Logistic Regression Models with GEE for the Secondary Outcomes in the VQI FBVAR Dataset

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Variables to adjust for

We used a correlation matrix to report the correlations between variables statistically. We also discussed with our collaborator on the choice of variables to adjust for. Here we did not report the correlation matrix.

- cluster on `CENTERID`

- adjust for `AGECAT`, `GENDER`, `PREOP_SMOKING`, `PRIOR_AORSURG`, `PRIOR_CHF`, `PREOP_DIALYSIS`

- adjust for `PATHOLOGY`, `extent`

*In the model, we merge groups for the **extent**: merge "Juxtarenal AAA" with "Type 4 TAAA"; "Type 1 TAAA", "Type 2 TAAA", "Type 3 TAAA", with "Type 5 TAAA". Now **extent** is a binary variable, Juxtarenal or not.*

- categorical secondary outcomes: `POSTOP_CEREBROSX`, `POSTOP_SPINAL_ISCHEMIA`, `POSTOP_DIALYSIS`, `POSTOP_LOS`, `POSTOP_COMPLICATIONS`, `POSTOP_LEGEMBO`, `POSTOP_RESPIRATORY`, `RETX_R_RTOR`, `BRANCH_POST`, `TOTAL_LOS`,`ICUSTAY`, `POSTOP_INTISCH`

logistic regression with Generalized Estimating Equations for categorical secondary outcomes

- continuous secondary outcomes: `POSTOP_PRBC`

linear regression with Generalized Estimating Equations for continuous secondary outcomes

`POSTOP_GFR`

TOTAL_LOS: Length of stay in days between admission date and discharge date

Characteristic	TOTAL_LOS Length of Stay in days		
	OR[1]	95% CI[1]	p-value
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	5.14	4.11, 6.43	**<0.001**

[1]OR = Odds Ratio, CI = Confidence Interval

	TOTAL_LOS Length of Stay in days		
Characteristic	**OR[1]**	**95% CI[1]**	**p-value**
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	3.79	2.99, 4.81	**<0.001**
AGECAT			
<50	—	—	
>79	1.91	0.88, 4.15	0.10
50-59	1.89	0.82, 4.36	0.13
60-69	1.32	0.63, 2.77	0.47
70-79	2.16	1.02, 4.55	**0.043**
GENDER			
female	—	—	
male	0.62	0.51, 0.75	**<0.001**
PREOP_SMOKING			
No	—	—	
Yes	0.99	0.76, 1.29	0.94
PRIOR_AORSURG			
Both	—	—	
Endo	1.59	0.93, 2.71	0.091
None	1.08	0.65, 1.80	0.76
Open	1.43	0.83, 2.47	0.20
PRIOR_CHF			
No	—	—	
Yes	1.51	1.21, 1.89	**<0.001**
PREOP_DIALYSIS			
No	—	—	
Yes	1.87	1.10, 3.16	**0.020**
PATHOLOGY			
Aneurysm	—	—	
Aneurysm from dissection	1.83	1.16, 2.87	**0.009**
Dissection	1.77	1.02, 3.06	**0.041**
PAU/IMH	1.94	0.90, 4.20	0.093
extent			

[1]OR = Odds Ratio, CI = Confidence Interval

Characteristic	TOTAL_LOS Length of Stay in days		
	OR[1]	95% CI[1]	p-value
Juxtarenal	—	—	
No	2.10	1.72, 2.57	**<0.001**

[1]OR = Odds Ratio, CI = Confidence Interval

ICUSTAY: ICU Stay

Characteristic	ICU Stay		
	OR[1]	95% CI[1]	p-value
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	3.11	2.43, 3.97	**<0.001**

[1]OR = Odds Ratio, CI = Confidence Interval

Characteristic	ICU Stay		
	OR[1]	95% CI[1]	p-value
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	2.08	1.59, 2.71	**<0.001**
AGECAT			
<50	—	—	
>79	1.31	0.51, 3.37	0.58
50-59	1.30	0.47, 3.58	0.62
60-69	0.96	0.38, 2.42	0.93
70-79	1.28	0.50, 3.25	0.61
GENDER			
female	—	—	
male	0.60	0.49, 0.74	**<0.001**
PREOP_SMOKING			
No	—	—	
Yes	1.02	0.75, 1.38	0.92
PRIOR_AORSURG			
Both	—	—	
Endo	1.36	0.77, 2.41	0.29
None	0.75	0.43, 1.32	0.32
Open	1.31	0.72, 2.38	0.38
PRIOR_CHF			
No	—	—	
Yes	1.21	0.93, 1.57	0.17
PREOP_DIALYSIS			

[1]OR = Odds Ratio, CI = Confidence Interval

	ICU Stay		
Characteristic	**OR^1**	**95% CI^1**	**p-value**
No	—	—	
Yes	1.84	1.07, 3.19	**0.028**
PATHOLOGY			
Aneurysm	—	—	
Aneurysm from dissection	1.35	0.81, 2.25	0.25
Dissection	1.72	0.93, 3.19	0.084
PAU/IMH	1.25	0.50, 3.12	0.63
extent			
Juxtarenal	—	—	
No	2.23	1.78, 2.80	**<0.001**

^{1}OR = Odds Ratio, CI = Confidence Interval

POSTOP_PRBC: Transfusion # Units PRBC

	Transfusion # Units PRBC		
Characteristic	**Beta**	**95% CI**[1]	**p-value**
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	0.95	0.52, 1.4	**<0.001**

[1]CI = Confidence Interval

POSTOP_INTISCH: Post-op Intestinal Ischemia

	Intestinal Ischemia		
Characteristic	**OR**[1]	**95% CI**[1]	**p-value**
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	1.13	0.56, 2.26	0.74

[1]OR = Odds Ratio, CI = Confidence Interval

	Intestinal Ischemia		
Characteristic	**OR**[1]	**95% CI**[1]	**p-value**
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	1.07	0.50, 2.30	0.87
AGECAT			
<50	—	—	
>79	0.41	0.07, 2.37	0.32
50-59	0.49	0.06, 4.15	0.51
60-69	0.36	0.06, 2.15	0.26
70-79	0.45	0.08, 2.48	0.36
GENDER			
female	—	—	
male	0.62	0.37, 1.03	0.063
PREOP_SMOKING			
No	—	—	
Yes	0.86	0.43, 1.70	0.66
PRIOR_AORSURG			
Both	—	—	
Endo	1.94	0.23, 16.6	0.55
None	1.84	0.22, 15.8	0.58
Open	1.62	0.16, 15.9	0.68
PRIOR_CHF			
No	—	—	
Yes	1.05	0.53, 2.08	0.89
PREOP_DIALYSIS			

