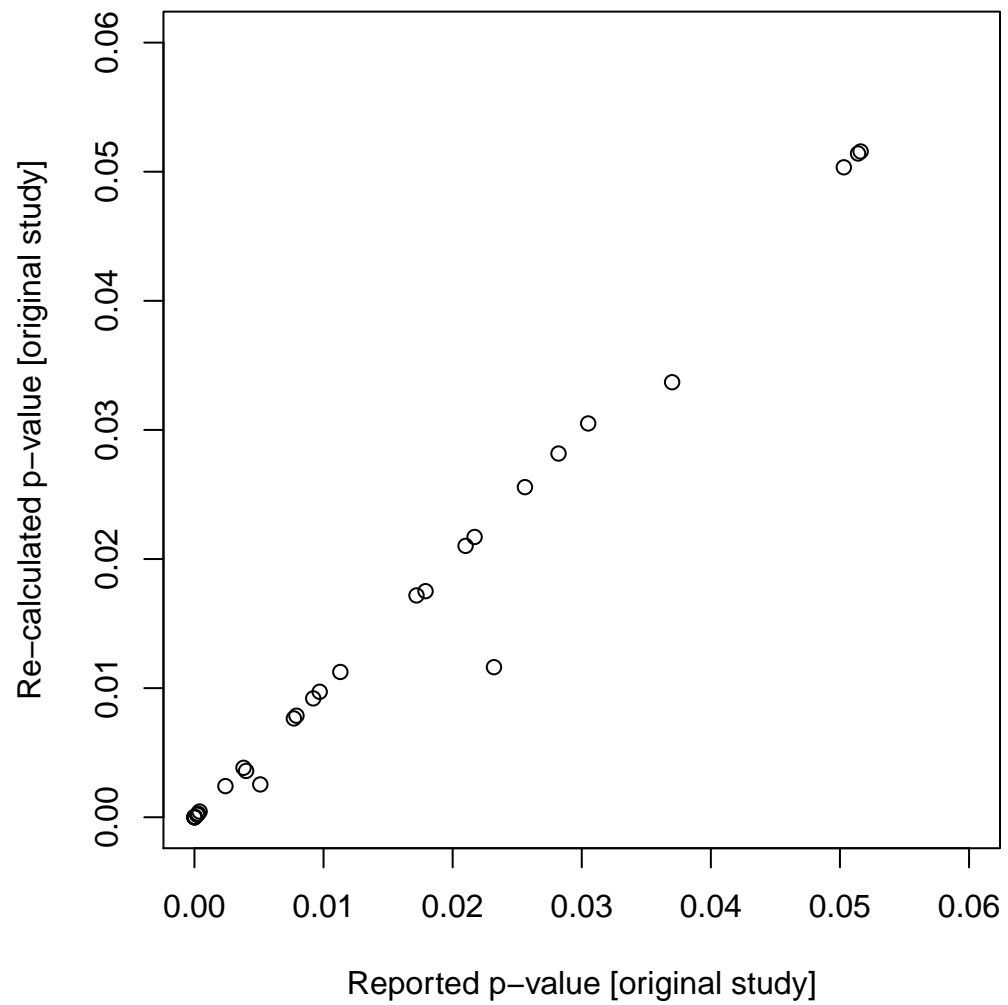
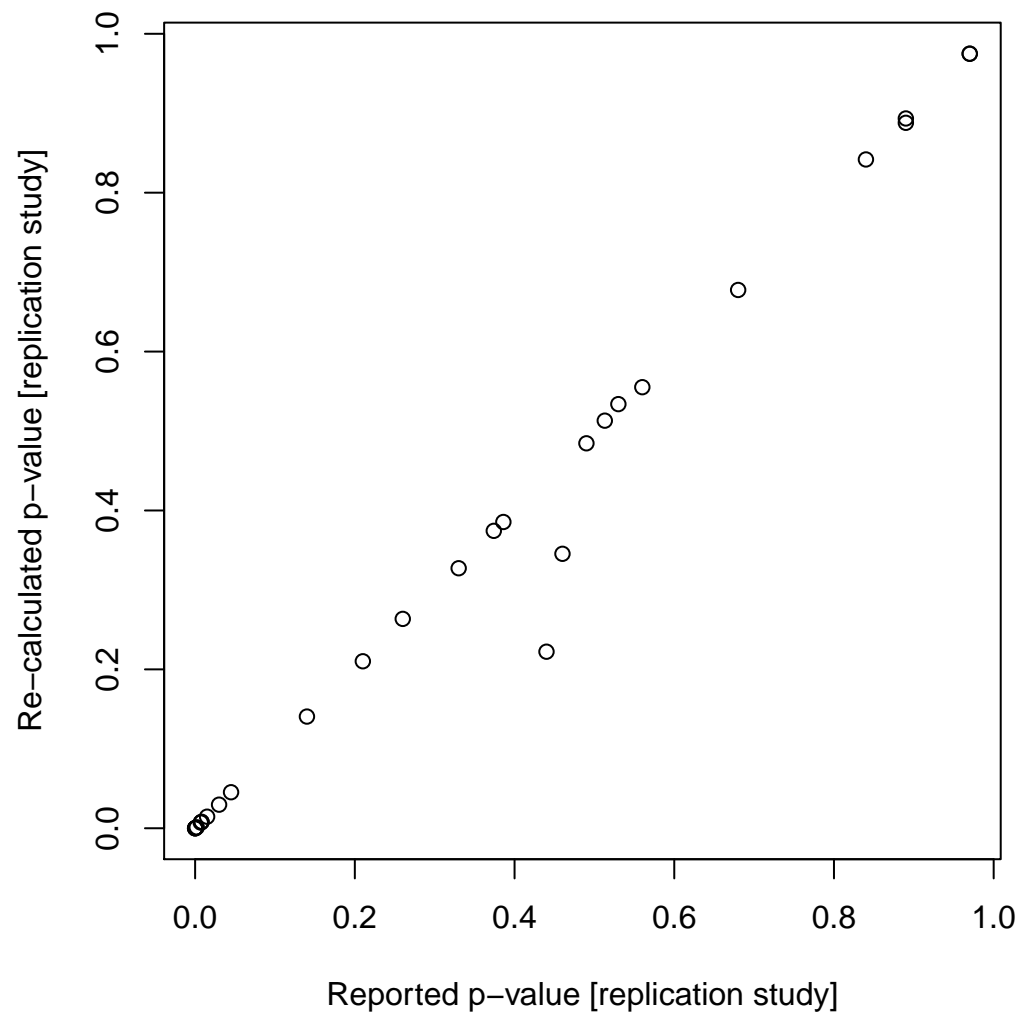


