g008.sas: No 0 margins and n>=20, loglinear model (fixed effects)
Sorted by n

Obs	id	y00	y01	y10	y11	n	zero_margins	modality
1	Lee 2014	1	5	2	21	29	0	3
2	Reyes 2016	0	3	3	28	34	0	1
3	Boerwinkle 2017	0	2	7	27	36	0	4
4	Chen 2017	4	6	2	30	42	0	0
5	Bettus 2010	12	6	10	16	44	0	1
6	Khoo 2019	18	7	8	16	49	0	3
7	Boerwinkle 2019	38	1	3	22	64	0	4
		73	*30*	*35*	*160*	*298*		

g008.sas: No 0 margins and n>=20, loglinear model (fixed effects)
Variables

variable	*LABEL*
compar	Comparative (1=-, 2=+)
count	
id	Study ID
modality	Modality (0/1/2/3/4)
n	Sample size
rsfMRI	rsfMRI (1=-, 2=+)

g008.sas: No 0 margins and n>=20, loglinear model (fixed effects)
1. Log(odds ratio): 0

The GENMOD Procedure

Model Information	
Data Set	WORK.A
Distribution	Poisson
Link Function	Log
Dependent Variable	count

Number of Observations Read	28
Number of Observations Used	28

Class Level Information

Class	*Levels*	*Values*
id	7	Bettus 2010 Boerwinkle 2017 Boerwinkle 2019 Chen 2017 Khoo 2019 Lee 2014 Reyes 2016
rsfMRI	2	1 2
compar	2	1 2

Parameter Information

Parameter	*Effect*	*id*	*rsfMRI*	*compar*
Prm1	Intercept			
Prm2	id	Bettus 2010		
Prm3	id	Boerwinkle 2017		
Prm4	id	Boerwinkle 2019		
Prm5	id	Chen 2017		
Prm6	id	Khoo 2019		
Prm7	id	Lee 2014		
Prm8	id	Reyes 2016		
Prm9	rsfMRI		1	
Prm10	rsfMRI		2	
Prm11	id*rsfMRI	Bettus 2010	1	
Prm12	id*rsfMRI	Bettus 2010	2	
Prm13	id*rsfMRI	Boerwinkle 2017	1	
Prm14	id*rsfMRI	Boerwinkle 2017	2	
Prm15	id*rsfMRI	Boerwinkle 2019	1	
Prm16	id*rsfMRI	Boerwinkle 2019	2	
Prm17	id*rsfMRI	Chen 2017	1	
Prm18	id*rsfMRI	Chen 2017	2	
Prm19	id*rsfMRI	Khoo 2019	1	
Prm20	id*rsfMRI	Khoo 2019	2	
Prm21	id*rsfMRI	Lee 2014	1	
Prm22	id*rsfMRI	Lee 2014	2	

g008.sas: No 0 margins and n>=20, loglinear model (fixed effects)
1. Log(odds ratio): 0

The GENMOD Procedure

Parameter Information

Parameter	*Effect*	*id*	*rsfMRI*	*compar*
Prm23	id*rsfMRI	Reyes 2016	1	
Prm24	id*rsfMRI	Reyes 2016	2	
Prm25	compar			1
Prm26	compar			2
Prm27	id*compar	Bettus 2010		1
Prm28	id*compar	Bettus 2010		2
Prm29	id*compar	Boerwinkle 2017		1
Prm30	id*compar	Boerwinkle 2017		2
Prm31	id*compar	Boerwinkle 2019		1
Prm32	id*compar	Boerwinkle 2019		2
Prm33	id*compar	Chen 2017		1
Prm34	id*compar	Chen 2017		2
Prm35	id*compar	Khoo 2019		1
Prm36	id*compar	Khoo 2019		2
Prm37	id*compar	Lee 2014		1
Prm38	id*compar	Lee 2014		2
Prm39	id*compar	Reyes 2016		1
Prm40	id*compar	Reyes 2016		2

Criteria For Assessing Goodness Of Fit

Criterion	*DF*	*Value*	*Value/DF*
Deviance	7	74.7190	10.6741
Scaled Deviance	7	74.7190	10.6741
Pearson Chi-Square	7	67.2790	9.6113
Scaled Pearson X2	7	67.2790	9.6113
Log Likelihood		505.7443	
Full Log Likelihood		-87.2452	
AIC (smaller is better)		216.4903	
AICC (smaller is better)		370.4903	
BIC (smaller is better)		244.4666	

Algorithm converged.

g008.sas: No 0 margins and n>=20, loglinear model (fixed effects)
1. Log(odds ratio): 0

The GENMOD Procedure

Analysis Of Maximum Likelihood Parameter Estimates

Parameter			*DF*	*Estimate*	*Standard Error*	*Wald 95% Confidence Limits*		*Wald Chi-Square*	*Pr > ChiSq*
Intercept			1	3.3416	0.1874	2.9744	3.7088	318.09	<.0001
id	Bettus 2010		1	-0.7767	0.3103	-1.3849	-0.1685	6.26	0.0123
id	Boerwinkle 2017		1	-0.0315	0.2669	-0.5545	0.4916	0.01	0.9061
id	Boerwinkle 2019		1	-1.1461	0.3209	-1.7750	-0.5172	12.76	0.0004
id	Chen 2017		1	-0.0300	0.2652	-0.5498	0.4897	0.01	0.9098
id	Khoo 2019		1	-0.9199	0.3160	-1.5392	-0.3006	8.48	0.0036
id	Lee 2014		1	-0.3153	0.2873	-0.8785	0.2478	1.20	0.2725
id	Reyes 2016		0	0.0000	0.0000	0.0000	0.0000	.	.
rsfMRI	1		1	-2.3354	0.6046	-3.5205	-1.1503	14.92	0.0001
rsfMRI	2		0	0.0000	0.0000	0.0000	0.0000	.	.
*id*rsfMRI*	Bettus 2010	1	1	1.9677	0.6779	0.6389	3.2964	8.42	0.0037
*id*rsfMRI*	Bettus 2010	2	0	0.0000	0.0000	0.0000	0.0000	.	.
*id*rsfMRI*	Boerwinkle 2017	1	1	-0.4978	0.9460	-2.3521	1.3564	0.28	0.5987
*id*rsfMRI*	Boerwinkle 2017	2	0	0.0000	0.0000	0.0000	0.0000	.	.
*id*rsfMRI*	Boerwinkle 2019	1	1	2.7801	0.6567	1.4930	4.0671	17.92	<.0001
*id*rsfMRI*	Boerwinkle 2019	2	0	0.0000	0.0000	0.0000	0.0000	.	.
*id*rsfMRI*	Chen 2017	1	1	1.1722	0.7049	-0.2093	2.5537	2.77	0.0963
*id*rsfMRI*	Chen 2017	2	0	0.0000	0.0000	0.0000	0.0000	.	.
*id*rsfMRI*	Khoo 2019	1	1	2.3762	0.6688	1.0654	3.6870	12.62	0.0004
*id*rsfMRI*	Khoo 2019	2	0	0.0000	0.0000	0.0000	0.0000	.	.
*id*rsfMRI*	Lee 2014	1	1	0.9916	0.7588	-0.4955	2.4788	1.71	0.1912
*id*rsfMRI*	Lee 2014	2	0	0.0000	0.0000	0.0000	0.0000	.	.
*id*rsfMRI*	Reyes 2016	1	0	0.0000	0.0000	0.0000	0.0000	.	.
*id*rsfMRI*	Reyes 2016	2	0	0.0000	0.0000	0.0000	0.0000	.	.
compar	1		1	-2.3354	0.6046	-3.5205	-1.1503	14.92	0.0001
compar	2		0	0.0000	0.0000	0.0000	0.0000	.	.
*id*compar*	Bettus 2010	1	1	2.3354	0.6756	1.0111	3.6596	11.95	0.0005
*id*compar*	Bettus 2010	2	0	0.0000	0.0000	0.0000	0.0000	.	.
*id*compar*	Boerwinkle 2017	1	1	0.9140	0.7368	-0.5302	2.3582	1.54	0.2148
*id*compar*	Boerwinkle 2017	2	0	0.0000	0.0000	0.0000	0.0000	.	.
*id*compar*	Boerwinkle 2019	1	1	2.9135	0.6584	1.6231	4.2038	19.58	<.0001
*id*compar*	Boerwinkle 2019	2	0	0.0000	0.0000	0.0000	0.0000	.	.
*id*compar*	Chen 2017	1	1	0.5436	0.7484	-0.9231	2.0104	0.53	0.4676
*id*compar*	Chen 2017	2	0	0.0000	0.0000	0.0000	0.0000	.	.
*id*compar*	Khoo 2019	1	1	2.4580	0.6690	1.1468	3.7691	13.50	0.0002
*id*compar*	Khoo 2019	2	0	0.0000	0.0000	0.0000	0.0000	.	.

g008.sas: No 0 margins and n>=20, loglinear model (fixed effects)
1. Log(odds ratio): 0

The GENMOD Procedure

Analysis Of Maximum Likelihood Parameter Estimates

Parameter			*DF*	*Estimate*	*Standard Error*	*Wald 95% Confidence Limits*		*Wald Chi-Square*	*Pr > ChiSq*
*id*compar*	Lee 2014	1	1	0.1759	0.8587	-1.5072	1.8589	0.04	0.8377
*id*compar*	Lee 2014	2	0	0.0000	0.0000	0.0000	0.0000	.	.
*id*compar*	Reyes 2016	1	0	0.0000	0.0000	0.0000	0.0000	.	.
*id*compar*	Reyes 2016	2	0	0.0000	0.0000	0.0000	0.0000	.	.
Scale			0	1.0000	0.0000	1.0000	1.0000		

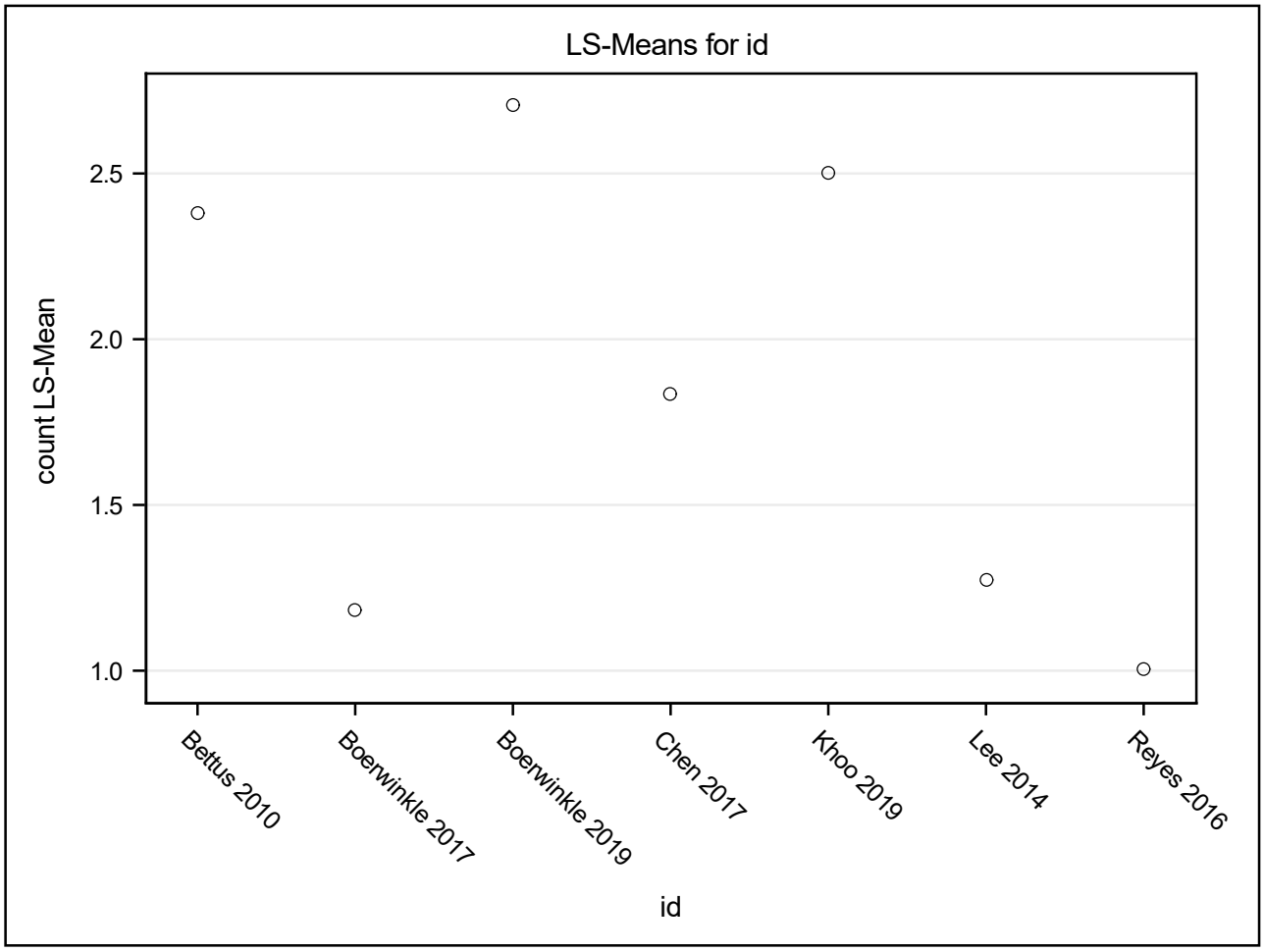
Note: The scale parameter was held fixed.

