

Diet

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Introduction

```

source("Survival/utils.R")

# Setup analysis environment
analysis_setup <- setup_analysis()
paths <- analysis_setup$paths
demo <- analysis_setup$demo

demo$FC <- log(demo$FC)

flare.df <- readRDS(paste0(paths$outdir, "flares-biochem.RDS"))
flare.cd.df <- readRDS(paste0(paths$outdir, "flares-biochem-cd.RDS"))
flare.uc.df <- readRDS(paste0(paths$outdir, "flares-biochem-uc.RDS"))

```

Total meat protein

Protein intake from animal sources is not found to be significantly associated with flares in CD. However, there is evidence of an association for UC. At present, it is difficult to explore this in more detail (e.g. by meat type).

Crohn's disease

Patient-reported flare

```

# Categorize meat protein by quantiles
flare.cd.df <- categorize_by_quantiles(flare.cd.df, "Meat_sum", reference_data = flare.df)

# Run survival analysis using utility function

```

```

analysis_result <- run_survival_analysis(
  data = flare.cd.df,
  var_name = "Meat_sum",
  outcome_time = "softflare_time",
  outcome_event = "softflare",
  legend_title = "Meat protein quantiles",
  plot_base_path = "plots/cd/soft-flare/diet/meat",
  break_time_by = 200
)

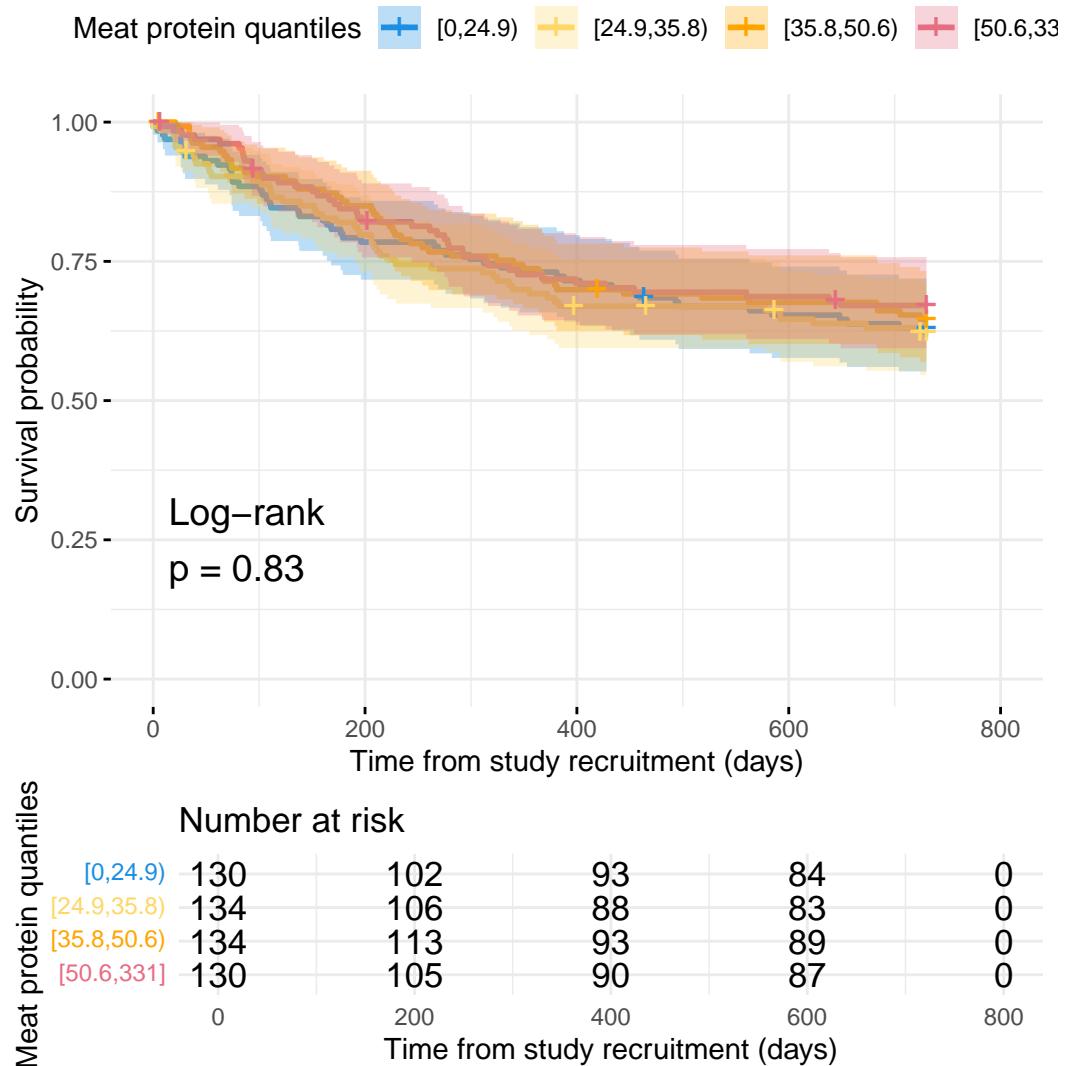
# Save plot as RDS
saveRDS(analysis_result$plot, paste0(paths$outdir, "meat-cd-soft.RDS"))

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(softflare_time, softflare) ~
    Sex + cat + IMD + dqi_tot + Meat_sum_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.cd.df
)

# Display plot and model summary
analysis_result$plot

```

Time to patient-reported flare



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.9330	1.3884	2.6912	0.0001
catFC 50-250	1.3110	0.9289	1.8504	0.1235
catFC > 250	1.9974	1.3682	2.9160	0.0003

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	0.7245	0.3828	1.3713	0.3222
IMD3	0.9050	0.4996	1.6395	0.7420
IMD4	0.8296	0.4564	1.5079	0.5400
IMD5	0.9966	0.5737	1.7313	0.9904
dqi_tot	1.0039	0.9902	1.0177	0.5800
Meat_sum_cat[24.9,35.8)	0.9972	0.6580	1.5114	0.9896
Meat_sum_cat[35.8,50.6)	0.8668	0.5687	1.3213	0.5064
Meat_sum_cat[50.6,331]	0.9280	0.5963	1.4442	0.7406

Diagnostics:

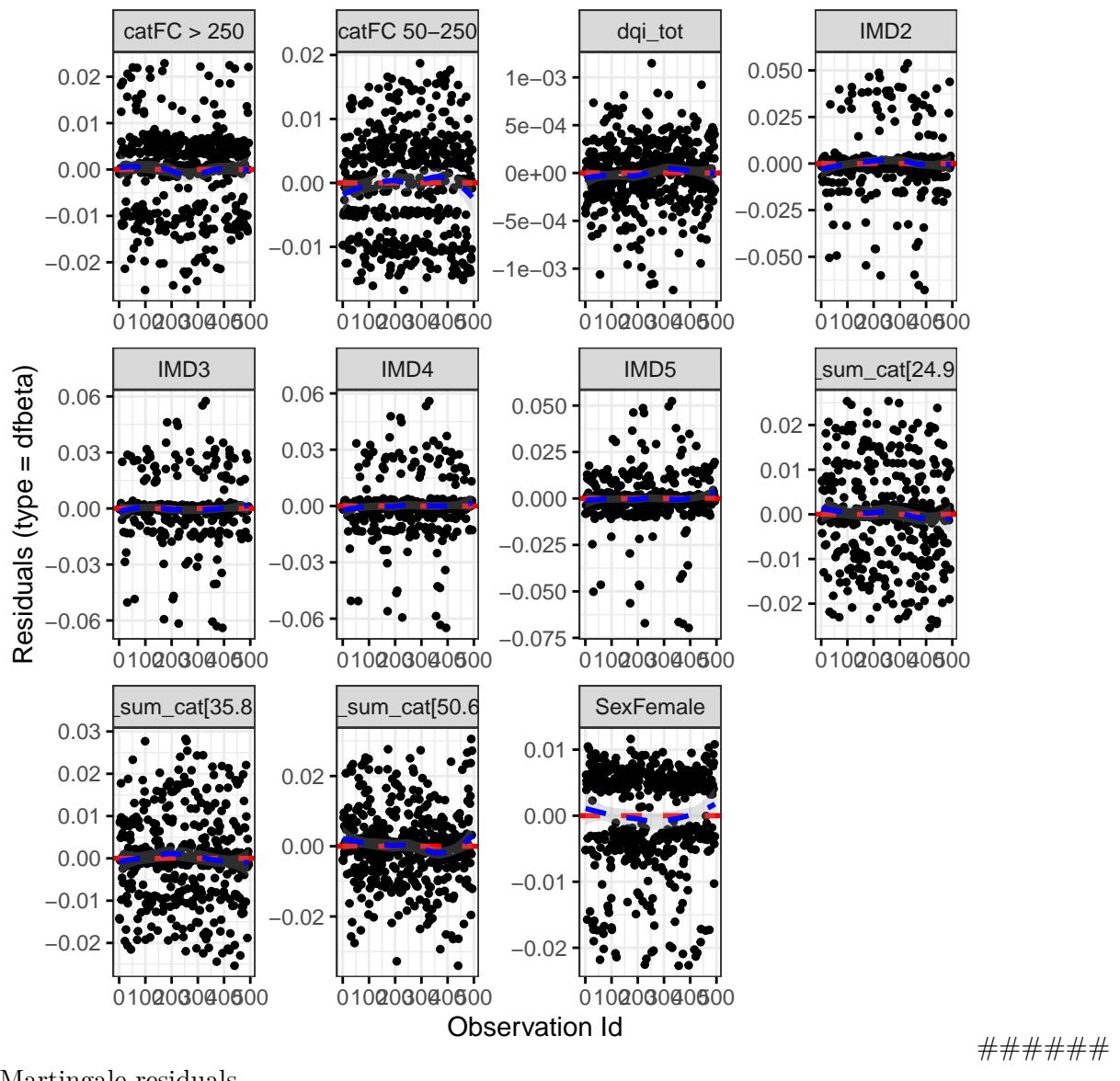
Proportional hazards assumption test

	Chi-squared statistic	DF	P-value
Sex	0.2035	1.0000	0.6519
cat	1.0755	2.0000	0.5841
IMD	3.0237	4.0000	0.5539
dqi_tot	0.1664	1.0000	0.6834
Meat_sum_cat	1.3198	3.0000	0.7244
GLOBAL	5.5992	11.0001	0.8987

DF betas

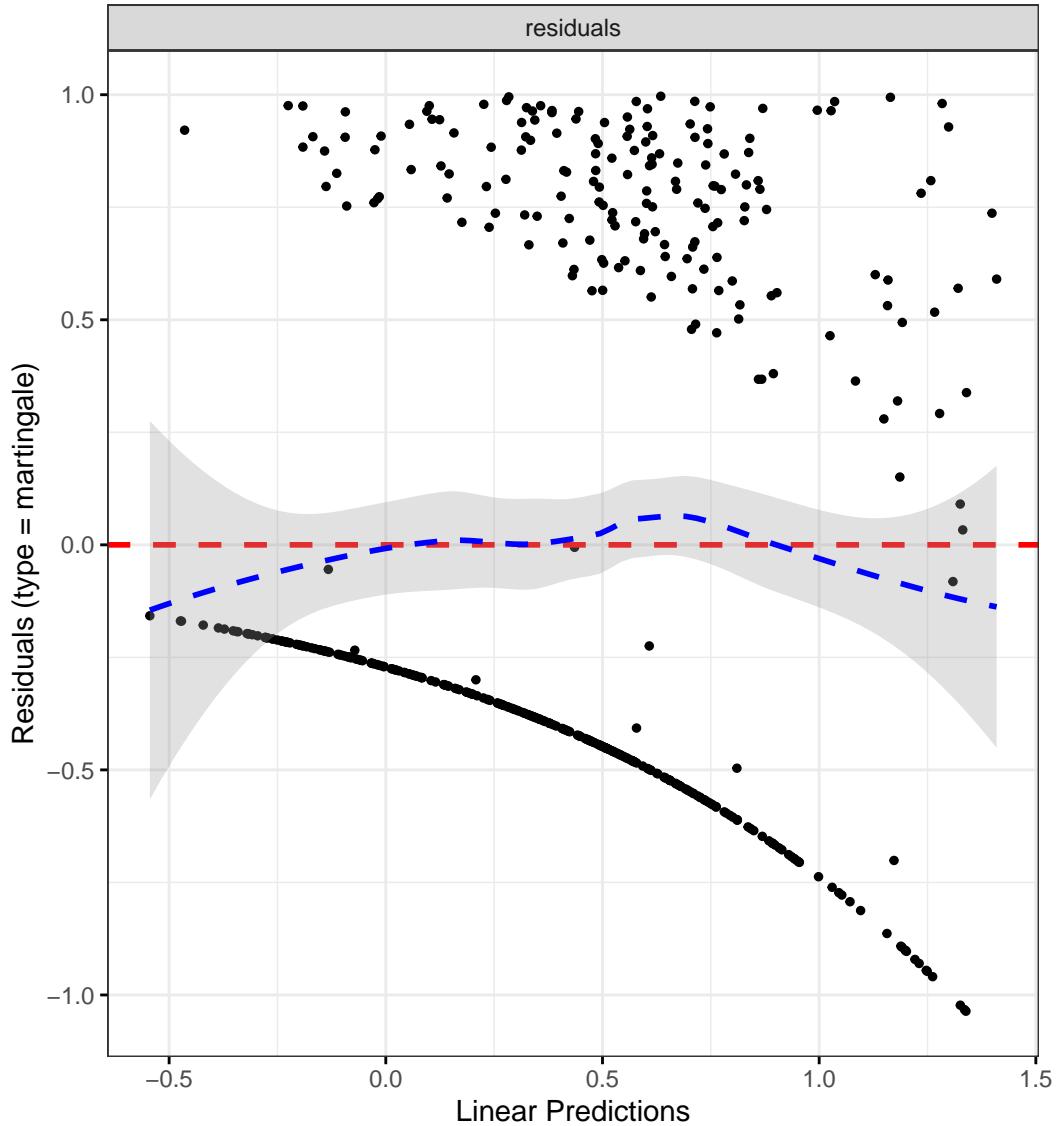
```
Warning: `gather_()` was deprecated in tidyverse 1.2.0.
i Please use `gather()` instead.
i The deprecated feature was likely used in the survminer package.
Please report the issue at <https://github.com/kassambara/survminer/issues>.
```

```
`geom_smooth()` using formula = 'y ~ x'
```



Martingale residuals

```
`geom_smooth()` using formula = 'y ~ x'
```



Hard flare

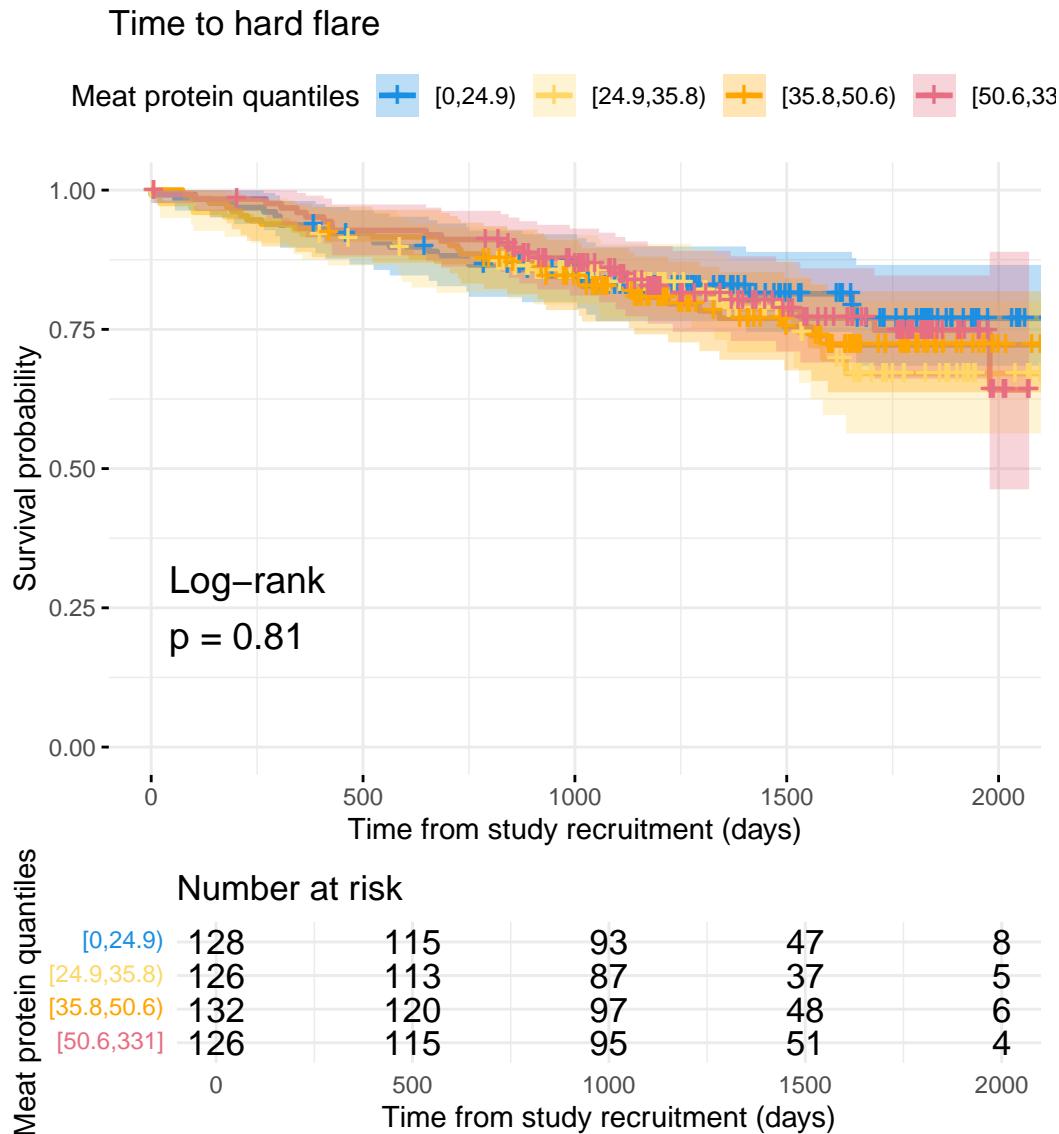
```
# Run survival analysis using utility function for hard flare
analysis_result <- run_survival_analysis(
  data = flare.cd.df,
  var_name = "Meat_sum",
  outcome_time = "hardflare_time",
  outcome_event = "hardflare",
  legend_title = "Meat protein quantiles",
```

```
plot_base_path = "plots/cd/hard-flare/diet/meat",
break_time_by = 500
)

# Save plot as RDS
saveRDS(analysis_result$plot, paste0(paths$outdir, "meat-cd-hard.RDS"))

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(hardflare_time, hardflare) ~
    Sex + cat + IMD + dqi_tot + Meat_sum_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.cd.df
)

# Display plot and model summary
analysis_result$plot
```



Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.2718	0.8442	1.9160	0.2501
catFC 50-250	1.9436	1.2242	3.0859	0.0048
catFC > 250	2.9448	1.7832	4.8629	0.0000

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	0.5613	0.2421	1.3010	0.1781
IMD3	0.7347	0.3371	1.6014	0.4381
IMD4	0.6942	0.3202	1.5051	0.3552
IMD5	0.6491	0.3135	1.3436	0.2443
dqi_tot	1.0027	0.9849	1.0208	0.7668
Meat_sum_cat[24.9,35.8)	1.3035	0.7468	2.2752	0.3509
Meat_sum_cat[35.8,50.6)	1.1908	0.6836	2.0743	0.5374
Meat_sum_cat[50.6,331]	0.9684	0.5387	1.7407	0.9145

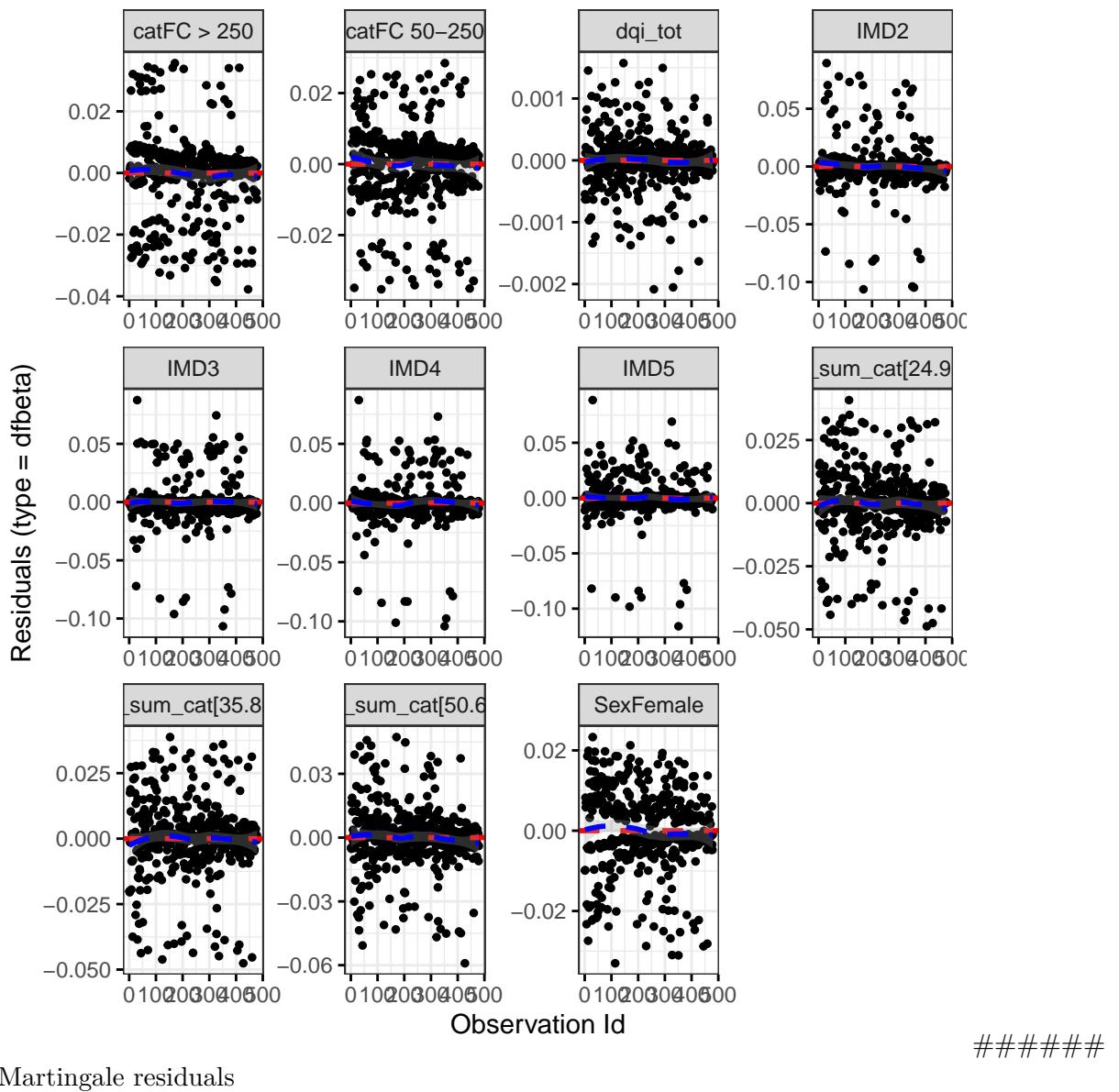
Diagnostics:

Proportional hazards assumption test

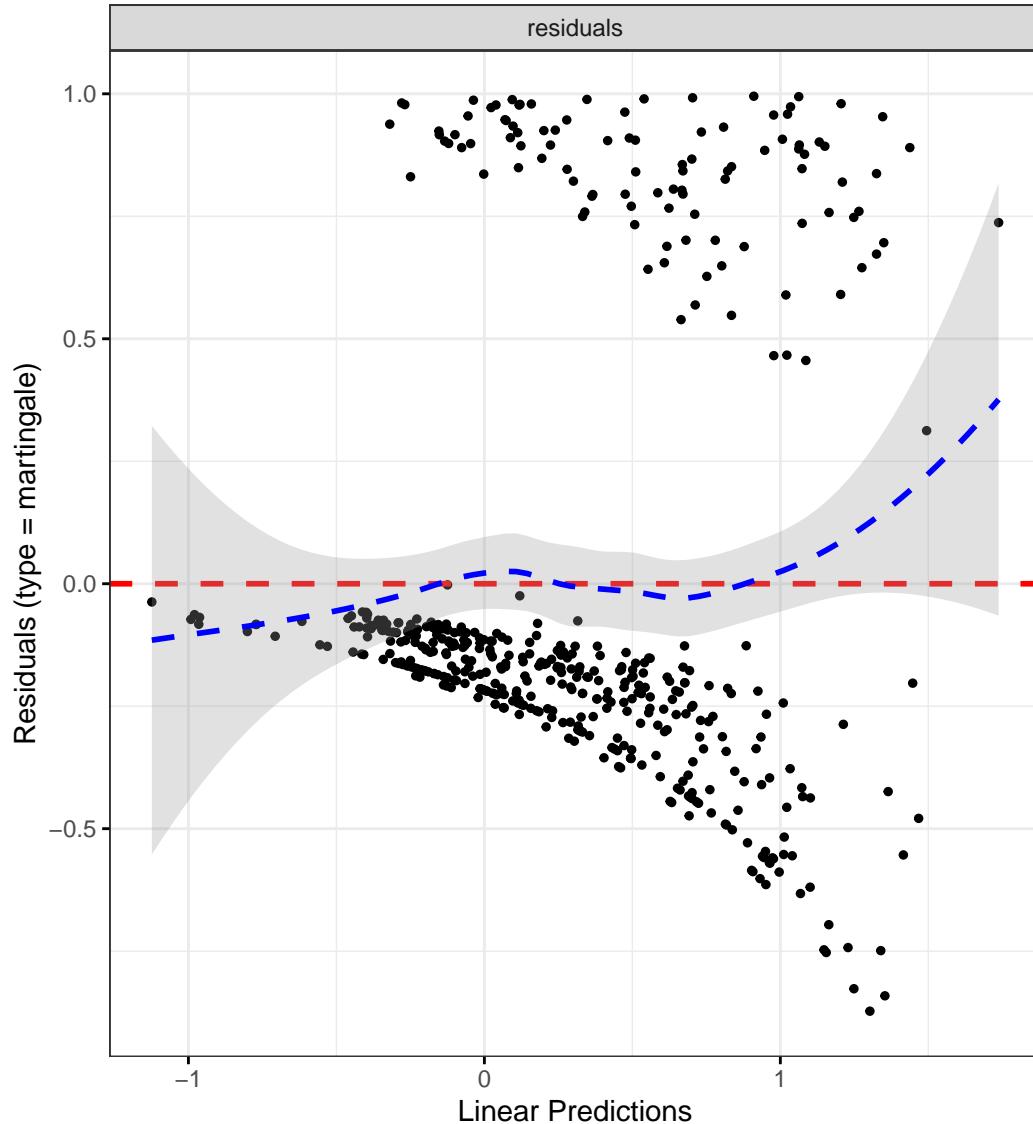
	Chi-squared statistic	DF	P-value
Sex	0.0858	0.9758	0.7605
cat	10.6562	1.9802	0.0047
IMD	2.8910	3.9262	0.5646
dqi_tot	2.8736	0.9913	0.0890
Meat_sum_cat	2.8562	2.9740	0.4098
GLOBAL	21.6864	17.0383	0.1989

DF betas

```
`geom_smooth()` using formula = 'y ~ x'
```



```
`geom_smooth()` using formula = 'y ~ x'
```



Ulcerative colitis

Patient-reported flare

```
# Categorize meat protein by quantiles
flare.uc.df <- categorize_by_quantiles(flare.uc.df, "Meat_sum", reference_data = flare.df)

# Run survival analysis using utility function
analysis_result <- run_survival_analysis()
```

```

data = flare.uc.df,
var_name = "Meat_sum",
outcome_time = "softflare_time",
outcome_event = "softflare",
legend_title = "Meat protein quantiles",
plot_base_path = "plots/uc/soft-flare/diet/meat",
break_time_by = 200
)

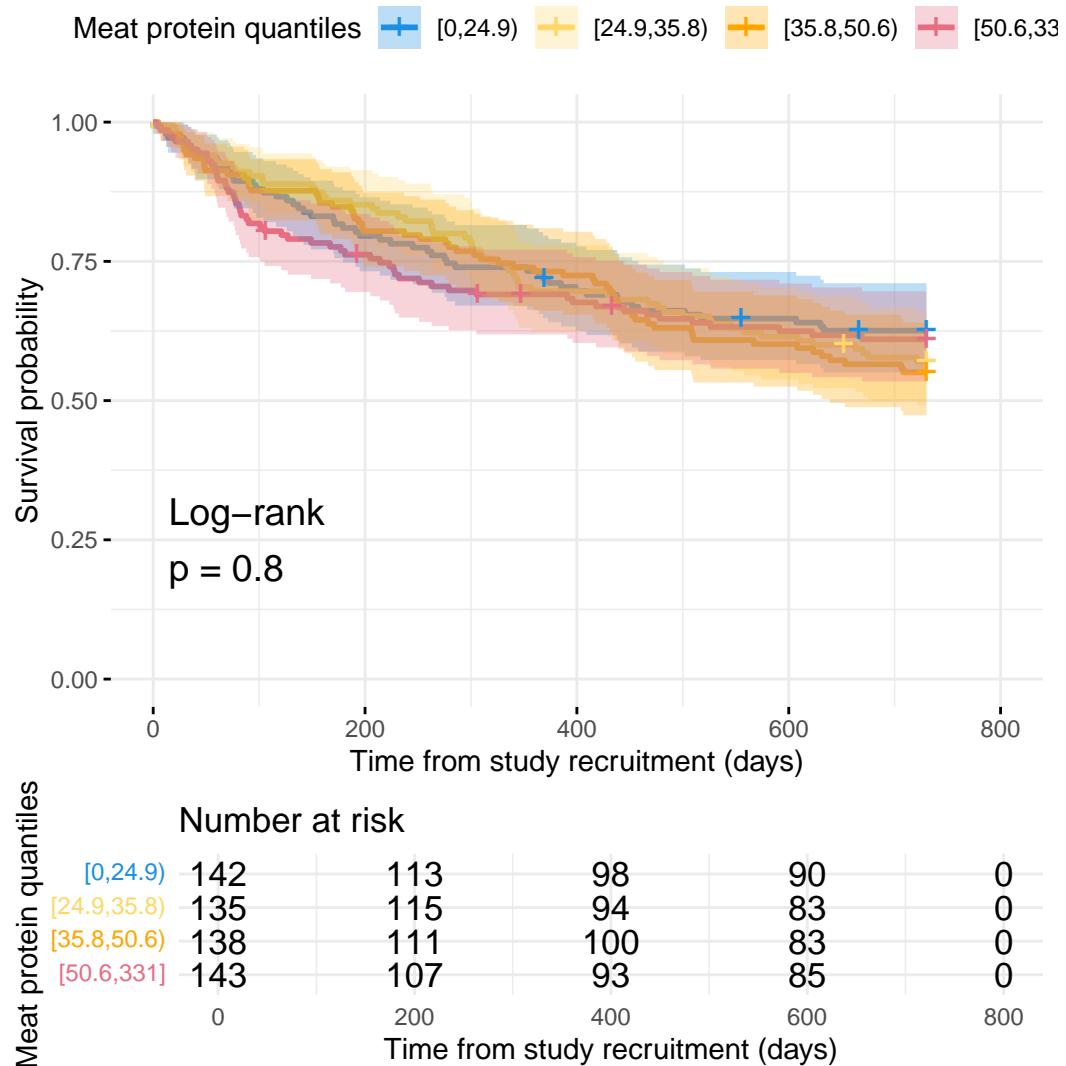
# Save plot as RDS
saveRDS(analysis_result$plot, paste0(paths$outdir, "meat-uc-soft.RDS"))

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(softflare_time, softflare) ~
    Sex + cat + IMD + dqi_tot + Meat_sum_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.uc.df
)

# Display plot and model summary
analysis_result$plot

```

Time to patient-reported flare



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.7482	1.3166	2.3214	0.0001
catFC 50-250	1.8207	1.3322	2.4883	0.0002
catFC > 250	2.1674	1.5186	3.0933	0.0000

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	1.5406	0.8082	2.9368	0.1892
IMD3	1.3026	0.7003	2.4229	0.4038
IMD4	1.4203	0.7876	2.5613	0.2434
IMD5	1.3201	0.7406	2.3529	0.3464
dqi_tot	1.0034	0.9904	1.0166	0.6107
Meat_sum_cat[24.9,35.8)	1.1736	0.7894	1.7448	0.4289
Meat_sum_cat[35.8,50.6)	1.3622	0.9159	2.0259	0.1270
Meat_sum_cat[50.6,331]	1.2700	0.8408	1.9185	0.2560

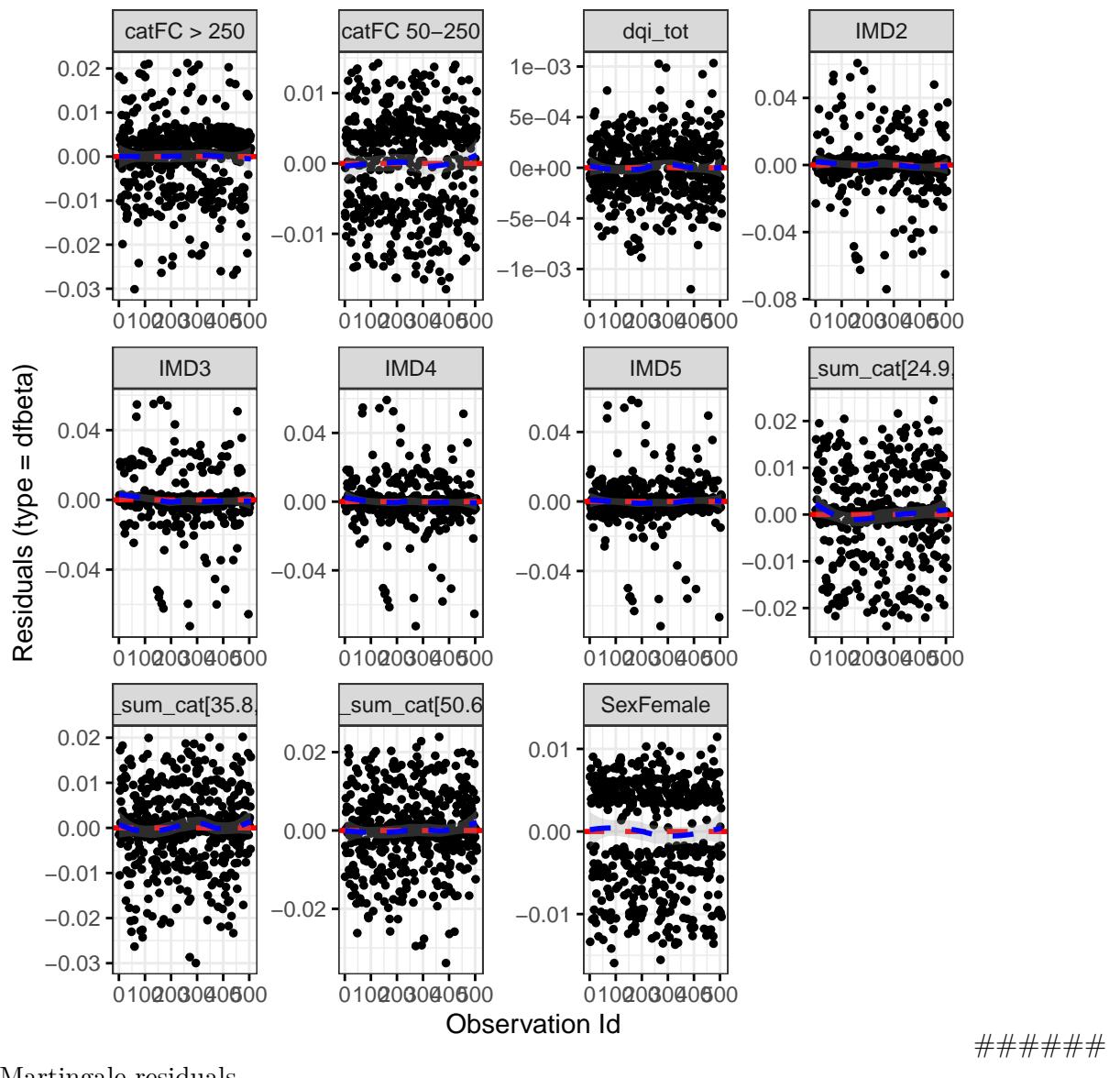
Diagnostics:

Proportional hazards assumption test

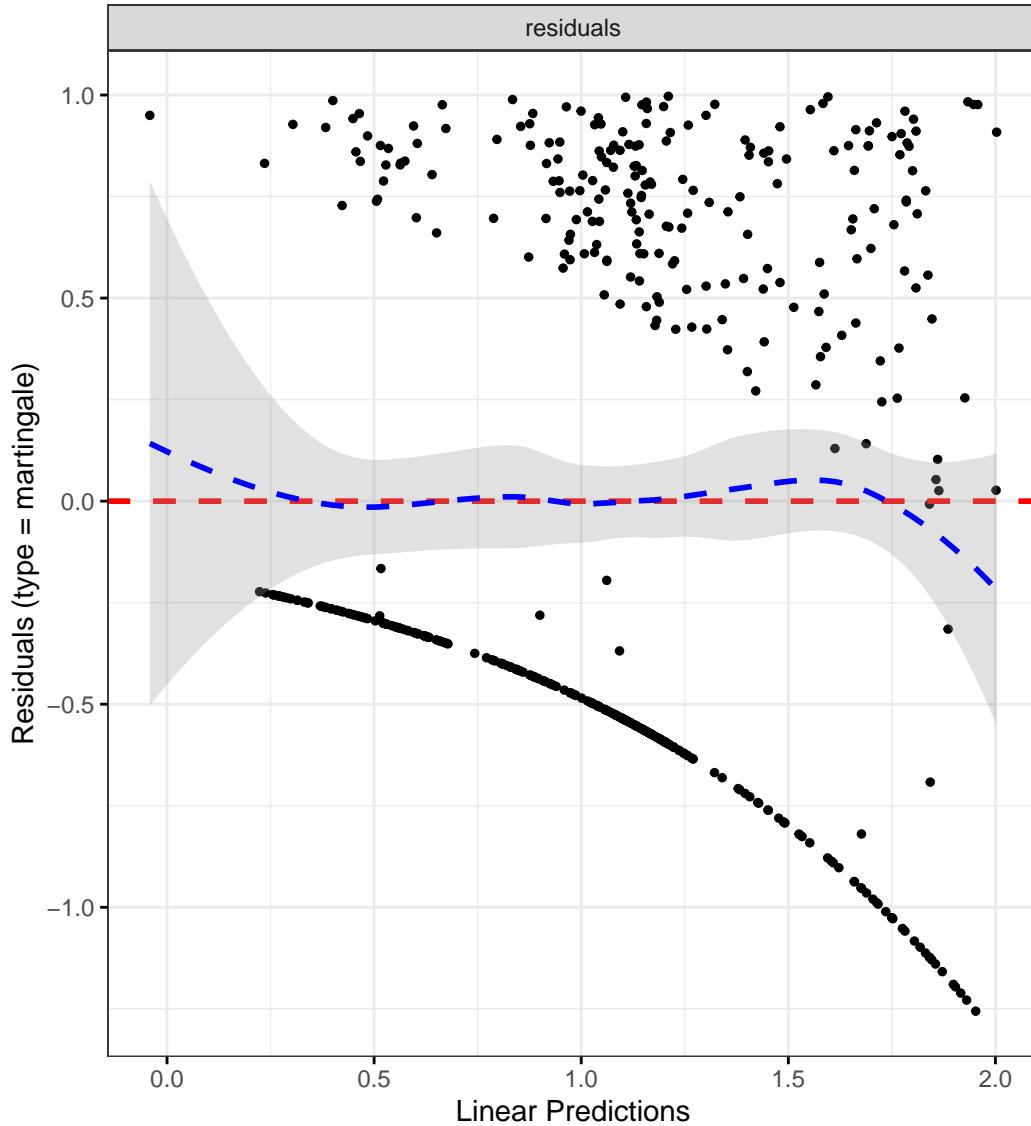
	Chi-squared statistic	DF	P-value
Sex	0.0456	0.9999	0.8309
cat	3.8911	1.9999	0.1429
IMD	2.6428	3.9999	0.6192
dqi_tot	0.6440	1.0000	0.4223
Meat_sum_cat	11.4044	2.9999	0.0097
GLOBAL	18.1848	11.0089	0.0776

DF betas

```
`geom_smooth()` using formula = 'y ~ x'
```



```
`geom_smooth()` using formula = 'y ~ x'
```



Hard flare

```
# Run survival analysis using utility function for hard flare
analysis_result <- run_survival_analysis(
  data = flare.uc.df,
  var_name = "Meat_sum",
  outcome_time = "hardflare_time",
  outcome_event = "hardflare",
  legend_title = "Meat protein quantiles",
```

```

plot_base_path = "plots/uc/hard-flare/diet/meat",
break_time_by = 500
)

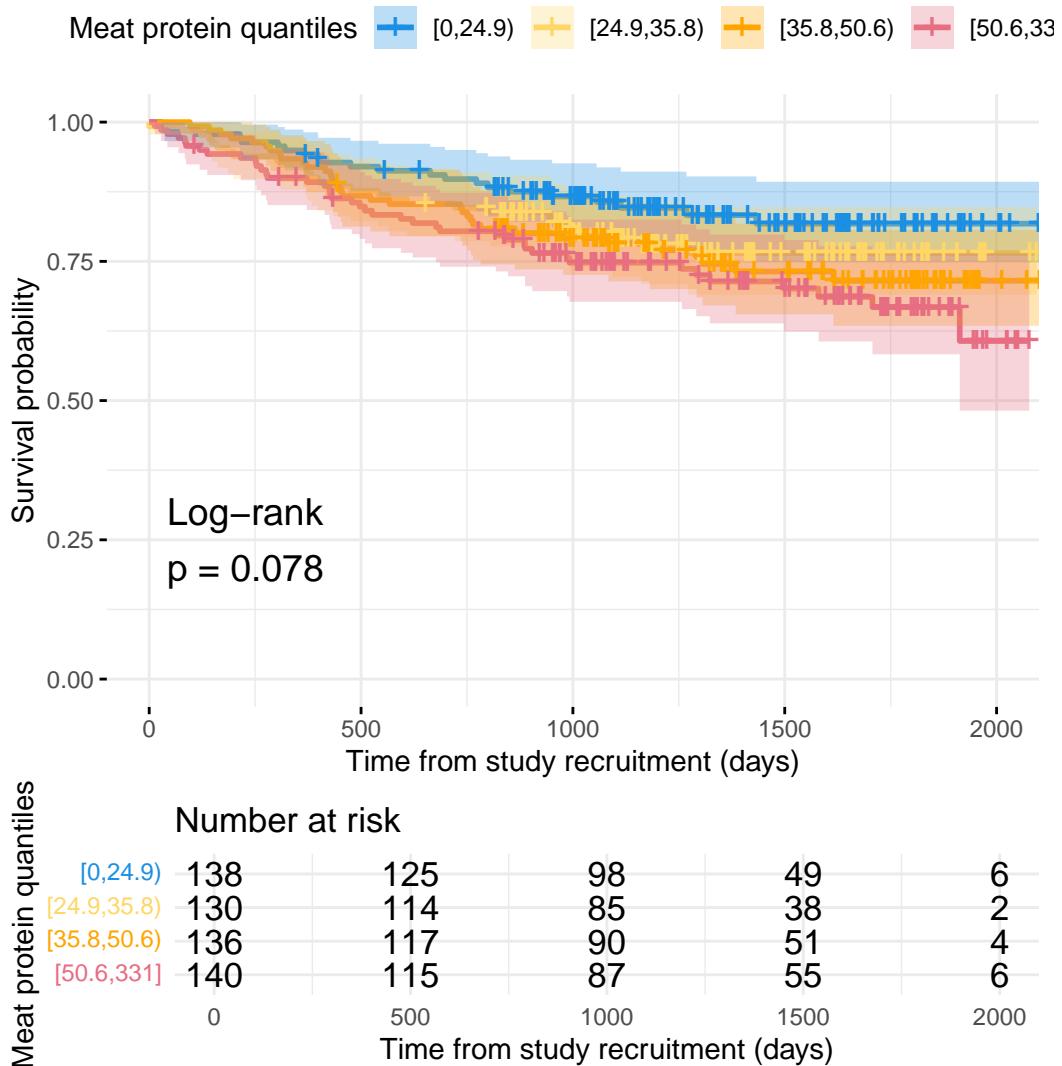
# Save plot as RDS
saveRDS(analysis_result$plot, paste0(paths$outdir, "meat-uc-hard.RDS"))

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(hardflare_time, hardflare) ~
    Sex + cat + IMD + dqi_tot + Meat_sum_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.uc.df
)

# Display plot and model summary
analysis_result$plot

```

Time to hard flare



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.2917	0.8895	1.8756	0.1787
catFC 50-250	1.9278	1.2624	2.9439	0.0024
catFC > 250	2.4267	1.4961	3.9360	0.0003

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	1.6747	0.6343	4.4215	0.2979
IMD3	1.5942	0.6246	4.0687	0.3293
IMD4	2.6769	1.1151	6.4257	0.0275
IMD5	1.6306	0.6779	3.9222	0.2749
dqi_tot	1.0115	0.9934	1.0301	0.2147
Meat_sum_cat[24.9,35.8)	1.3961	0.7831	2.4891	0.2580
Meat_sum_cat[35.8,50.6)	1.5504	0.8753	2.7461	0.1327
Meat_sum_cat[50.6,331]	2.1853	1.2371	3.8603	0.0071

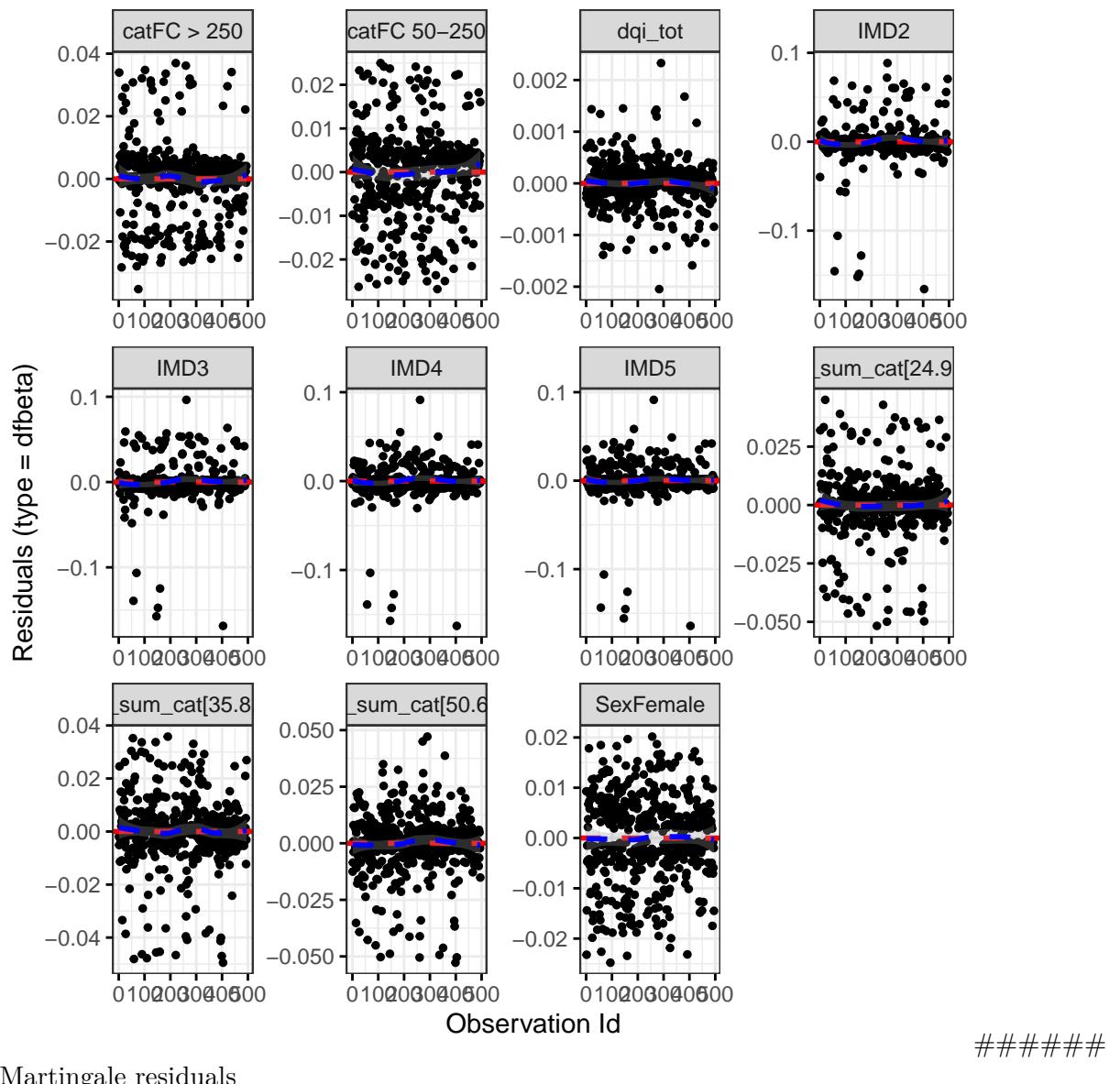
Diagnostics:

Proportional hazards assumption test

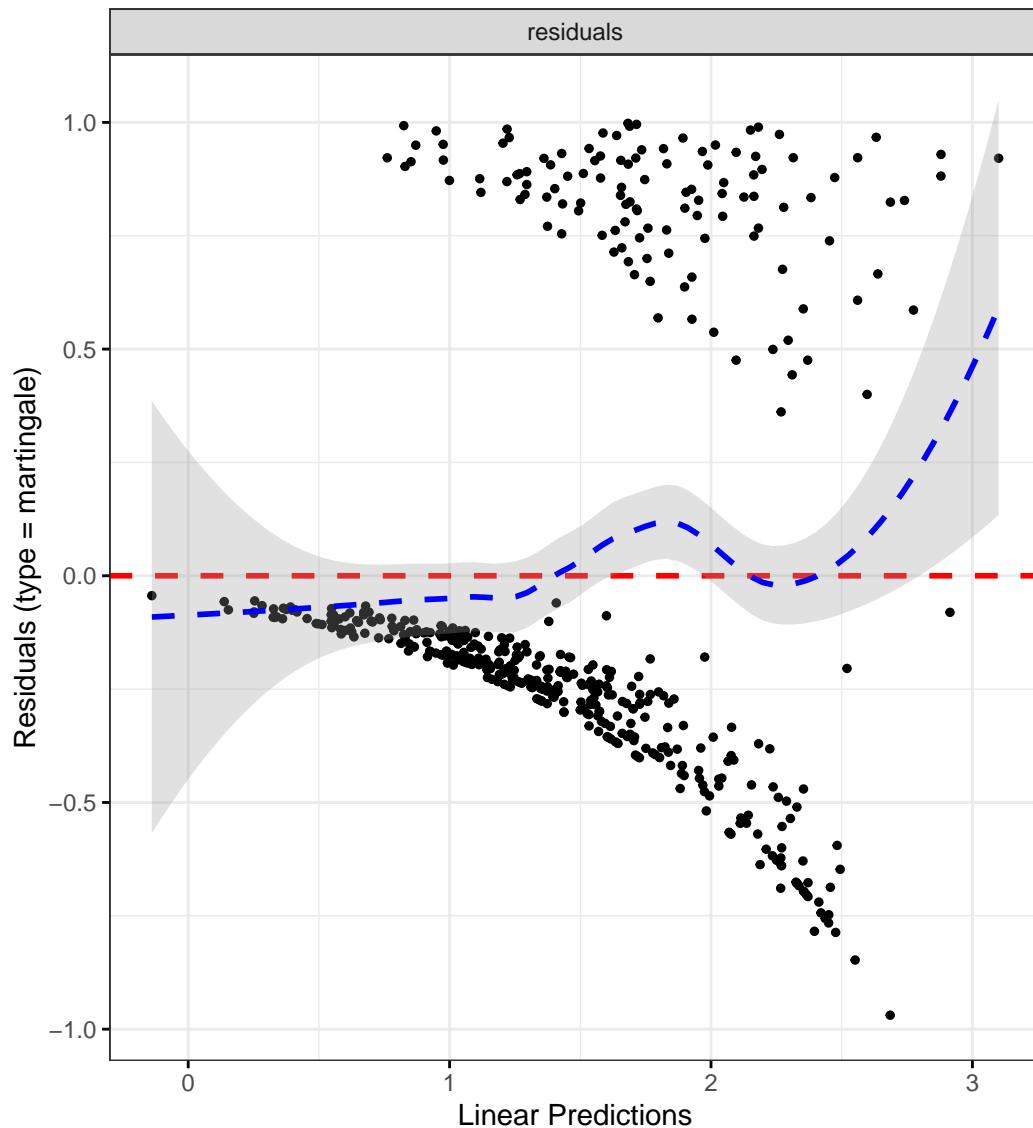
	Chi-squared statistic	DF	P-value
Sex	0.1730	0.9851	0.6714
cat	7.0075	1.9595	0.0288
IMD	1.8409	3.9355	0.7564
dqi_tot	0.0332	0.9866	0.8513
Meat_sum_cat	1.1868	2.9607	0.7498
GLOBAL	10.4857	18.8915	0.9376

DF betas

```
`geom_smooth()` using formula = 'y ~ x'
```



```
`geom_smooth()` using formula = 'y ~ x'
```



Inflammatory bowel disease

Patient-reported flare

```
# Categorize meat protein by quantiles
flare.df <- categorize_by_quantiles(flare.df, "Meat_sum", reference_data = flare.df)

# Run survival analysis using utility function
analysis_result <- run_survival_analysis()
```

```

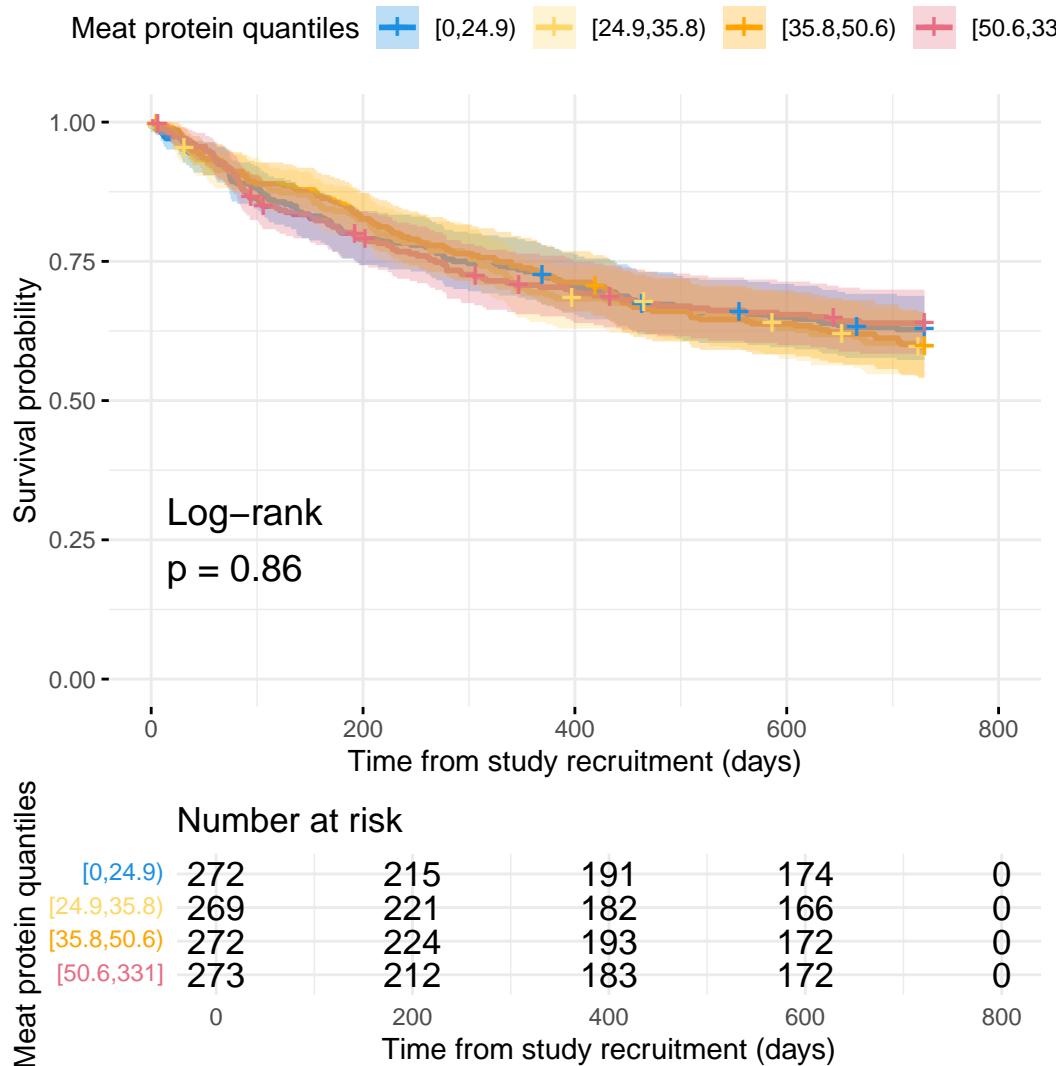
data = flare.df,
var_name = "Meat_sum",
outcome_time = "softflare_time",
outcome_event = "softflare",
legend_title = "Meat protein quantiles",
plot_base_path = "plots/ibd/soft-flare/diet/meat",
break_time_by = 200
)

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(softflare_time, softflare) ~
    Sex + cat + IMD + dqi_tot + Meat_sum_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.df
)

# Display plot and model summary
analysis_result$plot

```

Time to patient-reported flare



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.7655	1.4275	2.1834	0.0000
catFC 50-250	1.5389	1.2227	1.9369	0.0002
catFC > 250	2.0361	1.5728	2.6359	0.0000

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	1.0276	0.6548	1.6126	0.9059
IMD3	1.0568	0.6893	1.6202	0.7999
IMD4	1.1037	0.7289	1.6712	0.6412
IMD5	1.1073	0.7443	1.6474	0.6149
dqi_tot	1.0035	0.9941	1.0129	0.4646
Meat_sum_cat[24.9,35.8)	1.0840	0.8143	1.4429	0.5806
Meat_sum_cat[35.8,50.6)	1.1101	0.8338	1.4779	0.4743
Meat_sum_cat[50.6,331]	1.0996	0.8149	1.4839	0.5346

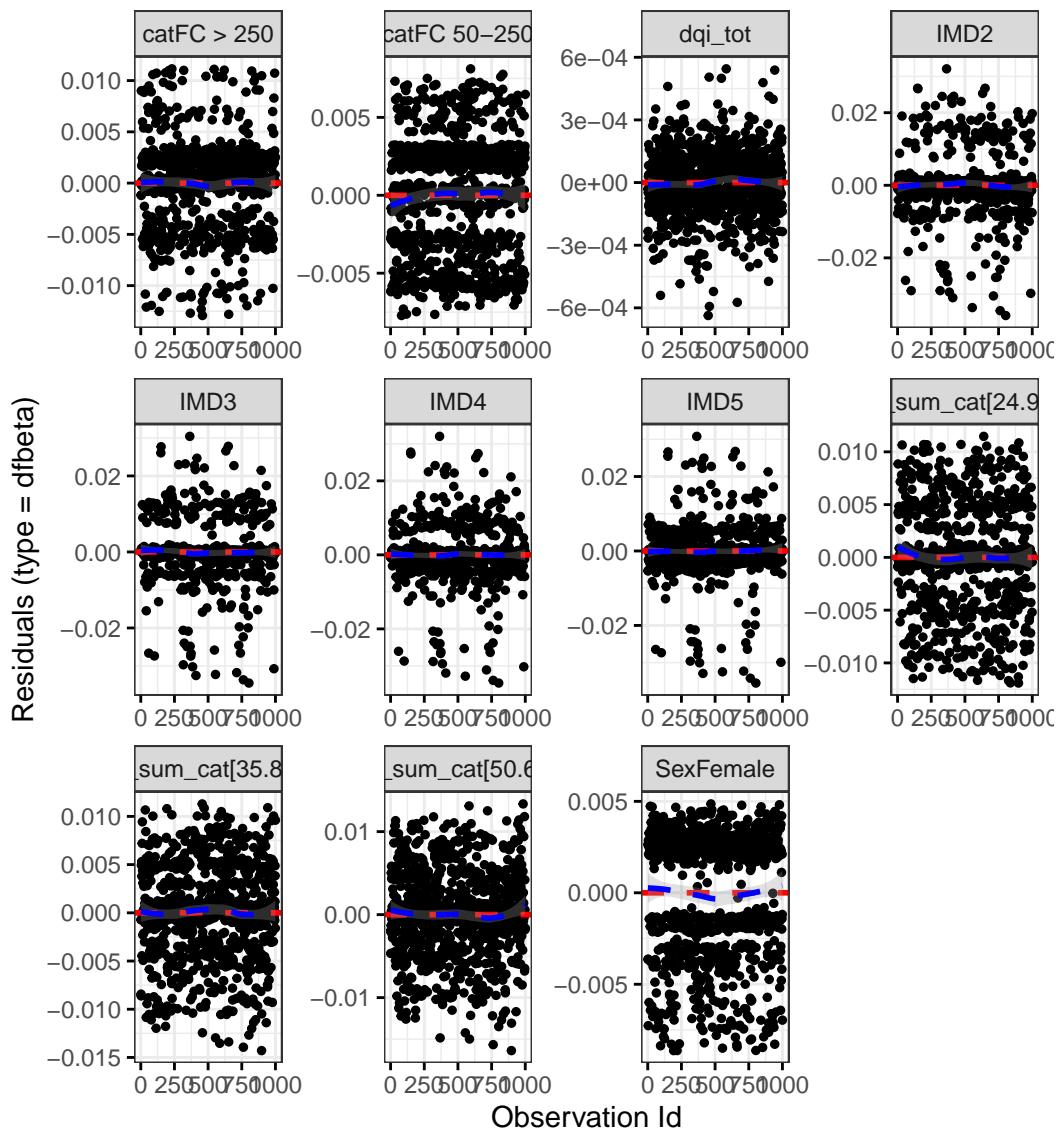
Diagnostics:

Proportional hazards assumption test

	Chi-squared statistic	DF	P-value
Sex	0.0003	1.0000	0.9858
cat	0.8204	2.0000	0.6635
IMD	4.6867	4.0000	0.3210
dqi_tot	0.9433	1.0000	0.3314
Meat_sum_cat	7.6387	3.0000	0.0541
GLOBAL	13.9143	11.0002	0.2378

DF betas

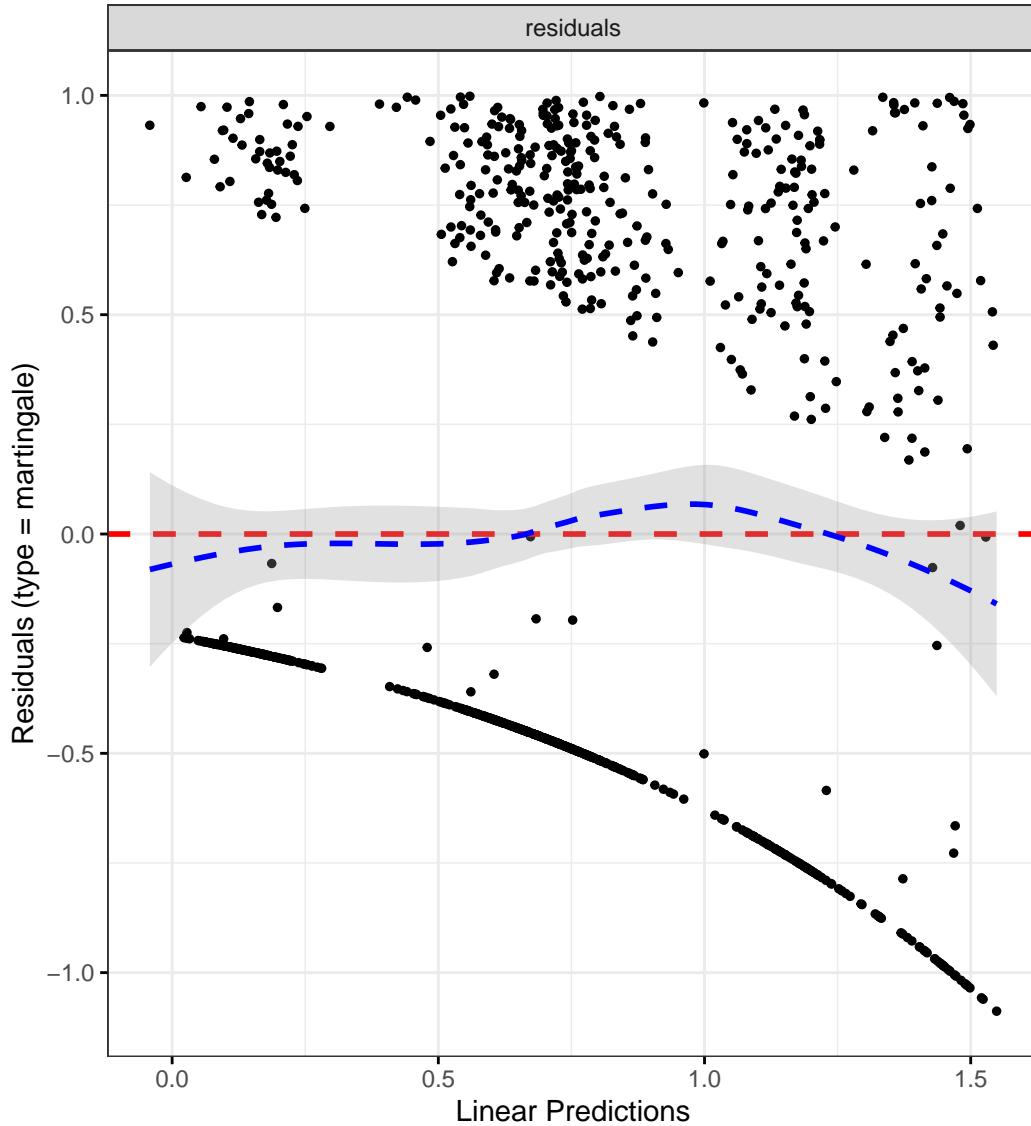
```
`geom_smooth()` using formula = 'y ~ x'
```



#####

Martingale residuals

```
`geom_smooth()` using formula = 'y ~ x'
```



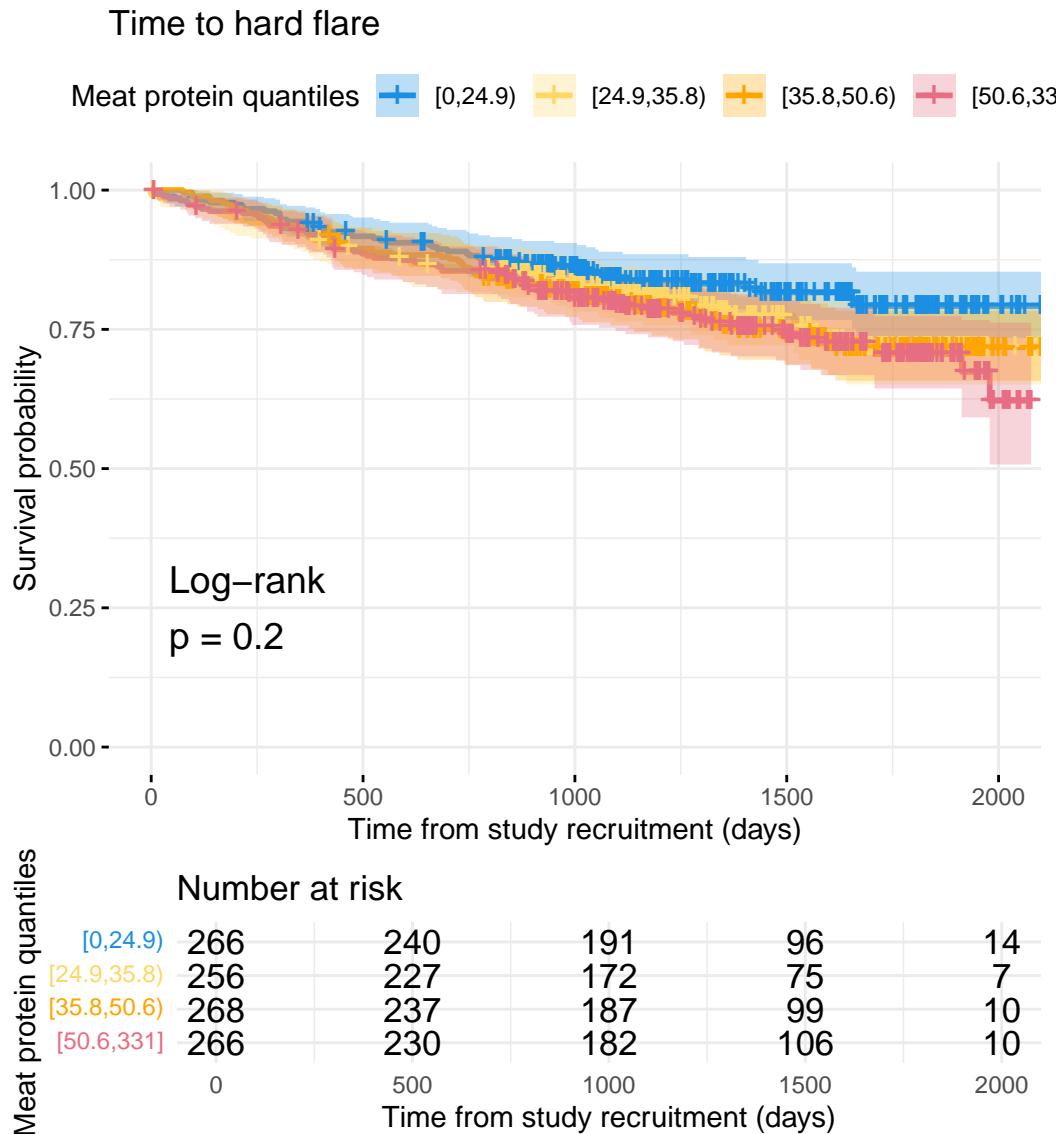
Hard flare

```
# Run survival analysis using utility function for hard flare
analysis_result <- run_survival_analysis(
  data = flare.df,
  var_name = "Meat_sum",
  outcome_time = "hardflare_time",
  outcome_event = "hardflare",
  legend_title = "Meat protein quantiles",
```

```
plot_base_path = "plots/ibd/hard-flare/diet/meat",
break_time_by = 500
)

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(hardflare_time, hardflare) ~
    Sex + cat + IMD + dqi_tot + Meat_sum_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.df
)

# Display plot and model summary
analysis_result$plot
```



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.2339	0.9394	1.6209	0.1309
catFC 50-250	1.8917	1.3882	2.5777	0.0001
catFC > 250	2.6316	1.8634	3.7165	0.0000

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	0.9745	0.5203	1.8252	0.9357
IMD3	1.0492	0.5795	1.8996	0.8740
IMD4	1.4170	0.8068	2.4888	0.2252
IMD5	1.0324	0.5939	1.7948	0.9100
dqi_tot	1.0063	0.9937	1.0191	0.3262
Meat_sum_cat[24.9,35.8)	1.3293	0.8923	1.9805	0.1616
Meat_sum_cat[35.8,50.6)	1.3662	0.9215	2.0256	0.1204
Meat_sum_cat[50.6,331]	1.5038	1.0091	2.2411	0.0450

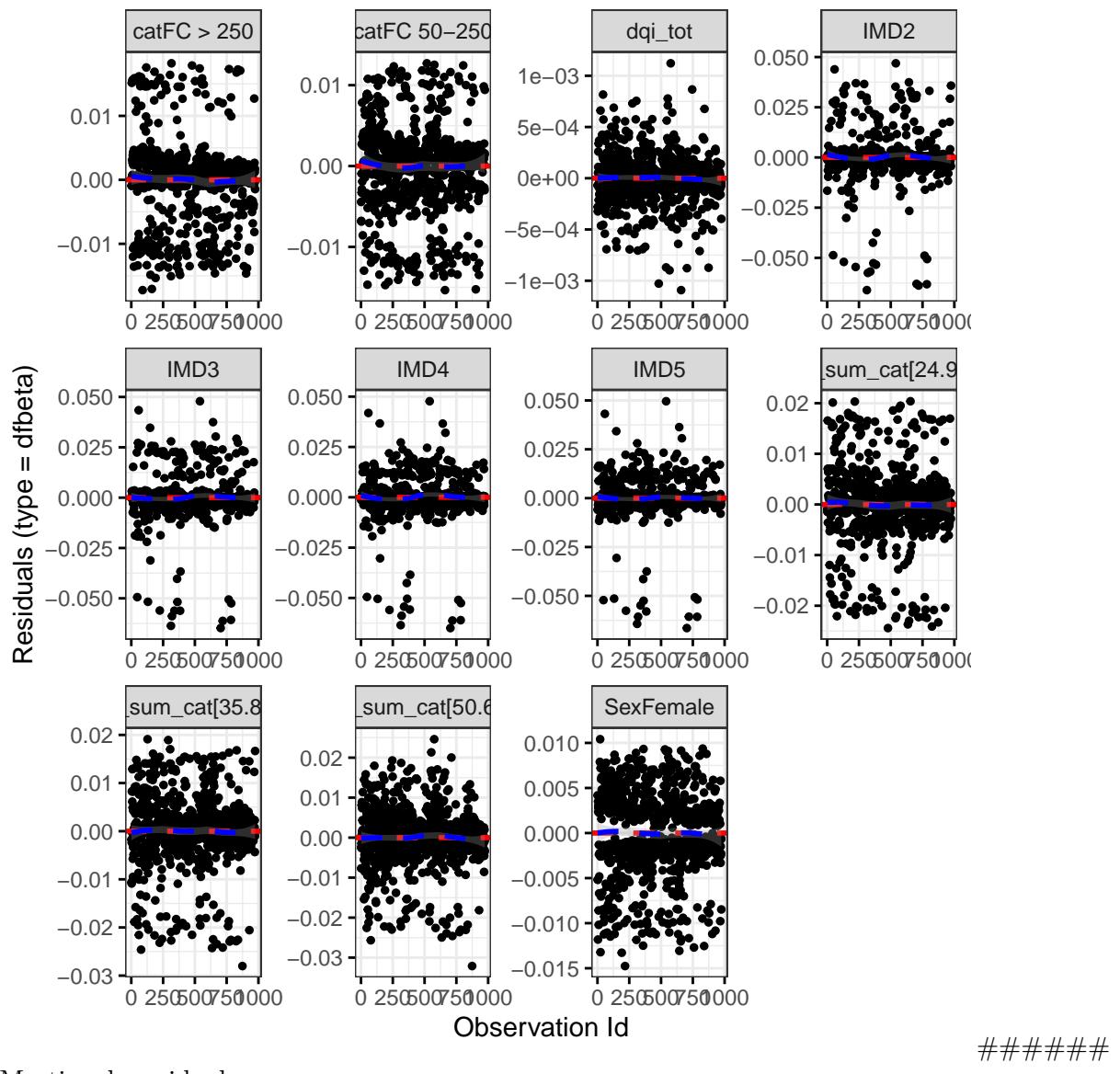
Diagnostics:

Proportional hazards assumption test

	Chi-squared statistic	DF	P-value
Sex	0.1190	0.9876	0.7253
cat	6.5934	1.9792	0.0362
IMD	2.3284	3.9449	0.6674
dqi_tot	1.4570	0.9915	0.2252
Meat_sum_cat	1.2857	2.9785	0.7289
GLOBAL	12.6525	22.9723	0.9587

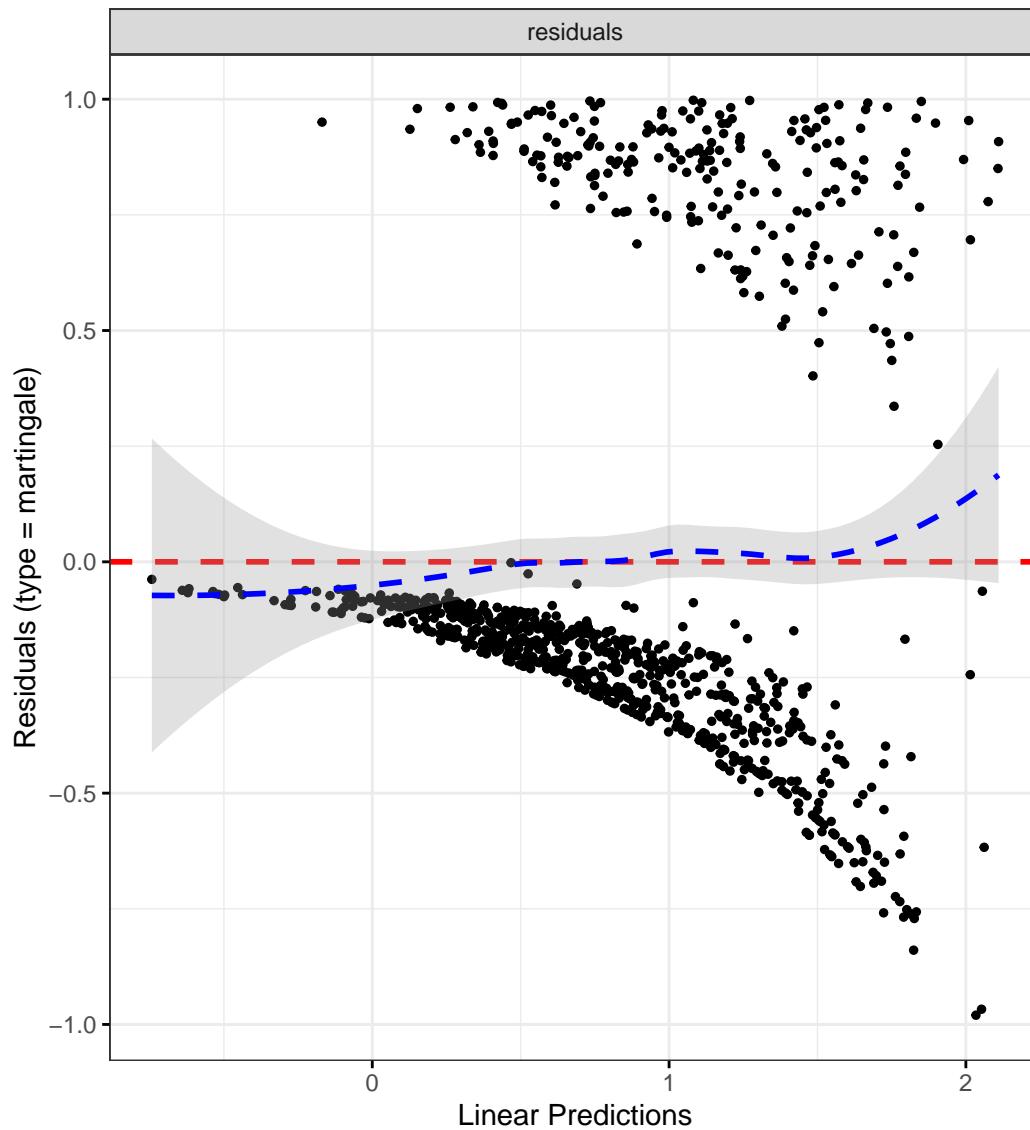
DF betas

```
`geom_smooth()` using formula = 'y ~ x'
```



Martingale residuals

```
`geom_smooth()` using formula = 'y ~ x'
```



Overall meat intake

Crohn's disease

Patient-reported flare

```
# Categorize overall meat intake by quantiles
```

```
flare.cd.df <- categorize_by_quantiles(flare.cd.df, "meat_overall", reference_data = flare.d
```

```

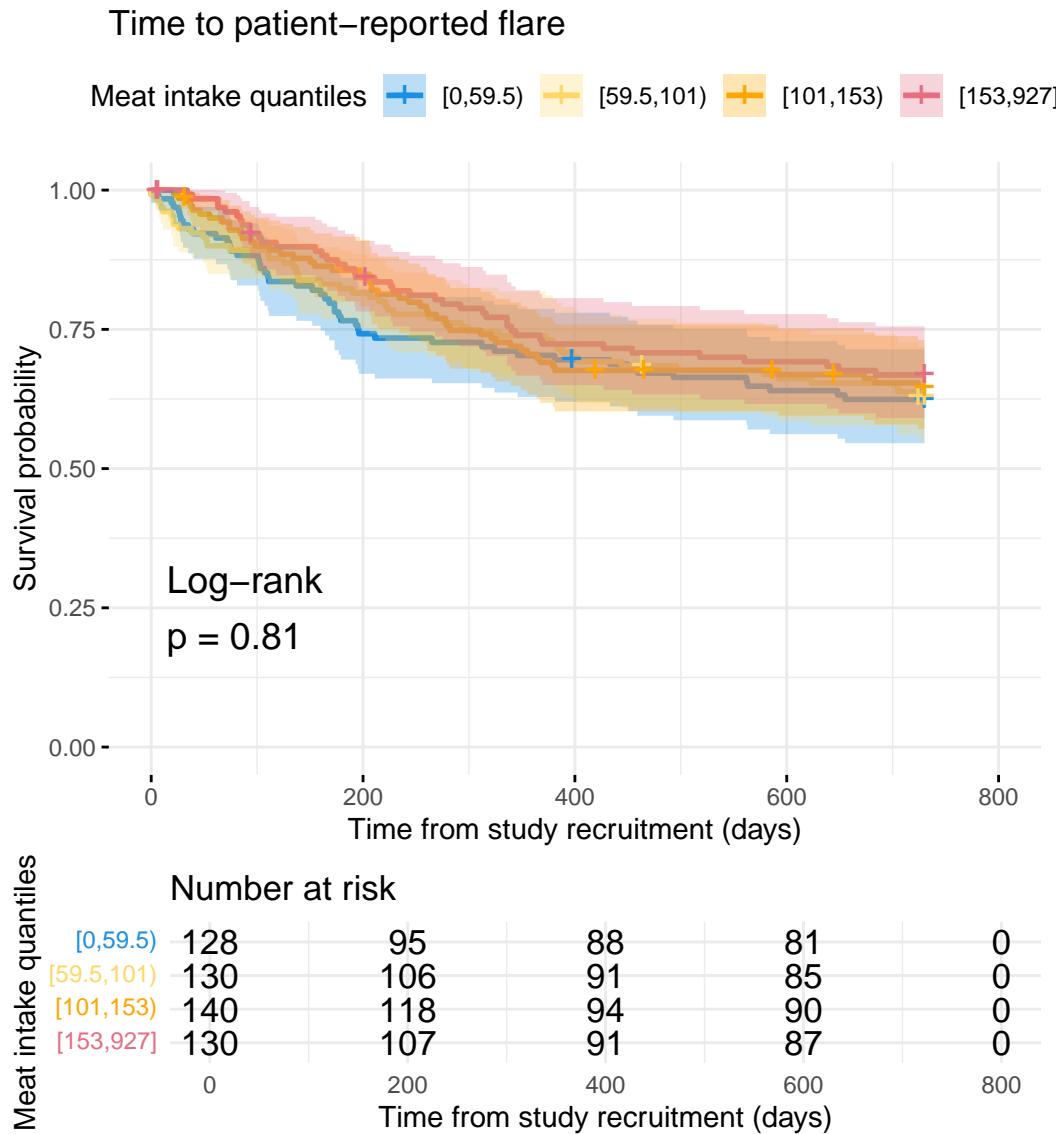
# Run survival analysis using utility function
analysis_result <- run_survival_analysis(
  data = flare.cd.df,
  var_name = "meat_overall",
  outcome_time = "softflare_time",
  outcome_event = "softflare",
  legend_title = "Meat intake quantiles",
  plot_base_path = "plots/cd/soft-flare/diet/meat_overall",
  break_time_by = 200
)

# Save plot as RDS
saveRDS(analysis_result$plot, paste0(paths$outdir, "meat-overall-cd-soft.RDS"))

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(softflare_time, softflare) ~
    Sex + cat + IMD + dqi_tot + meat_overall_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.cd.df
)

# Display plot and model summary
analysis_result$plot

```



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.9283	1.3852	2.6842	0.0001
catFC 50-250	1.3105	0.9275	1.8516	0.1252
catFC > 250	2.0021	1.3693	2.9275	0.0003

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	0.7228	0.3804	1.3732	0.3215
IMD3	0.8950	0.4922	1.6273	0.7161
IMD4	0.8338	0.4587	1.5153	0.5509
IMD5	0.9839	0.5656	1.7115	0.9542
dqi_tot	1.0027	0.9881	1.0175	0.7219
meat_overall_cat[59,5,101]	0.9729	0.6398	1.4793	0.8976
meat_overall_cat[101,153)	0.8923	0.5762	1.3816	0.6094
meat_overall_cat[153,927]	0.8927	0.5557	1.4341	0.6388

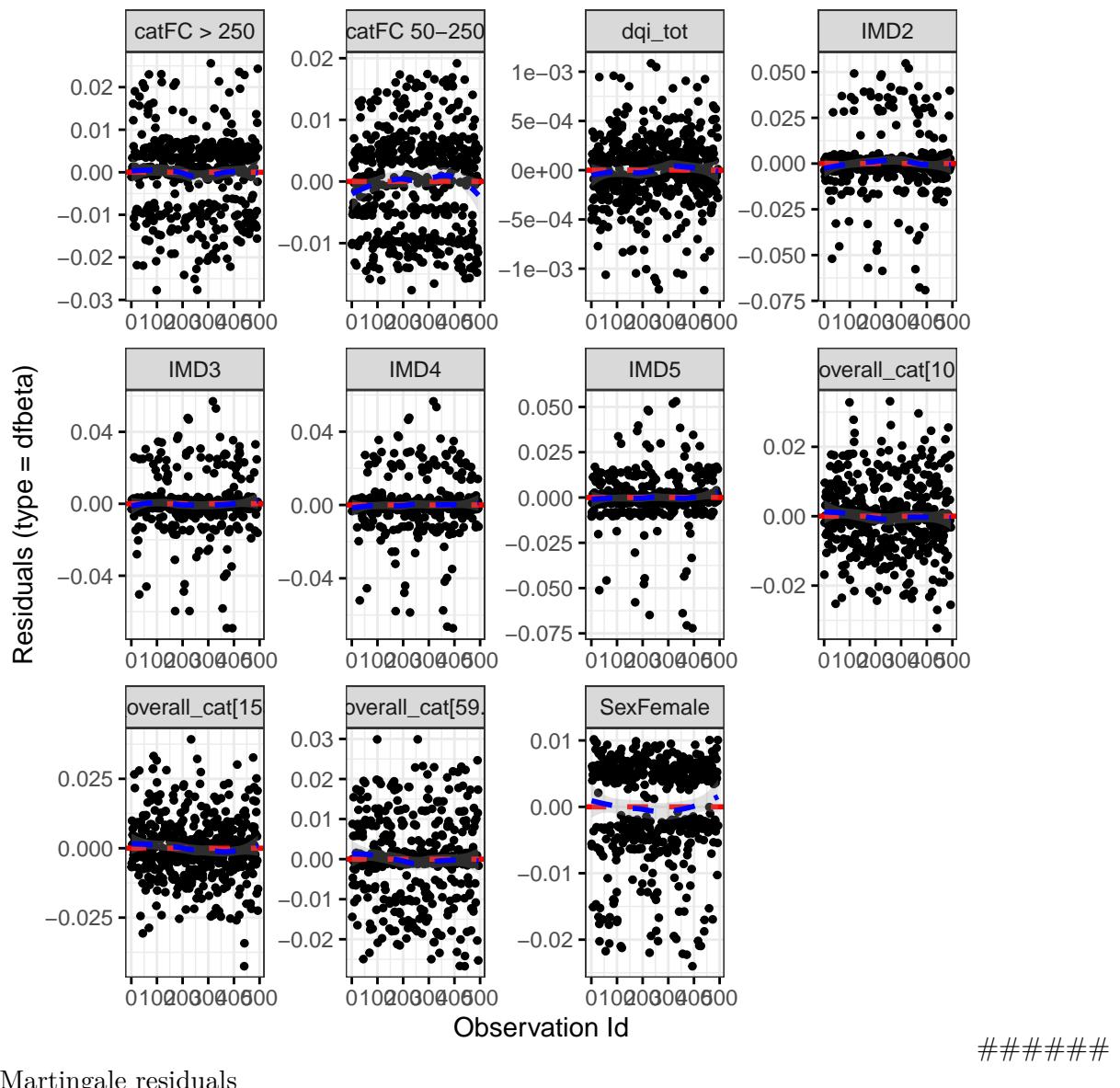
Diagnostics:

Proportional hazards assumption test

	Chi-squared statistic	DF	P-value
Sex	0.2004	1.0000	0.6544
cat	1.0758	2.0000	0.5840
IMD	3.0383	4.0000	0.5514
dqi_tot	0.1606	1.0000	0.6886
meat_overall_cat	2.8814	3.0000	0.4103
GLOBAL	8.0855	11.0001	0.7056

DF betas

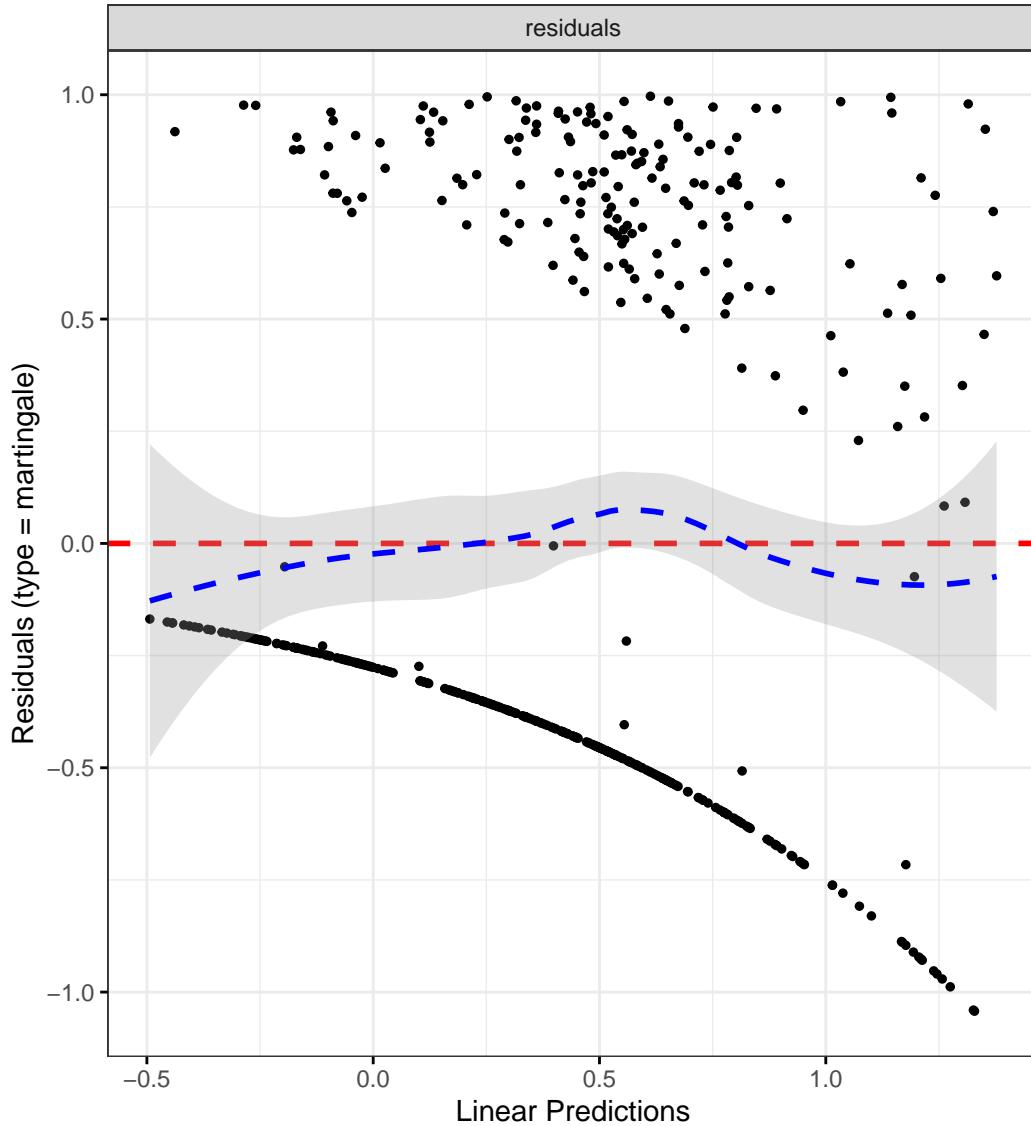
```
`geom_smooth()` using formula = 'y ~ x'
```



#####

Martingale residuals

```
`geom_smooth()` using formula = 'y ~ x'
```



Hard flare

```
# Run survival analysis using utility function for hard flare
analysis_result <- run_survival_analysis(
  data = flare.cd.df,
  var_name = "meat_overall",
  outcome_time = "hardflare_time",
  outcome_event = "hardflare",
  legend_title = "Meat intake quantiles",
```

```

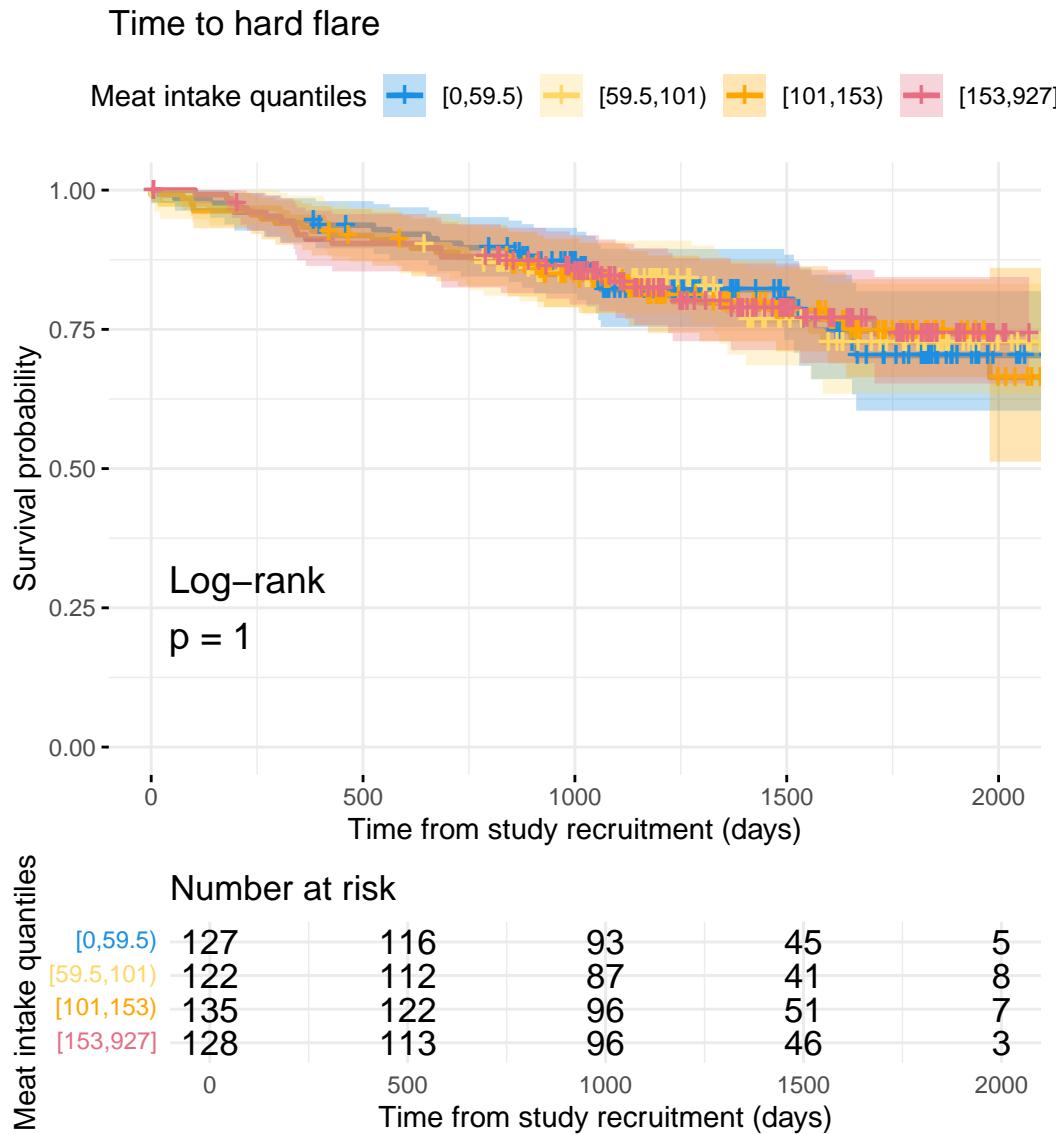
plot_base_path = "plots/cd/hard-flare/diet/meat_overall",
break_time_by = 500
)

# Save plot as RDS
saveRDS(analysis_result$plot, paste0(paths$outdir, "meat-overall-cd-hard.RDS"))

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(hardflare_time, hardflare) ~
    Sex + cat + IMD + dqi_tot + meat_overall_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.cd.df
)

# Display plot and model summary
analysis_result$plot

```



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.3000	0.8615	1.9619	0.2114
catFC 50-250	1.9286	1.2142	3.0635	0.0054
catFC > 250	2.9723	1.7957	4.9199	0.0000

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	0.5555	0.2385	1.2939	0.1730
IMD3	0.7479	0.3427	1.6325	0.4658
IMD4	0.7130	0.3285	1.5478	0.3924
IMD5	0.6695	0.3239	1.3842	0.2790
dqi_tot	1.0012	0.9821	1.0207	0.9048
meat_overall_cat[59.5,101]	0.8740	0.5032	1.5183	0.6328
meat_overall_cat[101,153)	0.9062	0.5151	1.5943	0.7326
meat_overall_cat[153,927]	0.8502	0.4650	1.5545	0.5981

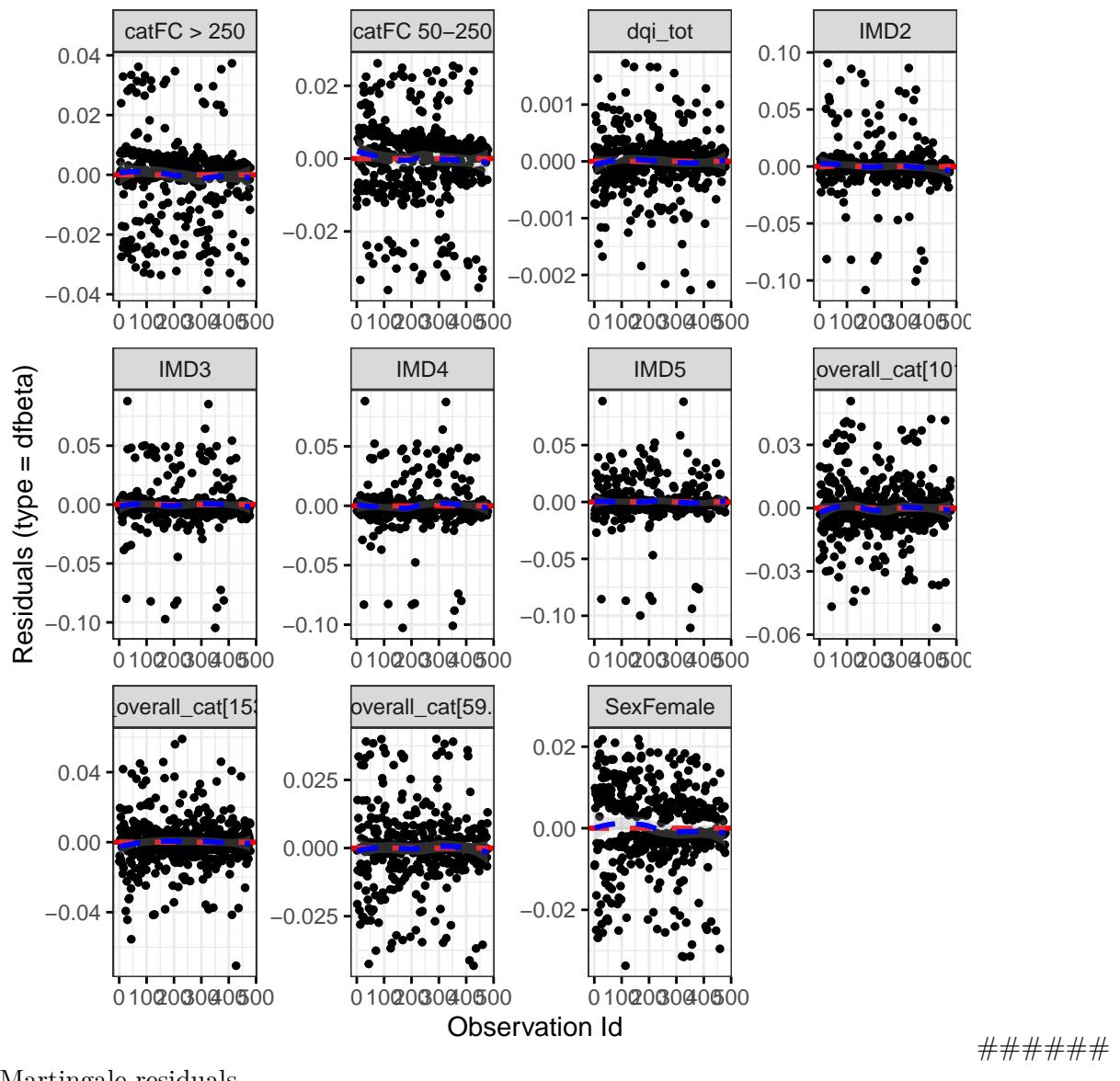
Diagnostics:

Proportional hazards assumption test

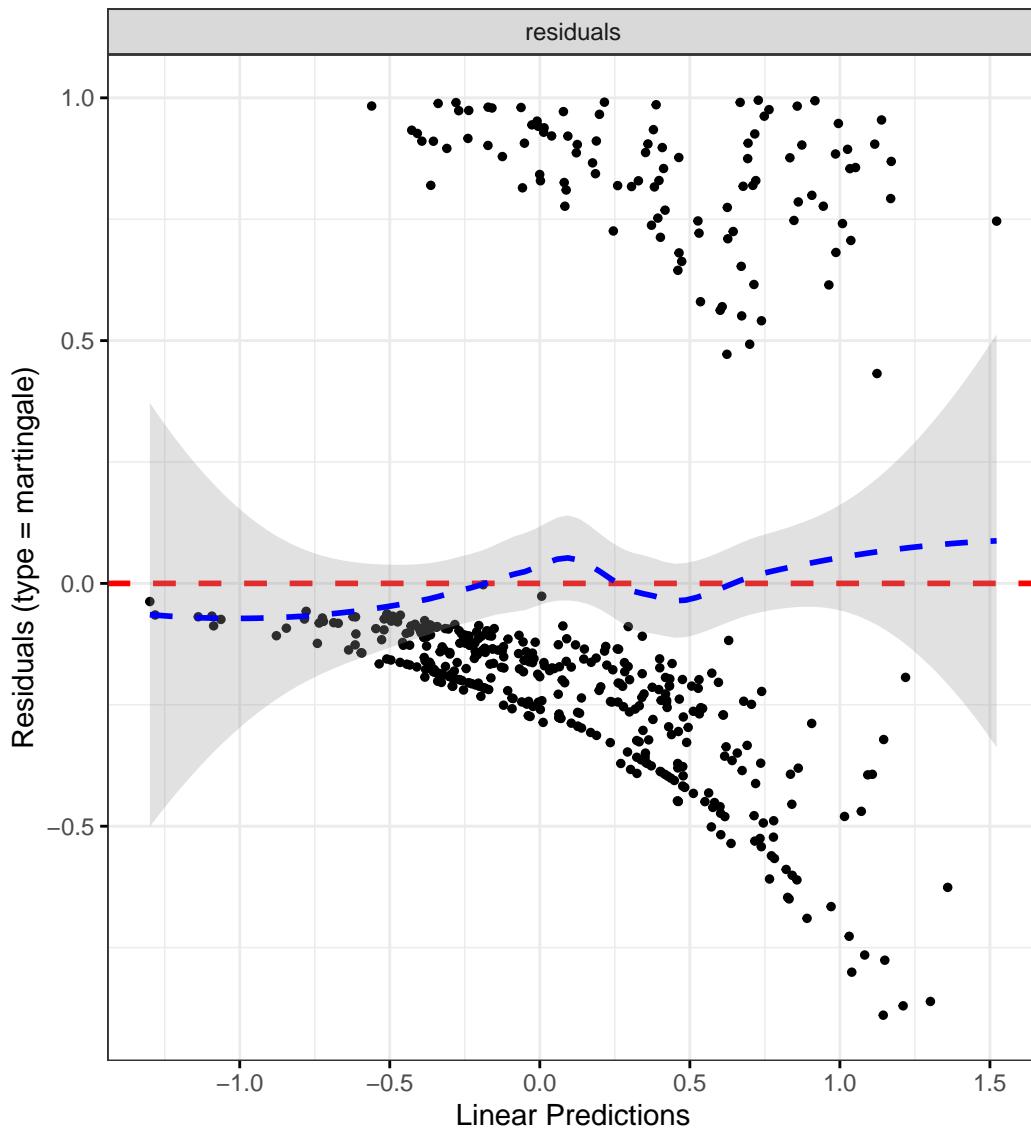
	Chi-squared statistic	DF	P-value
Sex	0.1074	0.9741	0.7330
cat	10.3961	1.9794	0.0054
IMD	2.7691	3.9317	0.5865
dqi_tot	2.8689	0.9910	0.0892
meat_overall_cat	0.4851	2.9711	0.9197
GLOBAL	16.1019	17.2467	0.5339

DF betas

```
`geom_smooth()` using formula = 'y ~ x'
```



```
`geom_smooth()` using formula = 'y ~ x'
```



Ulcerative colitis

Patient-reported flare

```
# Categorize overall meat intake by quantiles
flare.uc.df <- categorize_by_quantiles(flare.uc.df, "meat_overall", reference_data = flare.d
```

```
# Run survival analysis using utility function
analysis_result <- run_survival_analysis(
```

```

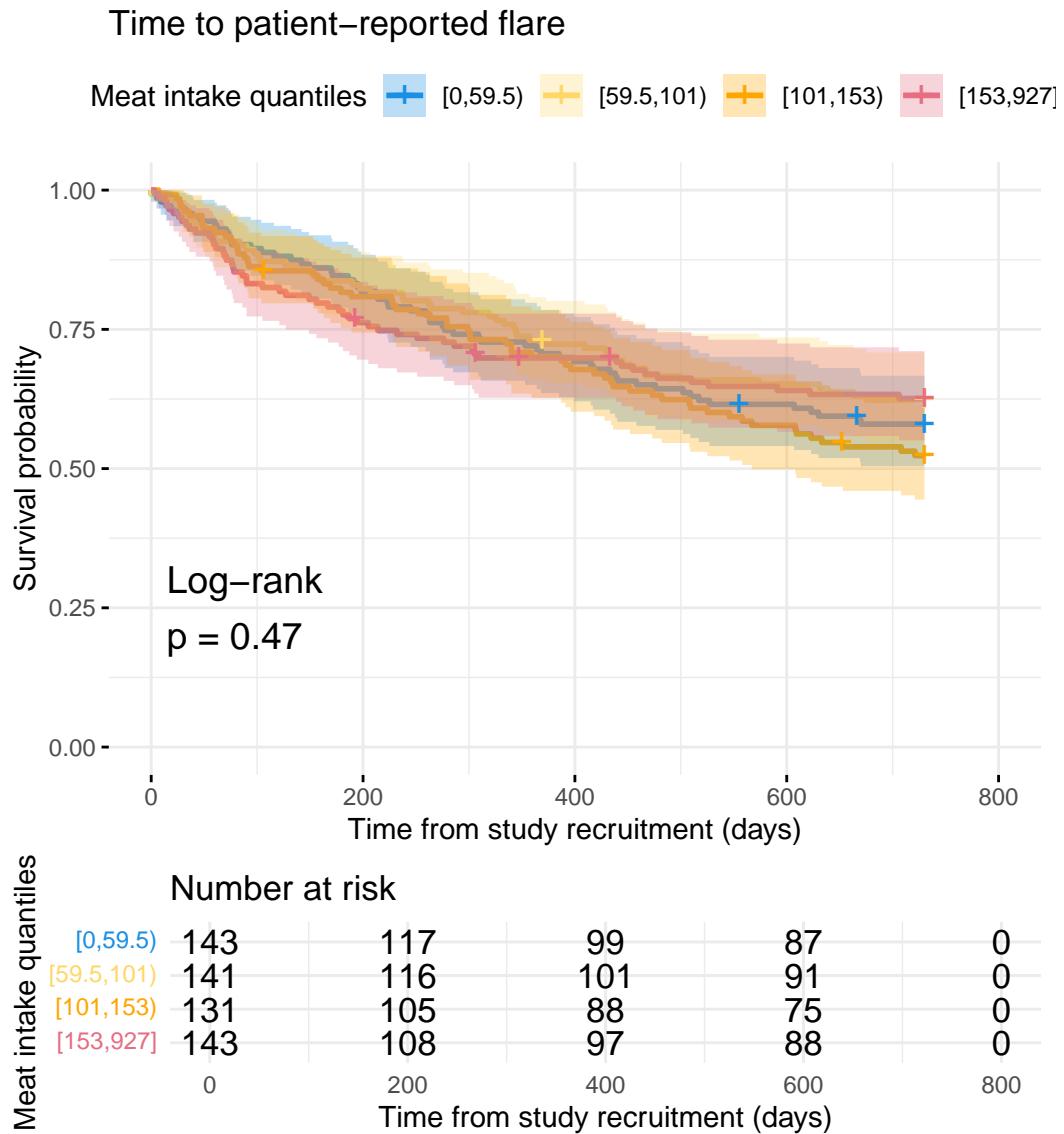
data = flare.uc.df,
var_name = "meat_overall",
outcome_time = "softflare_time",
outcome_event = "softflare",
legend_title = "Meat intake quantiles",
plot_base_path = "plots/uc/soft-flare/diet/meat_overall",
break_time_by = 200
)

# Save plot as RDS
saveRDS(analysis_result$plot, paste0(paths$outdir, "meat-overall-uc-soft.RDS"))

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(softflare_time, softflare) ~
    Sex + cat + IMD + dqi_tot + meat_overall_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.uc.df
)

# Display plot and model summary
analysis_result$plot

```



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.7285	1.2992	2.2997	0.0002
catFC 50-250	1.8389	1.3440	2.5161	0.0001
catFC > 250	2.1393	1.4976	3.0559	0.0000

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	1.4663	0.7712	2.7881	0.2431
IMD3	1.2909	0.6936	2.4025	0.4204
IMD4	1.3819	0.7648	2.4970	0.2839
IMD5	1.2718	0.7126	2.2698	0.4158
dqi_tot	1.0039	0.9895	1.0184	0.5978
meat_overall_cat[59.5,101]	0.9258	0.6231	1.3755	0.7026
meat_overall_cat[101,153)	1.2290	0.8270	1.8266	0.3077
meat_overall_cat[153,927]	1.0747	0.6919	1.6693	0.7484

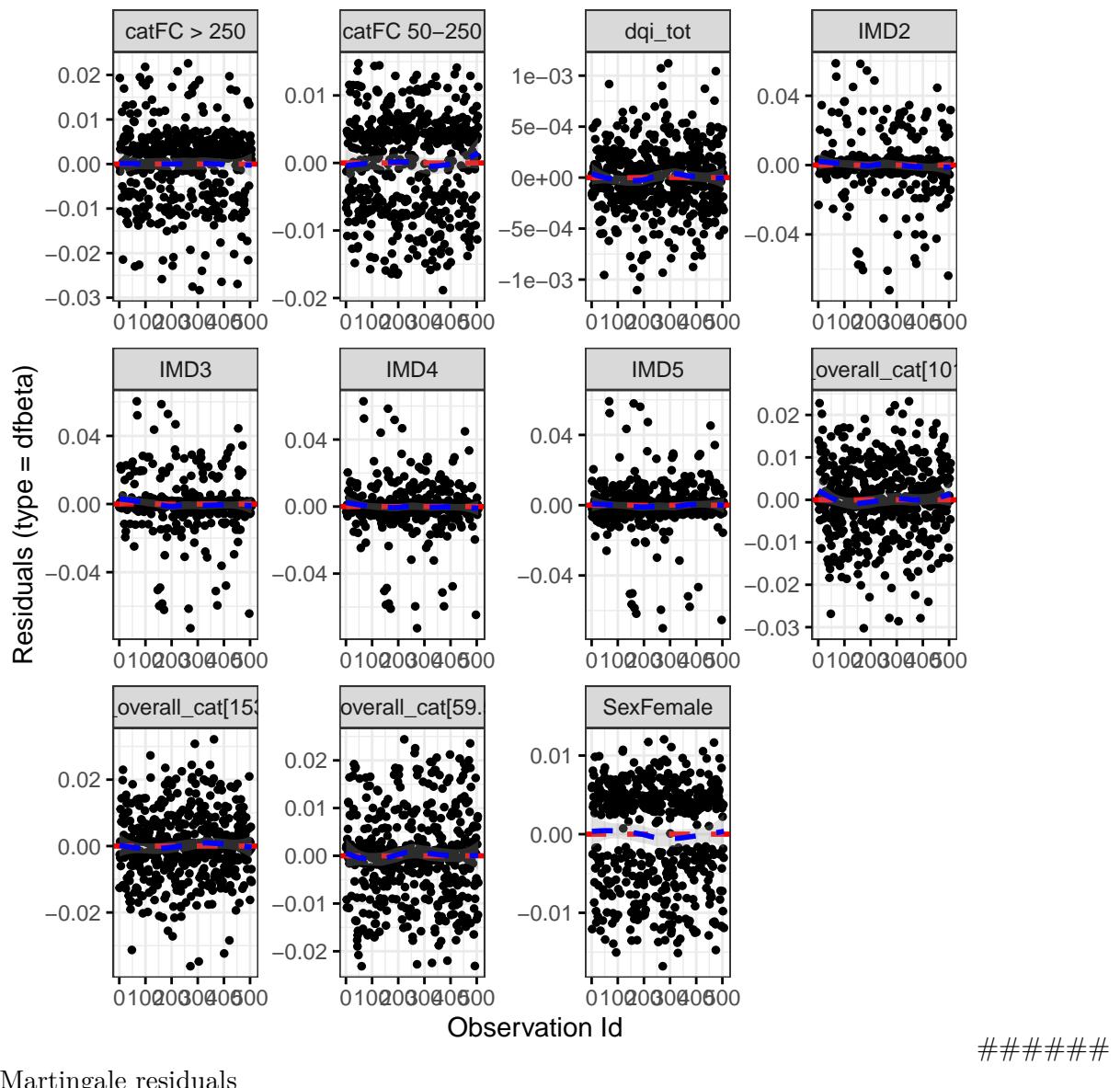
Diagnostics:

Proportional hazards assumption test

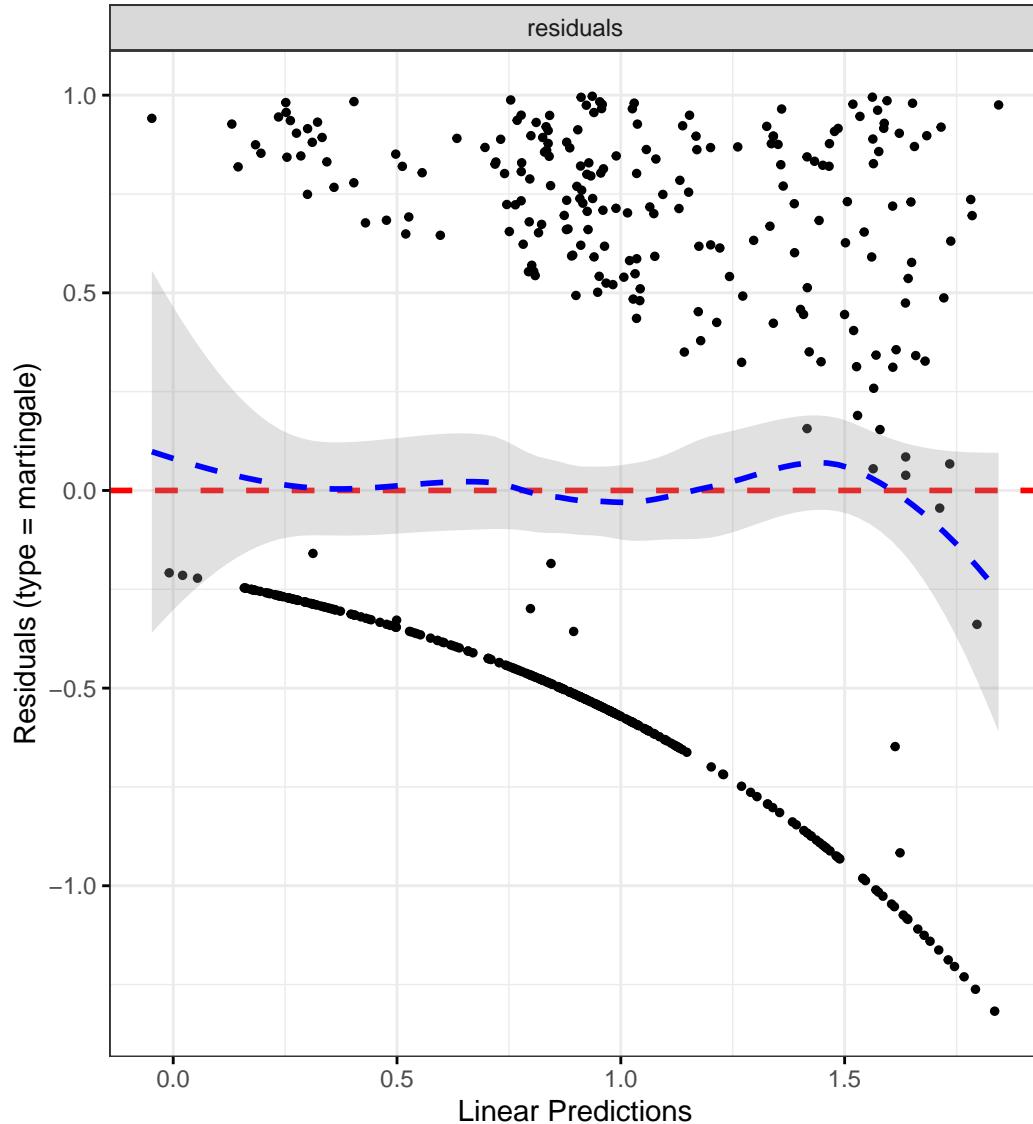
	Chi-squared statistic	DF	P-value
Sex	0.0329	1.0000	0.8562
cat	3.7928	2.0000	0.1501
IMD	2.6095	4.0000	0.6251
dqi_tot	0.6535	1.0000	0.4189
meat_overall_cat	8.7443	3.0000	0.0329
GLOBAL	15.7031	11.0001	0.1525

DF betas

```
`geom_smooth()` using formula = 'y ~ x'
```



```
`geom_smooth()` using formula = 'y ~ x'
```



Hard flare

```
# Run survival analysis using utility function for hard flare
analysis_result <- run_survival_analysis(
  data = flare.uc.df,
  var_name = "meat_overall",
  outcome_time = "hardflare_time",
  outcome_event = "hardflare",
  legend_title = "Meat intake quantiles",
```

```

plot_base_path = "plots/uc/hard-flare/diet/meat_overall",
break_time_by = 500
)

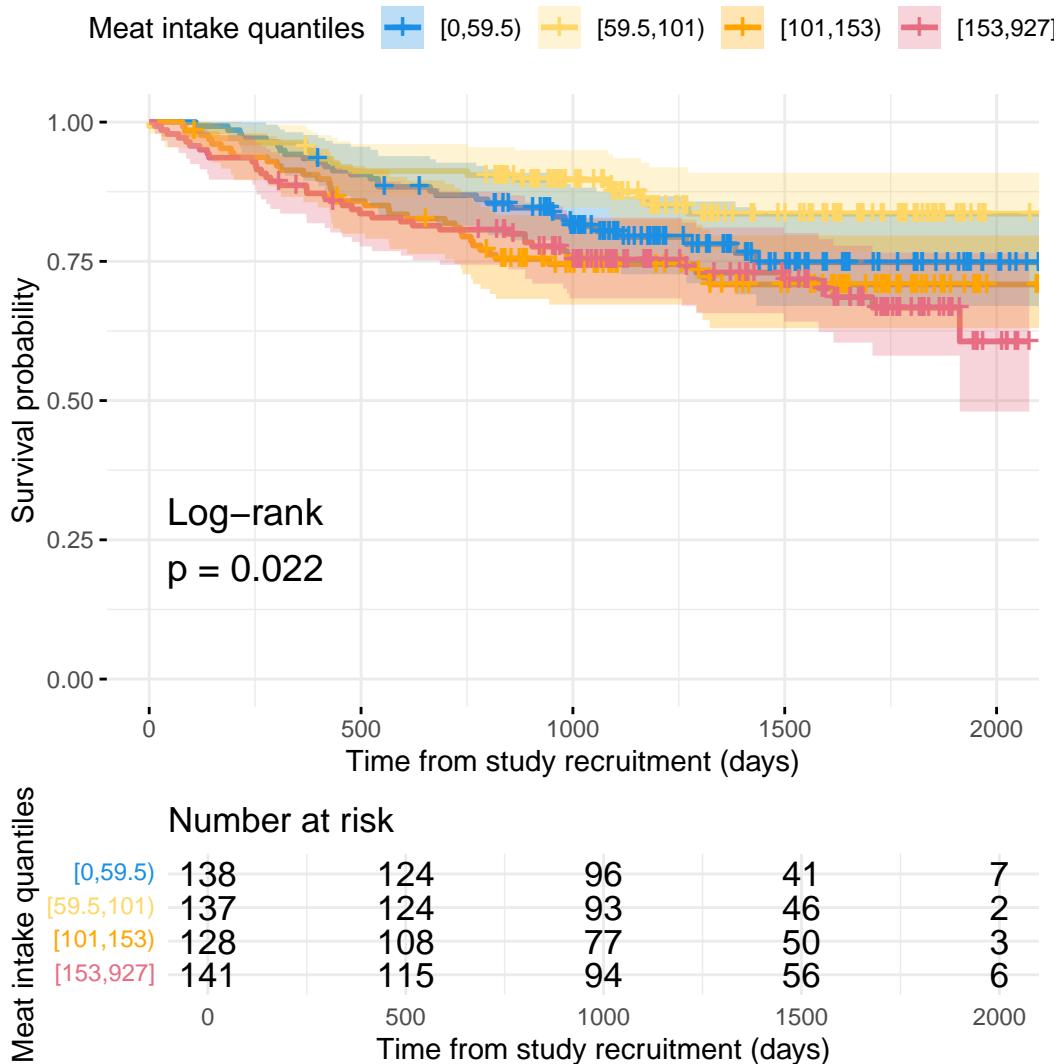
# Save plot as RDS
saveRDS(analysis_result$plot, paste0(paths$outdir, "meat-overall-uc-hard.RDS"))

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(hardflare_time, hardflare) ~
    Sex + cat + IMD + dqi_tot + meat_overall_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.uc.df
)

# Display plot and model summary
analysis_result$plot

```

Time to hard flare



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.3107	0.8948	1.9200	0.1648
catFC 50-250	1.9627	1.2813	3.0063	0.0019
catFC > 250	2.3648	1.4567	3.8391	0.0005

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	1.6660	0.6329	4.3854	0.3013
IMD3	1.5465	0.6044	3.9569	0.3631
IMD4	2.6029	1.0826	6.2585	0.0326
IMD5	1.5688	0.6520	3.7747	0.3148
dqi_tot	1.0190	0.9986	1.0398	0.0686
meat_overall_cat[59,5,101]	0.7688	0.4211	1.4037	0.3921
meat_overall_cat[101,153)	1.5264	0.8791	2.6503	0.1330
meat_overall_cat[153,927]	1.9492	1.0666	3.5619	0.0300

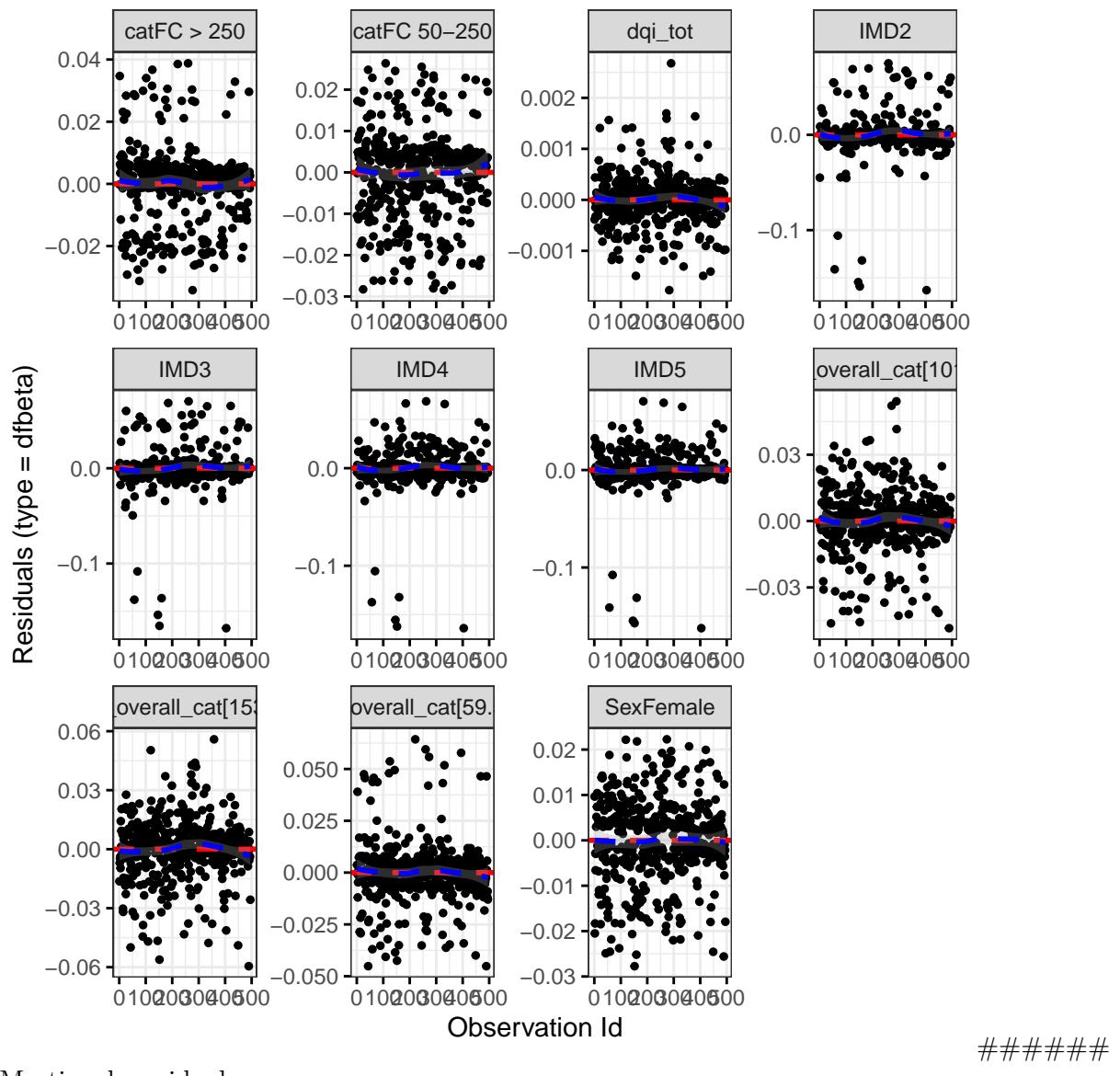
Diagnostics:

Proportional hazards assumption test

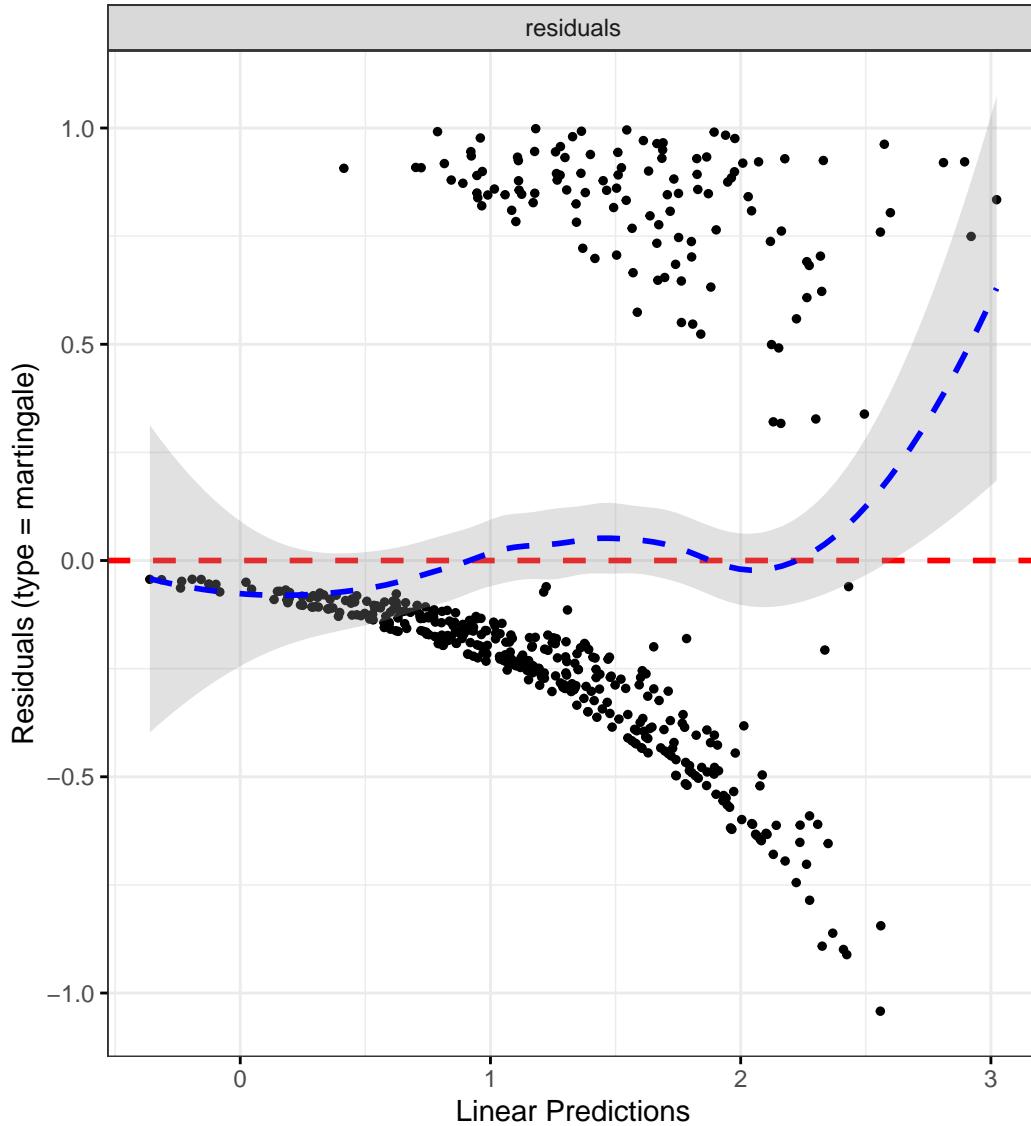
	Chi-squared statistic	DF	P-value
Sex	0.1586	0.9811	0.6827
cat	6.5851	1.9573	0.0356
IMD	1.8899	3.9269	0.7461
dqi_tot	0.0381	0.9811	0.8394
meat_overall_cat	1.1463	2.9449	0.7570
GLOBAL	10.6928	19.8397	0.9510

DF betas

```
`geom_smooth()` using formula = 'y ~ x'
```



```
`geom_smooth()` using formula = 'y ~ x'
```



Inflammatory bowel disease

Patient-reported flare

```
# Categorize overall meat intake by quantiles
flare.df <- categorize_by_quantiles(flare.df, "meat_overall", reference_data = flare.df)

# Run survival analysis using utility function
analysis_result <- run_survival_analysis()
```

```

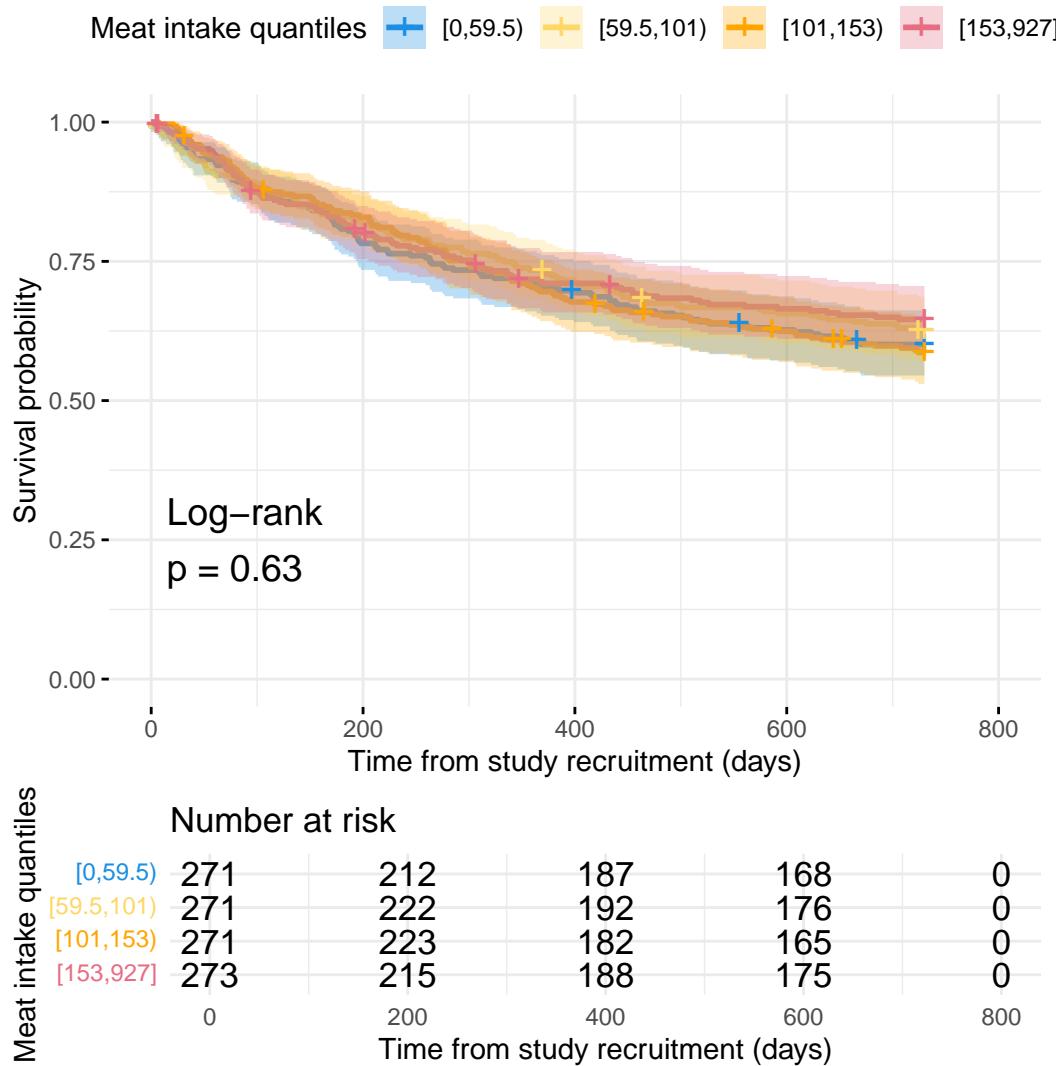
data = flare.df,
var_name = "meat_overall",
outcome_time = "softflare_time",
outcome_event = "softflare",
legend_title = "Meat intake quantiles",
plot_base_path = "plots/ibd/soft-flare/diet/meat_overall",
break_time_by = 200
)

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(softflare_time, softflare) ~
    Sex + cat + IMD + dqi_tot + meat_overall_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.df
)

# Display plot and model summary
analysis_result$plot

```

Time to patient-reported flare



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.7617	1.4244	2.1790	0.0000
catFC 50-250	1.5474	1.2287	1.9487	0.0002
catFC > 250	2.0422	1.5777	2.6433	0.0000

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	1.0254	0.6541	1.6076	0.9129
IMD3	1.0649	0.6939	1.6340	0.7736
IMD4	1.1039	0.7295	1.6704	0.6402
IMD5	1.1042	0.7422	1.6429	0.6247
dqi_tot	1.0034	0.9932	1.0137	0.5115
meat_overall_cat[59.5,101]	0.9658	0.7267	1.2835	0.8105
meat_overall_cat[101,153)	1.0830	0.8101	1.4477	0.5905
meat_overall_cat[153,927]	0.9958	0.7241	1.3696	0.9794

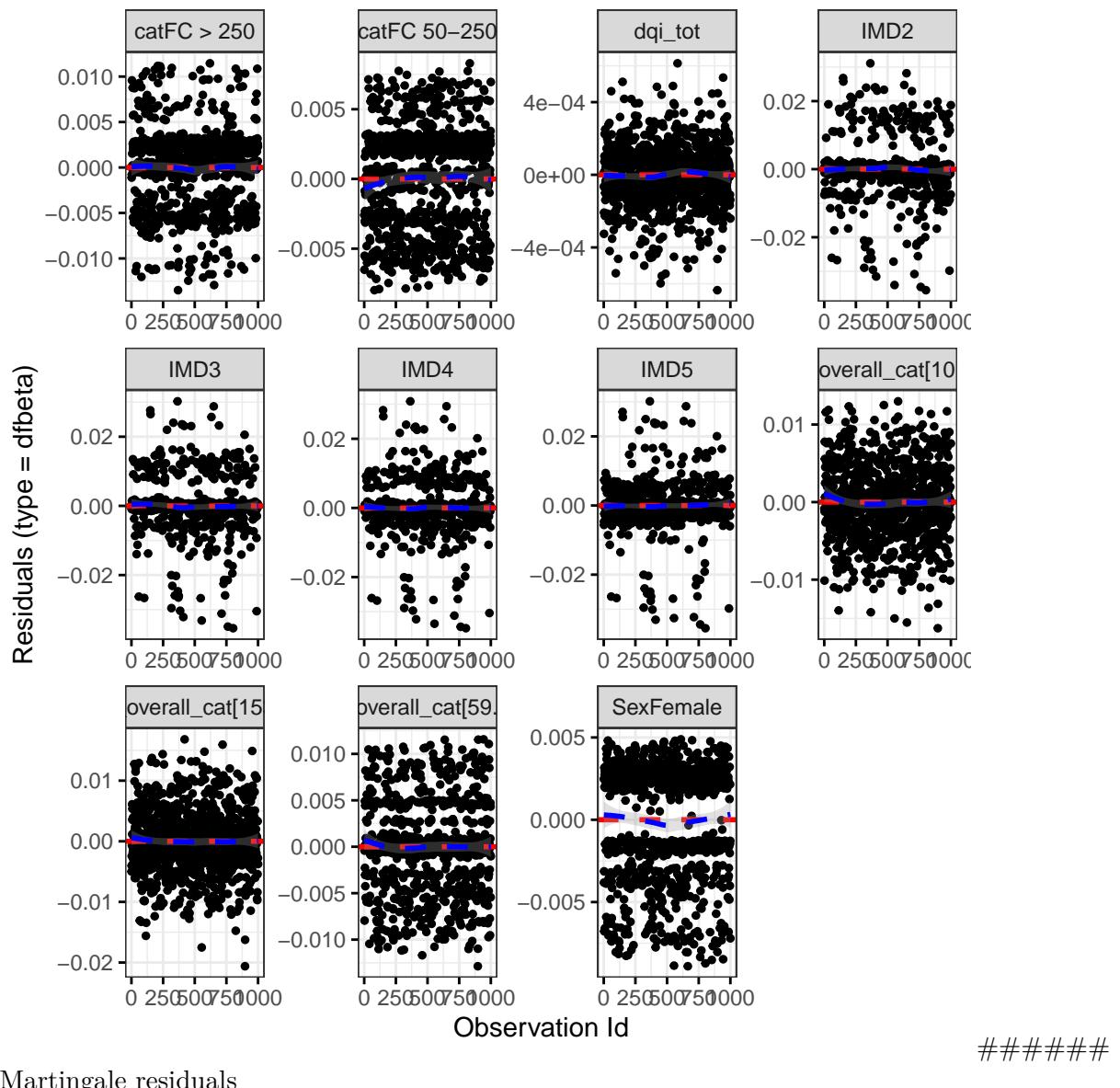
Diagnostics:

Proportional hazards assumption test

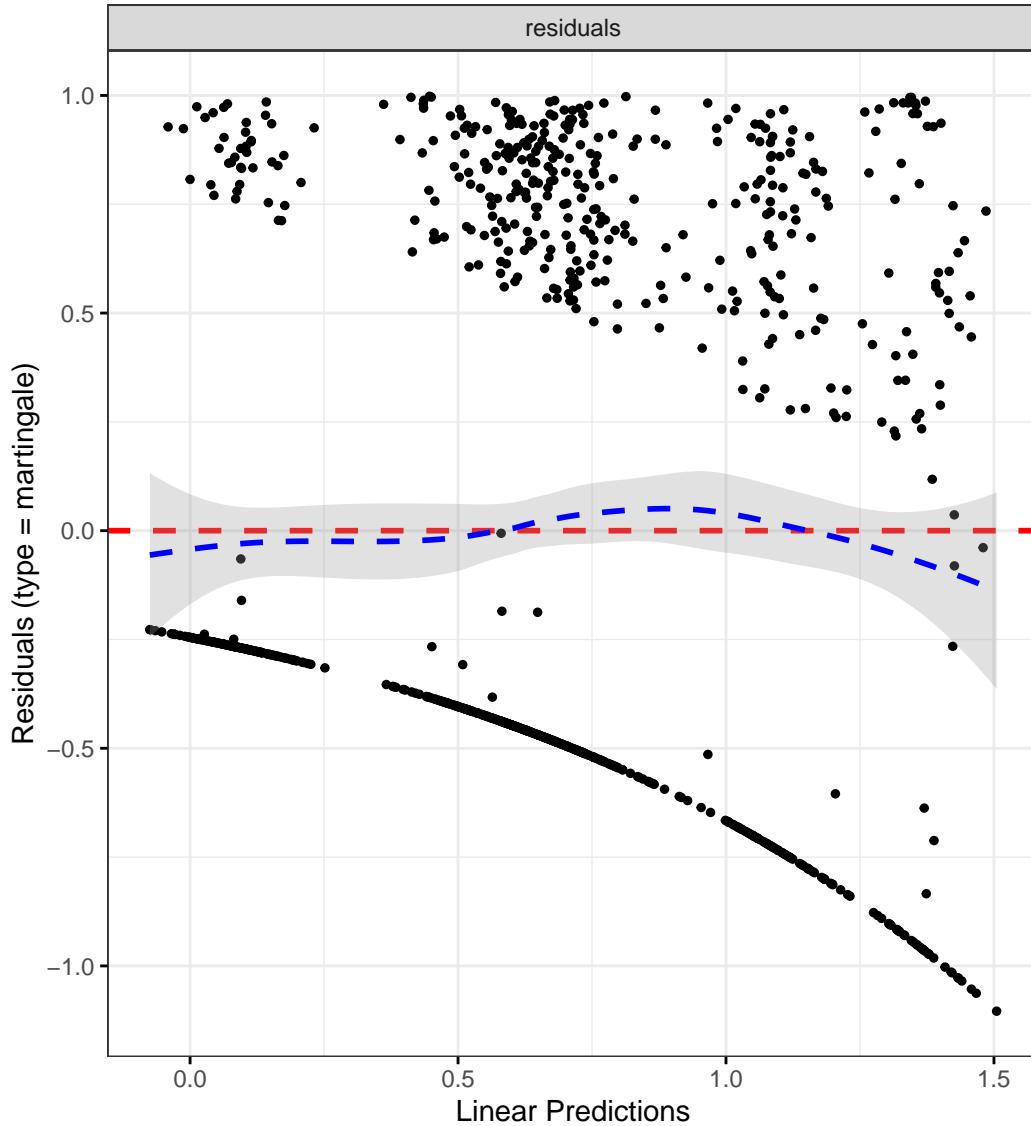
	Chi-squared statistic	DF	P-value
Sex	0.0001	1.0000	0.9915
cat	0.8075	2.0000	0.6678
IMD	4.6669	4.0000	0.3232
dqi_tot	0.9546	1.0000	0.3286
meat_overall_cat	3.7140	3.0000	0.2940
GLOBAL	10.0527	11.0002	0.5257

DF betas

```
`geom_smooth()` using formula = 'y ~ x'
```



```
`geom_smooth()` using formula = 'y ~ x'
```



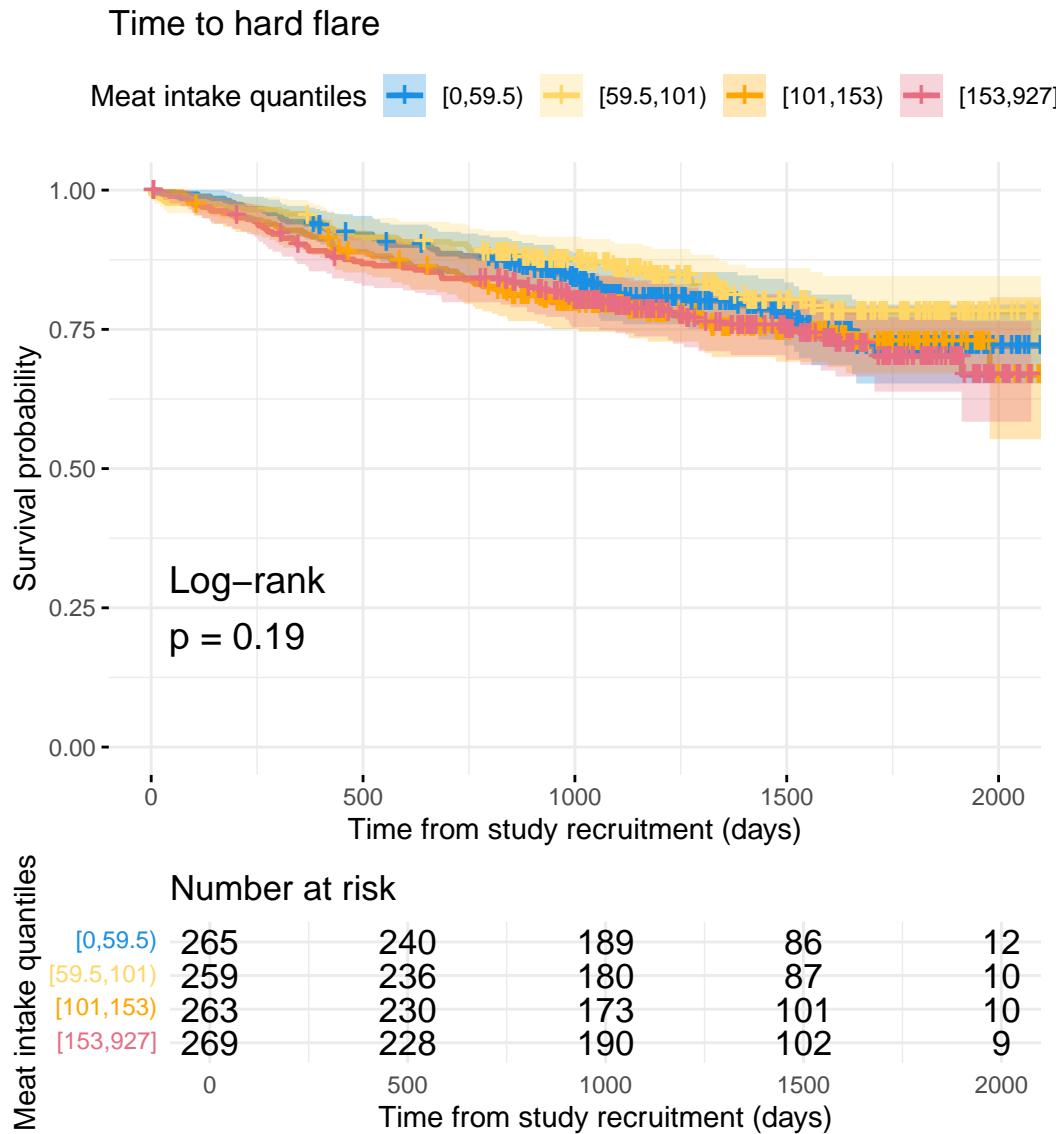
Hard flare

```
# Run survival analysis using utility function for hard flare
analysis_result <- run_survival_analysis(
  data = flare.df,
  var_name = "meat_overall",
  outcome_time = "hardflare_time",
  outcome_event = "hardflare",
  legend_title = "Meat intake quantiles",
```

```
plot_base_path = "plots/ibd/hard-flare/diet/meat_overall",
break_time_by = 500
)

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(hardflare_time, hardflare) ~
    Sex + cat + IMD + dqi_tot + meat_overall_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.df
)

# Display plot and model summary
analysis_result$plot
```



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.2443	0.9466	1.6356	0.1172
catFC 50-250	1.9230	1.4102	2.6222	0.0000
catFC > 250	2.6521	1.8787	3.7439	0.0000

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	0.9601	0.5133	1.7960	0.8987
IMD3	1.0478	0.5783	1.8982	0.8777
IMD4	1.4264	0.8129	2.5030	0.2157
IMD5	1.0348	0.5956	1.7981	0.9033
dqi_tot	1.0091	0.9953	1.0231	0.1972
meat_overall_cat[59.5,101]	0.8306	0.5560	1.2407	0.3646
meat_overall_cat[101,153)	1.2094	0.8216	1.7803	0.3352
meat_overall_cat[153,927]	1.3007	0.8612	1.9645	0.2114

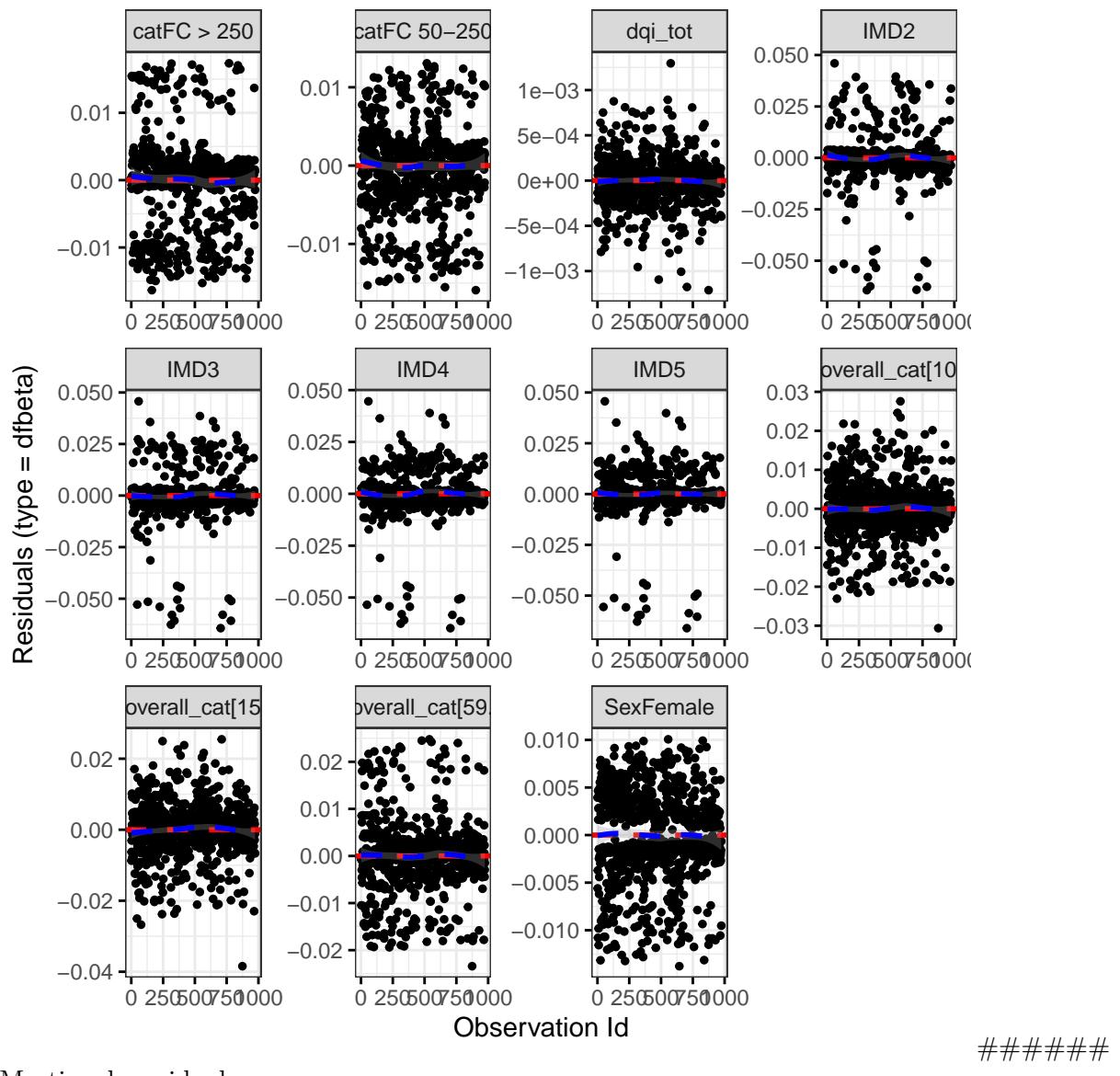
Diagnostics:

Proportional hazards assumption test

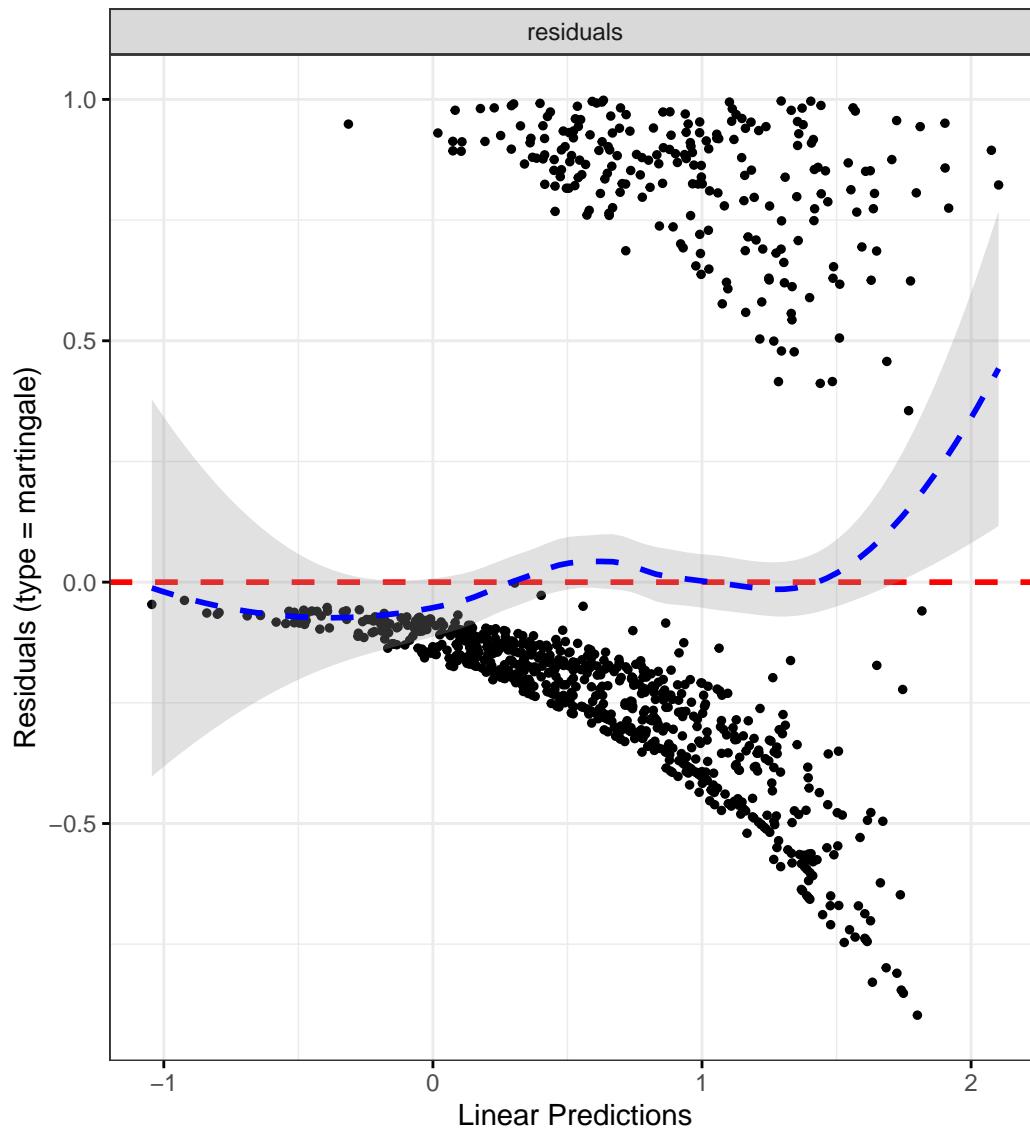
	Chi-squared statistic	DF	P-value
Sex	0.1207	0.9880	0.7236
cat	6.3624	1.9795	0.0407
IMD	2.4822	3.9450	0.6394
dqi_tot	1.4650	0.9898	0.2235
meat_overall_cat	1.9016	2.9717	0.5878
GLOBAL	11.7018	23.1150	0.9759

DF betas

```
`geom_smooth()` using formula = 'y ~ x'
```



```
`geom_smooth()` using formula = 'y ~ x'
```



Overall fish intake

Crohn's disease

Patient-reported flare

```
# Categorize overall fish intake by quantiles
```

```
flare.cd.df <- categorize_by_quantiles(flare.cd.df, "fish_overall", reference_data = flare.d
```

```

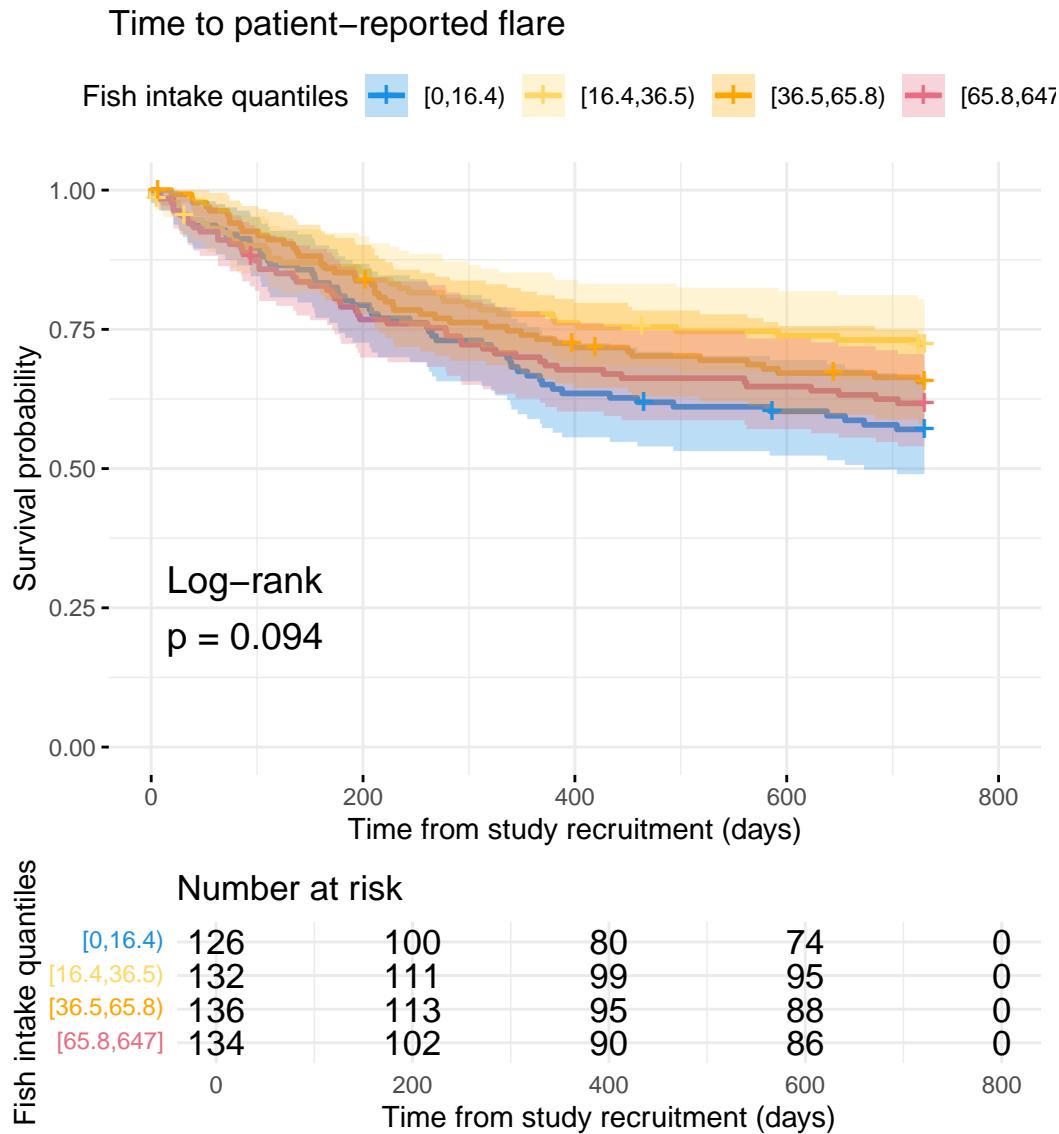
# Run survival analysis using utility function
analysis_result <- run_survival_analysis(
  data = flare.cd.df,
  var_name = "fish_overall",
  outcome_time = "softflare_time",
  outcome_event = "softflare",
  legend_title = "Fish intake quantiles",
  plot_base_path = "plots/cd/soft-flare/diet/fish_overall",
  break_time_by = 200
)

# Save plot as RDS
saveRDS(analysis_result$plot, paste0(paths$outdir, "fish-overall-cd-soft.RDS"))

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(softflare_time, softflare) ~
    Sex + cat + IMD + dqi_tot + fish_overall_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.cd.df
)

# Display plot and model summary
analysis_result$plot

```



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.8915	1.3593	2.6322	0.0002
catFC 50-250	1.3197	0.9329	1.8669	0.1171
catFC > 250	2.0898	1.4279	3.0585	0.0001

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	0.7647	0.4051	1.4436	0.4080
IMD3	0.9021	0.4976	1.6357	0.7344
IMD4	0.8322	0.4594	1.5075	0.5446
IMD5	1.0438	0.5998	1.8164	0.8795
dqi_tot	1.0058	0.9919	1.0199	0.4186
fish_overall_cat[16.4,36.	0.5914	0.3778	0.9256	0.0215
fish_overall_cat[36.5,65.	0.6846	0.4467	1.0493	0.0820
fish_overall_cat[65.8,647	0.8655	0.5684	1.3179	0.5006

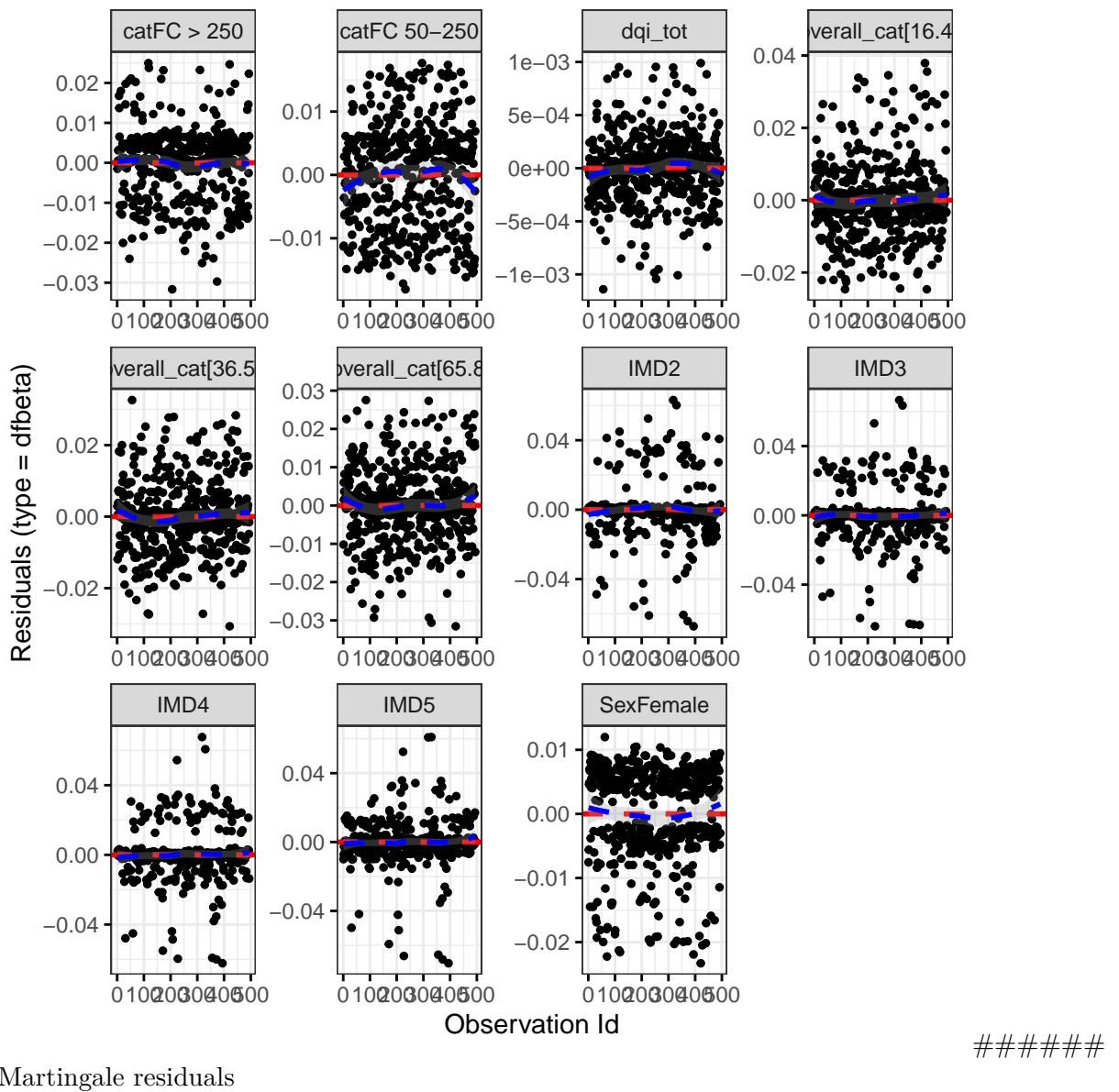
Diagnostics:

