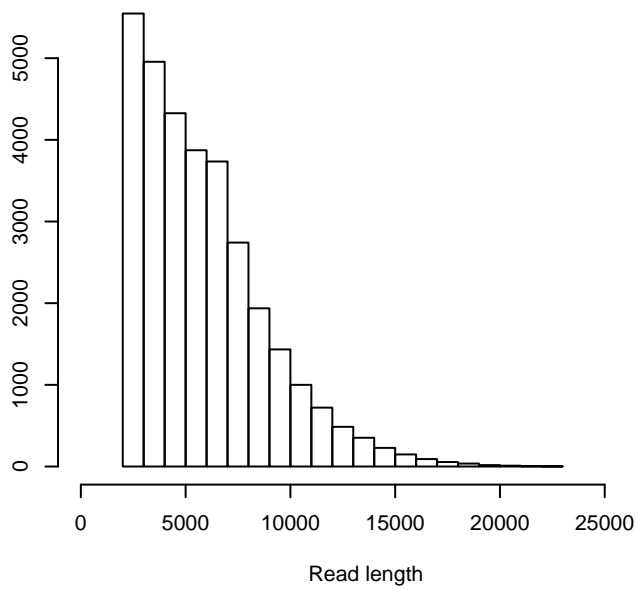
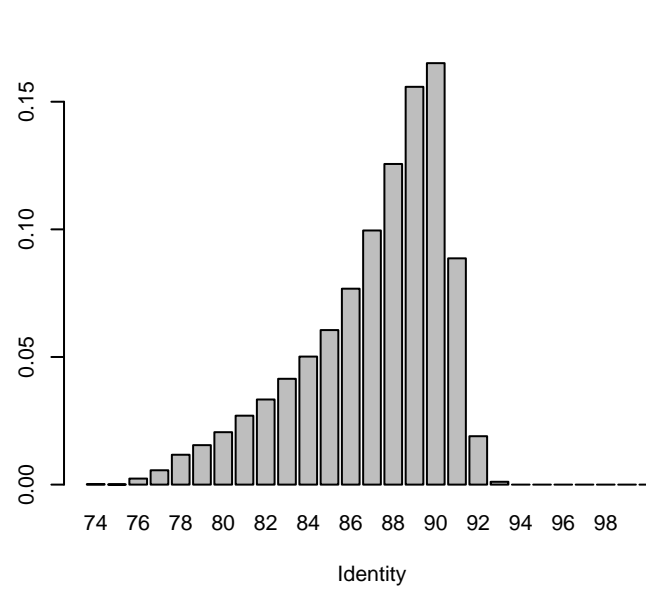


MetaMaps mapping summary for *Helicobacter pylori* 26695-1 (e-proteobacteria) (taxon ID x902) – 31700 mapped reads assigned

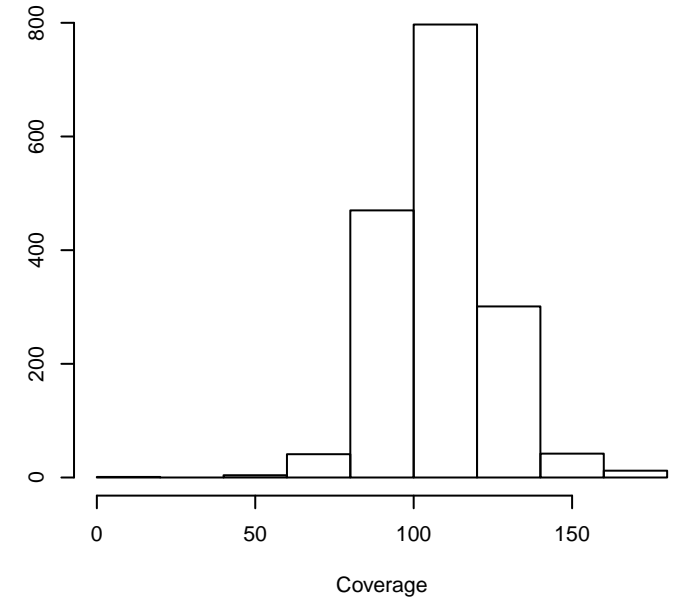
Read length histogram



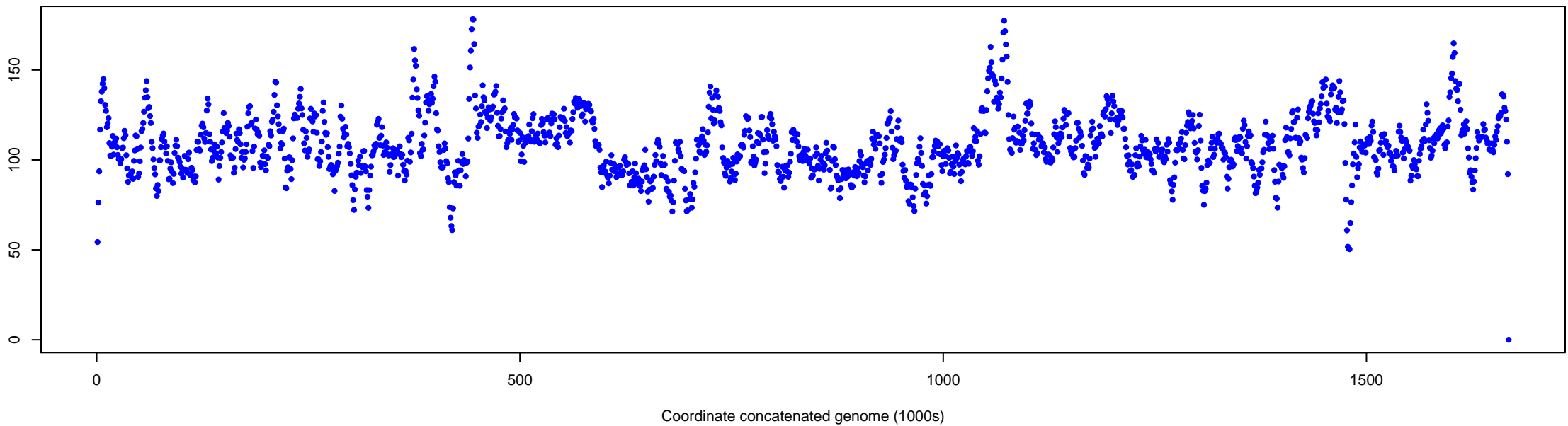
Read identities



Genome window coverage histogram

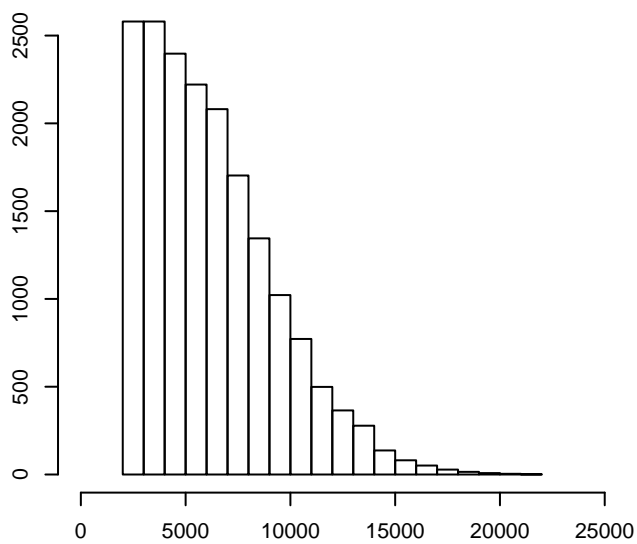


Genome-wide coverage over all contigs for *Helicobacter pylori* 26695-1 (e-proteobacteria) (taxon ID x902) – 31700 mapped reads assigned

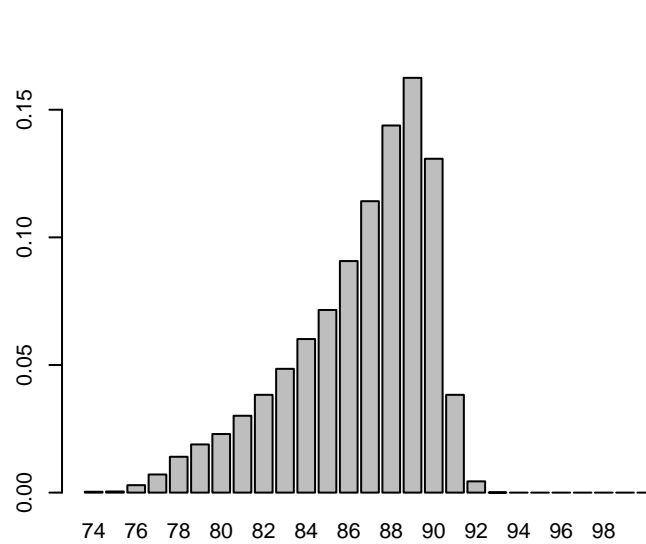


MetaMaps mapping summary for *Pseudomonas aeruginosa* PAO1 (taxon ID 208964) – 18168 mapped reads assigned

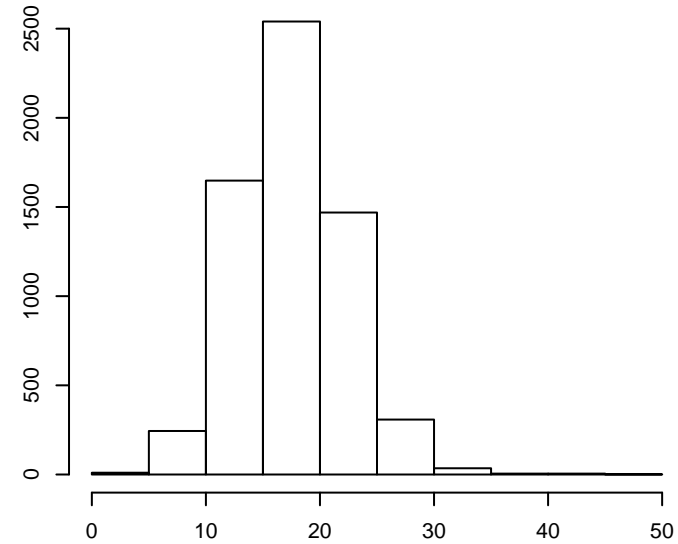
Read length histogram



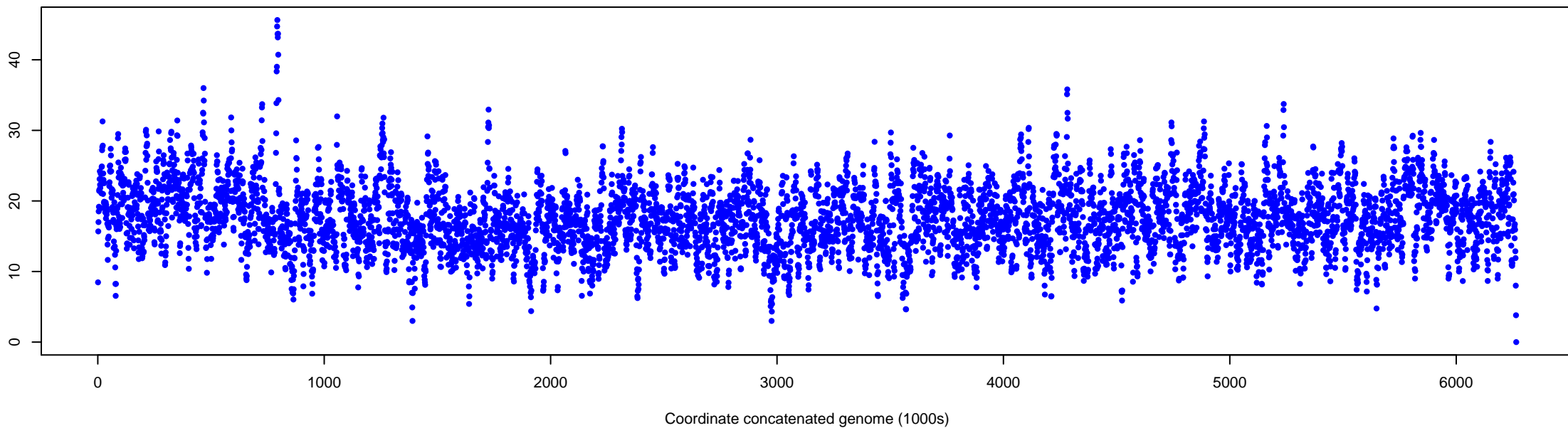
Read identities



Genome window coverage histogram

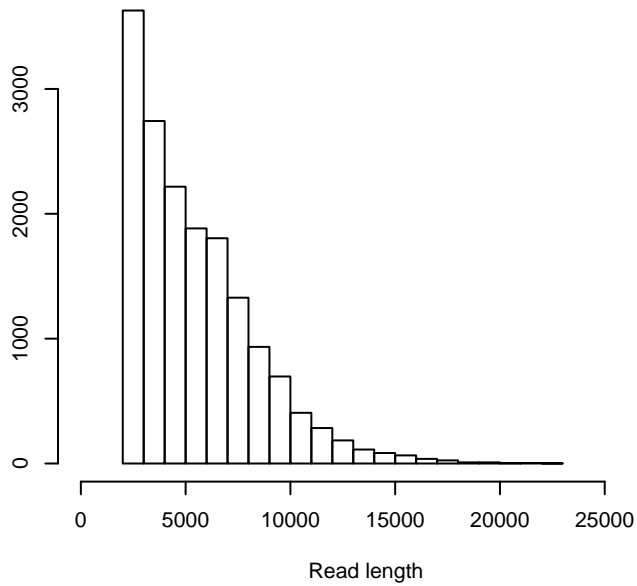


Genome-wide coverage over all contigs for *Pseudomonas aeruginosa* PAO1 (taxon ID 208964) – 18168 mapped reads assigned

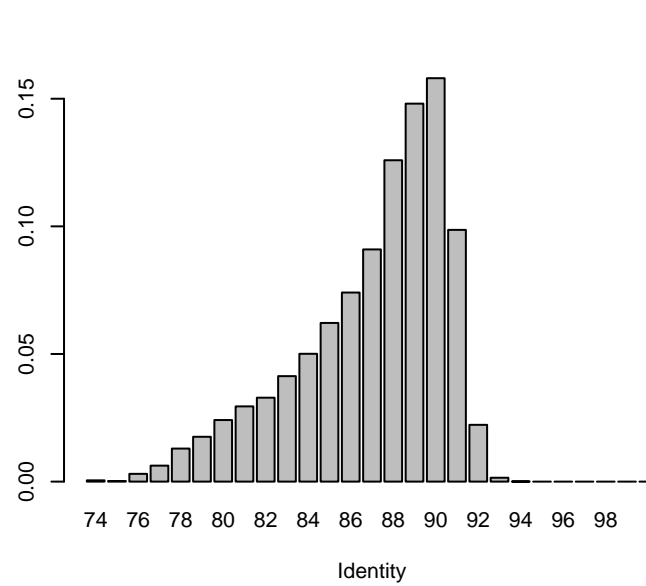


MetaMaps mapping summary for *Bacteroides vulgatus* ATCC 8482 (taxon ID 435590) – 16458 mapped reads assigned