[1]OR = Odds Ratio, CI = Confidence Interval

Characteristic	Intestinal Ischemia		
	OR[1]	95% CI[1]	p-value
No	—	—	
Yes	0.69	0.09, 5.12	0.71
PATHOLOGY			
Aneurysm	—	—	
Aneurysm from dissection	0.48	0.06, 3.66	0.48
Dissection	0.71	0.14, 3.71	0.69
PAU/IMH	1.28	0.16, 10.6	0.82
extent			
Juxtarenal	—	—	
No	0.94	0.53, 1.69	0.85

[1]OR = Odds Ratio, CI = Confidence Interval

POSTOP_CEREBROSX: Post-op Cerebrovascular Stroke:

Also account for `ARMNECK_ACCESS`

Characteristic	Post-op Cerebrovascular Stroke		
	OR[1]	95% CI[1]	p-value
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	3.42	1.83, 6.38	**<0.001**

[1]OR = Odds Ratio, CI = Confidence Interval

Characteristic	Post-op Cerebrovascular Stroke		
	OR[1]	95% CI[1]	p-value
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	1.81	0.91, 3.60	0.091
AGECAT			
<50	—	—	
>79	0.51	0.08, 3.29	0.48
50-59	0.79	0.13, 4.95	0.81
60-69	0.23	0.04, 1.45	0.12
70-79	0.62	0.11, 3.46	0.58
GENDER			
female	—	—	
male	0.49	0.26, 0.90	**0.023**
PREOP_SMOKING			
No	—	—	
Yes	0.73	0.34, 1.58	0.43
PRIOR_AORSURG			
Both	—	—	
Endo	1.20	0.24, 6.05	0.83
None	1.39	0.28, 6.92	0.69
Open	0.95	0.15, 5.88	0.95
PRIOR_CHF			
No	—	—	
Yes	2.14	1.07, 4.31	**0.032**

[1]OR = Odds Ratio, CI = Confidence Interval

Characteristic	Post-op Cerebrovascular Stroke		
	OR[1]	95% CI[1]	p-value
PREOP_DIALYSIS			
No	—	—	
Yes	1.97	0.46, 8.55	0.36
PATHOLOGY			
Aneurysm	—	—	
Aneurysm from dissection	3.44	1.03, 11.6	**0.045**
Dissection	2.56	0.57, 11.5	0.22
PAU/IMH	1.46	0.21, 10.2	0.70
extent			
Juxtarenal	—	—	
No	1.44	0.68, 3.04	0.34
ARMNECK_ACCESS			
No	—	—	
Yes	2.31	1.26, 4.25	**0.007**

[1]OR = Odds Ratio, CI = Confidence Interval

POSTOP_SPINAL_ISCHEMIA: Post-op Spinal Ischemia

Also account for `POSTOP_SPINALDRAIN` and `OCCLUDED_CELIAC`

Characteristic	OR[1]	95% CI[1]	p-value
	Post-op Spinal Ischemia		
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	2.56	1.70, 3.86	**<0.001**

[1]OR = Odds Ratio, CI = Confidence Interval

Characteristic	OR[1]	95% CI[1]	p-value
	Post-op Spinal Ischemia		
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	1.61	1.00, 2.60	**0.050**
AGECAT			
<50	—	—	
>79	2.19	0.27, 17.7	0.46
50-59	1.99	0.23, 17.3	0.53
60-69	1.63	0.21, 13.0	0.64
70-79	2.13	0.27, 16.6	0.47
GENDER			
female	—	—	
male	0.88	0.58, 1.36	0.58
PREOP_SMOKING			
No	—	—	
Yes	1.22	0.64, 2.32	0.55
PRIOR_AORSURG			
Both	—	—	
Endo	1.23	0.52, 2.95	0.64
None	1.46	0.63, 3.40	0.37
Open	1.47	0.60, 3.63	0.40
PRIOR_CHF			
No	—	—	
Yes	1.06	0.61, 1.83	0.84

[1]OR = Odds Ratio, CI = Confidence Interval

Characteristic	Post-op Spinal Ischemia		
	OR[1]	95% CI[1]	p-value
PREOP_DIALYSIS			
No	—	—	
Yes	1.16	0.48, 2.83	0.75
PATHOLOGY			
Aneurysm	—	—	
Aneurysm from dissection	0.98	0.43, 2.25	0.96
Dissection	1.08	0.36, 3.26	0.89
PAU/IMH	0.44	0.05, 3.63	0.45
extent			
Juxtarenal	—	—	
No	1.01	0.65, 1.57	0.97
POSTOP_SPINALDRAIN			
No	—	—	
Yes	19.0	11.1, 32.6	**<0.001**
OCCLUDED_CELIAC			
FALSE	—	—	
TRUE	1.57	0.83, 2.99	0.17

[1]OR = Odds Ratio, CI = Confidence Interval

POSTOP_LOS: Length of stay in days between surgery date and discharge date

Characteristic	Length of stay in days between surgery date and discharge date		
	OR[1]	95% CI[1]	p-value
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	3.39	2.69, 4.29	**<0.001**

[1]OR = Odds Ratio, CI = Confidence Interval

Characteristic	Length of stay in days between surgery date and discharge date		
	OR[1]	95% CI[1]	p-value
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	2.46	1.91, 3.17	**<0.001**
AGECAT			
<50	—	—	
>79	2.28	0.88, 5.88	0.089
50-59	1.93	0.72, 5.21	0.19
60-69	1.55	0.60, 3.96	0.36
70-79	2.49	0.98, 6.35	0.055
GENDER			
female	—	—	
male	0.62	0.50, 0.75	**<0.001**
PREOP_SMOKING			
No	—	—	
Yes	0.97	0.74, 1.28	0.82
PRIOR_AORSURG			
Both	—	—	
Endo	1.26	0.73, 2.19	0.41
None	0.96	0.57, 1.62	0.88
Open	1.36	0.76, 2.41	0.30
PRIOR_CHF			
No	—	—	
Yes	1.41	1.11, 1.80	**0.005**

