

Simulation results for PCEV

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A Session Information

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Introduction

We simulated 1000 datasets of size $n = 500$. The general model is given by the following multivariate linear model:

$$\mathbf{Y} = \beta X + \mathbf{E},$$

where \mathbf{Y} is of dimension p , $X \sim N(0, 1)$ and $\mathbf{E} \sim N(0, \Sigma)$. The goal of the simulations is to compare three different approaches to a multivariate association test between \mathbf{Y} and X .

- Univariate approach: a p-value \mathfrak{p}_j is computed for the association between Y_j and X , for $j = 1, \dots, p$. The overall p-value is given by

$$\mathfrak{p}_{univ} := \min(\mathfrak{p}_1, \dots, \mathfrak{p}_p) \cdot p,$$

where the multiplication by p is a Bonferroni correction for multiple testing.

- Principal components regression (PCR): a principal components analysis is performed on the vector \mathbf{Y} to extract the linear combination \tilde{Y} of the components with the largest variance. The p-value \mathfrak{p}_{PCR} is simply the p-value for the (univariate) association between \tilde{Y} and X .
- Principal components of explained variance (PCEV): very similar to PCR, but the linear combination \tilde{Y} is defined such that it maximizes the proportion of variance of \tilde{Y} being explained by the covariate X (this methodology was first introduced by [Ott and Rabinowitz \[1999\]](#)). The p-value \mathfrak{p}_{PCEV} is based on Wilk's lambda, which tests whether this proportion of explained variance is 0.

The dimension p of \mathbf{Y} takes the values 4, 10, 20, 100, 200, 300, 400. These p phenotypes are splitted in b blocks of equal size (with b equal to 2, 5, 10, 20). The covariance structure Σ depends on two parameters: the within-block correlation ρ_w and the between-block correlation ρ_b . Both quantities take value in $\{0, 0.5, 0.7\}$, with the convention that the between-block variance is never larger than the within-block variance, i.e. $\rho_w \geq \rho_b$. Finally, the association between X and a component of \mathbf{Y} is given in terms of the heritability h^2 ; this is related to the more familiar linear regression coefficient β via

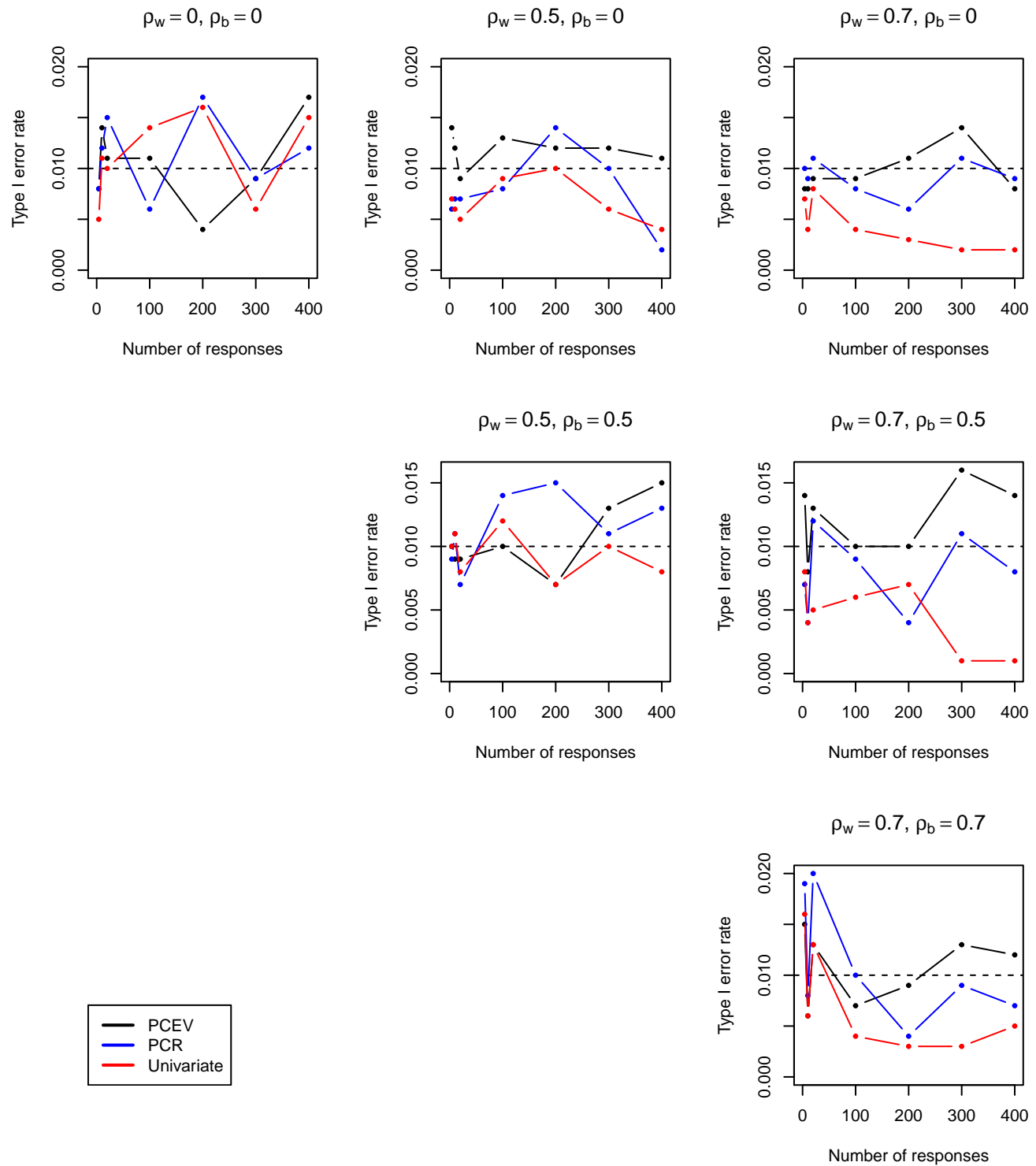
$$h^2 = \frac{\beta^2}{1 + \beta^2}.$$

The data is available in the R object `O11-simulation-results.RData`. There is a different matrix for each significance level $\alpha = 0.01, 0.05, 0.1$, each of the same form: the first six columns respectively correspond to 1) the simulation scenario, 2) the heritability h^2 , 3) the number of phenotypes p , 4) the number of blocks b , 5) the within-block correlation ρ_w , and 6) the between-block correlation ρ_b . The last four columns correspond to the four methods considered (we will ignore Hotteling's method).

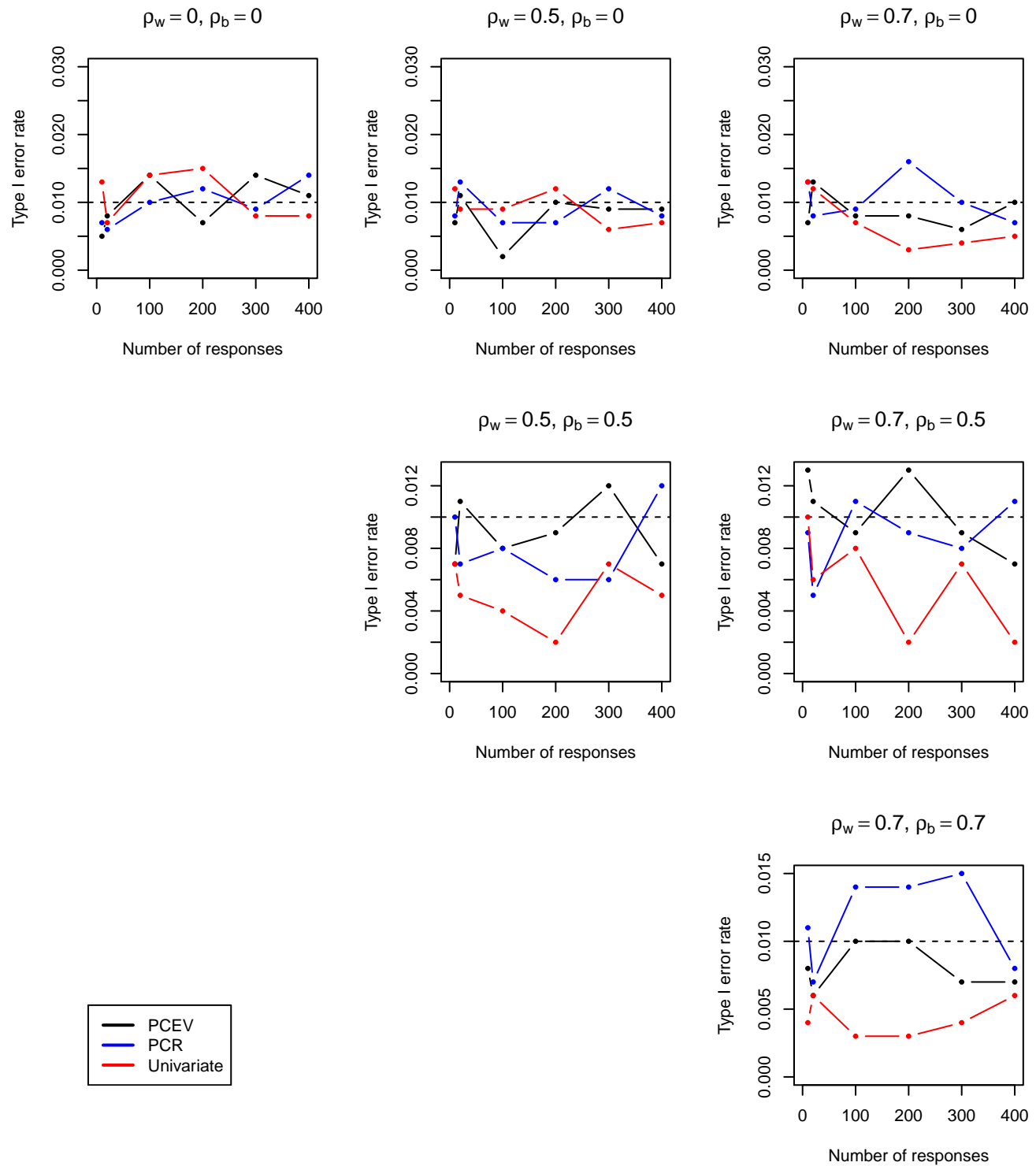
1 Simulation scenario 1

We simulated no association between the continuous covariate x and the multivariate phenotype \mathbf{Y} .

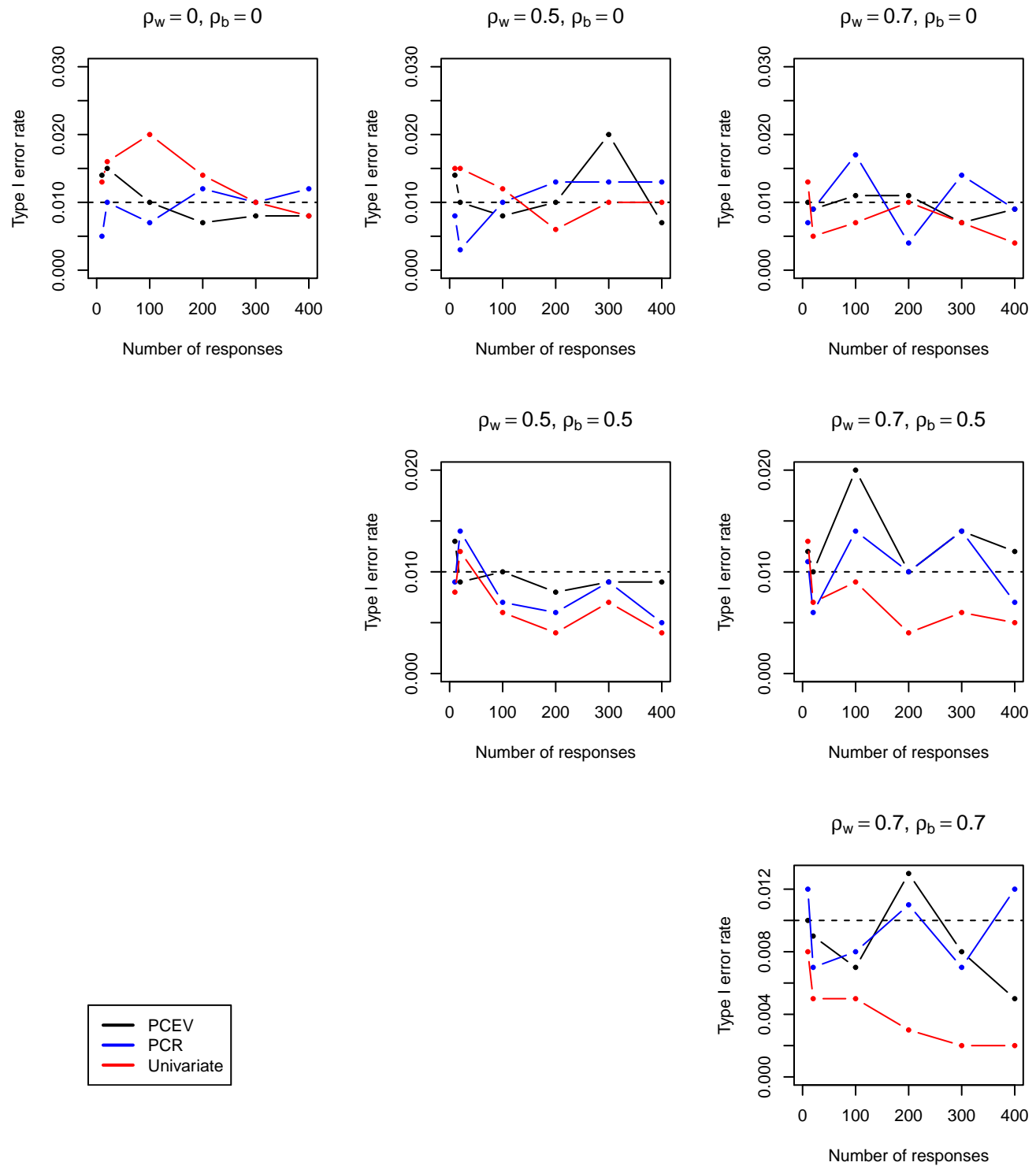
1.1 Significance level: 0.01, Number of blocks: 2



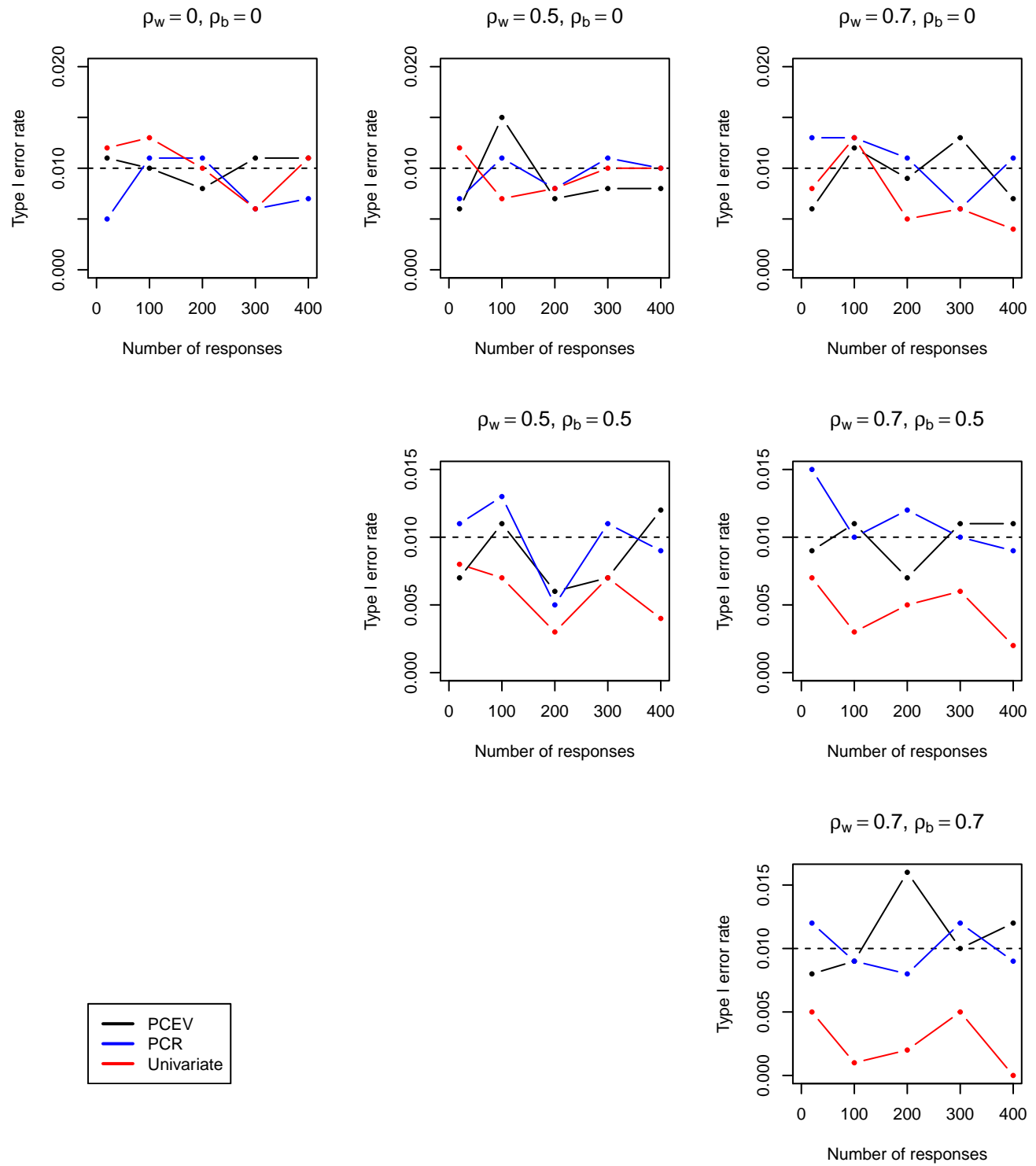
1.2 Significance level: 0.01, Number of blocks: 5



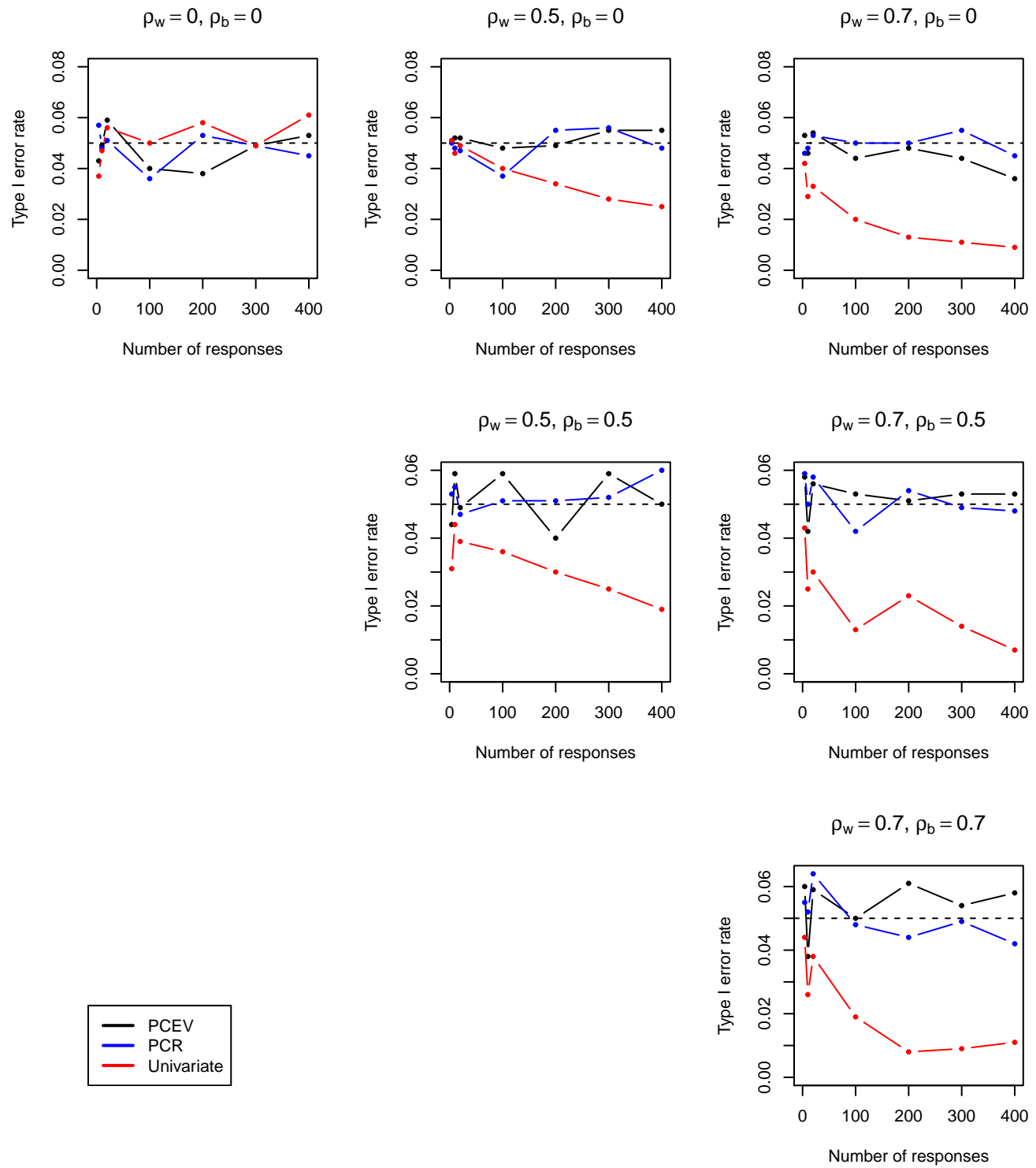
1.3 Significance level: 0.01, Number of blocks: 10



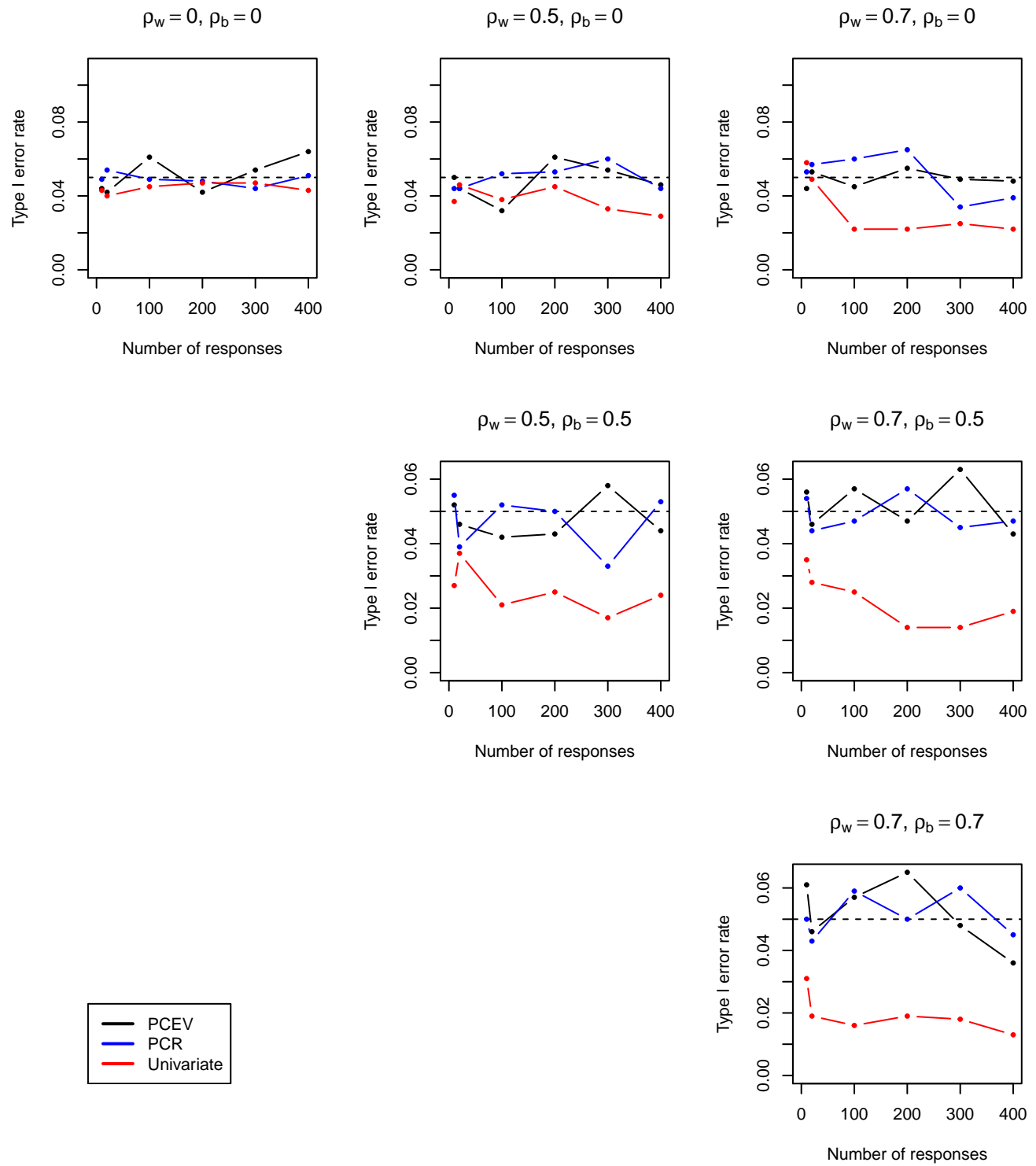
1.4 Significance level: 0.01, Number of blocks: 20



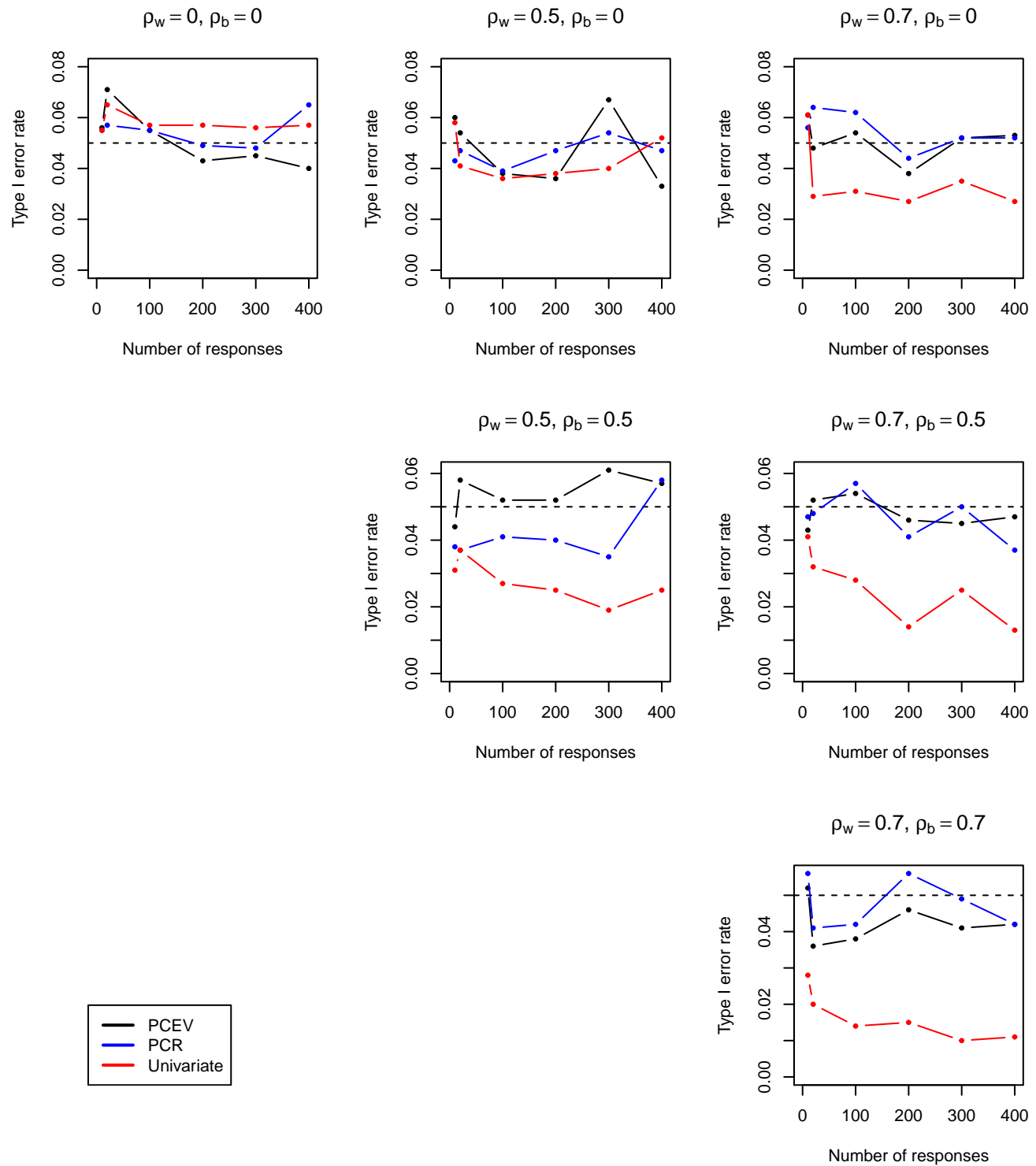
1.5 Significance level: 0.05, Number of blocks: 2



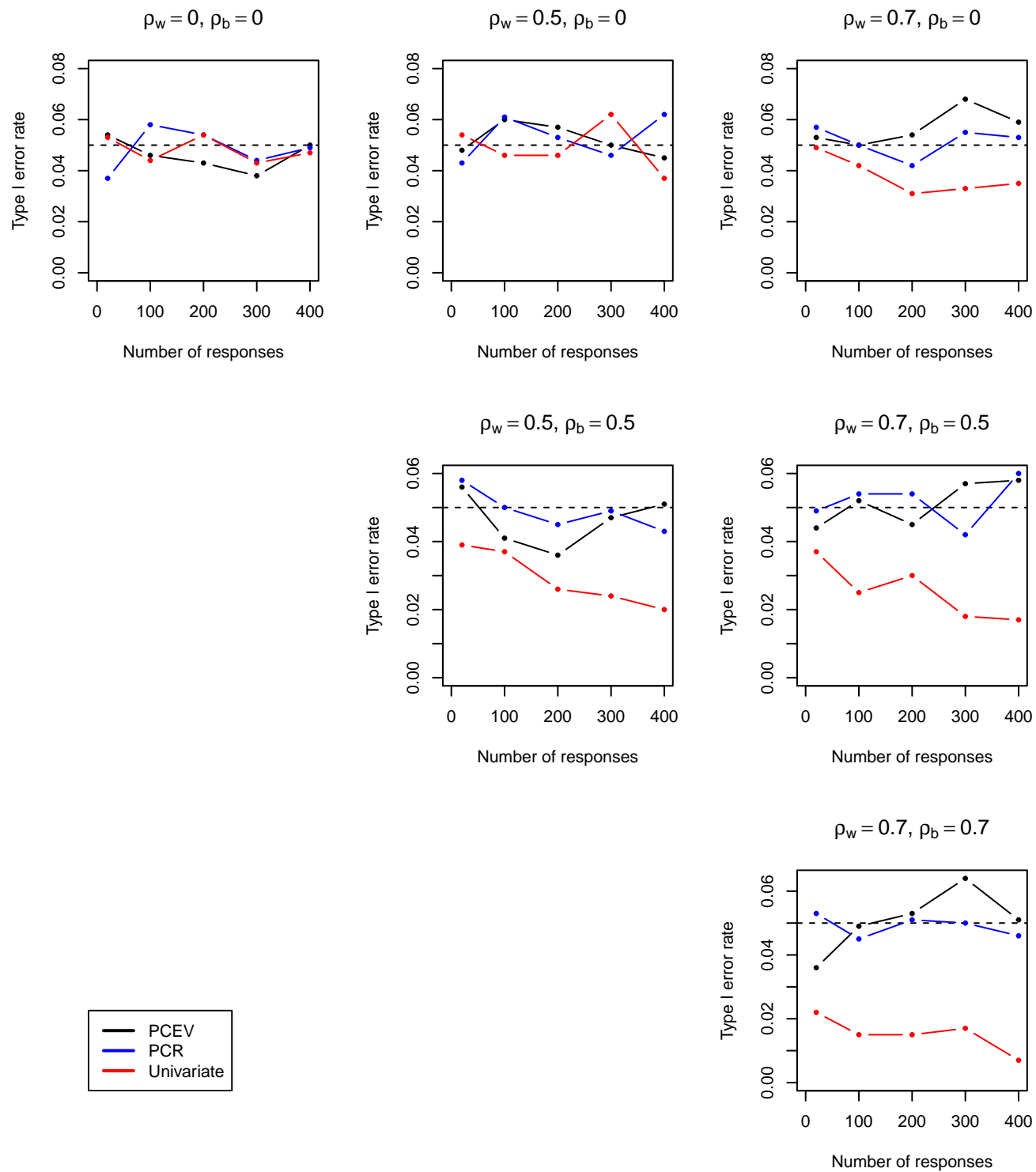
1.6 Significance level: 0.05, Number of blocks: 5



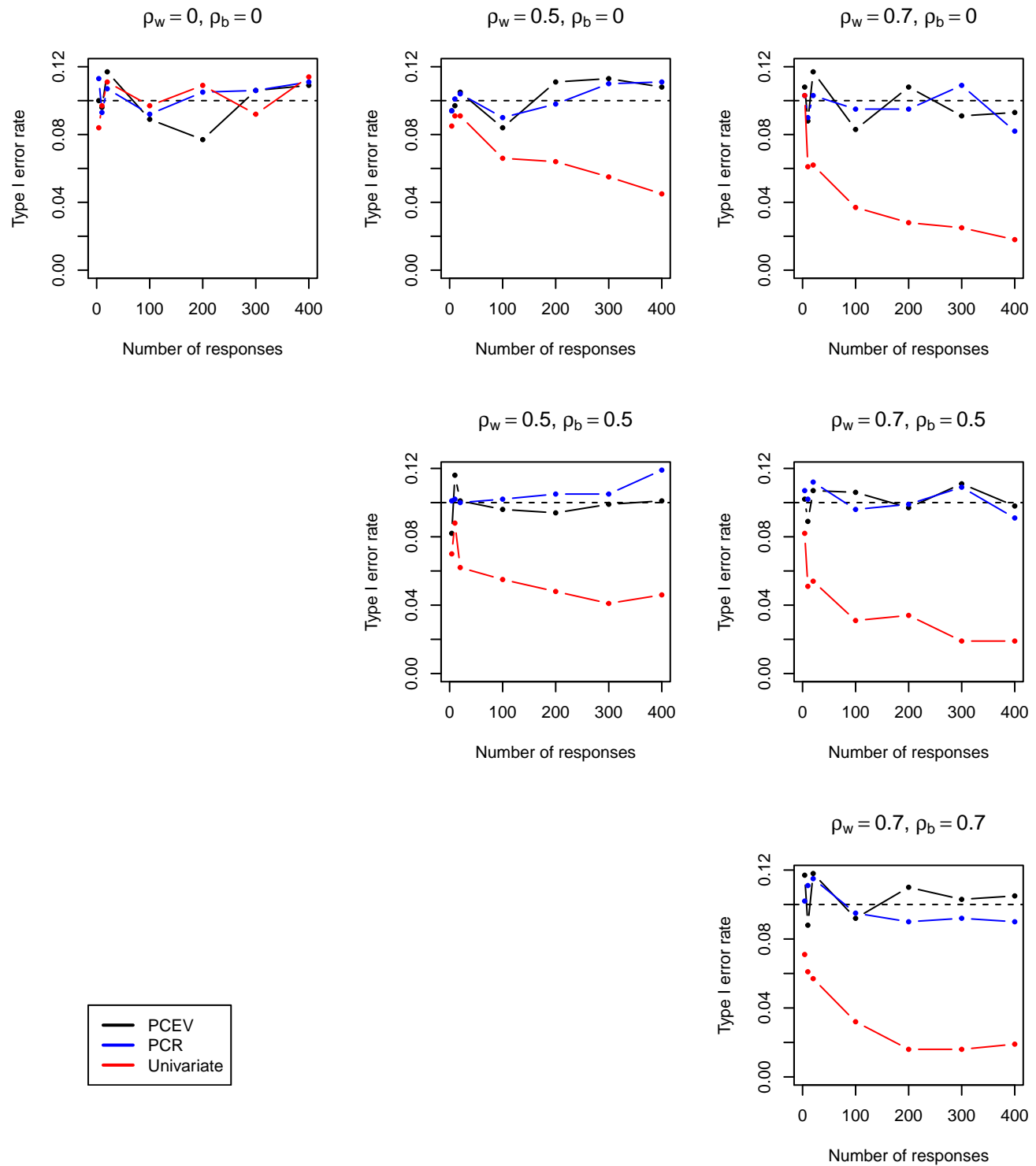
1.7 Significance level: 0.05, Number of blocks: 10



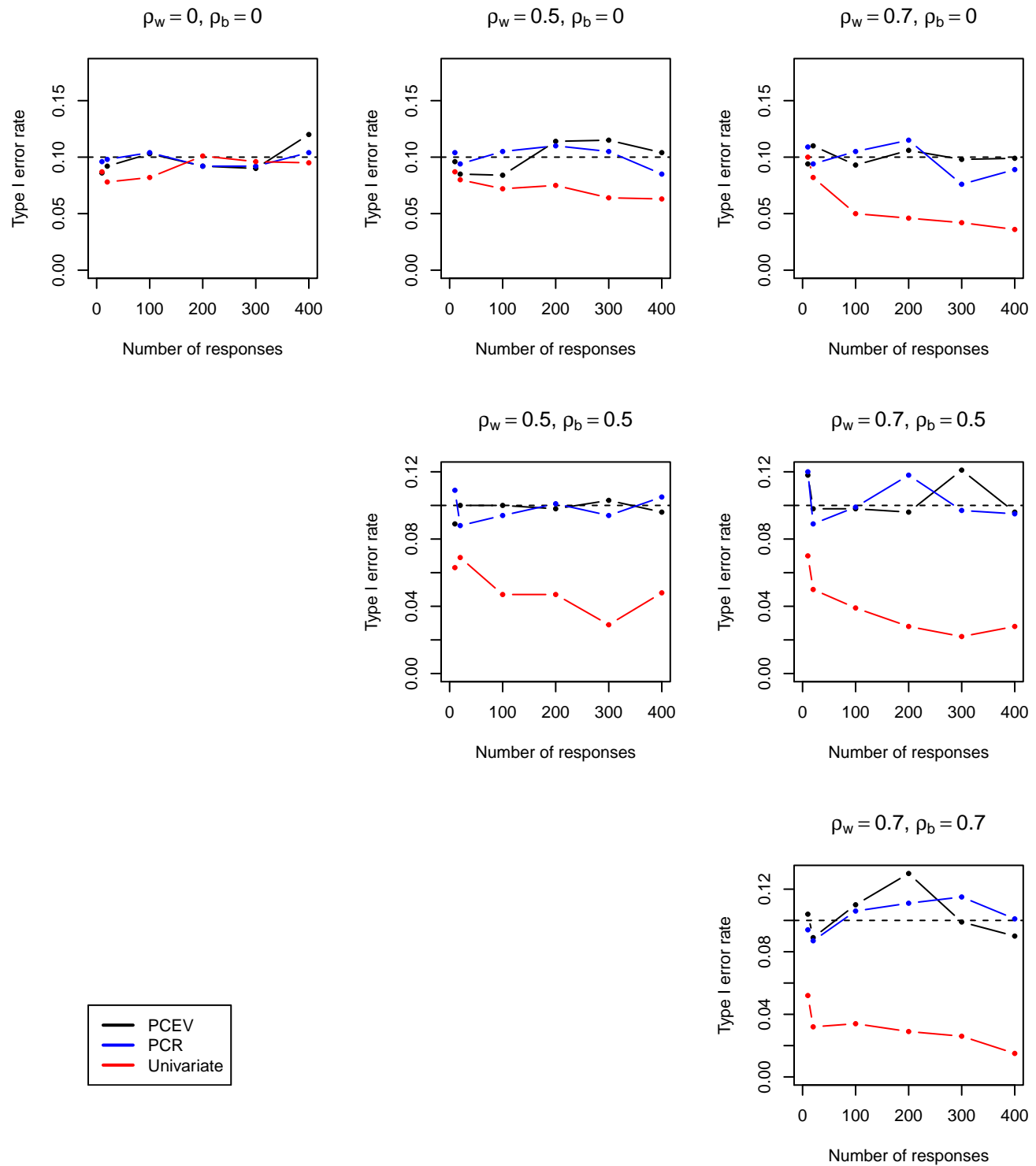
1.8 Significance level: 0.05, Number of blocks: 20



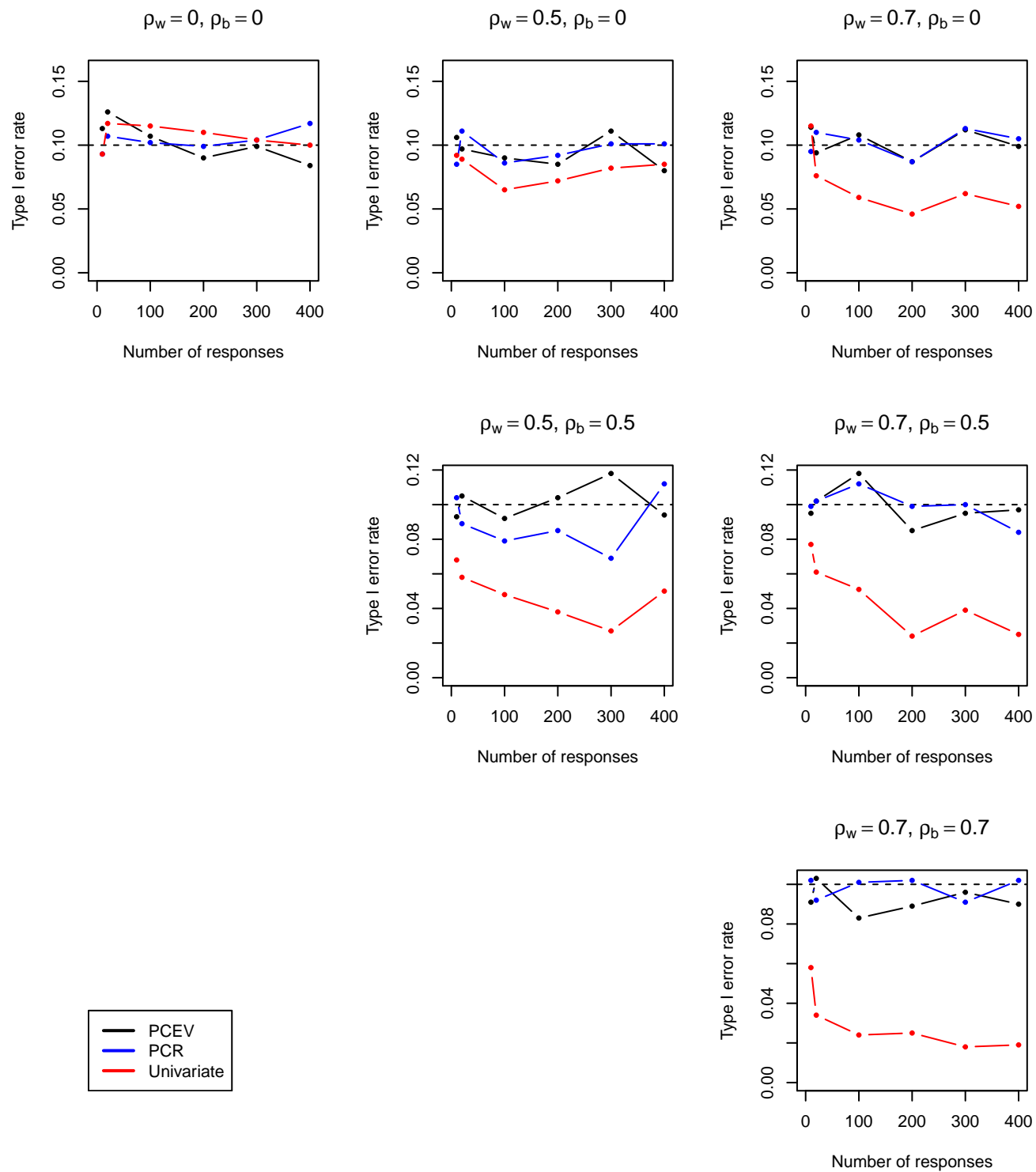
1.9 Significance level: 0.1, Number of blocks: 2



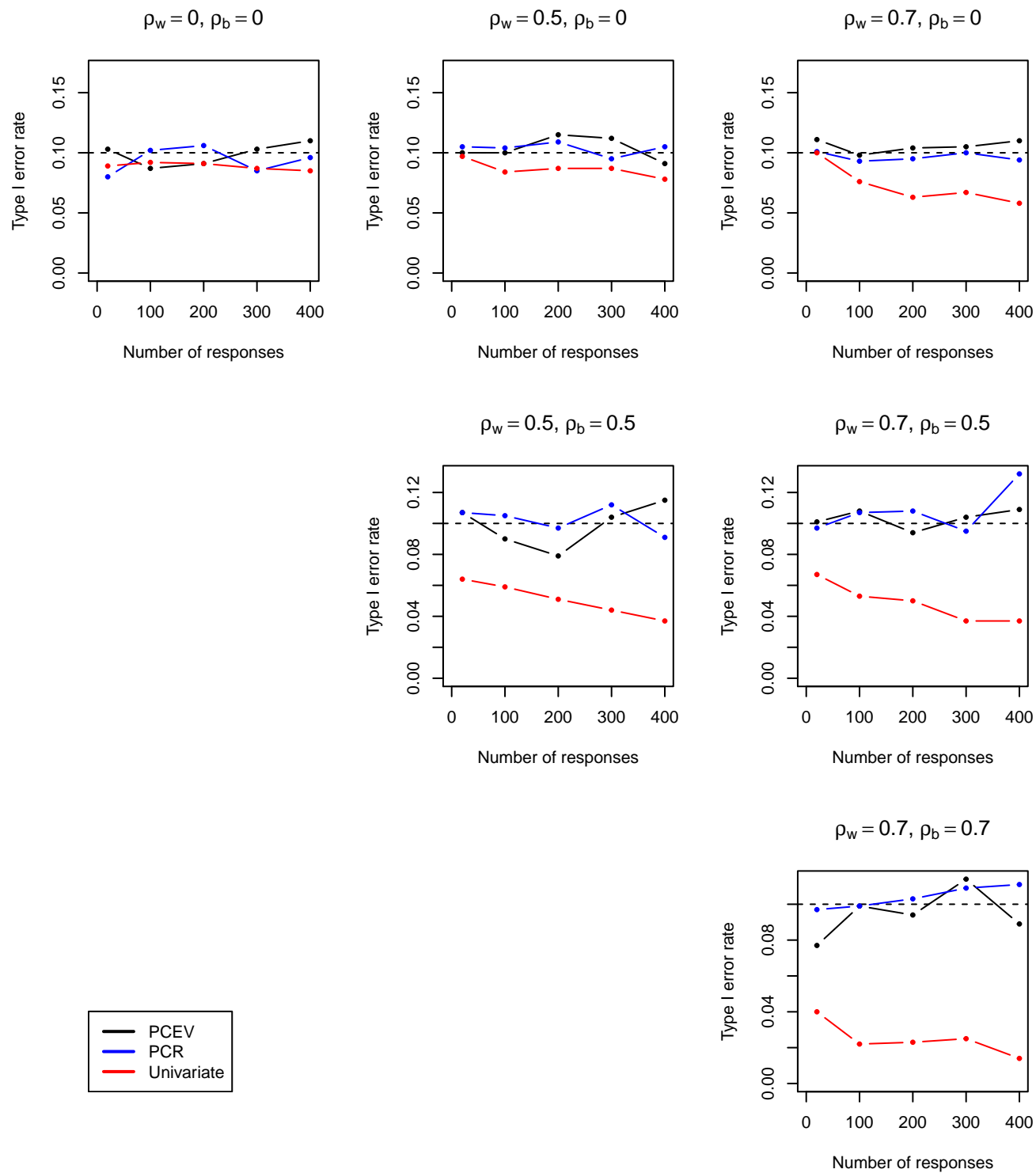
1.10 Significance level: 0.1, Number of blocks: 5



1.11 Significance level: 0.1, Number of blocks: 10



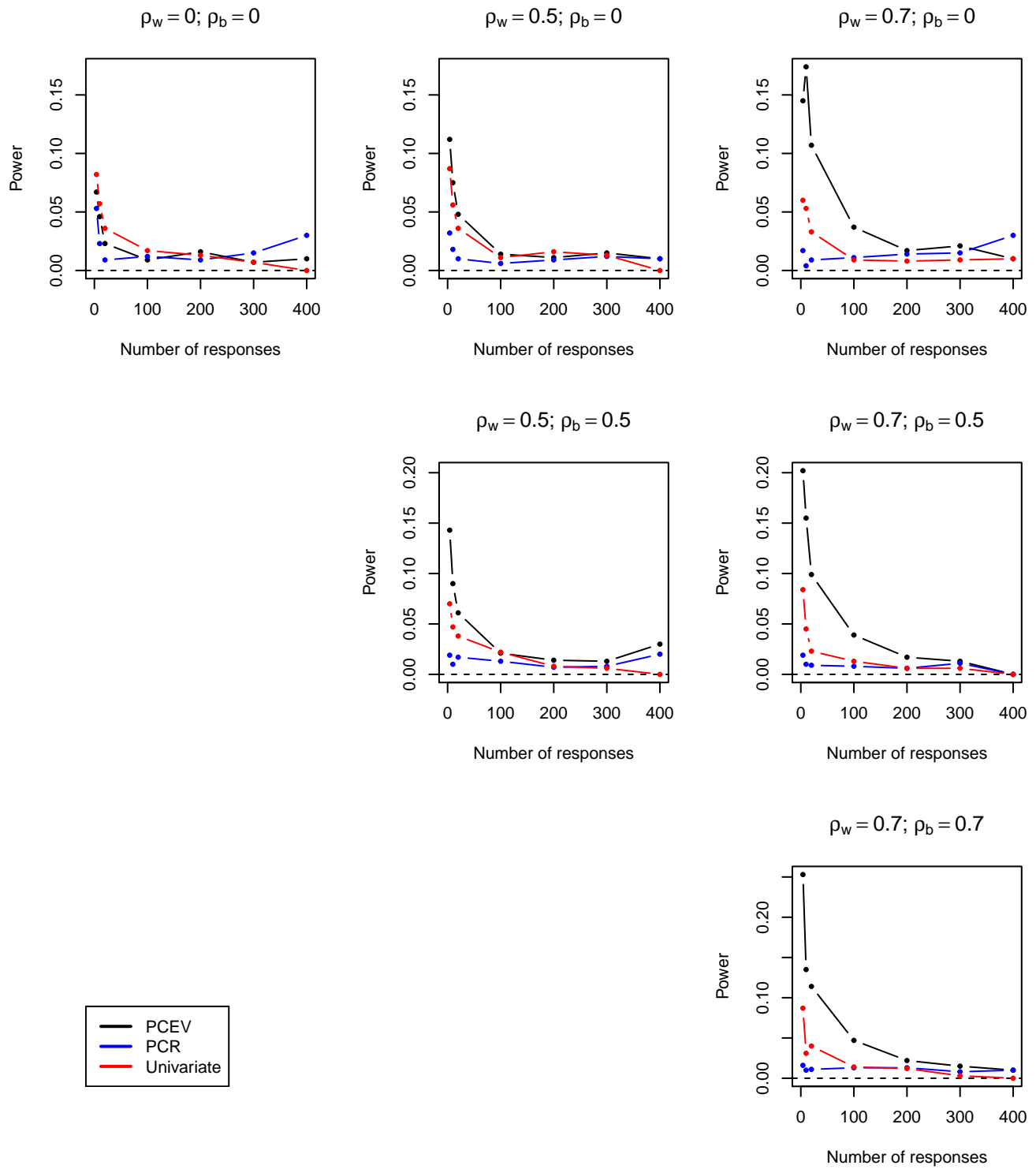
1.12 Significance level: 0.1, Number of blocks: 20



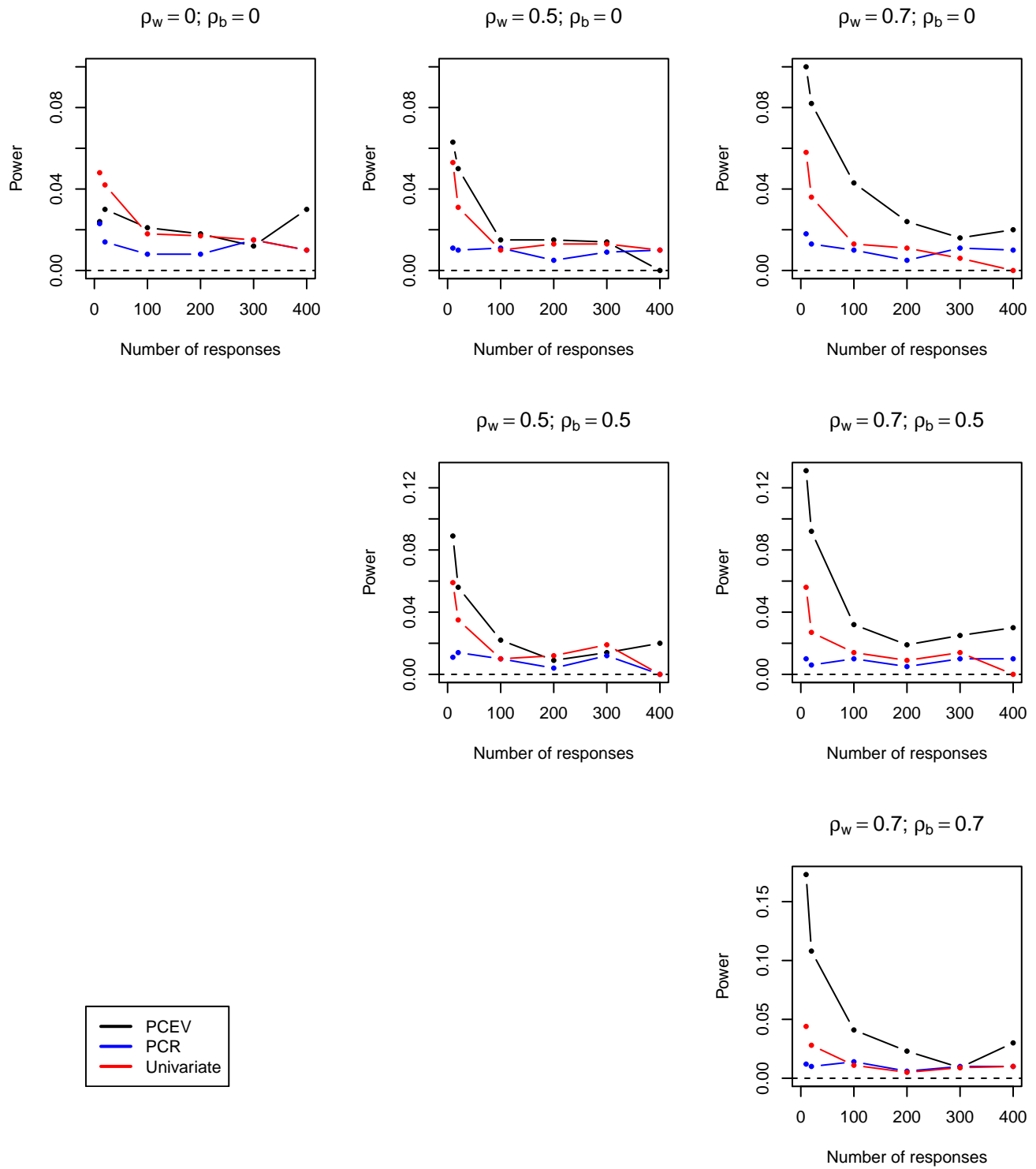
2 Simulation scenario 2

We simulated an association between the continuous covariate x and the first component of the multivariate phenotype \mathbf{Y} .

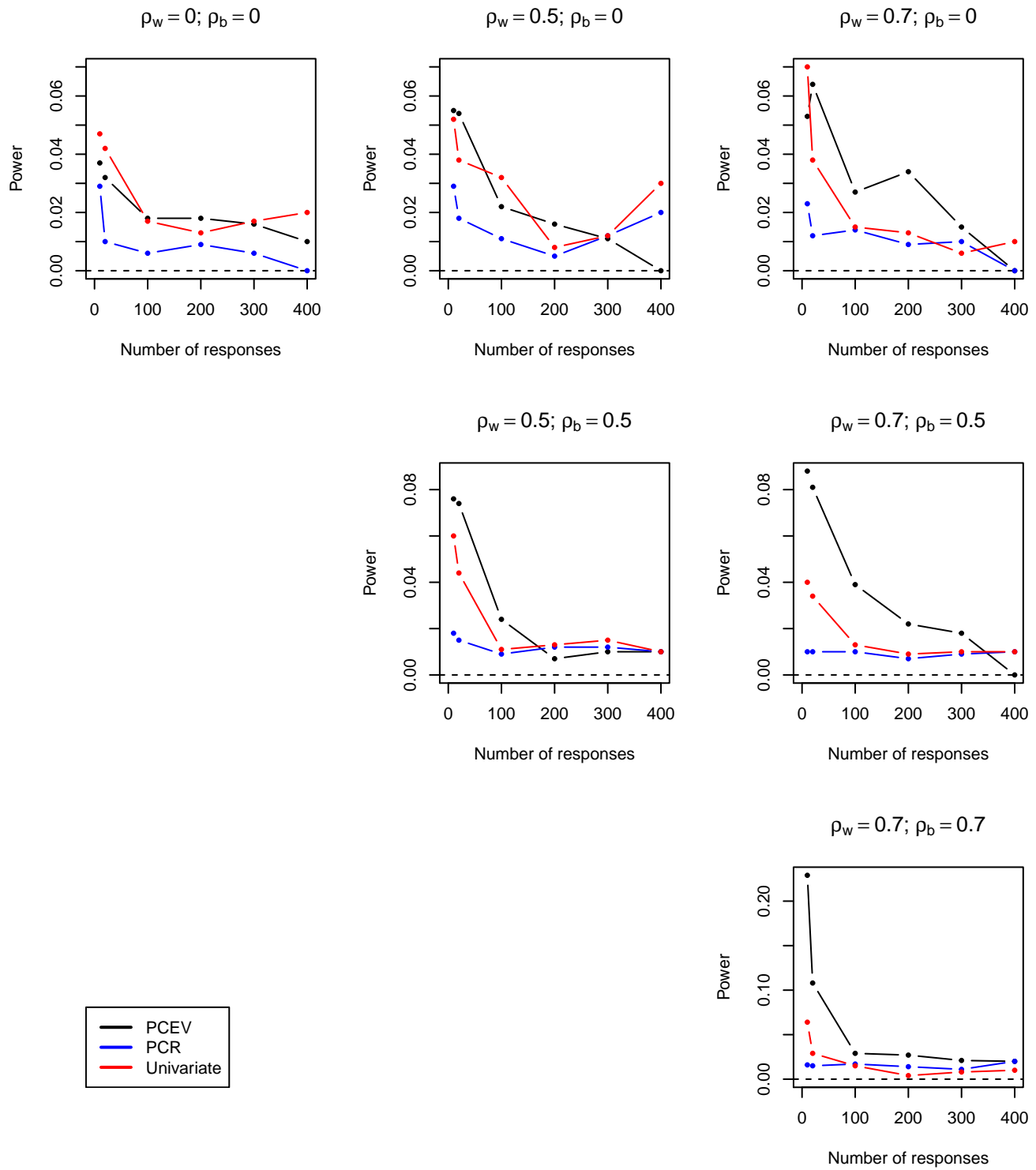
2.1 Significance level: 0.01, Heritability: 0.5%, Number of blocks: 2



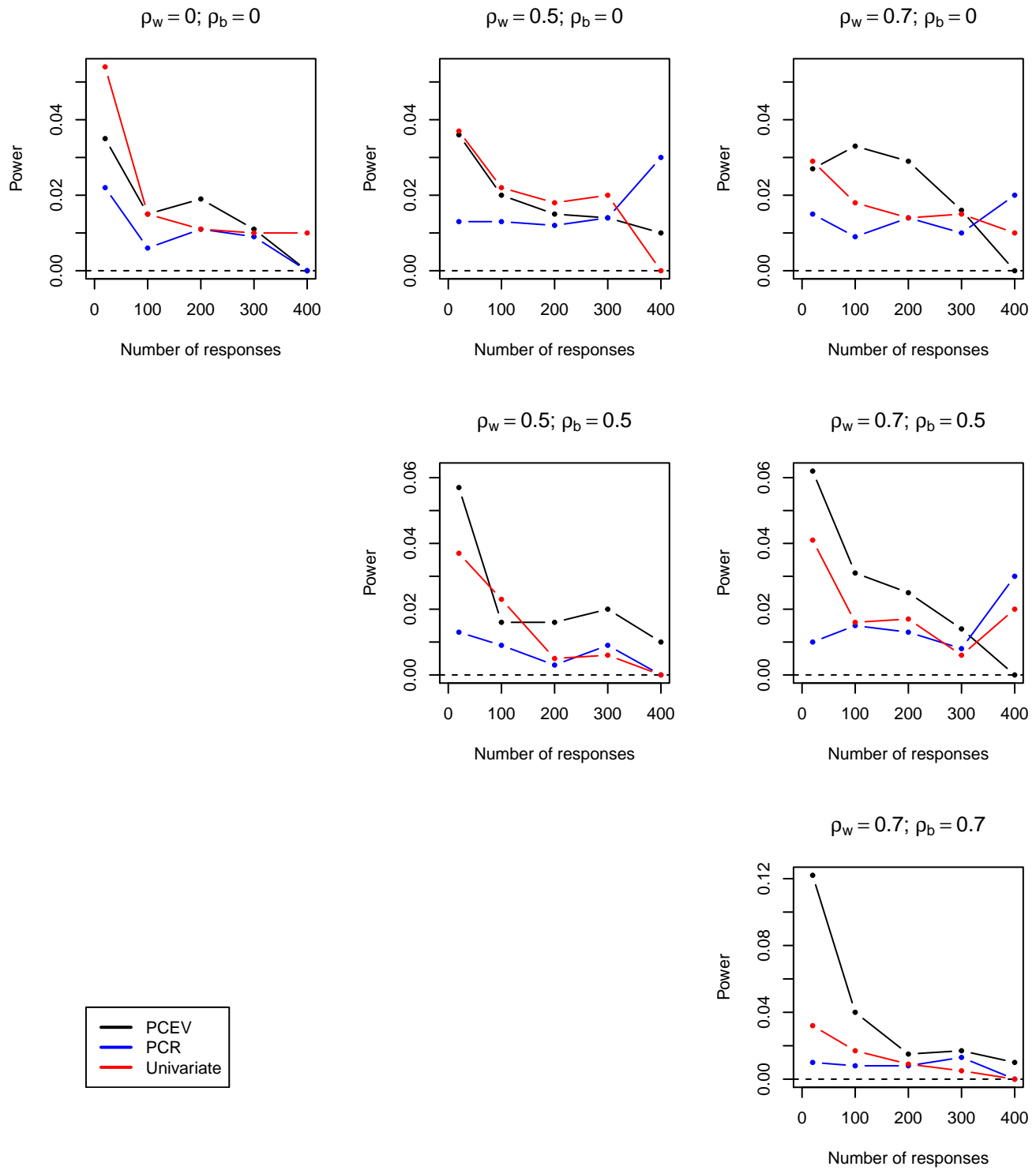
2.2 Significance level: 0.01, Heritability: 0.5%, Number of blocks: 5



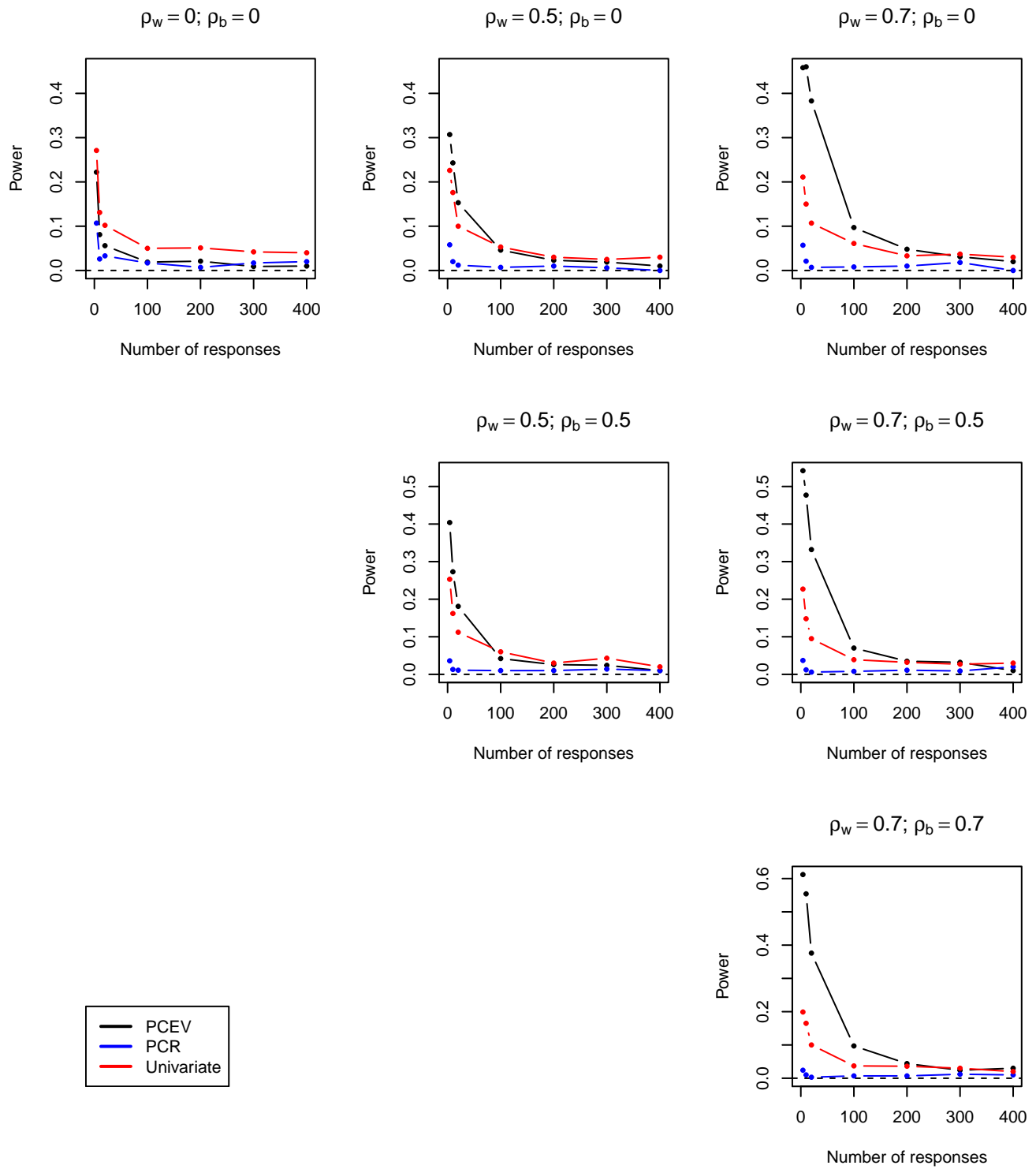
2.3 Significance level: 0.01, Heritability: 0.5%, Number of blocks: 10



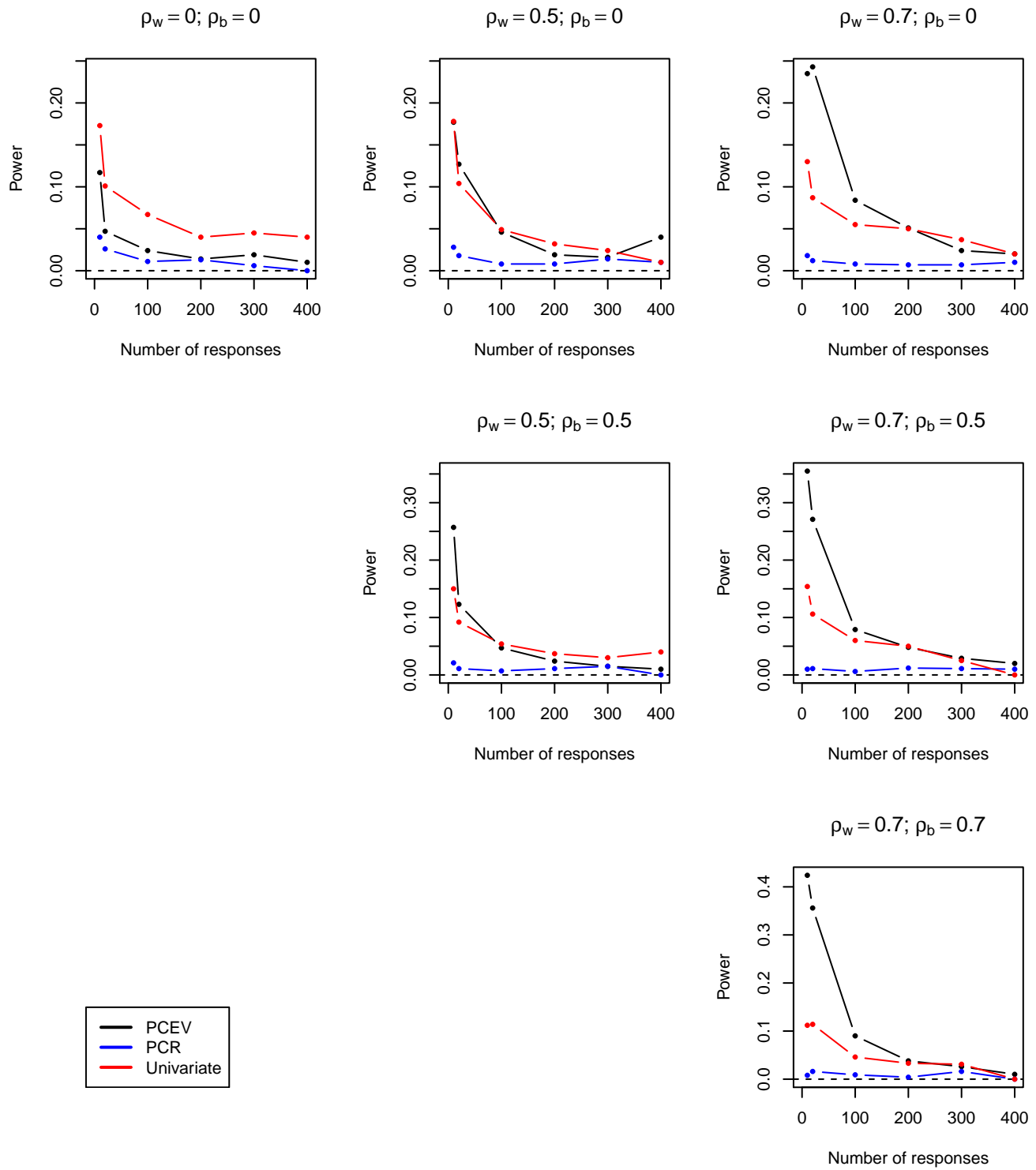
2.4 Significance level: 0.01, Heritability: 0.5%, Number of blocks: 20



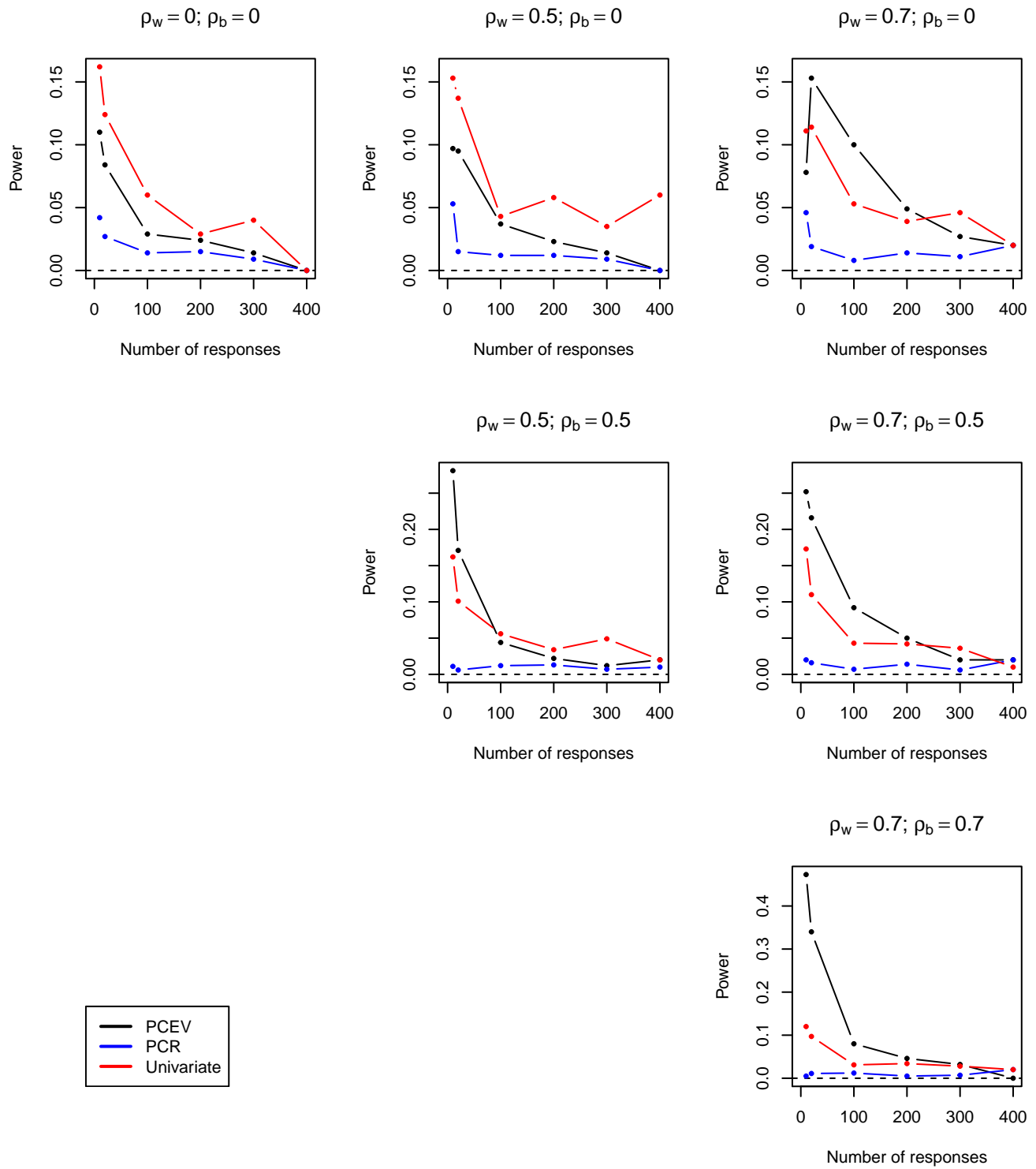
2.5 Significance level: 0.01, Heritability: 1%, Number of blocks: 2



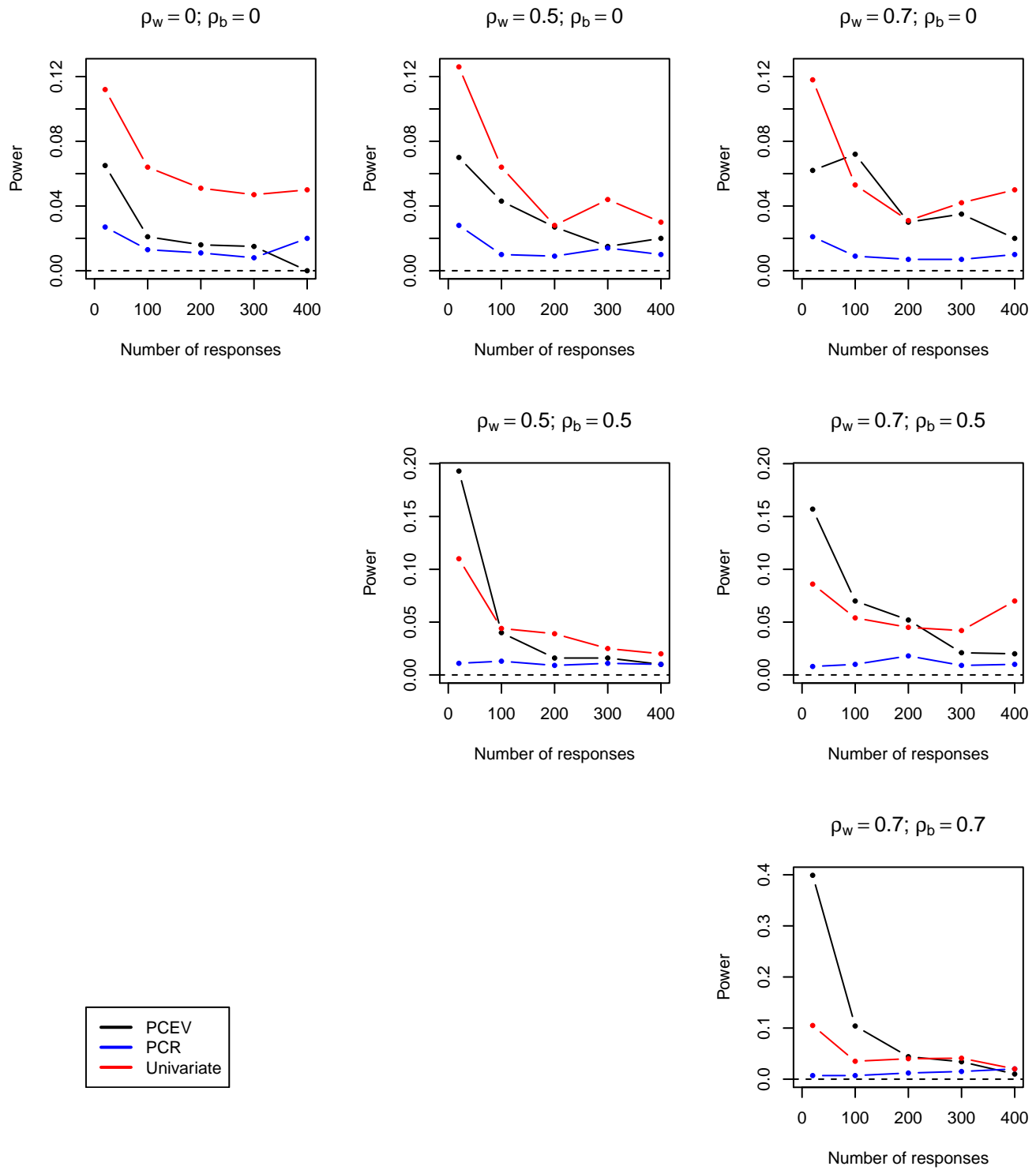
2.6 Significance level: 0.01, Heritability: 1%, Number of blocks: 5



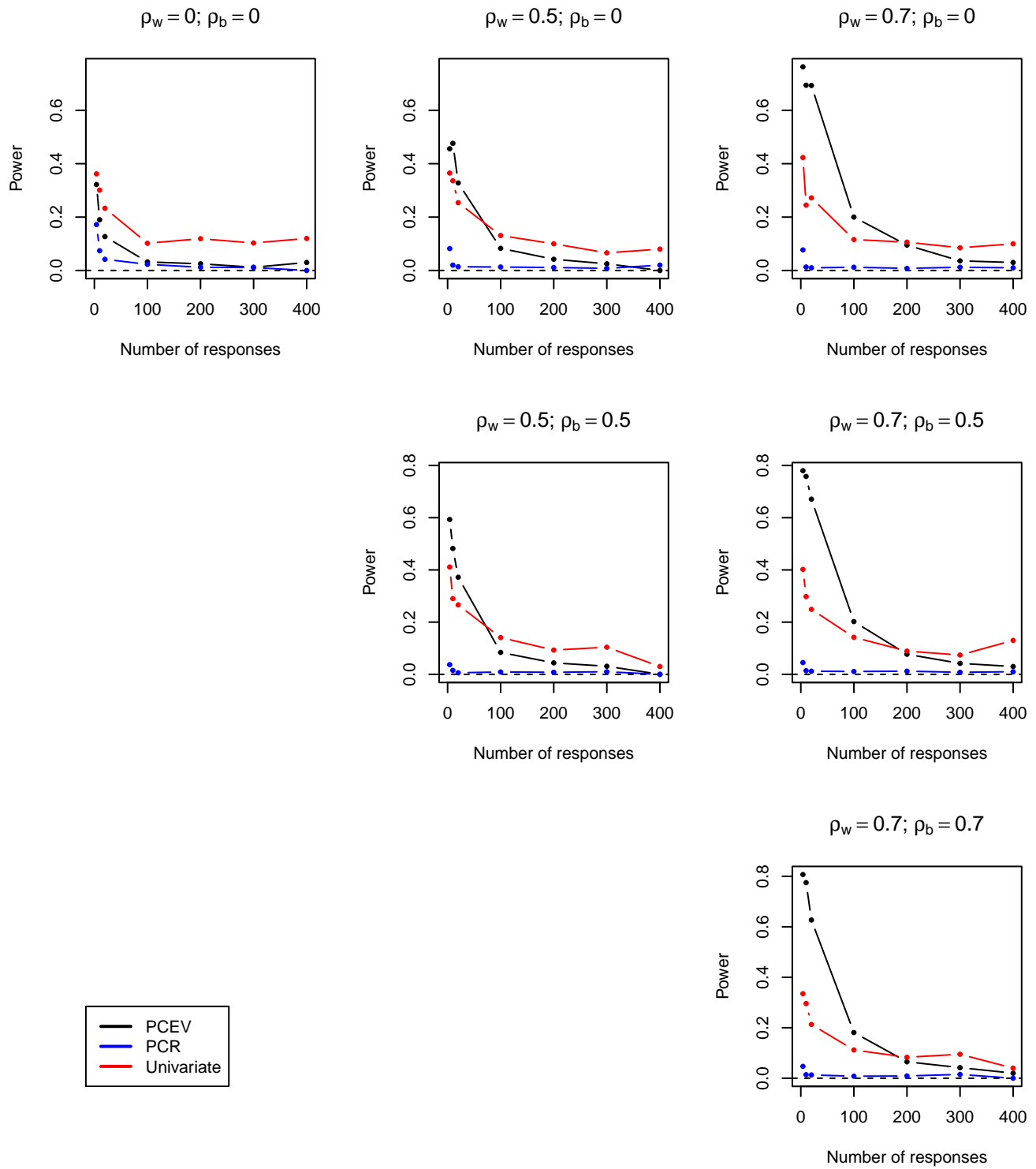
2.7 Significance level: 0.01, Heritability: 1%, Number of blocks: 10



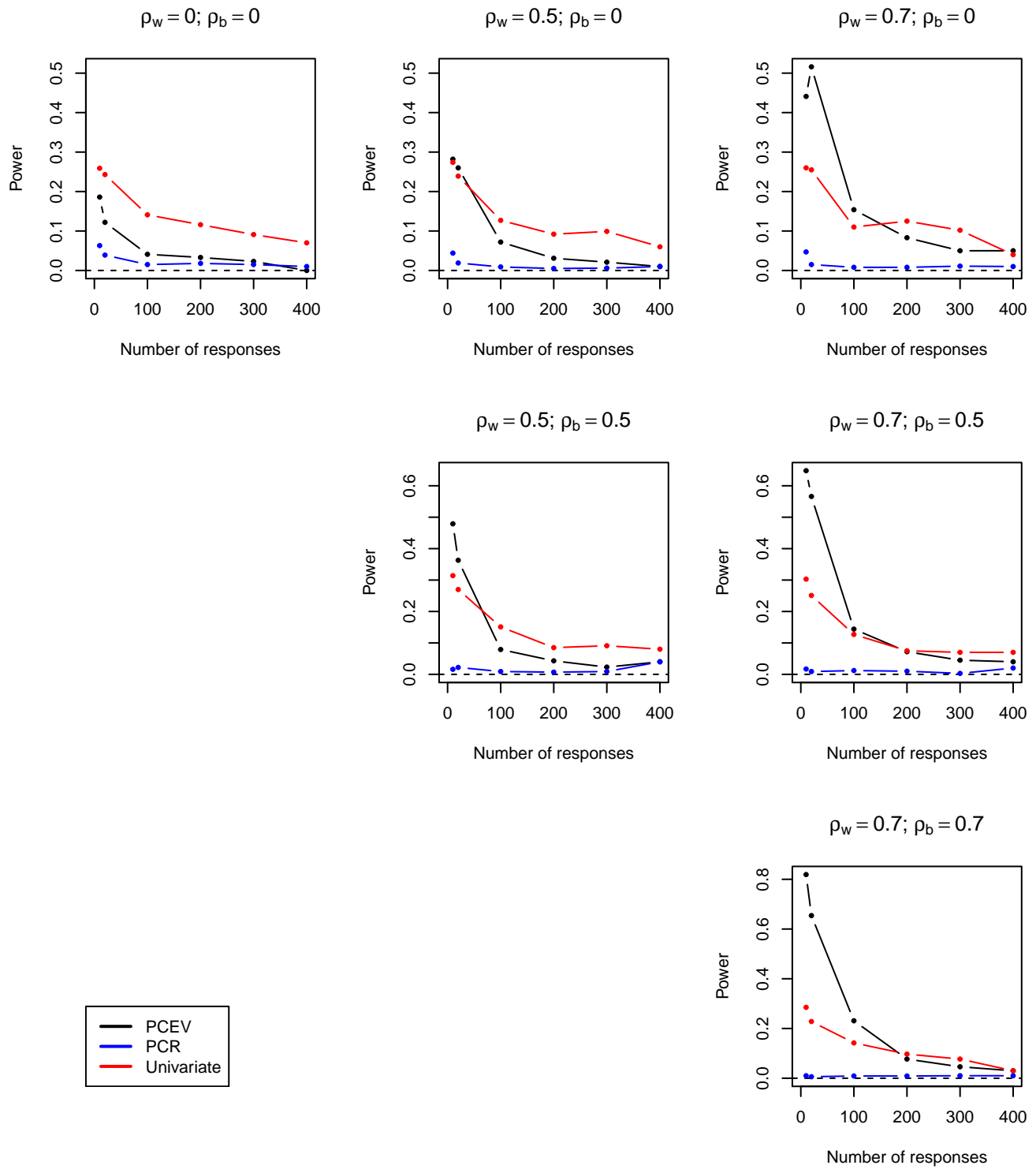
2.8 Significance level: 0.01, Heritability: 1%, Number of blocks: 20



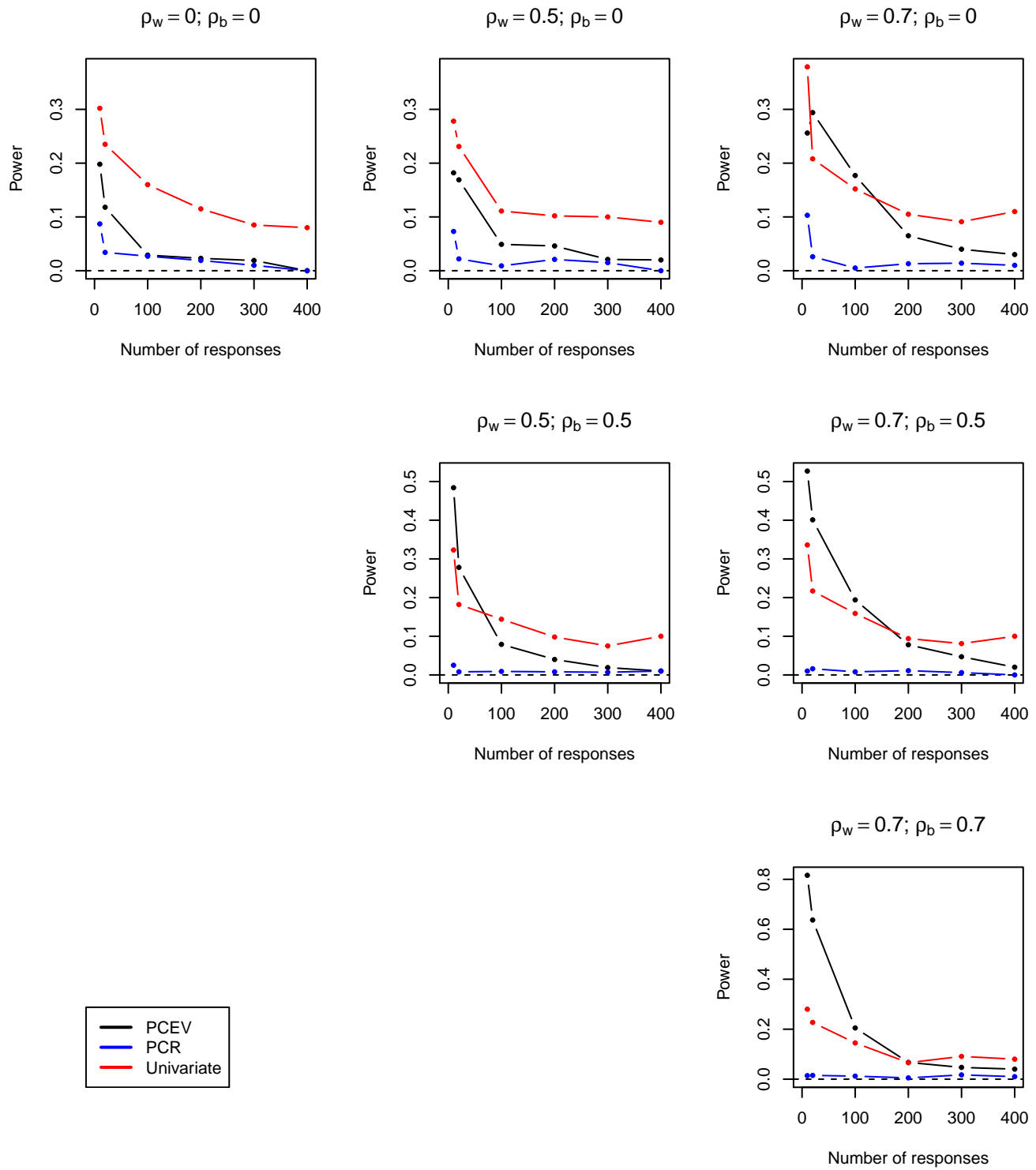
2.9 Significance level: 0.01, Heritability: 1.5%, Number of blocks: 2



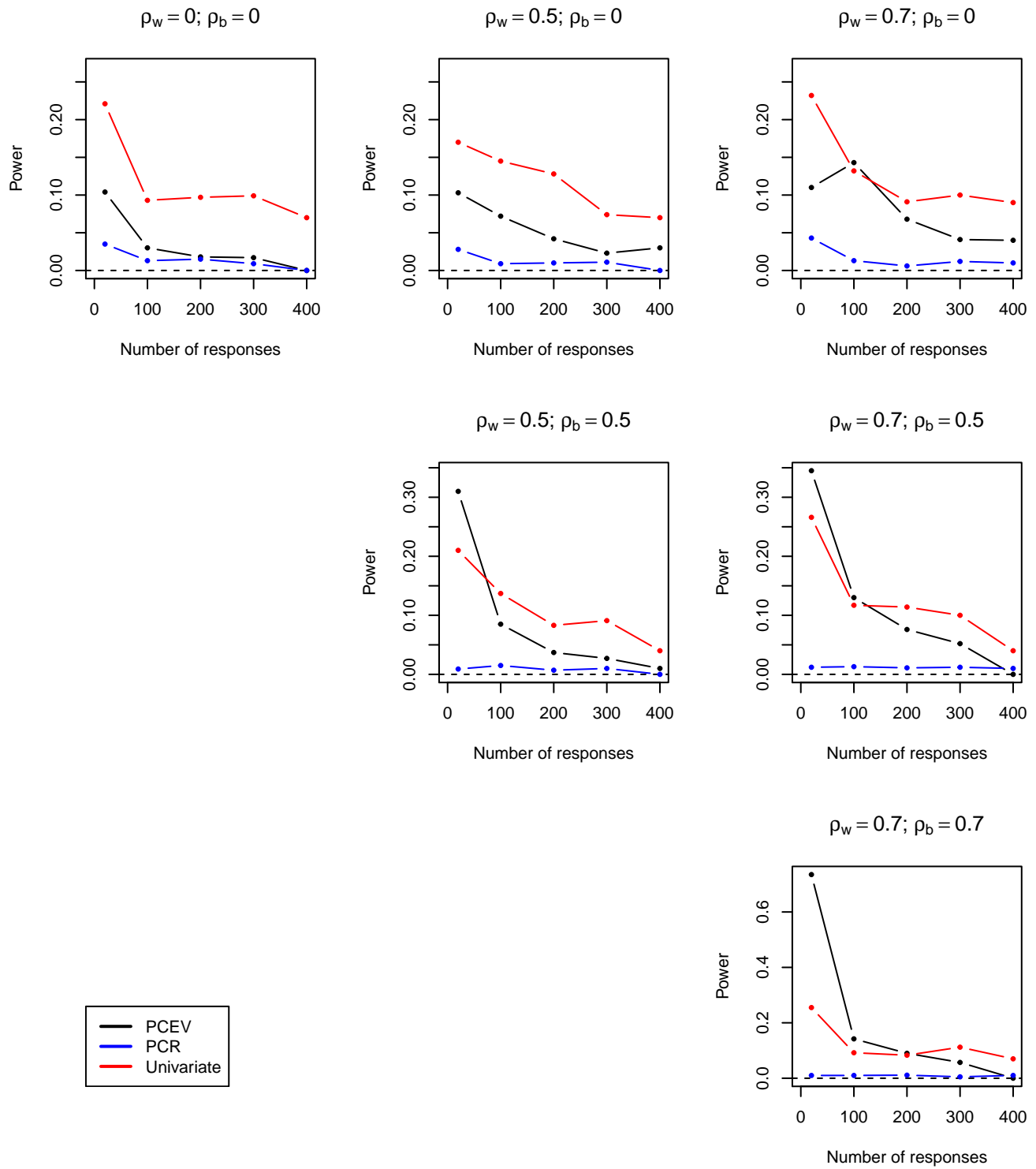
2.10 Significance level: 0.01, Heritability: 1.5%, Number of blocks: 5