Proportional hazards assumption test

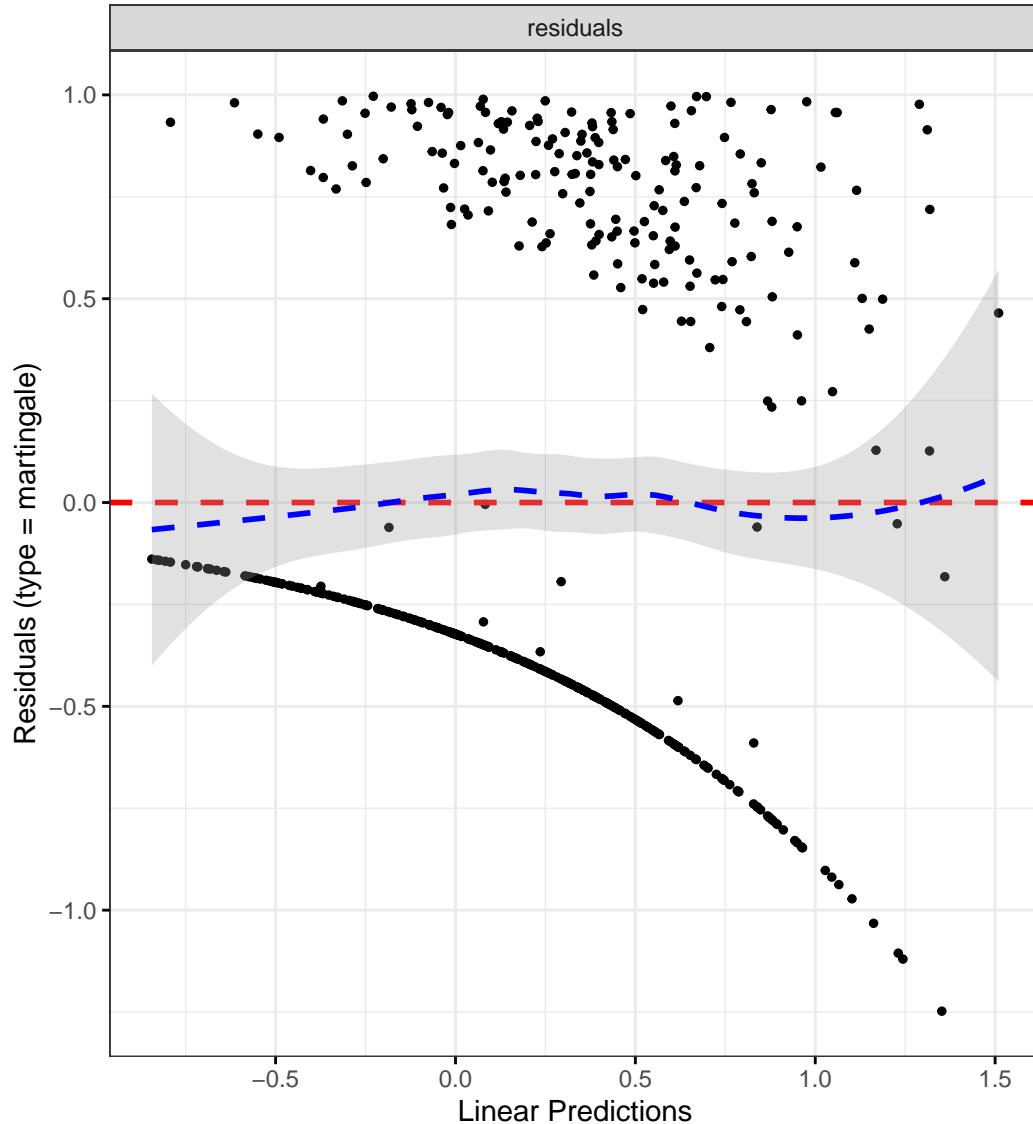
	Chi-squared statistic	DF	P-value
Sex	0.1702	1.0000	0.6800
cat	1.1851	2.0000	0.5529
IMD	2.9824	4.0000	0.5608
dqi_tot	0.1405	1.0000	0.7078
fish_overall_cat	2.7091	3.0000	0.4387
GLOBAL	7.8593	11.0001	0.7259

DF betas

```
`geom_smooth()` using formula = 'y ~ x'
```



```
`geom_smooth()` using formula = 'y ~ x'
```



Hard flare

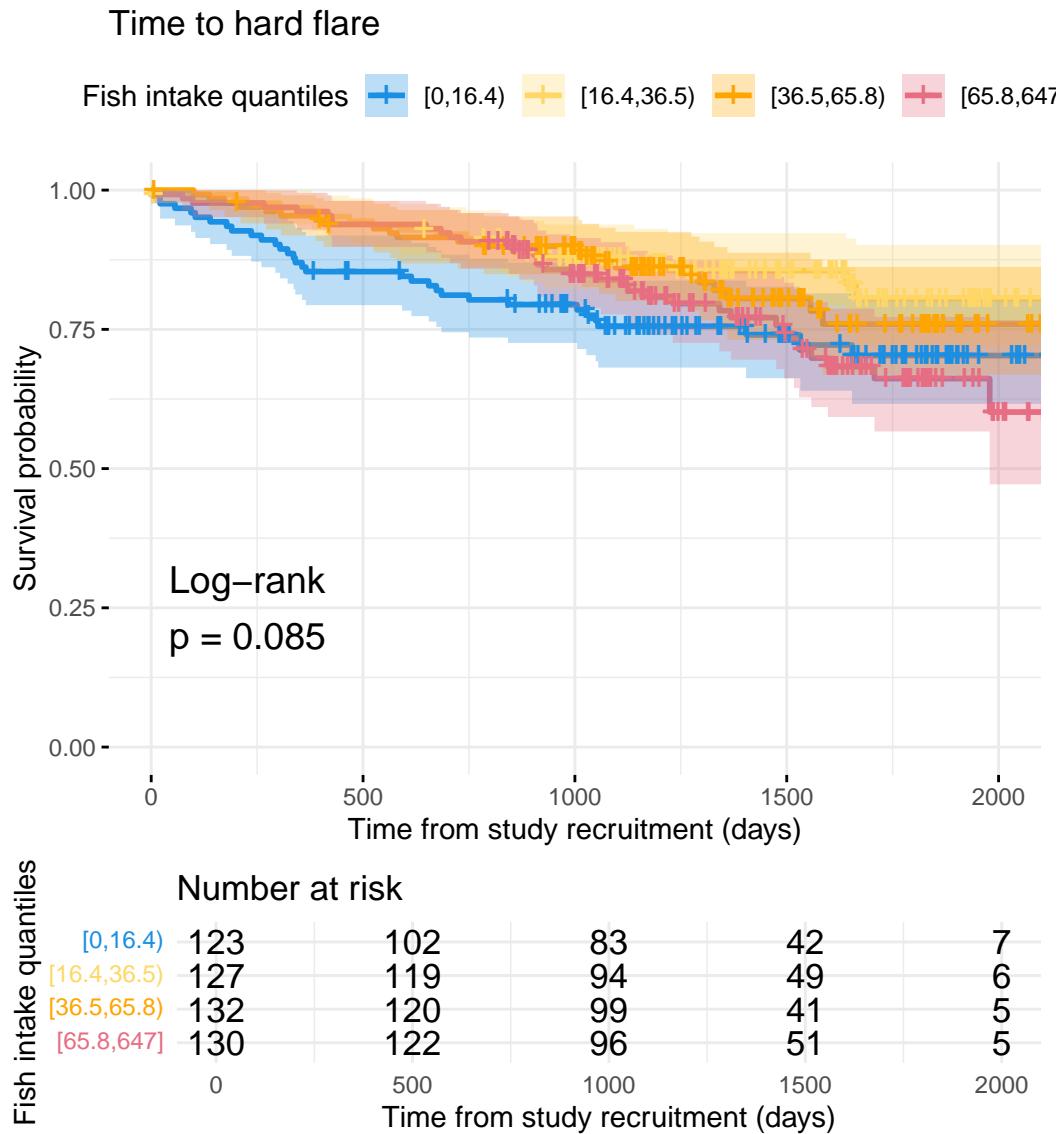
```
# Run survival analysis using utility function for hard flare
analysis_result <- run_survival_analysis(
  data = flare.cd.df,
  var_name = "fish_overall",
  outcome_time = "hardflare_time",
  outcome_event = "hardflare",
  legend_title = "Fish intake quantiles",
```

```
plot_base_path = "plots/cd/hard-flare/diet/fish_overall",
break_time_by = 500
)

# Save plot as RDS
saveRDS(analysis_result$plot, paste0(paths$outdir, "fish-overall-cd-hard.RDS"))

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(hardflare_time, hardflare) ~
    Sex + cat + IMD + dqi_tot + BMI + fish_overall_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.cd.df
)

# Display plot and model summary
analysis_result$plot
```



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.3102	0.8666	1.9809	0.2002
catFC 50-250	1.8784	1.1759	3.0005	0.0083
catFC > 250	3.1436	1.8906	5.2272	0.0000

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	0.6667	0.2863	1.5525	0.3472
IMD3	0.8078	0.3638	1.7937	0.6001
IMD4	0.7195	0.3301	1.5684	0.4077
IMD5	0.7555	0.3612	1.5801	0.4564
dqi_tot	1.0060	0.9875	1.0249	0.5266
BMI	1.0157	0.9803	1.0524	0.3885
fish_overall_cat[16.4,36.	0.4418	0.2418	0.8072	0.0079
fish_overall_cat[36.5,65.	0.5899	0.3344	1.0404	0.0683
fish_overall_cat[65.8,647	0.7671	0.4491	1.3102	0.3317

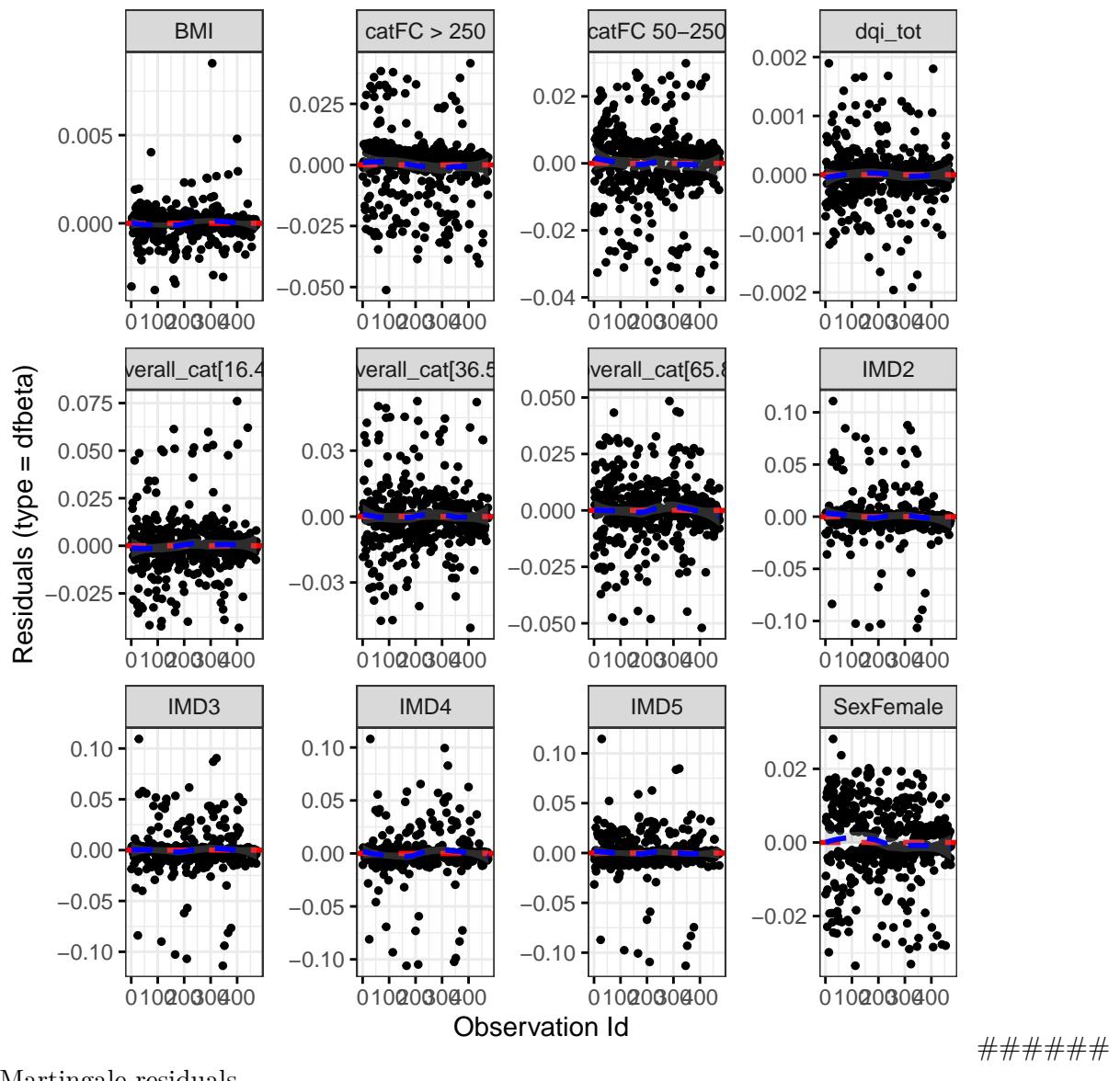
Diagnostics:

Proportional hazards assumption test

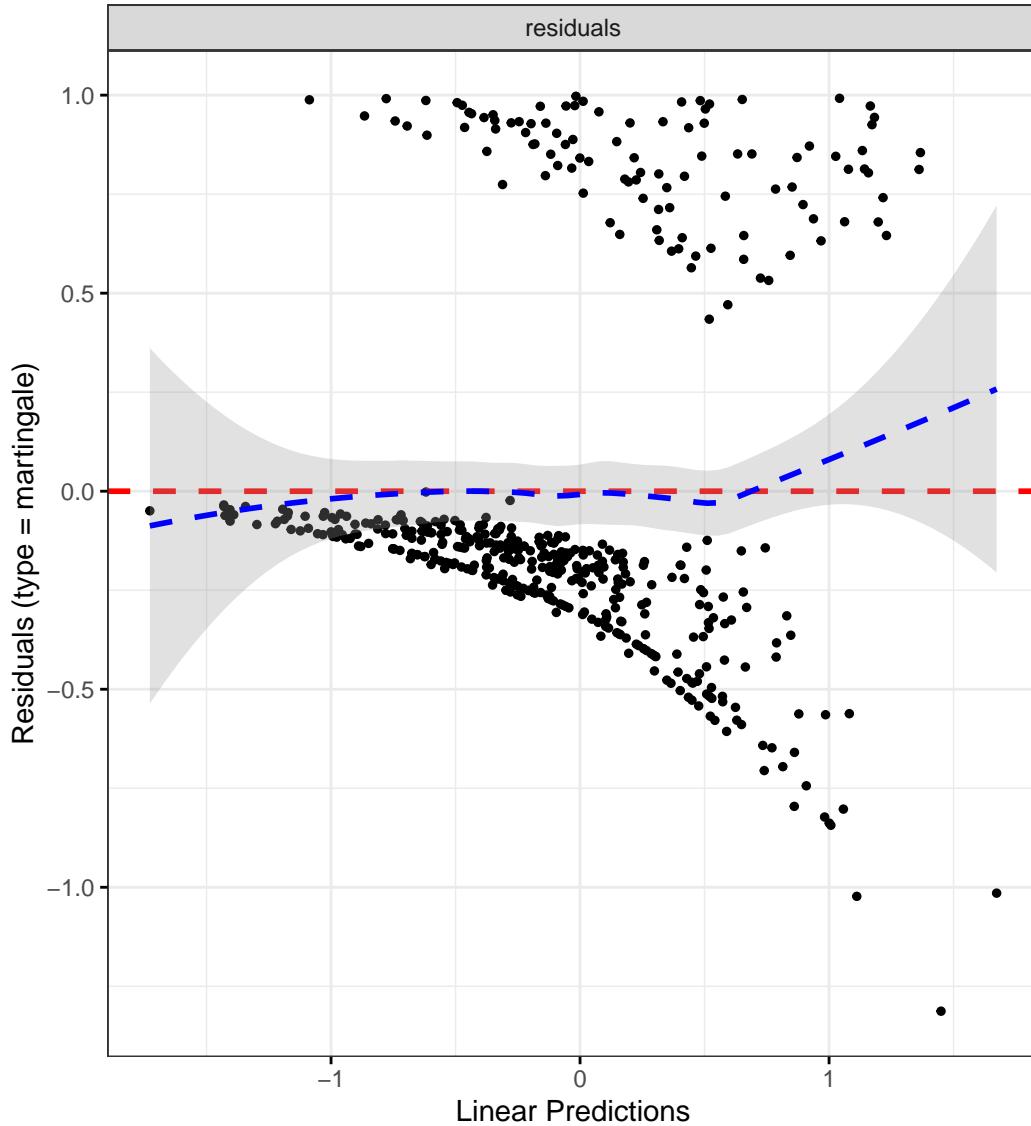
	Chi-squared statistic	DF	P-value
Sex	0.0875	0.9705	0.7562
cat	9.5266	1.9809	0.0083
IMD	2.6789	3.9281	0.6017
dqi_tot	2.6709	0.9911	0.1010
BMI	1.2451	0.9802	0.2588
fish_overall_cat	9.8922	2.9629	0.0189
GLOBAL	25.7218	17.9134	0.1038

DF betas

```
`geom_smooth()` using formula = 'y ~ x'
```



```
`geom_smooth()` using formula = 'y ~ x'
```



Ulcerative colitis

Patient-reported flare

```
# Categorize overall fish intake by quantiles
flare.uc.df <- categorize_by_quantiles(flare.uc.df, "fish_overall", reference_data = flare.d
```



```
# Run survival analysis using utility function
analysis_result <- run_survival_analysis(
```

```

data = flare.uc.df,
var_name = "fish_overall",
outcome_time = "softflare_time",
outcome_event = "softflare",
legend_title = "Fish intake quantiles",
plot_base_path = "plots/uc/soft-flare/diet/fish_overall",
break_time_by = 200
)

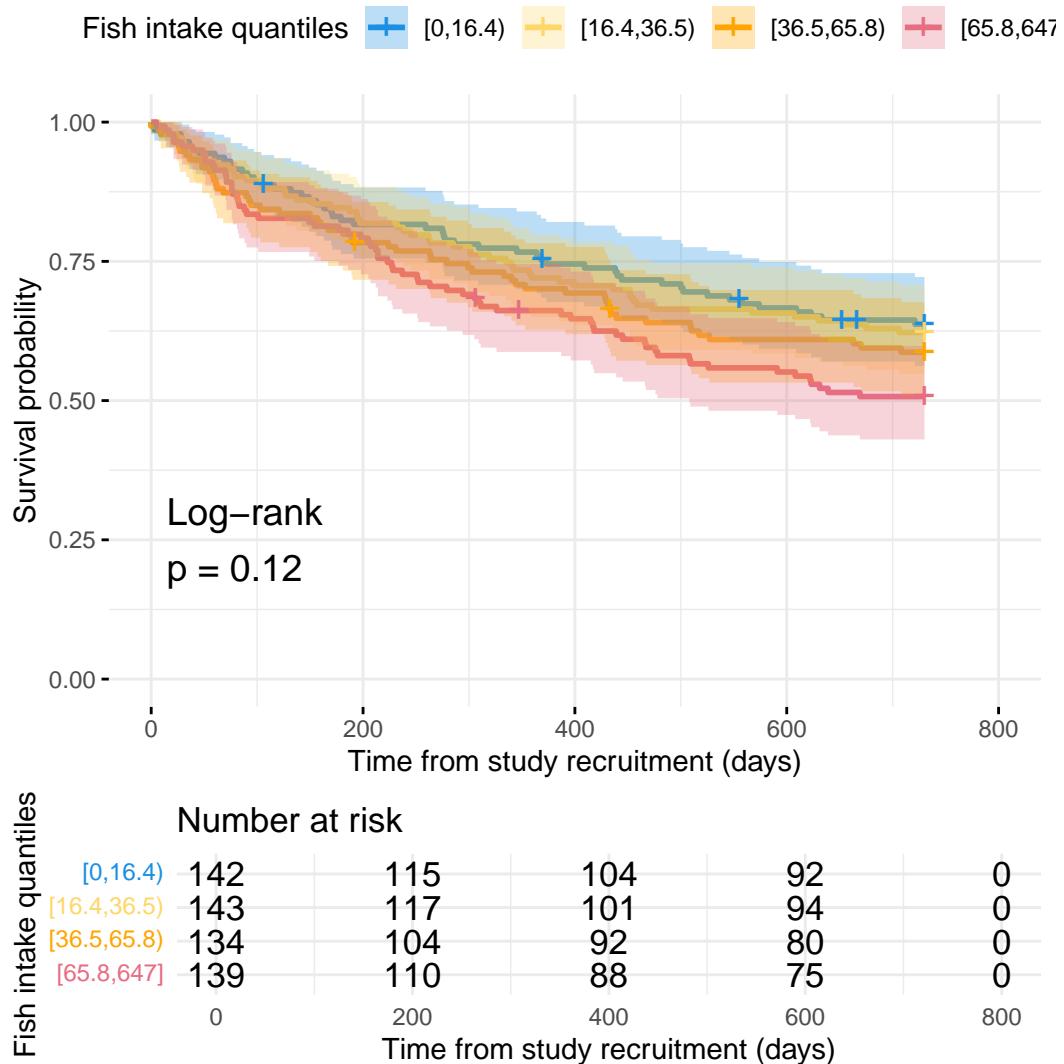
# Save plot as RDS
saveRDS(analysis_result$plot, paste0(paths$outdir, "fish-overall-uc-soft.RDS"))

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(softflare_time, softflare) ~
    Sex + cat + IMD + dqi_tot + BMI + fish_overall_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.uc.df
)

# Display plot and model summary
analysis_result$plot

```

Time to patient-reported flare



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.7033	1.2752	2.2751	0.0003
catFC 50-250	1.7671	1.2775	2.4443	0.0006
catFC > 250	2.0722	1.4510	2.9594	0.0001

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	1.5200	0.7951	2.9058	0.2054
IMD3	1.1686	0.6205	2.2008	0.6295
IMD4	1.4071	0.7743	2.5570	0.2624
IMD5	1.2361	0.6872	2.2233	0.4792
dqi_tot	0.9962	0.9830	1.0095	0.5737
BMI	0.9773	0.9481	1.0074	0.1383
fish_overall_cat[16.4,36.	1.1858	0.7883	1.7838	0.4132
fish_overall_cat[36.5,65.	1.1459	0.7555	1.7379	0.5216
fish_overall_cat[65.8,647	1.4914	1.0061	2.2109	0.0466

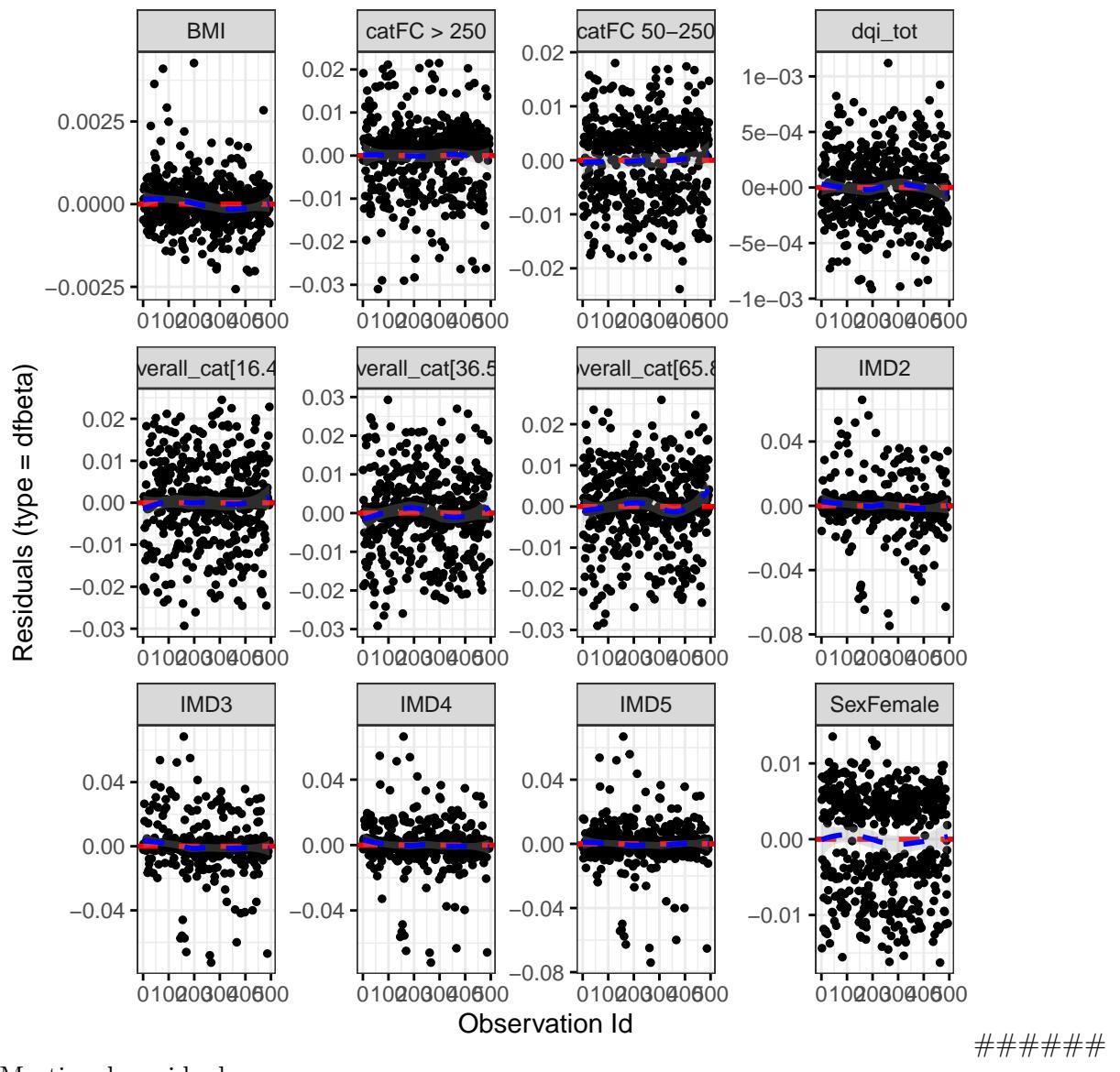
Diagnostics:

Proportional hazards assumption test

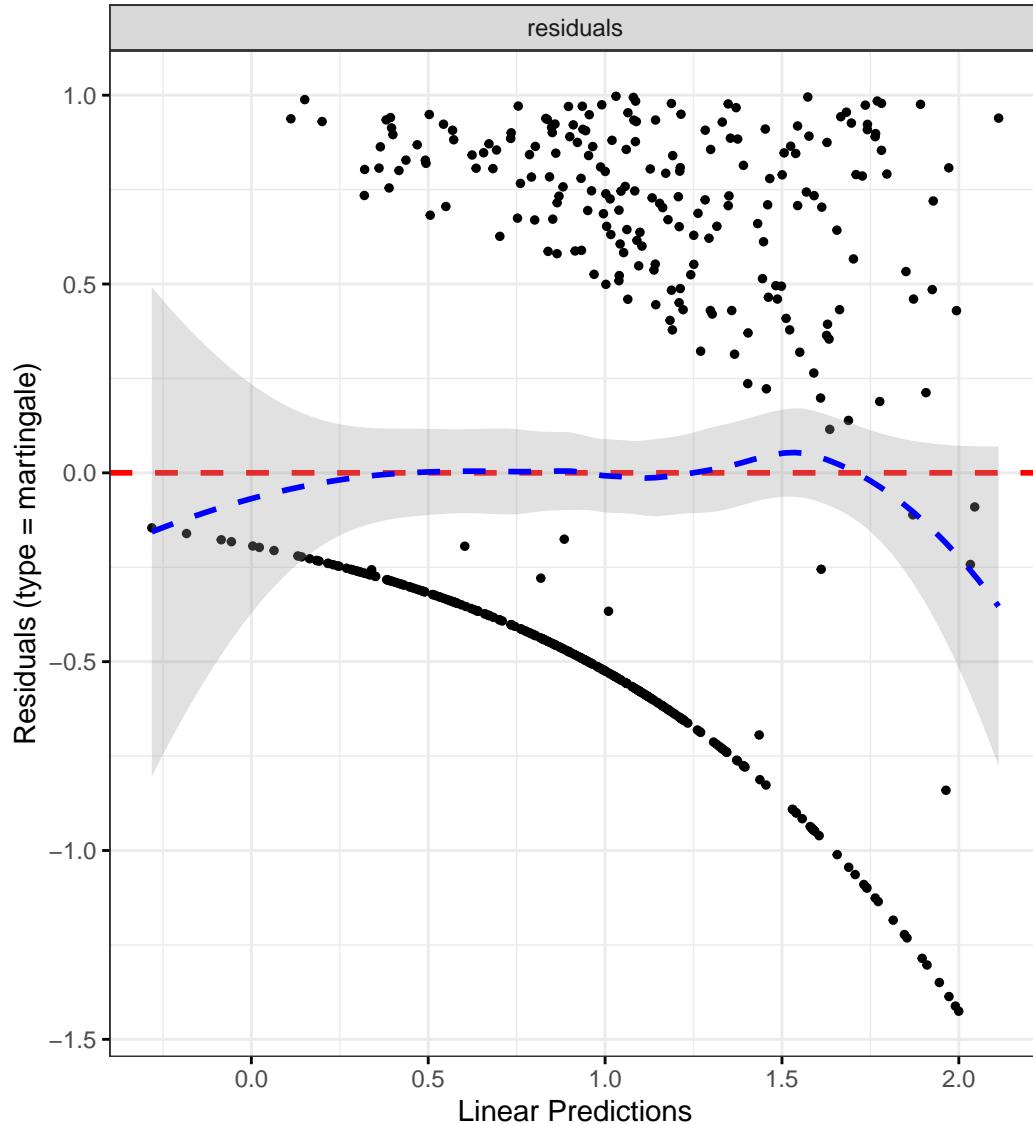
	Chi-squared statistic	DF	P-value
Sex	0.0111	1.0000	0.9161
cat	3.5361	2.0000	0.1707
IMD	2.6892	4.0000	0.6111
dqi_tot	0.7602	1.0000	0.3833
BMI	0.9453	1.0000	0.3309
fish_overall_cat	0.6666	3.0000	0.8810
GLOBAL	8.9045	12.0001	0.7111

DF betas

```
`geom_smooth()` using formula = 'y ~ x'
```



```
`geom_smooth()` using formula = 'y ~ x'
```



Hard flare

```
# Run survival analysis using utility function for hard flare
analysis_result <- run_survival_analysis(
  data = flare.uc.df,
  var_name = "fish_overall",
  outcome_time = "hardflare_time",
  outcome_event = "hardflare",
  legend_title = "Fish intake quantiles",
```

```

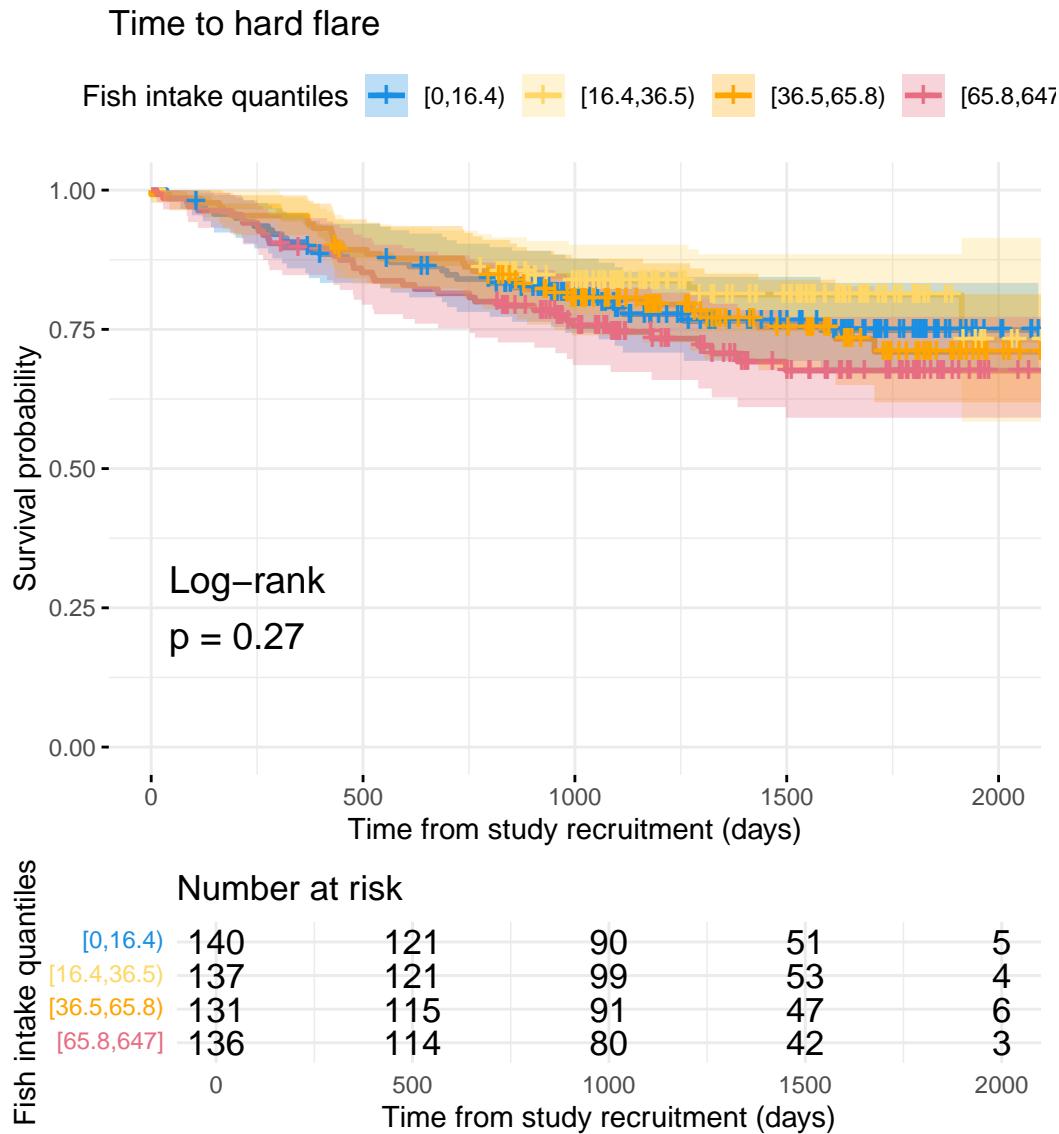
plot_base_path = "plots/uc/hard-flare/diet/fish_overall",
break_time_by = 500
)

# Save plot as RDS
saveRDS(analysis_result$plot, paste0(paths$outdir, "fish-overall-uc-hard.RDS"))

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(hardflare_time, hardflare) ~
    Sex + cat + IMD + dqi_tot + BMI + fish_overall_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.uc.df
)

# Display plot and model summary
analysis_result$plot

```



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.1941	0.8159	1.7478	0.3613
catFC 50-250	2.0229	1.2996	3.1488	0.0018
catFC > 250	2.4586	1.5117	3.9986	0.0003

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	1.6328	0.6183	4.3116	0.3223
IMD3	1.3160	0.5102	3.3947	0.5701
IMD4	2.4180	1.0087	5.7962	0.0478
IMD5	1.4286	0.5916	3.4499	0.4277
dqi_tot	1.0002	0.9821	1.0186	0.9857
BMI	0.9605	0.9204	1.0024	0.0641
fish_overall_cat[16.4,36.	0.8017	0.4619	1.3914	0.4320
fish_overall_cat[36.5,65.	0.8688	0.5070	1.4889	0.6088
fish_overall_cat[65.8,647	1.1617	0.6953	1.9410	0.5671

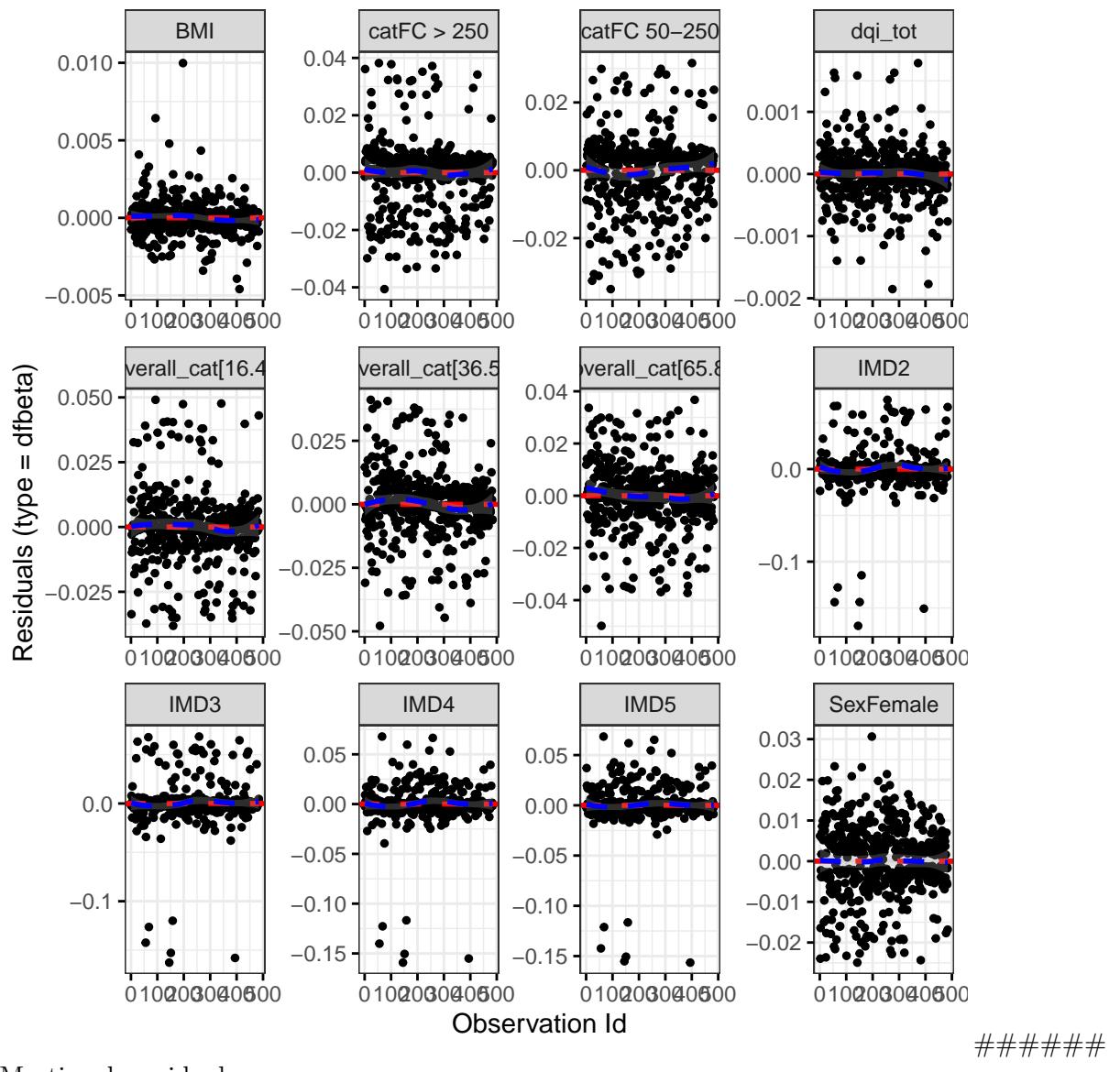
Diagnostics:

Proportional hazards assumption test

	Chi-squared statistic	DF	P-value
Sex	0.0334	0.9883	0.8515
cat	5.4126	1.9571	0.0641
IMD	1.2035	3.9340	0.8713
dqi_tot	0.0001	0.9865	0.9922
BMI	0.6022	0.9887	0.4334
fish_overall_cat	2.4436	2.9667	0.4794
GLOBAL	12.4545	18.9576	0.8637

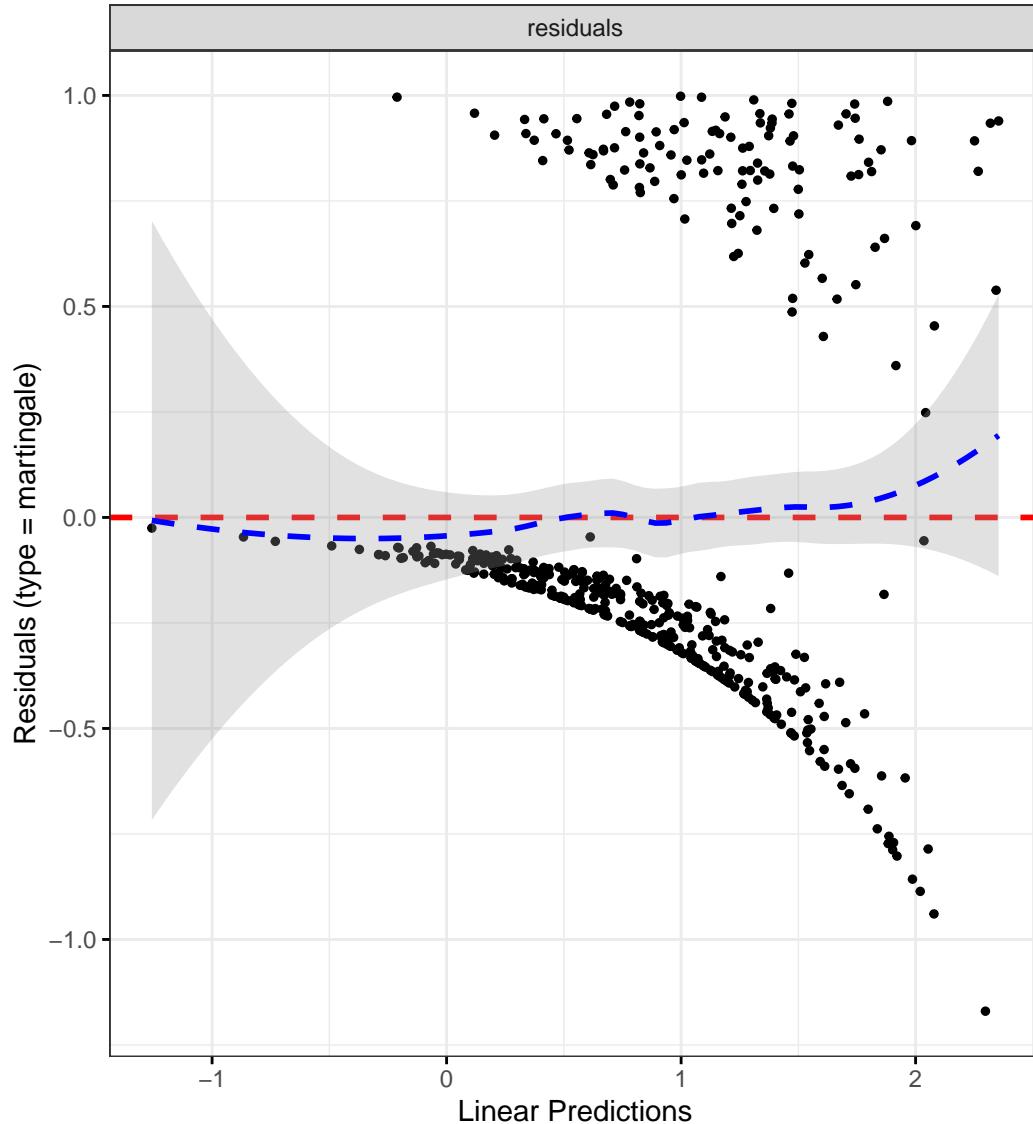
DF betas

```
`geom_smooth()` using formula = 'y ~ x'
```



Martingale residuals

```
`geom_smooth()` using formula = 'y ~ x'
```



Inflammatory bowel disease

Patient-reported flare

```
# Categorize overall fish intake by quantiles
flare.df <- categorize_by_quantiles(flare.df, "fish_overall", reference_data = flare.df)

# Run survival analysis using utility function
analysis_result <- run_survival_analysis()
```

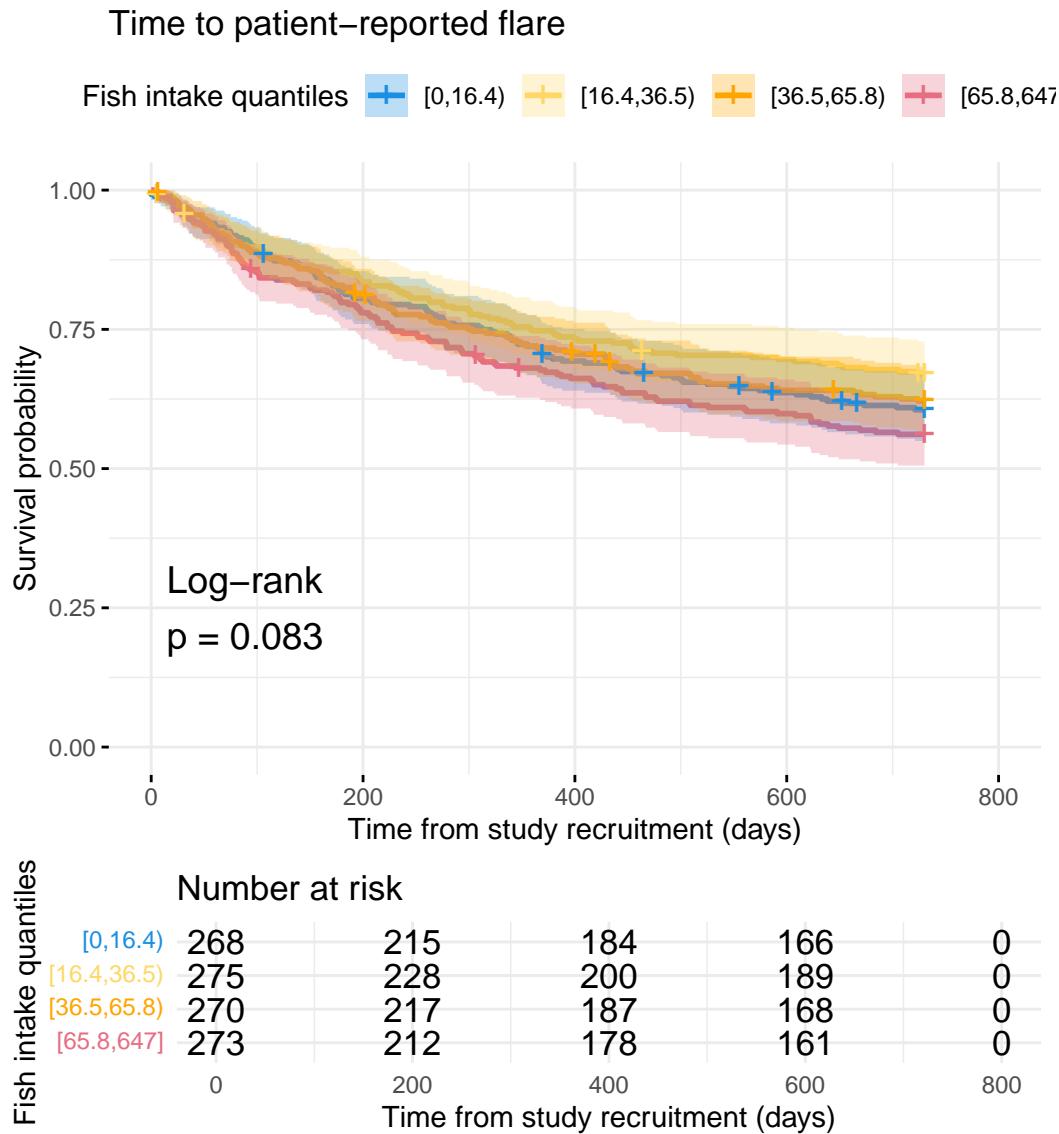
```

data = flare.df,
var_name = "fish_overall",
outcome_time = "softflare_time",
outcome_event = "softflare",
legend_title = "Fish intake quantiles",
plot_base_path = "plots/ibd/soft-flare/diet/fish_overall",
break_time_by = 200
)

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(softflare_time, softflare) ~
    Sex + cat + IMD + dqi_tot + BMI + fish_overall_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.df
)

# Display plot and model summary
analysis_result$plot

```



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.7632	1.4212	2.1875	0.0000
catFC 50-250	1.4793	1.1694	1.8713	0.0011
catFC > 250	2.0110	1.5523	2.6053	0.0000

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	1.0159	0.6451	1.5999	0.9458
IMD3	1.0071	0.6520	1.5557	0.9744
IMD4	1.1380	0.7503	1.7261	0.5429
IMD5	1.1013	0.7368	1.6461	0.6380
dqi_tot	1.0012	0.9916	1.0108	0.8128
BMI	0.9950	0.9753	1.0151	0.6231
fish_overall_cat[16.4,36.	0.8621	0.6390	1.1630	0.3313
fish_overall_cat[36.5,65.	0.9355	0.6958	1.2576	0.6586
fish_overall_cat[65.8,647	1.1716	0.8795	1.5608	0.2792

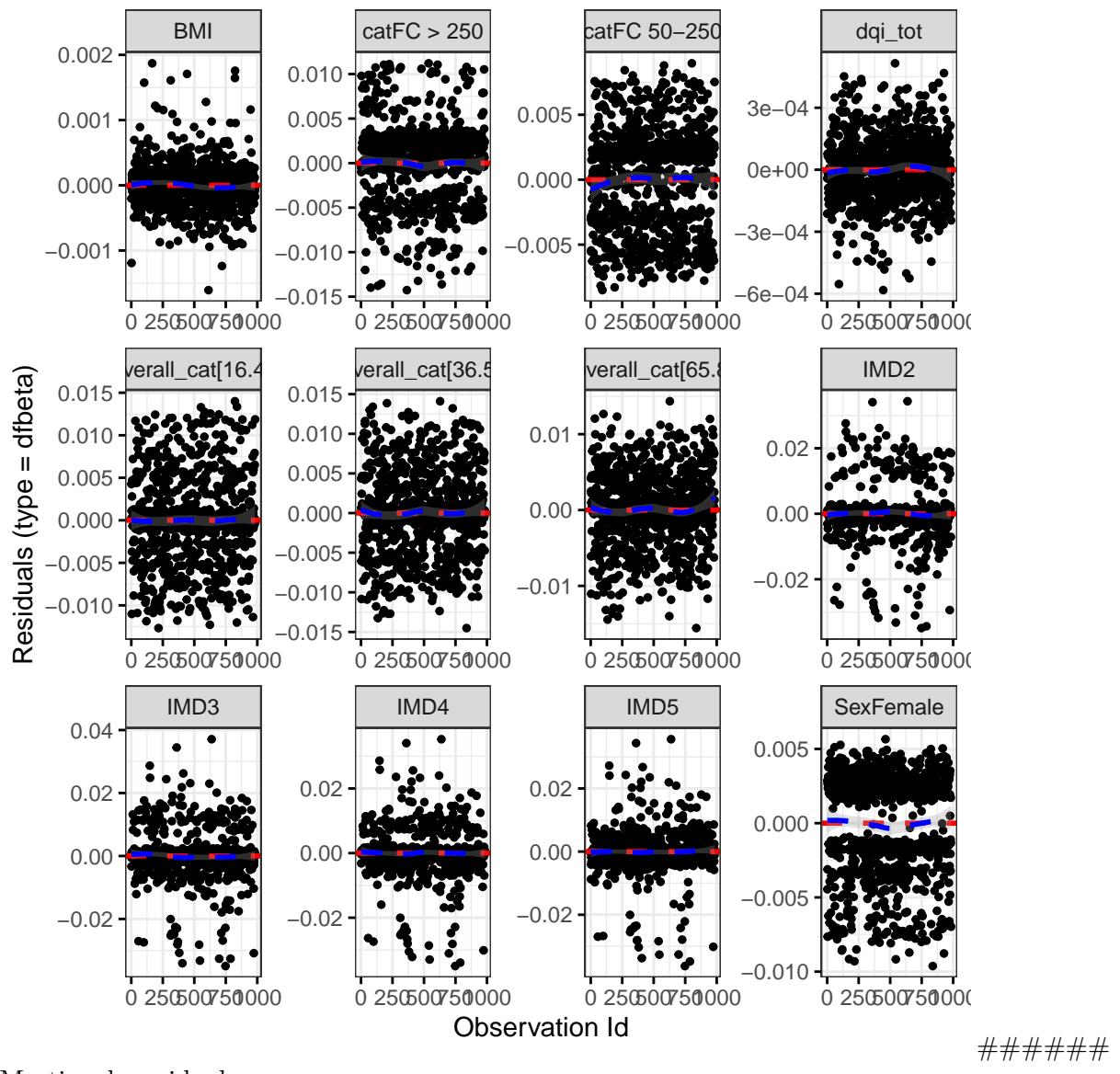
Diagnostics:

Proportional hazards assumption test

	Chi-squared statistic	DF	P-value
Sex	0.0037	1.0000	0.9515
cat	1.0850	2.0000	0.5813
IMD	5.0340	4.0000	0.2838
dqi_tot	1.3398	1.0000	0.2471
BMI	0.0088	1.0000	0.9255
fish_overall_cat	0.6613	3.0000	0.8823
GLOBAL	8.6555	12.0002	0.7321

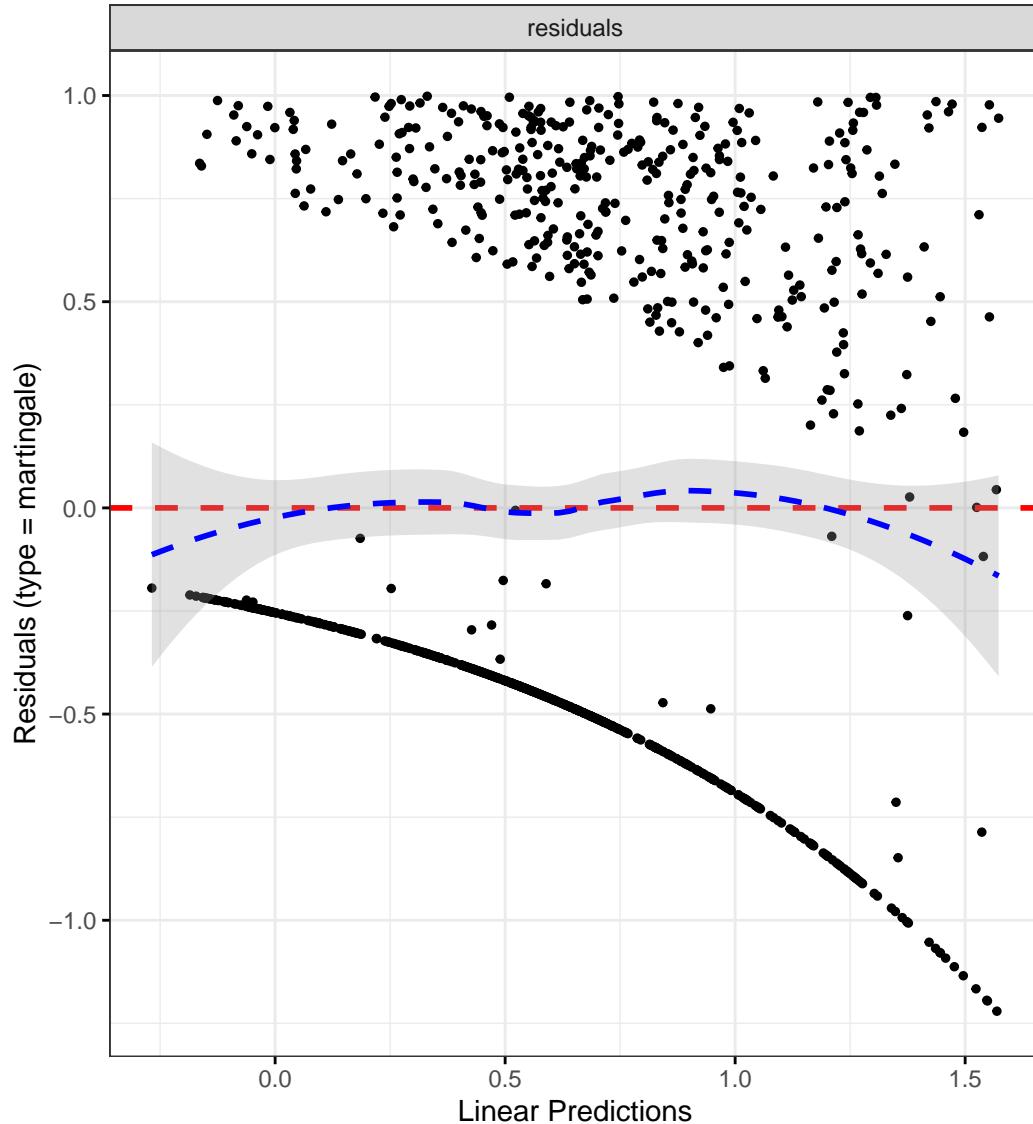
DF betas

```
`geom_smooth()` using formula = 'y ~ x'
```



Martingale residuals

```
`geom_smooth()` using formula = 'y ~ x'
```



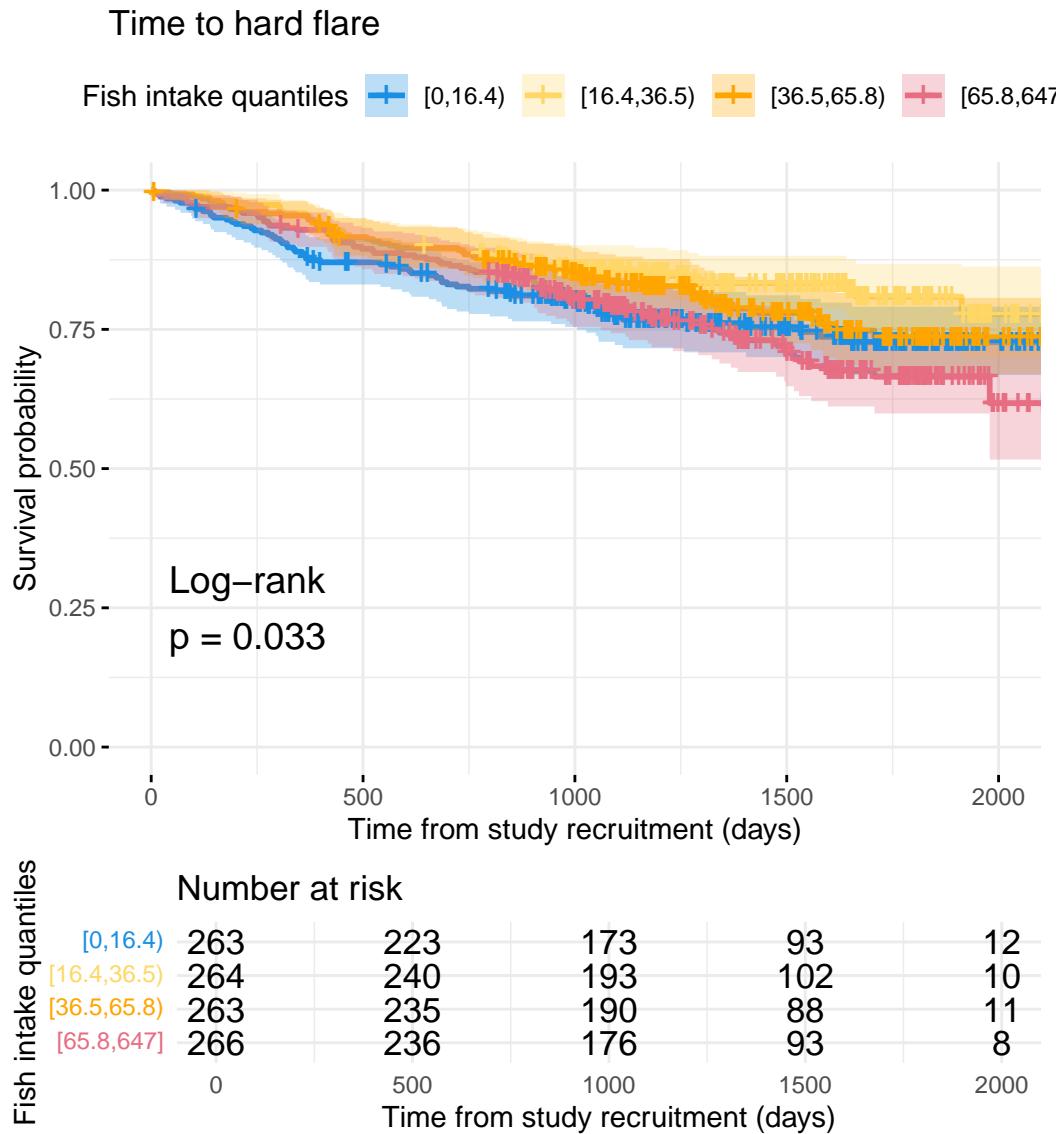
Hard flare

```
# Run survival analysis using utility function for hard flare
analysis_result <- run_survival_analysis(
  data = flare.df,
  var_name = "fish_overall",
  outcome_time = "hardflare_time",
  outcome_event = "hardflare",
  legend_title = "Fish intake quantiles",
```

```
plot_base_path = "plots/ibd/hard-flare/diet/fish_overall",
break_time_by = 500
)

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(hardflare_time, hardflare) ~
    Sex + cat + IMD + dqi_tot + BMI + fish_overall_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.df
)

# Display plot and model summary
analysis_result$plot
```



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.2361	0.9377	1.6295	0.1327
catFC 50-250	1.8663	1.3583	2.5642	0.0001
catFC > 250	2.6575	1.8774	3.7618	0.0000

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	0.9622	0.5142	1.8005	0.9040
IMD3	0.9640	0.5288	1.7574	0.9048
IMD4	1.3841	0.7874	2.4331	0.2587
IMD5	1.0097	0.5785	1.7622	0.9728
dqi_tot	1.0022	0.9894	1.0152	0.7350
BMI	0.9909	0.9645	1.0181	0.5086
fish_overall_cat[16.4,36.	0.6319	0.4235	0.9427	0.0245
fish_overall_cat[36.5,65.	0.7394	0.5040	1.0846	0.1225
fish_overall_cat[65.8,647	0.9716	0.6734	1.4018	0.8775

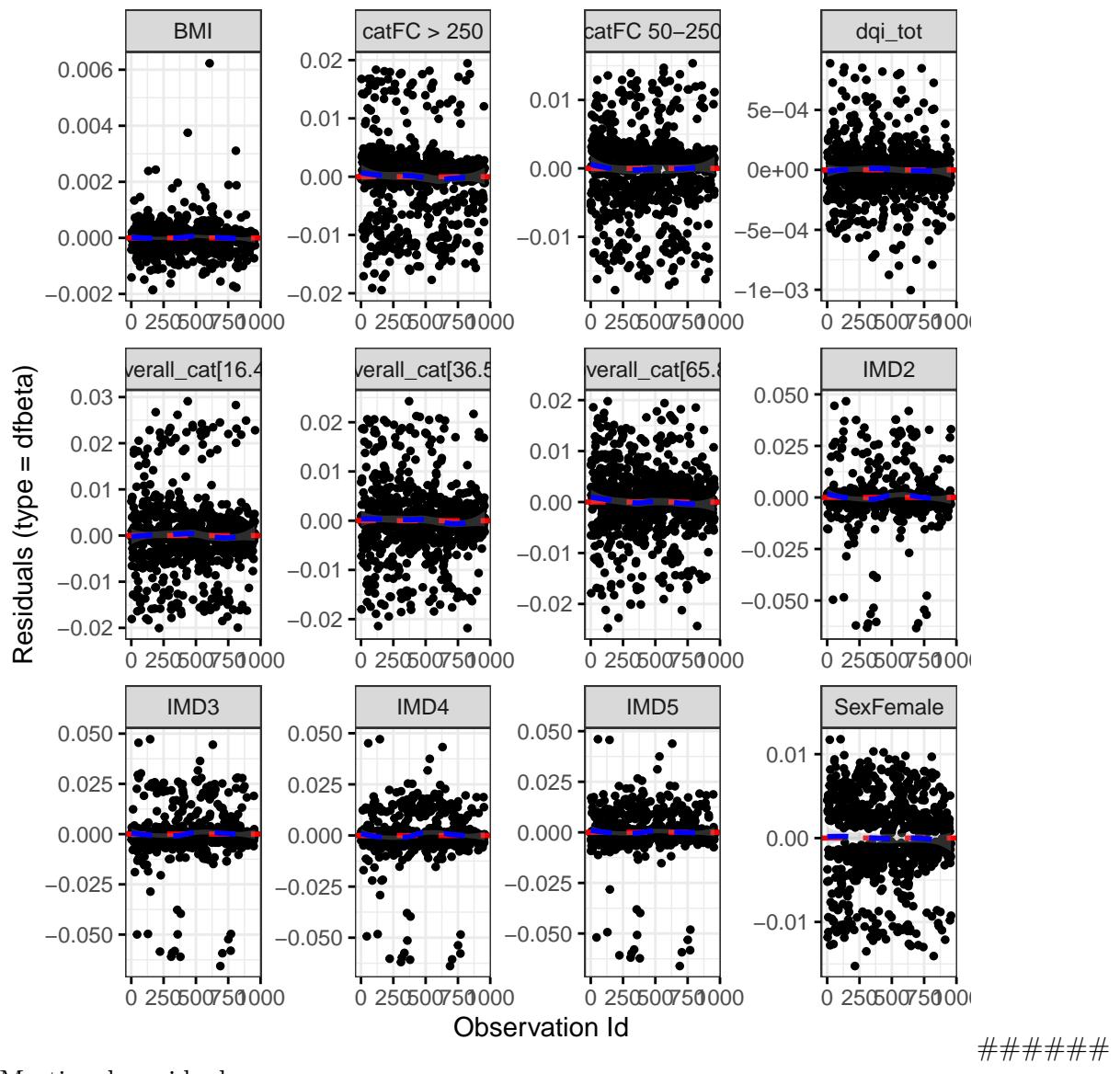
Diagnostics:

Proportional hazards assumption test

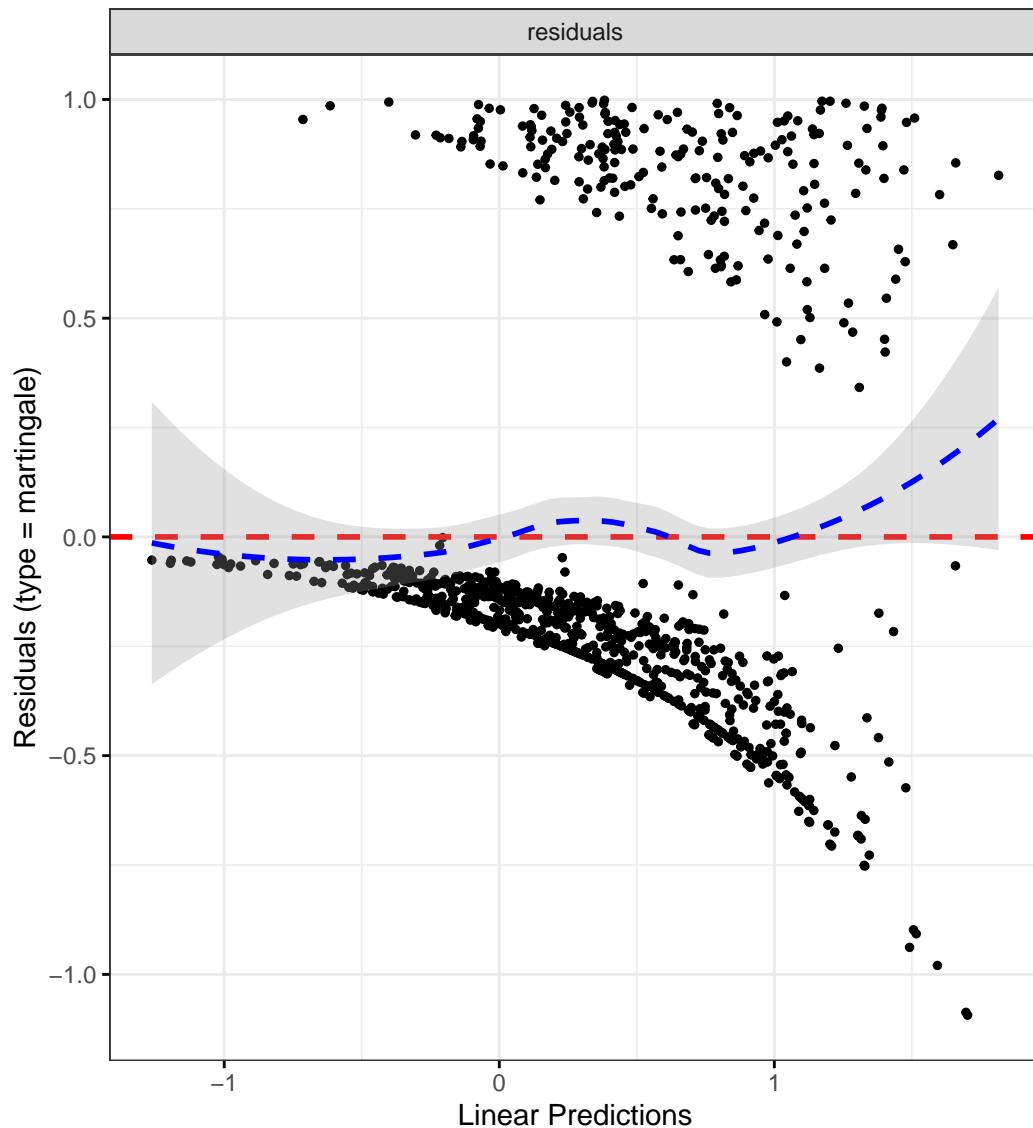
	Chi-squared statistic	DF	P-value
Sex	0.0378	0.9882	0.8422
cat	6.5833	1.9803	0.0365
IMD	1.5618	3.9428	0.8089
dqi_tot	1.8820	0.9922	0.1685
BMI	1.9590	0.9878	0.1592
fish_overall_cat	8.8737	2.9790	0.0305
GLOBAL	20.5269	22.9338	0.6061

DF betas

```
`geom_smooth()` using formula = 'y ~ x'
```



```
`geom_smooth()` using formula = 'y ~ x'
```



Dietary fibre

Crohn's disease

Patient-reported flare

```
# Categorize dietary fibre by quantiles
flare.cd.df <- categorize_by_quantiles(flare.cd.df, "fibre", reference_data = flare.df)
```

```

# Run survival analysis using utility function
analysis_result <- run_survival_analysis(
  data = flare.cd.df,
  var_name = "fibre",
  outcome_time = "softflare_time",
  outcome_event = "softflare",
  legend_title = "Fibre quantiles",
  plot_base_path = "plots/cd/soft-flare/diet/fibre",
  break_time_by = 200
)

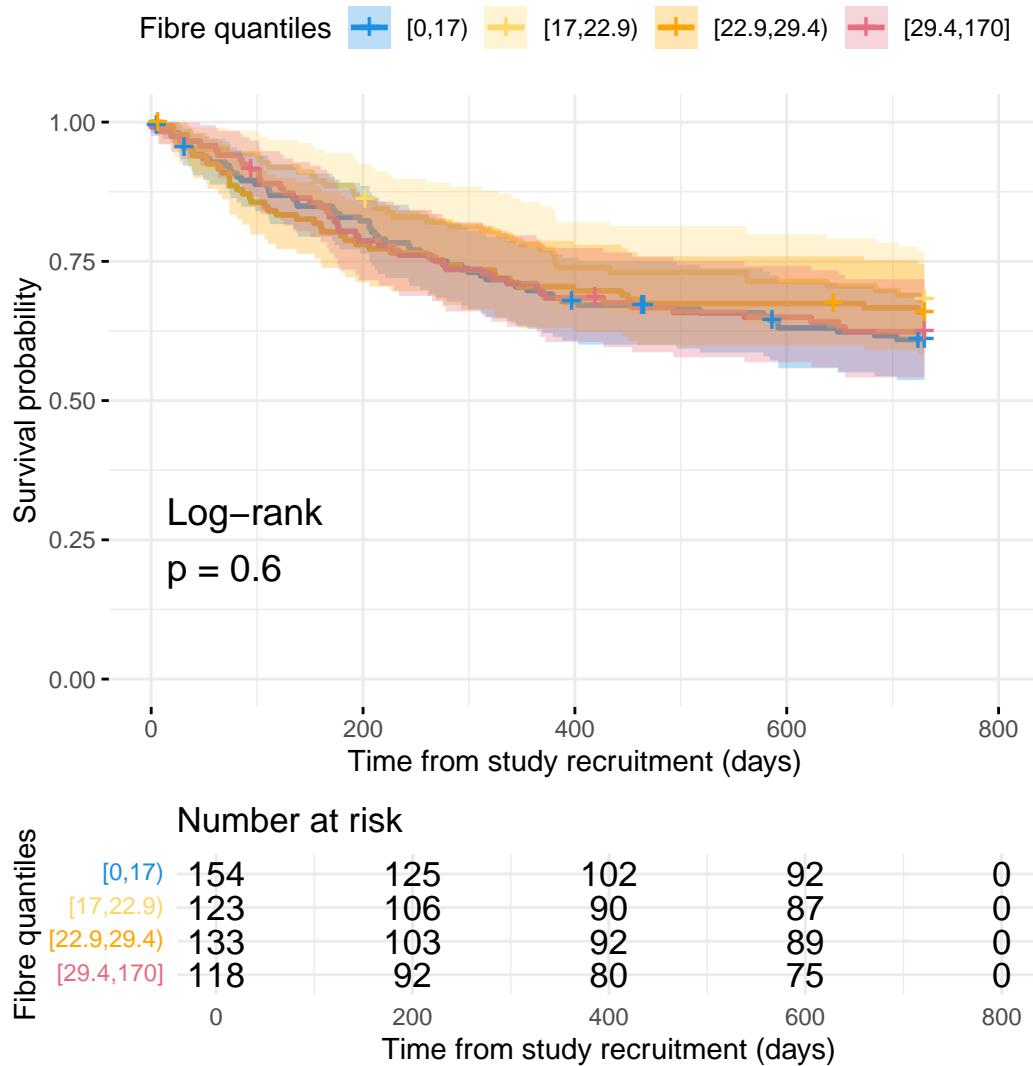
# Save plot as RDS
saveRDS(analysis_result$plot, paste0(paths$outdir, "fibre-cd-soft.RDS"))

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(softflare_time, softflare) ~
    Sex + cat + IMD + dqi_tot + BMI + fibre_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.cd.df
)

# Display plot and model summary
analysis_result$plot

```

Time to patient-reported flare



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.8864	1.3475	2.6408	0.0002
catFC 50-250	1.2975	0.9125	1.8450	0.1471
catFC > 250	2.0536	1.3992	3.0141	0.0002

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	0.6955	0.3632	1.3319	0.2733
IMD3	0.9297	0.5101	1.6947	0.8120
IMD4	0.8450	0.4668	1.5296	0.5780
IMD5	0.9776	0.5611	1.7032	0.9362
dqi_tot	1.0068	0.9912	1.0226	0.3971
BMI	1.0079	0.9804	1.0363	0.5756
fibre_cat[17,22.9)	0.7511	0.4878	1.1567	0.1939
fibre_cat[22.9,29.4)	0.8966	0.5804	1.3851	0.6228
fibre_cat[29.4,170]	0.9582	0.5984	1.5342	0.8588

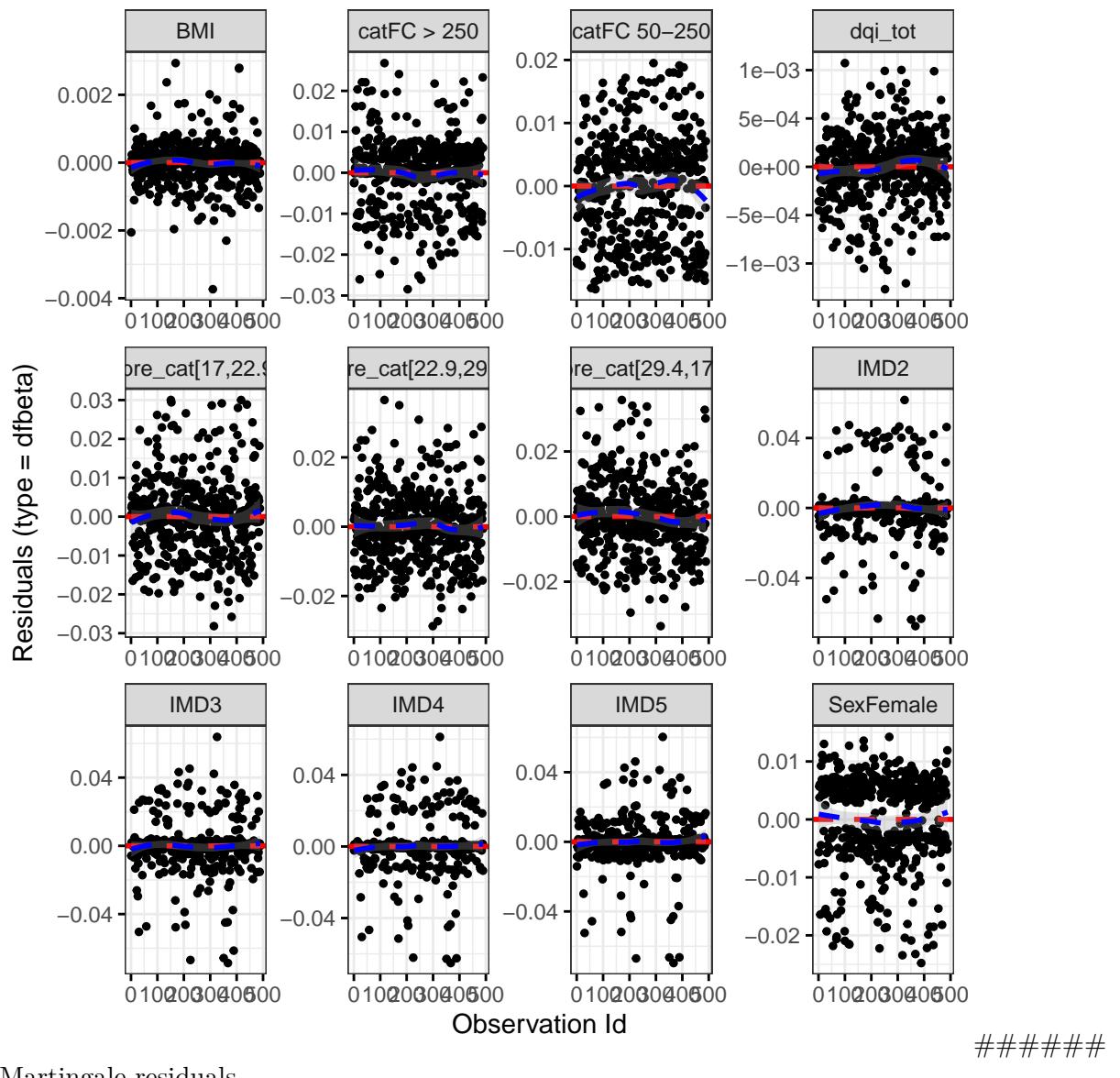
Diagnostics:

Proportional hazards assumption test

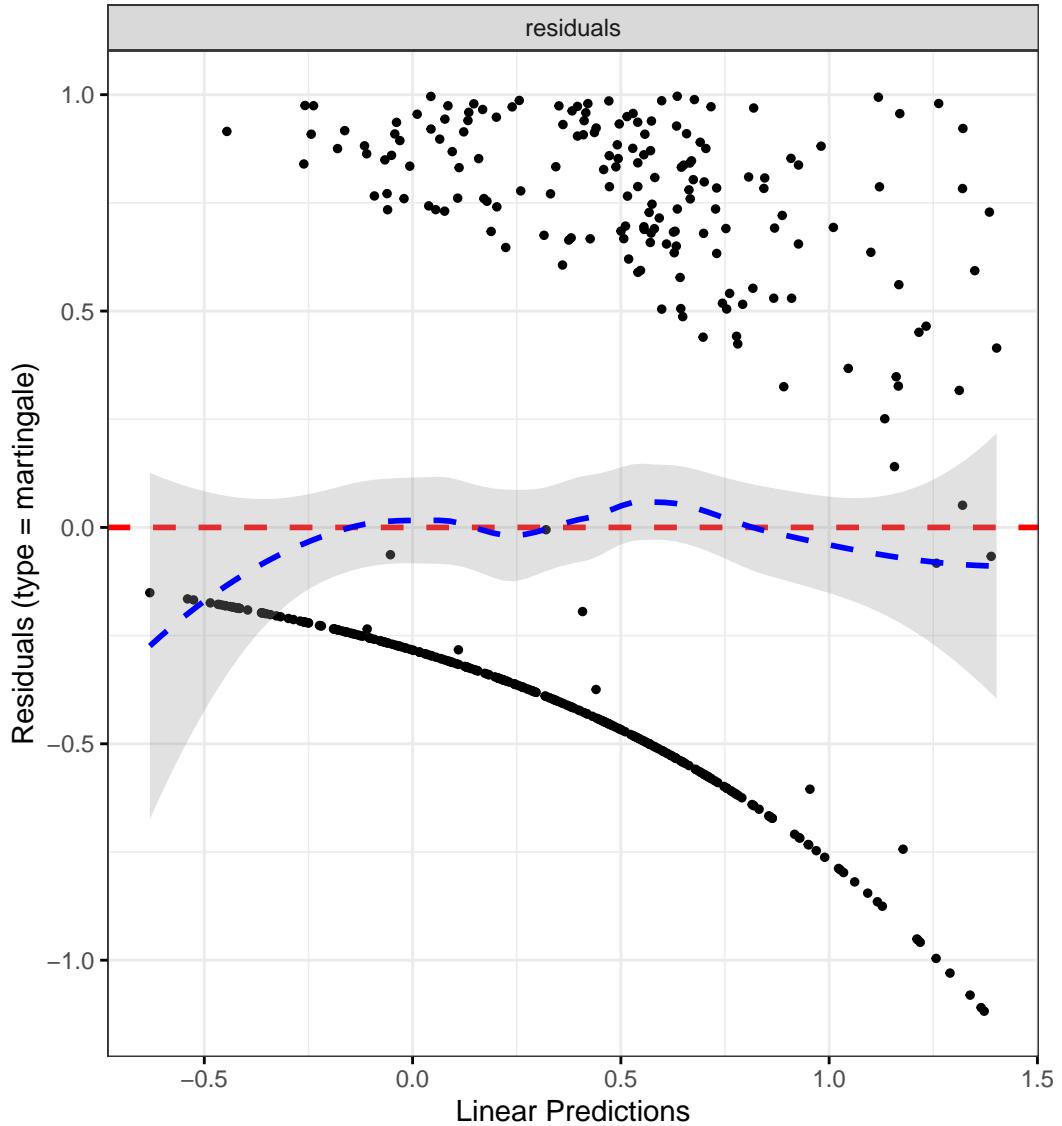
	Chi-squared statistic	DF	P-value
Sex	0.2744	1.0000	0.6004
cat	0.8152	2.0000	0.6652
IMD	3.0351	4.0000	0.5520
dqi_tot	0.3396	1.0000	0.5600
BMI	1.3198	1.0000	0.2506
fibre_cat	5.1069	3.0000	0.1641
GLOBAL	10.6138	12.0001	0.5623

DF betas

```
`geom_smooth()` using formula = 'y ~ x'
```



```
`geom_smooth()` using formula = 'y ~ x'
```



Hard flare

```
# Run survival analysis using utility function for hard flare
analysis_result <- run_survival_analysis(
  data = flare.cd.df,
  var_name = "fibre",
  outcome_time = "hardflare_time",
  outcome_event = "hardflare",
  legend_title = "Fibre quantiles",
```

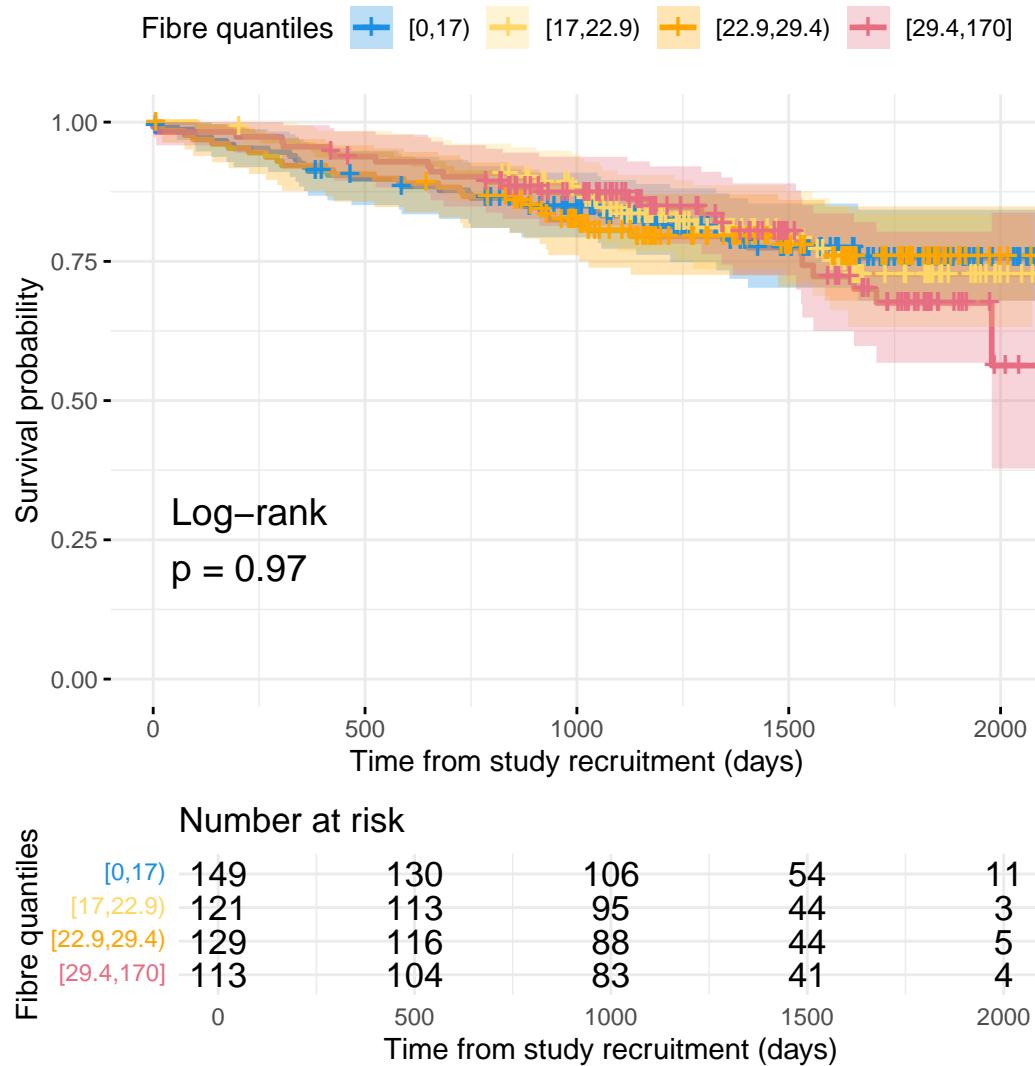
```
plot_base_path = "plots/cd/hard-flare/diet/fibre",
break_time_by = 500
)

# Save plot as RDS
saveRDS(analysis_result$plot, paste0(paths$outdir, "fibre-cd-hard.RDS"))

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(hardflare_time, hardflare) ~
    Sex + cat + IMD + dqi_tot + BMI + fibre_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.cd.df
)

# Display plot and model summary
analysis_result$plot
```

Time to hard flare



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.3807	0.9086	2.0981	0.1308
catFC 50-250	1.8701	1.1707	2.9872	0.0088
catFC > 250	3.1224	1.8748	5.2003	0.0000

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	0.6300	0.2709	1.4651	0.2833
IMD3	0.8054	0.3634	1.7849	0.5940
IMD4	0.7541	0.3466	1.6404	0.4766
IMD5	0.7123	0.3415	1.4858	0.3657
dqi_tot	0.9978	0.9779	1.0182	0.8345
BMI	1.0165	0.9811	1.0533	0.3648
fibre_cat[17,22.9)	1.0252	0.5798	1.8128	0.9319
fibre_cat[22.9,29.4)	1.4448	0.8175	2.5534	0.2053
fibre_cat[29.4,170]	1.3901	0.7530	2.5660	0.2923

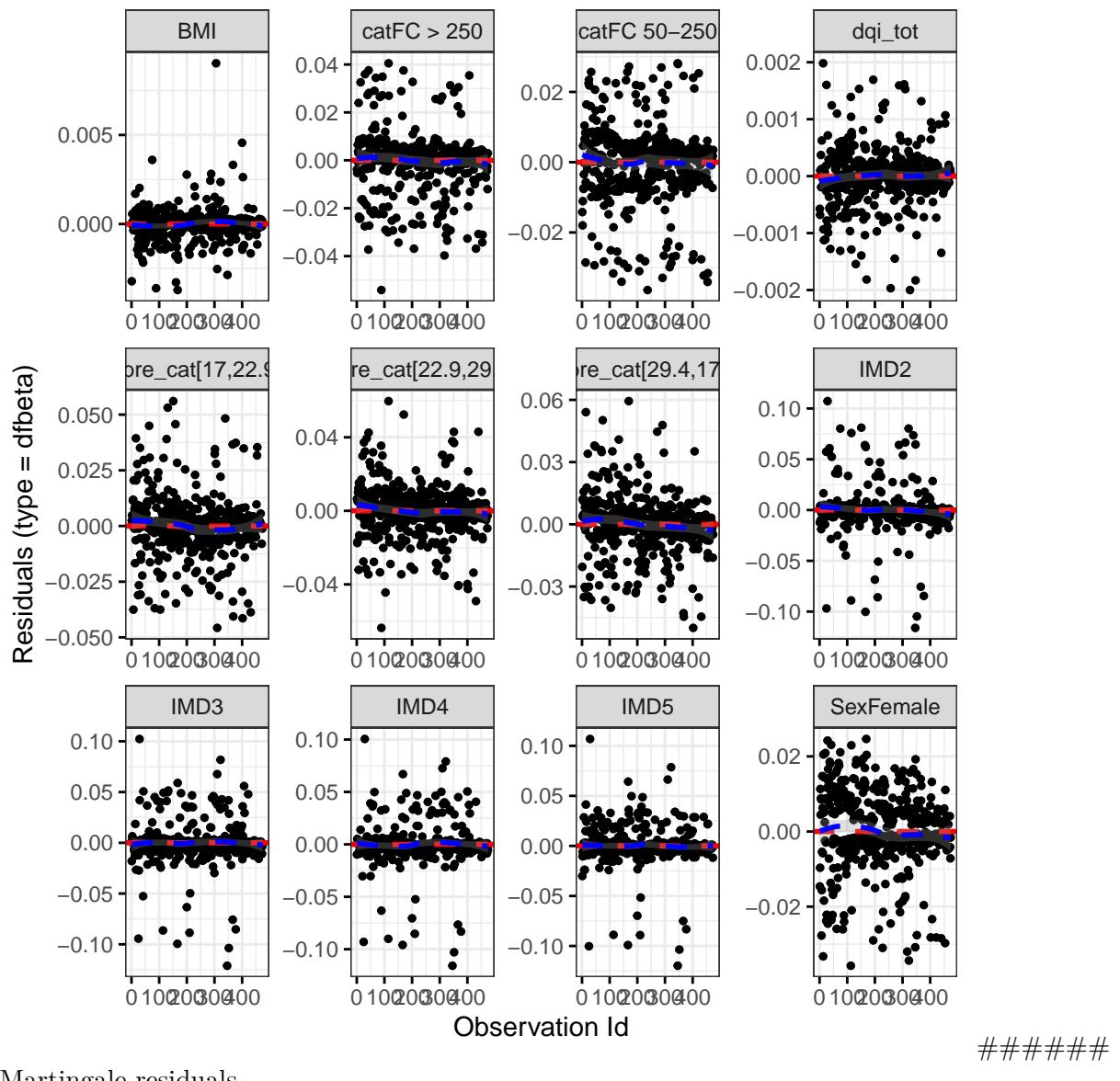
Diagnostics:

Proportional hazards assumption test

	Chi-squared statistic	DF	P-value
Sex	0.0861	0.9701	0.7579
cat	10.1182	1.9787	0.0062
IMD	2.6037	3.9266	0.6148
dqi_tot	2.7993	0.9906	0.0931
BMI	1.1389	0.9815	0.2803
fibre_cat	9.7004	2.9616	0.0206
GLOBAL	22.6456	18.6611	0.2362

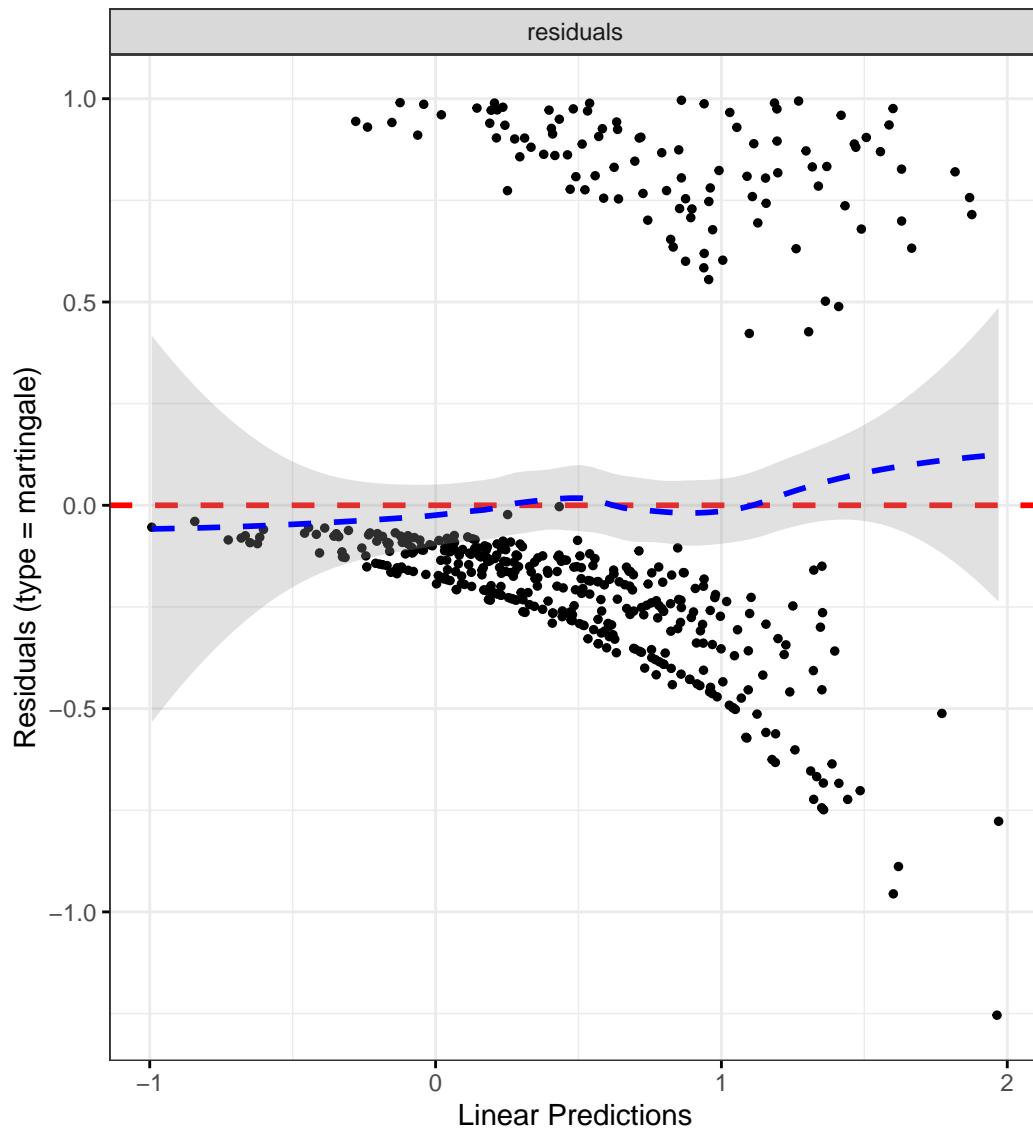
DF betas

```
`geom_smooth()` using formula = 'y ~ x'
```



Martingale residuals

```
`geom_smooth()` using formula = 'y ~ x'
```



Ulcerative colitis

Patient-reported flare

```
# Categorize fibre by quantiles
flare.uc.df <- categorize_by_quantiles(flare.uc.df, "fibre", reference_data = flare.df)

# Run survival analysis using utility function
analysis_result <- run_survival_analysis()
```

```

data = flare.uc.df,
var_name = "fibre",
outcome_time = "softflare_time",
outcome_event = "softflare",
legend_title = "Fibre quantiles",
plot_base_path = "plots/uc/soft-flare/diet/fibre",
break_time_by = 200
)

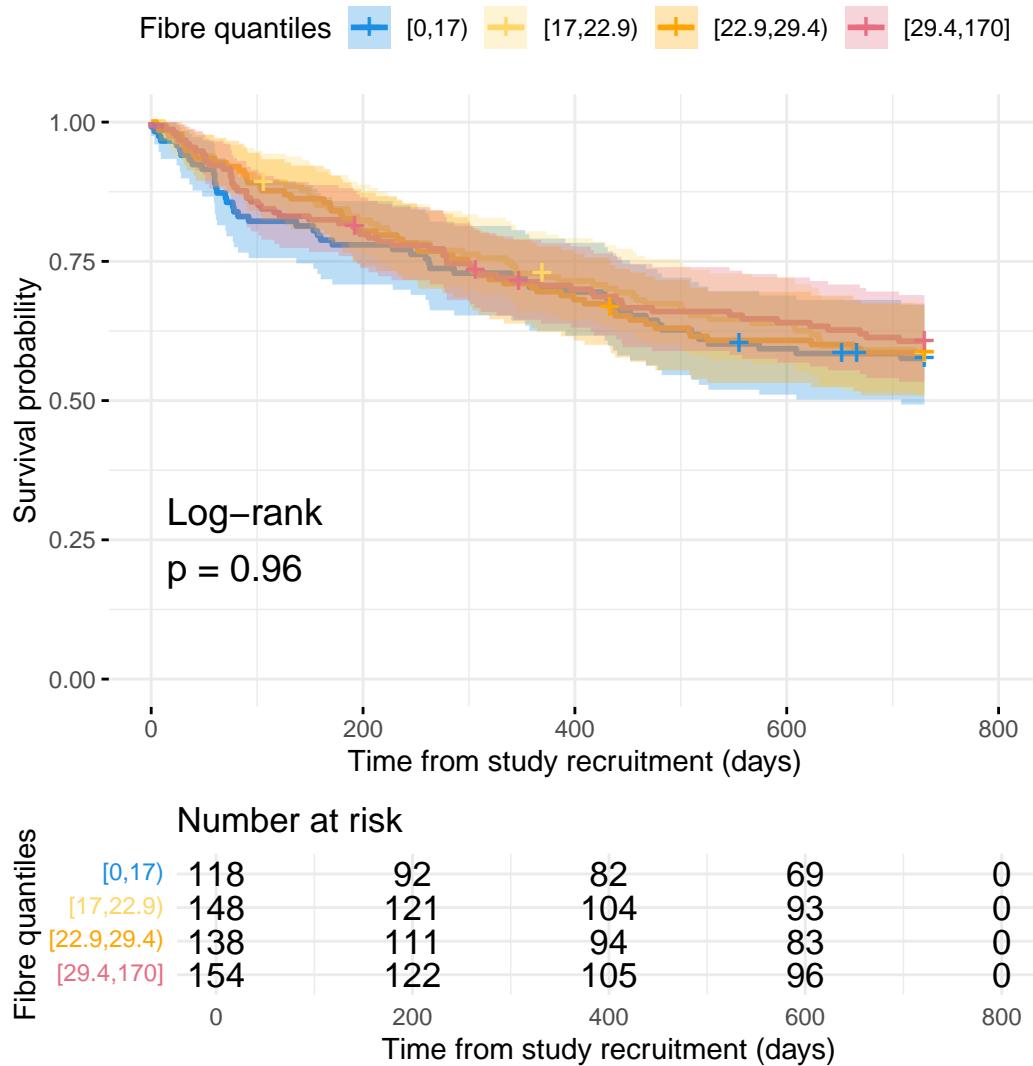
# Save plot as RDS
saveRDS(analysis_result$plot, paste0(paths$outdir, "fibre-uc-soft.RDS"))

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(softflare_time, softflare) ~
    Sex + cat + IMD + dqi_tot + BMI + fibre_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.uc.df
)

# Display plot and model summary
analysis_result$plot

```

Time to patient-reported flare



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.6926	1.2636	2.2672	0.0004
catFC 50-250	1.7837	1.2980	2.4513	0.0004
catFC > 250	2.1170	1.4803	3.0274	0.0000

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	1.3861	0.7239	2.6542	0.3246
IMD3	1.1466	0.6076	2.1636	0.6728
IMD4	1.3385	0.7390	2.4243	0.3361
IMD5	1.1956	0.6643	2.1520	0.5512
dqi_tot	1.0010	0.9871	1.0151	0.8880
BMI	0.9759	0.9471	1.0056	0.1111
fibre_cat[17,22.9)	0.8763	0.5895	1.3026	0.5138
fibre_cat[22.9,29.4)	0.9668	0.6292	1.4855	0.8776
fibre_cat[29.4,170]	0.8254	0.5346	1.2744	0.3866

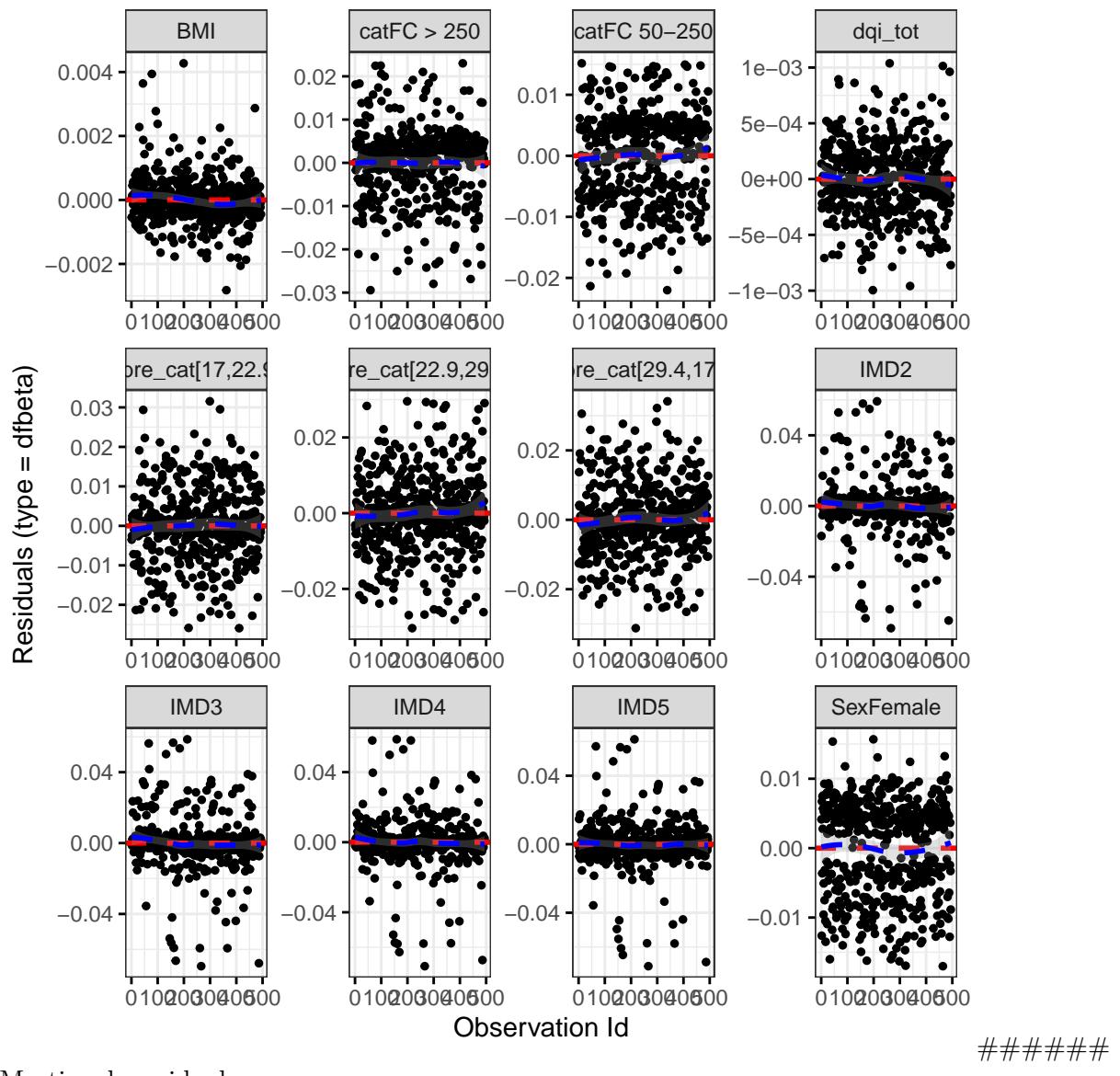
Diagnostics:

Proportional hazards assumption test

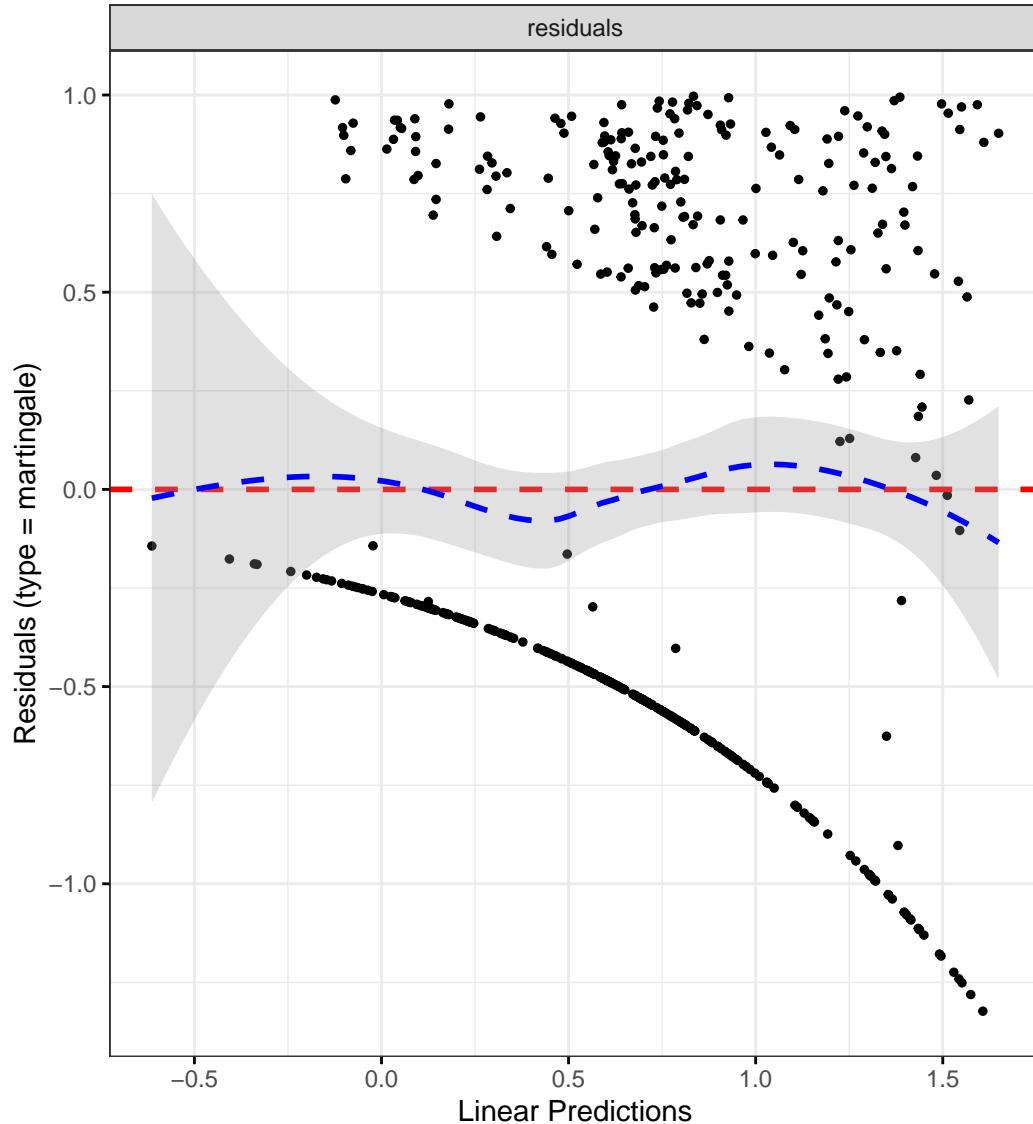
	Chi-squared statistic	DF	P-value
Sex	0.0057	1.0000	0.9400
cat	3.5363	2.0000	0.1706
IMD	2.6179	4.0000	0.6236
dqi_tot	0.7523	1.0000	0.3858
BMI	0.9507	1.0000	0.3295
fibre_cat	1.0506	3.0000	0.7890
GLOBAL	9.0611	12.0001	0.6977

DF betas

```
`geom_smooth()` using formula = 'y ~ x'
```



```
`geom_smooth()` using formula = 'y ~ x'
```



Hard flare

```
# Run survival analysis using utility function for hard flare
analysis_result <- run_survival_analysis(
  data = flare.uc.df,
  var_name = "fibre",
  outcome_time = "hardflare_time",
  outcome_event = "hardflare",
  legend_title = "Fibre quantiles",
```

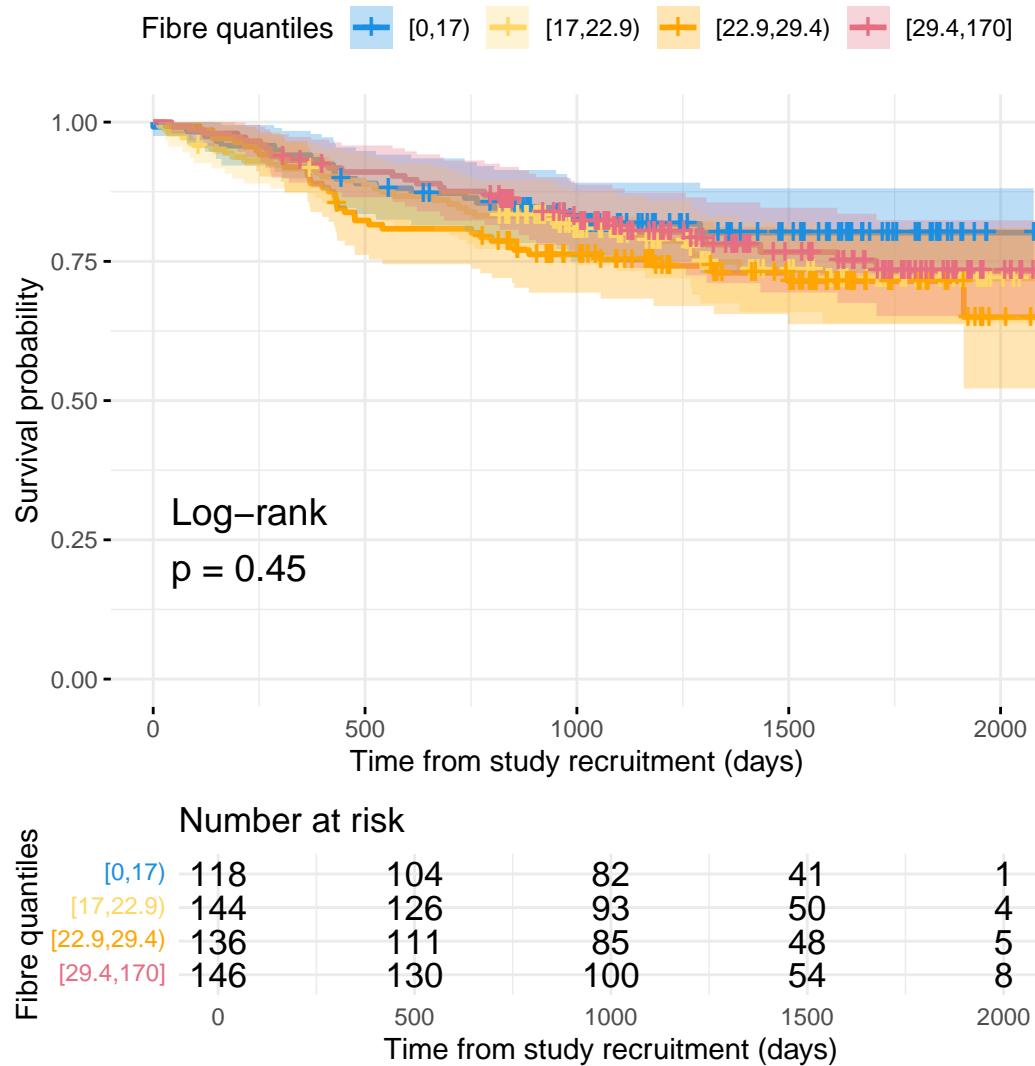
```
plot_base_path = "plots/uc/hard-flare/diet/fibre",
break_time_by = 500
)

# Save plot as RDS
saveRDS(analysis_result$plot, paste0(paths$outdir, "fibre-uc-hard.RDS"))

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(hardflare_time, hardflare) ~
    Sex + cat + IMD + dqi_tot + BMI + fibre_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.uc.df
)

# Display plot and model summary
analysis_result$plot
```

Time to hard flare



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.2319	0.8386	1.8095	0.2879
catFC 50-250	2.0087	1.3018	3.0992	0.0016
catFC > 250	2.4709	1.5197	4.0173	0.0003

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	1.7192	0.6445	4.5859	0.2790
IMD3	1.3779	0.5312	3.5743	0.5099
IMD4	2.4505	1.0190	5.8931	0.0453
IMD5	1.4399	0.5943	3.4885	0.4194
dqi_tot	0.9996	0.9808	1.0188	0.9682
BMI	0.9644	0.9247	1.0057	0.0900
fibre_cat[17,22.9)	1.2507	0.7094	2.2052	0.4394
fibre_cat[22.9,29.4)	1.4394	0.7917	2.6169	0.2324
fibre_cat[29.4,170]	1.1698	0.6416	2.1328	0.6088

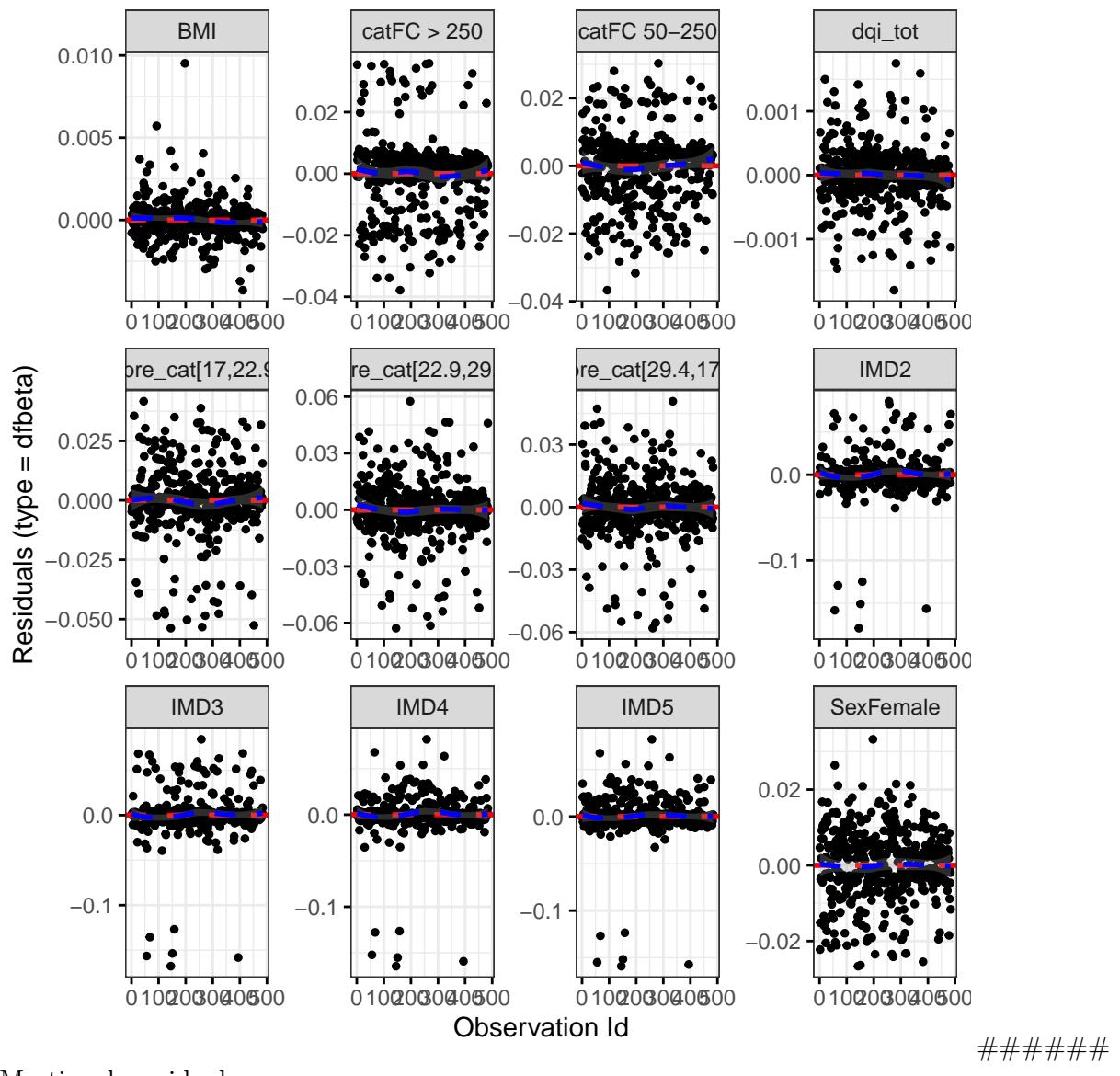
Diagnostics:

Proportional hazards assumption test

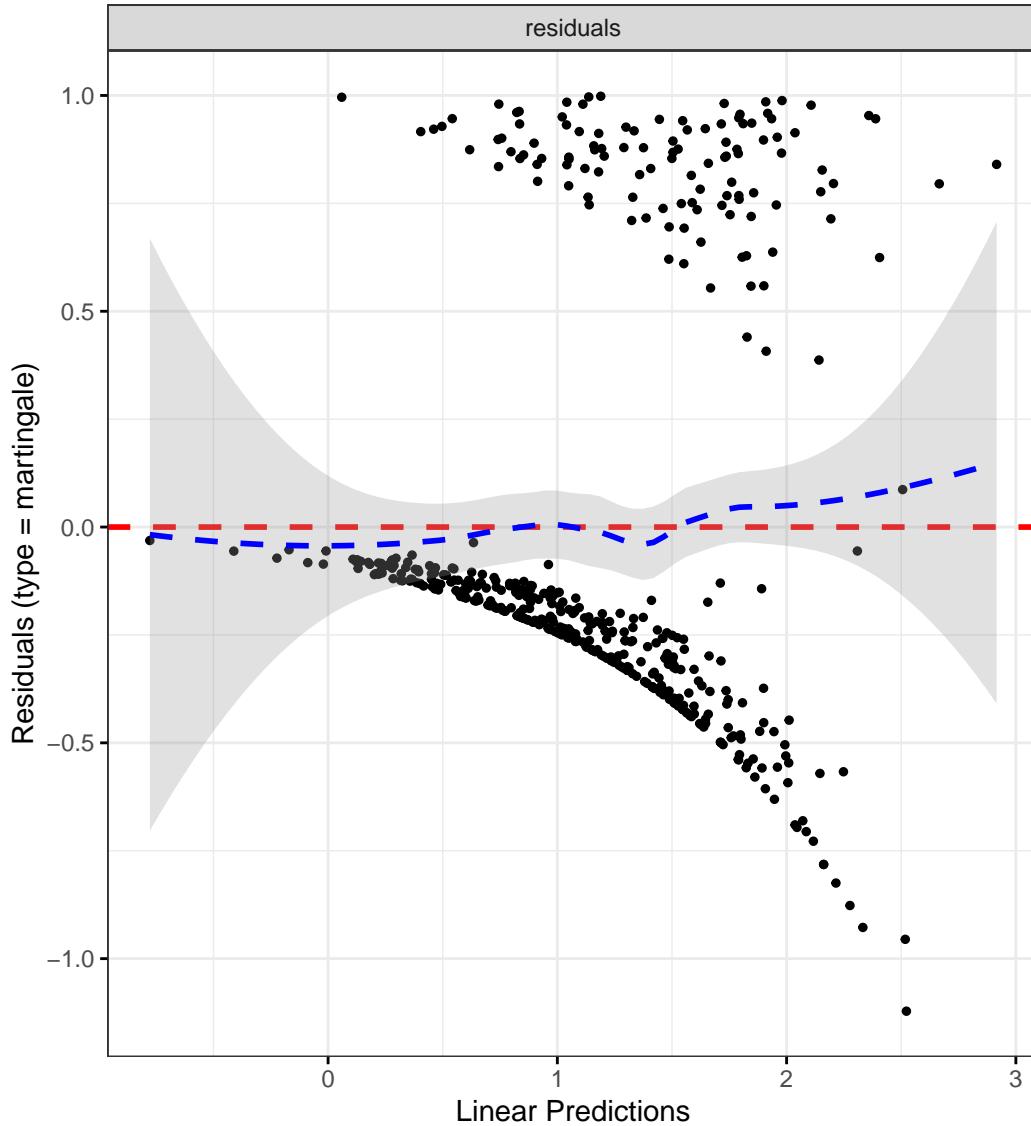
	Chi-squared statistic	DF	P-value
Sex	0.0292	0.9895	0.8613
cat	5.5323	1.9568	0.0604
IMD	1.1150	3.9308	0.8859
dqi_tot	0.0010	0.9893	0.9731
BMI	0.5841	0.9886	0.4403
fibre_cat	4.7052	2.9522	0.1893
GLOBAL	12.4623	19.3462	0.8777

DF betas

```
`geom_smooth()` using formula = 'y ~ x'
```



```
`geom_smooth()` using formula = 'y ~ x'
```



Inflammatory bowel disease

Patient-reported flare

```
# Categorize dietary fibre by quantiles
flare.df <- categorize_by_quantiles(flare.df, "fibre", reference_data = flare.df)

# Run survival analysis using utility function
analysis_result <- run_survival_analysis()
```

```

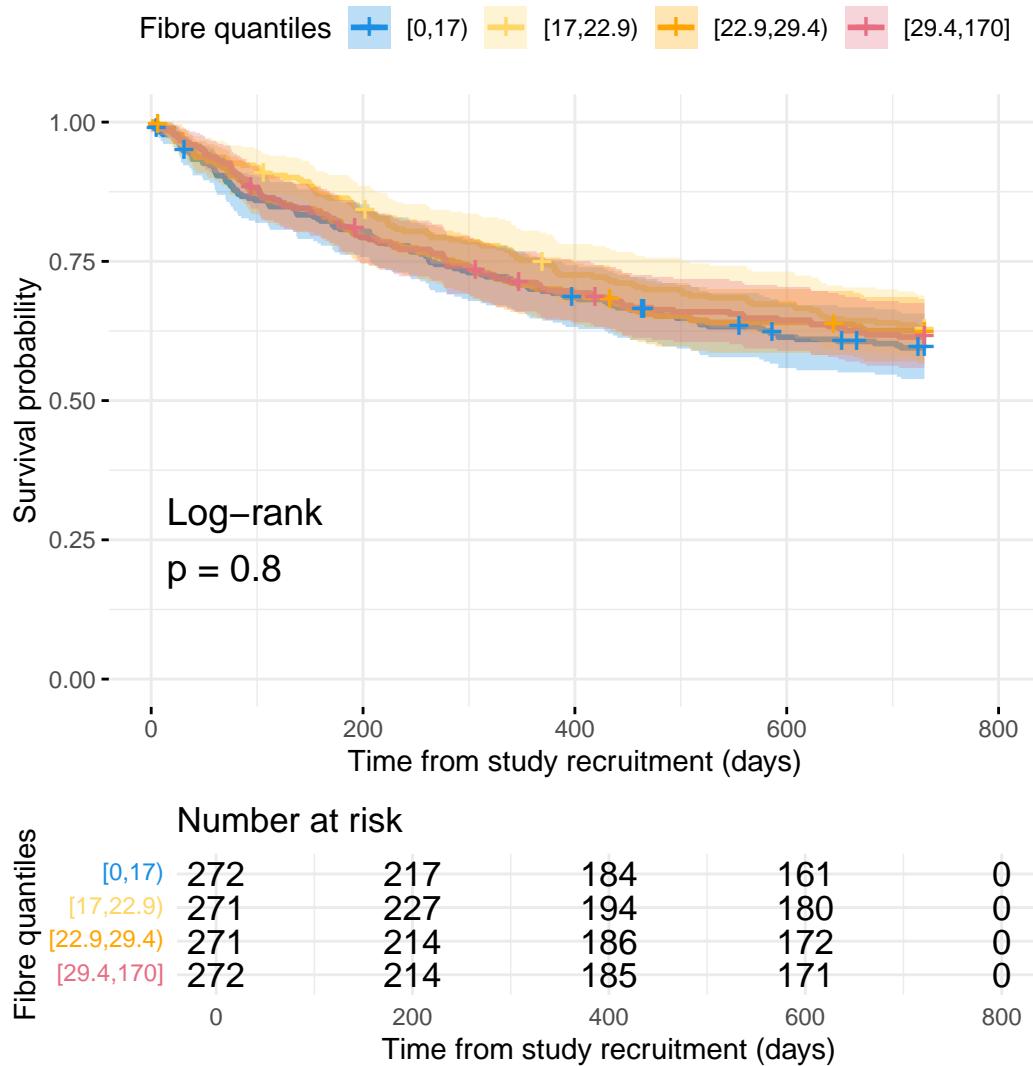
data = flare.df,
var_name = "fibre",
outcome_time = "softflare_time",
outcome_event = "softflare",
legend_title = "Fibre quantiles",
plot_base_path = "plots/ibd/soft-flare/diet/fibre",
break_time_by = 200
)

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(softflare_time, softflare) ~
    Sex + cat + IMD + dqi_tot + BMI + fibre_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.df
)

# Display plot and model summary
analysis_result$plot

```

Time to patient-reported flare



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.7669	1.4224	2.1947	0.0000
catFC 50-250	1.4980	1.1859	1.8921	0.0007
catFC > 250	2.0311	1.5676	2.6318	0.0000

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	0.9612	0.6100	1.5147	0.8645
IMD3	0.9914	0.6418	1.5315	0.9690
IMD4	1.0909	0.7201	1.6527	0.6815
IMD5	1.0688	0.7154	1.5967	0.7454
dqi_tot	1.0037	0.9935	1.0141	0.4747
BMI	0.9941	0.9744	1.0142	0.5609
fibre_cat[17,22.9)	0.8419	0.6320	1.1214	0.2393
fibre_cat[22.9,29.4)	0.9420	0.6978	1.2717	0.6964
fibre_cat[29.4,170]	0.8956	0.6554	1.2238	0.4888

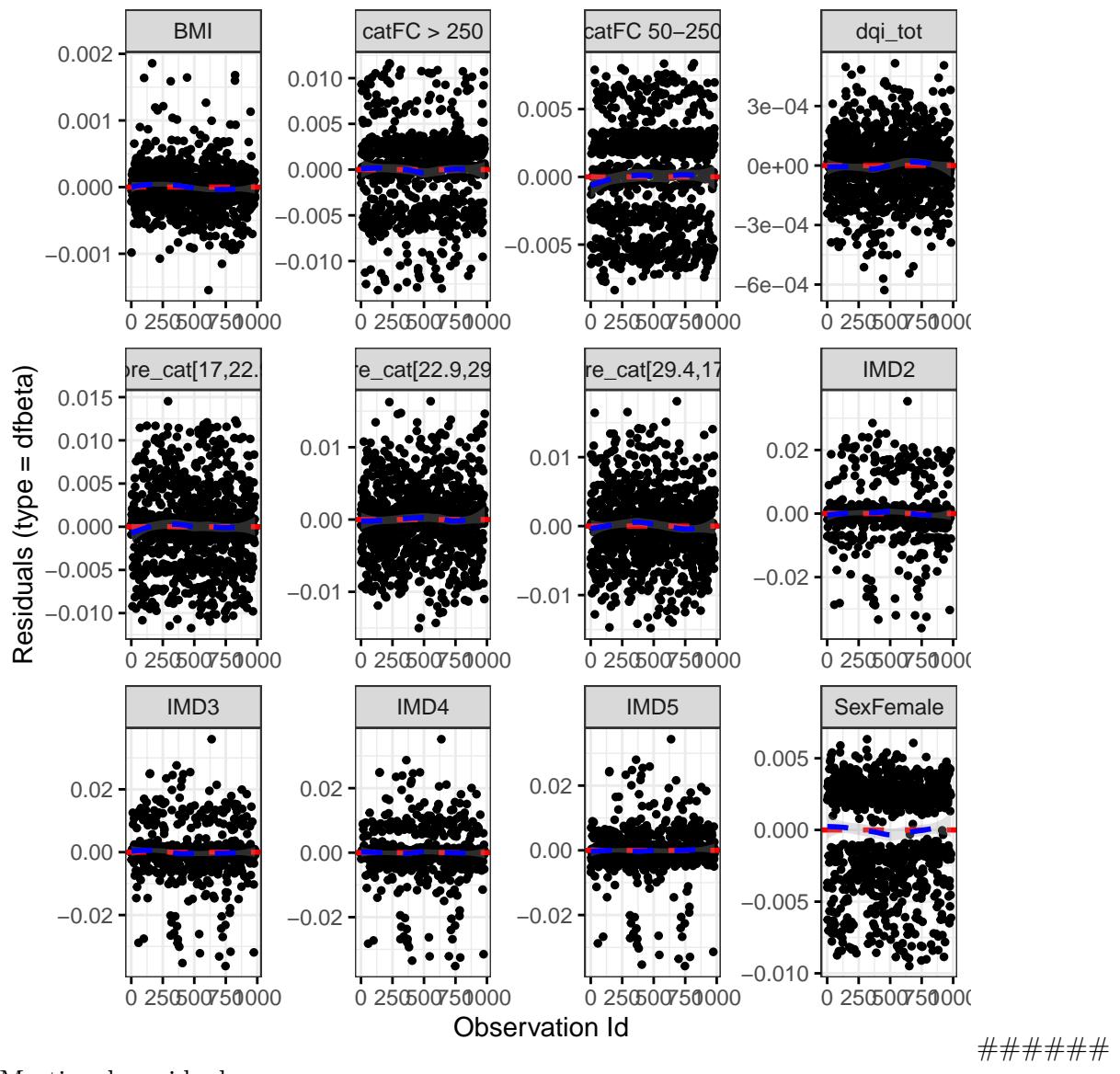
Diagnostics:

Proportional hazards assumption test

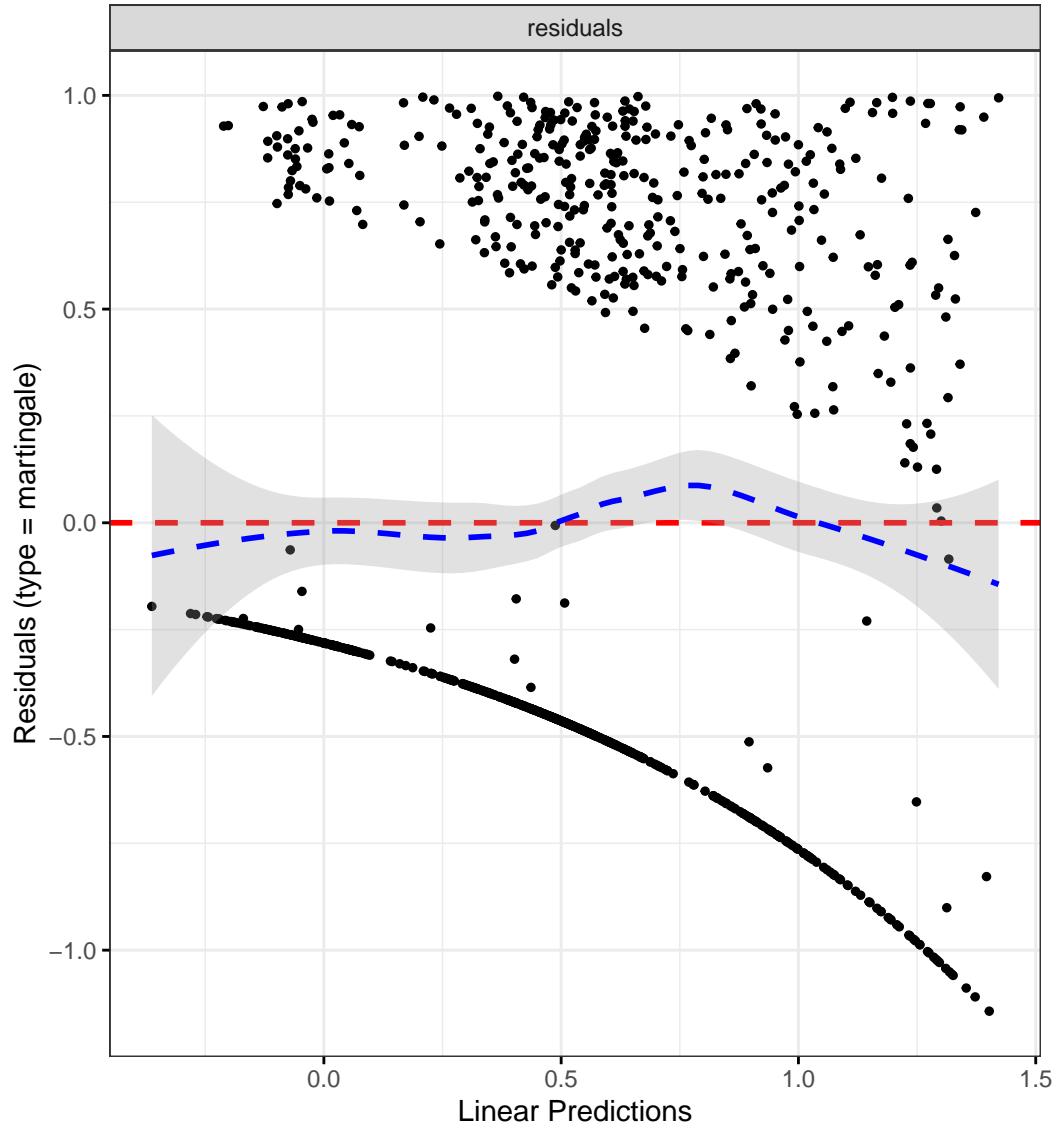
	Chi-squared statistic	DF	P-value
Sex	0.0038	1.0000	0.9511
cat	1.0906	2.0000	0.5797
IMD	5.0884	4.0000	0.2783
dqi_tot	1.3417	1.0000	0.2467
BMI	0.0088	1.0000	0.9251
fibre_cat	3.6398	3.0000	0.3031
GLOBAL	11.6255	12.0002	0.4762

DF betas

```
`geom_smooth()` using formula = 'y ~ x'
```



```
`geom_smooth()` using formula = 'y ~ x'
```



Hard flare

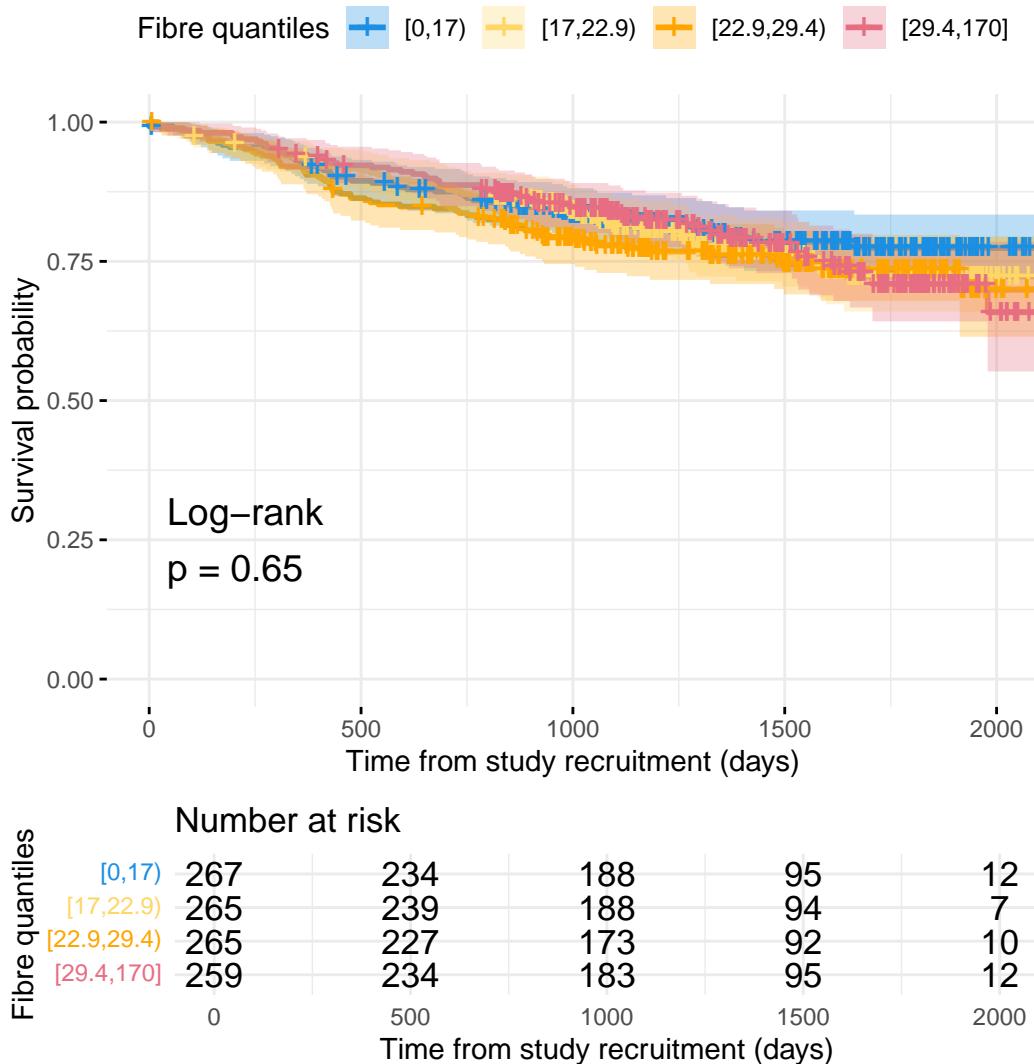
```
# Run survival analysis using utility function for hard flare
analysis_result <- run_survival_analysis(
  data = flare.df,
  var_name = "fibre",
  outcome_time = "hardflare_time",
  outcome_event = "hardflare",
  legend_title = "Fibre quantiles",
```

```
plot_base_path = "plots/ibd/hard-flare/diet/fibre",
break_time_by = 500
)

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(hardflare_time, hardflare) ~
    Sex + cat + IMD + dqi_tot + BMI + fibre_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.df
)

# Display plot and model summary
analysis_result$plot
```

Time to hard flare



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.2919	0.9786	1.7056	0.0707
catFC 50-250	1.8669	1.3629	2.5572	0.0001
catFC > 250	2.6881	1.8992	3.8048	0.0000

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	0.9718	0.5183	1.8219	0.9289
IMD3	0.9699	0.5321	1.7679	0.9206
IMD4	1.3801	0.7858	2.4238	0.2623
IMD5	0.9849	0.5646	1.7182	0.9573
dqi_tot	0.9985	0.9851	1.0122	0.8328
BMI	0.9923	0.9659	1.0194	0.5742
fibre_cat[17,22.9)	1.1513	0.7780	1.7040	0.4811
fibre_cat[22.9,29.4)	1.4022	0.9376	2.0971	0.0997
fibre_cat[29.4,170]	1.2760	0.8406	1.9370	0.2523

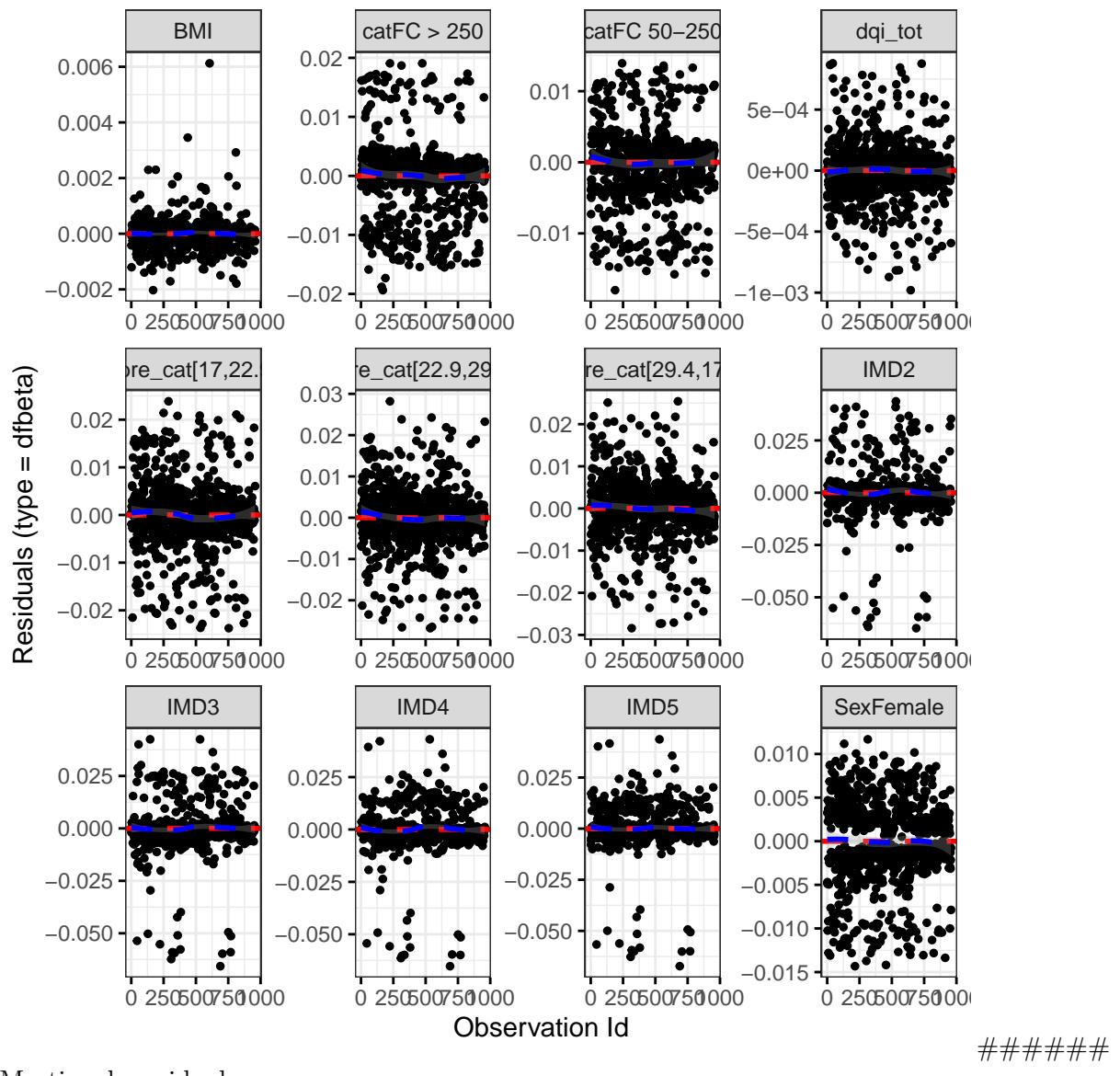
Diagnostics:

Proportional hazards assumption test

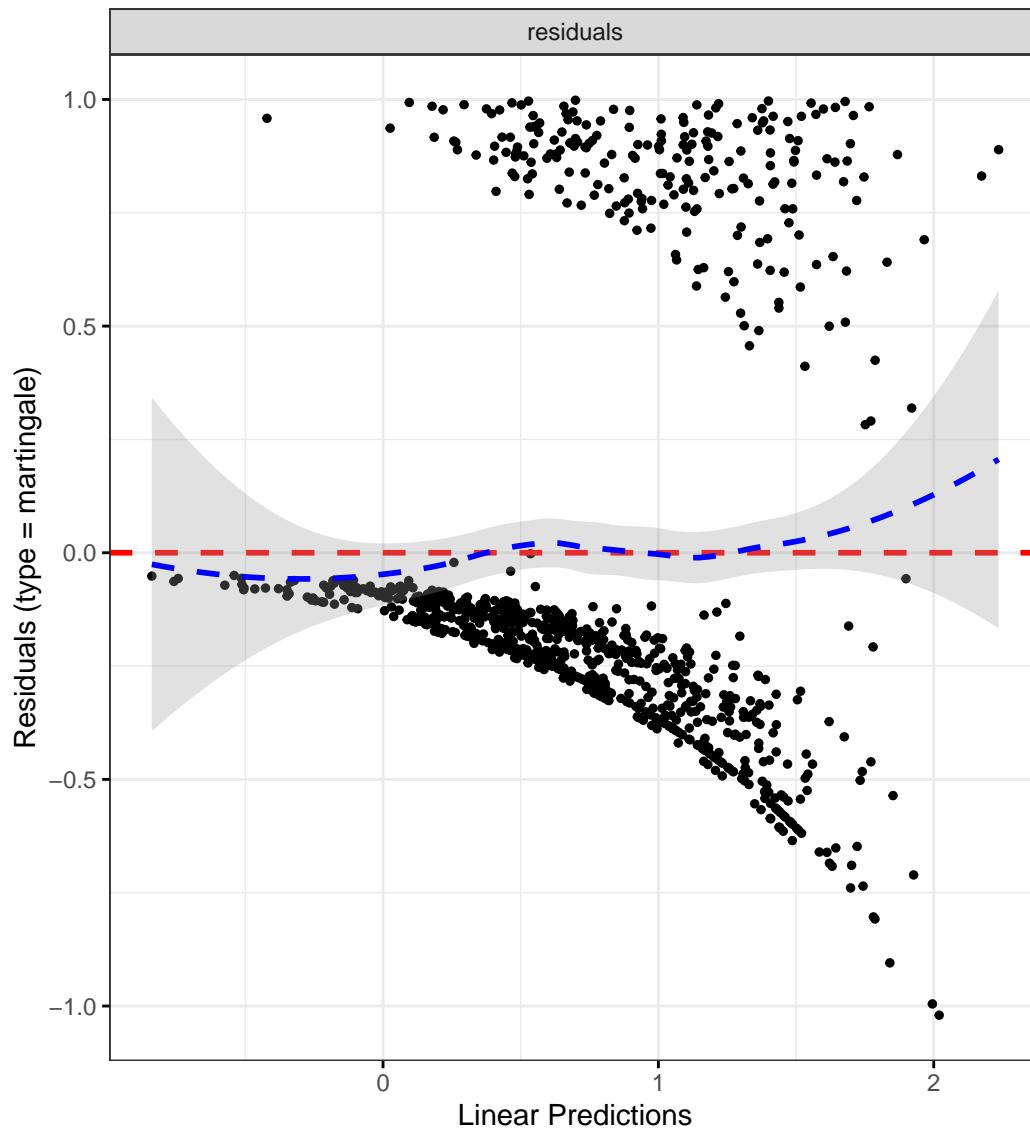
	Chi-squared statistic	DF	P-value
Sex	0.0422	0.9882	0.8334
cat	6.5765	1.9786	0.0365
IMD	1.6603	3.9441	0.7910
dqi_tot	2.0448	0.9939	0.1516
BMI	1.9420	0.9890	0.1612
fibre_cat	11.5963	2.9788	0.0087
GLOBAL	22.1617	22.8286	0.5002

DF betas

```
`geom_smooth()` using formula = 'y ~ x'
```



```
`geom_smooth()` using formula = 'y ~ x'
```



Polyunsaturated fatty acids

The SAP states n-6 PUFAs will be investigated. However, the FFQ data extract lists PUFA collectively, presumably describing both n-3 and n-6 PUFAs. For now, these data will be used.

