

Supplementary materials for *Small sample methods for cluster-robust variance estimation and hypothesis testing in fixed effects models*

July 15, 2016

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S1 Proof of Theorem 1

The Moore-Penrose inverse of \mathbf{B}_i can be computed from its eigen-decomposition. Let $b \leq n_i$ denote the rank of \mathbf{B}_i . Let \mathbf{A} be the $b \times b$ diagonal matrix of the positive eigenvalues of \mathbf{B}_i and \mathbf{V} be the $n_i \times b$ matrix of corresponding eigen-vectors, so that $\mathbf{B}_i = \mathbf{V}\mathbf{A}\mathbf{V}'$. Then $\mathbf{B}_i^+ = \mathbf{V}\mathbf{A}^{-1}\mathbf{V}'$ and $\mathbf{B}_i^{+1/2} = \mathbf{V}\mathbf{A}^{-1/2}\mathbf{V}'$. Now, observe that

$$\begin{aligned} \ddot{\mathbf{R}}_i' \mathbf{W}_i \mathbf{A}_i (\mathbf{I} - \mathbf{H}_{\mathbf{X}})_i \Phi (\mathbf{I} - \mathbf{H}_{\mathbf{X}})_i' \mathbf{A}_i' \mathbf{W}_i \ddot{\mathbf{R}}_i &= \ddot{\mathbf{R}}_i' \mathbf{W}_i \mathbf{D}_i \mathbf{B}_i^{+1/2} \mathbf{B}_i \mathbf{B}_i^{+1/2} \mathbf{D}_i' \mathbf{W}_i \ddot{\mathbf{R}}_i \\ &= \ddot{\mathbf{R}}_i' \mathbf{W}_i \mathbf{D}_i \mathbf{V} \mathbf{V}' \mathbf{D}_i' \mathbf{W}_i \ddot{\mathbf{R}}_i. \end{aligned} \quad (1)$$

Because \mathbf{D}_i , and Φ are positive definite and \mathbf{B}_i is symmetric, the eigen-vectors \mathbf{V} define an orthonormal basis for the column span of $(\mathbf{I} - \mathbf{H}_{\mathbf{X}})_i$. We now show that $\ddot{\mathbf{U}}_i$ is in the column space of $(\mathbf{I} - \mathbf{H}_{\mathbf{X}})_i$. Let \mathbf{Z}_i be an $n_i \times (r + s)$ matrix of zeros. Let $\mathbf{Z}_k = -\ddot{\mathbf{U}}_k \mathbf{L}^{-1} \mathbf{M}_{\ddot{\mathbf{U}}}^{-1}$, for $k \neq i$ and take $\mathbf{Z} = (\mathbf{Z}_1', \dots, \mathbf{Z}_m')'$. Now observe that $(\mathbf{I} - \mathbf{H}_{\mathbf{T}}) \mathbf{Z} = \mathbf{Z}$. It follows that

$$\begin{aligned} (\mathbf{I} - \mathbf{H}_{\mathbf{X}})_i \mathbf{Z} &= (\mathbf{I} - \mathbf{H}_{\ddot{\mathbf{U}}})_i (\mathbf{I} - \mathbf{H}_{\mathbf{T}}) \mathbf{Z} = (\mathbf{I} - \mathbf{H}_{\ddot{\mathbf{U}}})_i \mathbf{Z} \\ &= \mathbf{Z}_i - \ddot{\mathbf{U}}_i \mathbf{M}_{\ddot{\mathbf{U}}} \sum_{k=1}^m \ddot{\mathbf{U}}_k' \mathbf{W}_k \mathbf{Z}_k \\ &= \ddot{\mathbf{U}}_i \mathbf{M}_{\ddot{\mathbf{U}}} \left(\sum_{k \neq i} \ddot{\mathbf{U}}_k' \mathbf{W}_k \ddot{\mathbf{U}} \right) \mathbf{L}^{-1} \mathbf{M}_{\ddot{\mathbf{U}}}^{-1} = \ddot{\mathbf{U}}_i. \end{aligned}$$

Thus, there exists an $N \times (r + s)$ matrix \mathbf{Z} such that $(\mathbf{I} - \mathbf{H}_{\ddot{\mathbf{X}}})_i \mathbf{Z} = \ddot{\mathbf{U}}_i$, i.e., $\ddot{\mathbf{U}}_i$ is in the column span of $(\mathbf{I} - \mathbf{H}_{\mathbf{X}})_i$. Because $\mathbf{D}_i \mathbf{W}_i$ is positive definite and $\ddot{\mathbf{R}}_i$ is a sub-matrix of $\ddot{\mathbf{U}}_i$, $\mathbf{D}_i \mathbf{W}_i \ddot{\mathbf{R}}_i$ is also in the column span of $(\mathbf{I} - \mathbf{H}_{\mathbf{X}})_i$. It follows that

$$\ddot{\mathbf{R}}_i' \mathbf{W}_i \mathbf{D}_i \mathbf{V} \mathbf{V}' \mathbf{D}_i' \mathbf{W}_i \ddot{\mathbf{R}}_i = \ddot{\mathbf{R}}_i' \mathbf{W}_i \Phi \mathbf{W}_i \ddot{\mathbf{R}}_i. \quad (2)$$

Substituting (2) into (1) demonstrates that \mathbf{A}_i satisfies the generalized BRL criterion (Eq. 6 of the main paper).

Under the working model, the residuals from cluster i have mean $\mathbf{0}$ and variance

$$\text{Var}(\ddot{\mathbf{e}}_i) = (\mathbf{I} - \mathbf{H}_{\mathbf{X}})_i \Phi (\mathbf{I} - \mathbf{H}_{\mathbf{X}})_i',$$

It follows that

$$\begin{aligned} \mathbb{E}(\mathbf{V}^{CR2}) &= \mathbf{M}_{\ddot{\mathbf{R}}} \left[\sum_{i=1}^m \ddot{\mathbf{R}}_i' \mathbf{W}_i \mathbf{A}_i (\mathbf{I} - \mathbf{H}_{\mathbf{X}})_i \Phi (\mathbf{I} - \mathbf{H}_{\mathbf{X}})_i' \mathbf{A}_i' \mathbf{W}_i \ddot{\mathbf{R}}_i \right] \mathbf{M}_{\ddot{\mathbf{R}}} \\ &= \mathbf{M}_{\ddot{\mathbf{R}}} \left[\sum_{i=1}^m \ddot{\mathbf{R}}_i' \mathbf{W}_i \Phi \mathbf{W}_i \ddot{\mathbf{R}}_i \right] \mathbf{M}_{\ddot{\mathbf{R}}} \\ &= \text{Var}(\hat{\beta}) \end{aligned}$$

S2 Proof of Theorem 2

From the fact that $\ddot{\mathbf{U}}_i' \mathbf{W}_i \mathbf{T}_i = \mathbf{0}$ for $i = 1, \dots, m$, it follows that

$$\begin{aligned} \mathbf{B}_i &= \mathbf{D}_i (\mathbf{I} - \mathbf{H}_{\ddot{\mathbf{U}}})_i (\mathbf{I} - \mathbf{H}_{\mathbf{T}}) \Phi (\mathbf{I} - \mathbf{H}_{\mathbf{T}})' (\mathbf{I} - \mathbf{H}_{\ddot{\mathbf{U}}})_i' \mathbf{D}_i' \\ &= \mathbf{D}_i (\mathbf{I} - \mathbf{H}_{\ddot{\mathbf{U}}} - \mathbf{H}_{\mathbf{T}})_i \Phi (\mathbf{I} - \mathbf{H}_{\ddot{\mathbf{U}}} - \mathbf{H}_{\mathbf{T}})_i' \mathbf{D}_i' \\ &= \mathbf{D}_i \left(\Phi_i - \ddot{\mathbf{U}}_i \mathbf{M}_{\ddot{\mathbf{U}}} \ddot{\mathbf{U}}_i' - \mathbf{T}_i \mathbf{M}_{\mathbf{T}} \mathbf{T}_i' \right) \mathbf{D}_i' \end{aligned}$$

and

$$\mathbf{B}_i^+ = (\mathbf{D}_i')^{-1} \left(\Phi_i - \ddot{\mathbf{U}}_i \mathbf{M}_{\ddot{\mathbf{U}}} \ddot{\mathbf{U}}_i' - \mathbf{T}_i \mathbf{M}_{\mathbf{T}} \mathbf{T}_i' \right)^+ \mathbf{D}_i^{-1}. \quad (3)$$

Let $\Psi_i = \left(\Phi_i - \ddot{\mathbf{U}}_i \mathbf{M}_{\ddot{\mathbf{U}}} \ddot{\mathbf{U}}_i' \right)^+$. Using a generalized Woodbury identity (Henderson and Searle, 1981),

$$\Psi_i = \mathbf{W}_i + \mathbf{W}_i \ddot{\mathbf{U}}_i \mathbf{M}_{\ddot{\mathbf{U}}} \left(\mathbf{M}_{\ddot{\mathbf{U}}} - \mathbf{M}_{\ddot{\mathbf{U}}} \ddot{\mathbf{U}}_i' \mathbf{W}_i \ddot{\mathbf{U}}_i \mathbf{M}_{\ddot{\mathbf{U}}} \right)^+ \mathbf{M}_{\ddot{\mathbf{U}}} \ddot{\mathbf{U}}_i' \mathbf{W}_i.$$

It follows that $\Psi_i \mathbf{T}_i = \mathbf{W}_i \mathbf{T}_i$. Another application of the generalized Woodbury identity gives

$$\begin{aligned} \left(\Phi_i - \ddot{\mathbf{U}}_i \mathbf{M}_{\ddot{\mathbf{U}}} \ddot{\mathbf{U}}_i' - \mathbf{T}_i \mathbf{M}_{\mathbf{T}} \mathbf{T}_i' \right)^+ &= \Psi_i + \Psi_i \mathbf{T}_i \mathbf{M}_{\mathbf{T}} (\mathbf{M}_{\mathbf{T}} - \mathbf{M}_{\mathbf{T}} \mathbf{T}_i' \Psi_i \mathbf{T}_i \mathbf{M}_{\mathbf{T}})^+ \mathbf{M}_{\mathbf{T}} \mathbf{T}_i' \Psi_i \\ &= \Psi_i + \mathbf{W}_i \mathbf{T}_i \mathbf{M}_{\mathbf{T}} (\mathbf{M}_{\mathbf{T}} - \mathbf{M}_{\mathbf{T}} \mathbf{T}_i' \mathbf{W}_i \mathbf{T}_i \mathbf{M}_{\mathbf{T}})^+ \mathbf{M}_{\mathbf{T}} \mathbf{T}_i' \mathbf{W}_i \\ &= \Psi_i. \end{aligned}$$

The last equality follows from the fact that

$$\mathbf{T}_i \mathbf{M}_{\mathbf{T}} (\mathbf{M}_{\mathbf{T}} - \mathbf{M}_{\mathbf{T}} \mathbf{T}_i' \mathbf{W}_i \mathbf{T}_i \mathbf{M}_{\mathbf{T}})^- \mathbf{M}_{\mathbf{T}} \mathbf{T}_i' = \mathbf{0}$$

because the fixed effects are nested within clusters. Substituting into (3), we then have that $\mathbf{B}_i^+ = (\mathbf{D}_i')^{-1} \Psi_i \mathbf{D}_i^{-1}$. But

$$\tilde{\mathbf{B}}_i = \mathbf{D}_i (\mathbf{I} - \mathbf{H}_{\ddot{\mathbf{U}}})_i \Phi (\mathbf{I} - \mathbf{H}_{\ddot{\mathbf{U}}})_i' \mathbf{D}_i' = \mathbf{D}_i \left(\Phi_i - \ddot{\mathbf{U}}_i \mathbf{M}_{\ddot{\mathbf{U}}} \ddot{\mathbf{U}}_i' \right) \mathbf{D}_i' = \mathbf{D}_i \Psi_i^+ \mathbf{D}_i',$$

and so $\mathbf{B}_i^+ = \tilde{\mathbf{B}}_i^+$. It follows that $\mathbf{A}_i = \tilde{\mathbf{A}}_i$ for $i = 1, \dots, m$.

S3 Details of simulation study

This section provides further details regarding the design of the simulations reported in Section 4 of the main text. The simulations examined six distinct study designs. Outcomes are measured for n units (which may be individuals, as in a cluster-randomized or block-randomized design, or time-points, as in a difference-in-differences panel) in each of m clusters under one of three treatment conditions. Suppose that there are G sets of clusters, each of size m_g , where the clusters in each set have a distinct configuration of treatment assignments. Let n_{ghi} denote the number of units at which cluster i in configuration g is observed under condition h , for $i = 1, \dots, m$, $g = 1, \dots, G$, and $h = 1, 2, 3$. Table S1 summarizes the cluster-level sample sizes and unit-level patterns of treatment allocation for each of the six designs. The simulated designs included the following:

1. A balanced, block-randomized design, with an un-equal allocation within each block. In the balanced design, the treatment allocation is identical for each block, so $G = 1$.
2. An unbalanced, block-randomized design, with two different patterns of treatment allocation ($G = 2$).
3. A balanced, cluster-randomized design, in which units are nested within clusters and an equal number of clusters are assigned to each treatment condition.
4. An unbalanced, cluster-randomized design, in which units are nested within clusters but the number of clusters assigned to each condition is not equal.
5. A balanced difference-in-differences design with two patterns of treatment allocation ($G = 2$), in which half of the clusters are observed under the first treatment condition only and the remaining half are observed under all three conditions.
6. An unbalanced difference-in-differences design, again with two patterns of treatment allocation ($G = 2$), but where $2/3$ of the clusters are observed under the first treatment condition only and the remaining $1/3$ of clusters are observed under all three conditions.