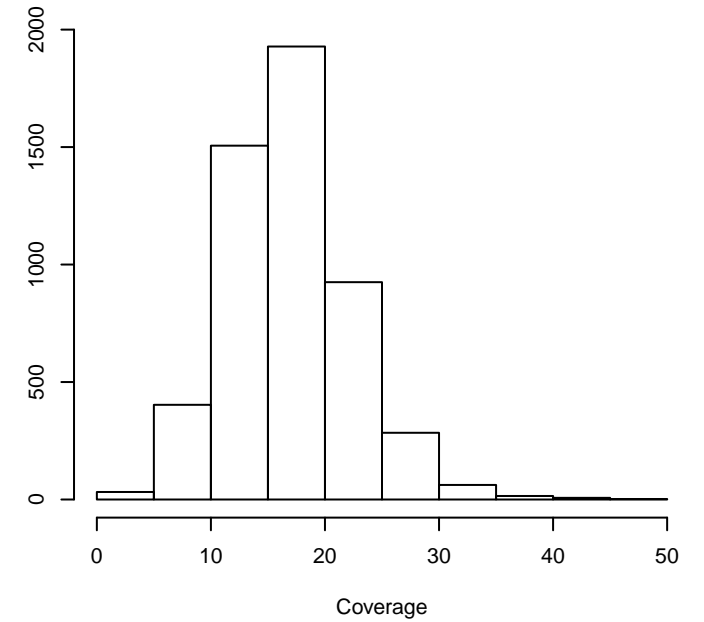
Read length histogram



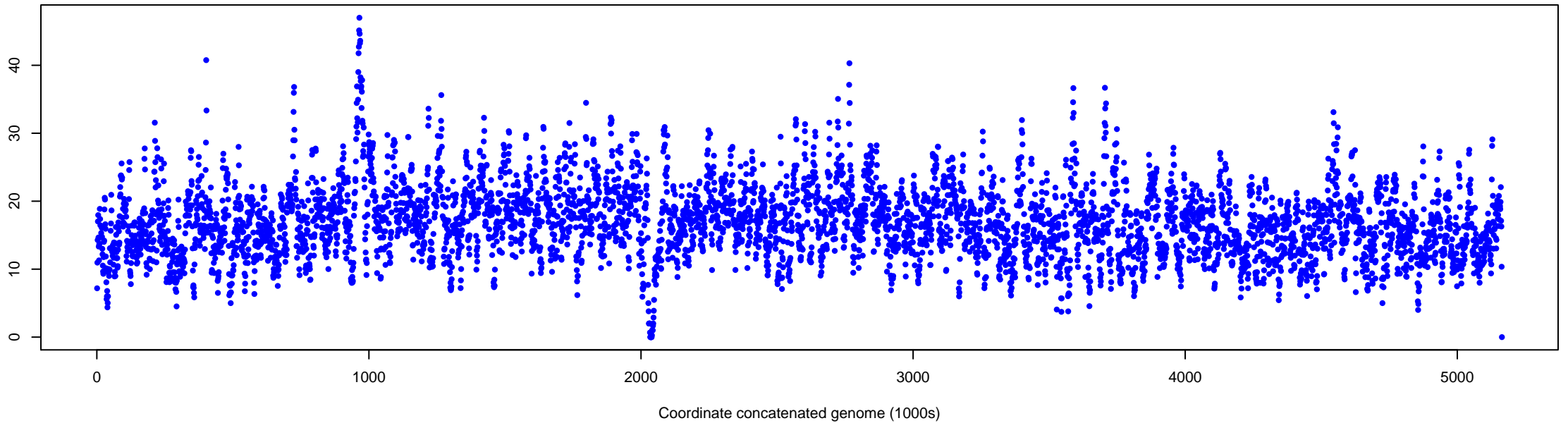
Read identities



Genome window coverage histogram

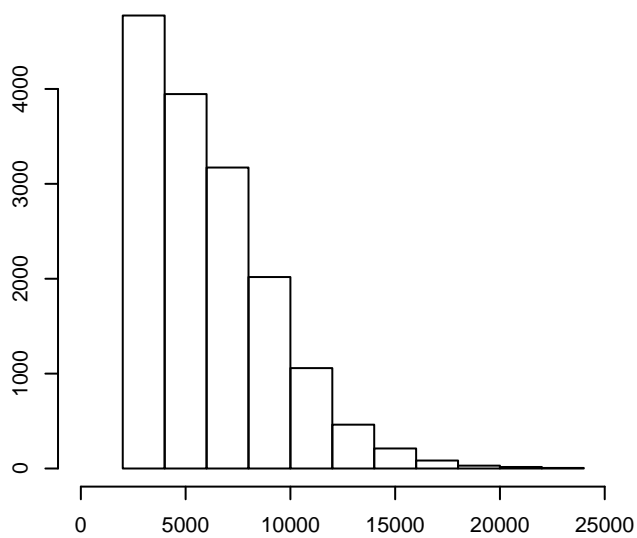


Genome-wide coverage over all contigs for *Bacteroides vulgatus* ATCC 8482 (taxon ID 435590) – 16458 mapped reads assigned

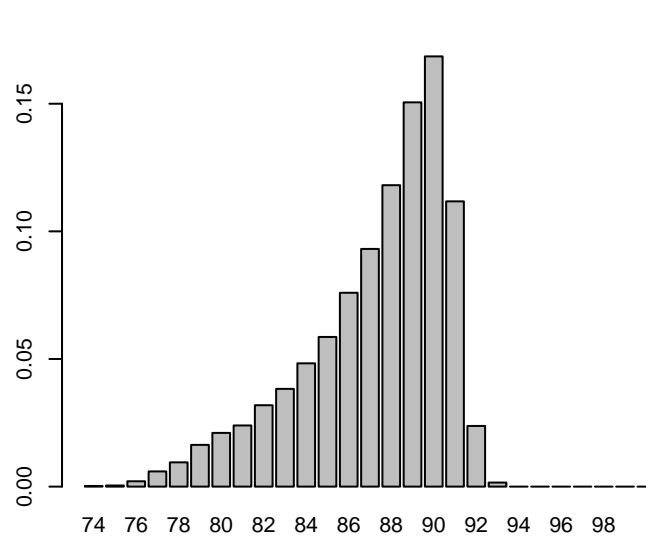


MetaMaps mapping summary for *Listeria monocytogenes* EGD-e (taxon ID 169963) – 15777 mapped reads assigned

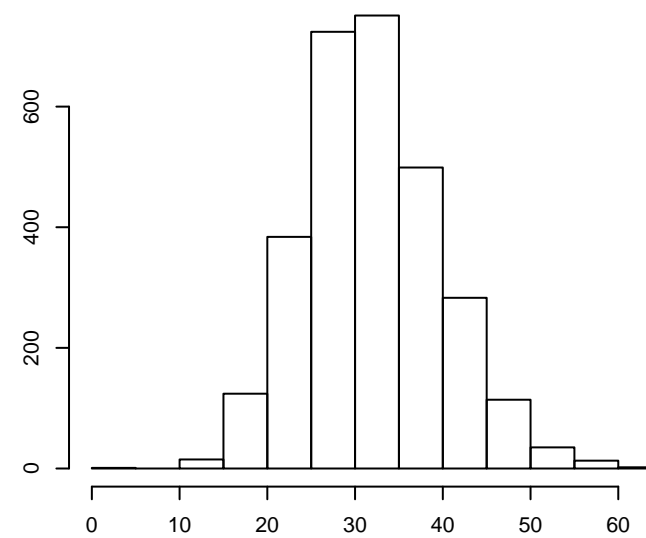
Read length histogram



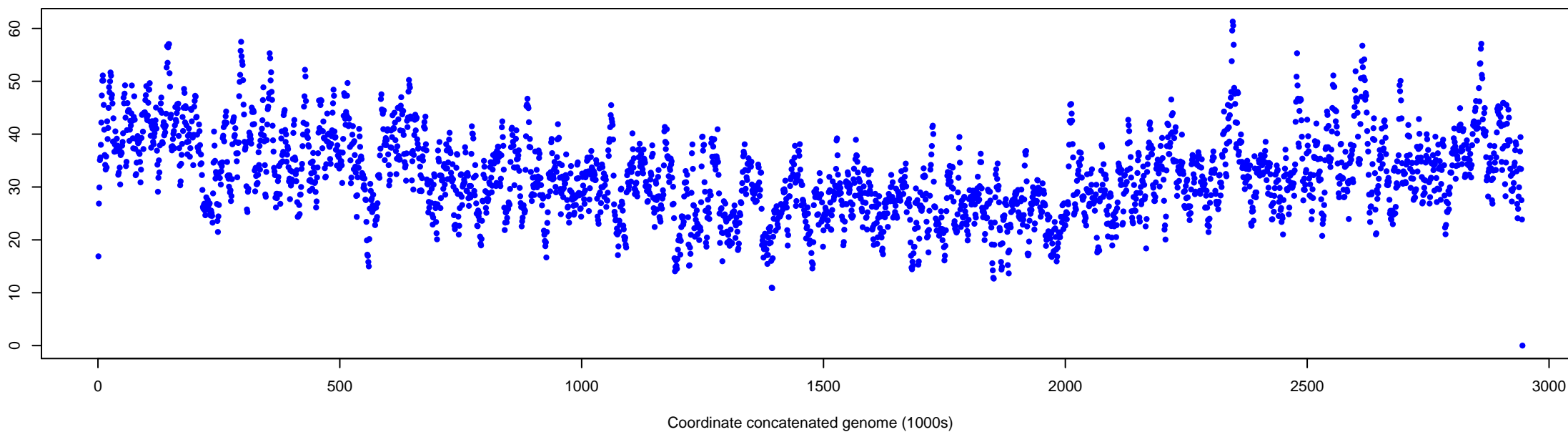
Read identities



Genome window coverage histogram

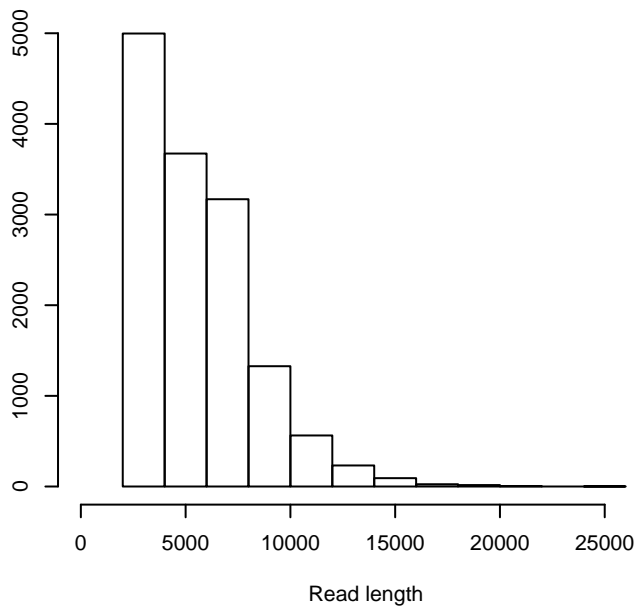


Genome-wide coverage over all contigs for *Listeria monocytogenes* EGD-e (taxon ID 169963) – 15777 mapped reads assigned

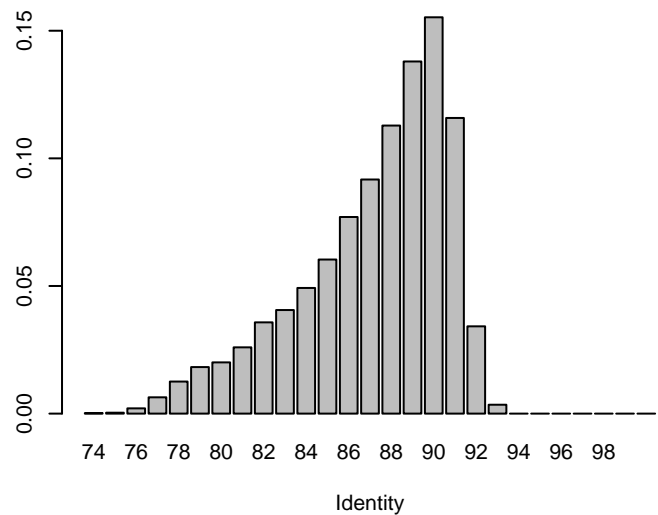


MetaMaps mapping summary for *Staphylococcus aureus* (firmicutes) (taxon ID x1770) – 14099 mapped reads assigned

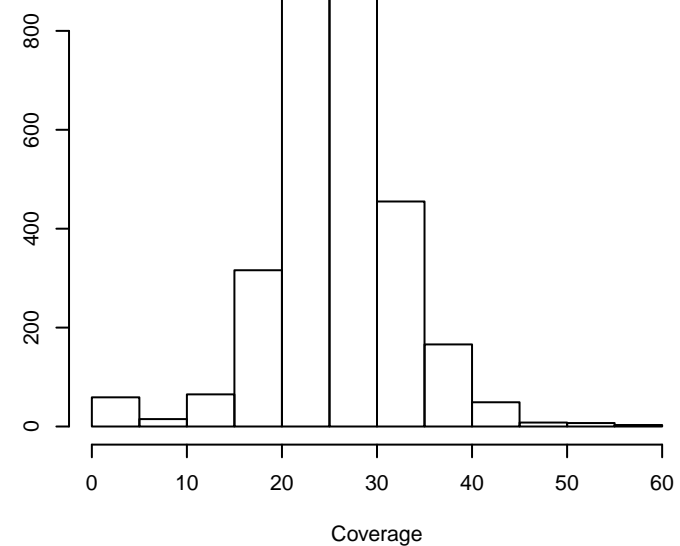
Read length histogram



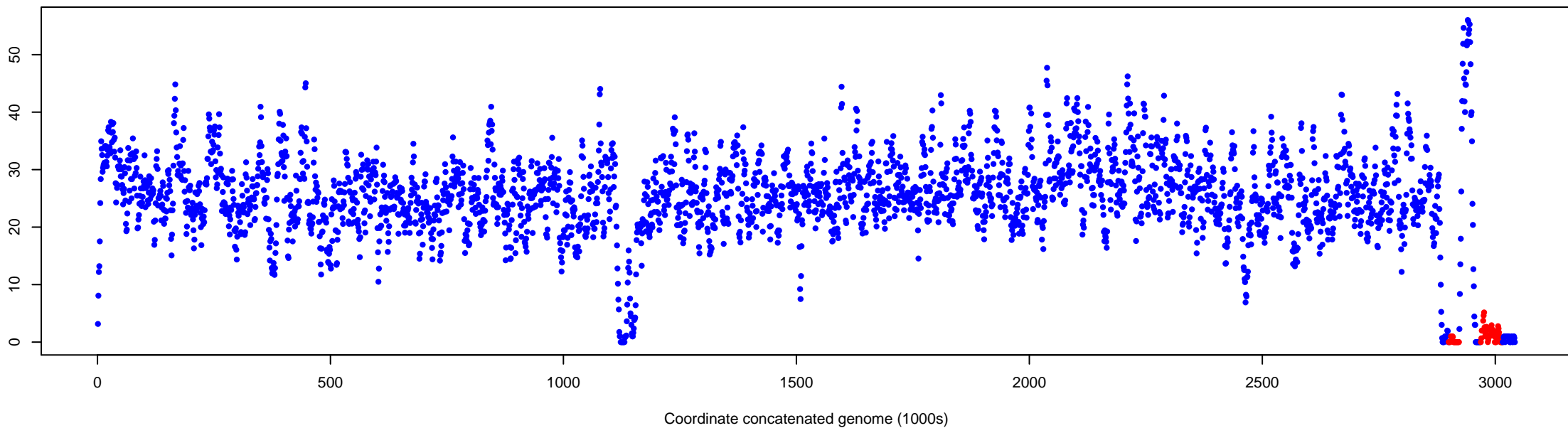
Read identities



Genome window coverage histogram

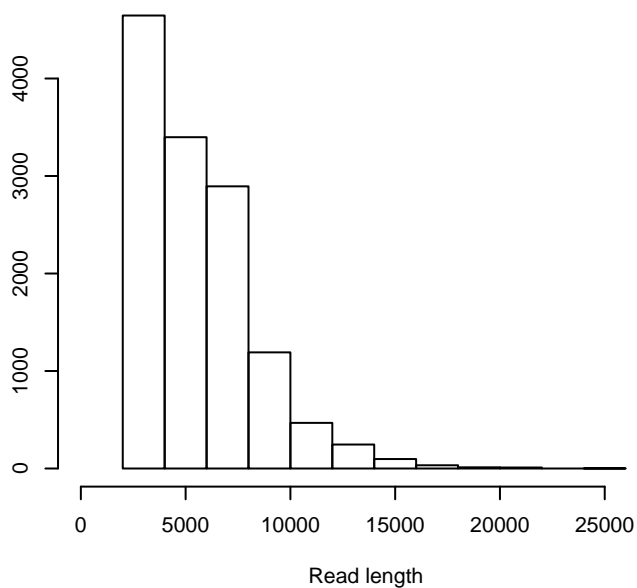


Genome-wide coverage over all contigs for *Staphylococcus aureus* (firmicutes) (taxon ID x1770) – 239 mapped reads assigned