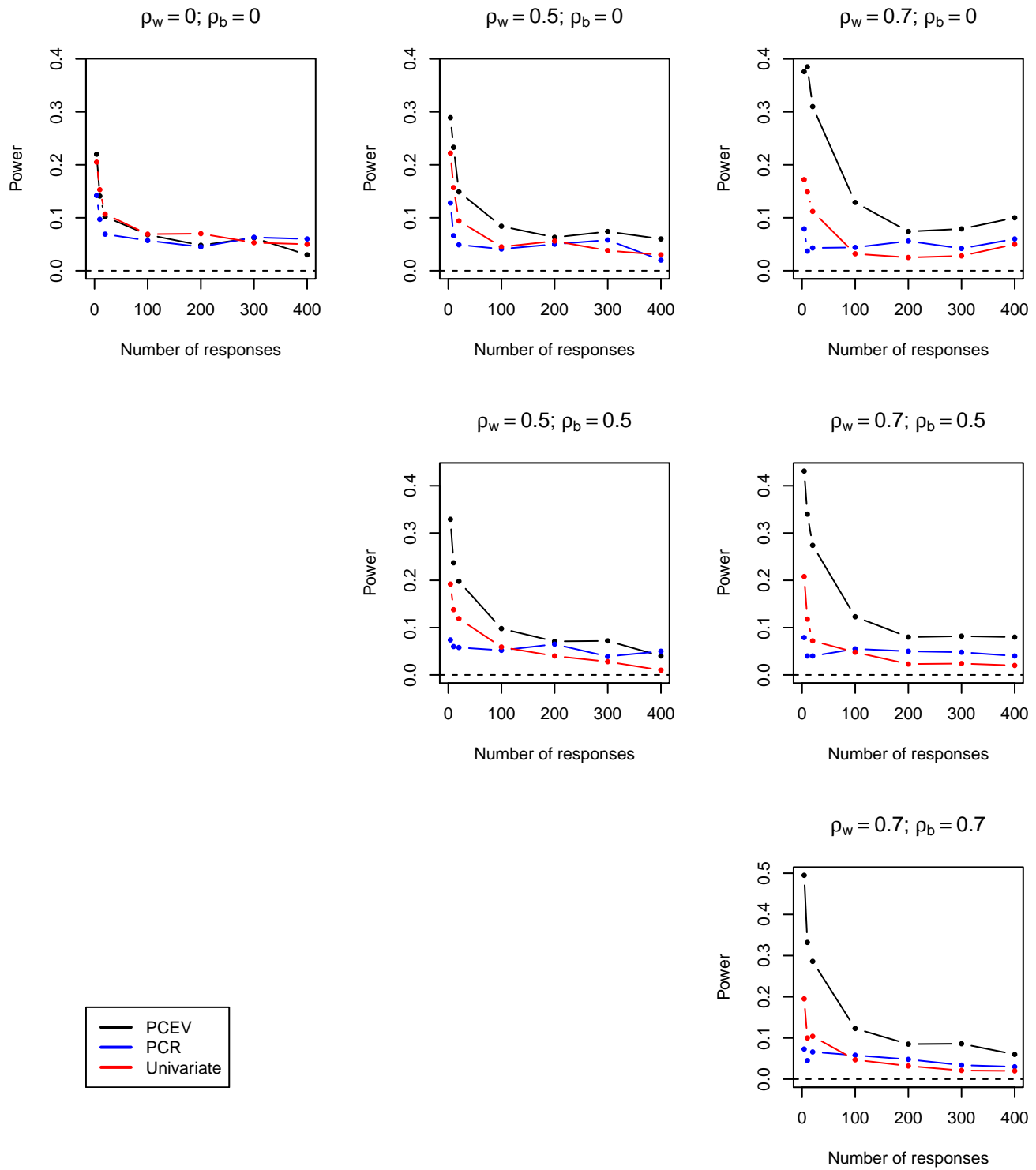
2.11 Significance level: 0.01, Heritability: 1.5%, Number of blocks: 10



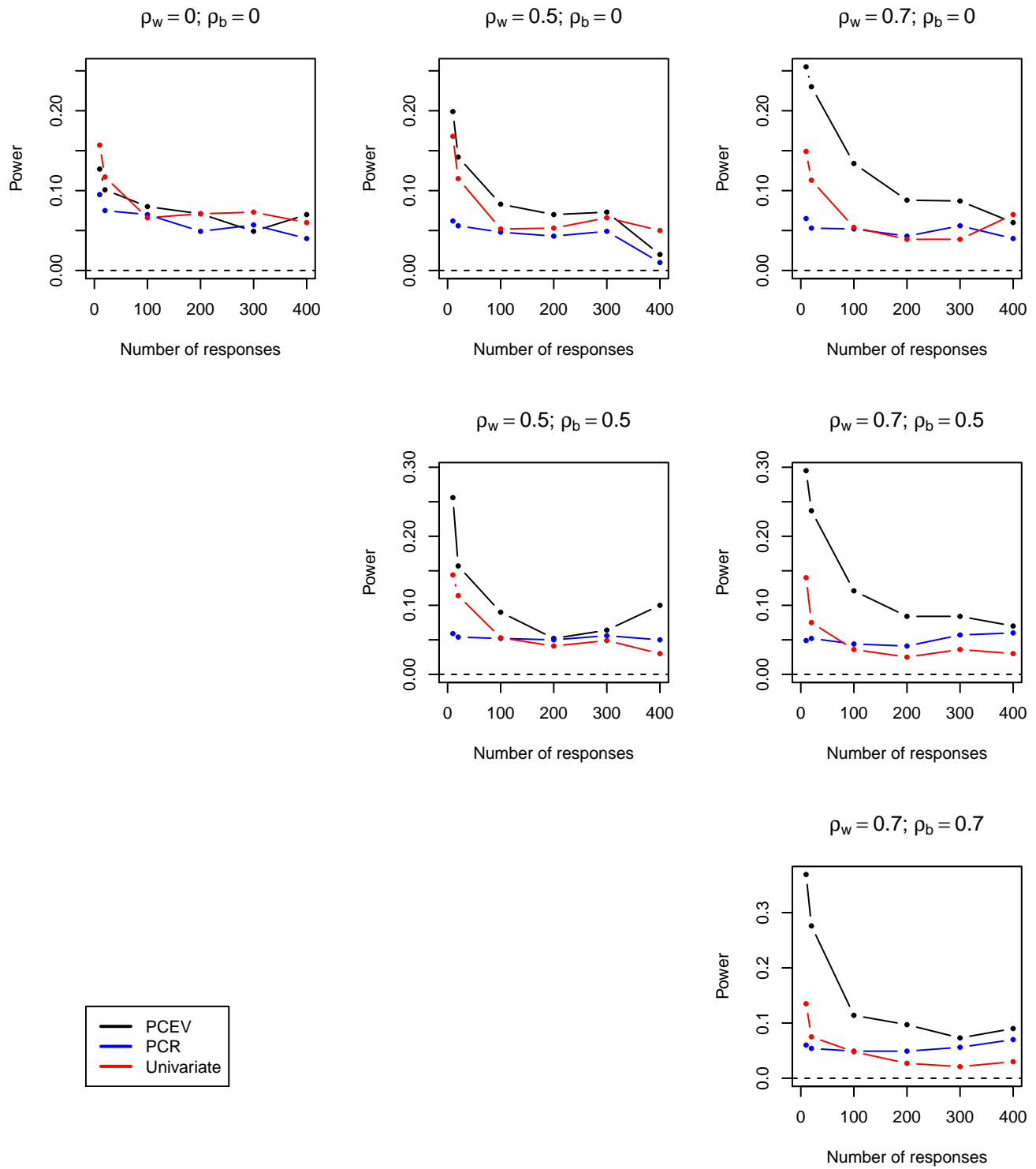
2.12 Significance level: 0.01, Heritability: 1.5%, Number of blocks: 20



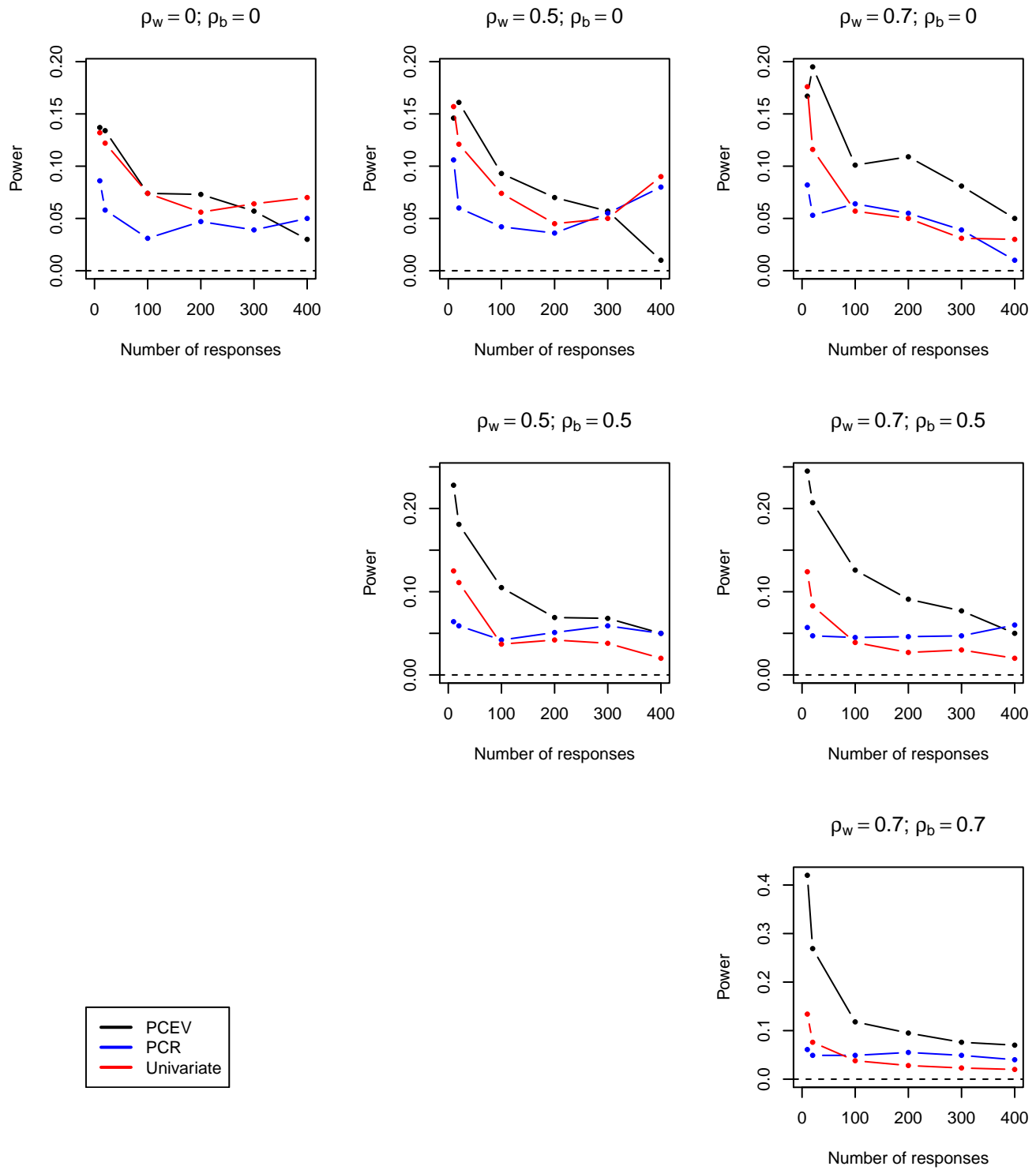
2.13 Significance level: 0.05, Heritability: 0.5%, Number of blocks: 2



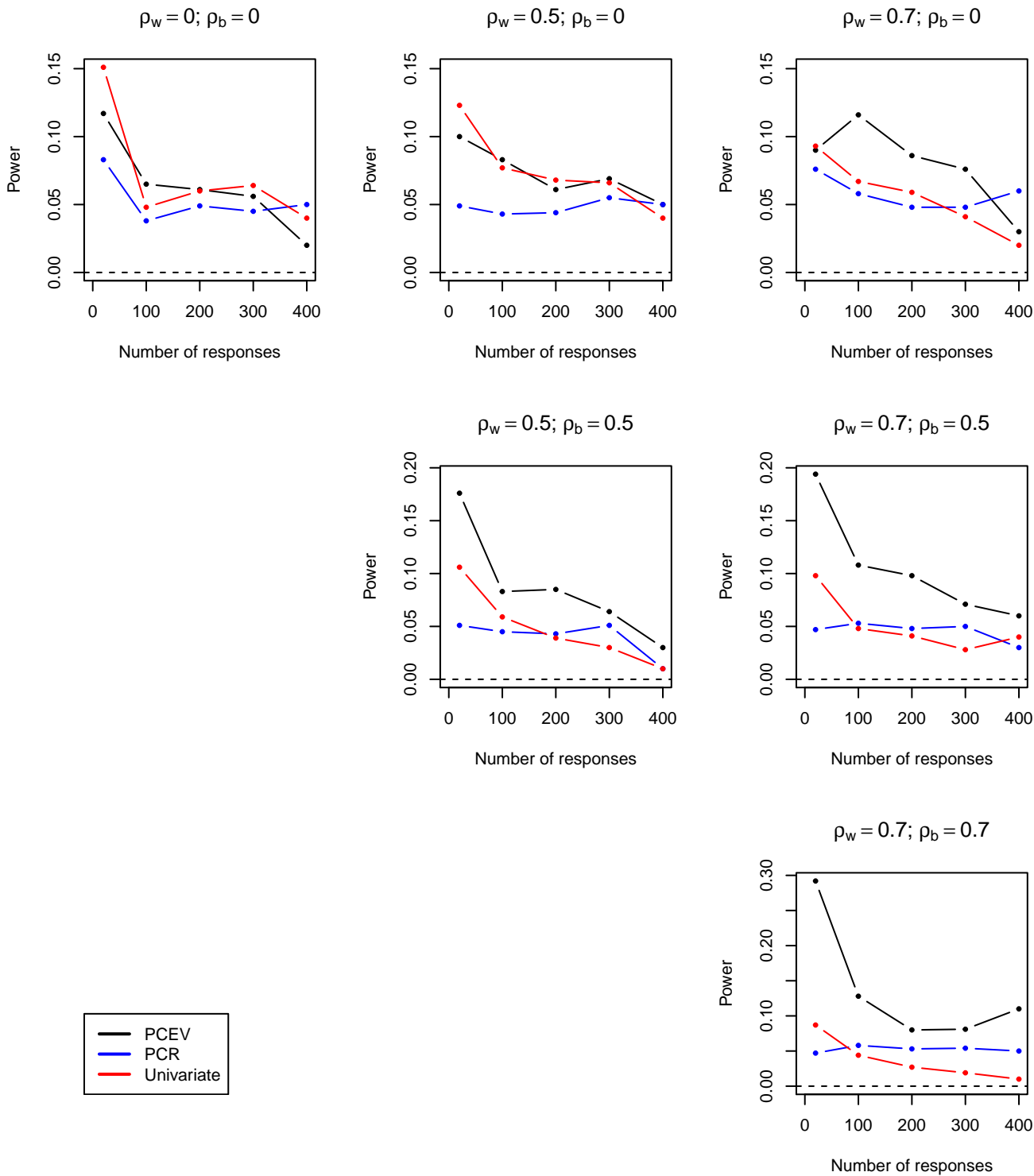
2.14 Significance level: 0.05, Heritability: 0.5%, Number of blocks: 5



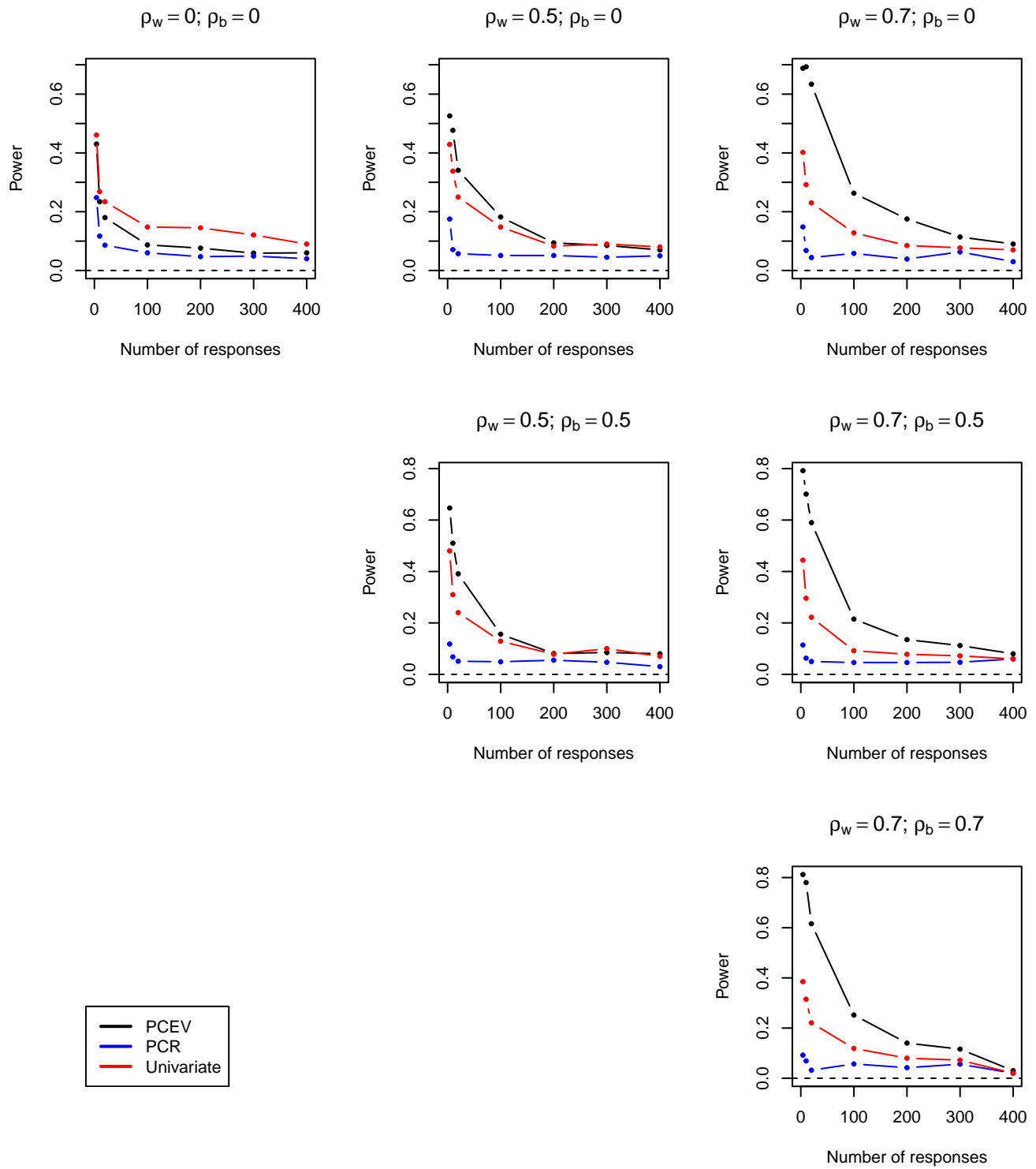
2.15 Significance level: 0.05, Heritability: 0.5%, Number of blocks: 10



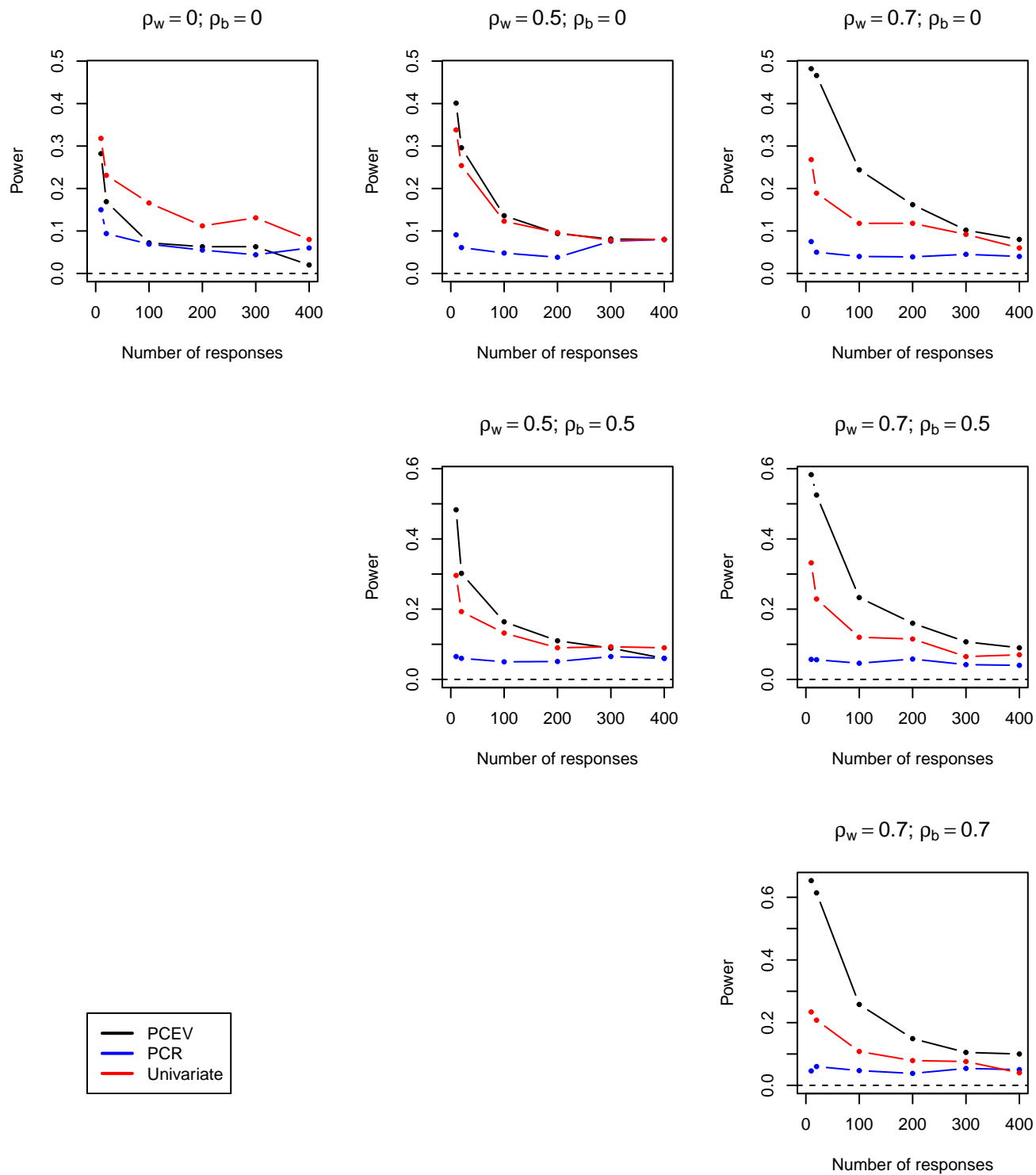
2.16 Significance level: 0.05, Heritability: 0.5%, Number of blocks: 20



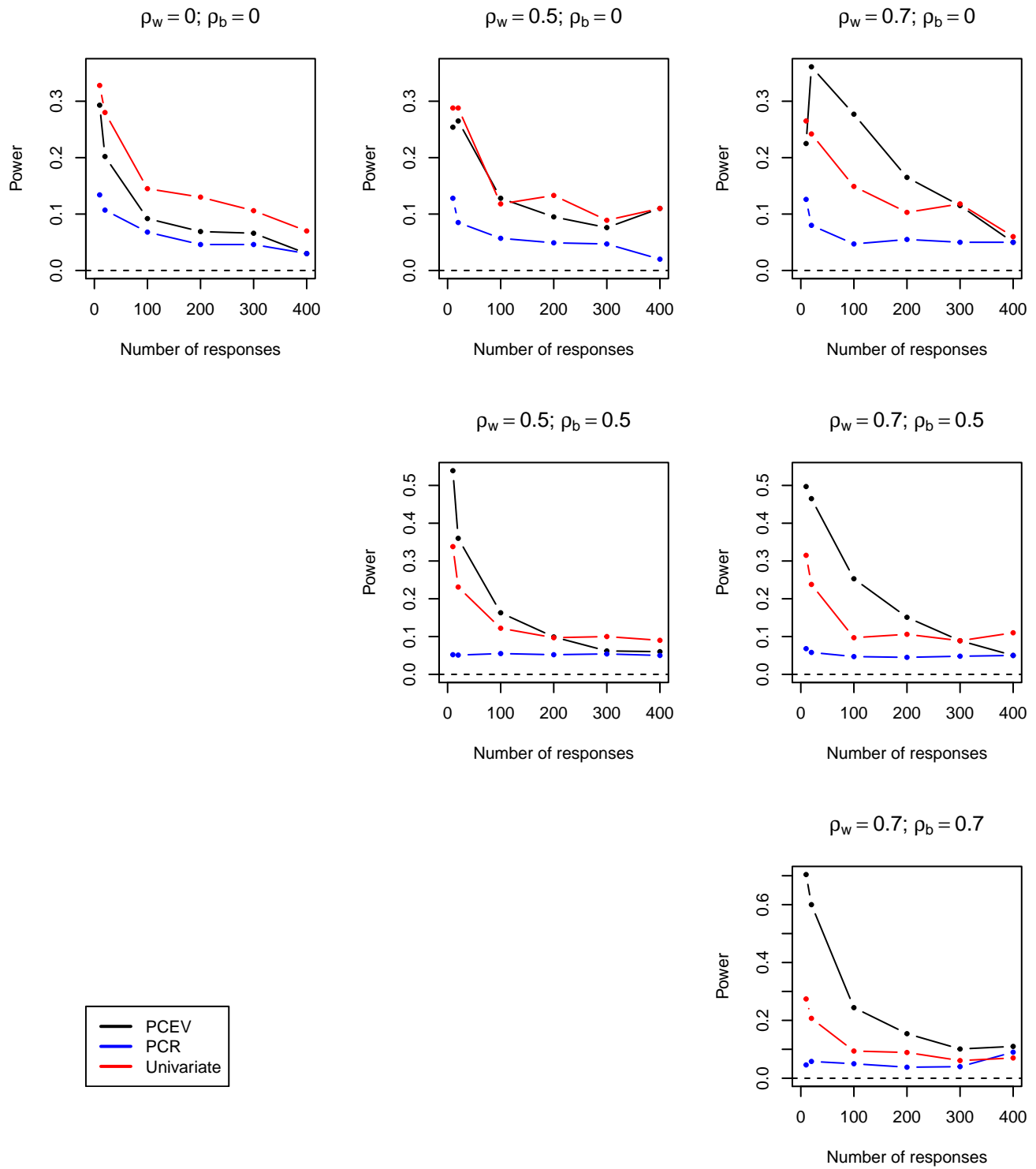
2.17 Significance level: 0.05, Heritability: 1%, Number of blocks: 2



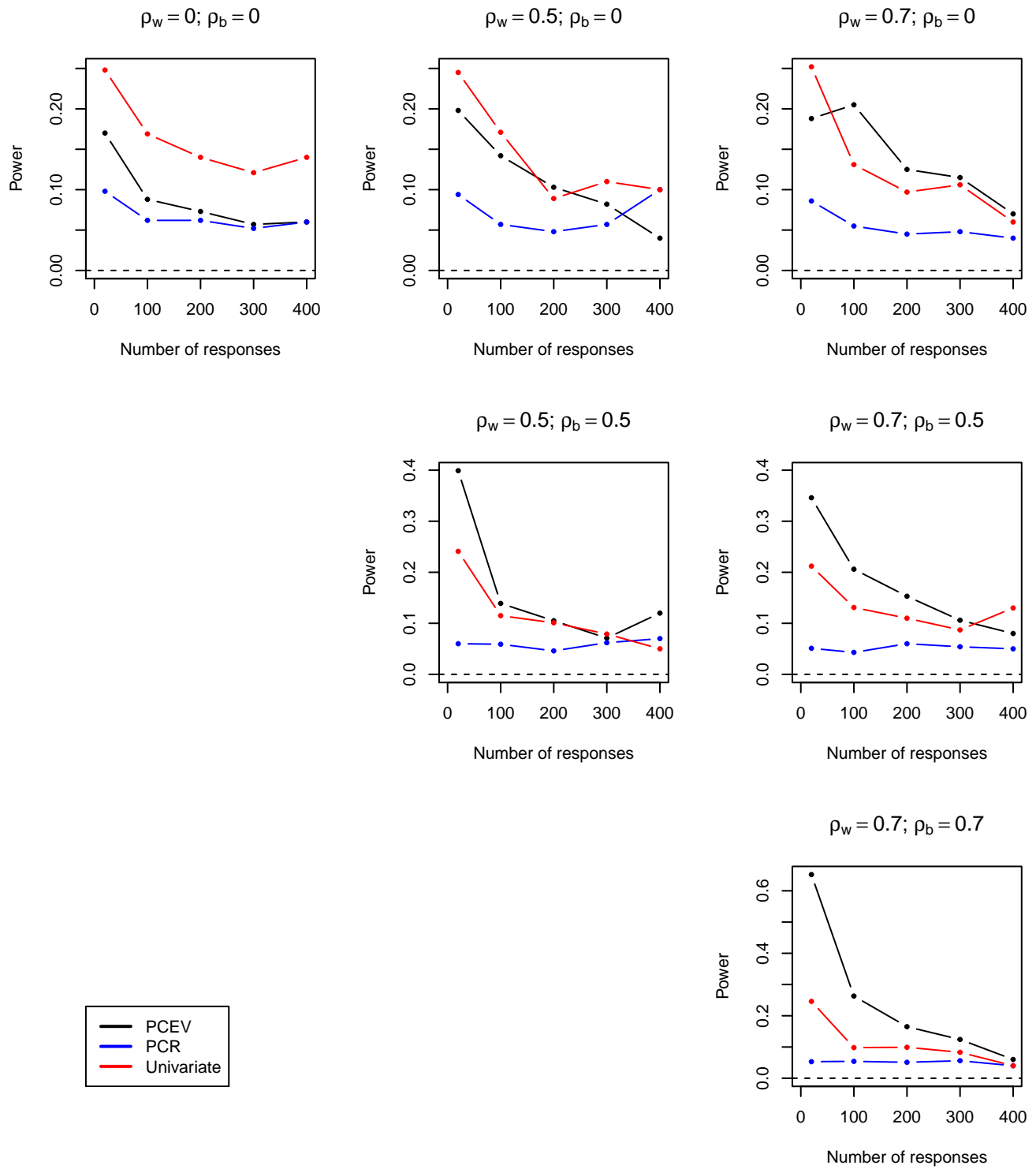
2.18 Significance level: 0.05, Heritability: 1%, Number of blocks: 5



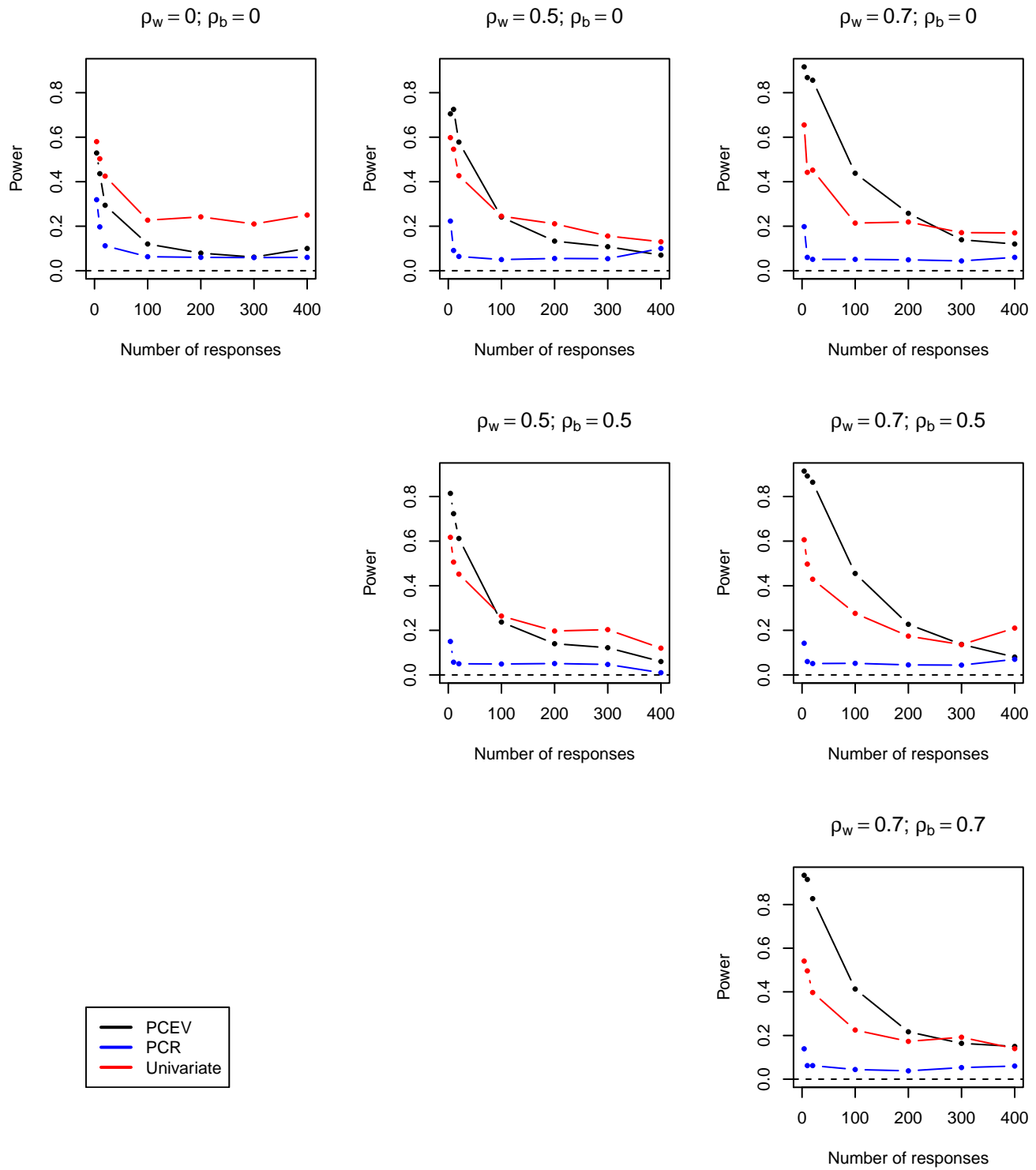
2.19 Significance level: 0.05, Heritability: 1%, Number of blocks: 10



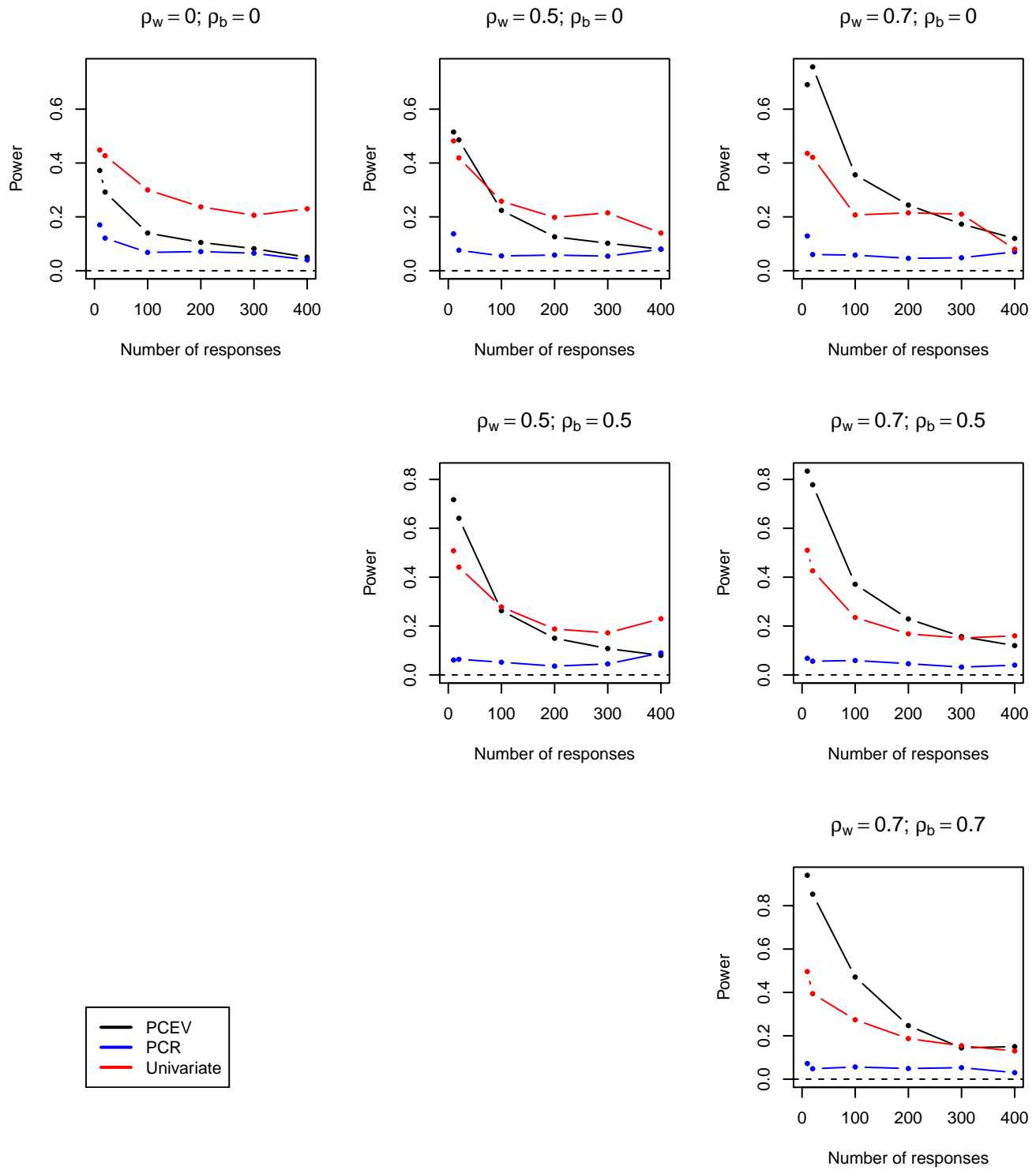
2.20 Significance level: 0.05, Heritability: 1%, Number of blocks: 20



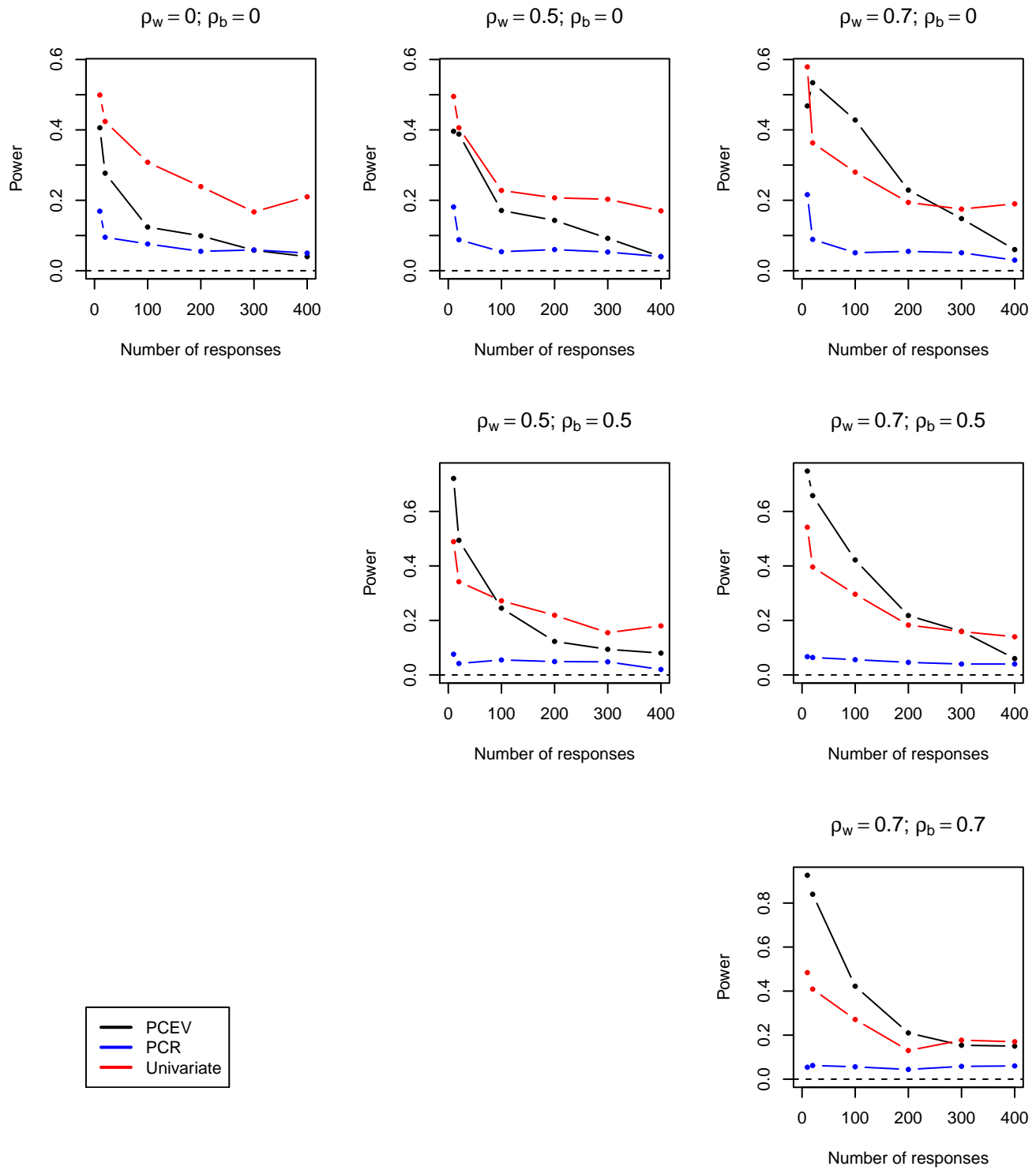
2.21 Significance level: 0.05, Heritability: 1.5%, Number of blocks: 2



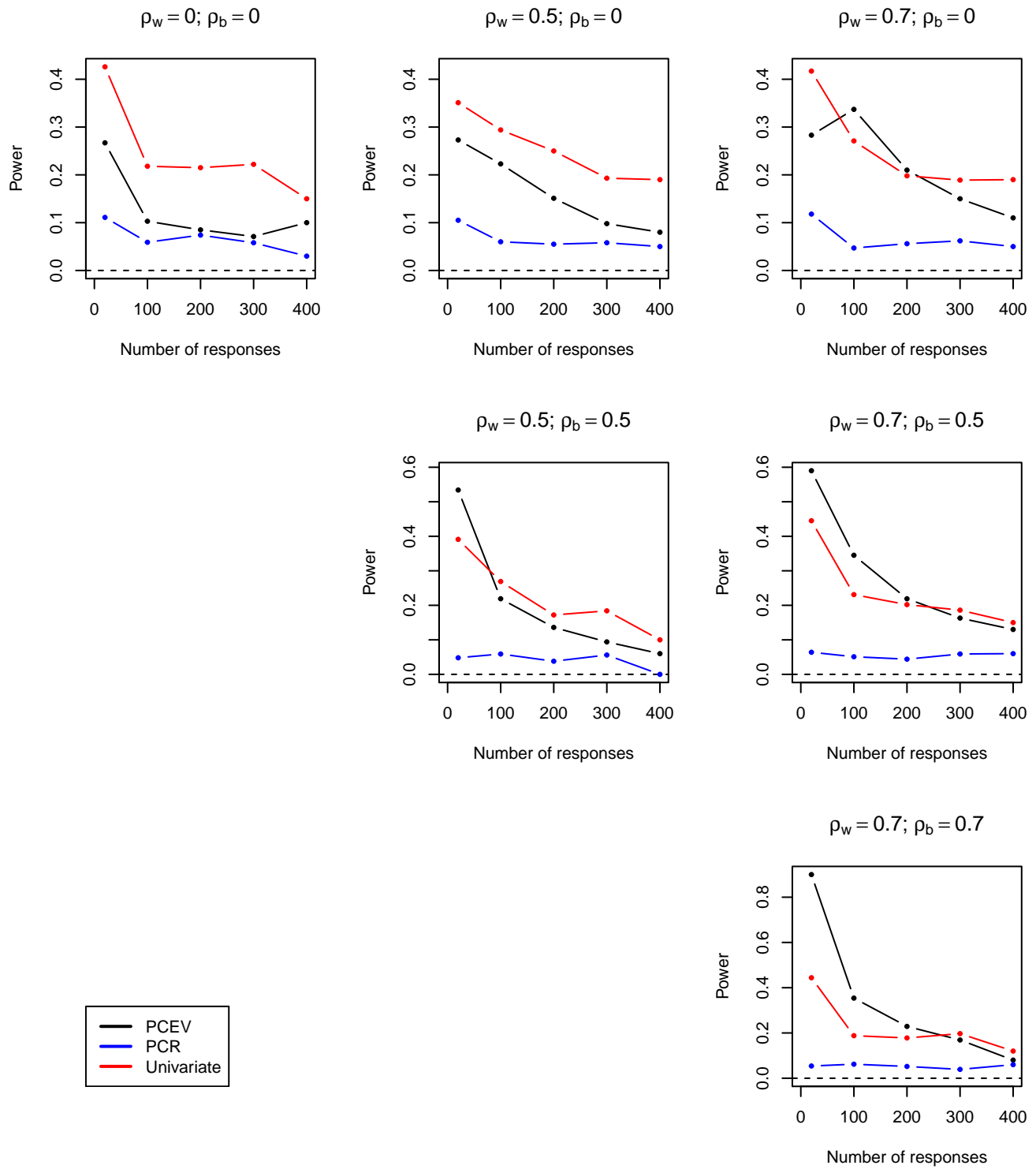
2.22 Significance level: 0.05, Heritability: 1.5%, Number of blocks: 5



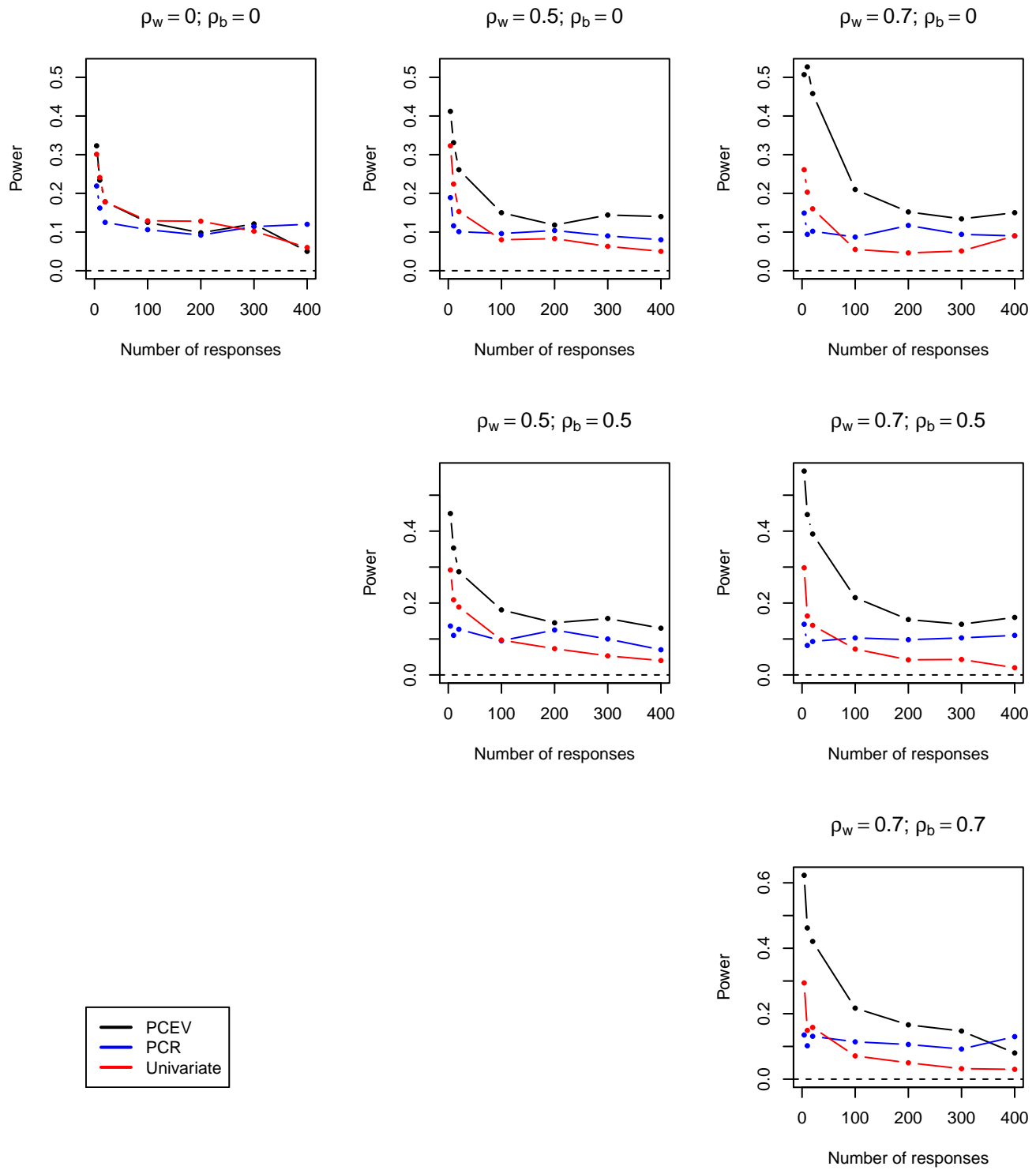
2.23 Significance level: 0.05, Heritability: 1.5%, Number of blocks: 10



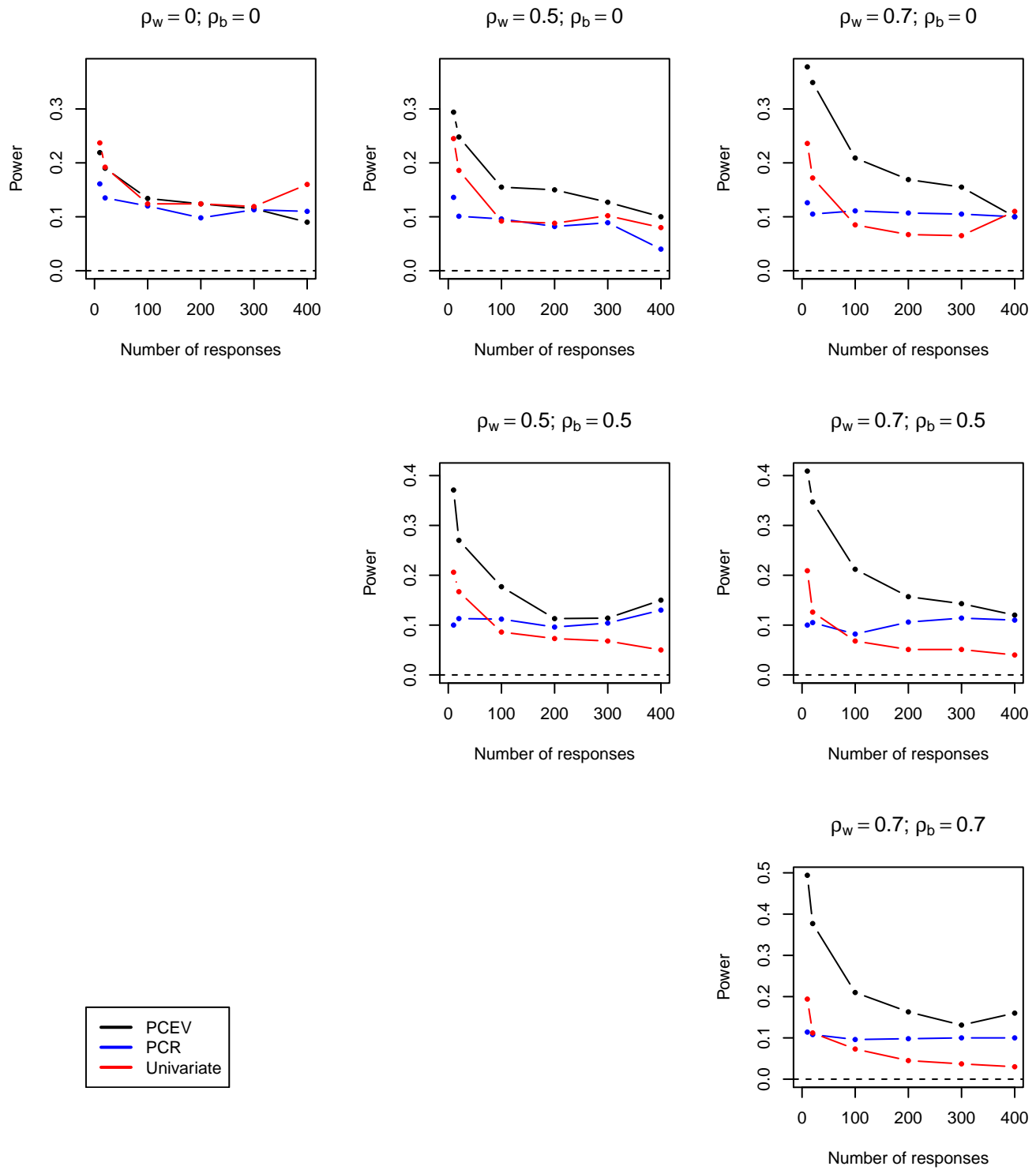
2.24 Significance level: 0.05, Heritability: 1.5%, Number of blocks: 20



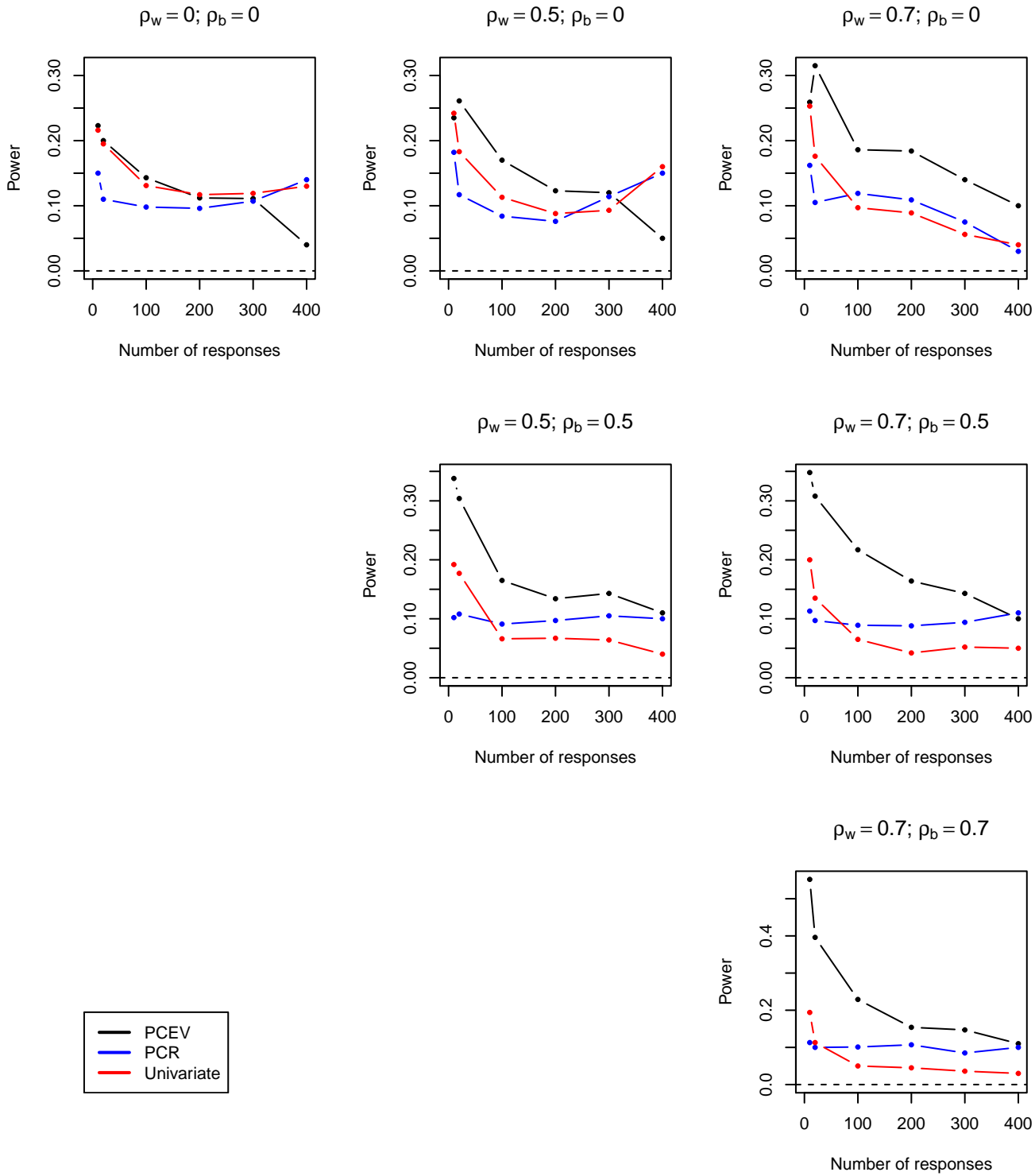
2.25 Significance level: 0.1, Heritability: 0.5%, Number of blocks: 2



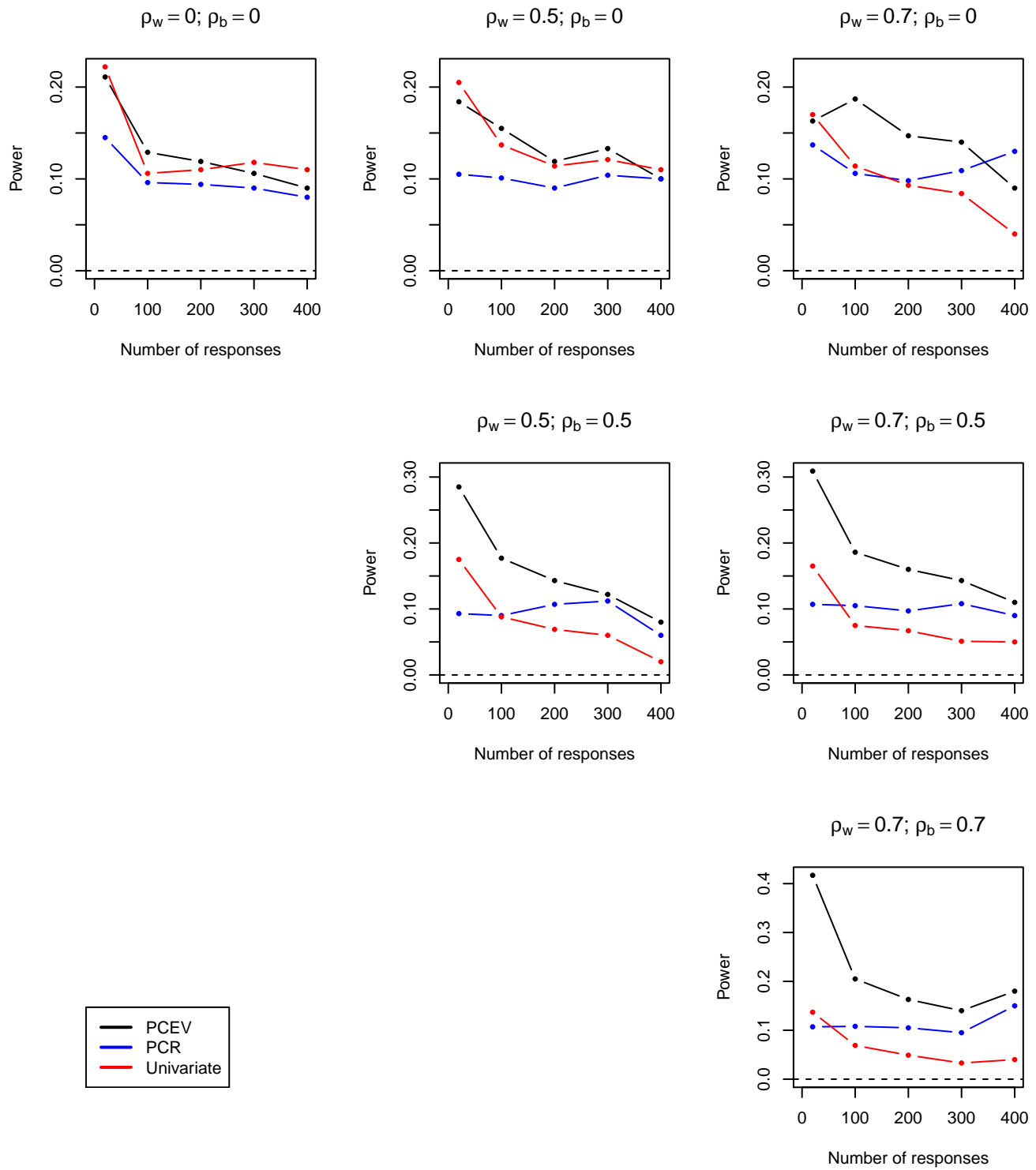
2.26 Significance level: 0.1, Heritability: 0.5%, Number of blocks: 5



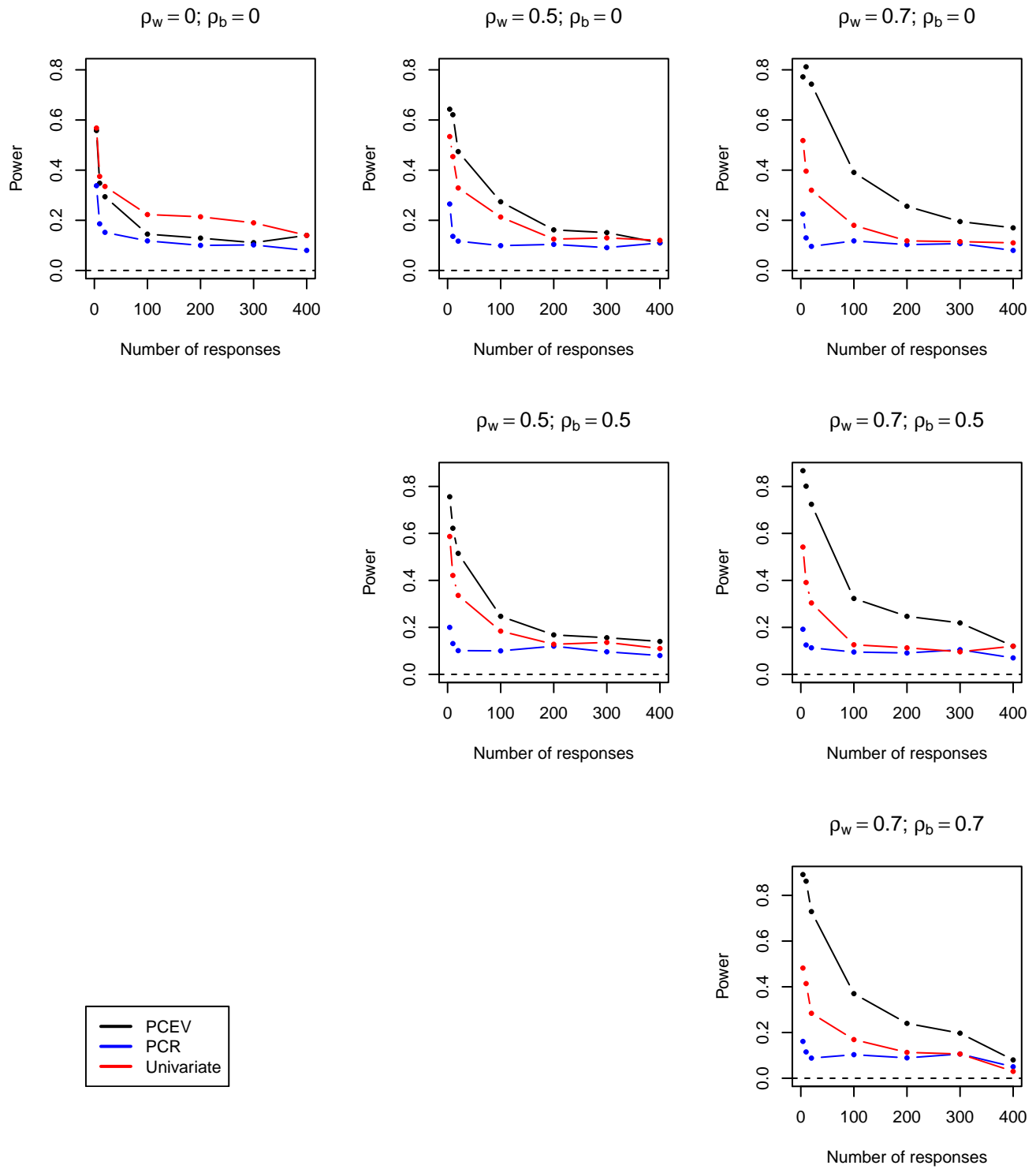
2.27 Significance level: 0.1, Heritability: 0.5%, Number of blocks: 10



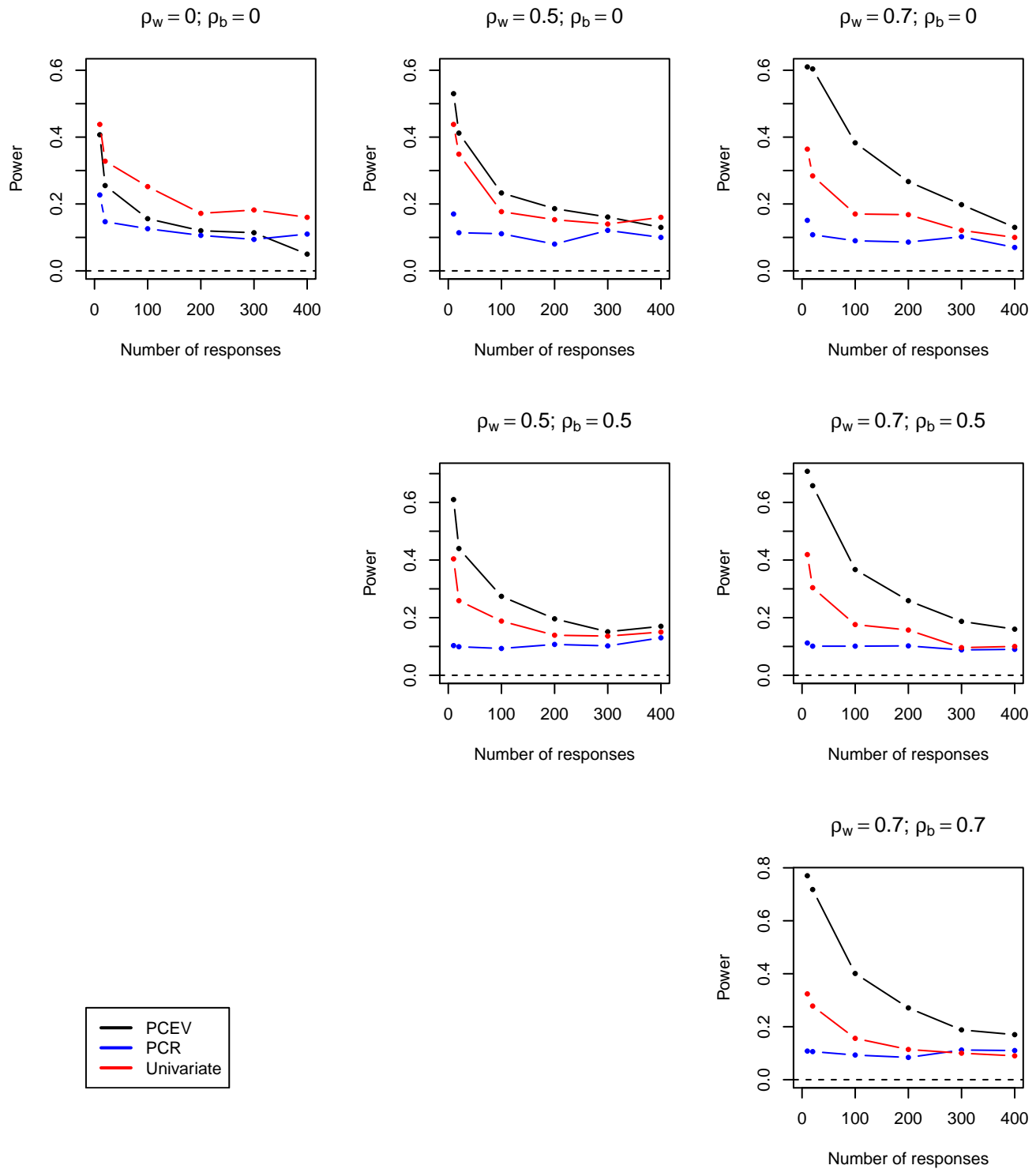
2.28 Significance level: 0.1, Heritability: 0.5%, Number of blocks: 20



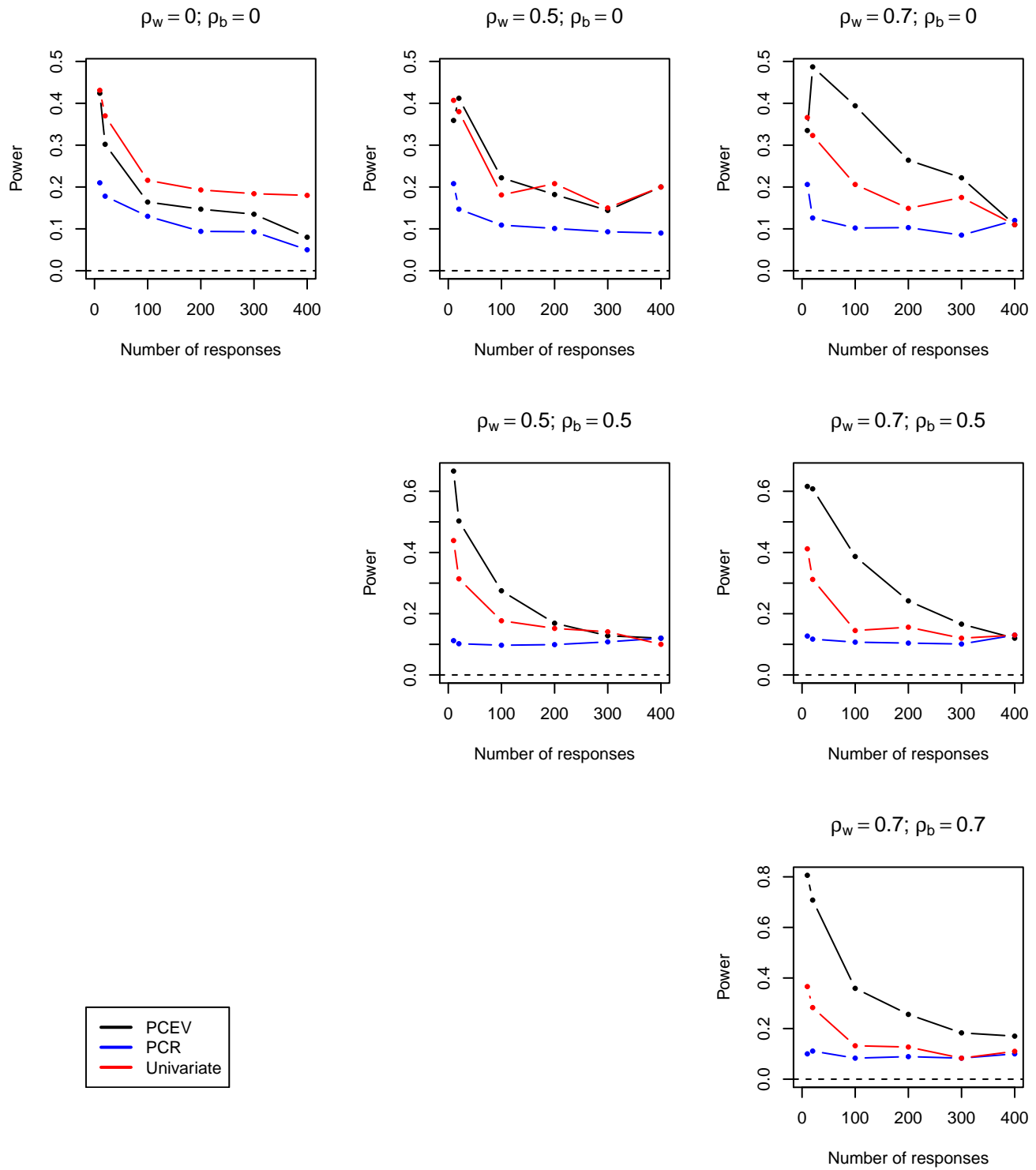
2.29 Significance level: 0.1, Heritability: 1%, Number of blocks: 2



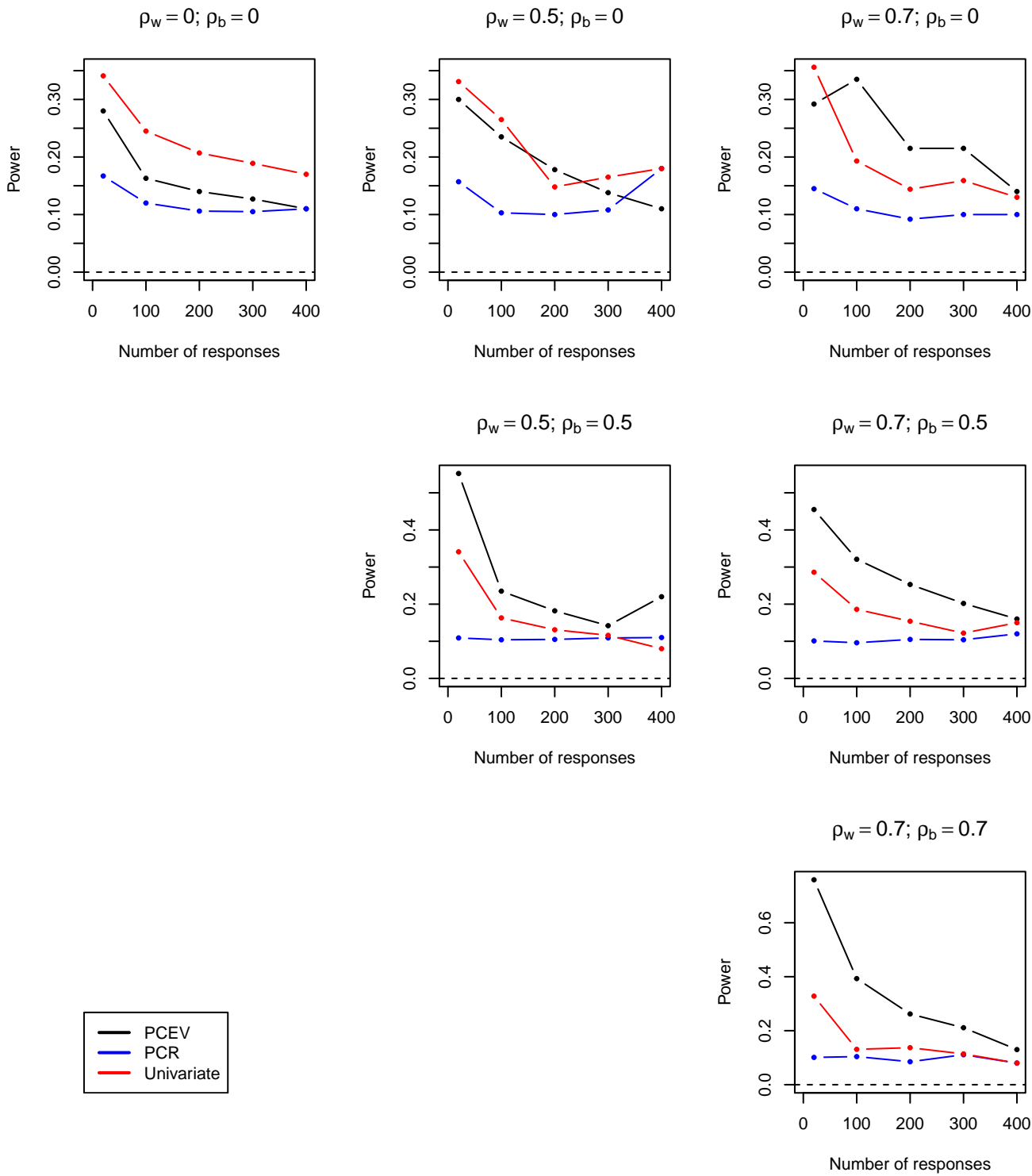
2.30 Significance level: 0.1, Heritability: 1%, Number of blocks: 5



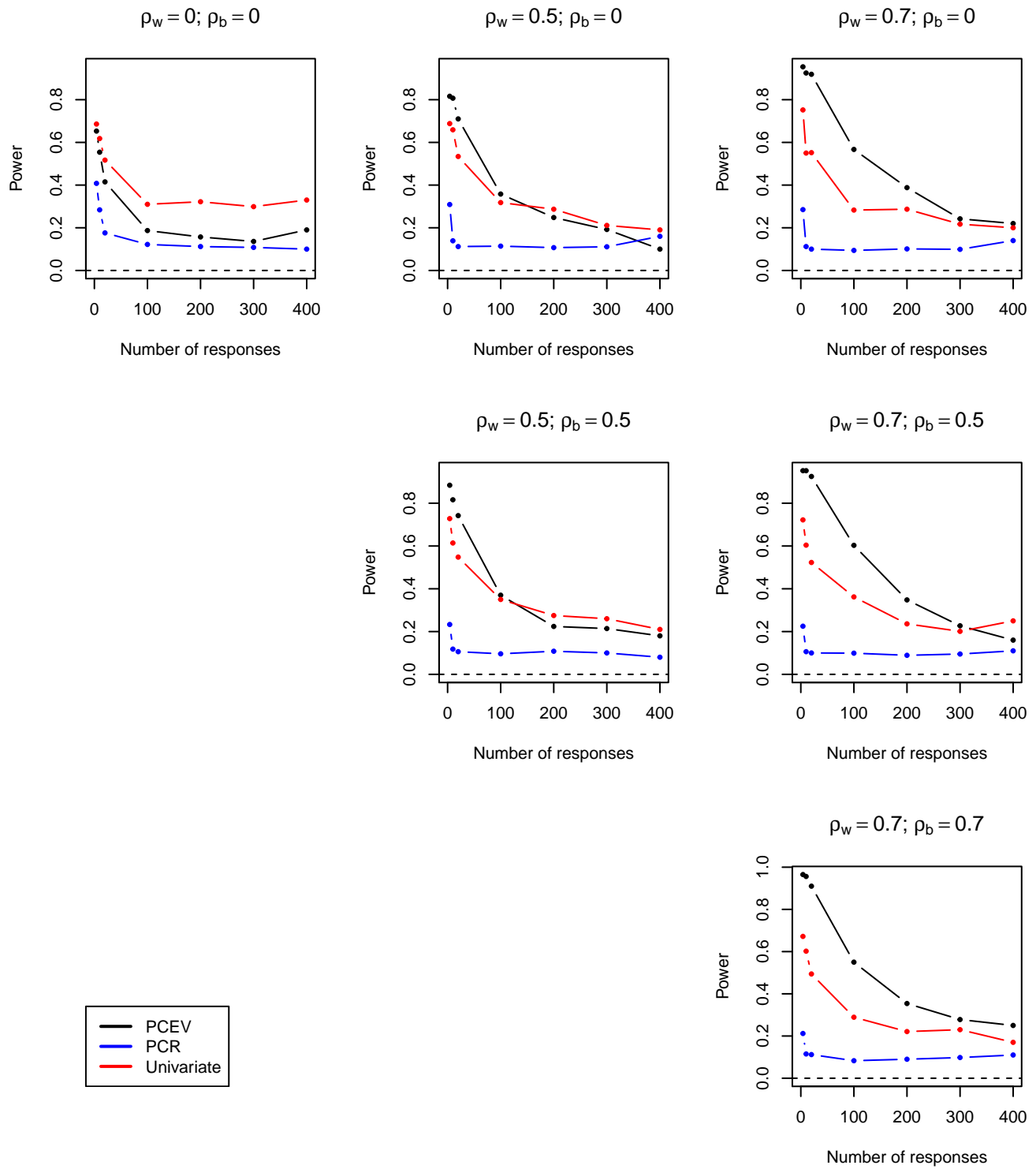
2.31 Significance level: 0.1, Heritability: 1%, Number of blocks: 10



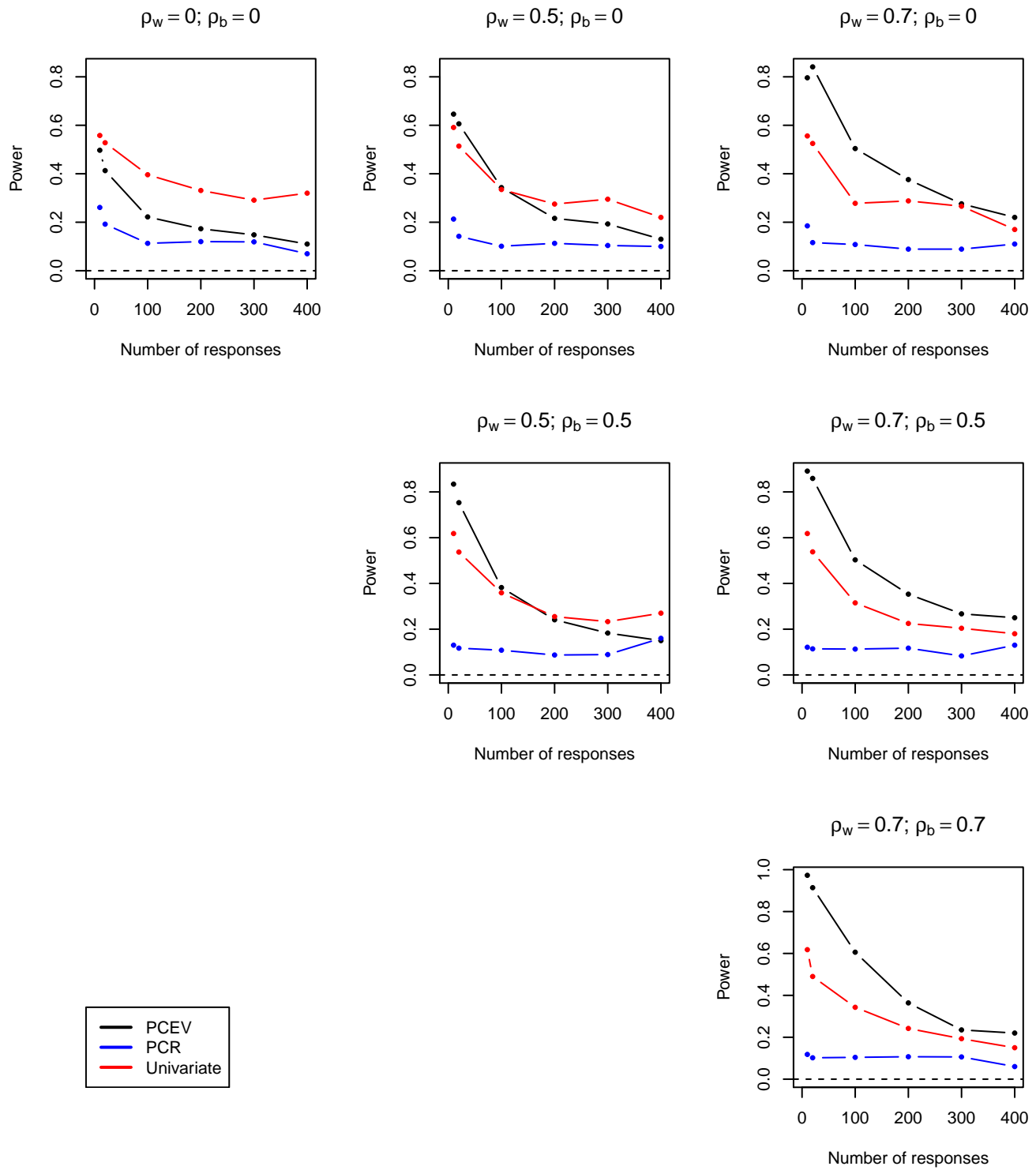
2.32 Significance level: 0.1, Heritability: 1%, Number of blocks: 20



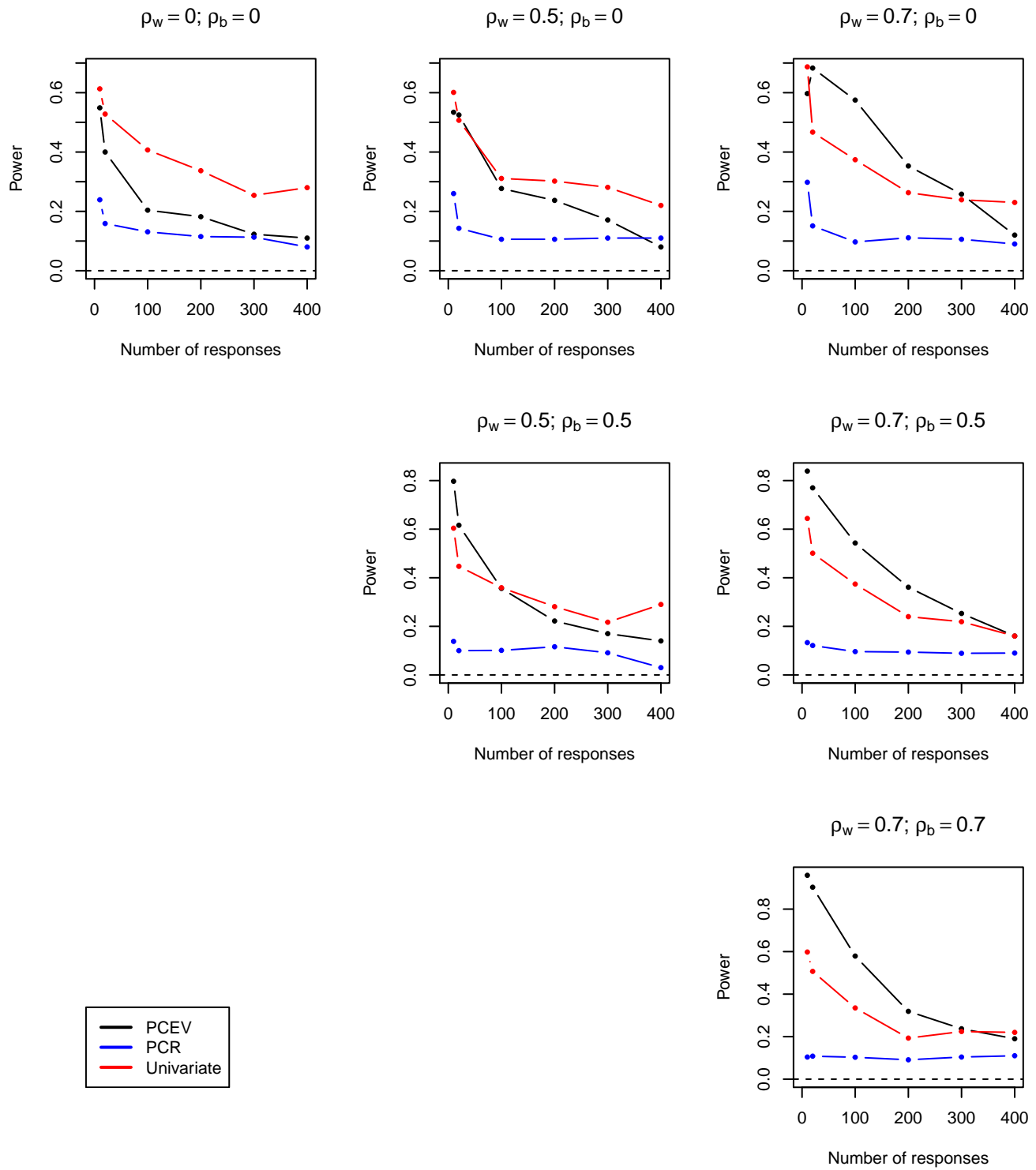
2.33 Significance level: 0.1, Heritability: 1.5%, Number of blocks: 2



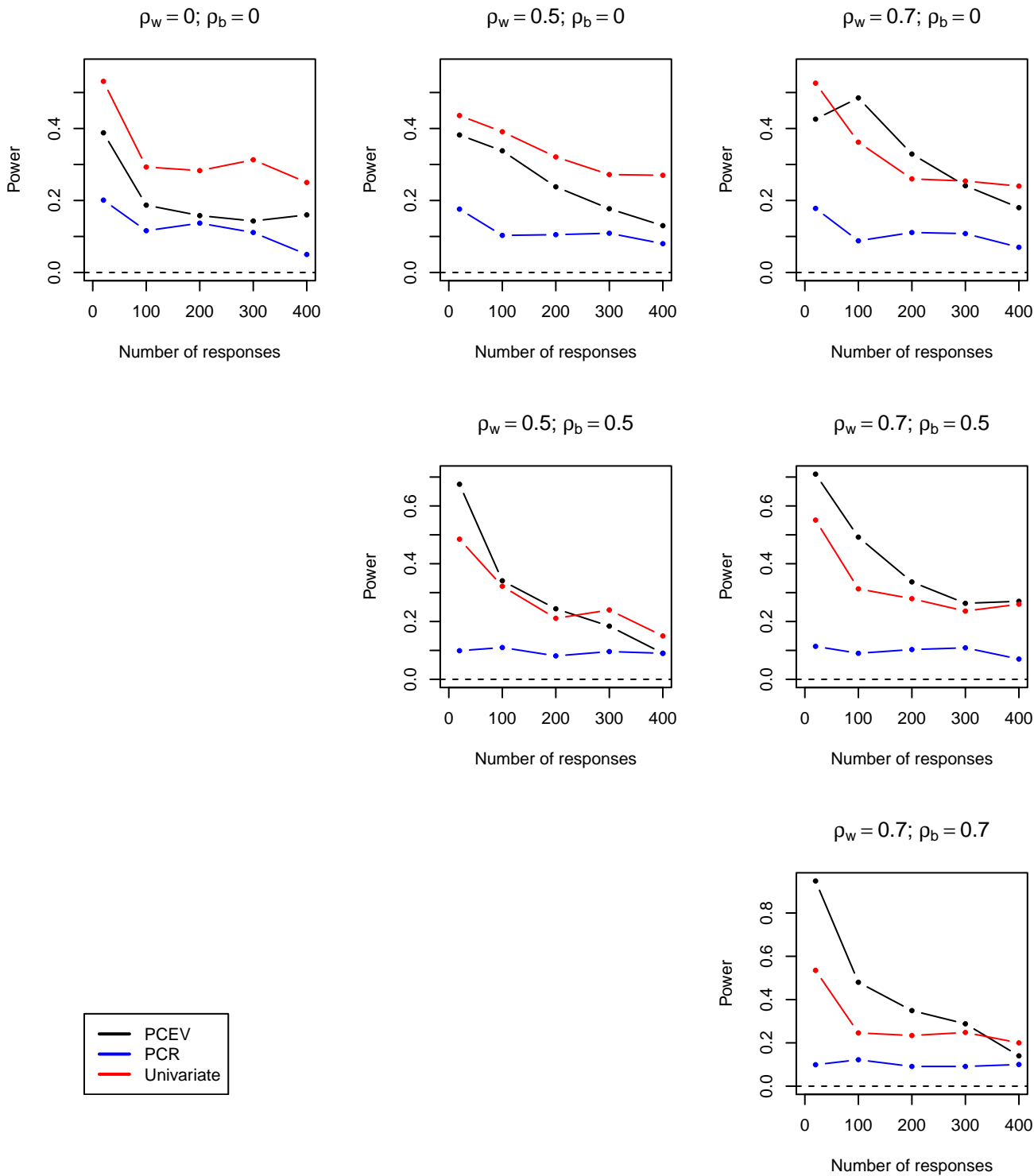
2.34 Significance level: 0.1, Heritability: 1.5%, Number of blocks: 5



2.35 Significance level: 0.1, Heritability: 1.5%, Number of blocks: 10



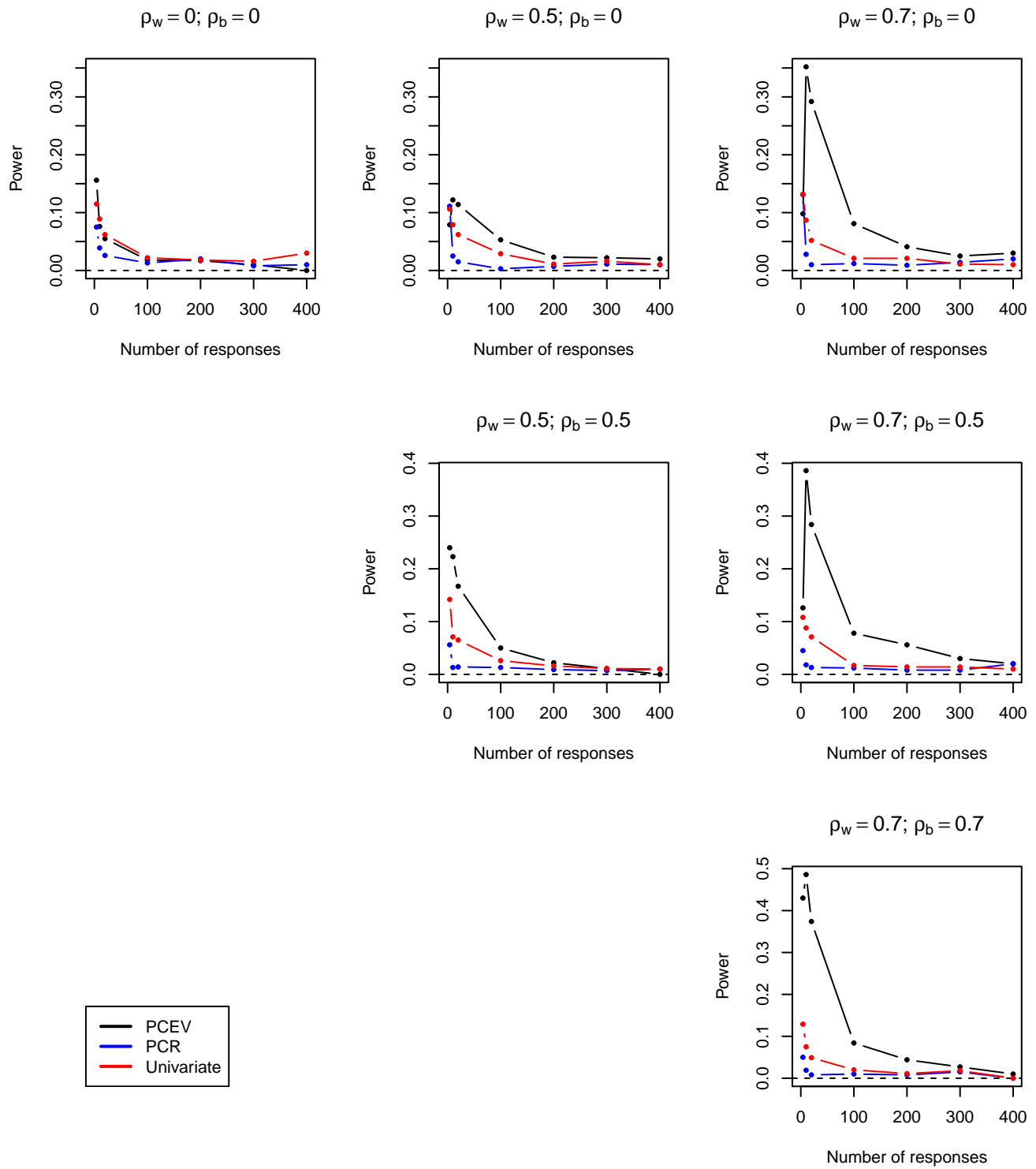
2.36 Significance level: 0.1, Heritability: 1.5%, Number of blocks: 20



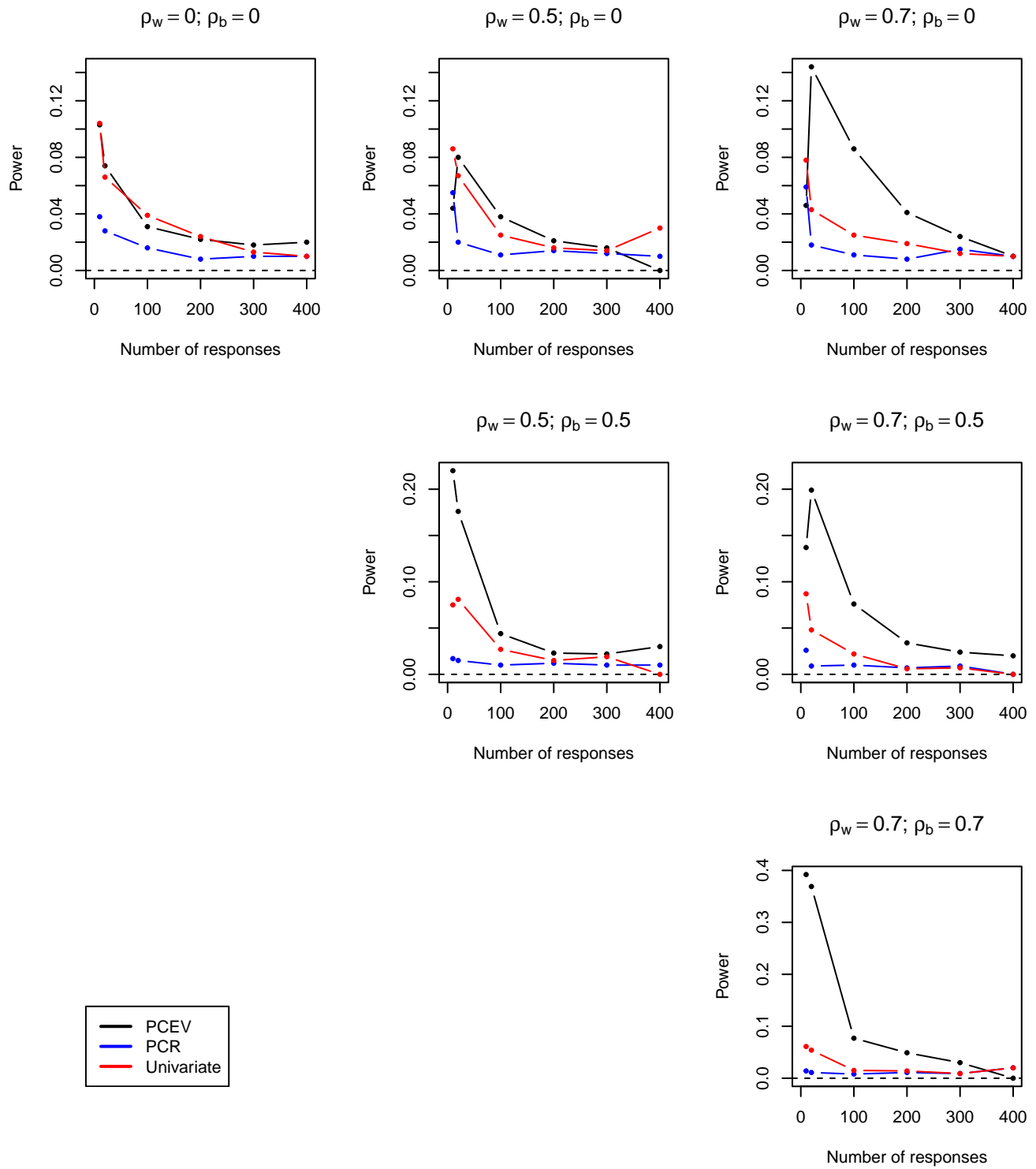
3 Simulation scenario 3

We simulated an association between the continuous covariate x and two components of the multivariate phenotype \mathbf{Y} : the associations are of the same size, in the same direction, and the two components lie in the same block.