Table S1: Study designs used for simulation

Study design	Balance	Configuration	Clusters	Treatment allocation
Randomized Block	Balanced	1	$m_1 = m$	$n_{11i} = n/2, n_{12i} = n/3, n_{13i} = n/6$
Randomized Block	Unbalanced	1 2	$m_1 = m/2$ $m_2 = m/2$	$n_{11i} = n/2, n_{12i} = n/3, n_{13i} = n/6$ $n_{21i} = n/3, n_{22i} = 5n/9, n_{23i} = n/9$
Cluster-Randomized	Balanced	1	$m_1 = m/3$	$n_{11i} = n$
		2	$m_2 = m/3$	$n_{22i} = n$
		3	$m_3 = m/3$	$n_{33i} = n$
Cluster-Randomized	Unbalanced	1	$m_1 = m/2$	$n_{11i} = n$
		2	$m_2 = 3m/10$	$n_{22i} = n$
		3	$m_3 = m/5$	$n_{33i} = n$
Difference-in-Differences	Balanced	1	$m_1 = m/2$	$n_{11i} = n$
		2	$m_2 = m/2$	$n_{21i} = n/2, n_{22i} = n/3, n_{23i} = n/6$
Difference-in-Differences	Unbalanced	1	$m_1 = 2m/3$	$n_{11i} = n$
		2	$m_2 = m/3$	$n_{21i} = n/2, n_{22i} = n/3, n_{23i} = n/6$

S4 Additional simulation results

S4.1 Rejection rates of AHT and standard tests

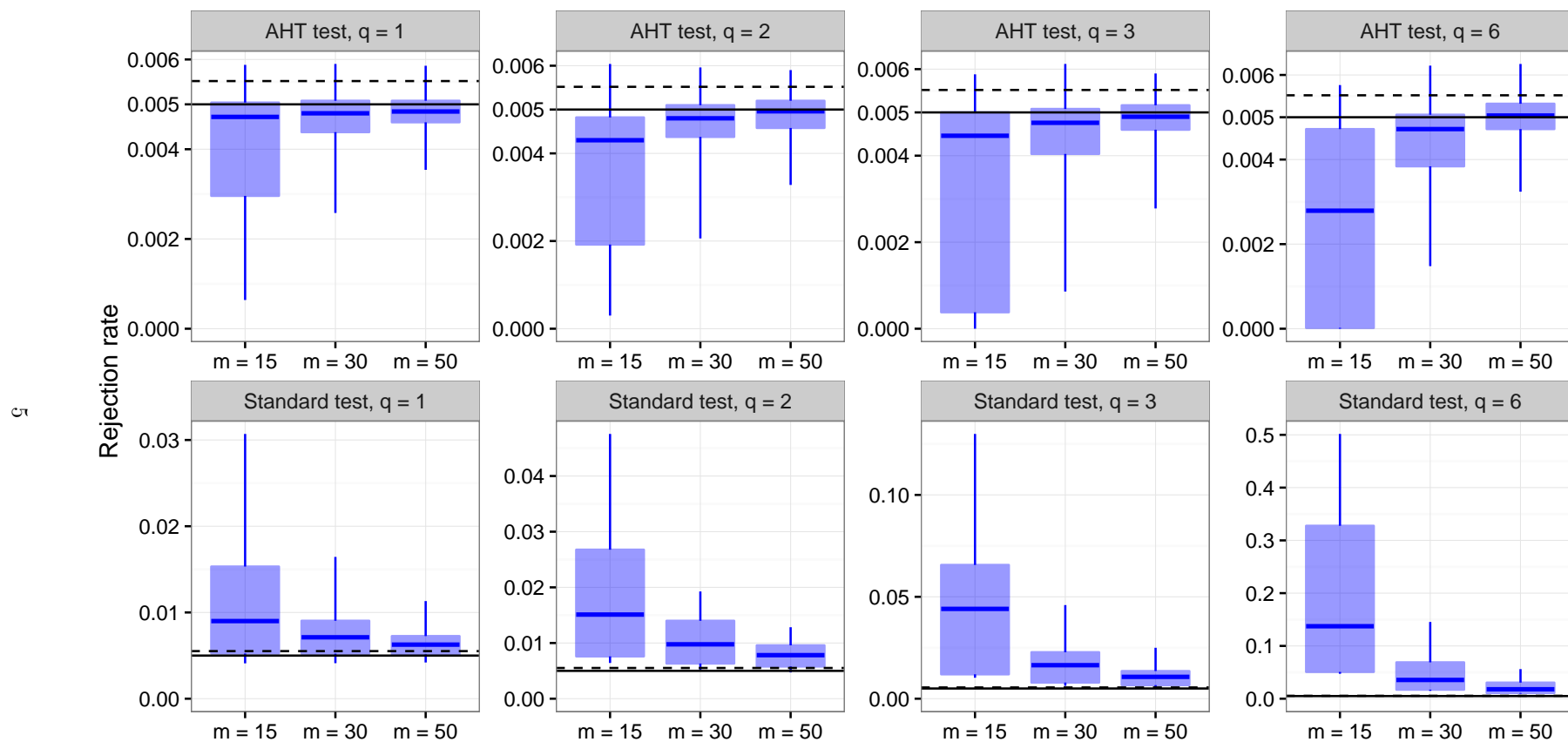


Figure S1: Rejection rates of AHT and standard tests for $\alpha = .005$, by dimension of hypothesis (q) and sample size (m).

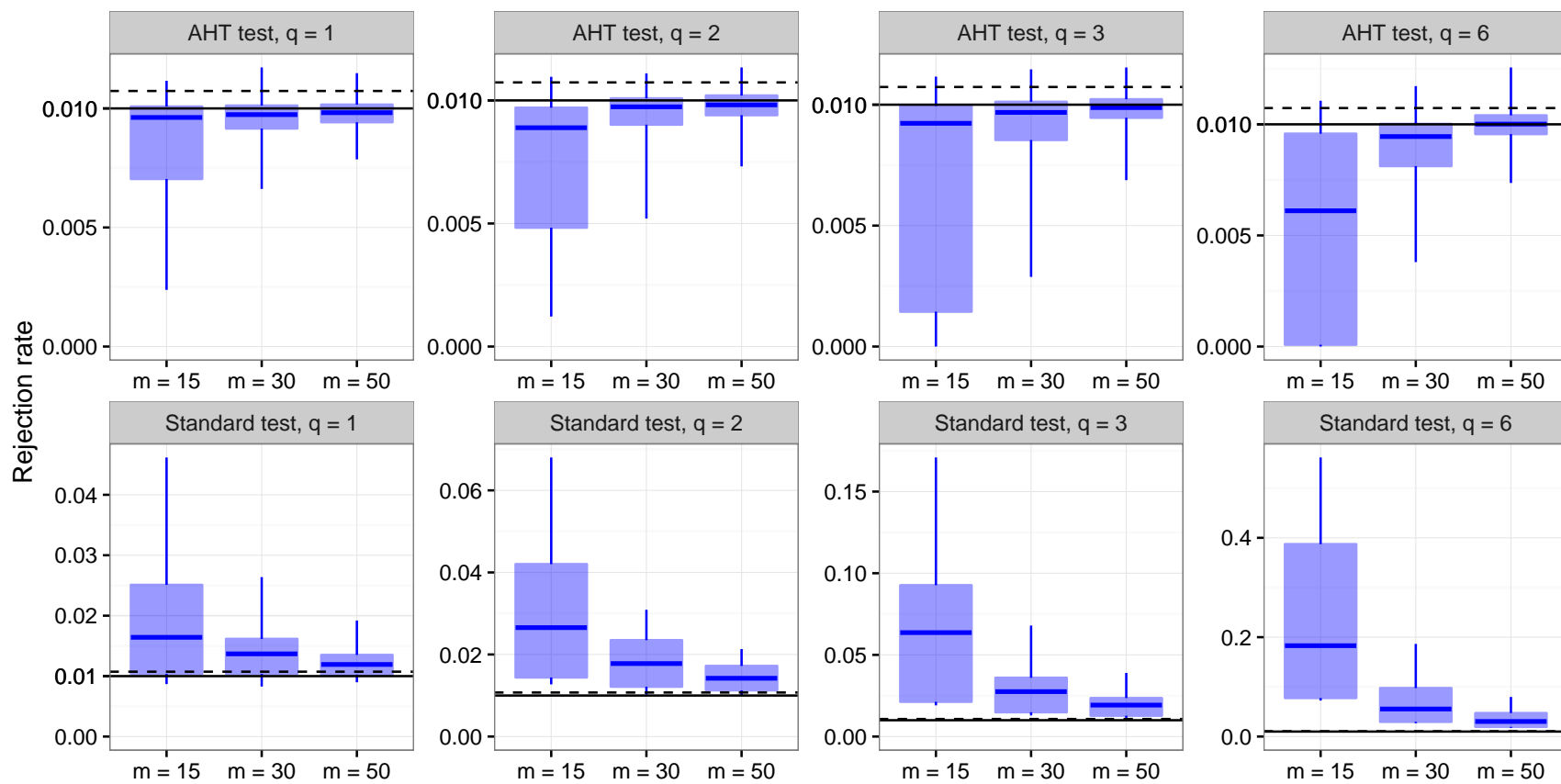


Figure S2: Rejection rates of AHT and standard tests for $\alpha = .01$, by dimension of hypothesis (q) and sample size (m).

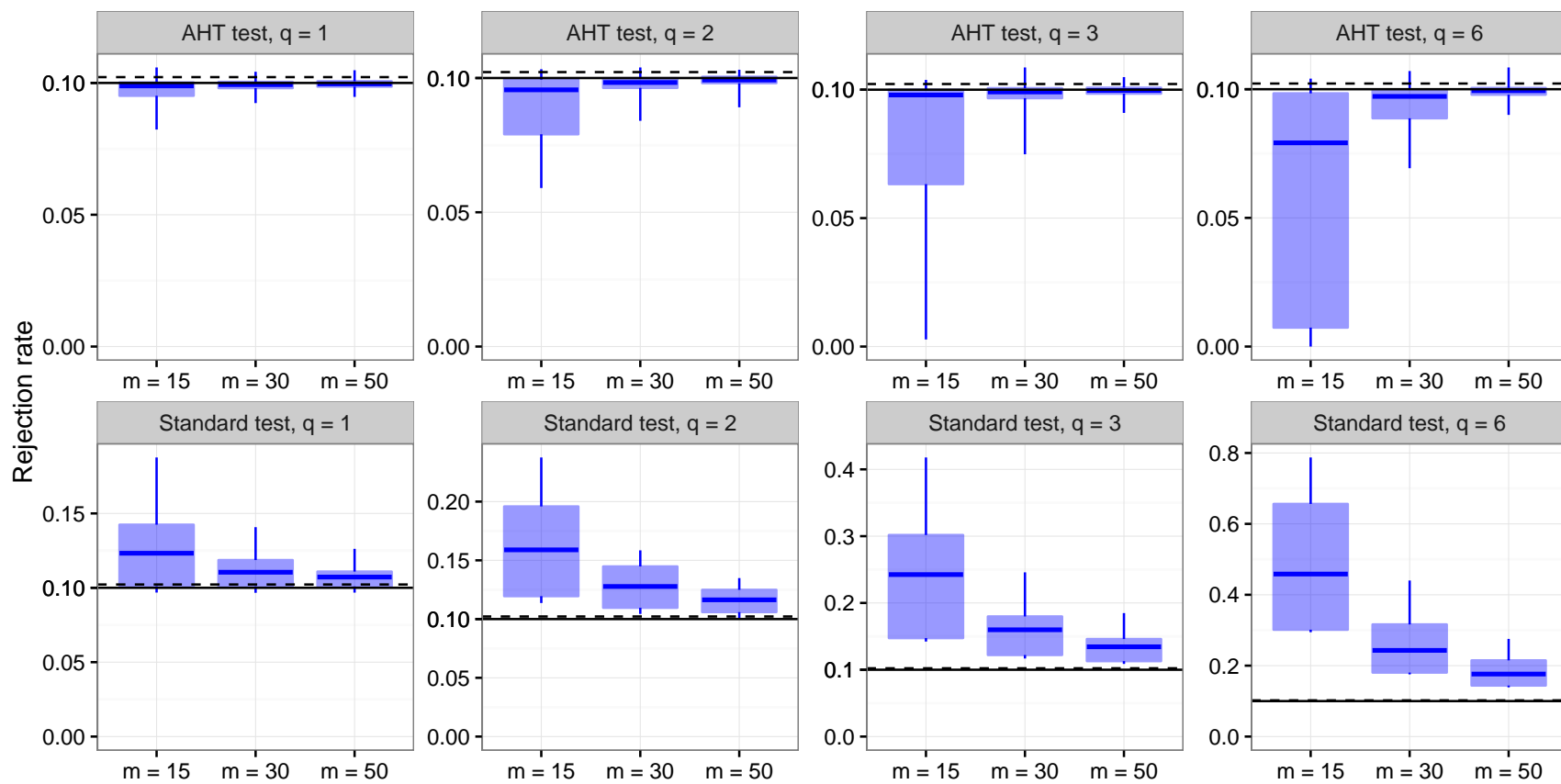


Figure S3: Rejection rates of AHT and standard tests for $\alpha = .10$, by dimension of hypothesis (q) and sample size (m).

