Supplement 2

Sites of pain

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Contents

Note: Sites RBP and RISI removed at data cleaning stage because n < 10.

Import and check data

```
# Import
data <- read_rds('data-cleaned/data-pain-sites.rds')
demo <- read_rds('data-cleaned/data-demographics.rds')

# Check
## Pain sites
dim(data)
```

```
## [1] 595  20
```

```
names(data)
```

```
##  [1] "ID"                "Head"              "Throat"
##  [4] "Shoulder"          "Arms"              "Elbows"
##  [7] "Wrists.Hands"      "Chest"             "Upper_back"
## [10] "Lower_back"        "Abdomen"           "Cervical_spine"
## [13] "Thoracic_spine"    "Lumbosacral_spine" "Groin"
## [16] "Hips"              "Legs"              "Knees"
## [19] "Ankles.Feet"       "Buttocks"
```

```
glimpse(data)
```

```
## Rows: 595
## Columns: 20
## $ ID                <chr> "RPB73", "RPB74", "RPB75", "RPB76", "RPB77", "RPB...
## $ Head              <chr> "No", "No", "No", "Yes", "Yes", "No", "No", "No",...
## $ Throat            <chr> "No", "No", "No", "No", "No", "No", "No", "No", "...
## $ Shoulder          <chr> "No", "No", "No", "No", "No", "No", "No", "No", "...
## $ Arms              <chr> "No", "No", "No", "No", "No", "No", "No", "No", "...
## $ Elbows            <chr> "No", "No", "No", "No", "No", "No", "No", "No", "...
## $ Wrists.Hands      <chr> "No", "No", "No", "No", "No", "No", "No", "No", "...
## $ Chest             <chr> "No", "No", "No", "Yes", "No", "No", "No", "No", ...
## $ Upper_back        <chr> "No", "No", "No", "No", "No", "No", "No", "No", "...
## $ Lower_back        <chr> "No", "No", "No", "No", "No", "No", "No", "No", "...
## $ Abdomen           <chr> "No", "No", "Yes", "Yes", "No", "No", "Yes", "No"...
## $ Cervical_spine    <chr> "No", "No", "No", "No", "No", "No", "No", "No", "...
## $ Thoracic_spine    <chr> "No", "No", "No", "No", "No", "No", "No", "No", "...
## $ Lumbosacral_spine <chr> "No", "No", "No", "No", "No", "No", "No", "No", "...
## $ Groin             <chr> "No", "No", "No", "No", "No", "No", "No", "No", "...
## $ Hips              <chr> "No", "No", "No", "No", "No", "No", "No", "Yes", ...
## $ Legs              <chr> "No", "No", "No", "No", "No", "Yes", "No", "Yes",...
## $ Knees             <chr> "No", "No", "No", "No", "No", "Yes", "No", "Yes",...
## $ Ankles.Feet       <chr> "No", "No", "No", "No", "No", "Yes", "No", "Yes",...
## $ Buttocks          <chr> "No", "No", "No", "No", "No", "No", "No", "Yes", ...
```

```
## Demographics
dim(demo)
```

```
## [1] 595   7
```

```
names(demo)
```

```
## [1] "ID"                "Sex"               "Age"
## [4] "Employment_status" "CD4_recent"        "ART_currently"
## [7] "Education"
```

```
glimpse(demo)
```

```
## Rows: 595
## Columns: 7
## $ ID                <chr> "RPB73", "RPB74", "RPB75", "RPB76", "RPB77", "RPB...
## $ Sex               <chr> "Female", "Female", "Female", "Female", "Female",...
## $ Age               <dbl> 36, 27, 39, 36, 31, 32, 28, 37, 31, 25, 31, 24, 3...
## $ Employment_status <chr> "Other", "Unemployed", "Other", "Unemployed", "Un...
## $ CD4_recent        <dbl> 391, 571, 591, 207, 126, 225, 543, 410, 74, 212, ...
## $ ART_currently     <chr> "Yes", "Yes", "Yes", "Yes", "Yes", "Yes", "Yes", ...
## $ Education         <chr> "Tertiary", "Secondary", "Secondary", "Primary", ...
```

Basic descriptive statistics

Pain sites

```
data %>%
    select(-ID) %>%
    mutate_if(is.character, factor) %>%
    skim()
```

Table 1: Data summary

Name	Piped data
Number of rows	595
Number of columns	19
Column type frequency:	
factor	19
Group variables	None

Variable type: factor

skim_variable	n_missing	complete_rate	n_unique	top_counts
Head	0	1	2	No: 401, Yes: 194
Throat	0	1	2	No: 576, Yes: 19
Shoulder	0	1	2	No: 547, Yes: 48
Arms	0	1	2	No: 570, Yes: 25
Elbows	0	1	2	No: 573, Yes: 22
Wrists.Hands	0	1	2	No: 560, Yes: 35
Chest	0	1	2	No: 479, Yes: 116
Upper_back	0	1	1	No: 595
Lower_back	0	1	2	No: 552, Yes: 43
Abdomen	0	1	2	No: 435, Yes: 160
Cervical_spine	0	1	2	No: 566, Yes: 29
Thoracic_spine	0	1	2	No: 522, Yes: 73
Lumbosacral_spine	0	1	2	No: 505, Yes: 90

skim_variable	n_missing	complete_rate	n_unique	top_counts
Groin	0	1	2	No: 541, Yes: 54
Hips	0	1	2	No: 556, Yes: 39
Legs	0	1	2	No: 497, Yes: 98
Knees	0	1	2	No: 512, Yes: 83
Ankles.Feet	0	1	2	No: 412, Yes: 183
Buttocks	0	1	2	No: 576, Yes: 19

Demographics

```
demo %>%
    select(-ID) %>%
    mutate_if(is.character, factor) %>%
    skim()
```

Table 3: Data summary

Name	Piped data
Number of rows	595
Number of columns	6
_____	
Column type frequency:	
factor	4
numeric	2
_____	
Group variables	None

Variable type: factor

skim_variable	n_missing	complete_rate	n_unique	top_counts
Sex	0	1.00	2	Fem: 479, Mal: 116
Employment_status	49	0.92	4	Une: 329, Ful: 131, Par: 52, Oth: 34
ART_currently	5	0.99	2	Yes: 459, No: 131
Education	37	0.94	3	Sec: 393, Pri: 100, Ter: 65

Variable type: numeric

skim_variable	n_missing	complete_rate	mean	sd	p0	p25	p50	p75	p100
Age	8	0.99	37.31	9.06	19	31	36.0	42.00	76
CD4_recent	99	0.83	337.17	400.32	1	155	261.5	437.75	7300

Boostrap functions

```
# Proportion
prop_func <- function(d, i){
```

```
    dat <- d[i, ]
    dat_vec <- dat[[1]]
    dat_prop <- mean(dat_vec == 'Yes')
    dat_prop
}
```

Proportion point estimates with 95% CIs

Process data

```
# Set seed
set.seed(2020)

# Remove ID and upper_back (only one outcome -- no pain) columns
prop <- data[, !(names(data) %in% c('ID', 'Upper_back'))]

# Bootstrap CIs
prop_boot <- prop %>%
    # Pivot to long format
    pivot_longer(cols = everything(),
                 names_to = 'site',
                 values_to = 'pain_present') %>%
    # Add body regions
    mutate(region = case_when(
        site == 'Chest' |
            site == 'Head' |
            site == 'Throat' |
            site == 'Shoulder' ~ 'Head and upper torso',
        site == 'Lower_back' |
            site == 'Abdomen' |
            site == 'Hips' |
            site == 'Buttocks' |
            site == 'Groin' ~ 'Lower torso',
        site == 'Legs' |
            site == 'Knees' |
            site == 'Ankles.Feet' ~ 'Lower limbs',
        site == 'Arms' |
            site == 'Elbows' |
            site == 'Wrists.Hands' ~ 'Upper limbs',
        site == 'Cervical_spine' |
            site == 'Thoracic_spine' |
            site == 'Lumbosacral_spine' ~ 'Spinal column',
        TRUE ~ 'other'
    )) %>%
    # Nest by body region and body site
    group_by(region, site) %>%
    nest() %>%
    # Boostrap data
    mutate(boot = map(.x = data,
```

```
                    ~ boot(data = .x,
                           statistic = prop_func,
                           R = 999,
                           stype = 'i',
                           parallel = 'multicore',
                           ncpus = 4))) %>%
    # Get CI
    mutate(ci = map(.x = boot,
                    ~ boot.ci(.x, type = 'perc'))) %>%
    # Extract ci data
    mutate(point_est = map(.x = ci,
                           ~ .x$t0),
           lower_ci = map(.x = ci,
                          ~ .x$percent[[4]]),
           upper_ci = map(.x = ci,
                          ~ .x$percent[[5]])) %>%
    # Remove columns
    select(-data, -boot, -ci) %>%
    # Unnest
    unnest(cols = c(point_est, lower_ci, upper_ci))

# Re-nest by body region and generate figures and tables
prop_boot2 <- prop_boot %>%
    group_by(region) %>%
    nest() %>%
    # Fix site labels
    mutate(data = map(.x = data,
                      ~ .x %>%
                          mutate(site = str_replace_all(site,
                                                        pattern = '_',
                                                        replacement = ' '),
                                 site = str_replace_all(site,
                                                        pattern = '\\.',
                                                        replacement = ' & ')))) %>%
    # Re-order sites by point_est
    mutate(data = map(.x = data,
                      ~ .x %>%
                          mutate(site = fct_reorder(site,
                                                    point_est)))) %>%
    # Plot data
    mutate(plots = map2(.x = data,
                        .y = region,
                        ~ .x %>%
                            ggplot(data = .) +
                            aes(x = site,
                                y = point_est,
                                ymin = lower_ci,
                                ymax = upper_ci) +
                            geom_linerange(size = 1) +
                            geom_point(size = 6) +
                            coord_flip() +
                             labs(title = .y,
                                  subtitle = '(Point estimate with 95%CI)',
```

```
                              y = 'Proportion with pain') +
                         scale_y_continuous(limits = c(0, 1)) +
                         theme_minimal(base_size = 18) +
                         theme(plot.title = element_text(size = 18),
                               plot.subtitle = element_text(size = 12),
                               axis.title.y = element_blank(),
                               panel.grid = element_blank(),
                               axis.text = element_text(colour = '#000000'),
                               axis.line = element_line(size = 0.5),
                               axis.ticks = element_line(size = 0.5)))) %>%
    # Tabulate data
    mutate(tables = map2(.x = data,
                         .y = region,
                         ~ .x %>%
                             kable(caption = .y,
                                   digits = 2)))
```

Tabulated proportions (with 95% CIs), by body region

```
walk(prop_boot2$tables, ~ print(.x))
```

Table 6: Head and upper torso

site	point_est	lower_ci	upper_ci
Head	0.33	0.29	0.37
Throat	0.03	0.02	0.05
Shoulder	0.08	0.06	0.10
Chest	0.19	0.16	0.23

Table 7: Upper limbs

site	point_est	lower_ci	upper_ci
Arms	0.04	0.03	0.06
Elbows	0.04	0.02	0.05
Wrists & Hands	0.06	0.04	0.08

Table 8: Lower torso

site	point_est	lower_ci	upper_ci
Lower back	0.07	0.05	0.09
Abdomen	0.27	0.23	0.30
Groin	0.09	0.07	0.12
Hips	0.07	0.05	0.09
Buttocks	0.03	0.02	0.05

Table 9: Spinal column

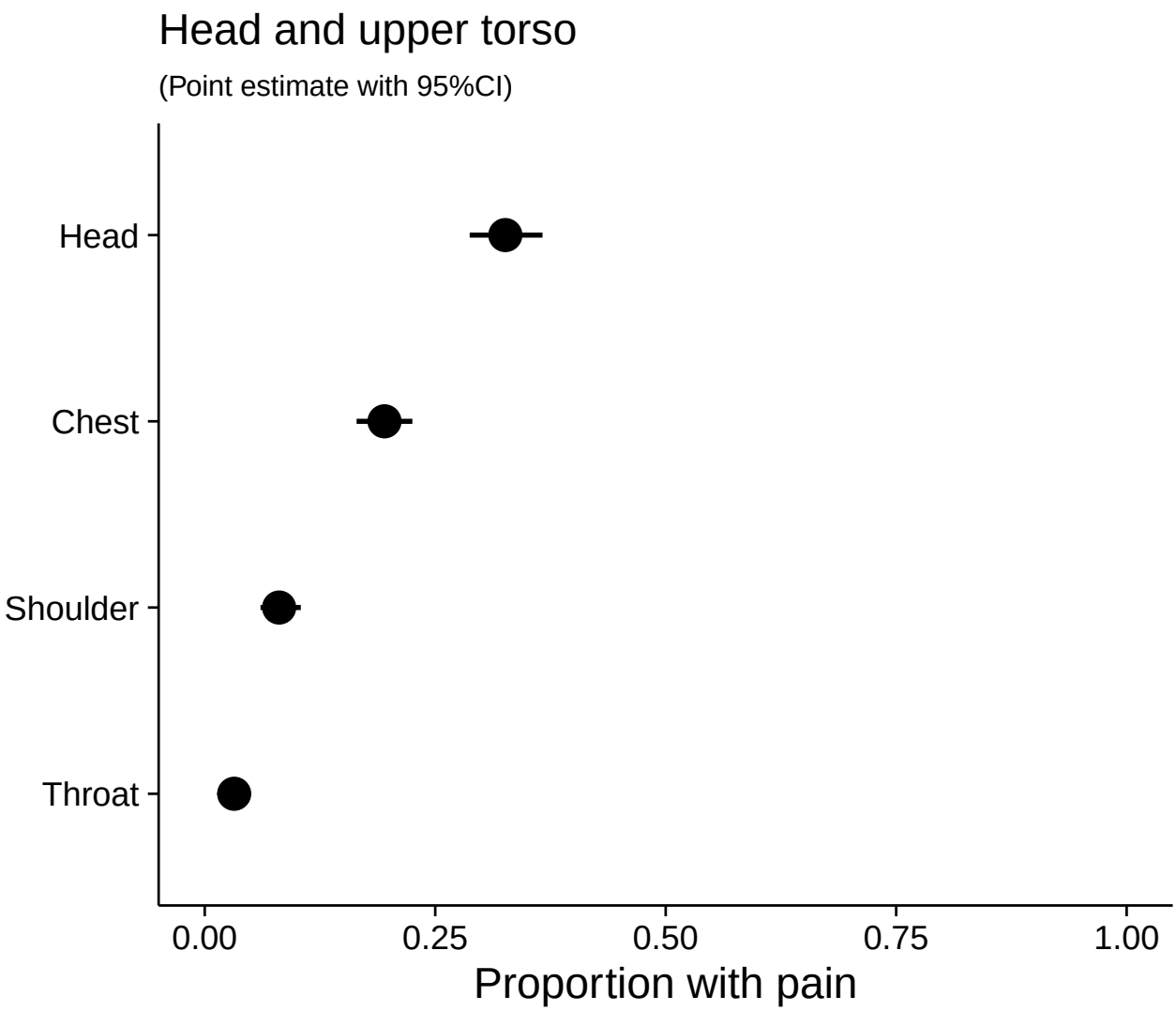
site	point_est	lower_ci	upper_ci
Cervical spine	0.05	0.03	0.07
Thoracic spine	0.12	0.10	0.15
Lumbosacral spine	0.15	0.12	0.18

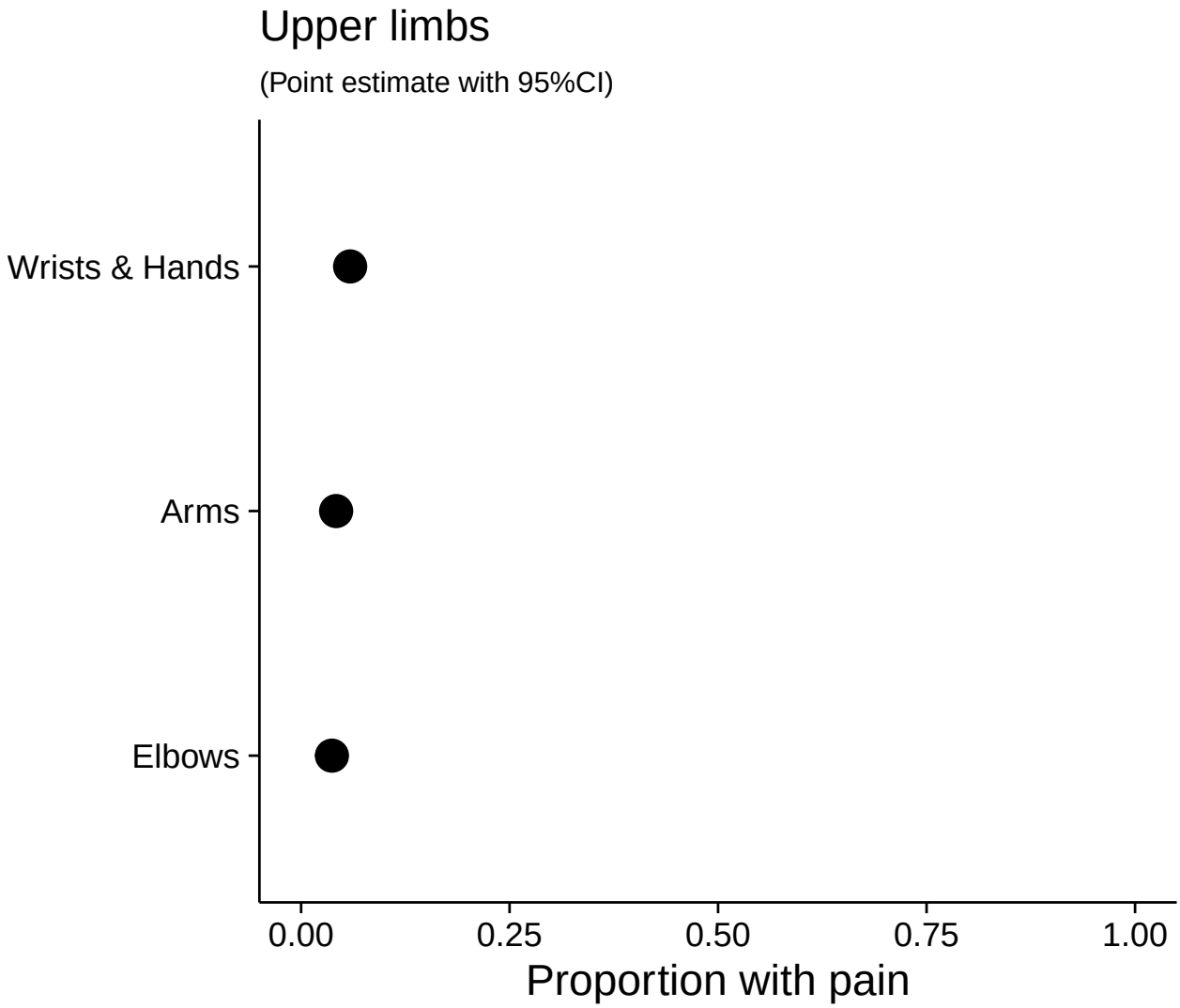
Table 10: Lower limbs

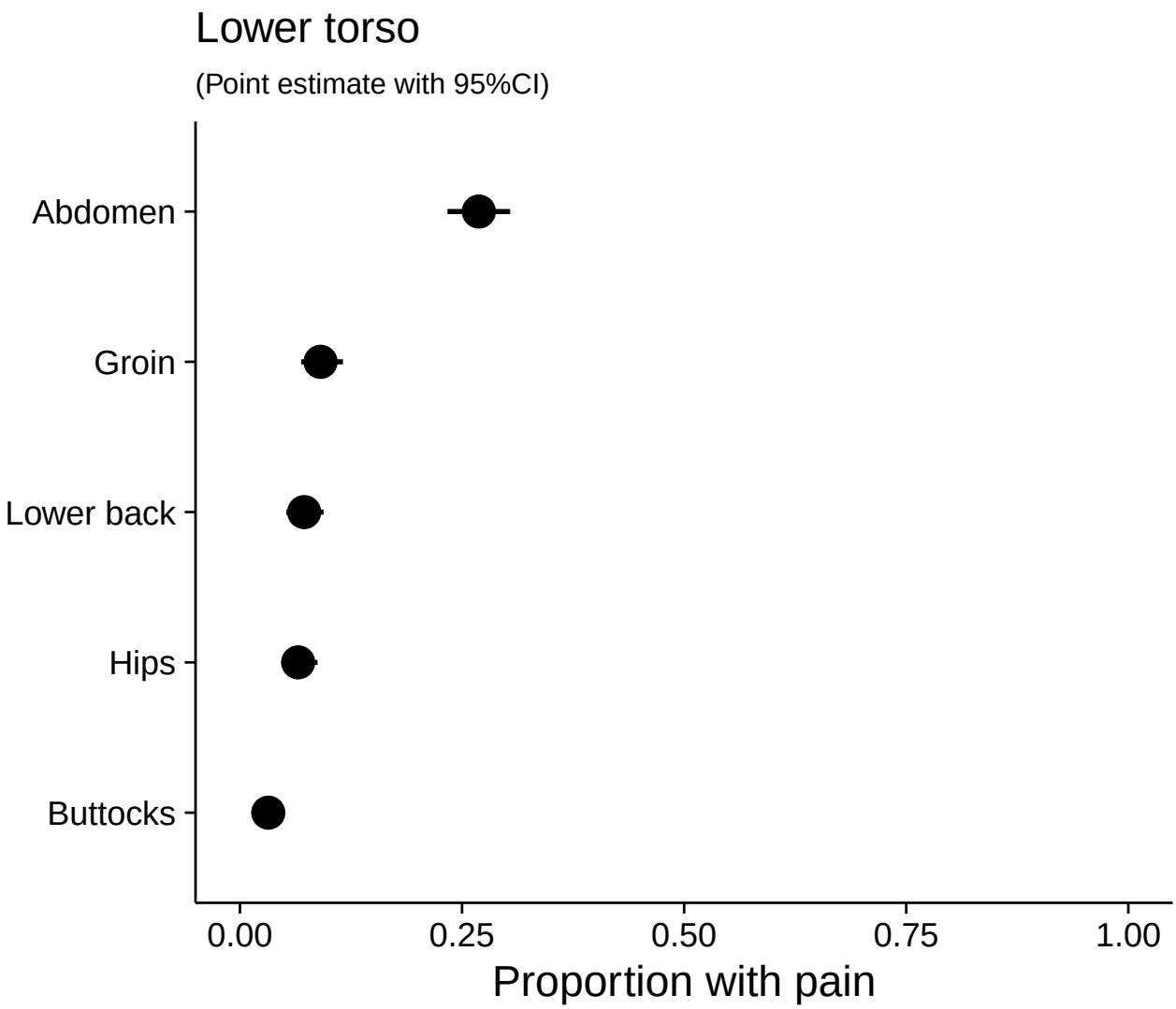
site	point_est	lower_ci	upper_ci
Legs	0.16	0.13	0.20
Knees	0.14	0.11	0.17
Ankles & Feet	0.31	0.27	0.35

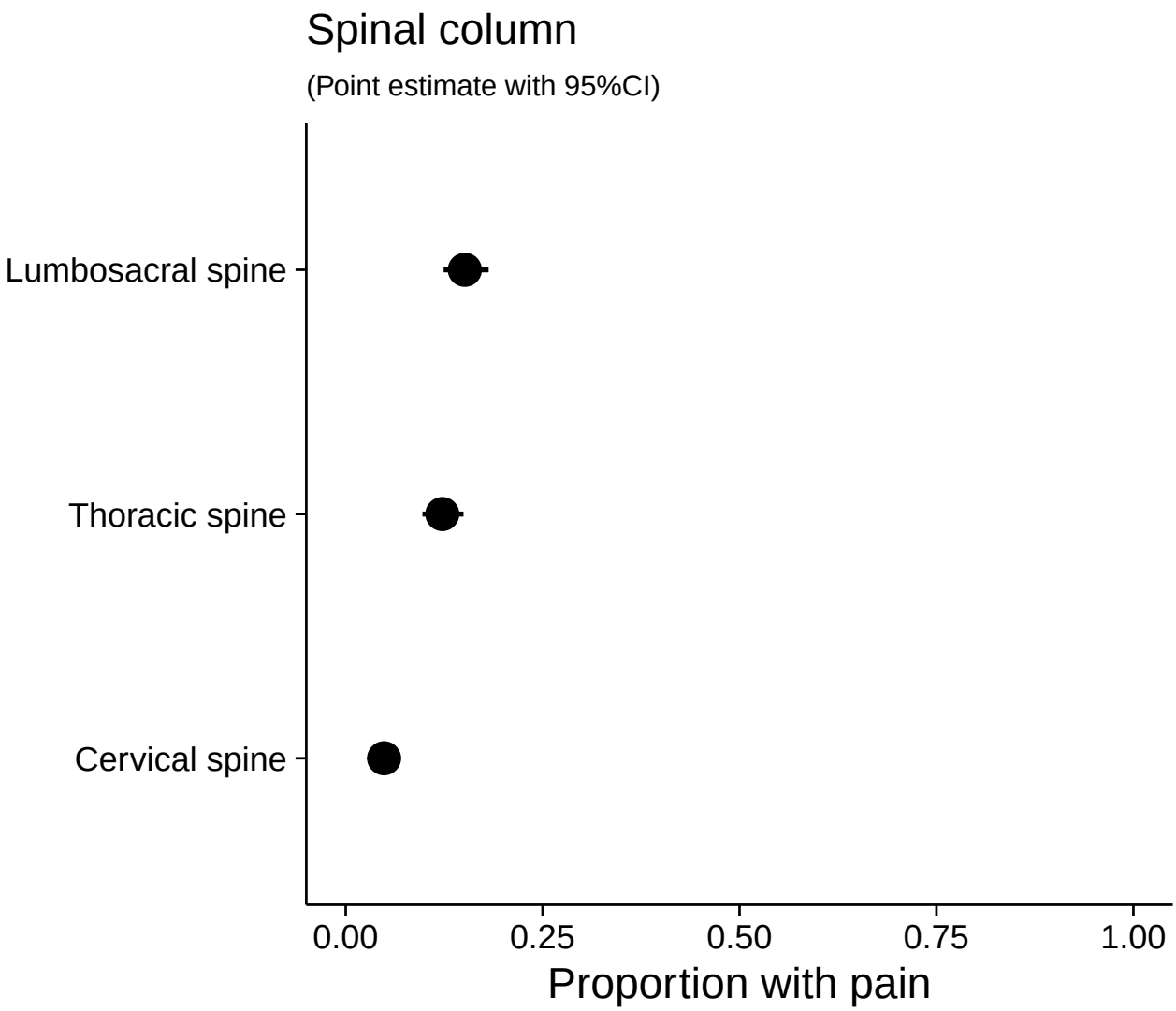
Plotted proportions (with 95% CIs), by body region

