	0.017	VBG
sex	Female	factor	-0.057	-0.017	VBG
serum_lac	NA	numeric	0.127	0.017	VBG
location	0	factor	-0.336	0.017	VBG
location	0	factor	-0.336	0.017	VBG
serum_cl	NA	numeric	-0.151	-0.017	VBG
asthma	0	factor	0.005	0.017	VBG
asthma	1	factor	-0.005	-0.017	VBG
wbc	NA	numeric	0.020	0.017	VBG
serum_cr	NA	numeric	0.098	0.017	VBG
wbc	NA	numeric	0.017	0.017	VBG
serum_phos	NA	numeric	0.074	0.017	VBG
hr	NA	numeric	0.145	0.017	VBG
asthma	1	factor	-0.005	-0.017	VBG
asthma	0	factor	0.005	0.017	VBG
location	0	factor	-0.336	0.017	VBG
temp_new	NA	numeric	-0.005	0.017	VBG
location	0	factor	-0.336	0.017	VBG
hr	NA	numeric	0.147	0.017	VBG
race_ethnicity	6	factor	0.205	-0.017	VBG
ckd	0	factor	-0.069	-0.017	VBG
ckd	1	factor	0.069	0.017	VBG
asthma	0	factor	0.005	0.017	VBG
asthma	1	factor	-0.005	-0.017	VBG
hr	NA	numeric	0.141	0.017	VBG
dbp	NA	numeric	-0.057	-0.017	VBG
asthma	0	factor	0.005	0.017	VBG
asthma	1	factor	-0.005	-0.017	VBG
plt	NA	numeric	-0.026	-0.017	VBG
serum_cr	NA	numeric	0.096	0.017	VBG
ckd	0	factor	-0.069	-0.017	VBG
ckd	1	factor	0.069	0.017	VBG
serum_cl	NA	numeric	-0.153	-0.017	VBG
asthma	1	factor	-0.005	-0.017	VBG
asthma	0	factor	0.005	0.017	VBG
asthma	0	factor	0.005	0.017	VBG
asthma	1	factor	-0.005	-0.017	VBG
wbc	NA	numeric	0.019	0.017	VBG
plt	NA	numeric	-0.029	-0.017	VBG
serum_cr	NA	numeric	0.095	0.017	VBG
race_ethnicity	6	factor	0.205	-0.017	VBG
wbc	NA	numeric	0.028	0.017	VBG
race_ethnicity	6	factor	0.205	-0.017	VBG

Table 20: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
plt	NA	numeric	-0.026	-0.017	VBG
wbc	NA	numeric	0.025	0.017	VBG
temp_new	NA	numeric	-0.021	0.017	VBG
temp_new	NA	numeric	0.004	0.017	VBG
asthma	1	factor	-0.005	-0.017	VBG
asthma	0	factor	0.005	0.017	VBG
plt	NA	numeric	-0.022	-0.017	VBG
serum_cr	NA	numeric	0.095	0.017	VBG
curr_bmi	NA	numeric	-0.218	-0.017	VBG
wbc	NA	numeric	0.016	0.017	VBG
serum_lac	NA	numeric	0.135	0.017	VBG
serum_lac	NA	numeric	0.135	0.017	VBG
temp_new	NA	numeric	-0.007	0.017	VBG
asthma	1	factor	-0.005	-0.017	VBG
asthma	0	factor	0.005	0.017	VBG
asthma	1	factor	-0.005	-0.017	VBG
asthma	0	factor	0.005	0.017	VBG
asthma	1	factor	-0.005	-0.017	VBG
asthma	0	factor	0.005	0.017	VBG
asthma	0	factor	0.005	0.017	VBG
asthma	1	factor	-0.005	-0.017	VBG
asthma	0	factor	0.005	0.017	VBG
asthma	0	factor	0.005	0.017	VBG
dbp	NA	numeric	-0.075	-0.017	VBG
asthma	0	factor	0.005	0.017	VBG
asthma	1	factor	-0.005	-0.017	VBG
serum_lac	NA	numeric	0.131	0.017	VBG
sbp	NA	numeric	-0.094	-0.017	VBG
serum_lac	NA	numeric	0.126	0.017	VBG
dbp	NA	numeric	-0.067	-0.017	VBG
location	0	factor	-0.336	0.017	VBG
dbp	NA	numeric	-0.084	-0.017	VBG
ckd	0	factor	-0.069	-0.017	VBG
ckd	1	factor	0.069	0.017	VBG
serum_phos	NA	numeric	0.068	0.017	VBG
plt	NA	numeric	-0.025	-0.017	VBG
serum_cr	NA	numeric	0.094	0.017	VBG
serum_hco3	NA	numeric	-0.070	0.017	VBG
asthma	1	factor	-0.005	-0.017	VBG
asthma	0	factor	0.005	0.017	VBG
serum_lac	NA	numeric	0.124	0.017	VBG
hr	NA	numeric	0.133	0.017	VBG
asthma	1	factor	-0.005	-0.017	VBG
asthma	0	factor	0.005	0.017	VBG
hr	NA	numeric	0.131	0.017	VBG
wbc	NA	numeric	0.017	0.017	VBG
serum_lac	NA	numeric	0.138	0.017	VBG
phtn	0	factor	-0.053	-0.017	VBG
phtn	1	factor	0.053	0.017	VBG
phtn	0	factor	-0.053	-0.017	VBG
phtn	1	factor	0.053	0.017	VBG
serum_phos	NA	numeric	0.076	0.017	VBG
serum_hco3	NA	numeric	-0.069	0.017	VBG
plt	NA	numeric	-0.027	-0.017	VBG
wbc	NA	numeric	0.017	0.017	VBG
race_ethnicity	6	factor	0.205	-0.017	VBG
serum_cl	NA	numeric	-0.151	-0.017	VBG
curr_bmi	NA	numeric	-0.214	-0.017	VBG
asthma	1	factor	-0.005	-0.017	VBG
asthma	0	factor	0.005	0.017	VBG
asthma	1	factor	-0.005	-0.017	VBG
asthma	0	factor	0.005	0.017	VBG
asthma	1	factor	-0.005	-0.017	VBG
asthma	0	factor	0.005	0.017	VBG
asthma	1	factor	-0.005	-0.017	VBG
asthma	0	factor	0.005	0.017	VBG
sex	Male	factor	0.057	0.017	VBG
sex	Female	factor	-0.057	-0.017	VBG
serum_cl	NA	numeric	-0.156	-0.017	VBG
serum_phos	NA	numeric	0.076	0.017	VBG

Table 20: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
dbp	NA	numeric	-0.061	-0.017	VBG
plt	NA	numeric	-0.025	-0.017	VBG
wbc	NA	numeric	0.021	0.017	VBG
serum_cl	NA	numeric	-0.155	-0.017	VBG
serum_lac	NA	numeric	0.131	0.017	VBG
serum_cr	NA	numeric	0.096	0.017	VBG
hr	NA	numeric	0.134	0.017	VBG
serum_lac	NA	numeric	0.133	0.017	VBG
plt	NA	numeric	-0.023	-0.016	VBG
wbc	NA	numeric	0.020	0.016	VBG
asthma	1	factor	-0.005	-0.016	VBG
asthma	0	factor	0.005	0.016	VBG
plt	NA	numeric	-0.027	-0.016	VBG
plt	NA	numeric	-0.025	-0.016	VBG
wbc	NA	numeric	0.017	0.016	VBG
location	0	factor	-0.336	0.016	VBG
location	0	factor	-0.336	0.016	VBG
serum_cr	NA	numeric	0.094	0.016	VBG
location	0	factor	-0.336	0.016	VBG
plt	NA	numeric	-0.024	-0.016	VBG
plt	NA	numeric	-0.030	-0.016	VBG
asthma	0	factor	0.005	0.016	VBG
asthma	1	factor	-0.005	-0.016	VBG
location	0	factor	-0.336	0.016	VBG
serum_hco3	NA	numeric	-0.073	0.016	VBG
wbc	NA	numeric	0.018	0.016	VBG
serum_lac	NA	numeric	0.139	0.016	VBG
hr	NA	numeric	0.140	0.016	VBG
serum_cr	NA	numeric	0.094	0.016	VBG
race_ethnicity	6	factor	0.205	-0.016	VBG
sbp	NA	numeric	-0.087	-0.016	VBG
serum_lac	NA	numeric	0.139	0.016	VBG
ckd	0	factor	-0.069	-0.016	VBG
ckd	1	factor	0.069	0.016	VBG
phtn	0	factor	-0.053	-0.016	VBG
phtn	1	factor	0.053	0.016	VBG
curr_bmi	NA	numeric	-0.221	-0.016	VBG
hr	NA	numeric	0.129	0.016	VBG
serum_cl	NA	numeric	-0.150	-0.016	VBG
asthma	1	factor	-0.005	-0.016	VBG
asthma	0	factor	0.005	0.016	VBG
curr_bmi	NA	numeric	-0.209	-0.016	VBG
ckd	1	factor	0.069	0.016	VBG
ckd	0	factor	-0.069	-0.016	VBG
ckd	0	factor	-0.069	-0.016	VBG
ckd	1	factor	0.069	0.016	VBG
hr	NA	numeric	0.140	0.016	VBG
ckd	0	factor	-0.069	-0.016	VBG
ckd	1	factor	0.069	0.016	VBG
ckd	0	factor	-0.069	-0.016	VBG
ckd	1	factor	0.069	0.016	VBG
hr	NA	numeric	0.133	0.016	VBG
hr	NA	numeric	0.132	0.016	VBG
location	0	factor	-0.336	0.016	VBG
sbp	NA	numeric	-0.096	-0.016	VBG
wbc	NA	numeric	0.017	0.016	VBG
sbp	NA	numeric	-0.097	-0.016	VBG
phtn	1	factor	0.053	0.016	VBG
phtn	0	factor	-0.053	-0.016	VBG
temp_new	NA	numeric	0.014	0.016	VBG
serum_lac	NA	numeric	0.118	0.016	VBG
hr	NA	numeric	0.130	0.016	VBG
wbc	NA	numeric	0.014	0.016	VBG

Table 20: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
race_ethnicity	6	factor	0.205	-0.016	VBG
hr	NA	numeric	0.144	0.016	VBG
ckd	0	factor	-0.069	-0.016	VBG
ckd	1	factor	0.069	0.016	VBG
plt	NA	numeric	-0.027	-0.016	VBG
sbp	NA	numeric	-0.094	-0.016	VBG
race_ethnicity	6	factor	0.205	-0.016	VBG
asthma	0	factor	0.005	0.016	VBG
asthma	1	factor	-0.005	-0.016	VBG
sbp	NA	numeric	-0.094	-0.016	VBG
hr	NA	numeric	0.123	0.016	VBG
curr_bmi	NA	numeric	-0.220	-0.016	VBG
plt	NA	numeric	-0.029	-0.016	VBG
serum_phos	NA	numeric	0.068	0.016	VBG
serum_phos	NA	numeric	0.072	0.016	VBG
plt	NA	numeric	-0.025	-0.016	VBG
serum_hco3	NA	numeric	-0.070	0.016	VBG
curr_bmi	NA	numeric	-0.209	-0.016	VBG
race_ethnicity	1	factor	0.042	0.016	VBG
sex	Female	factor	-0.057	-0.016	VBG
sex	Male	factor	0.057	0.016	VBG
plt	NA	numeric	-0.027	-0.016	VBG
serum_lac	NA	numeric	0.129	0.016	VBG
ckd	0	factor	-0.069	-0.016	VBG
ckd	1	factor	0.069	0.016	VBG
race_ethnicity	1	factor	0.042	0.016	VBG
race_ethnicity	6	factor	0.205	-0.016	VBG
ckd	1	factor	0.069	0.016	VBG
ckd	0	factor	-0.069	-0.016	VBG
asthma	0	factor	0.005	0.016	VBG
asthma	1	factor	-0.005	-0.016	VBG
plt	NA	numeric	-0.025	-0.016	VBG
serum_cl	NA	numeric	-0.152	-0.016	VBG
plt	NA	numeric	-0.025	-0.016	VBG
hr	NA	numeric	0.118	0.016	VBG
temp_new	NA	numeric	0.003	0.016	VBG
dbp	NA	numeric	-0.076	-0.016	VBG
phtn	0	factor	-0.053	-0.016	VBG
phtn	1	factor	0.053	0.016	VBG
serum_lac	NA	numeric	0.142	0.016	VBG
plt	NA	numeric	-0.028	-0.016	VBG
wbc	NA	numeric	0.026	0.016	VBG
ckd	1	factor	0.069	0.016	VBG
ckd	0	factor	-0.069	-0.016	VBG
plt	NA	numeric	-0.027	-0.016	VBG
sex	Male	factor	0.057	0.016	VBG
sex	Female	factor	-0.057	-0.016	VBG
wbc	NA	numeric	0.020	0.016	VBG
asthma	0	factor	0.005	0.016	VBG
asthma	1	factor	-0.005	-0.016	VBG
serum_lac	NA	numeric	0.133	0.016	VBG
asthma	1	factor	-0.005	-0.016	VBG
asthma	0	factor	0.005	0.016	VBG
asthma	0	factor	0.005	0.016	VBG
asthma	1	factor	-0.005	-0.016	VBG
wbc	NA	numeric	0.020	0.016	VBG
wbc	NA	numeric	0.017	0.016	VBG
wbc	NA	numeric	0.021	0.016	VBG
location	0	factor	-0.336	0.016	VBG
wbc	NA	numeric	0.016	0.016	VBG
serum_cr	NA	numeric	0.094	0.016	VBG
serum_hco3	NA	numeric	-0.069	0.016	VBG
asthma	0	factor	0.005	0.016	VBG
asthma	1	factor	-0.005	-0.016	VBG

Table 20: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
serum_cl	NA	numeric	-0.153	-0.016	VBG
wbc	NA	numeric	0.016	0.016	VBG
plt	NA	numeric	-0.019	-0.016	VBG
asthma	0	factor	0.005	0.016	VBG
asthma	1	factor	-0.005	-0.016	VBG
hr	NA	numeric	0.139	0.016	VBG
race_ethnicity	1	factor	0.042	0.016	VBG
location	0	factor	-0.336	0.016	VBG
serum_phos	NA	numeric	0.074	0.016	VBG
plt	NA	numeric	-0.023	-0.016	VBG
asthma	1	factor	-0.005	-0.016	VBG
asthma	0	factor	0.005	0.016	VBG
plt	NA	numeric	-0.028	-0.016	VBG
serum_cl	NA	numeric	-0.155	-0.015	VBG
serum_hco3	NA	numeric	-0.071	0.015	VBG
hr	NA	numeric	0.141	0.015	VBG
serum_hco3	NA	numeric	-0.072	0.015	VBG
location	0	factor	-0.336	0.015	VBG
hr	NA	numeric	0.137	0.015	VBG
race_ethnicity	6	factor	0.205	-0.015	VBG
ckd	0	factor	-0.069	-0.015	VBG
ckd	1	factor	0.069	0.015	VBG
plt	NA	numeric	-0.026	-0.015	VBG
plt	NA	numeric	-0.026	-0.015	VBG
hr	NA	numeric	0.147	0.015	VBG
race_ethnicity	1	factor	0.042	0.015	VBG
ckd	1	factor	0.069	0.015	VBG
ckd	0	factor	-0.069	-0.015	VBG
serum_hco3	NA	numeric	-0.073	0.015	VBG
race_ethnicity	6	factor	0.205	-0.015	VBG
location	0	factor	-0.336	0.015	VBG
plt	NA	numeric	-0.028	-0.015	VBG
location	0	factor	-0.336	0.015	VBG
wbc	NA	numeric	0.015	0.015	VBG
location	0	factor	-0.336	0.015	VBG
location	0	factor	-0.336	0.015	VBG
serum_hco3	NA	numeric	-0.071	0.015	VBG
serum_cr	NA	numeric	0.091	0.015	VBG
dbp	NA	numeric	-0.074	-0.015	VBG
serum_phos	NA	numeric	0.072	0.015	VBG
wbc	NA	numeric	0.014	0.015	VBG
wbc	NA	numeric	0.015	0.015	VBG
temp_new	NA	numeric	-0.004	0.015	VBG
location	0	factor	-0.336	0.015	VBG
wbc	NA	numeric	0.019	0.015	VBG
temp_new	NA	numeric	0.000	0.015	VBG
dbp	NA	numeric	-0.072	-0.015	VBG
sbp	NA	numeric	-0.091	-0.015	VBG
asthma	1	factor	-0.005	-0.015	VBG
asthma	0	factor	0.005	0.015	VBG
serum_cl	NA	numeric	-0.151	-0.015	VBG
location	0	factor	-0.336	0.015	VBG
wbc	NA	numeric	0.018	0.015	VBG
dbp	NA	numeric	-0.073	-0.015	VBG
hr	NA	numeric	0.137	0.015	VBG
serum_phos	NA	numeric	0.058	0.015	VBG
plt	NA	numeric	-0.029	-0.015	VBG
sbp	NA	numeric	-0.090	-0.015	VBG
sex	Male	factor	0.057	0.015	VBG
sex	Female	factor	-0.057	-0.015	VBG
sex	Female	factor	-0.057	-0.015	VBG
sex	Male	factor	0.057	0.015	VBG
serum_hco3	NA	numeric	-0.075	0.015	VBG

Table 20: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
asthma	0	factor	0.005	0.015	VBG
asthma	1	factor	-0.005	-0.015	VBG
hr	NA	numeric	0.127	0.015	VBG
location	0	factor	-0.336	0.015	VBG
wbc	NA	numeric	0.019	0.015	VBG
wbc	NA	numeric	0.017	0.015	VBG
hr	NA	numeric	0.126	0.015	VBG
curr_bmi	NA	numeric	-0.205	-0.015	VBG
serum_hco3	NA	numeric	-0.074	0.015	VBG
race_ethnicity	1	factor	0.042	0.015	VBG
sex	Female	factor	-0.057	-0.015	VBG
sex	Male	factor	0.057	0.015	VBG
curr_bmi	NA	numeric	-0.213	-0.015	VBG
serum_hco3	NA	numeric	-0.070	0.015	VBG
sex	Male	factor	0.057	0.015	VBG
sex	Female	factor	-0.057	-0.015	VBG
serum_hco3	NA	numeric	-0.071	0.015	VBG
location	0	factor	-0.336	0.015	VBG
plt	NA	numeric	-0.027	-0.015	VBG
serum_lac	NA	numeric	0.134	0.015	VBG
wbc	NA	numeric	0.017	0.015	VBG
ckd	0	factor	-0.069	-0.015	VBG
ckd	1	factor	0.069	0.015	VBG
dbp	NA	numeric	-0.069	-0.015	VBG
wbc	NA	numeric	0.013	0.015	VBG
dbp	NA	numeric	-0.058	-0.015	VBG
curr_bmi	NA	numeric	-0.230	-0.015	VBG
sex	Male	factor	0.057	0.015	VBG
sex	Female	factor	-0.057	-0.015	VBG
sex	Male	factor	0.057	0.015	VBG
sex	Female	factor	-0.057	-0.015	VBG
hr	NA	numeric	0.133	0.015	VBG
ckd	0	factor	-0.069	-0.015	VBG
ckd	1	factor	0.069	0.015	VBG
phtn	0	factor	-0.053	-0.015	VBG
phtn	1	factor	0.053	0.015	VBG
ckd	1	factor	0.069	0.015	VBG
ckd	0	factor	-0.069	-0.015	VBG
dbp	NA	numeric	-0.073	-0.015	VBG
curr_bmi	NA	numeric	-0.211	-0.015	VBG
serum_cl	NA	numeric	-0.153	-0.015	VBG
wbc	NA	numeric	0.022	0.015	VBG
sbp	NA	numeric	-0.091	-0.015	VBG
plt	NA	numeric	-0.025	-0.015	VBG
serum_cr	NA	numeric	0.091	0.015	VBG
ckd	1	factor	0.069	0.015	VBG
ckd	0	factor	-0.069	-0.015	VBG
asthma	0	factor	0.005	0.015	VBG
asthma	1	factor	-0.005	-0.015	VBG
serum_hco3	NA	numeric	-0.069	0.015	VBG
ckd	0	factor	-0.069	-0.015	VBG
ckd	1	factor	0.069	0.015	VBG
serum_hco3	NA	numeric	-0.068	0.015	VBG
ckd	1	factor	0.069	0.014	VBG
ckd	0	factor	-0.069	-0.014	VBG
serum_lac	NA	numeric	0.131	0.014	VBG
asthma	0	factor	0.005	0.014	VBG
asthma	1	factor	-0.005	-0.014	VBG
ckd	1	factor	0.069	0.014	VBG
ckd	0	factor	-0.069	-0.014	VBG
ckd	0	factor	-0.069	-0.014	VBG
ckd	1	factor	0.069	0.014	VBG
sex	Female	factor	-0.057	-0.014	VBG

Table 20: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
sex	Male	factor	0.057	0.014	VBG
serum_lac	NA	numeric	0.132	0.014	VBG
serum_phos	NA	numeric	0.082	0.014	VBG
phtn	0	factor	-0.053	-0.014	VBG
phtn	1	factor	0.053	0.014	VBG
serum_cr	NA	numeric	0.094	0.014	VBG
hr	NA	numeric	0.140	0.014	VBG
sex	Female	factor	-0.057	-0.014	VBG
sex	Male	factor	0.057	0.014	VBG
phtn	1	factor	0.053	0.014	VBG
phtn	0	factor	-0.053	-0.014	VBG
plt	NA	numeric	-0.024	-0.014	VBG
wbc	NA	numeric	0.018	0.014	VBG
location	0	factor	-0.336	0.014	VBG
race_ethnicity	1	factor	0.042	0.014	VBG
asthma	0	factor	0.005	0.014	VBG
asthma	1	factor	-0.005	-0.014	VBG
hr	NA	numeric	0.147	0.014	VBG
phtn	0	factor	-0.053	-0.014	VBG
phtn	1	factor	0.053	0.014	VBG
location	0	factor	-0.336	0.014	VBG
race_ethnicity	1	factor	0.042	0.014	VBG
serum_lac	NA	numeric	0.125	0.014	VBG
sex	Male	factor	0.057	0.014	VBG
sex	Female	factor	-0.057	-0.014	VBG
serum_lac	NA	numeric	0.121	0.014	VBG
serum_hco3	NA	numeric	-0.068	0.014	VBG
serum_hco3	NA	numeric	-0.072	0.014	VBG
hr	NA	numeric	0.134	0.014	VBG
race_ethnicity	1	factor	0.042	0.014	VBG
serum_hco3	NA	numeric	-0.072	0.014	VBG
serum_phos	NA	numeric	0.075	0.014	VBG
phtn	0	factor	-0.053	-0.014	VBG
phtn	1	factor	0.053	0.014	VBG
curr_bmi	NA	numeric	-0.227	-0.014	VBG
serum_phos	NA	numeric	0.072	0.014	VBG
sbp	NA	numeric	-0.092	-0.014	VBG
phtn	0	factor	-0.053	-0.014	VBG
phtn	1	factor	0.053	0.014	VBG
serum_cr	NA	numeric	0.095	0.014	VBG
race_ethnicity	1	factor	0.042	0.014	VBG
dbp	NA	numeric	-0.067	-0.014	VBG
phtn	1	factor	0.053	0.014	VBG
phtn	0	factor	-0.053	-0.014	VBG
wbc	NA	numeric	0.013	0.014	VBG
hr	NA	numeric	0.156	0.014	VBG
asthma	0	factor	0.005	0.014	VBG
asthma	1	factor	-0.005	-0.014	VBG
ckd	0	factor	-0.069	-0.014	VBG
ckd	1	factor	0.069	0.014	VBG
serum_hco3	NA	numeric	-0.070	0.014	VBG
serum_hco3	NA	numeric	-0.069	0.014	VBG
location	0	factor	-0.336	0.014	VBG
sex	Male	factor	0.057	0.014	VBG
sex	Female	factor	-0.057	-0.014	VBG
wbc	NA	numeric	0.018	0.014	VBG
sex	Male	factor	0.057	0.014	VBG
sex	Female	factor	-0.057	-0.014	VBG
sbp	NA	numeric	-0.095	-0.014	VBG
race_ethnicity	1	factor	0.042	0.014	VBG
serum_cl	NA	numeric	-0.148	-0.014	VBG
wbc	NA	numeric	0.022	0.014	VBG
serum_cr	NA	numeric	0.097	0.014	VBG
ckd	1	factor	0.069	0.014	VBG

Table 20: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
ckd	0	factor	-0.069	-0.014	VBG
plt	NA	numeric	-0.023	-0.014	VBG
wbc	NA	numeric	0.018	0.014	VBG
sbp	NA	numeric	-0.082	-0.014	VBG
wbc	NA	numeric	0.017	0.014	VBG
asthma	1	factor	-0.005	-0.014	VBG
asthma	0	factor	0.005	0.014	VBG
asthma	0	factor	0.005	0.014	VBG
asthma	1	factor	-0.005	-0.014	VBG
serum_hco3	NA	numeric	-0.070	0.014	VBG
wbc	NA	numeric	0.017	0.014	VBG
serum_lac	NA	numeric	0.135	0.014	VBG
plt	NA	numeric	-0.022	-0.014	VBG
plt	NA	numeric	-0.025	-0.014	VBG
wbc	NA	numeric	0.011	0.014	VBG
serum_cl	NA	numeric	-0.153	-0.014	VBG
hr	NA	numeric	0.136	0.014	VBG
race_ethnicity	1	factor	0.042	0.014	VBG
curr_bmi	NA	numeric	-0.234	-0.014	VBG
plt	NA	numeric	-0.028	-0.014	VBG
plt	NA	numeric	-0.025	-0.014	VBG
serum_hco3	NA	numeric	-0.070	0.014	VBG
temp_new	NA	numeric	0.000	0.014	VBG
sex	Male	factor	0.057	0.014	VBG
sex	Female	factor	-0.057	-0.014	VBG
plt	NA	numeric	-0.027	-0.014	VBG
location	0	factor	-0.336	0.014	VBG
ckd	0	factor	-0.069	-0.014	VBG
ckd	1	factor	0.069	0.014	VBG
serum_hco3	NA	numeric	-0.069	0.014	VBG
plt	NA	numeric	-0.031	-0.014	VBG
location	0	factor	-0.336	0.014	VBG
curr_bmi	NA	numeric	-0.216	-0.014	VBG
serum_hco3	NA	numeric	-0.071	0.014	VBG
hr	NA	numeric	0.147	0.014	VBG
sbp	NA	numeric	-0.100	-0.014	VBG
race_ethnicity	1	factor	0.042	0.014	VBG
asthma	1	factor	-0.005	-0.014	VBG
asthma	0	factor	0.005	0.014	VBG
plt	NA	numeric	-0.024	-0.014	VBG
plt	NA	numeric	-0.023	-0.014	VBG
asthma	1	factor	-0.005	-0.014	VBG
asthma	0	factor	0.005	0.014	VBG
plt	NA	numeric	-0.027	-0.014	VBG
wbc	NA	numeric	0.014	0.013	VBG
dbp	NA	numeric	-0.071	-0.013	VBG
serum_lac	NA	numeric	0.129	0.013	VBG
ckd	1	factor	0.069	0.013	VBG
ckd	0	factor	-0.069	-0.013	VBG
sex	Male	factor	0.057	0.013	VBG
sex	Female	factor	-0.057	-0.013	VBG
plt	NA	numeric	-0.025	-0.013	VBG
wbc	NA	numeric	0.019	0.013	VBG
race_ethnicity	1	factor	0.042	0.013	VBG
sex	Male	factor	0.057	0.013	VBG
sex	Female	factor	-0.057	-0.013	VBG
plt	NA	numeric	-0.026	-0.013	VBG
plt	NA	numeric	-0.018	-0.013	VBG
serum_phos	NA	numeric	0.094	0.013	VBG
sex	Female	factor	-0.057	-0.013	VBG
sex	Male	factor	0.057	0.013	VBG
sex	Female	factor	-0.057	-0.013	VBG
sex	Male	factor	0.057	0.013	VBG

Table 20: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
race_ethnicity	1	factor	0.042	0.013	VBG
sex	Male	factor	0.057	0.013	VBG
sex	Female	factor	-0.057	-0.013	VBG
ckd	0	factor	-0.069	-0.013	VBG
ckd	1	factor	0.069	0.013	VBG
phtn	1	factor	0.053	0.013	VBG
phtn	0	factor	-0.053	-0.013	VBG
curr_bmi	NA	numeric	-0.210	-0.013	VBG
phtn	1	factor	0.053	0.013	VBG
phtn	0	factor	-0.053	-0.013	VBG
sbp	NA	numeric	-0.089	-0.013	VBG
asthma	1	factor	-0.005	-0.013	VBG
asthma	0	factor	0.005	0.013	VBG
serum_lac	NA	numeric	0.129	0.013	VBG
dbp	NA	numeric	-0.079	-0.013	VBG
asthma	0	factor	0.005	0.013	VBG
asthma	1	factor	-0.005	-0.013	VBG
plt	NA	numeric	-0.029	-0.013	VBG
wbc	NA	numeric	0.018	0.013	VBG
phtn	0	factor	-0.053	-0.013	VBG
phtn	1	factor	0.053	0.013	VBG
curr_bmi	NA	numeric	-0.200	-0.013	VBG
sbp	NA	numeric	-0.096	-0.013	VBG
phtn	1	factor	0.053	0.013	VBG
phtn	0	factor	-0.053	-0.013	VBG
asthma	0	factor	0.005	0.013	VBG
asthma	1	factor	-0.005	-0.013	VBG
dbp	NA	numeric	-0.084	-0.013	VBG
curr_bmi	NA	numeric	-0.211	-0.013	VBG
phtn	0	factor	-0.053	-0.013	VBG
phtn	1	factor	0.053	0.013	VBG
hr	NA	numeric	0.144	0.013	VBG
dbp	NA	numeric	-0.072	-0.013	VBG
asthma	0	factor	0.005	0.013	VBG
asthma	1	factor	-0.005	-0.013	VBG
ckd	0	factor	-0.069	-0.013	VBG
ckd	1	factor	0.069	0.013	VBG
hr	NA	numeric	0.133	0.013	VBG
plt	NA	numeric	-0.023	-0.013	VBG
race_ethnicity	1	factor	0.042	0.013	VBG
serum_hco3	NA	numeric	-0.067	0.013	VBG
asthma	1	factor	-0.005	-0.013	VBG
asthma	0	factor	0.005	0.013	VBG
asthma	1	factor	-0.005	-0.013	VBG
asthma	0	factor	0.005	0.013	VBG
ckd	1	factor	0.069	0.013	VBG
ckd	0	factor	-0.069	-0.013	VBG
race_ethnicity	1	factor	0.042	0.013	VBG
race_ethnicity	1	factor	0.042	0.013	VBG
sex	Male	factor	0.057	0.013	VBG
sex	Female	factor	-0.057	-0.013	VBG
sex	Female	factor	-0.057	-0.013	VBG
sex	Male	factor	0.057	0.013	VBG
sbp	NA	numeric	-0.088	-0.013	VBG
serum_hco3	NA	numeric	-0.071	0.013	VBG
asthma	1	factor	-0.005	-0.013	VBG
asthma	0	factor	0.005	0.013	VBG
curr_bmi	NA	numeric	-0.219	-0.013	VBG
plt	NA	numeric	-0.024	-0.013	VBG
dbp	NA	numeric	-0.068	-0.013	VBG
hr	NA	numeric	0.133	0.013	VBG

Table 20: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
location	0	factor	-0.336	0.013	VBG
serum_hco3	NA	numeric	-0.072	0.013	VBG
sex	Female	factor	-0.057	-0.013	VBG
sex	Male	factor	0.057	0.013	VBG
sex	Male	factor	0.057	0.013	VBG
sex	Female	factor	-0.057	-0.013	VBG
hr	NA	numeric	0.141	0.013	VBG
hr	NA	numeric	0.138	0.013	VBG
dbp	NA	numeric	-0.067	-0.013	VBG
serum_hco3	NA	numeric	-0.073	0.013	VBG
serum_cl	NA	numeric	-0.151	-0.013	VBG
sex	Female	factor	-0.057	-0.013	VBG
sex	Male	factor	0.057	0.013	VBG
sex	Male	factor	0.057	0.013	VBG
sex	Female	factor	-0.057	-0.013	VBG
plt	NA	numeric	-0.025	-0.013	VBG
serum_cr	NA	numeric	0.093	0.013	VBG
phtn	0	factor	-0.053	-0.013	VBG
phtn	1	factor	0.053	0.013	VBG
curr_bmi	NA	numeric	-0.204	-0.013	VBG
phtn	0	factor	-0.053	-0.013	VBG
phtn	1	factor	0.053	0.013	VBG
ckd	1	factor	0.069	0.013	VBG
ckd	0	factor	-0.069	-0.013	VBG
race_ethnicity	1	factor	0.042	0.013	VBG
dm	0	factor	-0.082	0.013	VBG
dm	1	factor	0.082	-0.013	VBG
dbp	NA	numeric	-0.062	-0.013	VBG
hr	NA	numeric	0.131	0.013	VBG
sex	Male	factor	0.057	0.013	VBG
sex	Female	factor	-0.057	-0.013	VBG
dm	0	factor	-0.082	0.013	VBG
dm	1	factor	0.082	-0.013	VBG
asthma	1	factor	-0.005	-0.013	VBG
asthma	0	factor	0.005	0.013	VBG
serum_hco3	NA	numeric	-0.069	0.012	VBG
phtn	0	factor	-0.053	-0.012	VBG
phtn	1	factor	0.053	0.012	VBG
phtn	0	factor	-0.053	-0.012	VBG
phtn	1	factor	0.053	0.012	VBG
ckd	1	factor	0.069	0.012	VBG
ckd	0	factor	-0.069	-0.012	VBG
sbp	NA	numeric	-0.095	-0.012	VBG
plt	NA	numeric	-0.024	-0.012	VBG
serum_hco3	NA	numeric	-0.071	0.012	VBG
phtn	0	factor	-0.053	-0.012	VBG
phtn	1	factor	0.053	0.012	VBG
race_ethnicity	1	factor	0.042	0.012	VBG
wbc	NA	numeric	0.020	0.012	VBG
serum_cl	NA	numeric	-0.153	-0.012	VBG
sex	Male	factor	0.057	0.012	VBG
sex	Female	factor	-0.057	-0.012	VBG
ckd	0	factor	-0.069	-0.012	VBG
ckd	1	factor	0.069	0.012	VBG
serum_hco3	NA	numeric	-0.073	0.012	VBG
curr_bmi	NA	numeric	-0.209	-0.012	VBG
serum_hco3	NA	numeric	-0.069	0.012	VBG
plt	NA	numeric	-0.022	-0.012	VBG
ckd	1	factor	0.069	0.012	VBG
ckd	0	factor	-0.069	-0.012	VBG
ckd	1	factor	0.069	0.012	VBG
ckd	0	factor	-0.069	-0.012	VBG
sex	Male	factor	0.057	0.012	VBG
sex	Female	factor	-0.057	-0.012	VBG

Table 20: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
ckd	0	factor	-0.069	-0.012	VBG
ckd	1	factor	0.069	0.012	VBG
sbp	NA	numeric	-0.083	-0.012	VBG
serum_hco3	NA	numeric	-0.071	0.012	VBG
phtn	1	factor	0.053	0.012	VBG
phtn	0	factor	-0.053	-0.012	VBG
phtn	1	factor	0.053	0.012	VBG
phtn	0	factor	-0.053	-0.012	VBG
plt	NA	numeric	-0.027	-0.012	VBG
phtn	1	factor	0.053	0.012	VBG
phtn	0	factor	-0.053	-0.012	VBG
sbp	NA	numeric	-0.098	-0.012	VBG
plt	NA	numeric	-0.024	-0.012	VBG
ckd	0	factor	-0.069	-0.012	VBG
ckd	1	factor	0.069	0.012	VBG
ckd	0	factor	-0.069	-0.012	VBG
ckd	1	factor	0.069	0.012	VBG
dbp	NA	numeric	-0.068	-0.012	VBG
sex	Female	factor	-0.057	-0.012	VBG
sex	Male	factor	0.057	0.012	VBG
dbp	NA	numeric	-0.061	-0.012	VBG
dbp	NA	numeric	-0.076	-0.012	VBG
curr_bmi	NA	numeric	-0.213	-0.012	VBG
serum_hco3	NA	numeric	-0.074	0.012	VBG
wbc	NA	numeric	0.020	0.012	VBG
dbp	NA	numeric	-0.094	-0.012	VBG
phtn	1	factor	0.053	0.012	VBG
phtn	0	factor	-0.053	-0.012	VBG
sbp	NA	numeric	-0.096	-0.012	VBG
ckd	1	factor	0.069	0.012	VBG
ckd	0	factor	-0.069	-0.012	VBG
phtn	0	factor	-0.053	-0.012	VBG
phtn	1	factor	0.053	0.012	VBG
phtn	0	factor	-0.053	-0.012	VBG
ckd	1	factor	0.069	0.012	VBG
ckd	0	factor	-0.069	-0.012	VBG
race_ethnicity	0	factor	-0.194	0.012	VBG
serum_hco3	NA	numeric	-0.069	0.012	VBG
phtn	0	factor	-0.053	-0.012	VBG
phtn	1	factor	0.053	0.012	VBG
sex	Female	factor	-0.057	-0.012	VBG
sex	Male	factor	0.057	0.012	VBG
race_ethnicity	0	factor	-0.194	0.012	VBG
race_ethnicity	0	factor	-0.194	0.012	VBG
sex	Female	factor	-0.057	-0.012	VBG
sex	Male	factor	0.057	0.012	VBG
race_ethnicity	1	factor	0.042	0.012	VBG
race_ethnicity	1	factor	0.042	0.012	VBG
serum_hco3	NA	numeric	-0.071	0.012	VBG
ckd	0	factor	-0.069	-0.012	VBG
ckd	1	factor	0.069	0.012	VBG
race_ethnicity	1	factor	0.042	0.012	VBG
phtn	0	factor	-0.053	-0.012	VBG
phtn	1	factor	0.053	0.012	VBG
osa	1	factor	-0.025	-0.012	VBG
osa	0	factor	0.025	0.012	VBG
wbc	NA	numeric	0.020	0.012	VBG
curr_bmi	NA	numeric	-0.197	-0.012	VBG
sbp	NA	numeric	-0.092	-0.012	VBG
phtn	0	factor	-0.053	-0.012	VBG
phtn	1	factor	0.053	0.012	VBG
race_ethnicity	1	factor	0.042	0.012	VBG