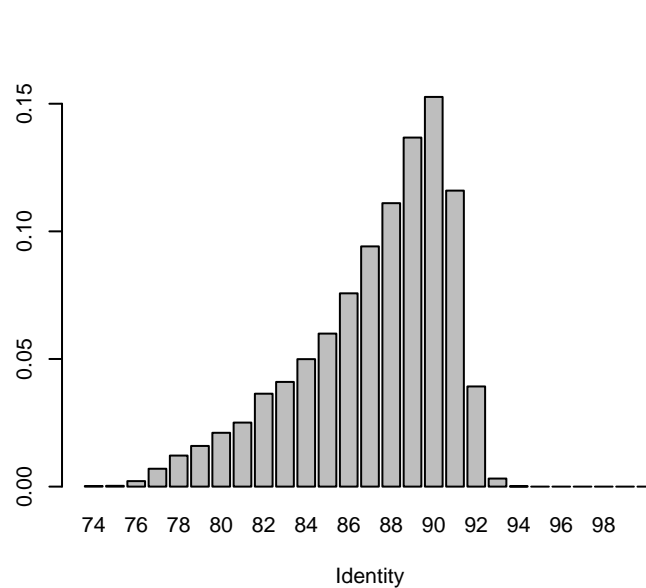


MetaMaps mapping summary for *Clostridium beijerinckii* NCIMB 8052 (taxon ID 290402) – 12996 mapped reads assigned

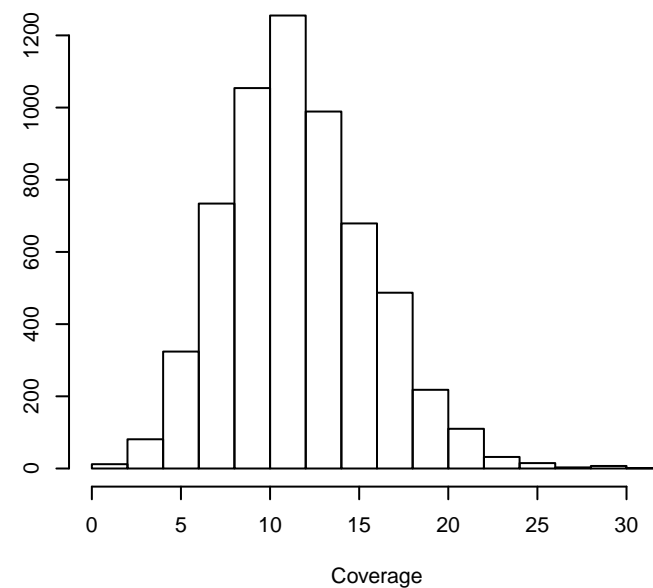
Read length histogram



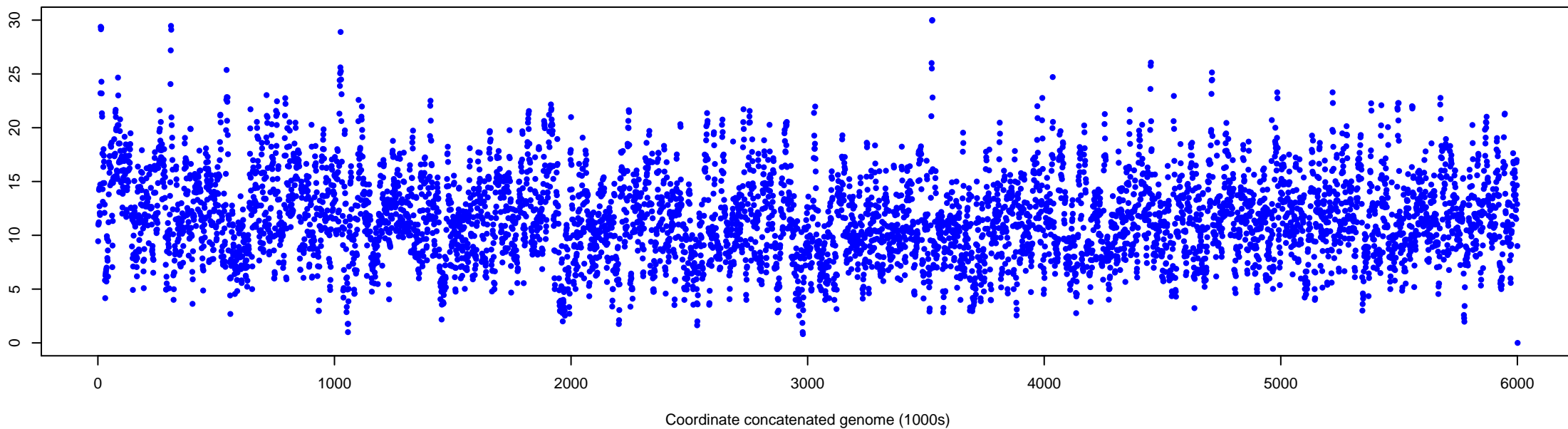
Read identities



Genome window coverage histogram

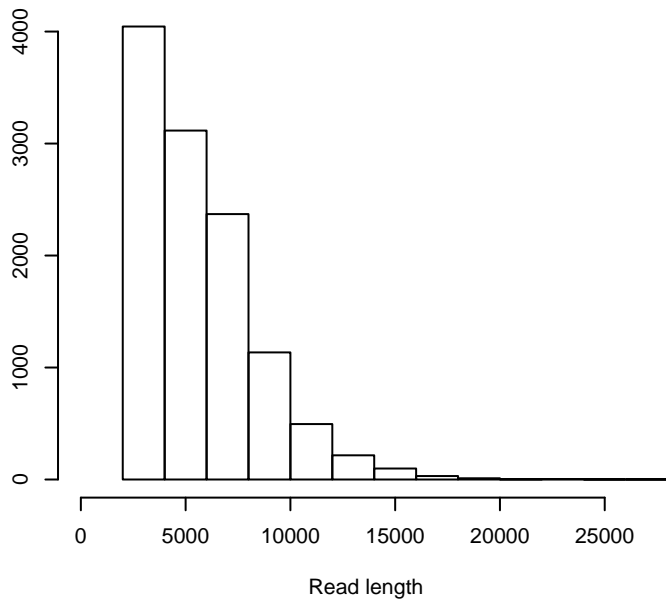


Genome-wide coverage over all contigs for *Clostridium beijerinckii* NCIMB 8052 (taxon ID 290402) – 12996 mapped reads assigned

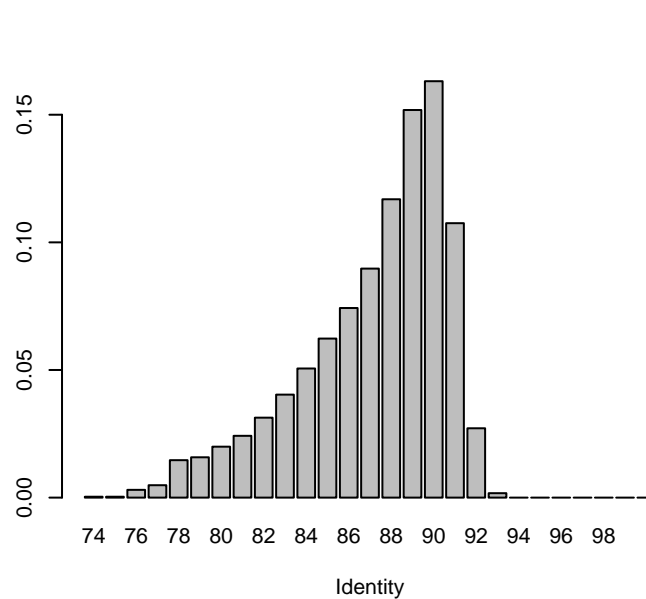


MetaMaps mapping summary for *Streptococcus mutans* UA159 (taxon ID 210007) – 11525 mapped reads assigned

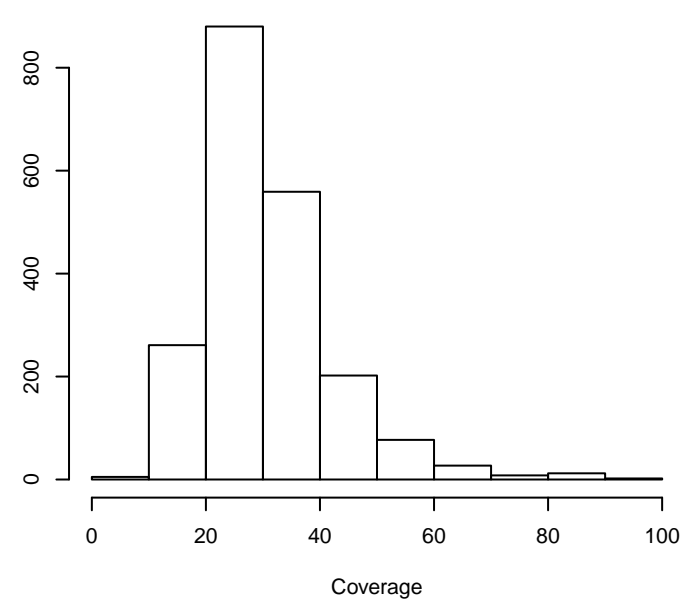
Read length histogram



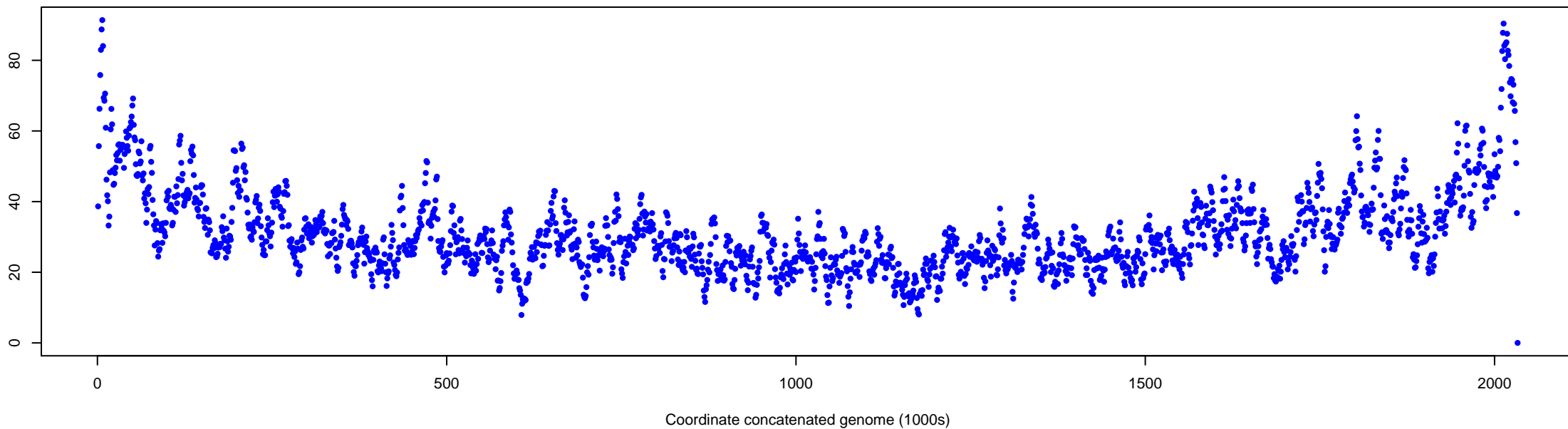
Read identities



Genome window coverage histogram

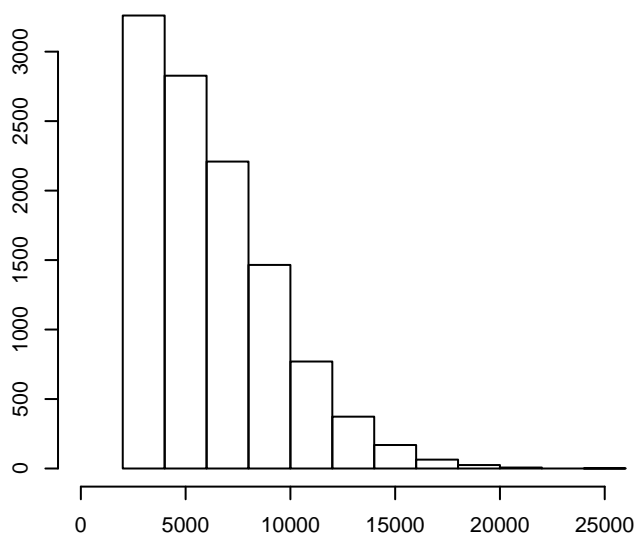


Genome-wide coverage over all contigs for *Streptococcus mutans* UA159 (taxon ID 210007) – 11525 mapped reads assigned

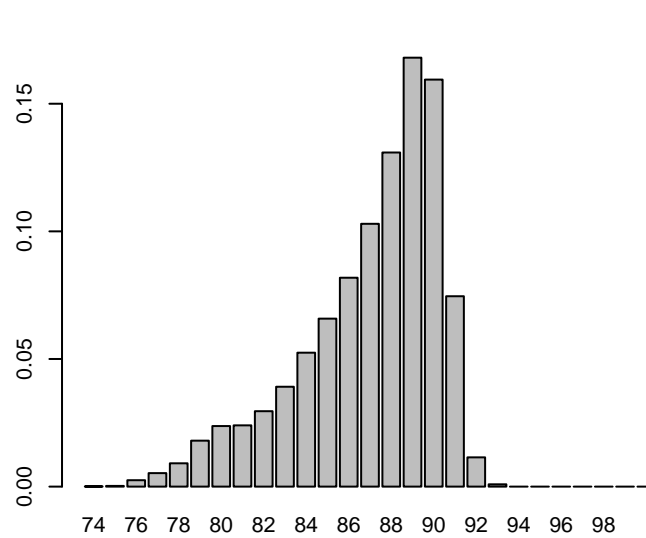


MetaMaps mapping summary for *Escherichia coli* str. K-12 substr. MG1655 (*E. coli*) (taxon ID x41) – 11170 mapped reads assigned

