

ABG-VBG Analysis

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1 Data Pre-processing

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
if (!requireNamespace("kableExtra", quietly = TRUE)) install.packages("kableExtra")
library(kableExtra)
library(gtsummary)

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

Setting theme "Compact"
```

```

# 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) {
  kbl <- gtsummary::as_kable(
    tbl,
    format      = "latex",
    booktabs    = TRUE,
    longtable = TRUE # allows multipage tables; repeats header with kableExtra option below
  )

  # 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)
  }

  kbl <- kableExtra::kable_styling(
    kbl,
    latex_options = c("repeat_header", "hold_position", "scale_down"),
    font_size     = font_size
  )

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

# 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"
)

# Install any missing packages (with dependencies)
missing_pkgs <- setdiff(required_pkgs, rownames(installed.packages()))

```

```
if (length(missing_pkgs)) {  
  install.packages(missing_pkgs, dependencies = TRUE)  
}  
  
# Load (or attach) all required packages  
invisible(lapply(required_pkgs, require, character.only = TRUE))
```

Loading required package: WeightIt

Loading required package: broom

Loading required package: cobalt

cobalt (Version 4.6.1, Build Date: 2025-08-20)

Loading required package: codebookr

Loading required package: dplyr

Attaching package: 'dplyr'

The following object is masked from 'package:kableExtra':

group_rows

The following objects are masked from 'package:stats':

filter, lag

```
The following objects are masked from 'package:base' :
```

```
  intersect, setdiff, setequal, union
```

```
Loading required package: flextable
```

```
Attaching package: 'flextable'
```

```
The following object is masked from 'package:gtsummary' :
```

```
continuous_summary
```

```
The following objects are masked from 'package:kableExtra' :
```

```
as_image, footnote
```

```
Loading required package: parallel
```

```
Loading required package: gbm
```

```
Loaded gbm 2.2.2
```

```
This version of gbm is no longer under development. Consider transitioning to gbm3, https://github.com/gbm-developers/gbm3
```

```
Loading required package: ggplot2
```

```
Loading required package: gt
```

```
Loading required package: haven
```

```
Loading required package: labelled
```

```
Loading required package: scales
```

```
Loading required package: modelsummary
```

```
Loading required package: officer
```

```
Loading required package: patchwork
```

```
Loading required package: rms
```

```
Loading required package: Hmisc
```

```
Attaching package: 'Hmisc'
```

```
The following object is masked from 'package:modelsummary':
```

```
Mean
```

```
The following objects are masked from 'package:gt':
```

```
html, latex
```

```
The following objects are masked from 'package:dplyr':
```

```
src, summarize
```

```
The following objects are masked from 'package:base':
```

```
format.pval, units
```

```
Attaching package: 'rms'
```

```
The following object is masked from 'package:WeightIt':
```

```
calibrate
```

```
Loading required package: survey
```

```
Loading required package: grid
```

```
Loading required package: Matrix
```

```
Loading required package: survival
```

```
Attaching package: 'survey'
```

```
The following object is masked from 'package:rms':
```

```
calibrate
```

```
The following object is masked from 'package:Hmisc':
```

```
deff
```

```
The following object is masked from 'package:WeightIt':
```

```
calibrate
```

The following object is masked from 'package:graphics':

dotchart

Loading required package: tibble

Loading required package: lubridate

Attaching package: 'lubridate'

The following objects are masked from 'package:base':

date, intersect, setdiff, union

Loading required package: sensitivitymw

```
# ensure predictable, writable figure path + robust PNG device
knitr::opts_chunk$set(
  fig.path = "figs/", # short local dir for figures
  dev     = "png",
  dpi     = 144
)
dir.create("figs", showWarnings = FALSE, recursive = TRUE)
# on macOS and some setups this prevents device headaches
options(bitmapType = "cairo")

if (!requireNamespace("shapviz", quietly = TRUE) ||
  packageVersion("shapviz") < "0.2.0") {
  install.packages("shapviz") # or: remotes::install_github("ModelOriented/shapviz")
}
```

```

if (interactive() && !requireNamespace("fastshap", quietly = TRUE)) {
  options(repos = c(CRAN = "https://cran.rstudio.com/"))
  install.packages("fastshap")
}

if (interactive() && !requireNamespace("fastshap", quietly = TRUE)) {
  options(repos = c(CRAN = "https://cran.rstudio.com/"))
  install.packages("DALEX")
}

if (interactive() && !requireNamespace("fastshap", quietly = TRUE)) {
  options(repos = c(CRAN = "https://cran.rstudio.com/"))
  install.packages("shapviz")
}

# 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.

```

# data_dir_name <- '/Users/blocke/Box Sync/Residency Personal Files/Scholarly Work/Locke Research Projects/abg-vbg-project/data'
data_dir_name <- '/Users/reblocke/Research/abg-vbg-project/data'

rdata_file <- file.path(data_dir_name, "full_trinetsx.rdata")
stata_file <- file.path(data_dir_name, "full_db.dta")

if (!dir.exists(data_dir_name)) {
  dir.create(data_dir_name)
  message("Directory 'data' created.")
} else {
  message("Directory 'data' already exists.")
}

```

Directory 'data' already exists.

```

if (file.exists(rdata_file)) {
  load(rdata_file)
  message("Loaded existing dataset from 'full_trinetsx.rdata'.")
} else {
  message("RData file not found. Reading Stata dataset...")
  stata_data <- read_dta(stata_file)

  message("Extracting variable labels...")
  var_label(stata_data)

  message("Extracting value labels...")
}

stata_data, function(x) if (is.labelled(x)) val_labels(x))

save(stata_data, file = rdata_file)
message("Dataset saved as 'full_trinetsx.rdata'.") 

load(rdata_file)
message("Loaded newly saved dataset from 'full_trinetsx.rdata'.")

```

```
}
```

```
Loaded existing dataset from 'full_trinetsx.rdata'.
```

```
Creating subset_data
```

```
set.seed(123)
rows_to_keep <- round(nrow(stata_data) * 1) #0.1
subset_data <- stata_data[sample(nrow(stata_data), rows_to_keep), ]  
  
subset_data <- subset_data %>%
  filter(encounter_type != 1)  
  
table(subset_data$encounter_type)
```

```
2      3  
171727 343559
```

```
dim(subset_data)
```

```
[1] 515286    546
```

```
Generating Codebook for the Full Dataset
```

```
message("Generating codebook for the dataset...")
```

```
Generating codebook for the dataset...
```

```

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 <- file.path(data_dir_name, "codebookr.docx")
print(study_codebook, codebook_file)
message("Codebook saved as 'codebookr.docx' in the data directory.")

```

Codebook saved as 'codebookr.docx' in the data directory.

New Variable - Death at 60 days

```

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
461485	53801	

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

0	0.89559
1	0.10441

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

	Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
0.0000	0.00000	0.00000	0.1044	0.0000	1.0000	1.0000

Table 1A and 1B:

```
# Robust derivation of analysis variables + helper for Table 1 production
# -----
# helper: label binary 0/1 → "No"/"Yes"
bin_lab <- function(x) factor(x, levels = c(0, 1), labels = c("No", "Yes"))

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

    ## derive ABG / VBG hypercapnia groups
    abg_group
    = case_when(
      has_abg == 0 ~ "No_ABG",
      has_abg == 1 & hypercap_on_abg == 0 ~ "ABG_NoHypercapnia",
      has_abg == 1 & hypercap_on_abg == 1 ~ "ABG_Hypercapnia",
      TRUE ~ "Missing"
```

```

),
vbg_group = case_when(
  has_vbg == 0 ~ "No_VBG",
  has_vbg == 1 & hypercap_on_vbg == 0 ~ "VBG_NoHypercapnia",
  has_vbg == 1 & hypercap_on_vbg == 1 ~ "VBG_Hypercapnia",
  TRUE ~ "Missing"
),

## factorise groups with explicit NA/missing level
abg_group = factor(
  abg_group,
  levels = c("No_ABG", "ABG_NoHypercapnia", "ABG_Hypercapnia", "Missing")
),
vbg_group = factor(
  vbg_group,
  levels = c("No_VBG", "VBG_NoHypercapnia", "VBG_Hypercapnia", "Missing")
),

## labelled covariates
sex_label = factor(sex, levels = c(0, 1), labels = c("Female", "Male")),
race_ethnicity_label = factor(
  race_ethnicity,
  levels = c(0, 1, 2, 3, 4, 5, 6),
  labels = c("White", "Black or African American", "Hispanic",
            "Asian", "American Indian", "Pacific Islander", "Unknown")
), location_label = factor(
  location,
  levels = c(0, 1, 2, 3),
  labels = c("South", "Northeast", "Midwest", "West")
), encounter_type_label = factor(
  encounter_type,
  levels = c(2, 3),
  labels = 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"
)

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

data %>%
  filter(!is.na(!group_sym), # drop explicit NA
        !group_sym != "Missing") %>%
  droplevels() %>% # drop "Missing" cohort
  select(all_of(c(group_var, vars))) %>%
  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"
) %>%
gtsummary::modify_header(label = "***Variable***") %>%
gtsummary::modify_caption(caption)
}

# 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")

table1A

```

table1B

Generating Word Doc for Table 1A & 1B

```

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 = "Table1_ABG_VBG.docx")

```

NEW Table 1

```

# Status factors (column labels are taken from factor levels)
subset_data <- subset_data %>%
mutate(

```

Variable	No ABG N = 328,044 ¹	ABG_NoHypercapnia N = 129,429 ¹	ABG_Hypercapnia
Age (years)	58.1 ± 18.1; 0.0/328,044.0 missing (0.0%)	60.8 ± 17.1; 0.0/129,429.0 missing (0.0%)	62.1 ± 16.4; 0.0/57,813.0
Current BMI kg/m ²	32.3 ± 8.7; 184,223.0/328,044.0 missing (56.2%)	28.6 ± 6.9; 75,826.0/129,429.0 missing (58.6%)	29.8 ± 7.9; 33,496.0/57,813
sex_label			
Female	169,023 (52%)	57,767 (45%)	27,116 (47%)
Male	159,021 (48%)	71,662 (55%)	30,697 (53%)
race_ethnicity_label			
White	200,033 (61%)	81,357 (63%)	39,784 (69%)
Black or African American	62,418 (19%)	19,197 (15%)	8,082 (14%)
Hispanic	23,548 (7.2%)	7,464 (5.8%)	2,757 (4.8%)
Asian	4,880 (1.5%)	2,739 (2.1%)	789 (1.4%)
American Indian	1,971 (0.6%)	1,768 (1.4%)	316 (0.5%)
Pacific Islander	460 (0.1%)	162 (0.1%)	56 (<0.1%)
Unknown	34,734 (11%)	16,742 (13%)	6,029 (10%)
location_label			
South	138,843 (42%)	70,729 (55%)	32,694 (57%)
Northeast	93,209 (28%)	23,262 (18%)	12,975 (22%)
Midwest	22,924 (7.0%)	10,703 (8.3%)	4,844 (8.4%)
West	73,068 (22%)	24,735 (19%)	7,300 (13%)
osa_label			
asthma_label	60,653 (18%)	17,709 (14%)	11,965 (21%)
copd_label	48,456 (15%)	13,049 (10%)	8,268 (14%)
chf_label	60,214 (18%)	21,195 (16%)	18,846 (33%)
nmd_label	59,770 (18%)	25,469 (20%)	16,219 (28%)
phtrn_label	11,891 (3.6%)	5,861 (4.5%)	2,487 (4.3%)
ckd_label	23,854 (7.3%)	10,513 (8.1%)	7,347 (13%)
diabetes_label	54,528 (17%)	24,849 (19%)	11,769 (20%)
encounter_type_label	93,007 (28%)	37,426 (29%)	18,521 (32%)
Emergency	142,713 (44%)	19,196 (15%)	9,818 (17%)
Inpatient	185,331 (56%)	110,233 (85%)	47,995 (83%)
VBG PCO2	45.5 ± 10.5; 233,430.0/328,044.0 missing (71.2%)	42.0 ± 11.2; 91,782.0/129,429.0 missing (70.9%)	57.4 ± 18.4; 40,411.0/57,813
Arterial PCO2	NA ± NA; 328,044.0/328,044.0 missing (100.0%)	35.5 ± 6.1; 0.0/129,429.0 missing (0.0%)	58.5 ± 20.4; 0.0/57,813.0

¹Mean ± SD; N Missing/No. obs. missing (% Missing); n (%)

Variable	No VBG N = 365,623 ¹	VBG_NoHypercapnia N = 105,646 ¹	VBG_Hypercapnia
Age (years)	59.4 ± 17.8; 0.0/365,623.0 missing (0.0%)	58.1 ± 17.8; 0.0/105,646.0 missing (0.0%)	61.0 ± 16.7; 0.0/44,017.0
Current BMI kg/m ²	31.8 ± 8.5; 192,892.0/365,623.0 missing (52.8%)	28.7 ± 7.2; 69,615.0/105,646.0 missing (65.9%)	29.3 ± 7.9; 31,038.0/44,017.0
sex_label			
Female	184,619 (50%)	48,931 (46%)	20,356 (46%)
Male	181,004 (50%)	56,715 (54%)	23,661 (54%)
race_ethnicity_label			
White	241,114 (66%)	55,100 (52%)	24,960 (57%)
Black or African American	61,814 (17%)	19,199 (18%)	8,684 (20%)
Hispanic	22,951 (6.3%)	8,354 (7.9%)	2,464 (5.6%)
Asian	5,439 (1.5%)	2,293 (2.2%)	676 (1.5%)
American Indian	2,128 (0.6%)	1,683 (1.6%)	244 (0.6%)
Pacific Islander	543 (0.1%)	110 (0.1%)	25 (<0.1%)
Unknown	31,634 (8.7%)	18,907 (18%)	6,964 (16%)
location_label			
South	196,774 (54%)	30,426 (29%)	15,066 (34%)
Northeast	65,537 (18%)	44,405 (42%)	19,504 (44%)
Midwest	24,891 (6.8%)	9,178 (8.7%)	4,402 (10%)
West	78,421 (21%)	21,637 (20%)	5,045 (11%)
osa_label	65,748 (18%)	15,634 (15%)	8,945 (20%)
asthma_label	49,810 (14%)	13,419 (13%)	6,544 (15%)
copd_label	70,950 (19%)	16,459 (16%)	12,846 (29%)
chf_label	68,964 (19%)	20,573 (19%)	11,921 (27%)
nmd_label	14,796 (4.0%)	3,754 (3.6%)	1,689 (3.8%)
phtn_label	27,731 (7.6%)	8,534 (8.1%)	5,449 (12%)
ckd_label	61,091 (17%)	21,290 (20%)	8,765 (20%)
diabetes_label	101,173 (28%)	33,665 (32%)	14,116 (32%)
encounter_type_label			
Emergency	124,405 (34%)	34,711 (33%)	12,611 (29%)
Inpatient	241,218 (66%)	70,935 (67%)	31,406 (71%)
VBG PCO2	NA ± NA; 365,623.0/365,623.0 missing (100.0%)	40.1 ± 6.6; 0.0/105,646.0 missing (0.0%)	60.2 ± 12.6; 0.0/44,017.0
Arterial PCO2	42.4 ± 15.5; 233,430.0/365,623.0 missing (63.8%)	38.6 ± 15.4; 68,334.0/105,646.0 missing (64.7%)	52.7 ± 19.6; 26,280.0/44,017.0

¹Mean ± SD; N Missing/No. obs. missing (% Missing); n (%)

```

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), 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 (no "Everyone" here)
tbl1_vbg <- subset_data %>%
  select(all_of(vars), 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::modify_header(label = "##Variable**")

library(gtsummary)

tbl1 <- tbl_merge(
  tbls = list(tbl1_abg, tbl1_vbg)
) %>%
  modify_caption("##Table 1. Baseline summary: Everyone, ABG status, and VBG status**")

tbl1

```

NEW Table 2

```

# Hypercapnia factors within measured cohorts
subset_data <- subset_data %>%
  mutate(
    hyper_abg = factor(hypercap_on_abg, levels = c(1, 0),
                        labels = c("Got ABG & Hypercapnia", "Got ABG & No hypercapnia")),
    hyper_vbg = factor(hypercap_on_vbg, levels = c(1, 0),
                        labels = c("Got VBG & Hypercapnia", "Got VBG & No hypercapnia"))
  )

# ABG cohort (has_abg == 1)
tbl2_abg <- subset_data %>%
  filter(has_abg == 1) %>%
  select(all_of(vars), hyper_abg) %>%
  gtsummary::tbl_summary(
    by = hyper_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})%"
    ),
  )

```

Table 1

Variable	Everyone ^t	Did not get ABG N = 328,044 ^t	Did get ABG N
Age (years)	59.2 ± 17.7; 0.0/515,286.0 missing (0.0%)	58.1 ± 18.1; 0.0/328,044.0 missing (0.0%)	61.2 ± 16.9; 0.0/187,247
Current BMI kg/m ²	31.1 ± 8.4; 293,545.0/515,286.0 missing (57.0%)	32.3 ± 8.7; 184,223.0/328,044.0 missing (56.2%)	29.0 ± 7.2; 109,322.0/187.5
sex_label			
Female	253,906 (49%)	169,023 (52%)	84,883 (48%)
Male	261,380 (51%)	159,021 (48%)	102,359 (51%)
race_ethnicity_label			
White	321,174 (62%)	200,033 (61%)	121,141 (62%)
Black or African American	89,697 (17%)	62,418 (19%)	27,279 (17%)
Hispanic	33,769 (6.6%)	23,548 (7.2%)	10,221 (5%)
Asian	8,408 (1.6%)	4,880 (1.5%)	3,528 (1.4%)
American Indian	4,055 (0.8%)	1,971 (0.6%)	2,084 (1.1%)
Pacific Islander	678 (0.1%)	460 (0.1%)	218 (0.1%)
Unknown	57,505 (11%)	34,734 (11%)	22,771 (11%)
location_label			
South	242,266 (47%)	138,843 (42%)	103,423 (52%)
Northeast	129,446 (25%)	93,209 (28%)	36,237 (18%)
Midwest	38,471 (7.5%)	22,924 (7.0%)	15,547 (8%)
West	105,103 (20%)	73,068 (22%)	32,035 (18%)
osa_label	90,327 (18%)	60,653 (18%)	29,674 (16%)
asthma_label	69,773 (14%)	48,456 (15%)	21,317 (13%)
copd_label	100,255 (19%)	60,214 (18%)	40,041 (21%)
chf_label	101,458 (20%)	59,770 (18%)	41,688 (22%)
nmd_label	20,239 (3.9%)	11,891 (3.6%)	8,348 (4.4%)
phtn_label	41,714 (8.1%)	23,854 (7.3%)	17,860 (9.4%)
ckd_label	91,146 (18%)	54,528 (17%)	36,618 (20%)
diabetes_label	148,954 (29%)	93,007 (28%)	55,947 (31%)
encounter_type_label			
Emergency	171,727 (33%)	142,713 (44%)	29,014 (15%)
Inpatient	343,559 (67%)	185,331 (56%)	158,228 (82%)
VBG PCO2	46.0 ± 12.7; 365,623.0/515,286.0 missing (71.0%)	45.5 ± 10.5; 233,430.0/328,044.0 missing (71.2%)	46.9 ± 15.6; 132,193.0/187,247 missing (100.0%)
Arterial PCO2	42.6 ± 16.3; 328,044.0/515,286.0 missing (63.7%)	NA ± NA; 328,044.0/328,044.0 missing (100.0%)	42.6 ± 16.3; 0.0/187,247 missing (100.0%)

^tMean ± SD; N Missing/No. obs. missing (% Missing); n (%)

```

digits = list(gtsummary::all_continuous() ~ 1),
missing = "no"
) %>%
gtsummary::modify_header(
  label = "**Variable**",
  stat_1 = "***Got ABG & Hypercapnia***",
  stat_2 = "***Got ABG & No hypercapnia***"
)

# VBG cohort (has_vbg == 1)
tbl2_vbg <- subset_data %>%
  filter(has_vbg == 1) %>%
  select(all_of(vars), hyper_vbg) %>%
gtsummary::tbl_summary(
  by = hyper_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 = "***Got VBG & Hypercapnia***",
  stat_2 = "***Got VBG & No hypercapnia***"
)

# Merge side-by-side (no spanners; 4 requested columns)
table2 <- gtsummary::tbl_merge(
  tbls = list(tbl2_abg, tbl2_vbg),
  tab_spinner = c(NULL, NULL)
) %>%

```

```
gtsummary::modify_caption("**Table 2. Baseline summary by hypercapnia within ABG and VBG cohorts**")  
table2
```

Generating Word Docs for New Table 1 and 2

```
library(gtsummary)  
library(flextable)  
library(officer)  
  
# gtsummary objects (example: table1, table2)  
ft1 <- as_flex_table(tbl1)  
ft2 <- as_flex_table(table2)  
  
doc <- read_docx() %>%  
  body_add_par("Table 1", style = "heading 1") %>%  
  body_add_flextable(ft1) %>%  
  body_add_par("Table 2", style = "heading 1") %>%  
  body_add_flextable(ft2)  
  
print(doc, target = "Tables.docx")
```

Unweighted, Hypercapnia (binary yes/no) Simple (1 predictor) Regressions:

Unweighted, ABG Group: hypercapnia treated as a binary (yes/no) predictor

```
logit_intubated_abg <- glm(imv_proc ~ hypercap_on_abg, data = subset_data, family = binomial)  
summary(logit_intubated_abg)
```

Call:
glm(formula = imv_proc ~ hypercap_on_abg, family = binomial,
 data = subset_data)

Table 1

Variable	Got ABG & Hypercapnia ¹	Got ABG & No hypercapnia ¹	Got VBG & Hypercapnia ¹
Age (years)	62.1 ± 16.4; 0.0/57,813.0 missing (0.0%)	60.8 ± 17.1; 0.0/129,429.0 missing (0.0%)	61.0 ± 16.7; 0.0/44,017.0 m
Current BMI kg/m ²	29.8 ± 7.9; 33,496.0/57,813.0 missing (57.9%)	28.6 ± 6.9; 75,826.0/129,429.0 missing (58.6%)	29.3 ± 7.9; 31,038.0/44,017.0 .
sex_label			
Female	27,116 (47%)	57,767 (45%)	20,356 (46%)
Male	30,697 (53%)	71,662 (55%)	23,661 (54%)
race_ethnicity_label			
White	39,784 (69%)	81,357 (63%)	24,960 (57%)
Black or African American	8,082 (14%)	19,197 (15%)	8,684 (20%)
Hispanic	2,757 (4.8%)	7,464 (5.8%)	2,464 (5.6%)
Asian	789 (1.4%)	2,739 (2.1%)	676 (1.5%)
American Indian	316 (0.5%)	1,768 (1.4%)	244 (0.6%)
Pacific Islander	56 (<0.1%)	162 (0.1%)	25 (<0.1%)
Unknown	6,029 (10%)	16,742 (13%)	6,964 (16%)
location_label			
South	32,694 (57%)	70,729 (55%)	15,066 (34%)
Northeast	12,975 (22%)	23,262 (18%)	19,504 (44%)
Midwest	4,844 (8.4%)	10,703 (8.3%)	4,402 (10%)
West	7,300 (13%)	24,735 (19%)	5,045 (11%)
osa_label			
asthma_label			
copd_label			
chf_label			
nmd_label			
phtn_label			
ckd_label			
diabetes_label			
encounter_type_label			
Emergency	9,818 (17%)	19,196 (15%)	12,611 (29%)
Inpatient	47,995 (83%)	110,233 (85%)	31,406 (71%)
VBG PCO2	57.4 ± 18.4; 40,411.0/57,813.0 missing (69.9%)	42.0 ± 11.2; 91,782.0/129,429.0 missing (70.9%)	60.2 ± 12.6; 0.0/44,017.0 m
Arterial PCO2	58.5 ± 20.4; 0.0/57,813.0 missing (0.0%)	35.5 ± 6.1; 0.0/129,429.0 missing (0.0%)	52.7 ± 19.6; 26,280.0/44,017.0

1Mean ± SD; N Missing/No. obs. missing (% Missing); n (%)

```

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept) -2.275471  0.005086 -447.4 <2e-16 ***
hypercap_on_abg 1.259993  0.010700  117.8 <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' '

```

(Dispersion parameter for binomial family taken to be 1)

```

Null deviance: 362580  on 515285 degrees of freedom
Residual deviance: 350435 on 515284 degrees of freedom
AIC: 350439

```

Number of Fisher Scoring iterations: 5

```

tidy(logit_intubated_abg,
  exponentiate = TRUE, # turns log-odds → OR
  conf.int = TRUE) # adds 95 % CI

```

term	estimate	std.error	statistic	p.value	conf.low	conf.high
(Intercept)	0.1027485	0.0050863	-447.3684	0	0.1017279	0.1037765
hypercap_on_abg	3.5253956	0.0106997	117.7601	0	3.4521736	3.6000445

```

logit_niv_abg <- glm(niv_proc ~ hypercap_on_abg, data = subset_data, family = binomial)
summary(logit_niv_abg)

```

Call:
`glm(formula = niv_proc ~ hypercap_on_abg, data = subset_data, family = binomial,
 data = subset_data)`

Coefficients:

```
(Intercept) -2.860418  0.006533 -437.84 <2e-16 ***
hypercap_on_abg 1.201665  0.013093  91.78 <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

(Dispersion parameter for binomial family taken to be 1)

```
Null deviance: 250639  on 515285  degrees of freedom
Residual deviance: 243461  on 515284  degrees of freedom
AIC: 243465
```

Number of Fisher Scoring iterations: 5

```
tidy(logit_niv_abg,
exponentiate = TRUE, # turns log-odds → OR
conf.int    = TRUE) # adds 95 % CI
```

term	estimate	std.error	statistic	p.value	conf.low	conf.high
(Intercept)	0.0572448	0.0065330	-437.84069	0	0.0565151	0.0579811
hypercap_on_abg	3.3256498	0.0130929	91.77958	0	3.2412752	3.4119744

```
logit_death_abg <- glm(death_60d ~ hypercap_on_abg, data = subset_data, family = binomial)
summary(logit_death_abg)
```

Call:
glm(formula = death_60d ~ hypercap_on_abg, family = binomial,
data = subset_data)

Coefficients:

```

Estimate Std. Error z value Pr(>|z|)
(Intercept) -2.258743 0.005052 -447.11 <2e-16 ***
hypercap_on_abg 0.756240 0.011903 63.53 <2e-16 ***
---
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

(Dispersion parameter for binomial family taken to be 1)

```

Null deviance: 344897 on 515285 degrees of freedom
Residual deviance: 341286 on 515284 degrees of freedom
AIC: 341290

```

Number of Fisher Scoring iterations: 5

```

tidy(logit_death_abg,
exponentiate = TRUE, # turns log-odds → OR
conf.int = TRUE) # adds 95 % CI

```

term	estimate	std.error	statistic	p.value	conf.low	conf.high
(Intercept)	0.1044817	0.0050519	-447.10674	0	0.1034509	0.105520
hypercap_on_abg	2.1302521	0.0119030	63.53375	0	2.0810535	2.180455

```

logit_icd_abg <- glm(hypercap_resp_failure ~ hypercap_on_abg, data = subset_data, family = binomial)
summary(logit_icd_abg)

```

Call:
`glm(formula = hypercap_resp_failure ~ hypercap_on_abg, family = binomial,
 data = subset_data)`

Coefficients:

Estimate	Std. Error	z value	Pr(> z)
----------	------------	---------	----------

```
(Intercept) -3.355697  0.008192 -409.6 <2e-16 ***
hypercap_on_abg 2.175594  0.012779  170.2 <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

(Dispersion parameter for binomial family taken to be 1)

```
Null deviance: 223278 on 515285 degrees of freedom
Residual deviance: 197920 on 515284 degrees of freedom
AIC: 197924
```

Number of Fisher Scoring iterations: 6

```
tidy(logit_icd_abg,
  exponentiate = TRUE, # turns log-odds → OR
  conf.int    = TRUE) # adds 95 % CI
```

term	estimate	std.error	statistic	p.value	conf.low	conf.high
(Intercept)	0.034885	0.0081920	-409.6314	0	0.034328	0.0354483
hypercap_on_abg	8.807416	0.0127795	170.2414	0	8.589528	9.0307810

Display the regression coefficients for the binary (hypercapnia yes/no) predictor logistic regressions

```
modelsummary(
  list("Intubated" = logit_intubated_abg,
       "NIV"      = logit_niv_abg,
       "Death"    = logit_death_abg,
       "ICD Hyper" = logit_icd_abg),
  exponentiate = TRUE,
  conf_level   = 0.95,
  estimate     = "estimate",
  statistic    = "{conf.low}, {conf.high}") ,
```

	Intubated	NIV	Death	ICD Hyper
hypercap_on_abg	3.53 (3.45, 3.60)	3.33 (3.24, 3.41)	2.13 (2.08, 2.18)	8.81 (8.59, 9.03)

```

coefomit = "(Intercept)" ,
gofomit = ".*",
fmt      = 2,
output   = "gt"
) |>
gt_pdf(title = "Odds Ratios for ABG Hypercapnia (>45 mmHg)'s association with...")
```

Profiled confidence intervals may take longer time to compute.

Use `ci_method="wald"` for faster computation of CIs.

Profiled confidence intervals may take longer time to compute.

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Profiled confidence intervals may take longer time to compute.

Use `ci_method="wald"` for faster computation of CIs.

