

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/01 09:29:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472834.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_SRR3472834 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472834.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 01 09:29:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472834.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,946,638
Mapped reads	2,604,615 / 88.39%
Unmapped reads	342,023 / 11.61%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,570 / 0.66%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	84,856 / 2.88%
Duplication rate	2.37%
Clipped reads	1,304,854 / 44.28%

2.2. ACGT Content

Number/percentage of A's	45,712,264 / 26.89%
Number/percentage of C's	33,274,543 / 19.58%
Number/percentage of T's	51,261,459 / 30.16%
Number/percentage of G's	39,728,363 / 23.37%
Number/percentage of N's	4,134 / 0%
GC Percentage	42.95%

2.3. Coverage

Mean	0.0549

Standard Deviation	0.3987
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2.4. Mapping Quality

Mean Mapping Quality	44.52
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2.5. Mismatches and indels

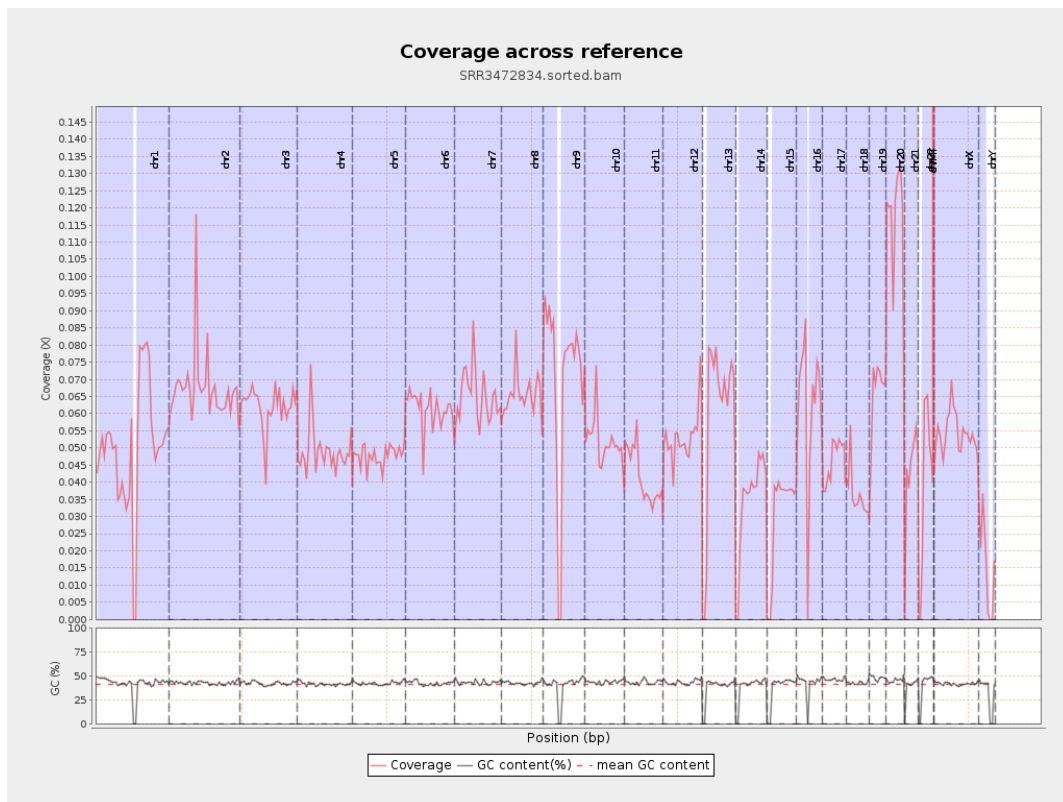
General error rate	0.87%
Mismatches	1,456,288
Insertions	13,252
Mapped reads with at least one insertion	0.5%
Deletions	38,655
Mapped reads with at least one deletion	1.47%
Homopolymer indels	45.08%

