

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 01:02:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004092.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_SRR6004092 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004092.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 01:02:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004092.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,734,346
Mapped reads	2,478,216 / 90.63%
Unmapped reads	256,130 / 9.37%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,813 / 0.76%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	104,635 / 3.83%
Duplication rate	3.29%
Clipped reads	1,170,053 / 42.79%

2.2. ACGT Content

Number/percentage of A's	45,933,574 / 28.08%
Number/percentage of C's	29,319,086 / 17.92%
Number/percentage of T's	52,211,751 / 31.92%
Number/percentage of G's	36,054,687 / 22.04%
Number/percentage of N's	72,421 / 0.04%
GC Percentage	39.96%

2.3. Coverage

Mean	0.0529

Standard Deviation	0.4234
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2.4. Mapping Quality

Mean Mapping Quality	45.52
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2.5. Mismatches and indels

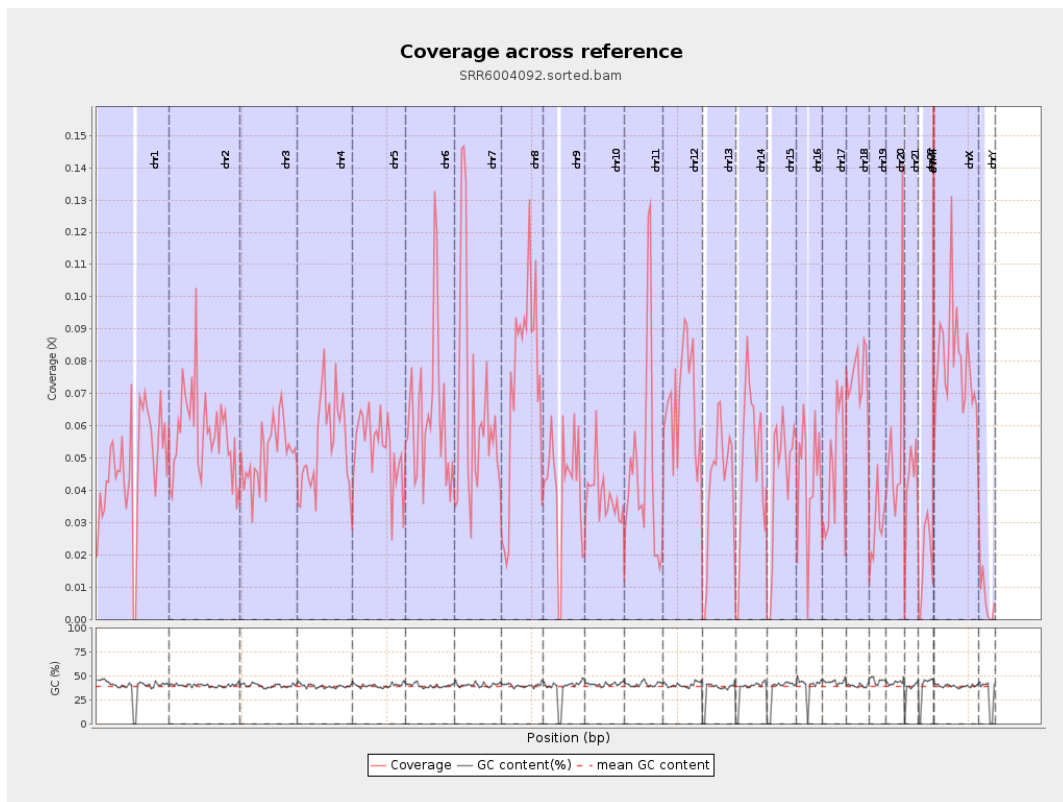
General error rate	0.86%
Mismatches	1,384,197
Insertions	11,988
Mapped reads with at least one insertion	0.48%
Deletions	57,497
Mapped reads with at least one deletion	2.29%
Homopolymer indels	44.55%