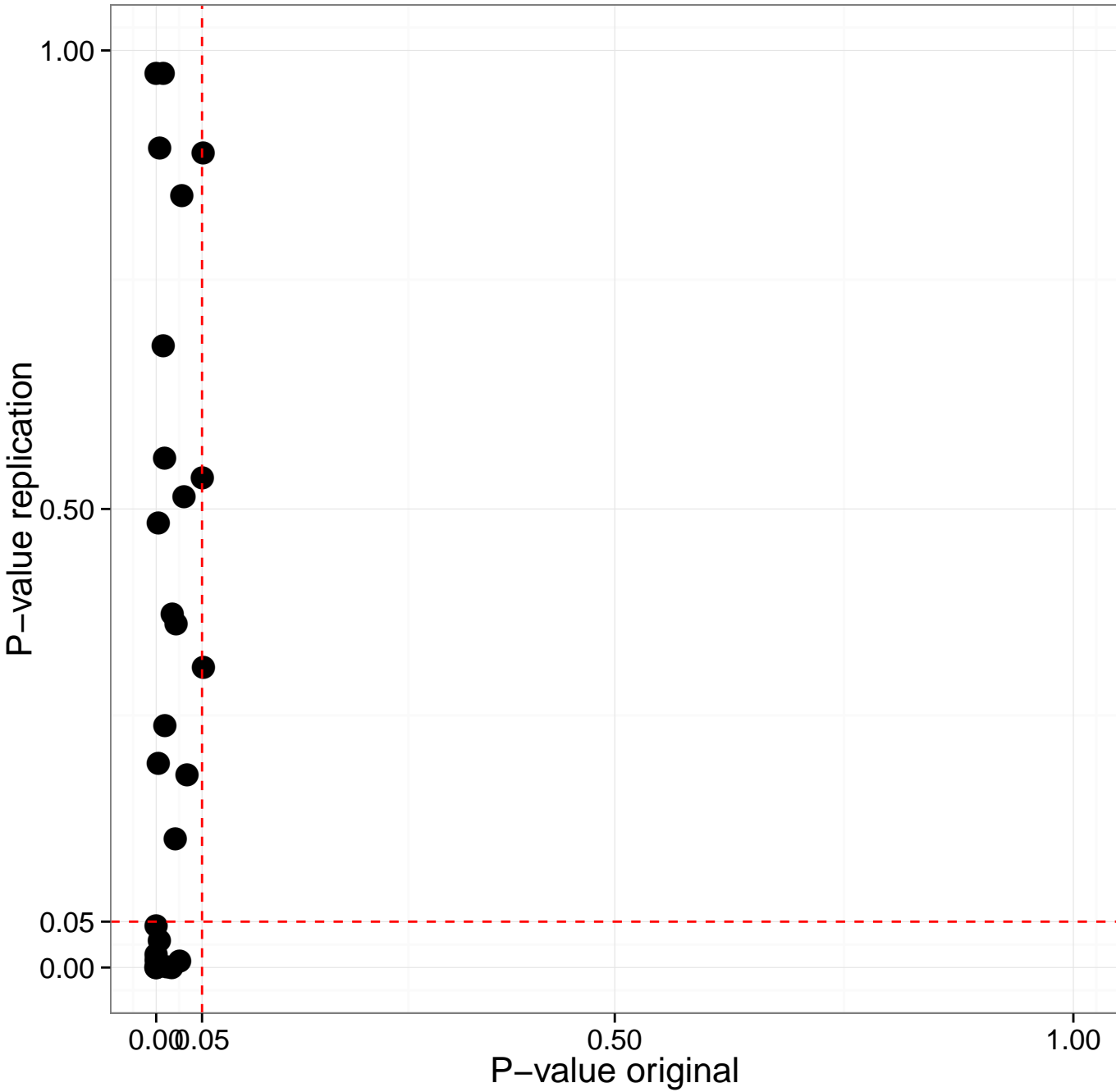
Recalculating p-values



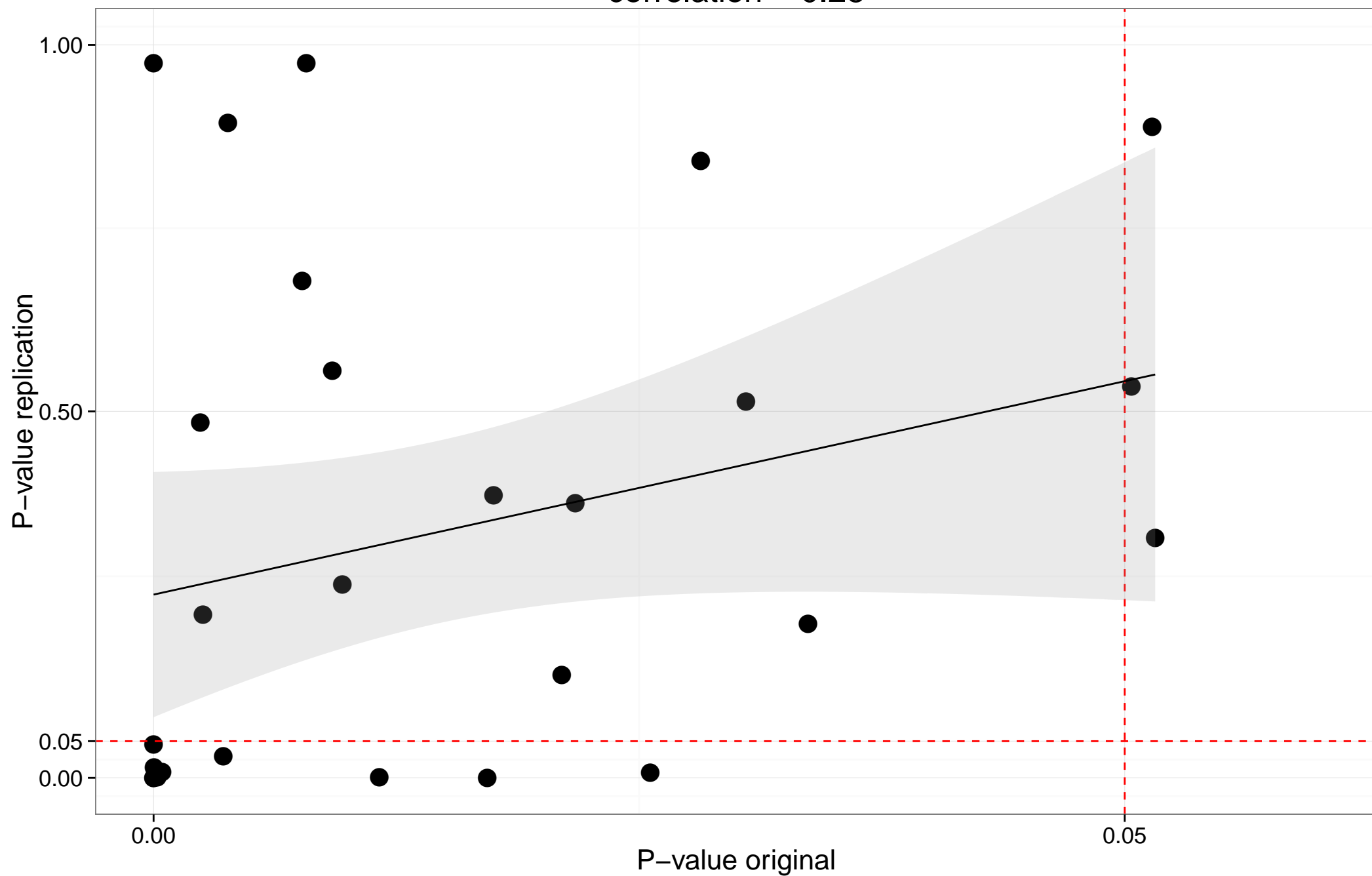