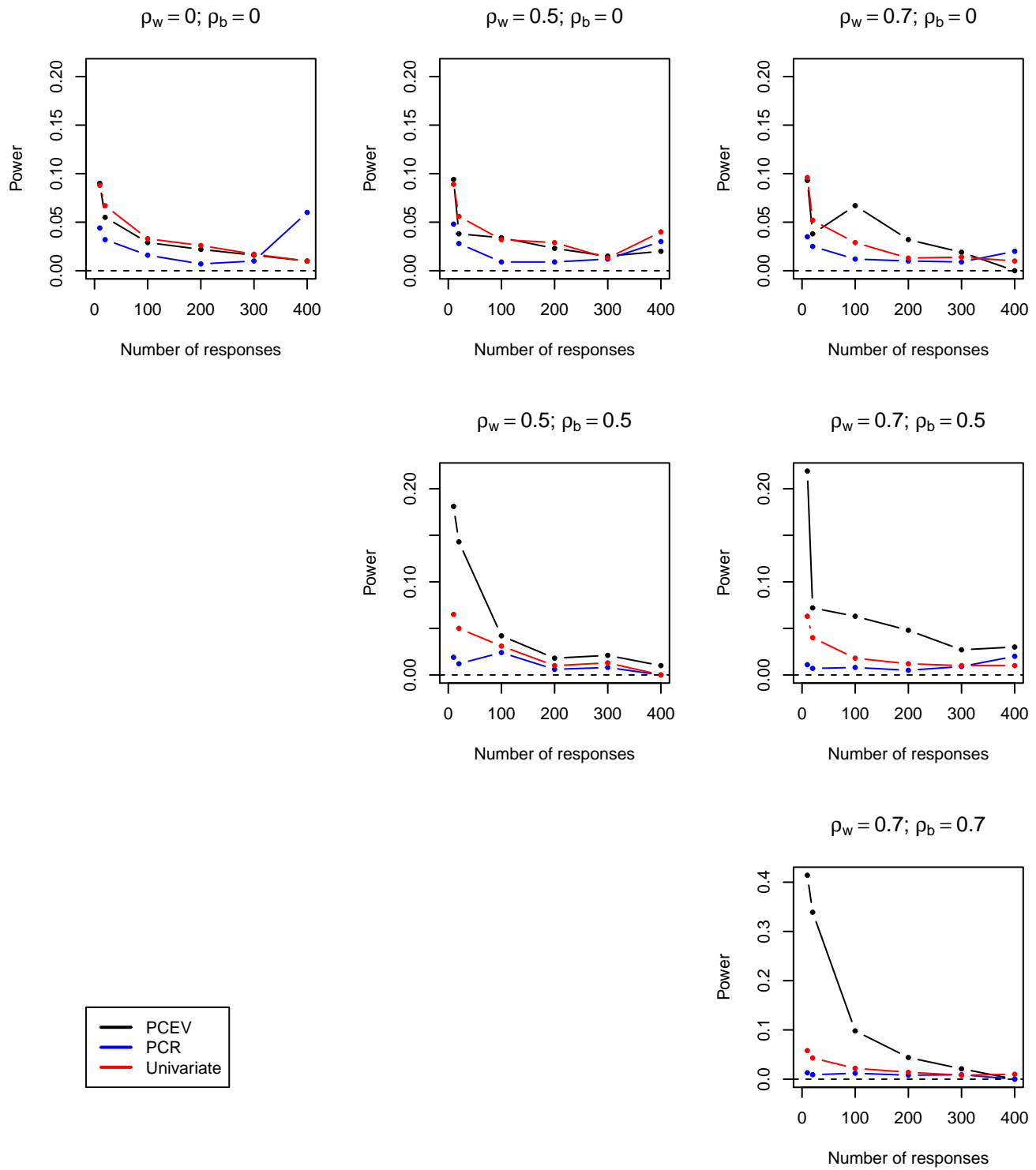
3.1 Significance level: 0.01, Heritability: 0.5%, Number of blocks: 2



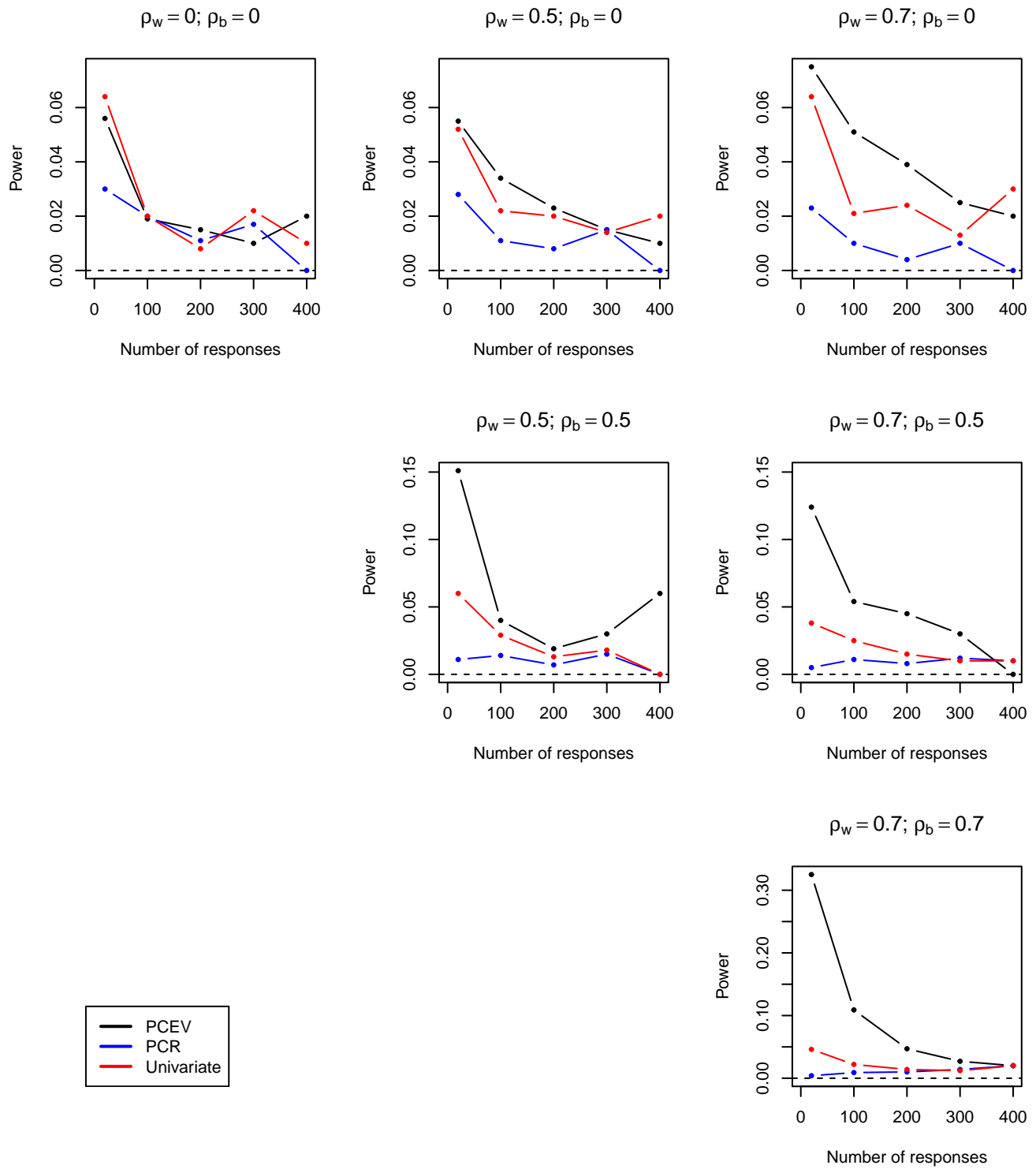
3.2 Significance level: 0.01, Heritability: 0.5%, Number of blocks: 5



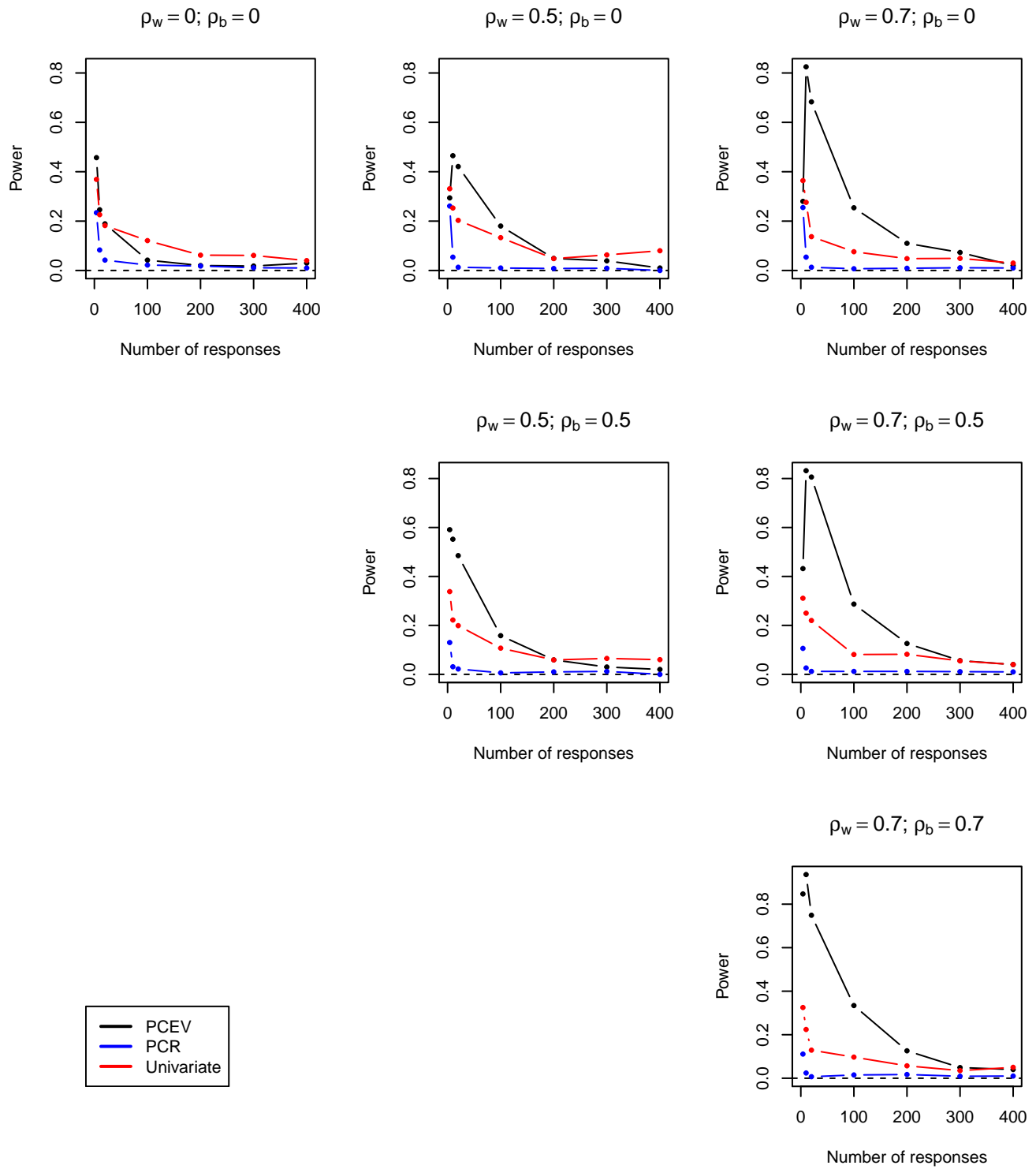
3.3 Significance level: 0.01, Heritability: 0.5%, Number of blocks: 10



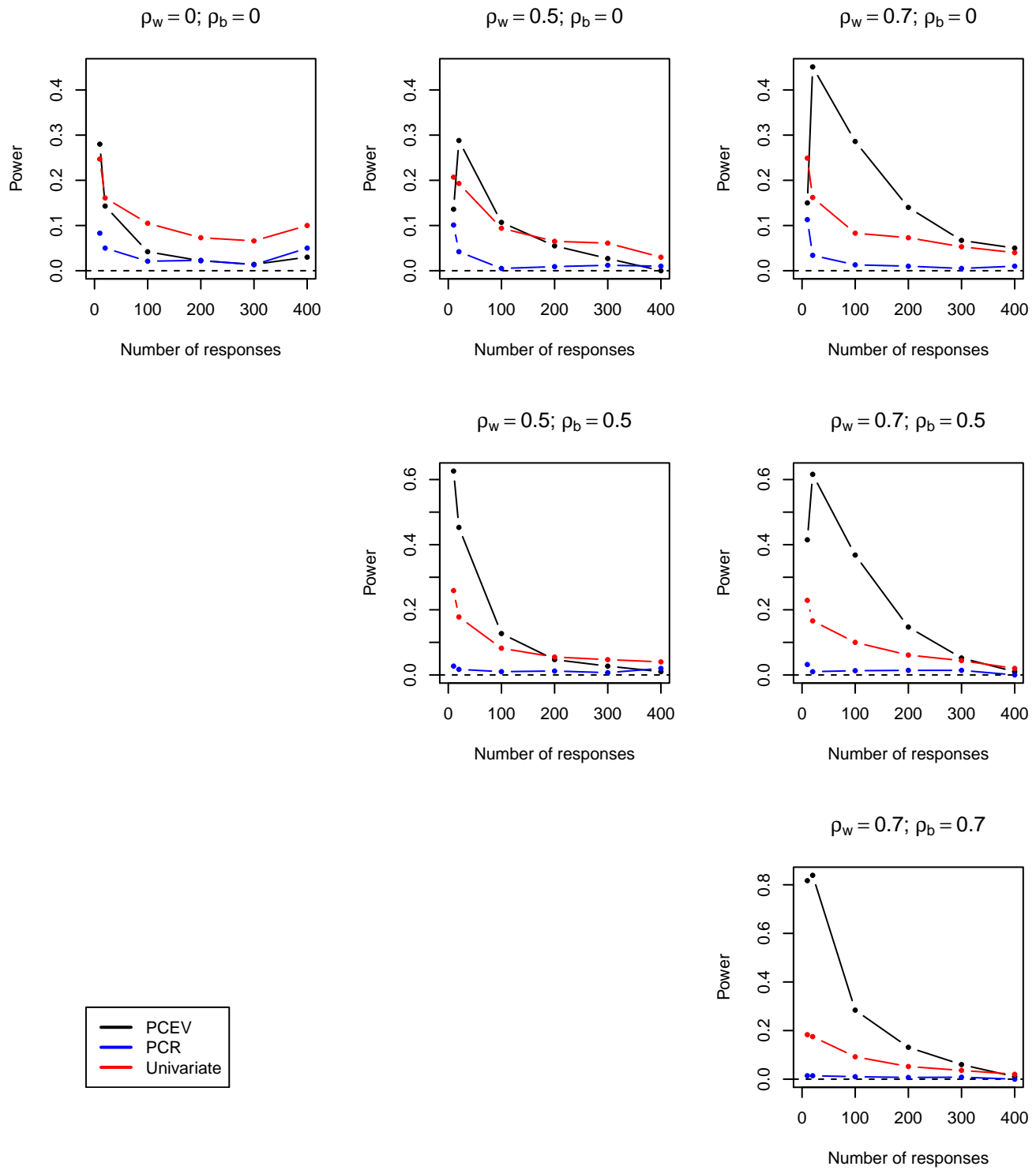
3.4 Significance level: 0.01, Heritability: 0.5%, Number of blocks: 20



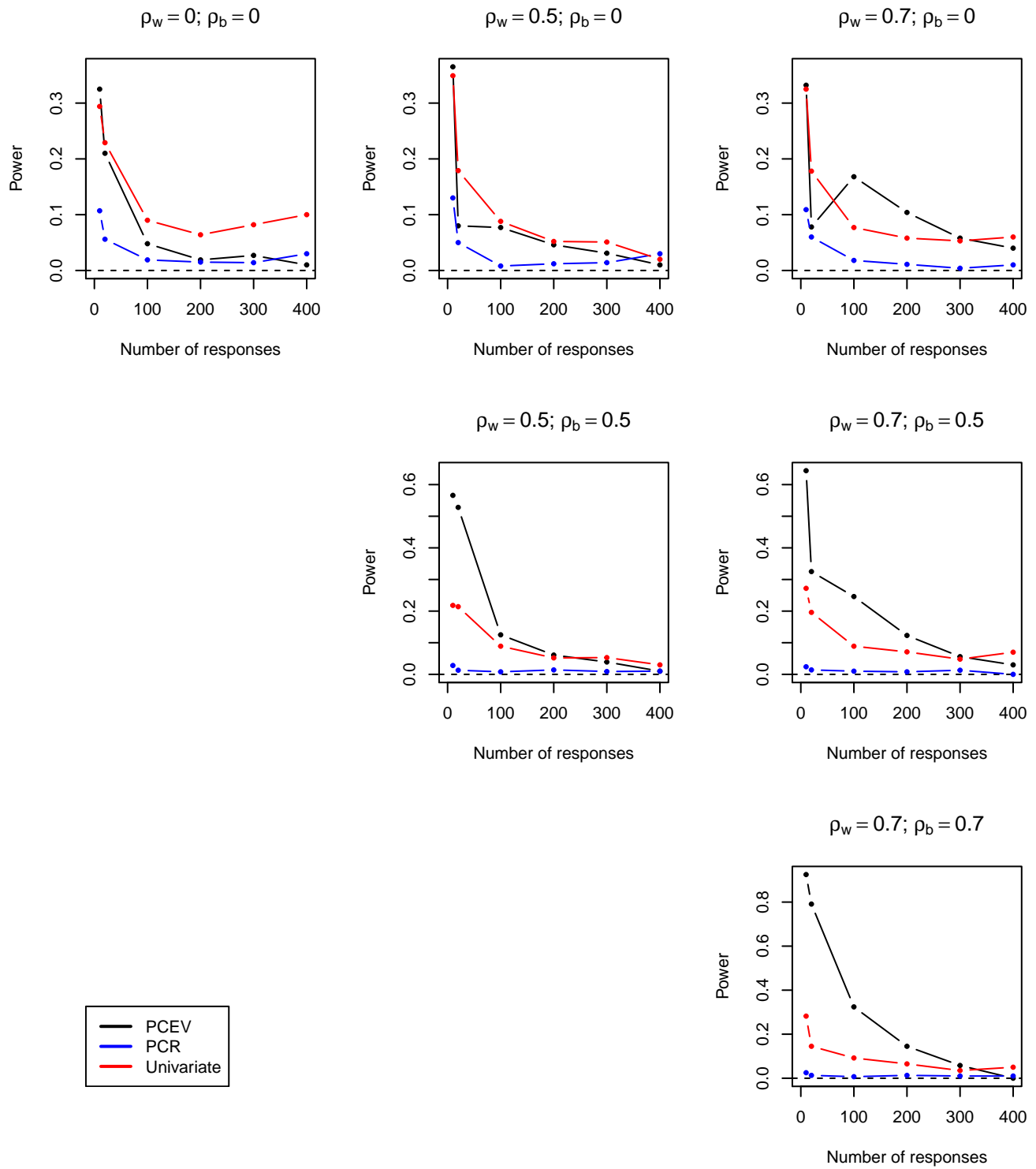
3.5 Significance level: 0.01, Heritability: 1%, Number of blocks: 2



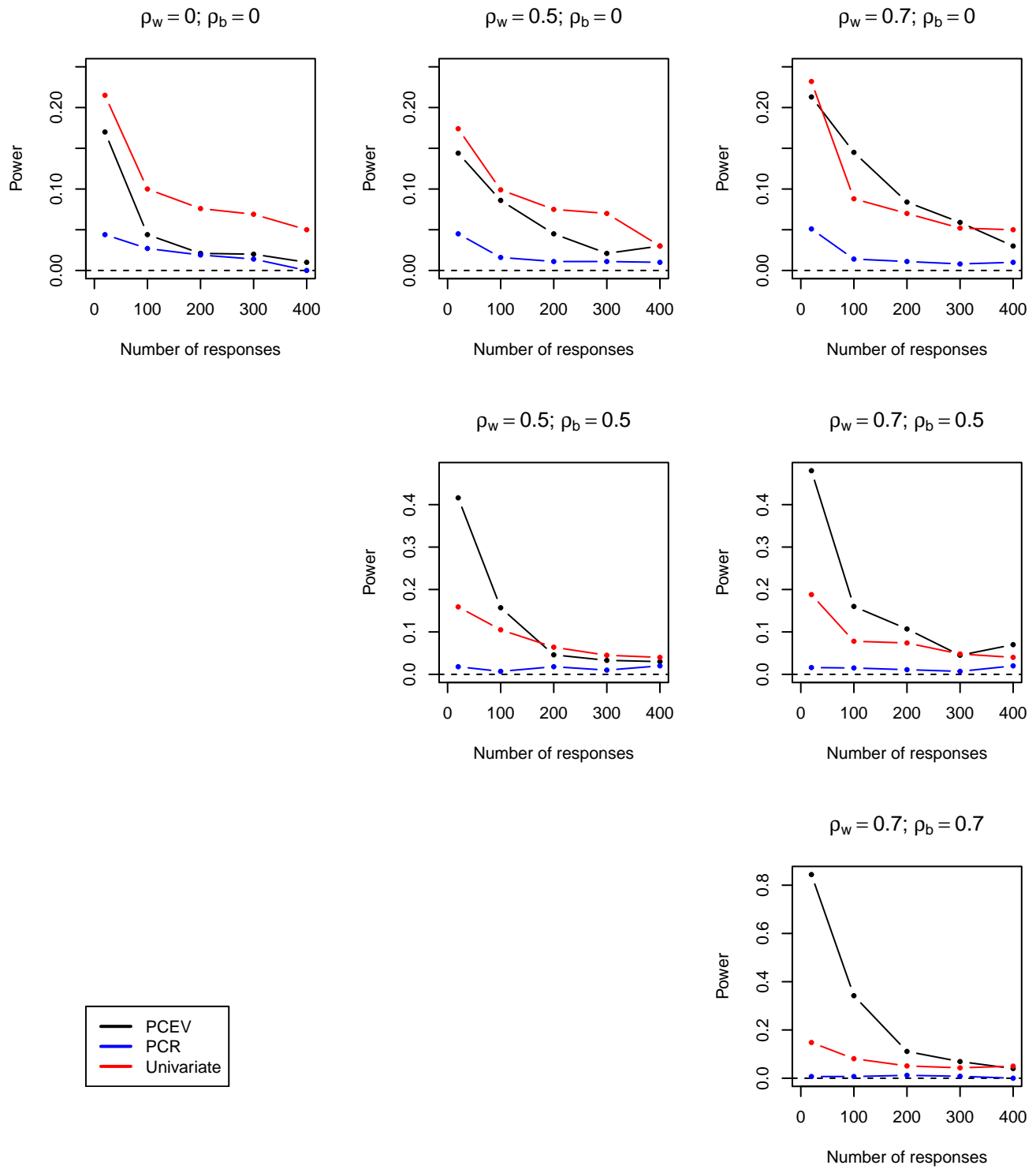
3.6 Significance level: 0.01, Heritability: 1%, Number of blocks: 5



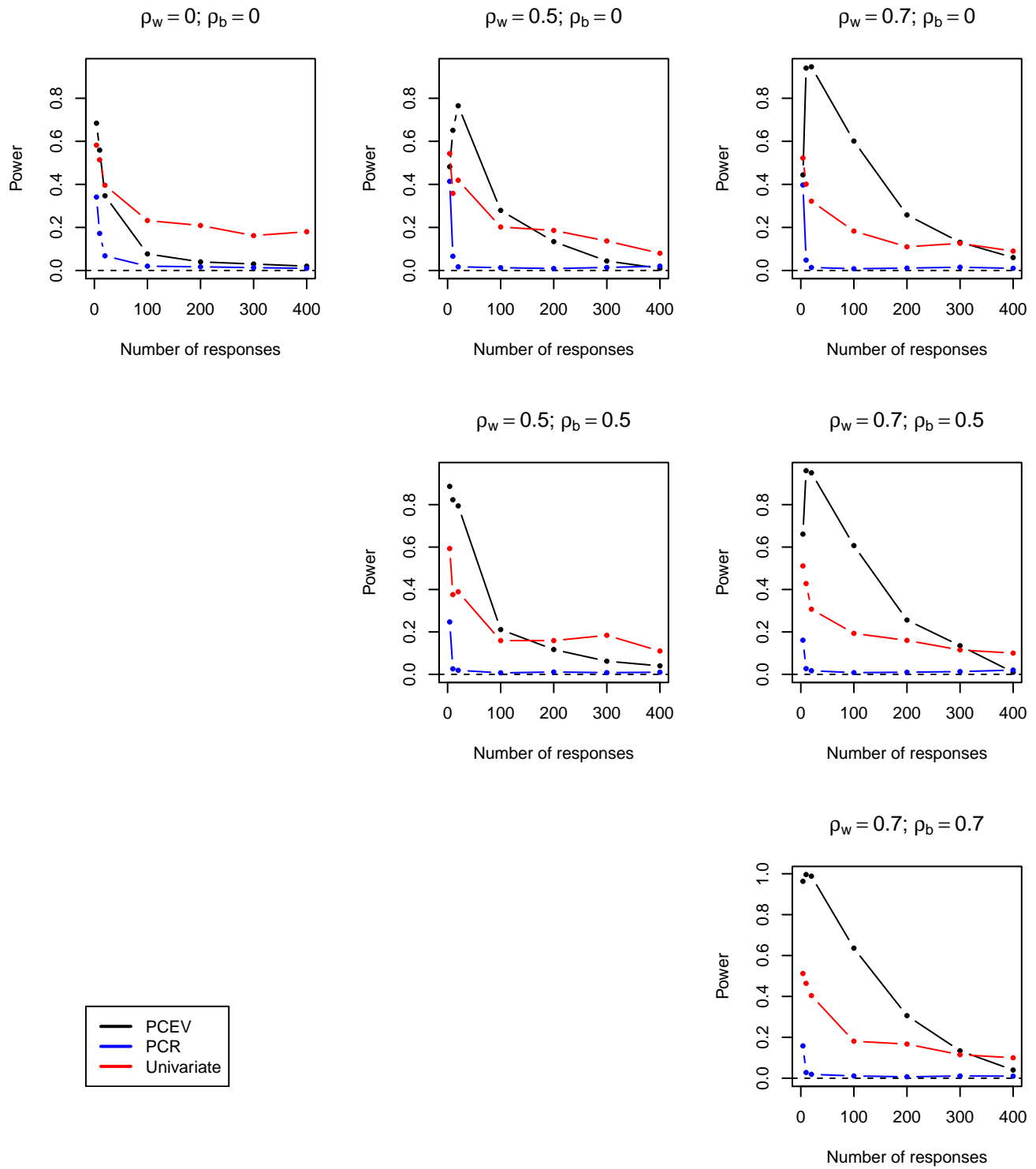
3.7 Significance level: 0.01, Heritability: 1%, Number of blocks: 10



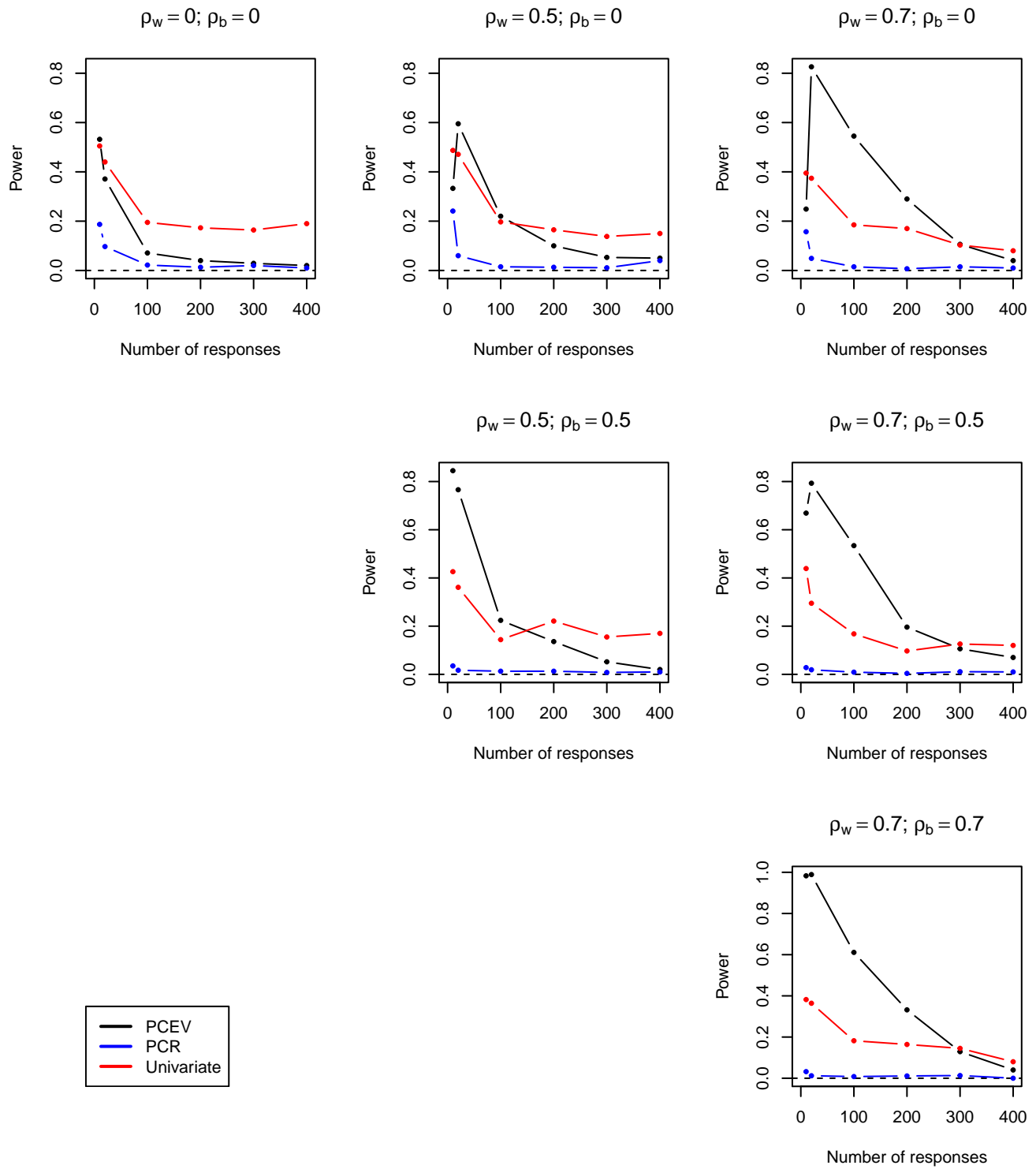
3.8 Significance level: 0.01, Heritability: 1%, Number of blocks: 20



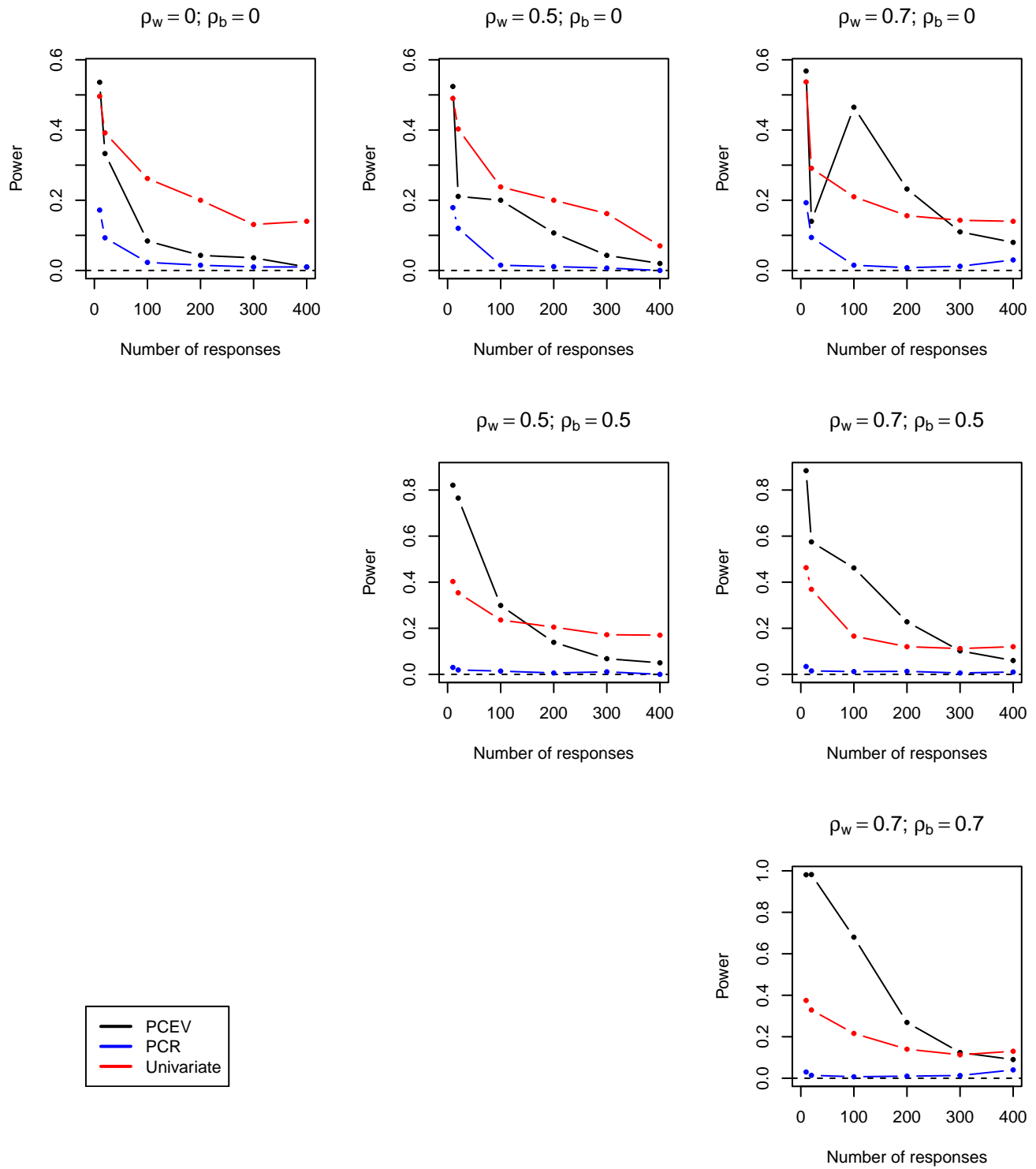
3.9 Significance level: 0.01, Heritability: 1.5%, Number of blocks: 2



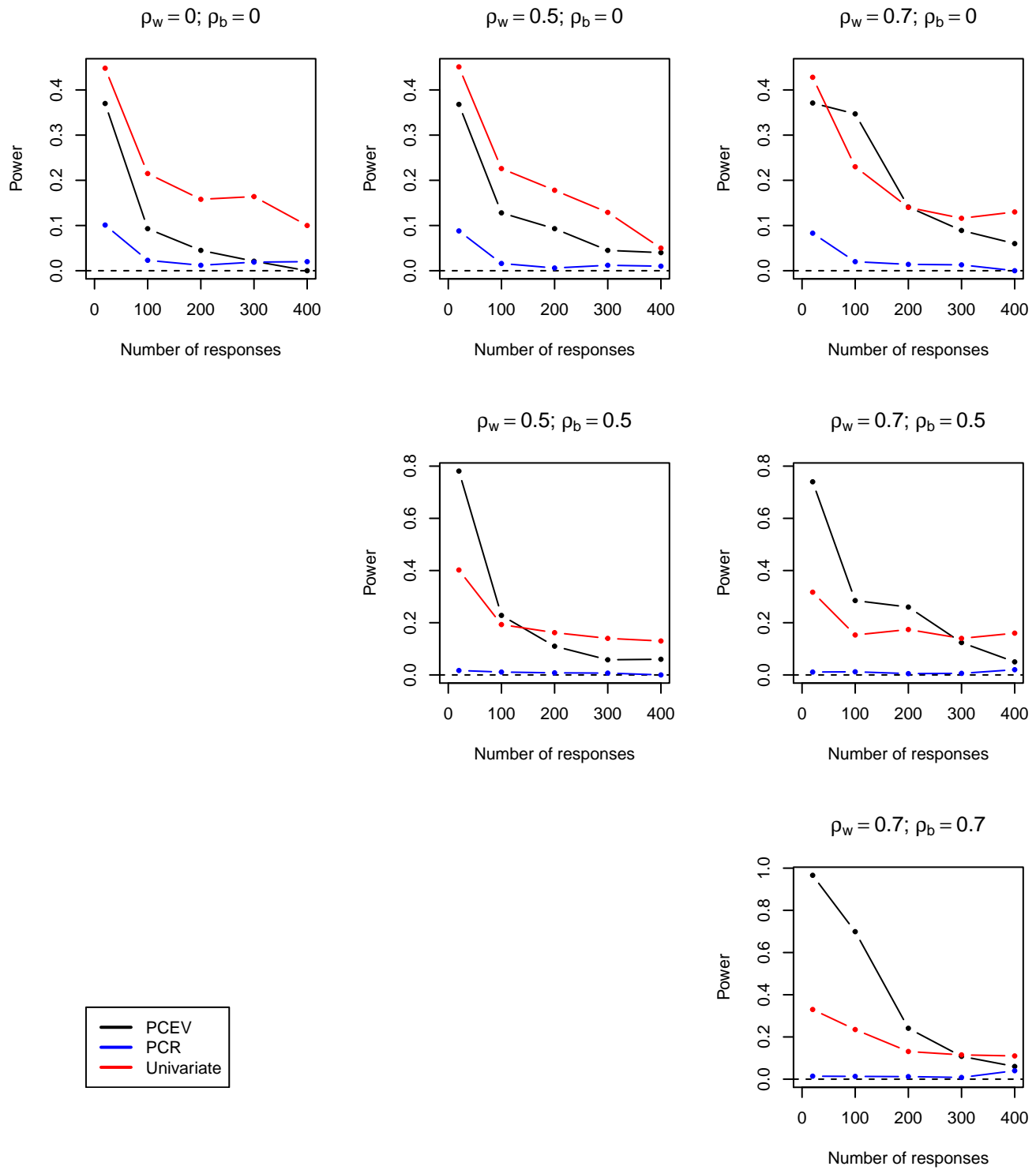
3.10 Significance level: 0.01, Heritability: 1.5%, Number of blocks: 5



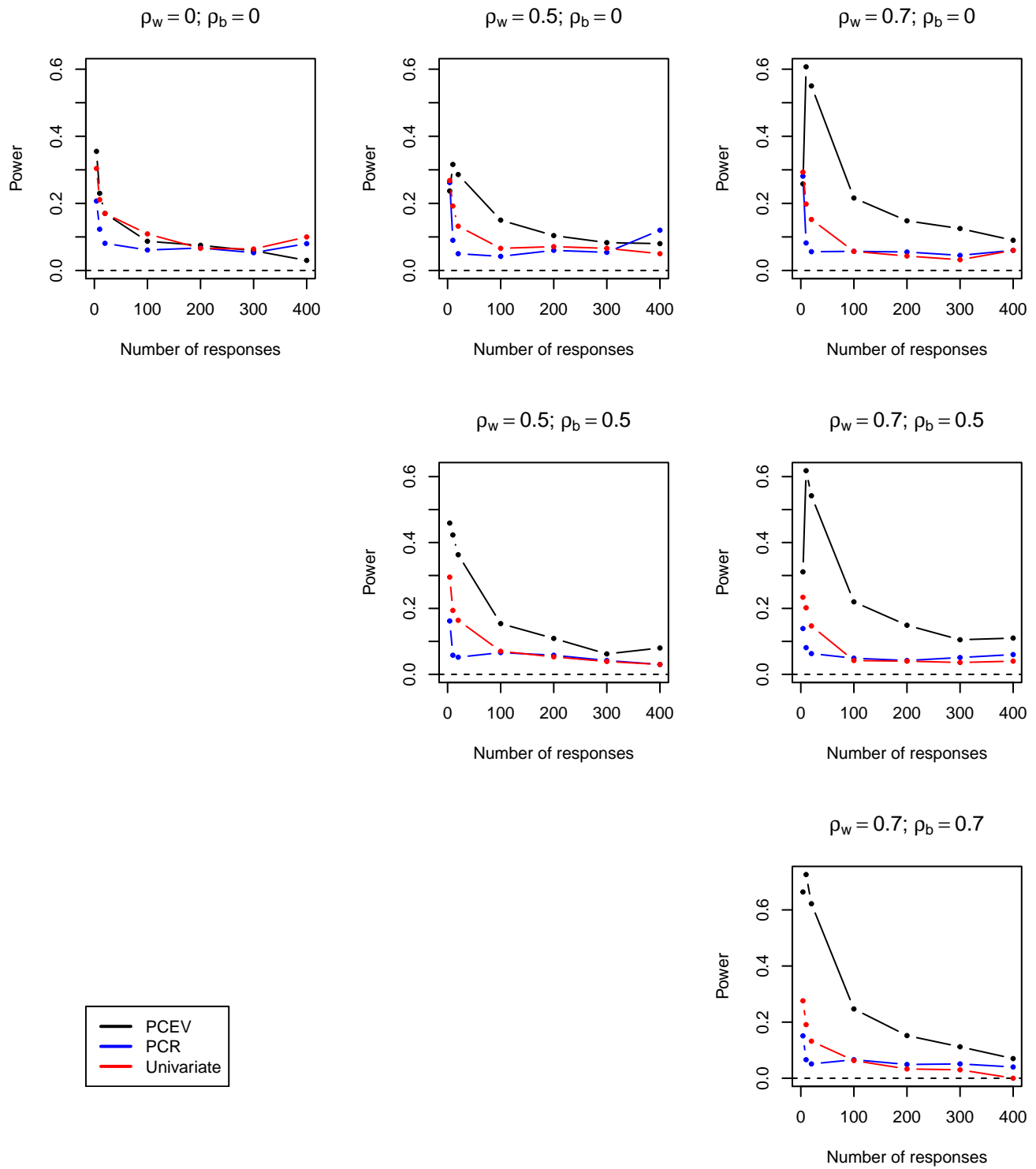
3.11 Significance level: 0.01, Heritability: 1.5%, Number of blocks: 10



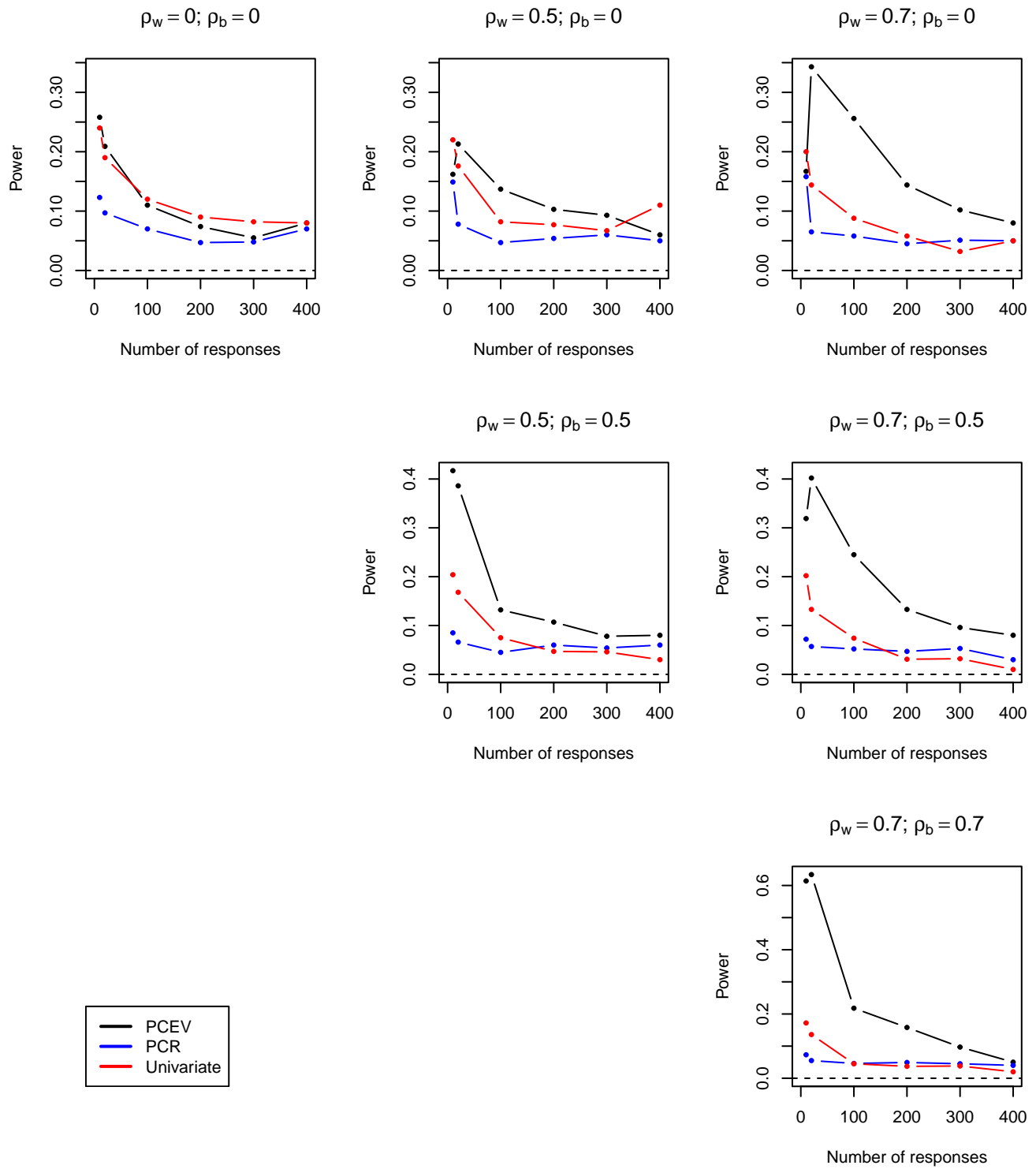
3.12 Significance level: 0.01, Heritability: 1.5%, Number of blocks: 20



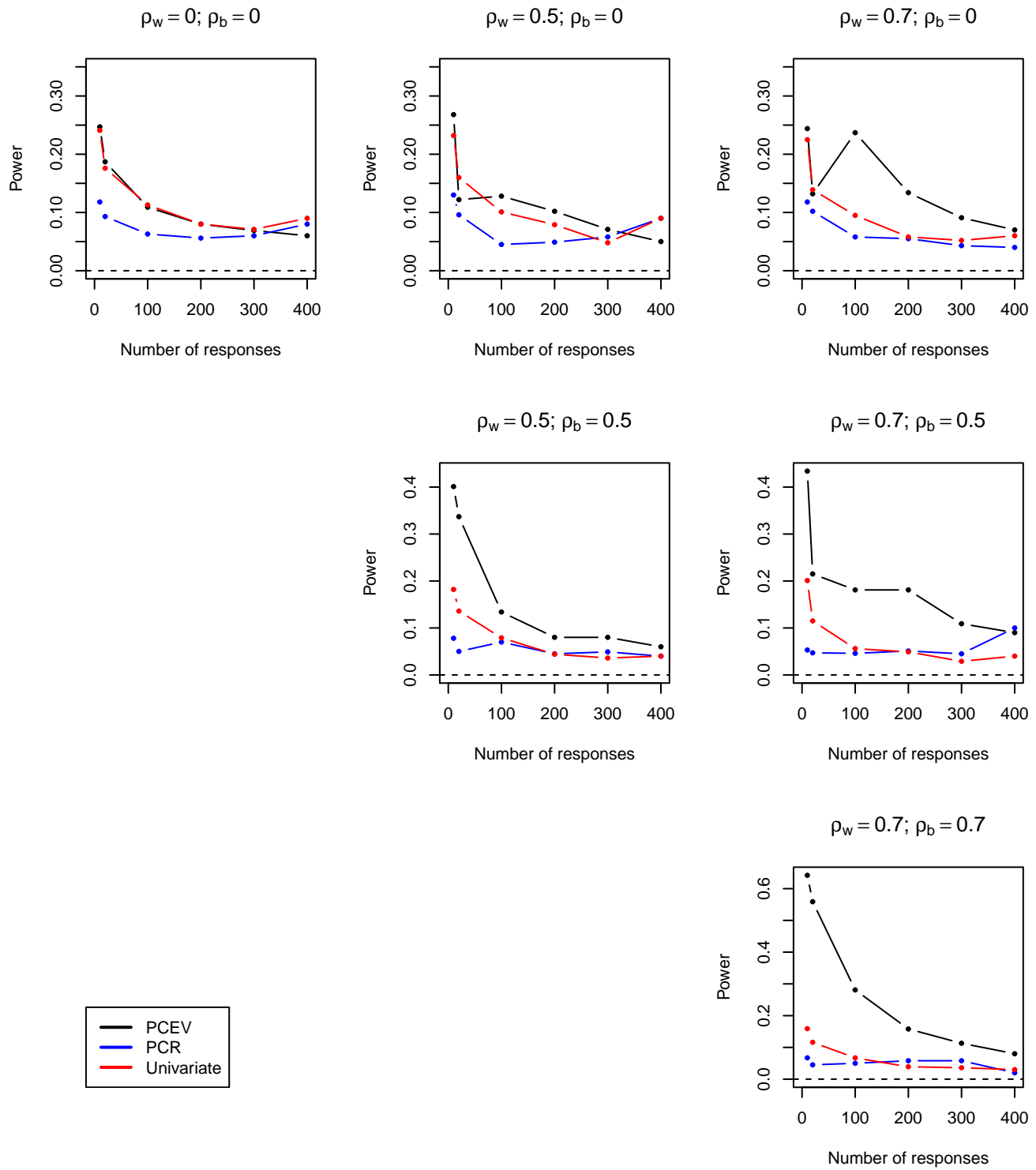
3.13 Significance level: 0.05, Heritability: 0.5%, Number of blocks: 2



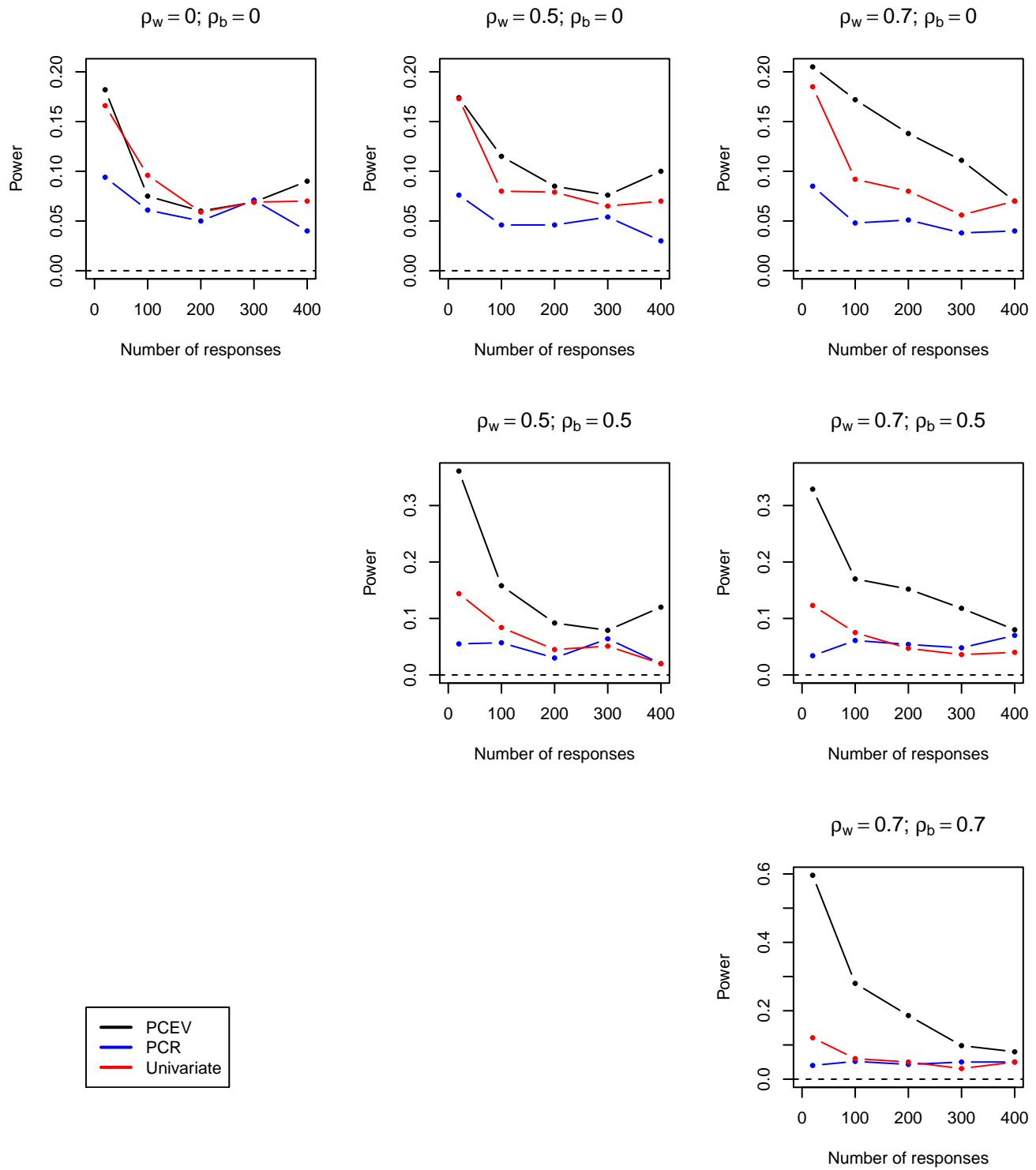
3.14 Significance level: 0.05, Heritability: 0.5%, Number of blocks: 5



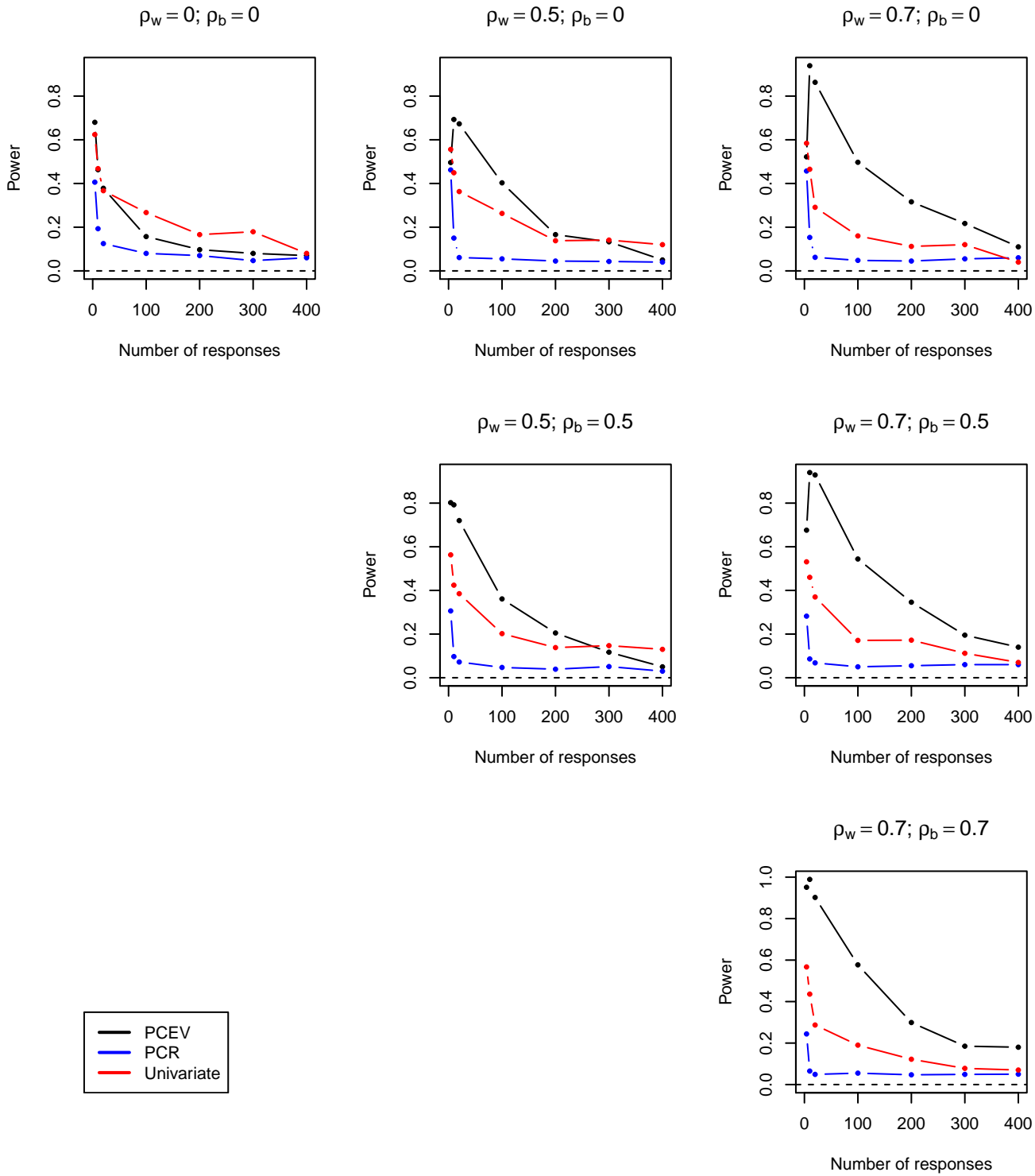
3.15 Significance level: 0.05, Heritability: 0.5%, Number of blocks: 10



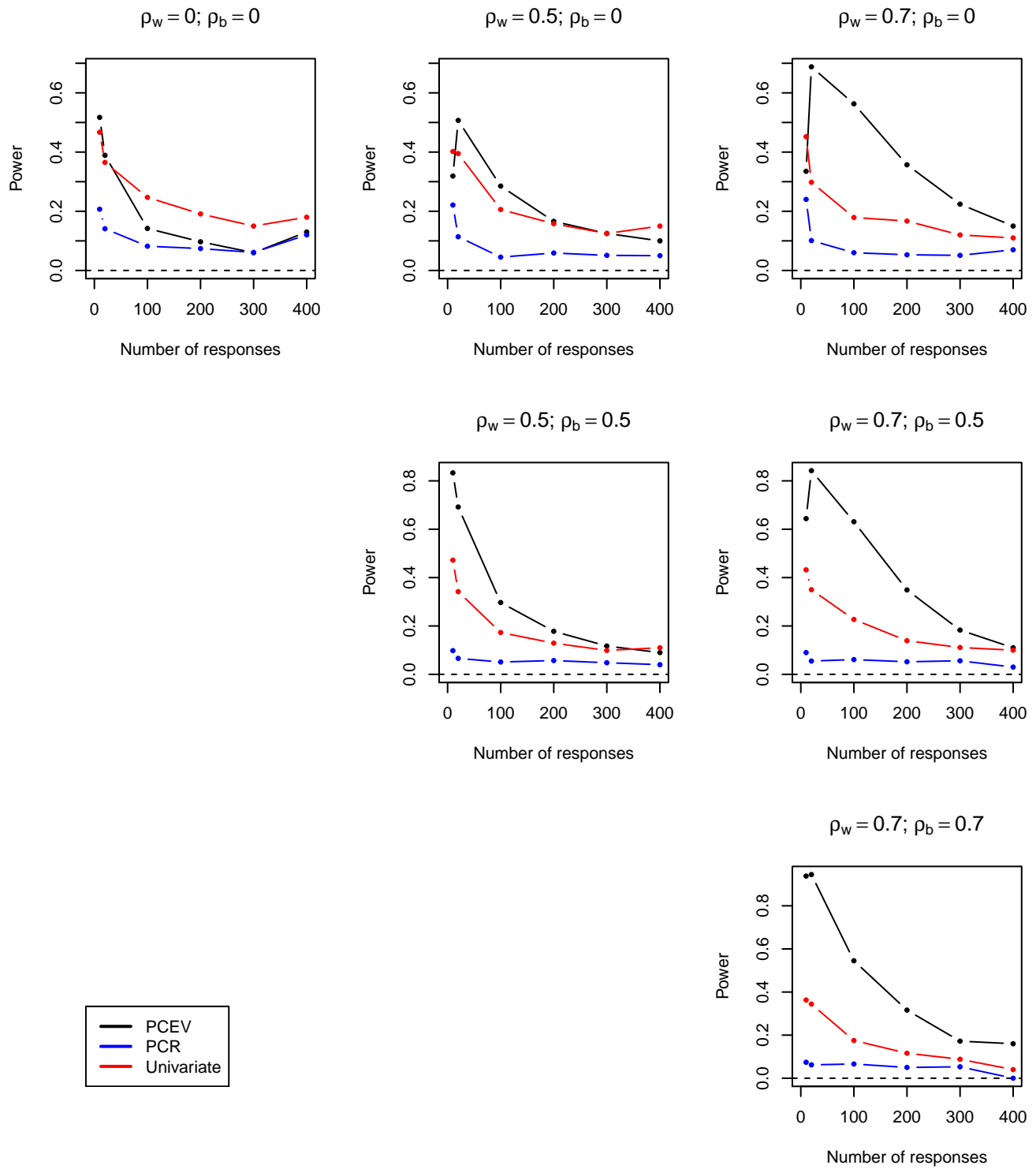
3.16 Significance level: 0.05, Heritability: 0.5%, Number of blocks: 20



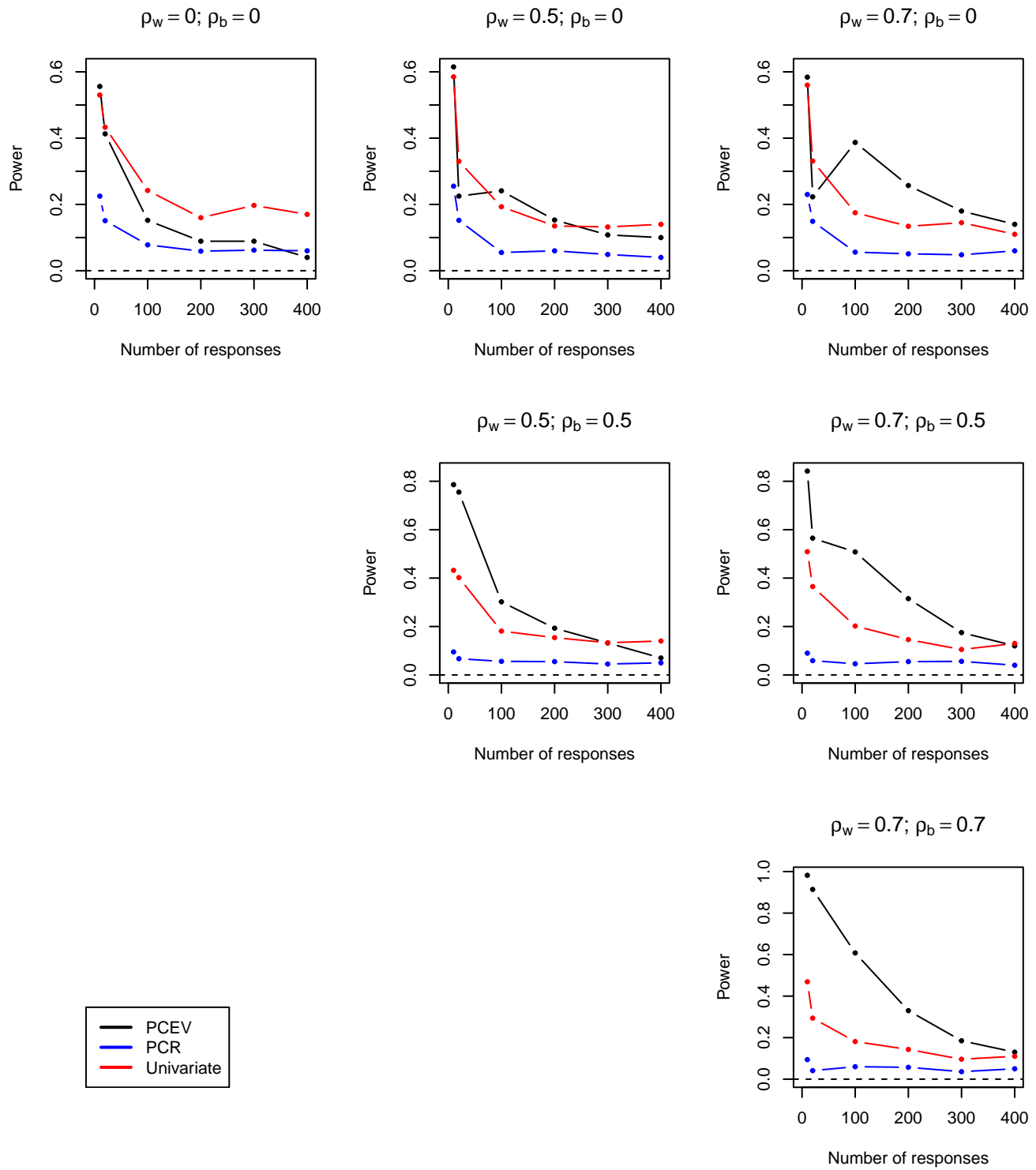
3.17 Significance level: 0.05, Heritability: 1%, Number of blocks: 2



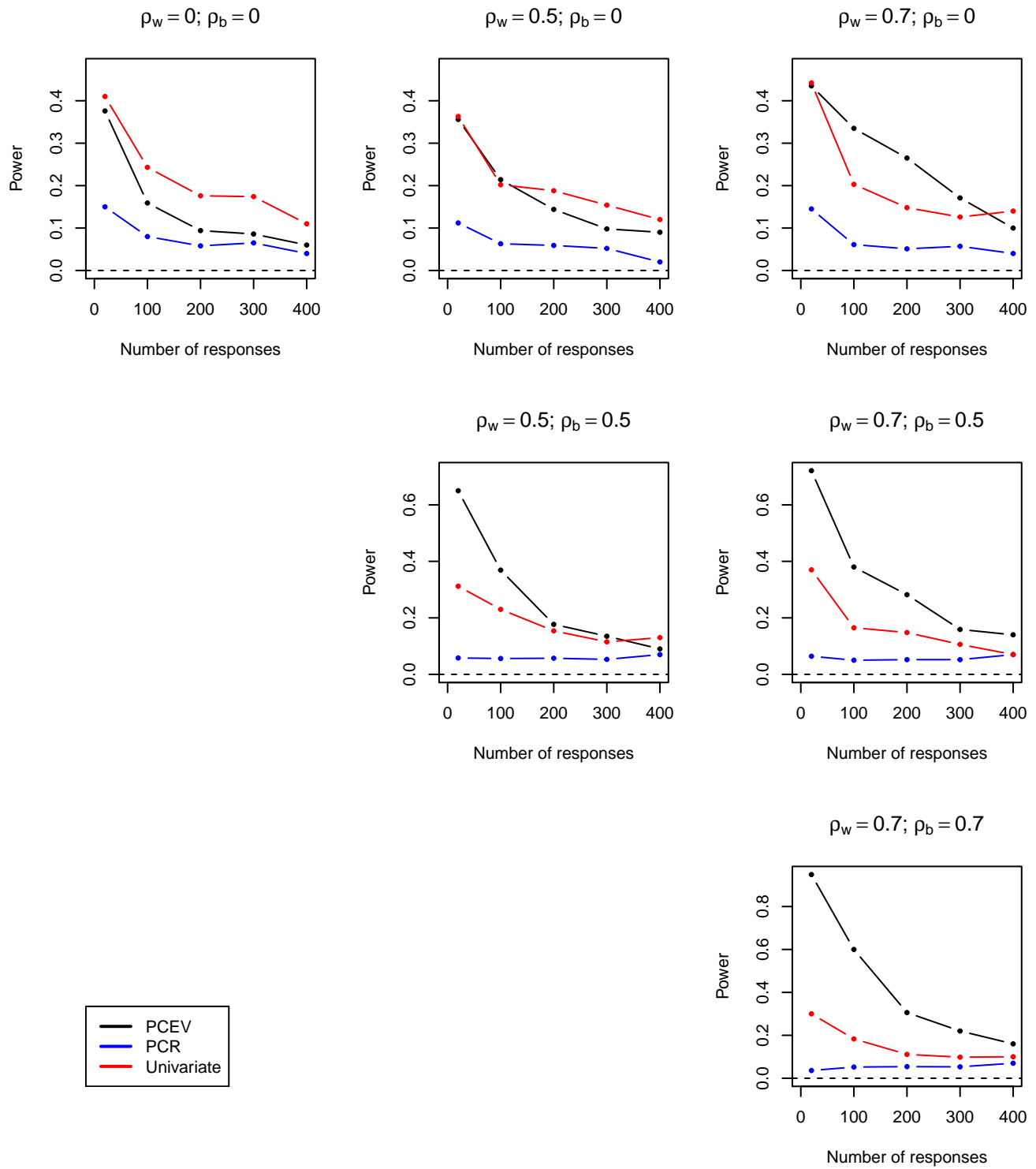
3.18 Significance level: 0.05, Heritability: 1%, Number of blocks: 5



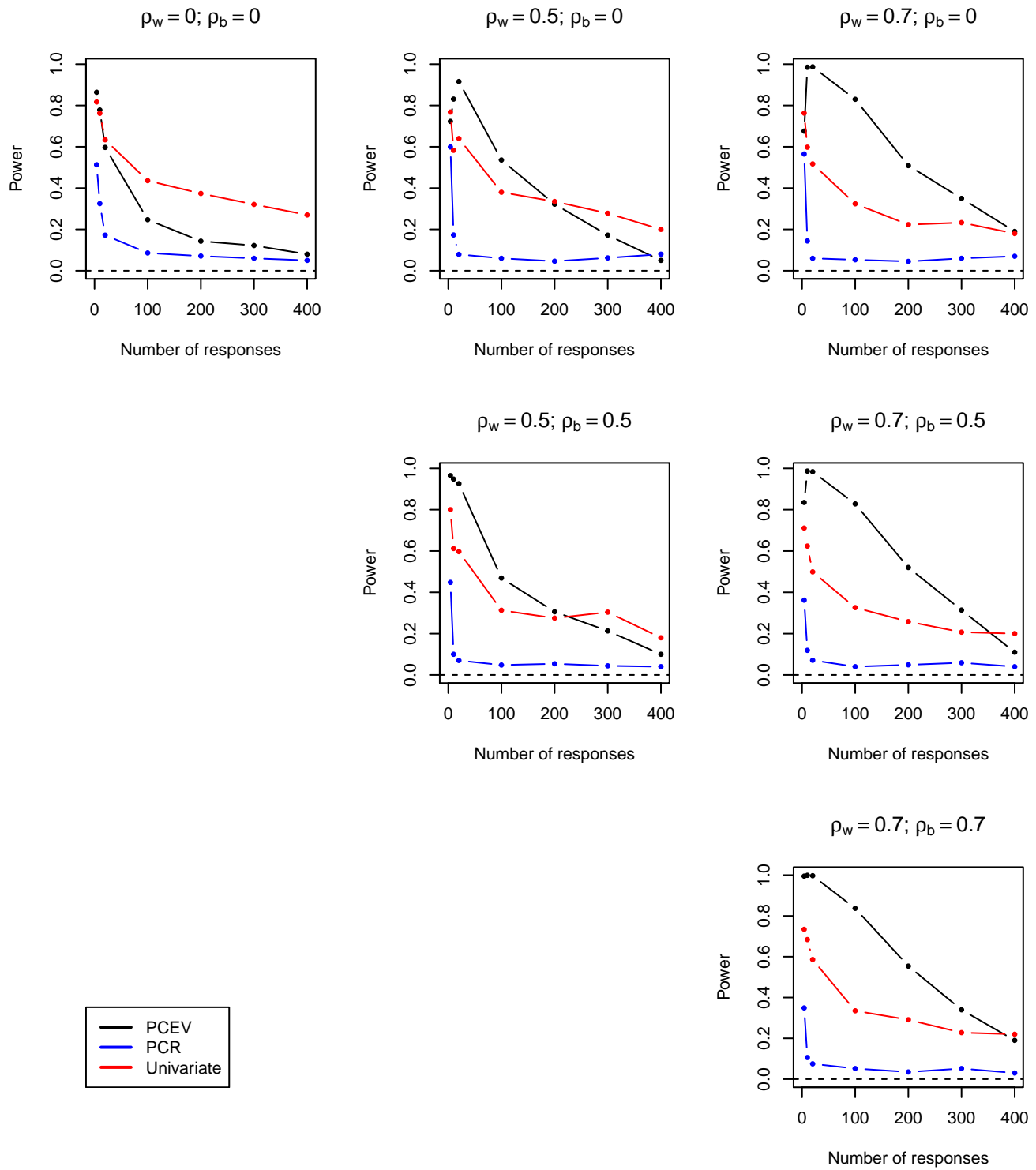
3.19 Significance level: 0.05, Heritability: 1%, Number of blocks: 10



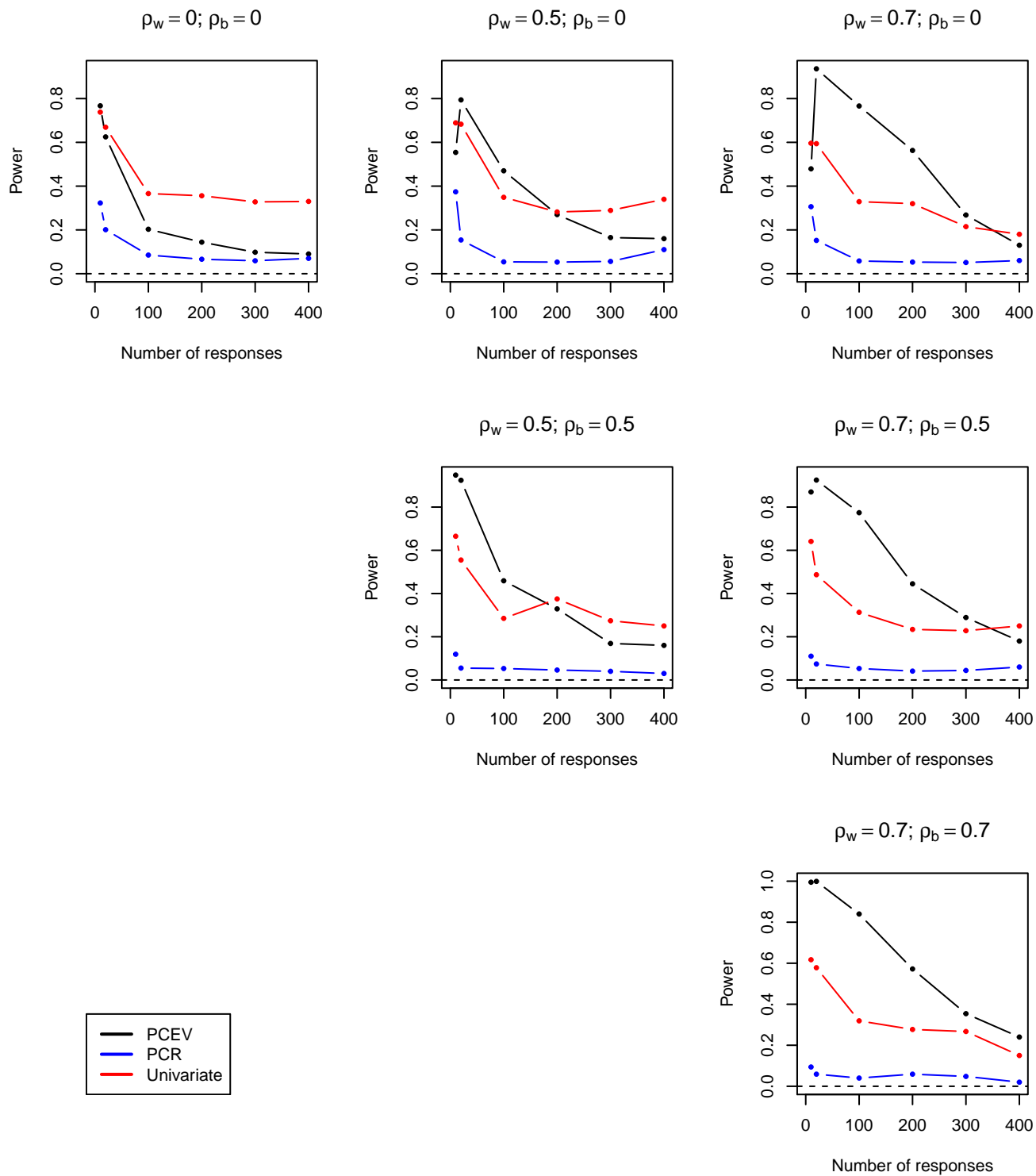
3.20 Significance level: 0.05, Heritability: 1%, Number of blocks: 20



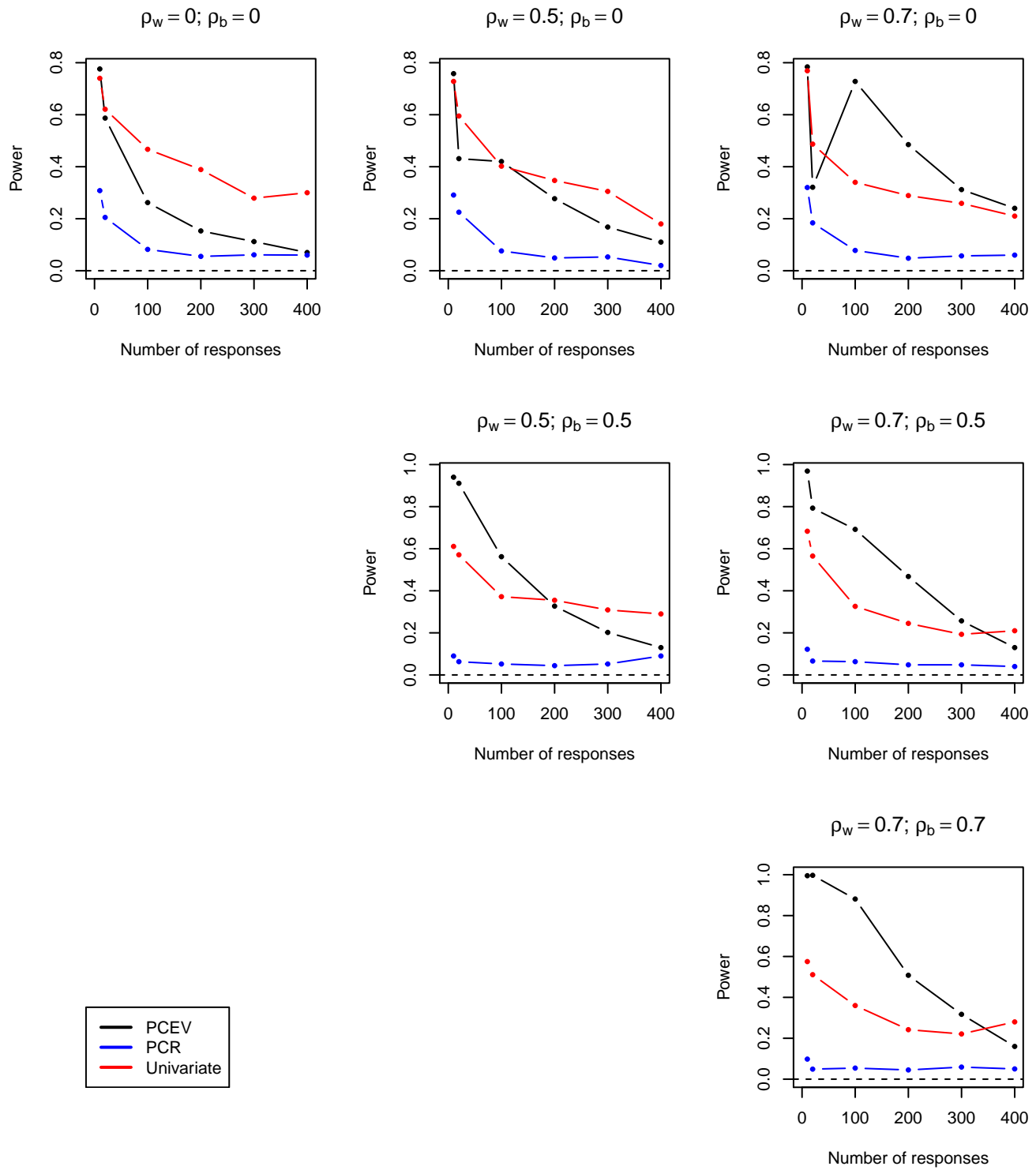
3.21 Significance level: 0.05, Heritability: 1.5%, Number of blocks: 2



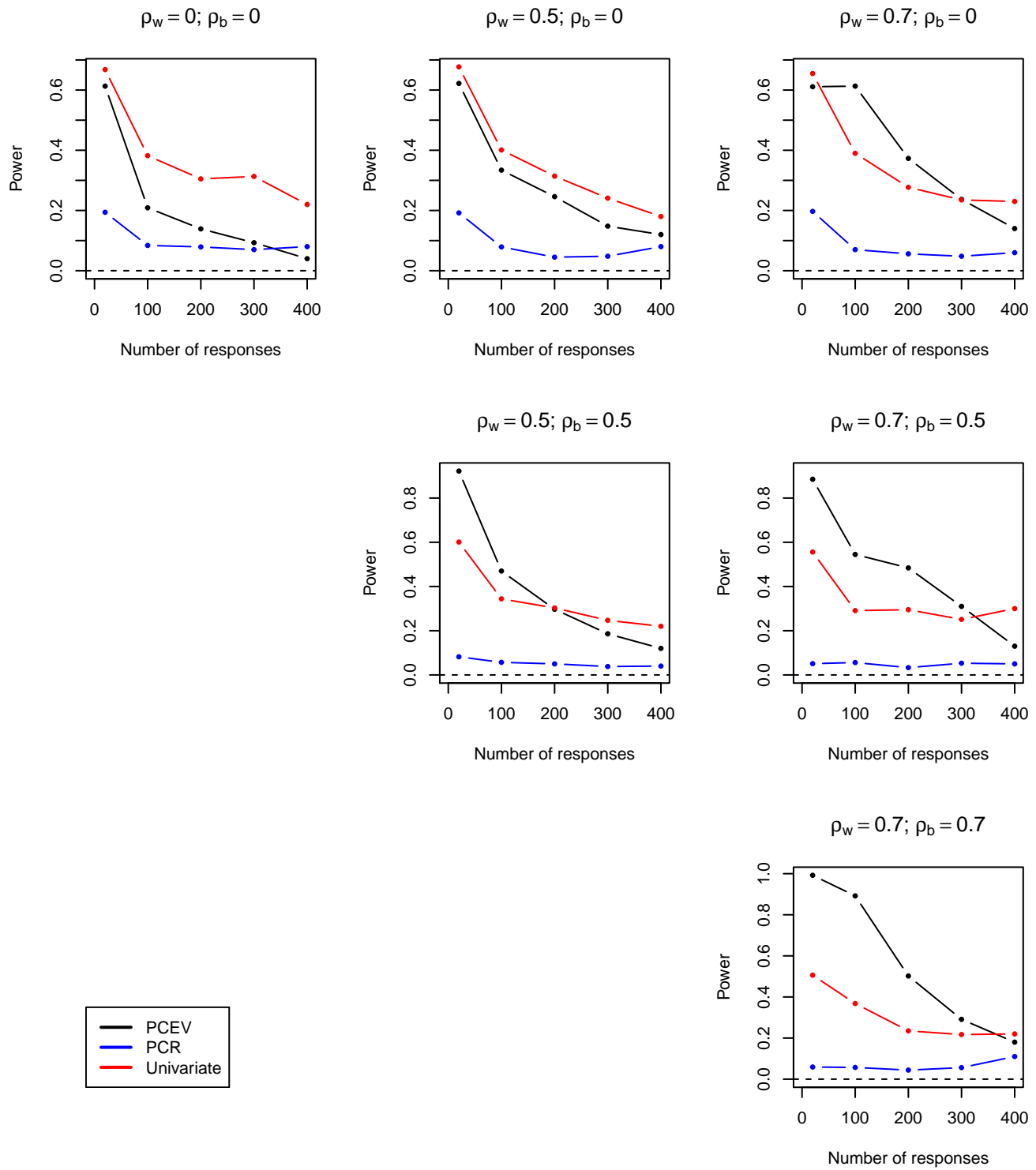
3.22 Significance level: 0.05, Heritability: 1.5%, Number of blocks: 5