2.6. Chromosome stats

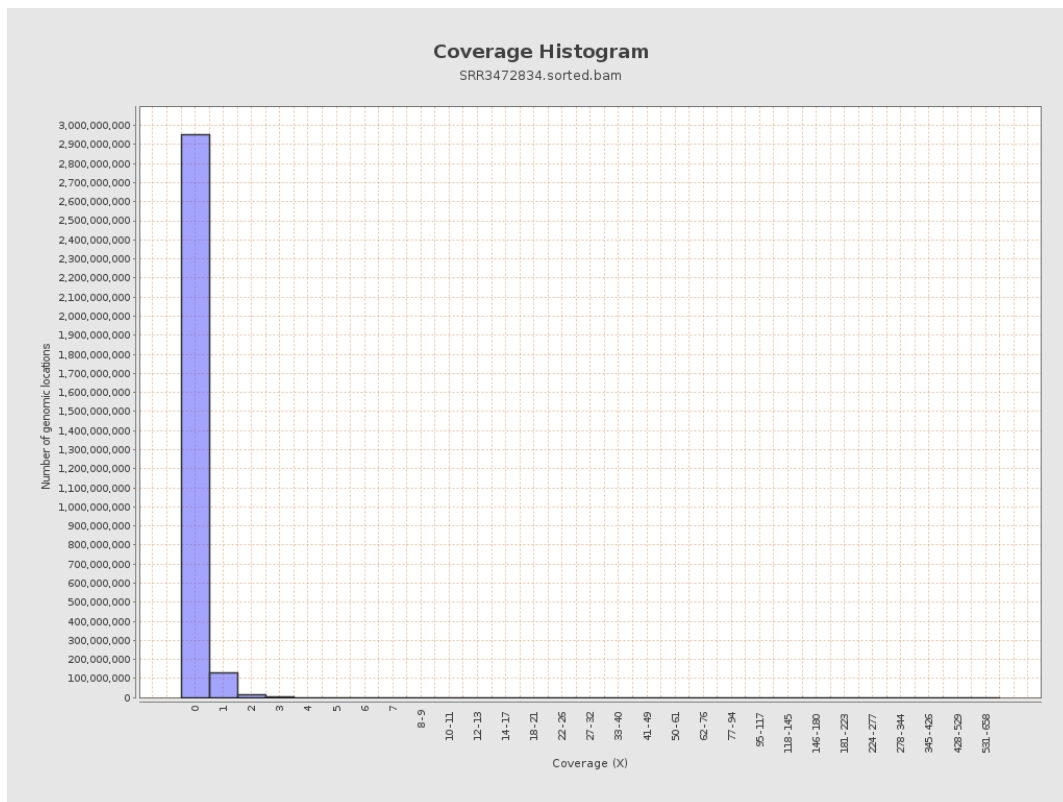
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	12460974	0.05	0.5378
chr2	243199373	16399299	0.0674	0.5915
chr3	198022430	12270371	0.062	0.2785
chr4	191154276	9337360	0.0488	0.2791
chr5	180915260	8643120	0.0478	0.2471
chr6	171115067	10475385	0.0612	0.3085
chr7	159138663	10388003	0.0653	0.5128

chr8	146364022	9582672	0.0655	0.4092
chr9	141213431	9914912	0.0702	0.4852
chr10	135534747	7029736	0.0519	0.3728
chr11	135006516	5598013	0.0415	0.3653
chr12	133851895	7109374	0.0531	0.2692
chr13	115169878	6846764	0.0594	0.2843
chr14	107349540	3733208	0.0348	0.249
chr15	102531392	3128072	0.0305	0.2172
chr16	90354753	5665294	0.0627	0.3162
chr17	81195210	3762205	0.0463	0.2669
chr18	78077248	2872683	0.0368	0.7824
chr19	59128983	3913166	0.0662	0.4176
chr20	63025520	7395794	0.1173	0.4089
chr21	48129895	2068693	0.043	0.2845
chr22	51304566	1966058	0.0383	0.2312
chrMT	16571	187796	11.3328	6.7377
chrX	155270560	8417738	0.0542	0.3045
chrY	59373566	882476	0.0149	0.1969