2.6. Chromosome stats

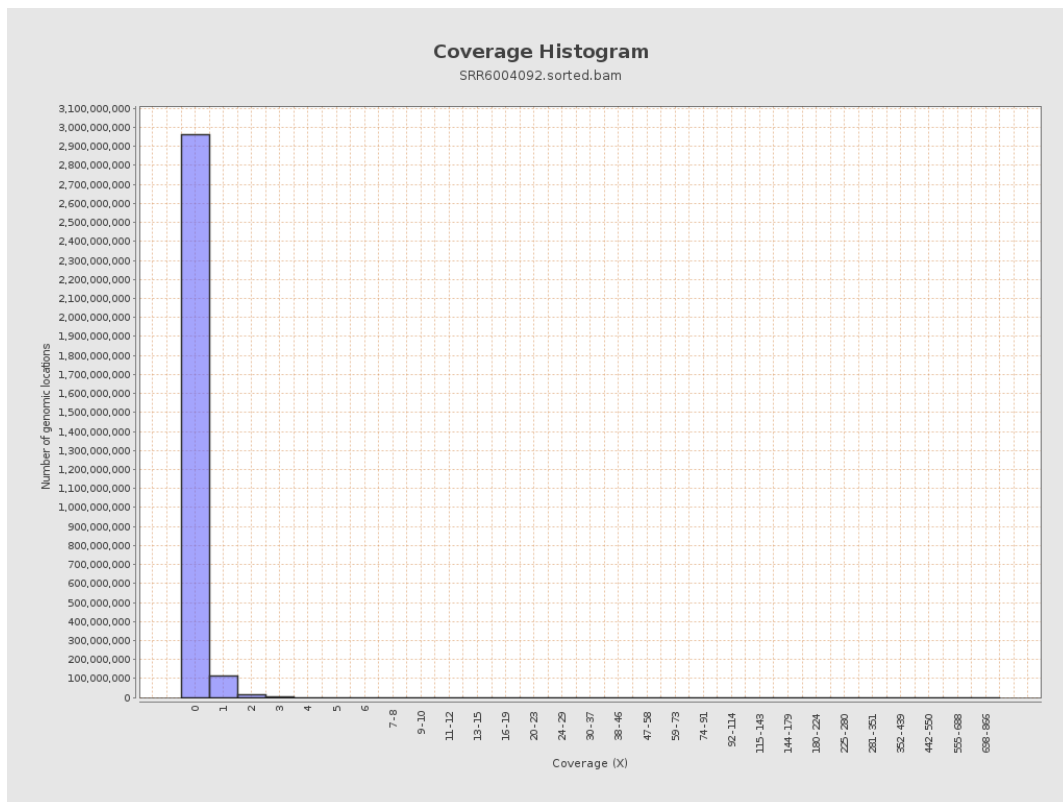
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	11789850	0.0473	0.7666
chr2	243199373	14036363	0.0577	0.555
chr3	198022430	10172471	0.0514	0.2615
chr4	191154276	10370257	0.0543	0.2761
chr5	180915260	9654500	0.0534	0.2715
chr6	171115067	10846551	0.0634	0.3422
chr7	159138663	10742583	0.0675	0.5274

chr8	146364022	10552428	0.0721	0.5464
chr9	141213431	5894479	0.0417	0.394
chr10	135534747	5191632	0.0383	0.3428
chr11	135006516	6331179	0.0469	0.3075
chr12	133851895	9087735	0.0679	0.3094
chr13	115169878	4764300	0.0414	0.2343
chr14	107349540	5264660	0.049	0.2766
chr15	102531392	4428240	0.0432	0.247
chr16	90354753	4008365	0.0444	0.2844
chr17	81195210	3703947	0.0456	0.2654
chr18	78077248	5895342	0.0755	0.6913
chr19	59128983	1734687	0.0293	0.5129
chr20	63025520	3622317	0.0575	0.2905
chr21	48129895	1974841	0.041	0.2539
chr22	51304566	938130	0.0183	0.1525
chrMT	16571	7394	0.4462	0.7441
chrX	155270560	12273847	0.079	0.3849
chrY	59373566	401397	0.0068	0.1218