Crohn's disease

Patient-reported flare

```
# Categorize PUFA by quantiles
flare.cd.df <- categorize_by_quantiles(flare.cd.df, "PUFA_percEng", reference_data = flare.d

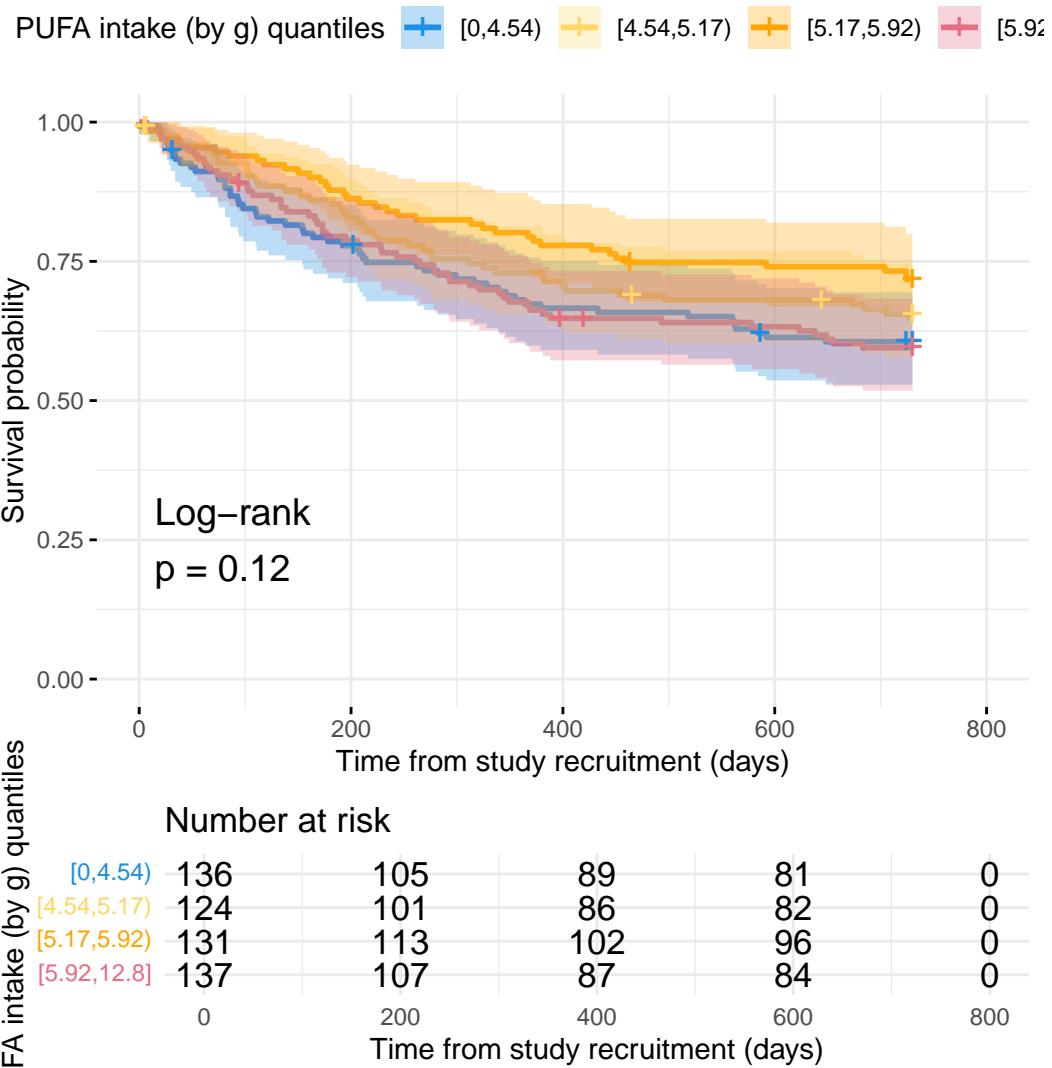
# Run survival analysis using utility function
analysis_result <- run_survival_analysis(
  data = flare.cd.df,
  var_name = "PUFA_percEng",
  outcome_time = "softflare_time",
  outcome_event = "softflare",
  legend_title = "PUFA intake (by g) quantiles",
  plot_base_path = "plots/cd/soft-flare/diet/pufa",
  break_time_by = 200
)

# Save plot as RDS
saveRDS(analysis_result$plot, paste0(paths$outdir, "pufa-cd-soft.RDS"))

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(softflare_time, softflare) ~
    Sex + cat + IMD + PUFA_percEng_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.cd.df
)

# Display plot and model summary
analysis_result$plot
```

Time to patient-reported flare



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.9094	1.3738	2.6539	0.0001
catFC 50-250	1.2909	0.9127	1.8257	0.1489
catFC > 250	1.9690	1.3482	2.8756	0.0005

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	0.7145	0.3783	1.3493	0.3000
IMD3	0.8979	0.4955	1.6269	0.7224
IMD4	0.8463	0.4671	1.5331	0.5819
IMD5	0.9825	0.5652	1.7079	0.9502
PUFA_percEng_cat[4.54,5.1]	0.7530	0.4955	1.1443	0.1839
PUFA_percEng_cat[5.17,5.9]	0.6531	0.4246	1.0045	0.0525
PUFA_percEng_cat[5.92,12.]	0.9356	0.6336	1.3814	0.7378

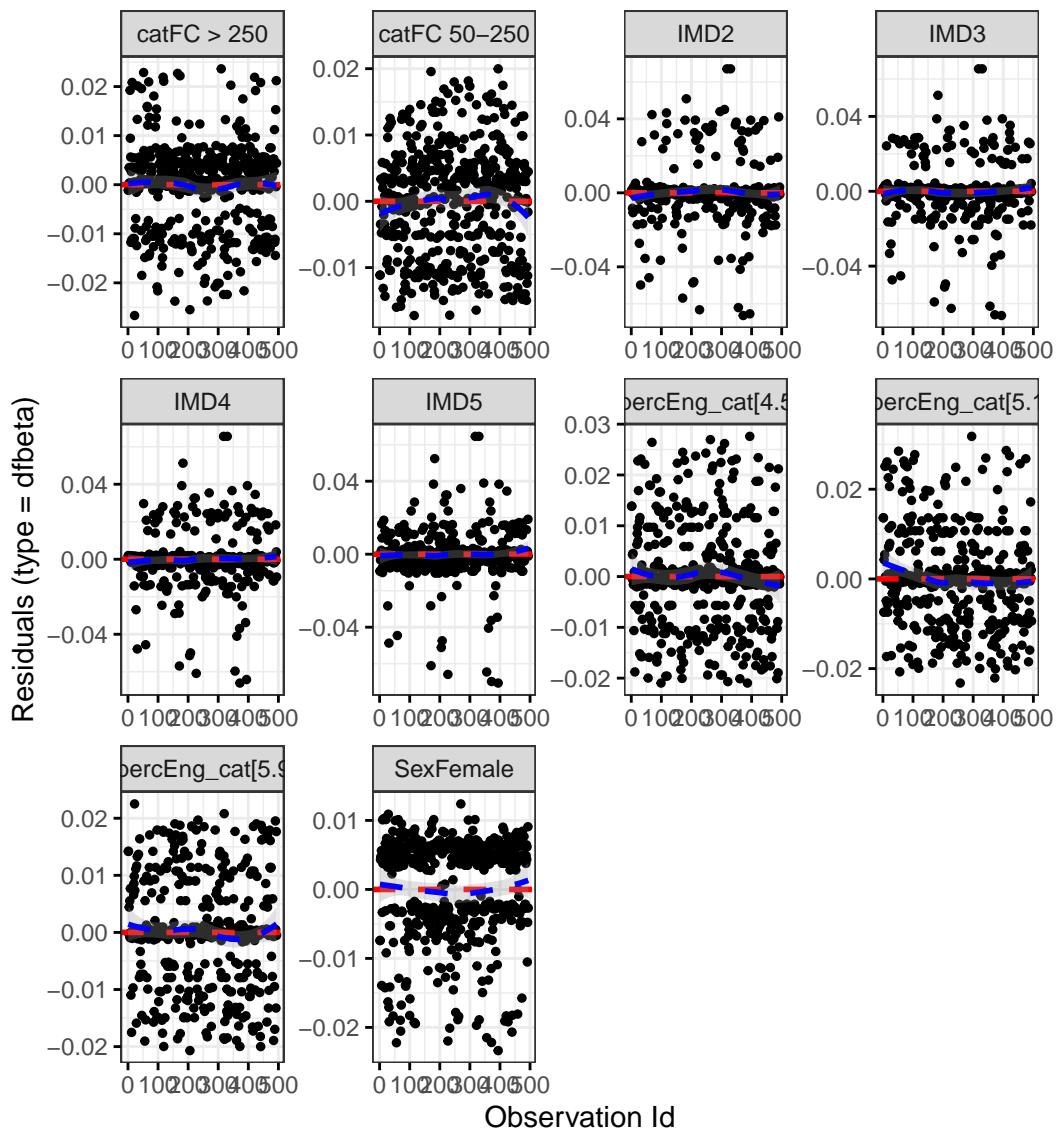
Diagnostics:

Proportional hazards assumption test

	Chi-squared statistic	DF	P-value
Sex	0.1923	1.0000	0.6610
cat	1.1166	2.0000	0.5722
IMD	3.2044	4.0000	0.5242
PUFA_percEng_cat	0.9104	3.0000	0.8229
GLOBAL	5.3470	10.0001	0.8668

DF betas

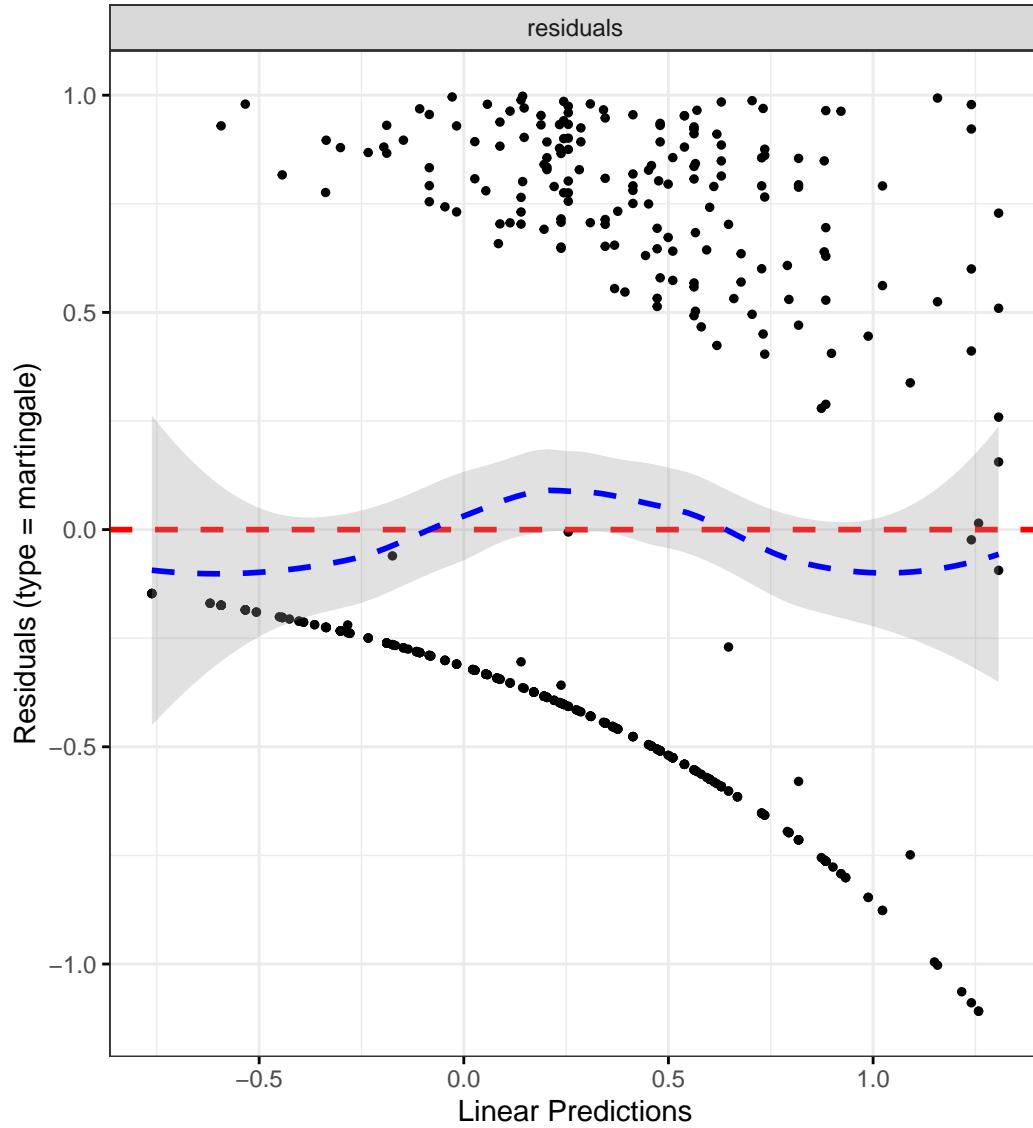
```
`geom_smooth()` using formula = 'y ~ x'
```



#####

Martingale residuals

```
`geom_smooth()` using formula = 'y ~ x'
```



Hard flare

```
# Run survival analysis using utility function for hard flare
analysis_result <- run_survival_analysis(
  data = flare.cd.df,
  var_name = "PUFA_percEng",
  outcome_time = "hardflare_time",
  outcome_event = "hardflare",
  legend_title = "PUFA intake (by g) quantiles",
```

```

plot_base_path = "plots/cd/hard-flare/diet/pufa",
break_time_by = 500
)

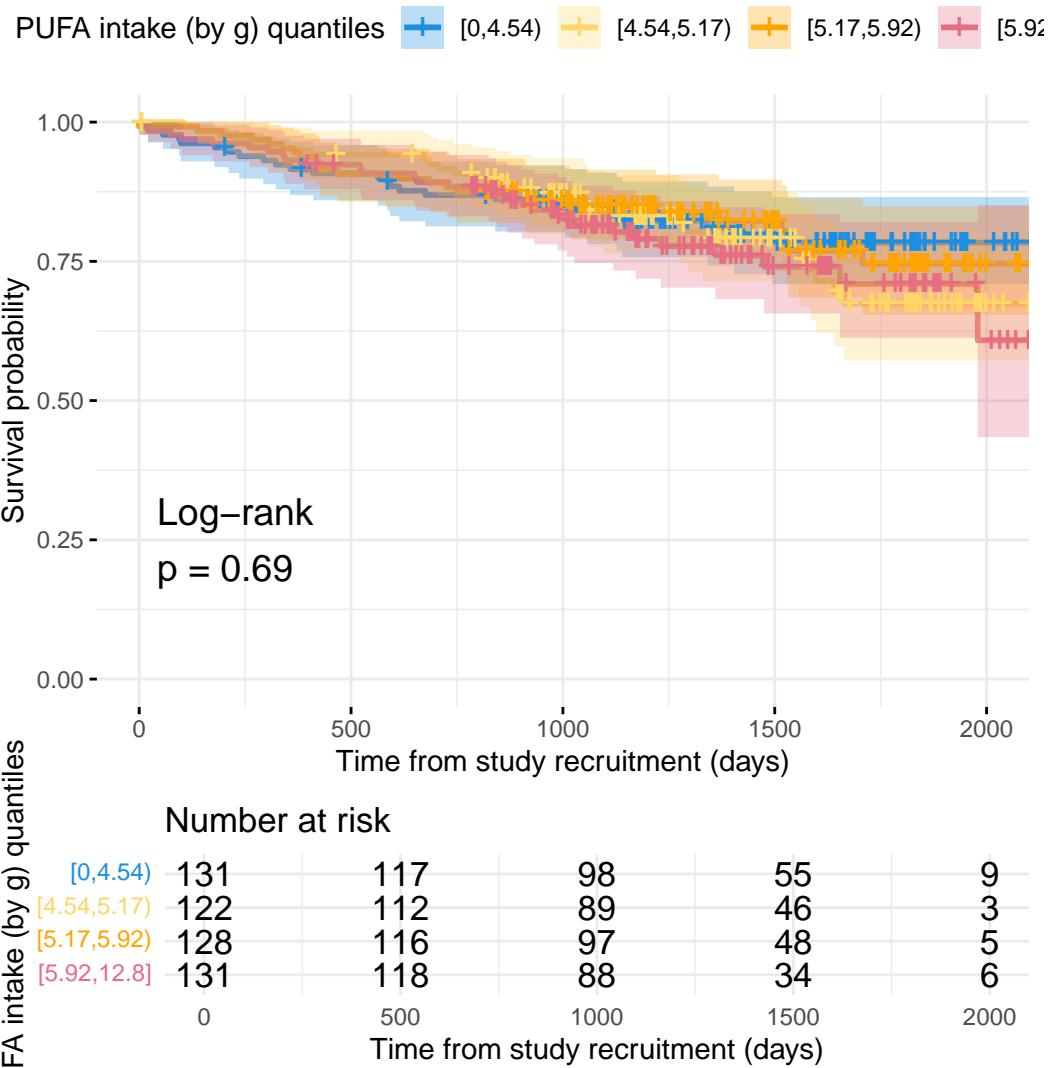
# Save plot as RDS
saveRDS(analysis_result$plot, paste0(paths$outdir, "pufa-cd-hard.RDS"))

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(hardflare_time, hardflare) ~
    Sex + cat + IMD + dqi_tot + BMI + PUFA_percEng_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.cd.df
)

# Display plot and model summary
analysis_result$plot

```

Time to hard flare



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.3456	0.8895	2.0355	0.1599
catFC 50-250	1.8559	1.1640	2.9588	0.0094
catFC > 250	2.8788	1.7356	4.7751	0.0000

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	0.6383	0.2747	1.4829	0.2965
IMD3	0.8351	0.3771	1.8497	0.6570
IMD4	0.7877	0.3621	1.7136	0.5473
IMD5	0.7257	0.3490	1.5090	0.3907
dqi_tot	1.0035	0.9857	1.0217	0.7013
BMI	1.0187	0.9834	1.0553	0.3026
PUFA_percEng_cat[4.54,5.1	1.1055	0.6301	1.9395	0.7266
PUFA_percEng_cat[5.17,5.9	1.0967	0.6237	1.9285	0.7486
PUFA_percEng_cat[5.92,12.	1.3012	0.7520	2.2517	0.3466

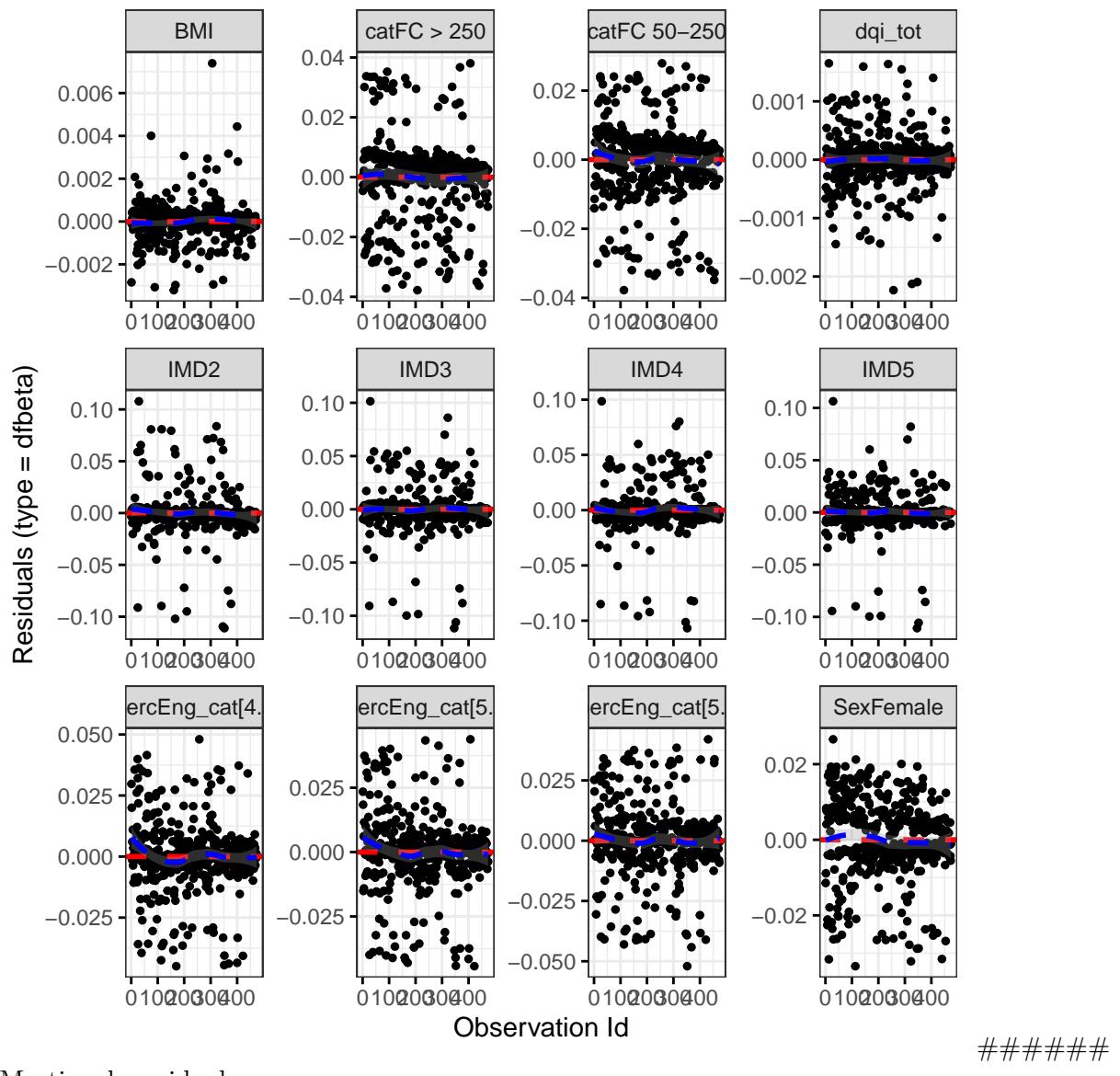
Diagnostics:

Proportional hazards assumption test

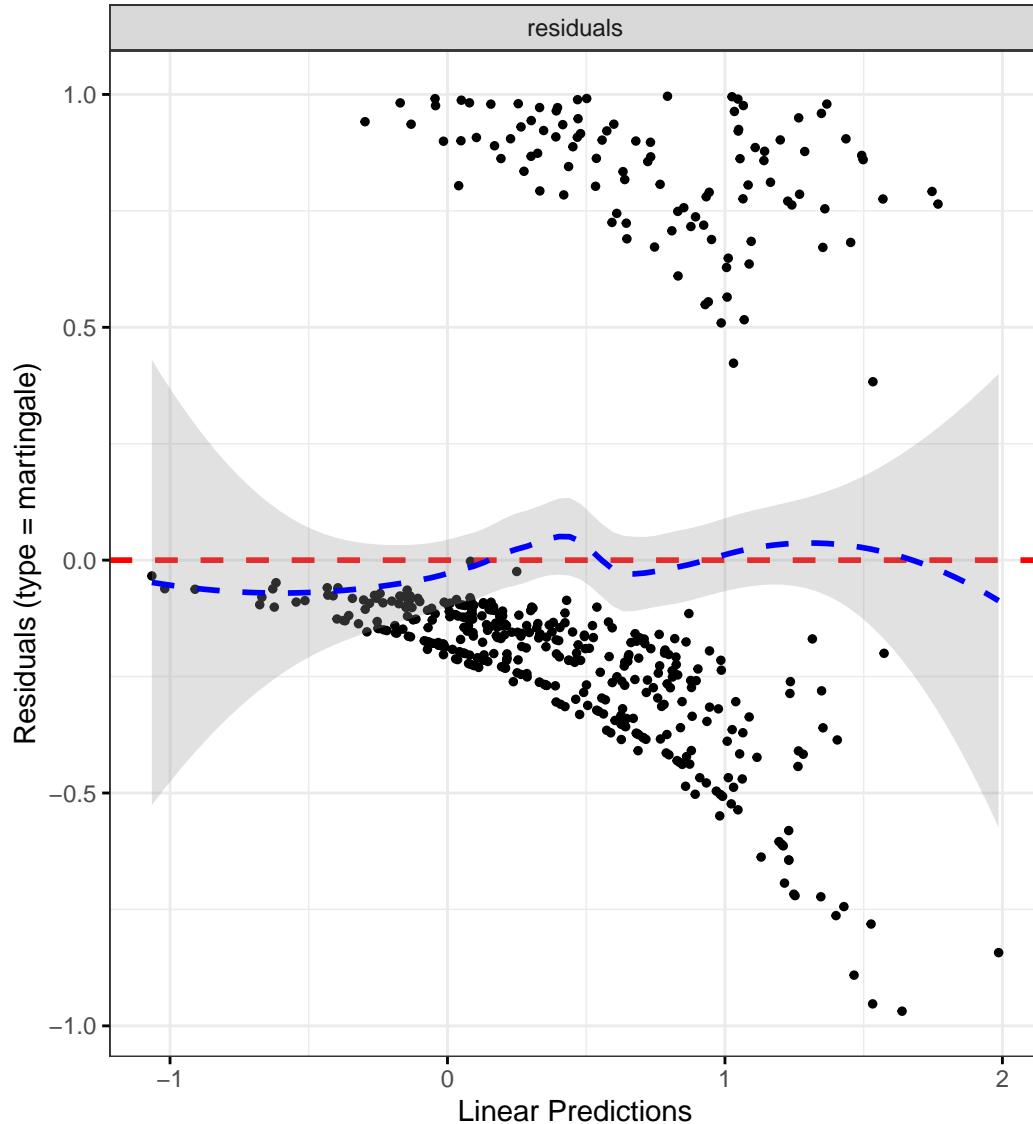
	Chi-squared statistic	DF	P-value
Sex	0.0505	0.9726	0.8128
cat	10.2964	1.9788	0.0057
IMD	2.7271	3.9317	0.5938
dqi_tot	2.8444	0.9892	0.0903
BMI	1.2067	0.9786	0.2657
PUFA_percEng_cat	8.4728	2.9524	0.0358
GLOBAL	27.3020	18.3585	0.0817

DF betas

```
`geom_smooth()` using formula = 'y ~ x'
```



```
`geom_smooth()` using formula = 'y ~ x'
```



Ulcerative colitis

Patient-reported flare

```
# Categorize PUFA by quantiles
flare.uc.df <- categorize_by_quantiles(flare.uc.df, "PUFA_percEng", reference_data = flare.d
```



```
# Run survival analysis using utility function
analysis_result <- run_survival_analysis(
```

```

data = flare.uc.df,
var_name = "PUFA_percEng",
outcome_time = "softflare_time",
outcome_event = "softflare",
legend_title = "PUFA intake (by g) quantiles",
plot_base_path = "plots/uc/soft-flare/diet/pufa",
break_time_by = 200
)

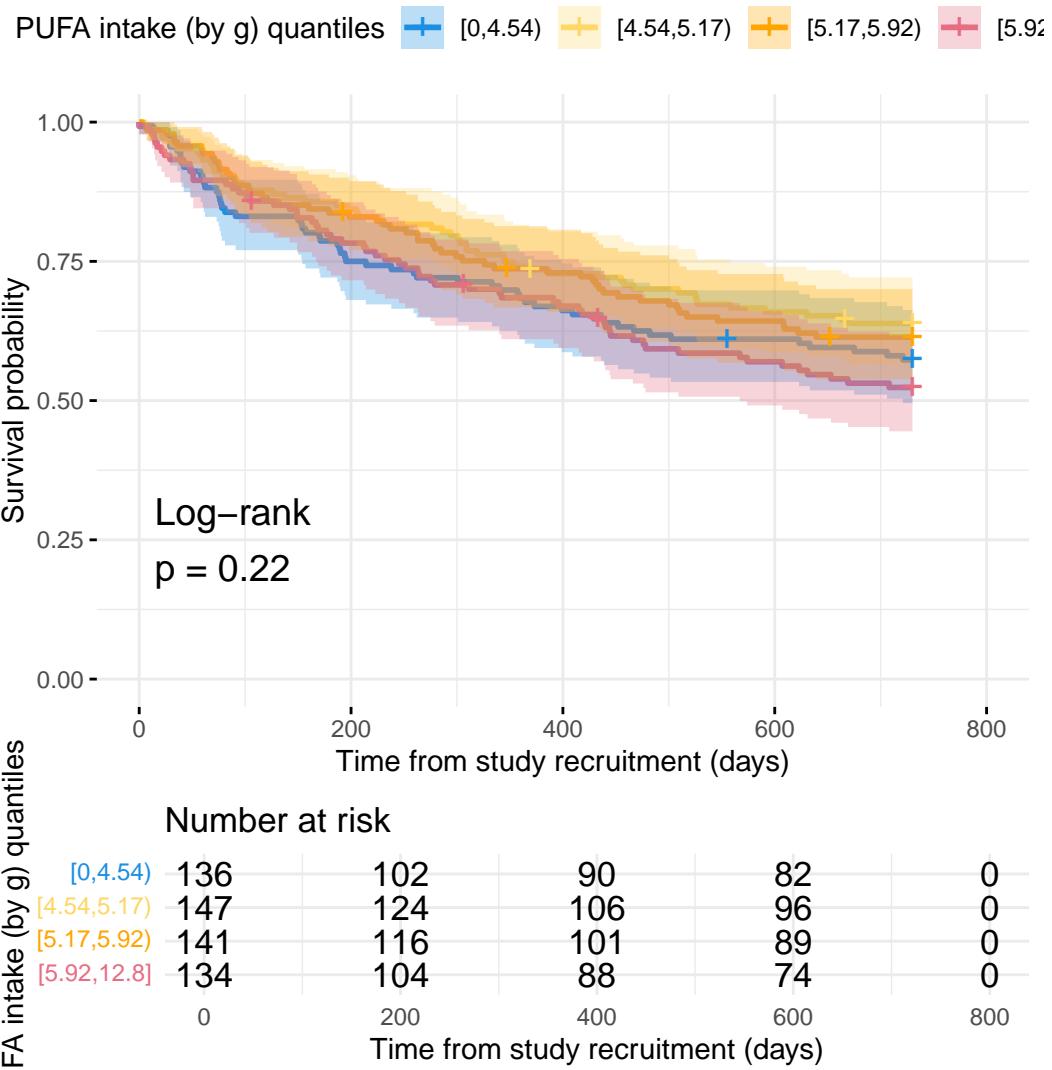
# Save plot as RDS
saveRDS(analysis_result$plot, paste0(paths$outdir, "pufa-uc-soft.RDS"))

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(softflare_time, softflare) ~
    Sex + cat + IMD + dqi_tot + BMI + PUFA_percEng_cat +
    frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.uc.df
)

# Display plot and model summary
analysis_result$plot

```

Time to patient-reported flare



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.6993	1.2731	2.2683	0.0003
catFC 50-250	1.8254	1.3279	2.5092	0.0002
catFC > 250	2.1008	1.4690	3.0042	0.0000

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	1.4206	0.7448	2.7094	0.2866
IMD3	1.1143	0.5917	2.0984	0.7375
IMD4	1.3211	0.7286	2.3953	0.3591
IMD5	1.1679	0.6490	2.1015	0.6047
dqi_tot	0.9995	0.9867	1.0125	0.9433
BMI	0.9799	0.9508	1.0099	0.1861
PUFA_percEng_cat[4.54,5.1	0.8929	0.6036	1.3208	0.5706
PUFA_percEng_cat[5.17,5.9	0.8670	0.5867	1.2811	0.4737
PUFA_percEng_cat[5.92,12.	1.1782	0.8065	1.7212	0.3965

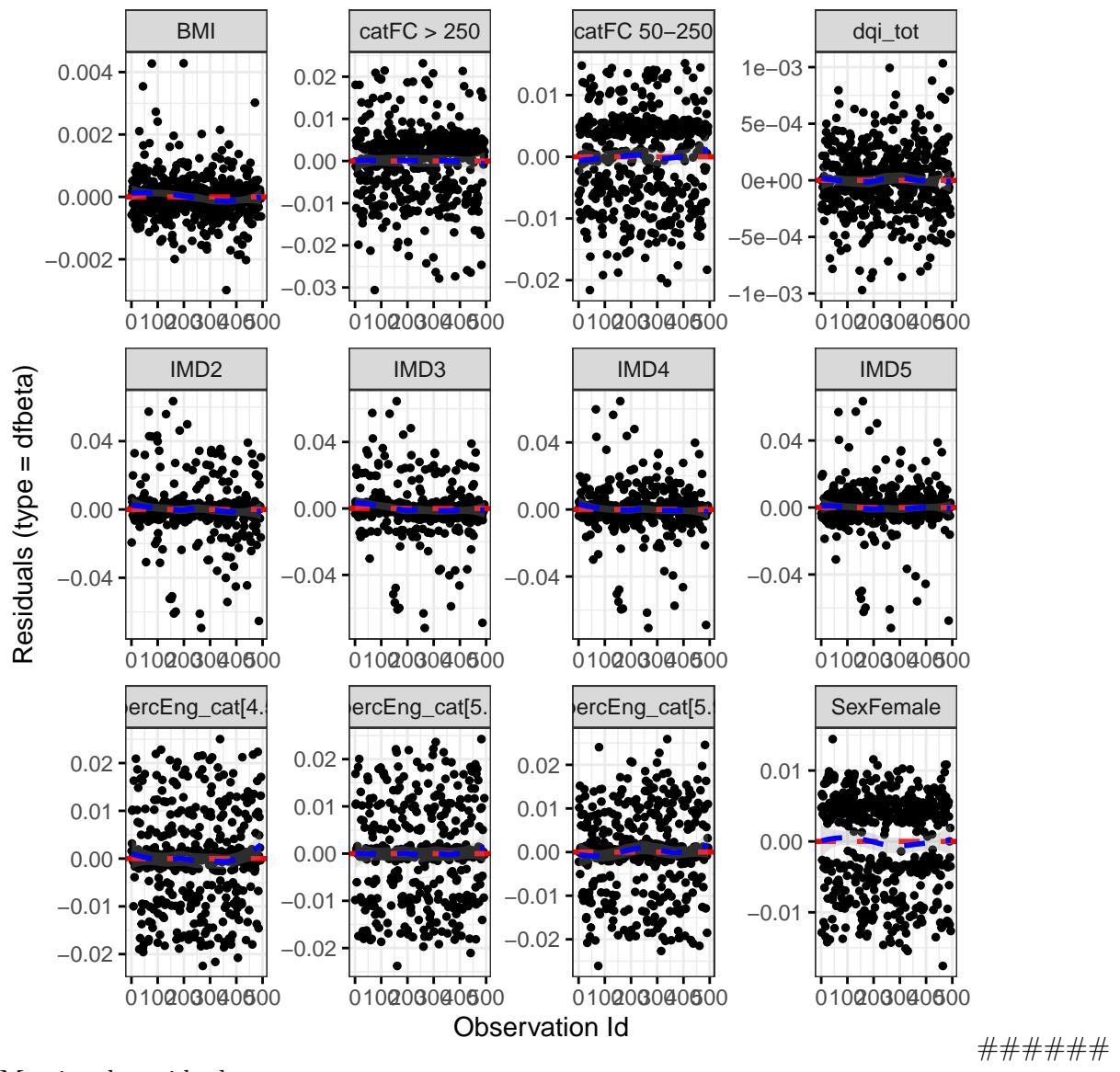
Diagnostics:

Proportional hazards assumption test

	Chi-squared statistic	DF	P-value
Sex	0.0129	1.0000	0.9097
cat	3.5443	2.0000	0.1700
IMD	2.6609	4.0000	0.6161
dqi_tot	0.7367	1.0000	0.3907
BMI	0.8724	1.0000	0.3503
PUFA_percEng_cat	2.7154	3.0000	0.4376
GLOBAL	11.2593	12.0001	0.5068

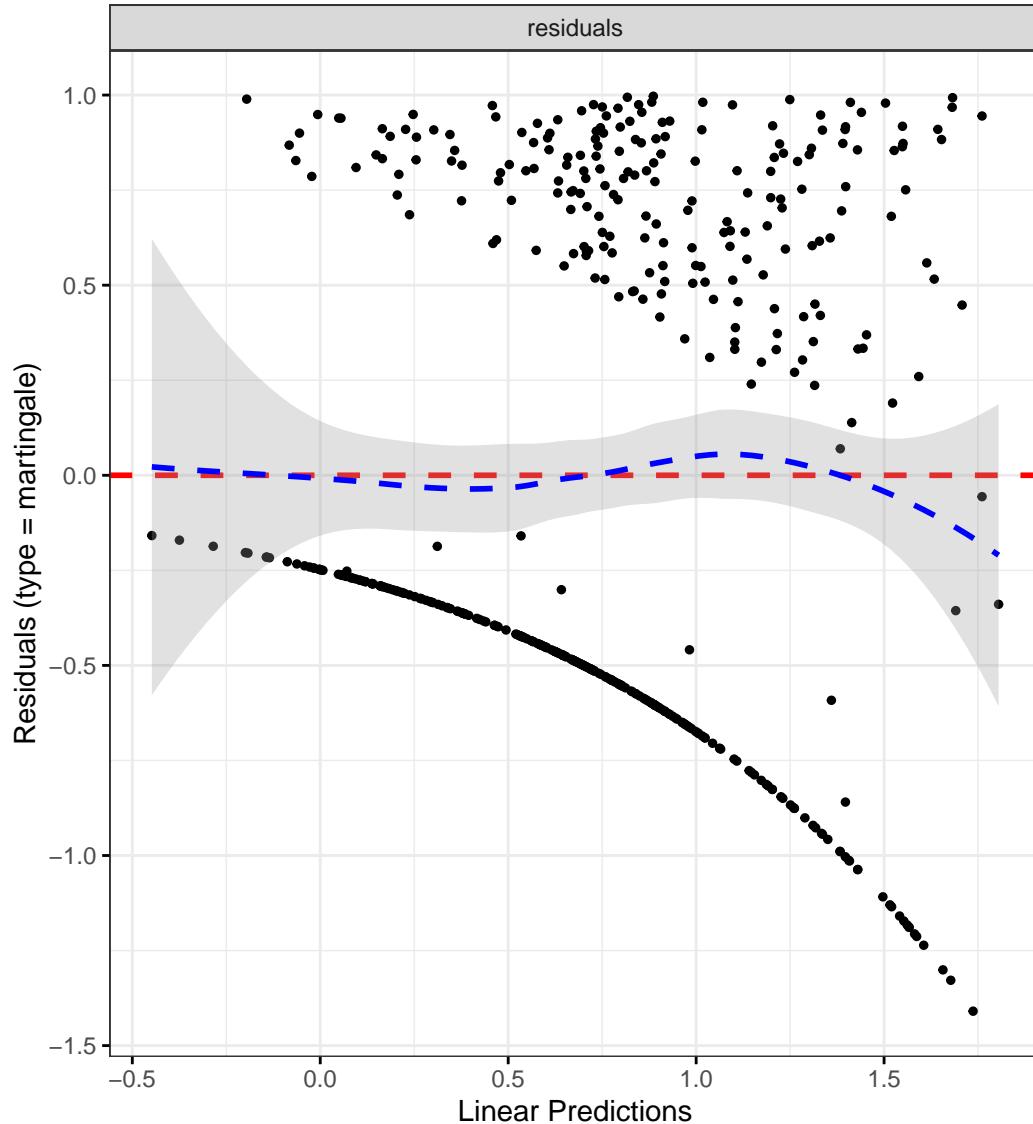
DF betas

```
`geom_smooth()` using formula = 'y ~ x'
```



Martingale residuals

```
`geom_smooth()` using formula = 'y ~ x'
```



Hard flare

```
# Run survival analysis using utility function for hard flare
analysis_result <- run_survival_analysis(
  data = flare.uc.df,
  var_name = "PUFA_percEng",
  outcome_time = "hardflare_time",
  outcome_event = "hardflare",
  legend_title = "PUFA intake (by g) quantiles",
```

```

plot_base_path = "plots/uc/hard-flare/diet/pufa",
break_time_by = 500
)

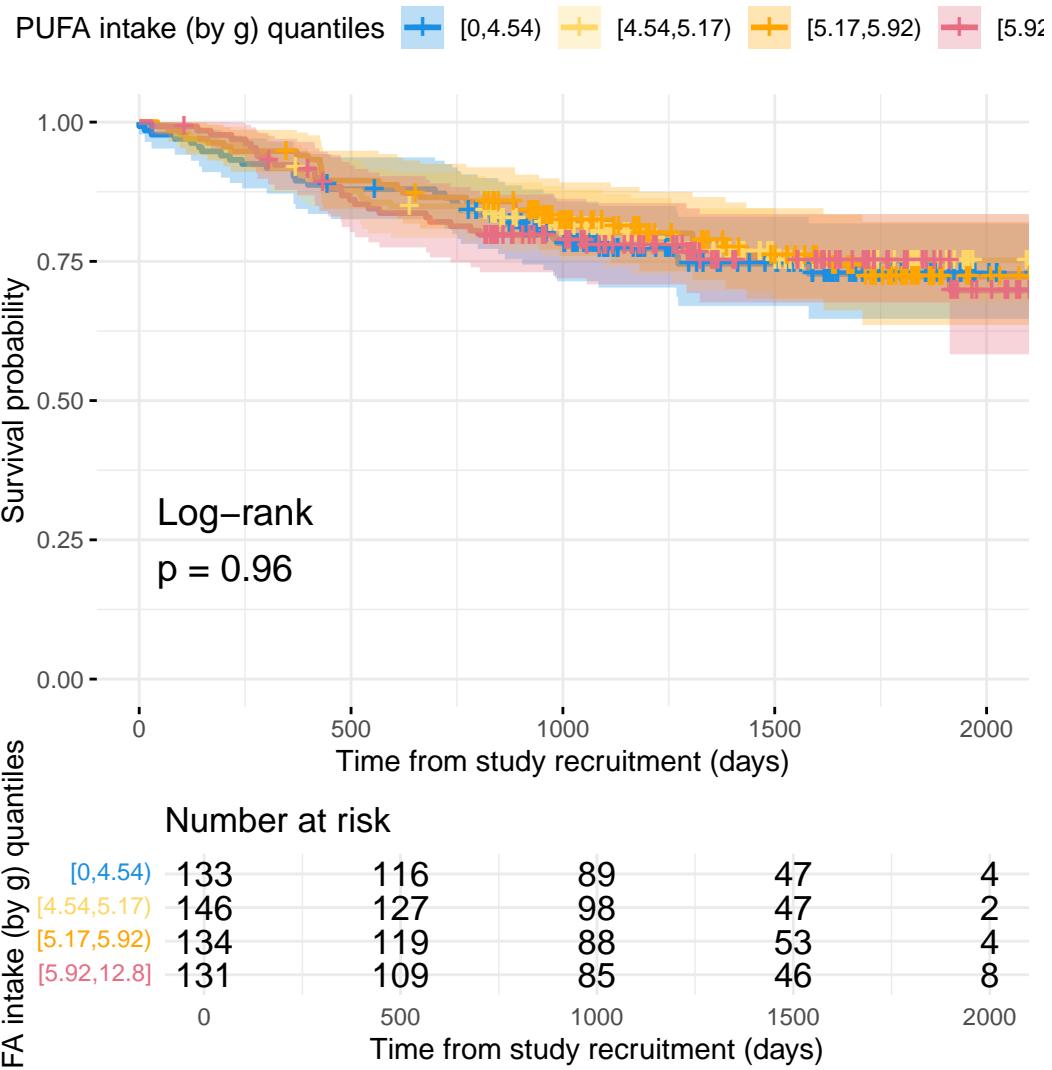
# Save plot as RDS
saveRDS(analysis_result$plot, paste0(paths$outdir, "pufa-uc-hard.RDS"))

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(hardflare_time, hardflare) ~
    Sex + cat + IMD + dqi_tot + BMI + PUFA_percEng_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.uc.df
)

# Display plot and model summary
analysis_result$plot

```

Time to hard flare



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.2077	0.8256	1.7666	0.3308
catFC 50-250	2.0348	1.3195	3.1378	0.0013
catFC > 250	2.5288	1.5496	4.1269	0.0002

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	1.5333	0.5814	4.0436	0.3877
IMD3	1.2567	0.4866	3.2454	0.6369
IMD4	2.2494	0.9365	5.4030	0.0698
IMD5	1.3583	0.5604	3.2920	0.4978
dqi_tot	1.0020	0.9844	1.0200	0.8236
BMI	0.9618	0.9219	1.0035	0.0722
PUFA_percEng_cat[4.54,5.1	0.9134	0.5480	1.5223	0.7281
PUFA_percEng_cat[5.17,5.9	0.7609	0.4497	1.2875	0.3086
PUFA_percEng_cat[5.92,12.	0.8666	0.5136	1.4621	0.5916

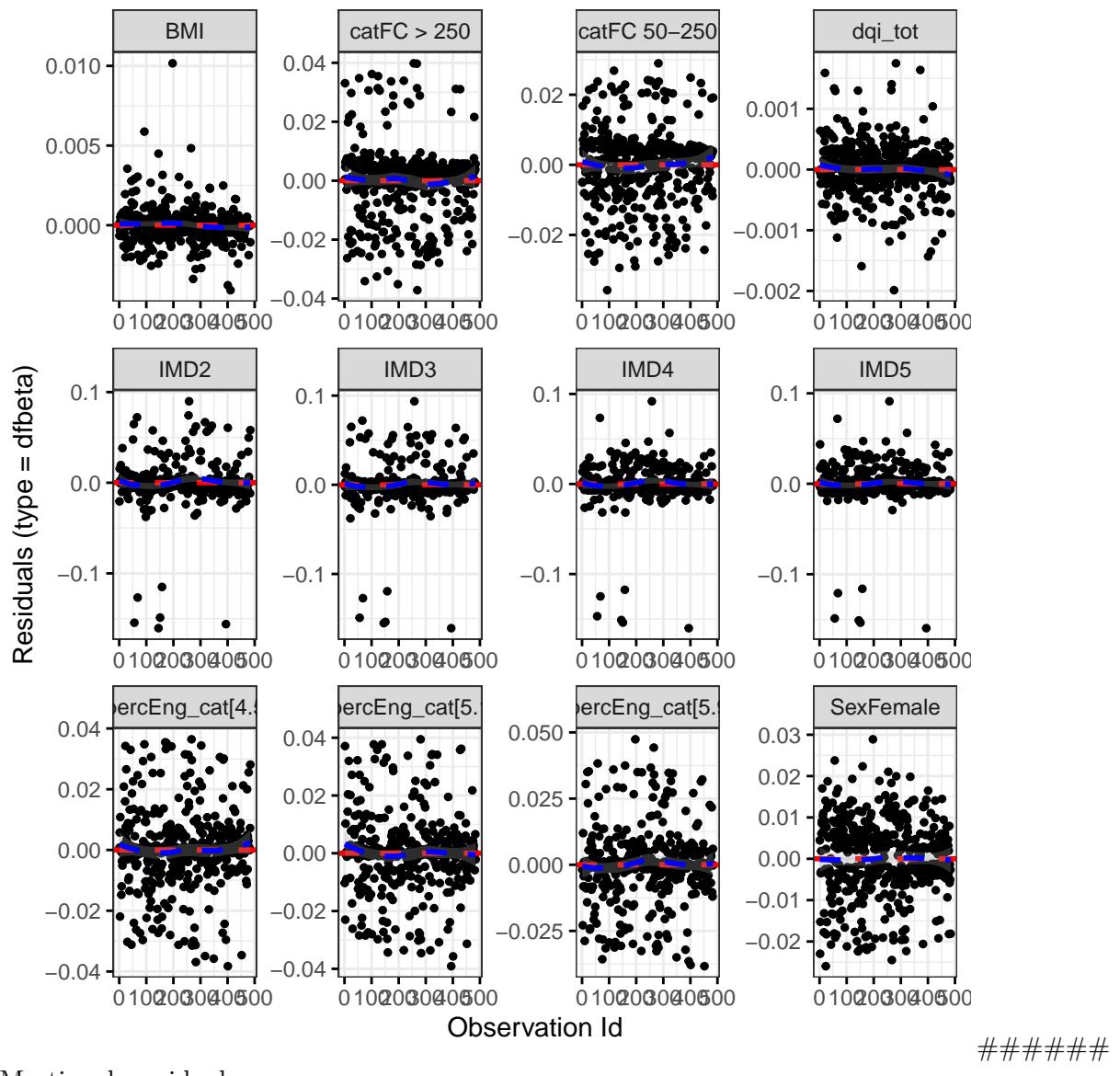
Diagnostics:

Proportional hazards assumption test

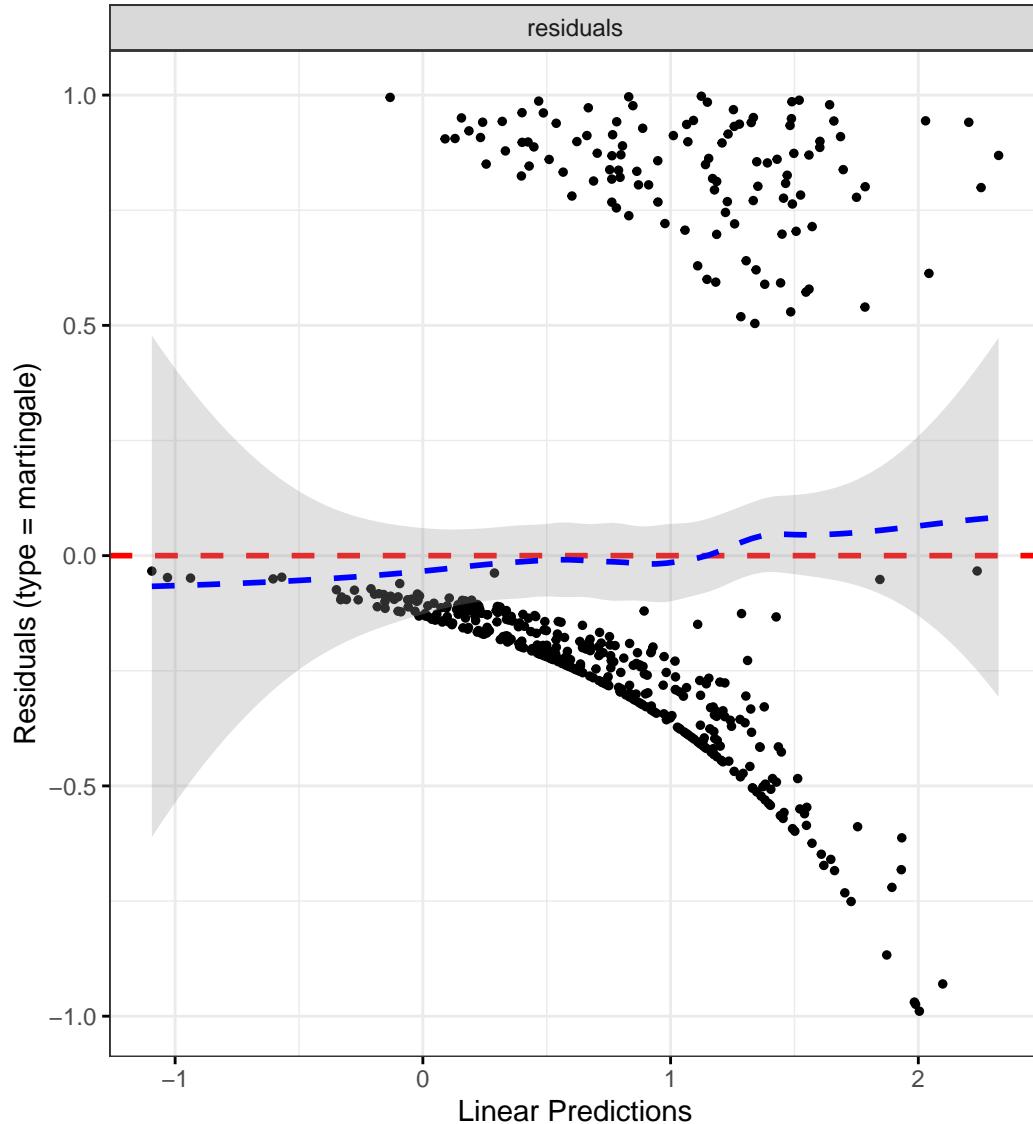
	Chi-squared statistic	DF	P-value
Sex	0.0277	0.9890	0.8646
cat	5.3713	1.9576	0.0655
IMD	1.1788	3.9319	0.8753
dqi_tot	0.0028	0.9861	0.9558
BMI	0.5505	0.9901	0.4542
PUFA_percEng_cat	3.2562	2.9455	0.3449
GLOBAL	11.7781	19.4010	0.9072

DF betas

```
`geom_smooth()` using formula = 'y ~ x'
```



```
`geom_smooth()` using formula = 'y ~ x'
```



Inflammatory bowel disease

Patient-reported flare

```
# Categorize PUFA by quantiles
flare.df <- categorize_by_quantiles(flare.df, "PUFA_percEng", reference_data = flare.df)

# Run survival analysis using utility function
analysis_result <- run_survival_analysis()
```

```

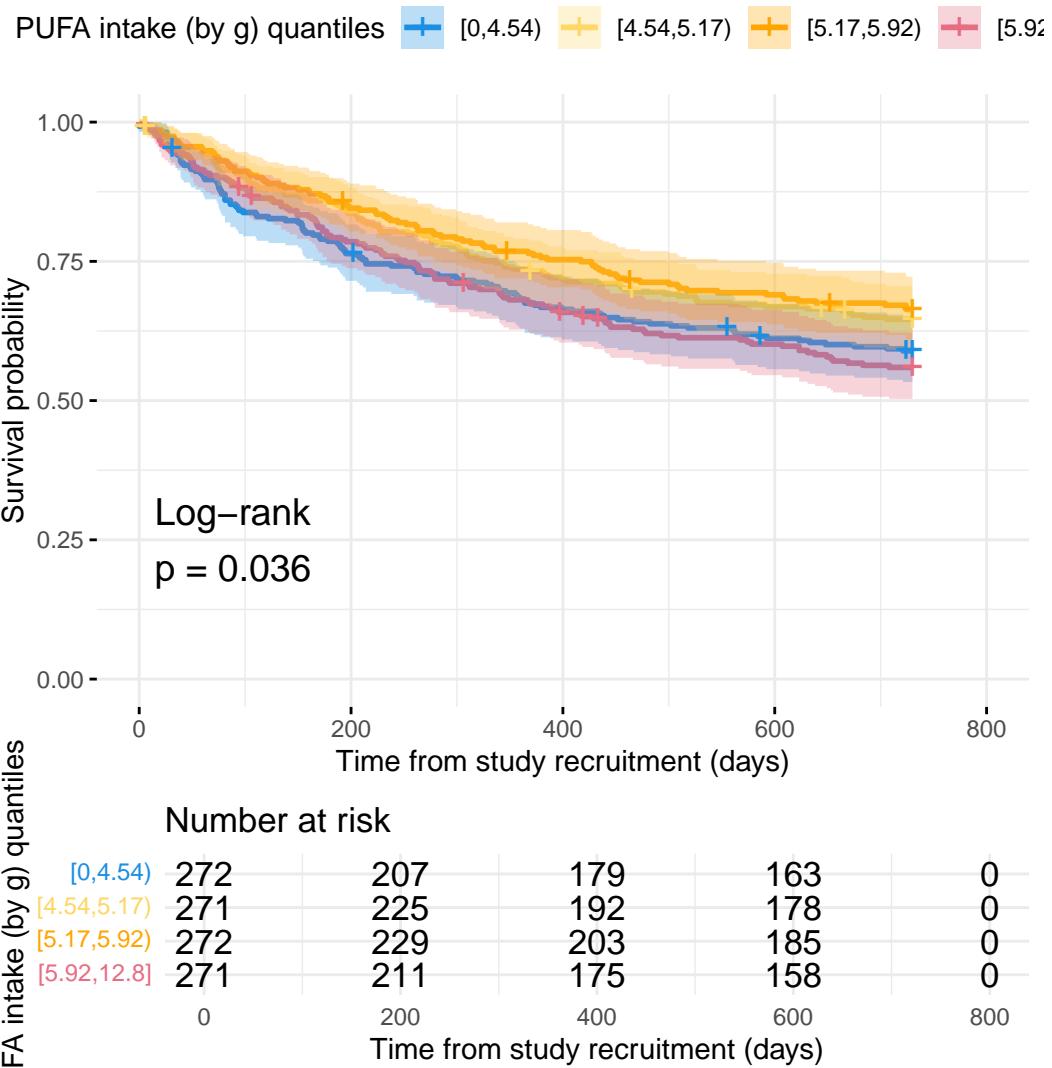
data = flare.df,
var_name = "PUFA_percEng",
outcome_time = "softflare_time",
outcome_event = "softflare",
legend_title = "PUFA intake (by g) quantiles",
plot_base_path = "plots/ibd/soft-flare/diet/pufa",
break_time_by = 200
)

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(softflare_time, softflare) ~
    Sex + cat + IMD + dqi_tot + BMI + PUFA_percEng_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.df
)

# Display plot and model summary
analysis_result$plot

```

Time to patient-reported flare



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.7648	1.4228	2.1890	0.0000
catFC 50-250	1.5003	1.1877	1.8953	0.0007
catFC > 250	2.0190	1.5584	2.6157	0.0000

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	0.9653	0.6131	1.5199	0.8789
IMD3	0.9886	0.6403	1.5266	0.9589
IMD4	1.0873	0.7173	1.6481	0.6933
IMD5	1.0602	0.7092	1.5850	0.7755
dqi_tot	1.0021	0.9928	1.0115	0.6604
BMI	0.9966	0.9768	1.0168	0.7386
PUFA_percEng_cat[4.54,5.1	0.8545	0.6423	1.1369	0.2805
PUFA_percEng_cat[5.17,5.9	0.7679	0.5757	1.0243	0.0724
PUFA_percEng_cat[5.92,12.	1.0490	0.7990	1.3772	0.7306

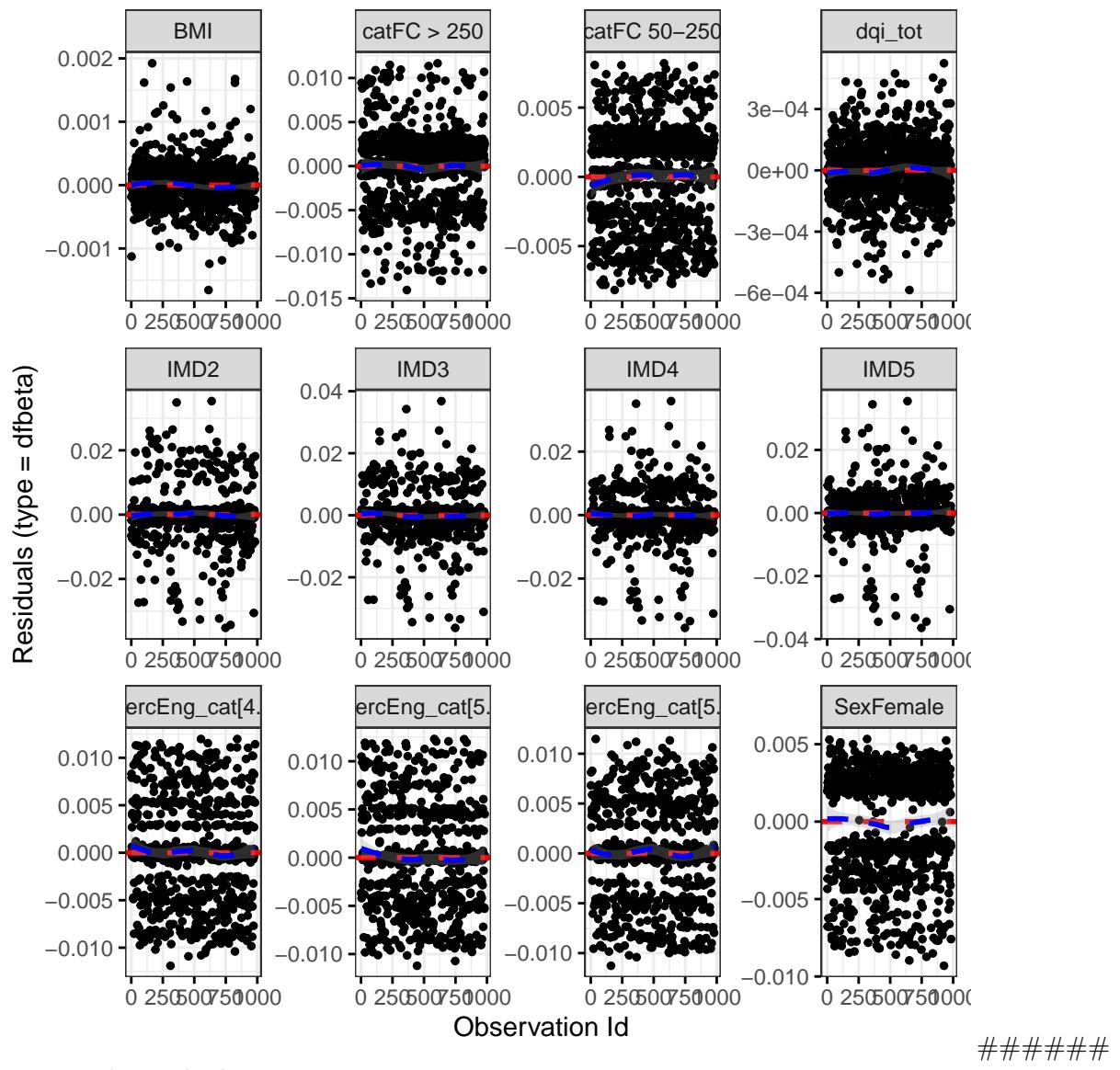
Diagnostics:

Proportional hazards assumption test

	Chi-squared statistic	DF	P-value
Sex	0.0016	1.0000	0.9682
cat	1.0598	2.0000	0.5887
IMD	5.2193	4.0000	0.2655
dqi_tot	1.3435	1.0000	0.2464
BMI	0.0112	1.0000	0.9155
PUFA_percEng_cat	3.8212	3.0000	0.2814
GLOBAL	11.7195	12.0002	0.4685

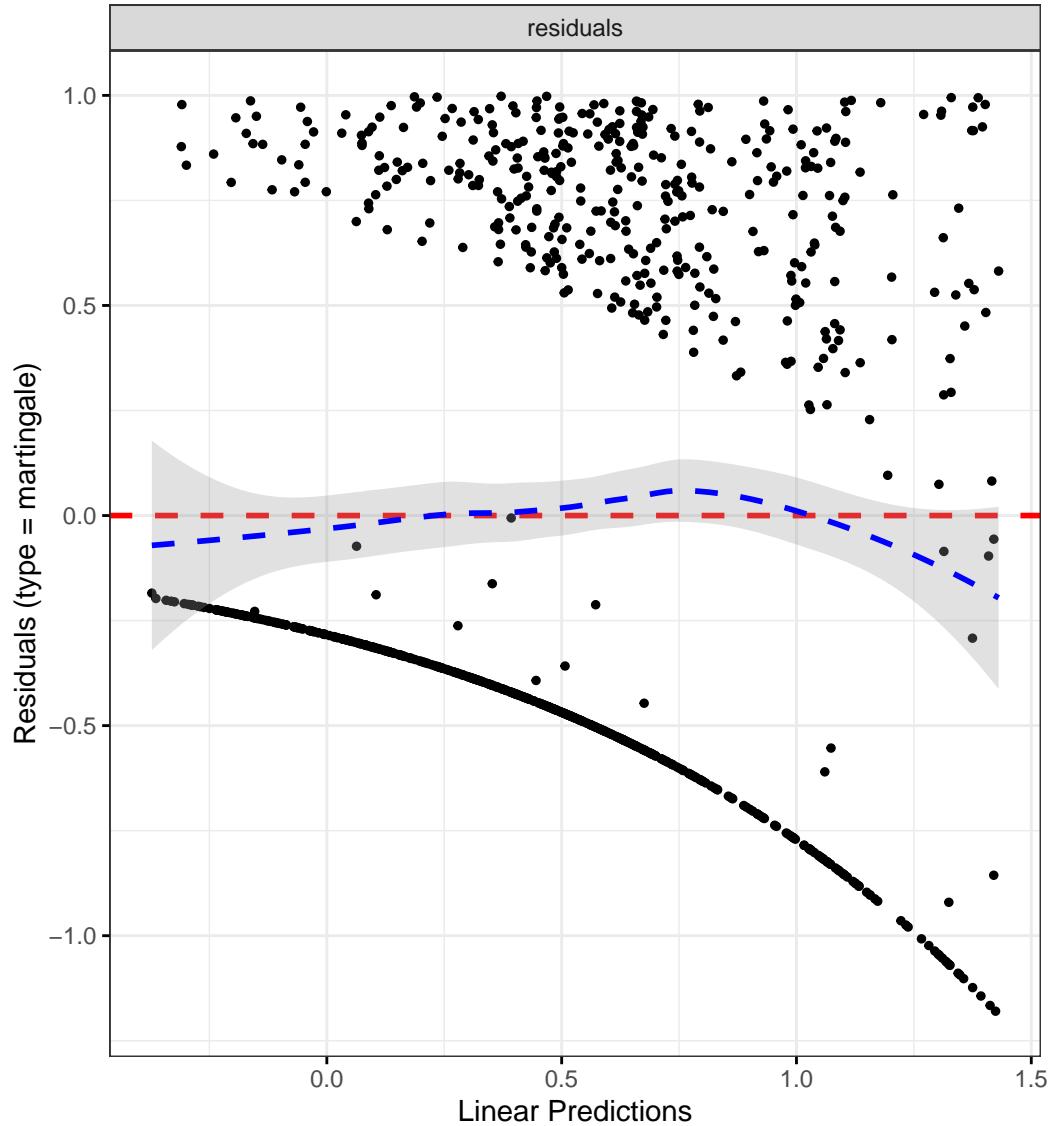
DF betas

```
`geom_smooth()` using formula = 'y ~ x'
```



Martingale residuals

```
`geom_smooth()` using formula = 'y ~ x'
```



Hard flare

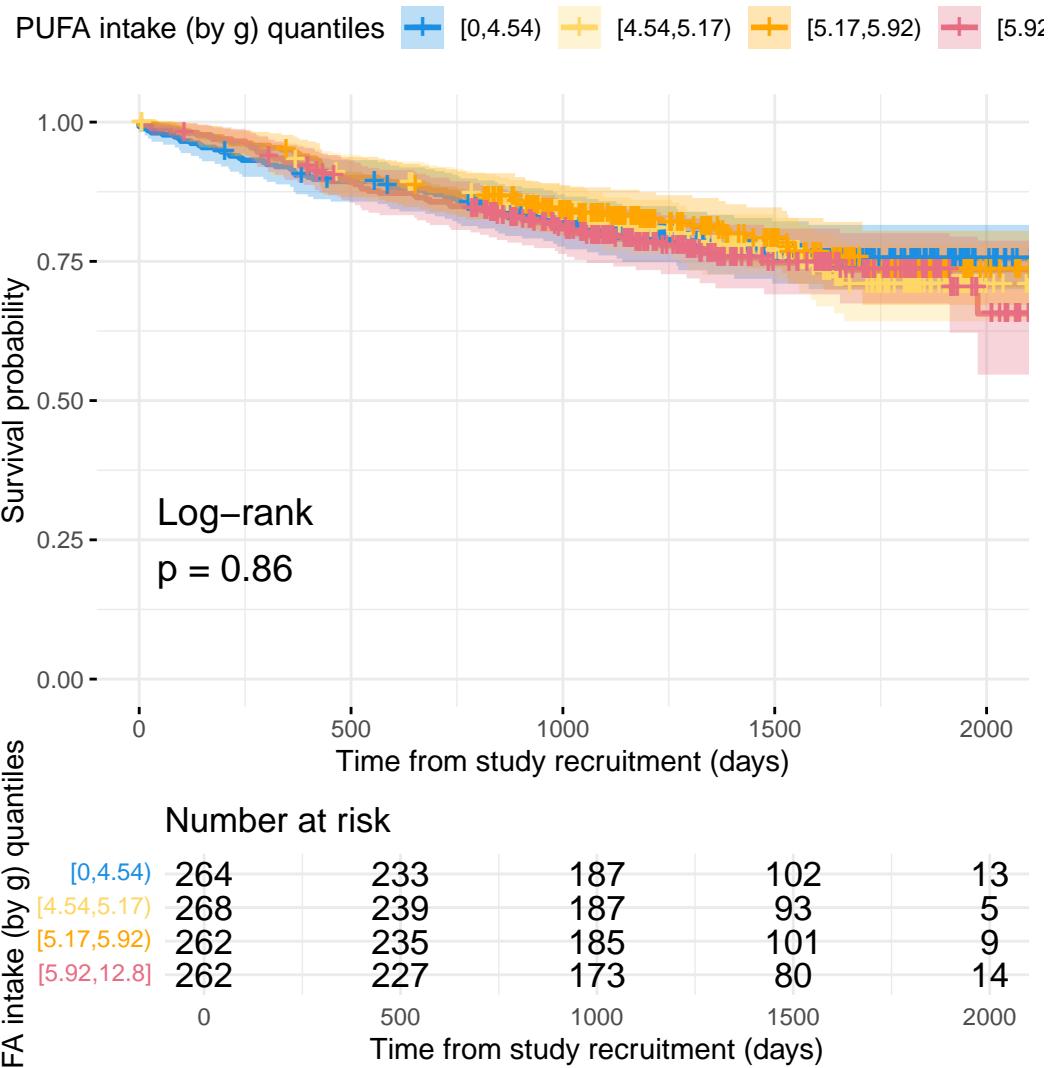
```
# Run survival analysis using utility function for hard flare
analysis_result <- run_survival_analysis(
  data = flare.df,
  var_name = "PUFA_percEng",
  outcome_time = "hardflare_time",
  outcome_event = "hardflare",
  legend_title = "PUFA intake (by g) quantiles",
```

```
plot_base_path = "plots/ibd/hard-flare/diet/pufa",
break_time_by = 500
)

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(hardflare_time, hardflare) ~
    Sex + cat + IMD + dqi_tot + BMI + PUFA_percEng_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.df
)

# Display plot and model summary
analysis_result$plot
```

Time to hard flare



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.2527	0.9498	1.6521	0.1107
catFC 50-250	1.8650	1.3617	2.5542	0.0001
catFC > 250	2.6139	1.8490	3.6952	0.0000

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	0.9178	0.4912	1.7151	0.7880
IMD3	0.9535	0.5230	1.7383	0.8765
IMD4	1.3506	0.7689	2.3724	0.2956
IMD5	0.9680	0.5550	1.6884	0.9088
dqi_tot	1.0025	0.9901	1.0151	0.6944
BMI	0.9926	0.9662	1.0197	0.5902
PUFA_percEng_cat[4.54,5.1	1.0478	0.7206	1.5234	0.8070
PUFA_percEng_cat[5.17,5.9	0.8868	0.6056	1.2986	0.5371
PUFA_percEng_cat[5.92,12.	1.0675	0.7343	1.5517	0.7323

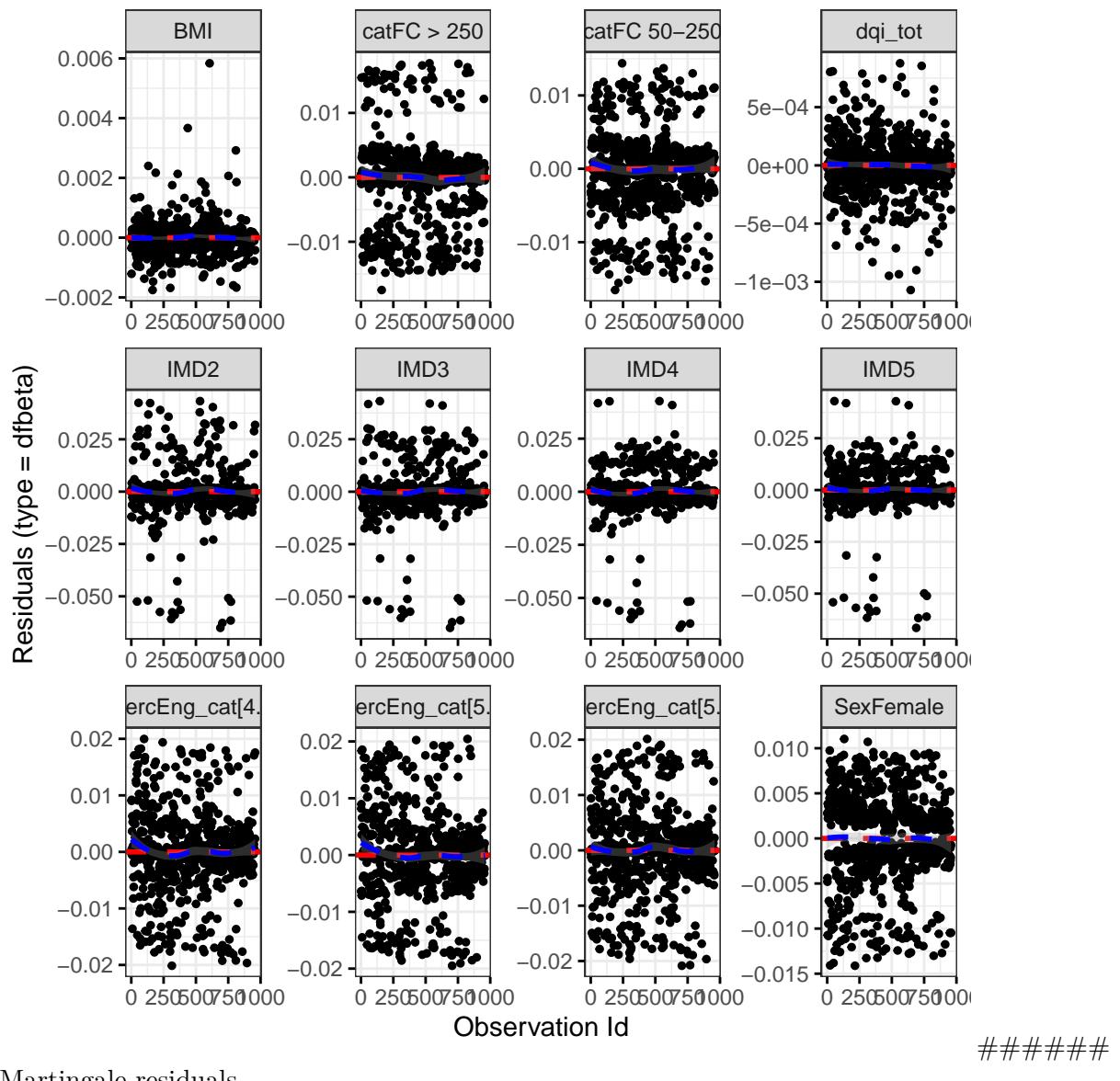
Diagnostics:

Proportional hazards assumption test

	Chi-squared statistic	DF	P-value
Sex	0.0286	0.9889	0.8625
cat	6.8811	1.9800	0.0314
IMD	1.6066	3.9463	0.8011
dqi_tot	2.0684	0.9924	0.1490
BMI	1.8498	0.9903	0.1718
PUFA_percEng_cat	5.0558	2.9659	0.1643
GLOBAL	17.2508	22.9415	0.7942

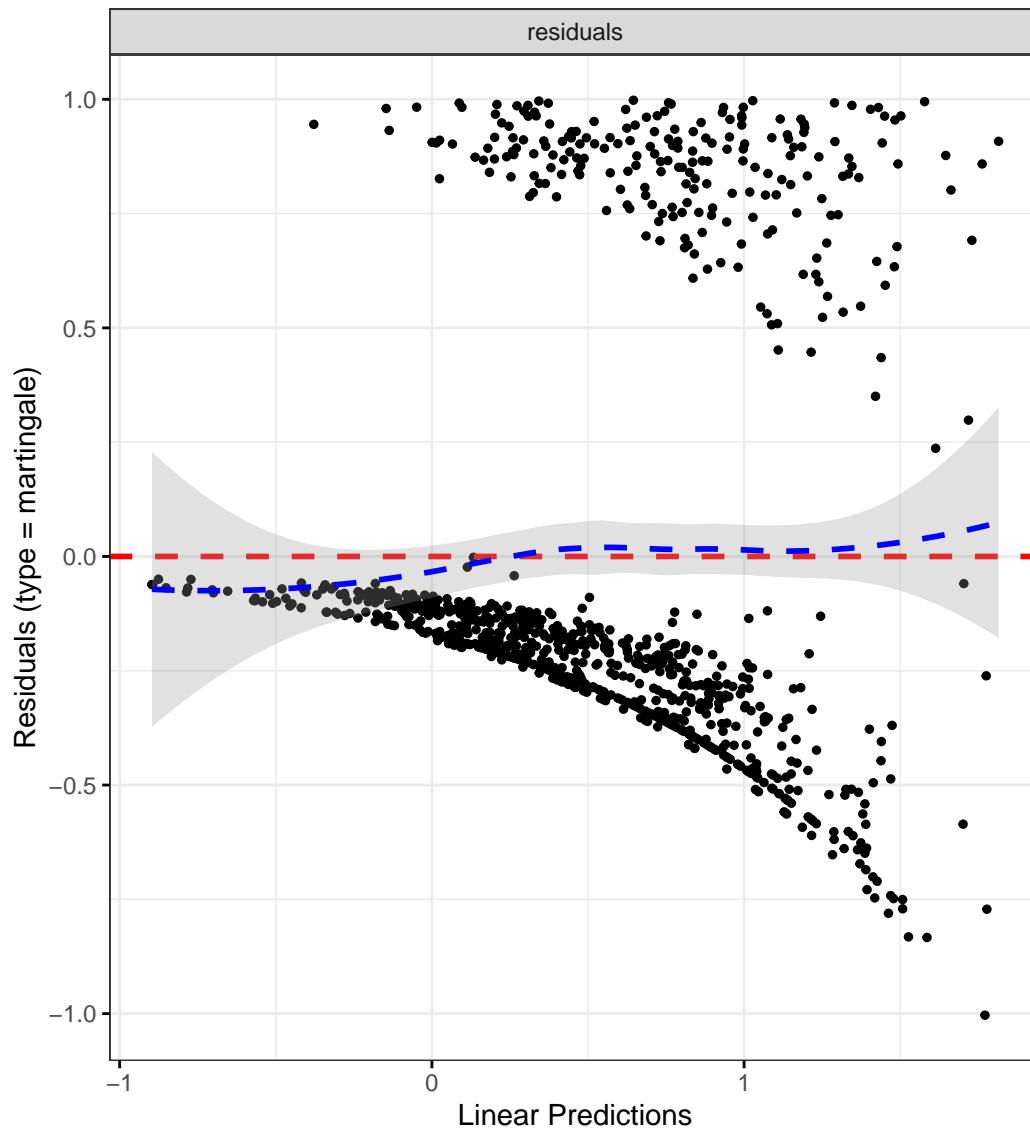
DF betas

```
`geom_smooth()` using formula = 'y ~ x'
```



Martingale residuals

```
`geom_smooth()` using formula = 'y ~ x'
```



NOVA score

The SAP states emulsifiers (specifically lecithin) will be investigated. However, data on emulsifiers are not available in the FFQ data extract. As a proxy for emulsifiers, this report will look at ultra-processed foods via Nova scores (Monteiro et al. 2017).

Crohn's disease

Patient-reported flare

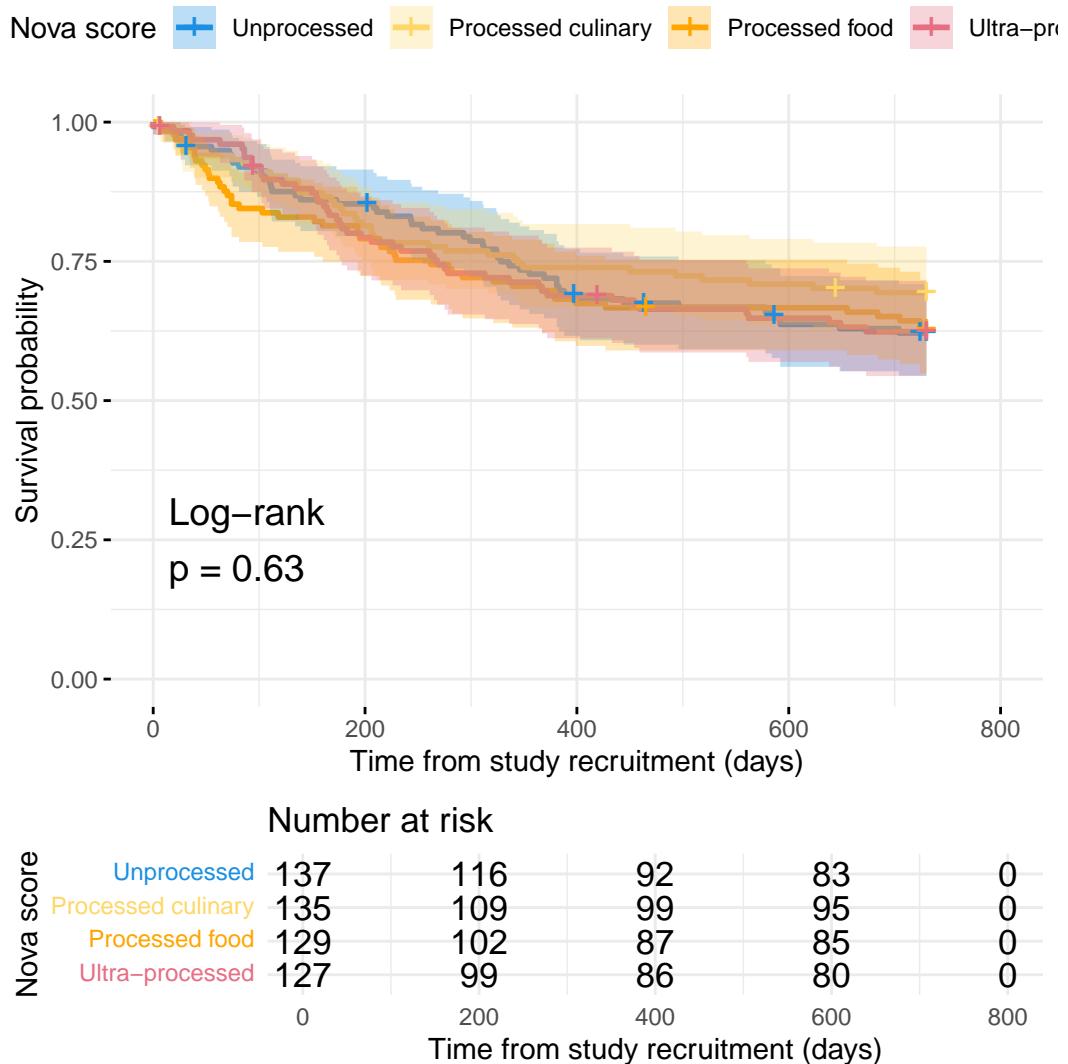
```
# Run survival analysis using utility function
analysis_result <- run_survival_analysis(
  data = flare.cd.df,
  var_name = "NOVAScore",
  outcome_time = "softflare_time",
  outcome_event = "softflare",
  legend_title = "Nova score",
  plot_base_path = "plots/cd/soft-flare/diet/nova",
  break_time_by = 200
)

# Save plot as RDS
saveRDS(analysis_result$plot, paste0(paths$outdir, "nova-cd-soft.RDS"))

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(softflare_time, softflare) ~
    Sex + cat + IMD + dqi_tot + BMI + NOVAScore_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.cd.df
)

# Display plot and model summary
analysis_result$plot
```

Time to patient-reported flare



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.9041	1.3630	2.6598	0.0002
catFC 50-250	1.2913	0.9079	1.8365	0.1549
catFC > 250	2.0473	1.3967	3.0011	0.0002

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	0.7306	0.3793	1.4071	0.3479
IMD3	0.9623	0.5254	1.7625	0.9009
IMD4	0.8866	0.4863	1.6165	0.6945
IMD5	1.0227	0.5837	1.7917	0.9376
dqi_tot	1.0058	0.9921	1.0196	0.4099
BMI	1.0091	0.9813	1.0377	0.5237
NOVAScore_catProcessed cu	0.9416	0.6123	1.4480	0.7841
NOVAScore_catProcessed fo	1.1200	0.7347	1.7074	0.5983
NOVAScore_catUltra-proces	1.0418	0.6817	1.5922	0.8497

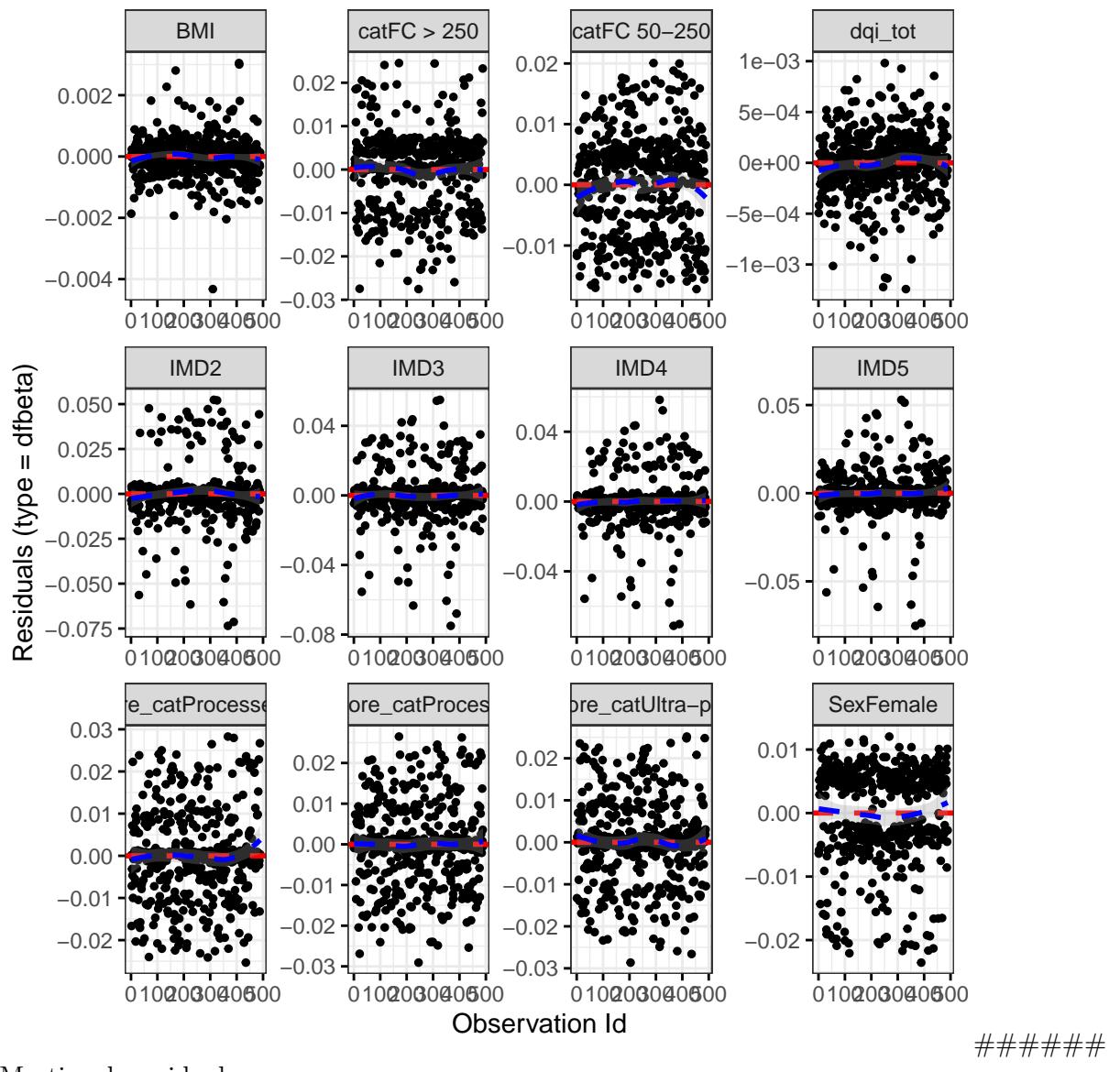
Diagnostics:

Proportional hazards assumption test

	Chi-squared statistic	DF	P-value
Sex	0.2700	1.0000	0.6033
cat	0.7511	2.0000	0.6869
IMD	3.0377	4.0000	0.5515
dqi_tot	0.3613	1.0000	0.5478
BMI	1.3237	1.0000	0.2499
NOVAScore_cat	3.3740	3.0000	0.3375
GLOBAL	7.9593	12.0001	0.7883

DF betas

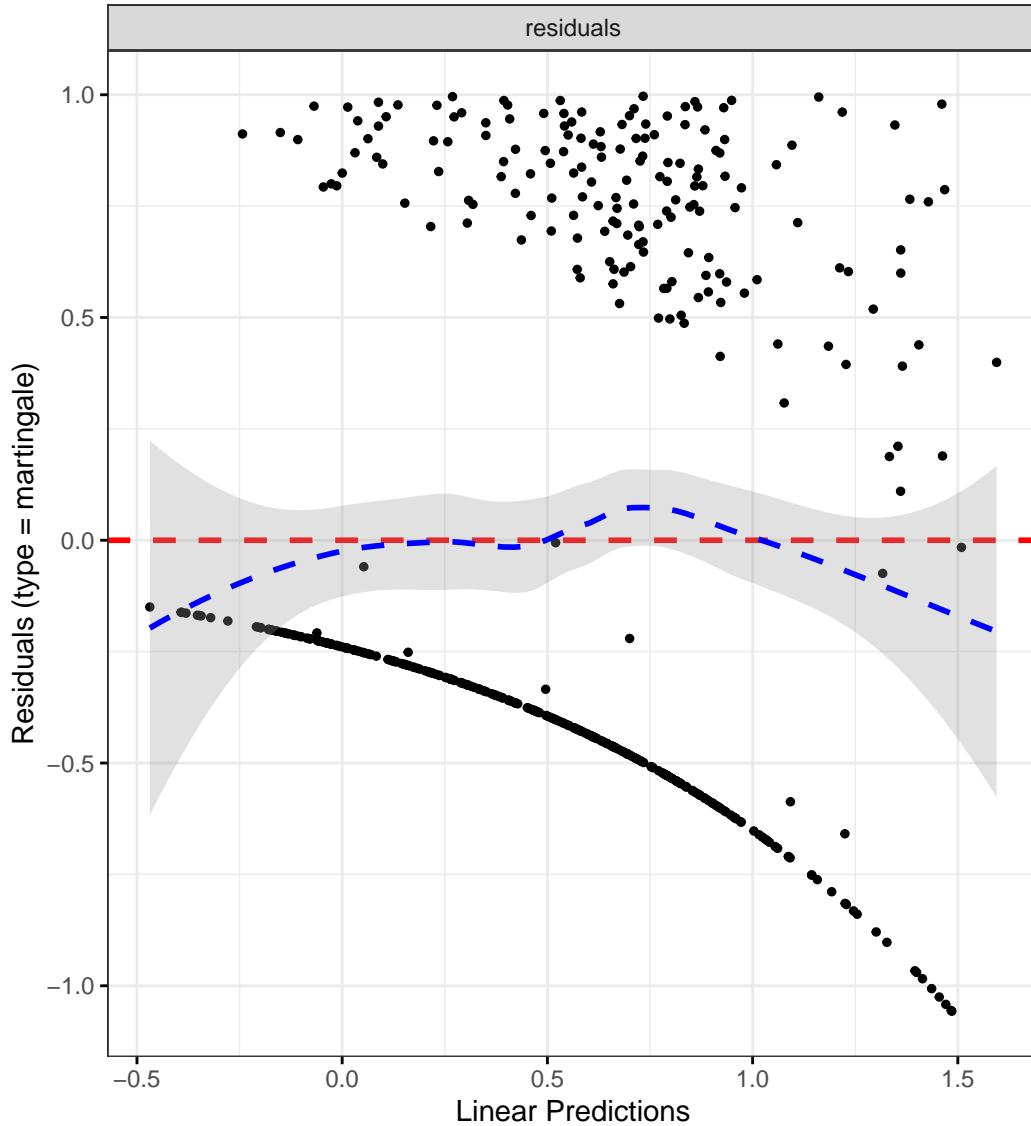
```
`geom_smooth()` using formula = 'y ~ x'
```



#####

Martingale residuals

```
`geom_smooth()` using formula = 'y ~ x'
```



Hard flare

```
# Run survival analysis using utility function for hard flare
analysis_result <- run_survival_analysis(
  data = flare.cd.df,
  var_name = "NOVAScore",
  outcome_time = "hardflare_time",
  outcome_event = "hardflare",
  legend_title = "Nova Score",
```

```

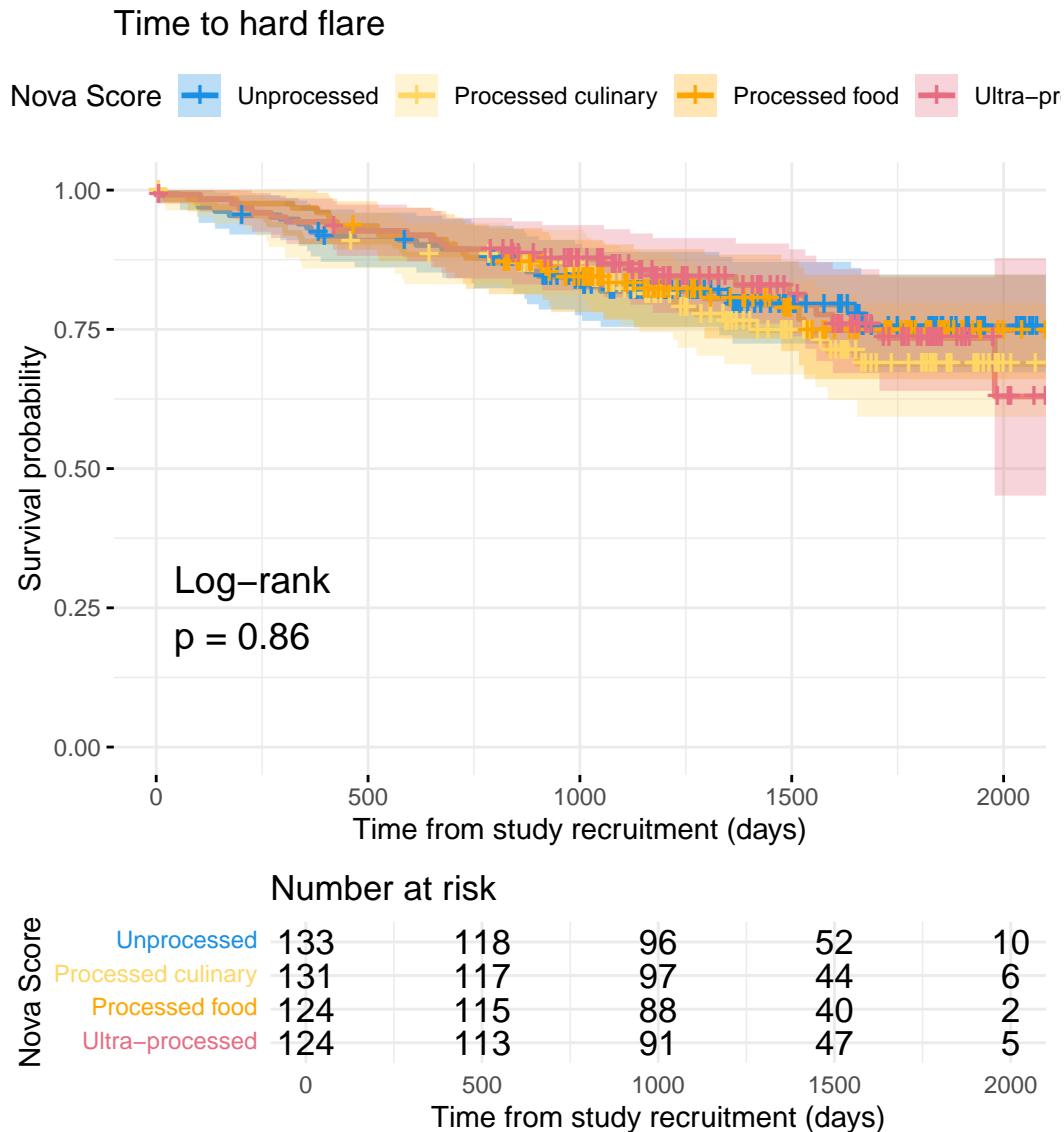
plot_base_path = "plots/cd/hard-flare/diet/nova",
break_time_by = 500
)

# Save plot as RDS
saveRDS(analysis_result$plot, paste0(paths$outdir, "nova-cd-hard.RDS"))

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(hardflare_time, hardflare) ~
    Sex + cat + IMD + dqi_tot + BMI + NOVAScore_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.cd.df
)

# Display plot and model summary
analysis_result$plot

```



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.3765	0.9071	2.0889	0.1332
catFC 50-250	1.9265	1.2064	3.0765	0.0060
catFC > 250	3.0753	1.8471	5.1204	0.0000

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	0.5750	0.2455	1.3464	0.2024
IMD3	0.7991	0.3604	1.7718	0.5810
IMD4	0.7288	0.3351	1.5848	0.4247
IMD5	0.6597	0.3155	1.3792	0.2689
dqi_tot	1.0045	0.9866	1.0228	0.6226
BMI	1.0213	0.9859	1.0579	0.2409
NOVAScore_catProcessed cu	1.4982	0.8659	2.5924	0.1484
NOVAScore_catProcessed fo	1.3744	0.7708	2.4508	0.2812
NOVAScore_catUltra-proces	1.0451	0.5865	1.8623	0.8809

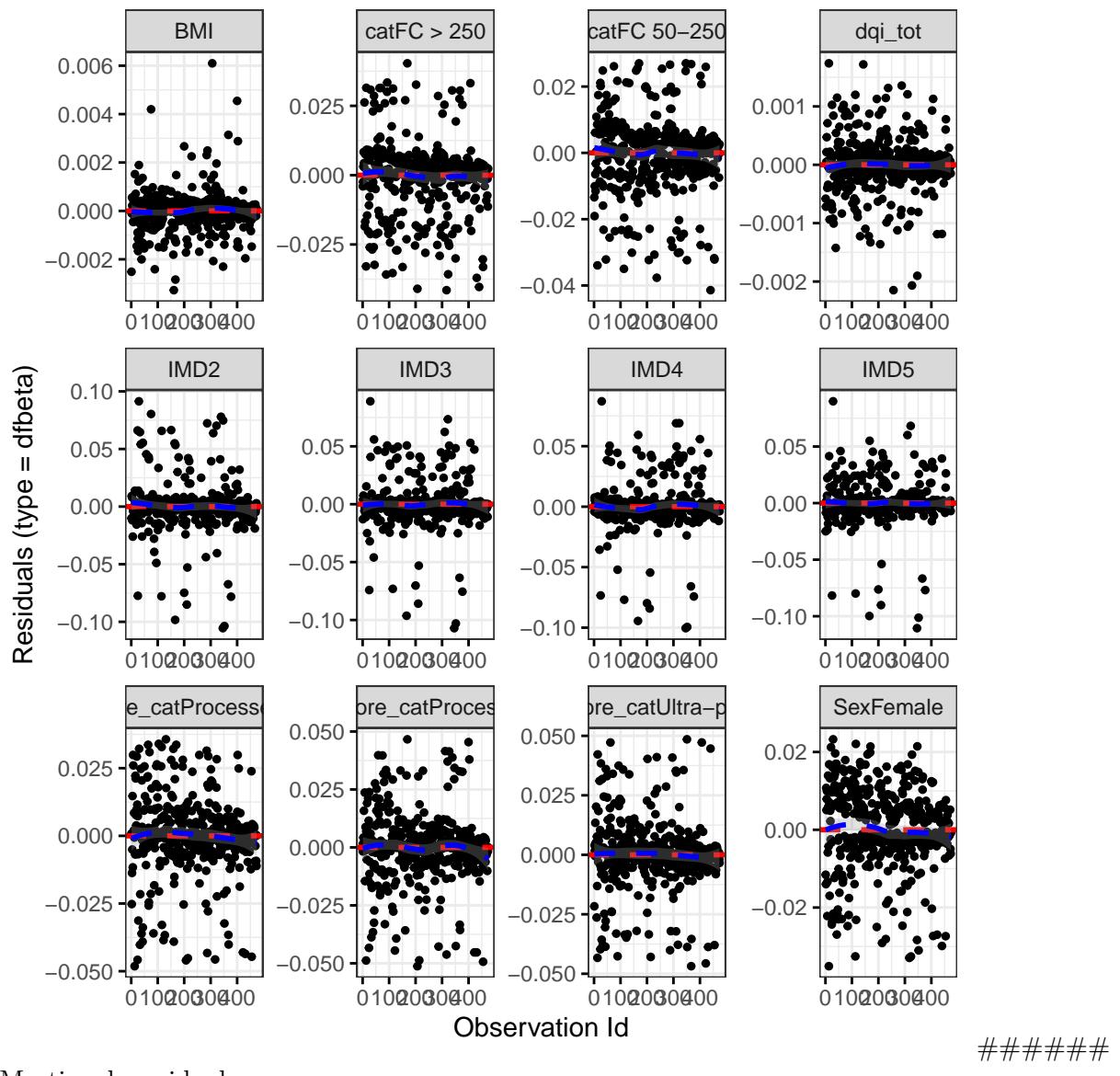
Diagnostics:

Proportional hazards assumption test

	Chi-squared statistic	DF	P-value
Sex	0.0551	0.9677	0.8032
cat	10.1241	1.9797	0.0062
IMD	2.6049	3.9203	0.6136
dqi_tot	2.6694	0.9897	0.1009
BMI	1.3680	0.9768	0.2359
NOVAScore_cat	2.7791	2.9458	0.4173
GLOBAL	17.0559	18.9993	0.5860

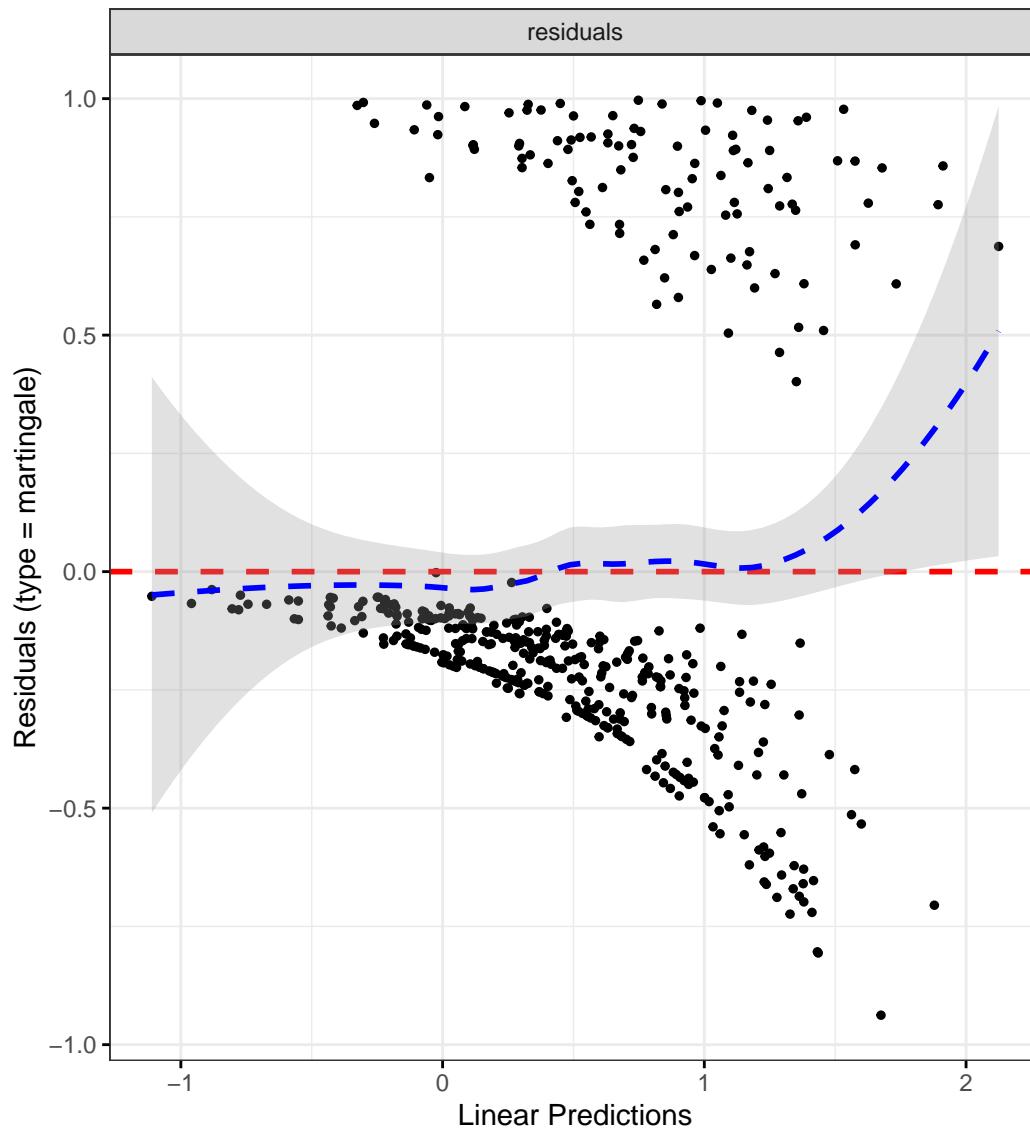
DF betas

```
`geom_smooth()` using formula = 'y ~ x'
```



Martingale residuals

```
`geom_smooth()` using formula = 'y ~ x'
```



Ulcerative colitis

Patient-reported flare

```
# Run survival analysis using utility function
analysis_result <- run_survival_analysis(
  data = flare.uc.df,
  var_name = "NOVAScore",
  outcome_time = "softflare_time",
```

```

  outcome_event = "softflare",
  legend_title = "Nova score",
  plot_base_path = "plots/uc/soft-flare/diet/nova",
  break_time_by = 200
)

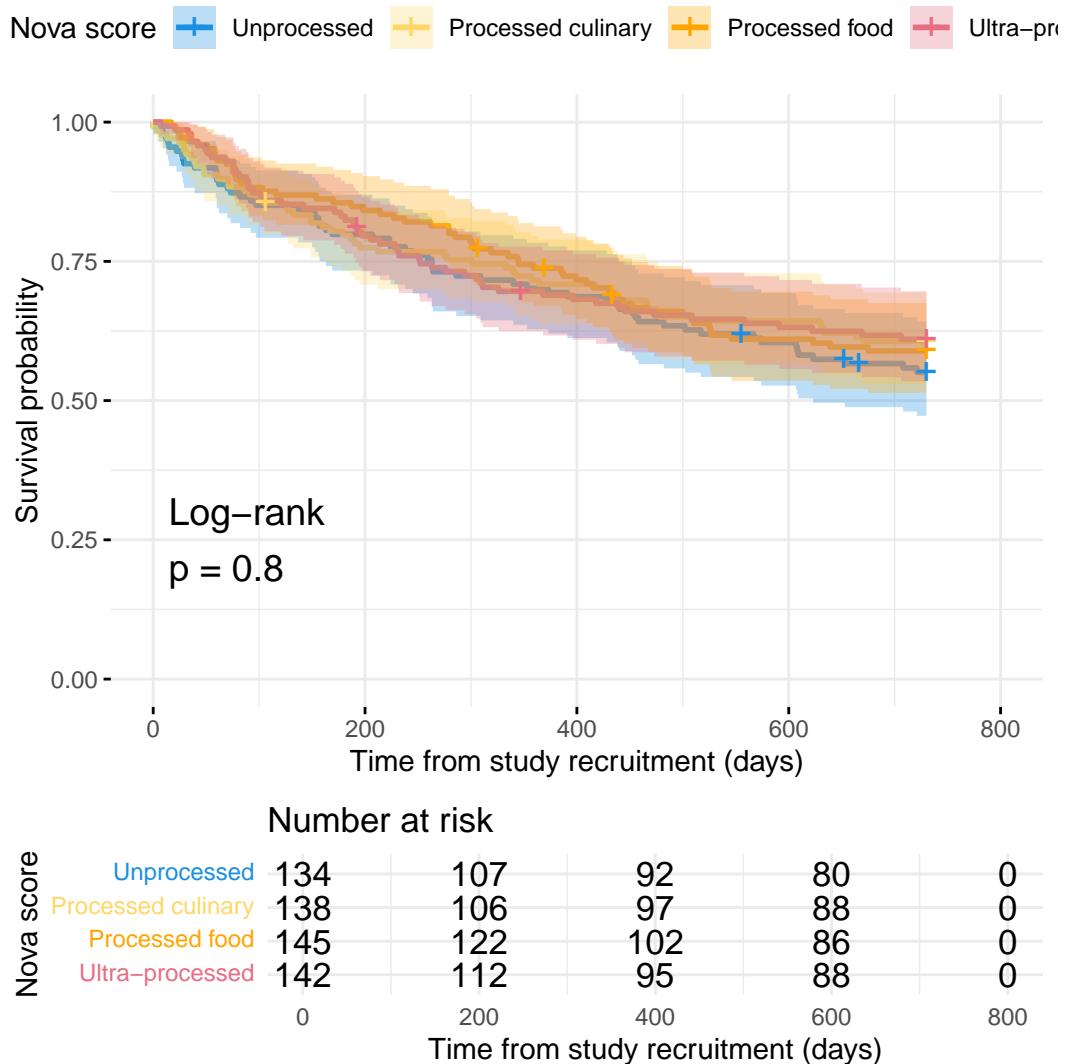
# Save plot as RDS
saveRDS(analysis_result$plot, paste0(paths$outdir, "nova-uc-soft.RDS"))

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(softflare_time, softflare) ~
    Sex + cat + IMD + dqi_tot + BMI + NOVAScore_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.uc.df
)

# Display plot and model summary
analysis_result$plot

```

Time to patient-reported flare



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.6755	1.2539	2.2390	0.0005
catFC 50-250	1.7983	1.3085	2.4713	0.0003
catFC > 250	2.0842	1.4585	2.9783	0.0001

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	1.3629	0.7130	2.6053	0.3490
IMD3	1.1200	0.5942	2.1110	0.7260
IMD4	1.3073	0.7193	2.3759	0.3794
IMD5	1.1683	0.6489	2.1034	0.6041
dqi_tot	0.9997	0.9869	1.0126	0.9617
BMI	0.9764	0.9475	1.0063	0.1206
NOVAScore_catProcessed cu	0.8762	0.5993	1.2810	0.4953
NOVAScore_catProcessed fo	0.8984	0.6159	1.3105	0.5781
NOVAScore_catUltra-proces	0.8615	0.5817	1.2758	0.4568

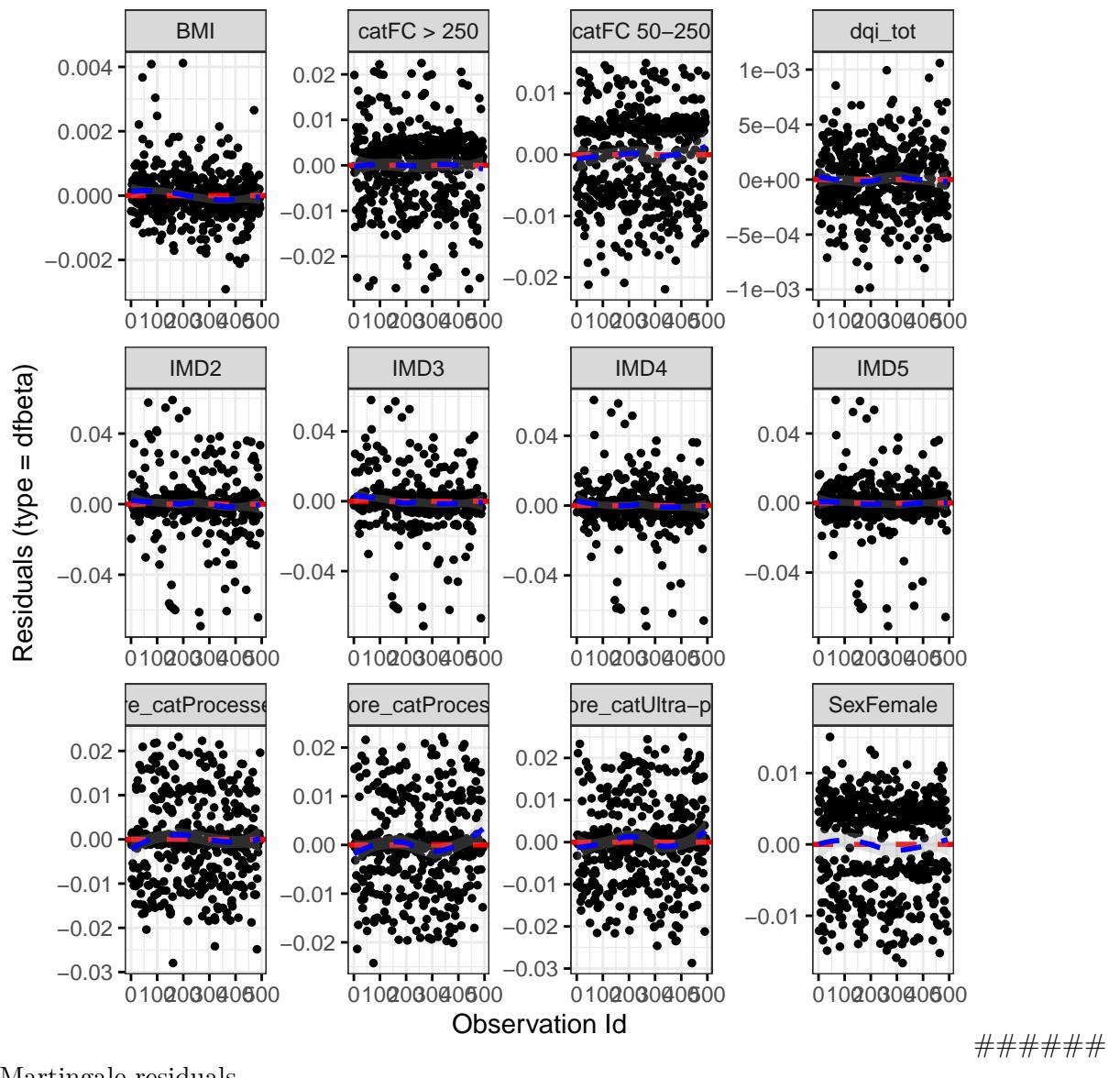
Diagnostics:

Proportional hazards assumption test

	Chi-squared statistic	DF	P-value
Sex	0.0068	1.0000	0.9341
cat	3.5965	2.0000	0.1656
IMD	2.6425	4.0000	0.6193
dqi_tot	0.7671	1.0000	0.3811
BMI	0.9279	1.0000	0.3354
NOVAScore_cat	2.4869	3.0000	0.4777
GLOBAL	11.7588	12.0001	0.4652

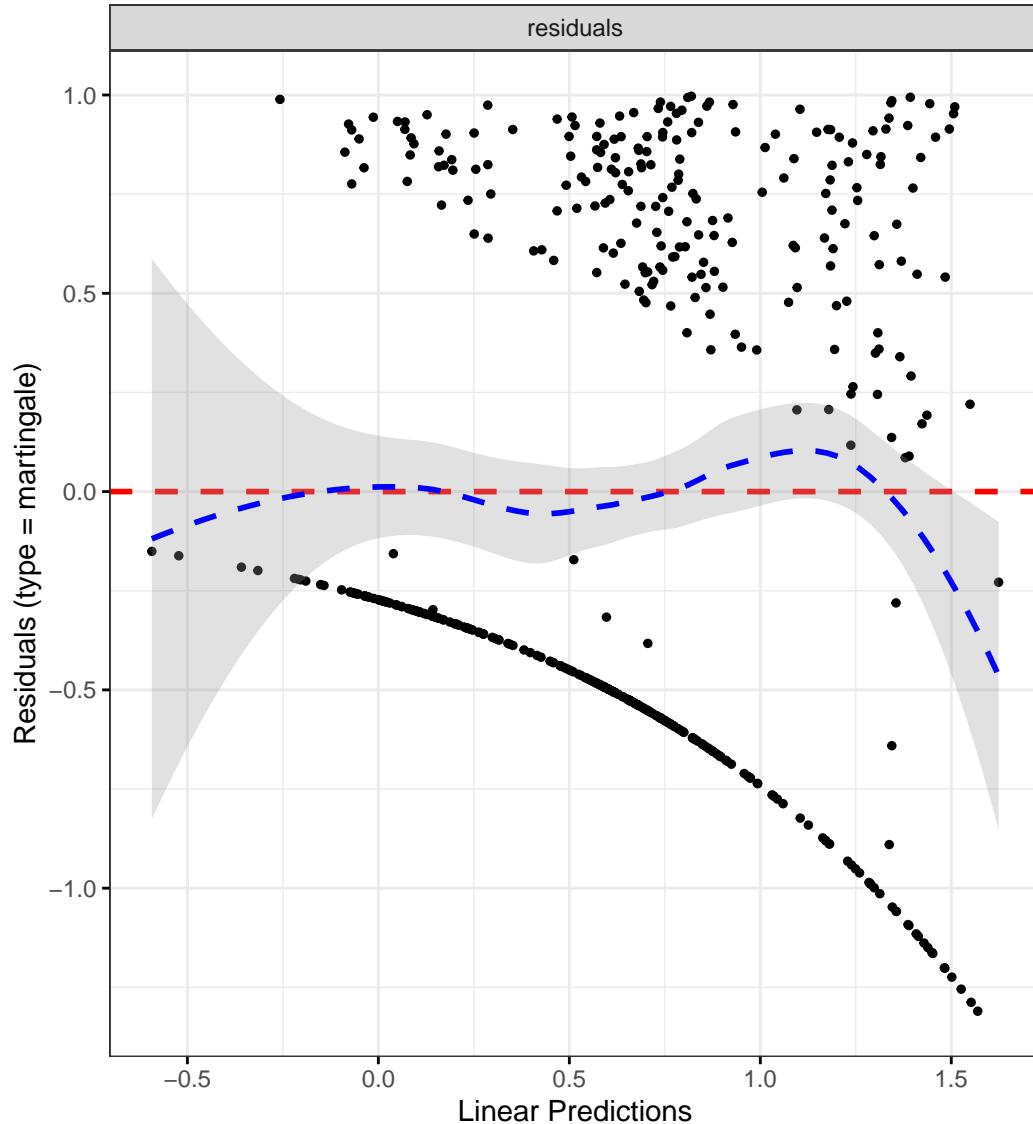
DF betas

```
`geom_smooth()` using formula = 'y ~ x'
```



Martingale residuals

```
`geom_smooth()` using formula = 'y ~ x'
```



Hard flare

```
# Run survival analysis using utility function for hard flare
analysis_result <- run_survival_analysis(
  data = flare.uc.df,
  var_name = "NOVAScore",
  outcome_time = "hardflare_time",
  outcome_event = "hardflare",
  legend_title = "Nova score",
```

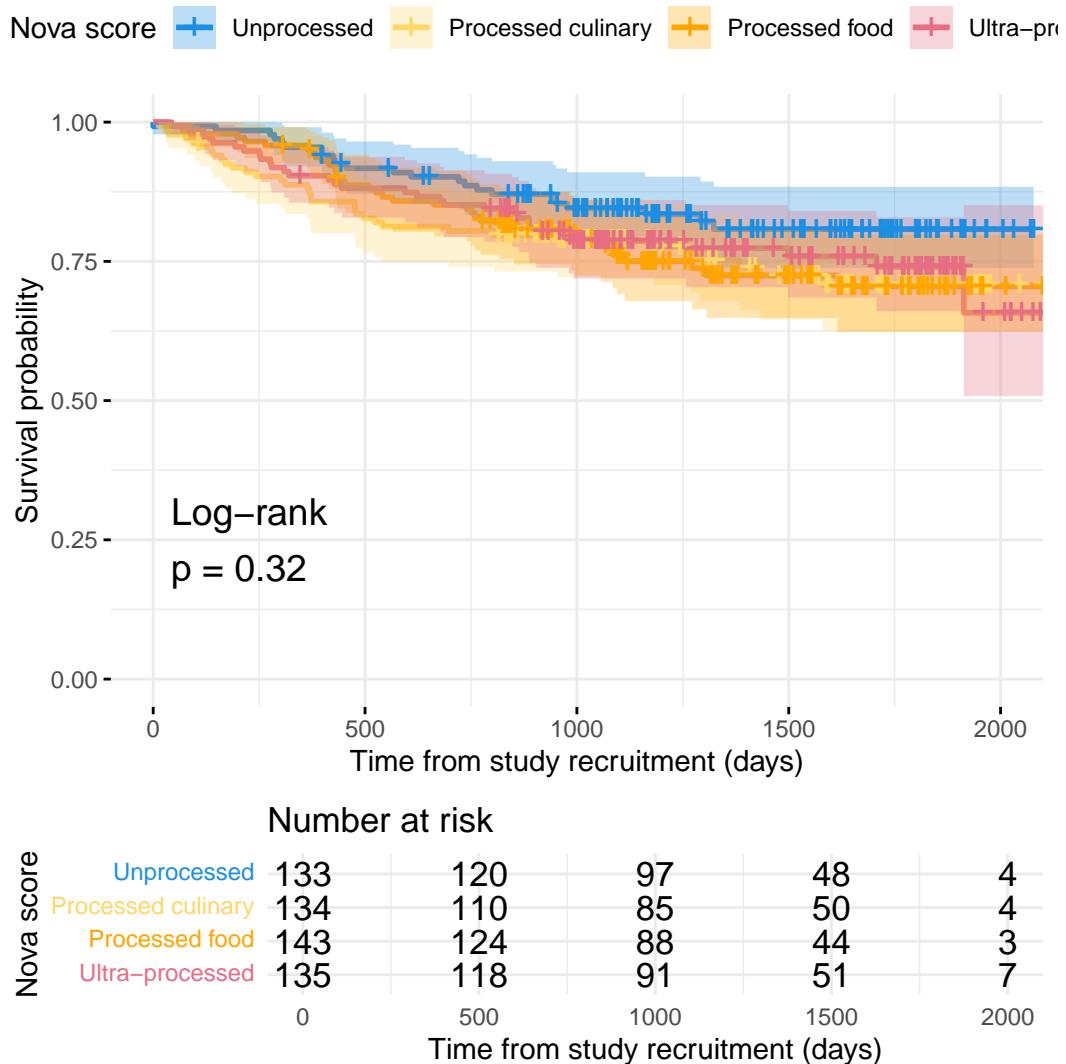
```
plot_base_path = "plots/uc/hard-flare/diet/nova",
break_time_by = 500
)

# Save plot as RDS
saveRDS(analysis_result$plot, paste0(paths$outdir, "nova-uc-hard.RDS"))

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(hardflare_time, hardflare) ~
    Sex + cat + IMD + dqi_tot + BMI + NOVAScore_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.uc.df
)

# Display plot and model summary
analysis_result$plot
```

Time to hard flare



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.2403	0.8458	1.8188	0.2703
catFC 50-250	2.0398	1.3207	3.1505	0.0013
catFC > 250	2.5646	1.5724	4.1832	0.0002

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	1.7138	0.6466	4.5423	0.2787
IMD3	1.4122	0.5442	3.6644	0.4781
IMD4	2.4869	1.0324	5.9903	0.0422
IMD5	1.4772	0.6083	3.5870	0.3888
dqi_tot	1.0022	0.9846	1.0200	0.8109
BMI	0.9636	0.9235	1.0053	0.0864
NOVAScore_catProcessed cu	1.5453	0.8991	2.6561	0.1153
NOVAScore_catProcessed fo	1.6050	0.9309	2.7674	0.0887
NOVAScore_catUltra-proces	1.4460	0.8215	2.5455	0.2011

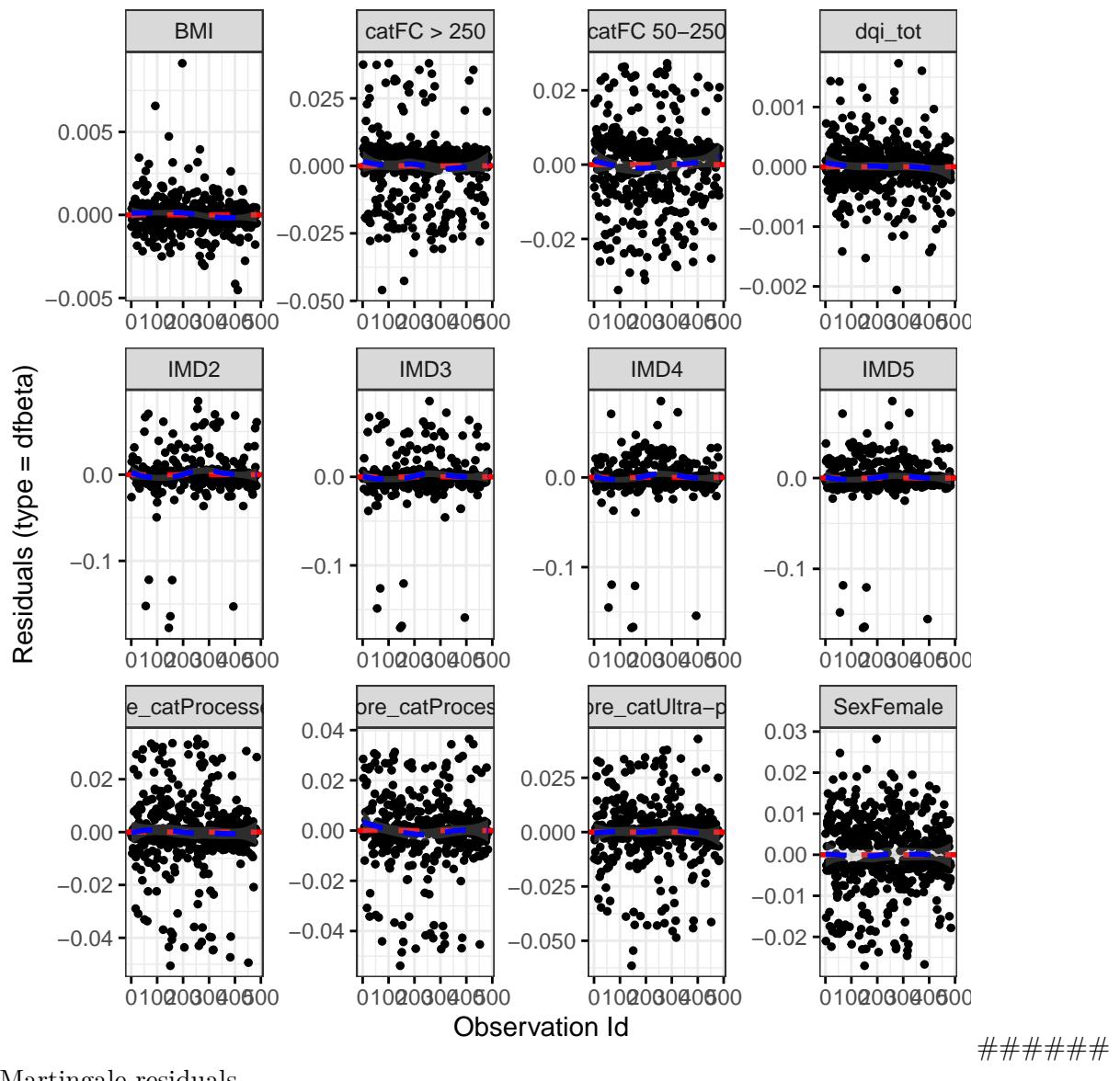
Diagnostics:

Proportional hazards assumption test

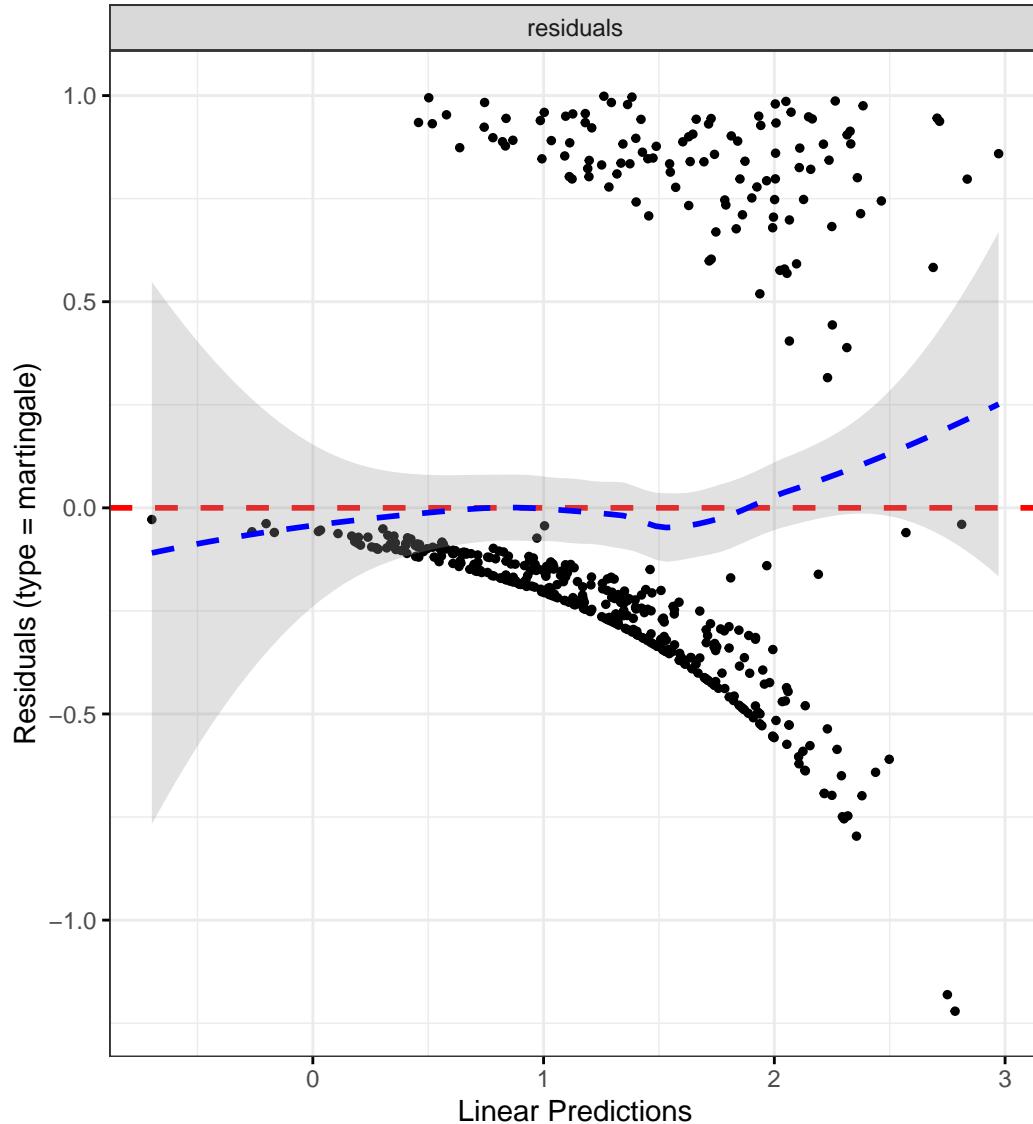
	Chi-squared statistic	DF	P-value
Sex	0.0230	0.9864	0.8756
cat	5.3361	1.9527	0.0664
IMD	1.1314	3.9238	0.8825
dqi_tot	0.0031	0.9868	0.9534
BMI	0.5418	0.9878	0.4569
NOVAScore_cat	5.2061	2.9510	0.1526
GLOBAL	12.9505	19.7960	0.8723

DF betas

```
`geom_smooth()` using formula = 'y ~ x'
```



```
`geom_smooth()` using formula = 'y ~ x'
```



Inflammatory bowel disease

Patient-reported flare

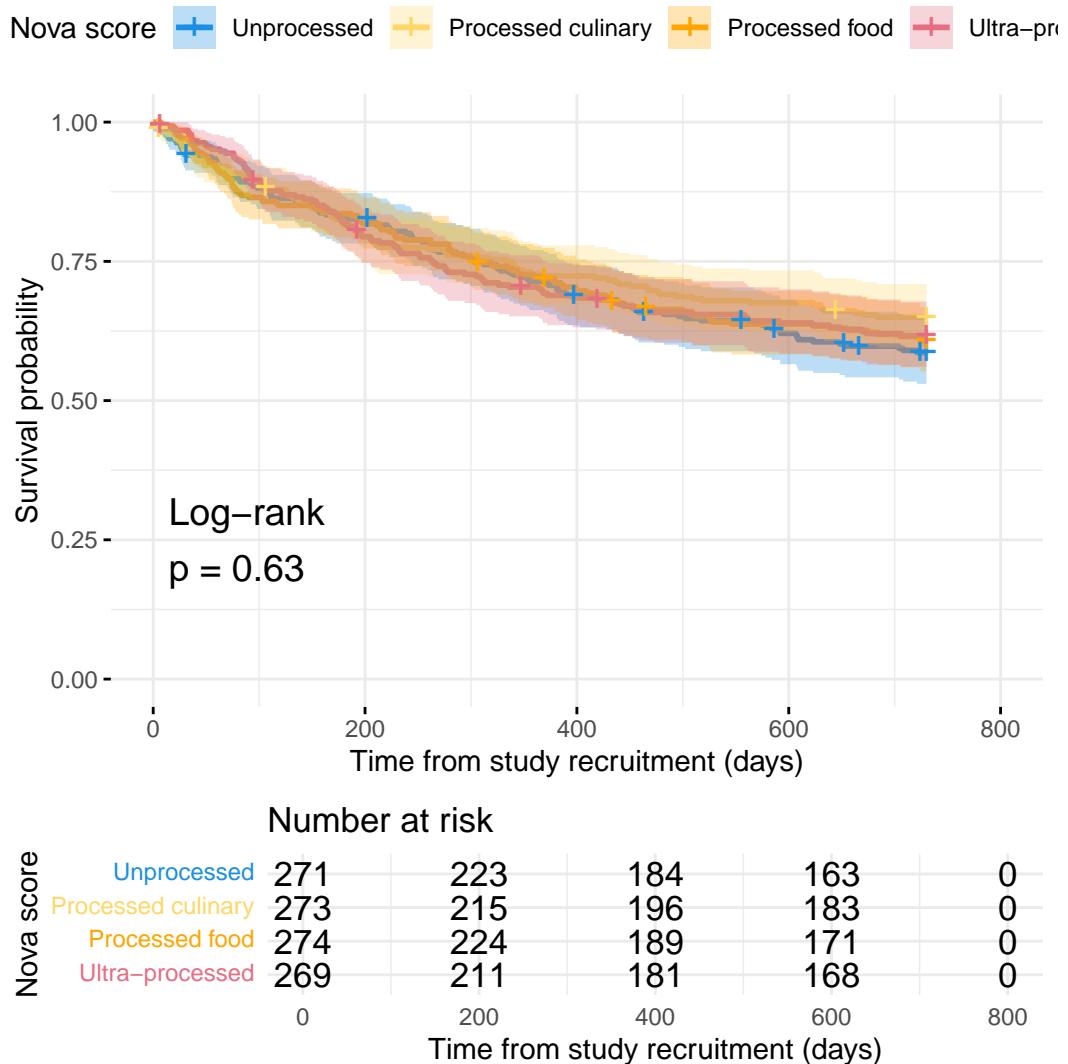
```
# Run survival analysis using utility function
analysis_result <- run_survival_analysis(
  data = flare.df,
  var_name = "NOVAScore",
  outcome_time = "softflare_time",
```

```
outcome_event = "softflare",
legend_title = "Nova score",
plot_base_path = "plots/ibd/soft-flare/diet/nova",
break_time_by = 200
)

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(softflare_time, softflare) ~
    Sex + cat + IMD + dqi_tot + BMI + NOVAScore_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.df
)

# Display plot and model summary
analysis_result$plot
```

Time to patient-reported flare



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.7682	1.4251	2.1939	0.0000
catFC 50-250	1.4961	1.1835	1.8912	0.0008
catFC > 250	2.0124	1.5527	2.6082	0.0000

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	0.9890	0.6278	1.5580	0.9620
IMD3	1.0112	0.6550	1.5611	0.9600
IMD4	1.1080	0.7308	1.6800	0.6290
IMD5	1.0847	0.7257	1.6212	0.6919
dqi_tot	1.0027	0.9935	1.0121	0.5656
BMI	0.9950	0.9752	1.0153	0.6287
NOVAScore_catProcessed cu	0.8931	0.6731	1.1849	0.4331
NOVAScore_catProcessed fo	0.9836	0.7431	1.3020	0.9081
NOVAScore_catUltra-proces	0.9197	0.6909	1.2243	0.5665

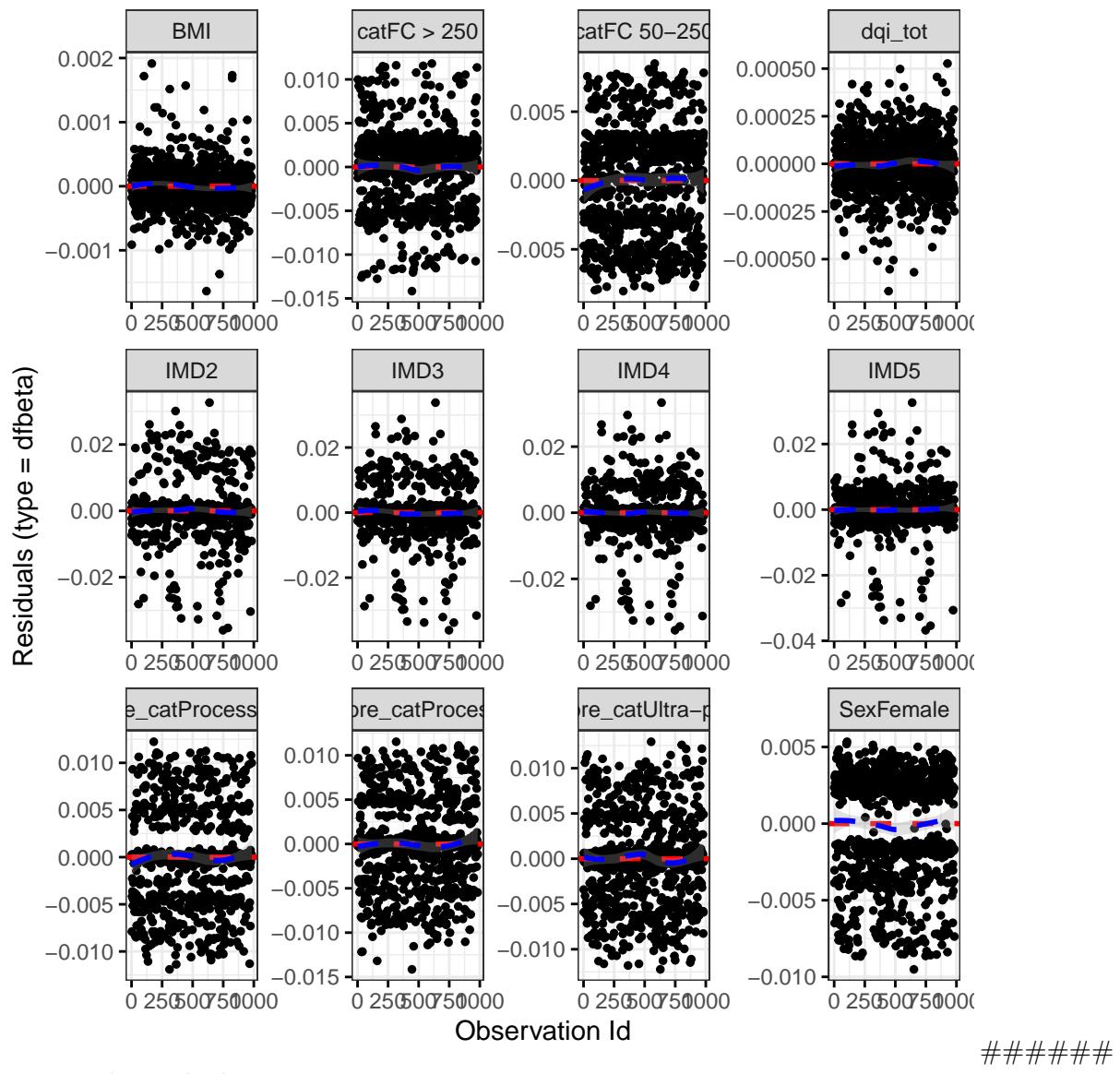
Diagnostics:

Proportional hazards assumption test

	Chi-squared statistic	DF	P-value
Sex	0.0048	1.0000	0.9445
cat	1.1276	2.0000	0.5690
IMD	5.0570	4.0000	0.2815
dqi_tot	1.3838	1.0000	0.2395
BMI	0.0111	1.0000	0.9162
NOVAScore_cat	3.0069	3.0000	0.3906
GLOBAL	10.9489	12.0002	0.5333

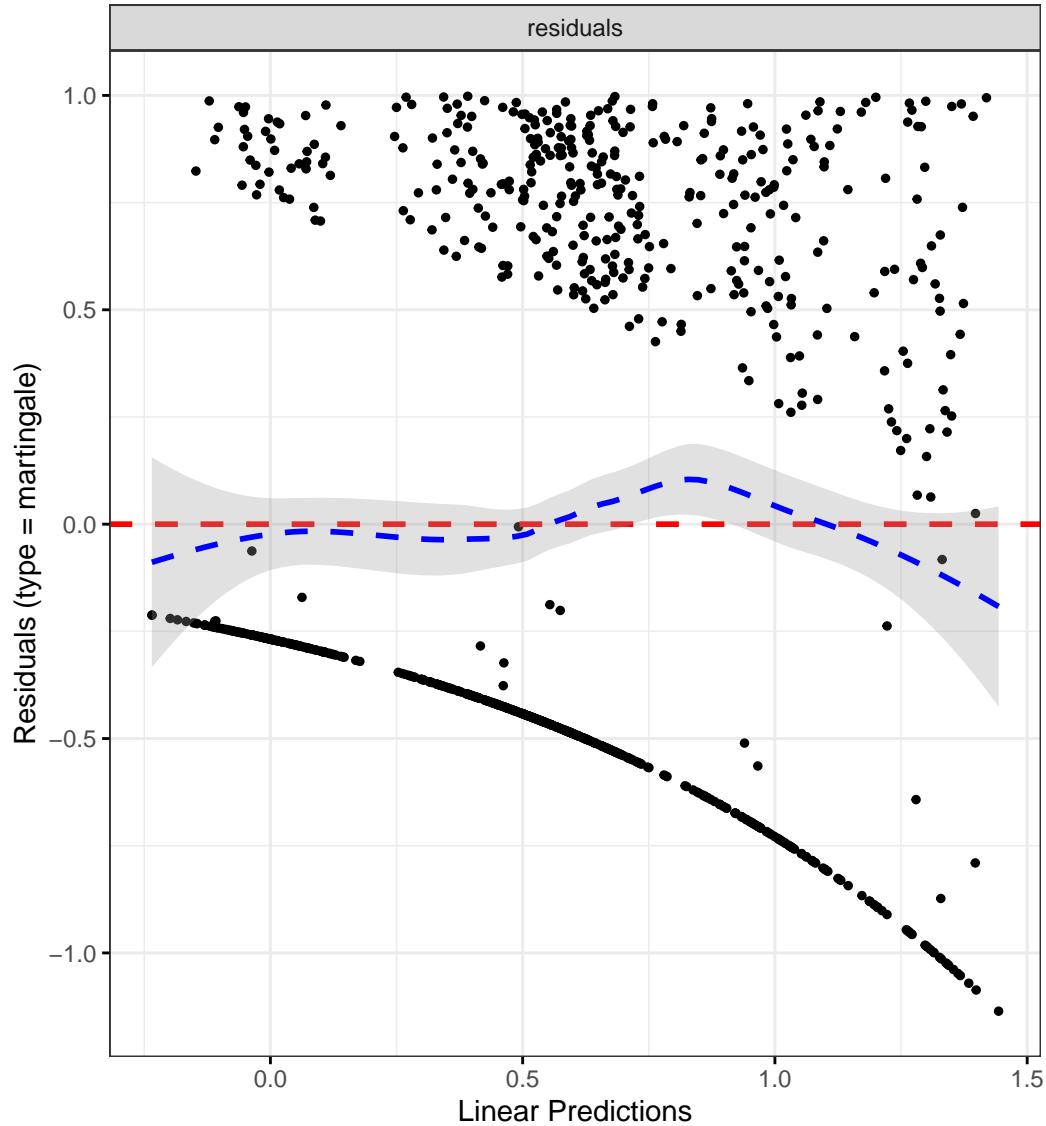
DF betas

```
`geom_smooth()` using formula = 'y ~ x'
```



Martingale residuals

```
`geom_smooth()` using formula = 'y ~ x'
```



Hard flare

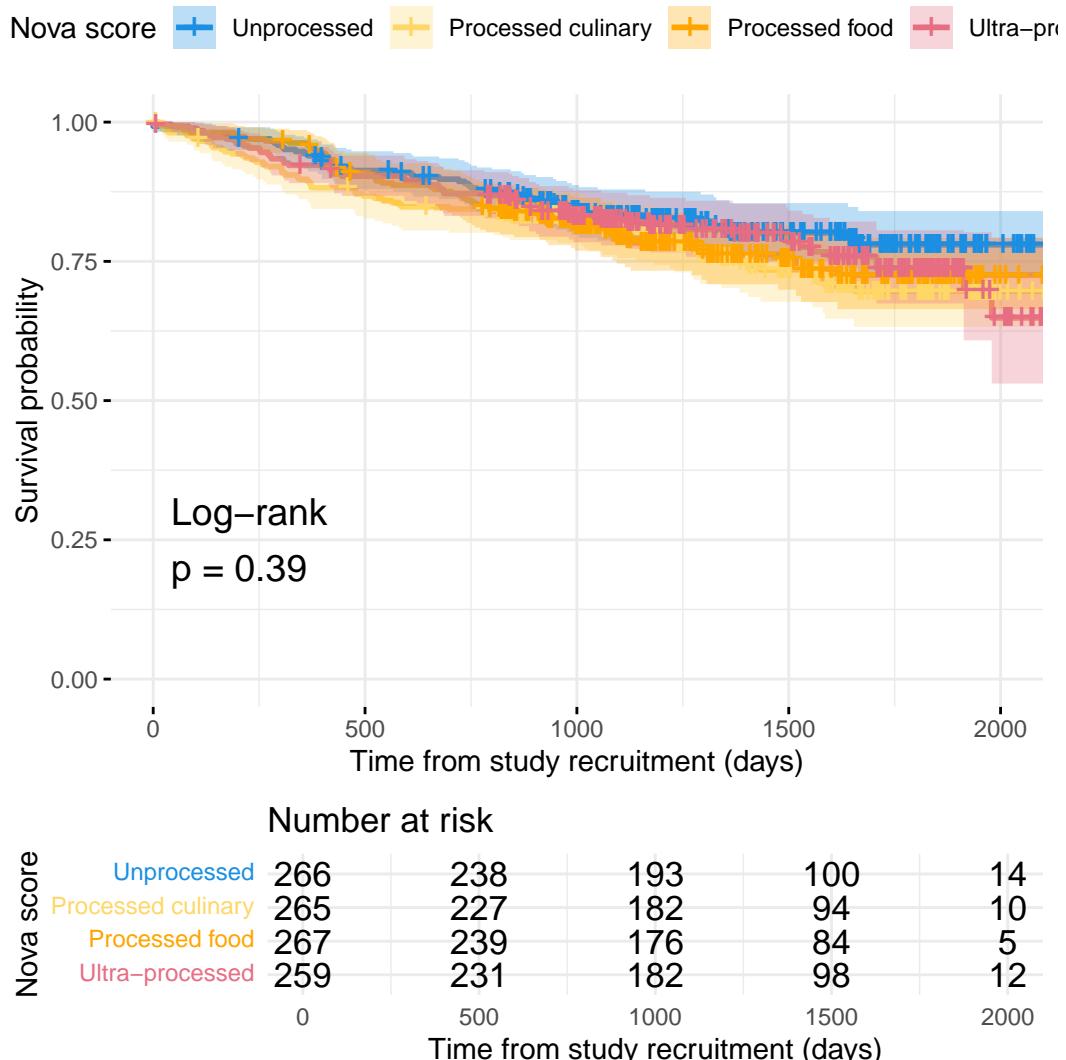
```
# Run survival analysis using utility function for hard flare
analysis_result <- run_survival_analysis(
  data = flare.df,
  var_name = "NOVAScore",
  outcome_time = "hardflare_time",
  outcome_event = "hardflare",
  legend_title = "Nova score",
```

```
plot_base_path = "plots/ibd/hard-flare/diet/nova",
break_time_by = 500
)

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(hardflare_time, hardflare) ~
    Sex + cat + IMD + dqi_tot + BMI + NOVAScore_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.df
)

# Display plot and model summary
analysis_result$plot
```

Time to hard flare



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.2847	0.9734	1.6954	0.0768
catFC 50-250	1.8810	1.3722	2.5785	0.0001
catFC > 250	2.7187	1.9203	3.8488	0.0000

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	0.9405	0.5026	1.7600	0.8479
IMD3	0.9990	0.5481	1.8208	0.9973
IMD4	1.3848	0.7883	2.4326	0.2575
IMD5	0.9837	0.5636	1.7171	0.9540
dqi_tot	1.0029	0.9906	1.0154	0.6447
BMI	0.9942	0.9677	1.0215	0.6741
NOVAScore_catProcessed cu	1.4771	1.0092	2.1621	0.0448
NOVAScore_catProcessed fo	1.4512	0.9798	2.1494	0.0631
NOVAScore_catUltra-proces	1.2239	0.8198	1.8272	0.3230

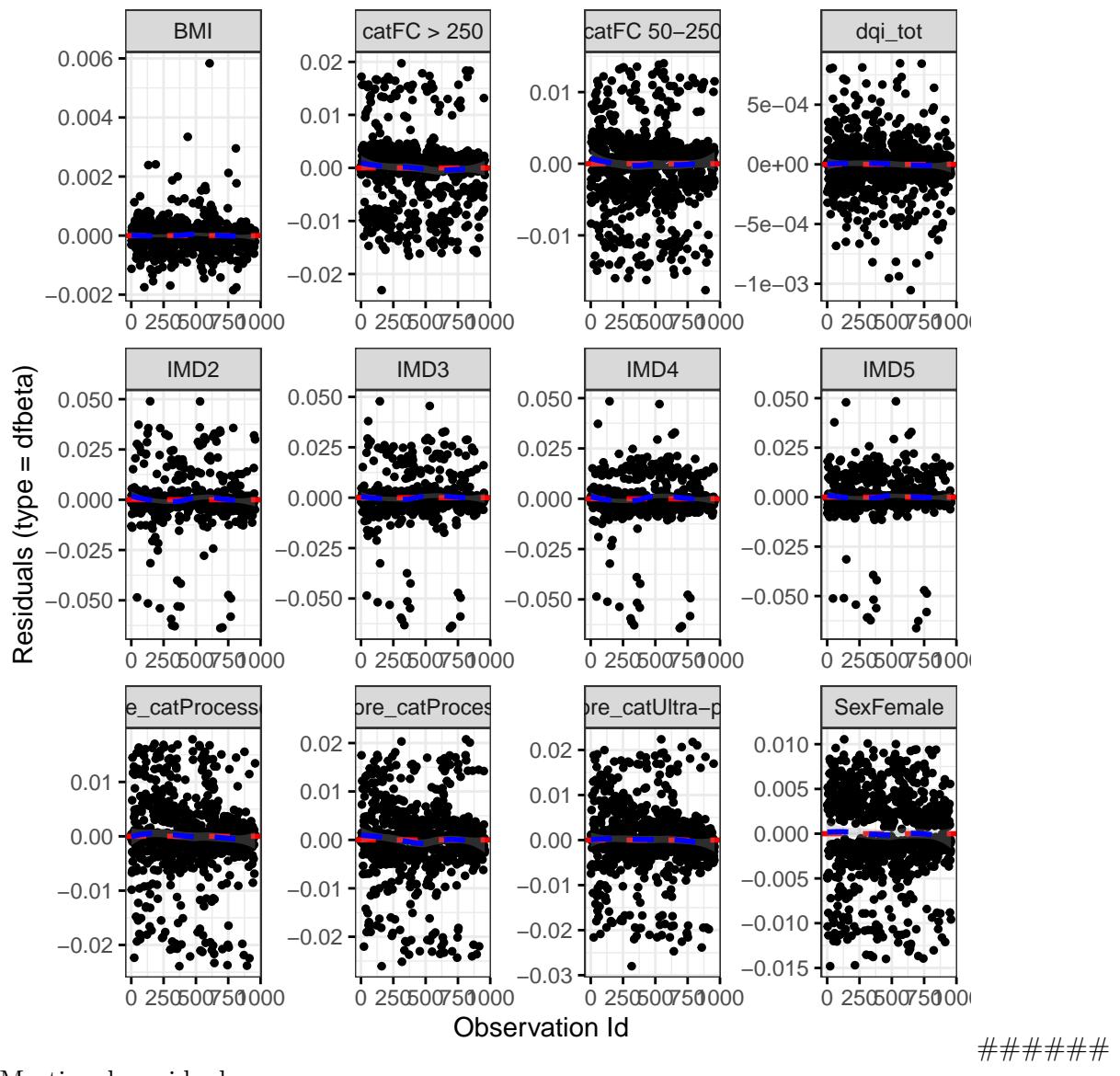
Diagnostics:

Proportional hazards assumption test

	Chi-squared statistic	DF	P-value
Sex	0.0289	0.9869	0.8611
cat	6.6825	1.9794	0.0347
IMD	1.5841	3.9431	0.8049
dqi_tot	1.9343	0.9922	0.1627
BMI	2.0039	0.9889	0.1547
NOVAScore_cat	2.8452	2.9706	0.4109
GLOBAL	13.9078	22.7588	0.9241

DF betas

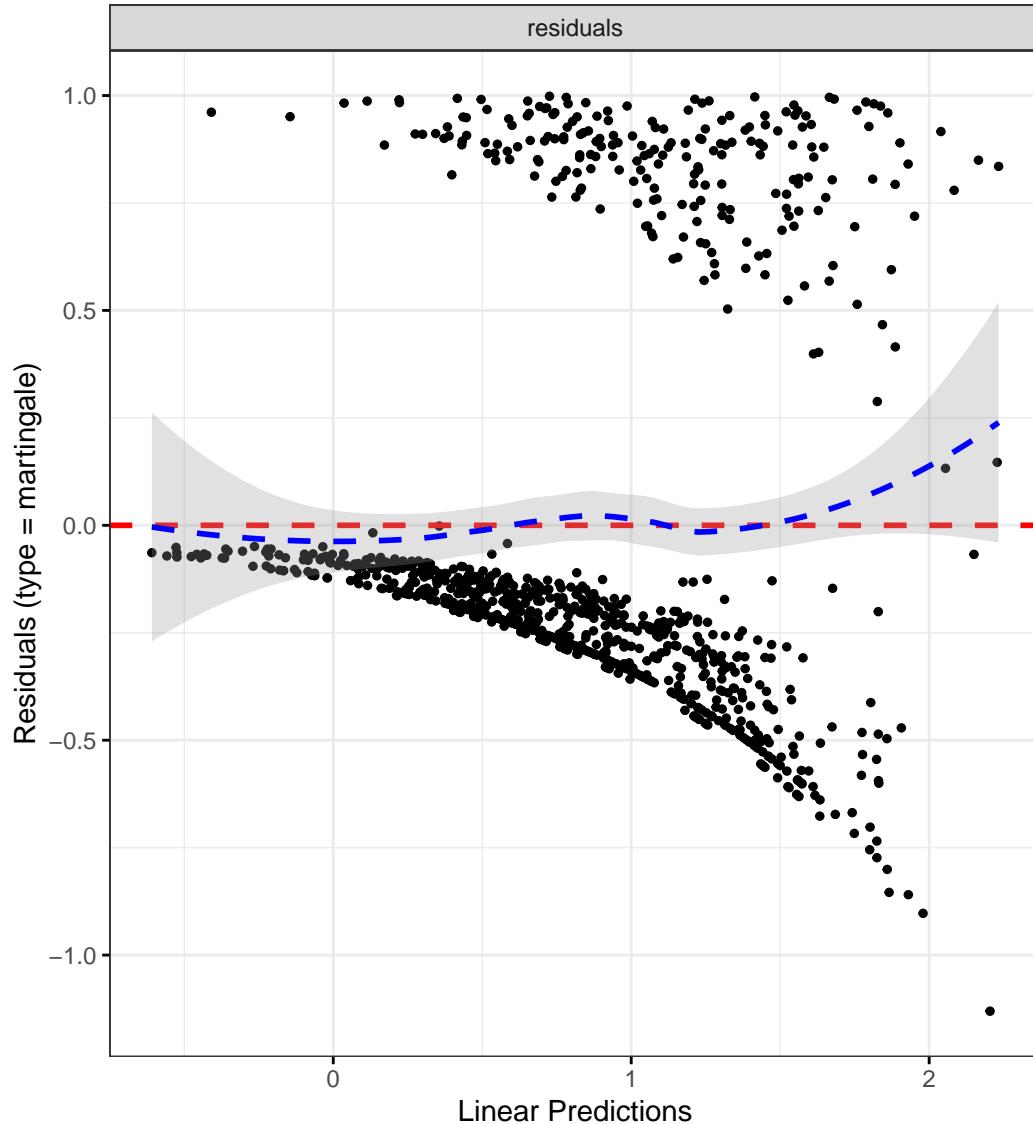
```
`geom_smooth()` using formula = 'y ~ x'
```



#####

Martingale residuals

```
`geom_smooth()` using formula = 'y ~ x'
```



UPF intake

As an alternative approach to characterising ultra-processed food, we considered the percentage of daily energy intake sourced from ultra-processed food and drink (Nova 4).

Crohn's disease

Patient-reported flare

```

# Categorize UPF percentage by quantiles
flare.cd.df <- categorize_by_quantiles(flare.cd.df, "UPF_perc", reference_data = flare.df)

# Run survival analysis using utility function
analysis_result <- run_survival_analysis(
  data = flare.cd.df,
  var_name = "UPF_perc",
  outcome_time = "softflare_time",
  outcome_event = "softflare",
  legend_title = "UPF as % of energy",
  plot_base_path = "plots/cd/soft-flare/diet/UPF",
  break_time_by = 200
)

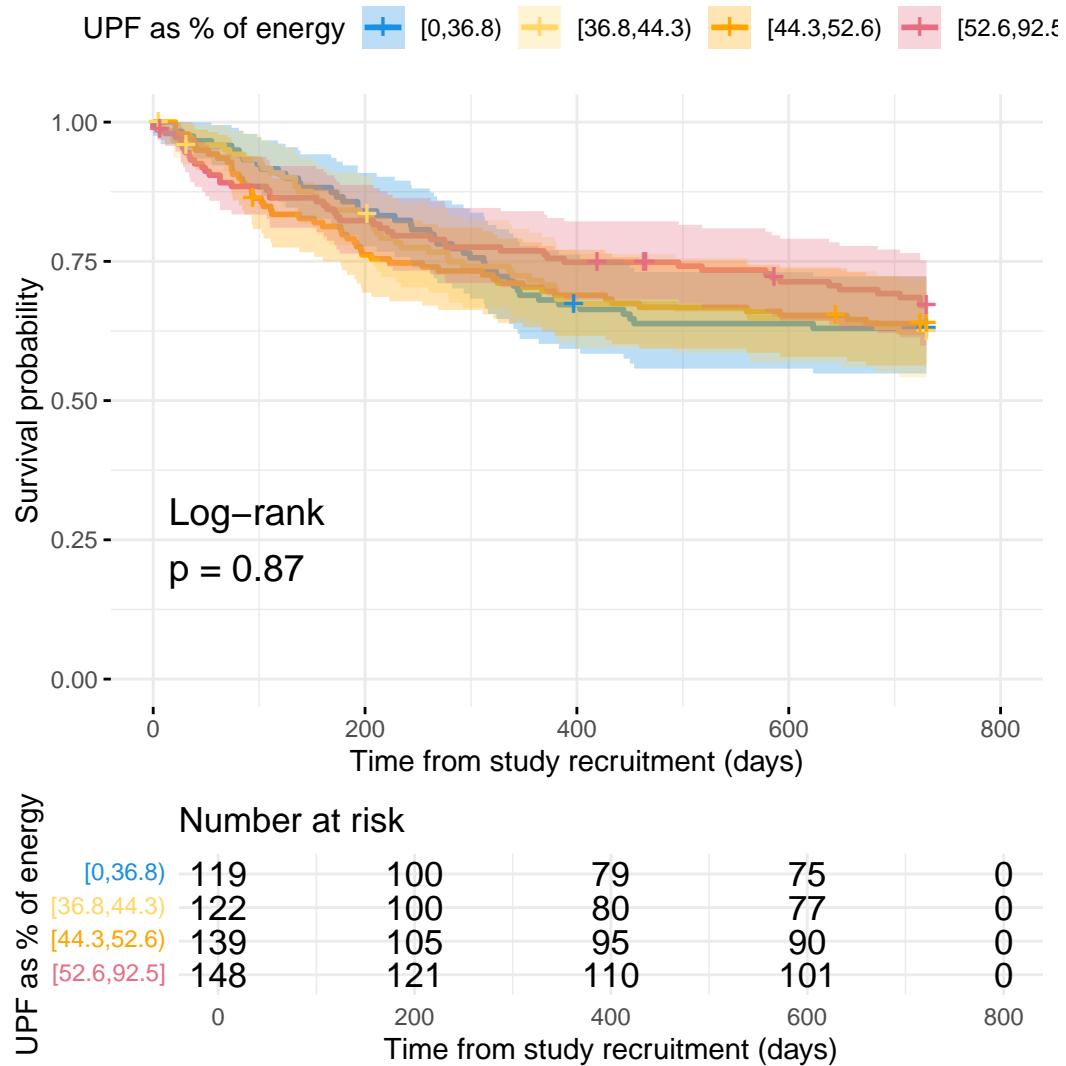
# Save plot as RDS
saveRDS(analysis_result$plot, paste0(paths$outdir, "upf-cd-soft.RDS"))

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(softflare_time, softflare) ~
    Sex + cat + IMD + dqi_tot + BMI + UPF_perc_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.cd.df
)

# Display plot and model summary
analysis_result$plot

```

Time to patient-reported flare



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.9145	1.3685	2.6784	0.0001
catFC 50-250	1.3268	0.9315	1.8898	0.1171
catFC > 250	2.0624	1.4060	3.0252	0.0002

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	0.6973	0.3640	1.3360	0.2772
IMD3	0.9313	0.5110	1.6972	0.8161
IMD4	0.8491	0.4683	1.5396	0.5901
IMD5	0.9655	0.5521	1.6885	0.9020
dqi_tot	1.0053	0.9913	1.0195	0.4614
BMI	1.0076	0.9802	1.0359	0.5903
UPF_perc_cat[36.8,44.3)	1.1193	0.7185	1.7437	0.6182
UPF_perc_cat[44.3,52.6)	1.1578	0.7484	1.7911	0.5104
UPF_perc_cat[52.6,92.5]	0.9745	0.6198	1.5322	0.9109

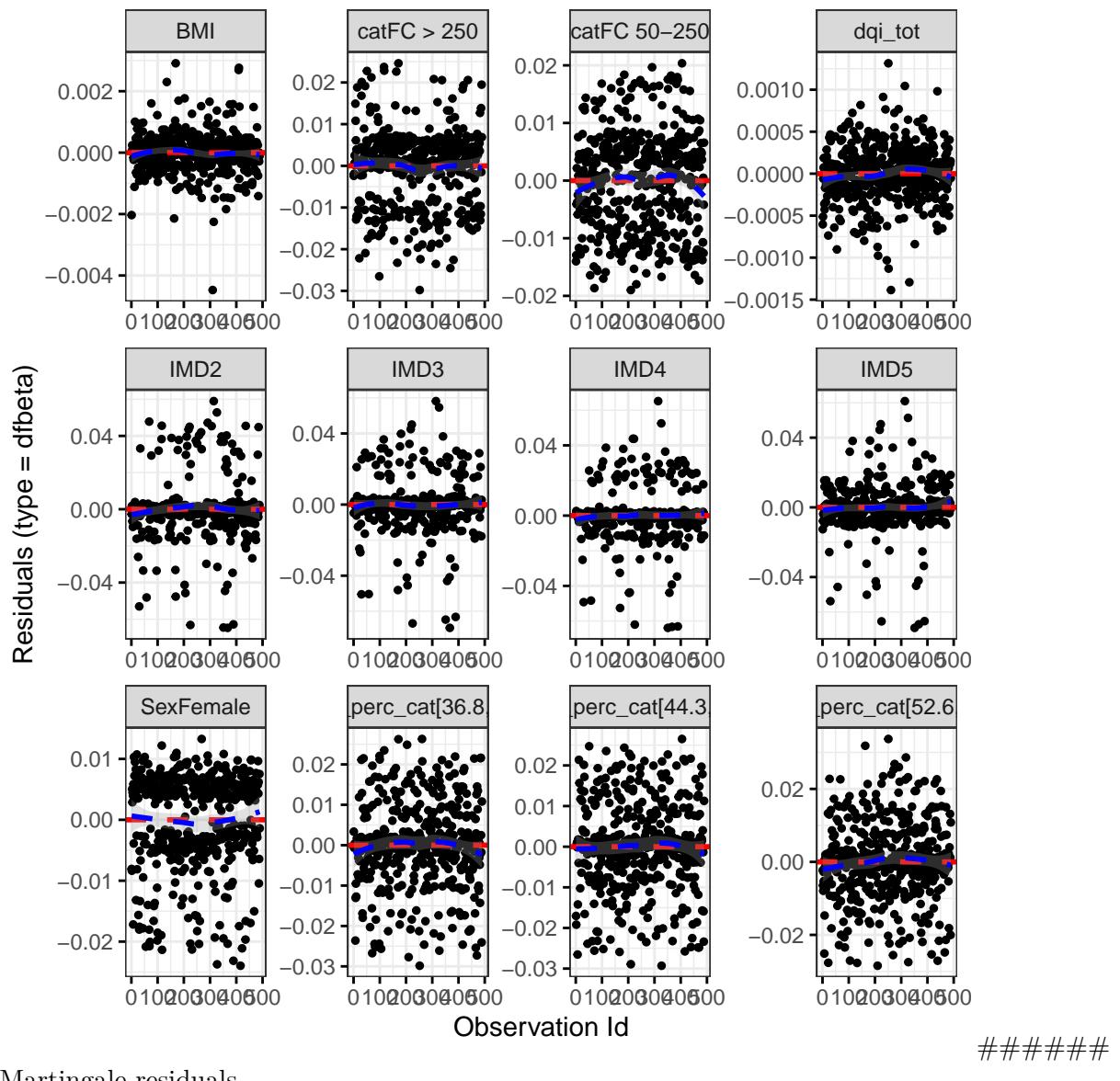
Diagnostics:

Proportional hazards assumption test

	Chi-squared statistic	DF	P-value
Sex	0.2738	1.0000	0.6008
cat	0.7941	2.0000	0.6723
IMD	3.0290	4.0000	0.5530
dqi_tot	0.3616	1.0000	0.5476
BMI	1.2818	1.0000	0.2576
UPF_perc_cat	5.2147	3.0000	0.1567
GLOBAL	10.1947	12.0001	0.5989

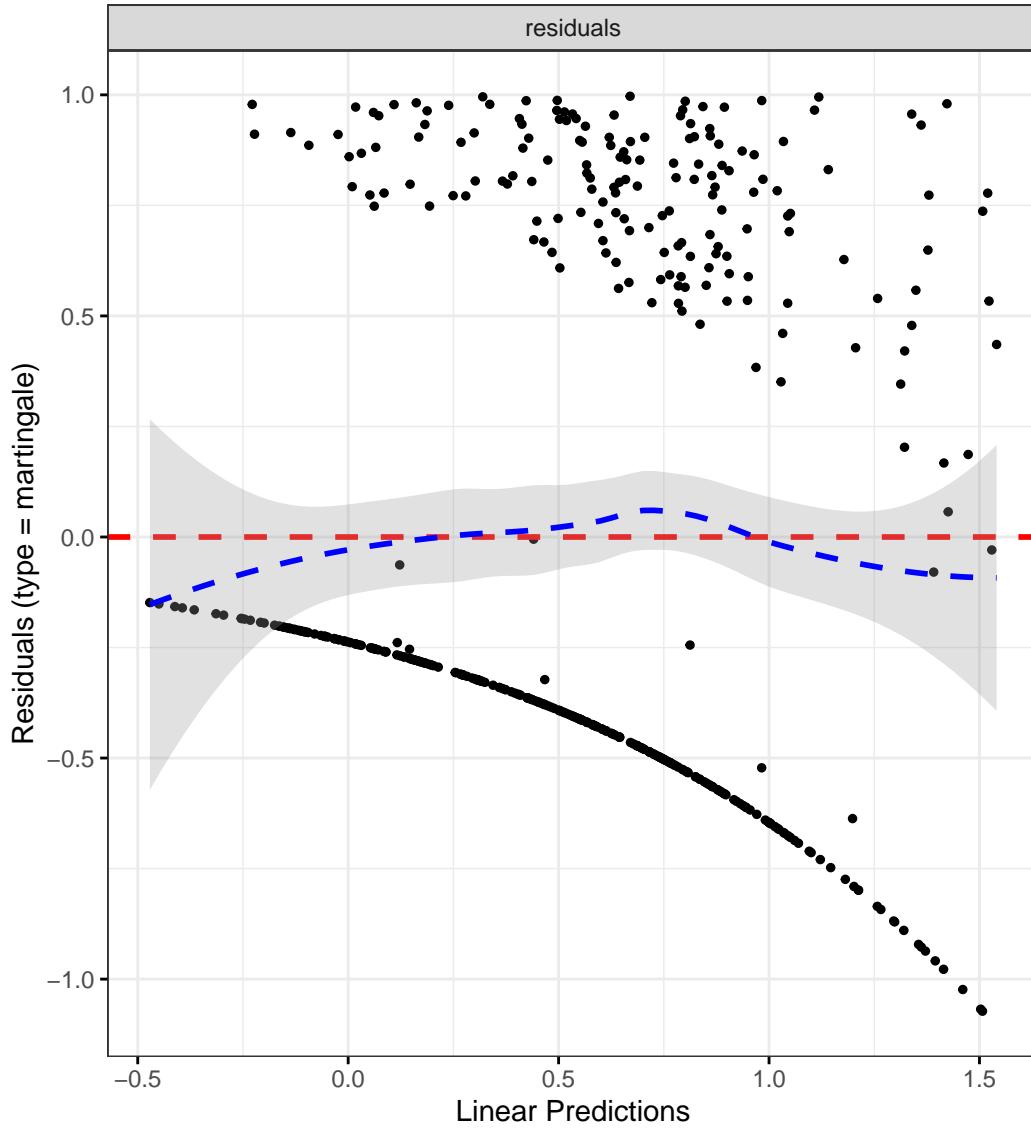
DF betas

```
`geom_smooth()` using formula = 'y ~ x'
```



Martingale residuals

```
`geom_smooth()` using formula = 'y ~ x'
```



Hard flare

```
# Run survival analysis using utility function for hard flare
analysis_result <- run_survival_analysis(
  data = flare.cd.df,
  var_name = "UPF_perc",
  outcome_time = "hardflare_time",
  outcome_event = "hardflare",
  legend_title = "UPF as % of energy",
```

```

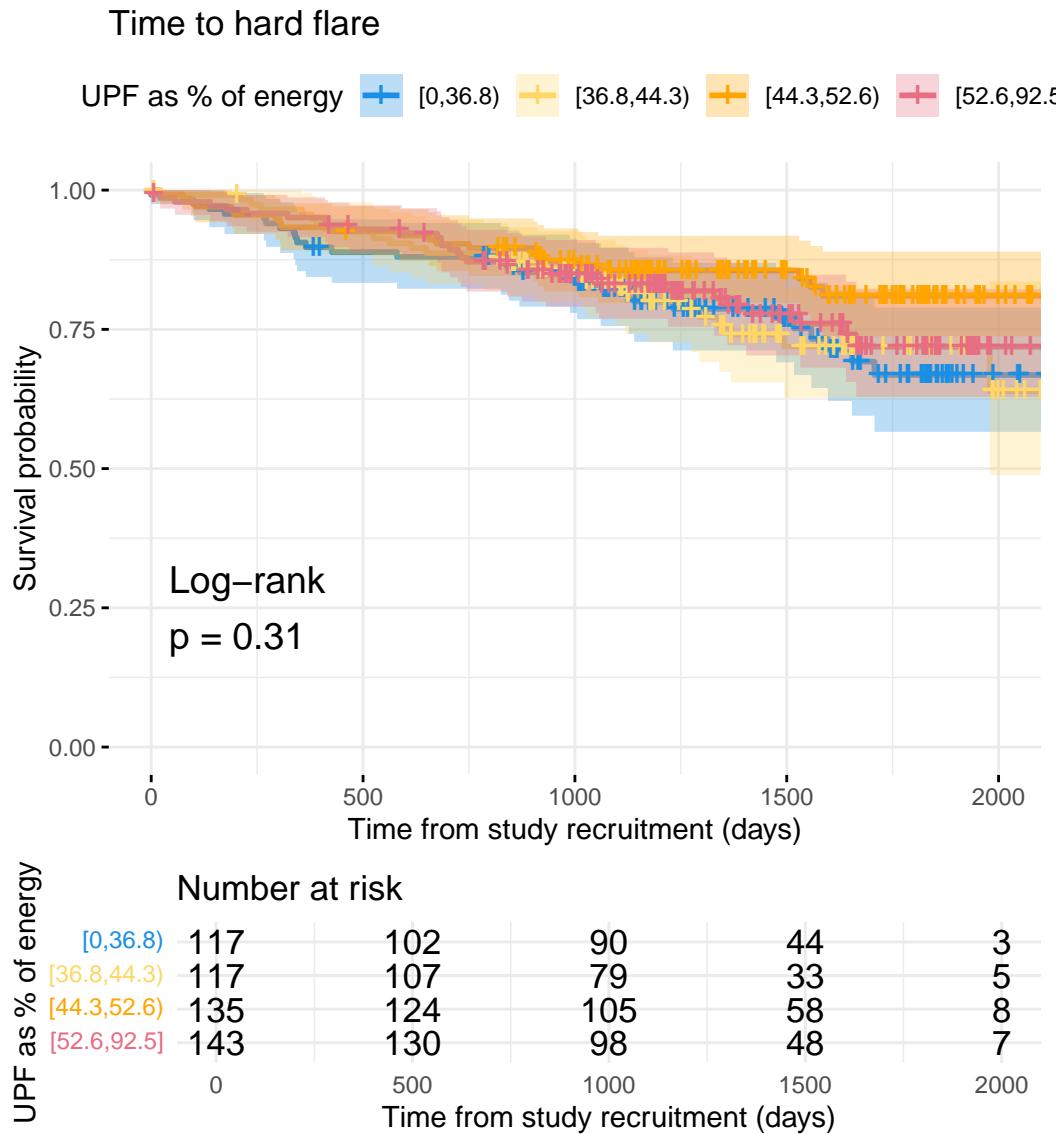
plot_base_path = "plots/cd/hard-flare/diet/UPF",
break_time_by = 500
)

# Save plot as RDS
saveRDS(analysis_result$plot, paste0(paths$outdir, "upf-cd-hard.RDS"))

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(hardflare_time, hardflare) ~
    Sex + cat + IMD + dqi_tot + BMI + UPF_perc_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.cd.df
)

# Display plot and model summary
analysis_result$plot

```



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.3186	0.8713	1.9957	0.1908
catFC 50-250	1.7965	1.1231	2.8737	0.0145
catFC > 250	2.8936	1.7406	4.8105	0.0000

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	0.6606	0.2850	1.5312	0.3337
IMD3	0.8629	0.3905	1.9070	0.7156
IMD4	0.8169	0.3771	1.7698	0.6081
IMD5	0.7533	0.3619	1.5679	0.4488
dqi_tot	1.0010	0.9826	1.0198	0.9154
BMI	1.0199	0.9848	1.0563	0.2691
UPF_perc_cat[36.8,44.3)	1.0173	0.5886	1.7582	0.9510
UPF_perc_cat[44.3,52.6)	0.6137	0.3424	1.1001	0.1011
UPF_perc_cat[52.6,92.5]	0.8593	0.4931	1.4977	0.5928

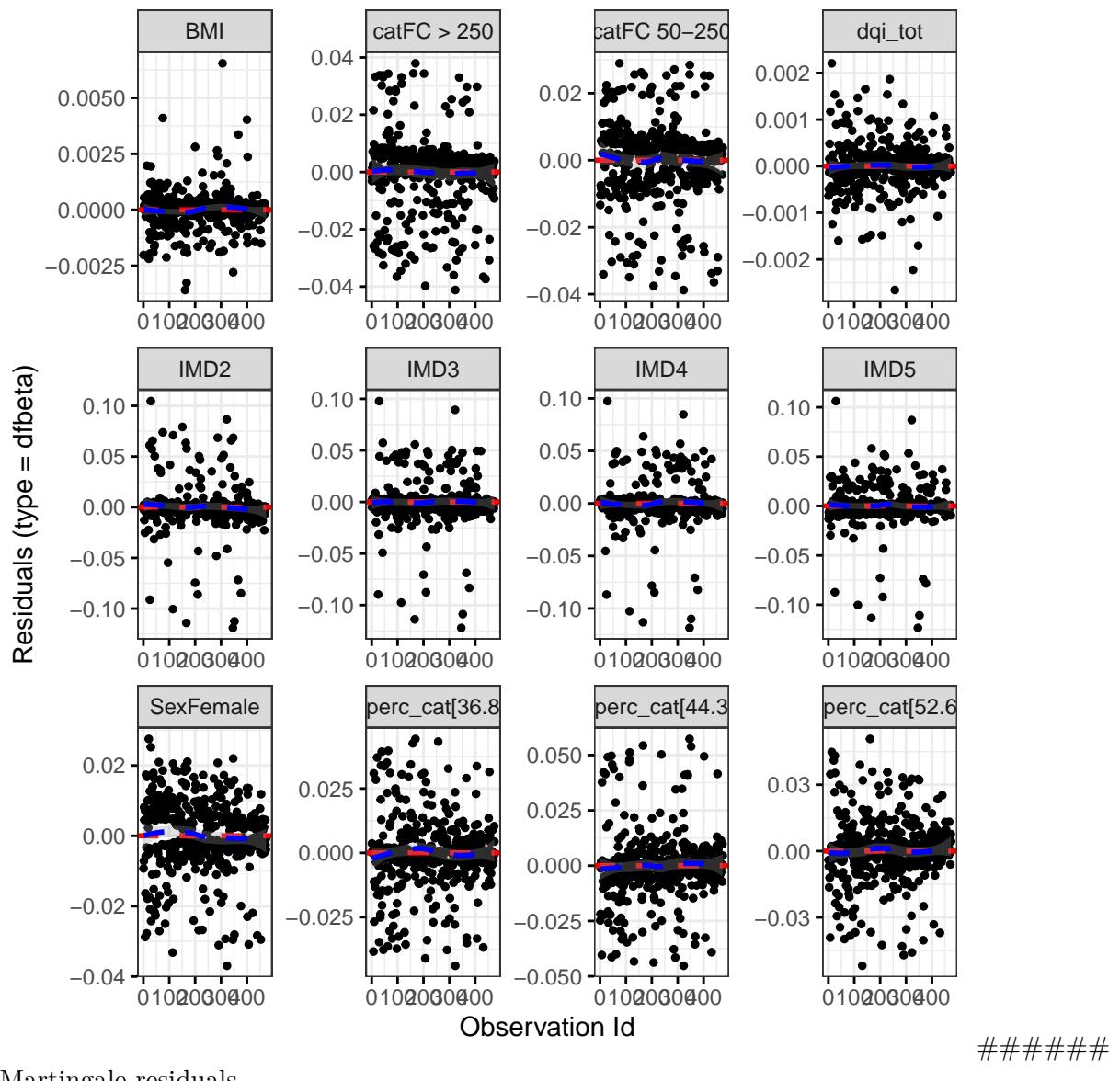
Diagnostics:

Proportional hazards assumption test

	Chi-squared statistic	DF	P-value
Sex	0.0409	0.9749	0.8316
cat	10.3600	1.9766	0.0055
IMD	2.6281	3.9274	0.6106
dqi_tot	2.6978	0.9900	0.0991
BMI	1.2001	0.9812	0.2678
UPF_perc_cat	1.9745	2.9726	0.5726
GLOBAL	18.0051	17.8046	0.4422

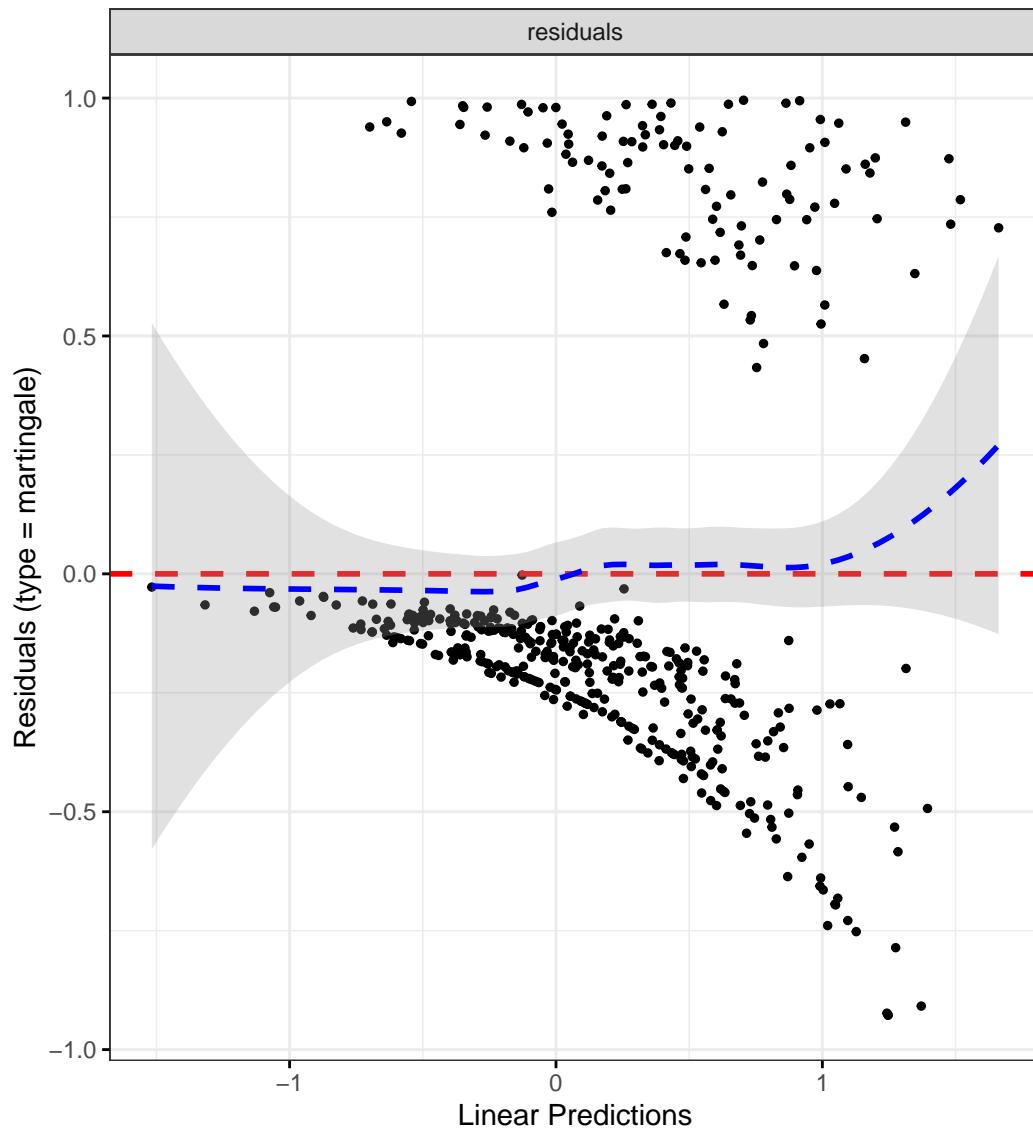
DF betas

```
`geom_smooth()` using formula = 'y ~ x'
```



Martingale residuals

```
`geom_smooth()` using formula = 'y ~ x'
```



Ulcerative colitis

Patient-reported flare

```
# Categorize UPF percentage by quantiles
flare.uc.df <- categorize_by_quantiles(flare.uc.df, "UPF_perc", reference_data = flare.df)

# Run survival analysis using utility function
analysis_result <- run_survival_analysis(
```

```

data = flare.uc.df,
var_name = "UPF_perc",
outcome_time = "softflare_time",
outcome_event = "softflare",
legend_title = "UPF as % of energy",
plot_base_path = "plots/uc/soft-flare/diet/UPF",
break_time_by = 200
)

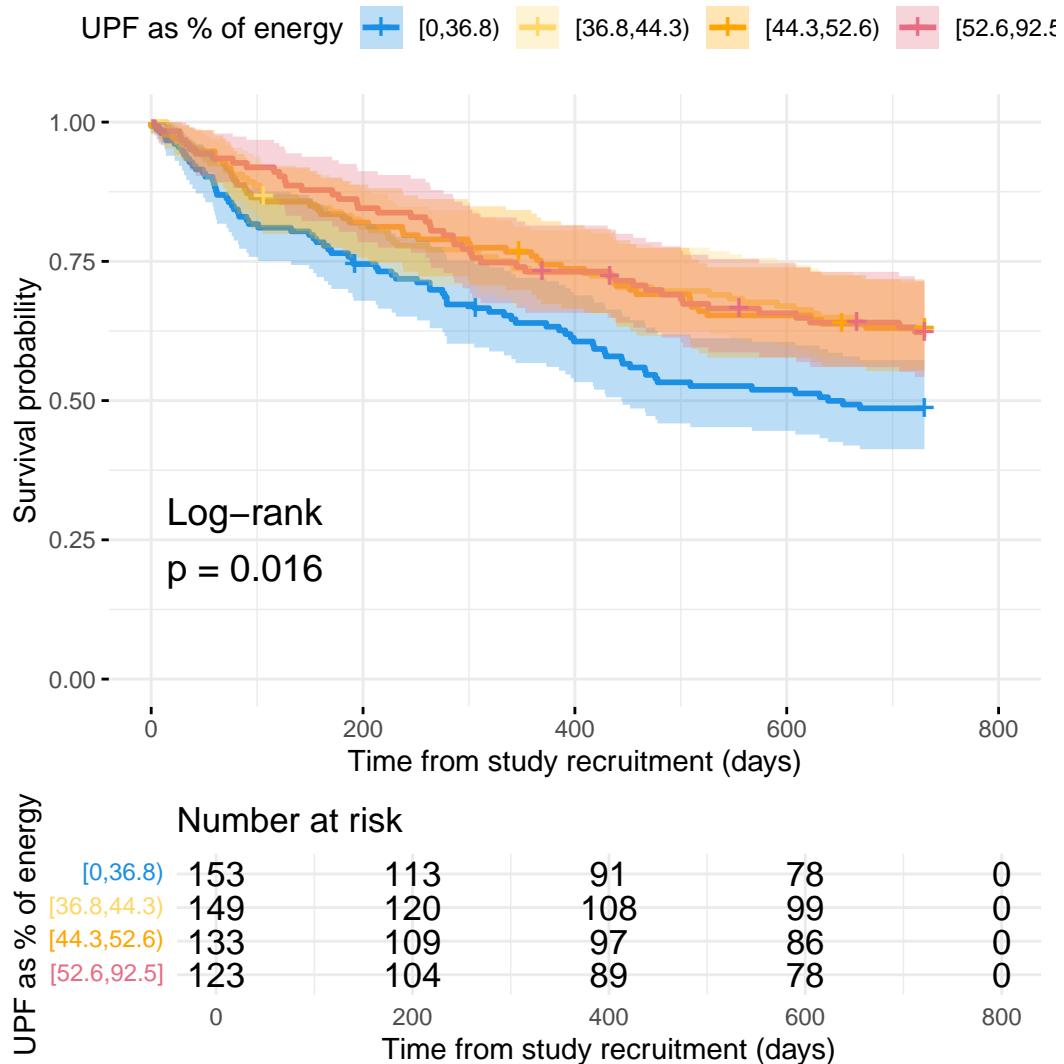
# Save plot as RDS
saveRDS(analysis_result$plot, paste0(paths$outdir, "upf-uc-soft.RDS"))

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(softflare_time, softflare) ~
    Sex + cat + IMD + dqi_tot + BMI + UPF_perc_cat +
    frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.uc.df
)

# Display plot and model summary
analysis_result$plot

```

Time to patient-reported flare



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.6886	1.2634	2.2567	0.0004
catFC 50-250	1.9565	1.4163	2.7028	0.0000
catFC > 250	2.2499	1.5707	3.2228	0.0000

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	1.3050	0.6834	2.4921	0.4200
IMD3	1.0649	0.5652	2.0063	0.8458
IMD4	1.2670	0.6990	2.2968	0.4355
IMD5	1.0858	0.6007	1.9625	0.7852
dqi_tot	0.9944	0.9811	1.0079	0.4132
BMI	0.9753	0.9466	1.0050	0.1018
UPF_perc_cat[36.8,44.3)	0.5985	0.4148	0.8636	0.0061
UPF_perc_cat[44.3,52.6)	0.5624	0.3809	0.8304	0.0038
UPF_perc_cat[52.6,92.5]	0.5871	0.3917	0.8800	0.0099