[1]OR = Odds Ratio, CI = Confidence Interval

	Length of stay in days between surgery date and discharge date		
Characteristic	**OR[1]**	**95% CI[1]**	**p-value**
PREOP_DIALYSIS			
No	—	—	
Yes	1.74	1.00, 3.00	**0.048**
PATHOLOGY			
Aneurysm	—	—	
Aneurysm from dissection	1.59	0.96, 2.63	0.069
Dissection	1.96	1.11, 3.45	**0.020**
PAU/IMH	1.82	0.90, 3.67	0.094
extent			
Juxtarenal	—	—	
No	1.97	1.60, 2.44	**<0.001**

[1]OR = Odds Ratio, CI = Confidence Interval

POSTOP_COMPLICATIONS: Any Complications Post-op

Characteristic	Any Complications Post-op		
	OR[1]	95% CI[1]	p-value
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	1.74	1.37, 2.21	**<0.001**

[1]OR = Odds Ratio, CI = Confidence Interval

Characteristic	Any Complications Post-op		
	OR[1]	95% CI[1]	p-value
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	1.44	1.12, 1.86	**0.004**
AGECAT			
<50	—	—	
>79	1.17	0.46, 2.97	0.74
50-59	1.29	0.49, 3.42	0.61
60-69	0.97	0.39, 2.41	0.94
70-79	1.32	0.53, 3.31	0.55
GENDER			
female	—	—	
male	0.65	0.54, 0.78	**<0.001**
PREOP_SMOKING			
No	—	—	
Yes	1.01	0.79, 1.31	0.91
PRIOR_AORSURG			
Both	—	—	
Endo	0.95	0.56, 1.60	0.84
None	1.00	0.60, 1.65	0.99
Open	1.41	0.82, 2.42	0.21
PRIOR_CHF			
No	—	—	
Yes	1.28	1.04, 1.58	**0.018**
PREOP_DIALYSIS			

[1]OR = Odds Ratio, CI = Confidence Interval

| | Any Complications Post-op | | |
Characteristic	OR[1]	95% CI[1]	p-value
No	—	—	
Yes	1.25	0.73, 2.15	0.41
PATHOLOGY			
Aneurysm	—	—	
Aneurysm from dissection	1.32	0.82, 2.12	0.26
Dissection	0.94	0.51, 1.73	0.84
PAU/IMH	0.77	0.35, 1.70	0.52
extent			
Juxtarenal	—	—	
No	1.47	1.21, 1.78	**<0.001**

[1]OR = Odds Ratio, CI = Confidence Interval

RETX_R_RTOR: Re-intervention

	Re-intervention		
Characteristic	**OR[1]**	**95% CI[1]**	**p-value**
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	1.86	1.33, 2.62	**<0.001**

[1]OR = Odds Ratio, CI = Confidence Interval

	Re-intervention		
Characteristic	**OR[1]**	**95% CI[1]**	**p-value**
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	1.48	1.04, 2.09	**0.029**
AGECAT			
<50	—	—	
>79	0.95	0.28, 3.27	0.93
50-59	1.41	0.38, 5.19	0.60
60-69	0.70	0.20, 2.44	0.58
70-79	0.94	0.28, 3.14	0.92
GENDER			
female	—	—	
male	0.59	0.45, 0.78	**<0.001**
PREOP_SMOKING			
No	—	—	
Yes	1.29	0.81, 2.05	0.28
PRIOR_AORSURG			
Both	—	—	
Endo	0.95	0.43, 2.09	0.90
None	1.01	0.47, 2.16	0.99
Open	0.67	0.27, 1.63	0.37
PRIOR_CHF			
No	—	—	
Yes	1.21	0.86, 1.72	0.27
PREOP_DIALYSIS			

[1]OR = Odds Ratio, CI = Confidence Interval

Characteristic	Re-intervention		
	OR[1]	95% CI[1]	p-value
No	—	—	
Yes	0.75	0.31, 1.81	0.52
PATHOLOGY			
Aneurysm	—	—	
Aneurysm from dissection	1.68	0.88, 3.19	0.12
Dissection	0.64	0.23, 1.78	0.39
PAU/IMH	1.77	0.70, 4.47	0.23
extent			
Juxtarenal	—	—	
No	1.56	1.15, 2.12	**0.004**

[1]OR = Odds Ratio, CI = Confidence Interval

BRANCH_POST: Post-treatment Status of All Branches

Characteristic	OR[1]	95% CI[1]	p-value
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	2.28	1.78, 2.91	**<0.001**

[1]OR = Odds Ratio, CI = Confidence Interval

Characteristic	OR[1]	95% CI[1]	p-value
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	1.64	1.24, 2.16	**<0.001**
AGECAT			
<50	—	—	
>79	0.78	0.32, 1.90	0.58
50-59	1.00	0.39, 2.58	>0.99
60-69	0.95	0.40, 2.27	0.91
70-79	0.90	0.38, 2.14	0.81
GENDER			
female	—	—	
male	0.47	0.39, 0.58	**<0.001**
PREOP_SMOKING			
No	—	—	
Yes	1.08	0.79, 1.48	0.63
PRIOR_AORSURG			
Both	—	—	
Endo	0.79	0.46, 1.35	0.38
None	0.52	0.31, 0.86	**0.011**
Open	0.69	0.39, 1.23	0.21
PRIOR_CHF			
No	—	—	
Yes	1.43	1.12, 1.82	**0.004**

[1]OR = Odds Ratio, CI = Confidence Interval

Characteristic	Post-treatment Status of All Branches		
	OR[1]	95% CI[1]	p-value
PREOP_DIALYSIS			
No	—	—	
Yes	7.90	4.70, 13.3	**<0.001**
PATHOLOGY			
Aneurysm	—	—	
Aneurysm from dissection	0.77	0.43, 1.37	0.37
Dissection	1.57	0.90, 2.74	0.12
PAU/IMH	0.45	0.16, 1.24	0.12
extent			
Juxtarenal	—	—	
No	1.56	1.25, 1.93	**<0.001**

[1]OR = Odds Ratio, CI = Confidence Interval

For the following variables, we need to merge age group "<50" and "50-59" so that there's no 0 patients on one level.