id Least Squares Means

Study ID	*Estimate*	*Standard Error*	*z Value*	*Pr > |z|*
Bettus 2010	2.3811	0.1533	15.53	<.0001
Boerwinkle 2017	1.1828	0.3859	3.07	0.0022
Boerwinkle 2019	2.7069	0.1332	20.32	<.0001
Chen 2017	1.8341	0.2400	7.64	<.0001
Khoo 2019	2.5034	0.1432	17.49	<.0001
Lee 2014	1.2747	0.3332	3.83	0.0001
Reyes 2016	1.0062	0.3916	2.57	0.0102

g008.sas: No 0 margins and n>=20, loglinear model (fixed effects)
1. Log(odds ratio): 0

The GENMOD Procedure

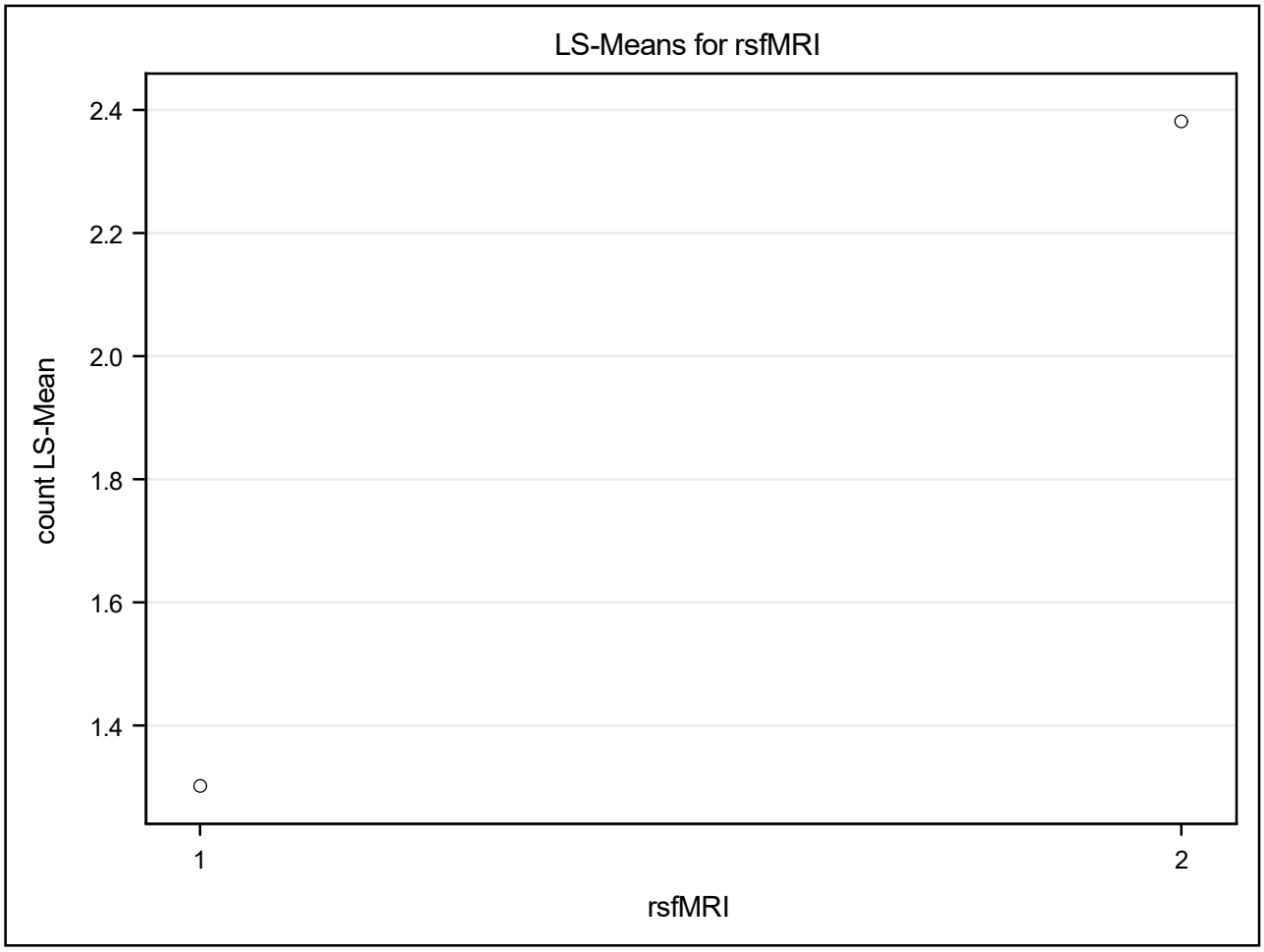


rsfMRI Least Squares Means

rsfMRI (1=-, 2=+)	*Estimate*	*Standard Error*	*z Value*	*Pr > |z|*
1	1.3015	0.1681	7.74	<.0001
2	2.3812	0.09256	25.73	<.0001

g008.sas: No 0 margins and n>=20, loglinear model (fixed effects)
1. Log(odds ratio): 0

The GENMOD Procedure

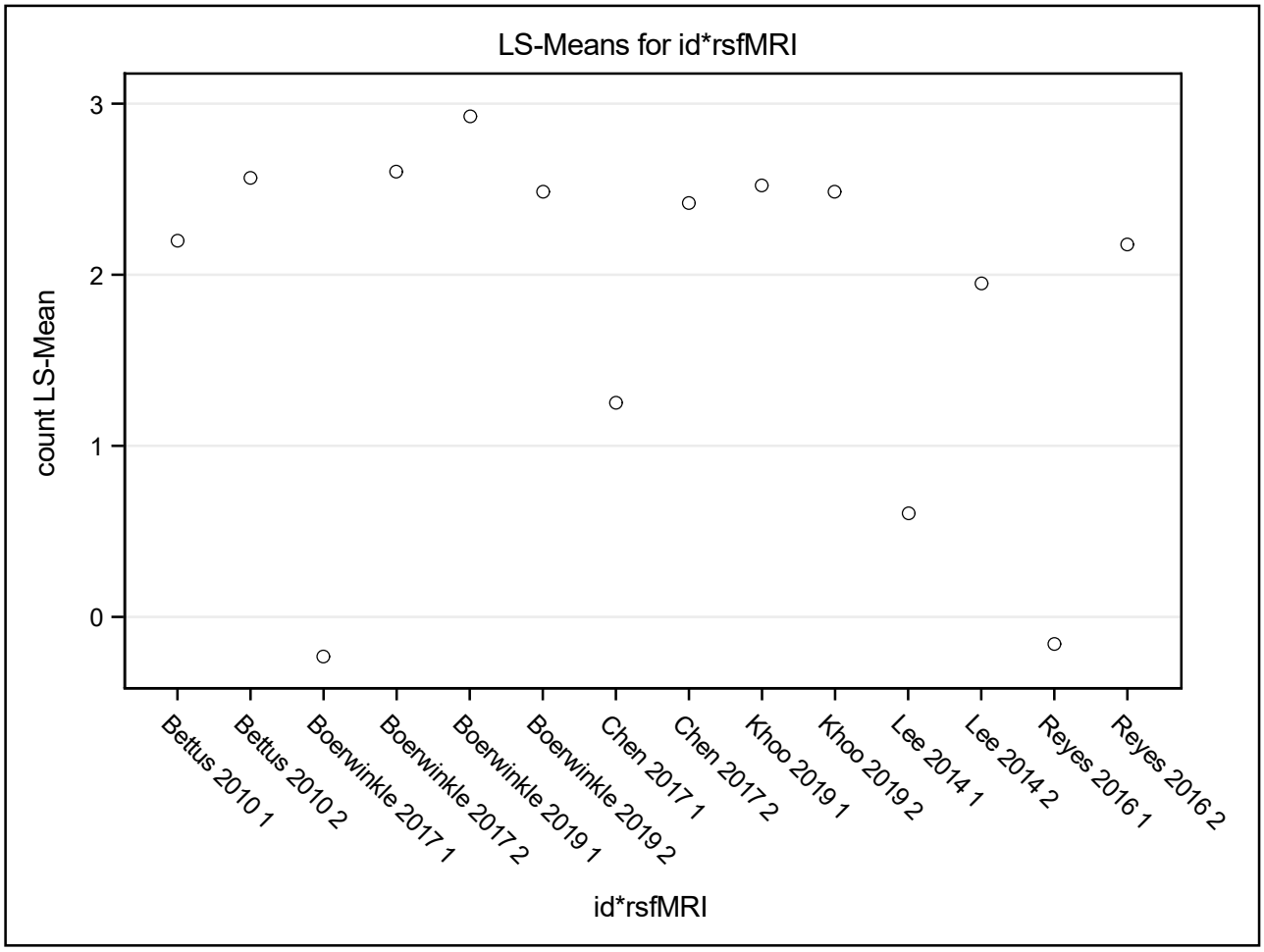


*id*rsfMRI Least Squares Means*

Study ID	*rsfMRI (1=-, 2=+)*	*Estimate*	*Standard Error*	*z Value*	*Pr > |z|*
Bettus 2010	1	2.1972	0.2357	9.32	<.0001
Bettus 2010	2	2.5649	0.1961	13.08	<.0001
Boerwinkle 2017	1	-0.2338	0.7187	-0.33	0.7450
Boerwinkle 2017	2	2.5994	0.2144	12.12	<.0001
Boerwinkle 2019	1	2.9292	0.1643	17.83	<.0001
Boerwinkle 2019	2	2.4845	0.2033	12.22	<.0001
Chen 2017	1	1.2526	0.3533	3.55	0.0004
Chen 2017	2	2.4157	0.2368	10.20	<.0001
Khoo 2019	1	2.5239	0.2002	12.61	<.0001
Khoo 2019	2	2.4830	0.2043	12.15	<.0001
Lee 2014	1	0.6028	0.4745	1.27	0.2039
Lee 2014	2	1.9466	0.3193	6.10	<.0001
Reyes 2016	1	-0.1614	0.6287	-0.26	0.7973
Reyes 2016	2	2.1739	0.3070	7.08	<.0001

g008.sas: No 0 margins and n>=20, loglinear model (fixed effects)
1. Log(odds ratio): 0