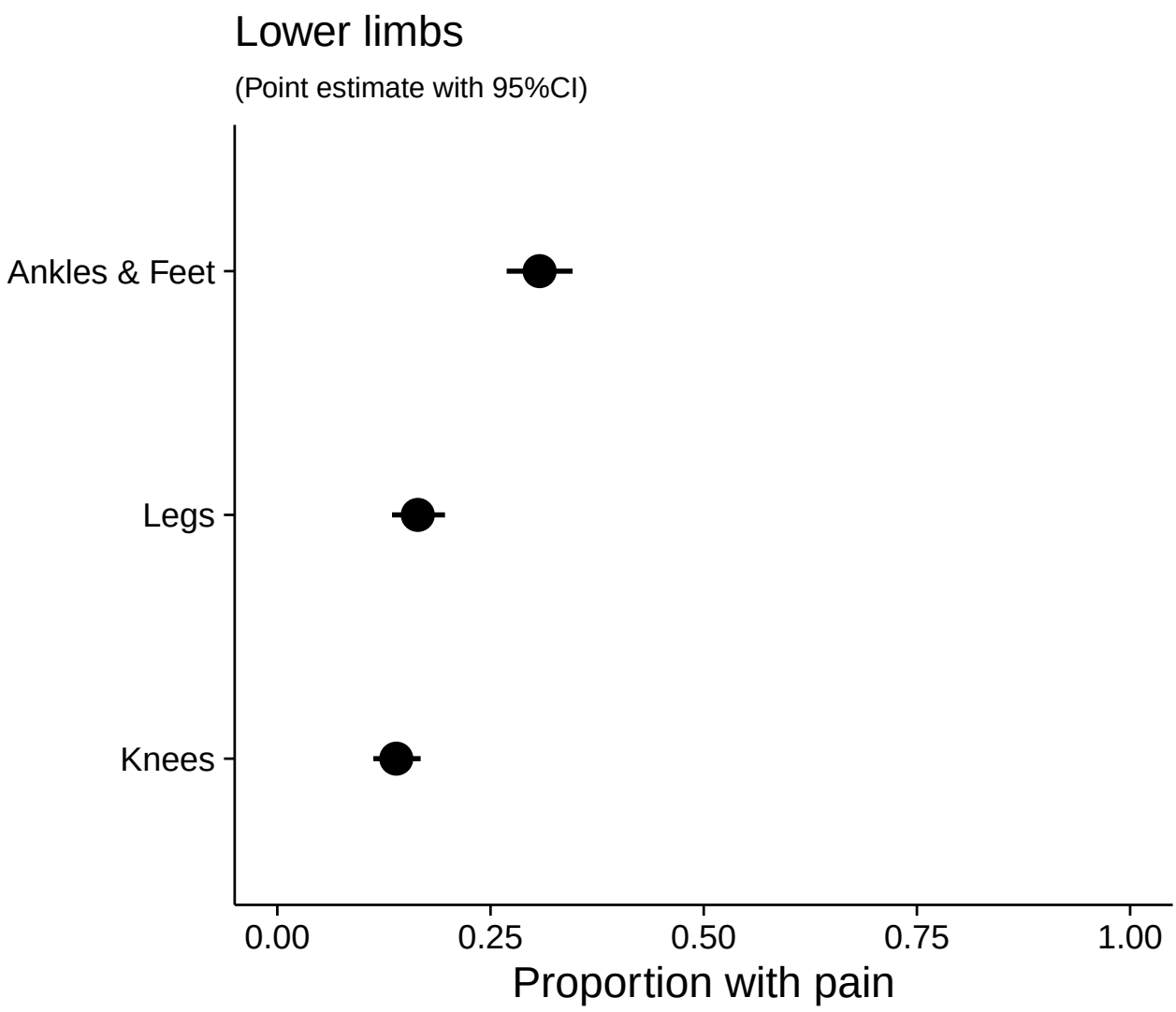
```
walk(prop_boot2$plots, ~ print(.x))
```


Head and upper torso
(Point estimate with 95%CI)
Head
Chest
Shoulder
Throat
0.00
0.25
0.50
0.75
1.00
Proportion with pain


Upper limbs
(Point estimate with 95%CI)
Wrists & Hands
Arms
Elbows
0.00
0.25
0.50
0.75
1.00
Proportion with pain


Lower torso
(Point estimate with 95%CI)
Abdomen
Groin
Lower back
Hips
Buttocks
0.00
0.25
0.50
0.75
1.00
Proportion with pain


Spinal column
(Point estimate with 95%CI)
Lumbosacral spine
Thoracic spine
Cervical spine
0.00
0.25
0.50
0.75
1.00
Proportion with pain



By sex

Process data

```
# Set seed
set.seed(2020)

# Select sex data
sex <- demo[, c('ID', 'Sex')]

# Join to boot_data & remove ID and Upper_back (only one outcome -- no pain)
sex <- left_join(data, sex) %>%
    select(-ID, -Upper_back)

# Bootstrap CIs
```

```r
sex_boot <- sex %>%
    # Pivot to long format
    pivot_longer(cols = -Sex,
                 names_to = 'site',
                 values_to = 'pain_present') %>%
    # Add body regions
    mutate(region = case_when(
        site == 'Chest' |
            site == 'Head' |
            site == 'Throat' |
            site == 'Shoulder' ~ 'Head and upper torso',
        site == 'Lower_back' |
            site == 'Abdomen' |
            site == 'Hips' |
            site == 'Buttocks' |
            site == 'Groin' ~ 'Lower torso',
        site == 'Legs' |
            site == 'Knees' |
            site == 'Ankles.Feet' ~ 'Lower limbs',
        site == 'Arms' |
            site == 'Elbows' |
            site == 'Wrists.Hands' ~ 'Upper limbs',
        site == 'Cervical_spine' |
            site == 'Thoracic_spine' |
            site == 'Lumbosacral_spine' ~ 'Spinal column',
        TRUE ~ 'other'
    )) %>%
    # Nest by body region and body site
    group_by(Sex, region, site) %>%
    nest() %>%
    # Boostrap data
    mutate(boot = map(.x = data,
                      ~ boot(data = .x,
                             statistic = prop_func,
                             R = 999,
                             stype = 'i',
                             parallel = 'multicore',
                             ncpus = 4))) %>%
    # Get CI
    mutate(ci = map(.x = boot,
                    ~ boot.ci(.x, type = 'perc'))) %>%
    # Extract ci data
    mutate(point_est = map(.x = ci,
                           ~ .x$t0),
           lower_ci = map(.x = ci,
                          ~ .x$percent[[4]]),
           upper_ci = map(.x = ci,
                          ~ .x$percent[[5]])) %>%
    # Remove columns
    select(-data, -boot, -ci) %>%
    # Unnest
    unnest(cols = c(point_est, lower_ci, upper_ci))
```

```r
# Re-nest by body region and generate figures and tables
sex_boot2 <- sex_boot %>%
    group_by(region) %>%
    nest() %>%
    # Fix site labels
    mutate(data = map(.x = data,
                      ~ .x %>%
                          mutate(site = str_replace_all(site,
                                                        pattern = '_',
                                                        replacement = ' '),
                                 site = str_replace_all(site,
                                                        pattern = '\\.',
                                                        replacement = ' & ')))) %>%
    # Re-order sites by point_est
    mutate(data = map(.x = data,
                      ~ .x %>%
                          mutate(site = fct_reorder(site,
                                                    point_est)))) %>%
    # Plot data
    mutate(plots = map2(.x = data,
                        .y = region,
                        ~ .x %>%
                            ggplot(data = .) +
                            aes(x = site,
                                y = point_est,
                                ymin = lower_ci,
                                ymax = upper_ci,
                                fill = Sex) +
                            geom_linerange(position = position_dodge2(width = 0.6),
                                           size = 1,
                                           colour = '#000000') +
                            geom_point(shape = 21,
                                       colour = '#000000',
                                       position = position_dodge2(width = 0.6),
                                       size = 6,
                                       stroke = 1) +
                            coord_flip() +
                            labs(title = .y,
                                 subtitle = '(Point estimate with 95%CI)',
                                 y = 'Proportion with pain') +
                            scale_y_continuous(limits = c(0, 1)) +
                            scale_fill_manual(values = c('#000000', '#FFFFFF')) +
                            theme_minimal(base_size = 18) +
                            theme(plot.title = element_text(size = 18),
                                  plot.subtitle = element_text(size = 12),
                                  legend.title = element_blank(),
                                  legend.position = 'top',
                                  axis.title.y = element_blank(),
                                  panel.grid = element_blank(),
                                  axis.text = element_text(colour = '#000000'),
                                  axis.line = element_line(size = 0.5),
                                  axis.ticks = element_line(size = 0.5)))) %>%
    # Tabulate data
```

```
    mutate(tables = map2(.x = data,
                         .y = region,
                         ~ .x %>%
                             kable(caption = .y,
                                   digits = 2)))
```

Tabulated proportions (with 95% CIs), by age and body region

```
walk(sex_boot2$tables, ~ print(.x))
```

Table 11: Head and upper torso

Sex	site	point_est	lower_ci	upper_ci
Female	Head	0.38	0.34	0.42
Female	Throat	0.03	0.01	0.05
Female	Shoulder	0.07	0.05	0.09
Female	Chest	0.19	0.16	0.23
Male	Head	0.12	0.07	0.18
Male	Throat	0.04	0.01	0.08
Male	Shoulder	0.12	0.07	0.18
Male	Chest	0.20	0.13	0.28

Table 12: Upper limbs

Sex	site	point_est	lower_ci	upper_ci
Female	Arms	0.04	0.03	0.06
Female	Elbows	0.03	0.02	0.05
Female	Wrists & Hands	0.06	0.04	0.09
Male	Arms	0.03	0.01	0.07
Male	Elbows	0.05	0.02	0.09
Male	Wrists & Hands	0.03	0.01	0.07

Table 13: Lower torso

Sex	site	point_est	lower_ci	upper_ci
Female	Lower back	0.08	0.05	0.10
Female	Abdomen	0.29	0.24	0.33
Female	Groin	0.10	0.07	0.12
Female	Hips	0.06	0.04	0.08
Female	Buttocks	0.03	0.01	0.05
Male	Lower back	0.06	0.02	0.10
Male	Abdomen	0.20	0.12	0.28
Male	Groin	0.07	0.03	0.12
Male	Hips	0.09	0.04	0.16
Male	Buttocks	0.04	0.01	0.09

Table 14: Spinal column

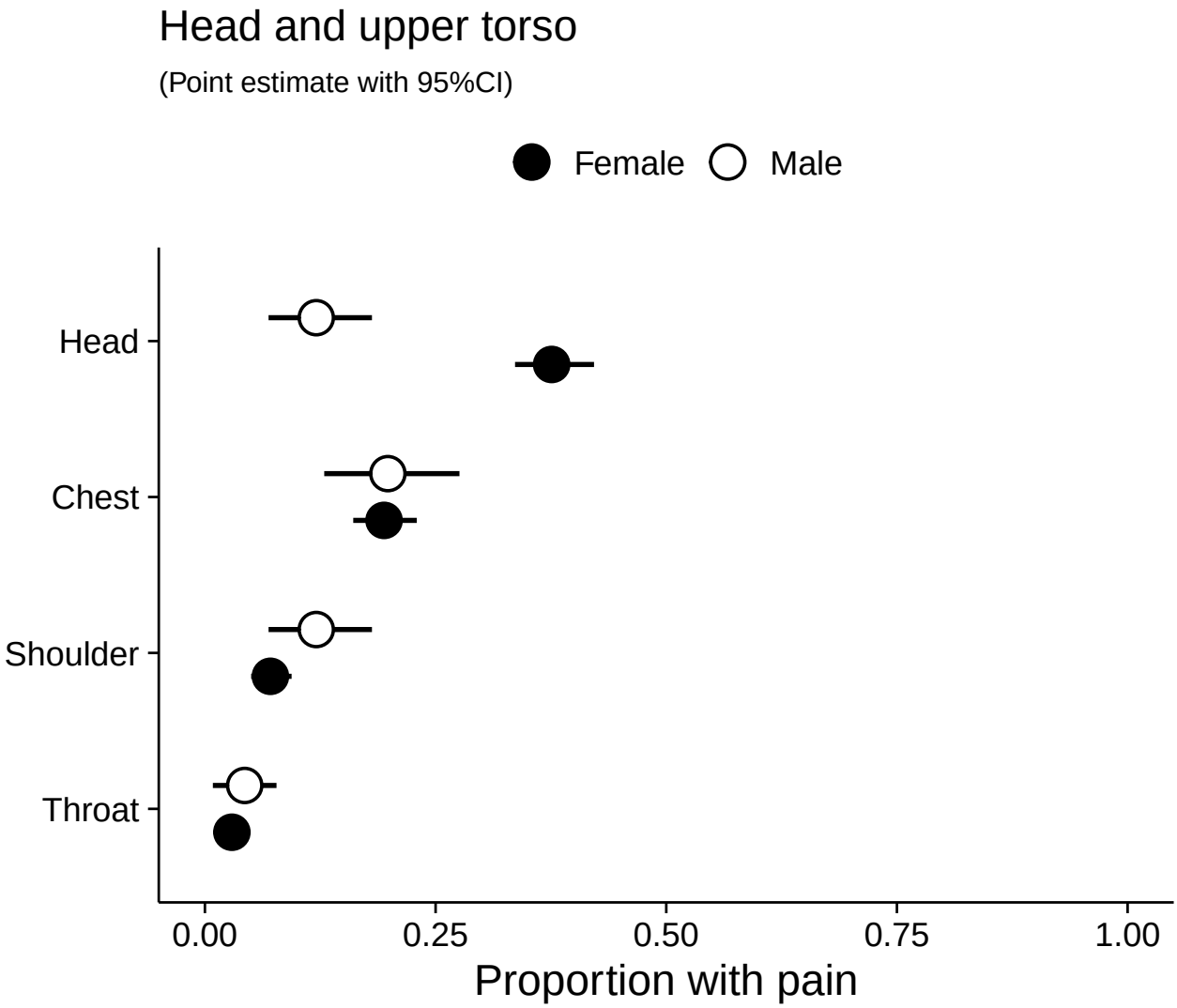
Sex	site	point_est	lower_ci	upper_ci
Female	Cervical spine	0.05	0.03	0.08
Female	Thoracic spine	0.14	0.11	0.17
Female	Lumbosacral spine	0.15	0.12	0.19
Male	Cervical spine	0.03	0.00	0.06
Male	Thoracic spine	0.07	0.03	0.11
Male	Lumbosacral spine	0.14	0.08	0.21

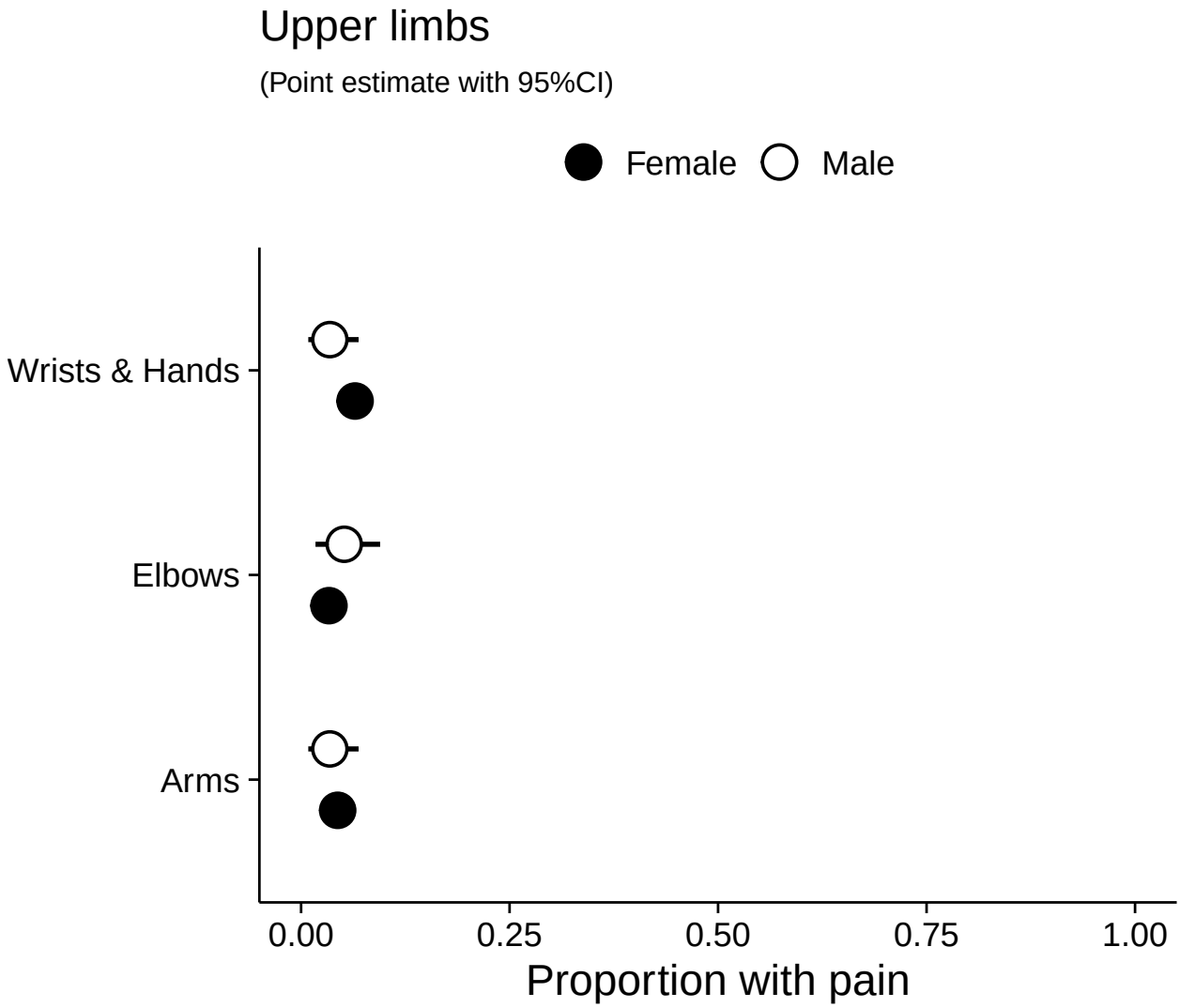
Table 15: Lower limbs

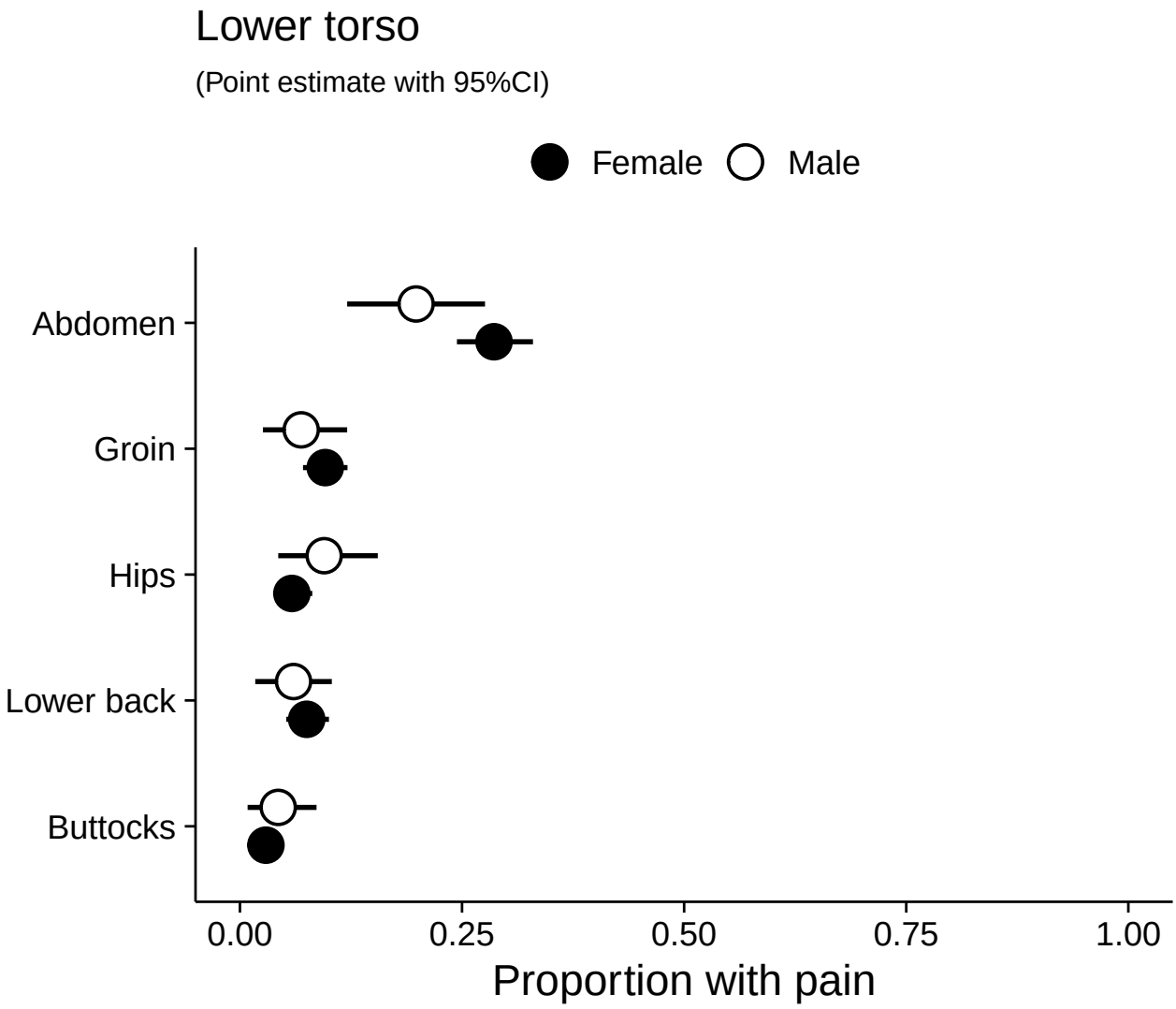
Sex	site	point_est	lower_ci	upper_ci
Female	Legs	0.15	0.12	0.18
Female	Knees	0.13	0.10	0.16
Female	Ankles & Feet	0.28	0.24	0.32
Male	Legs	0.23	0.16	0.31
Male	Knees	0.19	0.12	0.27
Male	Ankles & Feet	0.41	0.32	0.50

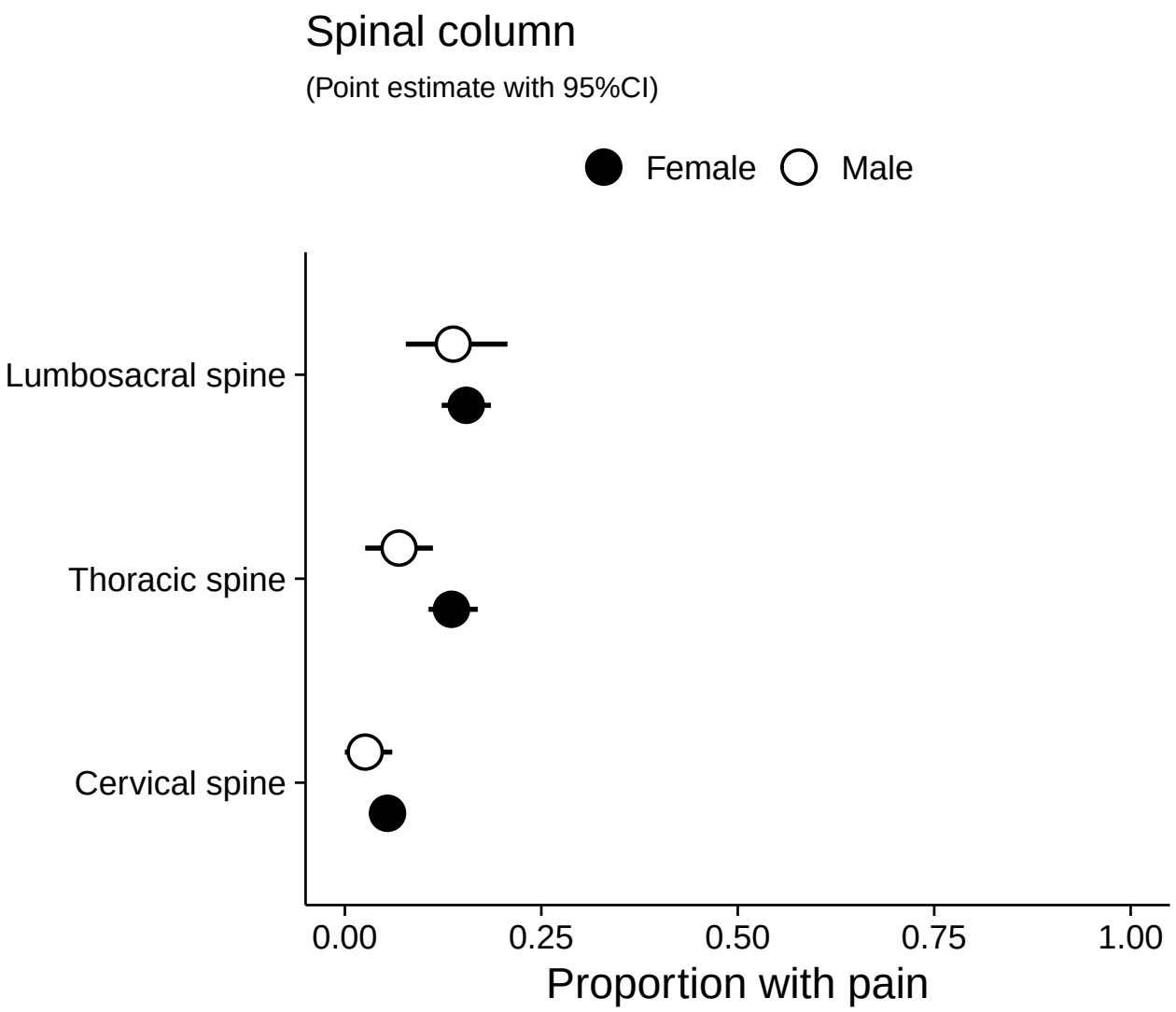
Plotted proportions (with 95% CIs), by age and body region

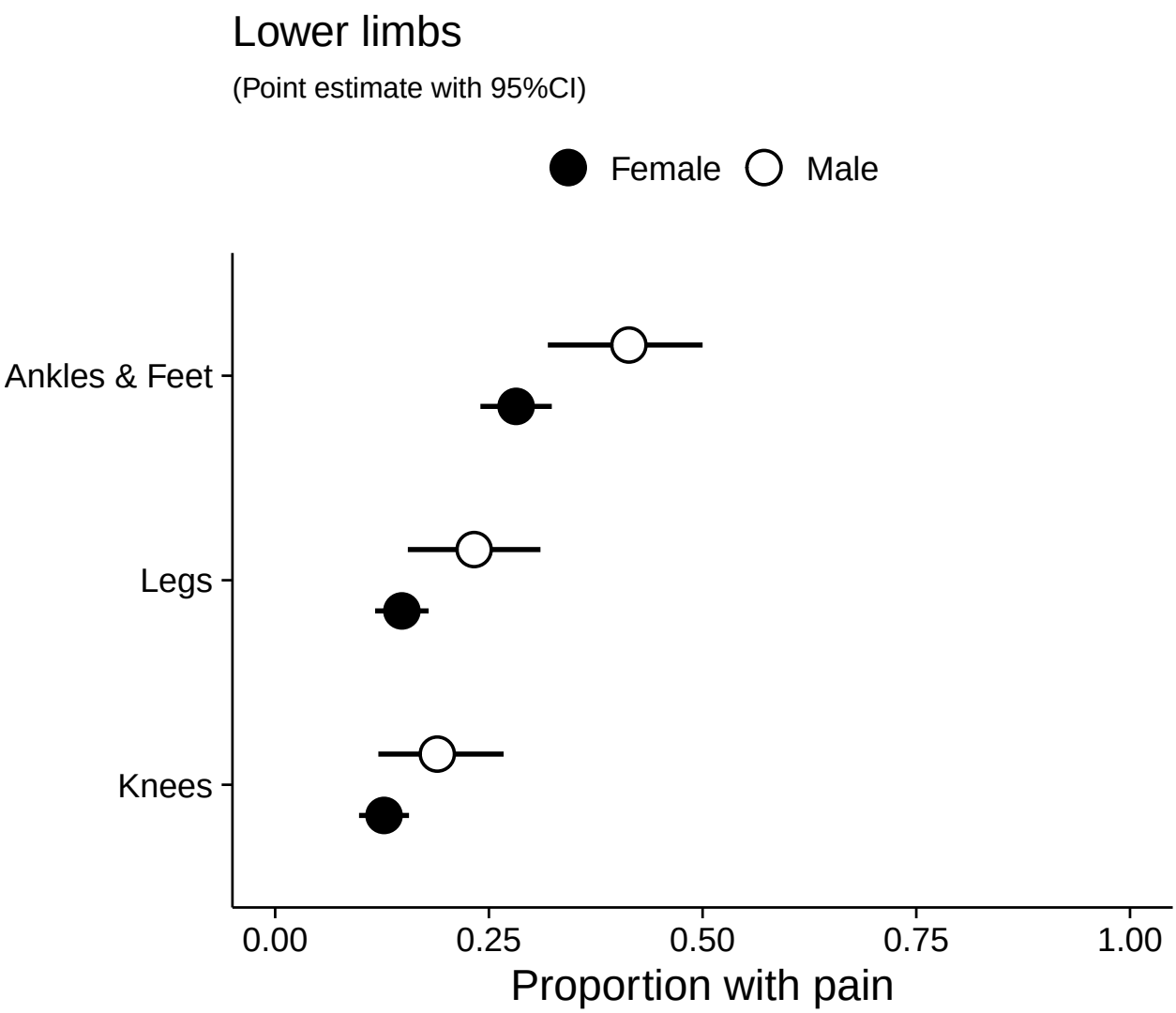
```
walk(sex_boot2$plots, ~ print(.x))
```


Head and upper torso
(Point estimate with 95%CI)
Female
Male
Head
Chest
Shoulder
Throat
0.00
0.25
0.50
0.75
1.00
Proportion with pain


Upper limbs
(Point estimate with 95%CI)
Female
Male
Wrists & Hands
Elbows
Arms
0.00
0.25
0.50
0.75
1.00
Proportion with pain