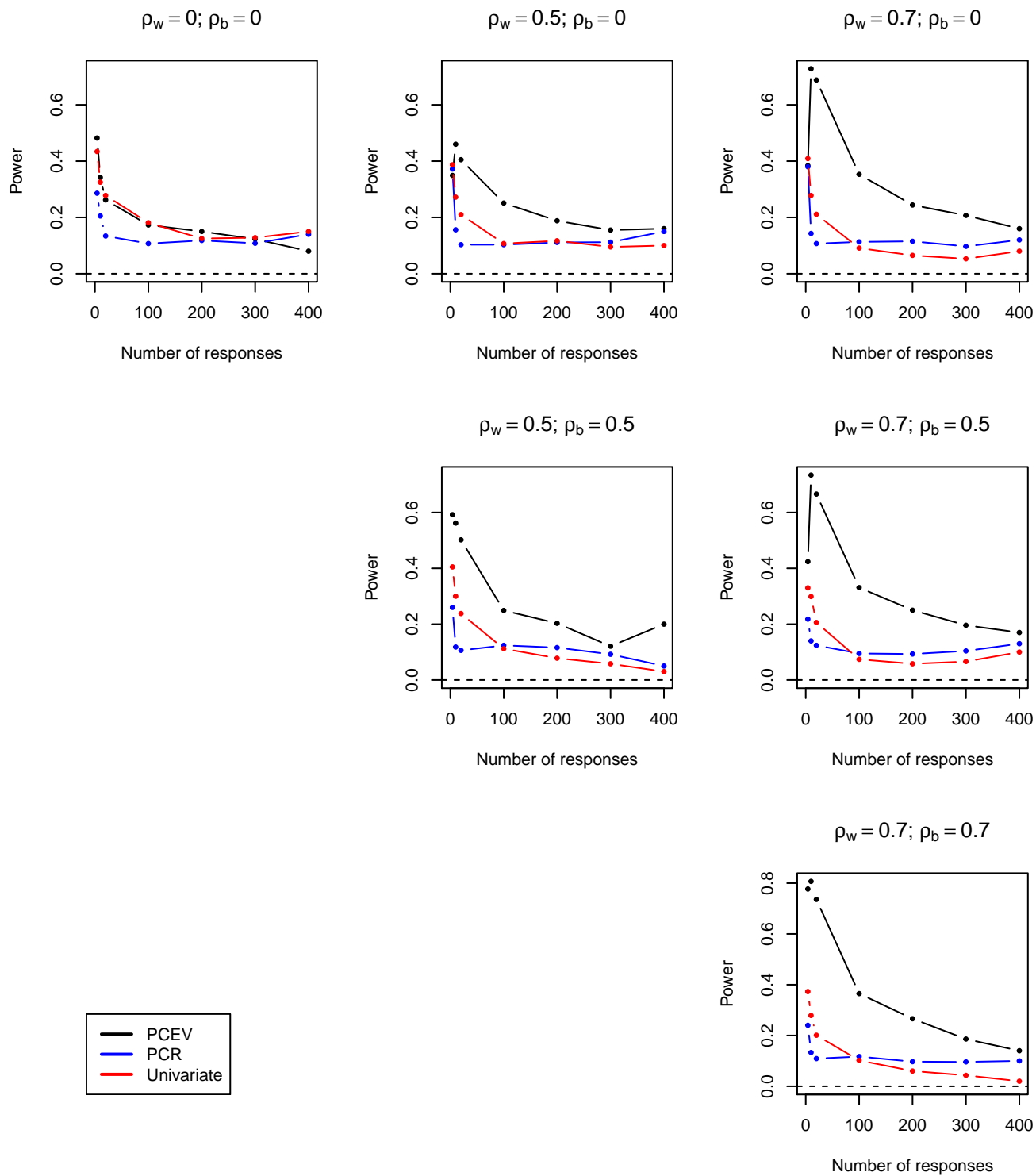
3.23 Significance level: 0.05, Heritability: 1.5%, Number of blocks: 10



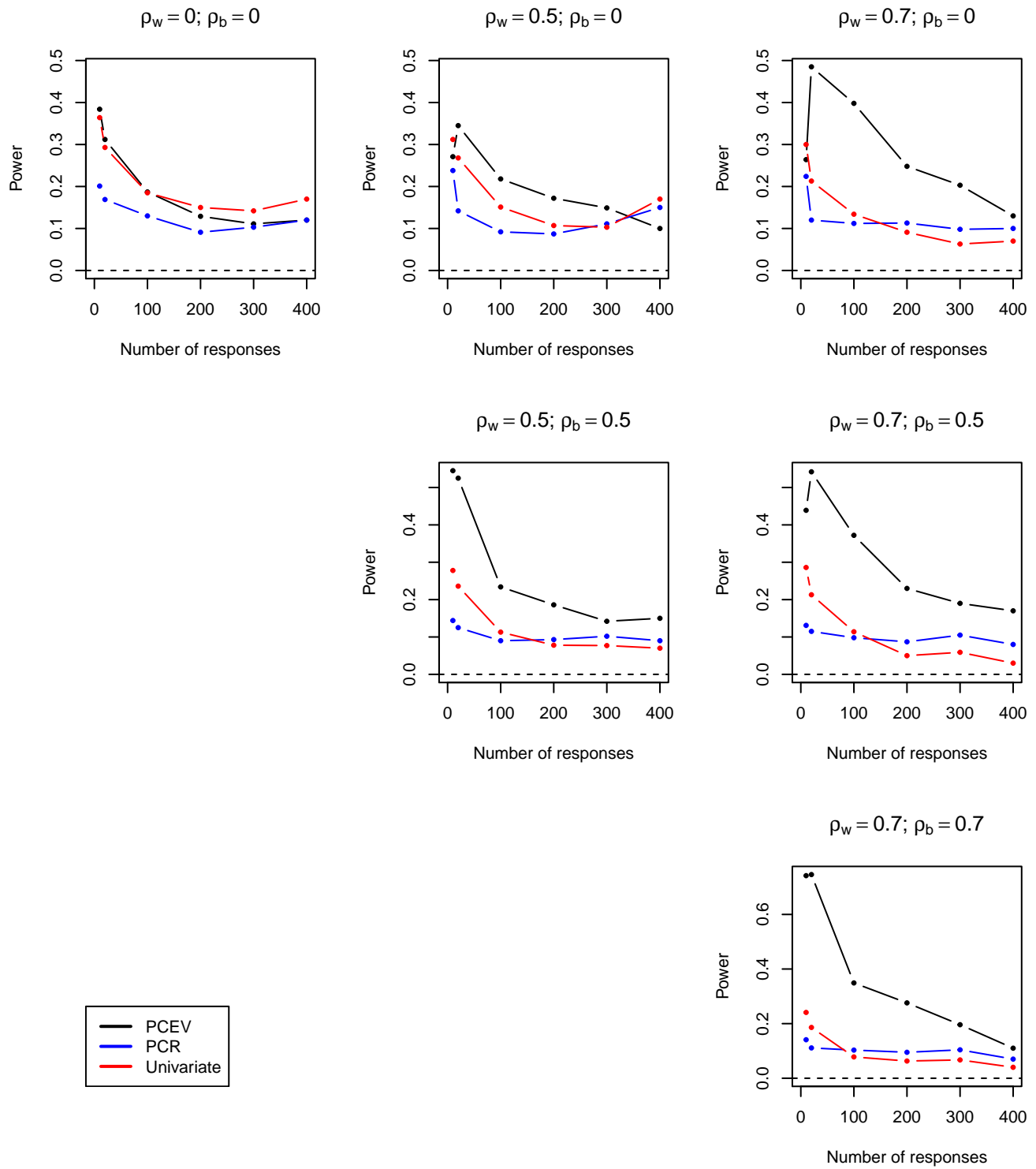
3.24 Significance level: 0.05, Heritability: 1.5%, Number of blocks: 20



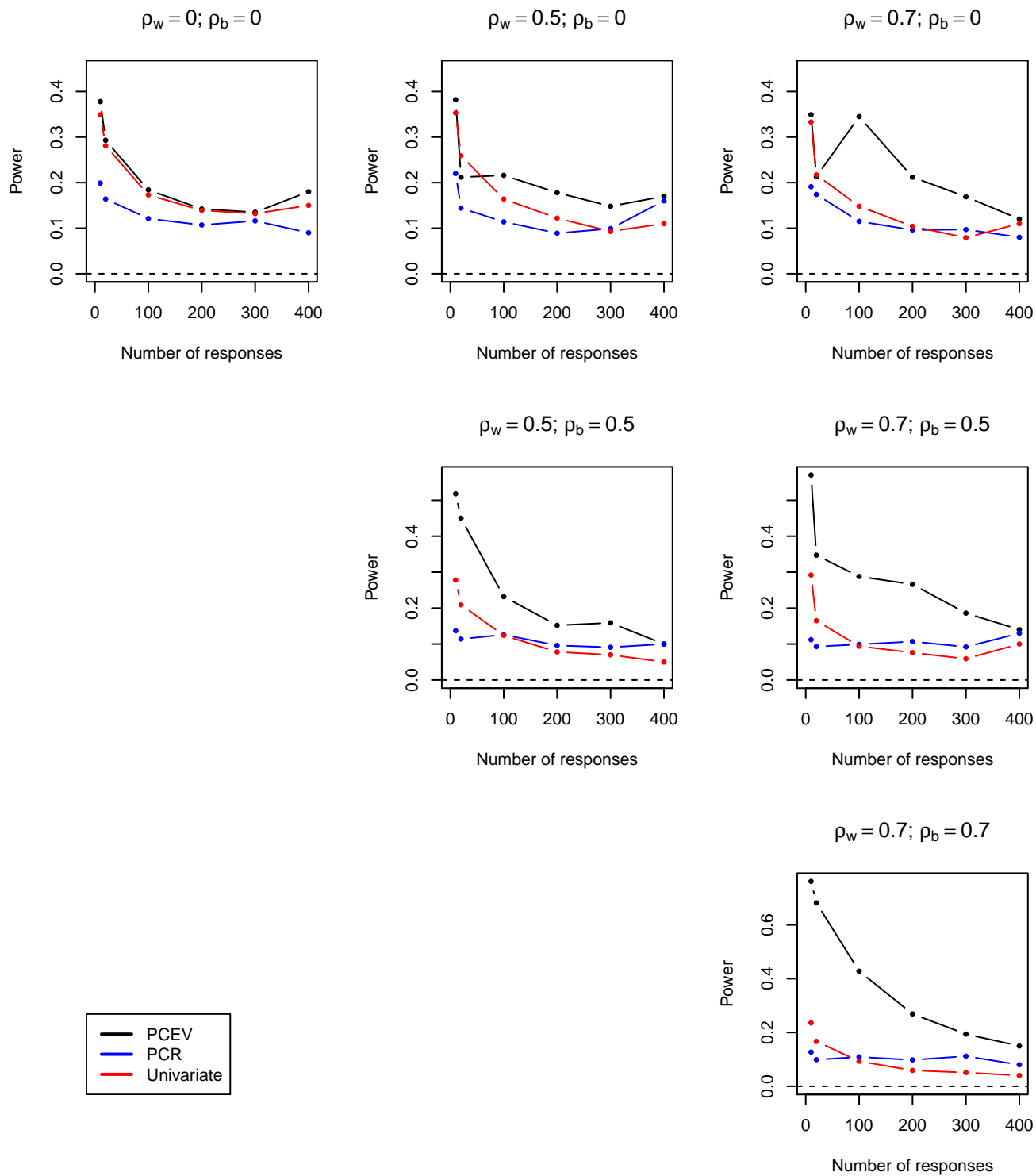
3.25 Significance level: 0.1, Heritability: 0.5%, Number of blocks: 2



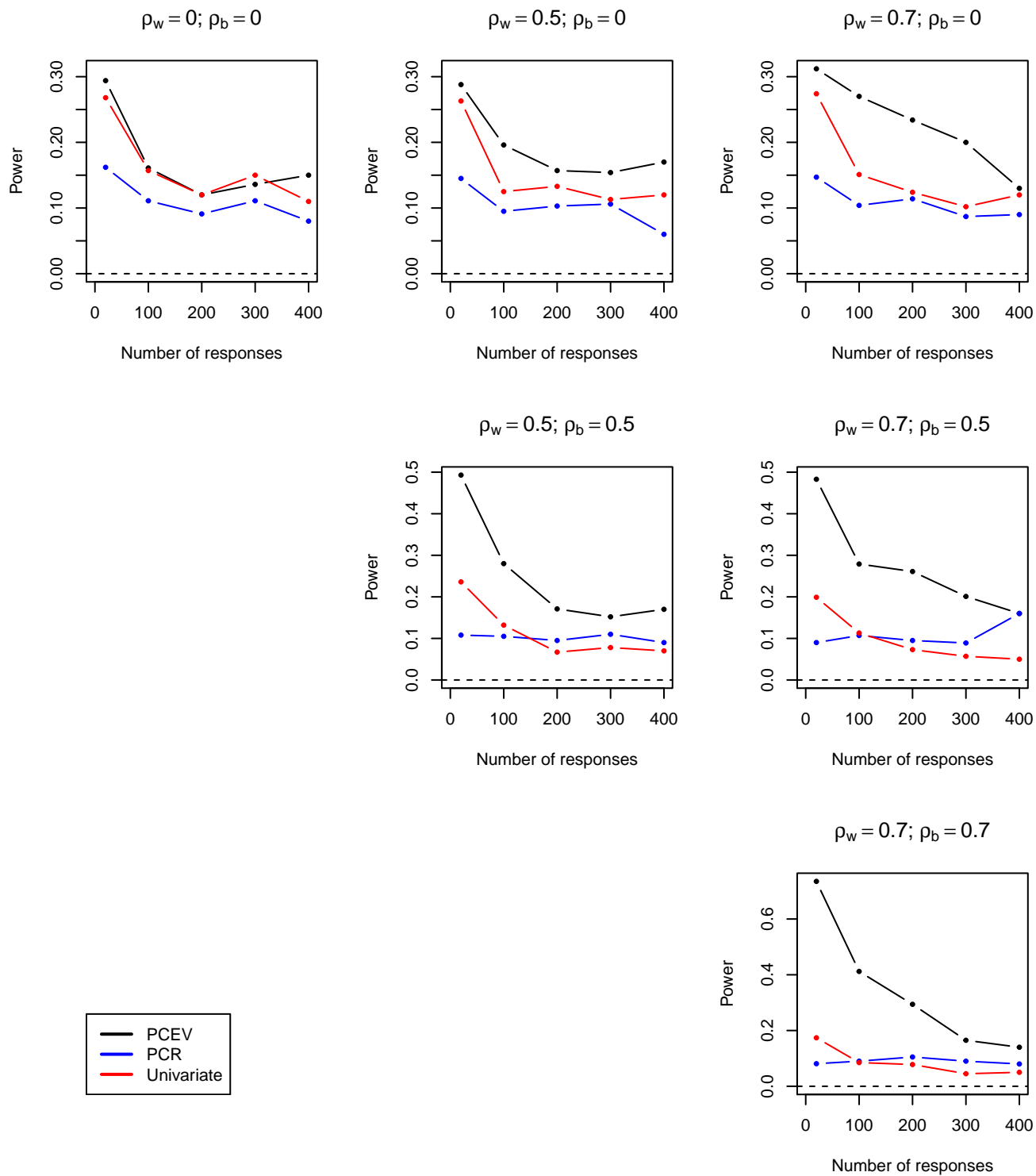
3.26 Significance level: 0.1, Heritability: 0.5%, Number of blocks: 5



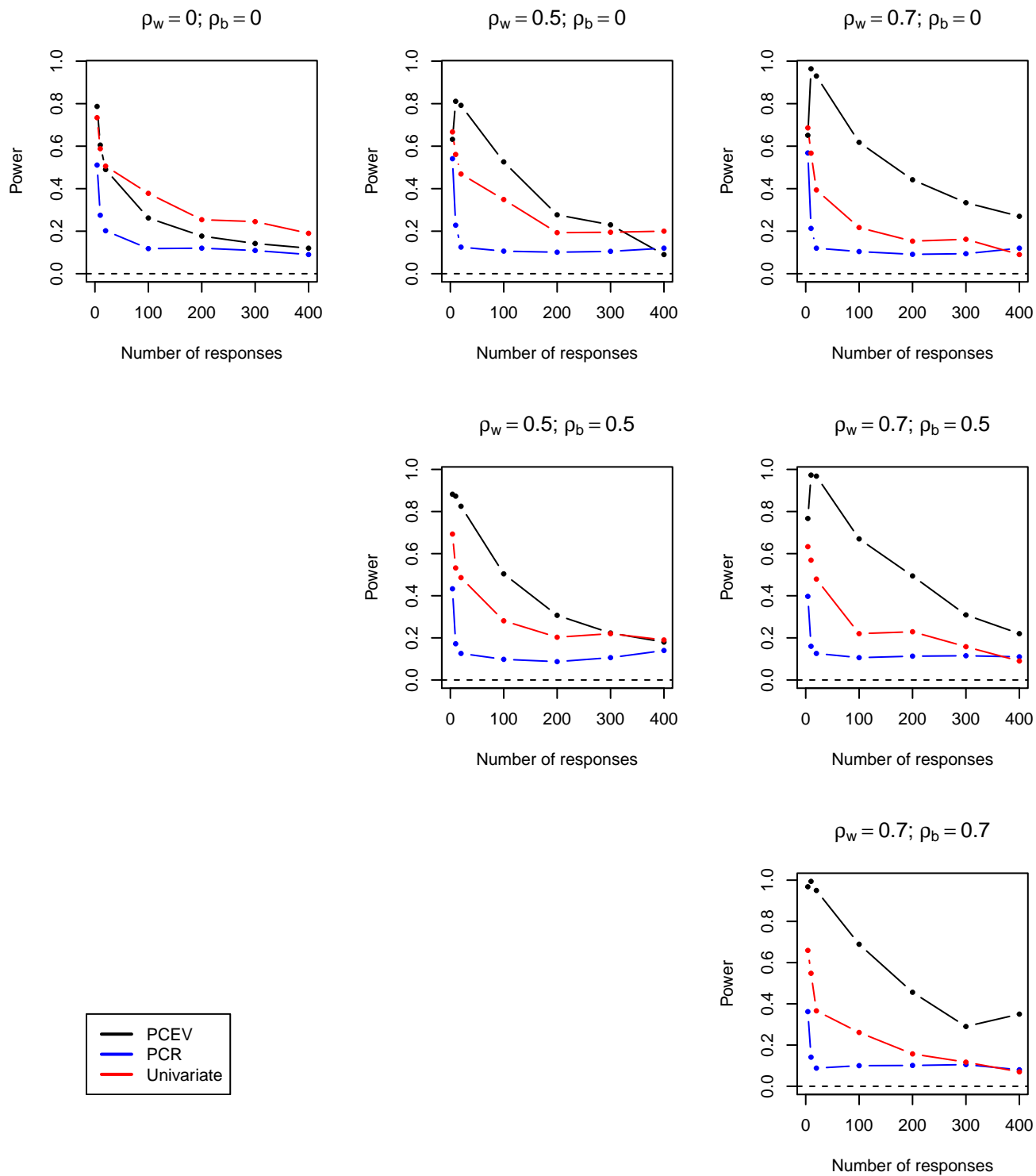
3.27 Significance level: 0.1, Heritability: 0.5%, Number of blocks: 10



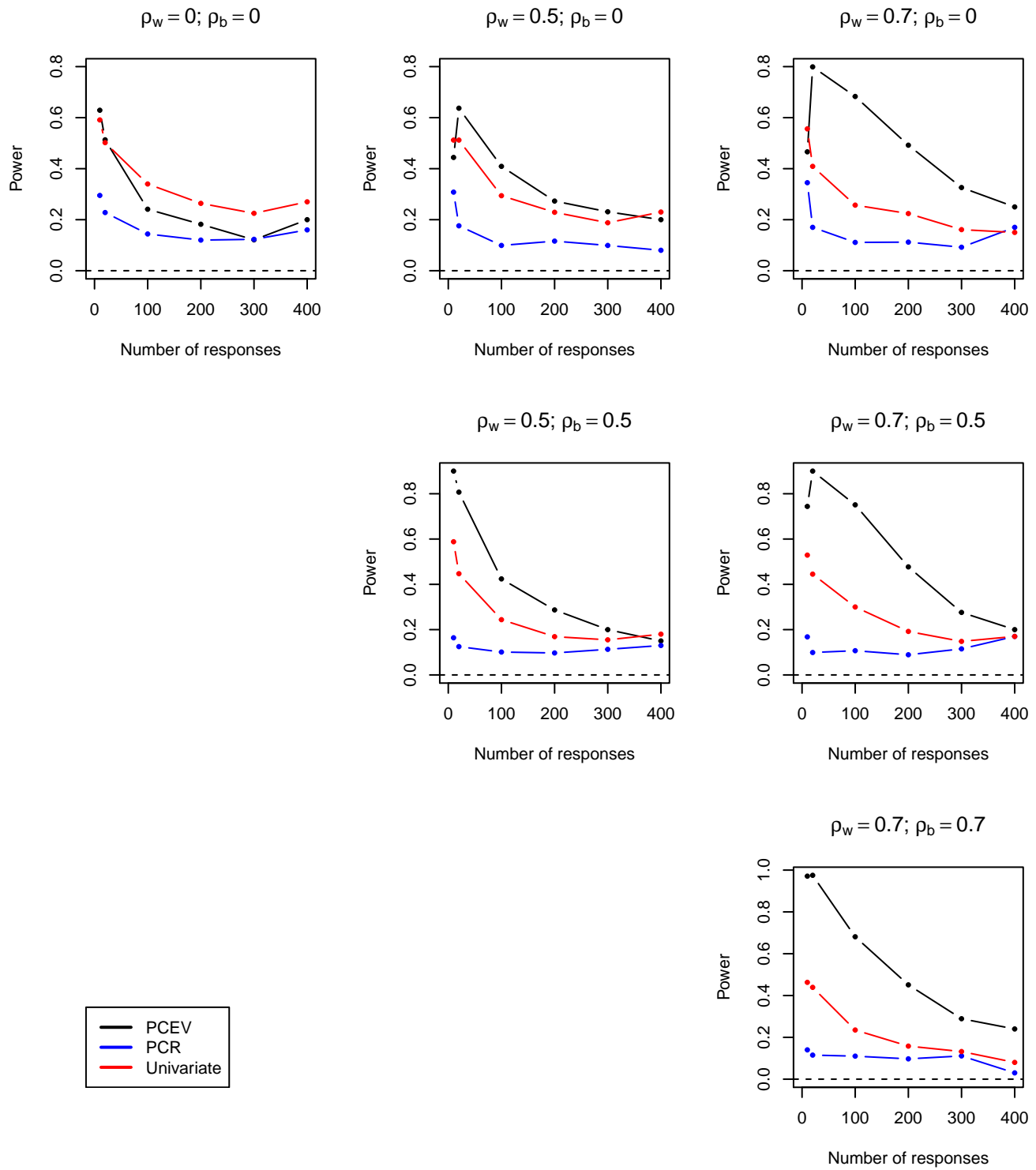
3.28 Significance level: 0.1, Heritability: 0.5%, Number of blocks: 20



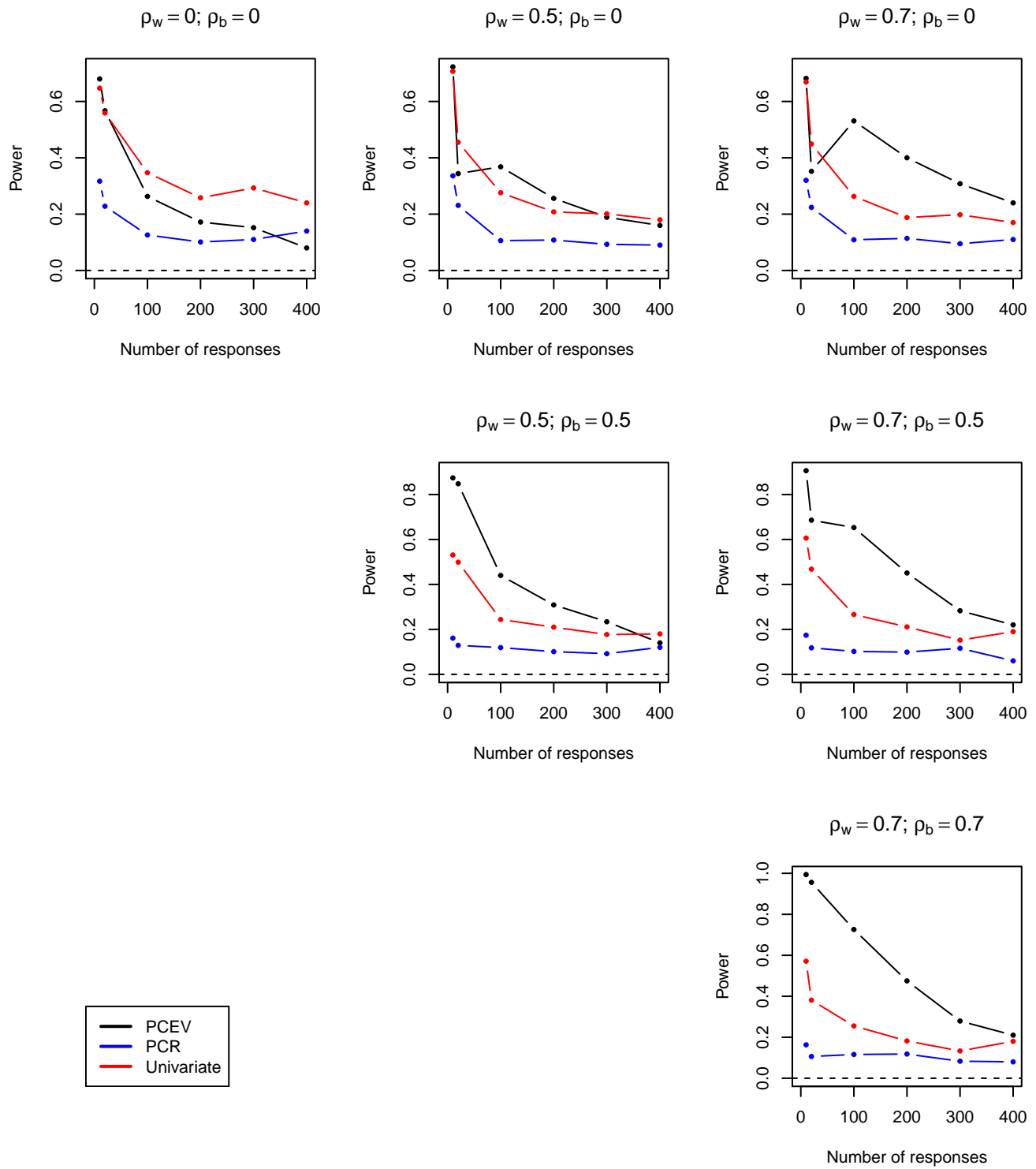
3.29 Significance level: 0.1, Heritability: 1%, Number of blocks: 2



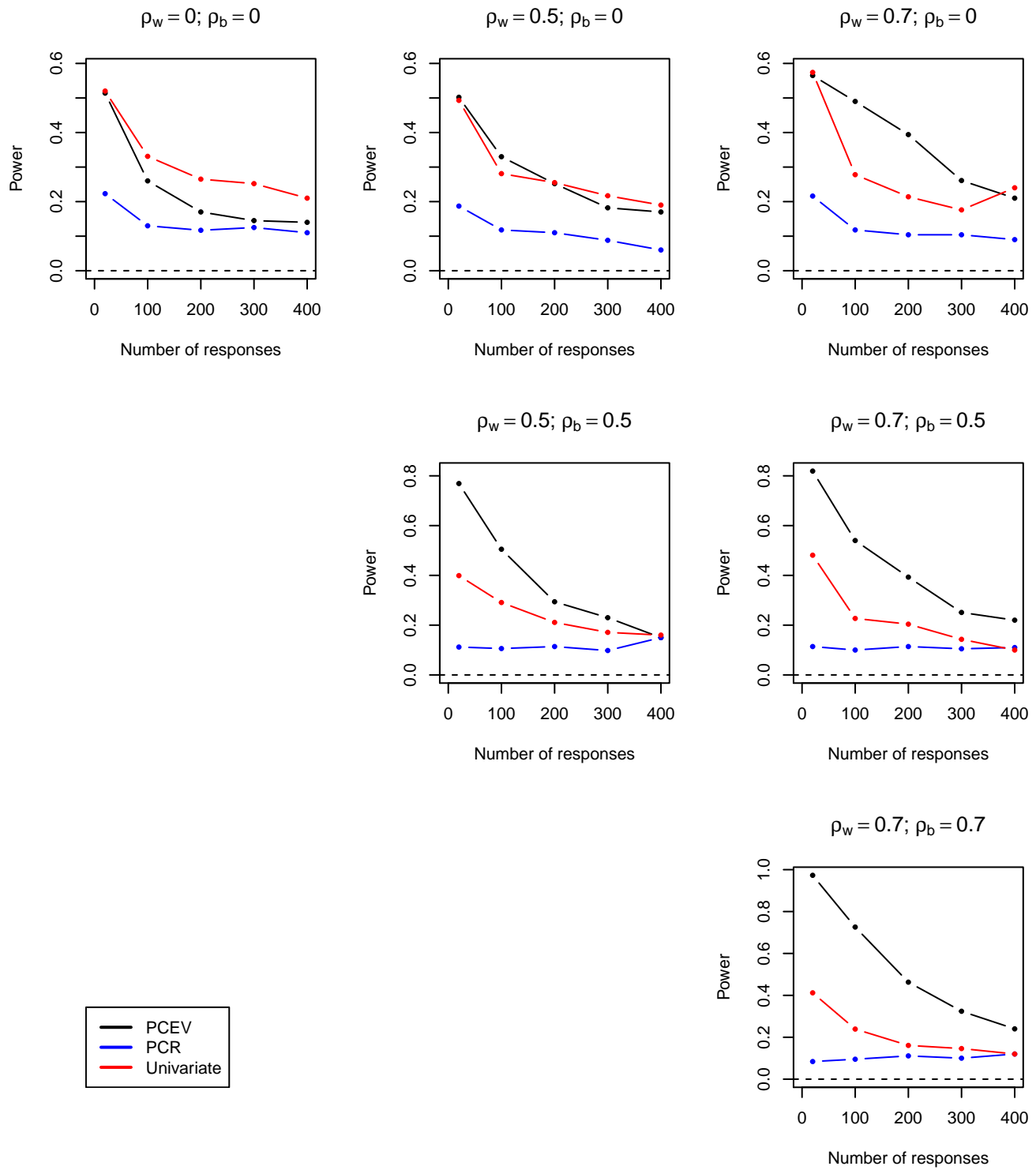
3.30 Significance level: 0.1, Heritability: 1%, Number of blocks: 5



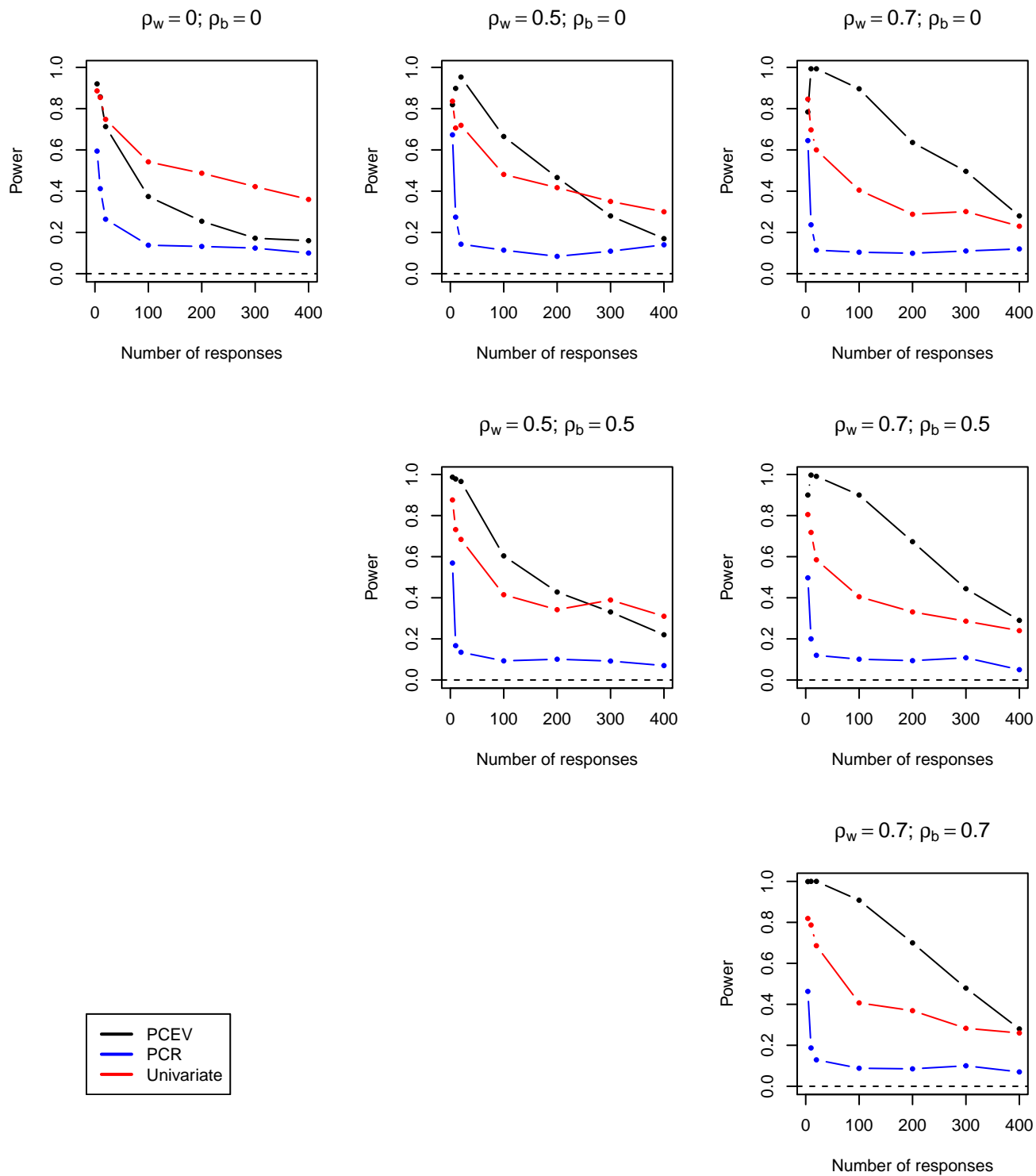
3.31 Significance level: 0.1, Heritability: 1%, Number of blocks: 10



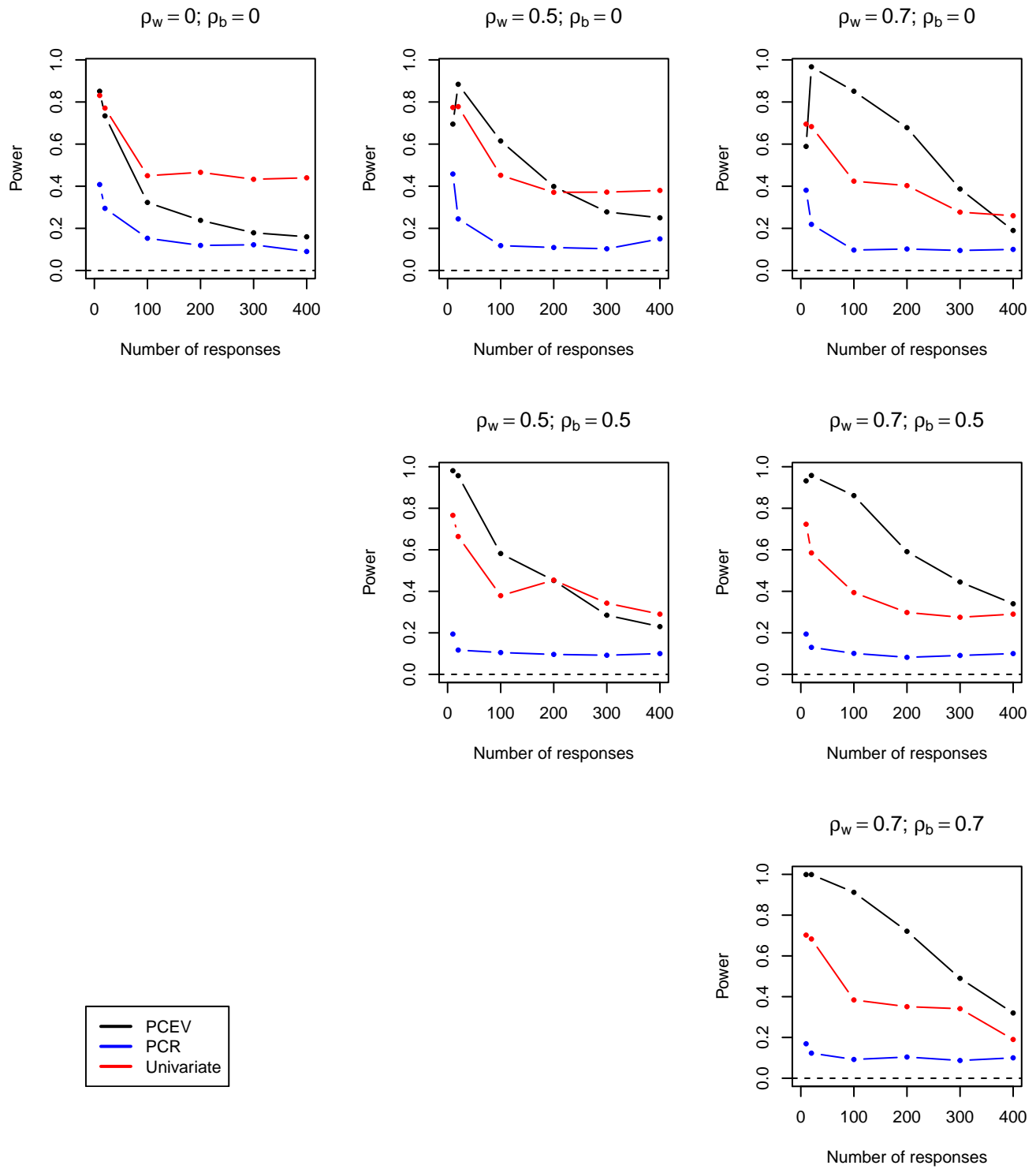
3.32 Significance level: 0.1, Heritability: 1%, Number of blocks: 20



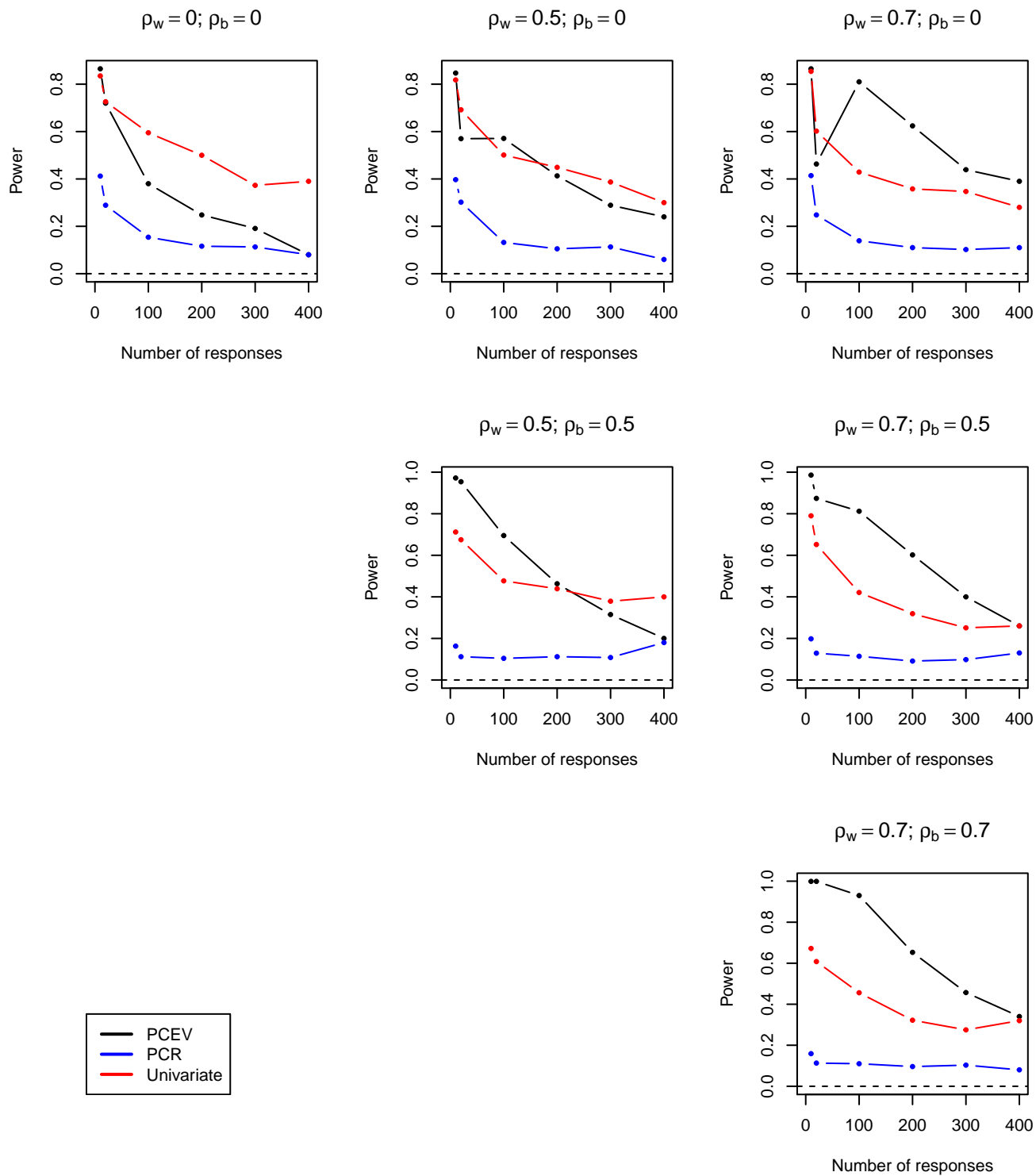
3.33 Significance level: 0.1, Heritability: 1.5%, Number of blocks: 2



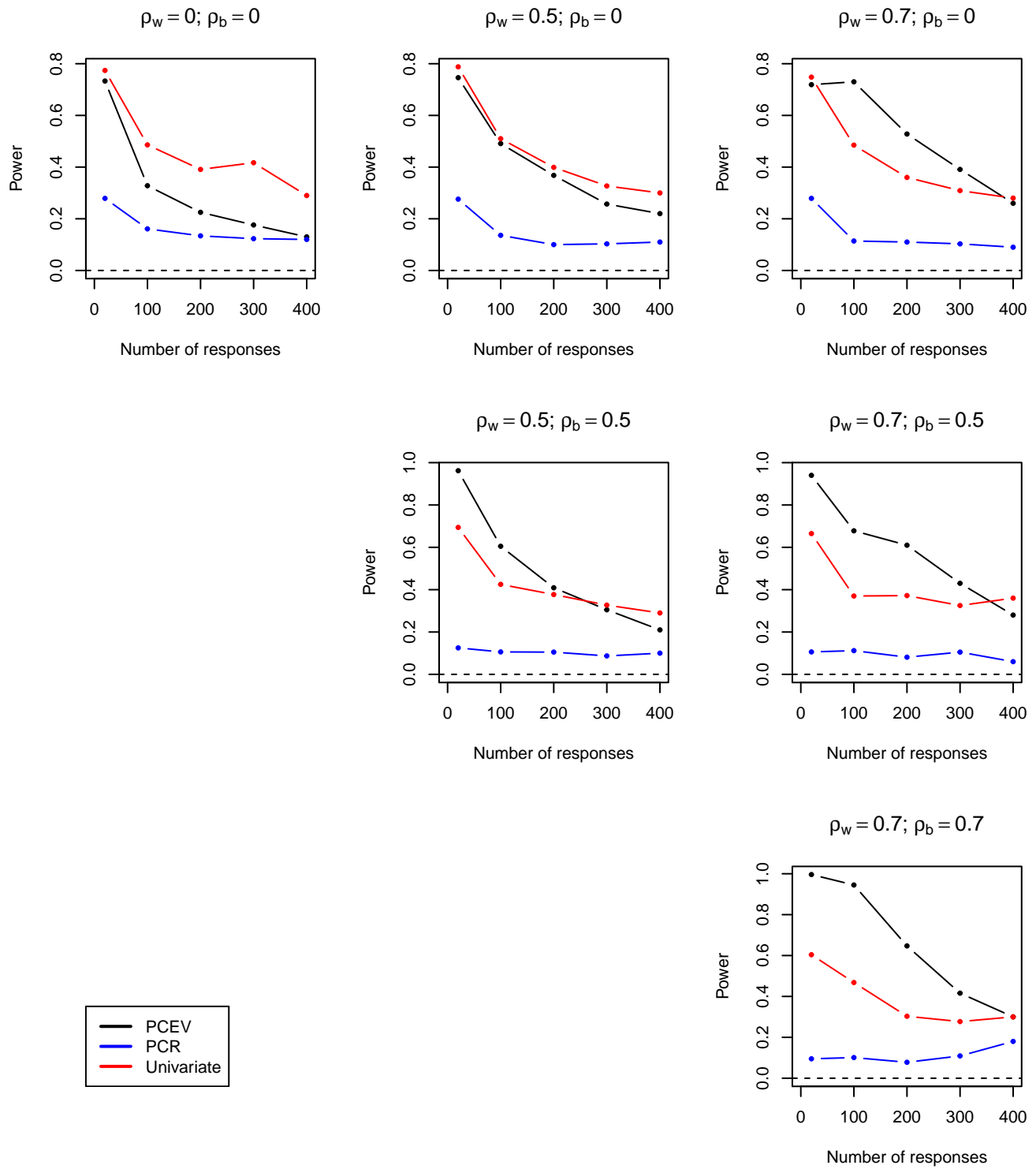
3.34 Significance level: 0.1, Heritability: 1.5%, Number of blocks: 5



3.35 Significance level: 0.1, Heritability: 1.5%, Number of blocks: 10



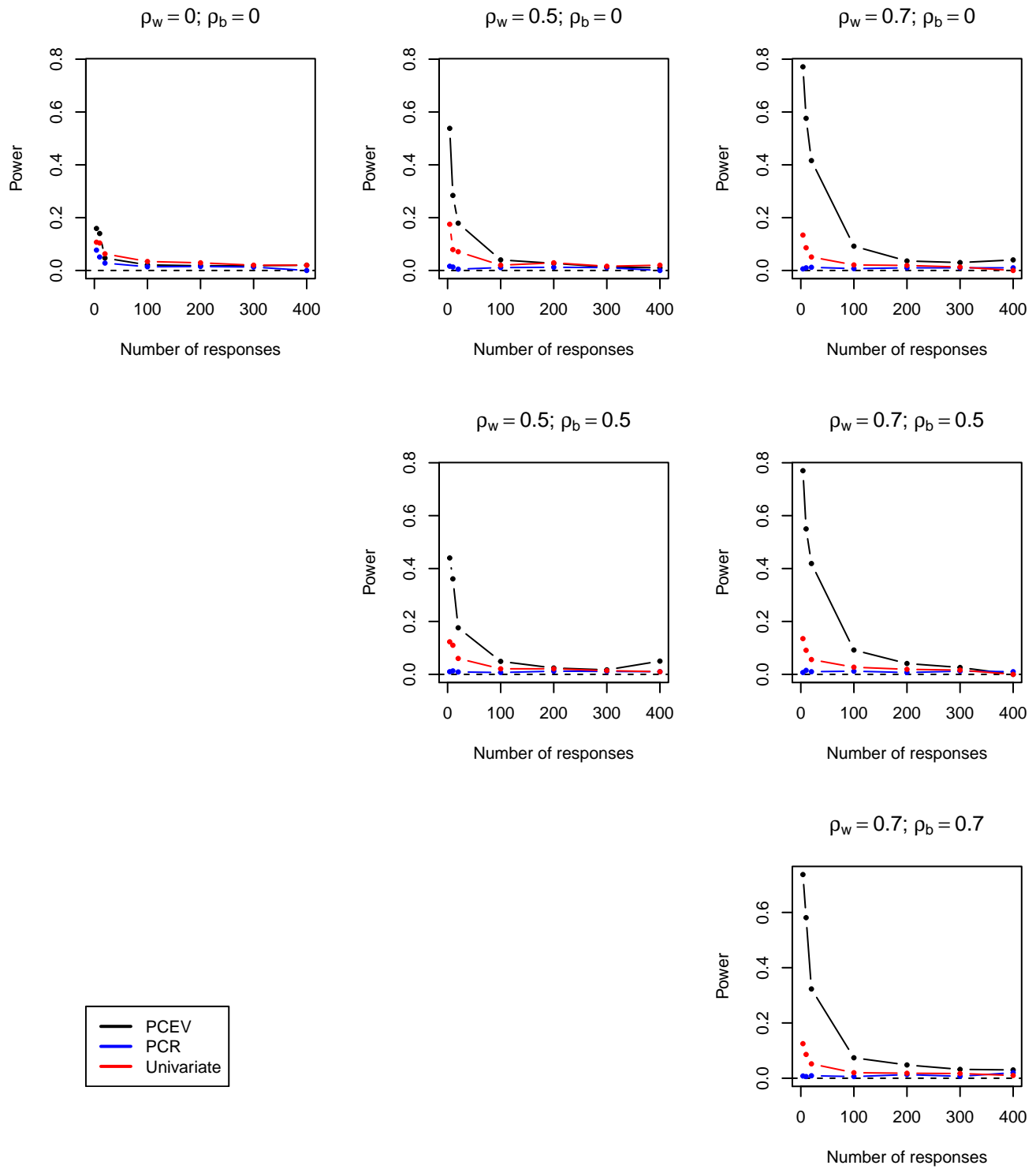
3.36 Significance level: 0.1, Heritability: 1.5%, Number of blocks: 20



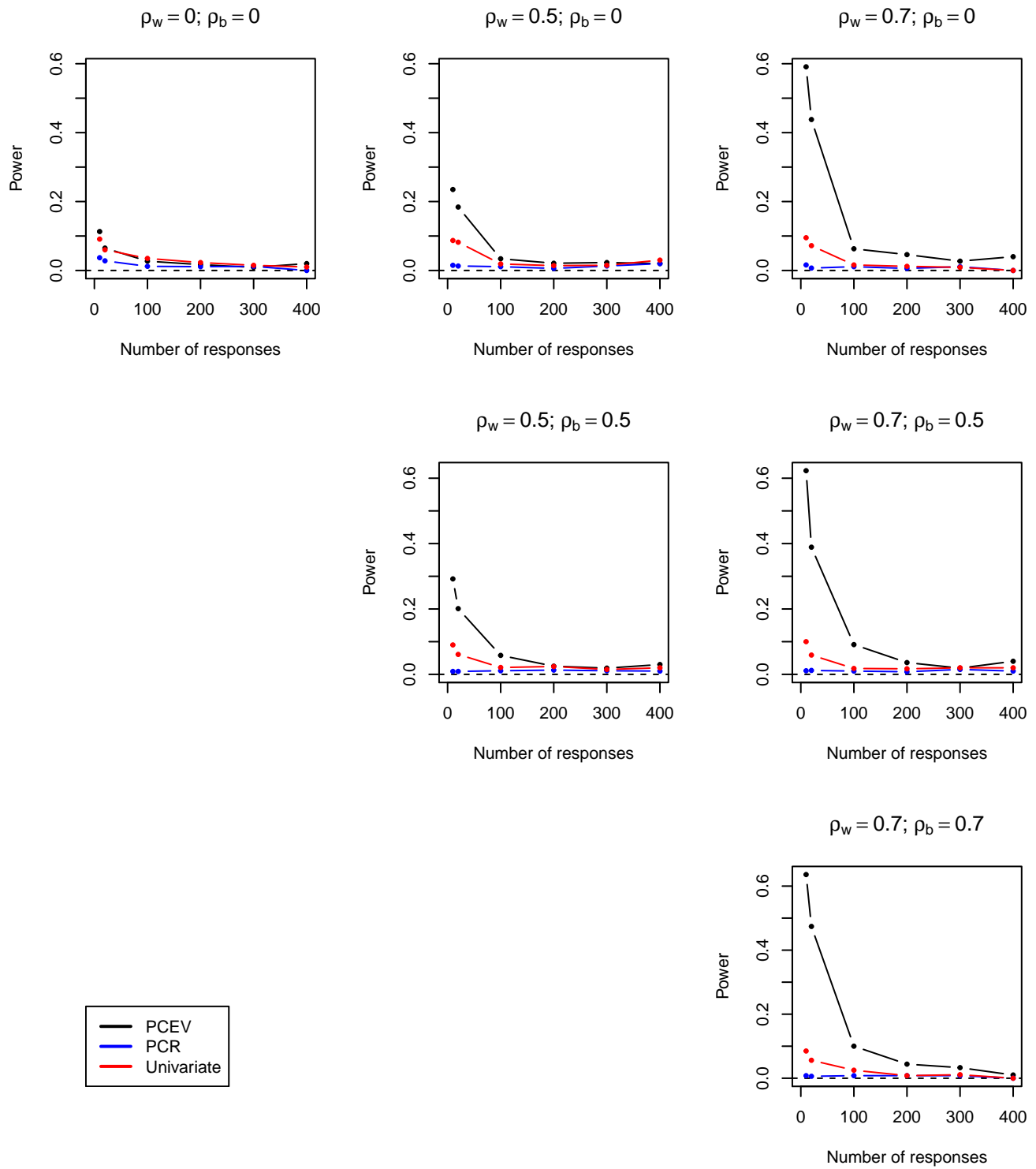
4 Simulation scenario 4

We simulated an association between the continuous covariate x and two components of the multivariate phenotype \mathbf{Y} : the associations are of the same size, in the opposite direction, and the two components lie in the same block.

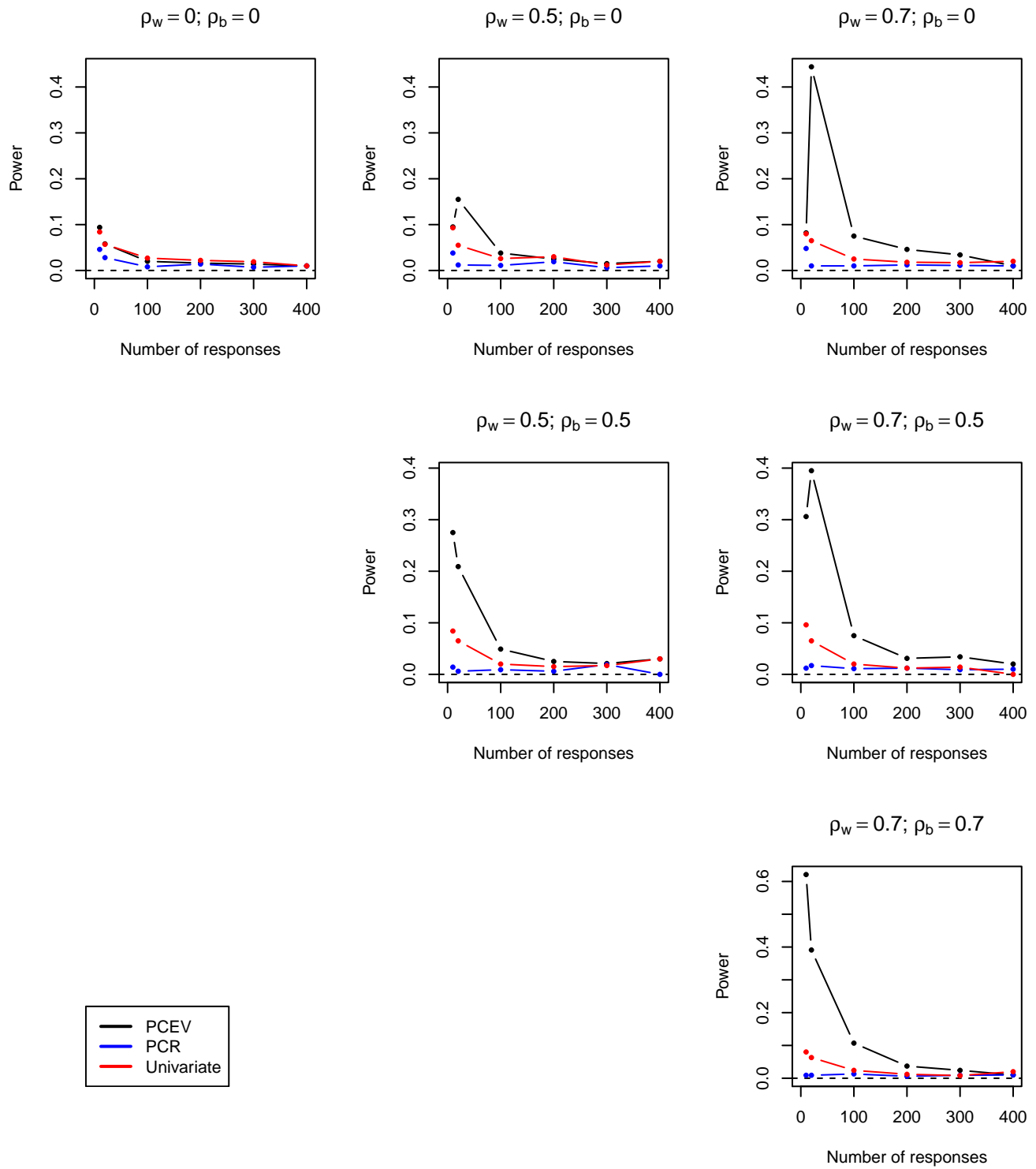
4.1 Significance level: 0.01, Heritability: 0.5%, Number of blocks: 2



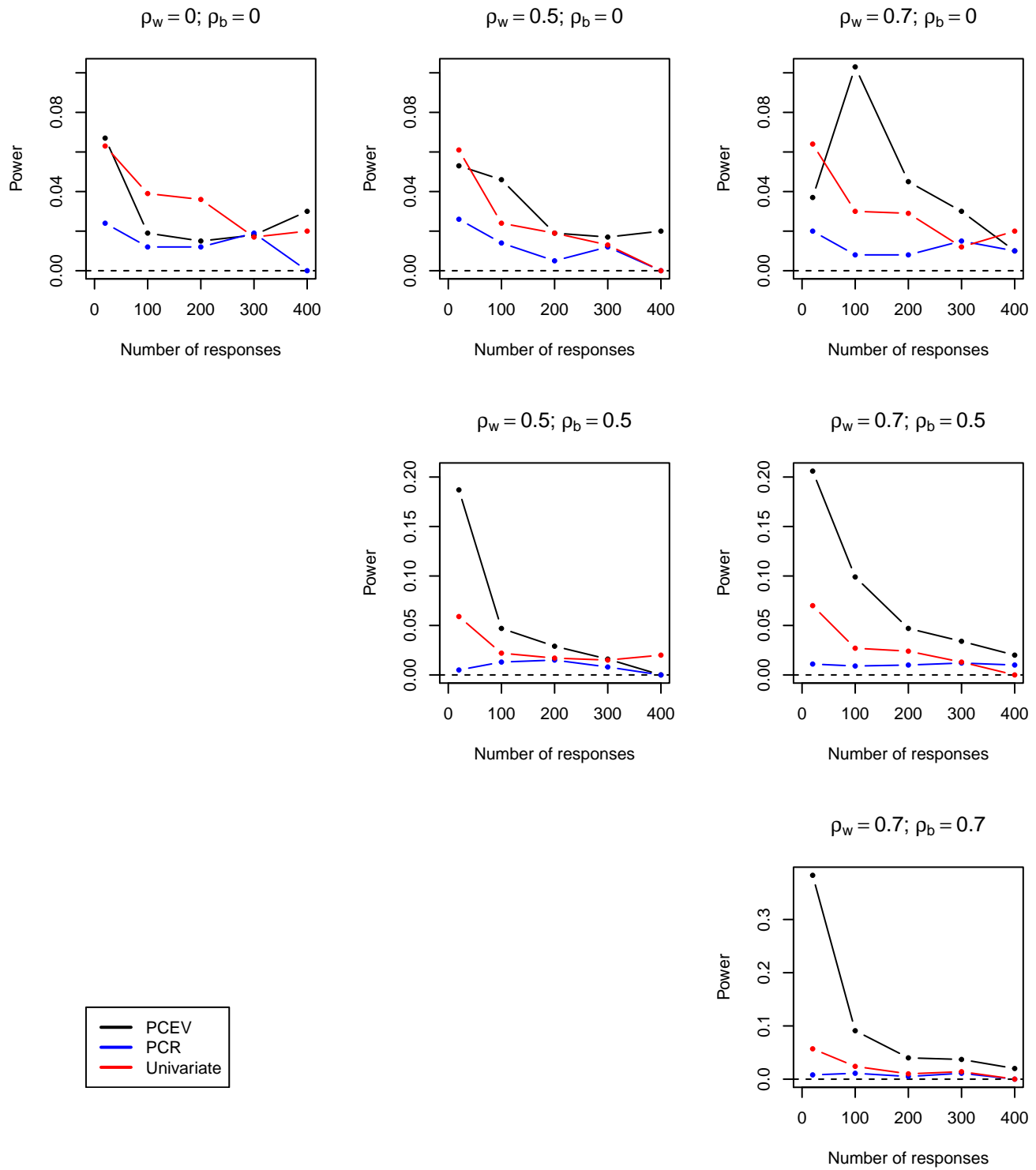
4.2 Significance level: 0.01, Heritability: 0.5%, Number of blocks: 5



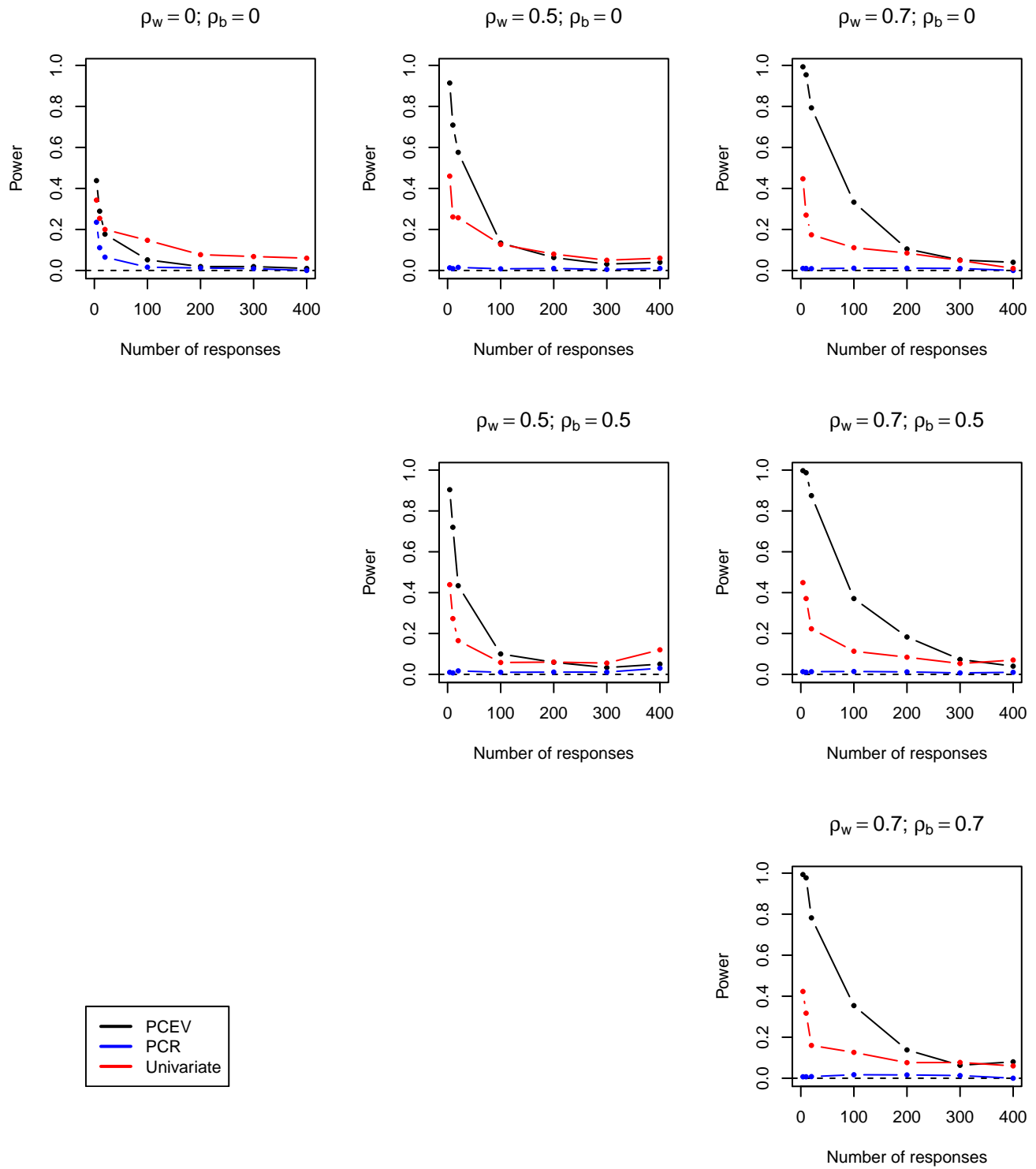
4.3 Significance level: 0.01, Heritability: 0.5%, Number of blocks: 10



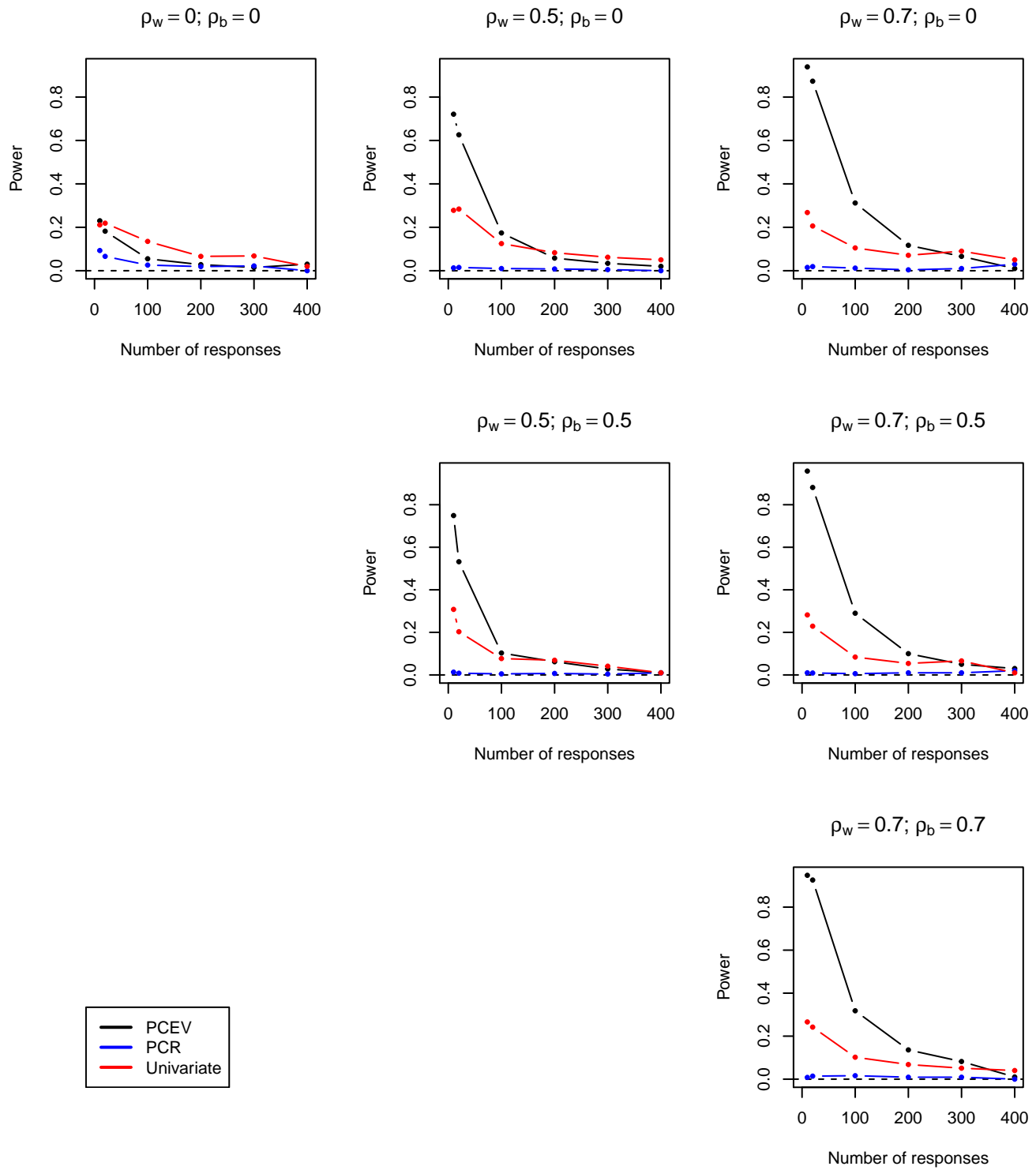
4.4 Significance level: 0.01, Heritability: 0.5%, Number of blocks: 20



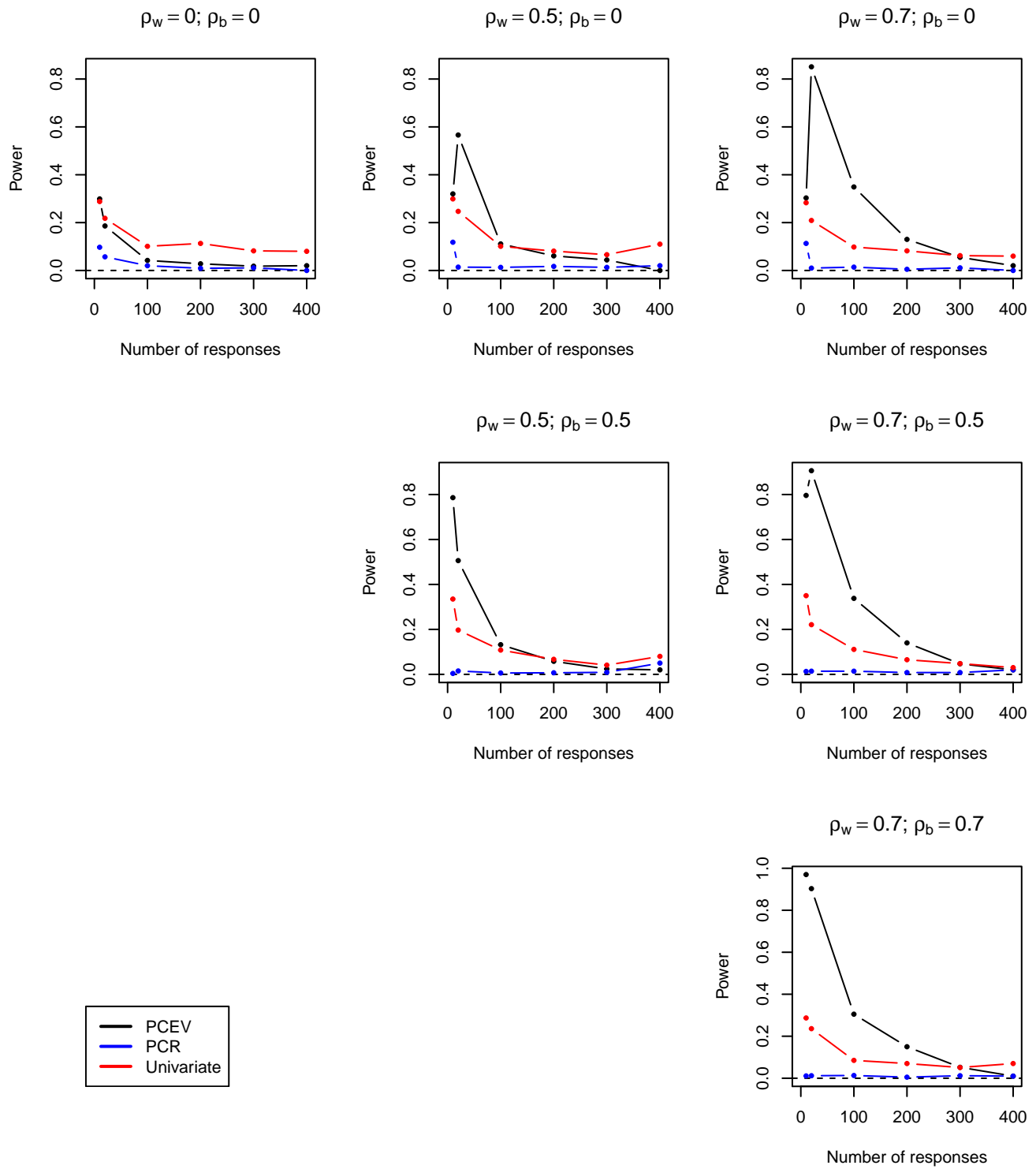
4.5 Significance level: 0.01, Heritability: 1%, Number of blocks: 2



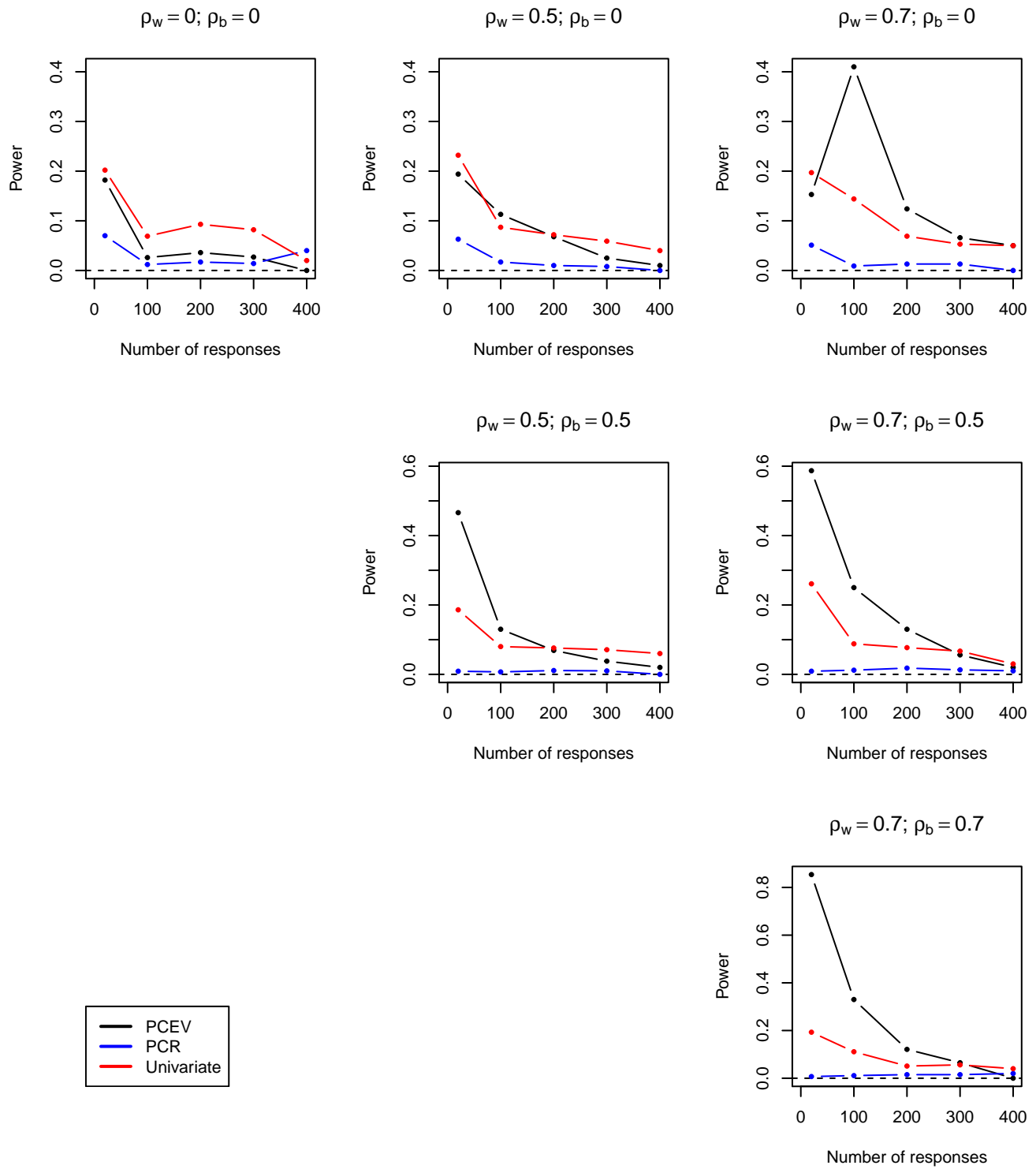
4.6 Significance level: 0.01, Heritability: 1%, Number of blocks: 5



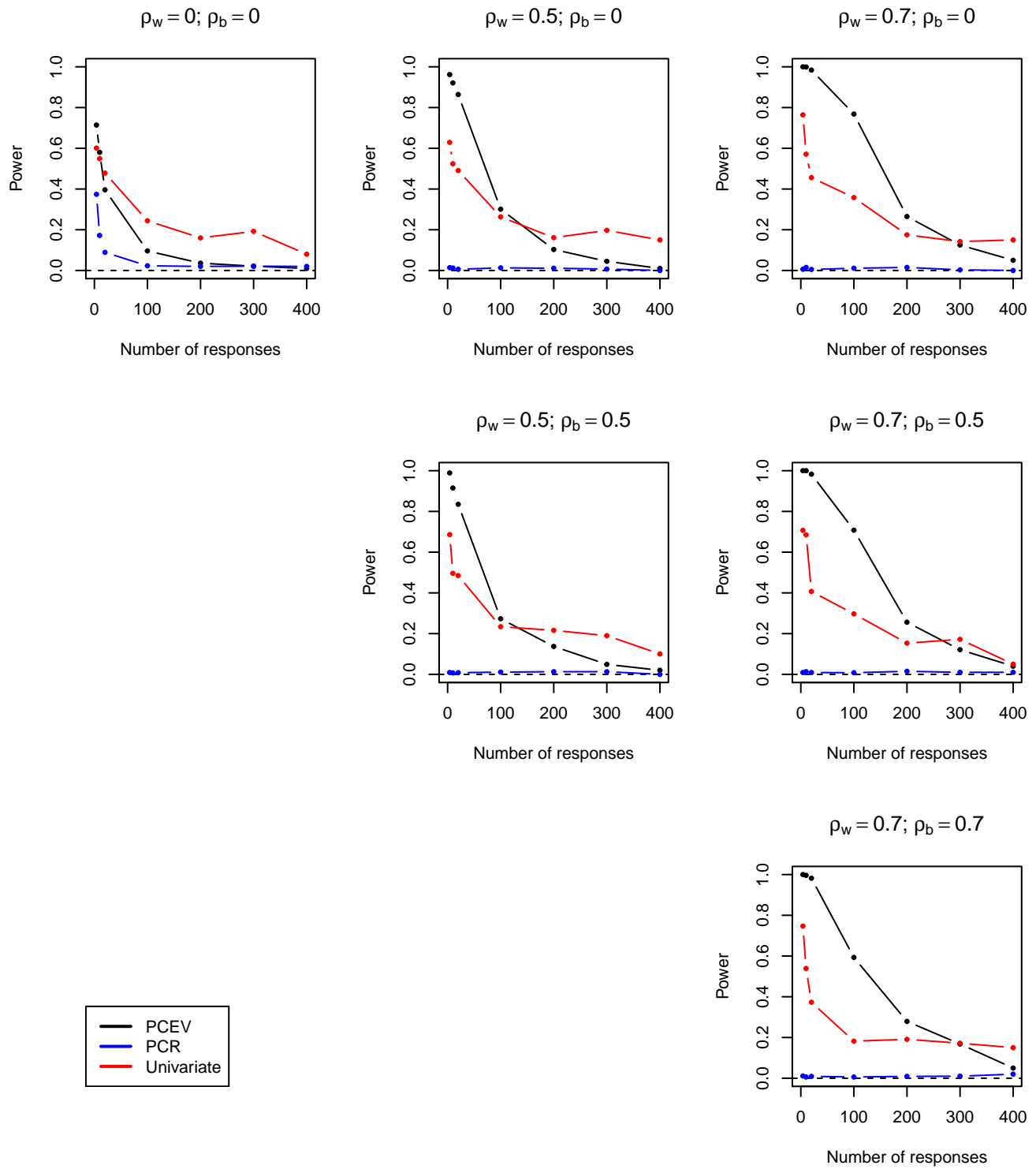
4.7 Significance level: 0.01, Heritability: 1%, Number of blocks: 10



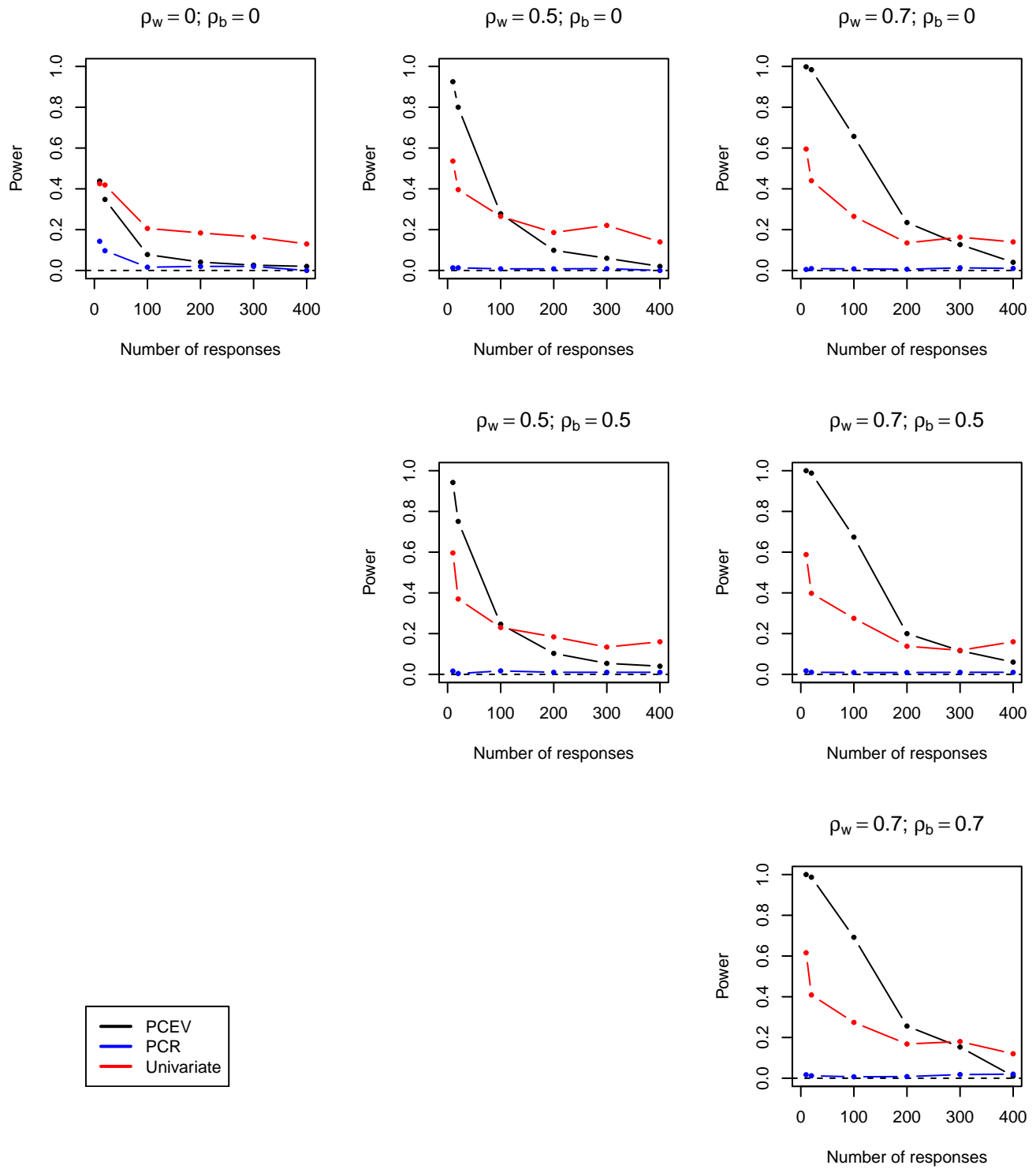
4.8 Significance level: 0.01, Heritability: 1%, Number of blocks: 20



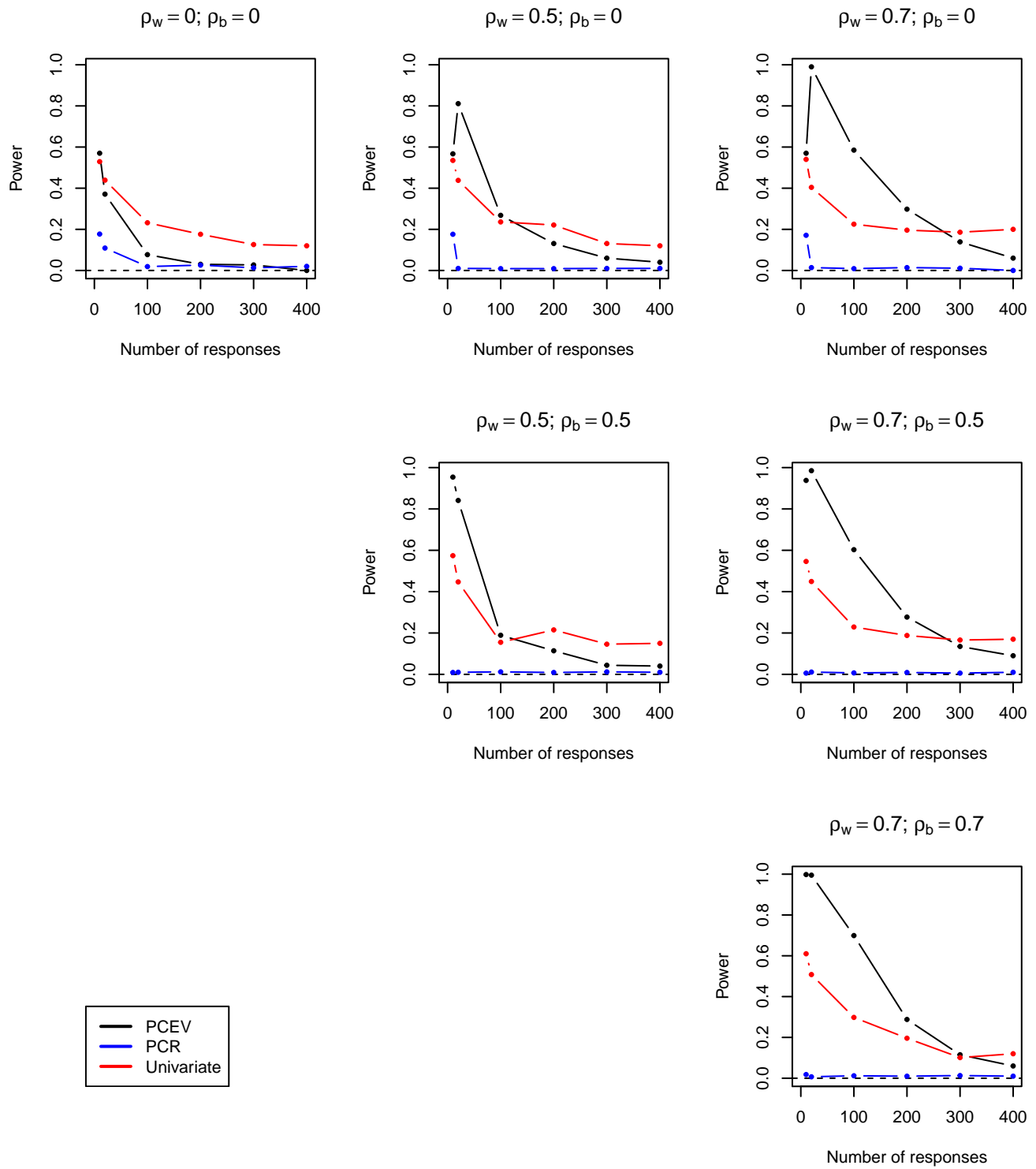
4.9 Significance level: 0.01, Heritability: 1.5%, Number of blocks: 2



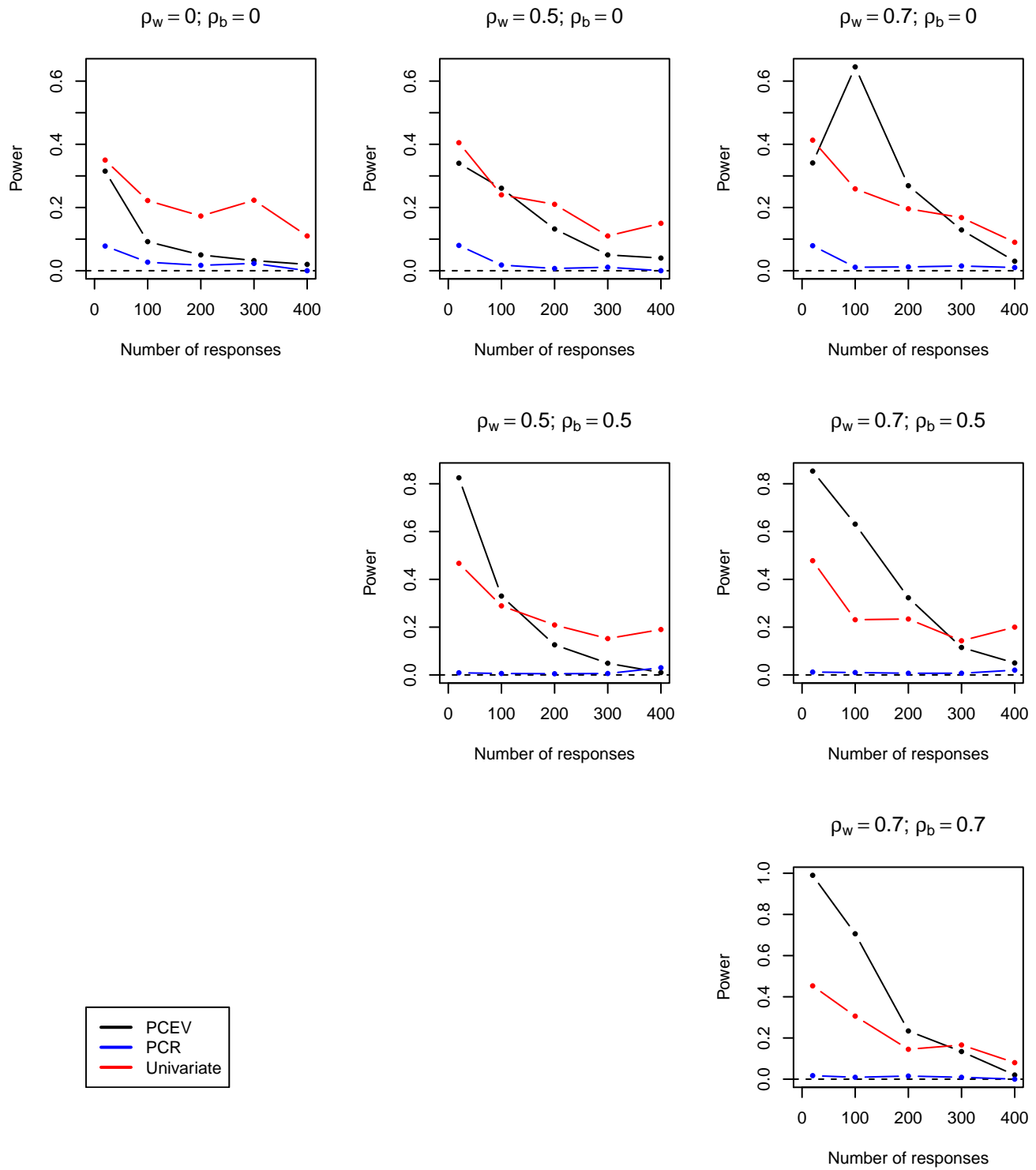
4.10 Significance level: 0.01, Heritability: 1.5%, Number of blocks: 5