POSTOP_DIALYSIS: Post-op Dialysis

Also account for `OCCLUDED_RENAL`

Characteristic	Post-op Dialysis OR[1]	95% CI[1]	p-value
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	2.42	1.44, 4.07	**<0.001**

[1]OR = Odds Ratio, CI = Confidence Interval

Characteristic	Post-op Dialysis OR[1]	95% CI[1]	p-value
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	1.78	1.01, 3.13	**0.047**
AGECAT			
<59	—	—	
60-69	0.53	0.22, 1.27	0.16
70-79	0.40	0.17, 0.97	**0.042**
>79	0.39	0.15, 1.01	0.053
GENDER			
female	—	—	
male	0.62	0.38, 1.00	**0.049**
PREOP_SMOKING			
No	—	—	
Yes	1.31	0.60, 2.86	0.49
PRIOR_AORSURG			
Both	—	—	
Endo	1.04	0.26, 4.10	0.95
None	0.82	0.22, 3.04	0.76
Open	0.58	0.12, 2.80	0.50
PRIOR_CHF			
No	—	—	
Yes	0.74	0.37, 1.45	0.38
PREOP_DIALYSIS			

[1]OR = Odds Ratio, CI = Confidence Interval

Characteristic	OR[1]	95% CI[1]	p-value
	Post-op Dialysis		
No	—	—	
Yes	0.00	0.00, 0.00	**<0.001**
PATHOLOGY			
Aneurysm	—	—	
Aneurysm from dissection	0.33	0.04, 2.96	0.32
Dissection	1.74	0.52, 5.82	0.37
PAU/IMH	2.33	0.51, 10.6	0.27
extent			
Juxtarenal	—	—	
No	0.99	0.58, 1.70	0.98
OCCLUDED_RENAL			
FALSE	—	—	
TRUE	4.82	2.33, 9.95	**<0.001**

[1]OR = Odds Ratio, CI = Confidence Interval

POSTOP_LEGEMBO: Leg Ischemia/Embol

Characteristic	Leg Ischemia/Embol		
	OR[1]	95% CI[1]	p-value
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	1.97	1.13, 3.46	**0.017**

[1]OR = Odds Ratio, CI = Confidence Interval

Characteristic	Leg Ischemia/Embol		
	OR[1]	95% CI[1]	p-value
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	1.74	0.94, 3.22	0.078
AGECAT			
<59	—	—	
60-69	0.80	0.28, 2.27	0.68
70-79	0.80	0.29, 2.23	0.67
>79	0.67	0.23, 2.00	0.48
GENDER			
female	—	—	
male	0.43	0.28, 0.67	**<0.001**
PREOP_SMOKING			
No	—	—	
Yes	2.61	0.98, 6.96	0.056
PRIOR_AORSURG			
Both	—	—	
Endo	139,944,960,652,840		
None	162,086,767,451,715		
Open	288,216,346,513,340		
PRIOR_CHF			
No	—	—	
Yes	0.85	0.44, 1.64	0.63
PREOP_DIALYSIS			
No	—	—	

[1]OR = Odds Ratio, CI = Confidence Interval

Characteristic	Leg Ischemia/Embol		
	OR[1]	95% CI[1]	p-value
Yes	0.58	0.08, 4.19	0.59
PATHOLOGY			
Aneurysm	—	—	
Aneurysm from dissection	0.87	0.20, 3.86	0.86
Dissection	0.60	0.08, 4.59	0.62
PAU/IMH	2.28	0.49, 10.6	0.29
extent			
Juxtarenal	—	—	
No	1.01	0.61, 1.66	0.98

[1]OR = Odds Ratio, CI = Confidence Interval

POSTOP_RESPIRATORY: Post-op Respiratory

	Post-op Respiratory		
Characteristic	OR[1]	95% CI[1]	p-value
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	2.65	1.87, 3.75	**<0.001**

[1]OR = Odds Ratio, CI = Confidence Interval

	Post-op Respiratory		
Characteristic	OR[1]	95% CI[1]	p-value
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	2.17	1.47, 3.21	**<0.001**
AGECAT			
<59	—	—	
60-69	0.94	0.44, 1.98	0.86
70-79	1.06	0.50, 2.25	0.87
>79	0.94	0.42, 2.06	0.87
GENDER			
female	—	—	
male	0.66	0.47, 0.92	**0.014**
PREOP_SMOKING			
No	—	—	
Yes	1.08	0.68, 1.72	0.75
PRIOR_AORSURG			
Both	—	—	
Endo	0.59	0.27, 1.30	0.19
None	0.55	0.26, 1.16	0.11
Open	0.67	0.28, 1.60	0.36
PRIOR_CHF			
No	—	—	
Yes	1.23	0.82, 1.84	0.31
PREOP_DIALYSIS			
No	—	—	

[1]OR = Odds Ratio, CI = Confidence Interval

Characteristic	Post-op Respiratory		
	OR[1]	95% CI[1]	p-value
Yes	0.78	0.27, 2.23	0.64
PATHOLOGY			
Aneurysm	—	—	
Aneurysm from dissection	0.60	0.23, 1.55	0.29
Dissection	0.83	0.29, 2.38	0.73
PAU/IMH	1.14	0.33, 4.02	0.83
extent			
Juxtarenal	—	—	
No	1.74	1.25, 2.41	**<0.001**