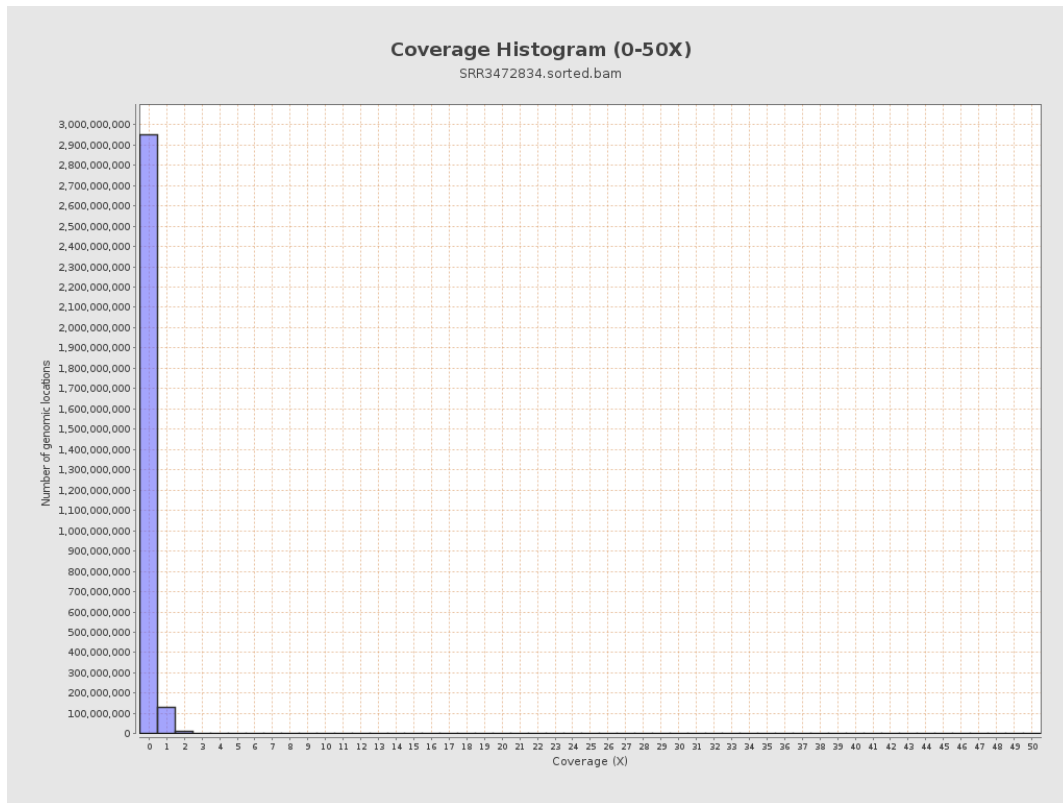
3. Results : Coverage across reference



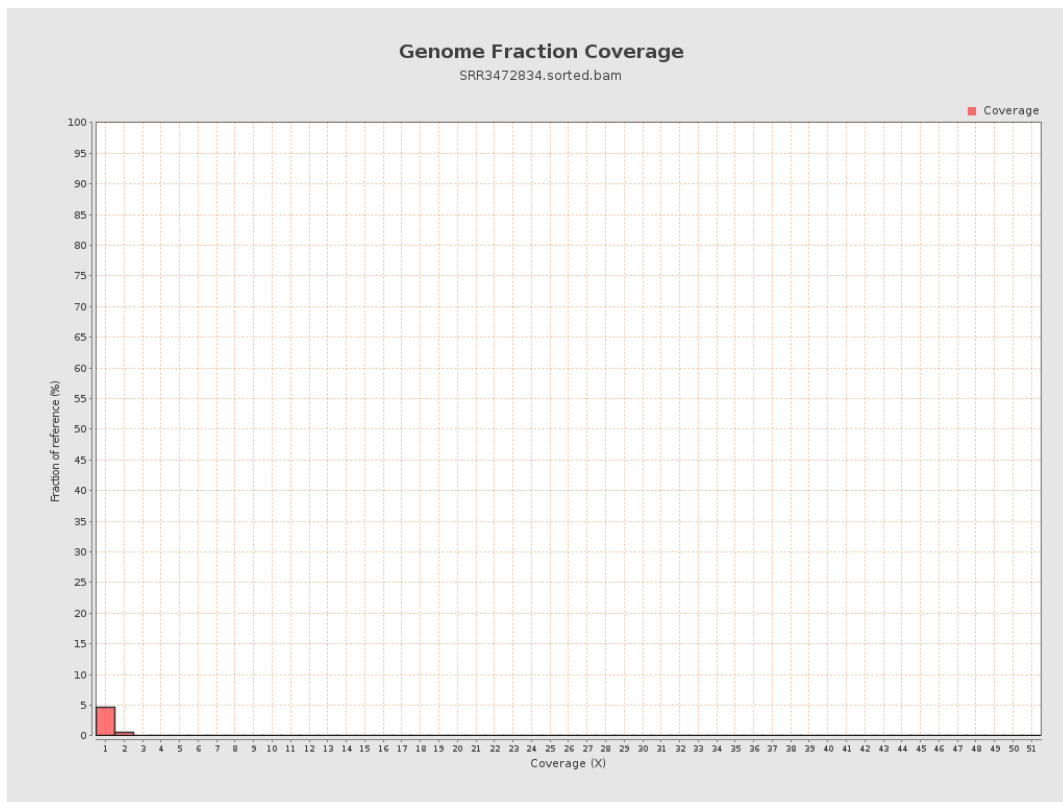