The GENMOD Procedure

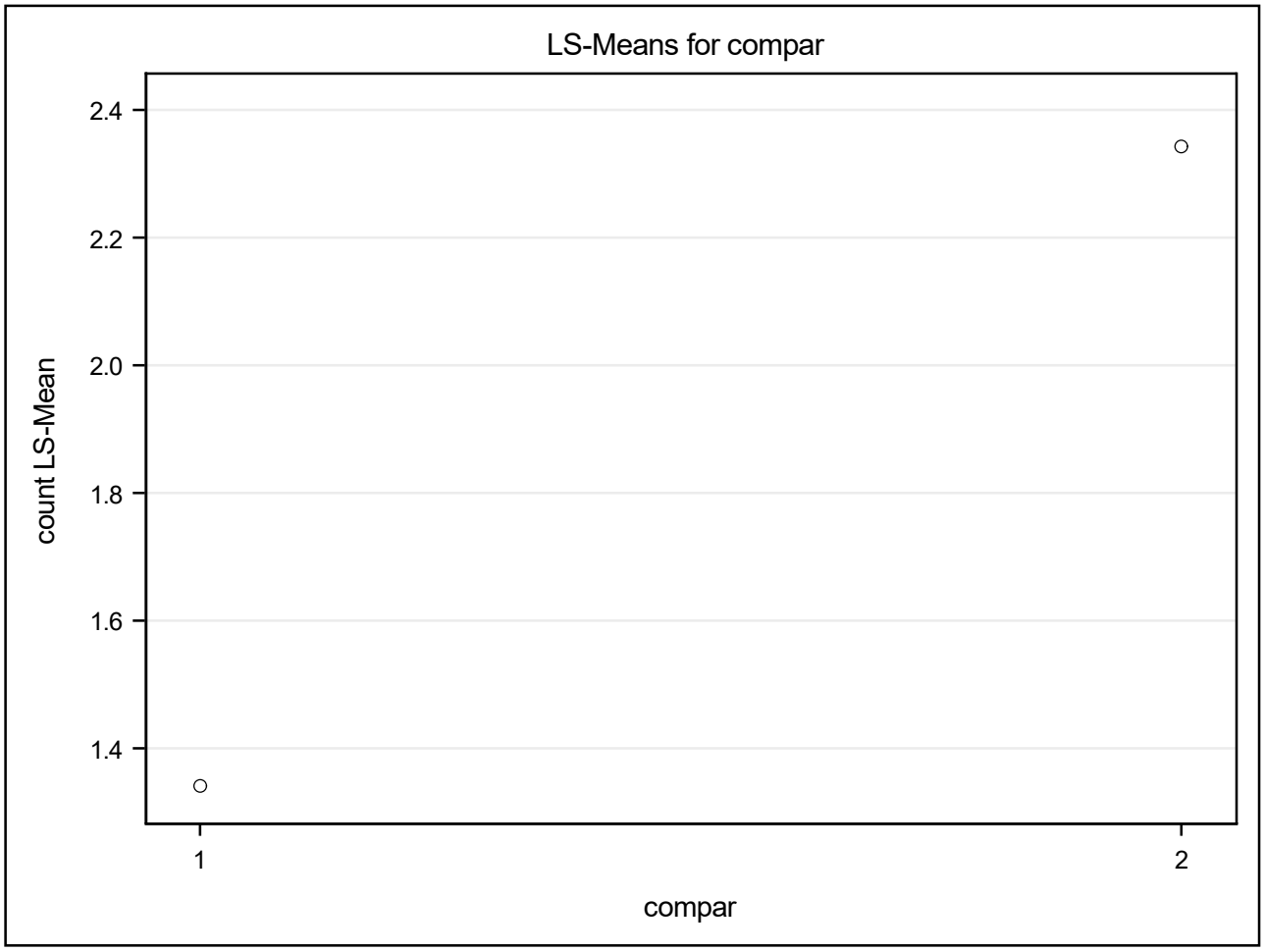


compar Least Squares Means

Comparative (1=-, 2=+)	*Estimate*	*Standard Error*	*z Value*	*Pr > |z|*
1	1.3408	0.1616	8.30	<.0001
2	2.3419	0.09695	24.15	<.0001

g008.sas: No 0 margins and n>=20, loglinear model (fixed effects)
1. Log(odds ratio): 0

The GENMOD Procedure

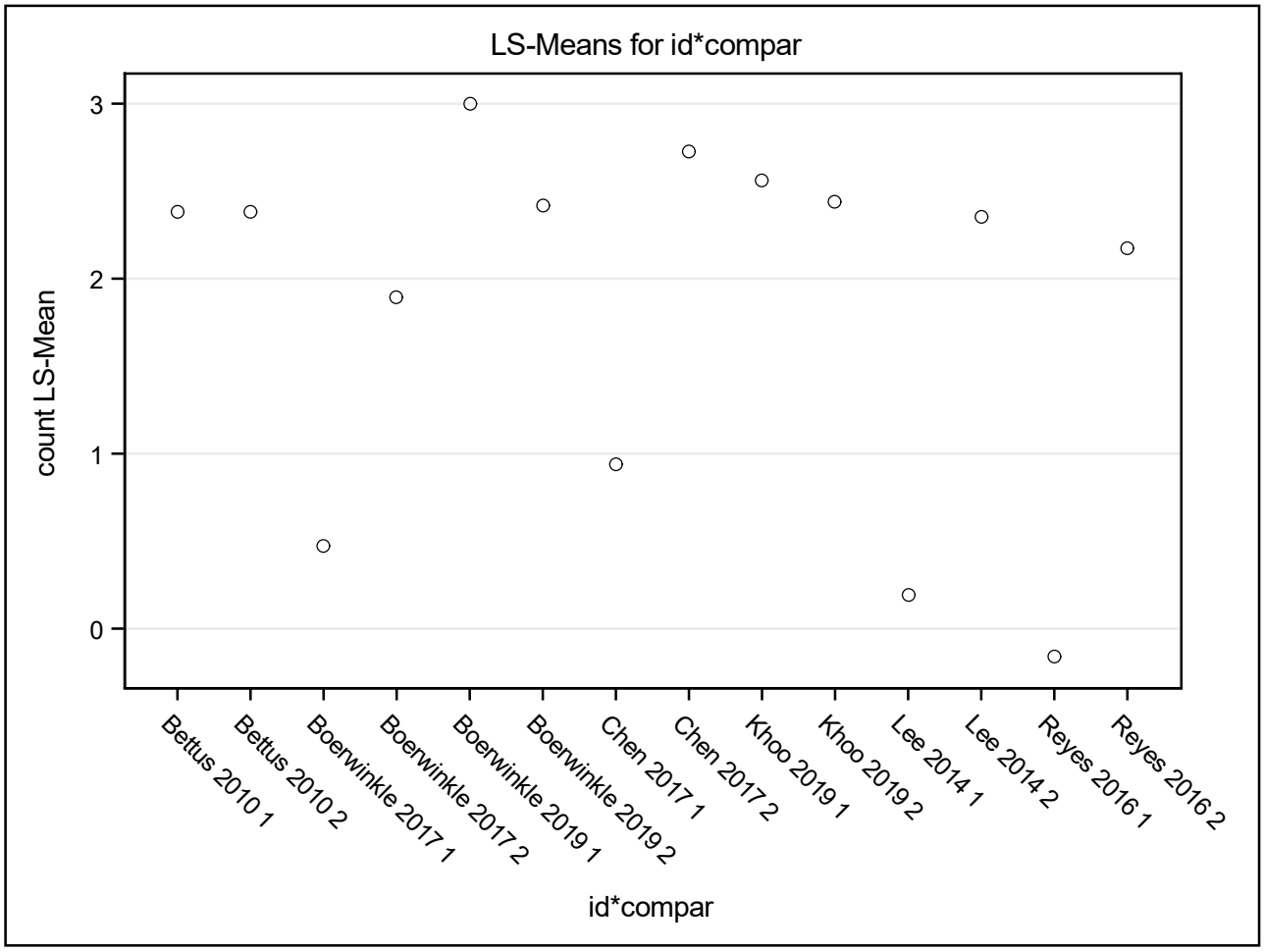


*id*compar Least Squares Means*

Study ID	*Comparative (1=-, 2=+)*	*Estimate*	*Standard Error*	*z Value*	*Pr > |z|*
Bettus 2010	1	2.3811	0.2150	11.07	<.0001
Bettus 2010	2	2.3811	0.2150	11.07	<.0001
Boerwinkle 2017	1	0.4721	0.4974	0.95	0.3425
Boerwinkle 2017	2	1.8935	0.3729	5.08	<.0001
Boerwinkle 2019	1	2.9959	0.1587	18.88	<.0001
Boerwinkle 2019	2	2.4178	0.2104	11.49	<.0001
Chen 2017	1	0.9383	0.4191	2.24	0.0252
Chen 2017	2	2.7300	0.1918	14.23	<.0001
Khoo 2019	1	2.5647	0.1961	13.08	<.0001
Khoo 2019	2	2.4421	0.2085	11.71	<.0001
Lee 2014	1	0.1949	0.5928	0.33	0.7423
Lee 2014	2	2.3544	0.2377	9.90	<.0001
Reyes 2016	1	-0.1614	0.6287	-0.26	0.7973
Reyes 2016	2	2.1739	0.3070	7.08	<.0001

g008.sas: No 0 margins and n>=20, loglinear model (fixed effects)
1. Log(odds ratio): 0

The GENMOD Procedure



g008.sas: No 0 margins and n>=20, loglinear model (fixed effects)
2. Log(odds ratio): 1

The GENMOD Procedure

Model Information	
Data Set	WORK.A
Distribution	Poisson
Link Function	Log
Dependent Variable	count

Number of Observations Read	28
Number of Observations Used	28

Class Level Information

Class	*Levels*	*Values*
id	7	Bettus 2010 Boerwinkle 2017 Boerwinkle 2019 Chen 2017 Khoo 2019 Lee 2014 Reyes 2016
rsfMRI	2	1 2
compar	2	1 2

Parameter Information

Parameter	*Effect*	*id*	*rsfMRI*	*compar*
Prm1	Intercept			
Prm2	id	Bettus 2010		
Prm3	id	Boerwinkle 2017		
Prm4	id	Boerwinkle 2019		
Prm5	id	Chen 2017		
Prm6	id	Khoo 2019		
Prm7	id	Lee 2014		
Prm8	id	Reyes 2016		
Prm9	rsfMRI		1	
Prm10	rsfMRI		2	
Prm11	id*rsfMRI	Bettus 2010	1	
Prm12	id*rsfMRI	Bettus 2010	2	
Prm13	id*rsfMRI	Boerwinkle 2017	1	
Prm14	id*rsfMRI	Boerwinkle 2017	2	
Prm15	id*rsfMRI	Boerwinkle 2019	1	
Prm16	id*rsfMRI	Boerwinkle 2019	2	
Prm17	id*rsfMRI	Chen 2017	1	
Prm18	id*rsfMRI	Chen 2017	2	
Prm19	id*rsfMRI	Khoo 2019	1	
Prm20	id*rsfMRI	Khoo 2019	2	
Prm21	id*rsfMRI	Lee 2014	1	
Prm22	id*rsfMRI	Lee 2014	2	

g008.sas: No 0 margins and n>=20, loglinear model (fixed effects)
2. Log(odds ratio): 1

The GENMOD Procedure

Parameter Information

Parameter	*Effect*	*id*	*rsfMRI*	*compar*
Prm23	id*rsfMRI	Reyes 2016	1	
Prm24	id*rsfMRI	Reyes 2016	2	
Prm25	compar			1
Prm26	compar			2
Prm27	id*compar	Bettus 2010		1
Prm28	id*compar	Bettus 2010		2
Prm29	id*compar	Boerwinkle 2017		1
Prm30	id*compar	Boerwinkle 2017		2
Prm31	id*compar	Boerwinkle 2019		1
Prm32	id*compar	Boerwinkle 2019		2
Prm33	id*compar	Chen 2017		1
Prm34	id*compar	Chen 2017		2
Prm35	id*compar	Khoo 2019		1
Prm36	id*compar	Khoo 2019		2
Prm37	id*compar	Lee 2014		1
Prm38	id*compar	Lee 2014		2
Prm39	id*compar	Reyes 2016		1
Prm40	id*compar	Reyes 2016		2
Prm41	rsfMRI*compar		1	1
Prm42	rsfMRI*compar		1	2
Prm43	rsfMRI*compar		2	1
Prm44	rsfMRI*compar		2	2