[1]OR = Odds Ratio, CI = Confidence Interval

Code Appendix

```r
knitr::opts_chunk$set(echo = FALSE,message = FALSE,warning = FALSE)
library(tidyverse)
library(table1)
library(dplyr)
library(geepack)
library(gtsummary)
library(broom.mixed)
## ------------- working directories for Lily ----------
wd_lily = '/Users/hanyiwang/Desktop/Comparative-analysis-of-treatments-of-CAA'
path_lily = c("../data/TEVAR_PROC.csv")

## ------------- read data ----------
setwd(wd_lily)
TEVAR_PROC = read.csv(path_lily)
# ### ---------- Correlation matrix ---------
# library(corrplot)
# library(tidyverse)
# library(caret)
# library(ggcorrplot)
#
# matrix <- PROC %>%
#     select_if(is.numeric) %>% subset(., select = -1)%>%
#     cor(.,use = "complete")
#
# corrplot(matrix, method="number")
#
# #select dataset that column are not numeric
# matrix <- PROC %>% select_if(negate(is.numeric))
#
# # find out the variables
# lapply(matrix[,], unique)
# sapply(lapply(matrix, unique), length)
#
# #select if more than one variable
# y<-matrix %>%select_if(function(col) length(unique(col))==2)
#
# # Convert all columns to factor
# data3 <- as.data.frame(unclass(y),
#                        stringsAsFactors = TRUE)
#
#  model.matrix(~0 +., data=data3) %>%
#    cor(use="pairwise.complete.obs") %>%
#    ggcorrplot(show.diag = F, type="lower", lab=TRUE, lab_size=2)
#
# str(y)
## ------------- modify dataset ----------
TEVAR_PROC = TEVAR_PROC %>%
  mutate(extent = factor(extent,levels = c("Juxtarenal AAA","Type 1 TAAA","Type 2 TAAA","Type 3 TAAA","

  mutate(TOTAL_LOS = case_when(TOTAL_LOS>7 ~ '>7',
                               TOTAL_LOS<=7 ~ '<=7')) %>%
  mutate(ICUSTAY = case_when(ICUSTAY>4 ~ '>4',
```

```
                                  ICUSTAY<=4 ~ '<=4')) %>%
    mutate(POSTOP_LOS = case_when(POSTOP_LOS>7 ~ '>7',
                                  POSTOP_LOS<=7 ~ '<=7')) %>%

    mutate(TOTAL_LOS = as.numeric(TOTAL_LOS != "<=7") ) %>%
    mutate(ICUSTAY = as.numeric(ICUSTAY != "<=4") ) %>%
    mutate(POSTOP_LOS = as.numeric(POSTOP_LOS != "<=7") ) %>%

    mutate(POSTOP_INTISCH = as.numeric(POSTOP_INTISCH == "Yes"))  %>%
    mutate(POSTOP_CEREBROSX = as.numeric(POSTOP_CEREBROSX == "Yes")) %>%
    mutate(POSTOP_SPINAL_ISCHEMIA = as.numeric(POSTOP_SPINAL_ISCHEMIA == "Yes")) %>%
    mutate(POSTOP_DIALYSIS = as.numeric(POSTOP_DIALYSIS == "Yes")) %>%
    mutate(POSTOP_COMPLICATIONS = as.numeric(POSTOP_COMPLICATIONS == "Yes")) %>%
    mutate(POSTOP_LEGEMBO = as.numeric(POSTOP_LEGEMBO == "Yes")) %>%
    mutate(POSTOP_RESPIRATORY = as.numeric(POSTOP_RESPIRATORY == "Yes")) %>%
    mutate(RETX_R_RTOR = as.numeric(RETX_R_RTOR == "Yes")) %>%
    mutate(BRANCH_POST = as.numeric(BRANCH_POST == "Yes"))

# remove missing values
TEVAR_PROC = subset(TEVAR_PROC, !is.na(extent))


## ------------- change class of variables ----------
names <- c('CENTERID','AGECAT', 'GENDER', 'PREOP_SMOKING', 'PRIOR_AORSURG', 'PRIOR_CHF', 'PREOP_DIALYSIS
TEVAR_PROC[,names] <- lapply(TEVAR_PROC[,names] , factor)

## ------------- Length of stay in days between admission date and discharge date ----------

#table(PROC$extent)
#PROCNM[is.na(PROCNM) | PROCNM=="Inf"] = NA
# repeated patients, need id, geeglm needs complete data, extent is not complete

## ------------- unadjusted ----------
LOS1<-geeglm(TOTAL_LOS~ PRESENTATION, data=TEVAR_PROC, family=binomial(link="logit"), id = CENTERID, co

t1<-LOS1 %>%
  tbl_regression(exponentiate=TRUE,
                 tidy_fun = broom.mixed::tidy,
                 pvalue_fun = function(x) style_pvalue(x, digits = 2))%>%
  bold_p(t = 0.05)

tbl_merge(tbls = list(t1),tab_spanner ="**TOTAL_LOS Length of Stay in days**")%>%as_flex_table()


## ------------- adjusted ----------
LOS2<-geeglm(TOTAL_LOS ~ PRESENTATION+AGECAT+GENDER+PREOP_SMOKING+PRIOR_AORSURG+PRIOR_CHF+PREOP_DIALYSIS
             , data=TEVAR_PROC, family=binomial(link="logit"),id = CENTERID, corstr = "independence")
t2<-LOS2 %>%
  tbl_regression(exponentiate=TRUE,tidy_fun = broom.mixed::tidy,
                 pvalue_fun = function(x) style_pvalue(x, digits = 2))%>%
  bold_p(t = 0.05)

tbl_merge(tbls = list(t2),tab_spanner ="**TOTAL_LOS Length of Stay in days**")%>%as_flex_table()
```

```r
#the difference in mean number of sessions attended comparing treatment to control


#adjust<-c('PRESENTATION','AGECAT', 'GENDER', 'PREOP_SMOKING','PRIOR_AORSURG', 'PRIOR_CHF','PATHOLOGY',
#PROC %>%
#  tbl_uvregression(
#    y = TOTAL_LOS,
#    x = PRESENTATION+AGECAT+GENDER+PREOP_SMOKING+PRIOR_AORSURG+PRIOR_CHF+PATHOLOGY+NUM_TREATED_BRANCHE
#    method = geepack::geeglm,
#    method.args = list(id = X+CENTERID, corstr = "independence"),
#    include = all_of(adjust)
#  ) %>%
#  as_kable()
## ------------ ICU Stay ----------

## ------------ unadjusted ----------
ICU1<-geeglm(ICUSTAY~ PRESENTATION, data=TEVAR_PROC, family=binomial(link="logit"), id = CENTERID, cors

