

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 01:29:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004099.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR6004099 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004099.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 01:29:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004099.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,007,006
Mapped reads	2,562,874 / 85.23%
Unmapped reads	444,132 / 14.77%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,991 / 0.76%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	169,450 / 5.64%
Duplication rate	5.32%
Clipped reads	1,106,222 / 36.79%

2.2. ACGT Content

Number/percentage of A's	48,087,100 / 27.84%
Number/percentage of C's	31,854,723 / 18.44%
Number/percentage of T's	56,052,656 / 32.45%
Number/percentage of G's	36,698,732 / 21.25%
Number/percentage of N's	23,339 / 0.01%
GC Percentage	39.69%

2.3. Coverage

Mean	0.0558

Standard Deviation	0.5036
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2.4. Mapping Quality

Mean Mapping Quality	47.45
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2.5. Mismatches and indels

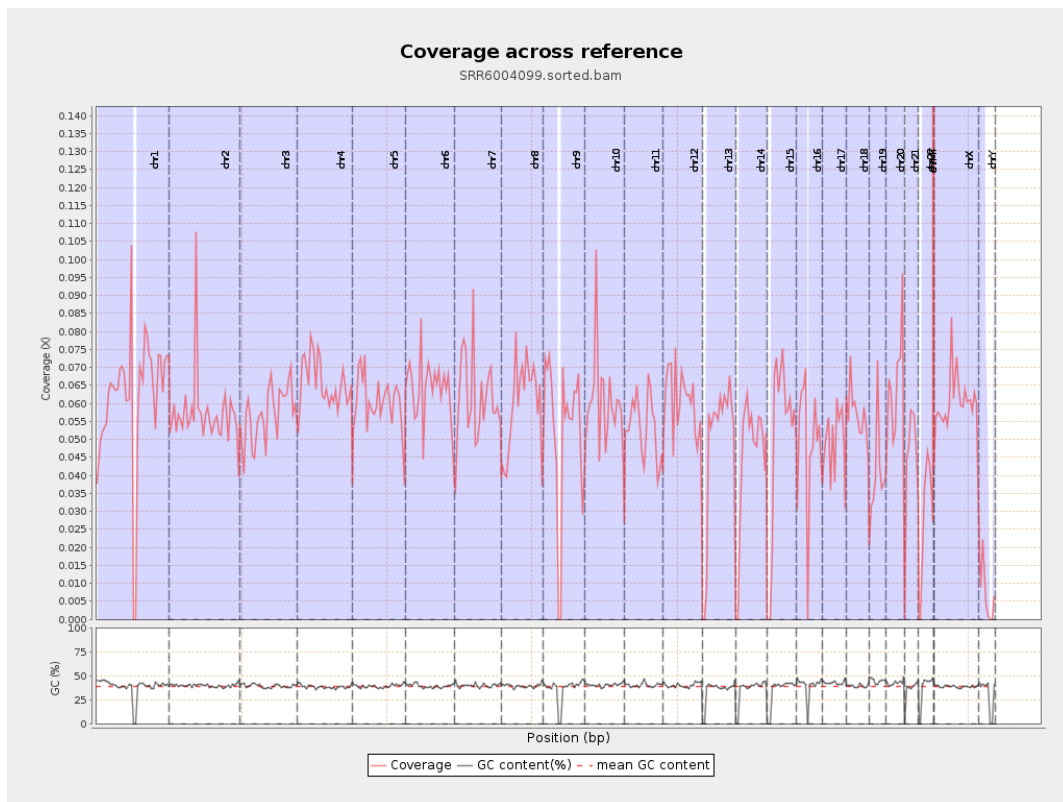
General error rate	0.97%
Mismatches	1,648,252
Insertions	13,697
Mapped reads with at least one insertion	0.53%
Deletions	45,292
Mapped reads with at least one deletion	1.75%
Homopolymer indels	47.94%

