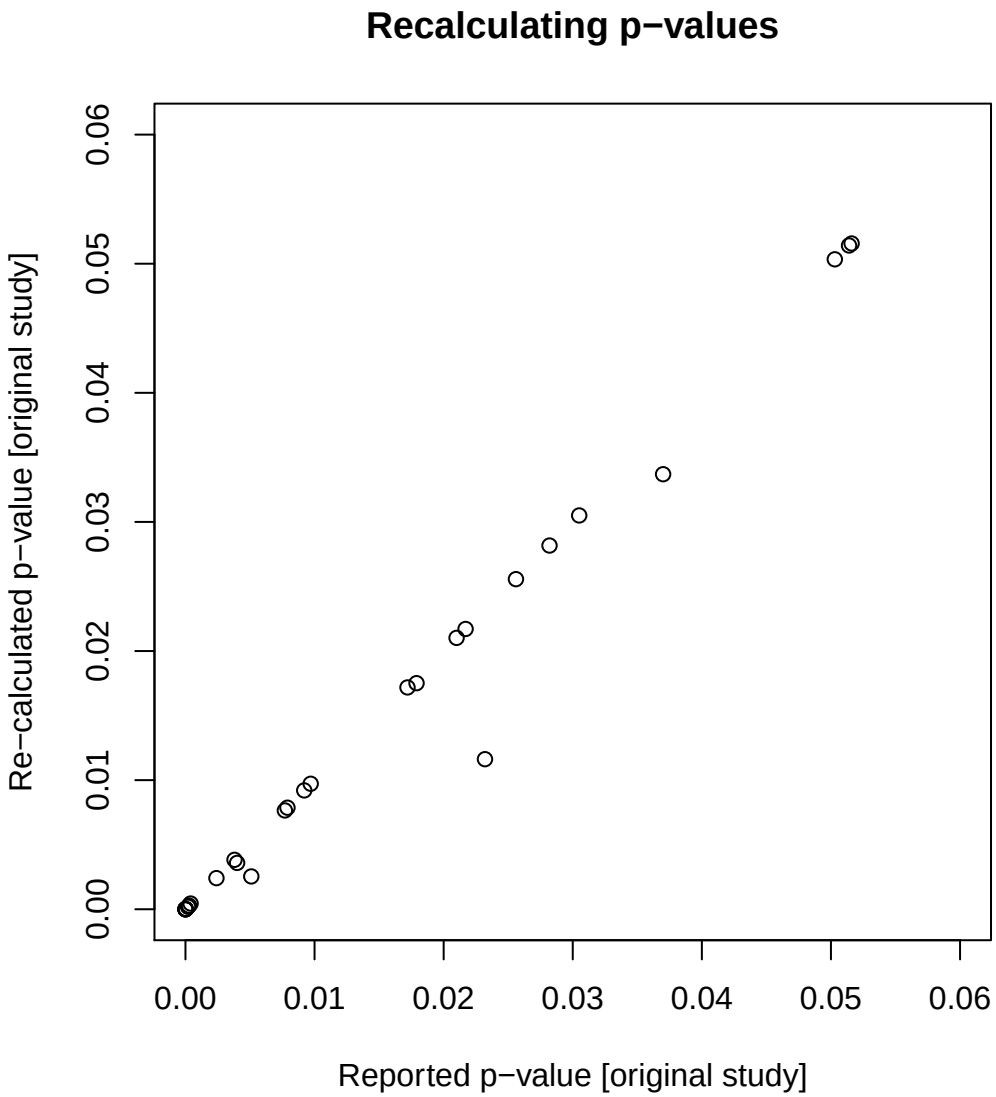
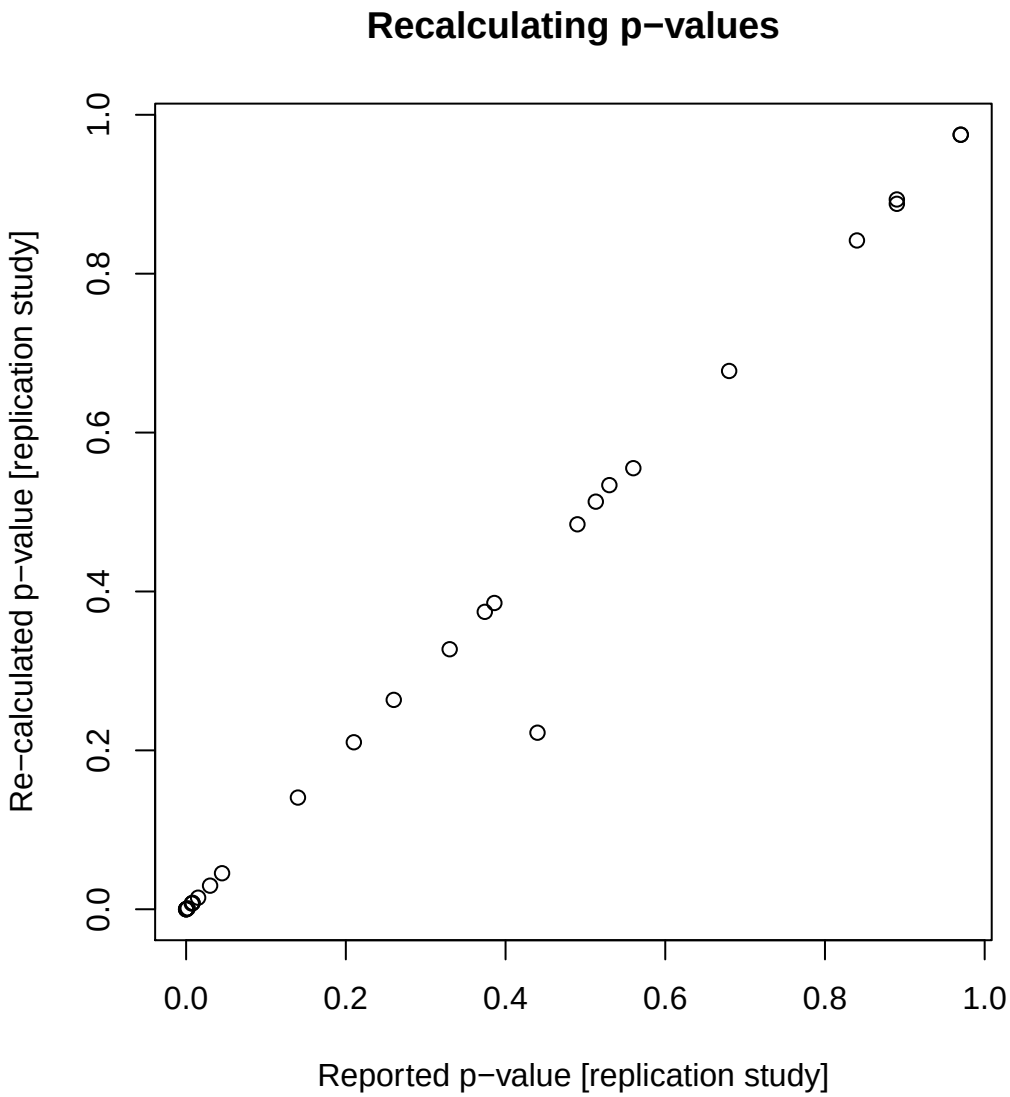
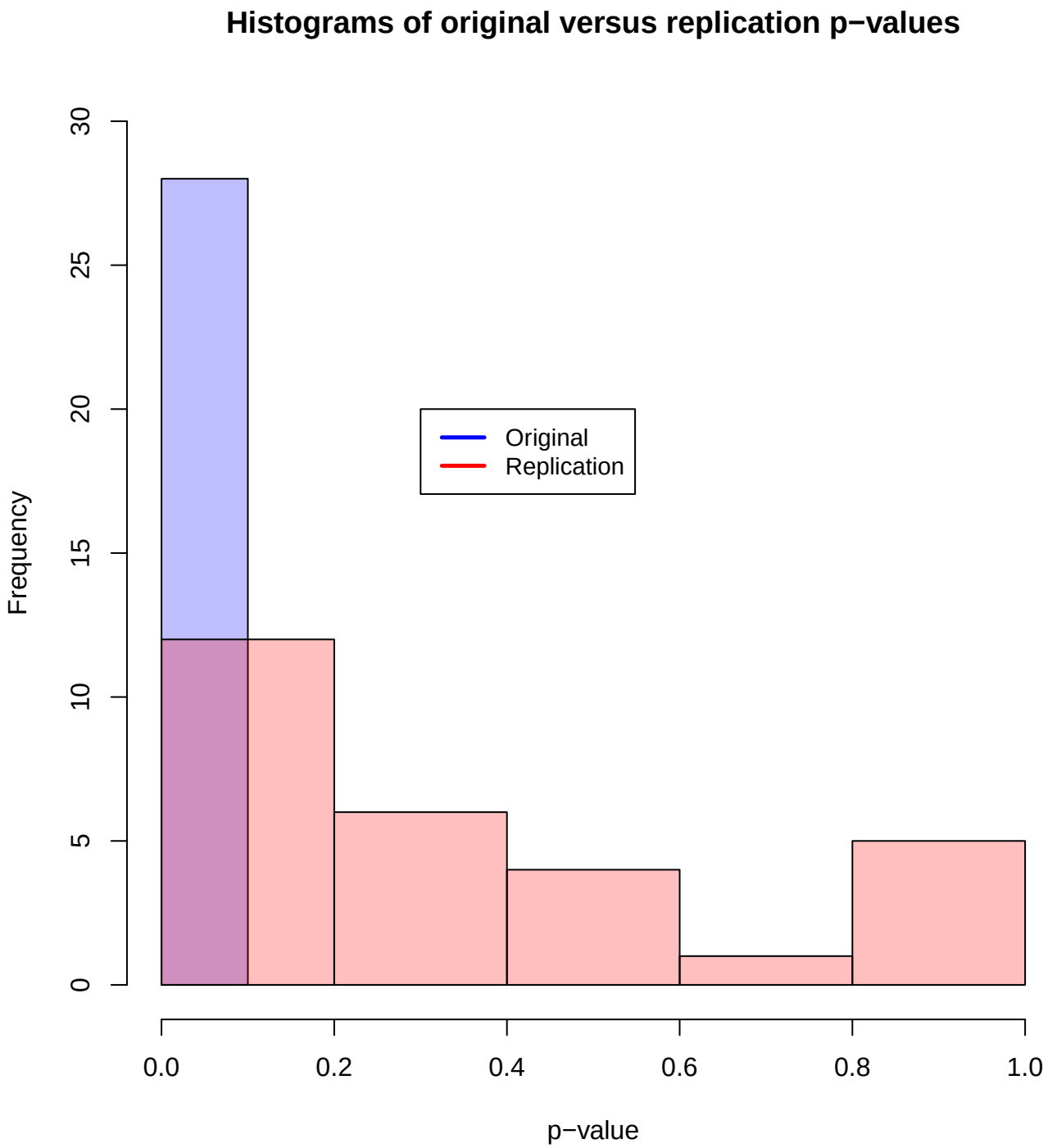