#summary(LOS2)
#summary(ICU1)

#ICU1<-geeglm(ICUSTAY ~ PRESENTATION, data=PROCNM,id = CENTERID, corstr = "independence")
t1<-ICU1 %>%tbl_regression(exponentiate=TRUE, tidy_fun = broom.mixed::tidy,
                           pvalue_fun = function(x) style_pvalue(x, digits = 2))%>%
  bold_p(t = 0.05)

tbl_merge(tbls = list(t1),tab_spanner ="**ICU Stay**")%>%as_flex_table()

## ------------ adjusted ----------
ICU2<-geeglm(ICUSTAY ~ PRESENTATION+AGECAT+GENDER+PREOP_SMOKING+PRIOR_AORSURG+PRIOR_CHF+PREOP_DIALYSIS+
            , family=binomial(link="logit"), data=TEVAR_PROC, id = CENTERID, corstr = "independence")
t2<- ICU2 %>%tbl_regression(exponentiate=TRUE,tidy_fun = broom.mixed::tidy,
                           pvalue_fun = function(x) style_pvalue(x, digits = 2))%>%
  bold_p(t = 0.05)

tbl_merge(tbls = list(t2),tab_spanner ="**ICU Stay**")%>%as_flex_table()
## ------------  Transfusion # Units PRBC ----------
## ------------ unadjusted ----------
POSTOP_PRBC1<-geeglm(POSTOP_PRBC ~ PRESENTATION, data=TEVAR_PROC,id = CENTERID, corstr = "independence")
t1<-POSTOP_PRBC1 %>%tbl_regression(tidy_fun = broom.mixed::tidy,
                                   pvalue_fun = function(x) style_pvalue(x, digits = 2))%>%
  bold_p(t = 0.05)

tbl_merge(tbls = list(t1),tab_spanner ="**Transfusion # Units PRBC**")%>%as_flex_table()


## ------------ adjusted ----------
# POSTOP_PRBC2<-geeglm(POSTOP_PRBC ~ PRESENTATION+AGECAT+GENDER+PREOP_SMOKING+PRIOR_AORSURG+PRIOR_CHF+P
# t2<- POSTOP_PRBC2 %>%tbl_regression(tidy_fun = broom.mixed::tidy,
#                                    pvalue_fun = function(x) style_pvalue(x, digits = 2))%>%
#   bold_p(t = 0.05)
# tbl_merge(tbls = list(t2),tab_spanner ="**Transfusion # Units PRBC**")%>%as_flex_table()
```

```r
## ------------ Post-op Intestinal Ischemia  ----------
## ------------- unadjusted ----------
POSTOP_INTISCH1<-geeglm(POSTOP_INTISCH ~ PRESENTATION, family=binomial(link="logit"), data=TEVAR_PROC,id

t1<-POSTOP_INTISCH1 %>%tbl_regression(exponentiate=TRUE,tidy_fun = broom.mixed::tidy,
                                      pvalue_fun = function(x) style_pvalue(x, digits = 2))%>%
  bold_p(t = 0.05)

tbl_merge(tbls = list(t1),tab_spanner ="**Intestinal Ischemia**")%>%as_flex_table()


## ------------- adjusted ----------
POSTOP_INTISCH2<-geeglm(POSTOP_INTISCH ~ PRESENTATION+AGECAT+GENDER+PREOP_SMOKING+PRIOR_AORSURG+PRIOR_CH
                        , data=TEVAR_PROC,family=binomial(link="logit"), id = CENTERID, corstr = "indepen
t2<- POSTOP_INTISCH2 %>%tbl_regression(exponentiate=TRUE,tidy_fun = broom.mixed::tidy,
                                       pvalue_fun = function(x) style_pvalue(x, digits = 2))%>%
  bold_p(t = 0.05)
tbl_merge(tbls = list(t2),tab_spanner ="**Intestinal Ischemia**")%>%as_flex_table()

# model<-geeglm(as.numeric(POSTOP_DIALYSIS)~PRESENTATION+AGECAT+GENDER+PREOP_SMOKING+PRIOR_AORSURG+PRIO

# model<-geeglm(outcome~predictor+confounder, family=binomial(link = "logit"),
# data=na.omit(data), corstr='ar1', id=id, std.err="san.se")
# TOTAL_LOS
# ICUSTAY
# POSTOP_PRBC
# POSTOP_HIGHCREAT
# POSTOP_INTISCH
## ------------- Post-op Cerebrovascular Stroke ----------
## ------------- unadjusted ----------
POSTOP_CEREBROSX1 = geeglm(POSTOP_CEREBROSX ~ PRESENTATION,
                           data=TEVAR_PROC, family=binomial(link="logit"),
                           id = CENTERID, corstr = "independence")

t1 = POSTOP_CEREBROSX1 %>%
  tbl_regression(exponentiate=TRUE, tidy_fun = broom.mixed::tidy,
                 pvalue_fun = function(x) style_pvalue(x, digits = 2))%>%
  bold_p(t = 0.05)

tbl_merge(tbls = list(t1),tab_spanner ="**Post-op Cerebrovascular Stroke**")%>%as_flex_table()

## ------------- adjusted ----------
POSTOP_CEREBROSX2 = geeglm(POSTOP_CEREBROSX ~ PRESENTATION+AGECAT+GENDER+PREOP_SMOKING+
                           PRIOR_AORSURG+PRIOR_CHF+PREOP_DIALYSIS+PATHOLOGY+extent+ARMNECK_ACCESS,
                           family=binomial(link="logit"), data=TEVAR_PROC,
                           id = CENTERID, corstr = "independence")

t2 = POSTOP_CEREBROSX2 %>%
  tbl_regression(exponentiate=TRUE,tidy_fun = broom.mixed::tidy,
                 pvalue_fun = function(x) style_pvalue(x, digits = 2))%>%
  bold_p(t = 0.05)
```

```
tbl_merge(tbls = list(t2),tab_spanner ="**Post-op Cerebrovascular Stroke**")%>%as_flex_table()
## ------------ Post-op Spinal Ischemia  ----------
## ------------ unadjusted ----------
POSTOP_SPINAL_ISCHEMIA1 = geeglm(POSTOP_SPINAL_ISCHEMIA ~ PRESENTATION,
                                 data=TEVAR_PROC,family=binomial(link="logit"),
                                 id = CENTERID, corstr = "independence")

t1 = POSTOP_SPINAL_ISCHEMIA1 %>%
  tbl_regression(exponentiate=TRUE, tidy_fun = broom.mixed::tidy,
              pvalue_fun = function(x) style_pvalue(x, digits = 2))%>%