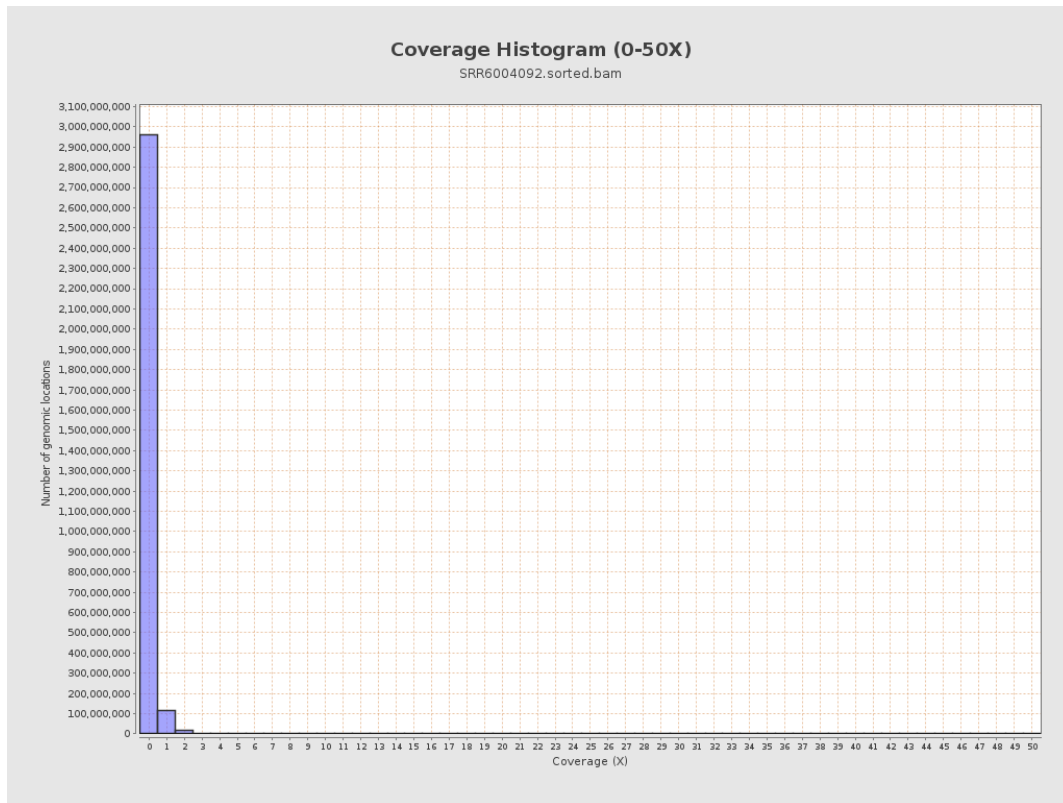
3. Results : Coverage across reference



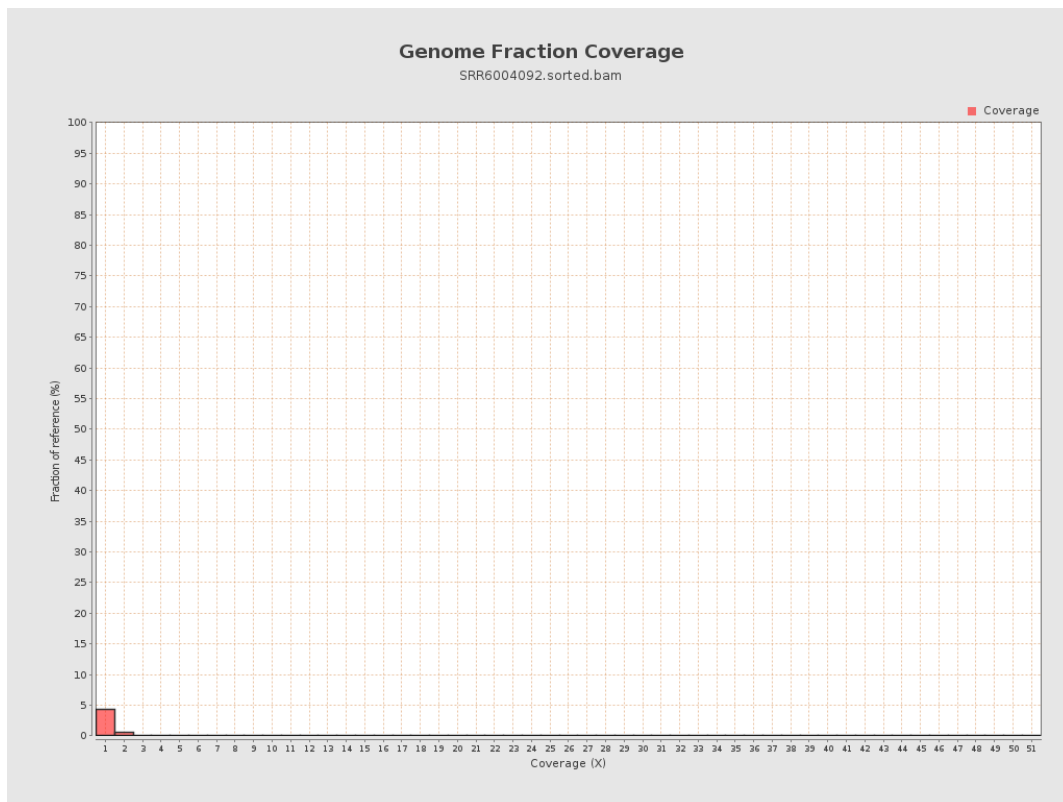