4. Results : Coverage Histogram



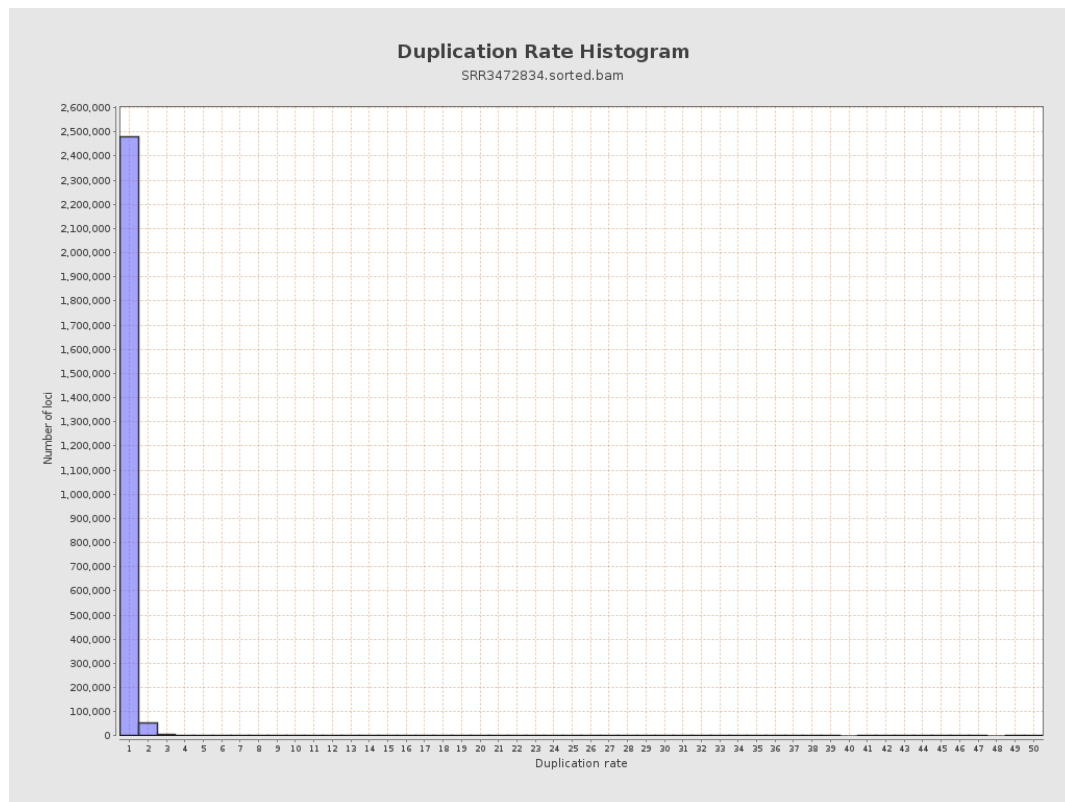
5. Results : Coverage Histogram (0-50X)