Recalculating p-values



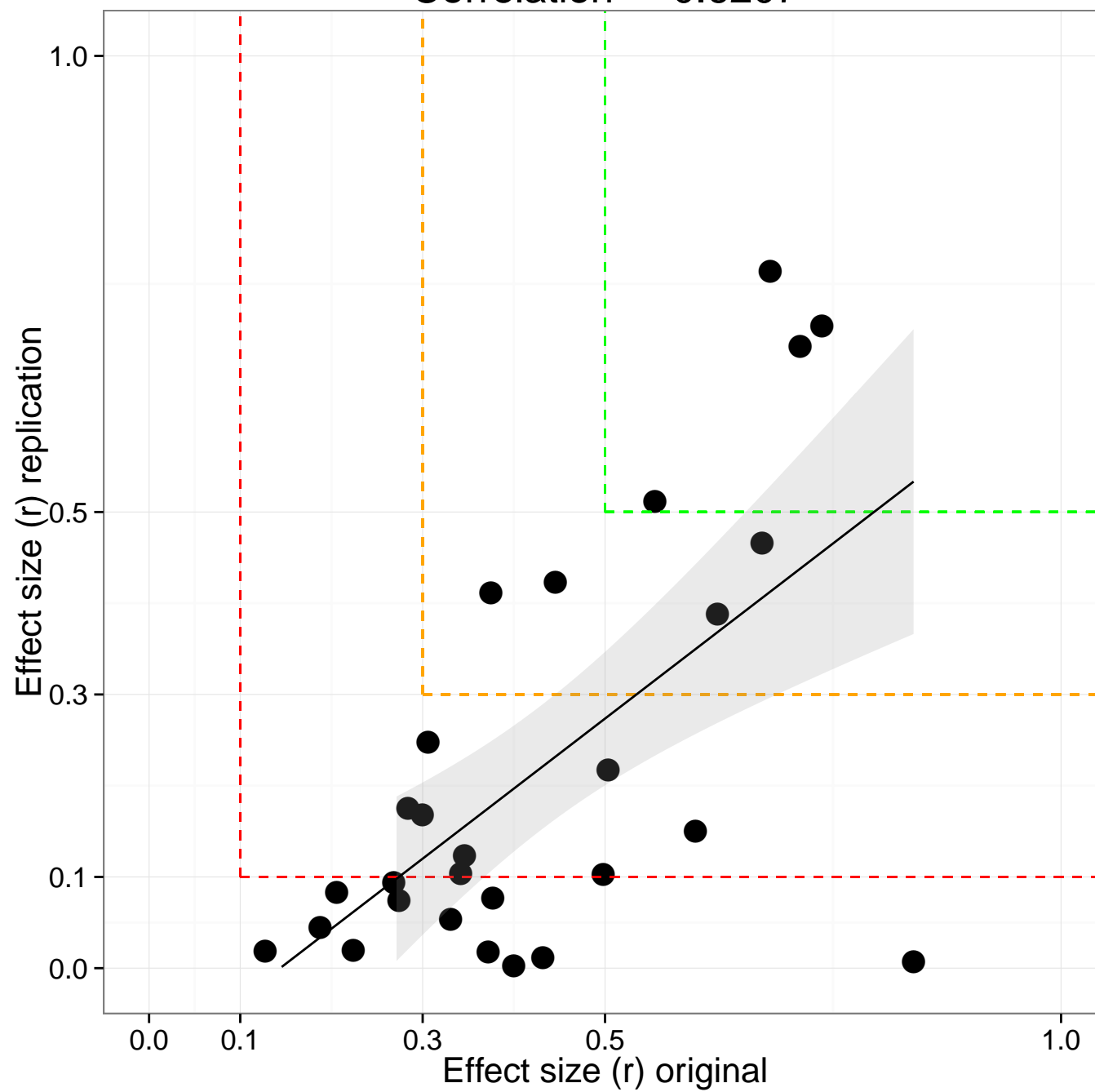
Original vs. Replication p-value
correlation = 0.28