  bold_p(t = 0.05)

tbl_merge(tbls = list(t1),tab_spanner ="**Post-op Spinal Ischemia**")%>%as_flex_table()

## ------------ adjusted ----------
POSTOP_SPINAL_ISCHEMIA2 = geeglm(POSTOP_SPINAL_ISCHEMIA ~ PRESENTATION+AGECAT+GENDER+
                                 PREOP_SMOKING+PRIOR_AORSURG+PRIOR_CHF+
                                 PREOP_DIALYSIS+PATHOLOGY+extent+
                                 POSTOP_SPINALDRAIN+OCCLUDED_CELIAC,
                    family=binomial(link="logit"), data=TEVAR_PROC,
                    id = CENTERID, corstr = "independence")

t2 = POSTOP_SPINAL_ISCHEMIA2 %>%
  tbl_regression(exponentiate=TRUE,tidy_fun = broom.mixed::tidy,
              pvalue_fun = function(x) style_pvalue(x, digits = 2))%>%
  bold_p(t = 0.05)

tbl_merge(tbls = list(t2),tab_spanner ="**Post-op Spinal Ischemia**")%>%as_flex_table()



## ------------ Length of stay in days between surgery date and discharge date  ----------
## ------------ unadjusted ----------
POSTOP_LOS1 = geeglm(POSTOP_LOS~ PRESENTATION,
                     data=TEVAR_PROC, family=binomial(link="logit"),
                     id = CENTERID, corstr = "independence")
# summary(POSTOP_LOS1)

t1 = POSTOP_LOS1 %>%
  tbl_regression(exponentiate=TRUE, tidy_fun = broom.mixed::tidy,
              pvalue_fun = function(x) style_pvalue(x, digits = 2))%>%
  bold_p(t = 0.05)

tbl_merge(tbls = list(t1),tab_spanner ="**Length of stay in days between surgery date and discharge date

## ------------ adjusted ----------
POSTOP_LOS2 = geeglm(POSTOP_LOS ~ PRESENTATION+AGECAT+GENDER+PREOP_SMOKING+
                     PRIOR_AORSURG+PRIOR_CHF+PREOP_DIALYSIS+PATHOLOGY+extent,
                    family=binomial(link="logit"), data=TEVAR_PROC,
                    id = CENTERID, corstr = "independence")

t2 = POSTOP_LOS2 %>%
  tbl_regression(exponentiate=TRUE,tidy_fun = broom.mixed::tidy,
```

```
                      pvalue_fun = function(x) style_pvalue(x, digits = 2))%>%
    bold_p(t = 0.05)

tbl_merge(tbls = list(t2),tab_spanner ="**Length of stay in days between surgery date and discharge date
## ------------ Any Complications Post-op  ----------
## ------------ unadjusted ----------
POSTOP_COMPLICATIONS1 = geeglm(POSTOP_COMPLICATIONS~ PRESENTATION,
                    data=TEVAR_PROC, family=binomial(link="logit"),
                    id = CENTERID, corstr = "independence")

t1 = POSTOP_COMPLICATIONS1 %>%
  tbl_regression(exponentiate=TRUE, tidy_fun = broom.mixed::tidy,
              pvalue_fun = function(x) style_pvalue(x, digits = 2))%>%
  bold_p(t = 0.05)

tbl_merge(tbls = list(t1),tab_spanner ="**Any Complications Post-op**")%>%as_flex_table()

## ------------- adjusted ----------
POSTOP_COMPLICATIONS2 = geeglm(POSTOP_COMPLICATIONS ~ PRESENTATION+AGECAT+GENDER+PREOP_SMOKING+
                      PRIOR_AORSURG+PRIOR_CHF+PREOP_DIALYSIS+PATHOLOGY+extent,
                    family=binomial(link="logit"), data=TEVAR_PROC,
                    id = CENTERID, corstr = "independence")

t2 = POSTOP_COMPLICATIONS2 %>%
  tbl_regression(exponentiate=TRUE,tidy_fun = broom.mixed::tidy,
              pvalue_fun = function(x) style_pvalue(x, digits = 2))%>%
  bold_p(t = 0.05)

tbl_merge(tbls = list(t2),tab_spanner ="**Any Complications Post-op**")%>%as_flex_table()
## ------------ Re-intervention  ----------
## ------------ unadjusted ----------
RETX_R_RTOR1 = geeglm(RETX_R_RTOR~ PRESENTATION,
                    data=TEVAR_PROC, family=binomial(link="logit"),
                    id = CENTERID, corstr = "independence")
# summary(POSTOP_LOS1)

t1 = RETX_R_RTOR1 %>%
  tbl_regression(exponentiate=TRUE, tidy_fun = broom.mixed::tidy,
              pvalue_fun = function(x) style_pvalue(x, digits = 2))%>%
  bold_p(t = 0.05)

tbl_merge(tbls = list(t1),tab_spanner ="**Re-intervention**")%>%as_flex_table()

## ------------- adjusted ----------
RETX_R_RTOR2 = geeglm(RETX_R_RTOR ~ PRESENTATION+AGECAT+GENDER+PREOP_SMOKING+
                      PRIOR_AORSURG+PRIOR_CHF+PREOP_DIALYSIS+PATHOLOGY+extent,
                    family=binomial(link="logit"), data=TEVAR_PROC,
                    id = CENTERID, corstr = "independence")

t2 = RETX_R_RTOR2 %>%
  tbl_regression(exponentiate=TRUE,tidy_fun = broom.mixed::tidy,
              pvalue_fun = function(x) style_pvalue(x, digits = 2))%>%
  bold_p(t = 0.05)
```

```r
tbl_merge(tbls = list(t2),tab_spanner ="**Re-intervention**")%>%as_flex_table()
## ------------ Post-treatment Status of All Branches  ----------
## ------------- unadjusted ----------
BRANCH_POST1 = geeglm(BRANCH_POST~ PRESENTATION,
                      data=TEVAR_PROC, family=binomial(link="logit"),
                      id = CENTERID, corstr = "independence")
# summary(POSTOP_LOS1)

t1 = BRANCH_POST1 %>%
  tbl_regression(exponentiate=TRUE, tidy_fun = broom.mixed::tidy,
                 pvalue_fun = function(x) style_pvalue(x, digits = 2))%>%