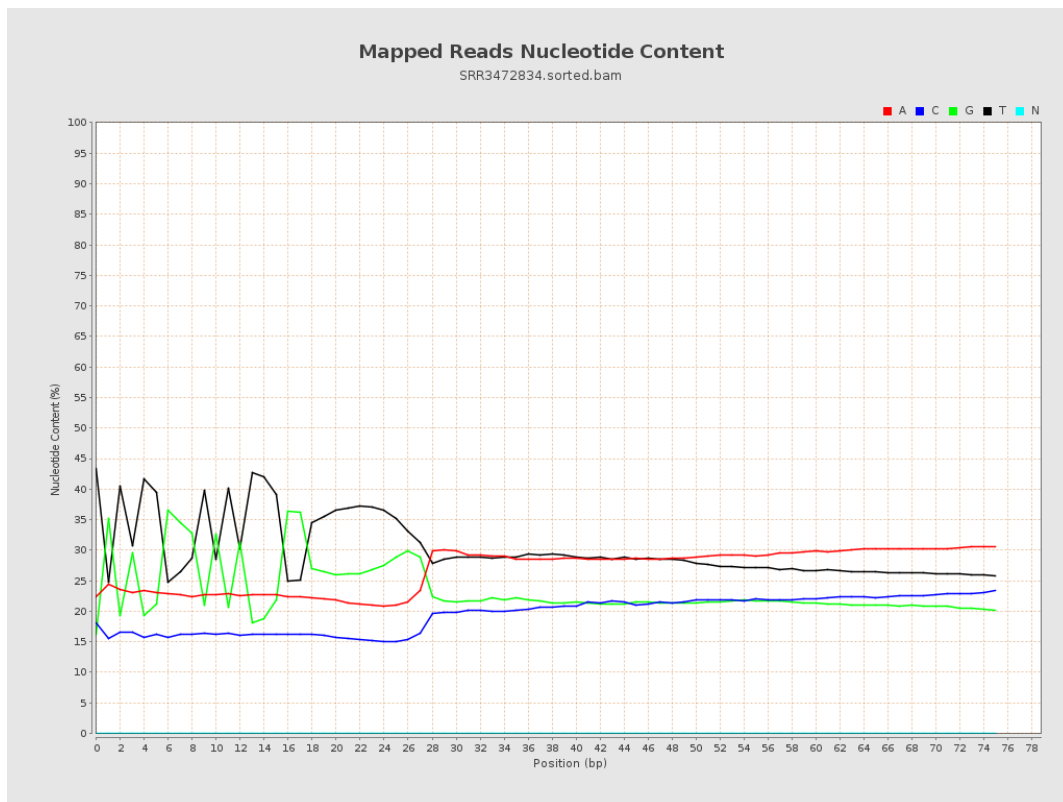
6. Results : Genome Fraction Coverage



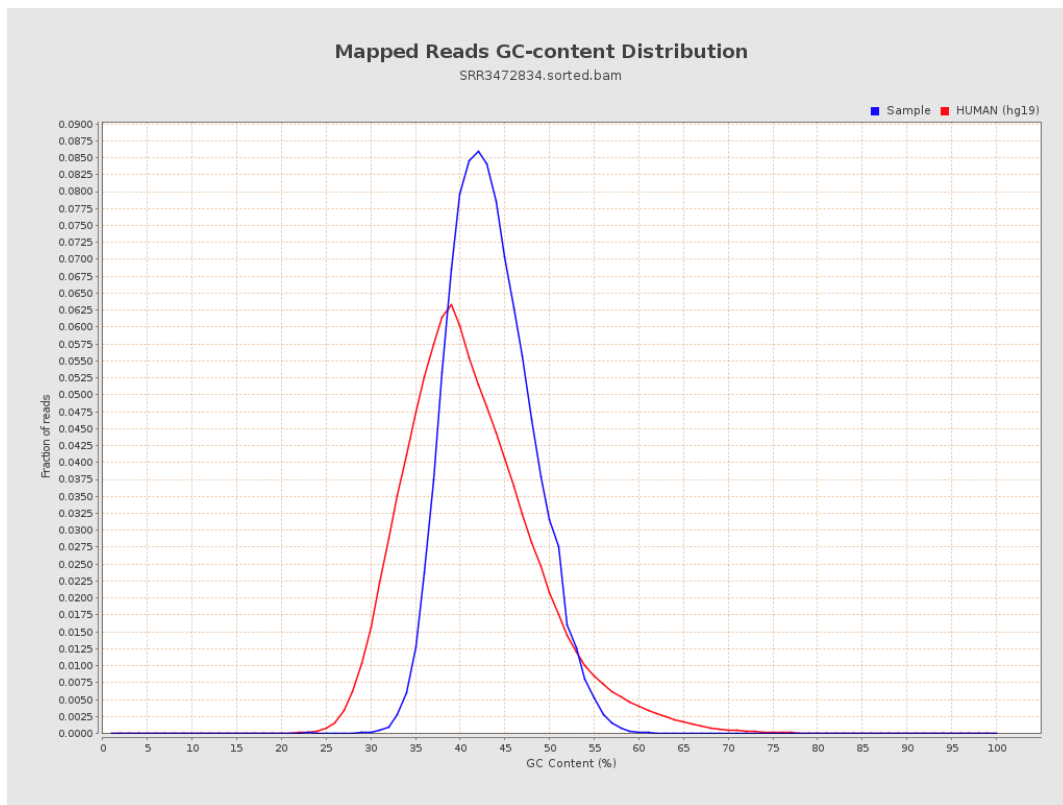
