

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 20:55:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6230386.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_SRR6230386 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6230386.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 20:55:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6230386.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,238,060
Mapped reads	1,667,390 / 74.5%
Unmapped reads	570,670 / 25.5%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,695 / 0.66%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	60,410 / 2.7%
Duplication rate	2.84%
Clipped reads	773,718 / 34.57%

2.2. ACGT Content

Number/percentage of A's	30,390,126 / 27.56%
Number/percentage of C's	19,334,111 / 17.53%
Number/percentage of T's	36,503,745 / 33.1%
Number/percentage of G's	23,838,473 / 21.62%
Number/percentage of N's	213,452 / 0.19%
GC Percentage	39.15%

2.3. Coverage

Mean	0.0356

Standard Deviation	0.3176
--------------------	--------

2.4. Mapping Quality

Mean Mapping Quality	47.13
----------------------	-------

2.5. Mismatches and indels

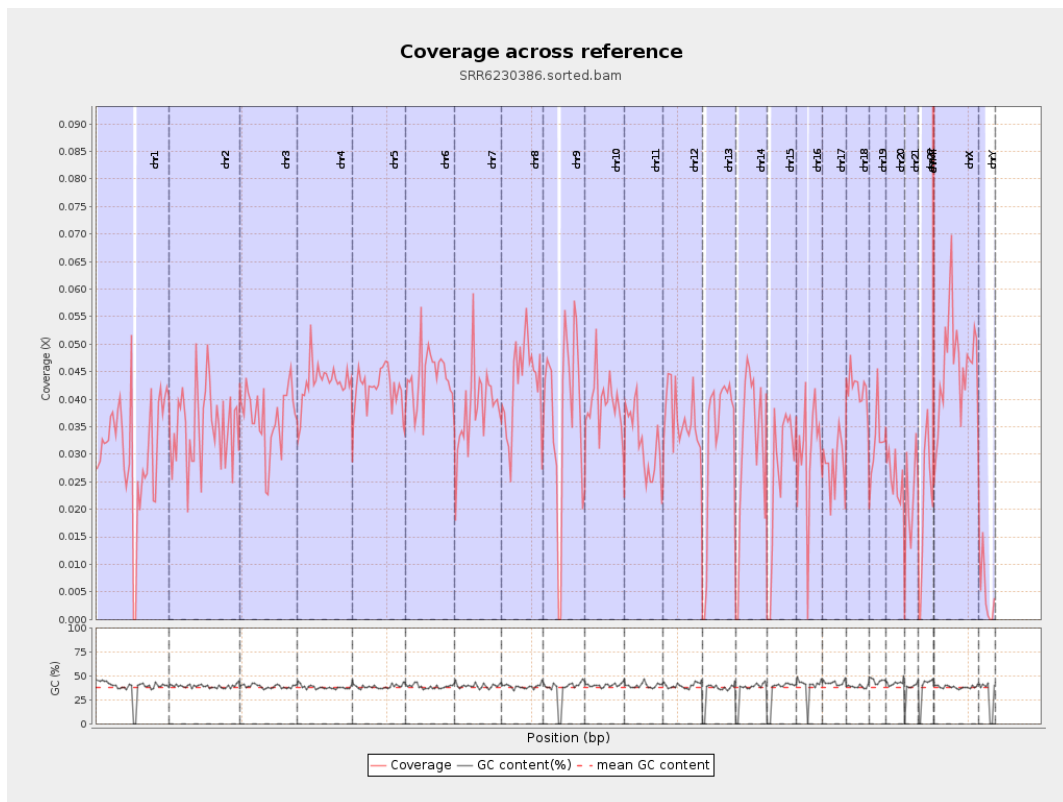
General error rate	1.06%
Mismatches	1,145,688
Insertions	9,806
Mapped reads with at least one insertion	0.58%
Deletions	29,312
Mapped reads with at least one deletion	1.74%
Homopolymer indels	48.27%