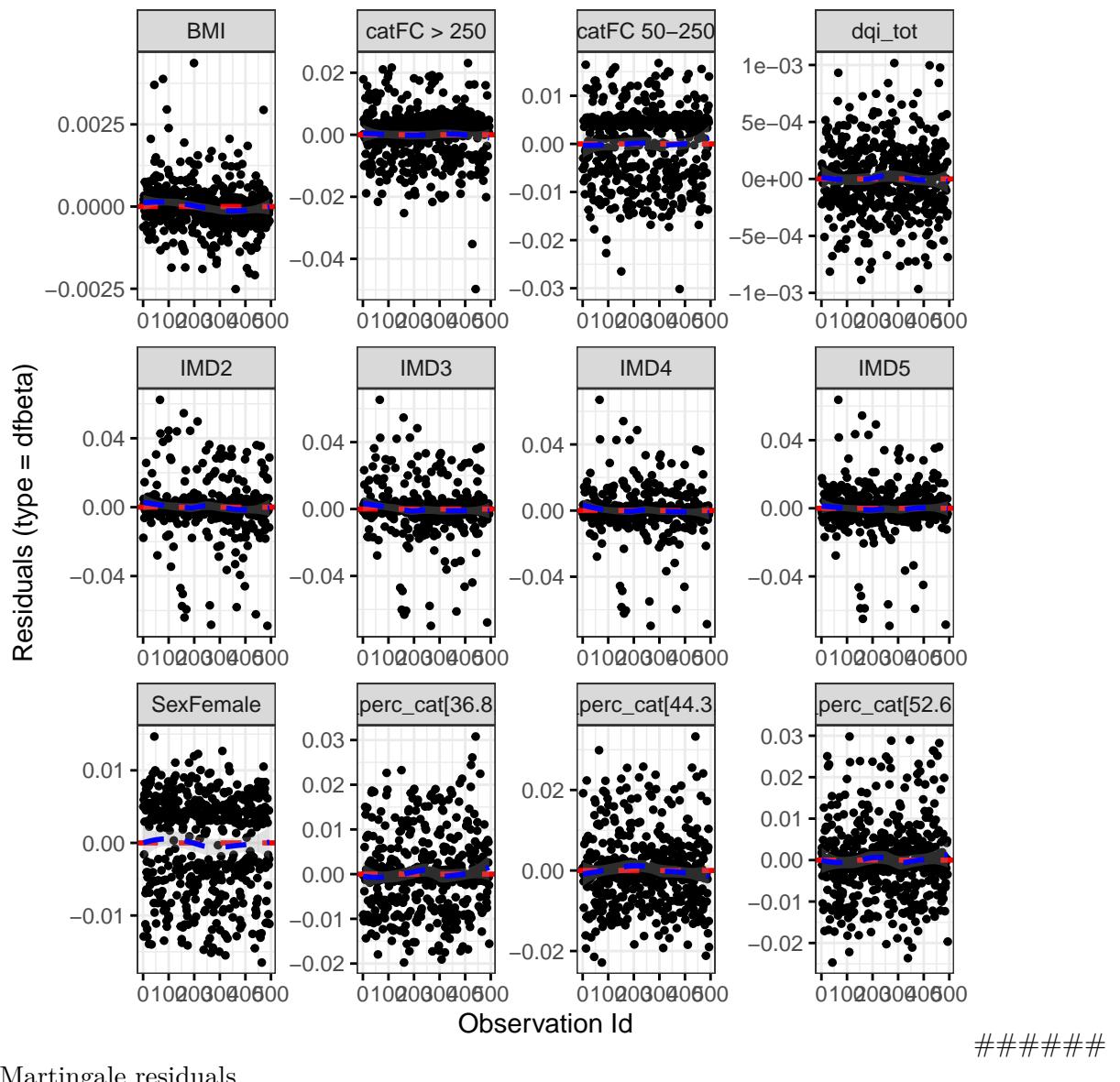
Diagnostics:

Proportional hazards assumption test

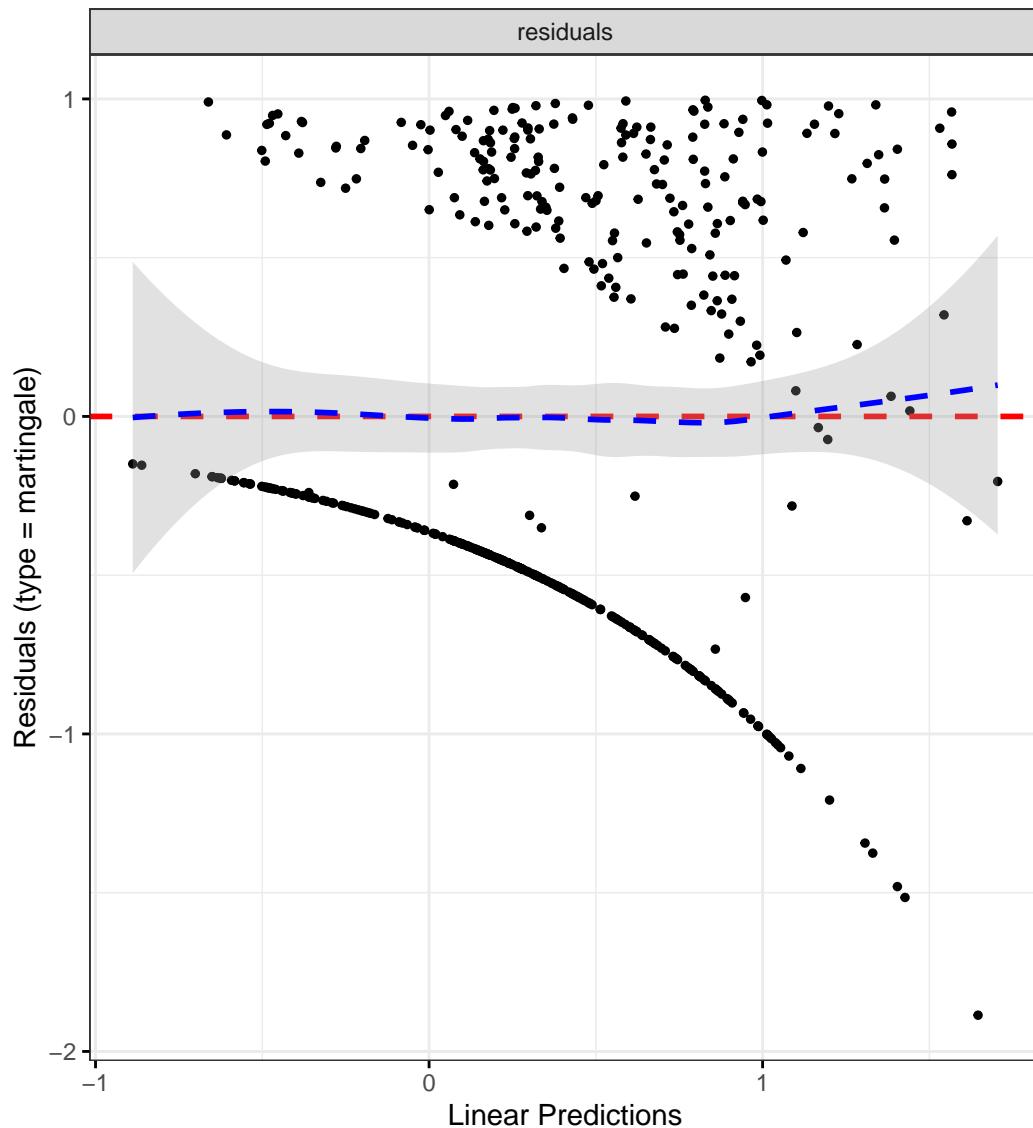
	Chi-squared statistic	DF	P-value
Sex	0.0065	0.9990	0.9358
cat	3.3668	1.9979	0.1854
IMD	2.4615	3.9959	0.6509
dqi_tot	0.7873	0.9996	0.3748
BMI	0.8257	0.9994	0.3633
UPF_perc_cat	0.3640	2.9981	0.9475
GLOBAL	8.8670	12.2308	0.7312

DF betas

```
`geom_smooth()` using formula = 'y ~ x'
```



```
`geom_smooth()` using formula = 'y ~ x'
```



Hard flare

```
# Run survival analysis using utility function for hard flare
analysis_result <- run_survival_analysis(
  data = flare.uc.df,
  var_name = "UPF_perc",
  outcome_time = "hardflare_time",
  outcome_event = "hardflare",
  legend_title = "UPF as % of energy",
```

```

plot_base_path = "plots/uc/hard-flare/diet/UPF",
break_time_by = 500
)

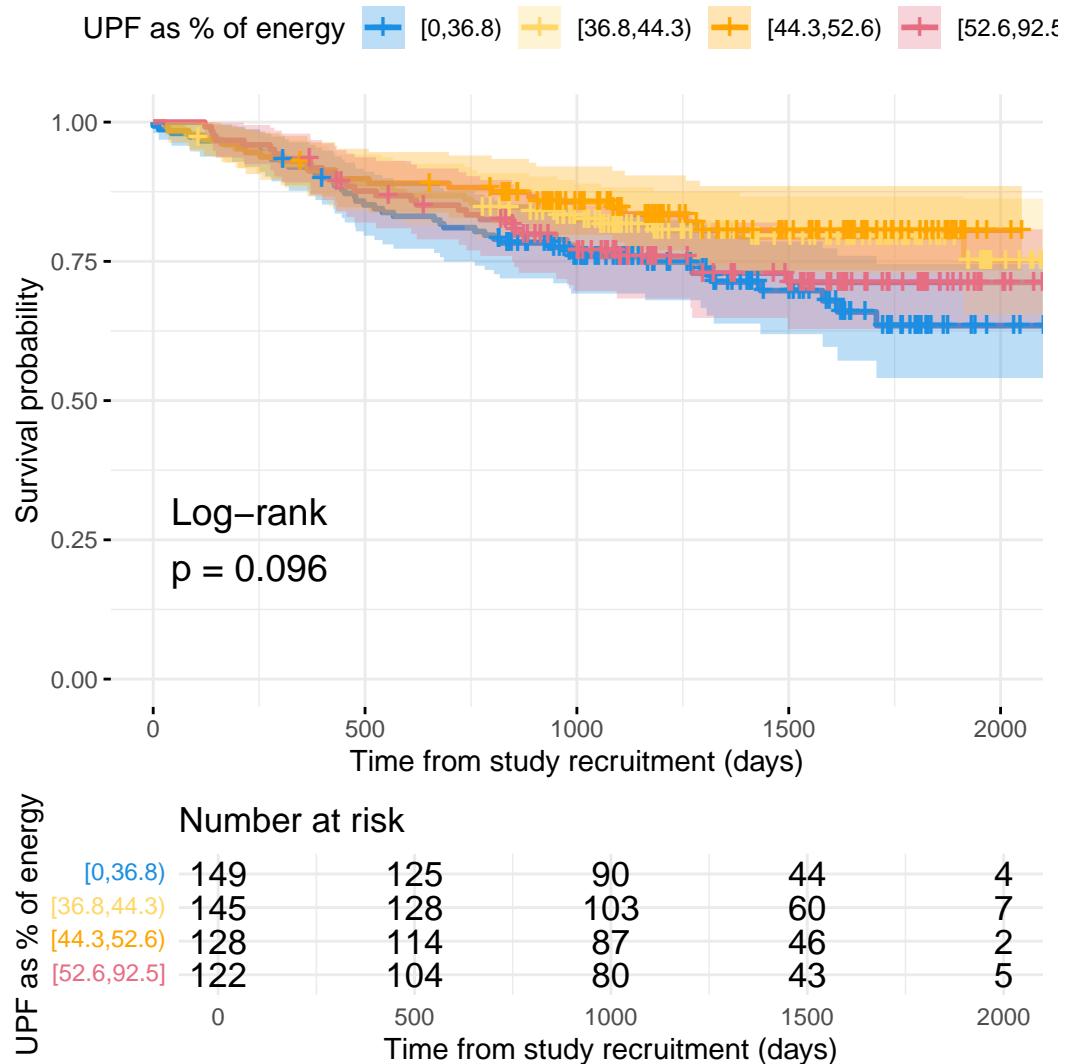
# Save plot as RDS
saveRDS(analysis_result$plot, paste0(paths$outdir, "upf-uc-hard.RDS"))

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(hardflare_time, hardflare) ~
    Sex + cat + IMD + dqi_tot + BMI + UPF_perc_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.uc.df
)

# Display plot and model summary
analysis_result$plot

```

Time to hard flare



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.2067	0.8251	1.7648	0.3327
catFC 50-250	2.1249	1.3740	3.2864	0.0007
catFC > 250	2.7076	1.6569	4.4246	0.0001

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	1.4523	0.5479	3.8496	0.4531
IMD3	1.2522	0.4827	3.2487	0.6437
IMD4	2.2537	0.9374	5.4182	0.0694
IMD5	1.3310	0.5463	3.2429	0.5292
dqi_tot	0.9973	0.9793	1.0157	0.7755
BMI	0.9576	0.9177	0.9992	0.0459
UPF_perc_cat[36.8,44.3)	0.5626	0.3412	0.9275	0.0241
UPF_perc_cat[44.3,52.6)	0.4536	0.2598	0.7919	0.0054
UPF_perc_cat[52.6,92.5]	0.7752	0.4700	1.2787	0.3187

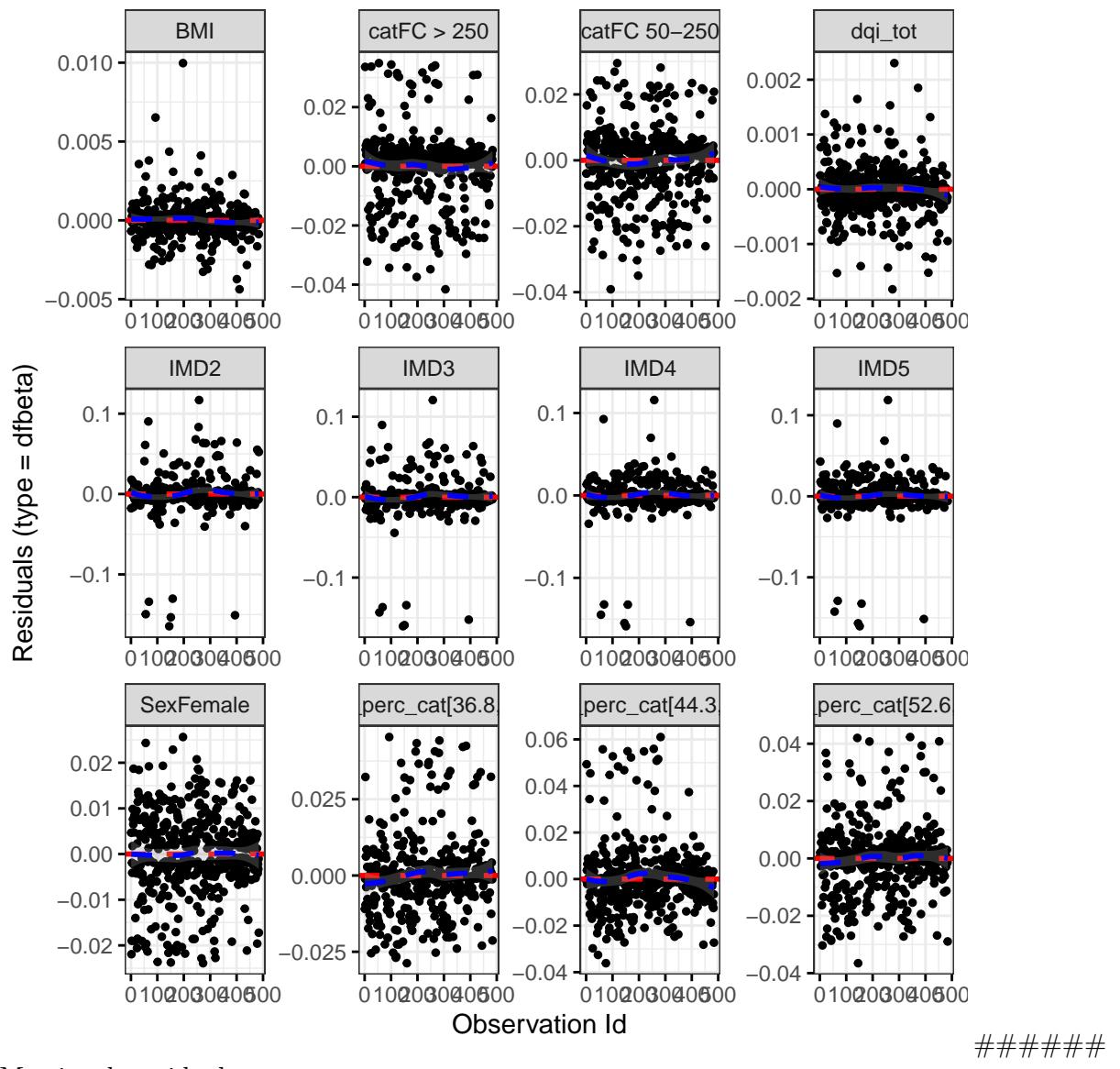
Diagnostics:

Proportional hazards assumption test

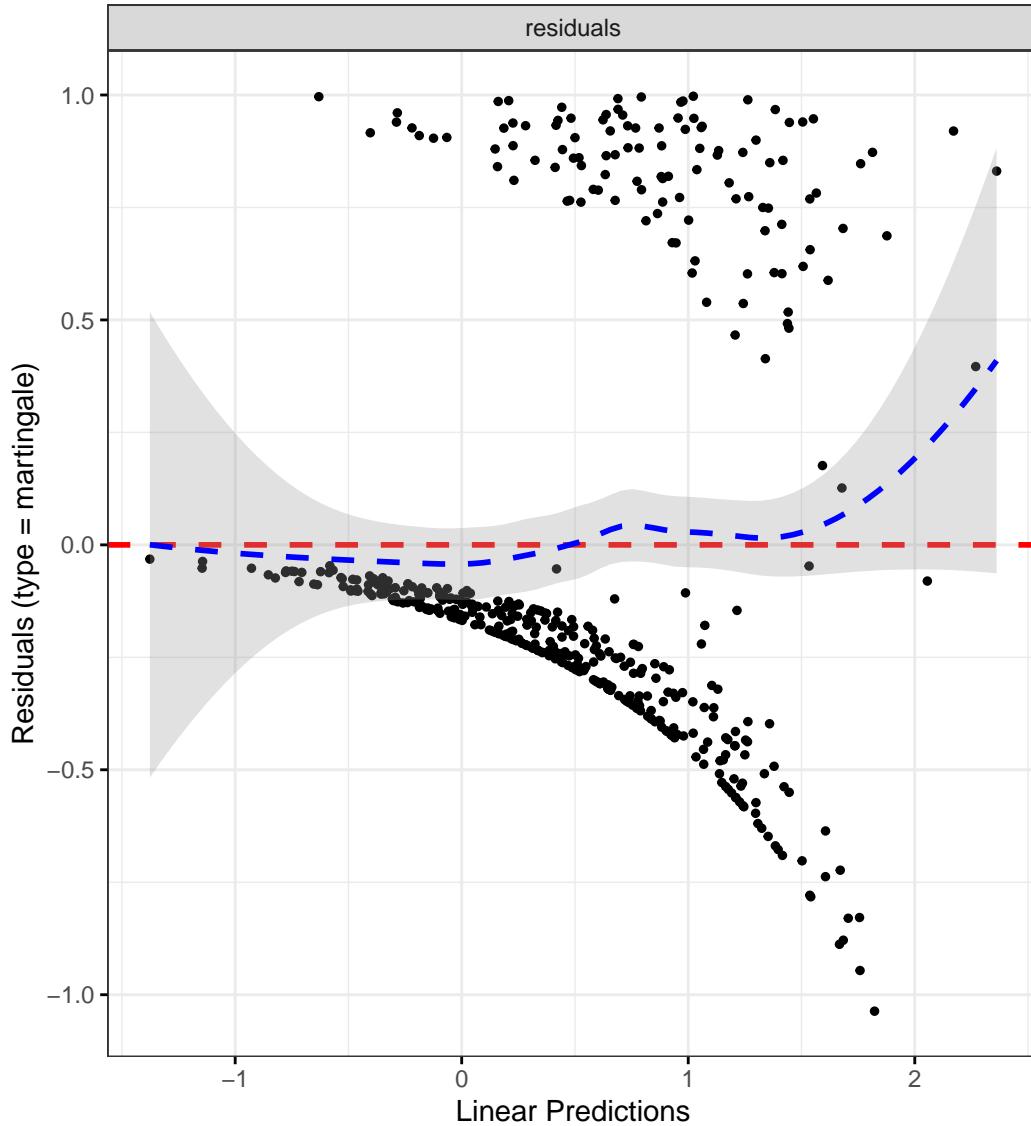
	Chi-squared statistic	DF	P-value
Sex	0.0395	0.9884	0.8387
cat	5.1651	1.9539	0.0724
IMD	1.1683	3.9311	0.8770
dqi_tot	0.0010	0.9856	0.9728
BMI	0.5583	0.9861	0.4495
UPF_perc_cat	6.7840	2.9591	0.0768
GLOBAL	13.2005	20.0426	0.8702

DF betas

```
`geom_smooth()` using formula = 'y ~ x'
```



```
`geom_smooth()` using formula = 'y ~ x'
```



Inflammatory bowel disease

Patient-reported flare

```
# Categorize UPF percentage by quantiles
flare.df <- categorize_by_quantiles(flare.df, "UPF_perc", reference_data = flare.df)

# Run survival analysis using utility function
analysis_result <- run_survival_analysis()
```

```

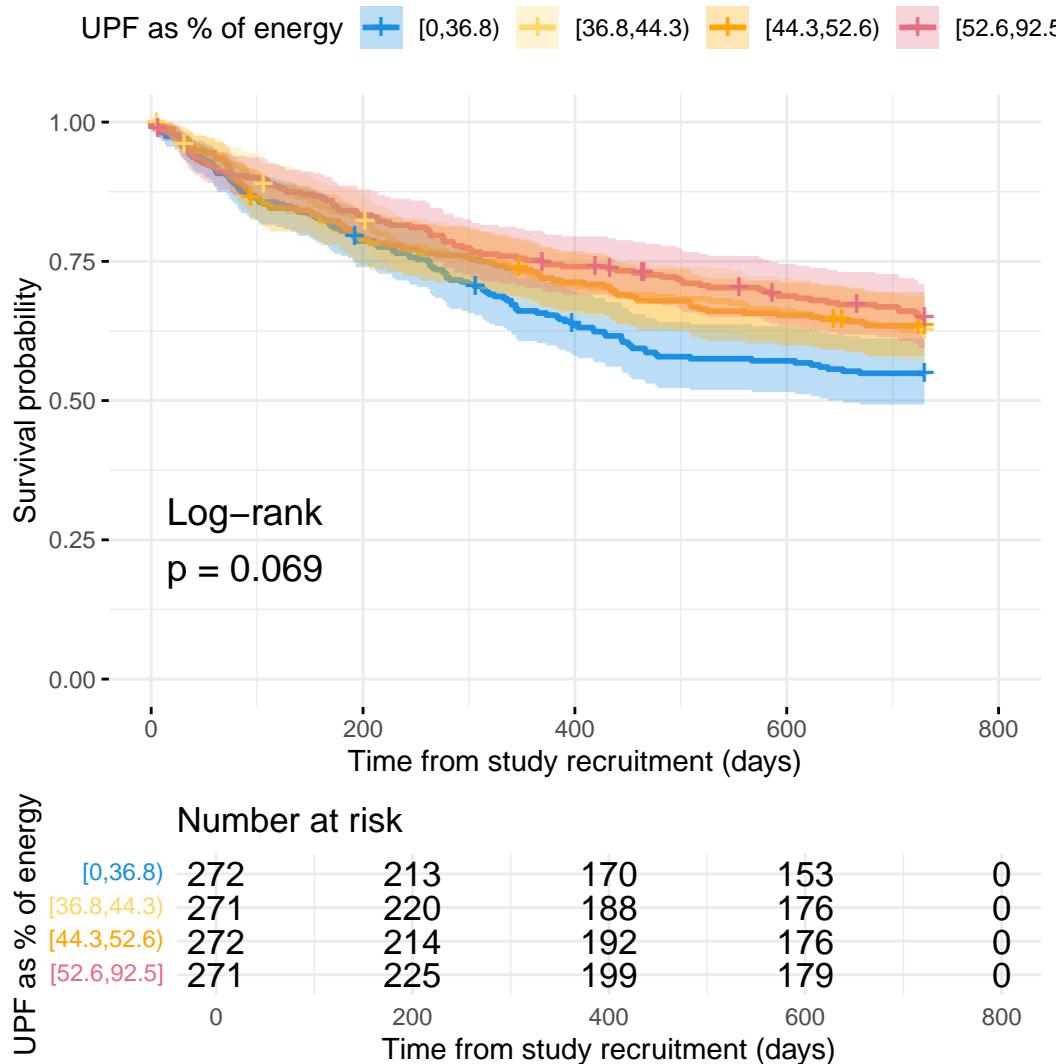
data = flare.df,
var_name = "UPF_perc",
outcome_time = "softflare_time",
outcome_event = "softflare",
legend_title = "UPF as % of energy",
plot_base_path = "plots/ibd/soft-flare/diet/UPF",
break_time_by = 200
)

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(softflare_time, softflare) ~
    Sex + cat + IMD + dqi_tot + BMI + UPF_perc_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.df
)

# Display plot and model summary
analysis_result$plot

```

Time to patient-reported flare



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.7470	1.4077	2.1679	0.0000
catFC 50-250	1.5065	1.1924	1.9034	0.0006
catFC > 250	2.0201	1.5599	2.6162	0.0000

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	0.9629	0.6117	1.5157	0.8702
IMD3	0.9912	0.6422	1.5298	0.9682
IMD4	1.0878	0.7179	1.6484	0.6914
IMD5	1.0509	0.7025	1.5720	0.8091
dqi_tot	1.0004	0.9909	1.0100	0.9335
BMI	0.9961	0.9765	1.0162	0.7034
UPF_perc_cat[36.8,44.3)	0.8250	0.6262	1.0868	0.1713
UPF_perc_cat[44.3,52.6)	0.8052	0.6071	1.0680	0.1328
UPF_perc_cat[52.6,92.5]	0.7405	0.5512	0.9948	0.0461

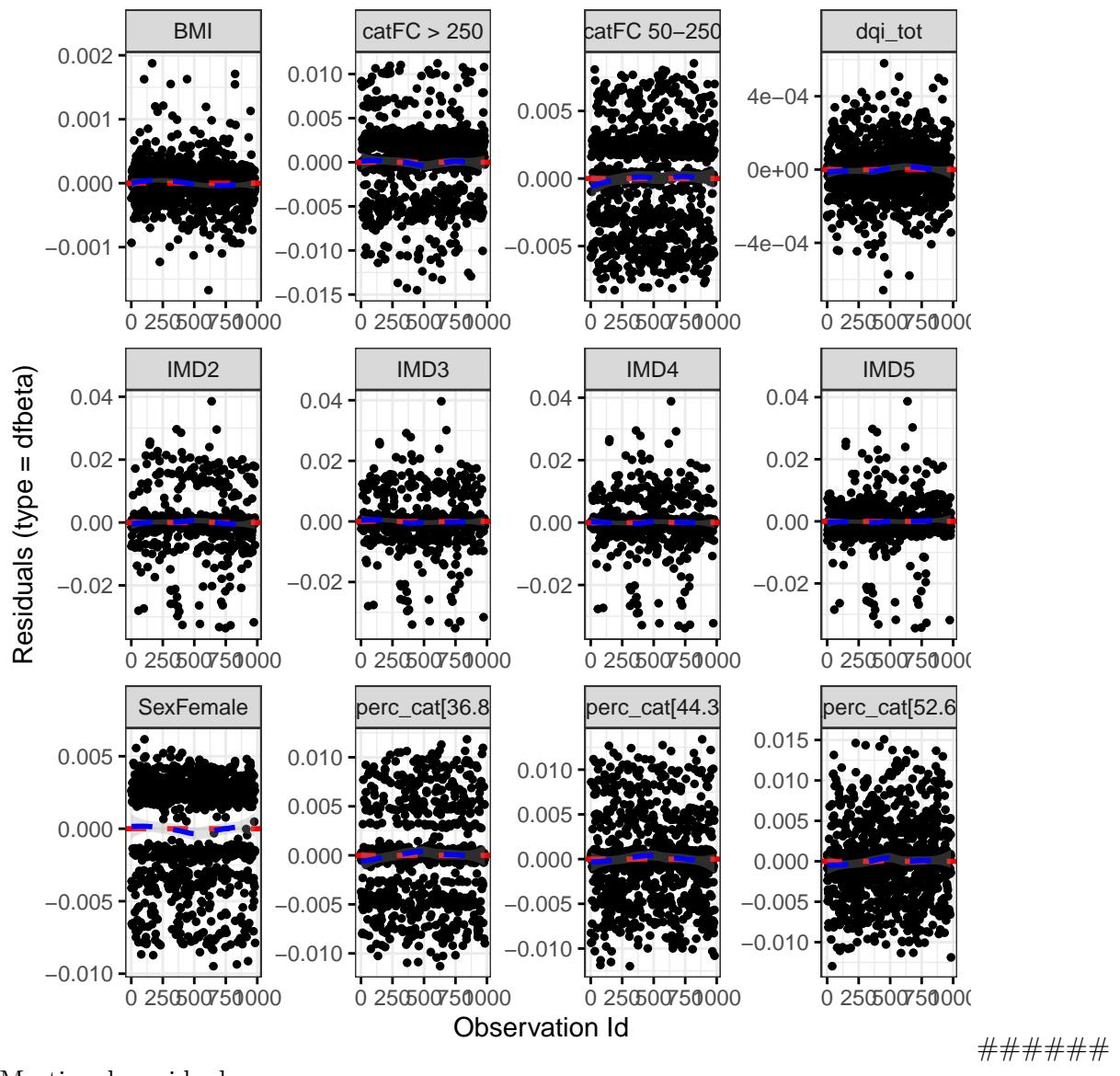
Diagnostics:

Proportional hazards assumption test

	Chi-squared statistic	DF	P-value
Sex	0.0061	1.0000	0.9379
cat	1.1551	2.0000	0.5613
IMD	4.9207	4.0000	0.2955
dqi_tot	1.3621	1.0000	0.2432
BMI	0.0163	1.0000	0.8983
UPF_perc_cat	2.1786	3.0000	0.5362
GLOBAL	9.4588	12.0002	0.6633

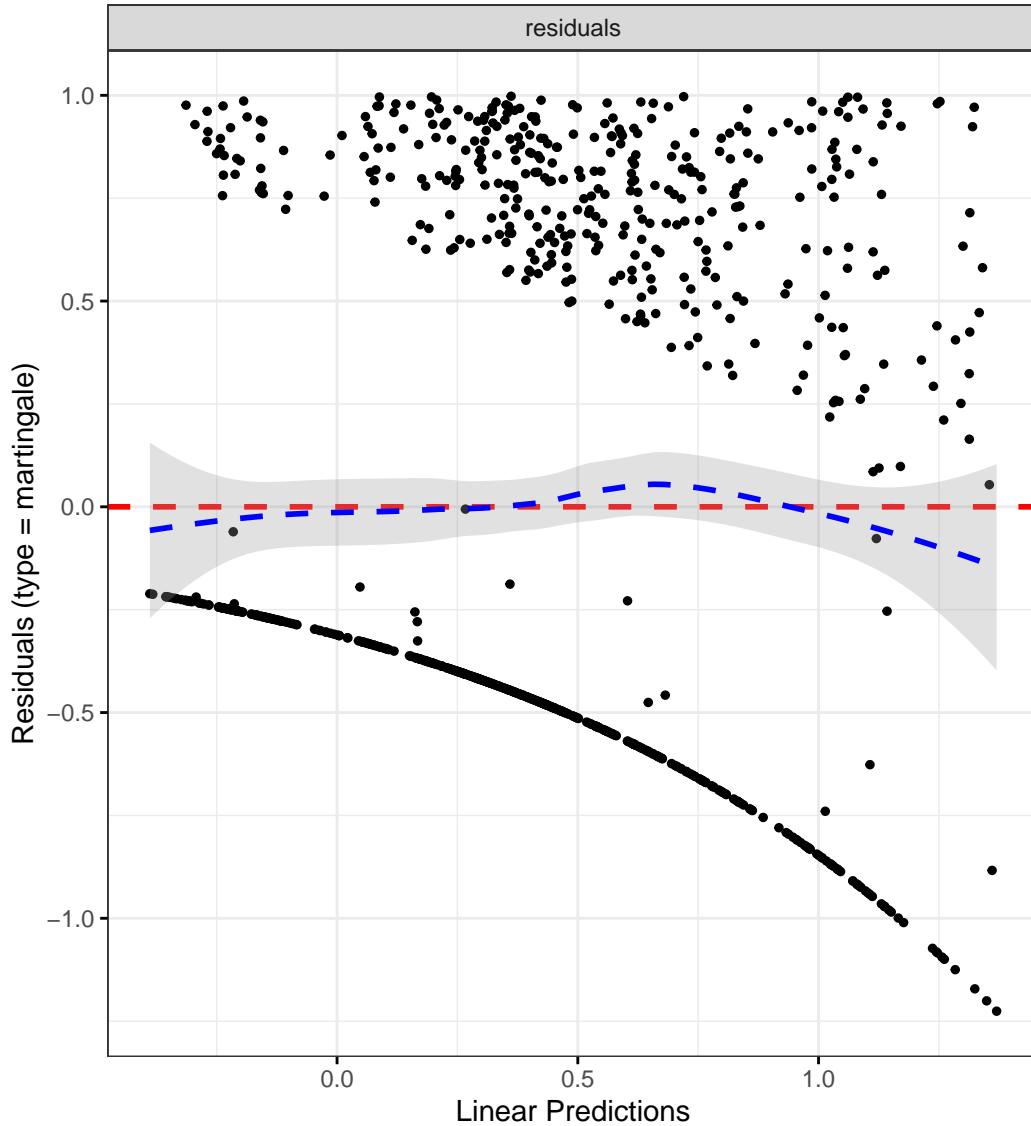
DF betas

```
`geom_smooth()` using formula = 'y ~ x'
```



Martingale residuals

```
`geom_smooth()` using formula = 'y ~ x'
```



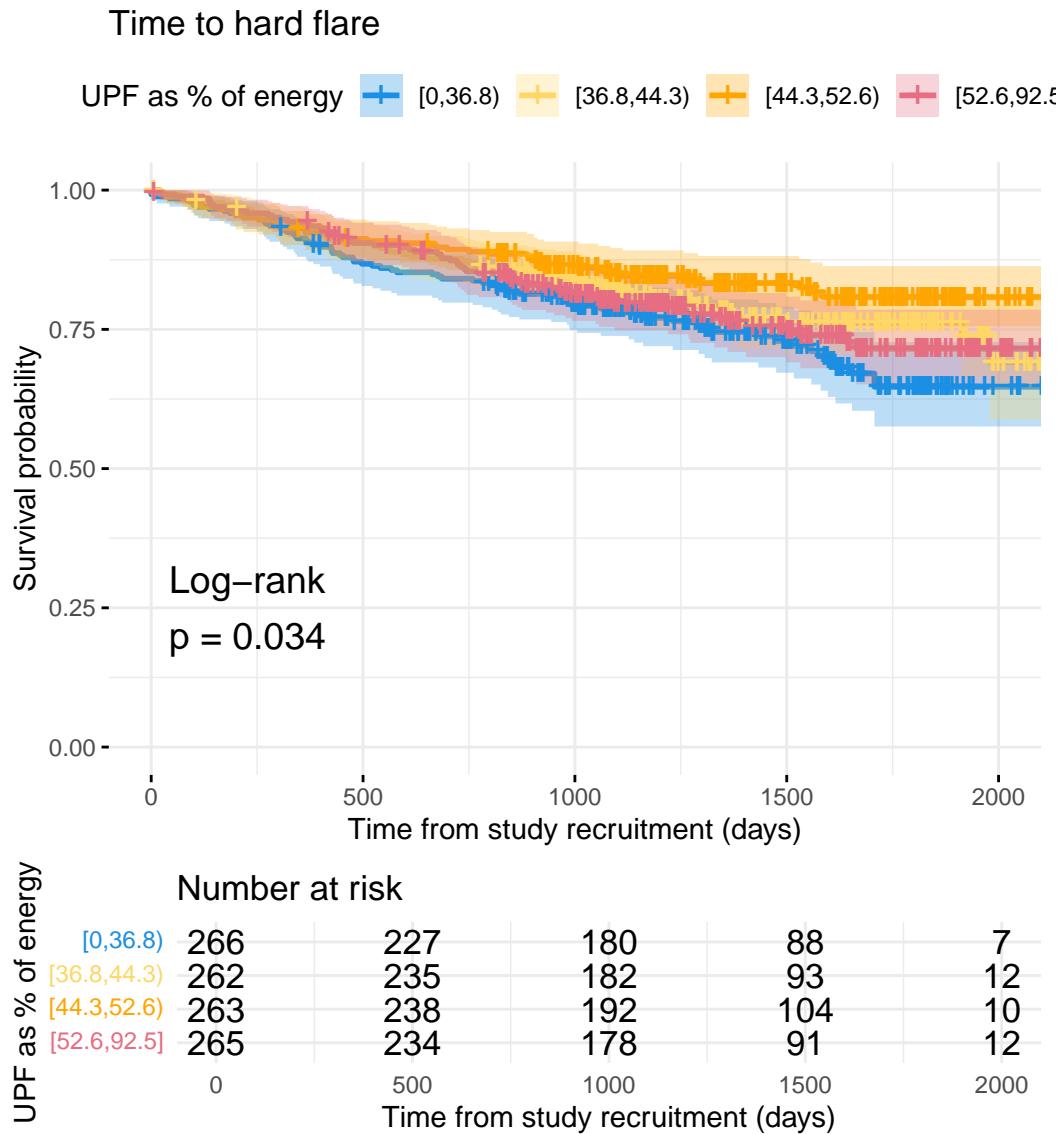
Hard flare

```
# Run survival analysis using utility function for hard flare
analysis_result <- run_survival_analysis(
  data = flare.df,
  var_name = "UPF_perc",
  outcome_time = "hardflare_time",
  outcome_event = "hardflare",
  legend_title = "UPF as % of energy",
```

```
plot_base_path = "plots/ibd/hard-flare/diet/UPF",
break_time_by = 500
)

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(hardflare_time, hardflare) ~
    Sex + cat + IMD + dqi_tot + BMI + UPF_perc_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.df
)

# Display plot and model summary
analysis_result$plot
```



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.2431	0.9425	1.6397	0.1234
catFC 50-250	1.8265	1.3343	2.5002	0.0002
catFC > 250	2.6243	1.8574	3.7077	0.0000

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	0.9195	0.4916	1.7197	0.7927
IMD3	0.9574	0.5250	1.7459	0.8871
IMD4	1.3706	0.7806	2.4066	0.2724
IMD5	0.9917	0.5670	1.7344	0.9766
dqi_tot	0.9998	0.9871	1.0127	0.9750
BMI	0.9922	0.9657	1.0193	0.5674
UPF_perc_cat[36.8,44.3)	0.7500	0.5232	1.0751	0.1173
UPF_perc_cat[44.3,52.6)	0.5211	0.3508	0.7741	0.0012
UPF_perc_cat[52.6,92.5]	0.8113	0.5607	1.1739	0.2672

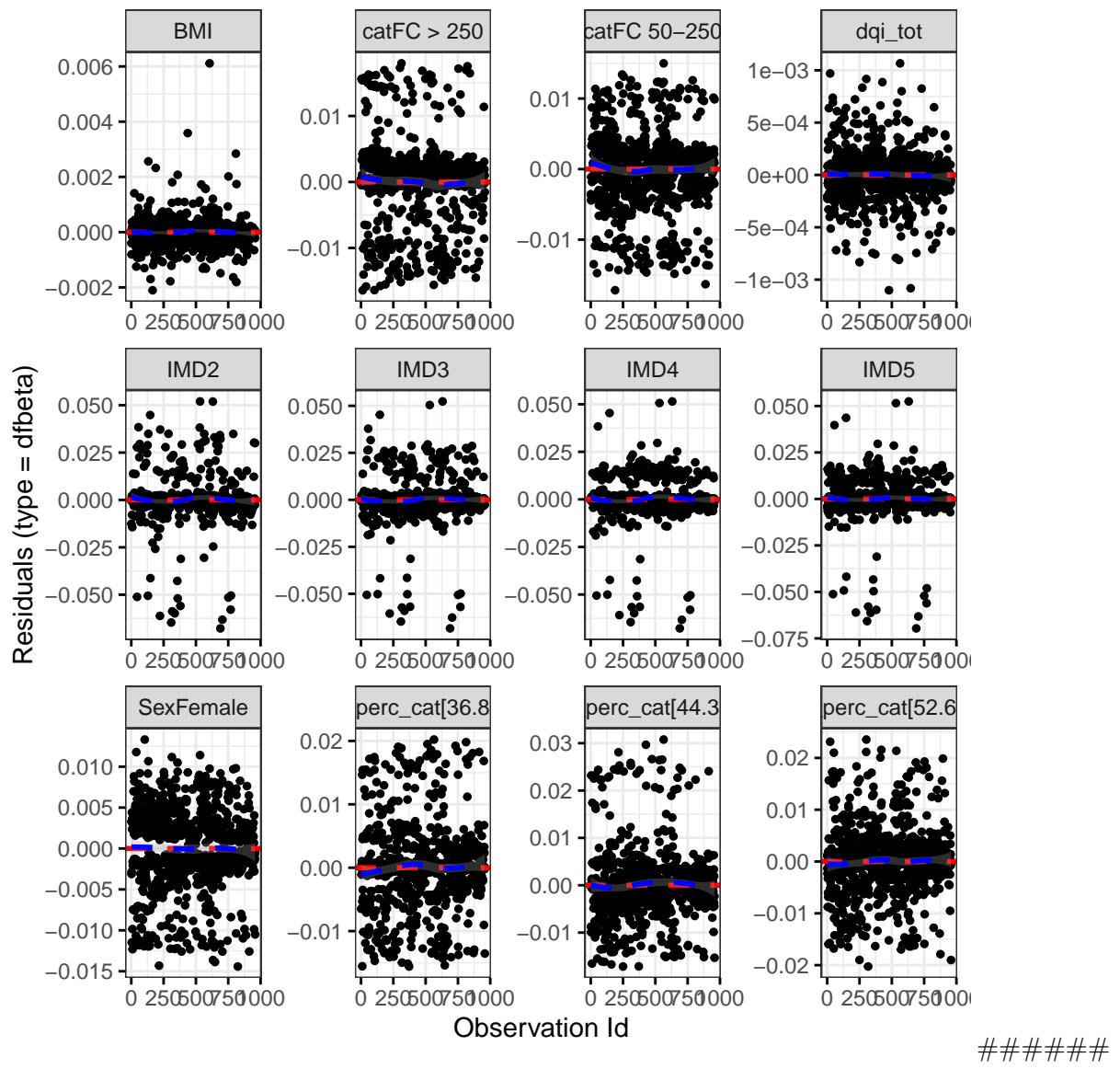
Diagnostics:

Proportional hazards assumption test

	Chi-squared statistic	DF	P-value
Sex	0.0227	0.9900	0.8776
cat	6.9955	1.9796	0.0296
IMD	1.4707	3.9447	0.8256
dqi_tot	1.8680	0.9920	0.1700
BMI	1.8535	0.9889	0.1710
UPF_perc_cat	4.0100	2.9741	0.2568
GLOBAL	15.7585	22.4833	0.8468

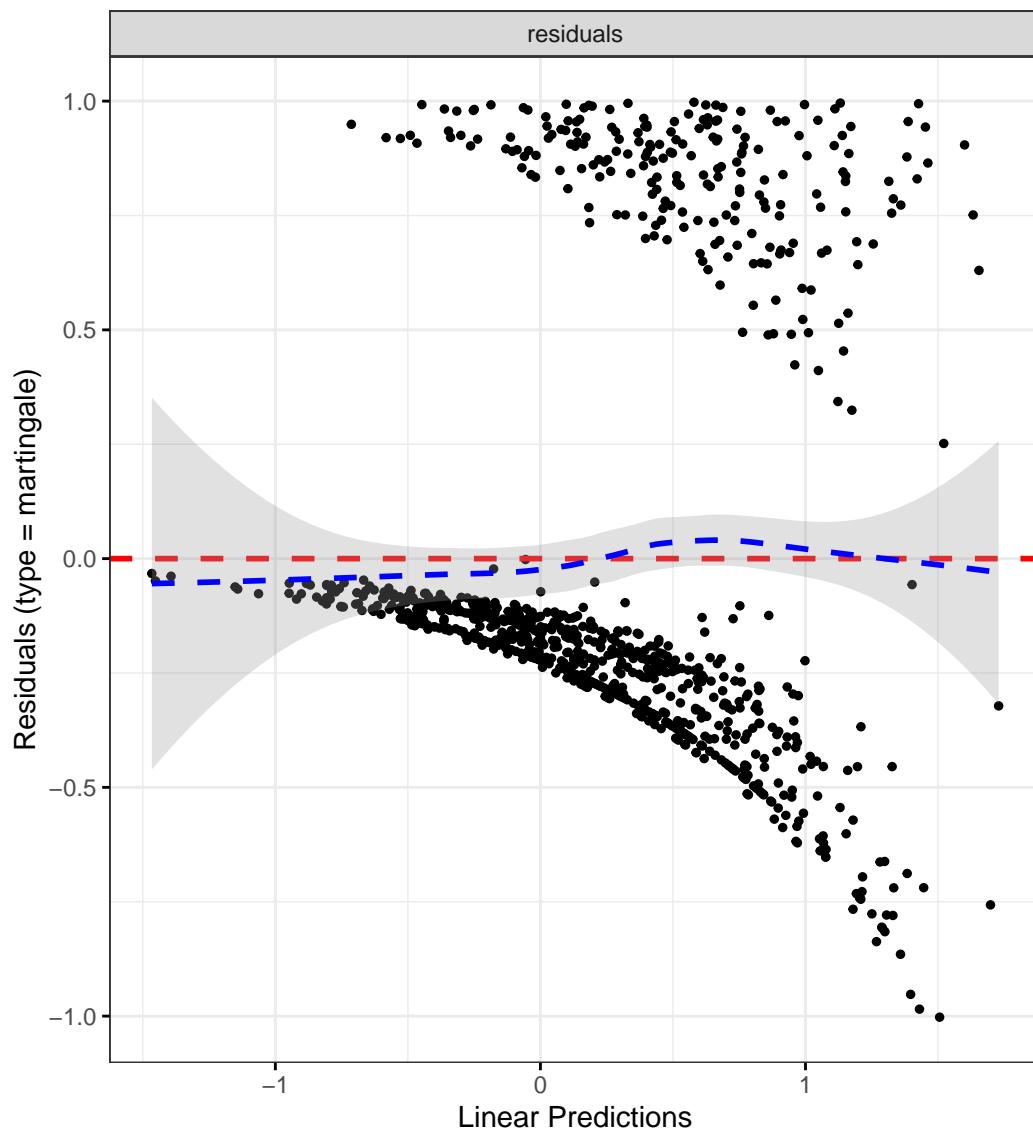
DF betas

```
`geom_smooth()` using formula = 'y ~ x'
```



Martingale residuals

```
`geom_smooth()` using formula = 'y ~ x'
```



Processed food subgroups

Breads and cereals

Crohn's disease

Patient-reported flare

```

# Categorize bread intake by quantiles
flare.cd.df <- categorize_by_quantiles(flare.cd.df, "breadIntake", reference_data = flare.df)

# Run survival analysis using utility function
analysis_result <- run_survival_analysis(
  data = flare.cd.df,
  var_name = "breadIntake",
  outcome_time = "softflare_time",
  outcome_event = "softflare",
  legend_title = "Bread/cereal intake quantiles",
  plot_base_path = "plots/cd/soft-flare/diet/breadIntake",
  break_time_by = 200
)

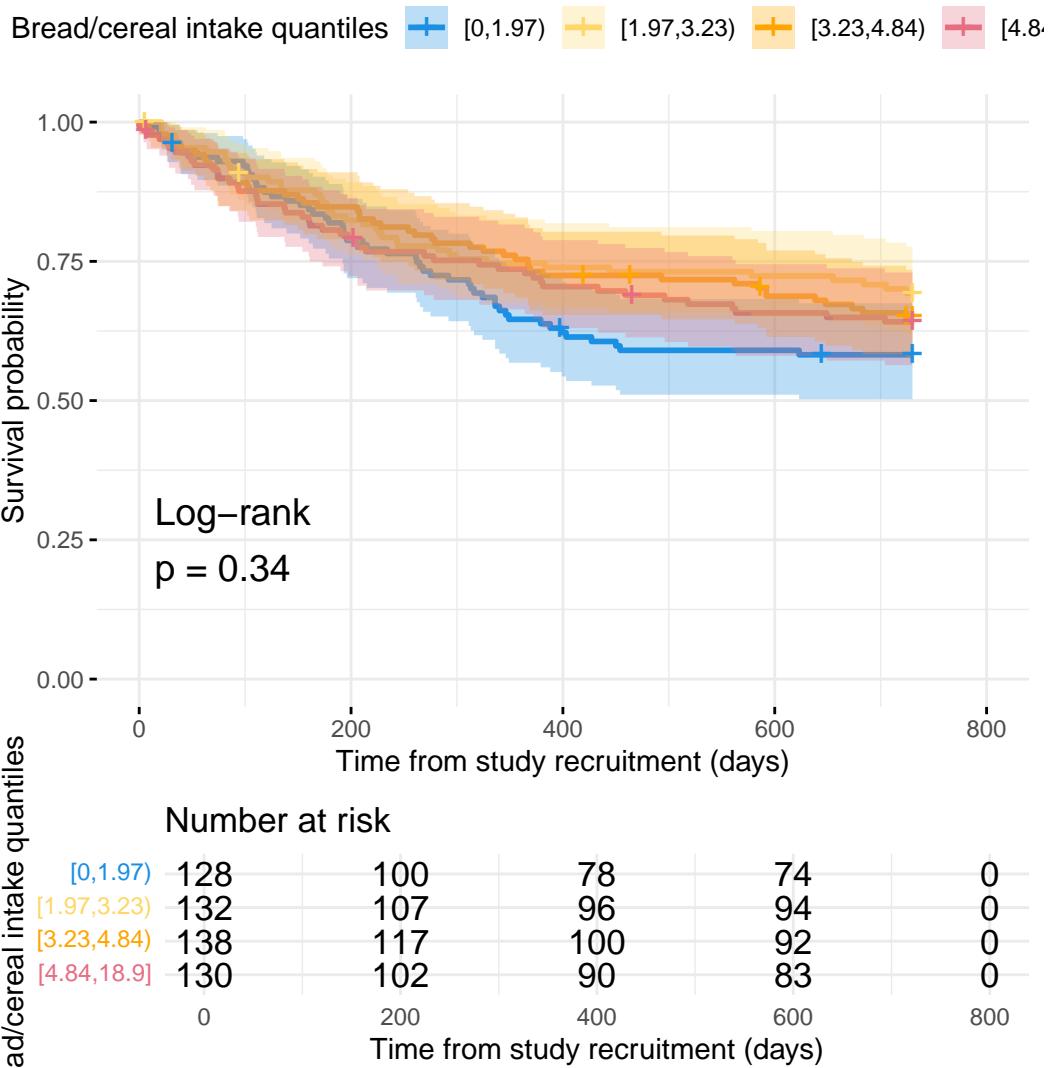
# Save plot as RDS
saveRDS(analysis_result$plot, paste0(paths$outdir, "breadIntake-cd-soft.RDS"))

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(softflare_time, softflare) ~
    Sex + cat + IMD + dqi_tot + BMI + breadIntake_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.cd.df
)

# Display plot and model summary
analysis_result$plot

```

Time to patient-reported flare



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.8549	1.3254	2.5960	0.0003
catFC 50-250	1.3338	0.9385	1.8956	0.1082
catFC > 250	2.0756	1.4177	3.0388	0.0002

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	0.7180	0.3723	1.3845	0.3227
IMD3	0.9704	0.5295	1.7787	0.9227
IMD4	0.8580	0.4716	1.5612	0.6161
IMD5	1.0216	0.5822	1.7927	0.9406
dqi_tot	1.0053	0.9918	1.0191	0.4432
BMI	1.0101	0.9820	1.0390	0.4866
breadIntake_cat[1.97,3.23	0.6838	0.4456	1.0492	0.0819
breadIntake_cat[3.23,4.84	0.7591	0.4942	1.1659	0.2080
breadIntake_cat[4.84,18.9	0.8312	0.5455	1.2665	0.3896

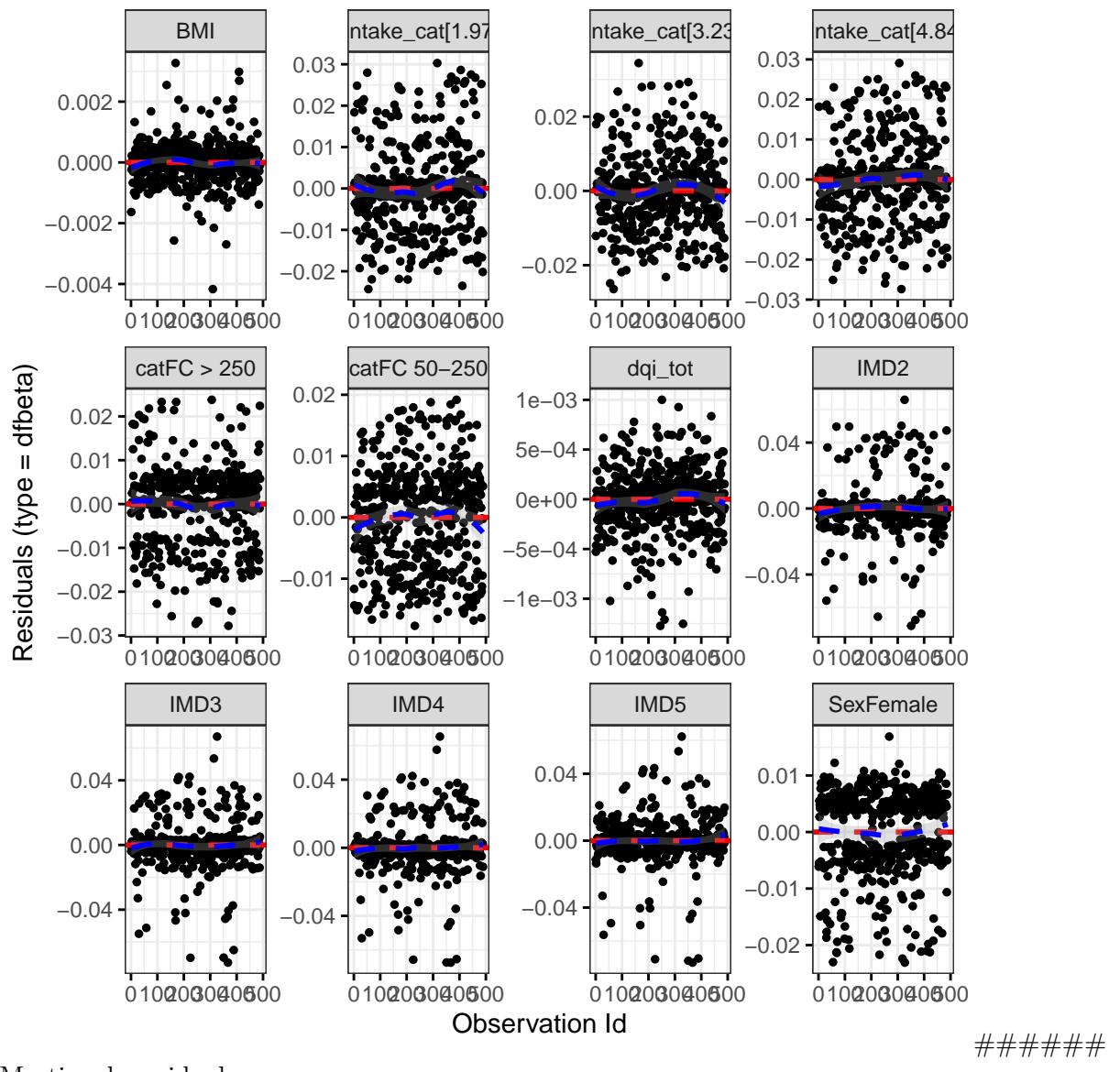
Diagnostics:

Proportional hazards assumption test

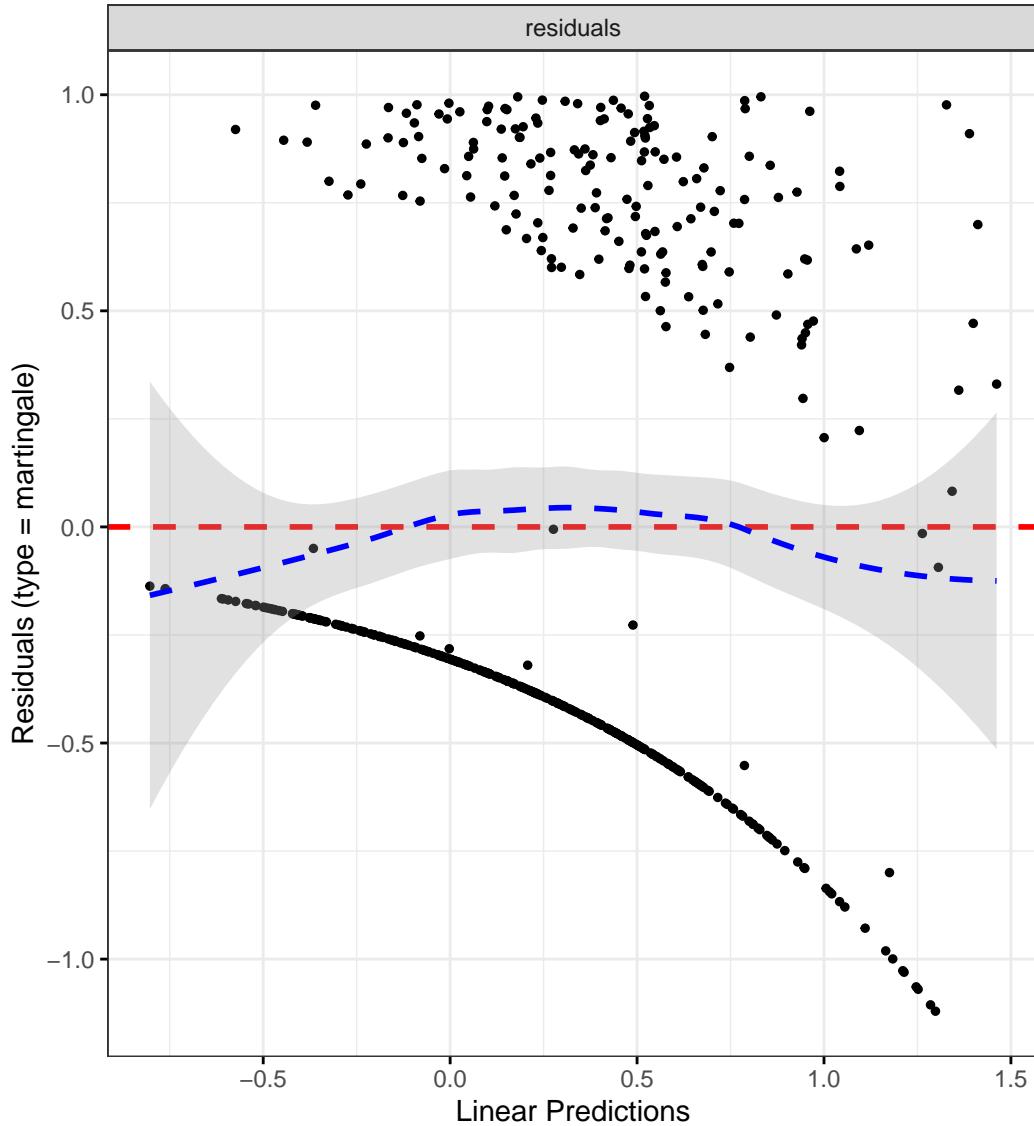
	Chi-squared statistic	DF	P-value
Sex	0.2772	1.0000	0.5985
cat	0.7971	2.0000	0.6713
IMD	2.9801	4.0000	0.5612
dqi_tot	0.3946	1.0000	0.5299
BMI	1.3054	1.0000	0.2532
breadIntake_cat	1.5017	3.0000	0.6819
GLOBAL	6.7240	12.0001	0.8753

DF betas

```
`geom_smooth()` using formula = 'y ~ x'
```



```
`geom_smooth()` using formula = 'y ~ x'
```



Hard flare

```
# Run survival analysis using utility function for hard flare
analysis_result <- run_survival_analysis(
  data = flare.cd.df,
  var_name = "breadIntake",
  outcome_time = "hardflare_time",
  outcome_event = "hardflare",
  legend_title = "Bread/cereal intake quantiles",
```

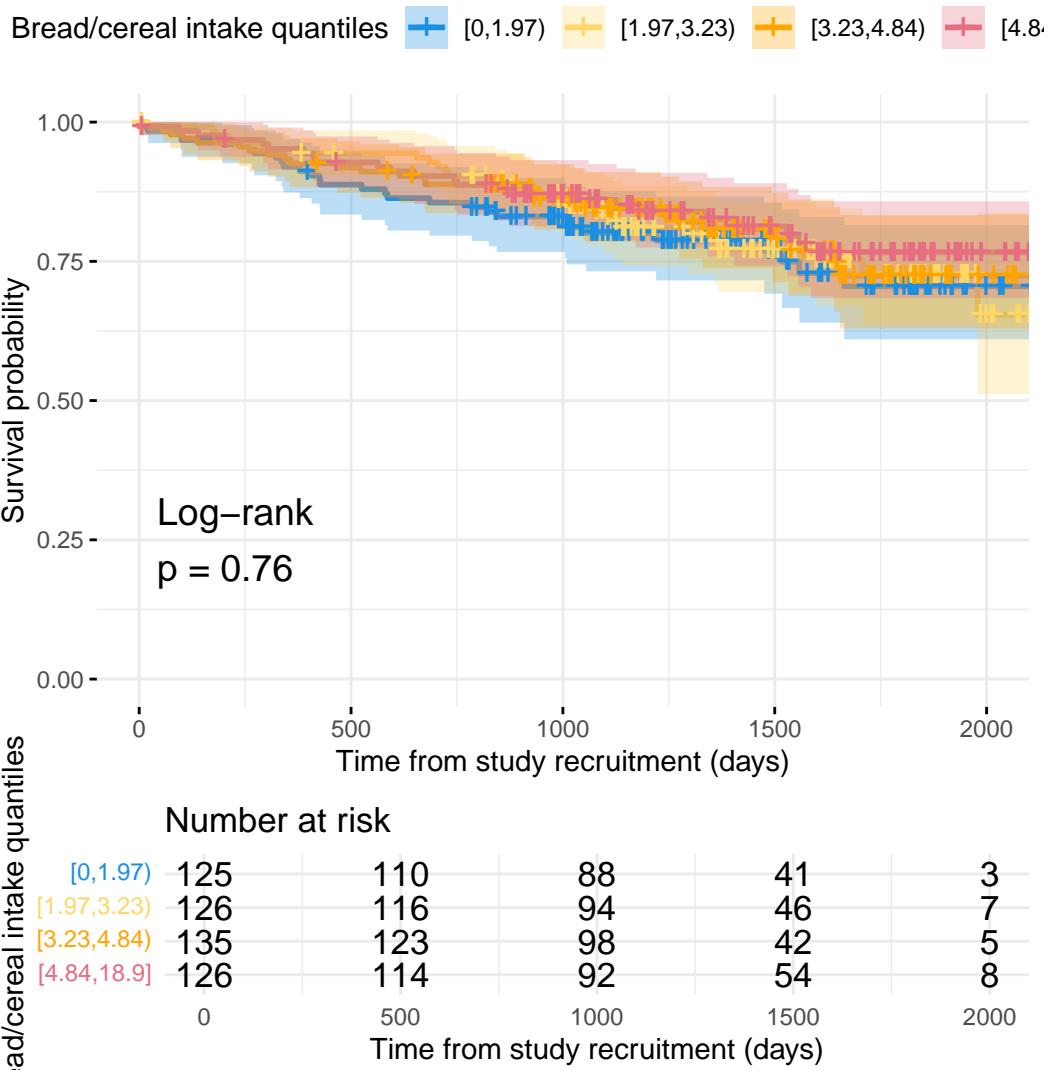
```
plot_base_path = "plots/cd/hard-flare/diet/breadIntake",
break_time_by = 500
)

# Save plot as RDS
saveRDS(analysis_result$plot, paste0(paths$outdir, "breadIntake-cd-hard.RDS"))

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(hardflare_time, hardflare) ~
    Sex + cat + IMD + dqi_tot + BMI + breadIntake_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.cd.df
)

# Display plot and model summary
analysis_result$plot
```

Time to hard flare



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.2818	0.8447	1.9450	0.2433
catFC 50-250	1.8953	1.1894	3.0202	0.0072
catFC > 250	2.9513	1.7806	4.8916	0.0000

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	0.6239	0.2670	1.4577	0.2759
IMD3	0.8269	0.3720	1.8380	0.6409
IMD4	0.7789	0.3576	1.6967	0.5294
IMD5	0.7324	0.3497	1.5338	0.4089
dqi_tot	1.0028	0.9848	1.0211	0.7634
BMI	1.0211	0.9852	1.0582	0.2523
breadIntake_cat[1.97,3.23	0.6760	0.3934	1.1616	0.1563
breadIntake_cat[3.23,4.84	0.6910	0.3951	1.2083	0.1948
breadIntake_cat[4.84,18.9	0.6121	0.3483	1.0758	0.0880

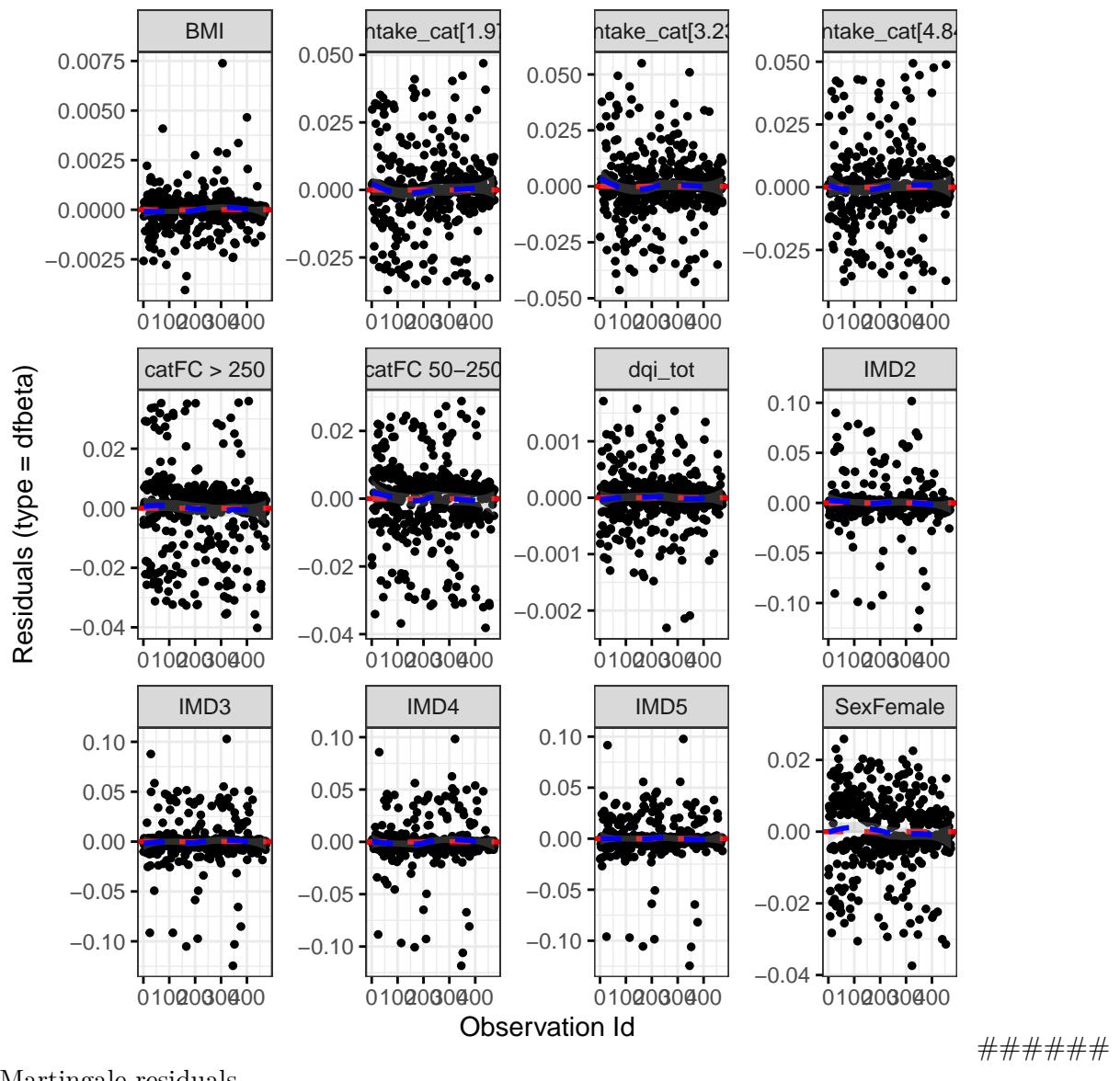
Diagnostics:

Proportional hazards assumption test

	Chi-squared statistic	DF	P-value
Sex	0.0425	0.9718	0.8275
cat	10.1284	1.9763	0.0061
IMD	2.7110	3.9248	0.5955
dqi_tot	2.7449	0.9888	0.0961
BMI	1.2185	0.9801	0.2639
breadIntake_cat	1.3541	2.9611	0.7096
GLOBAL	18.0861	18.7513	0.5002

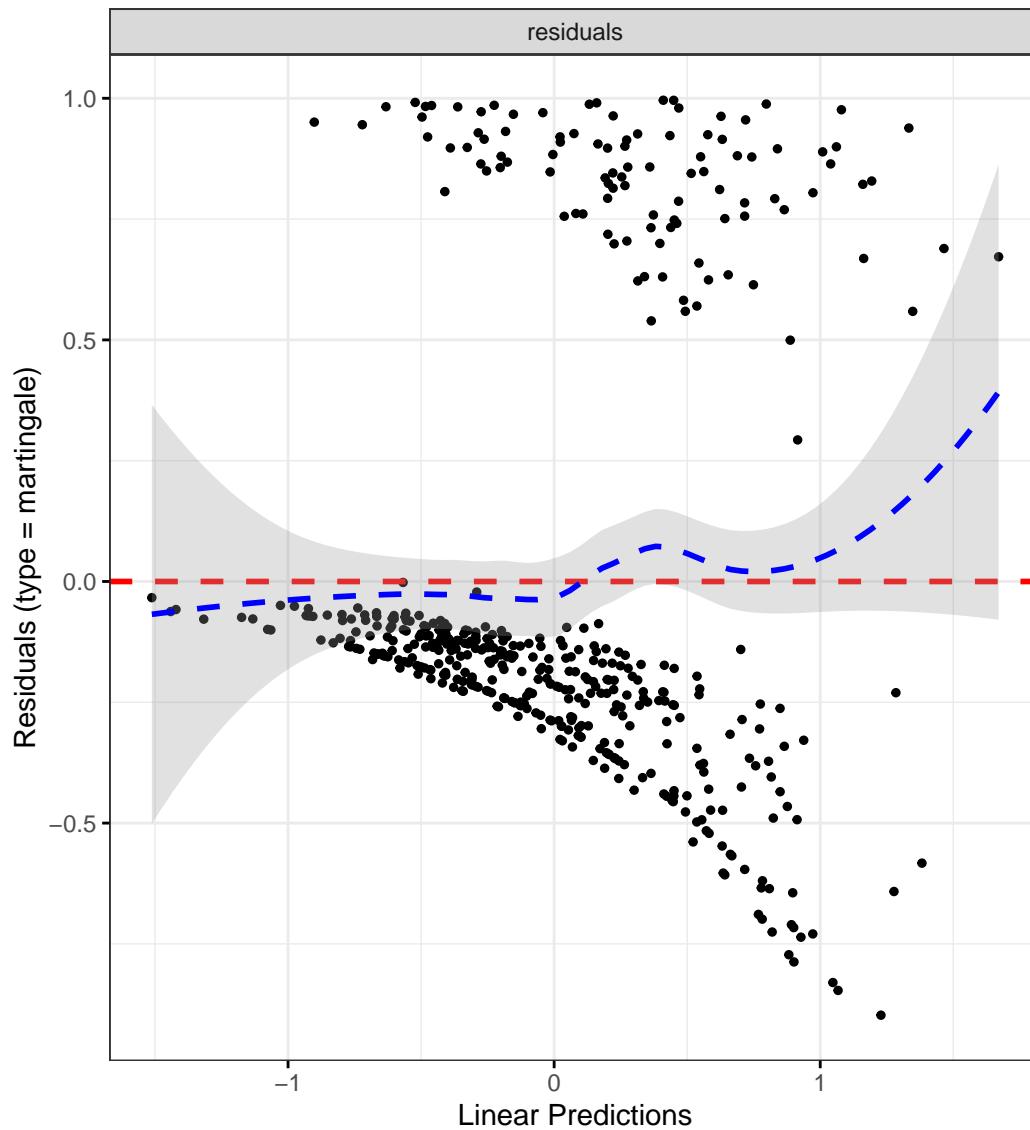
DF betas

```
`geom_smooth()` using formula = 'y ~ x'
```



Martingale residuals

```
`geom_smooth()` using formula = 'y ~ x'
```



Ulcerative colitis

Patient-reported flare

```
# Categorize bread intake by quantiles
flare.uc.df <- categorize_by_quantiles(flare.uc.df, "breadIntake", reference_data = flare.df)

# Run survival analysis using utility function
```

```

analysis_result <- run_survival_analysis(
  data = flare.uc.df,
  var_name = "breadIntake",
  outcome_time = "softflare_time",
  outcome_event = "softflare",
  legend_title = "Bread/cereal intake quantiles",
  plot_base_path = "plots/uc/soft-flare/diet/breadIntake",
  break_time_by = 200
)

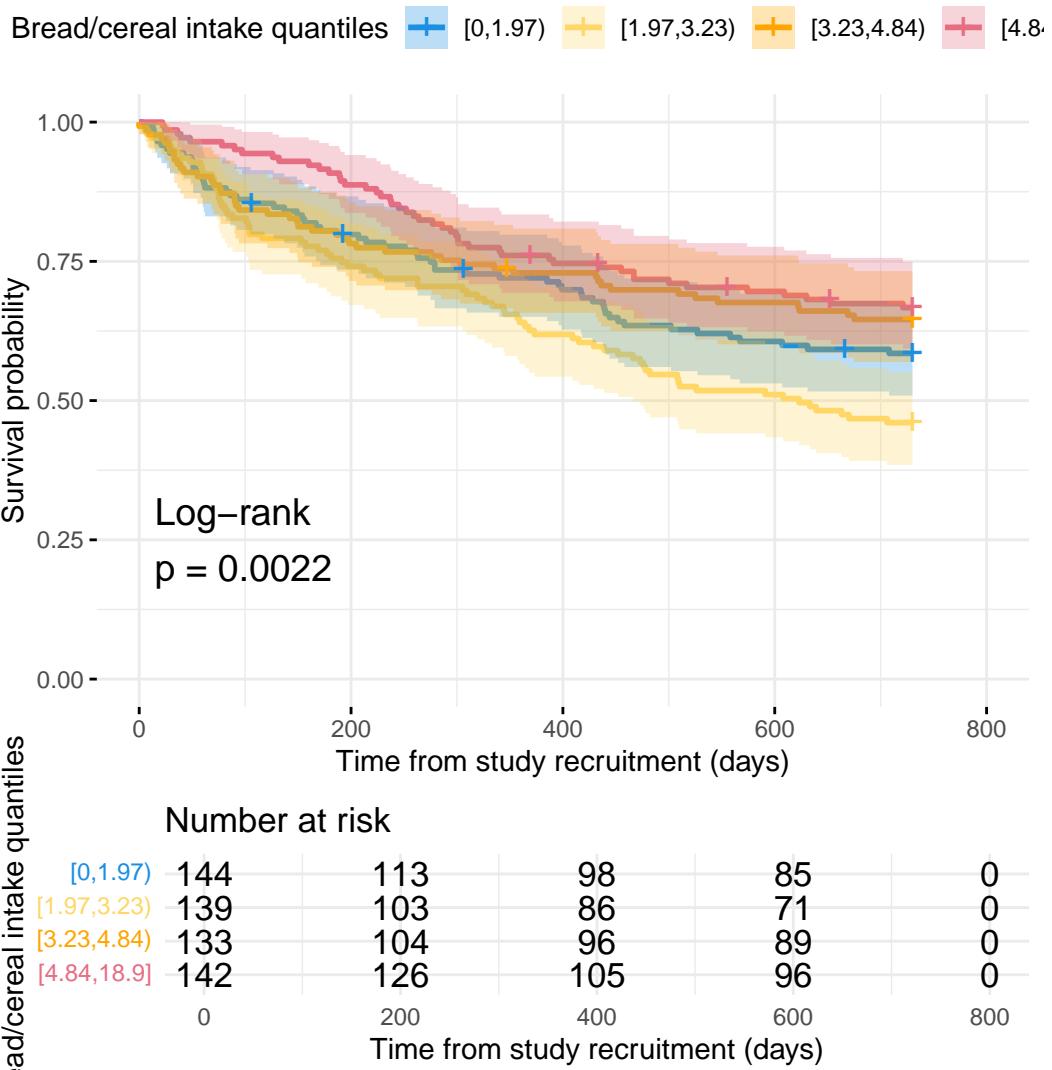
# Save plot as RDS
saveRDS(analysis_result$plot, paste0(paths$outdir, "breadIntake-uc-soft.RDS"))

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(softflare_time, softflare) ~
    Sex + cat + IMD + dqi_tot + BMI + breadIntake_cat +
    frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.uc.df
)

# Display plot and model summary
analysis_result$plot

```

Time to patient-reported flare



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.5974	1.1901	2.1439	0.0018
catFC 50-250	1.8289	1.3305	2.5139	0.0002
catFC > 250	2.0796	1.4545	2.9734	0.0001

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	1.3869	0.7273	2.6447	0.3206
IMD3	1.1062	0.5857	2.0892	0.7558
IMD4	1.2738	0.7010	2.3144	0.4271
IMD5	1.1090	0.6140	2.0030	0.7317
dqi_tot	0.9994	0.9868	1.0122	0.9267
BMI	0.9753	0.9463	1.0051	0.1038
breadIntake_cat[1.97,3.23	1.3883	0.9667	1.9938	0.0756
breadIntake_cat[3.23,4.84	0.9952	0.6658	1.4876	0.9815
breadIntake_cat[4.84,18.9	0.7822	0.5191	1.1787	0.2403

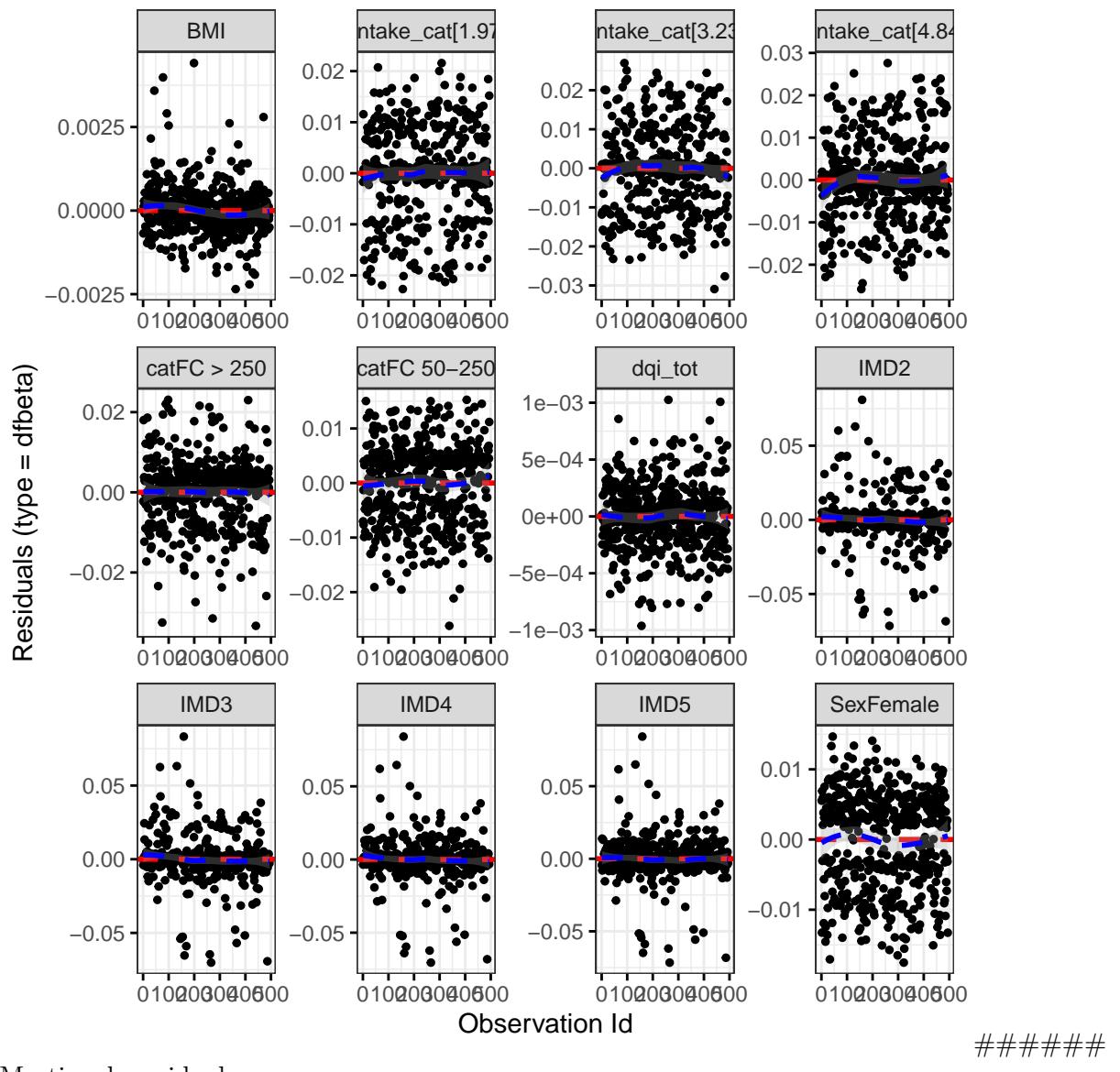
Diagnostics:

Proportional hazards assumption test

	Chi-squared statistic	DF	P-value
Sex	0.0088	1.0000	0.9253
cat	3.5302	2.0000	0.1712
IMD	2.4471	4.0000	0.6541
dqi_tot	0.7841	1.0000	0.3759
BMI	1.0910	1.0000	0.2962
breadIntake_cat	7.5792	3.0000	0.0556
GLOBAL	16.2972	12.0001	0.1780

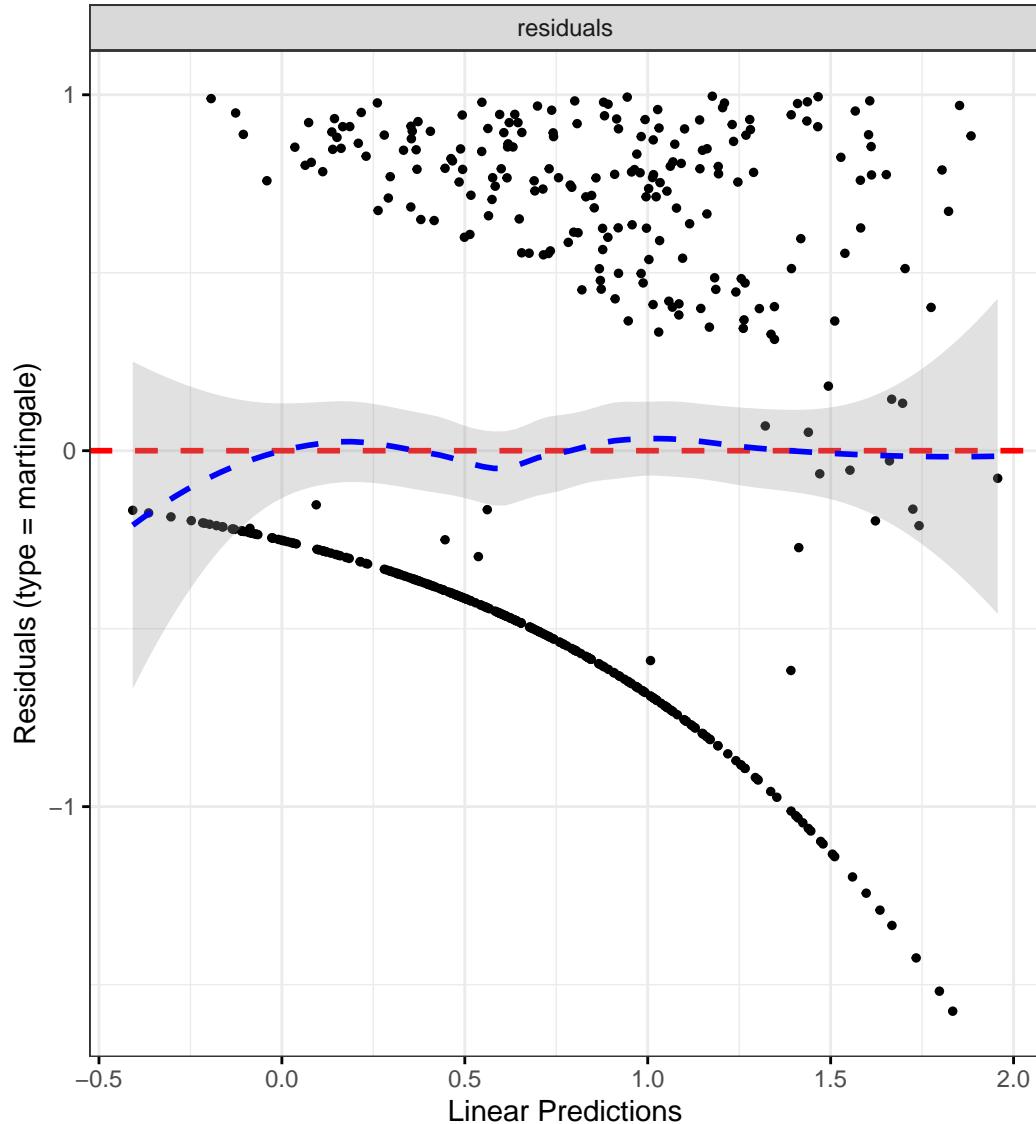
DF betas

```
`geom_smooth()` using formula = 'y ~ x'
```



Martingale residuals

```
`geom_smooth()` using formula = 'y ~ x'
```



Hard flare

```
# Run survival analysis using utility function for hard flare
analysis_result <- run_survival_analysis(
  data = flare.uc.df,
  var_name = "breadIntake",
  outcome_time = "hardflare_time",
  outcome_event = "hardflare",
  legend_title = "Bread/cereal intake quantiles",
```

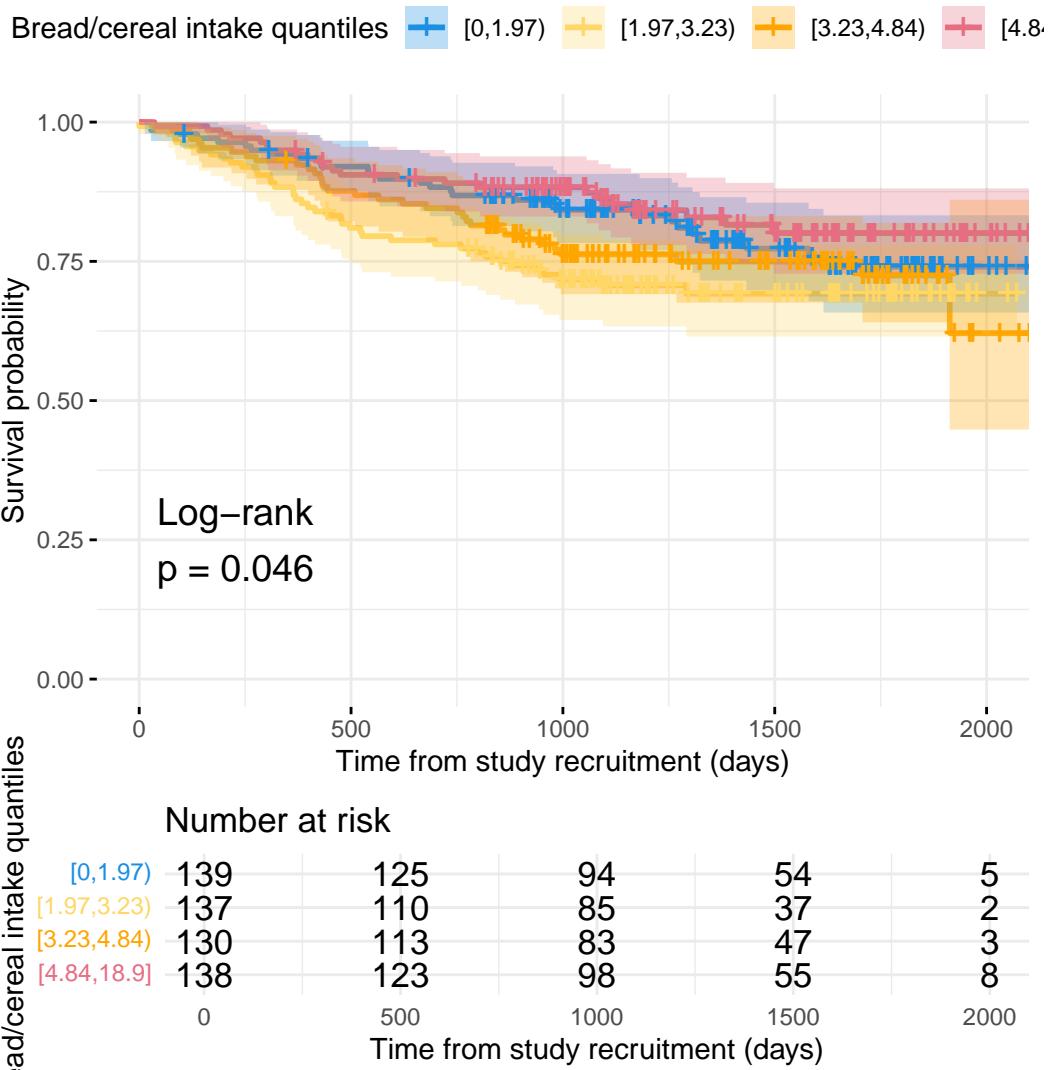
```
plot_base_path = "plots/uc/hard-flare/diet/breadIntake",
break_time_by = 500
)

# Save plot as RDS
saveRDS(analysis_result$plot, paste0(paths$outdir, "breadIntake-uc-hard.RDS"))

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(hardflare_time, hardflare) ~
    Sex + cat + IMD + dqi_tot + BMI + breadIntake_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.uc.df
)

# Display plot and model summary
analysis_result$plot
```

Time to hard flare



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.1108	0.7546	1.6353	0.5942
catFC 50-250	2.0656	1.3386	3.1876	0.0010
catFC > 250	2.5389	1.5578	4.1380	0.0002

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	1.4995	0.5674	3.9625	0.4138
IMD3	1.2679	0.4881	3.2937	0.6261
IMD4	2.2312	0.9250	5.3818	0.0740
IMD5	1.3244	0.5436	3.2265	0.5363
dqi_tot	1.0023	0.9846	1.0202	0.8025
BMI	0.9618	0.9222	1.0032	0.0700
breadIntake_cat[1.97,3.23	1.3021	0.7918	2.1411	0.2983
breadIntake_cat[3.23,4.84	1.1248	0.6651	1.9022	0.6609
breadIntake_cat[4.84,18.9	0.6735	0.3785	1.1986	0.1789

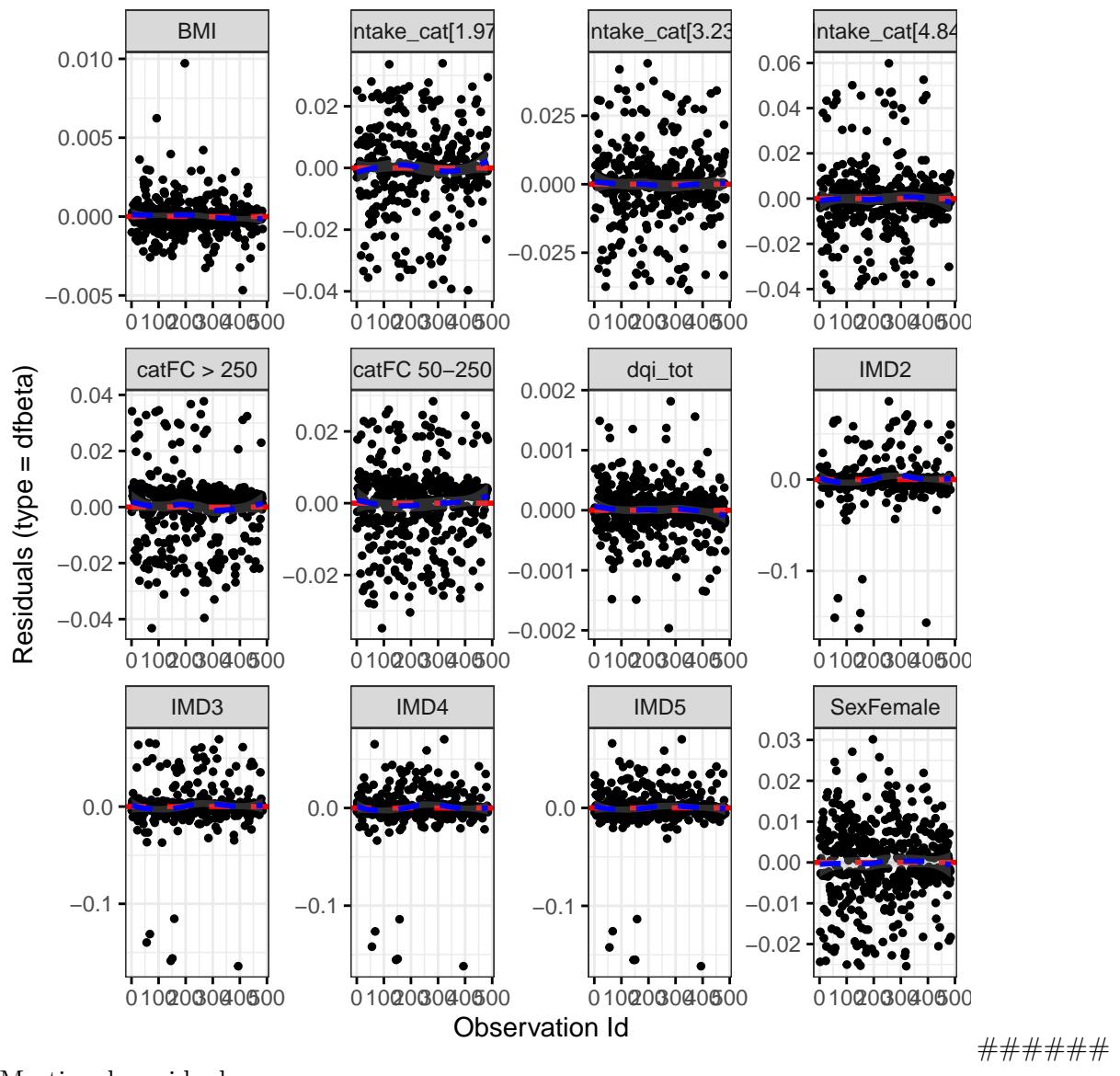
Diagnostics:

Proportional hazards assumption test

	Chi-squared statistic	DF	P-value
Sex	0.0579	0.9871	0.8054
cat	5.1146	1.9520	0.0742
IMD	1.2813	3.9305	0.8576
dqi_tot	0.0007	0.9866	0.9770
BMI	0.5239	0.9883	0.4645
breadIntake_cat	3.5288	2.9512	0.3095
GLOBAL	11.1126	19.6917	0.9368

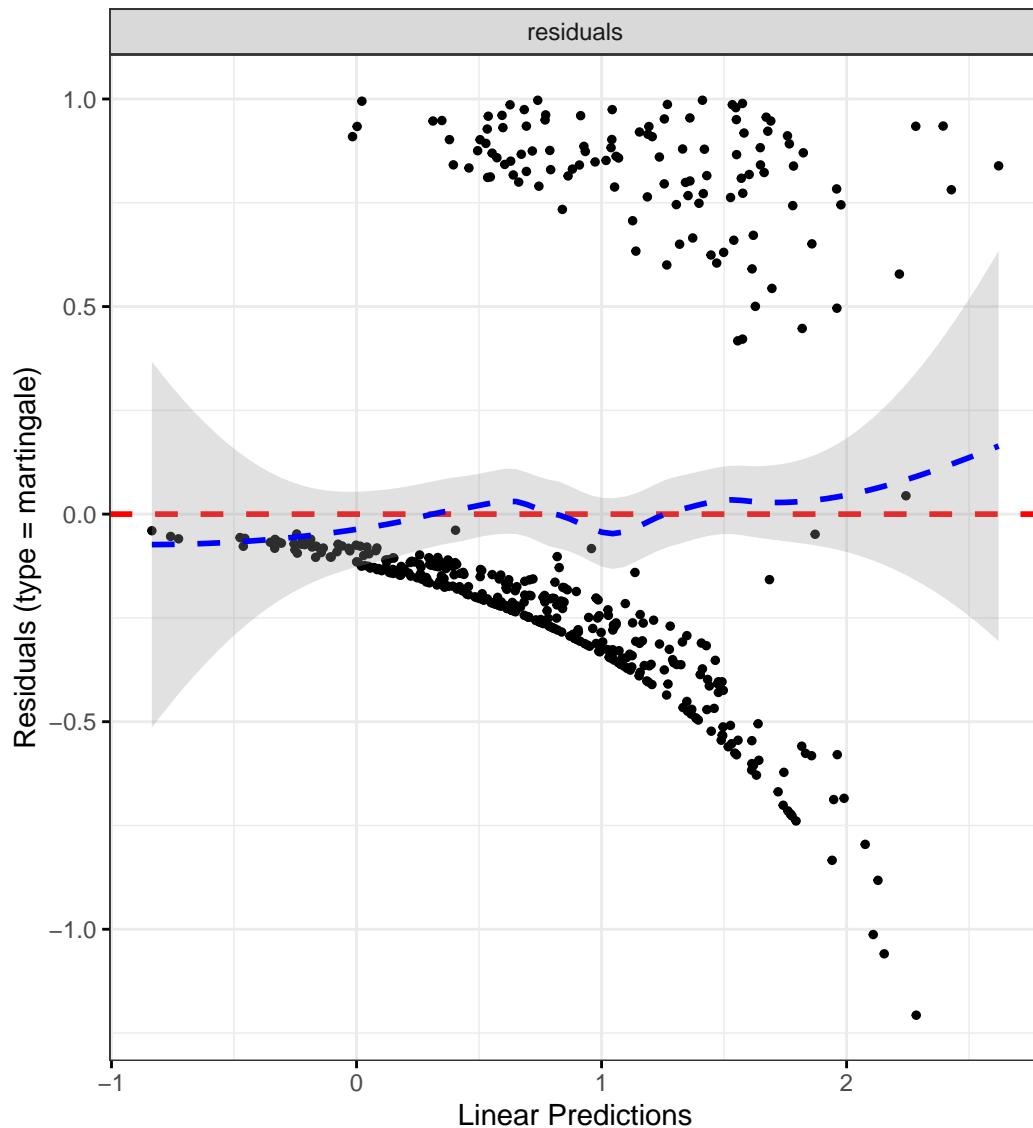
DF betas

```
`geom_smooth()` using formula = 'y ~ x'
```



Martingale residuals

```
`geom_smooth()` using formula = 'y ~ x'
```



Inflammatory bowel disease

Patient-reported flare

```
# Categorize bread intake by quantiles
flare.df <- categorize_by_quantiles(flare.df, "breadIntake", reference_data = flare.df)

# Run survival analysis using utility function
```

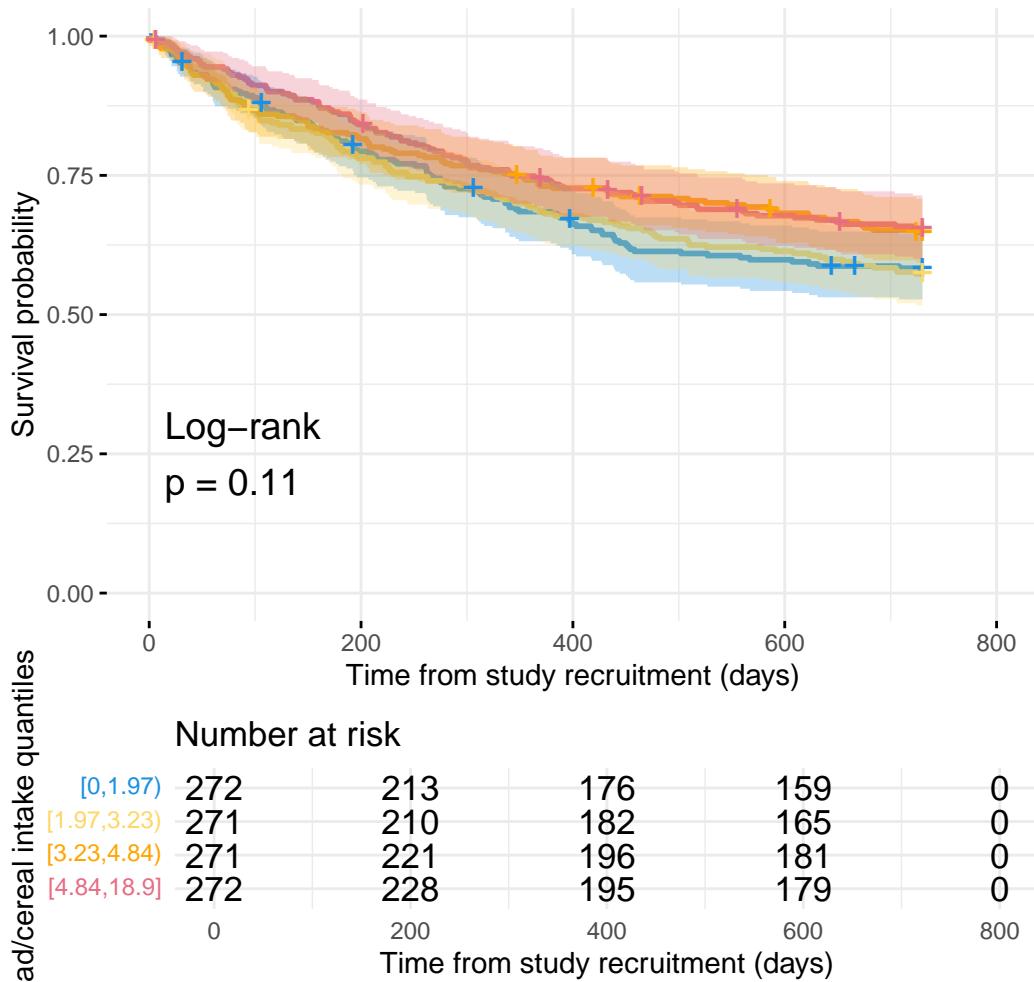
```
analysis_result <- run_survival_analysis(
  data = flare.df,
  var_name = "breadIntake",
  outcome_time = "softflare_time",
  outcome_event = "softflare",
  legend_title = "Bread/cereal intake quantiles",
  plot_base_path = "plots/ibd/soft-flare/diet/breadIntake",
  break_time_by = 200
)

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(softflare_time, softflare) ~
    Sex + cat + IMD + dqi_tot + BMI + breadIntake_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.df
)

# Display plot and model summary
analysis_result$plot
```

Time to patient-reported flare

Bread/cereal intake quantiles [0,1.97] [1.97,3.23] [3.23,4.84] [4.84,18.9]



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.7298	1.3914	2.1506	0.0000
catFC 50-250	1.5032	1.1900	1.8989	0.0006
catFC > 250	2.0014	1.5449	2.5927	0.0000

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	0.9930	0.6309	1.5629	0.9758
IMD3	1.0106	0.6549	1.5593	0.9621
IMD4	1.1187	0.7383	1.6949	0.5968
IMD5	1.0831	0.7252	1.6177	0.6966
dqi_tot	1.0025	0.9932	1.0118	0.6035
BMI	0.9952	0.9753	1.0154	0.6369
breadIntake_cat[1.97,3.23	1.0110	0.7695	1.3284	0.9371
breadIntake_cat[3.23,4.84	0.8747	0.6552	1.1678	0.3640
breadIntake_cat[4.84,18.9	0.8229	0.6141	1.1027	0.1918

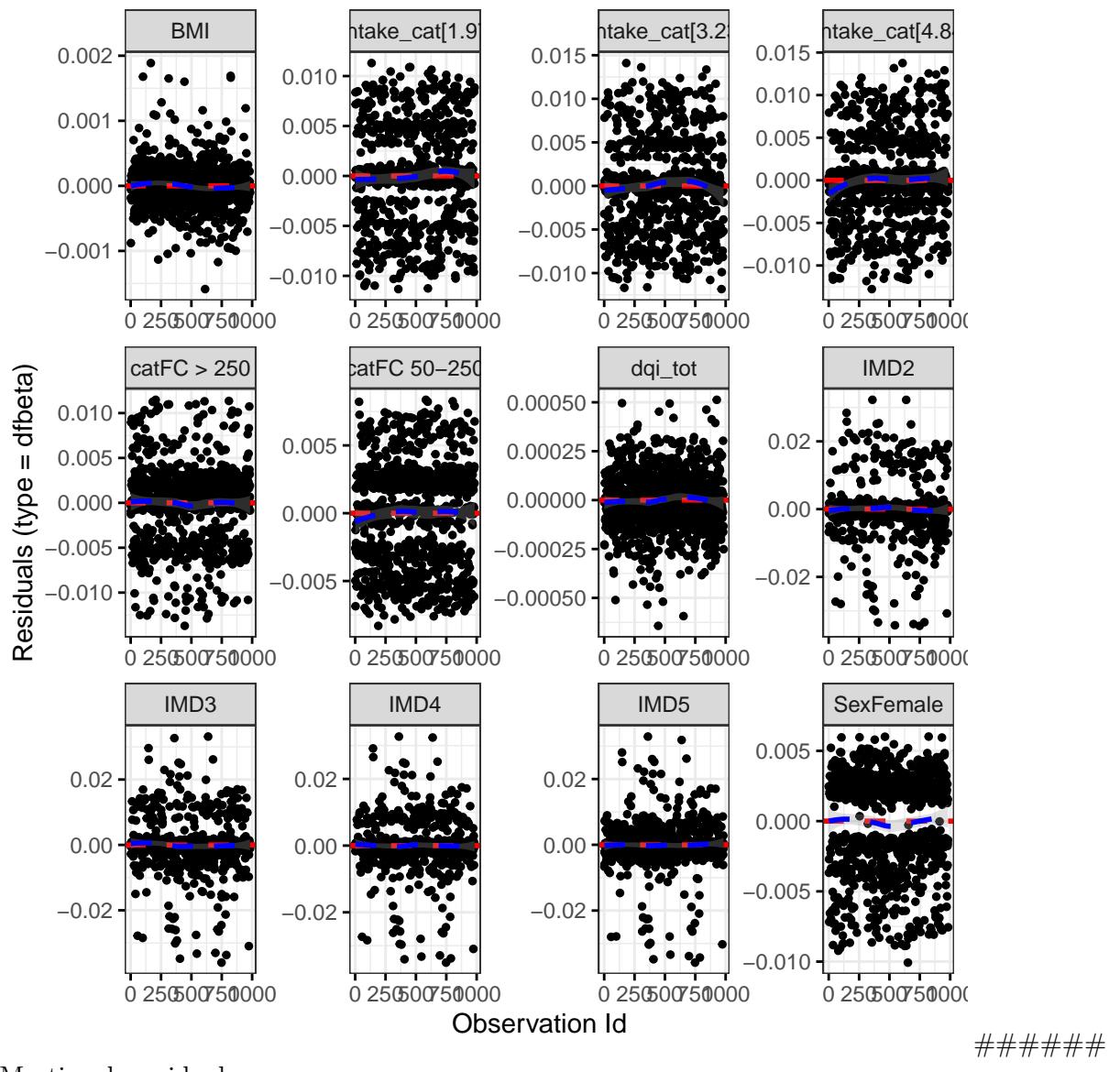
Diagnostics:

Proportional hazards assumption test

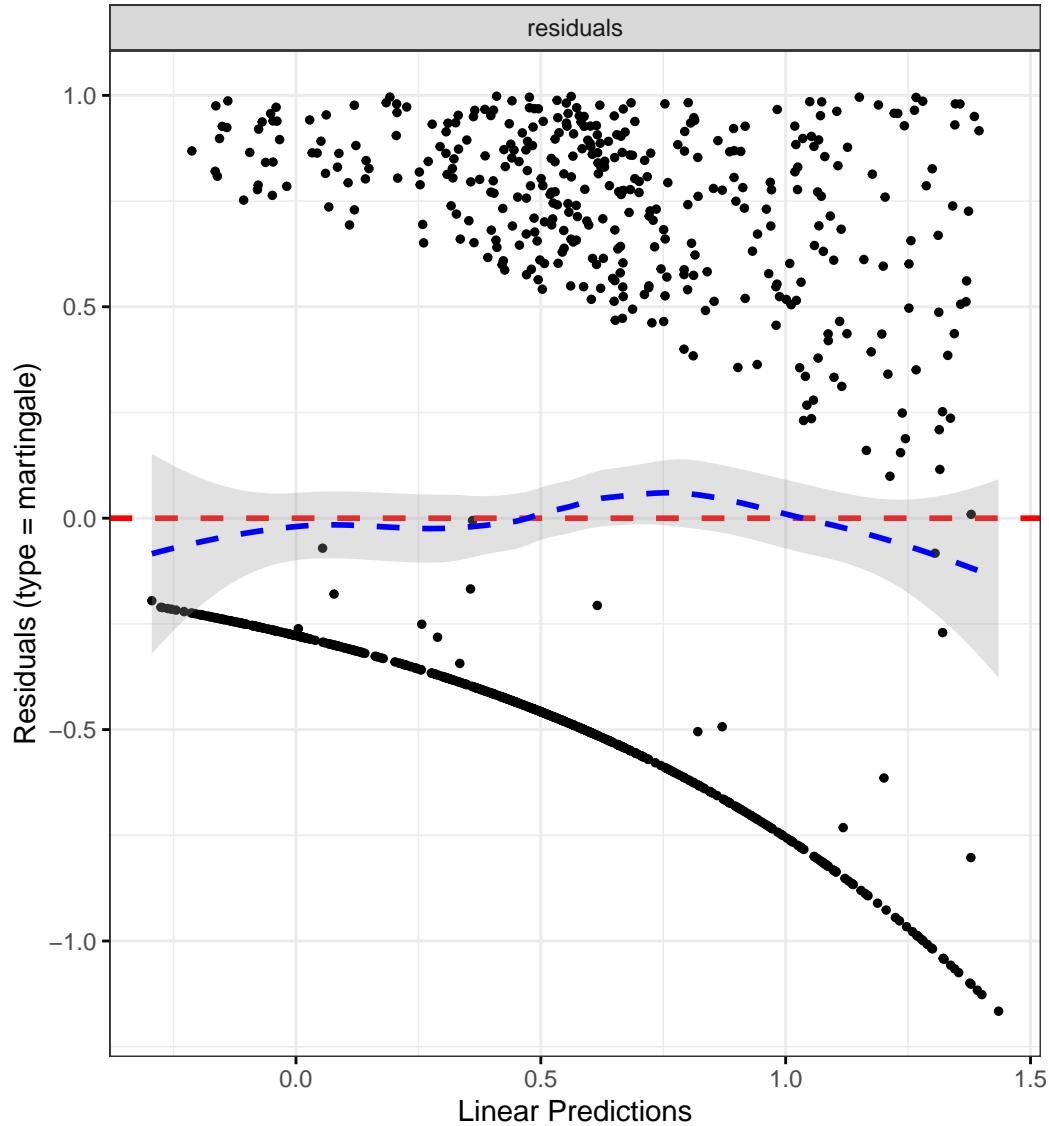
	Chi-squared statistic	DF	P-value
Sex	0.0067	1.0000	0.9346
cat	1.1012	2.0000	0.5766
IMD	4.9448	4.0000	0.2930
dqi_tot	1.4125	1.0000	0.2346
BMI	0.0107	1.0000	0.9175
breadIntake_cat	1.9383	3.0000	0.5853
GLOBAL	9.5634	12.0002	0.6542

DF betas

```
`geom_smooth()` using formula = 'y ~ x'
```



```
`geom_smooth()` using formula = 'y ~ x'
```



Hard flare

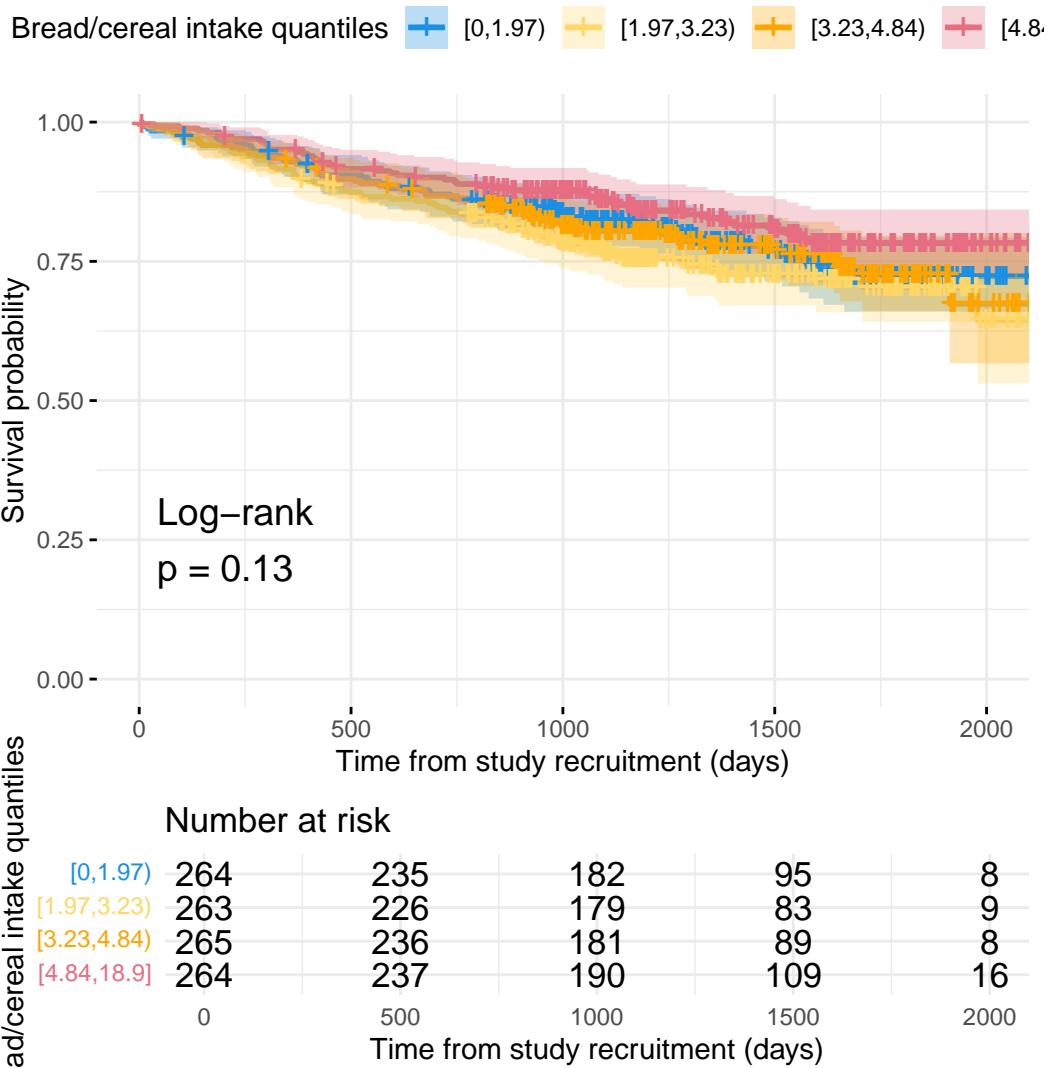
```
# Run survival analysis using utility function for hard flare
analysis_result <- run_survival_analysis(
  data = flare.df,
  var_name = "breadIntake",
  outcome_time = "hardflare_time",
  outcome_event = "hardflare",
  legend_title = "Bread/cereal intake quantiles",
```

```
plot_base_path = "plots/ibd/hard-flare/diet/breadIntake",
break_time_by = 500
)

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(hardflare_time, hardflare) ~
    Sex + cat + IMD + dqi_tot + BMI + breadIntake_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.df
)

# Display plot and model summary
analysis_result$plot
```

Time to hard flare



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.1999	0.9078	1.5860	0.2003
catFC 50-250	1.8702	1.3660	2.5605	0.0001
catFC > 250	2.6057	1.8425	3.6850	0.0000

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	0.9120	0.4876	1.7058	0.7731
IMD3	0.9527	0.5226	1.7370	0.8745
IMD4	1.3641	0.7767	2.3957	0.2798
IMD5	0.9665	0.5544	1.6848	0.9043
dqi_tot	1.0028	0.9903	1.0154	0.6668
BMI	0.9910	0.9646	1.0182	0.5140
breadIntake_cat[1.97,3.23	1.0072	0.7018	1.4455	0.9691
breadIntake_cat[3.23,4.84	0.9468	0.6516	1.3759	0.7744
breadIntake_cat[4.84,18.9	0.6680	0.4480	0.9960	0.0478

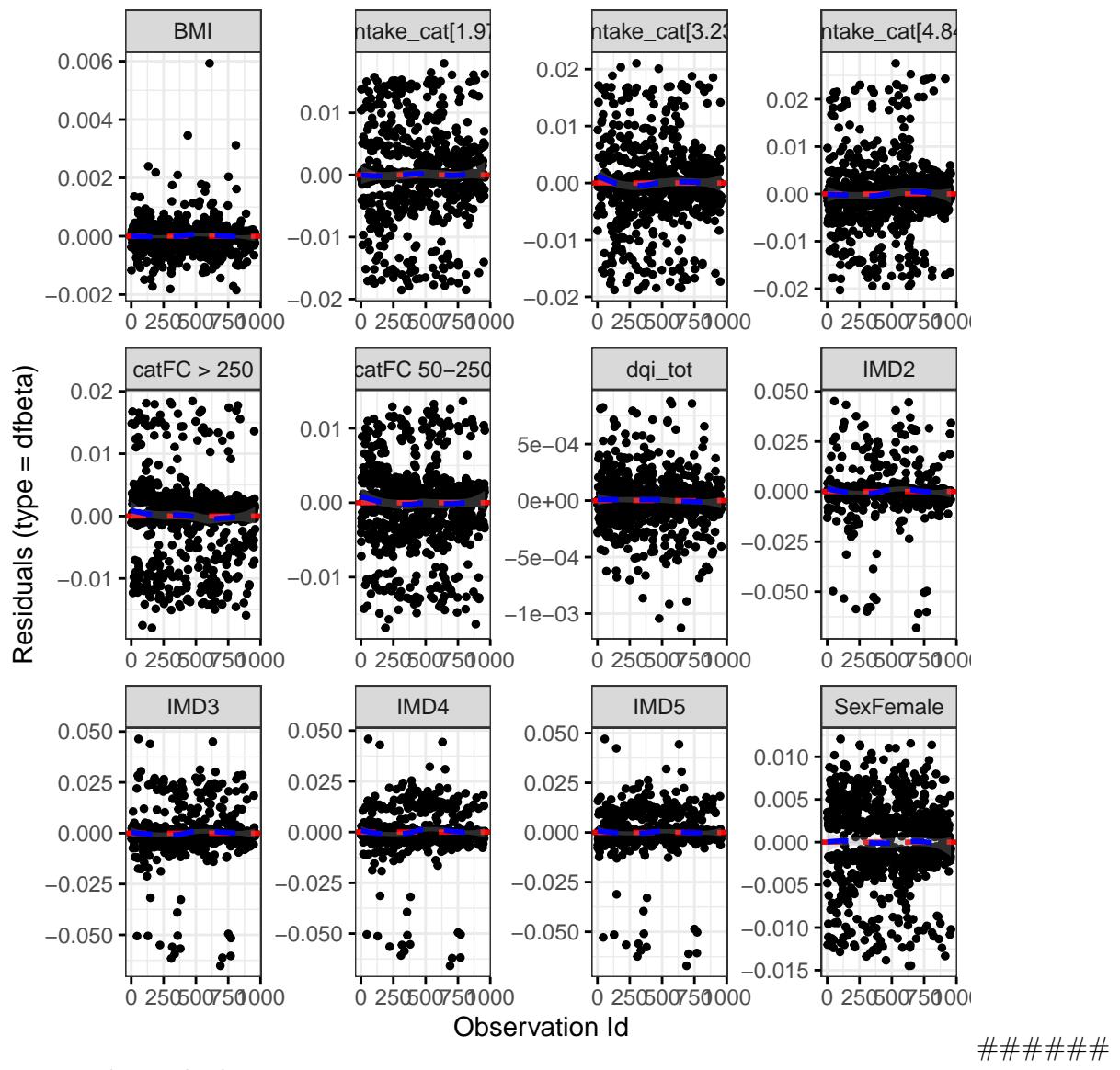
Diagnostics:

Proportional hazards assumption test

	Chi-squared statistic	DF	P-value
Sex	0.0416	0.9886	0.8347
cat	6.6262	1.9786	0.0356
IMD	1.6491	3.9447	0.7931
dqi_tot	1.9561	0.9920	0.1603
BMI	1.7776	0.9887	0.1800
breadIntake_cat	0.3860	2.9751	0.9414
GLOBAL	12.2429	22.9608	0.9661

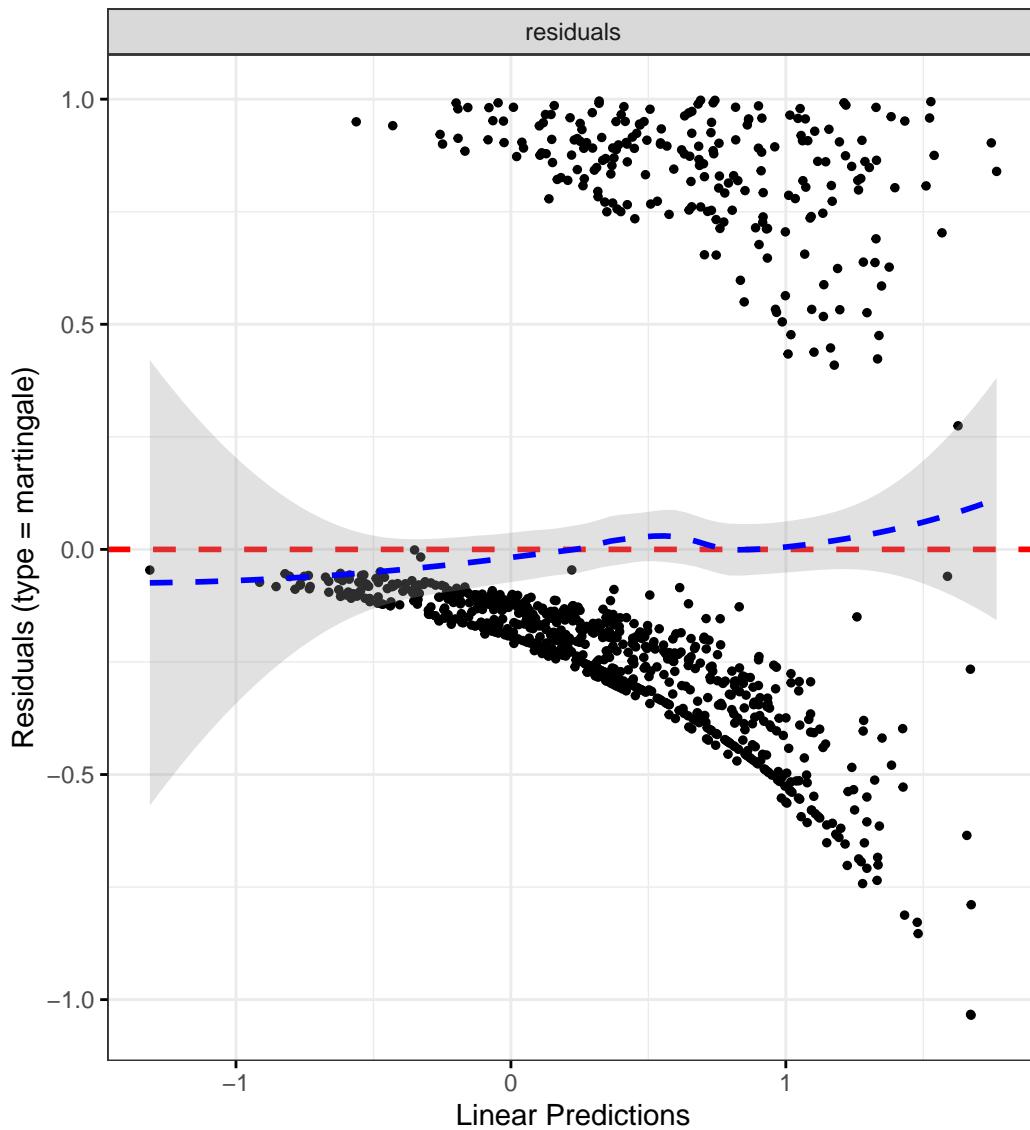
DF betas

```
`geom_smooth()` using formula = 'y ~ x'
```



Martingale residuals

```
`geom_smooth()` using formula = 'y ~ x'
```



Sweets and desserts/snack foods

Crohn's disease

Patient-reported flare

```
# Categorize sweet intake by quantiles
flare.cd.df <- categorize_by_quantiles(flare.cd.df, "sweetIntake", reference_data = flare.df)
```

```

# Run survival analysis using utility function
analysis_result <- run_survival_analysis(
  data = flare.cd.df,
  var_name = "sweetIntake",
  outcome_time = "softflare_time",
  outcome_event = "softflare",
  legend_title = "Sweet/dessert/snack intake quantiles",
  plot_base_path = "plots/cd/soft-flare/diet/sweetIntake",
  break_time_by = 200
)

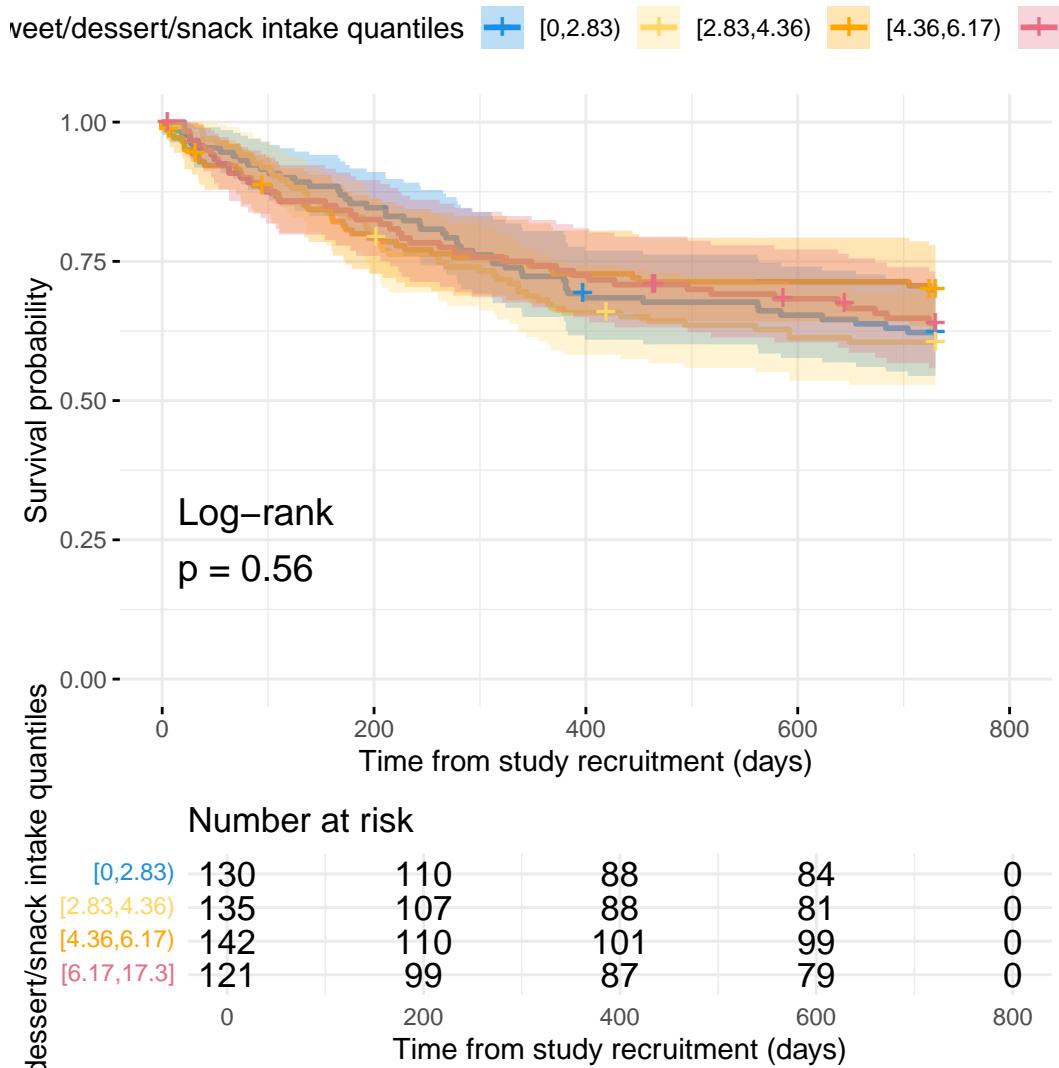
# Save plot as RDS
saveRDS(analysis_result$plot, paste0(paths$outdir, "sweetIntake-cd-soft.RDS"))

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(softflare_time, softflare) ~
    Sex + cat + IMD + dqi_tot + BMI + sweetIntake_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.cd.df
)

# Display plot and model summary
analysis_result$plot

```

Time to patient-reported flare



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.8949	1.3541	2.6516	0.0002
catFC 50-250	1.3187	0.9275	1.8750	0.1234
catFC > 250	2.0504	1.4008	3.0011	0.0002

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	0.7147	0.3722	1.3726	0.3131
IMD3	0.9678	0.5283	1.7728	0.9155
IMD4	0.8756	0.4816	1.5917	0.6630
IMD5	1.0159	0.5800	1.7795	0.9559
dqi_tot	1.0056	0.9918	1.0196	0.4272
BMI	1.0077	0.9799	1.0363	0.5920
sweetIntake_cat[2.83,4.36	1.0612	0.7023	1.6036	0.7778
sweetIntake_cat[4.36,6.17	0.8063	0.5172	1.2571	0.3421
sweetIntake_cat[6.17,17.3	1.0362	0.6645	1.6157	0.8754

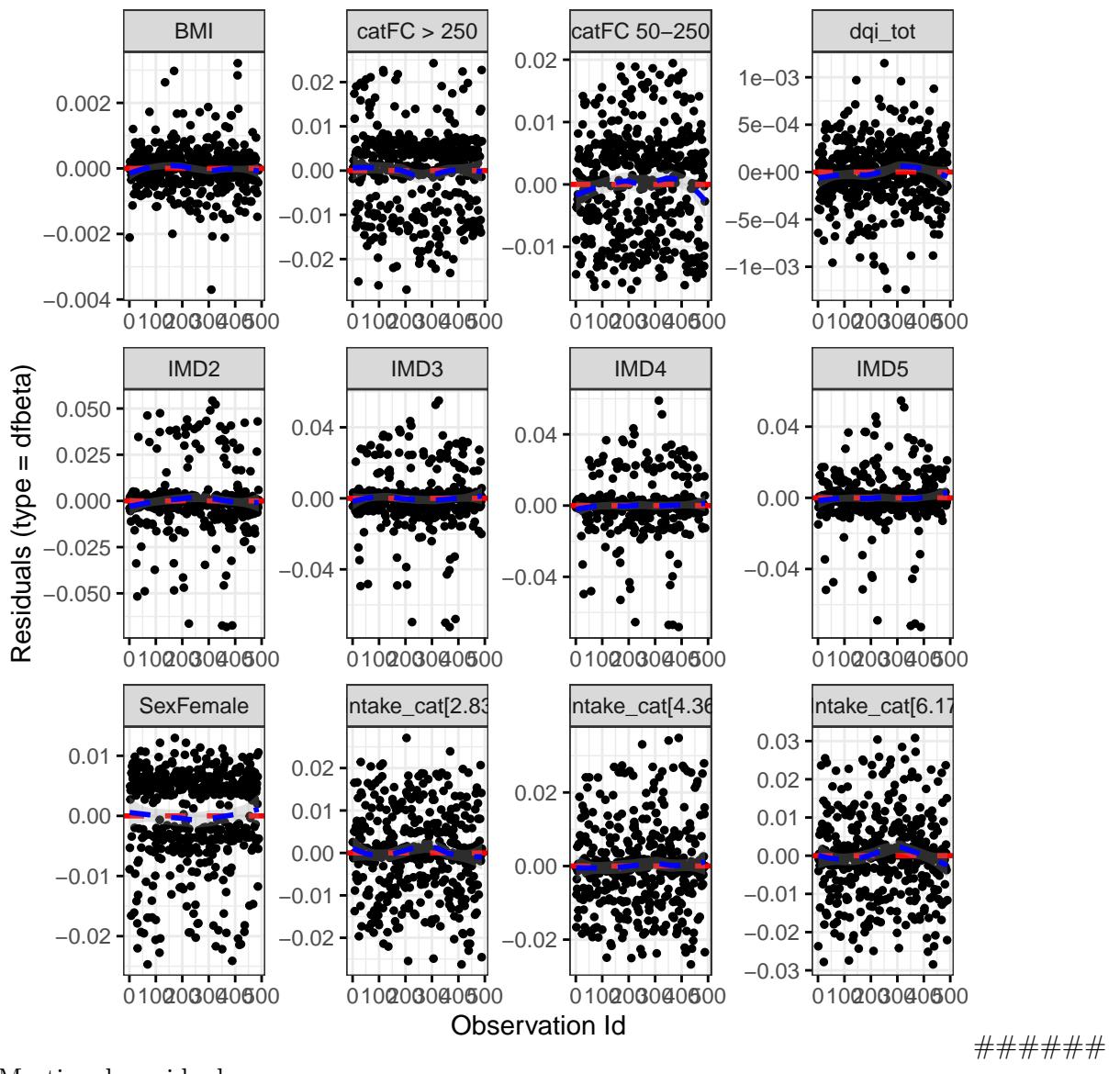
Diagnostics:

Proportional hazards assumption test

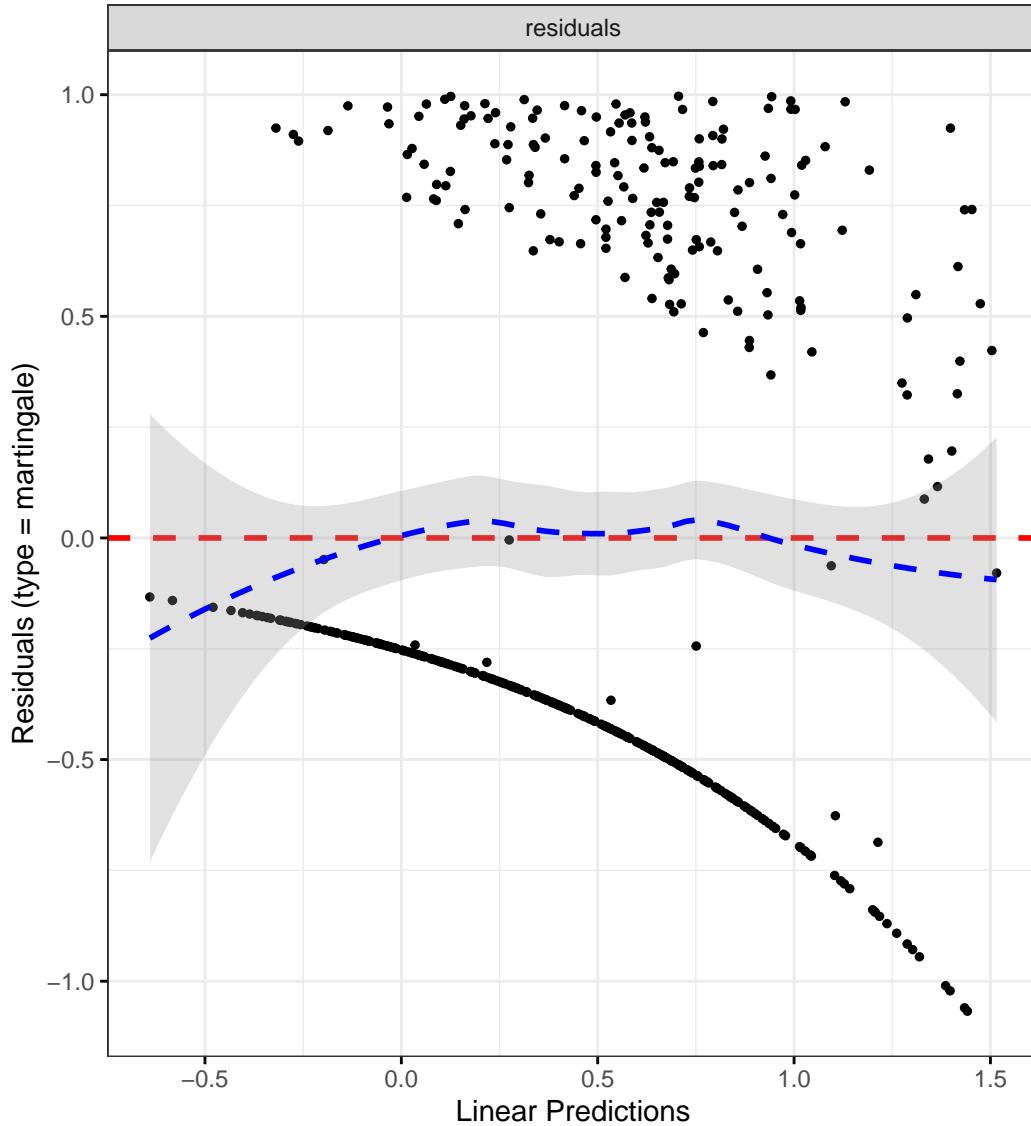
	Chi-squared statistic	DF	P-value
Sex	0.2861	1.0000	0.5928
cat	0.8500	2.0000	0.6538
IMD	3.0084	4.0000	0.5564
dqi_tot	0.3710	1.0000	0.5425
BMI	1.3535	1.0000	0.2447
sweetIntake_cat	10.1113	3.0000	0.0176
GLOBAL	15.2266	12.0001	0.2293

DF betas

```
`geom_smooth()` using formula = 'y ~ x'
```



```
`geom_smooth()` using formula = 'y ~ x'
```



Hard flare

```
# Run survival analysis using utility function for hard flare
analysis_result <- run_survival_analysis(
  data = flare.cd.df,
  var_name = "sweetIntake",
  outcome_time = "hardflare_time",
  outcome_event = "hardflare",
  legend_title = "Sweet/dessert/snack intake quantiles",
```

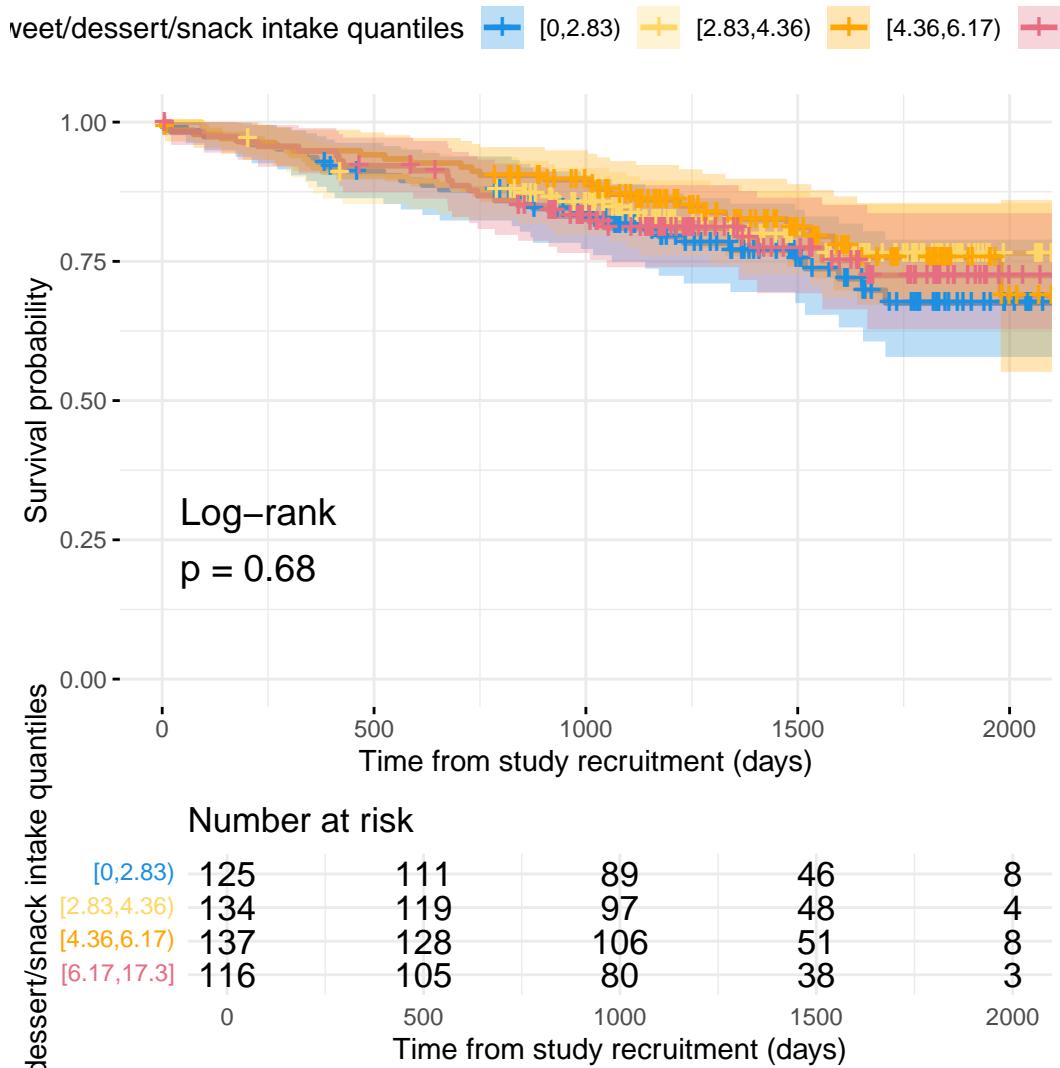
```
plot_base_path = "plots/cd/hard-flare/diet/sweetIntake",
break_time_by = 500
)

# Save plot as RDS
saveRDS(analysis_result$plot, paste0(paths$outdir, "sweetIntake-cd-hard.RDS"))

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(hardflare_time, hardflare) ~
    Sex + cat + IMD + dqi_tot + BMI + sweetIntake_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.cd.df
)

# Display plot and model summary
analysis_result$plot
```

Time to hard flare



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.3925	0.9159	2.1172	0.1214
catFC 50-250	1.8455	1.1581	2.9407	0.0100
catFC > 250	2.9263	1.7688	4.8413	0.0000

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	0.6548	0.2812	1.5249	0.3263
IMD3	0.8444	0.3807	1.8729	0.6774
IMD4	0.8018	0.3683	1.7454	0.5778
IMD5	0.7467	0.3585	1.5553	0.4352
dqi_tot	1.0025	0.9845	1.0209	0.7851
BMI	1.0194	0.9841	1.0561	0.2851
sweetIntake_cat[2.83,4.36	0.7477	0.4309	1.2972	0.3010
sweetIntake_cat[4.36,6.17	0.7720	0.4479	1.3306	0.3515
sweetIntake_cat[6.17,17.3	0.9325	0.5337	1.6294	0.8062

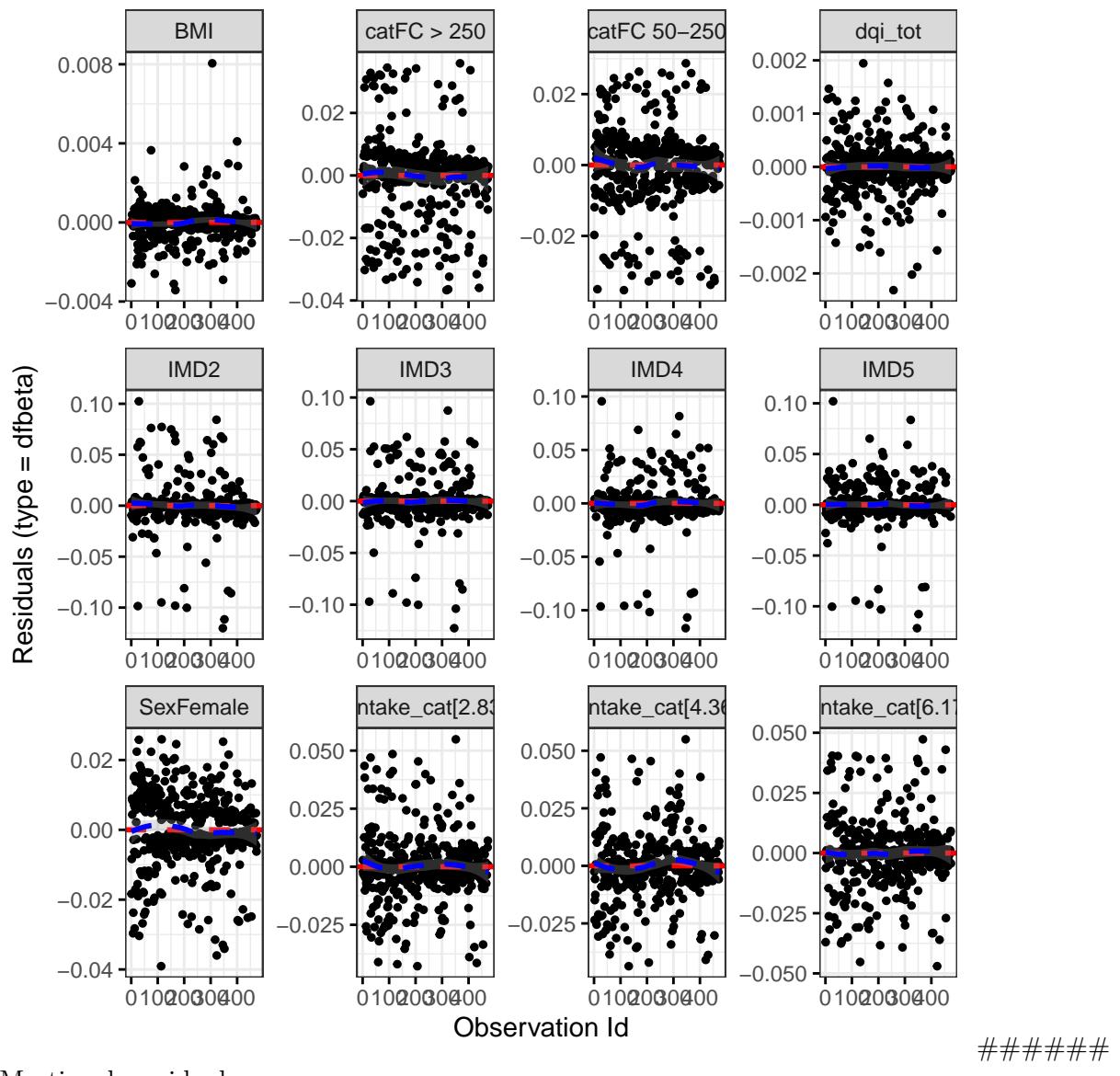
Diagnostics:

Proportional hazards assumption test

	Chi-squared statistic	DF	P-value
Sex	0.0651	0.9718	0.7885
cat	10.1084	1.9788	0.0062
IMD	2.6137	3.9315	0.6138
dqi_tot	2.7412	0.9905	0.0965
BMI	1.0543	0.9802	0.2983
sweetIntake_cat	0.6600	2.9648	0.8787
GLOBAL	17.0427	18.1954	0.5334

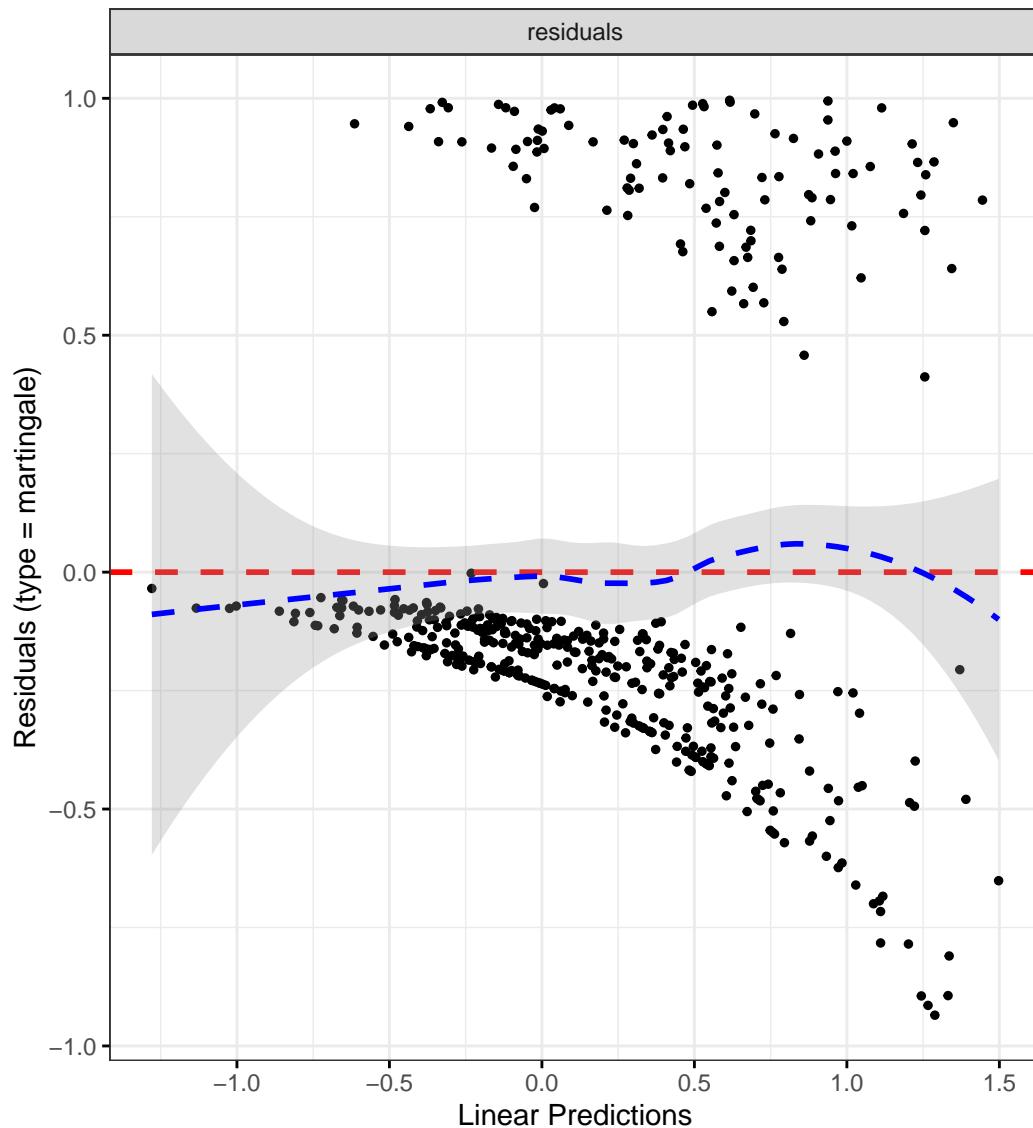
DF betas

```
`geom_smooth()` using formula = 'y ~ x'
```



Martingale residuals

```
`geom_smooth()` using formula = 'y ~ x'
```



Ulcerative colitis

Patient-reported flare

```
# Categorize sweet intake by quantiles
flare.uc.df <- categorize_by_quantiles(flare.uc.df, "sweetIntake", reference_data = flare.df)

# Run survival analysis using utility function
```

```

analysis_result <- run_survival_analysis(
  data = flare.uc.df,
  var_name = "sweetIntake",
  outcome_time = "softflare_time",
  outcome_event = "softflare",
  legend_title = "Sweet/dessert/snack intake quantiles",
  plot_base_path = "plots/uc/soft-flare/diet/sweetIntake",
  break_time_by = 200
)

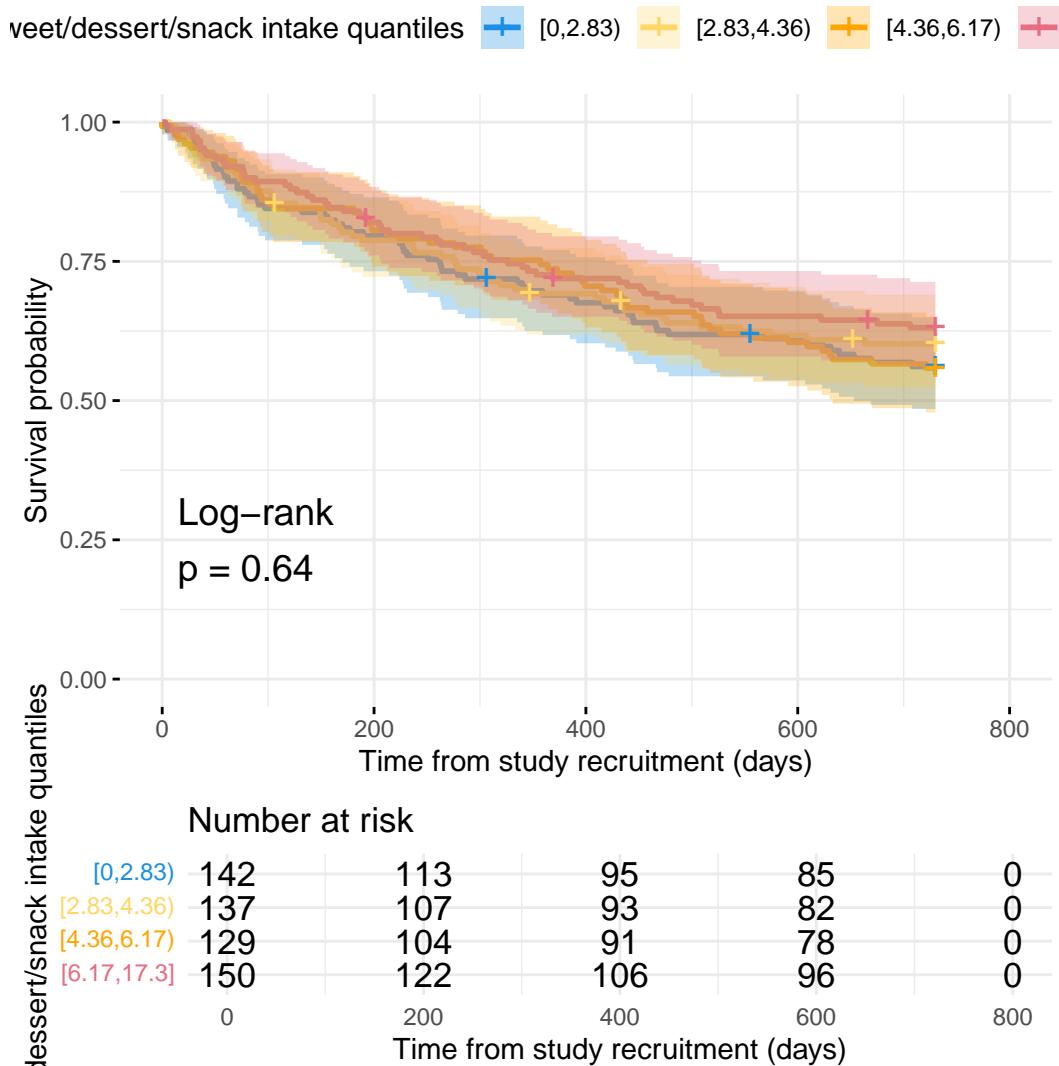
# Save plot as RDS
saveRDS(analysis_result$plot, paste0(paths$outdir, "sweetIntake-uc-soft.RDS"))

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(softflare_time, softflare) ~
    Sex + cat + IMD + dqi_tot + BMI + sweetIntake_cat +
    frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.uc.df
)

# Display plot and model summary
analysis_result$plot

```

Time to patient-reported flare



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.7292	1.2927	2.3131	0.0002
catFC 50-250	1.8689	1.3547	2.5782	0.0001
catFC > 250	2.0887	1.4617	2.9848	0.0001

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	1.3991	0.7344	2.6653	0.3071
IMD3	1.1566	0.6119	2.1863	0.6542
IMD4	1.3474	0.7434	2.4423	0.3258
IMD5	1.1844	0.6576	2.1333	0.5729
dqi_tot	0.9978	0.9850	1.0108	0.7425
BMI	0.9767	0.9479	1.0063	0.1216
sweetIntake_cat[2.83,4.36	0.7848	0.5340	1.1534	0.2174
sweetIntake_cat[4.36,6.17	0.7567	0.5144	1.1130	0.1568
sweetIntake_cat[6.17,17.3	0.7399	0.5054	1.0830	0.1212

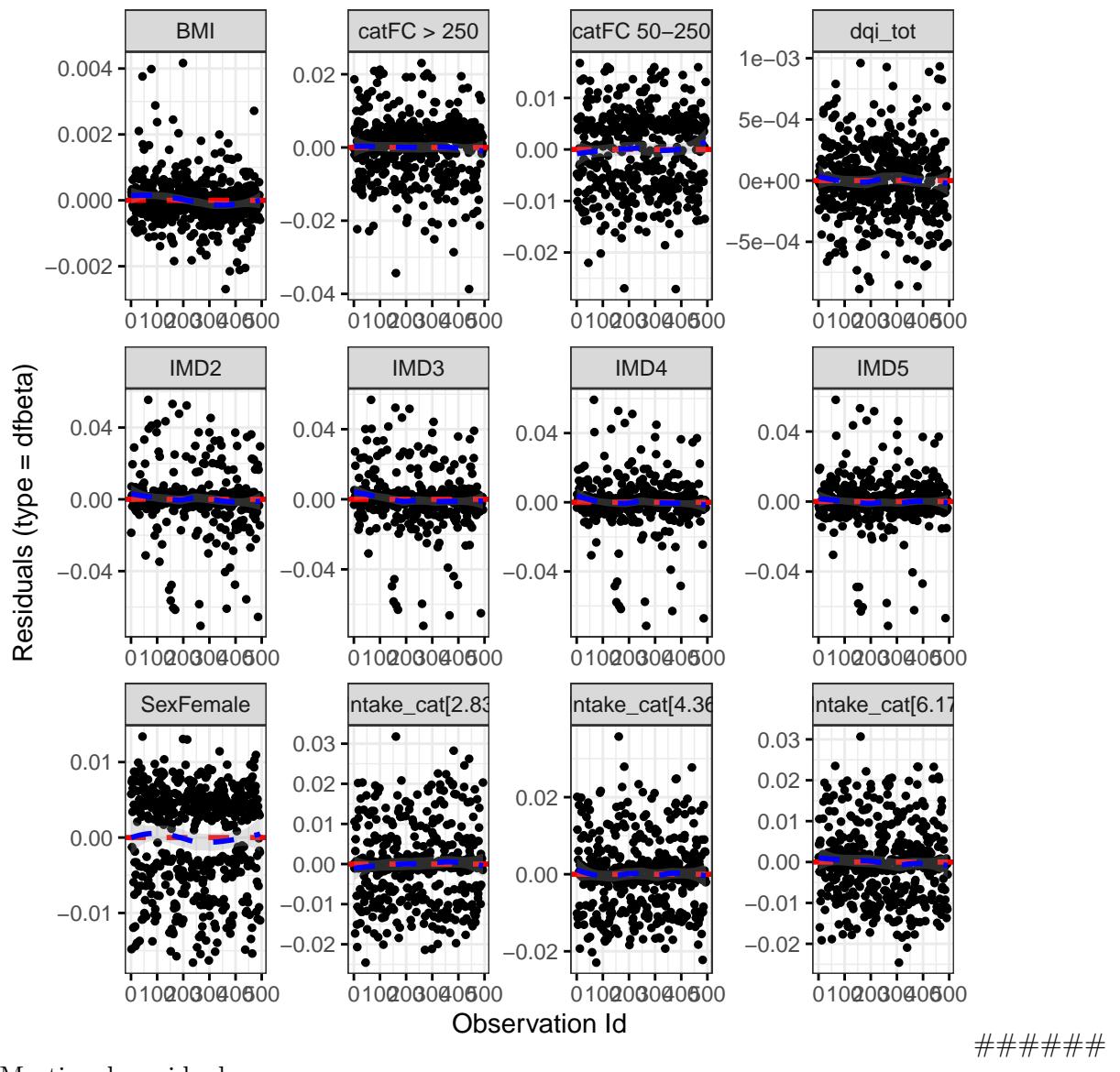
Diagnostics:

Proportional hazards assumption test

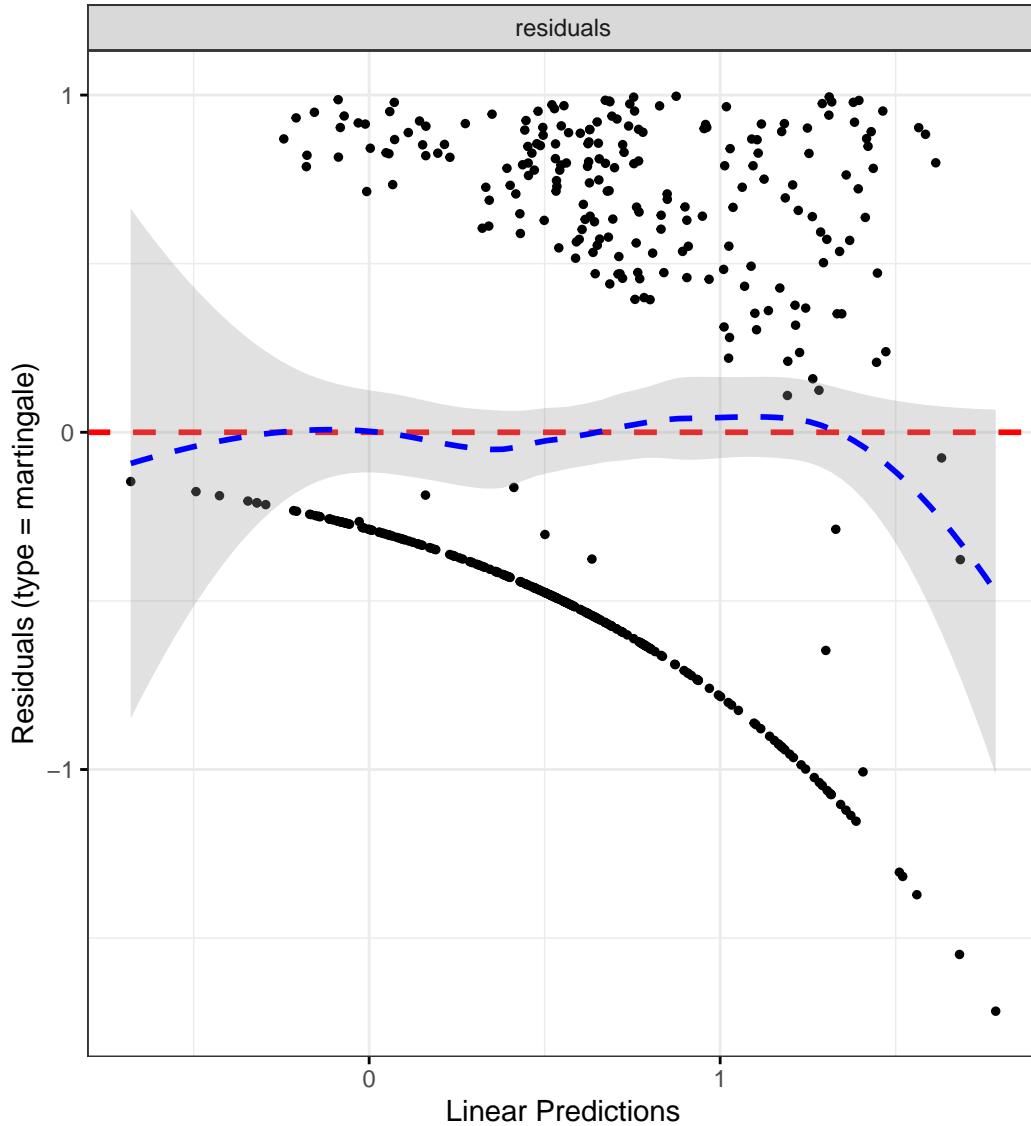
	Chi-squared statistic	DF	P-value
Sex	0.0034	1.0000	0.9532
cat	3.4572	2.0000	0.1775
IMD	2.5656	4.0000	0.6329
dqi_tot	0.7507	1.0000	0.3862
BMI	0.8299	1.0000	0.3623
sweetIntake_cat	1.0874	3.0000	0.7801
GLOBAL	9.2010	12.0001	0.6857

DF betas

```
`geom_smooth()` using formula = 'y ~ x'
```



```
`geom_smooth()` using formula = 'y ~ x'
```



Hard flare

```
# Run survival analysis using utility function for hard flare
analysis_result <- run_survival_analysis(
  data = flare.uc.df,
  var_name = "sweetIntake",
  outcome_time = "hardflare_time",
  outcome_event = "hardflare",
  legend_title = "Sweet/dessert/snack intake quantiles",
```

```

plot_base_path = "plots/uc/hard-flare/diet/sweetIntake",
break_time_by = 500
)

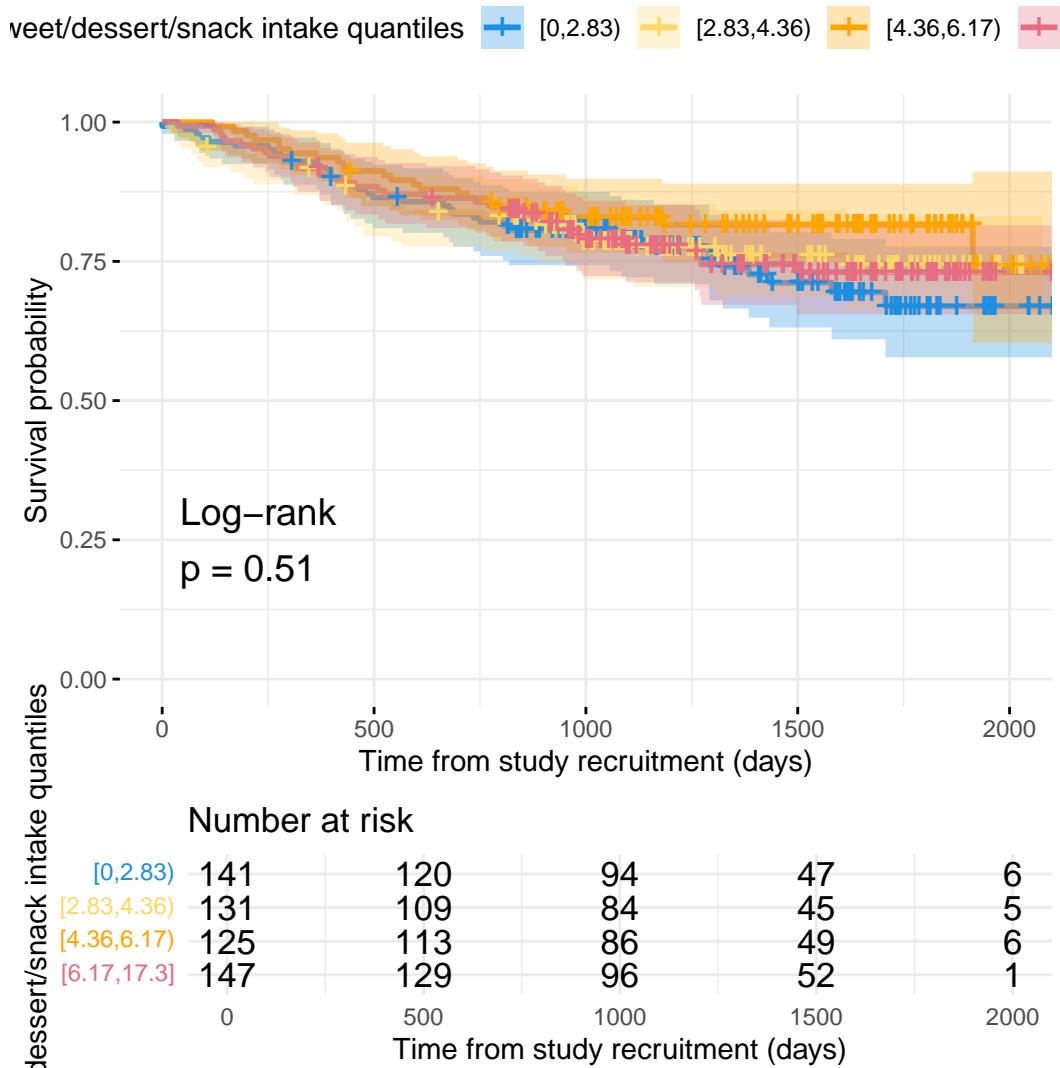
# Save plot as RDS
saveRDS(analysis_result$plot, paste0(paths$outdir, "sweetIntake-uc-hard.RDS"))

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(hardflare_time, hardflare) ~
    Sex + cat + IMD + dqi_tot + BMI + sweetIntake_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.uc.df
)

# Display plot and model summary
analysis_result$plot