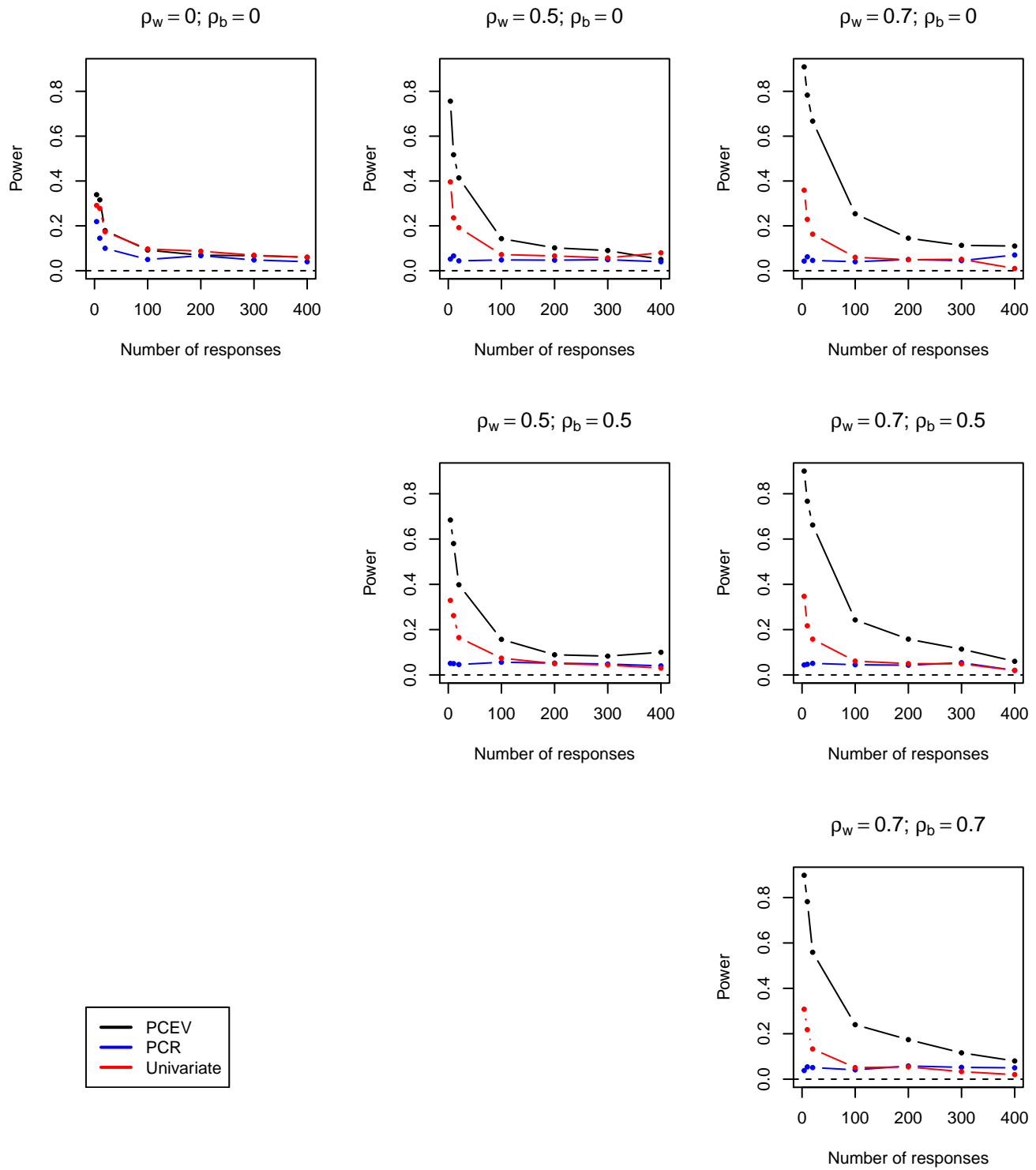
4.11 Significance level: 0.01, Heritability: 1.5%, Number of blocks: 10



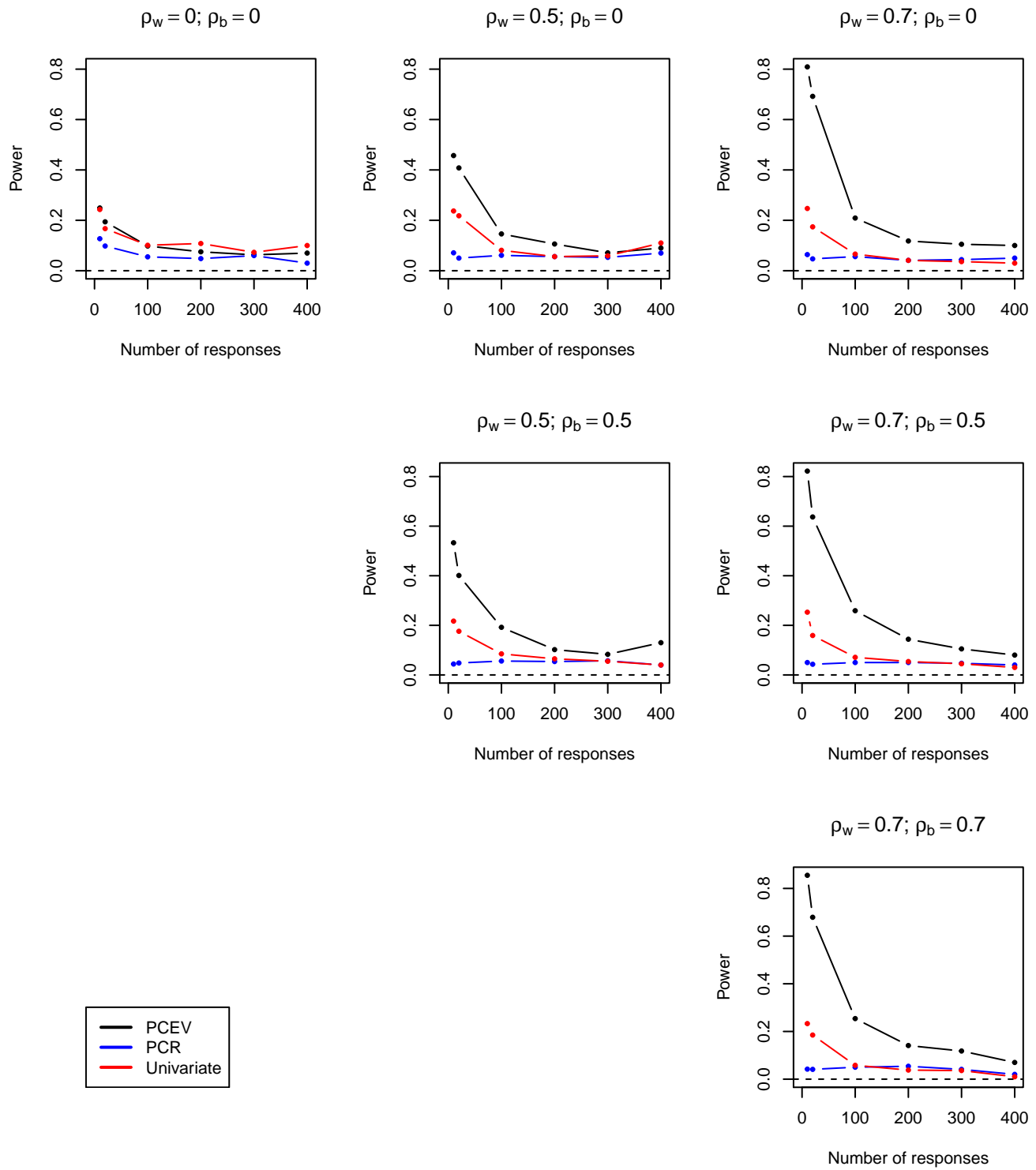
4.12 Significance level: 0.01, Heritability: 1.5%, Number of blocks: 20



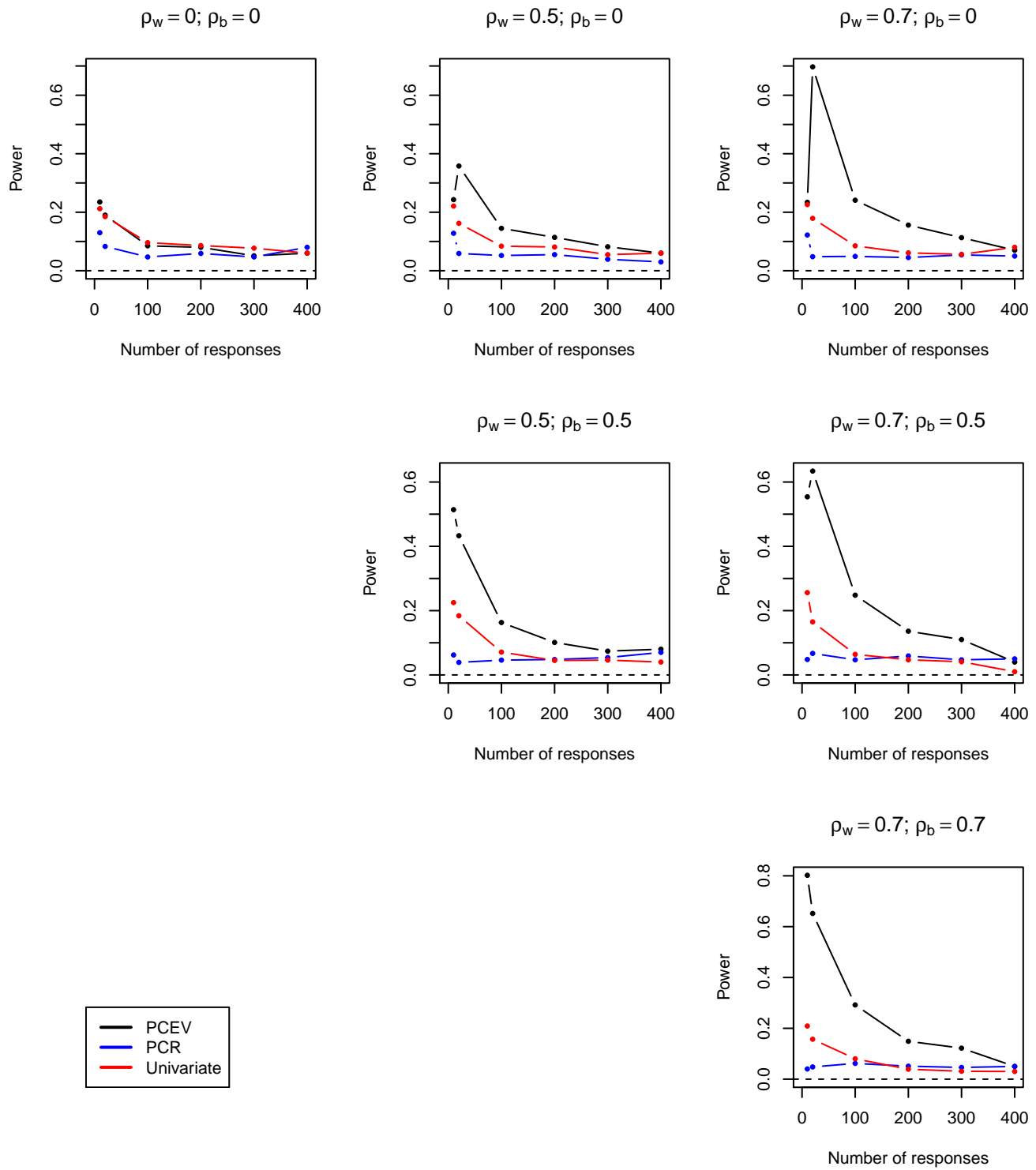
4.13 Significance level: 0.05, Heritability: 0.5%, Number of blocks: 2



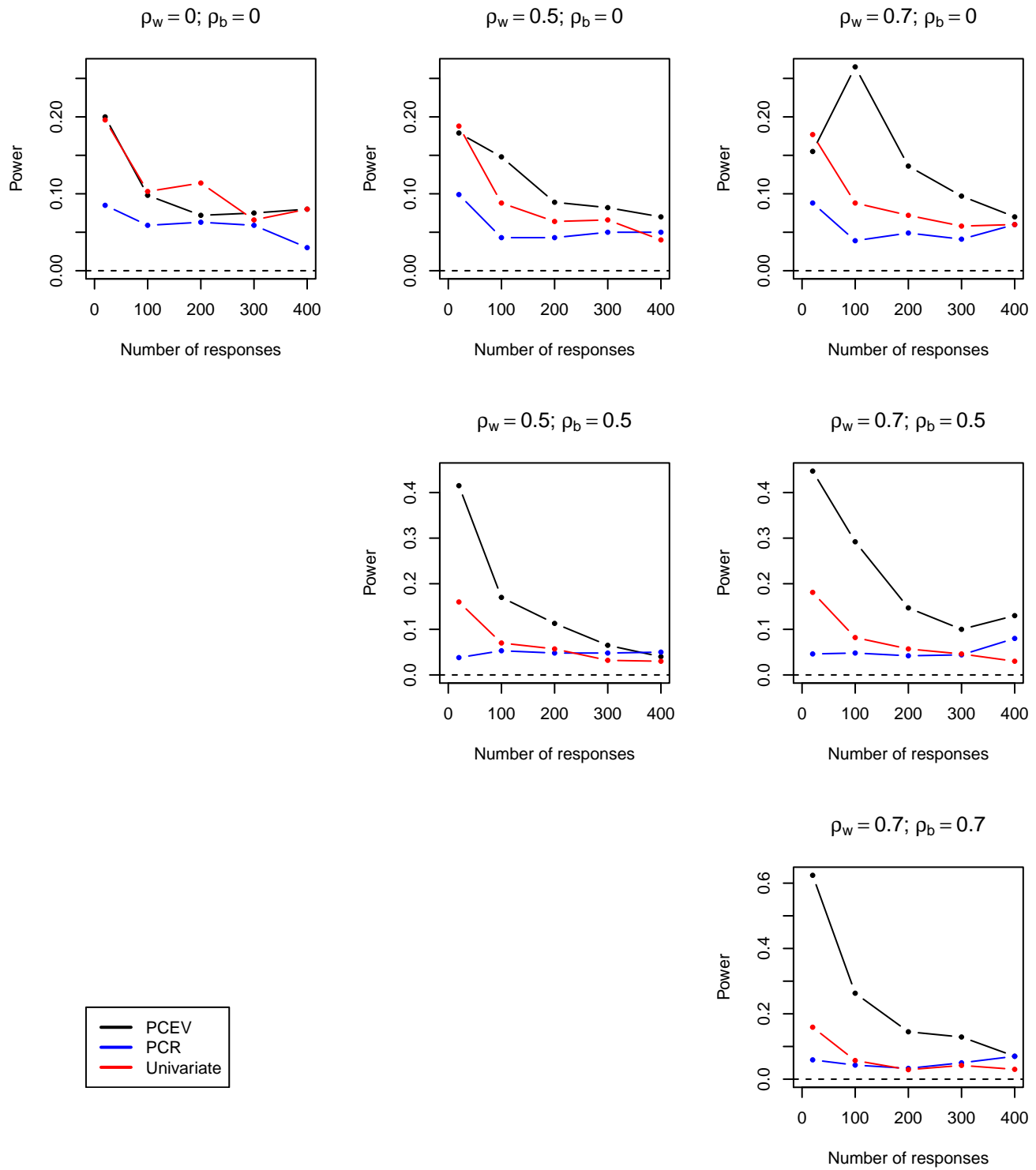
4.14 Significance level: 0.05, Heritability: 0.5%, Number of blocks: 5



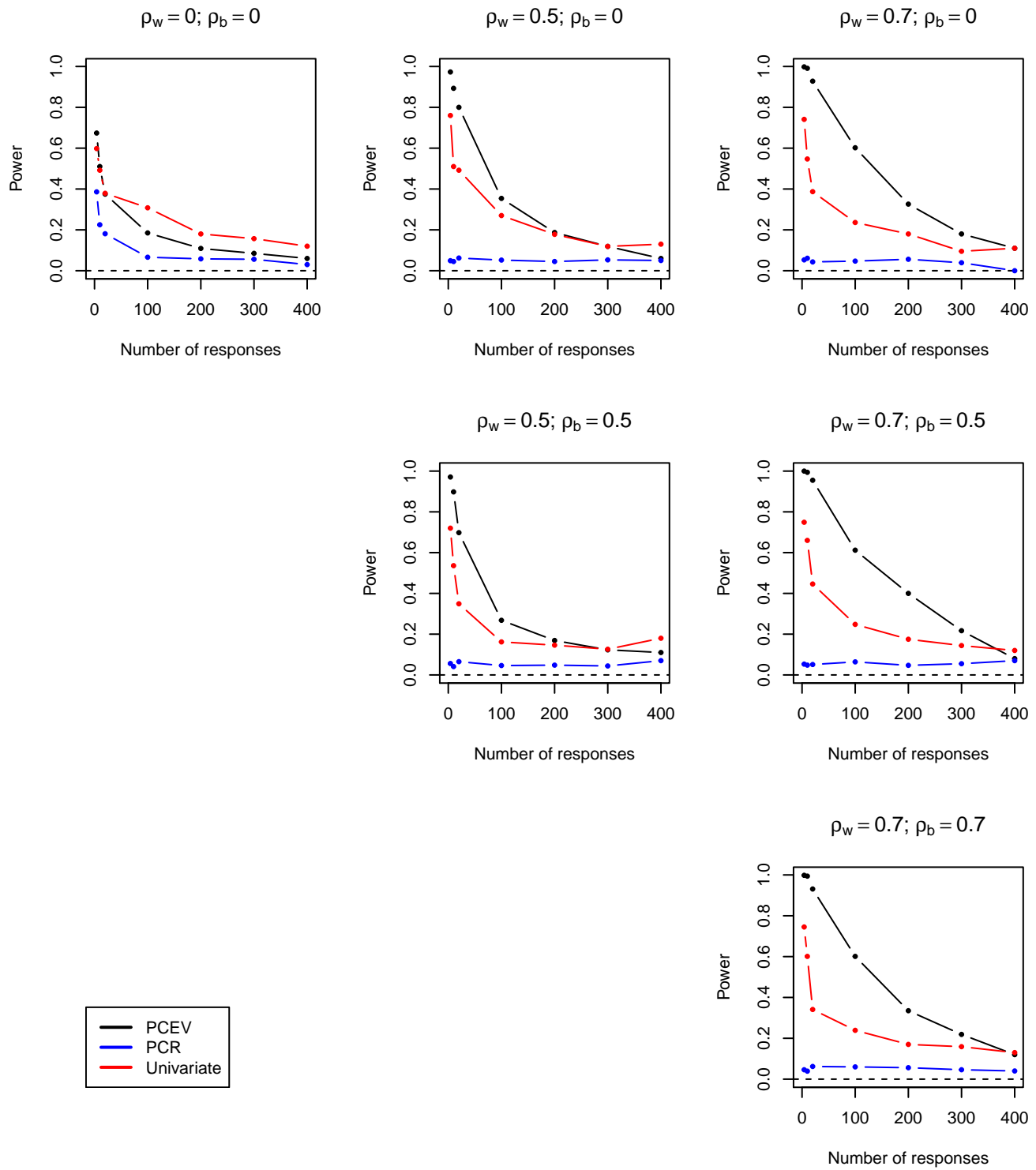
4.15 Significance level: 0.05, Heritability: 0.5%, Number of blocks: 10



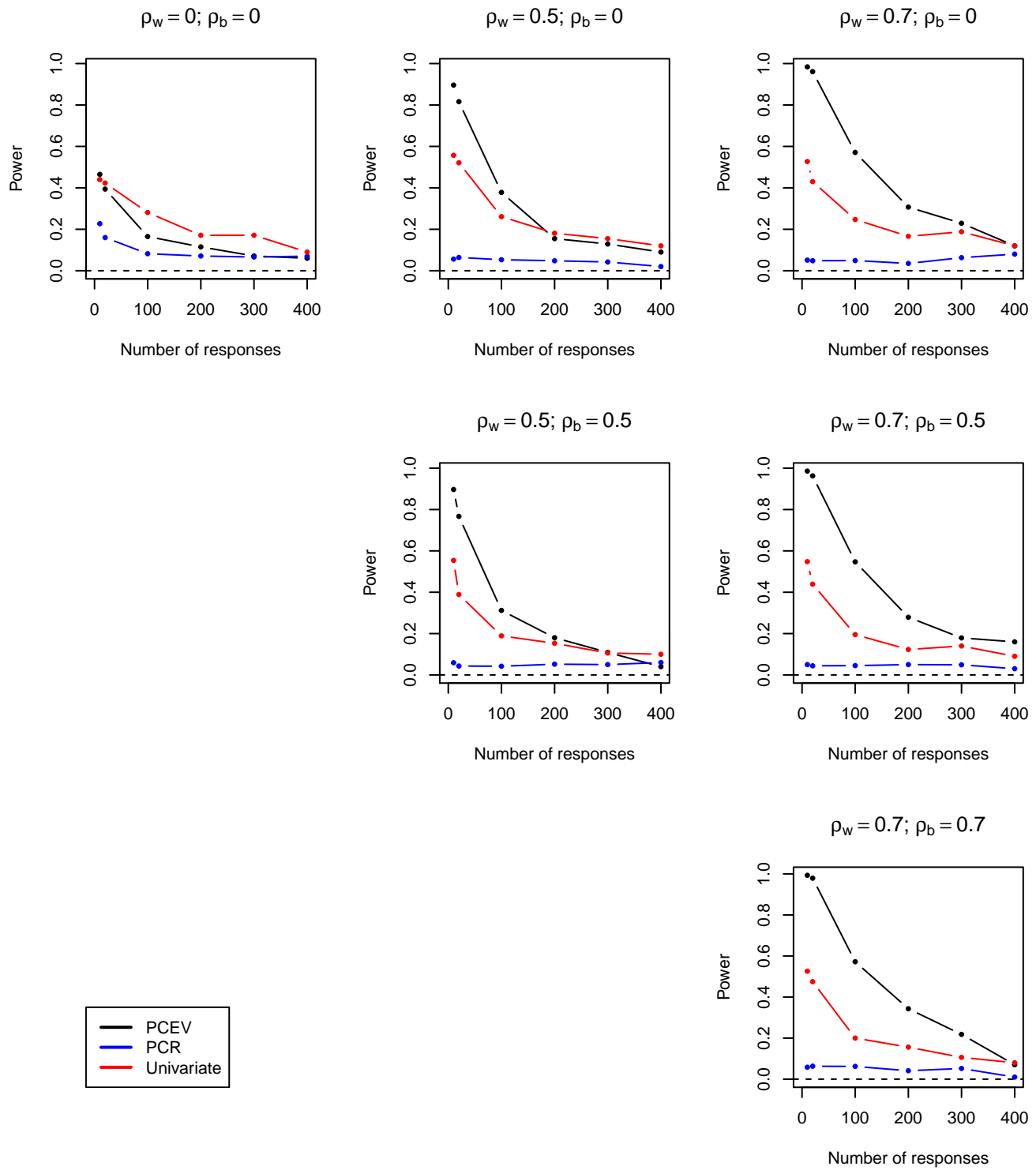
4.16 Significance level: 0.05, Heritability: 0.5%, Number of blocks: 20



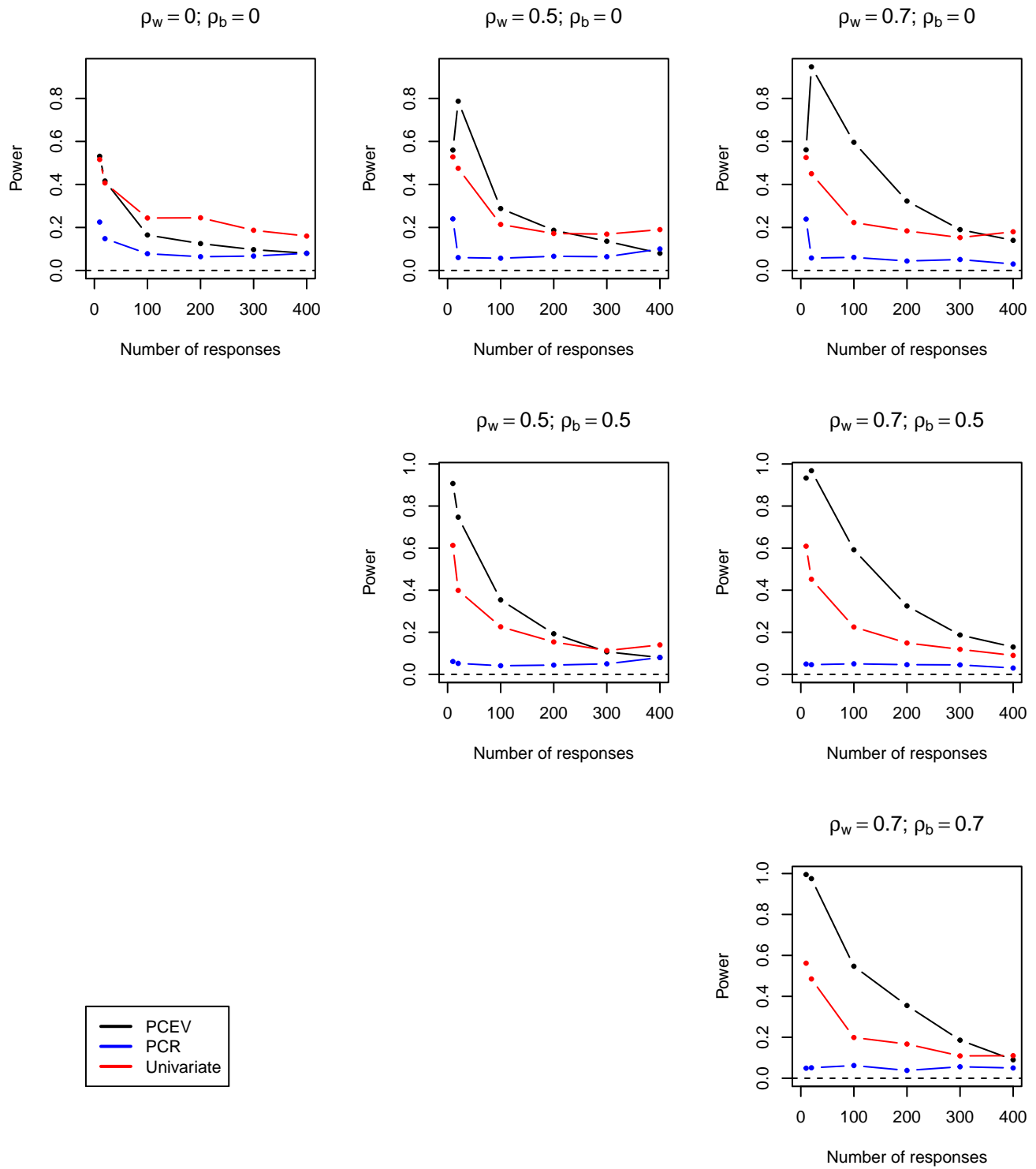
4.17 Significance level: 0.05, Heritability: 1%, Number of blocks: 2



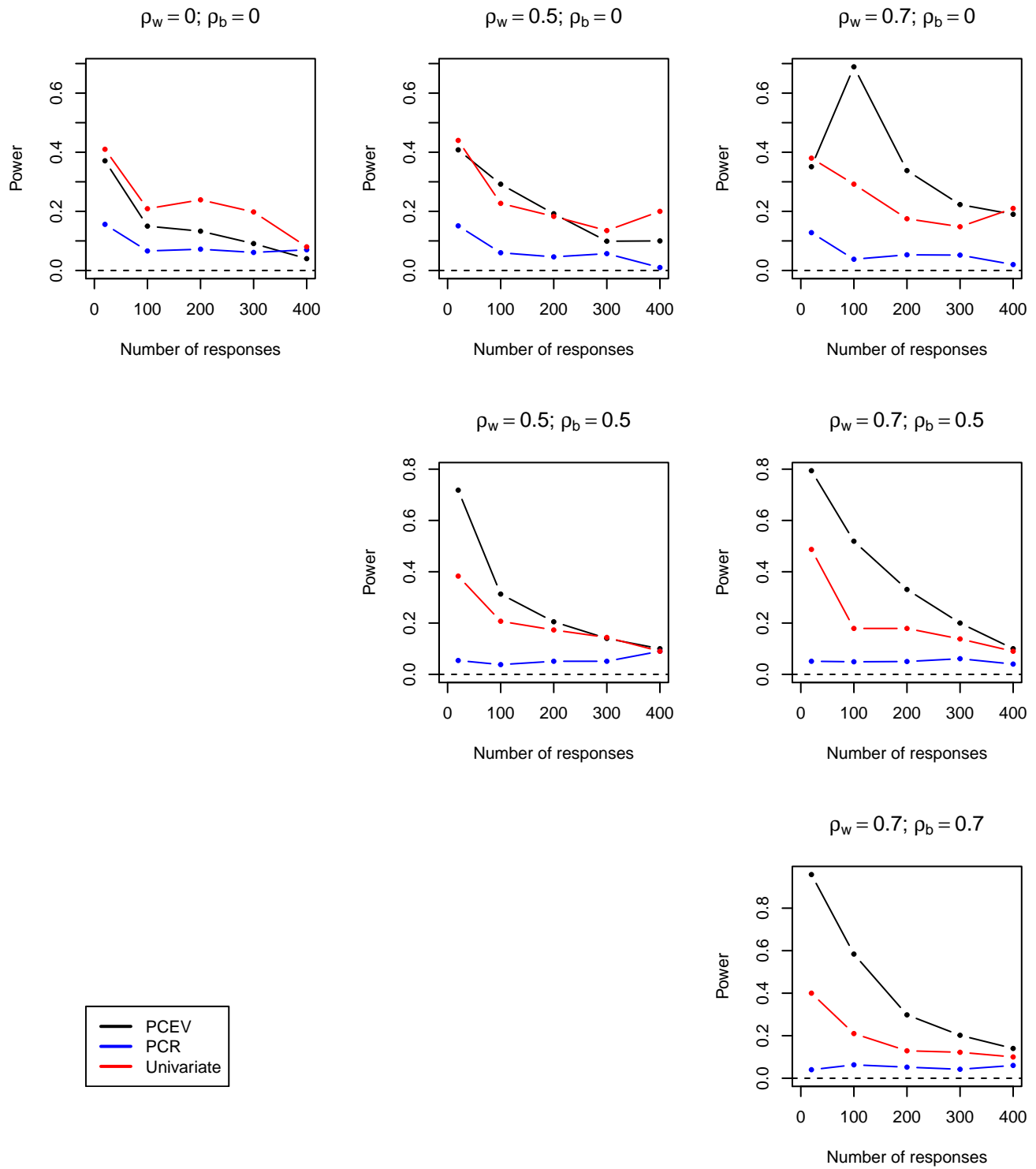
4.18 Significance level: 0.05, Heritability: 1%, Number of blocks: 5



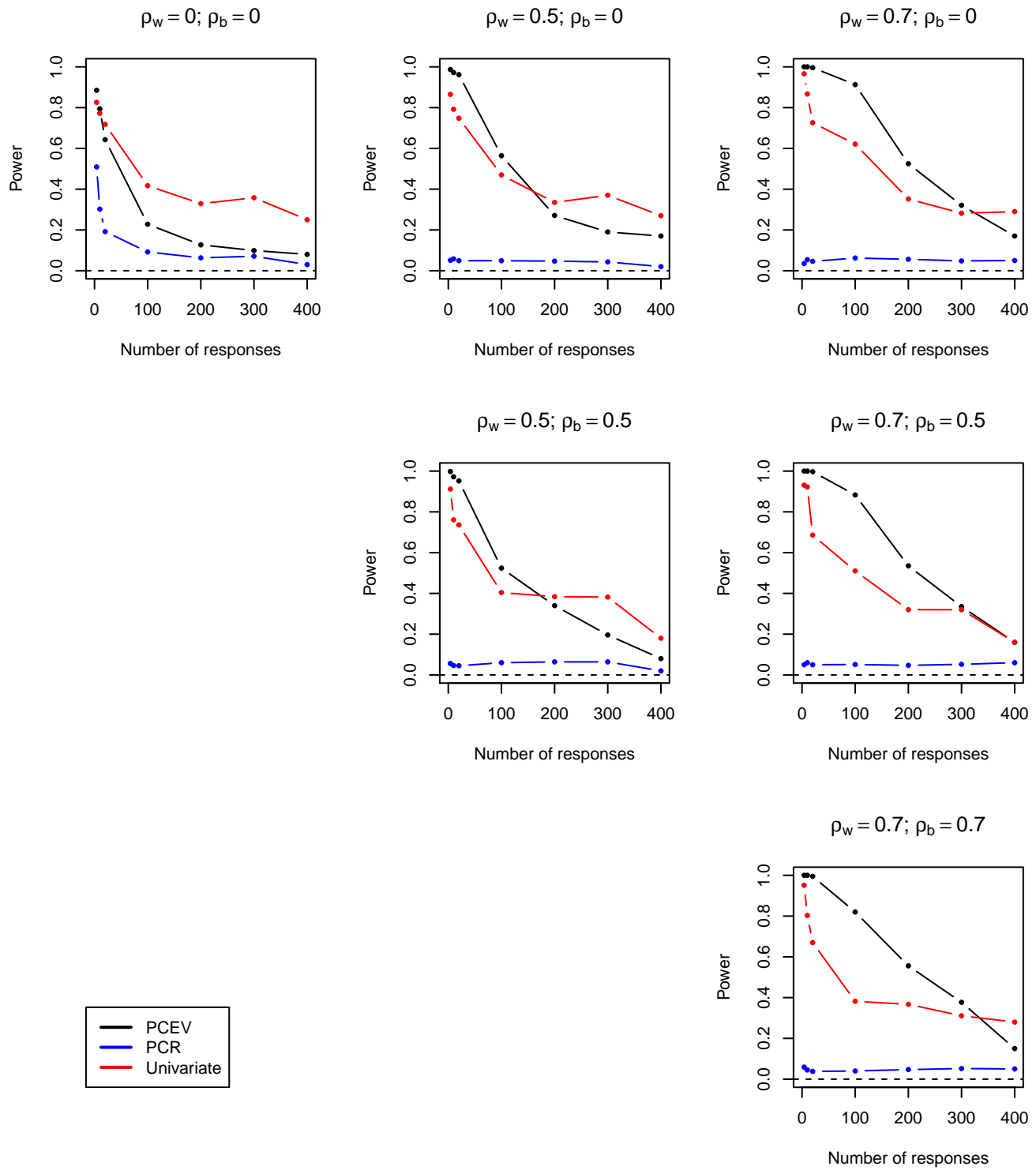
4.19 Significance level: 0.05, Heritability: 1%, Number of blocks: 10



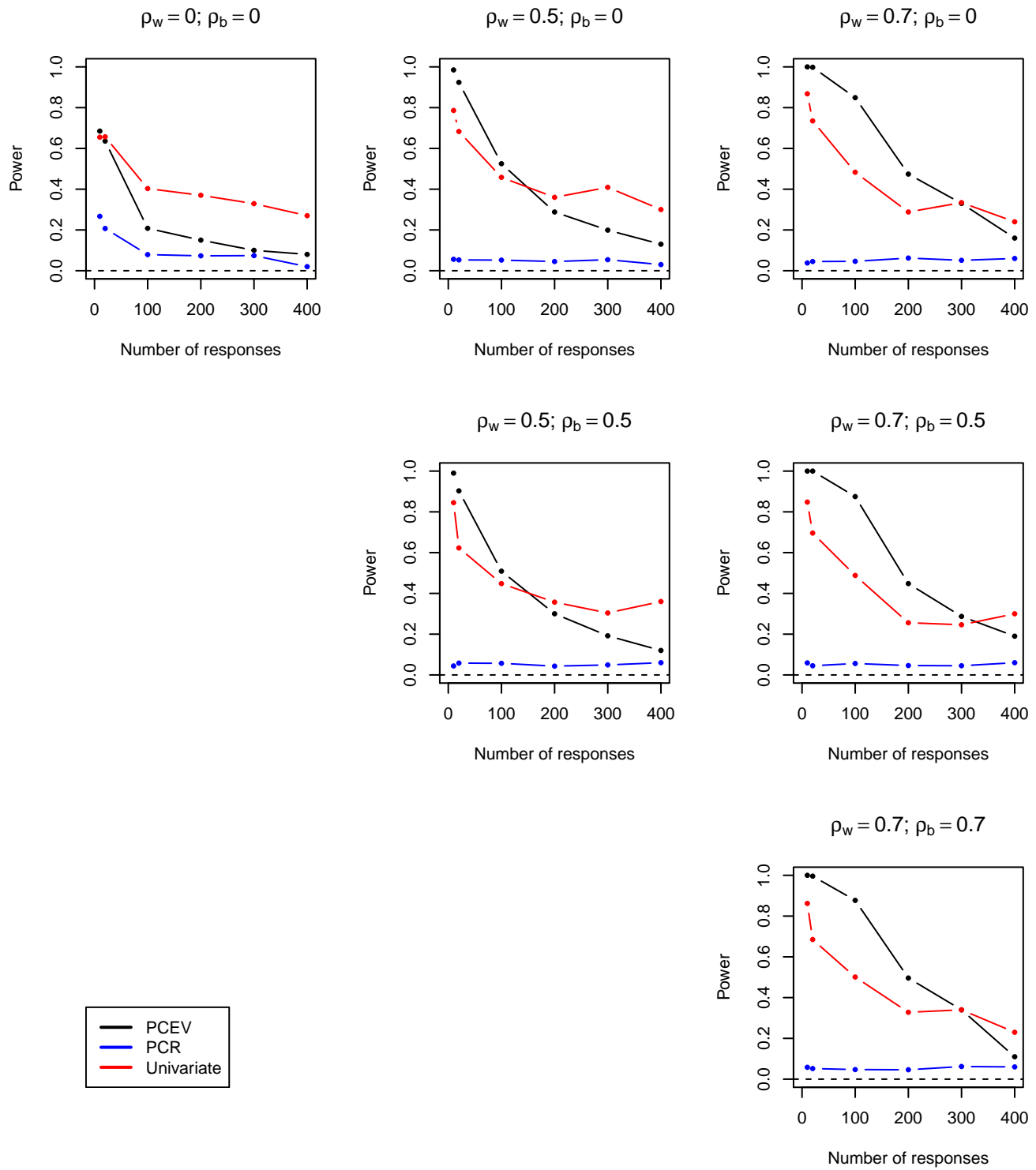
4.20 Significance level: 0.05, Heritability: 1%, Number of blocks: 20



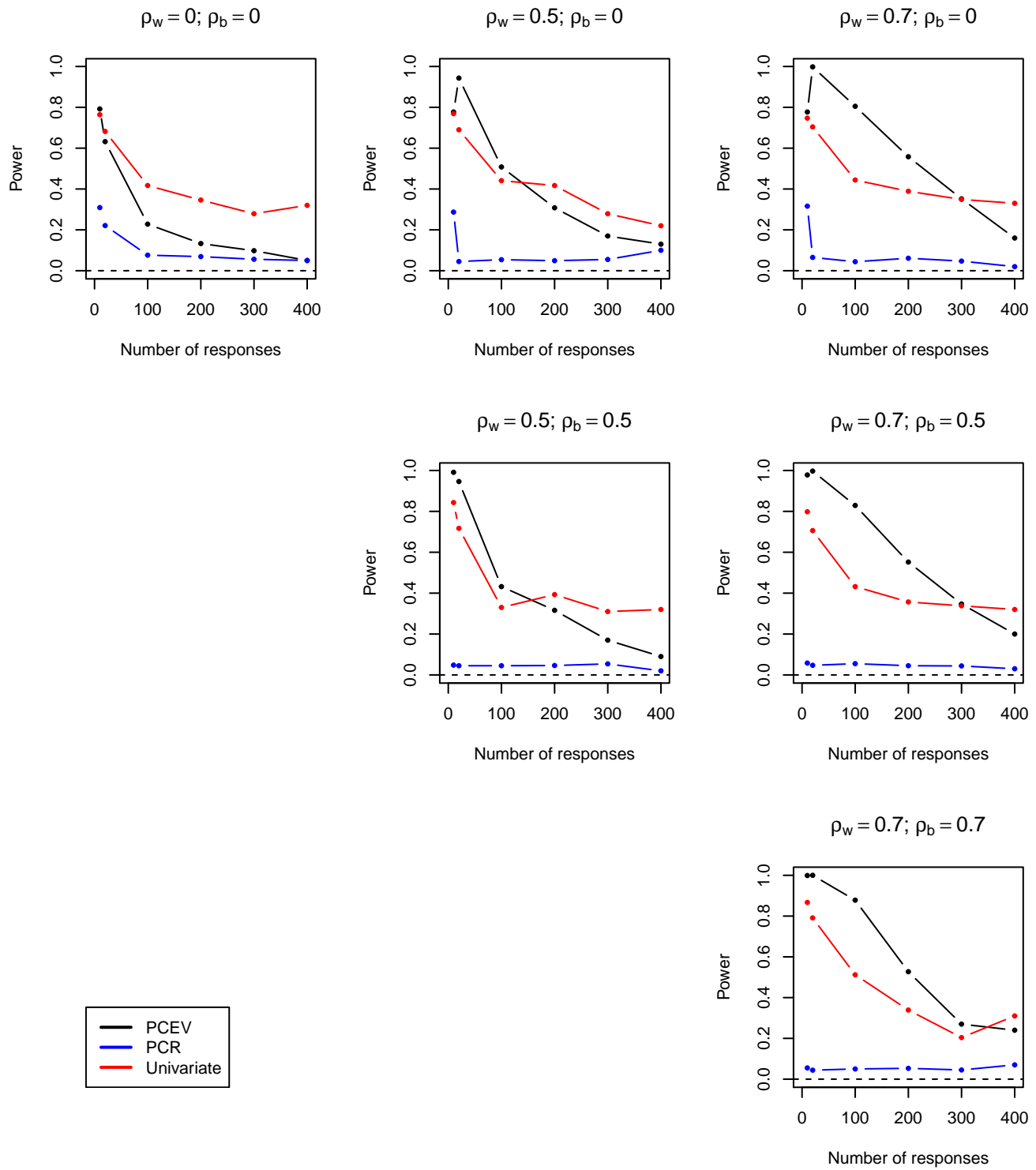
4.21 Significance level: 0.05, Heritability: 1.5%, Number of blocks: 2



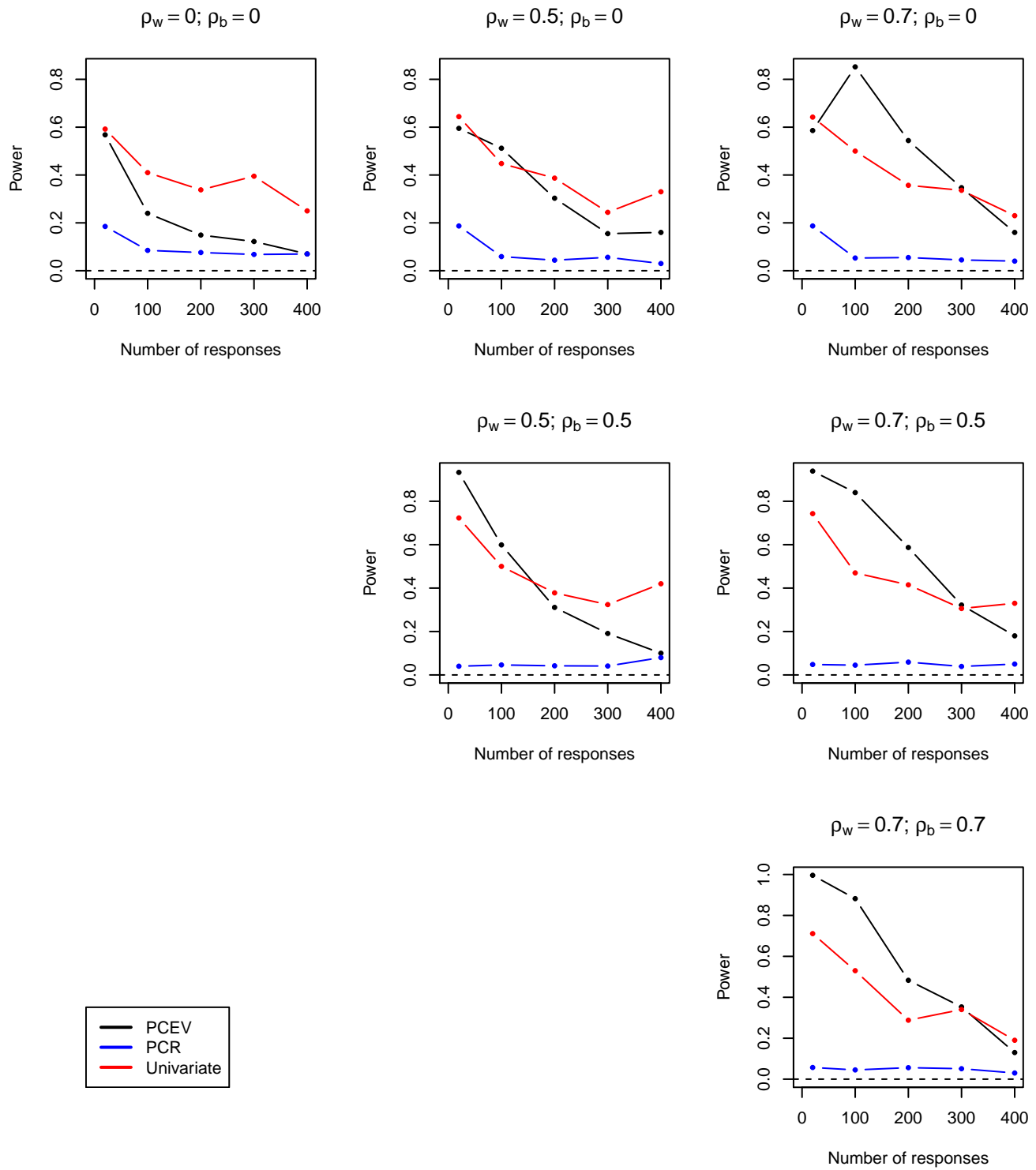
4.22 Significance level: 0.05, Heritability: 1.5%, Number of blocks: 5



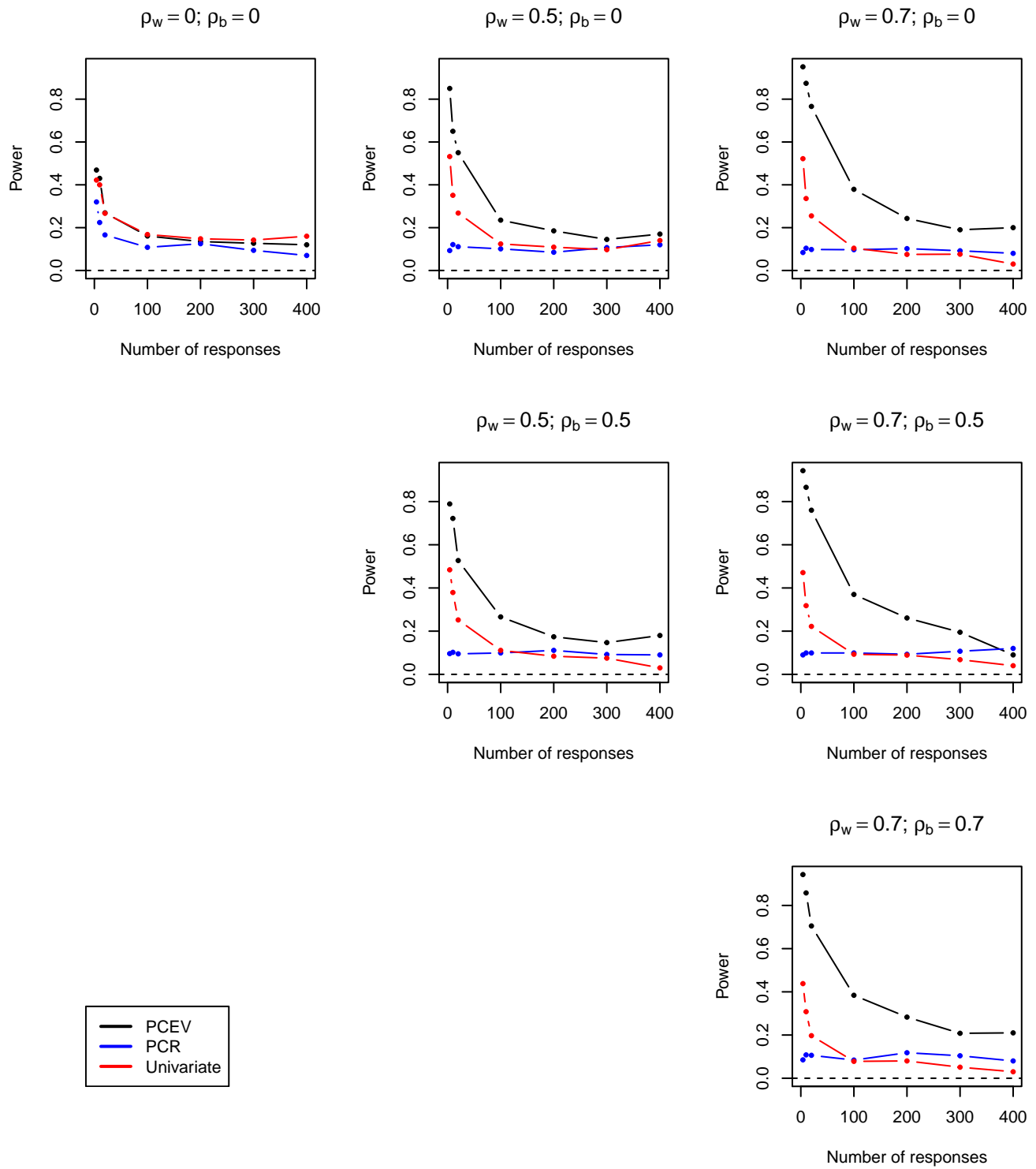
4.23 Significance level: 0.05, Heritability: 1.5%, Number of blocks: 10



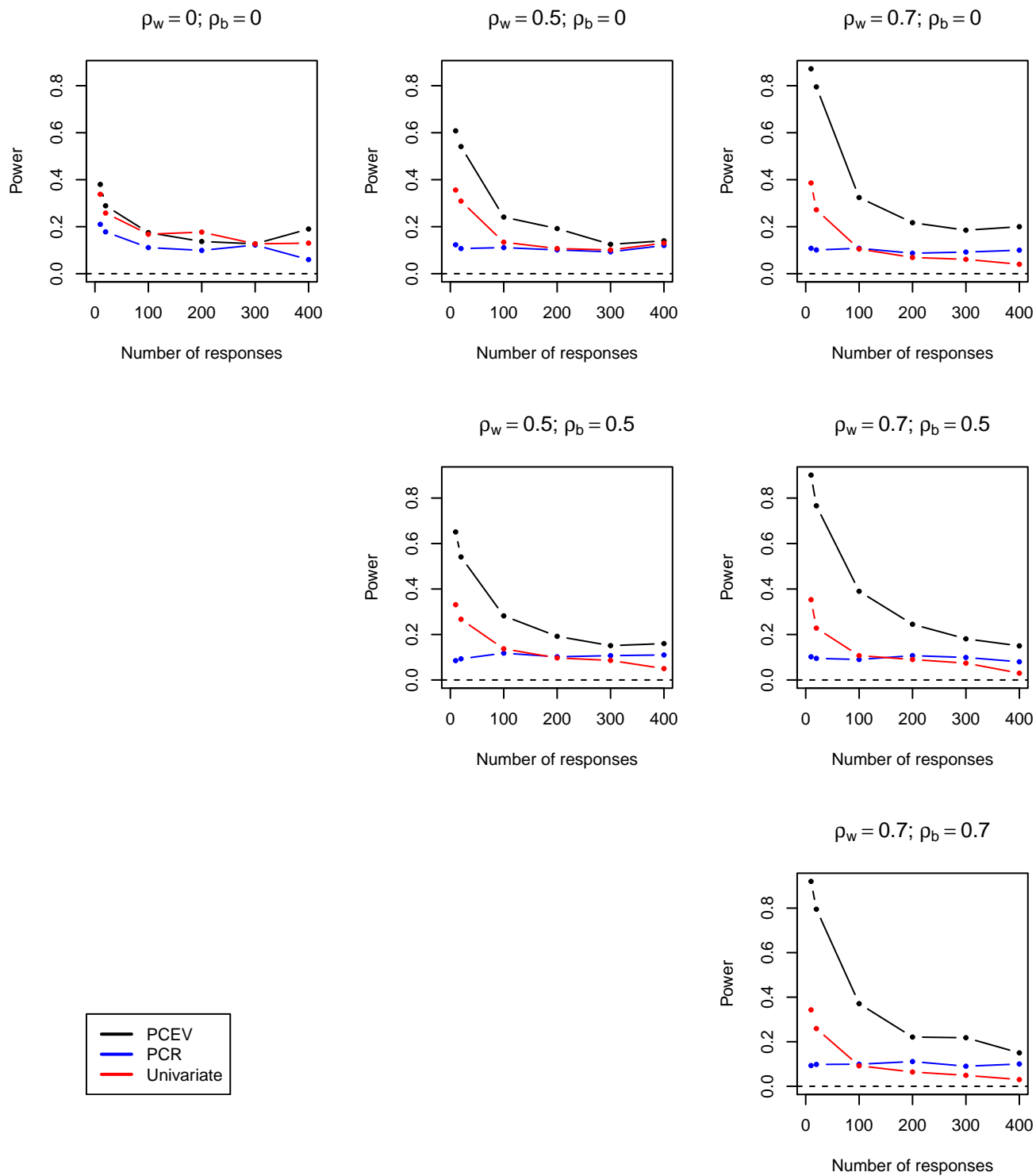
4.24 Significance level: 0.05, Heritability: 1.5%, Number of blocks: 20



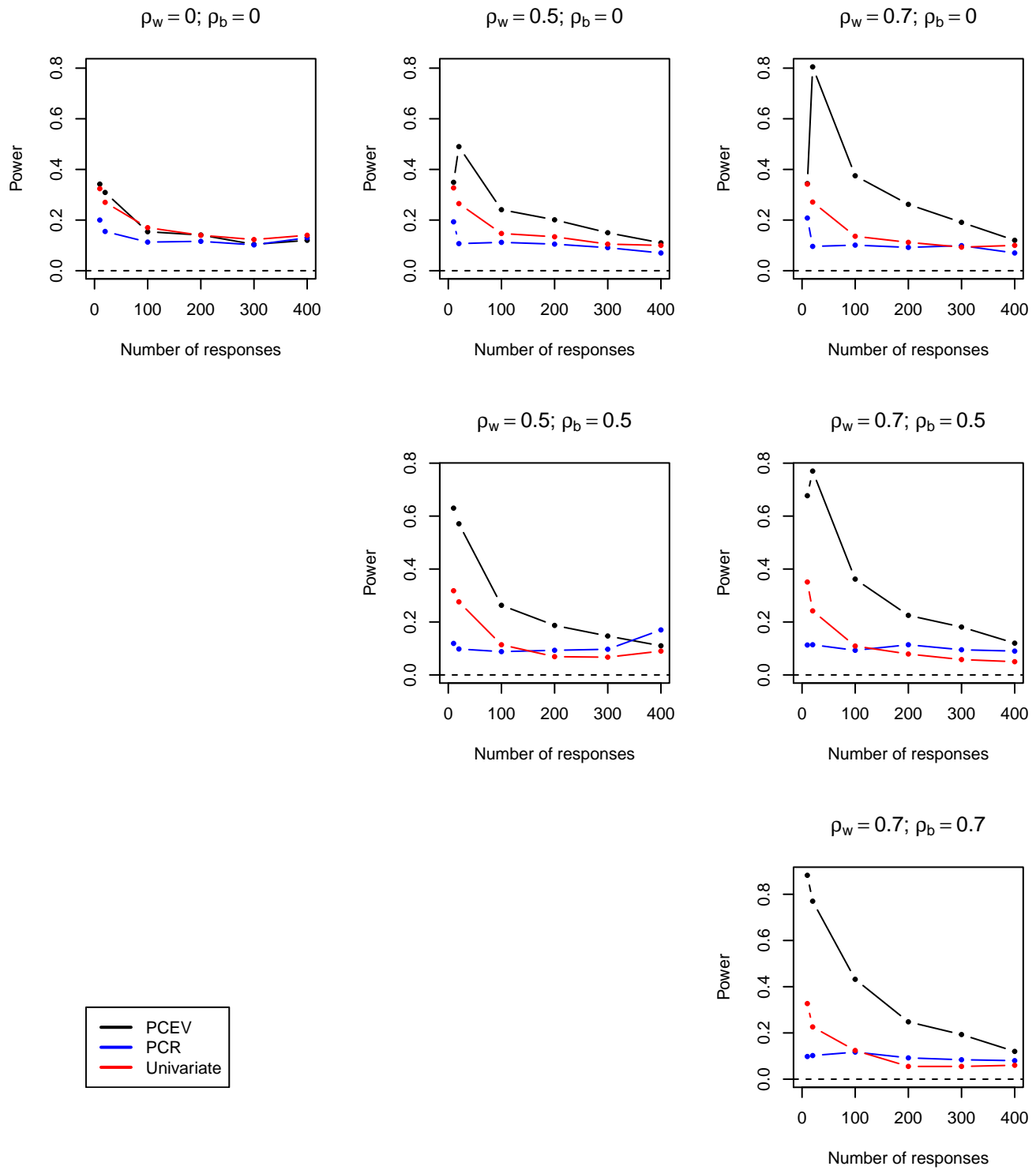
4.25 Significance level: 0.1, Heritability: 0.5%, Number of blocks: 2



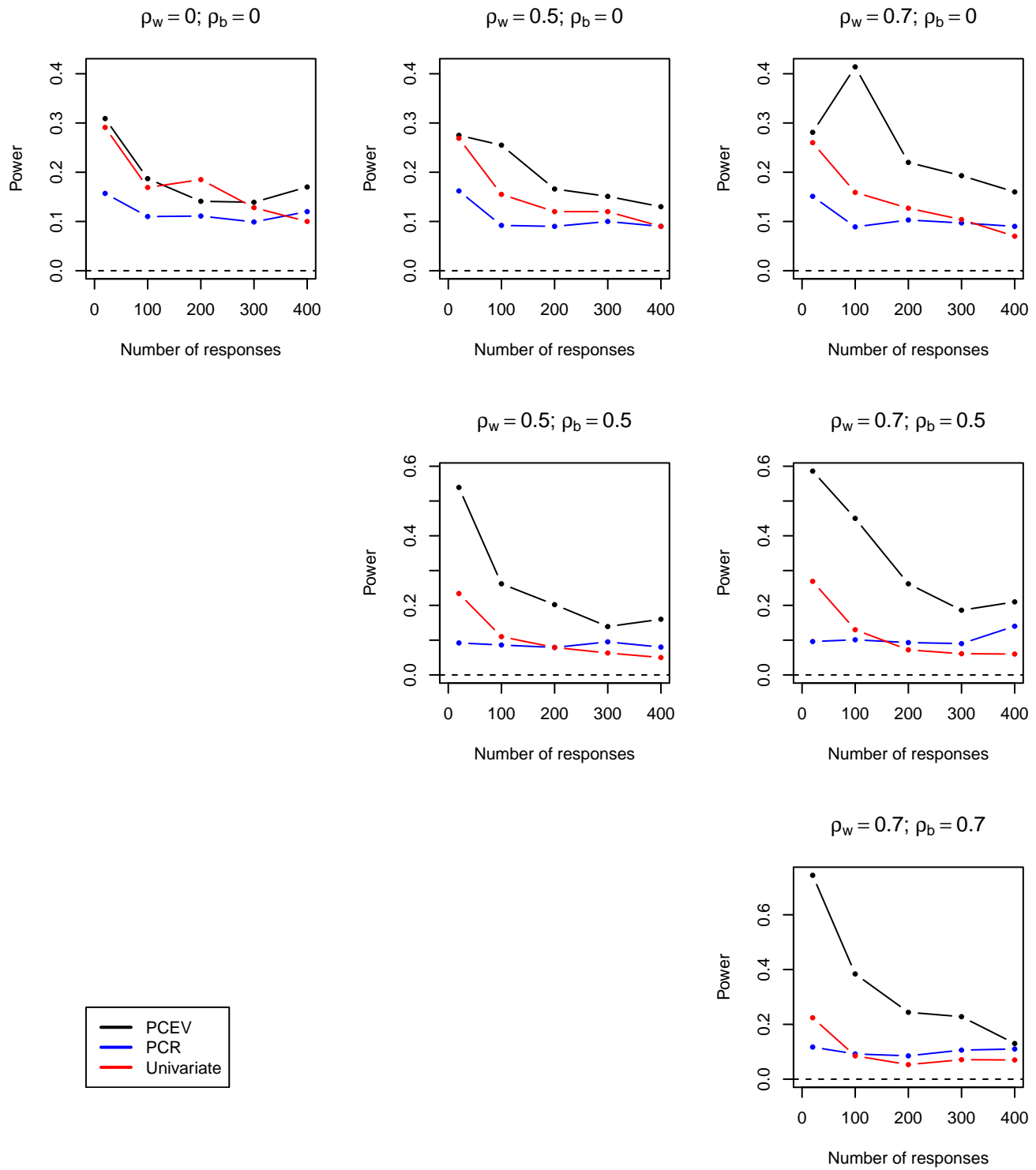
4.26 Significance level: 0.1, Heritability: 0.5%, Number of blocks: 5



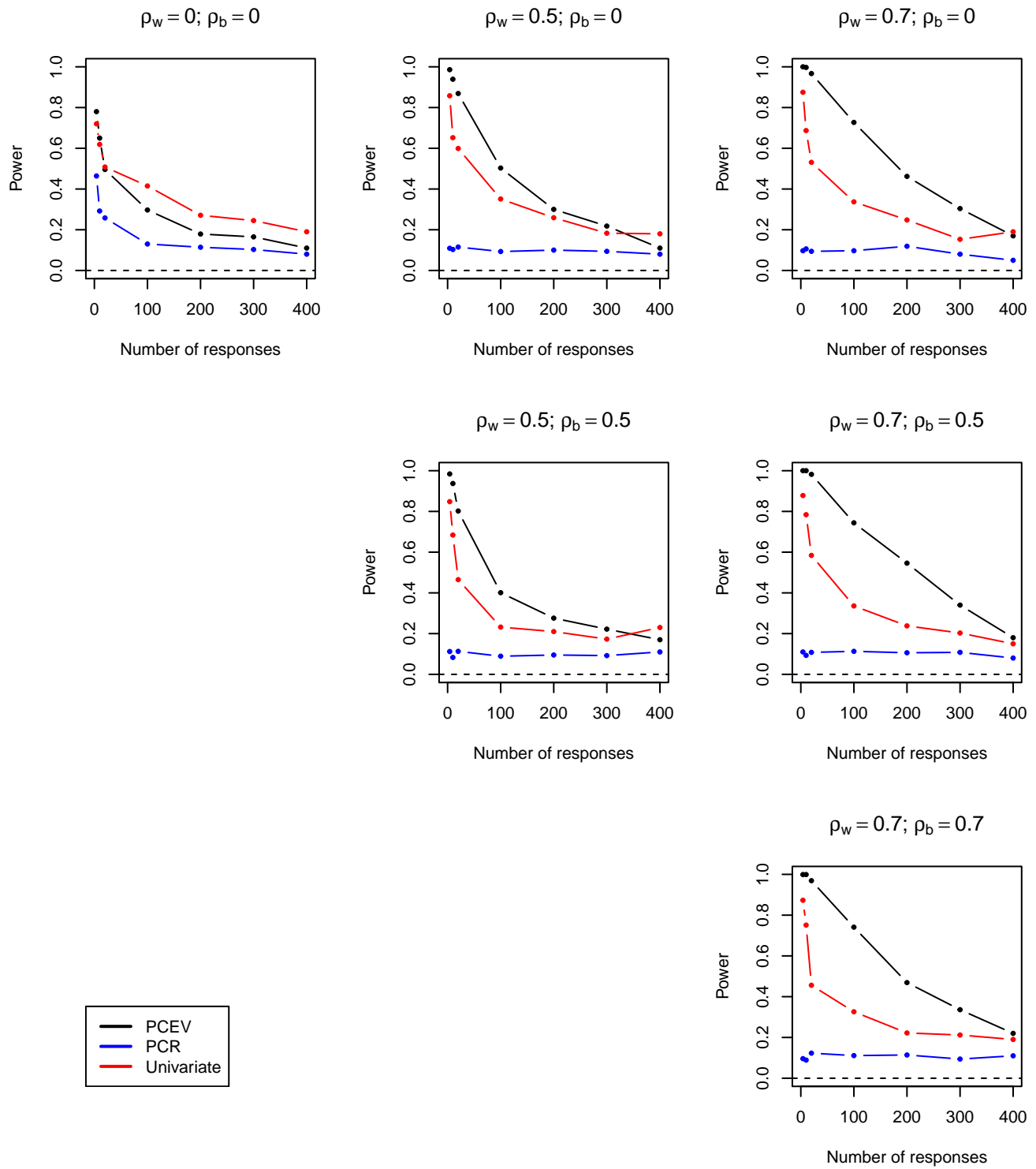
4.27 Significance level: 0.1, Heritability: 0.5%, Number of blocks: 10



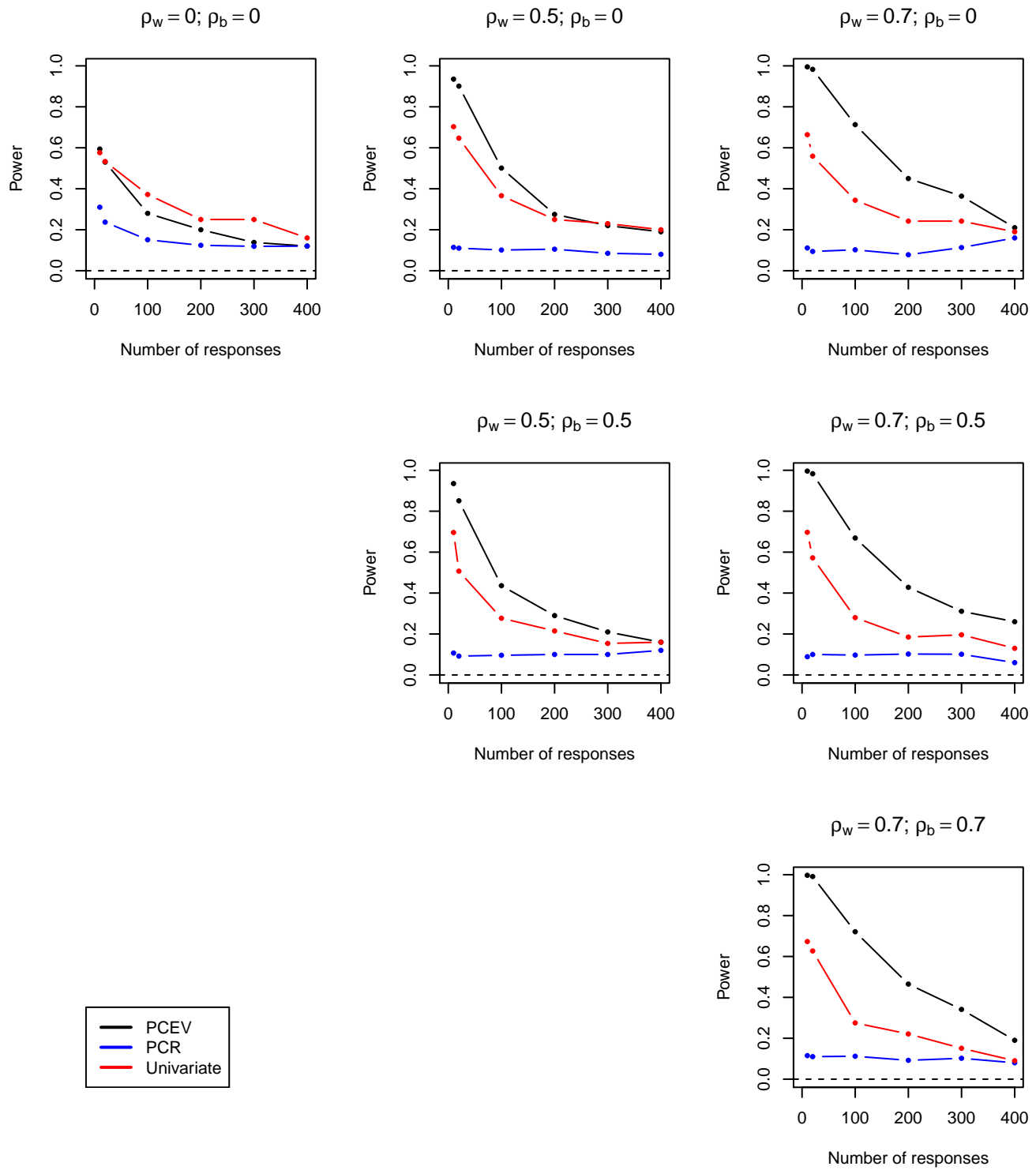
4.28 Significance level: 0.1, Heritability: 0.5%, Number of blocks: 20



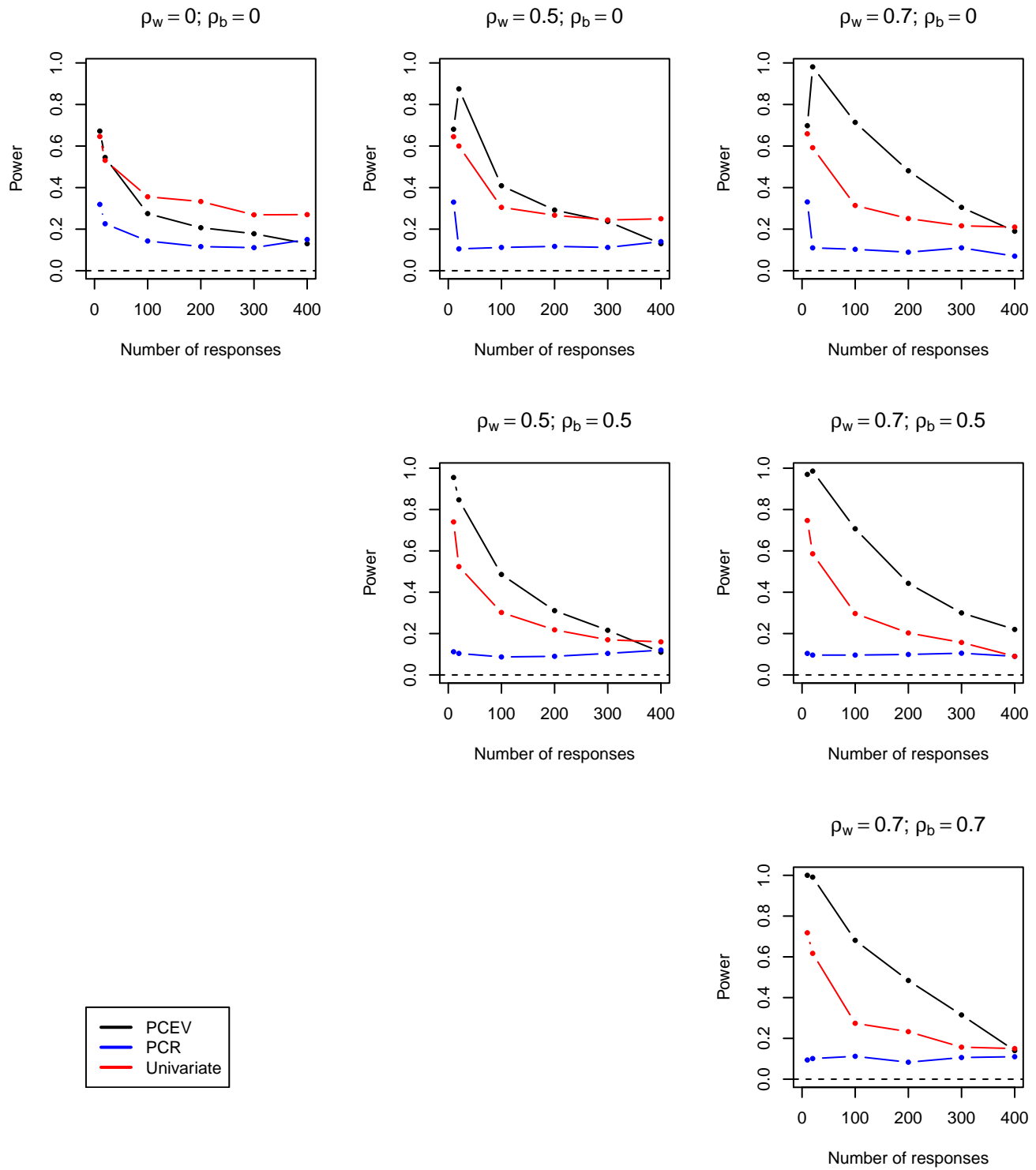
4.29 Significance level: 0.1, Heritability: 1%, Number of blocks: 2



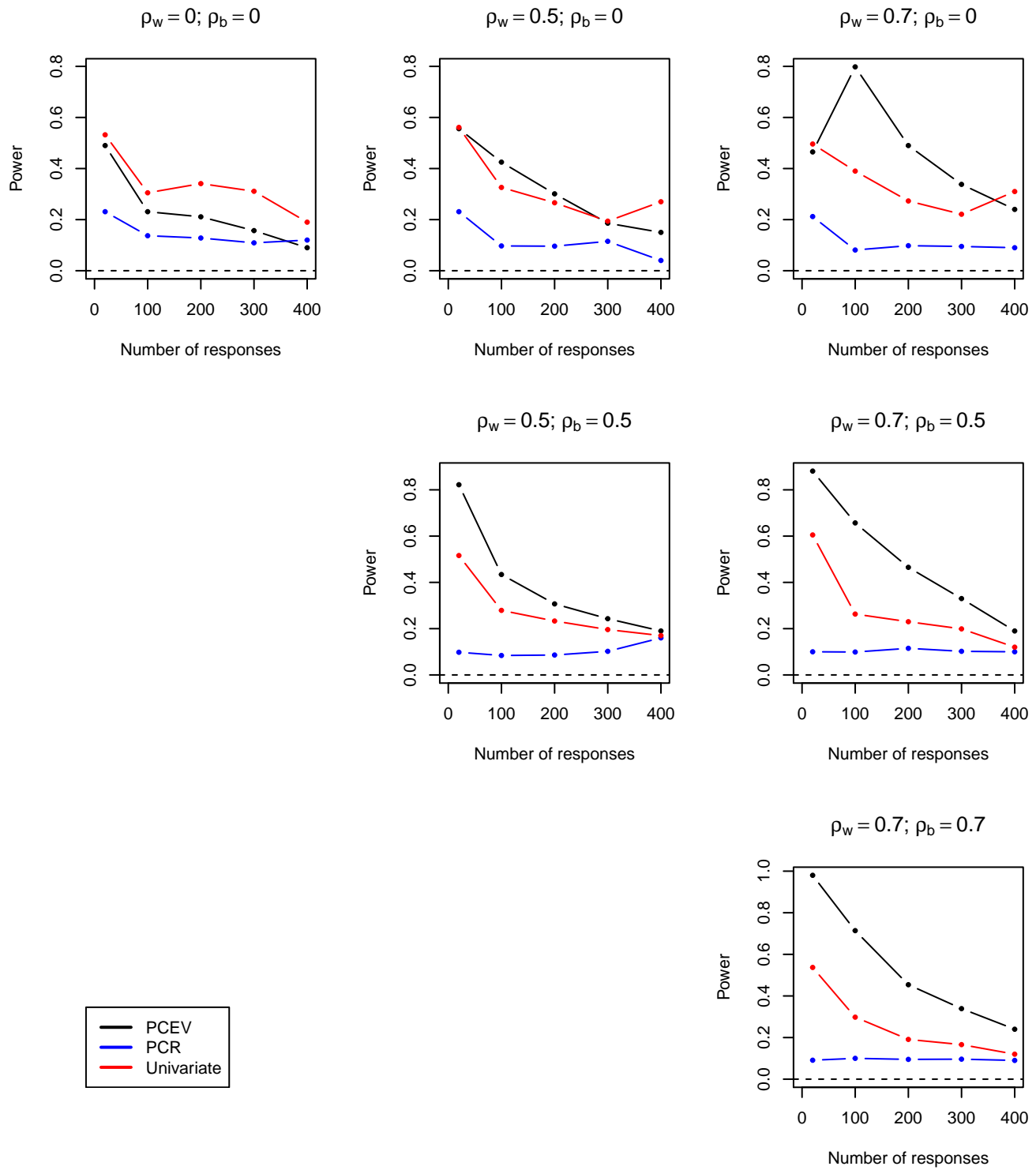
4.30 Significance level: 0.1, Heritability: 1%, Number of blocks: 5



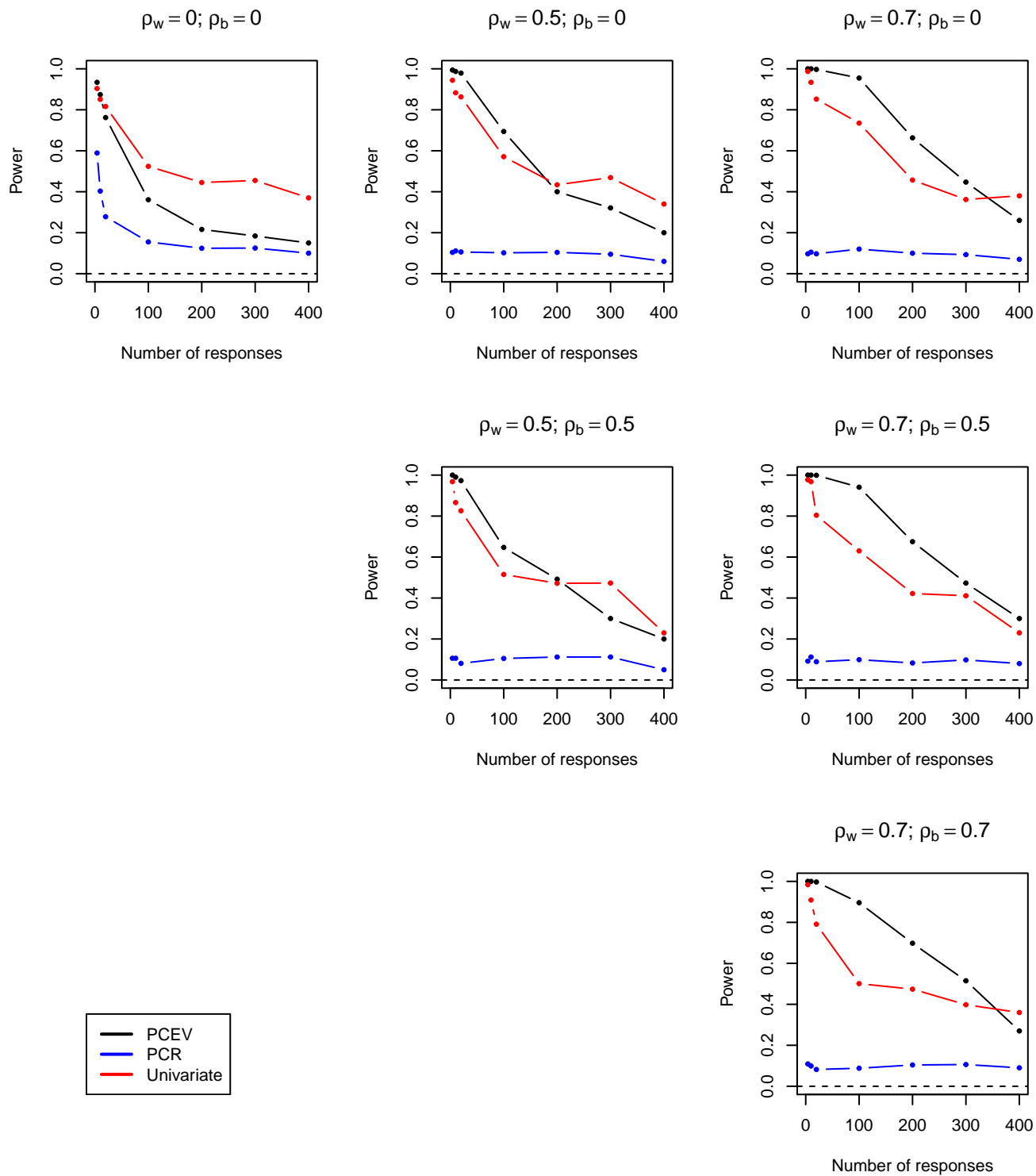
4.31 Significance level: 0.1, Heritability: 1%, Number of blocks: 10



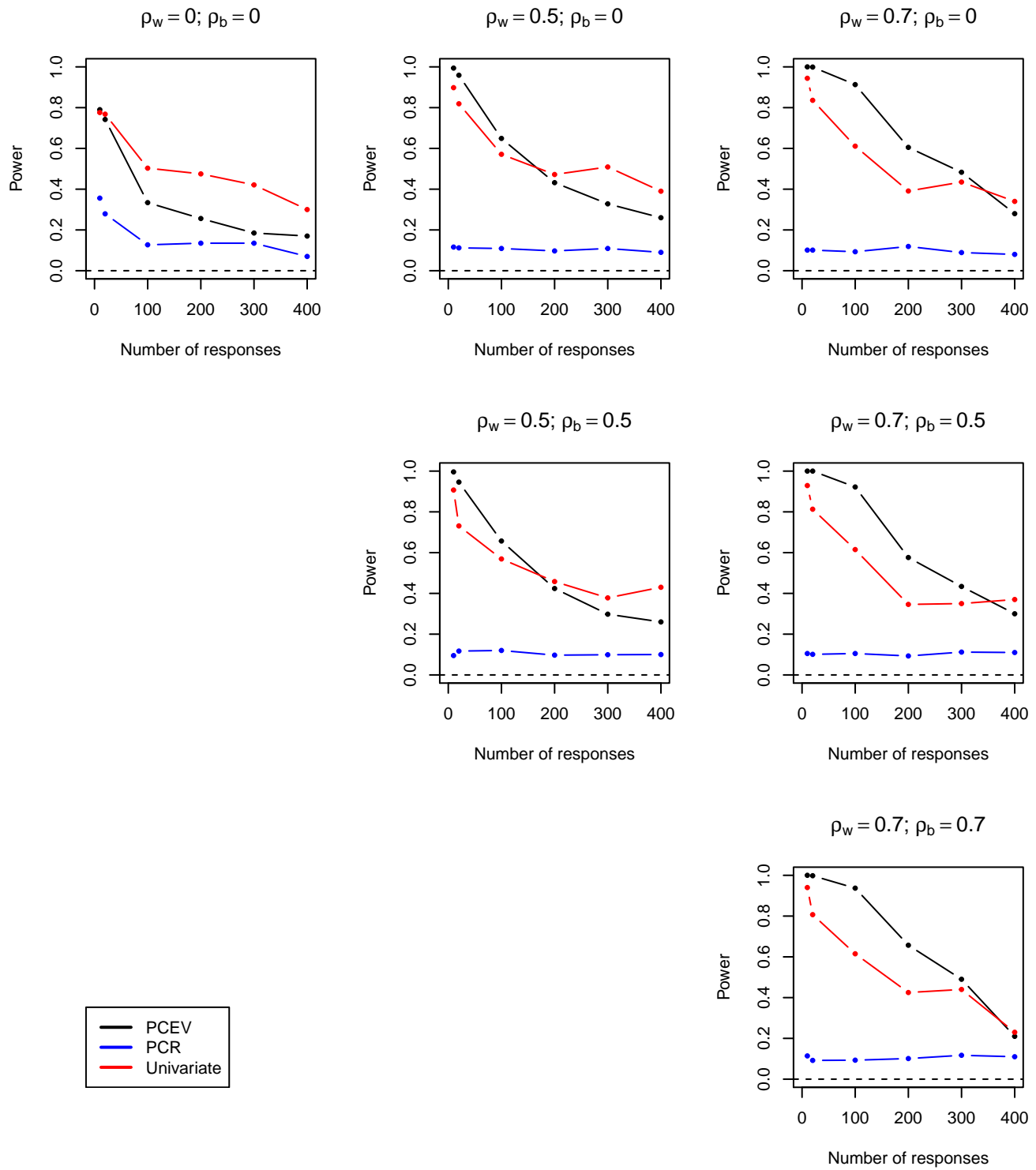
4.32 Significance level: 0.1, Heritability: 1%, Number of blocks: 20



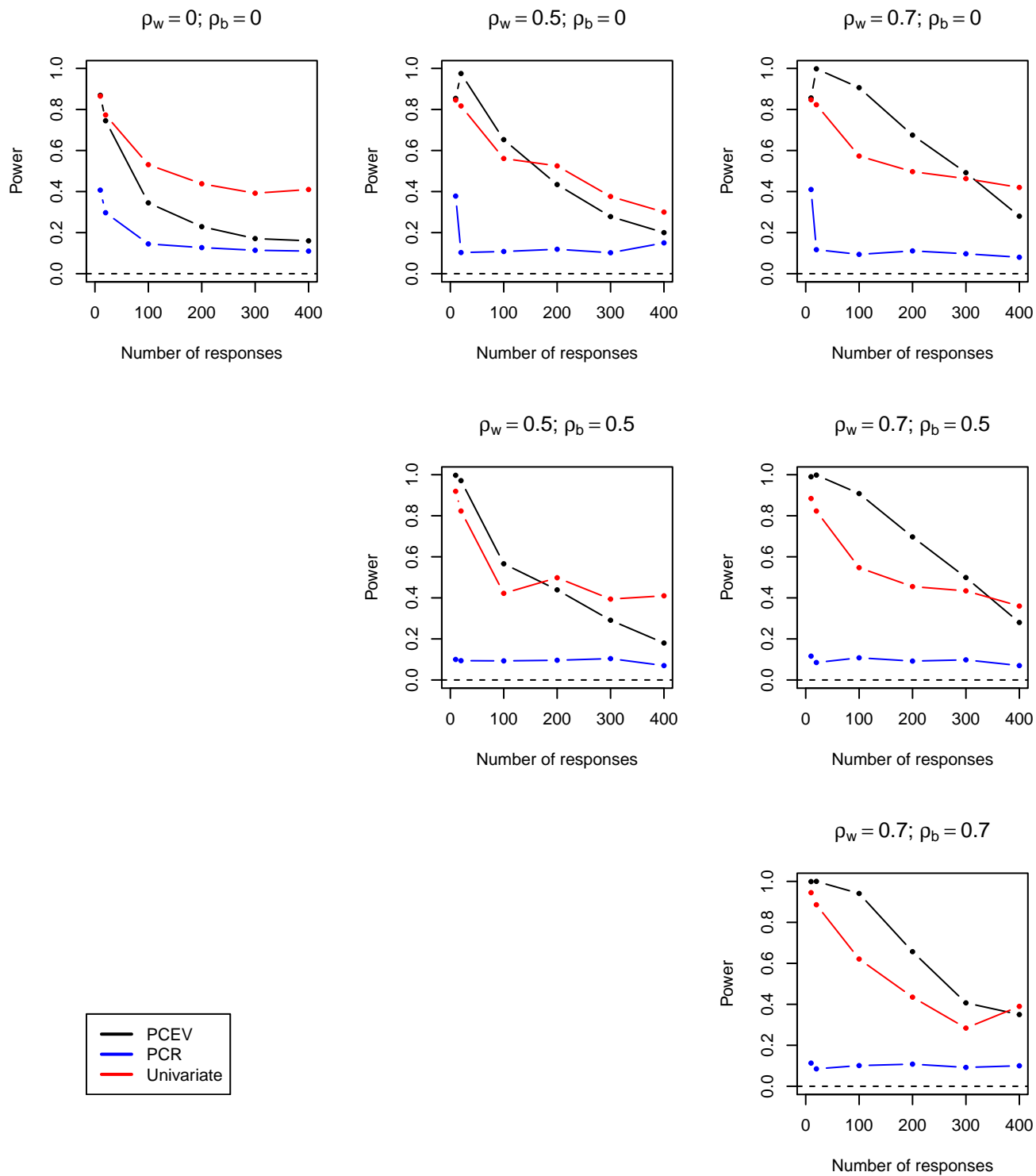
4.33 Significance level: 0.1, Heritability: 1.5%, Number of blocks: 2



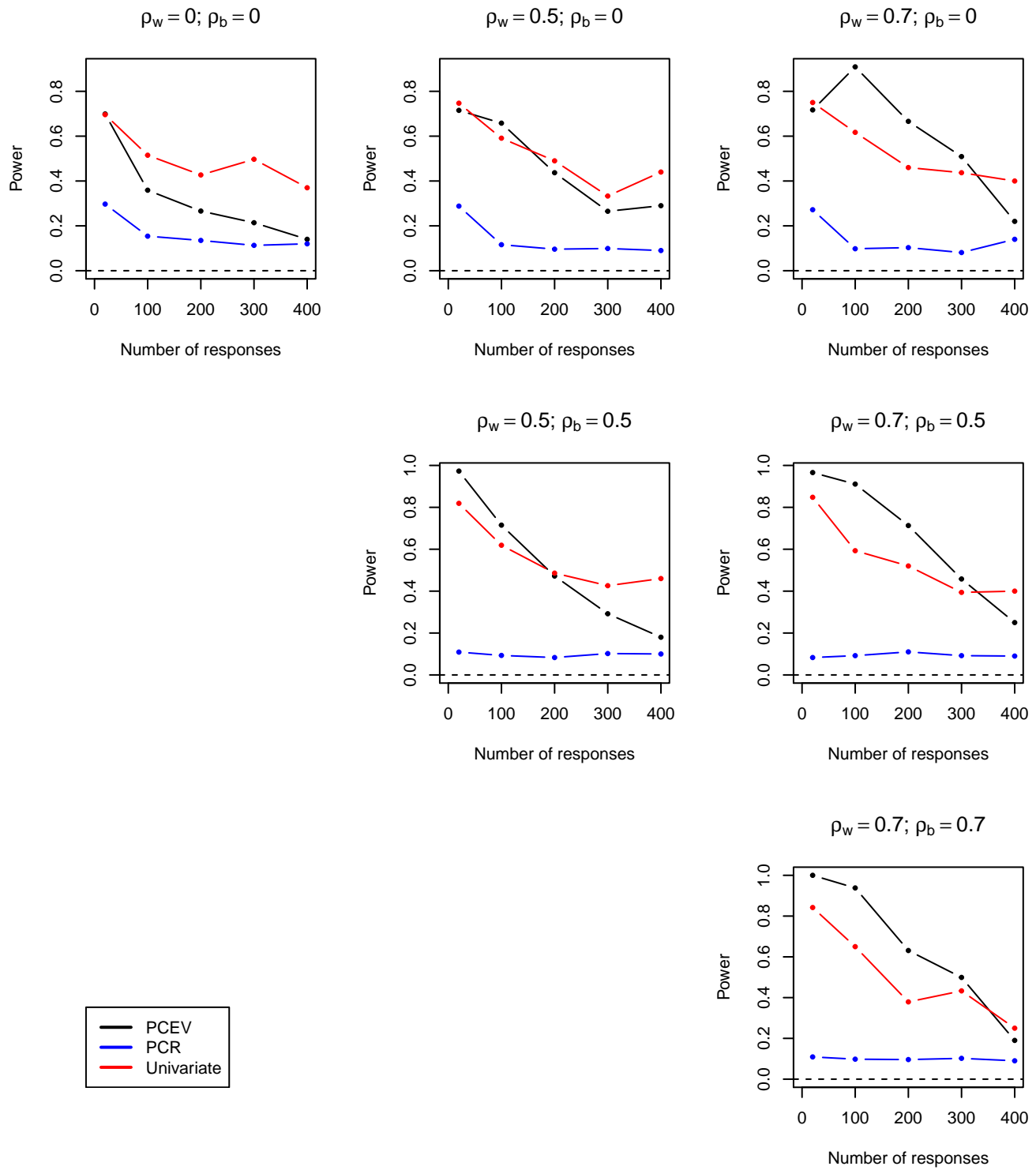
4.34 Significance level: 0.1, Heritability: 1.5%, Number of blocks: 5



4.35 Significance level: 0.1, Heritability: 1.5%, Number of blocks: 10



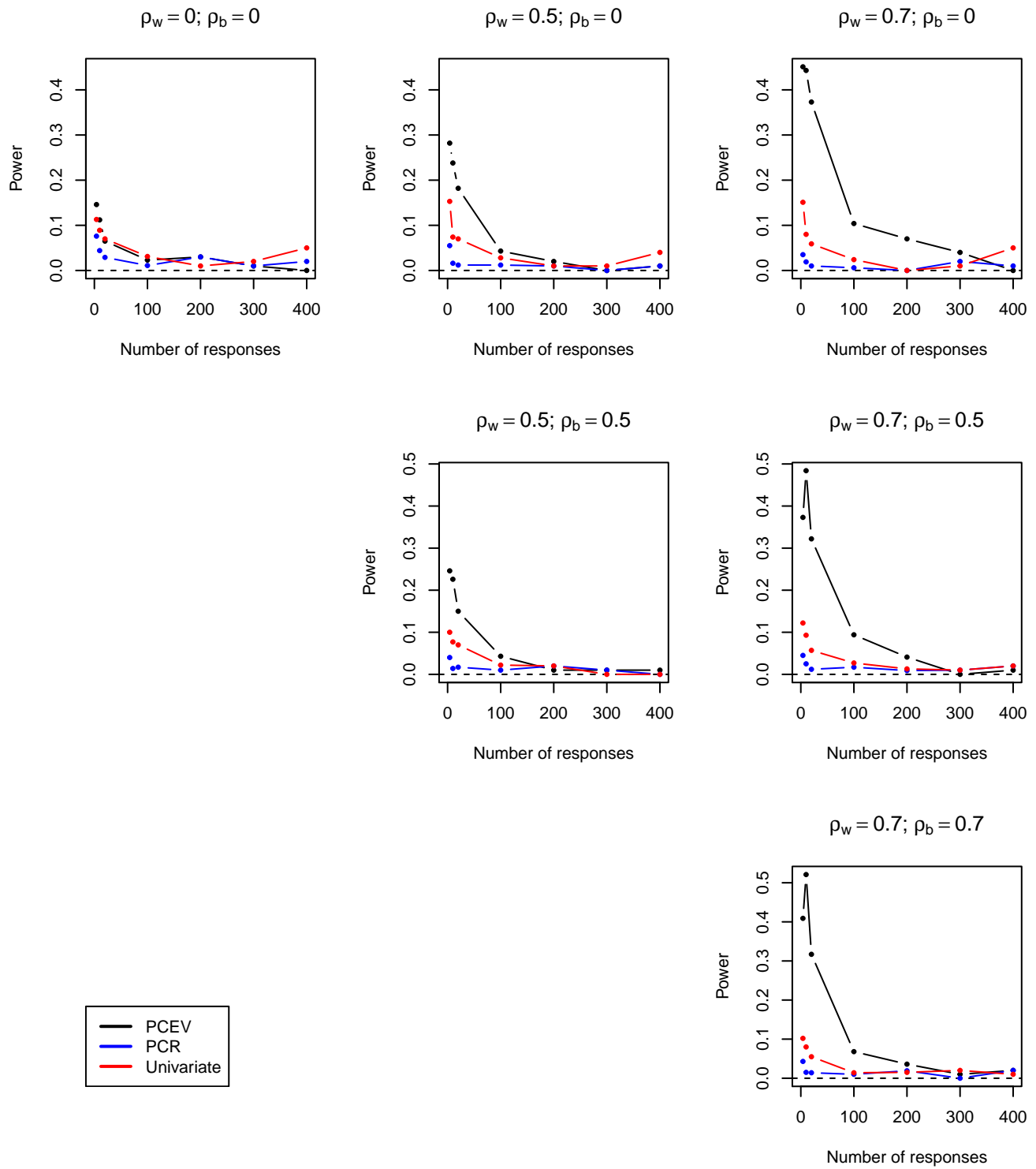
4.36 Significance level: 0.1, Heritability: 1.5%, Number of blocks: 20



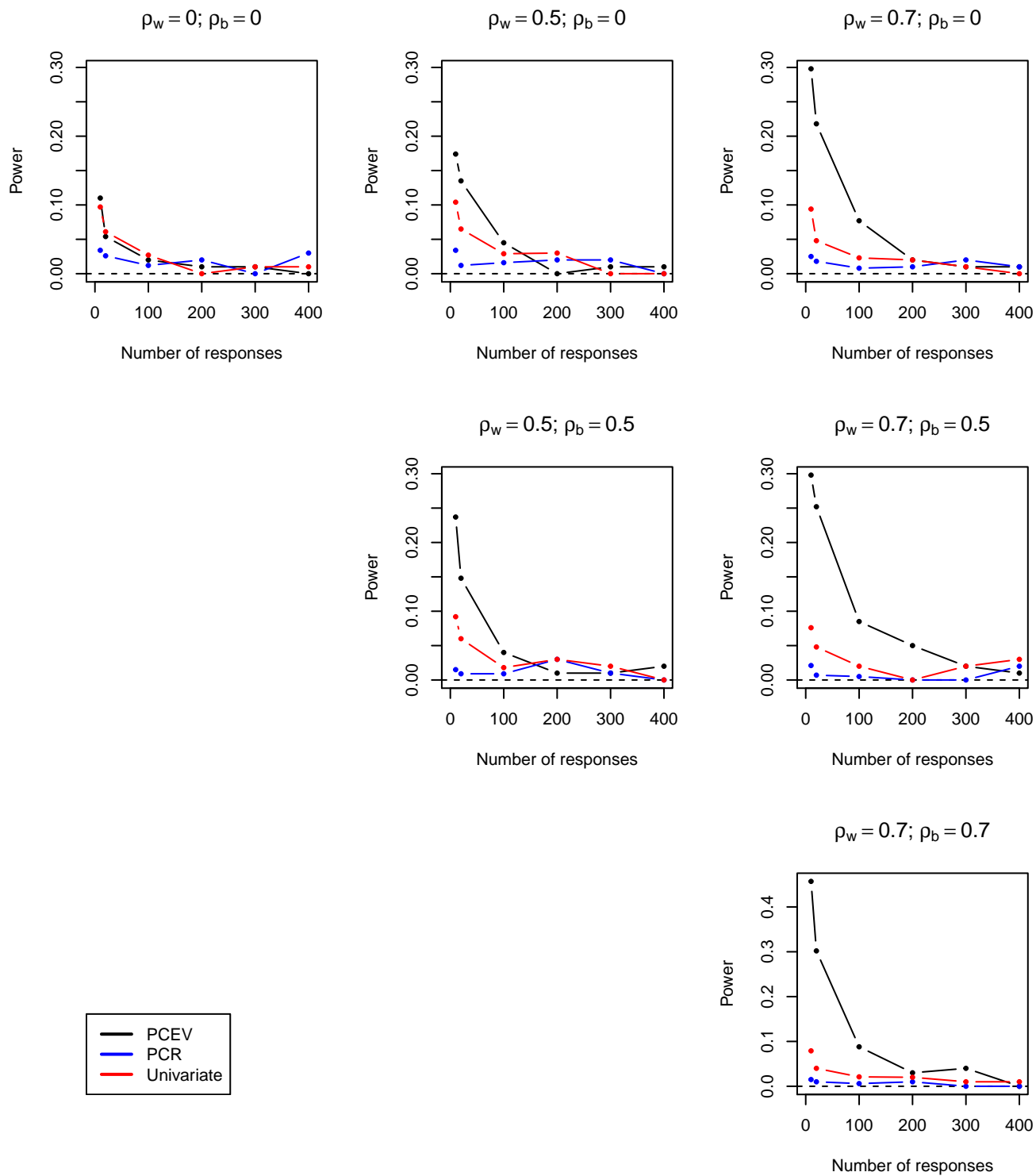
5 Simulation scenario 5

We simulated an association between the continuous covariate x and two components of the multivariate phenotype \mathbf{Y} : the associations are of the same size, in the same direction, and the two components lie in different blocks.