2.6. Chromosome stats

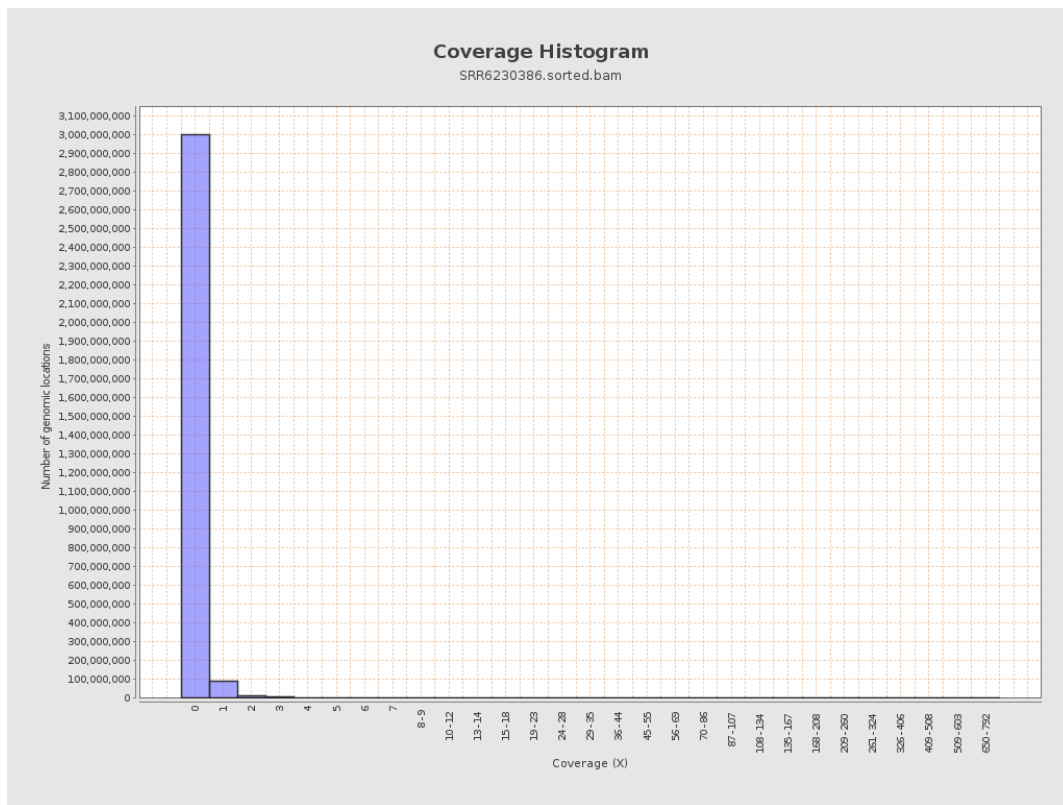
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	7676919	0.0308	0.533
chr2	243199373	8515207	0.035	0.2919
chr3	198022430	7311024	0.0369	0.2121
chr4	191154276	8226354	0.043	0.2417
chr5	180915260	7602194	0.042	0.2291
chr6	171115067	7511447	0.0439	0.2821
chr7	159138663	6129277	0.0385	0.4077

chr8	146364022	6243066	0.0427	0.5403
chr9	141213431	5374503	0.0381	0.3038
chr10	135534747	5338440	0.0394	0.2872
chr11	135006516	4253463	0.0315	0.2586
chr12	133851895	4853060	0.0363	0.2146
chr13	115169878	3743854	0.0325	0.2001
chr14	107349540	3388872	0.0316	0.2096
chr15	102531392	2722772	0.0266	0.1807
chr16	90354753	2744422	0.0304	0.2094
chr17	81195210	2259677	0.0278	0.1967
chr18	78077248	3275636	0.042	0.5506
chr19	59128983	1920207	0.0325	0.3639
chr20	63025520	1621704	0.0257	0.1894
chr21	48129895	1050876	0.0218	0.1816
chr22	51304566	1053608	0.0205	0.159
chrMT	16571	102629	6.1933	3.6699
chrX	155270560	7133057	0.0459	0.2633
chrY	59373566	276270	0.0047	0.1126

