

# Supplementary Material for Deep Learning on Chaos Game Representation for Proteins

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## Abstract

This section contains the AUCs for the test- training splits for the best hidden layer and FCGR configuration (Figure 1 and Figure 2), the mean errors (Figure 3 and Figure 4) and  $\langle \phi, \delta \rangle$  diagrams [Armano and Giuliani, 2018] for the encodings used in Heider et al. [2011] for all drugs (Figure 5), as well as for the CGR encoding for all configurations used in the current study (left column of Figure 7 - Figure 33). The difference between the average FCGR of positive and negative sequences in the datasets are shown in the middle column of Figure 7 to Figure 33, and the significance of the differences in log(p) values as calculated using a Bonferroni-corrected t-test in the right column. Blue pixels are significantly different between positively and negatively labeled sequences. Gray pixels contain no values or zeros.

## References

- Giuliano Armano and Alessandro Giuliani. A two-tiered 2d visual tool for assessing classifier performance. *Information Sciences*, jun 2018. doi: 10.1016/j.ins.2018.06.052. URL <https://doi.org/10.1016%2Fj.ins.2018.06.052>.
- Dominik Heider, Jens Verheyen, and Daniel Hoffmann. Machine learning on normalized protein sequences. *BMC research notes*, 4(1):94, 2011.
- Dominik Heider and Daniel Hoffmann. Interpol: An r package for preprocessing of protein sequences. *BioData mining*, 4(1):16, 2011.

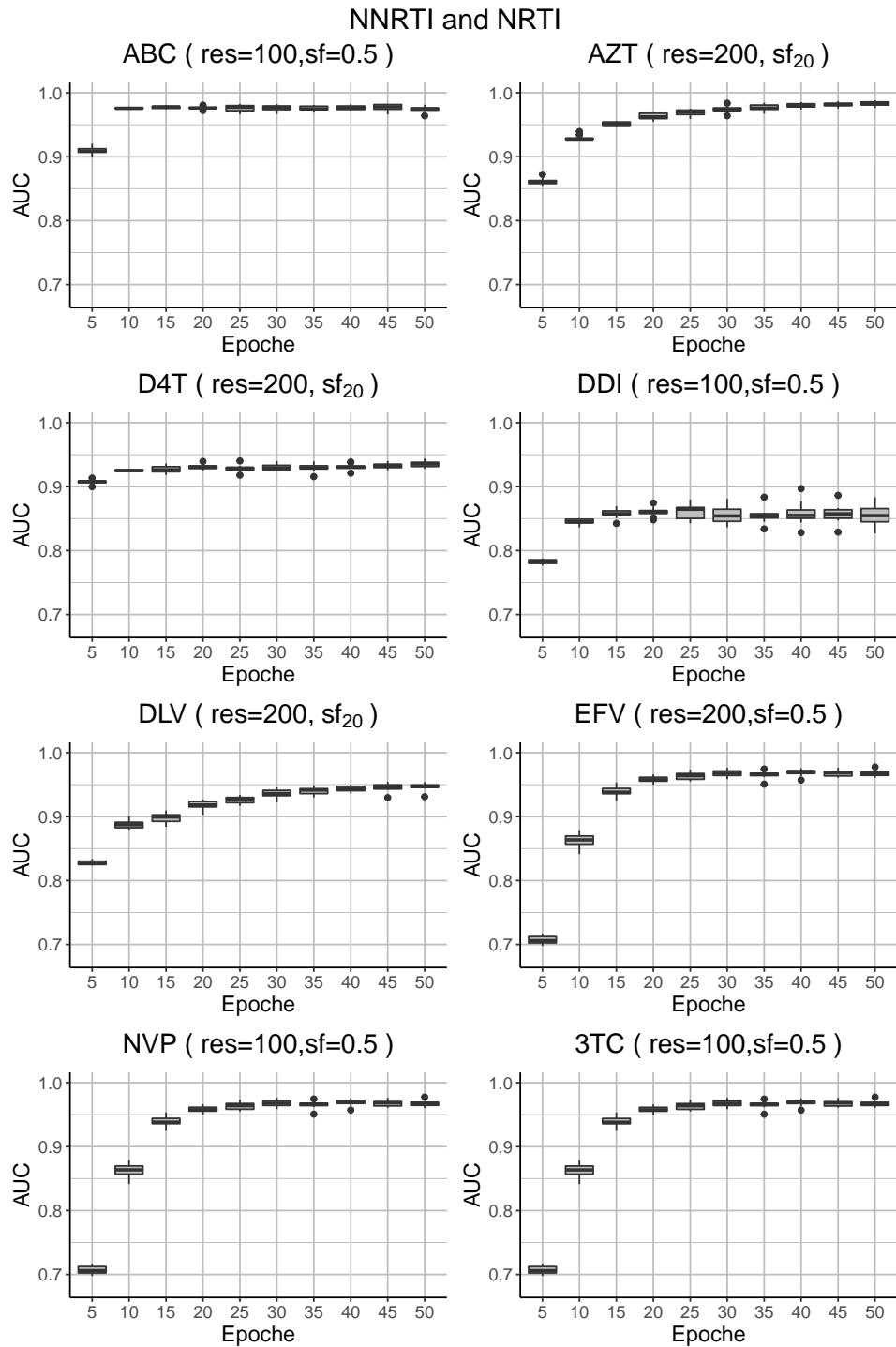


Figure 1: AUCs of NNRTIs and NRTIs for test- trainingsplits within best hiddenlayer and FCGR configurations

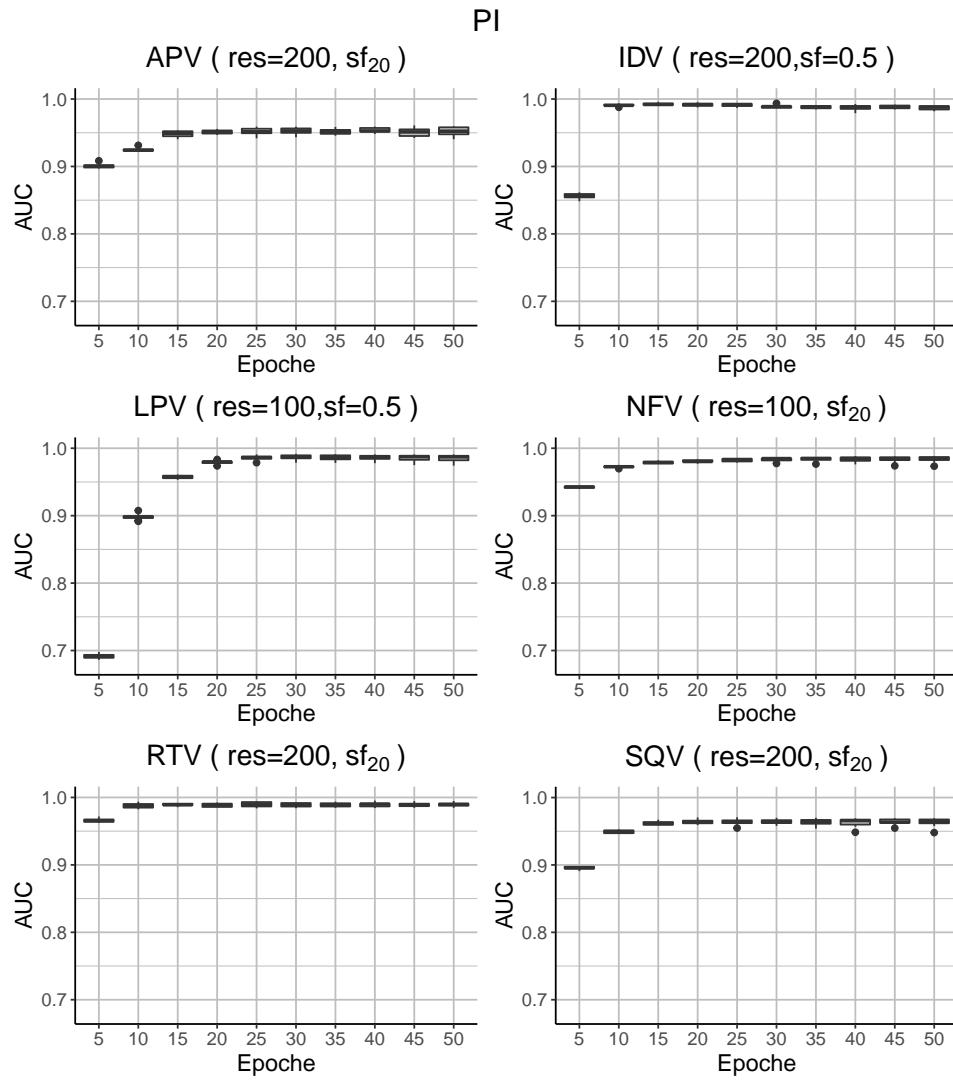


Figure 2: AUCs of PIs for test- trainingsplits within best hiddenlayer and FCGR configurations

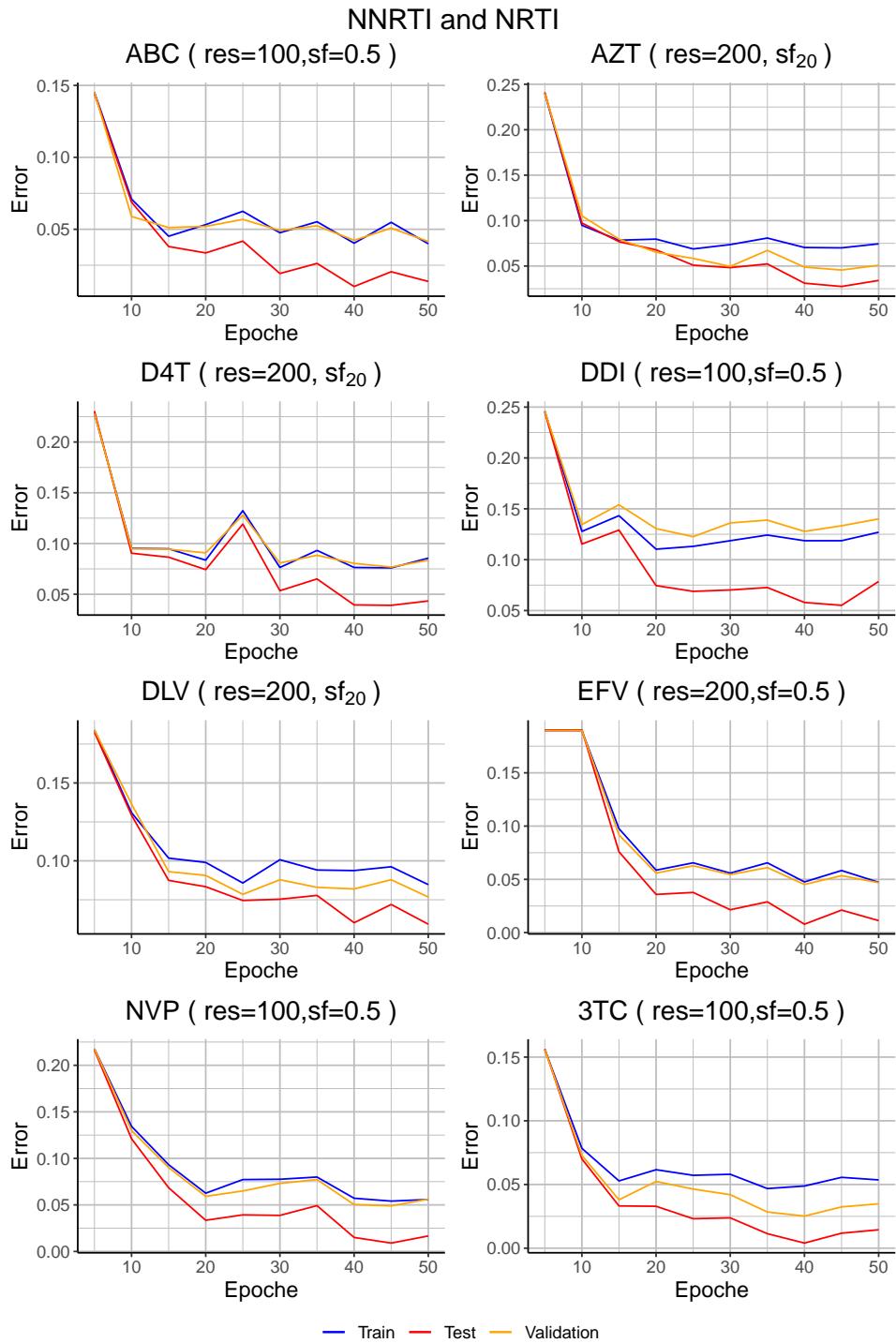


Figure 3: Mean error of NNRTIs and NRTIs for test- trainingsplits within best hiddenlayer and FCGR configurations

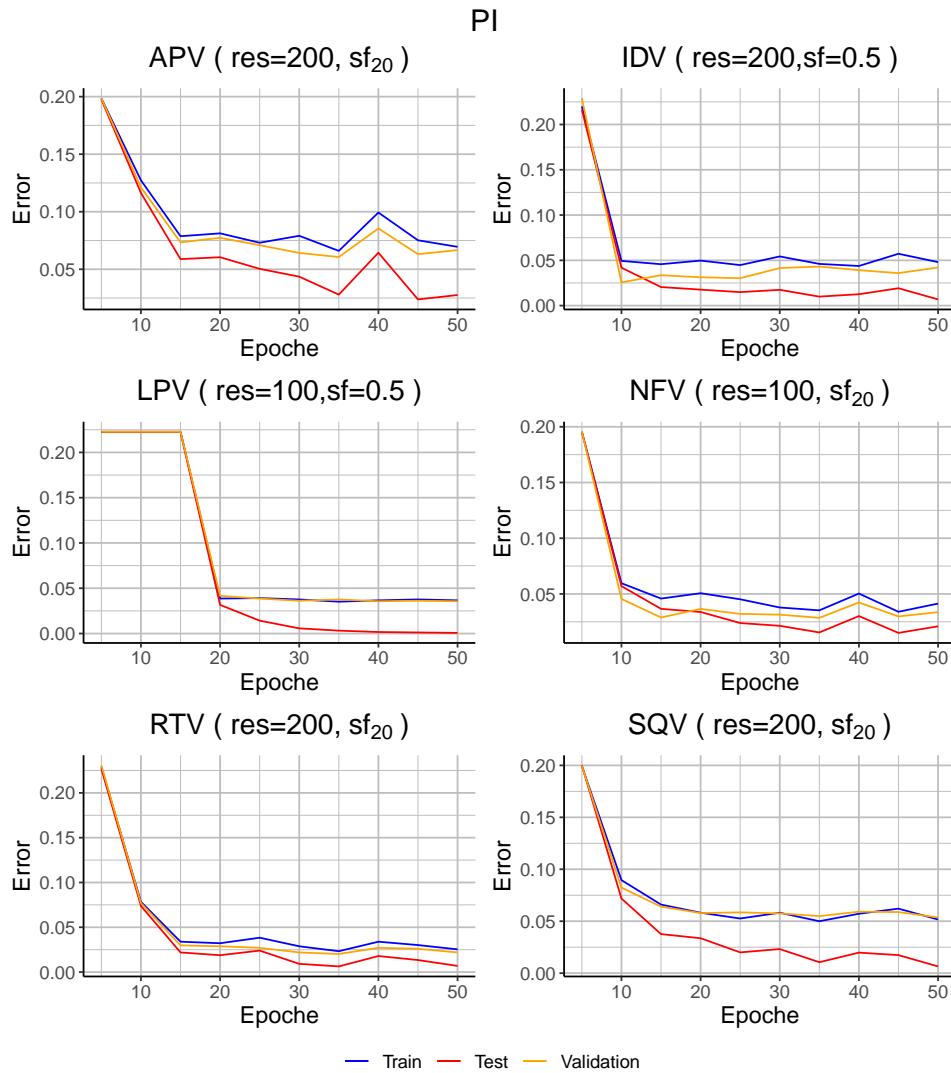


Figure 4: Mean error of PIs for test- trainingsplits within best hiddenlayer and FCGR configurations