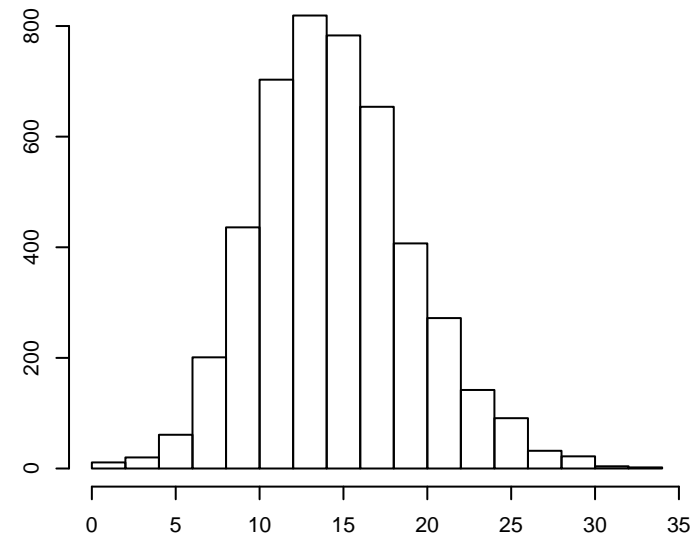
Read length histogram



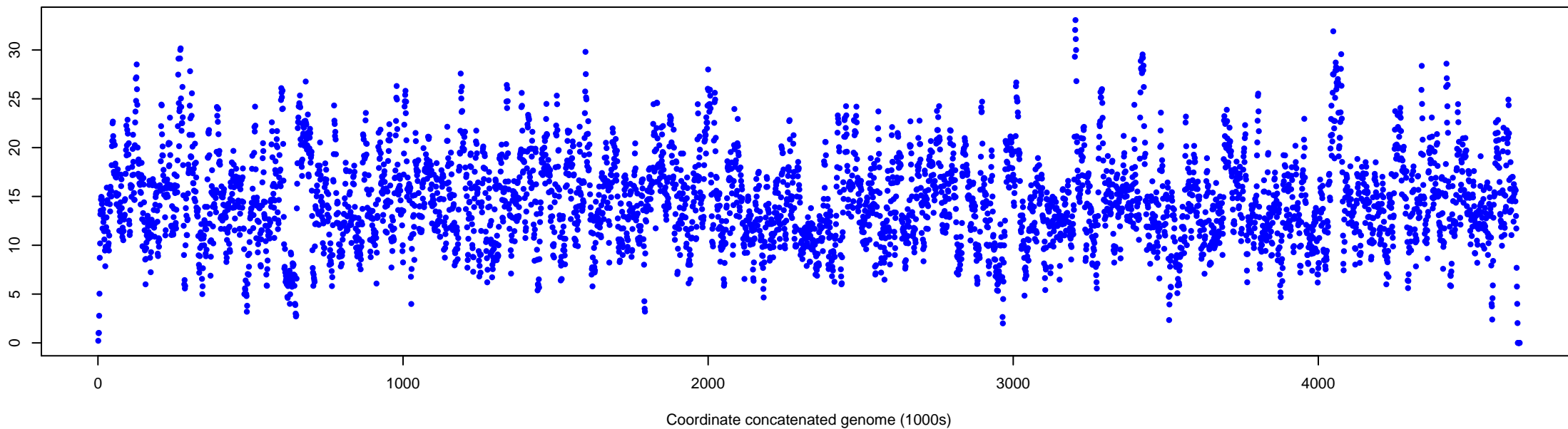
Read identities



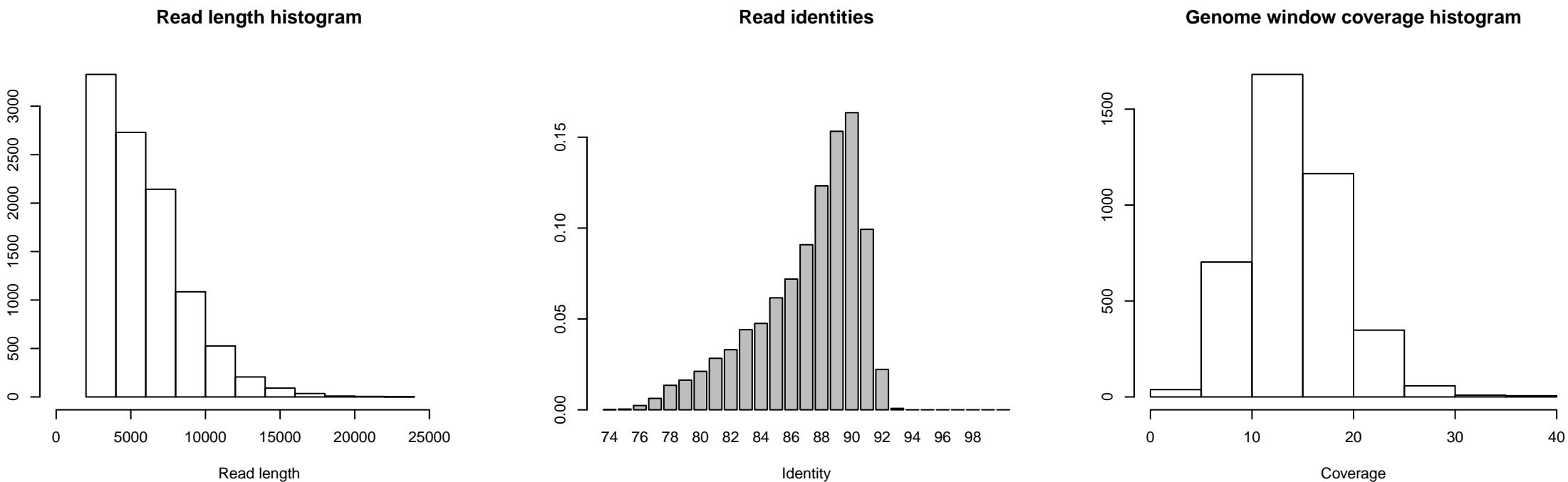
Genome window coverage histogram



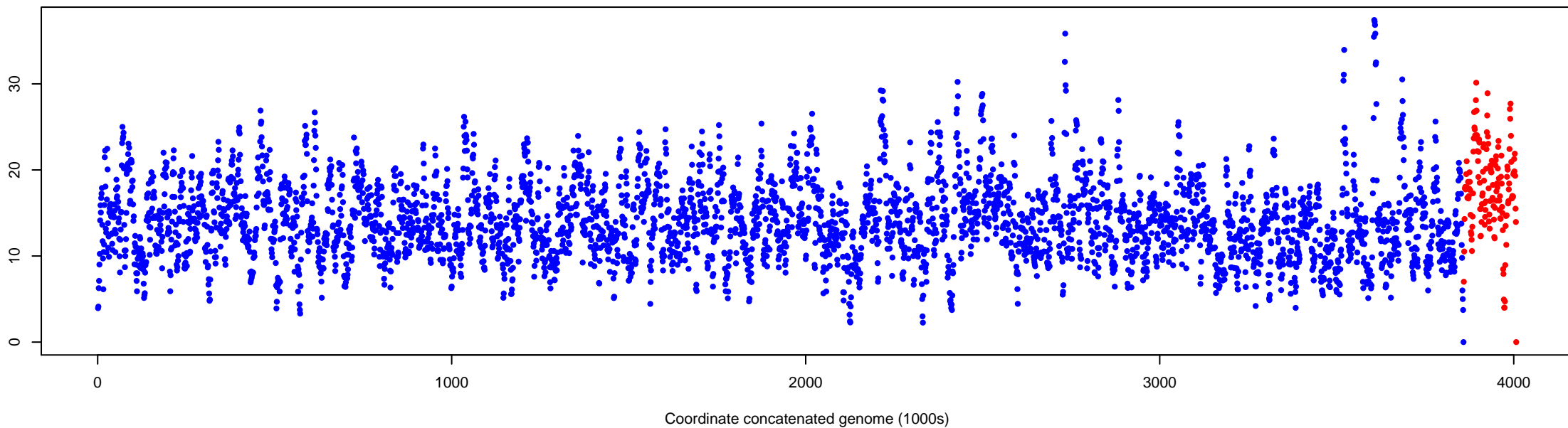
Genome-wide coverage over all contigs for *Escherichia coli* str. K-12 substr. MG1655 (*E. coli*) (taxon ID x41) – 11170 mapped reads assigned



MetaMaps mapping summary for *Acinetobacter baumannii* (g-proteobacteria) (taxon ID x1376) – 10160 mapped reads assigned

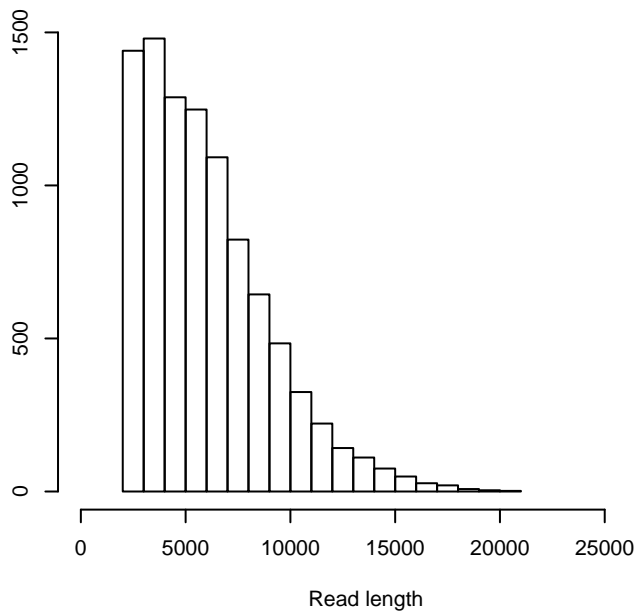


Genome-wide coverage over all contigs for *Acinetobacter baumannii* (g-proteobacteria) (taxon ID x1376) – 485 mapped reads assigned

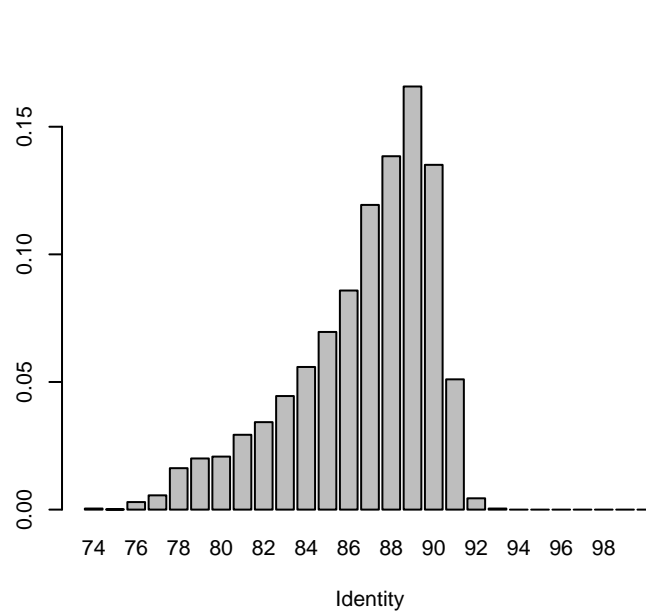


MetaMaps mapping summary for *Propionibacterium acnes* KPA171202 (taxon ID 267747) – 9484 mapped reads assigned

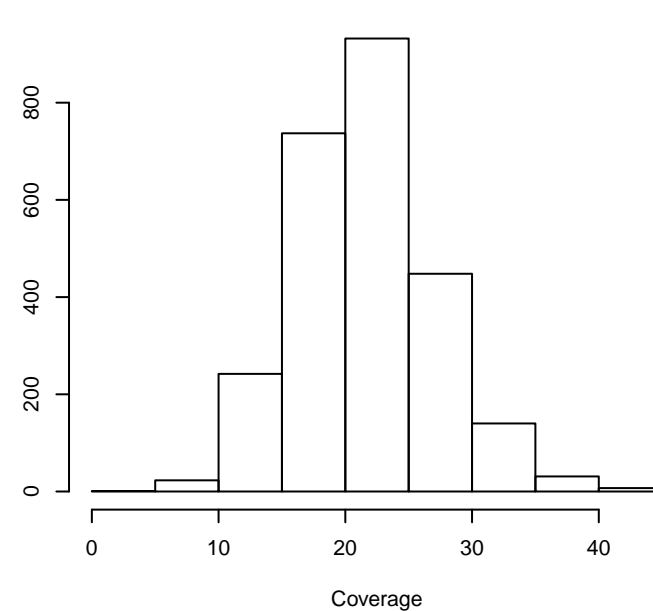
Read length histogram



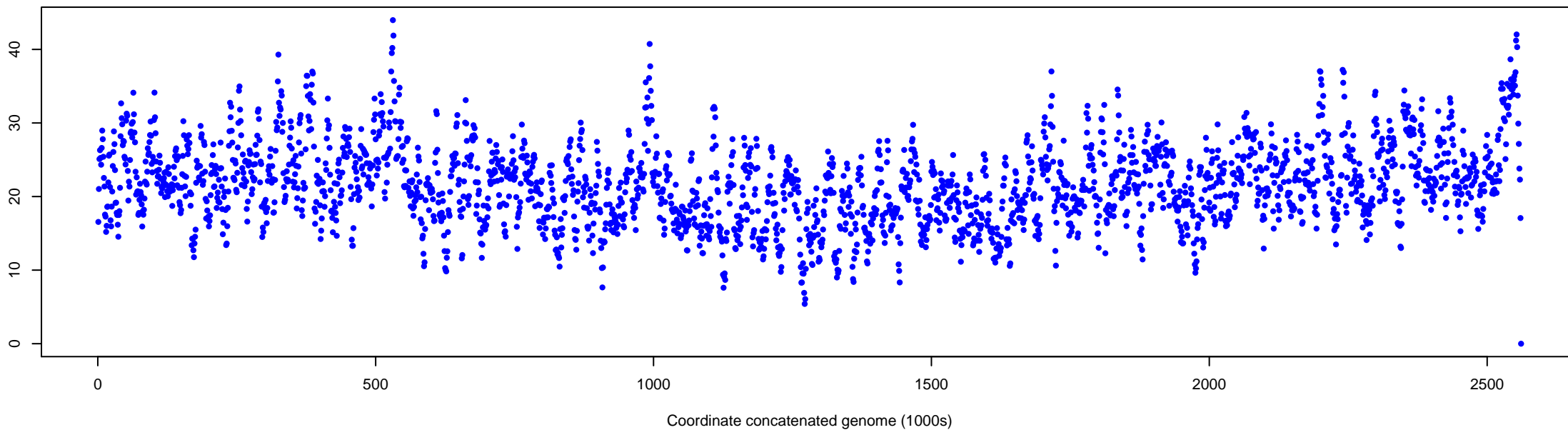
Read identities



Genome window coverage histogram

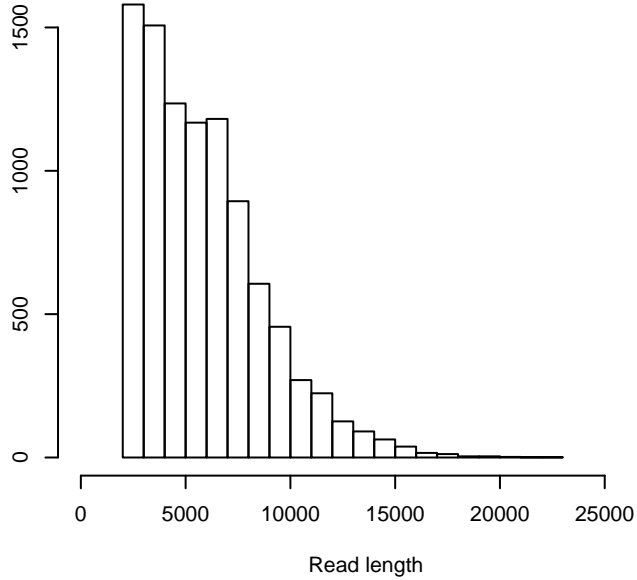


Genome-wide coverage over all contigs for *Propionibacterium acnes* KPA171202 (taxon ID 267747) – 9484 mapped reads assigned

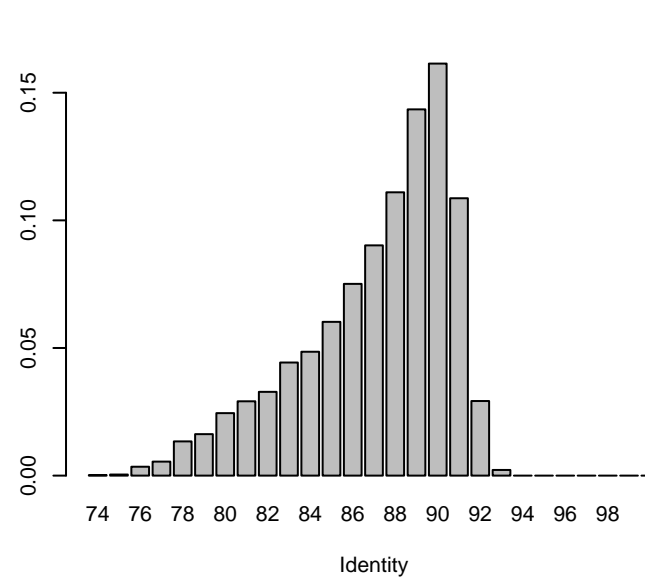


MetaMaps mapping summary for *Lactobacillus gasseri* ATCC 33323 = JCM 1131 (taxon ID 324831) – 9479 mapped reads assigned