Table 20: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
hr	NA	numeric	0.123	0.012	VBG
hr	NA	numeric	0.134	0.012	VBG
ckd	1	factor	0.069	0.012	VBG
ckd	0	factor	-0.069	-0.012	VBG
wbc	NA	numeric	0.018	0.012	VBG
sbp	NA	numeric	-0.104	-0.012	VBG
phtn	1	factor	0.053	0.012	VBG
phtn	0	factor	-0.053	-0.012	VBG
race_ethnicity	5	factor	-0.018	-0.012	VBG
phtn	1	factor	0.053	0.012	VBG
phtn	0	factor	-0.053	-0.012	VBG
sex	Male	factor	0.057	0.012	VBG
sex	Female	factor	-0.057	-0.012	VBG
wbc	NA	numeric	0.022	0.012	VBG
ckd	0	factor	-0.069	-0.012	VBG
ckd	1	factor	0.069	0.012	VBG
ckd	0	factor	-0.069	-0.012	VBG
ckd	1	factor	0.069	0.012	VBG
asthma	0	factor	0.005	0.012	VBG
asthma	1	factor	-0.005	-0.012	VBG
phtn	1	factor	0.053	0.012	VBG
phtn	0	factor	-0.053	-0.012	VBG
phtn	1	factor	0.053	0.012	VBG
phtn	0	factor	-0.053	-0.012	VBG
race_ethnicity	5	factor	-0.018	-0.012	VBG
serum_hco3	NA	numeric	-0.071	0.012	VBG
ckd	1	factor	0.069	0.012	VBG
ckd	0	factor	-0.069	-0.012	VBG
serum_hco3	NA	numeric	-0.068	0.012	VBG
hr	NA	numeric	0.136	0.012	VBG
sbp	NA	numeric	-0.095	-0.012	VBG
sex	Male	factor	0.057	0.012	VBG
sex	Female	factor	-0.057	-0.012	VBG
curr_bmi	NA	numeric	-0.210	-0.012	VBG
wbc	NA	numeric	0.015	0.012	VBG
race_ethnicity	1	factor	0.042	0.012	VBG
serum_cr	NA	numeric	0.095	0.012	VBG
dbp	NA	numeric	-0.077	-0.012	VBG
sbp	NA	numeric	-0.090	-0.012	VBG
phtn	1	factor	0.053	0.012	VBG
phtn	0	factor	-0.053	-0.012	VBG
dbp	NA	numeric	-0.067	-0.012	VBG
asthma	0	factor	0.005	0.012	VBG
asthma	1	factor	-0.005	-0.012	VBG
sex	Male	factor	0.057	0.012	VBG
sex	Female	factor	-0.057	-0.012	VBG
hr	NA	numeric	0.129	0.012	VBG
location	0	factor	-0.336	0.012	VBG
race_ethnicity	3	factor	0.029	0.012	VBG
sbp	NA	numeric	-0.082	-0.012	VBG
race_ethnicity	3	factor	0.029	0.012	VBG
ckd	0	factor	-0.069	-0.012	VBG
ckd	1	factor	0.069	0.012	VBG
sbp	NA	numeric	-0.099	-0.012	VBG
serum_hco3	NA	numeric	-0.069	0.012	VBG
serum_hco3	NA	numeric	-0.073	0.012	VBG
serum_hco3	NA	numeric	-0.073	0.012	VBG
ckd	0	factor	-0.069	-0.012	VBG
ckd	1	factor	0.069	0.012	VBG
osa	0	factor	0.025	0.012	VBG
osa	1	factor	-0.025	-0.012	VBG
race_ethnicity	1	factor	0.042	0.011	VBG
race_ethnicity	3	factor	0.029	0.011	VBG

Table 20: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
race_ethnicity	0	factor	-0.194	0.011	VBG
race_ethnicity	1	factor	0.042	0.011	VBG
sex	Male	factor	0.057	0.011	VBG
sex	Female	factor	-0.057	-0.011	VBG
sbp	NA	numeric	-0.101	-0.011	VBG
plt	NA	numeric	-0.027	-0.011	VBG
ckd	1	factor	0.069	0.011	VBG
ckd	0	factor	-0.069	-0.011	VBG
serum_hco3	NA	numeric	-0.072	0.011	VBG
phtn	1	factor	0.053	0.011	VBG
phtn	0	factor	-0.053	-0.011	VBG
sex	Female	factor	-0.057	-0.011	VBG
sex	Male	factor	0.057	0.011	VBG
race_ethnicity	5	factor	-0.018	-0.011	VBG
phtn	1	factor	0.053	0.011	VBG
phtn	0	factor	-0.053	-0.011	VBG
temp_new	NA	numeric	0.000	0.011	VBG
curr_bmi	NA	numeric	-0.223	-0.011	VBG
ckd	1	factor	0.069	0.011	VBG
ckd	0	factor	-0.069	-0.011	VBG
phtn	0	factor	-0.053	-0.011	VBG
phtn	1	factor	0.053	0.011	VBG
location	0	factor	-0.336	0.011	VBG
ckd	1	factor	0.069	0.011	VBG
ckd	0	factor	-0.069	-0.011	VBG
phtn	0	factor	-0.053	-0.011	VBG
phtn	1	factor	0.053	0.011	VBG
sbp	NA	numeric	-0.089	-0.011	VBG
race_ethnicity	1	factor	0.042	0.011	VBG
wbc	NA	numeric	0.020	0.011	VBG
ckd	0	factor	-0.069	-0.011	VBG
ckd	1	factor	0.069	0.011	VBG
serum_hco3	NA	numeric	-0.072	0.011	VBG
sbp	NA	numeric	-0.094	-0.011	VBG
dbp	NA	numeric	-0.073	-0.011	VBG
dbp	NA	numeric	-0.076	-0.011	VBG
serum_hco3	NA	numeric	-0.068	0.011	VBG
phtn	1	factor	0.053	0.011	VBG
phtn	0	factor	-0.053	-0.011	VBG
ckd	0	factor	-0.069	-0.011	VBG
ckd	1	factor	0.069	0.011	VBG
wbc	NA	numeric	0.018	0.011	VBG
wbc	NA	numeric	0.019	0.011	VBG
race_ethnicity	1	factor	0.042	0.011	VBG
serum_hco3	NA	numeric	-0.072	0.011	VBG
race_ethnicity	5	factor	-0.018	-0.011	VBG
wbc	NA	numeric	0.017	0.011	VBG
curr_bmi	NA	numeric	-0.200	-0.011	VBG
ckd	0	factor	-0.069	-0.011	VBG
ckd	1	factor	0.069	0.011	VBG
race_ethnicity	1	factor	0.042	0.011	VBG
dbp	NA	numeric	-0.067	-0.011	VBG
curr_bmi	NA	numeric	-0.216	-0.011	VBG
race_ethnicity	5	factor	-0.018	-0.011	VBG
sex	Male	factor	0.057	0.011	VBG
sex	Female	factor	-0.057	-0.011	VBG
sex	Female	factor	-0.057	-0.011	VBG
sex	Male	factor	0.057	0.011	VBG
race_ethnicity	5	factor	-0.018	-0.011	VBG
sbp	NA	numeric	-0.089	-0.011	VBG
dbp	NA	numeric	-0.073	-0.011	VBG
race_ethnicity	1	factor	0.042	0.011	VBG
serum_hco3	NA	numeric	-0.070	0.011	VBG
plt	NA	numeric	-0.027	-0.011	VBG

Table 20: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
sex	Male	factor	0.057	0.011	VBG
sex	Female	factor	-0.057	-0.011	VBG
ckd	0	factor	-0.069	-0.011	VBG
ckd	1	factor	0.069	0.011	VBG
hr	NA	numeric	0.134	0.011	VBG
phtn	0	factor	-0.053	-0.011	VBG
phtn	1	factor	0.053	0.011	VBG
ckd	0	factor	-0.069	-0.011	VBG
ckd	1	factor	0.069	0.011	VBG
phtn	0	factor	-0.053	-0.011	VBG
phtn	1	factor	0.053	0.011	VBG
race_ethnicity	1	factor	0.042	0.011	VBG
race_ethnicity	1	factor	0.042	0.011	VBG
race_ethnicity	3	factor	0.029	0.011	VBG
hr	NA	numeric	0.136	0.011	VBG
ckd	0	factor	-0.069	-0.011	VBG
ckd	1	factor	0.069	0.011	VBG
sex	Male	factor	0.057	0.011	VBG
sex	Female	factor	-0.057	-0.011	VBG
race_ethnicity	1	factor	0.042	0.011	VBG
race_ethnicity	5	factor	-0.018	-0.011	VBG
serum_hco3	NA	numeric	-0.072	0.011	VBG
phtn	1	factor	0.053	0.011	VBG
phtn	0	factor	-0.053	-0.011	VBG
serum_hco3	NA	numeric	-0.071	0.011	VBG
serum_hco3	NA	numeric	-0.071	0.011	VBG
sex	Female	factor	-0.057	-0.011	VBG
sex	Male	factor	0.057	0.011	VBG
ckd	0	factor	-0.069	-0.011	VBG
ckd	1	factor	0.069	0.011	VBG
race_ethnicity	1	factor	0.042	0.011	VBG
race_ethnicity	5	factor	-0.018	-0.011	VBG
temp_new	NA	numeric	-0.008	0.011	VBG
sex	Male	factor	0.057	0.011	VBG
sex	Female	factor	-0.057	-0.011	VBG
sbp	NA	numeric	-0.082	-0.011	VBG
phtn	1	factor	0.053	0.011	VBG
phtn	0	factor	-0.053	-0.011	VBG
sbp	NA	numeric	-0.082	-0.011	VBG
sex	Female	factor	-0.057	-0.011	VBG
sex	Male	factor	0.057	0.011	VBG
curr_bmi	NA	numeric	-0.212	-0.011	VBG
sbp	NA	numeric	-0.089	-0.011	VBG
race_ethnicity	1	factor	0.042	0.011	VBG
race_ethnicity	0	factor	-0.194	0.011	VBG
dbp	NA	numeric	-0.071	-0.011	VBG
serum_hco3	NA	numeric	-0.069	0.011	VBG
ckd	0	factor	-0.069	-0.011	VBG
ckd	1	factor	0.069	0.011	VBG
ckd	1	factor	0.069	0.011	VBG
ckd	0	factor	-0.069	-0.011	VBG
plt	NA	numeric	-0.023	-0.011	VBG
sbp	NA	numeric	-0.089	-0.010	VBG
chf	0	factor	-0.037	-0.010	VBG
chf	1	factor	0.037	0.010	VBG
chf	1	factor	0.037	0.010	VBG
chf	0	factor	-0.037	-0.010	VBG
race_ethnicity	1	factor	0.042	0.010	VBG
phtn	1	factor	0.053	0.010	VBG
phtn	0	factor	-0.053	-0.010	VBG
race_ethnicity	5	factor	-0.018	-0.010	VBG
race_ethnicity	1	factor	0.042	0.010	VBG
wbc	NA	numeric	0.013	0.010	VBG

Table 20: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
sex	Female	factor	-0.057	-0.010	VBG
sex	Male	factor	0.057	0.010	VBG
serum_hco3	NA	numeric	-0.071	0.010	VBG
ckd	0	factor	-0.069	-0.010	VBG
ckd	1	factor	0.069	0.010	VBG
sex	Female	factor	-0.057	-0.010	VBG
sex	Male	factor	0.057	0.010	VBG
race_ethnicity	5	factor	-0.018	-0.010	VBG
sex	Female	factor	-0.057	-0.010	VBG
sex	Male	factor	0.057	0.010	VBG
race_ethnicity	5	factor	-0.018	-0.010	VBG
sex	Male	factor	0.057	0.010	VBG
sex	Female	factor	-0.057	-0.010	VBG
sex	Female	factor	-0.057	-0.010	VBG
sex	Male	factor	0.057	0.010	VBG
sbp	NA	numeric	-0.092	-0.010	VBG
ckd	1	factor	0.069	0.010	VBG
ckd	0	factor	-0.069	-0.010	VBG
race_ethnicity	1	factor	0.042	0.010	VBG
race_ethnicity	1	factor	0.042	0.010	VBG
plt	NA	numeric	-0.024	-0.010	VBG
wbc	NA	numeric	0.010	0.010	VBG
phtn	0	factor	-0.053	-0.010	VBG
phtn	1	factor	0.053	0.010	VBG
race_ethnicity	5	factor	-0.018	-0.010	VBG
race_ethnicity	1	factor	0.042	0.010	VBG
race_ethnicity	3	factor	0.029	0.010	VBG
serum_phos	NA	numeric	0.074	0.010	VBG
race_ethnicity	0	factor	-0.194	0.010	VBG
race_ethnicity	1	factor	0.042	0.010	VBG
serum_hco3	NA	numeric	-0.071	0.010	VBG
serum_cr	NA	numeric	0.090	0.010	VBG
hr	NA	numeric	0.129	0.010	VBG
serum_hco3	NA	numeric	-0.072	0.010	VBG
race_ethnicity	0	factor	-0.194	0.010	VBG
serum_hco3	NA	numeric	-0.072	0.010	VBG
serum_hco3	NA	numeric	-0.073	0.010	VBG
sbp	NA	numeric	-0.087	-0.010	VBG
race_ethnicity	1	factor	0.042	0.010	VBG
sbp	NA	numeric	-0.089	-0.010	VBG
ckd	0	factor	-0.069	-0.010	VBG
ckd	1	factor	0.069	0.010	VBG
sex	Male	factor	0.057	0.010	VBG
sex	Female	factor	-0.057	-0.010	VBG
sbp	NA	numeric	-0.091	-0.010	VBG
race_ethnicity	5	factor	-0.018	-0.010	VBG
temp_new	NA	numeric	-0.010	0.010	VBG
plt	NA	numeric	-0.029	-0.010	VBG
serum_hco3	NA	numeric	-0.072	0.010	VBG
ckd	0	factor	-0.069	-0.010	VBG
ckd	1	factor	0.069	0.010	VBG
race_ethnicity	1	factor	0.042	0.010	VBG
dbp	NA	numeric	-0.060	-0.010	VBG
phtn	0	factor	-0.053	-0.010	VBG
phtn	1	factor	0.053	0.010	VBG
sbp	NA	numeric	-0.099	-0.010	VBG
wbc	NA	numeric	0.018	0.010	VBG
phtn	1	factor	0.053	0.010	VBG
phtn	0	factor	-0.053	-0.010	VBG
wbc	NA	numeric	0.018	0.010	VBG
wbc	NA	numeric	0.006	0.010	VBG
curr_bmi	NA	numeric	-0.223	-0.010	VBG
curr_bmi	NA	numeric	-0.219	-0.010	VBG

Table 20: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
sex	Male	factor	0.057	0.010	VBG
sex	Female	factor	-0.057	-0.010	VBG
curr_bmi	NA	numeric	-0.224	-0.010	VBG
phtn	0	factor	-0.053	-0.010	VBG
phtn	1	factor	0.053	0.010	VBG
dbp	NA	numeric	-0.076	-0.010	VBG
phtn	0	factor	-0.053	-0.010	VBG
phtn	1	factor	0.053	0.010	VBG
plt	NA	numeric	-0.026	-0.010	VBG
race_ethnicity	5	factor	-0.018	-0.010	VBG
phtn	0	factor	-0.053	-0.010	VBG
phtn	1	factor	0.053	0.010	VBG
race_ethnicity	1	factor	0.042	0.010	VBG
serum_hco3	NA	numeric	-0.067	0.010	VBG
phtn	0	factor	-0.053	-0.010	VBG
phtn	1	factor	0.053	0.010	VBG
sex	Female	factor	-0.057	-0.010	VBG
sex	Male	factor	0.057	0.010	VBG
race_ethnicity	1	factor	0.042	0.010	VBG
copd	0	factor	-0.008	-0.010	VBG
copd	1	factor	0.008	0.010	VBG
serum_hco3	NA	numeric	-0.072	0.010	VBG
dm	1	factor	0.082	-0.010	VBG
dm	0	factor	-0.082	0.010	VBG
sex	Female	factor	-0.057	-0.010	VBG
sex	Male	factor	0.057	0.010	VBG
phtn	0	factor	-0.053	-0.010	VBG
phtn	1	factor	0.053	0.010	VBG
race_ethnicity	1	factor	0.042	0.010	VBG
serum_hco3	NA	numeric	-0.072	0.010	VBG
race_ethnicity	1	factor	0.042	0.010	VBG
sex	Female	factor	-0.057	-0.010	VBG
sex	Male	factor	0.057	0.010	VBG
race_ethnicity	1	factor	0.042	0.010	VBG
sbp	NA	numeric	-0.100	-0.010	VBG
chf	0	factor	-0.037	-0.010	VBG
chf	1	factor	0.037	0.010	VBG
serum_hco3	NA	numeric	-0.069	0.010	VBG
race_ethnicity	0	factor	-0.194	0.010	VBG
phtn	1	factor	0.053	0.010	VBG
phtn	0	factor	-0.053	-0.010	VBG
chf	0	factor	-0.037	-0.010	VBG
chf	1	factor	0.037	0.010	VBG
chf	0	factor	-0.037	-0.010	VBG
chf	1	factor	0.037	0.010	VBG
curr_bmi	NA	numeric	-0.202	-0.010	VBG
serum_hco3	NA	numeric	-0.072	0.010	VBG
phtn	0	factor	-0.053	-0.010	VBG
phtn	1	factor	0.053	0.010	VBG
ckd	1	factor	0.069	0.010	VBG
ckd	0	factor	-0.069	-0.010	VBG
plt	NA	numeric	-0.021	-0.009	VBG
sbp	NA	numeric	-0.084	-0.009	VBG
phtn	1	factor	0.053	0.009	VBG
phtn	0	factor	-0.053	-0.009	VBG
sex	Male	factor	0.057	0.009	VBG
sex	Female	factor	-0.057	-0.009	VBG
race_ethnicity	2	factor	0.021	0.009	VBG
sbp	NA	numeric	-0.104	-0.009	VBG
race_ethnicity	5	factor	-0.018	-0.009	VBG
race_ethnicity	1	factor	0.042	0.009	VBG
race_ethnicity	1	factor	0.042	0.009	VBG
race_ethnicity	5	factor	-0.018	-0.009	VBG
race_ethnicity	1	factor	0.042	0.009	VBG

Table 20: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
curr_bmi	NA	numeric	-0.208	-0.009	VBG
hr	NA	numeric	0.124	0.009	VBG
sex	Female	factor	-0.057	-0.009	VBG
sex	Male	factor	0.057	0.009	VBG
race_ethnicity	5	factor	-0.018	-0.009	VBG
phtn	1	factor	0.053	0.009	VBG
phtn	0	factor	-0.053	-0.009	VBG
dbp	NA	numeric	-0.075	-0.009	VBG
race_ethnicity	5	factor	-0.018	-0.009	VBG
ckd	0	factor	-0.069	-0.009	VBG
ckd	1	factor	0.069	0.009	VBG
ckd	0	factor	-0.069	-0.009	VBG
curr_bmi	NA	numeric	-0.221	-0.009	VBG
phtn	0	factor	-0.053	-0.009	VBG
phtn	1	factor	0.053	0.009	VBG
race_ethnicity	5	factor	-0.018	-0.009	VBG
curr_bmi	NA	numeric	-0.210	-0.009	VBG
sex	Female	factor	-0.057	-0.009	VBG
sex	Male	factor	0.057	0.009	VBG
race_ethnicity	0	factor	-0.194	0.009	VBG
dbp	NA	numeric	-0.063	-0.009	VBG
race_ethnicity	1	factor	0.042	0.009	VBG
sbp	NA	numeric	-0.086	-0.009	VBG
race_ethnicity	5	factor	-0.018	-0.009	VBG
chf	0	factor	-0.037	-0.009	VBG
chf	1	factor	0.037	0.009	VBG
phtn	0	factor	-0.053	-0.009	VBG
phtn	1	factor	0.053	0.009	VBG
race_ethnicity	1	factor	0.042	0.009	VBG
race_ethnicity	0	factor	-0.194	0.009	VBG
wbc	NA	numeric	0.011	0.009	VBG
asthma	1	factor	-0.005	-0.009	VBG
asthma	0	factor	0.005	0.009	VBG
race_ethnicity	3	factor	0.029	0.009	VBG
sbp	NA	numeric	-0.095	-0.009	VBG
sbp	NA	numeric	-0.104	-0.009	VBG
chf	0	factor	-0.037	-0.009	VBG
chf	1	factor	0.037	0.009	VBG
race_ethnicity	0	factor	-0.194	0.009	VBG
sex	Female	factor	-0.057	-0.009	VBG
sex	Male	factor	0.057	0.009	VBG
serum_hco3	NA	numeric	-0.071	0.009	VBG
race_ethnicity	5	factor	-0.018	-0.009	VBG
race_ethnicity	3	factor	0.029	0.009	VBG
race_ethnicity	5	factor	-0.018	-0.009	VBG
race_ethnicity	0	factor	-0.194	0.009	VBG
race_ethnicity	1	factor	0.042	0.009	VBG
race_ethnicity	1	factor	0.042	0.009	VBG
race_ethnicity	1	factor	0.042	0.009	VBG
chf	1	factor	0.037	0.009	VBG
chf	0	factor	-0.037	-0.009	VBG
serum_hco3	NA	numeric	-0.072	0.009	VBG
sbp	NA	numeric	-0.094	-0.009	VBG
temp_new	NA	numeric	0.005	0.009	VBG
phtn	0	factor	-0.053	-0.009	VBG
phtn	1	factor	0.053	0.009	VBG
ckd	0	factor	-0.069	-0.009	VBG
ckd	1	factor	0.069	0.009	VBG
sex	Female	factor	-0.057	-0.009	VBG
sex	Male	factor	0.057	0.009	VBG
phtn	1	factor	0.053	0.009	VBG
phtn	0	factor	-0.053	-0.009	VBG

Table 20: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
race_ethnicity	0	factor	-0.194	0.009	VBG
dbp	NA	numeric	-0.075	-0.009	VBG
race_ethnicity	1	factor	0.042	0.009	VBG
sex	Female	factor	-0.057	-0.009	VBG
sex	Male	factor	0.057	0.009	VBG
curr_bmi	NA	numeric	-0.208	-0.009	VBG
race_ethnicity	1	factor	0.042	0.009	VBG
race_ethnicity	1	factor	0.042	0.009	VBG
serum_hco3	NA	numeric	-0.070	0.009	VBG
dbp	NA	numeric	-0.080	-0.009	VBG
phtn	0	factor	-0.053	-0.009	VBG
phtn	1	factor	0.053	0.009	VBG
plt	NA	numeric	-0.023	-0.009	VBG
plt	NA	numeric	-0.030	-0.009	VBG
osa	1	factor	-0.025	-0.009	VBG
osa	0	factor	0.025	0.009	VBG
ckd	1	factor	0.069	0.009	VBG
ckd	0	factor	-0.069	-0.009	VBG
sex	Female	factor	-0.057	-0.009	VBG
sex	Male	factor	0.057	0.009	VBG
race_ethnicity	0	factor	-0.194	0.009	VBG
race_ethnicity	5	factor	-0.018	-0.009	VBG
race_ethnicity	1	factor	0.042	0.008	VBG
sex	Female	factor	-0.057	-0.008	VBG
sex	Male	factor	0.057	0.008	VBG
sbp	NA	numeric	-0.087	-0.008	VBG
phtn	0	factor	-0.053	-0.008	VBG
phtn	1	factor	0.053	0.008	VBG
race_ethnicity	5	factor	-0.018	-0.008	VBG
copd	1	factor	0.008	0.008	VBG
copd	0	factor	-0.008	-0.008	VBG
phtn	1	factor	0.053	0.008	VBG
phtn	0	factor	-0.053	-0.008	VBG
race_ethnicity	3	factor	0.029	0.008	VBG
copd	1	factor	0.008	0.008	VBG
copd	0	factor	-0.008	-0.008	VBG
dm	1	factor	0.082	-0.008	VBG
dm	0	factor	-0.082	0.008	VBG
race_ethnicity	1	factor	0.042	0.008	VBG
race_ethnicity	3	factor	0.029	0.008	VBG
sex	Female	factor	-0.057	-0.008	VBG
sex	Male	factor	0.057	0.008	VBG
sbp	NA	numeric	-0.099	-0.008	VBG
race_ethnicity	0	factor	-0.194	0.008	VBG
curr_bmi	NA	numeric	-0.219	-0.008	VBG
copd	0	factor	-0.008	-0.008	VBG
copd	1	factor	0.008	0.008	VBG
race_ethnicity	3	factor	0.029	0.008	VBG
phtn	1	factor	0.053	0.008	VBG
phtn	0	factor	-0.053	-0.008	VBG
serum_hco3	NA	numeric	-0.070	0.008	VBG
sbp	NA	numeric	-0.098	-0.008	VBG
sex	Female	factor	-0.057	-0.008	VBG
sex	Male	factor	0.057	0.008	VBG
serum_k	NA	numeric	0.041	0.008	VBG
osa	0	factor	0.025	0.008	VBG
osa	1	factor	-0.025	-0.008	VBG
serum_phos	NA	numeric	0.066	0.008	VBG
race_ethnicity	5	factor	-0.018	-0.008	VBG
race_ethnicity	1	factor	0.042	0.008	VBG
dm	1	factor	0.082	-0.008	VBG
dm	0	factor	-0.082	0.008	VBG
phtn	0	factor	-0.053	-0.008	VBG

Table 20: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
phtn	1	factor	0.053	0.008	VBG
race_ethnicity	1	factor	0.042	0.008	VBG
osa	1	factor	-0.025	-0.008	VBG
osa	0	factor	0.025	0.008	VBG
race_ethnicity	5	factor	-0.018	-0.008	VBG
race_ethnicity	0	factor	-0.194	0.008	VBG
race_ethnicity	2	factor	0.021	-0.008	VBG
plt	NA	numeric	-0.023	-0.008	VBG
dbp	NA	numeric	-0.068	-0.008	VBG
wbc	NA	numeric	0.018	0.008	VBG
race_ethnicity	3	factor	0.029	0.008	VBG
curr_bmi	NA	numeric	-0.204	-0.008	VBG
osa	1	factor	-0.025	-0.008	VBG
osa	0	factor	0.025	0.008	VBG
race_ethnicity	0	factor	-0.194	0.008	VBG
race_ethnicity	5	factor	-0.018	-0.008	VBG
serum_k	NA	numeric	0.041	0.008	VBG
ckd	1	factor	0.069	0.008	VBG
ckd	0	factor	-0.069	-0.008	VBG
race_ethnicity	0	factor	-0.194	0.008	VBG
race_ethnicity	5	factor	-0.018	-0.008	VBG
sbp	NA	numeric	-0.094	-0.008	VBG
race_ethnicity	5	factor	-0.018	-0.008	VBG
race_ethnicity	1	factor	0.042	0.008	VBG
serum_hco3	NA	numeric	-0.070	0.008	VBG
race_ethnicity	1	factor	0.042	0.008	VBG
copd	0	factor	-0.008	-0.008	VBG
copd	1	factor	0.008	0.008	VBG
sbp	NA	numeric	-0.096	-0.008	VBG
ckd	0	factor	-0.069	-0.008	VBG
ckd	1	factor	0.069	0.008	VBG
chf	0	factor	-0.037	-0.008	VBG
chf	1	factor	0.037	0.008	VBG
phtn	0	factor	-0.053	-0.008	VBG
phtn	1	factor	0.053	0.008	VBG
race_ethnicity	5	factor	-0.018	-0.008	VBG
chf	0	factor	-0.037	-0.008	VBG
chf	1	factor	0.037	0.008	VBG
hr	NA	numeric	0.132	0.008	VBG
sodium	NA	numeric	-0.104	0.008	VBG
sex	Male	factor	0.057	0.008	VBG
sex	Female	factor	-0.057	-0.008	VBG
phtn	0	factor	-0.053	-0.008	VBG
phtn	1	factor	0.053	0.008	VBG
race_ethnicity	3	factor	0.029	0.008	VBG
dm	1	factor	0.082	-0.008	VBG
dm	0	factor	-0.082	0.008	VBG
race_ethnicity	3	factor	0.029	0.008	VBG
race_ethnicity	3	factor	0.029	0.008	VBG
serum_k	NA	numeric	0.044	0.008	VBG
race_ethnicity	3	factor	0.029	0.008	VBG
serum_hco3	NA	numeric	-0.072	0.008	VBG
serum_k	NA	numeric	0.046	0.008	VBG
race_ethnicity	0	factor	-0.194	0.008	VBG
race_ethnicity	5	factor	-0.018	-0.008	VBG
race_ethnicity	5	factor	-0.018	-0.008	VBG
chf	0	factor	-0.037	-0.008	VBG
chf	1	factor	0.037	0.008	VBG
copd	0	factor	-0.008	-0.008	VBG
copd	1	factor	0.008	0.008	VBG
sbp	NA	numeric	-0.096	-0.008	VBG
race_ethnicity	5	factor	-0.018	-0.008	VBG
location	1	factor	0.399	0.008	VBG
sex	Female	factor	-0.057	-0.008	VBG

Table 20: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
sex	Male	factor	0.057	0.008	VBG
location	2	factor	0.066	0.008	VBG
race_ethnicity	1	factor	0.042	0.007	VBG
location	2	factor	0.066	0.007	VBG
chf	0	factor	-0.037	-0.007	VBG
chf	1	factor	0.037	0.007	VBG
serum_k	NA	numeric	0.045	0.007	VBG
race_ethnicity	2	factor	0.021	-0.007	VBG
temp_new	NA	numeric	-0.010	0.007	VBG
race_ethnicity	0	factor	-0.194	0.007	VBG
race_ethnicity	3	factor	0.029	0.007	VBG
phtn	0	factor	-0.053	-0.007	VBG
phtn	1	factor	0.053	0.007	VBG
chf	1	factor	0.037	0.007	VBG
chf	0	factor	-0.037	-0.007	VBG
phtn	0	factor	-0.053	-0.007	VBG
phtn	1	factor	0.053	0.007	VBG
curr_bmi	NA	numeric	-0.207	-0.007	VBG
phtn	1	factor	0.053	0.007	VBG
phtn	0	factor	-0.053	-0.007	VBG
dbp	NA	numeric	-0.080	-0.007	VBG
dm	0	factor	-0.082	0.007	VBG
dm	1	factor	0.082	-0.007	VBG
race_ethnicity	5	factor	-0.018	-0.007	VBG
race_ethnicity	5	factor	-0.018	-0.007	VBG
chf	0	factor	-0.037	-0.007	VBG
chf	1	factor	0.037	0.007	VBG
race_ethnicity	1	factor	0.042	0.007	VBG
dm	1	factor	0.082	-0.007	VBG
dm	0	factor	-0.082	0.007	VBG
race_ethnicity	5	factor	-0.018	-0.007	VBG
hr	NA	numeric	0.137	0.007	VBG
dm	1	factor	0.082	-0.007	VBG
dm	0	factor	-0.082	0.007	VBG
dm	0	factor	-0.082	0.007	VBG
dm	1	factor	0.082	-0.007	VBG
race_ethnicity	1	factor	0.042	0.007	VBG
sodium	NA	numeric	-0.103	0.007	VBG
race_ethnicity	0	factor	-0.194	0.007	VBG
hr	NA	numeric	0.134	0.007	VBG
osa	1	factor	-0.025	-0.007	VBG
osa	0	factor	0.025	0.007	VBG
race_ethnicity	0	factor	-0.194	0.007	VBG
chf	1	factor	0.037	0.007	VBG
chf	0	factor	-0.037	-0.007	VBG
race_ethnicity	3	factor	0.029	0.007	VBG
serum_hco3	NA	numeric	-0.070	0.007	VBG
sodium	NA	numeric	-0.108	-0.007	VBG
sbp	NA	numeric	-0.094	-0.007	VBG
location	1	factor	0.399	0.007	VBG
sbp	NA	numeric	-0.091	-0.007	VBG
osa	0	factor	0.025	0.007	VBG
osa	1	factor	-0.025	-0.007	VBG
race_ethnicity	0	factor	-0.194	0.007	VBG
serum_k	NA	numeric	0.043	0.007	VBG
race_ethnicity	5	factor	-0.018	-0.007	VBG
race_ethnicity	5	factor	-0.018	-0.007	VBG
location	1	factor	0.399	0.007	VBG
location	2	factor	0.066	0.007	VBG
phtn	0	factor	-0.053	-0.007	VBG
phtn	1	factor	0.053	0.007	VBG
copd	0	factor	-0.008	-0.007	VBG
copd	1	factor	0.008	0.007	VBG

Table 20: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
race_ethnicity	0	factor	-0.194	0.007	VBG
race_ethnicity	0	factor	-0.194	0.007	VBG
copd	0	factor	-0.008	-0.007	VBG
copd	1	factor	0.008	0.007	VBG
race_ethnicity	3	factor	0.029	0.007	VBG
chf	0	factor	-0.037	-0.007	VBG
chf	1	factor	0.037	0.007	VBG
race_ethnicity	5	factor	-0.018	-0.007	VBG
copd	0	factor	-0.008	-0.007	VBG
copd	1	factor	0.008	0.007	VBG
race_ethnicity	3	factor	0.029	0.007	VBG
race_ethnicity	5	factor	-0.018	-0.007	VBG
copd	1	factor	0.008	0.007	VBG
copd	0	factor	-0.008	-0.007	VBG
dbp	NA	numeric	-0.063	-0.007	VBG
race_ethnicity	5	factor	-0.018	-0.007	VBG
race_ethnicity	0	factor	-0.194	0.007	VBG
location	1	factor	0.399	0.007	VBG
race_ethnicity	5	factor	-0.018	-0.007	VBG
race_ethnicity	0	factor	-0.194	0.007	VBG
location	1	factor	0.399	0.007	VBG
chf	1	factor	0.037	0.007	VBG
chf	0	factor	-0.037	-0.007	VBG
race_ethnicity	0	factor	-0.194	-0.007	VBG
location	1	factor	0.399	0.007	VBG
race_ethnicity	5	factor	-0.018	-0.007	VBG
serum_hco3	NA	numeric	-0.070	0.007	VBG
location	0	factor	-0.336	0.007	VBG
sbp	NA	numeric	-0.093	-0.007	VBG
race_ethnicity	3	factor	0.029	0.007	VBG
chf	1	factor	0.037	0.007	VBG
chf	0	factor	-0.037	-0.007	VBG
location	2	factor	0.066	0.007	VBG
copd	1	factor	0.008	0.007	VBG
copd	0	factor	-0.008	-0.007	VBG
race_ethnicity	0	factor	-0.194	0.007	VBG
hr	NA	numeric	0.138	0.007	VBG
osa	1	factor	-0.025	-0.006	VBG
osa	0	factor	0.025	0.006	VBG
sodium	NA	numeric	-0.103	0.006	VBG
serum_hco3	NA	numeric	-0.074	0.006	VBG
curr_bmi	NA	numeric	-0.191	-0.006	VBG
race_ethnicity	1	factor	0.042	0.006	VBG
race_ethnicity	0	factor	-0.194	0.006	VBG
sbp	NA	numeric	-0.082	-0.006	VBG
race_ethnicity	5	factor	-0.018	-0.006	VBG
race_ethnicity	2	factor	0.021	-0.006	VBG
ckd	1	factor	0.069	0.006	VBG
ckd	0	factor	-0.069	-0.006	VBG
ckd	1	factor	0.069	0.006	VBG
ckd	0	factor	-0.069	-0.006	VBG
race_ethnicity	0	factor	-0.194	0.006	VBG
serum_hco3	NA	numeric	-0.071	0.006	VBG
race_ethnicity	5	factor	-0.018	-0.006	VBG
race_ethnicity	1	factor	0.042	0.006	VBG
copd	1	factor	0.008	0.006	VBG
copd	0	factor	-0.008	-0.006	VBG
chf	1	factor	0.037	0.006	VBG
chf	0	factor	-0.037	-0.006	VBG
race_ethnicity	5	factor	-0.018	-0.006	VBG
race_ethnicity	3	factor	0.029	0.006	VBG
chf	1	factor	0.037	0.006	VBG
chf	0	factor	-0.037	-0.006	VBG