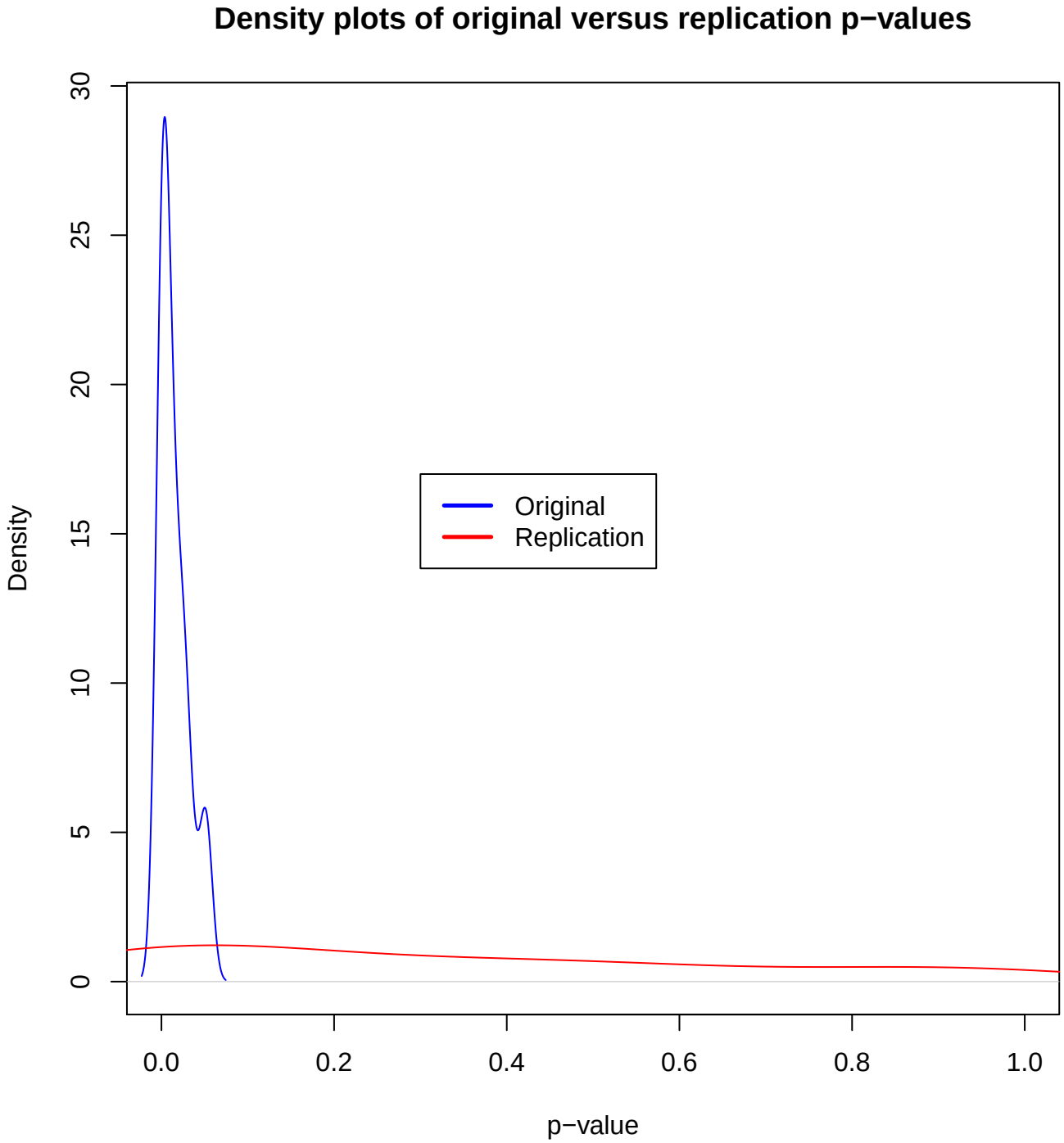
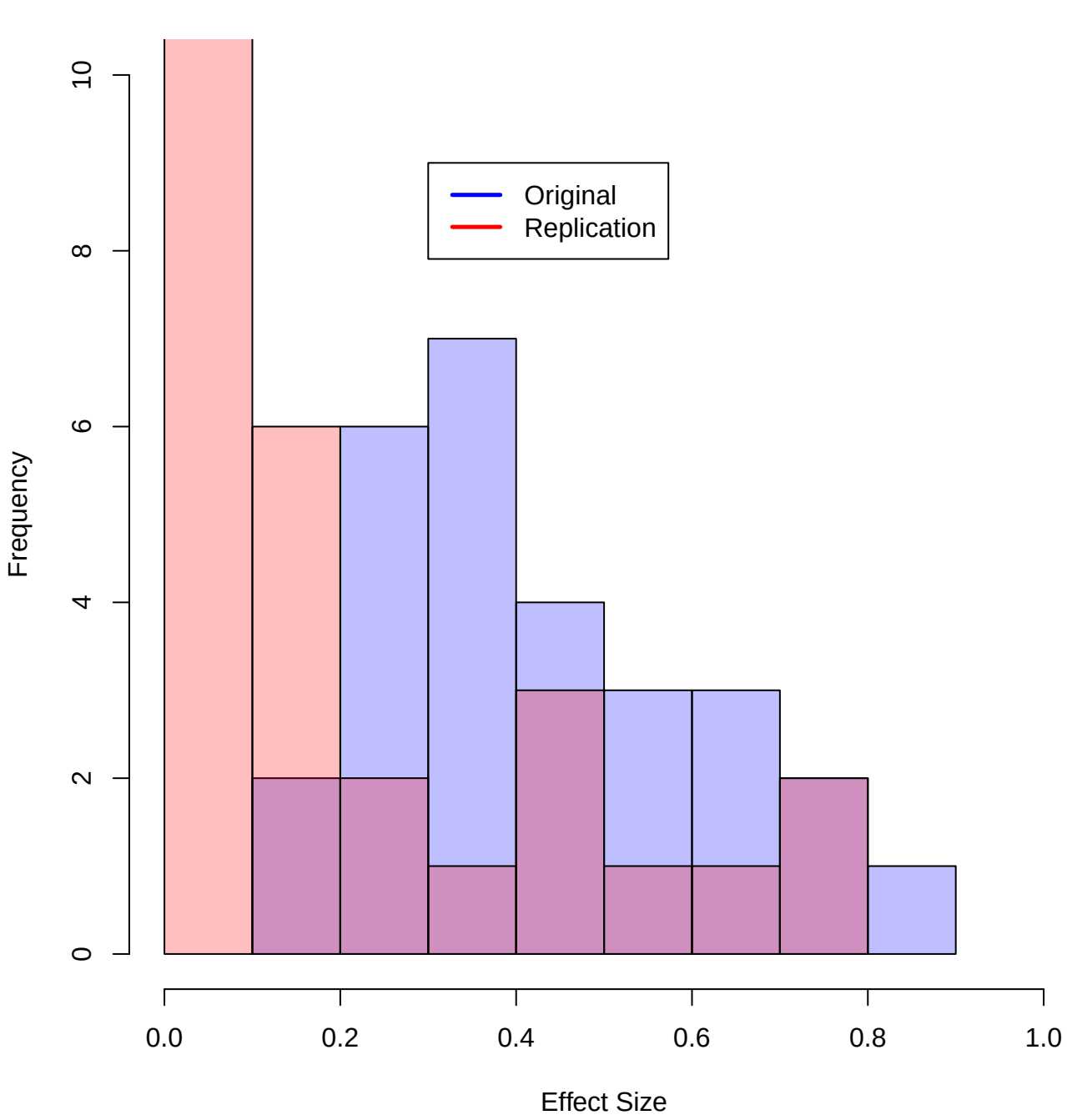
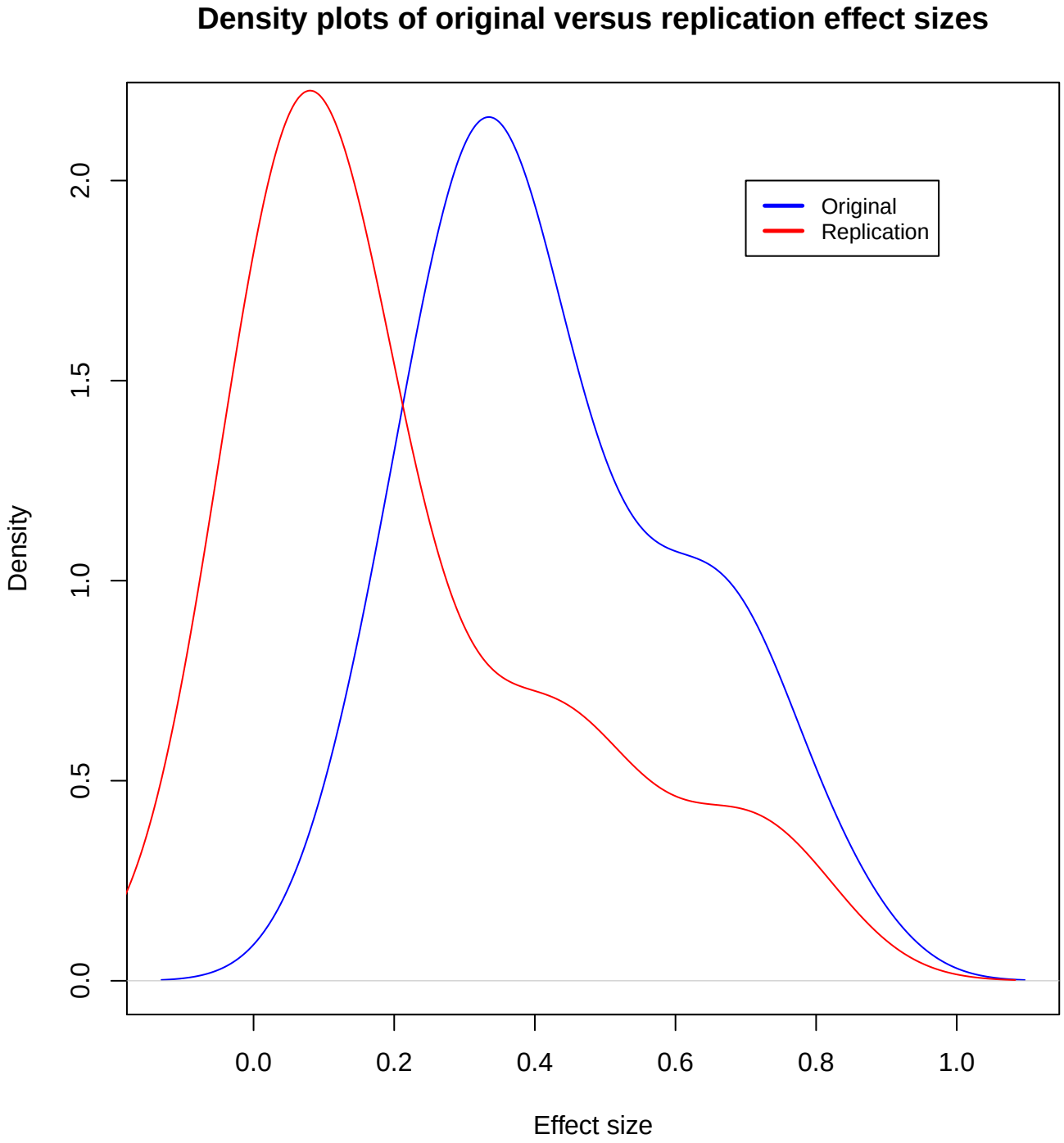