Unweighted VBG Group

```
logit_intubated_vbg <- glm(imv_proc ~ hypercap_on_vbg, data = subset_data, family = binomial)
summary(logit_intubated_vbg)
```

Call:
`glm(formula = imv_proc ~ hypercap_on_vbg, family = binomial,
 data = subset_data)`

Coefficients: Estimate Std. Error z value Pr(>|z|)

```
(Intercept) -2.134026  0.004735 -450.69 <2e-16 ***
hypercap_on_vbg 0.648004  0.013168  49.21 <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

(Dispersion parameter for binomial family taken to be 1)

```
Null deviance: 3625580 on 515285 degrees of freedom
Residual deviance: 360405 on 515284 degrees of freedom
AIC: 360409
```

Number of Fisher Scoring iterations: 4

```
tidy(logit_intubated_vbg,
exponentiate = TRUE, # turns log-odds → OR
conf.int = TRUE) # adds 95 % CI
```

term	estimate	std.error	statistic	p.value	conf.low	conf.high
(Intercept)	0.1183598	0.0047351	-450.68580	0	0.1172651	0.1194621
hypercap_on_vbg	1.9117219	0.0131682	49.20969	0	1.8629159	1.9616038

```
logit_niv_vbg <- glm(niv_proc ~ hypercap_on_vbg, data = subset_data, family = binomial)
summary(logit_niv_vbg)
```

Call:
`glm(formula = niv_proc ~ hypercap_on_vbg, family = binomial,
 data = subset_data)`

Coefficients:
`Estimate Std. Error z value Pr(>|z|)
(Intercept) -2.735699 0.006091 -449.13 <2e-16 ***`

```

hypercap_on_vbg 0.750555 0.015845 47.37 <2e-16 ***
---
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 250639 on 515285 degrees of freedom
Residual deviance: 248688 on 515284 degrees of freedom
AIC: 248692

```

Number of Fisher Scoring iterations: 5

```

tidy(logit_niv_vbg,
  exponentiate = TRUE, # turns log-odds → OR
  conf.int = TRUE) # adds 95 % CI

```

term	estimate	std.error	statistic	p.value	conf.low	conf.high
(Intercept)	0.0648486	0.0060911	-449.12691	0	0.0640777	0.0656261
hypercap_on_vbg	2.1181752	0.0158446	47.36965	0	2.0532293	2.1848014

```

logit_death_vbg <- glm(death_60d ~ hypercap_on_vbg, data = subset_data, family = binomial)
summary(logit_death_vbg)

```

Call:
`glm(formula = death_60d ~ hypercap_on_vbg, family = binomial,
 data = subset_data)`

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-2.197765	0.004856	-452.56	<2e-16 ***
hypercap_on_vbg	0.479895	0.014131	33.96	<2e-16 ***

```
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

(Dispersion parameter for binomial family taken to be 1)

```
Null deviance: 344897 on 515285 degrees of freedom
Residual deviance: 343841 on 515284 degrees of freedom
AIC: 343845
```

Number of Fisher Scoring iterations: 4

```
tidy(logit_death_vbg,
      exponentiate = TRUE, # turns log-odds to OR
      conf.int = TRUE) # adds 95 % CI
```

term	estimate	std.error	statistic	p.value	conf.low	conf.high
(Intercept)	0.1110511	0.0048563	-452.56297	0	0.1099977	0.1121119
hypercap_on_vbg	1.6159045	0.0141315	33.95924	0	1.5716549	1.6611746

```
logit_icd_vbg <- glm(hypercap_resp_failure ~ hypercap_on_vbg, data = subset_data, family = binomial)
summary(logit_icd_vbg)
```

Call:
glm(formula = hypercap_resp_failure ~ hypercap_on_vbg, family = binomial,
data = subset_data)

Coefficients:

```
Estimate Std. Error z value Pr(>|z|)
(Intercept) -3.136462 0.007293 -430.1 <2e-16 ***
hypercap_on_vbg 1.831609 0.013731 133.4 <2e-16 ***
---
```

```
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

(Dispersion parameter for binomial family taken to be 1)

```
Null deviance: 223278  on 515285 degrees of freedom
Residual deviance: 208772  on 515284 degrees of freedom
AIC: 208776
```

Number of Fisher Scoring iterations: 6

```
tidy(logit_icd_vbg,
  exponentiate = TRUE, # turns log-odds → OR
  conf.int = TRUE) # adds 95 % CI
```

term	estimate	std.error	statistic	p.value	conf.low	conf.high
(Intercept)	0.0434362	0.0072930	-430.0654	0	0.0428184	0.0440602
hypercap_on_vbg	6.2439262	0.0137314	133.3879	0	6.0779584	6.4140808

Display model coefficients for binary hypercapnia on VBG logistic regression

```
modelsummary(
  list("Intubated" = logit_intubated_vbg,
    "NIV" = logit_niv_vbg,
    "Death" = logit_death_vbg,
    "ICD Hyper" = logit_icd_vbg),
  exponentiate = TRUE,
  conf_level = 0.95,
  estimate = "{estimate}",
  statistic = "{conf.low}, {conf.high})",
  coef.omit = "(Intercept)",
  gof.omit = ".*",
  fmt = 2,
```

drop all goodness-of-fit rows
2 decimal places everywhere

```

hypercap_on_vbg
  Intubated      NIV      Death
  1.91      2.12      1.62
  (1.86, 1.96) (2.05, 2.18) (1.57, 1.66)
  (6.08, 6.41)

output = "gt"
) |>
gt_pdf(title = "Odds Ratios for VBG Hypercapnia (>45 mmHg)'s association with...")


```

Profiled confidence intervals may take longer time to compute.

Use `ci_method="wald"~` for faster computation of CIs.

Profiled confidence intervals may take longer time to compute.

Use `ci_method="wald"~` for faster computation of CIs.

Profiled confidence intervals may take longer time to compute.

Use `ci_method="wald"~` for faster computation of CIs.

Profiled confidence intervals may take longer time to compute.

Use `ci_method="wald"~` for faster computation of CIs.

Profiled confidence intervals may take longer time to compute.

Calculated ABG from VBG Using Farkas equation - binary predictor

```

subset_data <- subset_data %>%
  mutate(
    calc_abg = vbg_co2 - (0.22 * (93 - vbg_o2sat)))
  )
subset_data <- subset_data %>%
  mutate(
    hypercapnia_calc = ifelse(calc_abg > 45, 1, 0)
  )
with(subset_data, table(hypercapnia_calc,niv_proc))


```

niv_proc	hypercapnia_calc	0	1
0	47526	2877	
1	14146	2599	

```
logit_intubated_calc <- glm(imv_proc ~ hypercapnia_calc, data = subset_data, family = binomial)
summary(logit_intubated_calc)
```

Call:
`glm(formula = imv_proc ~ hypercapnia_calc, family = binomial,`

`data = subset_data)`

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-1.95271	0.01350	-144.62	<2e-16 ***
hypercapnia_calc	0.53248	0.02373	22.43	<2e-16 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 54823 on 67147 degrees of freedom

Residual deviance: 54341 on 67146 degrees of freedom

(448138 observations deleted due to missingness)

AIC: 54345

Number of Fisher Scoring iterations: 4

```
tidy(logit_intubated_calc,
exponentiate = TRUE, # turns log-odds → OR
conf.int = TRUE) # adds 95 % CI
```

term	estimate	std.error	statistic	p.value	conf.low	conf.high
(Intercept)	0.1418894	0.0135026	-144.61661	0	0.1381714	0.1456819
hypercapnia_calc	1.7031430	0.0237343	22.43489	0	1.6256101	1.7841152

```
logit_niv_calc <- glm(niv_proc ~ hypercapnia_calc, data = subset_data, family = binomial)
summary(logit_niv_calc)
```

Call:

```
glm(formula = niv_proc ~ hypercapnia_calc, family = binomial,
    data = subset_data)
```

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-2.80453	0.01920	-146.07	<2e-16 ***
hypercapnia_calc	1.11022	0.02871	38.67	<2e-16 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 37944 on 67147 degrees of freedom

Residual deviance: 36518 on 67146 degrees of freedom
(448138 observations deleted due to missingness)

AIC: 36522

Number of Fisher Scoring iterations: 5

```
tidy(logit_niv_calc,
  exponentiate = TRUE, # turns log-odds → OR
  conf.int = TRUE) # adds 95 % CI
```

term	estimate	std.error	statistic	p.value	conf.low	conf.high
(Intercept)	0.0605353	0.0191993	-146.07446	0	0.0582873	0.0628436
hypercapnia_calc	3.0350373	0.0287066	38.67487	0	2.8689300	3.2106486

```
logit_death_calc <- glm(death_60d ~ hypercapnia_calc, data = subset_data, family = binomial)
summary(logit_death_calc)
```

Call:
`glm(formula = death_60d ~ hypercapnia_calc, family = binomial,`

`data = subset_data)`

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-1.78892	0.01272	-140.681	< 2e-16 ***
hypercapnia_calc	0.15484	0.02447	6.327	2.49e-10 ***

Signif. codes:	0 '***'	0.001 '***'	0.01 '**'	0.05 '*'
	0.1	0.1	0.1	1

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 56349 on 67147 degrees of freedom

Residual deviance: 56310 on 67146 degrees of freedom
(448138 observations deleted due to missingness)

AIC: 56314

Number of Fisher Scoring iterations: 4

```
tidy(logit_death_calc,
exponentiate = TRUE, # turns log-odds → OR
conf.int = TRUE) # adds 95 % CI
```

term	estimate	std.error	statistic	p.value	conf.low	conf.high
(Intercept)	0.1671414	0.0127161	-140.68135	0	0.1630151	0.1713468
hypercapnia_calc	1.1674692	0.0244711	6.32739	0	1.1126631	1.2246862

```
logit_icd_calc <- glm(hypercap_resp_failure ~ hypercapnia_calc, data = subset_data, family = binomial)
summary(logit_icd_calc)
```

Call:
glm(formula = hypercap_resp_failure ~ hypercapnia_calc, family = binomial,
data = subset_data)

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-3.17657	0.02271	-139.85	<2e-16 ***
hypercapnia_calc	2.23074	0.02850	78.27	<2e-16 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 43605 on 67147 degrees of freedom

Residual deviance: 36797 on 67146 degrees of freedom

(448138 observations deleted due to missingness)

AIC: 36801

Number of Fisher Scoring iterations: 6

```
tidy(logit_icd_calc,
exponentiate = TRUE, # turns log-odds → OR
conf.int = TRUE) # adds 95 % CI
```

term	estimate	std.error	statistic	p.value	conf.low	conf.high
(Intercept)	0.0417287	0.0227148	-139.84562	0	0.039894	0.0436152
hypercapnia_calc	9.3067708	0.0285021	78.26601	0	8.8025311	9.8430989

	Intubated	NIV	Death	ICD Hyper
hypercapnia_calc	1.70 (1.63, 1.78)	3.04 (2.87, 3.21)	1.17 (1.11, 1.22)	9.31 (8.80, 9.84)

Display regression coefficients for binary Farkas adjustment (hypercapnia yes/no as predictor)

```
modelsummary(
  list("Intubated" = logit_intubated_calc,
       "NIV" = logit_niv_calc,
       "Death" = logit_death_calc,
       "ICD Hyper" = logit_icd_calc),
  exponentiate = TRUE,
  conf_level = 0.95,
  estimate = "estimate",
  statistic = "{conf.low}, {conf.high}",
  coef.omit = "(Intercept)",
  gof.omit = ".**",
  fmt = 2,
  output = "gt"
) |>
  gt_pdf(title = "Odds Ratios for Calculated Hypercapnia (>45 mmHg)'s association with...")
```

Profiled confidence intervals may take longer time to compute.

Use `ci_method="wald"` for faster computation of CIs.

Profiled confidence intervals may take longer time to compute.

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Odds Ratio Graph of all 3 simple, binary-predictor logistic regressions

```

tidy_with_labels <- function(model, group_label, outcome_label) {
  tidy(model, exponentiate = TRUE, conf.int = TRUE) %>%
    filter(term == "hypercap_on_abg" | term == "hypercap_niva_calc") %>%
    mutate(
      group = group_label,
      outcome = outcome_label
    )
}

# --- ABG Models ---
abg_intub <- tidy_with_labels(glm(imv_proc ~ hypercap_on_abg, data = subset_data, family = binomial), "ABG", "Intubation")
abg_niv <- tidy_with_labels(glm(niv_proc ~ hypercap_on_abg, data = subset_data, family = binomial), "ABG", "NIV")
abg_death <- tidy_with_labels(glm(death_60d ~ hypercap_on_abg, data = subset_data, family = binomial), "ABG", "Death")
abg_icd <- tidy_with_labels(glm(hypercap_resp_failure ~ hypercap_on_abg, data = subset_data, family = binomial), "ABG", "ICD")

# --- VBG Models ---
vbg_intub <- tidy_with_labels(glm(imv_proc ~ hypercap_on_vbg, data = subset_data, family = binomial), "VBG", "Intubation")
vbg_niv <- tidy_with_labels(glm(niv_proc ~ hypercap_on_vbg, data = subset_data, family = binomial), "VBG", "NIV")
vbg_death <- tidy_with_labels(glm(death_60d ~ hypercap_on_vbg, data = subset_data, family = binomial), "VBG", "Death")
vbg_icd <- tidy_with_labels(glm(hypercap_resp_failure ~ hypercap_on_vbg, data = subset_data, family = binomial), "VBG", "ICD")

# --- Calculated ABG Models ---
calc_intub <- tidy_with_labels(glm(imv_proc ~ hypercapnia_calc, data = subset_data, family = binomial), "Calculated ABG", "Intubated ABG")
calc_niv <- tidy_with_labels(glm(niv_proc ~ hypercapnia_calc, data = subset_data, family = binomial), "Calculated ABG", "NIV")
calc_death <- tidy_with_labels(glm(death_60d ~ hypercapnia_calc, data = subset_data, family = binomial), "Calculated ABG", "Death")
calc_icd <- tidy_with_labels(glm(hypercap_resp_failure ~ hypercapnia_calc, data = subset_data, family = binomial), "Calculated ABG", "ICD")

# --- Combine all model results ---
combined_or_df <- bind_rows(
  abg_intub, abg_niv, abg_death, abg_icd,
  vbg_intub, vbg_niv, vbg_death, vbg_icd,
  calc_intub, calc_niv, calc_death, calc_icd
)

```

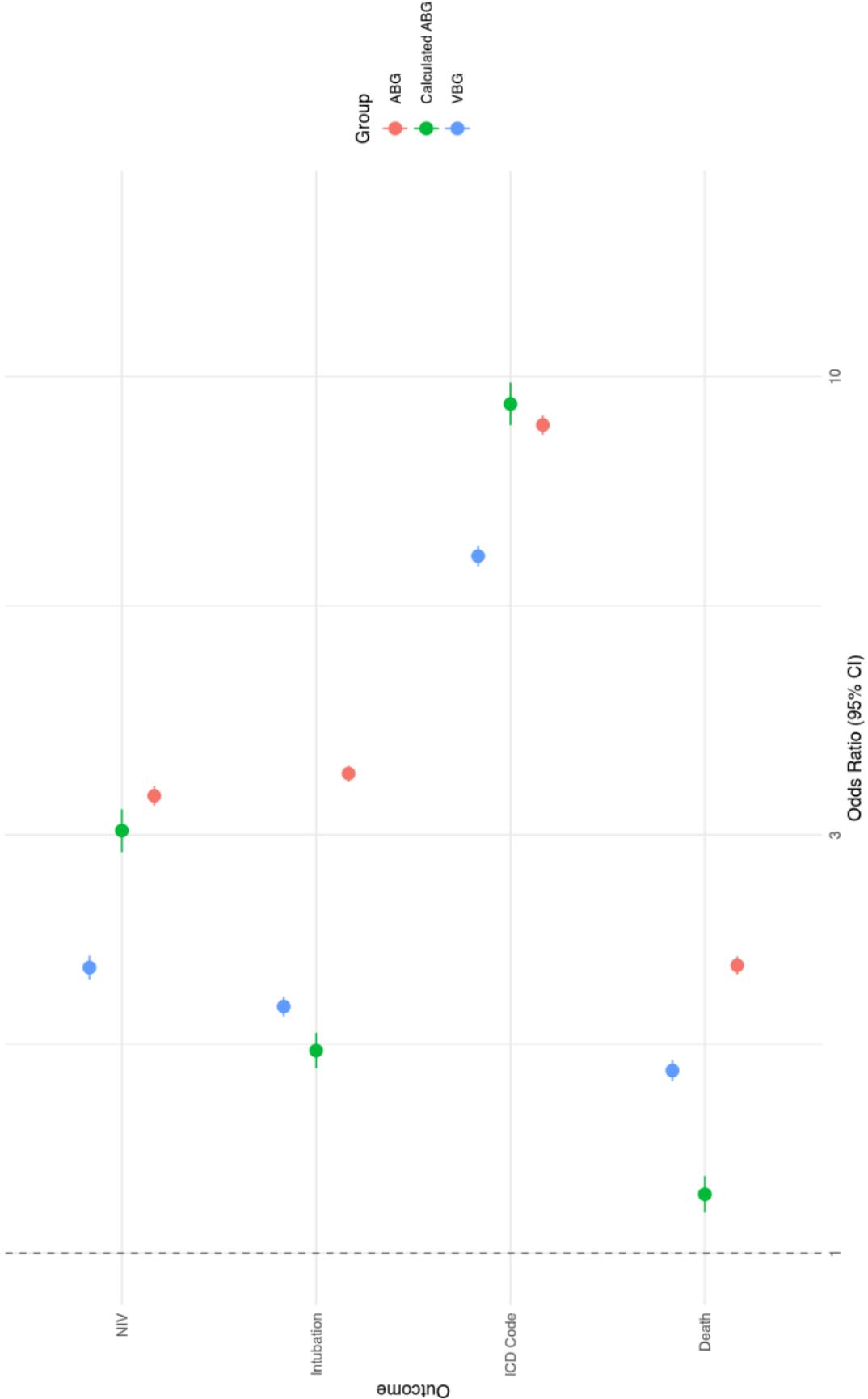
```

ggplot(combined_or_df, aes(x = outcome, y = estimate, ymin = conf.low, ymax = conf.high, color = group)) +
  geom_pointrange(position = position_dodge(width = 0.5), size = 0.6) +
  geom_hline(yintercept = 1, linetype = "dashed", color = "gray40") +
  coord_flip() +
  labs(
    title = "Unweighted, Unadjusted OR of Outcomes when Hypercapnia Present ABG, VBG, Farkas-VBG",
    x = "Outcome",
    y = "Odds Ratio (95% CI)",
    color = "Group"
  ) +
  scale_y_log10(limits = c(-0.5, 15)) + # optional log scale for better spacing
  theme_minimal(base_size = 10)

```

Warning in transform\$transform(limits): NaNs produced

Unweighted, Unadjusted OR of Outcomes when Hypercapnia Present ABG, VBG, Farkas-VBG



```
combined_or_df$group <- factor(combined_or_df$group,
levels = c("ABG", "VBG", "Calculated ABG"))
```

```

# prerequisites

# order groups before plotting
combined_or_df$group <- factor(
  combined_or_df$group,
  levels = c("ABG", "VBG", "Calculated ABG")
)

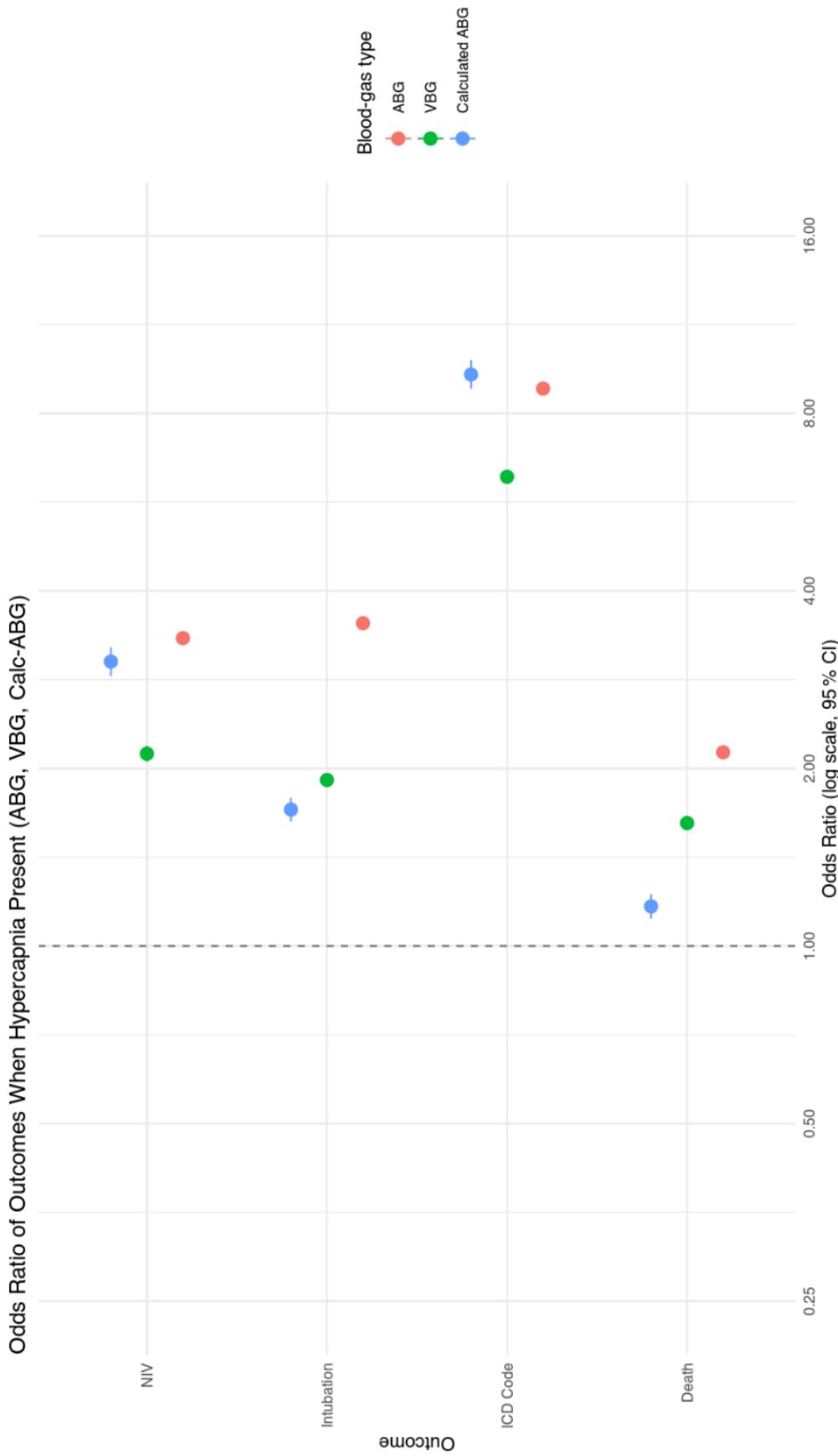
# plot
ggplot(
  combined_or_df,
  aes(
    x = outcome,
    y = estimate,
    ymin = conf.low,
    ymax = conf.high,
    color = group
  )
) +
  geom_pointrange(
    position = position_dodge(width = 0.6),
    size = 0.6
  ) +
  geom_hline(yintercept = 1, linetype = "dashed", colour = "grey40") +
  ## NOTE: scale_y_log10 applies to the axis that *becomes horizontal* after coord_flip()
  scale_y_log10(
    breaks = c(0.25, 0.5, 1, 2, 4, 8, 16),
    limits = c(0.25, 16),
    labels = number_format(accuracy = 0.01)
  ) +
  coord_flip() +
  labs(
    title = "Odds Ratio of Outcomes When Hypercapnia Present (ABG, VBG, Calc-ABG)",
    x = "Outcome",

```

```

y    = "Odds Ratio (log scale, 95 % CI)",
color = "Blood-gas type",
caption = paste(
  "Odds ratios are computed *within* each blood-gas cohort." ,
  "Numerator = patients who received that blood-gas and **had** hypercapnia;" ,
  "denominator = patients who received the same blood-gas and ***did not*** have hypercapnia." ,
  "Because the underlying cohorts differ (ABG, VBG, Calculated ABG) ,",
  "denominators are not identical across groups .",
  sep = "\n"
)
)
) +
theme_minimal(base_size = 10) +
theme(plot.caption = element_text(hjust = 0))

```



Now doing 3 groups instead of binary (above, normal and below)

```

subset_data <- subset_data %>%
  mutate(
    pco2_cat_abg = case_when(
      !is.na(paco2) & paco2 < 35 ~ "Below normal",
      !is.na(paco2) & paco2 > 45 ~ "Above normal",
      !is.na(paco2) ~ "Normal"
    ),
    pco2_cat_vbg = case_when(
      !is.na(vbg_co2) & vbg_co2 < 35 ~ "Below normal",
      !is.na(vbg_co2) & vbg_co2 > 50 ~ "Above normal",
      !is.na(vbg_co2) ~ "Normal"
    ),
    pco2_cat_calc = case_when(
      !is.na(calc_abg) & calc_abg < 35 ~ "Below normal",
      !is.na(calc_abg) & calc_abg > 45 ~ "Above normal",
      !is.na(calc_abg) ~ "Normal"
    )
  ) %>%
  mutate(
    across(starts_with("pco2_cat"),
      ~factor(.x, levels = c("Normal", "Below normal", "Above normal")))
  )

```

```

library(broom)
library(dplyr)

run_logit <- function(data, outcome, exposure, group_name) {
  f <- as.formula(paste(outcome, "~", exposure))
  glm(f, data = data, family = binomial) %>%
  tidy(exponentiate = TRUE, conf.int = TRUE) %>%
  filter(term != "(Intercept)") %>%
  mutate(
    outcome = outcome,
    group = group_name
  )
}

```

```

        )
    }

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

results <- bind_rows(
  lapply(outcomes, function(o) run_logit(subset_data, o, "pco2_cat_abg", "ABG")),
  lapply(outcomes, function(o) run_logit(subset_data, o, "pco2_cat_vbg", "VBG")),
  lapply(outcomes, function(o) run_logit(subset_data, o, "pco2_cat_calc", "Calculated ABG"))
)

combined_or_df <- results %>%
  mutate(
    exposure = recode(term,
      "pco2_cat_abgBelow normal" = "Below normal",
      "pco2_cat_abgAbove normal" = "Above normal",
      "pco2_cat_vbgBelow normal" = "Below normal",
      "pco2_cat_vbgAbove normal" = "Above normal",
      "pco2_cat_calcBelow normal" = "Below normal",
      "pco2_cat_calcAbove normal" = "Above normal"),
    outcome = recode(outcome,
      imv_proc = "Intubation",
      niv_proc = "NIV",
      death_60d = "Death (60d)",
      hypercap_resp_failure = "Hypercapnic RF")
  ) %>%
  select(outcome, group, exposure, estimate, conf.low, conf.high)

library(scales)

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

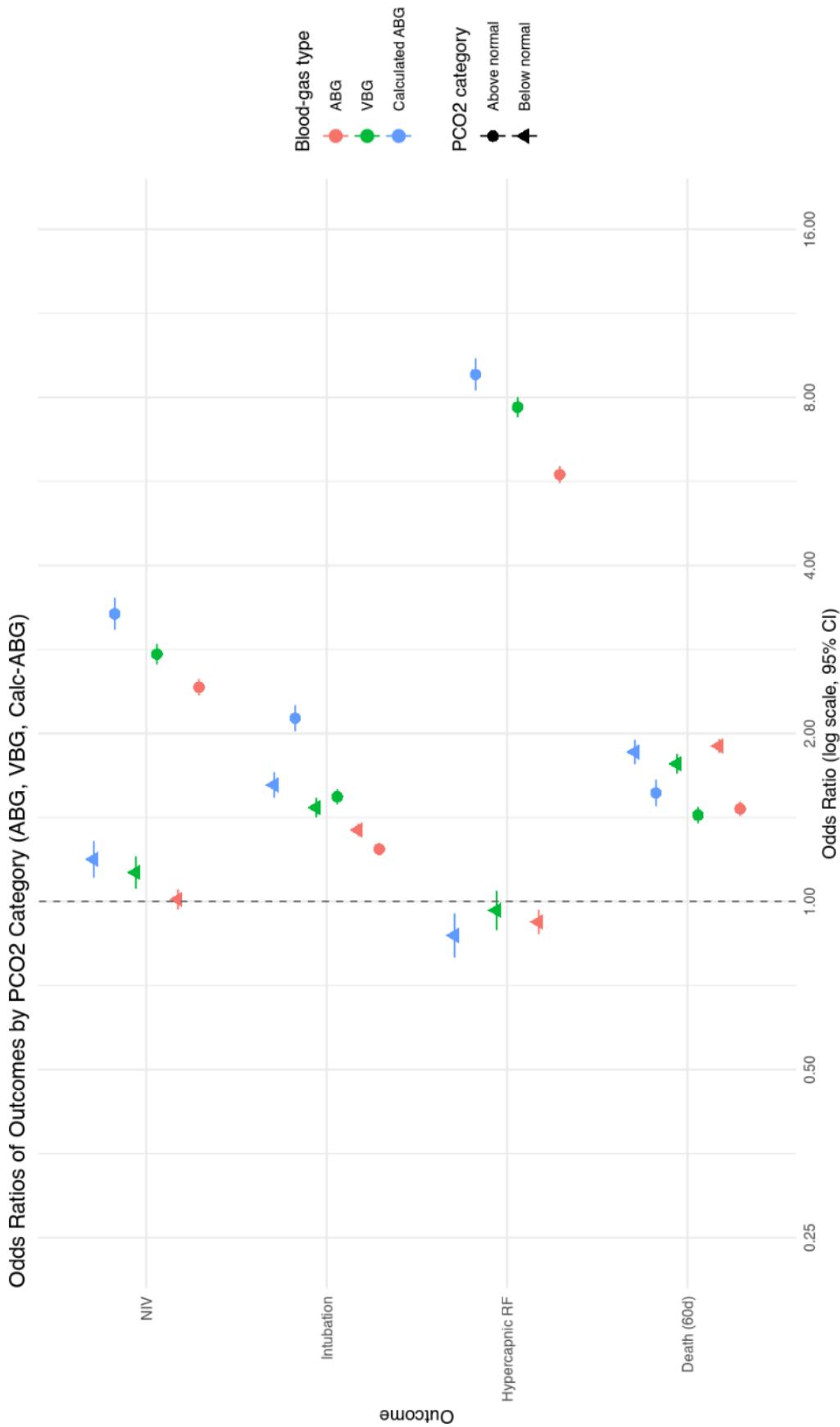
```

```

ggplot(
  combined_or_df,
  aes(
    x = outcome,
    y = estimate,
    ymin = conf.low,
    ymax = conf.high,
    color = group,
    shape = exposure
  )
) +
  geom_pointrange(
    position = position_dodge(width = 0.7),
    size = 0.6
  ) +
  geom_hline(yintercept = 1, linetype = "dashed", colour = "grey40") +
  scale_y_log10(
    breaks = c(0.25, 0.5, 1, 2, 4, 8, 16),
    limits = c(0.25, 16),
    labels = number_format(accuracy = 0.01)
  ) +
  coord_flip() +
  labs(
    title = "Odds Ratios of Outcomes by PCO2 Category (ABG, VBG, Calc-ABG)",
    x = "Outcome",
    y = "Odds Ratio (log scale, 95% CI)",
    color = "Blood-gas type",
    shape = "PCO2 category",
    caption = paste(
      "Odds ratios are computed within each blood-gas cohort.",
      "Reference = patients in the normal PCO2 range.",
      "Below normal: <35 mmHg (ABG, Calc-ABG) or >50 mmHg (VBG).",
      "Because the underlying cohorts differ (ABG, VBG, Calculated ABG), denominators are not identical across groups."
    )
  )

```

```
    sep = "\n"
)
) +
theme_minimal(base_size = 10) +
theme(plot.caption = element_text(hjust = 0))
```



Restricted Cubic Spline Regressions

```

# ABG spline dataset
subset_data_abg <- subset_data %>%
  select(paco2, imv_proc, niv_proc, death_60d, hypercap_resp_failure) %>%
  filter(!is.na(paco2))

dd_abg <- datadist(subset_data_abg)
options(datadist = "dd_abg")

```

Unweighted, Restricted Cubic Spline Regression - ABG by PaCO2

```

fit_imv <- lrm(imv_proc ~ rcs(paco2, 4), data = subset_data_abg)
pred_imv <- as.data.frame(Predict(fit_imv, paco2, fun = plogis))

plot_imv <- ggplot(pred_imv, aes(x = paco2, y = yhat)) +
  geom_line(color = "blue", size = 1.2) +
  geom_ribbon(aes(ymin = lower, ymax = upper), fill = "blue", alpha = 0.2) +
  labs(title = "Probability of Intubation by PaCO",
       x = "PaCO (mmHg)", y = "Predicted Probability") +
  theme_minimal()

```

Warning: Using `size` aesthetic for lines was deprecated in ggplot2 3.4.0.
 i Please use `lineweight` instead.