2.6. Chromosome stats

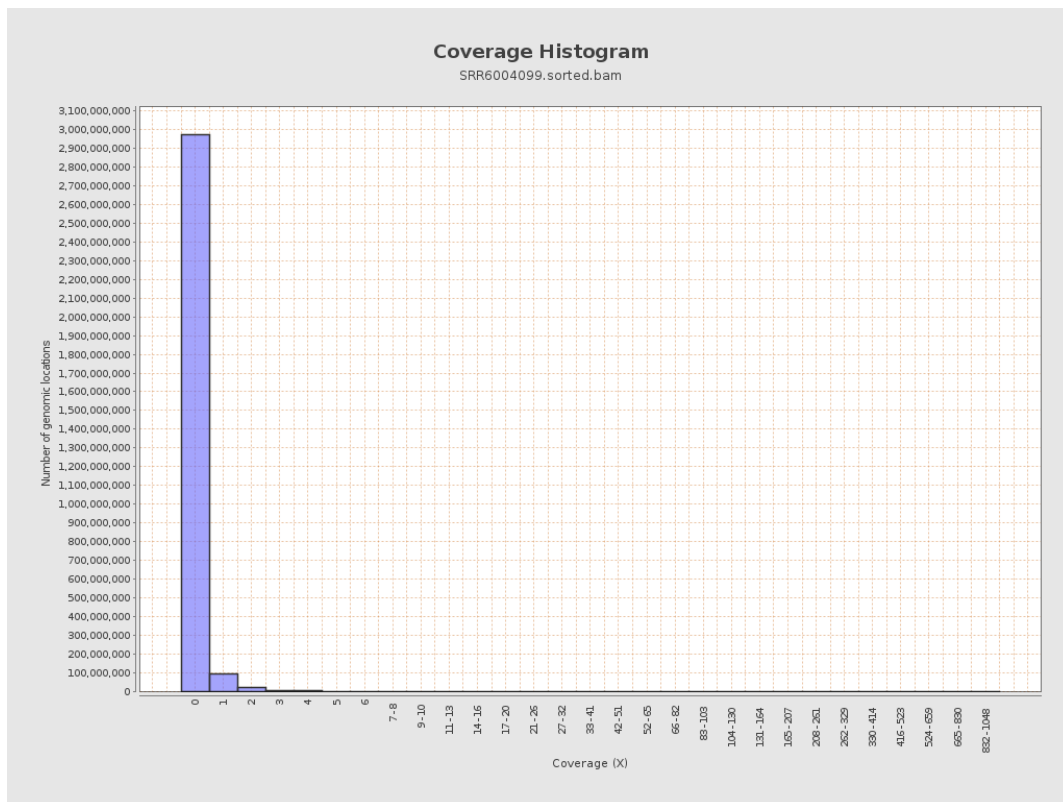
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	15380167	0.0617	0.9636
chr2	243199373	13911851	0.0572	0.5338
chr3	198022430	11322358	0.0572	0.3196
chr4	191154276	12533459	0.0656	0.35
chr5	180915260	10918097	0.0603	0.3265
chr6	171115067	10920507	0.0638	0.3958
chr7	159138663	9865709	0.062	0.6405

chr8	146364022	8724814	0.0596	0.6633
chr9	141213431	7439807	0.0527	0.4586
chr10	135534747	8166639	0.0603	0.511
chr11	135006516	7165083	0.0531	0.4235
chr12	133851895	8057934	0.0602	0.3327
chr13	115169878	5554991	0.0482	0.2892
chr14	107349540	4815721	0.0449	0.3078
chr15	102531392	5222632	0.0509	0.3009
chr16	90354753	4461471	0.0494	0.3249
chr17	81195210	3983126	0.0491	0.3366
chr18	78077248	4458744	0.0571	0.8271
chr19	59128983	2411148	0.0408	0.6178
chr20	63025520	4045739	0.0642	0.3477
chr21	48129895	2149970	0.0447	0.304
chr22	51304566	1428701	0.0278	0.2142
chrMT	16571	85257	5.145	3.9065
chrX	155270560	9348082	0.0602	0.3621
chrY	59373566	419086	0.0071	0.1519