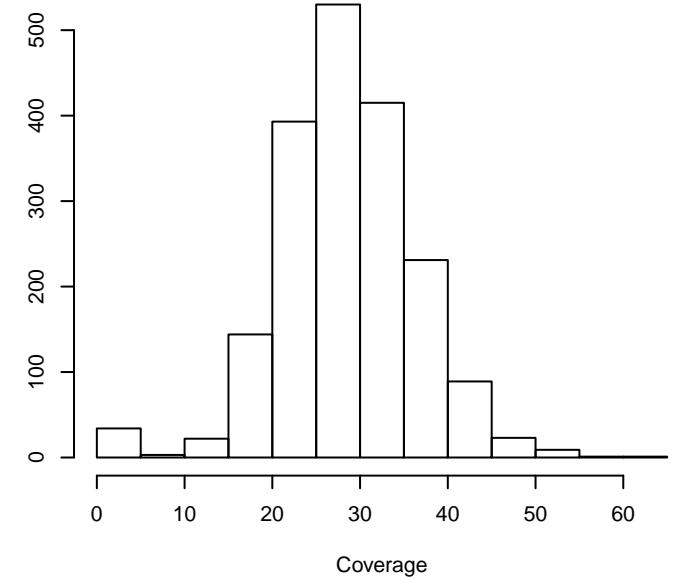
Read length histogram



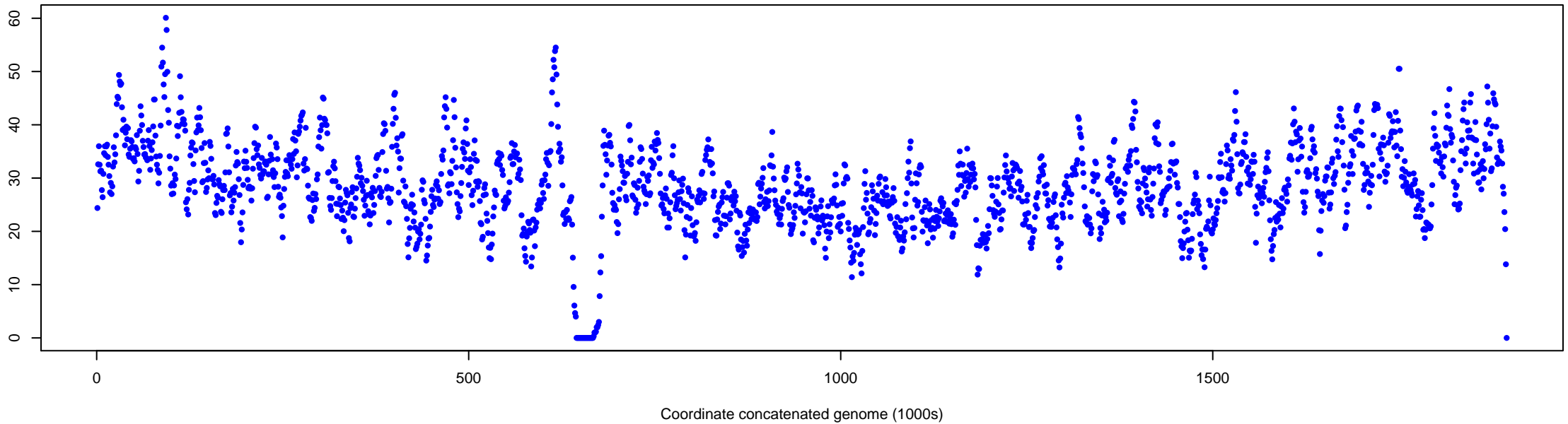
Read identities



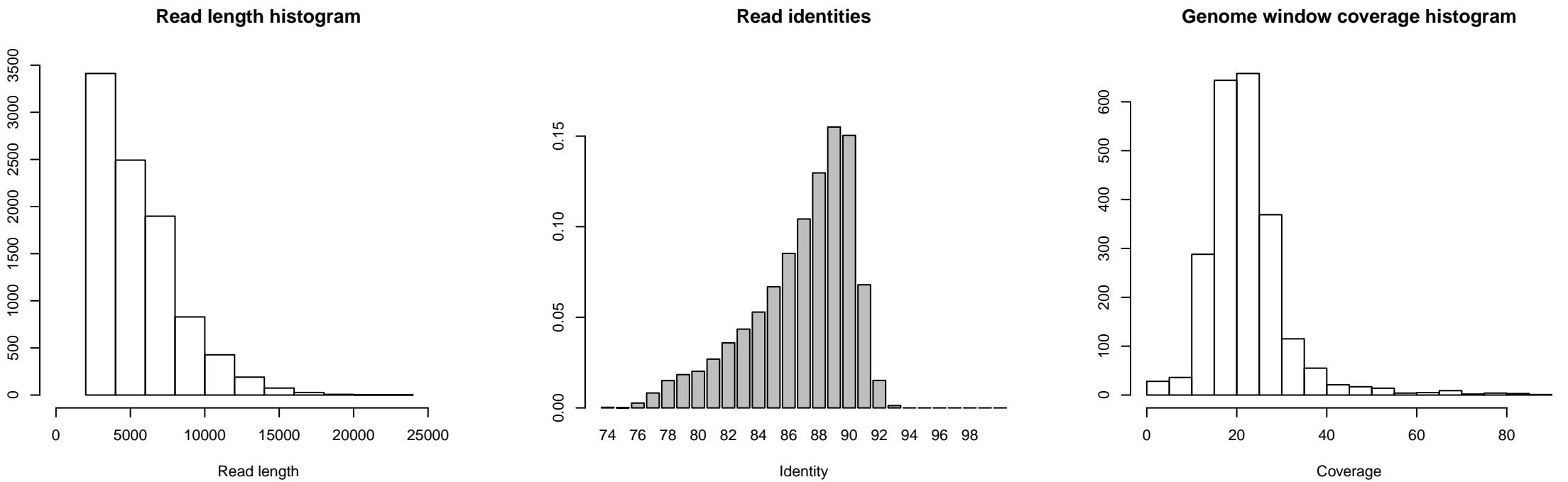
Genome window coverage histogram



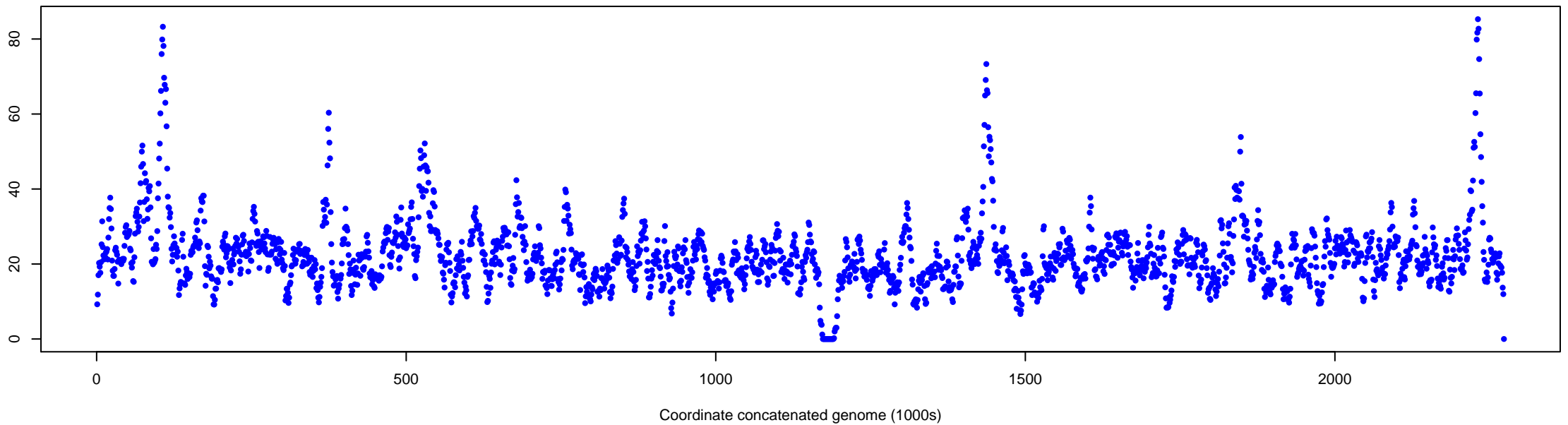
Genome-wide coverage over all contigs for *Lactobacillus gasseri* ATCC 33323 = JCM 1131 (taxon ID 324831) – 9479 mapped reads assigned



MetaMaps mapping summary for *Neisseria meningitidis* MC58 (taxon ID 122586) – 9361 mapped reads assigned

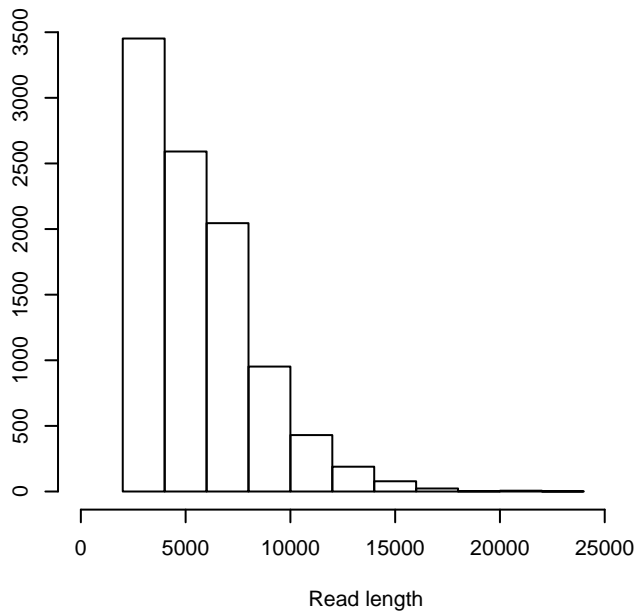


Genome-wide coverage over all contigs for *Neisseria meningitidis* MC58 (taxon ID 122586) – 9361 mapped reads assigned

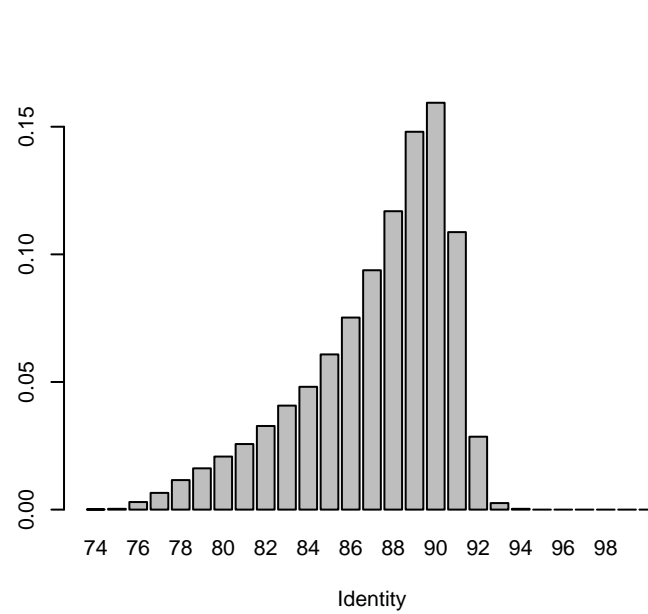


MetaMaps mapping summary for *Bacillus cereus* ATCC 10987 (taxon ID 222523) – 9769 mapped reads assigned

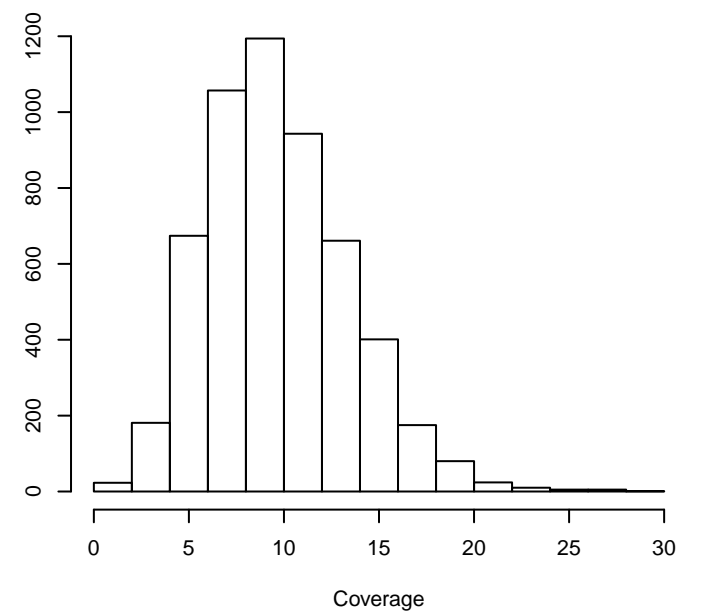
Read length histogram



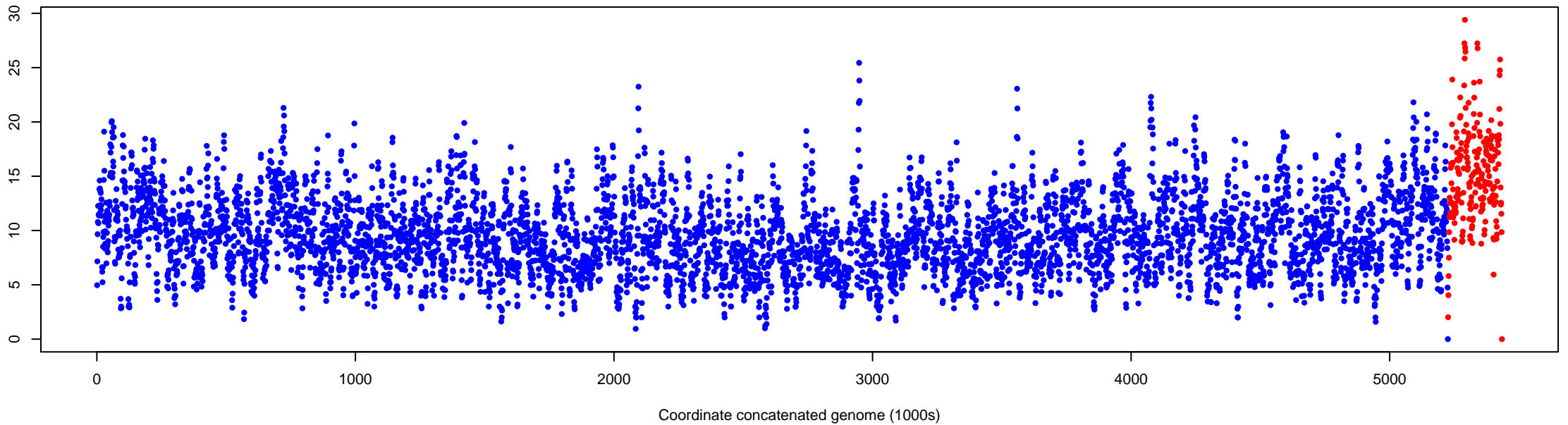
Read identities



Genome window coverage histogram

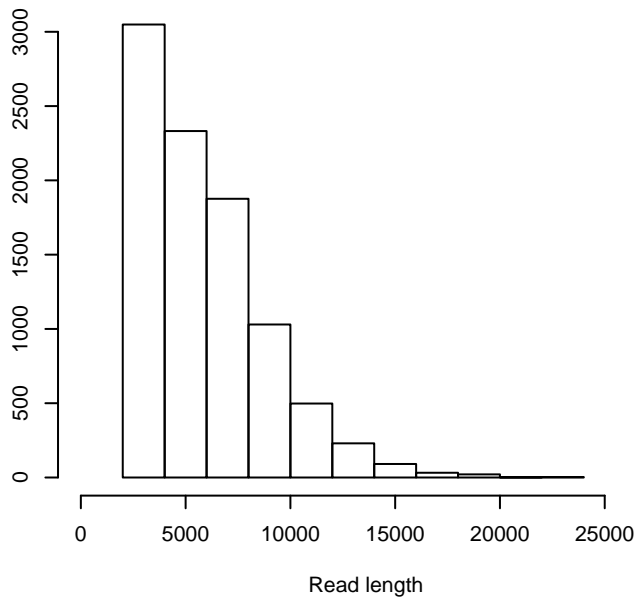


Genome-wide coverage over all contigs for *Bacillus cereus* ATCC 10987 (taxon ID 222523) – 604 mapped reads assigned

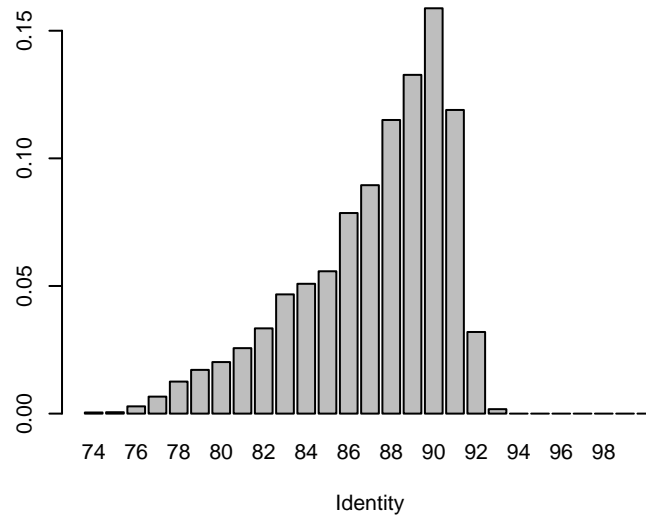


MetaMaps mapping summary for *Staphylococcus epidermidis* ATCC 12228 (taxon ID 176280) – 9163 mapped reads assigned