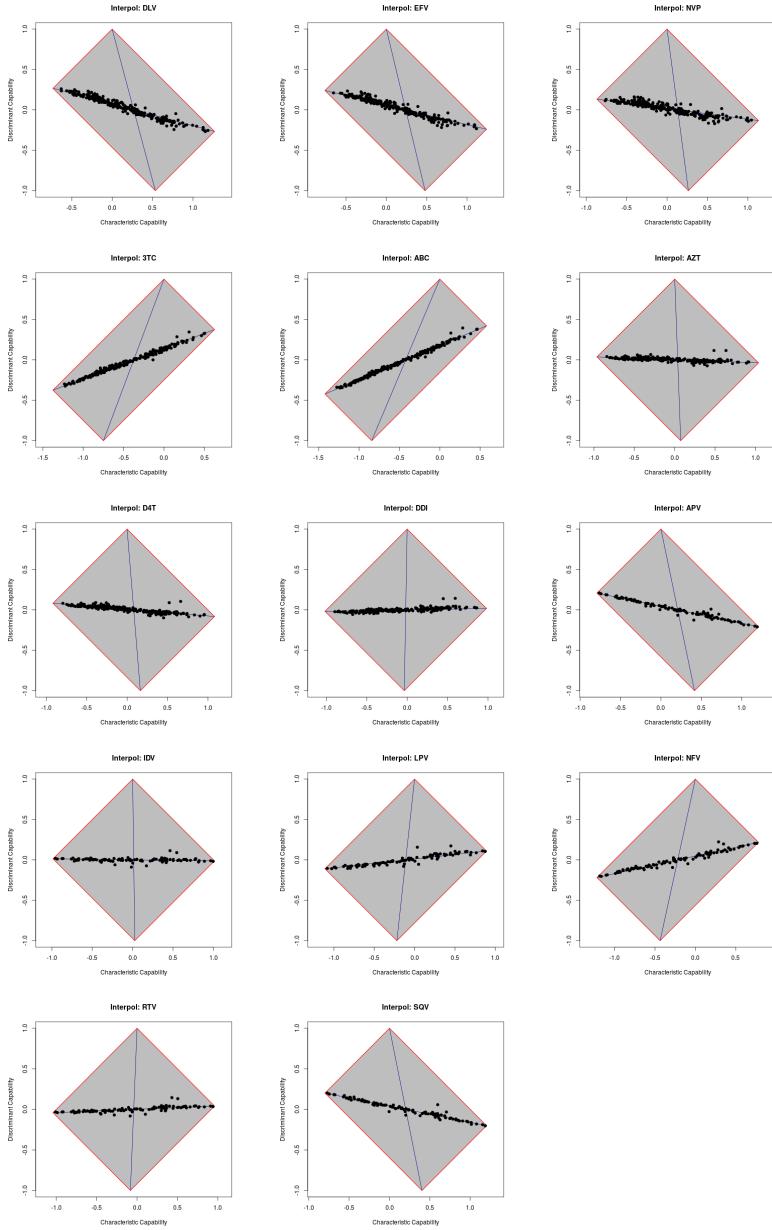


Figure 5:  $\langle \phi, \delta \rangle$  diagrams for feature encodings calculated using the R package Interpol [Heider and Hoffmann, 2011] as described in Heider et al. [2011]