Criteria For Assessing Goodness Of Fit

Criterion	*DF*	*Value*	*Value/DF*
Deviance	6	27.6083	4.6014
Scaled Deviance	6	27.6083	4.6014
Pearson Chi-Square	6	22.2452	3.7075
Scaled Pearson X2	6	22.2452	3.7075
Log Likelihood		529.2997	
Full Log Likelihood		-63.6898	
AIC (smaller is better)		171.3797	
AICC (smaller is better)		373.7797	
BIC (smaller is better)		200.6882	

Algorithm converged.

g008.sas: No 0 margins and n>=20, loglinear model (fixed effects)
2. Log(odds ratio): 1

The GENMOD Procedure

Analysis Of Maximum Likelihood Parameter Estimates

Parameter			*DF*	*Estimate*	*Standard Error*	*Wald 95% Confidence Limits*		*Wald Chi-Square*	*Pr > ChiSq*
Intercept			1	3.3691	0.1840	3.0084	3.7297	335.20	<.0001
id	Bettus 2010		1	-0.4763	0.2899	-1.0445	0.0919	2.70	0.1004
id	Boerwinkle 2017		1	-0.0282	0.2621	-0.5420	0.4855	0.01	0.9142
id	Boerwinkle 2019		1	-0.5983	0.2964	-1.1792	-0.0173	4.07	0.0435
id	Chen 2017		1	0.0243	0.2573	-0.4801	0.5287	0.01	0.9248
id	Khoo 2019		1	-0.5296	0.2928	-1.1035	0.0443	3.27	0.0705
id	Lee 2014		1	-0.2863	0.2800	-0.8351	0.2626	1.04	0.3067
id	Reyes 2016		0	0.0000	0.0000	0.0000	0.0000	.	.
rsfMRI	1		1	-2.7020	0.6373	-3.9510	-1.4530	17.98	<.0001
rsfMRI	2		0	0.0000	0.0000	0.0000	0.0000	.	.
*id*rsfMRI*	Bettus 2010	1	1	1.1848	0.7282	-0.2425	2.6121	2.65	0.1037
*id*rsfMRI*	Bettus 2010	2	0	0.0000	0.0000	0.0000	0.0000	.	.
*id*rsfMRI*	Boerwinkle 2017	1	1	-0.9166	0.9882	-2.8534	1.0203	0.86	0.3537
*id*rsfMRI*	Boerwinkle 2017	2	0	0.0000	0.0000	0.0000	0.0000	.	.
*id*rsfMRI*	Boerwinkle 2019	1	1	1.8812	0.7020	0.5054	3.2571	7.18	0.0074
*id*rsfMRI*	Boerwinkle 2019	2	0	0.0000	0.0000	0.0000	0.0000	.	.
*id*rsfMRI*	Chen 2017	1	1	1.1387	0.7426	-0.3167	2.5942	2.35	0.1252
*id*rsfMRI*	Chen 2017	2	0	0.0000	0.0000	0.0000	0.0000	.	.
*id*rsfMRI*	Khoo 2019	1	1	1.6363	0.7152	0.2346	3.0381	5.23	0.0221
*id*rsfMRI*	Khoo 2019	2	0	0.0000	0.0000	0.0000	0.0000	.	.
*id*rsfMRI*	Lee 2014	1	1	1.0496	0.7977	-0.5139	2.6131	1.73	0.1883
*id*rsfMRI*	Lee 2014	2	0	0.0000	0.0000	0.0000	0.0000	.	.
*id*rsfMRI*	Reyes 2016	1	0	0.0000	0.0000	0.0000	0.0000	.	.
*id*rsfMRI*	Reyes 2016	2	0	0.0000	0.0000	0.0000	0.0000	.	.
compar	1		1	-2.7020	0.6373	-3.9510	-1.4530	17.98	<.0001
compar	2		0	0.0000	0.0000	0.0000	0.0000	.	.
*id*compar*	Bettus 2010	1	1	1.8834	0.7180	0.4762	3.2906	6.88	0.0087
*id*compar*	Bettus 2010	2	0	0.0000	0.0000	0.0000	0.0000	.	.
*id*compar*	Boerwinkle 2017	1	1	1.1117	0.7696	-0.3967	2.6201	2.09	0.1486
*id*compar*	Boerwinkle 2017	2	0	0.0000	0.0000	0.0000	0.0000	.	.
*id*compar*	Boerwinkle 2019	1	1	2.1316	0.7004	0.7589	3.5044	9.26	0.0023
*id*compar*	Boerwinkle 2019	2	0	0.0000	0.0000	0.0000	0.0000	.	.
*id*compar*	Chen 2017	1	1	0.1126	0.7945	-1.4446	1.6699	0.02	0.8873
*id*compar*	Chen 2017	2	0	0.0000	0.0000	0.0000	0.0000	.	.
*id*compar*	Khoo 2019	1	1	1.7931	0.7135	0.3946	3.1915	6.32	0.0120
*id*compar*	Khoo 2019	2	0	0.0000	0.0000	0.0000	0.0000	.	.

g008.sas: No 0 margins and n>=20, loglinear model (fixed effects)
2. Log(odds ratio): 1

The GENMOD Procedure

Analysis Of Maximum Likelihood Parameter Estimates

Parameter			*DF*	*Estimate*	*Standard Error*	*Wald 95% Confidence Limits*		*Wald Chi-Square*	*Pr > ChiSq*
*id*compar*	Lee 2014	1	1	-0.2150	0.9079	-1.9943	1.5644	0.06	0.8128
*id*compar*	Lee 2014	2	0	0.0000	0.0000	0.0000	0.0000	.	.
*id*compar*	Reyes 2016	1	0	0.0000	0.0000	0.0000	0.0000	.	.
*id*compar*	Reyes 2016	2	0	0.0000	0.0000	0.0000	0.0000	.	.
*rsfMRI*compar*	1	1	1	2.0852	0.3189	1.4602	2.7102	42.76	<.0001
*rsfMRI*compar*	1	2	0	0.0000	0.0000	0.0000	0.0000	.	.
*rsfMRI*compar*	2	1	0	0.0000	0.0000	0.0000	0.0000	.	.
*rsfMRI*compar*	2	2	0	0.0000	0.0000	0.0000	0.0000	.	.
Scale			0	1.0000	0.0000	1.0000	1.0000		

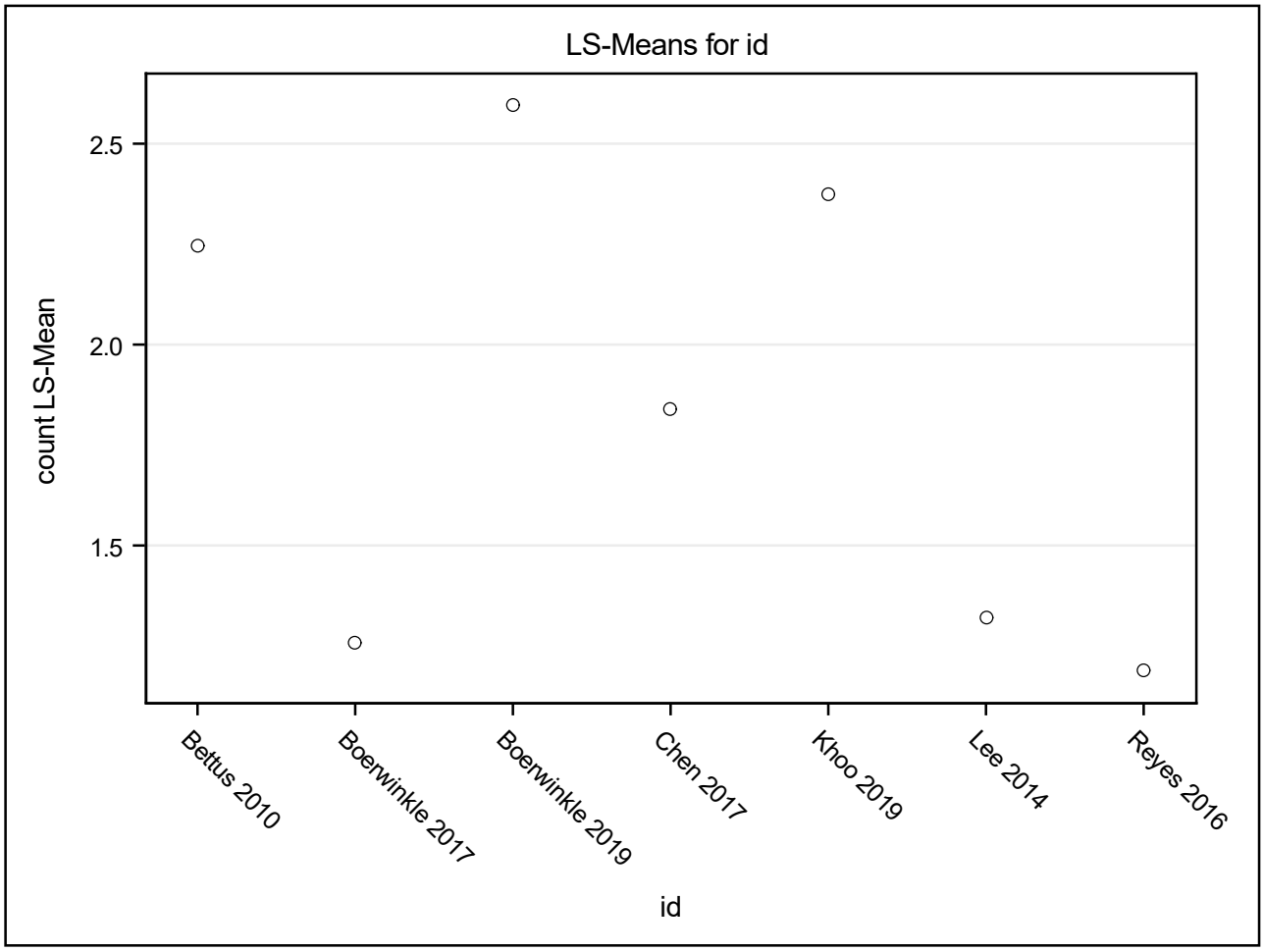
Note: The scale parameter was held fixed.

id Least Squares Means

Study ID	*Estimate*	*Standard Error*	*z Value*	*Pr > |z|*
Bettus 2010	2.2461	0.1591	14.12	<.0001
Boerwinkle 2017	1.2577	0.3673	3.42	0.0006
Boerwinkle 2019	2.5965	0.1359	19.11	<.0001
Chen 2017	1.8383	0.2255	8.15	<.0001
Khoo 2019	2.3735	0.1481	16.02	<.0001
Lee 2014	1.3194	0.3110	4.24	<.0001
Reyes 2016	1.1884	0.3545	3.35	0.0008

g008.sas: No 0 margins and n>=20, loglinear model (fixed effects)
2. Log(odds ratio): 1