  bold_p(t = 0.05)

tbl_merge(tbls = list(t1),tab_spanner ="**Post-treatment Status of All Branches**")%>%as_flex_table()

## ------------- adjusted ----------
BRANCH_POST2 = geeglm(BRANCH_POST ~ PRESENTATION+AGECAT+GENDER+PREOP_SMOKING+
                      PRIOR_AORSURG+PRIOR_CHF+PREOP_DIALYSIS+PATHOLOGY+extent,
                    family=binomial(link="logit"), data=TEVAR_PROC,
                    id = CENTERID, corstr = "independence")

t2 = BRANCH_POST2 %>%
  tbl_regression(exponentiate=TRUE,tidy_fun = broom.mixed::tidy,
                 pvalue_fun = function(x) style_pvalue(x, digits = 2))%>%
  bold_p(t = 0.05)

tbl_merge(tbls = list(t2),tab_spanner ="**Post-treatment Status of All Branches**")%>%as_flex_table()
## ------------- modify dataset ----------
TEVAR_PROC = TEVAR_PROC %>%
  mutate(AGECAT = factor(AGECAT,levels = c('<50','50-59','60-69','70-79','>79'),
                         labels = c('<59','<59','60-69','70-79','>79')))

## ------------ Post-op Dialysis  ----------
# table1(~ AGECAT | factor(POSTOP_DIALYSIS),data=subset(TEVAR_PROC, !is.na(POSTOP_DIALYSIS)))

## ------------- unadjusted ----------
POSTOP_DIALYSIS1 = geeglm(POSTOP_DIALYSIS ~ PRESENTATION,
                          data=TEVAR_PROC,family=binomial(link="logit"),
                          id = CENTERID, corstr = "independence")

t1 = POSTOP_DIALYSIS1 %>%
  tbl_regression(exponentiate=TRUE, tidy_fun = broom.mixed::tidy,
                 pvalue_fun = function(x) style_pvalue(x, digits = 2))%>%
  bold_p(t = 0.05)

tbl_merge(tbls = list(t1),tab_spanner ="**Post-op Dialysis**")%>%as_flex_table()

## ------------- adjusted ----------
POSTOP_DIALYSIS2 = geeglm(POSTOP_DIALYSIS ~ PRESENTATION+AGECAT+GENDER+
                          PREOP_SMOKING+PRIOR_AORSURG+PRIOR_CHF+
                          PREOP_DIALYSIS+PATHOLOGY+extent+
                          OCCLUDED_RENAL,
                    family=binomial(link="logit"), data=TEVAR_PROC,
```

```
                          id = CENTERID, corstr = "independence")

t2 = POSTOP_DIALYSIS2 %>%
  tbl_regression(exponentiate=TRUE,tidy_fun = broom.mixed::tidy,
                 pvalue_fun = function(x) style_pvalue(x, digits = 2))%>%
  bold_p(t = 0.05)

tbl_merge(tbls = list(t2),tab_spanner ="**Post-op Dialysis**")%>%as_flex_table()

## ------------ Leg Ischemia/Emboli  ----------
# table1(~ AGECAT | factor(POSTOP_LEGEMBO),data=subset(TEVAR_PROC, !is.na(POSTOP_LEGEMBO)))
## ------------- unadjusted ----------
POSTOP_LEGEMBO1 = geeglm(POSTOP_LEGEMBO~ PRESENTATION,
                    data=TEVAR_PROC, family=binomial(link="logit"),
                    id = CENTERID, corstr = "independence")
# summary(POSTOP_LOS1)

t1 = POSTOP_LEGEMBO1 %>%
  tbl_regression(exponentiate=TRUE, tidy_fun = broom.mixed::tidy,
                 pvalue_fun = function(x) style_pvalue(x, digits = 2))%>%
  bold_p(t = 0.05)

tbl_merge(tbls = list(t1),tab_spanner ="**Leg Ischemia/Embol**")%>%as_flex_table()

## ------------- adjusted ----------
POSTOP_LEGEMBO2 = geeglm(POSTOP_LEGEMBO ~ PRESENTATION+AGECAT+GENDER+PREOP_SMOKING+
                      PRIOR_AORSURG+PRIOR_CHF+PREOP_DIALYSIS+PATHOLOGY+extent,
                   family=binomial(link="logit"), data=TEVAR_PROC,
                   id = CENTERID, corstr = "independence")

t2 = POSTOP_LEGEMBO2 %>%
  tbl_regression(exponentiate=TRUE,tidy_fun = broom.mixed::tidy,
                 pvalue_fun = function(x) style_pvalue(x, digits = 2))%>%
  bold_p(t = 0.05)

tbl_merge(tbls = list(t2),tab_spanner ="**Leg Ischemia/Embol**")%>%as_flex_table()
## ------------- Post-op Respiratory  ----------
# table1(~ AGECAT | factor(POSTOP_RESPIRATORY),data=subset(TEVAR_PROC, !is.na(POSTOP_RESPIRATORY)))

## ------------- unadjusted ----------
POSTOP_RESPIRATORY1 = geeglm(POSTOP_RESPIRATORY~ PRESENTATION,
                    data=TEVAR_PROC, family=binomial(link="logit"),
                    id = CENTERID, corstr = "independence")

t1 = POSTOP_RESPIRATORY1 %>%
  tbl_regression(exponentiate=TRUE, tidy_fun = broom.mixed::tidy,
                 pvalue_fun = function(x) style_pvalue(x, digits = 2))%>%
  bold_p(t = 0.05)

tbl_merge(tbls = list(t1),tab_spanner ="**Post-op Respiratory**")%>%as_flex_table()

## ------------- adjusted ----------
POSTOP_RESPIRATORY2 = geeglm(POSTOP_RESPIRATORY ~ PRESENTATION+AGECAT+GENDER+PREOP_SMOKING+
```

```
                        PRIOR_AORSURG+PRIOR_CHF+PREOP_DIALYSIS+PATHOLOGY+extent,
                  family=binomial(link="logit"), data=TEVAR_PROC,
                  id = CENTERID, corstr = "independence")

t2 = POSTOP_RESPIRATORY2 %>%
  tbl_regression(exponentiate=TRUE,tidy_fun = broom.mixed::tidy,
                 pvalue_fun = function(x) style_pvalue(x, digits = 2))%>%
  bold_p(t = 0.05)

tbl_merge(tbls = list(t2),tab_spanner ="**Post-op Respiratory**")%>%as_flex_table()
```