Table 20: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
race_ethnicity	5	factor	-0.018	-0.006	VBG
serum_k	NA	numeric	0.040	0.006	VBG
race_ethnicity	5	factor	-0.018	-0.006	VBG
race_ethnicity	5	factor	-0.018	-0.006	VBG
curr_bmi	NA	numeric	-0.210	-0.006	VBG
race_ethnicity	0	factor	-0.194	0.006	VBG
sbp	NA	numeric	-0.103	-0.006	VBG
race_ethnicity	3	factor	0.029	0.006	VBG
race_ethnicity	3	factor	0.029	0.006	VBG
sodium	NA	numeric	-0.106	-0.006	VBG
race_ethnicity	5	factor	-0.018	-0.006	VBG
phtn	0	factor	-0.053	-0.006	VBG
phtn	1	factor	0.053	0.006	VBG
race_ethnicity	2	factor	0.021	-0.006	VBG
serum_k	NA	numeric	0.039	-0.006	VBG
dm	1	factor	0.082	-0.006	VBG
dm	0	factor	-0.082	0.006	VBG
location	2	factor	0.066	0.006	VBG
dbp	NA	numeric	-0.079	-0.006	VBG
sbp	NA	numeric	-0.096	-0.006	VBG
osa	1	factor	-0.025	-0.006	VBG
osa	0	factor	0.025	0.006	VBG
location	1	factor	0.399	0.006	VBG
serum_k	NA	numeric	0.040	0.006	VBG
race_ethnicity	2	factor	0.021	-0.006	VBG
race_ethnicity	3	factor	0.029	0.006	VBG
serum_k	NA	numeric	0.041	0.006	VBG
curr_bmi	NA	numeric	-0.204	-0.006	VBG
race_ethnicity	3	factor	0.029	0.006	VBG
dm	1	factor	0.082	-0.006	VBG
dm	0	factor	-0.082	0.006	VBG
location	2	factor	0.066	0.006	VBG
race_ethnicity	3	factor	0.029	0.006	VBG
phtn	1	factor	0.053	0.006	VBG
phtn	0	factor	-0.053	-0.006	VBG
race_ethnicity	0	factor	-0.194	0.006	VBG
race_ethnicity	0	factor	-0.194	0.006	VBG
race_ethnicity	3	factor	0.029	0.006	VBG
copd	0	factor	-0.008	-0.006	VBG
copd	1	factor	0.008	0.006	VBG
acute_nmd	0	factor	-0.009	0.006	VBG
acute_nmd	1	factor	0.009	-0.006	VBG
sex	Male	factor	0.057	0.006	VBG
sex	Female	factor	-0.057	-0.006	VBG
ckd	1	factor	0.069	0.006	VBG
ckd	0	factor	-0.069	-0.006	VBG
osa	0	factor	0.025	0.006	VBG
osa	1	factor	-0.025	-0.006	VBG
serum_hco3	NA	numeric	-0.072	0.006	VBG
copd	1	factor	0.008	0.006	VBG
copd	0	factor	-0.008	-0.006	VBG
serum_k	NA	numeric	0.044	0.006	VBG
race_ethnicity	1	factor	0.042	0.006	VBG
race_ethnicity	0	factor	-0.194	0.006	VBG
race_ethnicity	3	factor	0.029	0.006	VBG
race_ethnicity	5	factor	-0.018	-0.006	VBG
race_ethnicity	3	factor	0.029	0.006	VBG
sodium	NA	numeric	-0.105	0.006	VBG
acute_nmd	1	factor	0.009	-0.006	VBG
acute_nmd	0	factor	-0.009	0.006	VBG
chf	0	factor	-0.037	-0.006	VBG
chf	1	factor	0.037	0.006	VBG
chf	1	factor	0.037	0.006	VBG
chf	0	factor	-0.037	-0.006	VBG

Table 20: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
acute_nmd	0	factor	-0.009	0.006	VBG
acute_nmd	1	factor	0.009	-0.006	VBG
serum_k	NA	numeric	0.044	0.006	VBG
location	1	factor	0.399	0.006	VBG
race_ethnicity	2	factor	0.021	-0.006	VBG
race_ethnicity	2	factor	0.021	-0.006	VBG
sodium	NA	numeric	-0.108	-0.006	VBG
osa	1	factor	-0.025	-0.006	VBG
osa	0	factor	0.025	0.006	VBG
race_ethnicity	3	factor	0.029	0.006	VBG
location	2	factor	0.066	0.006	VBG
race_ethnicity	3	factor	0.029	0.006	VBG
copd	0	factor	-0.008	-0.006	VBG
copd	1	factor	0.008	0.006	VBG
copd	1	factor	0.008	0.006	VBG
copd	0	factor	-0.008	-0.006	VBG
sodium	NA	numeric	-0.104	0.006	VBG
race_ethnicity	3	factor	0.029	0.006	VBG
sodium	NA	numeric	-0.104	0.006	VBG
race_ethnicity	0	factor	-0.194	0.006	VBG
race_ethnicity	3	factor	0.029	0.006	VBG
race_ethnicity	3	factor	0.029	0.006	VBG
location	1	factor	0.399	0.006	VBG
race_ethnicity	0	factor	-0.194	0.006	VBG
race_ethnicity	3	factor	0.029	0.006	VBG
race_ethnicity	3	factor	0.029	0.006	VBG
copd	1	factor	0.008	0.006	VBG
copd	0	factor	-0.008	-0.006	VBG
osa	1	factor	-0.025	0.006	VBG
osa	0	factor	0.025	-0.006	VBG
sbp	NA	numeric	-0.088	-0.006	VBG
location	2	factor	0.066	-0.006	VBG
ckd	0	factor	-0.069	-0.006	VBG
ckd	1	factor	0.069	0.006	VBG
serum_hco3	NA	numeric	-0.072	0.006	VBG
osa	0	factor	0.025	-0.006	VBG
osa	1	factor	-0.025	0.006	VBG
race_ethnicity	0	factor	-0.194	0.006	VBG
race_ethnicity	3	factor	0.029	0.006	VBG
sbp	NA	numeric	-0.066	-0.005	VBG
race_ethnicity	0	factor	-0.194	0.005	VBG
acute_nmd	0	factor	-0.009	0.005	VBG
acute_nmd	1	factor	0.009	-0.005	VBG
chf	0	factor	-0.037	-0.005	VBG
chf	1	factor	0.037	0.005	VBG
race_ethnicity	3	factor	0.029	0.005	VBG
location	1	factor	0.399	0.005	VBG
serum_k	NA	numeric	0.044	-0.005	VBG
race_ethnicity	5	factor	-0.018	-0.005	VBG
race_ethnicity	5	factor	-0.018	-0.005	VBG
sodium	NA	numeric	-0.106	0.005	VBG
race_ethnicity	2	factor	0.021	-0.005	VBG
ckd	1	factor	0.069	0.005	VBG
ckd	0	factor	-0.069	-0.005	VBG
osa	0	factor	0.025	-0.005	VBG
osa	1	factor	-0.025	0.005	VBG
sbp	NA	numeric	-0.093	-0.005	VBG
location	2	factor	0.066	0.005	VBG
sbp	NA	numeric	-0.078	-0.005	VBG
location	1	factor	0.399	0.005	VBG
race_ethnicity	2	factor	0.021	-0.005	VBG
dm	0	factor	-0.082	0.005	VBG
dm	1	factor	0.082	-0.005	VBG

Table 20: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
chf	1	factor	0.037	0.005	VBG
chf	0	factor	-0.037	-0.005	VBG
race_ethnicity	2	factor	0.021	0.005	VBG
sodium	NA	numeric	-0.104	0.005	VBG
chf	0	factor	-0.037	-0.005	VBG
chf	1	factor	0.037	0.005	VBG
location	1	factor	0.399	0.005	VBG
race_ethnicity	1	factor	0.042	0.005	VBG
serum_hco3	NA	numeric	-0.068	0.005	VBG
race_ethnicity	3	factor	0.029	0.005	VBG
phtn	0	factor	-0.053	-0.005	VBG
phtn	1	factor	0.053	0.005	VBG
location	2	factor	0.066	0.005	VBG
acute_nmd	1	factor	0.009	-0.005	VBG
acute_nmd	0	factor	-0.009	0.005	VBG
race_ethnicity	0	factor	-0.194	0.005	VBG
serum_k	NA	numeric	0.042	0.005	VBG
race_ethnicity	0	factor	-0.194	0.005	VBG
race_ethnicity	1	factor	0.042	0.005	VBG
location	2	factor	0.066	0.005	VBG
acute_nmd	0	factor	-0.009	0.005	VBG
acute_nmd	1	factor	0.009	-0.005	VBG
race_ethnicity	3	factor	0.029	0.005	VBG
temp_new	NA	numeric	0.012	0.005	VBG
serum_k	NA	numeric	0.045	0.005	VBG
acute_nmd	1	factor	0.009	-0.005	VBG
acute_nmd	0	factor	-0.009	0.005	VBG
acute_nmd	0	factor	-0.009	0.005	VBG
acute_nmd	1	factor	0.009	-0.005	VBG
acute_nmd	0	factor	-0.009	0.005	VBG
acute_nmd	1	factor	0.009	-0.005	VBG
sbp	NA	numeric	-0.089	-0.005	VBG
race_ethnicity	0	factor	-0.194	0.005	VBG
race_ethnicity	0	factor	-0.194	0.005	VBG
race_ethnicity	0	factor	-0.194	0.005	VBG
copd	0	factor	-0.008	-0.005	VBG
copd	1	factor	0.008	0.005	VBG
location	1	factor	0.399	0.005	VBG
race_ethnicity	1	factor	0.042	0.005	VBG
race_ethnicity	3	factor	0.029	0.005	VBG
race_ethnicity	2	factor	0.021	-0.005	VBG
race_ethnicity	3	factor	0.029	0.005	VBG
race_ethnicity	5	factor	-0.018	-0.005	VBG
location	2	factor	0.066	0.005	VBG
curr_bmi	NA	numeric	-0.206	-0.005	VBG
sbp	NA	numeric	-0.089	-0.005	VBG
race_ethnicity	2	factor	0.021	-0.005	VBG
sbp	NA	numeric	-0.092	-0.005	VBG
dm	1	factor	0.082	-0.005	VBG
dm	0	factor	-0.082	0.005	VBG
dm	1	factor	0.082	-0.005	VBG
dm	0	factor	-0.082	0.005	VBG
race_ethnicity	2	factor	0.021	-0.005	VBG
chf	1	factor	0.037	-0.005	VBG
chf	0	factor	-0.037	0.005	VBG
copd	0	factor	-0.008	-0.005	VBG
copd	1	factor	0.008	0.005	VBG
serum_k	NA	numeric	0.037	-0.005	VBG
chf	0	factor	-0.037	-0.005	VBG
chf	1	factor	0.037	0.005	VBG
dm	1	factor	0.082	-0.005	VBG
dm	0	factor	-0.082	0.005	VBG
acute_nmd	1	factor	0.009	-0.005	VBG
acute_nmd	0	factor	-0.009	0.005	VBG
location	2	factor	0.066	0.005	VBG

Table 20: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
race_ethnicity	0	factor	-0.194	0.005	VBG
copd	1	factor	0.008	0.005	VBG
copd	0	factor	-0.008	-0.005	VBG
chf	0	factor	-0.037	-0.005	VBG
chf	1	factor	0.037	0.005	VBG
acute_nmd	1	factor	0.009	-0.005	VBG
acute_nmd	0	factor	-0.009	0.005	VBG
location	1	factor	0.399	0.005	VBG
race_ethnicity	2	factor	0.021	-0.005	VBG
acute_nmd	0	factor	-0.009	0.005	VBG
acute_nmd	1	factor	0.009	-0.005	VBG
chf	0	factor	-0.037	-0.005	VBG
chf	1	factor	0.037	0.005	VBG
race_ethnicity	0	factor	-0.194	-0.005	VBG
race_ethnicity	0	factor	-0.194	0.005	VBG
chf	0	factor	-0.037	-0.005	VBG
chf	1	factor	0.037	0.005	VBG
acute_nmd	1	factor	0.009	-0.005	VBG
acute_nmd	0	factor	-0.009	0.005	VBG
location	2	factor	0.066	0.005	VBG
race_ethnicity	3	factor	0.029	0.005	VBG
copd	1	factor	0.008	0.005	VBG
copd	0	factor	-0.008	-0.005	VBG
location	1	factor	0.399	0.005	VBG
sodium	NA	numeric	-0.106	-0.005	VBG
sodium	NA	numeric	-0.099	0.005	VBG
race_ethnicity	3	factor	0.029	0.005	VBG
osa	1	factor	-0.025	-0.005	VBG
osa	0	factor	0.025	0.005	VBG
sodium	NA	numeric	-0.104	0.005	VBG
race_ethnicity	0	factor	-0.194	0.005	VBG
chf	0	factor	-0.037	-0.005	VBG
chf	1	factor	0.037	0.005	VBG
serum_k	NA	numeric	0.041	-0.005	VBG
osa	0	factor	0.025	0.005	VBG
osa	1	factor	-0.025	-0.005	VBG
osa	0	factor	0.025	-0.005	VBG
osa	1	factor	-0.025	0.005	VBG
acute_nmd	0	factor	-0.009	0.005	VBG
acute_nmd	1	factor	0.009	-0.005	VBG
chf	0	factor	-0.037	-0.005	VBG
chf	1	factor	0.037	0.005	VBG
dm	1	factor	0.082	-0.005	VBG
dm	0	factor	-0.082	0.005	VBG
osa	1	factor	-0.025	-0.005	VBG
osa	0	factor	0.025	0.005	VBG
serum_k	NA	numeric	0.038	0.005	VBG
chf	0	factor	-0.037	-0.005	VBG
chf	1	factor	0.037	0.005	VBG
location	2	factor	0.066	0.005	VBG
race_ethnicity	5	factor	-0.018	-0.005	VBG
race_ethnicity	2	factor	0.021	0.005	VBG
dm	1	factor	0.082	-0.005	VBG
dm	0	factor	-0.082	0.005	VBG
location	2	factor	0.066	0.005	VBG
acute_nmd	0	factor	-0.009	0.005	VBG
acute_nmd	1	factor	0.009	-0.005	VBG
osa	0	factor	0.025	0.005	VBG
osa	1	factor	-0.025	-0.005	VBG
race_ethnicity	2	factor	0.021	0.005	VBG
race_ethnicity	3	factor	0.029	0.005	VBG
race_ethnicity	3	factor	0.029	0.005	VBG
serum_k	NA	numeric	0.042	0.005	VBG
race_ethnicity	3	factor	0.029	0.005	VBG

Table 20: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
sbp	NA	numeric	-0.094	-0.005	VBG
chf	1	factor	0.037	0.005	VBG
chf	0	factor	-0.037	-0.005	VBG
acute_nmd	0	factor	-0.009	0.005	VBG
acute_nmd	1	factor	0.009	-0.005	VBG
location	2	factor	0.066	0.005	VBG
copd	0	factor	-0.008	-0.005	VBG
copd	1	factor	0.008	0.005	VBG
acute_nmd	0	factor	-0.009	0.005	VBG
acute_nmd	1	factor	0.009	-0.005	VBG
dm	0	factor	-0.082	0.005	VBG
dm	1	factor	0.082	-0.005	VBG
dm	1	factor	0.082	-0.005	VBG
dm	0	factor	-0.082	0.005	VBG
dm	0	factor	-0.082	0.005	VBG
dm	1	factor	0.082	-0.005	VBG
race_ethnicity	5	factor	-0.018	-0.005	VBG
dm	1	factor	0.082	-0.005	VBG
dm	0	factor	-0.082	0.005	VBG
sodium	NA	numeric	-0.107	-0.005	VBG
acute_nmd	0	factor	-0.009	0.005	VBG
acute_nmd	1	factor	0.009	-0.005	VBG
location	1	factor	0.399	0.005	VBG
location	1	factor	0.399	0.004	VBG
race_ethnicity	0	factor	-0.194	0.004	VBG
copd	1	factor	0.008	0.004	VBG
copd	0	factor	-0.008	-0.004	VBG
dm	0	factor	-0.082	0.004	VBG
dm	1	factor	0.082	-0.004	VBG
sbp	NA	numeric	-0.097	-0.004	VBG
chf	1	factor	0.037	0.004	VBG
chf	0	factor	-0.037	-0.004	VBG
location	1	factor	0.399	0.004	VBG
race_ethnicity	2	factor	0.021	-0.004	VBG
serum_k	NA	numeric	0.043	0.004	VBG
location	1	factor	0.399	0.004	VBG
acute_nmd	0	factor	-0.009	0.004	VBG
acute_nmd	1	factor	0.009	-0.004	VBG
race_ethnicity	5	factor	-0.018	-0.004	VBG
location	1	factor	0.399	0.004	VBG
race_ethnicity	4	factor	0.068	0.004	VBG
location	2	factor	0.066	-0.004	VBG
copd	1	factor	0.008	0.004	VBG
copd	0	factor	-0.008	-0.004	VBG
race_ethnicity	0	factor	-0.194	0.004	VBG
race_ethnicity	2	factor	0.021	-0.004	VBG
chf	0	factor	-0.037	-0.004	VBG
chf	1	factor	0.037	0.004	VBG
osa	0	factor	0.025	-0.004	VBG
osa	1	factor	-0.025	0.004	VBG
acute_nmd	1	factor	0.009	-0.004	VBG
acute_nmd	0	factor	-0.009	0.004	VBG
osa	0	factor	0.025	-0.004	VBG
osa	1	factor	-0.025	0.004	VBG
sodium	NA	numeric	-0.106	0.004	VBG
sodium	NA	numeric	-0.105	0.004	VBG
acute_nmd	1	factor	0.009	-0.004	VBG
acute_nmd	0	factor	-0.009	0.004	VBG
race_ethnicity	5	factor	-0.018	-0.004	VBG
race_ethnicity	3	factor	0.029	0.004	VBG
location	1	factor	0.399	0.004	VBG
sodium	NA	numeric	-0.106	-0.004	VBG
sodium	NA	numeric	-0.105	0.004	VBG

Table 20: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
acute_nmd	0	factor	-0.009	-0.004	VBG
acute_nmd	1	factor	0.009	0.004	VBG
race_ethnicity	0	factor	-0.194	0.004	VBG
race_ethnicity	3	factor	0.029	0.004	VBG
acute_nmd	0	factor	-0.009	0.004	VBG
acute_nmd	1	factor	0.009	-0.004	VBG
chf	1	factor	0.037	0.004	VBG
chf	0	factor	-0.037	-0.004	VBG
serum_k	NA	numeric	0.045	0.004	VBG
race_ethnicity	0	factor	-0.194	0.004	VBG
sodium	NA	numeric	-0.108	-0.004	VBG
osa	0	factor	0.025	-0.004	VBG
osa	1	factor	-0.025	0.004	VBG
curr_bmi	NA	numeric	-0.204	-0.004	VBG
acute_nmd	0	factor	-0.009	0.004	VBG
acute_nmd	1	factor	0.009	-0.004	VBG
osa	0	factor	0.025	-0.004	VBG
osa	1	factor	-0.025	0.004	VBG
chf	0	factor	-0.037	-0.004	VBG
chf	1	factor	0.037	0.004	VBG
copd	1	factor	0.008	0.004	VBG
copd	0	factor	-0.008	-0.004	VBG
dm	1	factor	0.082	0.004	VBG
dm	0	factor	-0.082	-0.004	VBG
race_ethnicity	5	factor	-0.018	-0.004	VBG
race_ethnicity	0	factor	-0.194	0.004	VBG
serum_k	NA	numeric	0.039	0.004	VBG
copd	1	factor	0.008	0.004	VBG
copd	0	factor	-0.008	-0.004	VBG
race_ethnicity	1	factor	0.042	0.004	VBG
dm	0	factor	-0.082	0.004	VBG
dm	1	factor	0.082	-0.004	VBG
serum_k	NA	numeric	0.042	0.004	VBG
serum_k	NA	numeric	0.042	-0.004	VBG
sodium	NA	numeric	-0.104	0.004	VBG
dm	1	factor	0.082	-0.004	VBG
dm	0	factor	-0.082	0.004	VBG
race_ethnicity	2	factor	0.021	-0.004	VBG
copd	1	factor	0.008	0.004	VBG
copd	0	factor	-0.008	-0.004	VBG
race_ethnicity	5	factor	-0.018	-0.004	VBG
race_ethnicity	3	factor	0.029	0.004	VBG
osa	0	factor	0.025	-0.004	VBG
osa	1	factor	-0.025	0.004	VBG
dm	1	factor	0.082	-0.004	VBG
dm	0	factor	-0.082	0.004	VBG
chf	0	factor	-0.037	-0.004	VBG
chf	1	factor	0.037	0.004	VBG
race_ethnicity	2	factor	0.021	0.004	VBG
curr_bmi	NA	numeric	-0.203	-0.004	VBG
sodium	NA	numeric	-0.103	0.004	VBG
sodium	NA	numeric	-0.103	0.004	VBG
sodium	NA	numeric	-0.106	0.004	VBG
race_ethnicity	0	factor	-0.194	0.004	VBG
acute_nmd	0	factor	-0.009	0.004	VBG
acute_nmd	1	factor	0.009	-0.004	VBG
location	2	factor	0.066	0.004	VBG
sodium	NA	numeric	-0.107	-0.004	VBG
location	1	factor	0.399	0.004	VBG
race_ethnicity	0	factor	-0.194	0.004	VBG

Table 20: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
location	1	factor	0.399	0.004	VBG
race_ethnicity	2	factor	0.021	0.004	VBG
race_ethnicity	2	factor	0.021	-0.004	VBG
dm	0	factor	-0.082	-0.004	VBG
dm	1	factor	0.082	0.004	VBG
location	1	factor	0.399	0.004	VBG
sodium	NA	numeric	-0.104	-0.004	VBG
acute_nmd	1	factor	0.009	-0.004	VBG
acute_nmd	0	factor	-0.009	0.004	VBG
dm	1	factor	0.082	-0.004	VBG
dm	0	factor	-0.082	0.004	VBG
chf	1	factor	0.037	0.004	VBG
chf	0	factor	-0.037	-0.004	VBG
copd	1	factor	0.008	0.004	VBG
copd	0	factor	-0.008	-0.004	VBG
race_ethnicity	3	factor	0.029	0.004	VBG
osa	0	factor	0.025	0.004	VBG
osa	1	factor	-0.025	-0.004	VBG
chf	1	factor	0.037	0.004	VBG
chf	0	factor	-0.037	-0.004	VBG
location	2	factor	0.066	0.004	VBG
serum_k	NA	numeric	0.042	-0.004	VBG
sodium	NA	numeric	-0.104	0.004	VBG
osa	1	factor	-0.025	-0.004	VBG
osa	0	factor	0.025	0.004	VBG
dm	1	factor	0.082	-0.004	VBG
dm	0	factor	-0.082	0.004	VBG
race_ethnicity	5	factor	-0.018	-0.004	VBG
chf	1	factor	0.037	0.004	VBG
chf	0	factor	-0.037	-0.004	VBG
copd	0	factor	-0.008	-0.004	VBG
copd	1	factor	0.008	0.004	VBG
curr_bmi	NA	numeric	-0.228	-0.004	VBG
chf	0	factor	-0.037	-0.004	VBG
chf	1	factor	0.037	0.004	VBG
race_ethnicity	5	factor	-0.018	-0.004	VBG
copd	0	factor	-0.008	-0.004	VBG
copd	1	factor	0.008	0.004	VBG
location	1	factor	0.399	0.004	VBG
race_ethnicity	2	factor	0.021	-0.004	VBG
serum_k	NA	numeric	0.042	0.004	VBG
acute_nmd	0	factor	-0.009	0.004	VBG
acute_nmd	1	factor	0.009	-0.004	VBG
race_ethnicity	0	factor	-0.194	0.004	VBG
race_ethnicity	5	factor	-0.018	-0.004	VBG
osa	0	factor	0.025	0.004	VBG
osa	1	factor	-0.025	-0.004	VBG
acute_nmd	1	factor	0.009	-0.004	VBG
acute_nmd	0	factor	-0.009	0.004	VBG
acute_nmd	0	factor	-0.009	0.004	VBG
acute_nmd	1	factor	0.009	-0.004	VBG
location	2	factor	0.066	0.004	VBG
acute_nmd	0	factor	-0.009	0.004	VBG
acute_nmd	1	factor	0.009	-0.004	VBG
copd	1	factor	0.008	0.004	VBG
copd	0	factor	-0.008	-0.004	VBG
chf	1	factor	0.037	0.004	VBG
chf	0	factor	-0.037	-0.004	VBG
location	2	factor	0.066	0.004	VBG
race_ethnicity	5	factor	-0.018	-0.004	VBG
dm	1	factor	0.082	-0.004	VBG
dm	0	factor	-0.082	0.004	VBG
race_ethnicity	5	factor	-0.018	-0.004	VBG
race_ethnicity	2	factor	0.021	-0.004	VBG

Table 20: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
race_ethnicity	1	factor	0.042	0.004	VBG
dm	1	factor	0.082	0.004	VBG
dm	0	factor	-0.082	-0.004	VBG
sodium	NA	numeric	-0.104	0.004	VBG
location	1	factor	0.399	-0.004	VBG
race_ethnicity	2	factor	0.021	-0.004	VBG
sodium	NA	numeric	-0.102	0.004	VBG
acute_nmd	1	factor	0.009	-0.004	VBG
acute_nmd	0	factor	-0.009	0.004	VBG
race_ethnicity	2	factor	0.021	-0.004	VBG
chf	1	factor	0.037	0.004	VBG
chf	0	factor	-0.037	-0.004	VBG
serum_k	NA	numeric	0.043	0.004	VBG
copd	1	factor	0.008	-0.004	VBG
copd	0	factor	-0.008	0.004	VBG
race_ethnicity	2	factor	0.021	-0.004	VBG
osa	0	factor	0.025	0.004	VBG
osa	1	factor	-0.025	-0.004	VBG
copd	1	factor	0.008	0.004	VBG
copd	0	factor	-0.008	-0.004	VBG
acute_nmd	0	factor	-0.009	0.004	VBG
acute_nmd	1	factor	0.009	-0.004	VBG
sbp	NA	numeric	-0.089	-0.004	VBG
ckd	1	factor	0.069	0.004	VBG
ckd	0	factor	-0.069	-0.004	VBG
chf	0	factor	-0.037	-0.004	VBG
chf	1	factor	0.037	0.004	VBG
copd	0	factor	-0.008	0.004	VBG
copd	1	factor	0.008	-0.004	VBG
serum_k	NA	numeric	0.042	0.004	VBG
location	1	factor	0.399	0.004	VBG
race_ethnicity	2	factor	0.021	0.004	VBG
location	1	factor	0.399	0.004	VBG
race_ethnicity	0	factor	-0.194	0.004	VBG
serum_k	NA	numeric	0.043	0.004	VBG
serum_k	NA	numeric	0.041	0.004	VBG
acute_nmd	1	factor	0.009	-0.004	VBG
acute_nmd	0	factor	-0.009	0.004	VBG
race_ethnicity	5	factor	-0.018	-0.004	VBG
chf	0	factor	-0.037	-0.004	VBG
chf	1	factor	0.037	0.004	VBG
copd	1	factor	0.008	0.003	VBG
copd	0	factor	-0.008	-0.003	VBG
race_ethnicity	0	factor	-0.194	0.003	VBG
dm	1	factor	0.082	-0.003	VBG
dm	0	factor	-0.082	0.003	VBG
osa	1	factor	-0.025	0.003	VBG
osa	0	factor	0.025	-0.003	VBG
acute_nmd	1	factor	0.009	0.003	VBG
acute_nmd	0	factor	-0.009	-0.003	VBG
race_ethnicity	2	factor	0.021	-0.003	VBG
location	2	factor	0.066	-0.003	VBG
location	2	factor	0.066	0.003	VBG
dm	0	factor	-0.082	0.003	VBG
dm	1	factor	0.082	-0.003	VBG
chf	0	factor	-0.037	-0.003	VBG
chf	1	factor	0.037	0.003	VBG
sodium	NA	numeric	-0.104	0.003	VBG
chf	1	factor	0.037	0.003	VBG
chf	0	factor	-0.037	-0.003	VBG
dm	1	factor	0.082	-0.003	VBG
dm	0	factor	-0.082	0.003	VBG
location	2	factor	0.066	0.003	VBG

Table 20: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
copd	1	factor	0.008	0.003	VBG
copd	0	factor	-0.008	-0.003	VBG
race_ethnicity	4	factor	0.068	0.003	VBG
race_ethnicity	3	factor	0.029	0.003	VBG
dm	0	factor	-0.082	0.003	VBG
dm	1	factor	0.082	-0.003	VBG
location	1	factor	0.399	0.003	VBG
location	1	factor	0.399	0.003	VBG
copd	0	factor	-0.008	0.003	VBG
copd	1	factor	0.008	-0.003	VBG
race_ethnicity	2	factor	0.021	0.003	VBG
osa	0	factor	0.025	-0.003	VBG
osa	1	factor	-0.025	0.003	VBG
serum_k	NA	numeric	0.042	0.003	VBG
sbp	NA	numeric	-0.084	-0.003	VBG
location	1	factor	0.399	-0.003	VBG
location	2	factor	0.066	0.003	VBG
acute_nmd	1	factor	0.009	-0.003	VBG
acute_nmd	0	factor	-0.009	0.003	VBG
race_ethnicity	2	factor	0.021	0.003	VBG
race_ethnicity	2	factor	0.021	0.003	VBG
race_ethnicity	5	factor	-0.018	-0.003	VBG
dm	1	factor	0.082	-0.003	VBG
dm	0	factor	-0.082	0.003	VBG
race_ethnicity	0	factor	-0.194	-0.003	VBG
race_ethnicity	3	factor	0.029	0.003	VBG
race_ethnicity	3	factor	0.029	0.003	VBG
race_ethnicity	5	factor	-0.018	-0.003	VBG
race_ethnicity	5	factor	-0.018	-0.003	VBG
location	2	factor	0.066	0.003	VBG
race_ethnicity	3	factor	0.029	0.003	VBG
race_ethnicity	0	factor	-0.194	0.003	VBG
race_ethnicity	3	factor	0.029	0.003	VBG
osa	0	factor	0.025	0.003	VBG
osa	1	factor	-0.025	-0.003	VBG
acute_nmd	0	factor	-0.009	0.003	VBG
acute_nmd	1	factor	0.009	-0.003	VBG
location	1	factor	0.399	0.003	VBG
sodium	NA	numeric	-0.104	0.003	VBG
race_ethnicity	5	factor	-0.018	-0.003	VBG
race_ethnicity	3	factor	0.029	0.003	VBG
race_ethnicity	3	factor	0.029	0.003	VBG
race_ethnicity	3	factor	0.029	0.003	VBG
location	1	factor	0.399	0.003	VBG
osa	0	factor	0.025	-0.003	VBG
osa	1	factor	-0.025	0.003	VBG
serum_k	NA	numeric	0.039	0.003	VBG
acute_nmd	1	factor	0.009	-0.003	VBG
acute_nmd	0	factor	-0.009	0.003	VBG
location	1	factor	0.399	0.003	VBG
dm	0	factor	-0.082	0.003	VBG
dm	1	factor	0.082	-0.003	VBG
acute_nmd	0	factor	-0.009	0.003	VBG
acute_nmd	1	factor	0.009	-0.003	VBG
chf	1	factor	0.037	-0.003	VBG
chf	0	factor	-0.037	0.003	VBG
serum_k	NA	numeric	0.038	0.003	VBG
acute_nmd	0	factor	-0.009	-0.003	VBG
acute_nmd	1	factor	0.009	0.003	VBG
osa	1	factor	-0.025	-0.003	VBG
osa	0	factor	0.025	0.003	VBG
chf	0	factor	-0.037	-0.003	VBG
chf	1	factor	0.037	0.003	VBG

Table 20: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
race_ethnicity	0	factor	-0.194	0.003	VBG
race_ethnicity	2	factor	0.021	-0.003	VBG
race_ethnicity	3	factor	0.029	-0.003	VBG
osa	1	factor	-0.025	0.003	VBG
osa	0	factor	0.025	-0.003	VBG
location	2	factor	0.066	-0.003	VBG
dm	1	factor	0.082	0.003	VBG
dm	0	factor	-0.082	-0.003	VBG
chf	1	factor	0.037	0.003	VBG
chf	0	factor	-0.037	-0.003	VBG
dm	1	factor	0.082	-0.003	VBG
dm	0	factor	-0.082	0.003	VBG
location	2	factor	0.066	0.003	VBG
sbp	NA	numeric	-0.094	-0.003	VBG
copd	1	factor	0.008	0.003	VBG
copd	0	factor	-0.008	-0.003	VBG
serum_k	NA	numeric	0.039	-0.003	VBG
acute_nmd	0	factor	-0.009	0.003	VBG
acute_nmd	1	factor	0.009	-0.003	VBG
sodium	NA	numeric	-0.104	-0.003	VBG
race_ethnicity	2	factor	0.021	-0.003	VBG
copd	0	factor	-0.008	-0.003	VBG
copd	1	factor	0.008	0.003	VBG
race_ethnicity	3	factor	0.029	0.003	VBG
race_ethnicity	0	factor	-0.194	0.003	VBG
serum_k	NA	numeric	0.044	0.003	VBG
race_ethnicity	2	factor	0.021	0.003	VBG
sodium	NA	numeric	-0.106	0.003	VBG
sodium	NA	numeric	-0.107	0.003	VBG
race_ethnicity	5	factor	-0.018	-0.003	VBG
race_ethnicity	0	factor	-0.194	-0.003	VBG
acute_nmd	0	factor	-0.009	0.003	VBG
acute_nmd	1	factor	0.009	-0.003	VBG
osa	0	factor	0.025	-0.003	VBG
osa	1	factor	-0.025	0.003	VBG
race_ethnicity	0	factor	-0.194	-0.003	VBG
dm	0	factor	-0.082	0.003	VBG
dm	1	factor	0.082	-0.003	VBG
location	2	factor	0.066	0.003	VBG
copd	0	factor	-0.008	-0.003	VBG
copd	1	factor	0.008	0.003	VBG
copd	1	factor	0.008	-0.003	VBG
copd	0	factor	-0.008	0.003	VBG
osa	0	factor	0.025	-0.003	VBG
osa	1	factor	-0.025	0.003	VBG
osa	0	factor	0.025	-0.003	VBG
osa	1	factor	-0.025	0.003	VBG
serum_k	NA	numeric	0.042	0.003	VBG
acute_nmd	1	factor	0.009	-0.003	VBG
acute_nmd	0	factor	-0.009	0.003	VBG
location	1	factor	0.399	0.003	VBG
race_ethnicity	2	factor	0.021	-0.003	VBG
location	2	factor	0.066	0.003	VBG
race_ethnicity	0	factor	-0.194	0.003	VBG
sodium	NA	numeric	-0.106	0.003	VBG
copd	0	factor	-0.008	-0.003	VBG
copd	1	factor	0.008	0.003	VBG
race_ethnicity	5	factor	-0.018	-0.003	VBG
race_ethnicity	2	factor	0.021	-0.003	VBG
copd	1	factor	0.008	0.003	VBG
copd	0	factor	-0.008	-0.003	VBG
copd	0	factor	-0.008	0.003	VBG
copd	1	factor	0.008	-0.003	VBG
osa	0	factor	0.025	-0.003	VBG

Table 20: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
osa	1	factor	-0.025	0.003	VBG
sodium	NA	numeric	-0.106	-0.003	VBG
race_ethnicity	5	factor	-0.018	-0.003	VBG
race_ethnicity	5	factor	-0.018	-0.003	VBG
serum_k	NA	numeric	0.036	-0.003	VBG
race_ethnicity	0	factor	-0.194	0.003	VBG
acute_nmd	0	factor	-0.009	0.003	VBG
acute_nmd	1	factor	0.009	-0.003	VBG
copd	0	factor	-0.008	-0.003	VBG
copd	1	factor	0.008	0.003	VBG
acute_nmd	0	factor	-0.009	0.003	VBG
acute_nmd	1	factor	0.009	-0.003	VBG
race_ethnicity	0	factor	-0.194	0.003	VBG
race_ethnicity	0	factor	-0.194	0.003	VBG
dm	0	factor	-0.082	0.003	VBG
dm	1	factor	0.082	-0.003	VBG
sbp	NA	numeric	-0.081	-0.003	VBG
chf	1	factor	0.037	0.003	VBG
chf	0	factor	-0.037	-0.003	VBG
dm	1	factor	0.082	-0.003	VBG
dm	0	factor	-0.082	0.003	VBG
chf	0	factor	-0.037	-0.003	VBG
chf	1	factor	0.037	0.003	VBG
race_ethnicity	3	factor	0.029	-0.003	VBG
copd	1	factor	0.008	0.003	VBG
copd	0	factor	-0.008	-0.003	VBG
sodium	NA	numeric	-0.104	0.003	VBG
osa	0	factor	0.025	-0.003	VBG
osa	1	factor	-0.025	0.003	VBG
osa	1	factor	-0.025	0.003	VBG
osa	0	factor	0.025	-0.003	VBG
chf	1	factor	0.037	-0.003	VBG
chf	0	factor	-0.037	0.003	VBG
race_ethnicity	2	factor	0.021	0.003	VBG
acute_nmd	0	factor	-0.009	0.003	VBG
acute_nmd	1	factor	0.009	-0.003	VBG
copd	0	factor	-0.008	-0.003	VBG
copd	1	factor	0.008	0.003	VBG
copd	0	factor	0.037	0.003	VBG
chf	1	factor	-0.037	-0.003	VBG
dm	1	factor	0.082	-0.003	VBG
dm	0	factor	-0.082	0.003	VBG
osa	1	factor	-0.025	0.003	VBG
osa	0	factor	0.025	-0.003	VBG
location	2	factor	0.066	0.003	VBG
copd	0	factor	-0.008	-0.003	VBG
copd	1	factor	0.008	0.003	VBG
osa	1	factor	-0.025	-0.003	VBG
osa	0	factor	0.025	0.003	VBG
copd	0	factor	-0.008	-0.003	VBG
copd	1	factor	0.008	0.003	VBG
location	2	factor	0.066	0.003	VBG
location	2	factor	0.066	0.003	VBG
serum_k	NA	numeric	0.039	-0.003	VBG
race_ethnicity	2	factor	0.021	-0.003	VBG
serum_k	NA	numeric	0.044	0.003	VBG
location	2	factor	0.066	0.003	VBG
location	1	factor	0.399	0.003	VBG
sbp	NA	numeric	-0.094	-0.003	VBG
race_ethnicity	4	factor	0.068	-0.003	VBG
osa	0	factor	0.025	-0.003	VBG
osa	1	factor	-0.025	0.003	VBG
location	2	factor	0.066	-0.003	VBG