```

fit_niv <- lrm(niv_proc ~ rcs(paco2, 4), data = subset_data_abg)
pred_niv <- as.data.frame(Predict(fit_niv, paco2, fun = plogis))

plot_niv <- ggplot(pred_niv, aes(x = paco2, y = yhat)) +
  geom_line(color = "green", size = 1.2) +
  geom_ribbon(aes(ymin = lower, ymax = upper), fill = "green", alpha = 0.2) +
  labs(title = "Probability of NIV by PaCO",
       x = "PaCO (mmHg)", y = "Predicted Probability") +
  theme_minimal()

```

```

fit_death <- lrm(death_60d ~ rcs(paco2, 4), data = subset_data_abg)
pred_death <- as.data.frame(Predict(fit_death, paco2, fun = plogis))

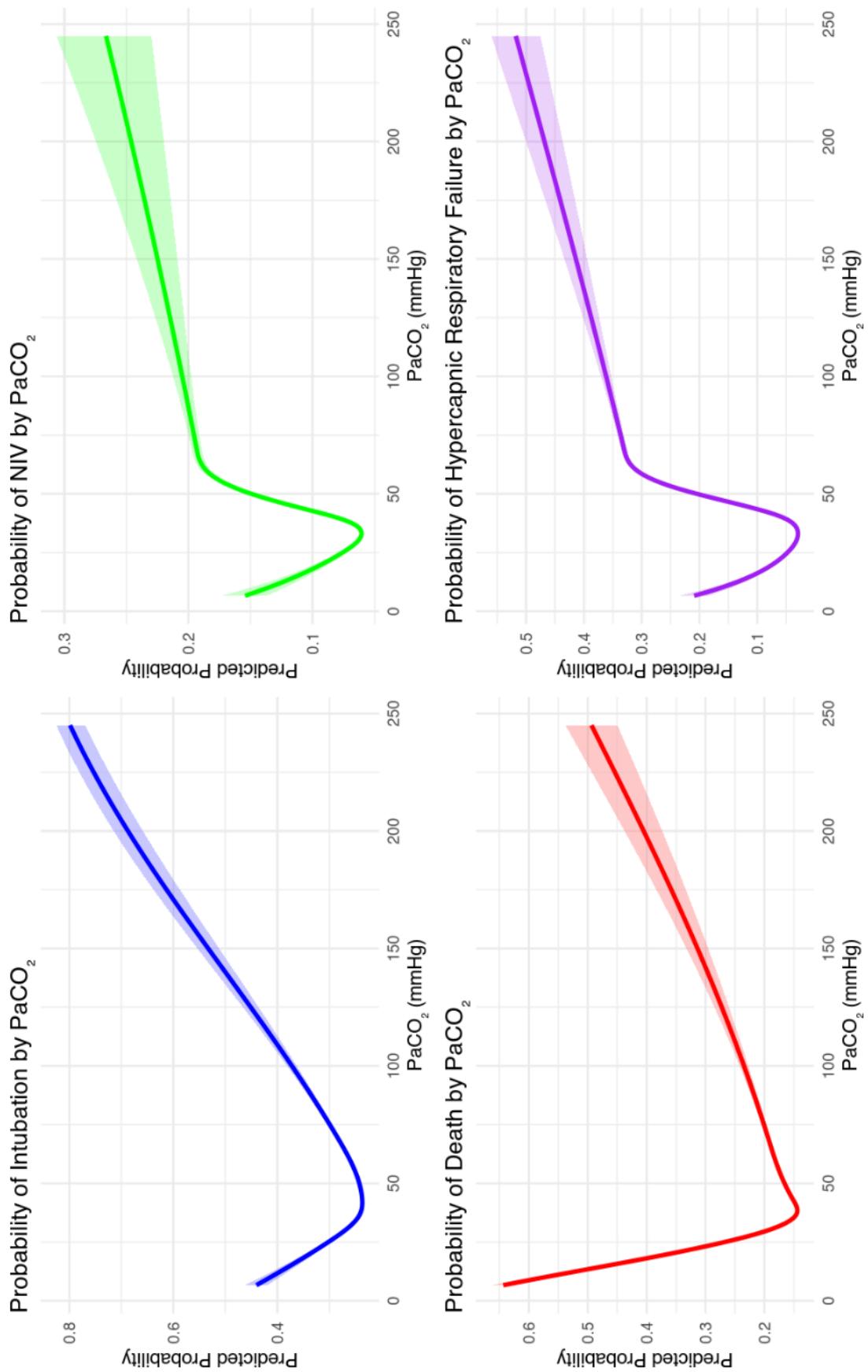
plot_death <- ggplot(pred_death, aes(x = paco2, y = yhat)) +
  geom_line(color = "red", size = 1.2) +
  geom_ribbon(aes(ymin = lower, ymax = upper), fill = "red", alpha = 0.2) +
  labs(title = "Probability of Death by PaCO",
       x = "PaCO (mmHg)", y = "Predicted Probability") +
  theme_minimal()

fit_hcrcf <- lrm(hypercap_resp_failure ~ rcs(paco2, 4), data = subset_data_abg)
pred_hcrcf <- as.data.frame(Predict(fit_hcrcf, paco2, fun = plogis))

plot_hcrcf <- ggplot(pred_hcrcf, aes(x = paco2, y = yhat)) +
  geom_line(color = "purple", size = 1.2) +
  geom_ribbon(aes(ymin = lower, ymax = upper), fill = "purple", alpha = 0.2) +
  labs(title = "Probability of Hypercapnic Respiratory Failure by PaCO",
       x = "PaCO (mmHg)", y = "Predicted Probability") +
  theme_minimal()

(plot_inv | plot_niv) / (plot_death | plot_hcrcf)

```



Unweighted, Restricted Cubic Spline - VBG

```

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

dd_vbg <- datadist(subset_data_vbg) # create datadist for VBG
# activate when doing VBG models:
options(datadist = "dd_vbg")

subset_data_vbg <- subset_data %>%
  select(vbg_co2, imv_proc, niv_proc, death_60d, hypercap_resp_failure) %>%
  filter(!is.na(vbg_co2) & complete.cases(.))

dd <- datadist(subset_data_vbg)
options(datadist = "dd")

pred_imv_vbg <- as.data.frame(Predict(fit_imv_vbg, vbg_co2, fun = plogis))
pred_niv_vbg <- as.data.frame(Predict(fit_niv_vbg, vbg_co2, fun = plogis))
pred_death_vbg <- as.data.frame(Predict(fit_death_vbg, vbg_co2, fun = plogis))
pred_hcrcf_vbg <- as.data.frame(Predict(fit_hcrcf_vbg, vbg_co2, fun = plogis))

plot_imv_vbg <- ggplot(pred_imv_vbg, aes(x = vbg_co2, y = yhat)) +
  geom_line(color = "blue") +
  geom_ribbon(aes(ymin = lower, ymax = upper), fill = "blue", alpha = 0.2) +
  labs(title = "IMV", x = "VBG CO (mmHg)", y = "Predicted Probability") +
  theme_minimal()

plot_niv_vbg <- ggplot(pred_niv_vbg, aes(x = vbg_co2, y = yhat)) +
  geom_line(color = "green") +

```

```

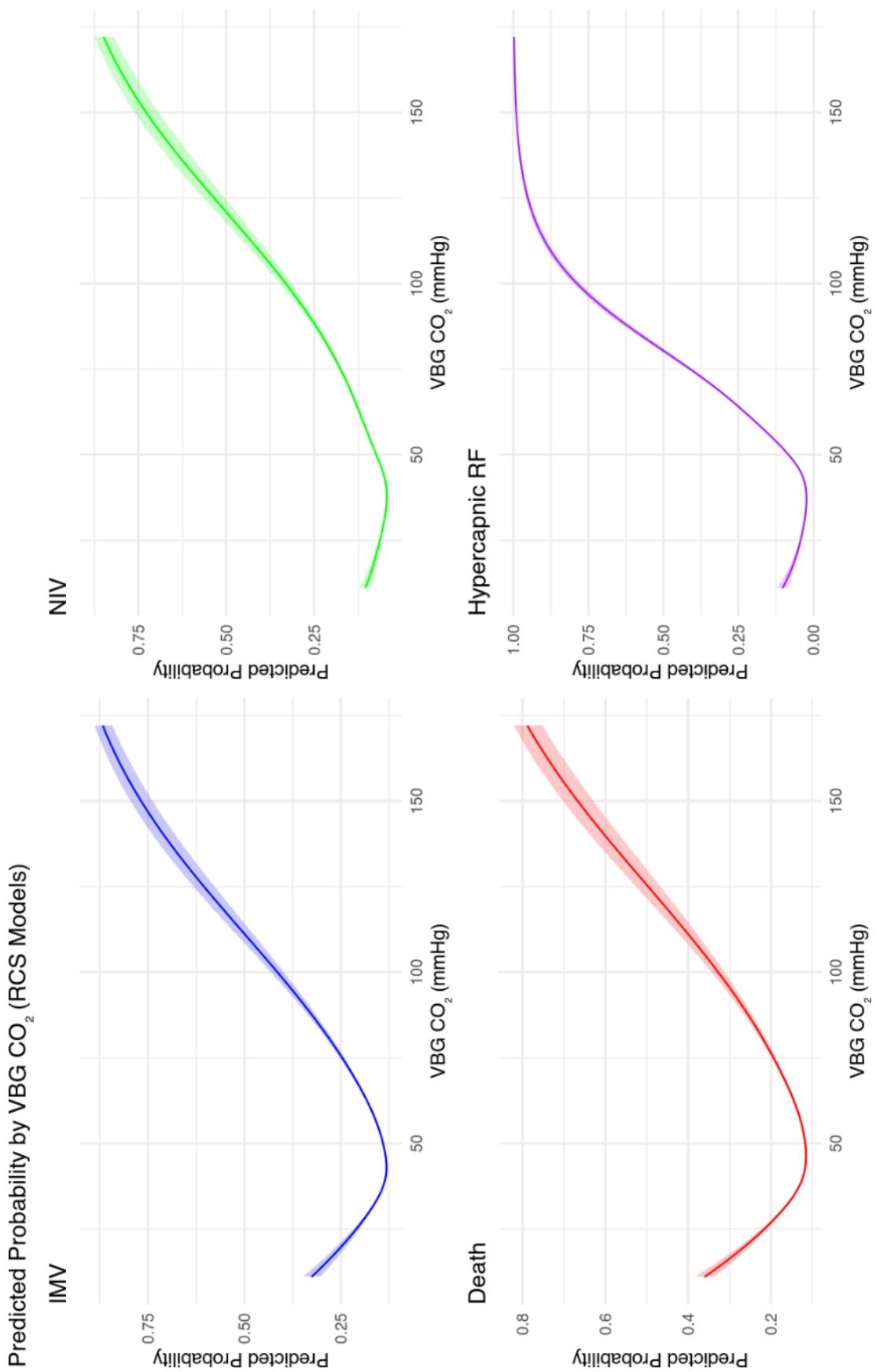
geom_ribbon(aes(ymin = lower, ymax = upper), fill = "green", alpha = 0.2) +
  labs(title = "NIV", x = "VBG CO (mmHg)", y = "Predicted Probability") +
  theme_minimal()

plot_death_vbg <- ggplot(pred_death_vbg, aes(x = vbg_co2, y = yhat)) +
  geom_line(color = "red") +
  geom_ribbon(aes(ymin = lower, ymax = upper), fill = "red", alpha = 0.2) +
  labs(title = "Death", x = "VBG CO (mmHg)", y = "Predicted Probability") +
  theme_minimal()

plot_hcrcf_vbg <- ggplot(pred_hcrcf_vbg, aes(x = vbg_co2, y = yhat)) +
  geom_line(color = "purple") +
  geom_ribbon(aes(ymin = lower, ymax = upper), fill = "purple", alpha = 0.2) +
  labs(title = "Hypercapnic RF", x = "VBG CO (mmHg)", y = "Predicted Probability") +
  theme_minimal()

((plot_imv_vbg | plot_niv_vbg) /
  (plot_death_vbg | plot_hcrcf_vbg)) +
  plot_annotation(title = "Predicted Probability by VBG CO (RCS Models)")

```



Unweighted, Restricted Cubic Spline Logistic Regression - Calculated VBG to ABG (Farkas VBG Adjustment)

```

subset_data_calc <- subset_data %>%
  select(calc_abg, imv_proc, niv_proc, death_60d, hypercap_resp_failure) %>%
  filter(!is.na(calc_abg) & complete.cases(.))

dd <- datadist(subset_data_calc)
options(datadist = "dd")

fit_imv_abg <- lrm(imv_proc ~ rcs(calc_abg, 4), data = subset_data_calc)
fit_niv_abg <- lrm(niv_proc ~ rcs(calc_abg, 4), data = subset_data_calc)
fit_death_abg <- lrm(death_60d ~ rcs(calc_abg, 4), data = subset_data_calc)
fit_hcrf_abg <- lrm(hypercap_resp_failure ~ rcs(calc_abg, 4), data = subset_data_calc)

pred_imv_abg <- as.data.frame(Predict(fit_imv_abg, calc_abg, fun = plogis))
pred_niv_abg <- as.data.frame(Predict(fit_niv_abg, calc_abg, fun = plogis))
pred_death_abg <- as.data.frame(Predict(fit_death_abg, calc_abg, fun = plogis))
pred_hcrf_abg <- as.data.frame(Predict(fit_hcrf_abg, calc_abg, fun = plogis))

plot_imv_abg <- ggplot(pred_imv_abg, aes(x = calc_abg, y = yhat)) +
  geom_line(color = "blue") +
  geom_ribbon(aes(ymin = lower, ymax = upper), fill = "blue", alpha = 0.2) +
  labs(title = "IMV", x = "Calculated ABG CO (mmHg)", y = "Predicted Probability") +
  theme_minimal()

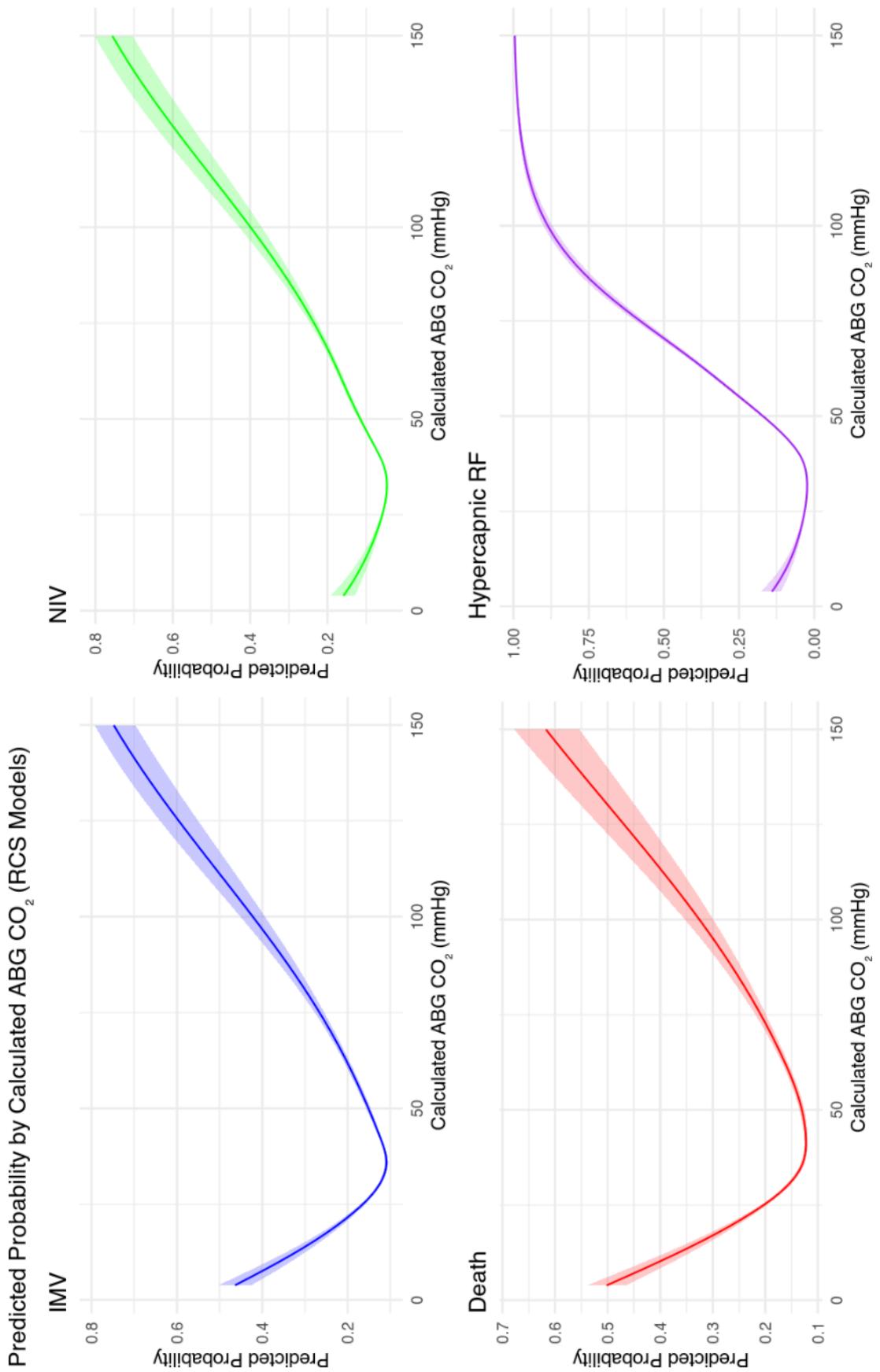
plot_niv_abg <- ggplot(pred_niv_abg, aes(x = calc_abg, y = yhat)) +
  geom_line(color = "green") +
  geom_ribbon(aes(ymin = lower, ymax = upper), fill = "green", alpha = 0.2) +
  labs(title = "NIV", x = "Calculated ABG CO (mmHg)", y = "Predicted Probability") +
  theme_minimal()

plot_death_abg <- ggplot(pred_death_abg, aes(x = calc_abg, y = yhat)) +
  geom_line(color = "red") +
  geom_ribbon(aes(ymin = lower, ymax = upper), fill = "red", alpha = 0.2) +
  labs(title = "Death", x = "Calculated ABG CO (mmHg)", y = "Predicted Probability") +
  theme_minimal()

```

```
plot_hcraf_abg <- ggplot(pred_hcraf_abg, aes(x = calc_abg, y = yhat)) +
  geom_line(color = "purple") +
  geom_ribbon(aes(ymin = lower, ymax = upper), fill = "purple", alpha = 0.2) +
  labs(title = "Hypercapnic RF", x = "Calculated ABG CO (mmHg)", y = "Predicted Probability") +
  theme_minimal()

((plot_imv_abg | plot_niv_abg) /
 (plot_death_abg | plot_hcraf_abg)) +
plot_annotation(title = "Predicted Probability by Calculated ABG CO (RCS Models)")
```



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 **age_at_encounter + sex + race_ethnicity** (remember - have to specify to use this as a factor variable) + **curr_bmi + copd + asthma + osa + chf + acute_nmd + phtn + location (as a factor variable)**

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

1. Smaller GBM & stopping rule → faster fit, avoids over-fitting, lighter tails (which lead to extreme weights that are problematic).
2. bal.tab() documents balance; aim is to adjust spec until standard mean difference (SMD) < 0.1.
3. Weight stabilization (divide by mean) mitigates a few huge weights. I also winsorized, which is a way to avoid very extreme weights (ie you set <1st percentile to the 1st percentile value, and >99th percentile to 99th percentile).
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.

```
subset_data$encounter_type <- factor(subset_data$encounter_type,
                                         levels = c(2, 3),
                                         labels = c("Emergency", "Inpatient"))
```

**Removed lactate from weights, decreased n.trees, increased bagging

```
# 1. fit GBM propensity model, ABG
set.seed(42)

weight_model <- weightit(
  has_abg ~ age_at_encounter + sex + factor(race_ethnicity) + curr_bmi + copd + asthma + osa + chf + acute_nmd + phtn + ckd +
  data = subset_data,
  method = "gbm",
  estimand = "ATE",
  missing = "ind",
  include.obj = TRUE, # ← REQUIRED for importance/SHAP
  n.trees = 1500, #decreased trees from 3000 to 1500
```

```

interaction.depth = 3,
shrinkage = 0.01,
bag.fraction= 0.8, #increased bagging 0.6 to 0.8 - less overfit extremes
cv.folds = 5,
stop.method = "es.mean",
n.cores = parallel::detectCores()
)

w_abg <- weight_model # Canonical alias so later code can use `w_abg`

# 2. Winsorise / stabilise weights (two-sided)
w <- weight_model$weights # original GBM weights
w <- w / mean(w) # stabilise
cut <- quantile(w, c(0.01, 1), na.rm = TRUE)
w <- pmin(pmax(w, cut[1]), cut[2]) # two-tail Winsorisation
w <- w / mean(w) # re-stabilise so E[w]=1

# overwrite inside the object and attach to data
weight_model$weights <- w
subset_data$w_abg <- w

# 3. balance diagnostics (only raw vs. IPW)
bal <- bal.tab(weight_model, un = TRUE, m.threshold = 0.1)

```

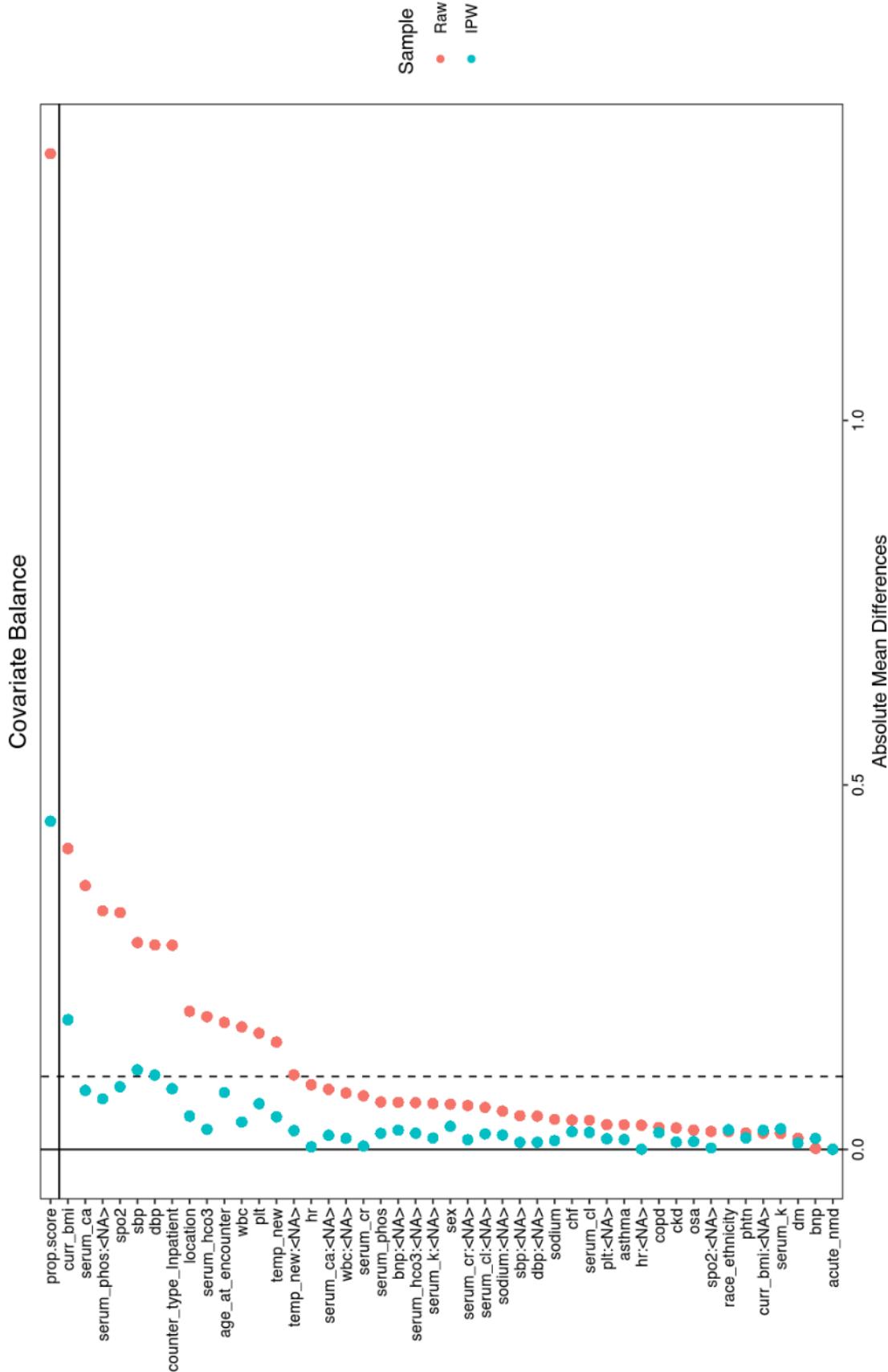
Warning: Missing values exist in the covariates. Displayed values omit these observations.

```

love.plot(
  bal,
  stats      = "m", # standardized mean differences only
  abs        = TRUE,
  var.order  = "unadjusted",
  sample.names = c("Raw", "IPW")
)

```

Warning: Standardized mean differences and raw mean differences are present in the same plot. Use the `stars` argument to distinguish between them and appropriately label the x-axis. See `?love.plot` for details.



```

# 4. survey design with the same weights
design <- svydesign(ids = ~1, weights = ~w_abg, data = subset_data)

# 5. outcome models (examples)
fit_niv <- svyglm(niv_proc ~ has_abg, design = design, family = quasibinomial())
fit_imv <- svyglm(imv_proc ~ has_abg, design = design, family = quasibinomial())
fit_death <- svyglm(death_60d ~ has_abg, design = design, family = quasibinomial())
fit_icd <- svyglm(hypercap_resp_failure ~ has_abg, design = design, family = quasibinomial())

# quick effect estimates
lapply(list(IMV = fit_imv, NIV = fit_niv, Death = fit_death, ICD = fit_icd), function(m) {
  c(OR = exp(coef(m)[2]),
    LCL = exp(confint(m)[2,1]),
    UCL = exp(confint(m)[2,2]))
})

```

	OR.has_abg	LCL	UCL
\$IMV	6.776346	6.606385	6.950680
\$NIV	1.881251	1.834660	1.929026
\$Death	2.104033	2.058994	2.150057
\$ICD	3.380855	3.284563	3.479970

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

```

# set.seed(42) # reproducible GBM fit
#
# # 1. inverse-probability weights for receiving an ABG
#
# # done in the last block, so not needed
#
#
# 2. analysis sample: rows with a measured PaCO
subset_data_abg <- subset_data %>%
  filter(!is.na(paco2)) %>%
  select(paco2, imv_proc, niv_proc, death_60d,
         hypercap_resp_failure, w_abg) %>%
  filter(complete.cases(.))
#
#
# 3. weighted logistic spline models with robust SEs
dd <- datadist(subset_data_abg); options(datadist = "dd")

```

- fitfun <- function(formula)


```

svyglm(
  formula,
  design = svydesign(ids = ~1, weights = ~w_abg, data = subset_data_abg),
  family = quasibinomial()
)

```
- fit_imv_abg <- fitfun(imv_proc ~ rcs(paco2, 4))
 fit_niv_abg <- fitfun(niv_proc ~ rcs(paco2, 4))
 fit_death_abg <- fitfun(death_60d ~ rcs(paco2, 4))
 fit_hcrf_abg <- fitfun(hypercap_resp_failure ~ rcs(paco2, 4))
4. prediction helper


```

mkpred <- function(fit, data_ref) {
  # 1. Grid of PaCO values
  newd <- data.frame(

```

```

pac02 = seq(min(data_ref$paco2, na.rm = TRUE),
            max(data_ref$paco2, na.rm = TRUE),
            length.out = 200)
      )

# 2. Design (model) matrix for the new data
mm <- model.matrix(delete.response(terms(fit)), # drop outcome
                    data = newd)

# 3. Linear predictor and its standard error
eta <- mm %*% coef(fit) # 'X
vcov <- vcov(fit) # robust VCOV from svyglm
se <- sqrt(rowSums((mm %*% vcov) * mm)) # √diag(X Σ X)

# 4. Transform to probability scale
transform(
  newd,
  yhat = plogis(eta),
  lower = plogis(eta - 1.96 * se),
  upper = plogis(eta + 1.96 * se)
)
}

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

plt <- function(dat, title)
  ggplot(dat, aes(paco2, yhat)) +
    geom_line() +

```

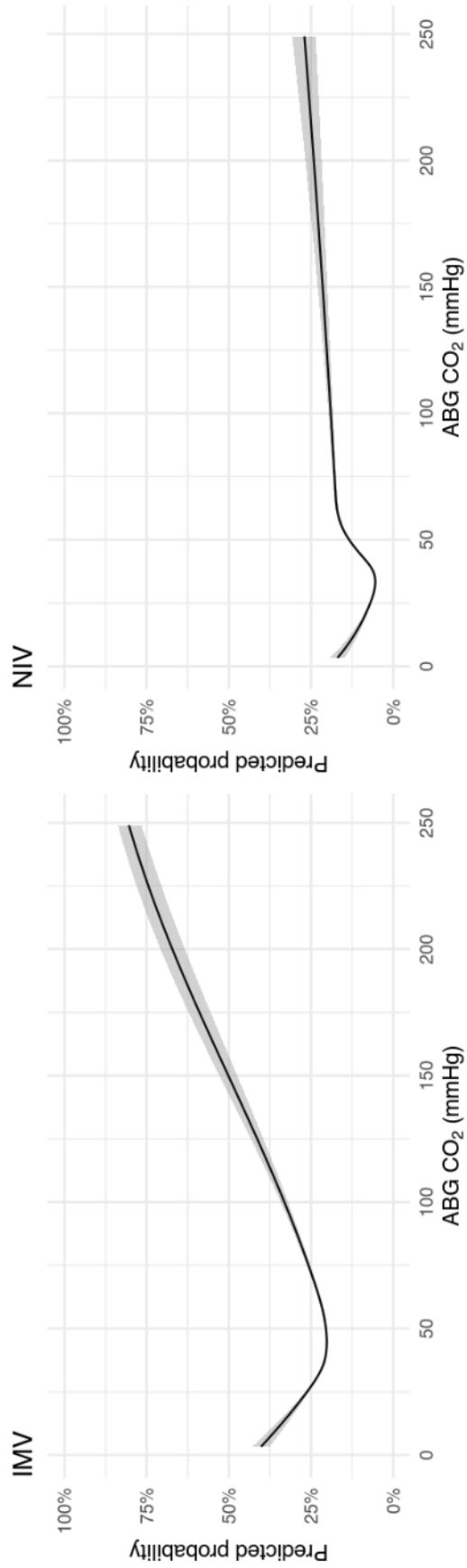
```

geom_ribbon(aes(ymin = lower, ymax = upper), alpha = 0.2) +
  scale_y_continuous(limits = c(0, 1), labels = percent_format(accuracy = 1)) +
  labs(title = title, x = xlab, y = "Predicted probability") +
  theme_minimal()

(patchwork::wrap_plots(
  plt(pred_imv_abg, "IMV"),
  plt(pred_niv_abg, "NIV"),
  plt(pred_death_abg, "Death"),
  plt(pred_hcrf_abg, "Hypercapnic RF"),
  ncol = 2
)
) +
  plot_annotation(
    title = expression(
      paste("Propensity-weighted predicted probability by ABG CO"[2],
            " (restricted cubic spline)"))
  )
)

```

Propensity-weighted predicted probability by ABG CO_2 (restricted cubic spline)

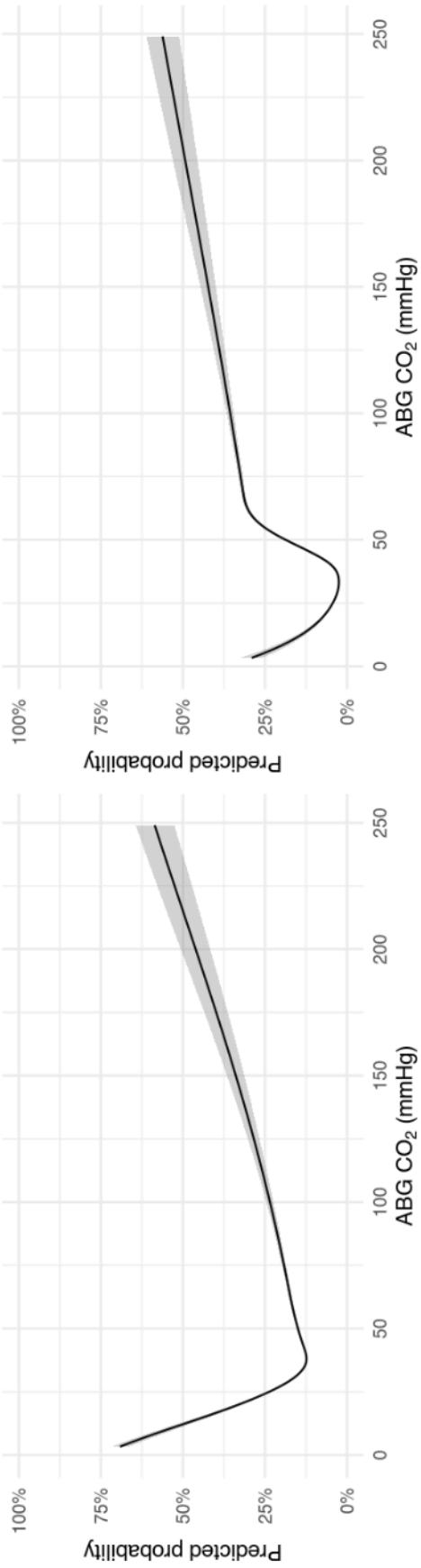


NIV

Hypercapnic RF

Death

Restricting plots bewtween 0.02 and 0.98



67

```

subset_data_abg <- subset_data %>%
  filter(!is.na(paco2)) %>%
  select(paco2, imv_proc, niv_proc, death_60d,
        hypercap_resp_failure, w_abg) %>%
  filter(complete.cases(.))