Recalculating p−values
Re−calculated p−value [original study]
Reported p−value [original study]
0.00
0.01
0.02
0.03
0.04
0.05
0.06

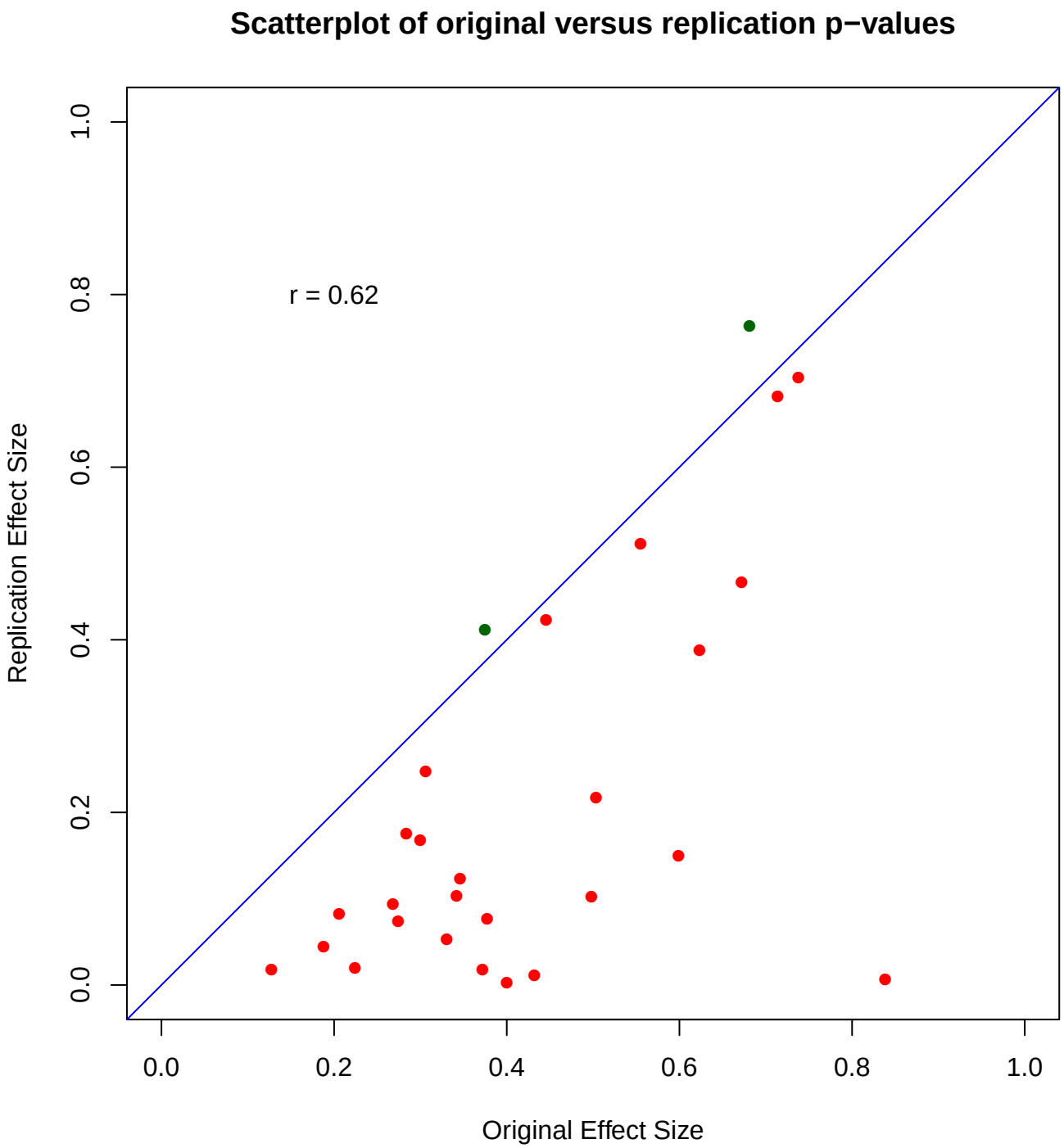

Recalculating p−values
Re−calculated p−value [replication study]
Reported p−value [replication study]
0.0
0.2
0.4
0.6
0.8
1.0

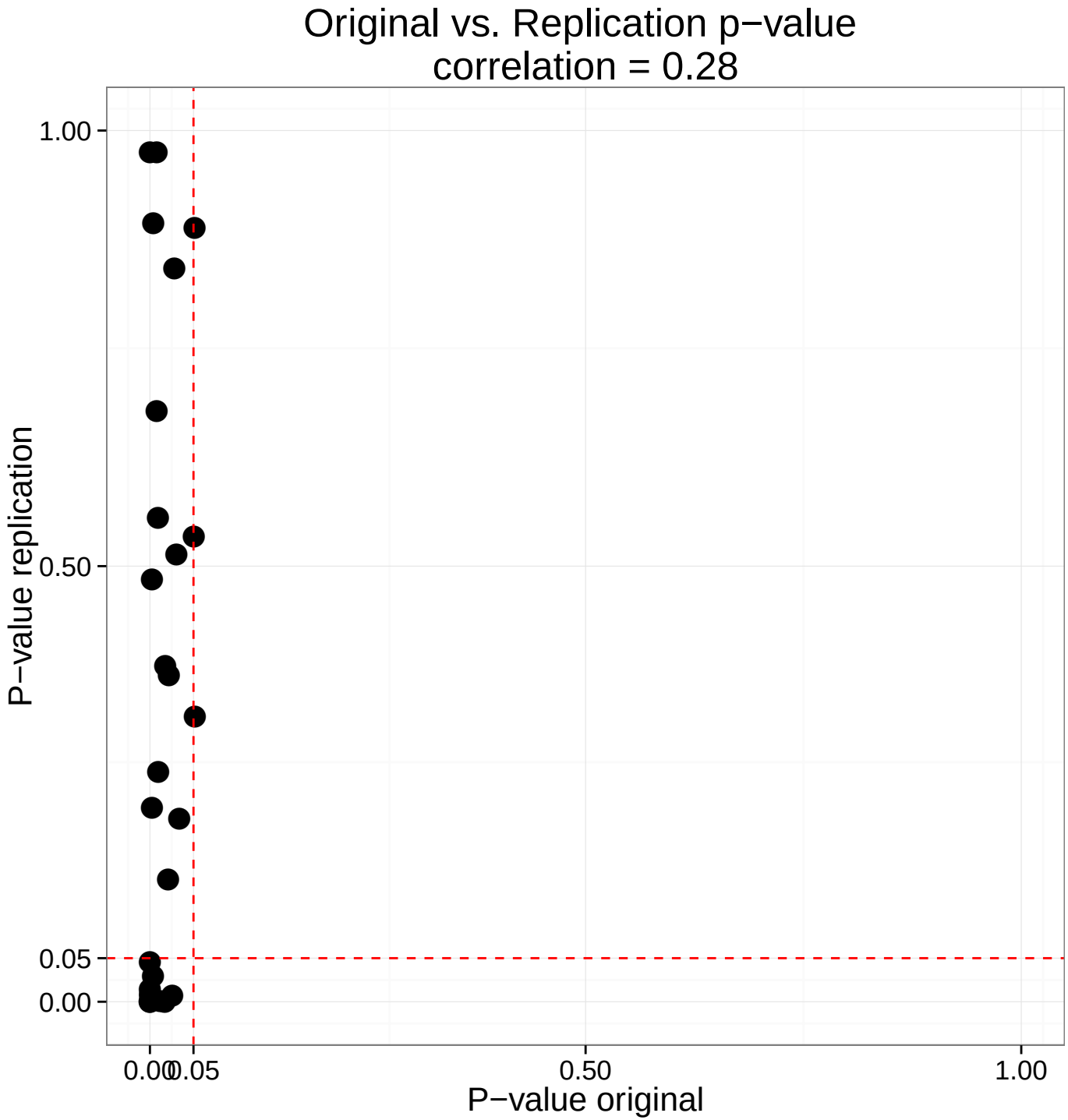

Histograms of original versus replication p−values
Frequency
0
5
10
15
20
25
30
Original
Replication
0.0
0.2
0.4
0.6
0.8
1.0
p−value