Table 20: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
race_ethnicity	0	factor	-0.194	0.003	VBG
acute_nmd	0	factor	-0.009	0.003	VBG
acute_nmd	1	factor	0.009	-0.003	VBG
serum_k	NA	numeric	0.041	0.003	VBG
location	1	factor	0.399	0.003	VBG
serum_k	NA	numeric	0.045	0.003	VBG
location	1	factor	0.399	0.003	VBG
chf	1	factor	0.037	0.003	VBG
chf	0	factor	-0.037	-0.003	VBG
sodium	NA	numeric	-0.103	-0.003	VBG
acute_nmd	0	factor	-0.009	0.002	VBG
acute_nmd	1	factor	0.009	-0.002	VBG
copd	0	factor	-0.008	-0.002	VBG
copd	1	factor	0.008	0.002	VBG
dm	0	factor	-0.082	0.002	VBG
dm	1	factor	0.082	-0.002	VBG
dm	0	factor	-0.082	0.002	VBG
dm	1	factor	0.082	-0.002	VBG
sodium	NA	numeric	-0.103	0.002	VBG
chf	0	factor	-0.037	-0.002	VBG
chf	1	factor	0.037	0.002	VBG
sodium	NA	numeric	-0.106	-0.002	VBG
location	1	factor	0.399	0.002	VBG
dm	1	factor	0.082	-0.002	VBG
dm	0	factor	-0.082	0.002	VBG
dm	1	factor	0.082	-0.002	VBG
dm	0	factor	-0.082	0.002	VBG
osa	0	factor	0.025	-0.002	VBG
osa	1	factor	-0.025	0.002	VBG
location	2	factor	0.066	0.002	VBG
serum_k	NA	numeric	0.040	0.002	VBG
acute_nmd	0	factor	-0.009	0.002	VBG
acute_nmd	1	factor	0.009	-0.002	VBG
serum_k	NA	numeric	0.040	0.002	VBG
race_ethnicity	2	factor	0.021	0.002	VBG
serum_k	NA	numeric	0.041	-0.002	VBG
serum_k	NA	numeric	0.040	0.002	VBG
sodium	NA	numeric	-0.104	0.002	VBG
race_ethnicity	2	factor	0.021	0.002	VBG
dm	0	factor	-0.082	-0.002	VBG
dm	1	factor	0.082	0.002	VBG
race_ethnicity	0	factor	-0.194	0.002	VBG
location	1	factor	0.399	0.002	VBG
race_ethnicity	2	factor	0.021	-0.002	VBG
dm	1	factor	0.082	-0.002	VBG
dm	0	factor	-0.082	0.002	VBG
race_ethnicity	2	factor	0.021	-0.002	VBG
copd	0	factor	-0.008	0.002	VBG
copd	1	factor	0.008	-0.002	VBG
sodium	NA	numeric	-0.102	-0.002	VBG
copd	1	factor	0.008	0.002	VBG
copd	0	factor	-0.008	-0.002	VBG
race_ethnicity	4	factor	0.068	-0.002	VBG
acute_nmd	0	factor	-0.009	0.002	VBG
acute_nmd	1	factor	0.009	-0.002	VBG
location	2	factor	0.066	0.002	VBG
dm	0	factor	-0.082	0.002	VBG
dm	1	factor	0.082	-0.002	VBG
race_ethnicity	4	factor	0.068	0.002	VBG
osa	1	factor	-0.025	-0.002	VBG
osa	0	factor	0.025	0.002	VBG
race_ethnicity	3	factor	0.029	0.002	VBG
race_ethnicity	2	factor	0.021	-0.002	VBG

Table 20: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
location	1	factor	0.399	0.002	VBG
race_ethnicity	2	factor	0.021	-0.002	VBG
serum_k	NA	numeric	0.044	0.002	VBG
race_ethnicity	2	factor	0.021	0.002	VBG
osa	0	factor	0.025	0.002	VBG
osa	1	factor	-0.025	-0.002	VBG
race_ethnicity	3	factor	0.029	0.002	VBG
acute_nmd	0	factor	-0.009	0.002	VBG
acute_nmd	1	factor	0.009	-0.002	VBG
location	1	factor	0.399	-0.002	VBG
osa	0	factor	0.025	0.002	VBG
osa	1	factor	-0.025	-0.002	VBG
acute_nmd	1	factor	0.009	0.002	VBG
acute_nmd	0	factor	-0.009	-0.002	VBG
osa	0	factor	0.025	0.002	VBG
osa	1	factor	-0.025	-0.002	VBG
copd	1	factor	0.008	0.002	VBG
copd	0	factor	-0.008	-0.002	VBG
osa	1	factor	-0.025	-0.002	VBG
osa	0	factor	0.025	0.002	VBG
acute_nmd	0	factor	-0.009	0.002	VBG
acute_nmd	1	factor	0.009	-0.002	VBG
acute_nmd	1	factor	0.009	-0.002	VBG
acute_nmd	0	factor	-0.009	0.002	VBG
dm	0	factor	-0.082	-0.002	VBG
dm	1	factor	0.082	0.002	VBG
location	1	factor	0.399	0.002	VBG
race_ethnicity	3	factor	0.029	0.002	VBG
race_ethnicity	2	factor	0.021	0.002	VBG
copd	1	factor	0.008	0.002	VBG
copd	0	factor	-0.008	-0.002	VBG
sbp	NA	numeric	-0.089	0.002	VBG
acute_nmd	1	factor	0.009	-0.002	VBG
acute_nmd	0	factor	-0.009	0.002	VBG
sodium	NA	numeric	-0.105	-0.002	VBG
sodium	NA	numeric	-0.104	-0.002	VBG
location	1	factor	0.399	0.002	VBG
serum_k	NA	numeric	0.038	0.002	VBG
osa	1	factor	-0.025	0.002	VBG
osa	0	factor	0.025	-0.002	VBG
race_ethnicity	3	factor	0.029	0.002	VBG
osa	1	factor	-0.025	0.002	VBG
osa	0	factor	0.025	-0.002	VBG
serum_k	NA	numeric	0.038	-0.002	VBG
copd	1	factor	0.008	0.002	VBG
copd	0	factor	-0.008	-0.002	VBG
location	1	factor	0.399	0.002	VBG
sodium	NA	numeric	-0.106	-0.002	VBG
sodium	NA	numeric	-0.103	0.002	VBG
race_ethnicity	4	factor	0.068	0.002	VBG
race_ethnicity	4	factor	0.068	0.002	VBG
location	2	factor	0.066	-0.002	VBG
race_ethnicity	2	factor	0.021	-0.002	VBG
location	2	factor	0.066	0.002	VBG
race_ethnicity	4	factor	0.068	-0.002	VBG
chf	1	factor	0.037	-0.002	VBG
chf	0	factor	-0.037	0.002	VBG
dm	0	factor	-0.082	0.002	VBG
dm	1	factor	0.082	-0.002	VBG
serum_k	NA	numeric	0.041	-0.002	VBG
location	1	factor	0.399	0.002	VBG
osa	1	factor	-0.025	-0.002	VBG
osa	0	factor	0.025	0.002	VBG
race_ethnicity	4	factor	0.068	0.002	VBG

Table 20: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
race_ethnicity	0	factor	-0.194	0.002	VBG
acute_nmd	1	factor	0.009	-0.002	VBG
acute_nmd	0	factor	-0.009	0.002	VBG
race_ethnicity	3	factor	0.029	0.002	VBG
acute_nmd	0	factor	-0.009	0.002	VBG
acute_nmd	1	factor	0.009	-0.002	VBG
race_ethnicity	2	factor	0.021	-0.002	VBG
dm	1	factor	0.082	-0.002	VBG
dm	0	factor	-0.082	0.002	VBG
serum_k	NA	numeric	0.037	0.002	VBG
sodium	NA	numeric	-0.103	-0.002	VBG
dm	1	factor	0.082	0.002	VBG
dm	0	factor	-0.082	-0.002	VBG
race_ethnicity	4	factor	0.068	-0.002	VBG
osa	0	factor	0.025	0.002	VBG
osa	1	factor	-0.025	-0.002	VBG
race_ethnicity	5	factor	-0.018	-0.002	VBG
serum_k	NA	numeric	0.043	-0.002	VBG
copd	1	factor	0.008	-0.002	VBG
copd	0	factor	-0.008	0.002	VBG
location	1	factor	0.399	0.002	VBG
chf	1	factor	0.037	0.002	VBG
chf	0	factor	-0.037	-0.002	VBG
race_ethnicity	4	factor	0.068	0.002	VBG
sodium	NA	numeric	-0.104	0.002	VBG
serum_k	NA	numeric	0.037	-0.002	VBG
dm	0	factor	-0.082	0.002	VBG
dm	1	factor	0.082	-0.002	VBG
location	1	factor	0.399	-0.002	VBG
race_ethnicity	4	factor	0.068	-0.002	VBG
chf	0	factor	-0.037	0.002	VBG
chf	1	factor	0.037	-0.002	VBG
dm	1	factor	0.082	-0.002	VBG
dm	0	factor	-0.082	0.002	VBG
copd	0	factor	-0.008	-0.002	VBG
copd	1	factor	0.008	0.002	VBG
location	2	factor	0.066	0.002	VBG
osa	1	factor	-0.025	-0.002	VBG
osa	0	factor	0.025	0.002	VBG
serum_k	NA	numeric	0.038	-0.002	VBG
chf	1	factor	0.037	0.002	VBG
chf	0	factor	-0.037	-0.002	VBG
location	2	factor	0.066	-0.002	VBG
dm	1	factor	0.082	-0.002	VBG
dm	0	factor	-0.082	0.002	VBG
race_ethnicity	5	factor	-0.018	-0.002	VBG
osa	1	factor	-0.025	0.002	VBG
osa	0	factor	0.025	-0.002	VBG
acute_nmd	1	factor	0.009	-0.002	VBG
acute_nmd	0	factor	-0.009	0.002	VBG
osa	1	factor	-0.025	0.002	VBG
osa	0	factor	0.025	-0.002	VBG
dm	1	factor	0.082	-0.002	VBG
dm	0	factor	-0.082	0.002	VBG
copd	0	factor	-0.008	0.002	VBG
copd	1	factor	0.008	-0.002	VBG
dm	0	factor	-0.082	0.002	VBG
dm	1	factor	0.082	-0.002	VBG
location	1	factor	0.399	0.002	VBG
osa	0	factor	0.025	-0.002	VBG
osa	1	factor	-0.025	0.002	VBG
serum_k	NA	numeric	0.040	0.002	VBG
race_ethnicity	3	factor	0.029	-0.002	VBG

Table 20: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
location	2	factor	0.066	-0.002	VBG
race_ethnicity	4	factor	0.068	-0.002	VBG
serum_k	NA	numeric	0.040	0.002	VBG
osa	1	factor	-0.025	0.002	VBG
osa	0	factor	0.025	-0.002	VBG
race_ethnicity	2	factor	0.021	0.002	VBG
race_ethnicity	0	factor	-0.194	0.002	VBG
serum_k	NA	numeric	0.038	0.002	VBG
acute_nmd	1	factor	0.009	-0.002	VBG
acute_nmd	0	factor	-0.009	0.002	VBG
location	1	factor	0.399	-0.002	VBG
sodium	NA	numeric	-0.105	0.002	VBG
sodium	NA	numeric	-0.106	-0.002	VBG
curr_bmi	NA	numeric	-0.217	0.002	VBG
dm	0	factor	-0.082	-0.002	VBG
dm	1	factor	0.082	0.002	VBG
sbp	NA	numeric	-0.092	-0.002	VBG
race_ethnicity	3	factor	0.029	0.002	VBG
location	2	factor	0.066	-0.002	VBG
race_ethnicity	4	factor	0.068	0.002	VBG
sodium	NA	numeric	-0.104	0.002	VBG
sodium	NA	numeric	-0.104	0.002	VBG
race_ethnicity	2	factor	0.021	-0.002	VBG
dm	0	factor	-0.082	0.002	VBG
dm	1	factor	0.082	-0.002	VBG
race_ethnicity	4	factor	0.068	0.002	VBG
location	2	factor	0.066	0.002	VBG
race_ethnicity	3	factor	0.029	0.002	VBG
copd	0	factor	-0.008	-0.002	VBG
copd	1	factor	0.008	0.002	VBG
location	2	factor	0.066	-0.002	VBG
race_ethnicity	4	factor	0.068	-0.002	VBG
osa	0	factor	0.025	-0.002	VBG
osa	1	factor	-0.025	0.002	VBG
serum_k	NA	numeric	0.040	0.002	VBG
acute_nmd	1	factor	0.009	0.002	VBG
acute_nmd	0	factor	-0.009	-0.002	VBG
race_ethnicity	2	factor	0.021	-0.002	VBG
chf	0	factor	-0.037	-0.002	VBG
chf	1	factor	0.037	0.002	VBG
dm	1	factor	0.082	0.002	VBG
dm	0	factor	-0.082	-0.002	VBG
sodium	NA	numeric	-0.106	-0.002	VBG
location	2	factor	0.066	-0.002	VBG
osa	0	factor	0.025	0.002	VBG
osa	1	factor	-0.025	-0.002	VBG
location	2	factor	0.066	0.002	VBG
race_ethnicity	2	factor	0.021	0.002	VBG
dm	0	factor	-0.082	0.002	VBG
dm	1	factor	0.082	-0.002	VBG
copd	0	factor	-0.008	0.002	VBG
copd	1	factor	0.008	-0.002	VBG
sodium	NA	numeric	-0.107	0.002	VBG
race_ethnicity	4	factor	0.068	-0.002	VBG
location	1	factor	0.399	0.002	VBG
chf	0	factor	-0.037	-0.002	VBG
chf	1	factor	0.037	0.002	VBG
location	2	factor	0.066	-0.002	VBG
race_ethnicity	0	factor	-0.194	0.002	VBG
race_ethnicity	4	factor	0.068	-0.002	VBG
copd	1	factor	0.008	-0.002	VBG
copd	0	factor	-0.008	0.002	VBG
copd	1	factor	0.008	-0.002	VBG

Table 20: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
copd	0	factor	-0.008	0.002	VBG
location	2	factor	0.066	-0.002	VBG
location	2	factor	0.066	0.002	VBG
race_ethnicity	3	factor	0.029	-0.002	VBG
race_ethnicity	3	factor	0.029	0.002	VBG
acute_nmd	0	factor	-0.009	0.002	VBG
acute_nmd	1	factor	0.009	-0.002	VBG
race_ethnicity	4	factor	0.068	-0.002	VBG
osa	0	factor	0.025	0.002	VBG
osa	1	factor	-0.025	-0.002	VBG
location	1	factor	0.399	0.002	VBG
acute_nmd	1	factor	0.009	-0.002	VBG
acute_nmd	0	factor	-0.009	0.002	VBG
sodium	NA	numeric	-0.105	-0.002	VBG
race_ethnicity	4	factor	0.068	-0.002	VBG
acute_nmd	1	factor	0.009	0.002	VBG
acute_nmd	0	factor	-0.009	-0.002	VBG
race_ethnicity	2	factor	0.021	0.002	VBG
location	2	factor	0.066	-0.002	VBG
osa	0	factor	0.025	0.002	VBG
osa	1	factor	-0.025	-0.002	VBG
copd	0	factor	-0.008	-0.002	VBG
copd	1	factor	0.008	0.002	VBG
serum_k	NA	numeric	0.041	-0.001	VBG
race_ethnicity	4	factor	0.068	0.001	VBG
location	1	factor	0.399	0.001	VBG
race_ethnicity	0	factor	-0.194	0.001	VBG
copd	1	factor	0.008	-0.001	VBG
copd	0	factor	-0.008	0.001	VBG
location	1	factor	0.399	0.001	VBG
race_ethnicity	4	factor	0.068	-0.001	VBG
location	2	factor	0.066	0.001	VBG
copd	0	factor	-0.008	-0.001	VBG
copd	1	factor	0.008	0.001	VBG
dm	0	factor	-0.082	0.001	VBG
dm	1	factor	0.082	-0.001	VBG
location	1	factor	0.399	0.001	VBG
copd	0	factor	-0.008	-0.001	VBG
copd	1	factor	0.008	0.001	VBG
race_ethnicity	2	factor	0.021	-0.001	VBG
race_ethnicity	2	factor	0.021	0.001	VBG
race_ethnicity	2	factor	0.021	-0.001	VBG
copd	0	factor	-0.008	0.001	VBG
copd	1	factor	0.008	-0.001	VBG
race_ethnicity	3	factor	0.029	0.001	VBG
race_ethnicity	2	factor	0.021	-0.001	VBG
location	2	factor	0.066	-0.001	VBG
race_ethnicity	4	factor	0.068	0.001	VBG
dm	1	factor	0.082	0.001	VBG
dm	0	factor	-0.082	-0.001	VBG
race_ethnicity	4	factor	0.068	-0.001	VBG
osa	0	factor	0.025	0.001	VBG
osa	1	factor	-0.025	-0.001	VBG
location	1	factor	0.399	-0.001	VBG
acute_nmd	1	factor	0.009	-0.001	VBG
acute_nmd	0	factor	-0.009	0.001	VBG
location	2	factor	0.066	0.001	VBG
acute_nmd	0	factor	-0.009	-0.001	VBG
acute_nmd	1	factor	0.009	0.001	VBG
race_ethnicity	4	factor	0.068	-0.001	VBG
race_ethnicity	4	factor	0.068	0.001	VBG
race_ethnicity	4	factor	0.068	-0.001	VBG
chf	0	factor	-0.037	-0.001	VBG
chf	1	factor	0.037	0.001	VBG

Table 20: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
race_ethnicity	5	factor	-0.018	-0.001	VBG
sodium	NA	numeric	-0.106	-0.001	VBG
race_ethnicity	4	factor	0.068	0.001	VBG
dm	1	factor	0.082	-0.001	VBG
dm	0	factor	-0.082	0.001	VBG
race_ethnicity	3	factor	0.029	0.001	VBG
location	2	factor	0.066	0.001	VBG
race_ethnicity	2	factor	0.021	-0.001	VBG
location	2	factor	0.066	0.001	VBG
copd	0	factor	-0.008	0.001	VBG
copd	1	factor	0.008	-0.001	VBG
sodium	NA	numeric	-0.104	-0.001	VBG
osa	0	factor	0.025	0.001	VBG
osa	1	factor	-0.025	-0.001	VBG
race_ethnicity	3	factor	0.029	0.001	VBG
location	2	factor	0.066	0.001	VBG
dm	1	factor	0.082	0.001	VBG
dm	0	factor	-0.082	-0.001	VBG
race_ethnicity	5	factor	-0.018	-0.001	VBG
race_ethnicity	4	factor	0.068	-0.001	VBG
race_ethnicity	2	factor	0.021	-0.001	VBG
race_ethnicity	0	factor	-0.194	-0.001	VBG
acute_nmd	0	factor	-0.009	0.001	VBG
acute_nmd	1	factor	0.009	-0.001	VBG
race_ethnicity	2	factor	0.021	-0.001	VBG
acute_nmd	1	factor	0.009	-0.001	VBG
acute_nmd	0	factor	-0.009	0.001	VBG
location	2	factor	0.066	-0.001	VBG
race_ethnicity	2	factor	0.021	-0.001	VBG
race_ethnicity	2	factor	0.021	0.001	VBG
copd	1	factor	0.008	-0.001	VBG
copd	0	factor	-0.008	0.001	VBG
race_ethnicity	2	factor	0.021	-0.001	VBG
sodium	NA	numeric	-0.104	-0.001	VBG
sodium	NA	numeric	-0.105	-0.001	VBG
race_ethnicity	4	factor	0.068	-0.001	VBG
copd	0	factor	-0.008	-0.001	VBG
copd	1	factor	0.008	0.001	VBG
location	1	factor	0.399	0.001	VBG
location	1	factor	0.399	0.001	VBG
race_ethnicity	4	factor	0.068	-0.001	VBG
race_ethnicity	4	factor	0.068	0.001	VBG
race_ethnicity	4	factor	0.068	-0.001	VBG
serum_k	NA	numeric	0.042	0.001	VBG
serum_k	NA	numeric	0.042	0.001	VBG
race_ethnicity	4	factor	0.068	-0.001	VBG
chf	0	factor	-0.037	-0.001	VBG
chf	1	factor	0.037	0.001	VBG
osa	1	factor	-0.025	-0.001	VBG
osa	0	factor	0.025	0.001	VBG
race_ethnicity	2	factor	0.021	0.001	VBG
location	1	factor	0.399	0.001	VBG
race_ethnicity	3	factor	0.029	0.001	VBG
race_ethnicity	4	factor	0.068	0.001	VBG
dm	0	factor	-0.082	-0.001	VBG
dm	1	factor	0.082	0.001	VBG
sodium	NA	numeric	-0.103	-0.001	VBG
acute_nmd	1	factor	0.009	0.001	VBG
acute_nmd	0	factor	-0.009	-0.001	VBG
location	2	factor	0.066	0.001	VBG
race_ethnicity	5	factor	-0.018	-0.001	VBG
sodium	NA	numeric	-0.105	0.001	VBG
dm	1	factor	0.082	-0.001	VBG

Table 20: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
dm	0	factor	-0.082	0.001	VBG
serum_k	NA	numeric	0.039	0.001	VBG
race_ethnicity	4	factor	0.068	-0.001	VBG
dm	0	factor	-0.082	0.001	VBG
dm	1	factor	0.082	-0.001	VBG
location	1	factor	0.399	0.001	VBG
copd	1	factor	0.008	0.001	VBG
copd	0	factor	-0.008	-0.001	VBG
copd	1	factor	0.008	-0.001	VBG
copd	0	factor	-0.008	0.001	VBG
serum_k	NA	numeric	0.041	0.001	VBG
serum_k	NA	numeric	0.041	-0.001	VBG
race_ethnicity	2	factor	0.021	-0.001	VBG
dm	1	factor	0.082	-0.001	VBG
dm	0	factor	-0.082	0.001	VBG
serum_k	NA	numeric	0.040	-0.001	VBG
osa	1	factor	-0.025	0.001	VBG
osa	0	factor	0.025	-0.001	VBG
serum_k	NA	numeric	0.045	-0.001	VBG
sodium	NA	numeric	-0.105	0.001	VBG
race_ethnicity	2	factor	0.021	-0.001	VBG
location	1	factor	0.399	0.001	VBG
dm	1	factor	0.082	-0.001	VBG
dm	0	factor	-0.082	0.001	VBG
osa	0	factor	0.025	0.001	VBG
osa	1	factor	-0.025	-0.001	VBG
race_ethnicity	4	factor	0.068	-0.001	VBG
race_ethnicity	2	factor	0.021	-0.001	VBG
race_ethnicity	4	factor	0.068	-0.001	VBG
acute_nmd	1	factor	0.009	-0.001	VBG
acute_nmd	0	factor	-0.009	0.001	VBG
race_ethnicity	4	factor	0.068	-0.001	VBG
acute_nmd	0	factor	-0.009	0.001	VBG
acute_nmd	1	factor	0.009	-0.001	VBG
location	2	factor	0.066	0.001	VBG
sodium	NA	numeric	-0.106	0.001	VBG
chf	0	factor	-0.037	0.001	VBG
chf	1	factor	0.037	-0.001	VBG
sodium	NA	numeric	-0.105	0.001	VBG
dm	1	factor	0.082	0.001	VBG
dm	0	factor	-0.082	-0.001	VBG
serum_k	NA	numeric	0.044	0.001	VBG
acute_nmd	0	factor	-0.009	-0.001	VBG
acute_nmd	1	factor	0.009	0.001	VBG
race_ethnicity	1	factor	0.042	0.001	VBG
copd	0	factor	-0.008	0.001	VBG
copd	1	factor	0.008	-0.001	VBG
acute_nmd	1	factor	0.009	0.001	VBG
acute_nmd	0	factor	-0.009	-0.001	VBG
serum_k	NA	numeric	0.042	-0.001	VBG
osa	1	factor	-0.025	0.001	VBG
osa	0	factor	0.025	-0.001	VBG
location	1	factor	0.399	0.001	VBG
location	1	factor	0.399	-0.001	VBG
serum_k	NA	numeric	0.042	-0.001	VBG
race_ethnicity	4	factor	0.068	-0.001	VBG
race_ethnicity	0	factor	-0.194	0.001	VBG
race_ethnicity	0	factor	-0.194	0.001	VBG
curr_bmi	NA	numeric	-0.231	-0.001	VBG
race_ethnicity	2	factor	0.021	0.001	VBG
race_ethnicity	4	factor	0.068	0.001	VBG
race_ethnicity	2	factor	0.021	0.001	VBG
location	2	factor	0.066	0.001	VBG

Table 20: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
osa	0	factor	0.025	0.001	VBG
osa	1	factor	-0.025	-0.001	VBG
acute_nmd	0	factor	-0.009	0.001	VBG
acute_nmd	1	factor	0.009	-0.001	VBG
sodium	NA	numeric	-0.104	0.001	VBG
acute_nmd	1	factor	0.009	-0.001	VBG
acute_nmd	0	factor	-0.009	0.001	VBG
location	2	factor	0.066	-0.001	VBG
race_ethnicity	4	factor	0.068	-0.001	VBG
race_ethnicity	2	factor	0.021	-0.001	VBG
race_ethnicity	3	factor	0.029	-0.001	VBG
osa	0	factor	0.025	-0.001	VBG
osa	1	factor	-0.025	0.001	VBG
race_ethnicity	4	factor	0.068	0.001	VBG
serum_k	NA	numeric	0.038	-0.001	VBG
location	1	factor	0.399	0.001	VBG
acute_nmd	0	factor	-0.009	-0.001	VBG
acute_nmd	1	factor	0.009	0.001	VBG
serum_k	NA	numeric	0.044	-0.001	VBG
location	2	factor	0.066	0.001	VBG
osa	1	factor	-0.025	0.001	VBG
osa	0	factor	0.025	-0.001	VBG
location	2	factor	0.066	0.001	VBG
chf	0	factor	-0.037	0.001	VBG
chf	1	factor	0.037	-0.001	VBG
osa	0	factor	0.025	-0.001	VBG
osa	1	factor	-0.025	0.001	VBG
race_ethnicity	0	factor	-0.194	-0.001	VBG
race_ethnicity	2	factor	0.021	-0.001	VBG
dm	1	factor	0.082	0.001	VBG
dm	0	factor	-0.082	-0.001	VBG
sodium	NA	numeric	-0.104	0.001	VBG
location	1	factor	0.399	0.001	VBG
copd	0	factor	-0.008	0.001	VBG
copd	1	factor	0.008	-0.001	VBG
race_ethnicity	4	factor	0.068	-0.001	VBG
serum_k	NA	numeric	0.040	-0.001	VBG
sodium	NA	numeric	-0.105	-0.001	VBG
race_ethnicity	4	factor	0.068	0.001	VBG
location	1	factor	0.399	-0.001	VBG
dm	0	factor	-0.082	0.001	VBG
dm	1	factor	0.082	-0.001	VBG
race_ethnicity	4	factor	0.068	-0.001	VBG
acute_nmd	0	factor	-0.009	-0.001	VBG
acute_nmd	1	factor	0.009	0.001	VBG
acute_nmd	0	factor	-0.009	-0.001	VBG
acute_nmd	1	factor	0.009	0.001	VBG
sodium	NA	numeric	-0.104	-0.001	VBG
location	2	factor	0.066	-0.001	VBG
chf	1	factor	0.037	-0.001	VBG
chf	0	factor	-0.037	0.001	VBG
race_ethnicity	4	factor	0.068	-0.001	VBG
sodium	NA	numeric	-0.105	-0.001	VBG
serum_k	NA	numeric	0.040	-0.001	VBG
race_ethnicity	2	factor	0.021	-0.001	VBG
serum_k	NA	numeric	0.039	0.001	VBG
location	1	factor	0.399	0.001	VBG
race_ethnicity	4	factor	0.068	-0.001	VBG
race_ethnicity	4	factor	0.068	-0.001	VBG
race_ethnicity	4	factor	0.068	-0.001	VBG
serum_k	NA	numeric	0.041	0.001	VBG
serum_k	NA	numeric	0.043	0.001	VBG
location	2	factor	0.066	0.001	VBG
dm	1	factor	0.082	-0.001	VBG

Table 20: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
dm	0	factor	-0.082	0.001	VBG
location	1	factor	0.399	-0.001	VBG
race_ethnicity	4	factor	0.068	-0.001	VBG
chf	0	factor	-0.037	-0.001	VBG
chf	1	factor	0.037	0.001	VBG
race_ethnicity	0	factor	-0.194	-0.001	VBG
race_ethnicity	4	factor	0.068	0.001	VBG
dm	0	factor	-0.082	0.001	VBG
dm	1	factor	0.082	-0.001	VBG
location	2	factor	0.066	0.001	VBG
location	1	factor	0.399	-0.001	VBG
location	2	factor	0.066	-0.001	VBG
race_ethnicity	3	factor	0.029	-0.001	VBG
sodium	NA	numeric	-0.104	-0.001	VBG
sodium	NA	numeric	-0.105	-0.001	VBG
chf	1	factor	0.037	0.001	VBG
chf	0	factor	-0.037	-0.001	VBG
chf	0	factor	-0.037	0.001	VBG
chf	1	factor	0.037	-0.001	VBG
chf	1	factor	0.037	-0.001	VBG
chf	0	factor	-0.037	0.001	VBG
race_ethnicity	4	factor	0.068	0.001	VBG
serum_k	NA	numeric	0.044	0.001	VBG
location	2	factor	0.066	0.001	VBG
race_ethnicity	4	factor	0.068	-0.001	VBG
race_ethnicity	4	factor	0.068	0.000	VBG
serum_k	NA	numeric	0.043	0.000	VBG
sodium	NA	numeric	-0.106	0.000	VBG
location	2	factor	0.066	0.000	VBG
race_ethnicity	4	factor	0.068	0.000	VBG
osa	0	factor	0.025	0.000	VBG
osa	1	factor	-0.025	0.000	VBG
race_ethnicity	4	factor	0.068	0.000	VBG
location	2	factor	0.066	0.000	VBG
osa	1	factor	-0.025	0.000	VBG
osa	0	factor	0.025	0.000	VBG
location	1	factor	0.399	0.000	VBG
location	2	factor	0.066	0.000	VBG
sbp	NA	numeric	-0.096	0.000	VBG
curr_bmi	NA	numeric	-0.203	0.000	VBG
copd	1	factor	0.008	0.000	VBG
copd	0	factor	-0.008	0.000	VBG
location	1	factor	0.399	0.000	VBG
serum_k	NA	numeric	0.043	0.000	VBG
copd	0	factor	-0.008	0.000	VBG
copd	1	factor	0.008	0.000	VBG
race_ethnicity	4	factor	0.068	0.000	VBG
race_ethnicity	4	factor	0.068	0.000	VBG
copd	0	factor	-0.008	0.000	VBG
copd	1	factor	0.008	0.000	VBG
race_ethnicity	4	factor	0.068	0.000	VBG
race_ethnicity	4	factor	0.068	0.000	VBG
copd	0	factor	-0.008	0.000	VBG
copd	1	factor	0.008	0.000	VBG
chf	1	factor	0.037	0.000	VBG
chf	0	factor	-0.037	0.000	VBG
location	2	factor	0.066	0.000	VBG
acute_nmd	0	factor	-0.009	0.000	VBG
acute_nmd	1	factor	0.009	0.000	VBG
race_ethnicity	4	factor	0.068	0.000	VBG
race_ethnicity	4	factor	0.068	0.000	VBG
location	2	factor	0.066	0.000	VBG
chf	1	factor	0.037	0.000	VBG

Table 20: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (continued)

variable	level	type	smd_pre	smd_post	group
chf	0	factor	-0.037	0.000	VBG
osa	1	factor	-0.025	0.000	VBG
osa	0	factor	0.025	0.000	VBG
serum_k	NA	numeric	0.039	0.000	VBG
race_ethnicity	4	factor	0.068	0.000	VBG
serum_k	NA	numeric	0.044	0.000	VBG
location	1	factor	0.399	0.000	VBG
sodium	NA	numeric	-0.108	0.000	VBG
race_ethnicity	4	factor	0.068	0.000	VBG
race_ethnicity	4	factor	0.068	0.000	VBG
location	2	factor	0.066	0.000	VBG
acute_nmd	1	factor	0.009	0.000	VBG
acute_nmd	0	factor	-0.009	0.000	VBG
race_ethnicity	2	factor	0.021	0.000	VBG
race_ethnicity	4	factor	0.068	0.000	VBG
race_ethnicity	4	factor	0.068	0.000	VBG
osa	0	factor	0.025	0.000	VBG
osa	1	factor	-0.025	0.000	VBG
sodium	NA	numeric	-0.110	0.000	VBG
location	2	factor	0.066	0.000	VBG
race_ethnicity	4	factor	0.068	0.000	VBG
osa	1	factor	-0.025	0.000	VBG
osa	0	factor	0.025	0.000	VBG
chf	0	factor	-0.037	0.000	VBG
chf	1	factor	0.037	0.000	VBG
location	2	factor	0.066	0.000	VBG
acute_nmd	0	factor	-0.009	0.000	VBG
acute_nmd	1	factor	0.009	0.000	VBG
copd	0	factor	-0.008	0.000	VBG
copd	1	factor	0.008	0.000	VBG
race_ethnicity	2	factor	0.021	0.000	VBG
race_ethnicity	4	factor	0.068	0.000	VBG
curr_bmi	NA	numeric	-0.232	0.000	VBG
race_ethnicity	2	factor	0.021	0.000	VBG
osa	0	factor	0.025	0.000	VBG
osa	1	factor	-0.025	0.000	VBG
race_ethnicity	2	factor	0.021	0.000	VBG
osa	1	factor	-0.025	0.000	VBG
osa	0	factor	0.025	0.000	VBG
copd	1	factor	0.008	0.000	VBG
copd	0	factor	-0.008	0.000	VBG
sbp	NA	numeric	-0.080	0.000	VBG
location	2	factor	0.066	0.000	VBG
location	1	factor	0.399	0.000	VBG
location	1	factor	0.399	0.000	VBG
acute_nmd	1	factor	0.009	0.000	VBG
acute_nmd	0	factor	-0.009	0.000	VBG
race_ethnicity	4	factor	0.068	0.000	VBG
sodium	NA	numeric	-0.105	0.000	VBG
location	1	factor	0.399	0.000	VBG
race_ethnicity	5	factor	-0.018	0.000	VBG
location	1	factor	0.399	0.000	VBG
dm	0	factor	-0.082	0.000	VBG
dm	1	factor	0.082	0.000	VBG
location	1	factor	0.399	0.000	VBG
dm	1	factor	0.082	0.000	VBG
dm	0	factor	-0.082	0.000	VBG
race_ethnicity	4	factor	0.068	0.000	VBG
race_ethnicity	4	factor	0.068	0.000	VBG
location	1	factor	0.399	0.000	VBG
location	1	factor	0.399	0.000	VBG
location	1	factor	0.399	0.000	VBG
race_ethnicity	3	factor	0.029	0.000	VBG

Table 20: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part A) (*continued*)

variable	level	type	smd_pre	smd_post	group
race_ethnicity	4	factor	0.068	0.000	VBG
location	2	factor	0.066	0.000	VBG
race_ethnicity	4	factor	0.068	0.000	VBG
race_ethnicity	4	factor	0.068	0.000	VBG
race_ethnicity	2	factor	0.021	0.000	VBG
race_ethnicity	4	factor	0.068	0.000	VBG
race_ethnicity	4	factor	0.068	0.000	VBG
sodium	NA	numeric	-0.101	0.000	VBG
race_ethnicity	4	factor	0.068	0.000	VBG
race_ethnicity	0	factor	-0.194	0.000	VBG
sodium	NA	numeric	-0.105	0.000	VBG
sodium	NA	numeric	-0.104	0.000	VBG
race_ethnicity	2	factor	0.021	0.000	VBG
race_ethnicity	4	factor	0.068	0.000	VBG
chf	1	factor	0.037	0.000	VBG
chf	0	factor	-0.037	0.000	VBG
race_ethnicity	4	factor	0.068	0.000	VBG
sodium	NA	numeric	-0.105	0.000	VBG
chf	0	factor	-0.037	0.000	VBG
chf	1	factor	0.037	0.000	VBG
chf	0	factor	-0.037	0.000	VBG
acute_nmd	0	factor	-0.009	0.000	VBG
acute_nmd	1	factor	0.009	0.000	VBG

Table 21: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part B)

imp	abs_post
26	0.051
26	0.051
68	0.049
68	0.049
36	0.049
36	0.049
9	0.048
9	0.048
53	0.048
53	0.048
60	0.048
27	0.048
27	0.048
25	0.048
25	0.048
24	0.047
49	0.047
49	0.047
52	0.047
52	0.047
37	0.047
37	0.047
35	0.047
35	0.047
16	0.047
16	0.047
74	0.046
74	0.046
31	0.046
31	0.046
45	0.046
45	0.046
13	0.046
62	0.046
62	0.046
70	0.046
70	0.046
10	0.046
10	0.046
7	0.046
77	0.046
77	0.046
80	0.046
80	0.046
56	0.045
19	0.045
19	0.045
33	0.045
33	0.045
64	0.045
64	0.045
25	0.045
79	0.045
79	0.045
78	0.045
78	0.045
18	0.045
61	0.045
61	0.045
65	0.045
65	0.045
6	0.045
24	0.045

Table 21: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
24	0.045
17	0.045
17	0.045
49	0.045
11	0.045
11	0.045
53	0.045
41	0.044
41	0.044
60	0.044
60	0.044
20	0.044
20	0.044
63	0.044
38	0.044
48	0.044
48	0.044
3	0.044
3	0.044
78	0.044
71	0.044
71	0.044
54	0.044
2	0.044
39	0.044
66	0.044
66	0.044
68	0.044
39	0.044
39	0.044
72	0.044
72	0.044
72	0.043
12	0.043
64	0.043
13	0.043
13	0.043
21	0.043
21	0.043
8	0.043
8	0.043
40	0.043
40	0.043
33	0.043
23	0.043
23	0.043
80	0.043
34	0.043
34	0.043
36	0.043
50	0.043
50	0.043
46	0.043
46	0.043
1	0.043
1	0.043
22	0.042
22	0.042
7	0.042
7	0.042
1	0.042
67	0.042
9	0.042