# 3. weighted logistic spline models with robust SEs
dd <- datadist(subset_data_abg); options(datadist = "dd")

fitfun <- function(formula)
{
  svyglm(
    formula,
    design = svydesign(ids = ~1, weights = ~w_abg, data = subset_data_abg),
    family = quasibinomial()
  )

  fit_imv_abg <- fitfun(imv_proc ~ rcs(paco2, 4))
  fit_niv_abg <- fitfun(niv_proc ~ rcs(paco2, 4))
  fit_death_abg <- fitfun(death_60d ~ rcs(paco2, 4))
  fit_hcrf_abg <- fitfun(hypercap_resp_failure ~ rcs(paco2, 4))

  # 4. prediction helper
  mkpred <- function(fit, data_ref) {
    # 1. Grid of PaCO values restricted to 2nd-98th percentile
    q <- quantile(data_ref$paco2, probs = c(0.02, 0.98), na.rm = TRUE)
    newd <- data.frame(
      paco2 = seq(q[1], q[2], length.out = 200)
    )
  }
}

# 2. Design (model) matrix for the new data
mm <- model.matrix(delete.response(terms(fit)), data = newd)

# 3. Linear predictor and its standard error

```

```

eta <- mm %*% coef(fit)
vcov <- vcov(fit)
se <- sqrt(crossprod((mm %*% vcov) * mm))

# 4. Transform to probability scale
transform(
  newd,
  yhat = plogis(eta),
  lower = plogis(eta - 1.96 * se),
  upper = plogis(eta + 1.96 * se)
)

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

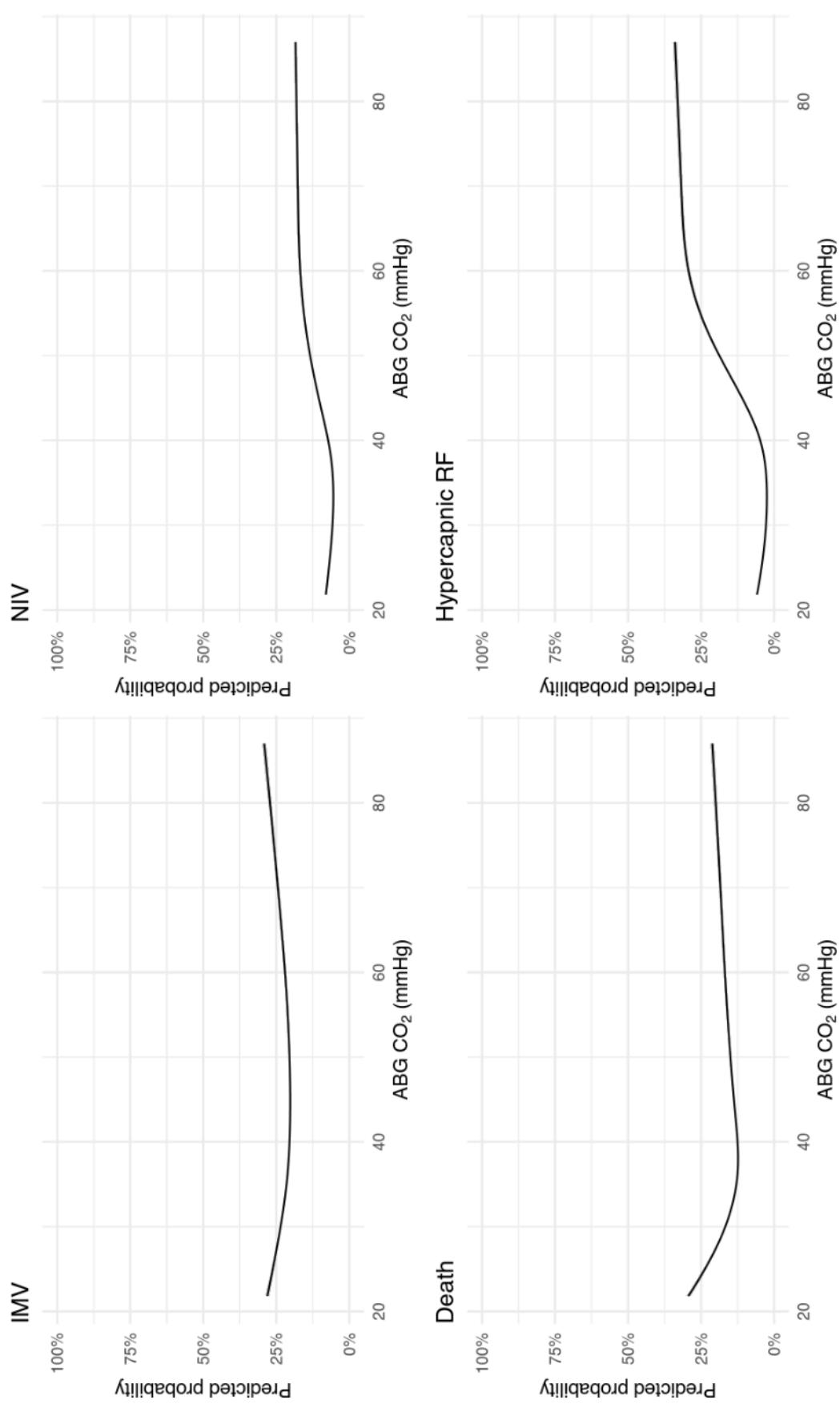
plt <- function(dat, title)
  ggplot(dat, aes(paco2, yhat)) +
    geom_line() +
    geom_ribbon(aes(ymin = lower, ymax = upper), alpha = 0.2) +
    scale_y_continuous(limits = c(0, 1), labels = percent_format(accuracy = 1)) +
    labs(title = title, x = xlab, y = "Predicted probability") +
    theme_minimal()

(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 = expression(
    paste("Propensity-weighted predicted probability by ABG CO"[2],
      " (restricted cubic spline)")
  )
)
```

Propensity-weighted predicted probability by ABG CO₂ (restricted cubic spline)



VBG - changed trees and bag fraction

```

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

set.seed(42)

# 1. IPW for VBG -----
w_vbg <- weightit(
  has_vbg ~ age_at_encounter + sex + factor(race_ethnicity) + curr_bmi +
    copd + asthma + osa + chf + acute_nmd + phtn + ckd + dm +
    factor(location) + factor(encounter_type) + temp_new + sbp + dbp + hr + spo2 + sodium + serum_cr + serum_hco3 + serum_cl +
    serum_k + wbc + plt + bnp + serum_phos + serum_ca,
  data = subset_data,
  method = "gbm",
  estimand = "ATE",
  missing = "ind",
  include.obj = TRUE, # ← REQUIRED for importance/SHAP
  n.trees = 1500,
  interaction.depth = 3,
  shrinkage = 0.01,
  bag.fraction= 0.8,
  cv.folds = 5,
  stop.method = "es.mean",
  ncores = parallel::detectCores()
)

# Stabilise & winsorise weights
w <- w_vbg$weights
w <- w / mean(w)
cut <- quantile(w, c(0.01, 1), na.rm = TRUE)
w <- pmin(pmax(w, cut[1]), cut[2])
w <- w / mean(w)

w_vbg$weights <- w
subset_data$w_vbg <- w

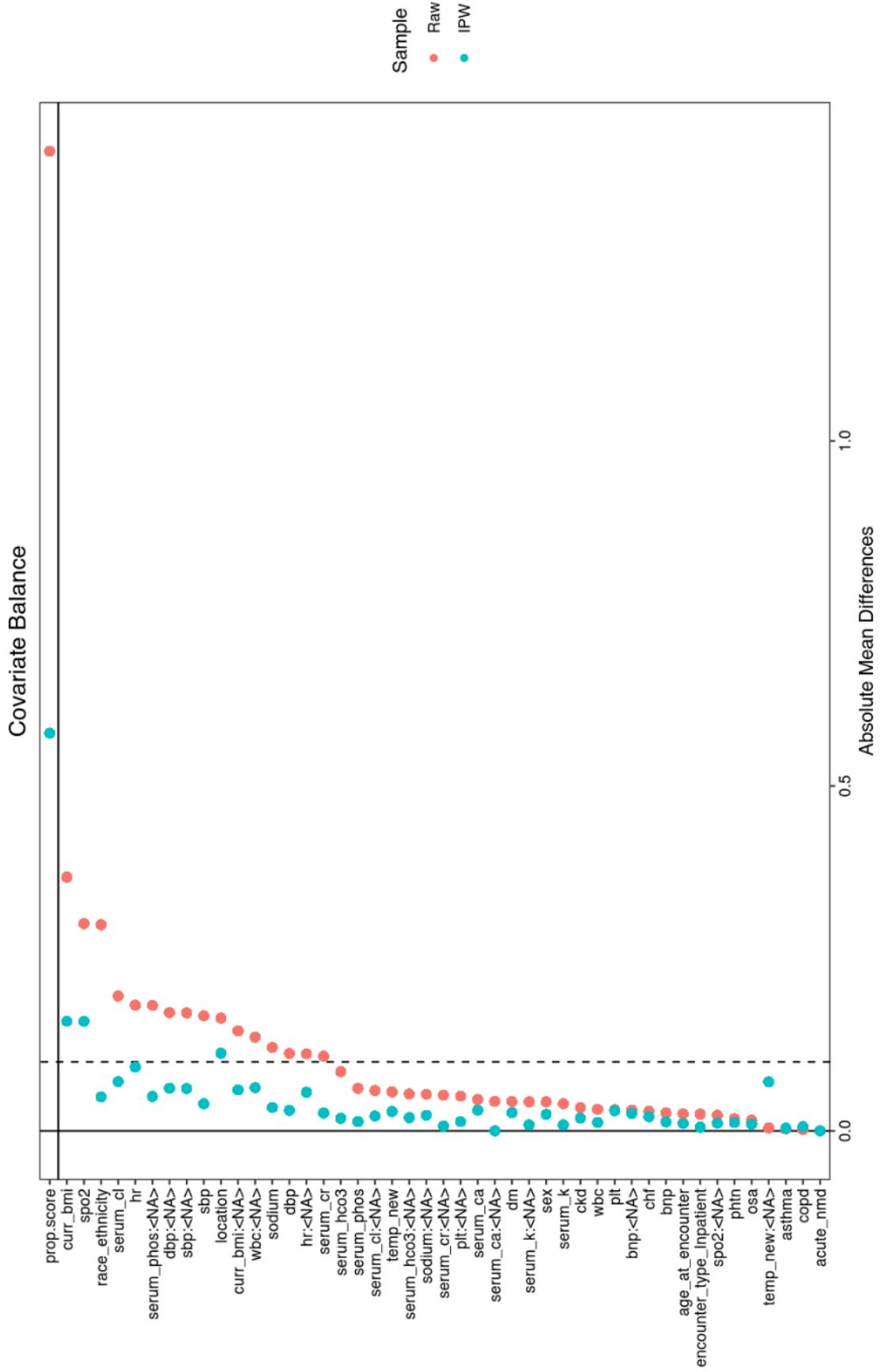
```

```
v_bal <- bal.tab(w_vbg, un = TRUE, m.threshold = 0.1)
```

Warning: Missing values exist in the covariates. Displayed values omit these observations.

```
love.plot(  
  v_bal,  
  stats      = "m",  
  # standardized mean differences only  
  abs        = TRUE,  
  var.order   = "unadjusted",  
  sample.names = c("Raw", "IPW")  
)
```

Warning: Standardized mean differences and raw mean differences are present in the same plot. Use the `stars` argument to distinguish between them and appropriately label the x-axis. See `?love.plot` for details.



```
# 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) %>%
filter(complete.cases(.))

# 3. Weighted spline models -----
dd_vbg <- datadist(subset_data_vbg)
options(datadist = "dd_vbg")

fitfun <- function(formula)

svyglm(
  formula,
  design = svydesign(ids = ~1, weights = ~w_vbg, data = subset_data_vbg),
  family = quasibinomial()
)

fit_imv_vbg <- fitfun(imv_proc
                        ~ rcs(vbg_co2, 4))
fit_niv_vbg <- fitfun(niv_proc
                        ~ rcs(vbg_co2, 4))
fit_death_vbg <- fitfun(death_60d
                        ~ rcs(vbg_co2, 4))
fit_hcrf_vbg <- fitfun(hypercap_resp_failure
                        ~ rcs(vbg_co2, 4))

# 4. Prediction helper -----
mkpred <- function(fit, data_ref) {
  newd <- data.frame(
    vbg_co2 = seq(min(data_ref$vbg_co2, na.rm = TRUE),
                  max(data_ref$vbg_co2, na.rm = TRUE),
                  length.out = 200)
  )
  mm <- model.matrix(delete.response(terms(fit)), newd)
  eta <- mm %*% coef(fit)
  vcov <- vcov(fit)
  se <- sqrt(rowSums((mm %*% vcov) * mm))
  transform(
    newd,
    yhat = plogis(eta),

```

```

    lower = plogis(eta - 1.96 * se),
    upper = plogis(eta + 1.96 * se)
  )

  pred_imv_vbg <- mkpred(fit_imv_vbg,
  subset_data_vbg)
  pred_niv_vbg <- mkpred(fit_niv_vbg,
  subset_data_vbg)
  pred_death_vbg <- mkpred(fit_death_vbg,
  subset_data_vbg)
  pred_hcrrf_vbg <- mkpred(fit_hcrrf_vbg,
  subset_data_vbg)

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

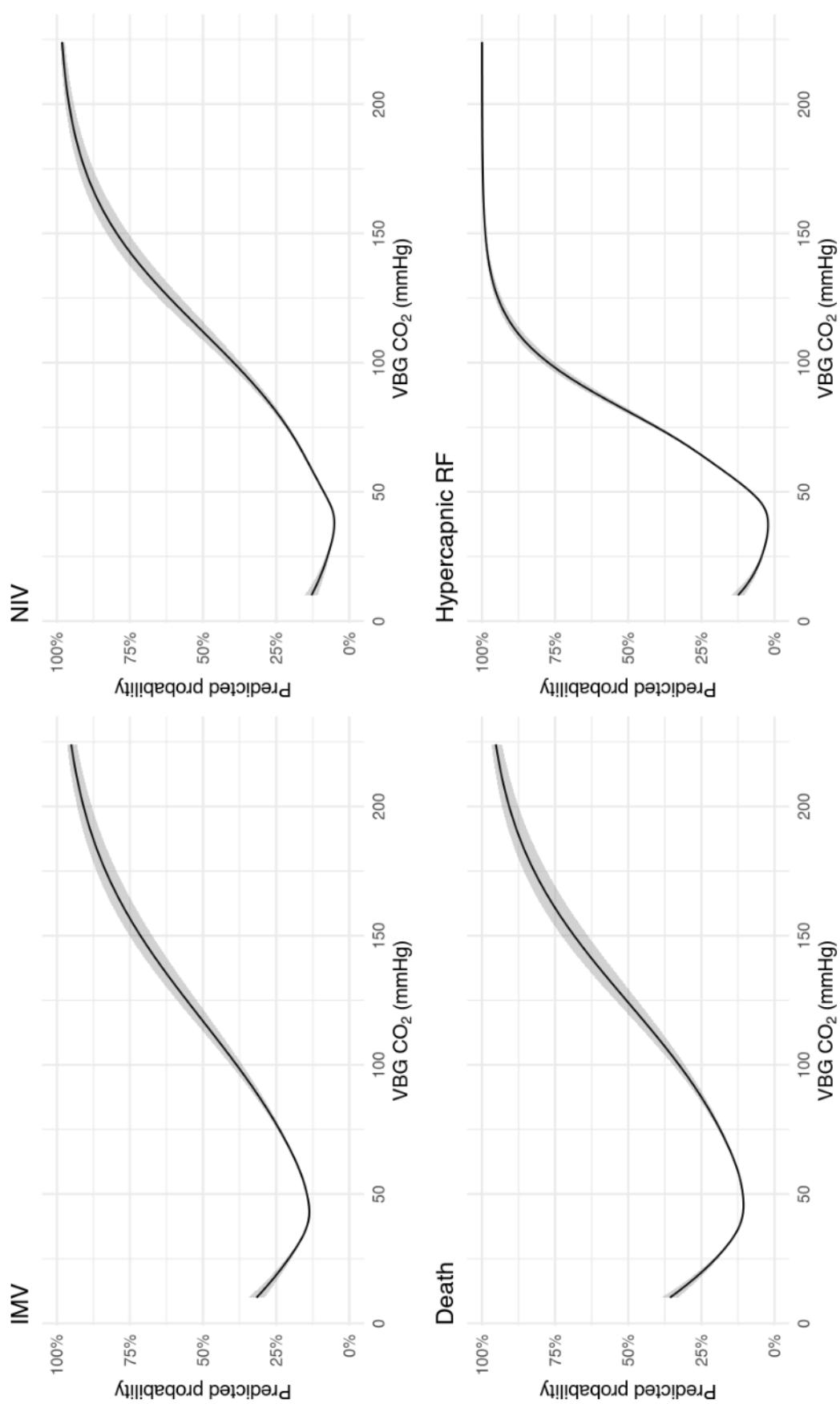
plt <- function(dat, title)
  ggplot(dat, aes(vbg_co2, yhat)) +
  geom_line() +
  geom_ribbon(aes(ymin = lower, ymax = upper), alpha = 0.2) +
  scale_y_continuous(limits = c(0, 1), labels = percent_format(accuracy = 1)) +
  labs(title = title, x = xlab, y = "Predicted probability") +
  theme_minimal()

(patchwork::wrap_plots(
  plt(pred_imv_vbg, "IMV"),
  plt(pred_niv_vbg, "NIV"),
  plt(pred_death_vbg, "Death"),
  plt(pred_hcrrf_vbg, "Hypercapnic RF"),
  ncol = 2
) +
  plot_annotation(
    title = expression(
      paste("Propensity-weighted predicted probability by VBG CO" [2],
        " (restricted cubic spline)"))
  )
)

```

)

Propensity-weighted predicted probability by VBG CO₂ (restricted cubic spline)



Calculated VBG to ABG / Farkas

```

# Propensity-weighted spline models for **Calculated ABG CO ***
# (weights still derive from propensity to receive a VBG)

# 1. define the new treatment variable -----
subset_data <- subset_data %>%
  mutate(
    has_vbg_co2_o2_sat = if_else(
      !is.na(vbg_co2) & vbg_co2 != 0 &
      !is.na(vbg_o2sat) & vbg_o2sat != 0,
      1, 0
    )
  )

# quick sanity check
# table(subset_data$has_vbg_co2_o2_sat, useNA = "ifany")

# 2. fit the GBM propensity model -----
set.seed(42)

w_vbg_calc <- weightit(
  has_vbg_co2_o2_sat ~ age_at_encounter + sex + factor(race_ethnicity) + curr_bmi + copd + asthma + osa + chf + acute_nmd + phcf,
  data = subset_data,
  method = "gbm",
  estimand = "ATE",
  missing = "ind",
  include.obj = TRUE,
  n.trees = 3000,
  interaction.depth = 3,
  shrinkage = 0.01,
  bag.fraction= 0.6,
  cv.folds = 5,
  stop.method = "es.mean",
  n.cores = parallel::detectCores()
)

```

```

# 3. (optional) stabilise + two-sided Winsorisation -----
w <- w_vbg_calc$weights
w <- w / mean(w)

cut <- quantile(w, c(0.01, 1), na.rm = TRUE)
w <- pmin(pmax(w, cut[1]), cut[2])
w <- w / mean(w)

subset_data$w_vbg_calc <- w          # attach to data frame
w_vbg_calc$weights <- w              # overwrite inside object for diagnostics

v_calc_bal <- bal.tab(w_vbg_calc, un = TRUE, m.threshold = 0.1) # inspect balance

```

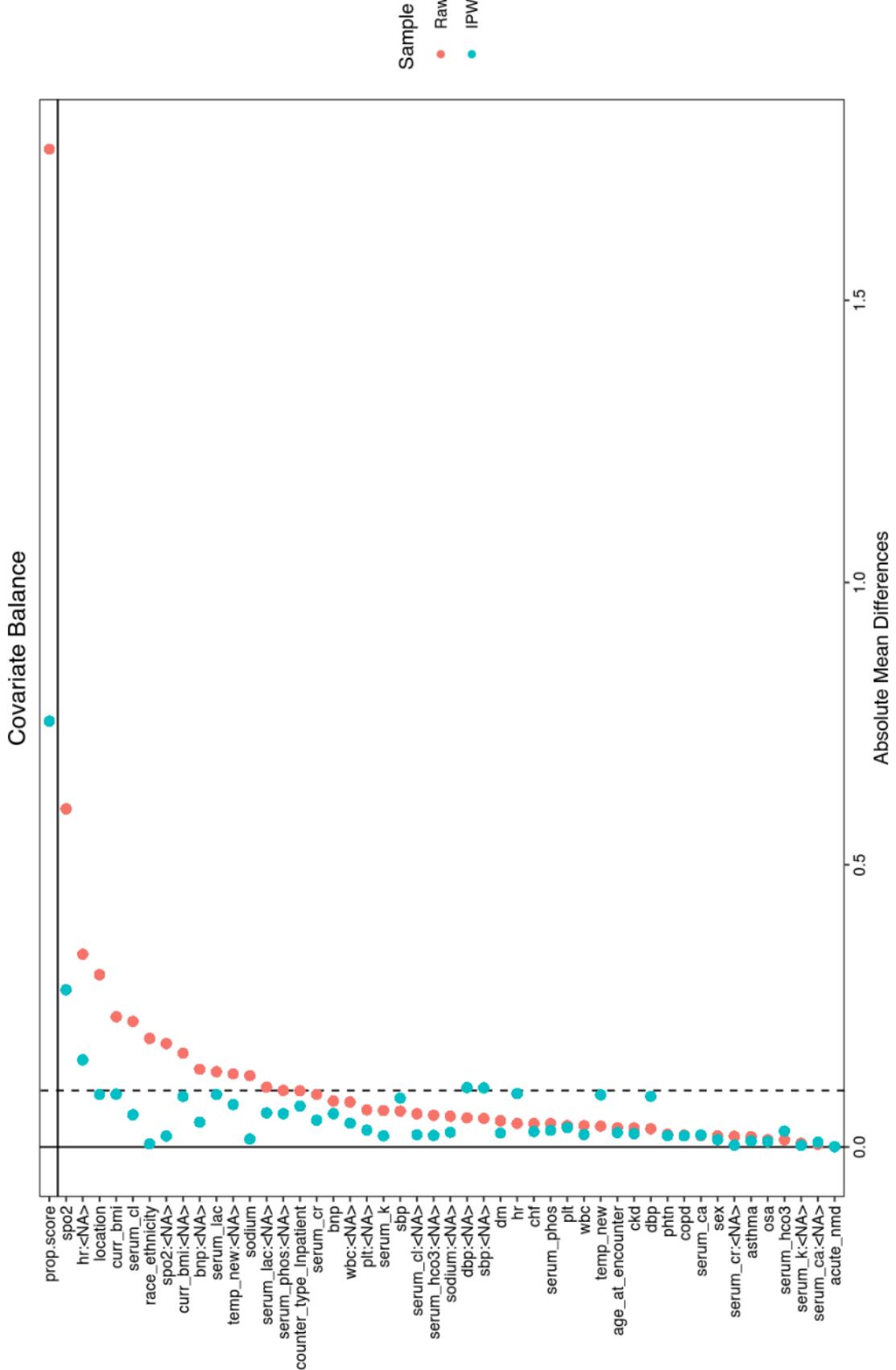
Warning: Missing values exist in the covariates. Displayed values omit these observations.

```

love.plot(
  v_calc_bal,
  stats      = "m",           # standardized mean differences only
  abs        = TRUE,
  var.order  = "unadjusted",
  sample.names = c("Raw", "IPW")
)

```

Warning: Standardized mean differences and raw mean differences are present in the same plot. Use the `stars` argument to distinguish between them and appropriately label the x-axis. See `?love.plot` for details.



```
# 2. Analysis sample: rows with a calculated ABG CO
subset_data_calc <- subset_data %>%
  filter(!is.na(calculator_abg)) %>%
# implies has_vbg == 1
```

```

select(calc_abg, imv_proc, niv_proc, death_60d,
      hypercap_resp_failure, w_vbg_calc) %>%
filter(complete.cases(.))