The GENMOD Procedure

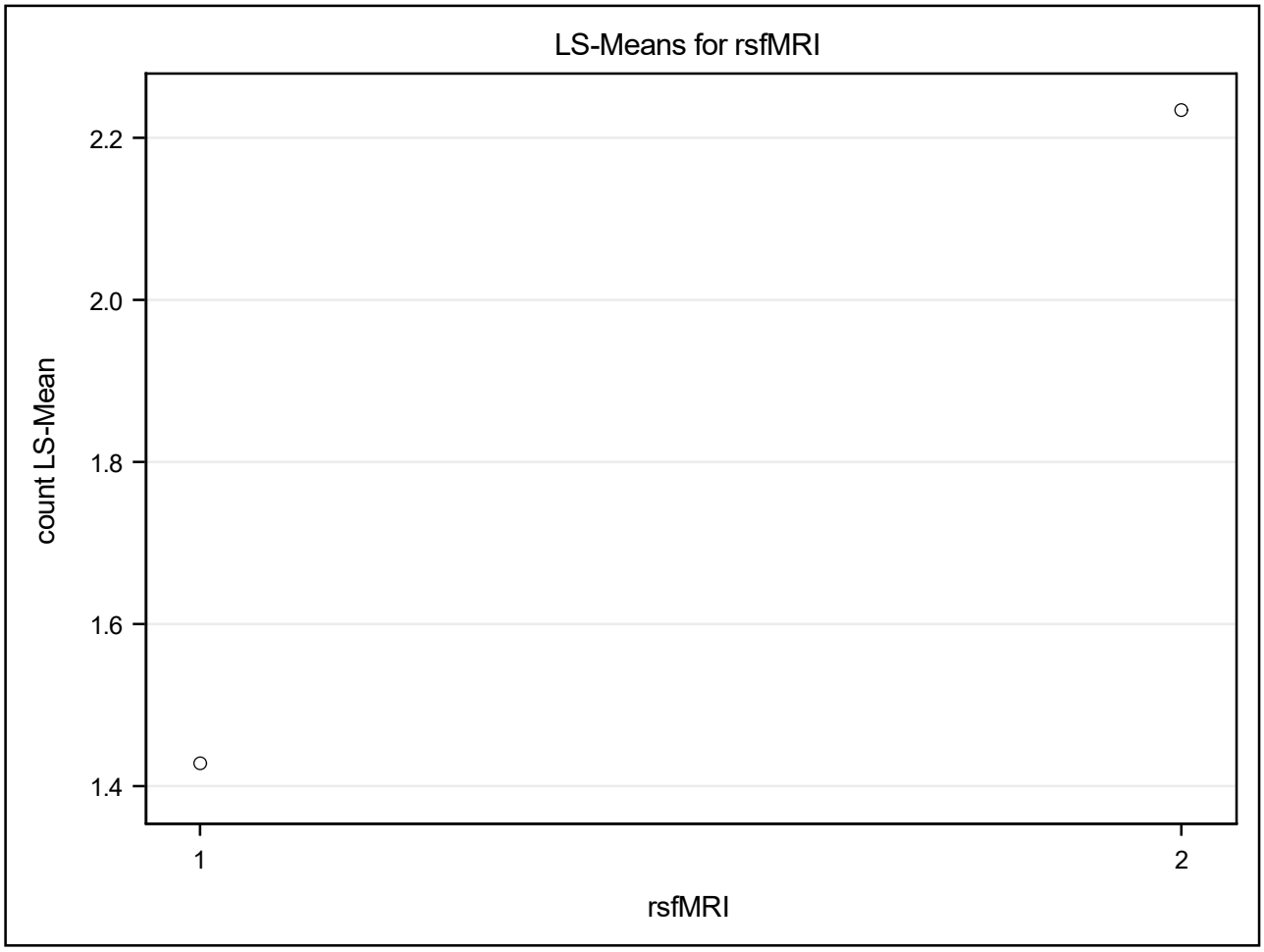


rsfMRI Least Squares Means

rsfMRI (1=-, 2=+)	*Estimate*	*Standard Error*	*z Value*	*Pr > |z|*
1	1.4284	0.1622	8.81	<.0001
2	2.2344	0.1074	20.81	<.0001

g008.sas: No 0 margins and n>=20, loglinear model (fixed effects)
2. Log(odds ratio): 1

The GENMOD Procedure

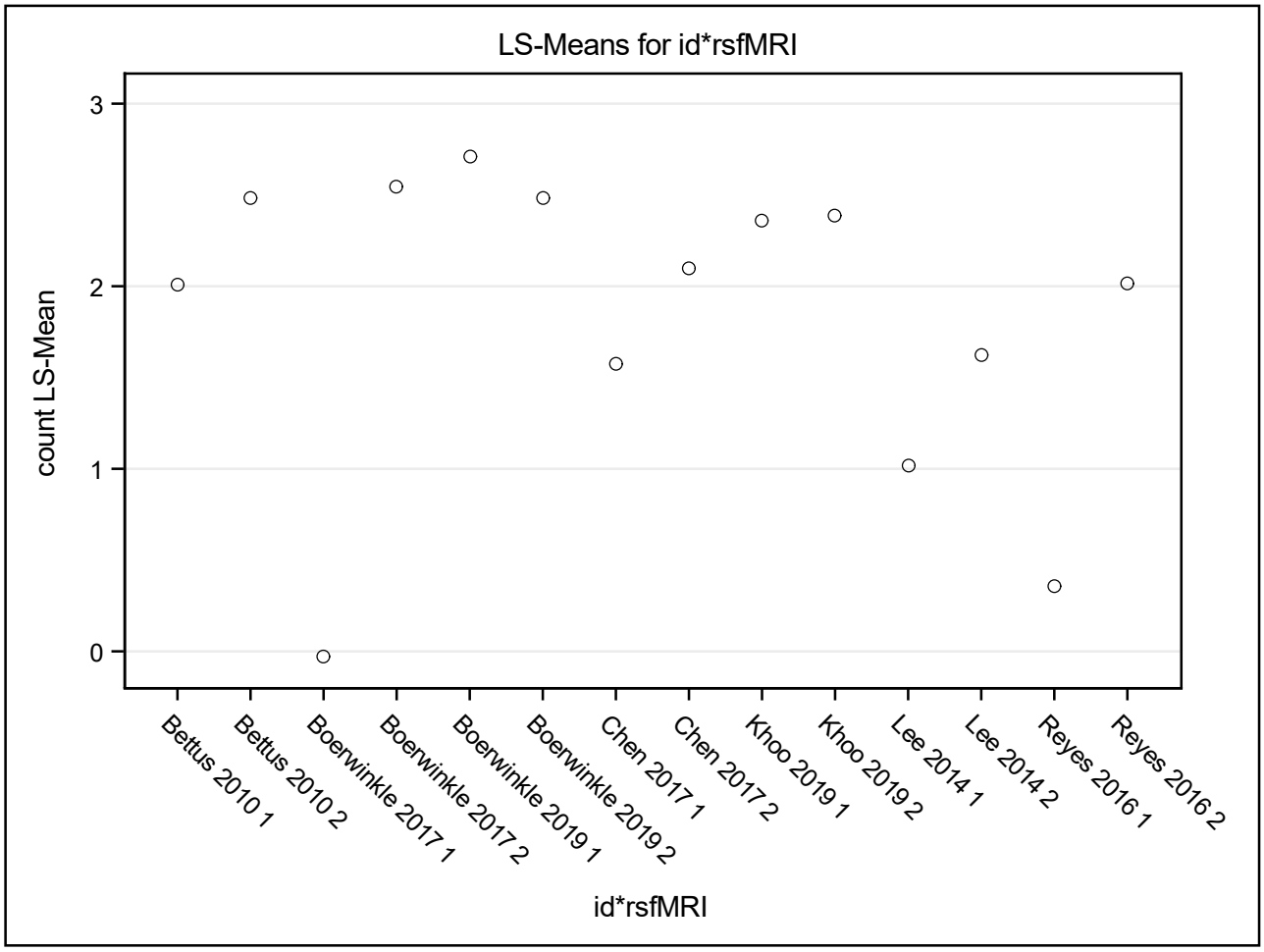


*id*rsfMRI Least Squares Means*

Study ID	*rsfMRI (1=-, 2=+)*	*Estimate*	*Standard Error*	*z Value*	*Pr > |z|*
Bettus 2010	1	2.0088	0.2607	7.71	<.0001
Bettus 2010	2	2.4834	0.2081	11.93	<.0001
Boerwinkle 2017	1	-0.03030	0.7100	-0.04	0.9660
Boerwinkle 2017	2	2.5457	0.2243	11.35	<.0001
Boerwinkle 2019	1	2.7074	0.1926	14.05	<.0001
Boerwinkle 2019	2	2.4856	0.2053	12.11	<.0001
Chen 2017	1	1.5780	0.3222	4.90	<.0001
Chen 2017	2	2.0987	0.2799	7.50	<.0001
Khoo 2019	1	2.3619	0.2221	10.63	<.0001
Khoo 2019	2	2.3850	0.2180	10.94	<.0001
Lee 2014	1	1.0145	0.4287	2.37	0.0179
Lee 2014	2	1.6243	0.3655	4.44	<.0001
Reyes 2016	1	0.3586	0.5860	0.61	0.5406
Reyes 2016	2	2.0181	0.3315	6.09	<.0001

g008.sas: No 0 margins and n>=20, loglinear model (fixed effects)
2. Log(odds ratio): 1

The GENMOD Procedure

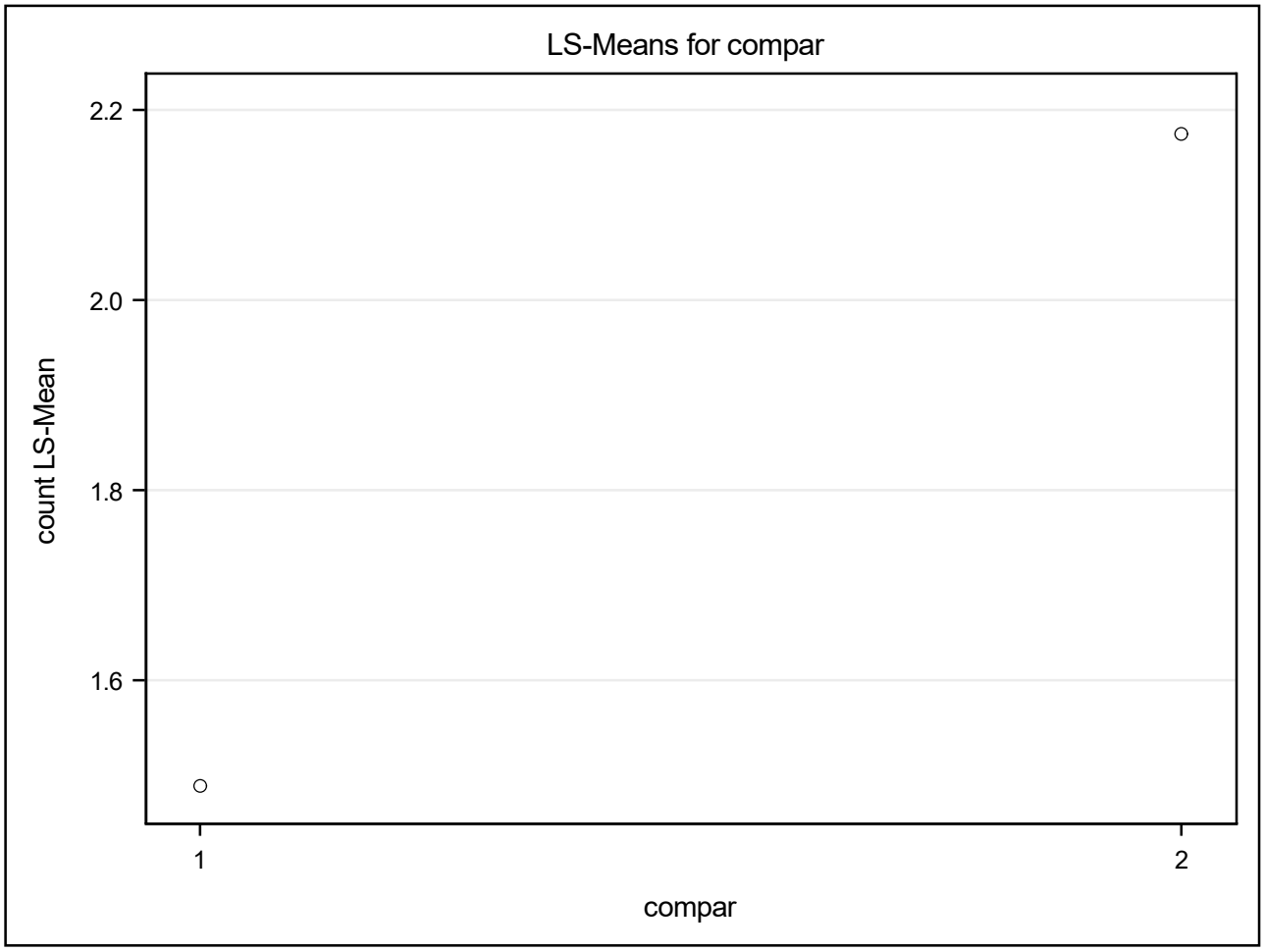


compar Least Squares Means

Comparative (1=-, 2=+)	*Estimate*	*Standard Error*	*z Value*	*Pr > |z|*
1	1.4887	0.1550	9.60	<.0001
2	2.1742	0.1133	19.19	<.0001

g008.sas: No 0 margins and n>=20, loglinear model (fixed effects)
2. Log(odds ratio): 1