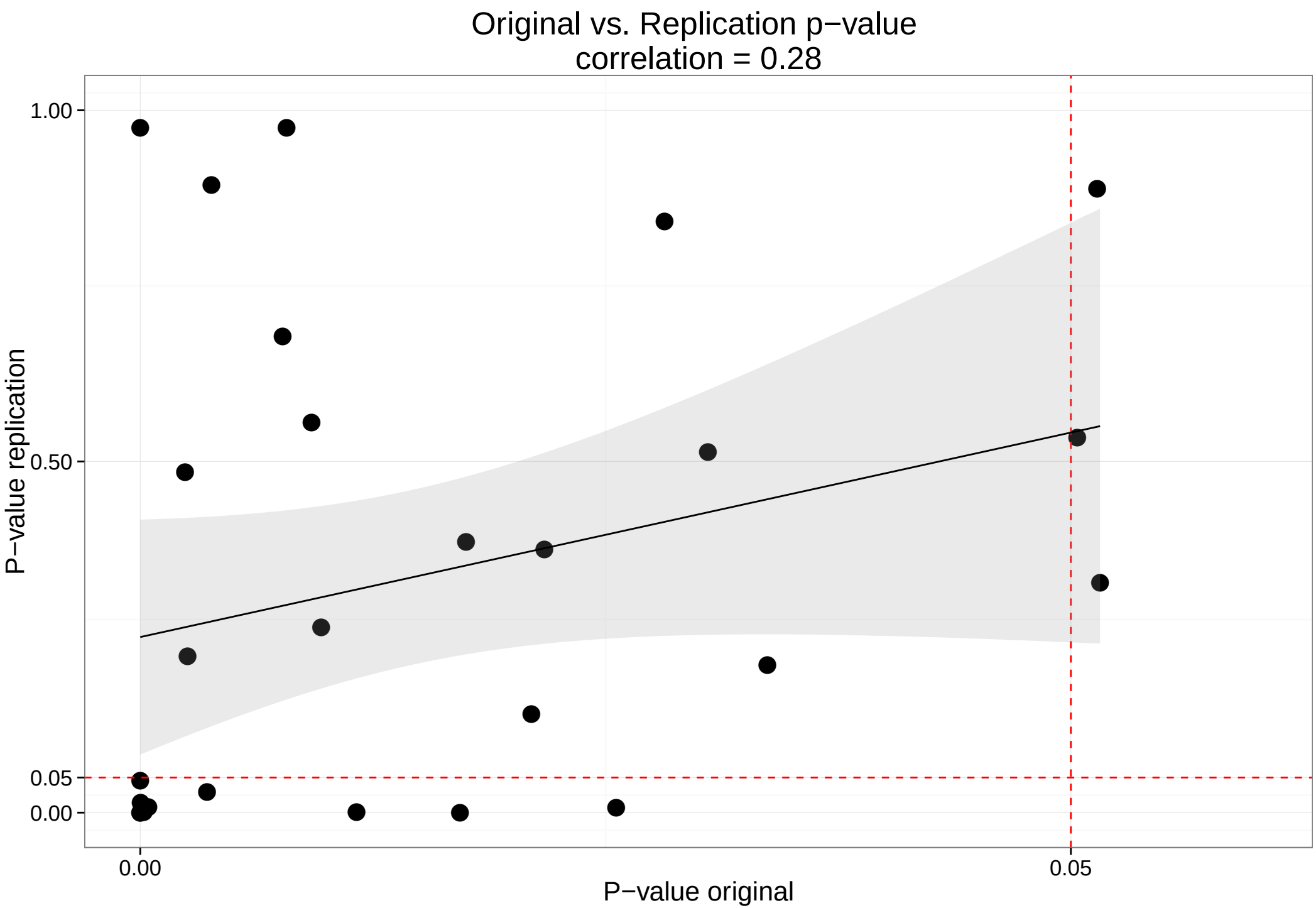

Density plots of original versus replication p−values
Density
0
5
10
15
20
25
30
0.0
0.2
0.4
0.6
0.8
1.0
p−value
Original
Replication

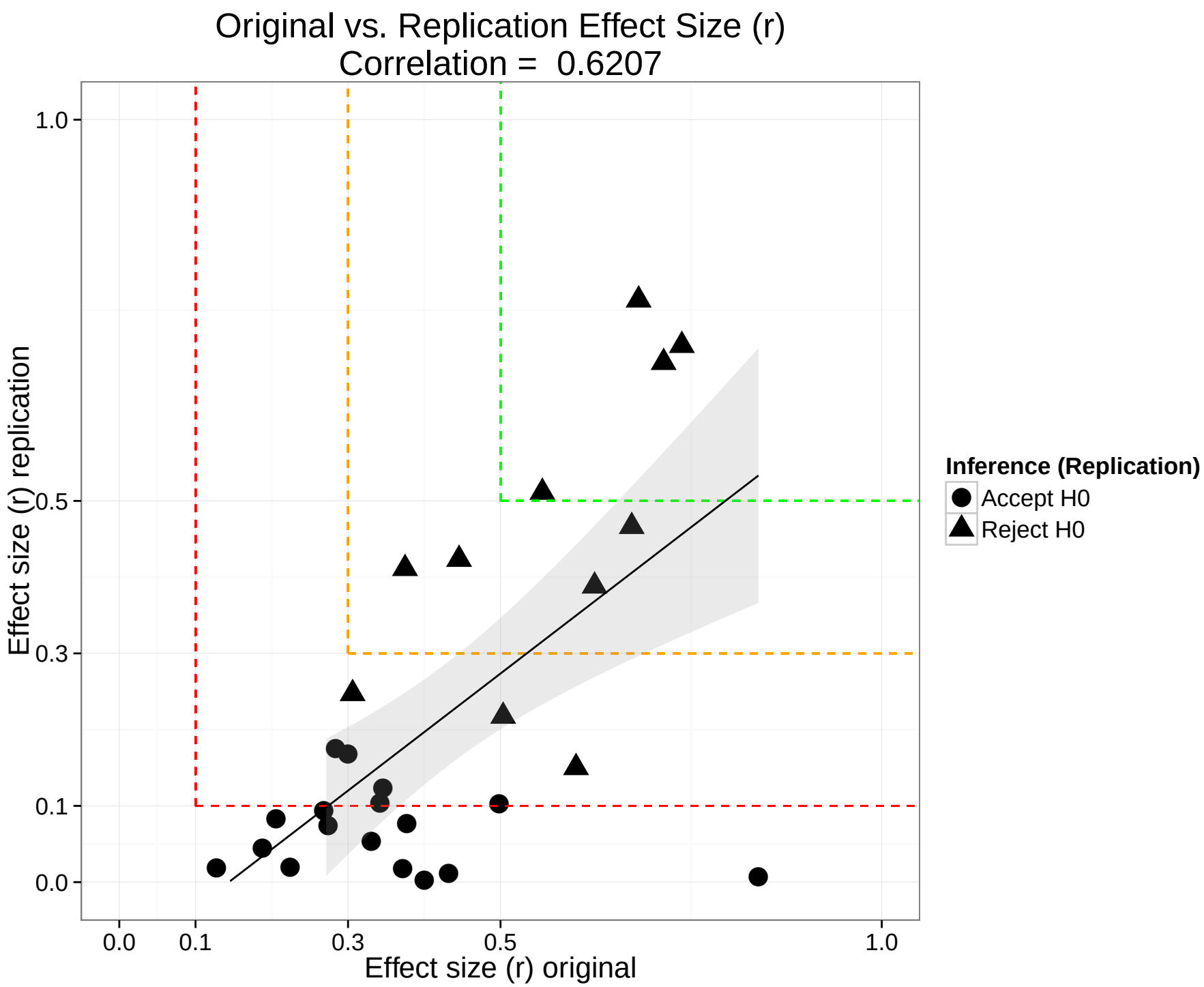

Histograms of original versus replication effect sizes
Original
Replication
Frequency
0
2
4
6
8
10
0.0
0.2
0.4
0.6
0.8
1.0
Effect Size

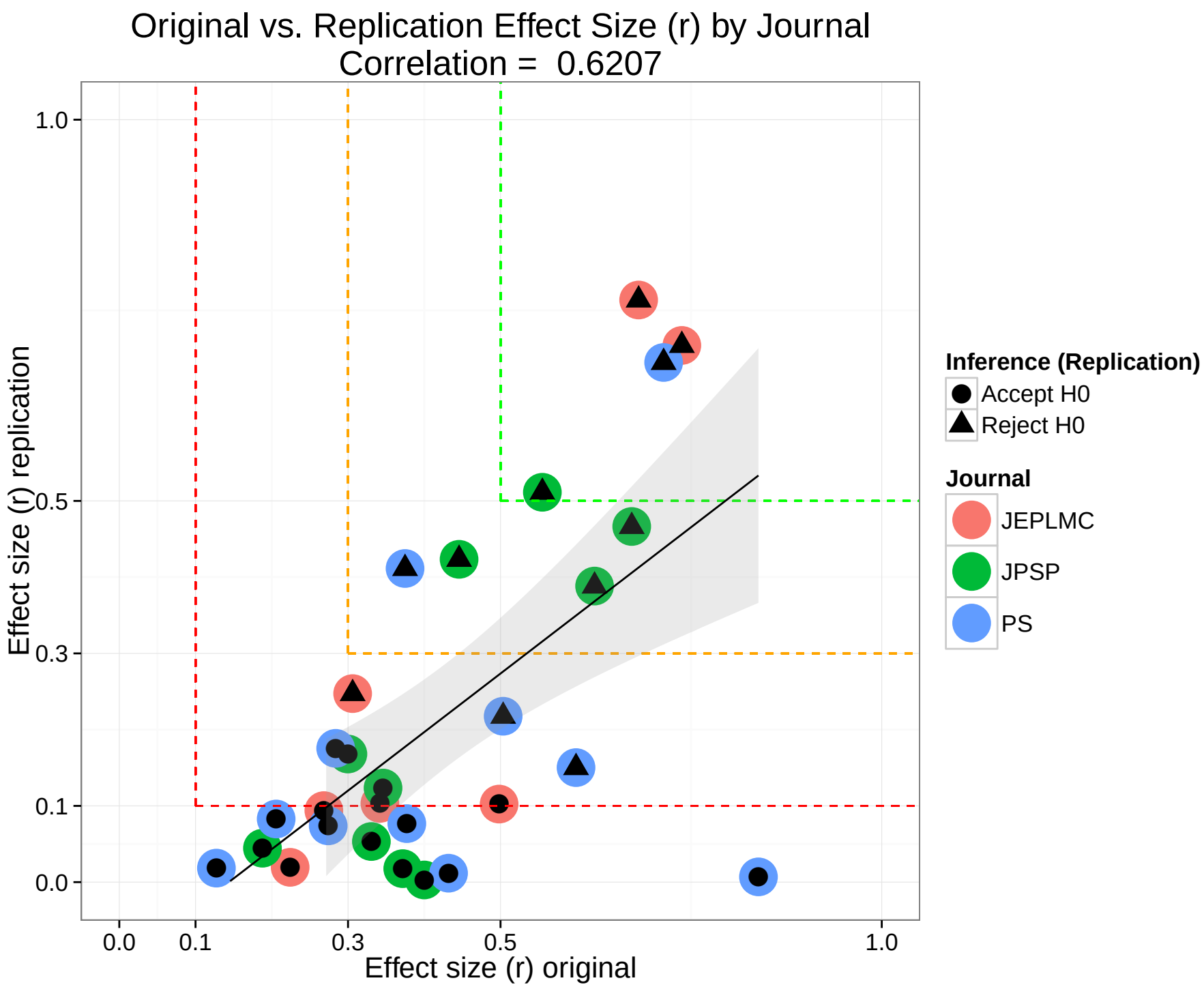

Density plots of original versus replication effect sizes
Original
Replication
Density
0.0
0.5
1.0
1.5
2.0
0.0
0.2
0.4
0.6
0.8
1.0
Effect size