7. Results : Duplication Rate Histogram



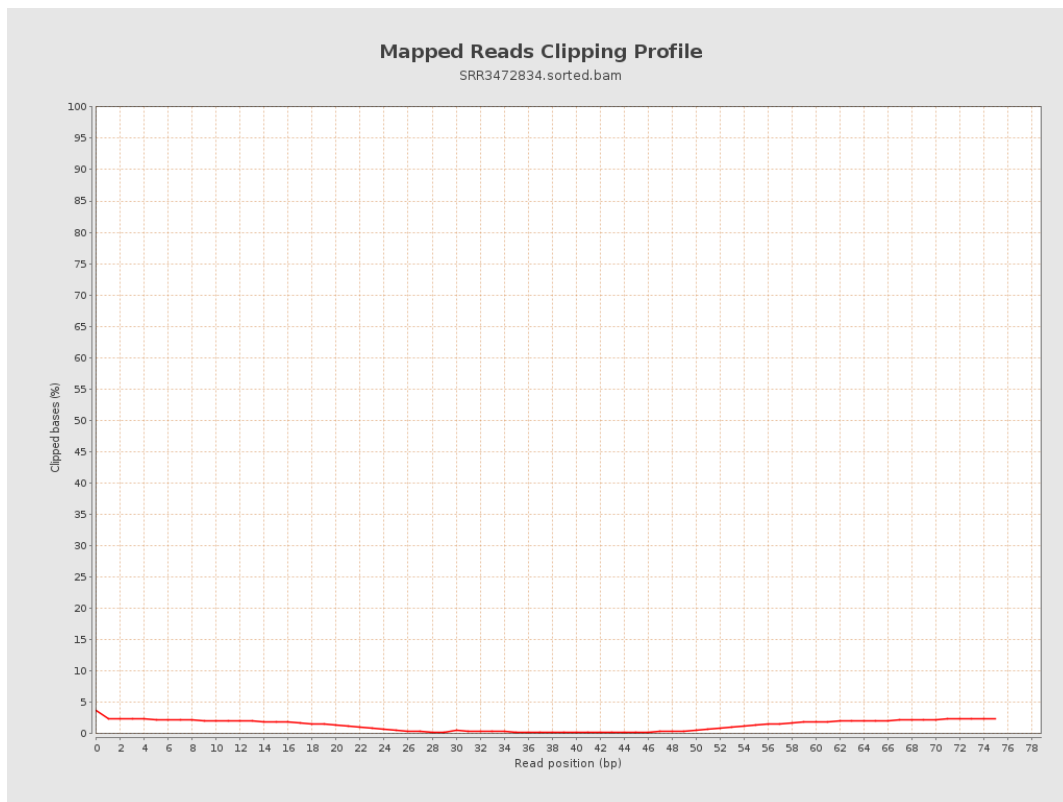
8. Results : Mapped Reads Nucleotide Content



