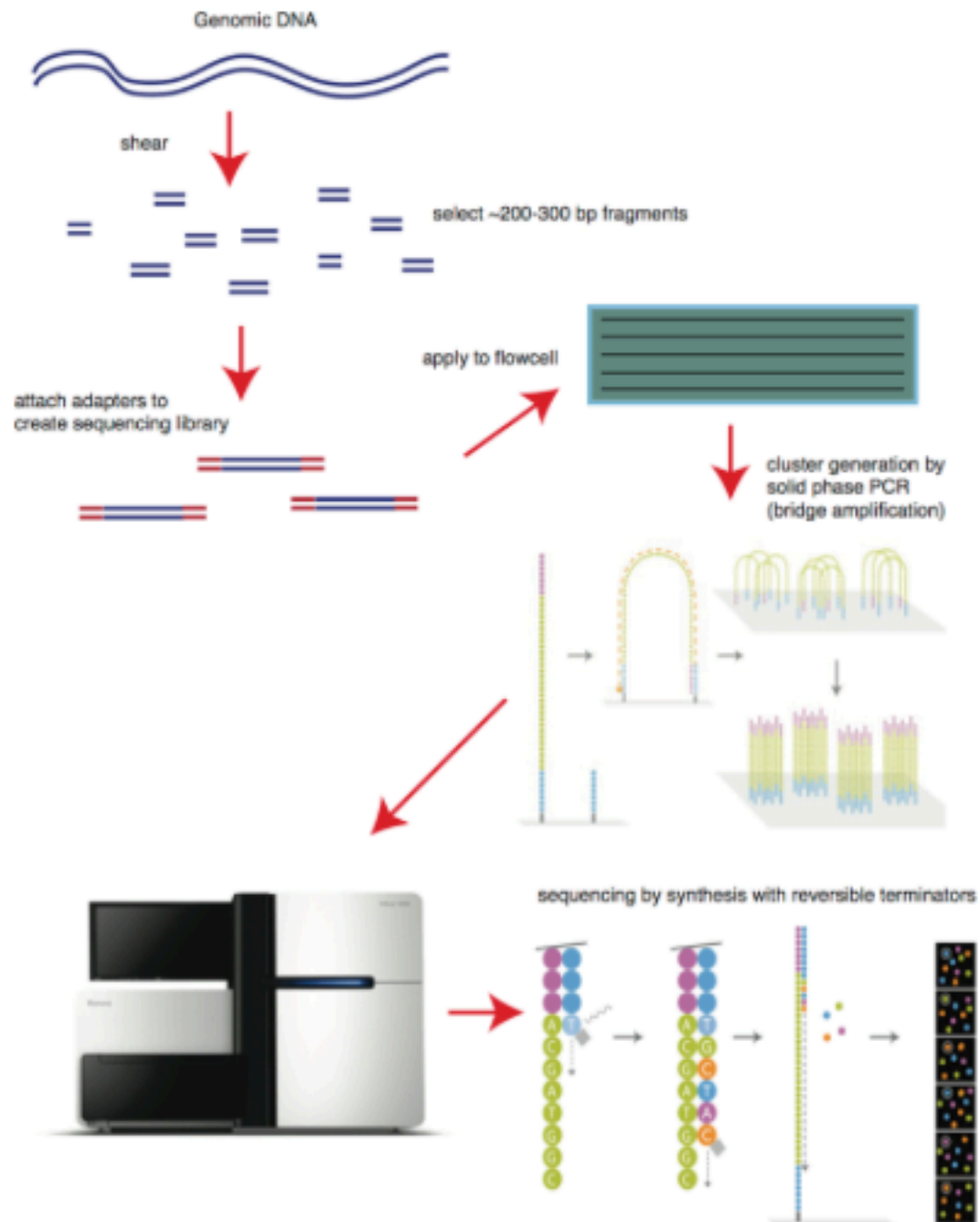
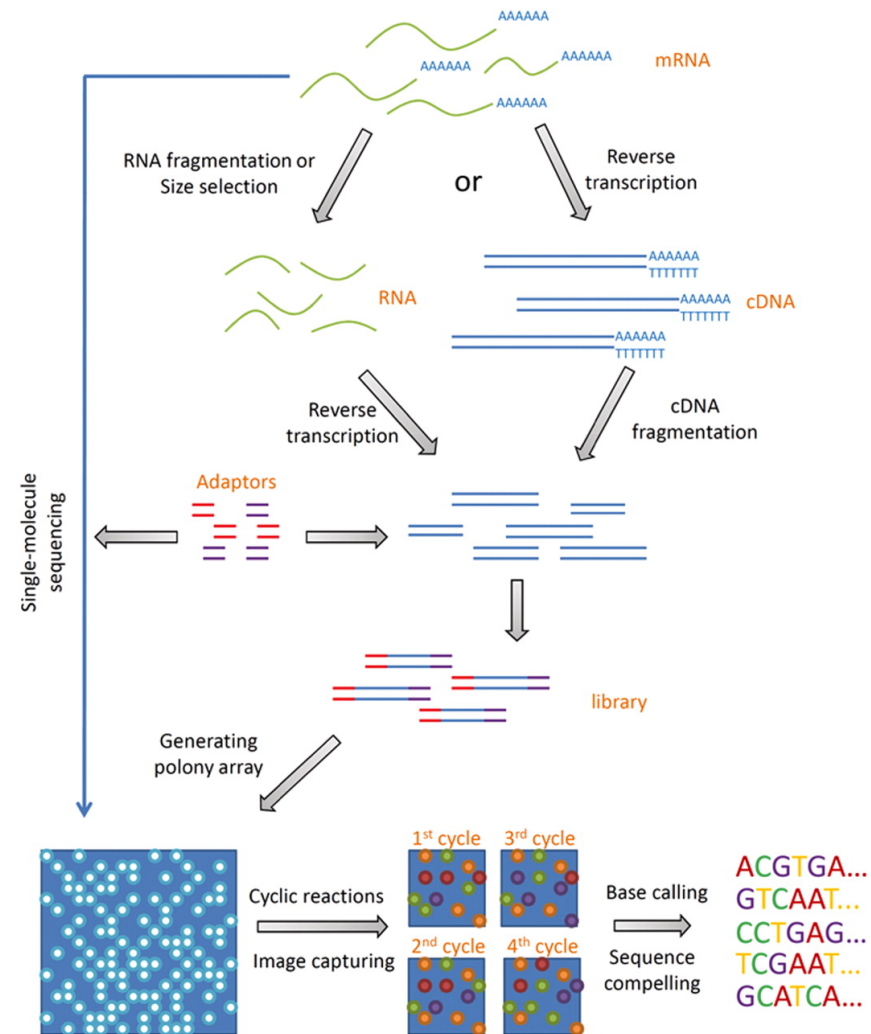