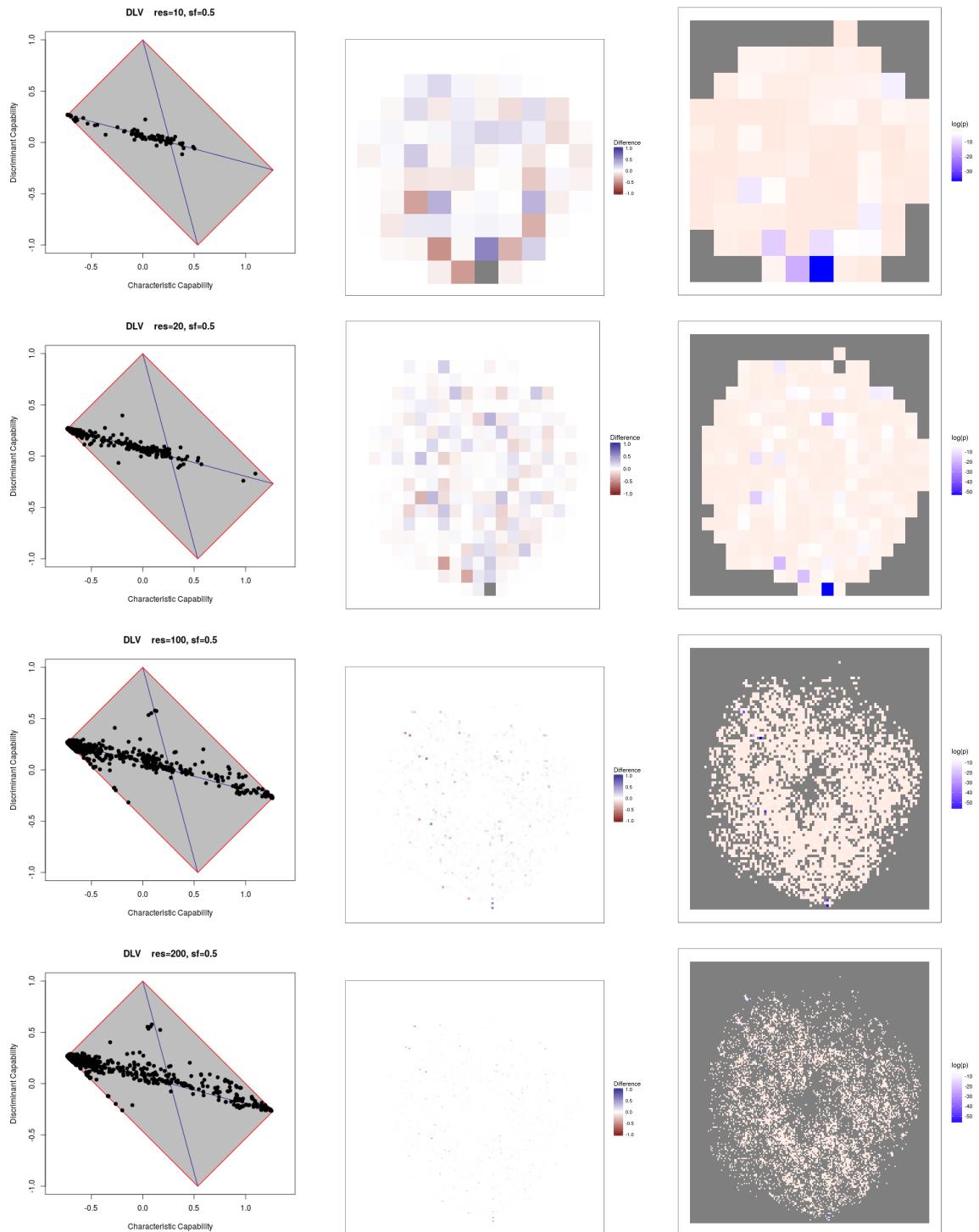


Figure 6: DLV,  $sf = 0.5$

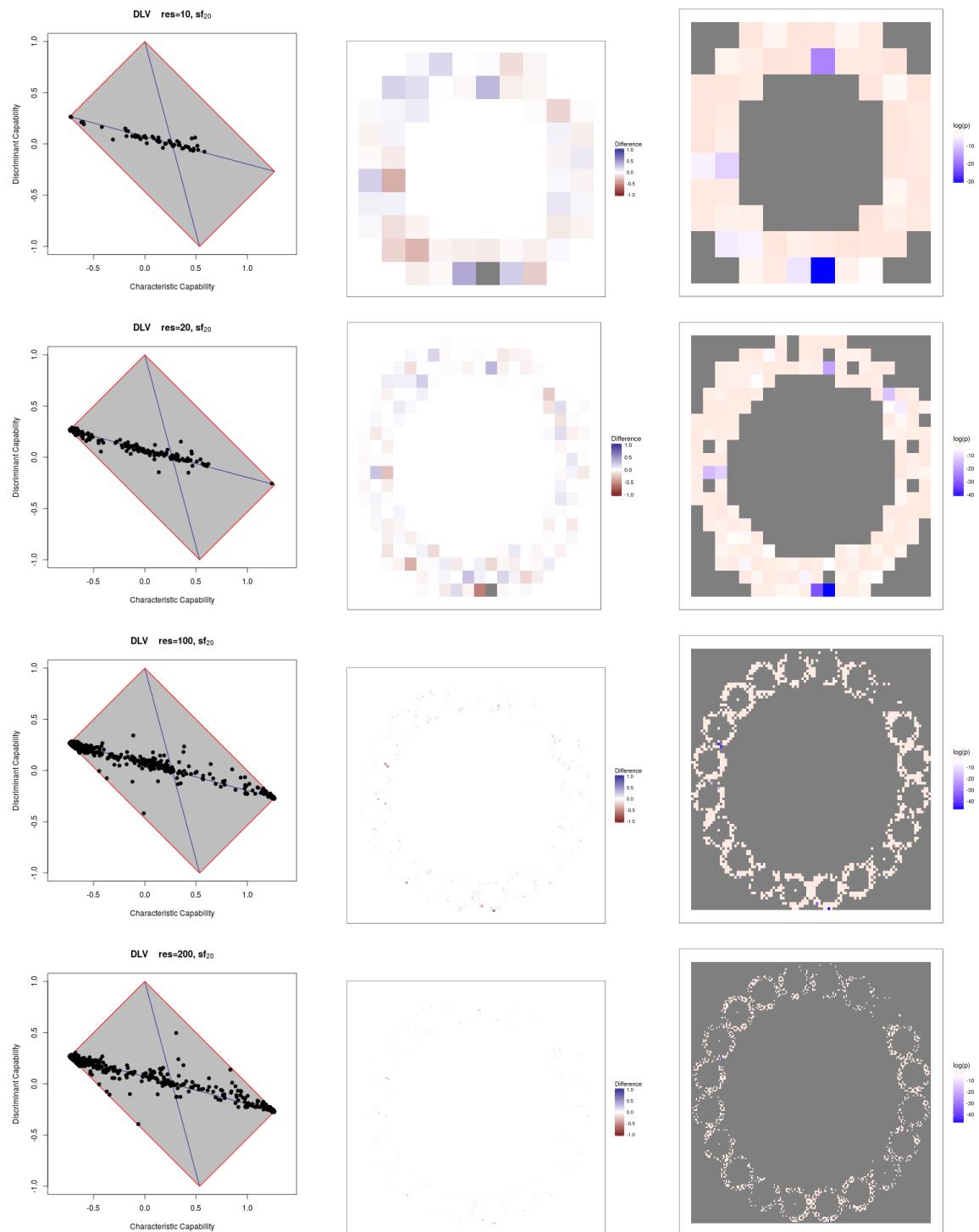


Figure 7: DLV,  $sf_{20}$

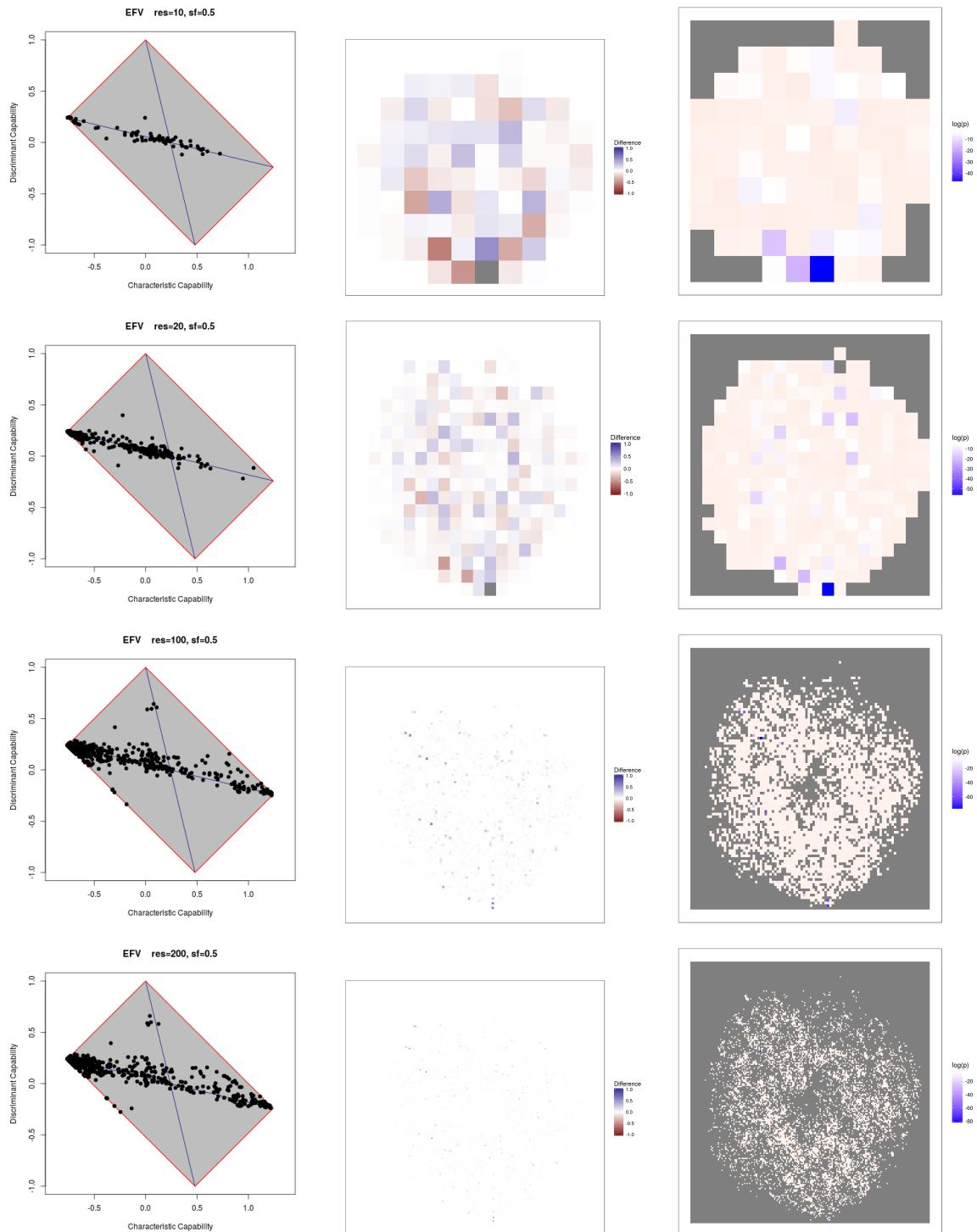


Figure 8: EFV,  $sf = 0.5$

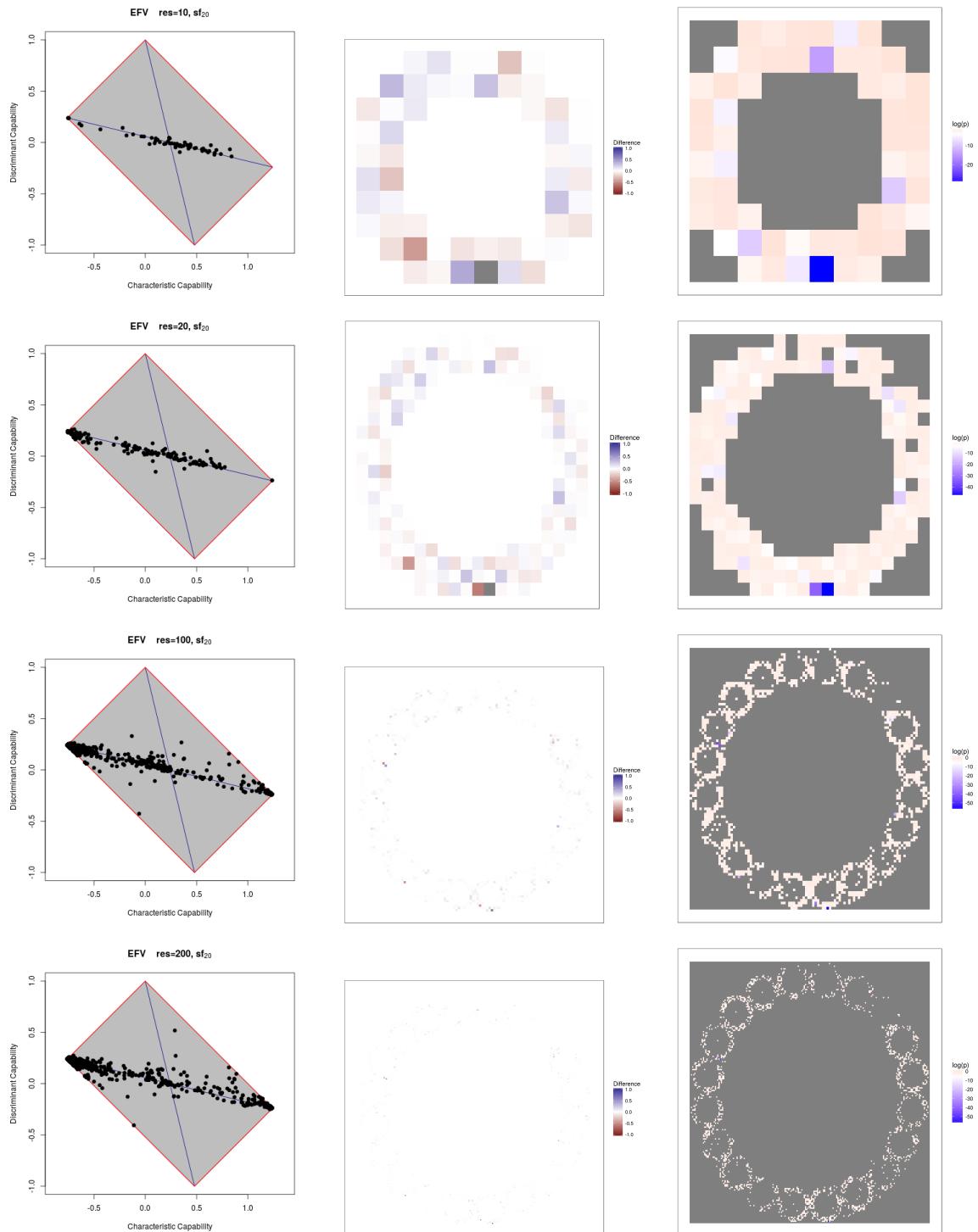


Figure 9: EFV,  $sf_{20}$

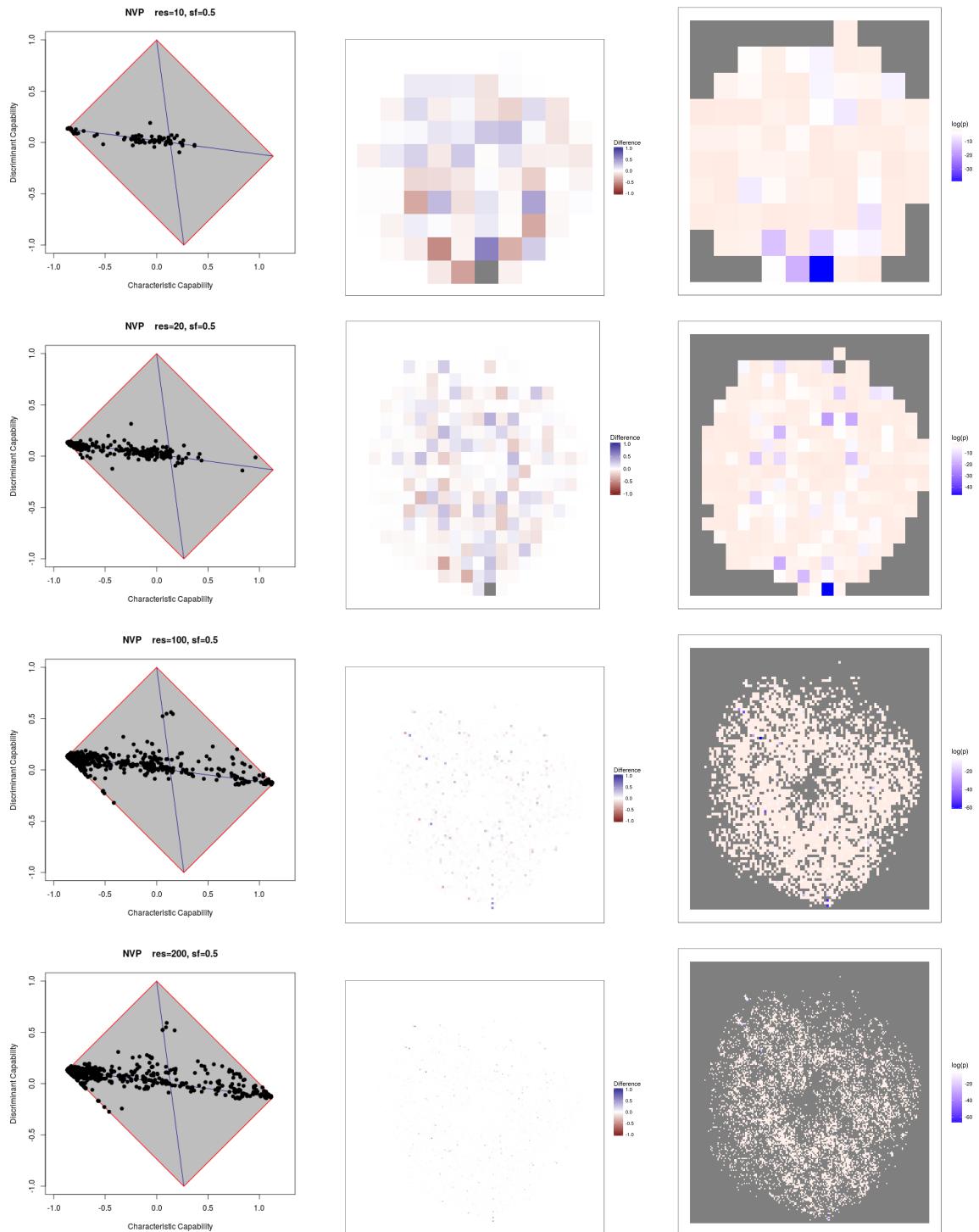