The GENMOD Procedure

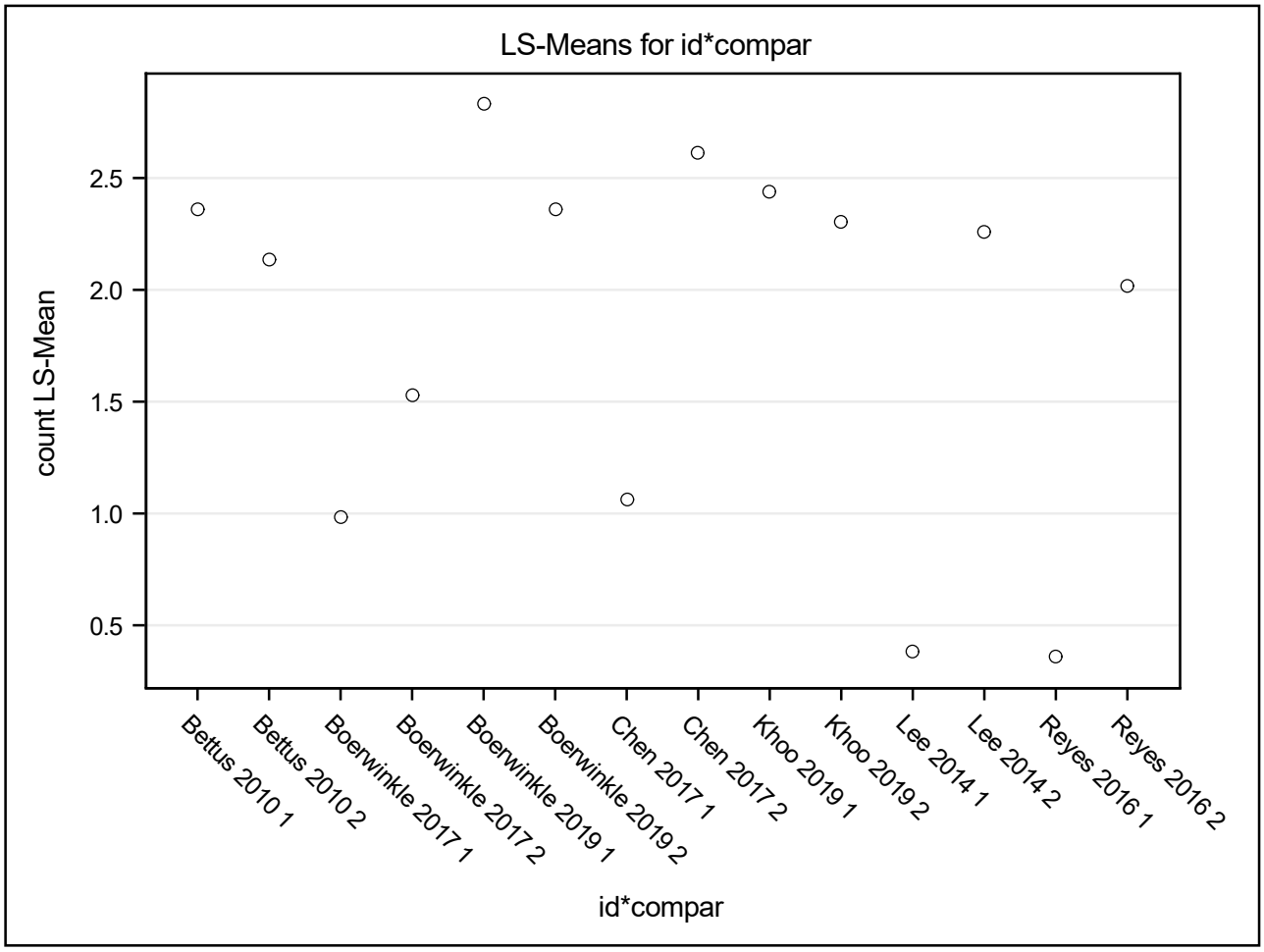


*id*compar Least Squares Means*

Study ID	*Comparative (1=-, 2=+)*	*Estimate*	*Standard Error*	*z Value*	*Pr > |z|*
Bettus 2010	1	2.3581	0.2192	10.76	<.0001
Bettus 2010	2	2.1342	0.2483	8.60	<.0001
Boerwinkle 2017	1	0.9838	0.4515	2.18	0.0293
Boerwinkle 2017	2	1.5315	0.4121	3.72	0.0002
Boerwinkle 2019	1	2.8326	0.1797	15.76	<.0001
Boerwinkle 2019	2	2.3604	0.2191	10.77	<.0001
Chen 2017	1	1.0649	0.4125	2.58	0.0098
Chen 2017	2	2.6117	0.2111	12.37	<.0001
Khoo 2019	1	2.4403	0.2133	11.44	<.0001
Khoo 2019	2	2.3066	0.2269	10.16	<.0001
Lee 2014	1	0.3822	0.5804	0.66	0.5101
Lee 2014	2	2.2566	0.2570	8.78	<.0001
Reyes 2016	1	0.3586	0.5860	0.61	0.5406
Reyes 2016	2	2.0181	0.3315	6.09	<.0001

g008.sas: No 0 margins and n>=20, loglinear model (fixed effects)
2. Log(odds ratio): 1

The GENMOD Procedure

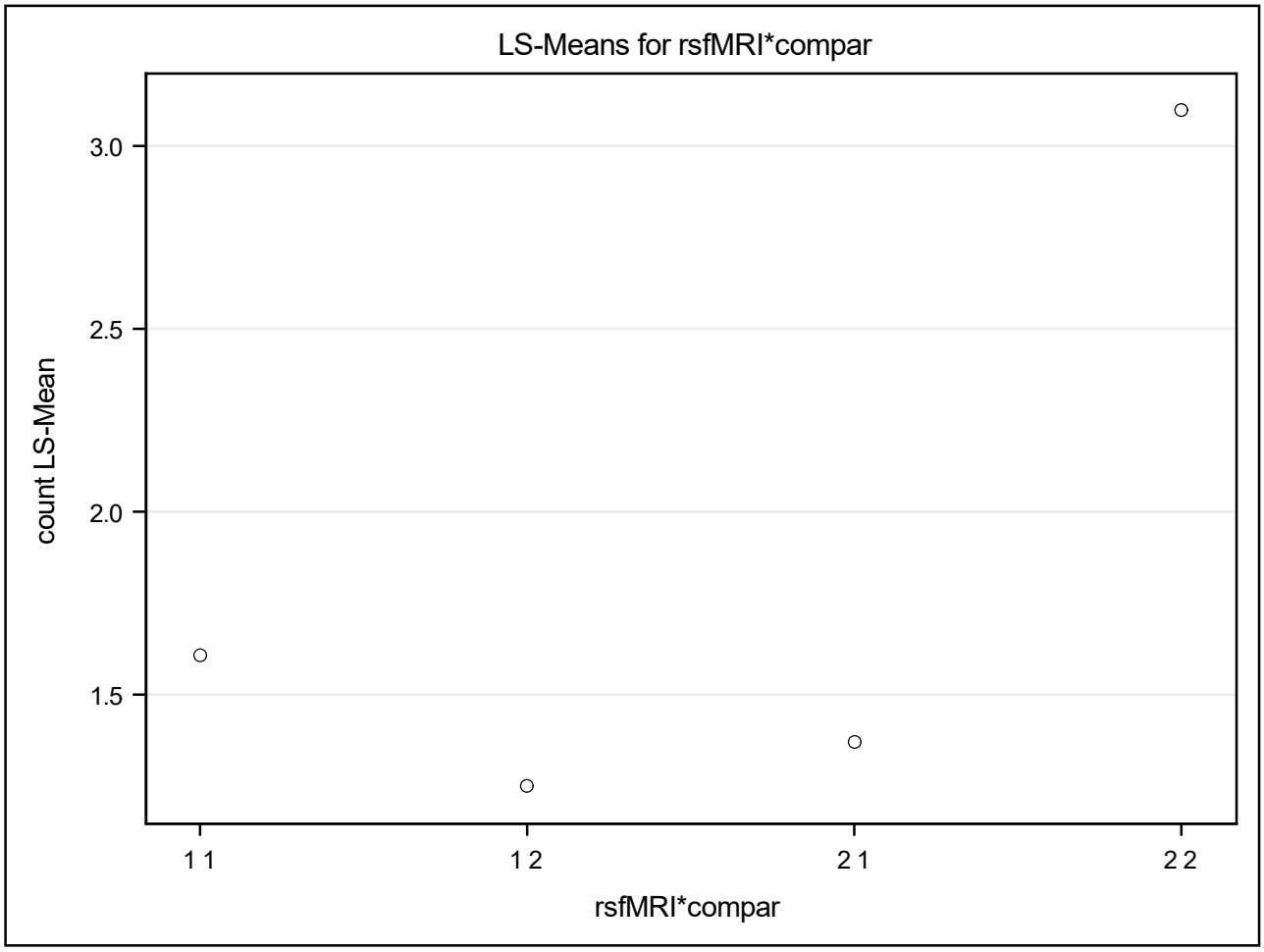


*rsfMRI*compar Least Squares Means*

rsfMRI (1=-, 2=+)	*Comparative (1=-, 2=+)*	*Estimate*	*Standard Error*	*z Value*	*Pr > |z|*
1	1	1.6070	0.2045	7.86	<.0001
1	2	1.2499	0.2126	5.88	<.0001
2	1	1.3703	0.2002	6.85	<.0001
2	2	3.0984	0.08140	38.07	<.0001

g008.sas: No 0 margins and n>=20, loglinear model (fixed effects)
2. Log(odds ratio): 1

The GENMOD Procedure



g008.sas: No 0 margins and n>=20, loglinear model (fixed effects)
3. Log(odds ratio): 1+modality

The GENMOD Procedure

Model Information	
Data Set	WORK.A
Distribution	Poisson
Link Function	Log
Dependent Variable	count

Number of Observations Read	28
Number of Observations Used	28

Class Level Information

Class	*Levels*	*Values*
id	7	Bettus 2010 Boerwinkle 2017 Boerwinkle 2019 Chen 2017 Khoo 2019 Lee 2014 Reyes 2016
rsfMRI	2	1 2
compar	2	1 2
modality	4	0 1 3 4

Parameter Information

Parameter	*Effect*	*id*	*rsfMRI*	*compar*	*modality*
Prm1	Intercept				
Prm2	id	Bettus 2010			
Prm3	id	Boerwinkle 2017			
Prm4	id	Boerwinkle 2019			
Prm5	id	Chen 2017			
Prm6	id	Khoo 2019			
Prm7	id	Lee 2014			
Prm8	id	Reyes 2016			
Prm9	rsfMRI		1		
Prm10	rsfMRI		2		
Prm11	id*rsfMRI	Bettus 2010	1		
Prm12	id*rsfMRI	Bettus 2010	2		
Prm13	id*rsfMRI	Boerwinkle 2017	1		
Prm14	id*rsfMRI	Boerwinkle 2017	2		
Prm15	id*rsfMRI	Boerwinkle 2019	1		
Prm16	id*rsfMRI	Boerwinkle 2019	2		
Prm17	id*rsfMRI	Chen 2017	1		
Prm18	id*rsfMRI	Chen 2017	2		
Prm19	id*rsfMRI	Khoo 2019	1		
Prm20	id*rsfMRI	Khoo 2019	2		
Prm21	id*rsfMRI	Lee 2014	1		

g008.sas: No 0 margins and n>=20, loglinear model (fixed effects)
3. Log(odds ratio): 1+modality