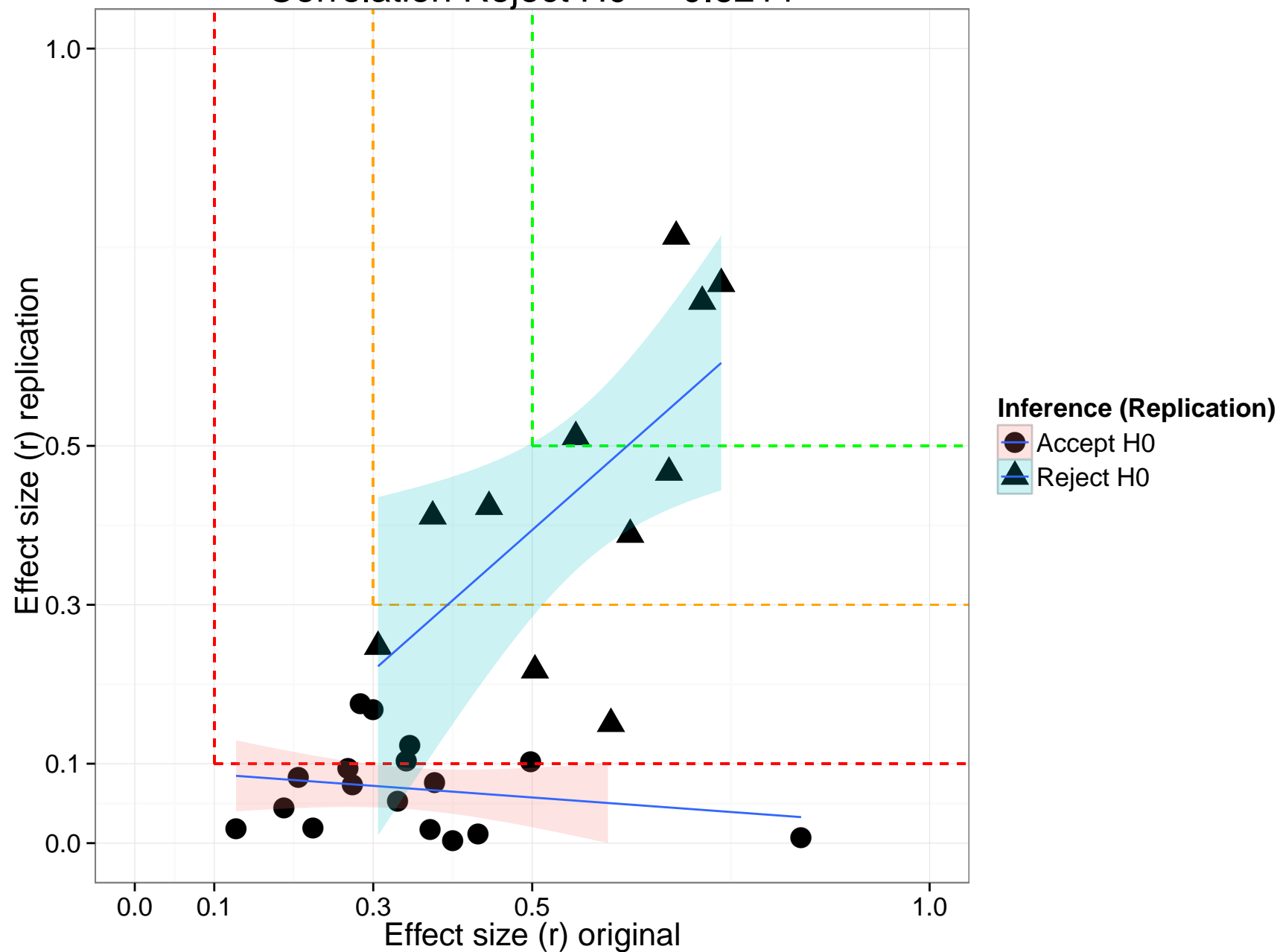
Original vs. Replication p-value
correlation = 0.28



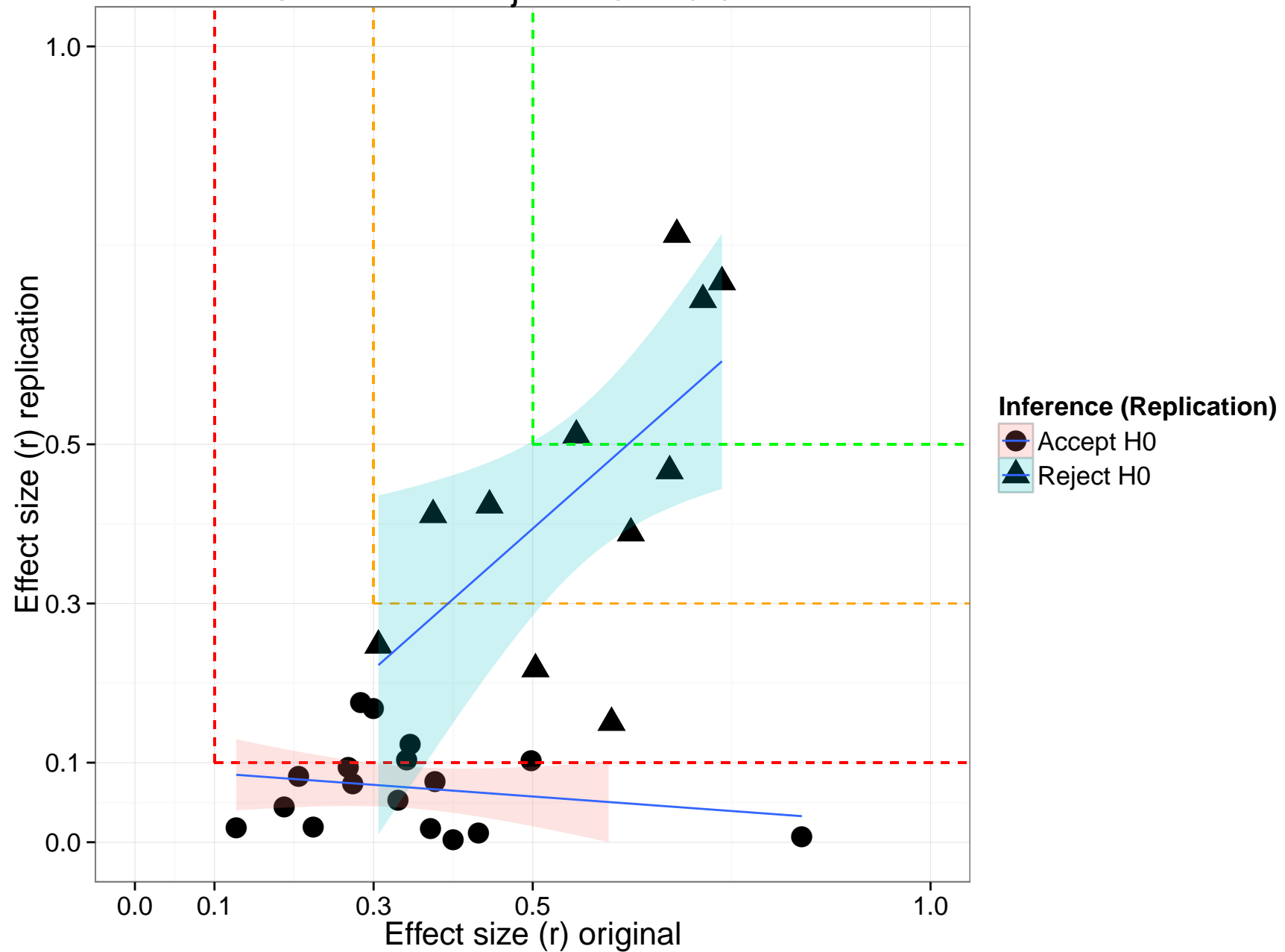
Original vs. Replication Effect Size (r)
Correlation = 0.6207