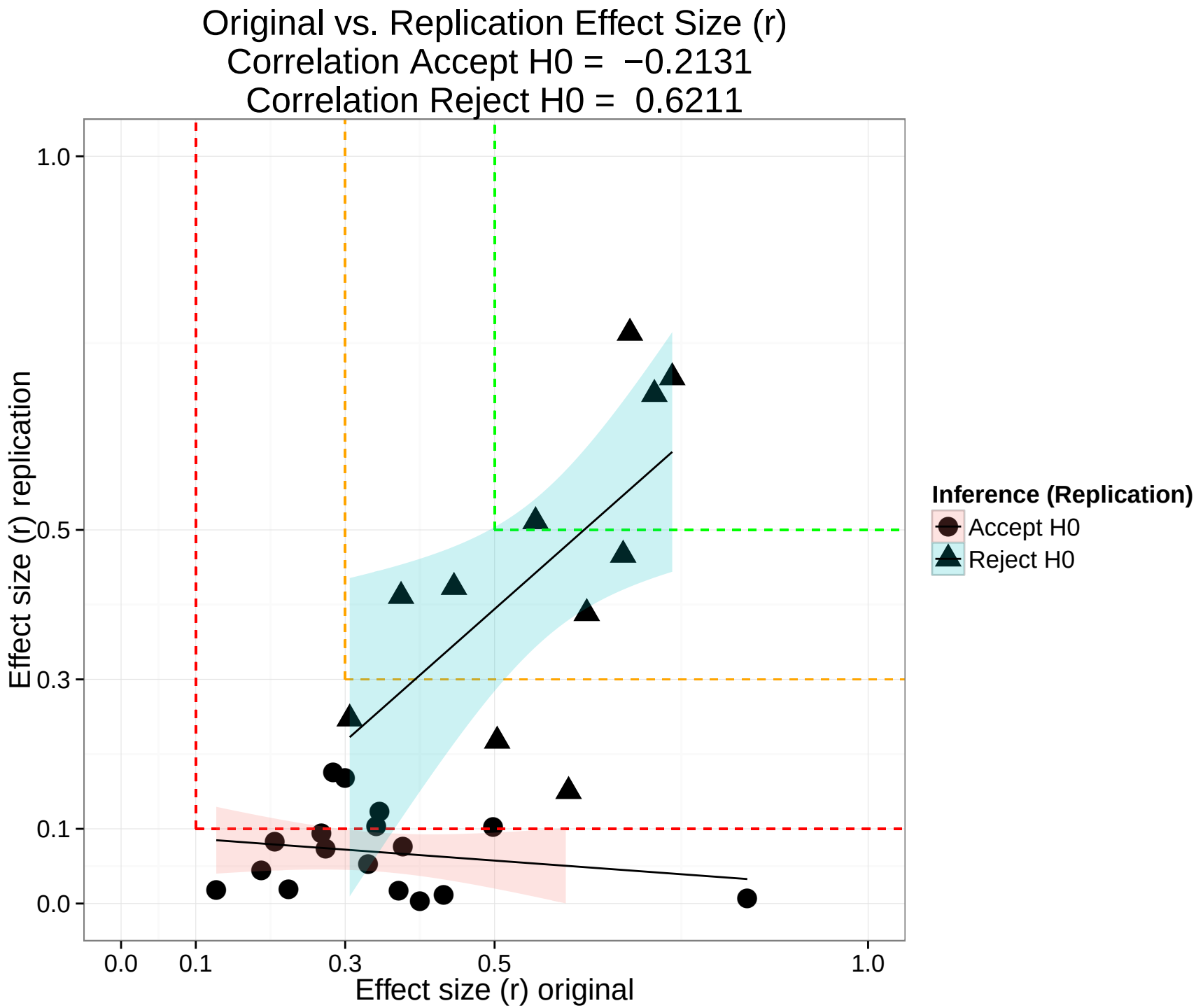

Scatterplot of original versus replication p−values
r = 0.62
Replication Effect Size
Original Effect Size
0.0
0.2
0.4
0.6
0.8
1.0

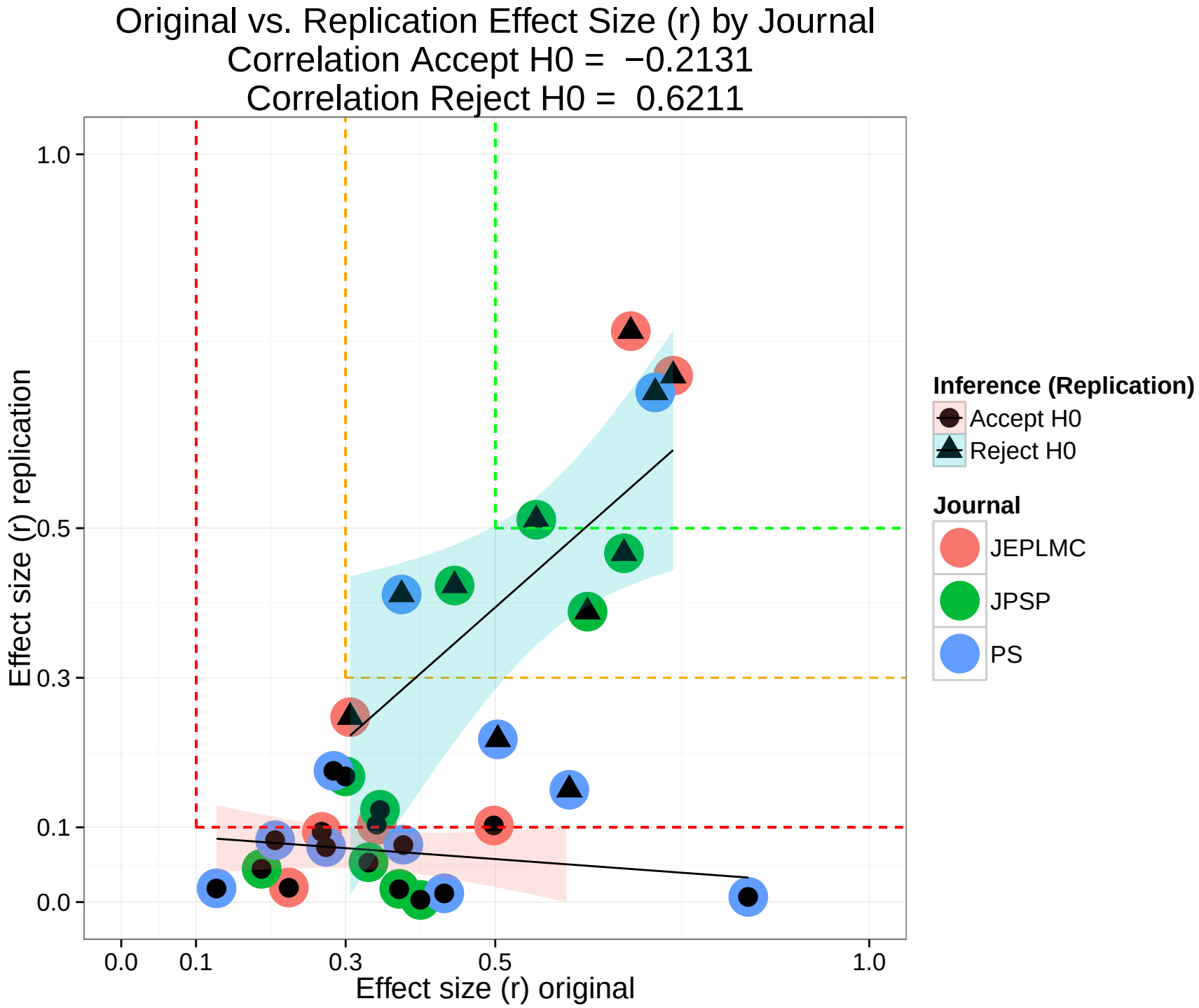

Original vs. Replication p−value
correlation = 0.28
P−value replication
1.00
0.50
0.05
0.00
0.00
0.05
0.50
1.00
P−value original