```

Time to hard flare



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.2478	0.8519	1.8277	0.2555
catFC 50-250	2.2171	1.4295	3.4385	0.0004
catFC > 250	2.6535	1.6269	4.3280	0.0001

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	1.4938	0.5653	3.9472	0.4182
IMD3	1.2641	0.4863	3.2855	0.6306
IMD4	2.3158	0.9616	5.5768	0.0611
IMD5	1.4183	0.5832	3.4491	0.4409
dqi_tot	1.0008	0.9832	1.0187	0.9302
BMI	0.9600	0.9204	1.0014	0.0584
sweetIntake_cat[2.83,4.36	0.6915	0.4125	1.1592	0.1617
sweetIntake_cat[4.36,6.17	0.5093	0.2909	0.8916	0.0182
sweetIntake_cat[6.17,17.3	0.8931	0.5484	1.4543	0.6495

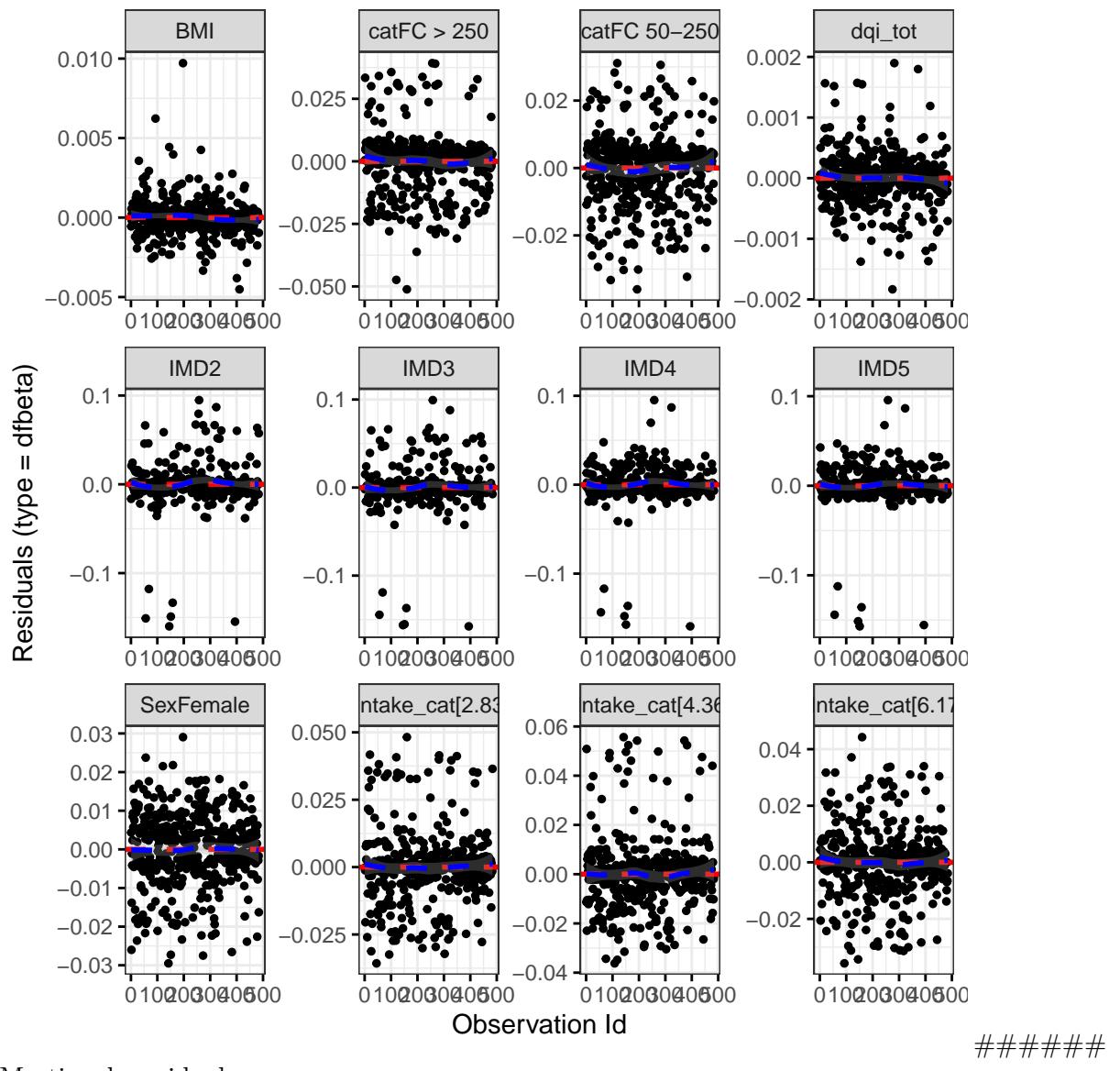
Diagnostics:

Proportional hazards assumption test

	Chi-squared statistic	DF	P-value
Sex	0.0144	0.9879	0.9017
cat	5.0681	1.9578	0.0763
IMD	1.2835	3.9288	0.8571
dqi_tot	0.0006	0.9853	0.9790
BMI	0.6578	0.9881	0.4128
sweetIntake_cat	1.2028	2.9501	0.7441
GLOBAL	8.3018	19.3980	0.9862

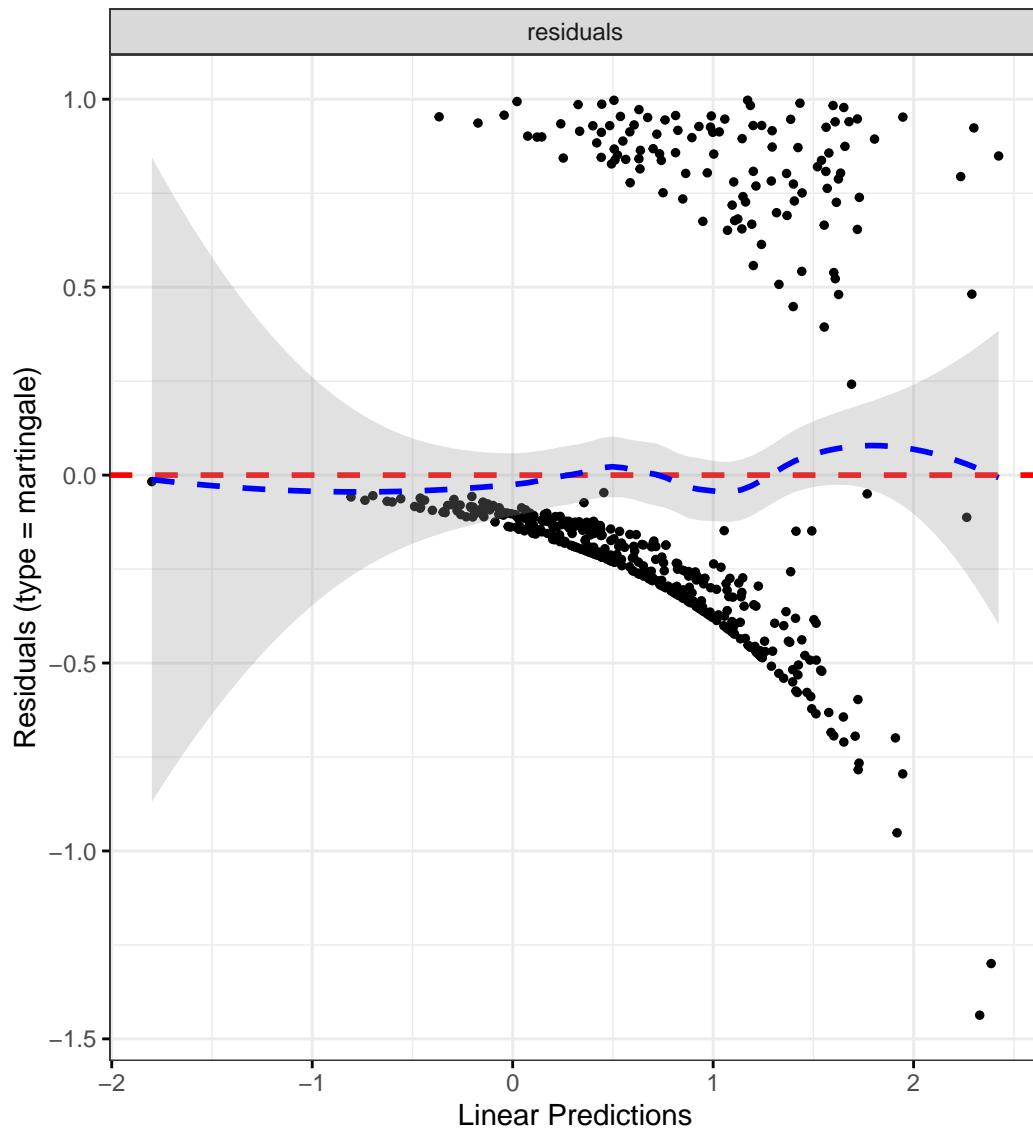
DF betas

```
`geom_smooth()` using formula = 'y ~ x'
```



Martingale residuals

```
`geom_smooth()` using formula = 'y ~ x'
```



Inflammatory bowel disease

Patient-reported flare

```
# Categorize sweet intake by quantiles
flare.df <- categorize_by_quantiles(flare.df, "sweetIntake", reference_data = flare.df)

# Run survival analysis using utility function
```

```

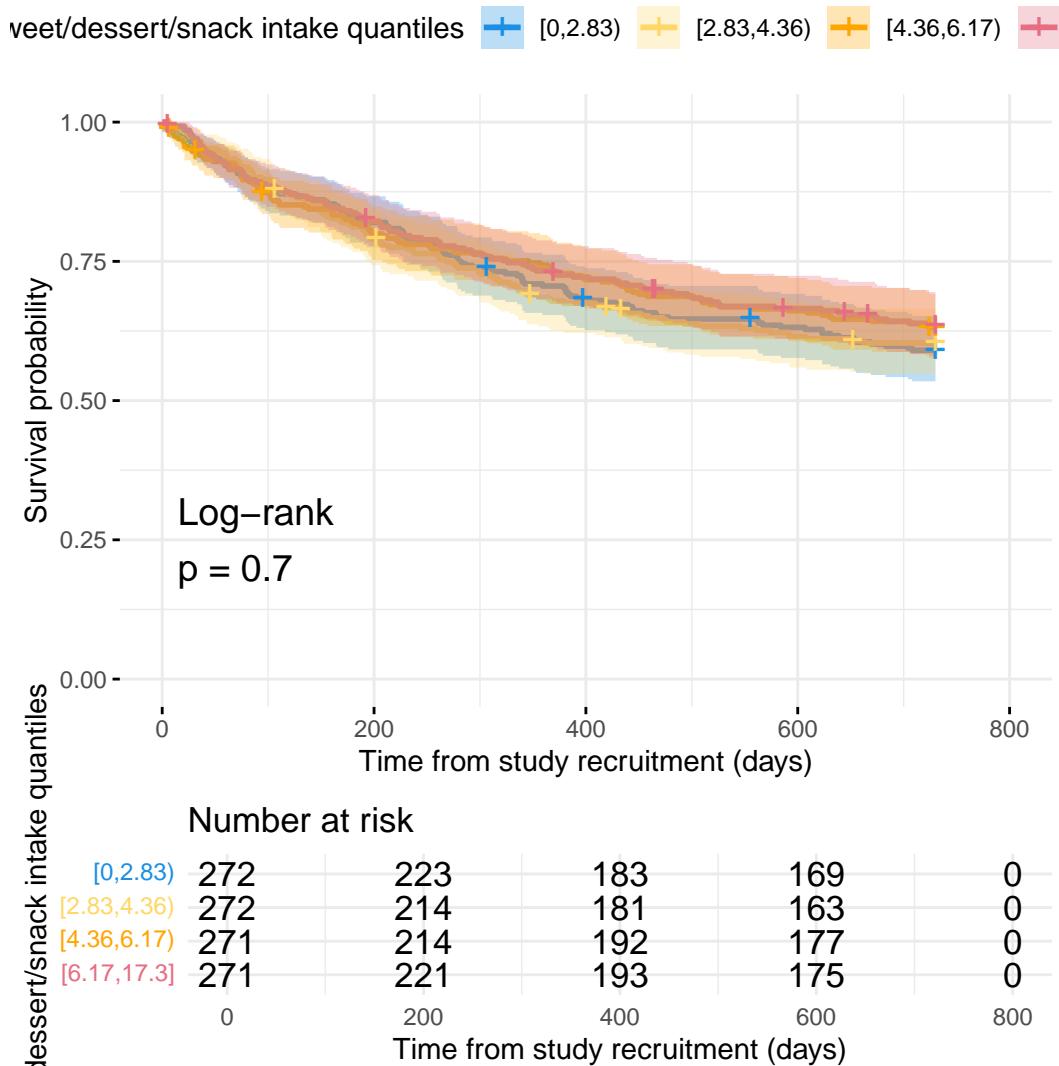
analysis_result <- run_survival_analysis(
  data = flare.df,
  var_name = "sweetIntake",
  outcome_time = "softflare_time",
  outcome_event = "softflare",
  legend_title = "Sweet/dessert/snack intake quantiles",
  plot_base_path = "plots/ibd/soft-flare/diet/sweetIntake",
  break_time_by = 200
)

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(softflare_time, softflare) ~
    Sex + cat + IMD + dqi_tot + BMI + sweetIntake_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.df
)

# Display plot and model summary
analysis_result$plot

```

Time to patient-reported flare



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.7904	1.4429	2.2216	0.0000
catFC 50-250	1.5176	1.2007	1.9180	0.0005
catFC > 250	2.0398	1.5742	2.6432	0.0000

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	0.9882	0.6277	1.5558	0.9591
IMD3	1.0169	0.6583	1.5708	0.9398
IMD4	1.1179	0.7371	1.6953	0.6000
IMD5	1.0921	0.7300	1.6340	0.6680
dqi_tot	1.0016	0.9923	1.0111	0.7334
BMI	0.9945	0.9747	1.0147	0.5895
sweetIntake_cat[2.83,4.36	0.9113	0.6895	1.2045	0.5140
sweetIntake_cat[4.36,6.17	0.7899	0.5917	1.0544	0.1095
sweetIntake_cat[6.17,17.3	0.8874	0.6664	1.1815	0.4133

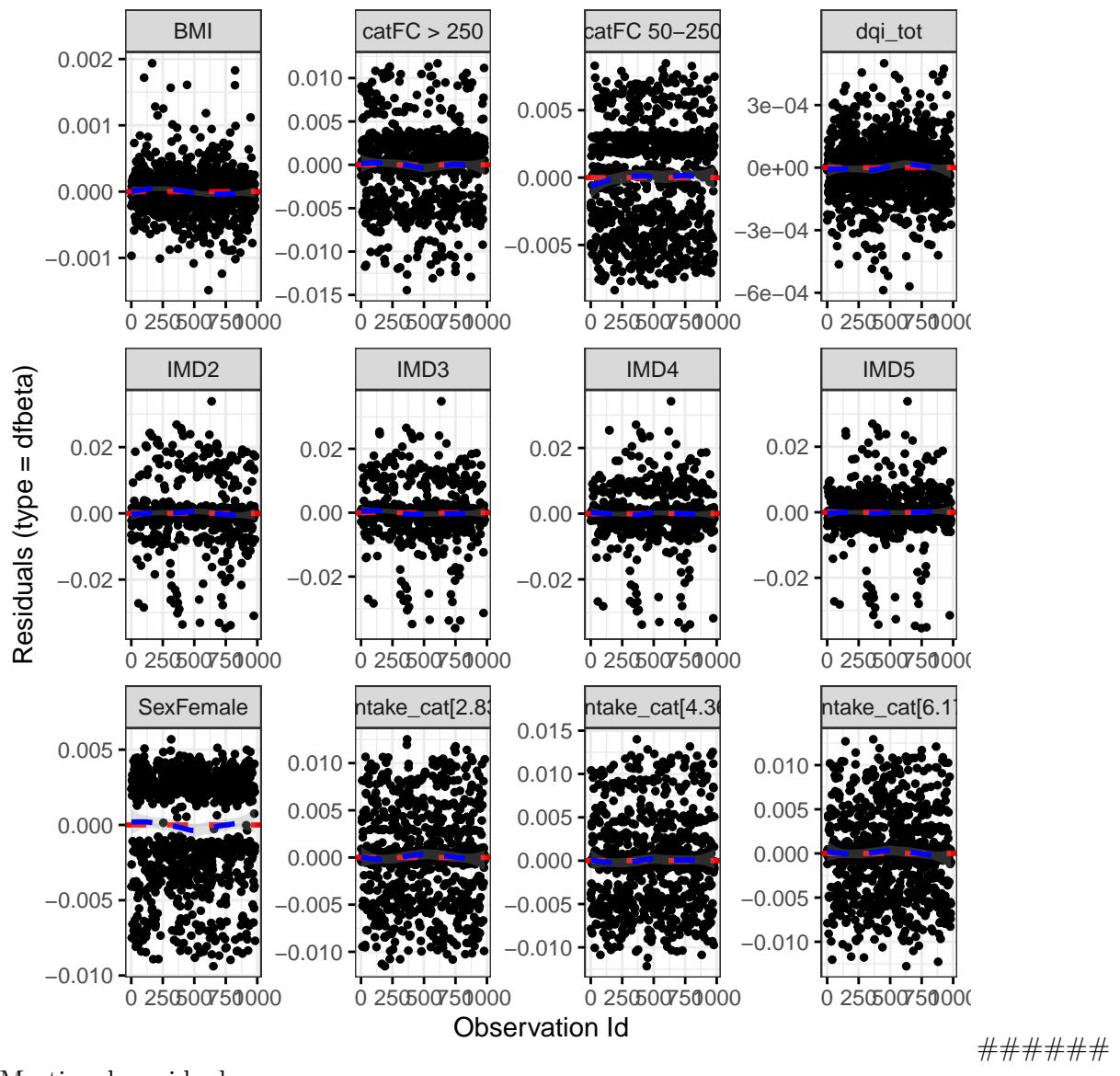
Diagnostics:

Proportional hazards assumption test

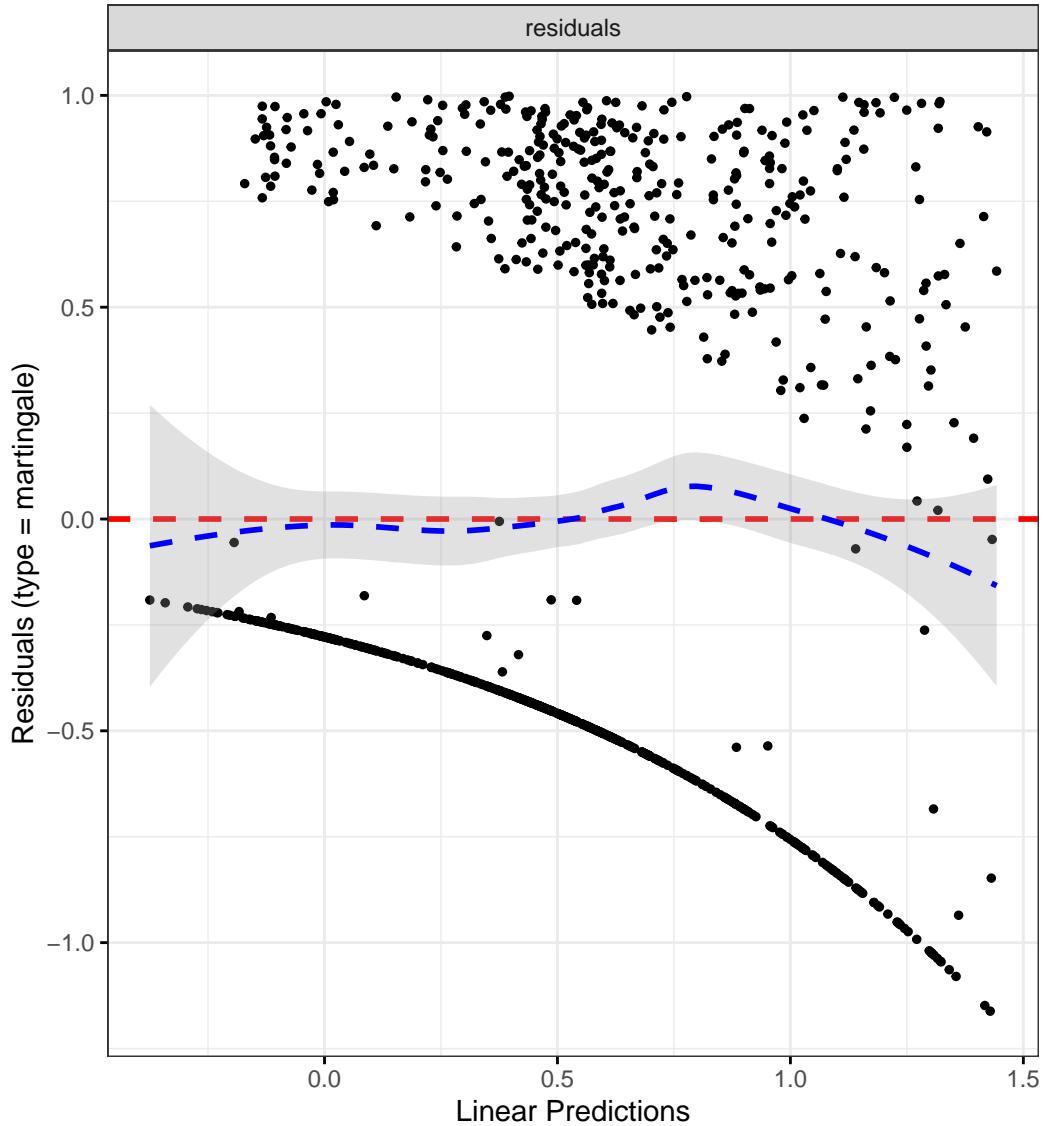
	Chi-squared statistic	DF	P-value
Sex	0.0085	1.0000	0.9267
cat	1.1156	2.0000	0.5725
IMD	4.9991	4.0000	0.2874
dqi_tot	1.3854	1.0000	0.2392
BMI	0.0158	1.0000	0.9000
sweetIntake_cat	3.4165	3.0000	0.3318
GLOBAL	10.7231	12.0002	0.5528

DF betas

```
`geom_smooth()` using formula = 'y ~ x'
```



```
`geom_smooth()` using formula = 'y ~ x'
```



Hard flare

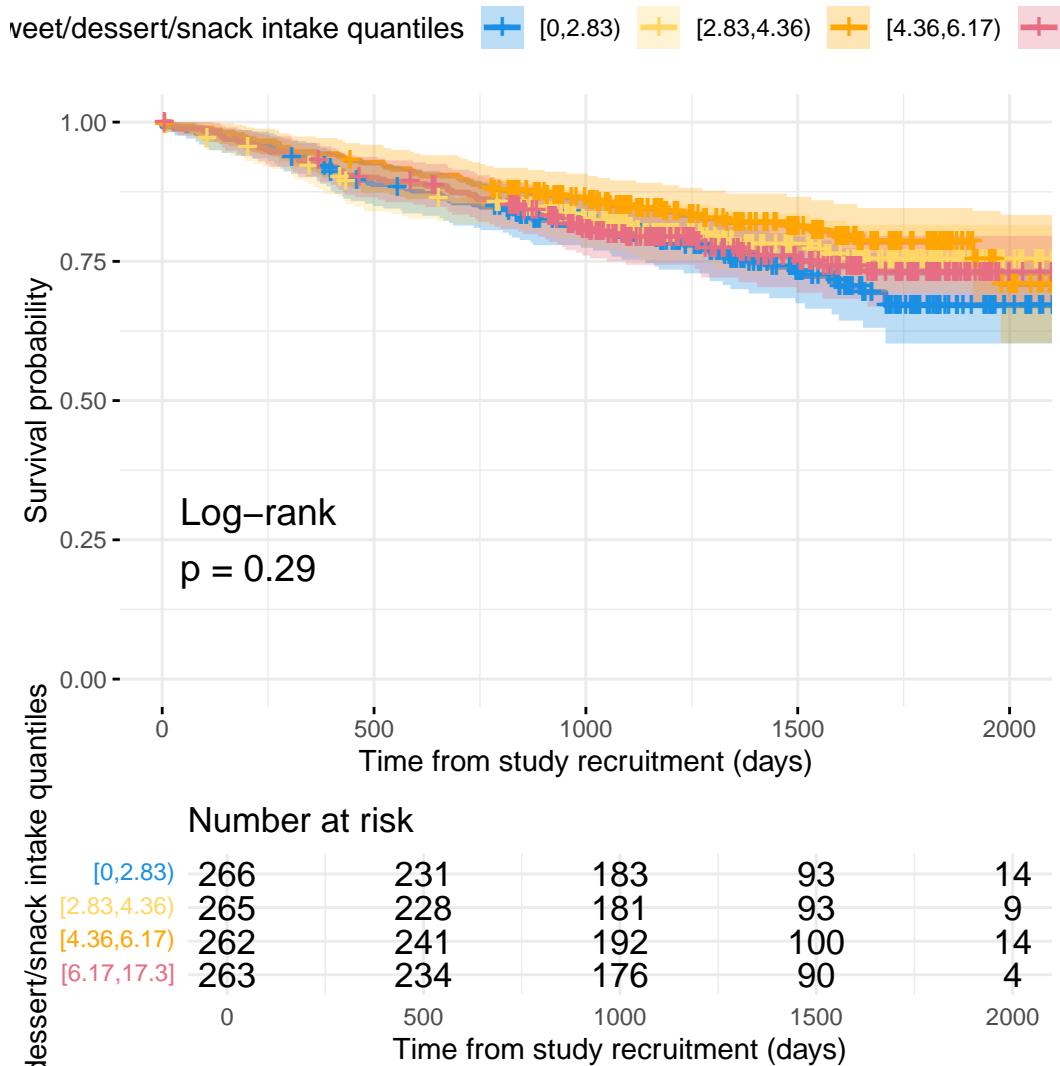
```
# Run survival analysis using utility function for hard flare
analysis_result <- run_survival_analysis(
  data = flare.df,
  var_name = "sweetIntake",
  outcome_time = "hardflare_time",
  outcome_event = "hardflare",
  legend_title = "Sweet/dessert/snack intake quantiles",
```

```
plot_base_path = "plots/ibd/hard-flare/diet/sweetIntake",
break_time_by = 500
)

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(hardflare_time, hardflare) ~
    Sex + cat + IMD + dqi_tot + BMI + sweetIntake_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.df
)

# Display plot and model summary
analysis_result$plot
```

Time to hard flare



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.3142	0.9958	1.7344	0.0536
catFC 50-250	1.9148	1.3966	2.6252	0.0001
catFC > 250	2.7022	1.9120	3.8189	0.0000

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	0.9503	0.5082	1.7771	0.8732
IMD3	0.9898	0.5425	1.8057	0.9733
IMD4	1.4306	0.8128	2.5181	0.2145
IMD5	1.0293	0.5888	1.7993	0.9193
dqi_tot	1.0008	0.9883	1.0135	0.8997
BMI	0.9918	0.9652	1.0191	0.5507
sweetIntake_cat[2.83,4.36	0.7056	0.4852	1.0260	0.0679
sweetIntake_cat[4.36,6.17	0.6232	0.4235	0.9171	0.0164
sweetIntake_cat[6.17,17.3	0.9359	0.6504	1.3467	0.7213

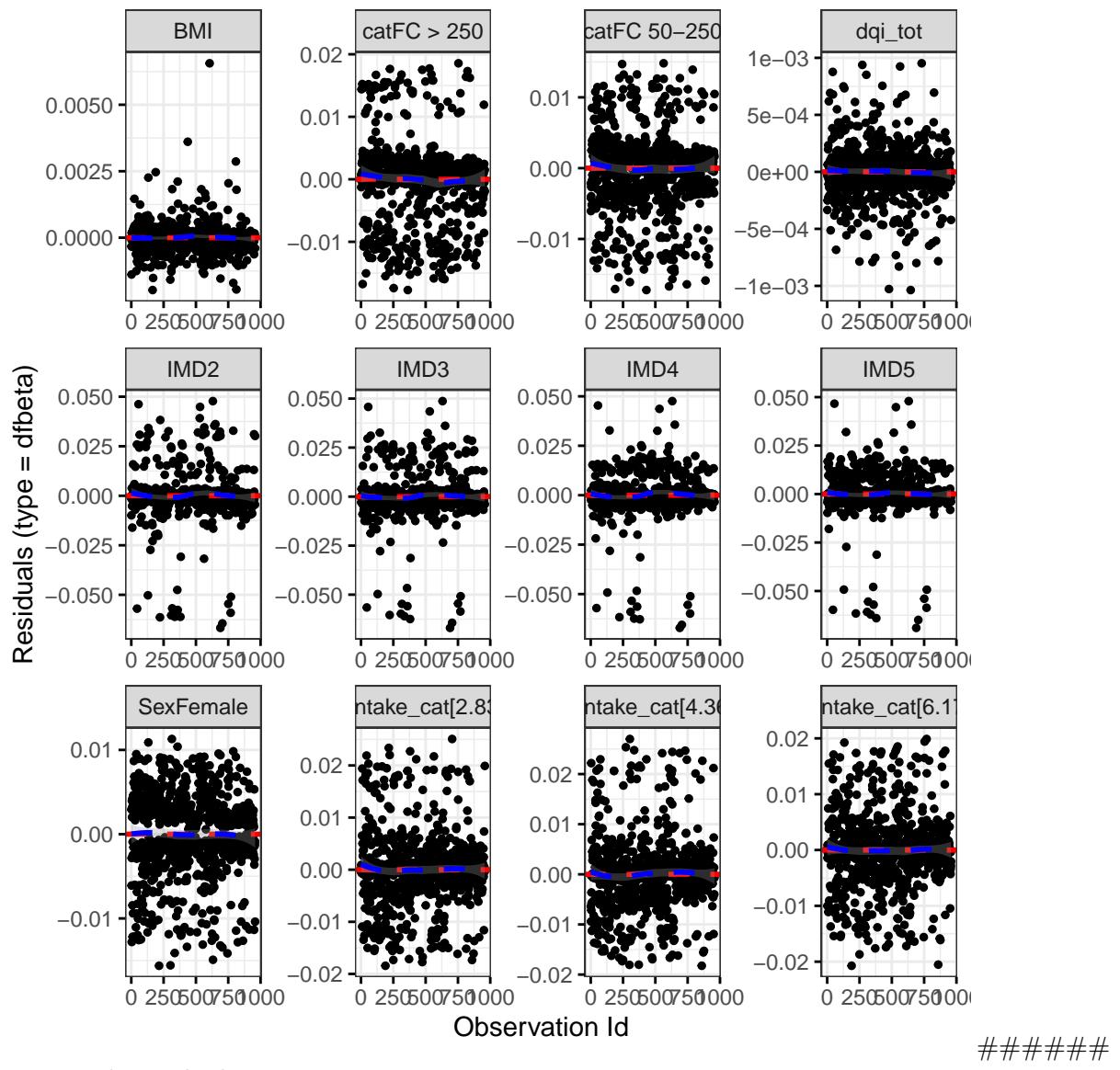
Diagnostics:

Proportional hazards assumption test

	Chi-squared statistic	DF	P-value
Sex	0.0198	0.9883	0.8850
cat	6.5739	1.9810	0.0367
IMD	1.5344	3.9465	0.8143
dqi_tot	1.9481	0.9928	0.1614
BMI	1.8910	0.9895	0.1669
sweetIntake_cat	1.2166	2.9700	0.7441
GLOBAL	13.0420	22.4327	0.9409

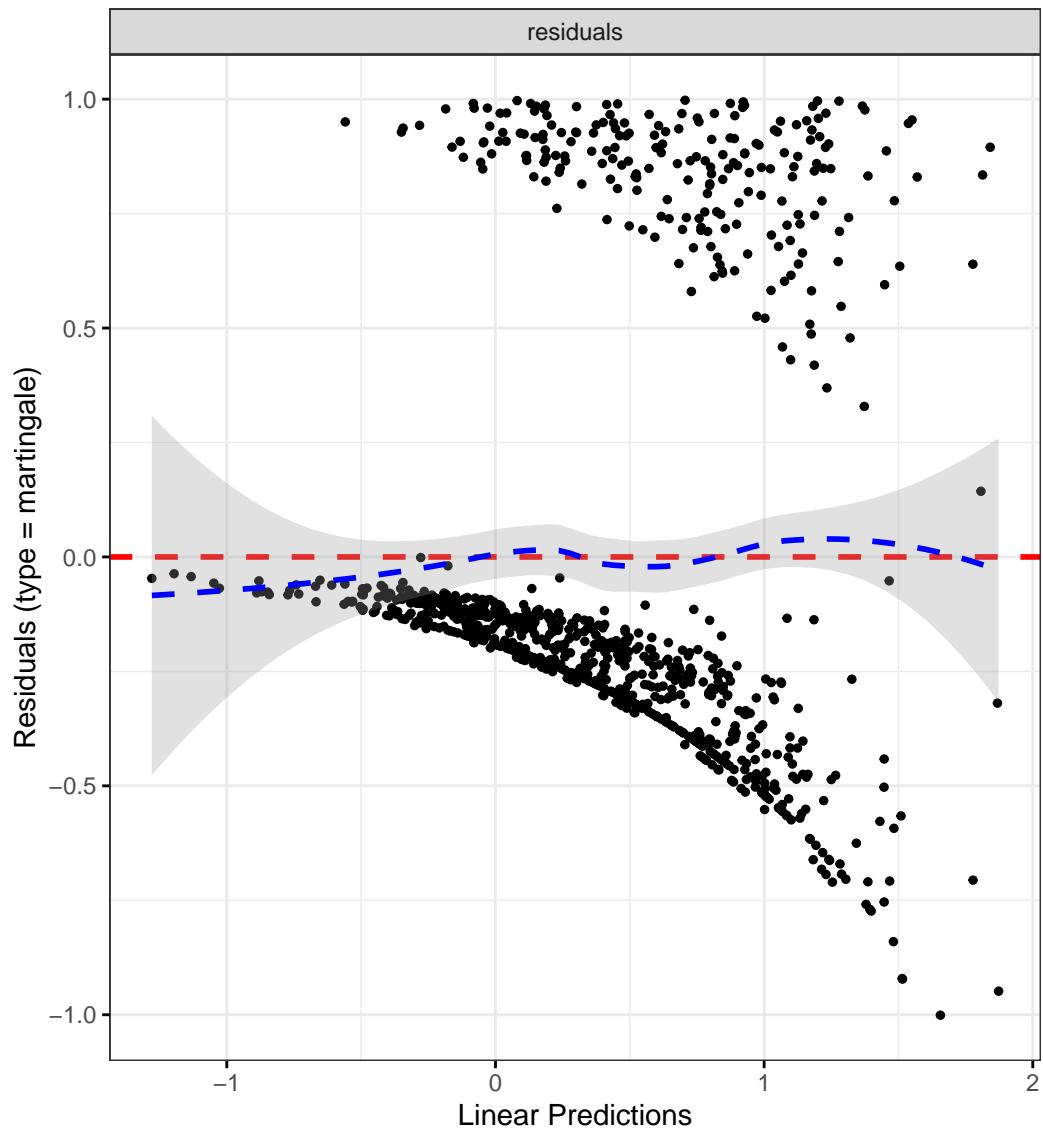
DF betas

```
`geom_smooth()` using formula = 'y ~ x'
```



Martingale residuals

```
`geom_smooth()` using formula = 'y ~ x'
```



Artificially and sugar-sweetened beverages

Crohn's disease

Patient-reported flare

```
# Categorize drink intake by quantiles
flare.cd.df <- categorize_by_quantiles(flare.cd.df, "drinkIntake", reference_data = flare.df)
```

```

# Run survival analysis using utility function
analysis_result <- run_survival_analysis(
  data = flare.cd.df,
  var_name = "drinkIntake",
  outcome_time = "softflare_time",
  outcome_event = "softflare",
  legend_title = "Artificially and sugar-sweetened drink intake quantiles",
  plot_base_path = "plots/cd/soft-flare/diet/drinkIntake",
  break_time_by = 200
)

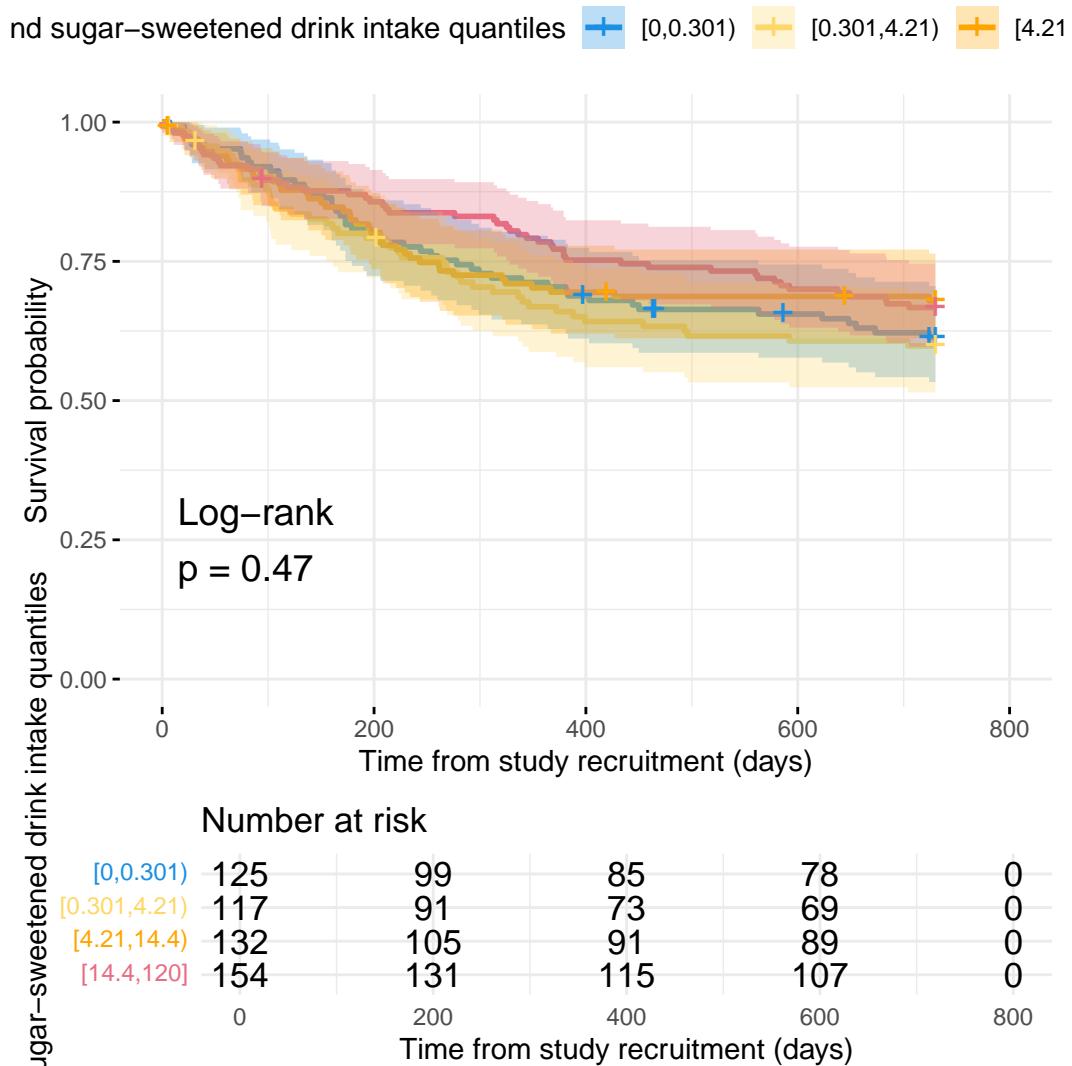
# Save plot as RDS
saveRDS(analysis_result$plot, paste0(paths$outdir, "drinkIntake-cd-soft.RDS"))

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(softflare_time, softflare) ~
    Sex + cat + IMD + dqi_tot + BMI + drinkIntake_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.cd.df
)

# Display plot and model summary
analysis_result$plot

```

Time to patient-reported flare



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.9387	1.3871	2.7097	0.0001
catFC 50-250	1.3069	0.9204	1.8556	0.1346
catFC > 250	2.0454	1.3967	2.9956	0.0002

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	0.6844	0.3543	1.3220	0.2589
IMD3	0.9238	0.5071	1.6829	0.7957
IMD4	0.8419	0.4637	1.5286	0.5717
IMD5	0.9577	0.5483	1.6727	0.8792
dqi_tot	1.0050	0.9913	1.0189	0.4744
BMI	1.0118	0.9847	1.0397	0.3967
drinkIntake_cat[0.301,4.2	0.9939	0.6424	1.5378	0.9781
drinkIntake_cat[4.21,14.4	0.9088	0.5884	1.4038	0.6665
drinkIntake_cat[14.4,120]	0.7704	0.5103	1.1632	0.2147

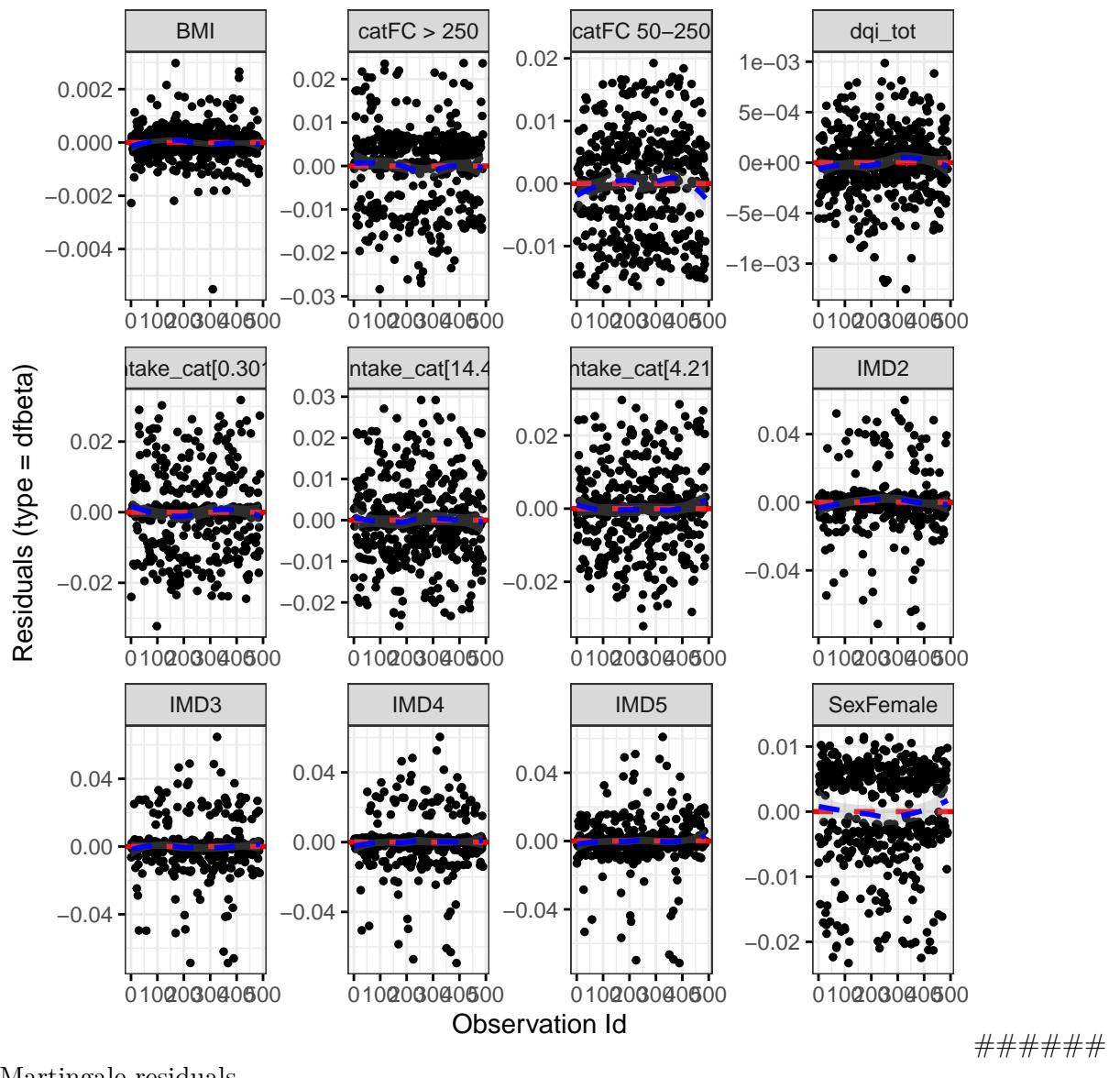
Diagnostics:

Proportional hazards assumption test

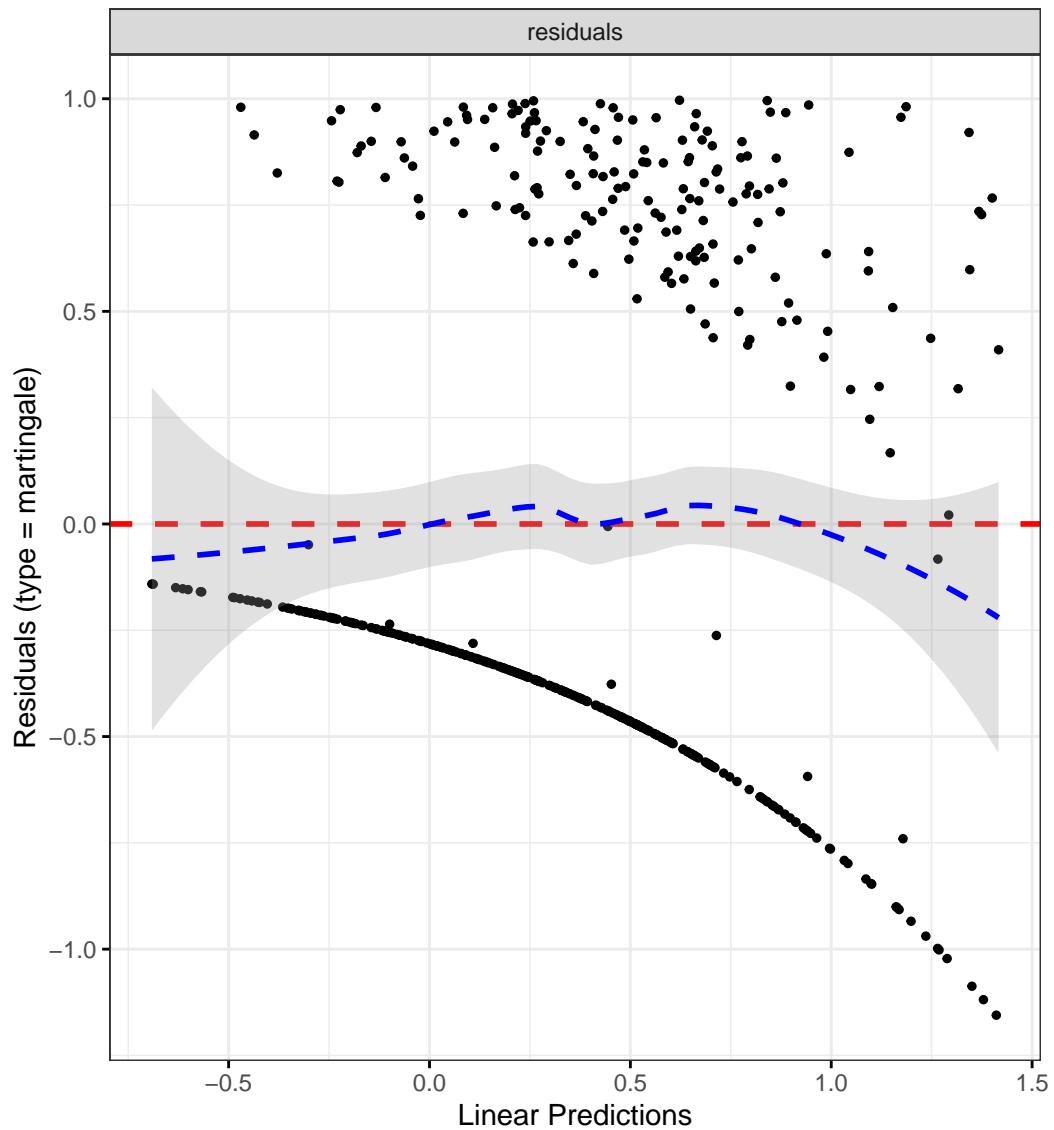
	Chi-squared statistic	DF	P-value
Sex	0.2680	1.0000	0.6047
cat	0.7967	2.0000	0.6714
IMD	3.0215	4.0000	0.5542
dqi_tot	0.3622	1.0000	0.5473
BMI	1.2701	1.0000	0.2597
drinkIntake_cat	3.7125	3.0000	0.2942
GLOBAL	8.2120	12.0001	0.7684

DF betas

```
`geom_smooth()` using formula = 'y ~ x'
```



```
`geom_smooth()` using formula = 'y ~ x'
```



Hard flare

```
# Run survival analysis using utility function for hard flare
analysis_result <- run_survival_analysis(
  data = flare.cd.df,
  var_name = "drinkIntake",
  outcome_time = "hardflare_time",
  outcome_event = "hardflare",
  legend_title = "Artificially and sugar-sweetened drink intake quantiles",
```

```

plot_base_path = "plots/cd/hard-flare/diet/drinkIntake",
break_time_by = 500
)

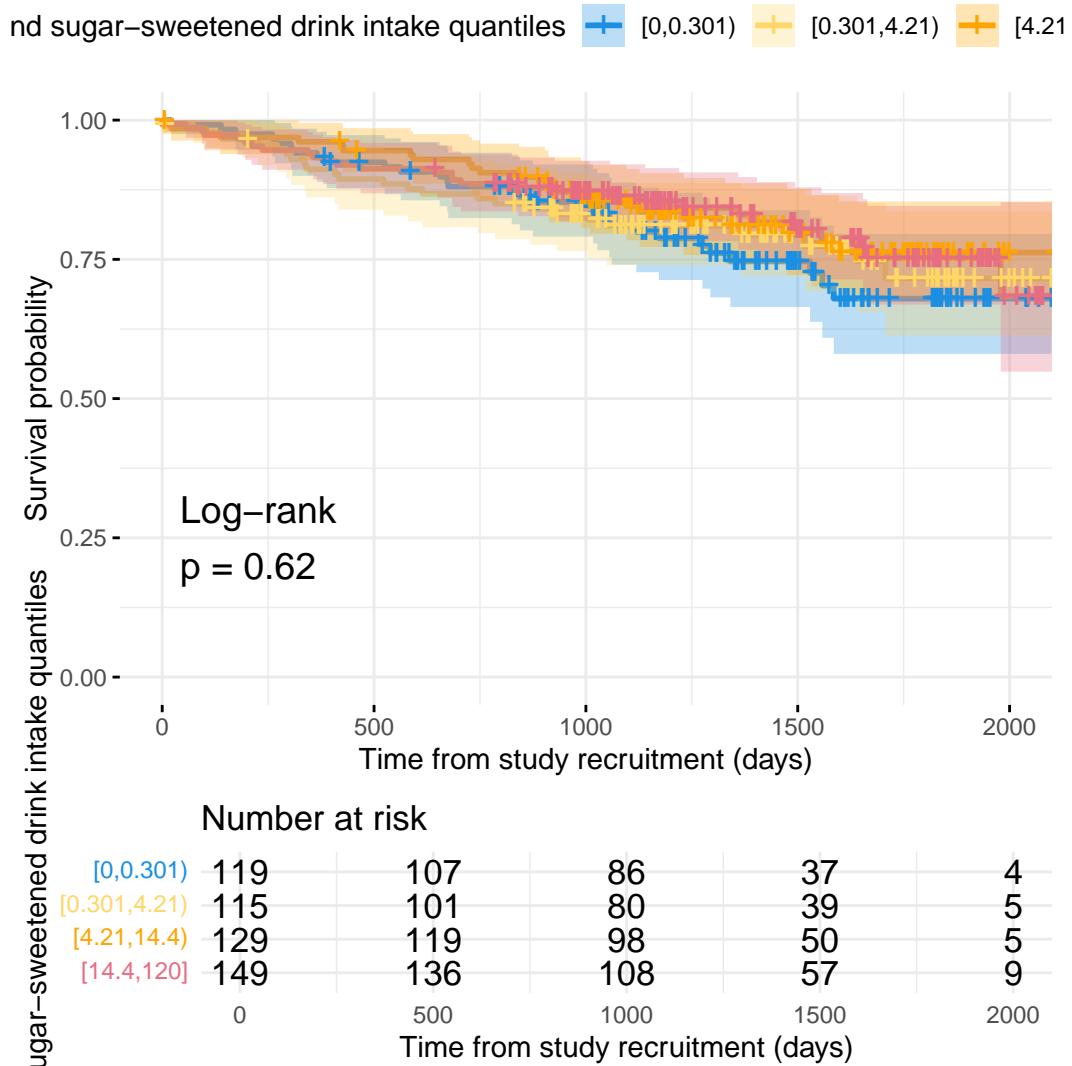
# Save plot as RDS
saveRDS(analysis_result$plot, paste0(paths$outdir, "drinkIntake-cd-hard.RDS"))

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(hardflare_time, hardflare) ~
    Sex + cat + IMD + dqi_tot + BMI + drinkIntake_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.cd.df
)

# Display plot and model summary
analysis_result$plot

```

Time to hard flare



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.3563	0.8966	2.0518	0.1490
catFC 50-250	1.8557	1.1651	2.9557	0.0092
catFC > 250	2.8668	1.7284	4.7549	0.0000

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	0.6255	0.2693	1.4530	0.2752
IMD3	0.8000	0.3630	1.7633	0.5800
IMD4	0.7414	0.3439	1.5984	0.4452
IMD5	0.6791	0.3274	1.4089	0.2987
dqi_tot	1.0016	0.9835	1.0200	0.8630
BMI	1.0224	0.9879	1.0582	0.2055
drinkIntake_cat[0.301,4.2	0.9249	0.5338	1.6026	0.7807
drinkIntake_cat[4.21,14.4	0.7356	0.4179	1.2950	0.2873
drinkIntake_cat[14.4,120]	0.7043	0.4133	1.2000	0.1973

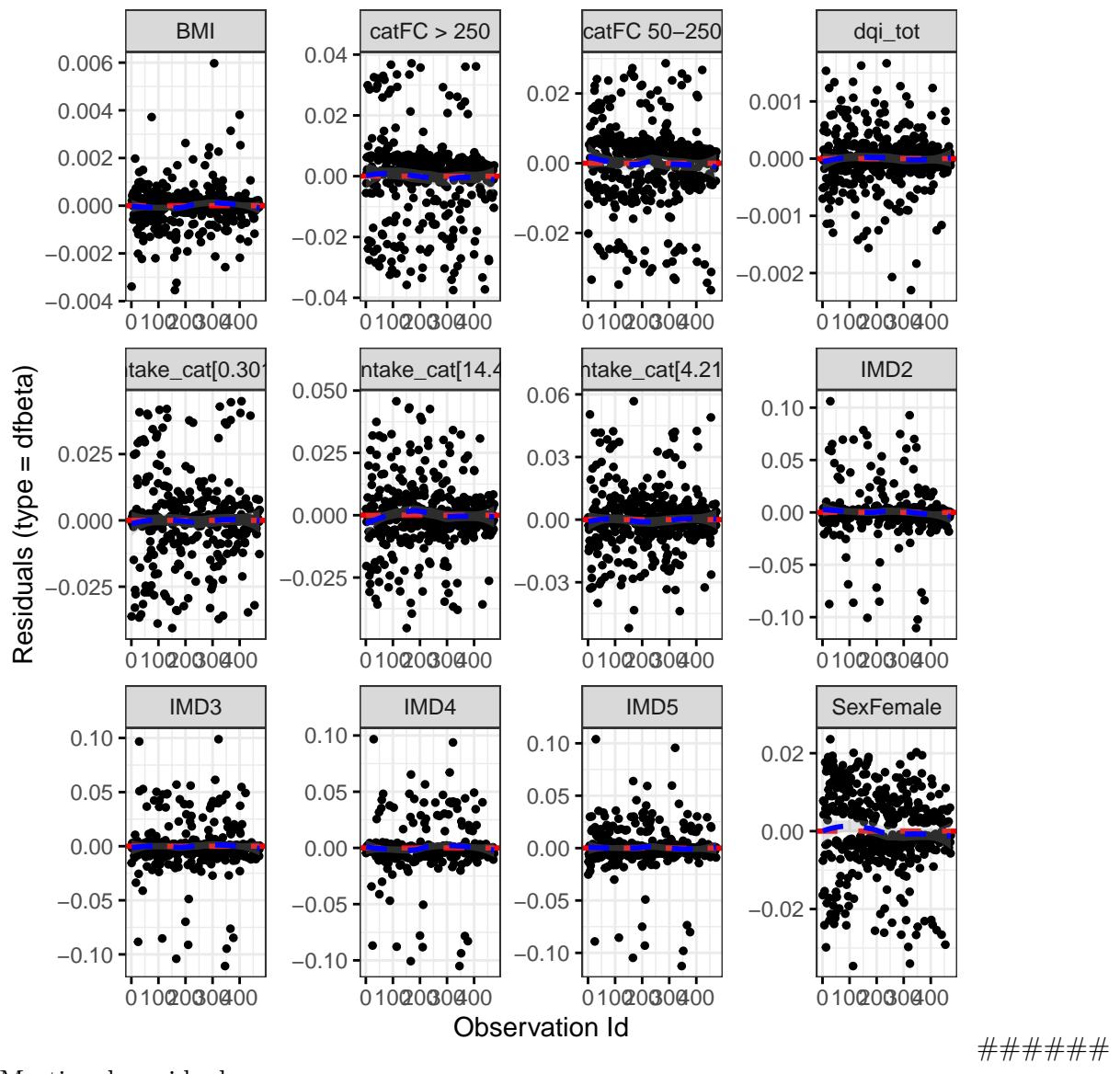
Diagnostics:

Proportional hazards assumption test

	Chi-squared statistic	DF	P-value
Sex	0.0773	0.9732	0.7711
cat	10.2074	1.9787	0.0059
IMD	2.6390	3.9298	0.6090
dqi_tot	2.8909	0.9919	0.0881
BMI	1.1251	0.9790	0.2824
drinkIntake_cat	1.3282	2.9696	0.7173
GLOBAL	18.0110	17.9838	0.4538

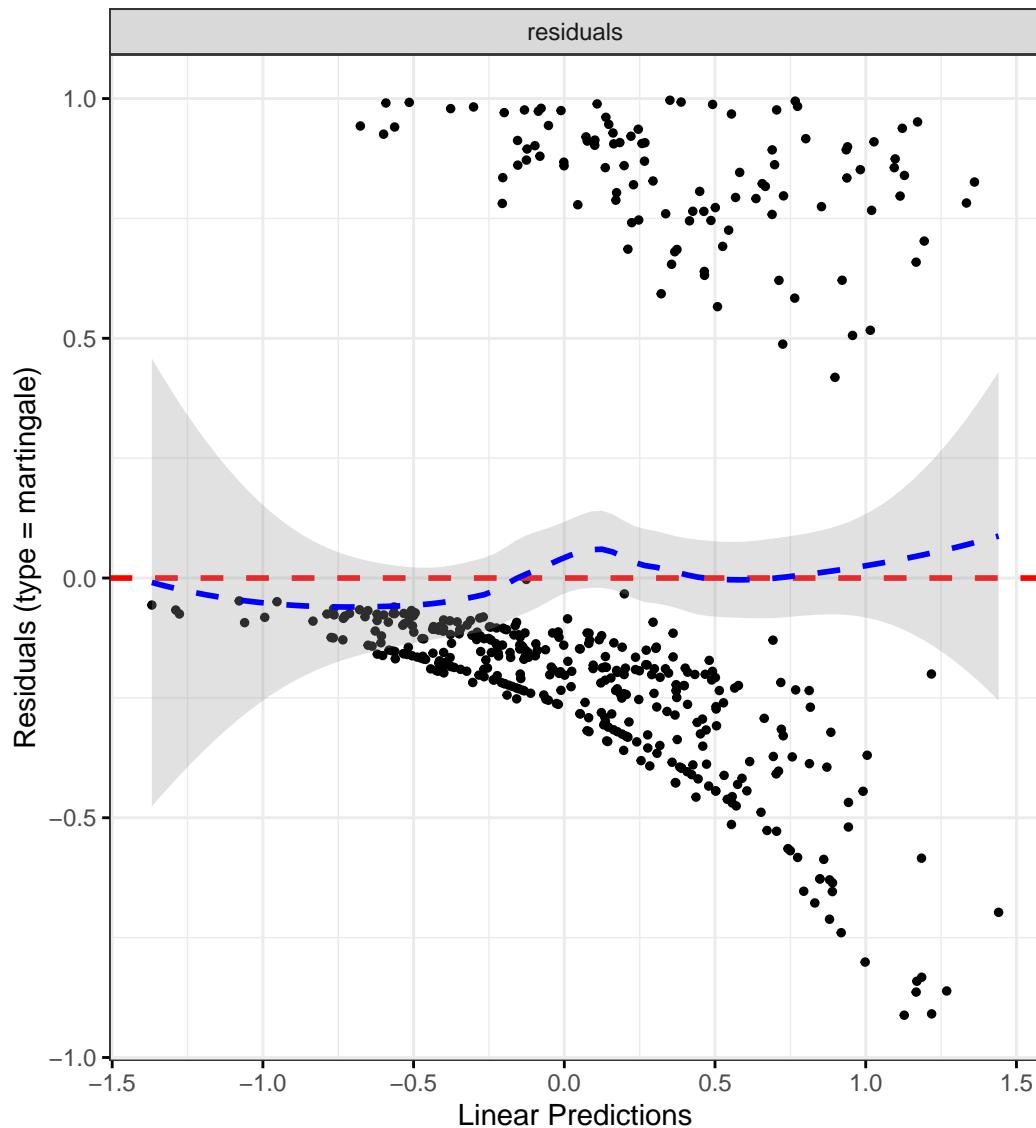
DF betas

```
`geom_smooth()` using formula = 'y ~ x'
```



Martingale residuals

```
`geom_smooth()` using formula = 'y ~ x'
```



Ulcerative colitis

Patient-reported flare

```
# Categorize drink intake by quantiles
flare.uc.df <- categorize_by_quantiles(flare.uc.df, "drinkIntake", reference_data = flare.df)

# Run survival analysis using utility function
```

```

analysis_result <- run_survival_analysis(
  data = flare.uc.df,
  var_name = "drinkIntake",
  outcome_time = "softflare_time",
  outcome_event = "softflare",
  legend_title = "Artificially and sugar-sweetened drink intake quantiles",
  plot_base_path = "plots/uc/soft-flare/diet/drinkIntake",
  break_time_by = 200
)

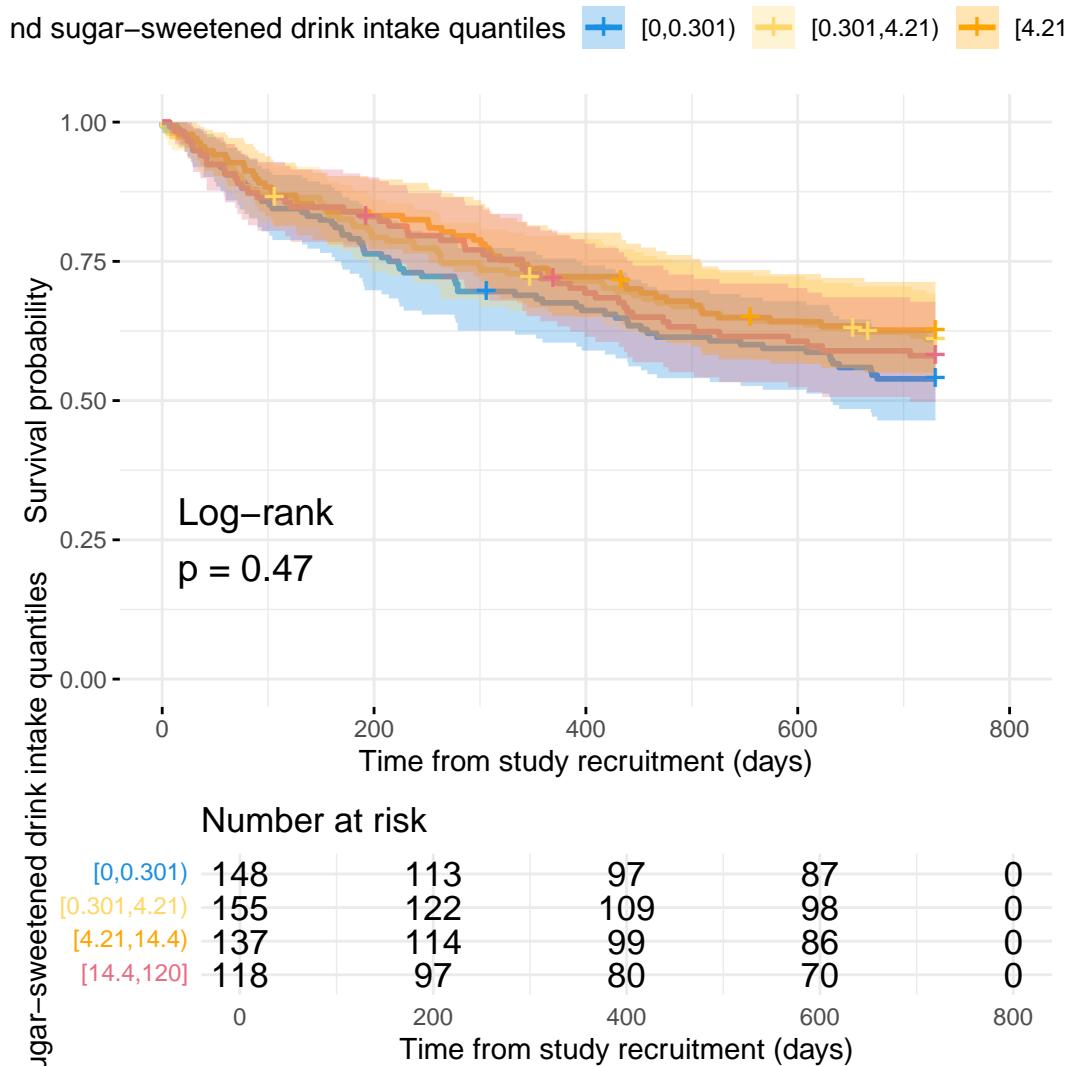
# Save plot as RDS
saveRDS(analysis_result$plot, paste0(paths$outdir, "drinkIntake-uc-soft.RDS"))

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(softflare_time, softflare) ~
    Sex + cat + IMD + dqi_tot + BMI + drinkIntake_cat +
    frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.uc.df
)

# Display plot and model summary
analysis_result$plot

```

Time to patient-reported flare



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.7014	1.2739	2.2724	0.0003
catFC 50-250	1.7909	1.3030	2.4616	0.0003
catFC > 250	2.1016	1.4714	3.0016	0.0000

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	1.4569	0.7625	2.7838	0.2546
IMD3	1.1699	0.6213	2.2028	0.6270
IMD4	1.3703	0.7558	2.4846	0.2994
IMD5	1.1926	0.6627	2.1462	0.5568
dqi_tot	0.9987	0.9859	1.0117	0.8487
BMI	0.9755	0.9462	1.0058	0.1118
drinkIntake_cat[0.301,4.2	0.8015	0.5556	1.1561	0.2364
drinkIntake_cat[4.21,14.4	0.9130	0.6222	1.3397	0.6418
drinkIntake_cat[14.4,120]	0.8593	0.5746	1.2849	0.4600

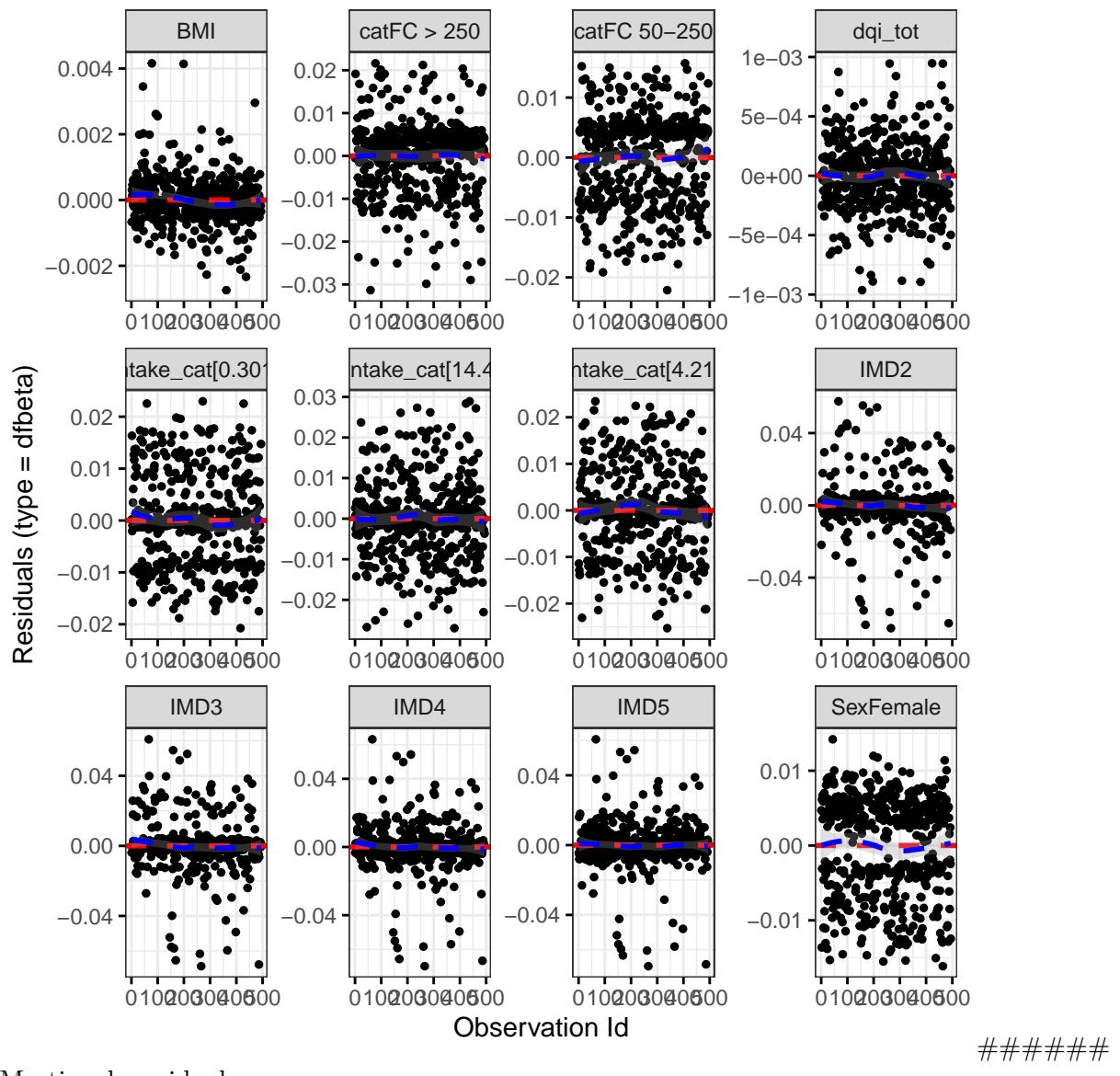
Diagnostics:

Proportional hazards assumption test

	Chi-squared statistic	DF	P-value
Sex	0.0079	1.0000	0.9293
cat	3.6394	2.0000	0.1621
IMD	2.6102	4.0000	0.6250
dqi_tot	0.7818	1.0000	0.3766
BMI	0.9537	1.0000	0.3288
drinkIntake_cat	0.5990	3.0000	0.8967
GLOBAL	9.3916	12.0001	0.6692

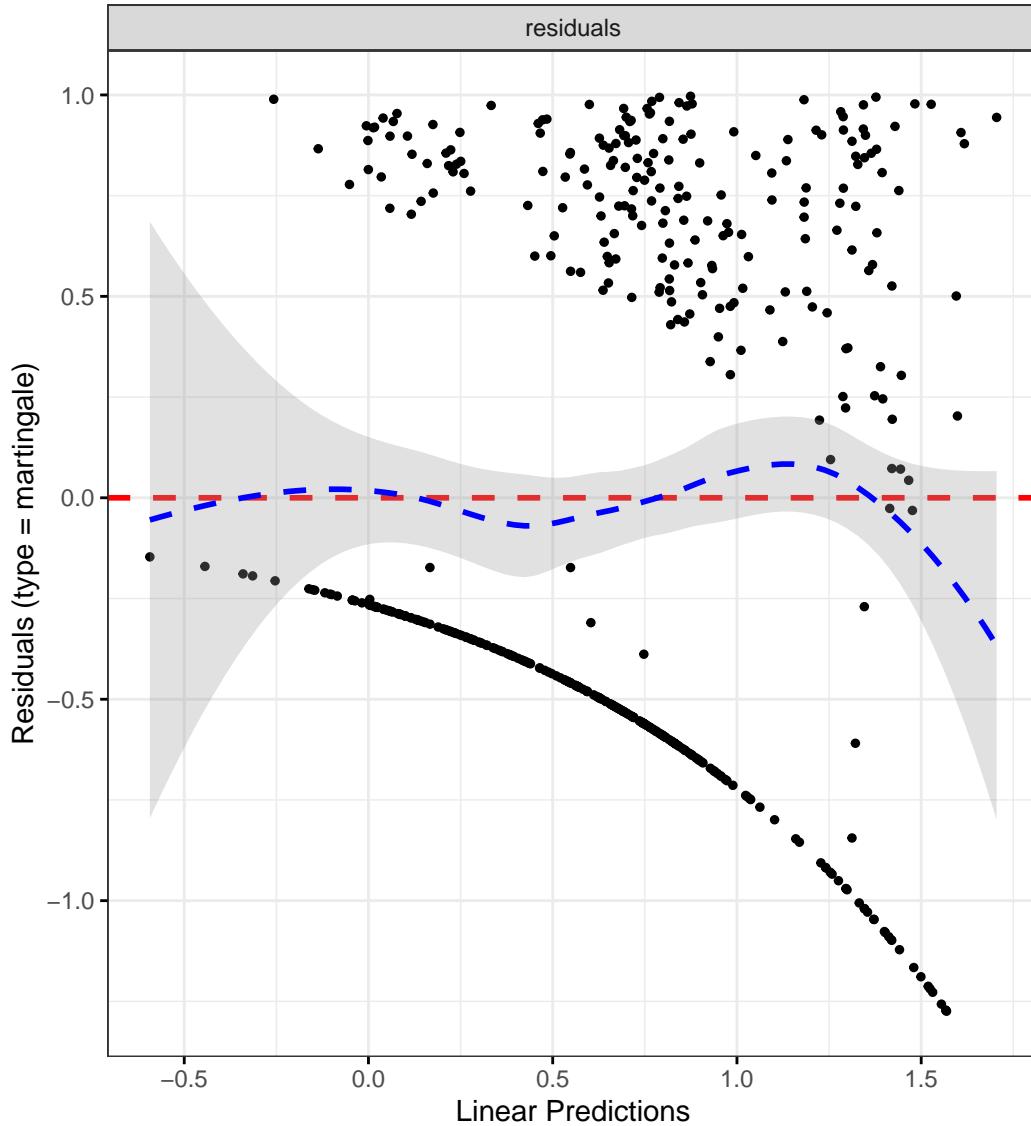
DF betas

```
`geom_smooth()` using formula = 'y ~ x'
```



Martingale residuals

```
`geom_smooth()` using formula = 'y ~ x'
```



Hard flare

```
# Run survival analysis using utility function for hard flare
analysis_result <- run_survival_analysis(
  data = flare.uc.df,
  var_name = "drinkIntake",
  outcome_time = "hardflare_time",
  outcome_event = "hardflare",
  legend_title = "Artificially and sugar-sweetened drink intake quantiles",
```

```

plot_base_path = "plots/uc/hard-flare/diet/drinkIntake",
break_time_by = 500
)

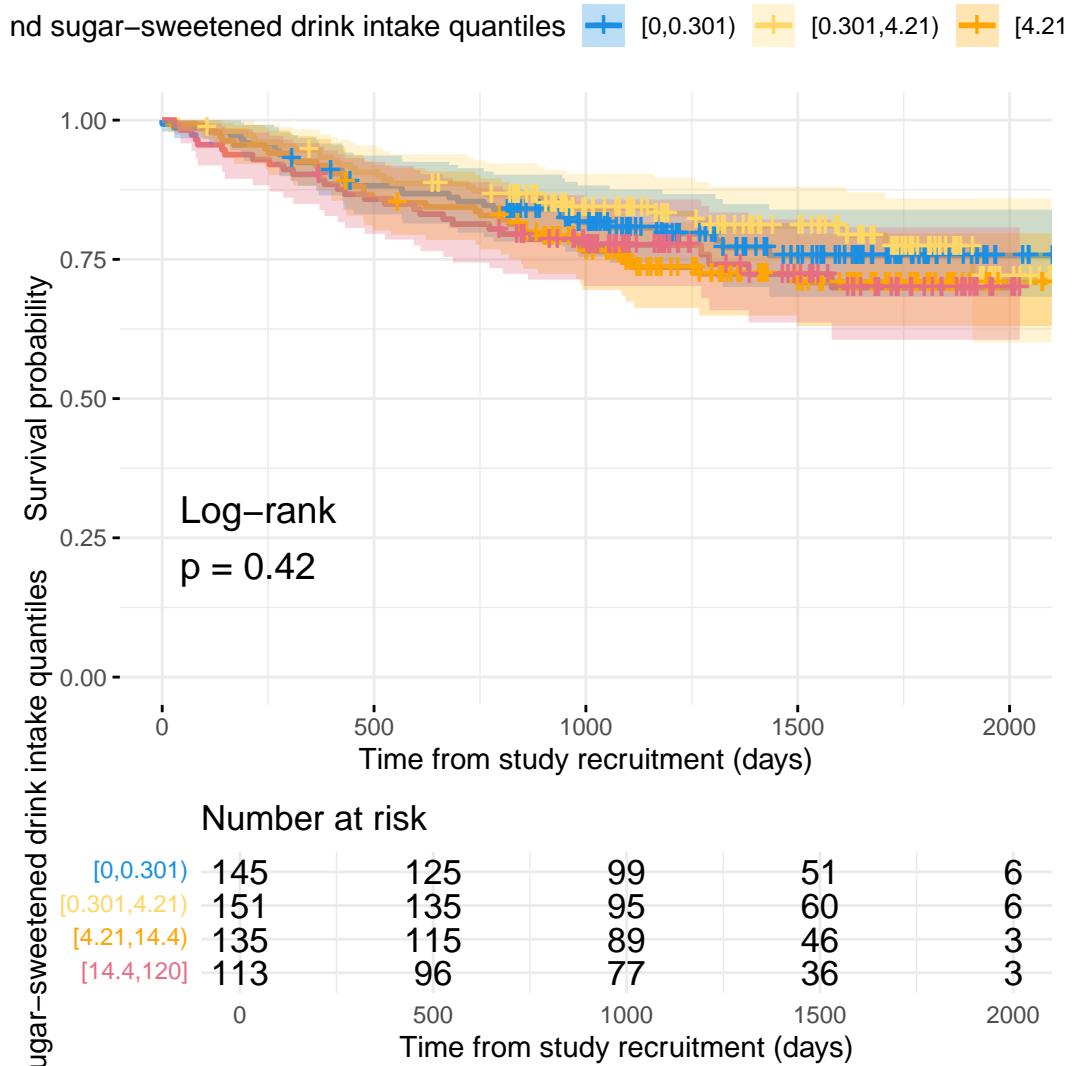
# Save plot as RDS
saveRDS(analysis_result$plot, paste0(paths$outdir, "drinkIntake-uc-hard.RDS"))

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(hardflare_time, hardflare) ~
    Sex + cat + IMD + dqi_tot + BMI + drinkIntake_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.uc.df
)

# Display plot and model summary
analysis_result$plot

```

Time to hard flare



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.2449	0.8499	1.8236	0.2607
catFC 50-250	2.1052	1.3646	3.2477	0.0008
catFC > 250	2.4862	1.5237	4.0568	0.0003

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	1.7016	0.6410	4.5171	0.2859
IMD3	1.4188	0.5468	3.6820	0.4721
IMD4	2.3502	0.9770	5.6535	0.0564
IMD5	1.5243	0.6283	3.6983	0.3512
dqi_tot	1.0026	0.9849	1.0206	0.7761
BMI	0.9550	0.9149	0.9969	0.0356
drinkIntake_cat[0.301,4.2	0.7606	0.4436	1.3041	0.3199
drinkIntake_cat[4.21,14.4	1.3462	0.7968	2.2744	0.2666
drinkIntake_cat[14.4,120]	1.2901	0.7450	2.2340	0.3632

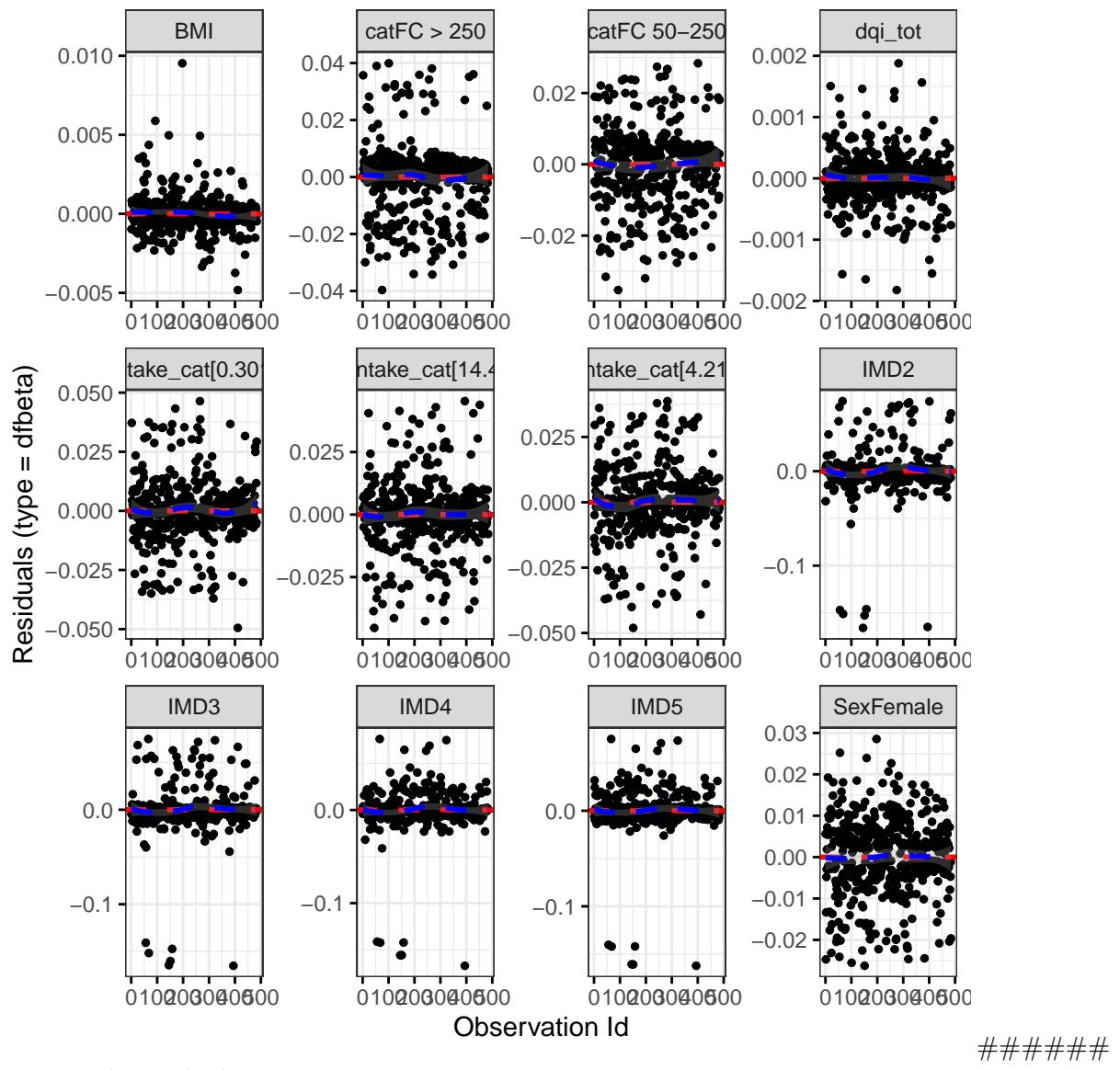
Diagnostics:

Proportional hazards assumption test

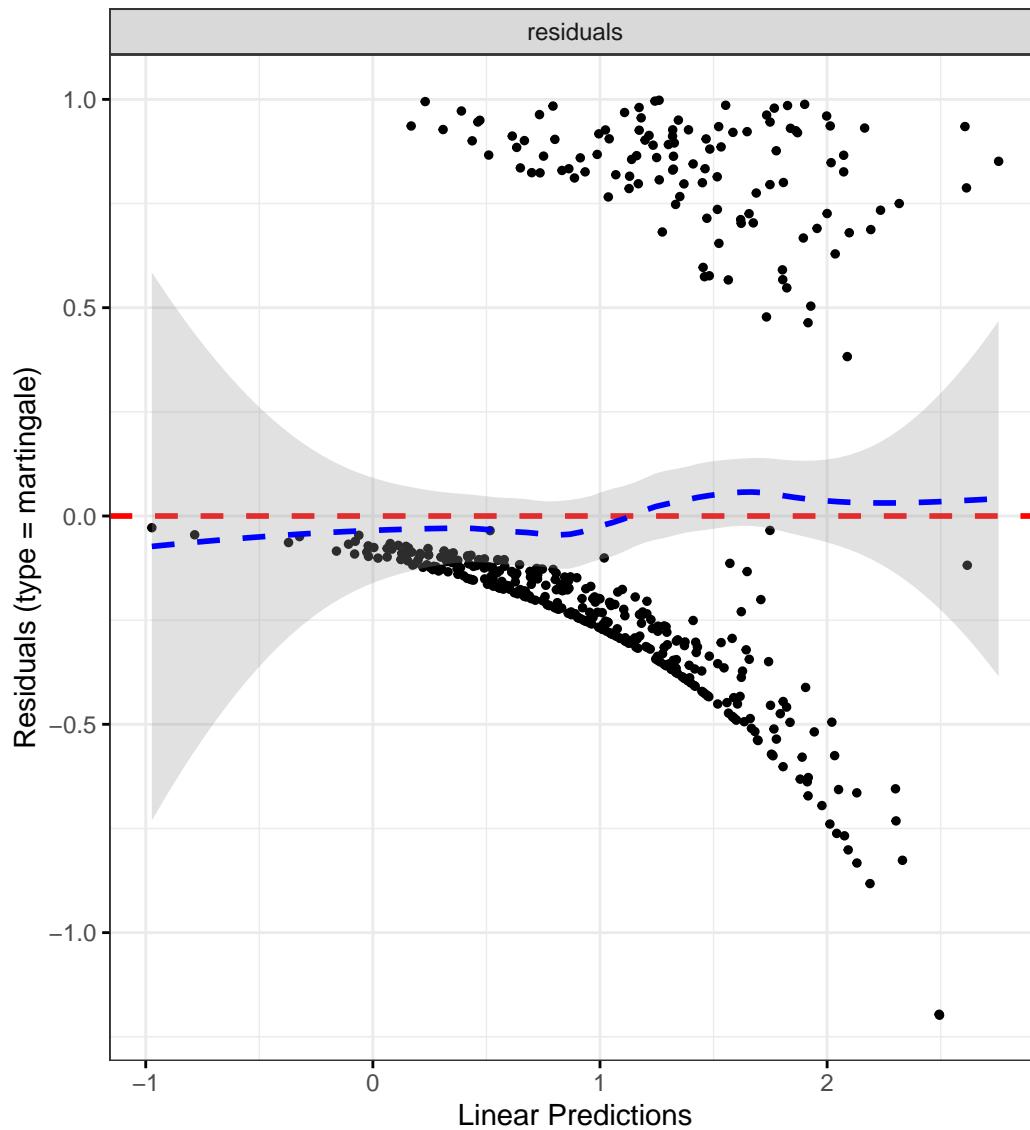
	Chi-squared statistic	DF	P-value
Sex	0.0245	0.9892	0.8725
cat	5.2533	1.9559	0.0694
IMD	1.2098	3.9323	0.8701
dqi_tot	0.0022	0.9840	0.9609
BMI	0.5083	0.9895	0.4717
drinkIntake_cat	0.7603	2.9415	0.8516
GLOBAL	8.8895	19.2237	0.9776

DF betas

```
`geom_smooth()` using formula = 'y ~ x'
```



```
`geom_smooth()` using formula = 'y ~ x'
```



Inflammatory bowel disease

Patient-reported flare

```
# Categorize drink intake by quantiles
flare.df <- categorize_by_quantiles(flare.df, "drinkIntake", reference_data = flare.df)

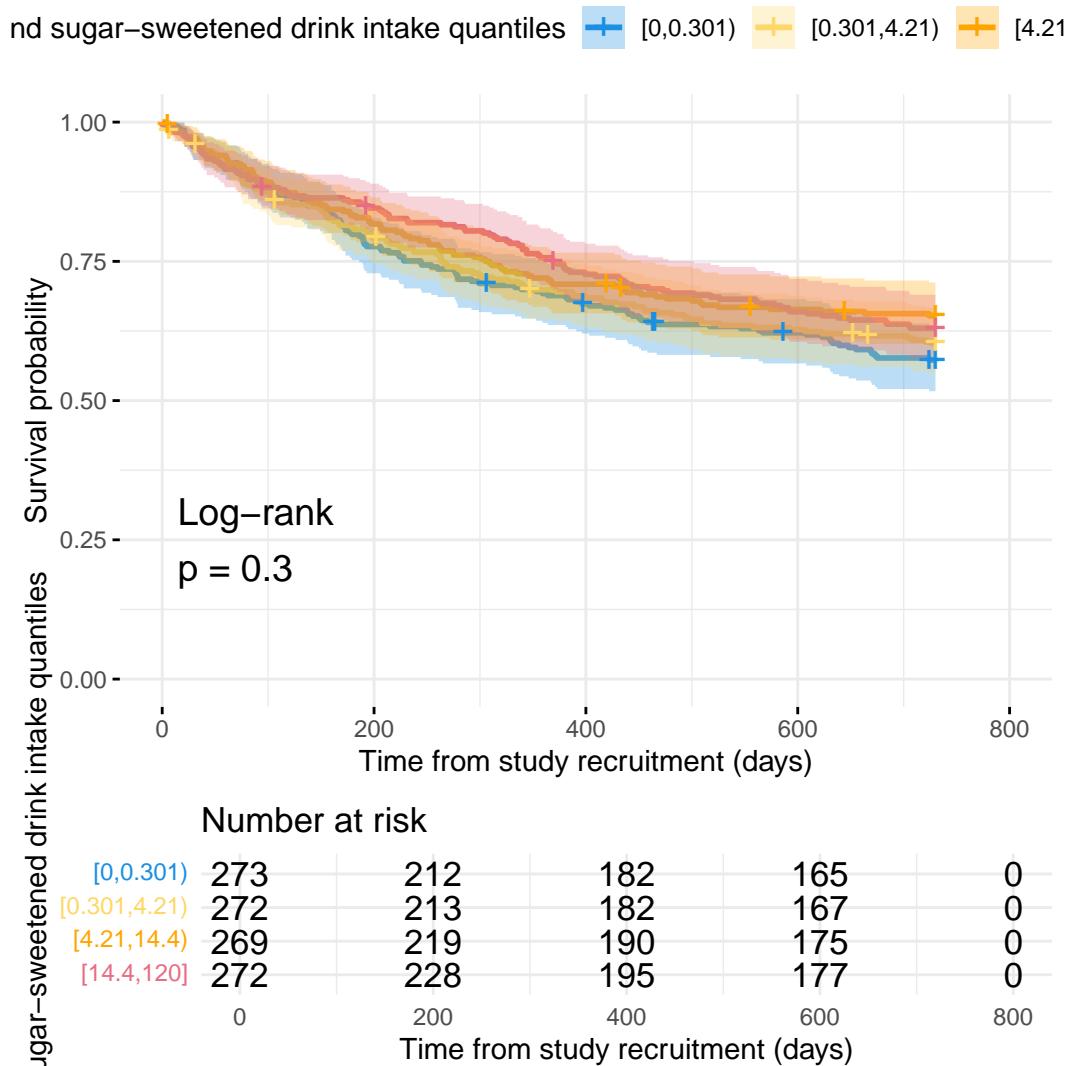
# Run survival analysis using utility function
```

```
analysis_result <- run_survival_analysis(
  data = flare.df,
  var_name = "drinkIntake",
  outcome_time = "softflare_time",
  outcome_event = "softflare",
  legend_title = "Artificially and sugar-sweetened drink intake quantiles",
  plot_base_path = "plots/ibd/soft-flare/diet/drinkIntake",
  break_time_by = 200
)

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(softflare_time, softflare) ~
    Sex + cat + IMD + dqi_tot + BMI + drinkIntake_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.df
)

# Display plot and model summary
analysis_result$plot
```

Time to patient-reported flare



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.7889	1.4415	2.2201	0.0000
catFC 50-250	1.5012	1.1881	1.8969	0.0007
catFC > 250	2.0239	1.5627	2.6213	0.0000

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	0.9935	0.6312	1.5639	0.9776
IMD3	1.0123	0.6563	1.5615	0.9558
IMD4	1.1166	0.7371	1.6915	0.6028
IMD5	1.0689	0.7158	1.5962	0.7446
dqi_tot	1.0018	0.9925	1.0112	0.7089
BMI	0.9969	0.9771	1.0171	0.7582
drinkIntake_cat[0.301,4.2	0.8903	0.6737	1.1767	0.4143
drinkIntake_cat[4.21,14.4	0.8810	0.6620	1.1724	0.3847
drinkIntake_cat[14.4,120]	0.7940	0.5968	1.0562	0.1131

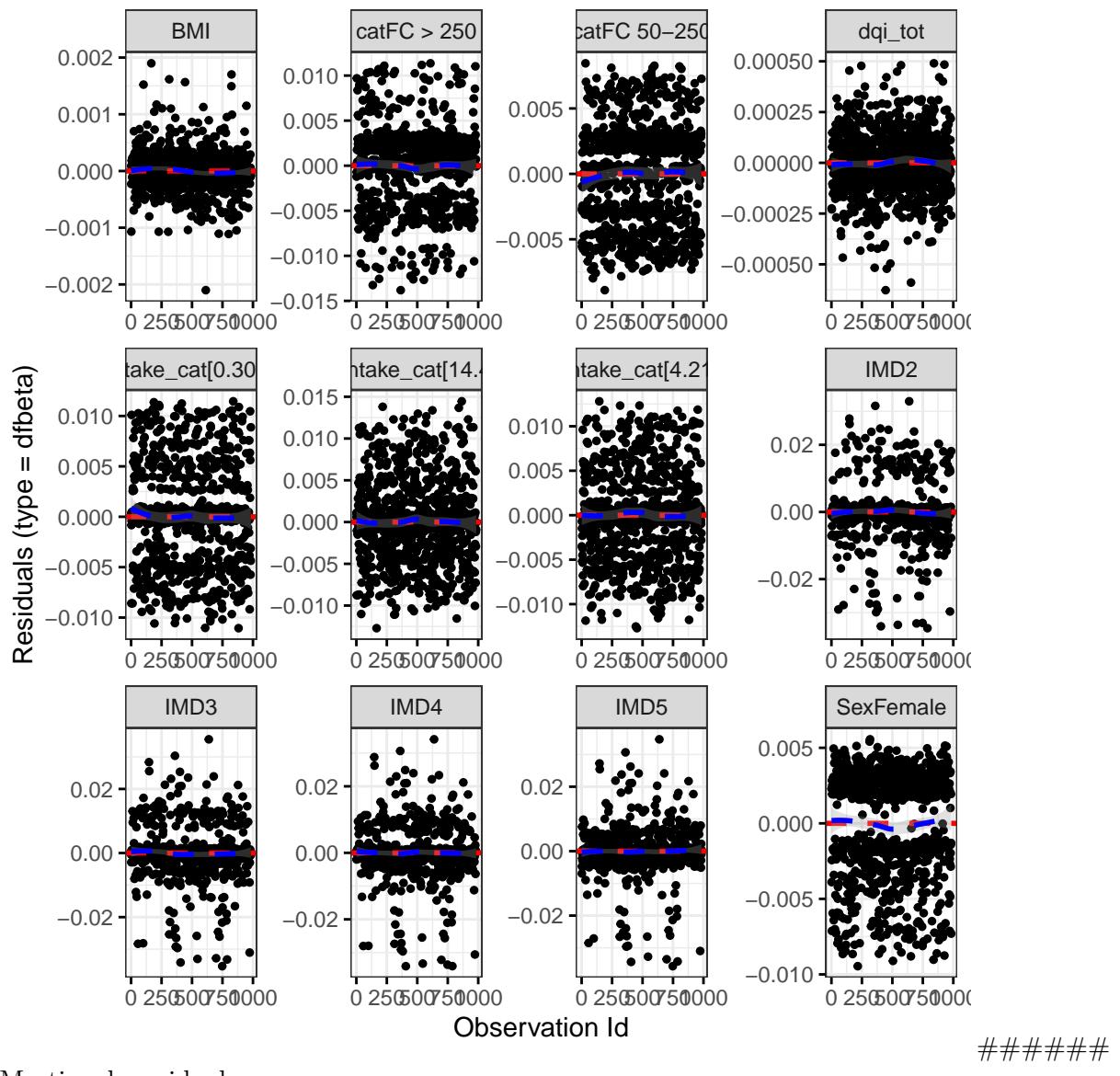
Diagnostics:

Proportional hazards assumption test

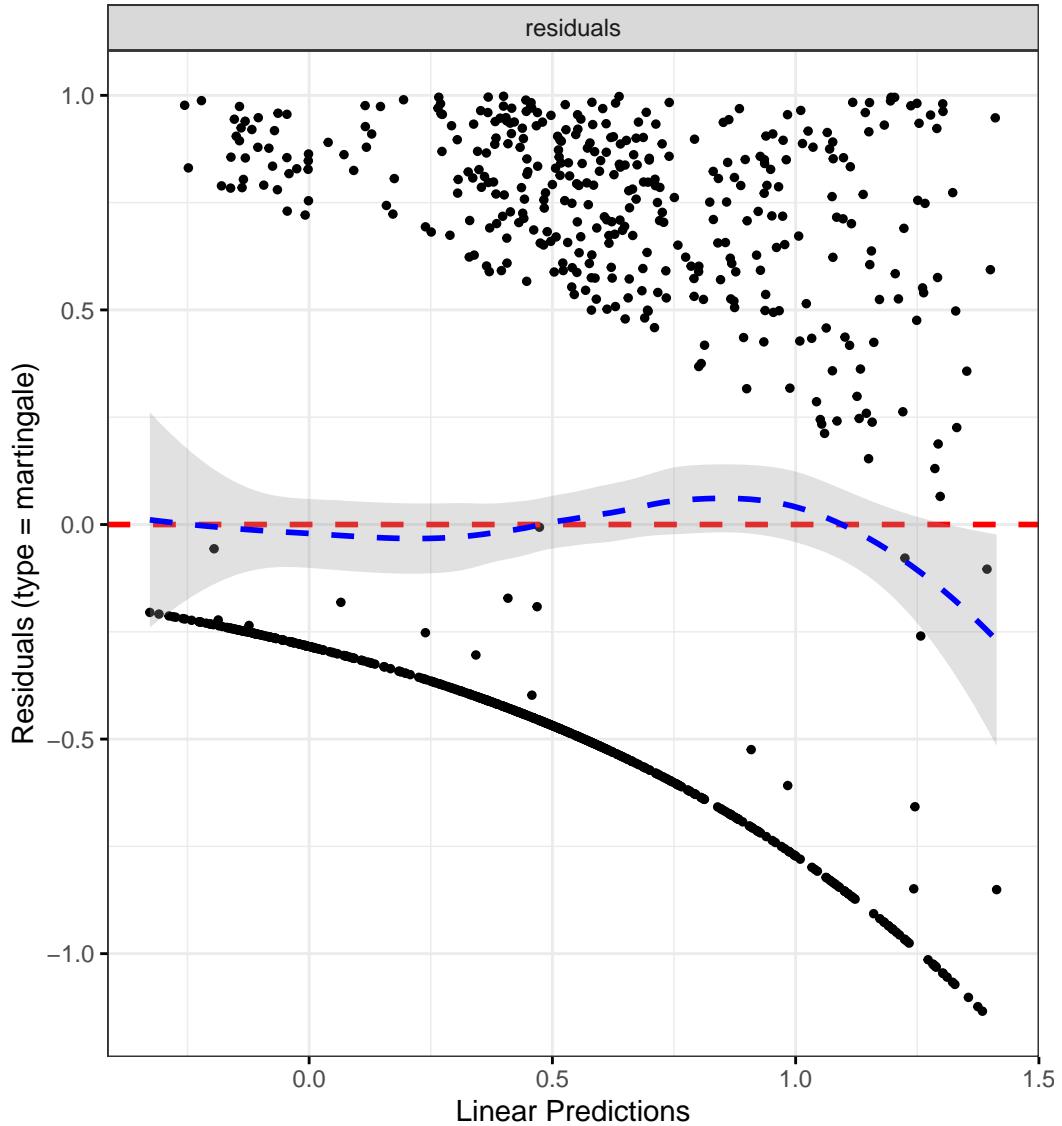
	Chi-squared statistic	DF	P-value
Sex	0.0048	1.0000	0.9450
cat	1.0779	2.0000	0.5834
IMD	5.0199	4.0000	0.2853
dqi_tot	1.3981	1.0000	0.2370
BMI	0.0131	1.0000	0.9090
drinkIntake_cat	2.4121	3.0000	0.4914
GLOBAL	10.1127	12.0002	0.6061

DF betas

```
`geom_smooth()` using formula = 'y ~ x'
```



```
`geom_smooth()` using formula = 'y ~ x'
```



Hard flare

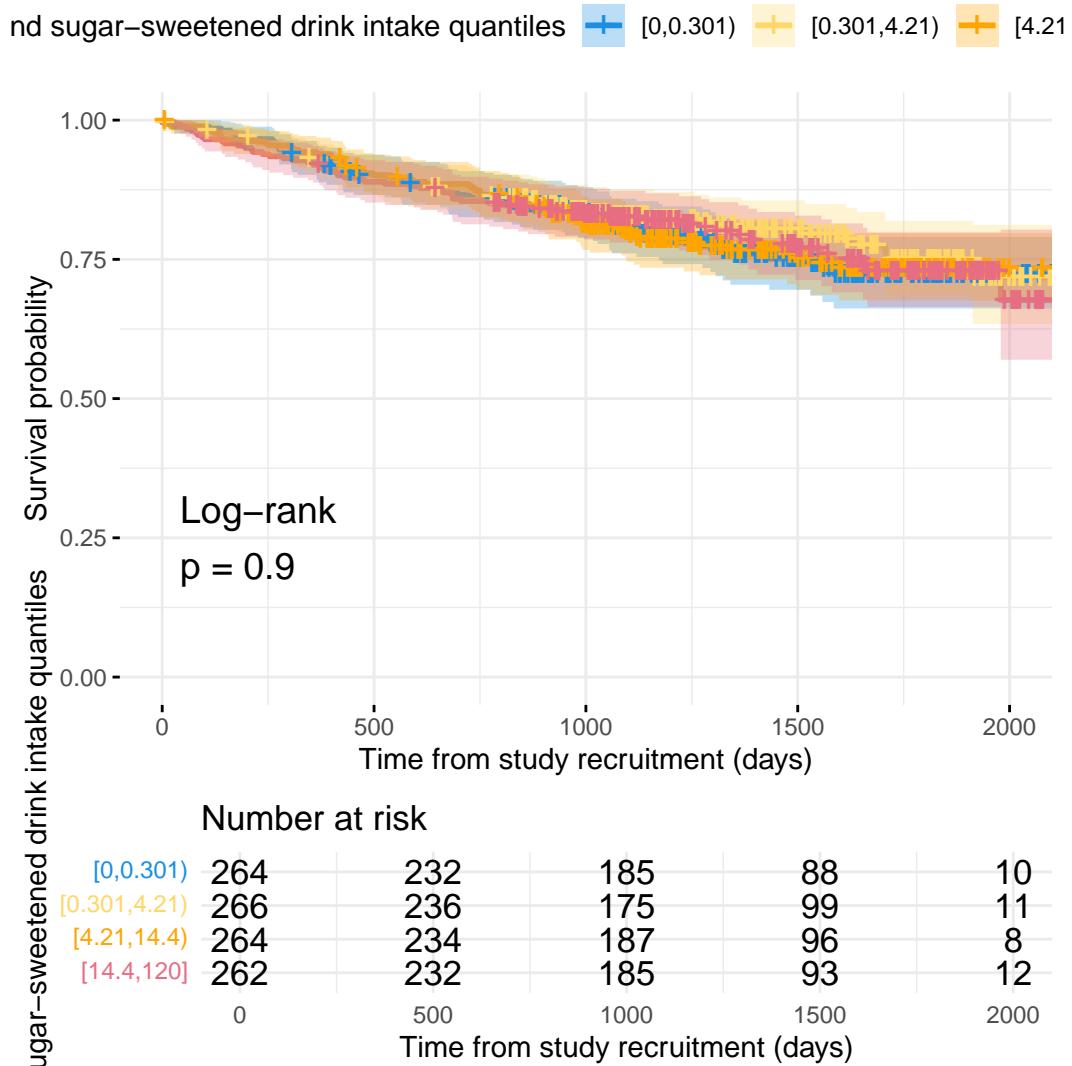
```
# Run survival analysis using utility function for hard flare
analysis_result <- run_survival_analysis(
  data = flare.df,
  var_name = "drinkIntake",
  outcome_time = "hardflare_time",
  outcome_event = "hardflare",
  legend_title = "Artificially and sugar-sweetened drink intake quantiles",
```

```
plot_base_path = "plots/ibd/hard-flare/diet/drinkIntake",
break_time_by = 500
)

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(hardflare_time, hardflare) ~
    Sex + cat + IMD + dqi_tot + BMI + drinkIntake_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.df
)

# Display plot and model summary
analysis_result$plot
```

Time to hard flare



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.2599	0.9561	1.6602	0.1007
catFC 50-250	1.8566	1.3558	2.5423	0.0001
catFC > 250	2.6100	1.8476	3.6871	0.0000

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	0.9362	0.5011	1.7492	0.8362
IMD3	0.9624	0.5281	1.7539	0.9003
IMD4	1.3519	0.7701	2.3734	0.2937
IMD5	0.9825	0.5630	1.7147	0.9506
dqi_tot	1.0025	0.9901	1.0151	0.6931
BMI	0.9913	0.9647	1.0187	0.5304
drinkIntake_cat[0.301,4.2	0.8415	0.5749	1.2319	0.3749
drinkIntake_cat[4.21,14.4	0.9888	0.6803	1.4373	0.9531
drinkIntake_cat[14.4,120]	0.9565	0.6543	1.3981	0.8183

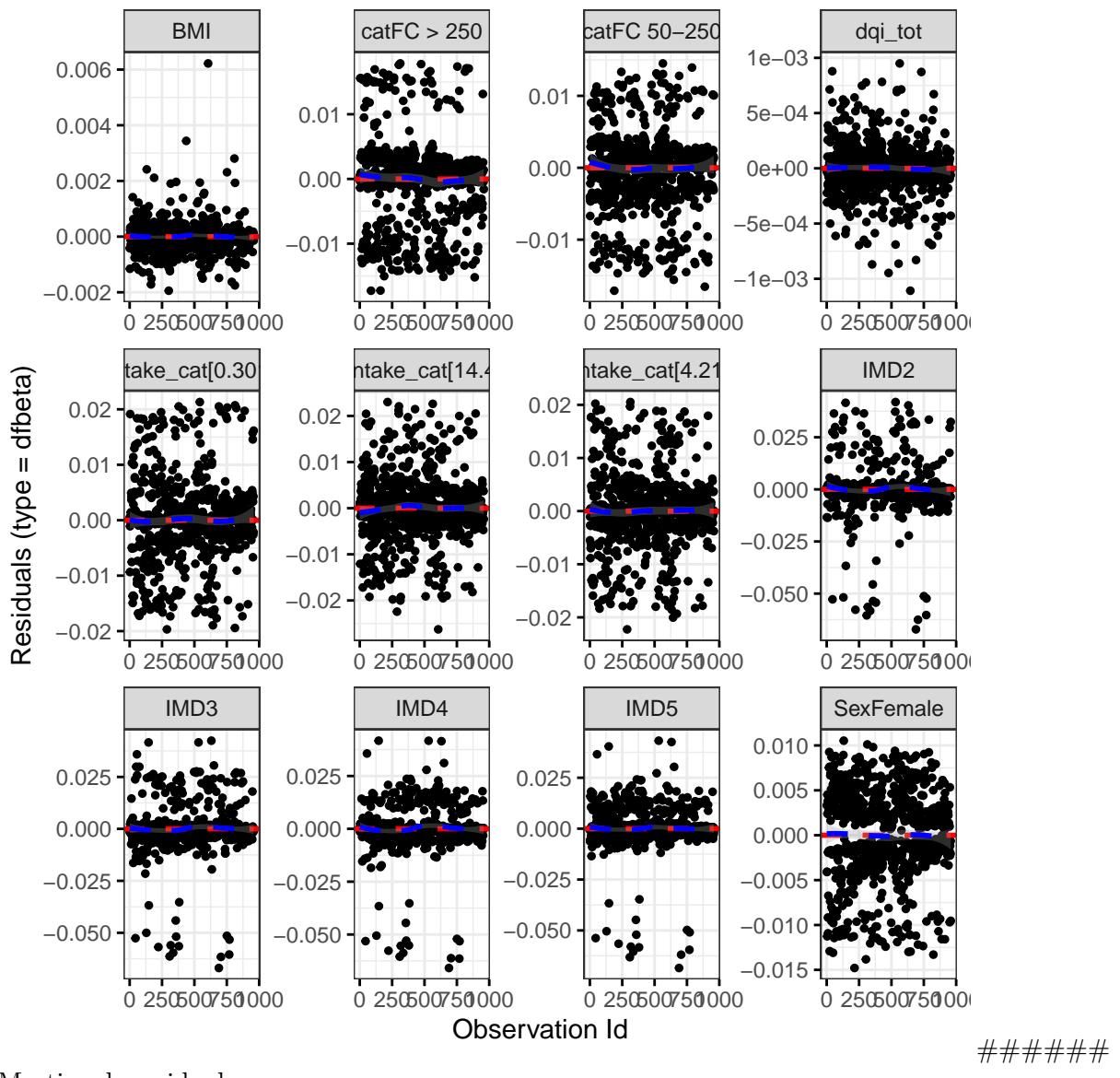
Diagnostics:

Proportional hazards assumption test

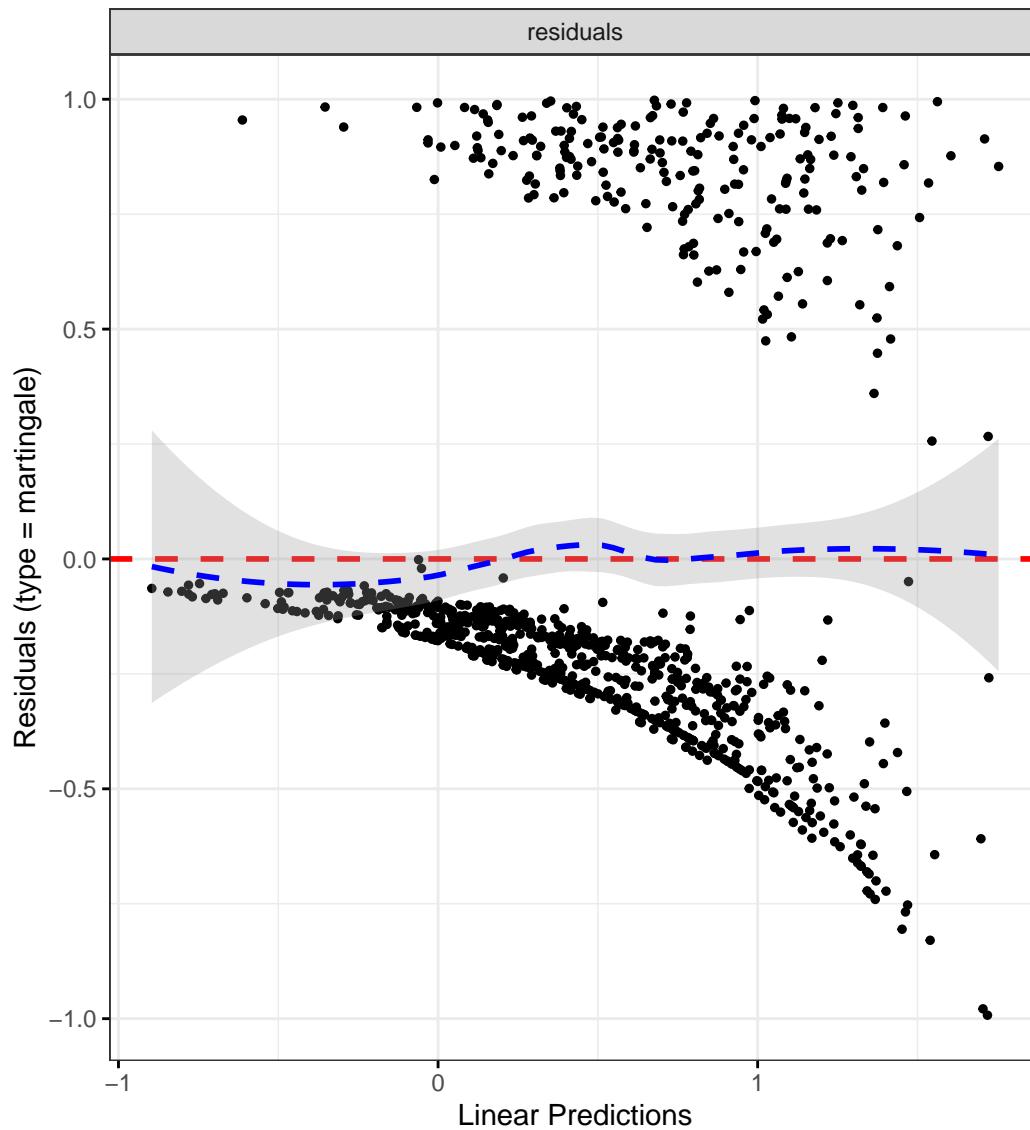
	Chi-squared statistic	DF	P-value
Sex	0.0391	0.9891	0.8399
cat	6.9377	1.9802	0.0305
IMD	1.5860	3.9442	0.8046
dqi_tot	1.9924	0.9924	0.1566
BMI	1.8574	0.9907	0.1710
drinkIntake_cat	0.6547	2.9754	0.8811
GLOBAL	12.9558	22.6243	0.9466

DF betas

```
`geom_smooth()` using formula = 'y ~ x'
```



```
`geom_smooth()` using formula = 'y ~ x'
```



Animal-based products (processed meat)

Crohn's disease

Patient-reported flare

```
# Categorize processed meat intake by quantiles  
flare.cd.df <- categorize_by_quantiles(flare.cd.df, "processedMeatIntake", reference_data = )
```

```

# Run survival analysis using utility function
analysis_result <- run_survival_analysis(
  data = flare.cd.df,
  var_name = "processedMeatIntake",
  outcome_time = "softflare_time",
  outcome_event = "softflare",
  legend_title = "Processed meat intake quantiles",
  plot_base_path = "plots/cd/soft-flare/diet/processedMeatIntake",
  break_time_by = 200
)

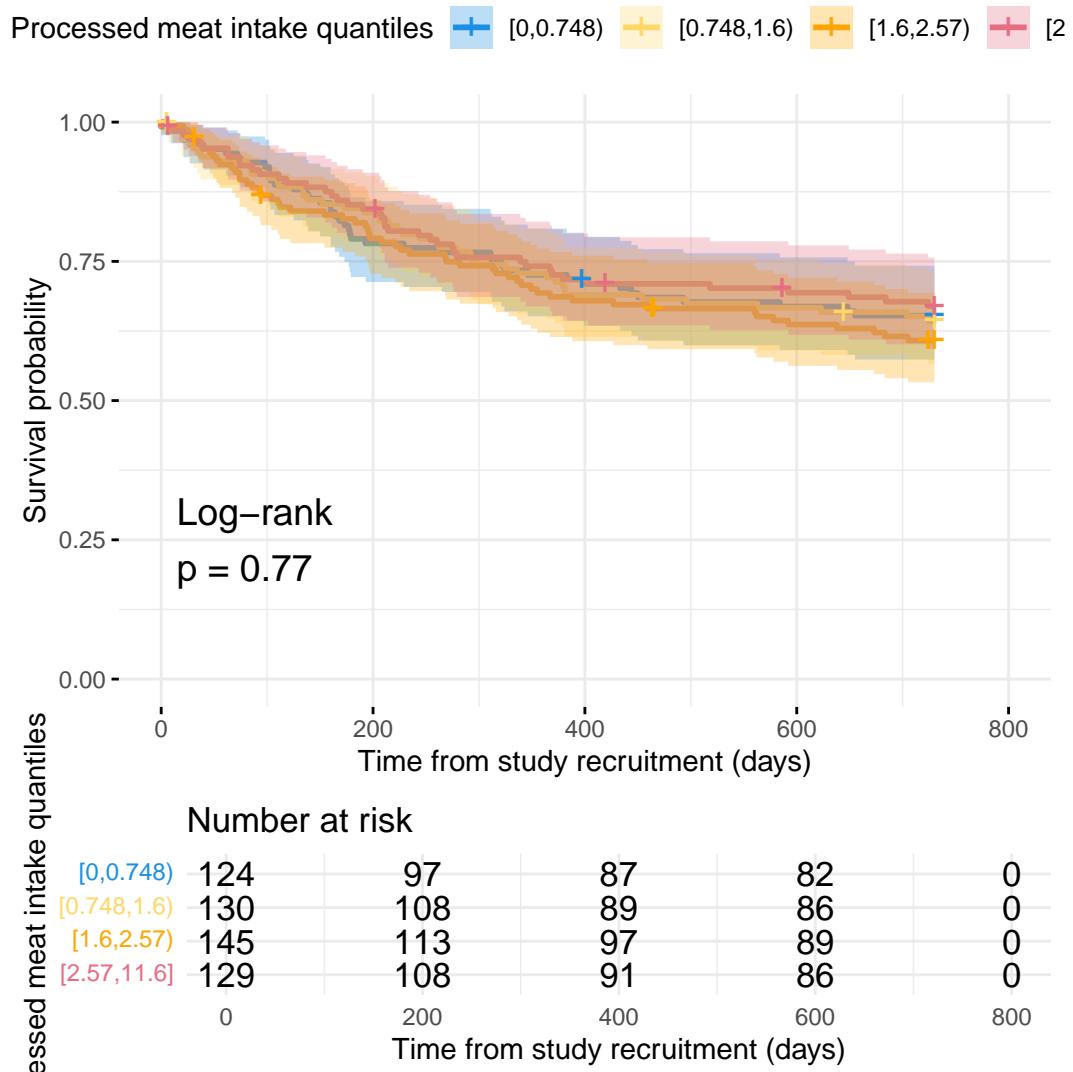
# Save plot as RDS
saveRDS(analysis_result$plot, paste0(paths$outdir, "processedMeatIntake-cd-soft.RDS"))

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(softflare_time, softflare) ~
    Sex + cat + IMD + dqi_tot + BMI + processedMeatIntake_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.cd.df
)

# Display plot and model summary
analysis_result$plot

```

Time to patient-reported flare



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.9199	1.3724	2.6857	0.0001
catFC 50-250	1.2723	0.8939	1.8109	0.1811
catFC > 250	1.9885	1.3563	2.9153	0.0004

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	0.7296	0.3805	1.3992	0.3427
IMD3	0.9467	0.5172	1.7326	0.8589
IMD4	0.8582	0.4738	1.5542	0.6137
IMD5	1.0046	0.5749	1.7554	0.9872
dqi_tot	1.0084	0.9938	1.0232	0.2606
BMI	1.0066	0.9790	1.0350	0.6424
processedMeatIntake_cat[0]	1.0300	0.6543	1.6213	0.8984
processedMeatIntake_cat[1]	1.2643	0.8094	1.9749	0.3026
processedMeatIntake_cat[2]	1.1644	0.7125	1.9030	0.5437

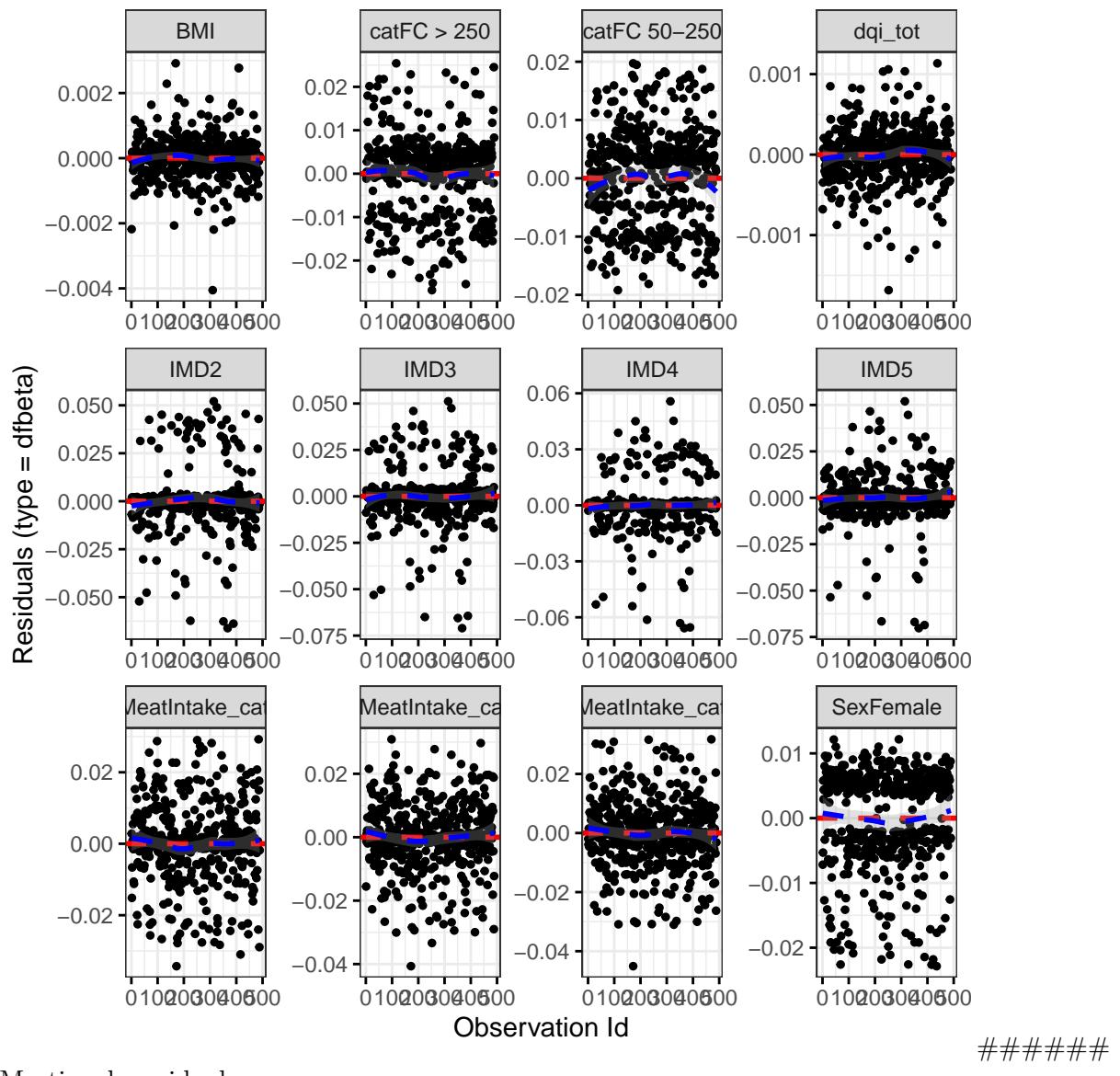
Diagnostics:

Proportional hazards assumption test

	Chi-squared statistic	DF	P-value
Sex	0.2725	1.0000	0.6016
cat	0.7333	2.0000	0.6931
IMD	2.9914	4.0000	0.5593
dqi_tot	0.3530	1.0000	0.5524
BMI	1.3234	1.0000	0.2500
processedMeatIntake_cat	0.6750	3.0000	0.8791
GLOBAL	5.8796	12.0001	0.9220

DF betas

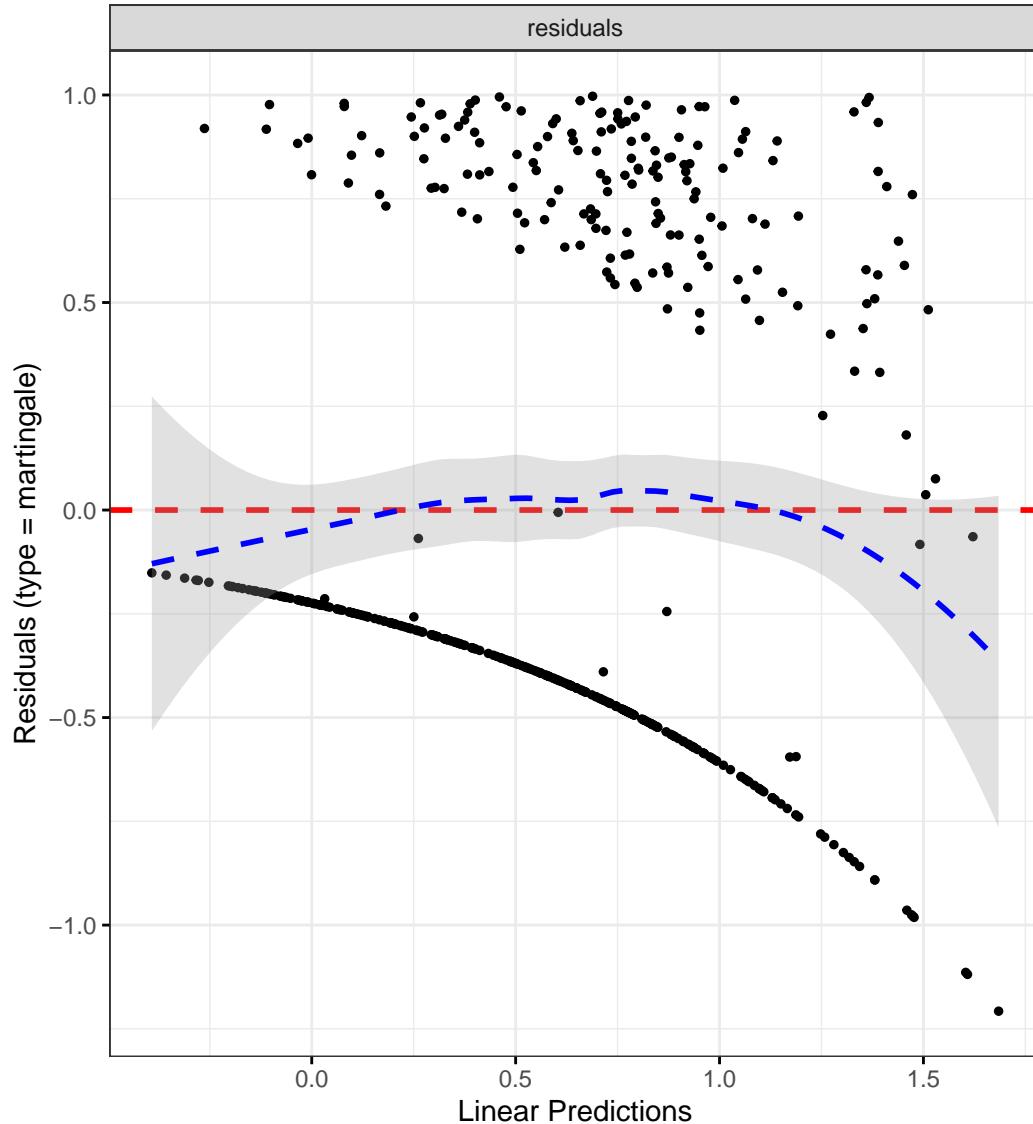
```
`geom_smooth()` using formula = 'y ~ x'
```



#####

Martingale residuals

```
`geom_smooth()` using formula = 'y ~ x'
```



Hard flare

```
# Run survival analysis using utility function for hard flare
analysis_result <- run_survival_analysis(
  data = flare.cd.df,
  var_name = "processedMeatIntake",
  outcome_time = "hardflare_time",
  outcome_event = "hardflare",
  legend_title = "Processed meat intake quantiles",
```

```

plot_base_path = "plots/cd/hard-flare/diet/processedMeatIntake",
break_time_by = 500
)

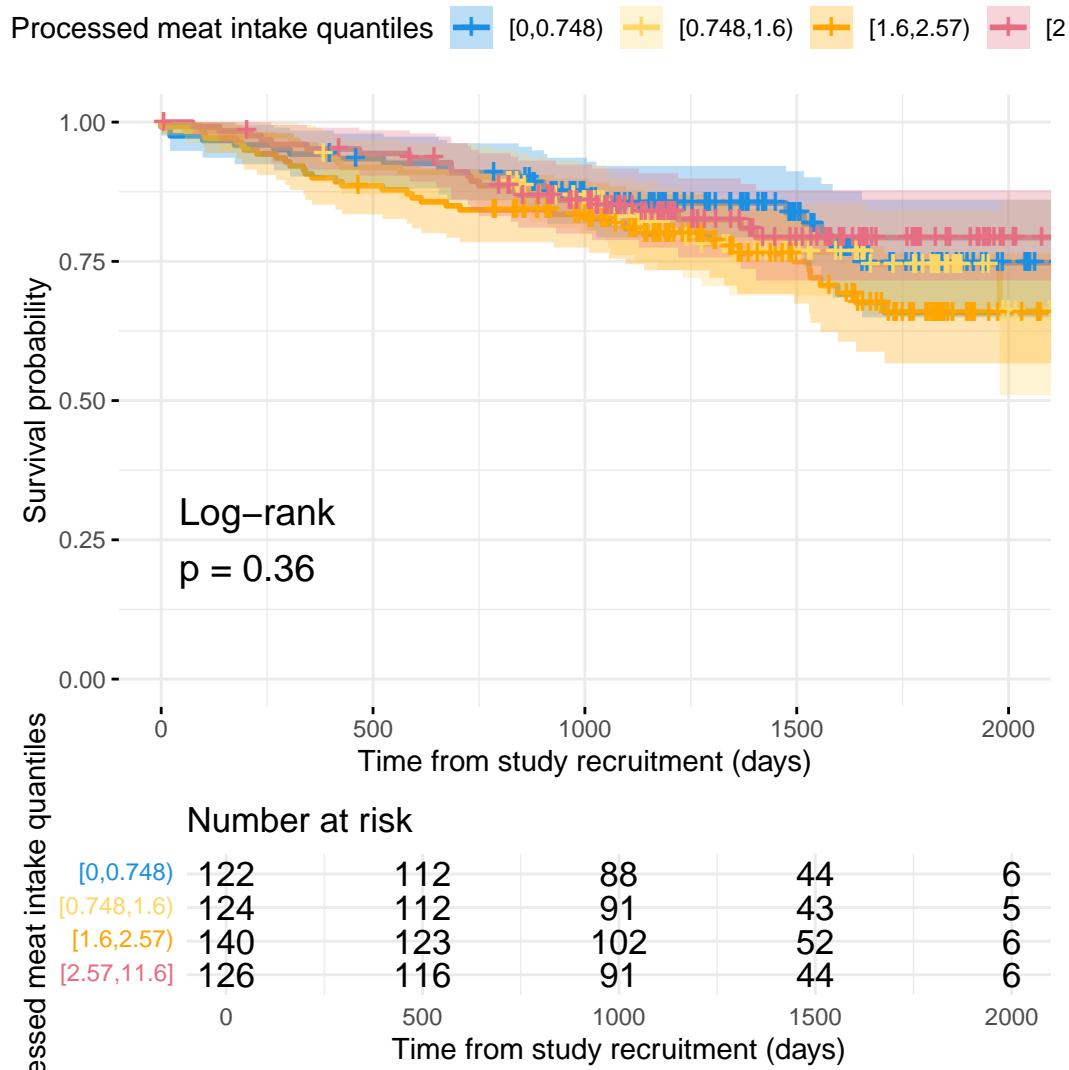
# Save plot as RDS
saveRDS(analysis_result$plot, paste0(paths$outdir, "processedMeatIntake-cd-hard.RDS"))

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(hardflare_time, hardflare) ~
    Sex + cat + IMD + dqi_tot + BMI + processedMeatIntake_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.cd.df
)

# Display plot and model summary
analysis_result$plot

```

Time to hard flare



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.3115	0.8651	1.9881	0.2015
catFC 50-250	1.8233	1.1442	2.9052	0.0115
catFC > 250	2.8472	1.7164	4.7231	0.0001

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	0.6080	0.2606	1.4187	0.2498
IMD3	0.7856	0.3533	1.7468	0.5539
IMD4	0.7381	0.3410	1.5978	0.4409
IMD5	0.6906	0.3291	1.4492	0.3276
dqi_tot	1.0026	0.9834	1.0222	0.7908
BMI	1.0181	0.9829	1.0546	0.3168
processedMeatIntake_cat[0]	1.0403	0.5762	1.8782	0.8958
processedMeatIntake_cat[1]	1.2417	0.7073	2.1799	0.4509
processedMeatIntake_cat[2]	0.8596	0.4488	1.6465	0.6482

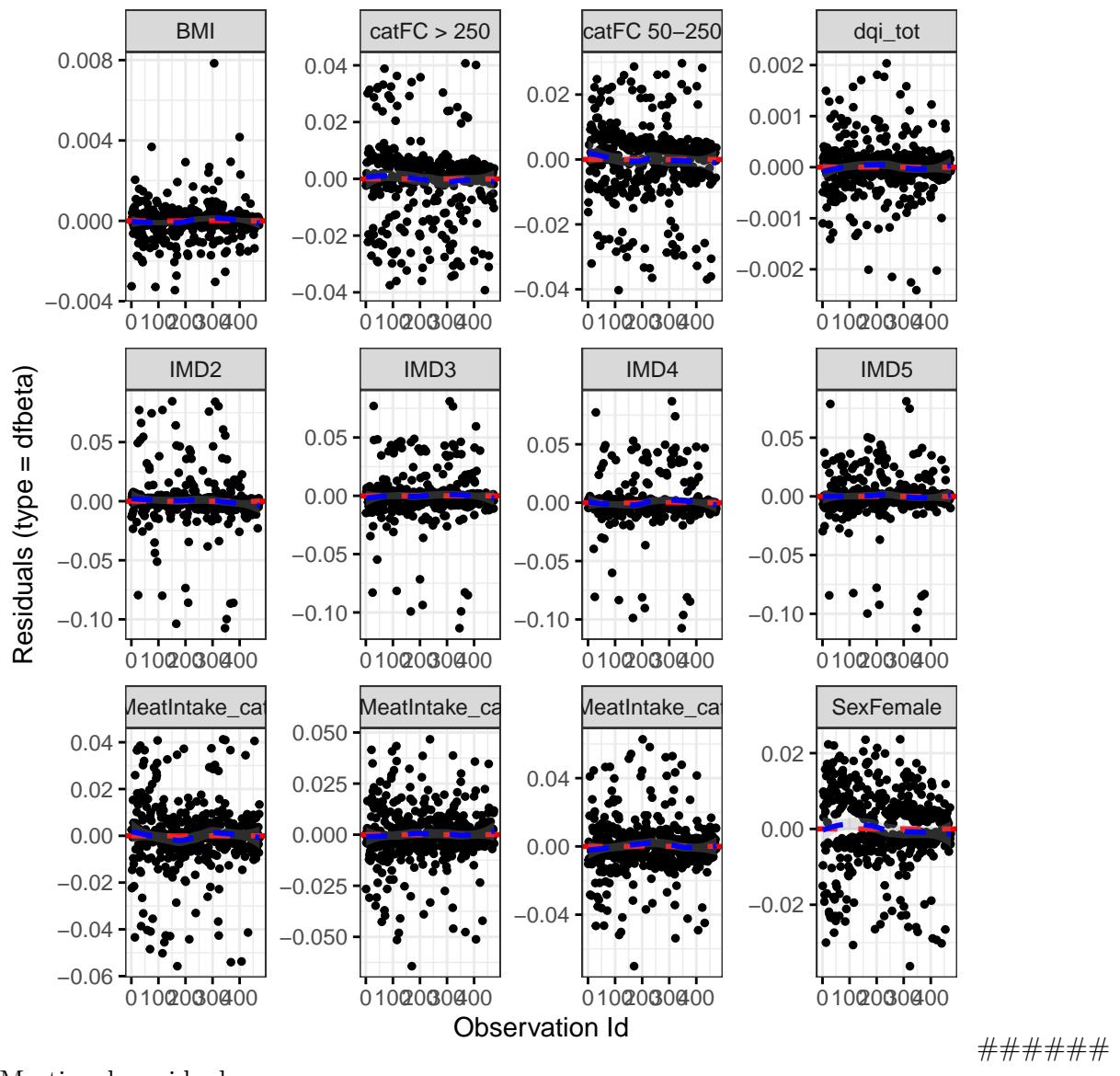
Diagnostics:

Proportional hazards assumption test

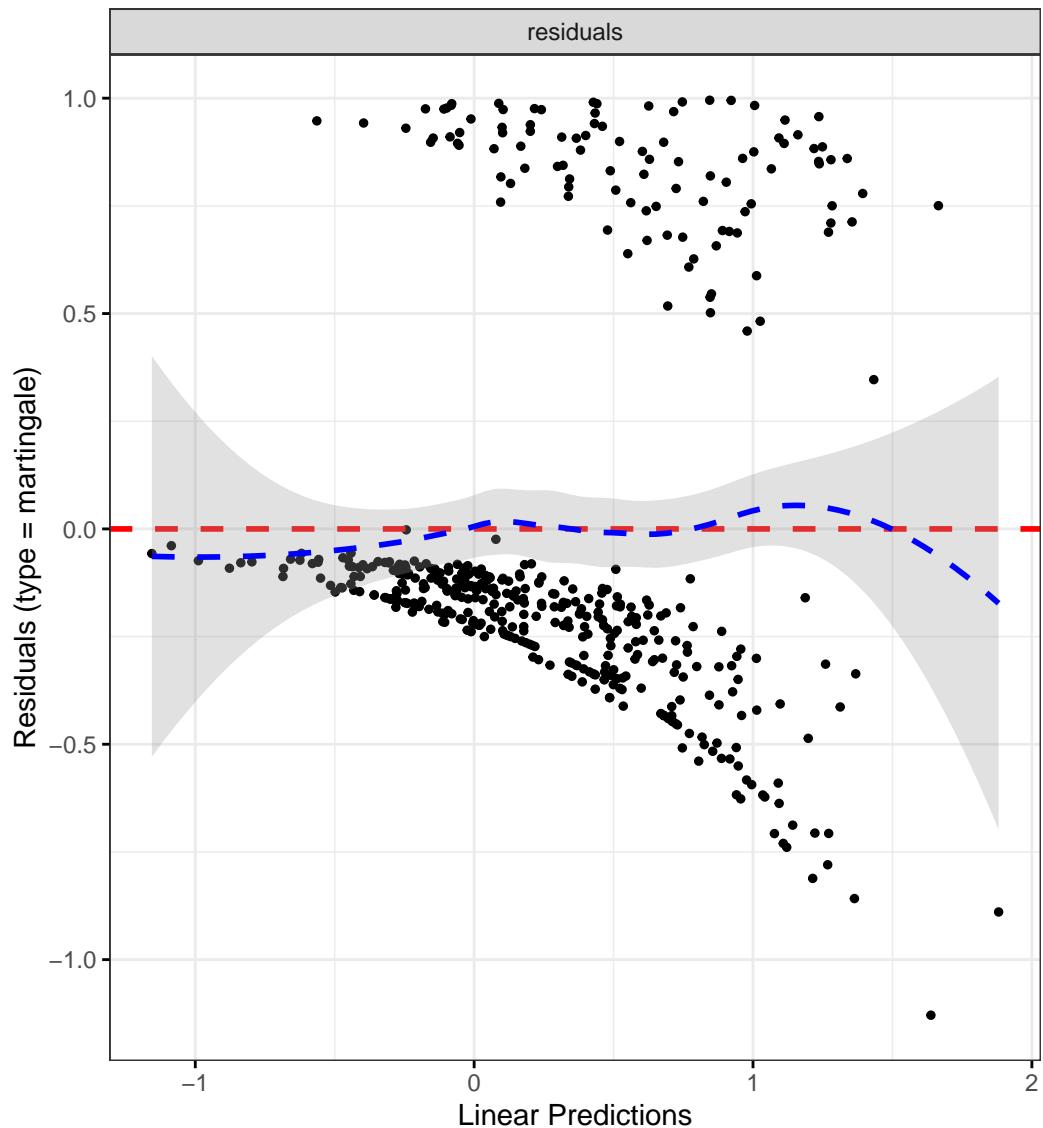
	Chi-squared statistic	DF	P-value
Sex	0.0592	0.9759	0.7994
cat	10.2015	1.9786	0.0059
IMD	2.7767	3.9304	0.5849
dqi_tot	2.8063	0.9895	0.0926
BMI	1.0919	0.9828	0.2907
processedMeatIntake_cat	0.6043	2.9621	0.8915
GLOBAL	17.3198	18.0697	0.5060

DF betas

```
`geom_smooth()` using formula = 'y ~ x'
```



```
`geom_smooth()` using formula = 'y ~ x'
```



Ulcerative colitis

Patient-reported flare

```
# Categorize processed meat intake by quantiles
flare.uc.df <- categorize_by_quantiles(flare.uc.df, "processedMeatIntake", reference_data = ...)

# Run survival analysis using utility function
```

```

analysis_result <- run_survival_analysis(
  data = flare.uc.df,
  var_name = "processedMeatIntake",
  outcome_time = "softflare_time",
  outcome_event = "softflare",
  legend_title = "Processed meat intake quantiles",
  plot_base_path = "plots/uc/soft-flare/diet/processedMeatIntake",
  break_time_by = 200
)

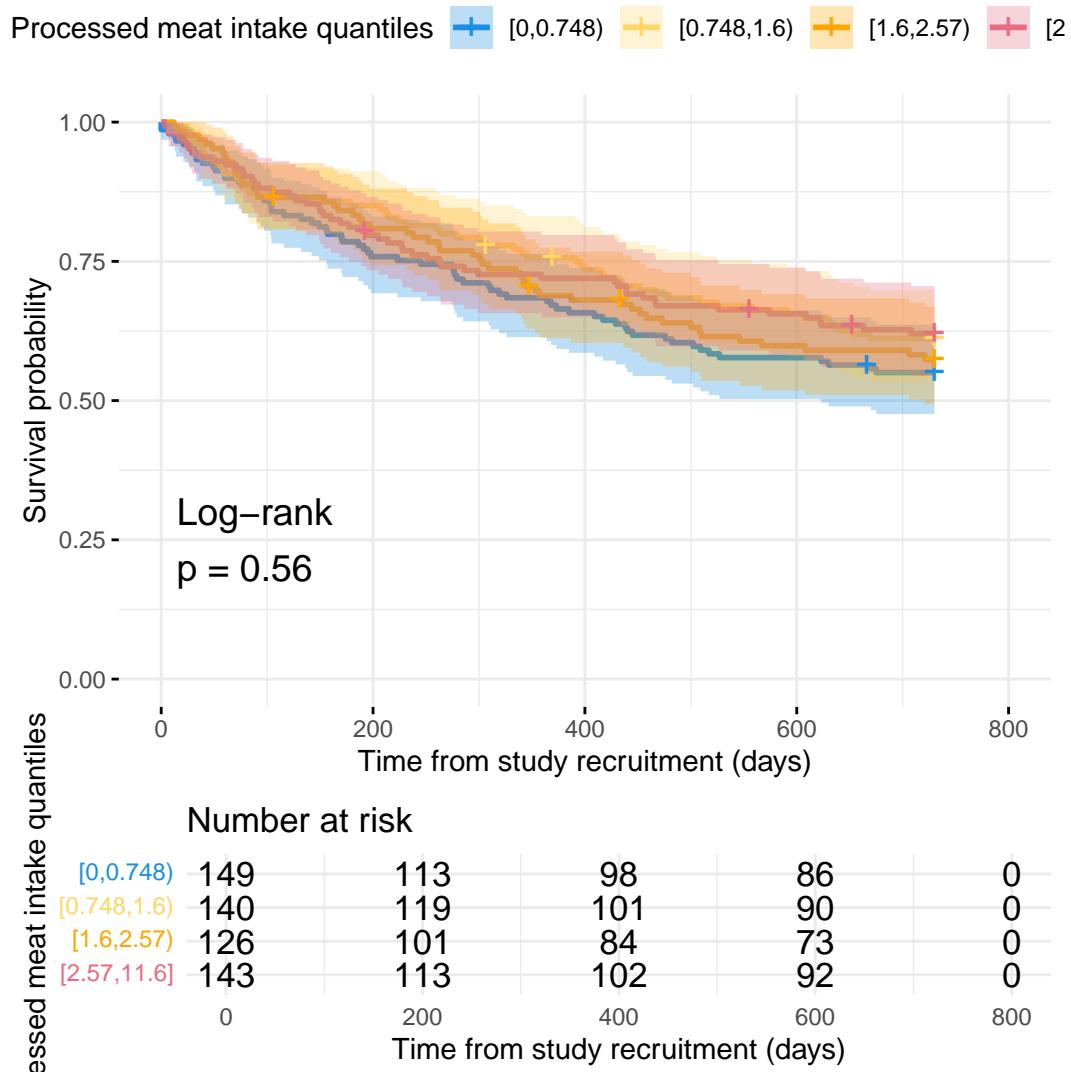
# Save plot as RDS
saveRDS(analysis_result$plot, paste0(paths$outdir, "processedMeatIntake-uc-soft.RDS"))

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(softflare_time, softflare) ~
    Sex + cat + IMD + dqi_tot + BMI + processedMeatIntake_cat +
    frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.uc.df
)

# Display plot and model summary
analysis_result$plot

```

Time to patient-reported flare



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.6876	1.2597	2.2607	0.0005
catFC 50-250	1.8379	1.3343	2.5317	0.0002
catFC > 250	2.1064	1.4712	3.0160	0.0000

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	1.3897	0.7283	2.6515	0.3182
IMD3	1.1285	0.5988	2.1269	0.7085
IMD4	1.3316	0.7349	2.4125	0.3450
IMD5	1.1648	0.6464	2.0992	0.6116
dqi_tot	0.9975	0.9837	1.0116	0.7285
BMI	0.9775	0.9486	1.0074	0.1392
processedMeatIntake_cat[0]	0.7309	0.4976	1.0736	0.1100
processedMeatIntake_cat[1]	0.8183	0.5511	1.2152	0.3204
processedMeatIntake_cat[2]	0.8006	0.5248	1.2213	0.3020

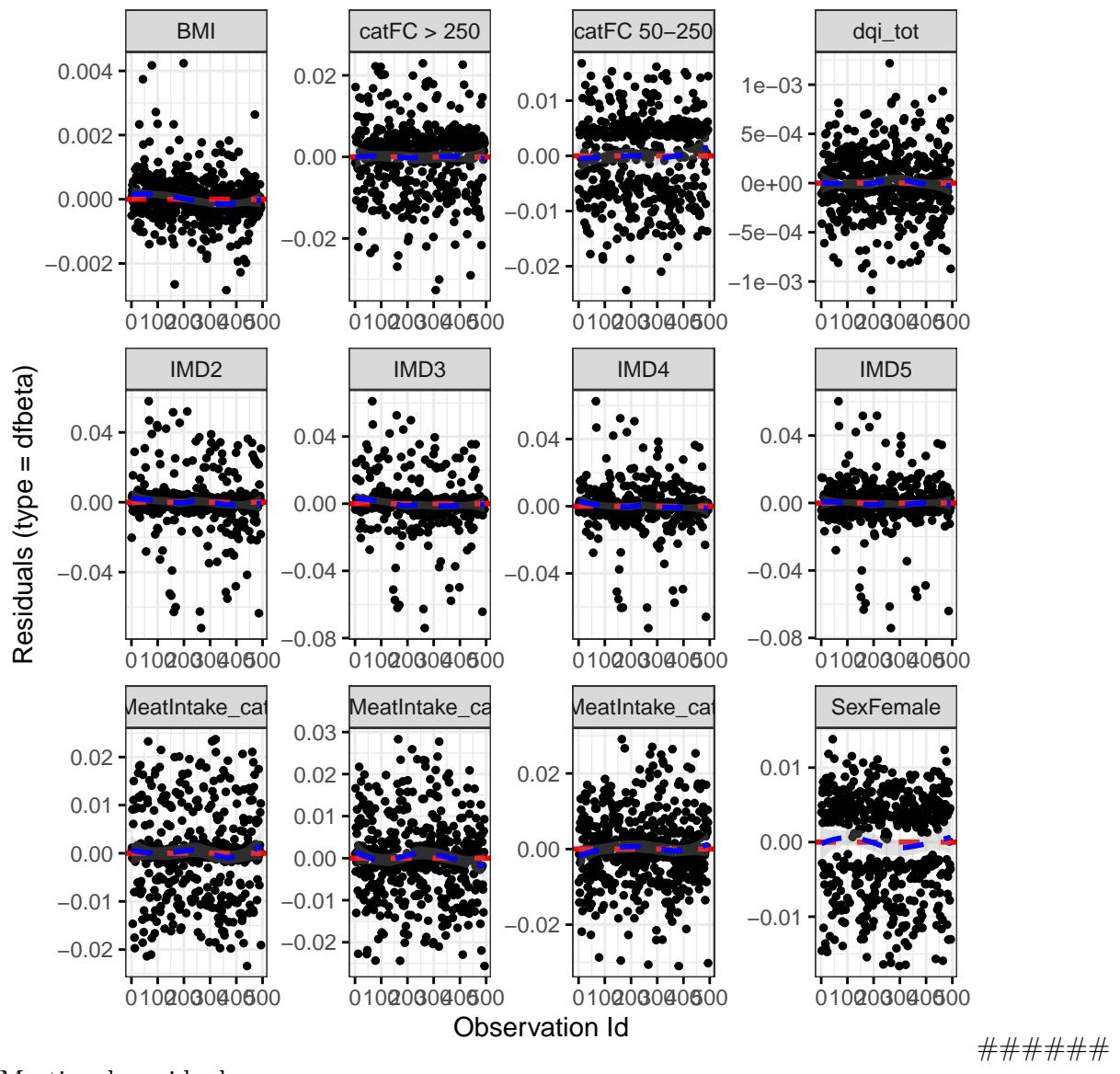
Diagnostics:

Proportional hazards assumption test

	Chi-squared statistic	DF	P-value
Sex	0.0021	1.0000	0.9639
cat	3.5998	2.0000	0.1653
IMD	2.6384	4.0000	0.6200
dqi_tot	0.7445	1.0000	0.3882
BMI	0.9629	1.0000	0.3265
processedMeatIntake_cat	1.8816	3.0000	0.5973
GLOBAL	11.4615	12.0001	0.4898

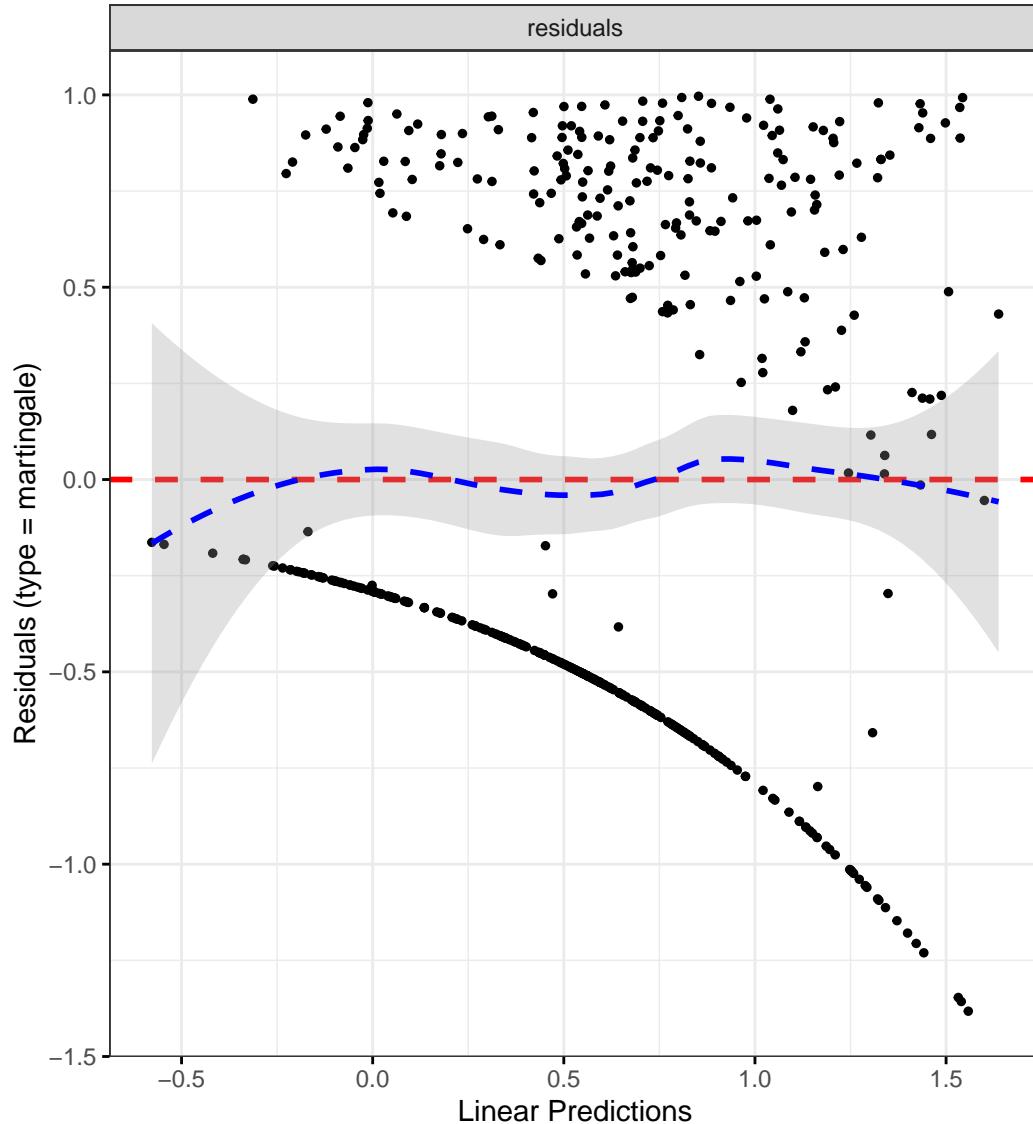
DF betas

```
`geom_smooth()` using formula = 'y ~ x'
```



Martingale residuals

```
`geom_smooth()` using formula = 'y ~ x'
```



Hard flare

```
# Run survival analysis using utility function for hard flare
analysis_result <- run_survival_analysis(
  data = flare.uc.df,
  var_name = "processedMeatIntake",
  outcome_time = "hardflare_time",
  outcome_event = "hardflare",
  legend_title = "Processed meat intake quantiles",
```

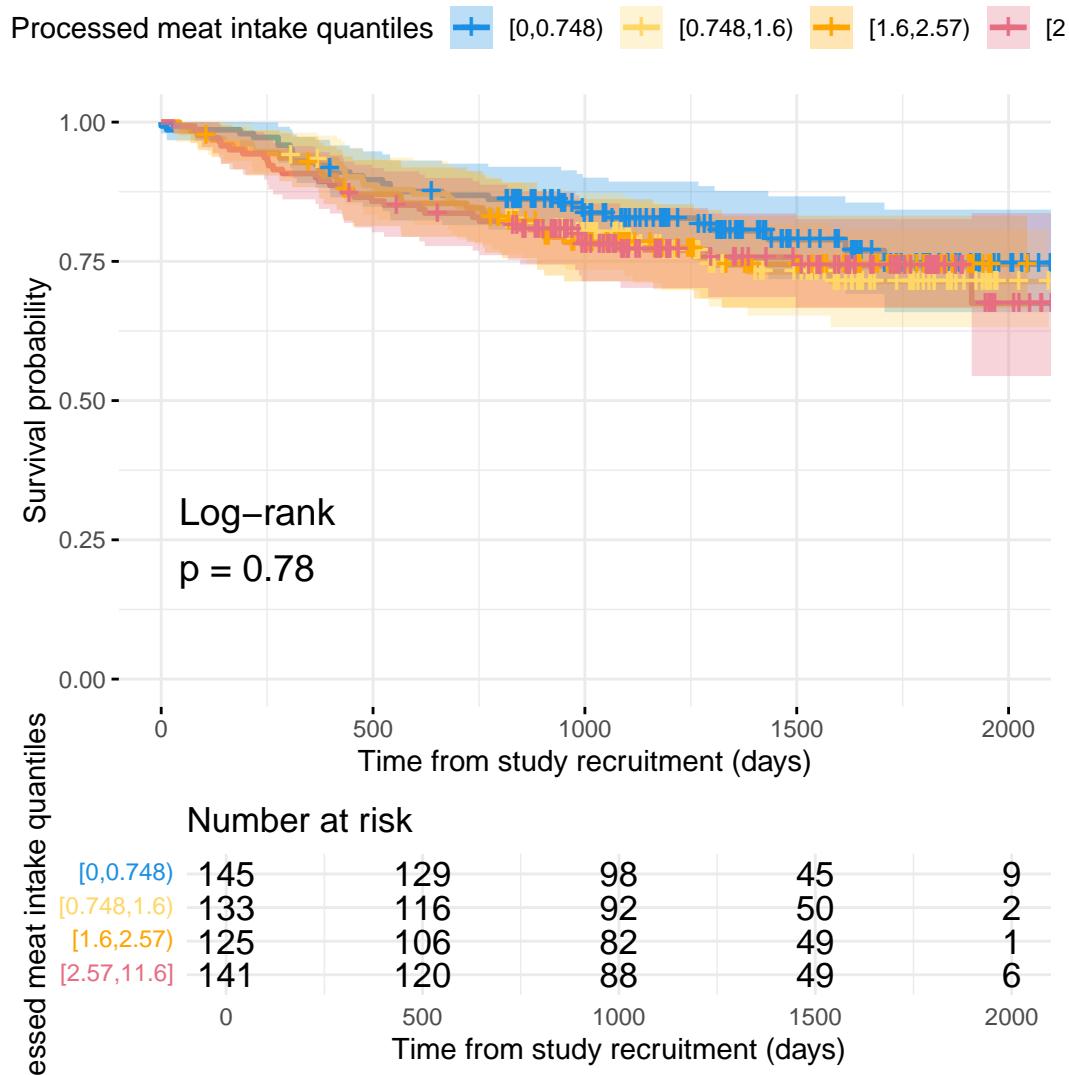
```
plot_base_path = "plots/uc/hard-flare/diet/processedMeatIntake",
break_time_by = 500
)

# Save plot as RDS
saveRDS(analysis_result$plot, paste0(paths$outdir, "processedMeatIntake-uc-hard.RDS"))

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(hardflare_time, hardflare) ~
    Sex + cat + IMD + dqi_tot + BMI + processedMeatIntake_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.uc.df
)

# Display plot and model summary
analysis_result$plot
```

Time to hard flare



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.2333	0.8371	1.8170	0.2889
catFC 50-250	1.9897	1.2858	3.0790	0.0020
catFC > 250	2.4280	1.4846	3.9708	0.0004

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	1.6005	0.6064	4.2242	0.3422
IMD3	1.3379	0.5162	3.4673	0.5491
IMD4	2.3690	0.9851	5.6971	0.0540
IMD5	1.4421	0.5929	3.5077	0.4195
dqi_tot	1.0050	0.9861	1.0244	0.6065
BMI	0.9602	0.9204	1.0017	0.0600
processedMeatIntake_cat[0]	1.1841	0.7006	2.0012	0.5279
processedMeatIntake_cat[1]	1.1236	0.6408	1.9702	0.6842
processedMeatIntake_cat[2]	1.3063	0.7237	2.3581	0.3752

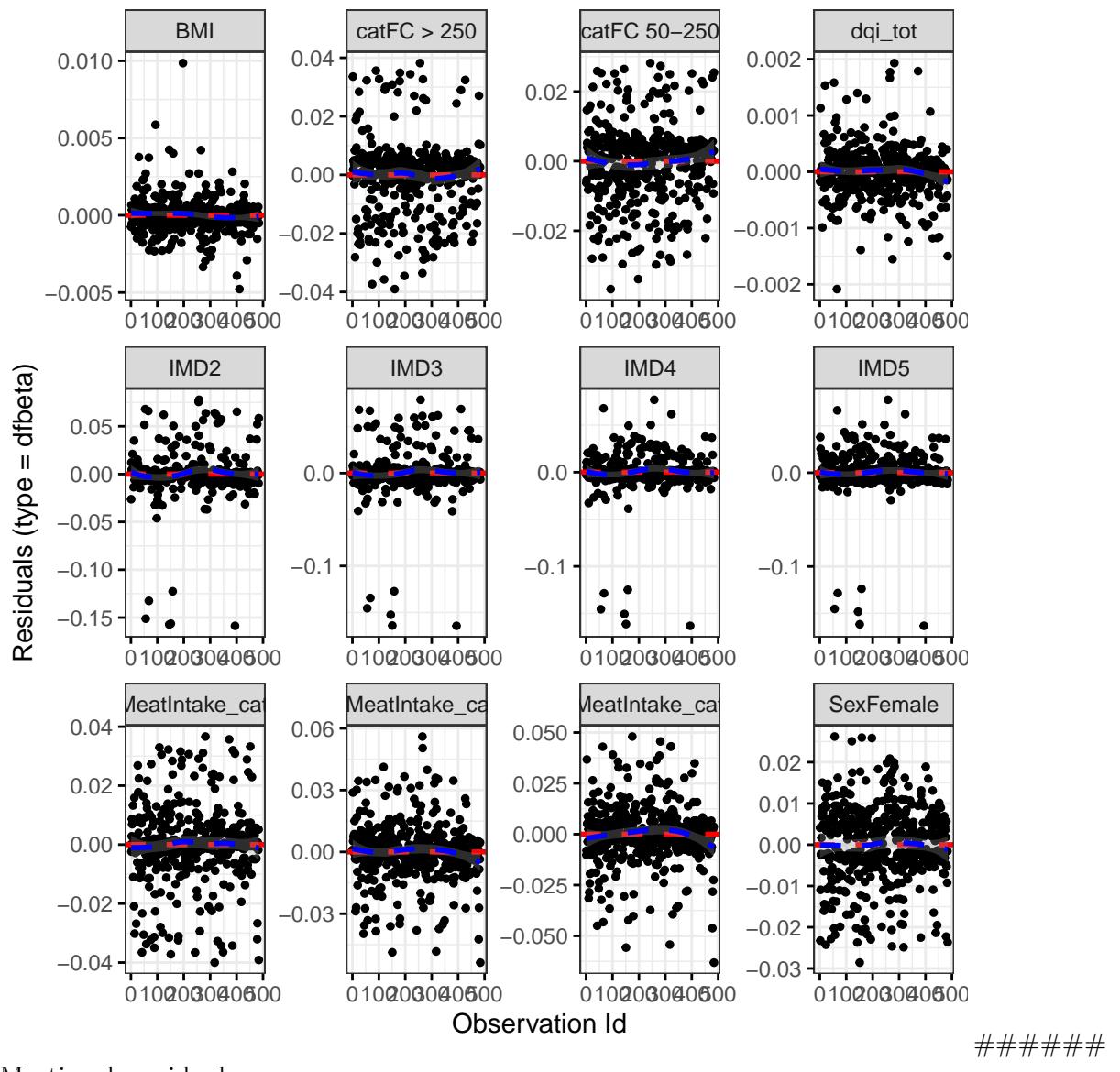
Diagnostics:

Proportional hazards assumption test

	Chi-squared statistic	DF	P-value
Sex	0.0299	0.9888	0.8593
cat	5.5116	1.9552	0.0609
IMD	1.2369	3.9299	0.8652
dqi_tot	0.0003	0.9856	0.9847
BMI	0.5831	0.9897	0.4411
processedMeatIntake_cat	3.3900	2.9535	0.3279
GLOBAL	11.4414	19.6258	0.9251

DF betas

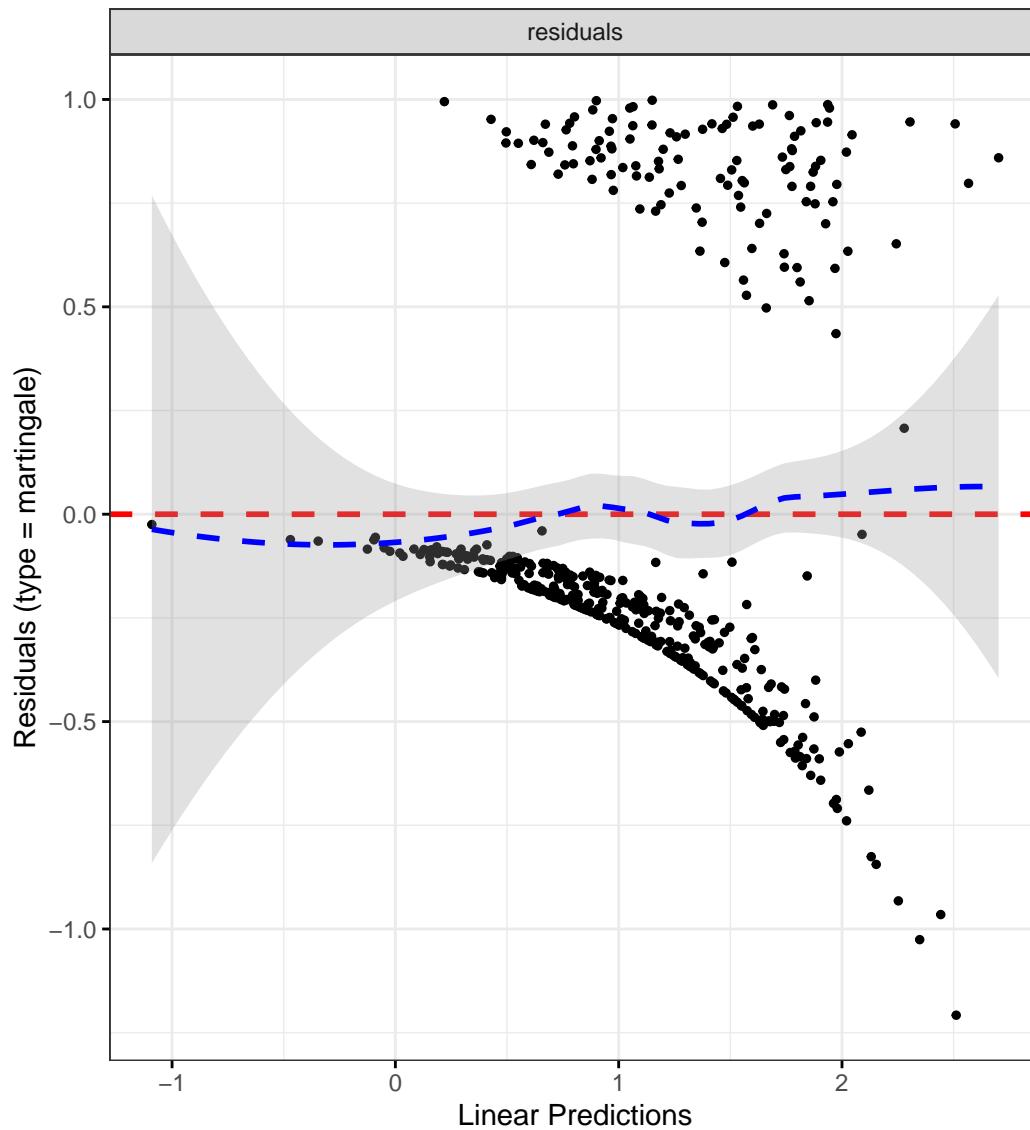
```
`geom_smooth()` using formula = 'y ~ x'
```