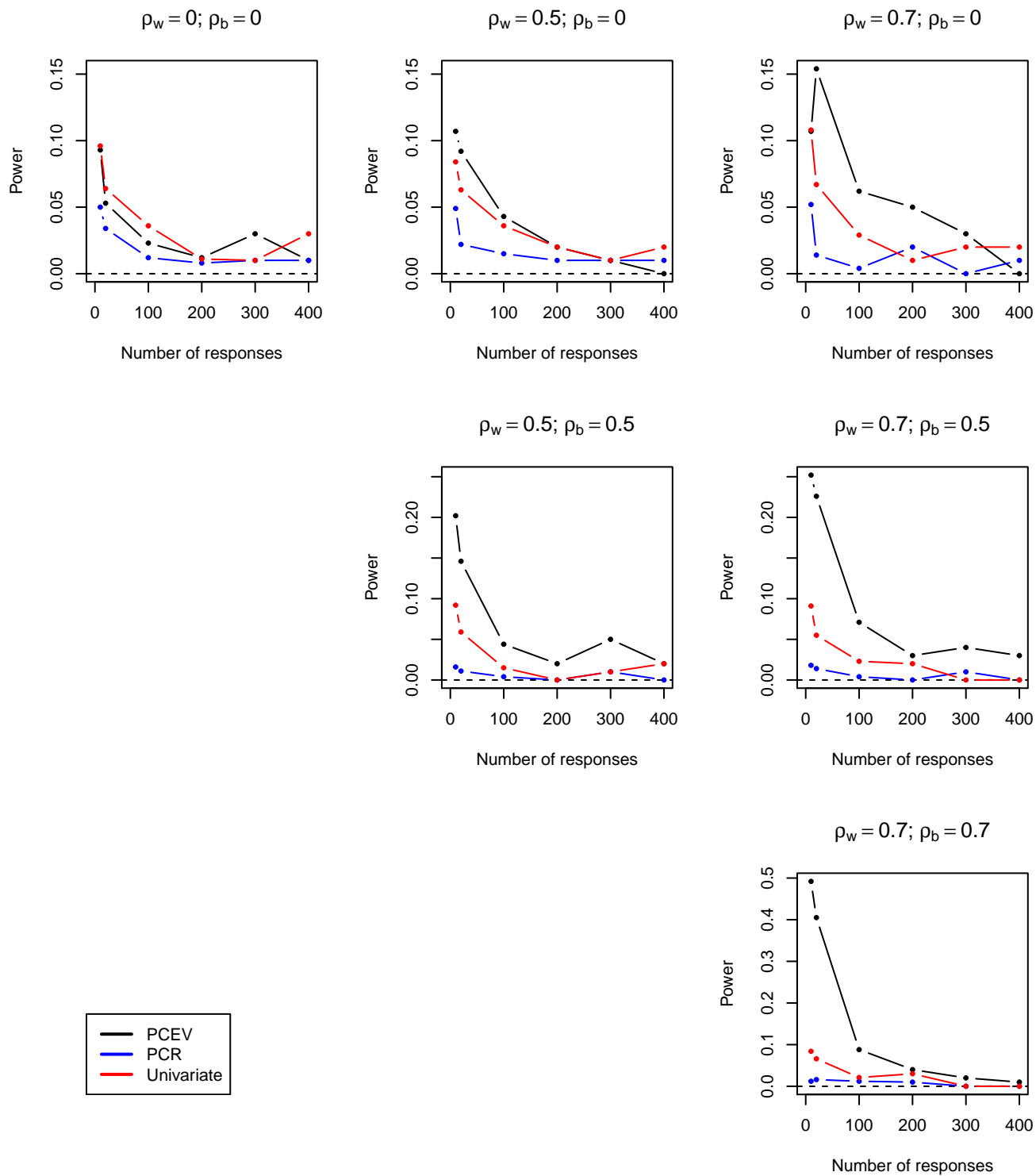
5.1 Significance level: 0.01, Heritability: 0.5%, Number of blocks: 2



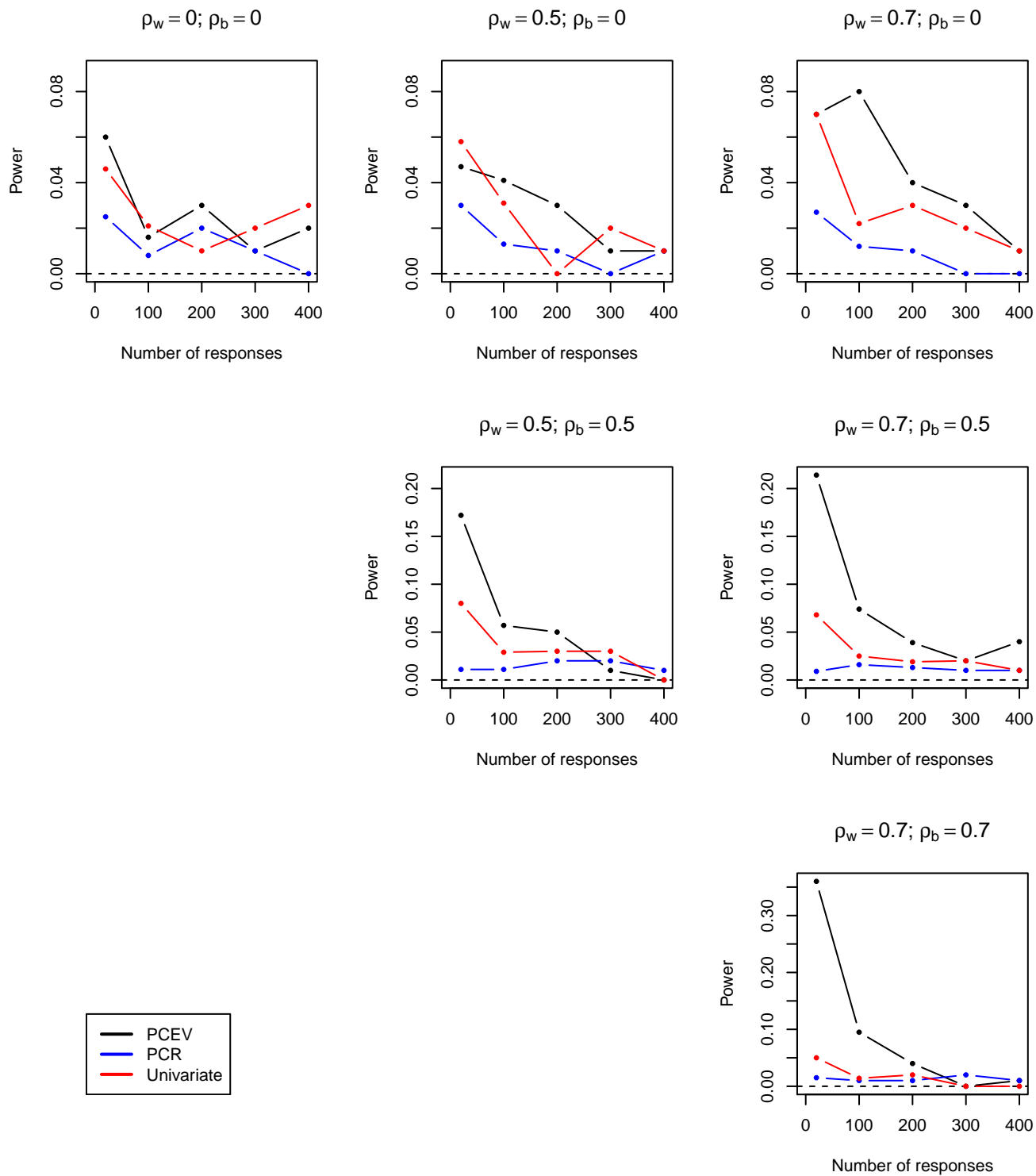
5.2 Significance level: 0.01, Heritability: 0.5%, Number of blocks: 5



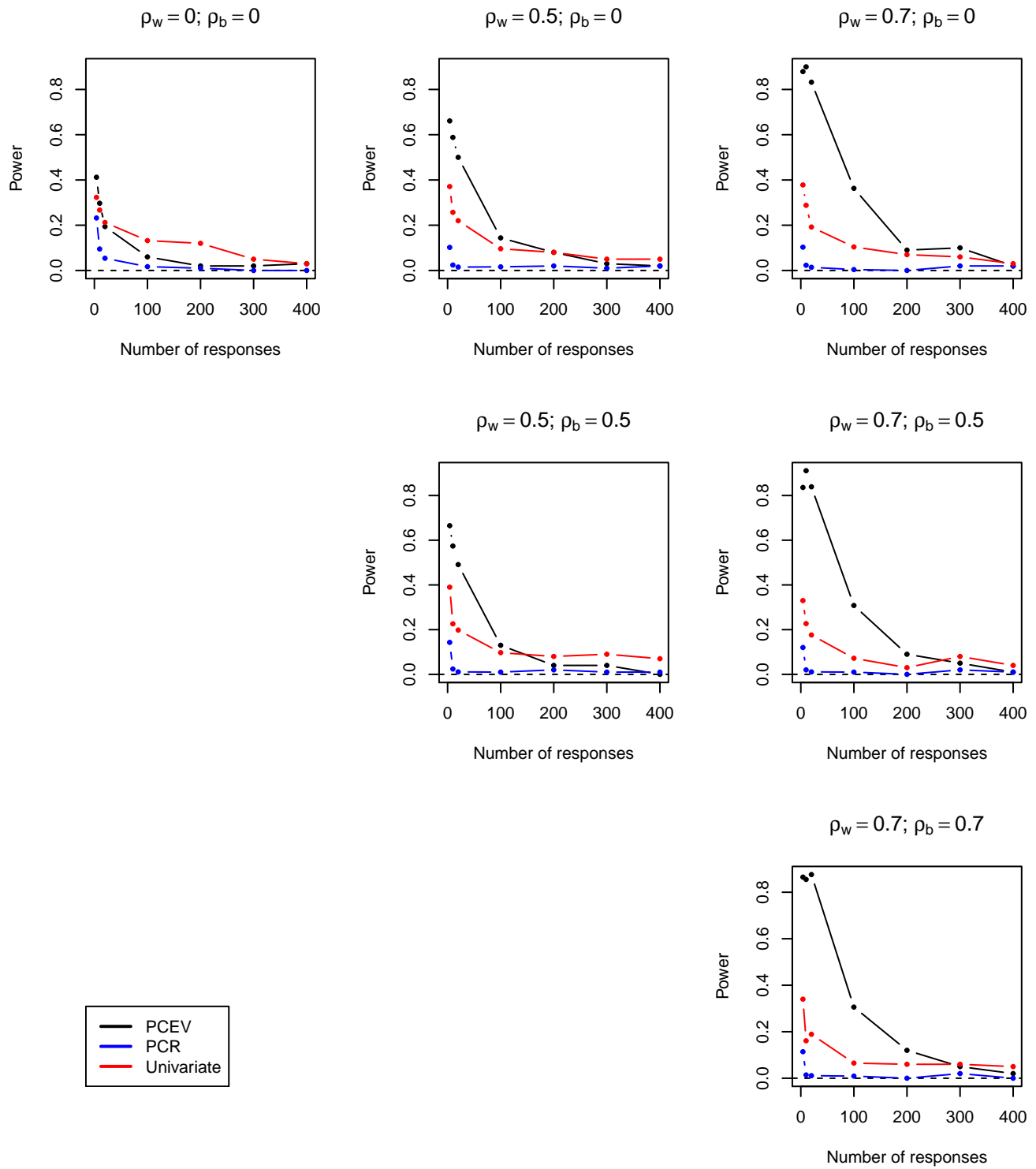
5.3 Significance level: 0.01, Heritability: 0.5%, Number of blocks: 10



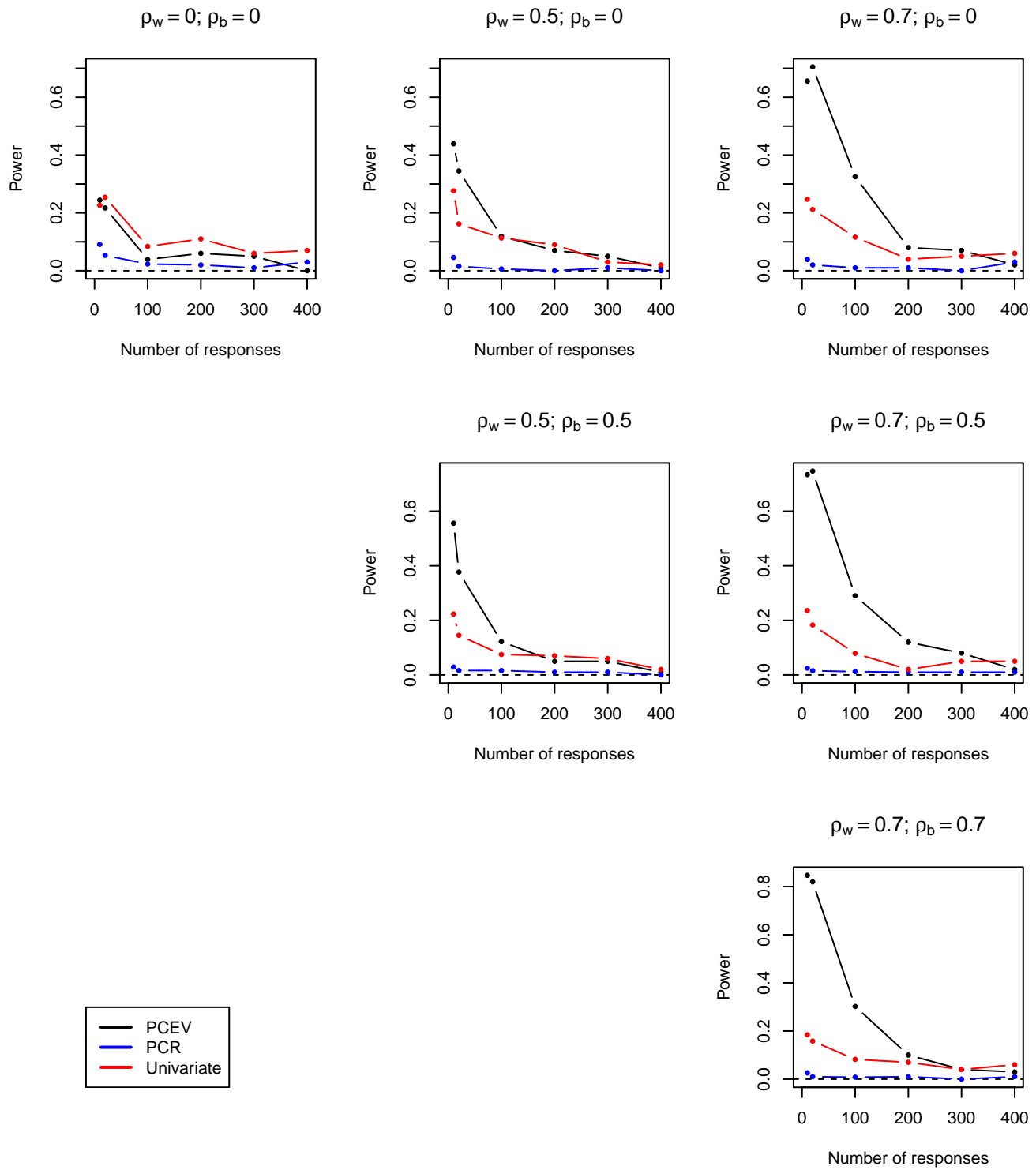
5.4 Significance level: 0.01, Heritability: 0.5%, Number of blocks: 20



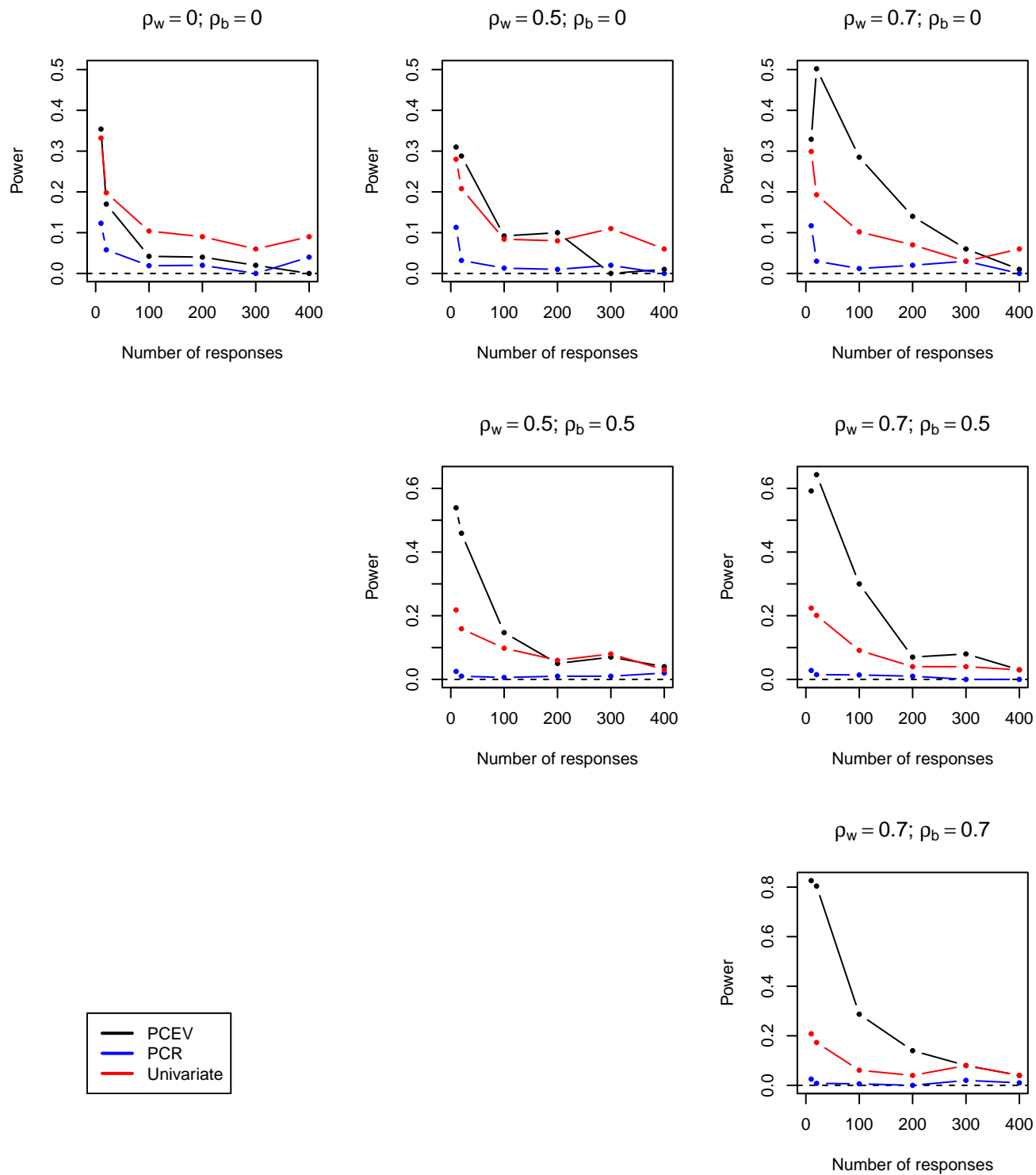
5.5 Significance level: 0.01, Heritability: 1%, Number of blocks: 2



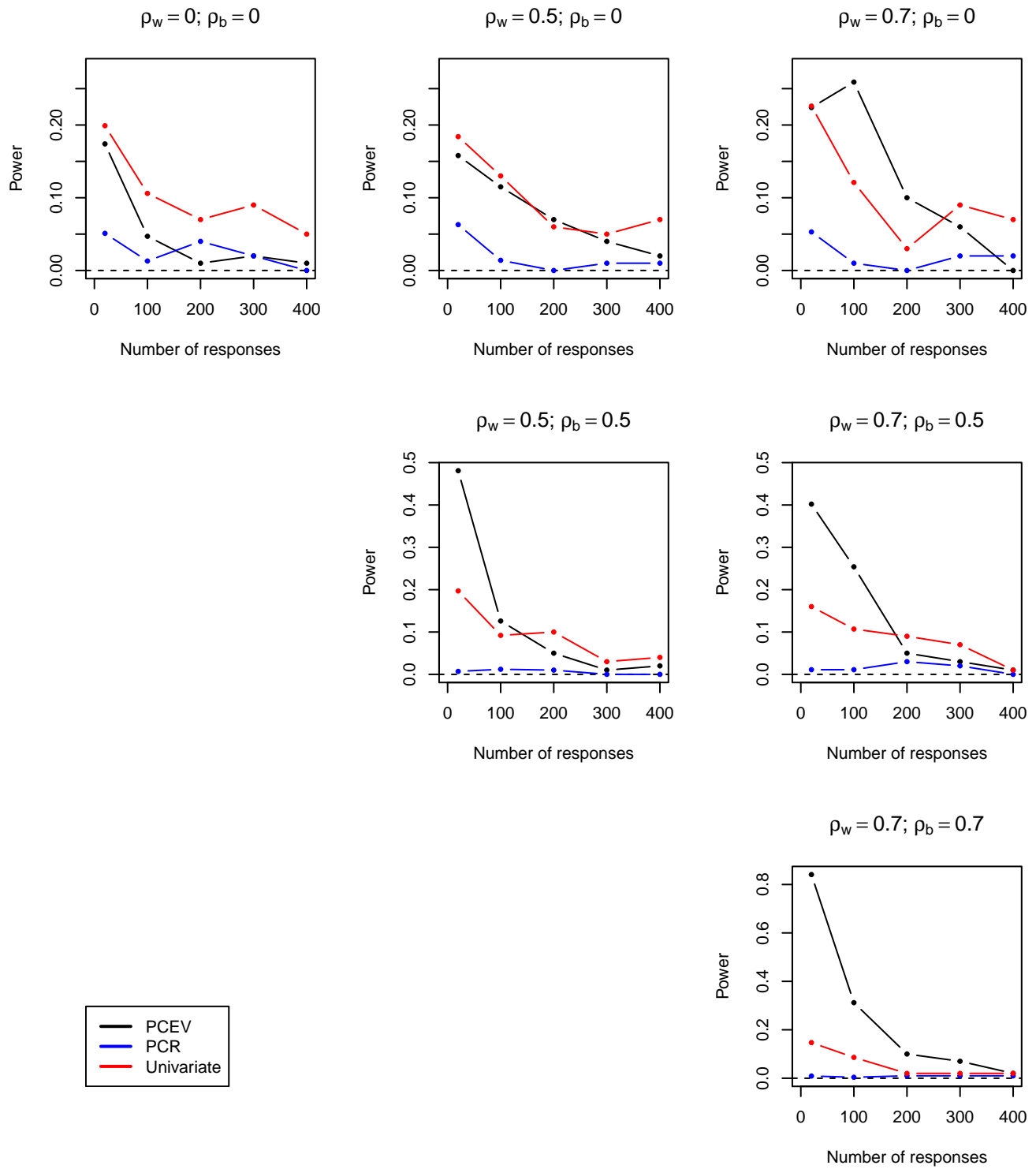
5.6 Significance level: 0.01, Heritability: 1%, Number of blocks: 5



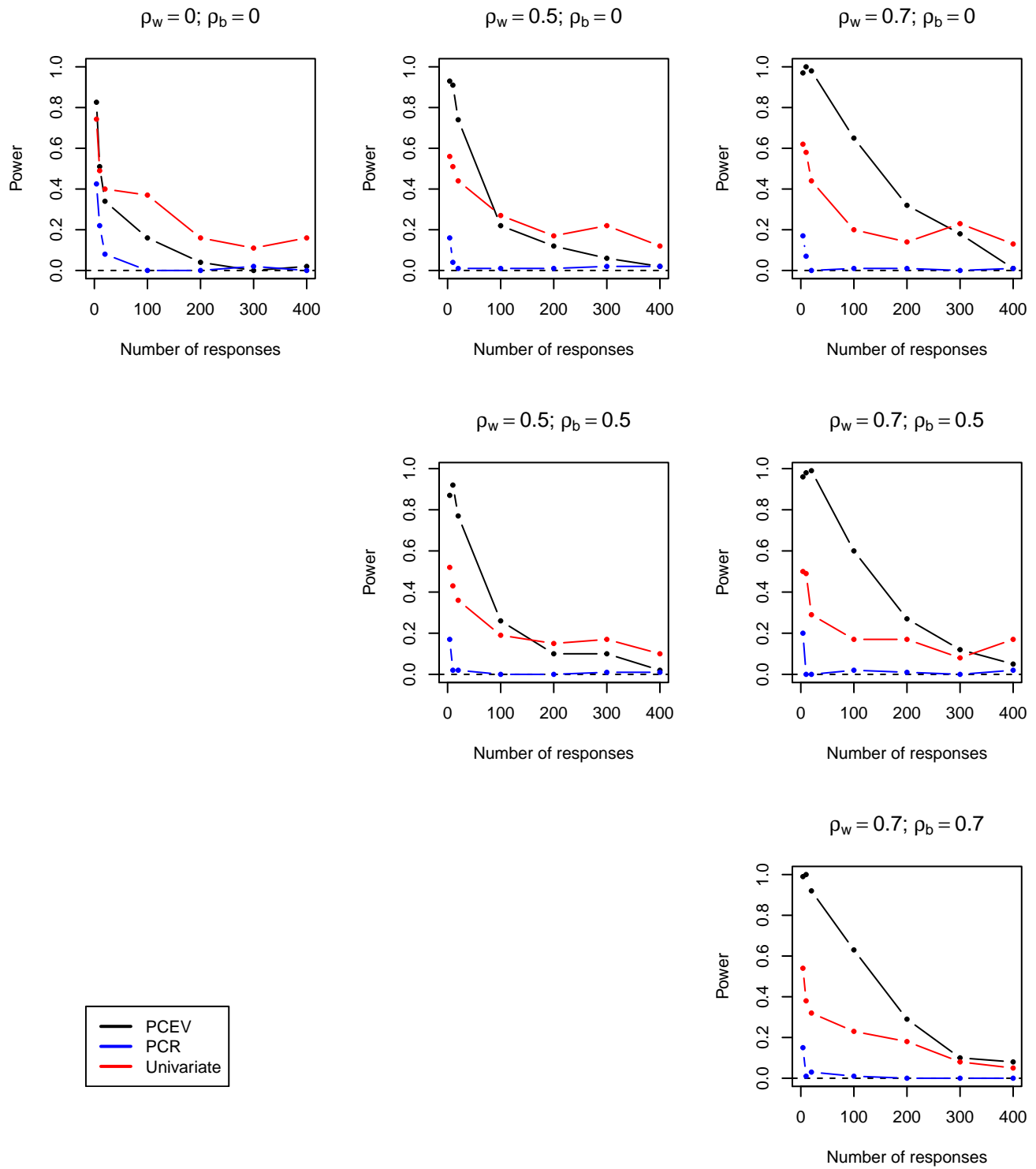
5.7 Significance level: 0.01, Heritability: 1%, Number of blocks: 10



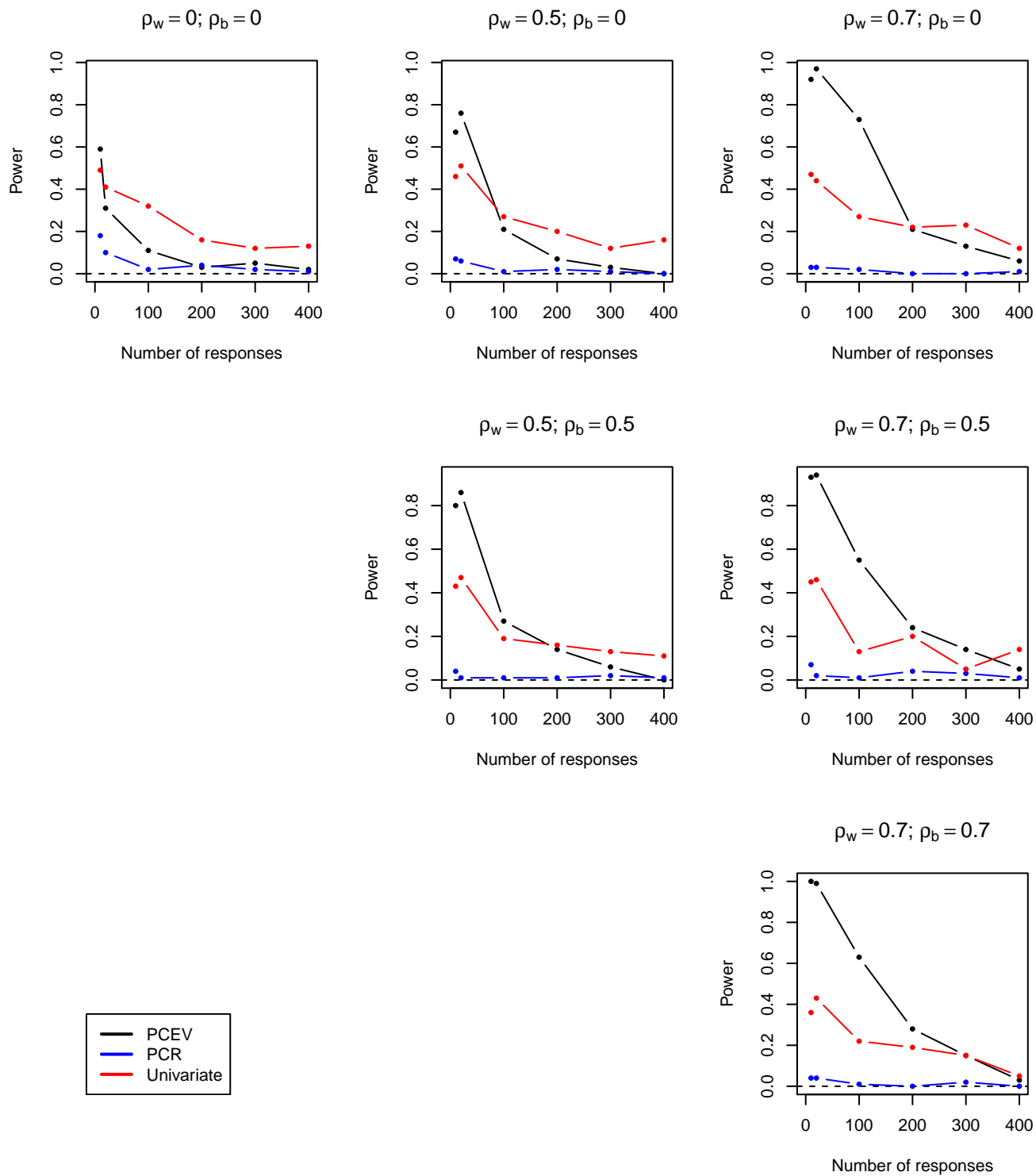
5.8 Significance level: 0.01, Heritability: 1%, Number of blocks: 20



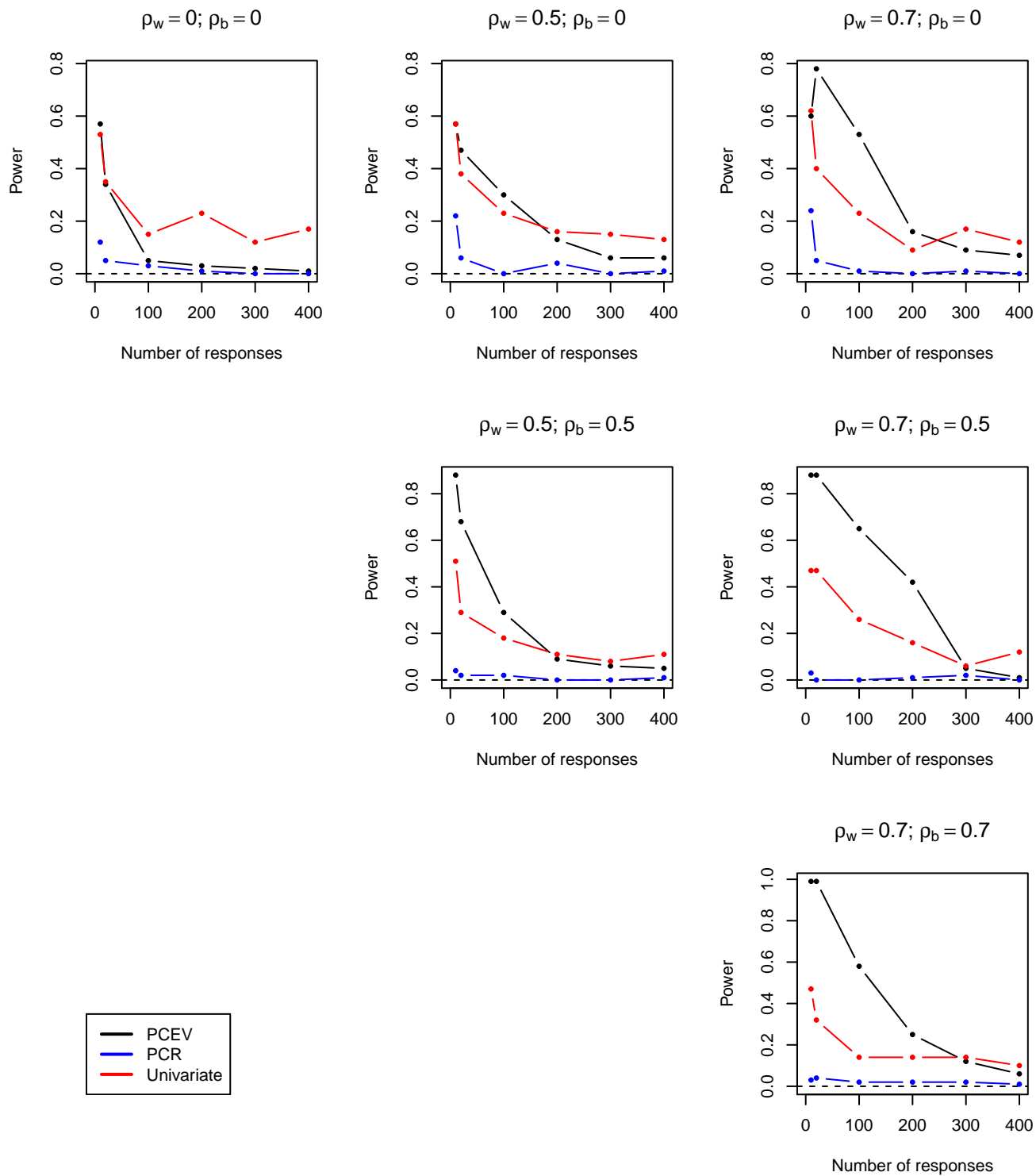
5.9 Significance level: 0.01, Heritability: 1.5%, Number of blocks: 2



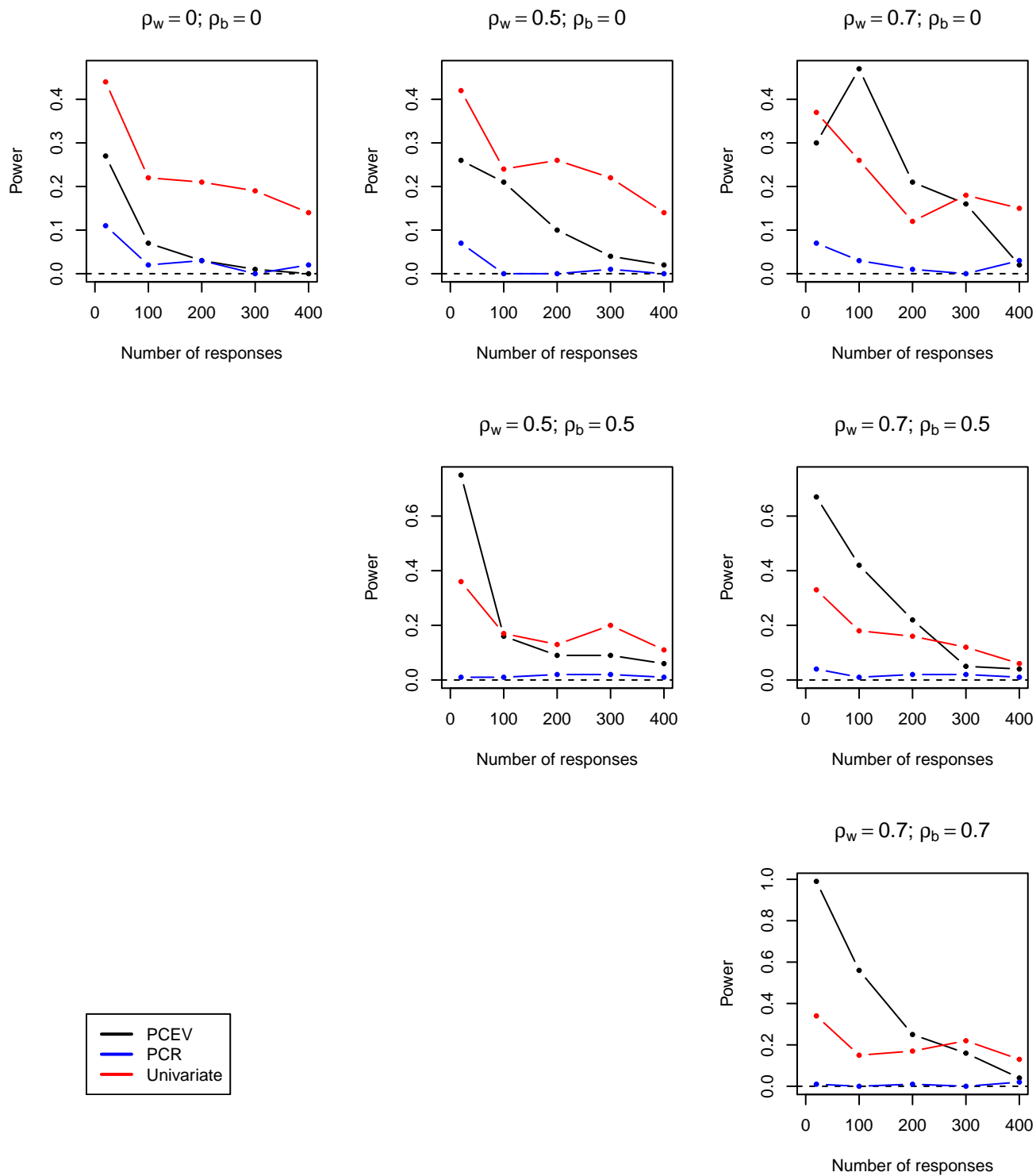
5.10 Significance level: 0.01, Heritability: 1.5%, Number of blocks: 5



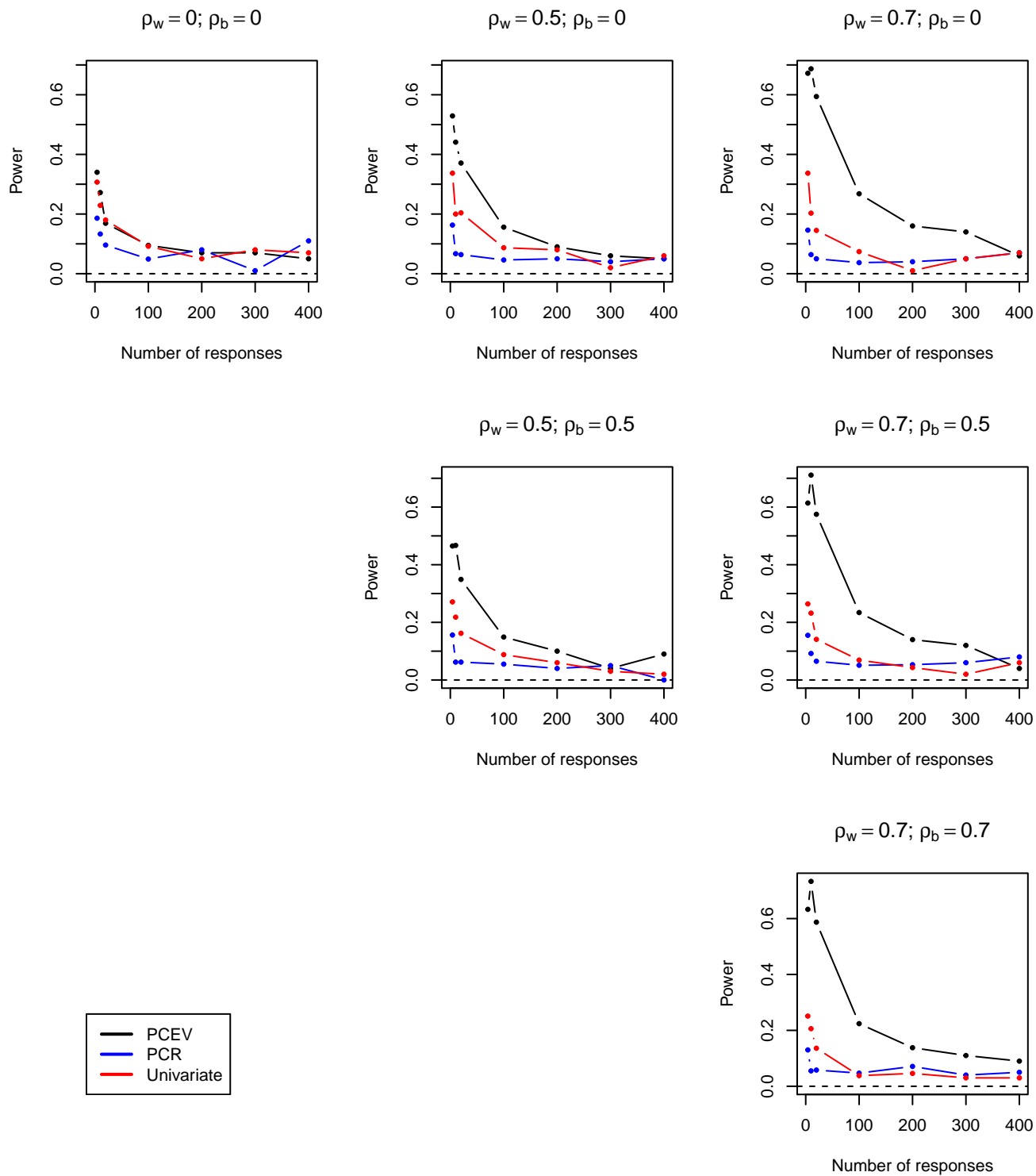
5.11 Significance level: 0.01, Heritability: 1.5%, Number of blocks: 10



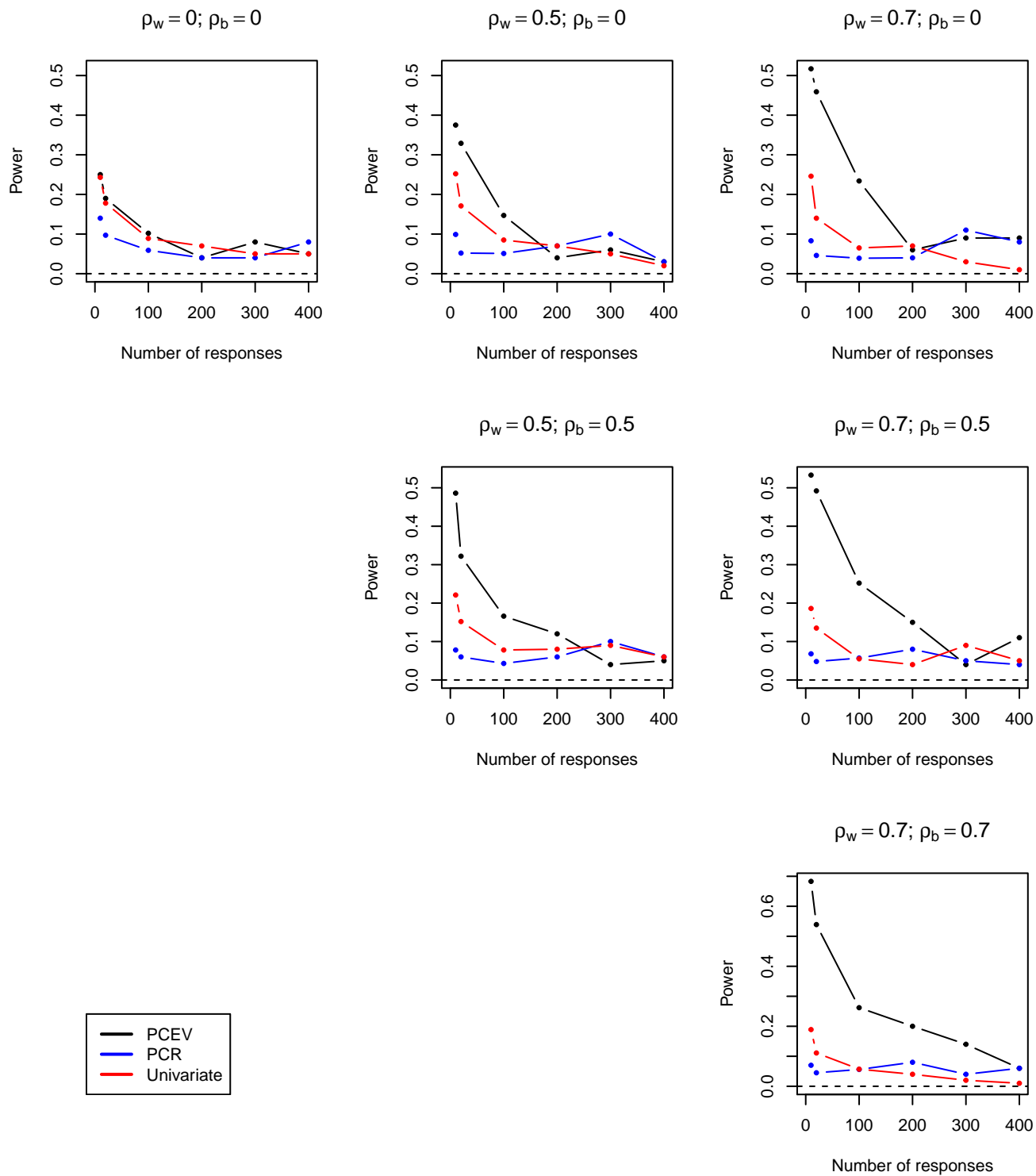
5.12 Significance level: 0.01, Heritability: 1.5%, Number of blocks: 20



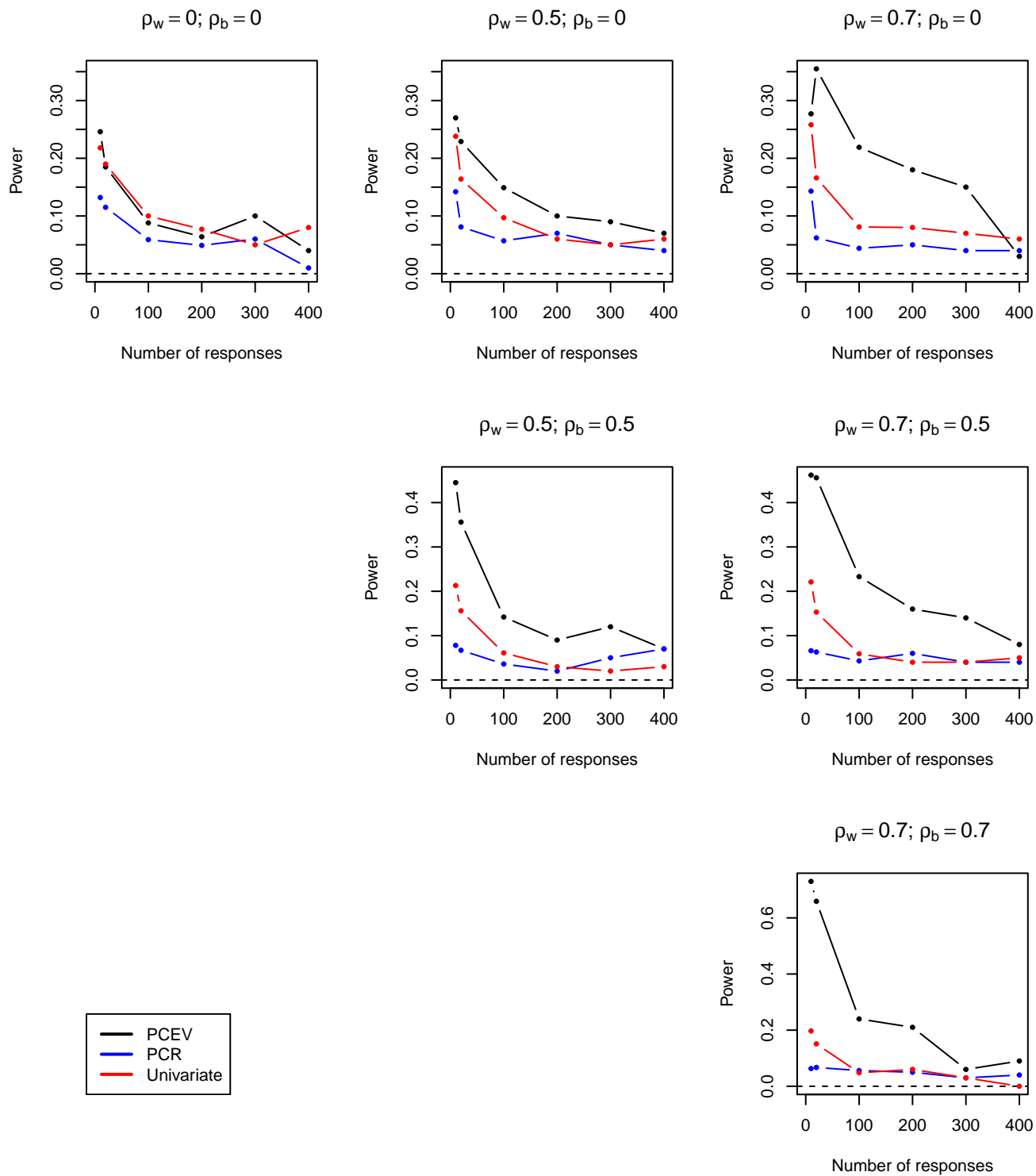
5.13 Significance level: 0.05, Heritability: 0.5%, Number of blocks: 2



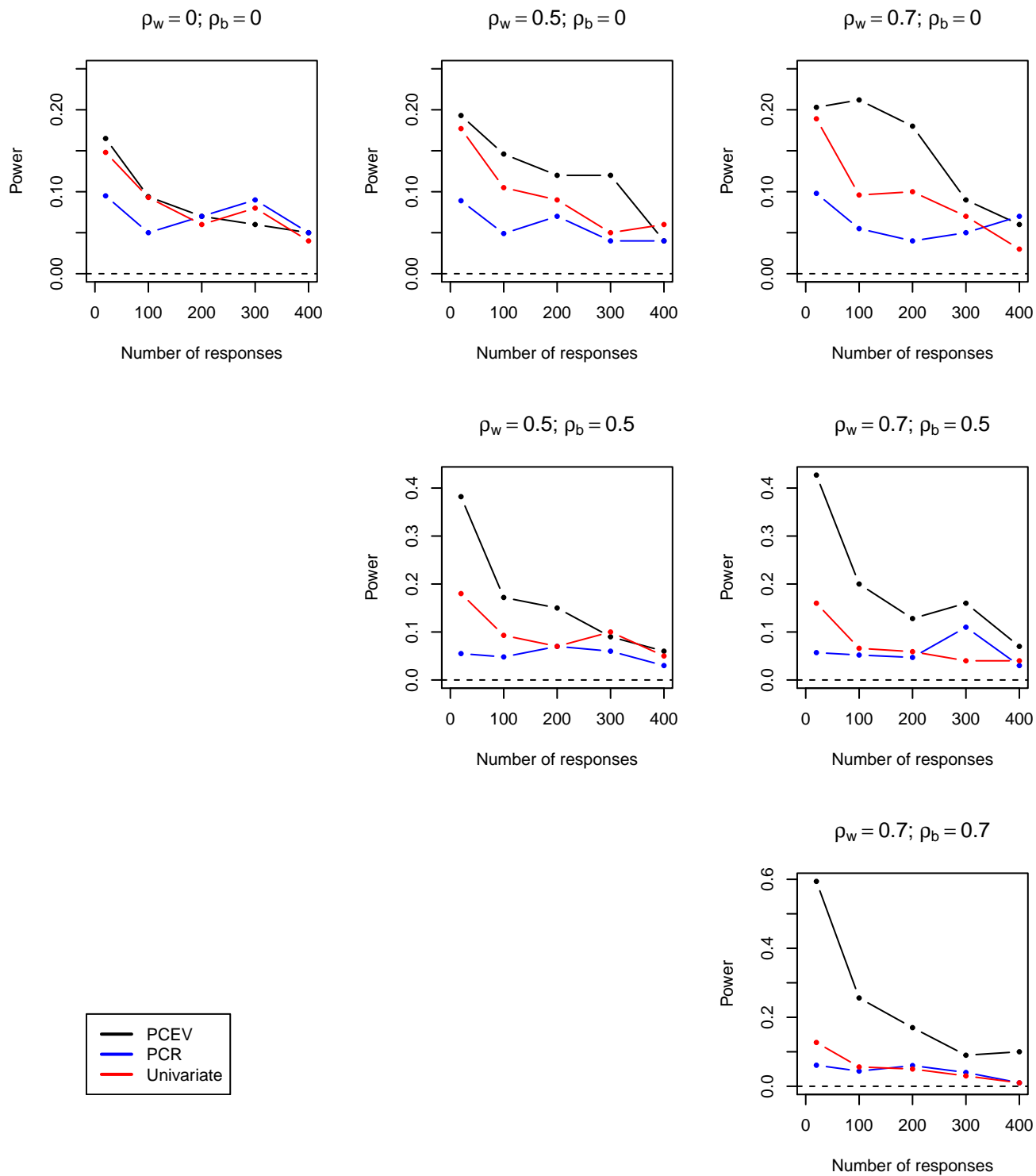
5.14 Significance level: 0.05, Heritability: 0.5%, Number of blocks: 5



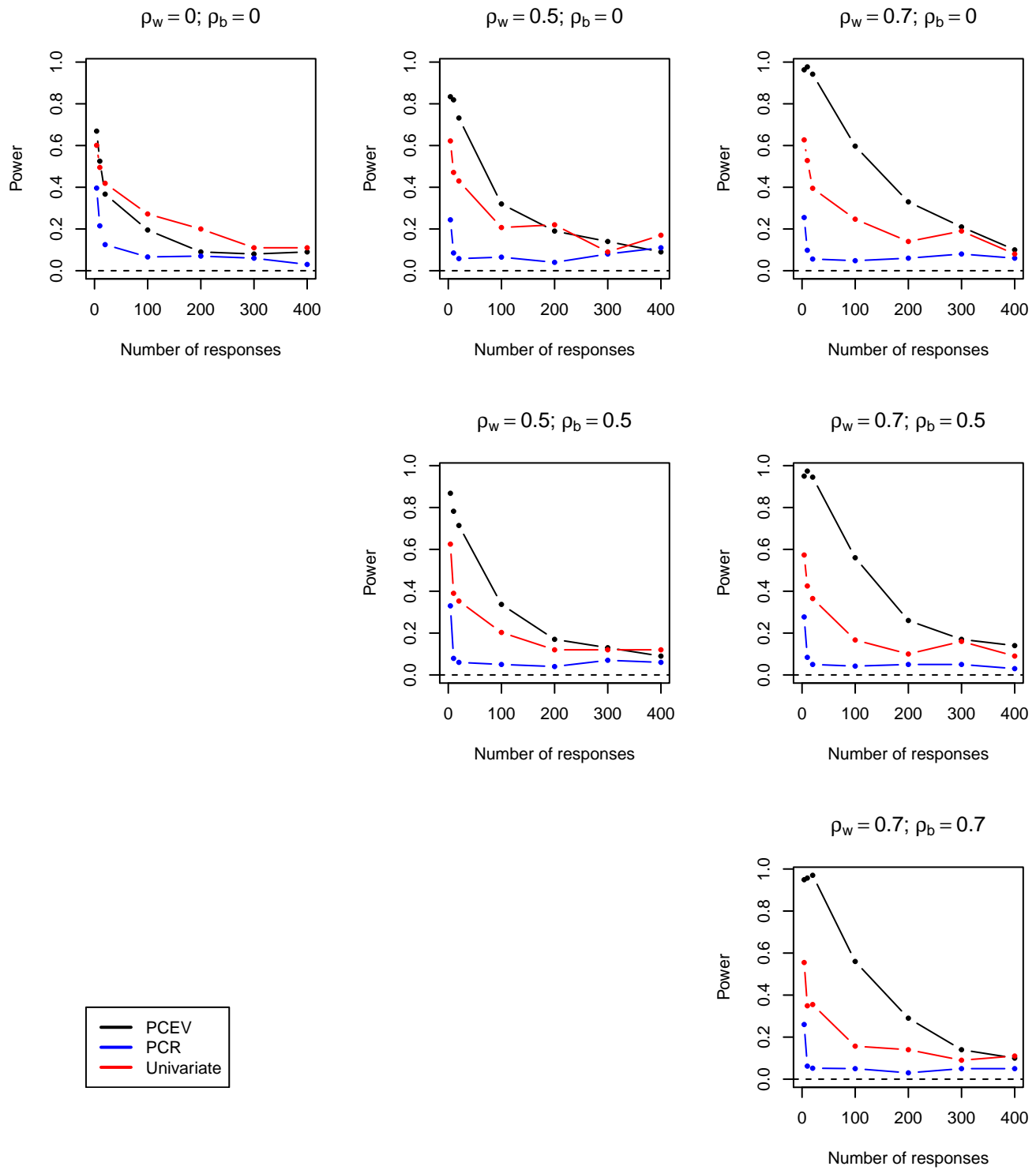
5.15 Significance level: 0.05, Heritability: 0.5%, Number of blocks: 10



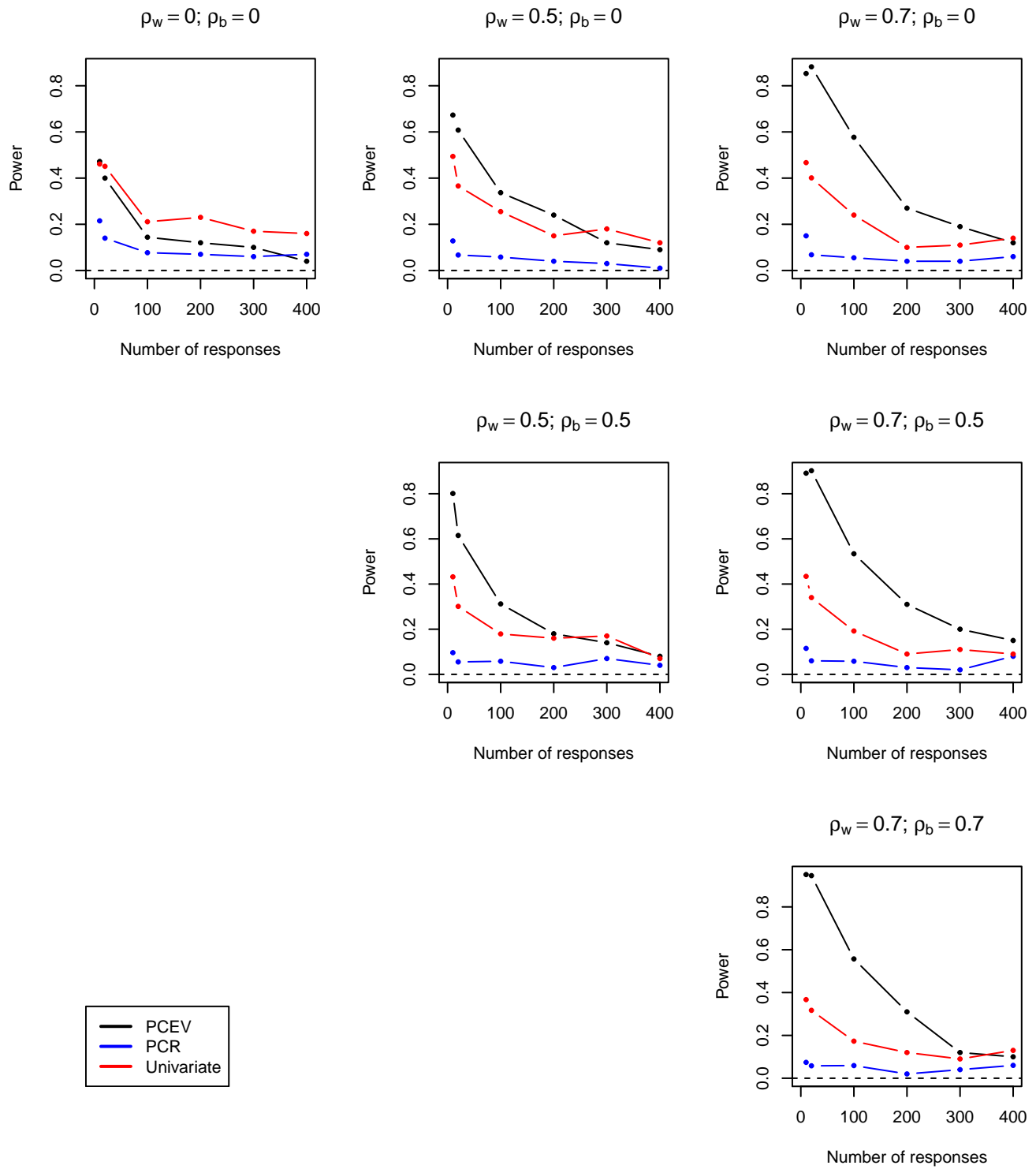
5.16 Significance level: 0.05, Heritability: 0.5%, Number of blocks: 20



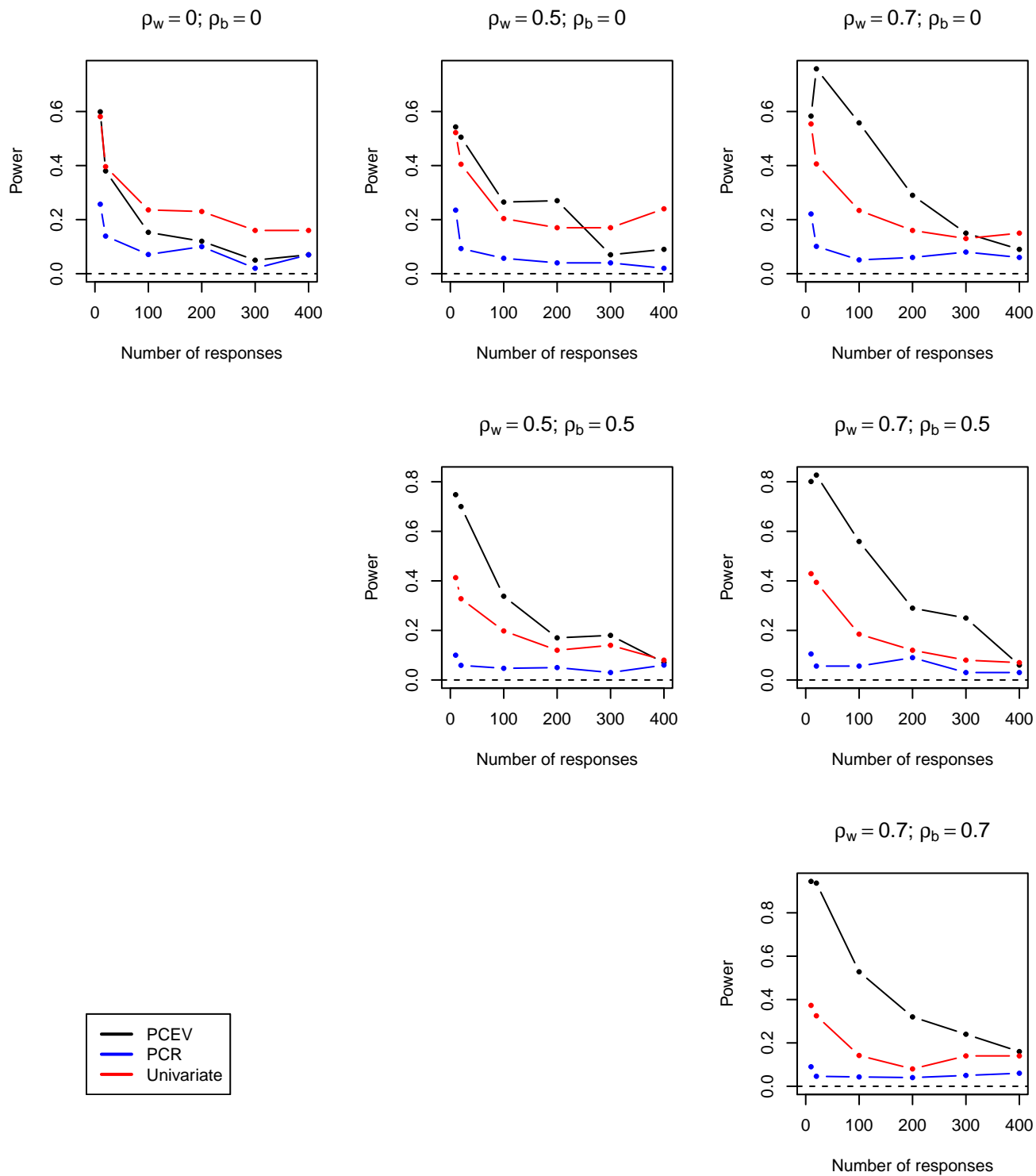
5.17 Significance level: 0.05, Heritability: 1%, Number of blocks: 2



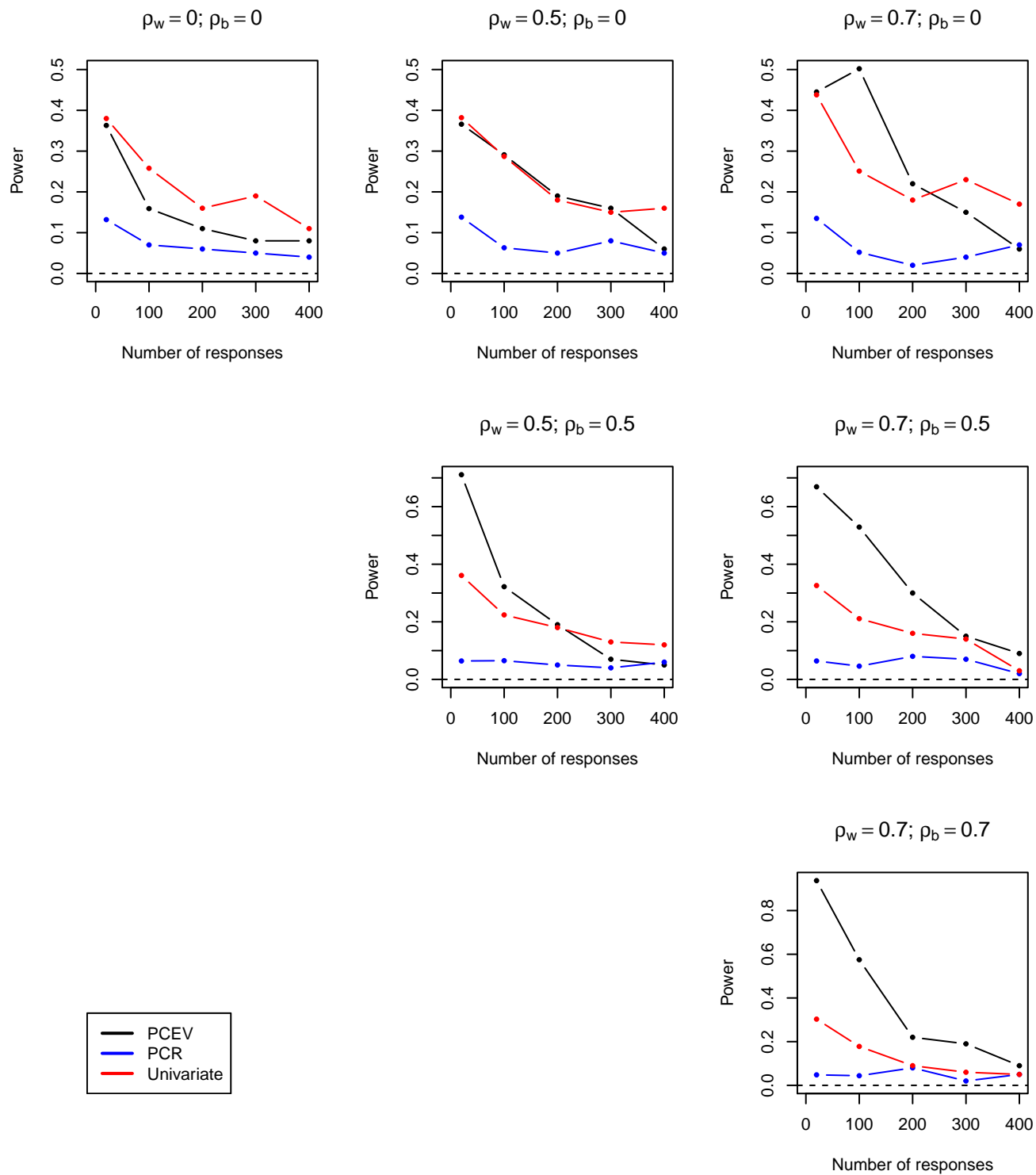
5.18 Significance level: 0.05, Heritability: 1%, Number of blocks: 5



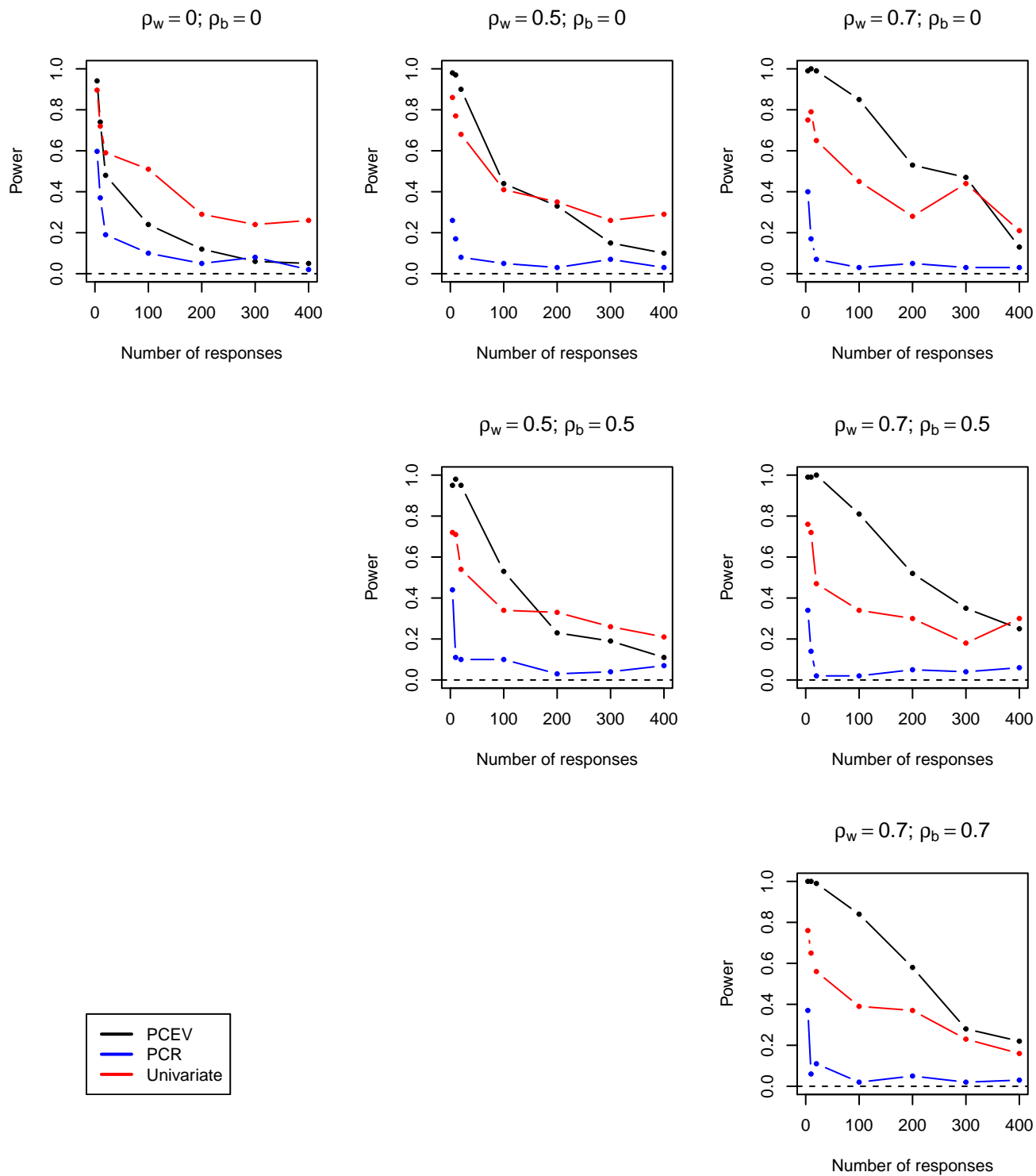
5.19 Significance level: 0.05, Heritability: 1%, Number of blocks: 10



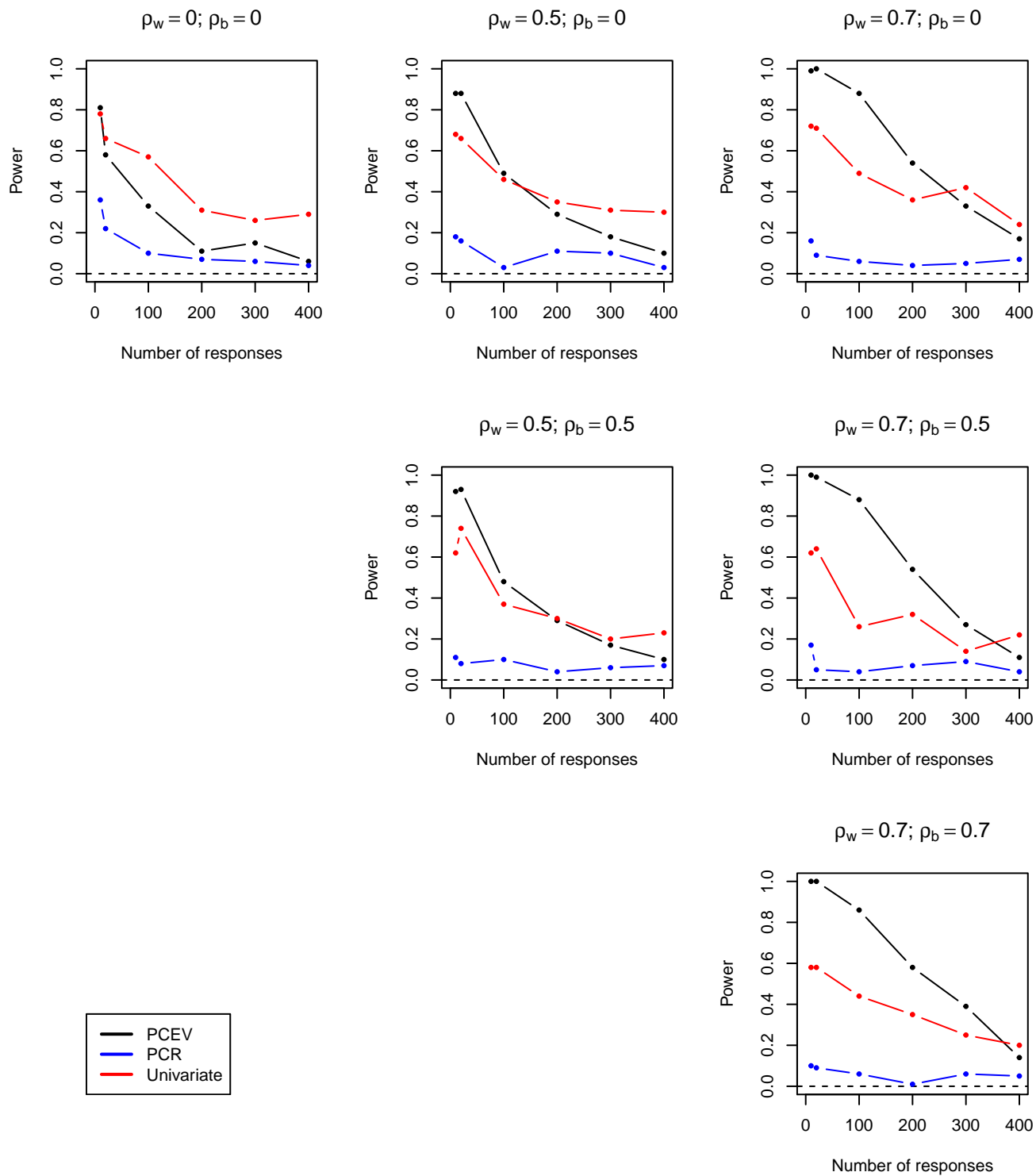
5.20 Significance level: 0.05, Heritability: 1%, Number of blocks: 20



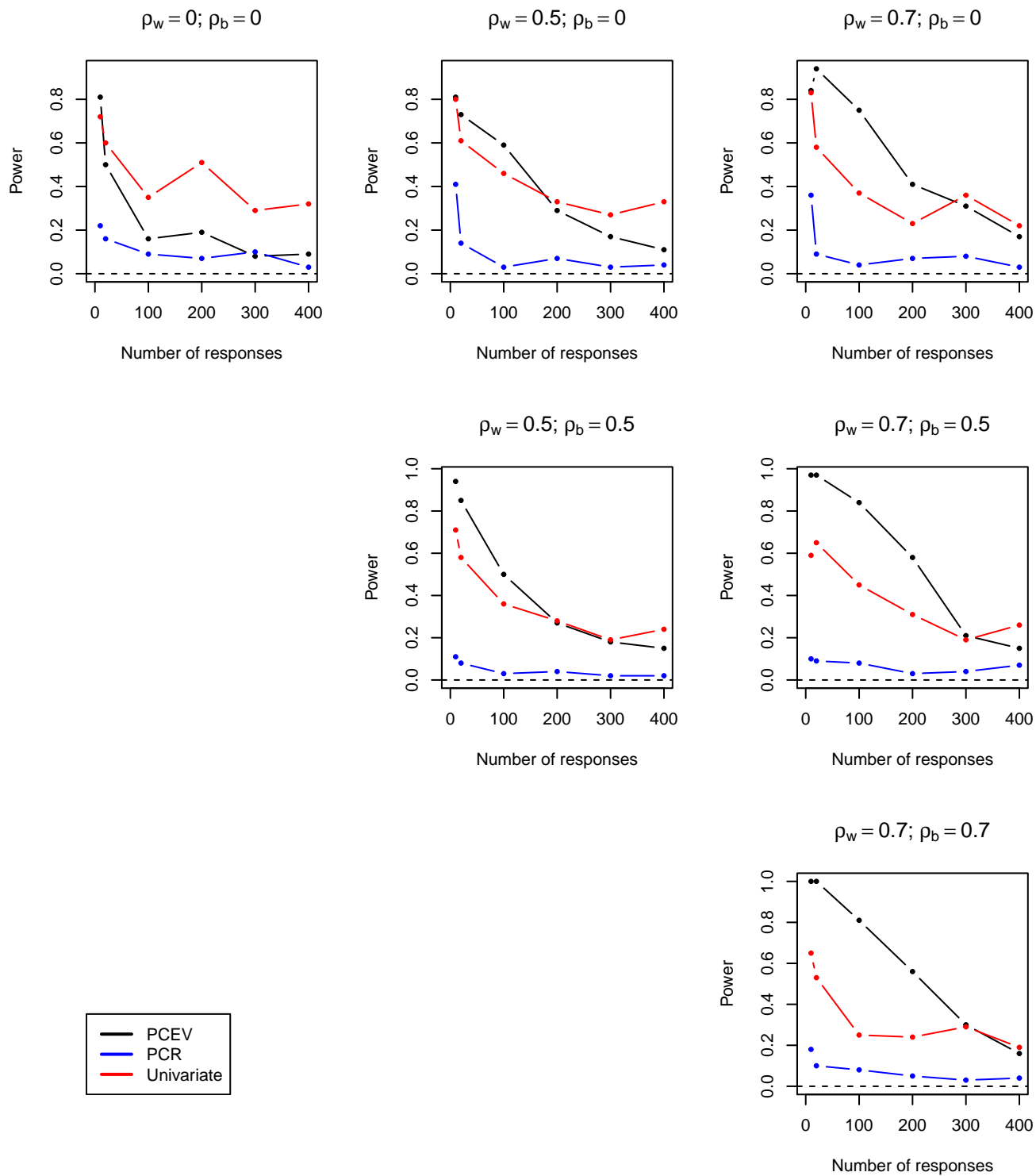
5.21 Significance level: 0.05, Heritability: 1.5%, Number of blocks: 2



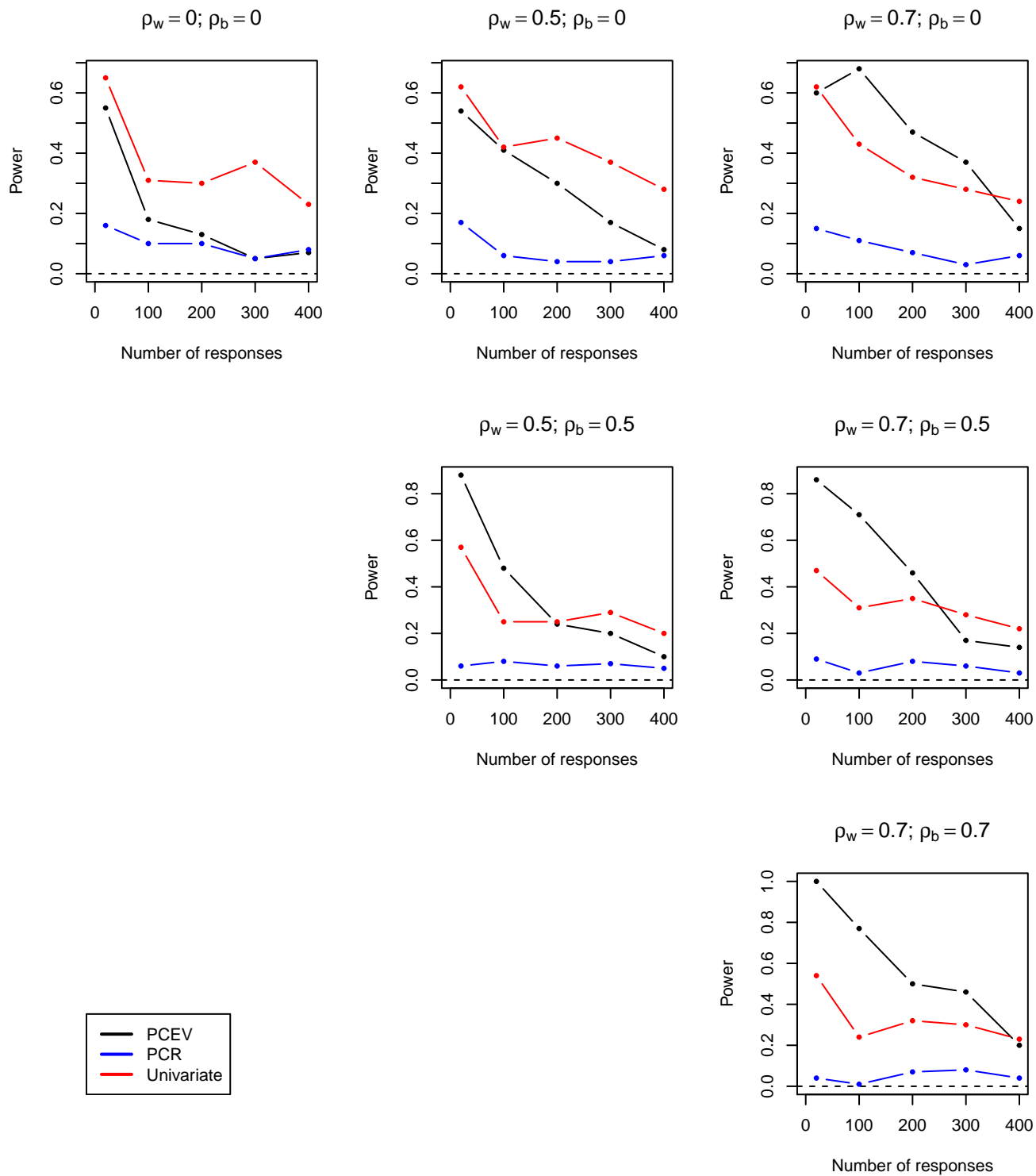
5.22 Significance level: 0.05, Heritability: 1.5%, Number of blocks: 5