Table 21: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
69	0.042
69	0.042
6	0.042
6	0.042
46	0.042
14	0.042
14	0.042
52	0.042
73	0.042
73	0.042
15	0.042
15	0.042
27	0.042
44	0.042
44	0.042
79	0.042
56	0.042
56	0.042
47	0.042
74	0.042
67	0.042
67	0.042
4	0.042
4	0.042
50	0.042
58	0.042
58	0.041
58	0.041
48	0.041
71	0.041
55	0.041
55	0.041
18	0.041
18	0.041
8	0.041
75	0.041
75	0.041
31	0.041
77	0.041
3	0.041
32	0.041
32	0.041
61	0.041
23	0.041
28	0.041
28	0.041
47	0.041
47	0.041
76	0.041
76	0.041
30	0.041
30	0.041
30	0.041
16	0.041
67	0.041
21	0.041
55	0.040
17	0.040
26	0.040
51	0.040
51	0.040
34	0.040
63	0.040
63	0.040

Table 21: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
29	0.040
4	0.040
2	0.040
2	0.040
29	0.040
70	0.040
29	0.040
29	0.040
15	0.040
76	0.040
62	0.040
14	0.040
19	0.040
5	0.040
5	0.040
41	0.040
42	0.040
42	0.040
54	0.039
25	0.039
43	0.039
43	0.039
11	0.039
59	0.039
59	0.039
57	0.039
10	0.038
65	0.038
24	0.038
22	0.038
38	0.038
38	0.038
28	0.038
57	0.038
57	0.038
32	0.038
5	0.038
23	0.038
73	0.038
12	0.038
12	0.038
45	0.038
45	0.038
51	0.038
43	0.037
34	0.037
33	0.037
13	0.037
9	0.037
59	0.037
40	0.037
20	0.037
66	0.037
54	0.036
54	0.036
69	0.036
22	0.036
59	0.036
52	0.036
75	0.036
30	0.036
75	0.036
63	0.036

Table 21: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
73	0.036
4	0.035
38	0.035
41	0.035
10	0.035
71	0.035
51	0.035
17	0.035
44	0.035
37	0.035
43	0.035
21	0.035
1	0.035
27	0.035
42	0.035
8	0.035
65	0.034
39	0.034
14	0.034
36	0.034
20	0.034
56	0.034
6	0.033
79	0.033
66	0.033
70	0.033
11	0.033
64	0.033
52	0.033
5	0.033
19	0.033
26	0.033
49	0.033
46	0.033
35	0.033
53	0.033
21	0.033
40	0.033
49	0.033
61	0.033
42	0.032
80	0.032
60	0.032
53	0.032
71	0.032
28	0.032
12	0.032
47	0.032
24	0.032
3	0.032
61	0.032
22	0.032
37	0.032
27	0.032
15	0.032
72	0.032
48	0.032
79	0.031
15	0.031
55	0.031
16	0.031
44	0.031
9	0.031

Table 21: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
43	0.031
16	0.031
77	0.031
52	0.031
35	0.031
35	0.031
23	0.031
68	0.031
18	0.030
74	0.030
25	0.030
62	0.030
68	0.030
45	0.030
20	0.030
24	0.030
58	0.030
67	0.030
28	0.030
40	0.030
78	0.030
76	0.030
11	0.030
19	0.029
59	0.029
10	0.029
62	0.029
39	0.029
38	0.029
74	0.029
60	0.029
40	0.029
80	0.029
16	0.029
57	0.029
10	0.029
64	0.029
37	0.029
57	0.029
18	0.029
1	0.028
51	0.028
30	0.028
25	0.028
53	0.028
23	0.028
80	0.028
8	0.028
56	0.028
3	0.028
61	0.028
32	0.028
58	0.028
56	0.028
9	0.028
7	0.028
10	0.028
50	0.028
28	0.028
69	0.027
21	0.027
74	0.027
2	0.027
71	0.027

Table 21: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
80	0.027
2	0.027
63	0.027
79	0.027
70	0.027
76	0.027
76	0.027
54	0.027
14	0.027
36	0.027
56	0.027
17	0.027
78	0.027
54	0.027
12	0.027
46	0.027
71	0.027
7	0.027
38	0.027
66	0.026
76	0.026
15	0.026
46	0.026
46	0.026
2	0.026
26	0.026
58	0.026
55	0.026
72	0.026
50	0.026
13	0.026
5	0.026
38	0.026
41	0.026
65	0.026
6	0.026
74	0.026
69	0.026
16	0.026
32	0.026
76	0.026
4	0.026
78	0.026
69	0.026
68	0.026
33	0.026
31	0.026
49	0.025
18	0.025
57	0.025
77	0.025
9	0.025
21	0.025
29	0.025
62	0.025
35	0.025
8	0.025
6	0.025
18	0.025
73	0.025
75	0.025
55	0.025
23	0.025

Table 21: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
45	0.025
49	0.025
21	0.025
58	0.025
52	0.025
13	0.025
54	0.025
25	0.025
62	0.025
20	0.025
21	0.025
17	0.025
1	0.025
51	0.025
25	0.025
21	0.025
79	0.025
17	0.025
13	0.025
66	0.025
10	0.025
21	0.025
58	0.024
8	0.024
15	0.024
42	0.024
31	0.024
69	0.024
14	0.024
33	0.024
73	0.024
60	0.024
48	0.024
60	0.024
29	0.024
55	0.024
27	0.024
65	0.024
49	0.024
40	0.024
32	0.024
30	0.024
16	0.024
1	0.024
26	0.024
45	0.024
64	0.024
50	0.024
2	0.024
6	0.024
61	0.024
62	0.024
47	0.024
34	0.024
15	0.024
6	0.024
65	0.024
39	0.024
65	0.024
61	0.024
16	0.024
76	0.024
27	0.024

Table 21: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
27	0.024
20	0.024
12	0.024
7	0.024
50	0.023
19	0.023
37	0.023
70	0.023
57	0.023
56	0.023
4	0.023
58	0.023
66	0.023
28	0.023
28	0.023
74	0.023
43	0.023
3	0.023
8	0.023
8	0.023
49	0.023
49	0.023
44	0.023
64	0.023
64	0.023
78	0.023
62	0.023
56	0.023
38	0.023
66	0.023
36	0.023
19	0.023
44	0.023
71	0.023
35	0.023
61	0.023
11	0.023
79	0.023
15	0.023
43	0.023
13	0.023
19	0.023
60	0.023
20	0.023
73	0.023
39	0.023
47	0.023
14	0.023
34	0.023
34	0.023
48	0.023
70	0.023
14	0.023
6	0.023
6	0.023
27	0.023
19	0.023
45	0.023
70	0.023
18	0.023
66	0.023
1	0.023
70	0.023
2	0.023

Table 21: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
28	0.023
69	0.023
53	0.023
37	0.023
65	0.023
46	0.023
2	0.023
47	0.023
24	0.023
26	0.023
51	0.023
42	0.023
74	0.023
1	0.023
33	0.023
65	0.023
58	0.023
47	0.023
12	0.023
30	0.023
18	0.023
17	0.022
38	0.022
64	0.022
77	0.022
18	0.022
25	0.022
56	0.022
48	0.022
49	0.022
71	0.022
13	0.022
51	0.022
58	0.022
55	0.022
1	0.022
29	0.022
49	0.022
26	0.022
66	0.022
40	0.022
13	0.022
33	0.022
44	0.022
15	0.022
77	0.022
22	0.022
8	0.022
76	0.022
34	0.022
75	0.022
59	0.022
53	0.022
42	0.022
80	0.022
6	0.022
20	0.022
80	0.022
51	0.022
10	0.022
72	0.022
1	0.022
29	0.022

Table 21: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
68	0.022
73	0.022
40	0.022
32	0.022
70	0.022
67	0.022
65	0.022
24	0.022
45	0.022
73	0.022
22	0.022
41	0.022
2	0.022
40	0.022
52	0.022
54	0.022
77	0.022
58	0.022
72	0.022
11	0.022
6	0.022
42	0.022
23	0.022
31	0.022
12	0.022
53	0.022
12	0.022
12	0.022
41	0.022
36	0.022
33	0.022
39	0.022
56	0.022
79	0.022
3	0.022
79	0.022
53	0.022
3	0.022
12	0.022
70	0.022
1	0.022
44	0.022
80	0.022
71	0.022
8	0.022
31	0.022
5	0.022
40	0.022
8	0.022
28	0.021
6	0.021
35	0.021
11	0.021
5	0.021
7	0.021
67	0.021
62	0.021
30	0.021
79	0.021
34	0.021
38	0.021
45	0.021
41	0.021

Table 21: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
40	0.021
48	0.021
67	0.021
37	0.021
9	0.021
58	0.021
3	0.021
70	0.021
25	0.021
54	0.021
22	0.021
27	0.021
28	0.021
7	0.021
22	0.021
46	0.021
66	0.021
39	0.021
10	0.021
7	0.021
7	0.021
49	0.021
61	0.021
65	0.021
65	0.021
41	0.021
41	0.021
52	0.021
5	0.021
27	0.021
43	0.021
25	0.021
67	0.021
31	0.021
9	0.021
52	0.021
10	0.021
7	0.021
10	0.021
10	0.021
12	0.021
12	0.021
64	0.021
74	0.021
72	0.021
5	0.021
56	0.021
56	0.021
65	0.021
42	0.021
78	0.021
59	0.021
3	0.021
3	0.021
17	0.021
12	0.021
27	0.021
64	0.021
37	0.021
75	0.021
46	0.021
20	0.021
59	0.021
61	0.021

Table 21: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
51	0.021
63	0.021
76	0.021
3	0.021
1	0.021
61	0.021
30	0.021
34	0.021
47	0.021
57	0.021
16	0.021
48	0.021
5	0.021
76	0.021
22	0.021
56	0.021
56	0.021
76	0.021
12	0.020
30	0.020
28	0.020
64	0.020
23	0.020
23	0.020
19	0.020
70	0.020
70	0.020
61	0.020
33	0.020
80	0.020
13	0.020
29	0.020
13	0.020
2	0.020
59	0.020
40	0.020
43	0.020
8	0.020
4	0.020
5	0.020
63	0.020
70	0.020
24	0.020
51	0.020
30	0.020
3	0.020
3	0.020
24	0.020
24	0.020
44	0.020
24	0.020
63	0.020
33	0.020
69	0.020
37	0.020
16	0.020
59	0.020
41	0.020
61	0.020
23	0.020
33	0.020
16	0.020
63	0.020

Table 21: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
64	0.020
49	0.020
1	0.020
3	0.020
22	0.020
79	0.020
42	0.020
11	0.020
19	0.020
50	0.020
59	0.020
59	0.020
14	0.020
59	0.020
39	0.020
13	0.020
13	0.020
52	0.020
75	0.020
42	0.020
42	0.020
28	0.020
4	0.020
77	0.020
42	0.020
54	0.020
1	0.020
23	0.020
78	0.020
28	0.020
38	0.020
60	0.020
75	0.020
42	0.020
7	0.020
70	0.020
48	0.020
19	0.020
21	0.020
80	0.020
80	0.020
67	0.020
26	0.020
11	0.020
68	0.020
56	0.020
47	0.020
35	0.019
2	0.019
2	0.019
41	0.019
33	0.019
24	0.019
34	0.019
65	0.019
43	0.019
43	0.019
40	0.019
7	0.019
6	0.019
46	0.019
15	0.019
18	0.019

Table 21: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
14	0.019
13	0.019
72	0.019
58	0.019
37	0.019
37	0.019
71	0.019
54	0.019
45	0.019
11	0.019
22	0.019
55	0.019
44	0.019
33	0.019
33	0.019
7	0.019
7	0.019
47	0.019
26	0.019
11	0.019
28	0.019
38	0.019
38	0.019
62	0.019
39	0.019
39	0.019
63	0.019
63	0.019
6	0.019
27	0.019
77	0.019
4	0.019
4	0.019
49	0.019
72	0.019
26	0.019
74	0.019
78	0.019
45	0.019
45	0.019
49	0.019
69	0.019
69	0.019
27	0.019
38	0.019
10	0.019
38	0.019
39	0.019
72	0.019
72	0.019
63	0.019
66	0.019
8	0.019
8	0.019
41	0.019
80	0.019
35	0.019
48	0.019
17	0.019
29	0.019
25	0.019
25	0.019
75	0.019
78	0.019

Table 21: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
68	0.019
79	0.019
57	0.019
31	0.019
14	0.019
26	0.019
56	0.019
34	0.019
32	0.019
20	0.019
38	0.019
76	0.019
70	0.019
54	0.019
5	0.019
5	0.019
60	0.019
60	0.019
53	0.019
65	0.019
1	0.019
59	0.019
25	0.019
79	0.019
26	0.019
68	0.019
68	0.019
22	0.019
22	0.019
32	0.019
55	0.019
52	0.019
39	0.019
42	0.019
74	0.019
39	0.019
67	0.019
12	0.019
52	0.019
35	0.019
48	0.019
71	0.019
33	0.018
65	0.018
72	0.018
45	0.018
19	0.018
19	0.018
48	0.018
33	0.018
52	0.018
49	0.018
68	0.018
15	0.018
23	0.018
56	0.018
35	0.018
35	0.018
49	0.018
2	0.018
8	0.018
50	0.018
63	0.018

Table 21: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
71	0.018
71	0.018
42	0.018
65	0.018
65	0.018
25	0.018
25	0.018
9	0.018
40	0.018
20	0.018
74	0.018
57	0.018
73	0.018
73	0.018
52	0.018
52	0.018
68	0.018
25	0.018
79	0.018
36	0.018
36	0.018
39	0.018
30	0.018
62	0.018
14	0.018
74	0.018
74	0.018
50	0.018
31	0.018
51	0.018
9	0.018
73	0.018
73	0.018
23	0.018
36	0.018
20	0.018
54	0.018
54	0.018
77	0.018
1	0.018
69	0.018
35	0.018
47	0.018
32	0.018
52	0.018
52	0.018
31	0.018
47	0.018
55	0.018
54	0.018
76	0.018
66	0.018
44	0.018
52	0.018
68	0.018
37	0.018
73	0.018
74	0.018
4	0.018
45	0.018
2	0.018
68	0.018
68	0.018

Table 21: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
6	0.018
66	0.018
66	0.018
31	0.018
31	0.018
14	0.018
14	0.018
24	0.018
55	0.018
55	0.018
63	0.018
15	0.018
4	0.018
32	0.018
59	0.018
12	0.018
55	0.018
37	0.018
41	0.018
49	0.017
49	0.017
65	0.017
65	0.017
75	0.017
1	0.017
42	0.017
60	0.017
16	0.017
16	0.017
63	0.017
47	0.017
74	0.017
67	0.017
26	0.017
15	0.017
15	0.017
59	0.017
73	0.017
34	0.017
13	0.017
43	0.017
66	0.017
66	0.017
1	0.017
1	0.017
51	0.017
26	0.017
72	0.017
72	0.017
43	0.017
12	0.017
6	0.017
6	0.017
68	0.017
13	0.017
13	0.017
75	0.017
75	0.017
17	0.017
29	0.017
60	0.017
65	0.017
5	0.017
26	0.017

Table 21: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
58	0.017
60	0.017
27	0.017
9	0.017
78	0.017
78	0.017
52	0.017
44	0.017
22	0.017
52	0.017
46	0.017
37	0.017
17	0.017
51	0.017
51	0.017
36	0.017
36	0.017
50	0.017
50	0.017
43	0.017
18	0.017
18	0.017
45	0.017
7	0.017
16	0.017
27	0.017
26	0.017
29	0.017
56	0.017
56	0.017
25	0.017
3	0.017
78	0.017
75	0.017
70	0.017
70	0.017
50	0.017
59	0.017
24	0.017
24	0.017
4	0.017
24	0.017
23	0.017
54	0.017
54	0.017
48	0.017
48	0.017
72	0.017
26	0.017
69	0.017
14	0.017
24	0.017
17	0.017
30	0.017
79	0.017
79	0.017
19	0.017
67	0.017
67	0.017
40	0.017
40	0.017
69	0.017
32	0.017

Table 21: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
72	0.017
23	0.017
72	0.017
66	0.017
63	0.017
18	0.017
32	0.017
64	0.017
77	0.016
50	0.016
53	0.016
53	0.016
35	0.016
20	0.016
22	0.016
76	0.016
18	0.016
50	0.016
73	0.016
32	0.016
73	0.016
77	0.016
77	0.016
55	0.016
70	0.016
29	0.016
31	0.016
31	0.016
4	0.016
23	0.016
44	0.016
29	0.016
58	0.016
58	0.016
24	0.016
24	0.016
63	0.016
35	0.016
78	0.016
5	0.016
5	0.016
61	0.016
3	0.016
3	0.016
28	0.016
28	0.016
25	0.016
25	0.016
25	0.016
73	0.016
73	0.016
18	0.016
2	0.016
6	0.016
66	0.016
78	0.016
49	0.016
46	0.016
46	0.016
13	0.016
20	0.016
42	0.016
44	0.016

Table 21: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
48	0.016
23	0.016
46	0.016
46	0.016
36	0.016
51	0.016
13	0.016
62	0.016
62	0.016
14	0.016
55	0.016
52	0.016
74	0.016
73	0.016
57	0.016
10	0.016
57	0.016
7	0.016
28	0.016
27	0.016
27	0.016
68	0.016
70	0.016
68	0.016
68	0.016
44	0.016
21	0.016
62	0.016
62	0.016
58	0.016
58	0.016
67	0.016
3	0.016
53	0.016
77	0.016
56	0.016
55	0.016
17	0.016
17	0.016
80	0.016
59	0.016
53	0.016
79	0.016
79	0.016
60	0.016
21	0.016
21	0.016
6	0.016
30	0.016
30	0.016
69	0.016
74	0.016
74	0.016
12	0.016
12	0.016
70	0.016
48	0.016
49	0.016
66	0.016
64	0.016
71	0.016
28	0.016
59	0.016
59	0.016

Table 21: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
67	0.016
27	0.016
6	0.016
14	0.016
14	0.016
19	0.016
65	0.016
80	0.016
35	0.016
21	0.016
26	0.016
26	0.016
78	0.016
11	0.015
54	0.015
68	0.015
12	0.015
58	0.015
80	0.015
44	0.015
69	0.015
69	0.015
19	0.015
30	0.015
43	0.015
7	0.015
64	0.015
64	0.015
62	0.015
35	0.015
32	0.015
42	0.015
33	0.015
66	0.015
2	0.015
72	0.015
43	0.015
59	0.015
69	0.015
78	0.015
77	0.015
25	0.015
14	0.015
47	0.015
30	0.015
60	0.015
2	0.015
47	0.015
11	0.015
11	0.015
31	0.015
24	0.015
16	0.015
36	0.015
14	0.015
41	0.015
50	0.015
6	0.015
8	0.015
8	0.015
18	0.015
18	0.015
47	0.015

Table 21: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
9	0.015
9	0.015
60	0.015
30	0.015
15	0.015
23	0.015
36	0.015
3	0.015
18	0.015
10	0.015
15	0.015
15	0.015
40	0.015
38	0.015
60	0.015
60	0.015
67	0.015
70	0.015
80	0.015
62	0.015
65	0.015
65	0.015
65	0.015
35	0.015
55	0.015
18	0.015
47	0.015
16	0.015
16	0.015
32	0.015
32	0.015
76	0.015
72	0.015
72	0.015
2	0.015
2	0.015
8	0.015
8	0.015
28	0.015
35	0.015
45	0.015
10	0.015
18	0.015
48	0.015
9	0.015
74	0.015
74	0.015
48	0.015
48	0.015
58	0.015
24	0.015
24	0.015
37	0.015
1	0.014
1	0.014
36	0.014
17	0.014
17	0.014
33	0.014
33	0.014
48	0.014
48	0.014
41	0.014

Table 21: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
41	0.014
43	0.014
75	0.014
38	0.014
38	0.014
51	0.014
12	0.014
64	0.014
64	0.014
44	0.014
44	0.014
34	0.014
71	0.014
21	0.014
14	0.014
31	0.014
31	0.014
66	0.014
47	0.014
47	0.014
13	0.014
22	0.014
5	0.014
51	0.014
51	0.014
57	0.014
46	0.014
16	0.014
33	0.014
42	0.014
64	0.014
51	0.014
63	0.014
63	0.014
38	0.014
43	0.014
29	0.014
72	0.014
72	0.014
75	0.014
38	0.014
22	0.014
62	0.014
62	0.014
7	0.014
16	0.014
80	0.014
80	0.014
31	0.014
31	0.014
27	0.014
60	0.014
54	0.014
24	0.014
24	0.014
75	0.014
39	0.014
39	0.014
15	0.014
70	0.014
37	0.014
18	0.014
31	0.014
16	0.014

Table 21: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
16	0.014
22	0.014
62	0.014
21	0.014
12	0.014
34	0.014
34	0.014
47	0.014
47	0.014
10	0.014
28	0.014
17	0.014
5	0.014
17	0.014
20	0.014
72	0.014
28	0.014
17	0.014
41	0.014
61	0.014
8	0.014
19	0.014
3	0.014
19	0.014
19	0.014
26	0.014
31	0.014
53	0.014
53	0.014
29	0.014
18	0.014
14	0.014
46	0.014
48	0.014
45	0.014
27	0.014
58	0.014
57	0.014
57	0.014
71	0.014
64	0.014
21	0.014
21	0.014
40	0.014
41	0.013
77	0.013
9	0.013
60	0.013
60	0.013
45	0.013
45	0.013
15	0.013
34	0.013
26	0.013
62	0.013
62	0.013
51	0.013
7	0.013
47	0.013
63	0.013
63	0.013
34	0.013
34	0.013

Table 21: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
32	0.013
48	0.013
48	0.013
67	0.013
67	0.013
73	0.013
73	0.013
27	0.013
53	0.013
53	0.013
19	0.013
38	0.013
38	0.013
67	0.013
41	0.013
61	0.013
61	0.013
62	0.013
37	0.013
40	0.013
40	0.013
73	0.013
3	0.013
36	0.013
36	0.013
4	0.013
4	0.013
49	0.013
39	0.013
34	0.013
34	0.013
21	0.013
64	0.013
44	0.013
44	0.013
43	0.013
43	0.013
29	0.013
14	0.013
21	0.013
11	0.013
54	0.013
54	0.013
40	0.013
40	0.013
9	0.013
9	0.013
21	0.013
21	0.013
73	0.013
2	0.013
55	0.013
55	0.013
3	0.013
3	0.013
32	0.013
73	0.013
46	0.013
46	0.013
20	0.013
76	0.013
7	0.013
46	0.013

Table 21: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
77	0.013
56	0.013
71	0.013
71	0.013
80	0.013
80	0.013
57	0.013
75	0.013
30	0.013
15	0.013
36	0.013
47	0.013
47	0.013
77	0.013
77	0.013
41	0.013
32	0.013
56	0.013
56	0.013
68	0.013
78	0.013
78	0.013
4	0.013
4	0.013
61	0.013
37	0.013
37	0.013
60	0.013
39	0.013
30	0.013
30	0.013
17	0.013
17	0.013
2	0.013
2	0.013
21	0.012
43	0.012
43	0.012
25	0.012
25	0.012
44	0.012
44	0.012
35	0.012
72	0.012
17	0.012
11	0.012
11	0.012
45	0.012
19	0.012
53	0.012
10	0.012
10	0.012
11	0.012
11	0.012
74	0.012
78	0.012
76	0.012
11	0.012
20	0.012
20	0.012
77	0.012
77	0.012
54	0.012
54	0.012

Table 21: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
40	0.012
40	0.012
43	0.012
25	0.012
18	0.012
18	0.012
4	0.012
4	0.012
55	0.012
26	0.012
26	0.012
60	0.012
46	0.012
71	0.012
71	0.012
15	0.012
15	0.012
76	0.012
7	0.012
7	0.012
11	0.012
12	0.012
8	0.012
5	0.012
69	0.012
37	0.012
74	0.012
74	0.012
9	0.012
55	0.012
55	0.012
6	0.012
6	0.012
14	0.012
14	0.012
45	0.012
45	0.012
57	0.012
53	0.012
3	0.012
3	0.012
50	0.012
50	0.012
78	0.012
24	0.012
26	0.012
26	0.012
59	0.012
33	0.012
79	0.012
49	0.012
49	0.012
40	0.012
45	0.012
45	0.012
67	0.012
67	0.012
54	0.012
43	0.012
8	0.012
66	0.012
66	0.012
47	0.012

Table 21: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
10	0.012
54	0.012
19	0.012
19	0.012
61	0.012
78	0.012
7	0.012
7	0.012
11	0.012
29	0.012
29	0.012
9	0.012
9	0.012
80	0.012
27	0.012
27	0.012
63	0.012
63	0.012
32	0.012
32	0.012
61	0.012
61	0.012
58	0.012
58	0.012
50	0.012
61	0.012
36	0.012
36	0.012
3	0.012
63	0.012
63	0.012
20	0.012
20	0.012
10	0.012
36	0.012
80	0.012
57	0.012
74	0.012
69	0.012
50	0.012
50	0.012
62	0.012
20	0.012
20	0.012
23	0.012
23	0.012
50	0.012
44	0.012
27	0.012
59	0.012
25	0.012
13	0.012
13	0.012
68	0.012
30	0.012
55	0.012
31	0.012
38	0.012
38	0.012
30	0.012
30	0.012
37	0.011
23	0.011

Table 21: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
9	0.011
36	0.011
11	0.011
11	0.011
48	0.011
27	0.011
23	0.011
23	0.011
40	0.011
64	0.011
64	0.011
58	0.011
58	0.011
41	0.011
1	0.011
1	0.011
67	0.011
50	0.011
41	0.011
41	0.011
13	0.011
13	0.011
15	0.011
30	0.011
30	0.011
80	0.011
80	0.011
75	0.011
53	0.011
46	0.011
29	0.011
29	0.011
68	0.011
22	0.011
80	0.011
9	0.011
1	0.011
19	0.011
19	0.011
59	0.011
59	0.011
73	0.011
9	0.011
43	0.011
2	0.011
13	0.011
68	0.011
16	0.011
7	0.011
7	0.011
20	0.011
44	0.011
67	0.011
61	0.011
33	0.011
33	0.011
76	0.011
76	0.011
44	0.011
54	0.011
53	0.011
41	0.011
41	0.011
65	0.011

Table 21: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
4	0.011
4	0.011
78	0.011
78	0.011
22	0.011
9	0.011
9	0.011
52	0.011
52	0.011
16	0.011
16	0.011
29	0.011
76	0.011
77	0.011
15	0.011
70	0.011
70	0.011
5	0.011
5	0.011
12	0.011
24	0.011
8	0.011
41	0.011
41	0.011
7	0.011
39	0.011
12	0.011
12	0.011
35	0.011
35	0.011
13	0.011
54	0.011
36	0.011
79	0.011
79	0.011
50	0.011
37	0.011
37	0.011
58	0.011
28	0.011
28	0.011
54	0.011
17	0.011
30	0.011
79	0.011
38	0.011
78	0.011
10	0.011
10	0.011
75	0.011
75	0.011
38	0.011
46	0.010
31	0.010
31	0.010
9	0.010
9	0.010
16	0.010
75	0.010
75	0.010
71	0.010
67	0.010
32	0.010

Table 21: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
67	0.010
67	0.010
71	0.010
61	0.010
61	0.010
68	0.010
68	0.010
67	0.010
2	0.010
2	0.010
31	0.010
37	0.010
37	0.010
35	0.010
35	0.010
23	0.010
22	0.010
22	0.010
46	0.010
50	0.010
79	0.010
2	0.010
70	0.010
70	0.010
55	0.010
11	0.010
5	0.010
64	0.010
71	0.010
8	0.010
6	0.010
35	0.010
53	0.010
50	0.010
50	0.010
69	0.010
13	0.010
67	0.010
34	0.010
10	0.010
47	0.010
47	0.010
22	0.010
22	0.010
52	0.010
22	0.010
77	0.010
75	0.010
20	0.010
42	0.010
42	0.010
56	0.010
46	0.010
27	0.010
27	0.010
39	0.010
21	0.010
79	0.010
79	0.010
11	0.010
4	0.010
29	0.010
71	0.010

Table 21: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
75	0.010
75	0.010
34	0.010
8	0.010
8	0.010
34	0.010
69	0.010
69	0.010
16	0.010
58	0.010
10	0.010
10	0.010
23	0.010
36	0.010
20	0.010
20	0.010
31	0.010
31	0.010
55	0.010
63	0.010
63	0.010
59	0.010
70	0.010
70	0.010
61	0.010
61	0.010
15	0.010
15	0.010
68	0.010
65	0.010
75	0.010
43	0.010
43	0.010
4	0.010
40	0.010
39	0.010
39	0.010
44	0.010
60	0.010
60	0.010
60	0.010
13	0.010
13	0.010
2	0.010
2	0.010
11	0.010
32	0.010
59	0.010
59	0.010
17	0.010
17	0.010
56	0.009
37	0.009
39	0.009
39	0.009
53	0.009
53	0.009
23	0.009
25	0.009
57	0.009
60	0.009
6	0.009
59	0.009
72	0.009

Table 21: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
60	0.009
71	0.009
29	0.009
29	0.009
39	0.009
57	0.009
57	0.009
73	0.009
75	0.009
50	0.009
50	0.009
57	0.009
57	0.009
4	0.009
35	0.009
35	0.009
33	0.009
5	0.009
46	0.009
46	0.009
48	0.009
57	0.009
79	0.009
71	0.009
47	0.009
36	0.009
36	0.009
71	0.009
71	0.009
3	0.009
62	0.009
39	0.009
29	0.009
29	0.009
13	0.009
31	0.009
20	0.009
12	0.009
12	0.009
18	0.009
78	0.009
78	0.009
72	0.009
14	0.009
36	0.009
43	0.009
74	0.009
39	0.009
54	0.009
64	0.009
80	0.009
80	0.009
9	0.009
80	0.009
29	0.009
32	0.009
32	0.009
39	0.009
39	0.009
66	0.009
66	0.009
33	0.009
33	0.009

Table 21: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
25	0.009
58	0.009
9	0.009
42	0.009
42	0.009
28	0.009
52	0.009
5	0.009
22	0.009
63	0.009
22	0.009
22	0.009
57	0.009
44	0.009
71	0.009
71	0.009
18	0.009
18	0.009
17	0.009
17	0.009
63	0.009
26	0.009
27	0.008
36	0.008
36	0.008
38	0.008
42	0.008
42	0.008
69	0.008
32	0.008
32	0.008
77	0.008
77	0.008
1	0.008
80	0.008
80	0.008
3	0.008
3	0.008
49	0.008
39	0.008
44	0.008
44	0.008
42	0.008
29	0.008
25	0.008
2	0.008
2	0.008
76	0.008
30	0.008
30	0.008
4	0.008
36	0.008
6	0.008
6	0.008
58	0.008
56	0.008
56	0.008
15	0.008
53	0.008
19	0.008
76	0.008
76	0.008
52	0.008

Table 21: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
52	0.008
31	0.008
61	0.008
61	0.008
64	0.008
53	0.008
27	0.008
31	0.008
4	0.008
43	0.008
14	0.008
19	0.008
35	0.008
35	0.008
27	0.008
10	0.008
36	0.008
14	0.008
14	0.008
31	0.008
51	0.008
1	0.008
3	0.008
63	0.008
45	0.008
51	0.008
70	0.008
70	0.008
45	0.008
76	0.008
76	0.008
7	0.008
7	0.008
55	0.008
55	0.008
40	0.008
54	0.008
54	0.008
24	0.008
72	0.008
1	0.008
1	0.008
28	0.008
28	0.008
73	0.008
10	0.008
10	0.008
80	0.008
46	0.008
34	0.008
71	0.008
66	0.008
72	0.008
51	0.008
70	0.008
25	0.008
46	0.008
46	0.008
26	0.008
26	0.008
61	0.008
15	0.008
48	0.008
69	0.008

Table 21: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
69	0.008
15	0.008
66	0.007
2	0.007
72	0.007
72	0.007
65	0.007
29	0.007
8	0.007
30	0.007
70	0.007
51	0.007
51	0.007
65	0.007
65	0.007
5	0.007
5	0.007
69	0.007
23	0.007
23	0.007
17	0.007
57	0.007
57	0.007
79	0.007
18	0.007
56	0.007
56	0.007
57	0.007
67	0.007
67	0.007
35	0.007
69	0.007
63	0.007
63	0.007
51	0.007
51	0.007
25	0.007
55	0.007
19	0.007
56	0.007
34	0.007
34	0.007
16	0.007
16	0.007
16	0.007
51	0.007
34	0.007
21	0.007
13	0.007
24	0.007
4	0.007
22	0.007
22	0.007
69	0.007
56	0.007
6	0.007
76	0.007
59	0.007
28	0.007
67	0.007
67	0.007
69	0.007
69	0.007

Table 21: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
39	0.007
4	0.007
24	0.007
24	0.007
45	0.007
40	0.007
40	0.007
20	0.007
40	0.007
40	0.007
64	0.007
16	0.007
48	0.007
48	0.007
10	0.007
28	0.007
49	0.007
30	0.007
60	0.007
67	0.007
77	0.007
26	0.007
26	0.007
35	0.007
22	0.007
1	0.007
33	0.007
48	0.007
16	0.007
49	0.007
4	0.007
4	0.007
48	0.007
57	0.007
57	0.007
20	0.007
72	0.007
76	0.006
76	0.006
11	0.006
77	0.006
37	0.006
62	0.006
36	0.006
79	0.006
2	0.006
65	0.006
5	0.006
5	0.006
37	0.006
37	0.006
37	0.006
51	0.006
48	0.006
69	0.006
8	0.006
8	0.006
32	0.006
32	0.006
36	0.006
43	0.006
57	0.006
57	0.006

Table 21: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
8	0.006
53	0.006
65	0.006
34	0.006
45	0.006
8	0.006
33	0.006
20	0.006
72	0.006
71	0.006
7	0.006
76	0.006
76	0.006
63	0.006
75	0.006
47	0.006
47	0.006
1	0.006
50	0.006
77	0.006
52	0.006
52	0.006
13	0.006
49	0.006
16	0.006
75	0.006
12	0.006
64	0.006
11	0.006
28	0.006
28	0.006
70	0.006
68	0.006
49	0.006
49	0.006
17	0.006
59	0.006
9	0.006
29	0.006
29	0.006
25	0.006
25	0.006
57	0.006
57	0.006
32	0.006
32	0.006
19	0.006
19	0.006
23	0.006
39	0.006
39	0.006
31	0.006
74	0.006
3	0.006
66	0.006
27	0.006
41	0.006
25	0.006
38	0.006
38	0.006
63	0.006
63	0.006
25	0.006
25	0.006

Table 21: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
72	0.006
72	0.006
62	0.006
44	0.006
17	0.006
9	0.006
77	0.006
27	0.006
27	0.006
15	0.006
46	0.006
55	0.006
64	0.006
64	0.006
65	0.006
65	0.006
67	0.006
6	0.006
17	0.006
58	0.006
18	0.006
10	0.006
80	0.006
68	0.006
16	0.006
48	0.006
9	0.006
9	0.006
25	0.006
25	0.006
28	0.006
51	0.006
34	0.006
34	0.006
42	0.006
48	0.006
48	0.006
77	0.006
40	0.006
24	0.005
66	0.005
29	0.005
29	0.005
50	0.005
50	0.005
67	0.005
31	0.005
55	0.005
17	0.005
37	0.005
35	0.005
48	0.005
26	0.005
26	0.005
54	0.005
54	0.005
2	0.005
78	0.005
30	0.005
18	0.005
36	0.005
77	0.005
77	0.005

Table 21: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
62	0.005
62	0.005
6	0.005
69	0.005
53	0.005
53	0.005
61	0.005
77	0.005
14	0.005
47	0.005
21	0.005
21	0.005
24	0.005
8	0.005
8	0.005
54	0.005
33	0.005
41	0.005
18	0.005
36	0.005
35	0.005
35	0.005
33	0.005
63	0.005
6	0.005
41	0.005
41	0.005
26	0.005
26	0.005
64	0.005
80	0.005
52	0.005
47	0.005
36	0.005
36	0.005
58	0.005
78	0.005
63	0.005
58	0.005
19	0.005
23	0.005
69	0.005
57	0.005
11	0.005
24	0.005
12	0.005
26	0.005
26	0.005
32	0.005
32	0.005
26	0.005
35	0.005
35	0.005
38	0.005
38	0.005
15	0.005
64	0.005
64	0.005
49	0.005
49	0.005
75	0.005
75	0.005
58	0.005

Table 21: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
56	0.005
72	0.005
72	0.005
55	0.005
55	0.005
70	0.005
70	0.005
32	0.005
47	0.005
59	0.005
59	0.005
43	0.005
43	0.005
23	0.005
5	0.005
15	0.005
15	0.005
58	0.005
58	0.005
7	0.005
29	0.005
41	0.005
41	0.005
33	0.005
13	0.005
58	0.005
61	0.005
11	0.005
11	0.005
9	0.005
55	0.005
58	0.005
58	0.005
9	0.005
17	0.005
17	0.005
36	0.005
36	0.005
63	0.005
63	0.005
6	0.005
6	0.005
29	0.005
29	0.005
49	0.005
49	0.005
14	0.005
59	0.005
59	0.005
6	0.005
77	0.005
21	0.005
6	0.005
6	0.005
11	0.005
3	0.005
3	0.005
57	0.005
57	0.005
14	0.005
65	0.005
37	0.005
13	0.005
8	0.005