Lower torso
(Point estimate with 95%CI)
Female
Male
Abdomen
Groin
Hips
Lower back
Buttocks
0.00
0.25
0.50
0.75
1.00
Proportion with pain


Spinal column
(Point estimate with 95%CI)
Female
Male
Lumbosacral spine
Thoracic spine
Cervical spine
0.00
0.25
0.50
0.75
1.00
Proportion with pain



By age

Process data

```
# Set seed
set.seed(2020)

# Select age data
age <- demo[, c('ID', 'Age')]

# Join to boot_data & remove ID and Upper_back (only one outcome -- no pain)
age <- left_join(data, age) %>%
    select(-ID, -Upper_back)

# Get complete cases
```

```r
age <- age[complete.cases(age), ]

# Pivot and add age group categories (10 year periods)
age_boot <- age %>%
    # Pivot to long format
    pivot_longer(cols = -Age,
                 names_to = 'site',
                 values_to = 'pain_present') %>%
    # Add age categories
    mutate(age_group = case_when(
        Age < 28 ~ '18-27',
        Age >= 28 & Age < 38 ~ '28-37',
        Age >= 38 & Age < 48 ~ '38-47',
        Age >= 48 & Age < 58 ~ '48-57',
        Age >= 58 & Age < 68 ~ '58-67',
        Age >= 68 & Age < 78 ~ '68-77',
        Age >= 78 & Age < 88 ~ '78-87'
    ))

# Print count per age group
age_boot %>%
    group_by(site, age_group) %>%
    summarise(count = n()) %>%
    filter(site == 'Abdomen') %>%
    ungroup() %>%
    select(-site) %>%
    kable(caption = 'Participant count per age group')
```

Table 16: Participant count per age group

age_group	count
18-27	64
28-37	284
38-47	158
48-57	59
58-67	20
68-77	2

```r
# Generate CIs
age_boot2 <- age_boot %>%
    # Remove age
    select(-Age) %>%
    # Remove categories with less than 20 counts
    filter(age_group != '68-77') %>%
    # Nest by age group and body site
    group_by(age_group, site) %>%
    nest() %>%
    # Boostrap data
    mutate(boot = map(.x = data,
                      ~ boot(data = .x,
                             statistic = prop_func,
                             R = 999,
```

```
                            stype = 'i',
                            parallel = 'multicore',
                            ncpus = 4))) %>%
    # Get CI
    mutate(ci = map(.x = boot,
                    ~ boot.ci(.x, type = 'perc'))) %>%
    # Extract ci data
    mutate(point_est = map(.x = ci,
                           ~ .x$t0),
           lower_ci = map(.x = ci,
                          ~ .x$percent[[4]]),
           upper_ci = map(.x = ci,
                          ~ .x$percent[[5]])) %>%
    # Remove columns
    select(-data, -boot, -ci) %>%
    # Unnest
    unnest(cols = c(point_est, lower_ci, upper_ci)) %>%
    ungroup()

# Re-nest by body region and generate figures and tables
age_boot2 <- age_boot2 %>%
    # Fix site labels
    mutate(site = str_replace_all(site,
                                  pattern = '_',
                                  replacement = ' '),
           site = str_replace_all(site,
                                  pattern = '\\.',
                                  replacement = ' & ')) %>%
    # Group and nest
    group_by(site) %>%
    nest() %>%
    # Arrange age groups
    # Plot data
    mutate(plots = map2(.x = data,
                        .y = site,
                        ~ .x %>%
                            ggplot(data = .) +
                            aes(x = age_group,
                                y = point_est,
                                ymin = lower_ci,
                                ymax = upper_ci) +
                            geom_linerange(size = 1,
                                           colour = '#000000') +
                            geom_point(colour = '#000000',
                                       size = 6) +
                            labs(title = .y,
                                 subtitle = '(Point estimate with 95%CI)',
                                 caption = 'Age group 68-77 years removed because n = 2',
                                 x = 'Age group (Years)',
                                 y = 'Proportion with pain') +
                            scale_y_continuous(limits = c(0, 1)) +
                            theme_minimal(base_size = 18) +
                            theme(plot.title = element_text(size = 18),
```

```
                                plot.subtitle = element_text(size = 12),
                                plot.caption = element_text(size = 12),
                                panel.grid = element_blank(),
                                axis.text = element_text(colour = '#000000'),
                                axis.line = element_line(size = 0.5),
                                axis.ticks = element_line(size = 0.5)))) %>%
    # Tabulate data
    mutate(tables = map2(.x = data,
                         .y = site,
                         ~ .x %>%
                             arrange(age_group) %>%
                             kable(caption = str_glue('{.y} (Age group 68-77 years removed because n = 2
                                   digits = 2)))
```

Tabulated proportions (with 95% CIs), by age group and body site

```
walk(age_boot2$tables, ~ print(.x))
```

Table 17: Head (Age group 68-77 years removed because n = 2)

age_group	point_est	lower_ci	upper_ci
18-27	0.45	0.33	0.58
28-37	0.33	0.28	0.39
38-47	0.31	0.24	0.39
48-57	0.17	0.08	0.27
58-67	0.35	0.15	0.60

Table 18: Throat (Age group 68-77 years removed because n = 2)

age_group	point_est	lower_ci	upper_ci
18-27	0.05	0.00	0.11
28-37	0.03	0.01	0.05
38-47	0.03	0.01	0.06
48-57	0.05	0.00	0.12
58-67	0.00	0.00	0.00

Table 19: Shoulder (Age group 68-77 years removed because n = 2)

age_group	point_est	lower_ci	upper_ci
18-27	0.12	0.05	0.22
28-37	0.07	0.04	0.10
38-47	0.09	0.05	0.15
48-57	0.07	0.02	0.14
58-67	0.05	0.00	0.15

Table 20: Arms (Age group 68-77 years removed because n = 2)

age_group	point_est	lower_ci	upper_ci
18-27	0.02	0.00	0.05
28-37	0.04	0.02	0.07
38-47	0.06	0.03	0.09
48-57	0.05	0.00	0.12
58-67	0.00	0.00	0.00

Table 21: Elbows (Age group 68-77 years removed because n = 2)

age_group	point_est	lower_ci	upper_ci
18-27	0.00	0.00	0.00
28-37	0.03	0.01	0.05
38-47	0.04	0.01	0.07
48-57	0.05	0.00	0.10
58-67	0.15	0.00	0.30

Table 22: Wrists & Hands (Age group 68-77 years removed because n = 2)

age_group	point_est	lower_ci	upper_ci
18-27	0.02	0.00	0.05
28-37	0.07	0.04	0.10
38-47	0.04	0.01	0.08
48-57	0.07	0.02	0.14
58-67	0.15	0.00	0.30

Table 23: Chest (Age group 68-77 years removed because n = 2)

age_group	point_est	lower_ci	upper_ci
18-27	0.17	0.09	0.27
28-37	0.20	0.16	0.25
38-47	0.20	0.14	0.27
48-57	0.19	0.10	0.29
58-67	0.20	0.05	0.40

Table 24: Lower back (Age group 68-77 years removed because n = 2)

age_group	point_est	lower_ci	upper_ci
18-27	0.09	0.03	0.17
28-37	0.07	0.04	0.10
38-47	0.05	0.02	0.09
48-57	0.10	0.03	0.19

age_group	point_est	lower_ci	upper_ci
58-67	0.10	0.00	0.25

Table 25: Abdomen (Age group 68-77 years removed because n = 2)

age_group	point_est	lower_ci	upper_ci
18-27	0.22	0.12	0.33
28-37	0.32	0.26	0.37
38-47	0.30	0.23	0.37
48-57	0.12	0.03	0.20
58-67	0.05	0.00	0.15

Table 26: Cervical spine (Age group 68-77 years removed because n = 2)

age_group	point_est	lower_ci	upper_ci
18-27	0.12	0.05	0.22
28-37	0.05	0.02	0.08
38-47	0.04	0.01	0.08
48-57	0.00	0.00	0.00
58-67	0.00	0.00	0.00

Table 27: Thoracic spine (Age group 68-77 years removed because n = 2)

age_group	point_est	lower_ci	upper_ci
18-27	0.17	0.09	0.27
28-37	0.14	0.10	0.18
38-47	0.06	0.03	0.11
48-57	0.10	0.03	0.19
58-67	0.25	0.05	0.45

Table 28: Lumbosacral spine (Age group 68-77 years removed because n = 2)

age_group	point_est	lower_ci	upper_ci
18-27	0.17	0.09	0.27
28-37	0.15	0.11	0.19
38-47	0.11	0.06	0.16
48-57	0.15	0.07	0.25
58-67	0.40	0.20	0.60

Table 29: Groin (Age group 68-77 years removed because n = 2)

age_group	point_est	lower_ci	upper_ci
18-27	0.09	0.03	0.17
28-37	0.10	0.07	0.14
38-47	0.09	0.04	0.14
48-57	0.05	0.00	0.12
58-67	0.05	0.00	0.15

Table 30: Hips (Age group 68-77 years removed because n = 2)

age_group	point_est	lower_ci	upper_ci
18-27	0.03	0.00	0.08
28-37	0.05	0.02	0.07
38-47	0.09	0.04	0.13
48-57	0.14	0.05	0.22
58-67	0.10	0.00	0.25

Table 31: Legs (Age group 68-77 years removed because n = 2)

age_group	point_est	lower_ci	upper_ci
18-27	0.12	0.05	0.22
28-37	0.13	0.09	0.17
38-47	0.21	0.15	0.27
48-57	0.29	0.17	0.41
58-67	0.20	0.05	0.40

Table 32: Knees (Age group 68-77 years removed because n = 2)

age_group	point_est	lower_ci	upper_ci
18-27	0.11	0.05	0.19
28-37	0.10	0.07	0.14
38-47	0.16	0.11	0.22
48-57	0.22	0.12	0.32
58-67	0.30	0.10	0.50

Table 33: Ankles & Feet (Age group 68-77 years removed because n = 2)

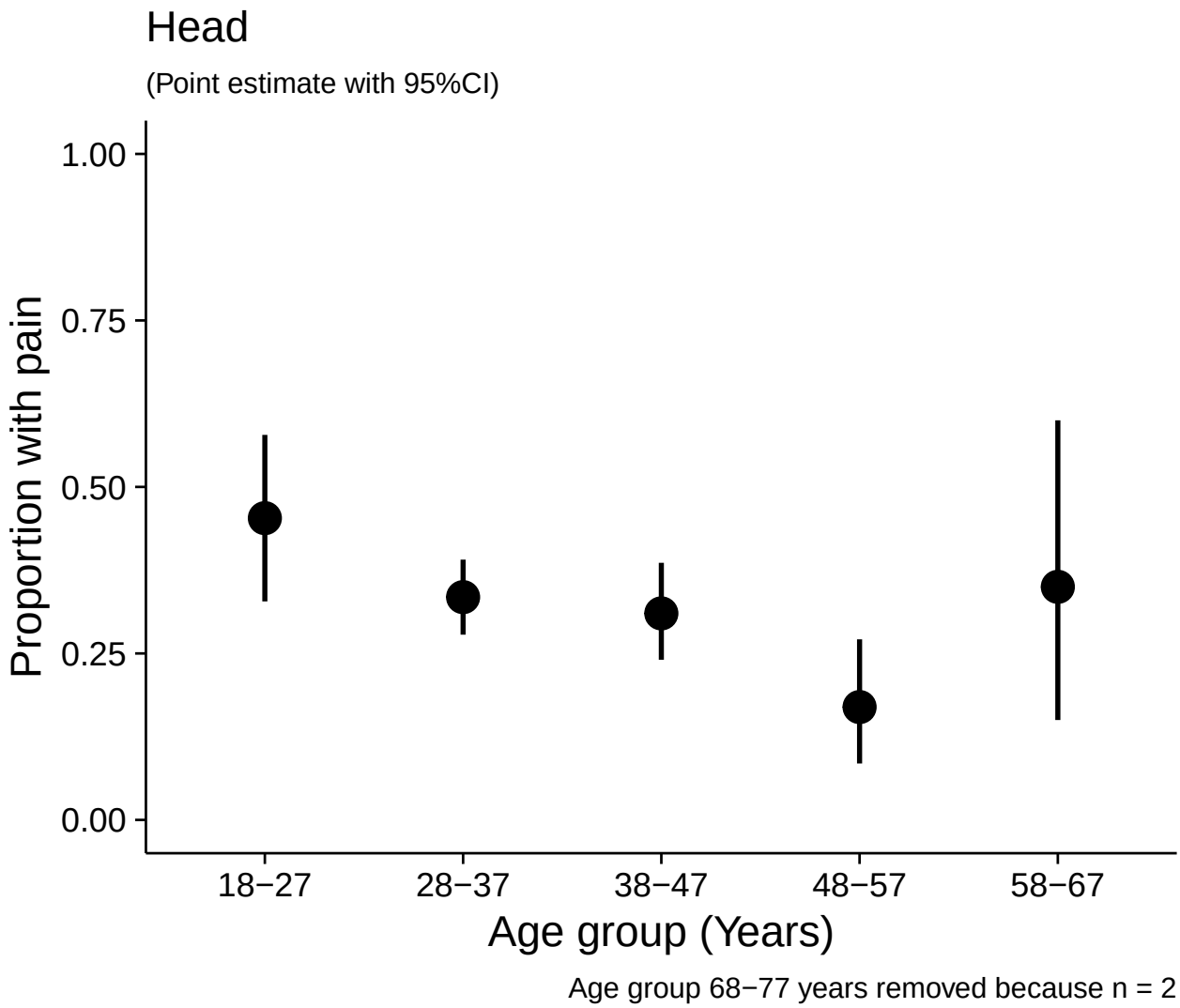
age_group	point_est	lower_ci	upper_ci
18-27	0.22	0.12	0.33
28-37	0.24	0.19	0.29
38-47	0.37	0.29	0.44
48-57	0.51	0.39	0.63
58-67	0.55	0.35	0.75

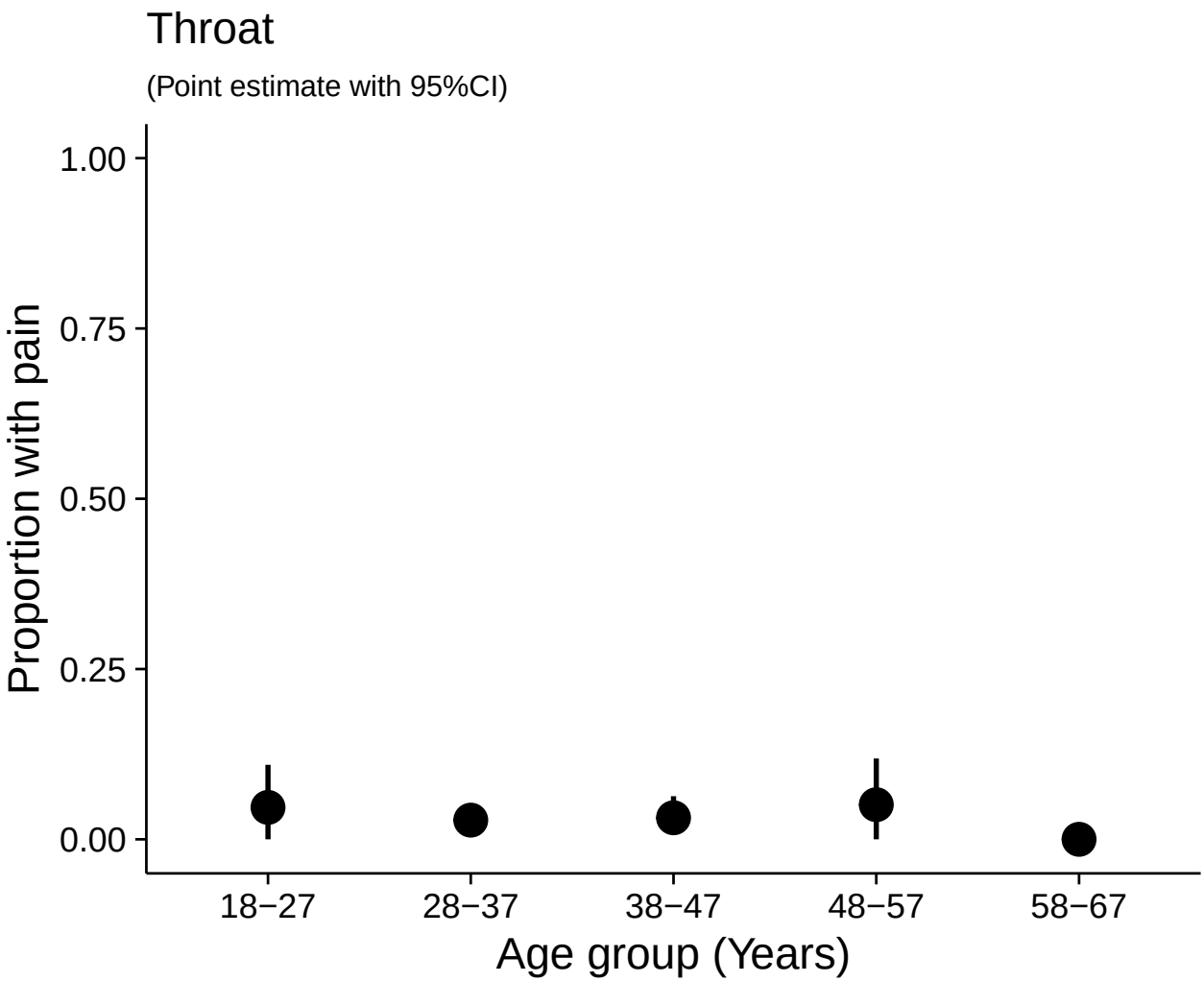
Table 34: Buttocks (Age group 68-77 years removed because n = 2)

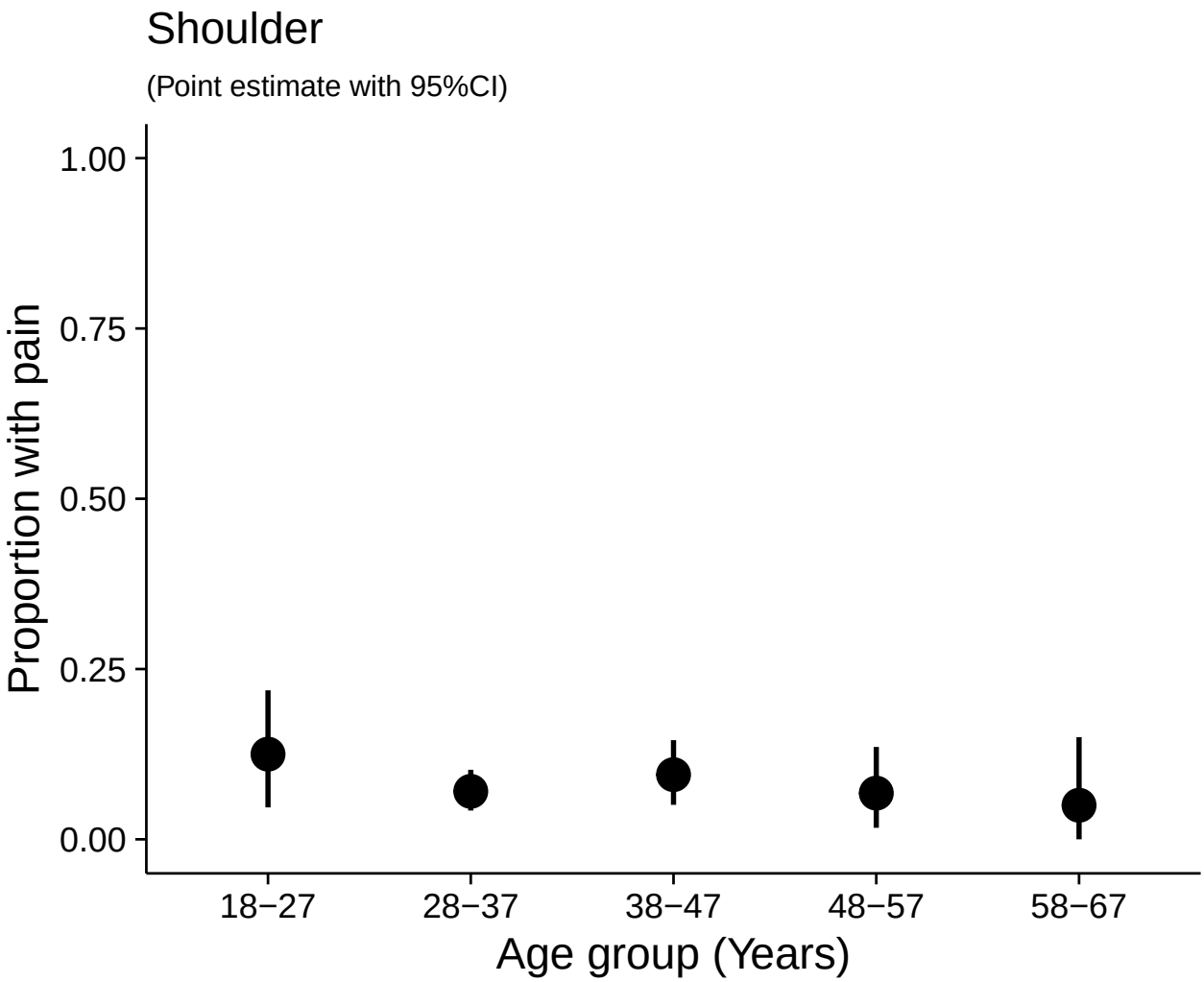
age_group	point_est	lower_ci	upper_ci
18-27	0.03	0.00	0.08
28-37	0.04	0.02	0.06
38-47	0.03	0.01	0.05
48-57	0.02	0.00	0.05
58-67	0.05	0.00	0.15

Plotted proportions (with 95% CIs), by age group and body site

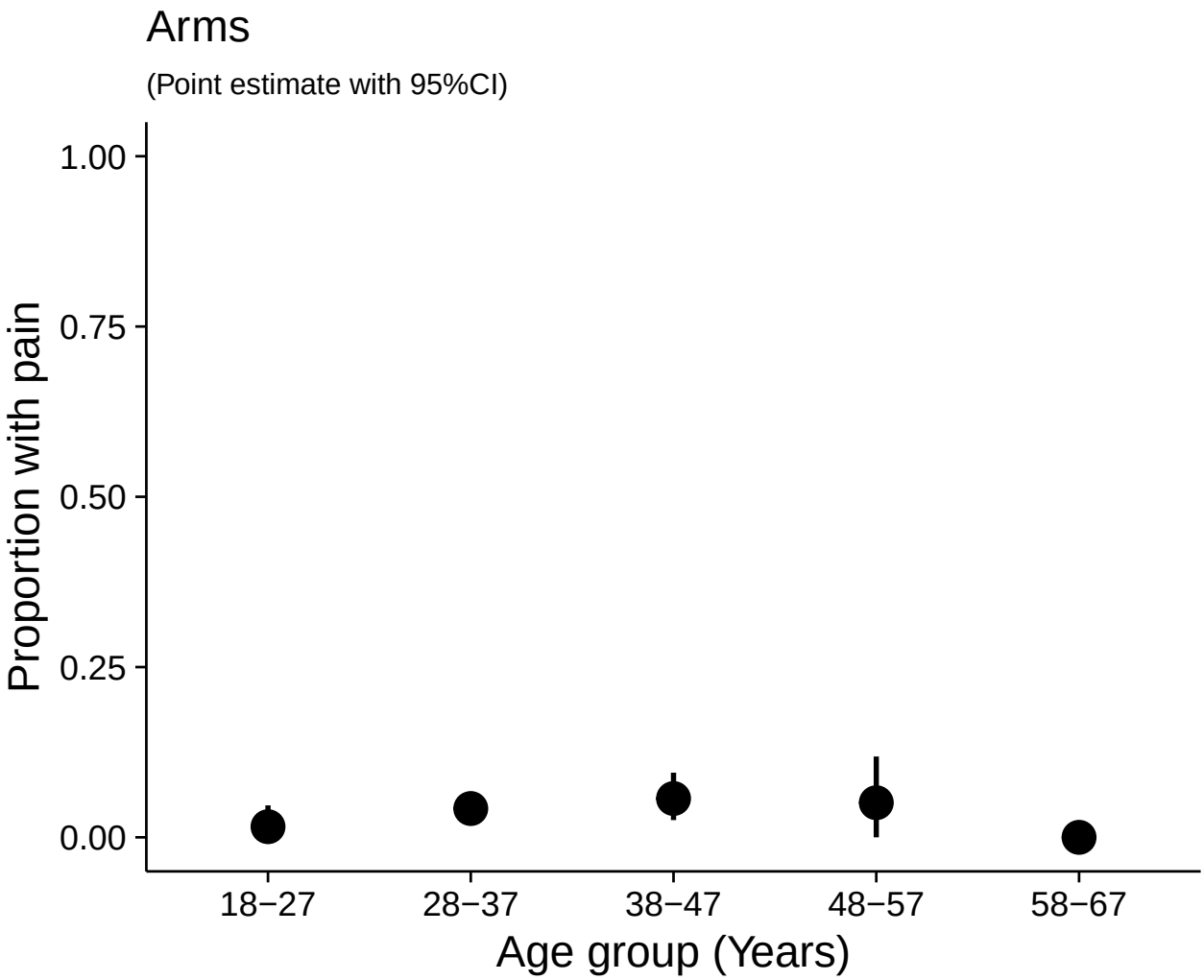
```
walk(age_boot2$plots, ~ print(.x))
```



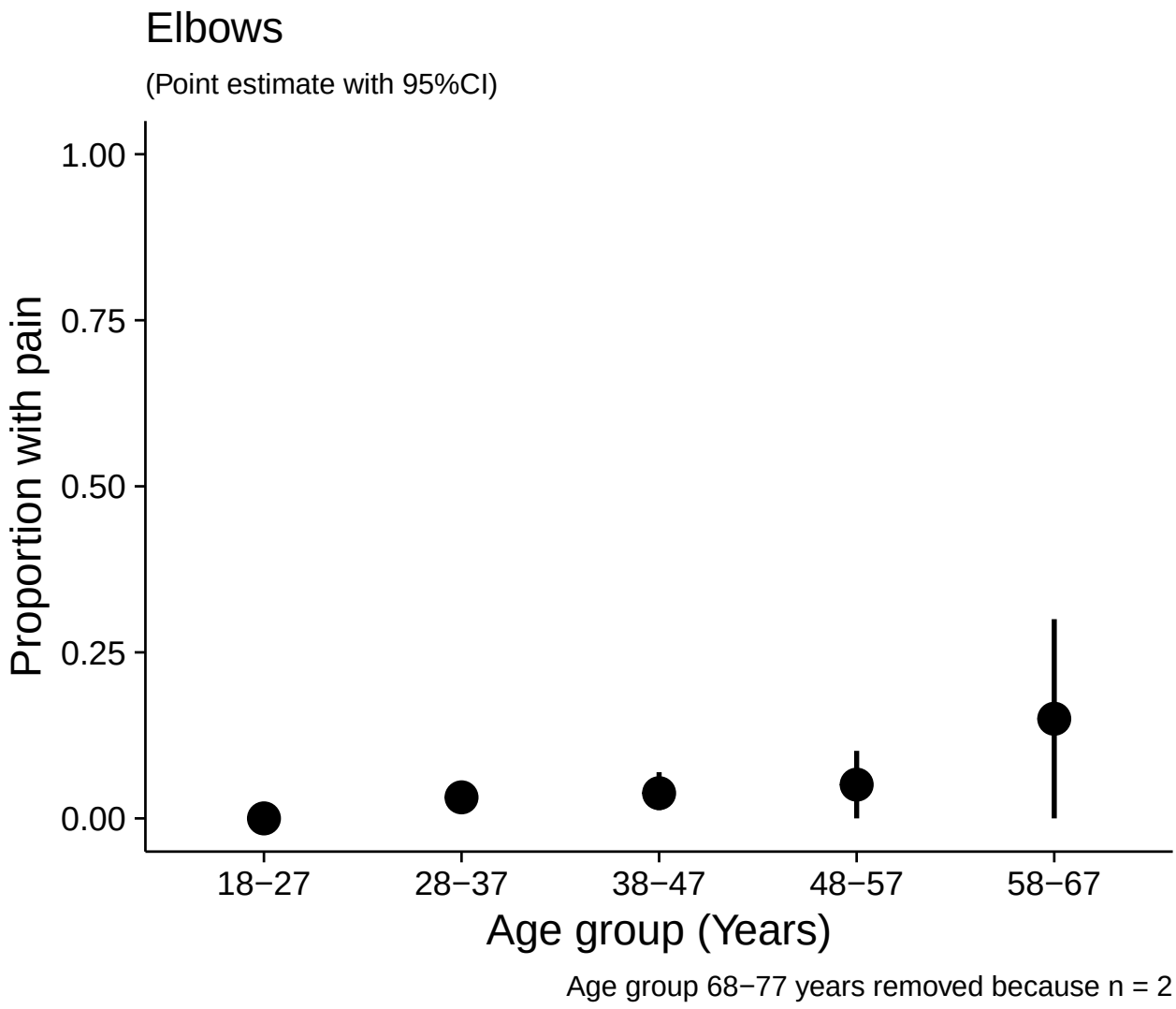

Throat
(Point estimate with 95%CI)
1.00
0.75
0.50
0.25
0.00
Proportion with pain
18−27
28−37
38−47
48−57
58−67
Age group (Years)
Age group 68−77 years removed because n = 2