# 3. Weighted logistic spline models with robust SEs
dd <- datadist(subset_data_calc); options(datadist = "dd")

fitfun <- function(formula)
svyglm(
  formula,
  design = svydesign(ids = ~1, weights = ~w_vbg_calc, data = subset_data_calc),
  family = quasibinomial()
)

fit_imv_calc <- fitfun(imv_proc ~ rcs(calc_abg, 4))
fit_niv_calc <- fitfun(niv_proc ~ rcs(calc_abg, 4))
fit_death_calc <- fitfun(death_60d ~ rcs(calc_abg, 4))
fit_hcrf_calc <- fitfun(hypercap_resp_failure ~ rcs(calc_abg, 4))

# 4. Prediction helper
mkpred <- function(fit, data_ref) {
  newd <- data.frame(
    calc_abg = seq(min(data_ref$calc_abg, na.rm = TRUE),
                   max(data_ref$calc_abg, na.rm = TRUE),
                   length.out = 200)
  )
  mm <- model.matrix(delete.response(terms(fit)), newd)
  eta <- mm %*% coef(fit)
  vcov <- vcov(fit)
  se <- sqrt(rowSums((mm %*% vcov) * mm))
  transform(
    newd,
    yhat = plogis(eta),
    lower = plogis(eta - 1.96 * se),
    upper = plogis(eta + 1.96 * se)
  )
}

```

```

    upper = plogis(eta + 1.96 * se)
  )
}

pred_imv_calc <- mkpred(fit_imv_calc, subset_data_calc)
pred_niv_calc <- mkpred(fit_niv_calc, subset_data_calc)
pred_death_calc <- mkpred(fit_death_calc, subset_data_calc)
pred_hcrcf_calc <- mkpred(fit_hcrcf_calc, subset_data_calc)

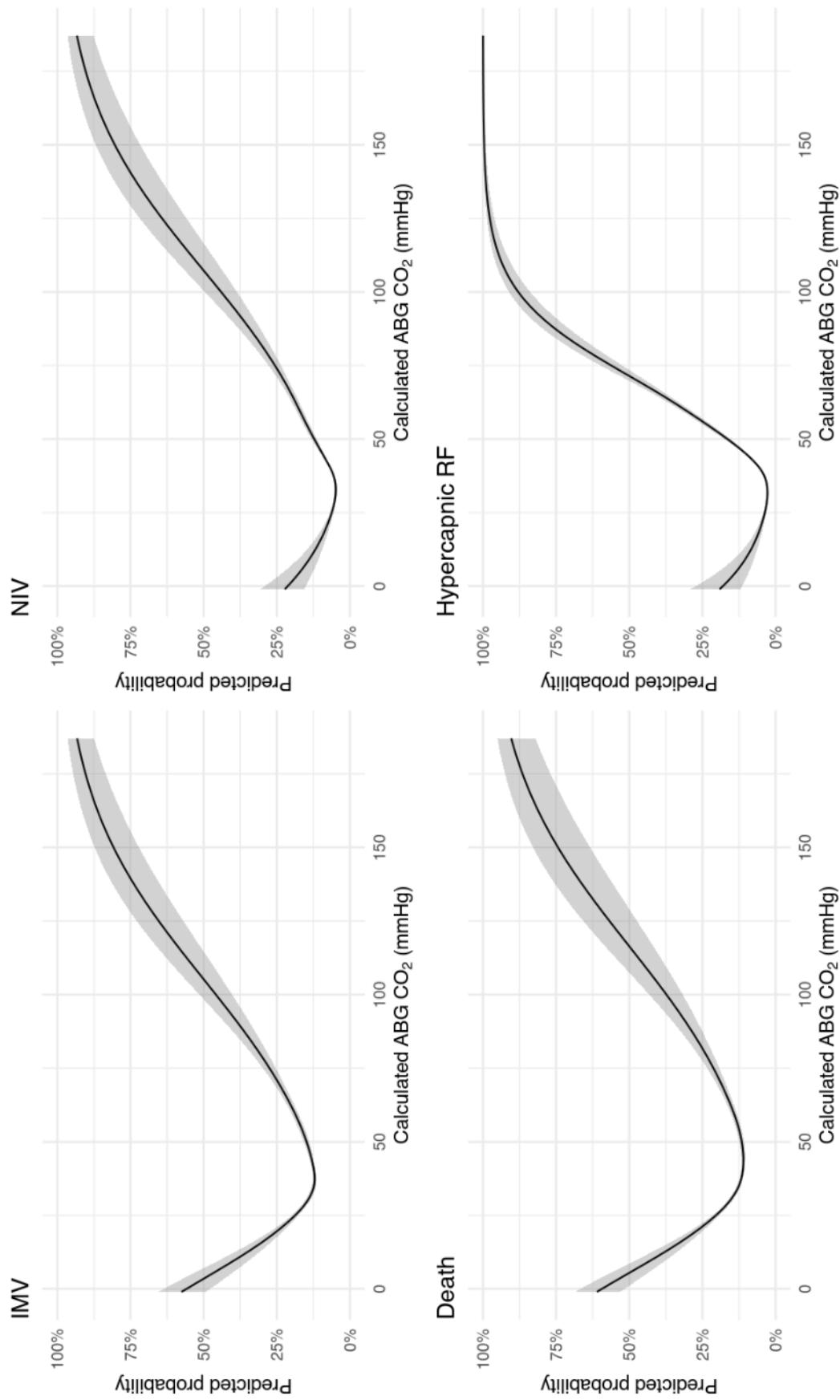
# 5. Plotting -----
xlab <- expression(paste("Calculated ABG CO"[2], " (mmHg)"))

plt <- function(dat, title)
  ggplot(dat, aes(calc_abg, yhat)) +
  geom_line() +
  geom_ribbon(aes(ymin = lower, ymax = upper), alpha = 0.2) +
  scale_y_continuous(limits = c(0, 1), labels = percent_format(accuracy = 1)) +
  labs(title = title, x = xlab, y = "Predicted probability") +
  theme_minimal()

(patchwork::wrap_plots(
  plt(pred_imv_calc, "IMV"),
  plt(pred_niv_calc, "NIV"),
  plt(pred_death_calc, "Death"),
  plt(pred_hcrcf_calc, "Hypercapnic RF"),
  ncol = 2
) +
  plot_annotation(
    title = expression(
      paste("Propensity-weighted predicted probability by Calculated ABG CO"[2],
            " (restricted cubic spline)")
    )
)

```

Propensity-weighted predicted probability by Calculated ABG CO₂ (restricted cubic spline)



Superimposing ABG and VBG weighted restricted cubic splines

```

library(dplyr)
library(ggplot2)
library(patchwork)
library(scales)
library(rms)

# ABG spline fits (unweighted, rms::lrm)
fit_imv_abg <- lrm(imv_proc ~ rcs(paco2, 4), data = subset_data_abg)
fit_niv_abg <- lrm(niv_proc ~ rcs(paco2, 4), data = subset_data_abg)
fit_death_abg <- lrm(death_60d ~ rcs(paco2, 4), data = subset_data_abg)
fit_hcrf_abg <- lrm(hypercap_resp_failure ~ rcs(paco2, 4), data = subset_data_abg)

# VBG spline fits (mirror pattern)
fit_imv_vbg <- lrm(imv_proc ~ rcs(vbg_co2, 4), data = subset_data_vbg)
fit_niv_vbg <- lrm(niv_proc ~ rcs(vbg_co2, 4), data = subset_data_vbg)
fit_death_vbg <- lrm(death_60d ~ rcs(vbg_co2, 4), data = subset_data_vbg)
fit_hcrf_vbg <- lrm(hypercap_resp_failure ~ rcs(vbg_co2, 4), data = subset_data_vbg)

library(rms) # ensure lrm() and Predict() are available

# Helper to make predictions with standardized columns: co2, yhat, lower, upper, group
mkpred <- function(fit, data_ref, xvar, group_label, n = 200) {
  stopifnot(is.character(xvar), length(xvar) == 1, xvar %in% names(data_ref))
  xseq <- seq(min(data_ref[[xvar]]), na.rm = TRUE),
        max(data_ref[[xvar]]), na.rm = TRUE),
  length.out = n
}

if (inherits(fit, "lrm")) {
  # Predict() needs a datadist object visible by name set in options(datadist=)
  dd <- rms::datadist(data_ref)
  old <- options(datadist = "dd")
  on.exit(options(old), add = TRUE)
  assign("dd", dd, envir = .GlobalEnv)
}

```

```

# IMPORTANT: name the model argument 'object', not 'fit'
args <- c(list(object = fit, fun = plogis),
         stats::setNames(list(xseq), xvar))
p <- do.call(rms::Predict, args)
out <- as.data.frame(p)

# standardize column names used by plotting code
names(out)[names(out) == xvar] <- "co2"
out$group <- group_label
out[, c("co2", "yhat", "lower", "upper", "group")]
} else {
  # glm/svyglm path
  newd <- stats::setNames(data.frame(xseq), xvar)
  X <- stats::model.matrix(stats::delete.response(stats::terms(fit)), newd)
  beta <- stats::coef(fit)
  eta <- drop(X %*% beta)
  V <- stats::vcov(fit)
  se <- sqrt(rowSums((X %*% V) * X))

  data.frame(
    co2      = xseq,
    yhat     = plogis(eta),
    lower   = plogis(eta - 1.96 * se),
    upper   = plogis(eta + 1.96 * se),
    group   = group_label,
    check.names = FALSE
  )
}

# Generate predictions
# VBG
pred_imv_vbg <- mkpred(fit_imv_vbg, subset_data_vbg, "vbg_co2", "VBG")
pred_niv_vbg <- mkpred(fit_niv_vbg, subset_data_vbg, "vbg_co2", "VBG")
pred_death_vbg <- mkpred(fit_death_vbg, subset_data_vbg, "vbg_co2", "VBG")
pred_hcfr_vbg <- mkpred(fit_hcfr_vbg, subset_data_vbg, "vbg_co2", "VBG")

```

```

# ABG
pred_imv_abg <- mkpred(fit_imv_abg,
pred_niv_abg <- mkpred(fit_niv_abg,
pred_death_abg <- mkpred(fit_death_abg,
pred_hcrf_abg <- mkpred(fit_hcrf_abg,
subset_data_abg, "paco2", "ABG")

# Combine
pred_imv <- bind_rows(pred_imv_vbg,
pred_niv <- bind_rows(pred_niv_vbg,
pred_death <- bind_rows(pred_death_vbg,
pred_hcrf <- bind_rows(pred_hcrf_vbg,
pred_imv_abg)
pred_niv_abg)
pred_death_abg)
pred_hcrf_abg)

# Plotting function in grayscale with distinguishable ribbons
plt_gray <- function(dat, title) {
  ggplot(dat, aes(x = co2, y = yhat, linetype = group)) +
    geom_line(color = "black", linewidth = 1) +
    geom_ribbon(aes(ymin = lower, ymax = upper, fill = group),
                alpha = 0.3, color = NA) +
    scale_fill_manual(values = c("ABG" = "gray90", "VBG" = "gray20")) + # different gray shades
    scale_linetype_manual(values = c("ABG" = "solid", "VBG" = "dashed")) +
    scale_y_continuous(limits = c(0, 1),
                       labels = scales::percent_format(accuracy = 1)) +
    labs(title = title,
         x = expression(CO[2]~"(mmHg)"),
         y = "Predicted probability",
         fill = "Group",
         linetype = "Group") +
    theme_minimal() +
    theme(legend.position = "bottom")
}

# Patchwork layout with gray shades
(patchwork::wrap_plots(

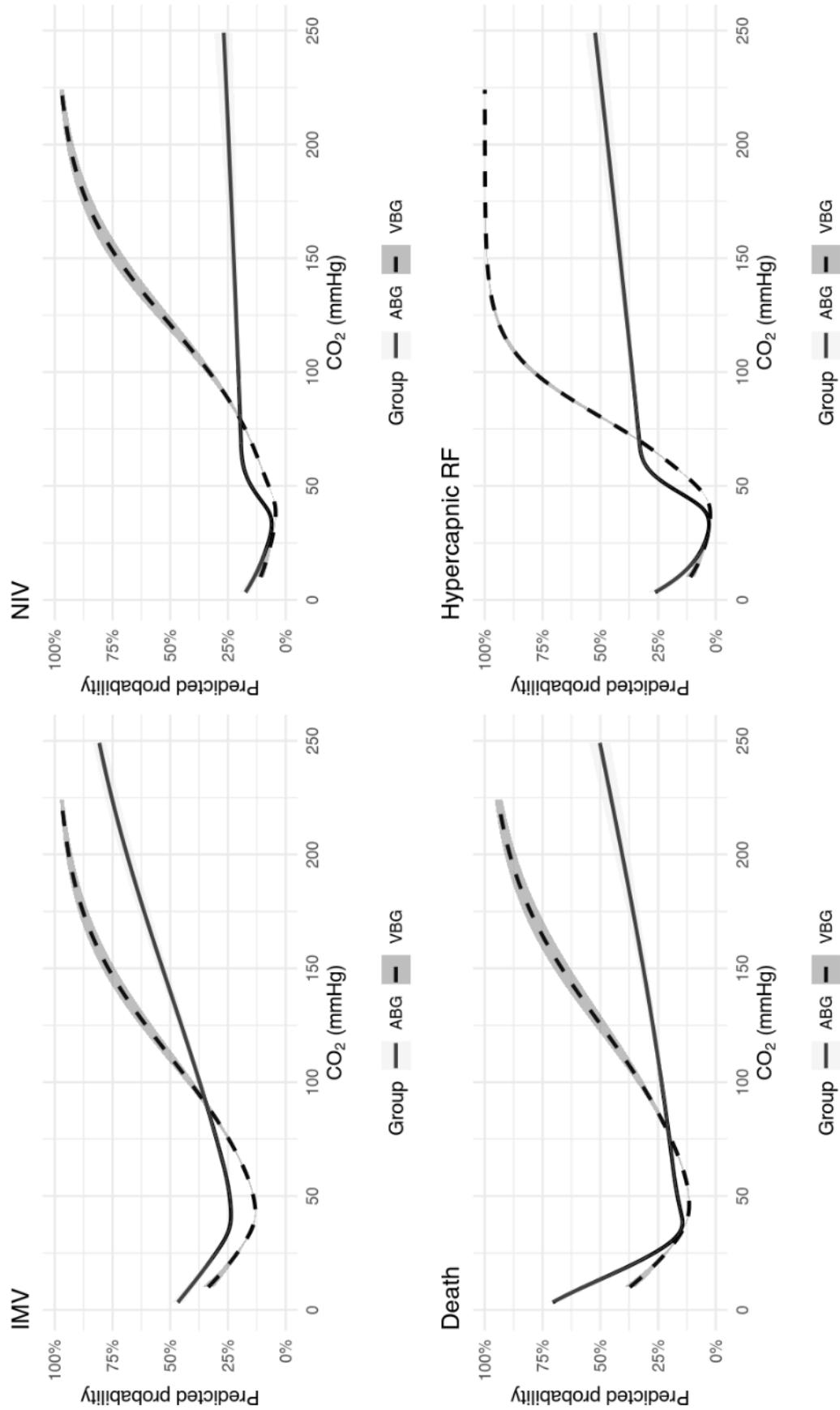
```

```

plt_gray(pred_imv,
plt_gray(pred_niv,
plt_gray(pred_death, "Death"),
plt_gray(pred_hcrf, "Hypercapnic RF"),
ncol = 2
)
)
+
plot_annotation(
  title = expression(
    paste("Propensity-weighted predicted probability by ABG vs VBG CO" [2],
      " (restricted cubic splines, gray scheme)"))
)

```

Propensity-weighted predicted probability by ABG vs VBG CO_2 (restricted cubic splines, gray scheme)



Restricting the plot to 0.02 to 0.99 (since this puts it at about 100mmHg for CO_2)

```

library(dplyr)
library(ggplot2)
library(patchwork)
library(scales)
library(rms)

# ABG spline fits (unweighted, rms::lrm)
fit_imv_abg <- lrm(imv_proc ~ rcs(paco2, 4), data = subset_data_abg)
fit_niv_abg <- lrm(niv_proc ~ rcs(paco2, 4), data = subset_data_abg)
fit_death_abg <- lrm(death_60d ~ rcs(paco2, 4), data = subset_data_abg)
fit_hcrf_abg <- lrm(hypercap_resp_failure ~ rcs(paco2, 4), data = subset_data_abg)

# VBG spline fits (mirror pattern)
fit_imv_vbg <- lrm(imv_proc ~ rcs(vbg_co2, 4), data = subset_data_vbg)
fit_niv_vbg <- lrm(niv_proc ~ rcs(vbg_co2, 4), data = subset_data_vbg)
fit_death_vbg <- lrm(death_60d ~ rcs(vbg_co2, 4), data = subset_data_vbg)
fit_hcrf_vbg <- lrm(hypercap_resp_failure ~ rcs(vbg_co2, 4), data = subset_data_vbg)

library(rms) # ensure lrm() and Predict() are available

# Helper to make predictions with standardized columns: co2, yhat, lower, upper, group
mkpred <- function(fit, data_ref, xvar, group_label, n = 200) {
  stopifnot(is.character(xvar), length(xvar) == 1, xvar %in% names(data_ref))

  # Restrict to 2nd and 98th percentiles
  rng <- quantile(data_ref[[xvar]], probs = c(0.02, 0.98), na.rm = TRUE)
  xseq <- seq(rng[1], rng[2], length.out = n)

  if (inherits(fit, "lrm")) {
    dd <- rms::datadist(data_ref)
    old <- options(datadist = "dd")
    on.exit(options(old), add = TRUE)
    assign("dd", dd, envir = .GlobalEnv)
  }
}

```

```

args <- c(list(object = fit, fun = plogis,
               stats::setNames(list(xseq), xvar))
p <- do.call(rms::Predict, args)
out <- as.data.frame(p)
names(out)[names(out) == xvar] <- "co2"
out$group <- group_label
out[, c("co2", "yhat", "lower", "upper", "group")]
} else {
  newd <- stats::setNames(data.frame(xseq), xvar)
  X <- stats::model.matrix(stats::delete.response(stats::terms(fit)), newd)
  beta <- stats::coef(fit)
  eta <- drop(X %*% beta)
  V <- stats::vcov(fit)
  se <- sqrt(rowSums((X %*% V) * X))
  data.frame(
    co2 = xseq,
    yhat = plogis(eta),
    lower = plogis(eta - 1.96 * se),
    upper = plogis(eta + 1.96 * se),
    group = group_label,
    check.names = FALSE
  )
}
}

# Generate predictions
# VBG
pred_imv_vbg <- mkpred(fit_imv_vbg, subset_data_vbg, "vbg_co2", "VBG")
pred_niv_vbg <- mkpred(fit_niv_vbg, subset_data_vbg, "vbg_co2", "VBG")
pred_death_vbg <- mkpred(fit_death_vbg, subset_data_vbg, "vbg_co2", "VBG")
pred_hcfr_vbg <- mkpred(fit_hcfr_vbg, subset_data_vbg, "vbg_co2", "VBG")

# ABG
pred_imv_abg <- mkpred(fit_imv_abg, subset_data_abg, "paco2", "ABG")

```

```

pred_niv_abg <- mkpred(fit_niv_abg, subset_data_abg, "paco2", "ABG")
pred_death_abg <- mkpred(fit_death_abg, subset_data_abg, "paco2", "ABG")
pred_hcfr_abg <- mkpred(fit_hcfr_abg, subset_data_abg, "paco2", "ABG")

# Combine
pred_imv <- bind_rows(pred_imv_vbg, pred_imv_abg)
pred_niv <- bind_rows(pred_niv_vbg, pred_niv_abg)
pred_death <- bind_rows(pred_death_vbg, pred_death_abg)
pred_hcfr <- bind_rows(pred_hcfr_vbg, pred_hcfr_abg)

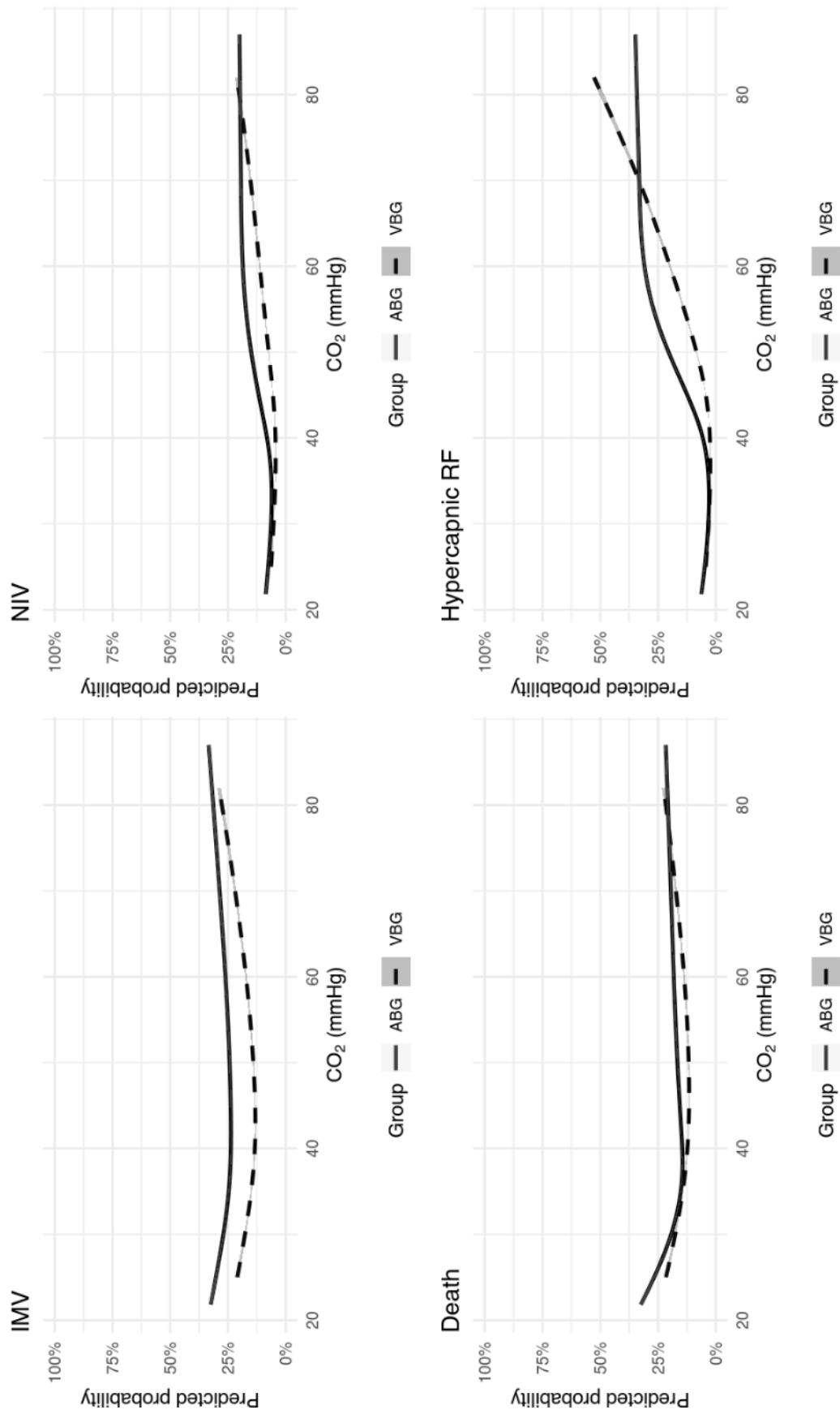
# Plotting function in grayscale with distinguishable ribbons
plt_gray <- function(dat, title) {
  ggplot(dat, aes(x = co2, y = yhat, linetype = group)) +
    geom_line(color = "black", linewidth = 1) +
    geom_ribbon(aes(ymin = lower, ymax = upper, fill = group),
                alpha = 0.3, color = NA) +
    scale_fill_manual(values = c("ABG" = "gray90", "VBG" = "gray20")) + # different gray shades
    scale_linetype_manual(values = c("ABG" = "solid", "VBG" = "dashed")) +
    scale_y_continuous(limits = c(0, 1),
                       labels = scales::percent_format(accuracy = 1)) +
    labs(title = title,
         x = expression(CO[2]~"(mmHg)"),
         y = "Predicted probability",
         fill = "Group",
         linetype = "Group") +
    theme_minimal() +
    theme(legend.position = "bottom")
}

# Patchwork layout with gray shades
(patchwork::wrap_plots(
  plt_gray(pred_imv, "IMV"),
  plt_gray(pred_niv, "NIV"),
  plt_gray(pred_death, "Death"),
  )
)

```

```
plt_gray(pred_hcrf, "Hypercapnic RF"),
ncol = 2
)
) +
plot_annotation(
title = expression(
paste("Propensity-weighted predicted probability by ABG vs VBG CD"[2],
" (restricted cubic splines, gray scheme)"))
)
)
```

Propensity-weighted predicted probability by ABG vs VBG CO_2 (restricted cubic splines, gray scheme)



Feature importance: *global* contribution of a feature to the model's predictive performance on the training distribution. Quick global triage—which variables the model leaned on to fit propensity. Good for model debugging, feature pruning, and tracking drift across refits (qualitatively).

SHAP: a *local*, signed attribution for that subject: “by how much did feature j push this person’s log-odds of receiving the test up or down vs baseline?; then global shap is mean absolute SHAP across subjects—i.e., the **typical magnitude** of a feature’s contribution to predictions in your population. Good for auditability and **directional insight**—*who is assigned higher/lower propensity by which features, spot proxies, and communicate fairness/operational drivers. Aggregate with mean |SHAP| for a global ranking with direction available when needed.*

TODO: Can label y-axis in plots: contribution to the log odds of receiving an ABG or VBG for the SHAP values.

ABG

For the top SHAP-ranked predictors we computed partial- and accumulated-local-effects (ALE) to estimate the marginal change in predicted risk across clinically relevant ranges, robust to covariate correlation. We complemented this with SHAP dependence plots (colored by plausible interactions) and fitted transparent spline-logistic models to identify turn-points (‘knees’) where marginal log-odds slope changed.

```
# --- deps -----
library(WeightIt)
library(gbm)
library(dplyr)
library(ggplot2)
library(fastshap)

# --- 0) Canonicalize object name -----
# Your 9-26.qmd labeled the ABG propensity object `weight_model` .
if (!exists("w_abg", inherits = TRUE) && exists("weight_model", inherits = TRUE)) {
  w_abg <- weight_model
}

stopifnot(exists("w_abg", inherits = TRUE))

# --- 1) Ensure the WeightIt object stores the GBM + covariate matrix -----
ensure_gbm_obj <- function(W) {
  stopifnot(inherits(W, "weightit"))
  has_obj <- !is.null(W$obj) || !is.null(W$info$obj) || !is.null(W$model.obj)
  has_cov <- !is.null(W$covs)
  if (has_obj && has_cov) return(W)
```

```

cl <- as.list(W$call); cl[[1]] <- WeightIt::weightit
if (!is.null(cl[["missing."]]) ) { cl$missing <- cl[["missing."]]; cl[[["missing."]]] <- NULL }
if (is.null(cl$missing)) cl$missing <- "ind"
cl$include.obj <- TRUE
if (is.null(cl$method)) cl$method <- "gbm"
if (is.language(cl$formula)) cl$formula <- eval(cl$formula, envir = .GlobalEnv)
if (is.language(cl$data)) cl$data <- eval(cl$data, envir = .GlobalEnv)
do.call(WeightIt::weightit, cl[-1])
}

w_abg <- ensure_gbm_obj(w_abg)

# --- 2) Helpers: design alignment, importance, fast SHAP (logit scale) -----
prep_design <- function(W) {
  stopifnot(inherits(W, "weightit"))
  gbm_fit <- if (!is.null(W$obj)) W$obj else if (!is.null(W$info$obj)) W$info$obj else W$model.obj
  stopifnot(inherits(gbm_fit, "gbm"))
  stopifnot(!is.null(W$covs))
}

X <- W$covs
if (inherits(X, "tbl")) X <- as.data.frame(X)
if (inherits(X, "Matrix")) X <- as.matrix(X)
X <- as.data.frame(X, stringsAsFactors = FALSE)

# conservative coercion: only numeric-like strings → numeric
for (nm in names(X)) {
  if (is.factor(X[[nm]])) X[[nm]] <- as.character(X[[nm]])
  if (is.character(X[[nm]])) {
    ok <- grep1("^-+]?[0-9.]+$", X[[nm]] %||% "")
    if (all(ok | is.na(X[[nm]]))) suppressWarnings(X[[nm]] <- as.numeric(X[[nm]]))
  }
}

vars <- gbm_fit$var.names
miss <- setdiff(vars, colnames(X))
}

```

```

if (length(miss)) for (nm in miss) X[[nm]] <- 0
X <- X[, vars, drop = FALSE]

best_tree <- if (!is.null(W$info$best.tree)) W$info$best.tree else gbm_fit$n.trees
list(X = X, gbm_fit = gbm_fit, best_tree = best_tree)
}

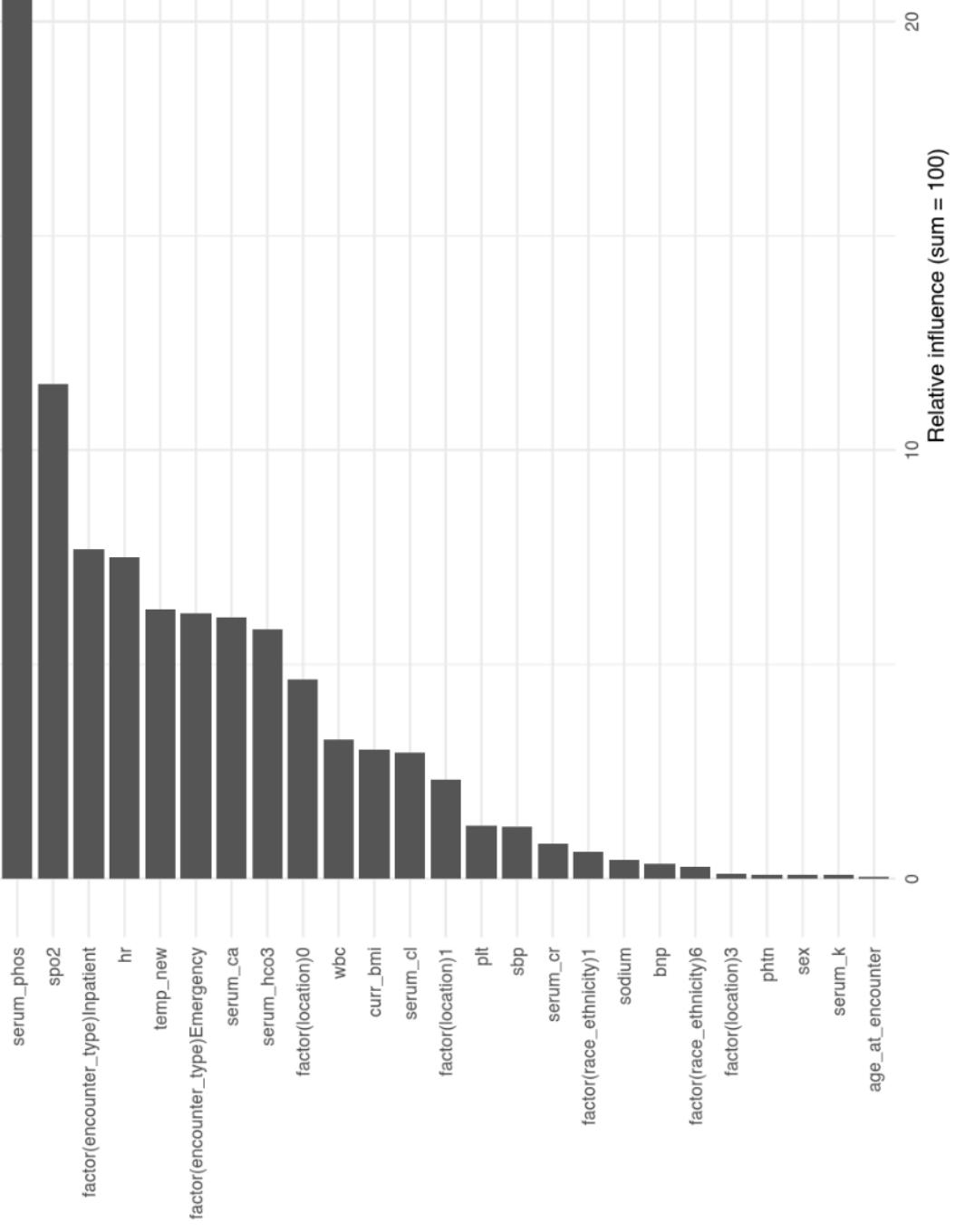
extract_gbm_importance <- function(W, top_n = 25) {
  mats <- prep_design(W)
  as.data.frame(summary(mats$gbm_fit, n.trees = mats$best_tree, plotit = FALSE)) |>
    arrange(desc(rel.inf)) |>
    slice_head(n = top_n)
}

plot_gbm_importance <- function(imp_df, title = "GBM variable importance (relative influence)") {
  ggplot(imp_df, aes(x = rel.inf, y = reorder(var, rel.inf))) +
    geom_col(width = 0.85) +
    labs(x = "Relative influence (sum = 100)", y = NULL, title = title) +
    theme_minimal(base_size = 11)
}

# --- 3) Run: ABG selection model - importance + fast SHAP -----
imp_abg <- extract_gbm_importance(w_abg, top_n = 25)
p_imp_abg <- plot_gbm_importance(imp_abg, "ABG selection model - GBM relative influence")
p_imp_abg

```

ABG selection model – GBM relative influence



```
# ---- Build shapviz object robustly ----  
library(shapviz)
```

```

# fast SHAP on LOGIT scale; prunes zero-variance features; subsamples rows
compute_shap_fast <- function(W, top_k = 30, nsim = 64, frac_rows = 0.50,
                                max_rows = 100000, seed = 123) {
  mats <- prep_design(W); X <- mats$X; gbm_fit <- mats$gbm_fit; best_tree <- mats$best_tree

  imp <- as.data.frame(summary(gbm_fit, n.trees = best_tree, plotit = FALSE))
  top_feats <- head(imp$var, min(top_k, nrow(imp)))
  top_feats <- intersect(top_feats, colnames(X))

  # drop constant features (avoid flat SHAP/plots)
  nzv <- sapply(X[, top_feats, drop = FALSE], function(z) sd(z, na.rm = TRUE) > 0)
  top_feats <- top_feats[nzv]
  if (!length(top_feats)) stop("All candidate features are near-constant in this subset.")

  n <- nrow(X); target_n <- min(n, max_rows, ceiling(frac_rows * n))
  set.seed(seed)

  Xsub <- if (target_n < n) X[sample.int(n, target_n), , drop = FALSE] else X

  # SHAP on logit scale for contrast/stability
  pfun <- function(object, newdata)
    predict(object, newdata = newdata, n.trees = best_tree, type = "link")

  fs_formals <- names(formals(fastshap::explain))
  args <- list(object = gbm_fit, X = Xsub, pred_wrapper = pfun, nsim = nsim, adjust = TRUE)
  if ("feature_names" %in% fs_formals) args$feature_names <- top_feats

  set.seed(seed)
  S <- do.call(fastshap::explain, args) # matrix or data.frame of SHAP
  list(shap = S, X = Xsub, top_feats = top_feats, imp = imp)
}

t0 <- Sys.time()
sh_abg_fast <- compute_shap_fast(w_abg, top_k = 100, nsim = 32, frac_rows = 0.25, max_rows = 100000)

```

```

t1 <- Sys.time(); message(sprintf("[compute_shap_fast] %.2f s", as.numeric(difftime(t1, t0, units="secs"))))

[compute_shap_fast] 19204.68 s

# 1) Take SHAP and design from your fast SHAP object
S <- as.matrix(sh_abg_fast$shap) # n x p SHAP matrix
X <- as.data.frame(sh_abg_fast$x) # matching rows, p columns