RNA Sequence



Overview of RNA-seq experimental procedures.



Wang L et al. Briefings in Functional Genomics
2010;9:118-128

FASTQ format

**SRA ID &
pair info**

Machine ID

Flowcell lane

Flowcell coordinates

Sequence

@SRR769604.1 HWI-ST765:7:1101:1319:2156 length=101

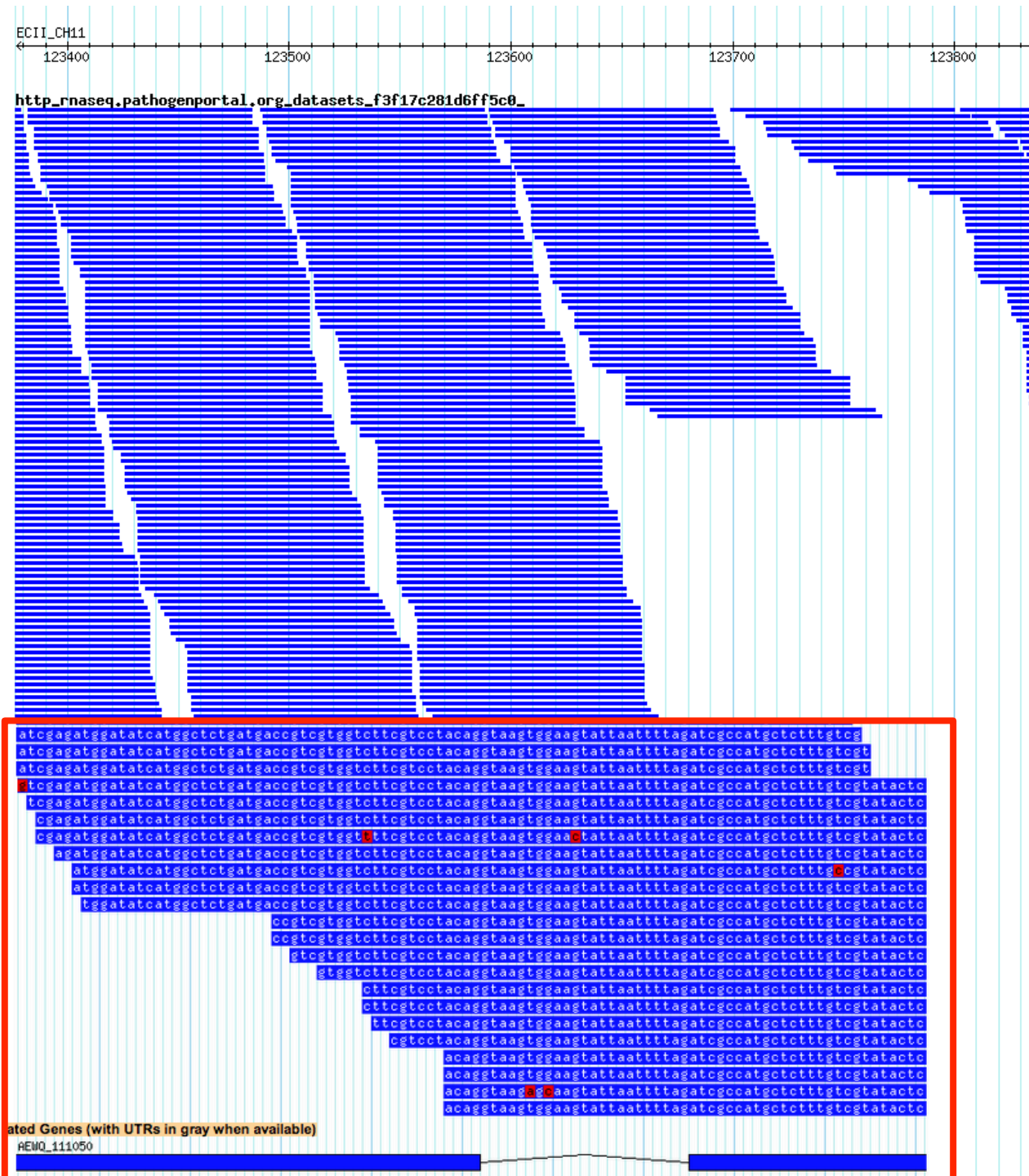
TGCAATGCCTAGAAATGGGGGCTGTGGAAACGCTTATAGTTTATGAGGGCTTATCTGAGCTCAAGGATGAGGAATTGTTTGTGGACTGGATTGCTGAGAAC