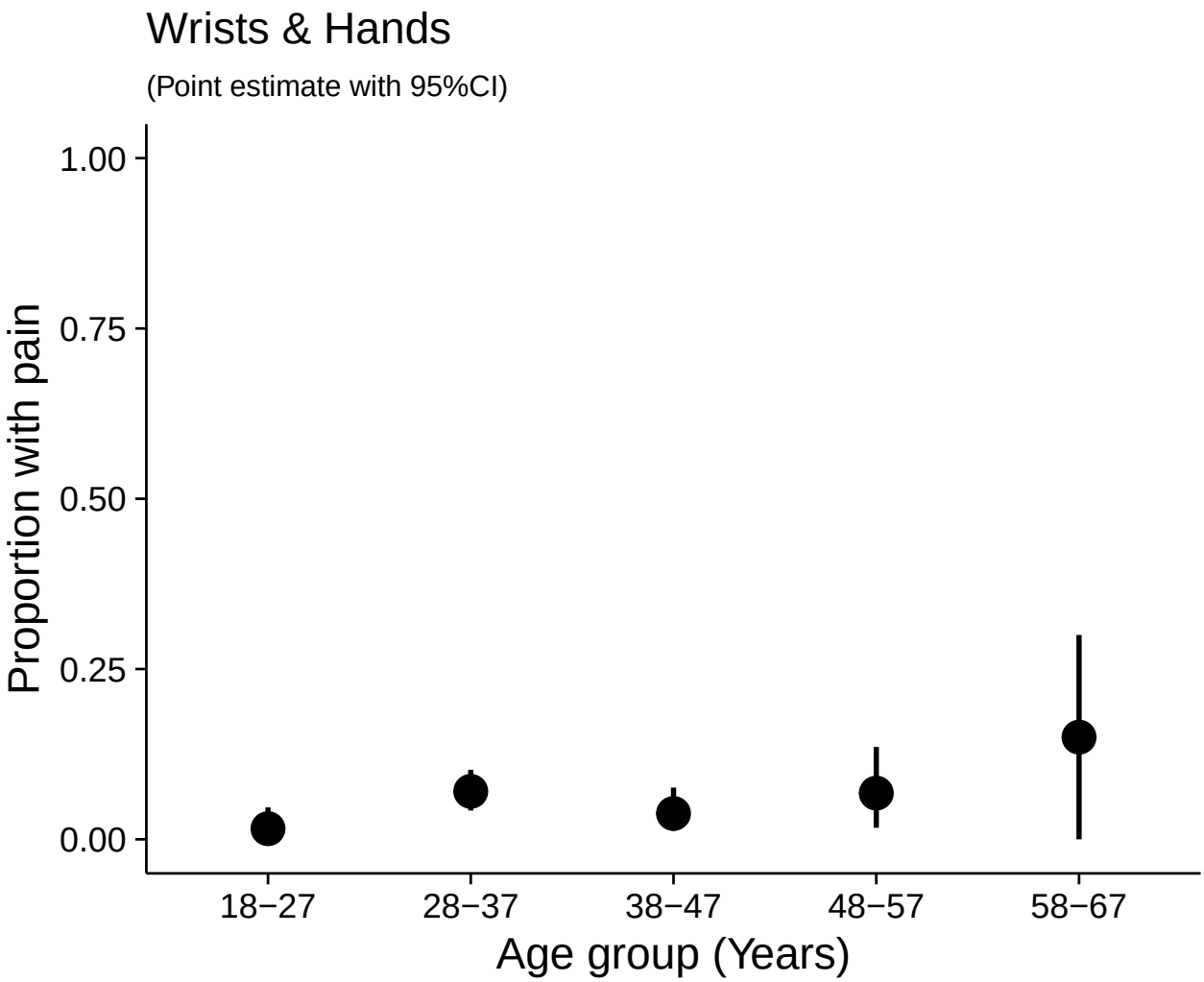


Age group 68−77 years removed because n = 2

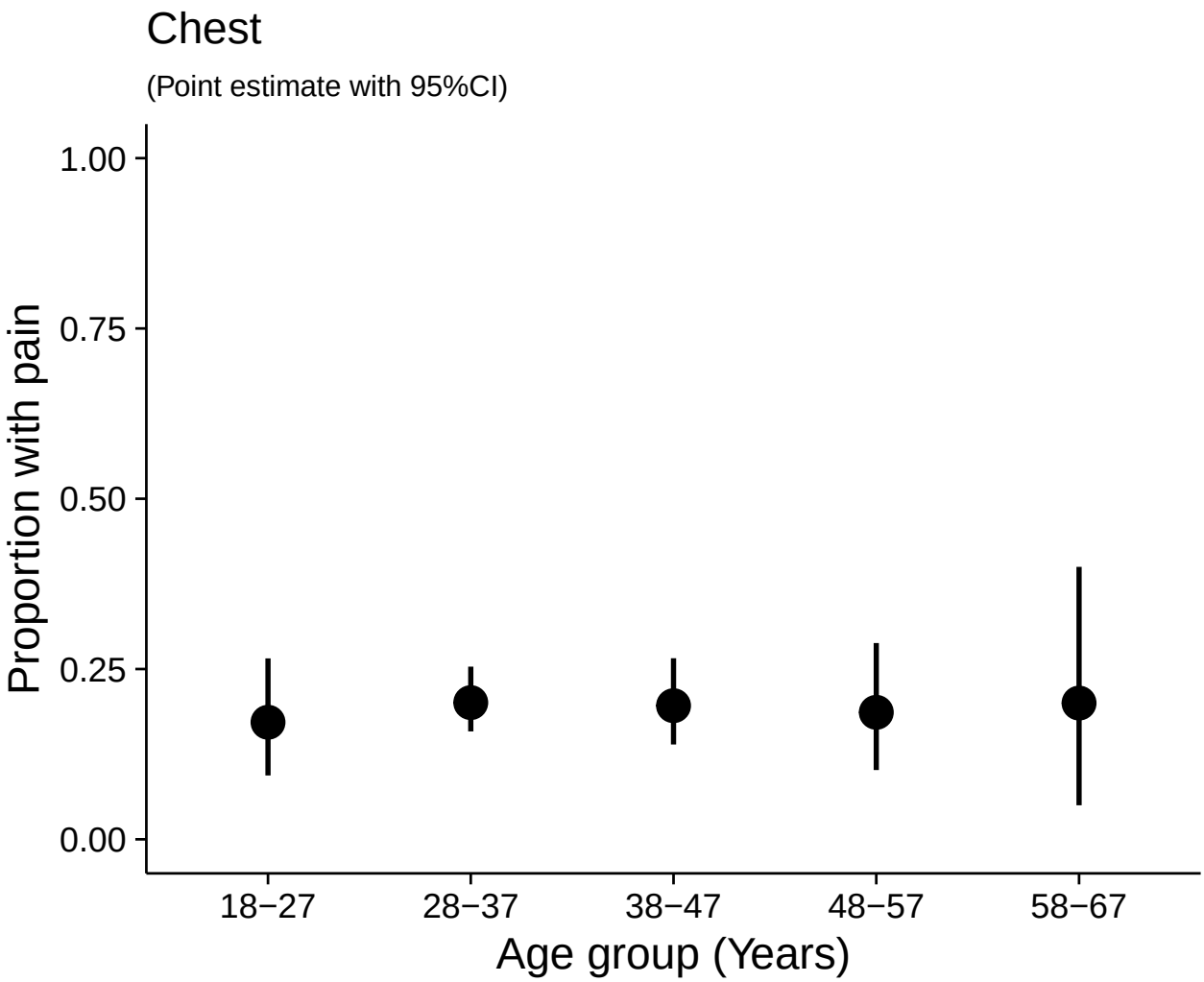


Age group 68−77 years removed because n = 2

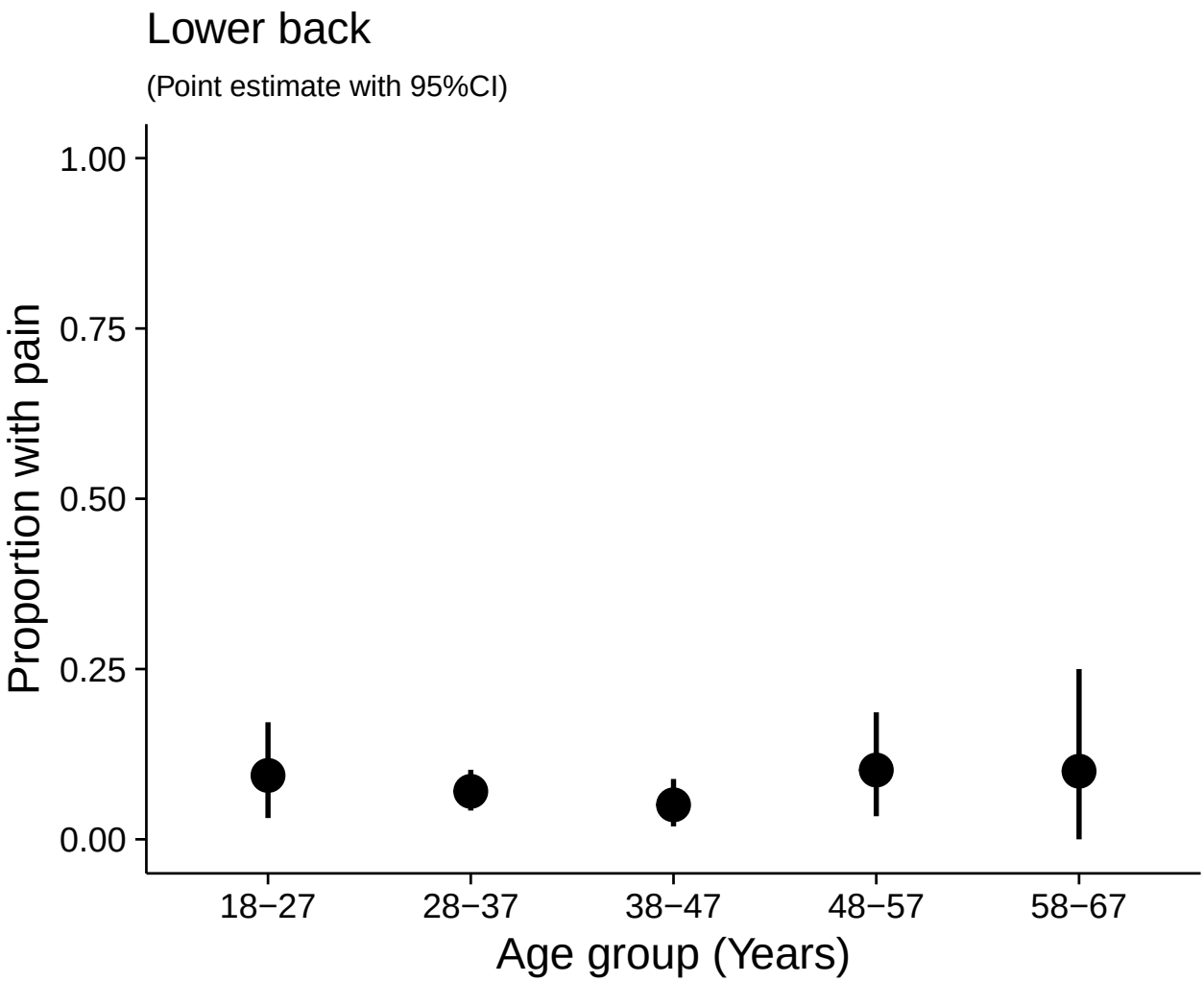

Elbows
(Point estimate with 95%CI)
1.00
0.75
0.50
0.25
0.00
Proportion with pain
18−27
28−37
38−47
48−57
58−67
Age group (Years)
Age group 68−77 years removed because n = 2

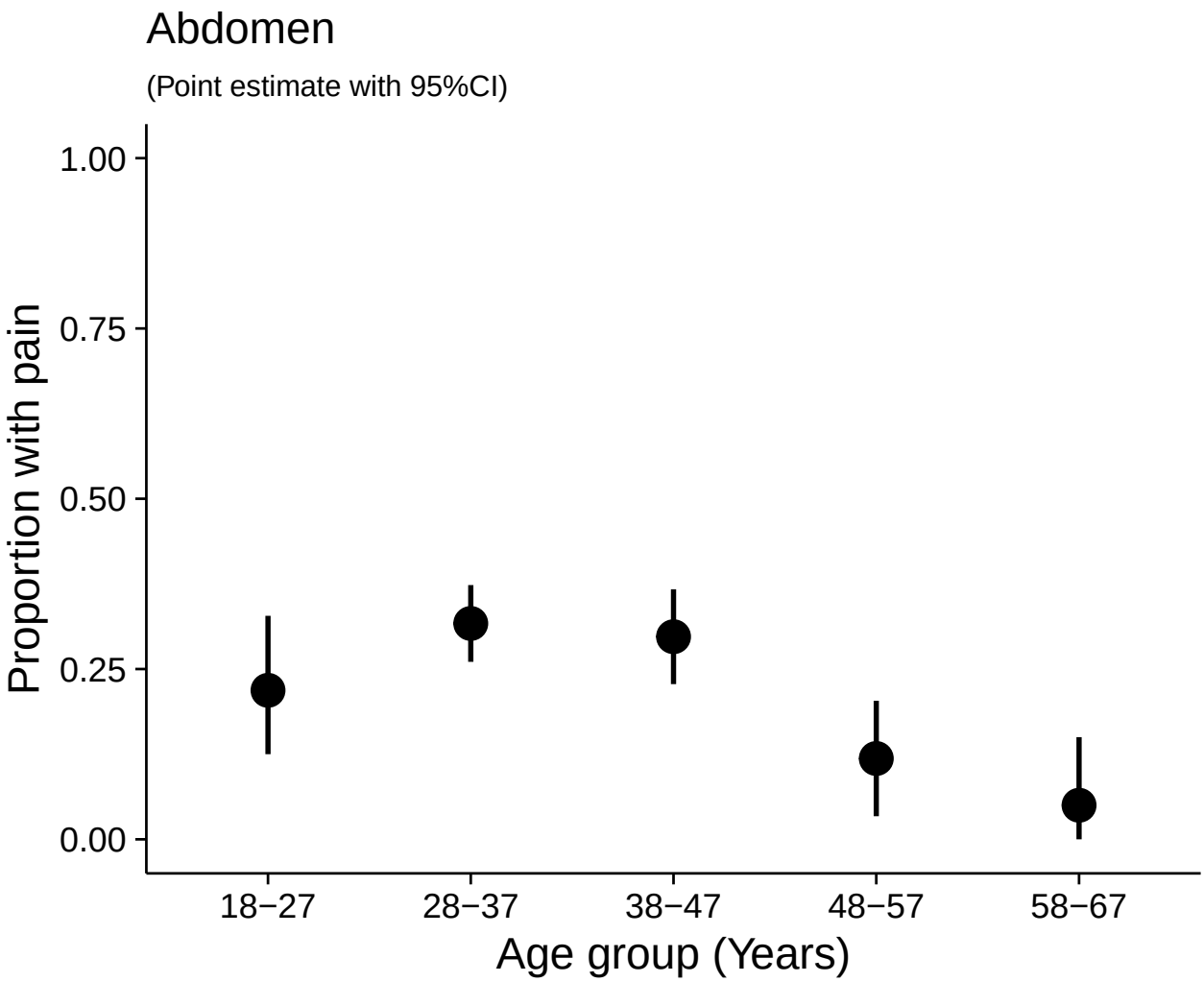


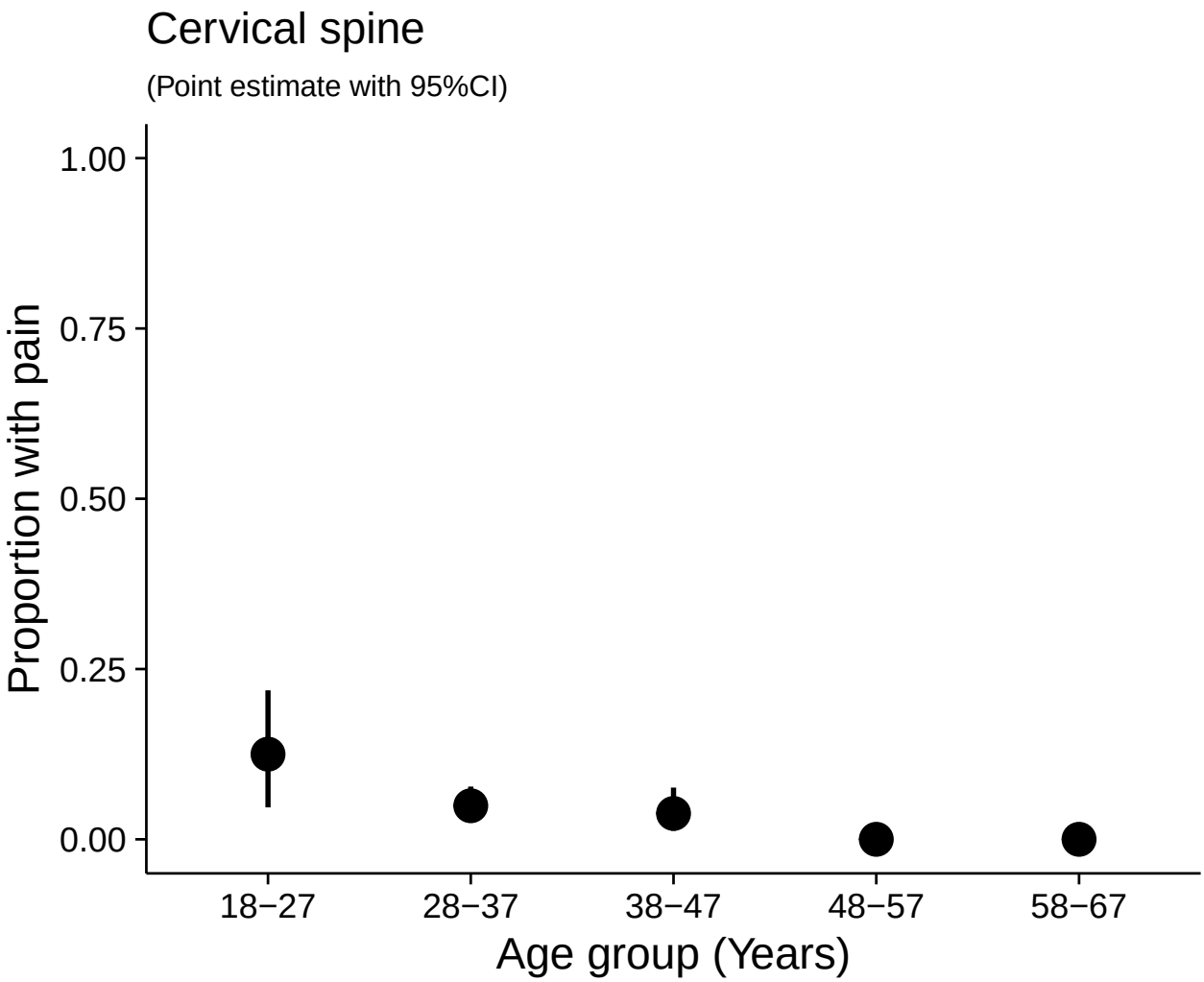
Age group 68−77 years removed because n = 2



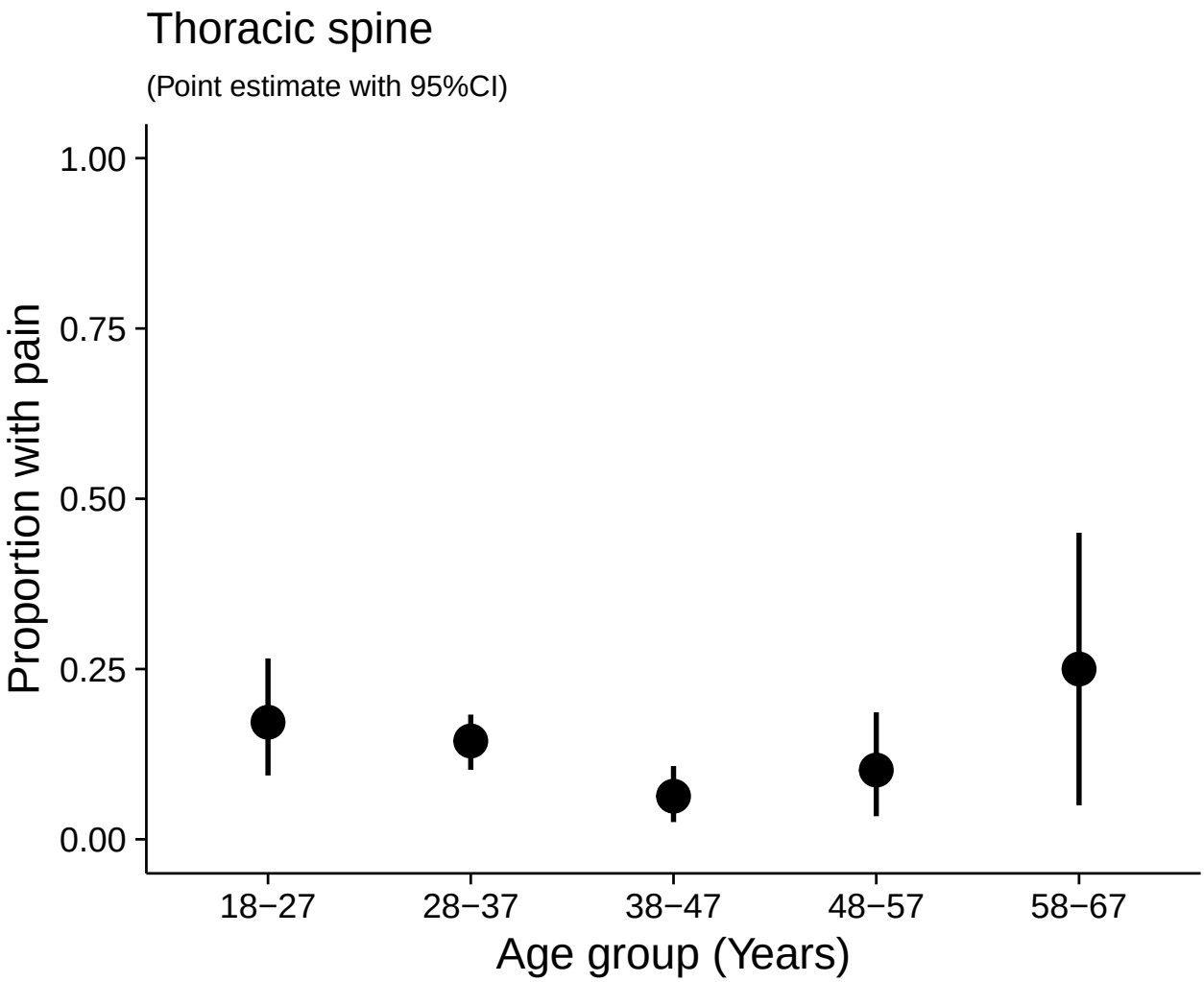
Age group 68−77 years removed because n = 2


Lower back
(Point estimate with 95%CI)
1.00
0.75
0.50
0.25
0.00
Proportion with pain
18−27
28−37
38−47
48−57
58−67
Age group (Years)
Age group 68−77 years removed because n = 2

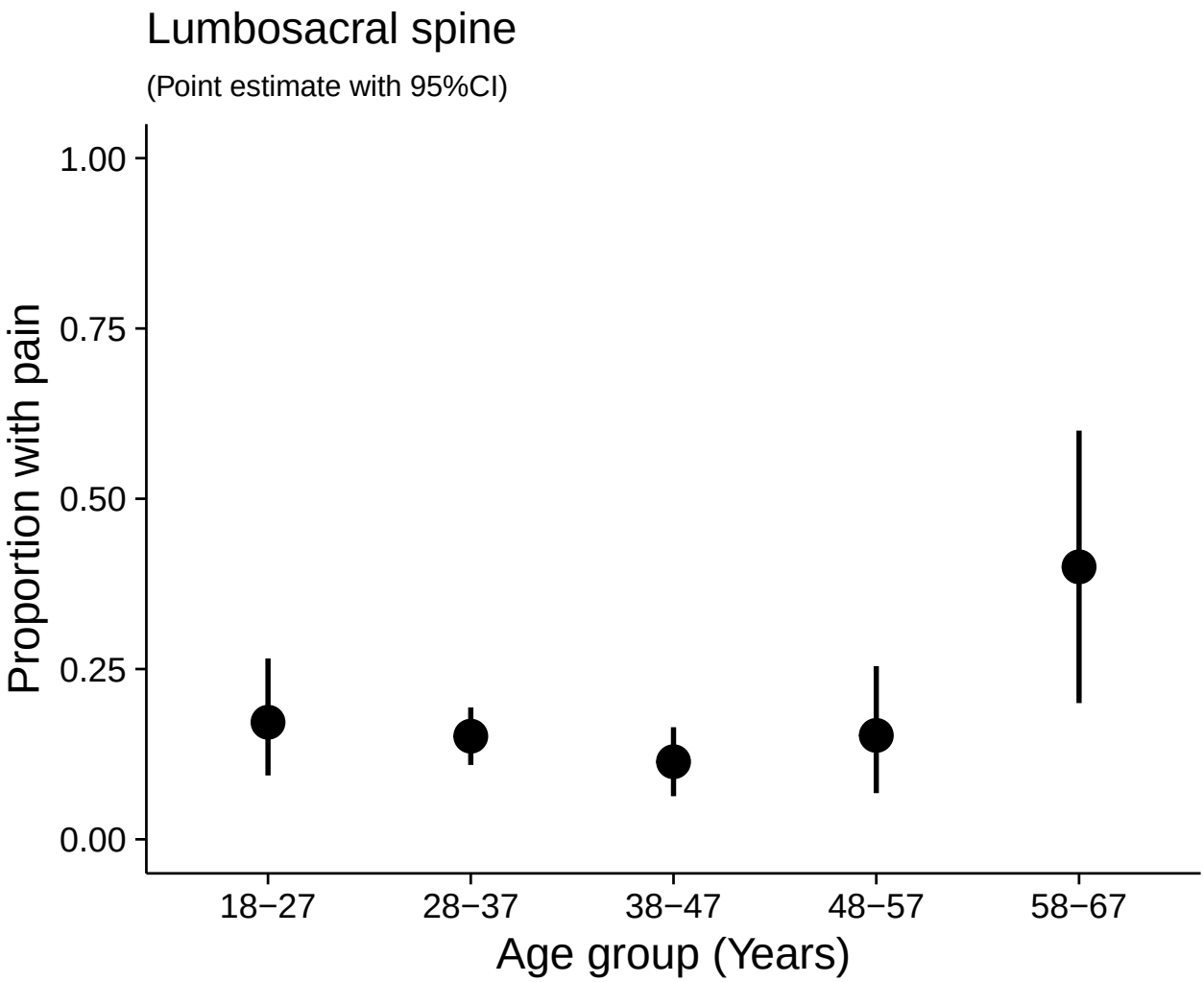

Abdomen
(Point estimate with 95%CI)
1.00
0.75
0.50
0.25
0.00
Proportion with pain
18−27
28−37
38−47
48−57
58−67
Age group (Years)
Age group 68−77 years removed because n = 2