S4.2 Rejection rates of AHT and standard tests by study design

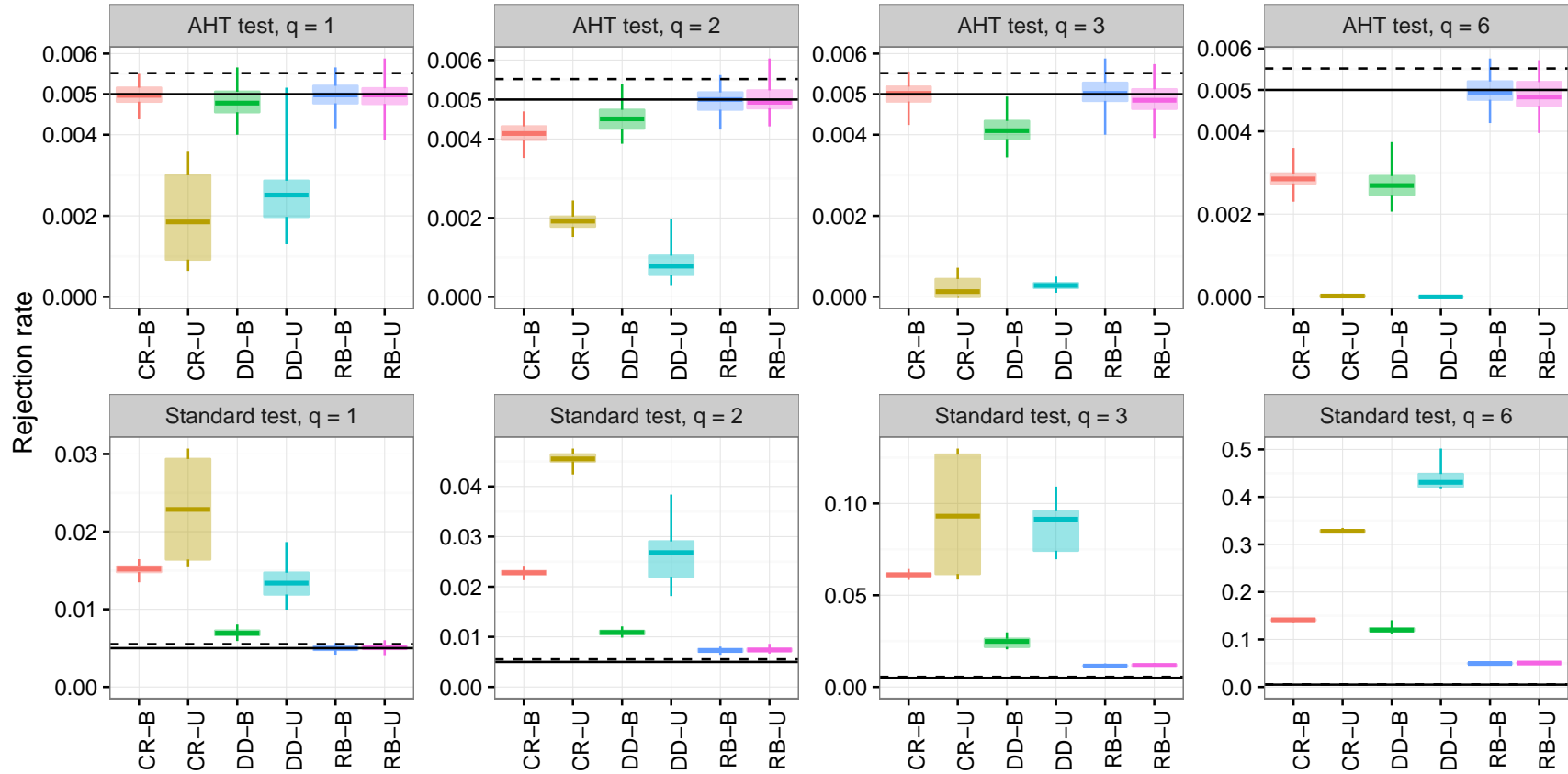


Figure S4: Rejection rates of AHT and standard tests, by study design and dimension of hypothesis (q) for $\alpha = .005$ and $m = 15$. CR = cluster-randomized design; DD = difference-in-differences design; RB = randomized block design; B = balanced; U = unbalanced.

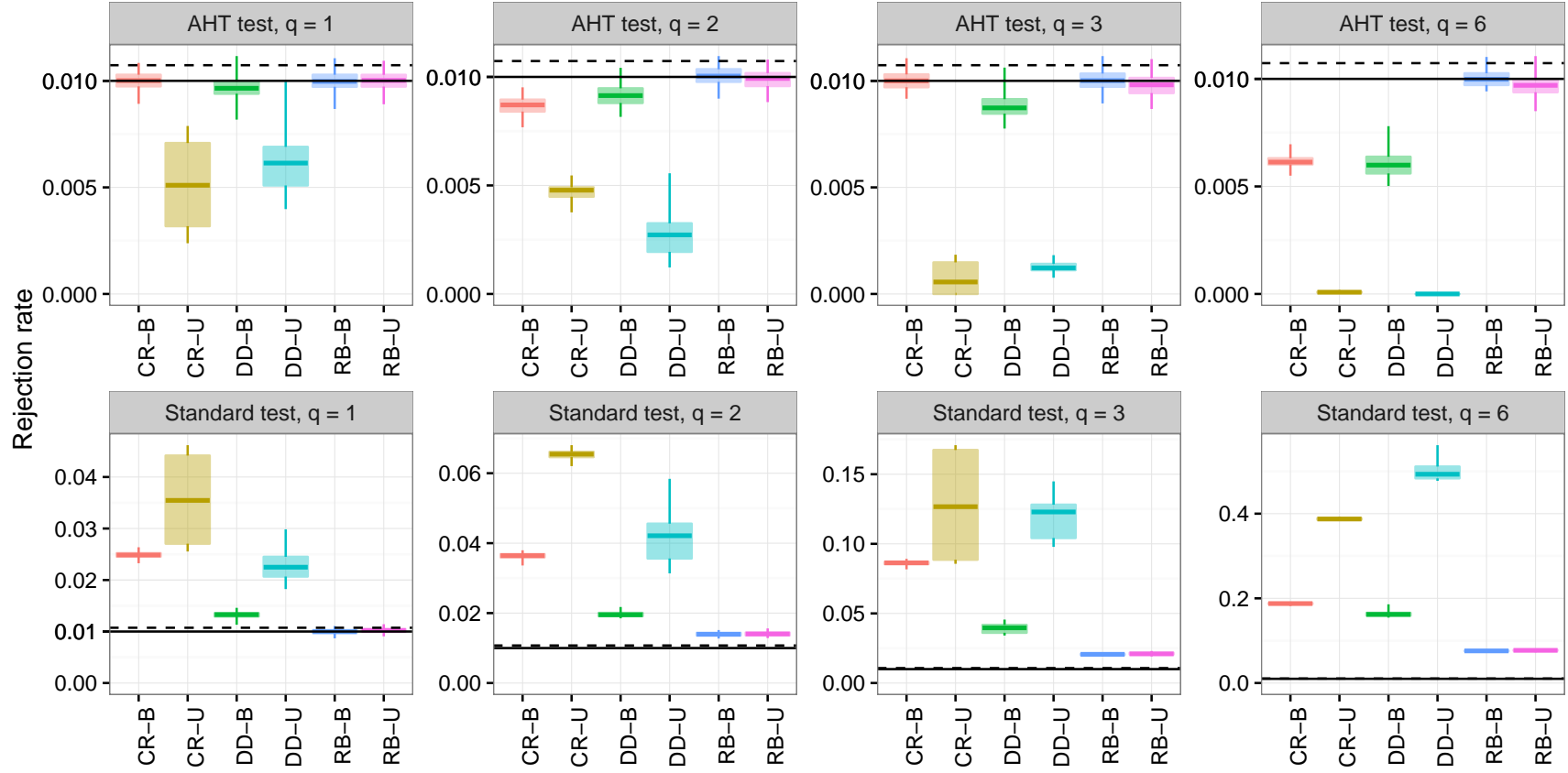


Figure S5: Rejection rates of AHT and standard tests, by study design and dimension of hypothesis (q) for $\alpha = .01$ and $m = 15$. CR = cluster-randomized design; DD = difference-in-differences design; RB = randomized block design; B = balanced; U = unbalanced.

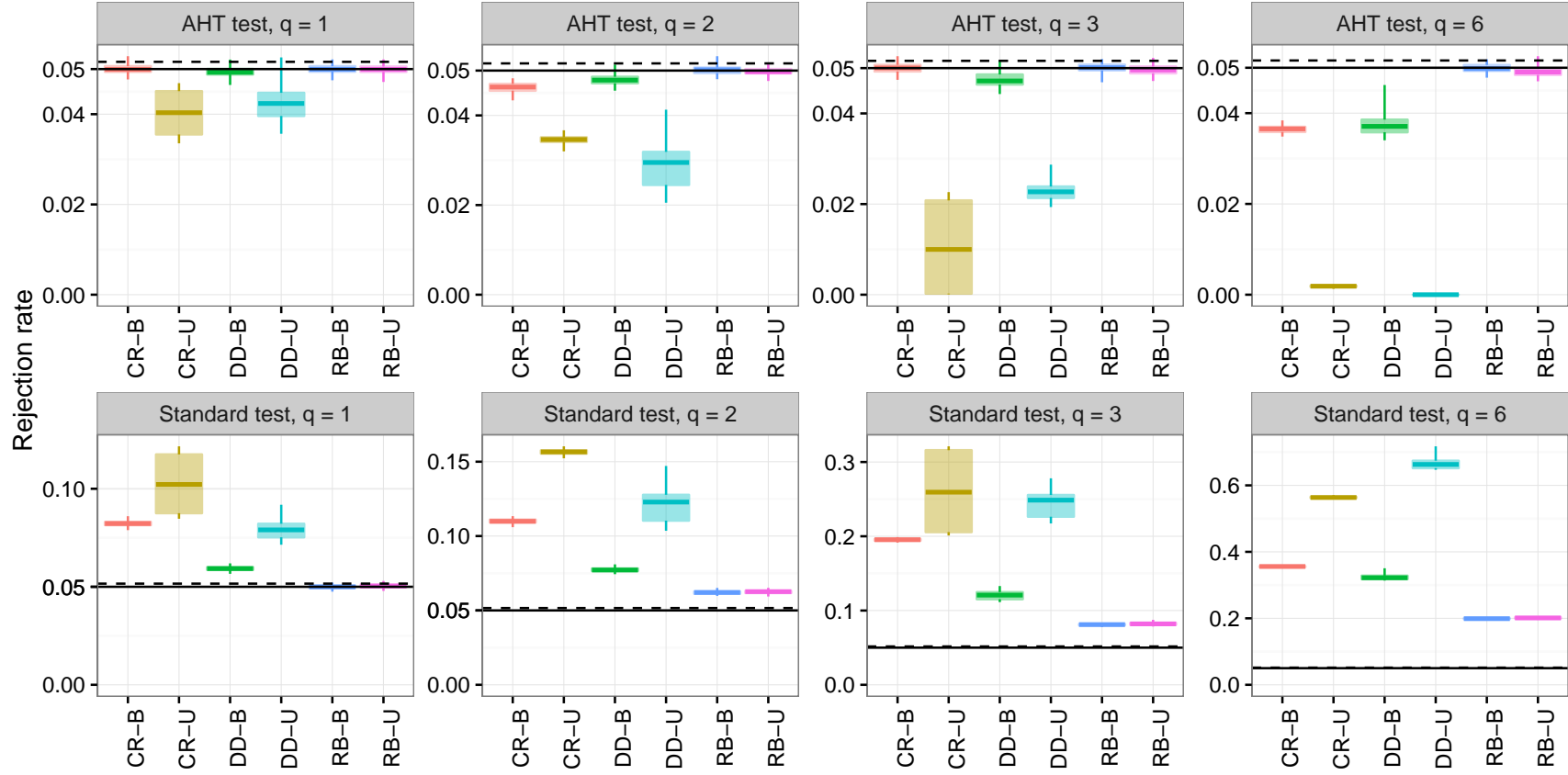


Figure S6: Rejection rates of AHT and standard tests, by study design and dimension of hypothesis (q) for $\alpha = .05$ and $m = 15$. CR = cluster-randomized design; DD = difference-in-differences design; RB = randomized block design; B = balanced; U = unbalanced.