Figure 10: NVP,  $sf = 0.5$

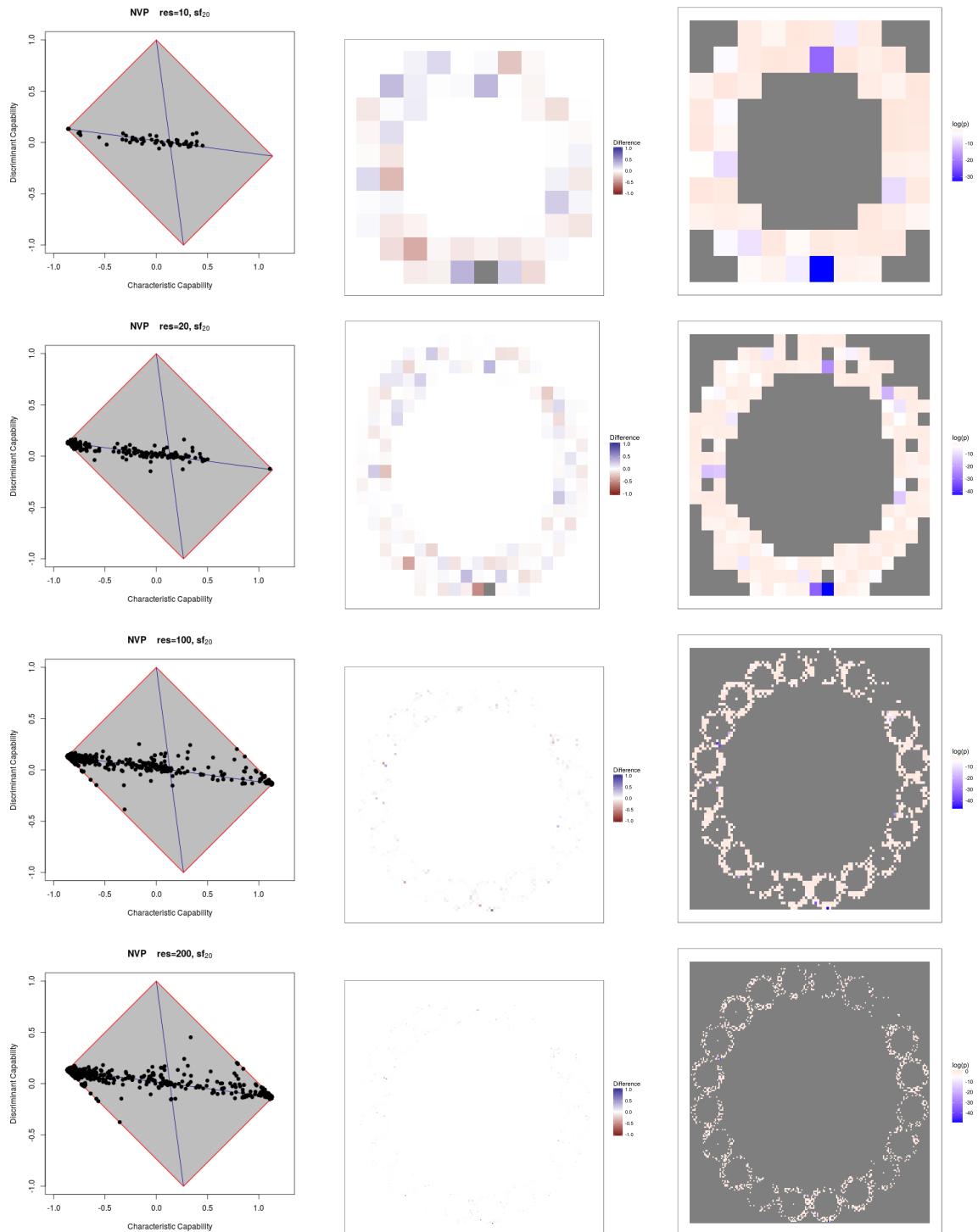


Figure 11: NFV,  $sf_{20}$

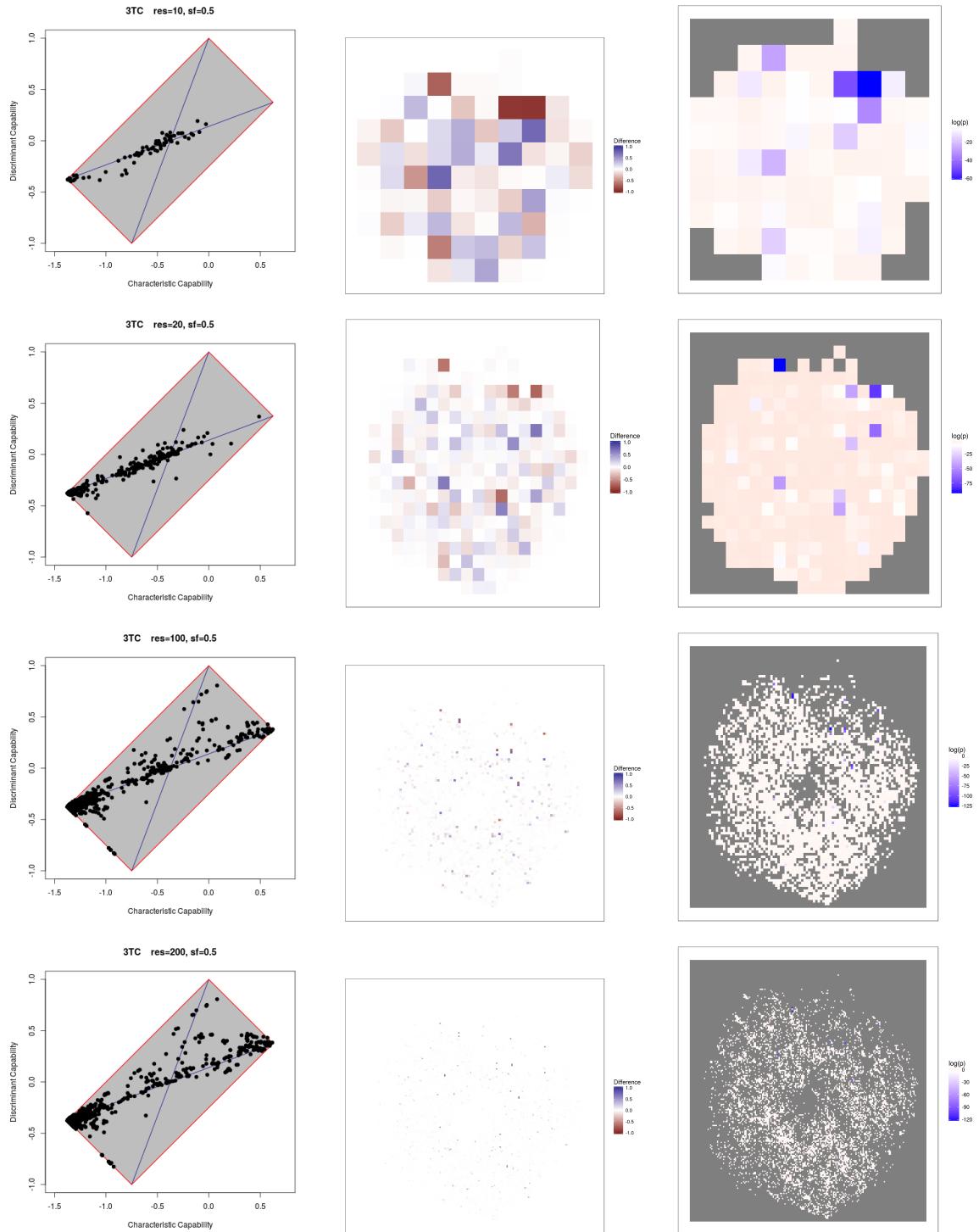


Figure 12: 3TC,  $sf = 0.5$

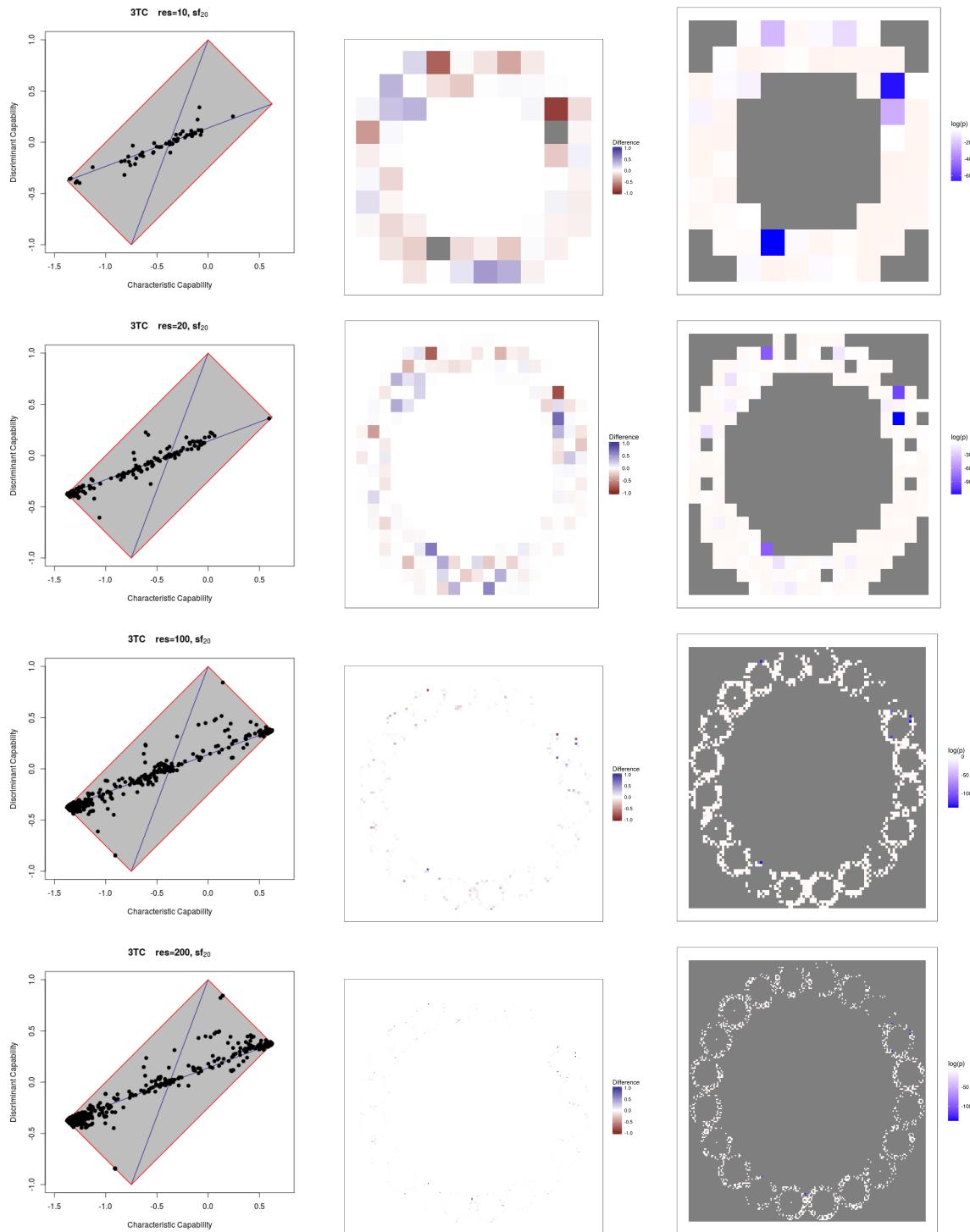


Figure 13: 3TC,  $sf_{20}$

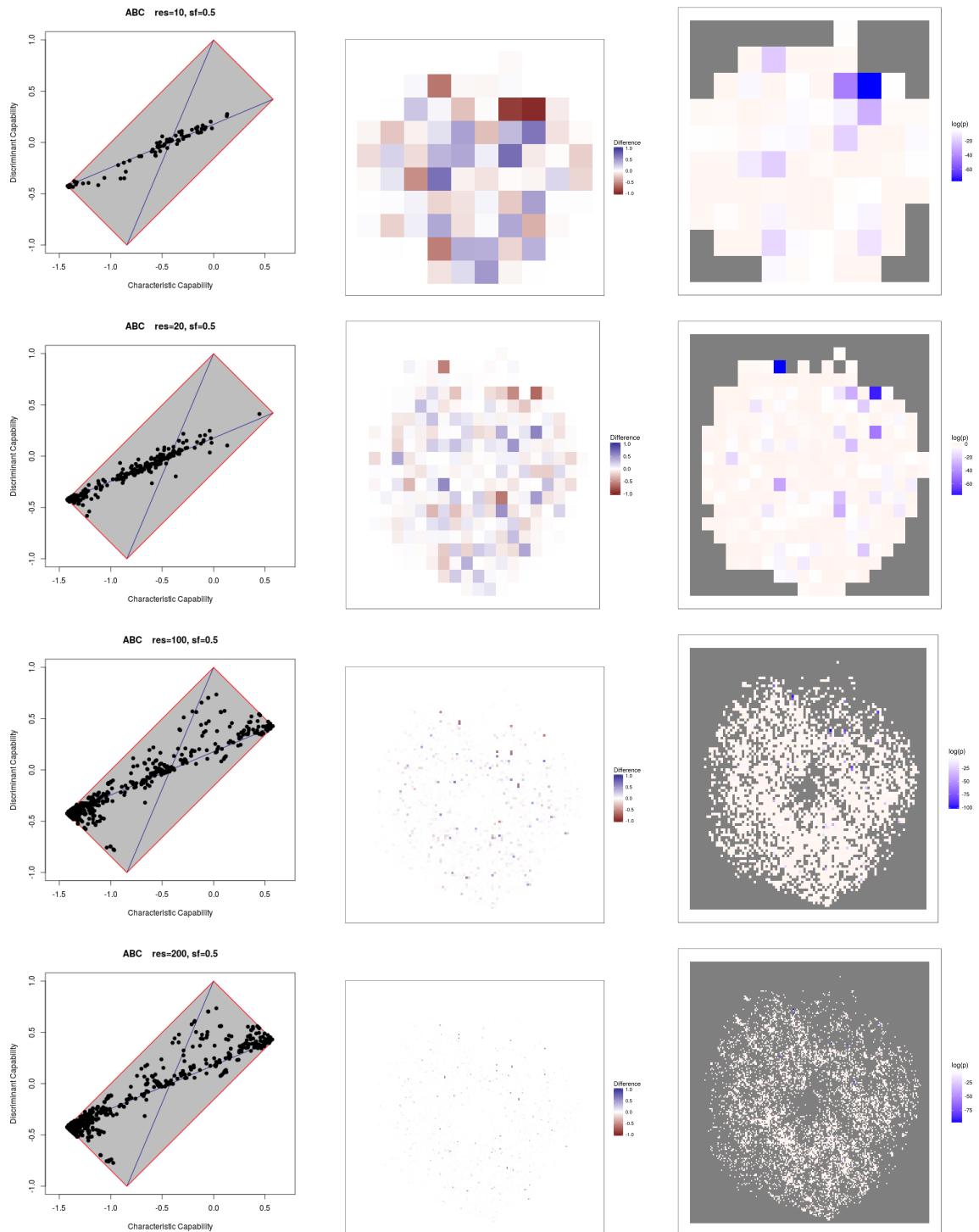


Figure 14: ABC,  $sf = 0.5$

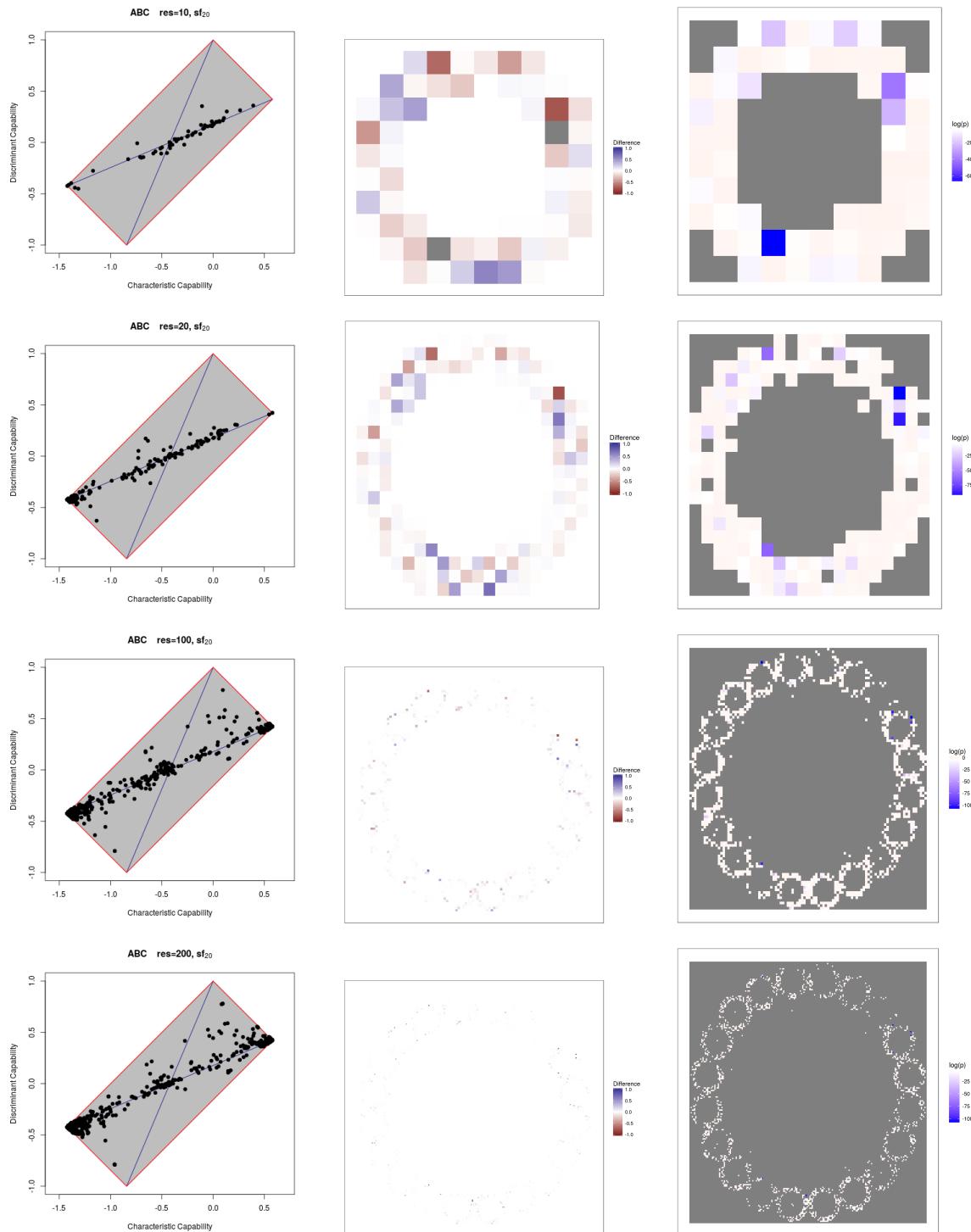