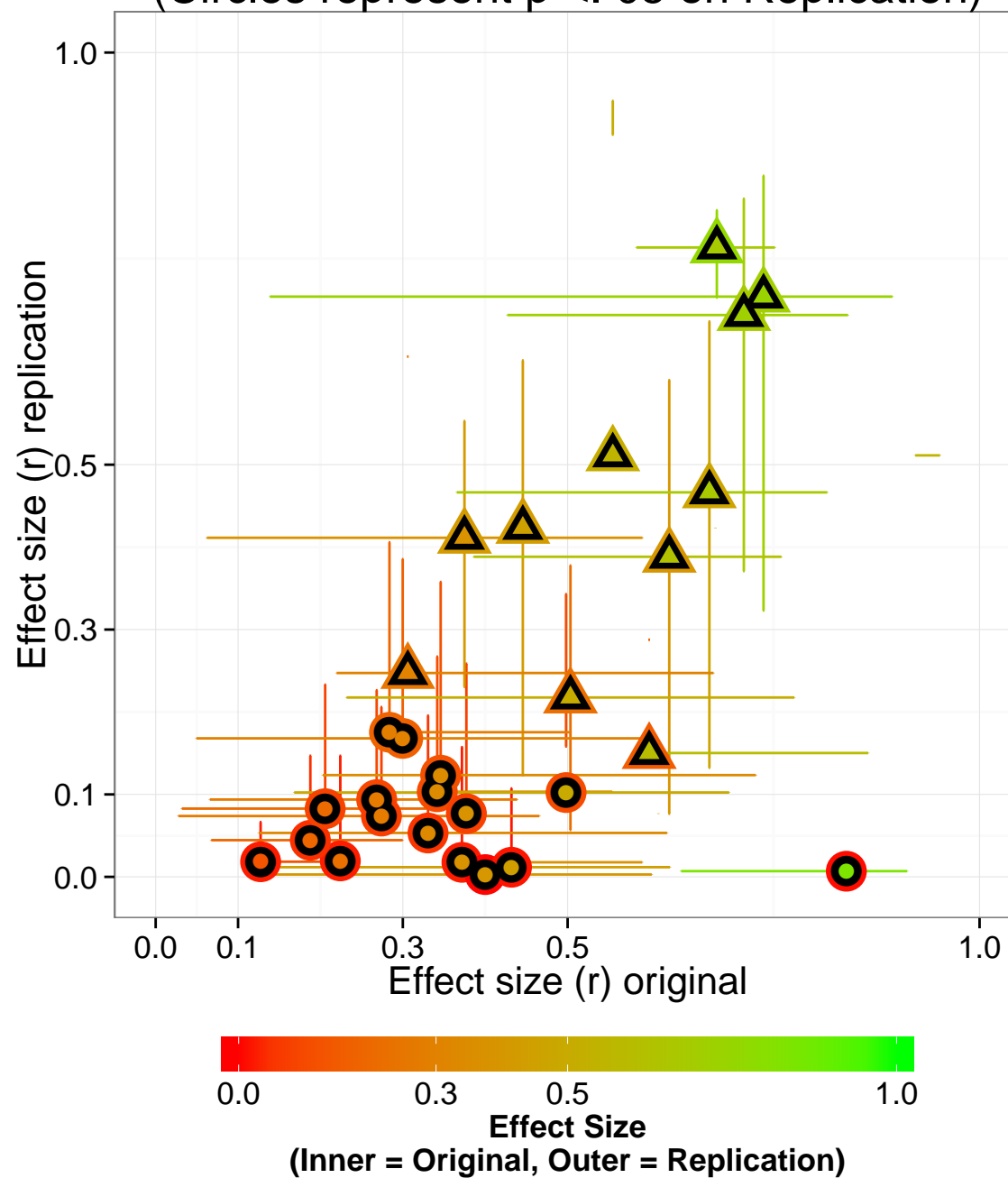
Original vs. Replication Effect Size (r)
Correlation Accept H0 = -0.2131
Correlation Reject H0 = 0.6211



Original vs. Replication Effect Size (r)
Correlation Accept H0 = -0.2131
Correlation Reject H0 = 0.6211