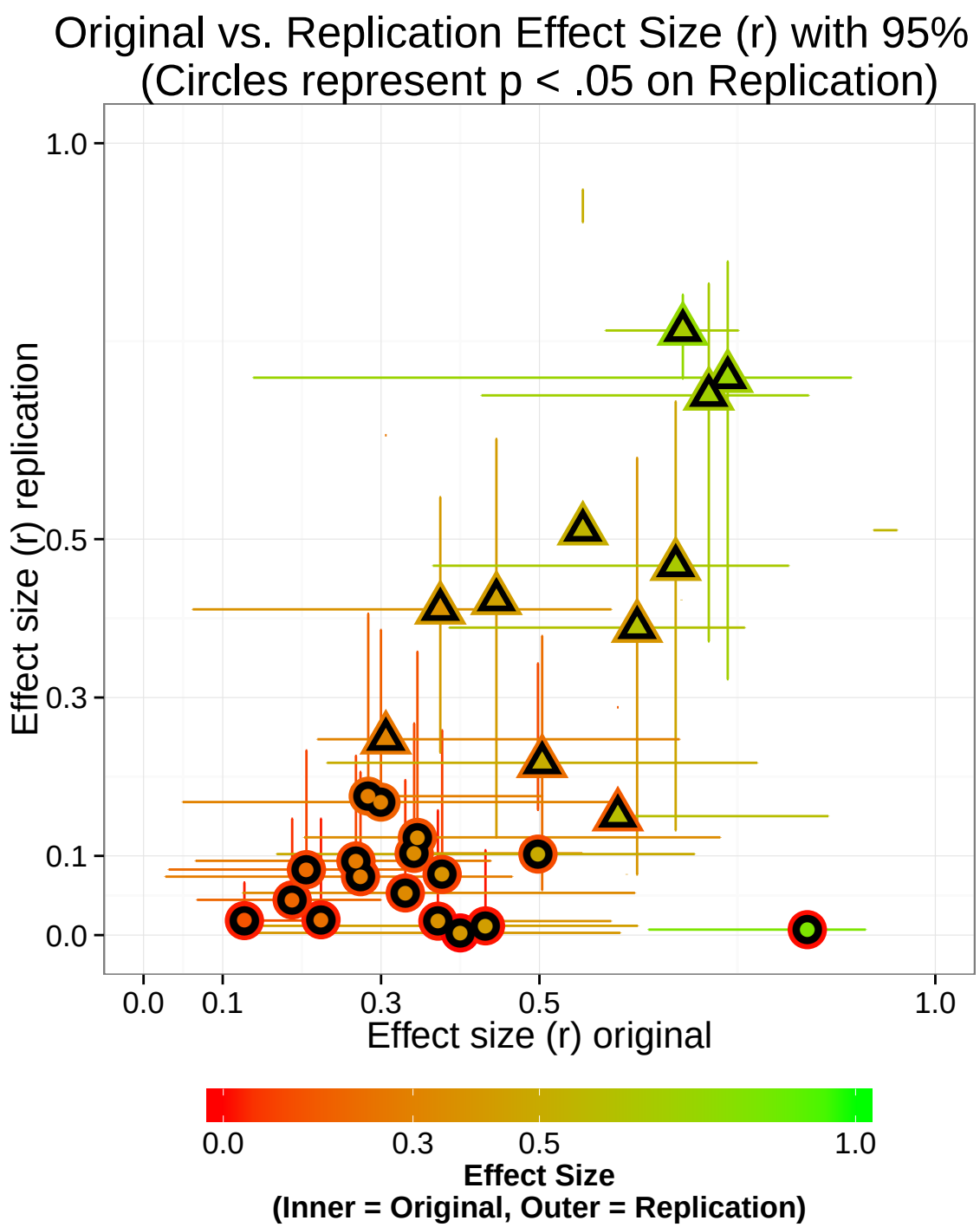

Original vs. Replication p−value
correlation = 0.28
1.00
0.50
0.05
0.00
P−value replication
0.00
0.05
P−value original


Original vs. Replication Effect Size (r)
Correlation = 0.6207
Effect size (r) replication
1.0
0.5
0.3
0.1
0.0
0.0
0.1
0.3
0.5
1.0
Effect size (r) original
Inference (Replication)
Accept H0
Reject H0

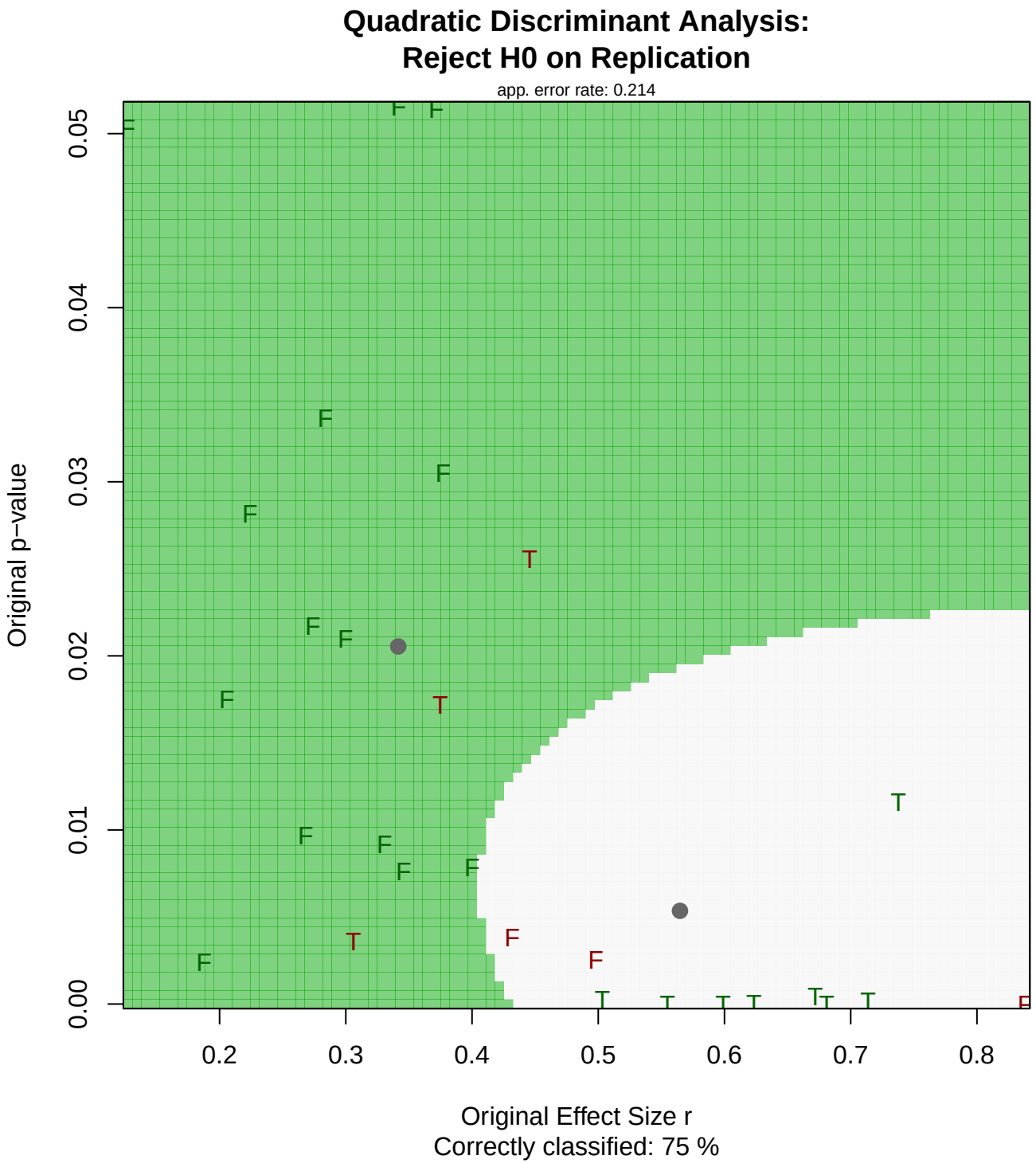

Original vs. Replication Effect Size (r) by Journal
Correlation = 0.6207
Effect size (r) replication
Effect size (r) original
1.0
0.5
0.3
0.1
0.0
0.0
0.1
0.3
0.5
1.0
Inference (Replication)
Accept H0
Reject H0
Journal
JEPLMC
JPSP
PS

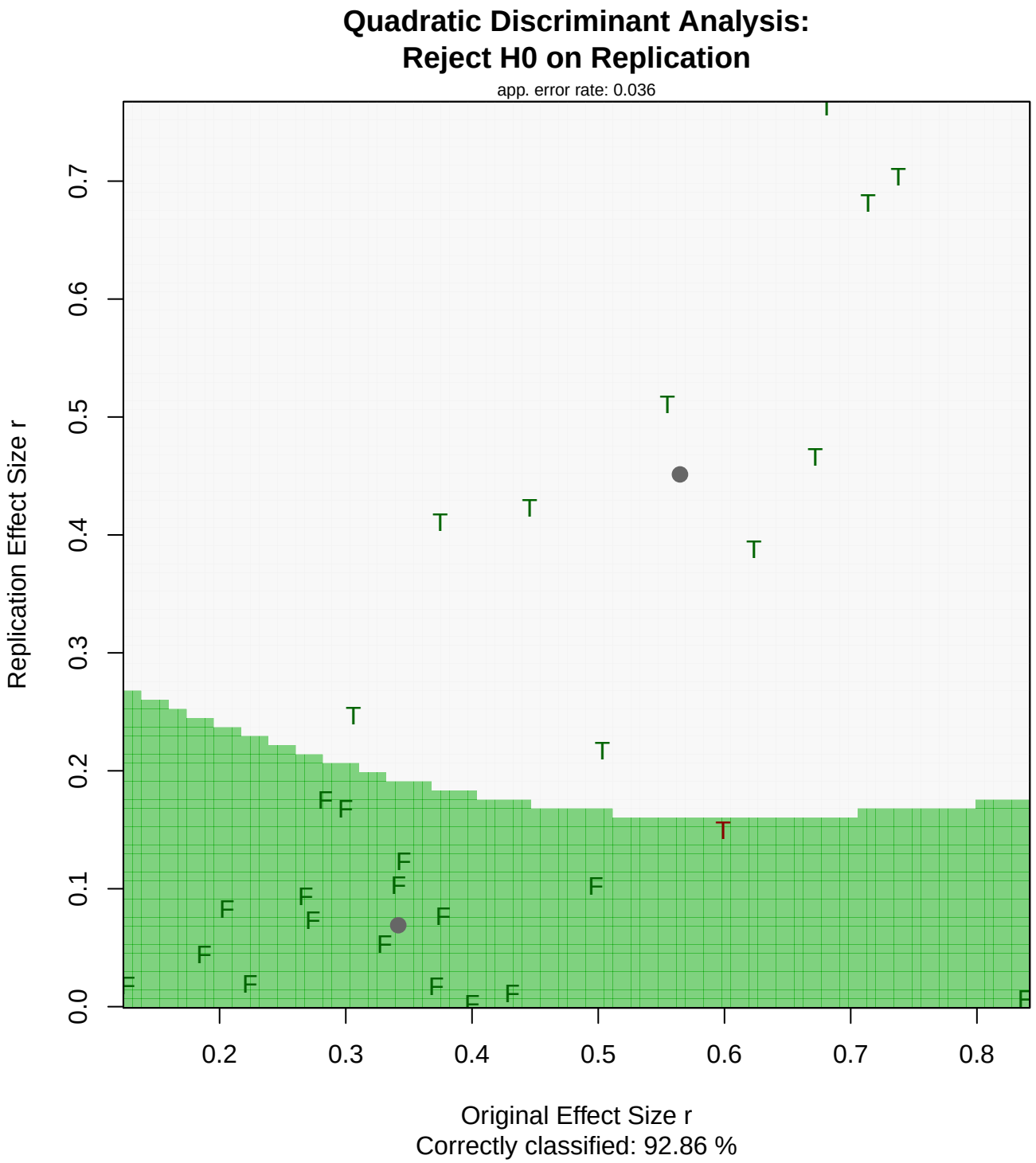

Original vs. Replication Effect Size (r)
Correlation Accept H0 = −0.2131
Correlation Reject H0 = 0.6211
Effect size (r) replication
1.0
0.5
0.3
0.1
0.0
0.0
0.1
0.3
0.5
1.0
Effect size (r) original
Inference (Replication)
Accept H0
Reject H0