Figure 15: ABC,  $sf_{20}$

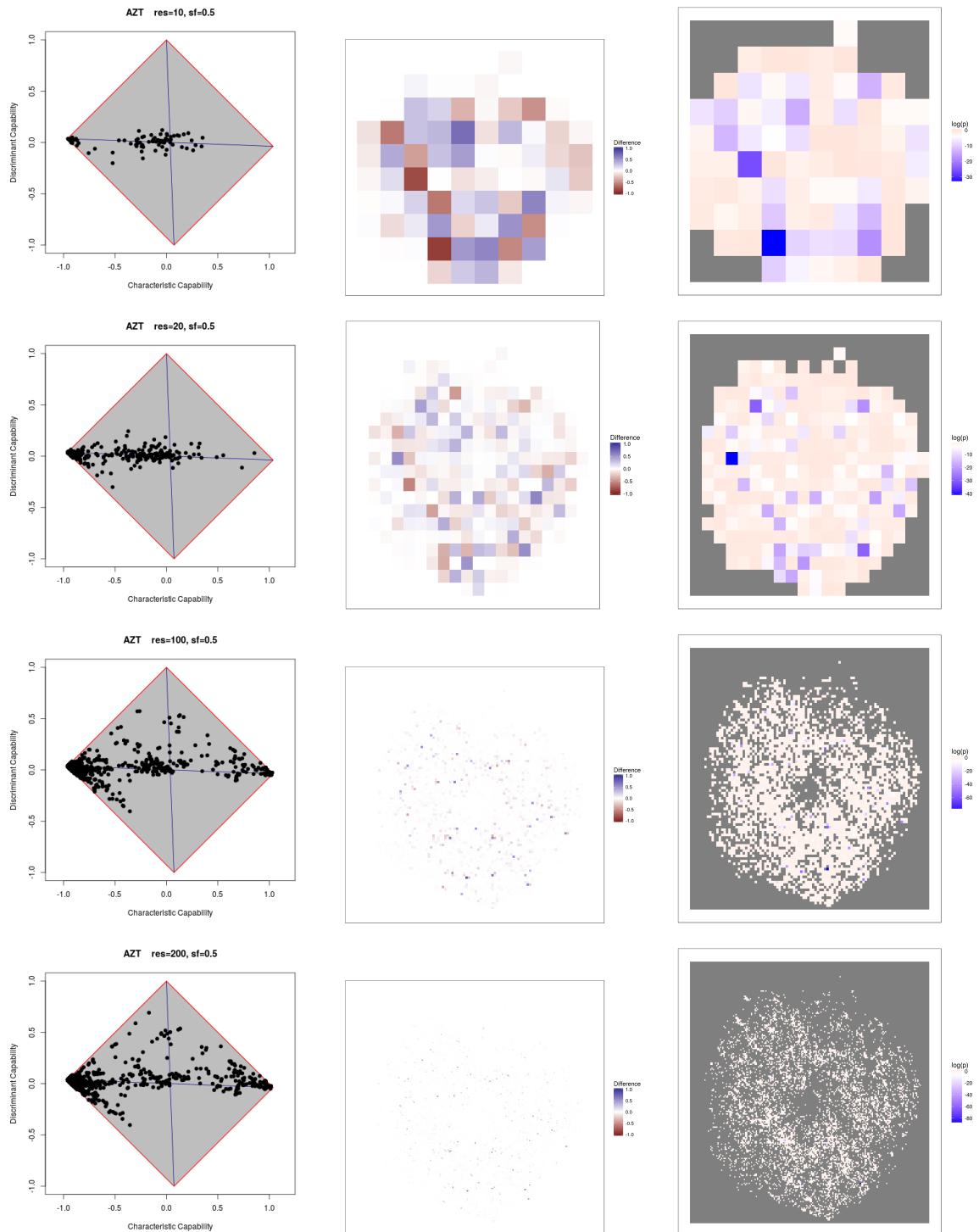


Figure 16: AZT,  $sf = 0.5$

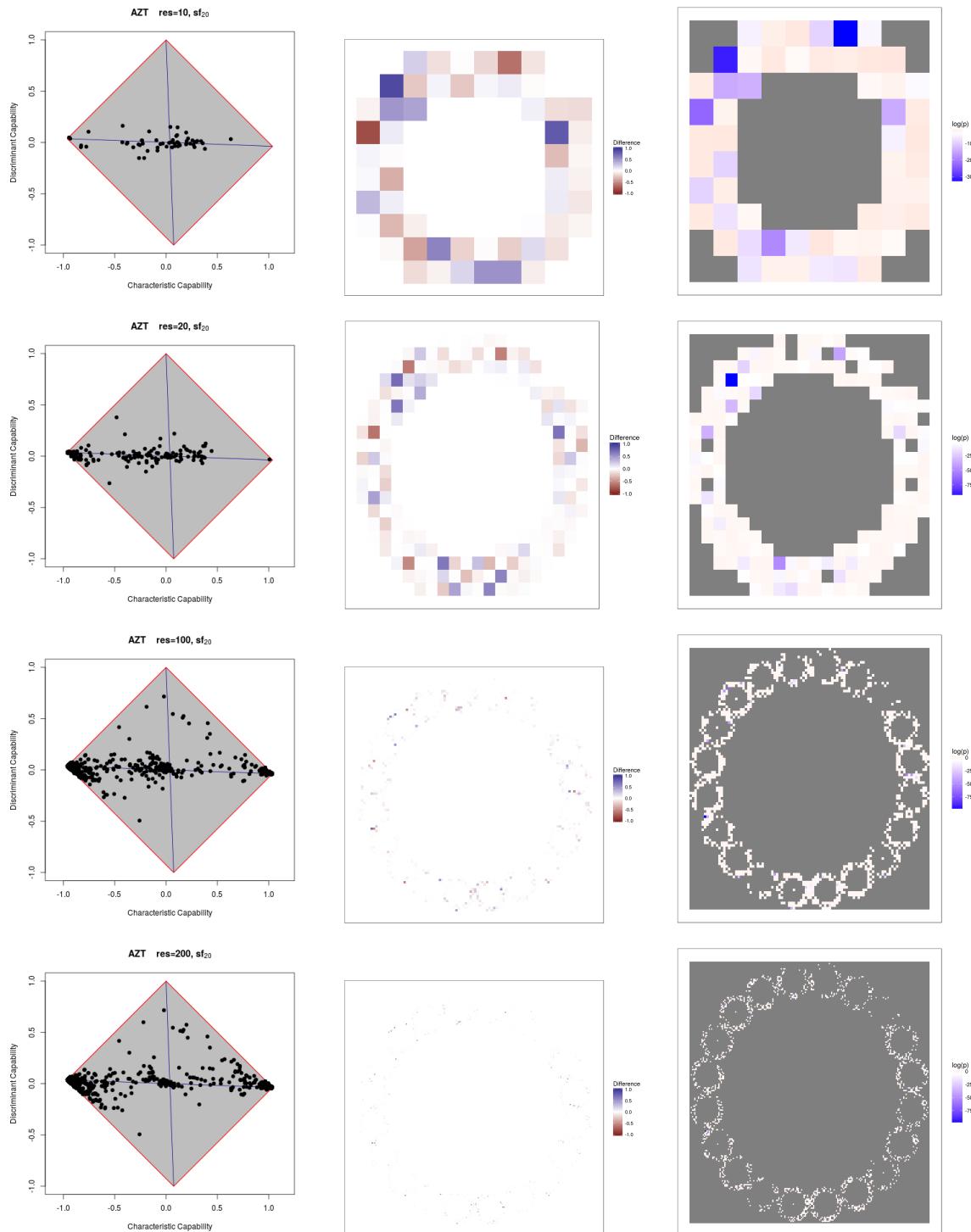


Figure 17: AZT,  $sf_{20}$

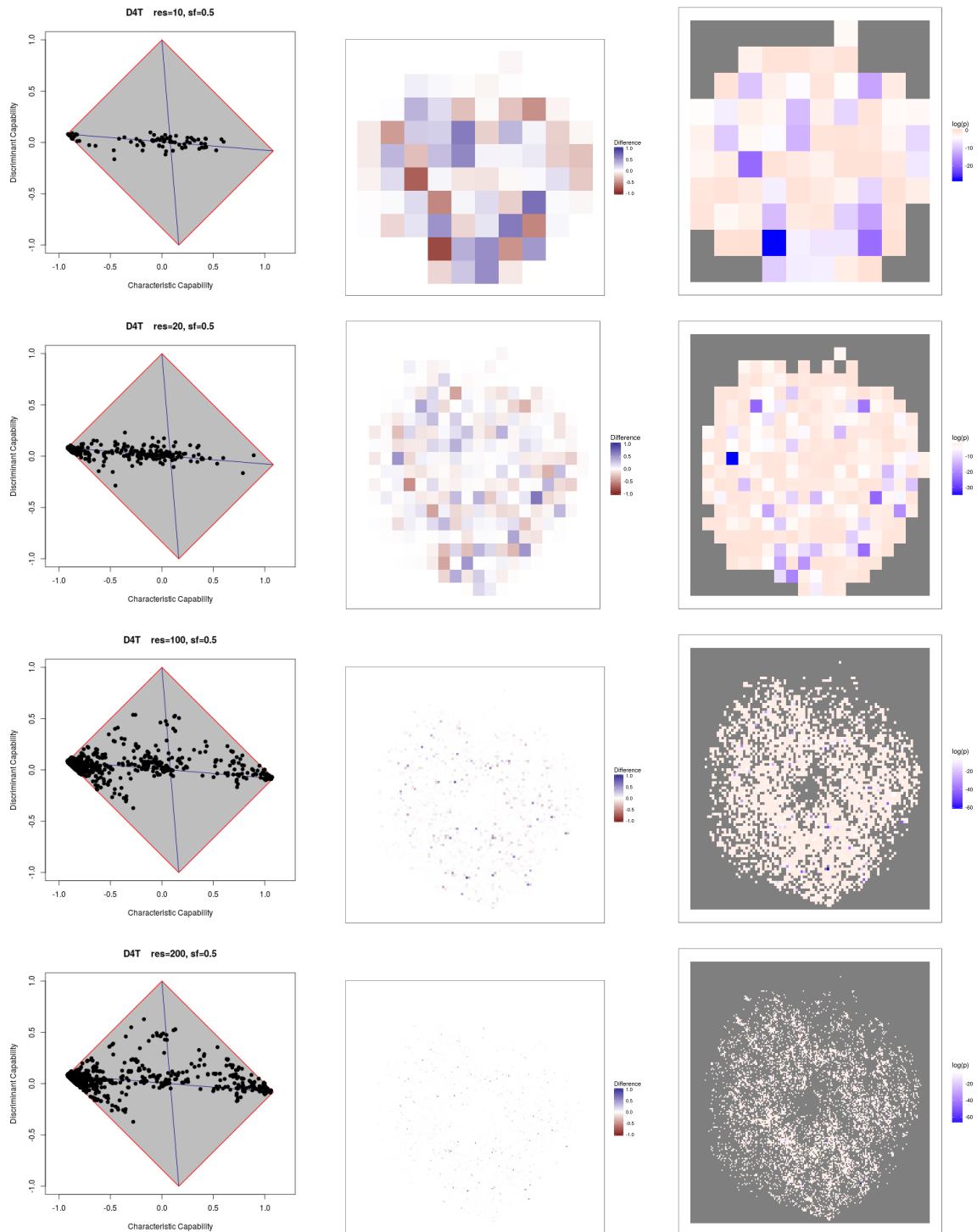


Figure 18: D4T,  $sf = 0.5$

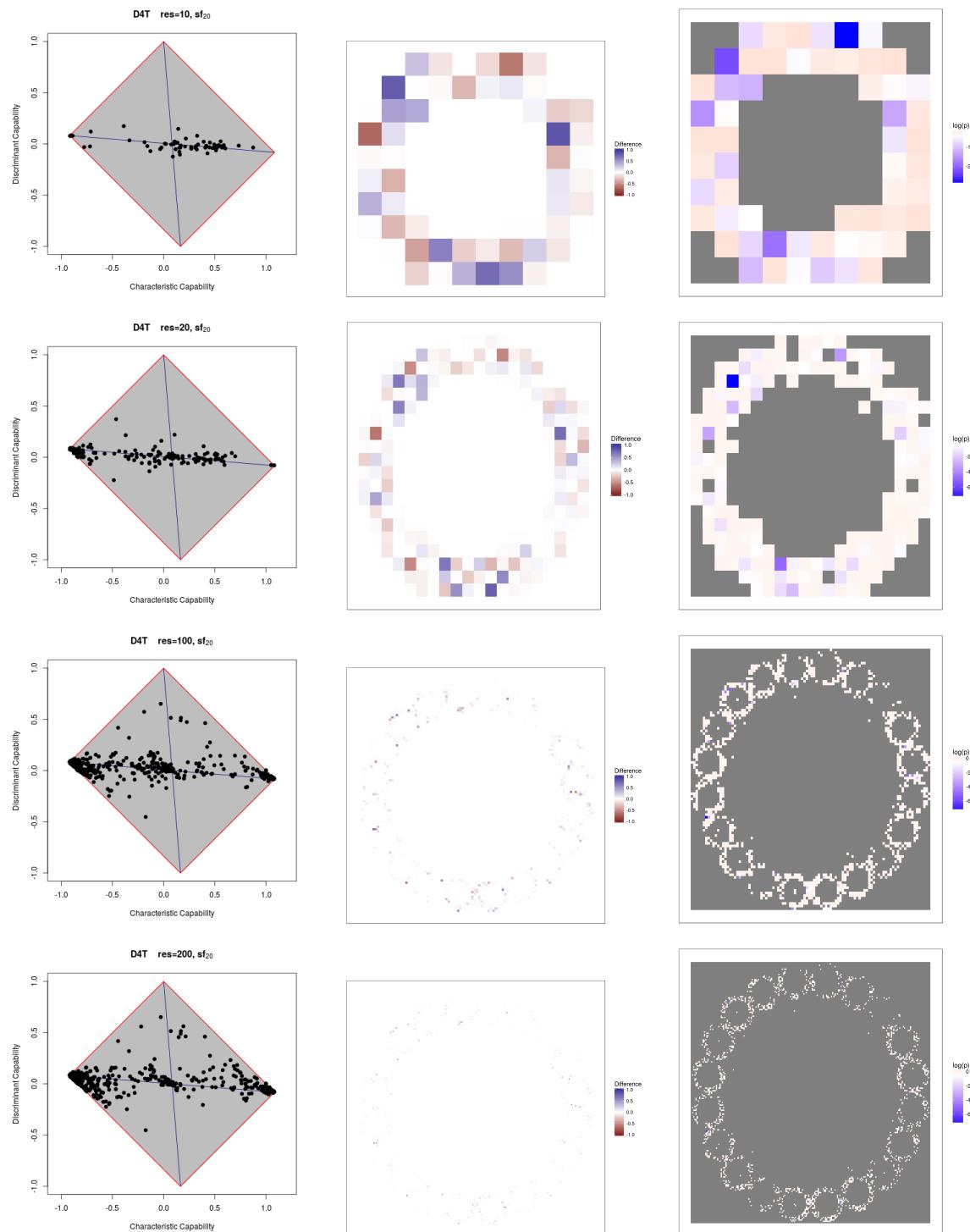


Figure 19: D4T,  $sf_{20}$