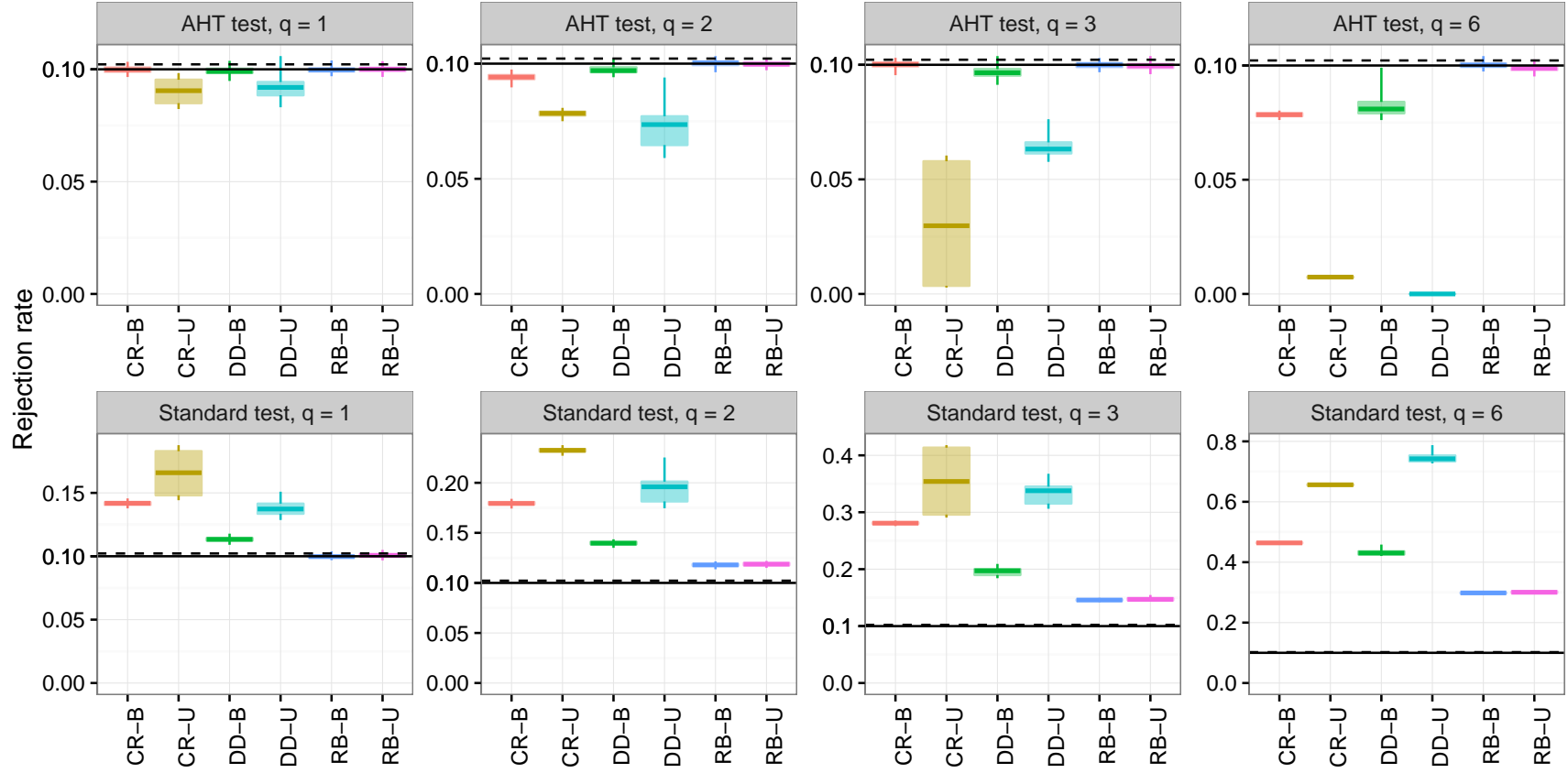


Figure S7: Rejection rates of AHT and standard tests, by study design and dimension of hypothesis (q) for $\alpha = .10$ and $m = 15$. CR = cluster-randomized design; DD = difference-in-differences design; RB = randomized block design; B = balanced; U = unbalanced.

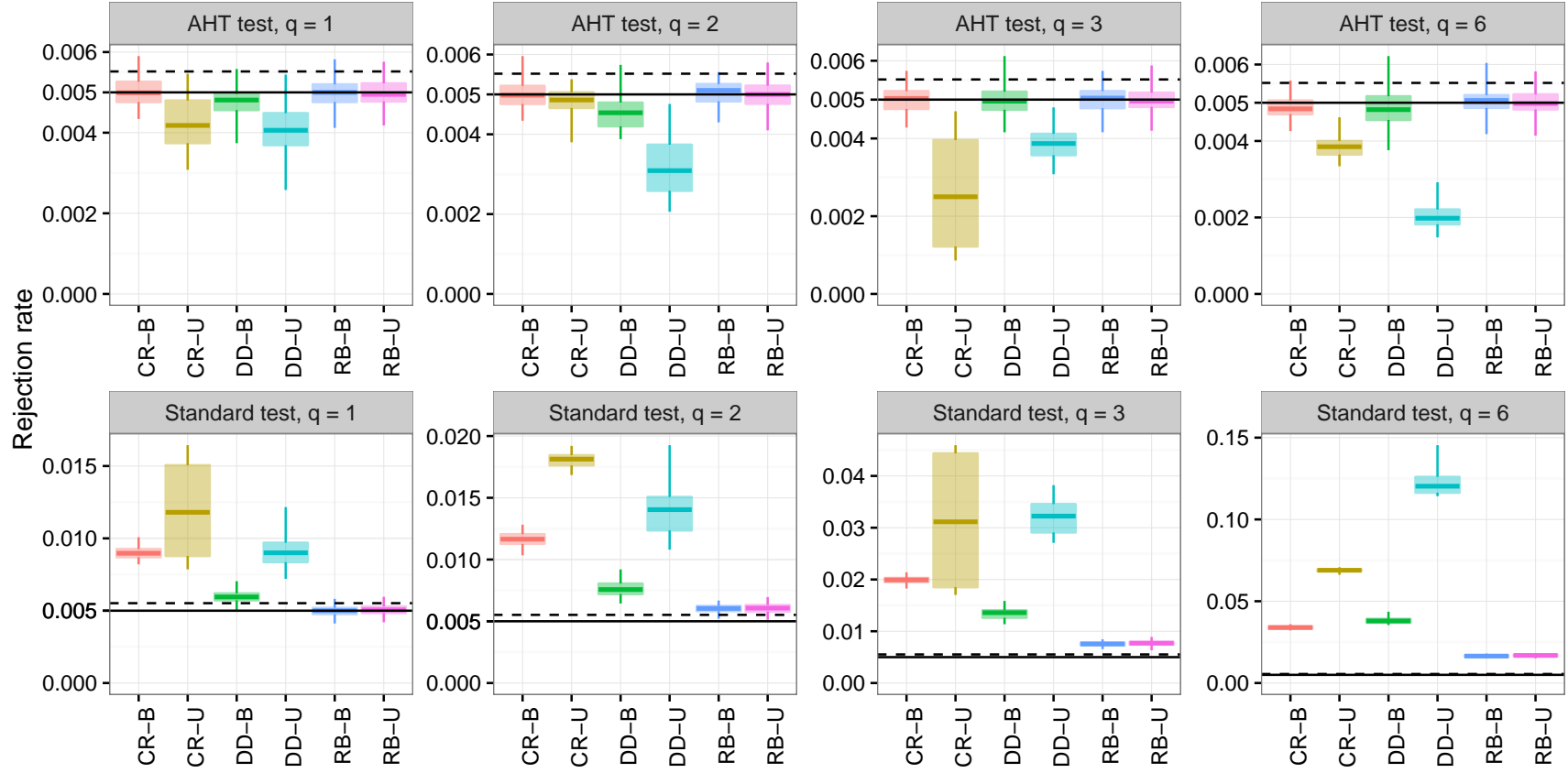


Figure S8: Rejection rates of AHT and standard tests, by study design and dimension of hypothesis (q) for $\alpha = .005$ and $m = 30$. CR = cluster-randomized design; DD = difference-in-differences design; RB = randomized block design; B = balanced; U = unbalanced.

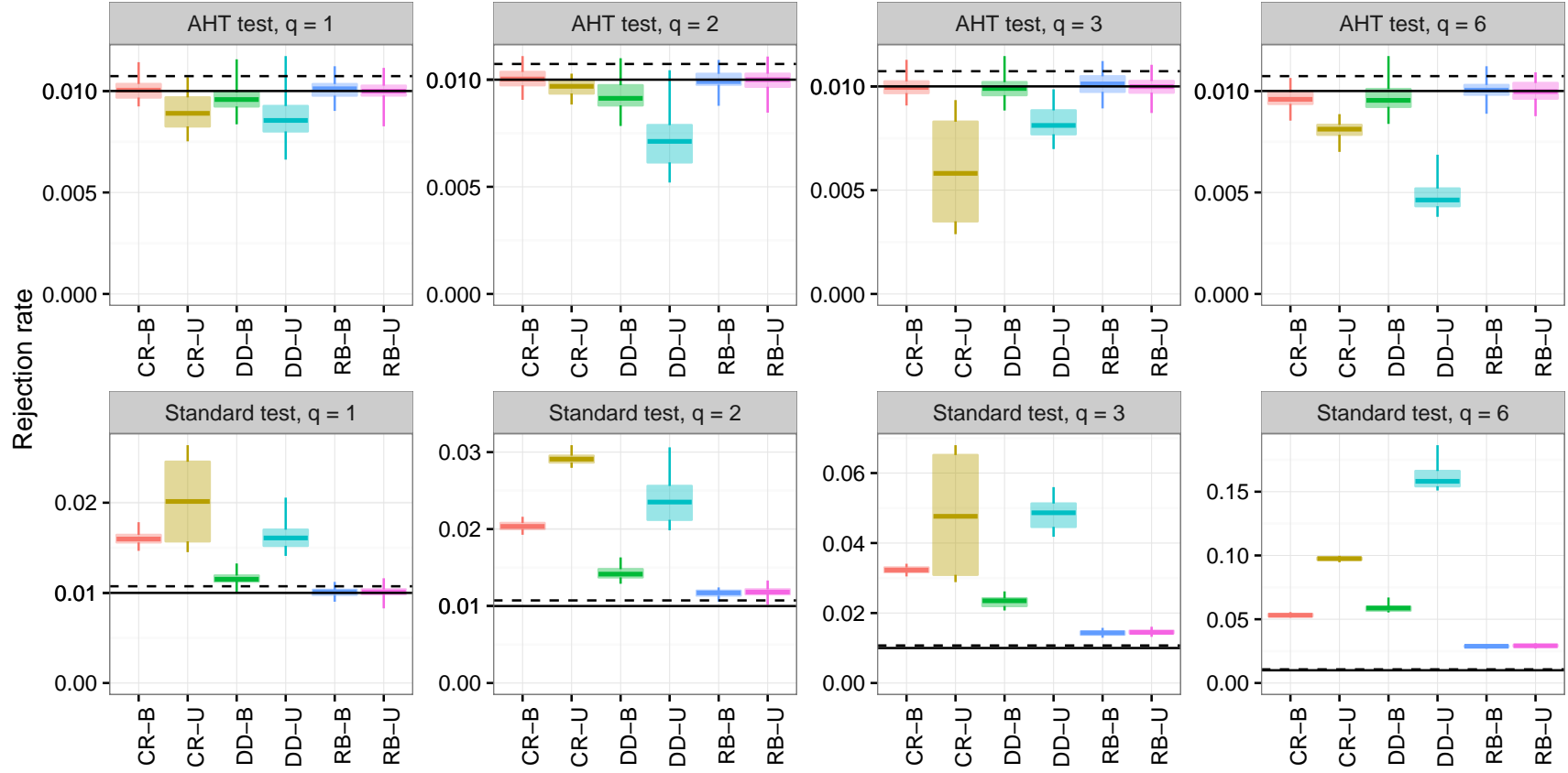


Figure S9: Rejection rates of AHT and standard tests, by study design and dimension of hypothesis (q) for $\alpha = .01$ and $m = 30$. CR = cluster-randomized design; DD = difference-in-differences design; RB = randomized block design; B = balanced; U = unbalanced.

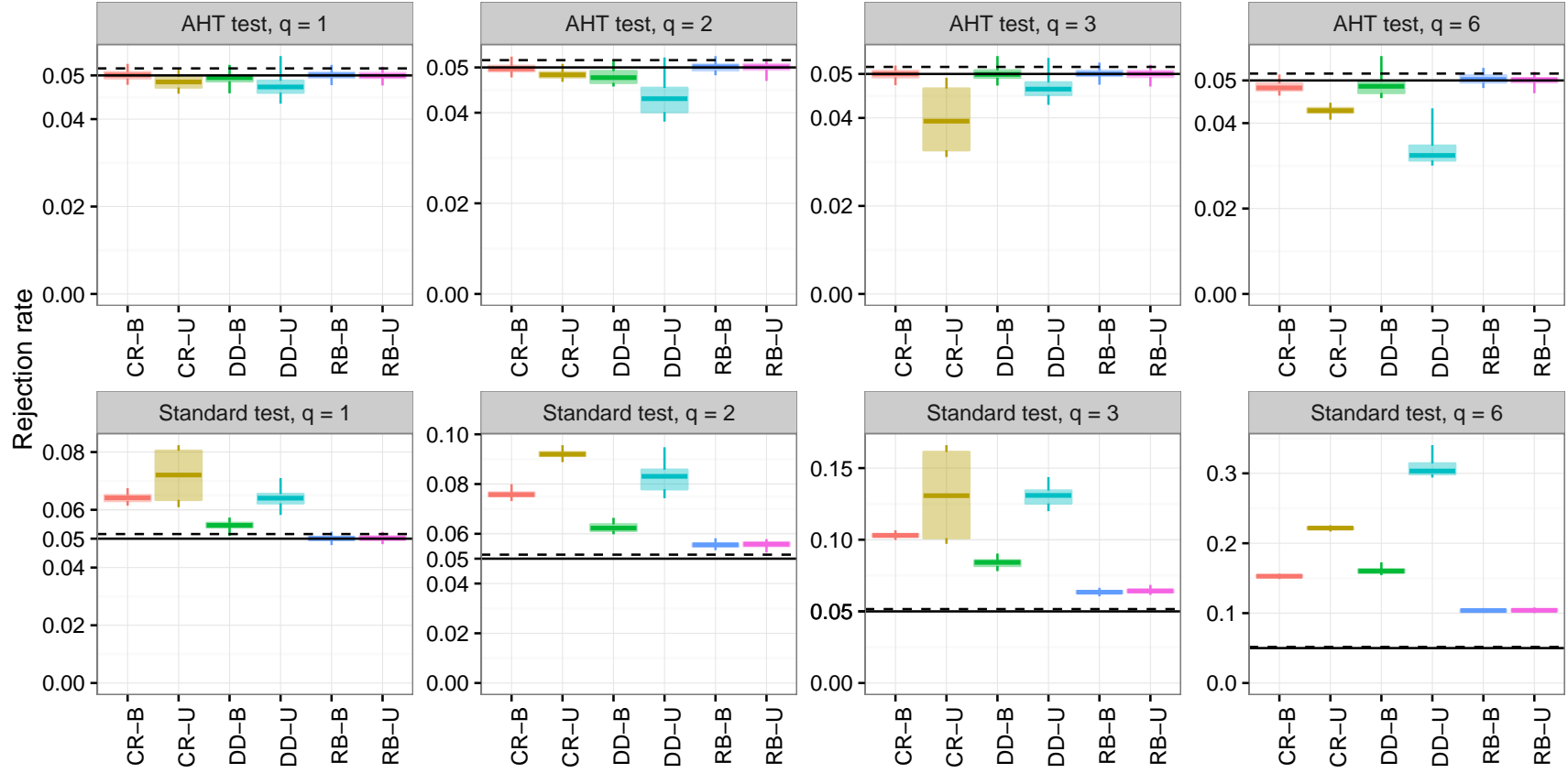


Figure S10: Rejection rates of AHT and standard tests, by study design and dimension of hypothesis (q) for $\alpha = .05$ and $m = 30$. CR = cluster-randomized design; DD = difference-in-differences design; RB = randomized block design; B = balanced; U = unbalanced.