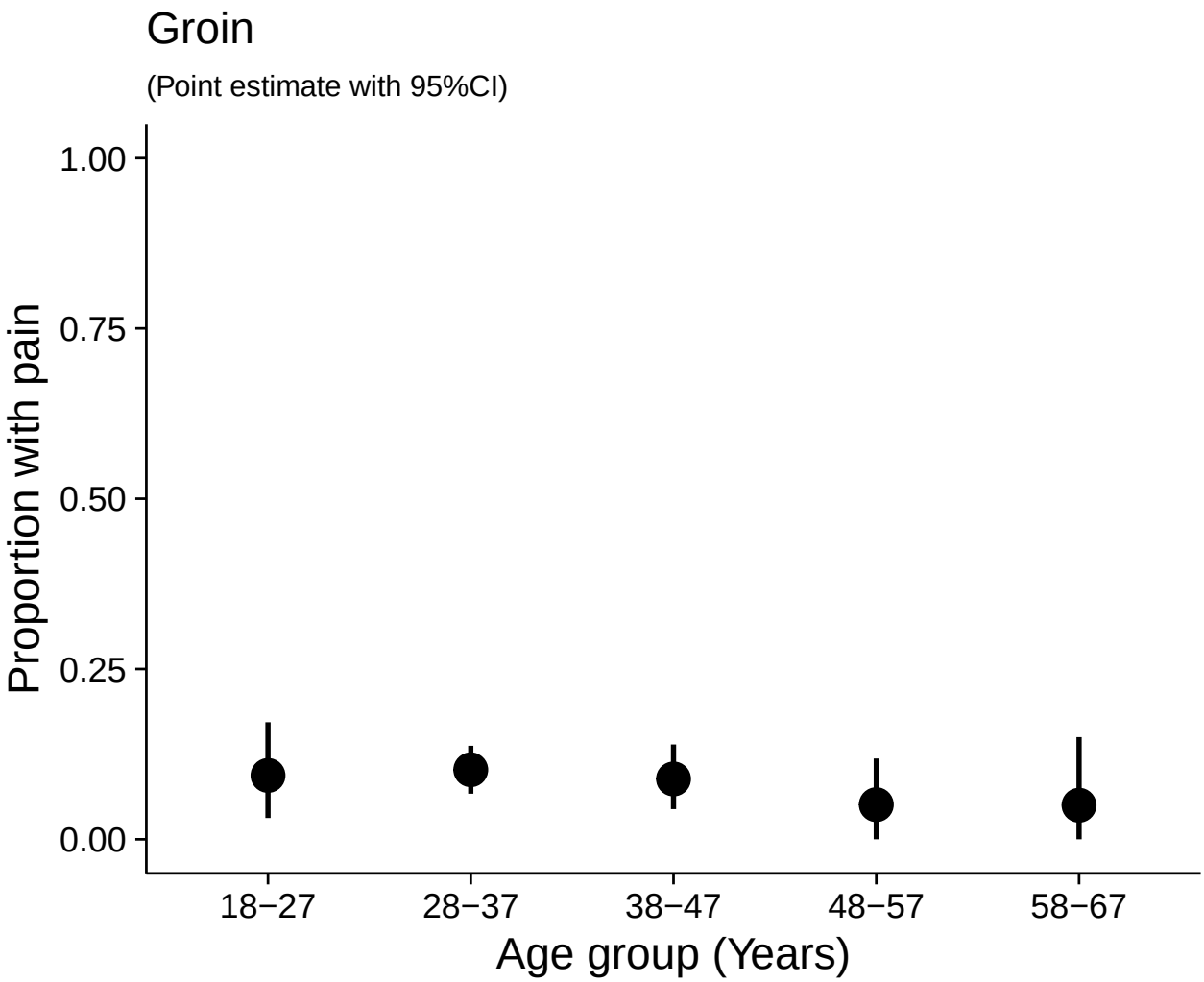
Age group 68−77 years removed because n = 2



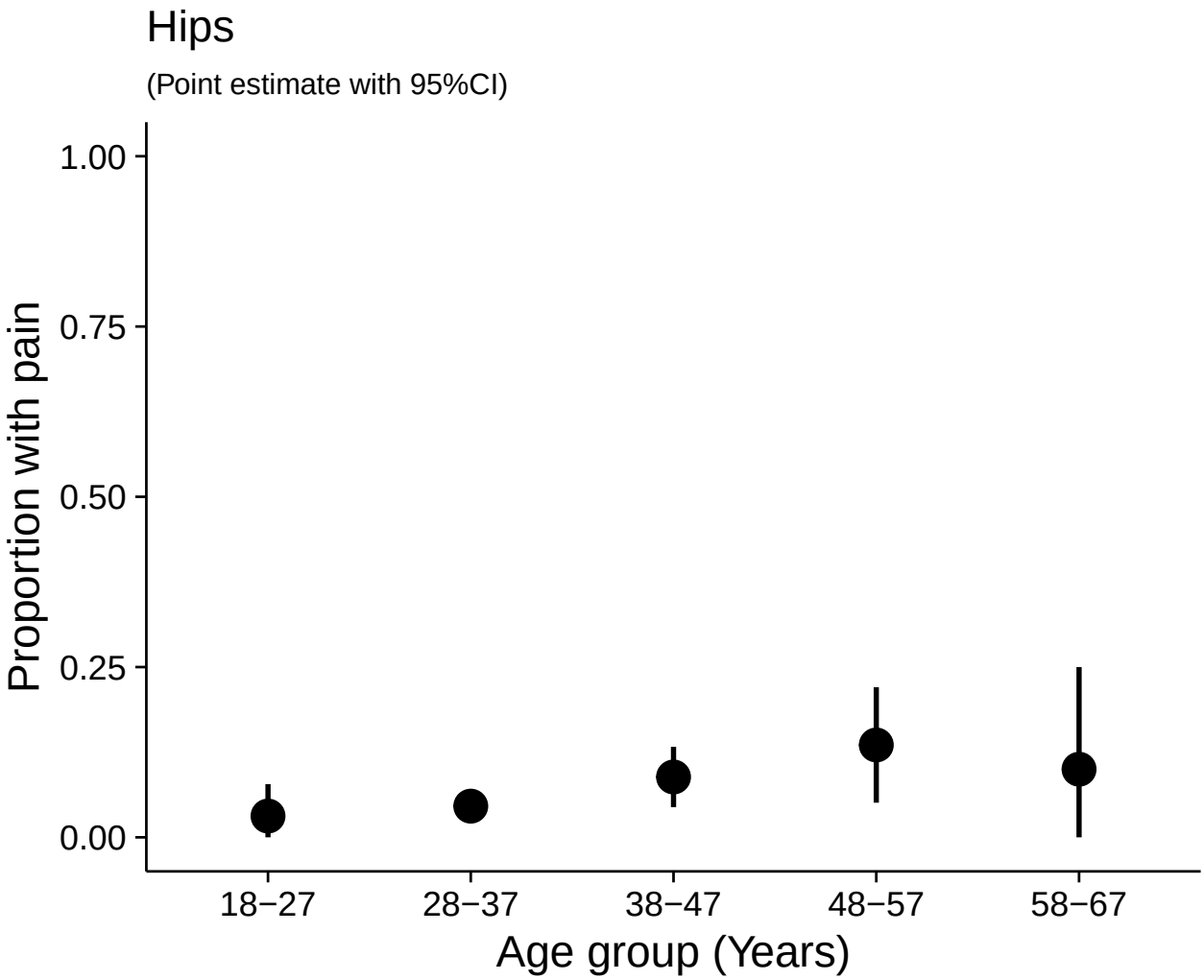
Age group 68−77 years removed because n = 2



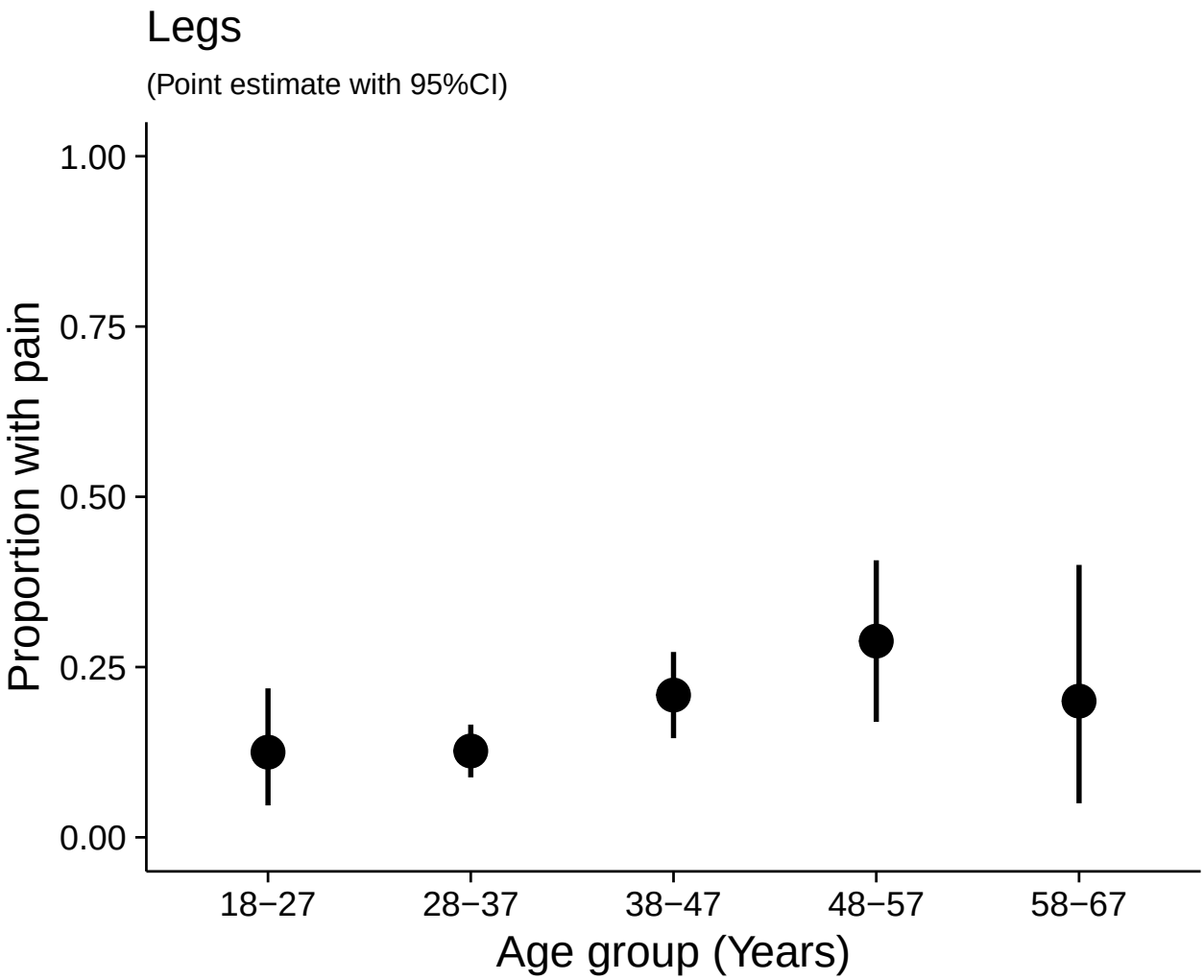
Age group 68−77 years removed because n = 2



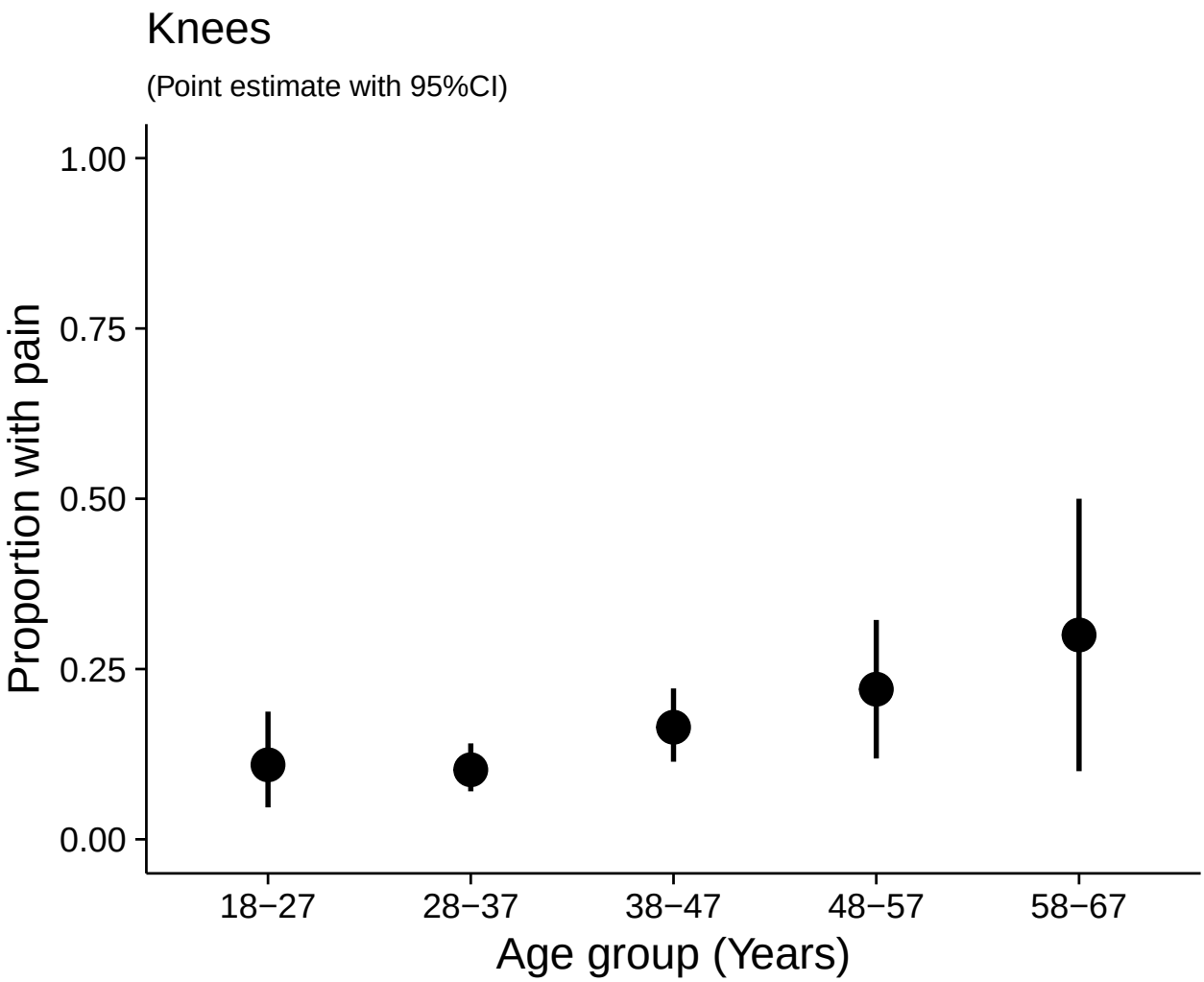
Age group 68−77 years removed because n = 2



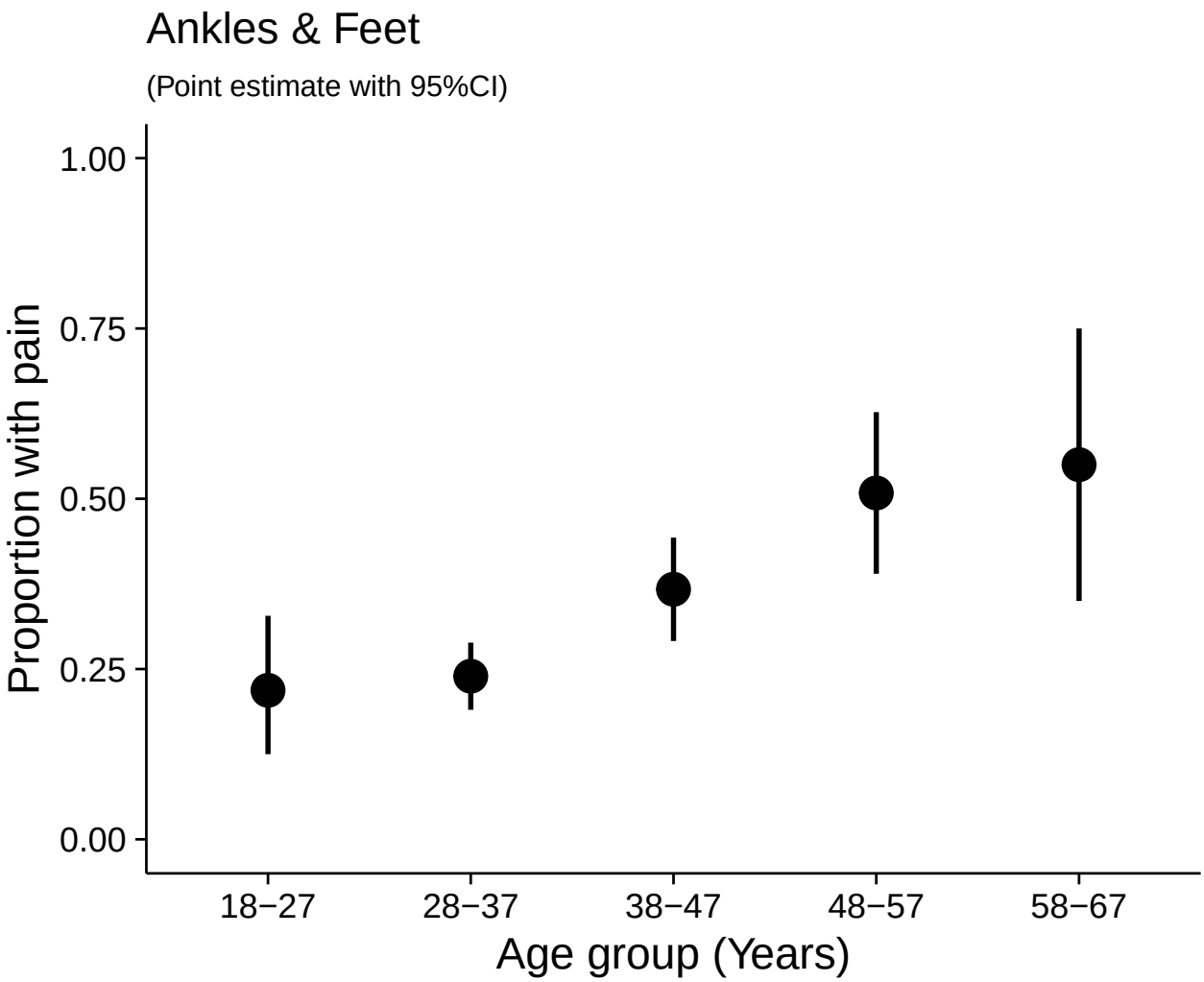
Age group 68−77 years removed because n = 2



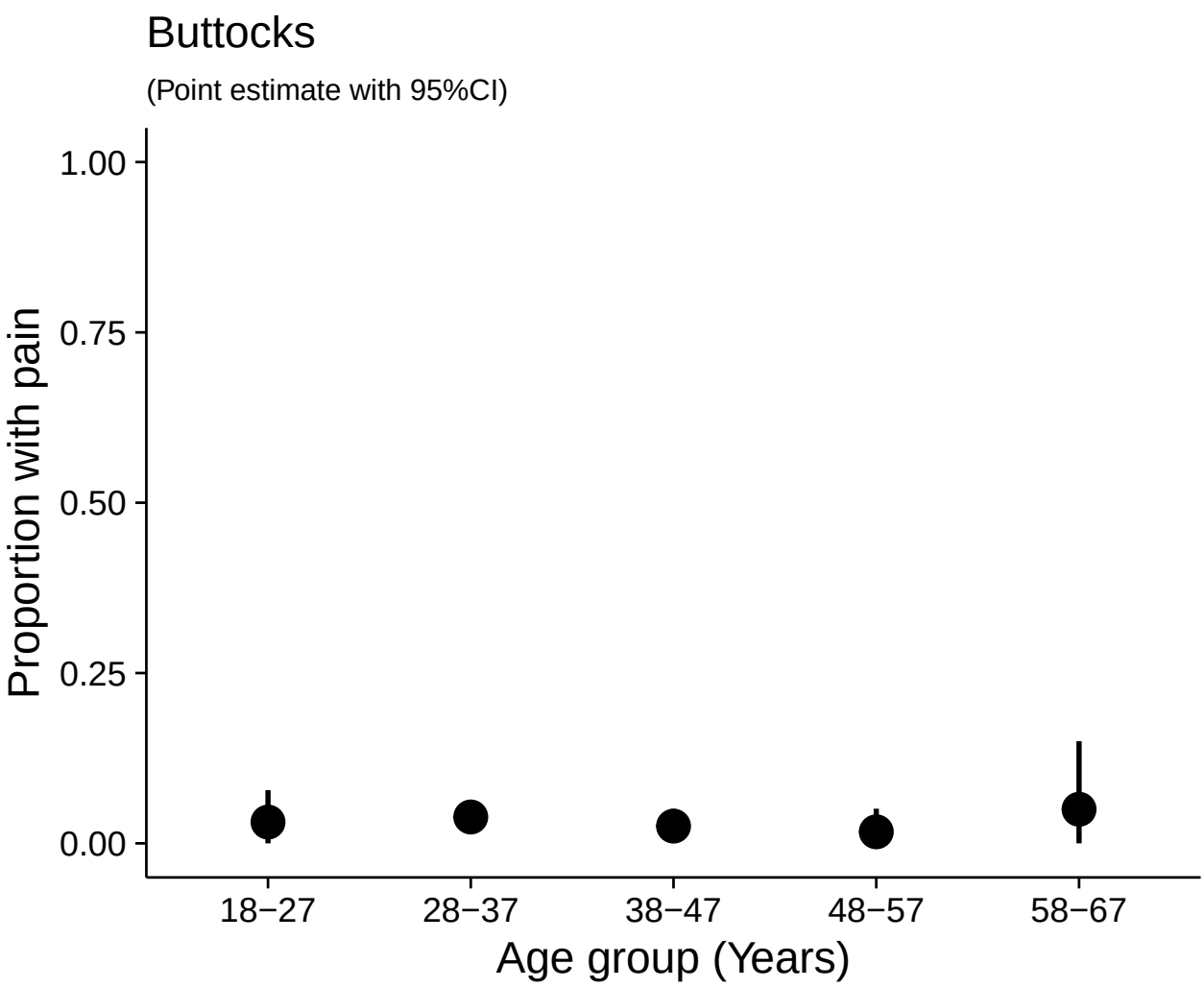
Age group 68−77 years removed because n = 2



Age group 68−77 years removed because n = 2



Age group 68−77 years removed because n = 2



By most recent CD4 T-cell count

Process data

```
# Set seed
set.seed(2020)

# Select CD4 recent data
cd4 <- demo[, c('ID', 'CD4_recent')]

# Join to boot_data & remove ID and Upper_back (only one outcome -- no pain)
cd4 <- left_join(data, cd4) %>%
    select(-ID, -Upper_back)

# Get complete cases
```

```r
cd4 <- cd4[complete.cases(cd4), ]

# Pivot and add CD4 recent group categories (counts of 100)
cd4_boot <- cd4 %>%
    # Pivot to long format
    pivot_longer(cols = -CD4_recent,
                 names_to = 'site',
                 values_to = 'pain_present') %>%
    # Add CD4 recent categories
    mutate(cd4_group = case_when(
        CD4_recent < 100 ~ '0-99',
        CD4_recent >= 100 & CD4_recent < 200 ~ '100-199',
        CD4_recent >= 200 & CD4_recent < 300 ~ '200-299',
        CD4_recent >= 300 & CD4_recent < 400 ~ '300-399',
        CD4_recent >= 400 & CD4_recent < 500 ~ '400-499',
        CD4_recent >= 500 ~ '500+'
    ))

# Print count per CD4 recent group
cd4_boot %>%
    group_by(site, cd4_group) %>%
    summarise(count = n()) %>%
    filter(site == 'Abdomen') %>%
    ungroup() %>%
    select(-site) %>%
    kable(caption = 'Participant count per CD4 group')
```

Table 35: Participant count per CD4 group

cd4_group	count
0-99	68
100-199	105
200-299	108
300-399	76
400-499	46
500+	93

```r
# Generate CIs
cd4_boot2 <- cd4_boot %>%
    # Remove CD4 recent
    select(-CD4_recent) %>%
    # Nest by CD4 recent group and body site
    group_by(cd4_group, site) %>%
    nest() %>%
    # Boostrap data
    mutate(boot = map(.x = data,
                      ~ boot(data = .x,
                             statistic = prop_func,
                             R = 999,
                             stype = 'i',
                             parallel = 'multicore',
                             ncpus = 4))) %>%
```

```
    # Get CI
    mutate(ci = map(.x = boot,
                    ~ boot.ci(.x, type = 'perc'))) %>%
    # Extract ci data
    mutate(point_est = map(.x = ci,
                           ~ .x$t0),
           lower_ci = map(.x = ci,
                          ~ .x$percent[[4]]),
           upper_ci = map(.x = ci,
                          ~ .x$percent[[5]])) %>%
    # Remove columns
    select(-data, -boot, -ci) %>%
    # Unnest
    unnest(cols = c(point_est, lower_ci, upper_ci)) %>%
    ungroup()

# Re-nest by body region and generate figures and tables
cd4_boot2 <- cd4_boot2 %>%
    # Fix site labels
    mutate(site = str_replace_all(site,
                                  pattern = '_',
                                  replacement = ' '),
           site = str_replace_all(site,
                                  pattern = '\\.',
                                  replacement = ' & ')) %>%
    # Group and nest
    group_by(site) %>%
    nest() %>%
    # Arrange CD4 recent groups
    # Plot data
    mutate(plots = map2(.x = data,
                        .y = site,
                        ~ .x %>%
                            ggplot(data = .) +
                            aes(x = cd4_group,
                                y = point_est,
                                ymin = lower_ci,
                                ymax = upper_ci) +
                            geom_linerange(size = 1,
                                           colour = '#000000') +
                            geom_point(colour = '#000000',
                                       size = 6) +
                            labs(title = .y,
                                 subtitle = '(Point estimate with 95%CI)',
                                 x = expression('CD4 group (cells.mm'^-3*')'),
                                 y = 'Proportion with pain') +
                            scale_y_continuous(limits = c(0, 1)) +
                            theme_minimal(base_size = 18) +
                            theme(plot.title = element_text(size = 18),
                                  plot.subtitle = element_text(size = 12),
                                  panel.grid = element_blank(),
                                  axis.text = element_text(colour = '#000000'),
                                  axis.line = element_line(size = 0.5),
```

```
                                axis.ticks = element_line(size = 0.5)))) %>%
    # Tabulate data
    mutate(tables = map2(.x = data,
                         .y = site,
                         ~ .x %>%
                             arrange(cd4_group) %>%
                             kable(caption = .y,
                                   digits = 2)))
```

Tabulated proportions (with 95% CIs), by CD4 (recent) group and body site

```
walk(cd4_boot2$tables, ~ print(.x))
```

Table 36: Head

cd4_group	point_est	lower_ci	upper_ci
0-99	0.26	0.18	0.37
100-199	0.39	0.30	0.49
200-299	0.32	0.24	0.42
300-399	0.37	0.26	0.49
400-499	0.30	0.17	0.43
500+	0.25	0.17	0.33

Table 37: Throat

cd4_group	point_est	lower_ci	upper_ci
0-99	0.07	0.01	0.15
100-199	0.02	0.00	0.05
200-299	0.03	0.00	0.06
300-399	0.01	0.00	0.04
400-499	0.04	0.00	0.11
500+	0.00	0.00	0.00

Table 38: Shoulder

cd4_group	point_est	lower_ci	upper_ci
0-99	0.07	0.01	0.15
100-199	0.10	0.05	0.16
200-299	0.06	0.02	0.11
300-399	0.05	0.01	0.11
400-499	0.15	0.04	0.26
500+	0.09	0.03	0.15

Table 39: Arms

cd4_group	point_est	lower_ci	upper_ci
0-99	0.06	0.01	0.12
100-199	0.09	0.04	0.14
200-299	0.00	0.00	0.00
300-399	0.04	0.00	0.08
400-499	0.02	0.00	0.07
500+	0.05	0.02	0.11

Table 40: Elbows

cd4_group	point_est	lower_ci	upper_ci
0-99	0.01	0.00	0.04
100-199	0.05	0.01	0.10
200-299	0.02	0.00	0.06
300-399	0.04	0.00	0.09
400-499	0.07	0.00	0.15
500+	0.06	0.02	0.12

Table 41: Wrists & Hands

cd4_group	point_est	lower_ci	upper_ci
0-99	0.01	0.00	0.04
100-199	0.06	0.02	0.10
200-299	0.06	0.02	0.10
300-399	0.07	0.01	0.13
400-499	0.07	0.00	0.15
500+	0.14	0.08	0.22

Table 42: Chest

cd4_group	point_est	lower_ci	upper_ci
0-99	0.34	0.22	0.46
100-199	0.22	0.14	0.30
200-299	0.17	0.10	0.23
300-399	0.17	0.09	0.26
400-499	0.17	0.09	0.28
500+	0.11	0.04	0.17