The GENMOD Procedure

Parameter Information

Parameter	*Effect*	*id*	*rsfMRI*	*compar*	*modality*
Prm22	id*rsfMRI	Lee 2014	2		
Prm23	id*rsfMRI	Reyes 2016	1		
Prm24	id*rsfMRI	Reyes 2016	2		
Prm25	compar			1	
Prm26	compar			2	
Prm27	id*compar	Bettus 2010		1	
Prm28	id*compar	Bettus 2010		2	
Prm29	id*compar	Boerwinkle 2017		1	
Prm30	id*compar	Boerwinkle 2017		2	
Prm31	id*compar	Boerwinkle 2019		1	
Prm32	id*compar	Boerwinkle 2019		2	
Prm33	id*compar	Chen 2017		1	
Prm34	id*compar	Chen 2017		2	
Prm35	id*compar	Khoo 2019		1	
Prm36	id*compar	Khoo 2019		2	
Prm37	id*compar	Lee 2014		1	
Prm38	id*compar	Lee 2014		2	
Prm39	id*compar	Reyes 2016		1	
Prm40	id*compar	Reyes 2016		2	
Prm41	rsfMRI*compar		1	1	
Prm42	rsfMRI*compar		1	2	
Prm43	rsfMRI*compar		2	1	
Prm44	rsfMRI*compar		2	2	
Prm45	modality				0
Prm46	modality				1
Prm47	modality				3
Prm48	modality				4
Prm49	rsfMRI*modality		1		0
Prm50	rsfMRI*modality		1		1
Prm51	rsfMRI*modality		1		3
Prm52	rsfMRI*modality		1		4
Prm53	rsfMRI*modality		2		0
Prm54	rsfMRI*modality		2		1
Prm55	rsfMRI*modality		2		3
Prm56	rsfMRI*modality		2		4
Prm57	compar*modality			1	0
Prm58	compar*modality			1	1
Prm59	compar*modality			1	3

g008.sas: No 0 margins and n>=20, loglinear model (fixed effects)
3. Log(odds ratio): 1+modality

The GENMOD Procedure

Parameter Information

Parameter	*Effect*	*id*	*rsfMRI*	*compar*	*modality*
Prm60	compar*modality			1	4
Prm61	compar*modality			2	0
Prm62	compar*modality			2	1
Prm63	compar*modality			2	3
Prm64	compar*modality			2	4
Prm65	rsfMRI*compar*modali		1	1	0
Prm66	rsfMRI*compar*modali		1	1	1
Prm67	rsfMRI*compar*modali		1	1	3
Prm68	rsfMRI*compar*modali		1	1	4
Prm69	rsfMRI*compar*modali		1	2	0
Prm70	rsfMRI*compar*modali		1	2	1
Prm71	rsfMRI*compar*modali		1	2	3
Prm72	rsfMRI*compar*modali		1	2	4
Prm73	rsfMRI*compar*modali		2	1	0
Prm74	rsfMRI*compar*modali		2	1	1
Prm75	rsfMRI*compar*modali		2	1	3
Prm76	rsfMRI*compar*modali		2	1	4
Prm77	rsfMRI*compar*modali		2	2	0
Prm78	rsfMRI*compar*modali		2	2	1
Prm79	rsfMRI*compar*modali		2	2	3
Prm80	rsfMRI*compar*modali		2	2	4

Criteria For Assessing Goodness Of Fit

Criterion	*DF*	*Value*	*Value/DF*
Deviance	3	14.5974	4.8658
Scaled Deviance	3	14.5974	4.8658
Pearson Chi-Square	3	23.5714	7.8571
Scaled Pearson X2	3	23.5714	7.8571
Log Likelihood		535.8051	
Full Log Likelihood		-57.1844	
AIC (smaller is better)		164.3688	
AICC (smaller is better)		814.3688	
BIC (smaller is better)		197.6739	

Algorithm converged.

g008.sas: No 0 margins and n>=20, loglinear model (fixed effects)
3. Log(odds ratio): 1+modality

The GENMOD Procedure

Estimated Covariance Matrix

	Prm1	*Prm2*	*Prm3*	*Prm4*	*Prm5*	*Prm6*	*Prm7*	*Prm9*	*Prm11*
Prm1	0.03464	-0.03390	-0.03464	-0.03464	-0.03464	-0.03464	-0.03464	-0.03002	0.02756
Prm2	-0.03390	0.09651	0.03390	0.03390	0.03390	0.03390	0.03390	0.02077	-0.07845
Prm3	-0.03464	0.03390	0.06917	0.03489	0.03464	0.03464	0.03464	0.03002	-0.02756
Prm4	-0.03464	0.03390	0.03489	0.08381	0.03464	0.03464	0.03464	0.03002	-0.02756
Prm5	-0.03464	0.03390	0.03464	0.03464	0.06797	0.03464	0.03464	0.03002	-0.02756
Prm6	-0.03464	0.03390	0.03464	0.03464	0.03464	0.09682	0.03616	0.03002	-0.02756
Prm7	-0.03464	0.03390	0.03464	0.03464	0.03464	0.03616	0.08018	0.03002	-0.02756
Prm9	-0.03002	0.02077	0.03002	0.03002	0.03002	0.03002	0.03002	0.37881	-0.34769
Prm11	0.02756	-0.07845	-0.02756	-0.02756	-0.02756	-0.02756	-0.02756	-0.34769	0.51880
Prm13	0.03002	-0.02077	-0.03712	-0.06944	-0.03002	-0.03002	-0.03002	-0.37881	0.34769
Prm15	0.03002	-0.02077	-0.03210	-0.07660	-0.03002	-0.03002	-0.03002	-0.37881	0.34769
Prm17	0.03002	-0.02077	-0.03002	-0.03002	-0.06336	-0.03002	-0.03002	-0.37881	0.34769
Prm19	0.03002	-0.02077	-0.03002	-0.03002	-0.03002	-0.08783	-0.03471	-0.37881	0.34769
Prm21	0.03002	-0.02077	-0.03002	-0.03002	-0.03002	-0.03868	-0.07038	-0.37881	0.34769
Prm25	-0.03002	0.02077	0.03002	0.03002	0.03002	0.03002	0.03002	-0.02819	0.05930
Prm27	0.02822	-0.08032	-0.02822	-0.02822	-0.02822	-0.02822	-0.02822	0.05101	-0.02866
Prm29	0.03002	-0.02077	-0.06356	-0.03169	-0.03002	-0.03002	-0.03002	0.02819	-0.05930
Prm31	0.03002	-0.02077	-0.03134	-0.07768	-0.03002	-0.03002	-0.03002	0.02819	-0.05930
Prm33	0.03002	-0.02077	-0.03002	-0.03002	-0.06336	-0.03002	-0.03002	0.02819	-0.05930
Prm35	0.03002	-0.02077	-0.03002	-0.03002	-0.03002	-0.08835	-0.03434	0.02819	-0.05930
Prm37	0.03002	-0.02077	-0.03002	-0.03002	-0.03002	-0.05241	-0.06041	0.02819	-0.05930
Prm41	-1.31E-16	2.816E-17	0.003281	0.04486	1.299E-16	1.596E-16	1.188E-16	1.508E-15	-1.12E-15
Prm65	7.37E-17	3.775E-17	-0.003281	-0.04486	0.03333	-8.33E-17	-5.81E-17	-1.17E-15	7.989E-16
Prm66	0.004531	0.05180	-0.007811	-0.04939	-0.004531	-0.004531	-0.004531	-0.05717	-0.13223
Prm67	1.172E-16	-4.29E-17	-0.003281	-0.04486	-1.2E-16	0.05210	0.008832	-1.25E-15	9.314E-16

g008.sas: No 0 margins and n>=20, loglinear model (fixed effects)
3. Log(odds ratio): 1+modality

The GENMOD Procedure

Estimated Covariance Matrix

	Prm13	*Prm15*	*Prm17*	*Prm19*	*Prm21*	*Prm25*	*Prm27*	*Prm29*	*Prm31*
Prm1	0.03002	0.03002	0.03002	0.03002	0.03002	-0.03002	0.02822	0.03002	0.03002
Prm2	-0.02077	-0.02077	-0.02077	-0.02077	-0.02077	0.02077	-0.08032	-0.02077	-0.02077
Prm3	-0.03712	-0.03210	-0.03002	-0.03002	-0.03002	0.03002	-0.02822	-0.06356	-0.03134
Prm4	-0.06944	-0.07660	-0.03002	-0.03002	-0.03002	0.03002	-0.02822	-0.03169	-0.07768
Prm5	-0.03002	-0.03002	-0.06336	-0.03002	-0.03002	0.03002	-0.02822	-0.03002	-0.03002
Prm6	-0.03002	-0.03002	-0.03002	-0.08783	-0.03868	0.03002	-0.02822	-0.03002	-0.03002
Prm7	-0.03002	-0.03002	-0.03002	-0.03471	-0.07038	0.03002	-0.02822	-0.03002	-0.03002
Prm9	-0.37881	-0.37881	-0.37881	-0.37881	-0.37881	-0.02819	0.05101	0.02819	0.02819
Prm11	0.34769	0.34769	0.34769	0.34769	0.34769	0.05930	-0.02866	-0.05930	-0.05930
Prm13	1.48048	0.70103	0.37881	0.37881	0.37881	0.02819	-0.05101	-0.17449	0.17652
Prm15	0.70103	0.75959	0.37881	0.37881	0.37881	0.02819	-0.05101	-0.01459	0.005966
Prm17	0.37881	0.37881	0.57881	0.37881	0.37881	0.02819	-0.05101	-0.02819	-0.02819
Prm19	0.37881	0.37881	0.37881	0.55749	0.40556	0.02819	-0.05101	-0.02819	-0.02819
Prm21	0.37881	0.37881	0.37881	0.40556	0.60899	0.02819	-0.05101	-0.02819	-0.02819
Prm25	0.02819	0.02819	0.02819	0.02819	0.02819	0.37881	-0.35599	-0.37881	-0.37881
Prm27	-0.05101	-0.05101	-0.05101	-0.05101	-0.05101	-0.35599	0.48447	0.35599	0.35599
Prm29	-0.17449	-0.01459	-0.02819	-0.02819	-0.02819	-0.37881	0.35599	0.59867	0.38745
Prm31	0.17652	0.005966	-0.02819	-0.02819	-0.02819	-0.37881	0.35599	0.38745	0.62633
Prm33	-0.02819	-0.02819	0.005143	-0.02819	-0.02819	-0.37881	0.35599	0.37881	0.37881
Prm35	-0.02819	-0.02819	-0.02819	0.01771	-0.003584	-0.37881	0.35599	0.37881	0.37881
Prm37	-0.02819	-0.02819	-0.02819	0.04102	-0.07422	-0.37881	0.35599	0.37881	0.37881
Prm41	-0.50950	-0.36671	-1.54E-15	-1.65E-15	-1.51E-15	3.556E-17	1.422E-16	-0.02150	-0.23298
Prm65	0.50950	0.36671	-0.20000	1.291E-15	1.173E-15	2.246E-16	-4.02E-16	0.02150	0.23298
Prm66	0.56667	0.42388	0.05717	0.05717	0.05717	-0.05717	-0.08175	0.07867	0.29014
Prm67	0.50950	0.36671	1.324E-15	-0.16104	-0.05037	2.206E-16	-3.06E-16	0.02150	0.23298

g008.sas: No 0 margins and n>=20, loglinear model (fixed effects)
3. Log(odds ratio): 1+modality