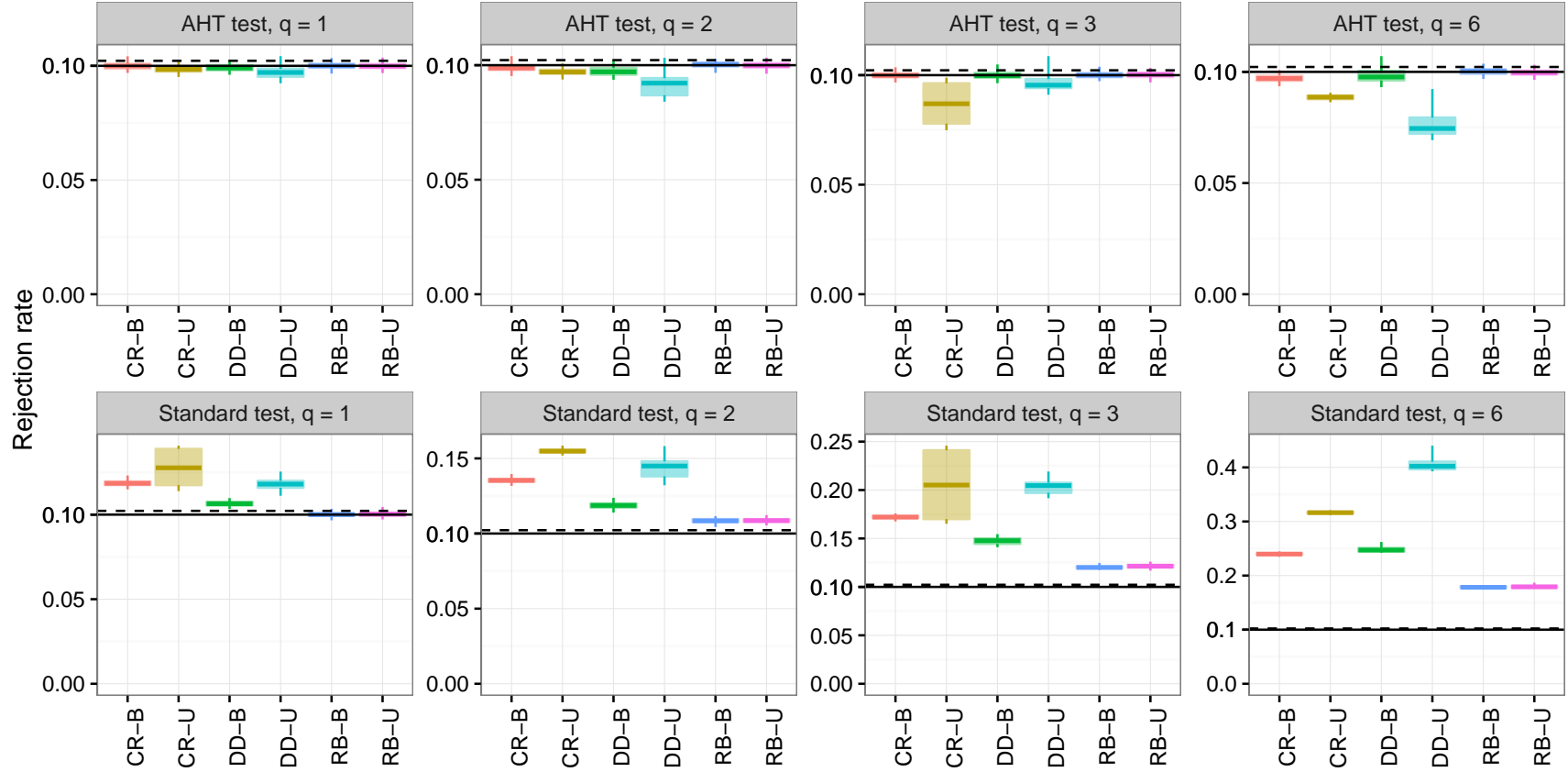


Figure S11: Rejection rates of AHT and standard tests, by study design and dimension of hypothesis (q) for $\alpha = .10$ and $m = 30$. CR = cluster-randomized design; DD = difference-in-differences design; RB = randomized block design; B = balanced; U = unbalanced.

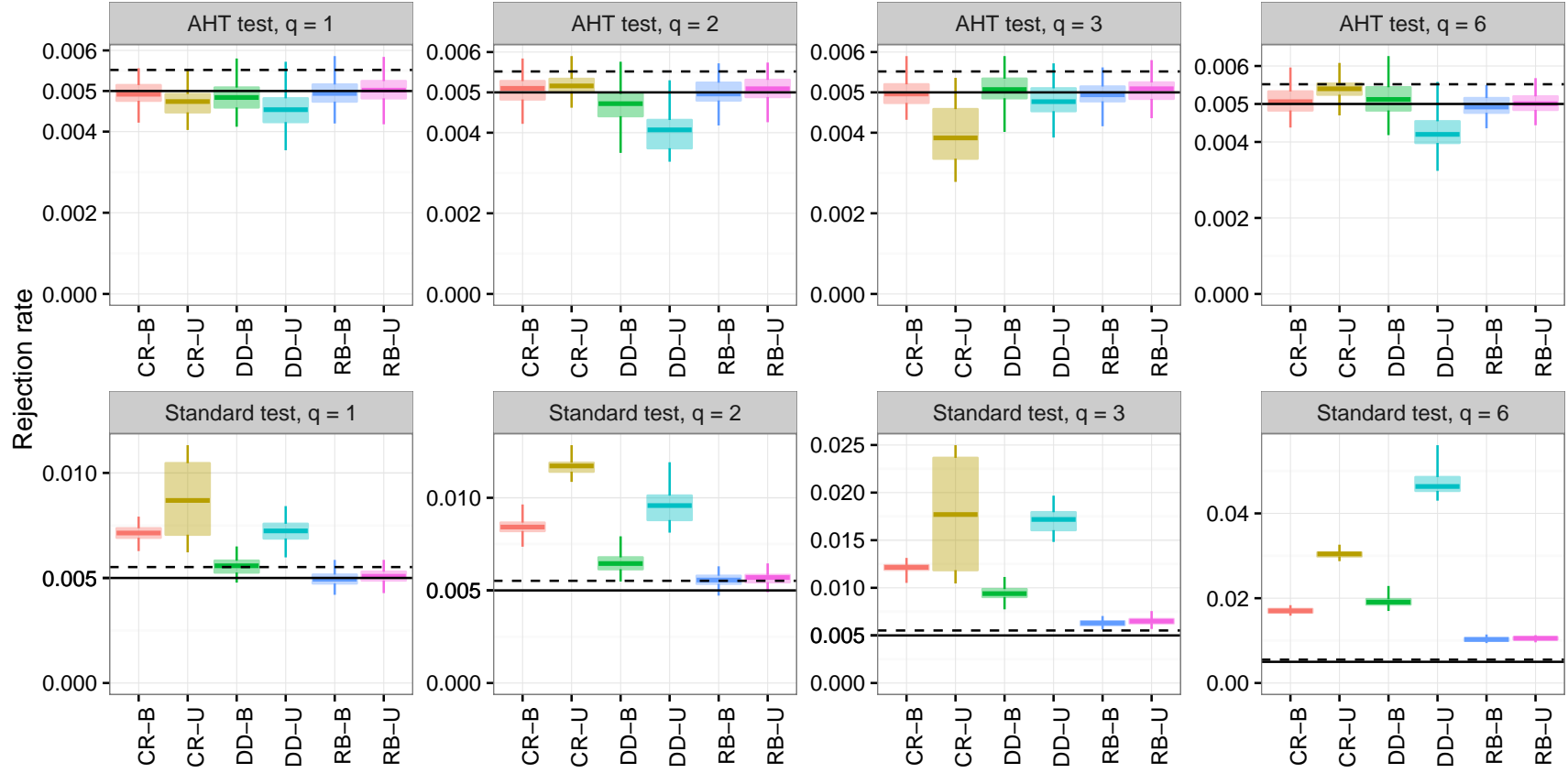


Figure S12: Rejection rates of AHT and standard tests, by study design and dimension of hypothesis (q) for $\alpha = .005$ and $m = 50$. CR = cluster-randomized design; DD = difference-in-differences design; RB = randomized block design; B = balanced; U = unbalanced.

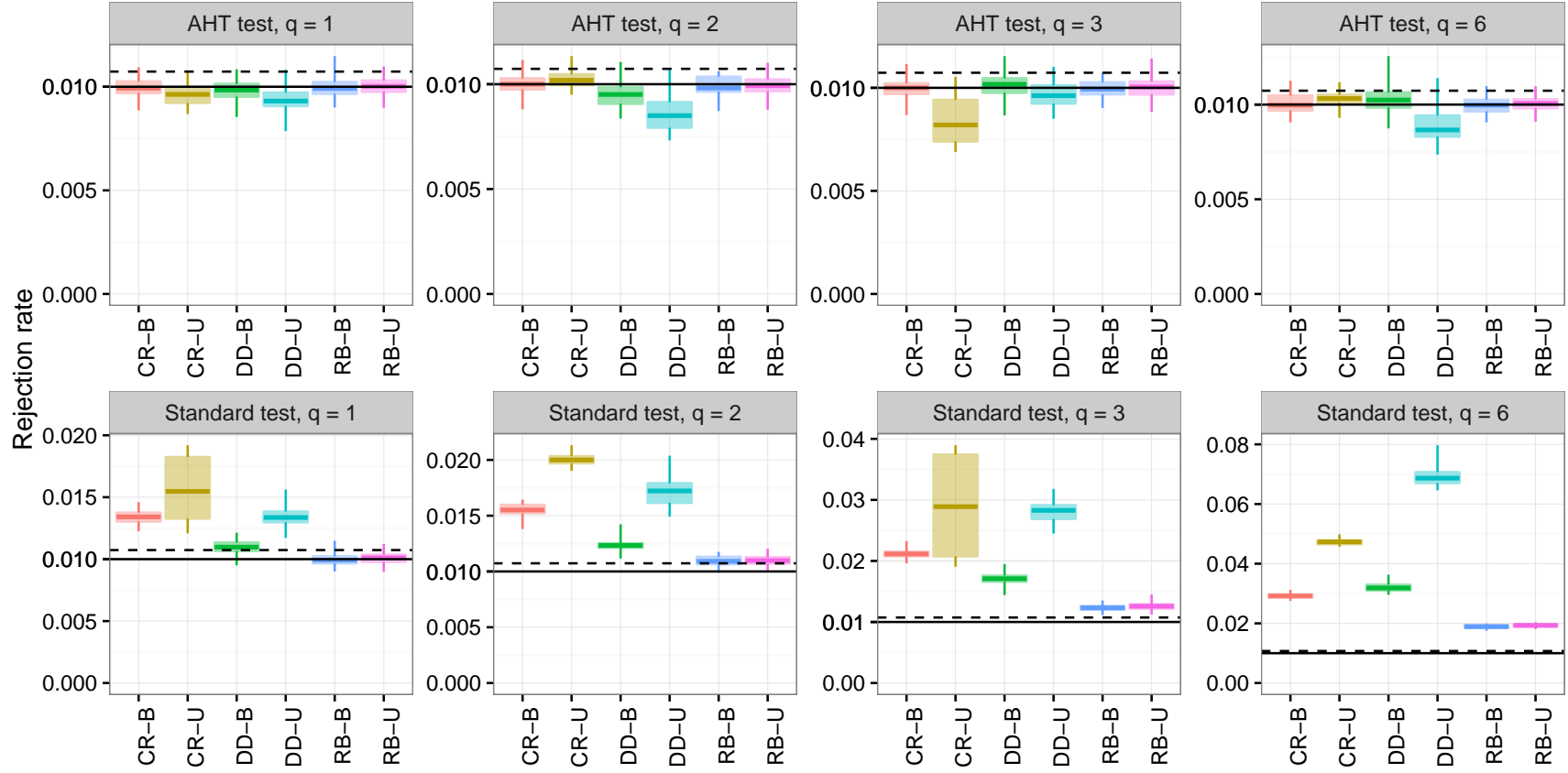


Figure S13: Rejection rates of AHT and standard tests, by study design and dimension of hypothesis (q) for $\alpha = .01$ and $m = 50$. CR = cluster-randomized design; DD = difference-in-differences design; RB = randomized block design; B = balanced; U = unbalanced.