Table 43: Lower back

cd4_group	point_est	lower_ci	upper_ci
0-99	0.06	0.01	0.12
100-199	0.08	0.03	0.13
200-299	0.06	0.02	0.10
300-399	0.07	0.01	0.13

cd4_group	point_est	lower_ci	upper_ci
400-499	0.11	0.02	0.20
500+	0.11	0.04	0.17

Table 44: Abdomen

cd4_group	point_est	lower_ci	upper_ci
0-99	0.34	0.22	0.46
100-199	0.30	0.21	0.38
200-299	0.27	0.19	0.36
300-399	0.22	0.13	0.32
400-499	0.30	0.17	0.46
500+	0.24	0.16	0.32

Table 45: Cervical spine

cd4_group	point_est	lower_ci	upper_ci
0-99	0.04	0.00	0.10
100-199	0.09	0.04	0.14
200-299	0.02	0.00	0.05
300-399	0.07	0.01	0.13
400-499	0.09	0.02	0.17
500+	0.03	0.00	0.08

Table 46: Thoracic spine

cd4_group	point_est	lower_ci	upper_ci
0-99	0.13	0.06	0.22
100-199	0.10	0.05	0.17
200-299	0.10	0.05	0.16
300-399	0.14	0.08	0.22
400-499	0.22	0.11	0.35
500+	0.15	0.09	0.23

Table 47: Lumbosacral spine

cd4_group	point_est	lower_ci	upper_ci
0-99	0.09	0.03	0.16
100-199	0.13	0.07	0.20
200-299	0.15	0.08	0.21
300-399	0.17	0.09	0.26
400-499	0.30	0.17	0.43
500+	0.20	0.13	0.29

Table 48: Groin

cd4_group	point_est	lower_ci	upper_ci
0-99	0.10	0.03	0.18
100-199	0.12	0.07	0.19
200-299	0.09	0.05	0.16
300-399	0.12	0.05	0.20
400-499	0.11	0.02	0.20
500+	0.08	0.02	0.13

Table 49: Hips

cd4_group	point_est	lower_ci	upper_ci
0-99	0.01	0.00	0.06
100-199	0.06	0.02	0.10
200-299	0.05	0.01	0.09
300-399	0.05	0.01	0.11
400-499	0.11	0.02	0.20
500+	0.13	0.06	0.20

Table 50: Legs

cd4_group	point_est	lower_ci	upper_ci
0-99	0.13	0.06	0.22
100-199	0.11	0.06	0.18
200-299	0.15	0.08	0.21
300-399	0.18	0.11	0.28
400-499	0.20	0.09	0.30
500+	0.22	0.13	0.31

Table 51: Knees

cd4_group	point_est	lower_ci	upper_ci
0-99	0.12	0.04	0.19
100-199	0.11	0.06	0.17
200-299	0.15	0.08	0.21
300-399	0.12	0.05	0.20
400-499	0.17	0.07	0.28
500+	0.20	0.13	0.29

Table 52: Ankles & Feet

cd4_group	point_est	lower_ci	upper_ci
0-99	0.26	0.16	0.37
100-199	0.30	0.22	0.39
200-299	0.31	0.23	0.41

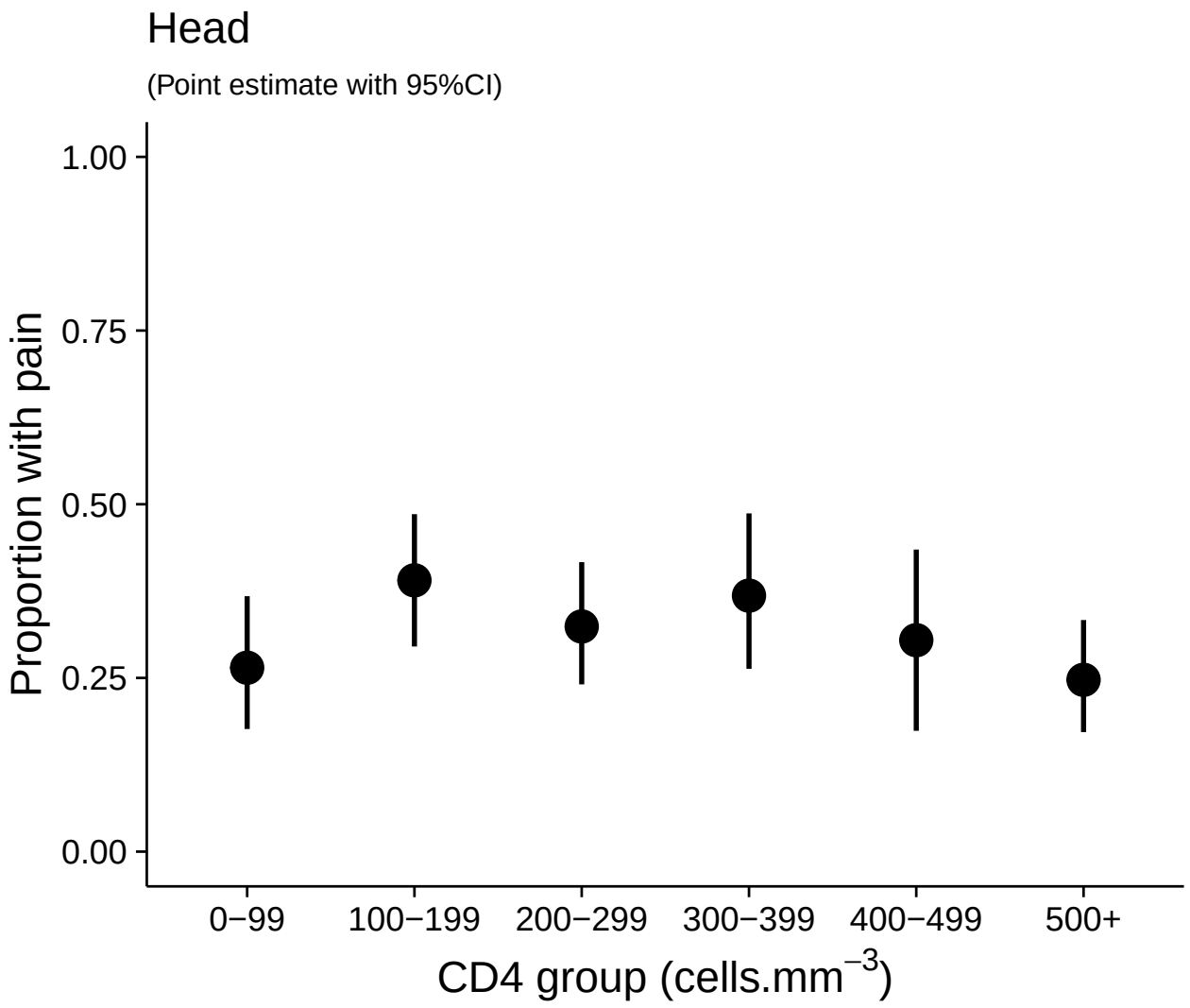
cd4_group	point_est	lower_ci	upper_ci
300-399	0.25	0.16	0.36
400-499	0.26	0.15	0.39
500+	0.33	0.24	0.43

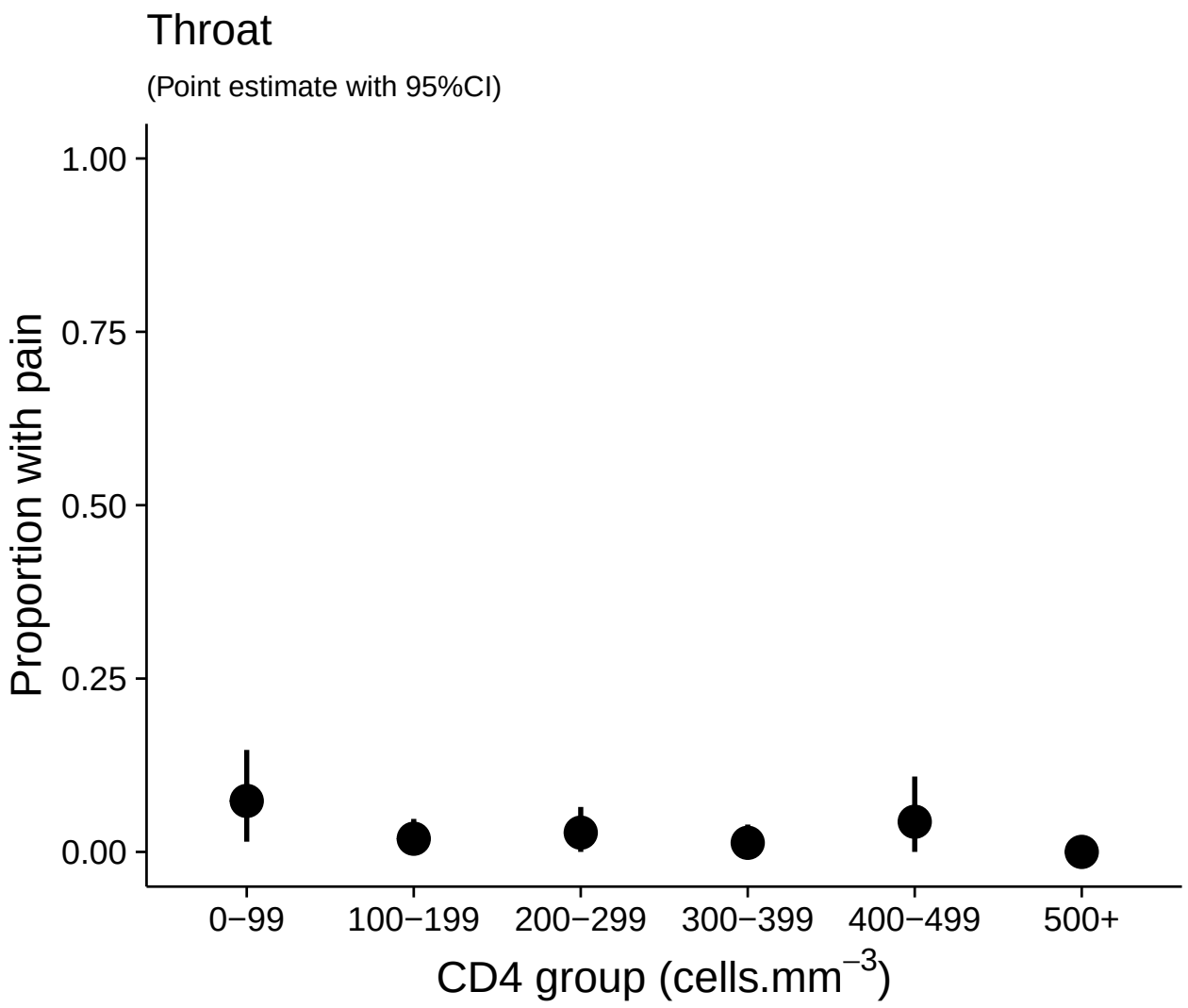
Table 53: Buttocks

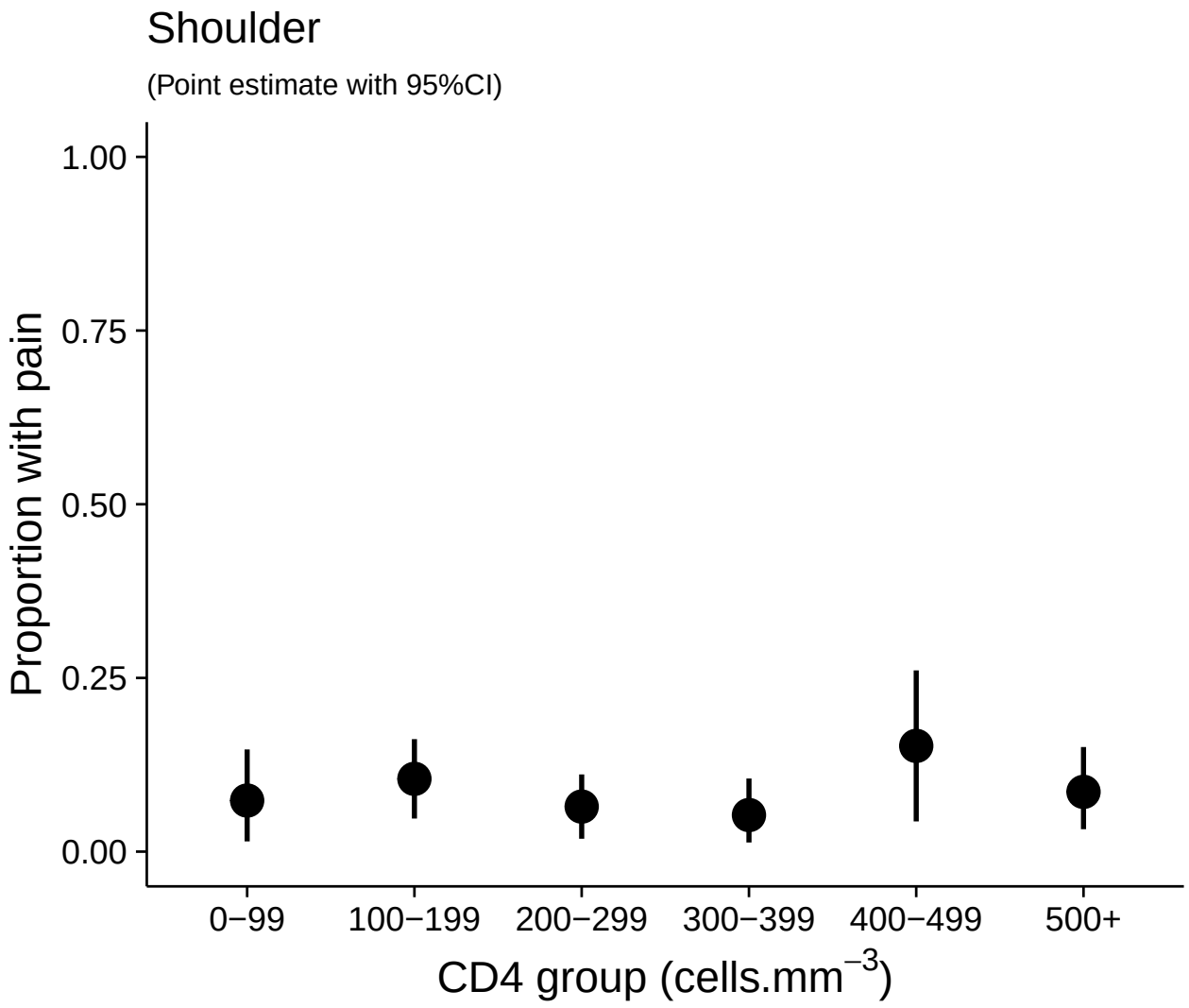
cd4_group	point_est	lower_ci	upper_ci
0-99	0.04	0.00	0.10
100-199	0.01	0.00	0.03
200-299	0.03	0.00	0.06
300-399	0.05	0.01	0.12
400-499	0.04	0.00	0.11
500+	0.06	0.02	0.12

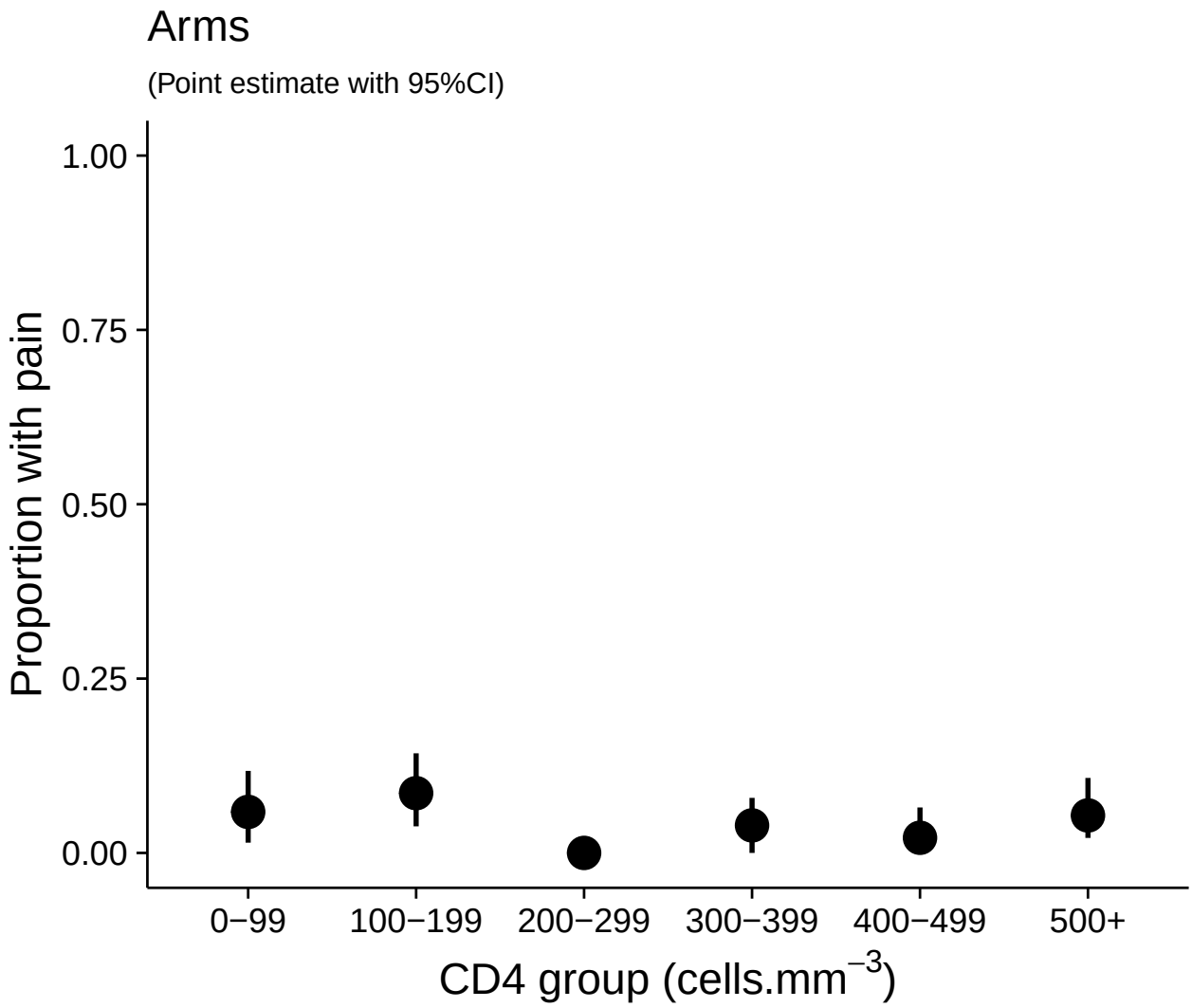
Plotted proportions (with 95% CIs), by CD4 (recent) group and body site

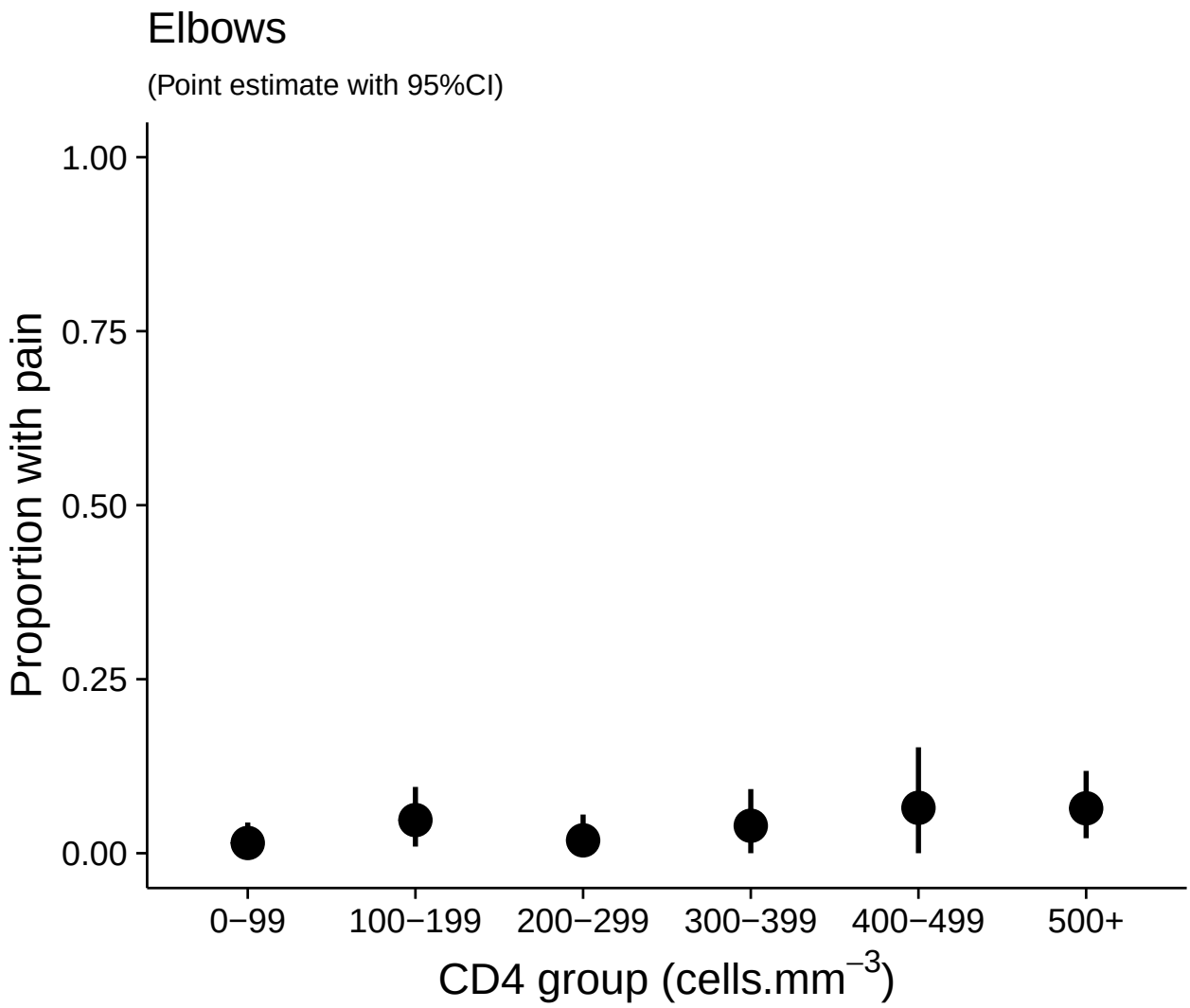
```
walk(cd4_boot2$plots, ~ print(.x))
```

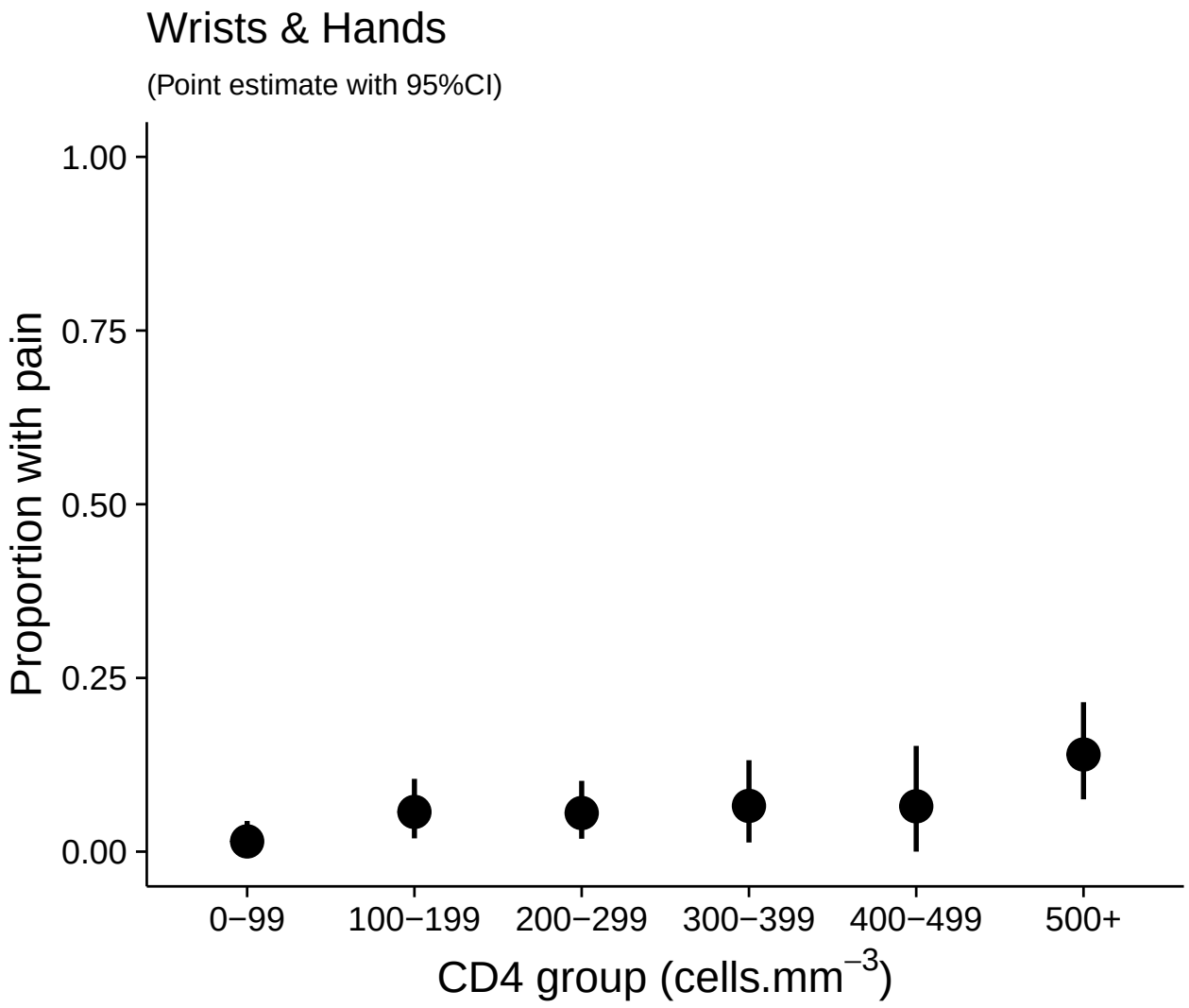

Head
(Point estimate with 95%CI)
Proportion with pain
1.00
0.75
0.50
0.25
0.00
0−99
100−199
200−299
300−399
400−499
500+
CD4 group (cells.mm^{-3})

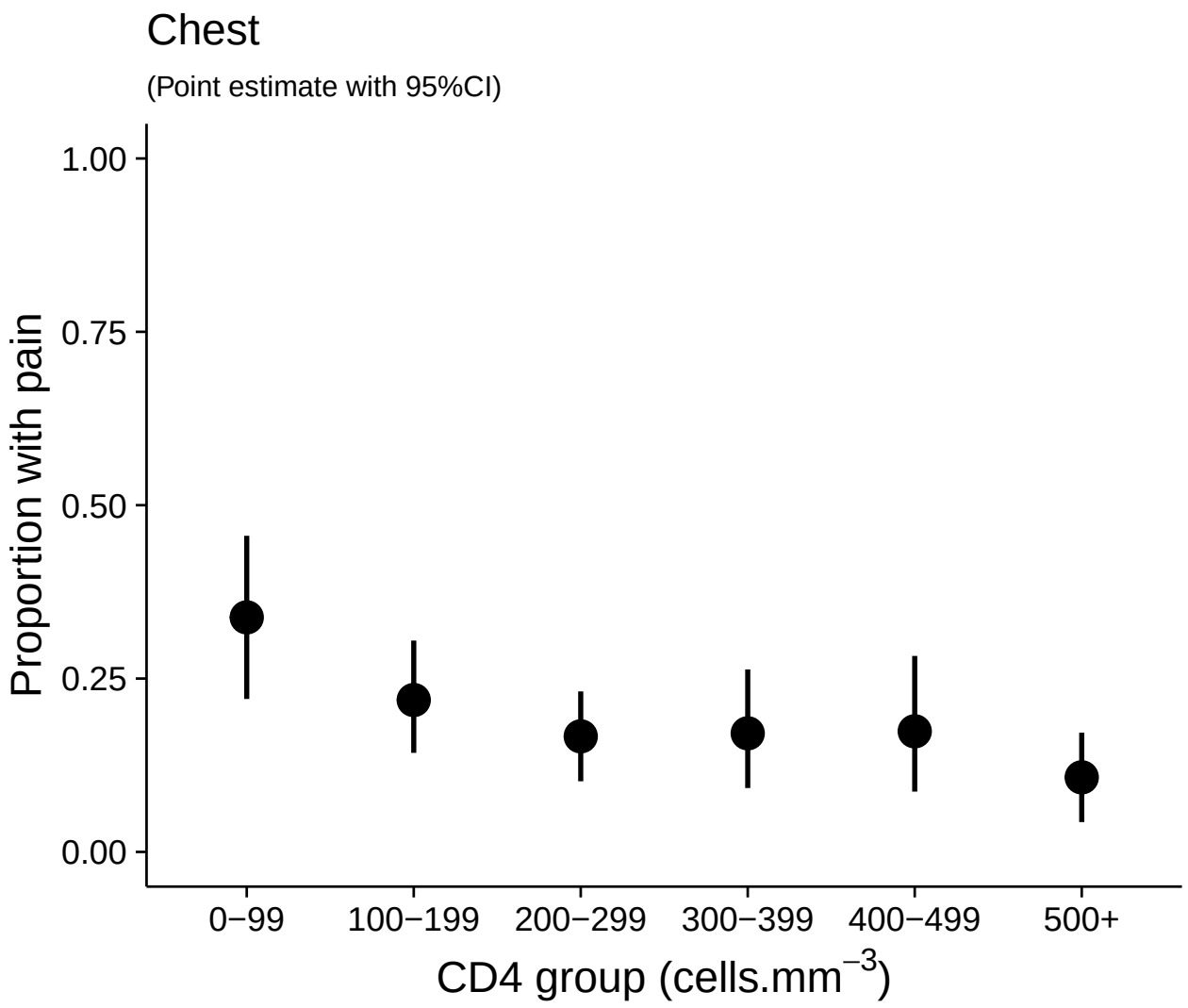

Throat
(Point estimate with 95%CI)
Proportion with pain
1.00
0.75
0.50
0.25
0.00
0−99
100−199
200−299
300−399
400−499
500+
CD4 group (cells.mm^{-3})