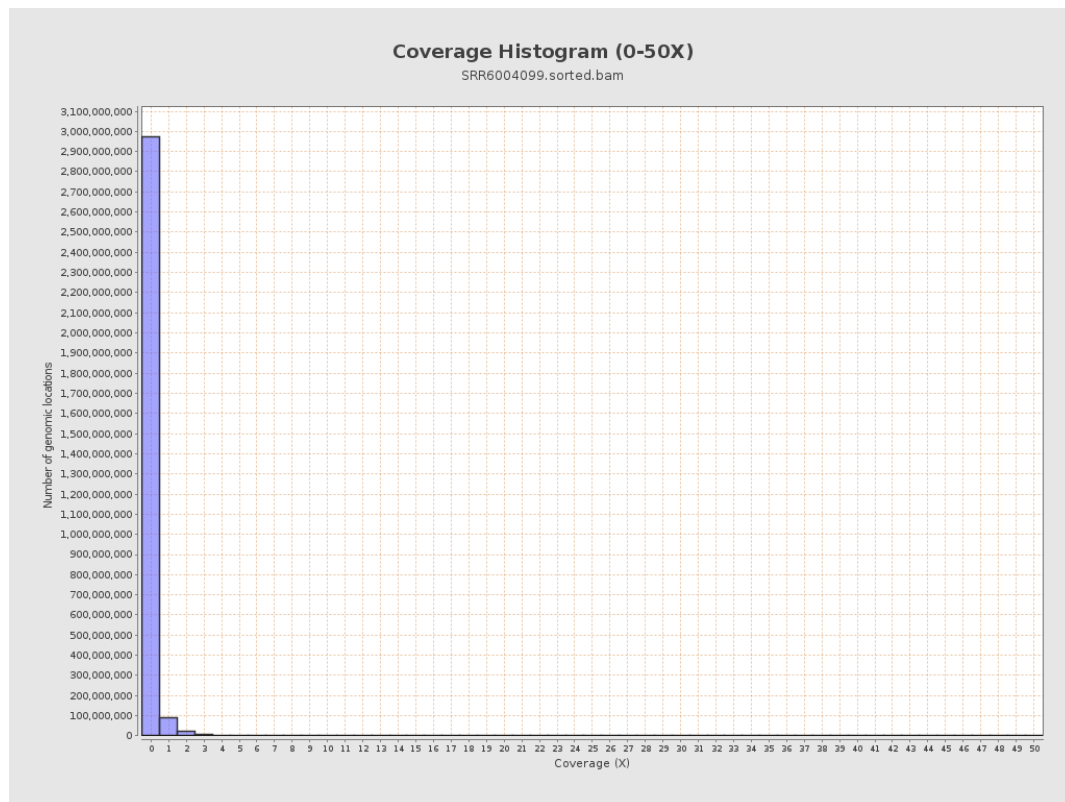
3. Results : Coverage across reference



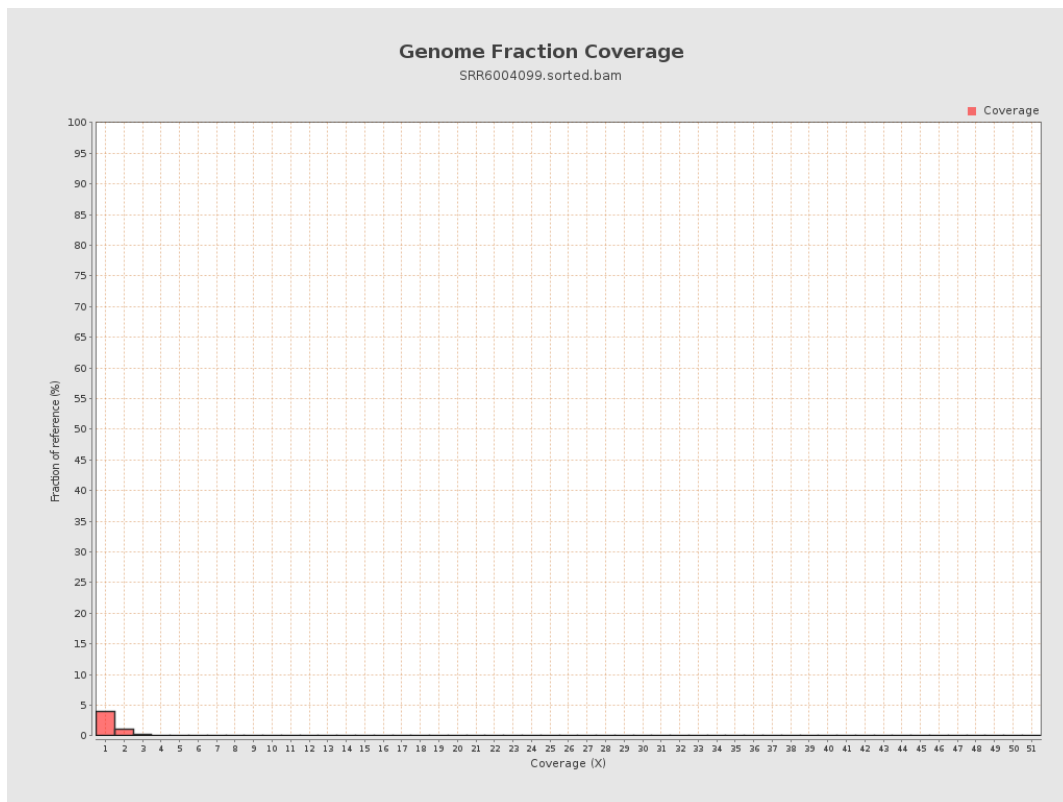