# 2) Make X numeric-only (handles factors / labelled types safely)
for (nm in names(X)) {
  if (inherits(X[[nm]], "haven_labelled")) {
    X[[nm]] <- labelled::to_factor(X[[nm]])
  }
  if (is.factor(X[[nm]])) X[[nm]] <- as.character(X[[nm]])
  if (is.character(X[[nm]])) suppressWarnings(X[[nm]] <- as.numeric(X[[nm]]))
}

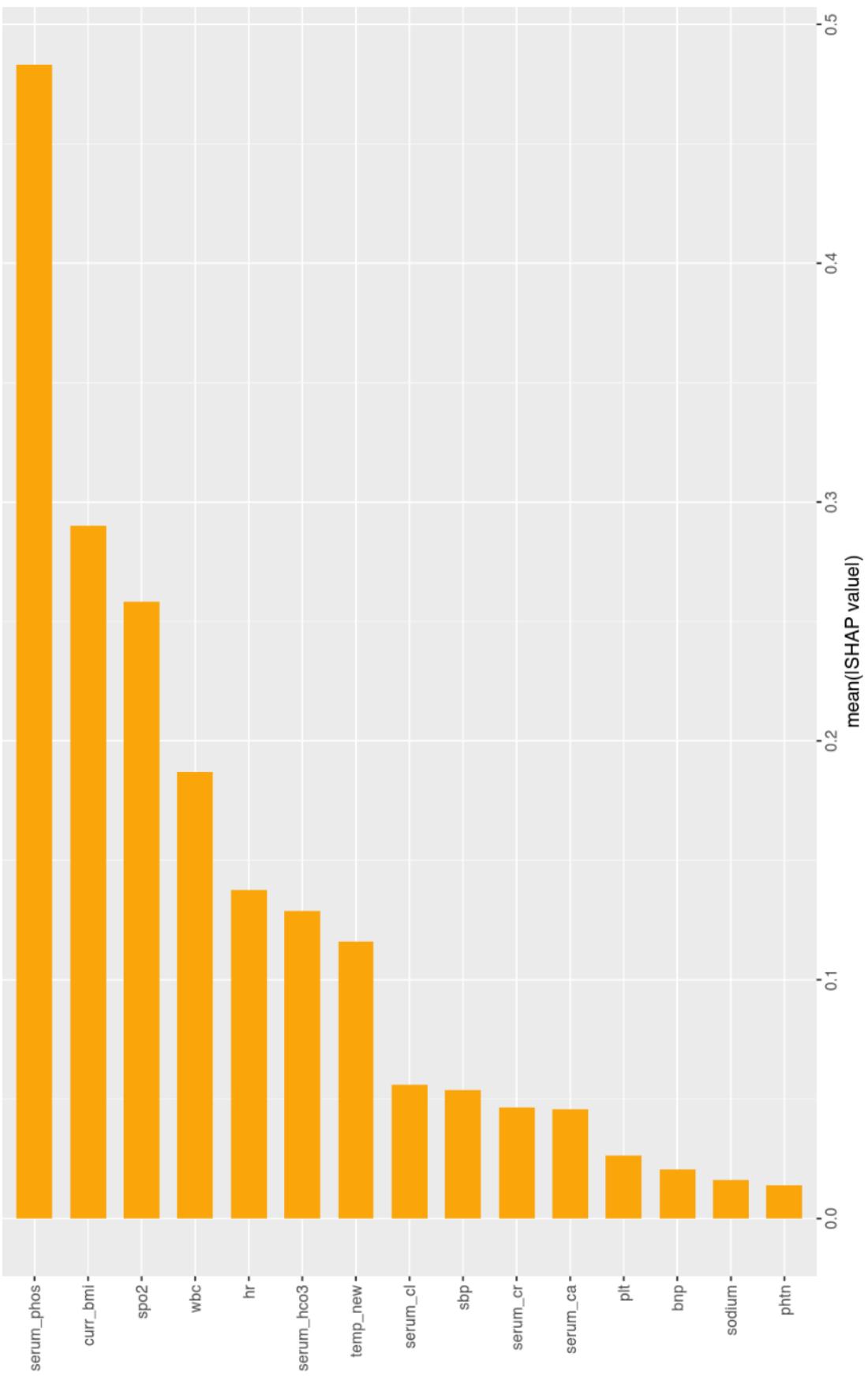
# 3) Align names/order between S and X (and give S names if missing)
if (is.null(colnames(S))) colnames(S) <- colnames(X)
S <- S[, intersect(colnames(S), colnames(X)), drop = FALSE]
X <- X[, colnames(S), drop = FALSE]

# 4) Construct shapviz object: PASS S POSITIONALLY (no name) to avoid dispatch bug
sv <- shapviz(S, X = as.matrix(X))

# --- Examples -----
# Bar plot of top 30 (global |SHAP|)
ord <- order(colMeans(abs(S), na.rm = TRUE), decreasing = TRUE)
topK <- colnames(S)[ord[1:min(30, ncol(S))]]
sv_importance(sv, kind = "bar", v = topK)

```

Warning: `label` cannot be a `<ggplot2::element_blank>` object.



```
library(shapviz)
```

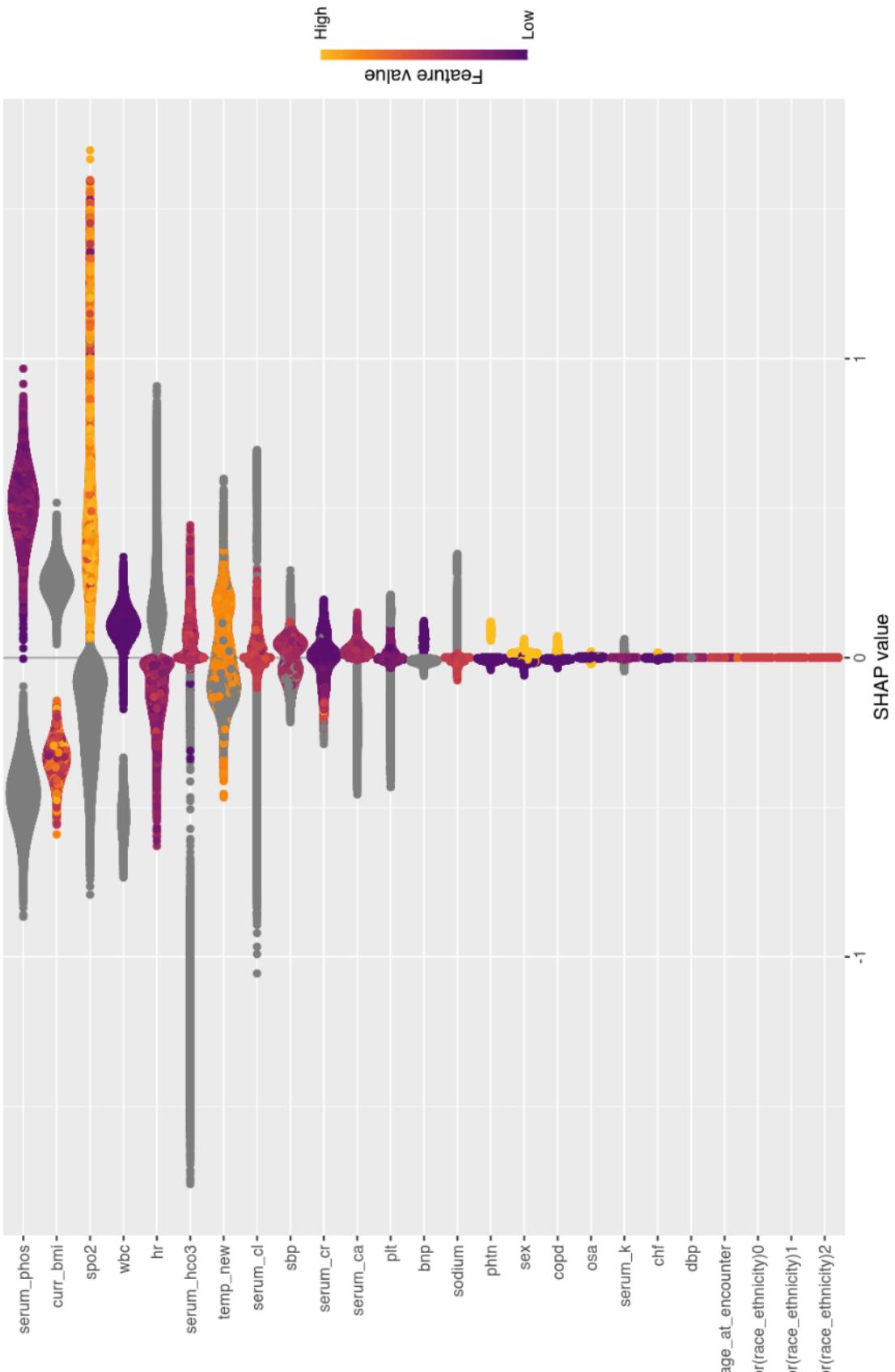
```
S <- as.matrix(sh_abg_fast$shap) # n x p SHAP values
```

```
X <- as.data.frame(sh_abg_fast$X) # same rows, p columns (features)

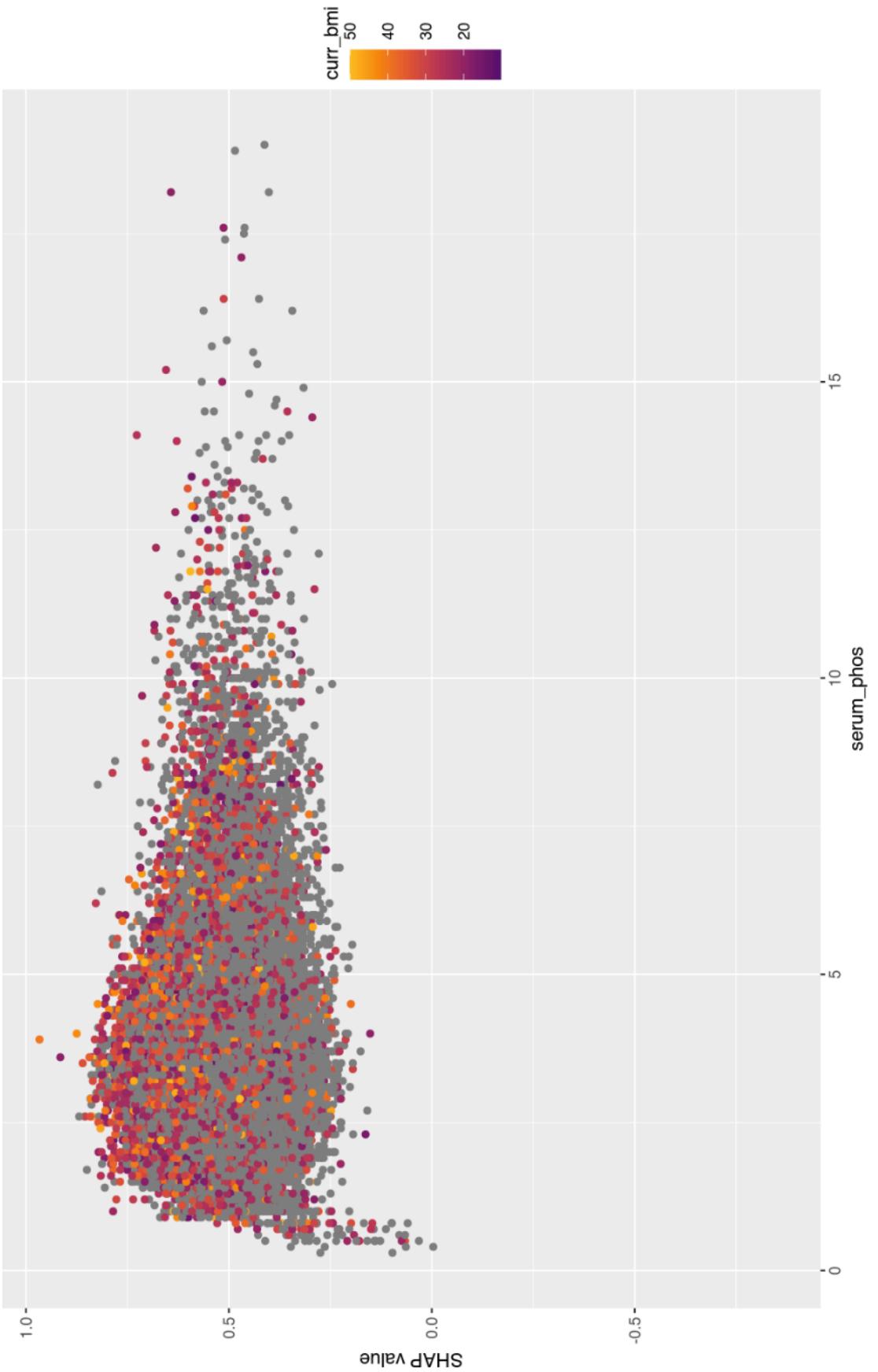
# Build shapviz object
sv <- shapviz(S, X = as.matrix(X))

# Beeswarm-style SHAP summary (like Python SHAP)
sv_importance(sv, kind = "beeswarm", max_display = 25) # overall
```

Warning: `label` cannot be a <ggplot2::element_blank> object.



```
# Primary = top feature; color by next feature
imp_order <- colnames(S)[ord]
sv_dependence(sv, v = imp_order[1], color_var = imp_order[2], smooth = TRUE)
```



```
# --- Compact 5x5 SHAP dependence grid with shared axes and a single small legend ----  
library(shapviz)  
library(ggplot2)
```

```

library(patchwork)
library(grid) # for unit()

# If needed, recover S and X_sv from 'sv'
if (!exists("S")) S <- sv$S
if (!exists("X_sv")) X_sv <- as.data.frame(sv$X)
stopifnot(is.matrix(S), is.data.frame(X_sv))

# 1) Top-5 by global mean |SHAP|
ranked <- colnames(S)[order(colMeans(abs(S), na.rm = TRUE), decreasing = TRUE)]
top5 <- head(ranked, 5)

# 2) Shared y-range across all top-5 features
y_rng <- range(unlist(lapply(top5, function(v) S[, v])), finite = TRUE)

# 3) Small theme helpers
theme_axes_compact <- function(show_y = FALSE, show_x = FALSE, base = 8) {
  theme_minimal(base_size = base) +
  theme(
    axis.title.y = if (show_y) element_text(size = base) else element_blank(),
    axis.text.y = if (show_y) element_text(size = base - 1) else element_blank(),
    axis.ticks.y = if (show_y) element_line(linewidth = 0.2) else element_blank(),
    axis.title.x = if (show_x) element_text(size = base) else element_blank(),
    axis.text.x = if (show_x) element_text(size = base - 1) else element_blank(),
    plot.title = element_text(size = base, hjust = 0),
    legend.title = element_text(size = base - 1),
    legend.text = element_text(size = base - 2),
    legend.key.height = unit(22, "pt"),
    legend.key.width = unit(3, "pt"),
    legend.margin = margin(0, 0, 0, "pt"),
    legend.box.margin = margin(0, 0, 0, "pt")
  )
}

}

```

```

# 4) One cell builder
cell_plot <- function(v_row, v_col, i, j, n) {
  show_y <- (j == 1) # y-axis only on first column
  show_x <- (i == n) # x-axis only on bottom row

  if (identical(v_row, v_col)) {
    # diagonal: unshaded scatter (no legend)
    df <- data.frame(
      x = as.numeric(X_sv[[v_row]]),
      shap = as.numeric(S[, v_row])
    )
    df <- df[is.finite(df$x) & is.finite(df$shap), , drop = FALSE]

    ggplot(df, aes(x = x, y = shap)) +
      geom_point(alpha = 0.30, size = 0.45, na.rm = TRUE) +
      scale_y_continuous(limits = y_rng) +
      labs(title = v_row, x = v_row, y = "SHAP") +
      theme_axes_compact(show_y = show_y, show_x = show_x, base = 8) +
      theme(legend.position = "none")
  } else {
    # off-diagonal: color by partner feature
    p <- shapviz::sv_dependence(sv, v = v_row, color_var = v_col, size = 0.4) +
      scale_y_continuous(limits = y_rng) +
      labs(title = paste0(v_row, " | color: ", v_col),
           x = v_row, y = "SHAP")
  }
}

# keep a single, small legend on the top-right panel only
keep_legend <- (i == 1 && j == length(top5))
p +
  theme_axes_compact(show_y = show_y, show_x = show_x, base = 8) +
  guides(colour = guide_colorbar(
    barheight = unit(24, "pt"),
    barwidth = unit(3, "pt"),
    title.position = "top",
  ))

```

```

    title.hjust   = 0.5,
    label.position = "right"
  )) +
  theme(legend.position = if (keep_legend) "right" else "none")
}

# 5) Build grid row-wise
n <- length(top5)
plots <- vector("list", n * n)
idx <- 1
for (i in seq_len(n)) {
  for (j in seq_len(n)) {
    vr <- top5[i];
    vc <- top5[j]
    plots[[idx]] <- cell_plot(vr, vc, i, j, n)
    idx <- idx + 1
  }
}

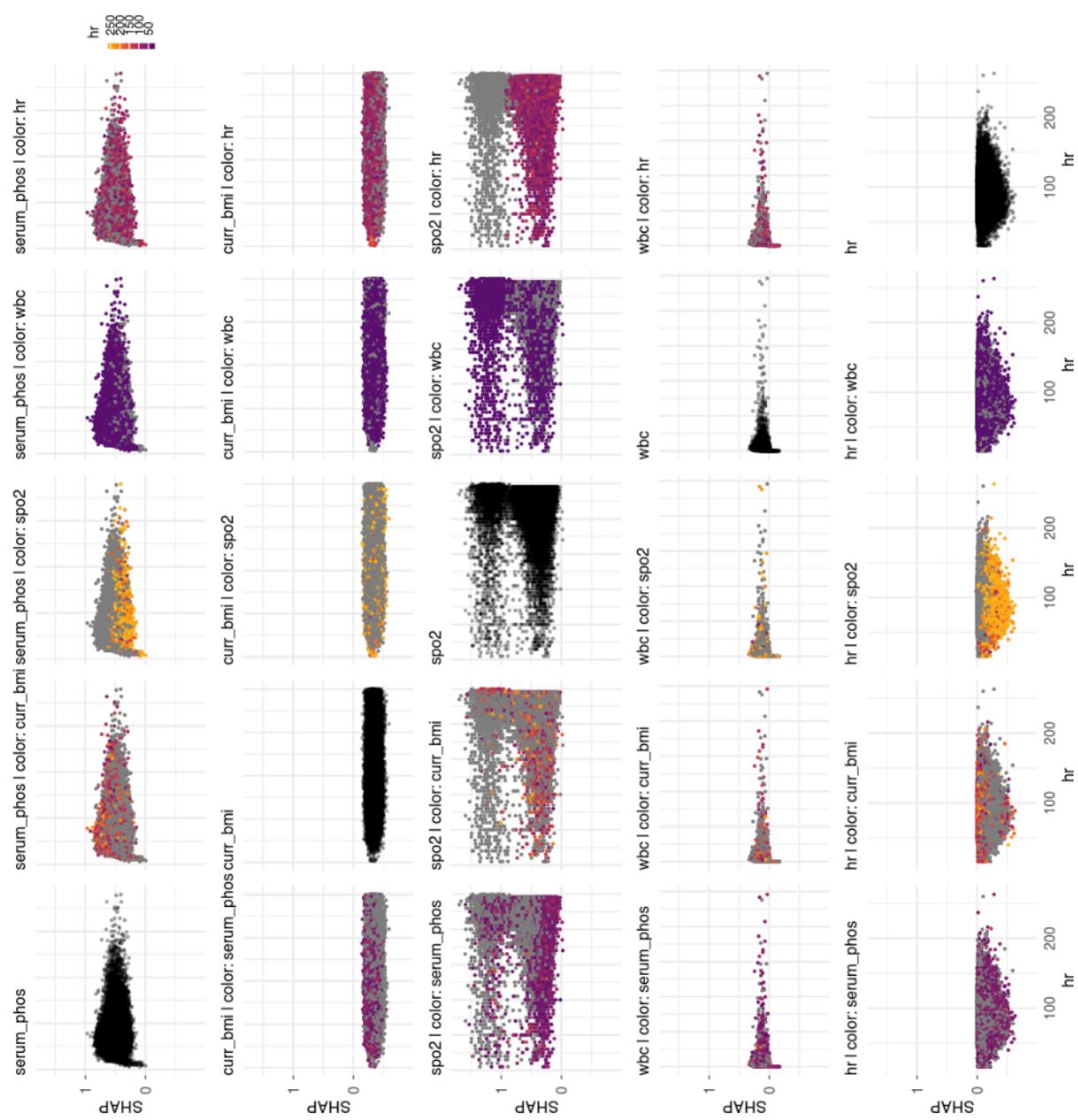
```

```

# 6) Draw: 5 columns, shared layout; keep (not collect) legends so only the chosen one stays
patchwork::wrap_plots(plots, ncol = n, guides = "keep") +
plot_annotation(title = "Top-5 SHAP dependence: interactions (off-diagonal) and main effects (diagonal)")

```

Top-5 SHAP dependence: interactions (off-diagonal) and main effects (diagonal)



VBG

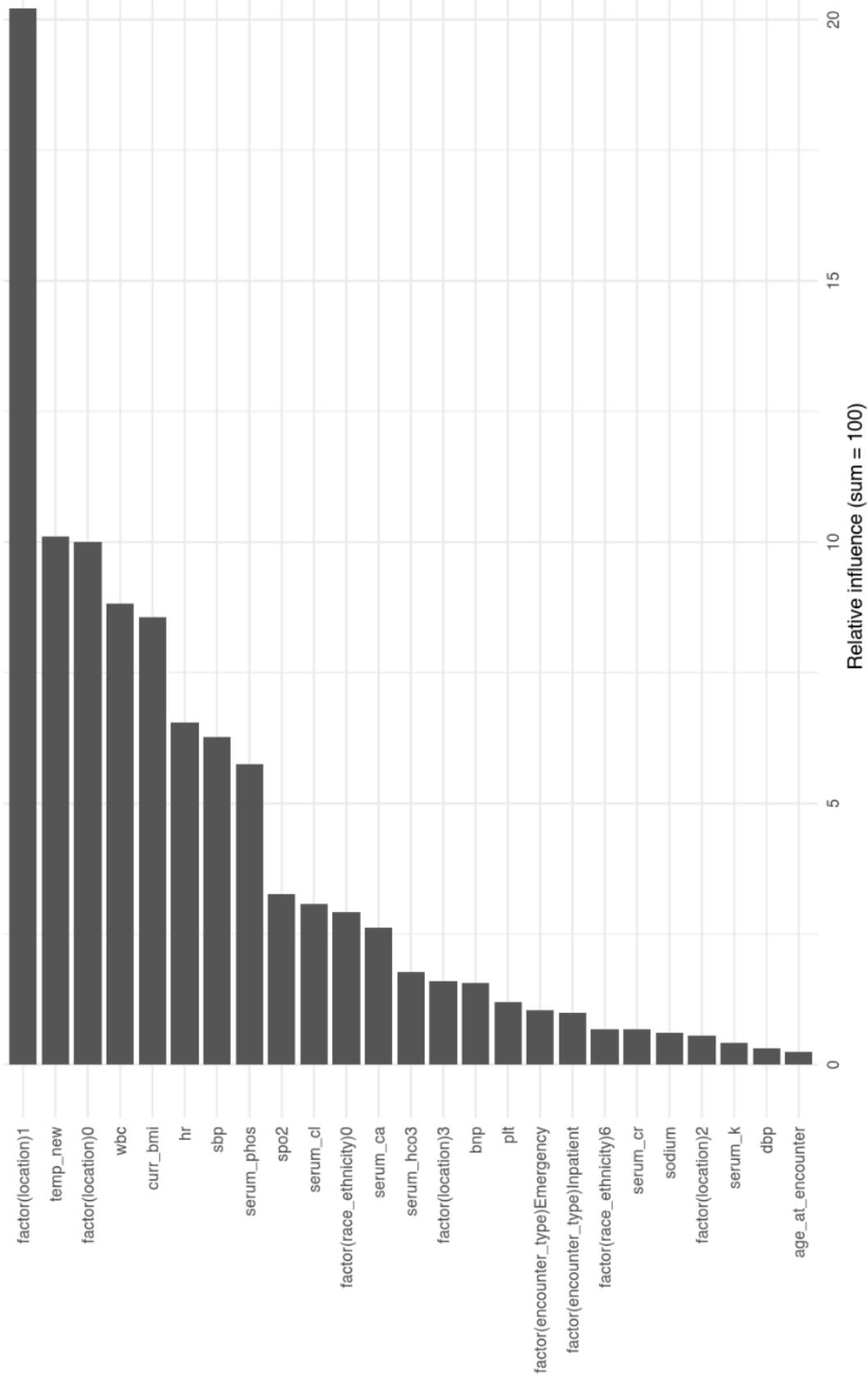
VBG Explainability

```
library(WeightIt); library(gbm); library(dplyr); library(ggplot2)

stopifnot(exists("w_vbg", inherits = TRUE))
w_vbg <- ensure_gbm_obj(w_vbg)

imp_vbg <- extract_gbm_importance(w_vbg, top_n = 25)
p_imp_vbg <- plot_gbm_importance(imp_vbg, "VBG selection model - GBM relative influence")
p_imp_vbg
```

VBG selection model – GBM relative influence



```
library(shapviz); library(fastrshap)
```

```
t0 <- Sys.time()
```

```

sh_vbg_fast <- compute_shap_fast(w_vbg, top_k = 100, nsim = 32, frac_rows = 0.25, max_rows = 1000000)
t1 <- Sys.time(); message(sprintf(" [compute_shap_fast VBG] %.2f s", as.numeric(difftime(t1, t0, units="secs"))))

S_vbg <- as.matrix(sh_vbg_fast$shap)
X_vbg <- as.data.frame(sh_vbg_fast$X)

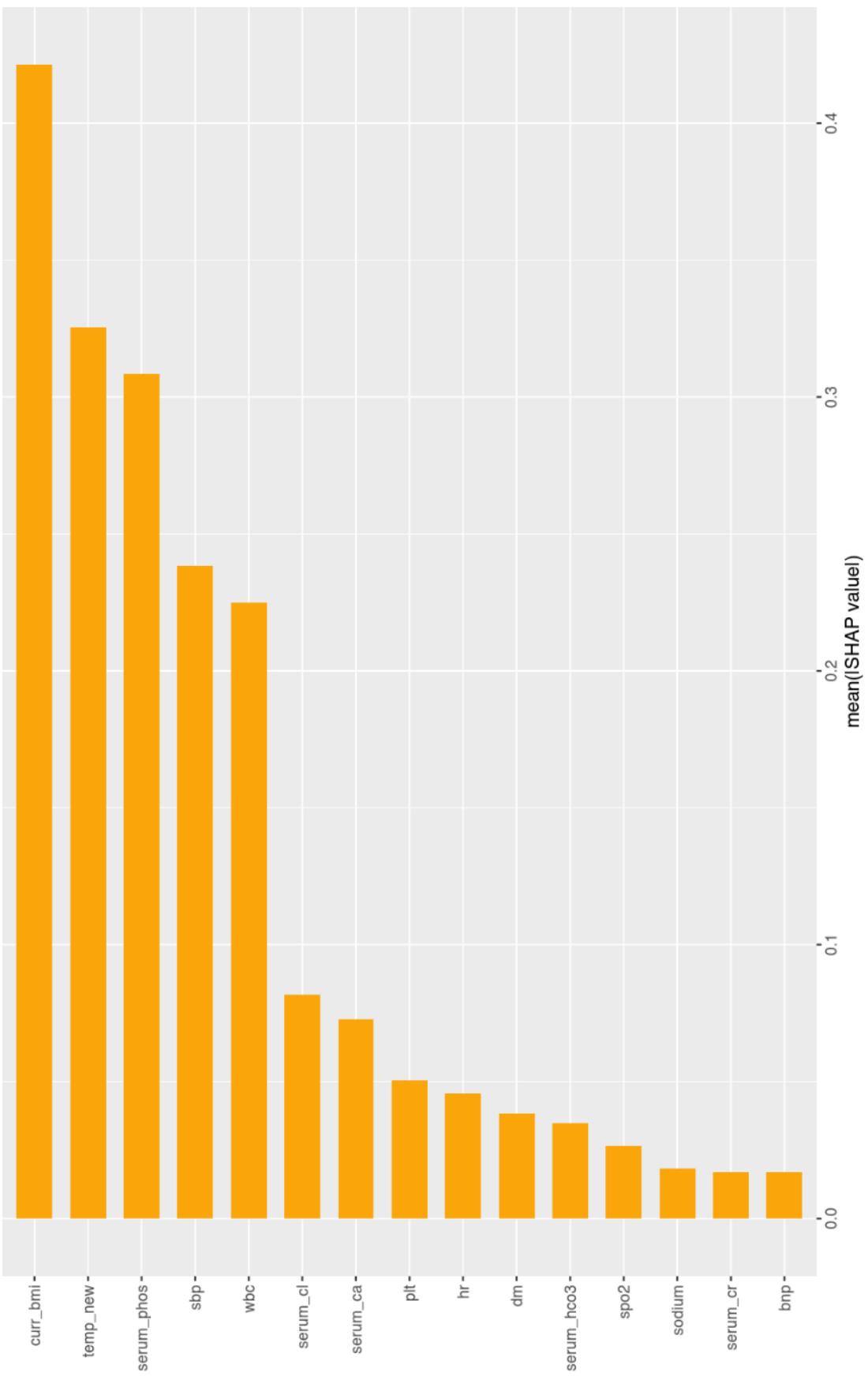
for (nm in names(X_vbg)) {
  if (inherits(X_vbg[[nm]], "haven_labelled")) X_vbg[[nm]] <- labelled::to_factor(X_vbg[[nm]])
  if (is.factor(X_vbg[[nm]])) X_vbg[[nm]] <- as.character(X_vbg[[nm]])
  if (is.character(X_vbg[[nm]])) suppressWarnings(X_vbg[[nm]] <- as.numeric(X_vbg[[nm]]))
}

if (is.null(colnames(S_vbg))) colnames(S_vbg) <- colnames(X_vbg)
S_vbg <- S_vbg[, intersect(colnames(S_vbg), colnames(X_vbg)), drop = FALSE]
X_vbg <- X_vbg[, colnames(S_vbg), drop = FALSE]