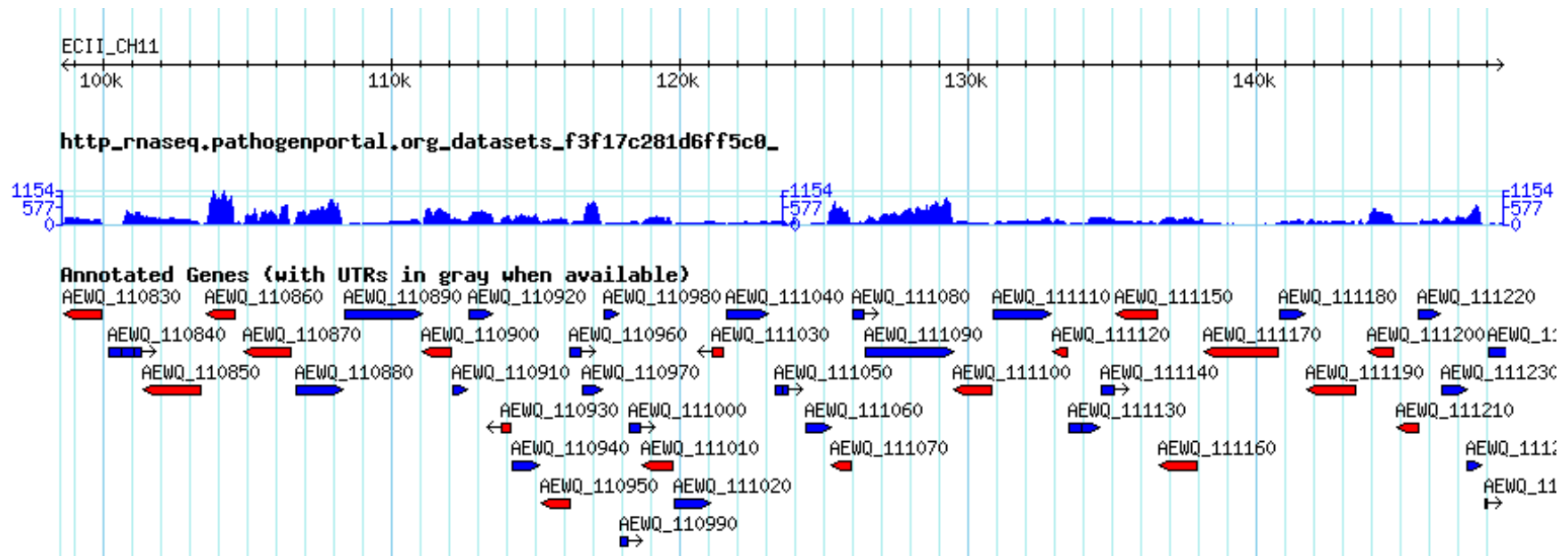
+SRR769604.1 HWI-ST765:7:1101:1319:2156 length=101

bbbeeeeeggggghhiiiiihhigghiihiiiihahdfhafheghhhiieiidghfgggefgeeedacbdcdabbcb`bc`bcccccccabbbb`accb

**Quality score
encoded in ASCII
to save space**

Sequence
reads aligned
using TopHat





Relative expression of transcript (determined by CuffLinks) represented as RPKMs or FPKMs

RPKM: Reads Per Kilobase of transcript per Million mapped reads.

FPKM: Fragments Per Kilobase of transcript per Million mapped reads.