Supplementary

Figure S1: Lengths of query sequences
The longest 2181 sequences from NCBI non-redundant nucleotide database

Figure S2: Lengths of database sequences
(a) speedup of Qsmall queries on human genome database

(b) speedup of Qmedium queries on human genome database

(c) speedup of Qlarge queries on human genome database
(d) speedup of Qbac queries on human genome database

(e) speedup of Qsmall queries on mouse genome database

(f) speedup of Qmedium queries on mouse genome database
(g) speedup of Qlarge queries on mouse genome database

(h) speedup of Qbac queries on mouse genome database

Figure S3: speedup of **megablast** mode (G780 vs. i7-3820; speedup-1 is for 1 CPU core, speedup-4 is for 4 CPU cores)
(a) Speedup of Qbac queries on human genome database

(b) Speedup of Qsmall queries on mouse genome database

(c) Speedup of Qmedium queries on mouse genome database
(d) speedup of Qlarge queries on mouse genome database

(e) speedup of Qbac queries on mouse genome database

Figure S4: speedup of megablast mode (G780 vs. E5620; speedup-1 is for 1 CPU core, speedup-4 is for 4 CPU cores, speedup-8 is for 8 CPU cores)
Figure S5: Speedups of blastn mode (G780 vs. i7-3820; speedup-1 is for 1 CPU core, speedup-4 is for 4 CPU cores)
speedup of Qbac on human genome database

speedup of Qbac on mouse genome database

speedup of Qbac on NCBI nt genome database

Figure S6: speedups of blastn mode (G780 vs. E5620; speedup-1 is for 1 CPU core, speedup-4 is for 4 CPU cores, speedup-8 is for 8 CPU cores)
Figure S7: the time distribution of Qbac on Human genome database. Remark: In (b), the time of ungapped extension is too short to be noticeable.