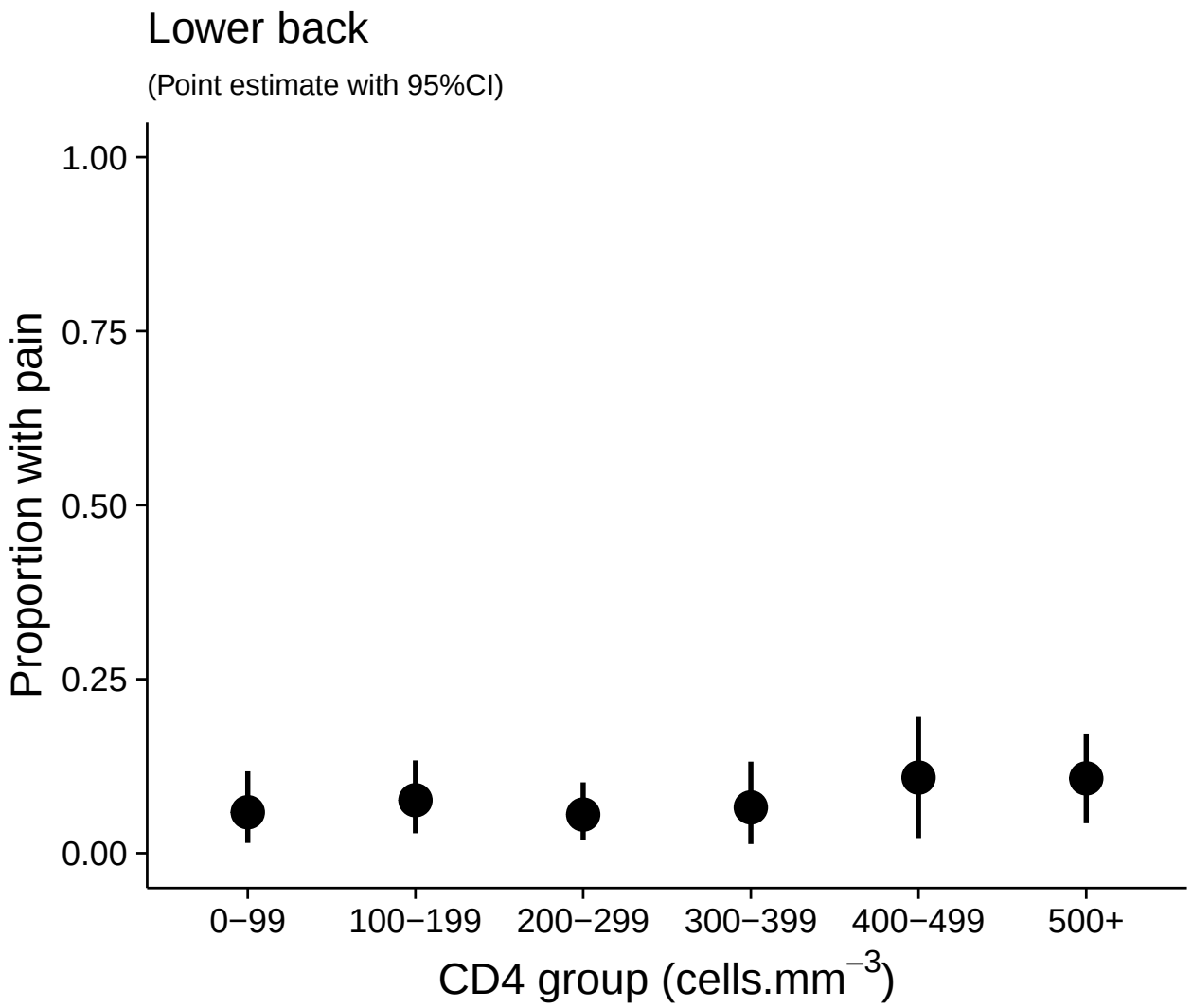

Shoulder
(Point estimate with 95%CI)
Proportion with pain
1.00
0.75
0.50
0.25
0.00
0−99
100−199
200−299
300−399
400−499
500+
CD4 group (cells.mm^{-3})

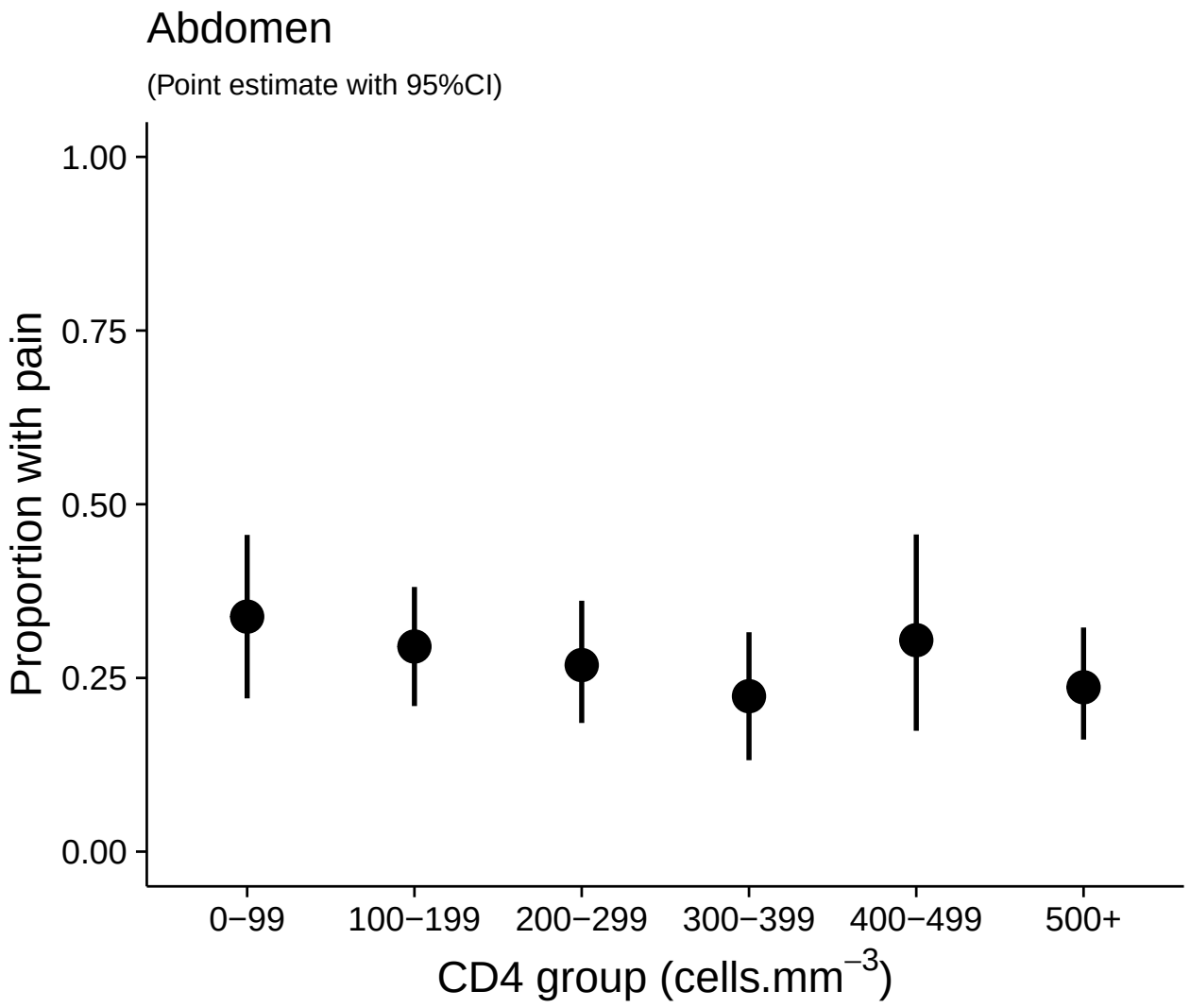

Arms
(Point estimate with 95%CI)
1.00
0.75
0.50
0.25
0.00
Proportion with pain
0−99
100−199
200−299
300−399
400−499
500+
CD4 group (cells.mm^{-3})

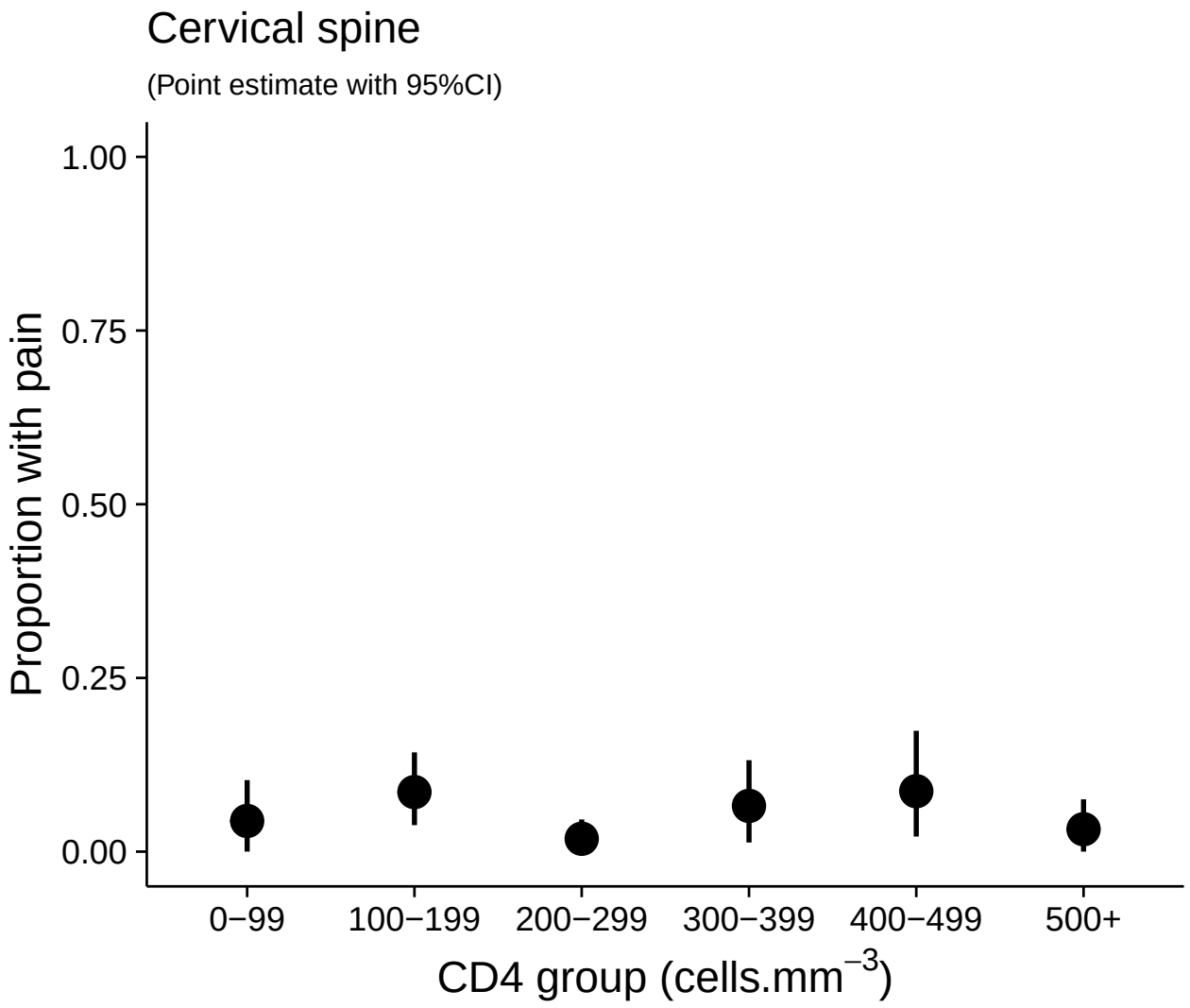

Elbows
(Point estimate with 95%CI)
Proportion with pain
1.00
0.75
0.50
0.25
0.00
0−99
100−199
200−299
300−399
400−499
500+
CD4 group (cells.mm^{-3})

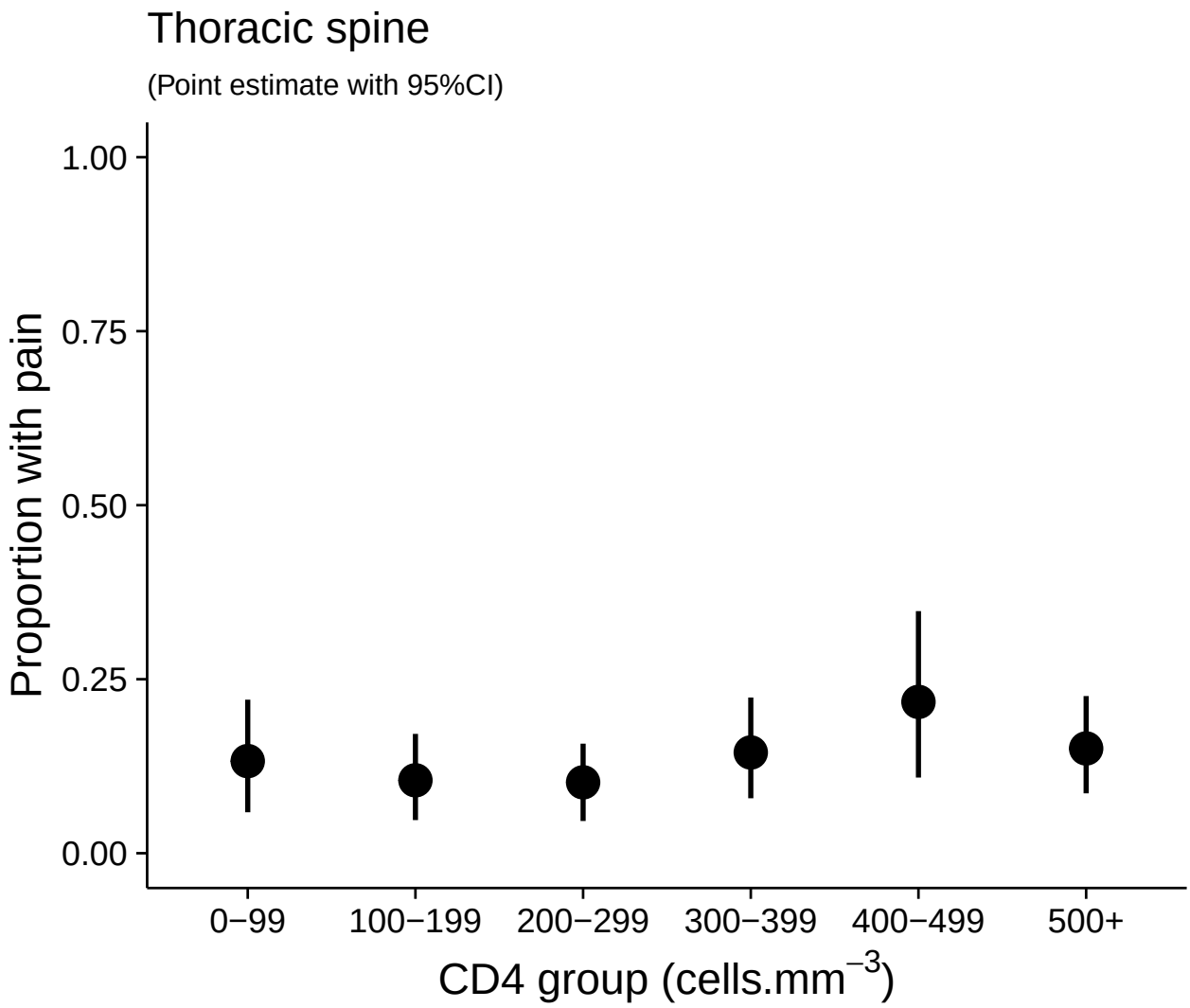

Wrists & Hands
(Point estimate with 95%CI)
Proportion with pain
1.00
0.75
0.50
0.25
0.00
0−99
100−199
200−299
300−399
400−499
500+
CD4 group (cells.mm^{-3})

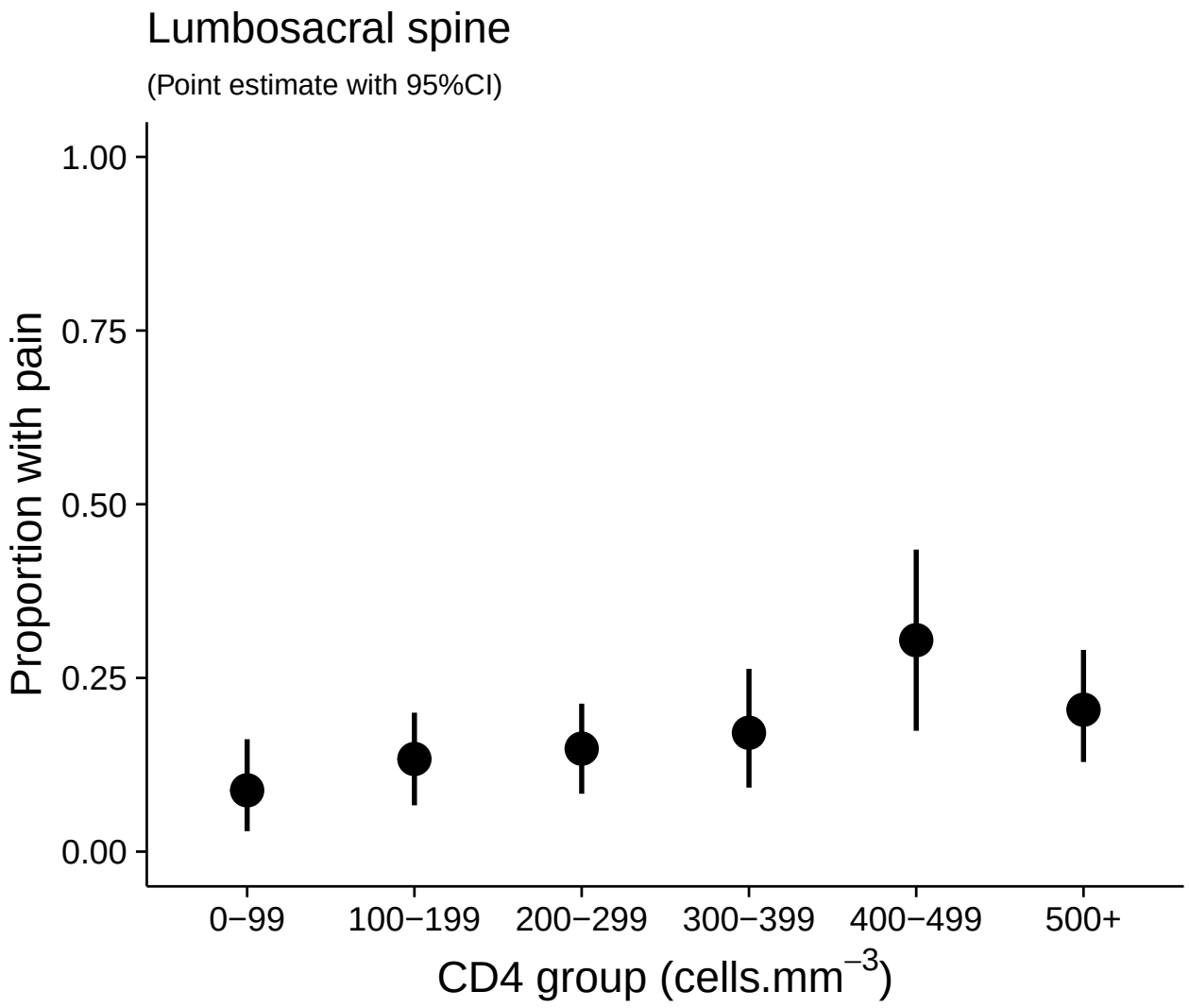

Chest
(Point estimate with 95%CI)
Proportion with pain
1.00
0.75
0.50
0.25
0.00
0−99
100−199
200−299
300−399
400−499
500+
CD4 group (cells.mm^{-3})

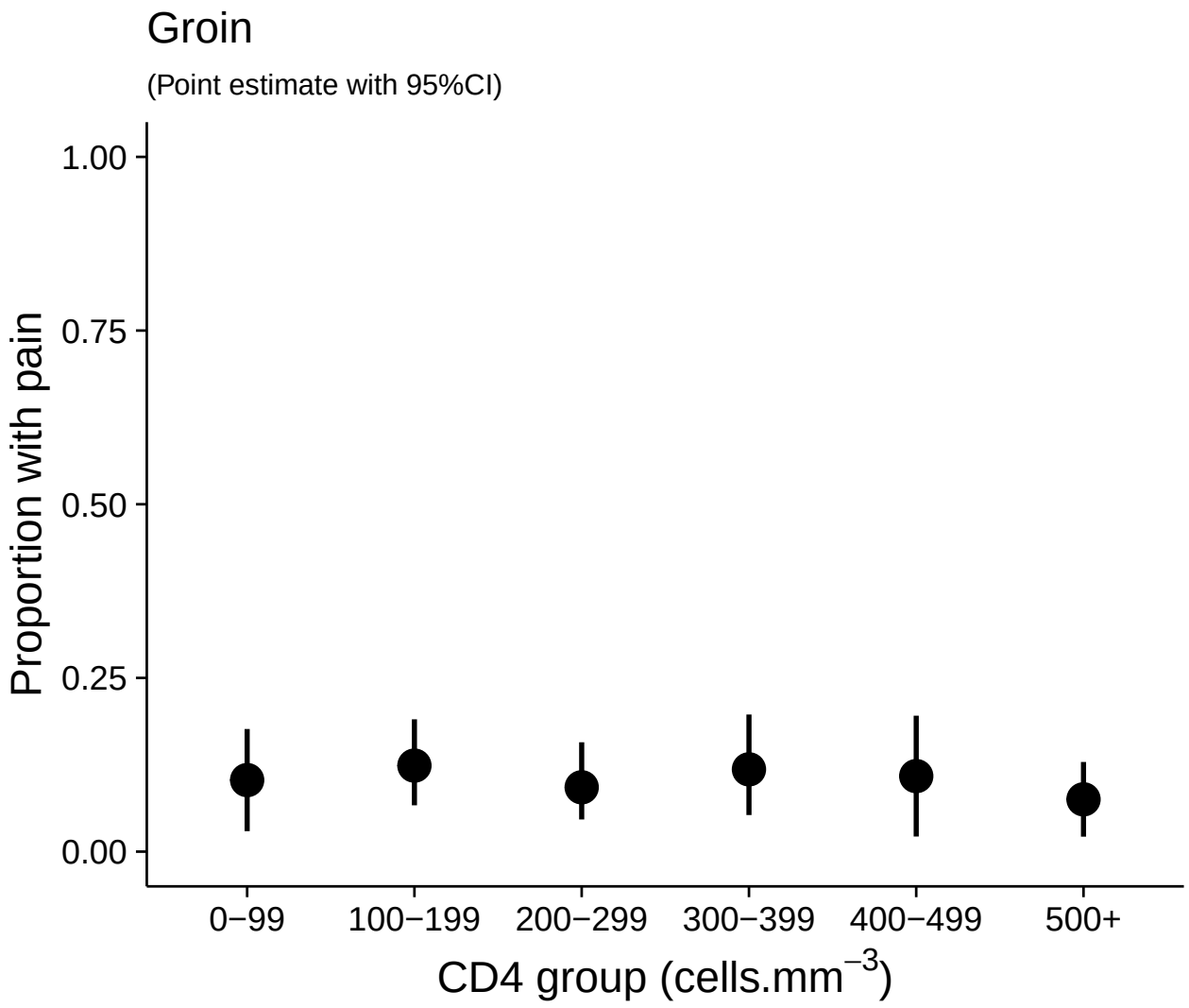

Lower back
(Point estimate with 95%CI)
Proportion with pain
1.00
0.75
0.50
0.25
0.00
0−99
100−199
200−299
300−399
400−499
500+
CD4 group (cells.mm^{-3})

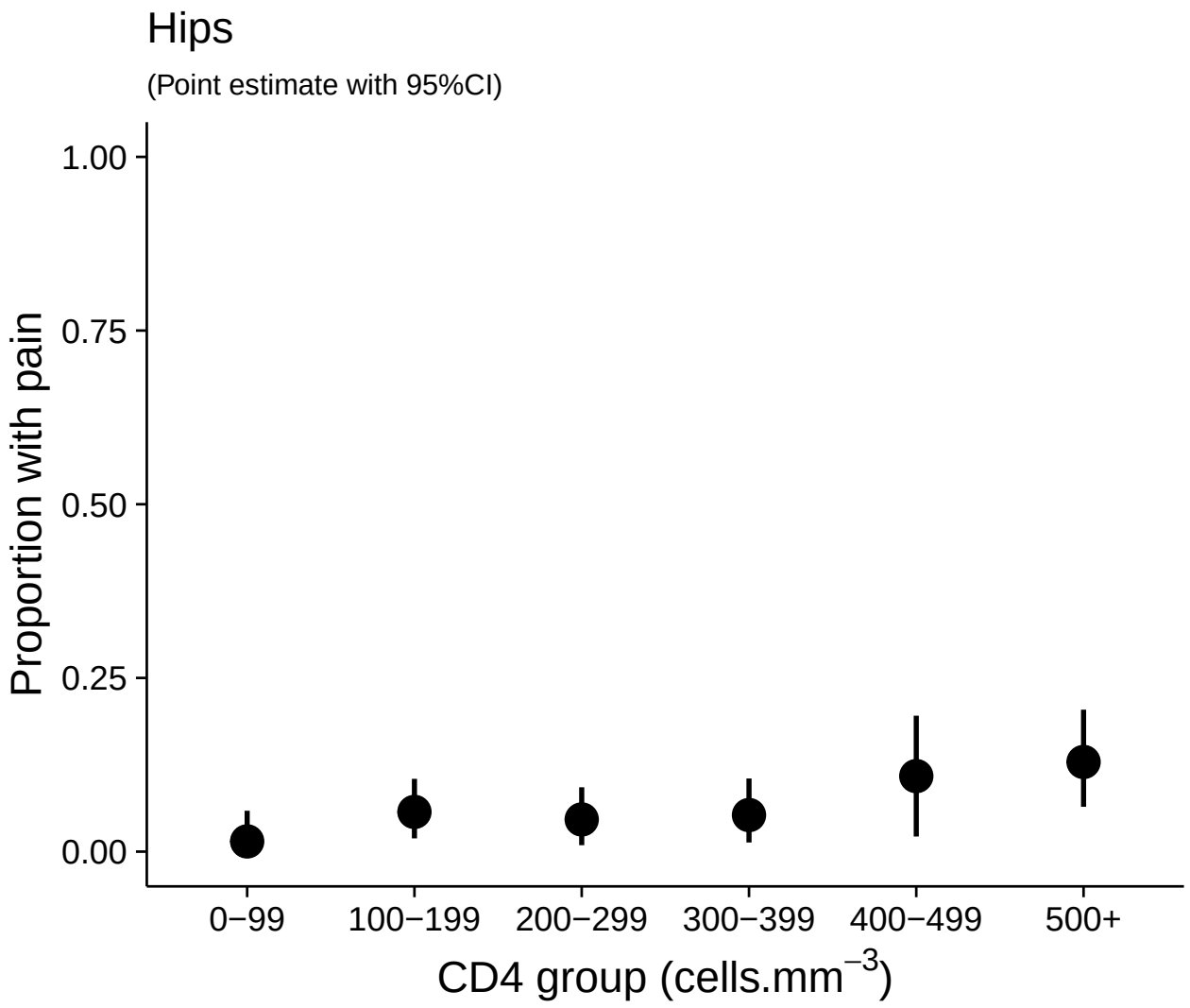

Abdomen
(Point estimate with 95%CI)
Proportion with pain
1.00
0.75
0.50
0.25
0.00
0−99
100−199
200−299
300−399
400−499
500+
CD4 group (cells.mm−3)