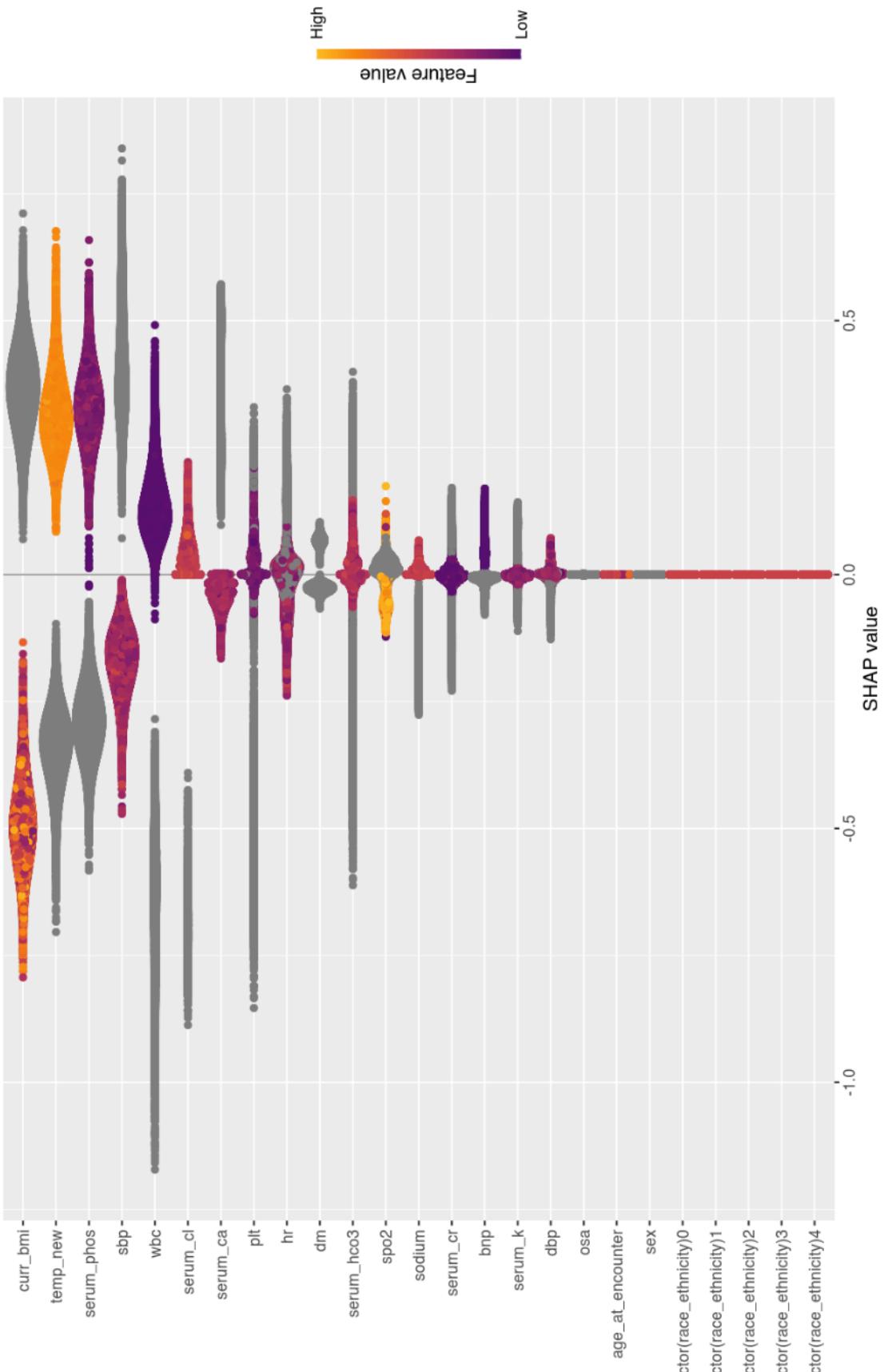
sv_vbg <- shapviz::shapviz(S_vbg, X = as.matrix(X_vbg))

ord_vbg <- order(colMeans(abs(S_vbg), na.rm = TRUE), decreasing = TRUE)
topK_vbg <- colnames(S_vbg)[ord_vbg[1:min(30, ncol(S_vbg))]]
sv_importance(sv_vbg, kind = "bar", v = topK_vbg)

```



```
library(shapviz)
sv_importance(sv_vbg, kind = "beeswarm", max_display = 25)
```



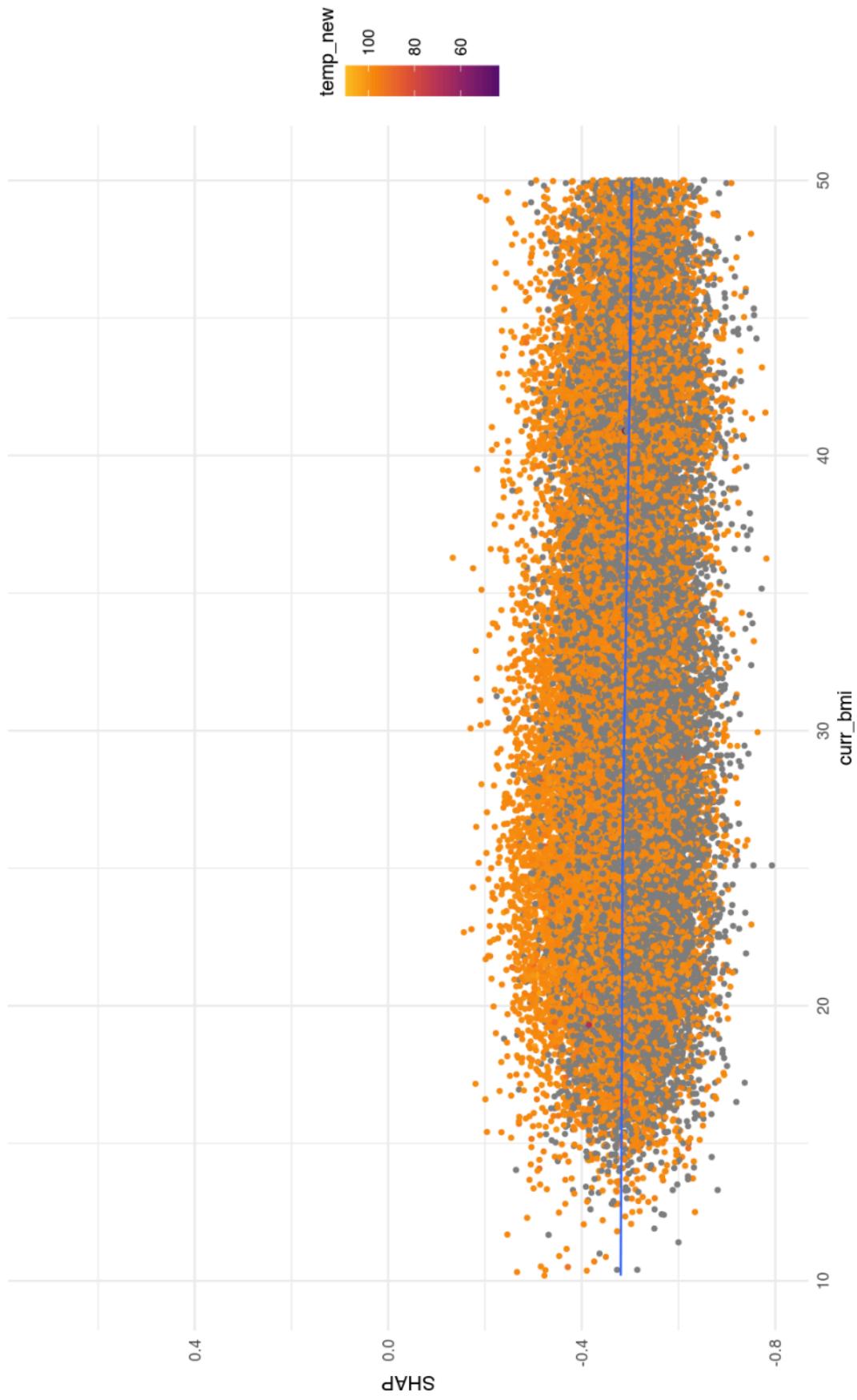
```
library(ggplot2)
```

```
imp_order_vbg <- colnames(S_vbg)[order(colMeans(abs(S_vbg)), na.rm = TRUE), decreasing = TRUE)]
```

```
pri_vbg <- imp_order_vbg[1]
aux_vbg <- imp_order_vbg[2]
if (identical(aux_vbg, pri_vbg) || !(aux_vbg %in% colnames(X_vbg))) aux_vbg <- imp_order_vbg[3]

shapviz::sv_dependence(sv_vbg, v = pri_vbg, color_var = aux_vbg, size = 1) +
  geom_smooth(se = FALSE, method = "loess", formula = y ~ x, linewidth = 0.6) +
  labs(title = sprintf("VBG propensity - SHAP dependence: %s (color: %s)", pri_vbg, aux_vbg),
       x = pri_vbg, y = "SHAP") +
  theme_minimal(base_size = 11)
```

VBG propensity – SHAP dependence: curr_bmi (color: temp_new)



```
library(shapviz); library(ggplot2); library(patchwork); library(grid)
```

```
stopifnot(is.matrix(S_vbg), is.data.frame(X_vbg))
```

```

ranked_vbg <- colnames(S_vbg)[order(colMeans(abs(S_vbg), na.rm = TRUE), decreasing = TRUE)]
top5_vbg <- head(ranked_vbg, 5)
y_rng_vbg <- range(unlist(lapply(top5_vbg, function(v) S_vbg[, v])), finite = TRUE)

theme_axes_compact <- function(show_y = FALSE, show_x = FALSE, base = 8) {
  theme_minimal(base_size = base) +
    theme(
      axis.title.y = if (show_y) element_text(size = base) else element_blank(),
      axis.text.y = if (show_y) element_text(size = base - 1) else element_blank(),
      axis.ticks.y = if (show_y) element_line(linewidth = 0.2) else element_blank(),
      axis.title.x = if (show_x) element_text(size = base) else element_blank(),
      axis.text.x = if (show_x) element_text(size = base - 1) else element_blank(),
      plot.title = element_text(size = base, hjust = 0),
      legend.title = element_text(size = base - 1),
      legend.text = element_text(size = base - 2),
      legend.key.height = unit(22, "pt"),
      legend.key.width = unit(3, "pt"),
      legend.margin = margin(0, 0, 0, "pt"),
      legend.box.margin = margin(0, 0, 0, "pt")
    )
}

cell_plot_vbg <- function(v_row, v_col, i, j, n) {
  show_y <- (j == 1); show_x <- (i == n)
  if (identical(v_row, v_col)) {
    df <- data.frame(x = as.numeric(X_vbg[[v_row]]), shape = as.numeric(S_vbg[, v_row]))
    df <- df[is.finite(df$x) & is.finite(df$shape), , drop = FALSE]
    ggplot(df, aes(x = x, y = shape)) +
      geom_point(alpha = 0.30, size = 0.45, na.rm = TRUE) +
      scale_y_continuous(limits = y_rng_vbg) +
      labs(title = v_row, x = v_row, y = "SHAP") +
      theme_axes_compact(show_y, show_x, base = 8) +
      theme(legend.position = "none")
  }
}

```

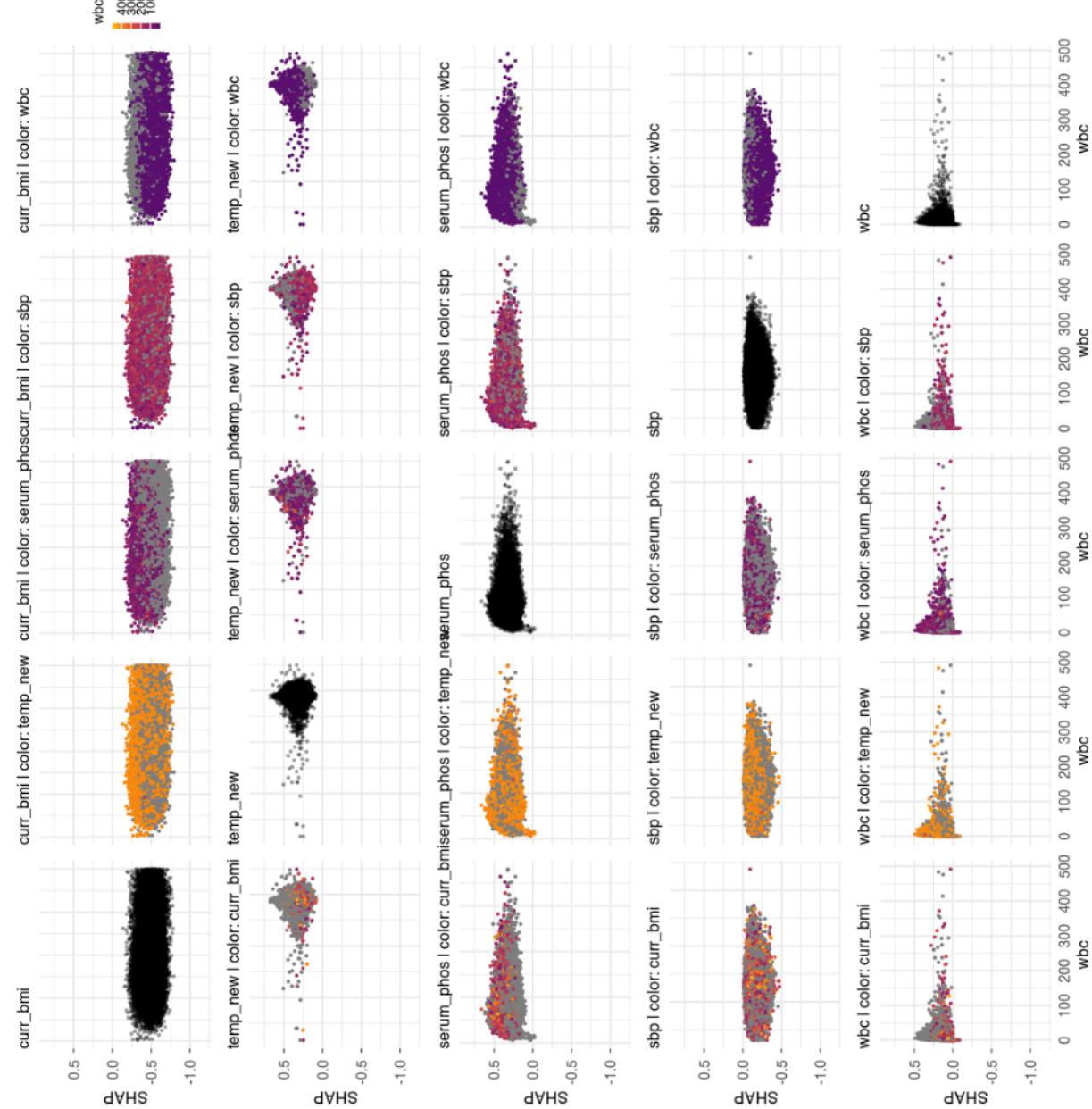
```

} else {
  keep_legend <- (i == 1 && j == length(top5_vbg))
  shapviz::sv_dependence(sv_vbg, v = v_row, color_var = v_col, size = 0.4) +
    scale_y_continuous(limits = y_rng_vbg) +
    labs(title = paste0(v_row, " | color:", " ", v_col), x = v_row, y = "SHAP") +
    theme_axes_compact(show_y, show_x, base = 8) +
    guides(colour = guide_colorbar(barheight = unit(24, "pt"), barwidth = unit(3, "pt")),
           title.position = "top", title.hjust = 0.5, label.position = "right")) +
    theme(legend.position = if (keep_legend) "right" else "none")
}

n <- length(top5_vbg); plots <- vector("list", n * n); k <- 1
for (i in seq_len(n)) for (j in seq_len(n)) {
  plots[[k]] <- cell_plot_vbg(top5_vbg[i], top5_vbg[j], i, j, n); k <- k + 1
}
patchwork::wrap_plots(plots, ncol = n, guides = "keep") +
  plot_annotation(title = "VBG propensity - Top-5 SHAP dependence (off-diagonal interactions, diagonal main effects)")

```

VBG propensity — Top-5 SHAP dependence (off-diagonal interactions, diagonal main effects)



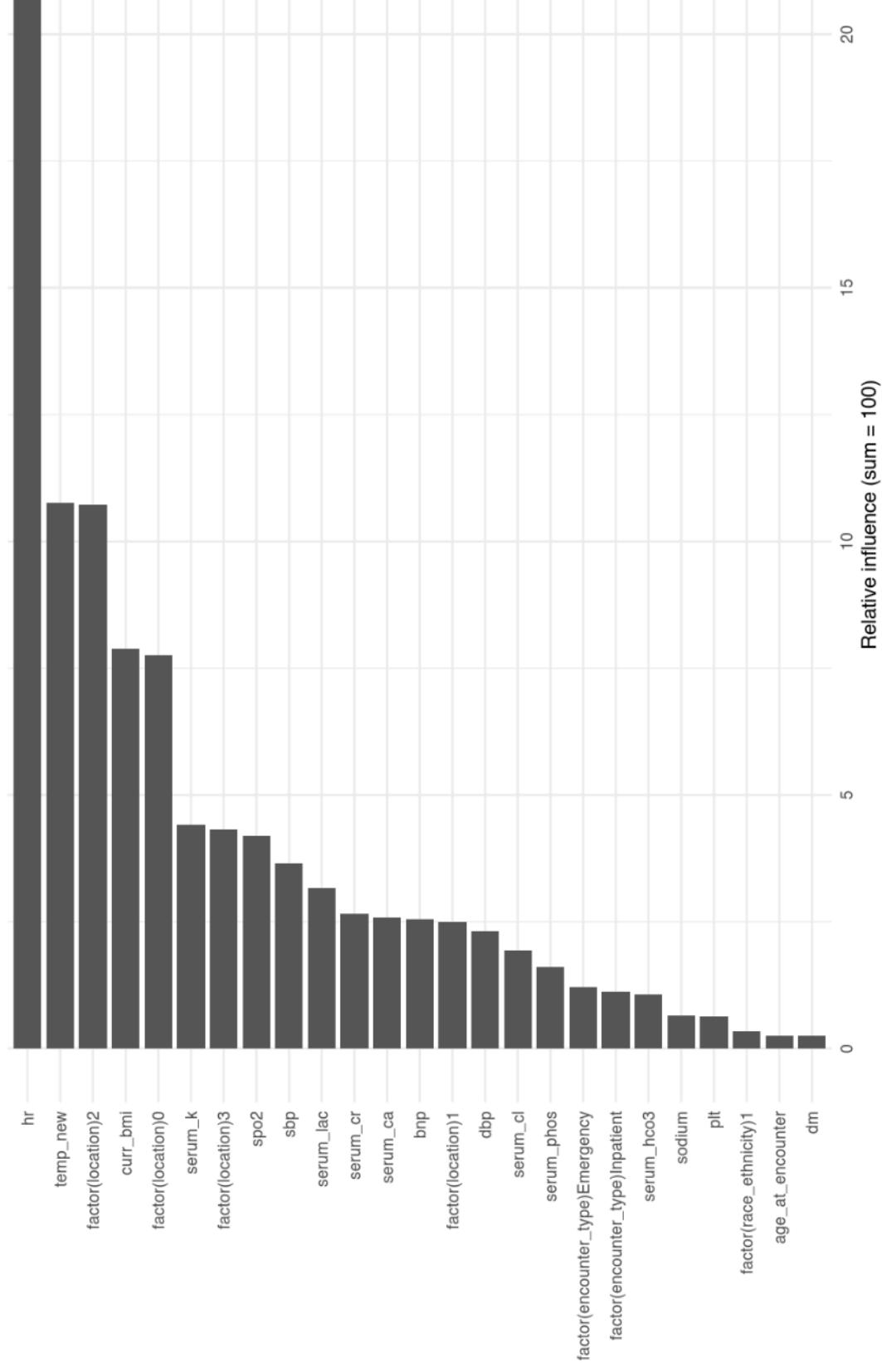
VBG-Calc

```
library(WeightIt); library(gbm); library(dplyr); library(ggplot2)

stopifnot(exists("w_vbg_calc", inherits = TRUE))
w_vbg_calc <- ensure_gbm_obj(w_vbg_calc)

imp_calc  <- extract_gbm_importance(w_vbg_calc, top_n = 25)
p_imp_calc <- plot_gbm_importance(imp_calc, "Calculated ABG selection model - GBM relative influence")
p_imp_calc
```

Calculated ABG selection model — GBM relative influence



```
library(shapviz); library(fastrshap)
```

```
t0 <- Sys.time()
```

```

sh_calc_fast <- compute_shap_fast(w_vbg_calc, top_k = 100, nsim = 32, frac_rows = 0.25, max_rows = 100000)
t1 <- Sys.time(); message(sprintf("[compute_shap_fast Calc-ABG] %.2f s", as.numeric(difftime(t1, t0, units="secs"))))

S_calc <- as.matrix(sh_calc_fast$shap)
X_calc <- as.data.frame(sh_calc_fast$X)

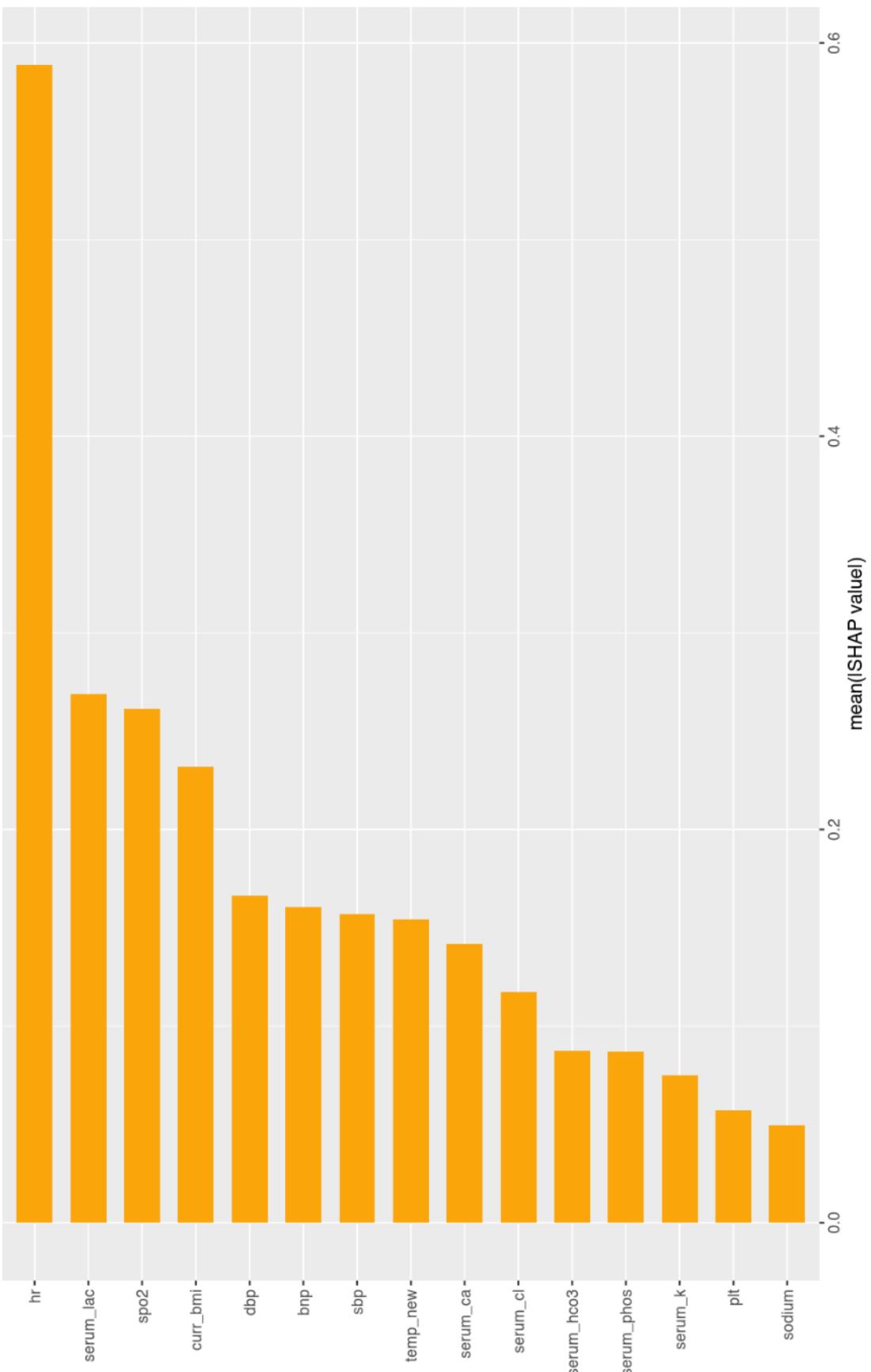
for (nm in names(X_calc)) {
  if (inherits(X_calc[[nm]], "haven_labelled")) X_calc[[nm]] <- labelled::to_factor(X_calc[[nm]])
  if (is.factor(X_calc[[nm]])) X_calc[[nm]] <- as.character(X_calc[[nm]])
  if (is.character(X_calc[[nm]])) suppressWarnings(X_calc[[nm]] <- as.numeric(X_calc[[nm]]))
}

if (is.null(colnames(S_calc)) colnames(S_calc) <- colnames(X_calc)
S_calc <- S_calc[, intersect(colnames(S_calc), colnames(X_calc)), drop = FALSE]
X_calc <- X_calc[, colnames(S_calc), drop = FALSE]

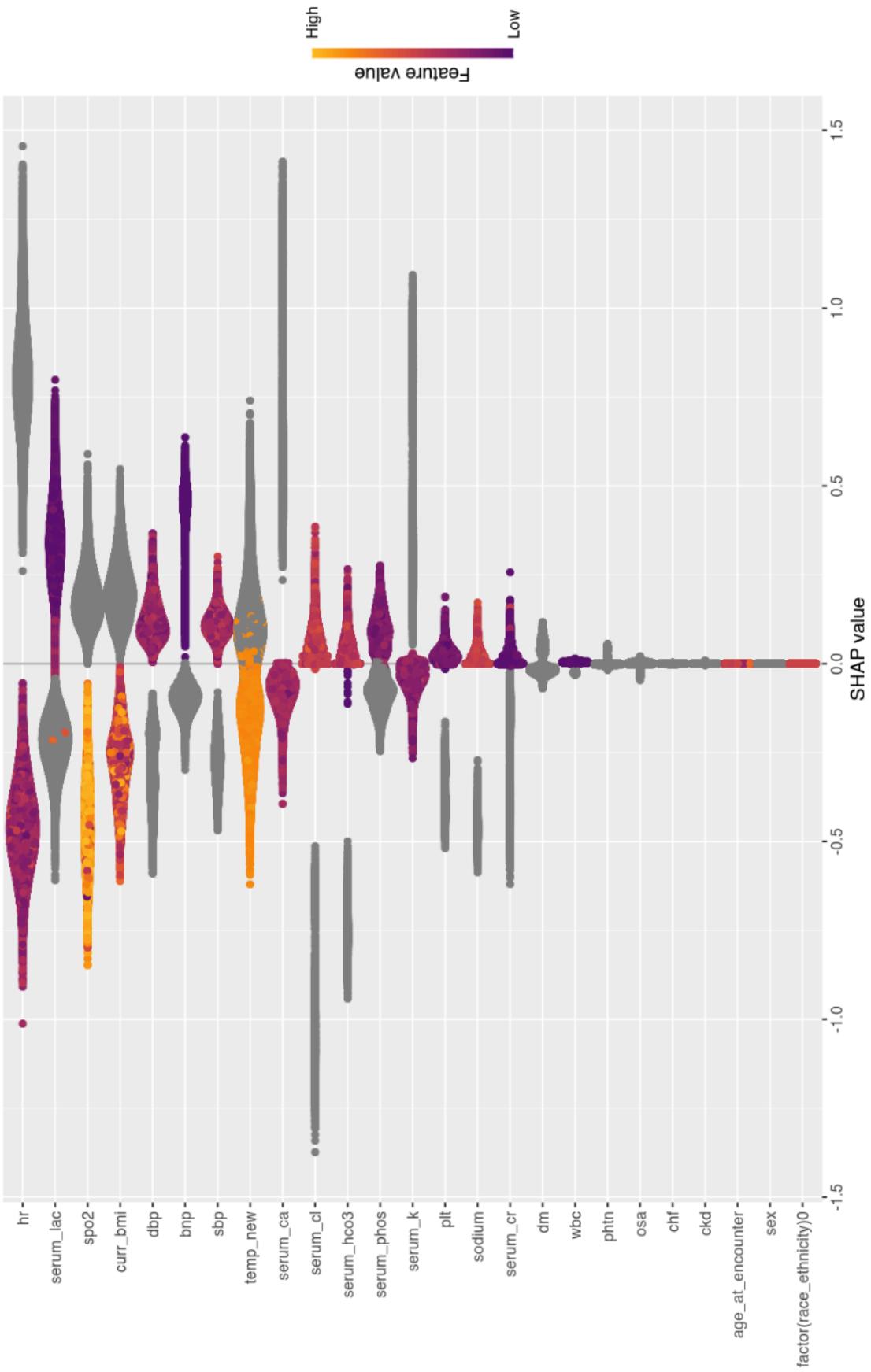
sv_calc <- shapviz::shapviz(S_calc, X = as.matrix(X_calc))

ord_calc <- order(colMeans(abs(S_calc), na.rm = TRUE), decreasing = TRUE)
topK_calc <- colnames(S_calc)[ord_calc[1:min(30, ncol(S_calc))]]
sv_importance(sv_calc, kind = "bar", v = topK_calc)

```



```
library(shapviz)
sv_importance(sv_calc, kind = "beeswarm", max_display = 25)
```



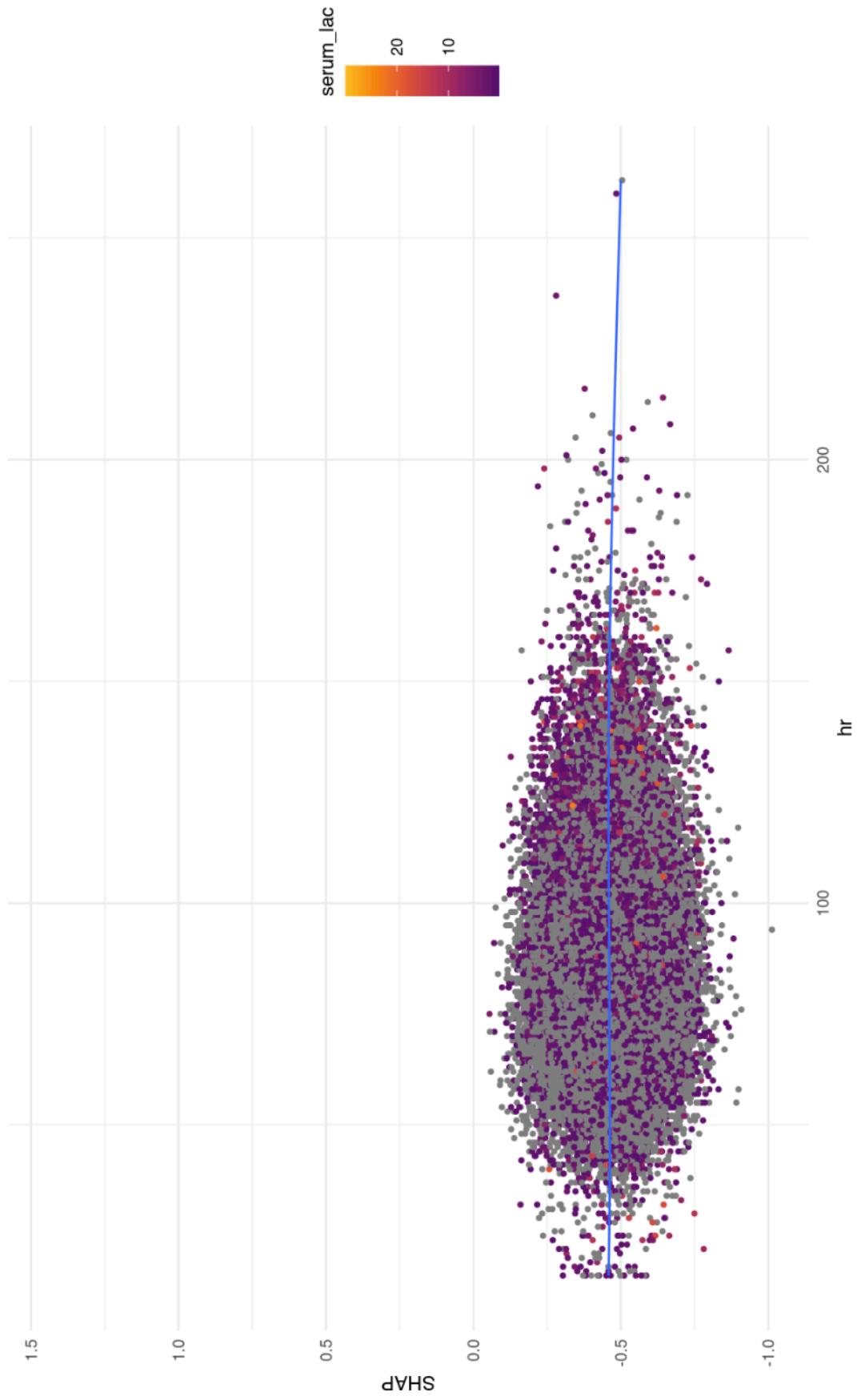
```
library(ggplot2)
```