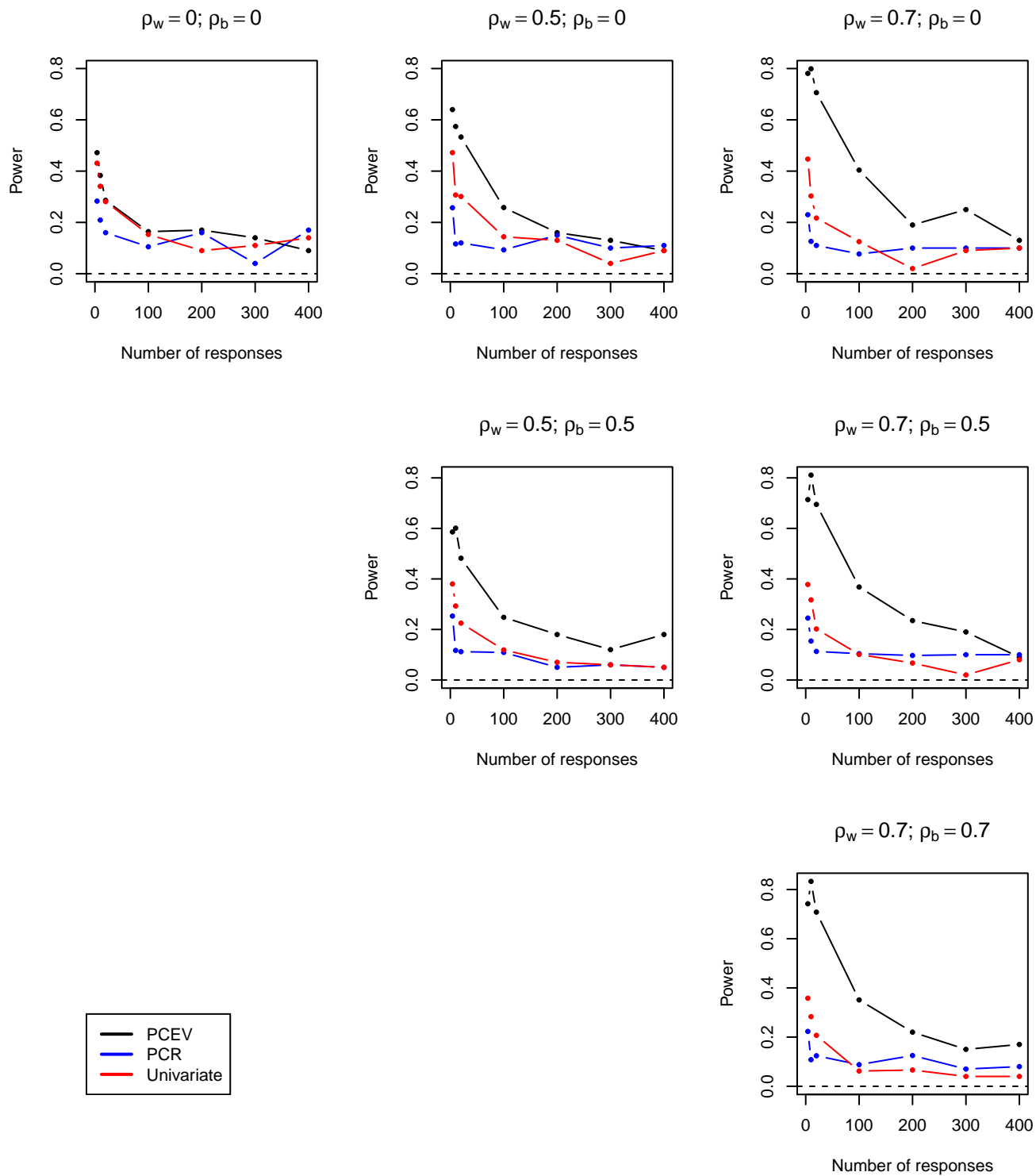
5.23 Significance level: 0.05, Heritability: 1.5%, Number of blocks: 10



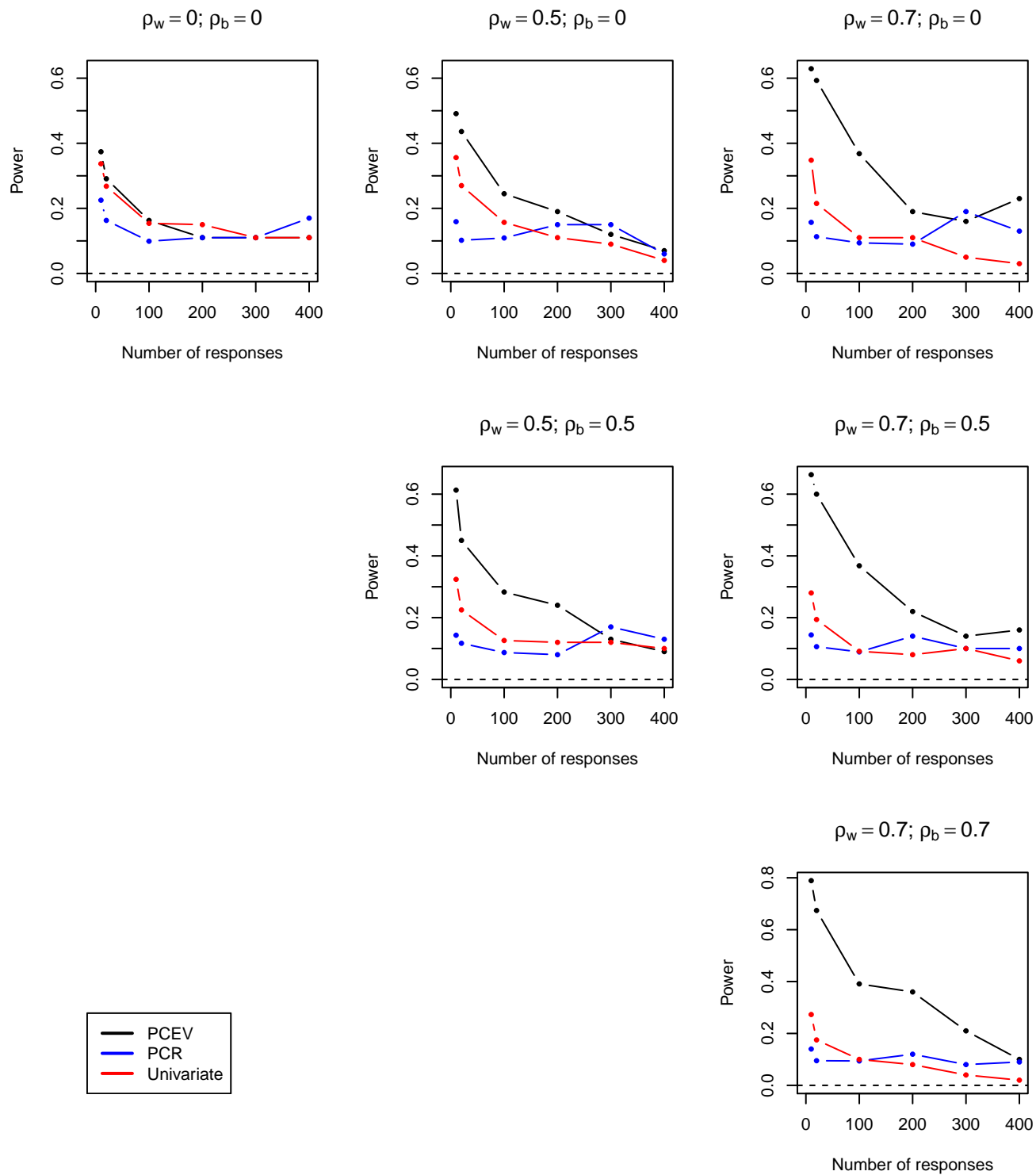
5.24 Significance level: 0.05, Heritability: 1.5%, Number of blocks: 20



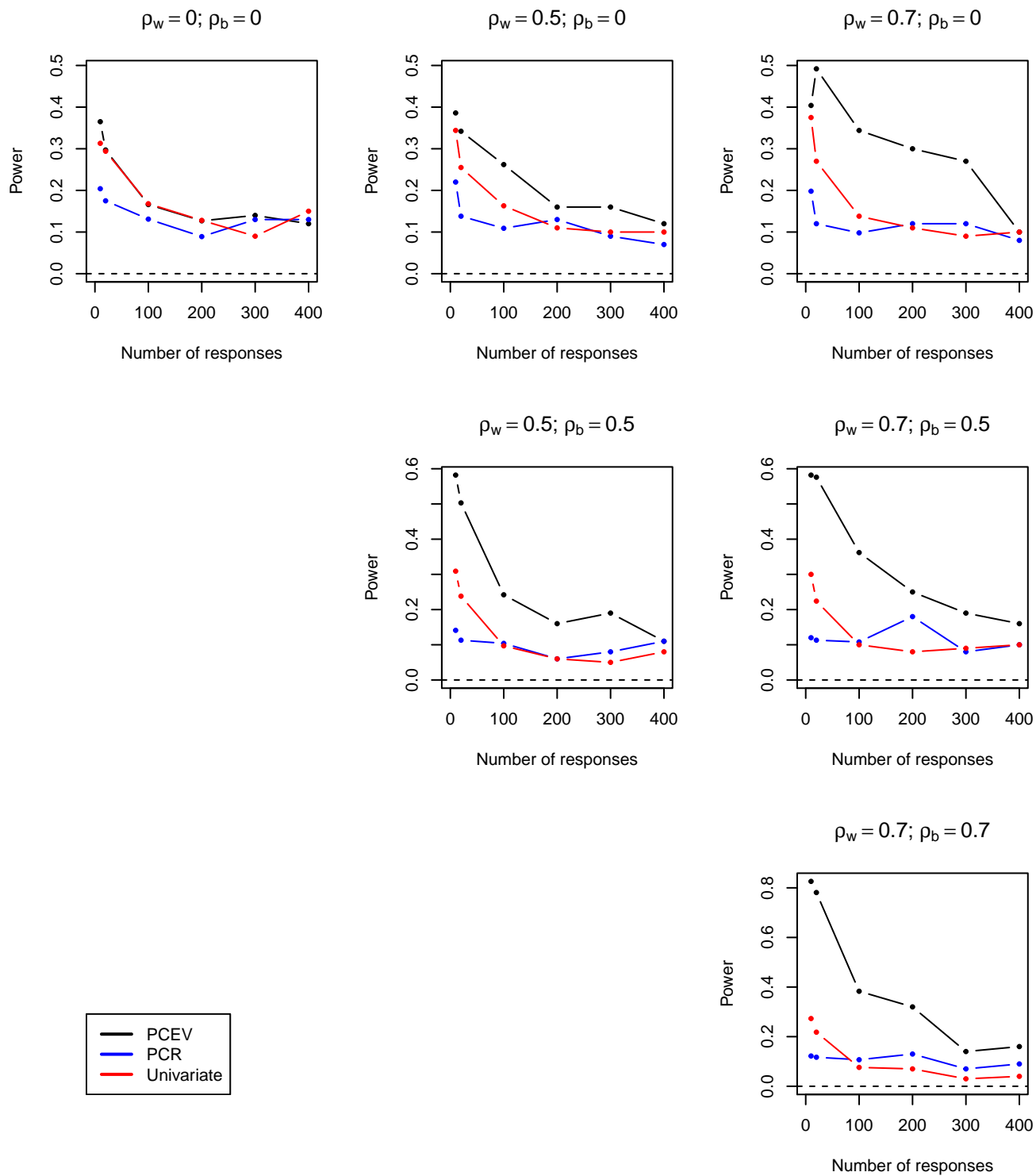
5.25 Significance level: 0.1, Heritability: 0.5%, Number of blocks: 2



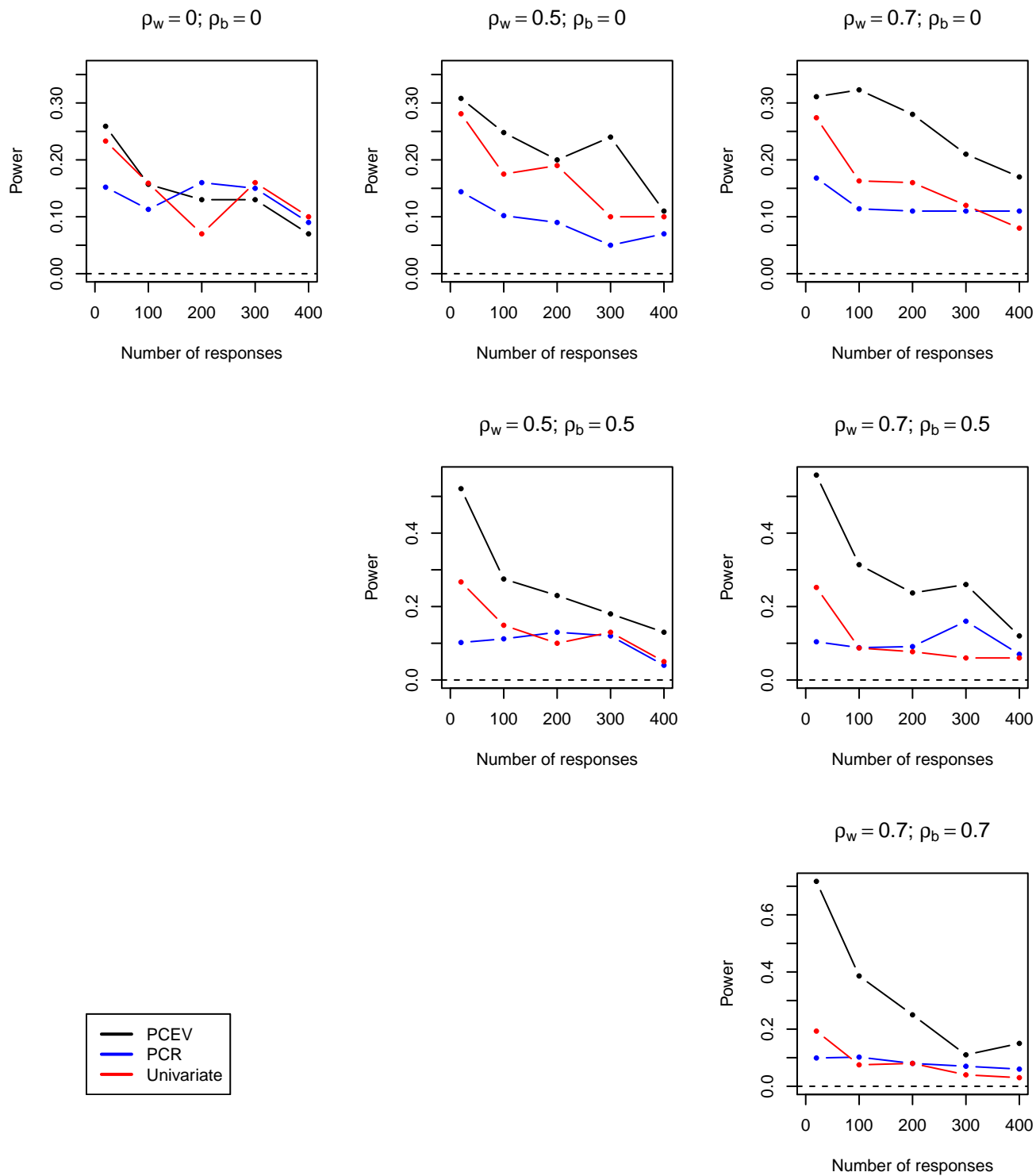
5.26 Significance level: 0.1, Heritability: 0.5%, Number of blocks: 5



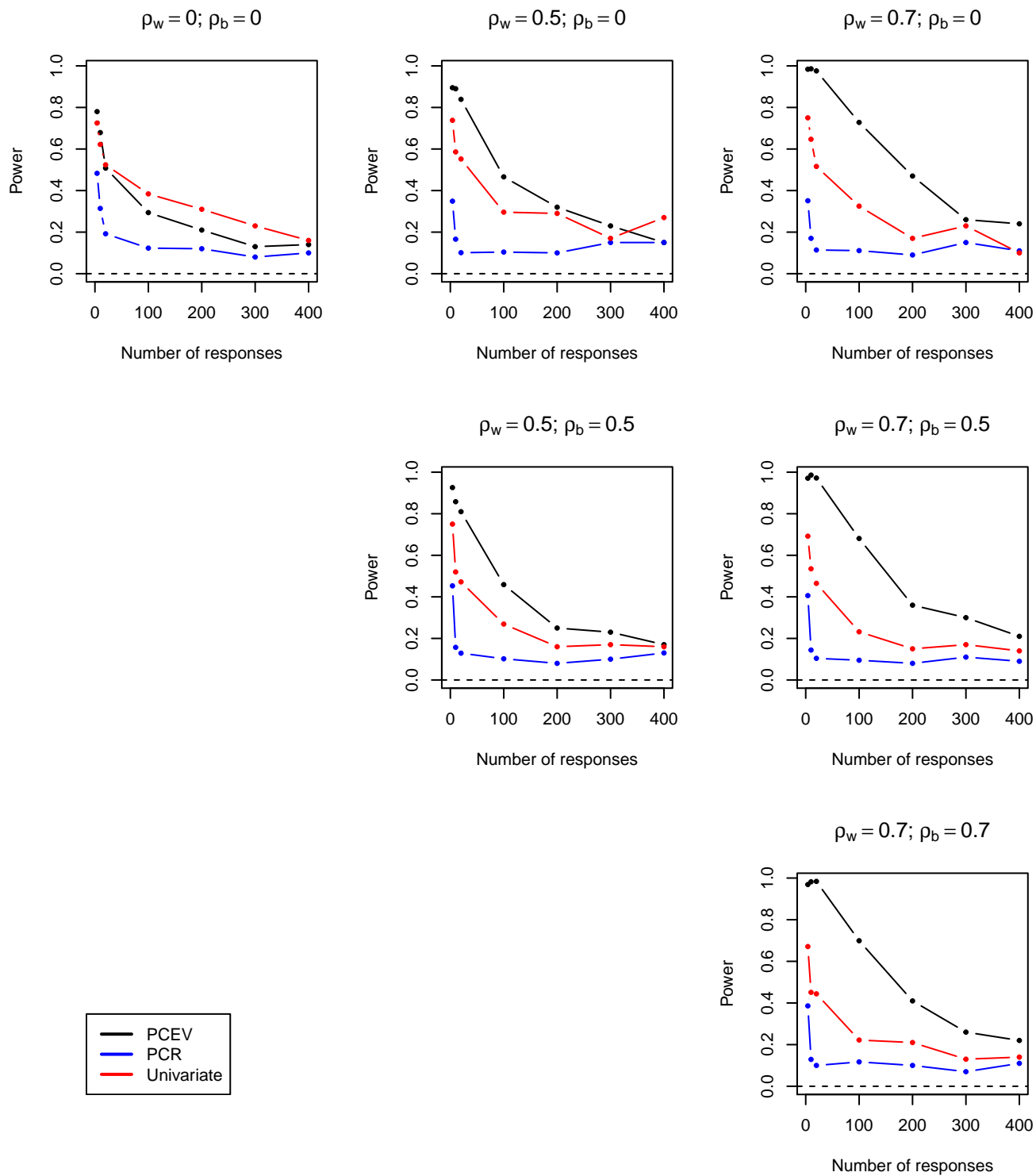
5.27 Significance level: 0.1, Heritability: 0.5%, Number of blocks: 10



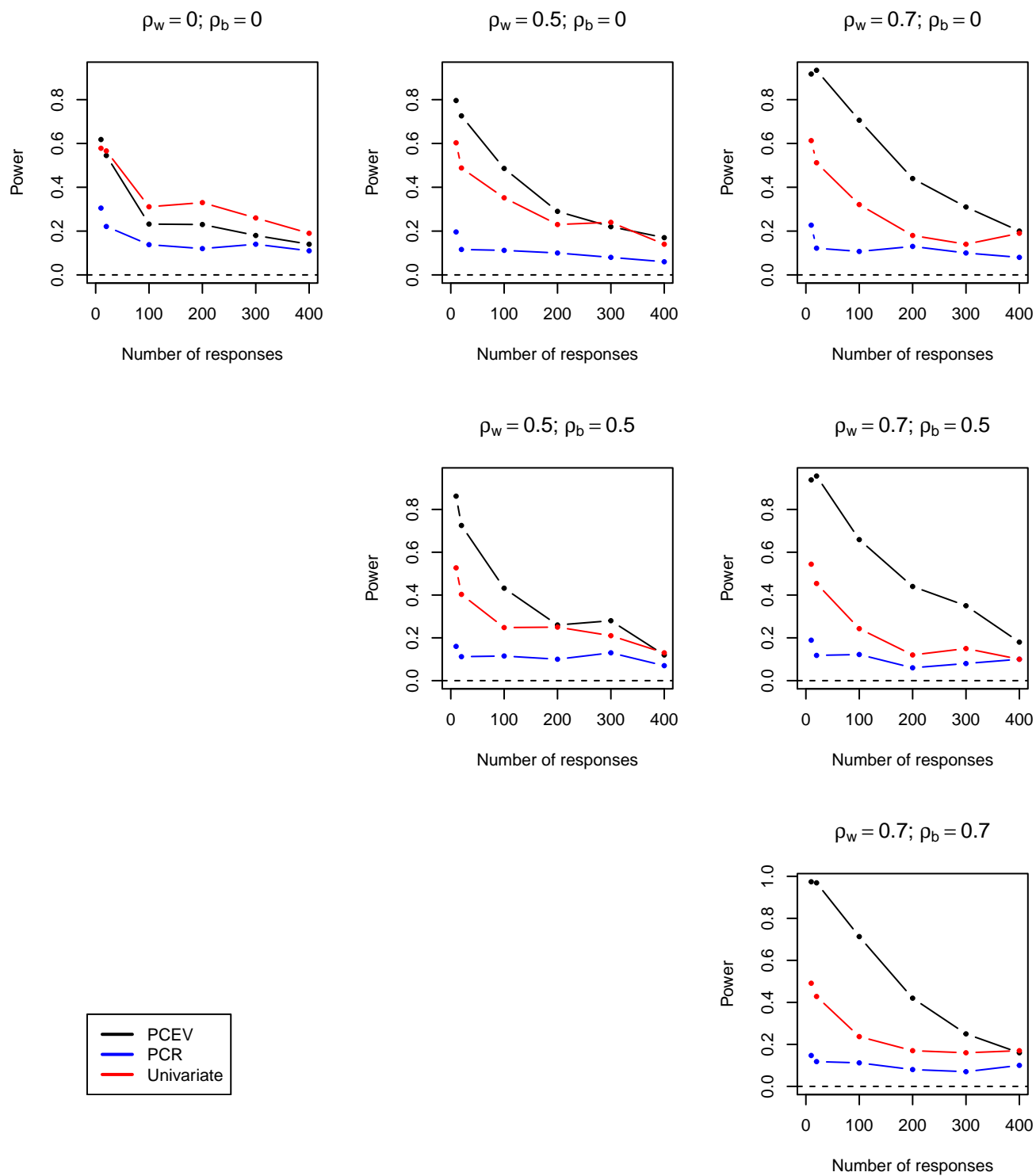
5.28 Significance level: 0.1, Heritability: 0.5%, Number of blocks: 20



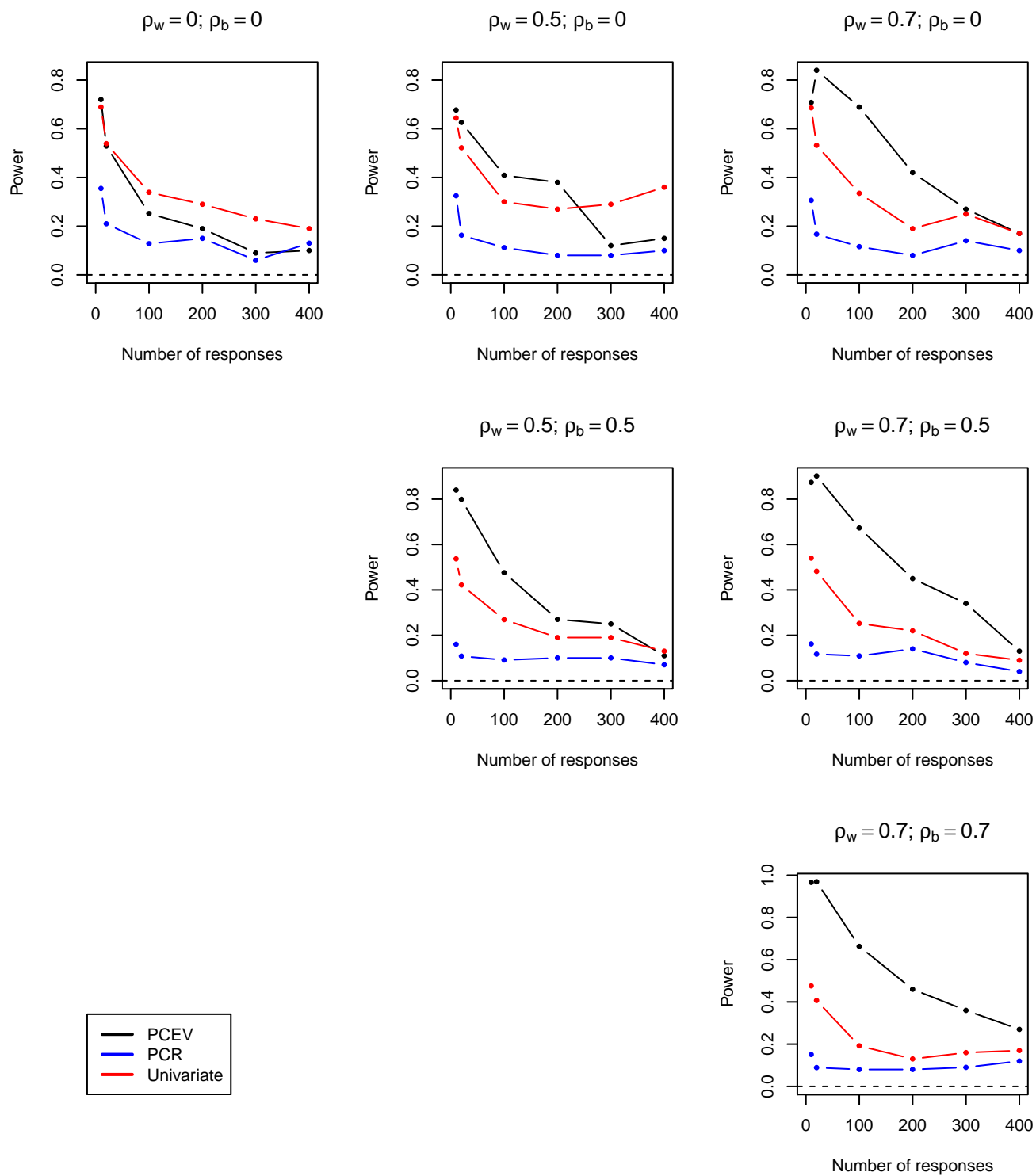
5.29 Significance level: 0.1, Heritability: 1%, Number of blocks: 2



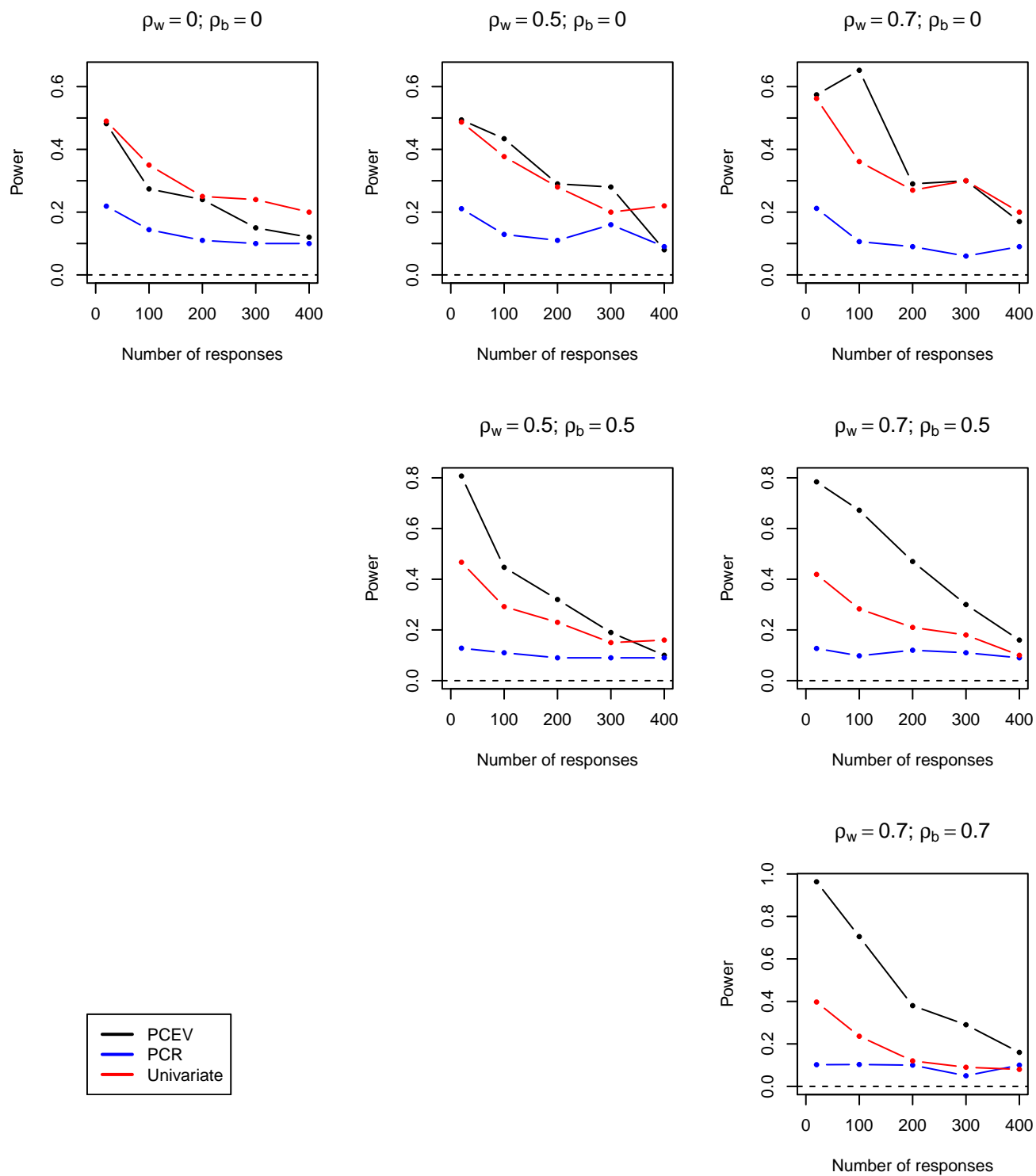
5.30 Significance level: 0.1, Heritability: 1%, Number of blocks: 5



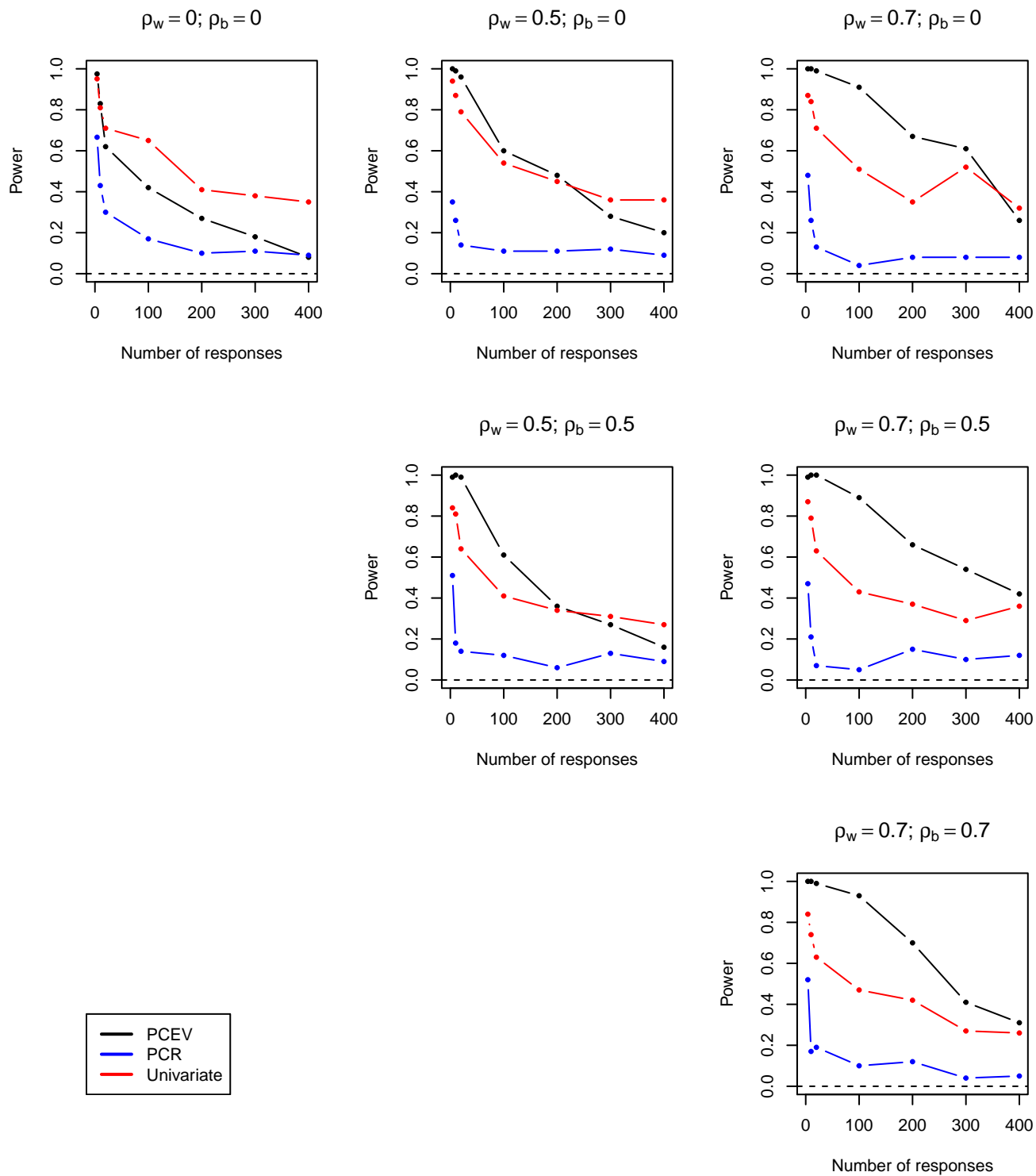
5.31 Significance level: 0.1, Heritability: 1%, Number of blocks: 10



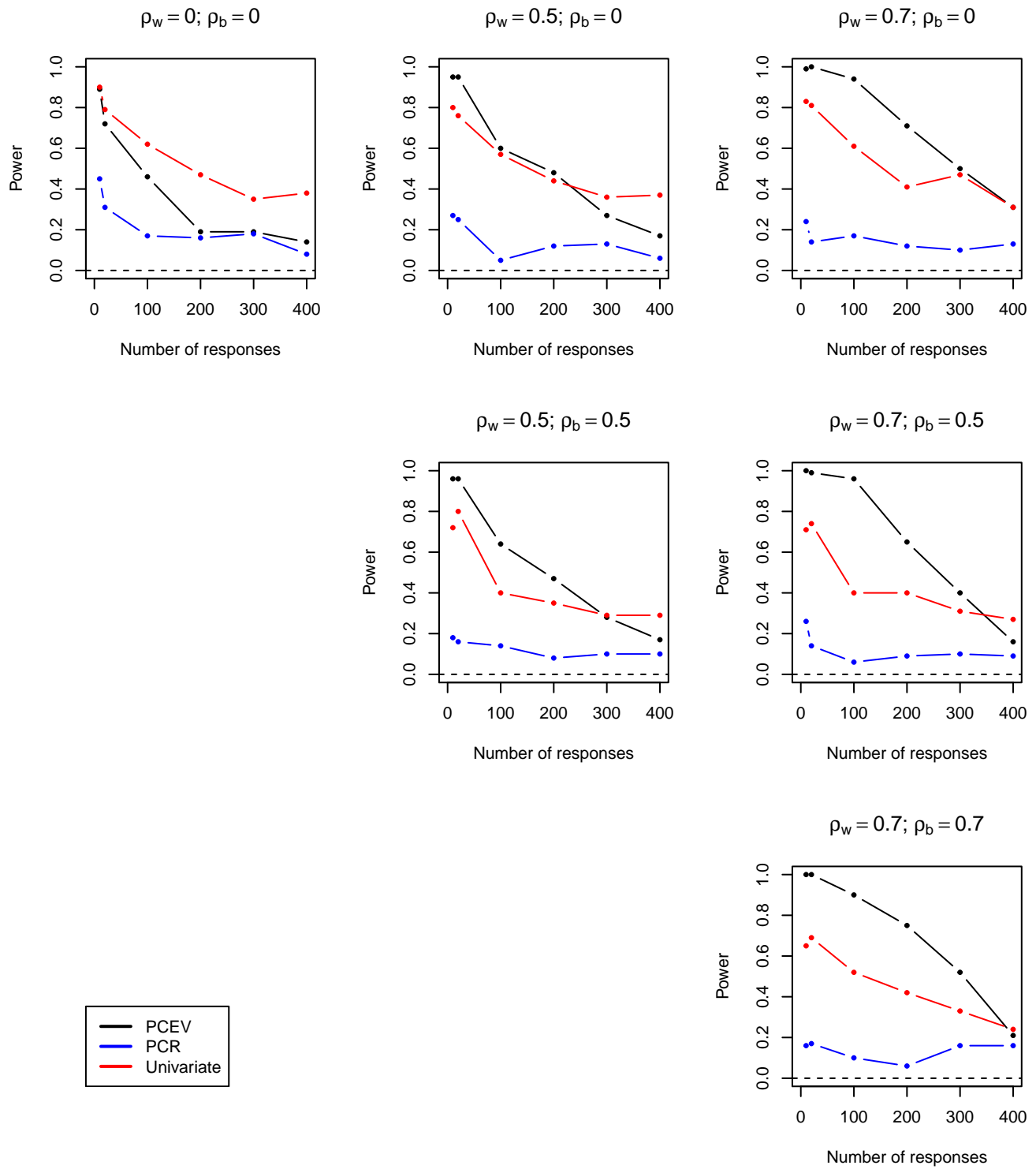
5.32 Significance level: 0.1, Heritability: 1%, Number of blocks: 20



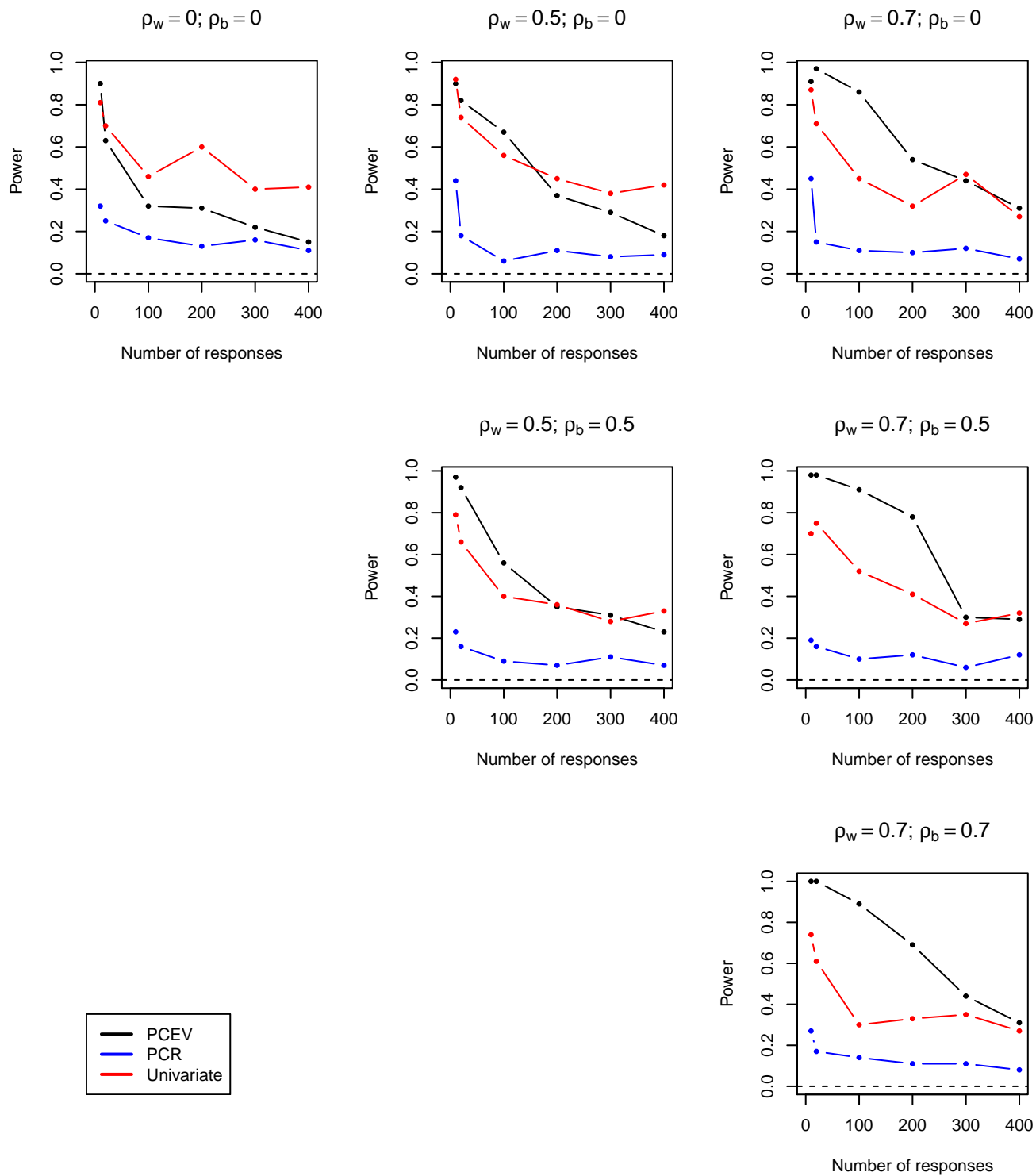
5.33 Significance level: 0.1, Heritability: 1.5%, Number of blocks: 2



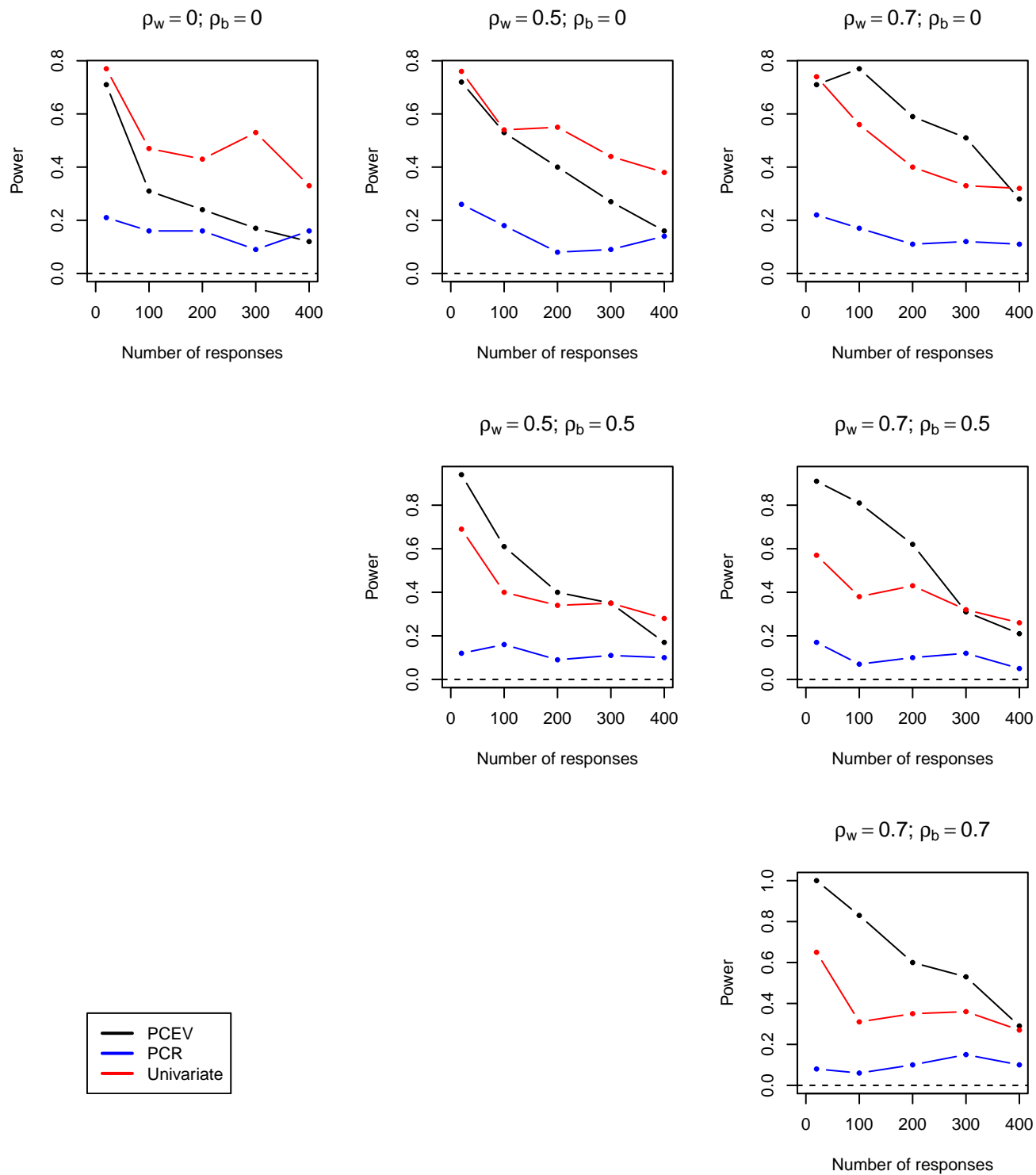
5.34 Significance level: 0.1, Heritability: 1.5%, Number of blocks: 5



5.35 Significance level: 0.1, Heritability: 1.5%, Number of blocks: 10



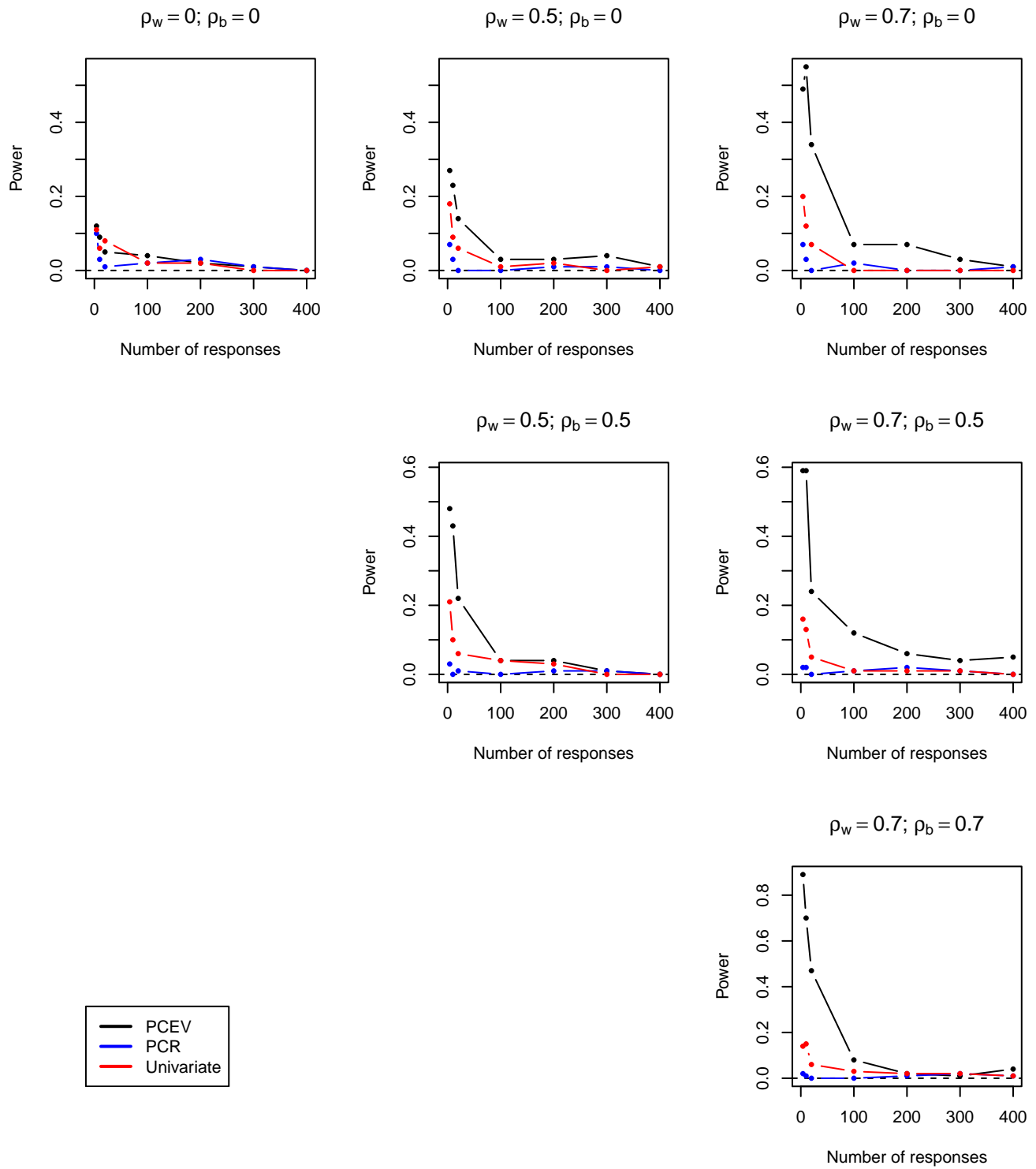
5.36 Significance level: 0.1, Heritability: 1.5%, Number of blocks: 20



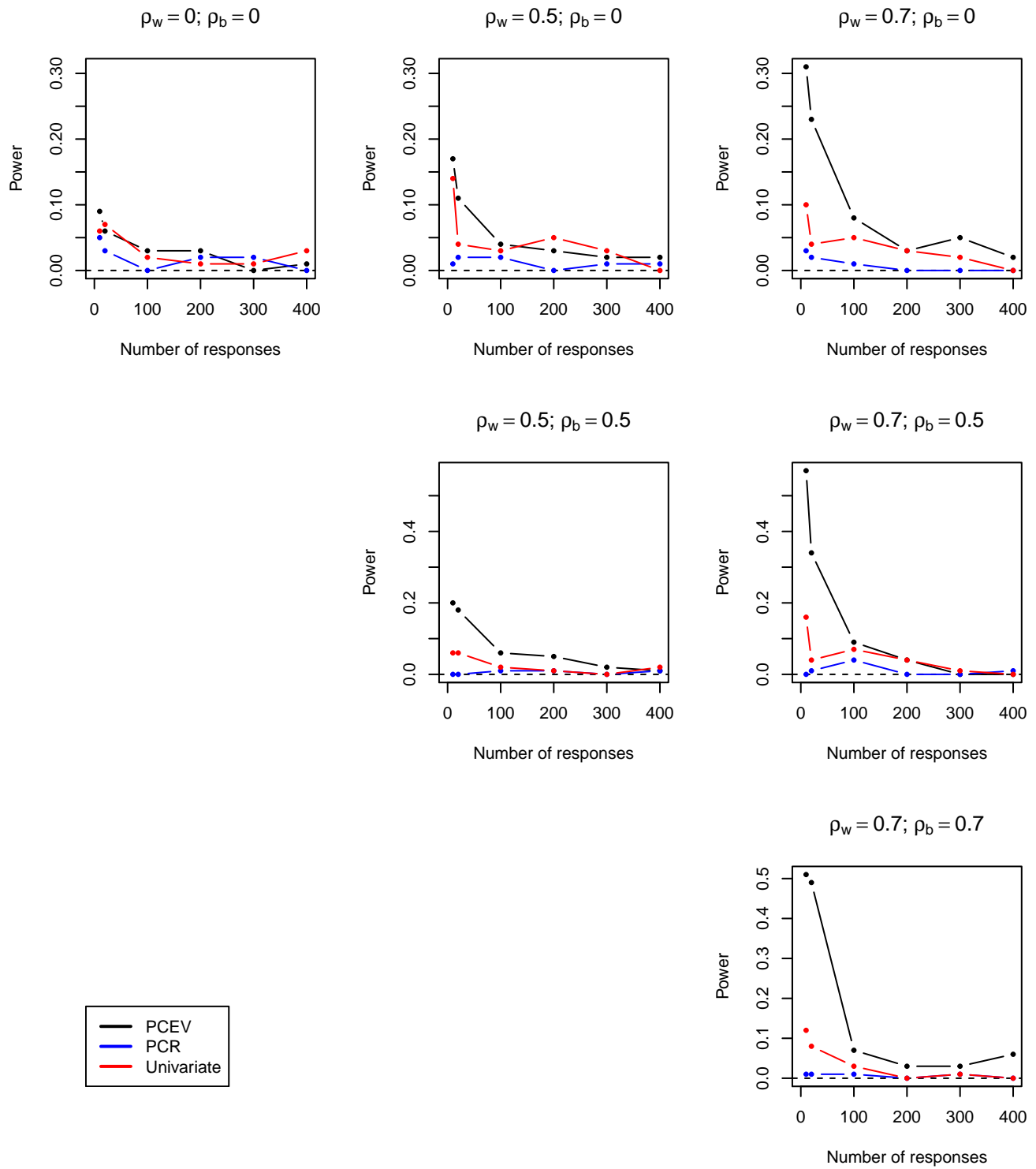
6 Simulation scenario 6

We simulated an association between the continuous covariate x and two components of the multivariate phenotype \mathbf{Y} : the associations are of the same size, in the opposite direction, and the two components lie in different blocks.

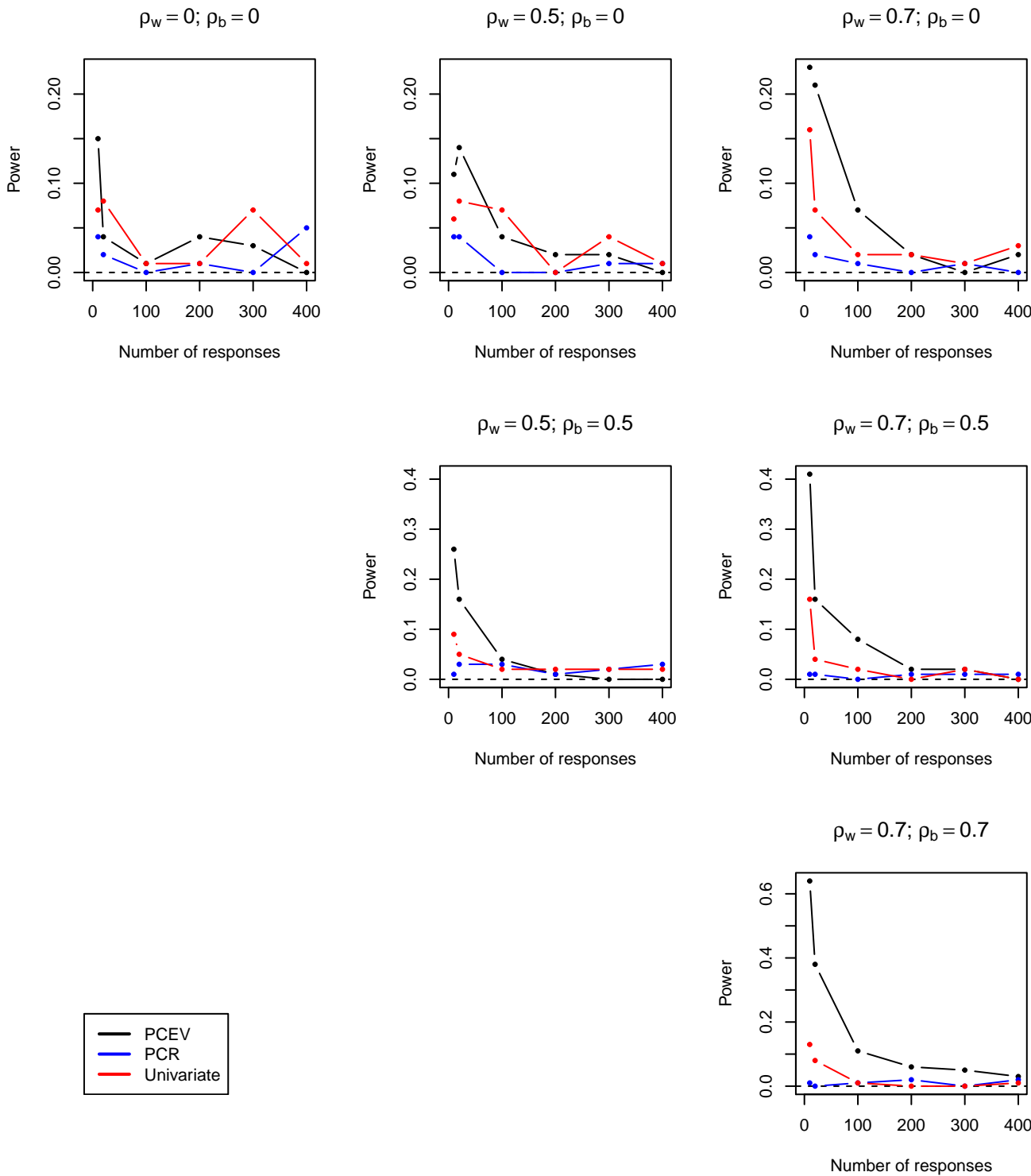
6.1 Significance level: 0.01, Heritability: 0.5%, Number of blocks: 2



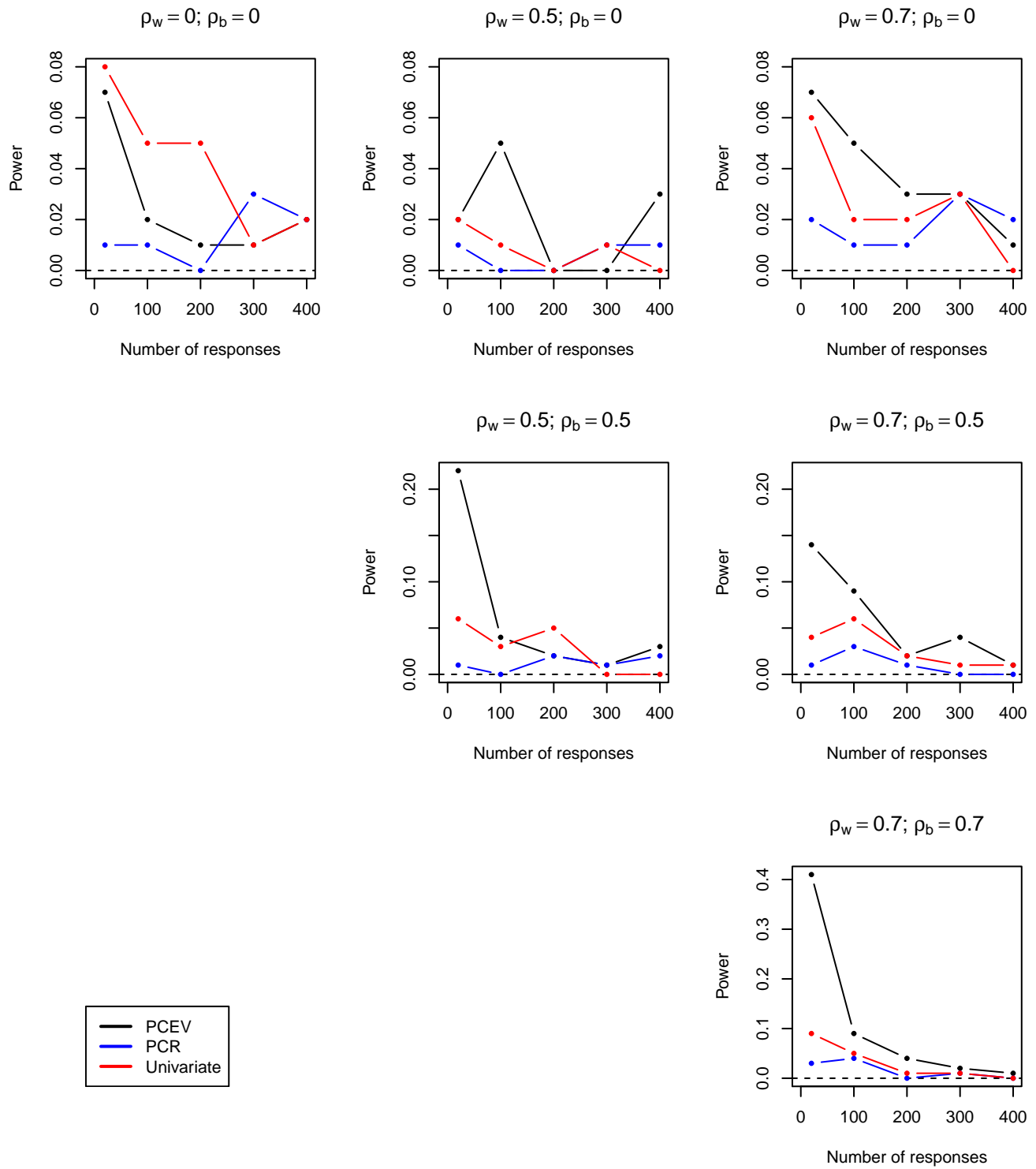
6.2 Significance level: 0.01, Heritability: 0.5%, Number of blocks: 5



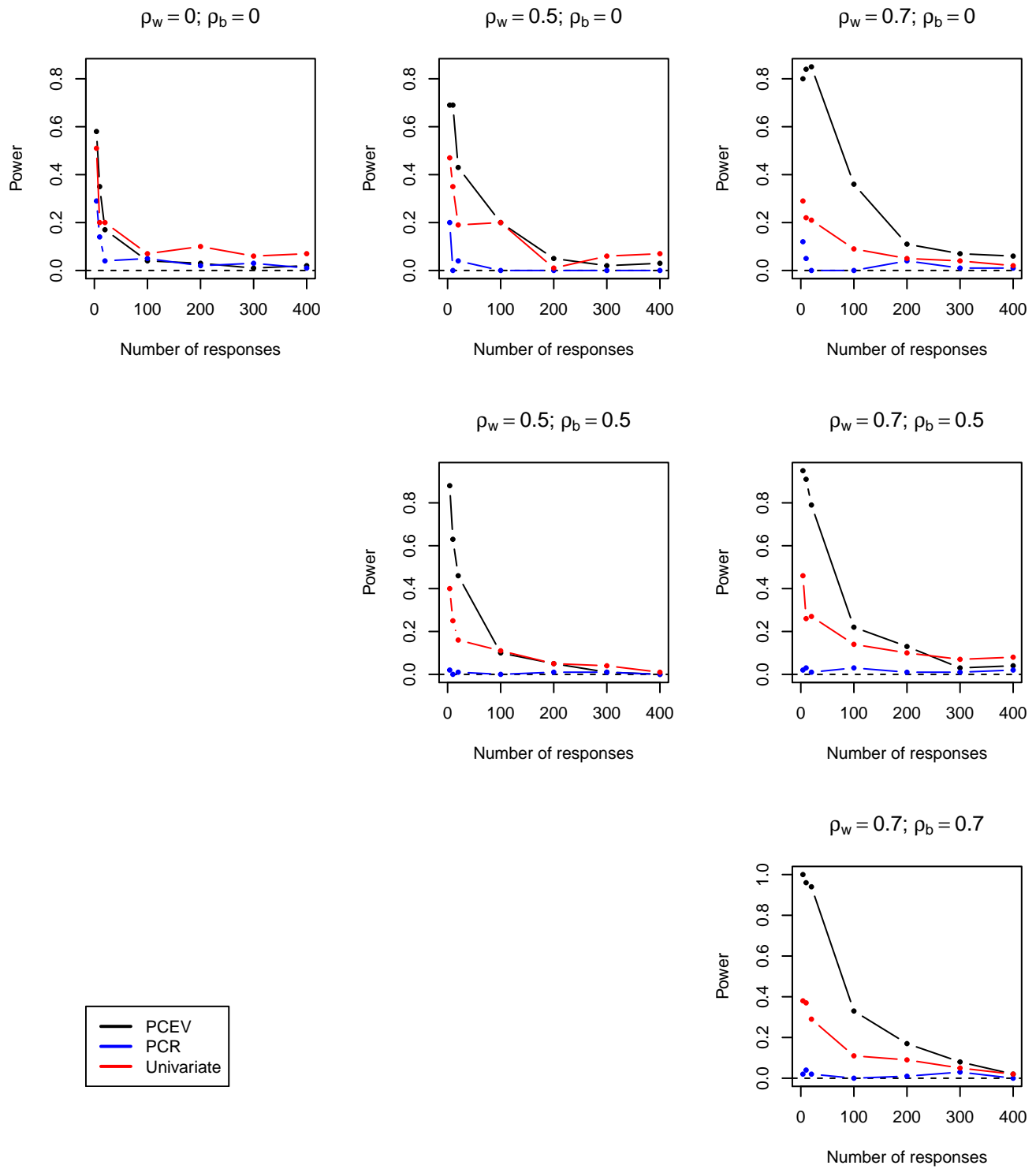
6.3 Significance level: 0.01, Heritability: 0.5%, Number of blocks: 10



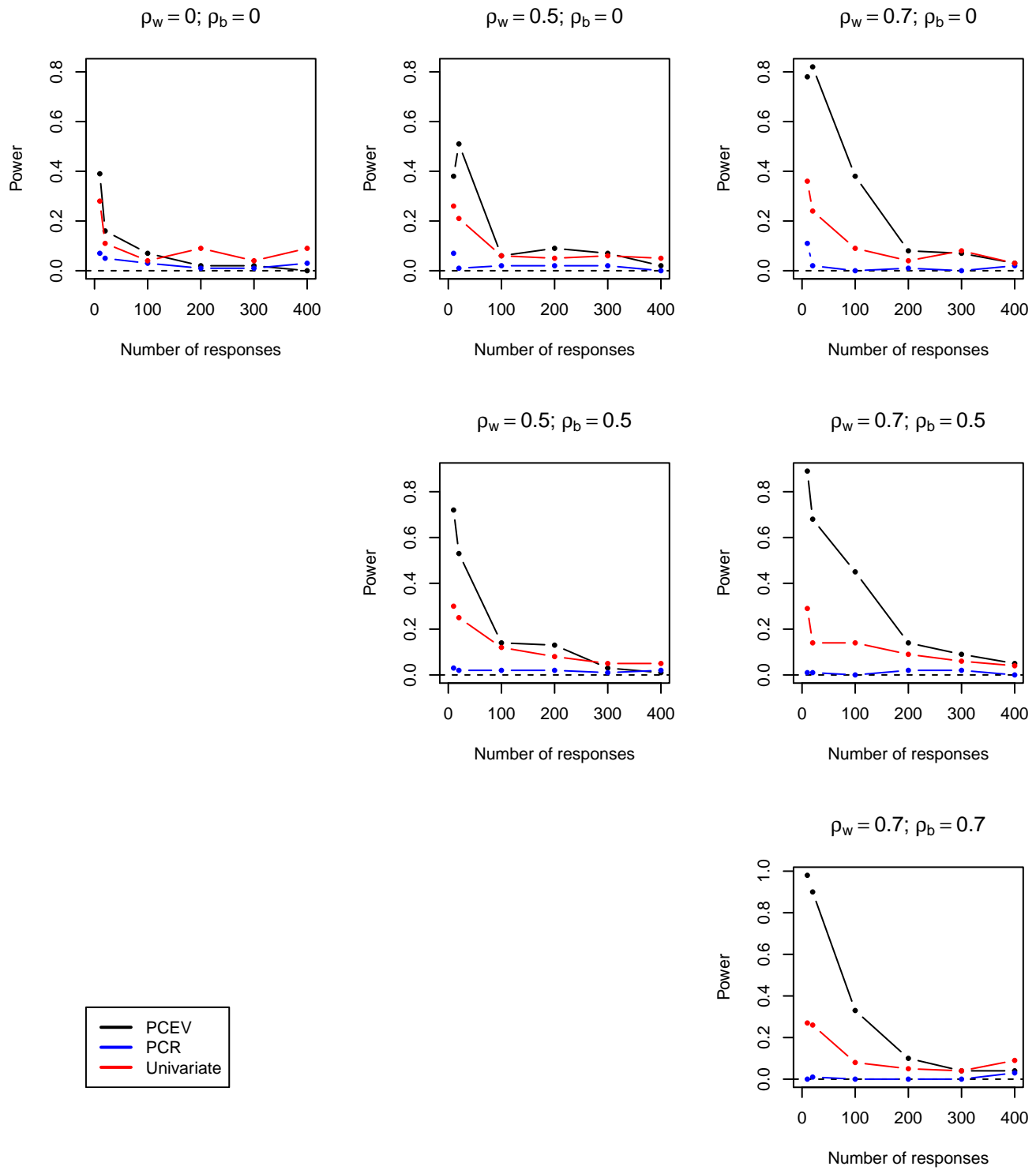
6.4 Significance level: 0.01, Heritability: 0.5%, Number of blocks: 20



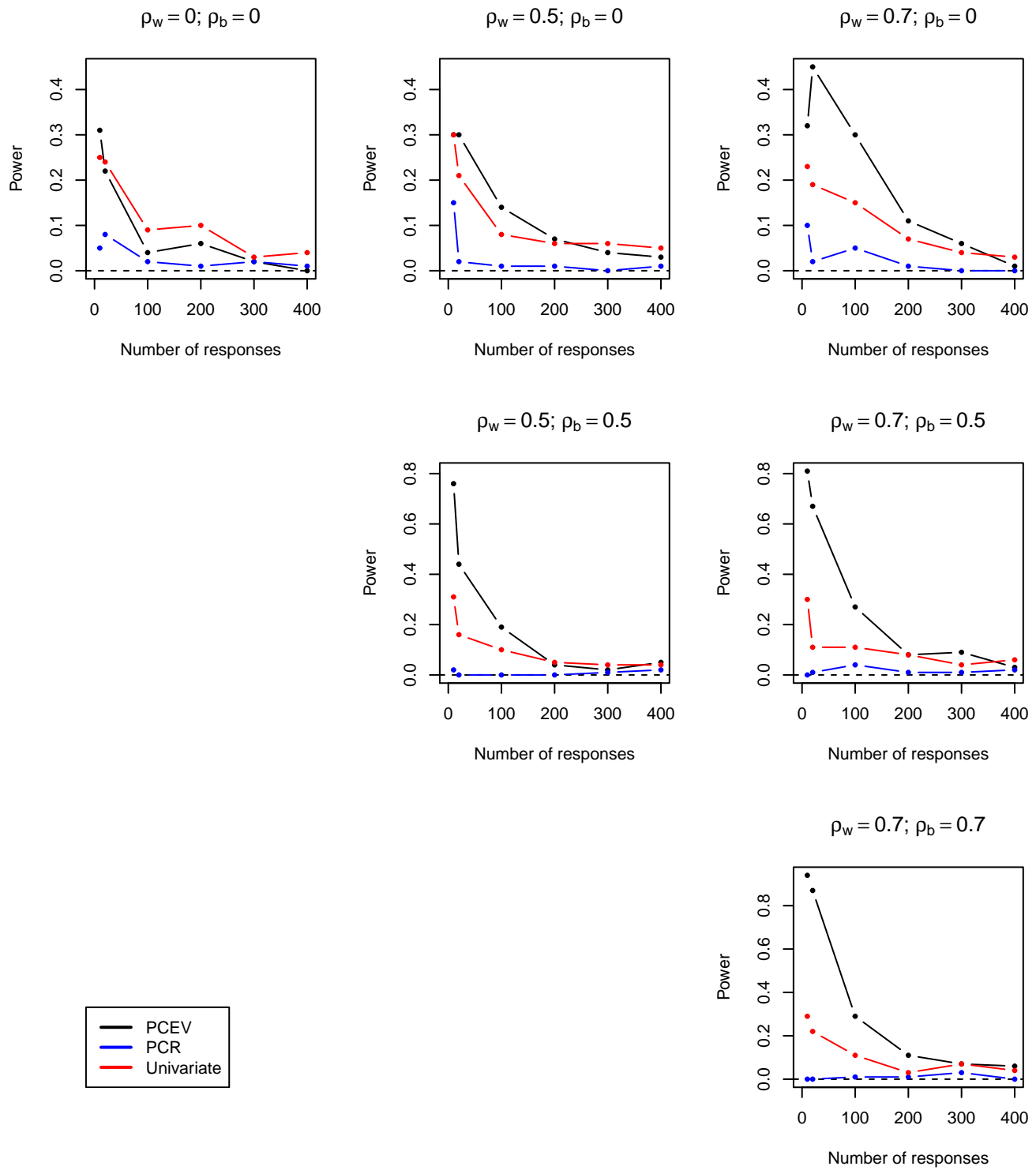
6.5 Significance level: 0.01, Heritability: 1%, Number of blocks: 2



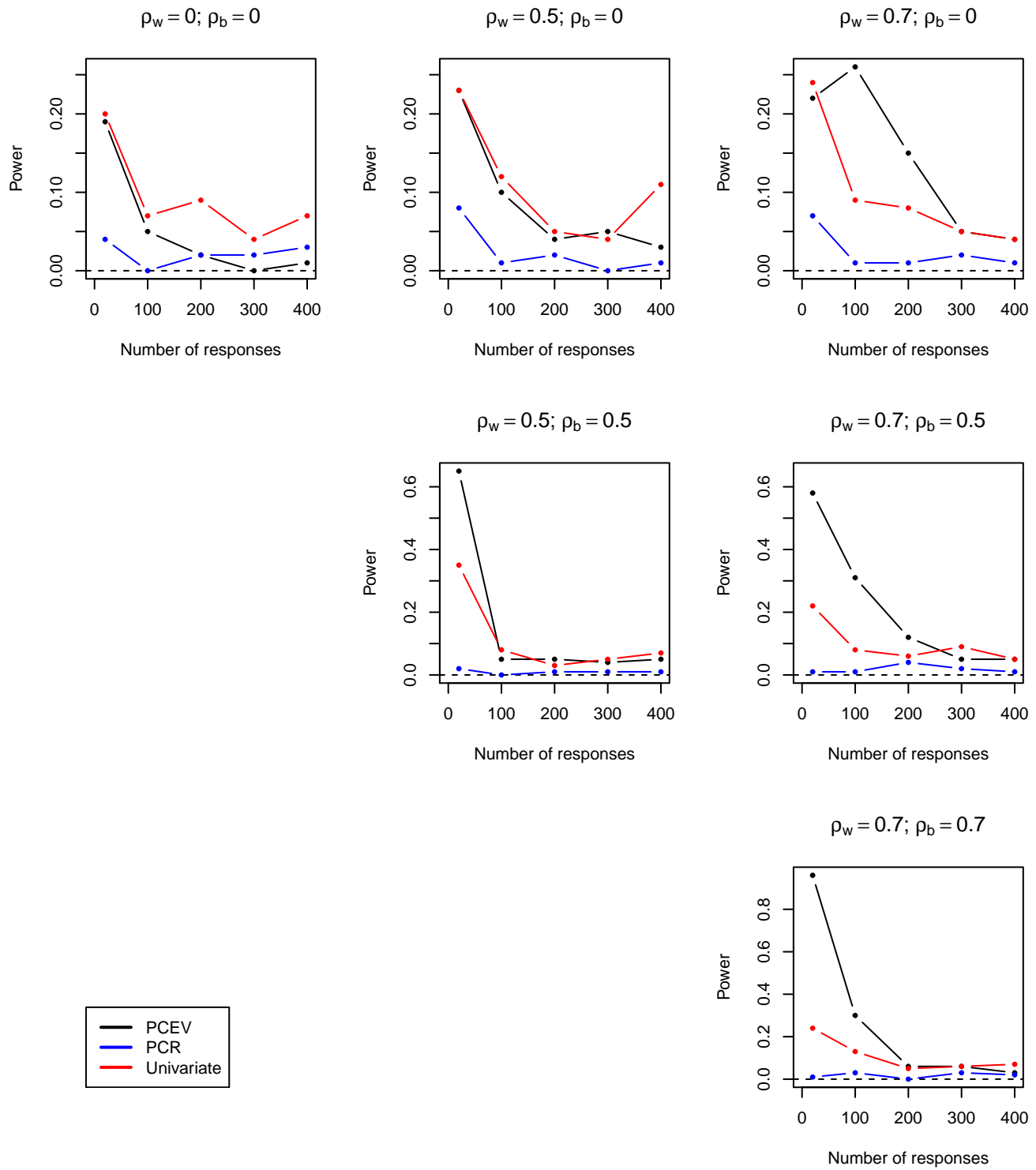
6.6 Significance level: 0.01, Heritability: 1%, Number of blocks: 5



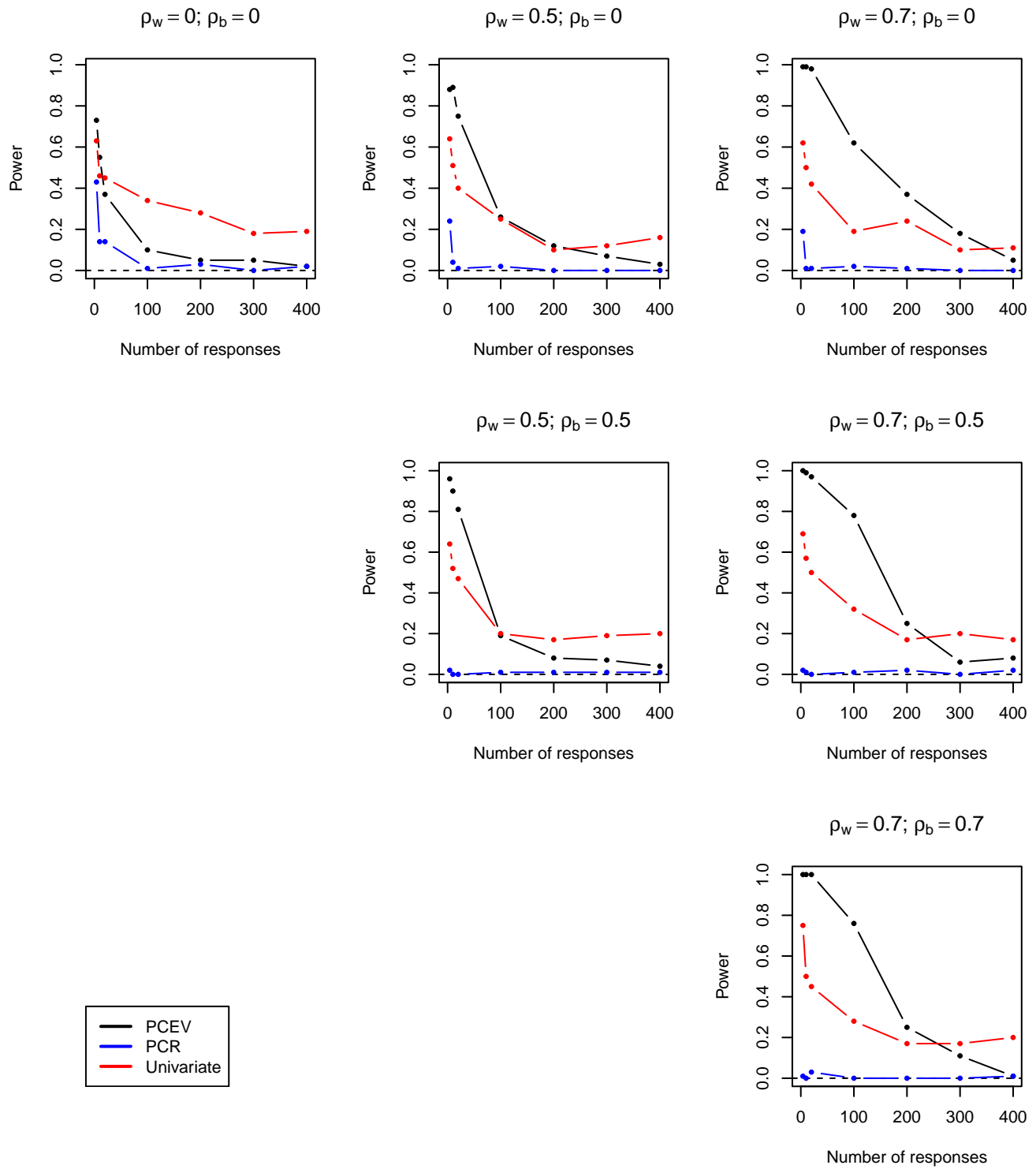
6.7 Significance level: 0.01, Heritability: 1%, Number of blocks: 10



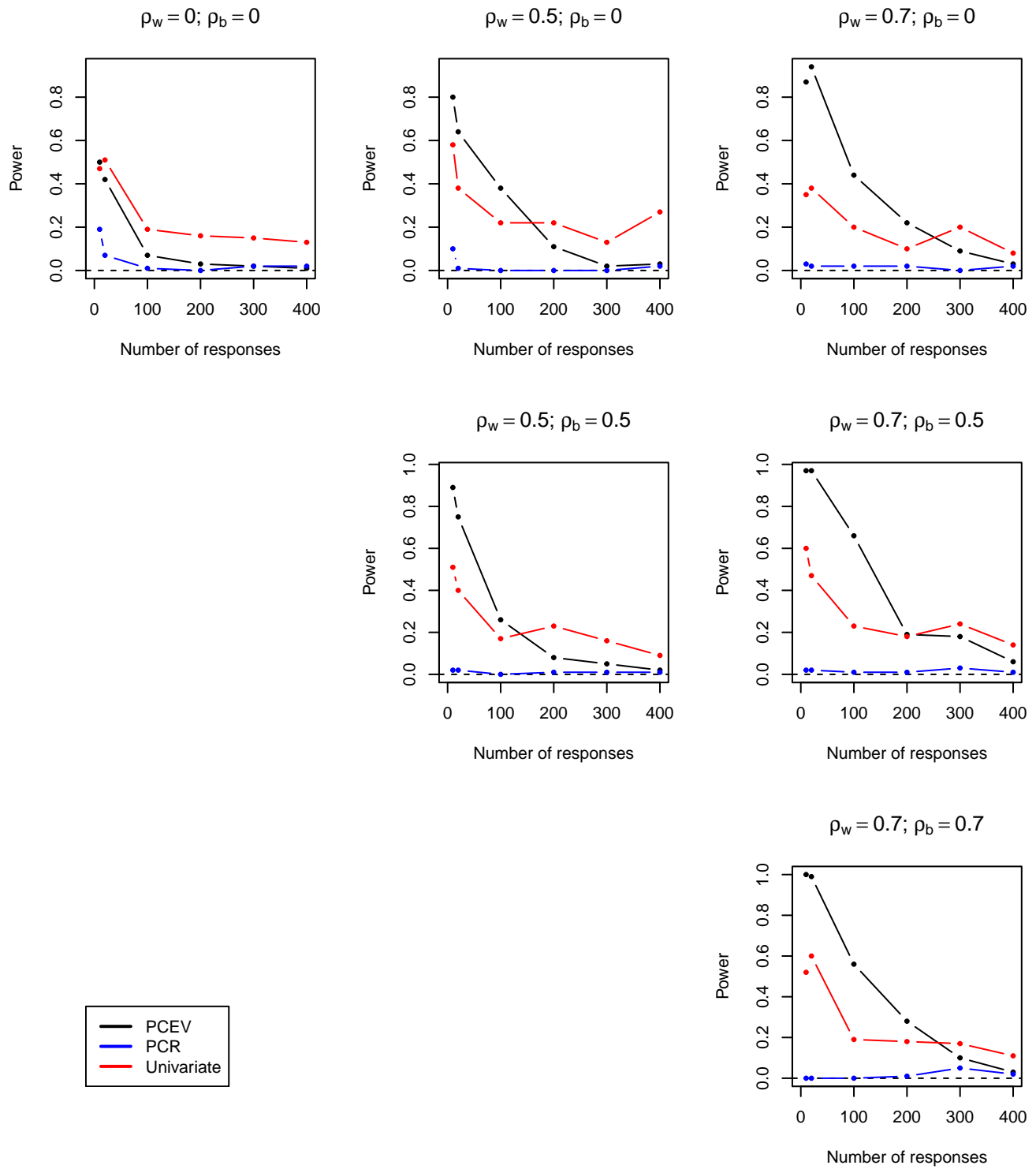
6.8 Significance level: 0.01, Heritability: 1%, Number of blocks: 20



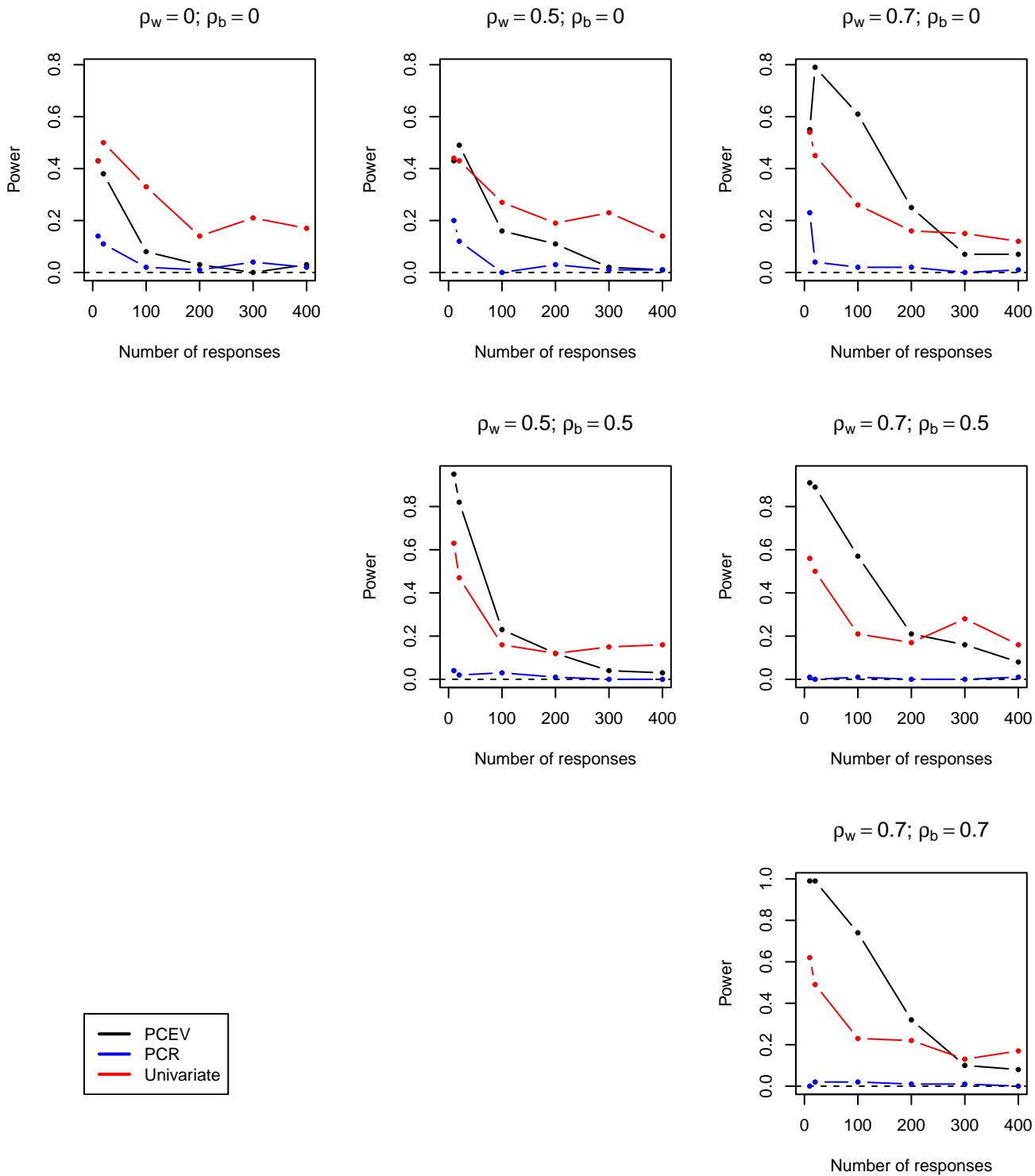
6.9 Significance level: 0.01, Heritability: 1.5%, Number of blocks: 2



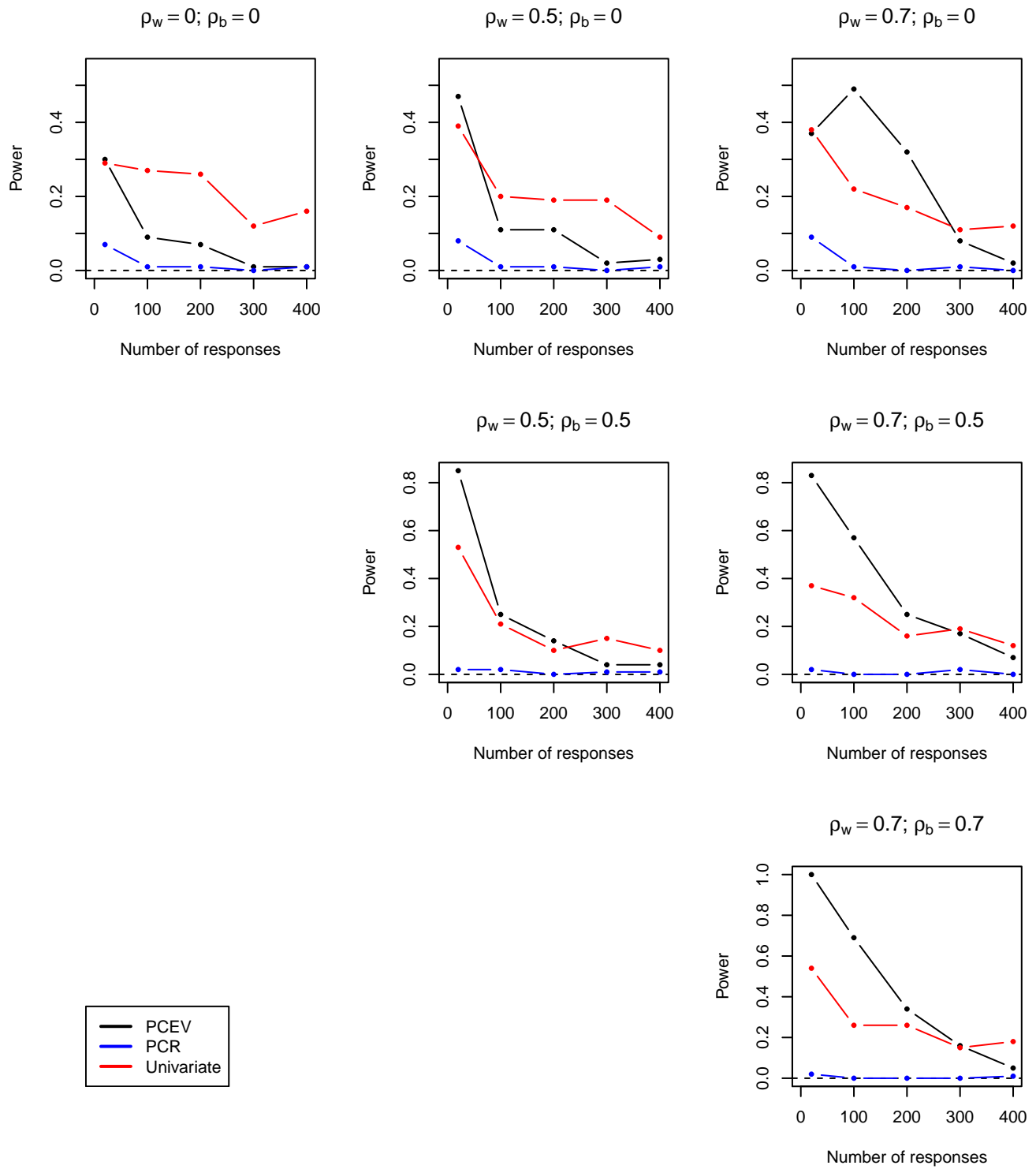
6.10 Significance level: 0.01, Heritability: 1.5%, Number of blocks: 5