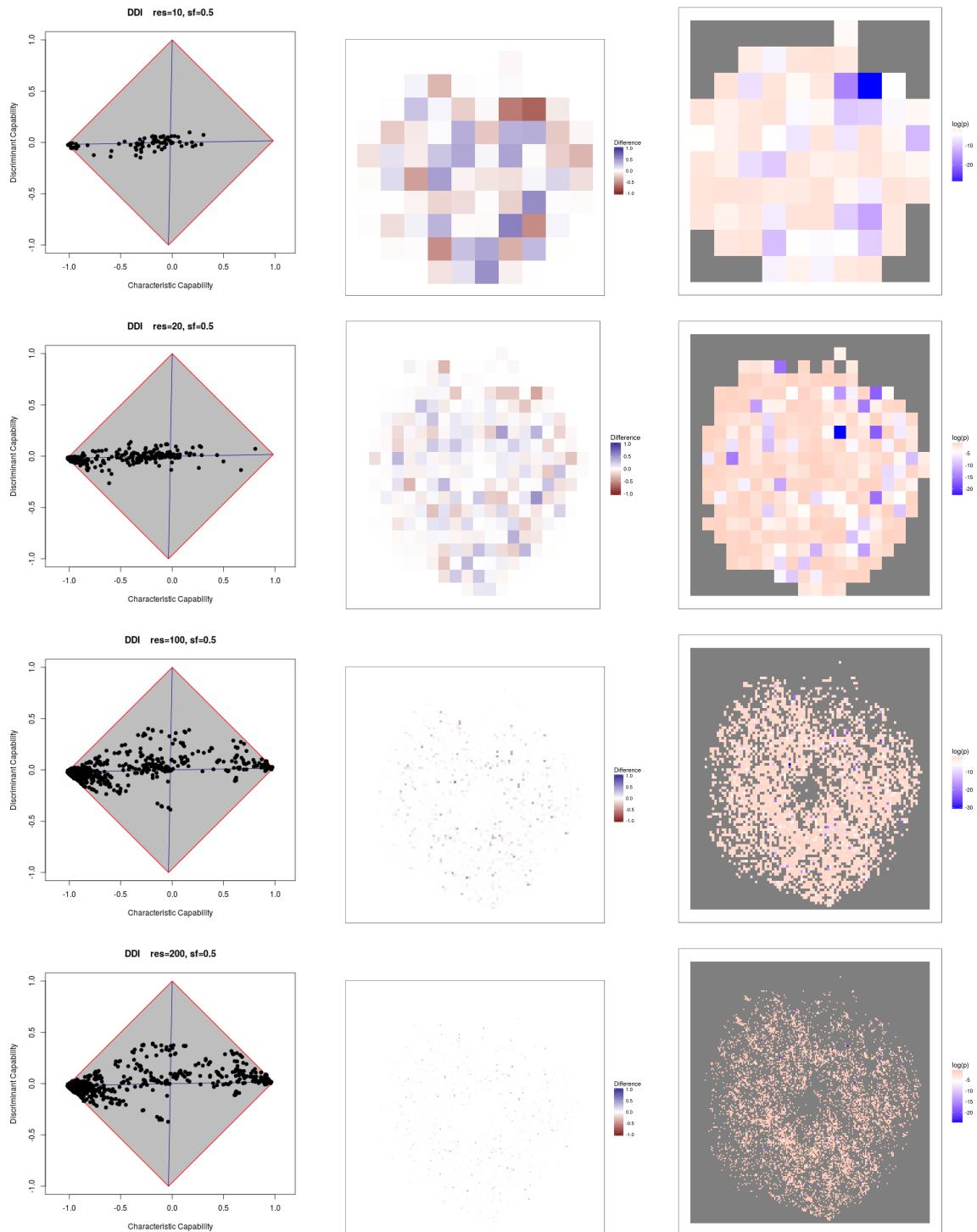


Figure 20: DDI,  $sf = 0.5$

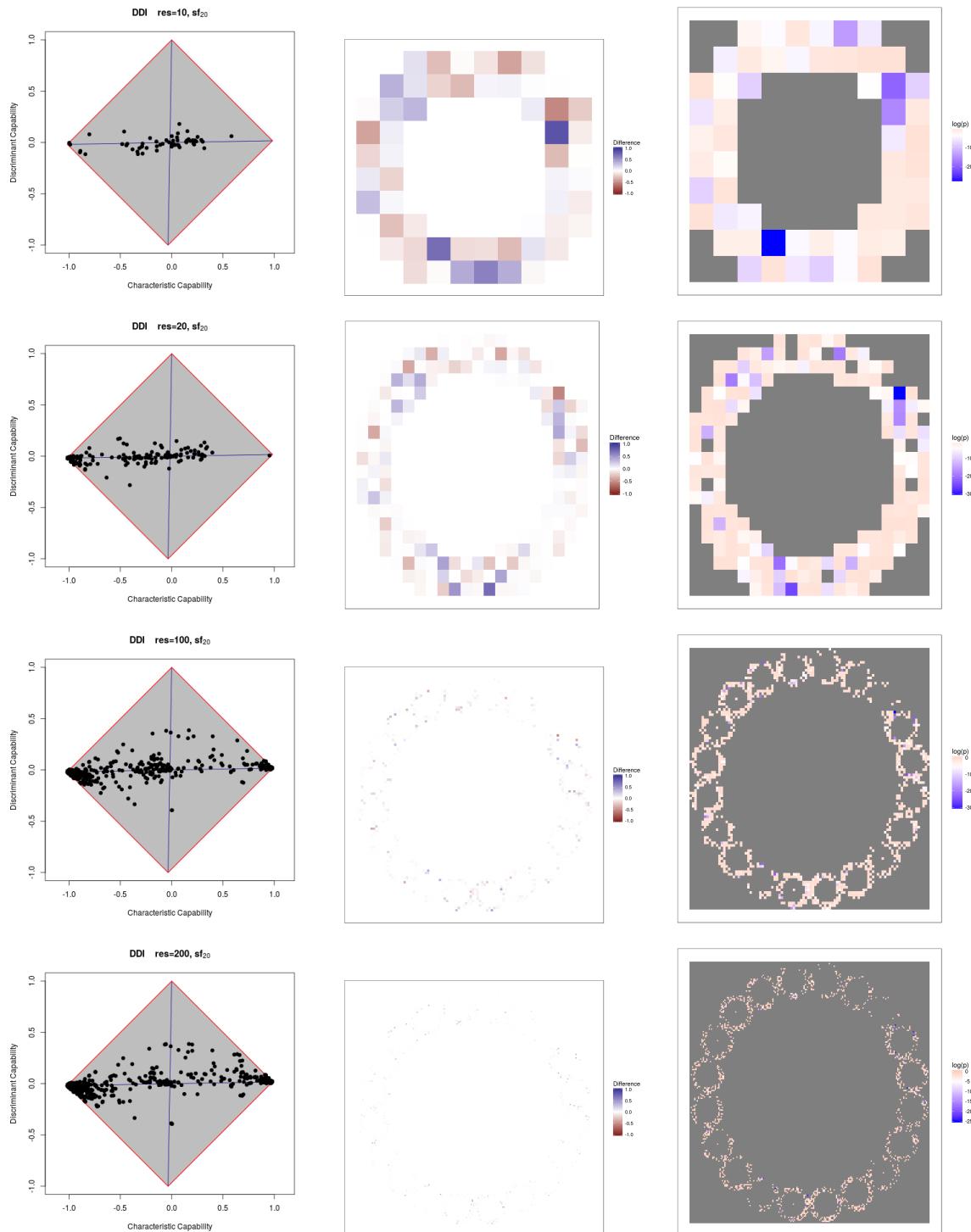


Figure 21: DDI,  $sf_{20}$

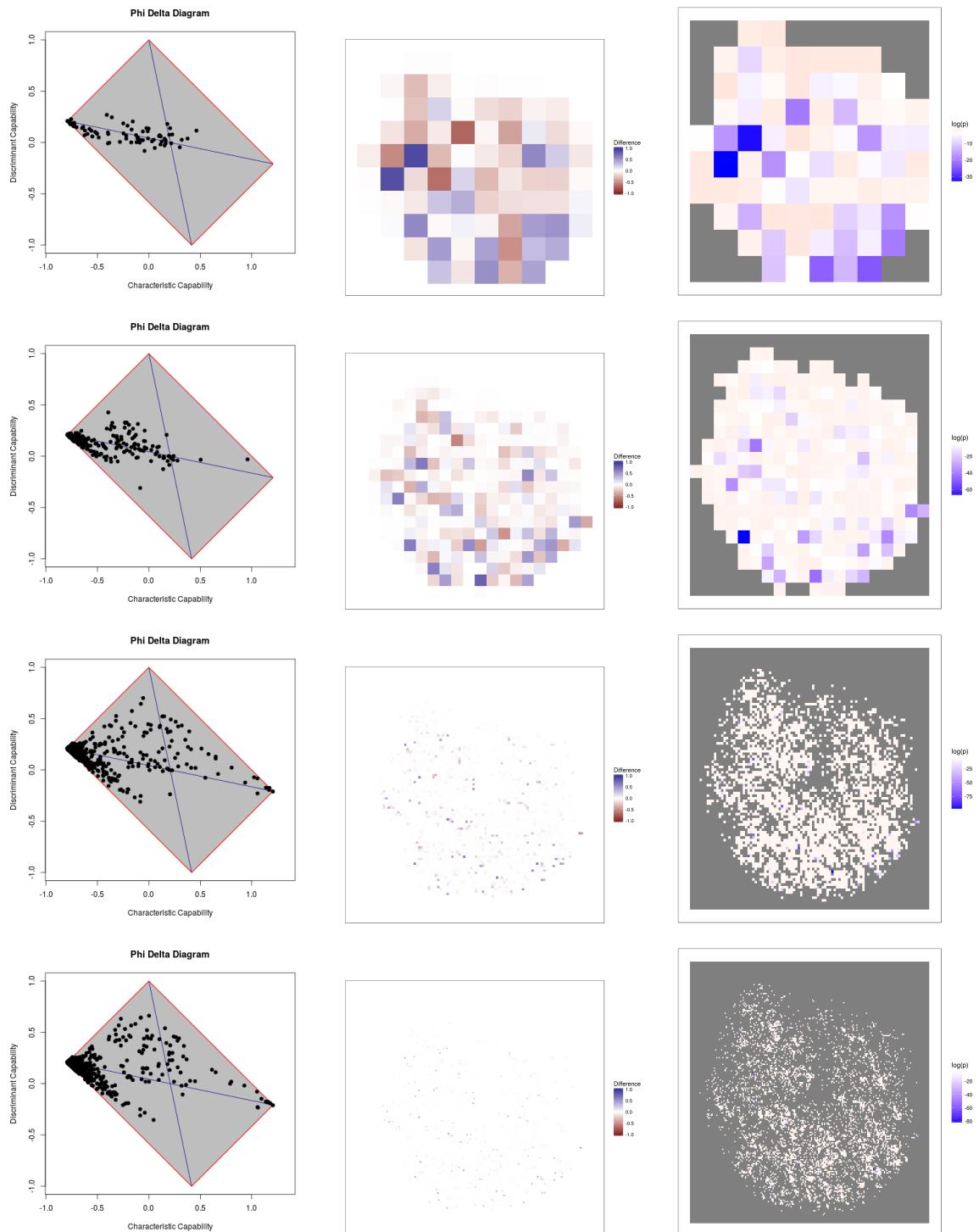


Figure 22: APV,  $sf = 0.5$

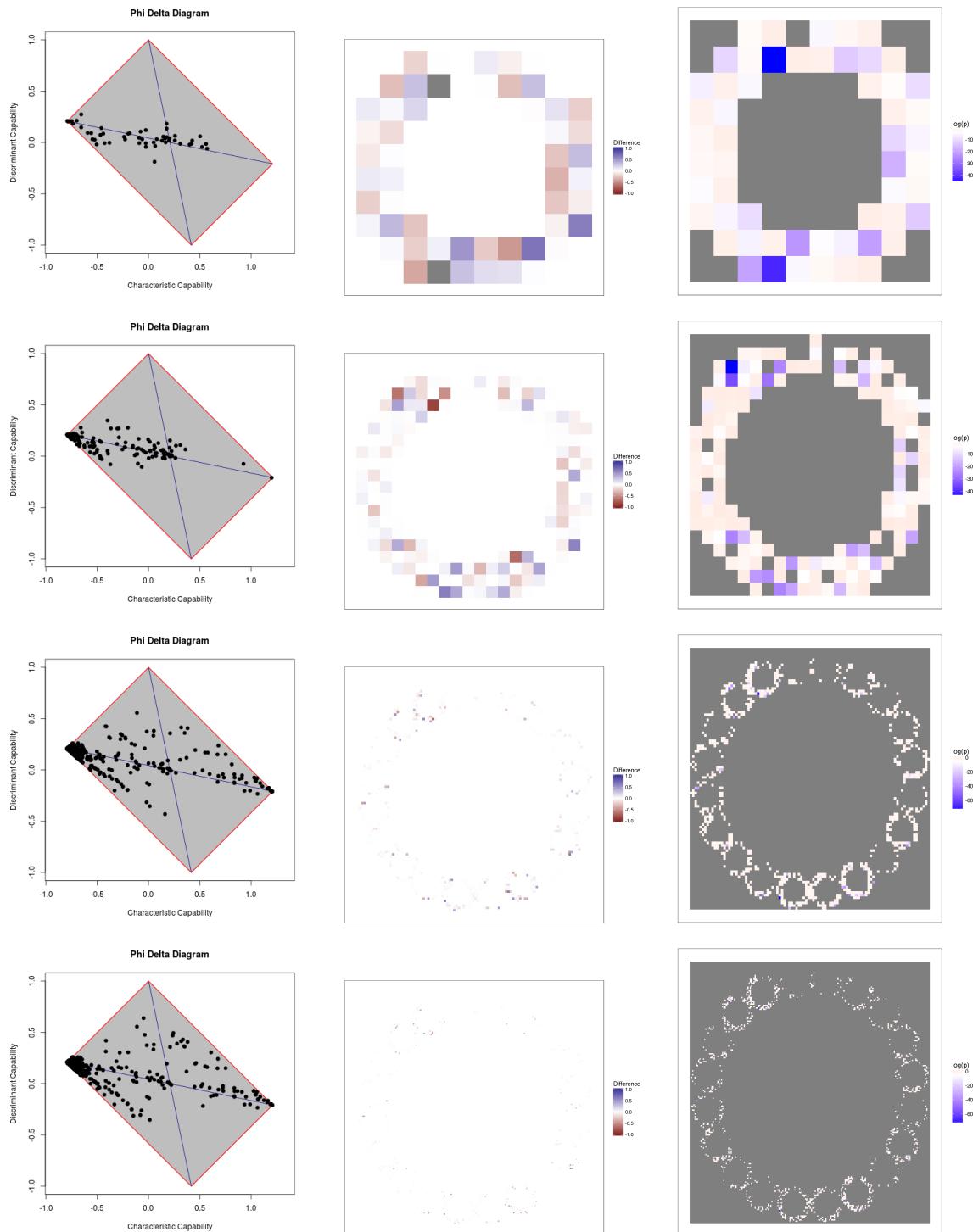


Figure 23: APV,  $s f_{20}$

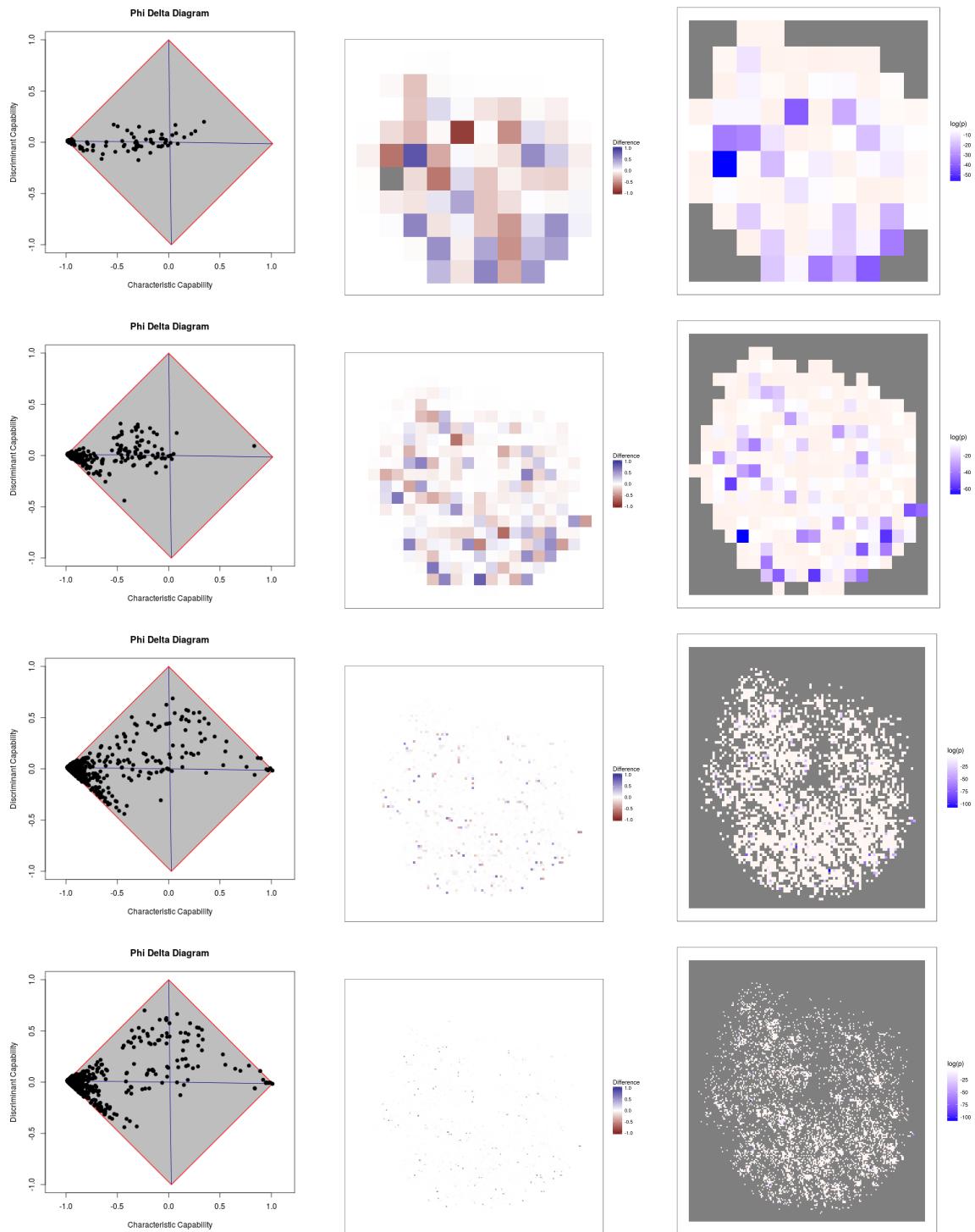