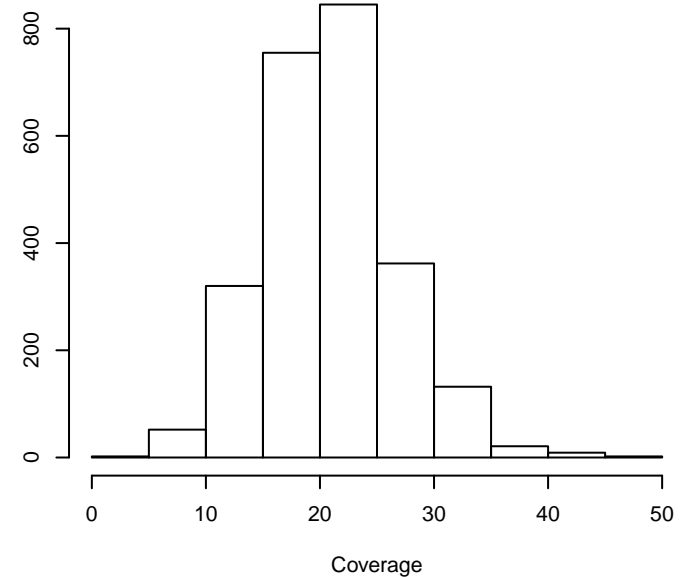
Read length histogram



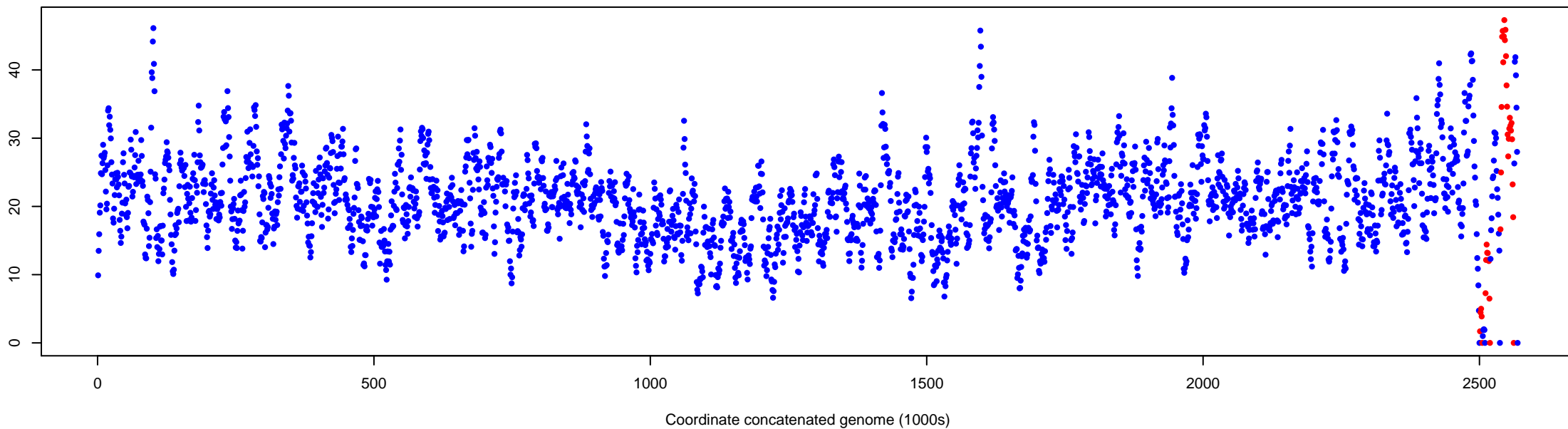
Read identities



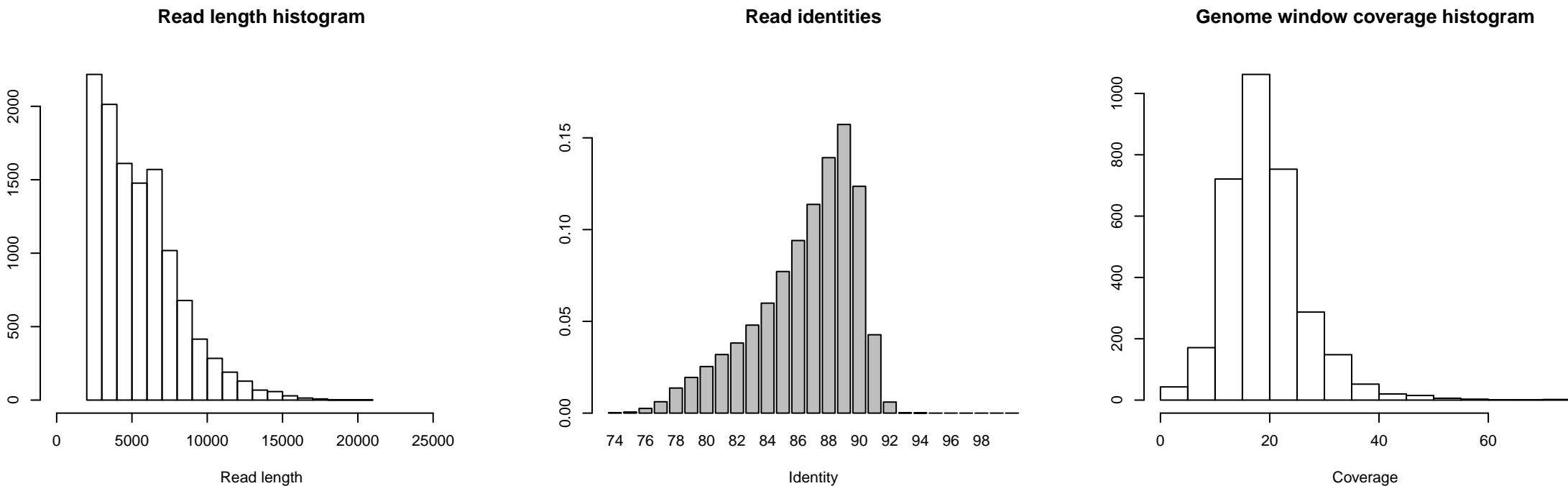
Genome window coverage histogram



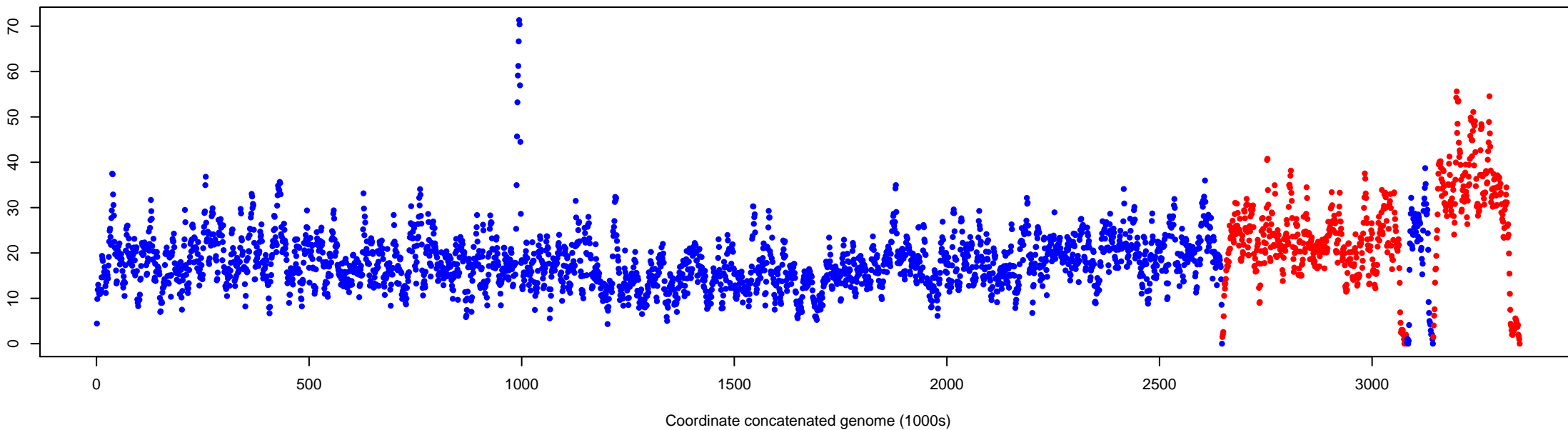
Genome-wide coverage over all contigs for *Staphylococcus epidermidis* ATCC 12228 (taxon ID 176280) – 9169 mapped reads assigned



MetaMaps mapping summary for *Deinococcus radiodurans* R1 (bacteria) (taxon ID x1049) – 11782 mapped reads assigned

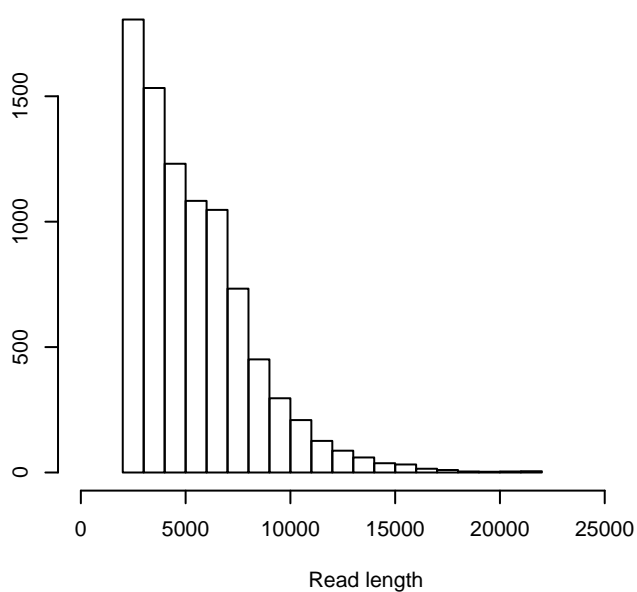


Genome-wide coverage over all contigs for *Deinococcus radiodurans* R1 (bacteria) (taxon ID x1049) – 1214 mapped reads assigned

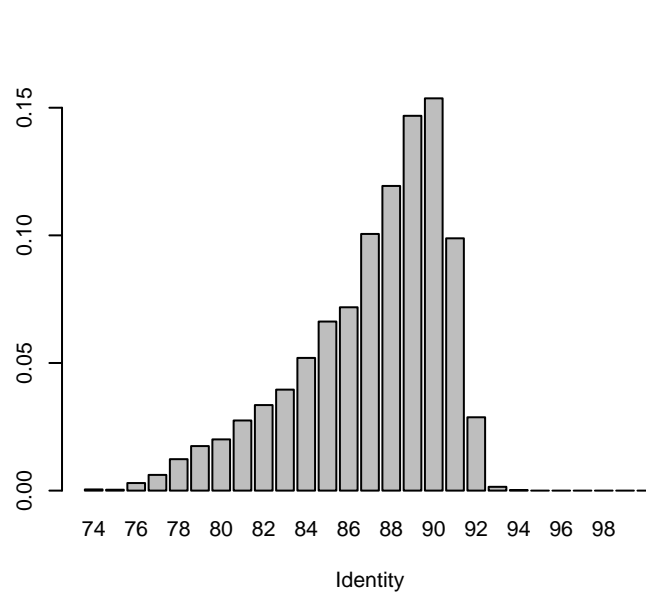


MetaMaps mapping summary for *Enterococcus faecalis* OG1RF (taxon ID 474186) – 8772 mapped reads assigned