Original vs. Replication Effect Size (r) by Journal
Correlation Accept H0 = −0.2131
Correlation Reject H0 = 0.6211
Effect size (r) replication
1.0
0.5
0.3
0.1
0.0
0.0
0.1
0.3
0.5
1.0
Effect size (r) original
Inference (Replication)
Accept H0
Reject H0
Journal
JEPLMC
JPSP
PS

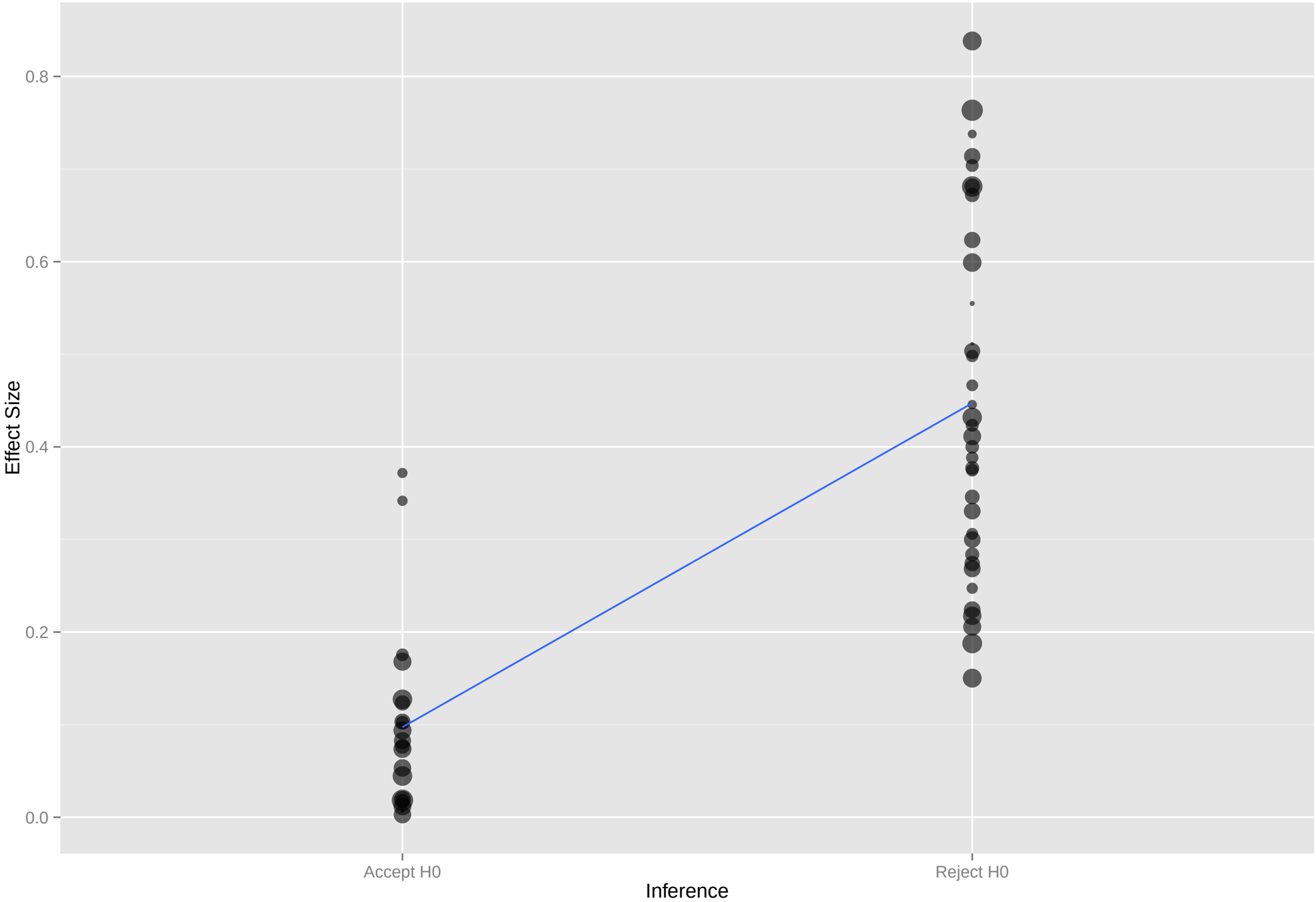

Original vs. Replication Effect Size (r) with 95% CI
(Circles represent p < .05 on Replication)
Effect size (r) replication
1.0
0.5
0.3
0.1
0.0
0.0
0.1
0.3
0.5
1.0
Effect size (r) original
0.0
0.3
0.5
1.0
Effect Size
(Inner = Original, Outer = Replication)

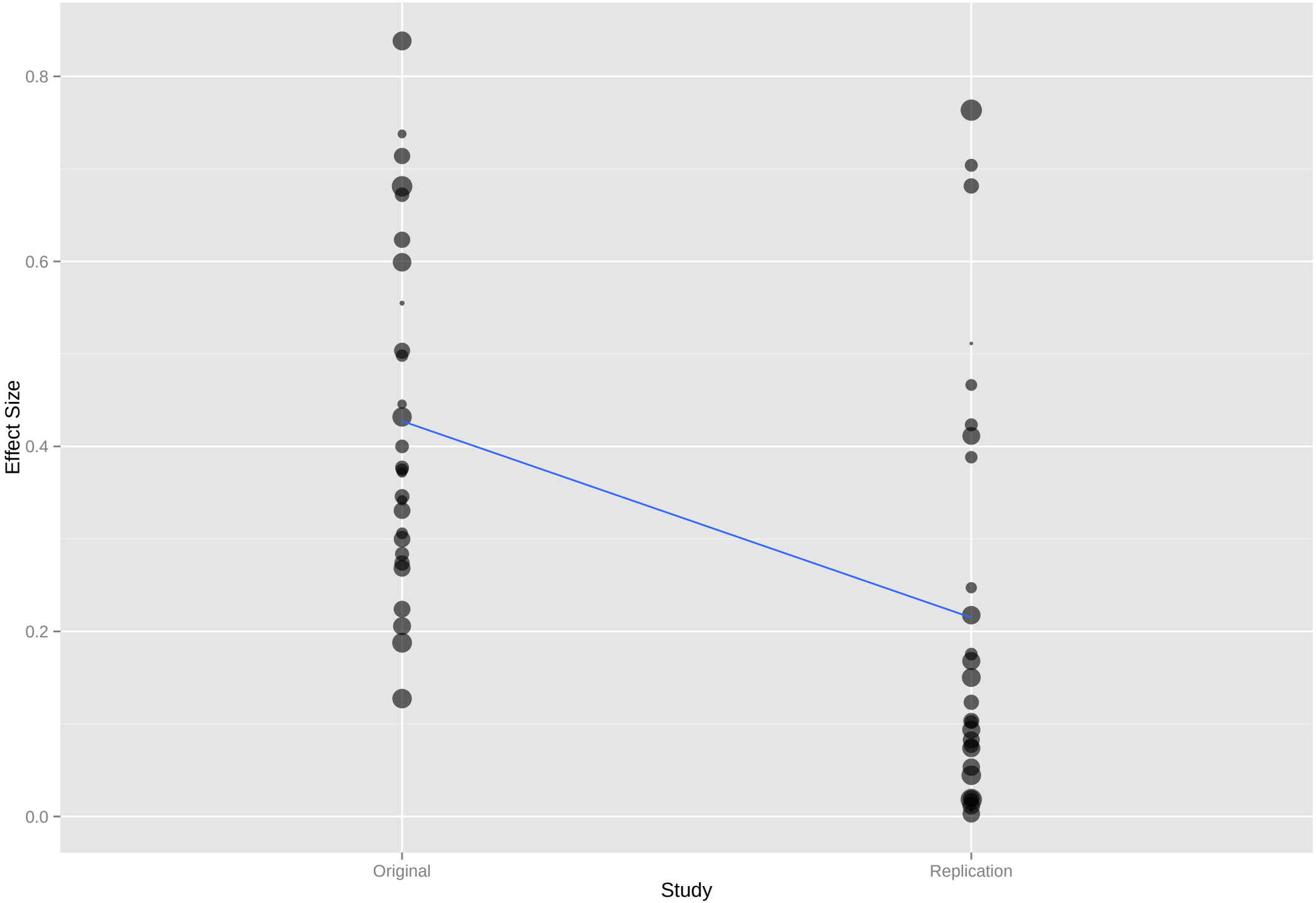
	FALSE	TRUE
FALSE	13	4
TRUE	3	8


Quadratic Discriminant Analysis:
Reject H0 on Replication
app. error rate: 0.214
Original p−value
0.00
0.01
0.02
0.03
0.04
0.05
0.2
0.3
0.4
0.5
0.6
0.7
0.8
Original Effect Size r
Correctly classified: 75 %