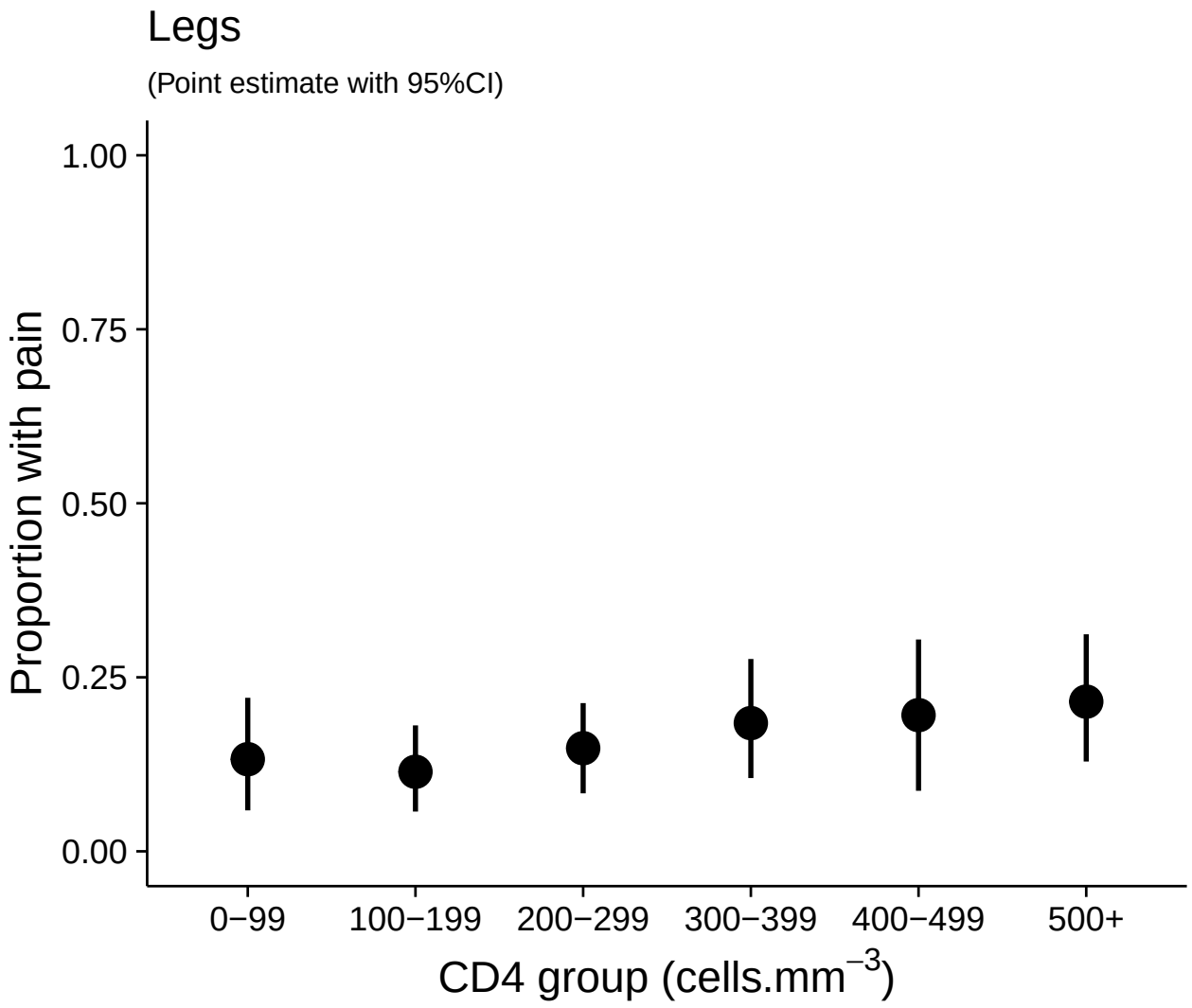

Cervical spine
(Point estimate with 95%CI)
Proportion with pain
1.00
0.75
0.50
0.25
0.00
0−99
100−199
200−299
300−399
400−499
500+
CD4 group (cells.mm−3)

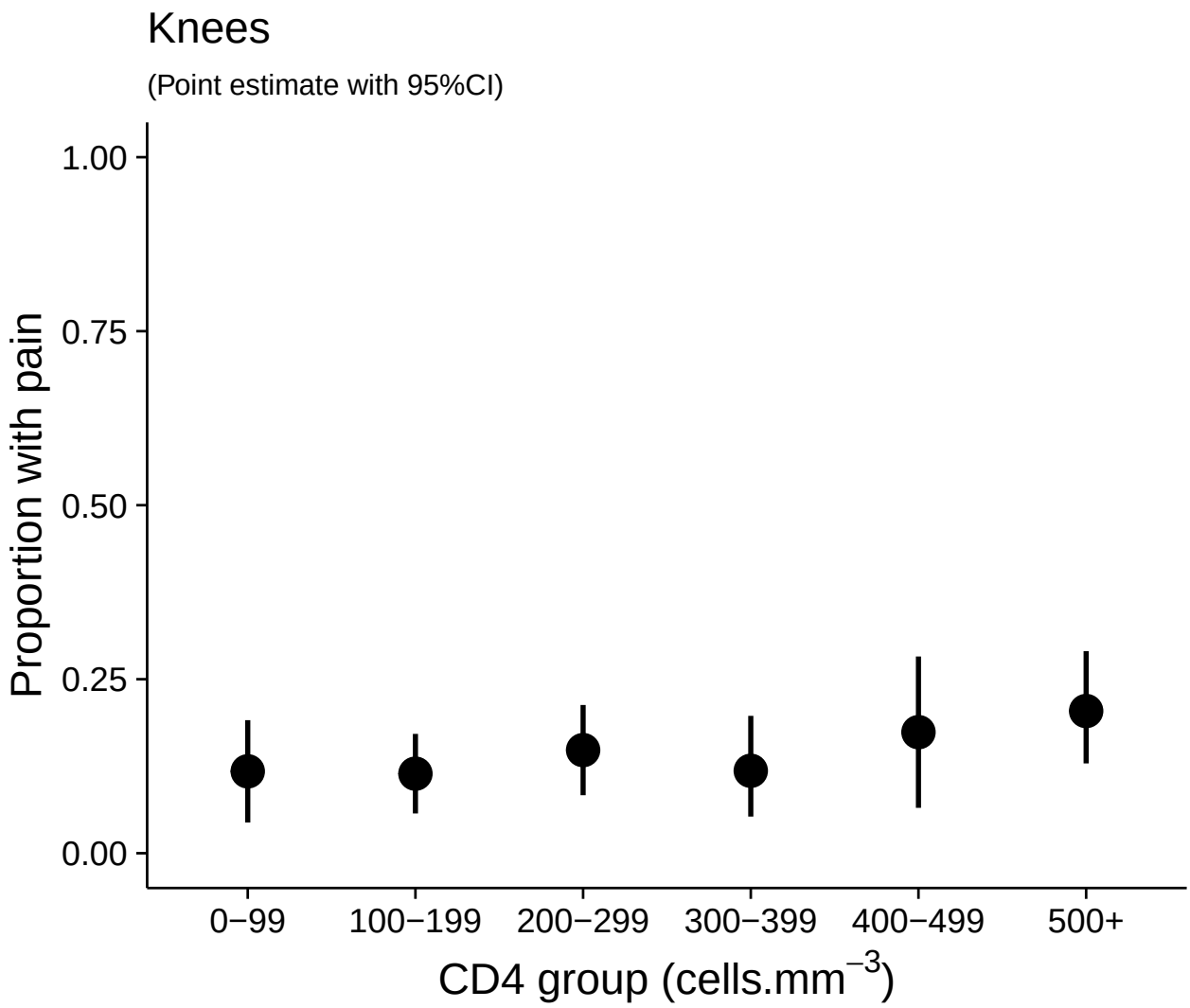

Thoracic spine
(Point estimate with 95%CI)
Proportion with pain
1.00
0.75
0.50
0.25
0.00
0−99
100−199
200−299
300−399
400−499
500+
CD4 group (cells.mm−3)

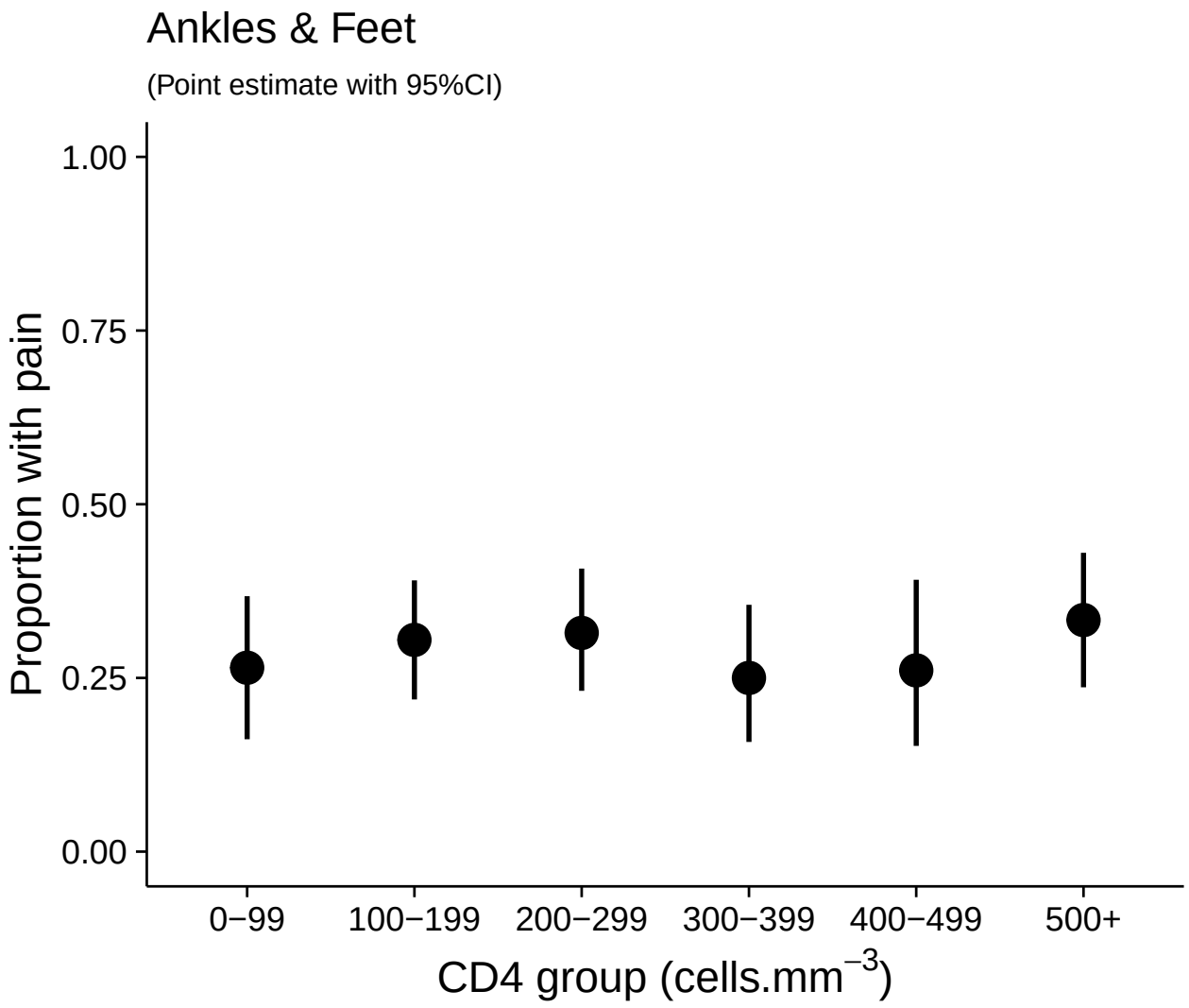

Lumbosacral spine
(Point estimate with 95%CI)
Proportion with pain
1.00
0.75
0.50
0.25
0.00
0−99
100−199
200−299
300−399
400−499
500+
CD4 group (cells.mm−3)

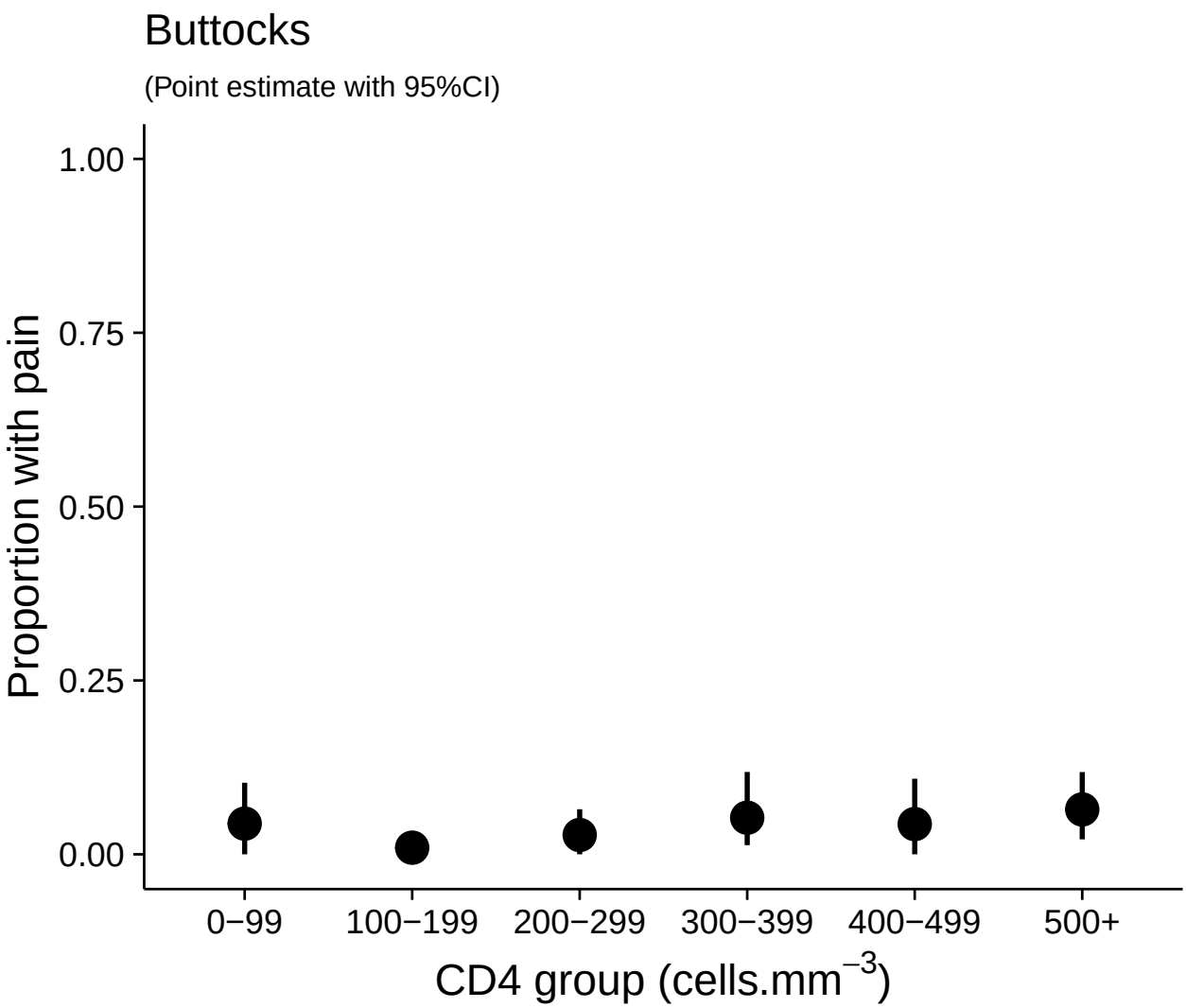

Groin
(Point estimate with 95%CI)
1.00
0.75
0.50
0.25
0.00
Proportion with pain
0−99
100−199
200−299
300−399
400−499
500+
CD4 group (cells.mm−3)


Hips
(Point estimate with 95%CI)
Proportion with pain
1.00
0.75
0.50
0.25
0.00
0−99
100−199
200−299
300−399
400−499
500+
CD4 group (cells.mm^{-3})


Legs
(Point estimate with 95%CI)
Proportion with pain
1.00
0.75
0.50
0.25
0.00
0−99
100−199
200−299
300−399
400−499
500+
CD4 group (cells.mm^{-3})


Knees
(Point estimate with 95%CI)
1.00
0.75
0.50
0.25
0.00
Proportion with pain
0−99
100−199
200−299
300−399
400−499
500+
CD4 group (cells.mm−3)


Ankles & Feet
(Point estimate with 95%CI)
Proportion with pain
1.00
0.75
0.50
0.25
0.00
0−99
100−199
200−299
300−399
400−499
500+
CD4 group (cells.mm−3)



Logistic regression (generalised linear mixed model)

Note: Age treated as a continuous variable, not like the categories used in the figures shwon above.

Process data

Extract cases with complete data for CD4 T-cell count, age, and sex.

```
# Select demographic data
demo_glmm <- demo[, c('ID', 'CD4_recent', 'Sex', 'Age')] %>%
    # Generate site codes
    mutate(Study_site = str_remove(ID,
                                   pattern = '[0-9][0-9]?[0-9]?[0-9]?[0-9]?')) %>%
    # Set column names
    set_names(nm = c('ID', 'CD4_recent', 'Sex', 'Age', 'Study_site'))
```

```r
# Process data and remove incomplete cases
data_glmm <- data %>%
    # Join with extracted demographics data (demo_reduced)
    left_join(demo_glmm) %>%
    # Remove upper back (only one outcome -- no pain) and ID
    select(-ID, -Upper_back) %>%
    # Extract complete cases
    filter(complete.cases(.))

# Convert data_glm to long format
data_glmm.long <- data_glmm %>%
    pivot_longer(cols = -c(CD4_recent, Age, Sex, Study_site),
                 names_to = 'Pain_site',
                 values_to = 'Pain_present')

# Extract vector of body sites where the proportion with pain was >= 10%
## Stops "Singular" fit warning when performing GLMM
high_prop <- data_glmm.long %>%
    group_by(Pain_site, Pain_present) %>%
    summarise(n = n()) %>%
    mutate(total = sum(n),
           prop = n/total) %>%
    filter(Pain_present == 'Yes') %>%
    filter(prop >= 0.10) %>%
    .$Pain_site

# Filter for pain sites selected above
data_glmm.filtered <- data_glmm.long %>%
    filter(Pain_site %in% high_prop)
```

Tabulate number of cases in original and GLM datasets

```r
# Get number of cases in original data
nrow(demo_glmm)
```

```
## [1] 595
```

```r
# Get number of cases in data_reduced
nrow(data_glmm)
```

```
## [1] 492
```

```r
# Tabulate number of cases by each study sits: original vs glm
original <- demo_glmm %>%
    group_by(Study_site) %>%
    summarise(Count1 = n())

glmm <- data_glmm %>%
    group_by(Study_site) %>%
    summarise(Count2 = n())

original %>%
    left_join(glmm) %>%
```

```
    kable(caption = 'Number of cases at each study site (original dataset)',
          col.names = c('Study site', 'Original', 'GLM'))
```

Table 54: Number of cases at each study site (original dataset)

Study site	Original	GLM
DD	60	42
NM	240	200
RESI	99	83
RPA	20	20
RPB	102	98
RPC	14	13
RPD	10	10
STIG	50	26

Tabulate the pain sites removed

Sites removed because proportion of cases with pain at each site was < 0.1.

```
data_glmm.long %>%
    filter(!Pain_site %in% high_prop) %>%
    select(Pain_site) %>%
    distinct() %>%
    mutate(Pain_site = str_replace(Pain_site,
                                   pattern = '_',
                                   replacement = ' '),
           Pain_site = str_replace(Pain_site,
                                   pattern = '\\.',
                                   replacement = ' & ')) %>%
    kable(caption = 'Removed pain sites',
          col.names = 'Pain sites')
```

Table 55: Removed pain sites

Pain sites
Throat
Shoulder
Arms
Elbows
Wrists & Hands
Lower back
Cervical spine
Hips
Buttocks

GLMM

```
# Perform GLMM on each remaining body site
glmm_mods <- data_glmm.filtered %>%
```

```
    # Scale Age and CD4_recent
    mutate_if(is.numeric, scale) %>%
    # Dummy code outcome variable
    mutate(Pain_present = ifelse(Pain_present == 'No',
                                 yes = 0,
                                 no = 1)) %>%
    # Group and then nest by Pain_site
    group_by(Pain_site) %>%
    nest() %>%
    # Perform logistic regression
    mutate(logistic = map(.x = data,
                          ~ glmer(Pain_present ~
                                    Age +
                                    Sex +
                                    CD4_recent +
                                    (1|Study_site),
                                  data = .x,
                                  family = binomial(),
                                  control = glmerControl(optimizer =
                                                           c('bobyqa',
                                                             'bobyqa'))))) %>%
    # Extract effect sizes and p-values
    mutate(OR = map(.x = logistic,
                    ~ exp(fixef(.x))),
           CI = map(.x = logistic,
                    ~ exp(confint.merMod(.x,
                                         method = 'Wald')[2:5, ])),
           p_value = map(.x = logistic,
                         ~ coef(summary(.x))[, 4])) %>%
    # Bind data into a dataframe and tabulate,
    mutate(df = pmap(.l = list(OR, CI, p_value, Pain_site),
                     ~ cbind(..1, ..2, ..3) %>%
                       kable(caption = ..4,
                             col.names = c('OR', 'Wald lower 95%CI',
                                           'Wald upper 95%CI', 'p-value'))))

# Print OR for fixed effects with Wald-type 95% CIs and p-values
walk(glmm_mods$df, ~print(.x))
```

Table 56: Head

	OR	Wald lower 95%CI	Wald upper 95%CI	p-value
(Intercept)	0.6025967	0.4111281	0.8832352	0.0094192
Age	0.9603824	0.7571667	1.2181392	0.7389474
SexMale	0.2483928	0.1168182	0.5281623	0.0002964
CD4_recent	0.7781325	0.5417471	1.1176622	0.1745119

Table 57: Chest

	OR	Wald lower 95%CI	Wald upper 95%CI	p-value
(Intercept)	0.1758590	0.1089509	0.2838563	0.0000000
Age	1.0270898	0.7939823	1.3286360	0.8387355

	OR	Wald lower 95%CI	Wald upper 95%CI	p-value
SexMale	0.9685384	0.5232464	1.7927819	0.9189509
CD4_recent	0.6066731	0.3740876	0.9838663	0.0427752

Table 58: Abdomen

	OR	Wald lower 95%CI	Wald upper 95%CI	p-value
(Intercept)	0.3934898	0.3105894	0.4985173	0.0000000
Age	0.8090008	0.6496259	1.0074758	0.0583007
SexMale	0.7543714	0.4217431	1.3493432	0.3420755
CD4_recent	1.0881886	0.8936920	1.3250140	0.4002194

Table 59: Thoracic_spine

	OR	Wald lower 95%CI	Wald upper 95%CI	p-value
(Intercept)	0.1734972	0.1289240	0.2334809	0.0000000
Age	0.9735667	0.7334718	1.2922543	0.8529032
SexMale	0.4232540	0.1665901	1.0753582	0.0707238
CD4_recent	1.1116459	0.8966374	1.3782122	0.3344899

Table 60: Lumbosacral_spine

	OR	Wald lower 95%CI	Wald upper 95%CI	p-value
(Intercept)	0.2151228	0.1511716	0.3061278	0.0000000
Age	1.0538056	0.8202668	1.3538355	0.6818089
SexMale	0.9184730	0.4740011	1.7797271	0.8010620
CD4_recent	1.0644237	0.8679756	1.3053338	0.5486620

Table 61: Groin

	OR	Wald lower 95%CI	Wald upper 95%CI	p-value
(Intercept)	0.0487589	0.0179773	0.1322464	0.0000000
Age	0.9692042	0.7021360	1.3378559	0.8491598
SexMale	0.5147107	0.2176283	1.2173374	0.1304876
CD4_recent	1.0812723	0.8215002	1.4231888	0.5772630

Table 62: Legs

	OR	Wald lower 95%CI	Wald upper 95%CI	p-value
(Intercept)	0.1715287	0.1164429	0.2526742	0.0000000
Age	1.2124724	0.9419946	1.5606134	0.1346604
SexMale	1.8610046	1.0339894	3.3494909	0.0383181
CD4_recent	1.0060419	0.8130468	1.2448486	0.9557953

Table 63: Knees

	OR	Wald lower 95%CI	Wald upper 95%CI	p-value
(Intercept)	0.1580291	0.1025172	0.2436002	0.0000000
Age	1.3641246	1.0557327	1.7626015	0.0175612
SexMale	1.5342243	0.8263945	2.8483301	0.1751272
CD4_recent	0.9808591	0.7710007	1.2478388	0.8749729

Table 64: Ankles.Feet

	OR	Wald lower 95%CI	Wald upper 95%CI	p-value
(Intercept)	0.3801689	0.2550638	0.566636	0.0000020
Age	1.3849495	1.1025712	1.739647	0.0051216
SexMale	1.4774529	0.8761858	2.491329	0.1431536
CD4_recent	0.8825650	0.6731476	1.157132	0.3660350

Session information

```
sessionInfo()
```

```
## R version 3.6.3 (2020-02-29)
## Platform: x86_64-apple-darwin15.6.0 (64-bit)
## Running under: macOS Catalina 10.15.4
##
## Matrix products: default
## BLAS:   /Library/Frameworks/R.framework/Versions/3.6/Resources/lib/libRblas.0.dylib
## LAPACK: /Library/Frameworks/R.framework/Versions/3.6/Resources/lib/libRlapack.dylib
##
## locale:
## [1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
##
## attached base packages:
## [1] stats     graphics  grDevices utils     datasets  methods   base
##
## other attached packages:
##  [1] lme4_1.1-21        Matrix_1.2-18      boot_1.3-24        knitr_1.28
##  [5] skimr_2.1          forcats_0.5.0      stringr_1.4.0      dplyr_0.8.5
##  [9] purrr_0.3.3        readr_1.3.1        tidyr_1.0.2        tibble_3.0.0
## [13] ggplot2_3.3.0.9000 tidyverse_1.3.0
##
## loaded via a namespace (and not attached):
##  [1] Rcpp_1.0.4       lubridate_1.7.4  lattice_0.20-38  utf8_1.1.4
##  [5] assertthat_0.2.1 digest_0.6.25    R6_2.4.1         cellranger_1.1.0
##  [9] repr_1.1.0       backports_1.1.5  reprex_0.3.0     evaluate_0.14
## [13] highr_0.8        httr_1.4.1       pillar_1.4.3     rlang_0.4.5
## [17] readxl_1.3.1     rstudioapi_0.11  minqa_1.2.4      nloptr_1.2.2.1
## [21] rmarkdown_2.1    labeling_0.3     splines_3.6.3    munsell_0.5.0
```

```
## [25] broom_0.5.5      compiler_3.6.3   modelr_0.1.6     xfun_0.12
## [29] pkgconfig_2.0.3  base64enc_0.1-3  htmltools_0.4.0  tidyselect_1.0.0
## [33] fansi_0.4.1      crayon_1.3.4     dbplyr_1.4.2     withr_2.1.2
## [37] MASS_7.3-51.5    grid_3.6.3       nlme_3.1-145     jsonlite_1.6.1
## [41] gtable_0.3.0     lifecycle_0.2.0  DBI_1.1.0        magrittr_1.5
## [45] scales_1.1.0     cli_2.0.2        stringi_1.4.6    farver_2.0.3
## [49] fs_1.3.1         xml2_1.3.0       ellipsis_0.3.0   generics_0.0.2
## [53] vctrs_0.2.4      tools_3.6.3      glue_1.3.2       hms_0.5.3
## [57] parallel_3.6.3   yaml_2.2.1       colorspace_1.4-1 rvest_0.3.5
## [61] haven_2.2.0
```