ginal Genome   Reduc

```
              Started job on |   Jul 28 10:21:35
         Started mapping on (info)   Jul 28 10:27:16
                 Finished on |   Jul 28 11:00:27
Million of reads per hour |   52.47

        Number of input reads |   29019229
   Average input read length |   300
              UNIQUE READS:
quely mapped reads number |   21592189
     Uniquely mapped reads % |   74.41%
       Average mapped length |   295.39
    Number of splices: Total |   23433957
splices: Annotated (sjdb) |   23357405
      Number of splices: GT/AG |   22613228
      Number of splices: GC/AG |   270444
      Number of splices: AT/AC |   27760
of splices: Non-canonical |   522525
Mismatch rate per base, % |   1.05%
      Deletion rate per base |   0.08%
    Deletion average length |   3.02
     Insertion rate per base |   0.09%
   Insertion average length |   1.92
         MULTI-MAPPING READS:
s mapped to multiple loci |   3658588
s mapped to multiple loci |   12.61%
s mapped to too many loci |   47106
s mapped to too many loci |   0.16%
              UNMAPPED READS:
pped: too many mismatches |   0.00%
reads unmapped: too short |   12.09%
of reads unmapped: other |   0.74%
              CHIMERIC READS:
Number of chimeric reads |   0
       % of chimeric reads |   0.00%
```

Mapping speed, Milli

N
Avera

Uniquely
Uni
A
Numb
Number of splic
Numb
Numb
Numb
Number of sp
Misma
De
Del
Ins
Inse

Number of reads map
% of reads map
Number of reads map
% of reads map

% of reads unmapped:
% of reads
% of r

Numb