Figure 24: IDV,  $sf = 0.5$

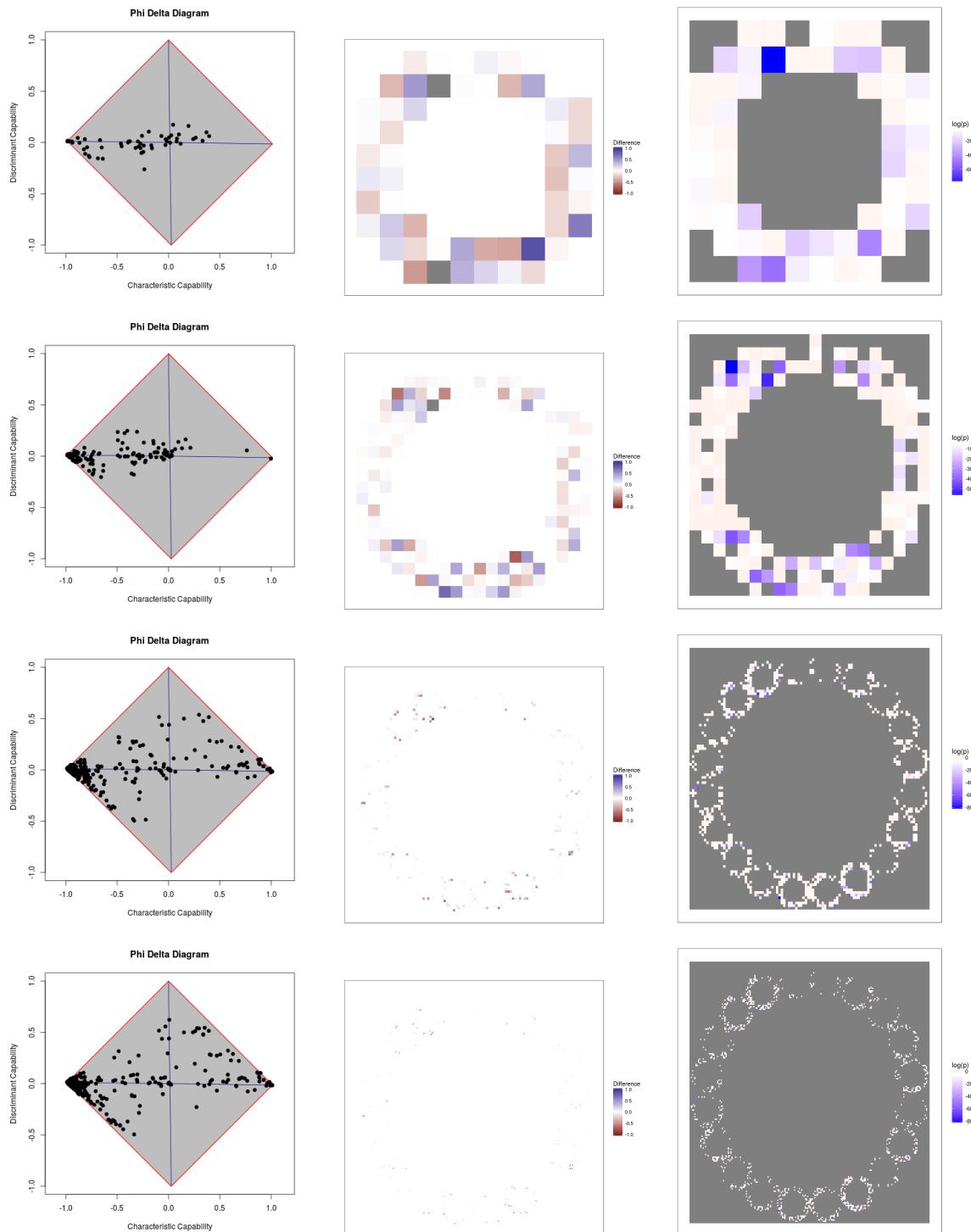


Figure 25: IDV,  $s f_{20}$

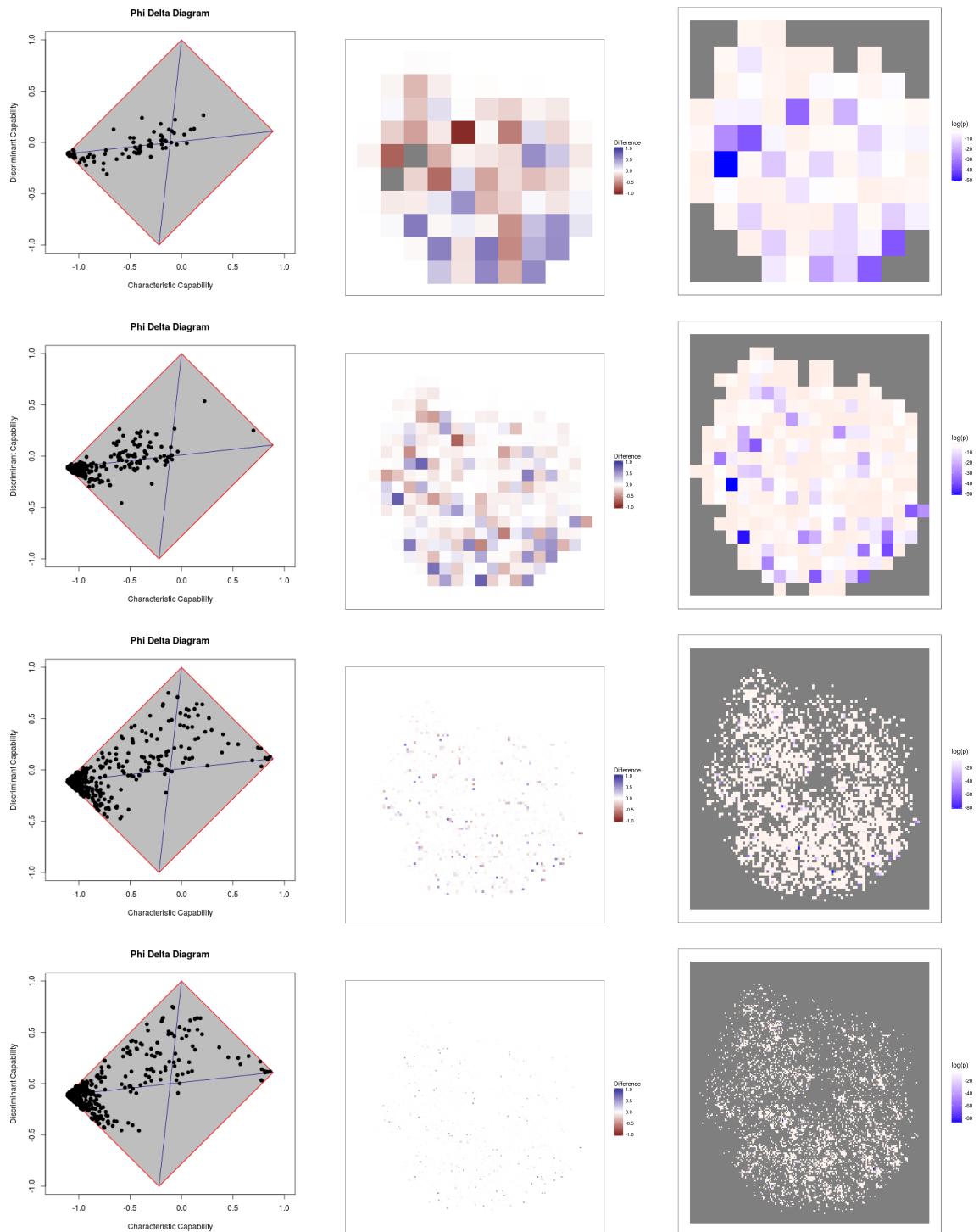


Figure 26: LPV,  $sf = 0.5$

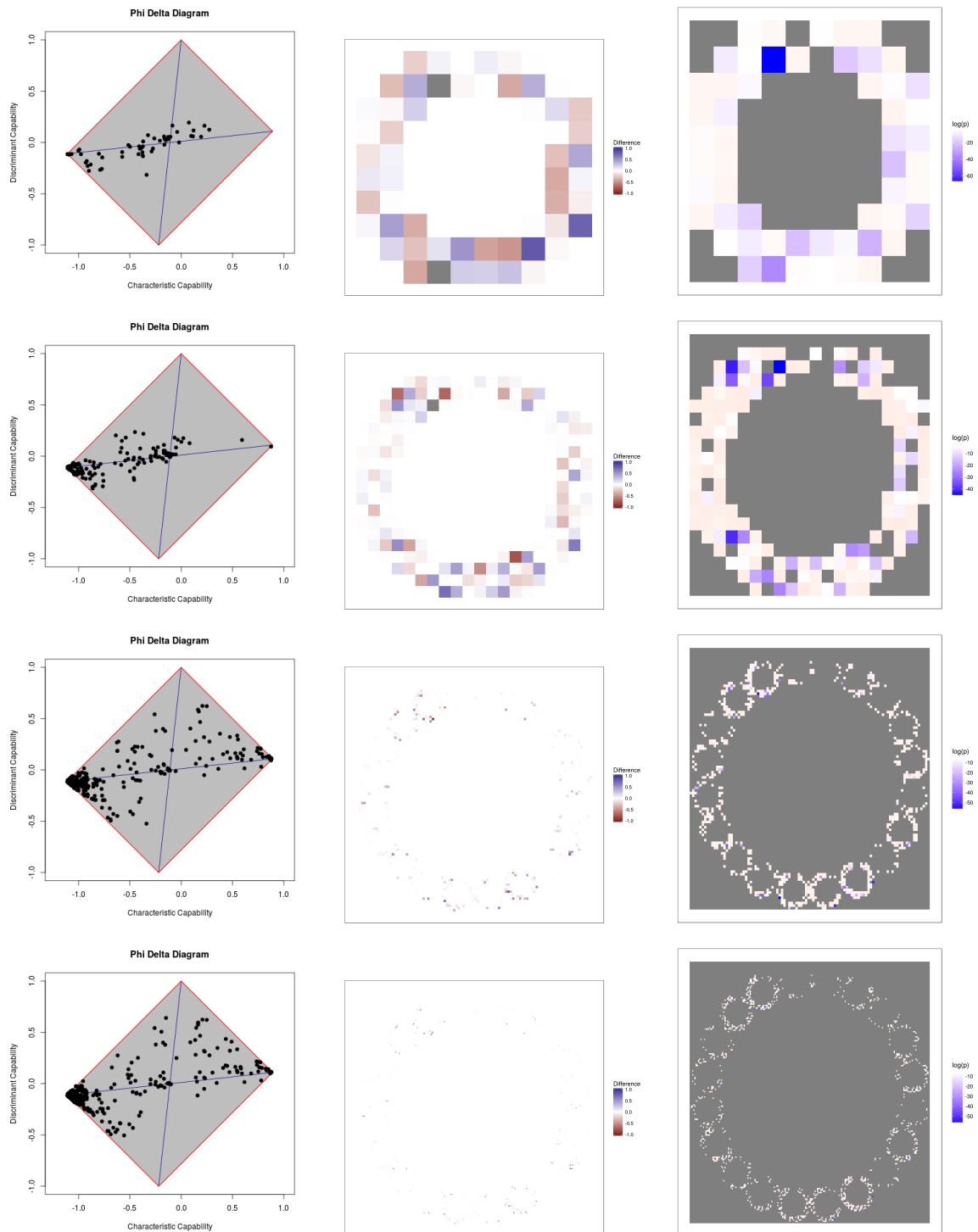


Figure 27: LPV,  $sf_{20}$

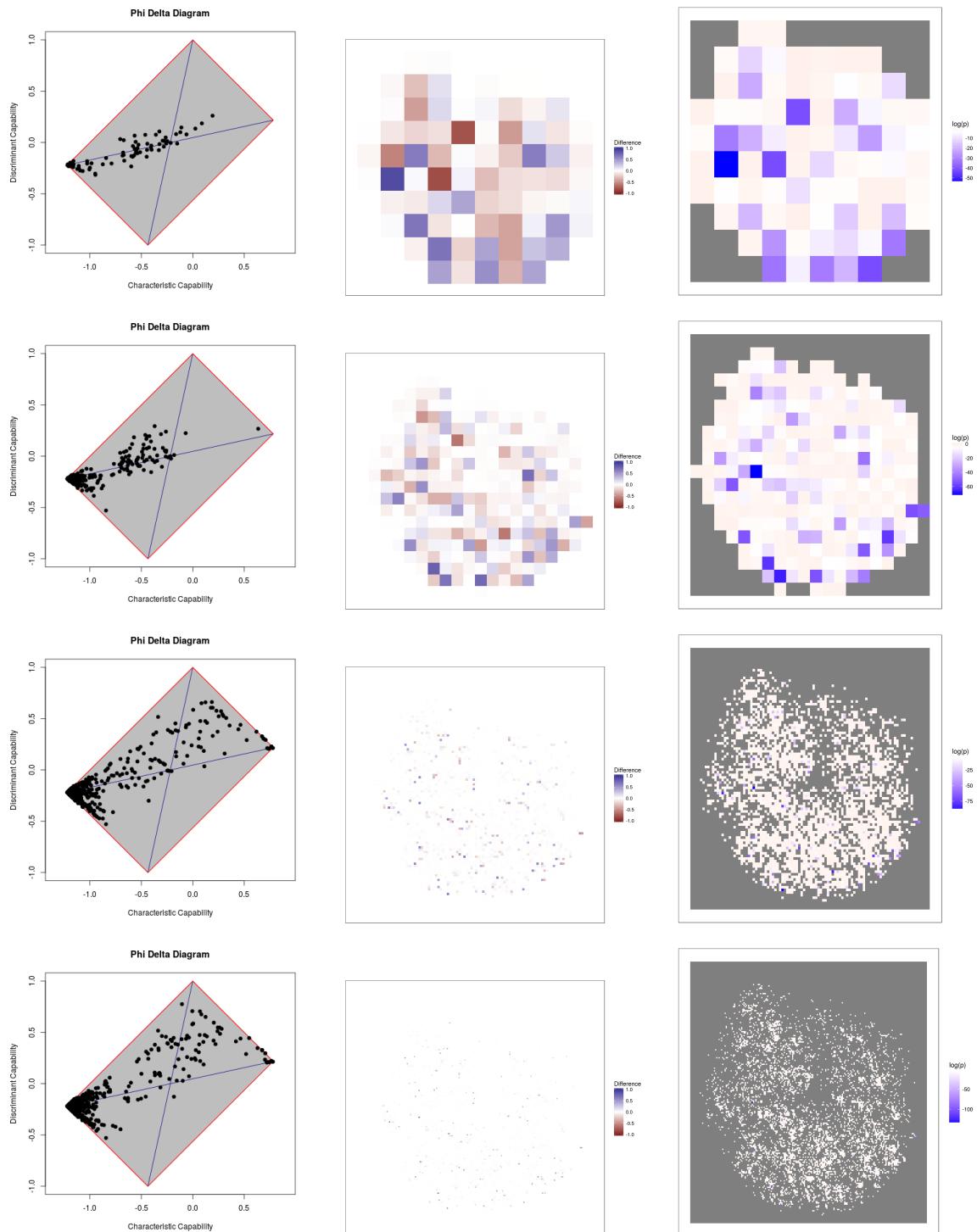


Figure 28: NFV,  $sf = 0.5$

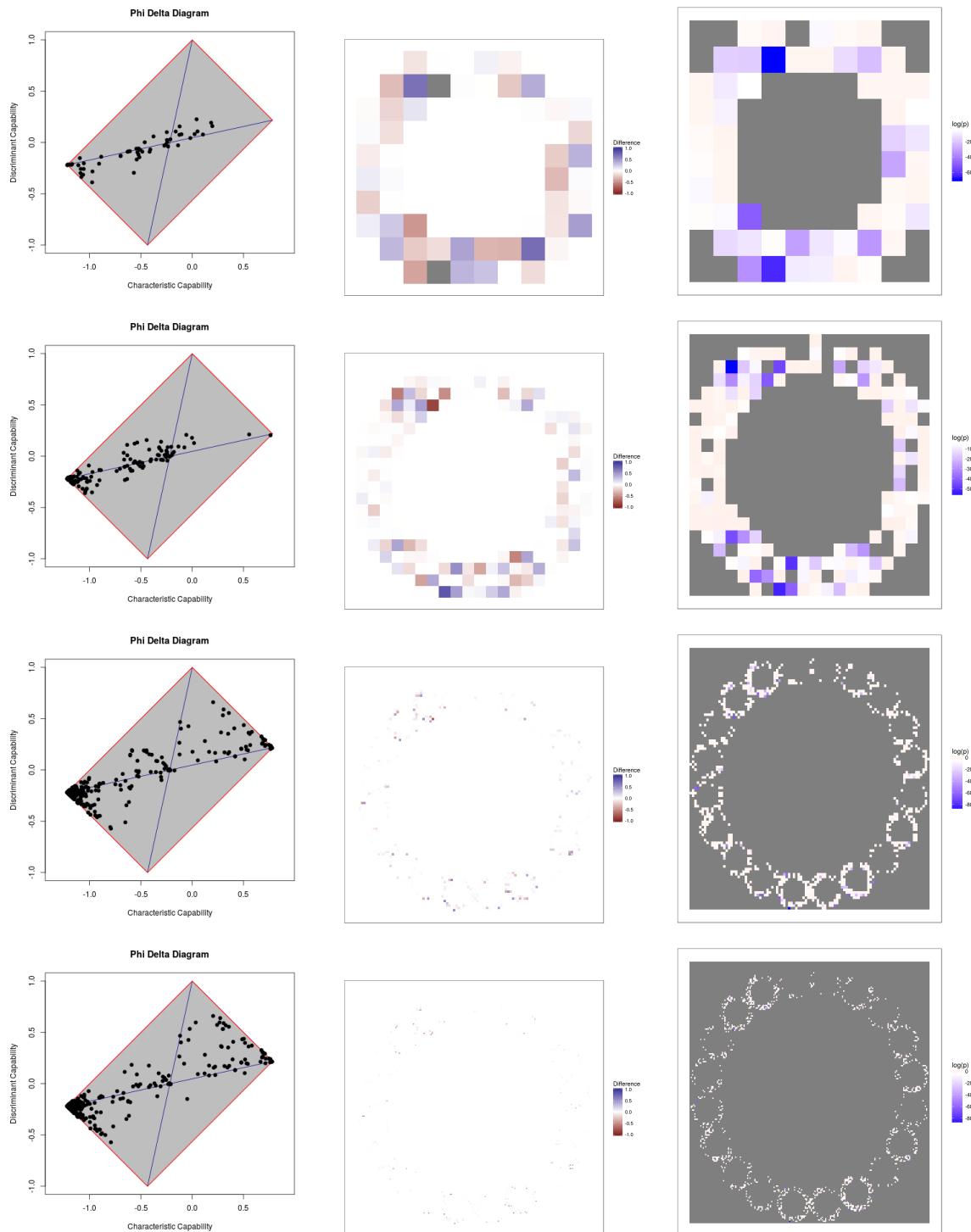