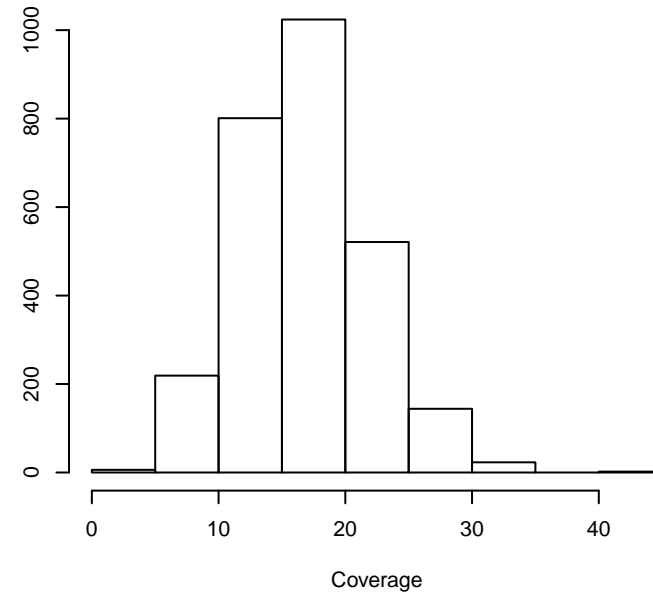
Read length histogram



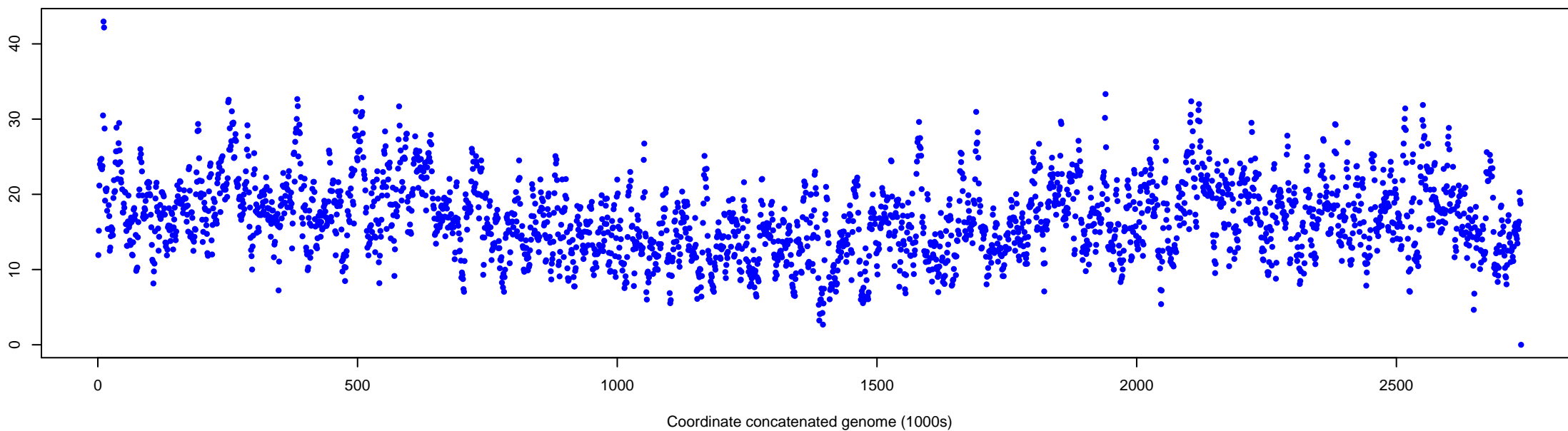
Read identities



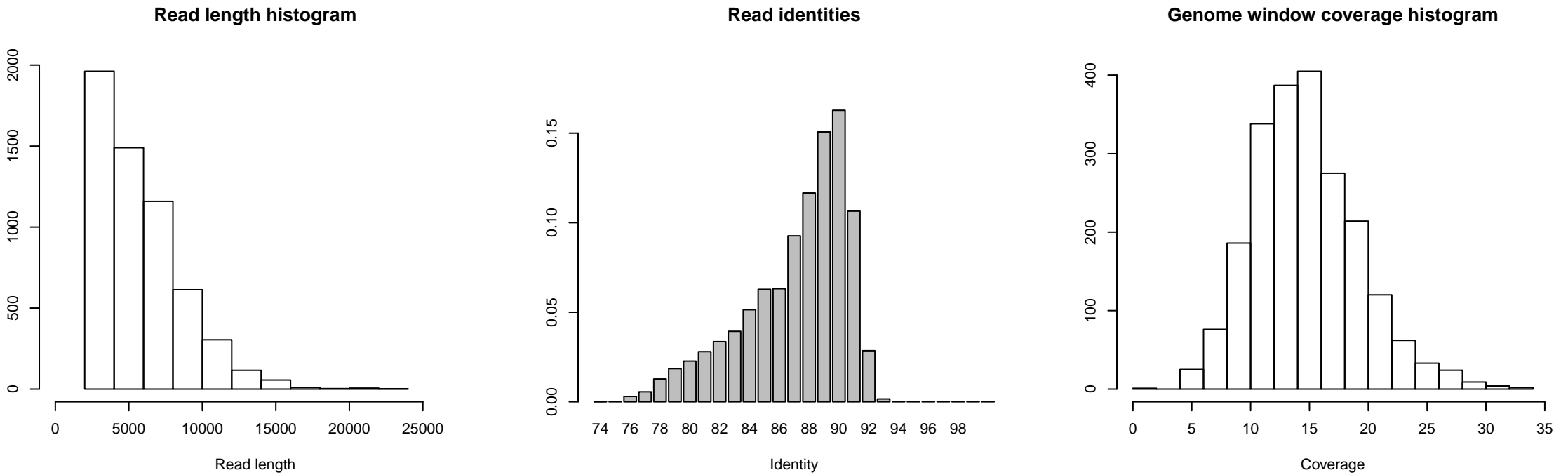
Genome window coverage histogram



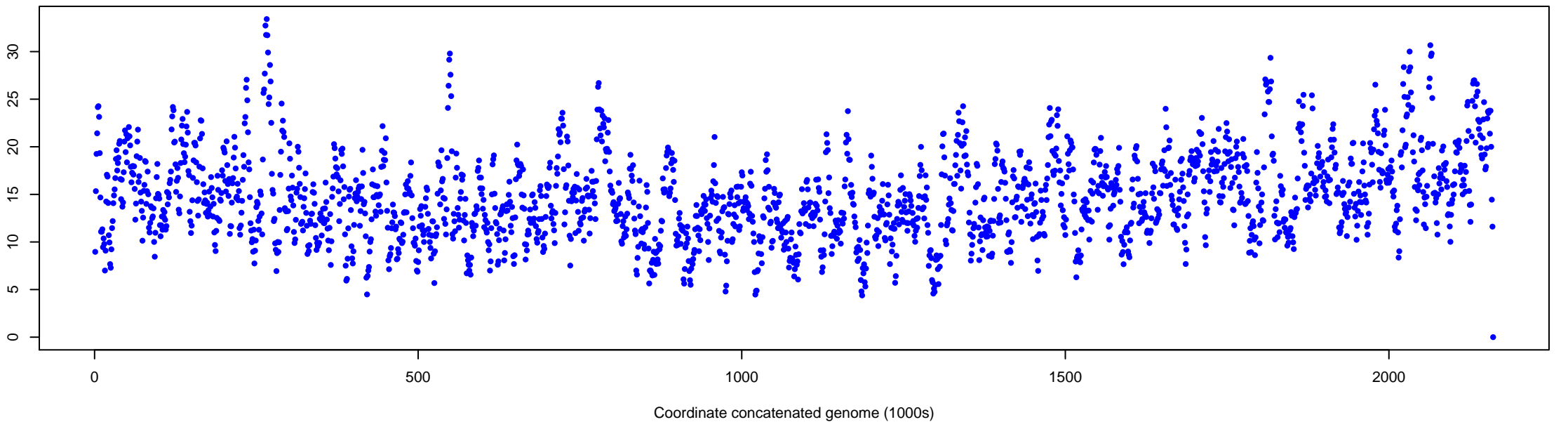
Genome-wide coverage over all contigs for *Enterococcus faecalis* OG1RF (taxon ID 474186) – 8772 mapped reads assigned



MetaMaps mapping summary for *Streptococcus agalactiae* 2603V/R (taxon ID 208435) – 5721 mapped reads assigned

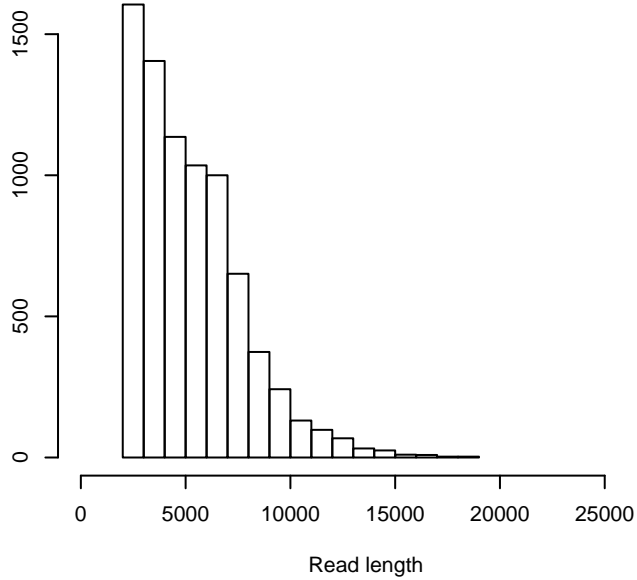


Genome-wide coverage over all contigs for *Streptococcus agalactiae* 2603V/R (taxon ID 208435) – 5721 mapped reads assigned

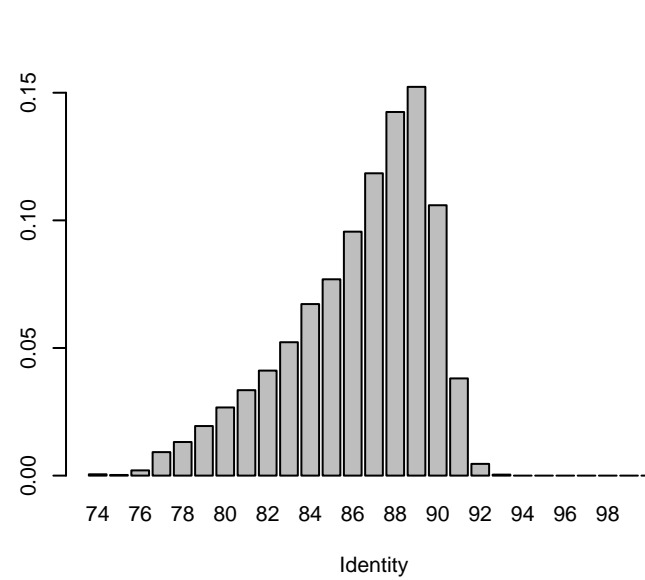


MetaMaps mapping summary for *Rhodobacter sphaeroides* (α-proteobacteria) (taxon ID x1520) – 7827 mapped reads assigned

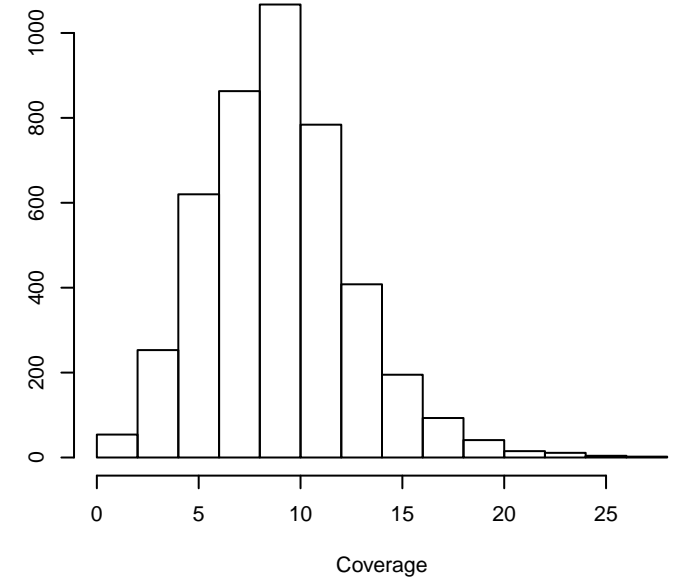
Read length histogram



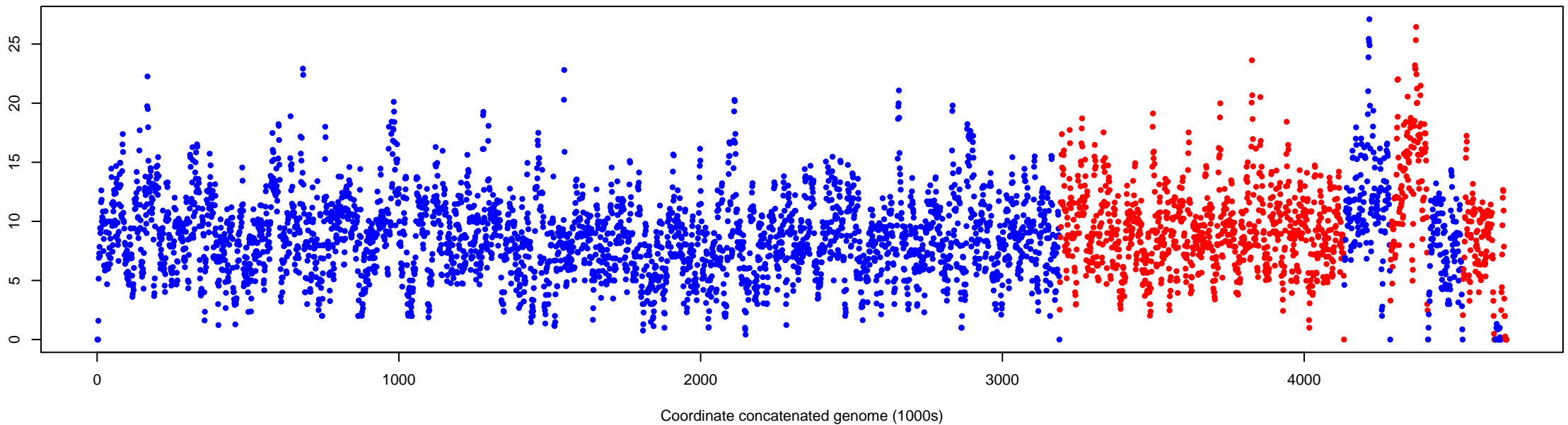
Read identities



Genome window coverage histogram

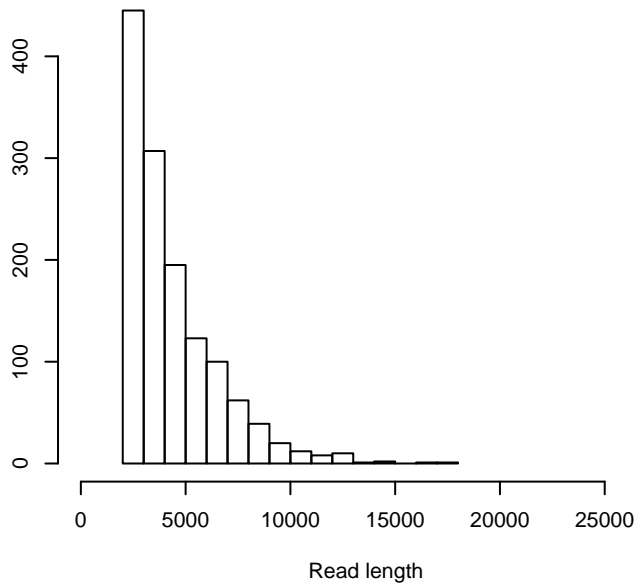


Genome-wide coverage over all contigs for *Rhodobacter sphaeroides* (α-proteobacteria) (taxon ID x1520) – 354 mapped reads assigned

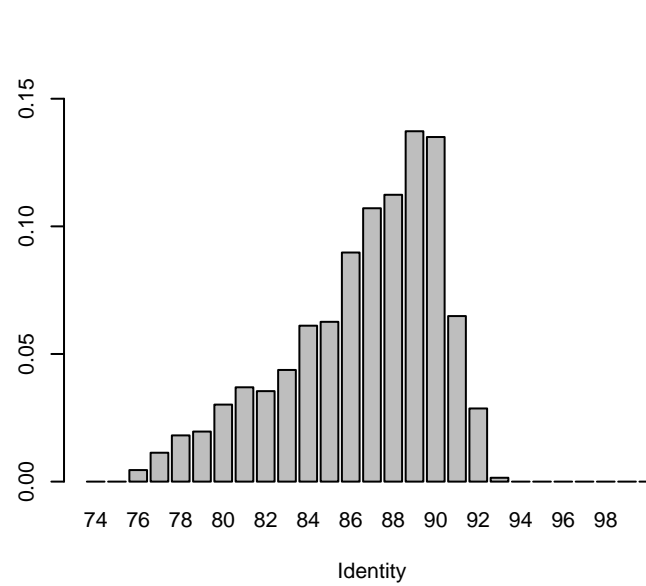


MetaMaps mapping summary for *Streptococcus pneumoniae* TIGR4 (taxon ID 170187) – 1326 mapped reads assigned

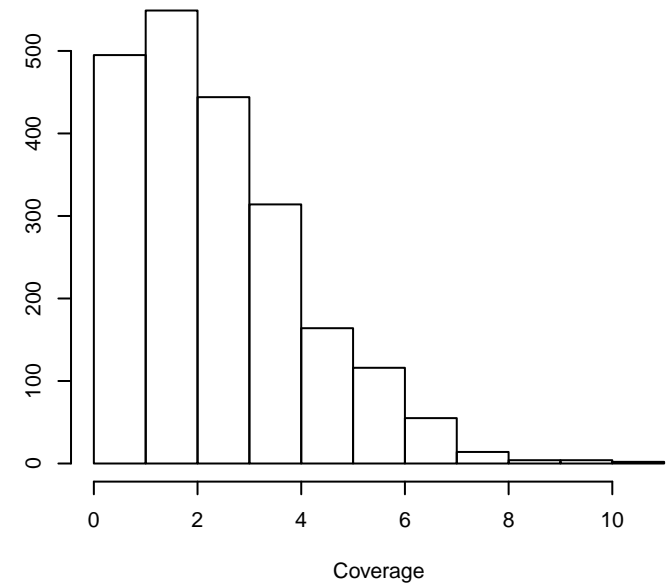
Read length histogram



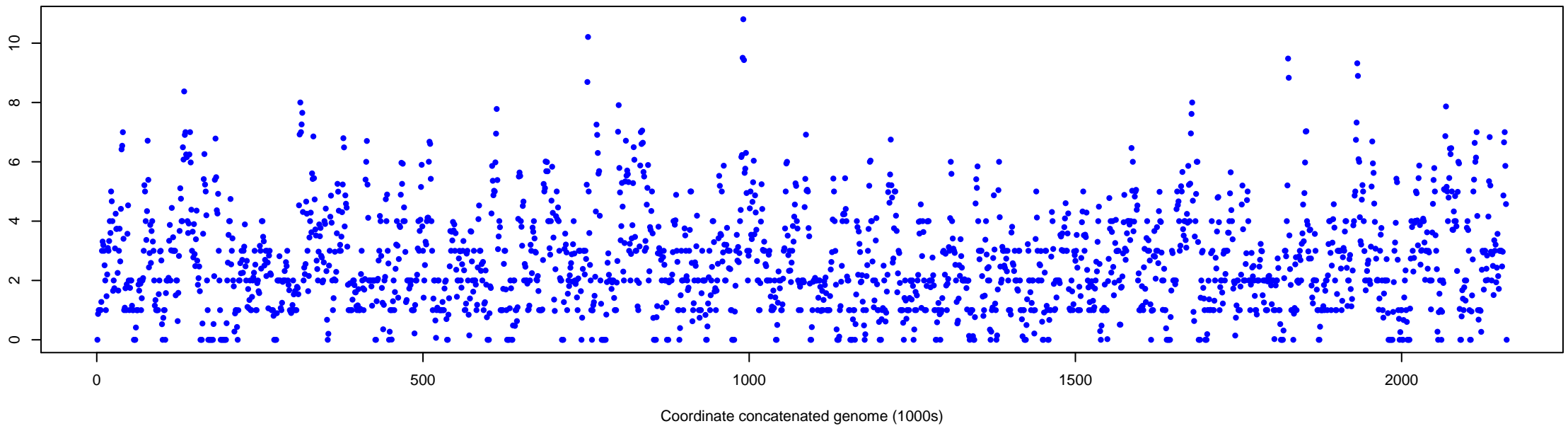
Read identities



Genome window coverage histogram

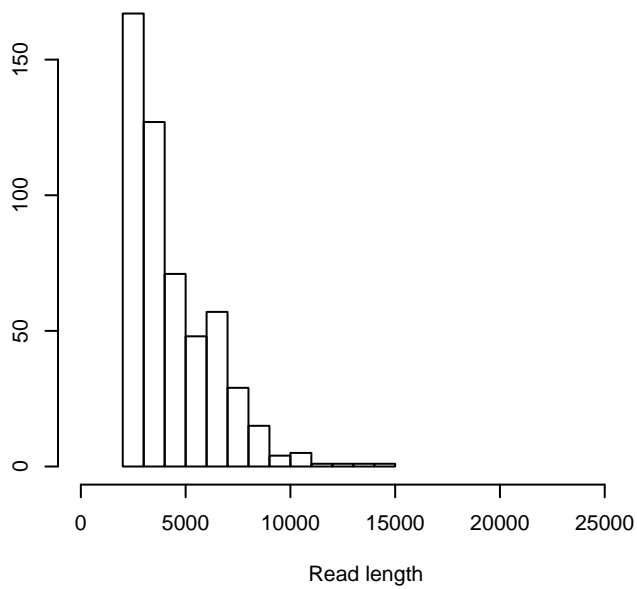


Genome-wide coverage over all contigs for *Streptococcus pneumoniae* TIGR4 (taxon ID 170187) – 1326 mapped reads assigned