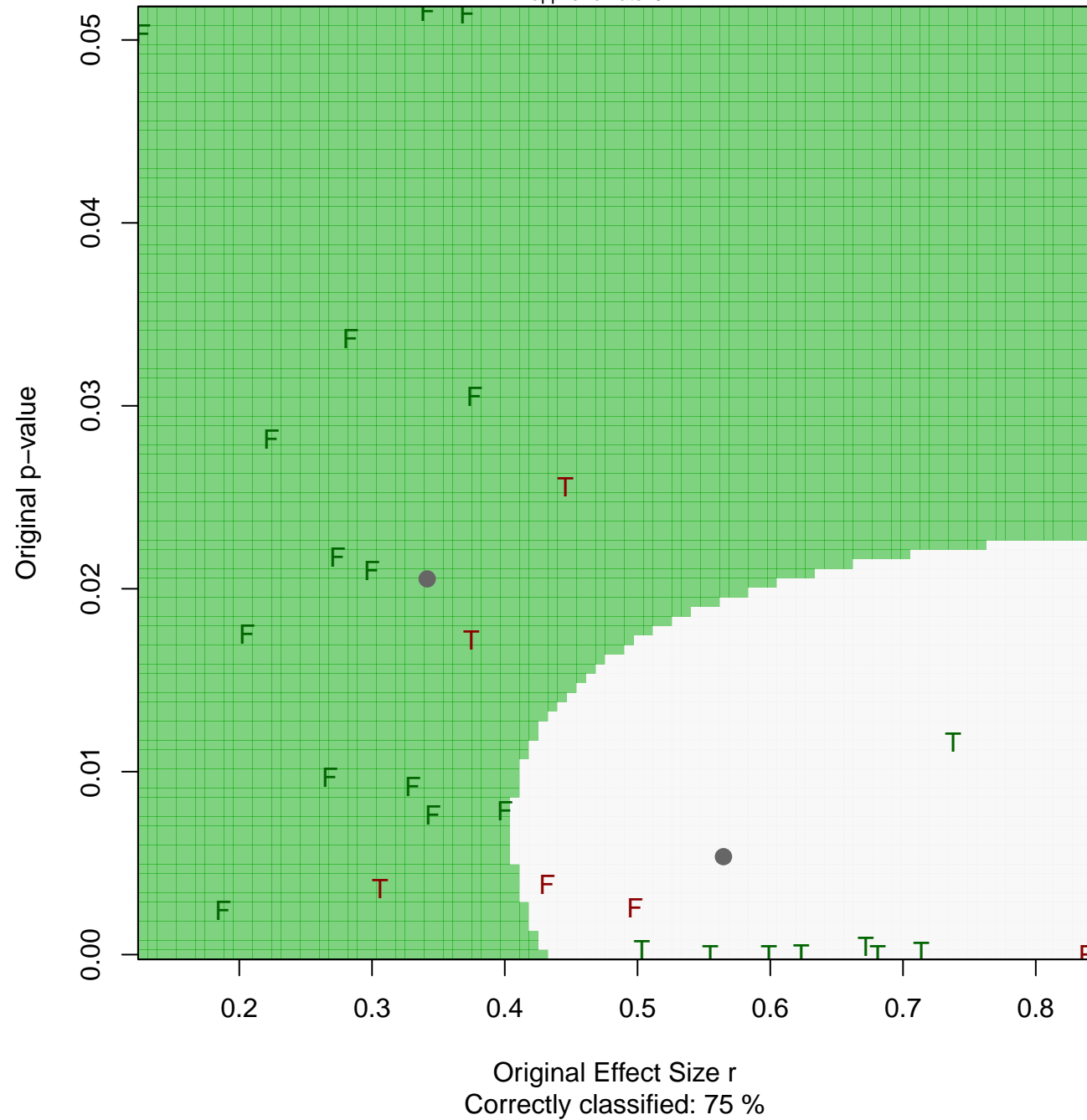
Original vs. Replication Effect Size (r) with 95% CI
(Circles represent $p < .05$ on Replication)



	FALSE	TRUE
FALSE	13	4
TRUE	3	8

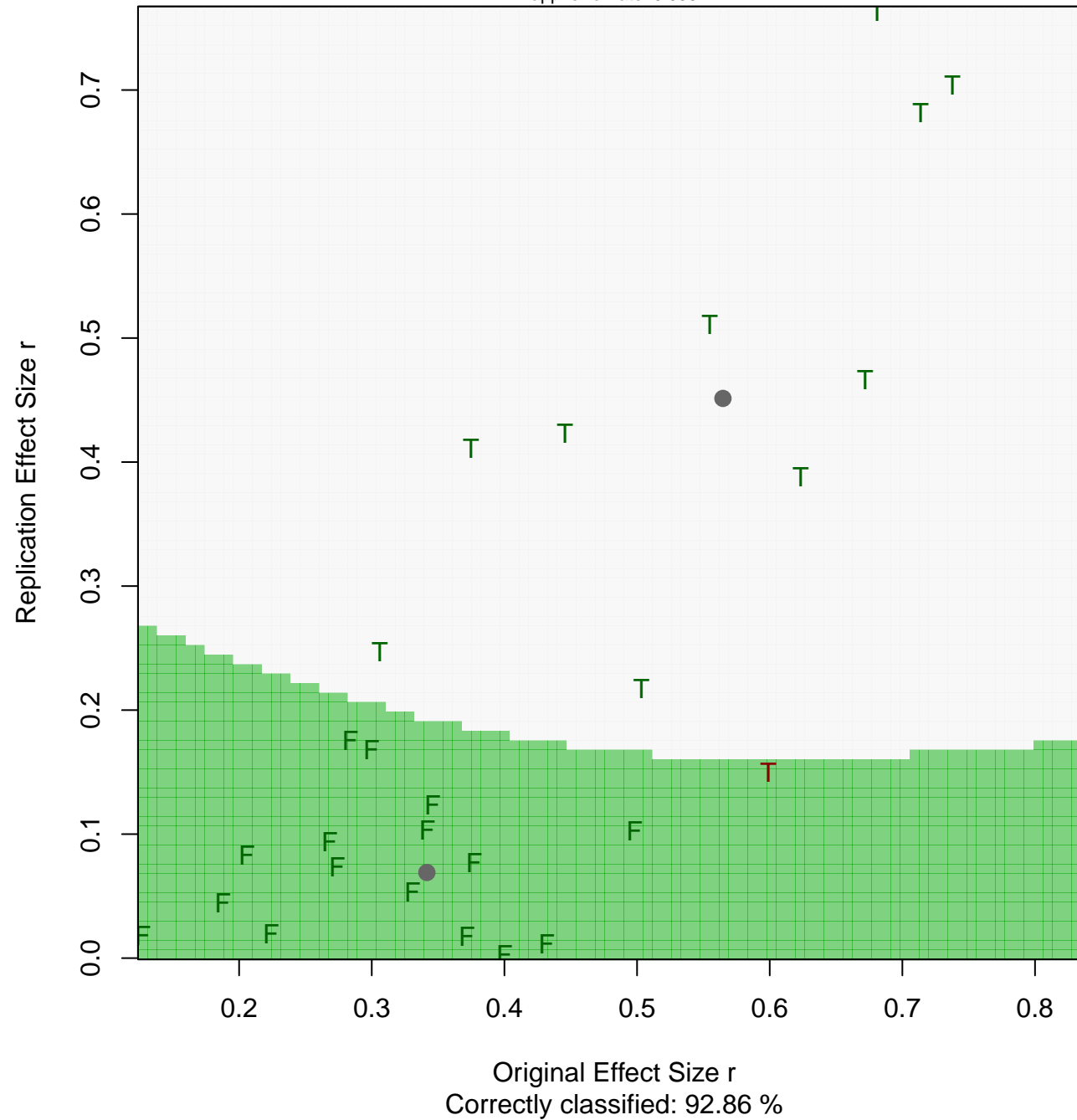
Quadratic Discriminant Analysis: Reject H0 on Replication

app. error rate: 0.214



Quadratic Discriminant Analysis: Reject H0 on Replication

app. error rate: 0.036



Mixed-Effects Model (k = 56; tau^2 estimator: REML)

	logLik	deviance	AIC	BIC	AICc
	18.3144	-36.6287	-26.6287	-16.8725	-25.3244

tau^2 (estimated amount of residual heterogeneity): 0.0202 (SE = 0.0061)
tau (square root of estimated tau^2 value): 0.1421
I^2 (residual heterogeneity / unaccounted variability): 71.18%
H^2 (unaccounted variability / sampling variability): 3.47
R^2 (amount of heterogeneity accounted for): 56.56%