4. Results : Coverage Histogram



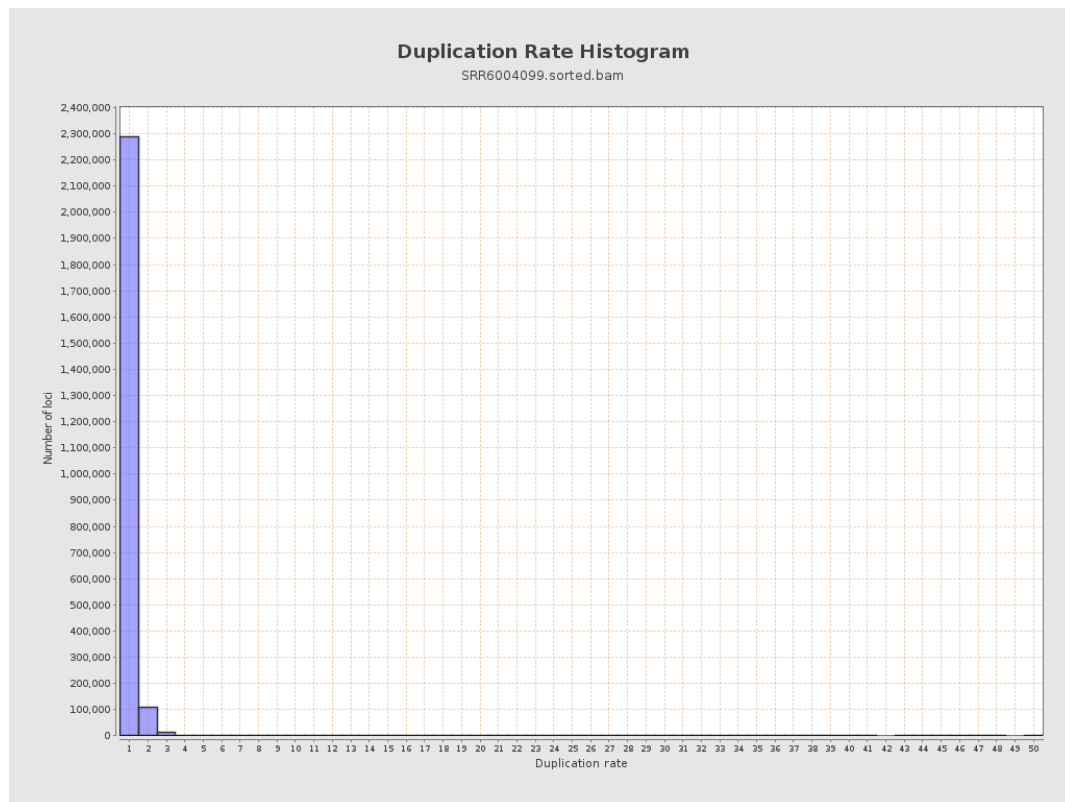
5. Results : Coverage Histogram (0-50X)