Table 21: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
34	0.005
68	0.005
68	0.005
32	0.005
32	0.005
21	0.005
21	0.005
21	0.005
4	0.005
4	0.005
11	0.005
11	0.005
64	0.005
64	0.005
33	0.005
33	0.005
56	0.005
42	0.005
42	0.005
22	0.005
77	0.005
77	0.005
23	0.005
54	0.004
11	0.004
18	0.004
18	0.004
19	0.004
19	0.004
56	0.004
44	0.004
44	0.004
15	0.004
37	0.004
46	0.004
70	0.004
20	0.004
20	0.004
49	0.004
52	0.004
28	0.004
56	0.004
54	0.004
54	0.004
64	0.004
30	0.004
29	0.004
29	0.004
24	0.004
24	0.004
7	0.004
7	0.004
72	0.004
72	0.004
24	0.004
60	0.004
43	0.004
43	0.004
9	0.004
24	0.004
66	0.004
32	0.004
46	0.004

Table 21: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
53	0.004
53	0.004
72	0.004
58	0.004
16	0.004
16	0.004
1	0.004
1	0.004
17	0.004
45	0.004
45	0.004
8	0.004
40	0.004
50	0.004
50	0.004
50	0.004
53	0.004
51	0.004
51	0.004
39	0.004
39	0.004
27	0.004
27	0.004
58	0.004
58	0.004
25	0.004
25	0.004
66	0.004
75	0.004
59	0.004
59	0.004
59	0.004
48	0.004
5	0.004
5	0.004
69	0.004
25	0.004
80	0.004
24	0.004
24	0.004
78	0.004
3	0.004
3	0.004
38	0.004
26	0.004
58	0.004
58	0.004
35	0.004
35	0.004
66	0.004
66	0.004
75	0.004
79	0.004
68	0.004
47	0.004
36	0.004
76	0.004
9	0.004
9	0.004
18	0.004
76	0.004
76	0.004
34	0.004

Table 21: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
39	0.004
34	0.004
59	0.004
66	0.004
66	0.004
55	0.004
8	0.004
71	0.004
71	0.004
78	0.004
78	0.004
48	0.004
48	0.004
77	0.004
77	0.004
2	0.004
79	0.004
79	0.004
41	0.004
41	0.004
14	0.004
32	0.004
52	0.004
42	0.004
42	0.004
53	0.004
53	0.004
21	0.004
20	0.004
20	0.004
47	0.004
47	0.004
75	0.004
38	0.004
38	0.004
30	0.004
49	0.004
49	0.004
21	0.004
80	0.004
21	0.004
5	0.004
5	0.004
73	0.004
19	0.004
21	0.004
21	0.004
78	0.004
78	0.004
73	0.004
73	0.004
66	0.004
10	0.004
10	0.004
51	0.004
51	0.004
73	0.004
73	0.004
30	0.004
32	0.004
71	0.004
71	0.004
5	0.004
19	0.004

Table 21: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
71	0.004
80	0.004
80	0.004
64	0.004
7	0.004
60	0.004
12	0.004
36	0.004
36	0.004
74	0.004
23	0.004
23	0.004
23	0.004
76	0.004
76	0.004
50	0.004
32	0.004
32	0.004
19	0.004
19	0.004
27	0.004
27	0.004
41	0.004
51	0.004
51	0.004
61	0.004
61	0.004
45	0.004
45	0.004
41	0.004
72	0.004
2	0.004
42	0.004
12	0.004
68	0.004
78	0.004
76	0.004
76	0.004
42	0.004
71	0.004
71	0.004
68	0.003
68	0.003
61	0.003
7	0.003
7	0.003
9	0.003
9	0.003
50	0.003
50	0.003
73	0.003
71	0.003
77	0.003
68	0.003
68	0.003
24	0.003
24	0.003
39	0.003
33	0.003
33	0.003
56	0.003
56	0.003
73	0.003

Table 21: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
22	0.003
22	0.003
6	0.003
22	0.003
30	0.003
30	0.003
47	0.003
14	0.003
30	0.003
30	0.003
4	0.003
63	0.003
63	0.003
74	0.003
55	0.003
17	0.003
63	0.003
67	0.003
67	0.003
46	0.003
77	0.003
52	0.003
15	0.003
15	0.003
14	0.003
74	0.003
56	0.003
29	0.003
74	0.003
61	0.003
60	0.003
46	0.003
31	0.003
77	0.003
77	0.003
1	0.003
1	0.003
74	0.003
57	0.003
68	0.003
34	0.003
44	0.003
57	0.003
46	0.003
31	0.003
31	0.003
61	0.003
54	0.003
54	0.003
2	0.003
48	0.003
48	0.003
21	0.003
21	0.003
5	0.003
5	0.003
42	0.003
40	0.003
40	0.003
74	0.003
74	0.003
69	0.003
69	0.003

Table 21: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
7	0.003
56	0.003
7	0.003
55	0.003
55	0.003
8	0.003
36	0.003
36	0.003
18	0.003
18	0.003
54	0.003
54	0.003
49	0.003
5	0.003
16	0.003
16	0.003
39	0.003
11	0.003
11	0.003
65	0.003
67	0.003
43	0.003
43	0.003
21	0.003
32	0.003
29	0.003
55	0.003
16	0.003
78	0.003
62	0.003
21	0.003
62	0.003
62	0.003
69	0.003
69	0.003
1	0.003
9	0.003
9	0.003
80	0.003
5	0.003
5	0.003
66	0.003
66	0.003
28	0.003
28	0.003
13	0.003
13	0.003
28	0.003
13	0.003
13	0.003
65	0.003
15	0.003
10	0.003
22	0.003
3	0.003
46	0.003
46	0.003
46	0.003
32	0.003
62	0.003
62	0.003
20	0.003
20	0.003
2	0.003

Table 21: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
2	0.003
33	0.003
12	0.003
4	0.003
4	0.003
26	0.003
24	0.003
24	0.003
56	0.003
56	0.003
69	0.003
69	0.003
33	0.003
42	0.003
8	0.003
8	0.003
76	0.003
52	0.003
52	0.003
39	0.003
39	0.003
70	0.003
70	0.003
4	0.003
60	0.003
60	0.003
49	0.003
70	0.003
70	0.003
18	0.003
18	0.003
76	0.003
76	0.003
3	0.003
44	0.003
44	0.003
55	0.003
55	0.003
19	0.003
19	0.003
73	0.003
73	0.003
20	0.003
20	0.003
50	0.003
11	0.003
11	0.003
78	0.003
78	0.003
34	0.003
34	0.003
19	0.003
13	0.003
47	0.003
79	0.003
38	0.003
31	0.003
56	0.003
57	0.003
10	0.003
68	0.003
68	0.003
16	0.003

Table 21: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
43	0.003
61	0.003
61	0.003
44	0.003
67	0.003
16	0.003
6	0.003
51	0.003
51	0.003
56	0.003
74	0.002
74	0.002
7	0.002
7	0.002
62	0.002
62	0.002
60	0.002
60	0.002
38	0.002
47	0.002
47	0.002
59	0.002
73	0.002
43	0.002
43	0.002
55	0.002
55	0.002
66	0.002
66	0.002
20	0.002
71	0.002
55	0.002
55	0.002
76	0.002
35	0.002
18	0.002
66	0.002
73	0.002
12	0.002
2	0.002
2	0.002
38	0.002
1	0.002
38	0.002
23	0.002
23	0.002
18	0.002
42	0.002
42	0.002
34	0.002
79	0.002
79	0.002
53	0.002
49	0.002
49	0.002
32	0.002
22	0.002
22	0.002
13	0.002
29	0.002
29	0.002
69	0.002
57	0.002

Table 21: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
19	0.002
42	0.002
2	0.002
69	0.002
51	0.002
51	0.002
35	0.002
23	0.002
23	0.002
20	0.002
73	0.002
73	0.002
39	0.002
39	0.002
23	0.002
23	0.002
52	0.002
52	0.002
15	0.002
15	0.002
37	0.002
37	0.002
19	0.002
19	0.002
72	0.002
72	0.002
78	0.002
54	0.002
64	0.002
4	0.002
4	0.002
74	0.002
28	0.002
28	0.002
61	0.002
4	0.002
35	0.002
7	0.002
44	0.002
44	0.002
59	0.002
62	0.002
62	0.002
43	0.002
12	0.002
12	0.002
26	0.002
1	0.002
70	0.002
36	0.002
7	0.002
4	0.002
53	0.002
34	0.002
79	0.002
49	0.002
49	0.002
1	0.002
1	0.002
64	0.002
11	0.002
6	0.002
6	0.002
77	0.002

Table 21: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
10	0.002
60	0.002
60	0.002
28	0.002
18	0.002
18	0.002
43	0.002
34	0.002
34	0.002
73	0.002
62	0.002
65	0.002
65	0.002
5	0.002
4	0.002
4	0.002
80	0.002
51	0.002
78	0.002
78	0.002
63	0.002
14	0.002
14	0.002
24	0.002
27	0.002
67	0.002
52	0.002
52	0.002
68	0.002
44	0.002
17	0.002
17	0.002
41	0.002
41	0.002
10	0.002
10	0.002
47	0.002
46	0.002
46	0.002
3	0.002
60	0.002
60	0.002
75	0.002
12	0.002
12	0.002
73	0.002
16	0.002
16	0.002
6	0.002
6	0.002
80	0.002
80	0.002
46	0.002
46	0.002
17	0.002
17	0.002
74	0.002
74	0.002
12	0.002
5	0.002
5	0.002
79	0.002
53	0.002

Table 21: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
9	0.002
48	0.002
1	0.002
12	0.002
12	0.002
52	0.002
28	0.002
19	0.002
52	0.002
52	0.002
9	0.002
43	0.002
20	0.002
9	0.002
38	0.002
38	0.002
62	0.002
3	0.002
38	0.002
30	0.002
28	0.002
29	0.002
44	0.002
69	0.002
69	0.002
49	0.002
76	0.002
62	0.002
27	0.002
27	0.002
64	0.002
78	0.002
38	0.002
38	0.002
20	0.002
79	0.002
79	0.002
20	0.002
11	0.002
11	0.002
44	0.002
44	0.002
23	0.002
79	0.002
14	0.002
14	0.002
53	0.002
62	0.002
18	0.002
18	0.002
37	0.002
37	0.002
6	0.002
80	0.002
75	0.002
78	0.002
78	0.002
26	0.002
45	0.002
61	0.002
74	0.002
74	0.002
67	0.002

Table 21: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
67	0.002
42	0.002
44	0.002
42	0.002
38	0.002
15	0.002
15	0.002
41	0.002
8	0.002
8	0.002
43	0.002
64	0.002
64	0.002
5	0.002
74	0.002
17	0.002
17	0.002
54	0.002
22	0.002
75	0.002
75	0.002
53	0.002
53	0.002
57	0.001
68	0.001
41	0.001
65	0.001
28	0.001
28	0.001
25	0.001
42	0.001
67	0.001
71	0.001
71	0.001
16	0.001
16	0.001
40	0.001
13	0.001
13	0.001
51	0.001
11	0.001
72	0.001
14	0.001
14	0.001
79	0.001
76	0.001
72	0.001
60	0.001
20	0.001
20	0.001
20	0.001
60	0.001
60	0.001
28	0.001
56	0.001
56	0.001
68	0.001
22	0.001
22	0.001
9	0.001
45	0.001
2	0.001
67	0.001
67	0.001

Table 21: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
63	0.001
2	0.001
23	0.001
4	0.001
4	0.001
12	0.001
29	0.001
10	0.001
23	0.001
23	0.001
23	0.001
66	0.001
37	0.001
37	0.001
52	0.001
25	0.001
79	0.001
79	0.001
72	0.001
50	0.001
22	0.001
44	0.001
57	0.001
57	0.001
7	0.001
12	0.001
12	0.001
12	0.001
49	0.001
33	0.001
35	0.001
35	0.001
25	0.001
14	0.001
44	0.001
75	0.001
44	0.001
44	0.001
36	0.001
16	0.001
46	0.001
51	0.001
62	0.001
54	0.001
37	0.001
25	0.001
42	0.001
42	0.001
26	0.001
26	0.001
13	0.001
38	0.001
32	0.001
27	0.001
31	0.001
31	0.001
18	0.001
46	0.001
46	0.001
27	0.001
78	0.001
79	0.001
45	0.001

Table 21: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
45	0.001
22	0.001
57	0.001
40	0.001
40	0.001
49	0.001
25	0.001
25	0.001
15	0.001
15	0.001
17	0.001
26	0.001
40	0.001
13	0.001
13	0.001
24	0.001
53	0.001
53	0.001
52	0.001
7	0.001
68	0.001
27	0.001
61	0.001
61	0.001
45	0.001
45	0.001
33	0.001
71	0.001
18	0.001
30	0.001
30	0.001
14	0.001
34	0.001
34	0.001
41	0.001
53	0.001
22	0.001
22	0.001
10	0.001
14	0.001
14	0.001
10	0.001
80	0.001
80	0.001
24	0.001
75	0.001
75	0.001
14	0.001
14	0.001
80	0.001
40	0.001
40	0.001
51	0.001
79	0.001
5	0.001
67	0.001
2	0.001
6	0.001
51	0.001
1	0.001
73	0.001
45	0.001
57	0.001

Table 21: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
33	0.001
33	0.001
31	0.001
31	0.001
63	0.001
47	0.001
47	0.001
65	0.001
64	0.001
28	0.001
50	0.001
64	0.001
64	0.001
56	0.001
27	0.001
34	0.001
66	0.001
66	0.001
35	0.001
55	0.001
3	0.001
3	0.001
43	0.001
8	0.001
8	0.001
47	0.001
47	0.001
15	0.001
31	0.001
75	0.001
75	0.001
37	0.001
71	0.001
61	0.001
61	0.001
66	0.001
48	0.001
75	0.001
16	0.001
57	0.001
21	0.001
21	0.001
3	0.001
45	0.001
45	0.001
68	0.001
68	0.001
26	0.001
45	0.001
10	0.001
10	0.001
47	0.001
74	0.001
40	0.001
61	0.001
30	0.001
3	0.001
54	0.001
70	0.001
11	0.001
11	0.001
70	0.001
59	0.001
58	0.001

Table 21: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
58	0.001
37	0.001
76	0.001
28	0.001
28	0.001
13	0.001
8	0.001
59	0.001
59	0.001
39	0.001
45	0.001
54	0.001
30	0.001
15	0.001
51	0.001
77	0.001
77	0.001
21	0.001
21	0.001
34	0.001
34	0.001
77	0.001
3	0.001
55	0.001
22	0.000
50	0.000
31	0.000
62	0.000
29	0.000
41	0.000
41	0.000
19	0.000
60	0.000
65	0.000
65	0.000
62	0.000
74	0.000
53	0.000
62	0.000
33	0.000
33	0.000
8	0.000
45	0.000
31	0.000
31	0.000
37	0.000
45	0.000
73	0.000
73	0.000
1	0.000
65	0.000
50	0.000
50	0.000
30	0.000
30	0.000
33	0.000
48	0.000
48	0.000
26	0.000
38	0.000
40	0.000
75	0.000

Table 21: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
75	0.000
59	0.000
59	0.000
60	0.000
17	0.000
63	0.000
5	0.000
30	0.000
4	0.000
12	0.000
17	0.000
65	0.000
65	0.000
66	0.000
32	0.000
58	0.000
43	0.000
43	0.000
42	0.000
52	0.000
71	0.000
7	0.000
7	0.000
74	0.000
74	0.000
37	0.000
42	0.000
42	0.000
6	0.000
6	0.000
5	0.000
59	0.000
17	0.000
41	0.000
10	0.000
10	0.000
70	0.000
1	0.000
1	0.000
1	0.000
1	0.000
73	0.000
35	0.000
64	0.000
69	0.000
33	0.000
33	0.000
31	0.000
19	0.000
50	0.000
45	0.000
4	0.000
27	0.000
27	0.000
53	0.000
50	0.000
50	0.000
35	0.000
40	0.000
60	0.000
29	0.000
10	0.000
78	0.000

Table 21: VBG: target SMD rows across imputations (sorted by $|SMD|$) (Part B) (*continued*)

imp	abs_post
63	0.000
5	0.000
69	0.000
72	0.000
39	0.000
43	0.000
21	0.000
54	0.000
15	0.000
70	0.000
41	0.000
48	0.000
8	0.000
52	0.000
3	0.000
3	0.000
39	0.000
40	0.000
37	0.000
37	0.000
79	0.000
79	0.000
2	0.000
2	0.000

```

vbg_imp_summary <- bal_imp_vbg$bal_imp_summary |>
  summarise(
    med = median(max_abs_post, na.rm = TRUE),
    p90 = quantile(max_abs_post, 0.9, na.rm = TRUE),
    max = max(max_abs_post, na.rm = TRUE)
  )
render_table_pdf(
  vbg_imp_summary,
  caption = "VBG: max |Target SMD| summary across imputations",
  file_stub = "vbg_target_smd_summary",
  digits = 3
)

```

Table 22: VBG: max |Target SMD| summary across imputations

med	p90	max
0.044	0.047	0.051

3.4 11) Weighted outcome models within each imputation + pooling

Within each imputation, fit covariate-adjusted CO2 spline outcome models **only in the measured cohort** (has_abg==1 for PaCO2; has_vbg==1 for VBG CO2), using IPSW weights to address nonrandom testing. Curves are pooled pointwise across imputations (Rubin's rules on the log-OR scale) and displayed as odds ratios relative to CO2_ref at a reference covariate profile.

3.4.1 11.1 Helper: fit + extract log-OR and SE from svyglm

```

stopifnot(exists("fit_spline_imp"), exists("pool_spline_curve"),
          exists("pool_spline_coefs"), exists("pool_terms"))

stopifnot(exists("mi_single_pass_done"), isTRUE(mi_single_pass_done))
stopifnot(exists("abg_spline"), exists("abg_curves"), exists("abg_coefs"))
message("ABG MI spline results were computed in the single-pass MI loop above.")

```

3.4.2 11.3 VBG: MI pooled spline models (treated cohort only)

```
stopifnot(exists("mi_single_pass_done"), isTRUE(mi_single_pass_done))
stopifnot(exists("vbg_spline"), exists("vbg_curves"), exists("vbg_coefs"))
message("VBG MI spline results were computed in the single-pass MI loop above.")
```

3.5 12) Explainability on one representative imputation

MI propensity scores are estimated via logistic regression with splines; SHAP summaries are not computed for the MI PS model. A placeholder diagnostic file is written for audit completeness.

```
shap_stability_file <- results_path("diag-ps-shap-stability.csv")
shap_stub <- data.frame(
  cohort = character(),
  feature = character(),
  mean_abs_seed1 = numeric(),
  mean_abs_seed2 = numeric(),
  run_id = character(),
  stringsAsFactors = FALSE
)
write_csv_safely(shap_stub, shap_stability_file, row_names = FALSE)
```

3.6 13) MI three-level PCO2 helpers and checks

```
stopifnot(exists("pool_terms"))
message("MI 3-level helpers defined in the single-pass MI section.")
```

3.7 14) MI + IPW three-level PCO2 (ABG & VBG)

3.7.1 14.1 ABG: MI + IPW, three-level PCO2 outcomes

```
stopifnot(exists("mi_single_pass_done"), isTRUE(mi_single_pass_done))
stopifnot(exists("abg_cat_results"))

mi_abg_cat_forms <- list(
  "MI IPW ABG 3-level: IMV ~ CO2 category + X"      = reformulate(c("co2_cat", adj_core), response = "imv_proc"),
  "MI IPW ABG 3-level: NIV ~ CO2 category + X"      = reformulate(c("co2_cat", adj_core), response = "niv_proc"),
  "MI IPW ABG 3-level: Death60d ~ CO2 category + X" = reformulate(c("co2_cat", adj_core), response = "death_60d"),
  "MI IPW ABG 3-level: HCRF ~ CO2 category + X"      = reformulate(c("co2_cat", adj_core), response = "hypercap_resp_failure")
)
register_model_diagrams(mi_abg_cat_forms)
message("ABG MI 3-level results were computed in the single-pass MI loop above.")
```

3.7.2 14.2 VBG: MI + IPW, three-level PCO2 outcomes

```
stopifnot(exists("mi_single_pass_done"), isTRUE(mi_single_pass_done))
stopifnot(exists("vbg_cat_results"))

mi_vbg_cat_forms <- list(
  "MI IPW VBG 3-level: IMV ~ CO2 category + X"      = reformulate(c("co2_cat", adj_core), response = "imv_proc"),
  "MI IPW VBG 3-level: NIV ~ CO2 category + X"      = reformulate(c("co2_cat", adj_core), response = "niv_proc"),
  "MI IPW VBG 3-level: Death60d ~ CO2 category + X" = reformulate(c("co2_cat", adj_core), response = "death_60d"),
  "MI IPW VBG 3-level: HCRF ~ CO2 category + X"      = reformulate(c("co2_cat", adj_core), response = "hypercap_resp_failure")
)
register_model_diagrams(mi_vbg_cat_forms)
message("VBG MI 3-level results were computed in the single-pass MI loop above.")
```

3.7.3 14.3 Table 3: MI-pooled IPW associations (3-level CO)

```
stopifnot(exists("abg_cat_results"), exists("vbg_cat_results"))

mi_threel level_results <- dplyr::bind_rows(
  dplyr::mutate(abg_cat_results, group = "ABG"),
  dplyr::mutate(vbg_cat_results, group = "V рG")
) |>
  dplyr::mutate(method = "IPW + MI adjusted")

table3_df <- dplyr::bind_rows(
  dplyr::mutate(abg_cat_results, group = "ABG"),
  dplyr::mutate(vbg_cat_results, group = "V рG")
) |>
  dplyr::mutate(
    exposure = gsub("^co2_cat", "", term),
    contrast = dplyr::recode(exposure,
      Low = "Low vs normal",
      High = "High vs normal",
      .default = exposure),
    outcome_label = dplyr::recode(
      outcome,
      IMV = "IMV",
      NIV = "NIV",
      Death60d = "Death (60d)",
      HCRF = "Hypercapnic RF"
    ),
    or_ci = sprintf("%.2f (%.2f, %.2f)", OR, LCL, UCL)
  ) |>
  dplyr::select(group, outcome_label, contrast, or_ci)

table3_wide <- table3_df |>
  tidyr::pivot_wider(names_from = contrast, values_from = or_ci) |>
  dplyr::arrange(
    factor(group, levels = c("ABG", "V рG")),
```

Table 3. MI-pooled IPW associations between CO category and outcomes (adjusted)

Cohort	Outcome	Low vs normal OR (95% CI)	High vs normal OR (95% CI)
ABG	IMV	1.27 (1.11, 1.45)	1.26 (1.10, 1.44)
ABG	NIV	1.14 (0.91, 1.44)	3.06 (2.52, 3.70)
ABG	Death (60d)	1.63 (1.40, 1.90)	1.30 (1.12, 1.52)
ABG	Hypercapnic RF	1.03 (0.79, 1.35)	7.66 (6.29, 9.32)
VBG	IMV	1.50 (1.23, 1.82)	1.54 (1.27, 1.87)
VBG	NIV	0.91 (0.68, 1.24)	2.83 (2.21, 3.63)
VBG	Death (60d)	1.75 (1.42, 2.15)	1.42 (1.16, 1.74)
VBG	Hypercapnic RF	0.68 (0.46, 1.00)	6.53 (5.08, 8.38)

Weighted survey GLMs adjusted for baseline covariates; weights = MI-specific GLM (RCS) IPW; m = 80 imputations (seed 20251206); reference = Normal.

```

  factor(outcome_label, levels = c("IMV", "NIV", "Death (60d)", "Hypercapnic RF"))
)

gt::gt(table3_wide) |>
  gt::tab_header(title = "Table 3. MI-pooled IPW associations between CO\u2082 category and outcomes (adjusted)") |>
  gt::cols_label(
    group      = "Cohort",
    outcome_label  = "Outcome",
    `Low vs normal` = "Low vs normal OR (95% CI)",
    `High vs normal` = "High vs normal OR (95% CI)"
  ) |>
  gt::fmt_missing(columns = gt::everything(), missing_text = "-") |>
  gt::tab_source_note(
    paste0(
      "Weighted survey GLMs adjusted for baseline covariates; weights = MI-specific GLM (RCS) IPW; m = ", M_IMP,
      " imputations (seed ", MI_SEED, "); reference = Normal."
    )
  )
)

```

3.7.4 14.4 Summary: adjusted CO2-category associations across analysis tracks

```
label_outcome <- function(x) {
  dplyr::recode(
    x,
    imv_proc = "IMV",
    niv_proc = "NIV",
    death_60d = "Death (60d)",
    hypercap_resp_failure = "Hypercapnic RF",
    IMV = "IMV",
    NIV = "NIV",
    Death60d = "Death (60d)",
    HCRF = "Hypercapnic RF"
  )
}

map_contrast <- function(term) {
  dplyr::case_when(
    grepl("Low", term) ~ "Low vs normal",
    grepl("High", term) ~ "High vs normal",
    TRUE ~ NA_character_
  )
}

prep_threellevel <- function(df, estimate_col, lcl_col, ucl_col, method_label) {
  df |>
    dplyr::mutate(
      contrast = map_contrast(term),
      outcome_label = label_outcome(outcome),
      OR = .data[[estimate_col]],
      LCL = .data[[lcl_col]],
      UCL = .data[[ucl_col]],
      method = method_label
    ) |>
    dplyr::filter(!is.na(contrast)) |>
```

```

dplyr::select(method, group, outcome_label, contrast, OR, LCL, UCL)
}

count_model <- function(data, outcome, exposure, adj_vars,
                        treat_var = NULL, weight_var = NULL) {
  d <- data
  if (!is.null(treat_var)) d <- d[d[[treat_var]] == 1, , drop = FALSE]
  vars <- c(outcome, exposure, adj_vars)
  if (!is.null(weight_var)) vars <- c(vars, weight_var)
  d <- d[, vars, drop = FALSE]
  d <- d[complete.cases(d), , drop = FALSE]
  if (!is.null(weight_var)) {
    w <- suppressWarnings(as.numeric(d[[weight_var]]))
    d <- d[is.finite(w) & w > 0, , drop = FALSE]
  }
  if (nrow(d) == 0L) {
    return(tibble::tibble(n_model = 0L, events = 0L))
  }
  d[[outcome]] <- to01(d[[outcome]])
  tibble::tibble(
    n_model = nrow(d),
    events = sum(d[[outcome]] == 1, na.rm = TRUE)
  )
}

count_group <- function(group, method) {
  exp_var <- if (group == "ABG") "pc02_cat_abg" else "pc02_cat_vbg"
  treat_var <- if (group == "ABG") "has_abg" else "has_vbg"
  weight_var <- if (method == "IPW adjusted") {
    if (group == "ABG") "w_abg" else "w_vbg"
  } else {
    NULL
  }
  outcomes <- c("imv_proc", "niv_proc", "death_60d", "hypercap_resp_failure")
  purrr::map_dfr(outcomes, function(outcome) {
    cnt <- count_model(subset_data, outcome, exp_var, adj_core,

```

```

            treat_var = treat_var, weight_var = weight_var)
dplyr::mutate(cnt,
              method = method,
              group = group,
              outcome_label = label_outcome(outcome)))
})
}

mi_counts_threelvel <- function(outcome, group) {
  imp_n <- imp$m
  counts <- lapply(seq_len(imp_n), function(i) {
    d <- get_imp(i)
    if (group == "ABG") {
      co2_var <- "paco2"
      treat_var <- "has_abg"
      w <- mi_logistic_ps_abg_list[[i]]$weights
      low_cut <- ABG_CO2_LOW
      high_cut <- ABG_CO2_HIGH
    } else {
      co2_var <- "vbg_co2"
      treat_var <- "has_vbg"
      w <- mi_logistic_ps_vbg_list[[i]]$weights
      low_cut <- VBG_CO2_LOW
      high_cut <- VBG_CO2_HIGH
    }
    d[[co2_var]] <- suppressWarnings(as.numeric(d[[co2_var]]))
    keep <- d[[treat_var]] == 1 & is.finite(d[[co2_var]])
    if (!any(keep)) return(c(n_model = 0, events = 0))
    d2 <- d[keep, , drop = FALSE]
    w2 <- w[keep]
    d2$co2_cat <- make_co2_cat3(d2[[co2_var]], low_cut, high_cut)
    keep2 <- !is.na(d2$co2_cat)
    d2 <- d2[keep2, , drop = FALSE]
    w2 <- w2[keep2]
    if (nrow(d2) == 0L) return(c(n_model = 0, events = 0))
    d2[[outcome]] <- to01(d2[[outcome]])
  })
}

```

```

complete_ok <- complete.cases(d2[, c(outcome, adj_core, "co2_cat")], drop = FALSE)
w_ok <- is.finite(w2) & w2 > 0
d2 <- d2[complete_ok & w_ok, , drop = FALSE]
if (nrow(d2) == 0L) return(c(n_model = 0, events = 0))
c(n_model = nrow(d2), events = sum(d2[[outcome]] == 1, na.rm = TRUE))
})
n_vals <- vapply(counts, `[[`, numeric(1), "n_model")
e_vals <- vapply(counts, `[[`, numeric(1), "events")
tibble::tibble(
  n_model = round(stats::median(n_vals, na.rm = TRUE)),
  events = round(stats::median(e_vals, na.rm = TRUE))
)
}

mi_counts <- function(group) {
  outcomes <- c("imv_proc", "niv_proc", "death_60d", "hypercap_resp_failure")
  purrr::map_dfr(outcomes, function(outcome) {
    cnt <- mi_counts_threel level(outcome, group)
    dplyr::mutate(cnt,
                  method = "IPW + MI adjusted",
                  group = group,
                  outcome_label = label_outcome(outcome))
  })
}

counts_tbl <- dplyr::bind_rows(
  count_group("ABG", "Unweighted adjusted"),
  count_group("VBG", "Unweighted adjusted"),
  count_group("ABG", "IPW adjusted"),
  count_group("VBG", "IPW adjusted"),
  mi_counts("ABG"),
  mi_counts("VBG")
)

or_all <- dplyr::bind_rows(
  prep_threel level(unw_threel level_results, "estimate", "conf.low", "conf.high", "Unweighted adjusted"),

```

```

prep_threelvel(ipw_threelvel_results, "estimate", "conf.low", "conf.high", "IPW adjusted"),
prep_threelvel(mi_threelvel_results, "OR", "LCL", "UCL", "IPW + MI adjusted")
) |>
dplyr::left_join(counts_tbl, by = c("method", "group", "outcome_label"))

table_summary <- or_all |>
dplyr::mutate(or_ci = sprintf("%.2f (%.2f, %.2f)", OR, LCL, UCL)) |>
dplyr::select(method, group, outcome_label, n_model, events, contrast, or_ci) |>
tidyrr::pivot_wider(names_from = contrast, values_from = or_ci) |>
dplyr::arrange(
  factor(method, levels = c("Unweighted adjusted", "IPW adjusted", "IPW + MI adjusted")),
  factor(group, levels = c("ABG", "VBG")),
  factor(outcome_label, levels = c("IMV", "NIV", "Death (60d)", "Hypercapnic RF"))
)

render_table_pdf(
  table_summary,
  caption = "Adjusted odds ratios (low/high vs normal) across analysis tracks; n/events reflect model sample size (median across
file_stub = "table_summary_adjusted_threelvel",
digits = 2
)

```

Table 23: Adjusted odds ratios (low/high vs normal) across analysis tracks; n/events reflect model sample size (median across imputations for MI). (Part A)

method	group	outcome_label	n_model	events	Low vs normal
Unweighted adjusted	ABG	IMV	9362	2391	1.28 (1.14, 1.43)
Unweighted adjusted	ABG	NIV	9362	896	1.08 (0.89, 1.31)
Unweighted adjusted	ABG	Death (60d)	9362	1645	1.72 (1.51, 1.97)
Unweighted adjusted	ABG	Hypercapnic RF	9362	992	0.96 (0.76, 1.21)
Unweighted adjusted	VBG	IMV	7460	1162	1.30 (1.11, 1.53)
Unweighted adjusted	VBG	NIV	7460	554	0.98 (0.76, 1.25)
Unweighted adjusted	VBG	Death (60d)	7460	1044	1.71 (1.45, 2.01)
Unweighted adjusted	VBG	Hypercapnic RF	7460	692	0.66 (0.49, 0.89)
IPW adjusted	ABG	IMV	9362	2391	1.26 (1.11, 1.43)
IPW adjusted	ABG	NIV	9362	896	1.15 (0.93, 1.44)
IPW adjusted	ABG	Death (60d)	9362	1645	1.63 (1.41, 1.89)
IPW adjusted	ABG	Hypercapnic RF	9362	992	1.08 (0.83, 1.40)
IPW adjusted	VBG	IMV	7460	1162	1.41 (1.18, 1.69)
IPW adjusted	VBG	NIV	7460	554	0.96 (0.73, 1.27)
IPW adjusted	VBG	Death (60d)	7460	1044	1.76 (1.46, 2.11)
IPW adjusted	VBG	Hypercapnic RF	7460	692	0.72 (0.52, 1.00)
IPW + MI adjusted	ABG	IMV	9362	2391	1.27 (1.11, 1.45)
IPW + MI adjusted	ABG	NIV	9362	896	1.14 (0.91, 1.44)
IPW + MI adjusted	ABG	Death (60d)	9362	1645	1.63 (1.40, 1.90)
IPW + MI adjusted	ABG	Hypercapnic RF	9362	992	1.03 (0.79, 1.35)
IPW + MI adjusted	VBG	IMV	7460	1162	1.50 (1.23, 1.82)
IPW + MI adjusted	VBG	NIV	7460	554	0.91 (0.68, 1.24)
IPW + MI adjusted	VBG	Death (60d)	7460	1044	1.75 (1.42, 2.15)
IPW + MI adjusted	VBG	Hypercapnic RF	7460	692	0.68 (0.46, 1.00)

Table 24: Adjusted odds ratios (low/high vs normal) across analysis tracks; n/events reflect model sample size (median across imputations for MI). (Part B)

High vs normal
1.27 (1.14, 1.43)
2.90 (2.46, 3.41)
1.38 (1.20, 1.57)
6.78 (5.75, 8.03)
1.54 (1.32, 1.80)
2.74 (2.22, 3.37)
1.35 (1.14, 1.59)
7.21 (5.92, 8.82)
1.20 (1.05, 1.36)
3.01 (2.50, 3.61)
1.31 (1.13, 1.52)
7.79 (6.46, 9.39)
1.51 (1.26, 1.80)
2.95 (2.35, 3.71)
1.52 (1.26, 1.83)
7.99 (6.39, 9.98)
1.26 (1.10, 1.44)
3.06 (2.52, 3.70)
1.30 (1.12, 1.52)
7.66 (6.29, 9.32)
1.54 (1.27, 1.87)
2.83 (2.21, 3.63)
1.42 (1.16, 1.74)
6.53 (5.08, 8.38)

```

append_mem_snapshot("stage1", "end", "post")
stage1_rm <- c(
  "unw_results_crude", "unw_results_adj", "unw_threel level_results",
  "unw_combined_or_df", "unw_plot_df", "unw_p_or", "unw_axis_spec", "outcomes_unw"
)
missing_stage1 <- setdiff(stage1_rm, ls())
stopifnot(length(missing_stage1) == 0)
rm(list = stage1_rm)
invisible(gc())
append_mem_snapshot("stage1", "cleanup", "post")

```

3.8 Manuscript outputs summary

```

# Cohort flow / sample sizes
flow_tbl <- tibble::tibble(
  metric = c(
    "Full cohort (raw)",
    "Analytic subset",
    "ABG tested",
    "ABG with PaCO2",
    "VBG tested",
    "VBG with VBG CO2"
  ),
  n = c(
    nrow(stata_data),
    nrow(subset_data),
    sum(subset_data$has_abg == 1, na.rm = TRUE),
    sum(subset_data$has_abg == 1 & !is.na(subset_data$paco2), na.rm = TRUE),
    sum(subset_data$has_vbg == 1, na.rm = TRUE),
    sum(subset_data$has_vbg == 1 & !is.na(subset_data$vbg_co2), na.rm = TRUE)
  )
)
render_table_pdf_maybe(flow_tbl, "Cohort flow summary", "cohort_flow_summary",
  digits = 0, show = SHOW_LOW_VALUE_TABLES)

```

```

# Event counts by cohort
outcome_vars <- c("imv_proc", "niv_proc", "death_60d", "hypercap_resp_failure")
outcome_labels <- c(
  imv_proc = "IMV",
  niv_proc = "NIV",
  death_60d = "Death (60d)",
  hypercap_resp_failure = "Hypercapnic RF"
)
event_tbl <- dplyr::bind_rows(
  lapply(outcome_vars, function(o) {
    dplyr::tibble(
      outcome = outcome_labels[[o]],
      group = "ABG",
      n = sum(subset_data$has_abg == 1 & !is.na(subset_data[[o]]), na.rm = TRUE),
      events = sum(subset_data$has_abg == 1 & subset_data[[o]] == 1, na.rm = TRUE)
    )
  }),
  lapply(outcome_vars, function(o) {
    dplyr::tibble(
      outcome = outcome_labels[[o]],
      group = "VBG",
      n = sum(subset_data$has_vbg == 1 & !is.na(subset_data[[o]]), na.rm = TRUE),
      events = sum(subset_data$has_vbg == 1 & subset_data[[o]] == 1, na.rm = TRUE)
    )
  })
)
event_tbl <- event_tbl |>
  dplyr::mutate(pct = ifelse(n > 0, 100 * events / n, NA_real_))
render_table_pdf_maybe(event_tbl,
  "Outcome counts by cohort (ABG/VBG tested)",
  "outcome_counts_by_cohort",
  digits = 1, show = SHOW_LOW_VALUE_TABLES)

# Weighting diagnostics (non-MI weights)
stopifnot(all(c("w_abg", "w_vbg", "ps_abg", "ps_vbg") %in% names(subset_data)))