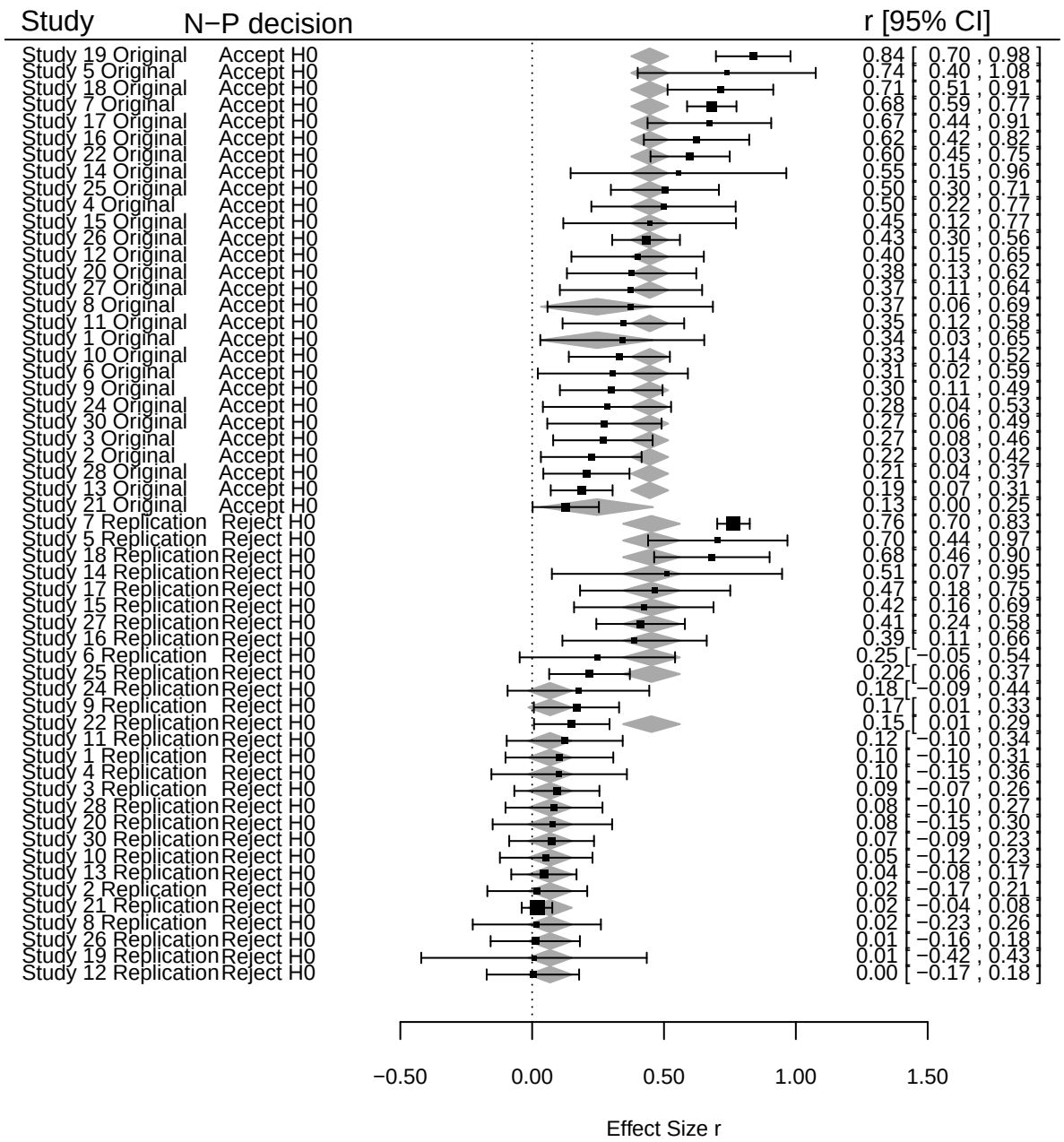

Quadratic Discriminant Analysis:
Reject H0 on Replication
app. error rate: 0.036
Replication Effect Size r
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.2
0.3
0.4
0.5
0.6
0.7
0.8
Original Effect Size r
Correctly classified: 92.86 %

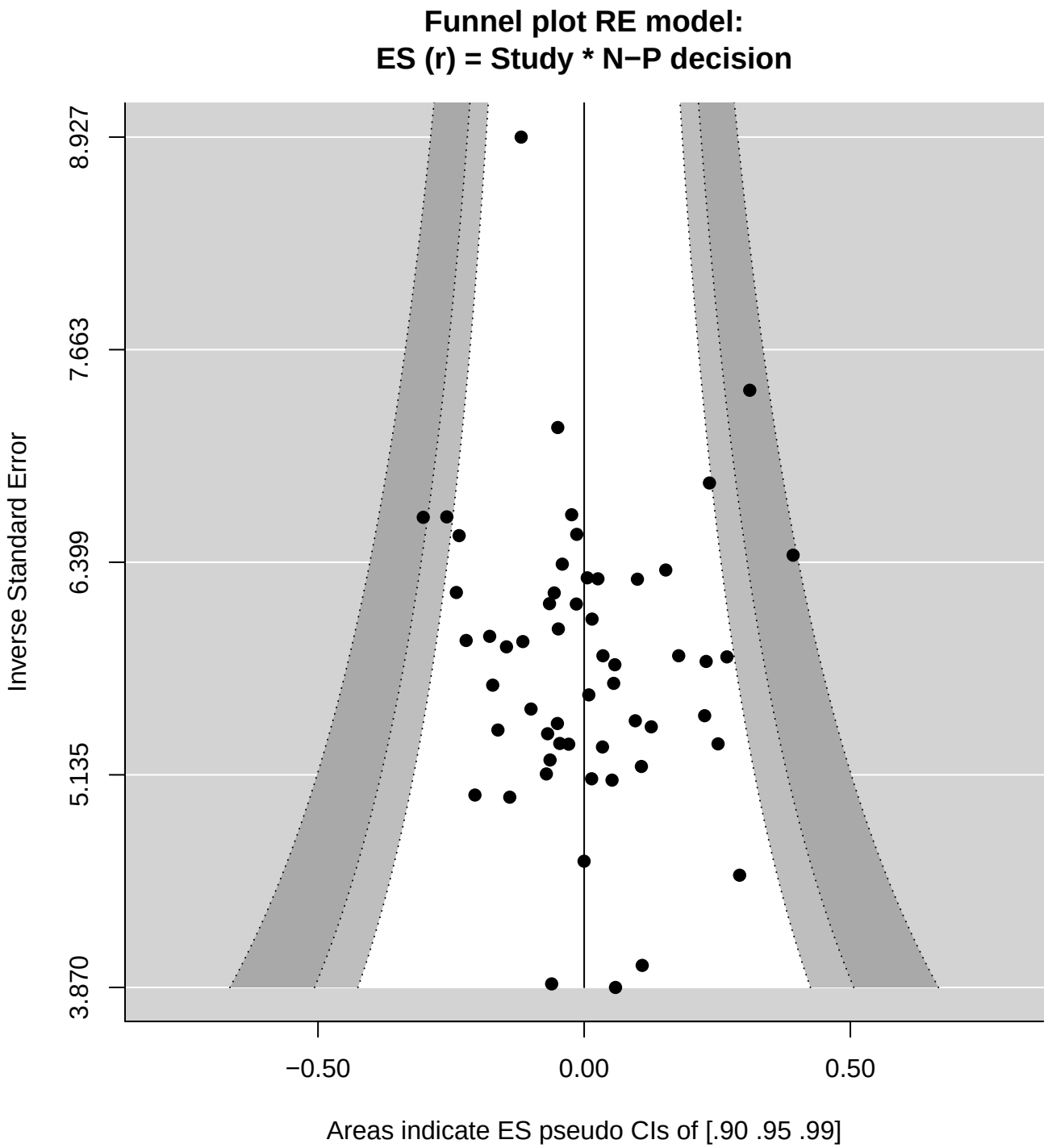
```
Mixed-Effects Model (k = 56; tau^2 estimator: REML)

  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
```

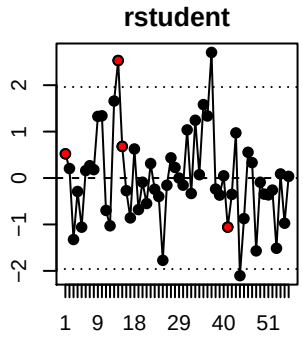

0.8
0.6
0.4
0.2
0.0
Effect Size
Accept H0
Reject H0
Inference

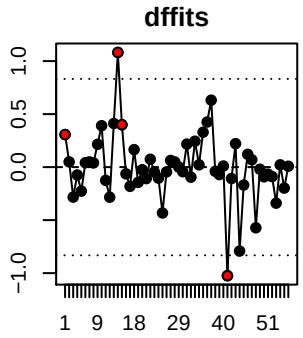

0.8
0.6
0.4
0.2
0.0
Effect Size
Original
Replication
Study

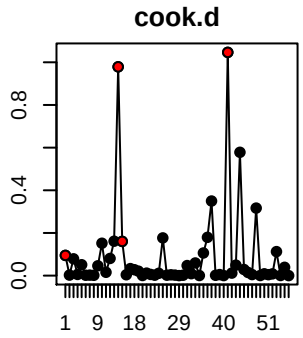
Forest plot RE model:
ES (r) = Study * N−P decision

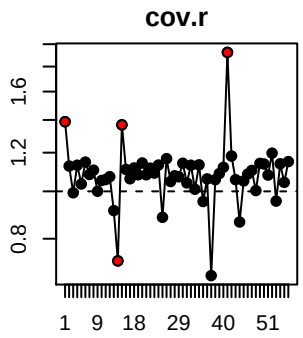


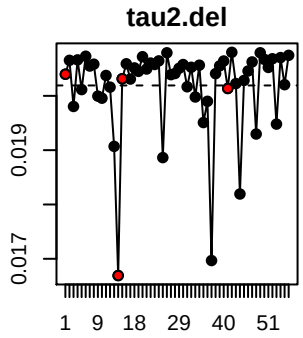

Funnel plot RE model:
ES (r) = Study * N−P decision
Inverse Standard Error
8.927
7.663
6.399
5.135
3.870
−0.50
0.00
0.50
Areas indicate ES pseudo CIs of [.90 .95 .99]

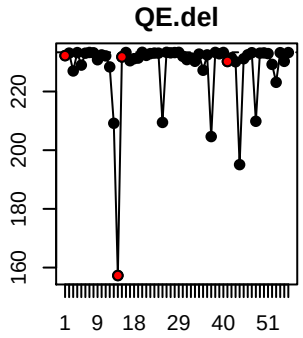

rstudent
2
1
0
−1
−2
1 9 18 29 40 51

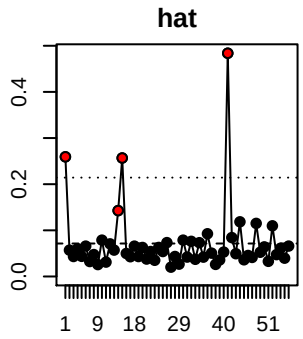

dffits
1.0
0.5
0.0
−1.0
1 9 18 29 40 51

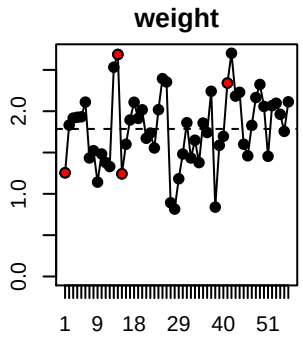

cook.d
0.8
0.4
0.0
1 9 18 29 40 51


cov.r
1.6
1.2
0.8
1 9 18 29 40 51


tau2.del
0.019
0.017
1 9 18 29 40 51


QE.del
220
200
180
160
1 9 18 29 40 51


hat
0.4
0.2
0.0
1 9 18 29 40 51


weight
2.0
1.0
0.0
1 9 18 29 40 51