4. Results : Coverage Histogram



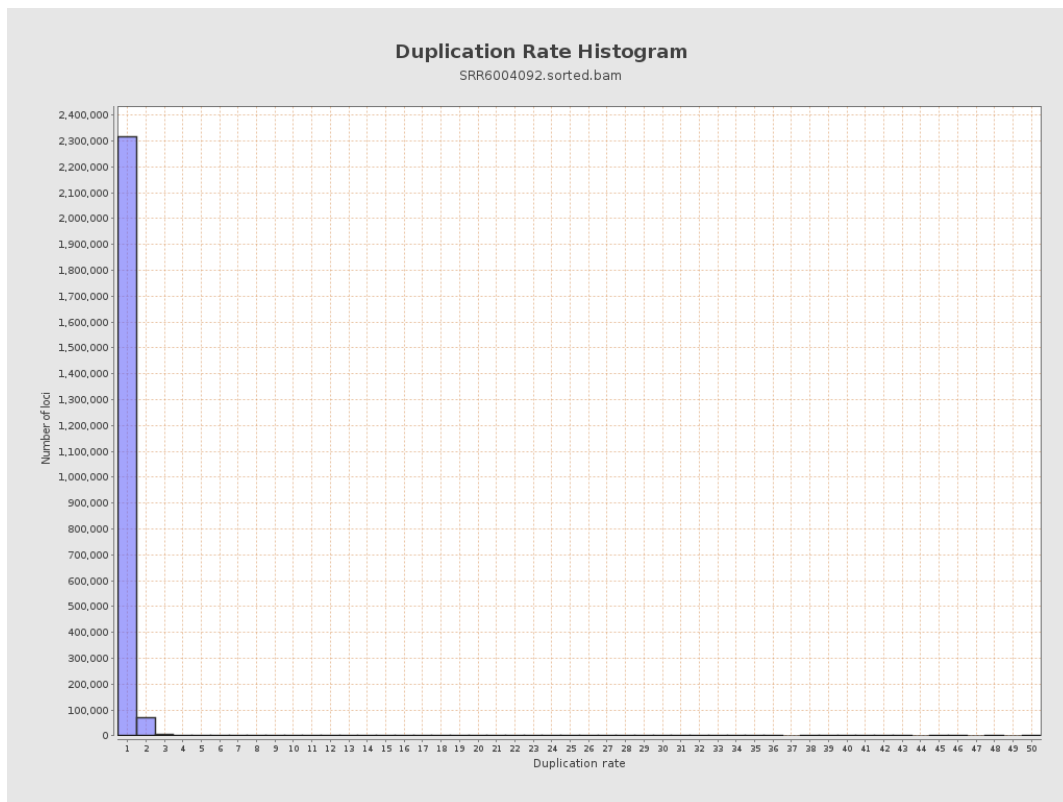
5. Results : Coverage Histogram (0-50X)