#####

Martingale residuals

```
`geom_smooth()` using formula = 'y ~ x'
```



Inflammatory bowel disease

Patient-reported flare

```
# Categorize processed meat intake by quantiles
flare.df <- categorize_by_quantiles(flare.df, "processedMeatIntake", reference_data = flare.o

# Run survival analysis using utility function
```

```

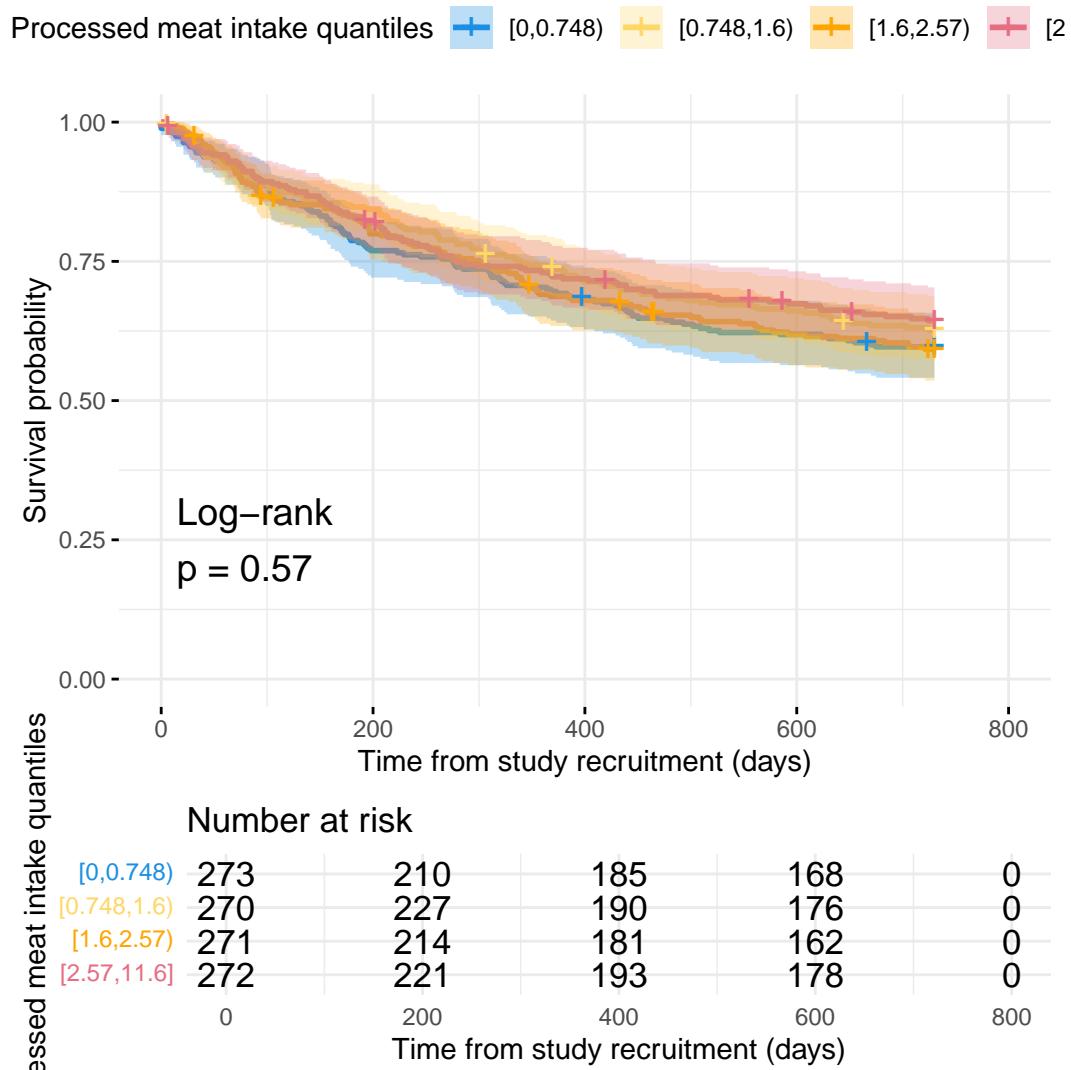
analysis_result <- run_survival_analysis(
  data = flare.df,
  var_name = "processedMeatIntake",
  outcome_time = "softflare_time",
  outcome_event = "softflare",
  legend_title = "Processed meat intake quantiles",
  plot_base_path = "plots/ibd/soft-flare/diet/processedMeatIntake",
  break_time_by = 200
)

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(softflare_time, softflare) ~
    Sex + cat + IMD + dqi_tot + BMI + processedMeatIntake_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.df
)

# Display plot and model summary
analysis_result$plot

```

Time to patient-reported flare



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.7738	1.4278	2.2036	0.0000
catFC 50-250	1.5001	1.1855	1.8983	0.0007
catFC > 250	2.0101	1.5496	2.6074	0.0000

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	0.9877	0.6276	1.5545	0.9575
IMD3	1.0248	0.6636	1.5825	0.9122
IMD4	1.1136	0.7352	1.6867	0.6116
IMD5	1.0896	0.7293	1.6280	0.6754
dqi_tot	1.0029	0.9929	1.0129	0.5767
BMI	0.9945	0.9747	1.0148	0.5936
processedMeatIntake_cat[0]	0.8575	0.6408	1.1474	0.3008
processedMeatIntake_cat[1]	1.0003	0.7466	1.3401	0.9984
processedMeatIntake_cat[2]	0.9493	0.6912	1.3037	0.7479

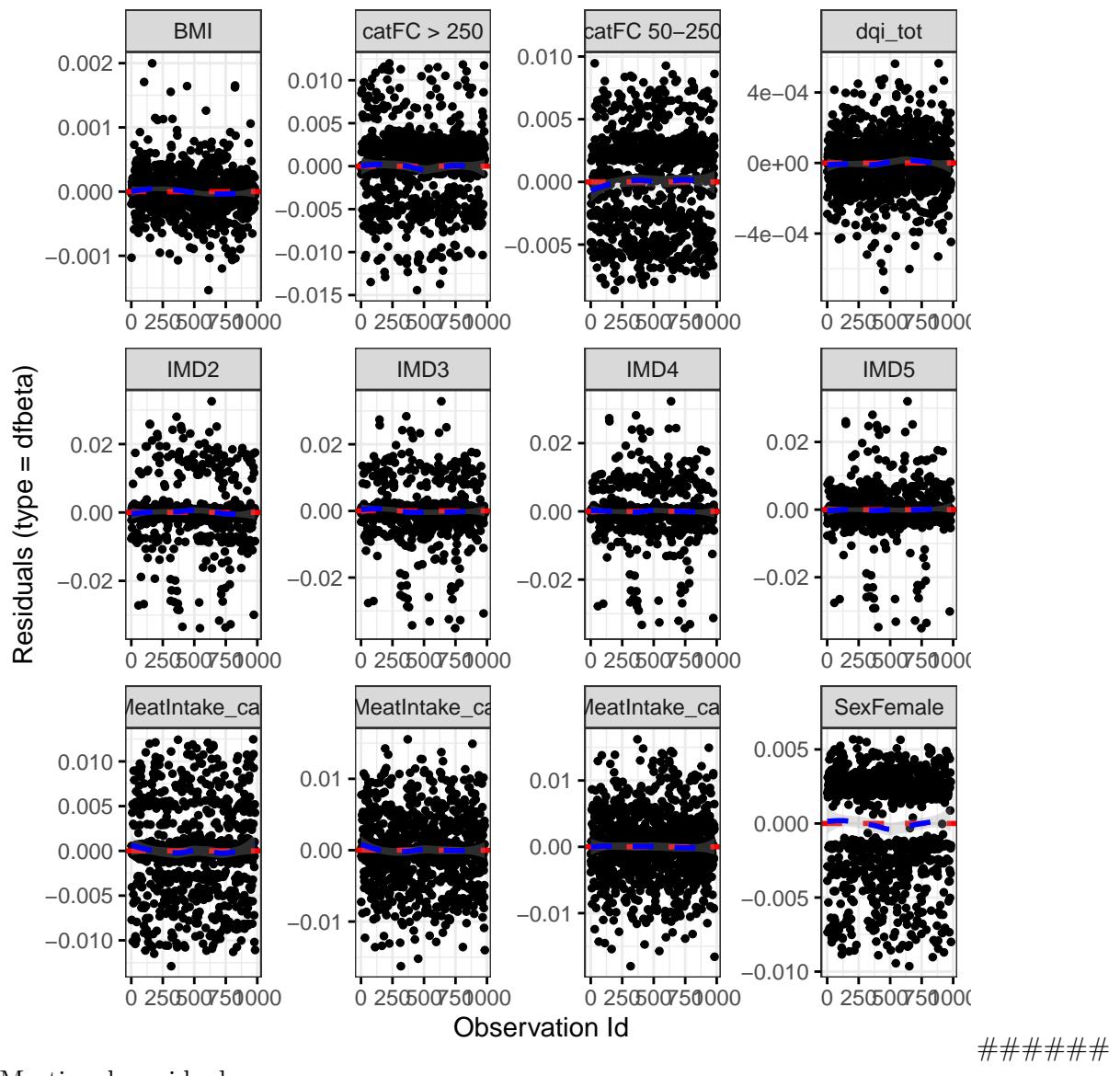
Diagnostics:

Proportional hazards assumption test

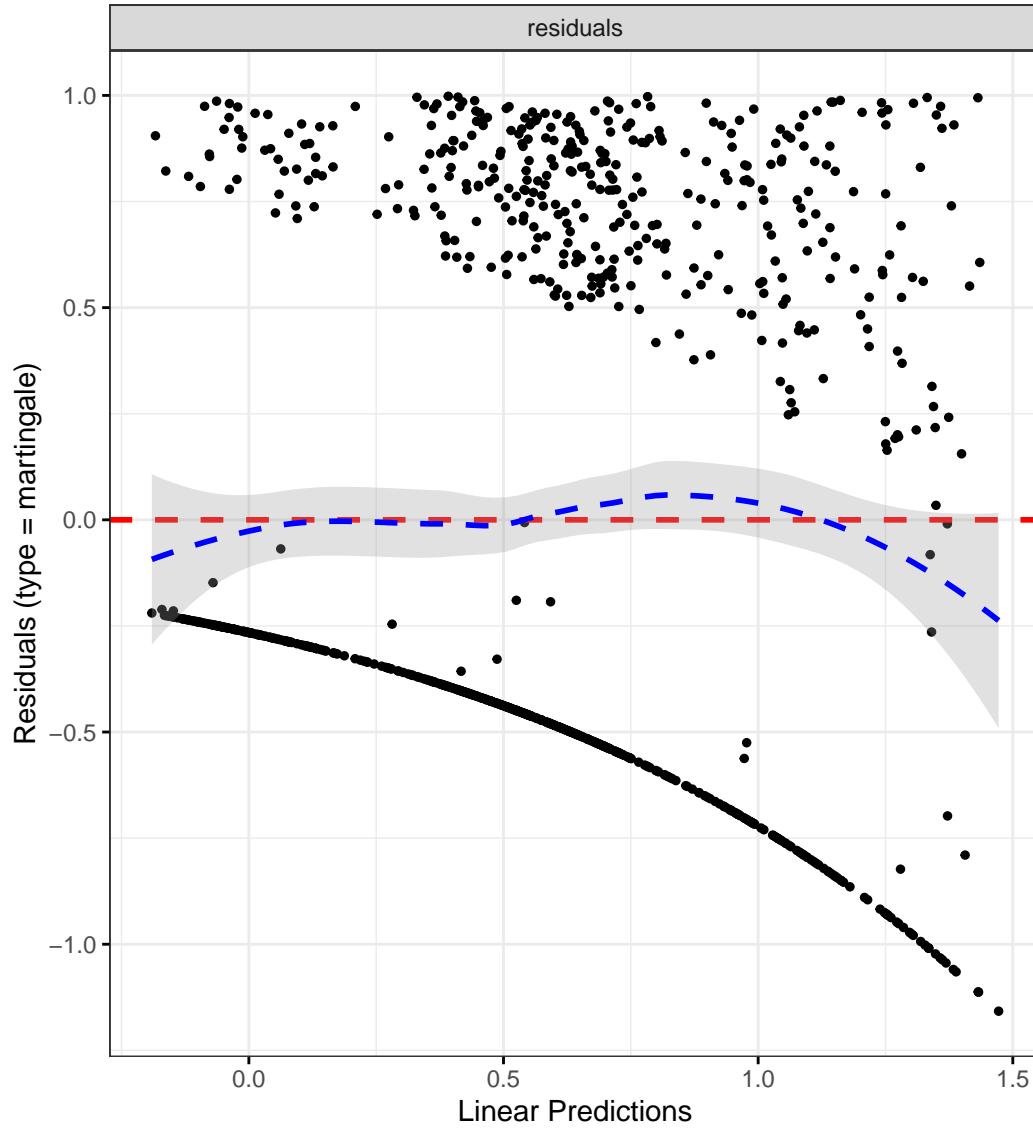
	Chi-squared statistic	DF	P-value
Sex	0.0058	1.0000	0.9393
cat	1.0843	2.0000	0.5815
IMD	5.0889	4.0000	0.2783
dqi_tot	1.4005	1.0000	0.2366
BMI	0.0083	1.0000	0.9273
processedMeatIntake_cat	1.8553	3.0000	0.6030
GLOBAL	10.5504	12.0002	0.5678

DF betas

```
`geom_smooth()` using formula = 'y ~ x'
```



```
`geom_smooth()` using formula = 'y ~ x'
```



Hard flare

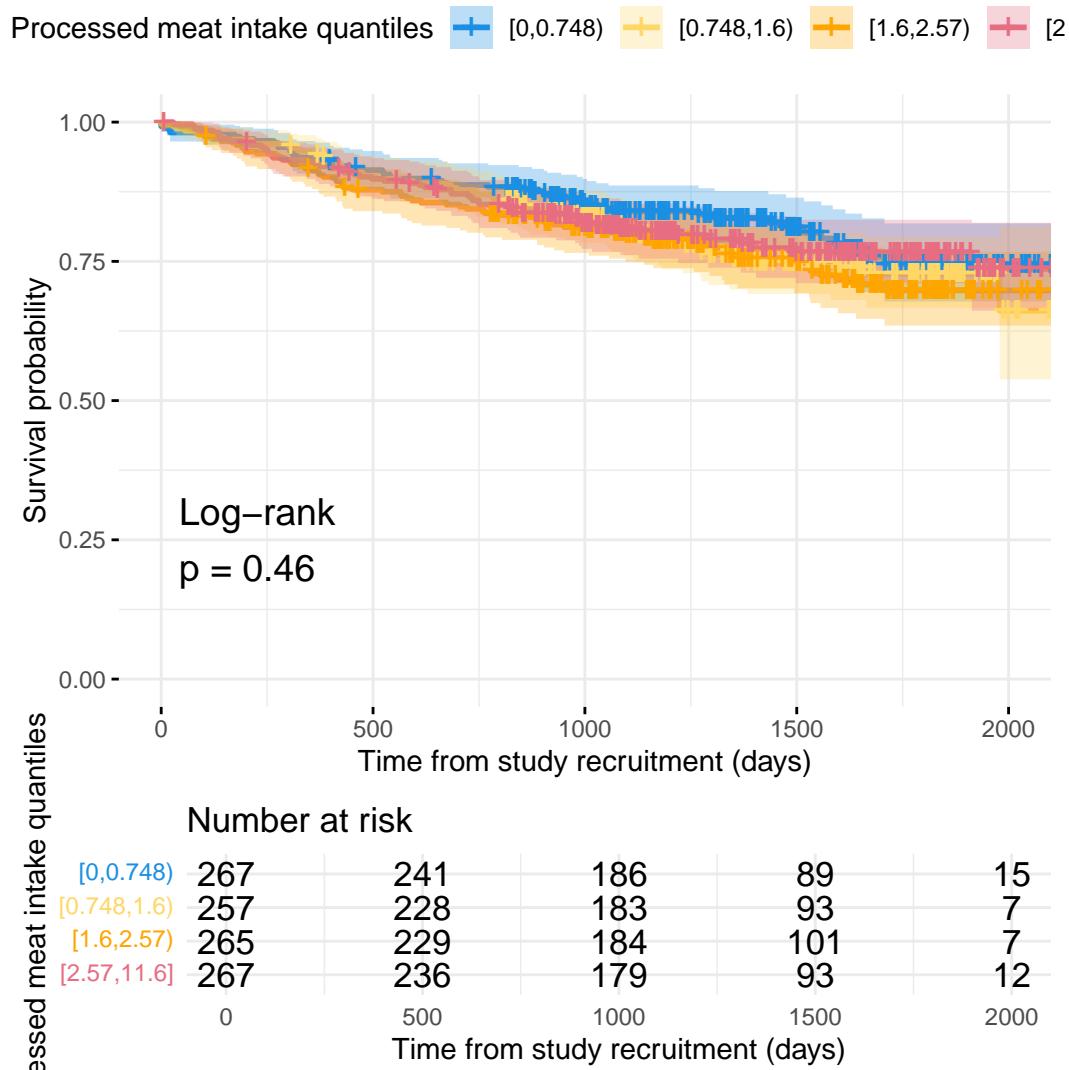
```
# Run survival analysis using utility function for hard flare
analysis_result <- run_survival_analysis(
  data = flare.df,
  var_name = "processedMeatIntake",
  outcome_time = "hardflare_time",
  outcome_event = "hardflare",
  legend_title = "Processed meat intake quantiles",
```

```
plot_base_path = "plots/ibd/hard-flare/diet/processedMeatIntake",
break_time_by = 500
)

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(hardflare_time, hardflare) ~
    Sex + cat + IMD + dqi_tot + BMI + processedMeatIntake_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.df
)

# Display plot and model summary
analysis_result$plot
```

Time to hard flare



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.2601	0.9534	1.6654	0.1043
catFC 50-250	1.8272	1.3323	2.5059	0.0002
catFC > 250	2.5606	1.8081	3.6263	0.0000

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	0.9287	0.4958	1.7396	0.8173
IMD3	0.9532	0.5216	1.7420	0.8762
IMD4	1.3466	0.7662	2.3665	0.3010
IMD5	0.9717	0.5549	1.7016	0.9200
dqi_tot	1.0034	0.9900	1.0170	0.6229
BMI	0.9921	0.9656	1.0192	0.5622
processedMeatIntake_cat[0]	1.0861	0.7356	1.6036	0.6779
processedMeatIntake_cat[1]	1.1960	0.8077	1.7709	0.3716
processedMeatIntake_cat[2]	1.0518	0.6819	1.6223	0.8194

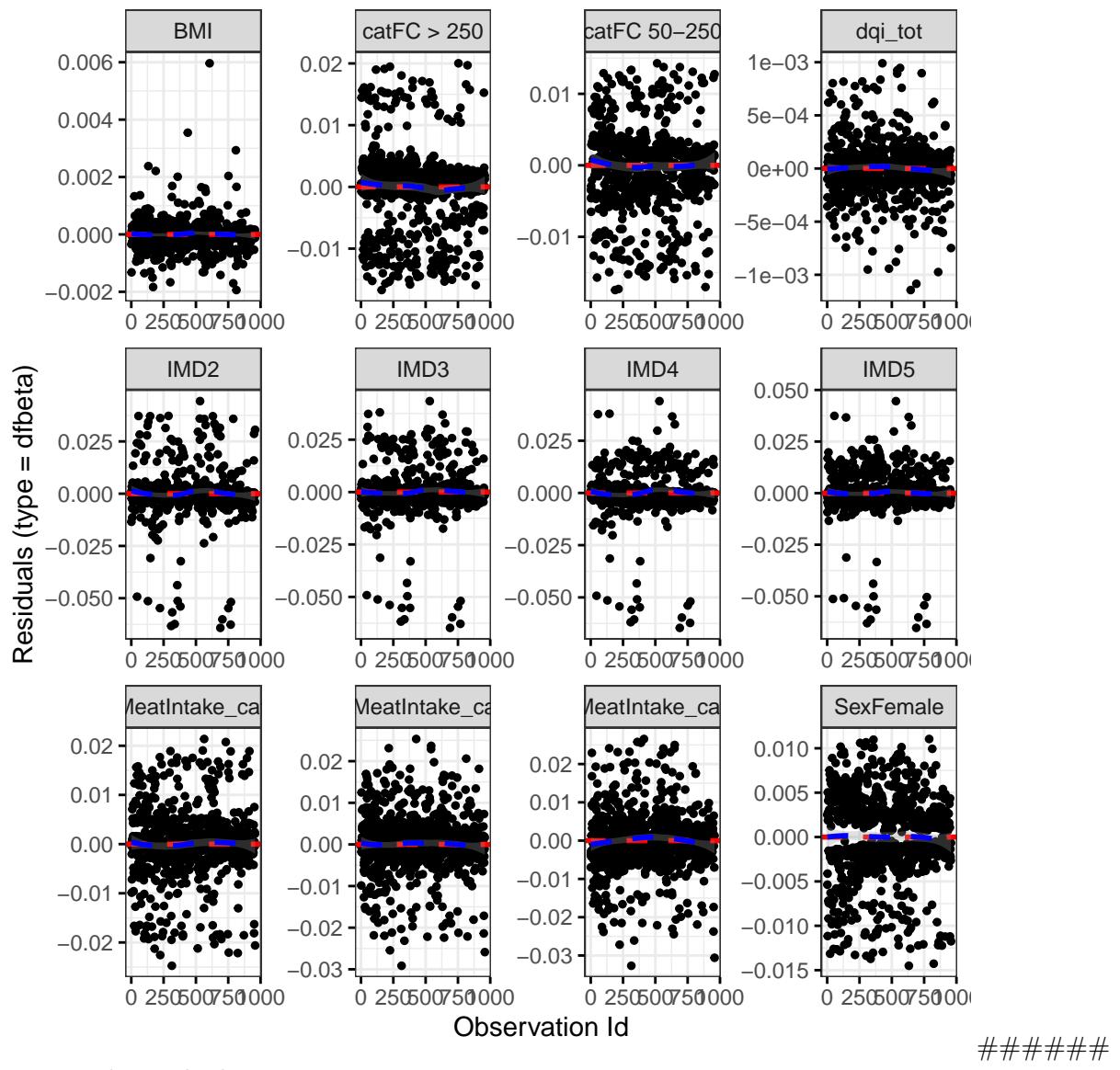
Diagnostics:

Proportional hazards assumption test

	Chi-squared statistic	DF	P-value
Sex	0.0299	0.9898	0.8597
cat	6.8809	1.9794	0.0314
IMD	1.6227	3.9444	0.7979
dqi_tot	2.0094	0.9907	0.1545
BMI	1.9520	0.9903	0.1604
processedMeatIntake_cat	2.9126	2.9733	0.4006
GLOBAL	14.6590	22.6204	0.8958

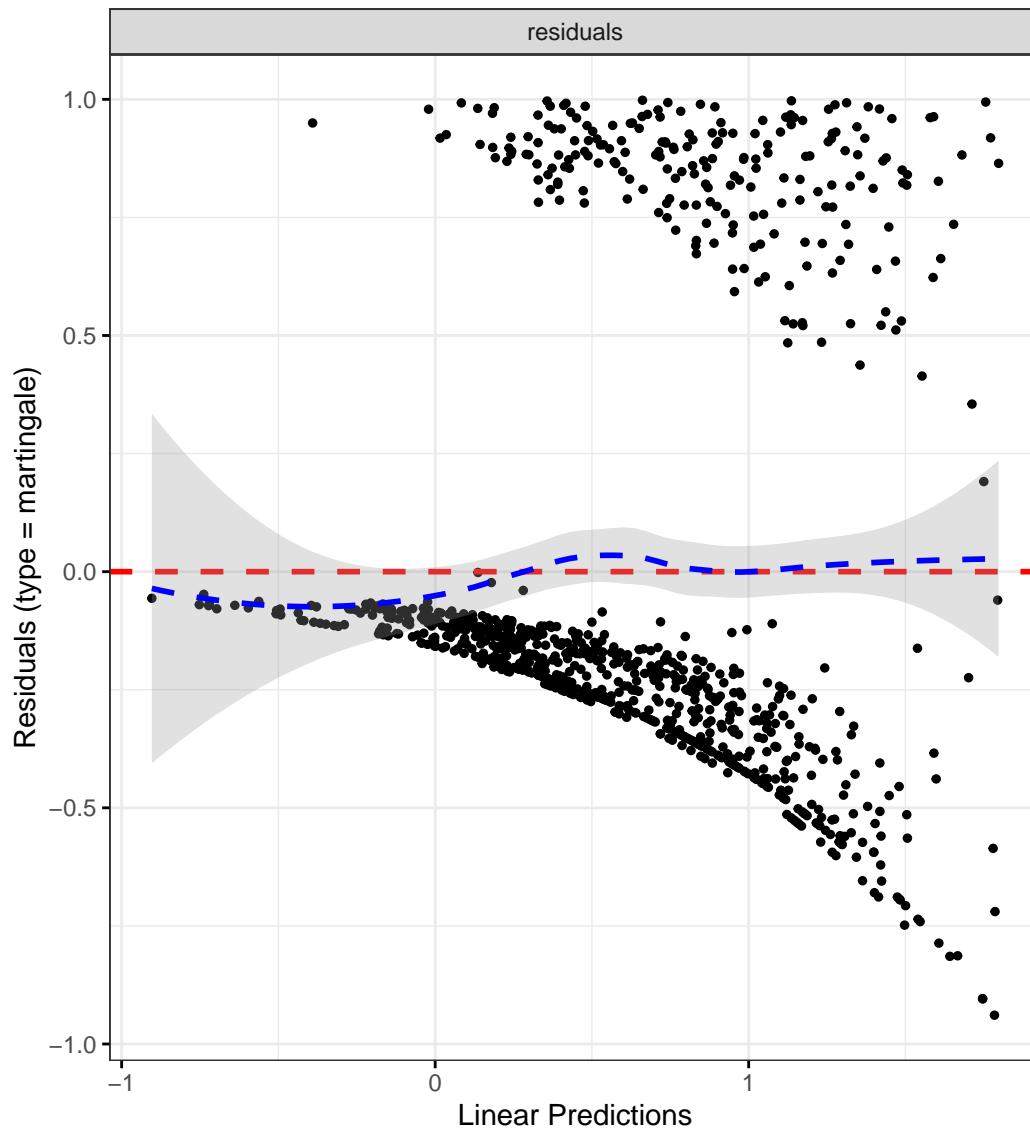
DF betas

```
`geom_smooth()` using formula = 'y ~ x'
```



Martingale residuals

```
`geom_smooth()` using formula = 'y ~ x'
```



Plant-based alternatives

Crohn's disease

Patient-reported flare

```
# Categorize processed plant intake by quantiles  
flare.cd.df <- categorize_by_quantiles(flare.cd.df, "processedPlantIntake", reference_data =
```

```

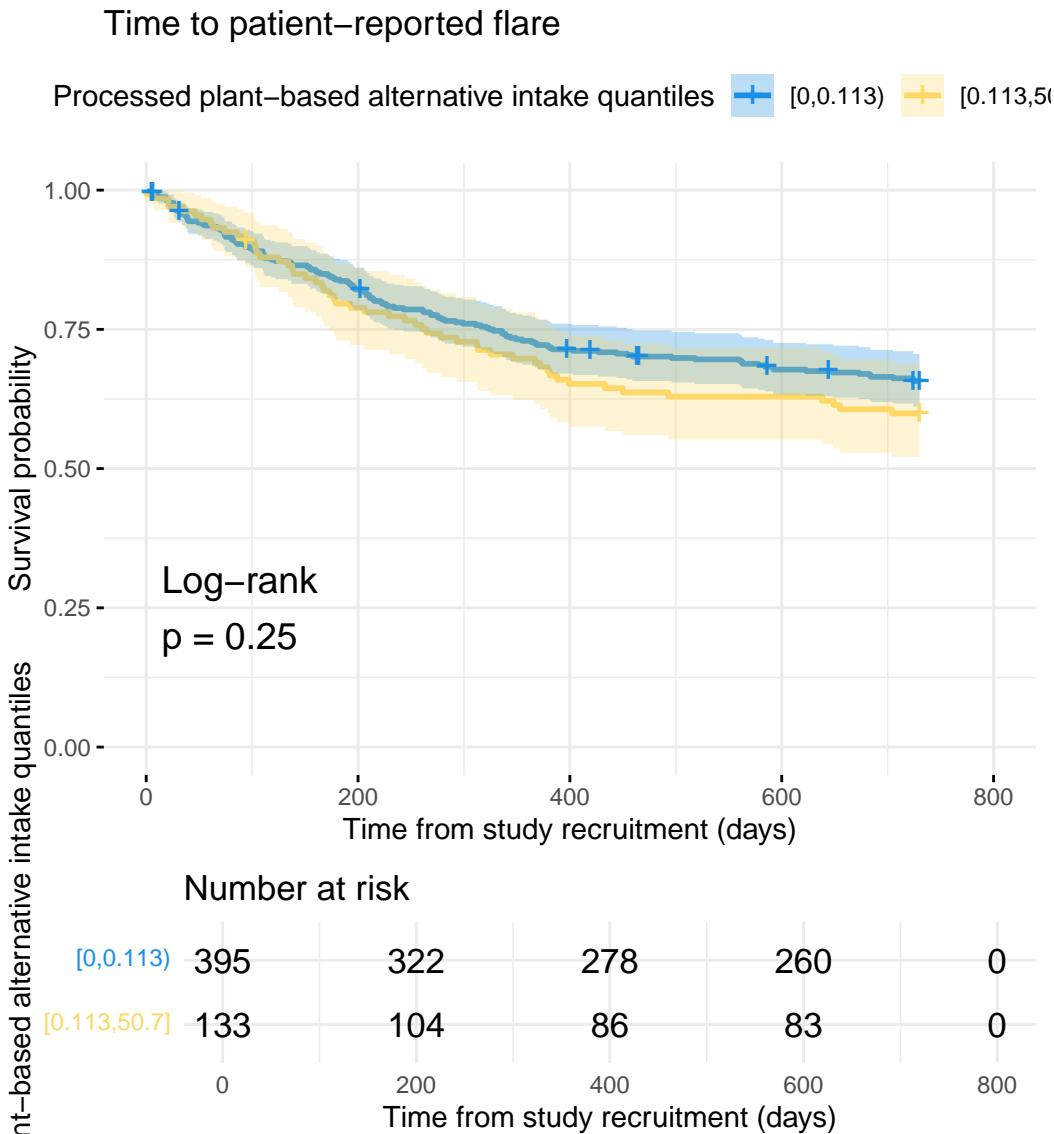
# Run survival analysis using utility function
analysis_result <- run_survival_analysis(
  data = flare.cd.df,
  var_name = "processedPlantIntake",
  outcome_time = "softflare_time",
  outcome_event = "softflare",
  legend_title = "Processed plant-based alternative intake quantiles",
  plot_base_path = "plots/cd/soft-flare/diet/processedPlantIntake",
  break_time_by = 200
)

# Save plot as RDS
saveRDS(analysis_result$plot, paste0(paths$outdir, "processedPlantIntake-cd-soft.RDS"))

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(softflare_time, softflare) ~
    Sex + cat + IMD + dqi_tot + BMI + processedPlantIntake_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.cd.df
)

# Display plot and model summary
analysis_result$plot

```



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.9000	1.3617	2.6512	0.0002
catFC 50-250	1.2962	0.9130	1.8402	0.1468
catFC > 250	2.0441	1.3974	2.9900	0.0002

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	0.6911	0.3602	1.3258	0.2663
IMD3	0.9222	0.5061	1.6805	0.7914
IMD4	0.8536	0.4718	1.5443	0.6008
IMD5	0.9828	0.5640	1.7128	0.9513
dqi_tot	1.0050	0.9912	1.0190	0.4807
BMI	1.0083	0.9809	1.0364	0.5561
processedPlantIntake_cat[1.1581	0.8189	1.6379	0.4064

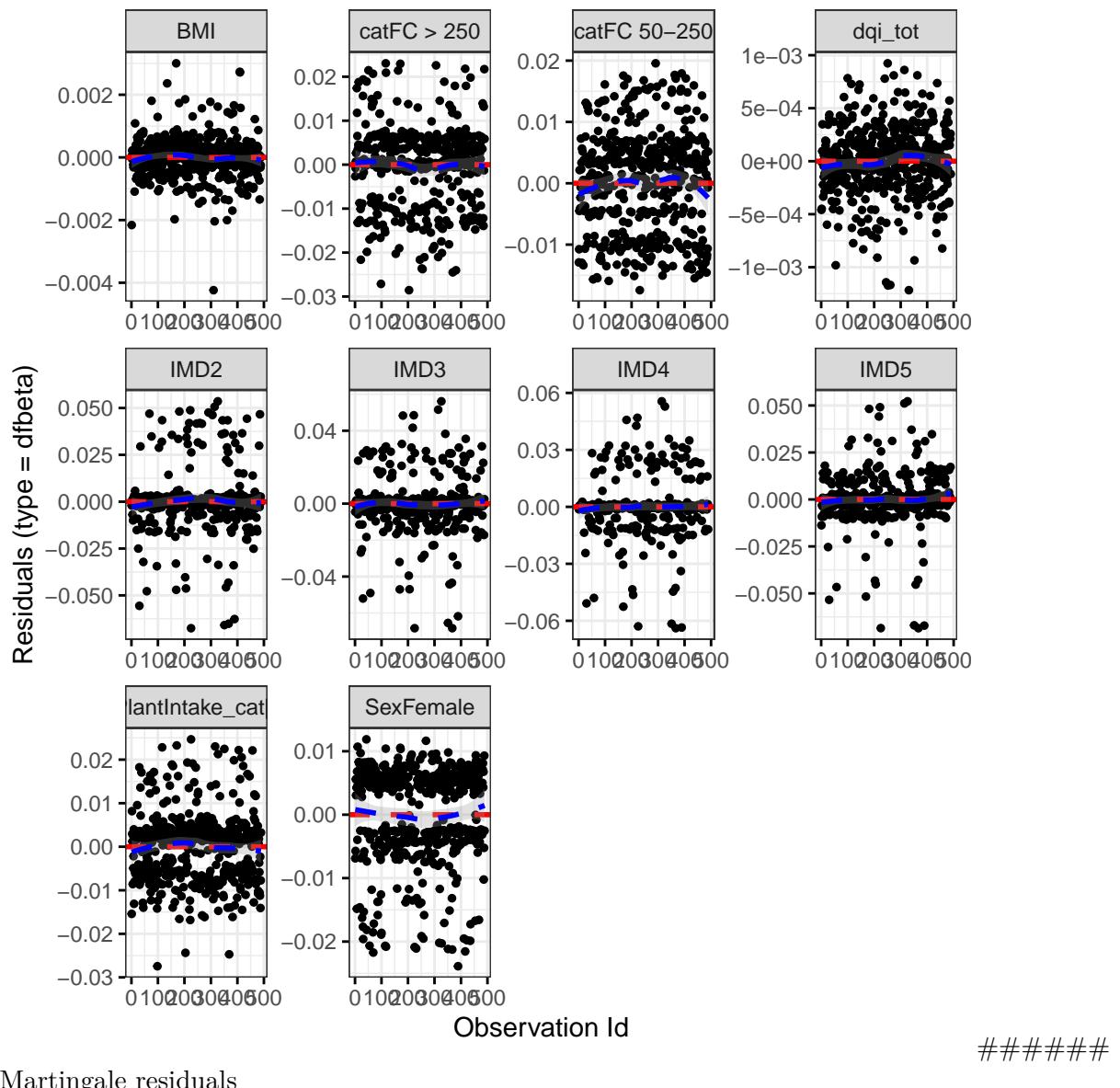
Diagnostics:

Proportional hazards assumption test

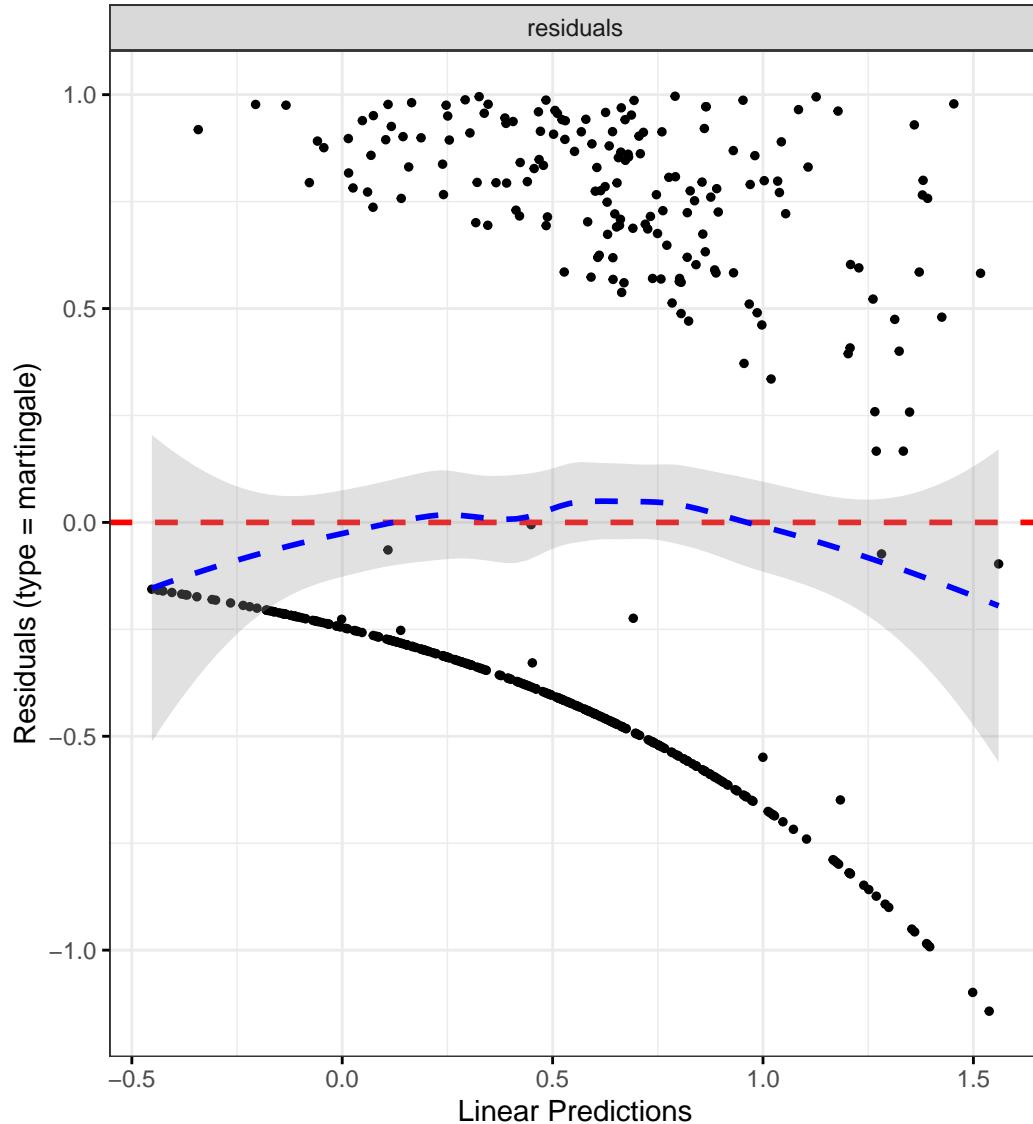
	Chi-squared statistic	DF	P-value
Sex	0.2615	1.0000	0.6091
cat	0.7725	2.0000	0.6796
IMD	3.0236	4.0000	0.5539
dqi_tot	0.3814	1.0000	0.5369
BMI	1.2745	1.0000	0.2589
processedPlantIntake_cat	0.1920	1.0000	0.6613
GLOBAL	5.5195	10.0001	0.8539

DF betas

```
`geom_smooth()` using formula = 'y ~ x'
```



```
`geom_smooth()` using formula = 'y ~ x'
```



Hard flare

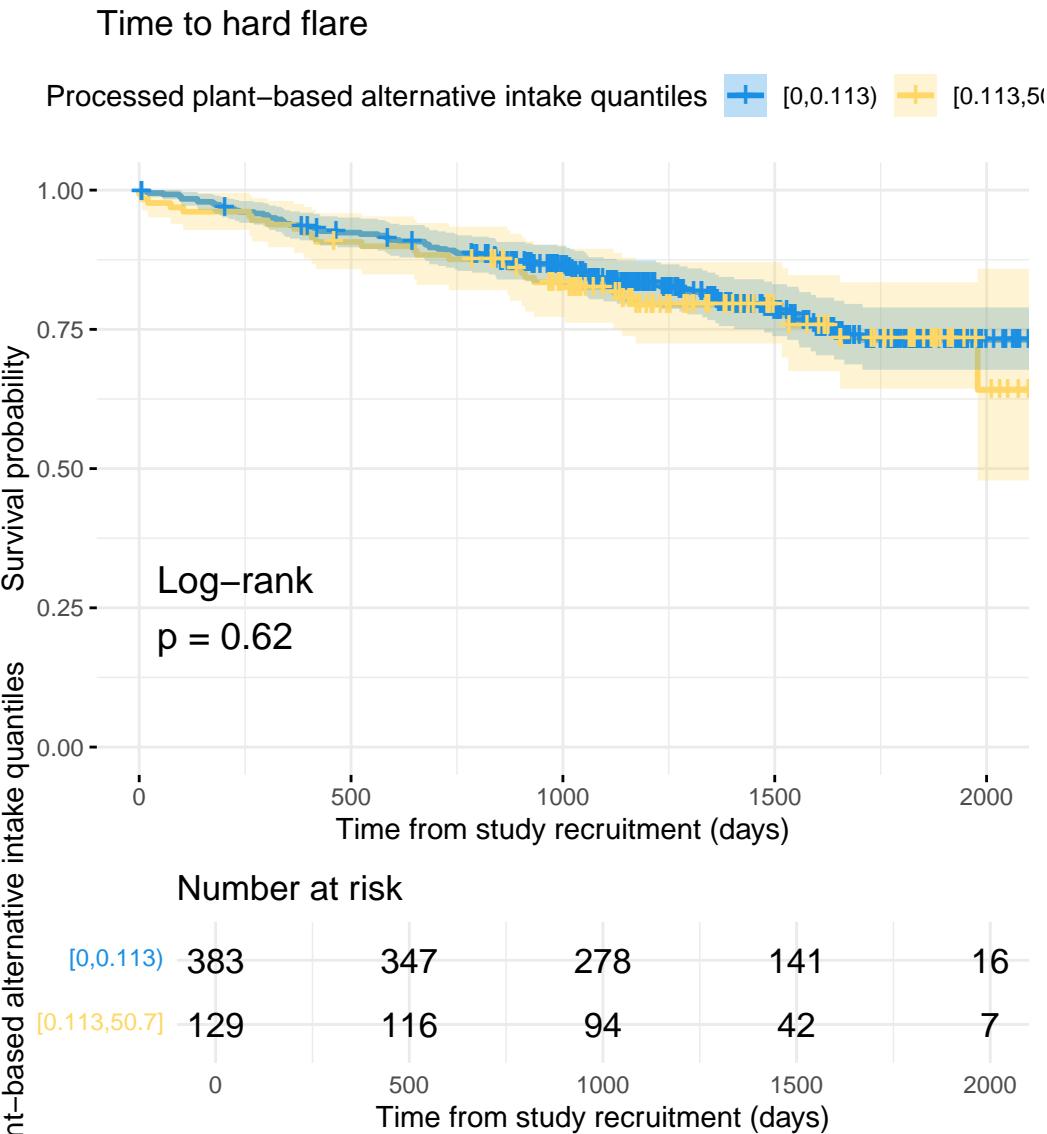
```
# Run survival analysis using utility function for hard flare
analysis_result <- run_survival_analysis(
  data = flare.cd.df,
  var_name = "processedPlantIntake",
  outcome_time = "hardflare_time",
  outcome_event = "hardflare",
  legend_title = "Processed plant-based alternative intake quantiles",
```

```
plot_base_path = "plots/cd/hard-flare/diet/processedPlantIntake",
break_time_by = 500
)

# Save plot as RDS
saveRDS(analysis_result$plot, paste0(paths$outdir, "processedPlantIntake-cd-hard.RDS"))

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(hardflare_time, hardflare) ~
    Sex + cat + IMD + dqi_tot + BMI + processedPlantIntake_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.cd.df
)

# Display plot and model summary
analysis_result$plot
```



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.3411	0.8879	2.0257	0.1630
catFC 50-250	1.8471	1.1607	2.9394	0.0096
catFC > 250	2.9260	1.7696	4.8379	0.0000

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	0.6122	0.2647	1.4157	0.2513
IMD3	0.8044	0.3653	1.7712	0.5889
IMD4	0.7524	0.3492	1.6211	0.4676
IMD5	0.7063	0.3416	1.4603	0.3480
dqi_tot	1.0025	0.9844	1.0210	0.7861
BMI	1.0184	0.9834	1.0547	0.3070
processedPlantIntake_cat[1.1481	0.7332	1.7978	0.5461

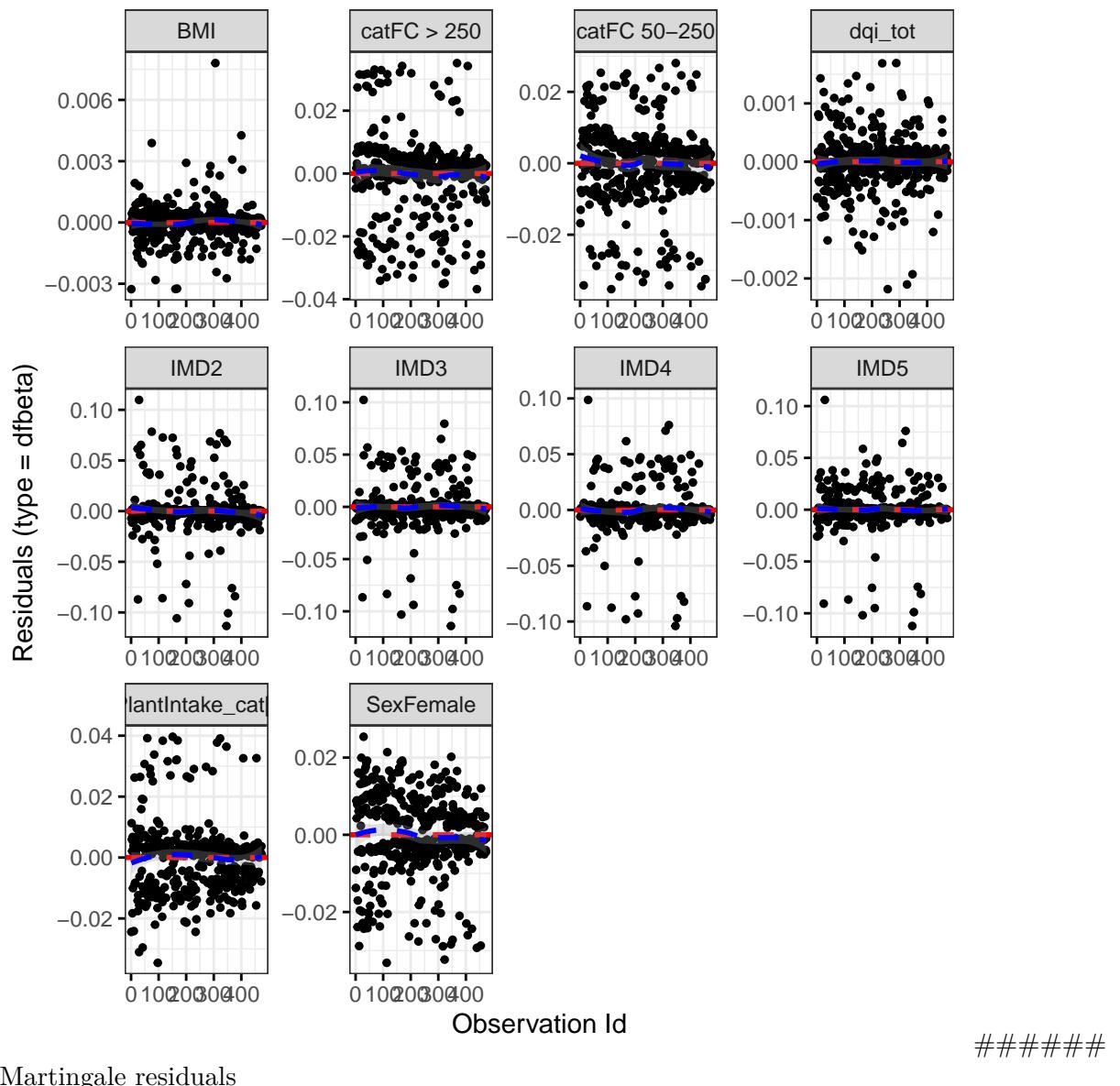
Diagnostics:

Proportional hazards assumption test

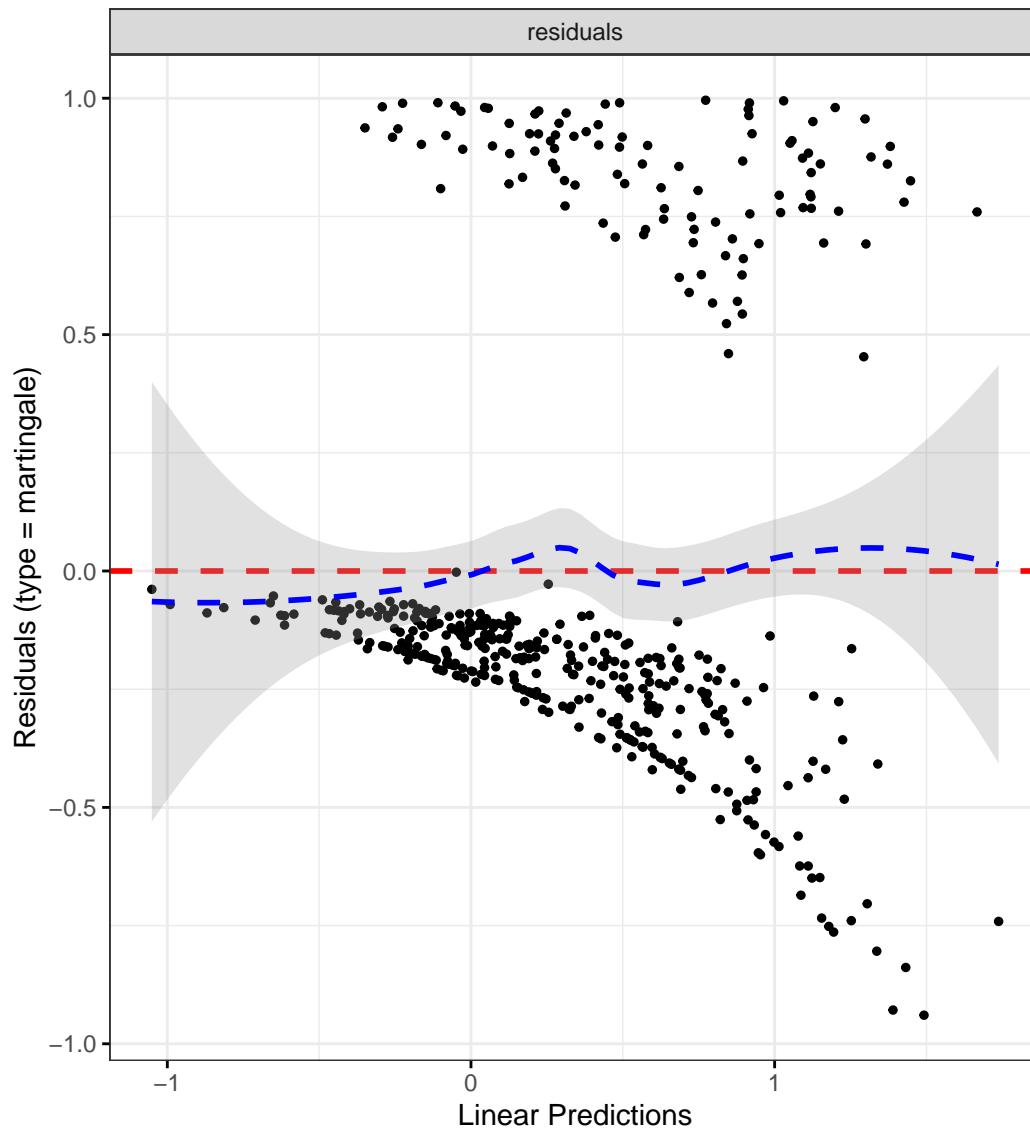
	Chi-squared statistic	DF	P-value
Sex	0.0587	0.9730	0.7991
cat	10.3351	1.9797	0.0056
IMD	2.6687	3.9328	0.6042
dqi_tot	2.7554	0.9896	0.0956
BMI	1.1366	0.9814	0.2807
processedPlantIntake_cat	0.0891	0.9900	0.7616
GLOBAL	17.0586	15.8412	0.3711

DF betas

```
`geom_smooth()` using formula = 'y ~ x'
```



```
`geom_smooth()` using formula = 'y ~ x'
```



Ulcerative colitis

Patient-reported flare

```
# Categorize processed plant intake by quantiles
flare.uc.df <- categorize_by_quantiles(flare.uc.df, "processedPlantIntake", reference_data = )

# Run survival analysis using utility function
```

```

analysis_result <- run_survival_analysis(
  data = flare.uc.df,
  var_name = "processedPlantIntake",
  outcome_time = "softflare_time",
  outcome_event = "softflare",
  legend_title = "Processed plant-based alternative intake quantiles",
  plot_base_path = "plots/uc/soft-flare/diet/processedPlantIntake",
  break_time_by = 200
)

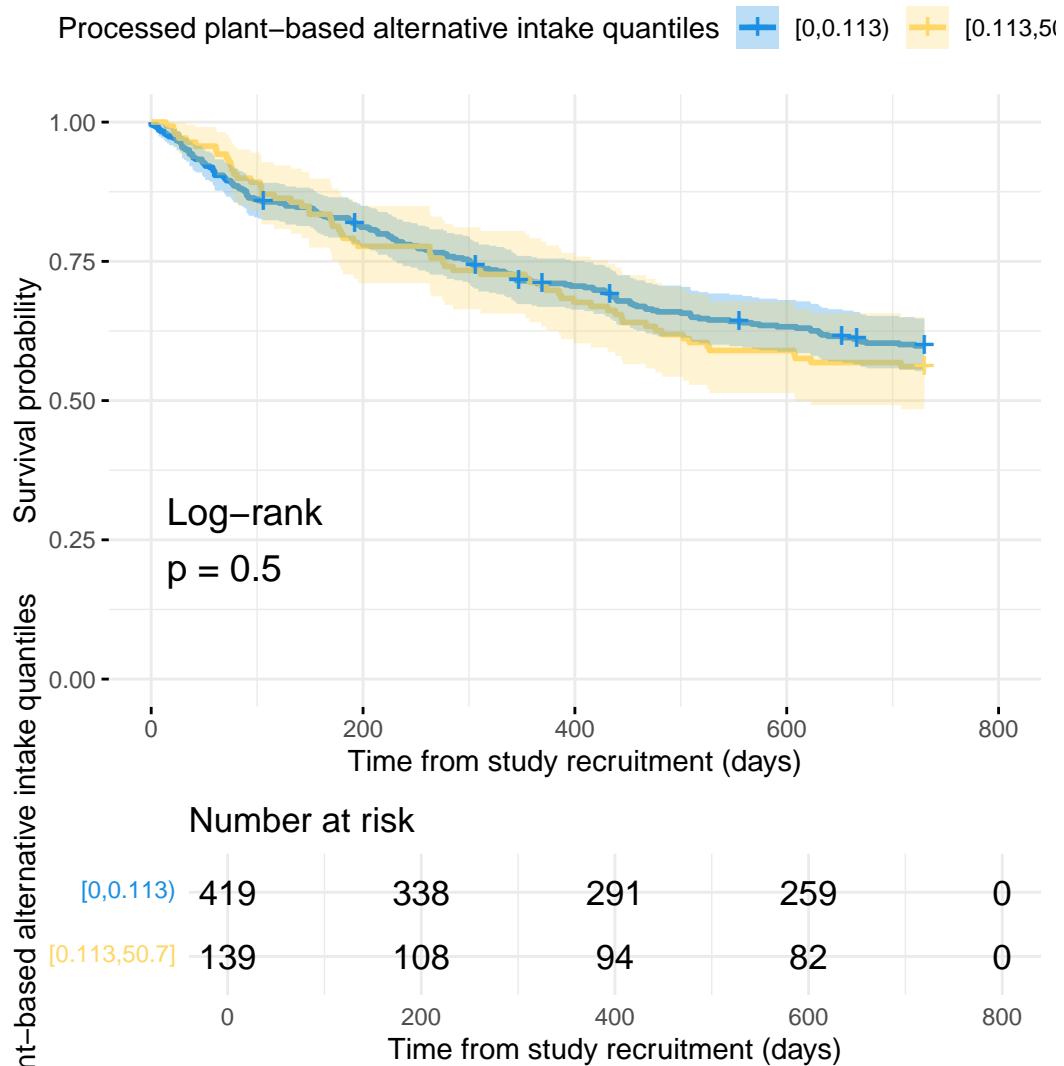
# Save plot as RDS
saveRDS(analysis_result$plot, paste0(paths$outdir, "processedPlantIntake-uc-soft.RDS"))

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(softflare_time, softflare) ~
    Sex + cat + IMD + dqi_tot + BMI + processedPlantIntake_cat +
    frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.uc.df
)

# Display plot and model summary
analysis_result$plot

```

Time to patient-reported flare



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.6856	1.2624	2.2507	0.0004
catFC 50-250	1.8090	1.3150	2.4885	0.0003
catFC > 250	2.0717	1.4515	2.9570	0.0001

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	1.4160	0.7437	2.6958	0.2897
IMD3	1.1473	0.6108	2.1551	0.6693
IMD4	1.3481	0.7453	2.4385	0.3233
IMD5	1.1873	0.6609	2.1331	0.5657
dqi_tot	0.9989	0.9860	1.0119	0.8640
BMI	0.9761	0.9474	1.0056	0.1119
processedPlantIntake_cat[1.0707	0.7769	1.4755	0.6765

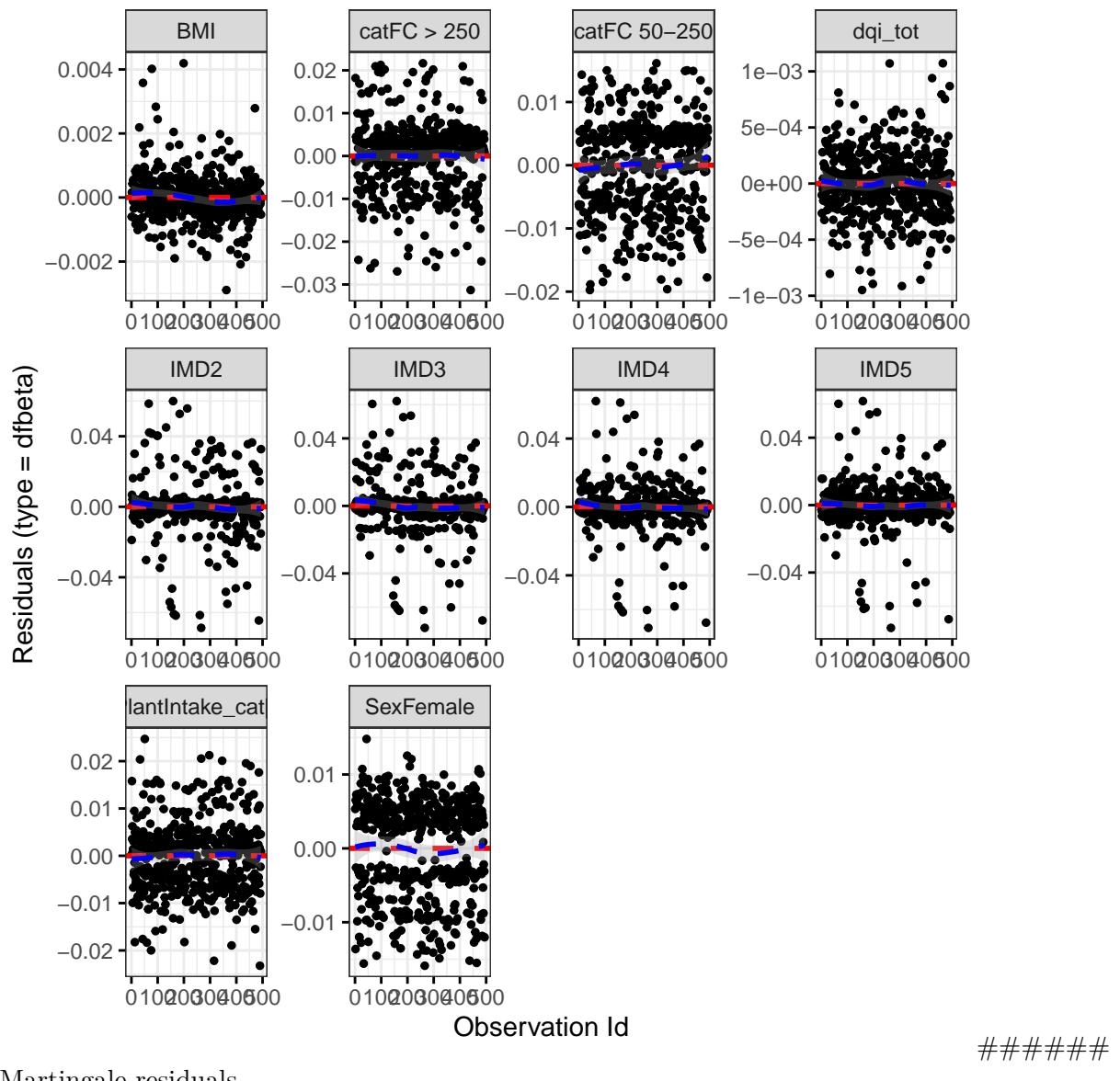
Diagnostics:

Proportional hazards assumption test

	Chi-squared statistic	DF	P-value
Sex	0.0050	1.0000	0.9435
cat	3.5698	2.0000	0.1678
IMD	2.5950	4.0000	0.6277
dqi_tot	0.7488	1.0000	0.3869
BMI	0.9742	1.0000	0.3236
processedPlantIntake_cat	1.1736	1.0000	0.2787
GLOBAL	8.8987	10.0001	0.5418

DF betas

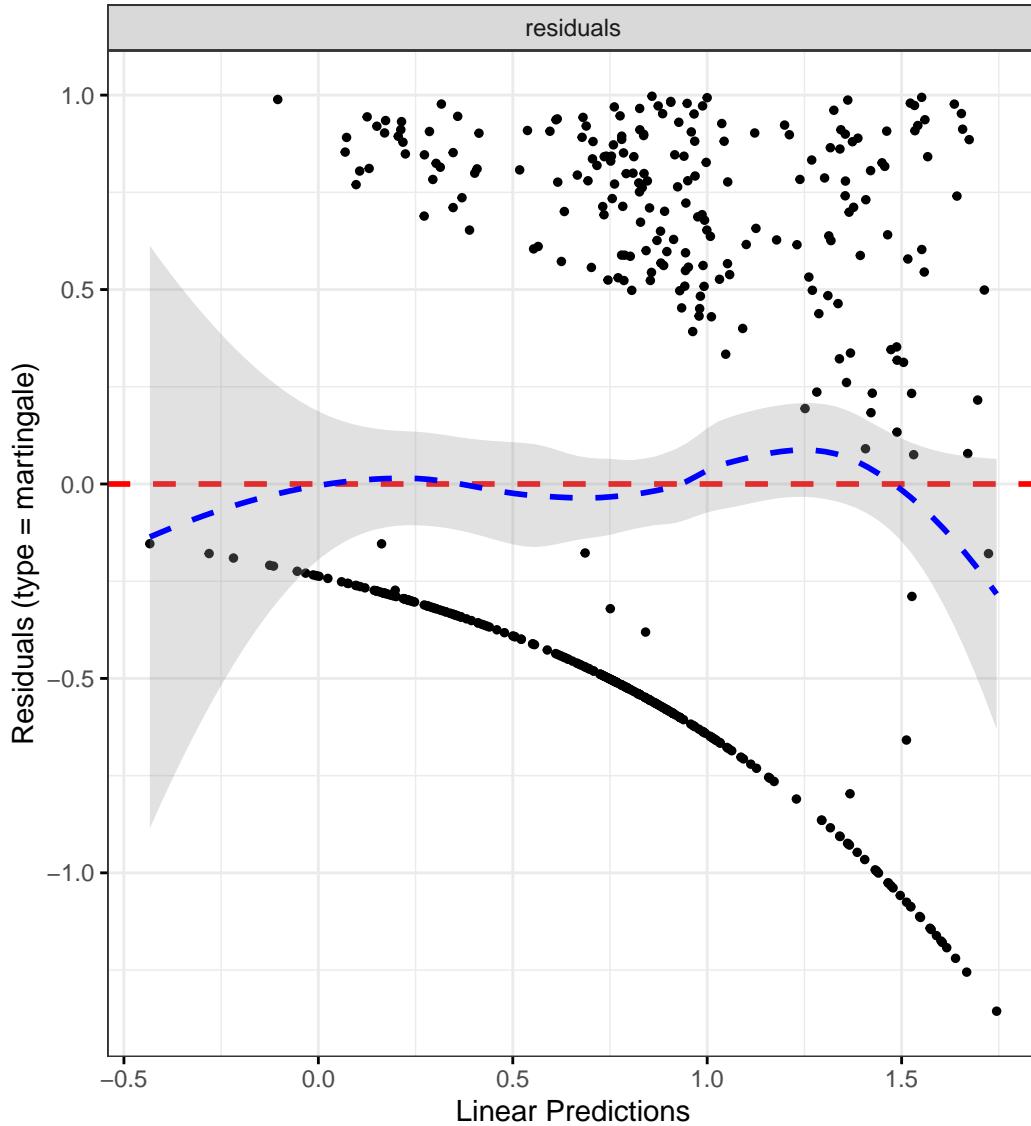
```
`geom_smooth()` using formula = 'y ~ x'
```



#####

Martingale residuals

```
`geom_smooth()` using formula = 'y ~ x'
```



Hard flare

```
# Run survival analysis using utility function for hard flare
analysis_result <- run_survival_analysis(
  data = flare.uc.df,
  var_name = "processedPlantIntake",
  outcome_time = "hardflare_time",
  outcome_event = "hardflare",
  legend_title = "Processed plant-based alternative intake quantiles",
```

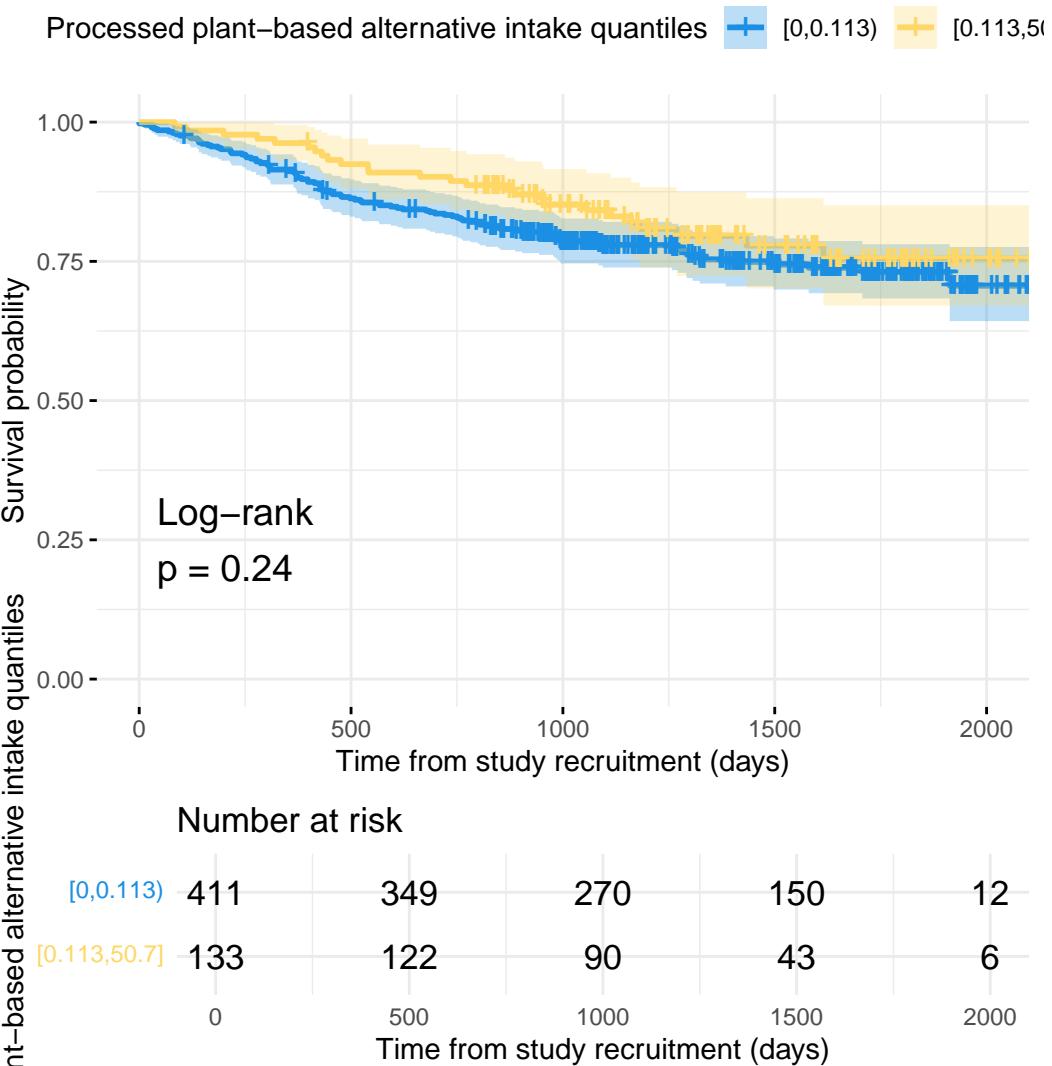
```
plot_base_path = "plots/uc/hard-flare/diet/processedPlantIntake",
break_time_by = 500
)

# Save plot as RDS
saveRDS(analysis_result$plot, paste0(paths$outdir, "processedPlantIntake-uc-hard.RDS"))

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(hardflare_time, hardflare) ~
    Sex + cat + IMD + dqi_tot + BMI + processedPlantIntake_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.uc.df
)

# Display plot and model summary
analysis_result$plot
```

Time to hard flare



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.2233	0.8353	1.7915	0.3005
catFC 50-250	1.9811	1.2828	3.0596	0.0020
catFC > 250	2.4871	1.5282	4.0477	0.0002

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	1.5340	0.5818	4.0444	0.3870
IMD3	1.2889	0.5001	3.3218	0.5993
IMD4	2.3256	0.9708	5.5712	0.0583
IMD5	1.3975	0.5782	3.3777	0.4573
dqi_tot	1.0036	0.9859	1.0217	0.6899
BMI	0.9612	0.9217	1.0025	0.0649
processedPlantIntake_cat[0.7892	0.4980	1.2506	0.3136

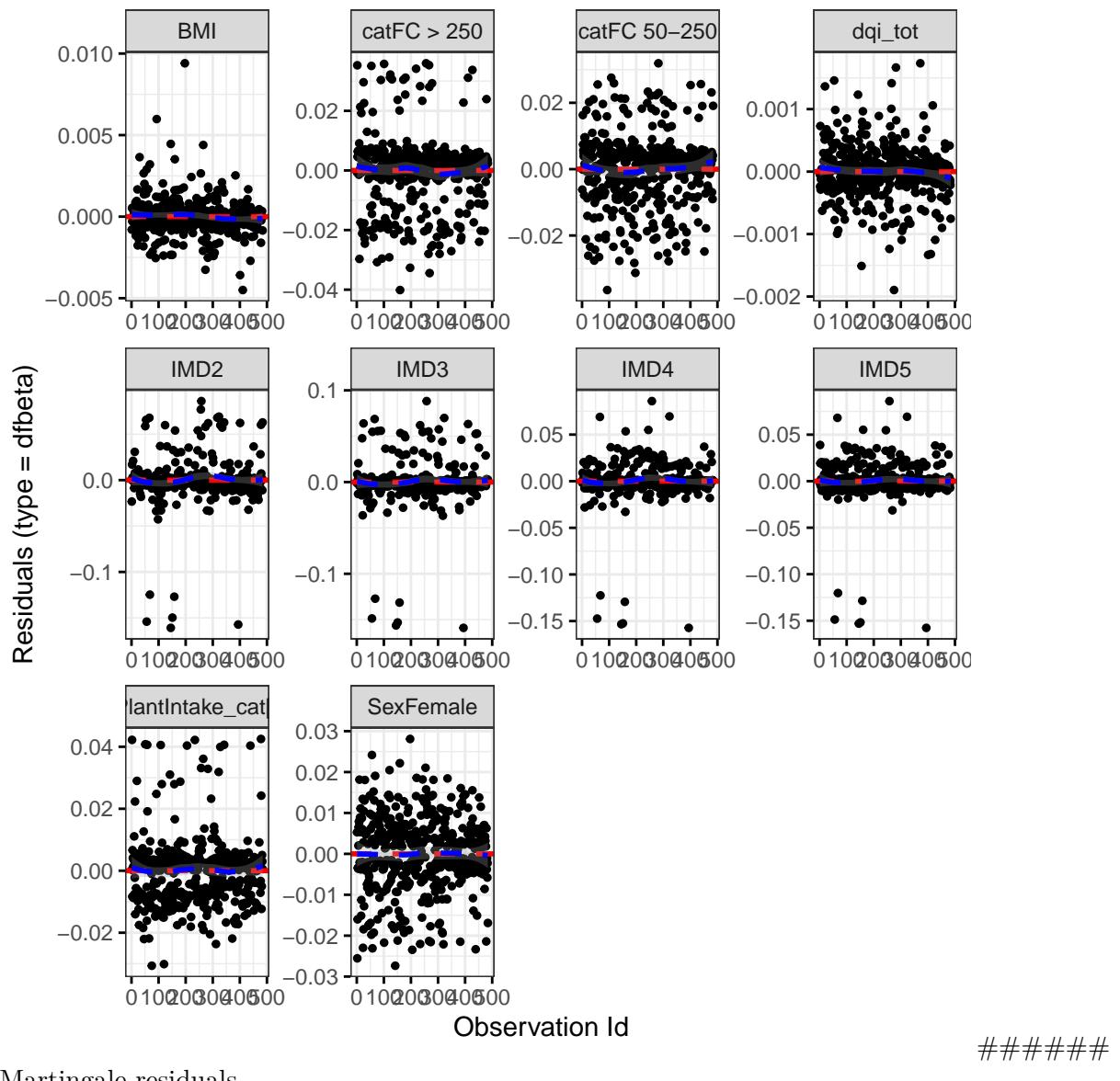
Diagnostics:

Proportional hazards assumption test

	Chi-squared statistic	DF	P-value
Sex	0.0305	0.9874	0.8577
cat	5.4999	1.9554	0.0613
IMD	1.2414	3.9288	0.8643
dqi_tot	0.0020	0.9851	0.9621
BMI	0.5662	0.9888	0.4474
processedPlantIntake_cat	3.4042	0.9842	0.0636
GLOBAL	11.1370	17.6787	0.8769

DF betas

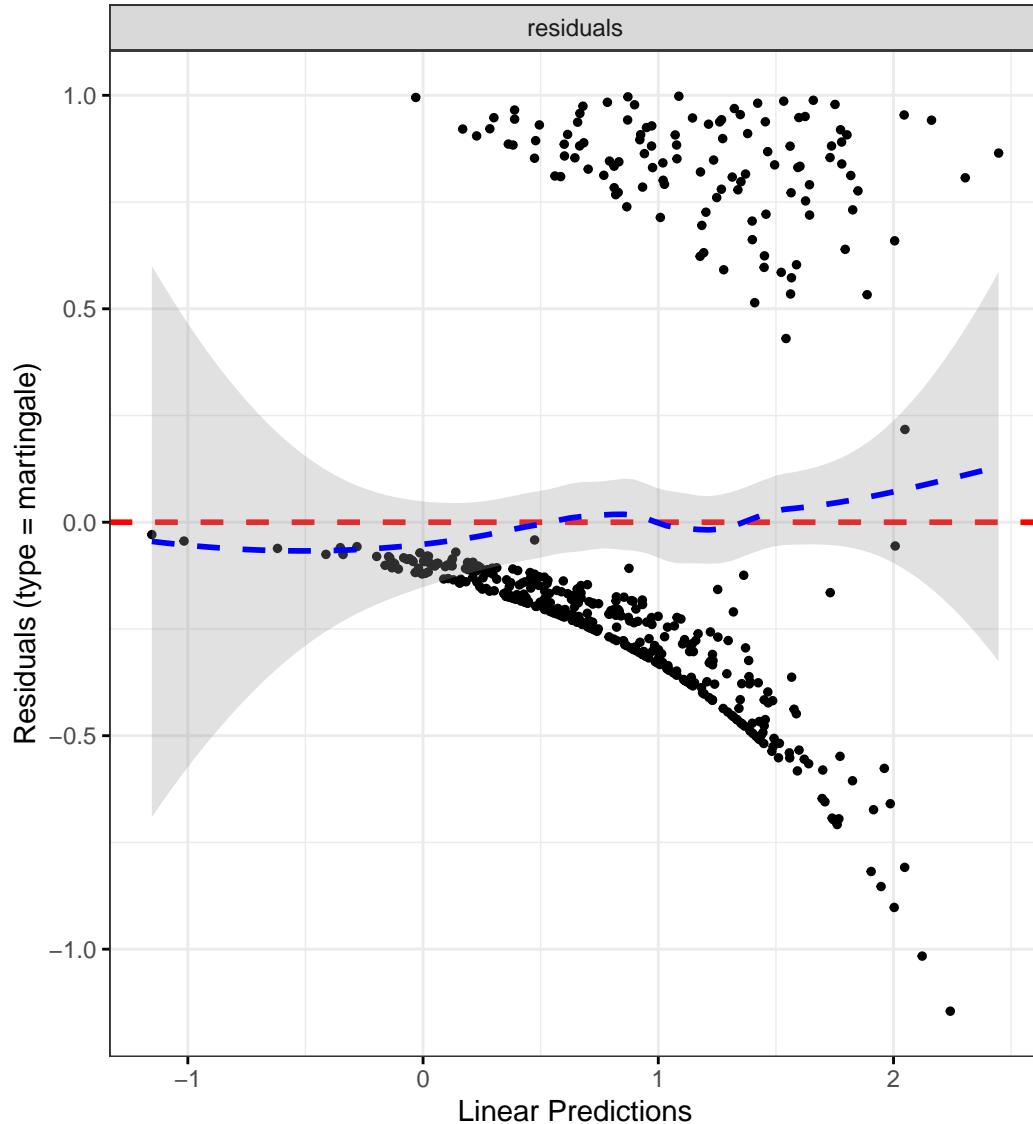
```
`geom_smooth()` using formula = 'y ~ x'
```



#####

Martingale residuals

```
`geom_smooth()` using formula = 'y ~ x'
```



Inflammatory bowel disease

Patient-reported flare

```
# Categorize processed plant intake by quantiles
flare.df <- categorize_by_quantiles(flare.df, "processedPlantIntake", reference_data = flare)

# Run survival analysis using utility function
```

```

analysis_result <- run_survival_analysis(
  data = flare.df,
  var_name = "processedPlantIntake",
  outcome_time = "softflare_time",
  outcome_event = "softflare",
  legend_title = "Processed plant-based alternative intake quantiles",
  plot_base_path = "plots/ibd/soft-flare/diet/processedPlantIntake",
  break_time_by = 200
)

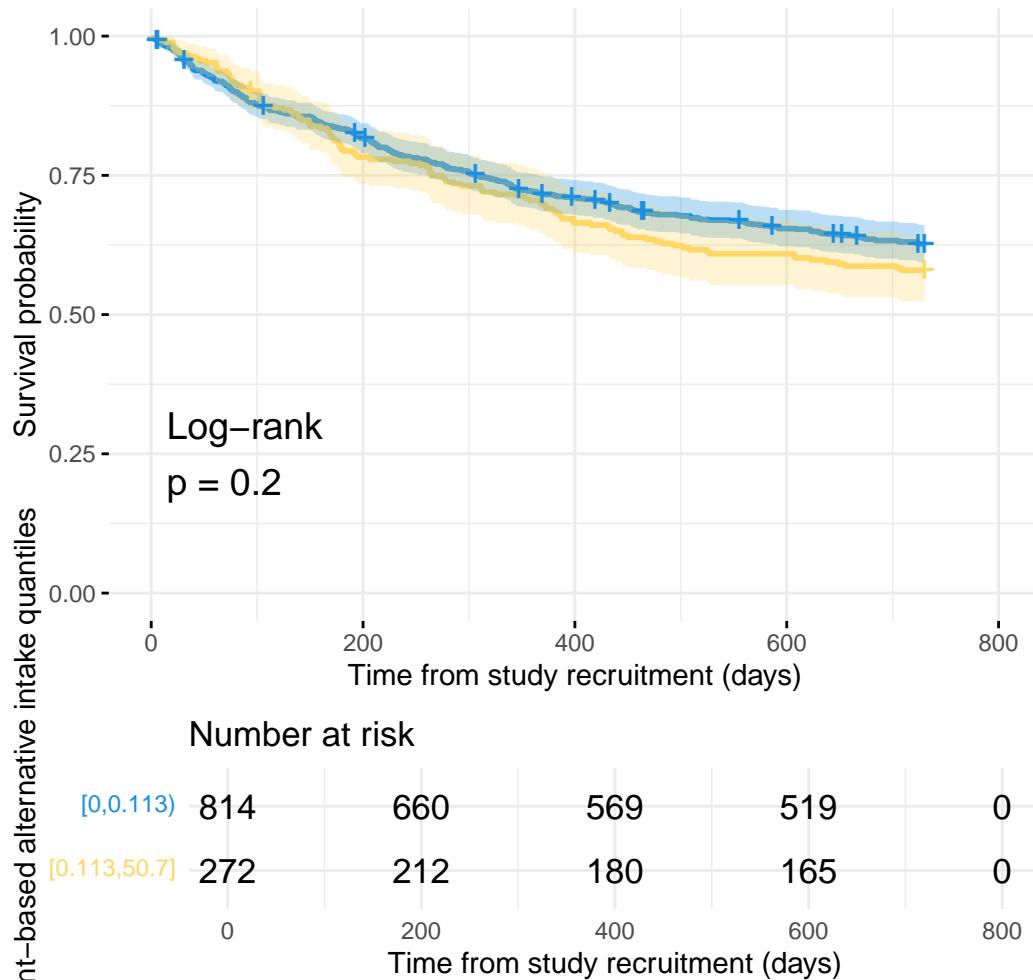
# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(softflare_time, softflare) ~
    Sex + cat + IMD + dqi_tot + BMI + processedPlantIntake_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.df
)

# Display plot and model summary
analysis_result$plot

```

Time to patient-reported flare

Processed plant-based alternative intake quantiles [0,0.113] [0.113,50.7]



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.7684	1.4261	2.1928	0.0000
catFC 50-250	1.5022	1.1893	1.8975	0.0006
catFC > 250	2.0154	1.5564	2.6099	0.0000

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	0.9812	0.6238	1.5434	0.9347
IMD3	1.0036	0.6504	1.5486	0.9872
IMD4	1.1042	0.7291	1.6722	0.6397
IMD5	1.0751	0.7199	1.6056	0.7233
dqi_tot	1.0021	0.9927	1.0115	0.6643
BMI	0.9945	0.9749	1.0145	0.5870
processedPlantIntake_cat[1.0751	0.8519	1.3569	0.5419

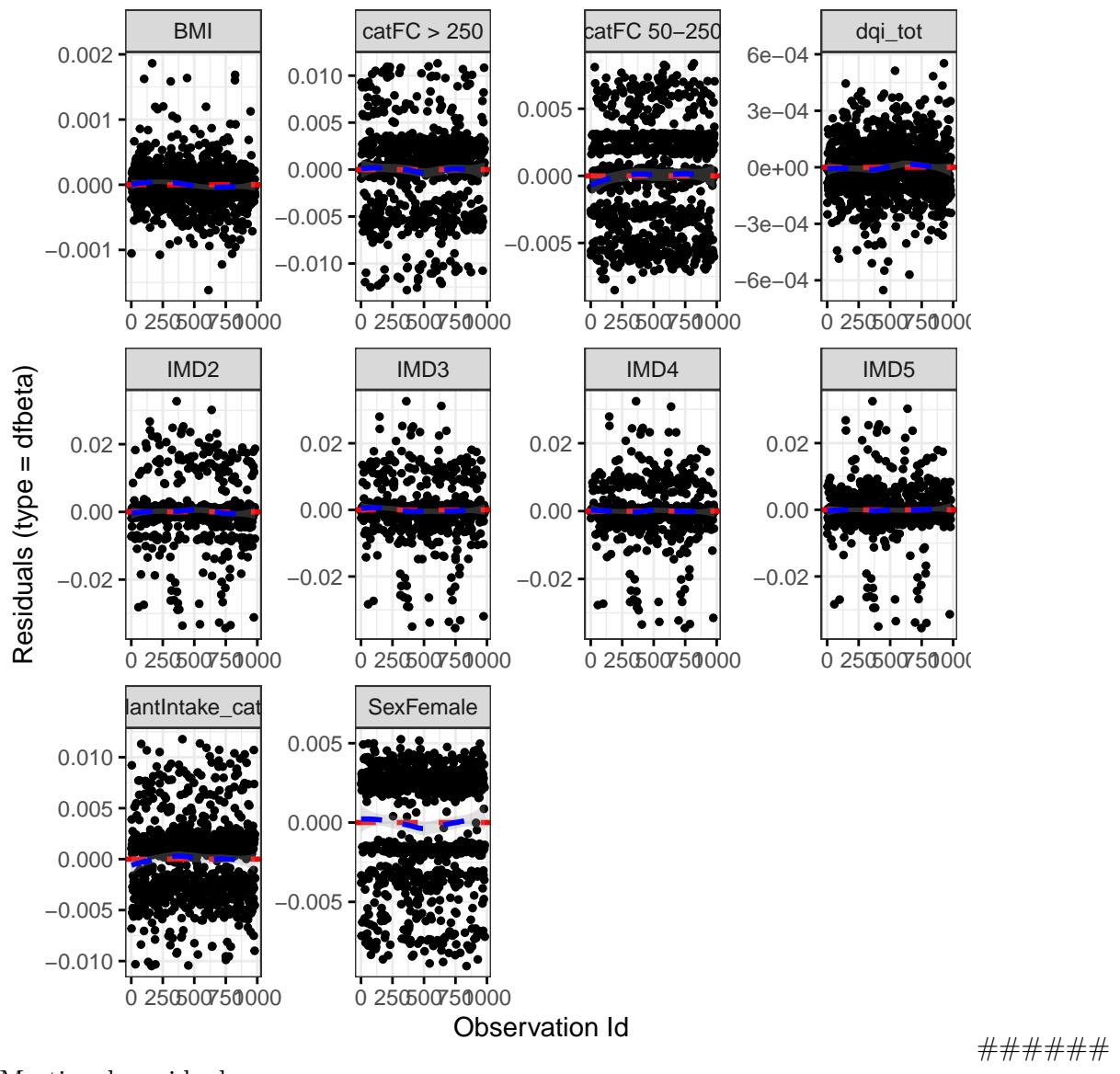
Diagnostics:

Proportional hazards assumption test

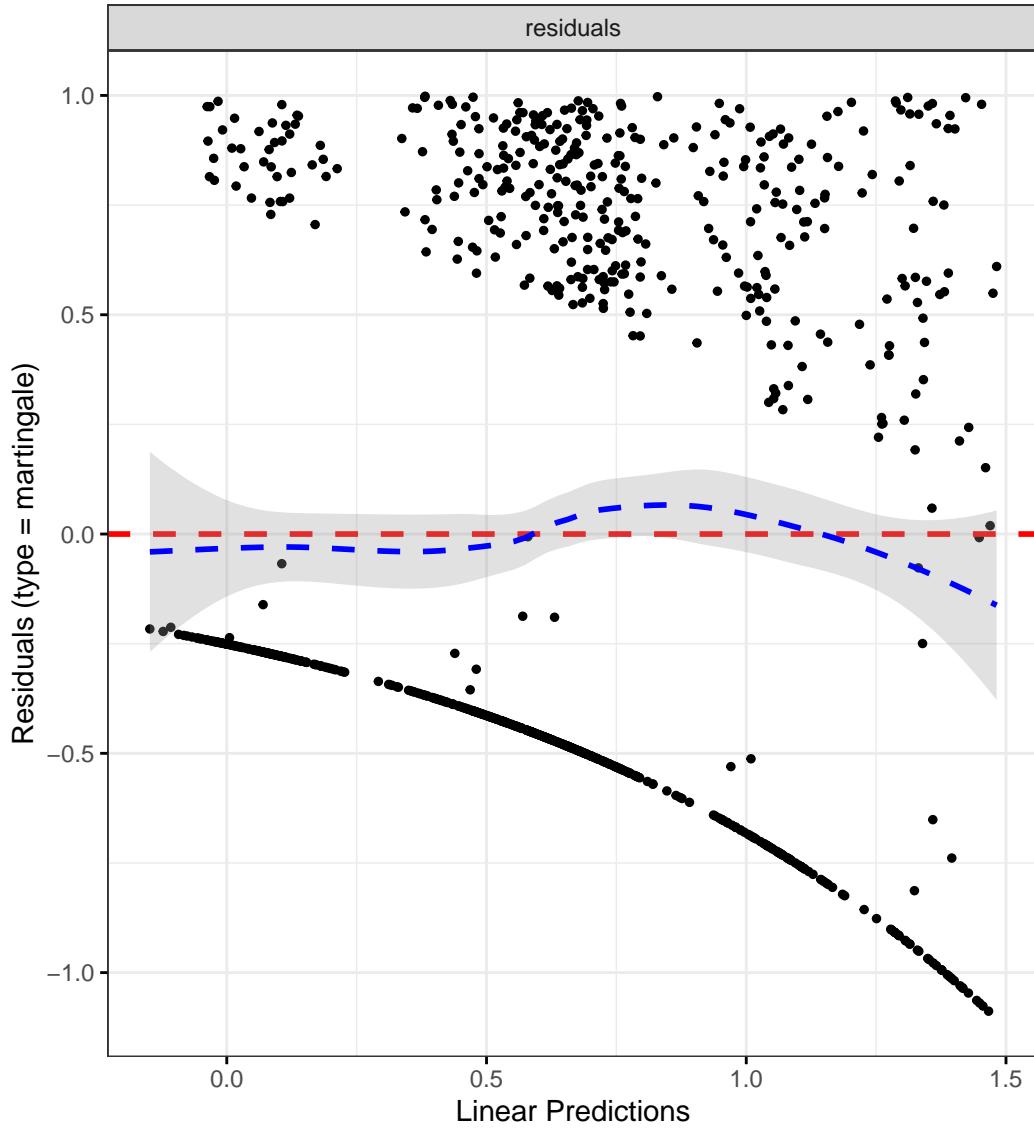
	Chi-squared statistic	DF	P-value
Sex	0.0052	1.0000	0.9428
cat	1.0830	2.0000	0.5819
IMD	5.0486	4.0000	0.2824
dqi_tot	1.3966	1.0000	0.2373
BMI	0.0079	1.0000	0.9290
processedPlantIntake_cat	1.0240	1.0000	0.3116
GLOBAL	8.6179	10.0002	0.5687

DF betas

```
`geom_smooth()` using formula = 'y ~ x'
```



```
`geom_smooth()` using formula = 'y ~ x'
```



Hard flare

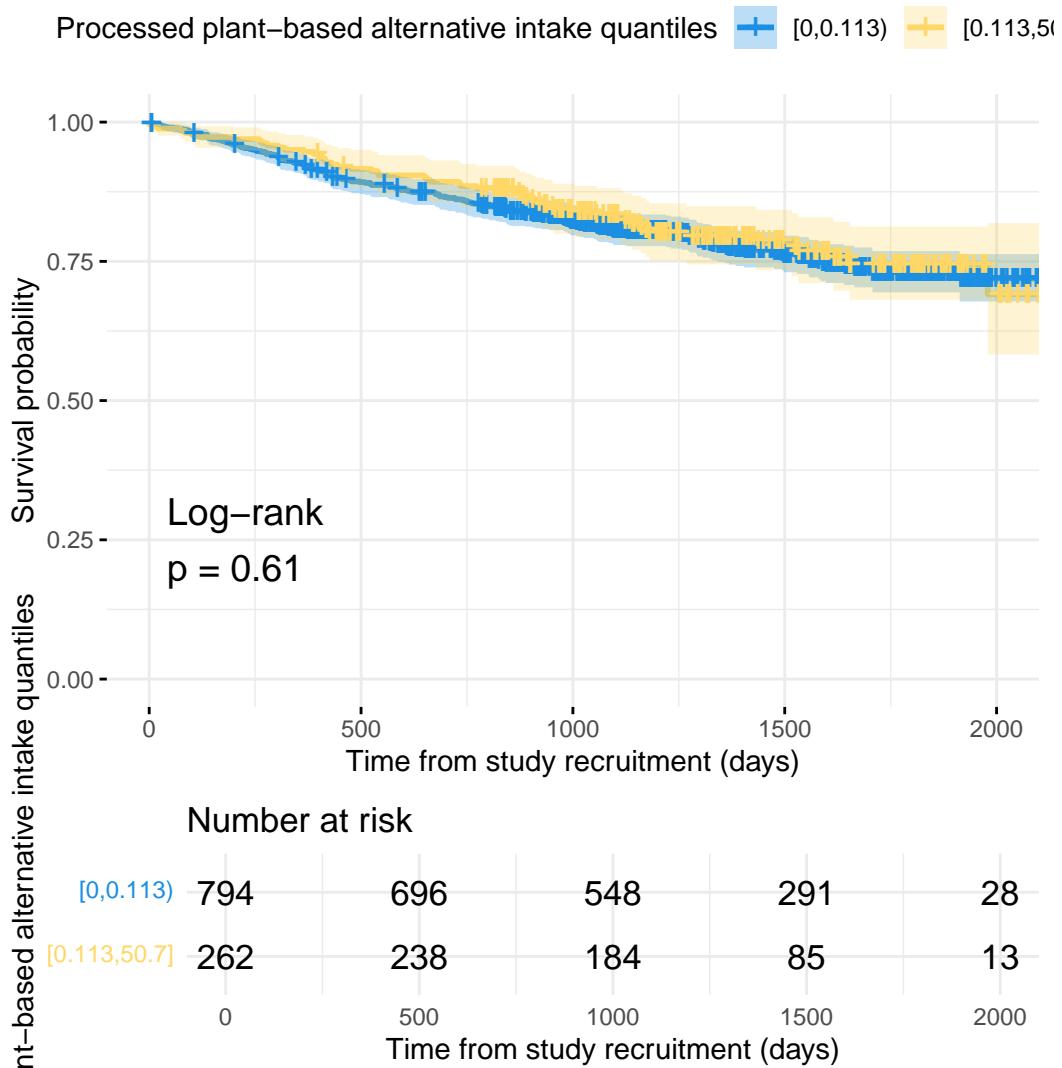
```
# Run survival analysis using utility function for hard flare
analysis_result <- run_survival_analysis(
  data = flare.df,
  var_name = "processedPlantIntake",
  outcome_time = "hardflare_time",
  outcome_event = "hardflare",
  legend_title = "Processed plant-based alternative intake quantiles",
```

```
plot_base_path = "plots/ibd/hard-flare/diet/processedPlantIntake",
break_time_by = 500
)

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(hardflare_time, hardflare) ~
    Sex + cat + IMD + dqi_tot + BMI + processedPlantIntake_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.df
)

# Display plot and model summary
analysis_result$plot
```

Time to hard flare



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.2614	0.9571	1.6624	0.0992
catFC 50-250	1.8514	1.3523	2.5348	0.0001
catFC > 250	2.6033	1.8429	3.6774	0.0000

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	0.9248	0.4953	1.7265	0.8060
IMD3	0.9545	0.5242	1.7380	0.8790
IMD4	1.3442	0.7663	2.3579	0.3023
IMD5	0.9743	0.5590	1.6982	0.9268
dqi_tot	1.0029	0.9904	1.0156	0.6504
BMI	0.9920	0.9657	1.0191	0.5609
processedPlantIntake_cat[0.9551	0.6958	1.3110	0.7761

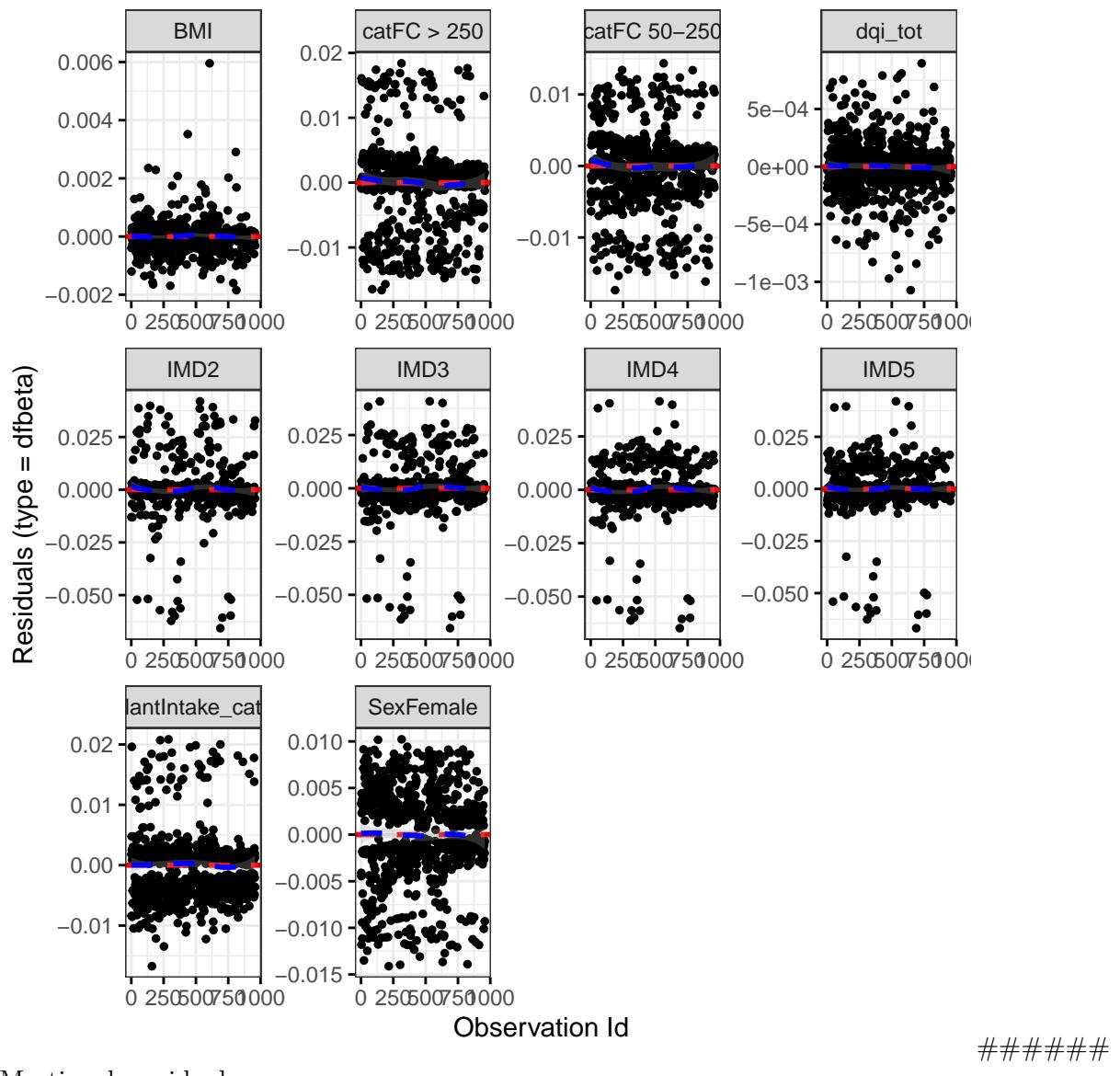
Diagnostics:

Proportional hazards assumption test

	Chi-squared statistic	DF	P-value
Sex	0.0338	0.9886	0.8506
cat	6.8441	1.9799	0.0320
IMD	1.6035	3.9456	0.8016
dqi_tot	2.0050	0.9925	0.1553
BMI	1.8960	0.9889	0.1663
processedPlantIntake_cat	1.4651	0.9928	0.2243
GLOBAL	13.3482	20.6346	0.8844

DF betas

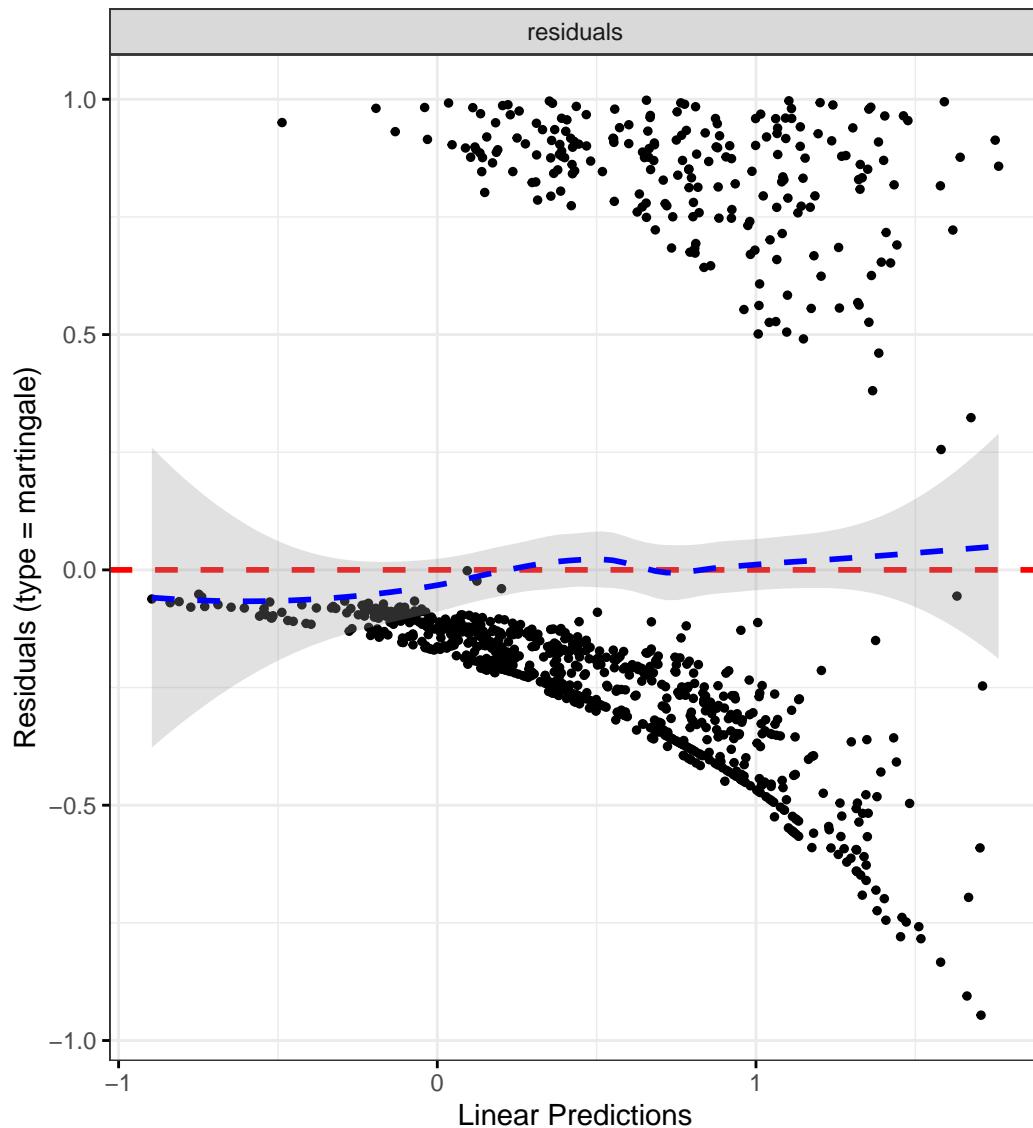
```
`geom_smooth()` using formula = 'y ~ x'
```



#####

Martingale residuals

```
`geom_smooth()` using formula = 'y ~ x'
```



Un-processed/minimally processed food subgroups

Fruit

Crohn's disease

Patient-reported flare

```

# Categorize fruit intake by quantiles
flare.cd.df <- categorize_by_quantiles(flare.cd.df, "fruitIntake", reference_data = flare.df)

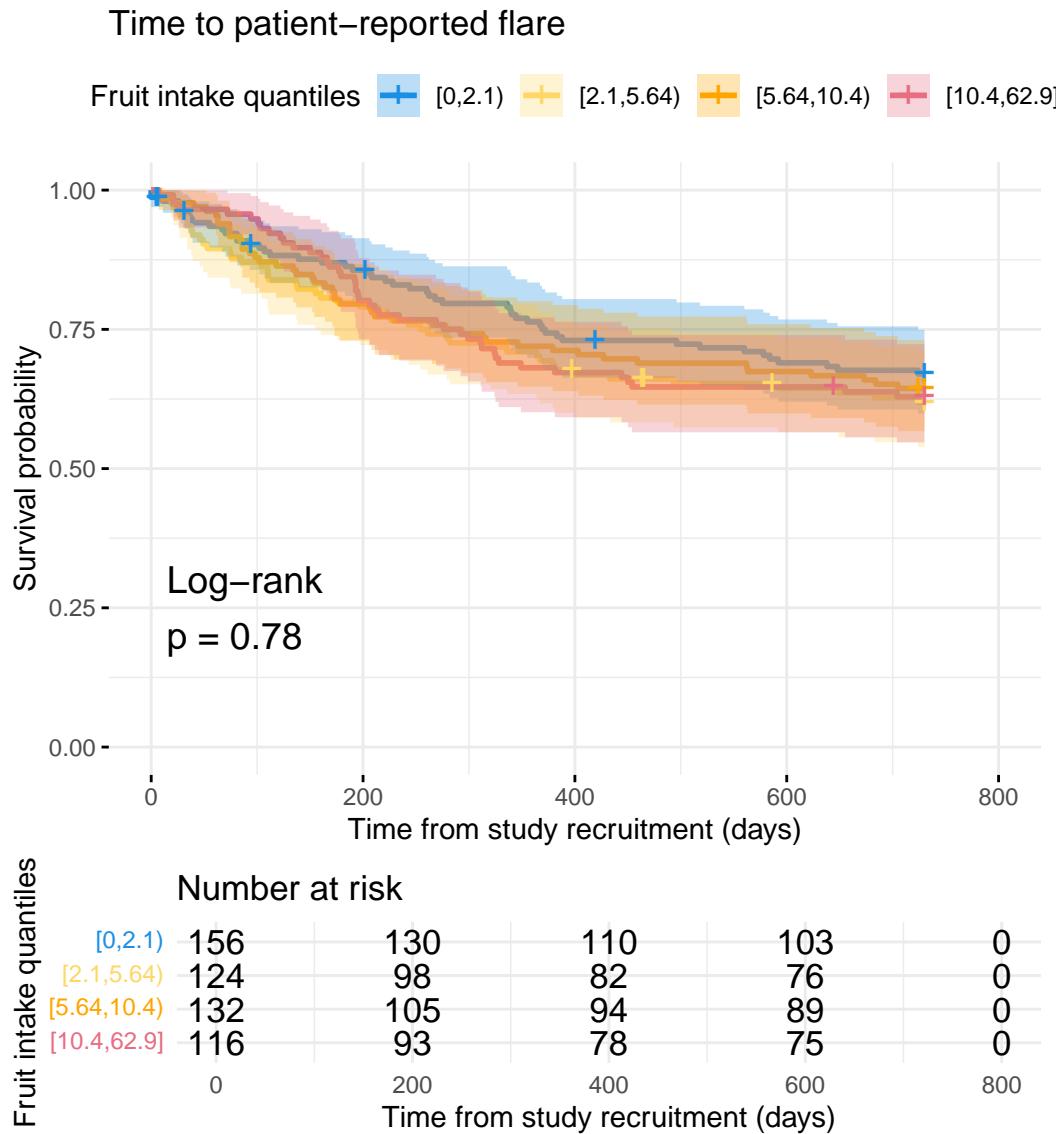
# Run survival analysis using utility function
analysis_result <- run_survival_analysis(
  data = flare.cd.df,
  var_name = "fruitIntake",
  outcome_time = "softflare_time",
  outcome_event = "softflare",
  legend_title = "Fruit intake quantiles",
  plot_base_path = "plots/cd/soft-flare/diet/fruitIntake",
  break_time_by = 200
)

# Save plot as RDS
saveRDS(analysis_result$plot, paste0(paths$outdir, "fruitIntake-cd-soft.RDS"))

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(softflare_time, softflare) ~
    Sex + cat + IMD + dqi_tot + BMI + fruitIntake_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.cd.df
)

# Display plot and model summary
analysis_result$plot

```



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.8801	1.3416	2.6347	0.0002
catFC 50-250	1.3110	0.9224	1.8633	0.1311
catFC > 250	2.0366	1.3915	2.9809	0.0003

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	0.7110	0.3703	1.3654	0.3056
IMD3	0.9318	0.5089	1.7062	0.8189
IMD4	0.8559	0.4727	1.5497	0.6075
IMD5	0.9888	0.5665	1.7259	0.9684
dqi_tot	1.0053	0.9897	1.0212	0.5090
BMI	1.0086	0.9813	1.0367	0.5410
fruitIntake_cat[2.1,5.64)	1.1255	0.7253	1.7464	0.5980
fruitIntake_cat[5.64,10.4	1.0556	0.6734	1.6548	0.8136
fruitIntake_cat[10.4,62.9	1.0500	0.6325	1.7433	0.8503

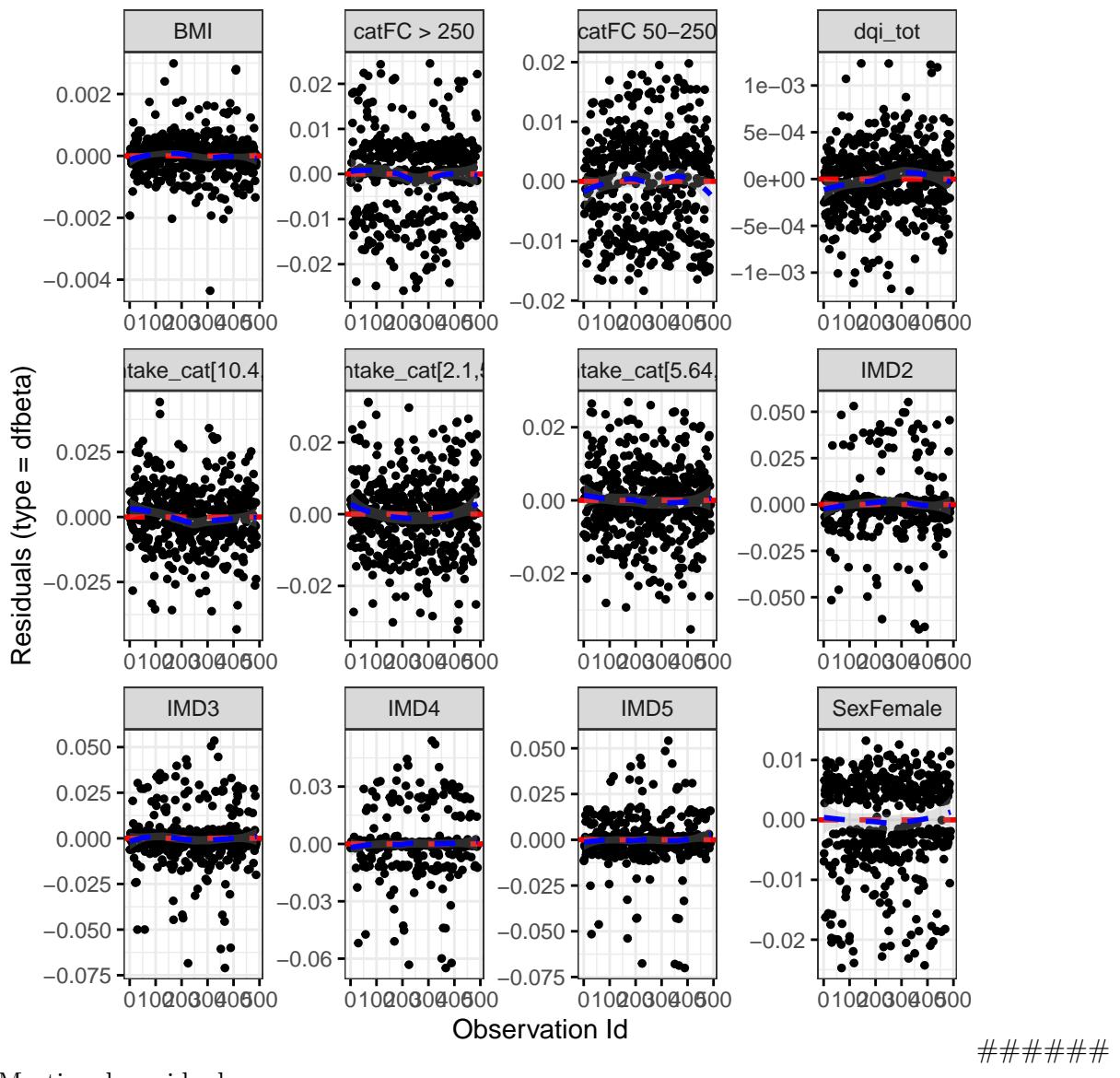
Diagnostics:

Proportional hazards assumption test

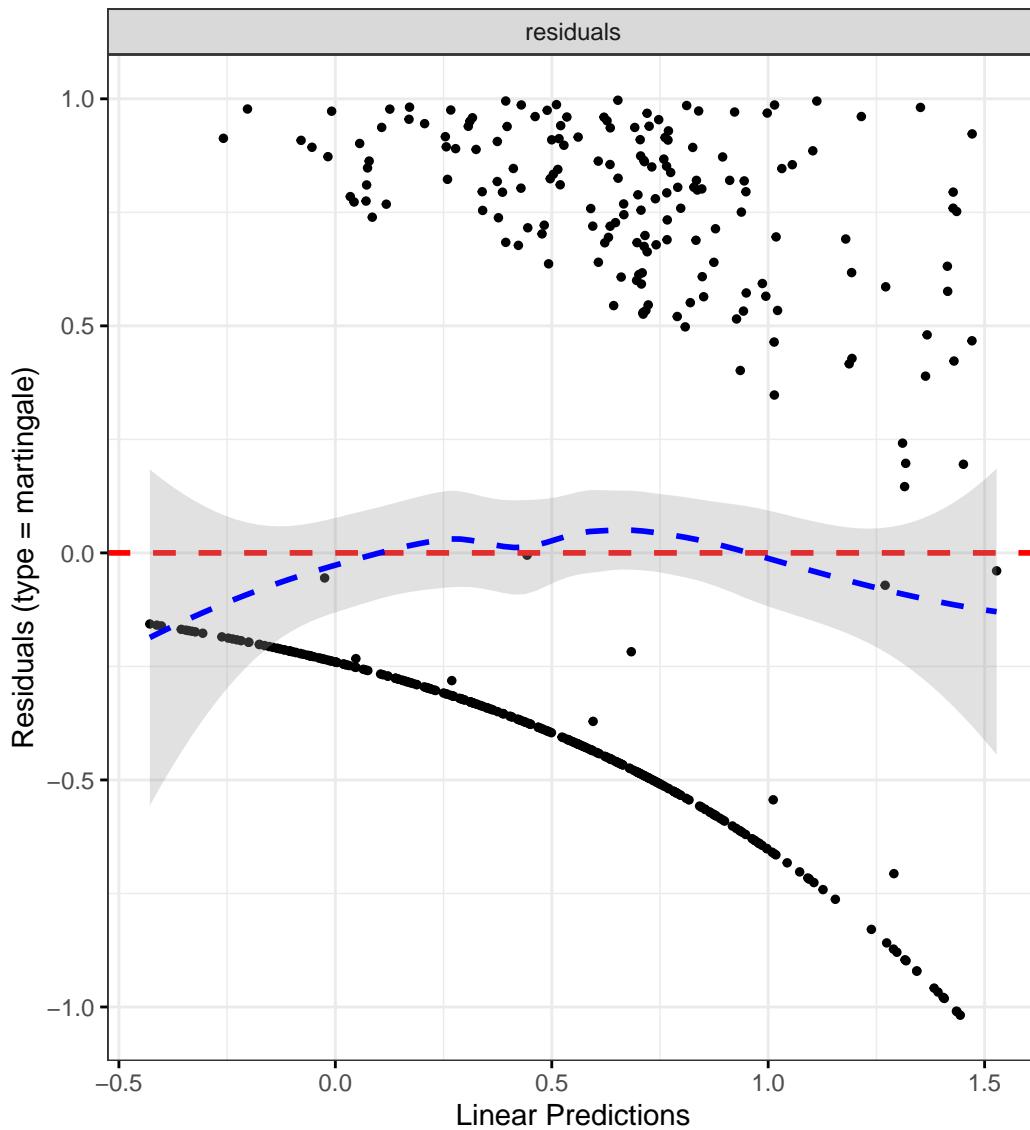
	Chi-squared statistic	DF	P-value
Sex	0.2610	1.0000	0.6094
cat	0.8034	2.0000	0.6692
IMD	3.0519	4.0000	0.5492
dqi_tot	0.3626	1.0000	0.5470
BMI	1.3223	1.0000	0.2502
fruitIntake_cat	0.5976	3.0000	0.8970
GLOBAL	6.3144	12.0001	0.8994

DF betas

```
`geom_smooth()` using formula = 'y ~ x'
```



```
`geom_smooth()` using formula = 'y ~ x'
```



Hard flare

```
# Run survival analysis using utility function for hard flare
analysis_result <- run_survival_analysis(
  data = flare.cd.df,
  var_name = "fruitIntake",
  outcome_time = "hardflare_time",
  outcome_event = "hardflare",
  legend_title = "Fruit intake quantiles",
```

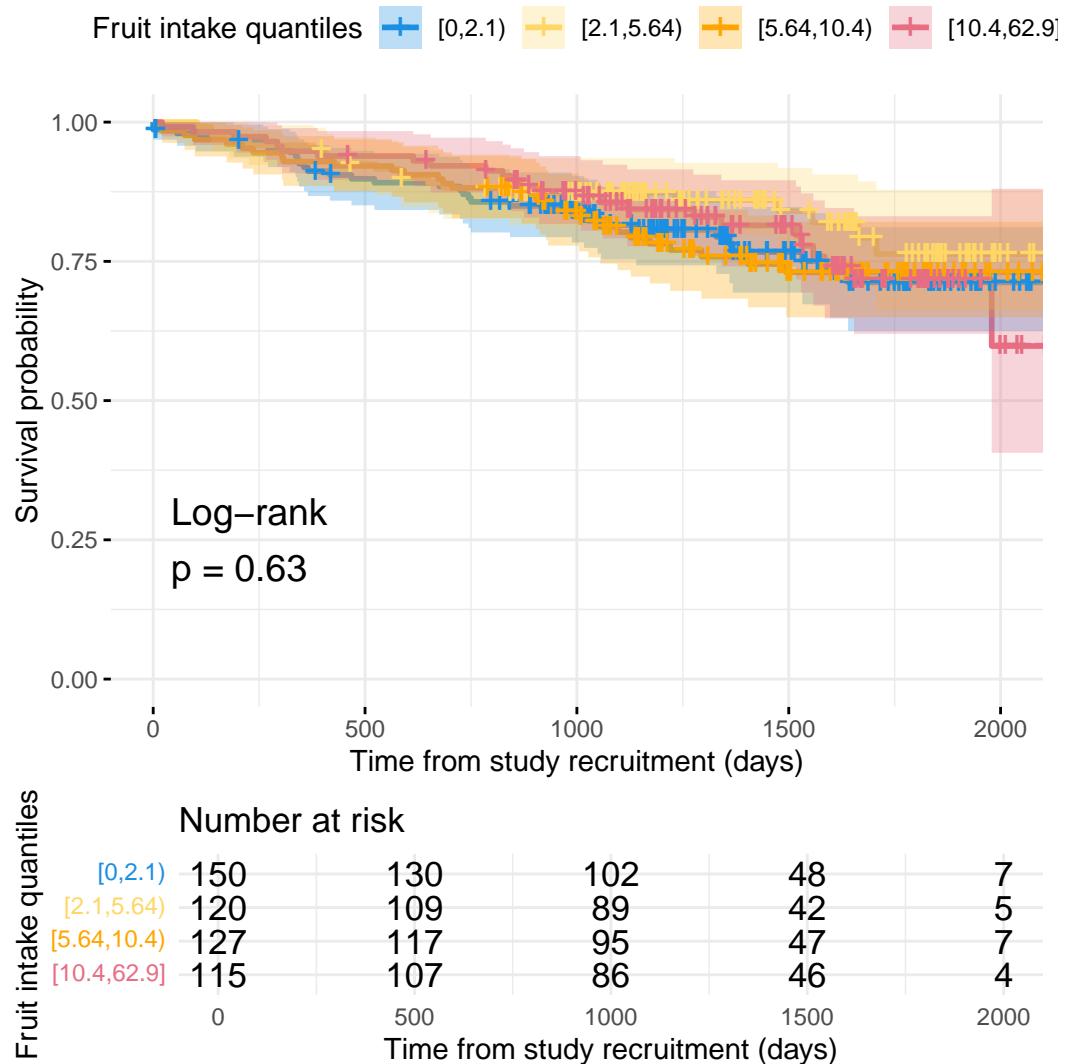
```
plot_base_path = "plots/cd/hard-flare/diet/fruitIntake",
break_time_by = 500
)

# Save plot as RDS
saveRDS(analysis_result$plot, paste0(paths$outdir, "fruitIntake-cd-hard.RDS"))

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(hardflare_time, hardflare) ~
    Sex + cat + IMD + dqi_tot + BMI + fruitIntake_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.cd.df
)

# Display plot and model summary
analysis_result$plot
```

Time to hard flare



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.3601	0.8927	2.0723	0.1522
catFC 50-250	1.8300	1.1495	2.9135	0.0109
catFC > 250	2.8711	1.7311	4.7617	0.0000

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	0.5956	0.2560	1.3853	0.2289
IMD3	0.8086	0.3627	1.8027	0.6035
IMD4	0.7497	0.3465	1.6220	0.4644
IMD5	0.7014	0.3375	1.4576	0.3419
dqi_tot	1.0057	0.9851	1.0267	0.5919
BMI	1.0174	0.9824	1.0537	0.3336
fruitIntake_cat[2.1,5.64)	0.7104	0.3904	1.2927	0.2630
fruitIntake_cat[5.64,10.4	0.9883	0.5654	1.7277	0.9672
fruitIntake_cat[10.4,62.9	0.8585	0.4521	1.6301	0.6409

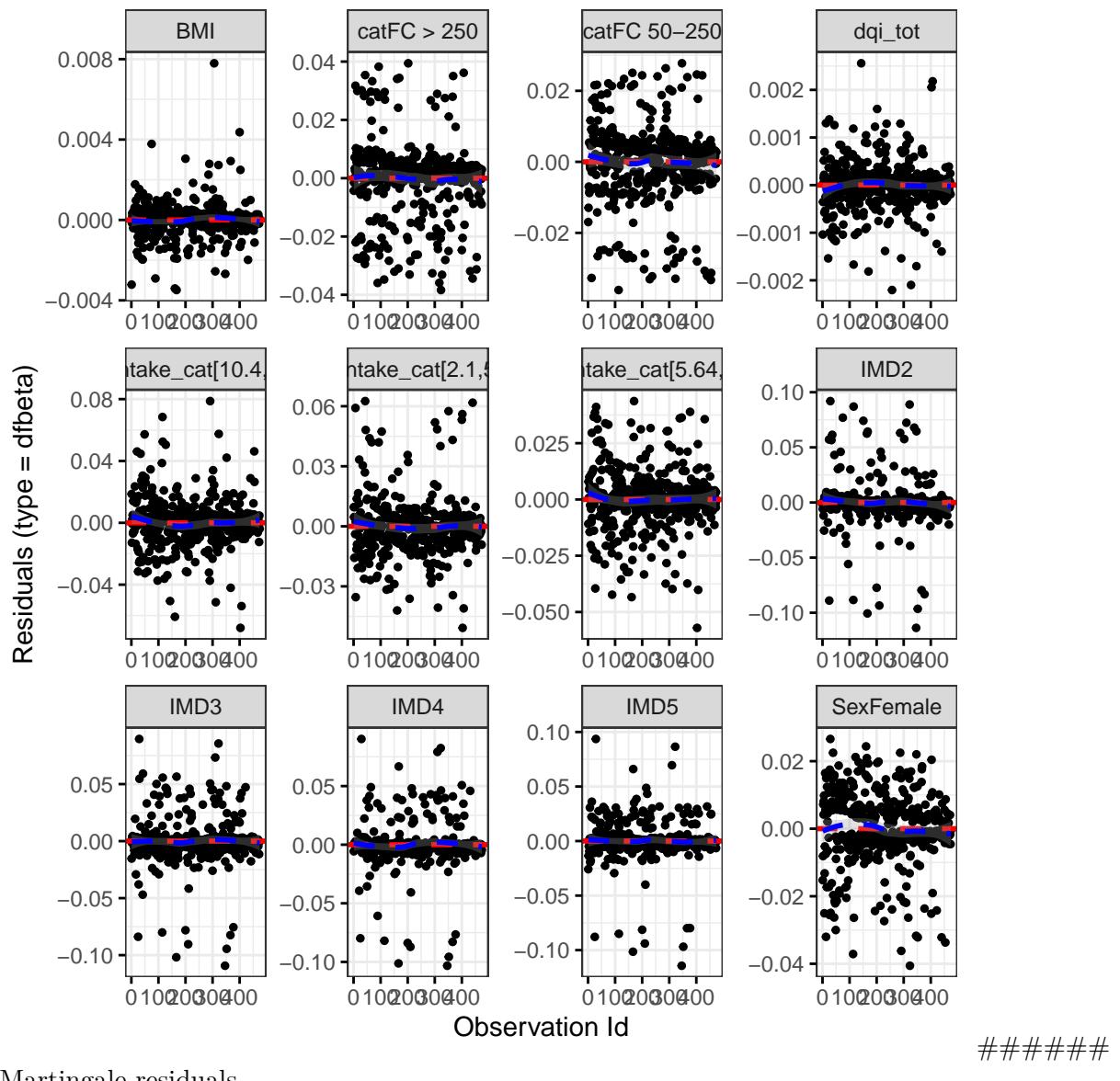
Diagnostics:

Proportional hazards assumption test

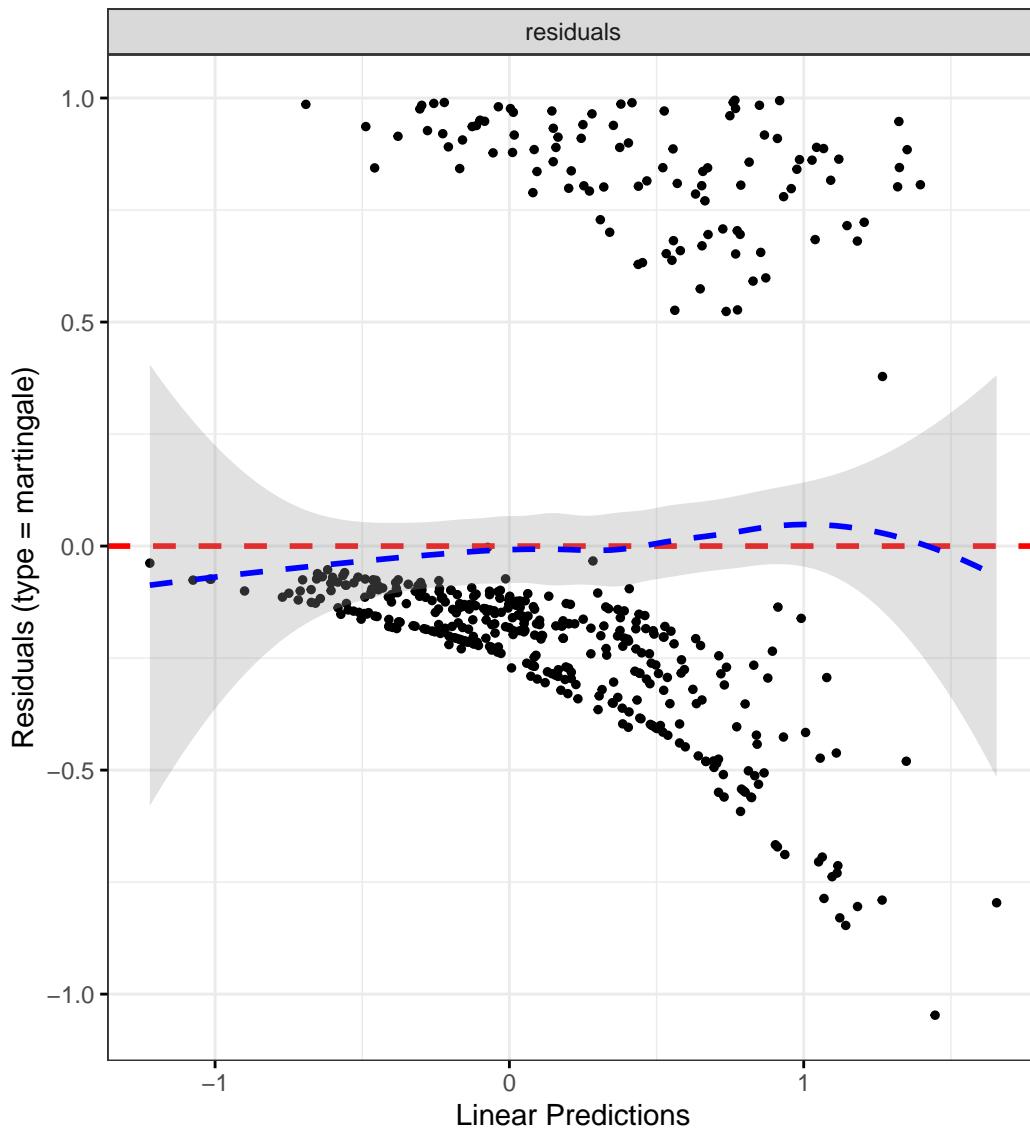
	Chi-squared statistic	DF	P-value
Sex	0.0676	0.9724	0.7850
cat	10.3750	1.9788	0.0054
IMD	2.7906	3.9322	0.5828
dqi_tot	2.6125	0.9875	0.1043
BMI	1.0987	0.9792	0.2881
fruitIntake_cat	2.0898	2.9692	0.5482
GLOBAL	18.2208	18.2141	0.4555

DF betas

```
`geom_smooth()` using formula = 'y ~ x'
```



```
`geom_smooth()` using formula = 'y ~ x'
```



Ulcerative colitis

Patient-reported flare

```
# Categorize fruit intake by quantiles
flare.uc.df <- categorize_by_quantiles(flare.uc.df, "fruitIntake", reference_data = flare.df)

# Run survival analysis using utility function
```

```

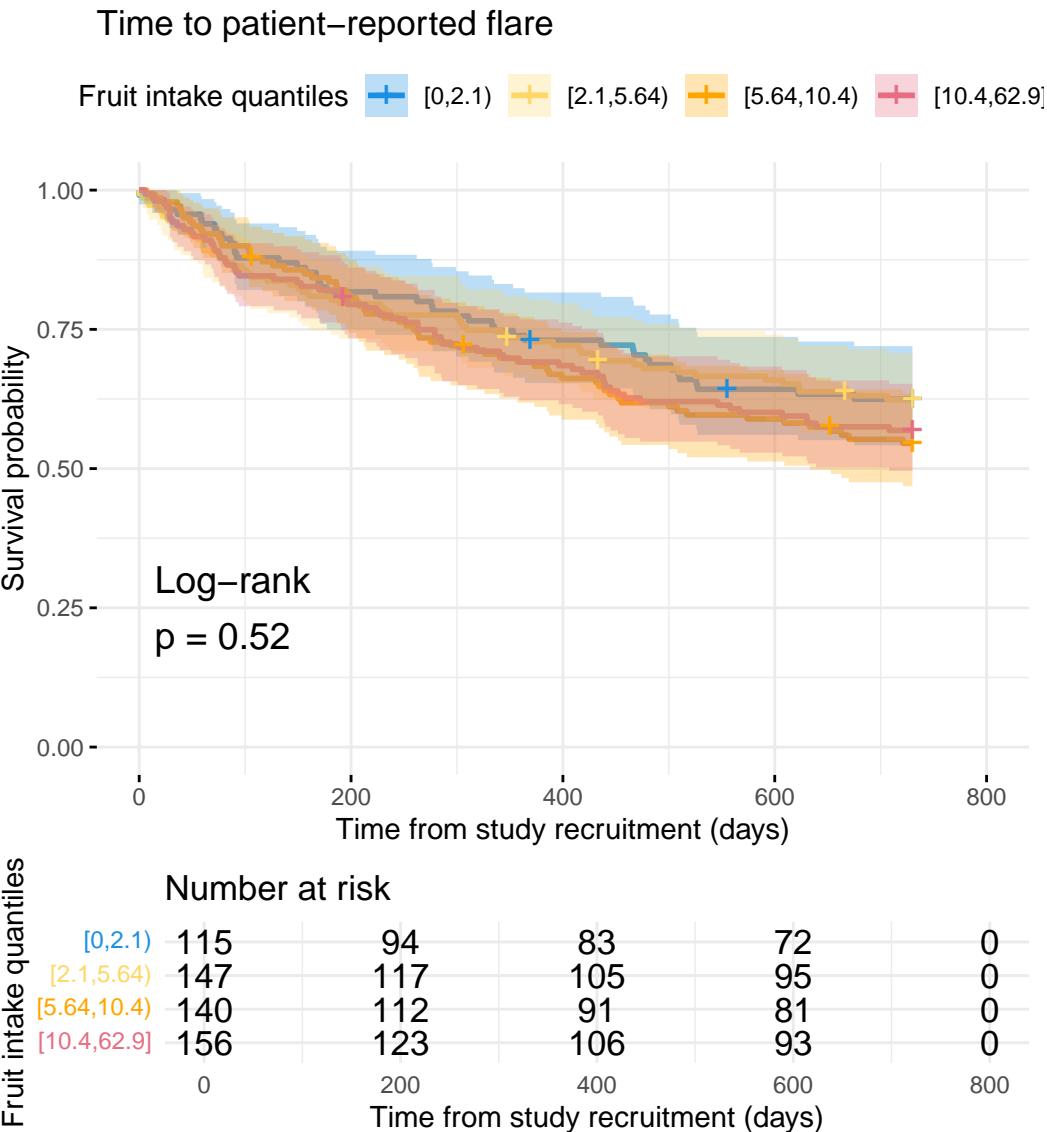
analysis_result <- run_survival_analysis(
  data = flare.uc.df,
  var_name = "fruitIntake",
  outcome_time = "softflare_time",
  outcome_event = "softflare",
  legend_title = "Fruit intake quantiles",
  plot_base_path = "plots/uc/soft-flare/diet/fruitIntake",
  break_time_by = 200
)

# Save plot as RDS
saveRDS(analysis_result$plot, paste0(paths$outdir, "fruitIntake-uc-soft.RDS"))

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(softflare_time, softflare) ~
    Sex + cat + IMD + dqi_tot + BMI + fruitIntake_cat +
    frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.uc.df
)

# Display plot and model summary
analysis_result$plot

```



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.6800	1.2564	2.2464	0.0005
catFC 50-250	1.8014	1.3116	2.4740	0.0003
catFC > 250	2.0619	1.4435	2.9454	0.0001

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	1.3888	0.7267	2.6541	0.3202
IMD3	1.1294	0.5995	2.1278	0.7064
IMD4	1.3261	0.7313	2.4046	0.3527
IMD5	1.1680	0.6472	2.1076	0.6062
dqi_tot	0.9984	0.9842	1.0129	0.8291
BMI	0.9761	0.9474	1.0056	0.1114
fruitIntake_cat[2.1,5.64)	1.0907	0.7154	1.6630	0.6866
fruitIntake_cat[5.64,10.4	1.1470	0.7525	1.7482	0.5237
fruitIntake_cat[10.4,62.9	1.0947	0.6921	1.7314	0.6989

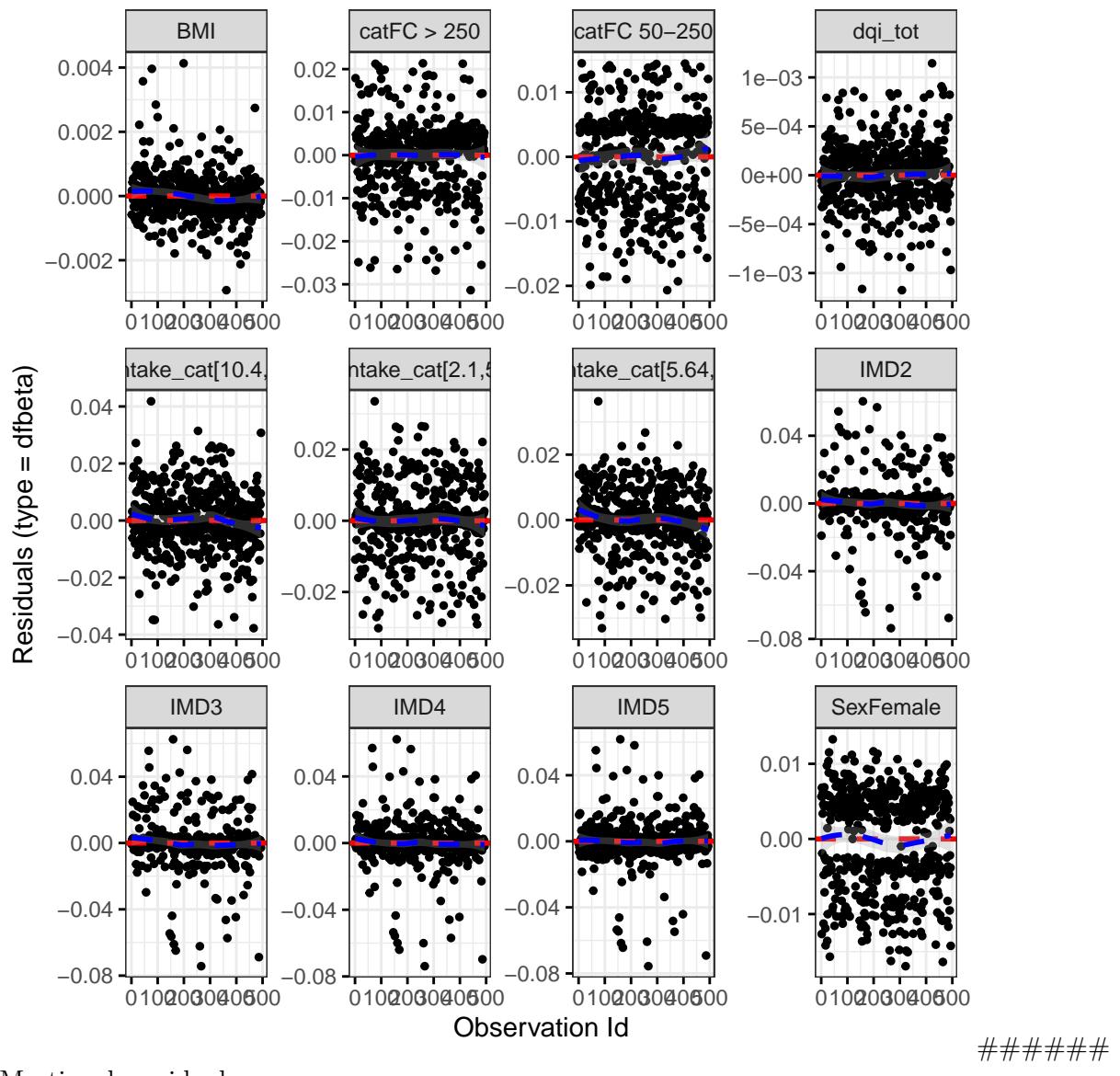
Diagnostics:

Proportional hazards assumption test

	Chi-squared statistic	DF	P-value
Sex	0.0057	1.0000	0.9399
cat	3.5410	2.0000	0.1702
IMD	2.6427	4.0000	0.6193
dqi_tot	0.7629	1.0000	0.3824
BMI	0.9614	1.0000	0.3268
fruitIntake_cat	3.2348	3.0000	0.3568
GLOBAL	11.2109	12.0001	0.5109

DF betas

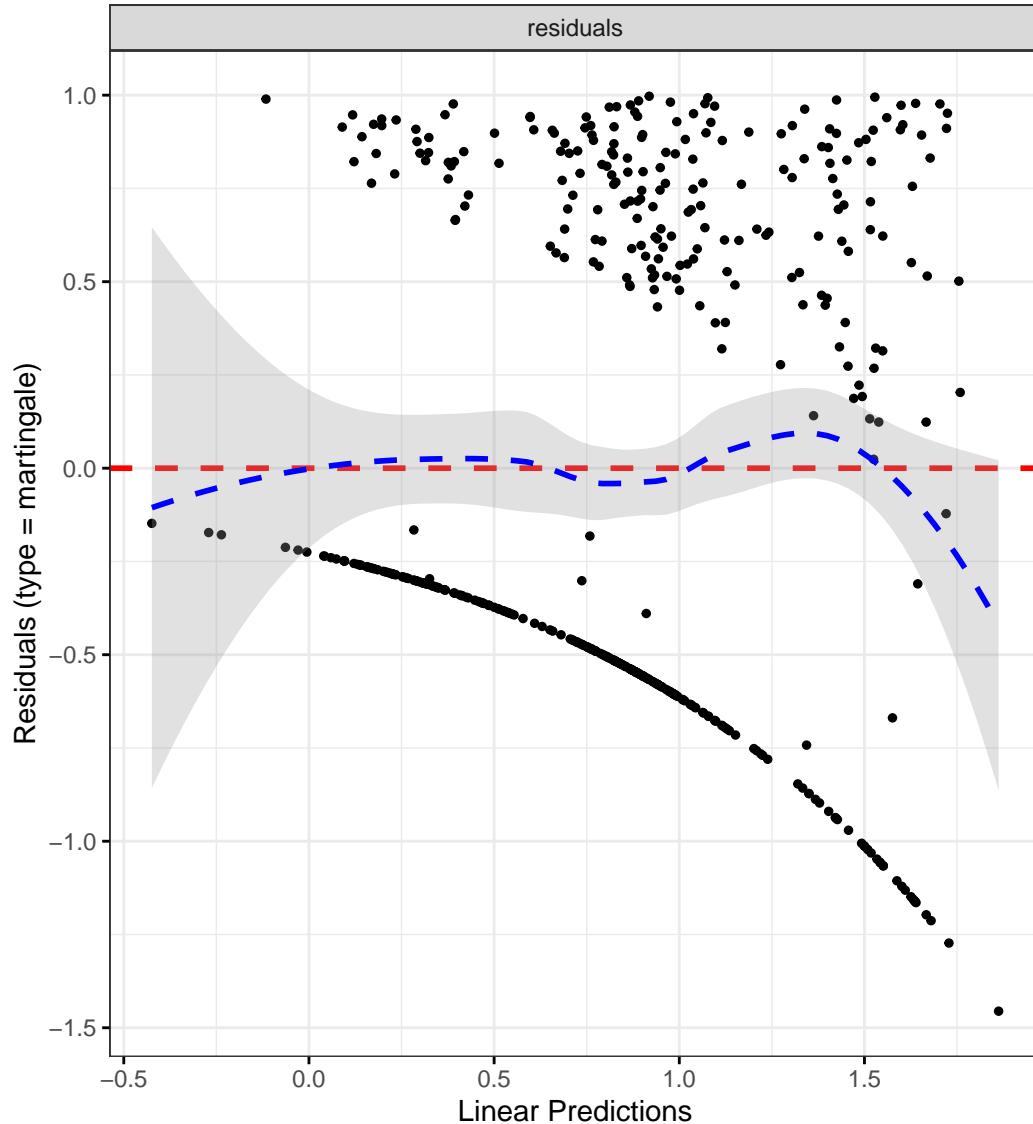
```
`geom_smooth()` using formula = 'y ~ x'
```



Martingale residuals

#####

```
`geom_smooth()` using formula = 'y ~ x'
```



Hard flare

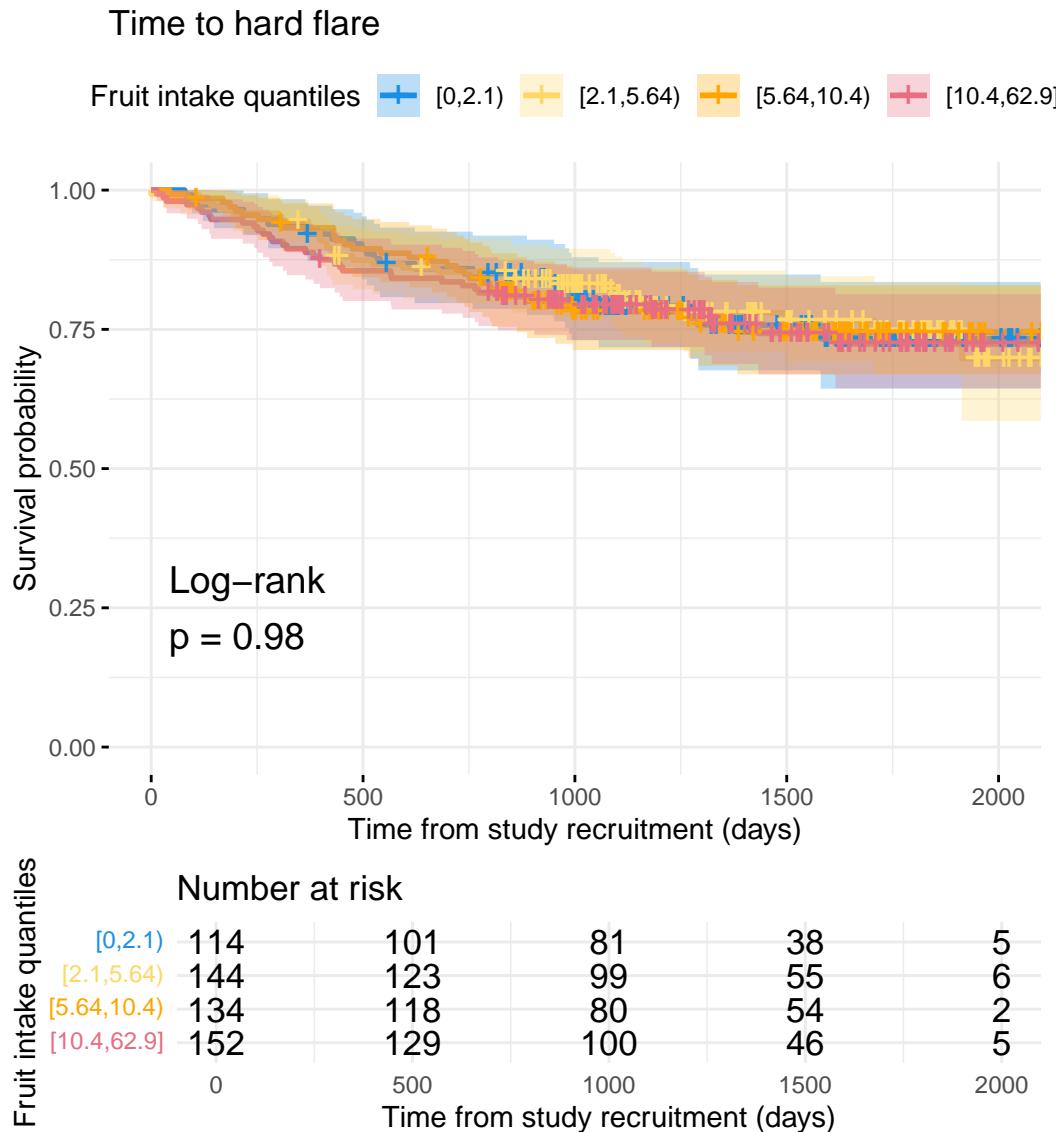
```
# Run survival analysis using utility function for hard flare
analysis_result <- run_survival_analysis(
  data = flare.uc.df,
  var_name = "fruitIntake",
  outcome_time = "hardflare_time",
  outcome_event = "hardflare",
  legend_title = "Fruit intake quantiles",
```

```
plot_base_path = "plots/uc/hard-flare/diet/fruitIntake",
break_time_by = 500
)

# Save plot as RDS
saveRDS(analysis_result$plot, paste0(paths$outdir, "fruitIntake-uc-hard.RDS"))

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(hardflare_time, hardflare) ~
    Sex + cat + IMD + fruitIntake_cat + dqi_tot + BMI + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.uc.df
)

# Display plot and model summary
analysis_result$plot
```



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.2010	0.8195	1.7602	0.3476
catFC 50-250	2.0242	1.3124	3.1221	0.0014
catFC > 250	2.4981	1.5330	4.0708	0.0002

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	1.5567	0.5886	4.1174	0.3725
IMD3	1.3012	0.5039	3.3603	0.5865
IMD4	2.3414	0.9743	5.6269	0.0572
IMD5	1.4003	0.5763	3.4025	0.4574
fruitIntake_cat[2.1,5.64)	0.9611	0.5489	1.6828	0.8895
fruitIntake_cat[5.64,10.4	0.8897	0.5009	1.5806	0.6903
fruitIntake_cat[10.4,62.9	1.1199	0.6155	2.0375	0.7108
dqi_tot	0.9998	0.9802	1.0198	0.9862
BMI	0.9617	0.9220	1.0030	0.0686

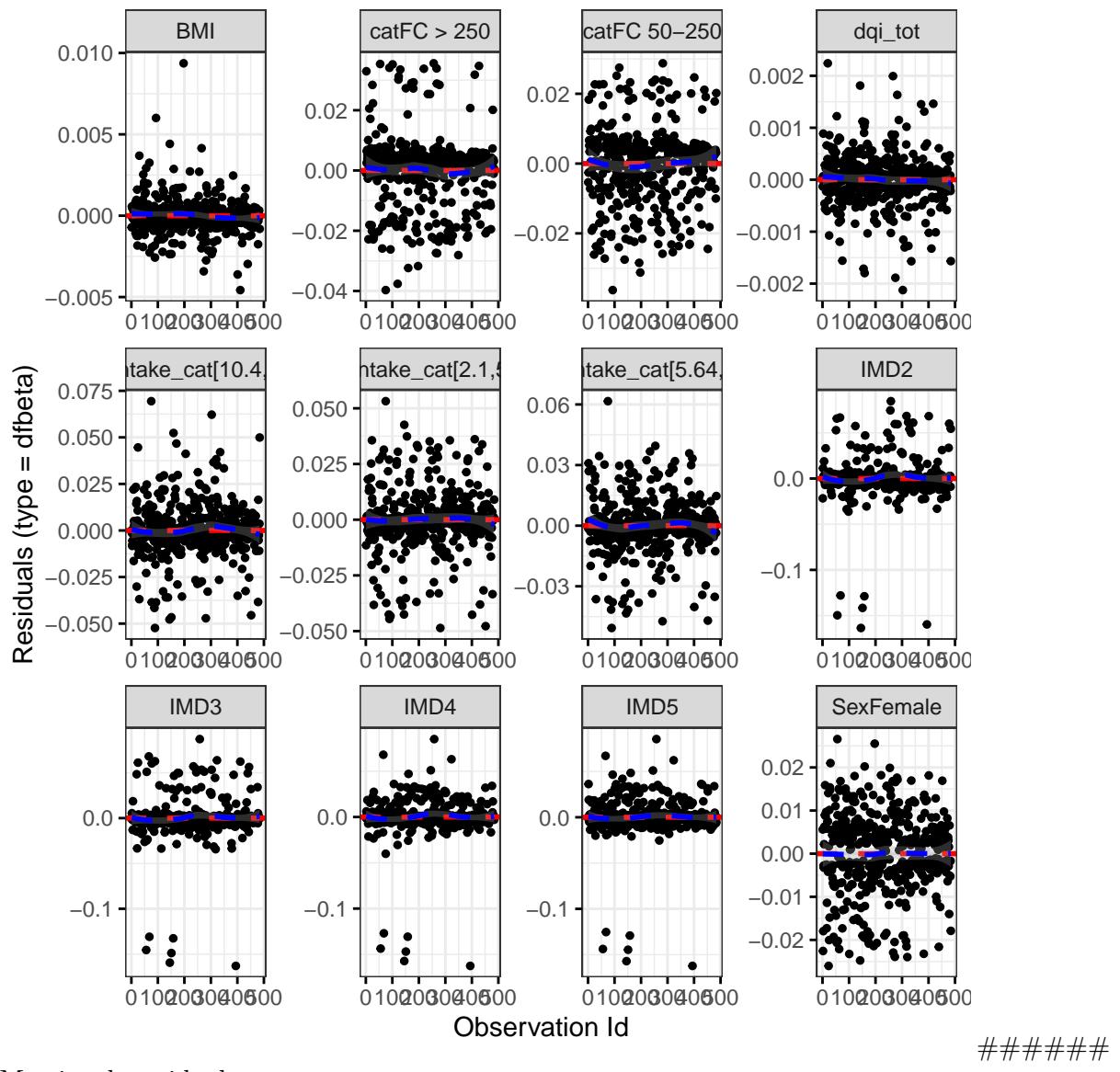
Diagnostics:

Proportional hazards assumption test

	Chi-squared statistic	DF	P-value
Sex	0.0255	0.9883	0.8699
cat	5.4338	1.9546	0.0633
IMD	1.1608	3.9313	0.8783
fruitIntake_cat	1.5003	2.9573	0.6746
dqi_tot	0.0000	0.9856	0.9977
BMI	0.5821	0.9901	0.4416
GLOBAL	9.7198	19.5655	0.9677

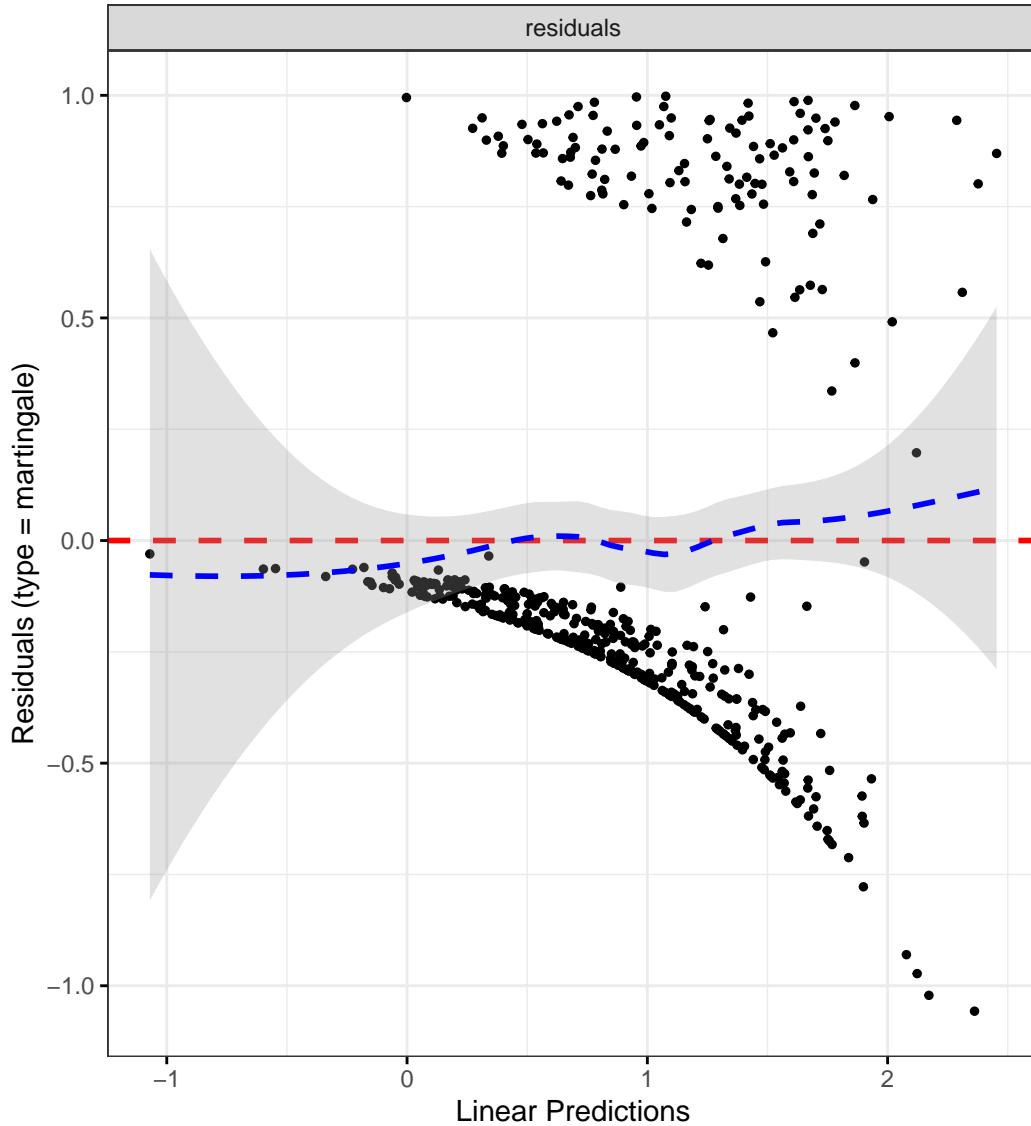
DF betas

```
`geom_smooth()` using formula = 'y ~ x'
```



Martingale residuals

```
`geom_smooth()` using formula = 'y ~ x'
```



Inflammatory bowel disease

Patient-reported flare

```
# Categorize fruit intake by quantiles
flare.df <- categorize_by_quantiles(flare.df, "fruitIntake", reference_data = flare.df)

# Run survival analysis using utility function
```

```

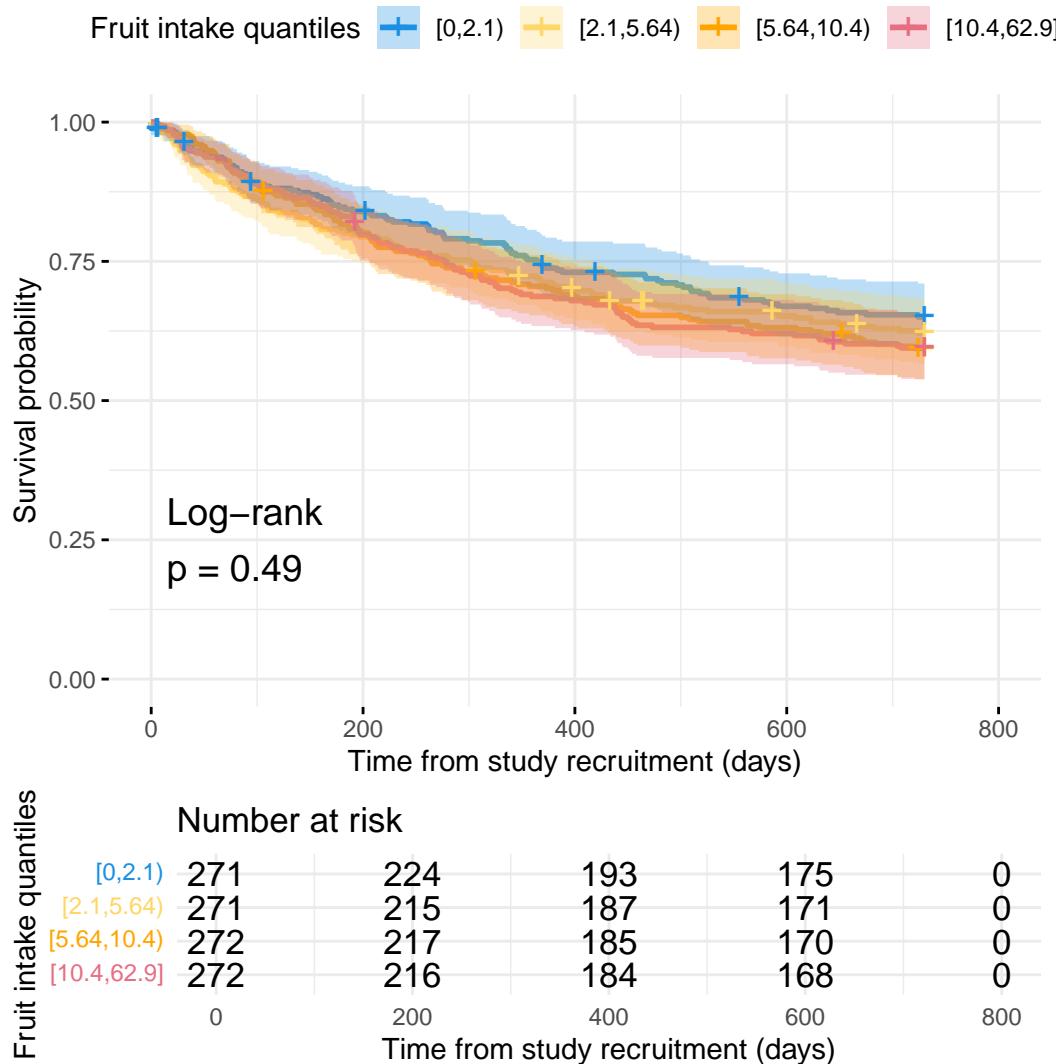
analysis_result <- run_survival_analysis(
  data = flare.df,
  var_name = "fruitIntake",
  outcome_time = "softflare_time",
  outcome_event = "softflare",
  legend_title = "Fruit intake quantiles",
  plot_base_path = "plots/ibd/soft-flare/diet/fruitIntake",
  break_time_by = 200
)

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(softflare_time, softflare) ~
    Sex + cat + IMD + dqi_tot + BMI + fruitIntake_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.df
)

# Display plot and model summary
analysis_result$plot

```

Time to patient-reported flare



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.7482	1.4072	2.1718	0.0000
catFC 50-250	1.5051	1.1912	1.9018	0.0006
catFC > 250	2.0149	1.5550	2.6107	0.0000

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	0.9835	0.6254	1.5468	0.9426
IMD3	1.0060	0.6519	1.5525	0.9785
IMD4	1.0986	0.7253	1.6641	0.6572
IMD5	1.0673	0.7144	1.5946	0.7504
dqi_tot	1.0008	0.9903	1.0114	0.8837
BMI	0.9945	0.9749	1.0145	0.5853
fruitIntake_cat[2.1,5.64)	1.1596	0.8572	1.5687	0.3369
fruitIntake_cat[5.64,10.4	1.1359	0.8380	1.5398	0.4115
fruitIntake_cat[10.4,62.9	1.1427	0.8171	1.5981	0.4357

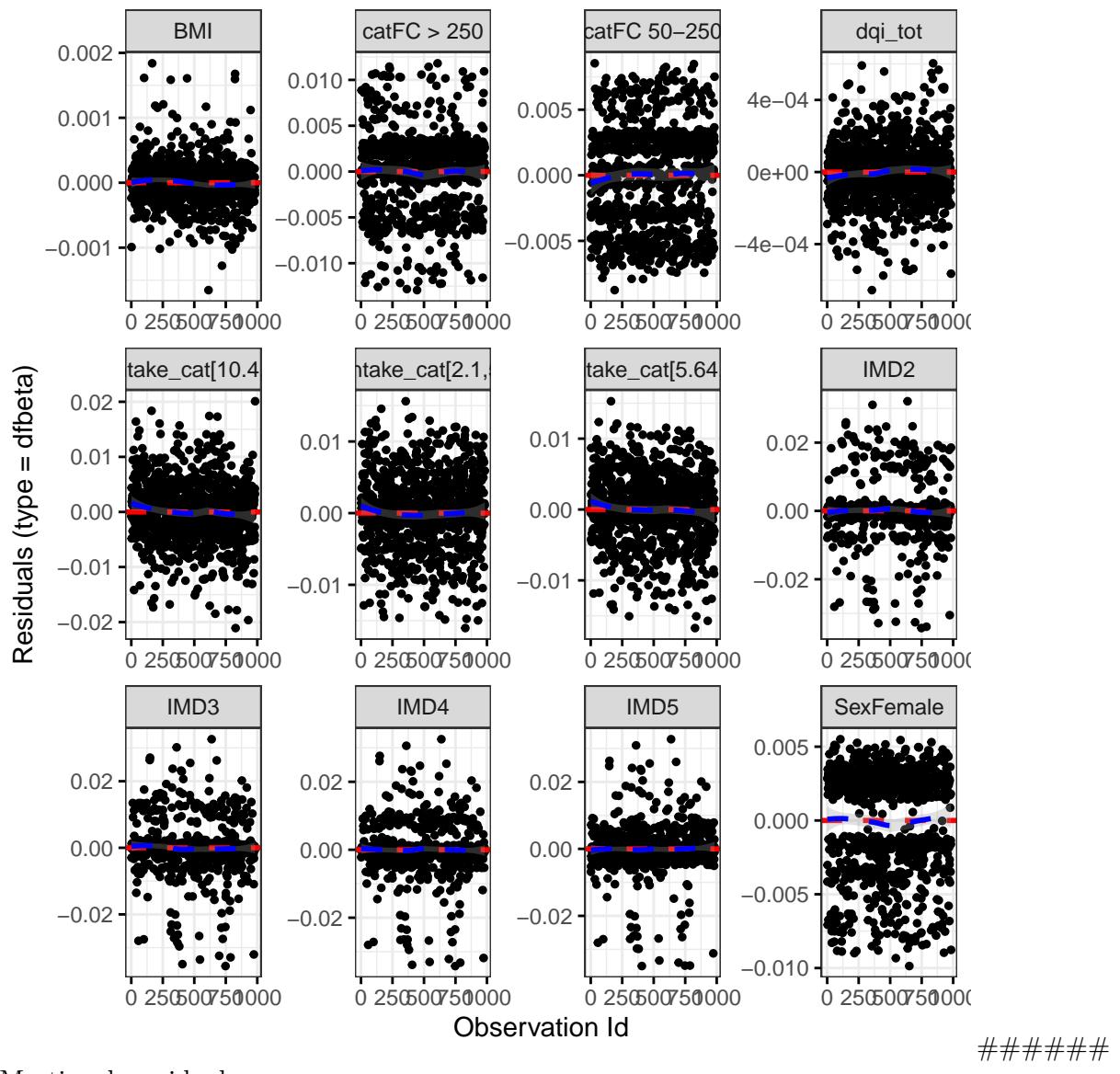
Diagnostics:

Proportional hazards assumption test

	Chi-squared statistic	DF	P-value
Sex	0.0033	1.0000	0.9544
cat	1.0633	2.0000	0.5876
IMD	5.0824	4.0000	0.2789
dqi_tot	1.4036	1.0000	0.2361
BMI	0.0121	1.0000	0.9125
fruitIntake_cat	2.9476	3.0000	0.3998
GLOBAL	10.9461	12.0002	0.5336