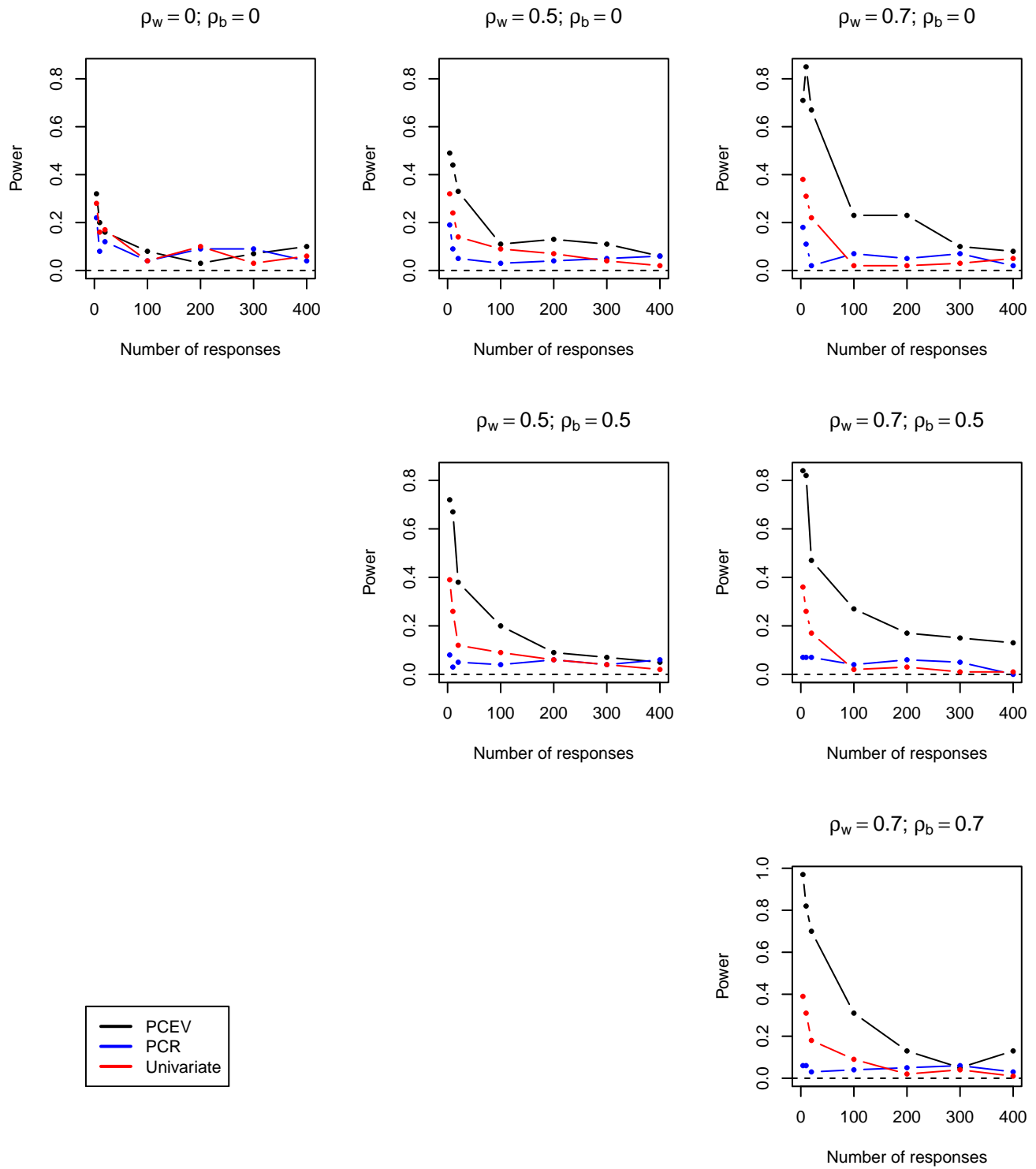
6.11 Significance level: 0.01, Heritability: 1.5%, Number of blocks: 10



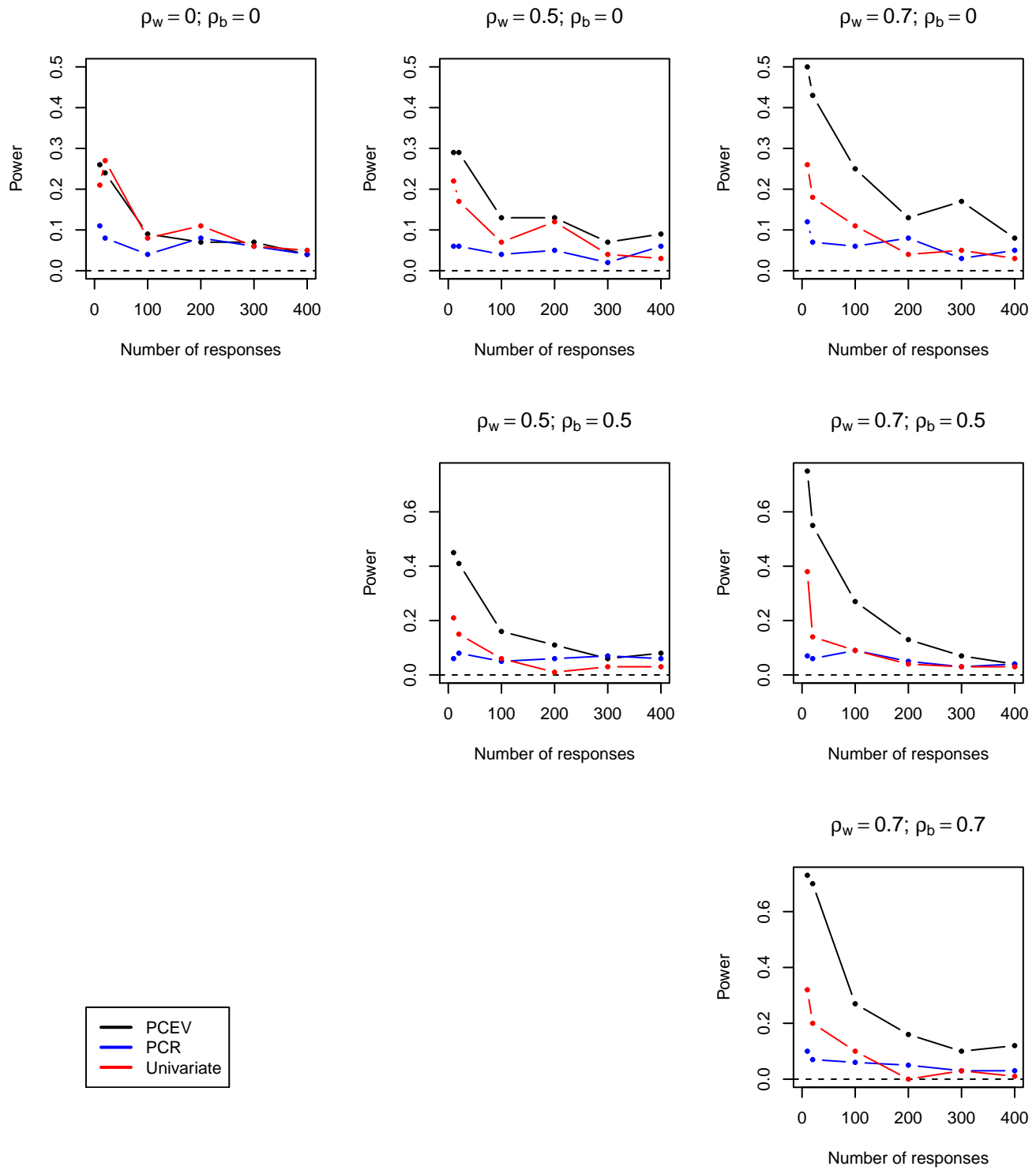
6.12 Significance level: 0.01, Heritability: 1.5%, Number of blocks: 20



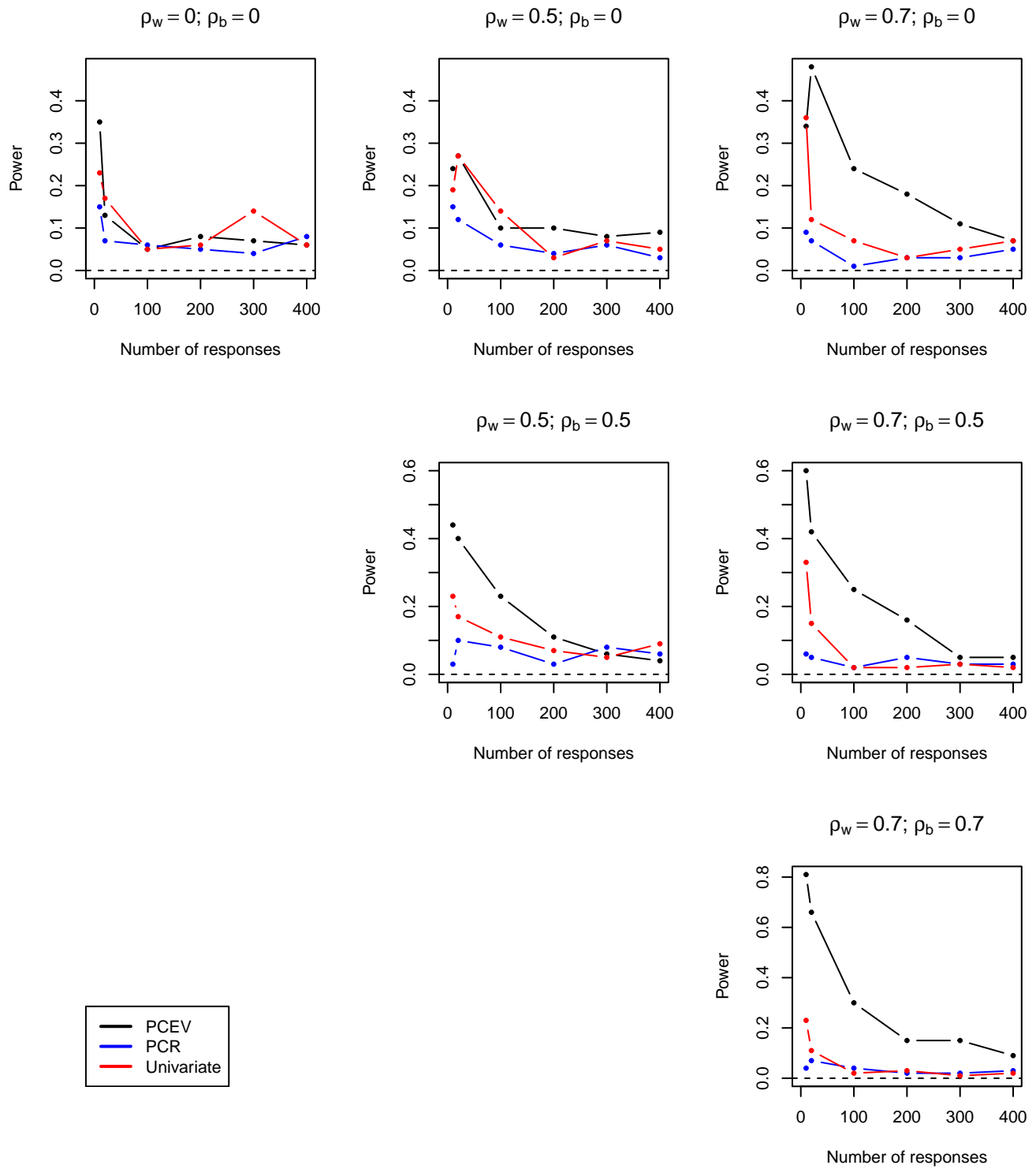
6.13 Significance level: 0.05, Heritability: 0.5%, Number of blocks: 2



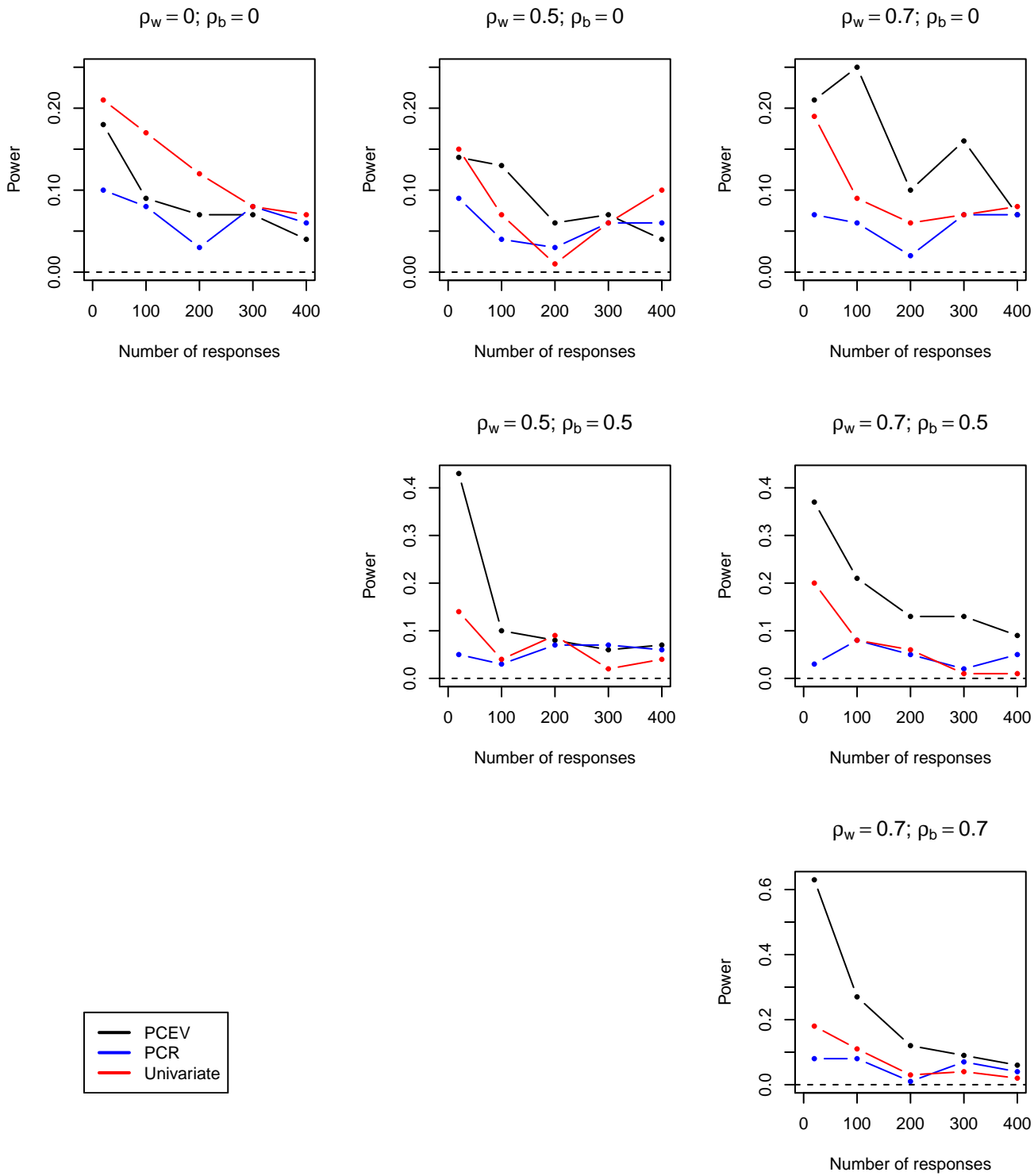
6.14 Significance level: 0.05, Heritability: 0.5%, Number of blocks: 5



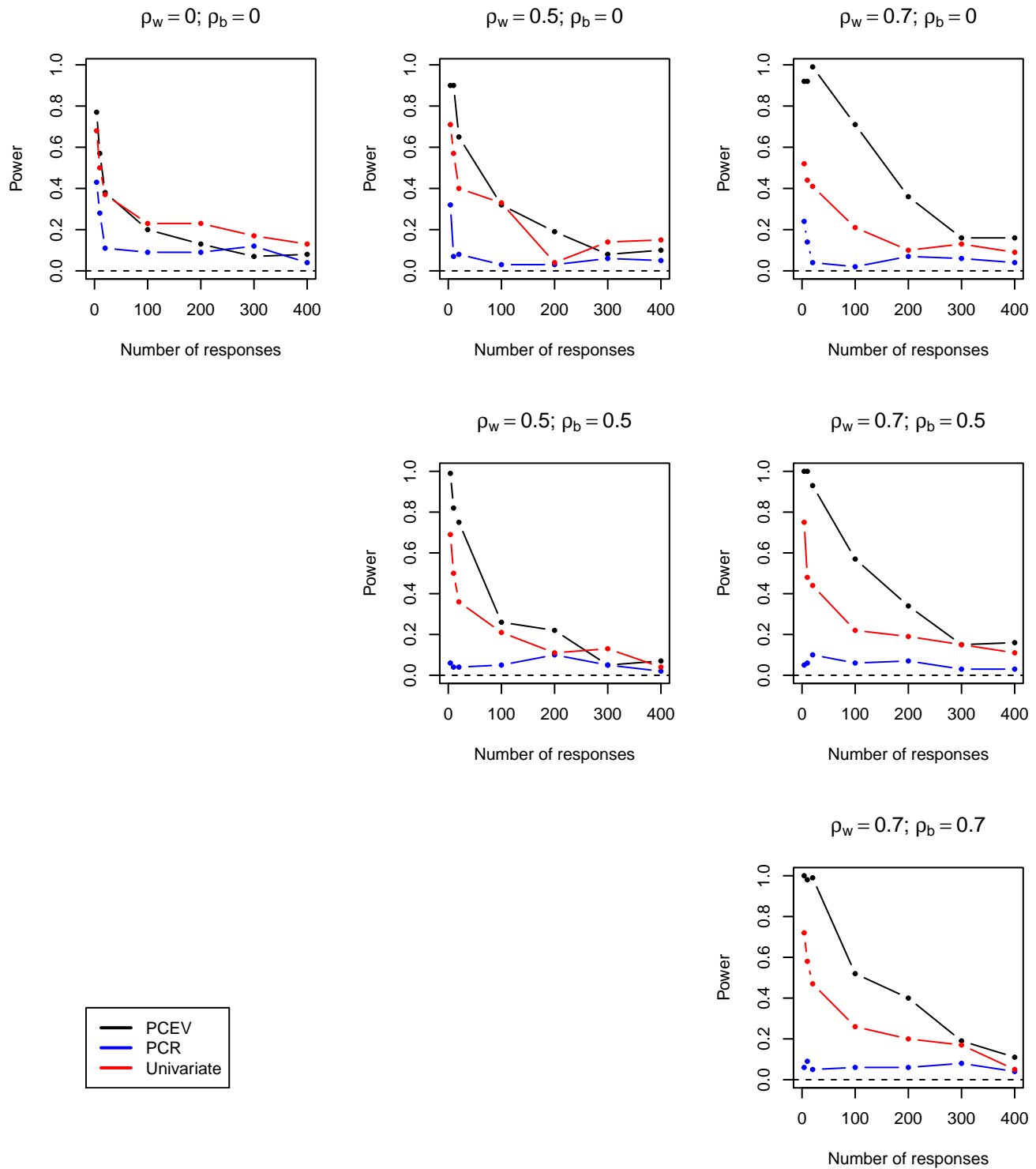
6.15 Significance level: 0.05, Heritability: 0.5%, Number of blocks: 10



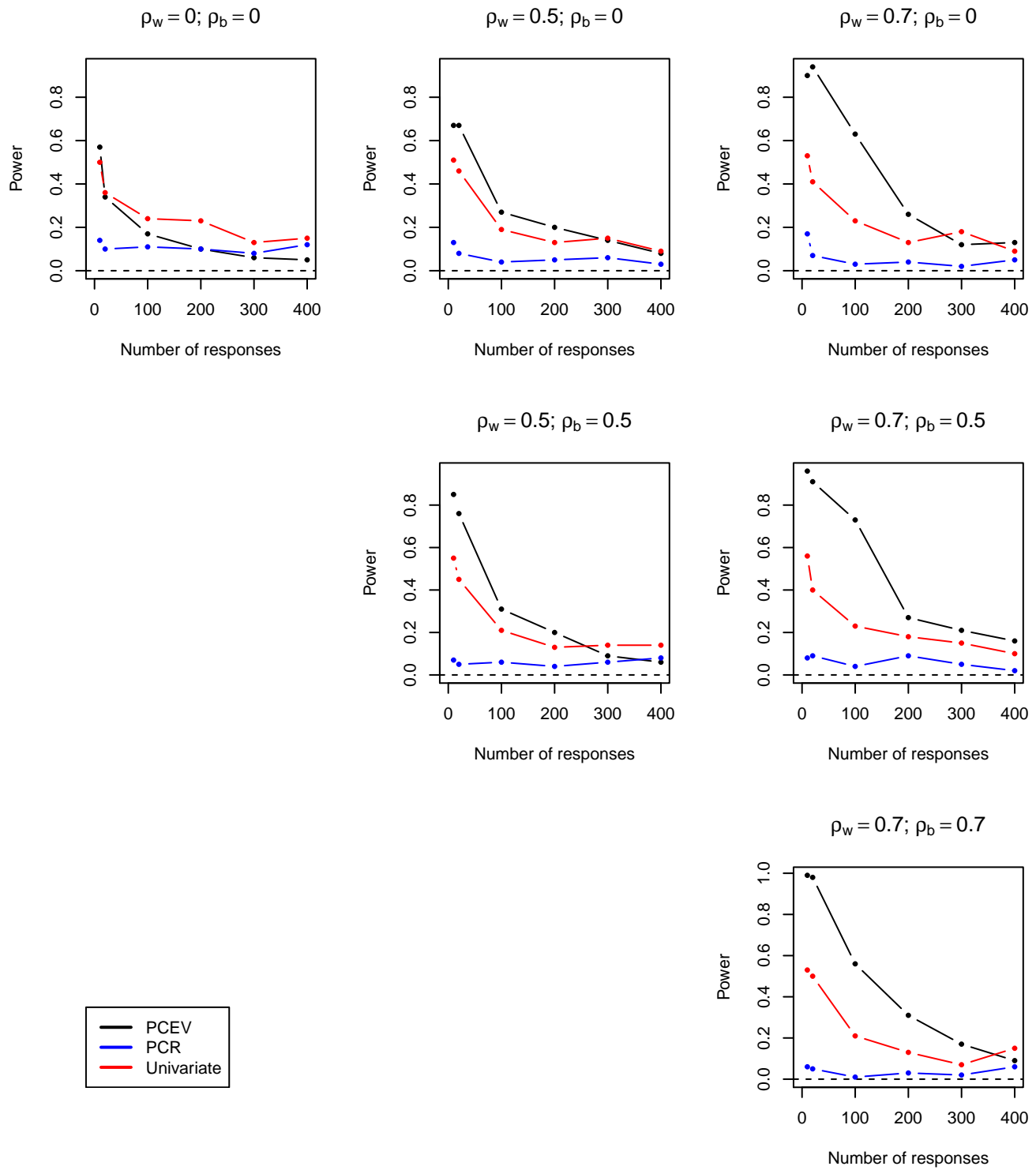
6.16 Significance level: 0.05, Heritability: 0.5%, Number of blocks: 20



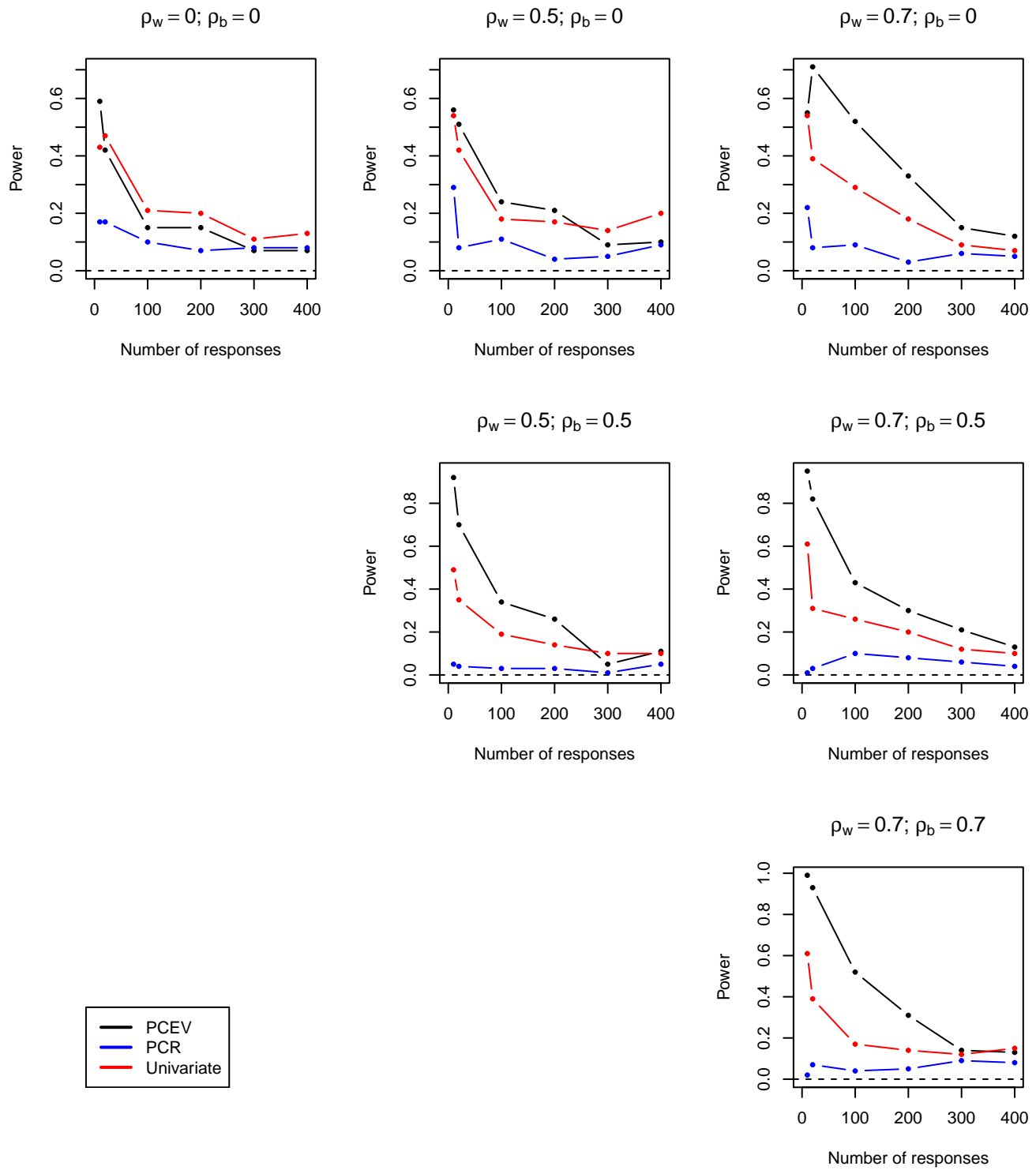
6.17 Significance level: 0.05, Heritability: 1%, Number of blocks: 2



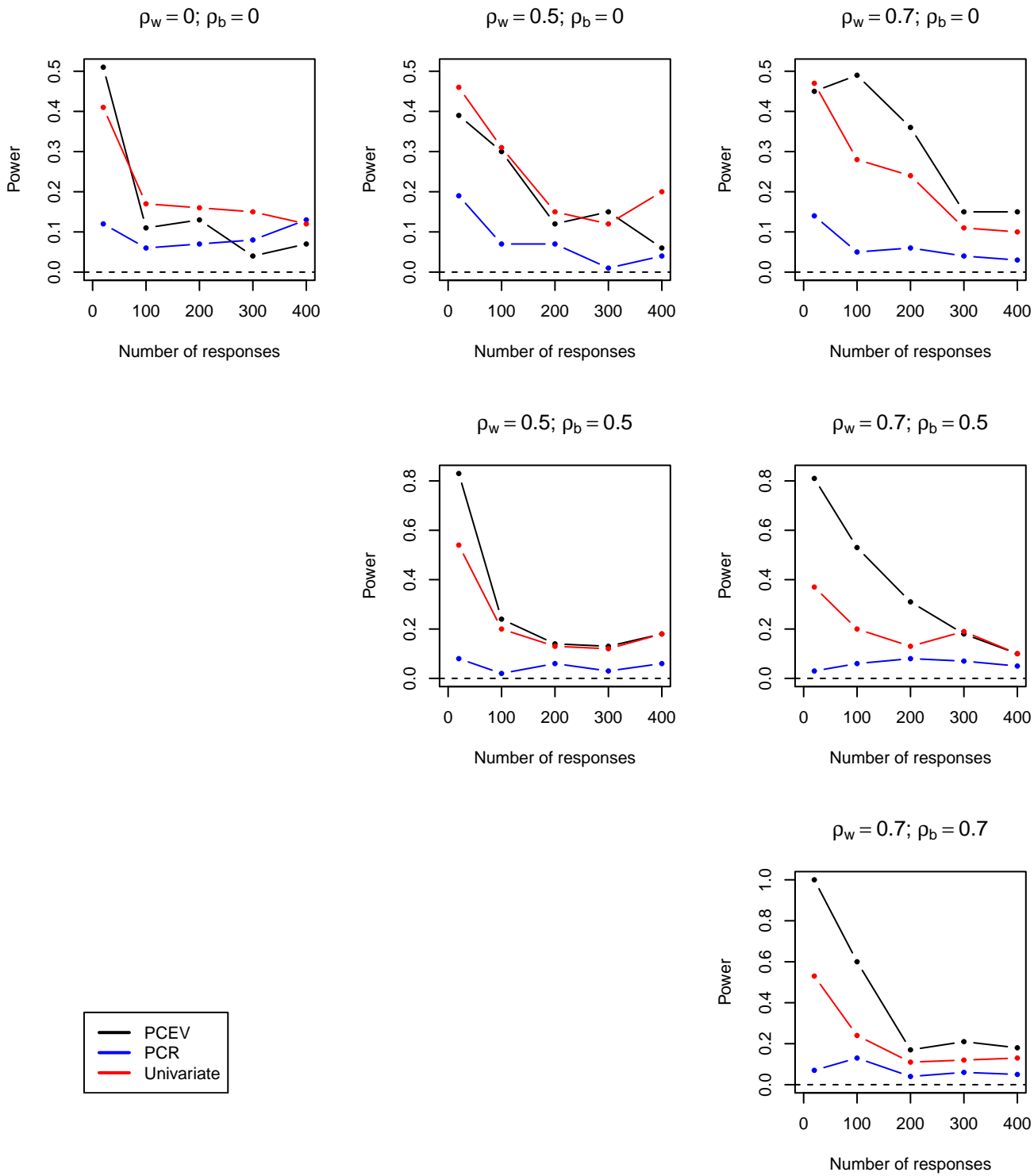
6.18 Significance level: 0.05, Heritability: 1%, Number of blocks: 5



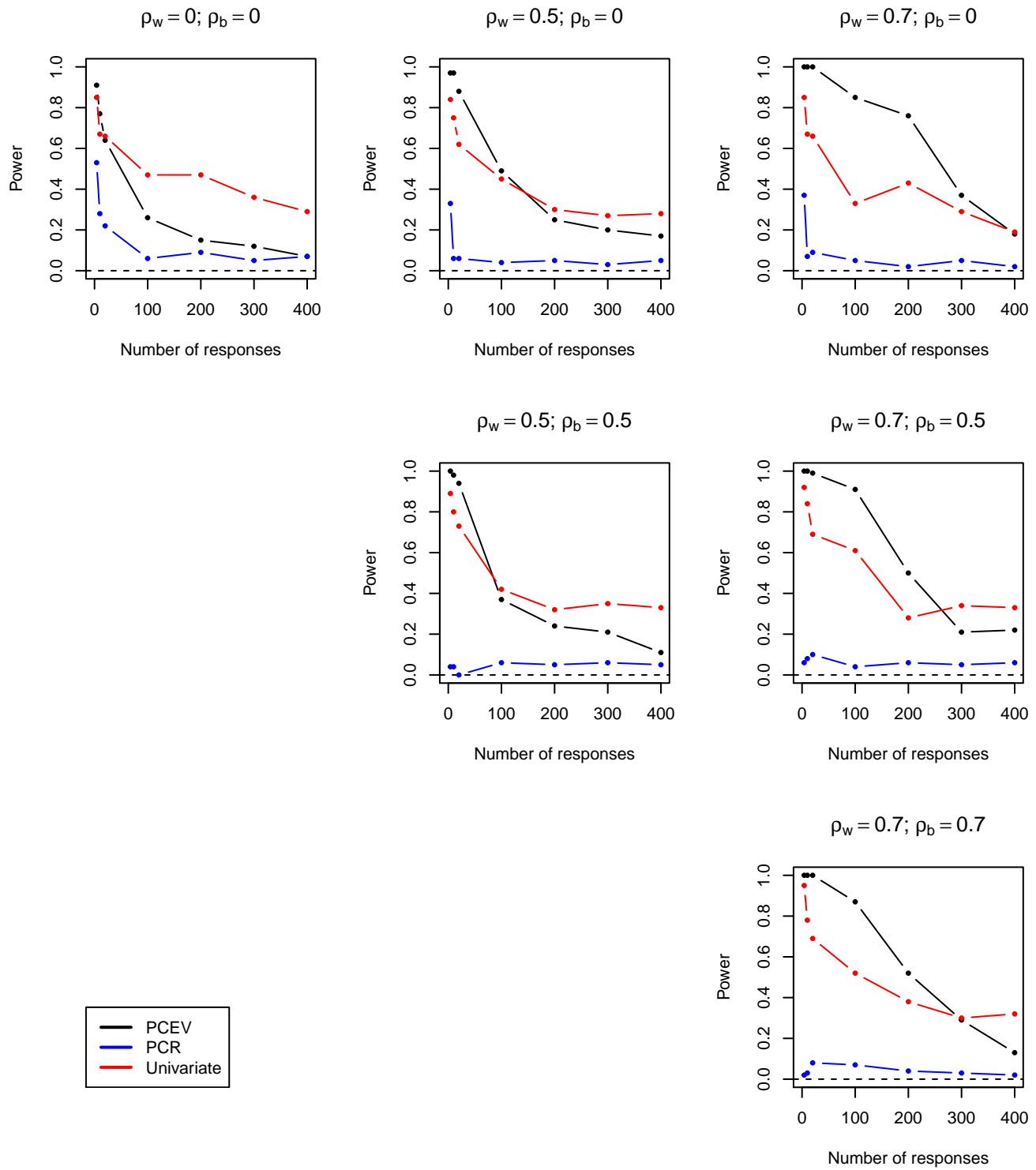
6.19 Significance level: 0.05, Heritability: 1%, Number of blocks: 10



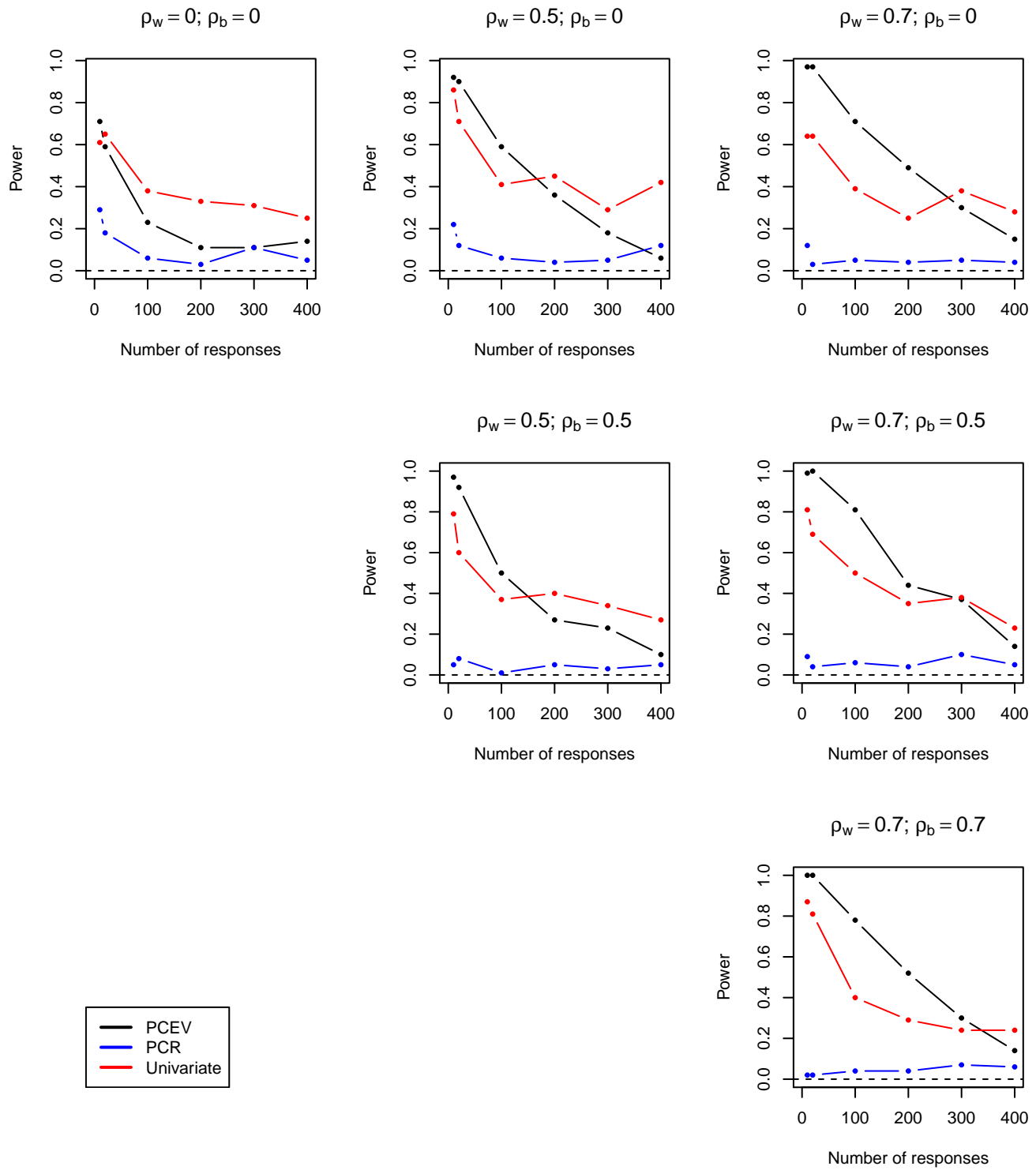
6.20 Significance level: 0.05, Heritability: 1%, Number of blocks: 20



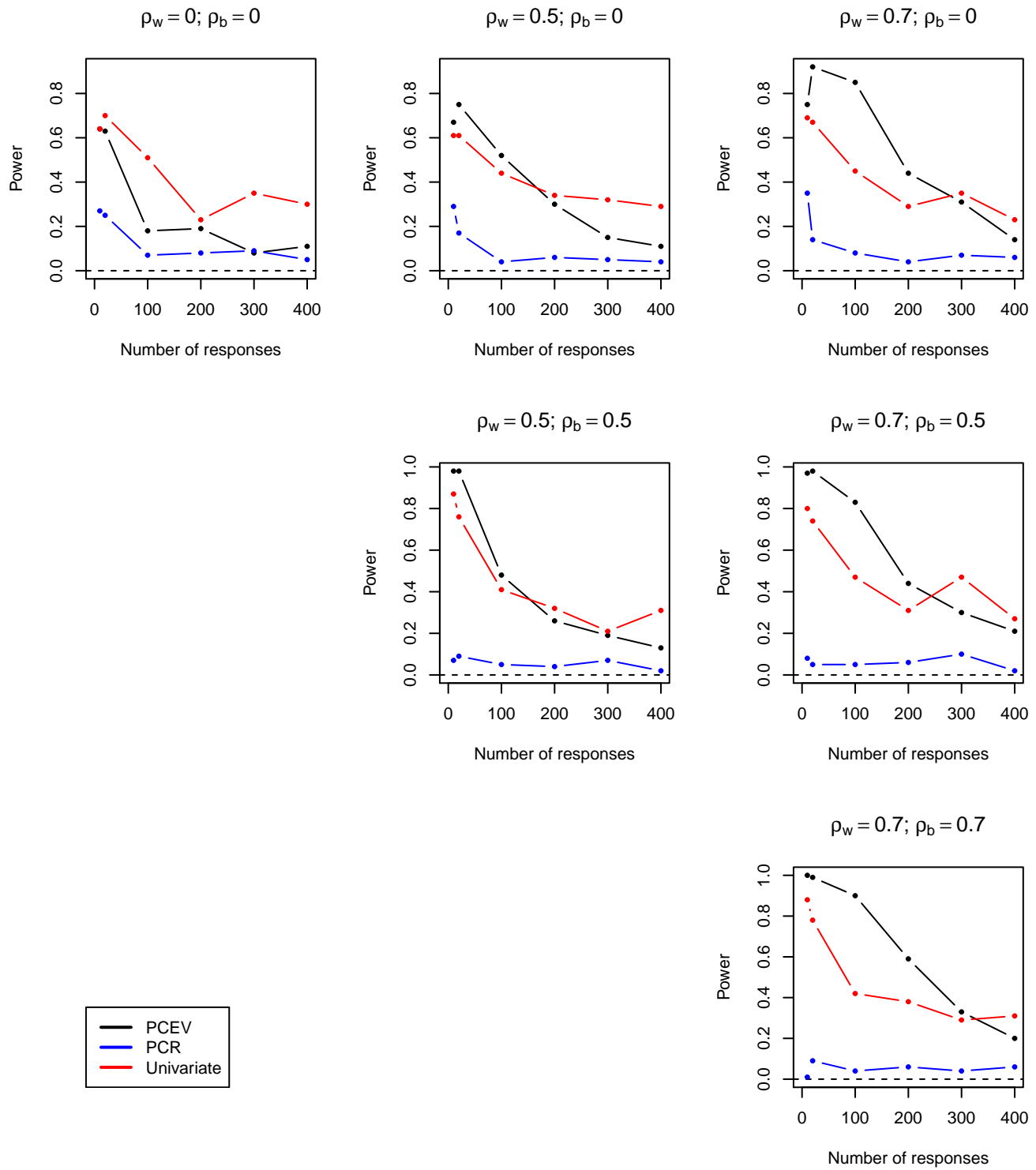
6.21 Significance level: 0.05, Heritability: 1.5%, Number of blocks: 2



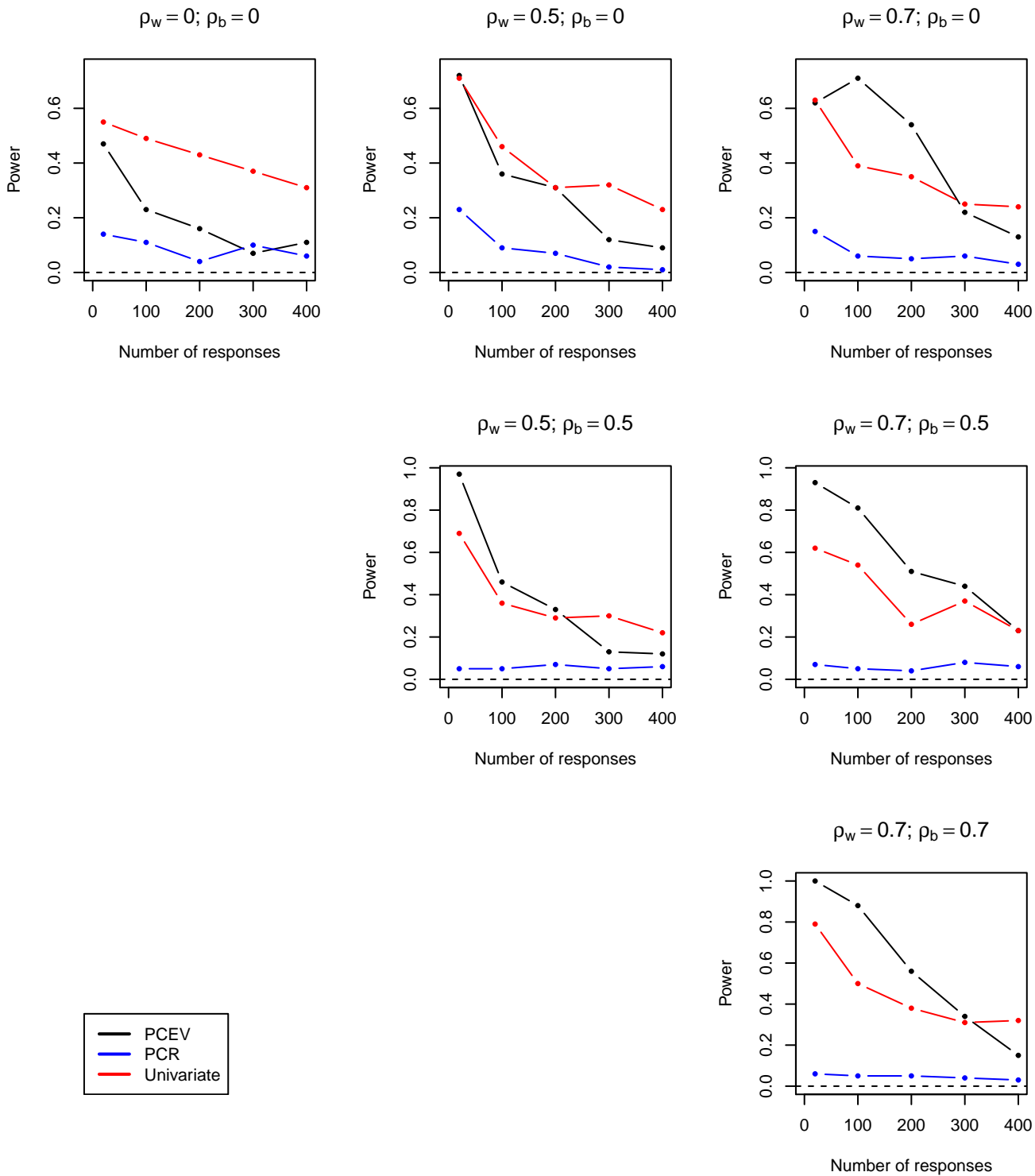
6.22 Significance level: 0.05, Heritability: 1.5%, Number of blocks: 5



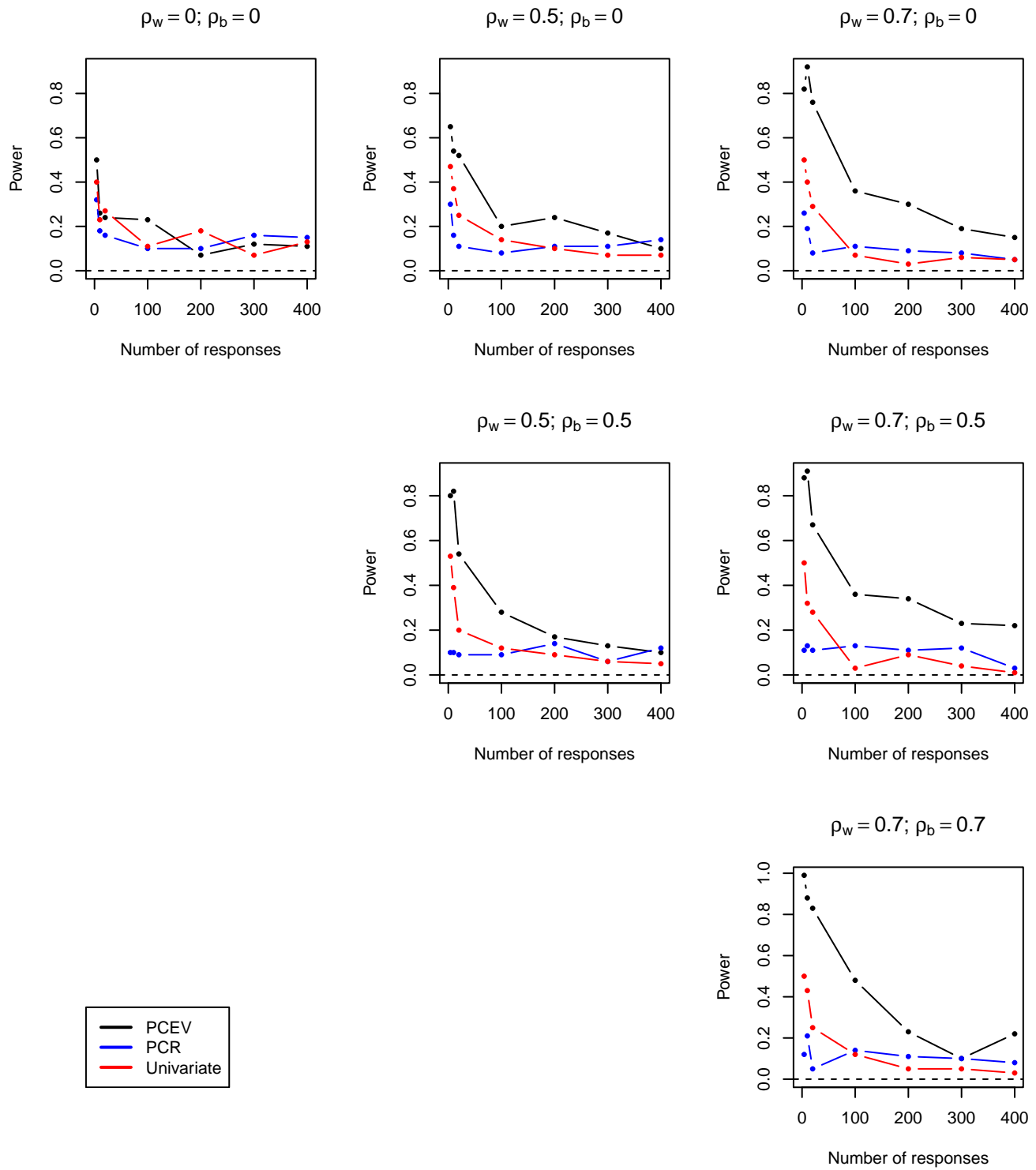
6.23 Significance level: 0.05, Heritability: 1.5%, Number of blocks: 10



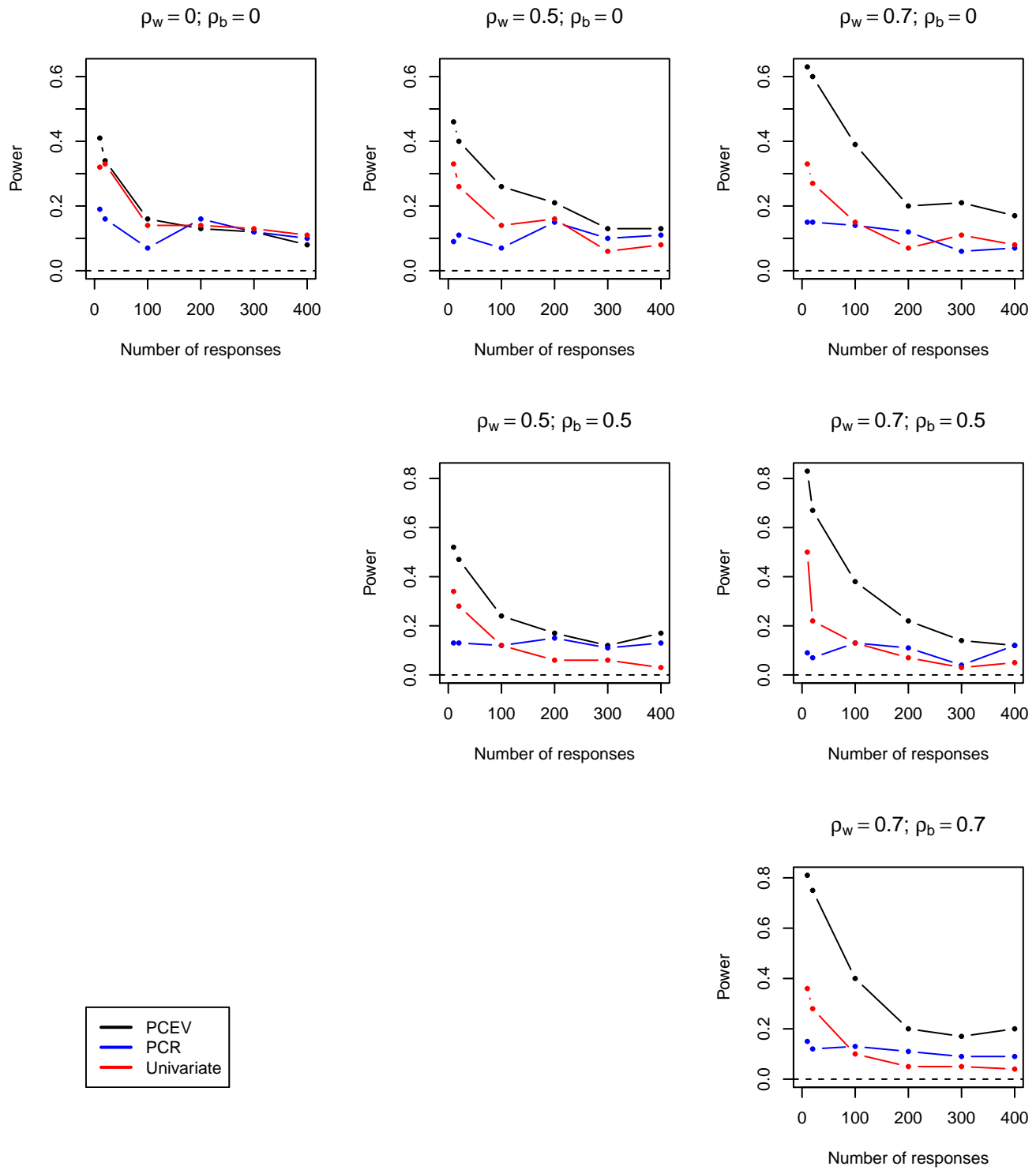
6.24 Significance level: 0.05, Heritability: 1.5%, Number of blocks: 20



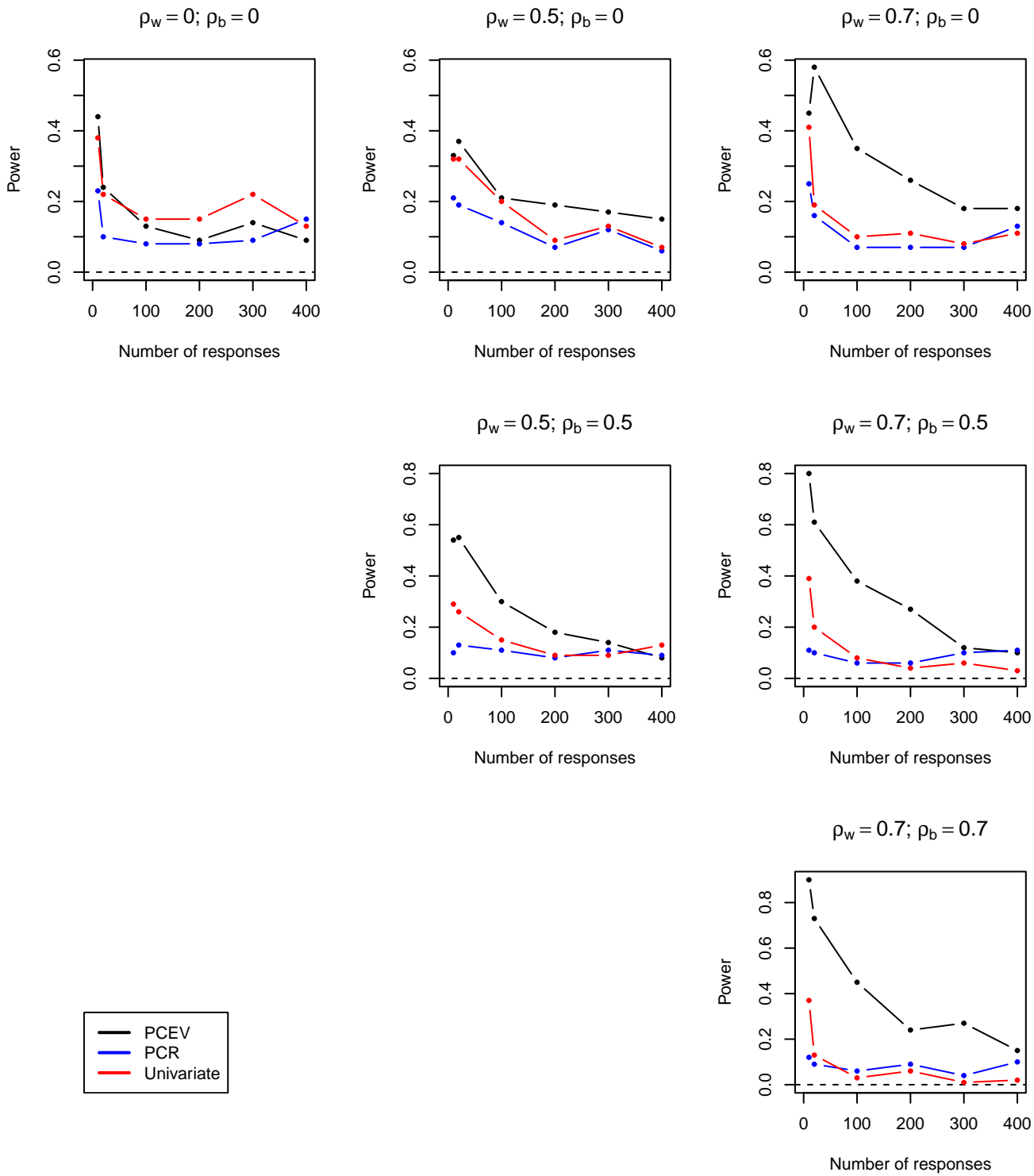
6.25 Significance level: 0.1, Heritability: 0.5%, Number of blocks: 2



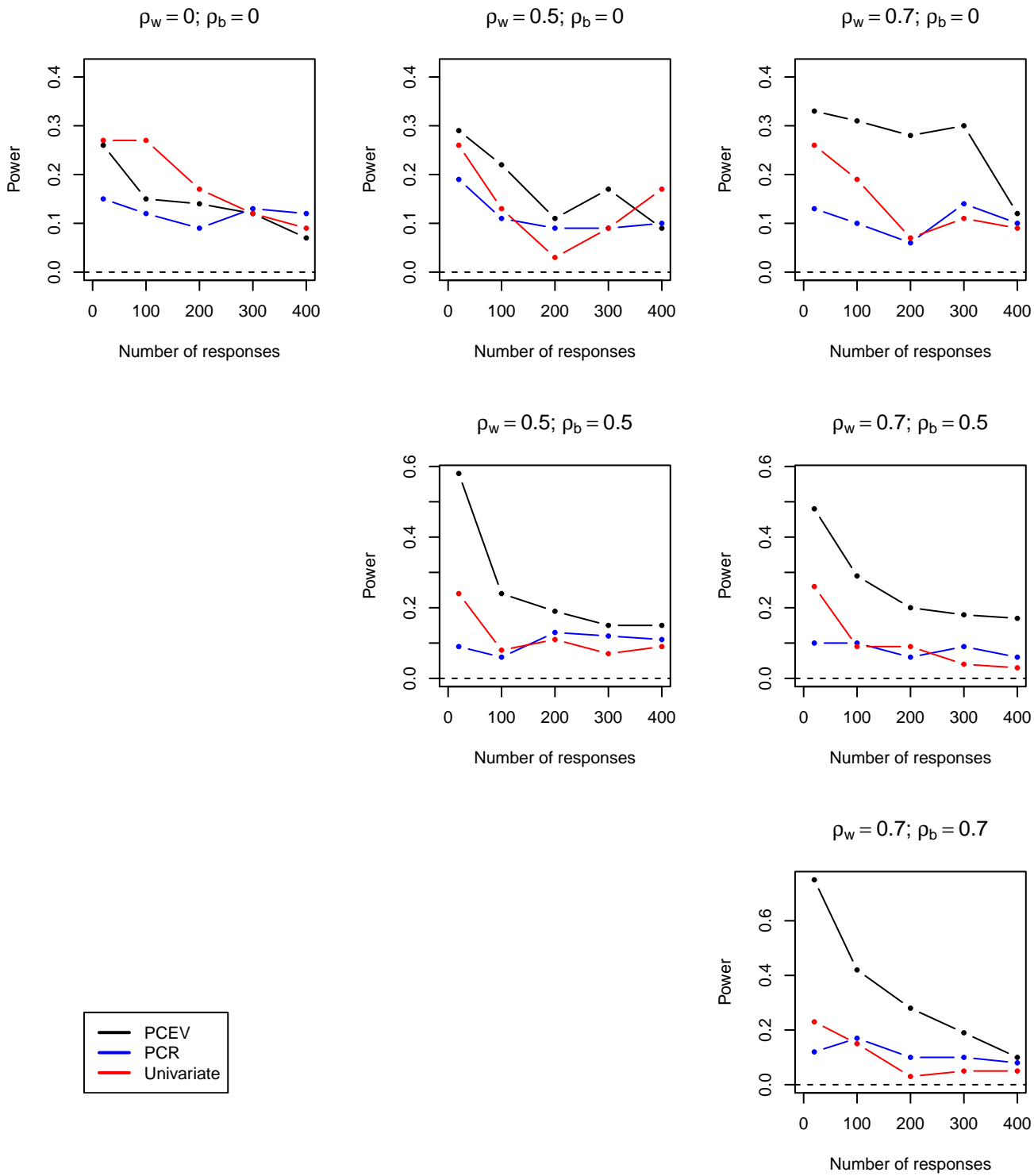
6.26 Significance level: 0.1, Heritability: 0.5%, Number of blocks: 5



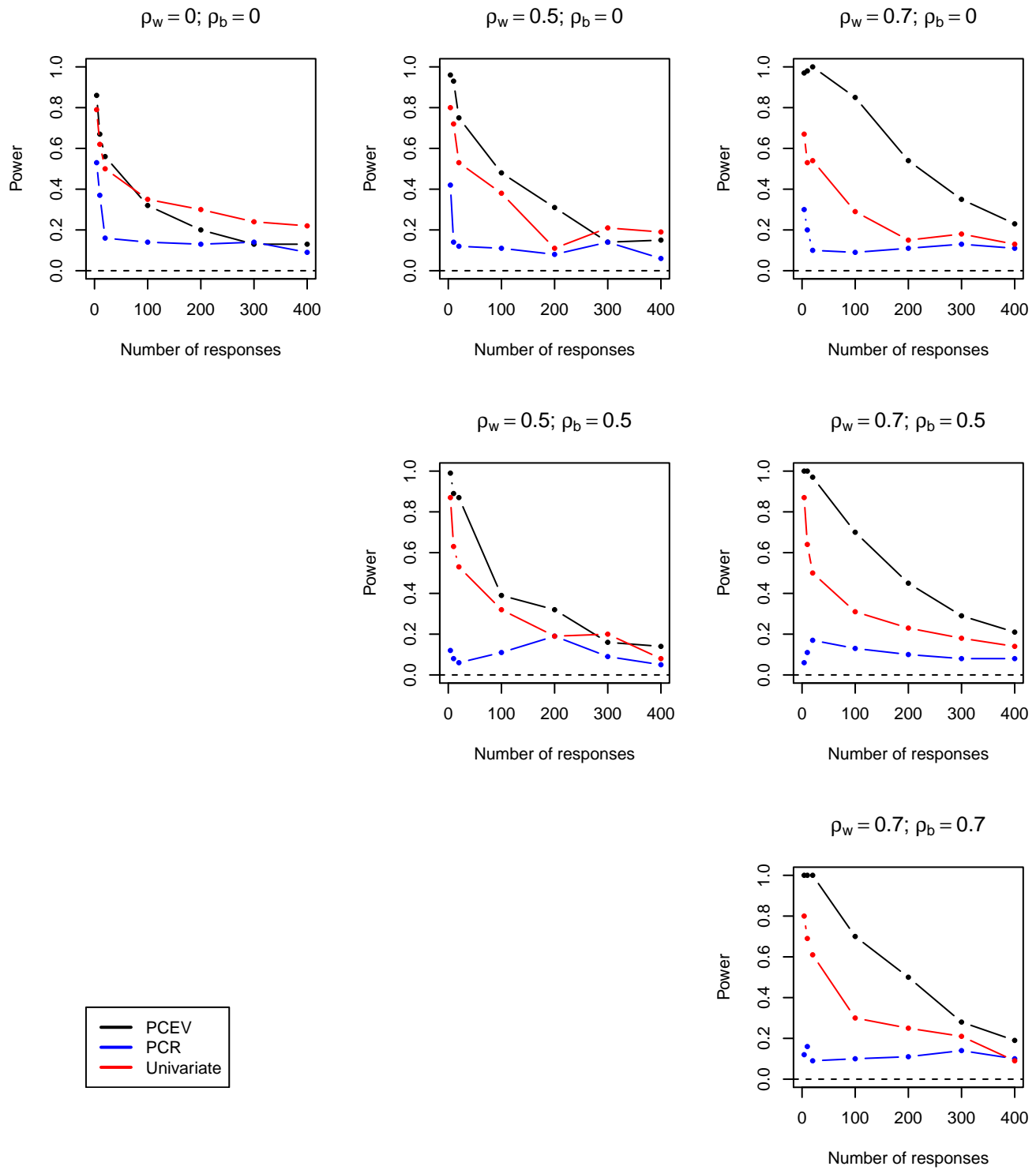
6.27 Significance level: 0.1, Heritability: 0.5%, Number of blocks: 10



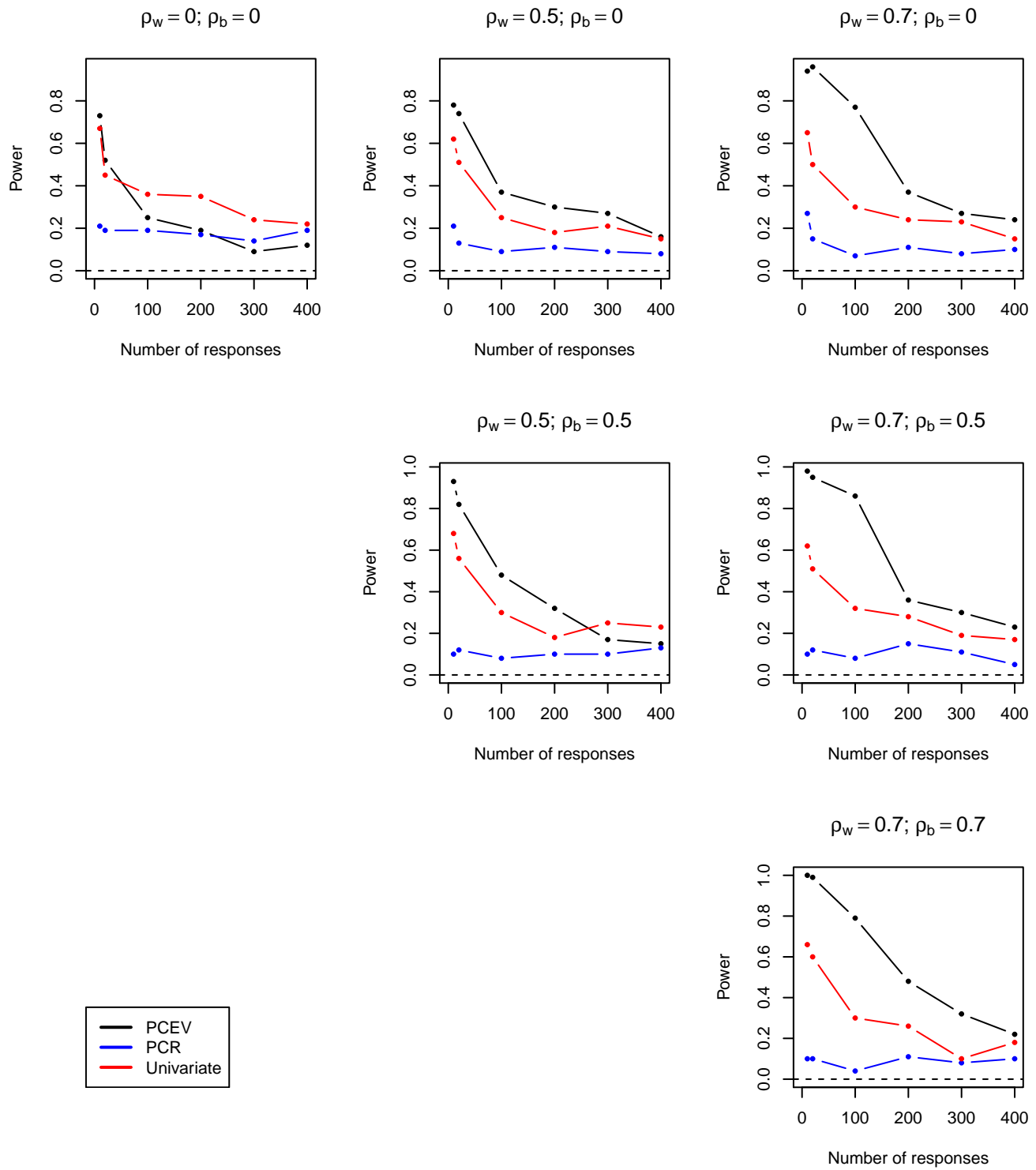
6.28 Significance level: 0.1, Heritability: 0.5%, Number of blocks: 20



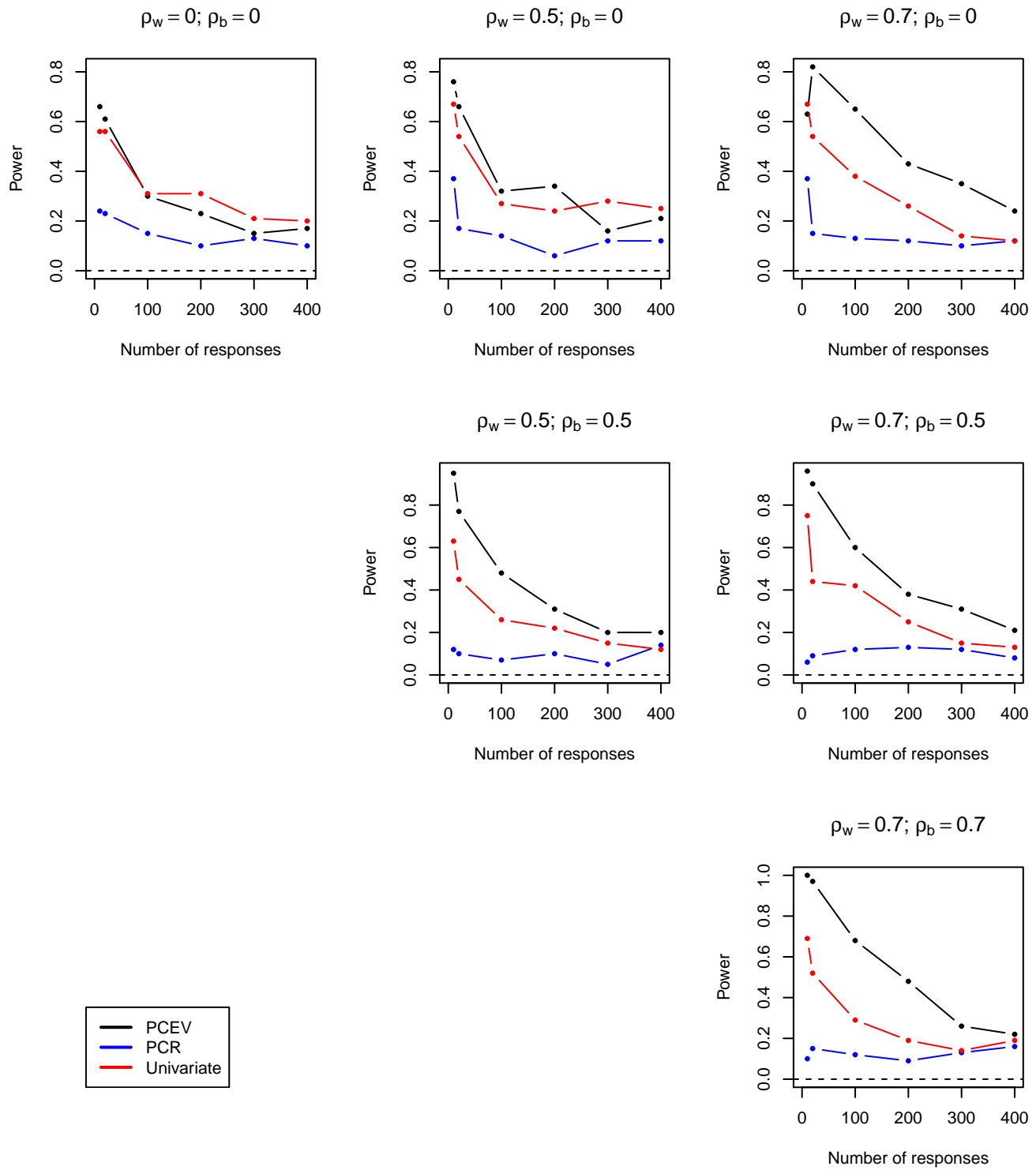
6.29 Significance level: 0.1, Heritability: 1%, Number of blocks: 2



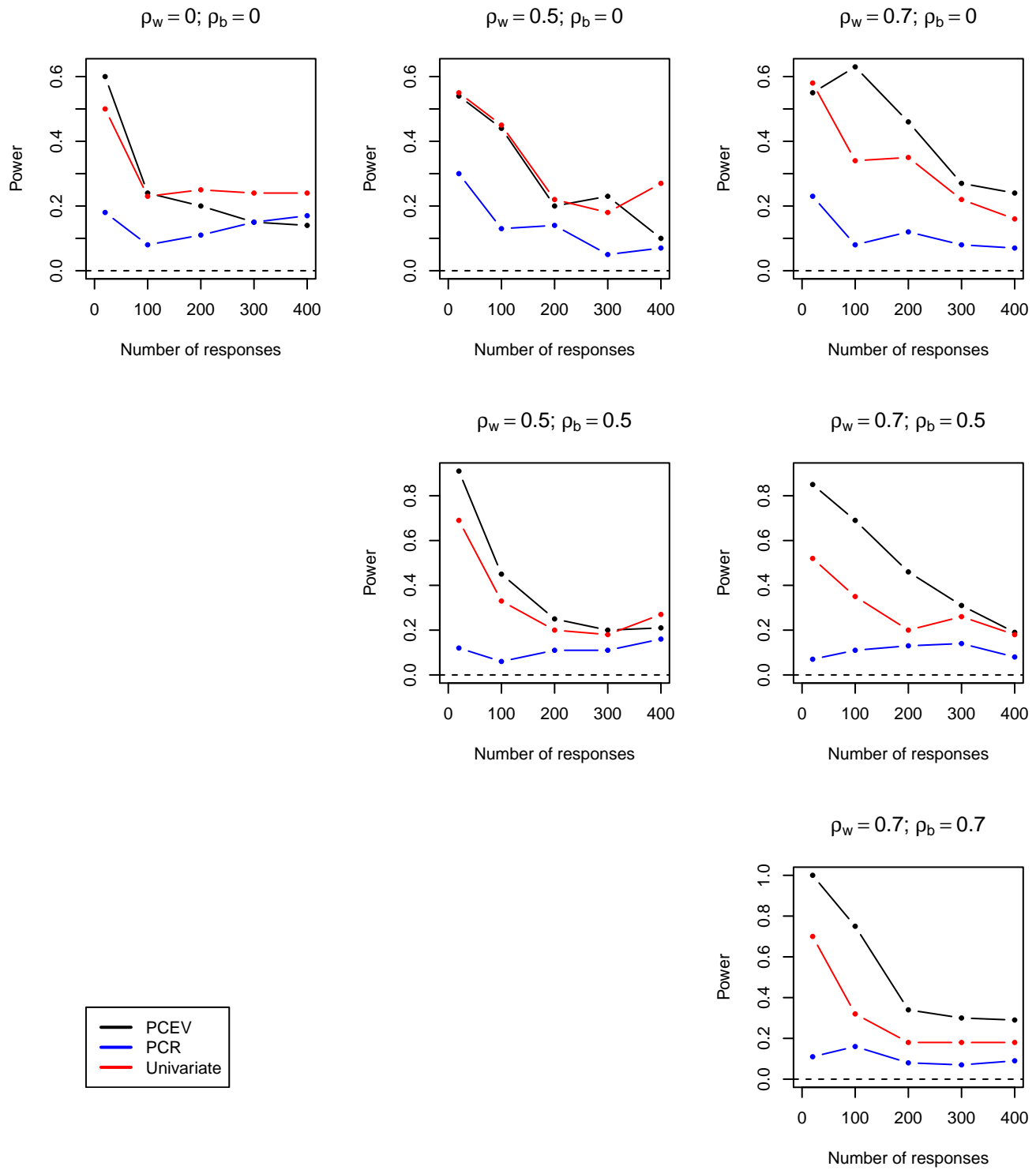
6.30 Significance level: 0.1, Heritability: 1%, Number of blocks: 5



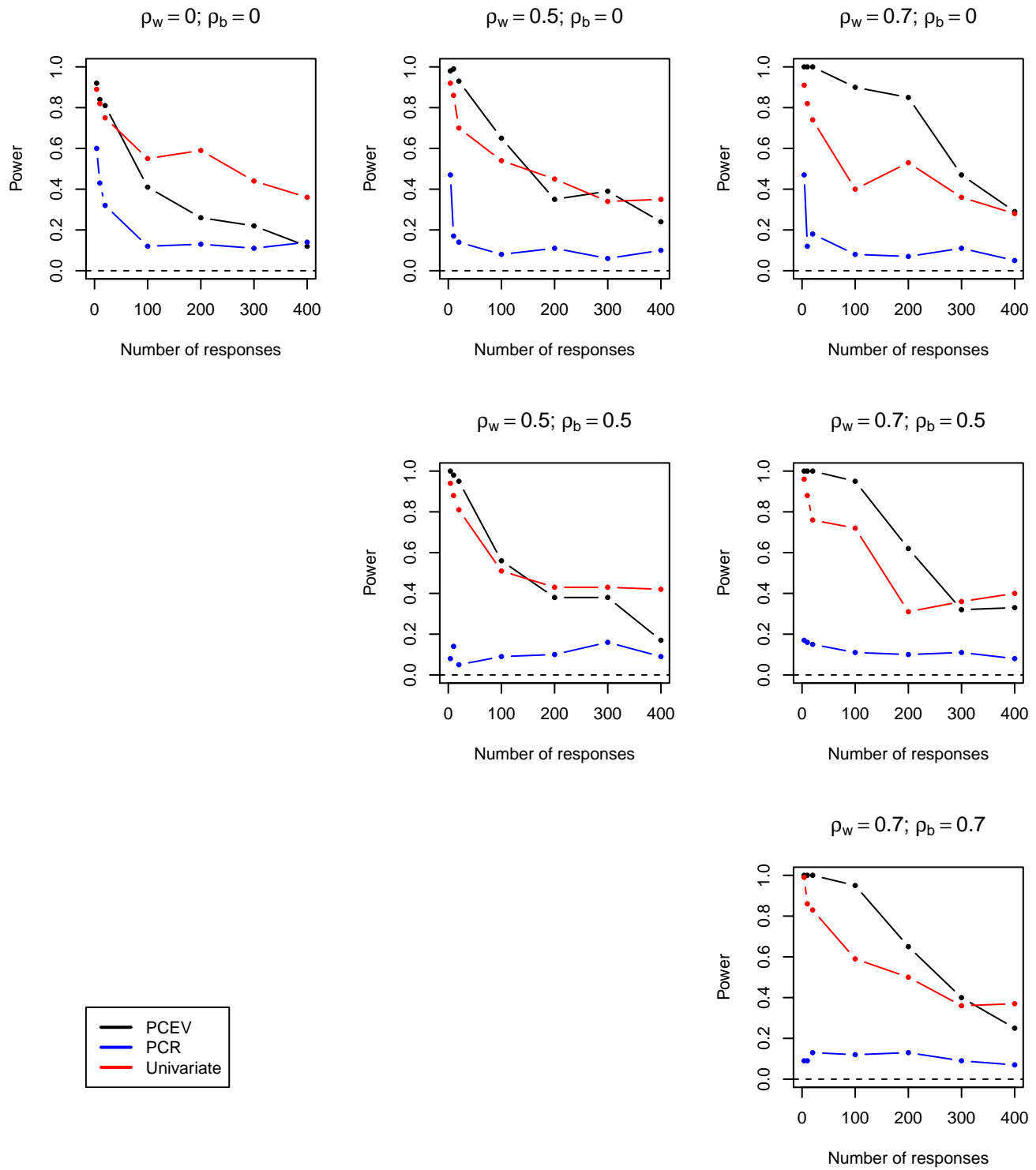
6.31 Significance level: 0.1, Heritability: 1%, Number of blocks: 10



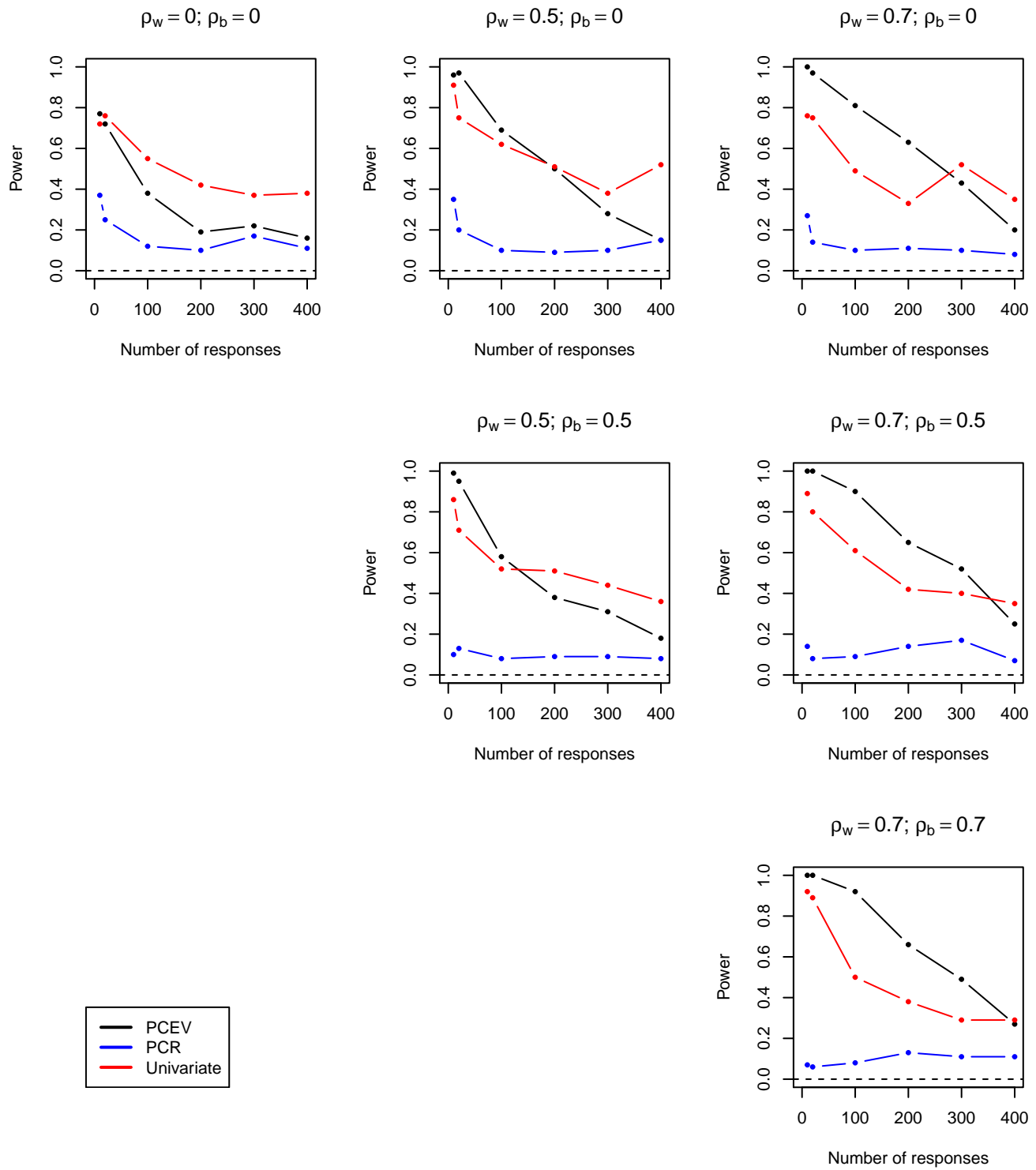
6.32 Significance level: 0.1, Heritability: 1%, Number of blocks: 20



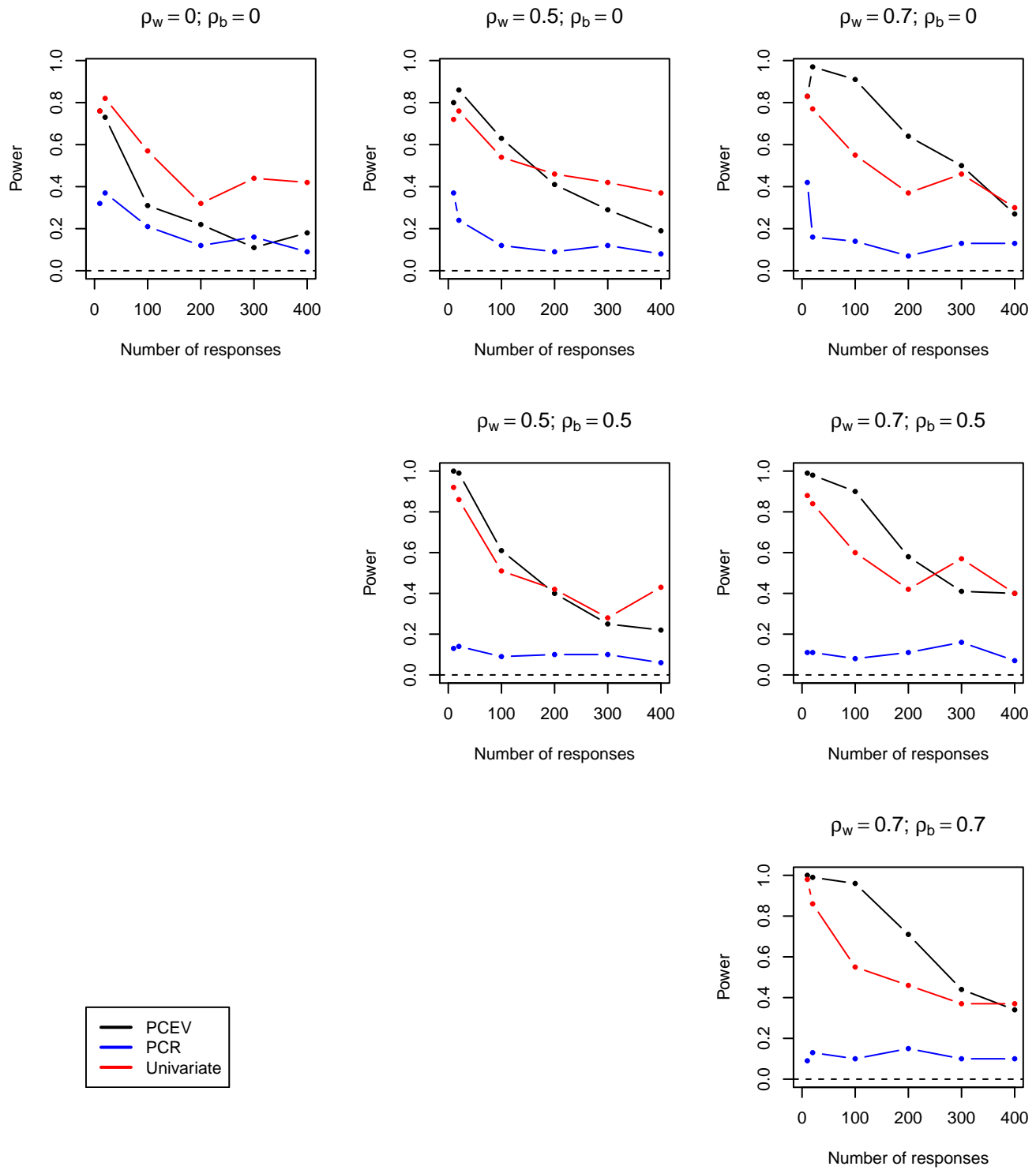
6.33 Significance level: 0.1, Heritability: 1.5%, Number of blocks: 2



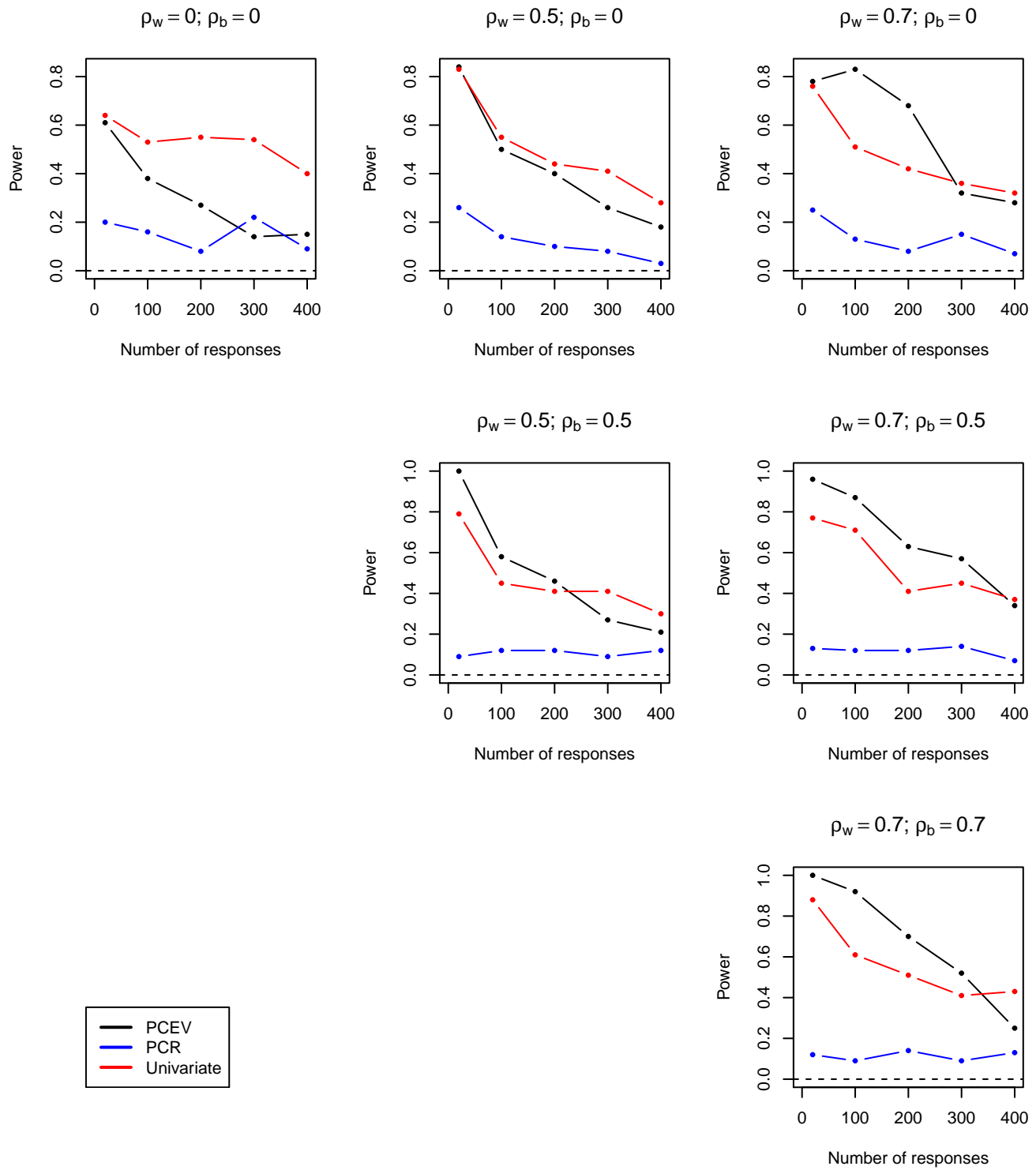
6.34 Significance level: 0.1, Heritability: 1.5%, Number of blocks: 5



6.35 Significance level: 0.1, Heritability: 1.5%, Number of blocks: 10



6.36 Significance level: 0.1, Heritability: 1.5%, Number of blocks: 20



References

Jurg Ott and Daniel Rabinowitz. A principal-components approach based on heritability for combining phenotype information. *Human heredity*, 49(2):106–111, 1999. 6

A Session Information

```
sessionInfo()

## R version 3.6.0 (2019-04-26)
## Platform: x86_64-pc-linux-gnu (64-bit)
## Running under: Pop!_OS 18.10
##
## Matrix products: default
## BLAS: /usr/lib/x86_64-linux-gnu/blas/libblas.so.3.8.0
## LAPACK: /usr/lib/x86_64-linux-gnu/lapack/liblapack.so.3.8.0
##
## locale:
##  [1] LC_CTYPE=en_CA.UTF-8      LC_NUMERIC=C
##  [3] LC_TIME=en_CA.UTF-8      LC_COLLATE=en_CA.UTF-8
##  [5] LC_MONETARY=en_CA.UTF-8  LC_MESSAGES=en_CA.UTF-8
##  [7] LC_PAPER=en_CA.UTF-8     LC_NAME=C
##  [9] LC_ADDRESS=C             LC_TELEPHONE=C
## [11] LC_MEASUREMENT=en_CA.UTF-8 LC_IDENTIFICATION=C
##
## attached base packages:
## [1] stats      graphics  grDevices  utils      datasets
## [6] methods    base
##
## other attached packages:
## [1] knitr_1.22
##
## loaded via a namespace (and not attached):
## [1] compiler_3.6.0 magrittr_1.5  formatR_1.6
## [4] tools_3.6.0     stringi_1.4.3 stringr_1.4.0
## [7] xfun_0.6        evaluate_0.13
```