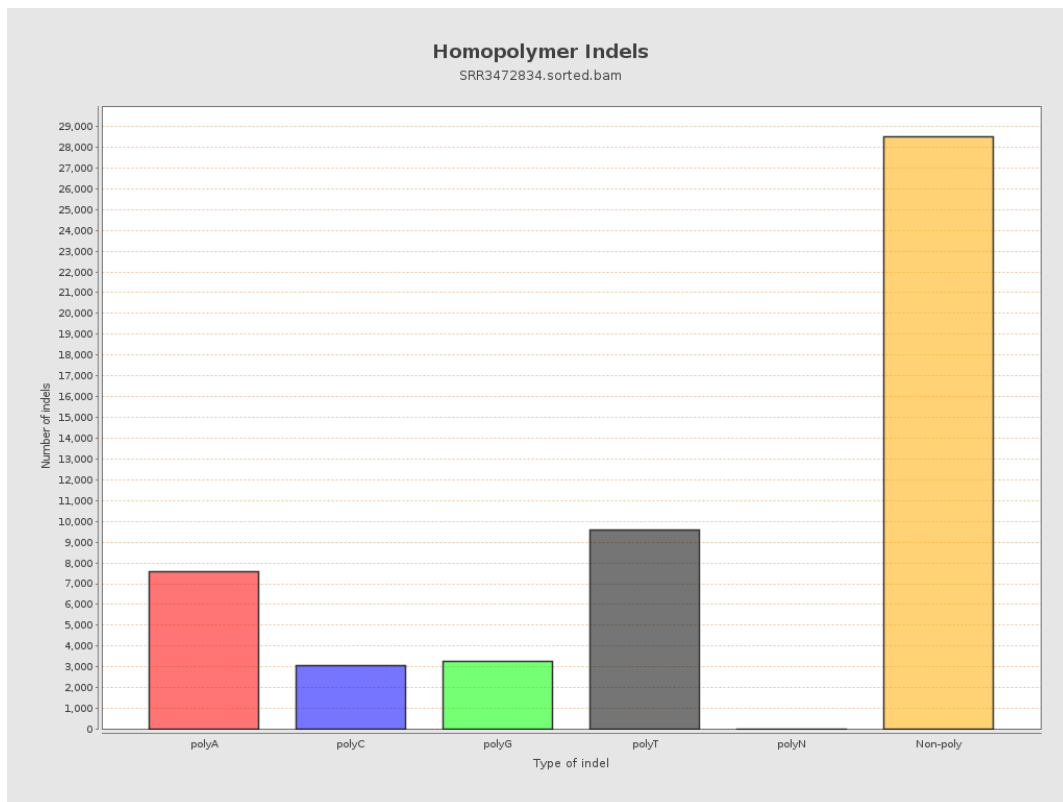
9. Results : Mapped Reads GC-content Distribution



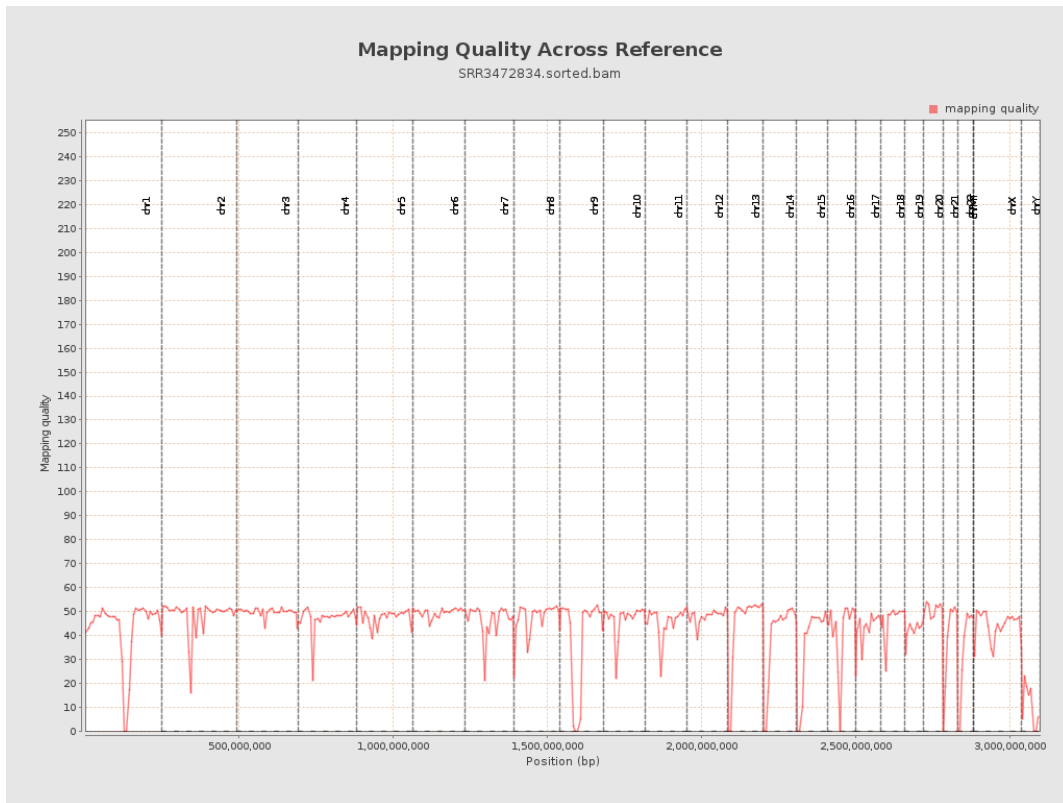
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