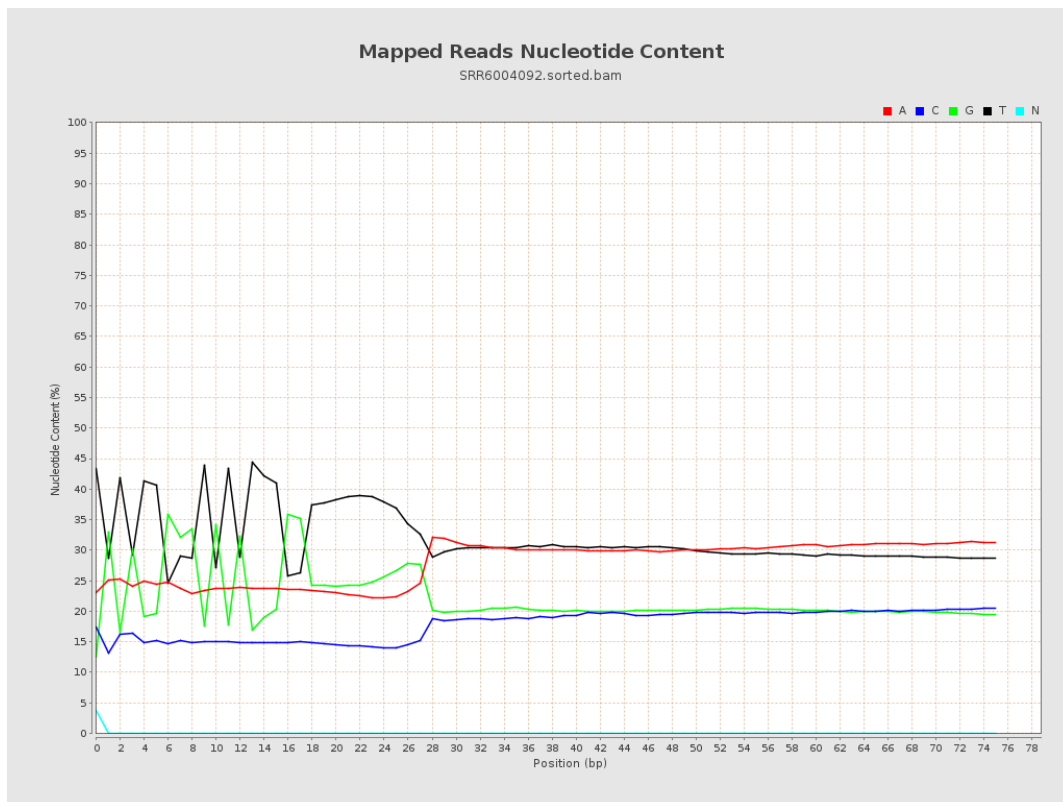
6. Results : Genome Fraction Coverage



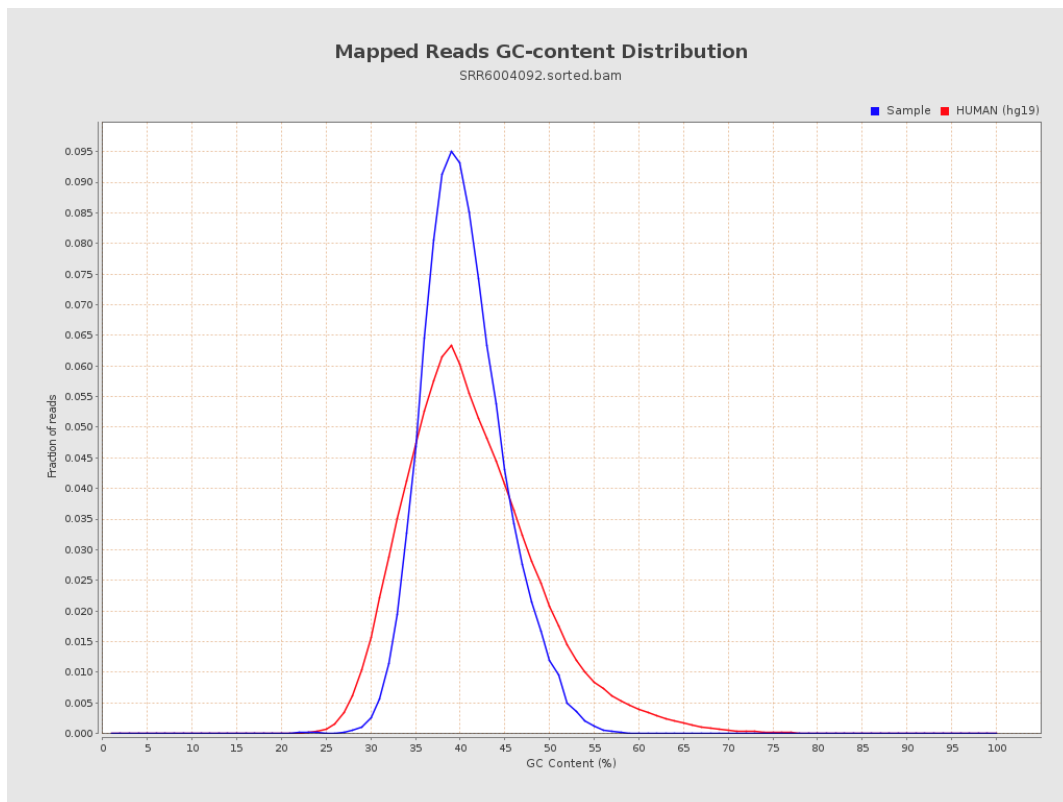
