S6 Figure. Robustness of the independent components

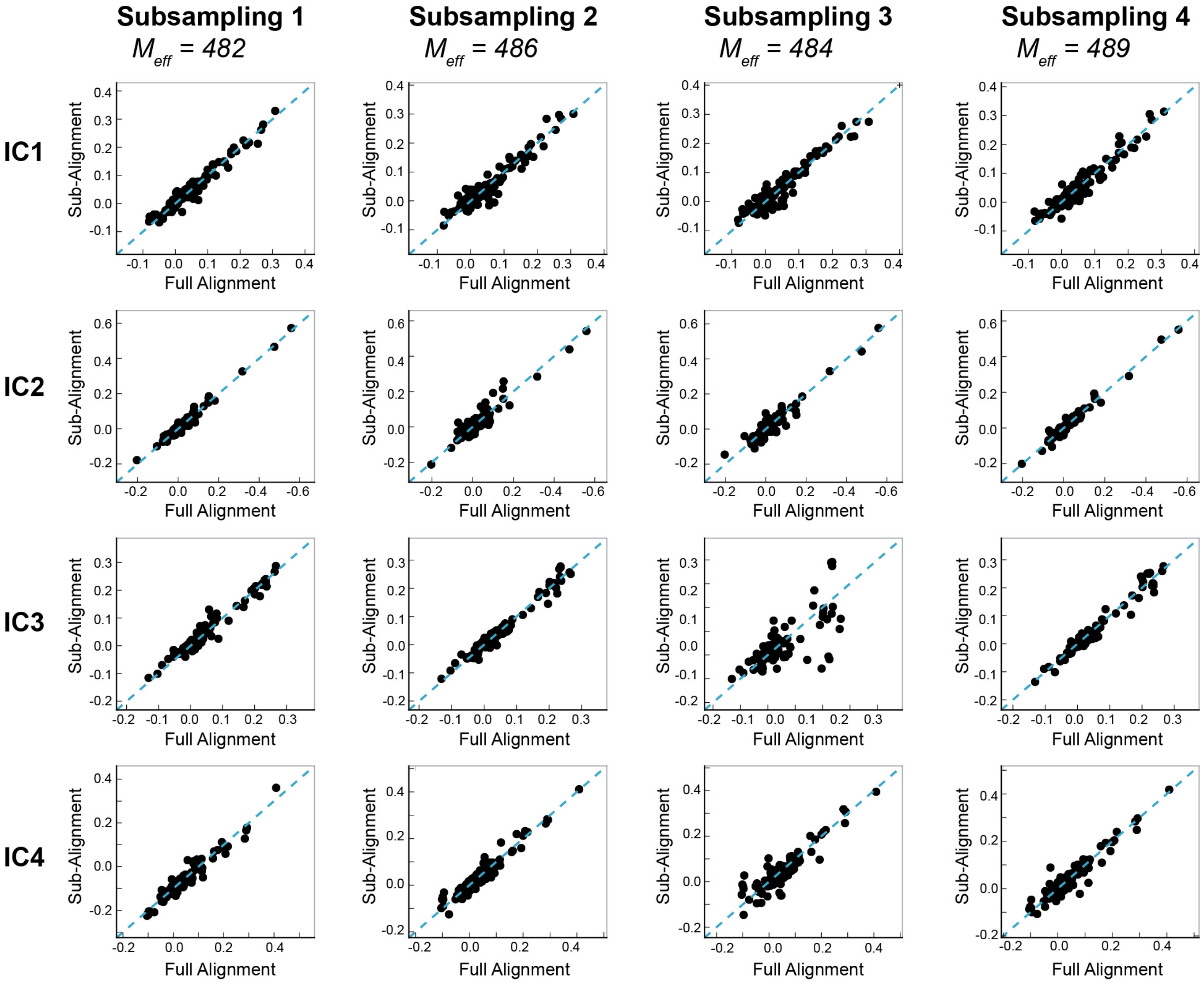

FIG. 6 **The robustness of the independent components (ICs) of the $\tilde{C}_{ij}$ matrix to alignment sub-sampling.** Scatterplots of the top four independent components (ICs) for the full alignment of G proteins ($M_{eff} = 3366$) against those for four trials of sub-sampling the alignment to ≈ 15% of sequences. The analysis shows that the composition of ICs (and therefore sector definitions and sequence projections) are highly robust to the number of effective sequences in the alignment.