

Table 9: Reduction of mapping artifacts by the intersection of mapping algorithms using the 0.01% quantile. Two Illumina paired end data sets with different insert sizes and read length were derived from pooled genomic DNA (natural *D. simulans* population) and mapped to the reference genome. Allele frequency differences between the libraries were computed using Fisher’s exact test [$-\log(\text{p-value}) = \text{fet-value}$]. To test which combination of alignment algorithms most efficiently reduces outlier peaks we intersected all pairwise combinations of alignment algorithms, i.e. we use SNPs identified with both algorithms and use the lowest *fet-value* found with any of the two algorithms. Below the diagonal we report the number SNPs (in million) common to both algorithms. For comparison, the number of SNPs identified with a single mapping algorithm are shown next to the list of mappers on the left side. Above the diagonal we report the 0.01% quantile of most differentiated SNPs (around 400 SNPs). For comparison, the outlier quantiles identified with a single mapping algorithm are shown next to the list of mappers on the upper side. We marked the five best combinations yielding the least pronounced outlier loci (green).

	bowtie2(g) 5.62	bwa aln 7.08	clc4(g) 6.91	ngm(g) 8.27	novoalign(g) 7.33	segemehl 9.48	bowtie2(l) 7.26	bwa bwaw 4.92	bwa mem 6.46	clc4(l) 5.91	gsnap 11.49	ngm(l) 6.25	novoalign(l) 5.96
bowtie2(g) 4.91		4.02	3.77	3.85	3.81	4.34	3.75	3.67	3.85	3.56	3.73	3.63	3.50
bwa aln 5.03	4.27		3.91	3.92	4.01	3.94	3.93	3.81	4.04	3.89	3.95	3.87	3.66
clc4(g) 6.61	4.10	4.27		4.88	3.91	3.89	3.73	3.62	3.85	4.80	3.92	3.97	3.57
ngm(g) 8.43	4.18	4.29	5.94		3.90	4.08	3.79	3.68	3.82	4.04	3.88	4.94	3.58
novoalign(g) 4.96	4.19	4.51	4.21	4.27		4.22	3.96	3.77	4.88	3.75	4.29	3.82	5.17
segemehl 4.87	4.05	3.91	3.97	4.12	3.92		3.88	3.67	4.21	3.76	4.06	3.74	3.84
bowtie2(l) 4.75	4.09	4.45	4.17	4.21	4.49	3.85		3.83	4.00	3.84	4.27	3.92	3.77
bwa bwaw 4.53	4.07	4.23	3.96	4.01	4.32	3.81	4.33		3.93	3.81	3.89	3.83	3.67
bwa mem 4.79	4.18	4.45	4.14	4.19	4.68	3.90	4.46	4.36		3.88	4.06	3.83	4.45
clc4(l) 4.71	4.01	4.32	4.35	4.20	1.48	3.80	4.37	4.21	4.28		3.87	4.33	3.64
gsnap 4.9	4.12	4.38	4.15	4.20	4.47	3.90	4.47	4.36	4.44	4.34		4.00	3.85
ngm(l) 5.05	4.15	4.45	4.40	4.60	4.45	3.96	4.51	4.32	4.40	4.54	4.48		3.59
novoalign(l) 4.39	3.84	4.12	3.88	3.85	4.35	3.62	4.20	4.13	4.28	4.07	4.19	4.13	