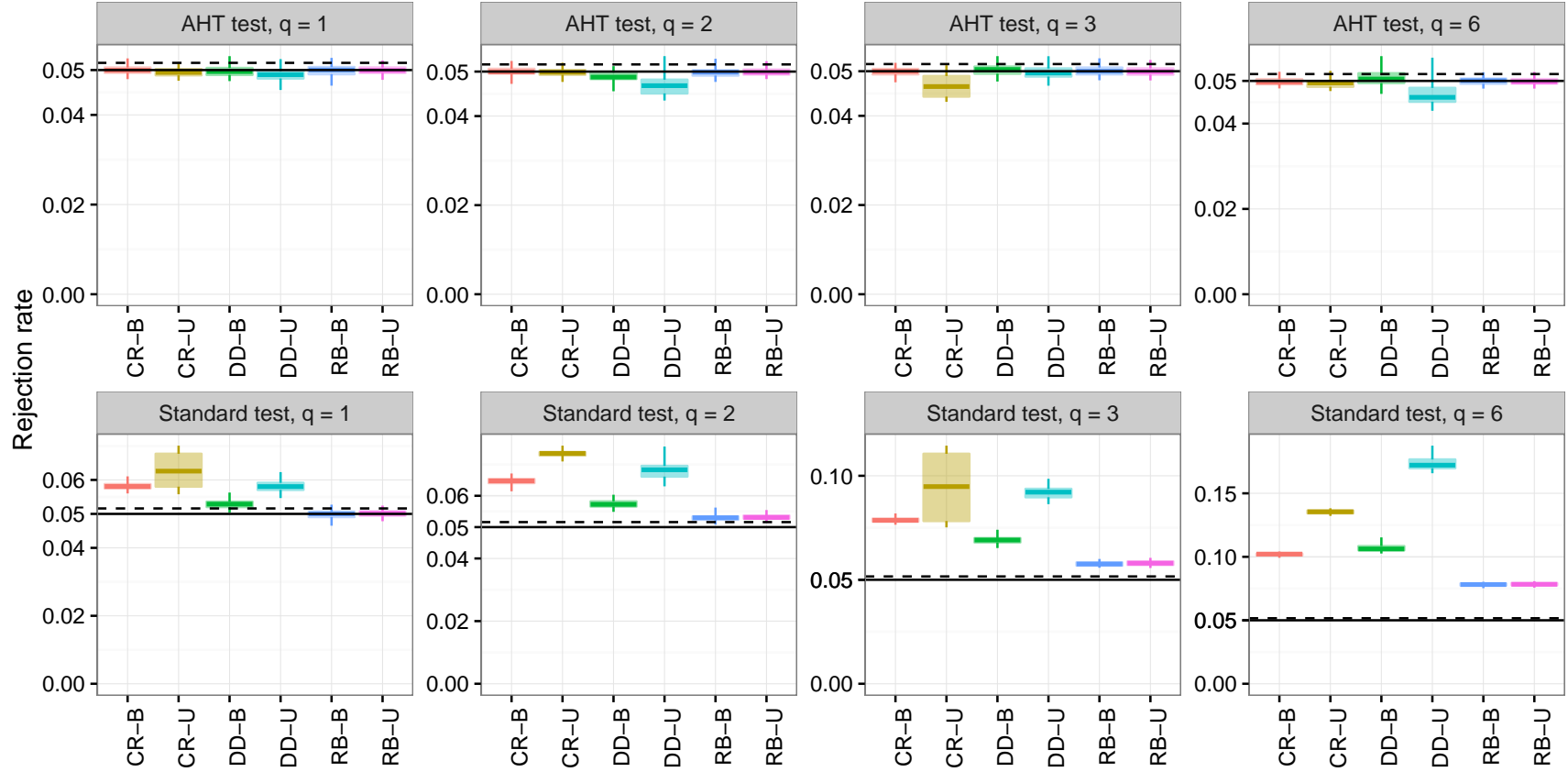


Figure S14: Rejection rates of AHT and standard tests, by study design and dimension of hypothesis (q) for $\alpha = .05$ and $m = 50$. CR = cluster-randomized design; DD = difference-in-differences design; RB = randomized block design; B = balanced; U = unbalanced.

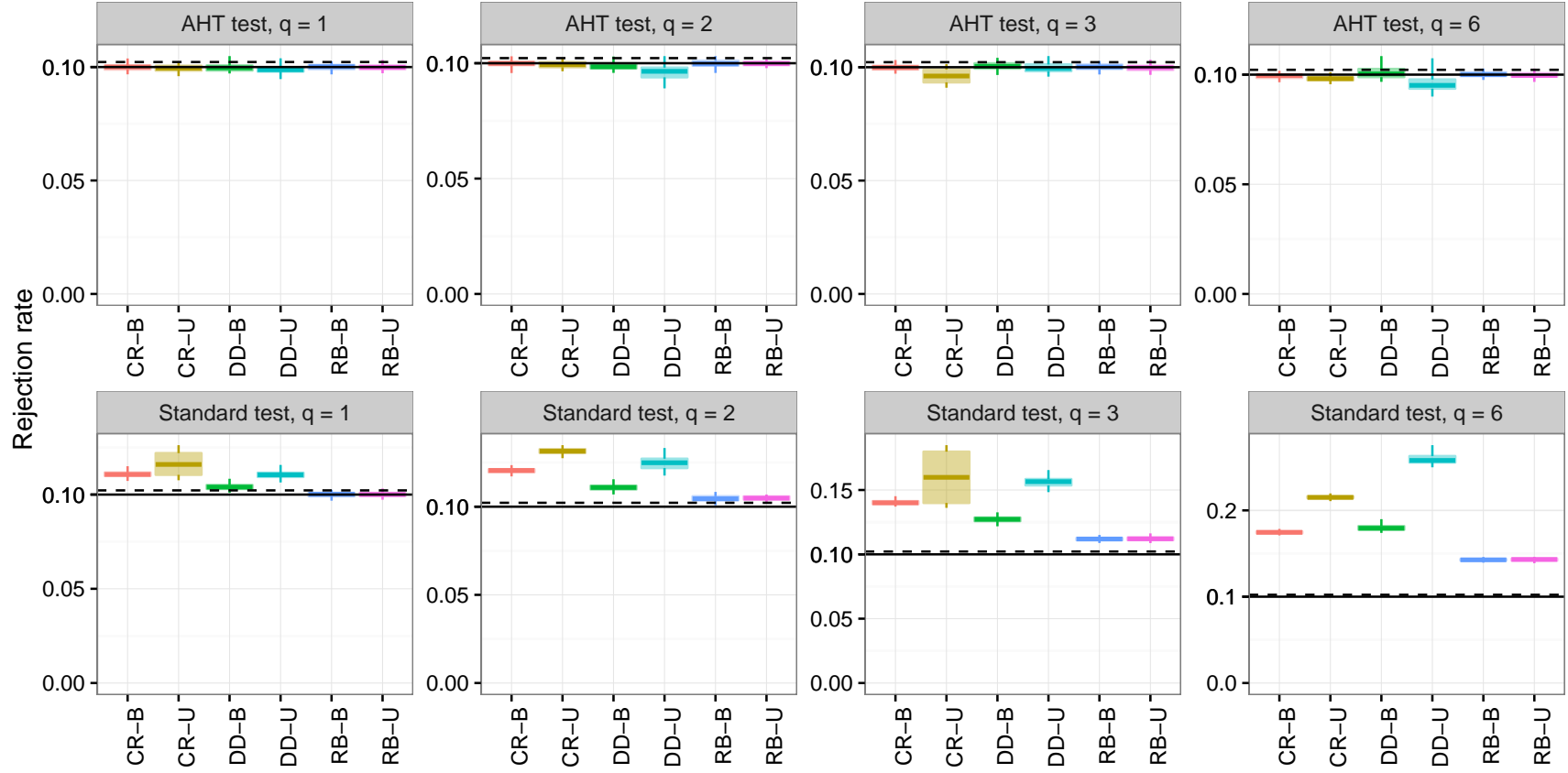


Figure S15: Rejection rates of AHT and standard tests, by study design and dimension of hypothesis (q) for $\alpha = .10$ and $m = 50$. CR = cluster-randomized design; DD = difference-in-differences design; RB = randomized block design; B = balanced; U = unbalanced.

S4.3 Rejection rates of AHT test using CR1 or CR2, with and without accounting for absorption

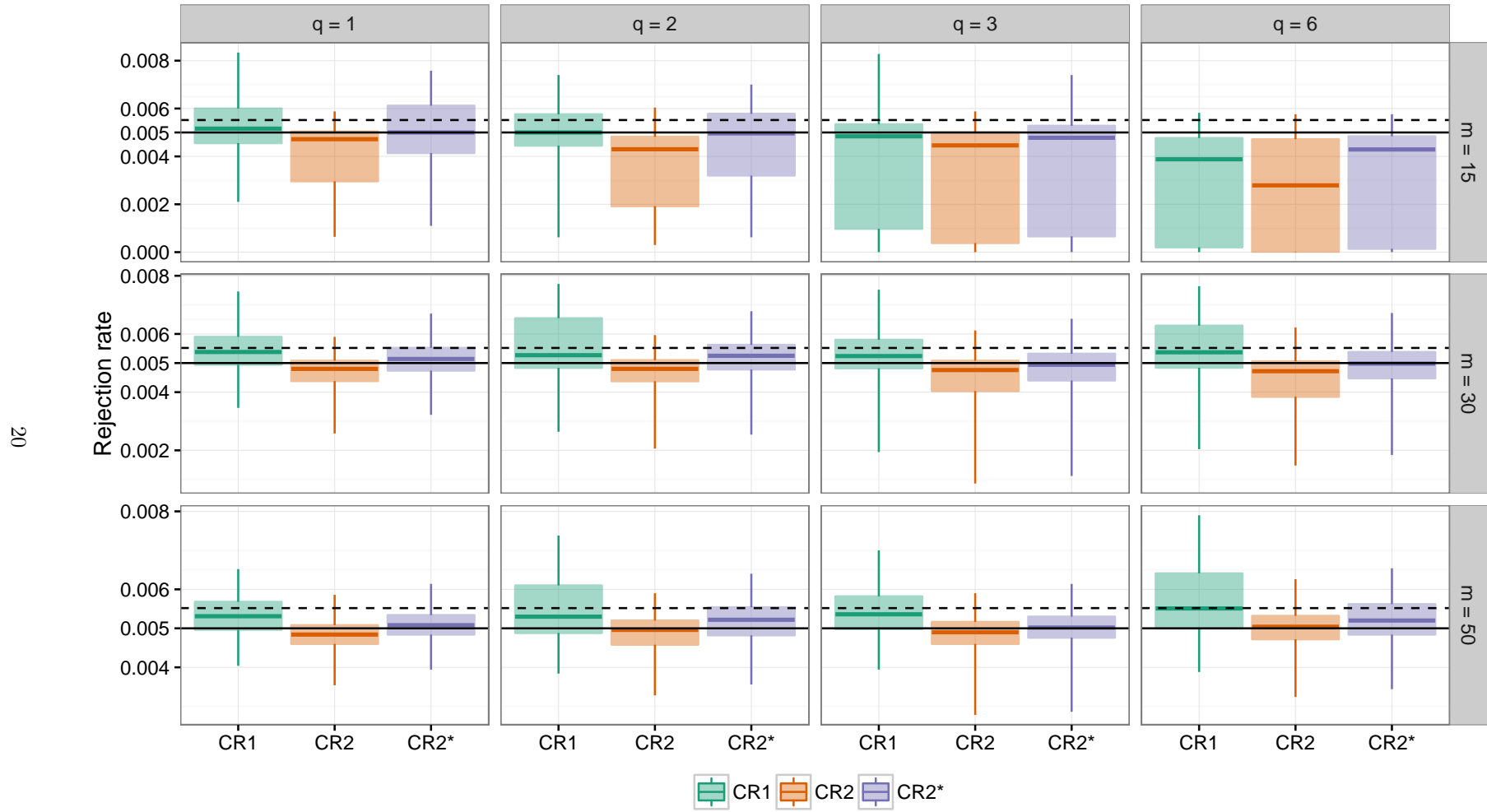


Figure S16: Rejection rates of AHT tests using CR1, CR2, or CR2 calculated without accounting for absorption of fixed effects (CR2*), by sample size (m) and dimension of hypothesis (q), for $\alpha = .005$.