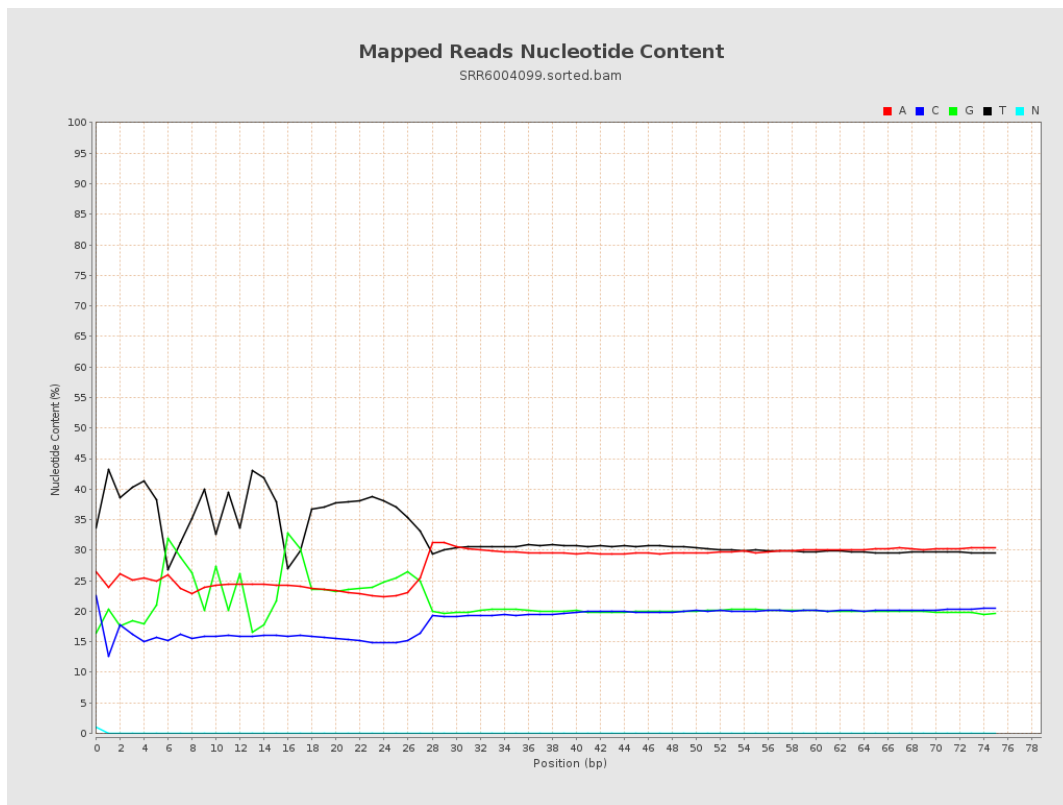
6. Results : Genome Fraction Coverage



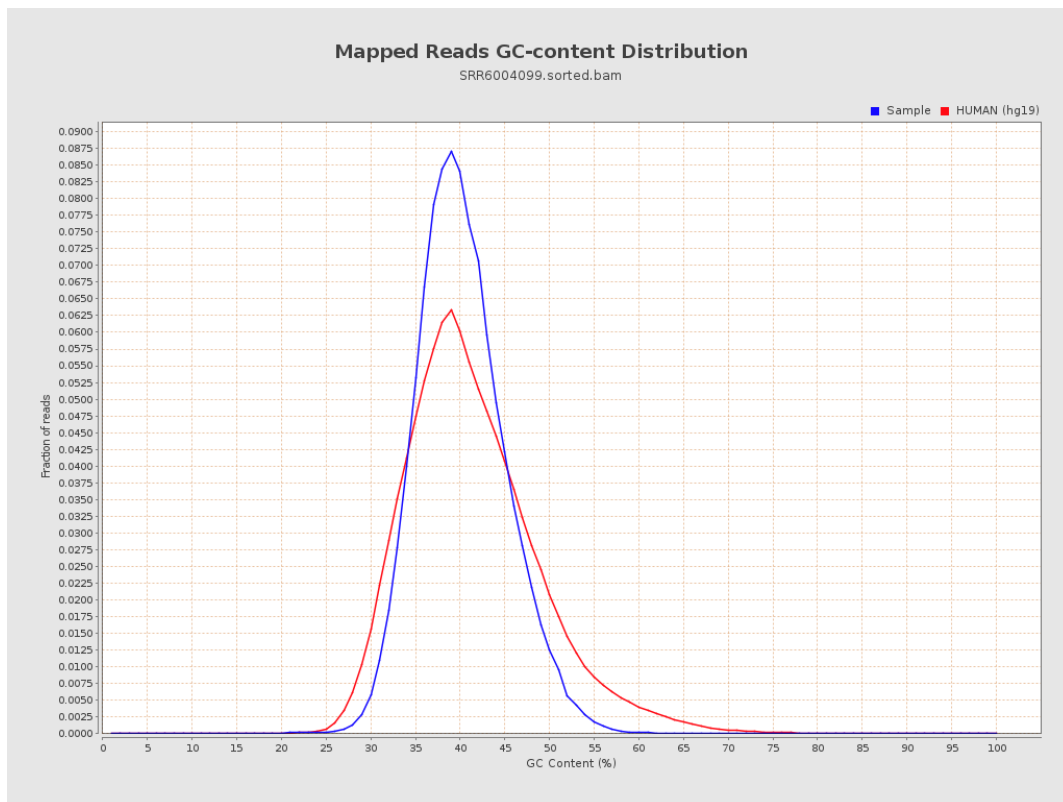