```

```

wt_abg <- subset_data$w_abg[subset_data$has_abg == 1]
wt_vbg <- subset_data$w_vbg[subset_data$has_vbg == 1]
ps_abg <- subset_data$ps_abg[subset_data$has_abg == 1]
ps_vbg <- subset_data$ps_vbg[subset_data$has_vbg == 1]
trunc_abg <- subset_data$trunc_abg[subset_data$has_abg == 1]
trunc_vbg <- subset_data$trunc_vbg[subset_data$has_vbg == 1]

wt_sum <- dplyr::bind_rows(
  weight_summary(wt_abg, ps = ps_abg, ps_floor = ps_floor_abg,
    truncated = trunc_abg) |>
    dplyr::mutate(group = "ABG"),
  weight_summary(wt_vbg, ps = ps_vbg, ps_floor = ps_floor_vbg,
    truncated = trunc_vbg) |>
    dplyr::mutate(group = "VBG")
)
wt_sum_display <- wt_sum |>
  dplyr::select(group, n, ess, min, p99, max, trunc_rate, ps_p01) |>
  dplyr::rename(
    trunc = trunc_rate,
    p01_ps = ps_p01
  )
render_table_pdf_maybe(wt_sum_display,
  "Weighting diagnostics summary (non-MI)",
  "weighting_diagnostics_non_mi",
  wide = TRUE,
  digits = 3,
  show = SHOW_LOW_VALUE_TABLES)

# Missingness + MI spec summary
miss_vars <- c(covars_ps, "paco2", "vbg_co2",
  "imv_proc", "niv_proc", "death_60d", "hypercap_resp_failure")
miss_vars <- intersect(miss_vars, names(subset_data_raw))
miss_tbl <- subset_data_raw |>
  dplyr::summarise(dplyr::across(dplyr::all_of(miss_vars), ~ mean(is.na(.)) * 100)) |>
  tidyr::pivot_longer(dplyr::everything(), names_to = "variable", values_to = "pct_missing") |>
  dplyr::arrange(dplyr::desc(pct_missing))

```

```

render_table_pdf_maybe(miss_tbl,
                      "Variables by missingness (pre-imputation)",
                      "missingness_all",
                      digits = 1,
                      show = SHOW_LOW_VALUE_TABLES)

mi_spec_tbl <- tibble::tibble(
  m = imp$m,
  maxit = MAXIT_MI,
  methods = paste(unique(imp$method[imp$method != ""]),
                  collapse = ", "),
  ps_model = MI_PS_METHOD,
  ps_spline_k = MI_PS_SPLINE_K,
  ps_glm_maxit = MI_GLM_MAXIT
)
render_table_pdf_maybe(mi_spec_tbl,
                      "MI specification (methods used)",
                      "mi_specification",
                      show = SHOW_LOW_VALUE_TABLES)

```

```

stopifnot(exists("imp"))
imp_n <- imp$m
get_imp <- function(i, imp_obj = imp) { normalize_types(mice::complete(imp_obj, action = i), levels_ref) }

# 1) must exist and be numeric
d1 <- get_imp(1)
stopifnot(all(c("paco2", "vbg_co2") %in% names(d1)))
stopifnot(is.numeric(d1$paco2), is.numeric(d1$vbg_co2))

# 2) confirm at least two PaCO2 levels among those with ABG in each imputation
table(vapply(seq_len(imp_n), function(i) {
  d <- get_imp(i)
  dplyr::n_distinct(d$paco2[d$has_abg == 1 & is.finite(d$paco2)])
}, integer(1)) > 1)

```

```
TRUE
```

```
80
```

```
# 3) light sanity check: ensure pooled MI cat3 results exist  
stopifnot(exists("abg_cat_results"), nrow(abg_cat_results) > 0)
```

3.8.1 14.3 Visualization: pooled three-level ORs

```
stopifnot(exists("abg_cat_results"), exists("vbg_cat_results"))

mi_combined_or_df <- dplyr::bind_rows(
  dplyr::mutate(abg_cat_results, group = "ABG"),
  dplyr::mutate(vbg_cat_results, group = "VBG")
) |>
  dplyr::mutate(
    outcome = factor(outcome,
                     levels = c("IMV", "NIV", "Death60d", "HCRF"),
                     labels = c("IMV", "NIV", "Death (60d)", "Hypercapnic RF")),
    group = factor(group, levels = c("ABG", "VBG"))
  )

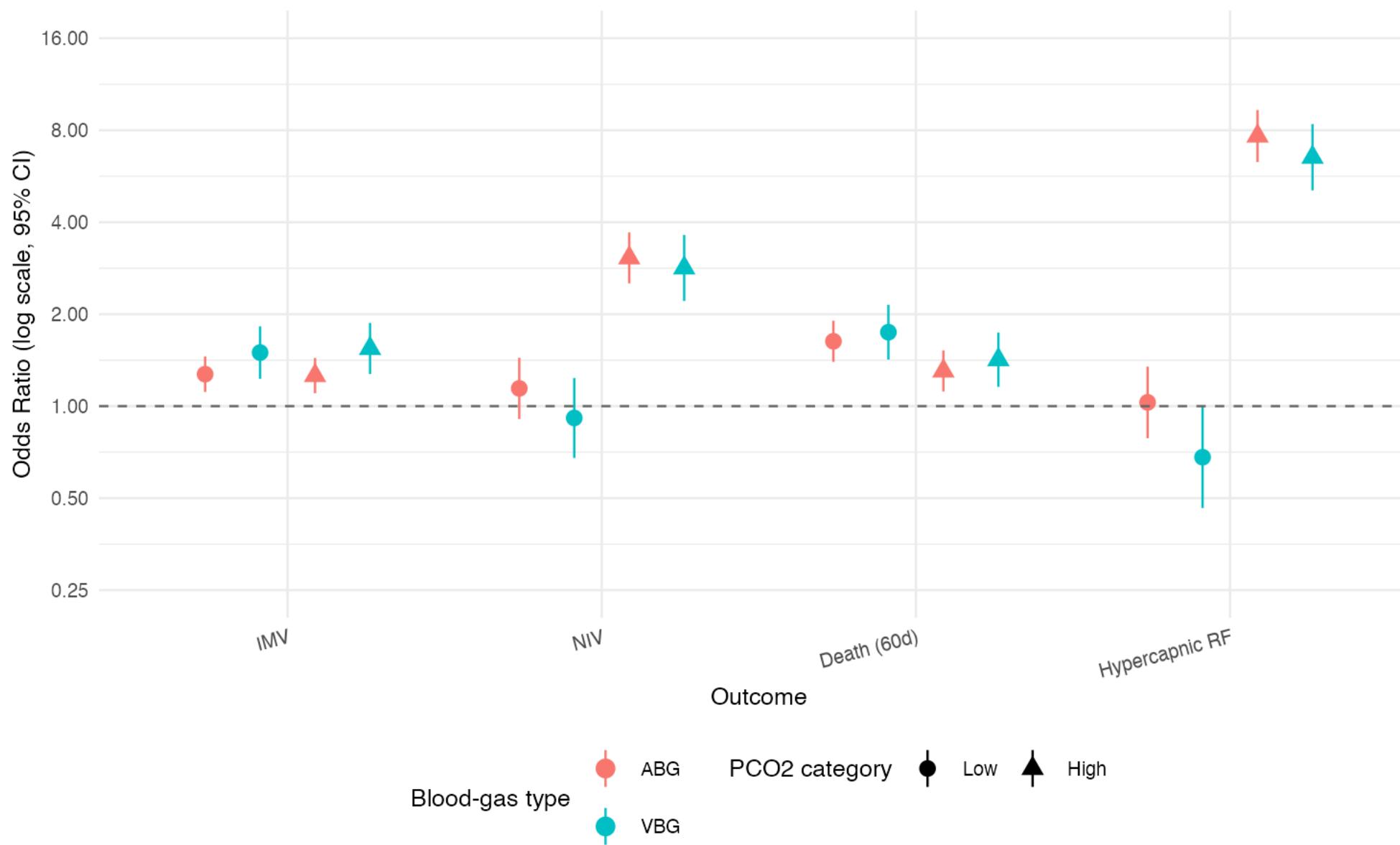
mi_combined_or_df <- map_or_exposure(mi_combined_or_df, "or-plot-mi-weighted")
mi_plot_df <- mi_combined_or_df |>
  dplyr::mutate(estimate = OR, conf.low = LCL, conf.high = UCL) |>
  dplyr::select(-OR, -LCL, -UCL)

mi_plot_df <- build_or_plot_df(
  mi_plot_df,
  "or-plot-mi-weighted",
  expected_exposure_levels = CO2_CAT_CONTRAST_LEVELS
)
mi_axis_spec <- compute_or_axis_spec(list(mi_plot_df), lo_col = "conf.low", hi_col = "conf.high")

mi_p_or <- plot_or_safe(
```

```
mi_plot_df,  
plot_name = "or-plot-mi-weighted",  
axis_spec = mi_axis_spec,  
title = "MI-pooled, IPW-adjusted odds ratios by PC02 category (ABG vs VBG)"  
)  
print_plot_once(mi_p_or, "or-plot-mi-weighted", width = 7.5, height = 4.8)
```

MI-pooled, IPW-adjusted odds ratios by PCO₂ category (ABG vs VBG)



3.8.2 15.3 Visualization

```
library(dplyr)
library(ggplot2)
library(patchwork)
library(purrr)

mi_ipw_rcs_forms <- list(
  "MI IPW spline (adjusted) ABG: IMV ~ CO2 spline + X"      = make_spline_fml("imv_proc", "paco2", adj_core),
  "MI IPW spline (adjusted) ABG: NIV ~ CO2 spline + X"      = make_spline_fml("niv_proc", "paco2", adj_core),
  "MI IPW spline (adjusted) ABG: Death60d ~ CO2 spline + X" = make_spline_fml("death_60d", "paco2", adj_core),
  "MI IPW spline (adjusted) ABG: HCRF ~ CO2 spline + X"     = make_spline_fml("hypercap_resp_failure", "paco2", adj_core),
  "MI IPW spline (adjusted) VBG: IMV ~ CO2 spline + X"      = make_spline_fml("imv_proc", "vbg_co2", adj_core),
  "MI IPW spline (adjusted) VBG: NIV ~ CO2 spline + X"      = make_spline_fml("niv_proc", "vbg_co2", adj_core),
  "MI IPW spline (adjusted) VBG: Death60d ~ CO2 spline + X" = make_spline_fml("death_60d", "vbg_co2", adj_core),
  "MI IPW spline (adjusted) VBG: HCRF ~ CO2 spline + X"     = make_spline_fml("hypercap_resp_failure", "vbg_co2", adj_core)
)
register_model_diagrams(mi_ipw_rcs_forms)

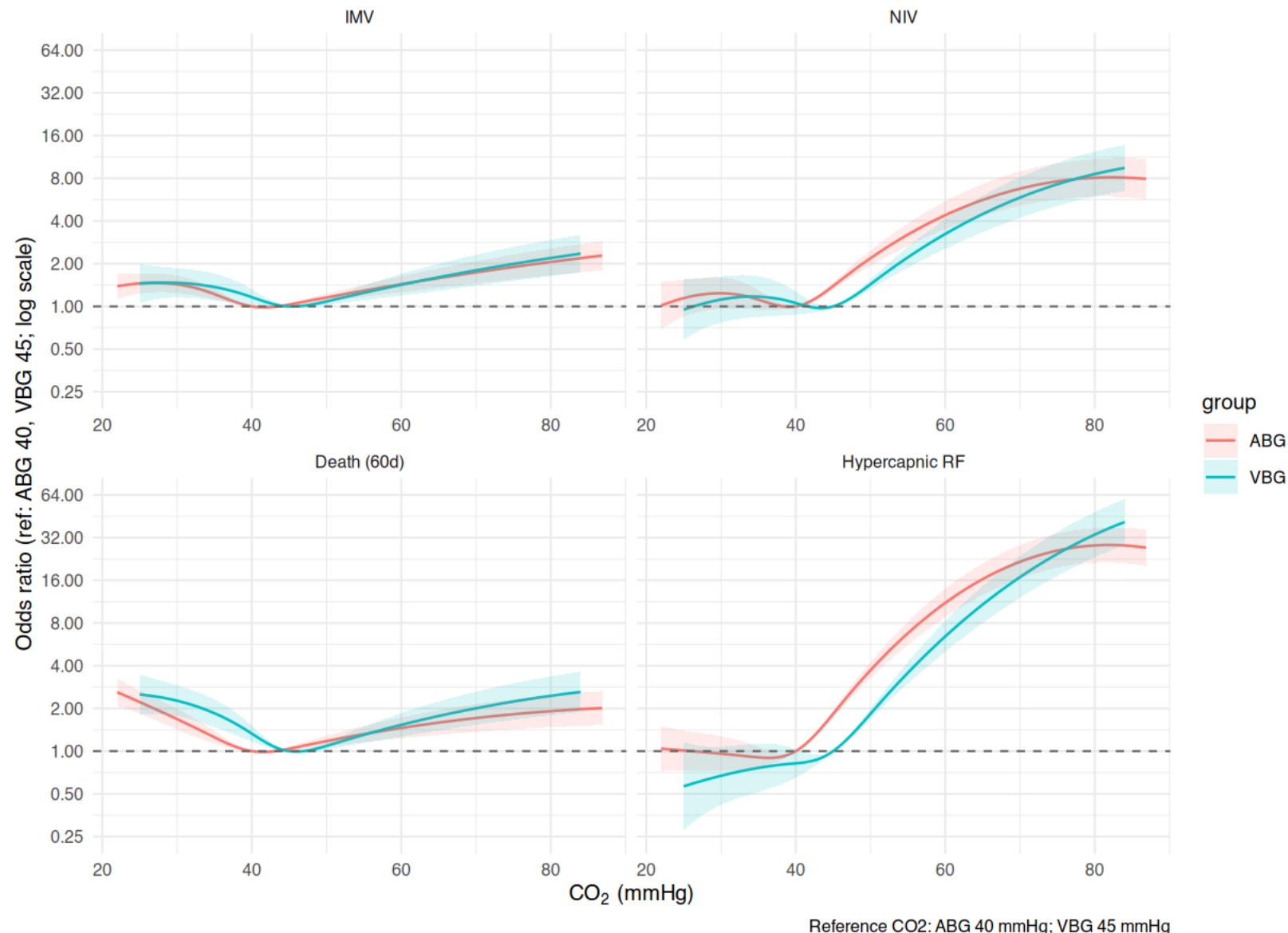
stopifnot(exists("abg_curves"), exists("vbg_curves"))

curve_abg <- abg_curves |>
  mutate(co2 = paco2) |>
  select(-paco2)
curve_vbg <- vbg_curves |>
  mutate(co2 = vbg_co2) |>
  select(-vbg_co2)
curve_all <- bind_rows(curve_abg, curve_vbg) |>
  mutate(outcome = factor(outcome,
                          levels = c("imv_proc", "niv_proc", "death_60d", "hypercap_resp_failure"),
                          labels = c("IMV", "NIV", "Death (60d)", "Hypercapnic RF")))
axis_mi_ipw <- compute_or_axis_spec(list(curve_abg, curve_vbg), lo_col = "LCL", hi_col = "UCL")

ggplot(curve_all, aes(x = co2, y = OR, color = group, fill = group)) +
  geom_line(linewidth = 0.6) +
```

```
geom_ribbon(aes(ymin = LCL, ymax = UCL), alpha = 0.15, color = NA) +
  geom_hline(yintercept = 1, linetype = "dashed", color = "grey40") +
  or_axis_scale(axis_mi_ipw) +
  facet_wrap(~ outcome, scales = "free_x") +
  labs(
    title = expression(
      paste("MI-pooled, IPSW-adjusted spline odds ratios: ABG vs VBG CO"[2]))
  ),
  x = expression(CO[2]~"(mmHg)"),
  y = paste0("Odds ratio (ref: ABG ", ABG_CO2_REF, ", VBG ", VBG_CO2_REF, "; log scale)"),
  caption = paste0("Reference CO2: ABG ", ABG_CO2_REF, " mmHg; VBG ", VBG_CO2_REF, " mmHg")
) +
  theme_minimal(base_size = 10)
```

MI-pooled, IPSW-adjusted spline odds ratios: ABG vs VBG CO₂



3.9 Diagnostics

```
stopifnot(gbm_params$stop.method == "smd.max")
stopifnot(exists("M_IMP"), exists("MAXIT_MI"), exists("MI_SEED"))
stopifnot(exists("imp"))
stopifnot(exists("mi_logistic_ps_abg_list"), exists("mi_logistic_ps_vbg_list"))
meth <- imp$method

diag_fig_dir <- results_path("figs")
fs::dir_create(diag_fig_dir)
```

3.9.1 MI convergence and mixing

```
stopifnot(exists("imp"))

log_events_summary_file <- results_path("mice_logged_events_summary.csv")
stopifnot(file.exists(log_events_summary_file))
log_events_summary <- tryCatch(
  utils::read.csv(log_events_summary_file, stringsAsFactors = FALSE),
  error = function(e) data.frame()
)
if (nrow(log_events_summary) && !("empty" %in% names(log_events_summary) && all(log_events_summary$empty))) {
  render_table_pdf_maybe(
    log_events_summary,
    caption = "Logged events (MI)",
    file_stub = "mice_logged_events_summary",
    digits = 0,
    show = SHOW_LOW_VALUE_TABLES
  )

  stopifnot(all(c("variable", "n") %in% names(log_events_summary)))
  total_events <- sum(log_events_summary$n, na.rm = TRUE)
  if (is.finite(total_events) && total_events > 1000) {
```

```

warning("MI loggedEvents count is high (", total_events, "). Review mice_logged_events_summary.csv.", call. = FALSE)
}
by_var <- log_events_summary |>
  dplyr::group_by(variable) |>
  dplyr::summarise(n = sum(n), .groups = "drop") |>
  dplyr::arrange(dplyr::desc(n))
if (nrow(by_var) && is.finite(total_events) && total_events > 0) {
  top_share <- by_var$n[1] / total_events
  if (top_share > 0.5) {
    warning("MI loggedEvents dominated by variable '", by_var$variable[1],
           "' (", round(100 * top_share, 1), "% of events).", call. = FALSE)
  }
}
} else {
  message("No logged events to summarize.")
}

stopifnot(exists("chain_diag"))
stopifnot(nrow(chain_diag) > 0)
n_imputed <- chain_diag_stats$n_imputed_vars
n_with_tail <- chain_diag_stats$n_with_drift_tail
message("Chain diagnostics: drift_tail available for ", n_with_tail, " / ", n_imputed, " imputed variables.")
stopifnot("drift_tail_scaled" %in% names(chain_diag))
frac_flagged <- mean(chain_diag$flag %in% TRUE, na.rm = TRUE)
med_scaled <- stats::median(chain_diag$drift_tail_scaled, na.rm = TRUE)
max_scaled <- max(chain_diag$drift_tail_scaled, na.rm = TRUE)
message("Chain diagnostics (scaled): flagged=", round(frac_flagged, 3),
       "; median drift_tail_scaled=", signif(med_scaled, 3),
       "; max drift_tail_scaled=", signif(max_scaled, 3))

top_flagged <- chain_diag |>
  dplyr::filter(flag %in% TRUE) |>
  dplyr::arrange(dplyr::desc(abs(drift_tail_scaled)))
if (nrow(top_flagged)) {
  render_table_pdf_maybe(
    top_flagged |>

```

```

dplyr::select(variable, method, drift_tail, drift_tail_scaled, slope, slope_scaled,
              tail_n_finite, tail_window_na_frac, flag_reason),
caption = "MICE chain diagnostics (flagged drift)",
file_stub = "mice_chain_diagnostics_flagged",
digits = 3,
show = SHOW_LOW_VALUE_TABLES
)
} else {
  message("No flagged drift in chain diagnostics.")
}

top_tail_na <- chain_diag |>
  dplyr::arrange(dplyr::desc(tail_window_na_frac))
if (nrow(top_tail_na)) {
  render_table_pdf_maybe(
    top_tail_na,
    caption = "MICE chain diagnostics (tail NA fraction)",
    file_stub = "mice_chain_diagnostics_tail_na",
    digits = 3,
    show = SHOW_LOW_VALUE_TABLES
  )
}

trace_vars <- intersect(c("curr_bmi", "serum_hco3", "hr", "sodium", "serum_cr"),
                         names(imp$data))

imp_trace <- imp
if (imp$m > 10) {
  set.seed(MI_SEED)
  idx <- sort(sample(seq_len(imp$m), 10))
  imp_trace$imp <- lapply(imp$imp, function(x) x[, idx, drop = FALSE])
  imp_trace$m <- length(idx)
}
if (length(trace_vars)) {
  tr_file <- results_path("figs", "diag-mi-trace-selected.png")
  grDevices::png(tr_file, width = 1800, height = 1200, res = 200)
}

```

```

    plot(imp_trace, trace_vars)
    grDevices::dev.off()
}

```

```

png
2

```

```

message("Using memory-safe observed vs imputed plots from mi-diagnostics (no mids densityplot/stripplot).")

```

3.9.2 MI stability across m

```

stopifnot(exists("imp"))
stopifnot(exists("mi_logistic_ps_abg_list"), exists("mi_logistic_ps_vbg_list"))
library(dplyr)

subset_mids <- function(imp_obj, m_keep) {
  if (imp_obj$m == m_keep) return(imp_obj)
  idx <- seq_len(m_keep)
  imp_new <- imp_obj
  imp_new$imp <- lapply(imp_obj$imp, function(x) x[, idx, drop = FALSE])
  imp_new$m <- m_keep
  imp_new
}

m_vals <- sort(unique(c(20, 50, M_IMP)))
m_vals <- m_vals[m_vals <= imp$m]

med_abg <- median(subset_data$paco2[subset_data$has_abg == 1 & !is.na(subset_data$paco2)], na.rm = TRUE)
med_vbg <- median(subset_data$vbg_co2[subset_data$has_vbg == 1 & !is.na(subset_data$vbg_co2)], na.rm = TRUE)
if (!is.finite(med_abg)) med_abg <- ABG_CO2_REF
if (!is.finite(med_vbg)) med_vbg <- VBG_CO2_REF
grid_abg_info_m <- make_co2_grid_ref("paco2", c(med_abg, ABG_CO2_REF), x_ref_abg, ABG_CO2_REF)
grid_vbg_info_m <- make_co2_grid_ref("vbg_co2", c(med_vbg, VBG_CO2_REF), x_ref_vbg, VBG_CO2_REF)

```

```

grid_abg_m <- grid_abg_info_m$grid
grid_vbg_m <- grid_vbg_info_m$grid
ref_idx_abg_m <- grid_abg_info_m$ref_idx
ref_idx_vbg_m <- grid_vbg_info_m$ref_idx
med_idx_abg <- match(med_abg, grid_abg_m$paco2)
med_idx_vbg <- match(med_vbg, grid_vbg_m$vbg_co2)
if (is.na(med_idx_abg)) med_idx_abg <- which.min(abs(grid_abg_m$paco2 - med_abg))
if (is.na(med_idx_vbg)) med_idx_vbg <- which.min(abs(grid_vbg_m$vbg_co2 - med_vbg))

stab_rows <- lapply(m_vals, function(mv) {
  imp_m <- subset_mids(imp, mv)
  get_imp_m <- function(i) normalize_types(mice::complete(imp_m, action = i), levels_ref)

  fits_abg <- lapply(seq_len(mv), function(i) {
    d <- get_imp_m(i)
    d <- d[, c("imv_proc", "has_abg", "paco2", adj_core), drop = FALSE]
    tryCatch(
      fit_spline_imp(
        d, mi_logistic_ps_abg_list[[i]]$weights, "imv_proc", "paco2", "has_abg",
        adj_vars = adj_core,
        spline_df = SPLINE_DF, spline_basis = SPLINE_BASIS, grid_df = grid_abg_m,
        ref_idx = ref_idx_abg_m,
        imp_index = i
      ),
      error = function(e) list(error = conditionMessage(e))
    )
  })
  collect_warnings_from_list(fits_abg)
  curve_abg <- pool_spline_curve(fits_abg, grid_abg_m, ref_idx_abg_m, ABG_CO2_REF,
                                   min_ok_frac = 0.9)

  fits_vbg <- lapply(seq_len(mv), function(i) {
    d <- get_imp_m(i)
    d <- d[, c("imv_proc", "has_vbg", "vbg_co2", adj_core), drop = FALSE]
    tryCatch(
      fit_spline_imp(

```

```

d, mi_logistic_ps_vbg_list[[i]]$weights, "imv_proc", "vbg_co2", "has_vbg",
adj_vars = adj_core,
spline_df = SPLINE_DF, spline_basis = SPLINE_BASIS, grid_df = grid_vbg_m,
ref_idx = ref_idx_vbg_m,
imp_index = i
),
error = function(e) list(error = conditionMessage(e))
)
})
collect_warnings_from_list(fits_vbg)
curve_vbg <- pool_spline_curve(fits_vbg, grid_vbg_m, ref_idx_vbg_m, VBG_CO2_REF,
min_ok_frac = 0.9)

bind_rows(
  tibble::tibble(group = "ABG", m = mv, OR = curve_abg$OR[med_idx_abg]),
  tibble::tibble(group = "VBG", m = mv, OR = curve_vbg$OR[med_idx_vbg])
)
})

stab_df <- bind_rows(stab_rows)
ref <- stab_df |> filter(m == max(m_vals)) |> select(group, OR) |> rename(OR_ref = OR)
stab_df <- stab_df |>
  left_join(ref, by = "group") |>
  mutate(abs_diff = OR - OR_ref,
    pct_diff = 100 * (OR - OR_ref) / OR_ref)

stab_file <- results_path("mi_m_stability.csv")
write_csv_safely(stab_df, stab_file, row_names = FALSE)

# FMI / relative efficiency for a representative unweighted model
cap_fmi <- capture_warnings(
  summary(mice::pool(with(imp, glm(imv_proc ~ has_abg + age_at_encounter + sex,
family = binomial())))),
context = make_context(
  stage = "diagnostics",
  component = "mi_fmi_glm",

```

```

analysis_variant = "mi",
model_type = "glm",
group = NA_character_,
outcome = "imv_proc",
imputation = NA_integer_,
batch = NA_integer_
)
)
append_warnings(cap_fmi$warnings)
fmi_tab <- cap_fmi$value
fmi_abg <- fmi_tab |> filter(term == "has_abg")
if (is.null(fmi_tab) || !"fmi" %in% names(fmi_tab)) {
  warning("FMI not available from mice::pool() summary; leaving FMI as NA.", call. = FALSE)
  fmi_abg <- fmi_abg |> mutate(fmi = NA_real_)
}
fmi_abg$rel_eff <- if (is.finite(fmi_abg$fmi[1])) 1 / (1 + fmi_abg$fmi[1] / M_IMP) else NA_real_

```

3.9.3 MI maxit sensitivity (sampled)

```

run_maxit_sensitivity <- TRUE
if (run_maxit_sensitivity) {
  stopifnot(exists("mi_df"), exists("meth"), exists("pred"))
  set.seed(MI_SEED)
  idx <- sample(seq_len(nrow(mi_df)), min(2000, nrow(mi_df)))
  mi_df_sens <- mi_df[idx, , drop = FALSE]

  m_sens <- min(20, M_IMP)
  maxit_short <- max(5, floor(MAXIT_MI / 2))

  cap_short <- capture_warnings(
    mice::mice(
      data           = mi_df_sens,
      m              = m_sens,
      maxit         = maxit_short,

```

```

predictorMatrix = pred,
method          = meth,
printFlag       = FALSE,
seed            = MI_SEED
),
context = make_context(
  stage = "MI",
  component = "mice_maxit_short",
  analysis_variant = "mi",
  model_type = "mice",
  group = NA_character_,
  outcome = NA_character_,
  imputation = NA_integer_,
  batch = NA_integer_
)
)
append_warnings(cap_short$warnings)
imp_short <- cap_short$value
le_short <- as.data.frame(imp_short$loggedEvents)
if (nrow(le_short)) {
  le_short$run_type <- "maxit_short"
}
write_csv_safely(le_short, results_path("mice_logged_events_maxit_short.csv"), row_names = FALSE)

cap_long <- capture_warnings(
  mice::mice(
    data           = mi_df_sens,
    m              = m_sens,
    maxit         = MAXIT_MI,
    predictorMatrix = pred,
    method         = meth,
    printFlag     = FALSE,
    seed          = MI_SEED + 1
),
  context = make_context(
    stage = "MI",

```

```

component = "mice_maxit_long",
analysis_variant = "mi",
model_type = "mice",
group = NA_character_,
outcome = NA_character_,
imputation = NA_integer_,
batch = NA_integer_
)
)
append_warnings(cap_long$warnings)
imp_long <- cap_long$value
le_long <- as.data.frame(imp_long$loggedEvents)
if (nrow(le_long)) {
  le_long$run_type <- "maxit_long"
}
write_csv_safely(le_long, results_path("mice_logged_events_maxit_long.csv"), row_names = FALSE)

mean_across_imps <- function(imp_obj, var) {
  means <- vapply(seq_len(imp_obj$m), function(i) {
    d <- mice::complete(imp_obj, action = i)
    mean(d[[var]], na.rm = TRUE)
  }, numeric(1))
  mean(means, na.rm = TRUE)
}

key_vars <- intersect(c("curr_bmi", "serum_hco3", "sodium", "serum_cr"), names(mi_df_sens))
sens_df <- lapply(key_vars, function(v) {
  m_short <- mean_across_imps(imp_short, v)
  m_long <- mean_across_imps(imp_long, v)
  data.frame(
    variable = v,
    mean_short = m_short,
    mean_long = m_long,
    diff       = m_long - m_short,
    stringsAsFactors = FALSE
)
})

```

```

}) |> bind_rows()

sens_file <- results_path("mi_maxit_sensitivity.csv")
write_csv_safely(sens_df, sens_file, row_names = FALSE)
}

stopifnot(all(c("w_abg", "w_vbg") %in% names(subset_data)))

wt_abg <- subset_data$w_abg[subset_data$has_abg == 1]
wt_vbg <- subset_data$w_vbg[subset_data$has_vbg == 1]
ps_abg <- subset_data$ps_abg[subset_data$has_abg == 1]
ps_vbg <- subset_data$ps_vbg[subset_data$has_vbg == 1]
trunc_abg <- subset_data$trunc_abg[subset_data$has_abg == 1]
trunc_vbg <- subset_data$trunc_vbg[subset_data$has_vbg == 1]

wt_sum <- bind_rows(
  weight_summary(wt_abg, ps = ps_abg, ps_floor = ps_floor_abg,
                 truncated = trunc_abg) |>
    mutate(group = "ABG"),
  weight_summary(wt_vbg, ps = ps_vbg, ps_floor = ps_floor_vbg,
                 truncated = trunc_vbg) |>
    mutate(group = "VBG")
)
wt_sum_file <- results_path("weight_summary.csv")
write_csv_safely(wt_sum, wt_sum_file, row_names = FALSE)

ps_stat <- function(ps, group) {
  ps_ok <- ps[is.finite(ps)]
  if (!length(ps_ok)) {
    return(data.frame(
      group = group,
      ps_min = NA_real_,
      ps_p01 = NA_real_,
      ps_p50 = NA_real_,
      ps_p99 = NA_real_,
      ps_max = NA_real_
    ))
  }
}

```

```

    stringsAsFactors = FALSE
  )))
}
data.frame(
  group = group,
  ps_min = min(ps_ok, na.rm = TRUE),
  ps_p01 = stats::quantile(ps_ok, 0.01, na.rm = TRUE),
  ps_p50 = stats::median(ps_ok, na.rm = TRUE),
  ps_p99 = stats::quantile(ps_ok, 0.99, na.rm = TRUE),
  ps_max = max(ps_ok, na.rm = TRUE),
  stringsAsFactors = FALSE
)
}

ps_summary <- dplyr::bind_rows(
  ps_stat(ps_abg, "ABG"),
  ps_stat(ps_vbg, "VBG")
)
write_csv_safely(ps_summary, results_path("ps_overlap_summary.csv"), row_names = FALSE)
render_table_pdf_maybe(
  ps_summary,
  caption = "Propensity score overlap (tested cohort)",
  file_stub = "ps_overlap_summary",
  digits = 3,
  show = SHOW_LOW_VALUE_TABLES
)

wt_df <- bind_rows(
  tibble::tibble(group = "ABG", ps = ps_abg, weight = wt_abg),
  tibble::tibble(group = "VBG", ps = ps_vbg, weight = wt_vbg)
) |>
  filter(is.finite(weight), is.finite(ps))

plot_hist <- function(df, title) {
  ggplot(df, aes(x = weight)) +
    geom_histogram(bins = 40, fill = "grey70", color = "white") +

```

```

    labs(title = title, x = "Weight", y = "Count") +
    theme_minimal(base_size = 10)
}

p_hist_abg <- plot_hist(filter(wt_df, group == "ABG"), "ABG weight distribution")
p_hist_vbg <- plot_hist(filter(wt_df, group == "VBG"), "VBG weight distribution")
save_diag_plot(p_hist_abg, results_path("figs", "diag-wt-weights-hist-abg.png"), width = 7, height = 5)
save_diag_plot(p_hist_vbg, results_path("figs", "diag-wt-weights-hist-vbg.png"), width = 7, height = 5)

plot_scatter <- function(df, title) {
  top_wt <- df |>
    slice_max(order_by = weight, n = min(20, nrow(df)))
  ggplot(df, aes(x = ps, y = weight)) +
    geom_point(alpha = 0.3, size = 0.7) +
    geom_point(data = top_wt, color = "red", size = 1.2) +
    scale_y_log10() +
    labs(title = title, x = "Propensity score", y = "Weight (log10)") +
    theme_minimal(base_size = 10)
}

p_scatter_abg <- plot_scatter(filter(wt_df, group == "ABG"),
                               "ABG weights vs propensity (top 20 highlighted)")
p_scatter_vbg <- plot_scatter(filter(wt_df, group == "VBG"),
                               "VBG weights vs propensity (top 20 highlighted)")
save_diag_plot(p_scatter_abg, results_path("figs", "diag-wt-weights-vs-ps-abg.png"), width = 7, height = 5)
save_diag_plot(p_scatter_vbg, results_path("figs", "diag-wt-weights-vs-ps-vbg.png"), width = 7, height = 5)

```

3.9.4 Balance diagnostics

```

stopifnot(exists("target_balance_table"))

covars_use <- intersect(covars_ps, names(subset_data))

bal_target_abg <- target_balance_table(subset_data, "has_abg", subset_data$w_abg, covars_use, levels_ref) |>

```

```

    mutate(group = "ABG")
bal_target_vbg <- target_balance_table(subset_data, "has_vbg", subset_data$w_vbg, covars_use, levels_ref) |>
  mutate(group = "VBG")

bal_target <- bind_rows(bal_target_abg, bal_target_vbg)
write_csv_safely(bal_target, results_path("balance_table.csv"), row_names = FALSE)

bal_target_sum <- bal_target |>
  group_by(group, variable) |>
  summarise(
    max_abs_pre = max(abs(smd_pre), na.rm = TRUE),
    max_abs_post = max(abs(smd_post), na.rm = TRUE),
    .groups = "drop"
  )
bal_worst <- bal_target_sum |>
  group_by(group) |>
  arrange(desc(max_abs_post)) |>
  ungroup()
write_csv_safely(bal_worst, results_path("balance_worst10.csv"), row_names = FALSE)
render_table_pdf(
  bal_worst,
  caption = "Target balance by covariate (sorted by max |SMD|)",
  file_stub = "balance_worst",
  digits = 3
)

```

Table 25: Target balance by covariate (sorted by max |SMD|)

group	variable	max_abs_pre	max_abs_post
ABG	curr_bmi	0.269	0.194
ABG	encounter_type	0.370	0.192
VBG	curr_bmi	0.273	0.180
VBG	location	0.399	0.151
ABG	location	0.166	0.114
ABG	sbp	0.179	0.087
ABG	serum_ca	0.224	0.085
ABG	age_at_encounter	0.106	0.082
VBG	serum_cl	0.146	0.079
VBG	race_ethnicity	0.205	0.078

Table 25: Target balance by covariate (sorted by max |SMD|) (*continued*)

group	variable	max_abs_pre	max_abs_post
ABG	copd	0.056	0.078
VBG	hr	0.131	0.074
ABG	chf	0.072	0.074
ABG	dbp	0.162	0.073
VBG	dm	0.082	0.072
VBG	dbp	0.093	0.067
ABG	sex	0.090	0.067
VBG	sbp	0.121	0.056
ABG	plt	0.106	0.054
ABG	phtn	0.049	0.054
VBG	ckd	0.069	0.054
ABG	wbc	0.099	0.054
VBG	serum_lac	0.097	0.048
ABG	temp_new	0.106	0.043
VBG	serum_cr	0.086	0.042
VBG	sodium	0.100	0.042
VBG	phtn	0.053	0.041
ABG	race_ethnicity	0.072	0.038
VBG	sex	0.057	0.035
VBG	serum_ca	0.027	0.031
ABG	asthma	0.059	0.029
ABG	serum_lac	0.051	0.029
VBG	chf	0.037	0.027
VBG	serum_phos	0.052	0.027
VBG	asthma	0.005	0.027
ABG	ckd	0.041	0.026
ABG	serum_phos	0.042	0.023
ABG	hr	0.064	0.022
ABG	osa	0.049	0.021
ABG	serum_k	0.014	0.020
VBG	age_at_encounter	0.018	0.020
VBG	osa	0.025	0.019
ABG	serum_hco3	0.121	0.018
VBG	plt	0.017	0.015
VBG	copd	0.008	0.015
ABG	serum_cl	0.033	0.013
VBG	wbc	0.017	0.012
VBG	temp_new	0.038	0.010
ABG	dm	0.004	0.010
VBG	acute_nmd	0.009	0.009
ABG	acute_nmd	0.002	0.007
ABG	serum_cr	0.045	0.006
VBG	serum_hco3	0.068	0.005
VBG	serum_k	0.036	0.005
ABG	sodium	0.023	0.003