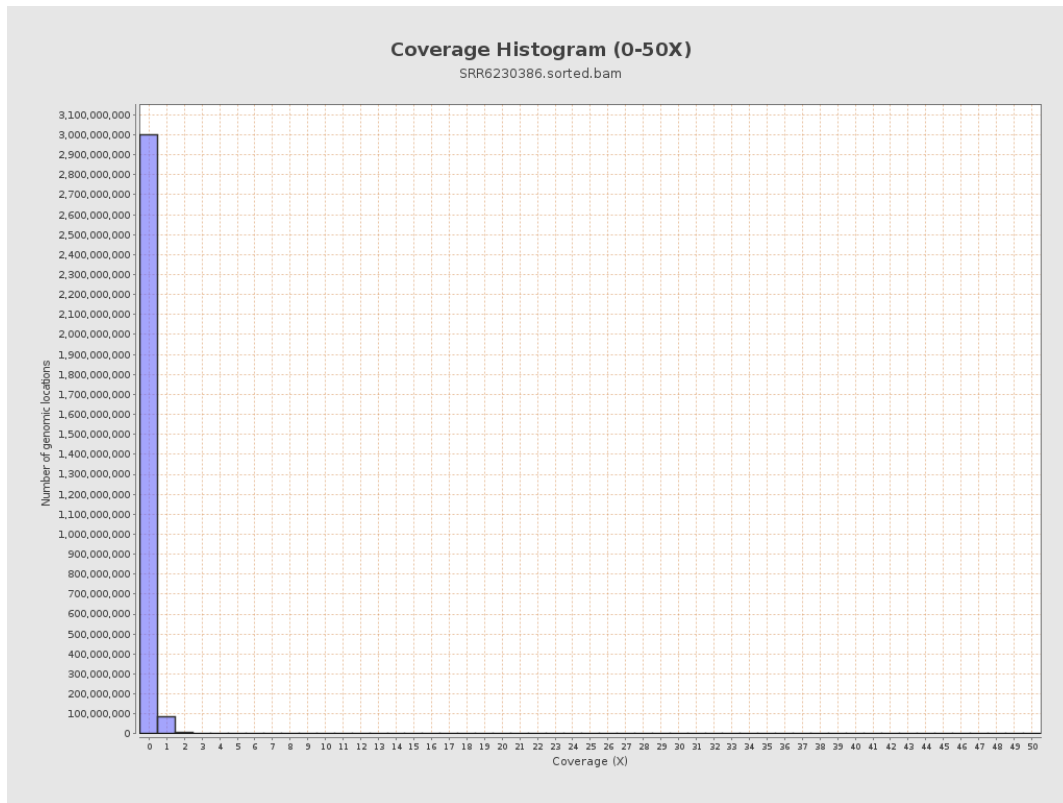
3. Results : Coverage across reference



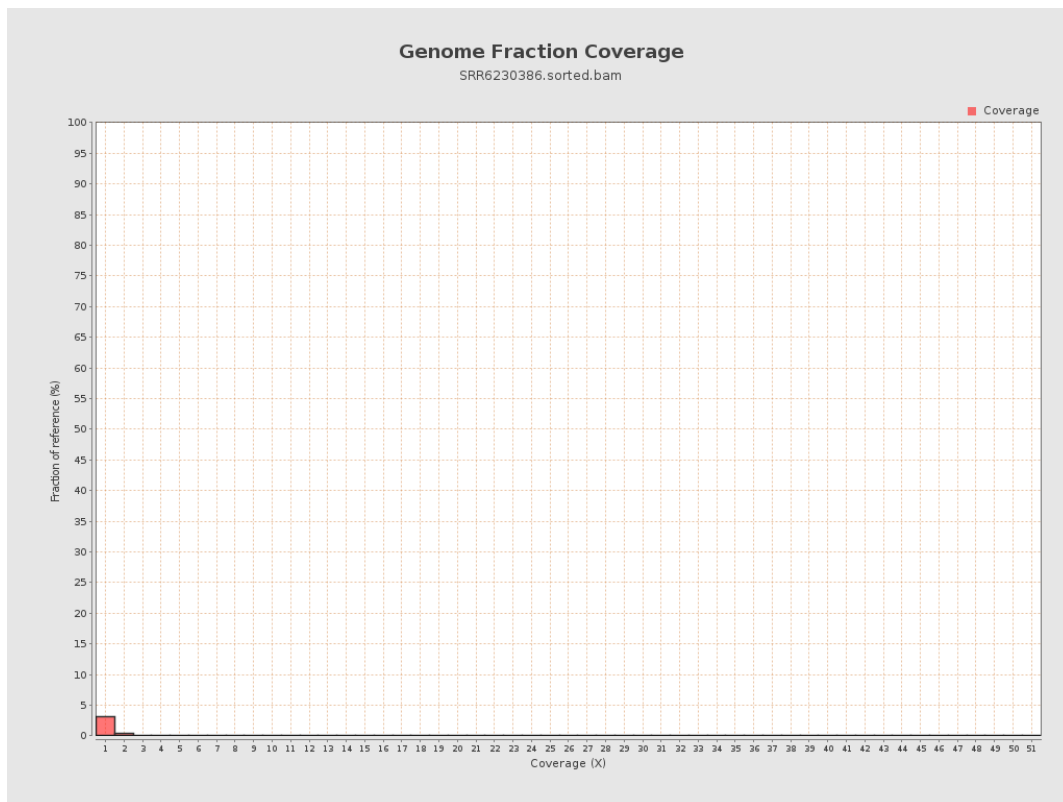