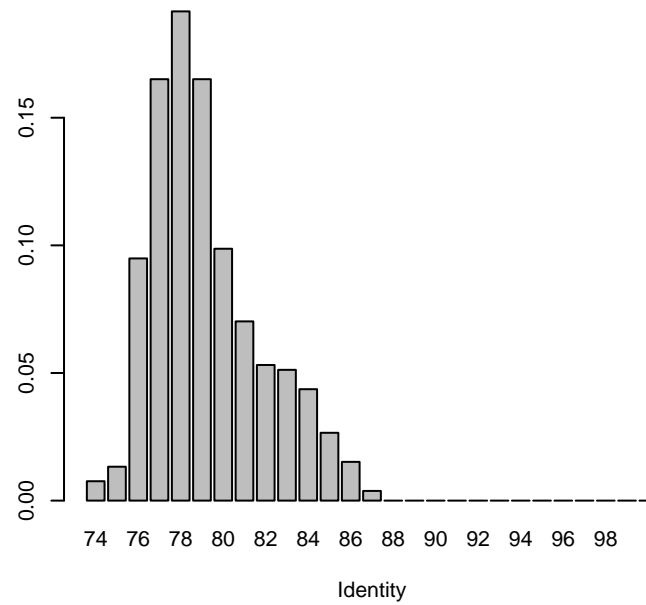


MetaMaps mapping summary for *Actinomyces meyeri* (taxon ID 52773) – 527 mapped reads assigned

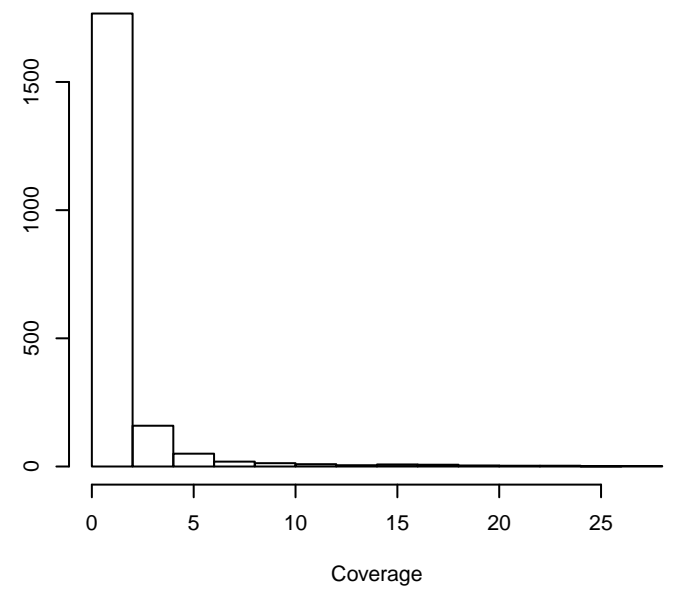
Read length histogram



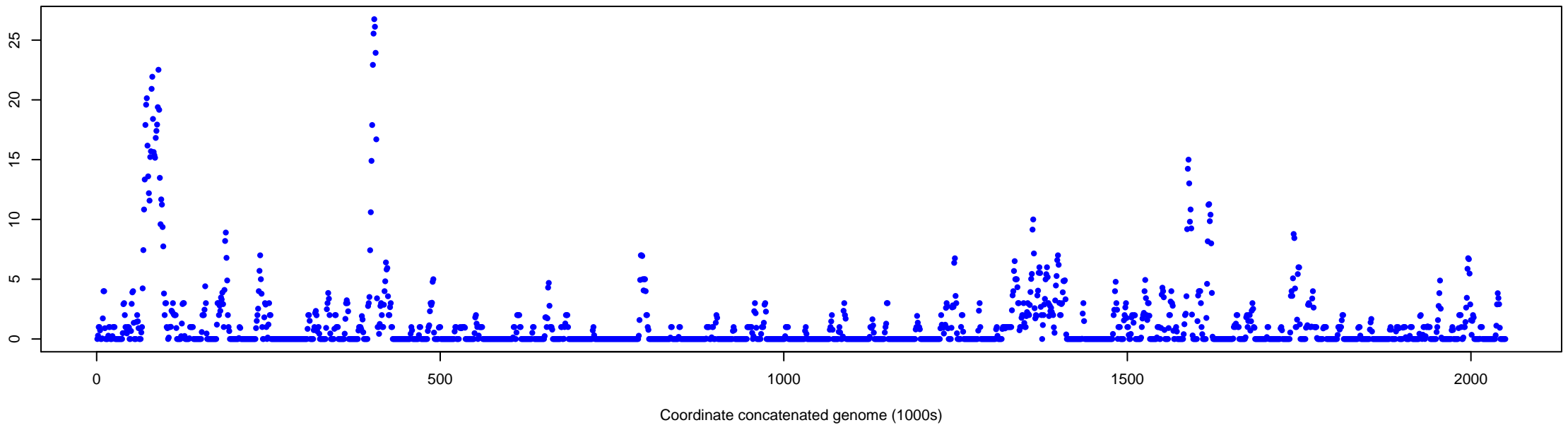
Read identities



Genome window coverage histogram

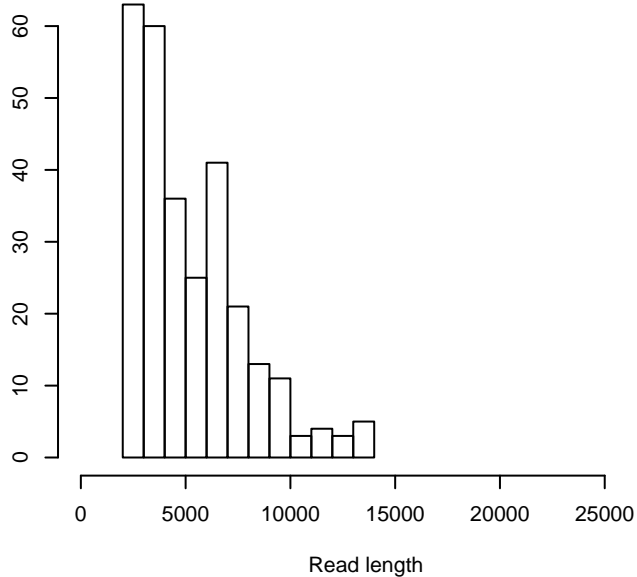


Genome-wide coverage over all contigs for *Actinomyces meyeri* (taxon ID 52773) – 527 mapped reads assigned

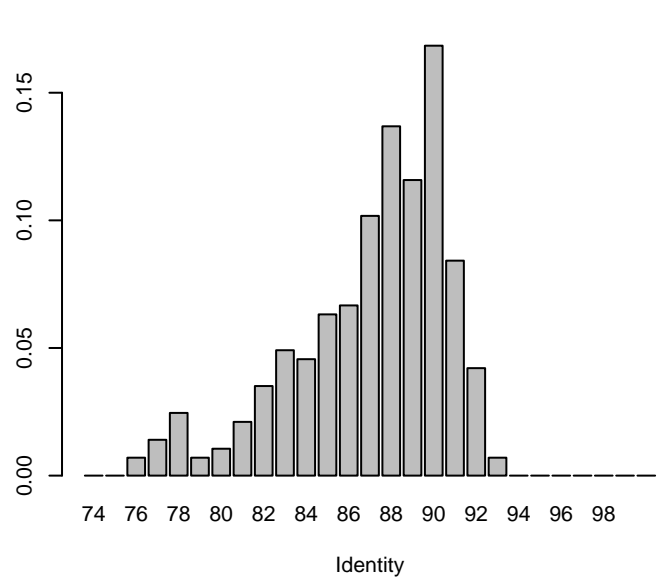


MetaMaps mapping summary for Staphylococcus phage 23MRA (taxon ID 1505027) – 285 mapped reads assigned

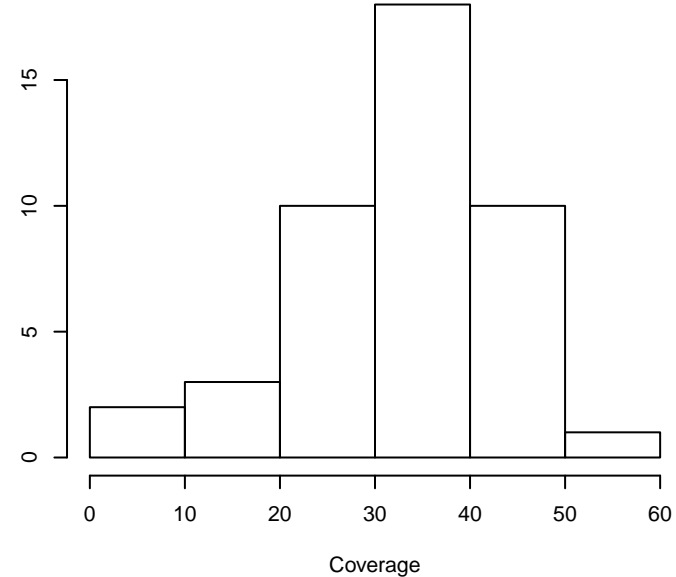
Read length histogram



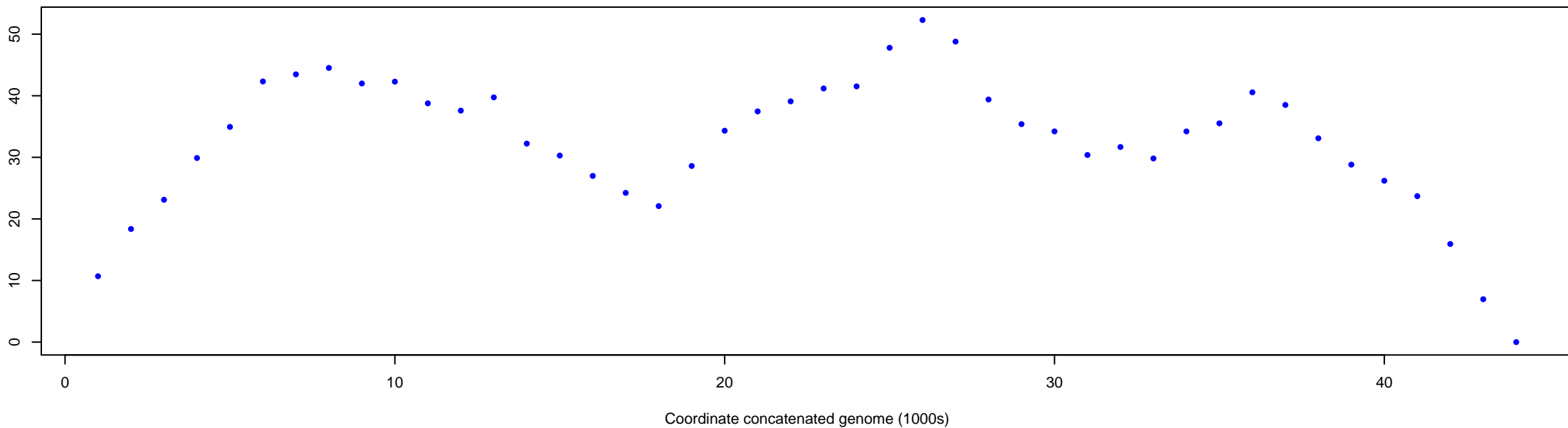
Read identities



Genome window coverage histogram

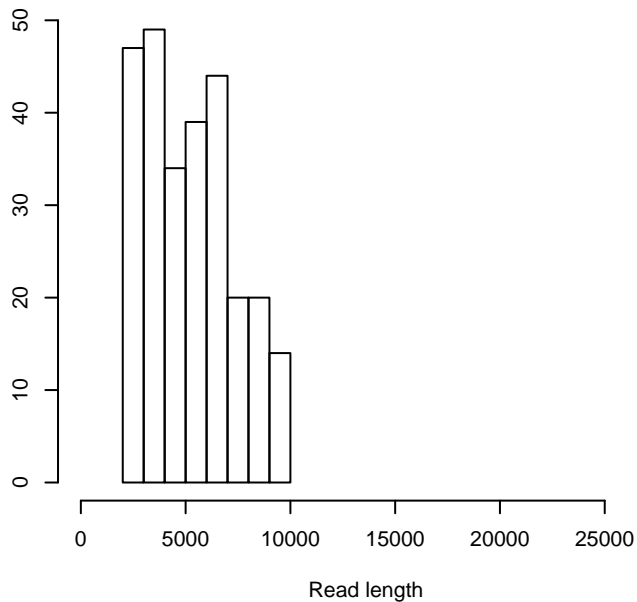


Genome-wide coverage over all contigs for Staphylococcus phage 23MRA (taxon ID 1505027) – 285 mapped reads assigned

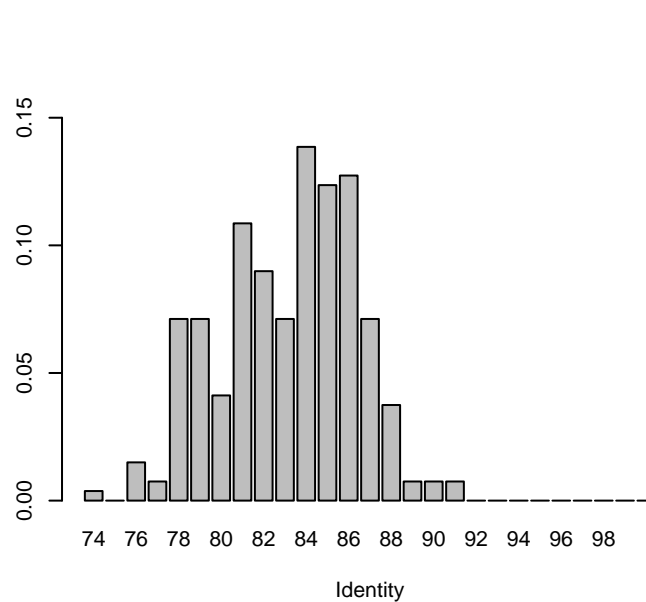


MetaMaps mapping summary for *Acinetobacter baumannii* AYE (taxon ID 509173) – 267 mapped reads assigned

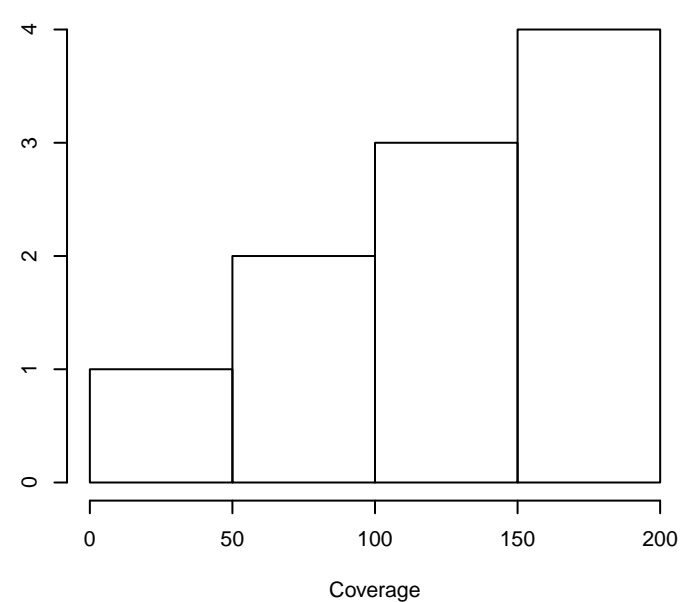
Read length histogram



Read identities



Genome window coverage histogram



Genome-wide coverage over all contigs for *Acinetobacter baumannii* AYE (taxon ID 509173) – 269 mapped reads assigned