7. Results : Duplication Rate Histogram



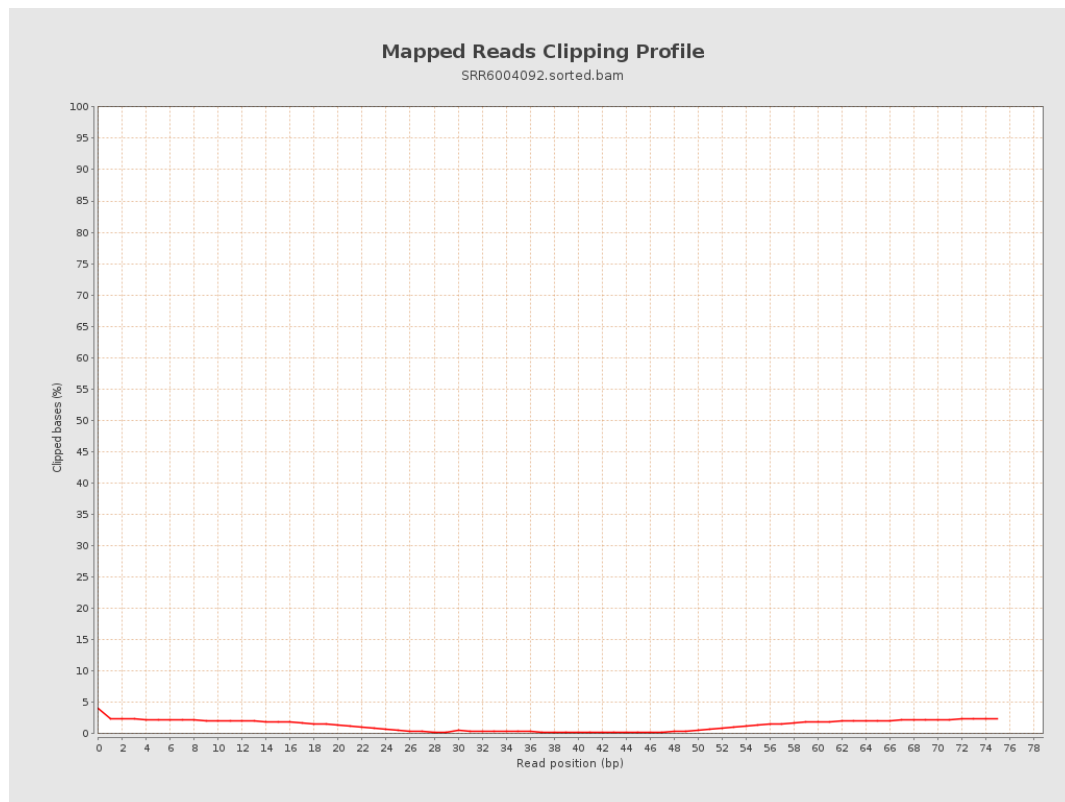
8. Results : Mapped Reads Nucleotide Content