4. Results : Coverage Histogram



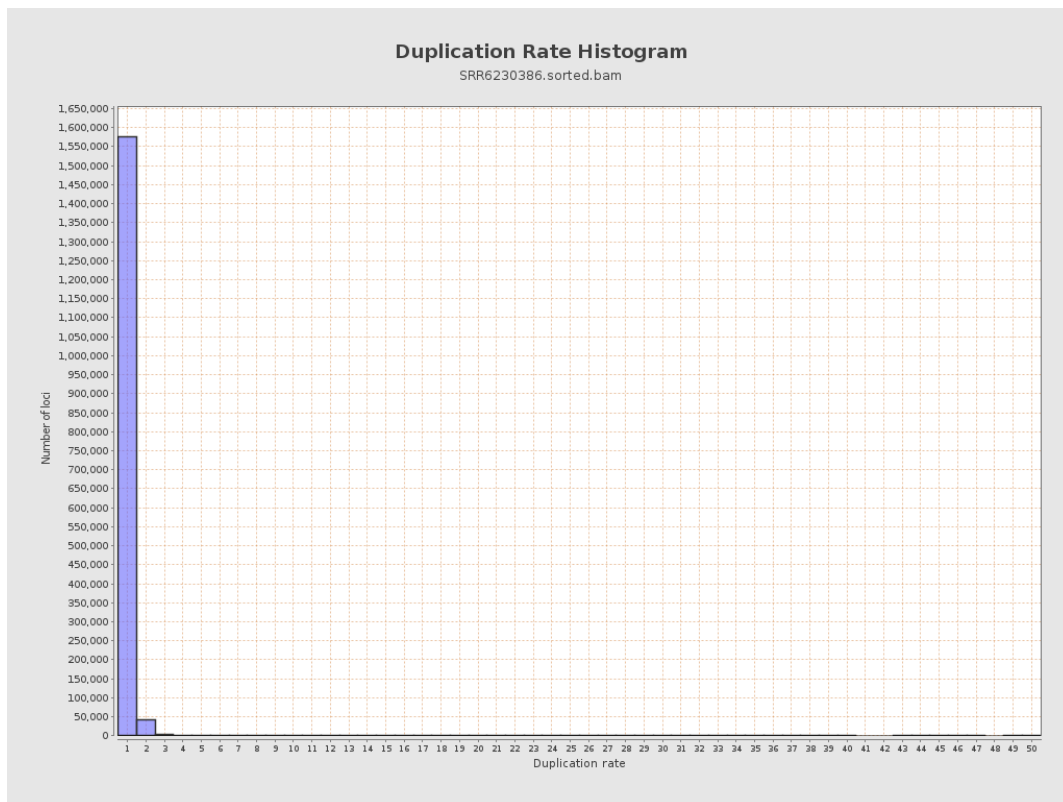
5. Results : Coverage Histogram (0-50X)