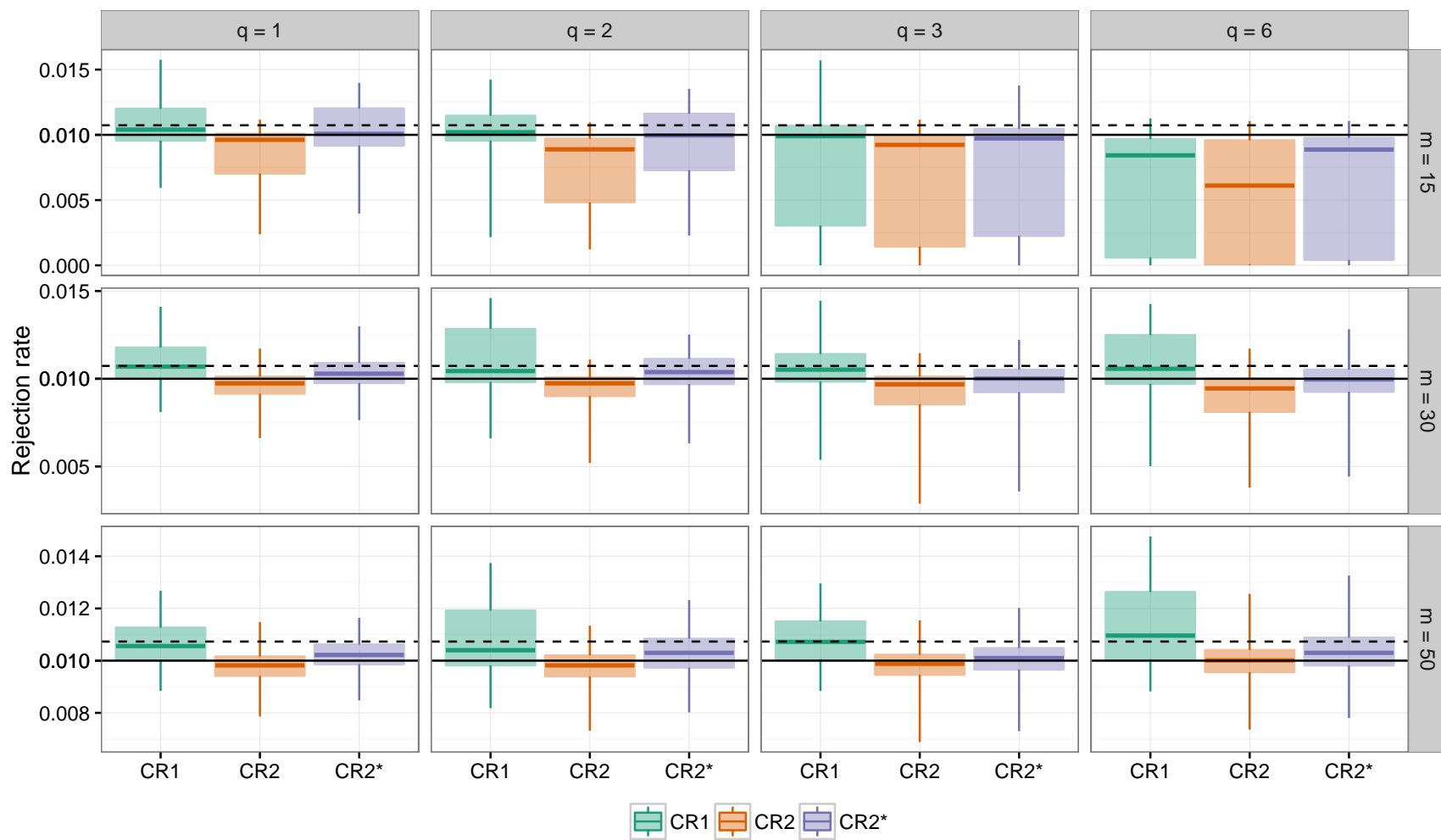


Figure S17: Rejection rates of AHT tests using CR1, CR2, or CR2 calculated without accounting for absorption of fixed effects (CR2*), by sample size (m) and dimension of hypothesis (q), for $\alpha = .01$.

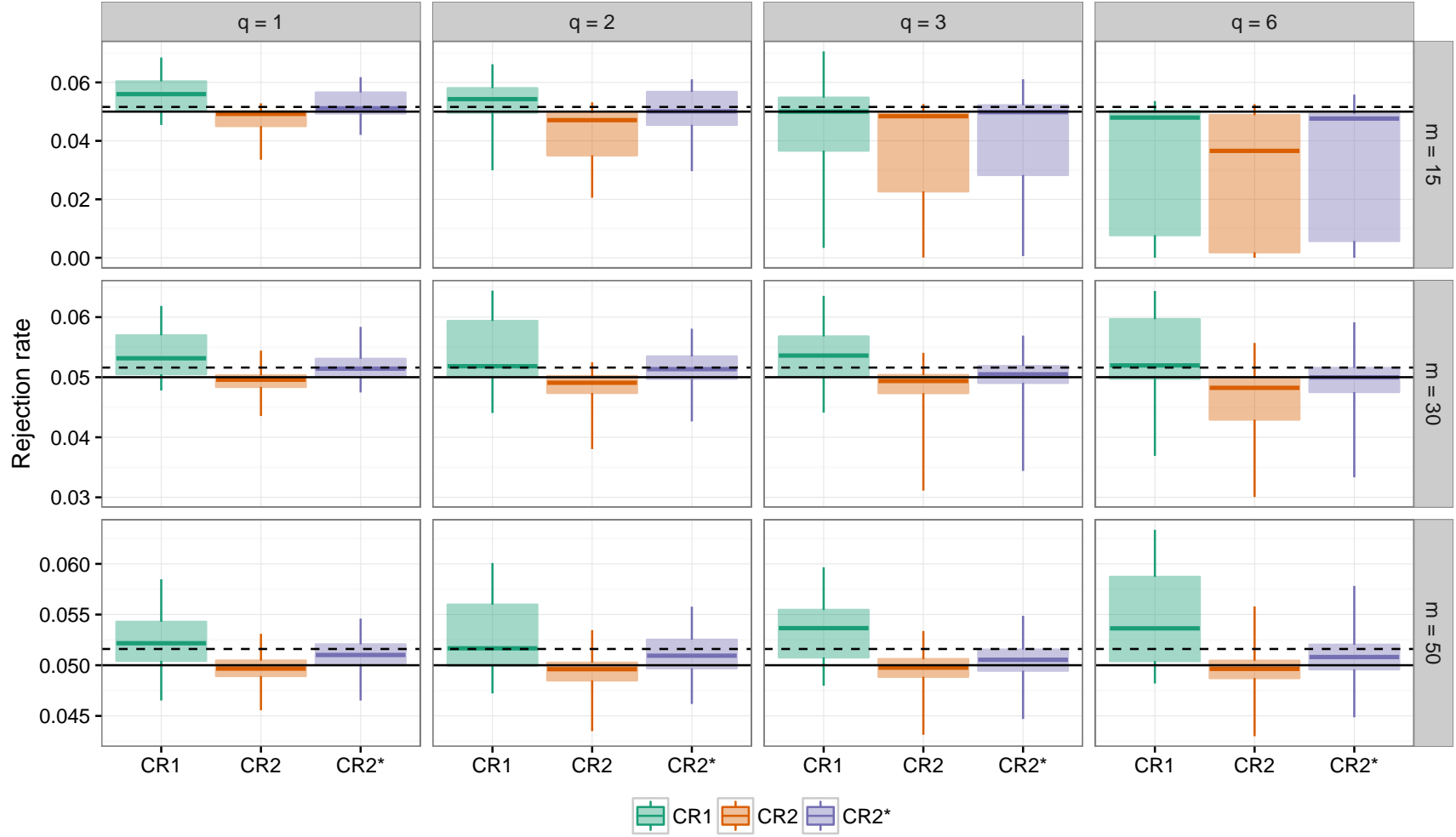


Figure S18: Rejection rates of AHT tests using CR1, CR2, or CR2 calculated without accounting for absorption of fixed effects (CR2*), by sample size (m) and dimension of hypothesis (q), for $\alpha = .05$.

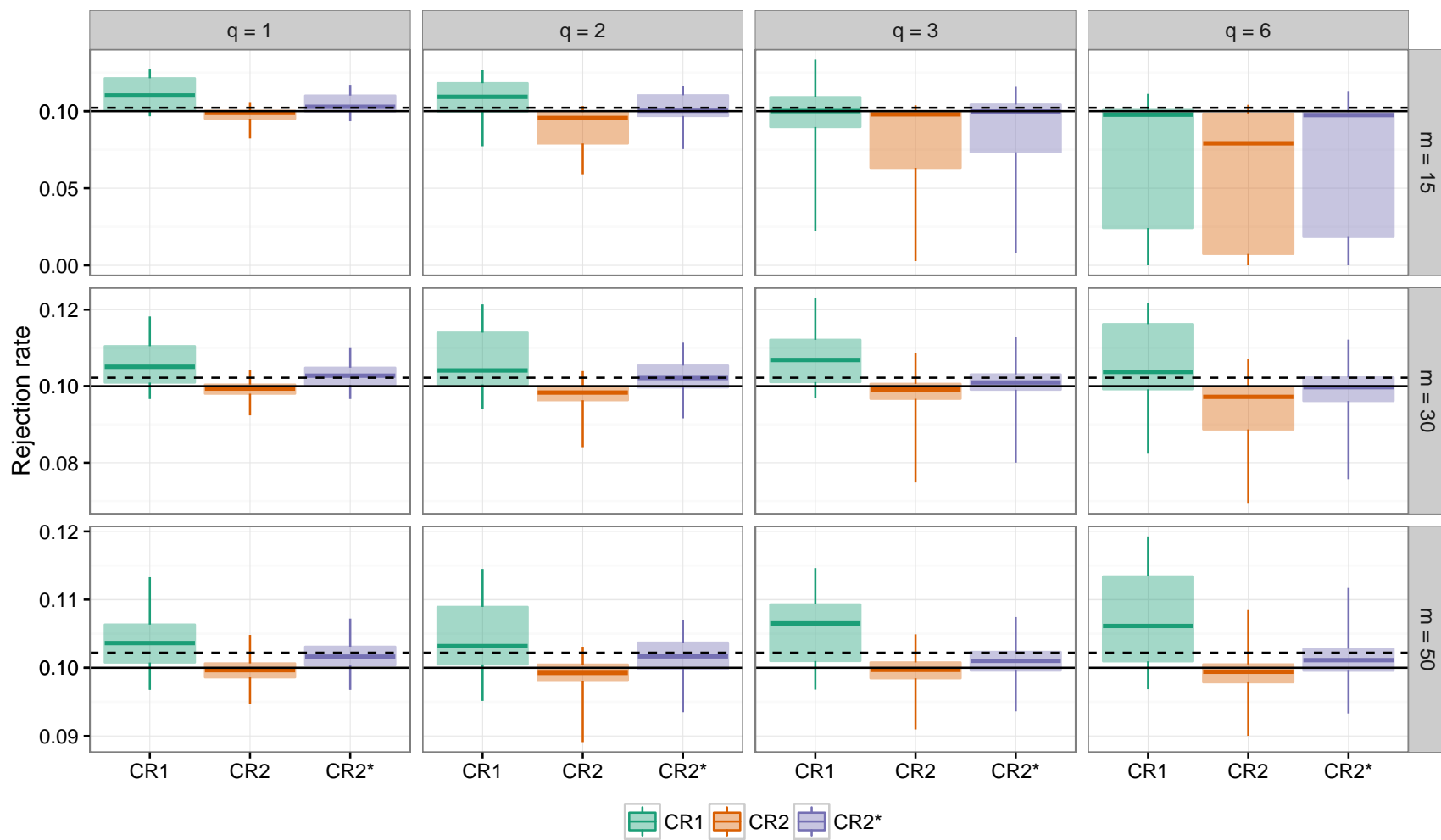


Figure S19: Rejection rates of AHT tests using CR1, CR2, or CR2 calculated without accounting for absorption of fixed effects (CR2*), by sample size (m) and dimension of hypothesis (q), for $\alpha = .10$.

S4.4 Rejection rates of AHT test by degree of working model misspecification

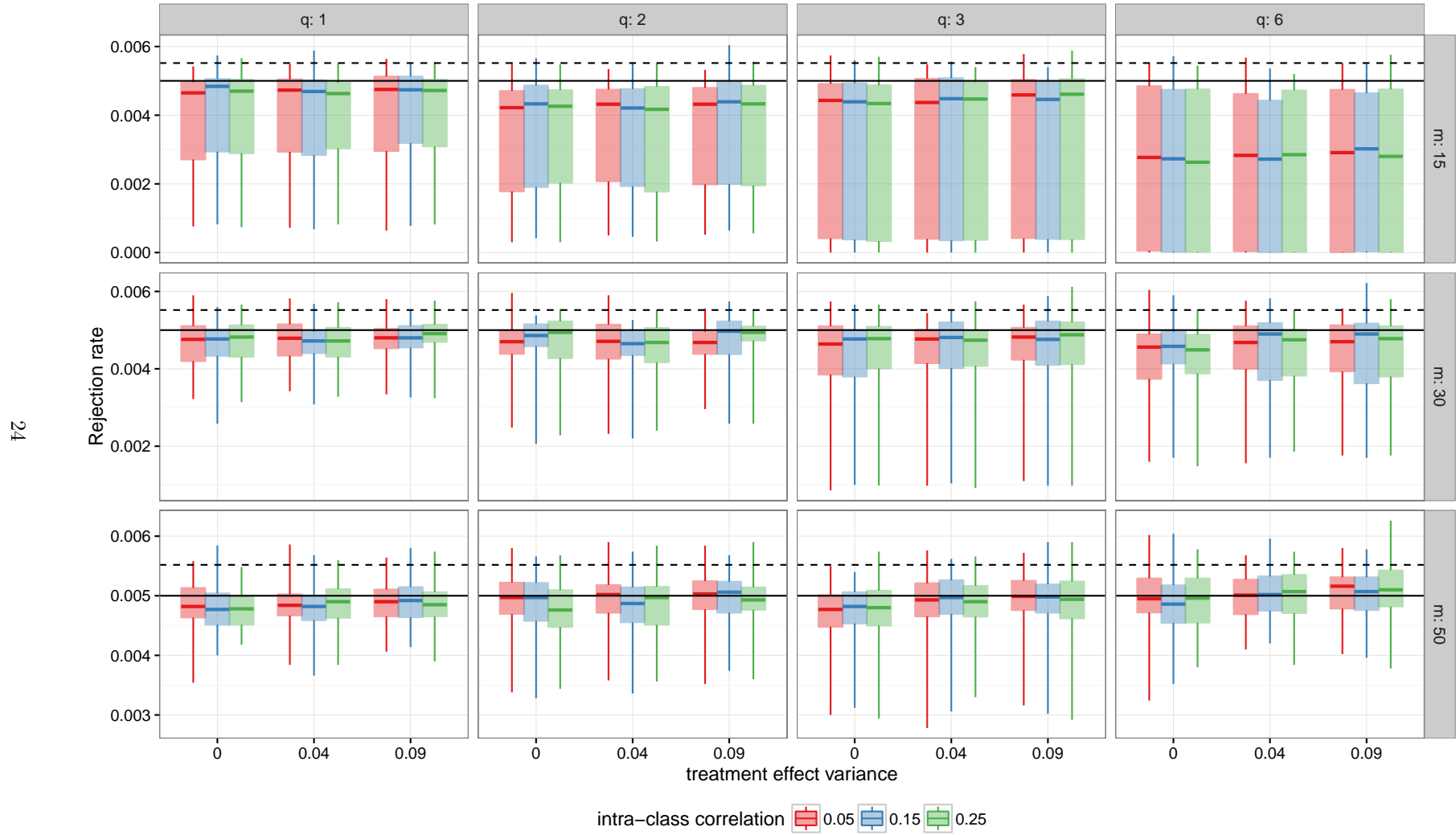


Figure S20: Rejection rates of CR2 AHT test, by treatment effect variance and intra-class correlation for $\alpha = .005$.