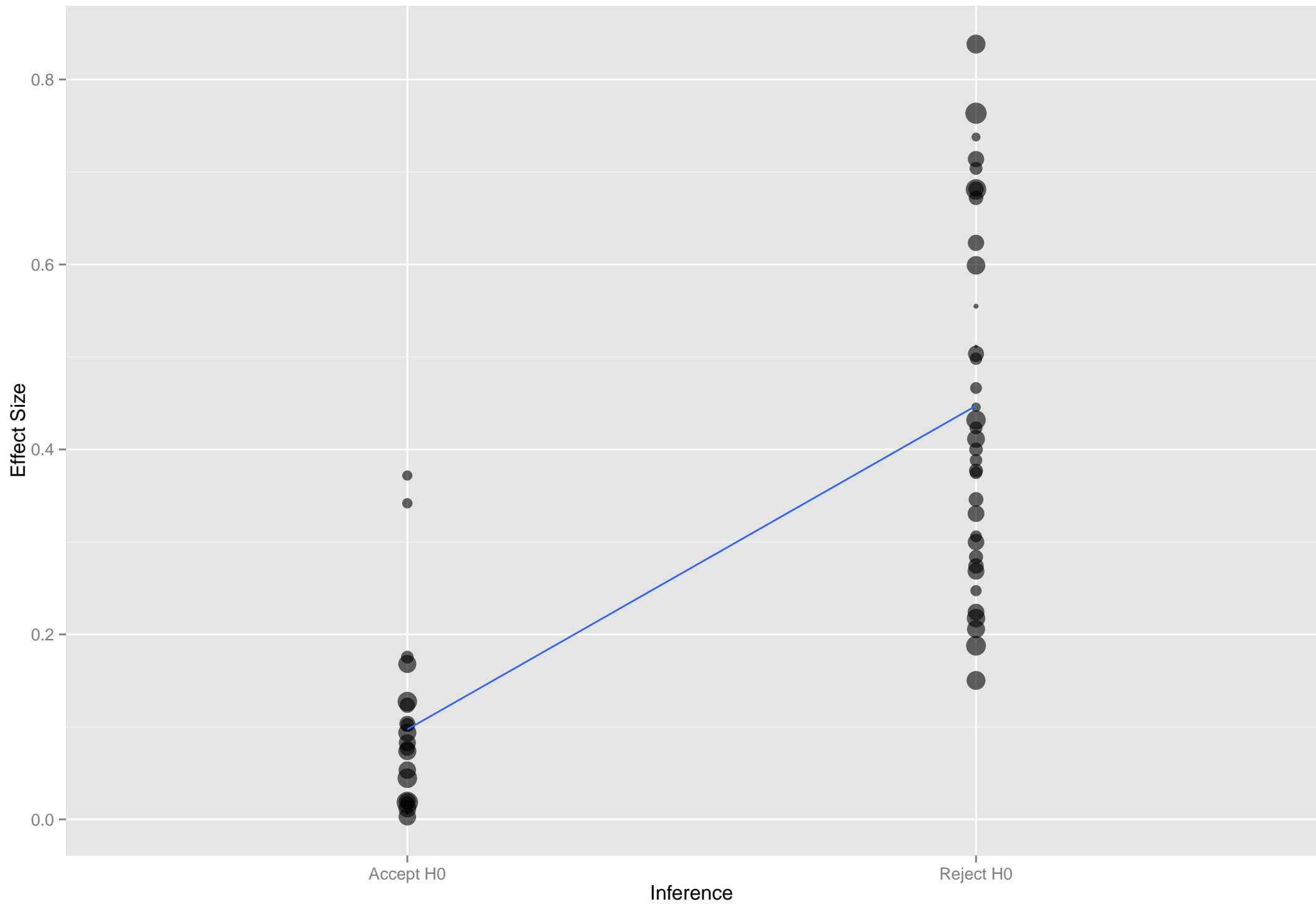
Test for Residual Heterogeneity:
QE(df = 52) = 233.3616, p-val < .0001

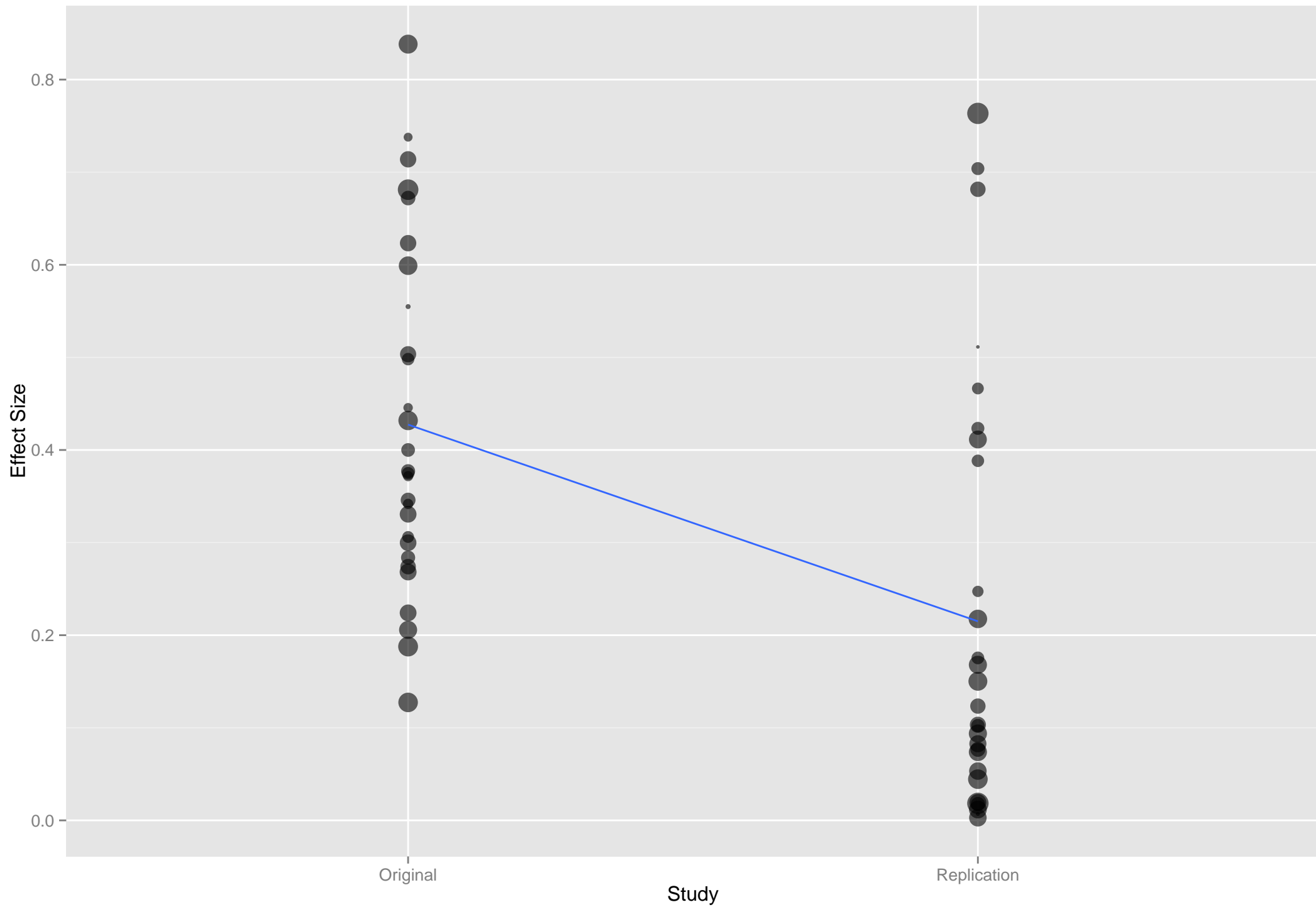
Test of Moderators (coefficient(s) 2,3,4):
QM(df = 3) = 54.3389, p-val < .0001