DF betas

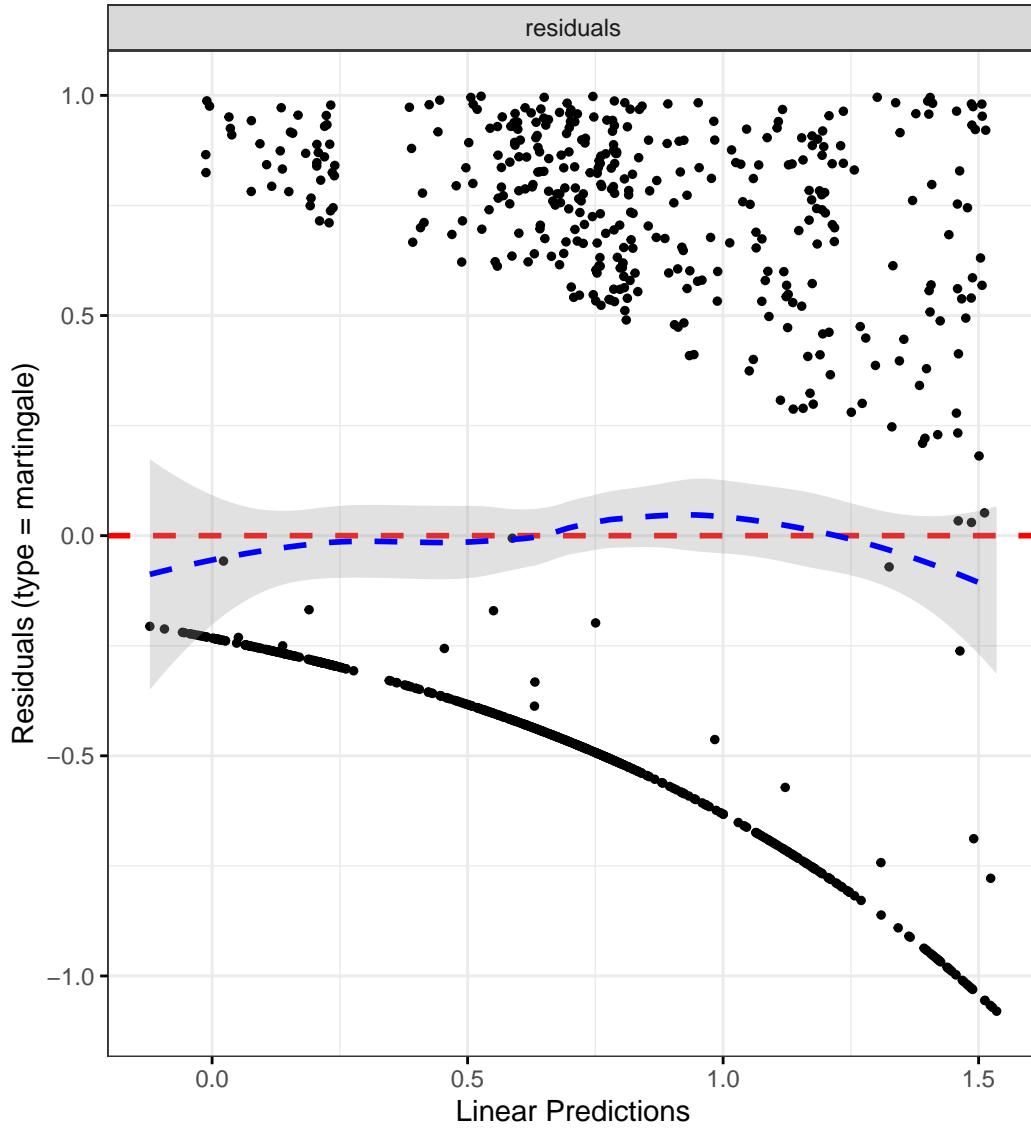
```
`geom_smooth()` using formula = 'y ~ x'
```



#####

Martingale residuals

```
`geom_smooth()` using formula = 'y ~ x'
```



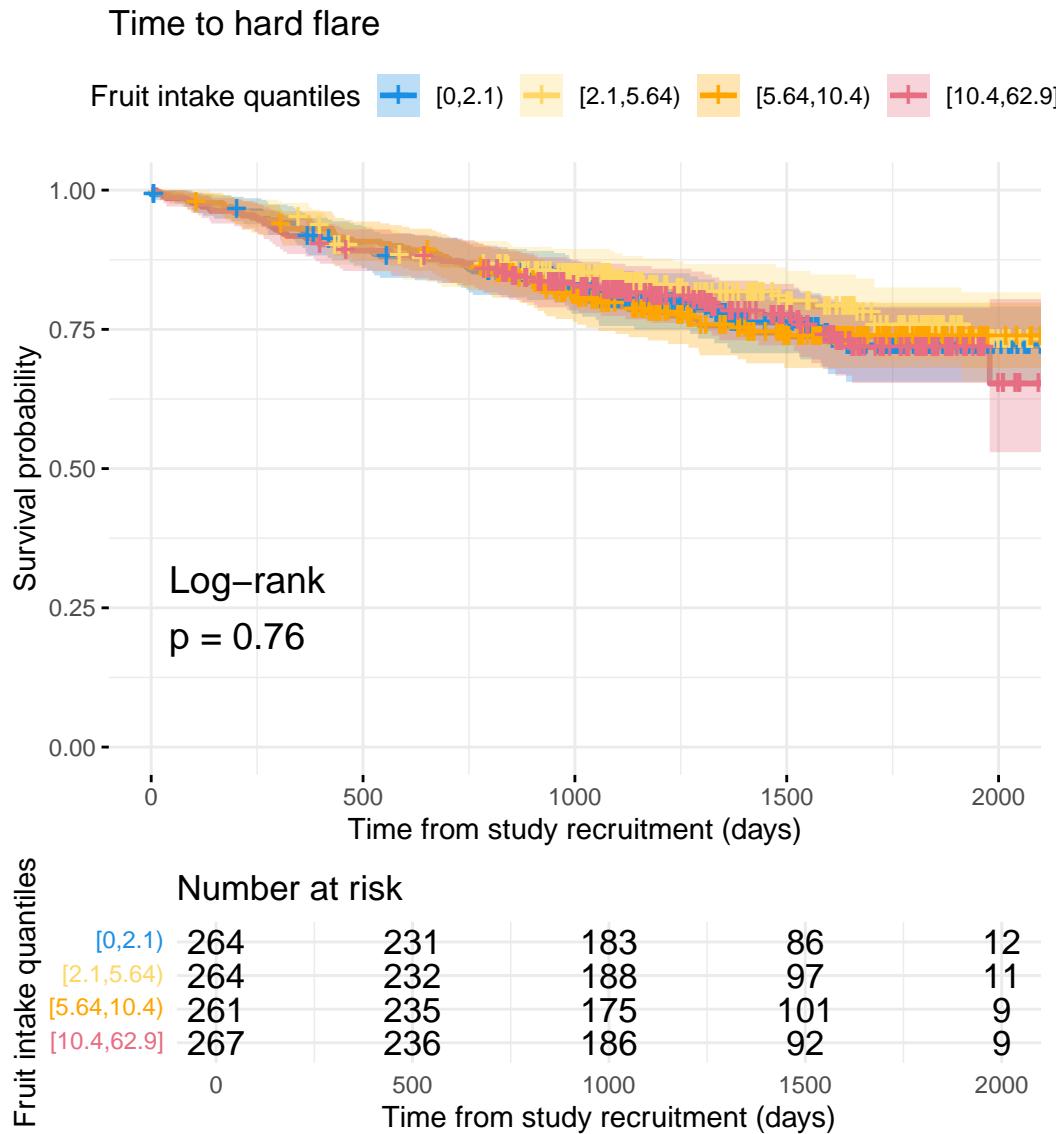
Hard flare

```
# Run survival analysis using utility function for hard flare
analysis_result <- run_survival_analysis(
  data = flare.df,
  var_name = "fruitIntake",
  outcome_time = "hardflare_time",
  outcome_event = "hardflare",
  legend_title = "Fruit intake quantiles",
```

```
plot_base_path = "plots/ibd/hard-flare/diet/fruitIntake",
break_time_by = 500
)

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(hardflare_time, hardflare) ~
    Sex + cat + IMD + dqi_tot + BMI + fruitIntake_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.df
)

# Display plot and model summary
analysis_result$plot
```



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.2627	0.9556	1.6686	0.1009
catFC 50-250	1.8532	1.3536	2.5373	0.0001
catFC > 250	2.5946	1.8348	3.6690	0.0000

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	0.9219	0.4934	1.7227	0.7988
IMD3	0.9605	0.5271	1.7503	0.8953
IMD4	1.3513	0.7700	2.3713	0.2941
IMD5	0.9789	0.5611	1.7078	0.9400
dqi_tot	1.0018	0.9878	1.0160	0.8014
BMI	0.9927	0.9663	1.0197	0.5921
fruitIntake_cat[2.1,5.64)	0.8518	0.5709	1.2710	0.4321
fruitIntake_cat[5.64,10.4	0.9814	0.6624	1.4539	0.9253
fruitIntake_cat[10.4,62.9	1.0112	0.6576	1.5550	0.9596

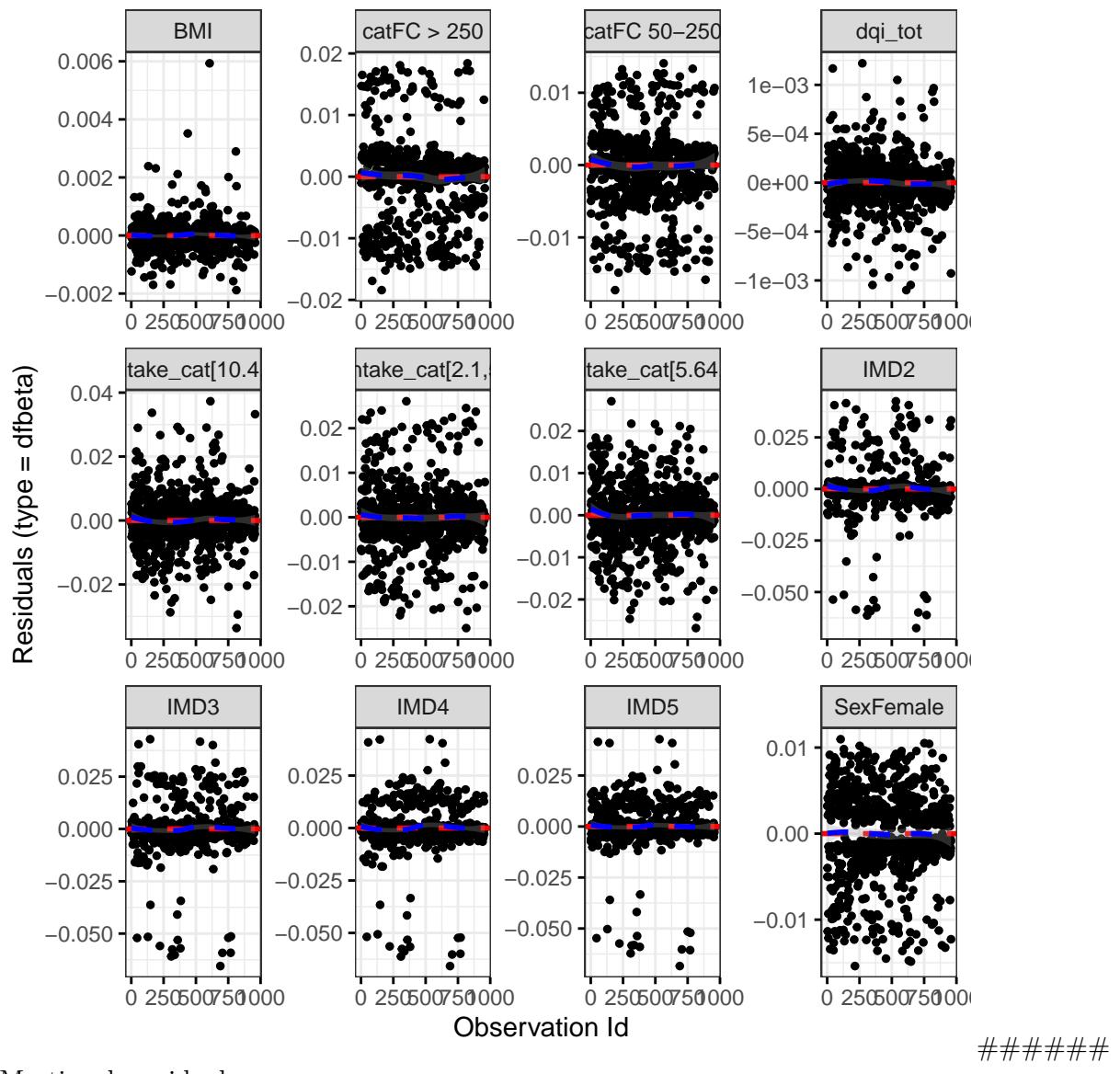
Diagnostics:

Proportional hazards assumption test

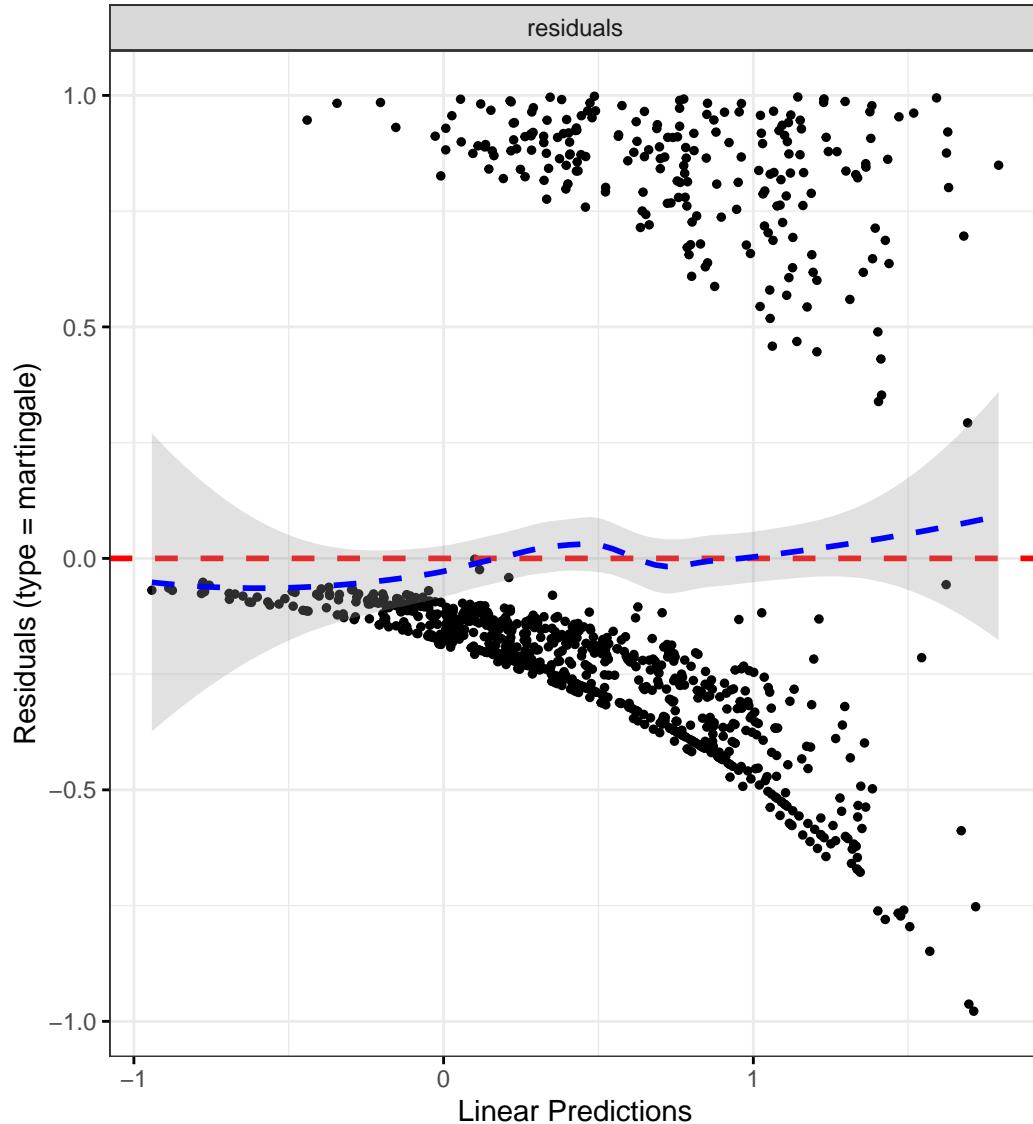
	Chi-squared statistic	DF	P-value
Sex	0.0368	0.9890	0.8445
cat	6.9646	1.9793	0.0301
IMD	1.6437	3.9450	0.7942
dqi_tot	1.9133	0.9931	0.1652
BMI	1.9272	0.9888	0.1628
fruitIntake_cat	0.2770	2.9729	0.9630
GLOBAL	12.8189	23.1032	0.9574

DF betas

```
`geom_smooth()` using formula = 'y ~ x'
```



```
`geom_smooth()` using formula = 'y ~ x'
```



Vegetable and legumes

Crohn's disease

Patient-reported flare

```
# Categorize vegetable intake by quantiles  
flare.cd.df <- categorize_by_quantiles(flare.cd.df, "vegIntake", reference_data = flare.df)
```

```

# Run survival analysis using utility function
analysis_result <- run_survival_analysis(
  data = flare.cd.df,
  var_name = "vegIntake",
  outcome_time = "softflare_time",
  outcome_event = "softflare",
  legend_title = "Vegetable/legume intake quantiles",
  plot_base_path = "plots/cd/soft-flare/diet/vegIntake",
  break_time_by = 200
)

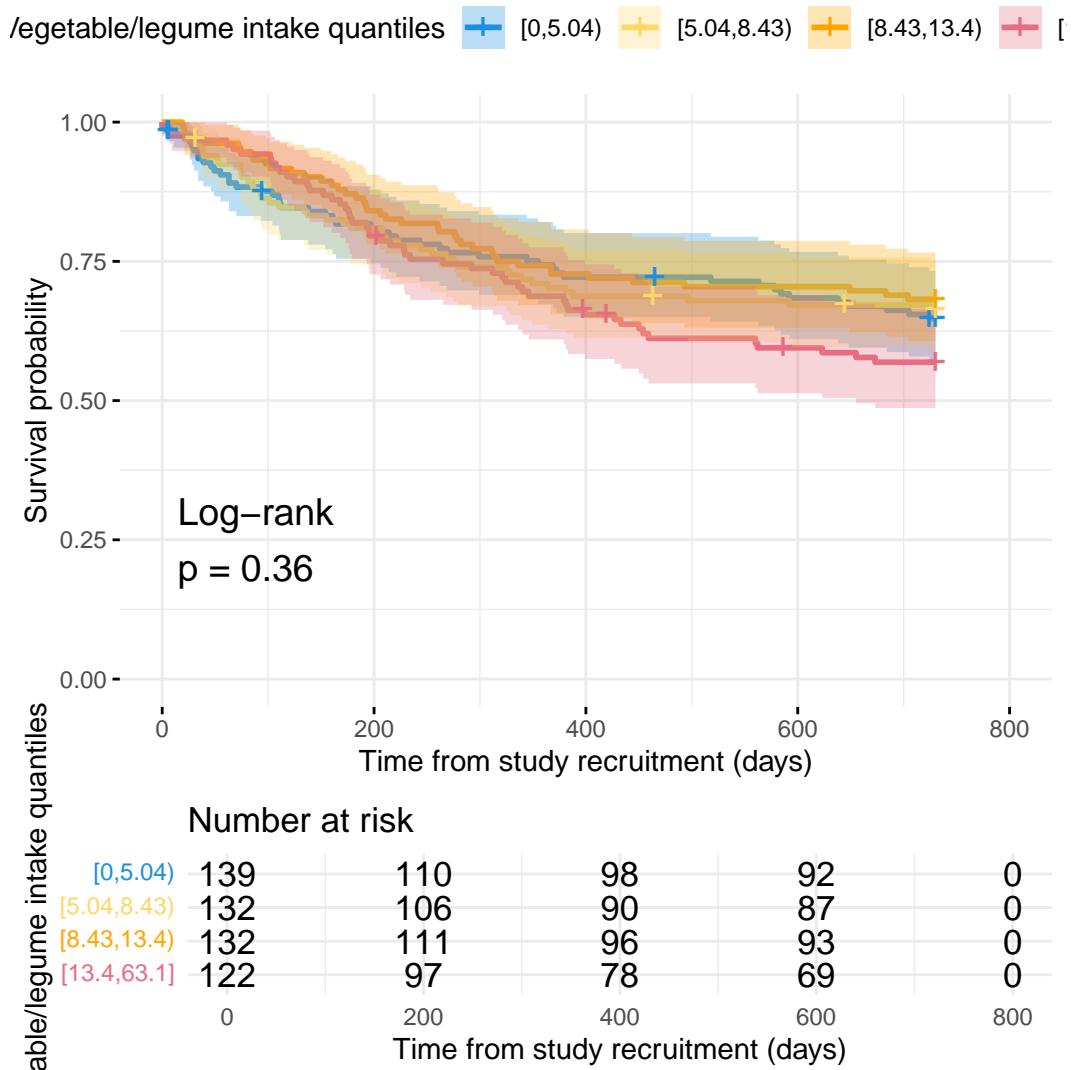
# Save plot as RDS
saveRDS(analysis_result$plot, paste0(paths$outdir, "vegIntake-cd-soft.RDS"))

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(softflare_time, softflare) ~
    Sex + cat + IMD + dqi_tot + BMI + vegIntake_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.cd.df
)

# Display plot and model summary
analysis_result$plot

```

Time to patient-reported flare



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.9542	1.3887	2.7500	0.0001
catFC 50-250	1.3117	0.9233	1.8633	0.1299
catFC > 250	2.0201	1.3811	2.9548	0.0003

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	0.7181	0.3746	1.3765	0.3185
IMD3	0.9734	0.5321	1.7806	0.9303
IMD4	0.8601	0.4742	1.5598	0.6197
IMD5	1.0221	0.5857	1.7837	0.9386
dqi_tot	1.0070	0.9917	1.0225	0.3717
BMI	1.0067	0.9794	1.0348	0.6325
vegIntake_cat[5.04,8.43)	0.9828	0.6360	1.5189	0.9379
vegIntake_cat[8.43,13.4)	0.7986	0.5053	1.2621	0.3355
vegIntake_cat[13.4,63.1]	0.9932	0.6210	1.5883	0.9772

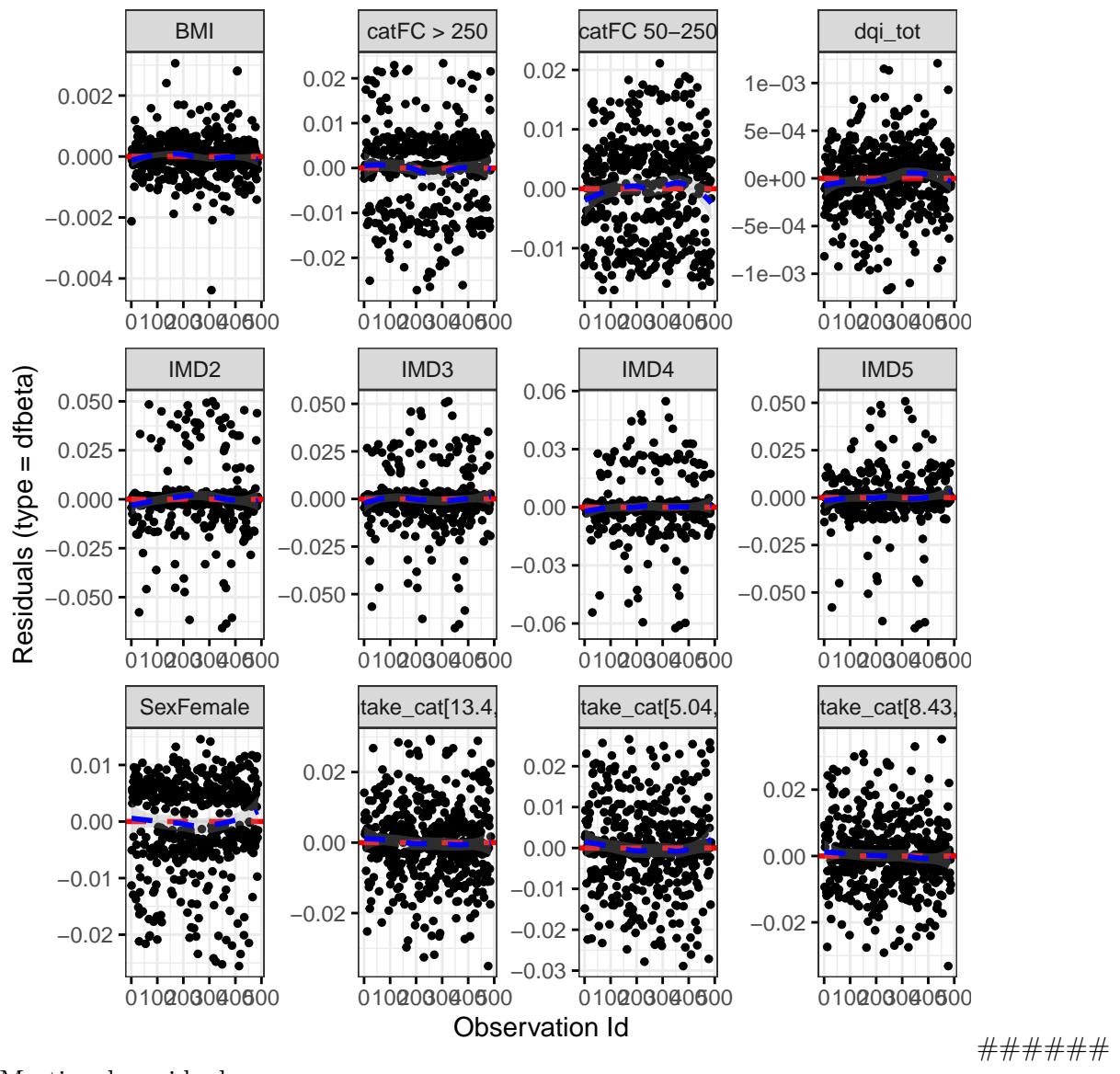
Diagnostics:

Proportional hazards assumption test

	Chi-squared statistic	DF	P-value
Sex	0.2757	1.0000	0.5995
cat	0.7686	2.0000	0.6809
IMD	3.1235	4.0000	0.5374
dqi_tot	0.3712	1.0000	0.5424
BMI	1.2712	1.0000	0.2595
vegIntake_cat	5.4228	3.0000	0.1433
GLOBAL	10.2926	12.0001	0.5903

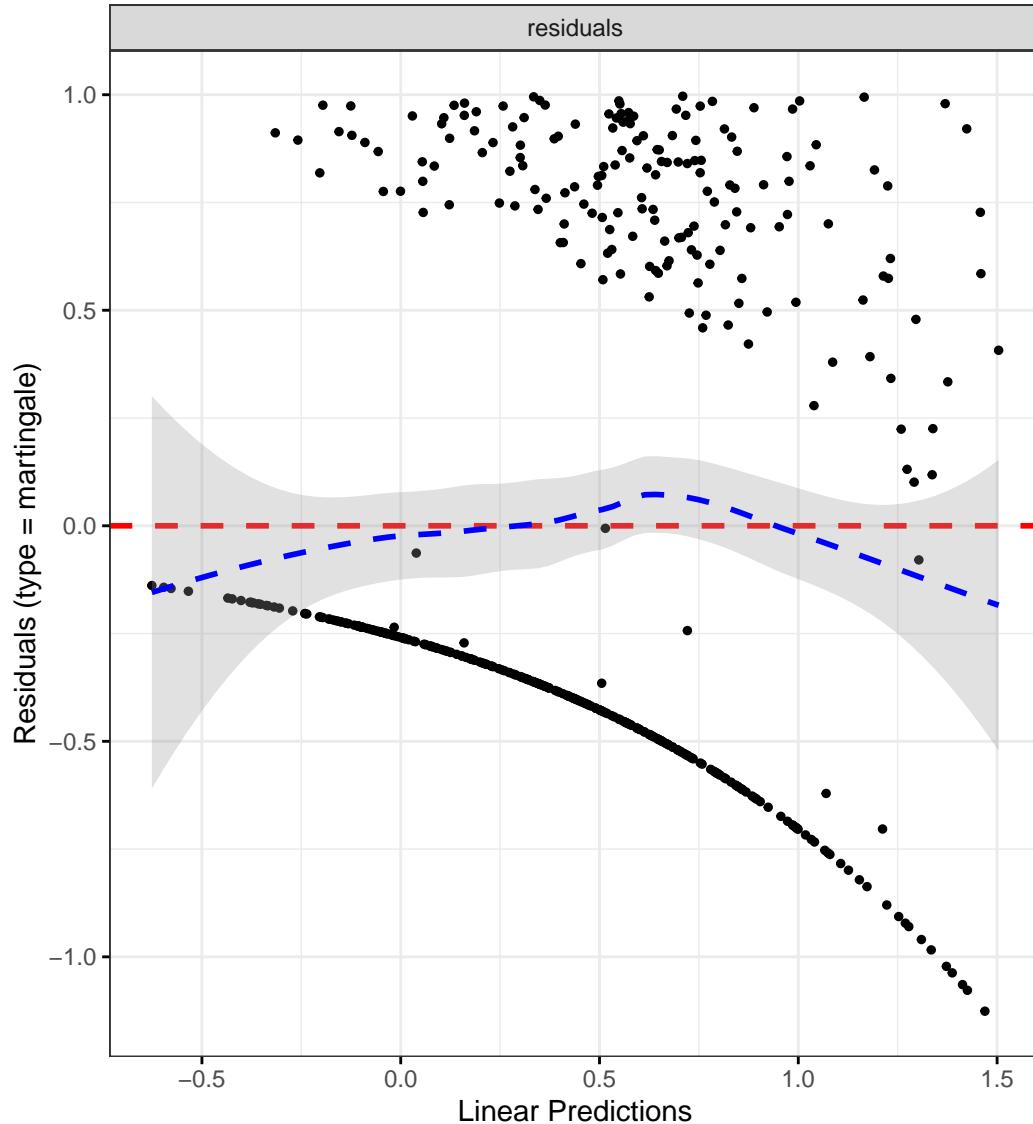
DF betas

```
`geom_smooth()` using formula = 'y ~ x'
```



Martingale residuals

```
`geom_smooth()` using formula = 'y ~ x'
```



Hard flare

```
# Run survival analysis using utility function for hard flare
analysis_result <- run_survival_analysis(
  data = flare.cd.df,
  var_name = "vegIntake",
  outcome_time = "hardflare_time",
  outcome_event = "hardflare",
  legend_title = "Vegetable/legume intake quantiles",
```

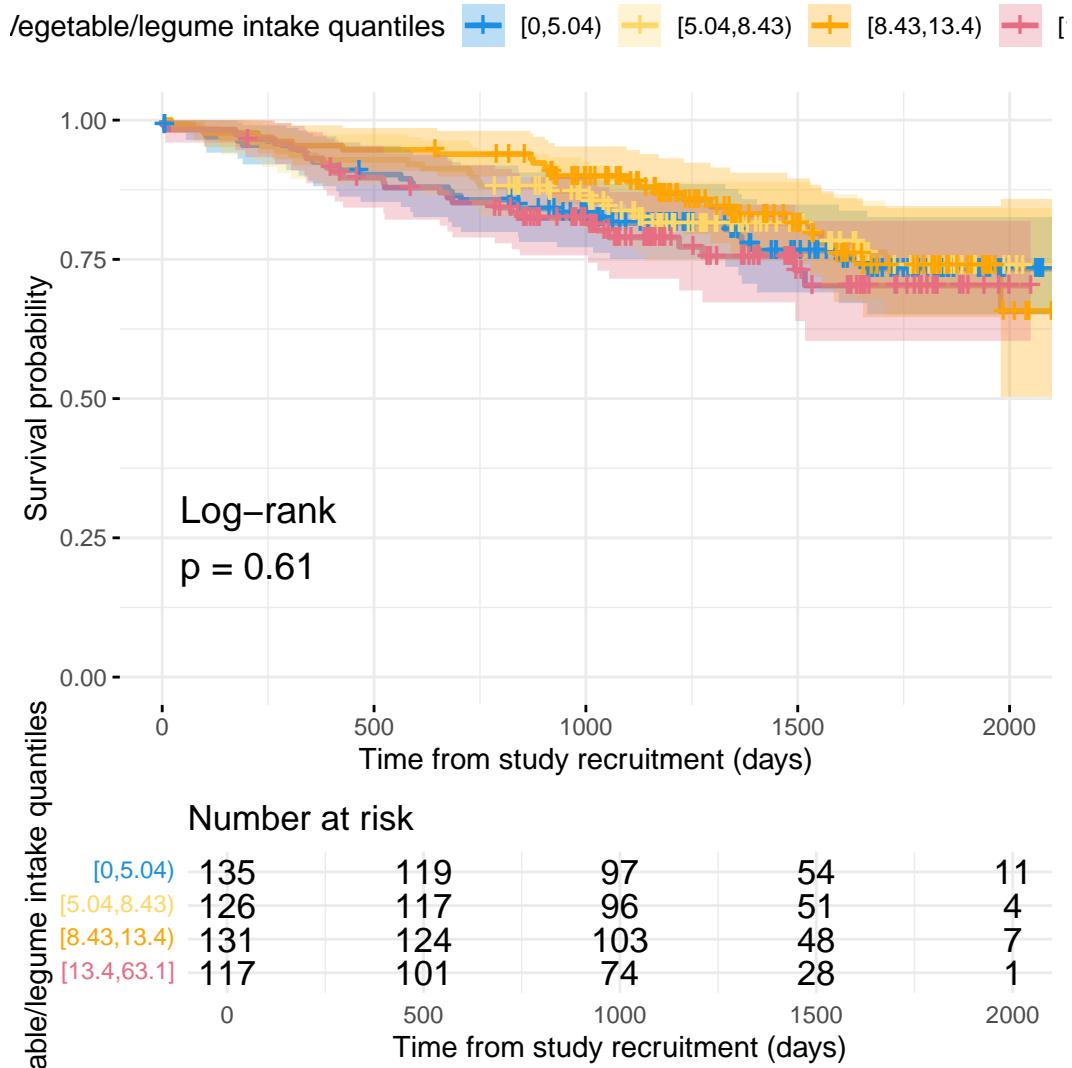
```
plot_base_path = "plots/cd/hard-flare/diet/vegIntake",
break_time_by = 500
)

# Save plot as RDS
saveRDS(analysis_result$plot, paste0(paths$outdir, "vegIntake-cd-hard.RDS"))

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(hardflare_time, hardflare) ~
    Sex + cat + IMD + dqi_tot + BMI + vegIntake_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.cd.df
)

# Display plot and model summary
analysis_result$plot
```

Time to hard flare



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.3135	0.8600	2.0063	0.2070
catFC 50-250	1.8911	1.1869	3.0133	0.0073
catFC > 250	2.9526	1.7842	4.8860	0.0000

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	0.6118	0.2620	1.4285	0.2561
IMD3	0.8509	0.3814	1.8985	0.6934
IMD4	0.7557	0.3466	1.6478	0.4813
IMD5	0.7251	0.3460	1.5195	0.3945
dqi_tot	1.0001	0.9802	1.0204	0.9941
BMI	1.0133	0.9781	1.0497	0.4642
vegIntake_cat[5.04,8.43)	0.9201	0.5234	1.6172	0.7722
vegIntake_cat[8.43,13.4)	0.8766	0.4838	1.5884	0.6641
vegIntake_cat[13.4,63.1]	1.4911	0.8106	2.7427	0.1989

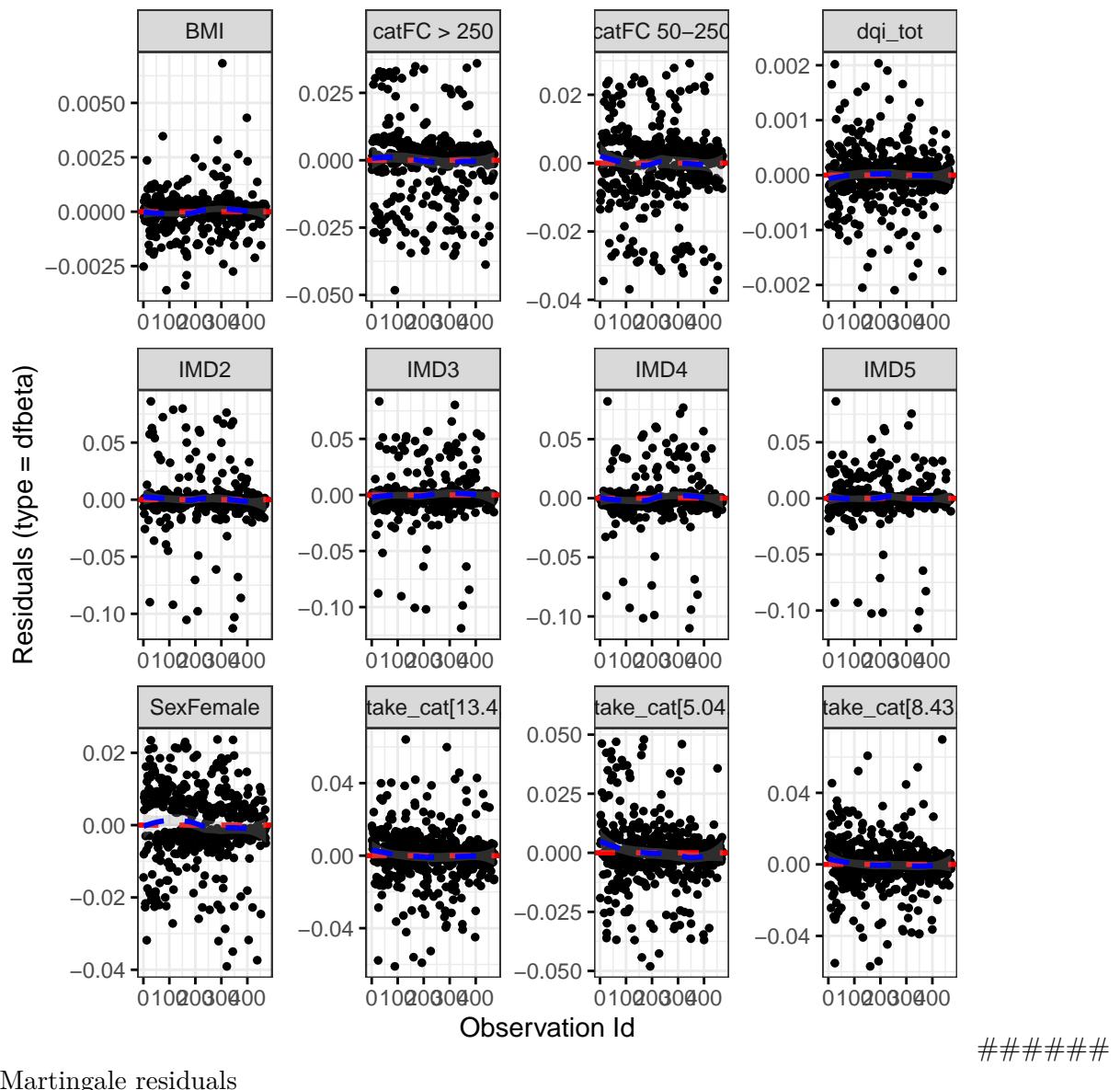
Diagnostics:

Proportional hazards assumption test

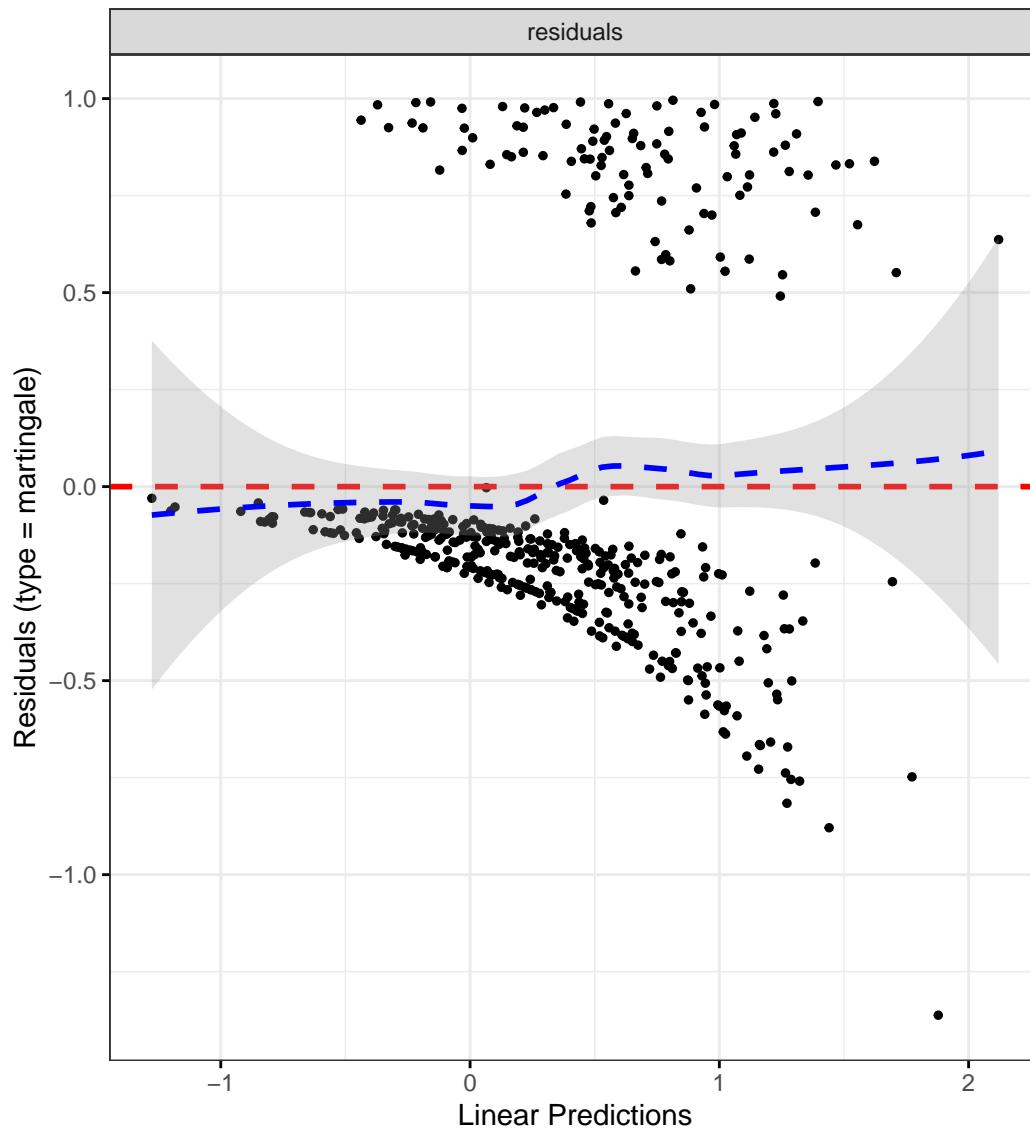
	Chi-squared statistic	DF	P-value
Sex	0.0507	0.9722	0.8124
cat	10.6924	1.9751	0.0046
IMD	2.6346	3.9177	0.6079
dqi_tot	2.9512	0.9900	0.0846
BMI	1.0876	0.9776	0.2900
vegIntake_cat	3.1115	2.9567	0.3674
GLOBAL	19.7739	19.3391	0.4299

DF betas

```
`geom_smooth()` using formula = 'y ~ x'
```



```
`geom_smooth()` using formula = 'y ~ x'
```



Ulcerative colitis

Patient-reported flare

```
# Categorize vegetable intake by quantiles
flare.uc.df <- categorize_by_quantiles(flare.uc.df, "vegIntake", reference_data = flare.df)

# Run survival analysis using utility function
```

```

analysis_result <- run_survival_analysis(
  data = flare.uc.df,
  var_name = "vegIntake",
  outcome_time = "softflare_time",
  outcome_event = "softflare",
  legend_title = "Vegetable/legume intake quantiles",
  plot_base_path = "plots/uc/soft-flare/diet/vegIntake",
  break_time_by = 200
)

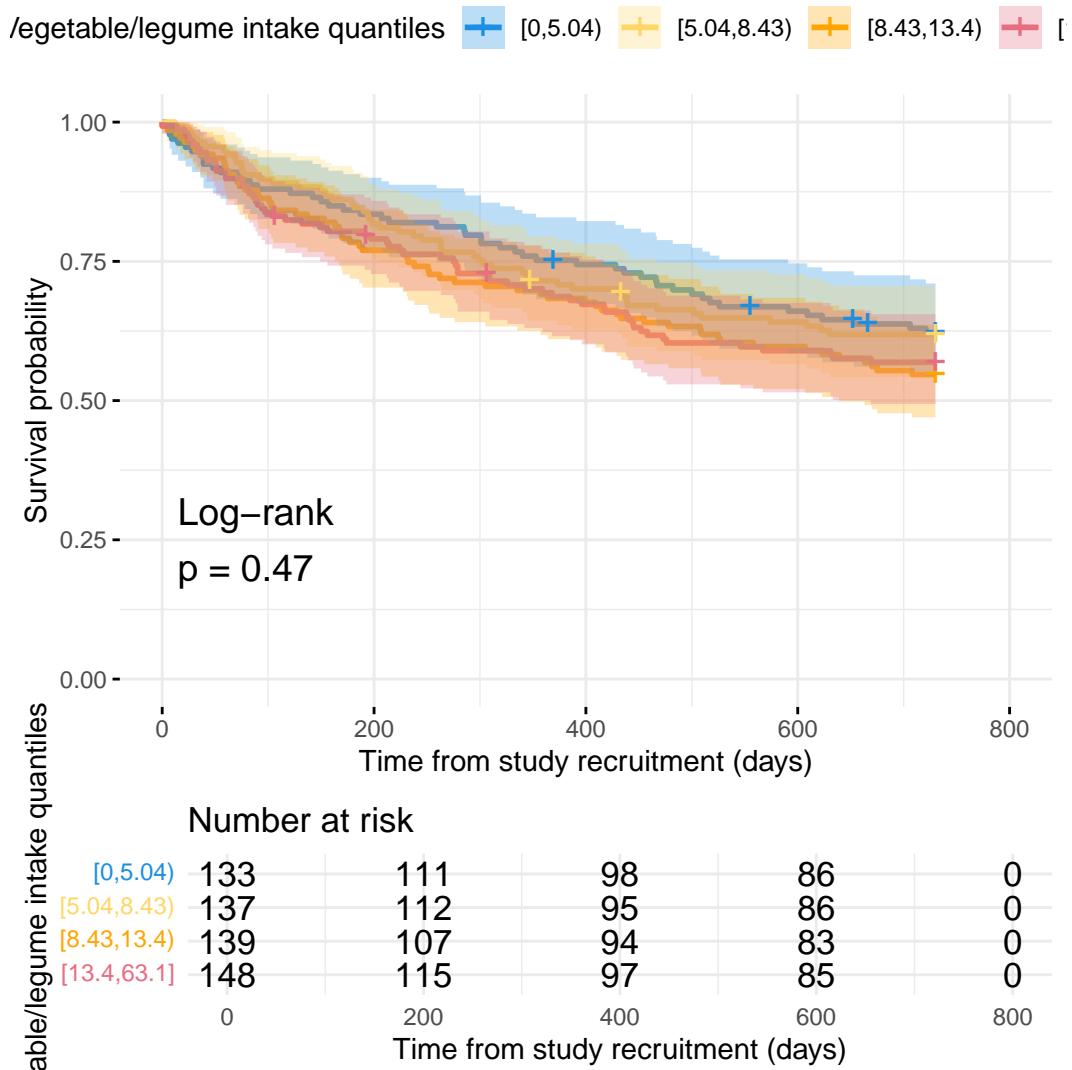
# Save plot as RDS
saveRDS(analysis_result$plot, paste0(paths$outdir, "vegIntake-uc-soft.RDS"))

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(softflare_time, softflare) ~
    Sex + cat + IMD + dqi_tot + BMI + vegIntake_cat +
    frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.uc.df
)

# Display plot and model summary
analysis_result$plot

```

Time to patient-reported flare



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.6437	1.2249	2.2056	0.0009
catFC 50-250	1.8196	1.3214	2.5058	0.0002
catFC > 250	2.0643	1.4466	2.9458	0.0001

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	1.3744	0.7202	2.6228	0.3348
IMD3	1.1272	0.5971	2.1278	0.7119
IMD4	1.3313	0.7335	2.4163	0.3468
IMD5	1.1300	0.6274	2.0353	0.6839
dqi_tot	0.9963	0.9824	1.0104	0.6053
BMI	0.9760	0.9473	1.0056	0.1106
vegIntake_cat[5.04,8.43)	1.0931	0.7228	1.6531	0.6731
vegIntake_cat[8.43,13.4)	1.2690	0.8365	1.9251	0.2625
vegIntake_cat[13.4,63.1]	1.2381	0.8002	1.9156	0.3374

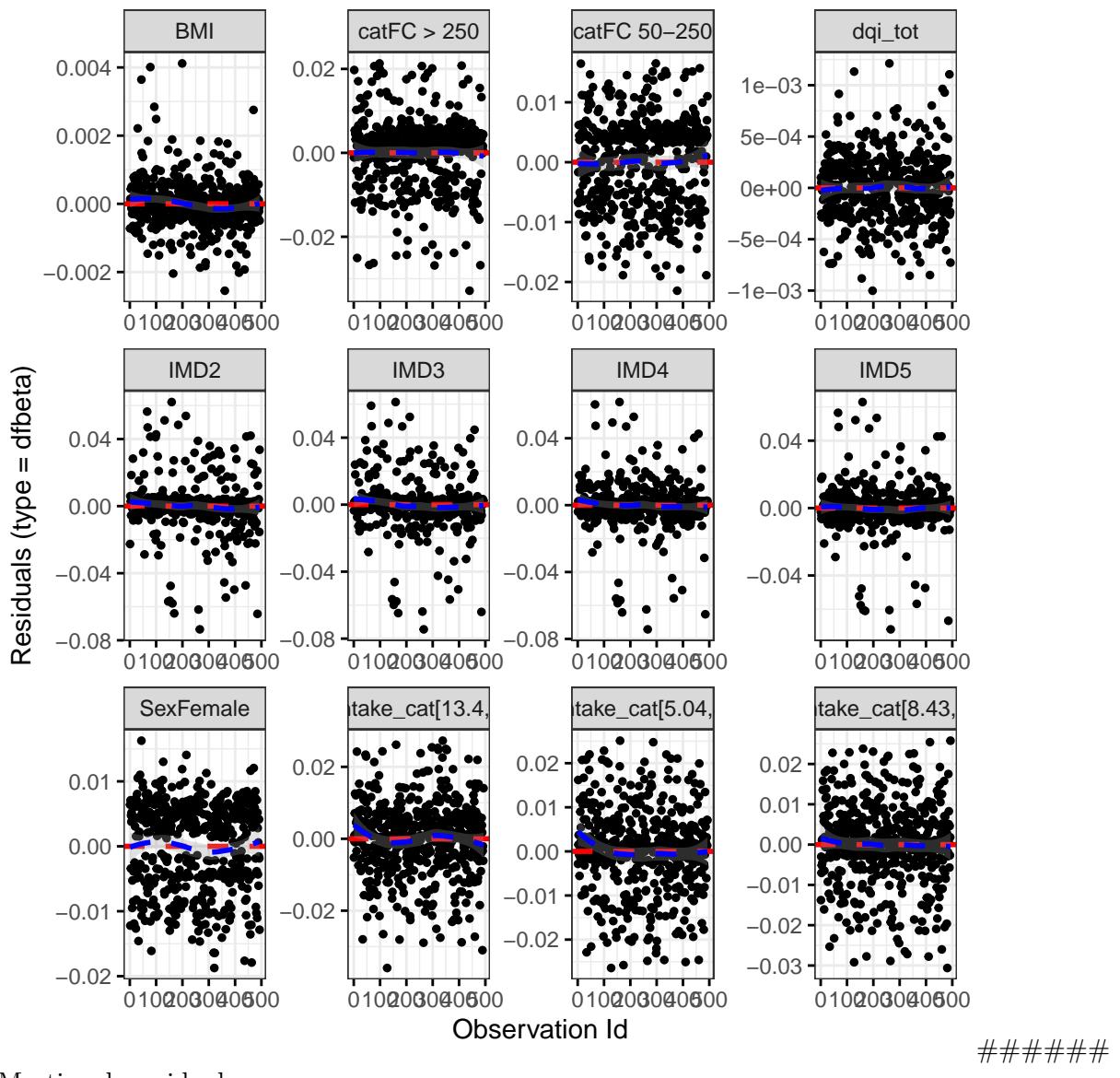
Diagnostics:

Proportional hazards assumption test

	Chi-squared statistic	DF	P-value
Sex	0.0077	1.0000	0.9303
cat	3.5328	2.0000	0.1709
IMD	2.6145	4.0000	0.6243
dqi_tot	0.7308	1.0000	0.3926
BMI	0.9252	1.0000	0.3361
vegIntake_cat	0.1588	3.0000	0.9839
GLOBAL	9.0796	12.0001	0.6961

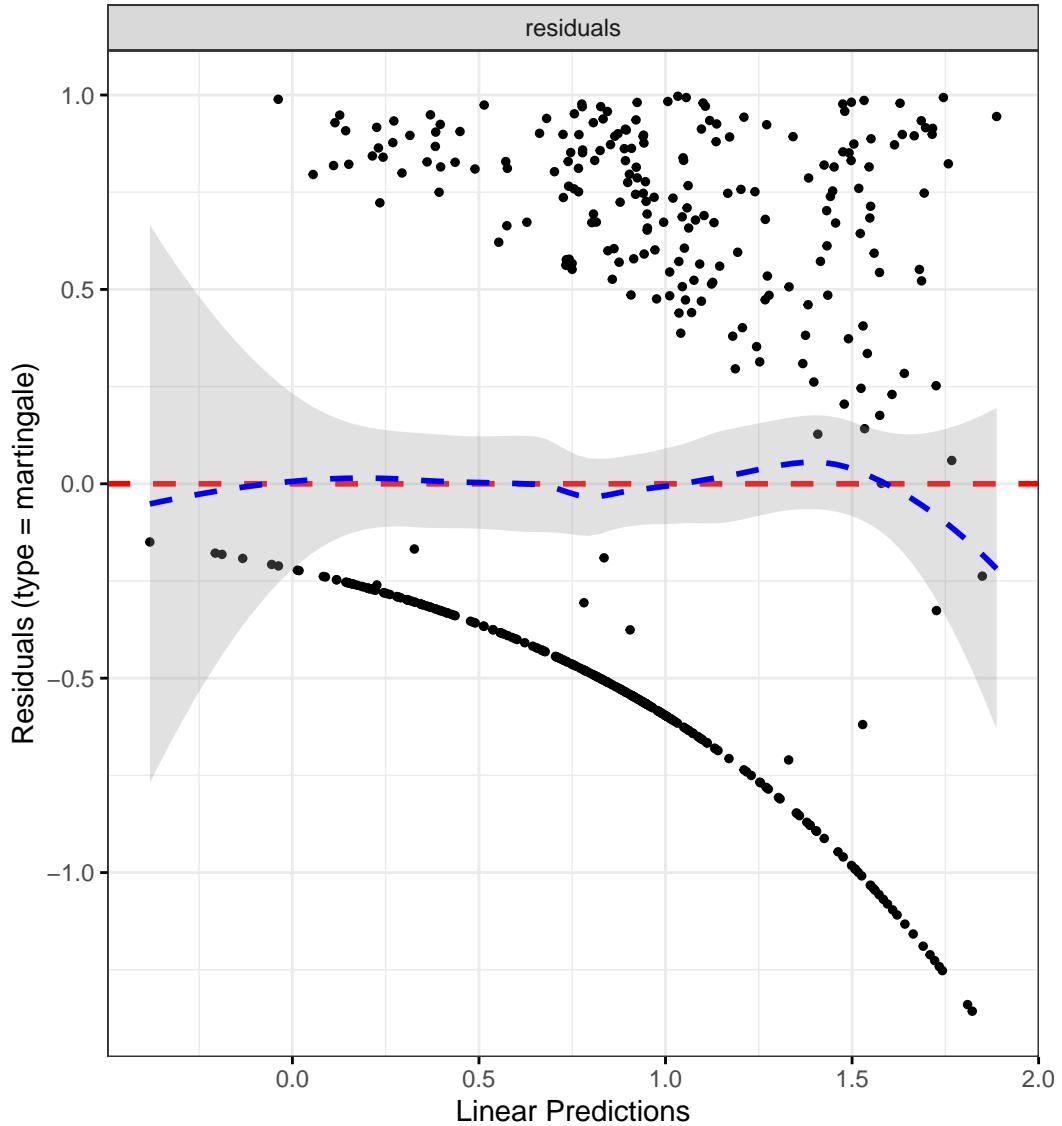
DF betas

```
`geom_smooth()` using formula = 'y ~ x'
```



Martingale residuals

```
`geom_smooth()` using formula = 'y ~ x'
```



Hard flare

```
# Run survival analysis using utility function for hard flare
analysis_result <- run_survival_analysis(
  data = flare.uc.df,
  var_name = "vegIntake",
  outcome_time = "hardflare_time",
  outcome_event = "hardflare",
  legend_title = "Vegetable/legume intake quantiles",
```

```

plot_base_path = "plots/uc/hard-flare/diet/vegIntake",
break_time_by = 500
)

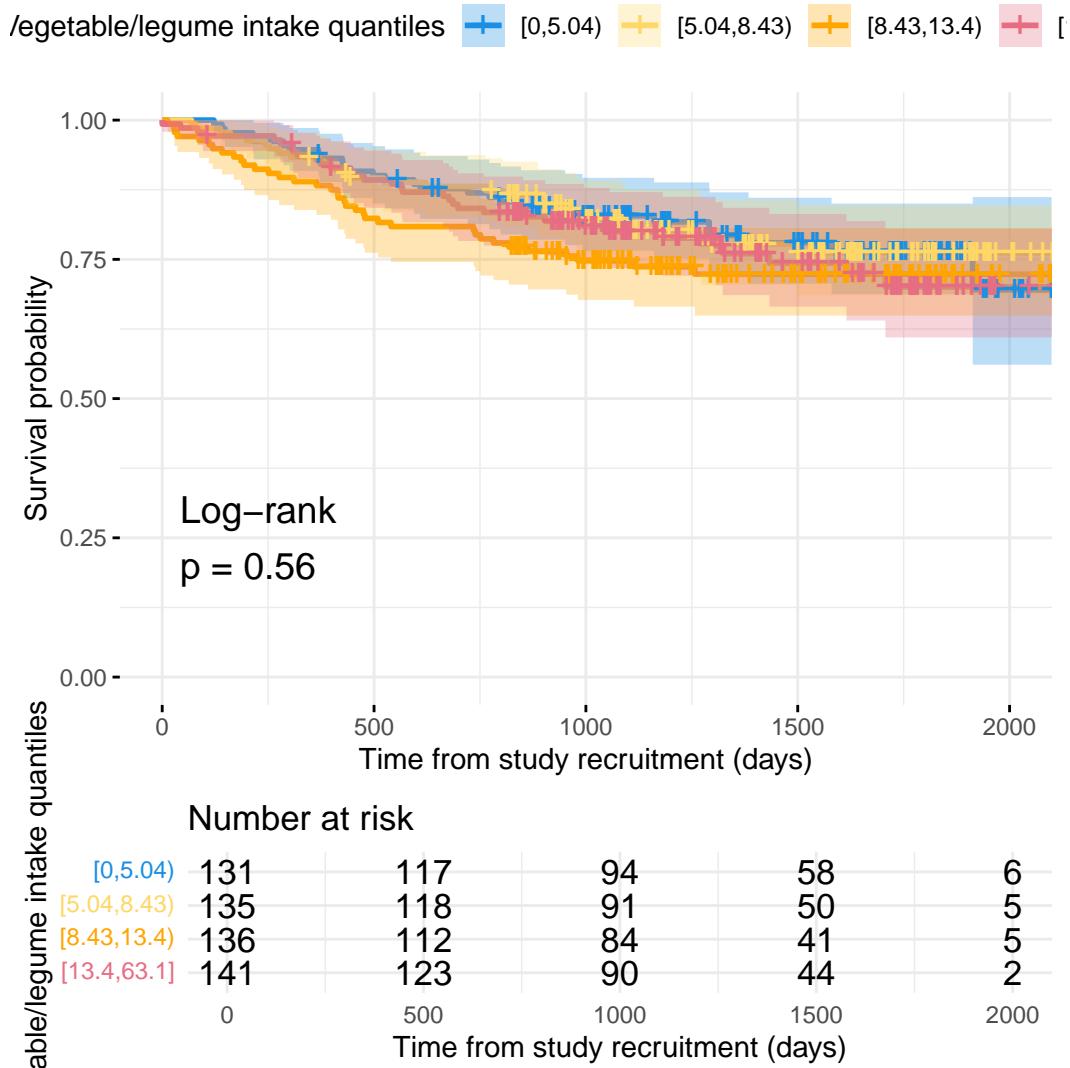
# Save plot as RDS
saveRDS(analysis_result$plot, paste0(paths$outdir, "vegIntake-uc-hard.RDS"))

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(hardflare_time, hardflare) ~
    Sex + cat + IMD + dqi_tot + BMI + vegIntake_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.uc.df
)

# Display plot and model summary
analysis_result$plot

```

Time to hard flare



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.1590	0.7857	1.7097	0.4569
catFC 50-250	2.0402	1.3207	3.1516	0.0013
catFC > 250	2.4817	1.5249	4.0390	0.0003

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	1.5765	0.5956	4.1727	0.3594
IMD3	1.3322	0.5147	3.4479	0.5544
IMD4	2.4411	1.0109	5.8950	0.0473
IMD5	1.3612	0.5603	3.3072	0.4960
dqi_tot	0.9959	0.9769	1.0153	0.6784
BMI	0.9614	0.9219	1.0027	0.0669
vegIntake_cat[5.04,8.43)	1.2609	0.7109	2.2363	0.4279
vegIntake_cat[8.43,13.4)	1.8195	1.0385	3.1880	0.0365
vegIntake_cat[13.4,63.1]	1.4784	0.8126	2.6896	0.2004

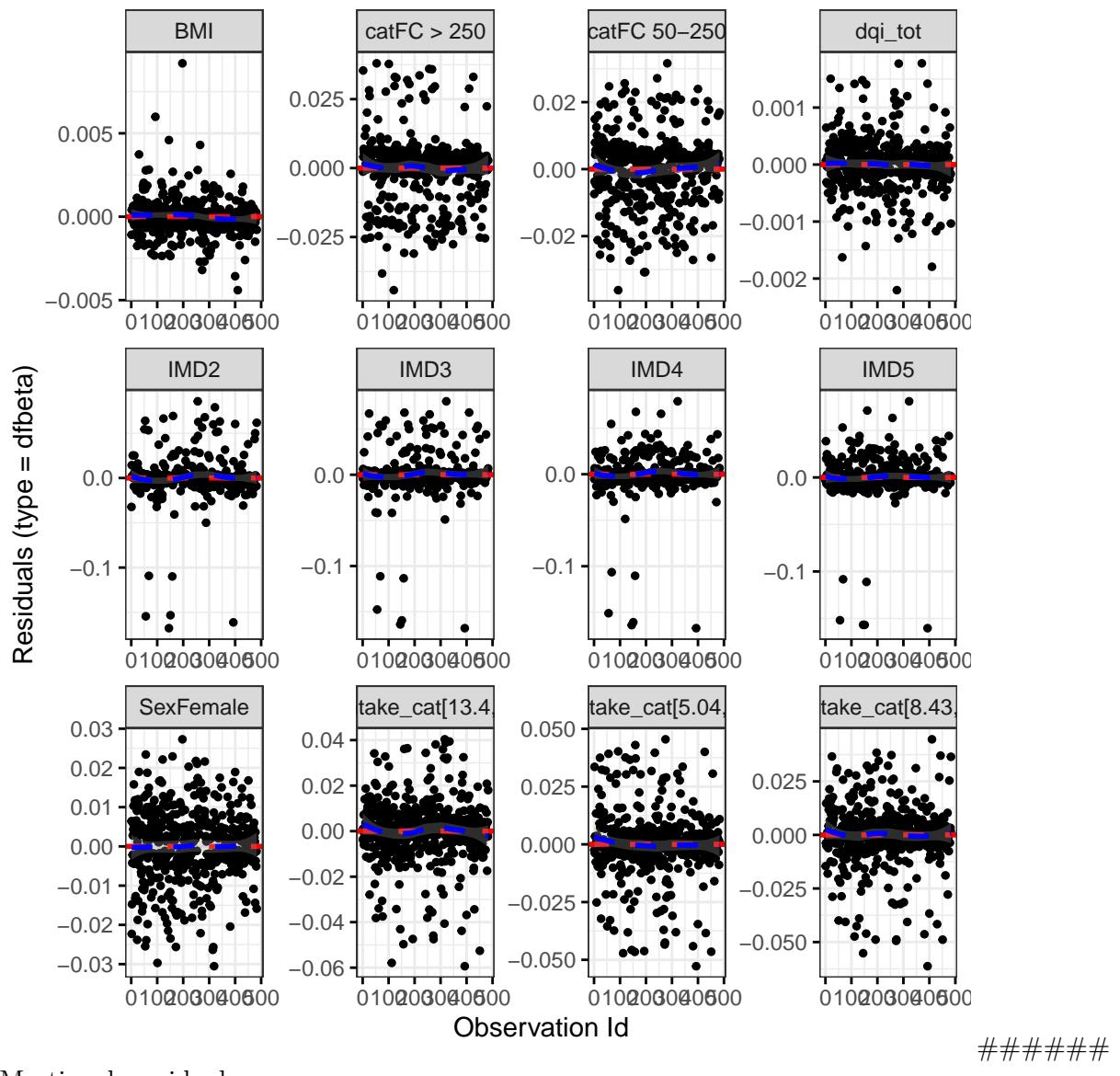
Diagnostics:

Proportional hazards assumption test

	Chi-squared statistic	DF	P-value
Sex	0.0269	0.9888	0.8664
cat	5.3609	1.9584	0.0659
IMD	1.2294	3.9333	0.8668
dqi_tot	0.0000	0.9881	0.9957
BMI	0.5082	0.9880	0.4711
vegIntake_cat	4.4812	2.9426	0.2070
GLOBAL	12.4241	18.9236	0.8638

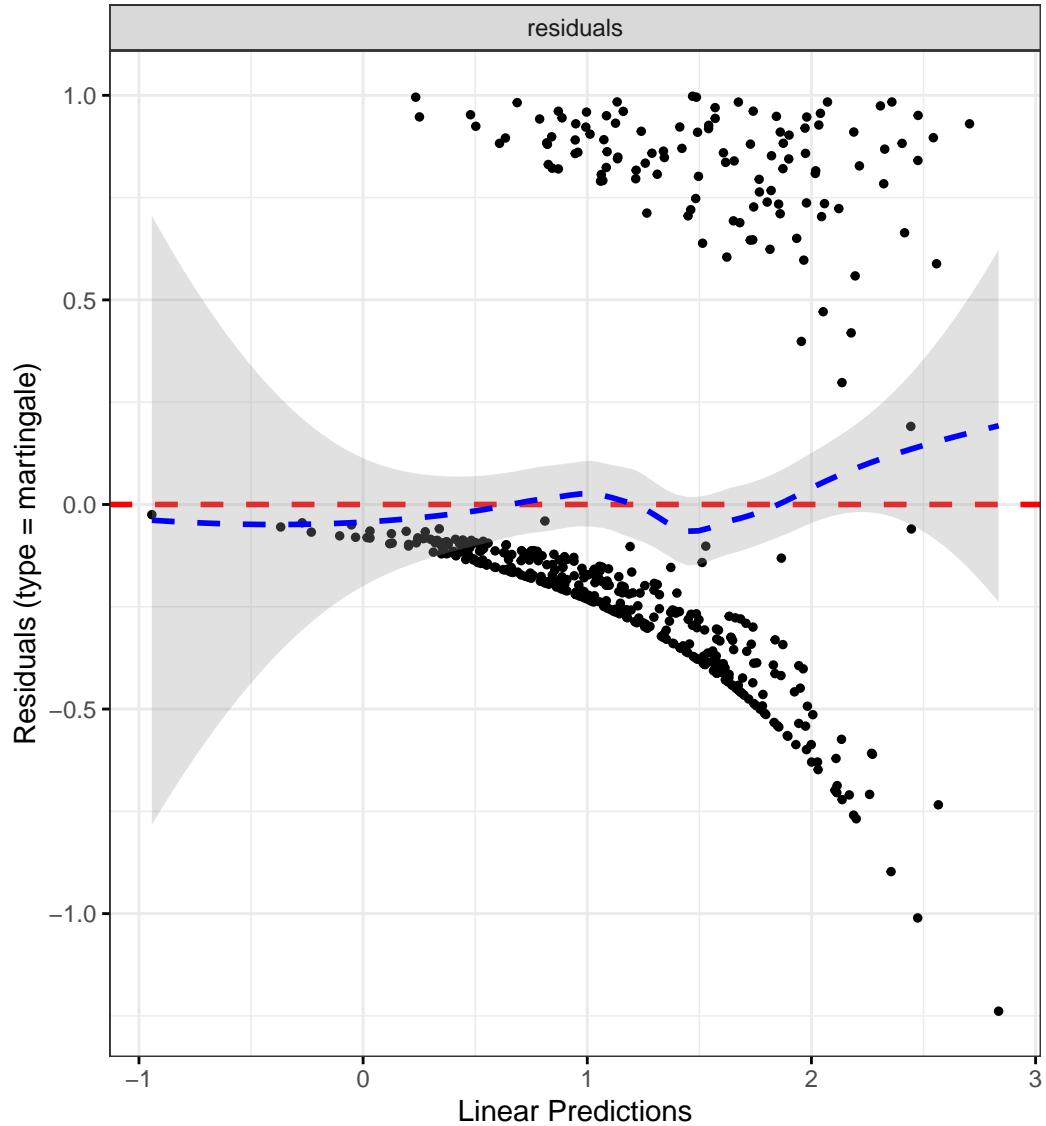
DF betas

```
`geom_smooth()` using formula = 'y ~ x'
```



Martingale residuals

```
`geom_smooth()` using formula = 'y ~ x'
```



Inflammatory bowel disease

Patient-reported flare

```
# Categorize vegetable intake by quantiles
flare.df <- categorize_by_quantiles(flare.df, "vegIntake", reference_data = flare.df)

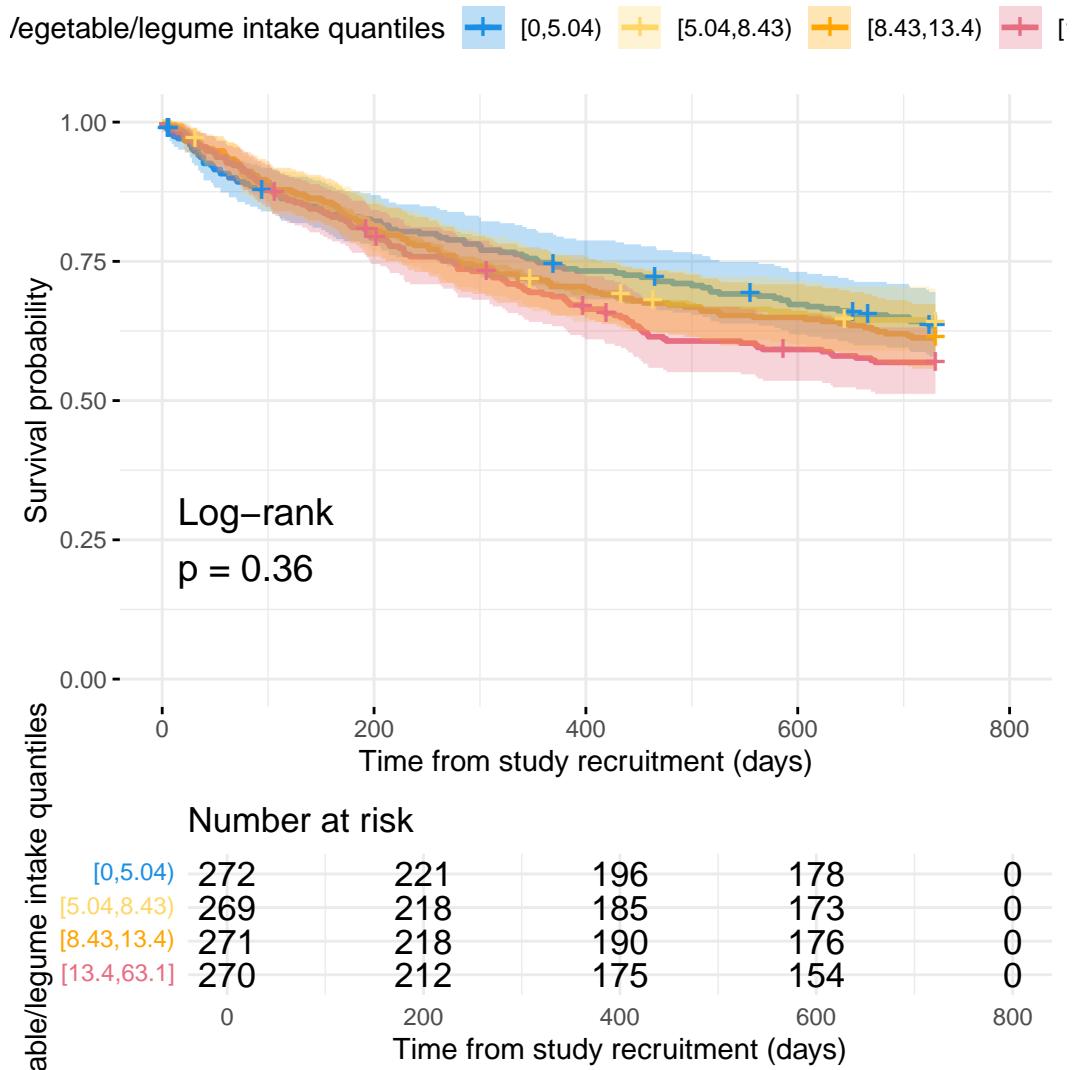
# Run survival analysis using utility function
```

```
analysis_result <- run_survival_analysis(
  data = flare.df,
  var_name = "vegIntake",
  outcome_time = "softflare_time",
  outcome_event = "softflare",
  legend_title = "Vegetable/legume intake quantiles",
  plot_base_path = "plots/ibd/soft-flare/diet/vegIntake",
  break_time_by = 200
)

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(softflare_time, softflare) ~
    Sex + cat + IMD + dqi_tot + BMI + vegIntake_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.df
)

# Display plot and model summary
analysis_result$plot
```

Time to patient-reported flare



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.7538	1.4078	2.1849	0.0000
catFC 50-250	1.5153	1.1992	1.9146	0.0005
catFC > 250	2.0105	1.5525	2.6035	0.0000

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	0.9657	0.6138	1.5195	0.8801
IMD3	0.9971	0.6460	1.5390	0.9895
IMD4	1.0856	0.7164	1.6451	0.6984
IMD5	1.0677	0.7144	1.5959	0.7492
dqi_tot	1.0014	0.9913	1.0117	0.7847
BMI	0.9938	0.9741	1.0138	0.5380
vegIntake_cat[5.04,8.43)	1.0054	0.7469	1.3533	0.9716
vegIntake_cat[8.43,13.4)	0.9993	0.7366	1.3557	0.9964
vegIntake_cat[13.4,63.1]	1.0946	0.7983	1.5010	0.5746

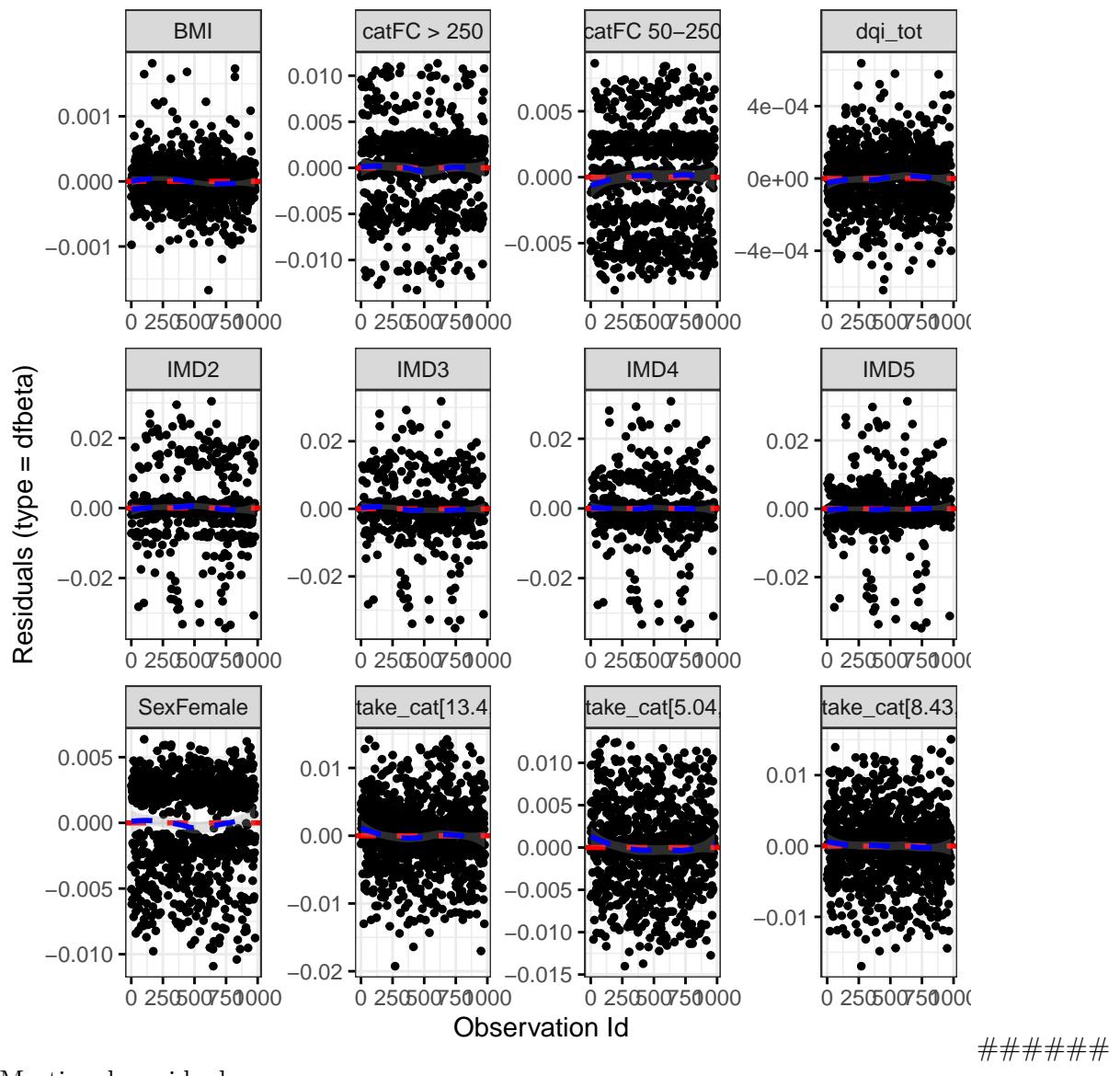
Diagnostics:

Proportional hazards assumption test

	Chi-squared statistic	DF	P-value
Sex	0.0050	1.0000	0.9435
cat	1.0871	2.0000	0.5807
IMD	5.0962	4.0000	0.2776
dqi_tot	1.3847	1.0000	0.2393
BMI	0.0088	1.0000	0.9254
vegIntake_cat	2.2038	3.0000	0.5312
GLOBAL	9.6259	12.0002	0.6488

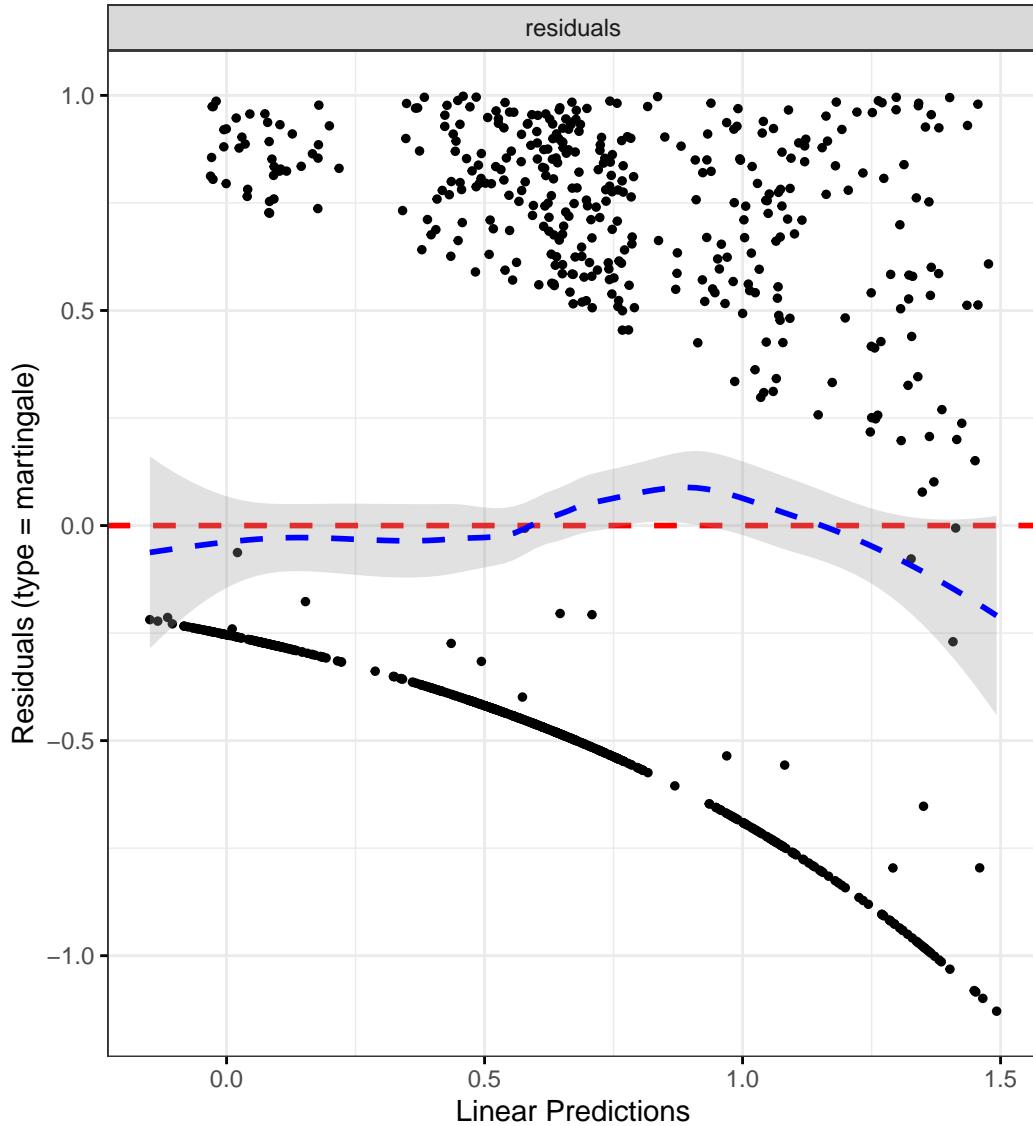
DF betas

```
`geom_smooth()` using formula = 'y ~ x'
```



Martingale residuals

```
`geom_smooth()` using formula = 'y ~ x'
```



Hard flare

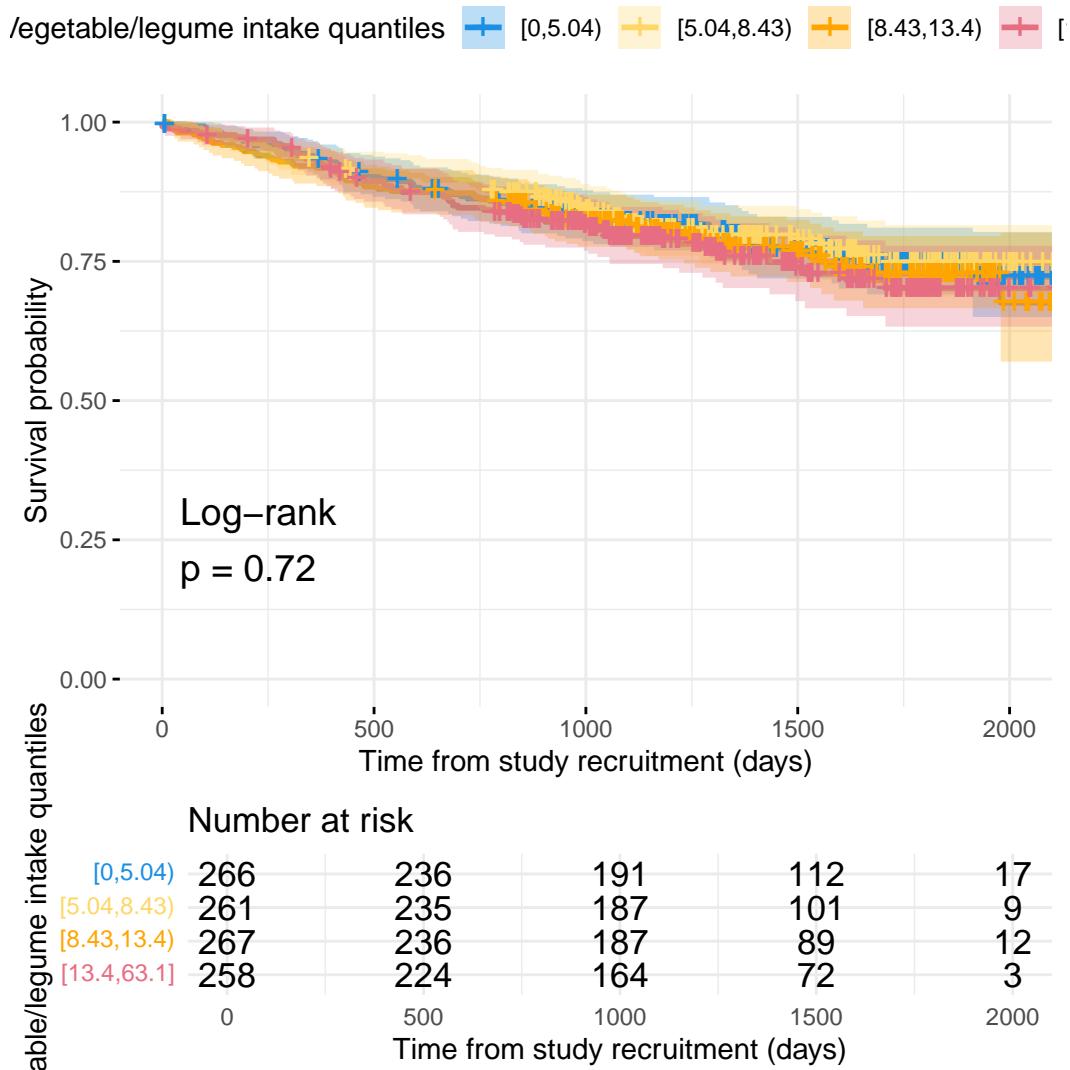
```
# Run survival analysis using utility function for hard flare
analysis_result <- run_survival_analysis(
  data = flare.df,
  var_name = "vegIntake",
  outcome_time = "hardflare_time",
  outcome_event = "hardflare",
  legend_title = "Vegetable/legume intake quantiles",
```

```
plot_base_path = "plots/ibd/hard-flare/diet/vegIntake",
break_time_by = 500
)

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(hardflare_time, hardflare) ~
    Sex + cat + IMD + dqi_tot + BMI + vegIntake_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.df
)

# Display plot and model summary
analysis_result$plot
```

Time to hard flare



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.1993	0.9045	1.5902	0.2067
catFC 50-250	1.8806	1.3731	2.5758	0.0001
catFC > 250	2.6248	1.8579	3.7082	0.0000

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	0.8961	0.4790	1.6765	0.7314
IMD3	0.9424	0.5168	1.7186	0.8465
IMD4	1.3206	0.7510	2.3225	0.3342
IMD5	0.9518	0.5448	1.6628	0.8621
dqi_tot	0.9980	0.9844	1.0117	0.7710
BMI	0.9912	0.9649	1.0182	0.5205
vegIntake_cat[5.04,8.43)	1.0275	0.6898	1.5306	0.8938
vegIntake_cat[8.43,13.4)	1.1983	0.8025	1.7892	0.3765
vegIntake_cat[13.4,63.1]	1.4011	0.9170	2.1406	0.1189

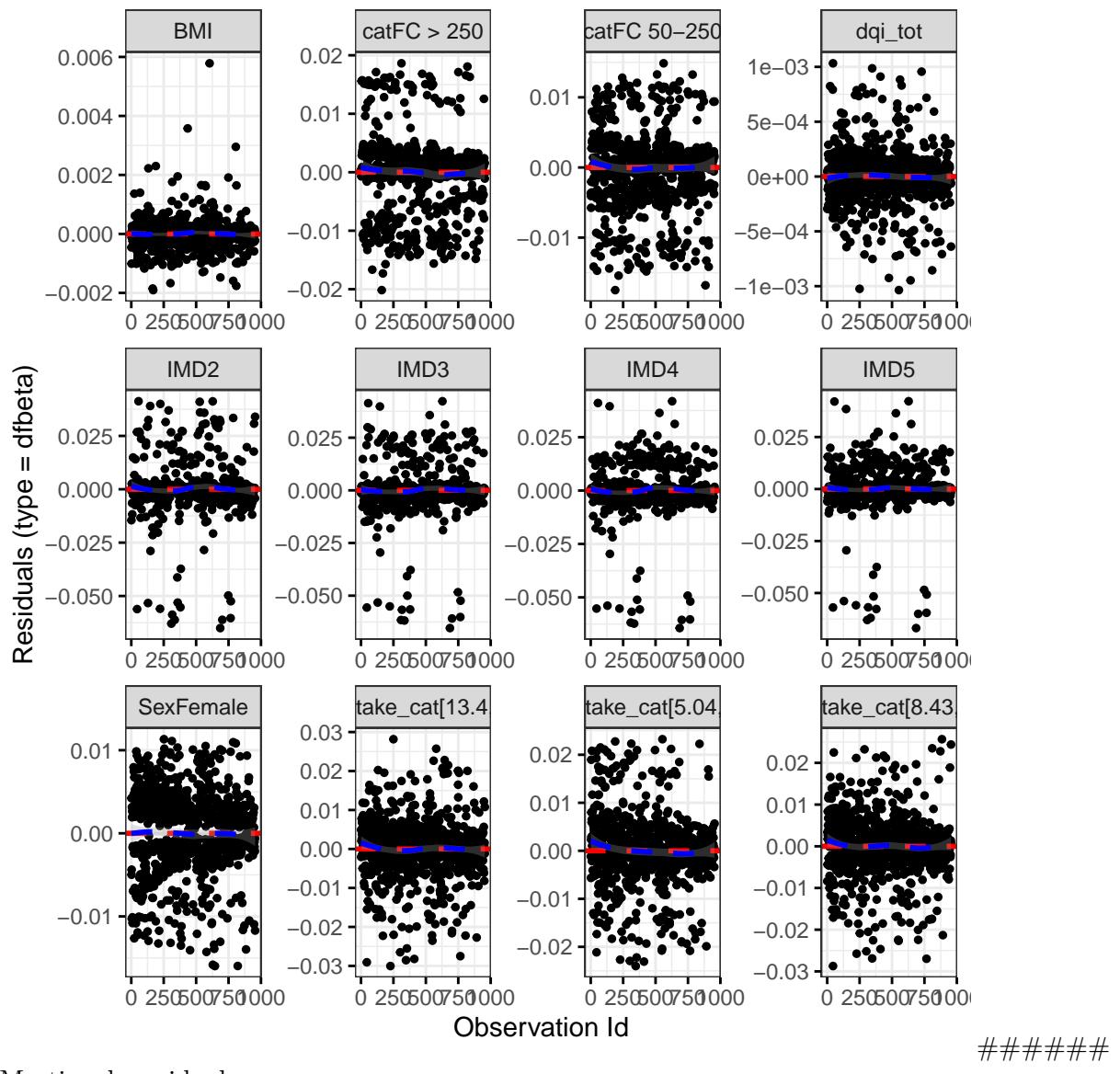
Diagnostics:

Proportional hazards assumption test

	Chi-squared statistic	DF	P-value
Sex	0.0275	0.9885	0.8649
cat	6.9737	1.9790	0.0299
IMD	1.6200	3.9445	0.7984
dqi_tot	2.0266	0.9941	0.1534
BMI	1.8300	0.9887	0.1737
vegIntake_cat	0.5625	2.9674	0.9018
GLOBAL	12.9337	22.7376	0.9491

DF betas

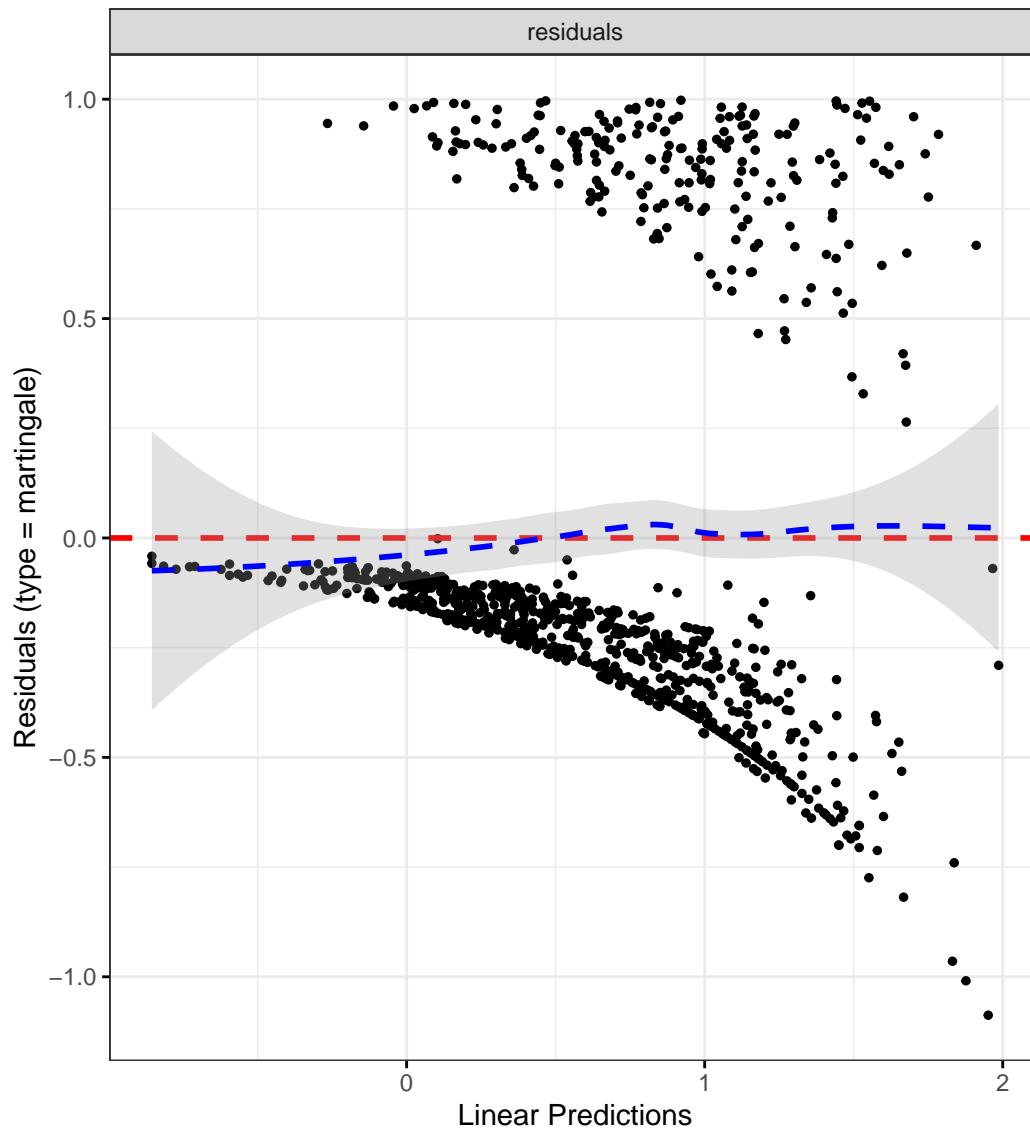
```
`geom_smooth()` using formula = 'y ~ x'
```



#####

Martingale residuals

```
`geom_smooth()` using formula = 'y ~ x'
```



Red meat

Crohn's disease

Patient-reported flare

```
# Categorize red meat intake by quantiles
```

```
flare.cd.df <- categorize_by_quantiles(flare.cd.df, "redMeatIntake", reference_data = flare.
```

```

# Run survival analysis using utility function
analysis_result <- run_survival_analysis(
  data = flare.cd.df,
  var_name = "redMeatIntake",
  outcome_time = "softflare_time",
  outcome_event = "softflare",
  legend_title = "Red meat intake quantiles",
  plot_base_path = "plots/cd/soft-flare/diet/redMeatIntake",
  break_time_by = 200
)

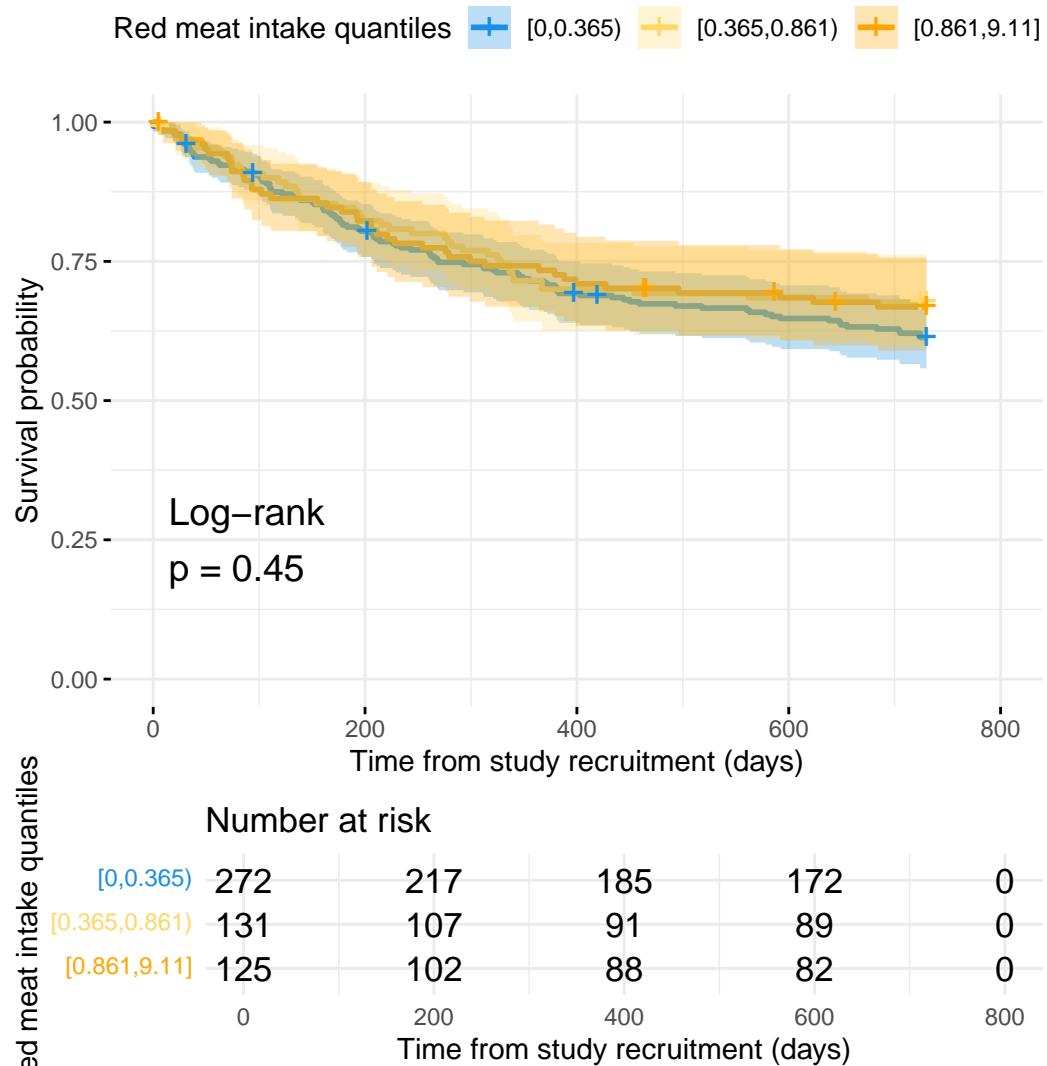
# Save plot as RDS
saveRDS(analysis_result$plot, paste0(paths$outdir, "redMeatIntake-cd-soft.RDS"))

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(softflare_time, softflare) ~
    Sex + cat + IMD + dqi_tot + BMI + redMeatIntake_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.cd.df
)

# Display plot and model summary
analysis_result$plot

```

Time to patient-reported flare



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.8753	1.3428	2.6191	0.0002
catFC 50-250	1.3044	0.9190	1.8513	0.1369
catFC > 250	2.0075	1.3712	2.9391	0.0003

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	0.7102	0.3706	1.3611	0.3025
IMD3	0.9471	0.5196	1.7263	0.8591
IMD4	0.8601	0.4753	1.5563	0.6183
IMD5	1.0063	0.5770	1.7550	0.9824
dqi_tot	1.0057	0.9921	1.0195	0.4115
BMI	1.0080	0.9805	1.0362	0.5723
redMeatIntake_cat[0.365,0	0.8424	0.5779	1.2279	0.3723
redMeatIntake_cat[0.861,9	0.9142	0.6253	1.3365	0.6433

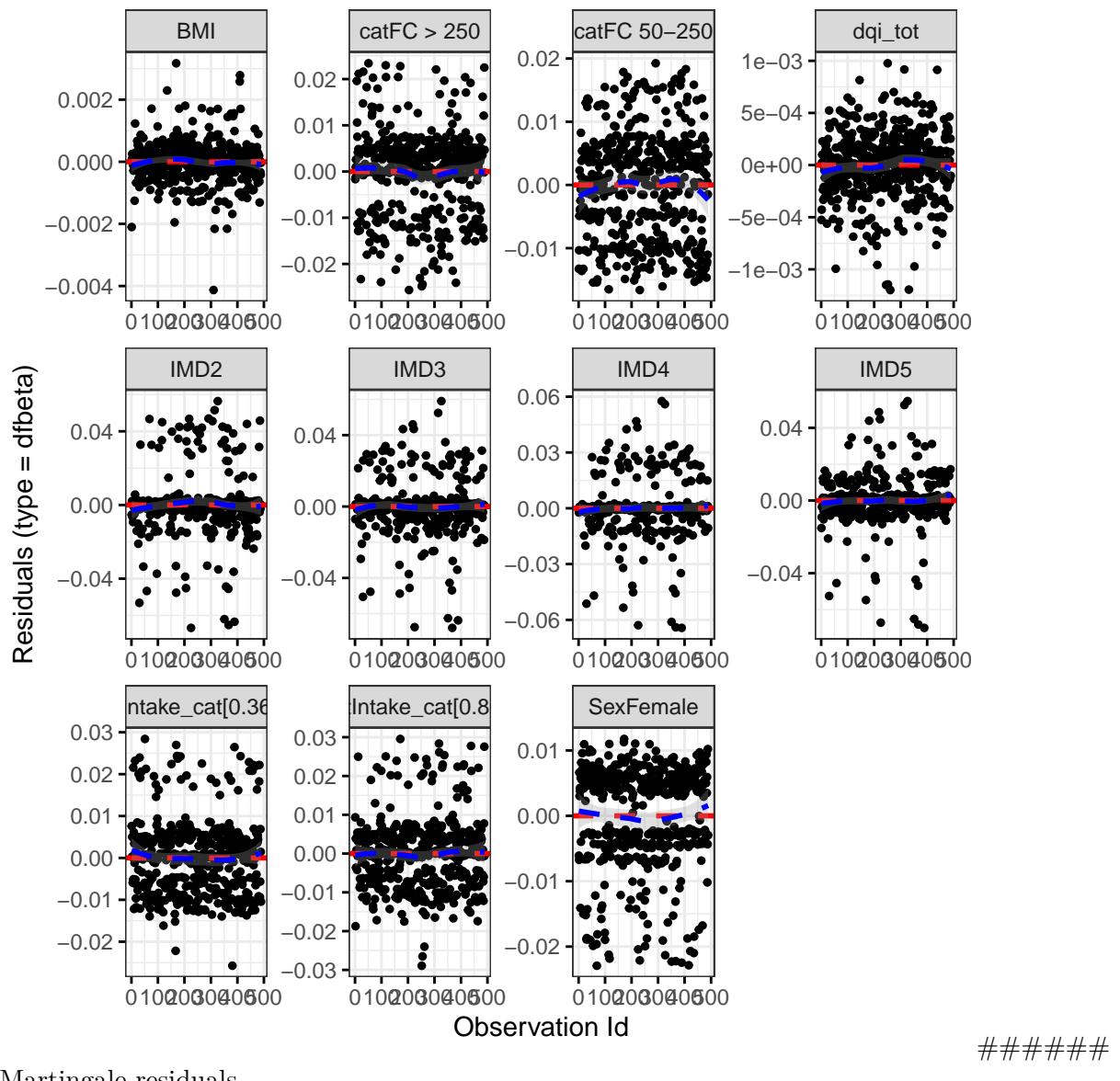
Diagnostics:

Proportional hazards assumption test

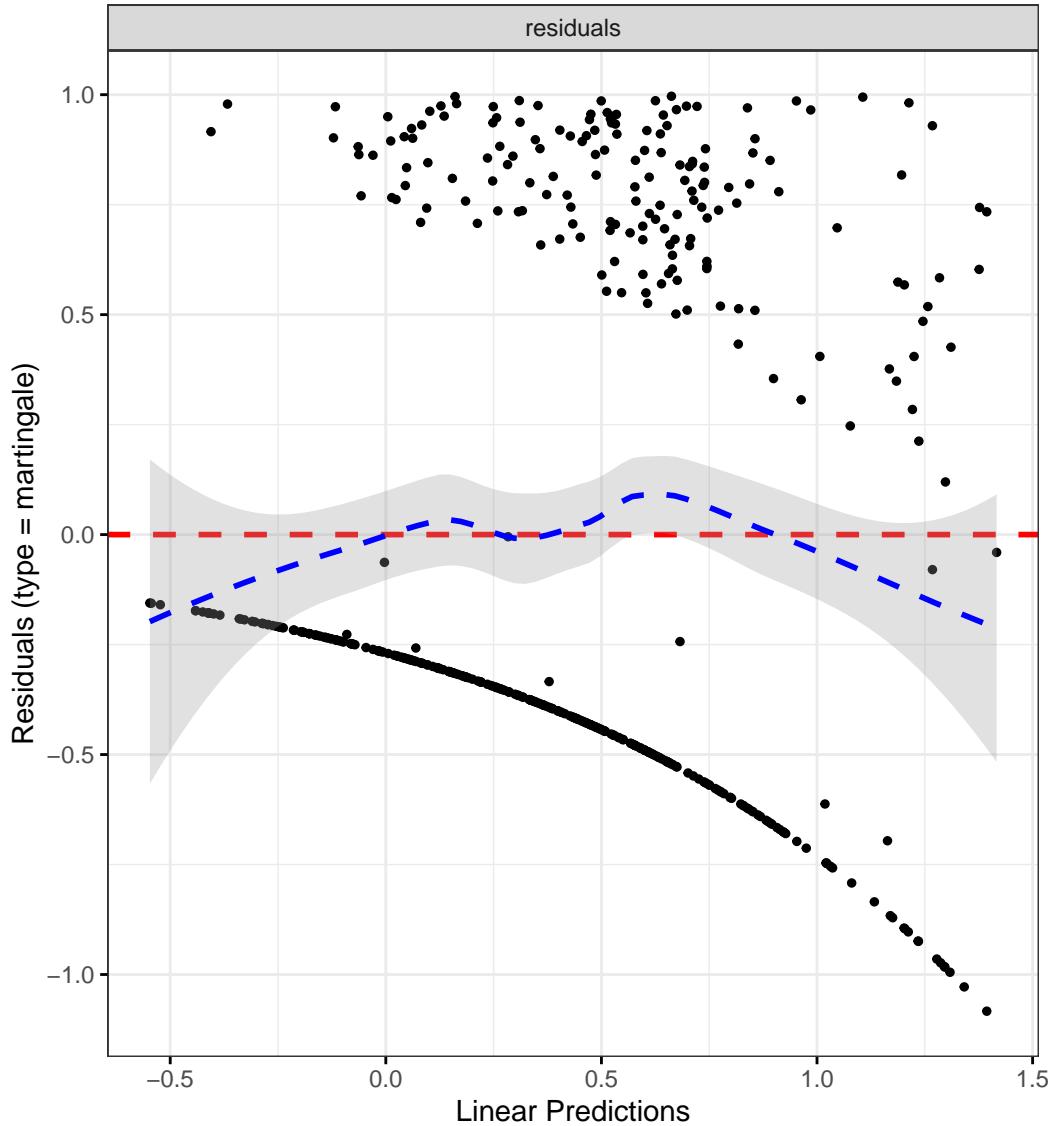
	Chi-squared statistic	DF	P-value
Sex	0.2574	1.0000	0.6119
cat	0.7623	2.0000	0.6831
IMD	3.0114	4.0000	0.5559
dqi_tot	0.3696	1.0000	0.5432
BMI	1.2684	1.0000	0.2601
redMeatIntake_cat	1.0317	2.0000	0.5970
GLOBAL	6.0729	11.0001	0.8685

DF betas

```
`geom_smooth()` using formula = 'y ~ x'
```



```
`geom_smooth()` using formula = 'y ~ x'
```



Hard flare

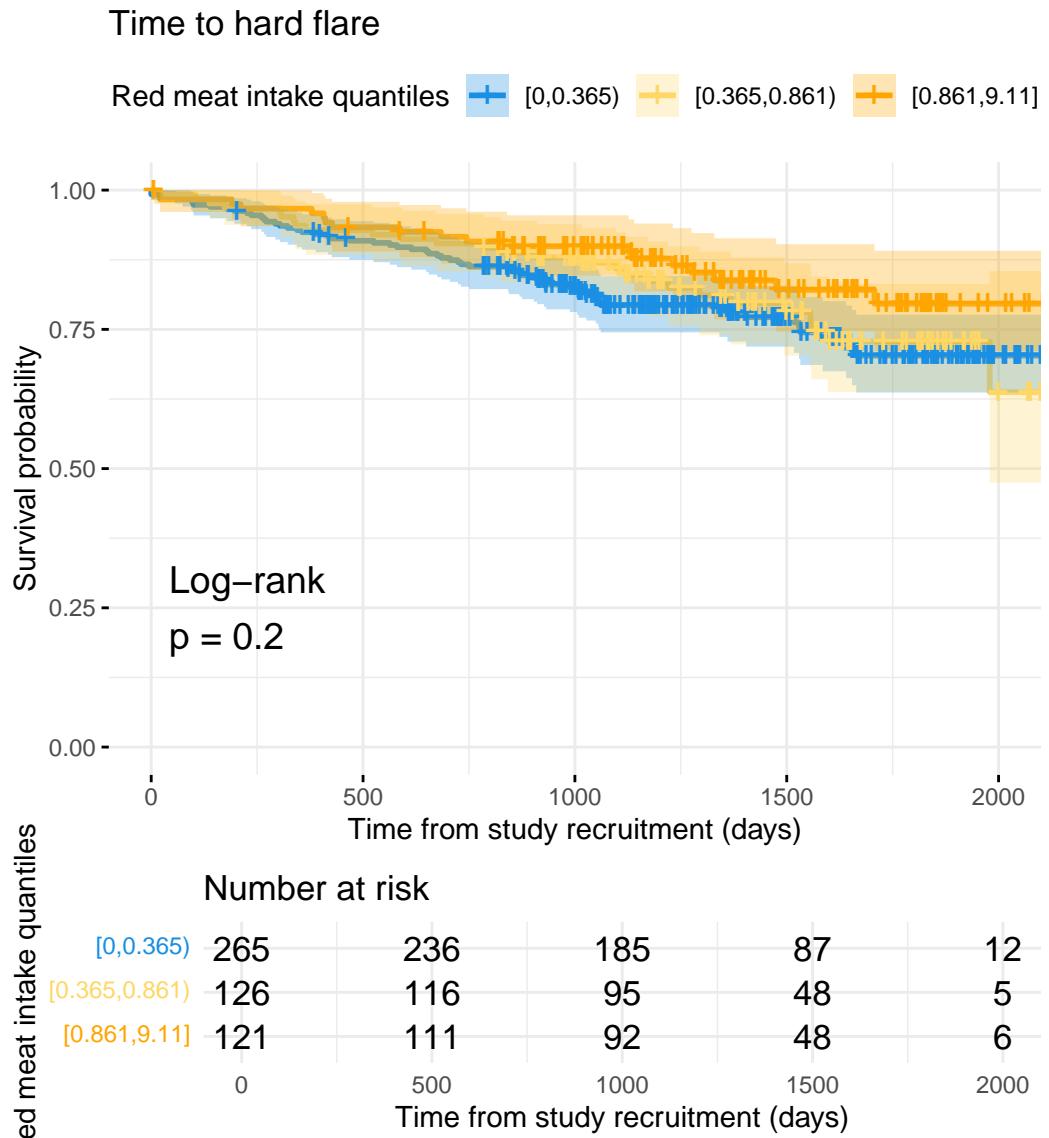
```
# Run survival analysis using utility function for hard flare
analysis_result <- run_survival_analysis(
  data = flare.cd.df,
  var_name = "redMeatIntake",
  outcome_time = "hardflare_time",
  outcome_event = "hardflare",
  legend_title = "Red meat intake quantiles",
```

```
plot_base_path = "plots/cd/hard-flare/diet/redMeatIntake",
break_time_by = 500
)

# Save plot as RDS
saveRDS(analysis_result$plot, paste0(paths$outdir, "redMeatIntake-cd-hard.RDS"))

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(hardflare_time, hardflare) ~
    Sex + cat + IMD + dqi_tot + BMI + redMeatIntake_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.cd.df
)

# Display plot and model summary
analysis_result$plot
```



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.2987	0.8610	1.9588	0.2127
catFC 50-250	1.8671	1.1739	2.9697	0.0084
catFC > 250	2.8795	1.7423	4.7592	0.0000

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	0.6504	0.2809	1.5058	0.3152
IMD3	0.8574	0.3876	1.8966	0.7040
IMD4	0.7642	0.3546	1.6468	0.4924
IMD5	0.7387	0.3565	1.5306	0.4151
dqi_tot	1.0026	0.9849	1.0206	0.7740
BMI	1.0202	0.9842	1.0574	0.2751
redMeatIntake_cat[0.365,0	0.8405	0.5244	1.3473	0.4704
redMeatIntake_cat[0.861,9	0.6369	0.3715	1.0919	0.1009

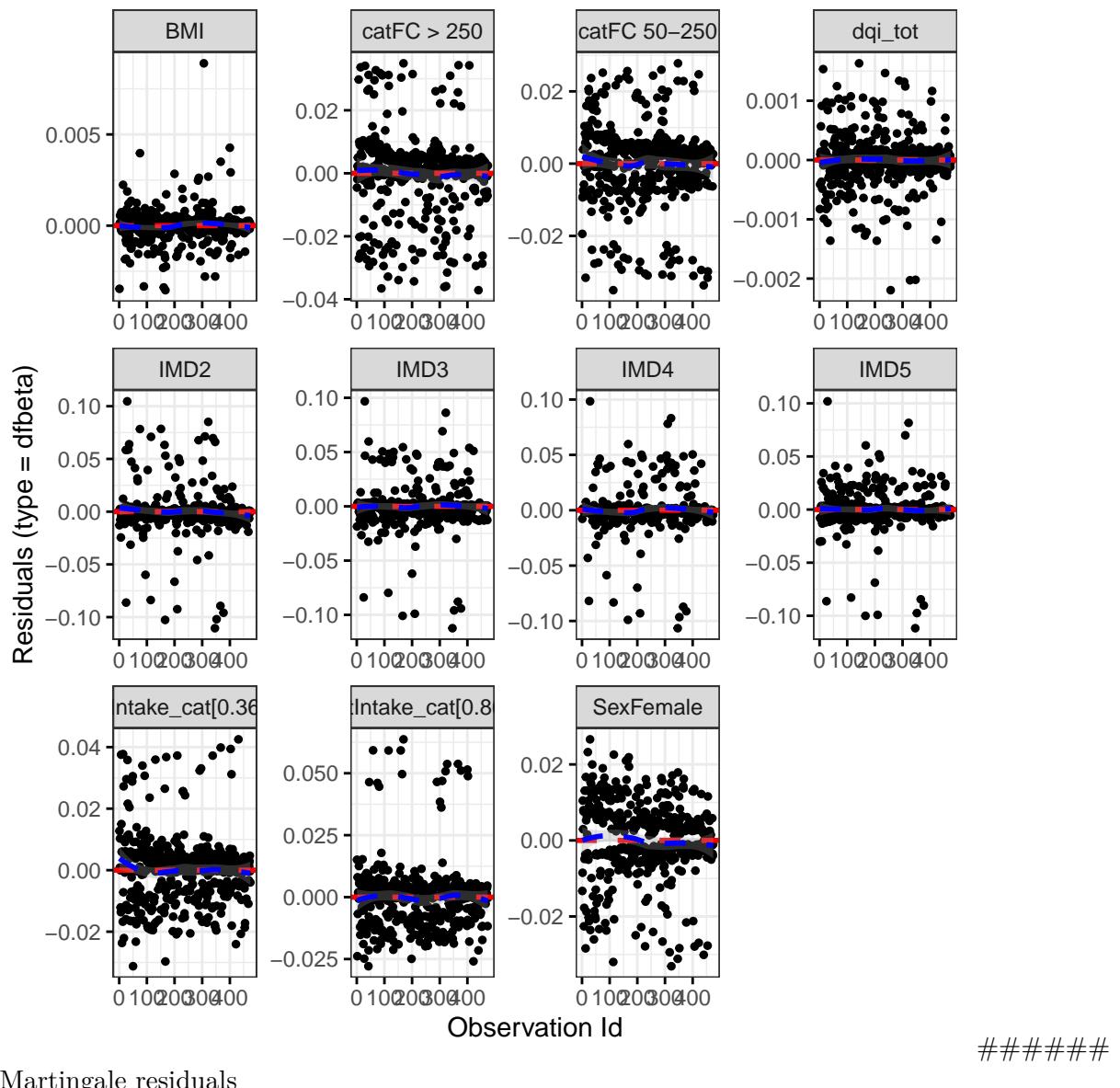
Diagnostics:

Proportional hazards assumption test

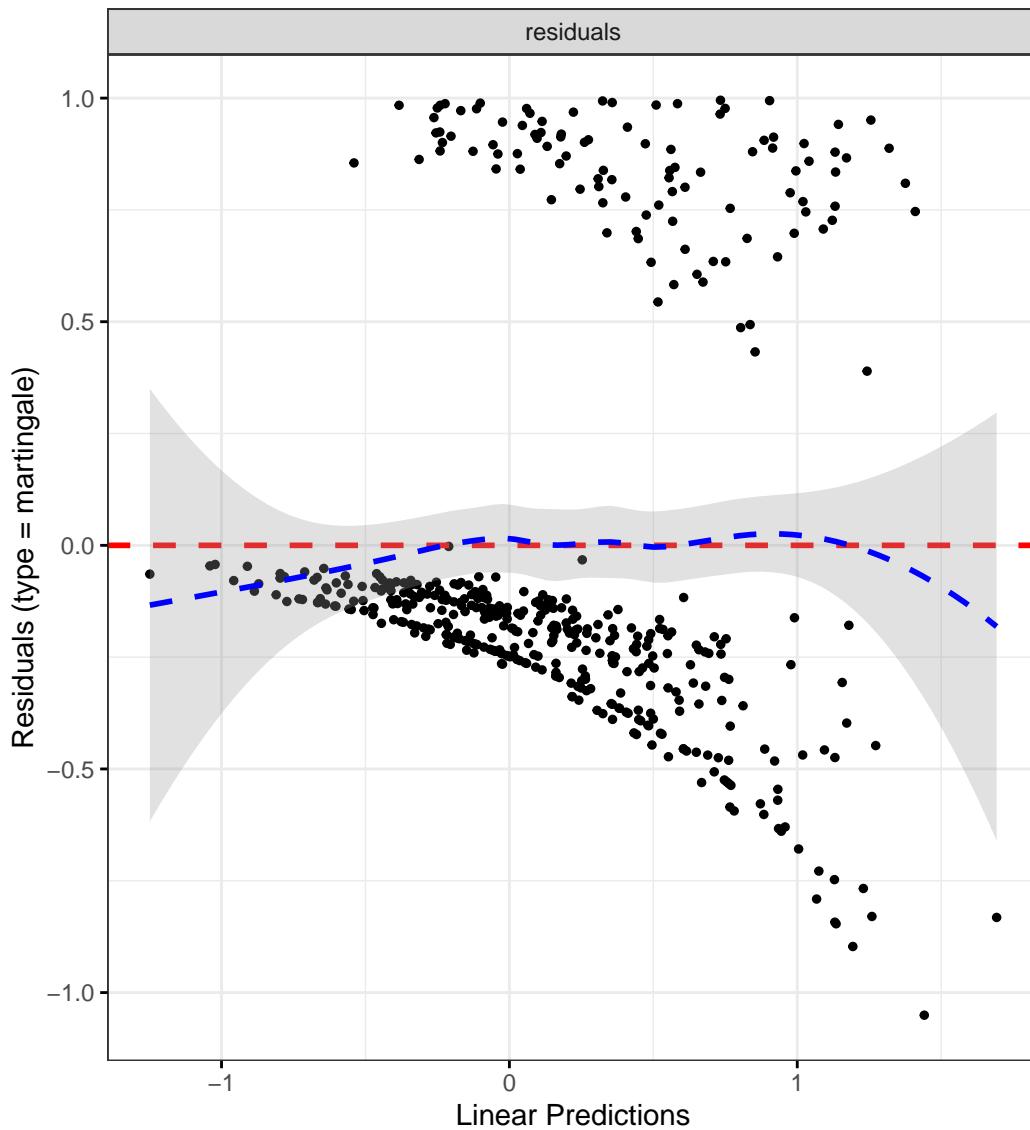
	Chi-squared statistic	DF	P-value
Sex	0.0659	0.9760	0.7888
cat	10.3796	1.9822	0.0055
IMD	2.5244	3.9375	0.6307
dqi_tot	2.6842	0.9914	0.1002
BMI	1.0069	0.9847	0.3107
redMeatIntake_cat	1.6621	1.9696	0.4285
GLOBAL	18.0302	15.9356	0.3181

DF betas

```
`geom_smooth()` using formula = 'y ~ x'
```



```
`geom_smooth()` using formula = 'y ~ x'
```



Ulcerative colitis

Patient-reported flare

```
# Categorize red meat intake by quantiles
flare.uc.df <- categorize_by_quantiles(flare.uc.df, "redMeatIntake", reference_data = flare.o)

# Run survival analysis using utility function
```

```

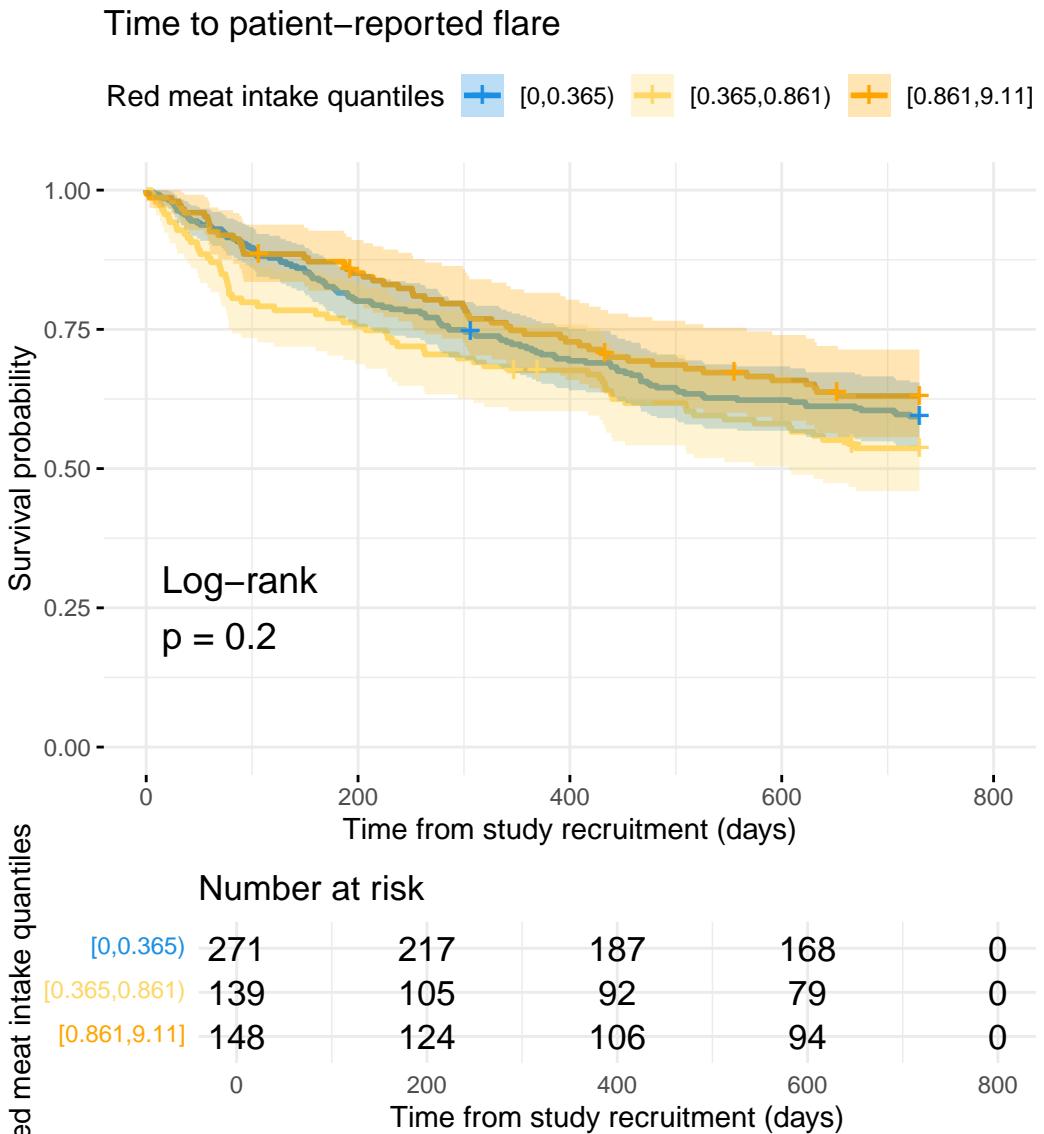
analysis_result <- run_survival_analysis(
  data = flare.uc.df,
  var_name = "redMeatIntake",
  outcome_time = "softflare_time",
  outcome_event = "softflare",
  legend_title = "Red meat intake quantiles",
  plot_base_path = "plots/uc/soft-flare/diet/redMeatIntake",
  break_time_by = 200
)

# Save plot as RDS
saveRDS(analysis_result$plot, paste0(paths$outdir, "redMeatIntake-uc-soft.RDS"))

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(softflare_time, softflare) ~
    Sex + cat + IMD + dqi_tot + BMI + redMeatIntake_cat +
    frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.uc.df
)

# Display plot and model summary
analysis_result$plot

```



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.7023	1.2751	2.2726	0.0003
catFC 50-250	1.7708	1.2882	2.4343	0.0004
catFC > 250	2.0473	1.4331	2.9247	0.0001

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	1.3587	0.7128	2.5898	0.3517
IMD3	1.1233	0.5974	2.1122	0.7182
IMD4	1.3179	0.7280	2.3857	0.3620
IMD5	1.1601	0.6446	2.0875	0.6204
dqi_tot	0.9987	0.9855	1.0120	0.8437
BMI	0.9773	0.9485	1.0070	0.1328
redMeatIntake_cat[0.365,0	1.1968	0.8642	1.6573	0.2796
redMeatIntake_cat[0.861,9	0.9164	0.6424	1.3072	0.6299

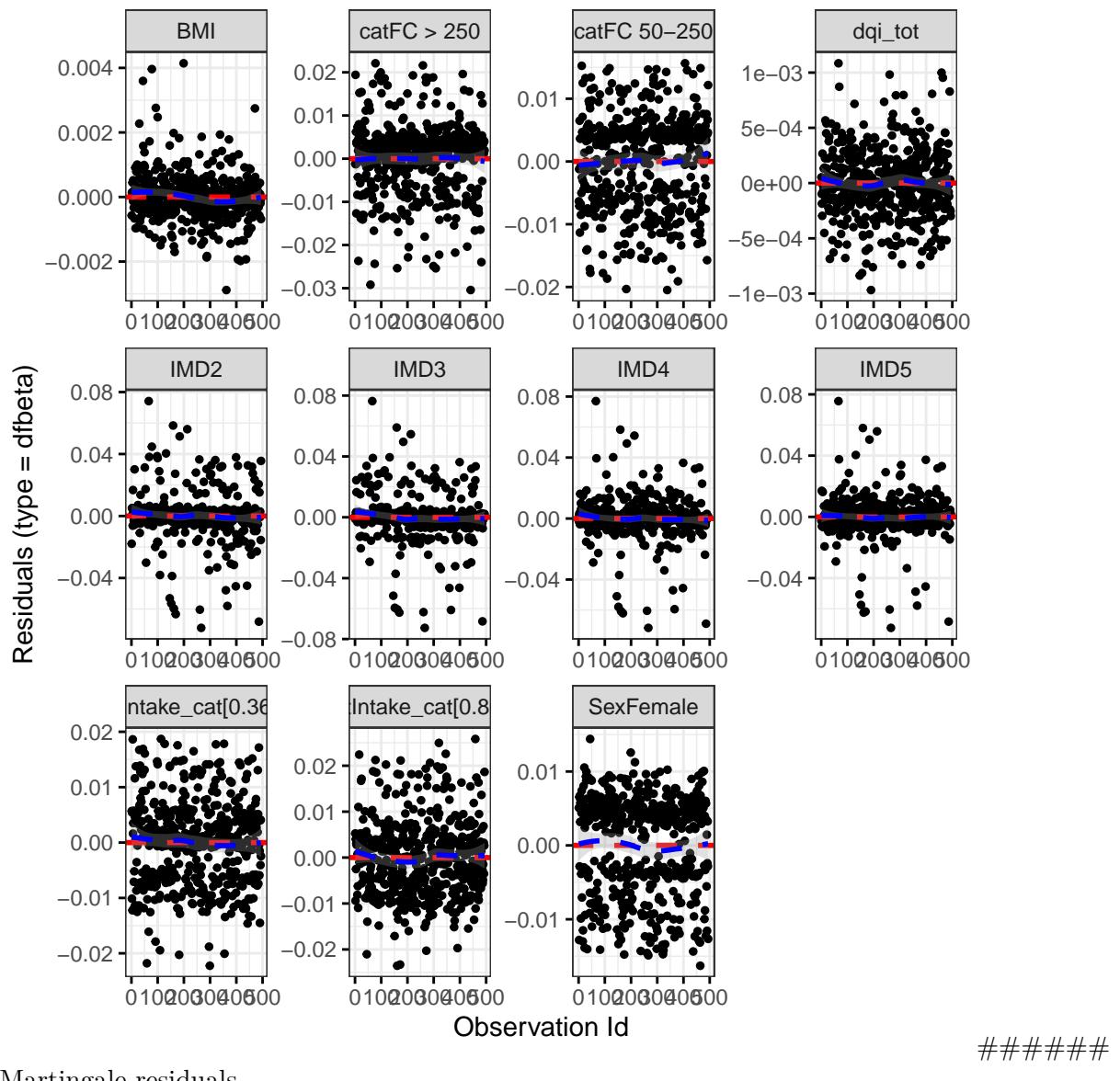
Diagnostics:

Proportional hazards assumption test

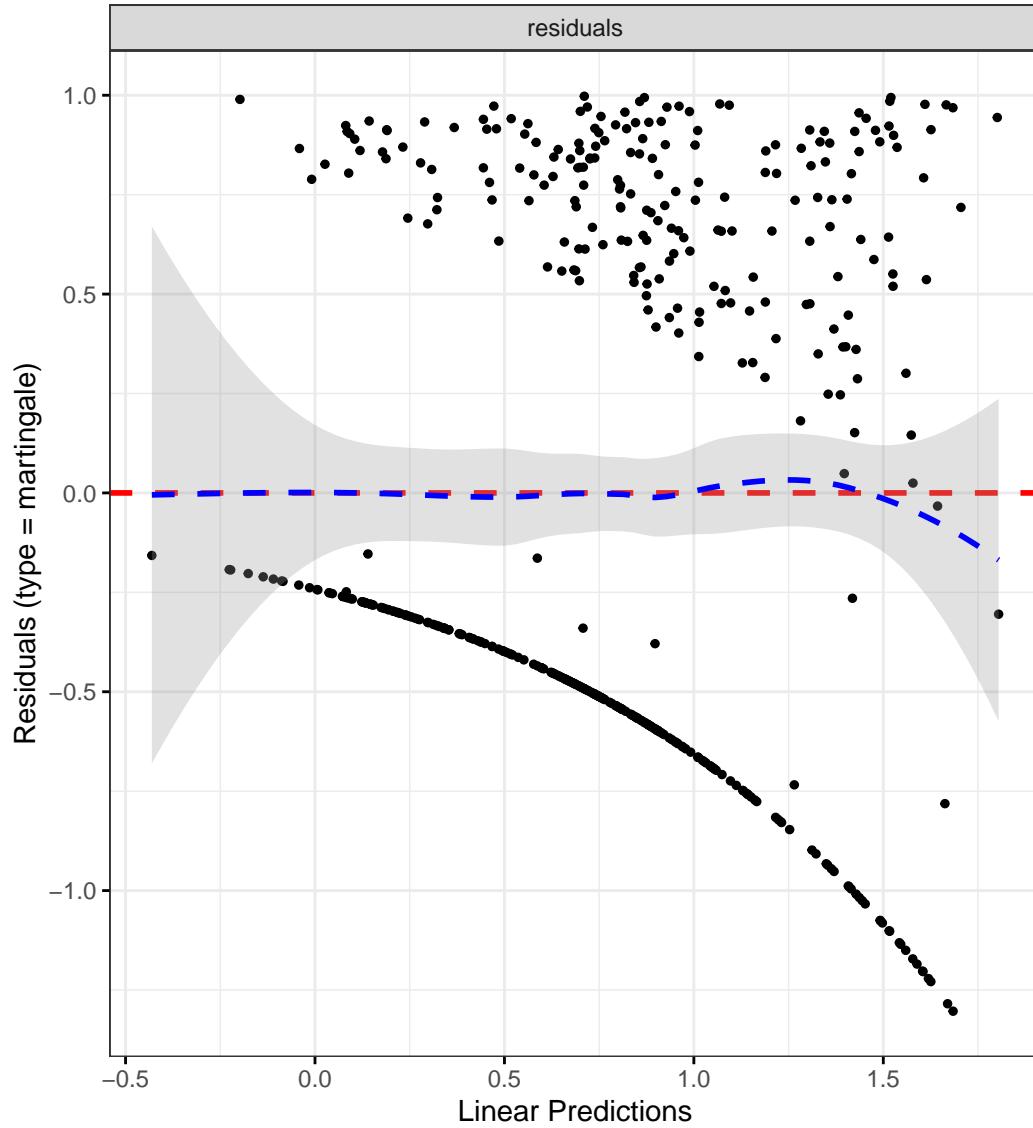
	Chi-squared statistic	DF	P-value
Sex	0.0027	1.0000	0.9587
cat	3.6510	2.0000	0.1611
IMD	2.6642	4.0000	0.6155
dqi_tot	0.7140	1.0000	0.3981
BMI	0.8837	1.0000	0.3472
redMeatIntake_cat	1.2673	2.0000	0.5307
GLOBAL	9.1883	11.0001	0.6045

DF betas

```
`geom_smooth()` using formula = 'y ~ x'
```



```
`geom_smooth()` using formula = 'y ~ x'
```



Hard flare

```
# Run survival analysis using utility function for hard flare
analysis_result <- run_survival_analysis(
  data = flare.uc.df,
  var_name = "redMeatIntake",
  outcome_time = "hardflare_time",
  outcome_event = "hardflare",
  legend_title = "Red meat intake quantiles",
```

```

plot_base_path = "plots/uc/hard-flare/diet/redMeatIntake",
break_time_by = 500
)

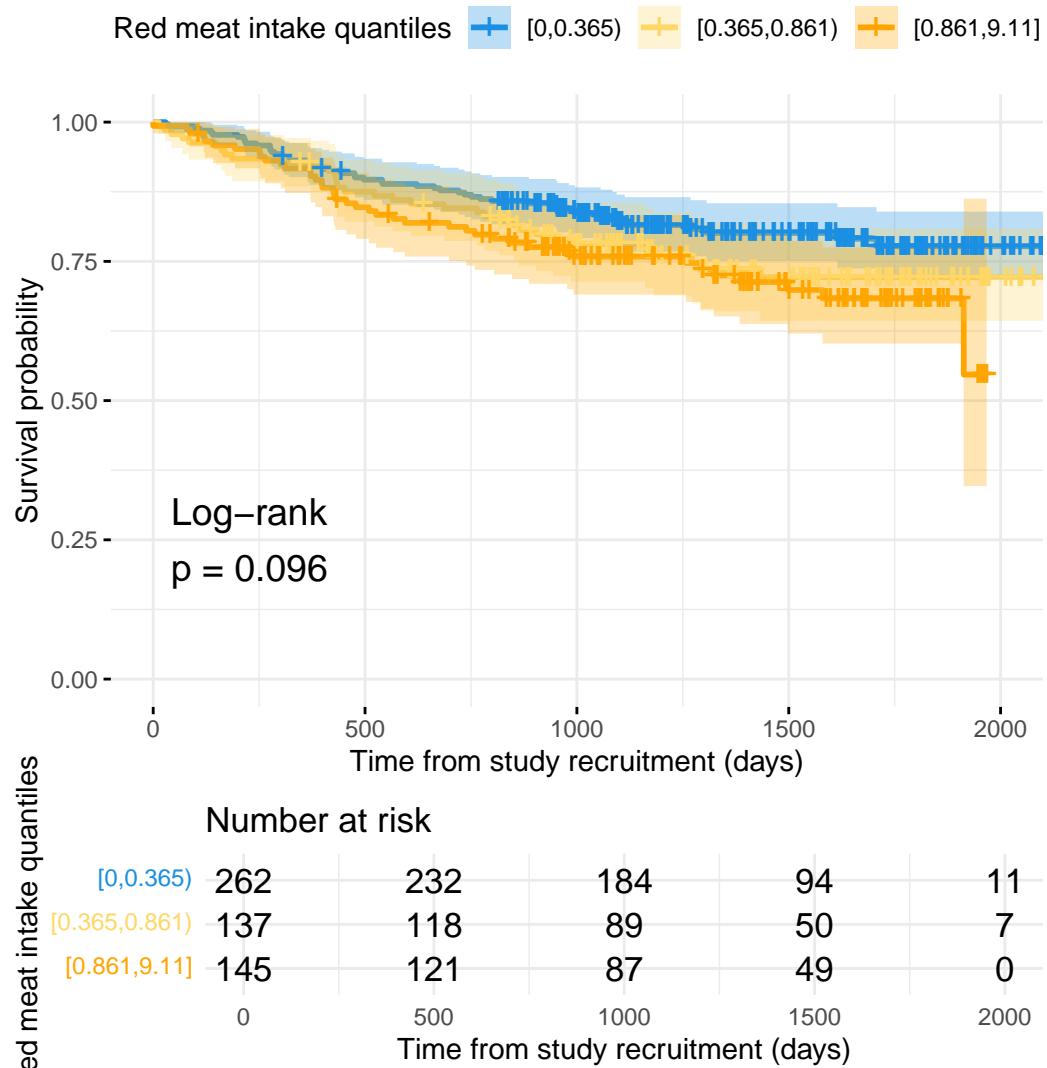
# Save plot as RDS
saveRDS(analysis_result$plot, paste0(paths$outdir, "redMeatIntake-uc-hard.RDS"))

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(hardflare_time, hardflare) ~
    Sex + cat + IMD + dqi_tot + BMI + redMeatIntake_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.uc.df
)

# Display plot and model summary
analysis_result$plot

```

Time to hard flare



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.2067	0.8255	1.7637	0.3320
catFC 50-250	1.9946	1.2929	3.0772	0.0018
catFC > 250	2.4769	1.5176	4.0427	0.0003

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	1.6324	0.6176	4.3146	0.3231
IMD3	1.3157	0.5099	3.3953	0.5705
IMD4	2.3450	0.9787	5.6188	0.0559
IMD5	1.4085	0.5827	3.4048	0.4469
dqi_tot	1.0085	0.9902	1.0270	0.3644
BMI	0.9567	0.9174	0.9978	0.0390
redMeatIntake_cat[0.365,0	1.3080	0.8204	2.0855	0.2592
redMeatIntake_cat[0.861,9	1.8056	1.1496	2.8358	0.0103

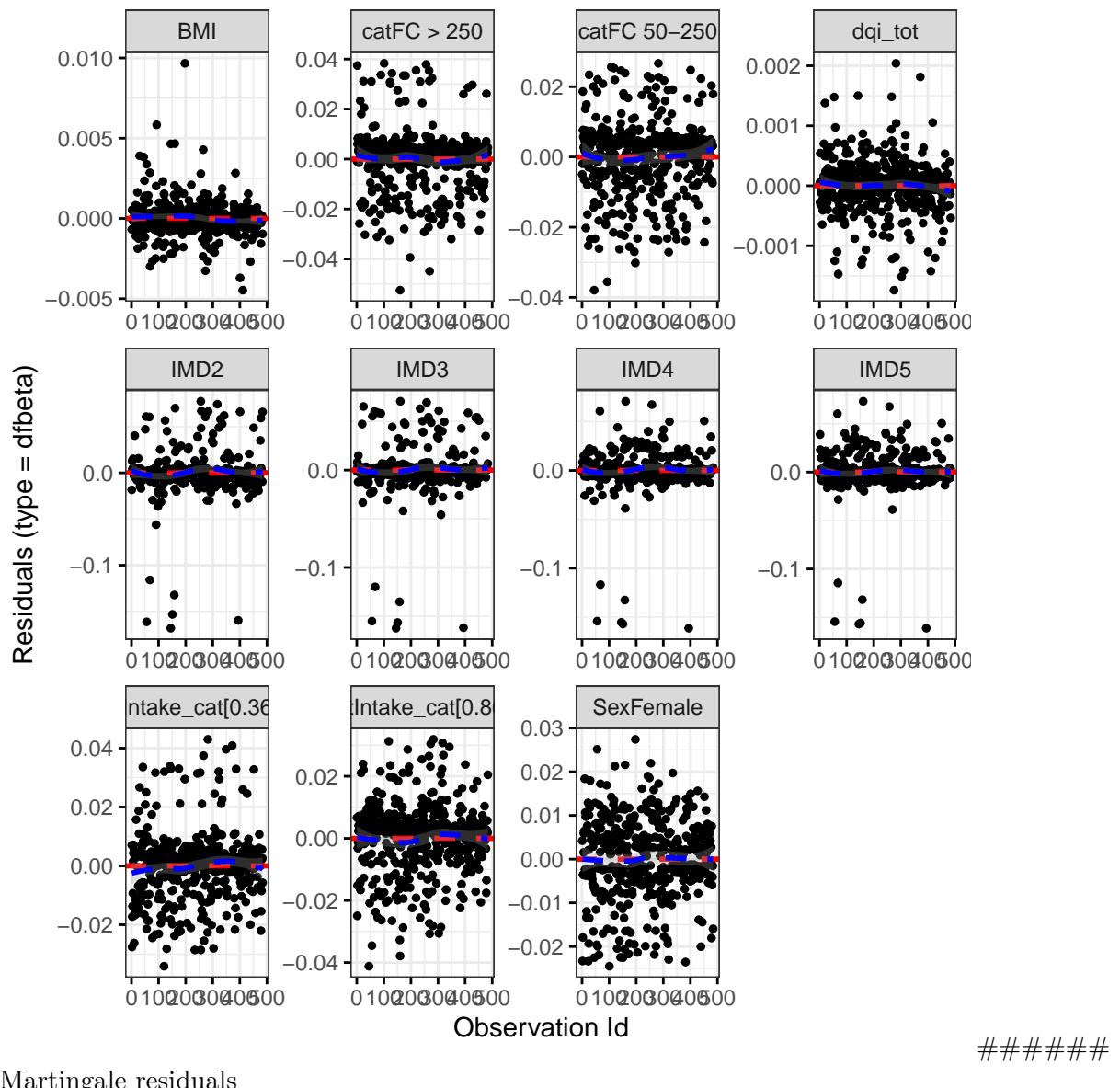
Diagnostics:

Proportional hazards assumption test

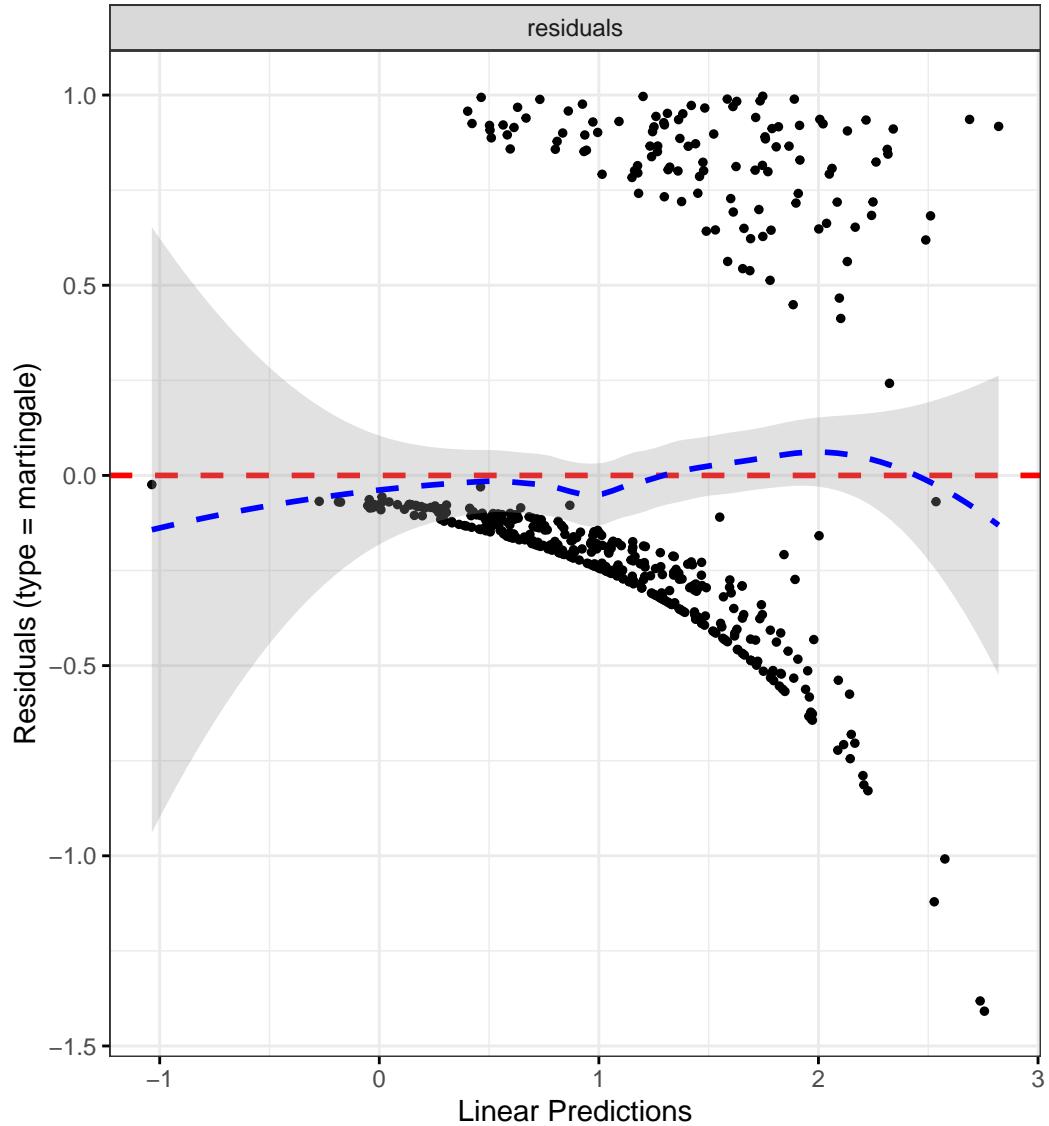
	Chi-squared statistic	DF	P-value
Sex	0.0459	0.9903	0.8271
cat	5.6937	1.9571	0.0557
IMD	1.1733	3.9294	0.8760
dqi_tot	0.0002	0.9859	0.9895
BMI	0.5398	0.9896	0.4584
redMeatIntake_cat	0.0083	1.9747	0.9955
GLOBAL	8.2307	17.8596	0.9734

DF betas

```
`geom_smooth()` using formula = 'y ~ x'
```



```
`geom_smooth()` using formula = 'y ~ x'
```



Inflammatory bowel disease

Patient-reported flare

```
# Categorize red meat intake by quantiles
flare.df <- categorize_by_quantiles(flare.df, "redMeatIntake", reference_data = flare.df)

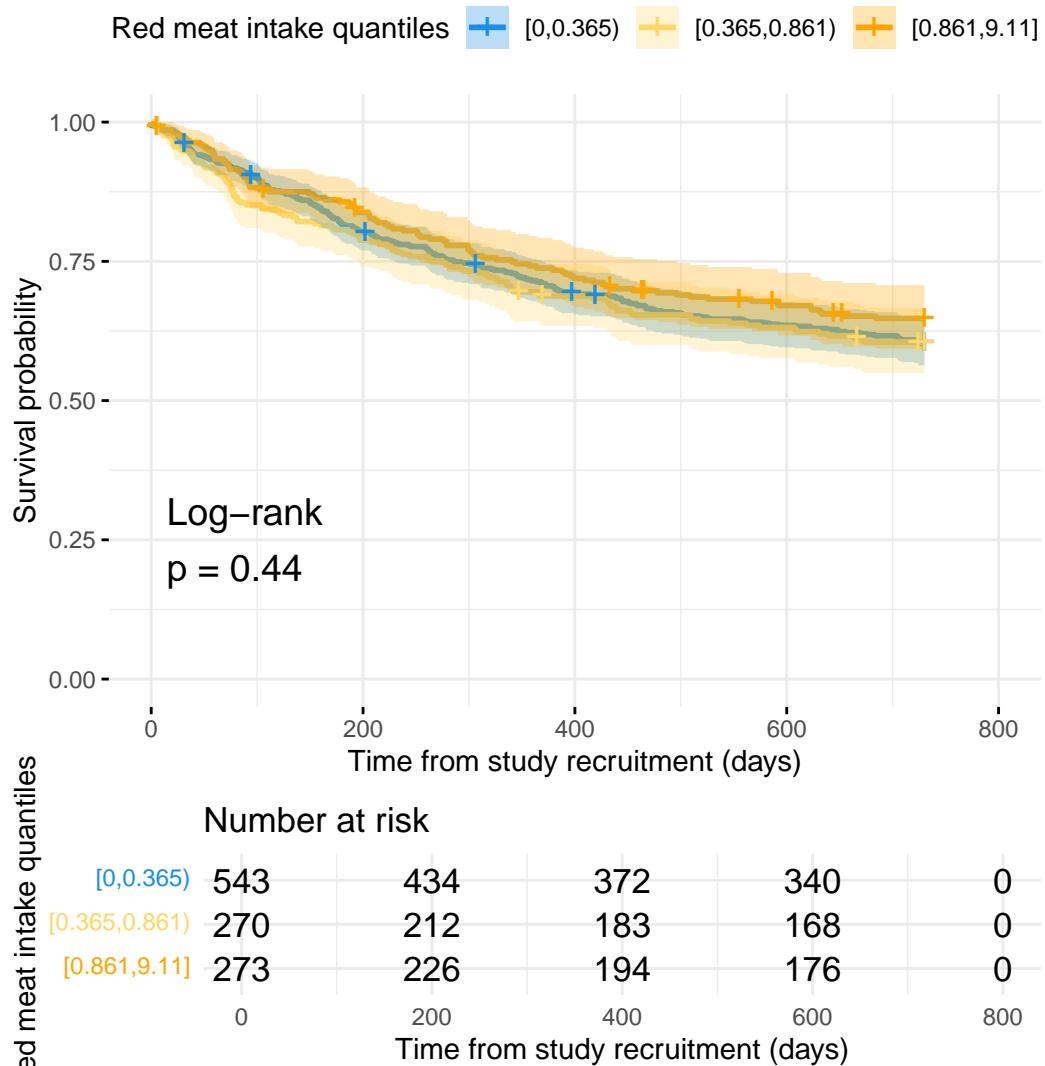
# Run survival analysis using utility function
```

```
analysis_result <- run_survival_analysis(
  data = flare.df,
  var_name = "redMeatIntake",
  outcome_time = "softflare_time",
  outcome_event = "softflare",
  legend_title = "Red meat intake quantiles",
  plot_base_path = "plots/ibd/soft-flare/diet/redMeatIntake",
  break_time_by = 200
)

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(softflare_time, softflare) ~
    Sex + cat + IMD + dqi_tot + BMI + redMeatIntake_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.df
)

# Display plot and model summary
analysis_result$plot
```

Time to patient-reported flare



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.7739	1.4304	2.1998	0.0000
catFC 50-250	1.4981	1.1860	1.8924	0.0007
catFC > 250	2.0132	1.5542	2.6076	0.0000

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	0.9808	0.6235	1.5427	0.9330
IMD3	1.0026	0.6497	1.5472	0.9906
IMD4	1.0998	0.7261	1.6658	0.6534
IMD5	1.0726	0.7180	1.6025	0.7321
dqi_tot	1.0022	0.9928	1.0116	0.6521
BMI	0.9951	0.9754	1.0152	0.6295
redMeatIntake_cat[0.365,0	1.0340	0.8098	1.3202	0.7888
redMeatIntake_cat[0.861,9	0.9216	0.7134	1.1905	0.5320

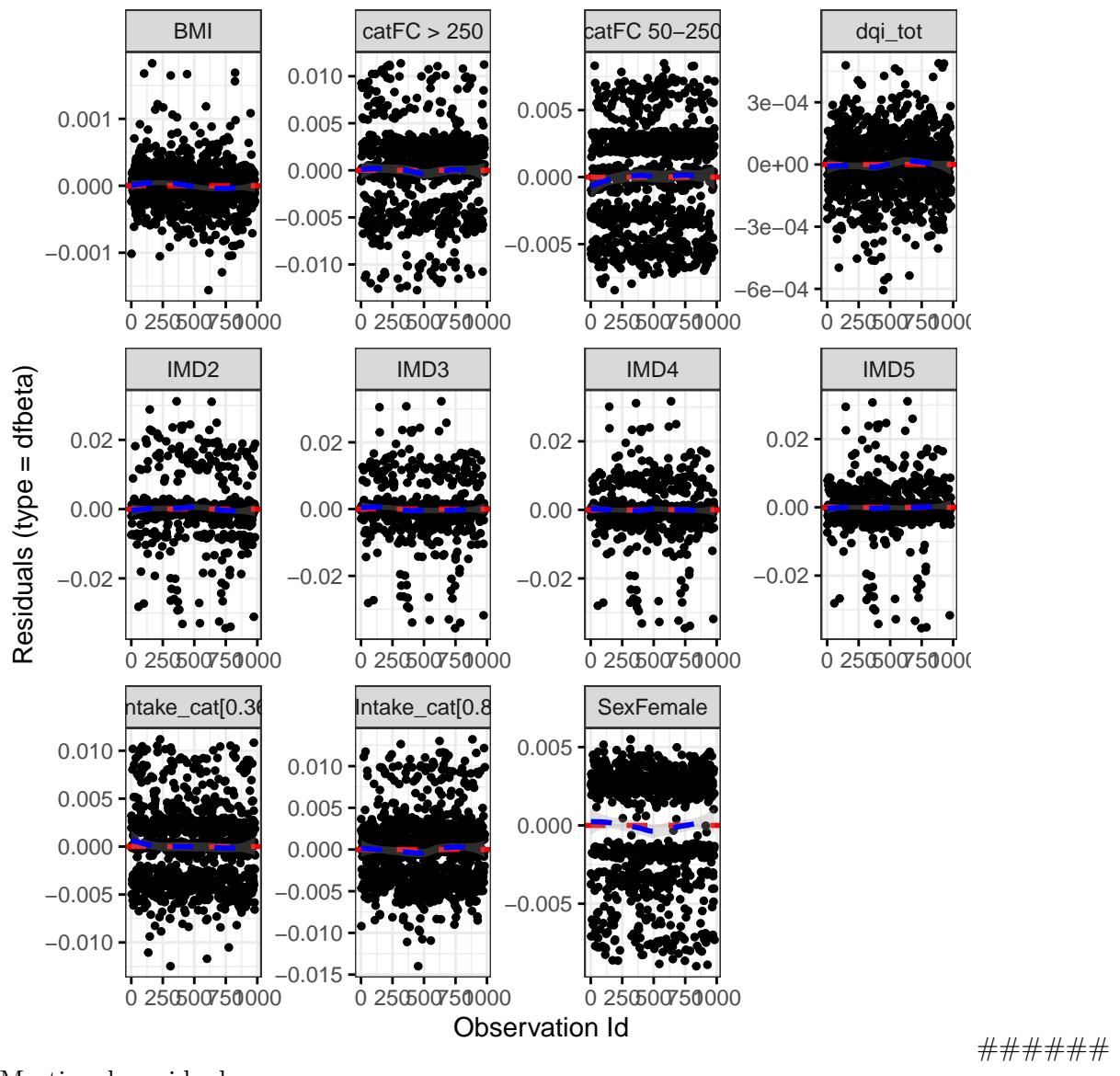
Diagnostics:

Proportional hazards assumption test

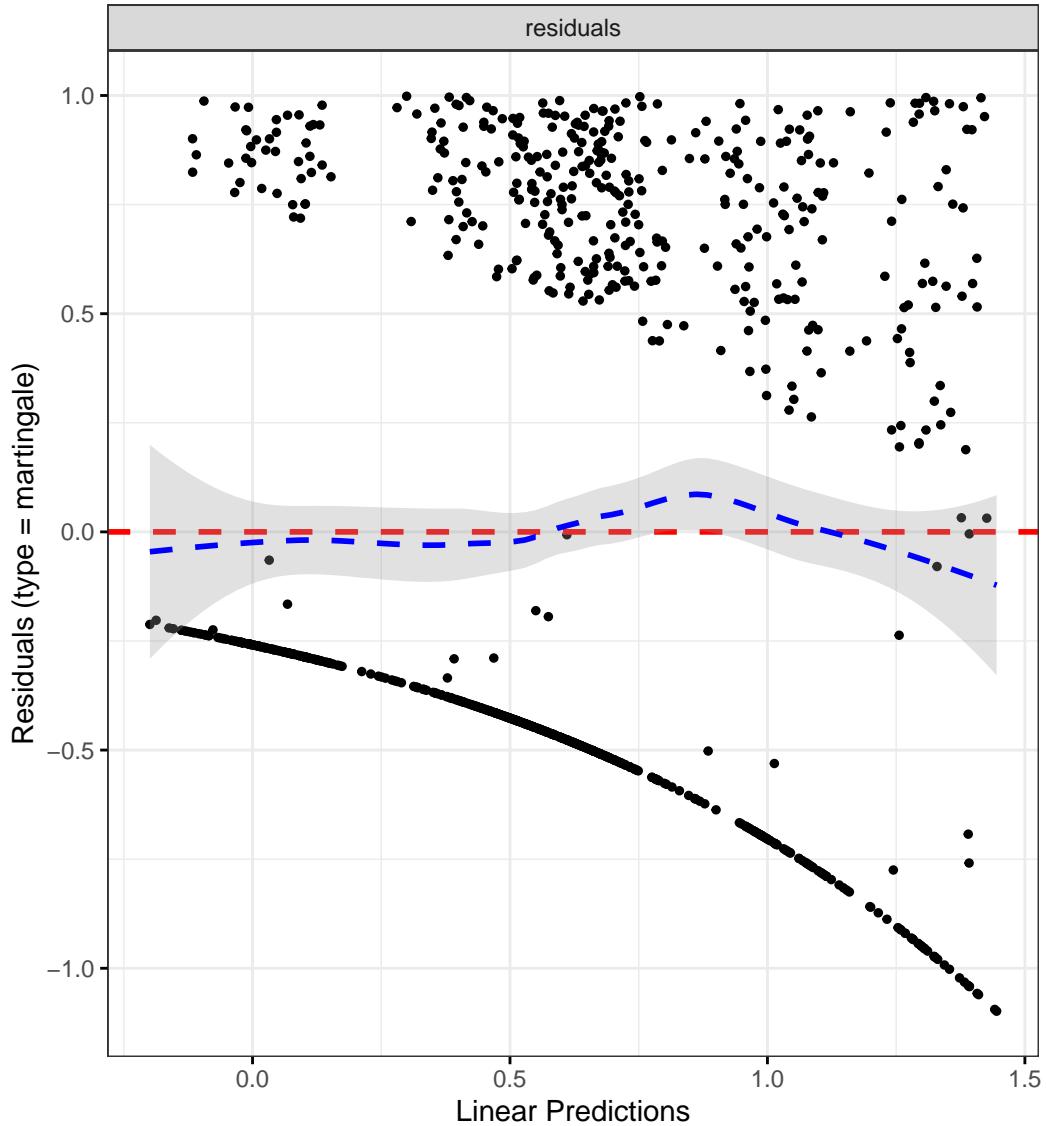
	Chi-squared statistic	DF	P-value
Sex	0.0059	1.0000	0.9388
cat	1.1034	2.0000	0.5760
IMD	5.0734	4.0000	0.2798
dqi_tot	1.3470	1.0000	0.2458
BMI	0.0112	1.0000	0.9159
redMeatIntake_cat	1.7438	2.0000	0.4182
GLOBAL	9.2067	11.0002	0.6028

DF betas

```
`geom_smooth()` using formula = 'y ~ x'
```



```
`geom_smooth()` using formula = 'y ~ x'
```



Hard flare

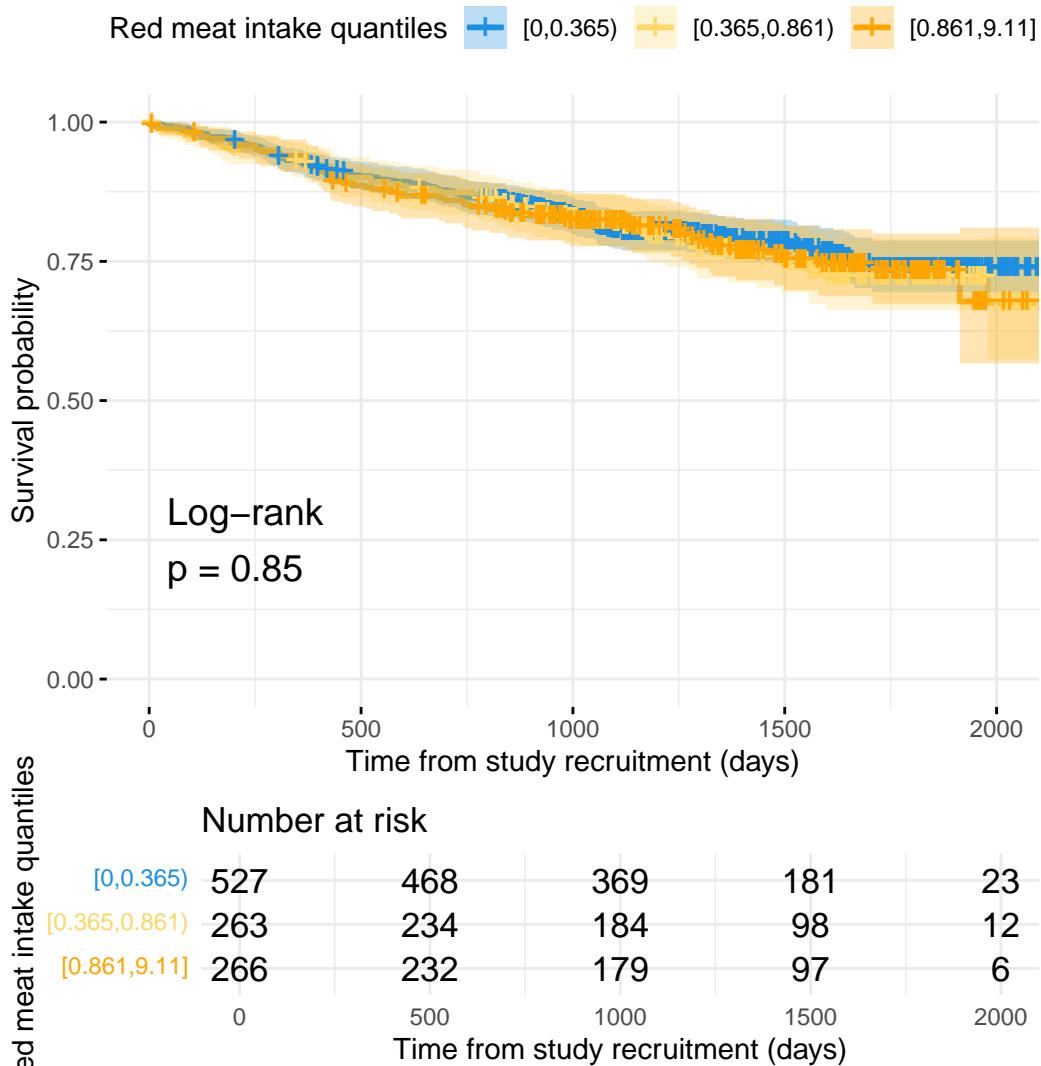
```
# Run survival analysis using utility function for hard flare
analysis_result <- run_survival_analysis(
  data = flare.df,
  var_name = "redMeatIntake",
  outcome_time = "hardflare_time",
  outcome_event = "hardflare",
  legend_title = "Red meat intake quantiles",
```

```
plot_base_path = "plots/ibd/hard-flare/diet/redMeatIntake",
break_time_by = 500
)

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(hardflare_time, hardflare) ~
    Sex + cat + IMD + dqi_tot + BMI + redMeatIntake_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.df
)

# Display plot and model summary
analysis_result$plot
```

Time to hard flare



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.2625	0.9578	1.6640	0.0981
catFC 50-250	1.8516	1.3519	2.5360	0.0001
catFC > 250	2.6146	1.8499	3.6954	0.0000

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	0.9265	0.4962	1.7300	0.8106
IMD3	0.9563	0.5248	1.7426	0.8839
IMD4	1.3470	0.7679	2.3628	0.2989
IMD5	0.9748	0.5591	1.6996	0.9283
dqi_tot	1.0031	0.9906	1.0158	0.6256
BMI	0.9914	0.9650	1.0185	0.5302
redMeatIntake_cat[0.365,0	1.0040	0.7241	1.3919	0.9811
redMeatIntake_cat[0.861,9	1.1188	0.8037	1.5573	0.5060

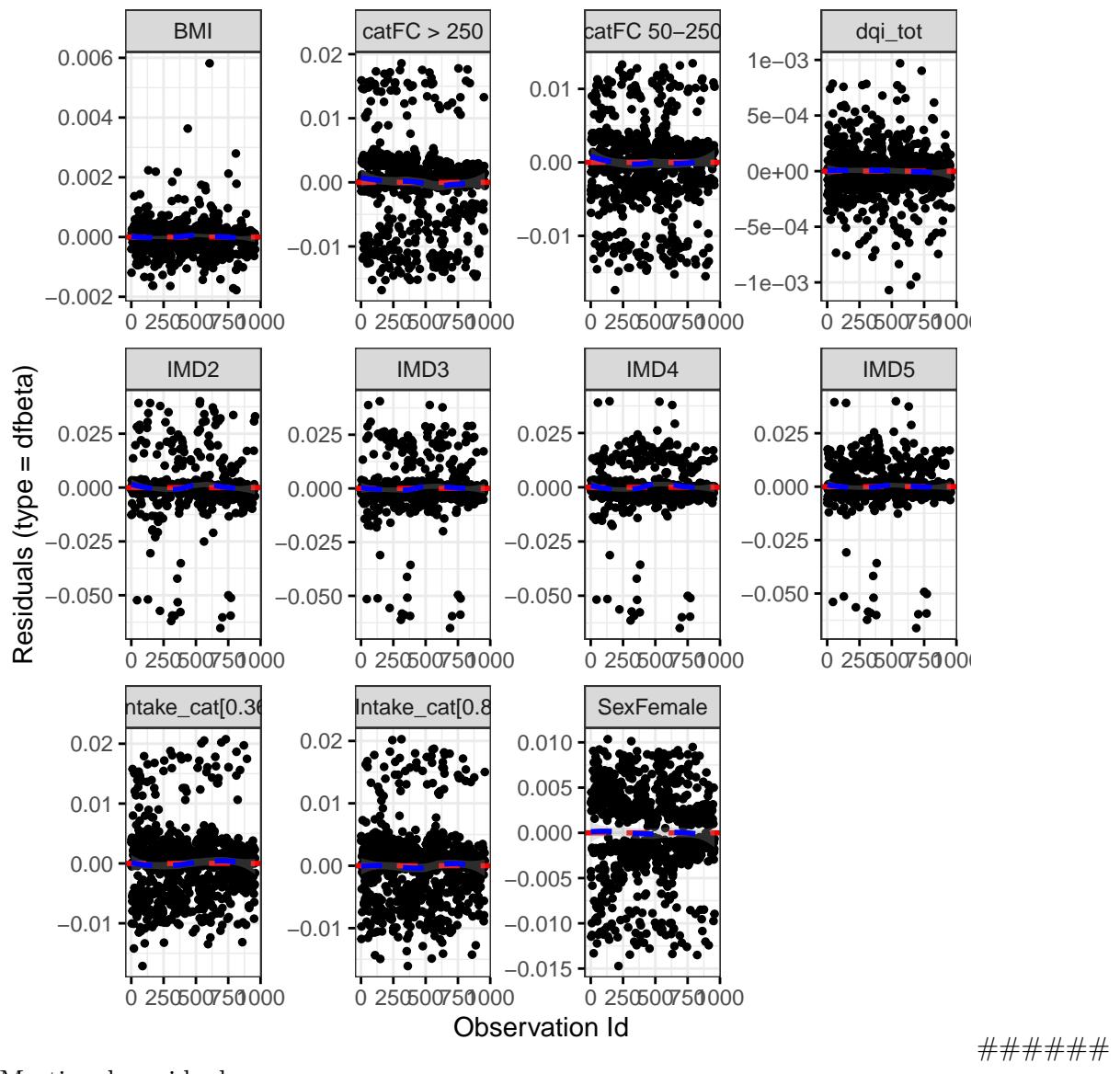
Diagnostics:

Proportional hazards assumption test

	Chi-squared statistic	DF	P-value
Sex	0.0348	0.9885	0.8484
cat	6.8825	1.9796	0.0314
IMD	1.6366	3.9457	0.7955
dqi_tot	1.9757	0.9920	0.1583
BMI	1.8905	0.9886	0.1668
redMeatIntake_cat	0.7511	1.9791	0.6820
GLOBAL	13.6333	21.6243	0.9038

DF betas

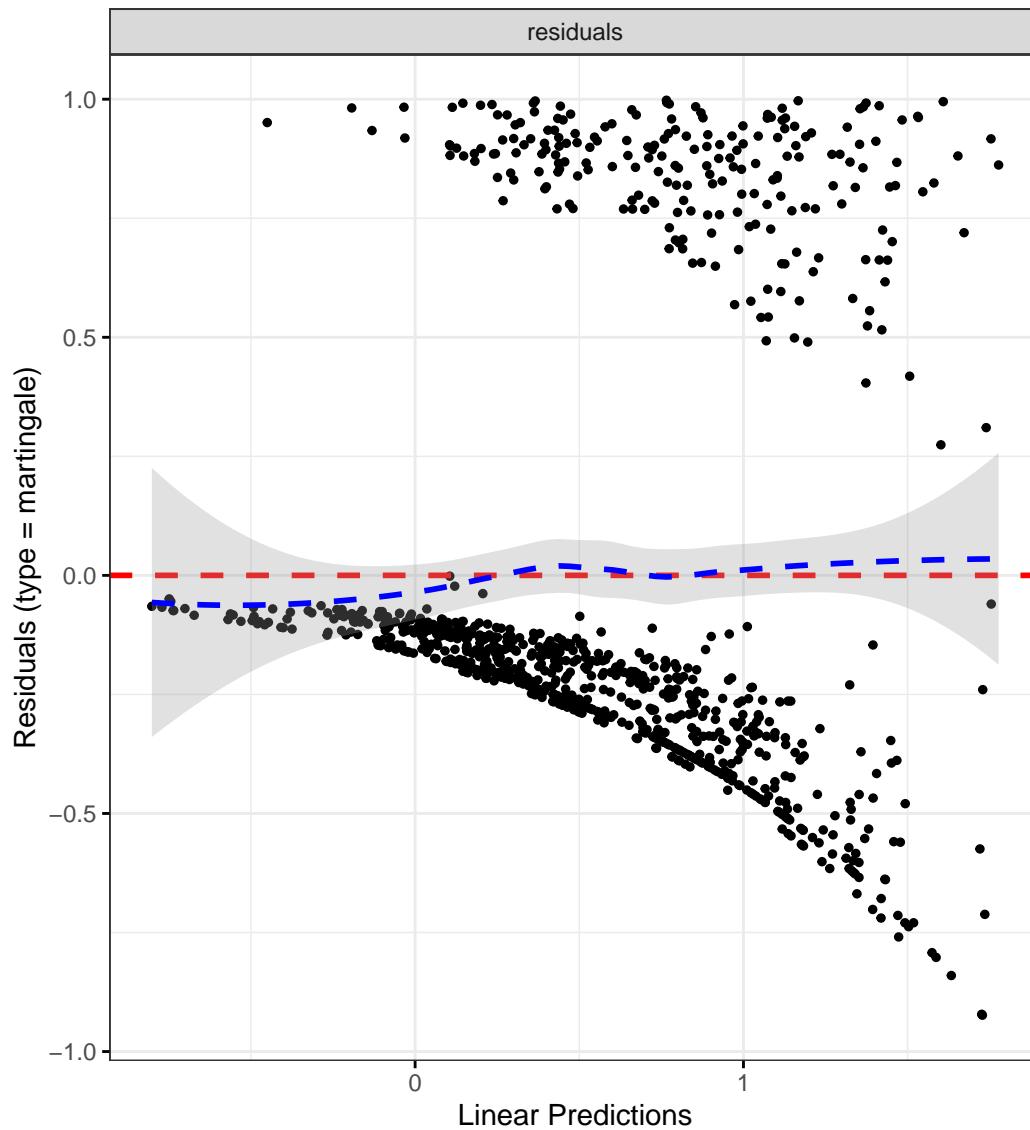
```
`geom_smooth()` using formula = 'y ~ x'
```



#####

Martingale residuals

```
`geom_smooth()` using formula = 'y ~ x'
```



White meat

Crohn's disease

Patient-reported flare

```
# Categorize white meat intake by quantiles  
flare.cd.df <- categorize_by_quantiles(flare.cd.df, "whiteMeatIntake", reference_data = flare
```

```

# Run survival analysis using utility function
analysis_result <- run_survival_analysis(
  data = flare.cd.df,
  var_name = "whiteMeatIntake",
  outcome_time = "softflare_time",
  outcome_event = "softflare",
  legend_title = "White meat intake quantiles",
  plot_base_path = "plots/cd/soft-flare/diet/whiteMeatIntake",
  break_time_by = 200
)

# Save plot as RDS
saveRDS(analysis_result$plot, paste0(paths$outdir, "whiteMeatIntake-cd-soft.RDS"))

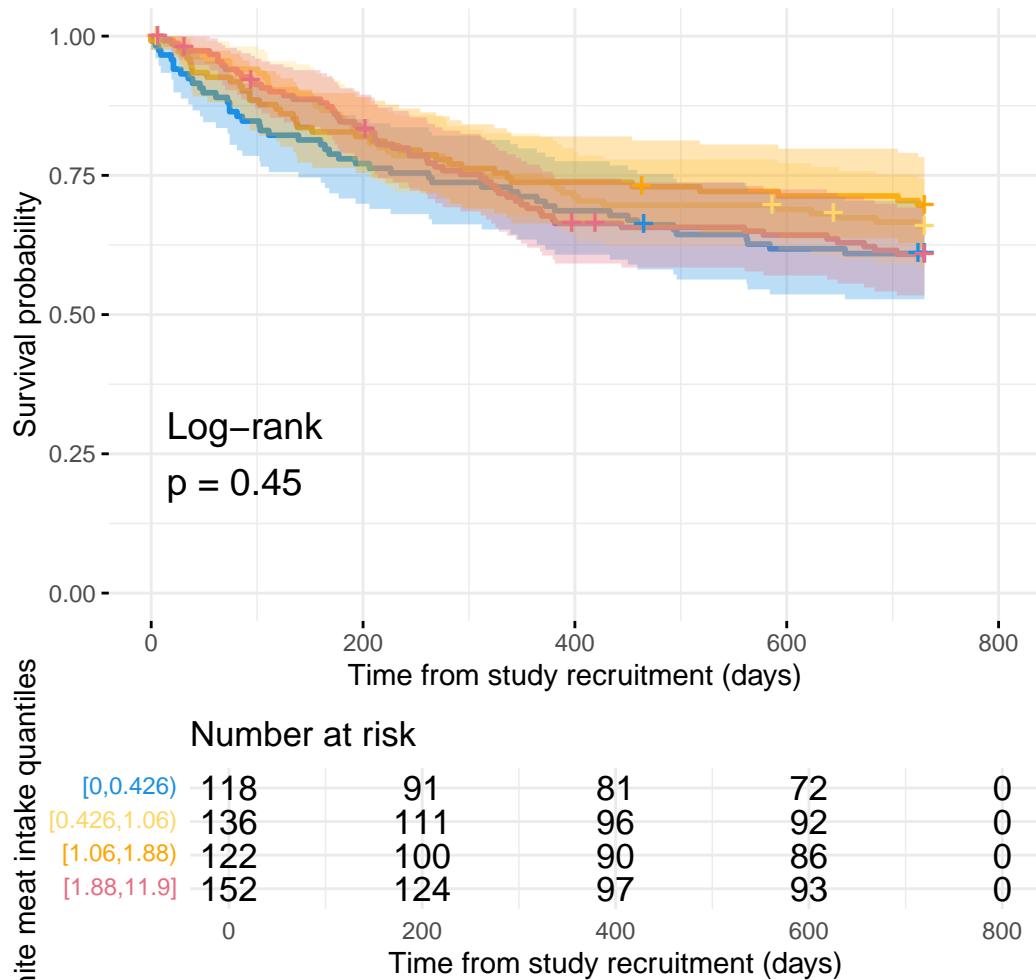
# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(softflare_time, softflare) ~
    Sex + cat + IMD + whiteMeatIntake_cat + dqi_tot + BMI + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.cd.df
)

# Display plot and model summary
analysis_result$plot

```

Time to patient-reported flare

White meat intake quantiles [0,0.426) [0.426,1.06) [1.06,1.88) [1.88,11.9]



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.8873	1.3481	2.6422	0.0002
catFC 50-250	1.3091	0.9213	1.8600	0.1329
catFC > 250	2.0572	1.4045	3.0132	0.0002

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	0.7018	0.3660	1.3458	0.2865
IMD3	0.9586	0.5255	1.7486	0.8904
IMD4	0.8582	0.4744	1.5526	0.6132
IMD5	0.9984	0.5725	1.7411	0.9955
whiteMeatIntake_cat[0.426	0.8350	0.5366	1.2994	0.4242
whiteMeatIntake_cat[1.06,	0.7647	0.4805	1.2169	0.2577
whiteMeatIntake_cat[1.88,	0.9321	0.6077	1.4296	0.7471
dqi_tot	1.0054	0.9917	1.0193	0.4407
BMI	1.0080	0.9805	1.0363	0.5706

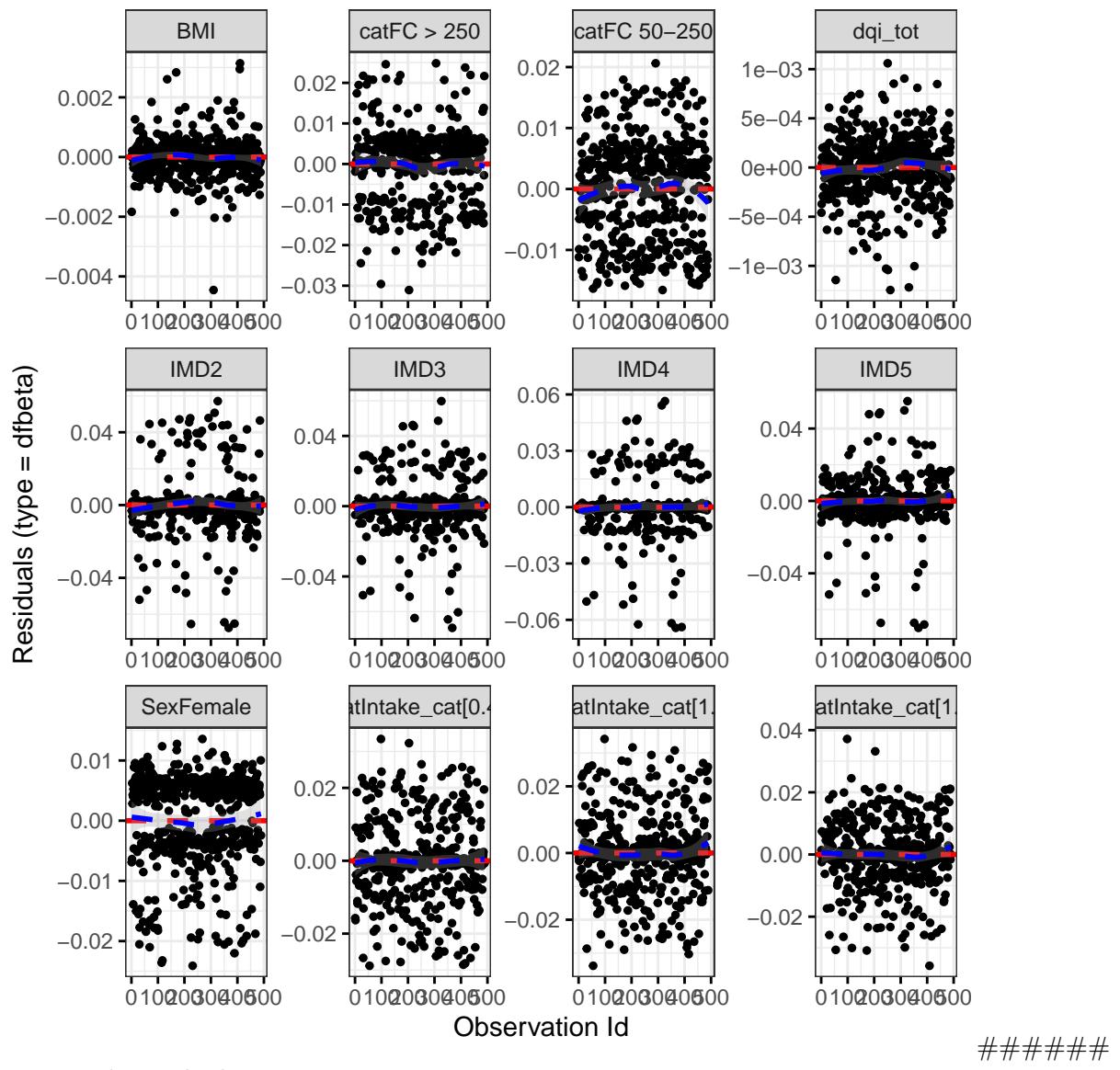
Diagnostics:

Proportional hazards assumption test

	Chi-squared statistic	DF	P-value
Sex	0.2479	1.0000	0.6186
cat	0.8277	2.0000	0.6611
IMD	3.0804	4.0000	0.5445
whiteMeatIntake_cat	8.1780	3.0000	0.0425
dqi_tot	0.3487	1.0000	0.5548
BMI	1.2754	1.0000	0.2588
GLOBAL	12.8119	12.0001	0.3829

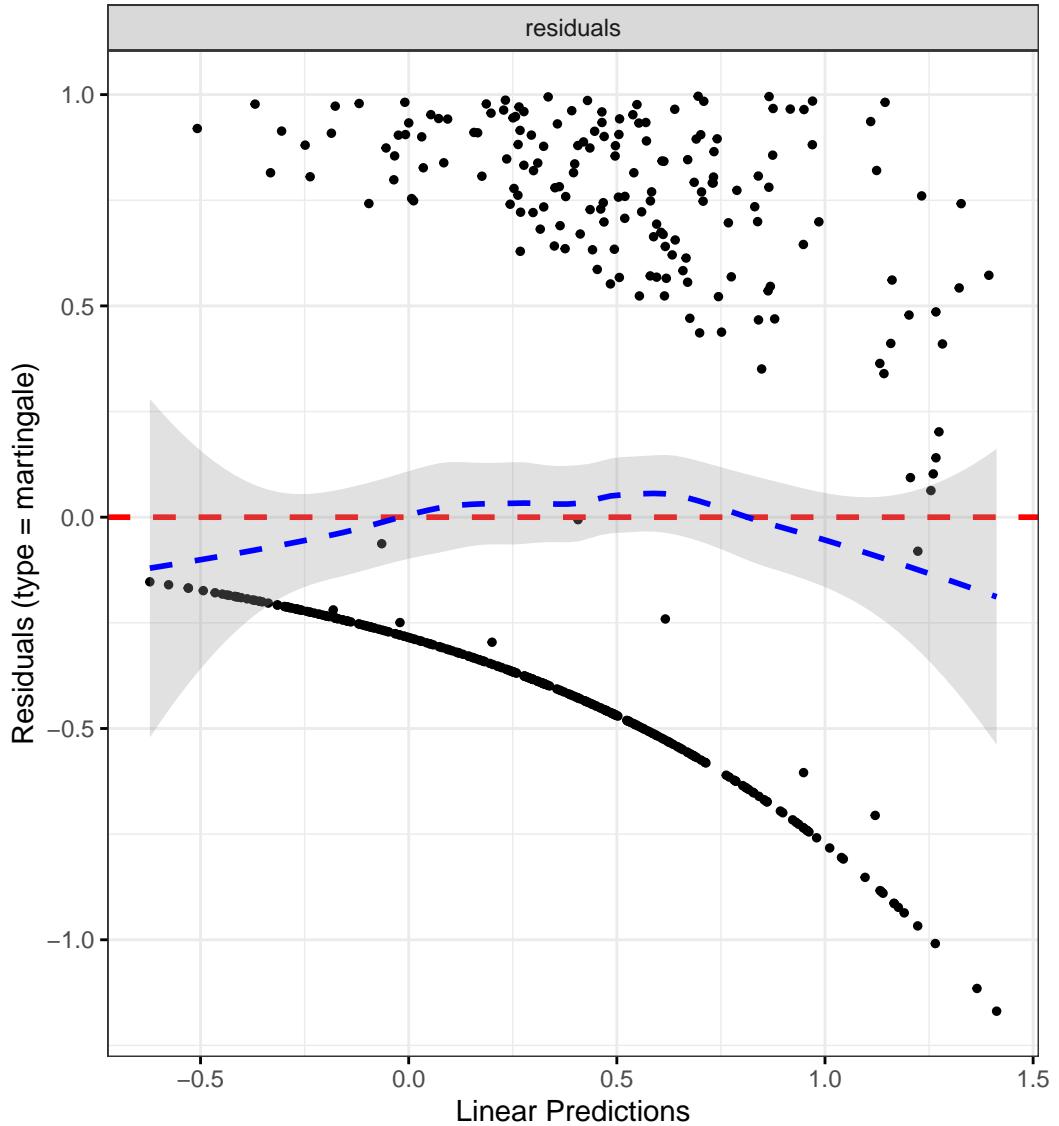
DF betas

```
`geom_smooth()` using formula = 'y ~ x'
```



Martingale residuals

```
`geom_smooth()` using formula = 'y ~ x'
```



Hard flare

```
# Run survival analysis using utility function for hard flare
analysis_result <- run_survival_analysis(
  data = flare.cd.df,
  var_name = "whiteMeatIntake",
  outcome_time = "hardflare_time",
  outcome_event = "hardflare",
  legend_title = "White meat intake quantiles",
```

```

plot_base_path = "plots/cd/hard-flare/diet/whiteMeatIntake",
break_time_by = 500
)

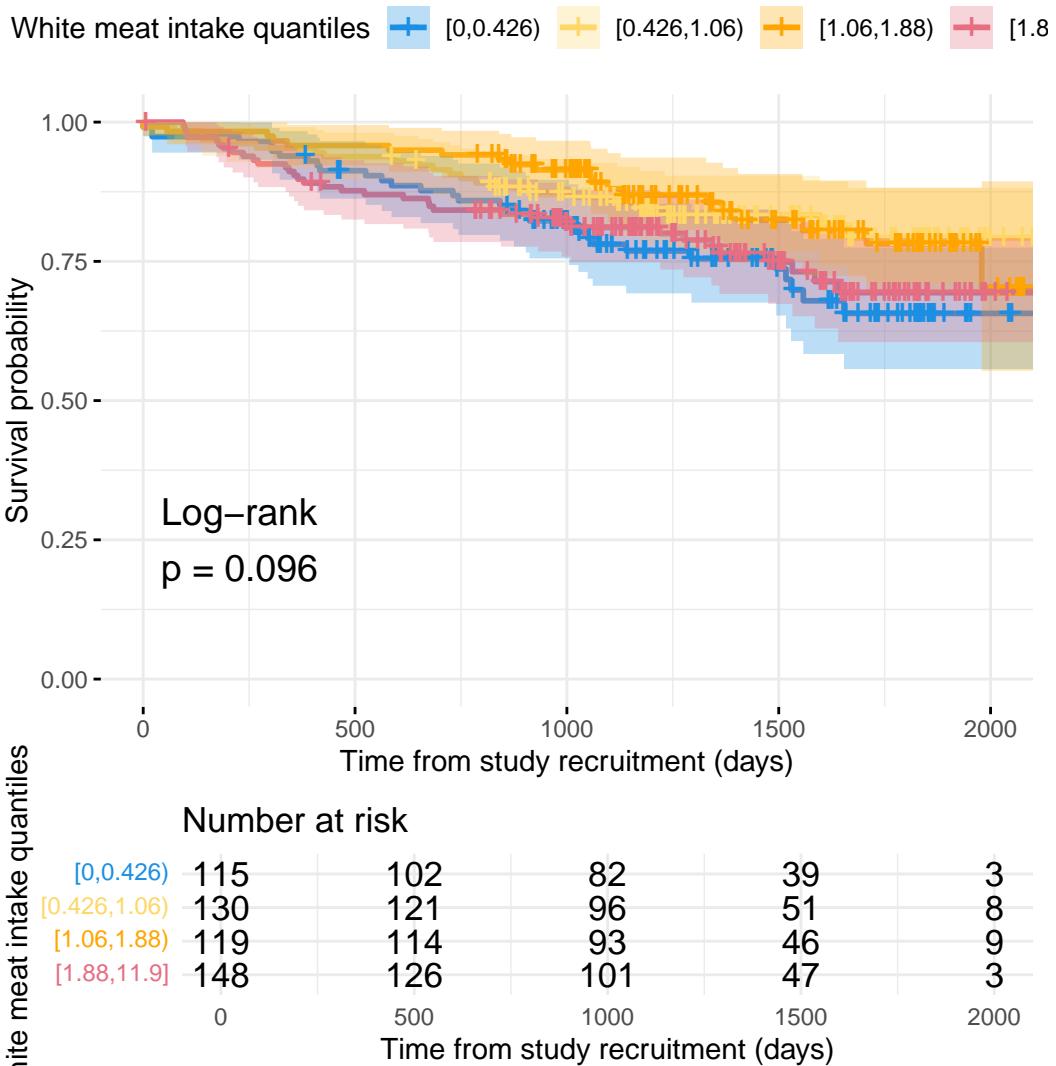
# Save plot as RDS
saveRDS(analysis_result$plot, paste0(paths$outdir, "whiteMeatIntake-cd-hard.RDS"))

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(hardflare_time, hardflare) ~
    Sex + cat + IMD + dqi_tot + BMI + whiteMeatIntake_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.cd.df
)

# Display plot and model summary
analysis_result$plot

```

Time to hard flare



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.3429	0.8871	2.0331	0.1635
catFC 50-250	1.8461	1.1560	2.9481	0.0103
catFC > 250	3.0321	1.8303	5.0229	0.0000

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	0.6183	0.2647	1.4442	0.2666
IMD3	0.8853	0.3981	1.9688	0.7652
IMD4	0.7618	0.3509	1.6538	0.4915
IMD5	0.7301	0.3506	1.5201	0.4005
dqi_tot	1.0022	0.9843	1.0204	0.8089
BMI	1.0190	0.9836	1.0557	0.2963
whiteMeatIntake_cat[0.426	0.5386	0.3076	0.9429	0.0303
whiteMeatIntake_cat[1.06,	0.5090	0.2848	0.9098	0.0227
whiteMeatIntake_cat[1.88,	0.7308	0.4351	1.2274	0.2358

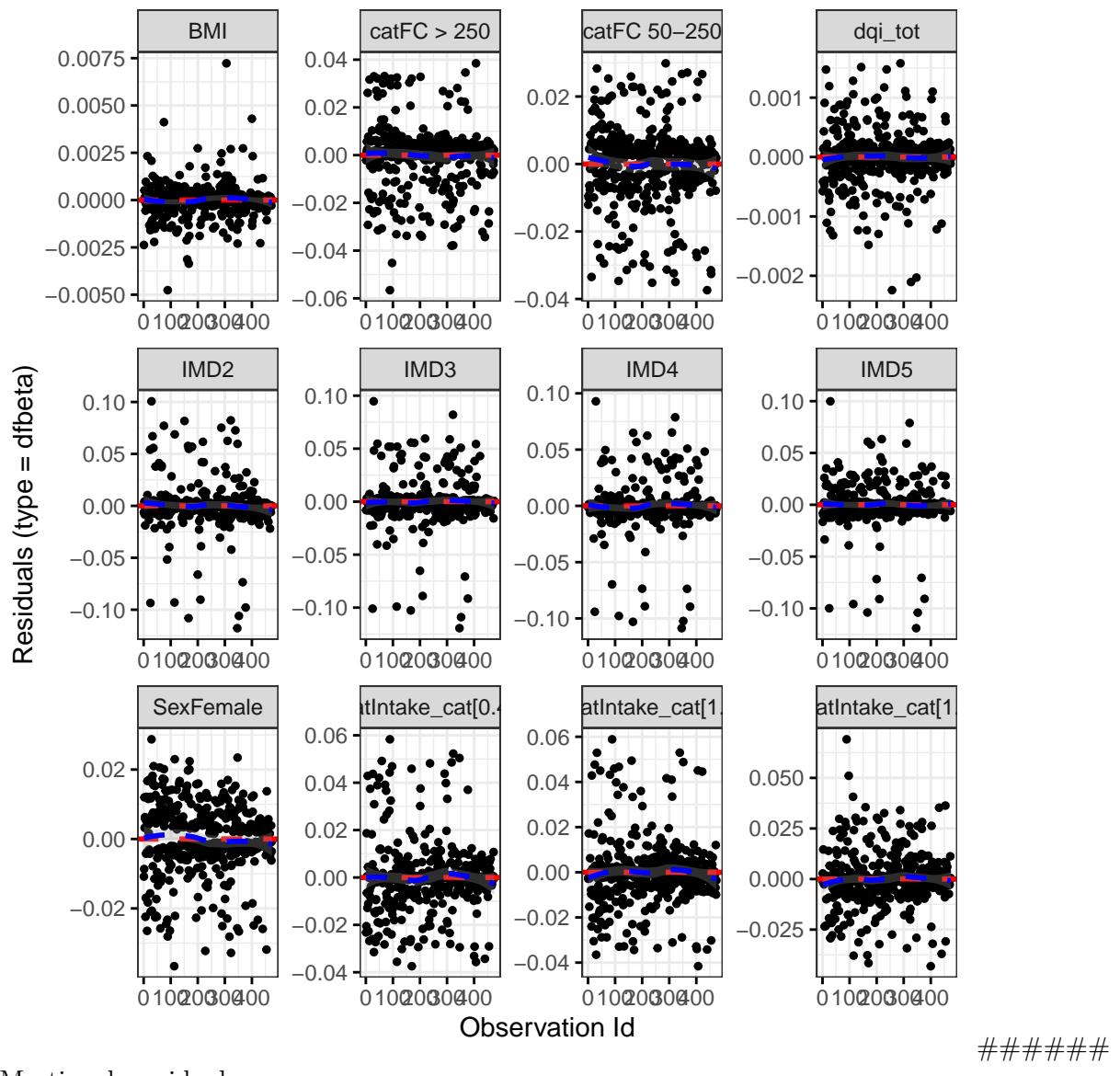
Diagnostics:

Proportional hazards assumption test

	Chi-squared statistic	DF	P-value
Sex	0.1198	0.9747	0.7192
cat	9.6209	1.9772	0.0079
IMD	2.7614	3.9308	0.5877
dqi_tot	3.1257	0.9909	0.0761
BMI	0.9814	0.9811	0.3157
whiteMeatIntake_cat	2.9394	2.9670	0.3953
GLOBAL	21.6390	17.8144	0.2388

DF betas

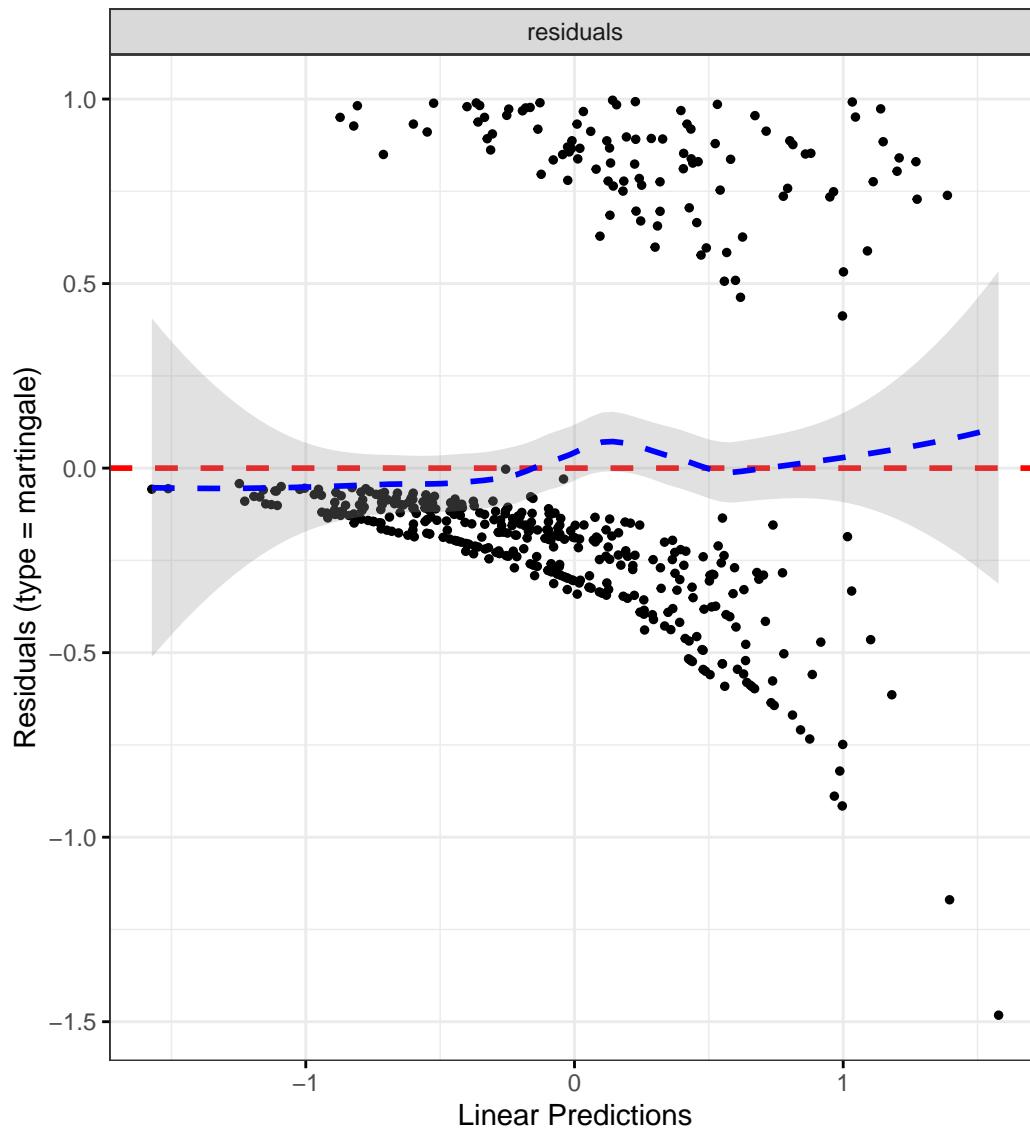
```
`geom_smooth()` using formula = 'y ~ x'
```



#####

Martingale residuals

```
`geom_smooth()` using formula = 'y ~ x'
```



Ulcerative colitis

Patient-reported flare

```
# Categorize white meat intake by quantiles
flare.uc.df <- categorize_by_quantiles(flare.uc.df, "whiteMeatIntake", reference_data = flare)

# Run survival analysis using utility function
```

```

analysis_result <- run_survival_analysis(
  data = flare.uc.df,
  var_name = "whiteMeatIntake",
  outcome_time = "softflare_time",
  outcome_event = "softflare",
  legend_title = "White meat intake quantiles",
  plot_base_path = "plots/uc/soft-flare/diet/whiteMeatIntake",
  break_time_by = 200
)

# Save plot as RDS
saveRDS(analysis_result$plot, paste0(paths$outdir, "whiteMeatIntake-uc-soft.RDS"))

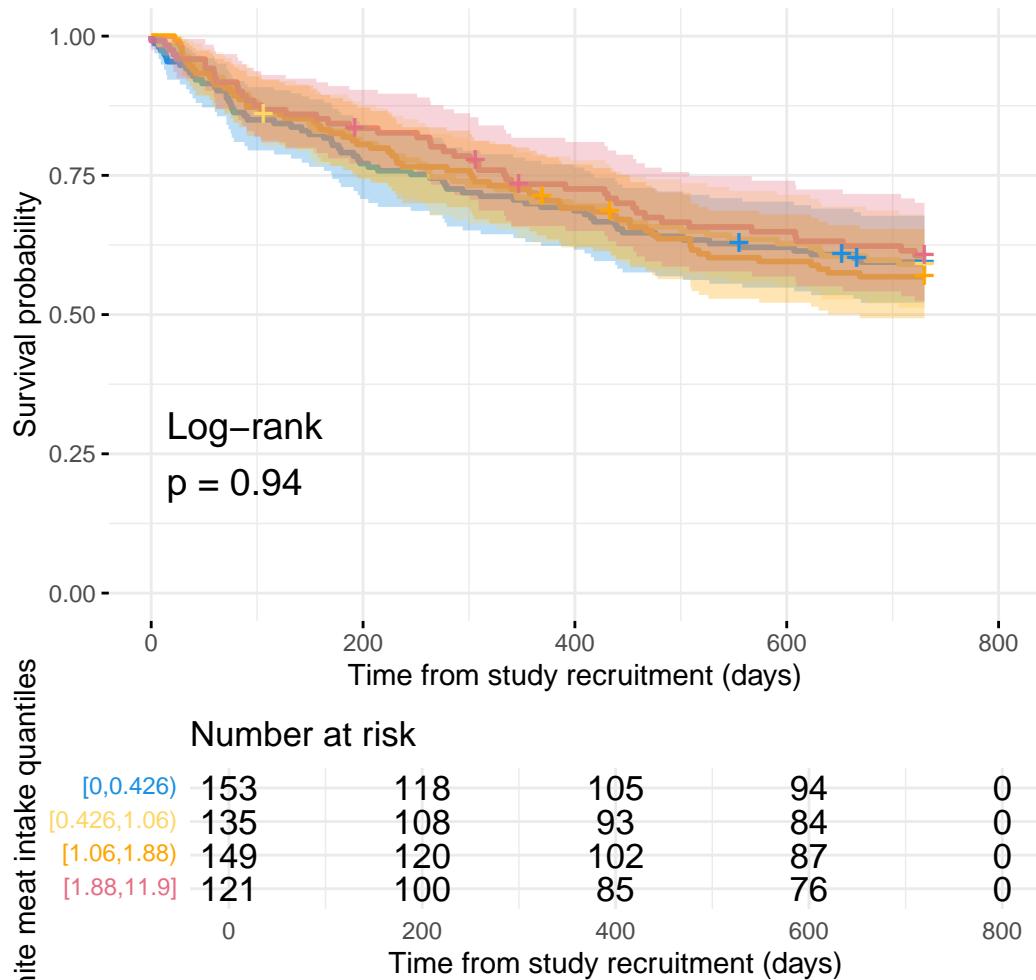
# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(softflare_time, softflare) ~
    Sex + cat + IMD + dqi_tot + BMI + whiteMeatIntake_cat +
    frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.uc.df
)

# Display plot and model summary
analysis_result$plot

```

Time to patient-reported flare

White meat intake quantiles [0,0.426) [0.426,1.06) [1.06,1.88) [1.88,11.9]



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.6907	1.2662	2.2575	0.0004
catFC 50-250	1.8008	1.3087	2.4779	0.0003
catFC > 250	2.0864	1.4592	2.9832	0.0001

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	1.4120	0.7410	2.6906	0.2943
IMD3	1.1432	0.6083	2.1485	0.6775
IMD4	1.3505	0.7457	2.4459	0.3213
IMD5	1.1880	0.6604	2.1369	0.5653
dqi_tot	0.9997	0.9868	1.0128	0.9689
BMI	0.9762	0.9473	1.0059	0.1145
whiteMeatIntake_cat[0.426	1.0801	0.7292	1.5998	0.7006
whiteMeatIntake_cat[1.06,	1.0490	0.7224	1.5235	0.8014
whiteMeatIntake_cat[1.88,	1.0258	0.6851	1.5359	0.9016

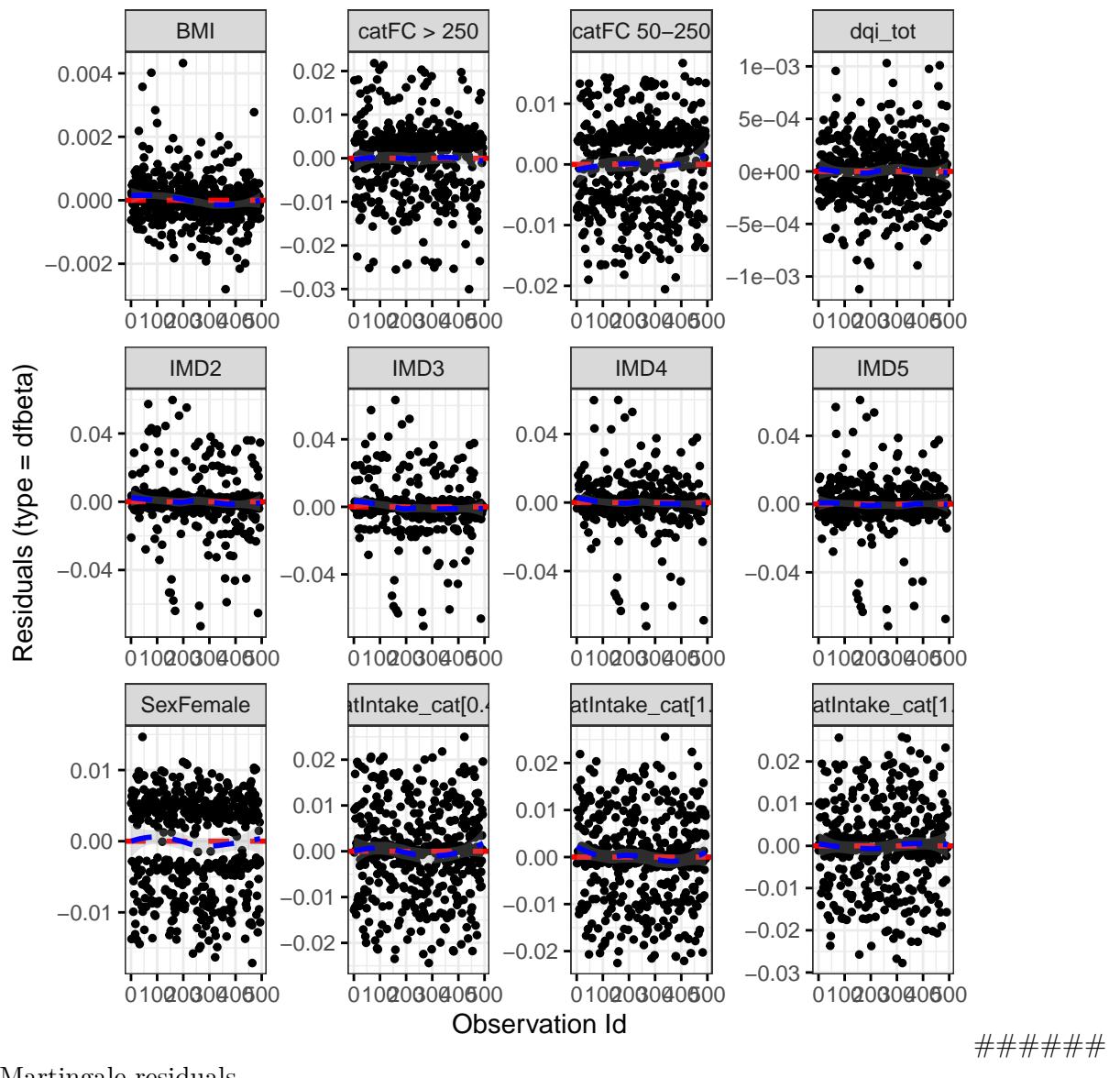
Diagnostics:

Proportional hazards assumption test

	Chi-squared statistic	DF	P-value
Sex	0.0061	1.0000	0.9378
cat	3.5527	2.0000	0.1693
IMD	2.6572	4.0000	0.6167
dqi_tot	0.7527	1.0000	0.3856
BMI	0.9437	1.0000	0.3313
whiteMeatIntake_cat	2.2827	3.0000	0.5158
GLOBAL	11.5067	12.0001	0.4861

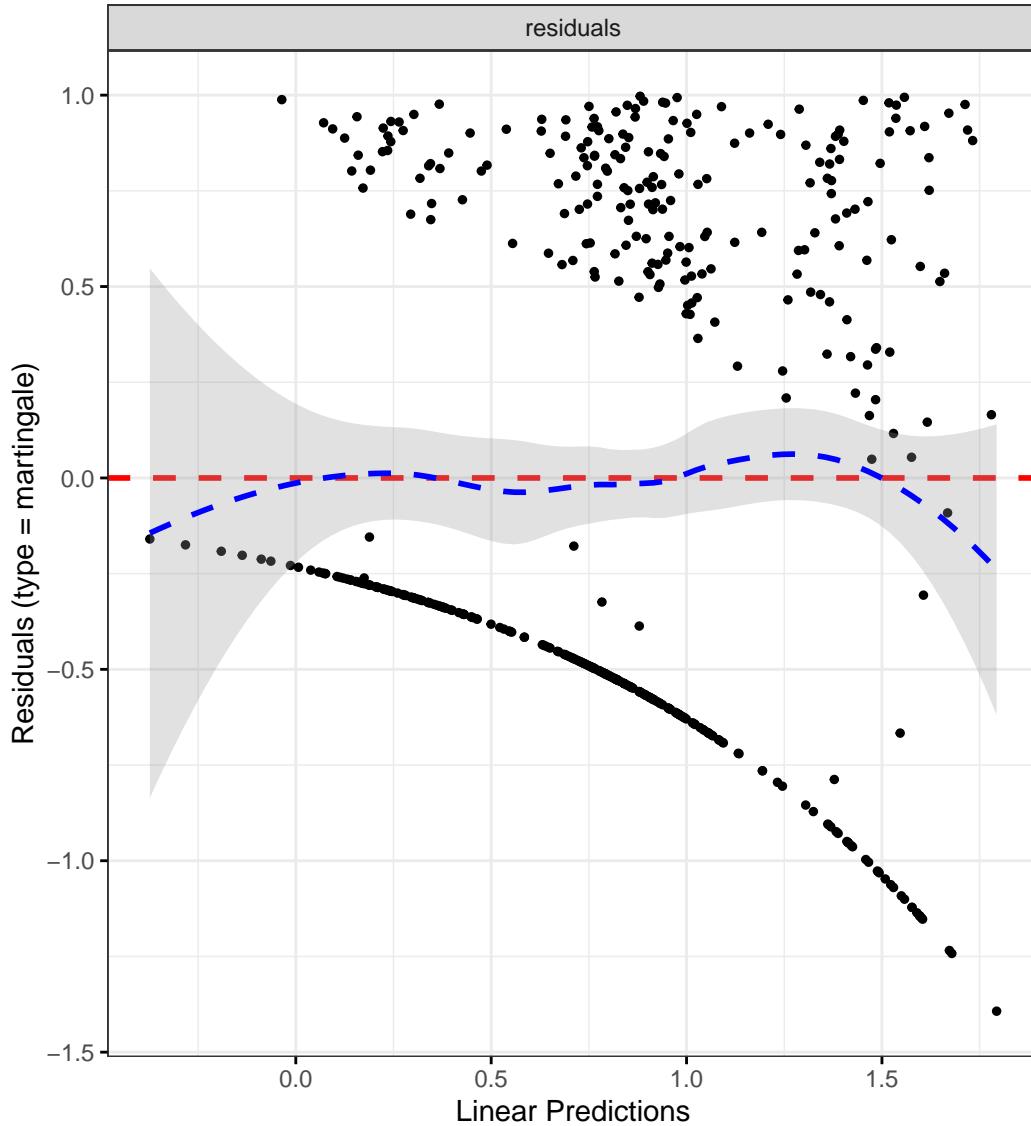
DF betas

```
`geom_smooth()` using formula = 'y ~ x'
```



Martingale residuals

```
`geom_smooth()` using formula = 'y ~ x'
```



Hard flare

```
# Run survival analysis using utility function for hard flare
analysis_result <- run_survival_analysis(
  data = flare.uc.df,
  var_name = "whiteMeatIntake",
  outcome_time = "hardflare_time",
  outcome_event = "hardflare",
  legend_title = "White meat intake quantiles",
```

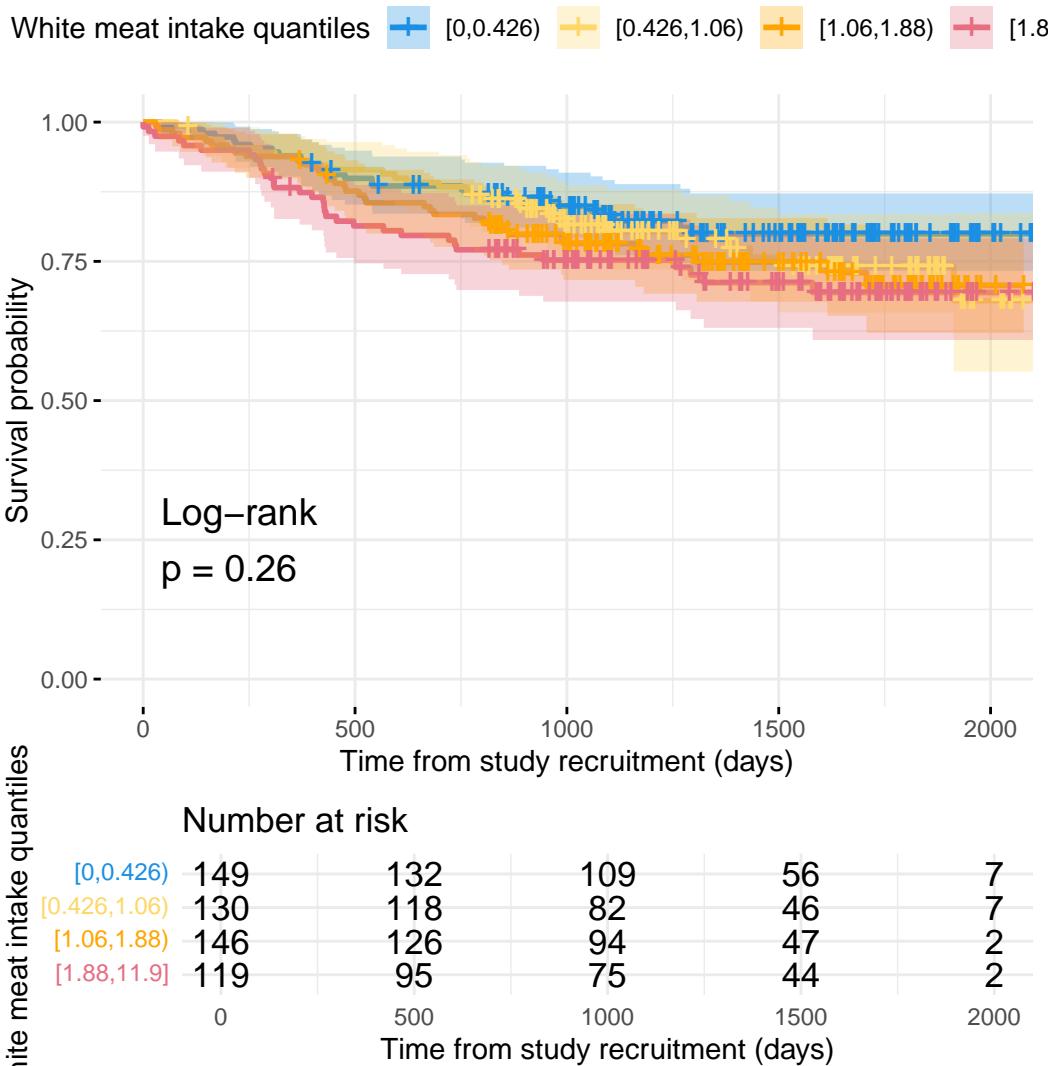
```
plot_base_path = "plots/uc/hard-flare/diet/whiteMeatIntake",
break_time_by = 500
)

# Save plot as RDS
saveRDS(analysis_result$plot, paste0(paths$outdir, "whiteMeatIntake-uc-hard.RDS"))

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(hardflare_time, hardflare) ~
    Sex + cat + IMD + dqi_tot + BMI + whiteMeatIntake_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.uc.df
)

# Display plot and model summary
analysis_result$plot
```

Time to hard flare



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.2080	0.8259	1.7669	0.3300
catFC 50-250	1.9895	1.2906	3.0669	0.0018
catFC > 250	2.5817	1.5809	4.2161	0.0002

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	1.6600	0.6280	4.3877	0.3068
IMD3	1.3605	0.5264	3.5165	0.5252
IMD4	2.3763	0.9885	5.7124	0.0531
IMD5	1.4230	0.5865	3.4523	0.4353
dqi_tot	1.0056	0.9877	1.0238	0.5438
BMI	0.9602	0.9204	1.0017	0.0601
whiteMeatIntake_cat[0.426	1.4066	0.8059	2.4551	0.2299
whiteMeatIntake_cat[1.06,	1.3778	0.8083	2.3483	0.2389
whiteMeatIntake_cat[1.88,	1.9050	1.1014	3.2949	0.0211

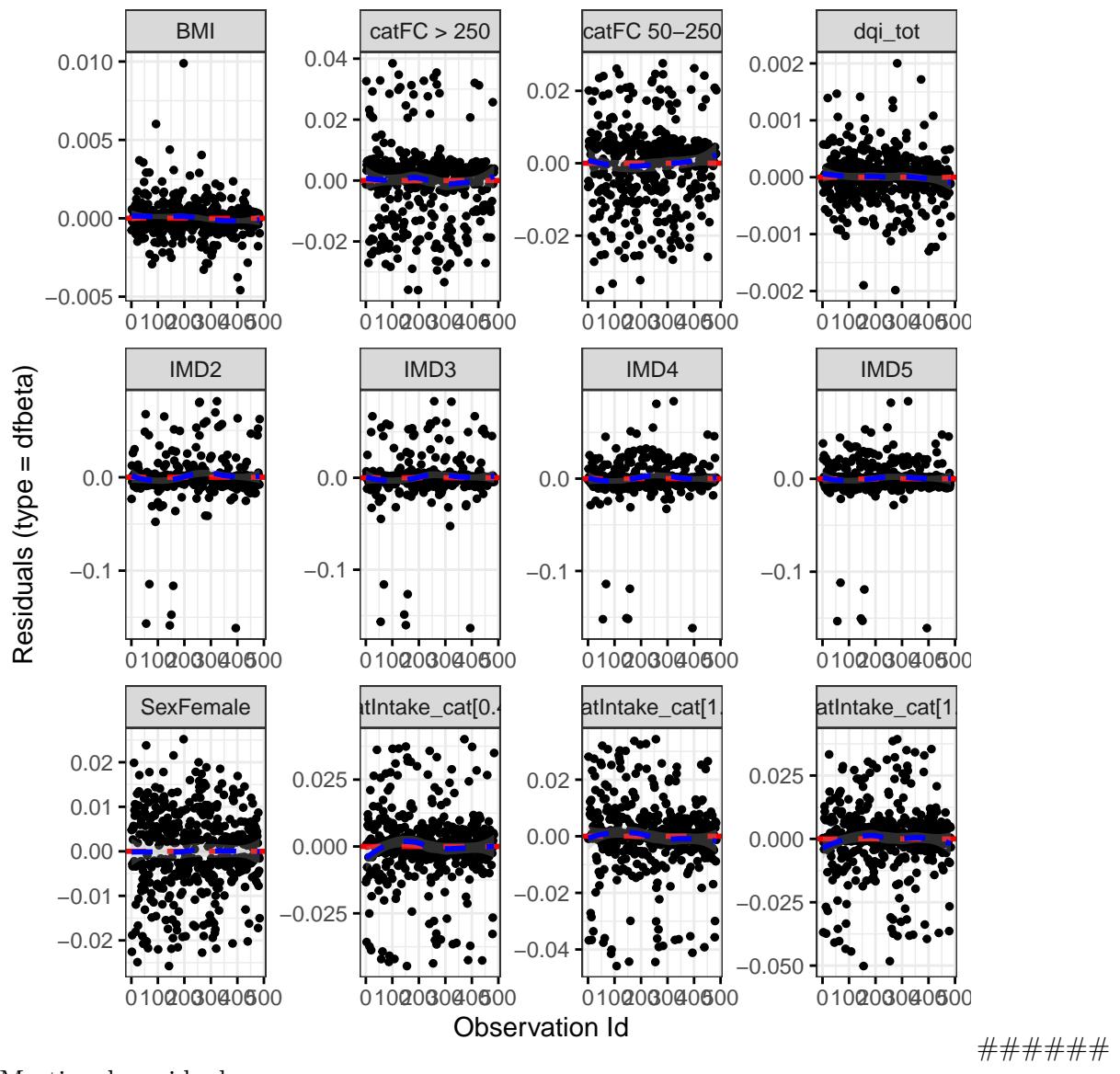
Diagnostics:

Proportional hazards assumption test

	Chi-squared statistic	DF	P-value
Sex	0.0465	0.9882	0.8254
cat	5.5121	1.9616	0.0613
IMD	1.2786	3.9366	0.8587
dqi_tot	0.0026	0.9885	0.9573
BMI	0.5757	0.9902	0.4442
whiteMeatIntake_cat	2.8092	2.9636	0.4155
GLOBAL	11.4009	18.5192	0.8947

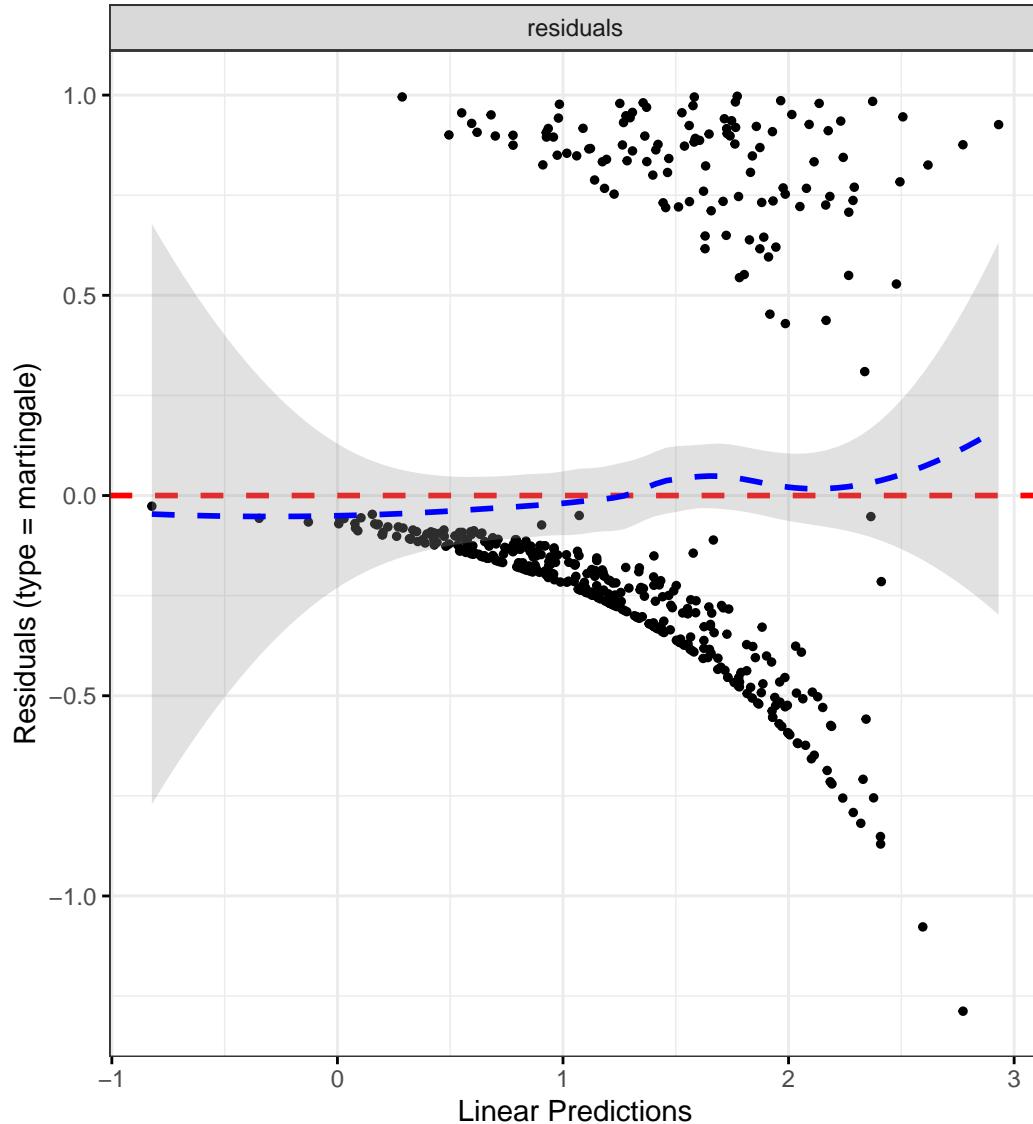
DF betas

```
`geom_smooth()` using formula = 'y ~ x'
```



Martingale residuals

```
`geom_smooth()` using formula = 'y ~ x'
```



Inflammatory bowel disease

Patient-reported flare

```
# Categorize white meat intake by quantiles
flare.df <- categorize_by_quantiles(flare.df, "whiteMeatIntake", reference_data = flare.df)

# Run survival analysis using utility function
```

```

analysis_result <- run_survival_analysis(
  data = flare.df,
  var_name = "whiteMeatIntake",
  outcome_time = "softflare_time",
  outcome_event = "softflare",
  legend_title = "White meat intake quantiles",
  plot_base_path = "plots/ibd/soft-flare/diet/whiteMeatIntake",
  break_time_by = 200
)

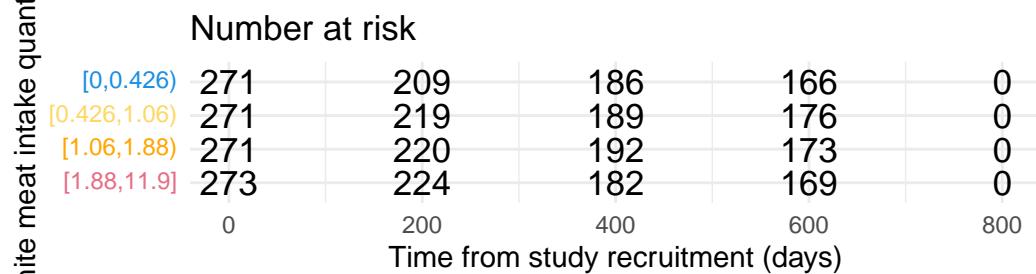
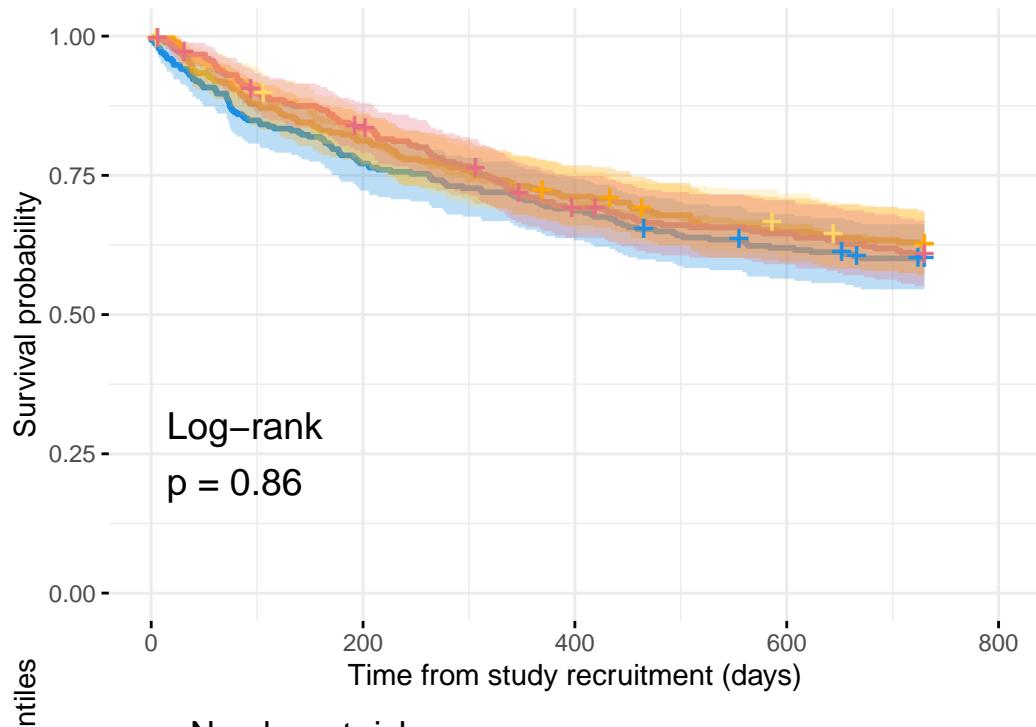
# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(softflare_time, softflare) ~
    Sex + cat + IMD + dqi_tot + BMI + whiteMeatIntake_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.df
)

# Display plot and model summary
analysis_result$plot

```

Time to patient-reported flare

White meat intake quantiles [0,0.426) [0.426,1.06) [1.06,1.88) [1.88,11.9]



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.7709	1.4269	2.1979	0.0000
catFC 50-250	1.5011	1.1882	1.8964	0.0007
catFC > 250	2.0189	1.5586	2.6150	0.0000

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	0.9841	0.6253	1.5487	0.9446
IMD3	1.0151	0.6575	1.5673	0.9460
IMD4	1.1060	0.7302	1.6753	0.6342
IMD5	1.0837	0.7255	1.6188	0.6946
dqi_tot	1.0024	0.9931	1.0118	0.6103
BMI	0.9941	0.9744	1.0142	0.5625
whiteMeatIntake_cat[0.426	0.9483	0.7088	1.2687	0.7208
whiteMeatIntake_cat[1.06,	0.9382	0.7025	1.2529	0.6656
whiteMeatIntake_cat[1.88,	0.9936	0.7452	1.3248	0.9650

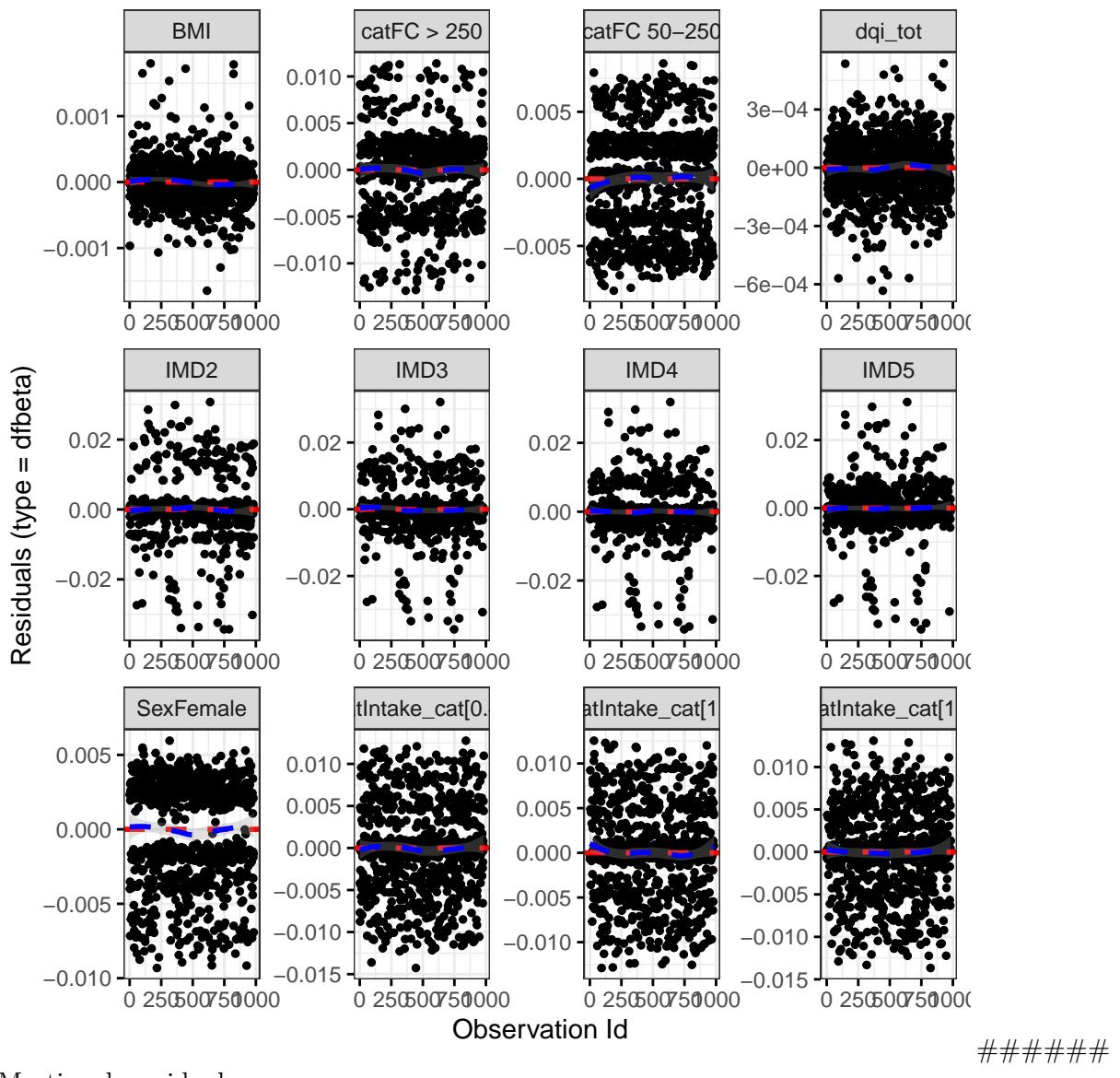
Diagnostics:

Proportional hazards assumption test

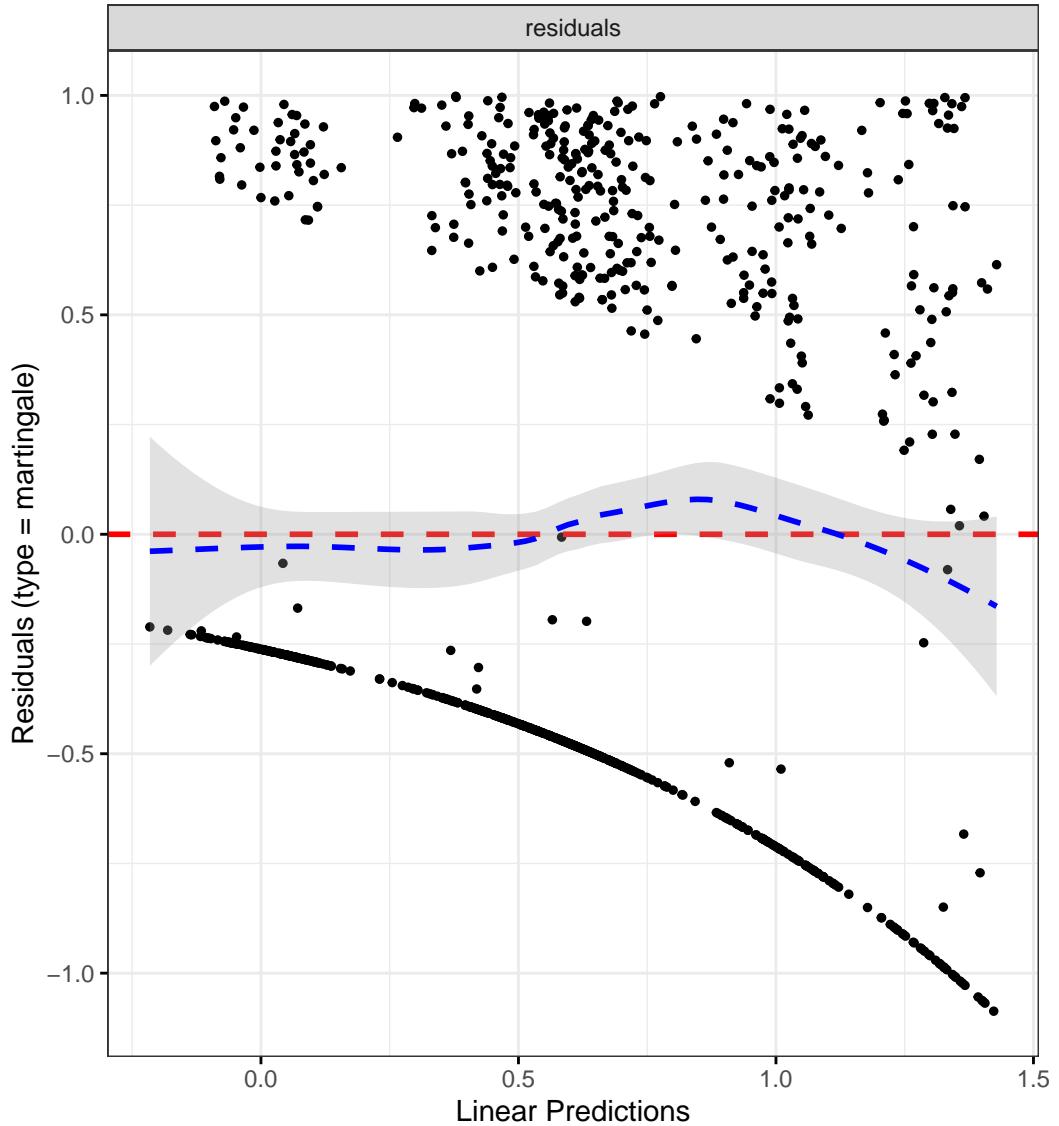
	Chi-squared statistic	DF	P-value
Sex	0.0045	1.0000	0.9466
cat	1.0963	2.0000	0.5780
IMD	5.0648	4.0000	0.2807
dqi_tot	1.3828	1.0000	0.2396
BMI	0.0090	1.0000	0.9246
whiteMeatIntake_cat	6.1537	3.0000	0.1044
GLOBAL	14.5079	12.0002	0.2695

DF betas

```
`geom_smooth()` using formula = 'y ~ x'
```



```
`geom_smooth()` using formula = 'y ~ x'
```



Hard flare

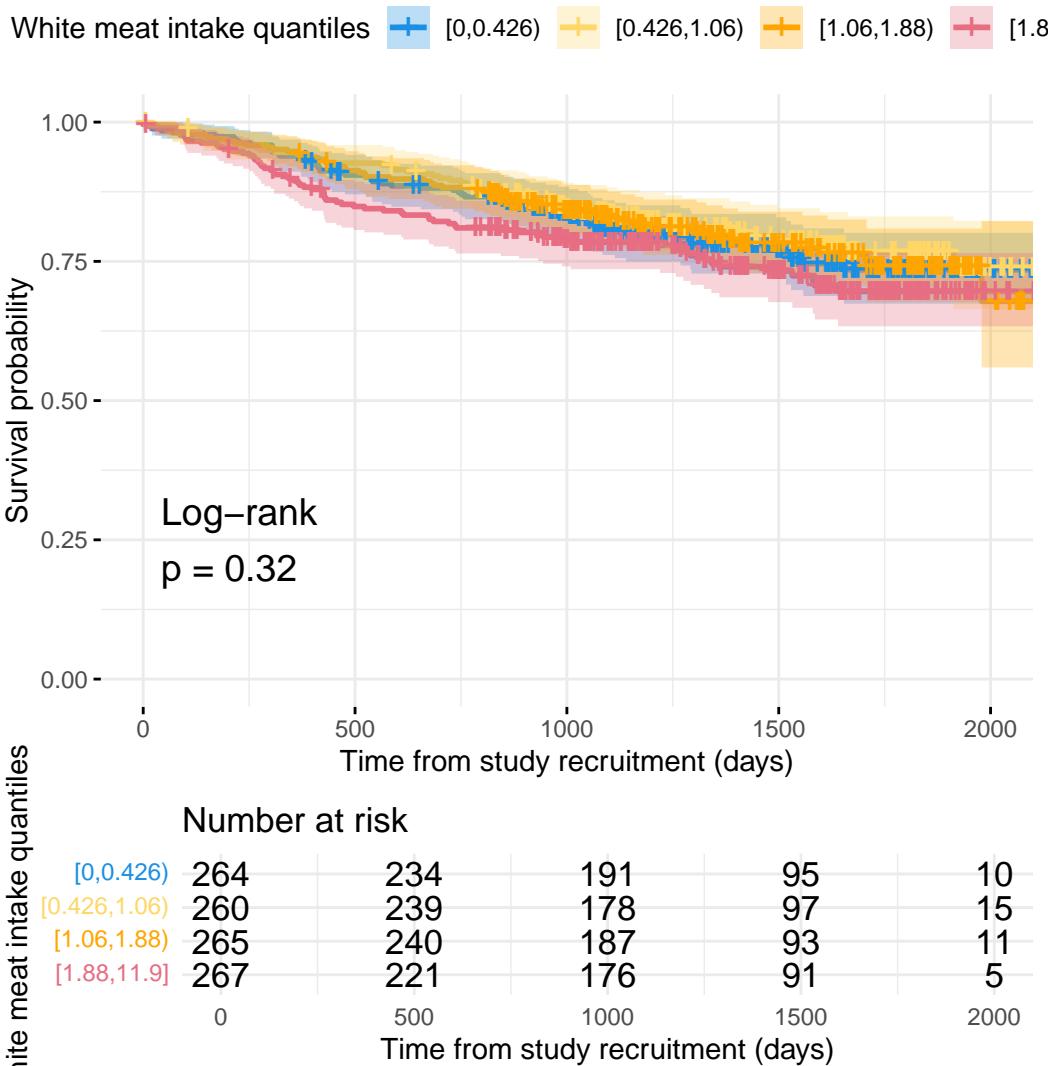
```
# Run survival analysis using utility function for hard flare
analysis_result <- run_survival_analysis(
  data = flare.df,
  var_name = "whiteMeatIntake",
  outcome_time = "hardflare_time",
  outcome_event = "hardflare",
  legend_title = "White meat intake quantiles",
```

```
plot_base_path = "plots/ibd/hard-flare/diet/whiteMeatIntake",
break_time_by = 500
)

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(hardflare_time, hardflare) ~
    Sex + cat + IMD + dqi_tot + BMI + whiteMeatIntake_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.df
)

# Display plot and model summary
analysis_result$plot
```

Time to hard flare



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.2445	0.9442	1.6403	0.1205
catFC 50-250	1.8704	1.3660	2.5610	0.0001
catFC > 250	2.6241	1.8565	3.7090	0.0000

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	0.9482	0.5073	1.7726	0.8678
IMD3	1.0017	0.5489	1.8280	0.9957
IMD4	1.3843	0.7884	2.4305	0.2576
IMD5	1.0005	0.5734	1.7457	0.9986
dqi_tot	1.0032	0.9907	1.0158	0.6189
BMI	0.9902	0.9639	1.0173	0.4741
whiteMeatIntake_cat[0.426	0.8970	0.6077	1.3241	0.5845
whiteMeatIntake_cat[1.06,	0.9039	0.6161	1.3261	0.6054
whiteMeatIntake_cat[1.88,	1.2086	0.8331	1.7532	0.3183

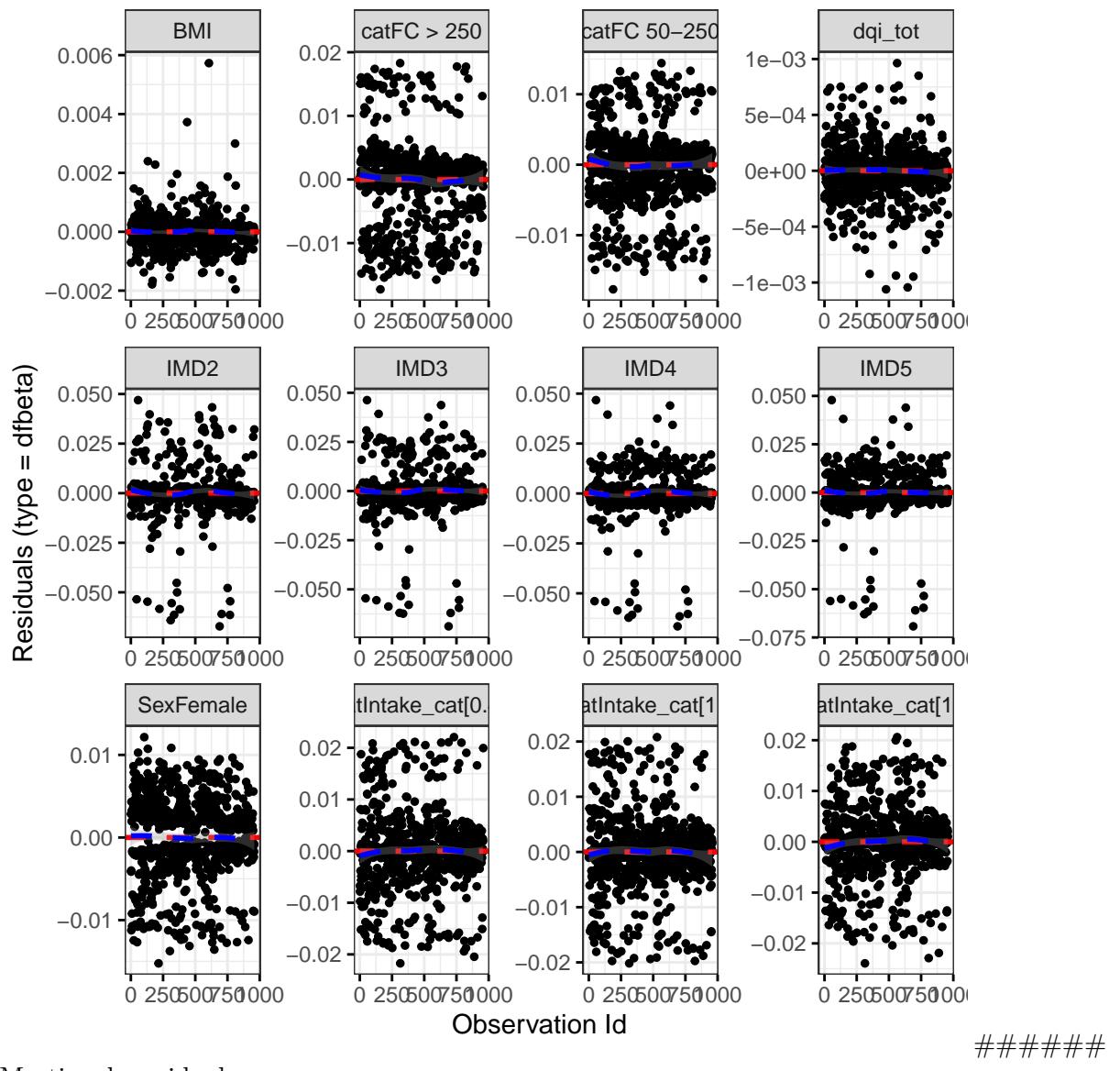
Diagnostics:

Proportional hazards assumption test

	Chi-squared statistic	DF	P-value
Sex	0.0306	0.9897	0.8581
cat	6.5690	1.9794	0.0367
IMD	1.4597	3.9463	0.8278
dqi_tot	2.0433	0.9929	0.1515
BMI	1.8532	0.9882	0.1709
whiteMeatIntake_cat	2.5360	2.9711	0.4635
GLOBAL	15.2956	22.6568	0.8726

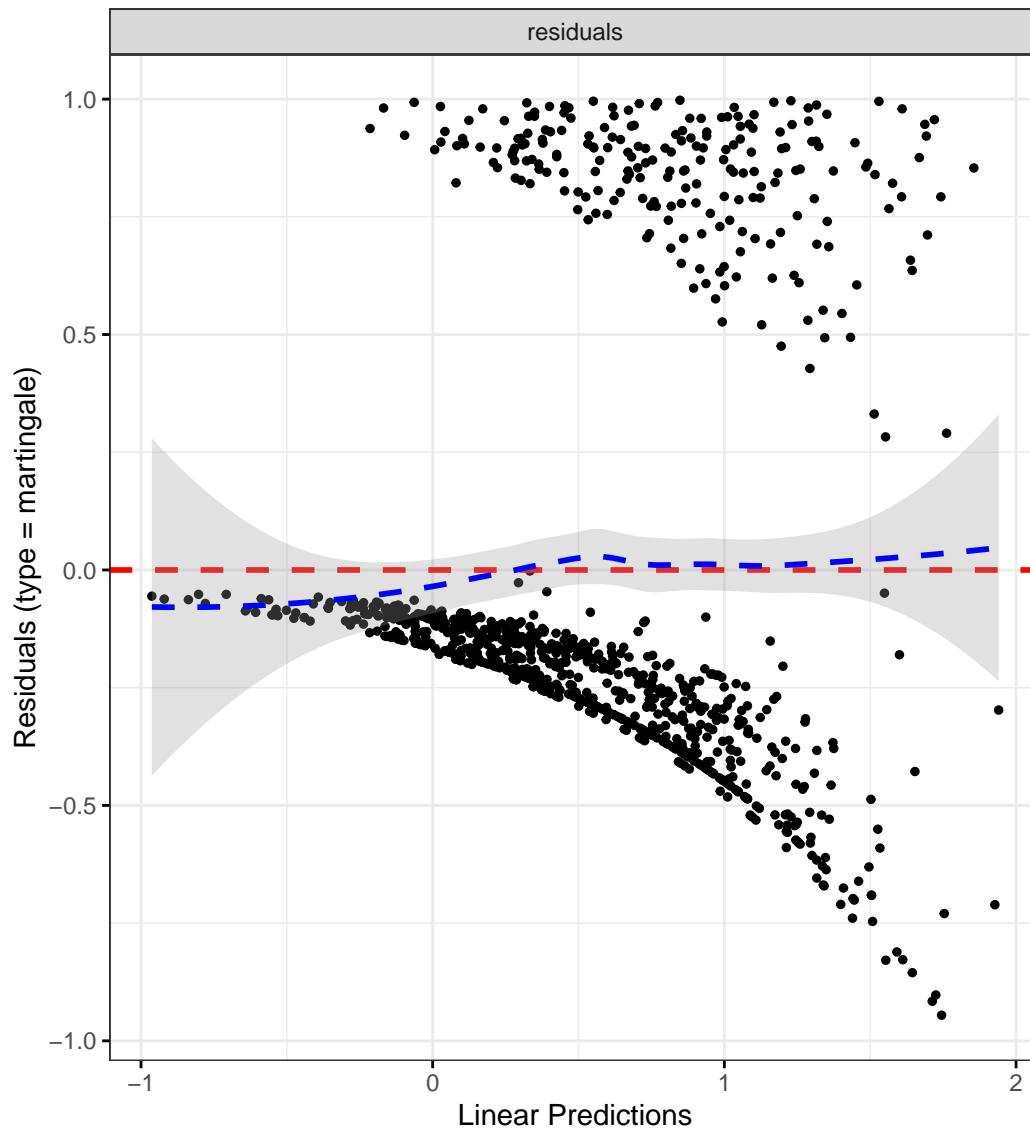
DF betas

```
`geom_smooth()` using formula = 'y ~ x'
```



Martingale residuals

```
`geom_smooth()` using formula = 'y ~ x'
```



Fish (white and oily)

Crohn's disease

Patient-reported flare

```
# Categorize white fish intake by quantiles  
flare.cd.df <- categorize_by_quantiles(flare.cd.df, "whiteFishIntake", reference_data = flare
```

```

# Run survival analysis using utility function
analysis_result <- run_survival_analysis(
  data = flare.cd.df,
  var_name = "whiteFishIntake",
  outcome_time = "softflare_time",
  outcome_event = "softflare",
  legend_title = "White fish intake quantiles",
  plot_base_path = "plots/cd/soft-flare/diet/whiteFishIntake",
  break_time_by = 200
)

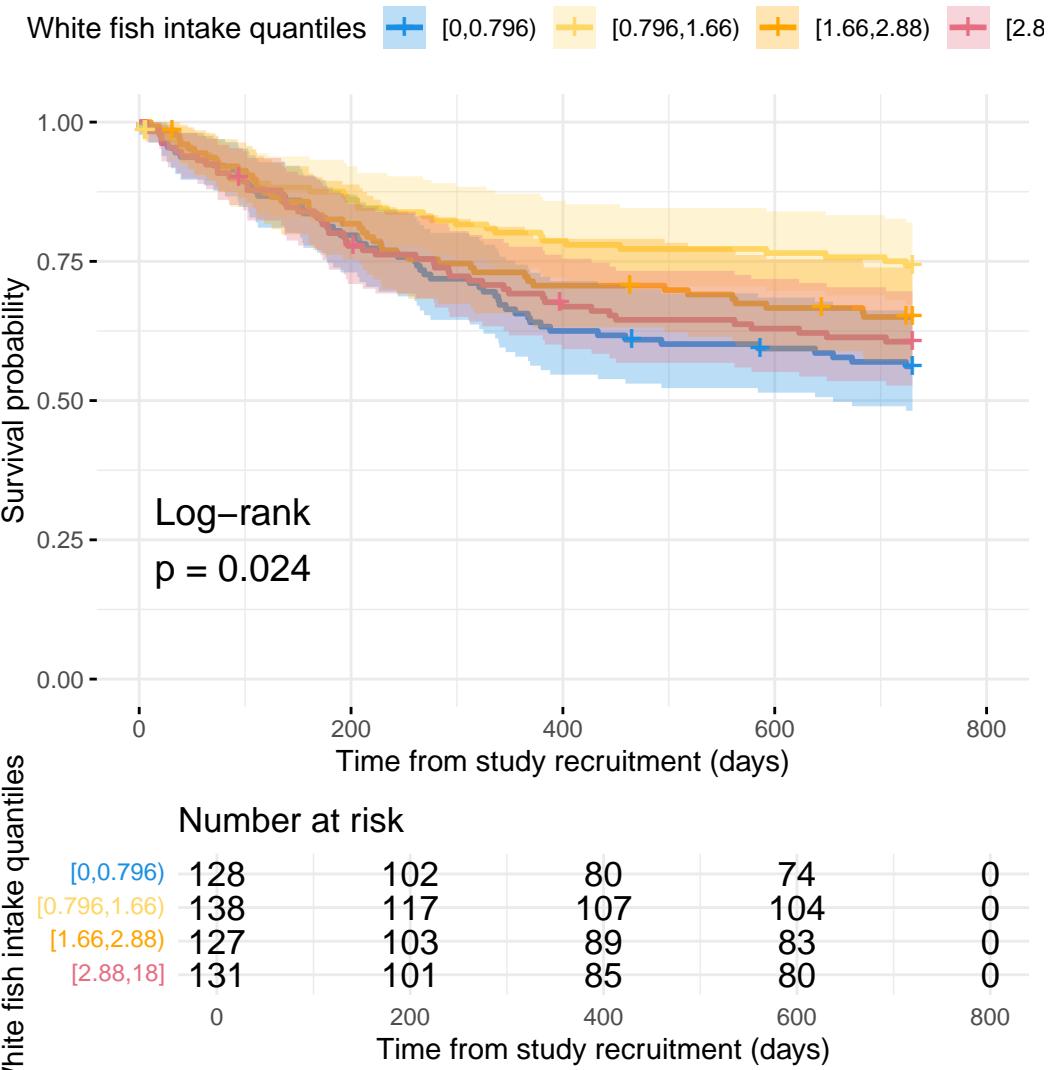
# Save plot as RDS
saveRDS(analysis_result$plot, paste0(paths$outdir, "whiteFishIntake-cd-soft.RDS"))

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(softflare_time, softflare) ~
    Sex + cat + IMD + dqi_tot + BMI + whiteFishIntake_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.cd.df
)

# Display plot and model summary
analysis_result$plot

```

Time to patient-reported flare



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.8518	1.3255	2.5870	0.0003
catFC 50-250	1.4540	1.0175	2.0779	0.0399
catFC > 250	2.1771	1.4827	3.1967	0.0001

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	0.7516	0.3920	1.4410	0.3899
IMD3	0.9740	0.5326	1.7812	0.9318
IMD4	0.8406	0.4630	1.5264	0.5684
IMD5	1.1131	0.6339	1.9545	0.7091
dqi_tot	1.0080	0.9939	1.0223	0.2698
BMI	1.0082	0.9809	1.0364	0.5585
whiteFishIntake_cat[0.796	0.4737	0.2988	0.7508	0.0015
whiteFishIntake_cat[1.66,	0.6477	0.4185	1.0024	0.0513
whiteFishIntake_cat[2.88,	0.7955	0.5209	1.2148	0.2895

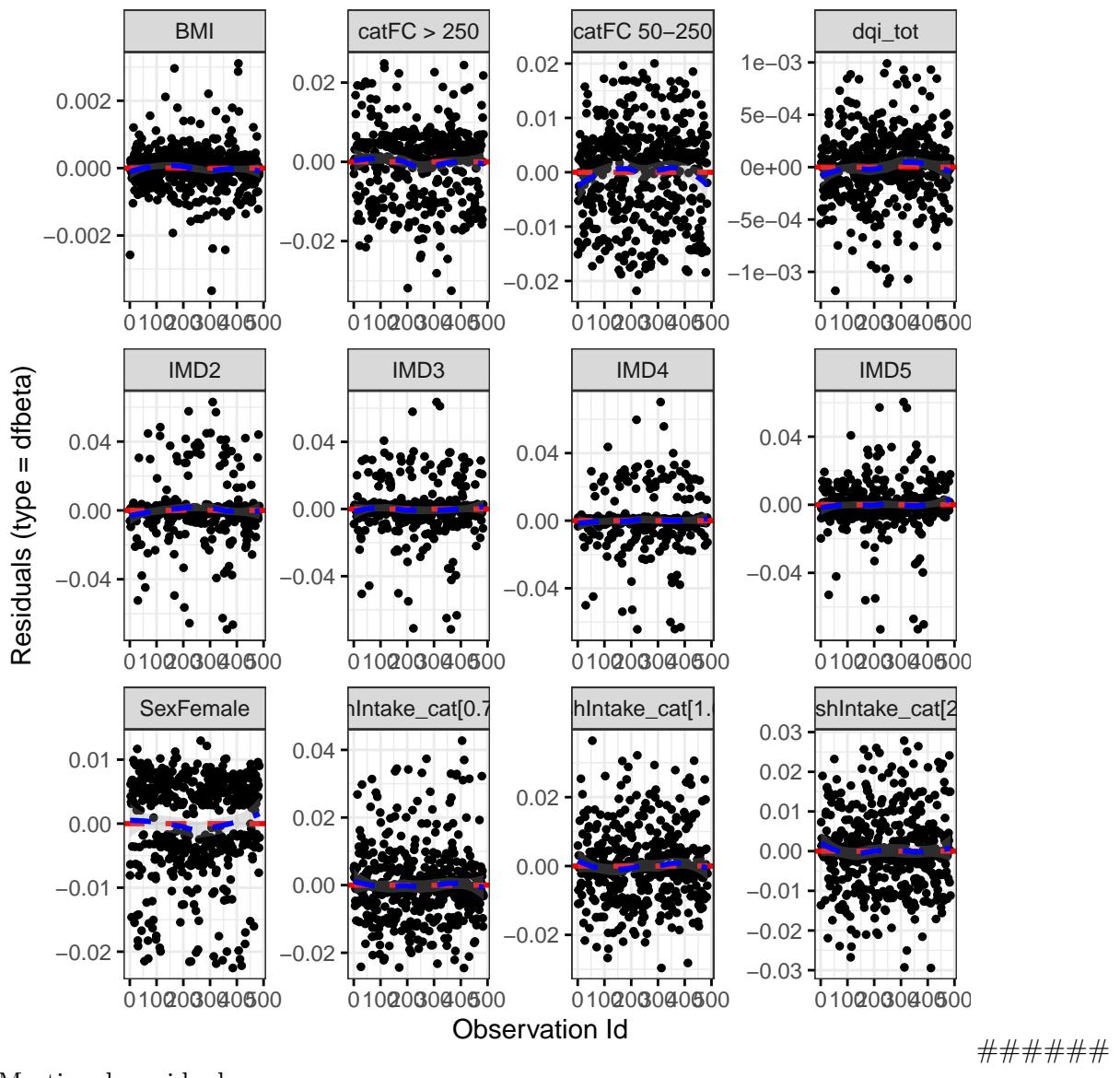
Diagnostics:

Proportional hazards assumption test

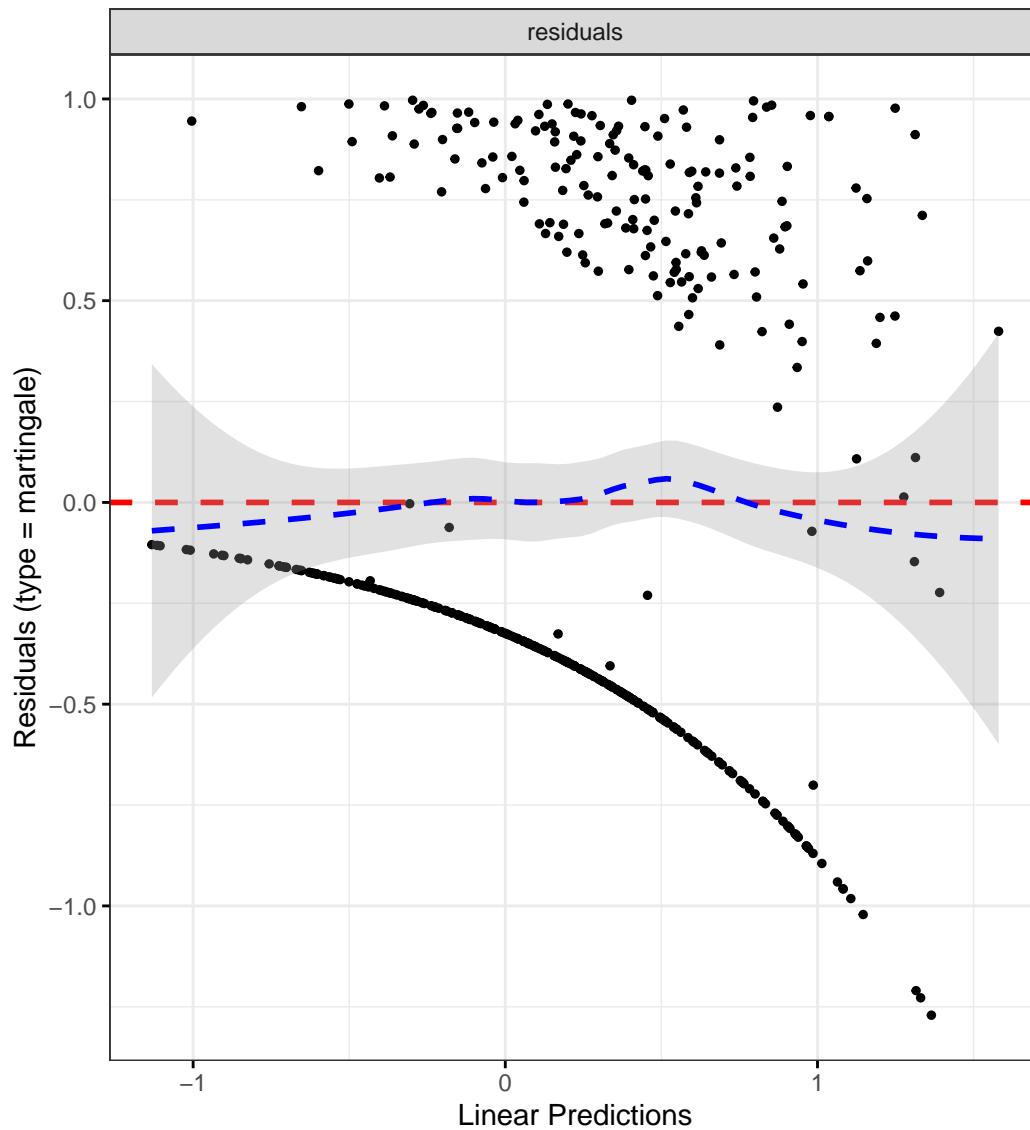
	Chi-squared statistic	DF	P-value
Sex	0.2468	1.0000	0.6193
cat	0.8197	2.0000	0.6638
IMD	3.1208	4.0000	0.5378
dqi_tot	0.2718	1.0000	0.6021
BMI	1.1602	1.0000	0.2814
whiteFishIntake_cat	1.4215	3.0000	0.7005
GLOBAL	6.9767	12.0001	0.8592

DF betas

```
`geom_smooth()` using formula = 'y ~ x'
```



```
`geom_smooth()` using formula = 'y ~ x'
```



Hard flare

```
# Run survival analysis using utility function for hard flare
analysis_result <- run_survival_analysis(
  data = flare.cd.df,
  var_name = "whiteFishIntake",
  outcome_time = "hardflare_time",
  outcome_event = "hardflare",
  legend_title = "White fish intake quantiles",
```

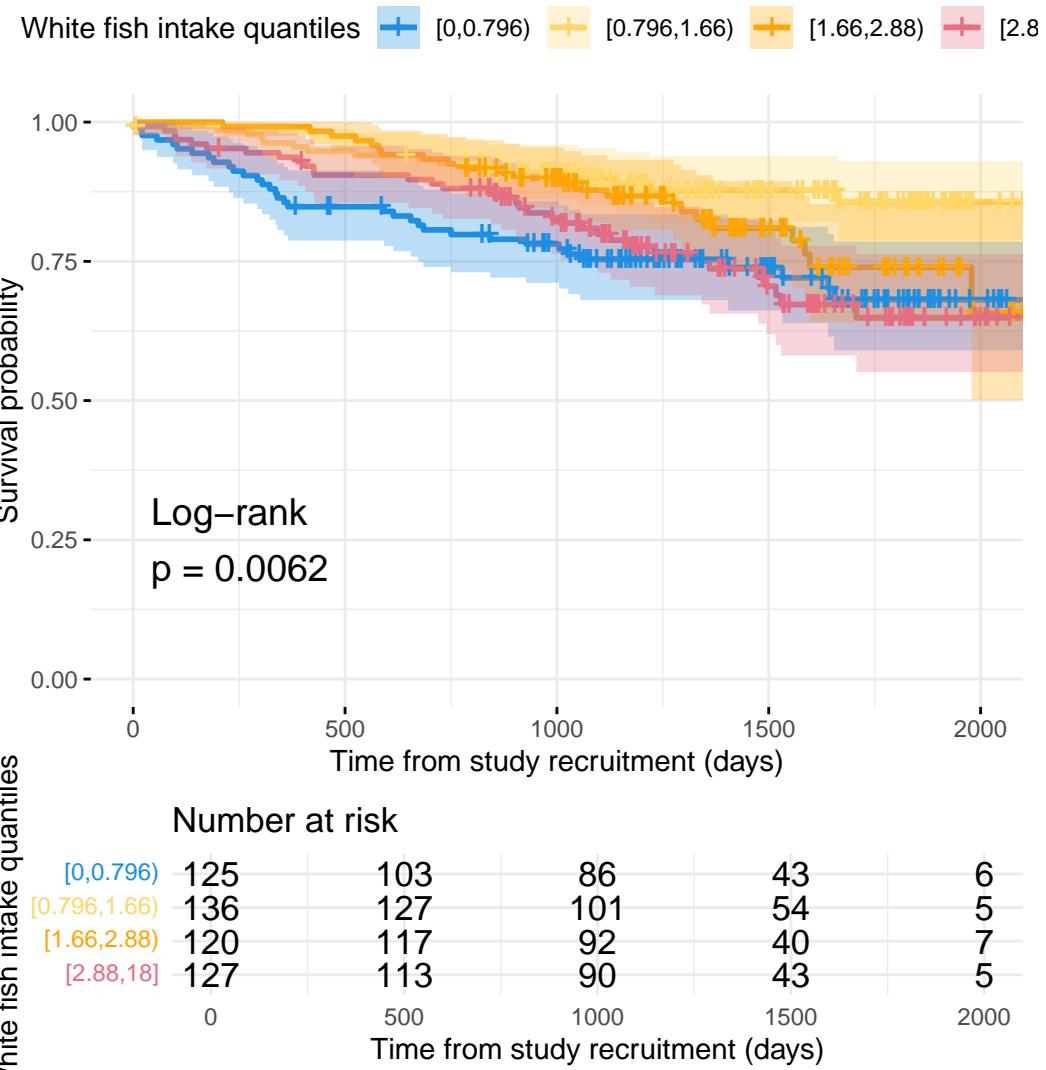
```
plot_base_path = "plots/cd/hard-flare/diet/whiteFishIntake",
break_time_by = 500
)

# Save plot as RDS
saveRDS(analysis_result$plot, paste0(paths$outdir, "whiteFishIntake-cd-hard.RDS"))

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(hardflare_time, hardflare) ~
    Sex + cat + IMD + dqi_tot + BMI + whiteFishIntake_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.cd.df
)

# Display plot and model summary
analysis_result$plot
```

Time to hard flare



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.3669	0.8962	2.0847	0.1467
catFC 50-250	2.0266	1.2588	3.2629	0.0036
catFC > 250	3.1633	1.8997	5.2672	0.0000

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	0.6713	0.2893	1.5580	0.3535
IMD3	0.8165	0.3672	1.8157	0.6191
IMD4	0.7617	0.3512	1.6518	0.4907
IMD5	0.7861	0.3748	1.6486	0.5242
dqi_tot	1.0052	0.9869	1.0240	0.5780
BMI	1.0167	0.9812	1.0534	0.3605
whiteFishIntake_cat[0.796	0.3096	0.1668	0.5748	0.0002
whiteFishIntake_cat[1.66,	0.5213	0.2928	0.9282	0.0269
whiteFishIntake_cat[2.88,	0.7569	0.4458	1.2851	0.3024

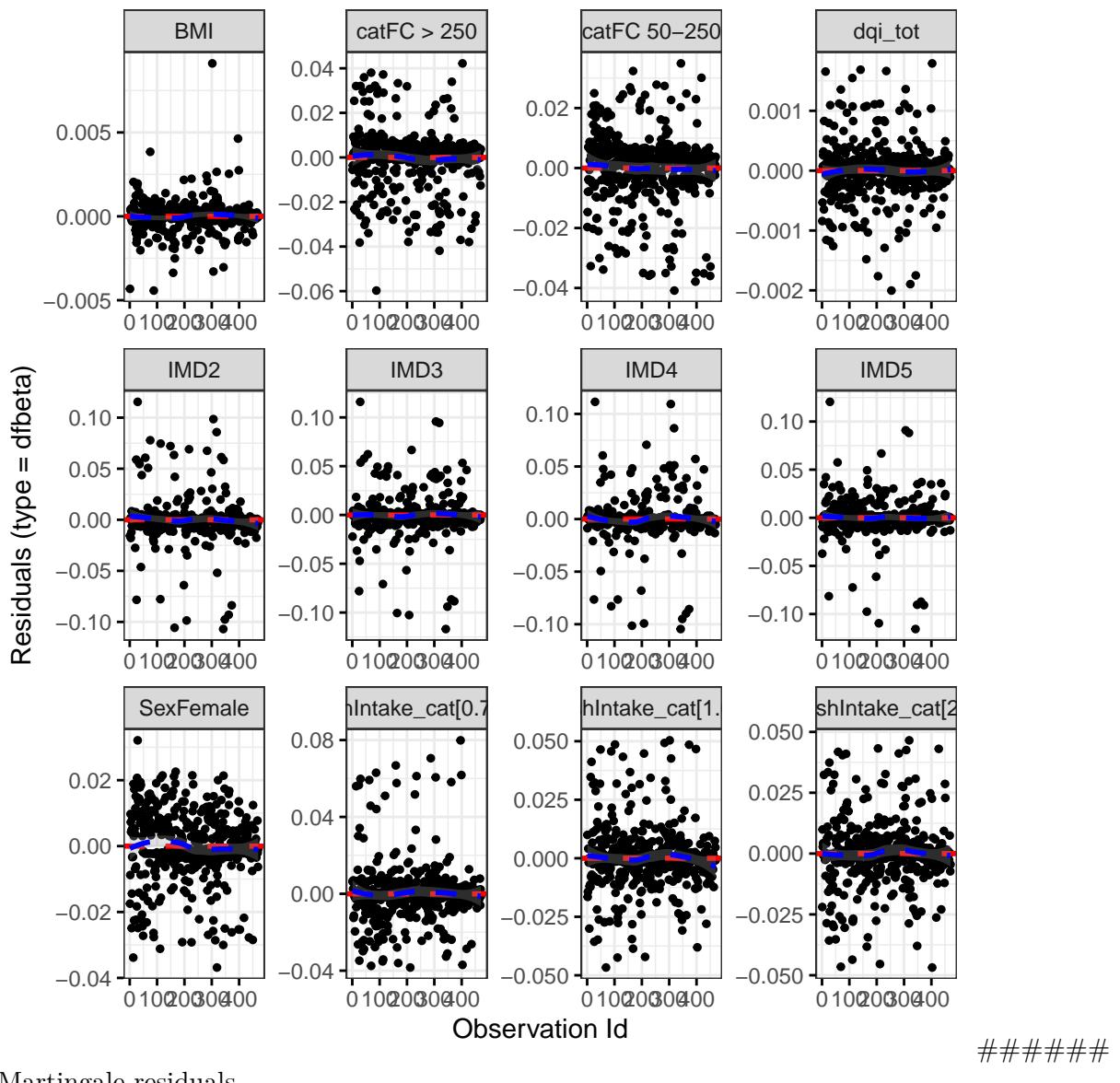
Diagnostics:

Proportional hazards assumption test

	Chi-squared statistic	DF	P-value
Sex	0.0086	0.9671	0.9192
cat	8.2453	1.9787	0.0158
IMD	3.3773	3.9247	0.4850
dqi_tot	2.4859	0.9898	0.1133
BMI	1.3059	0.9752	0.2463
whiteFishIntake_cat	11.0664	2.9536	0.0109
GLOBAL	27.4577	19.1135	0.0974

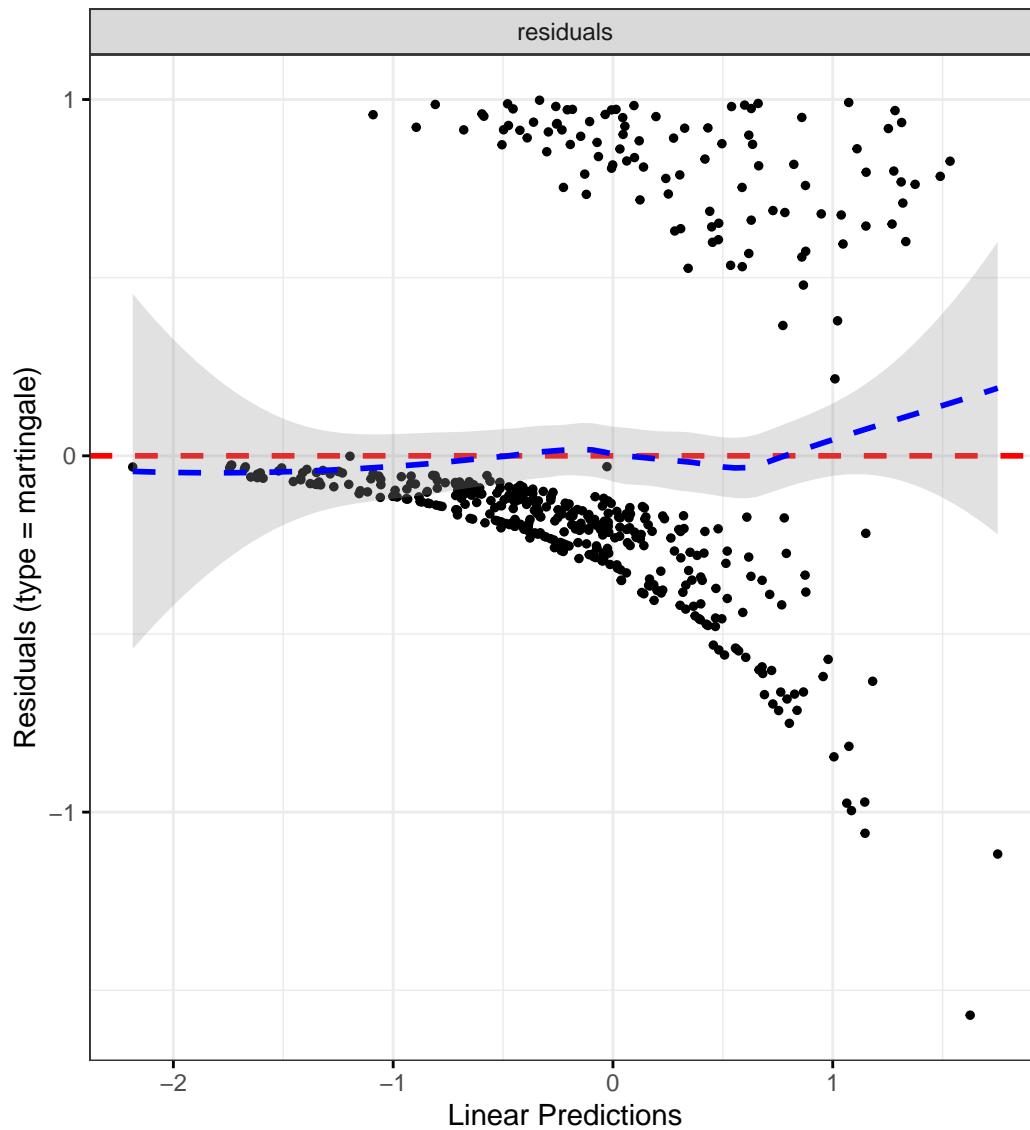
DF betas

```
`geom_smooth()` using formula = 'y ~ x'
```



Martingale residuals

```
`geom_smooth()` using formula = 'y ~ x'
```



Ulcerative colitis

Patient-reported flare

```
# Categorize white fish intake by quantiles
flare.uc.df <- categorize_by_quantiles(flare.uc.df, "whiteFishIntake", reference_data = flare)

# Run survival analysis using utility function
```

```

analysis_result <- run_survival_analysis(
  data = flare.uc.df,
  var_name = "whiteFishIntake",
  outcome_time = "softflare_time",
  outcome_event = "softflare",
  legend_title = "White fish intake quantiles",
  plot_base_path = "plots/uc/soft-flare/diet/whiteFishIntake",
  break_time_by = 200
)

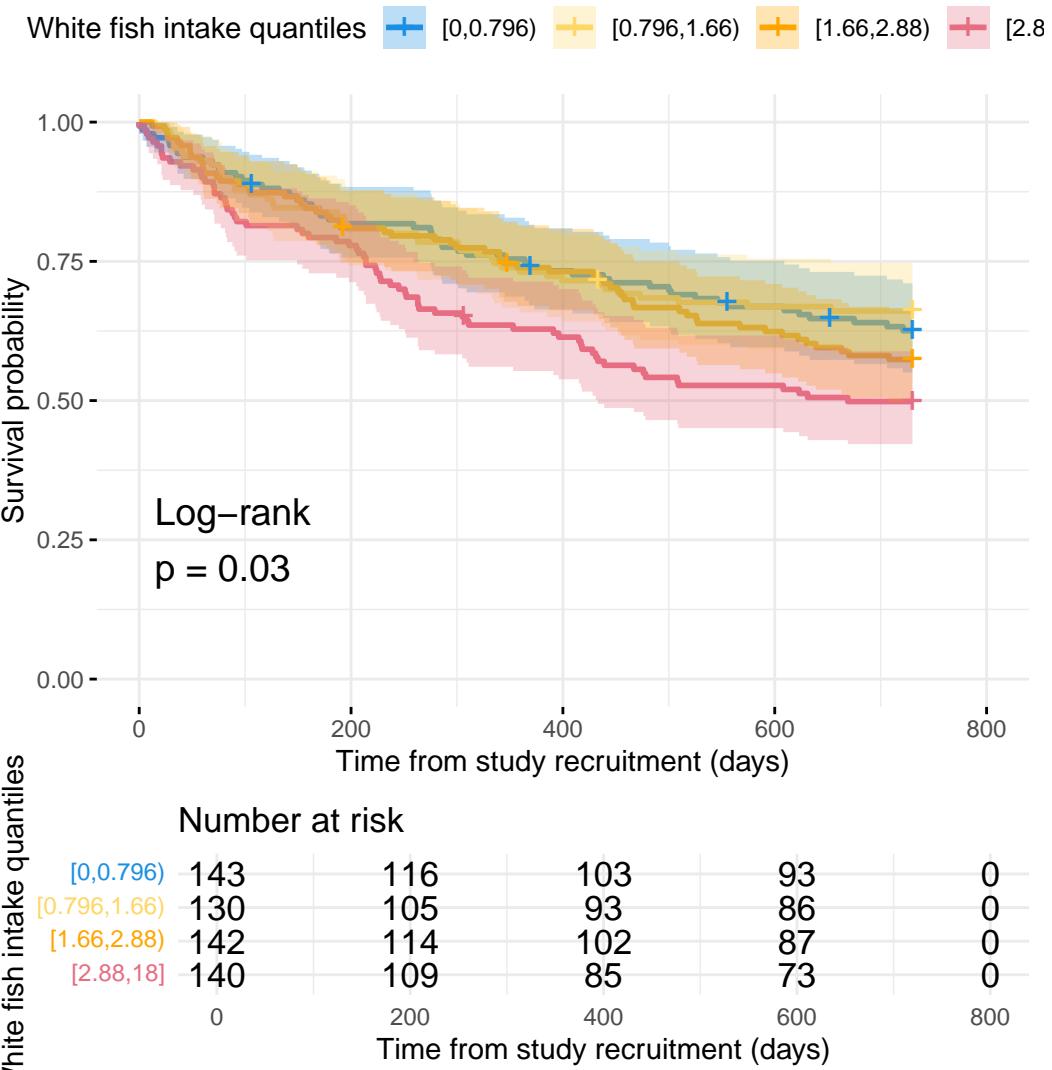
# Save plot as RDS
saveRDS(analysis_result$plot, paste0(paths$outdir, "whiteFishIntake-uc-soft.RDS"))

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(softflare_time, softflare) ~
    Sex + cat + IMD + dqi_tot + BMI + whiteFishIntake_cat +
    frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.uc.df
)

# Display plot and model summary
analysis_result$plot

```

Time to patient-reported flare



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.6795	1.2559	2.2461	0.0005
catFC 50-250	1.7231	1.2495	2.3763	0.0009
catFC > 250	2.0810	1.4563	2.9737	0.0001

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	1.4833	0.7781	2.8277	0.2310
IMD3	1.1348	0.6038	2.1329	0.6944
IMD4	1.3866	0.7641	2.5160	0.2824
IMD5	1.2546	0.6956	2.2629	0.4510
dqi_tot	0.9948	0.9814	1.0083	0.4482
BMI	0.9802	0.9511	1.0102	0.1930
whiteFishIntake_cat[0.796	1.1316	0.7406	1.7293	0.5676
whiteFishIntake_cat[1.66,	1.1029	0.7386	1.6471	0.6320
whiteFishIntake_cat[2.88,	1.5903	1.0731	2.3568	0.0208

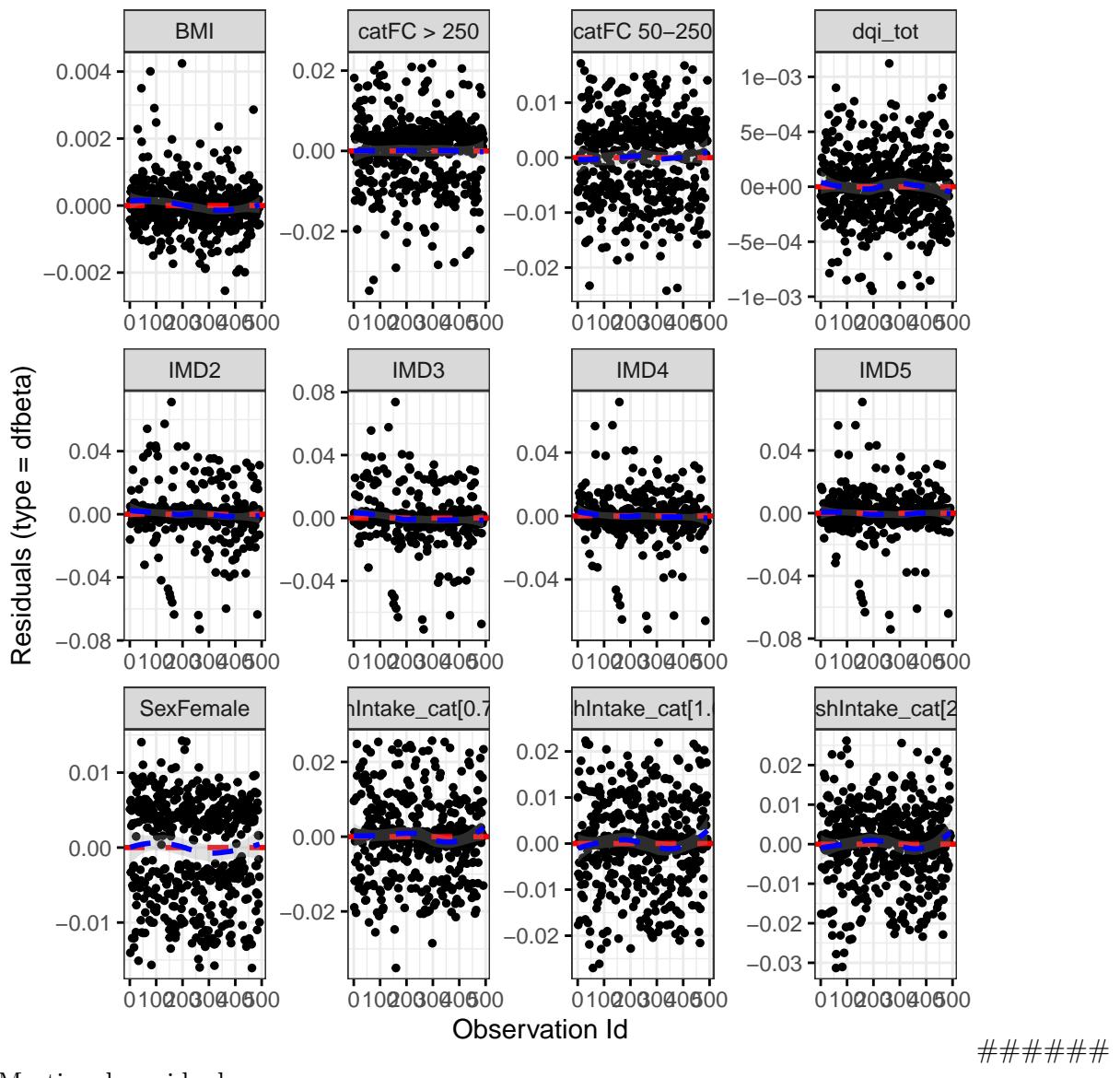
Diagnostics:

Proportional hazards assumption test

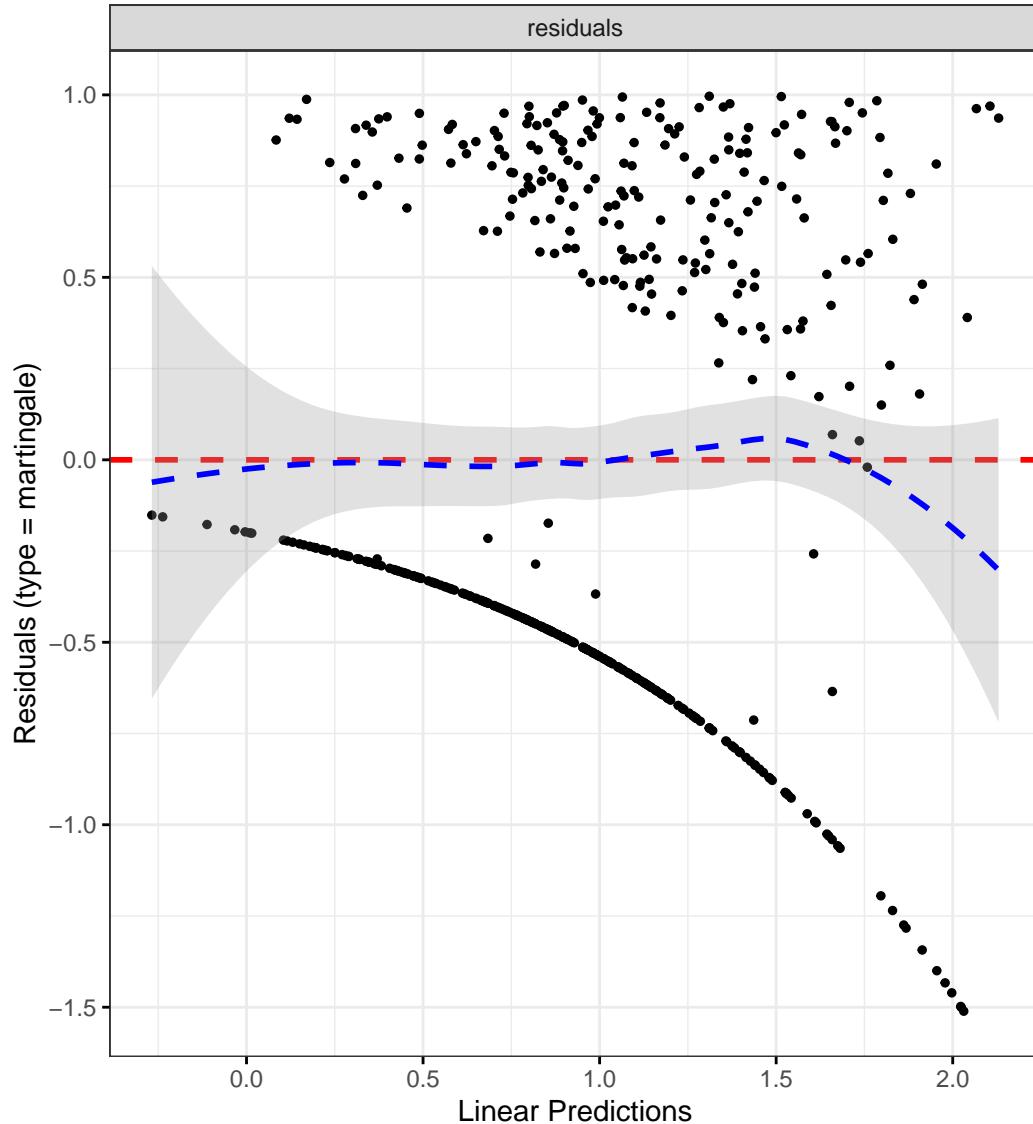
	Chi-squared statistic	DF	P-value
Sex	0.0023	1.0000	0.9620
cat	3.3157	2.0000	0.1905
IMD	2.6930	4.0000	0.6104
dqi_tot	0.8417	1.0000	0.3589
BMI	0.9320	1.0000	0.3343
whiteFishIntake_cat	4.3829	3.0000	0.2230
GLOBAL	13.7361	12.0001	0.3179

DF betas

```
`geom_smooth()` using formula = 'y ~ x'
```



```
`geom_smooth()` using formula = 'y ~ x'
```



Hard flare

```
# Run survival analysis using utility function for hard flare
analysis_result <- run_survival_analysis(
  data = flare.uc.df,
  var_name = "whiteFishIntake",
  outcome_time = "hardflare_time",
  outcome_event = "hardflare",
  legend_title = "White fish intake quantiles",
```

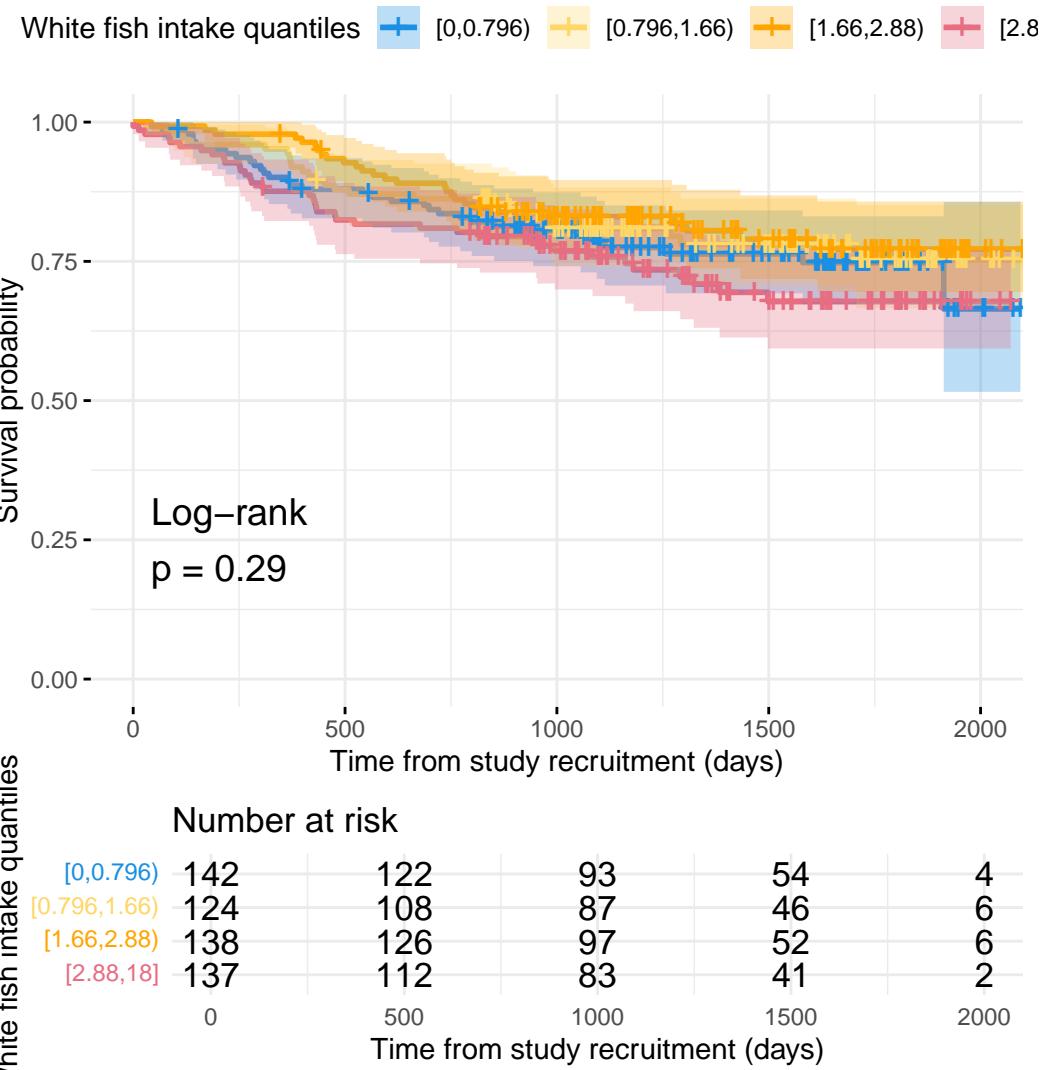
```
plot_base_path = "plots/uc/hard-flare/diet/whiteFishIntake",
break_time_by = 500
)

# Save plot as RDS
saveRDS(analysis_result$plot, paste0(paths$outdir, "whiteFishIntake-uc-hard.RDS"))

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(hardflare_time, hardflare) ~
    Sex + cat + IMD + dqi_tot + BMI + whiteFishIntake_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.uc.df
)

# Display plot and model summary
analysis_result$plot
```

Time to hard flare



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.2043	0.8203	1.7682	0.3427
catFC 50-250	2.1393	1.3771	3.3234	0.0007
catFC > 250	2.5089	1.5391	4.0897	0.0002

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	1.5800	0.6003	4.1587	0.3543
IMD3	1.3207	0.5126	3.4029	0.5645
IMD4	2.3071	0.9625	5.5300	0.0609
IMD5	1.3973	0.5772	3.3825	0.4583
dqi_tot	1.0029	0.9846	1.0215	0.7579
BMI	0.9582	0.9182	0.9999	0.0496
whiteFishIntake_cat[0.796	0.9208	0.5366	1.5801	0.7646
whiteFishIntake_cat[1.66,	0.7328	0.4234	1.2683	0.2666
whiteFishIntake_cat[2.88,	1.0419	0.6259	1.7342	0.8746

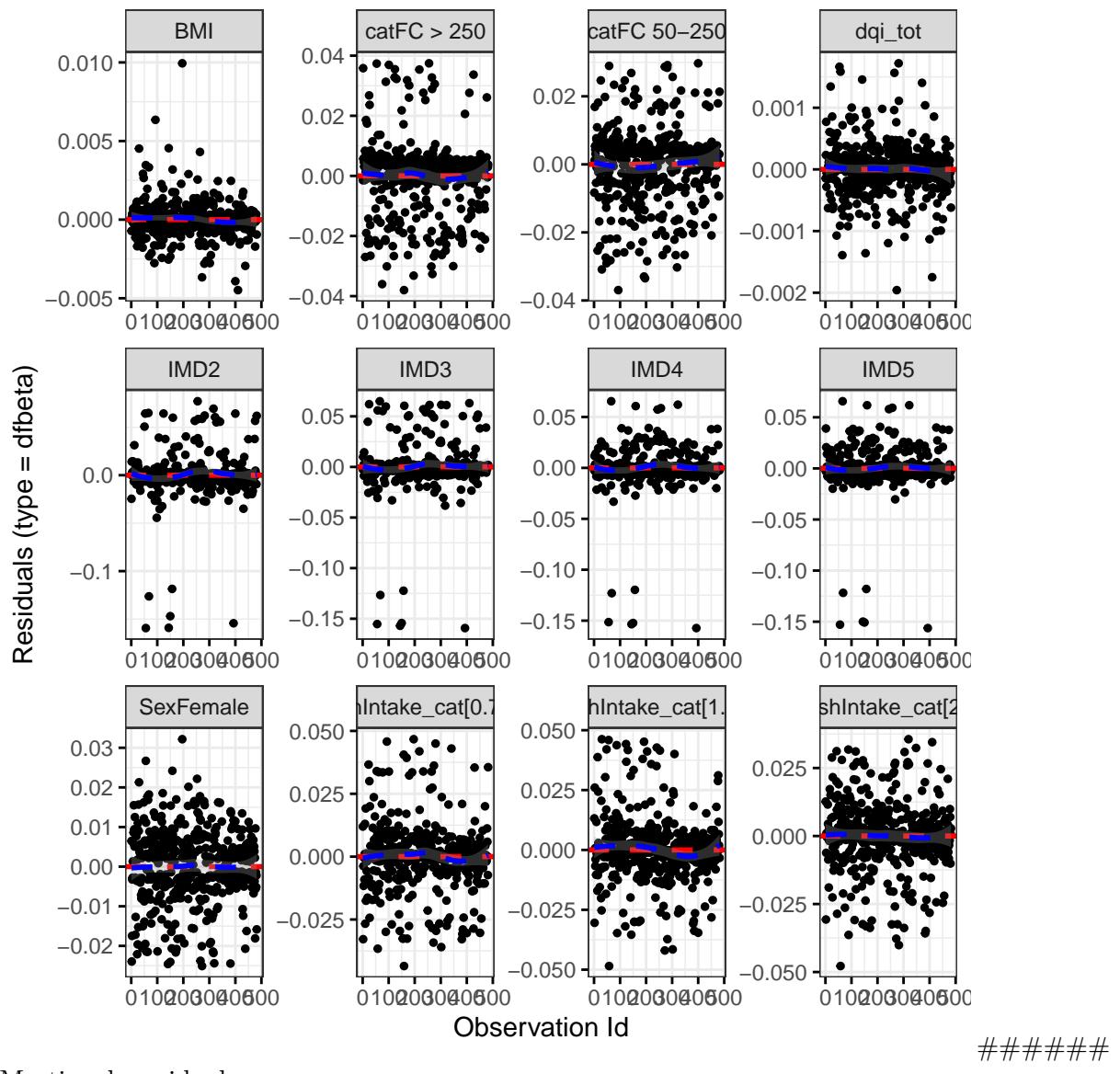
Diagnostics:

Proportional hazards assumption test

	Chi-squared statistic	DF	P-value
Sex	0.0197	0.9901	0.8859
cat	5.2113	1.9615	0.0713
IMD	0.9526	3.9382	0.9124
dqi_tot	0.0077	0.9884	0.9277
BMI	0.5184	0.9894	0.4673
whiteFishIntake_cat	5.4156	2.9592	0.1401
GLOBAL	13.7950	18.1517	0.7509

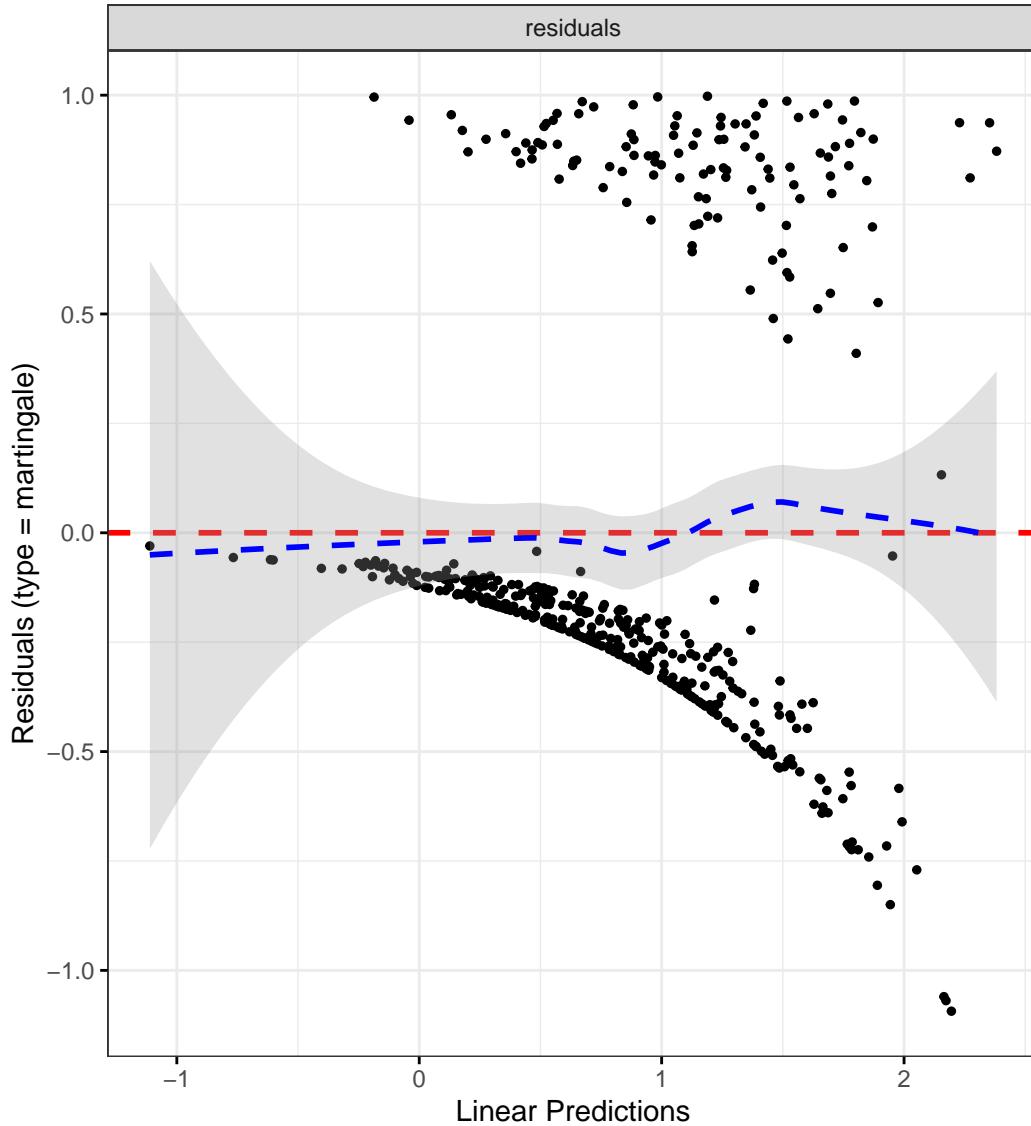
DF betas

```
`geom_smooth()` using formula = 'y ~ x'
```



Martingale residuals

```
`geom_smooth()` using formula = 'y ~ x'
```



Inflammatory bowel disease

Patient-reported flare

```
# Categorize white fish intake by quantiles
flare.df <- categorize_by_quantiles(flare.df, "whiteFishIntake", reference_data = flare.df)

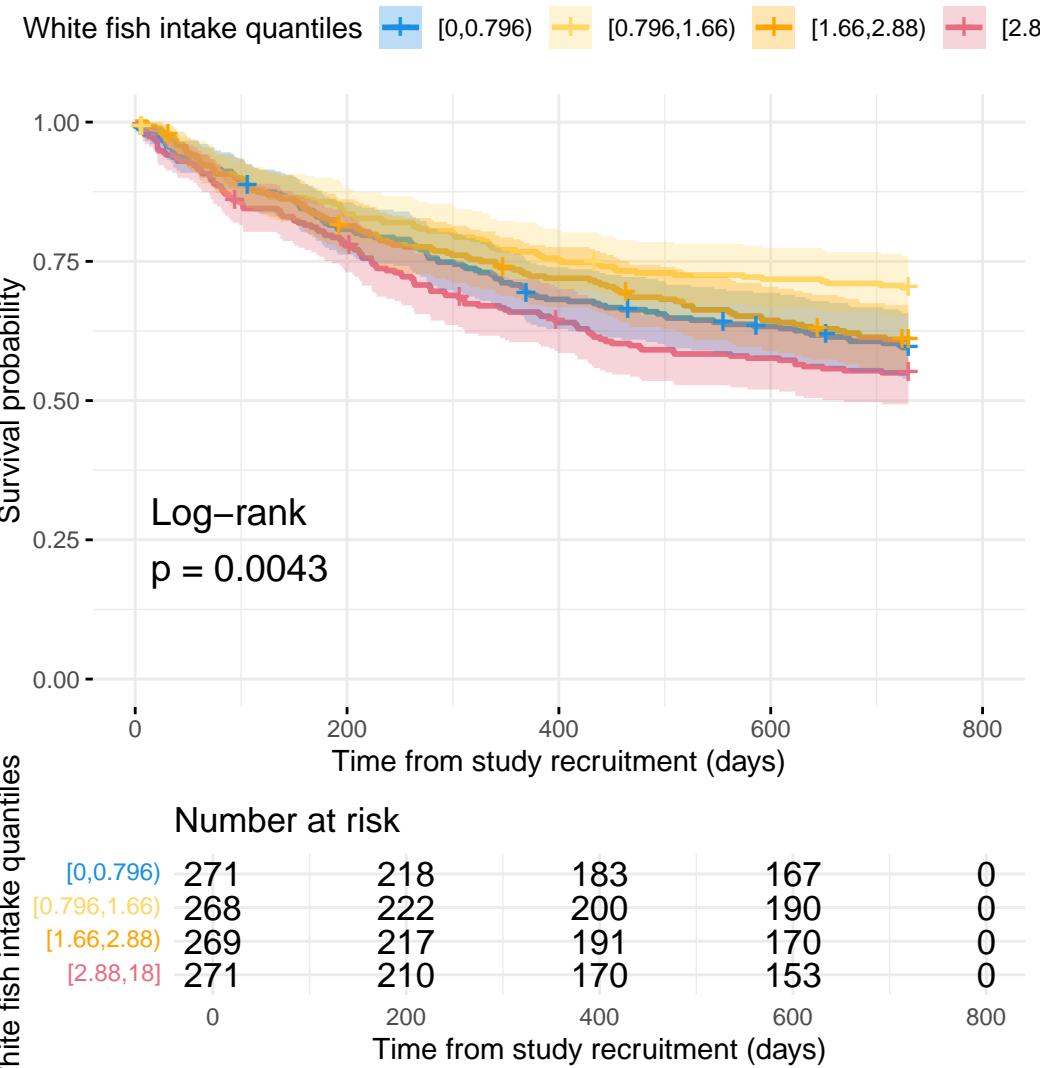
# Run survival analysis using utility function
```

```
analysis_result <- run_survival_analysis(
  data = flare.df,
  var_name = "whiteFishIntake",
  outcome_time = "softflare_time",
  outcome_event = "softflare",
  legend_title = "White fish intake quantiles",
  plot_base_path = "plots/ibd/soft-flare/diet/whiteFishIntake",
  break_time_by = 200
)

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(softflare_time, softflare) ~
    Sex + cat + IMD + dqi_tot + BMI + whiteFishIntake_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.df
)

# Display plot and model summary
analysis_result$plot
```

Time to patient-reported flare



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.7195	1.3854	2.1340	0.0000
catFC 50-250	1.5094	1.1920	1.9113	0.0006
catFC > 250	2.0167	1.5563	2.6132	0.0000

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	1.0305	0.6544	1.6227	0.8969
IMD3	1.0248	0.6636	1.5827	0.9119
IMD4	1.1336	0.7473	1.7196	0.5554
IMD5	1.1405	0.7619	1.7074	0.5230
dqi_tot	1.0008	0.9912	1.0105	0.8695
BMI	0.9957	0.9760	1.0157	0.6692
whiteFishIntake_cat[0.796	0.7342	0.5396	0.9990	0.0493
whiteFishIntake_cat[1.66,	0.8823	0.6588	1.1817	0.4009
whiteFishIntake_cat[2.88,	1.1629	0.8751	1.5452	0.2982

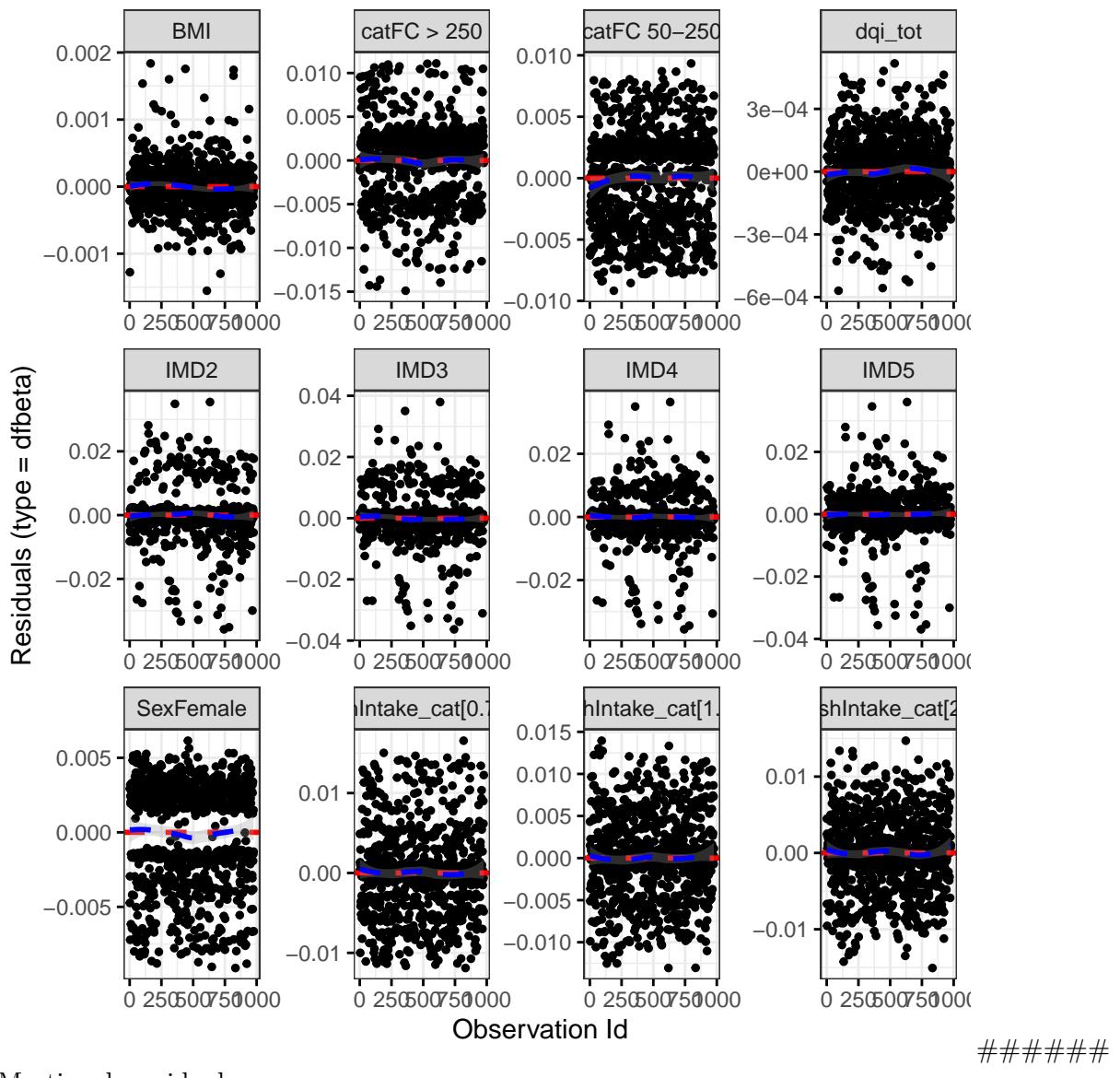
Diagnostics:

Proportional hazards assumption test

	Chi-squared statistic	DF	P-value
Sex	0.0136	1.0000	0.9072
cat	1.0328	2.0000	0.5967
IMD	5.1923	4.0000	0.2681
dqi_tot	1.3542	1.0000	0.2445
BMI	0.0006	1.0000	0.9813
whiteFishIntake_cat	4.4596	3.0000	0.2159
GLOBAL	11.8491	12.0002	0.4579

DF betas

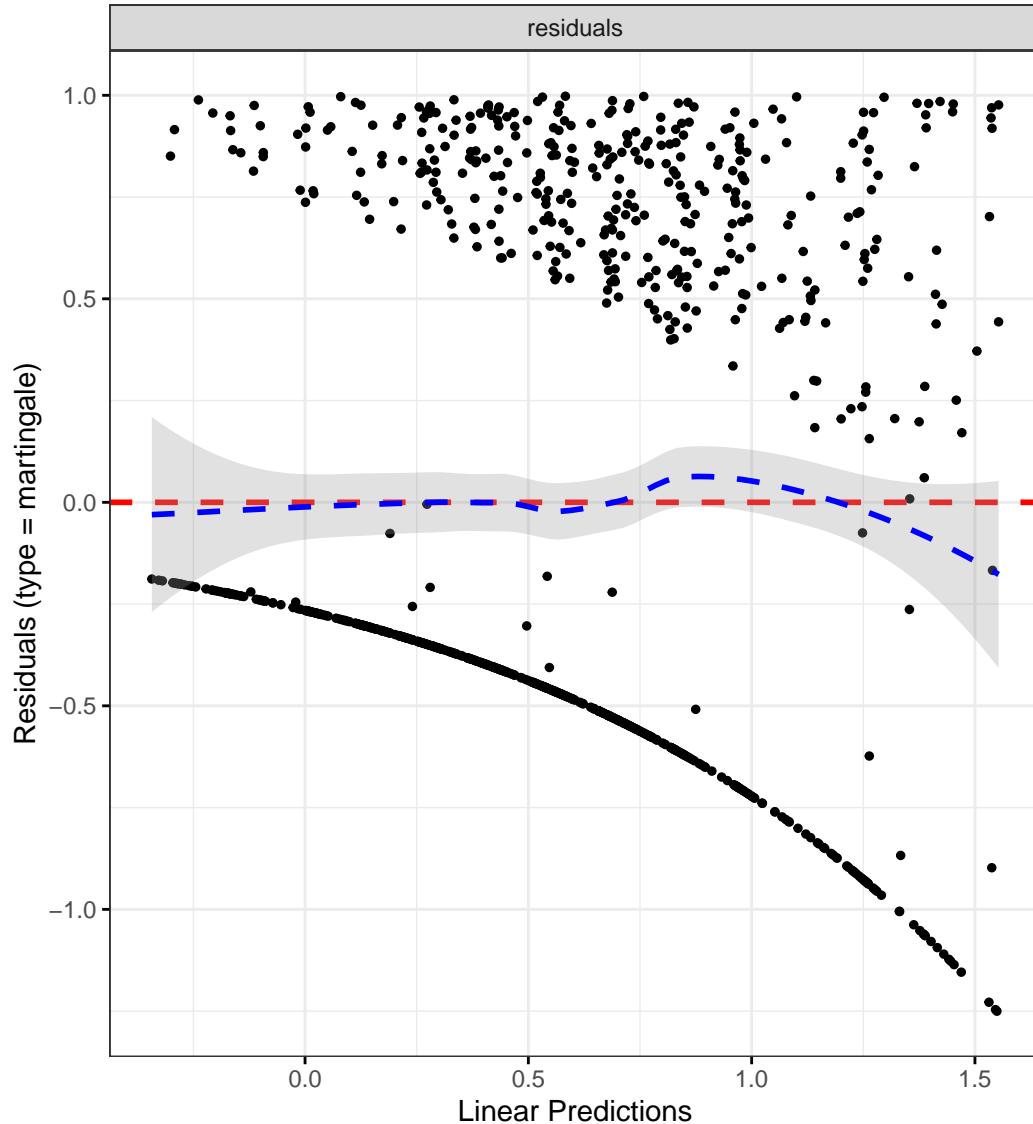
```
`geom_smooth()` using formula = 'y ~ x'
```



#####

Martingale residuals

```
`geom_smooth()` using formula = 'y ~ x'
```



Hard flare

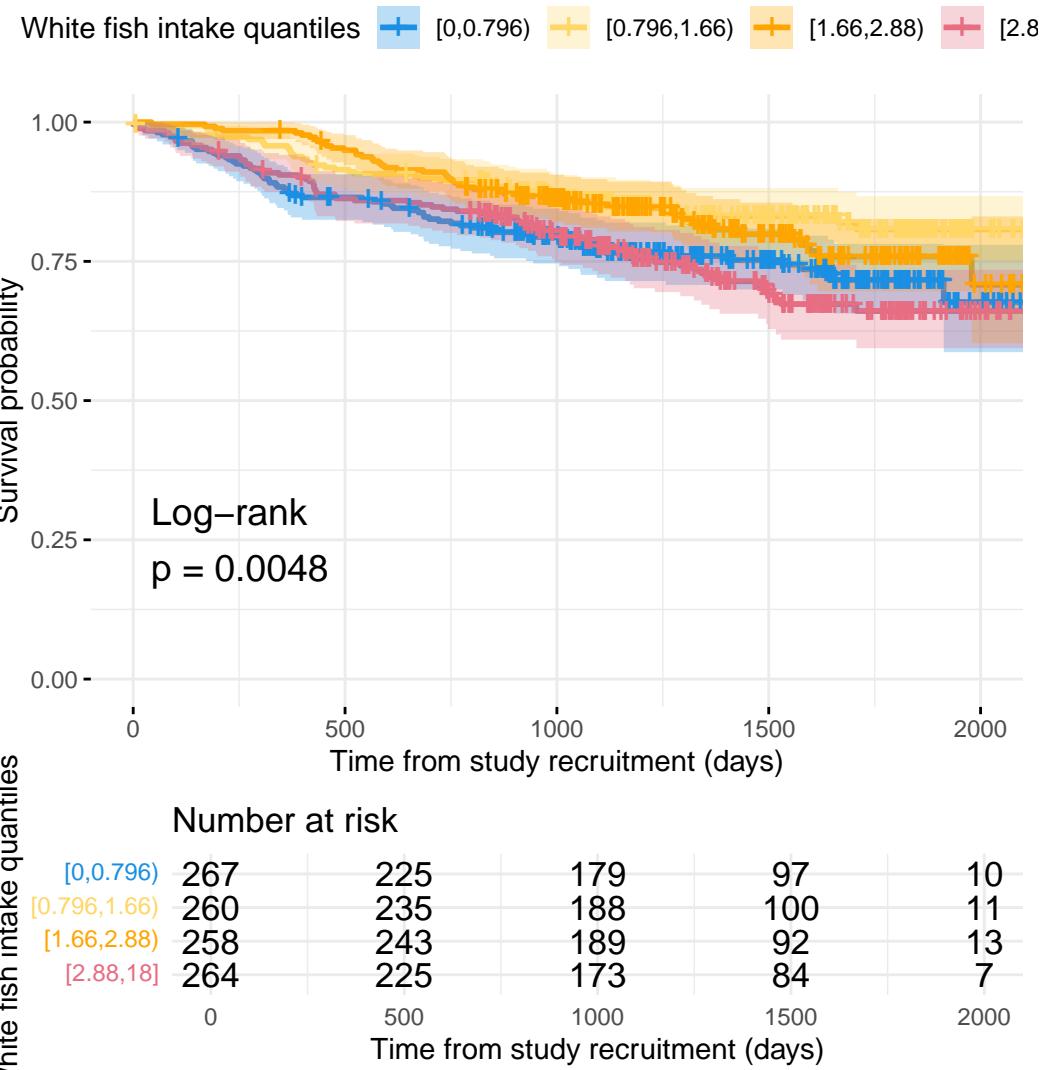
```
# Run survival analysis using utility function for hard flare
analysis_result <- run_survival_analysis(
  data = flare.df,
  var_name = "whiteFishIntake",
  outcome_time = "hardflare_time",
  outcome_event = "hardflare",
  legend_title = "White fish intake quantiles",
```

```
plot_base_path = "plots/ibd/hard-flare/diet/whiteFishIntake",
break_time_by = 500
)

# Run Cox model with categorical variable
fit.me <- coxph(
  Surv(hardflare_time, hardflare) ~
    Sex + cat + IMD + dqi_tot + BMI + whiteFishIntake_cat + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.df
)

# Display plot and model summary
analysis_result$plot
```

Time to hard flare



```
invisible(cox_summary(fit.me))
```

Cox model summary:

Variable	HR	Lower 95%	Upper 95%	P-value
SexFemale	1.2493	0.9455	1.6509	0.1174
catFC 50-250	1.9337	1.4033	2.6647	0.0001
catFC > 250	2.6610	1.8769	3.7726	0.0000

Variable	HR	Lower 95%	Upper 95%	P-value
IMD2	0.9543	0.5111	1.7819	0.8832
IMD3	0.9657	0.5304	1.7585	0.9092
IMD4	1.3903	0.7921	2.4401	0.2509
IMD5	1.0164	0.5819	1.7754	0.9545
dqi_tot	1.0030	0.9902	1.0160	0.6489
BMI	0.9895	0.9631	1.0167	0.4451
whiteFishIntake_cat[0.796	0.5553	0.3721	0.8287	0.0040
whiteFishIntake_cat[1.66,	0.6371	0.4306	0.9428	0.0241
whiteFishIntake_cat[2.88,	0.9103	0.6326	1.3099	0.6128

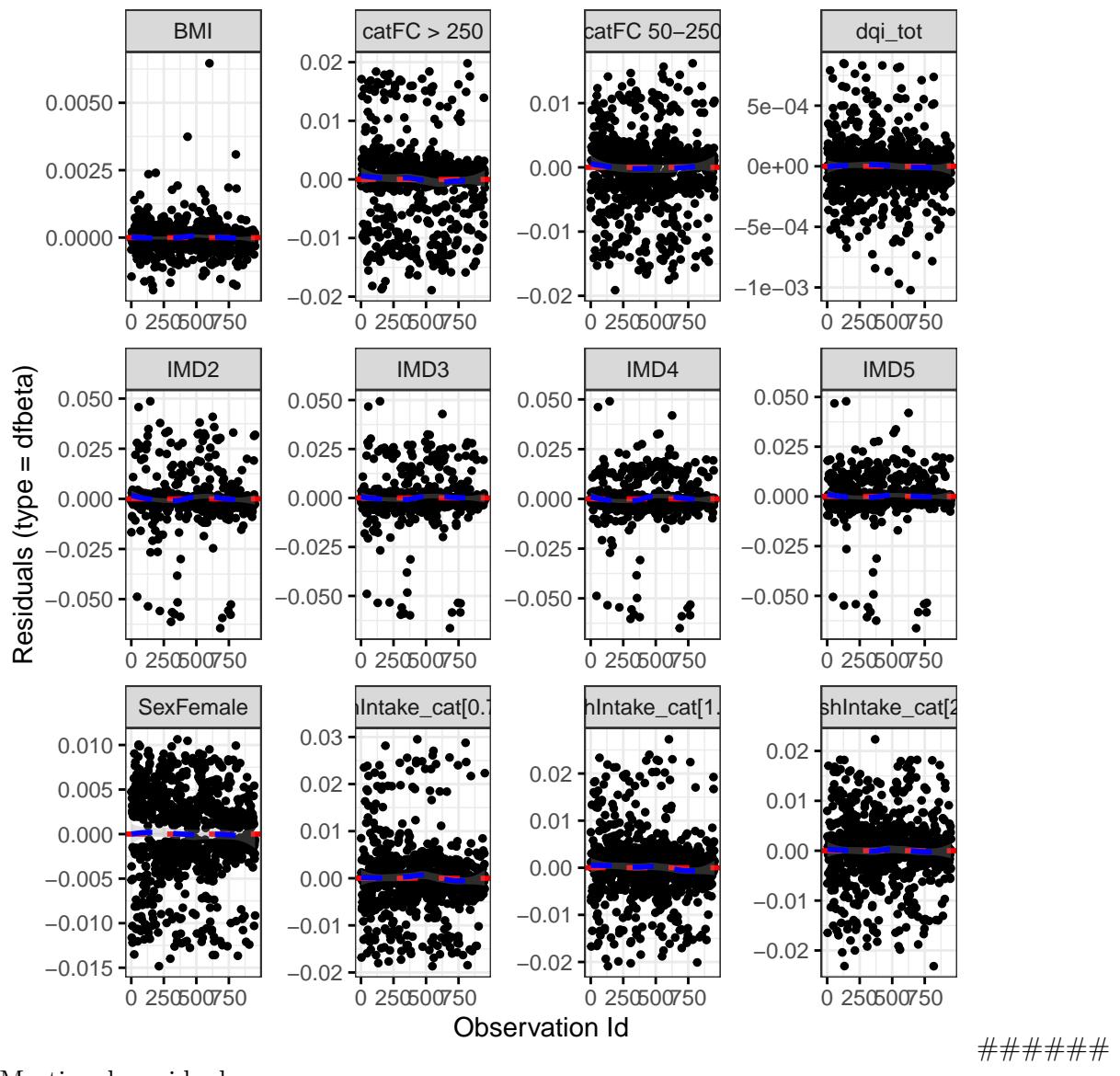
Diagnostics:

Proportional hazards assumption test

	Chi-squared statistic	DF	P-value
Sex	0.0005	0.9885	0.9822
cat	5.9214	1.9787	0.0507
IMD	1.5648	3.9443	0.8085
dqi_tot	1.8045	0.9919	0.1774
BMI	1.8165	0.9874	0.1750
whiteFishIntake_cat	13.4644	2.9681	0.0036
GLOBAL	24.5262	22.9639	0.3731

DF betas

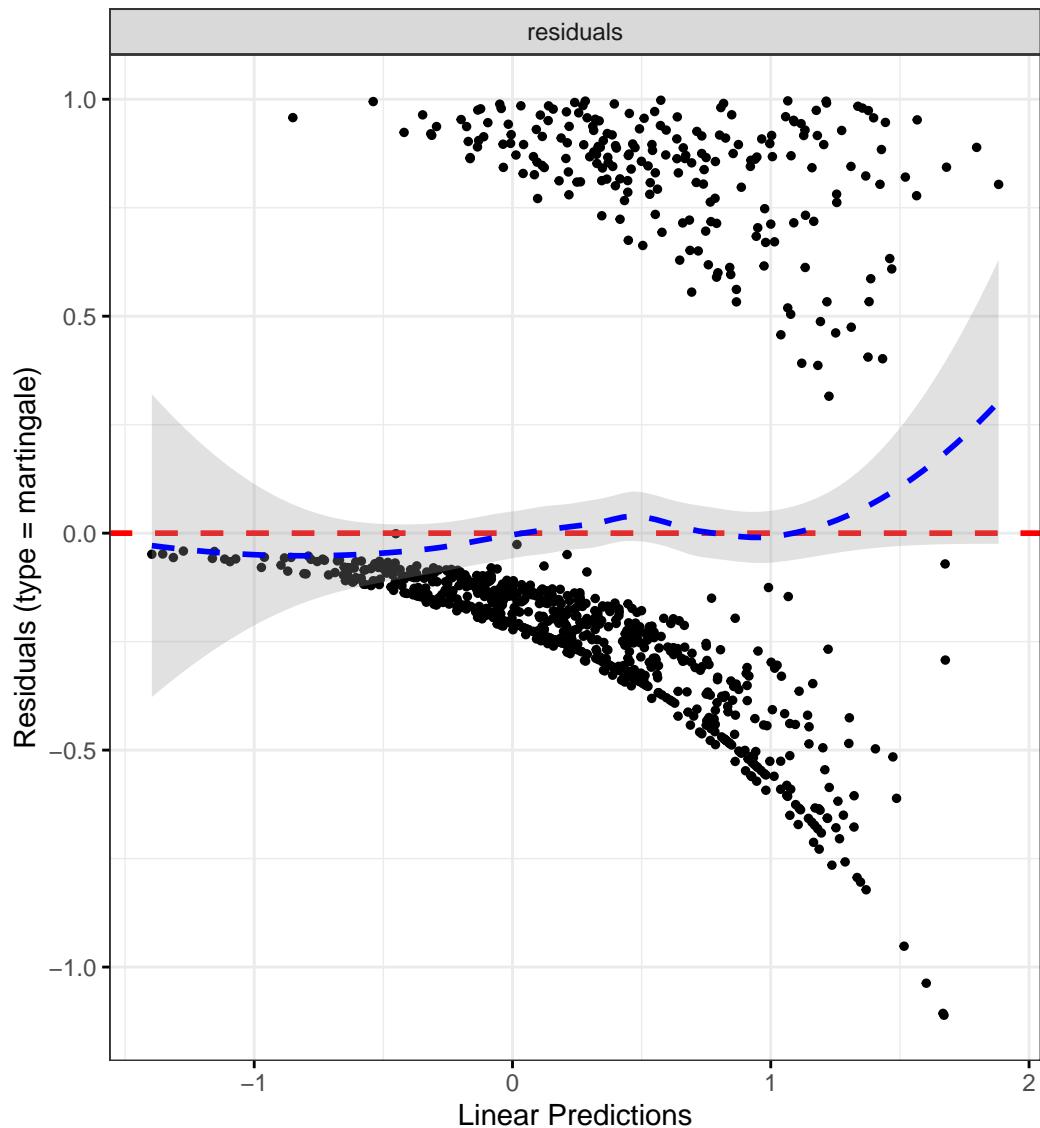
```
`geom_smooth()` using formula = 'y ~ x'
```



#####

Martingale residuals

```
`geom_smooth()` using formula = 'y ~ x'
```



Reproduction and reproducibility

Session info

R version 4.4.0 (2024-04-24)

Platform: aarch64-unknown-linux-gnu

locale: LC_CTYPE=en_US.UTF-8, LC_NUMERIC=C, LC_TIME=en_US.UTF-8,
LC_COLLATE=en_US.UTF-8, LC_MONETARY=en_US.UTF-8, LC_MESSAGES=en_US.UTF-

8, *LC_PAPER=en_US.UTF-8*, *LC_NAME=C*, *LC_ADDRESS=C*, *LC_TELEPHONE=C*, *LC_MEASUREMENT=en_US.UTF-8* and *LC_IDENTIFICATION=C*

attached base packages: *stats*, *graphics*, *grDevices*, *utils*, *datasets*, *methods* and *base*

other attached packages: *gtsummary(v.1.7.2)*, *DescTools(v.0.99.54)*, *finalfit(v.1.0.7)*, *coxme(v.2.2-20)*, *bdsmatrix(v.1.3-7)*, *pander(v.0.6.5)*, *survminer(v.0.4.9)*, *ggpubr(v.0.6.0)*, *survival(v.3.5-8)*, *datefixR(v.1.6.1)*, *lubridate(v.1.9.3)*, *forcats(v.1.0.0)*, *stringr(v.1.5.1)*, *dplyr(v.1.1.4)*, *purrr(v.1.0.2)*, *readr(v.2.1.5)*, *tidyR(v.1.3.1)*, *tibble(v.3.2.1)*, *ggplot2(v.3.5.1)*, *tidyverse(v.2.0.0)* and *readxl(v.1.4.3)*

loaded via a namespace (and not attached): *gridExtra(v.2.3)*, *gld(v.2.6.6)*, *rlang(v.1.1.3)*, *magrittr(v.2.0.3)*, *e1071(v.1.7-14)*, *compiler(v.4.4.0)*, *mgcv(v.1.9-1)*, *vcvers(v.0.6.5)*, *pkgconfig(v.2.0.3)*, *shape(v.1.4.6.1)*, *fastmap(v.1.2.0)*, *backports(v.1.5.0)*, *labeling(v.0.4.3)*, *KMsurv(v.0.1-5)*, *utf8(v.1.2.4)*, *rmarkdown(v.2.27)*, *markdown(v.1.12)*, *tzdb(v.0.4.0)*, *nloptr(v.2.0.3)*, *xfun(v.0.44)*, *glmnet(v.4.1-8)*, *jomo(v.2.7-6)*, *jsonlite(v.1.8.8)*, *pan(v.1.9)*, *broom(v.1.0.6)*, *R6(v.2.5.1)*, *stringi(v.1.8.4)*, *car(v.3.1-2)*, *boot(v.1.3-30)*, *rpart(v.4.1.23)*, *cellranger(v.1.1.0)*, *Rcpp(v.1.0.12)*, *iterators(v.1.0.14)*, *knitr(v.1.47)*, *zoo(v.1.8-12)*, *Matrix(v.1.7-0)*, *splines(v.4.4.0)*, *nnet(v.7.3-19)*, *timechange(v.0.3.0)*, *tidyselect(v.1.2.1)*, *rstudioapi(v.0.16.0)*, *abind(v.1.4-5)*, *yaml(v.2.3.8)*, *ggtext(v.0.1.2)*, *codetools(v.0.2-20)*, *lattice(v.0.22-6)*, *withr(v.3.0.0)*, *evaluate(v.0.23)*, *proxy(v.0.4-27)*, *xml2(v.1.3.6)*, *survMisc(v.0.5.6)*, *pillar(v.1.9.0)*, *carData(v.3.0-5)*, *mice(v.3.16.0)*, *foreach(v.1.5.2)*, *generics(v.0.1.3)*, *hms(v.1.1.3)*, *commonmark(v.1.9.1)*, *munsell(v.0.5.1)*, *scales(v.1.3.0)*, *rootSolve(v.1.8.2.4)*, *minqa(v.1.2.7)*, *xtable(v.1.8-4)*, *class(v.7.3-22)*, *glue(v.1.7.0)*, *lmom(v.3.0)*, *tools(v.4.4.0)*, *data.table(v.1.15.4)*, *lme4(v.1.1-35.3)*, *ggsignif(v.0.6.4)*, *Exact(v.3.2)*, *mvtnorm(v.1.2-5)*, *grid(v.4.4.0)*, *colorspace(v.2.1-0)*, *nlme(v.3.1-164)*, *cli(v.3.6.2)*, *km.ci(v.0.5-6)*, *fansi(v.1.0.6)*, *expm(v.0.999-9)*, *broom.helpers(v.1.15.0)*, *gt(v.0.10.1)*, *gttable(v.0.3.5)*, *rstatix(v.0.7.2)*, *digest(v.0.6.35)*, *farver(v.2.1.2)*, *htmltools(v.0.5.8.1)*, *lifecycle(v.1.0.4)*, *httr(v.1.4.7)*, *mitml(v.0.4-5)*, *gridtext(v.0.1.5)* and *MASS(v.7.3-60.2)*

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Monteiro, Carlos Augusto, Geoffrey Cannon, Jean-Claude Moubarac, Renata Bertazzi Levy, Maria Laura C Louzada, and Patrícia Constante Jaime. 2017. “The UN Decade of Nutrition, the NOVA Food Classification and the Trouble with Ultra-Processing.” *Public Health Nutrition* 21 (1): 5–17. <https://doi.org/10.1017/s1368980017000234>.