

	Original	Predicted	MergeLevels	GLADmerge
SSQ distance	12.5	0.87	0.50	0.30
MAD	0.053	0.008	0.002	0.002
Accuracy	0.958	0.999	0.997	0.997
Proportion of discordant pairs	-	0.633	0.005	0.003

Table S 3. Hupe et al. simulation model. Median of each performance measure for original log2 ratios, HMM predicted log2 ratios, HMM predicted log2 ratios merged by MergeLevels or by GLADmerge. Medians are based on 500 simulations.

	Original	Predicted	MergeLevels	GLADmerge
SSQ distance	12.5	0.616	0.389	0.376
MAD	0.053	0.007	0.002	0.002
Accuracy	0.958	0.998	0.998	0.997
Proportion of discordant pairs	-	0.441	0.004	0.004

Table S 4. Hupe et al. simulation model. Median of each performance measure for original log2 ratios, GLAD predicted log2 ratios, GLAD predicted log2 ratios merged by MergeLevels or by GLADmerge. Medians are based on 500 simulations.

	Original	Predicted	MergeLevels	GLADmerge
SSQ distance	12.5	0.315	0.184	0.168
MAD	0.053	0.006	0.002	0.002
Accuracy	0.958	0.9995	0.999	0.997
Proportion of discordant pairs	-	0.63	0.001	0.001

Table S 5. Hupe et al. simulation model. Median of each performance measure for original log2 ratios, DNACopy predicted log2 ratios, DNACopy predicted log2 ratios merged by MergeLevels or by GLAD. Medians are based on 500 simulations.