Model Results:

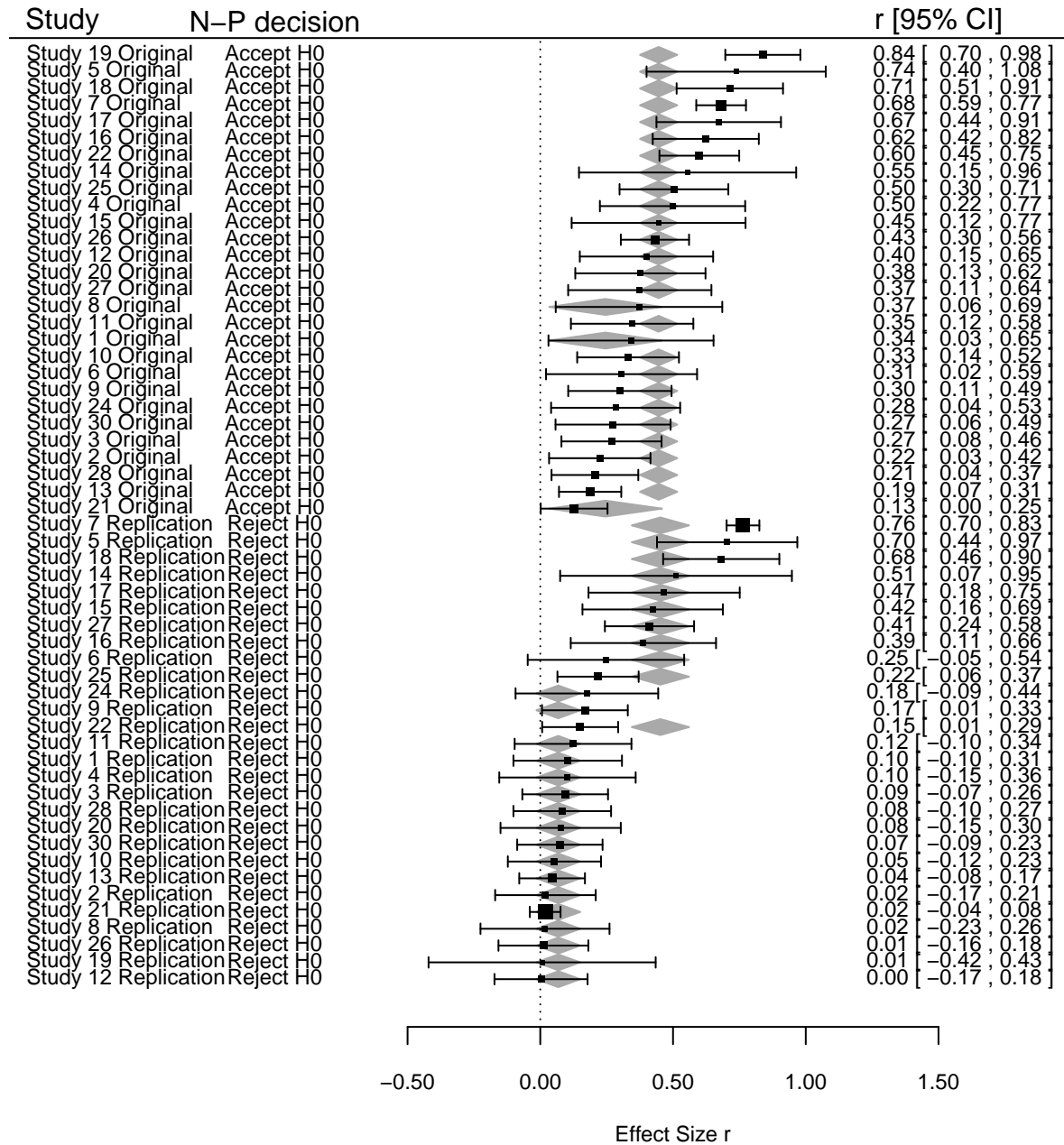
	estimate	se	zval	pval	ci.lb	ci.ub	
intrcpt	0.2458	0.1085	2.2660	0.0235	0.0332	0.4583	*
modReplication	-0.1778	0.1163	-1.5279	0.1265	-0.4058	0.0503	
mod1Reject H0	0.2001	0.1142	1.7515	0.0799	-0.0238	0.4239	.
modReplication:mod1Reject H0	0.1844	0.1336	1.3803	0.1675	-0.0774	0.4462	

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





Forest plot RE model: ES (r) = Study * N-P decision



Funnel plot RE model:
ES (r) = Study * N-P decision