7. Results : Duplication Rate Histogram



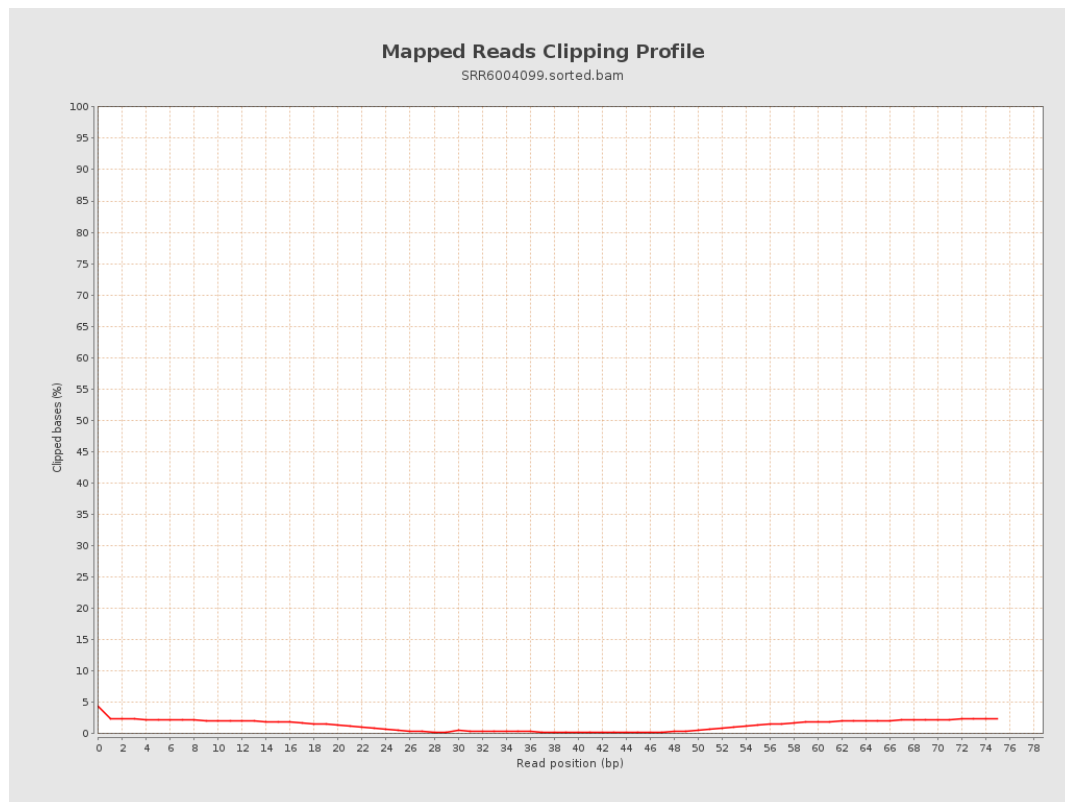
8. Results : Mapped Reads Nucleotide Content