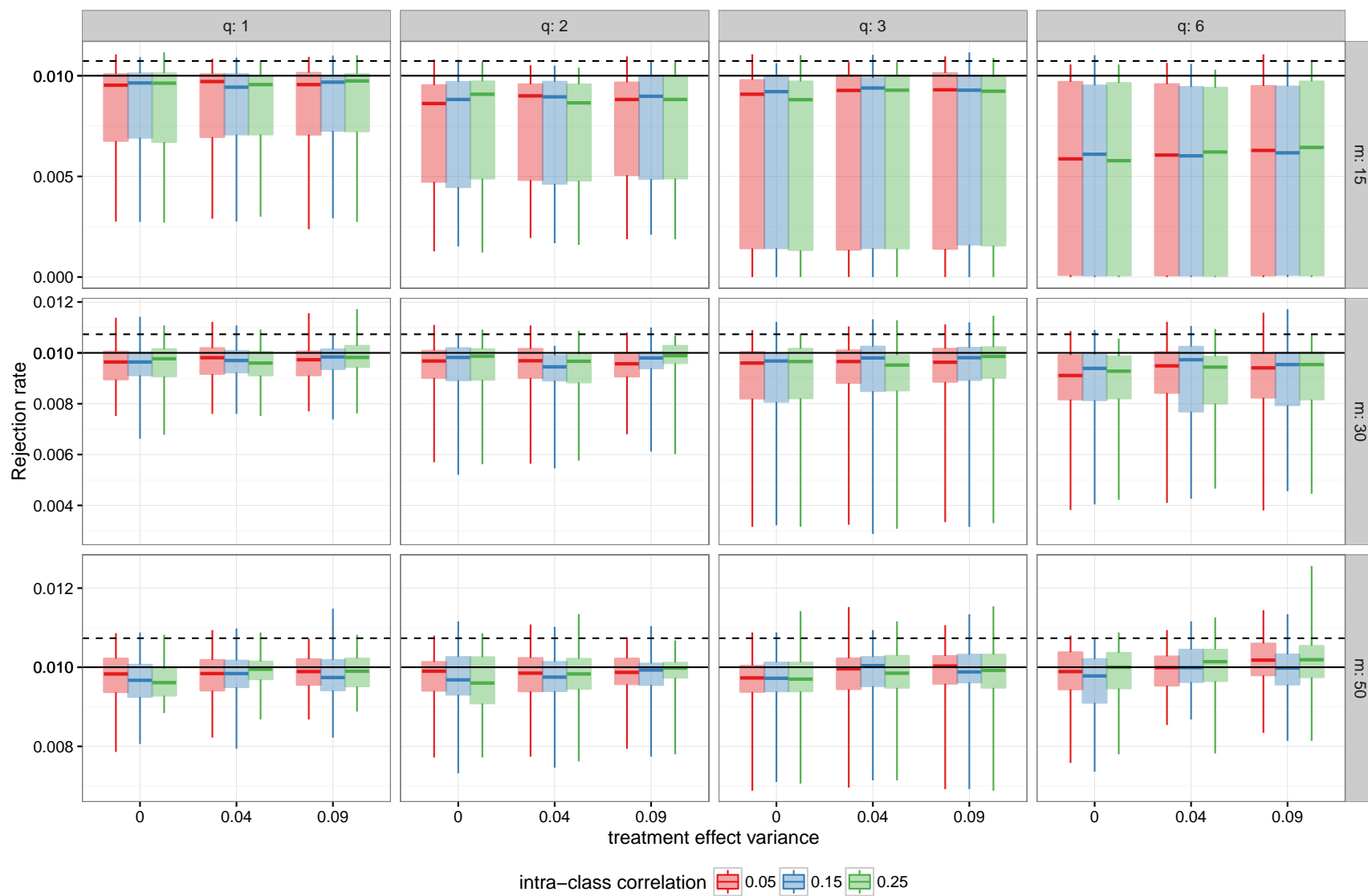


Figure S21: Rejection rates of CR2 AHT test, by treatment effect variance and intra-class correlation for $\alpha = .01$.

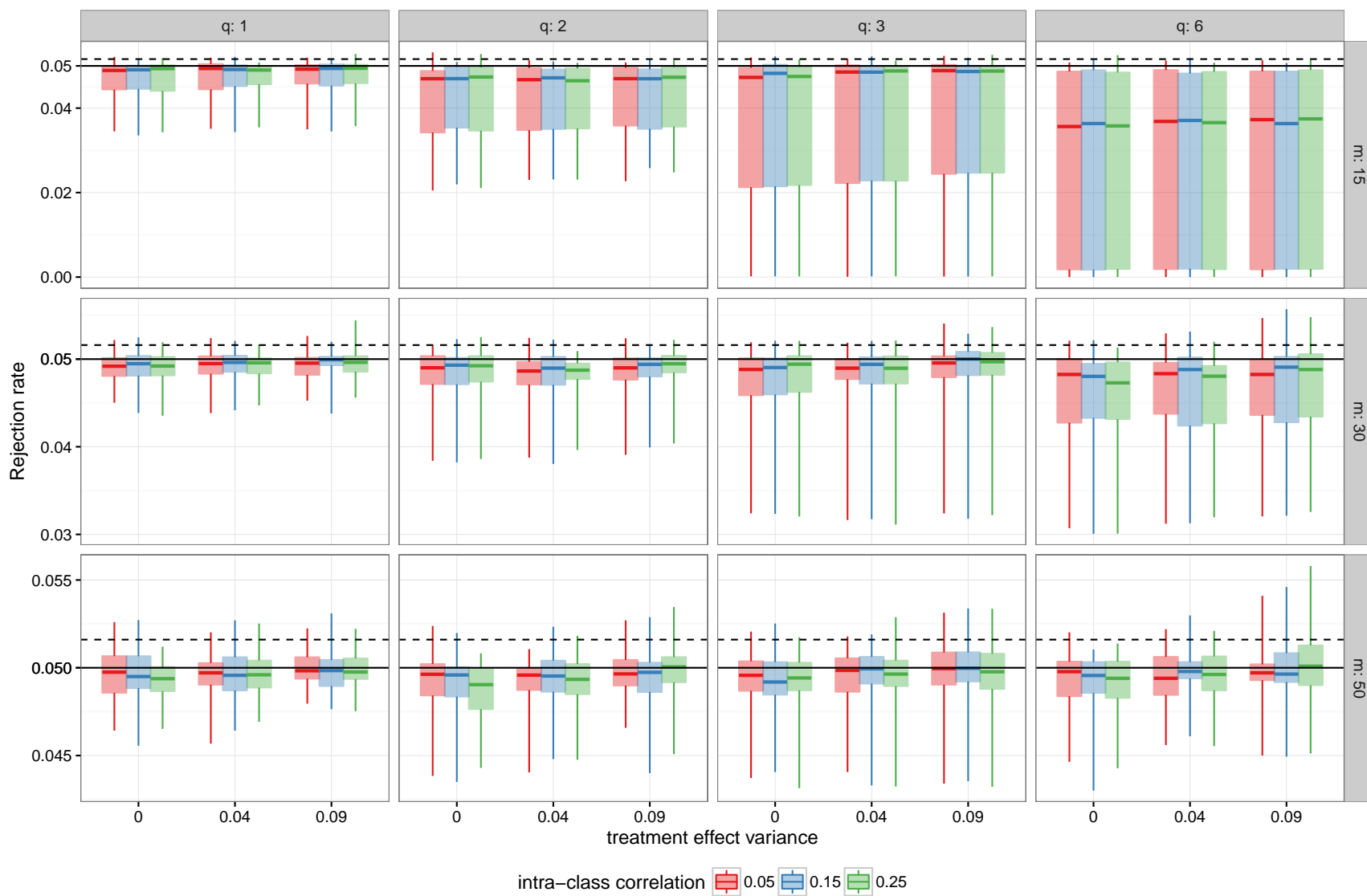


Figure S22: Rejection rates of CR2 AHT test, by treatment effect variance and intra-class correlation for $\alpha = .05$.

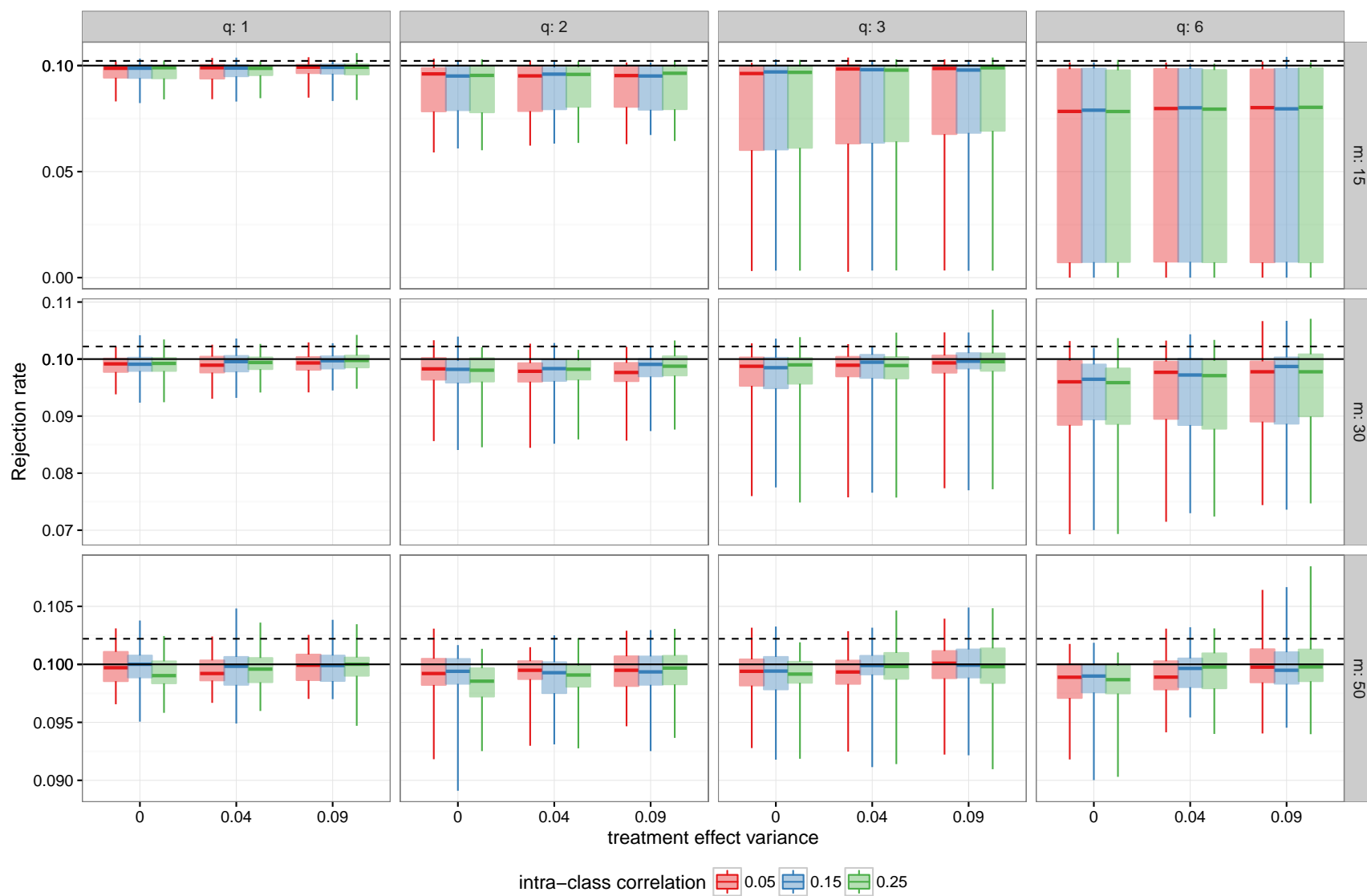


Figure S23: Rejection rates of CR2 AHT test, by treatment effect variance and intra-class correlation for $\alpha = .10$.

References

Henderson, H. V. and Searle, S. R. (1981), ‘On deriving the inverse of a sum of matrices’, *Siam Review* **23**(1), 53–60.