```
imp_order_calc <- colnames(S_calc)[order(colMeans(abs(S_calc)), na.rm = TRUE), decreasing = TRUE)]
```

```
pri_calc <- imp_order_calc[1]
aux_calc <- imp_order_calc[2]
if (identical(aux_calc, pri_calc) || !(aux_calc %in% colnames(X_calc))) aux_calc <- imp_order_calc[3]

shapviz::sv_dependence(sv_calc, v = pri_calc, color_var = aux_calc, size = 1) +
  geom_smooth(se = FALSE, method = "loess", formula = y ~ x, linewidth = 0.6) +
  labs(title = sprintf("Calculated-ABG propensity - SHAP dependence: %s (color: %s)", pri_calc, aux_calc),
       x = pri_calc, y = "SHAP") +
  theme_minimal(base_size = 11)
```

Calculated-ABG propensity – SHAP dependence: hr (color: serum_lac)



```
library(shapviz); library(ggplot2); library(patchwork); library(grid)
```

```
stopifnot(is.matrix(S_calc), is.data.frame(X_calc))
```

```

ranked_calc <- colnames(S_calc)[order(colMeans(abs(S_calc)), na.rm = TRUE), decreasing = TRUE]
top5_calc <- head(ranked_calc, 5)
y_rng_calc <- range(unlist(lapply(top5_calc, function(v) S_calc[, v])), finite = TRUE)

theme_axes_compact <- function(show_y = FALSE, show_x = FALSE, base = 8) {
  theme_minimal(base_size = base) +
    theme(
      axis.title.y = if (show_y) element_text(size = base) else element_blank(),
      axis.text.y = if (show_y) element_text(size = base - 1) else element_blank(),
      axis.ticks.y = if (show_y) element_line(linewidth = 0.2) else element_blank(),
      axis.title.x = if (show_x) element_text(size = base) else element_blank(),
      axis.text.x = if (show_x) element_text(size = base - 1) else element_blank(),
      plot.title = element_text(size = base, hjust = 0),
      legend.title = element_text(size = base - 1),
      legend.text = element_text(size = base - 2),
      legend.key.height = unit(22, "pt"),
      legend.key.width = unit(3, "pt"),
      legend.margin = margin(0, 0, 0, "pt"),
      legend.box.margin = margin(0, 0, 0, "pt")
    )
}

cell_plot_calc <- function(v_row, v_col, i, j, n) {
  show_y <- (j == 1); show_x <- (i == n)
  if (identical(v_row, v_col)) {
    df <- data.frame(x = as.numeric(X_calc[[v_row]]), shape = as.numeric(S_calc[, v_row]))
    df <- df[is.finite(df$x) & is.finite(df$shape), , drop = FALSE]
    ggplot(df, aes(x = x, y = shape)) +
      geom_point(alpha = 0.30, size = 0.45, na.rm = TRUE) +
      scale_y_continuous(limits = y_rng_calc) +
      labs(title = v_row, x = v_row, y = "SHAP") +
      theme_axes_compact(show_y, show_x, base = 8) +
      theme(legend.position = "none")
  }
}

```

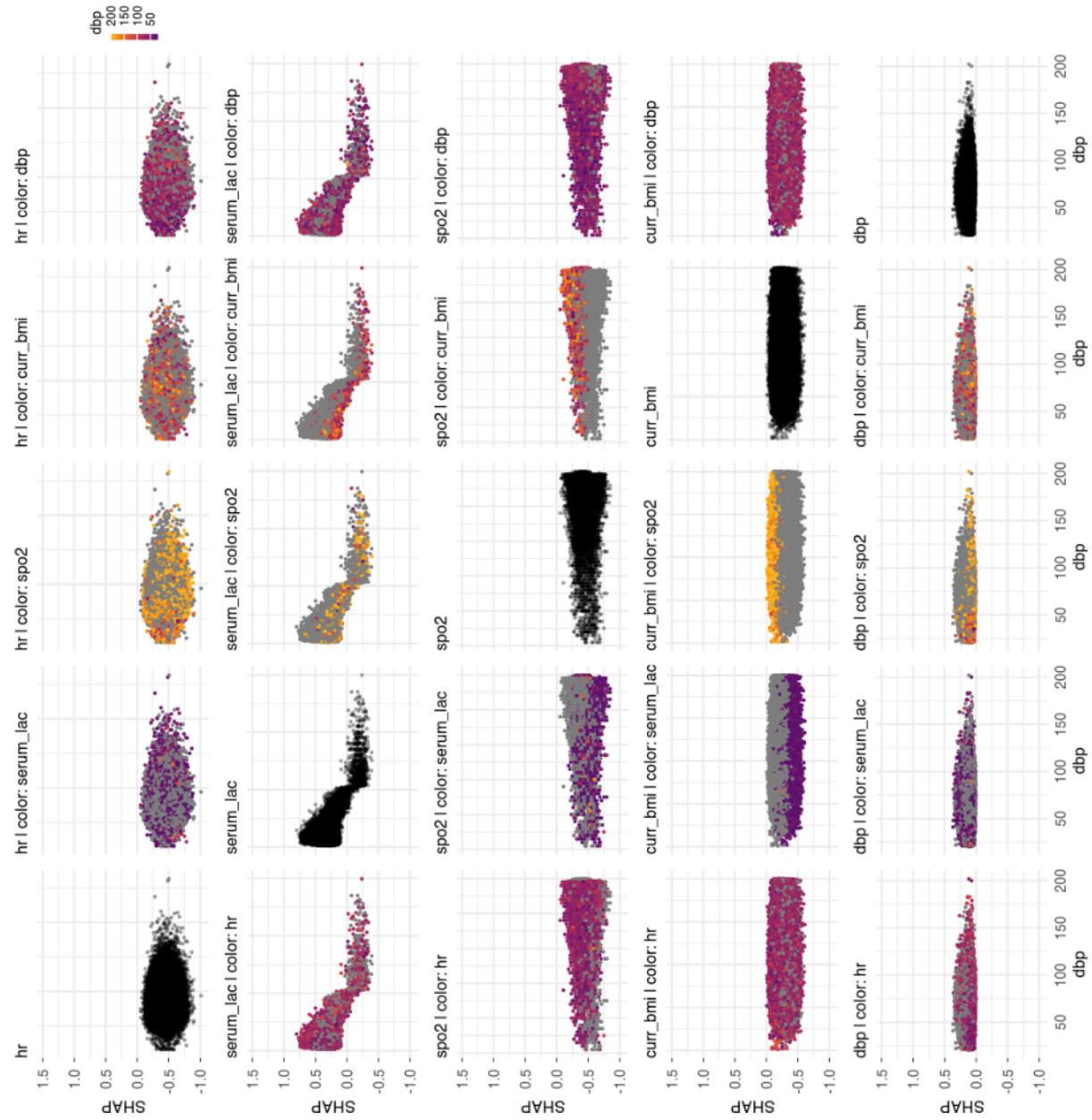
```

} else {
  keep_legend <- (i == 1 && j == length(top5_calc))
  shapviz::sv_dependence(sv_calc, v = v_row, color_var = v_col, size = 0.4) +
    scale_y_continuous(limits = y_rng_calc) +
    labs(title = paste0(v_row, " | color:", " ", v_col), x = v_row, y = "SHAP") +
    theme_axes_compact(show_y, show_x, base = 8) +
    guides(colour = guide_colorbar(barheight = unit(24, "pt"), barwidth = unit(3, "pt")),
           title.position = "top", title.hjust = 0.5, label.position = "right")) +
    theme(legend.position = if (keep_legend) "right" else "none")
}

n <- length(top5_calc); plots <- vector("list", n * n); k <- 1
for (i in seq_len(n)) for (j in seq_len(n)) {
  plots[[k]] <- cell_plot_calc(top5_calc[i], top5_calc[j], i, j, n); k <- k + 1
}
patchwork::wrap_plots(plots, ncol = n, guides = "keep") +
  plot_annotation(title = "Calculated-ABG propensity - Top-5 SHAP dependence (off-diagonal interactions, diagonal main effects"

```

Calculated-ABG propensity – Top-5 SHAP dependence (off-diagonal interactions, diagonal mask)



New weighted binary regression figures.

```
# IP-weighted odds-ratio plot (ABG, VBG, Calculated-ABG)
# - exact analogue of the un-weighted figure
#
# weights already attached earlier:
#   • w_abg      - propensity for *ABG* (column in subset_data)
#   • w_vbg      - propensity for *VBG* (column in subset_data)
#   • w_vbg_calc - same weights, used for calculated ABG CO

# 1. helper to fit an IP-weighted GLM and return tidy OR -----
tidy_ipw <- function(data, outcome, exposure, weight_var,
                      group_label, outcome_label) {
  des <- svydesign(ids = ~1, weights = as.formula(paste0("~", weight_var)),
                   data = data)

  mod <- svyglm(
    as.formula(paste0(outcome, " ~ ", exposure)),
    design = des,
    family = quasibinomial()
  )

  tidy(mod, exponentiate = TRUE, conf.int = TRUE) %>%
    filter(term == exposure) %>%
    mutate(group = group_label, outcome = outcome_label)
}

# 2. cohort-specific data frames -----
abg_df <- subset_data %>% filter(has_abg == 1)
vbg_df <- subset_data %>% filter(has_vbg == 1)
calc_df <- subset_data %>% filter(!is.na(calc_abg)) # implies VBG present

# 3. fit models & collect estimates -----
ipw_estimates <- bind_rows(
```

```

# ABC
tidy_ipw(abg_df, "imv_proc",
tidy_ipw(abg_df, "niv_proc",
tidy_ipw(abg_df, "death_60d",
tidy_ipw(abg_df, "hypercap_resp_failure",
tidy_ipw(abg_df, "hypercap_on_abg",
tidy_ipw(vbg_df, "imv_proc",
tidy_ipw(vbg_df, "niv_proc",
tidy_ipw(vbg_df, "death_60d",
tidy_ipw(vbg_df, "hypercap_resp_failure",
tidy_ipw(vbg_df, "hypercap_on_vbg",
tidy_ipw(calc_df, "imv_proc",
tidy_ipw(calc_df, "niv_proc",
tidy_ipw(calc_df, "death_60d",
tidy_ipw(calc_df, "hypercap_resp_failure",
)
# Calculated ABG
tidy_ipw(calc_df, "hypercapnia_calc",
tidy_ipw(calc_df, "hypercapnia_calc",
tidy_ipw(calc_df, "hypercapnia_calc",
tidy_ipw(calc_df, "hypercapnia_calc",
)
# 4. plotting -
ipw_estimates$group <- factor(
  ipw_estimates$group,
  levels = c("ABG", "VBG", "Calculated ABG")
)

```

```

ggplot(
  ipw_estimates,
  aes(
    x = outcome,
    y = estimate,
    ymin = conf.low,
    ymax = conf.high,
    color = group
  )
)

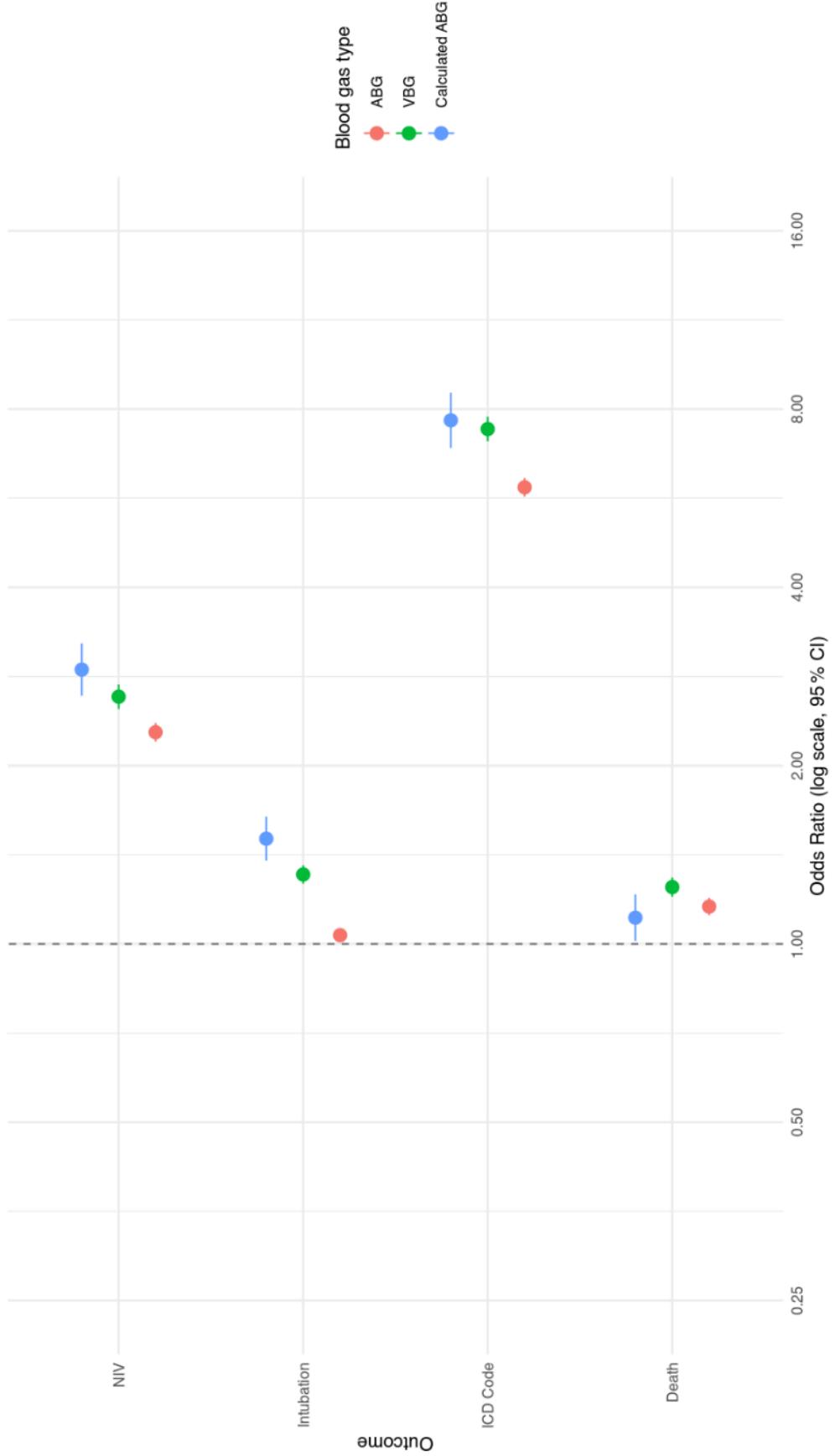
```

```

) +
  geom_pointrange(position = position_dodge(width = 0.6), size = 0.6) +
  geom_hline(yintercept = 1, linetype = "dashed", colour = "grey40") +
  scale_y_log10(
    breaks = c(0.25, 0.5, 1, 2, 4, 8, 16),
    limits = c(0.25, 16),
    labels = number_format(accuracy = 0.01)
  ) +
  coord_flip() +
  labs(
    title = "IP Weighted Odds Ratio of Outcomes When Hypercapnia Present",
    x = "Outcome",
    y = "Odds Ratio (log scale, 95 % CI)",
    color = "Blood gas type",
    caption = paste(
      "Inverse-probability weights adjust for covariates associated with receiving each blood-gas.",
      "Models are fitted within their respective cohorts:",
      "ABG (weights=w_abg), VBG (w_vbg), Calculated ABG (w_vbg_calc).",
      "Numerator = hypercapnic; denominator = normocapnic within cohort.",
      sep = "\n"
    )
  ) +
  theme_minimal(base_size = 10) +
  theme(plot.caption = element_text(hjust = 0))

```

IP Weighted Odds Ratio of Outcomes When Hypercapnia Present



Three Groups with Weights

```

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

# 1. Create PCO categories
subset_data <- subset_data %>%
  mutate(
    pco2_cat_abg = case_when(
      !is.na(paco2) & paco2 < 35 ~ "Below normal",
      !is.na(paco2) & paco2 >= 35 & paco2 <= 45 ~ "Normal",
      !is.na(paco2) & paco2 > 45 ~ "Above normal",
      TRUE ~ NA_character_
    ),
    pco2_cat_vbg = case_when(
      !is.na(vbg_co2) & vbg_co2 < 35 ~ "Below normal",
      !is.na(vbg_co2) & vbg_co2 >= 35 & vbg_co2 <= 50 ~ "Normal",
      !is.na(vbg_co2) & vbg_co2 > 50 ~ "Above normal",
      TRUE ~ NA_character_
    ),
    pco2_cat_calc = case_when(
      !is.na(calc_abg) & calc_abg < 35 ~ "Below normal",
      !is.na(calc_abg) & calc_abg >= 35 & calc_abg <= 45 ~ "Normal",
      !is.na(calc_abg) & calc_abg > 45 ~ "Above normal",
      TRUE ~ NA_character_
    )
  )
}

# 2. Function: weighted logistic regression & OR extraction
run_weighted_or <- function(data, outcome, cat_var, weight_var, group_name) {
  dat <- data %>%
    filter(
      !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 = c("Normal", "Below normal", "Above normal"))
) %>%
droplevels()

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

fit <- svyglm(as.formula(paste(outcome, "~", cat_var)),
  design = design, family = quasibinomial())
tidy(fit, exponentiate = TRUE, conf.int = TRUE) %>%
filter(term != "(Intercept)") %>%
mutate(
  group = group_name,
  outcome = outcome,
  exposure = gsub(paste0(cat_var, "", term) %>%
  gsub(~, "", .))
)
}

# 3. Run across outcomes & cohorts
outcomes <- c("imv_proc", "niv_proc", "death_60d", "hypercap_resp_failure")
combined_or_df <- bind_rows(
  lapply(outcomes, function(out)

```

```

run_weighted_or(subset_data, out, "pco2_cat_abg", "w_abg", "ABG"),
lapply(outcomes, function(out)
run_weighted_or(subset_data, out, "pco2_cat_vbg", "w_vbg", "VBG"),
lapply(outcomes, function(out)
run_weighted_or(subset_data, out, "pco2_cat_calc", "w_vbg_calc", "Calculated ABG"))
)

# Ensure nice ordering
combined_or_df$group <- factor(combined_or_df$group,
levels = c("ABG", "VBG", "Calculated ABG"))

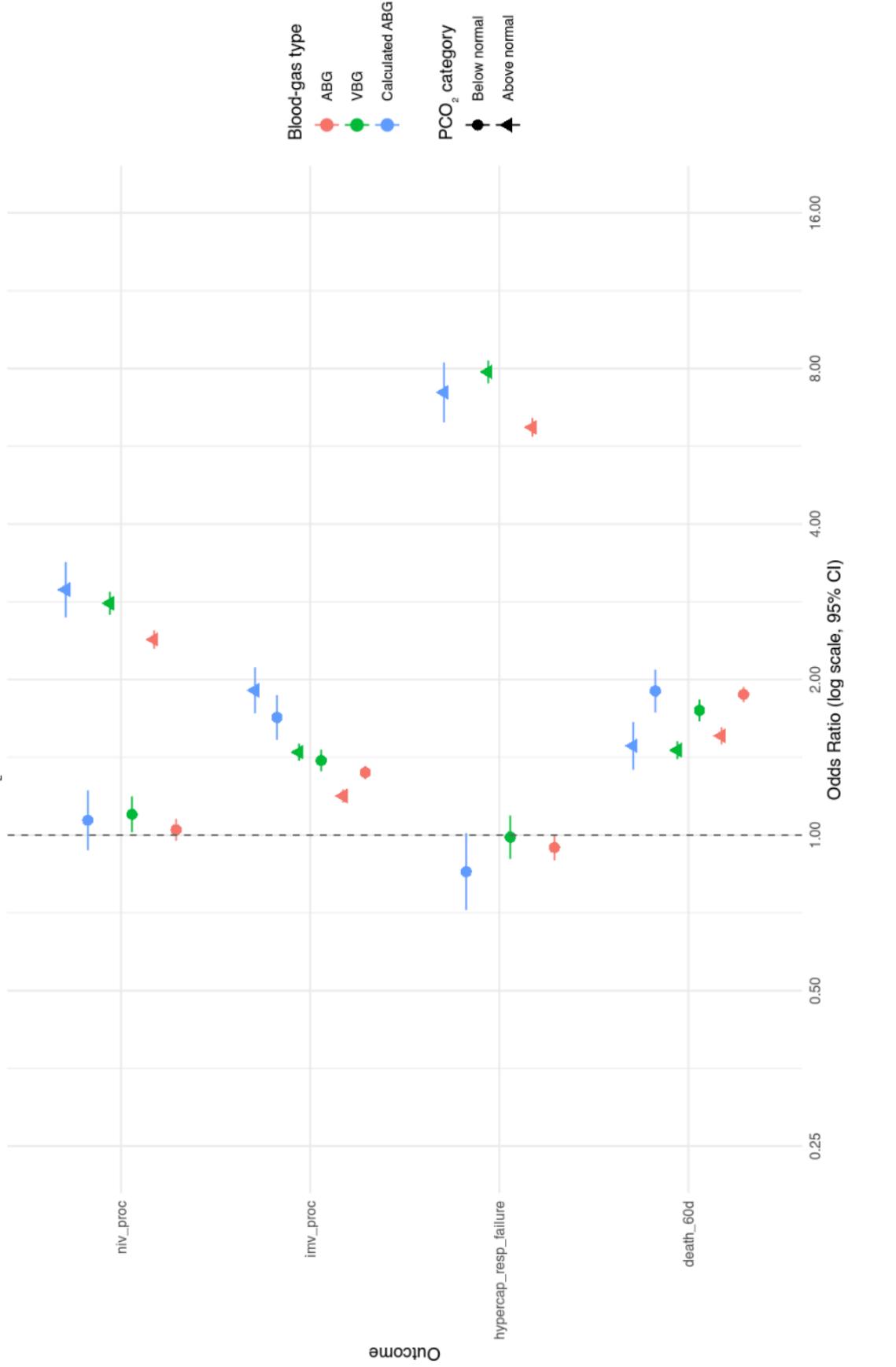
combined_or_df$exposure <- factor(combined_or_df$exposure,
levels = c("Below normal", "Above normal"))

# 4. Plot weighted odds ratios
ggplot(
  combined_or_df,
  aes(
    x = outcome,
    y = estimate,
    ymin = conf.low,
    ymax = conf.high,
    color = group,
    shape = exposure
  )
) +
  geom_pointrange(position = position_dodge(width = 0.7), size = 0.6) +
  geom_hline(yintercept = 1, linetype = "dashed", colour = "grey40") +
  scale_y_log10(
    breaks = c(0.25, 0.5, 1, 2, 4, 8, 16),
    limits = c(0.25, 16),
    labels = number_format(accuracy = 0.01)
  ) +
  coord_flip() +
  labs(

```

```
title = "Weighted Odds Ratios of Outcomes by PCO Category (ABG, VBG, Calc ABG)" ,  
x = "Outcome",  
y = "Odds Ratio (log scale, 95% CI)",  
color = "Blood-gas type",  
shape = "PCO category"  
) +  
theme_minimal(base_size = 10) +  
theme(plot.caption = element_text(hjust = 0))
```

Weighted Odds Ratios of Outcomes by PCO₂ Category (ABG, VBG, Calc ABG)



Plotting propensity scores

```

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

library(dplyr)
library(ggplot2)
library(scales)

# Resolve WeightIt objects regardless of naming used upstream
w_abg_obj <- if (exists("w_abg")) w_abg else if (exists("weight_model")) weight_model else NULL
w_vbg_obj <- if (exists("w_vbg")) w_vbg else NULL
w_vbg_calc_obj <- if (exists("w_vbg_calc")) w_vbg_calc else if (exists("w_vbg")) w_vbg else NULL

if (is.null(w_abg_obj)) stop("ABG WeightIt object not found. Define `w_abg` or `weight_model` before this block.")
if (!"has_abg" %in% names(subset_data)) stop("`subset_data` must contain `has_abg` for ABG PS plotting.")

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

if (!is.null(w_vbg_obj) && "has_vbg" %in% names(subset_data)) {
  ps_dfs$VBG <- data.frame(
    ps      = w_vbg_obj$ps,
    treat   = subset_data$has_vbg,
    ScoreType = "VBG"
  )
}

} else if (is.null(w_vbg_obj)) {
  message("Note: VBG WeightIt object `w_vbg` not found; skipping VBG panel.")
}

```

```

# Calculated ABG uses the VBG selection model; prefer a dedicated `w_vbg_calc` if present
if (!is.null(w_vbg_calc_obj) && "has_vbg_co2_o2_sat" %in% names(subset_data)) {
  psdfs$CalcABG <- data.frame(
    ps      = w_vbg_calc_obj$ps,
    treat   = subset_data$has_vbg_co2_o2_sat,
    ScoreType = "Calculated ABG"
  )
} else if (is.null(w_vbg_calc_obj)) {
  message("Note: Calculated-ABG WeightIt object `w_vbg_calc` (or fallback `w_vbg`) not found; skipping Calc-ABG panel.")
}

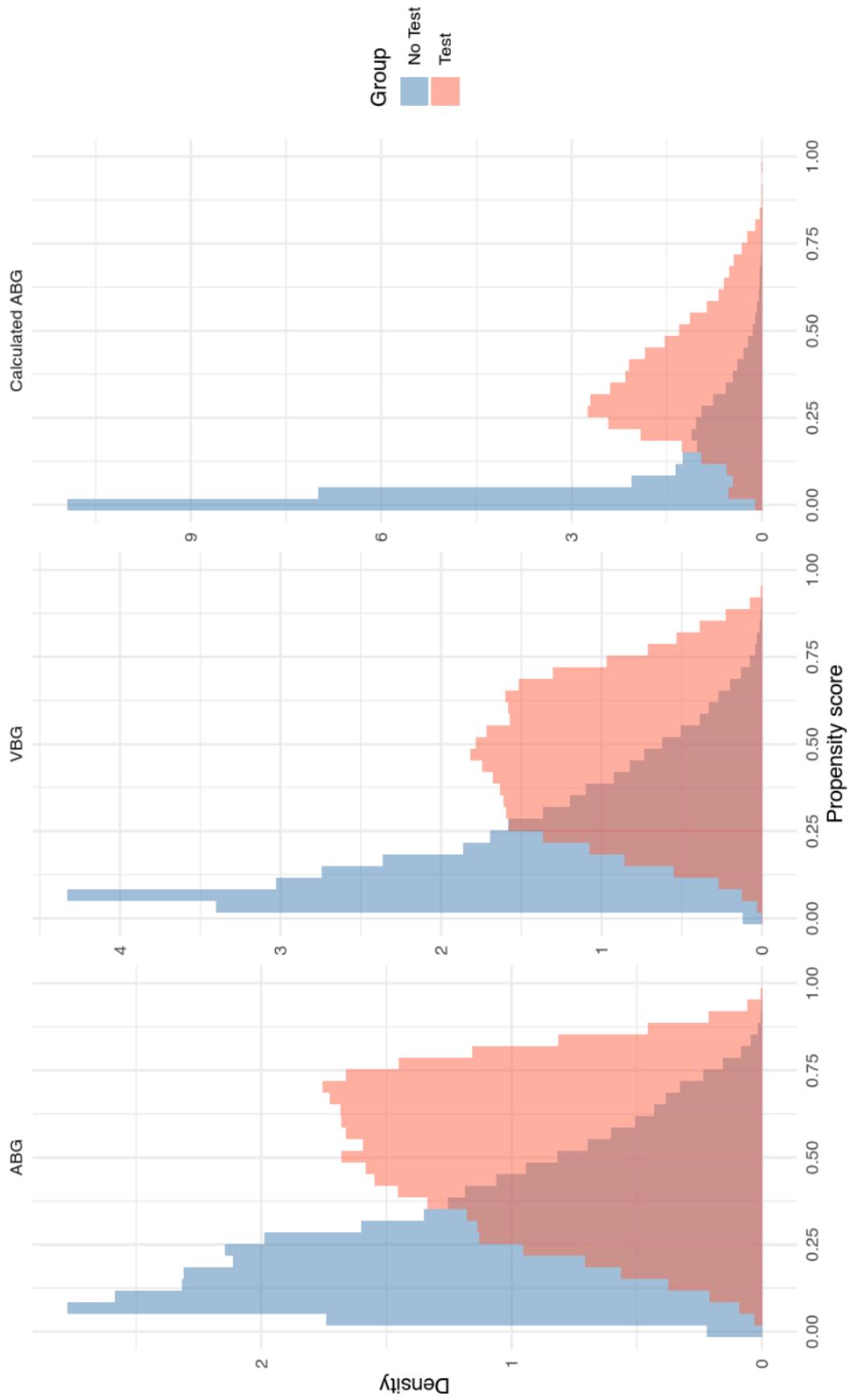
# Bind, clean, and factorize for plotting
df_ps <- bind_rows(psdfs) %>%
  filter(!is.na(ps), !is.na(treat)) %>%
  mutate(
    treat   = factor(treat, levels = c(0, 1), labels = c("No Test", "Test")),
    ScoreType = factor(ScoreType, levels = c("ABG", "VBG", "Calculated ABG"))
  )

# Plot
ggplot(df_ps, aes(x = ps, fill = treat)) +
  geom_histogram(aes(y = ..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)

```

Warning: The dot-dot notation (`..density..`) was deprecated in ggplot2 3.4.0.
i Please use `after_stat(density)` instead.

Propensity Score Distributions



```

df_ps <- bind_rows(
  data.frame(
    ps      = w_abg$ps,
    treat   = subset_data$has_abg,
    ScoreType = "ABG"
  ),
  data.frame(
    ps      = w_vbg$ps,
    treat   = subset_data$has_vbg,
    ScoreType = "VBG"
  ),
  data.frame(
    ps      = w_vbg_calc$ps,
    treat   = subset_data$has_vbg_co2_o2_sat,
    ScoreType = "Calculated ABG"
  )
) %>%
  mutate(
    treat = factor(treat, levels = c(0,1), labels = c("No Test", "Test"))
  )

ggplot(df_ps, aes(x = ps, fill = treat)) +
  geom_histogram(aes(y = ..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