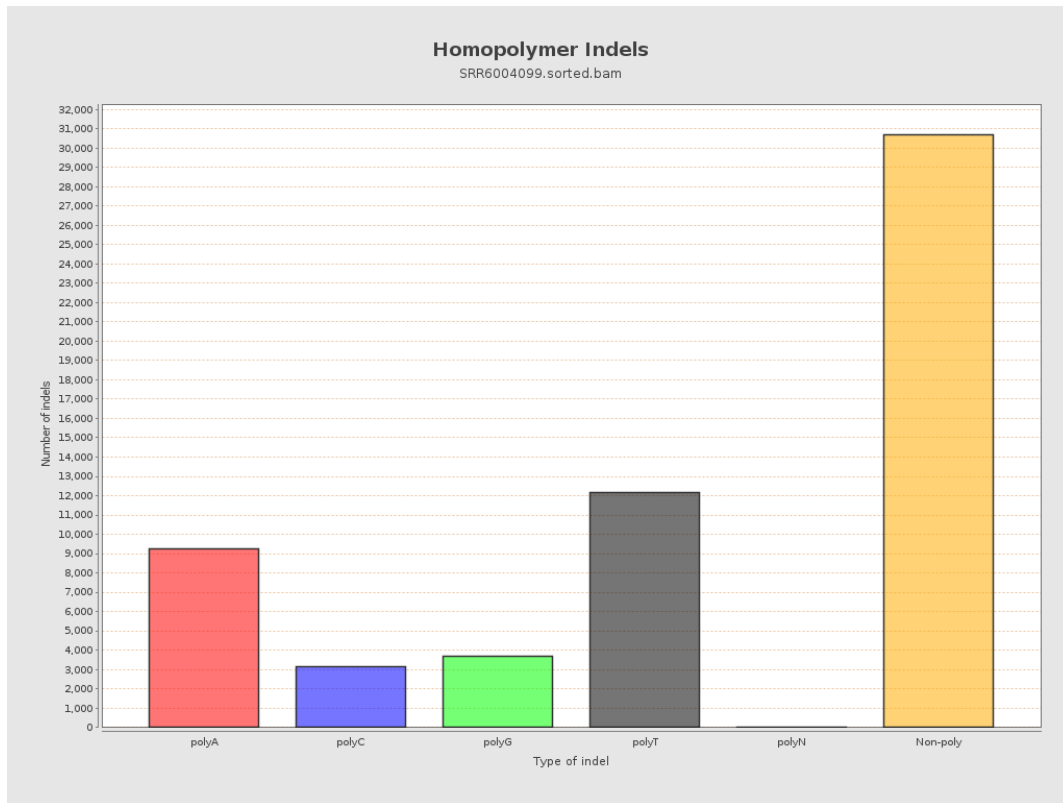
9. Results : Mapped Reads GC-content Distribution



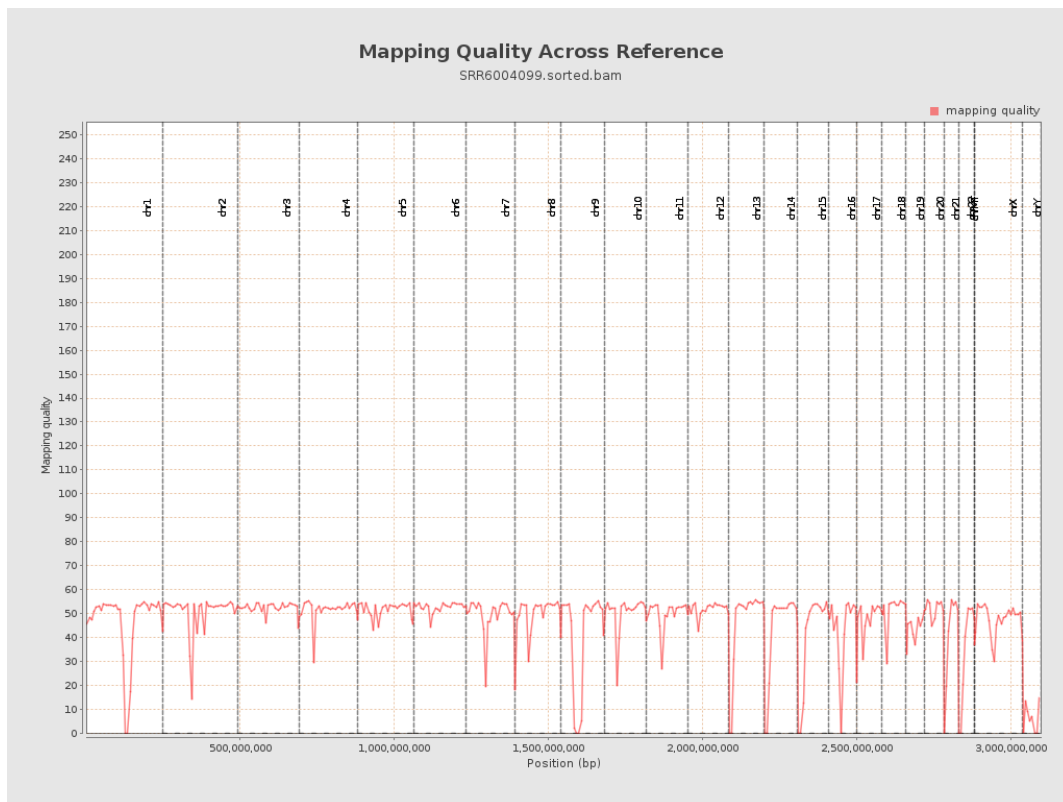
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