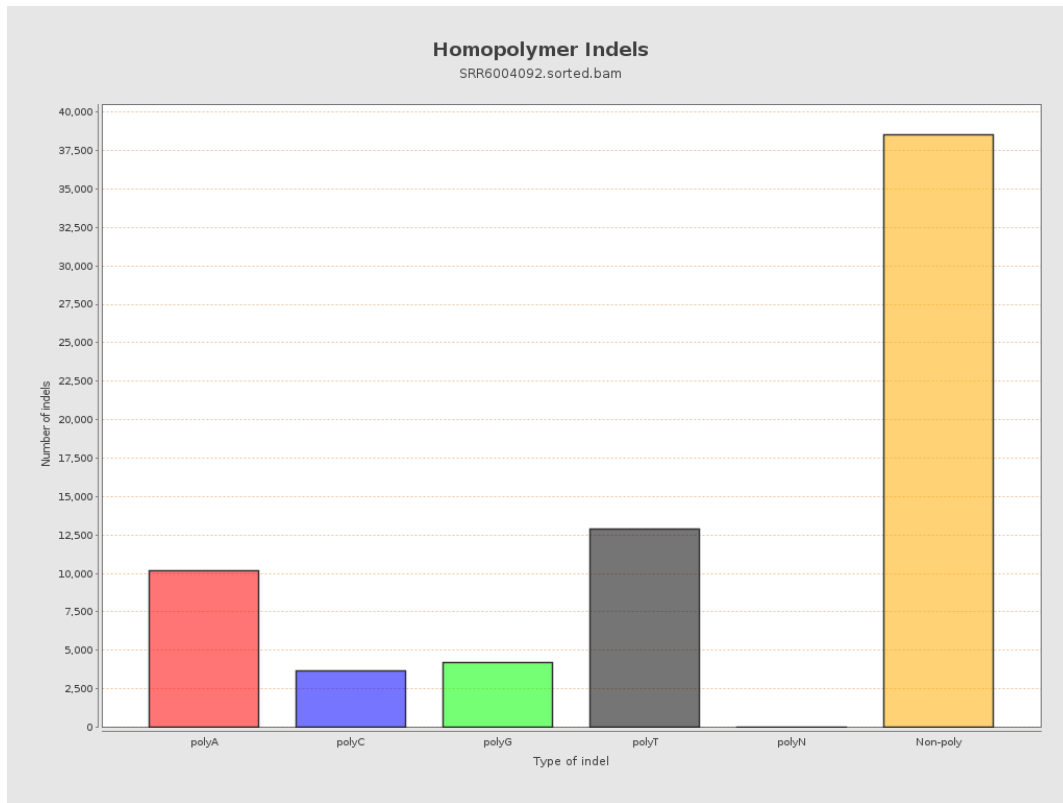
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