Table 25: Target balance by covariate (sorted by max |SMD|) (*continued*)

group	variable	max_abs_pre	max_abs_post
VBG	encounter_type	0.038	0.002

```

bal_plot_df <- bal_target |>
  mutate(label = ifelse(is.na(level), variable, paste0(variable, ":", level))) |>
  tidyr::pivot_longer(
    cols = c(smd_pre, smd_post),
    names_to = "stage",
    values_to = "smd"
  ) |>
  mutate(stage = recode(stage, smd_pre = "Pre", smd_post = "Post"))

p_bal_abg <- ggplot(filter(bal_plot_df, group == "ABG"),
                      aes(x = reorder(label, abs(smd)), y = smd, color = stage, shape = stage)) +
  geom_point(size = 1) +
  geom_hline(yintercept = c(-0.1, 0.1), linetype = 2, linewidth = 0.3) +
  geom_hline(yintercept = c(-0.05, 0.05), linetype = 3, linewidth = 0.3) +
  coord_flip() +
  labs(x = NULL, y = "Target SMD", title = "ABG target balance") +
  theme_minimal(base_size = 10)

p_bal_vbg <- ggplot(filter(bal_plot_df, group == "VBG"),
                      aes(x = reorder(label, abs(smd)), y = smd, color = stage, shape = stage)) +
  geom_point(size = 1) +
  geom_hline(yintercept = c(-0.1, 0.1), linetype = 2, linewidth = 0.3) +
  geom_hline(yintercept = c(-0.05, 0.05), linetype = 3, linewidth = 0.3) +
  coord_flip() +
  labs(x = NULL, y = "Target SMD", title = "VBG target balance") +
  theme_minimal(base_size = 10)

save_diag_plot(p_bal_abg, results_path("figs", "diag-balance-loveplot-abg.png"), width = 9, height = 7)
save_diag_plot(p_bal_vbg, results_path("figs", "diag-balance-loveplot-vbg.png"), width = 9, height = 7)

# MI target balance summaries across imputations

```

```

stopifnot(exists("bal_imp_abg"), exists("bal_imp_vbg"))
bal_imp <- bind_rows(bal_imp_abg$bal_long, bal_imp_vbg$bal_long)
bal_imp_summary <- bind_rows(bal_imp_abg$bal_imp_summary, bal_imp_vbg$bal_imp_summary)
worst_rows <- bind_rows(bal_imp_abg$worst_rows_overall, bal_imp_vbg$worst_rows_overall)
worst_by_imp <- bind_rows(bal_imp_abg$worst_by_imp, bal_imp_vbg$worst_by_imp)
worst_terms_by_imp <- bind_rows(bal_imp_abg$worst_terms_by_imp, bal_imp_vbg$worst_terms_by_imp)

write_csv_safely(bal_imp, results_path("balance_target_by_imp.csv"), row_names = FALSE)
write_csv_safely(bal_imp_summary, results_path("balance_target_imp_summary.csv"), row_names = FALSE)
write_csv_safely(worst_rows, results_path("balance_target_worst_rows.csv"), row_names = FALSE)
render_table_pdf_maybe(
  worst_rows,
  caption = "Target SMD rows across imputations (sorted by |SMD|)",
  file_stub = "balance_target_worst_rows",
  digits = 3,
  show = SHOW_LOW_VALUE_TABLES
)
write_csv_safely(worst_by_imp, results_path("balance_max_smd_by_imp.csv"), row_names = FALSE)
write_csv_safely(worst_terms_by_imp, results_path("balance_worst_terms.csv"), row_names = FALSE)
if (any(bal_imp_summary$max_abs_post > 0.10, na.rm = TRUE)) {
  warning("Target balance: max |SMD| > 0.10 in at least one imputation.", call. = FALSE)
}
if (nrow(bal_imp_summary)) {
  dist_tbl <- bal_imp_summary |>
    dplyr::group_by(group) |>
    dplyr::summarise(
      med = median(max_abs_post, na.rm = TRUE),
      iqr = IQR(max_abs_post, na.rm = TRUE),
      max = max(max_abs_post, na.rm = TRUE),
      .groups = "drop"
    )
  render_table_pdf_maybe(
    dist_tbl,
    caption = "Distribution of max |Target SMD| across imputations",
    file_stub = "balance_target_max_smd_distribution",
    digits = 3,
  )
}

```

```

    show = SHOW_LOW_VALUE_TABLES
  )
}

if (nrow(worst_terms_by_imp)) {
  worst_freq <- worst_terms_by_imp |>
    dplyr::count(group, term, sort = TRUE) |>
    dplyr::ungroup()
  render_table_pdf_maybe(
    worst_freq,
    caption = "Most frequent worst-balance terms",
    file_stub = "balance_worst_terms_freq",
    digits = 0,
    show = SHOW_LOW_VALUE_TABLES
  )
}

n_abg <- sum(subset_data$has_abg == 1, na.rm = TRUE)
n_vbg <- sum(subset_data$has_vbg == 1, na.rm = TRUE)

stopifnot(exists("wt_sum"))
ess_abg <- wt_sum$ess[wt_sum$group == "ABG"]
ess_vbg <- wt_sum$ess[wt_sum$group == "VBG"]

if (is.finite(ess_abg) && is.finite(n_abg) && ess_abg < 0.2 * n_abg) {
  warning("ABG balance: ESS < 0.2 * n_abg (", round(ess_abg, 1), " vs ", n_abg, ".)", call. = FALSE)
}
if (is.finite(ess_vbg) && is.finite(n_vbg) && ess_vbg < 0.2 * n_vbg) {
  warning("VBG balance: ESS < 0.2 * n_vbg (", round(ess_vbg, 1), " vs ", n_vbg, ".)", call. = FALSE)
}

```

3.9.5 Outcome diagnostics

```

stopifnot(exists("abg_curves"), exists("vbg_curves"))
curve_abg <- abg_curves |>

```

```

mutate(co2 = paco2) |>
  select(-paco2)
curve_vbg <- vbg_curves |>
  mutate(co2 = vbg_co2) |>
  select(-vbg_co2)
curve_all <- bind_rows(curve_abg, curve_vbg) |>
  mutate(outcome = factor(outcome,
                          levels = c("imv_proc", "niv_proc", "death_60d", "hypercap_resp_failure"),
                          labels = c("IMV", "NIV", "Death (60d)", "Hypercapnic RF")))
axis_mi_outcome <- compute_or_axis_spec(list(curve_abg, curve_vbg), lo_col = "LCL", hi_col = "UCL")

p_outcome <- ggplot(curve_all, aes(x = co2, y = OR, color = group, fill = group)) +
  geom_line(linewidth = 0.6) +
  geom_ribbon(aes(ymin = LCL, ymax = UCL), alpha = 0.15, color = NA) +
  geom_hline(yintercept = 1, linetype = "dashed", color = "grey40") +
  or_axis_scale(axis_mi_outcome) +
  facet_wrap(~ outcome, scales = "free_x") +
  labs(
    title = "MI-pooled IPSW spline odds ratios: ABG vs VBG",
    x = expression(CO[2]~"(mmHg)"),
    y = paste0("Odds ratio (ref: ABG ", ABG_CO2_REF, ", VBG ", VBG_CO2_REF, "; log scale)"),
    caption = paste0("Reference CO2: ABG ", ABG_CO2_REF, " mmHg; VBG ", VBG_CO2_REF, " mmHg")
  ) +
  theme_minimal(base_size = 10)
save_diag_plot(p_outcome, results_path("figs", "diag-outcome-or-vs-paco2.png"),
               width = 10, height = 8)

```

3.9.6 Diagnostics summary and audit

```

stopifnot(exists("bal_imp_summary"), exists("wt_sum"), exists("chain_diag_stats"))
target_abg_med <- median(bal_imp_summary$max_abs_post[bal_imp_summary$group == "ABG"], na.rm = TRUE)
target_abg_max <- max(bal_imp_summary$max_abs_post[bal_imp_summary$group == "ABG"], na.rm = TRUE)
target_vbg_med <- median(bal_imp_summary$max_abs_post[bal_imp_summary$group == "VBG"], na.rm = TRUE)
target_vbg_max <- max(bal_imp_summary$max_abs_post[bal_imp_summary$group == "VBG"], na.rm = TRUE)

```

```

runtime_proj_total_hrs <- NA_real_
if (is.finite(PILOT_FRAC) && PILOT_FRAC > 0 && PILOT_FRAC < 1) {
  runtime_log_curr <- runtime_log
  runtime_log_curr <- runtime_log_curr[runtime_log_curr$run_id == runtime_run_id, , drop = FALSE]
  scalable_steps <- c("mice_imputation", "mi_single_pass")
  scalable_secs <- runtime_log_curr |>
    dplyr::filter(step_name %in% scalable_steps) |>
    dplyr::summarise(total = sum(seconds, na.rm = TRUE)) |>
    dplyr::pull(total)
  if (length(scalable_secs) && is.finite(scalable_secs)) {
    runtime_proj_total_hrs <- scalable_secs / PILOT_FRAC / 3600
  }
}

get_wt_row <- function(group) {
  row <- wt_sum[wt_sum$group == group, , drop = FALSE]
  if (nrow(row) == 0L) {
    stop("Weight summary missing for group: ", group)
  }
  row[, c("ps_floor", "p01", "p05", "p95", "p99", "max", "sum_w", "ess",
         "top01_weight_share", "trunc_rate"), drop = FALSE]
}

wt_abg_row <- get_wt_row("ABG")
wt_vbg_row <- get_wt_row("VBG")

diag_summary <- bind_rows(
  tibble::tibble(
    block = "ABG weights",
    run_mode = RUN_MODE,
    m = M_IMP,
    maxit = MAXIT_MI,
    pilot_frac = PILOT_FRAC,
    stop_method = gbm_params$stop.method,
    ps_floor_quantile = ps_trunc_quantile,

```

```

ps_floor = wt_abg_row$ps_floor,
weight_p01 = wt_abg_row$p01,
weight_p05 = wt_abg_row$p05,
weight_p95 = wt_abg_row$p95,
weight_p99 = wt_abg_row$p99,
weight_max = wt_abg_row$max,
sum_w = wt_abg_row$sum_w,
ess = wt_abg_row$ess,
top1_weight_share = wt_abg_row$top01_weight_share,
trunc_rate = wt_abg_row$trunc_rate,
target_max_smd_post_med = target_abg_med,
target_max_smd_post_max = target_abg_max,
runtime_proj_total_hrs = runtime_proj_total_hrs,
chain_diag_n_imputed_vars = chain_diag_stats$n_imputed_vars,
chain_diag_n_with_chainMean = chain_diag_stats$n_with_chainMean,
chain_diag_n_with_drift_tail = chain_diag_stats$n_with_drift_tail,
chain_diag_drift_tail_na_frac = chain_diag_stats$drift_tail_na_frac,
chain_diag_tail_window_na_mean = chain_diag_stats$tail_window_na_mean
),
tibble::tibble(
  block = "VBG weights",
  run_mode = RUN_MODE,
  m = M_IMP,
  maxit = MAXIT_MI,
  pilot_frac = PILOT_FRAC,
  stop_method = gbm_params$stop.method,
  ps_floor_quantile = ps_trunc_quantile,
  ps_floor = wt_vbg_row$ps_floor,
  weight_p01 = wt_vbg_row$p01,
  weight_p05 = wt_vbg_row$p05,
  weight_p95 = wt_vbg_row$p95,
  weight_p99 = wt_vbg_row$p99,
  weight_max = wt_vbg_row$max,
  sum_w = wt_vbg_row$sum_w,
  ess = wt_vbg_row$ess,
  top1_weight_share = wt_vbg_row$top01_weight_share,

```

```

trunc_rate = wt_vbg_row$trunc_rate,
target_max_smd_post_med = target_vbg_med,
target_max_smd_post_max = target_vbg_max,
runtime_proj_total_hrs = runtime_proj_total_hrs,
chain_diag_n_imputed_vars = chain_diag_stats$n_imputed_vars,
chain_diag_n_with_chainMean = chain_diag_stats$n_with_chainMean,
chain_diag_n_with_drift_tail = chain_diag_stats$n_with_drift_tail,
chain_diag_drift_tail_na_frac = chain_diag_stats$drift_tail_na_frac,
chain_diag_tail_window_na_mean = chain_diag_stats$tail_window_na_mean
),
tibble::tibble(
  block = "ABG outcomes",
  run_mode = RUN_MODE,
  m = M_IMP,
  maxit = MAXIT_MI,
  pilot_frac = PILOT_FRAC,
  stop_method = gbm_params$stop.method,
  ps_floor_quantile = ps_trunc_quantile,
  ps_floor = wt_abg_row$ps_floor,
  weight_p01 = wt_abg_row$p01,
  weight_p05 = wt_abg_row$p05,
  weight_p95 = wt_abg_row$p95,
  weight_p99 = wt_abg_row$p99,
  weight_max = wt_abg_row$max,
  sum_w = wt_abg_row$sum_w,
  ess = wt_abg_row$ess,
  top1_weight_share = wt_abg_row$top01_weight_share,
  trunc_rate = wt_abg_row$trunc_rate,
  target_max_smd_post_med = target_abg_med,
  target_max_smd_post_max = target_abg_max,
  runtime_proj_total_hrs = runtime_proj_total_hrs,
  chain_diag_n_imputed_vars = chain_diag_stats$n_imputed_vars,
  chain_diag_n_with_chainMean = chain_diag_stats$n_with_chainMean,
  chain_diag_n_with_drift_tail = chain_diag_stats$n_with_drift_tail,
  chain_diag_drift_tail_na_frac = chain_diag_stats$drift_tail_na_frac,
  chain_diag_tail_window_na_mean = chain_diag_stats$tail_window_na_mean
)

```

```

),
tibble::tibble(
  block = "V рG outcomes",
  run_mode = RUN_MODE,
  m = M_IMP,
  maxit = MAXIT_MI,
  pilot_frac = PILOT_FRAC,
  stop_method = gbm_params$stop.method,
  ps_floor_quantile = ps_trunc_quantile,
  ps_floor = wt_vbg_row$ps_floor,
  weight_p01 = wt_vbg_row$p01,
  weight_p05 = wt_vbg_row$p05,
  weight_p95 = wt_vbg_row$p95,
  weight_p99 = wt_vbg_row$p99,
  weight_max = wt_vbg_row$max,
  sum_w = wt_vbg_row$sum_w,
  ess = wt_vbg_row$ess,
  top1_weight_share = wt_vbg_row$top01_weight_share,
  trunc_rate = wt_vbg_row$trunc_rate,
  target_max_smd_post_med = target_vbg_med,
  target_max_smd_post_max = target_vbg_max,
  runtime_proj_total_hrs = runtime_proj_total_hrs,
  chain_diag_n_imputed_vars = chain_diag_stats$n_imputed_vars,
  chain_diag_n_with_chainMean = chain_diag_stats$n_with_chainMean,
  chain_diag_n_with_drift_tail = chain_diag_stats$n_with_drift_tail,
  chain_diag_drift_tail_na_frac = chain_diag_stats$drift_tail_na_frac,
  chain_diag_tail_window_na_mean = chain_diag_stats$tail_window_na_mean
)
)

check_abg <- bal_imp_summary |>
  dplyr::filter(group == "ABG") |>
  dplyr::summarise(x = max(max_abs_post, na.rm = TRUE), .groups = "drop") |>
  dplyr::pull(x)
check_vbg <- bal_imp_summary |>
  dplyr::filter(group == "V рG") |>

```

```

dplyr::summarise(x = max(max_abs_post, na.rm = TRUE), .groups = "drop") |>
  dplyr::pull(x)
diag_abg <- diag_summary$target_max_smd_post_max[diag_summary$block == "ABG weights"]
diag_vbg <- diag_summary$target_max_smd_post_max[diag_summary$block == "VBG weights"]
if (length(diag_abg) && is.finite(check_abg)) {
  stopifnot(isTRUE(all.equal(check_abg, diag_abg, tolerance = 1e-8)))
}
if (length(diag_vbg) && is.finite(check_vbg)) {
  stopifnot(isTRUE(all.equal(check_vbg, diag_vbg, tolerance = 1e-8)))
}
stopifnot(exists("covars_use_abg"), exists("covars_use_vbg"))
stopifnot(setequal(covars_use_abg, covars_use_vbg))

diag_summary_file <- results_path("diagnostics_summary.csv")
write_csv_safely(diag_summary, diag_summary_file, row_names = FALSE)

diag_summary_display <- diag_summary |>
  dplyr::select(
    block,
    m,
    ess,
    trunc_rate,
    target_max_smd_post_med,
    target_max_smd_post_max
  ) |>
  dplyr::rename(
    `trunc` = trunc_rate,
    `med_max_smd` = target_max_smd_post_med,
    `max_max_smd` = target_max_smd_post_max
  )
render_table_pdf_maybe(diag_summary_display,
                      "Diagnostics summary (IPSW + MI)",
                      "diagnostics_summary_display",
                      wide = TRUE,
                      digits = 3,
                      show = SHOW_LOW_VALUE_TABLES)

```

```

audit_lines <- c(
  "# Diagnostics Audit",
  "",
  "## A1. MI workflow",
  "- Impute -> single-pass per-imputation loop (weights, target balance, 3-level outcomes, spline outcomes) -> pool curves and co.",
  "## A2. MI settings",
  paste0("- m = ", M_IMP, ", maxit = ", MAXIT_MI, ", seed = ", MI_SEED,
        "; treatments/outcomes/PaCO2/VBG CO2 are not imputed but are predictors (`mi-exec`)."),
  "## A3. Propensity weighting",
  "- Unimputed weighting uses WeightIt with method = \"gbm\" and balance-based stopping (stop.method = \"smd.max\"); no AUC-based",
  "- MI weighting uses logistic PS with restricted cubic splines (glm + rcs); no SHAP is computed for MI.",
  "## A4. One-sided IPSW + truncation",
  "- Weights are 1/ps for observed tests (ABG or VBG), truncated only for very small propensities (ps floor = 1st percentile), th",
  "## A5. Robust variance",
  "- Outcome models are survey::svyglm with svydesign (robust SEs), using spline(CO2) + X adjustment; ABG and VBG are fit separa",
  "## A6. Pooling",
  "- mitools::MIcombine pools coefficients and robust vcov from svyglm; spline curves are pooled pointwise on the log-OR scale re",
  "",
  "## Potential mismatches / risks",
  "- Target balance diagnostics compare weighted treated cohort to the full analytic sample (no treated-vs-control balance).",
  "- MI stability across m uses subsets of the first m imputations from the main mids object (not full re-imputation at each m).",
  "- Unweighted analyses remain earlier in the notebook for context; primary inference is based on weighted spline models."
)
audit_file <- results_path("diagnostics_audit.md")
write_diag_lines(audit_lines, audit_file)

```

3.9.7 Performance / runtime log

```

stopifnot(exists("mi_warn_log"), exists("mi_info_log"))
warn_df <- mi_warn_log
write_csv_safely(warn_df, results_path("mi_warnings_log.csv"), row_names = FALSE)
write_csv_safely(warn_df, results_path("warnings_log.csv"), row_names = FALSE)
write_csv_safely(mi_info_log, results_path("mi_info_log.csv"), row_names = FALSE)

```

```

if (nrow(warn_df)) {
  msg_counts <- warn_df |>
    dplyr::count(stage, component, message, sort = TRUE)
  render_table_pdf_maybe(
    msg_counts,
    caption = "Warning messages by stage/component",
    file_stub = "warnings_by_stage_component",
    digits = 0,
    show = SHOW_LOW_VALUE_TABLES
  )

  nonconv <- warn_df |>
    dplyr::filter(grepl("glm.fit: algorithm did not converge", message, fixed = TRUE))
  if (nrow(nonconv)) {
    nonconv_ctx <- nonconv |>
      dplyr::count(stage, component, analysis_variant, model_type, outcome, group, imputation, sort = TRUE)
    render_table_pdf_maybe(
      nonconv_ctx,
      caption = "Nonconvergence contexts",
      file_stub = "nonconvergence_contexts",
      digits = 0,
      show = SHOW_LOW_VALUE_TABLES
    )
  }
} else {
  message("No captured warnings.")
}

write_csv_safely(plot_drop_log(), results_path("plot_drop_log.csv"), row_names = FALSE)

stopifnot(exists("mi_outcome_diag"))
if (nrow(mi_outcome_diag) == 0L) {
  stop("mi_outcome_diag is empty; outcome diagnostics were not captured.")
}
out_diag_file <- results_path("model_fit_diagnostics.csv")

```

```

write_csv_safely(mi_outcome_diag, out_diag_file)
write_csv_safely(mi_outcome_diag, results_path("mi_outcome_fit_diagnostics.csv"))

nonconv <- mi_outcome_diag |>
  dplyr::filter(isTRUE(nonconv_flag) | isFALSE(converged))
sep <- mi_outcome_diag |>
  dplyr::filter(isTRUE(sep_flag))

if (nrow(nonconv)) {
  nonconv_counts <- nonconv |>
    dplyr::count(analysis_variant, group, outcome, model_type, sort = TRUE)
  render_table_pdf_maybe(
    nonconv_counts,
    caption = "Nonconverged fits by variant/group/outcome",
    file_stub = "nonconverged_fits_by_variant",
    digits = 0,
    show = SHOW_LOW_VALUE_TABLES
  )

  worst_imps <- nonconv |>
    dplyr::count(imputation, sort = TRUE)
  render_table_pdf_maybe(
    worst_imps,
    caption = "Imputations with most nonconverged fits",
    file_stub = "nonconverged_imputations",
    digits = 0,
    show = SHOW_LOW_VALUE_TABLES
  )
} else {
  message("No nonconverged outcome fits recorded.")
}

if (nrow(sep)) {
  sep_counts <- sep |>
    dplyr::count(analysis_variant, group, outcome, model_type, sort = TRUE)
  render_table_pdf_maybe(

```

```

sep_counts,
caption = "Separation flags by variant/group/outcome",
file_stub = "separation_flags_by_variant",
digits = 0,
show = SHOW_LOW_VALUE_TABLES
)
} else {
  message("No separation flags recorded.")
}

worst_phat <- mi_outcome_diag |>
  dplyr::filter(is.finite(min_phat) | is.finite(max_phat)) |>
  dplyr::mutate(extreme = pmin(min_phat, 1 - max_phat, na.rm = TRUE)) |>
  dplyr::arrange(extreme)
if (nrow(worst_phat)) {
  render_table_pdf_maybe(
    worst_phat,
    caption = "Worst fitted-probability extremes",
    file_stub = "worst_phat_extremes",
    digits = 3,
    show = SHOW_LOW_VALUE_TABLES
)
}

diag_df <- mi_outcome_diag
diag_df$sep_warn <- grepl("fitted probabilities numerically 0 or 1",
                           diag_df$top_warning, fixed = TRUE) |
  grepl("separat", diag_df$top_warning, ignore.case = TRUE)
diag_df$phat_extreme <- (diag_df$min_phat < PROB_EPS) |
  (diag_df$max_phat > 1 - PROB_EPS)
diag_df$sep_flag <- dplyr::coalesce(as.logical(diag_df$sep_flag), FALSE)
diag_df$nonconv_flag <- dplyr::coalesce(as.logical(diag_df$nonconv_flag), FALSE) |
  dplyr::coalesce(!as.logical(diag_df$converged), FALSE)

mi_variants <- intersect(c("mi_ipw", "weighted_imputed"), unique(diag_df$analysis_variant))
if (!length(mi_variants)) mi_variants <- unique(diag_df$analysis_variant)

```

```

issue_summary <- diag_df |>
  dplyr::filter(analysis_variant %in% mi_variants) |>
  dplyr::group_by(group, outcome, component, analysis_variant) |>
  dplyr::summarise(
    n_fits = dplyr::n(),
    n_nonconv = sum(nonconv_flag %in% TRUE, na.rm = TRUE),
    n_sep_warn = sum(sep_warn %in% TRUE, na.rm = TRUE),
    n_phat_extreme = sum(phat_extreme %in% TRUE, na.rm = TRUE),
    n_sep_flag = sum(sep_flag %in% TRUE, na.rm = TRUE),
    .groups = "drop"
  )
write_csv_safely(issue_summary, results_path("mi_fit_issue_summary.csv"))

# Top warning messages by stage/component
if (nrow(mi_warn_log)) {
  warn_top <- mi_warn_log |>
    dplyr::count(stage, component, analysis_variant, model_type, message, sort = TRUE)
  render_table_pdf_maybe(
    warn_top,
    caption = "Warnings by stage/component",
    file_stub = "warnings_by_stage_component_full",
    digits = 0,
    show = SHOW_LOW_VALUE_TABLES
  )
}

# Top MICE loggedEvents drivers
stopifnot(exists("log_events_summary"))
if (nrow(log_events_summary)) {
  render_table_pdf_maybe(
    log_events_summary,
    caption = "MICE loggedEvents drivers",
    file_stub = "mice_logged_events_drivers",
    digits = 0,
    show = SHOW_LOW_VALUE_TABLES
}

```

```

    )
}

# Replay debug mode (off by default)
MI_DEBUG_REPLAY <- FALSE
if (MI_DEBUG_REPLAY) {
  stopifnot(file.exists(results_path("model_fit_diagnostics.csv")))
  diag_df <- read.csv(results_path("model_fit_diagnostics.csv"), stringsAsFactors = FALSE)
  bad <- diag_df[isFALSE(diag_df$converged), , drop = FALSE]
  if (nrow(bad)) {
    row <- bad[1, , drop = FALSE]
    message("Replaying: group=", row$group, ", outcome=", row$outcome,
            ", model_type=", row$model_type, ", imputation=", row$imputation)
    options(warn = 1)
    stopifnot(exists("imp"))
    get_imp <- function(i, imp_obj = imp) {
      normalize_types(mice::complete(imp_obj, action = i), levels_ref)
    }
    d_dbg <- get_imp(row$imputation)
    if (row$group == "ABG") {
      d_dbg <- d_dbg[d_dbg$has_abg == 1 & is.finite(d_dbg$paco2), , drop = FALSE]
      w_dbg <- mi_logistic_ps_abg_list[[row$imputation]]$weights[d_dbg$has_abg == 1 & is.finite(d_dbg$paco2)]
      if (row$model_type == "spline") {
        d_dbg <- d_dbg[, c(row$outcome, "has_abg", "paco2", adj_core), drop = FALSE]
        fit_spline_imp(d_dbg, w_dbg, row$outcome, "paco2", "has_abg",
                      adj_vars = adj_core, spline_df = SPLINE_DF, spline_basis = SPLINE_BASIS,
                      grid_df = NULL, ref_idx = NULL, imp_index = row$imputation)
      } else {
        d_dbg$co2_cat <- make_co2_cat3(d_dbg$paco2, ABG_CO2_LOW, ABG_CO2_HIGH)
        d_dbg$co2_cat <- stats::relevel(base::droplevels(d_dbg$co2_cat), ref = "Normal")
        d_dbg[[row$outcome]] <- to01(d_dbg[[row$outcome]])
        des <- survey::svydesign(ids = ~1, weights = ~w_dbg, data = d_dbg)
        fml <- stats::reformulate(c("co2_cat", adj_core), response = row$outcome)
        survey::svyglm(fml, design = des, family = quasibinomial(),
                       control = stats::glm.control(maxit = 50))
      }
    }
  }
}

```

```

} else if (row$group == "VBG") {
  d_dbg <- d_dbg[d_dbg$has_vbg == 1 & is.finite(d_dbg$vbg_co2), , drop = FALSE]
  w_dbg <- mi_logistic_ps_vbg_list[[row$imputation]]$weights[d_dbg$has_vbg == 1 & is.finite(d_dbg$vbg_co2)]
  if (row$model_type == "spline") {
    d_dbg <- d_dbg[, c(row$outcome, "has_vbg", "vbg_co2", adj_core), drop = FALSE]
    fit_spline_imp(d_dbg, w_dbg, row$outcome, "vbg_co2", "has_vbg",
                    adj_vars = adj_core, spline_df = SPLINE_DF, spline_basis = SPLINE_BASIS,
                    grid_df = NULL, ref_idx = NULL, imp_index = row$imputation)
  } else {
    d_dbg$co2_cat <- make_co2_cat3(d_dbg$vbg_co2, VBG_CO2_LOW, VBG_CO2_HIGH)
    d_dbg$co2_cat <- stats::relevel(base::droplevels(d_dbg$co2_cat), ref = "Normal")
    d_dbg[[row$outcome]] <- to01(d_dbg[[row$outcome]])
    des <- survey::svydesign(ids = ~1, weights = ~w_dbg, data = d_dbg)
    fml <- stats::reformulate(c("co2_cat", adj_core), response = row$outcome)
    survey::svyglm(fml, design = des, family = quasibinomial(),
                   control = stats::glm.control(maxit = 50))
  }
}
options(warn = 0)
} else {
  message("MI_DEBUG_REPLAY=TRUE but no nonconverged rows found.")
}
}

```

3.9.8 Performance / runtime log

```

stopifnot(exists("runtime_log"), nrow(runtime_log) > 0)
runtime_log_curr <- runtime_log
runtime_log_curr <- runtime_log_curr[runtime_log_curr$run_id == runtime_run_id, , drop = FALSE]
runtime_log_file <- results_path("runtime_log.csv")
write_csv_safely(runtime_log_curr, runtime_log_file, row_names = FALSE)
top_steps <- runtime_log_curr |>
  arrange(desc(seconds))
top15_file <- results_path("runtime_summary_top15.csv")

```

```

write_csv_safely(top_steps, top15_file, row_names = FALSE)
render_table_pdf_maybe(
  top_steps,
  caption = "Runtime steps (seconds)",
  file_stub = "runtime_steps",
  digits = 3,
  show = SHOW_LOW_VALUE_TABLES
)

total_seconds <- sum(runtime_log_curr$seconds, na.rm = TRUE)
runtime_summary <- bind_rows(
  tibble::tibble(step_name = "TOTAL", seconds = total_seconds),
  runtime_log_curr |>
    arrange(desc(seconds)) |>
    select(step_name, seconds)
)
runtime_summary_file <- results_path("runtime_summary.csv")
write_csv_safely(runtime_summary, runtime_summary_file, row_names = FALSE)
render_table_pdf_maybe(
  runtime_summary,
  caption = "Runtime summary (total + all steps)",
  file_stub = "runtime_summary",
  digits = 3,
  show = SHOW_LOW_VALUE_TABLES
)

# GBM preflight diagnostics (CSV only)
write_csv_safely(memory_snapshots, results_path("memory_snapshots.csv"), row_names = FALSE)
write_csv_safely(gbm_preflight_design_dims, results_path("gbm_preflight_design_dims.csv"), row_names = FALSE)
write_csv_safely(gbm_preflight_warnings, results_path("gbm_preflight_warnings.csv"), row_names = FALSE)

if (is.finite(PILOT_FRAC) && PILOT_FRAC > 0 && PILOT_FRAC < 1) {
  scalable_steps <- c("mice_imputation", "mi_single_pass")
  proj <- runtime_log_curr |>
    filter(step_name %in% scalable_steps) |>
    mutate(projected_seconds = seconds / PILOT_FRAC,

```

```

    projected_hours = projected_seconds / 3600)
proj_total <- sum(proj$projected_hours, na.rm = TRUE)
render_table_pdf_maybe(
  proj |> select(step_name, seconds, projected_hours),
  caption = paste0("Runtime projection (scalable steps; pilot_frac = ", PILOT_FRAC, ")"),
  file_stub = "runtime_projection",
  digits = 3,
  show = SHOW_LOW_VALUE_TABLES
)
if (is.finite(proj_total) && proj_total > 10) {
  warning("Projected full-run time exceeds 10 hours (", round(proj_total, 1), "h).",
         call. = FALSE)
}
} else {
  message("Runtime projection skipped because PILOT_FRAC == 1 (full run).")
}

stopifnot(exists("get_imp_stats"))
get_imp_df <- data.frame(
  count = get_imp_stats$count,
  seconds = get_imp_stats$seconds,
  seconds_per_call = if (get_imp_stats$count > 0) get_imp_stats$seconds / get_imp_stats$count else NA_real_,
  run_id = runtime_run_id,
  run_mode = RUN_MODE,
  n_subset = nrow(subset_data),
  stringsAsFactors = FALSE
)
write_csv_safely(get_imp_df, results_path("get_imp_usage.csv"), row_names = FALSE)

```

```

expected_diag <- c(
  "runtime_log.csv", "runtime_summary.csv", "runtime_summary_top15.csv",
  "warnings_log.csv", "mi_warnings_log.csv", "mi_info_log.csv",
  "diagnostics_summary.csv", "diagnostics_missingness.csv",
  "diagnostics_missingness-by-strata.csv",
  "balance_target_imp_summary.csv", "balance_target_by_imp.csv",
  "balance_target_worst_rows.csv", "balance_max_smd_by_imp.csv",

```

```

"balance_worst_terms.csv", "balance_worst10.csv", "balance_table.csv",
"weight_summary.csv", "ps_overlap_summary.csv",
"model_fit_diagnostics.csv", "mi_outcome_fit_diagnostics.csv",
"mi_fit_issue_summary.csv", "mi_m_stability.csv", "mi_maxit_sensitivity.csv",
"mi_obs_vs_imp_summary.csv", "mi_spline_curve_abg.csv",
"mi_spline_curve_vbg.csv", "mi_spline_coef_abg.csv",
"mi_spline_coef_vbg.csv", "diag-ps-shap-stability.csv",
"mice_logged_events_raw.csv", "mice_logged_events_summary.csv",
"mice_pred_width_preflight.csv", "mice_chain_diagnostics.csv",
"mice_batches_log.csv", "missingness-by-strata.csv",
"missingness-drivers.csv", "missingness-pattern.csv", "plot_drop_log.csv",
"mice_smoketest.log"
)
missing_files <- expected_diag[!file.exists(results_path(expected_diag))]
stopifnot(length(missing_files) == 0)

run_id_mismatch <- character()
for (f in expected_diag) {
  path <- results_path(f)
  if (grepl("\\\\.csv$", f)) {
    df <- tryCatch(read.csv(path, nrows = 1), error = function(e) NULL)
    stopifnot(!is.null(df))
    stopifnot("run_id" %in% names(df))
    if (nrow(df) > 0 && !identical(as.character(df$run_id[1]), diag_run_id)) {
      run_id_mismatch <- c(run_id_mismatch, f)
    }
  }
}

if (length(missing_files) || length(run_id_mismatch)) {
  msg <- paste0(
    "Diagnostics completeness check failed: missing files [",
    paste(missing_files, collapse = ", "),
    "]; run_id mismatch [",
    paste(run_id_mismatch, collapse = ", "),
    "] ."
}

```

```
)  
stop(msg)  
}
```

3.10 16) Save, export, and session info

```
audit_script <- here::here("R", "diagnostics_audit.R")  
audit_md <- results_path("diagnostics_audit.md")  
stopifnot(file.exists(audit_script))  
  
audit_out <- tryCatch(  
  system2(  
    "Rscript",  
    args = c(shQuote(audit_script)),  
    env = c(paste0("DIAG_RESULTS_DIR=", results_dir)),  
    stdout = TRUE,  
    stderr = TRUE  
,  
  error = function(e) e  
)  
if (inherits(audit_out, "error")) {  
  warning("diagnostics_audit.R failed: ", conditionMessage(audit_out), call. = FALSE)  
} else {  
  status <- attr(audit_out, "status")  
  if (!is.null(status) && status != 0) {  
    warning("diagnostics_audit.R exited with status ", status, ".", call. = FALSE)  
  }  
}
```

```
audit_issues <- results_path("diagnostics_audit_issues.csv")  
if (file.exists(audit_issues)) {  
  issues_df <- read.csv(audit_issues)  
  issues_df <- issues_df |>  
  dplyr::arrange(factor(severity, levels = c("blocker", "high", "medium", "low")))
```

```

render_table_pdf_maybe(
  issues_df,
  caption = "Diagnostics audit issues (see Results/diagnostics_audit.md for details)",
  file_stub = "diagnostics_audit_issues",
  digits = 2,
  show = SHOW_LOW_VALUE_TABLES
)
} else {
  cat("Diagnostics audit summary not available.\n")
}

```

```

stopifnot(exists("abg_curves"), exists("vbg_curves"), exists("abg_coefs"), exists("vbg_coefs"))
saveRDS(
  list(
    abg_curves = abg_curves,
    vbg_curves = vbg_curves,
    abg_coefs = abg_coefs,
    vbg_coefs = vbg_coefs
  ),
  mi_pooled_file
)

```

```
writeLines(capture.output(sessionInfo()), results_path("sessionInfo.txt"))
```

```
cat("Software: R ", as.character(getRversion()),
  "; key packages: mice, WeightIt, cobalt, survey, rms.\n")
```

Software: R 4.5.2 ; key packages: mice, WeightIt, cobalt, survey, rms.

```

pdf_input <- knitr::current_input()
if (is.null(pdf_input) || !nzchar(pdf_input)) {
  pdf_input <- "ABG-VBG analysis 2025-12-11.qmd"
}
pdf_file <- results_path(paste0(tools::file_path_sans_ext(basename(pdf_input)), ".pdf"))
scan_out <- results_path("pdf_hygiene_scan.csv")

```

```
pdftotext_bin <- Sys.which("pdftotext")
if (!nzchar(pdftotext_bin) || !file.exists(pdf_file)) {
  write_csv_safely(data.frame(line = character()), scan_out, row_names = FALSE)
} else {
  tmp_txt <- tempfile(fileext = ".txt")
  system2(pdftotext_bin, c(pdf_file, tmp_txt))
  txt <- readLines(tmp_txt, warn = FALSE)
  bad <- txt[grep1("/Users/| [A-Z]:\\\\\\\\\\\\\\", txt)]
  scan_df <- data.frame(line = bad, stringsAsFactors = FALSE)
  write_csv_safely(scan_df, scan_out, row_names = FALSE)
  if (RUN_MODE == "full" && nrow(scan_df) > 0) {
    stop("PDF hygiene scan detected absolute paths; see ", scan_out)
  }
}
```