Figure 29: NFV,  $s f_{20}$

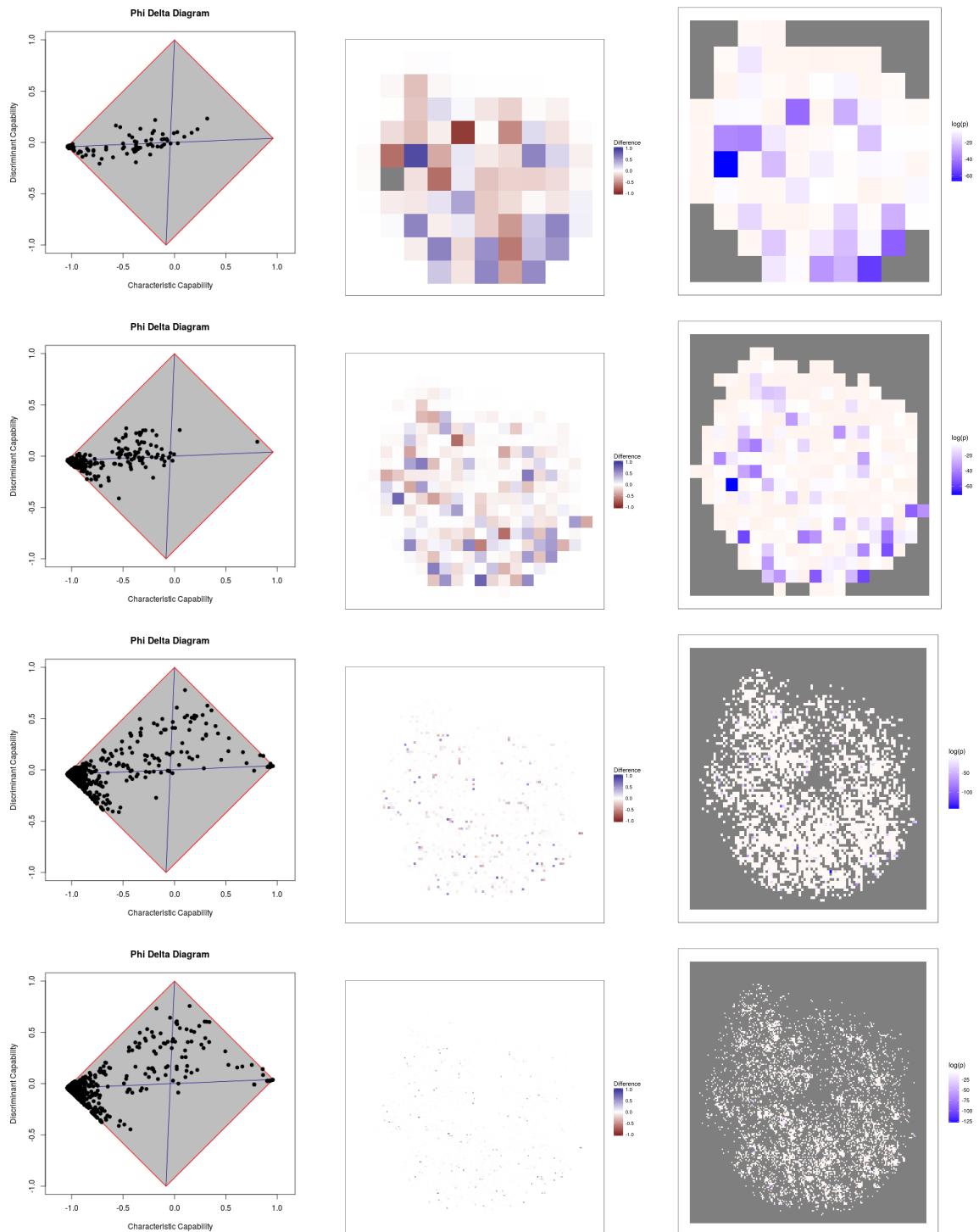


Figure 30: RTV,  $sf = 0.5$

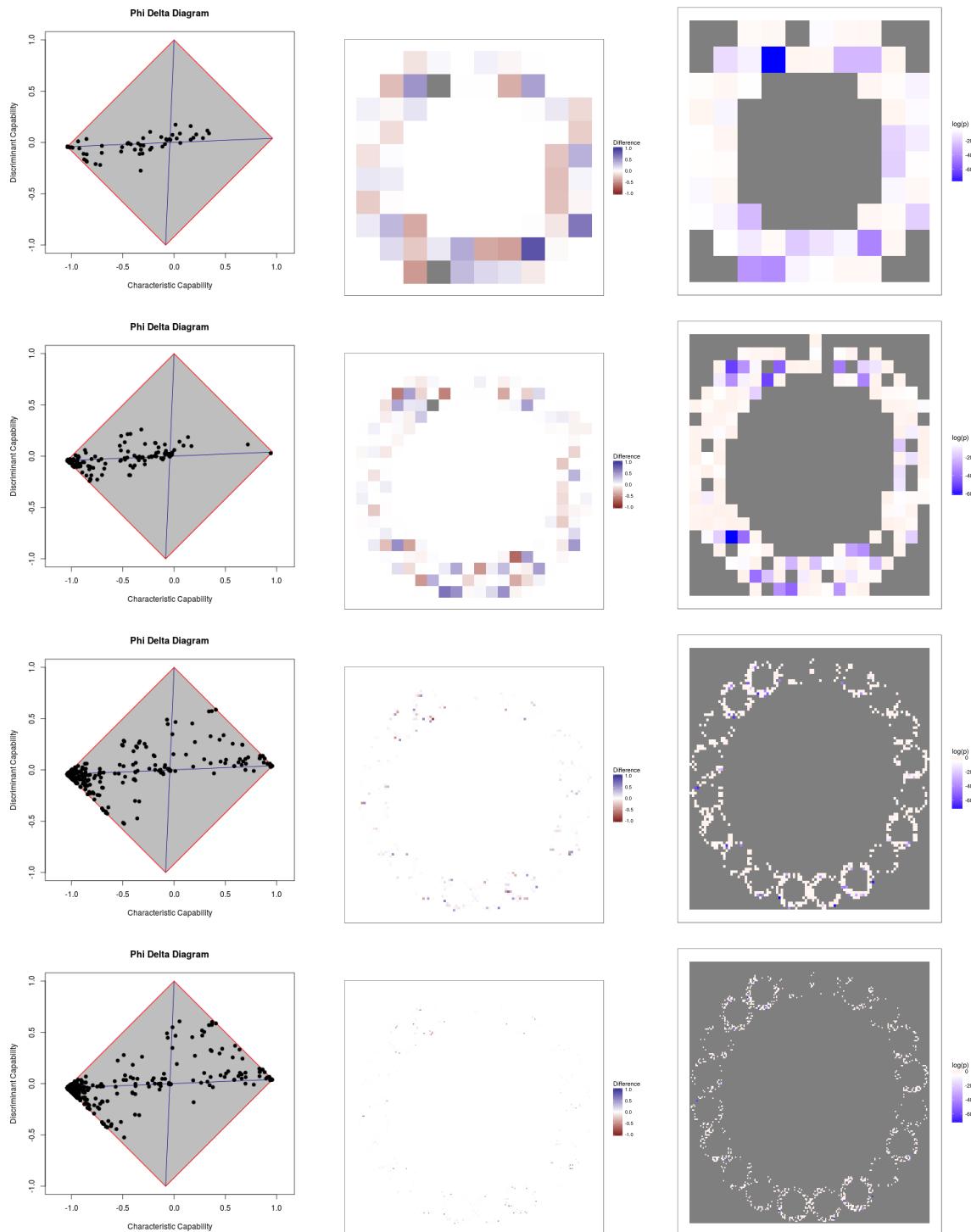


Figure 31: RTV,  $sf_{20}$

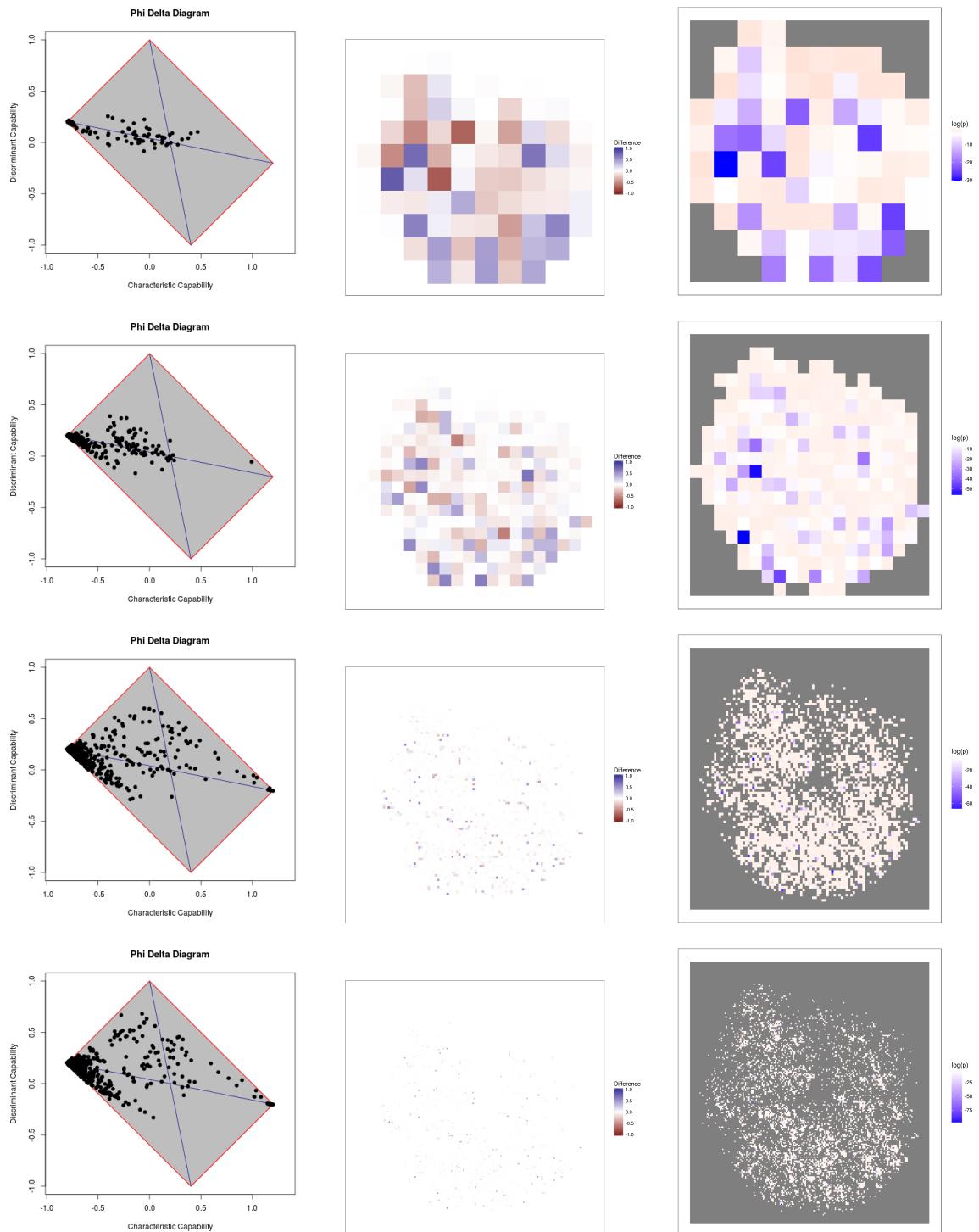


Figure 32: SQV,  $sf = 0.5$

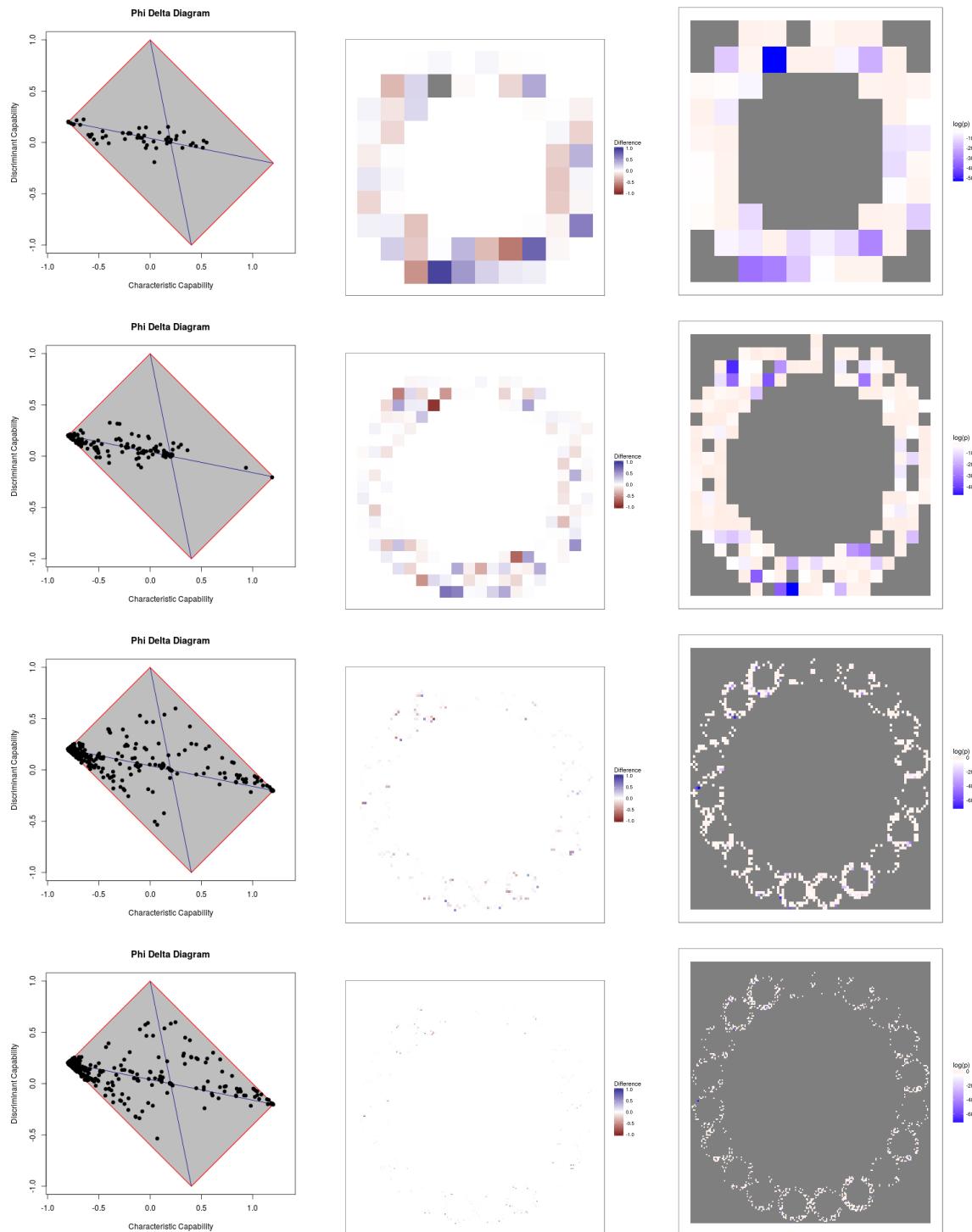


Figure 33: SQV,  $sf_{20}$