The GENMOD Procedure

Estimated Covariance Matrix

	Prm33	*Prm35*	*Prm37*	*Prm41*	*Prm65*	*Prm66*	*Prm67*
Prm1	0.03002	0.03002	0.03002	-1.31E-16	7.37E-17	0.004531	1.172E-16
Prm2	-0.02077	-0.02077	-0.02077	2.816E-17	3.775E-17	0.05180	-4.29E-17
Prm3	-0.03002	-0.03002	-0.03002	0.003281	-0.003281	-0.007811	-0.003281
Prm4	-0.03002	-0.03002	-0.03002	0.04486	-0.04486	-0.04939	-0.04486
Prm5	-0.06336	-0.03002	-0.03002	1.299E-16	0.03333	-0.004531	-1.2E-16
Prm6	-0.03002	-0.08835	-0.05241	1.596E-16	-8.33E-17	-0.004531	0.05210
Prm7	-0.03002	-0.03434	-0.06041	1.188E-16	-5.81E-17	-0.004531	0.008832
Prm9	0.02819	0.02819	0.02819	1.508E-15	-1.17E-15	-0.05717	-1.25E-15
Prm11	-0.05930	-0.05930	-0.05930	-1.12E-15	7.989E-16	-0.13223	9.314E-16
Prm13	-0.02819	-0.02819	-0.02819	-0.50950	0.50950	0.56667	0.50950
Prm15	-0.02819	-0.02819	-0.02819	-0.36671	0.36671	0.42388	0.36671
Prm17	0.005143	-0.02819	-0.02819	-1.54E-15	-0.20000	0.05717	1.324E-15
Prm19	-0.02819	0.01771	0.04102	-1.65E-15	1.291E-15	0.05717	-0.16104
Prm21	-0.02819	-0.003584	-0.07422	-1.51E-15	1.173E-15	0.05717	-0.05037
Prm25	-0.37881	-0.37881	-0.37881	3.556E-17	2.246E-16	-0.05717	2.206E-16
Prm27	0.35599	0.35599	0.35599	1.422E-16	-4.02E-16	-0.08175	-3.06E-16
Prm29	0.37881	0.37881	0.37881	-0.02150	0.02150	0.07867	0.02150
Prm31	0.37881	0.37881	0.37881	-0.23298	0.23298	0.29014	0.23298
Prm33	0.91214	0.37881	0.37881	-3.68E-17	-0.53333	0.05717	-2.45E-16
Prm35	0.37881	0.54464	0.44247	3.053E-16	-5.83E-16	0.05717	-0.14813
Prm37	0.37881	0.44247	0.82725	5.551E-17	-3.61E-16	0.05717	-0.13032
Prm41	-3.68E-17	3.053E-16	5.551E-17	0.57986	-0.57986	-0.57986	-0.57986
Prm65	-0.53333	-5.83E-16	-3.61E-16	-0.57986	1.52986	0.57986	0.57986
Prm66	0.05717	0.05717	0.05717	-0.57986	0.57986	0.92783	0.57986
Prm67	-2.45E-16	-0.14813	-0.13032	-0.57986	0.57986	0.57986	0.88310

Analysis Of Maximum Likelihood Parameter Estimates

Parameter		*DF*	*Estimate*	*Standard Error*	*Wald 95% Confidence Limits*		*Wald Chi-Square*	*Pr > ChiSq*
Intercept		1	3.3514	0.1861	2.9866	3.7162	324.27	<.0001
id	Bettus 2010	1	-0.6133	0.3107	-1.2222	-0.0045	3.90	0.0483
id	Boerwinkle 2017	1	0.0094	0.2630	-0.5060	0.5249	0.00	0.9714
id	Boerwinkle 2019	1	-0.3464	0.2895	-0.9138	0.2210	1.43	0.2315
id	Chen 2017	1	0.0498	0.2607	-0.4612	0.5608	0.04	0.8486
id	Khoo 2019	1	-0.6068	0.3112	-1.2166	0.0031	3.80	0.0512
id	Lee 2014	1	-0.2861	0.2832	-0.8411	0.2689	1.02	0.3123
id	Reyes 2016	0	0.0000	0.0000	0.0000	0.0000	.	.
rsfMRI	1	1	-2.4525	0.6155	-3.6588	-1.2462	15.88	<.0001

g008.sas: No 0 margins and n>=20, loglinear model (fixed effects)
3. Log(odds ratio): 1+modality

The GENMOD Procedure

Analysis Of Maximum Likelihood Parameter Estimates

Parameter			DF	Estimate	Standard Error	Wald 95% Confidence Limits		Wald Chi-Square	Pr > ChiSq
rsfMRI	2		0	0.0000	0.0000	0.0000	0.0000	.	.
id*rsfMRI	Bettus 2010	1	1	1.5928	0.7203	0.1811	3.0045	4.89	0.0270
id*rsfMRI	Bettus 2010	2	0	0.0000	0.0000	0.0000	0.0000	.	.
id*rsfMRI	Boerwinkle 2017	1	1	-2.5865	1.2167	-4.9713	-0.2017	4.52	0.0335
id*rsfMRI	Boerwinkle 2017	2	0	0.0000	0.0000	0.0000	0.0000	.	.
id*rsfMRI	Boerwinkle 2019	1	1	0.4818	0.8715	-1.2264	2.1900	0.31	0.5804
id*rsfMRI	Boerwinkle 2019	2	0	0.0000	0.0000	0.0000	0.0000	.	.
id*rsfMRI	Chen 2017	1	1	0.8430	0.7608	-0.6481	2.3341	1.23	0.2678
id*rsfMRI	Chen 2017	2	0	0.0000	0.0000	0.0000	0.0000	.	.
id*rsfMRI	Khoo 2019	1	1	1.7149	0.7466	0.2515	3.1783	5.28	0.0216
id*rsfMRI	Khoo 2019	2	0	0.0000	0.0000	0.0000	0.0000	.	.
id*rsfMRI	Lee 2014	1	1	0.9042	0.7804	-0.6253	2.4337	1.34	0.2466
id*rsfMRI	Lee 2014	2	0	0.0000	0.0000	0.0000	0.0000	.	.
id*rsfMRI	Reyes 2016	1	0	0.0000	0.0000	0.0000	0.0000	.	.
id*rsfMRI	Reyes 2016	2	0	0.0000	0.0000	0.0000	0.0000	.	.
compar	1		1	-2.4525	0.6155	-3.6588	-1.2462	15.88	<.0001
compar	2		0	0.0000	0.0000	0.0000	0.0000	.	.
id*compar	Bettus 2010	1	1	2.0699	0.6960	0.7056	3.4341	8.84	0.0029
id*compar	Bettus 2010	2	0	0.0000	0.0000	0.0000	0.0000	.	.
id*compar	Boerwinkle 2017	1	1	0.7377	0.7737	-0.7788	2.2542	0.91	0.3404
id*compar	Boerwinkle 2017	2	0	0.0000	0.0000	0.0000	0.0000	.	.
id*compar	Boerwinkle 2019	1	1	1.0188	0.7914	-0.5323	2.5699	1.66	0.1980
id*compar	Boerwinkle 2019	2	0	0.0000	0.0000	0.0000	0.0000	.	.
id*compar	Chen 2017	1	1	-0.2556	0.9551	-2.1275	1.6163	0.07	0.7890
id*compar	Chen 2017	2	0	0.0000	0.0000	0.0000	0.0000	.	.
id*compar	Khoo 2019	1	1	1.8410	0.7380	0.3945	3.2874	6.22	0.0126
id*compar	Khoo 2019	2	0	0.0000	0.0000	0.0000	0.0000	.	.
id*compar	Lee 2014	1	1	-0.1690	0.9095	-1.9517	1.6136	0.03	0.8526
id*compar	Lee 2014	2	0	0.0000	0.0000	0.0000	0.0000	.	.
id*compar	Reyes 2016	1	0	0.0000	0.0000	0.0000	0.0000	.	.
id*compar	Reyes 2016	2	0	0.0000	0.0000	0.0000	0.0000	.	.
rsfMRI*compar	1	1	1	3.9880	0.7615	2.4955	5.4805	27.43	<.0001
rsfMRI*compar	1	2	0	0.0000	0.0000	0.0000	0.0000	.	.
rsfMRI*compar	2	1	0	0.0000	0.0000	0.0000	0.0000	.	.
rsfMRI*compar	2	2	0	0.0000	0.0000	0.0000	0.0000	.	.
modality	0		0	0.0000	0.0000	0.0000	0.0000	.	.

g008.sas: No 0 margins and n>=20, loglinear model (fixed effects)
3. Log(odds ratio): 1+modality

The GENMOD Procedure

Analysis Of Maximum Likelihood Parameter Estimates

Parameter				DF	Estimate	Standard Error	Wald 95% Confidence Limits		Wald Chi-Square	Pr > ChiSq
modality	1			0	0.0000	0.0000	0.0000	0.0000	.	.
modality	3			0	0.0000	0.0000	0.0000	0.0000	.	.
modality	4			0	0.0000	0.0000	0.0000	0.0000	.	.
rsfMRI*modality	1	0		0	0.0000	0.0000	0.0000	0.0000	.	.
rsfMRI*modality	1	1		0	0.0000	0.0000	0.0000	0.0000	.	.
rsfMRI*modality	1	3		0	0.0000	0.0000	0.0000	0.0000	.	.
rsfMRI*modality	1	4		0	0.0000	0.0000	0.0000	0.0000	.	.
rsfMRI*modality	2	0		0	0.0000	0.0000	0.0000	0.0000	.	.
rsfMRI*modality	2	1		0	0.0000	0.0000	0.0000	0.0000	.	.
rsfMRI*modality	2	3		0	0.0000	0.0000	0.0000	0.0000	.	.
rsfMRI*modality	2	4		0	0.0000	0.0000	0.0000	0.0000	.	.
compar*modality	1	0		0	0.0000	0.0000	0.0000	0.0000	.	.
compar*modality	1	1		0	0.0000	0.0000	0.0000	0.0000	.	.
compar*modality	1	3		0	0.0000	0.0000	0.0000	0.0000	.	.
compar*modality	1	4		0	0.0000	0.0000	0.0000	0.0000	.	.
compar*modality	2	0		0	0.0000	0.0000	0.0000	0.0000	.	.
compar*modality	2	1		0	0.0000	0.0000	0.0000	0.0000	.	.
compar*modality	2	3		0	0.0000	0.0000	0.0000	0.0000	.	.
compar*modality	2	4		0	0.0000	0.0000	0.0000	0.0000	.	.
rsfMRI*compar*modali	1	1	0	1	-1.6854	1.2369	-4.1096	0.7388	1.86	0.1730
rsfMRI*compar*modali	1	1	1	1	-3.0452	0.9632	-4.9331	-1.1573	9.99	0.0016
rsfMRI*compar*modali	1	1	3	1	-2.5180	0.9397	-4.3598	-0.6762	7.18	0.0074
rsfMRI*compar*modali	1	1	4	0	0.0000	0.0000	0.0000	0.0000	.	.
rsfMRI*compar*modali	1	2	0	0	0.0000	0.0000	0.0000	0.0000	.	.
rsfMRI*compar*modali	1	2	1	0	0.0000	0.0000	0.0000	0.0000	.	.
rsfMRI*compar*modali	1	2	3	0	0.0000	0.0000	0.0000	0.0000	.	.
rsfMRI*compar*modali	1	2	4	0	0.0000	0.0000	0.0000	0.0000	.	.
rsfMRI*compar*modali	2	1	0	0	0.0000	0.0000	0.0000	0.0000	.	.
rsfMRI*compar*modali	2	1	1	0	0.0000	0.0000	0.0000	0.0000	.	.
rsfMRI*compar*modali	2	1	3	0	0.0000	0.0000	0.0000	0.0000	.	.
rsfMRI*compar*modali	2	1	4	0	0.0000	0.0000	0.0000	0.0000	.	.
rsfMRI*compar*modali	2	2	0	0	0.0000	0.0000	0.0000	0.0000	.	.
rsfMRI*compar*modali	2	2	1	0	0.0000	0.0000	0.0000	0.0000	.	.
rsfMRI*compar*modali	2	2	3	0	0.0000	0.0000	0.0000	0.0000	.	.
rsfMRI*compar*modali	2	2	4	0	0.0000	0.0000	0.0000	0.0000	.	.
Scale				0	1.0000	0.0000	1.0000	1.0000		

g008.sas: No 0 margins and n>=20, loglinear model (fixed effects)
3. Log(odds ratio): 1+modality

The GENMOD Procedure

Note: The scale parameter was held fixed.