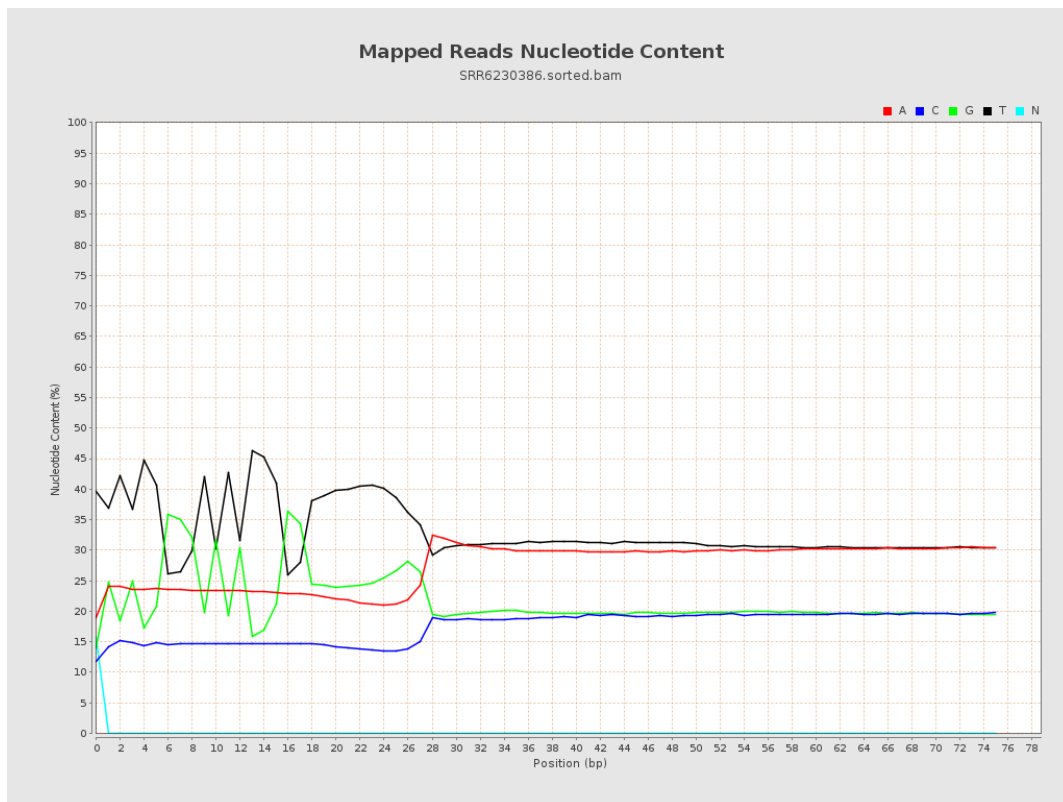
6. Results : Genome Fraction Coverage



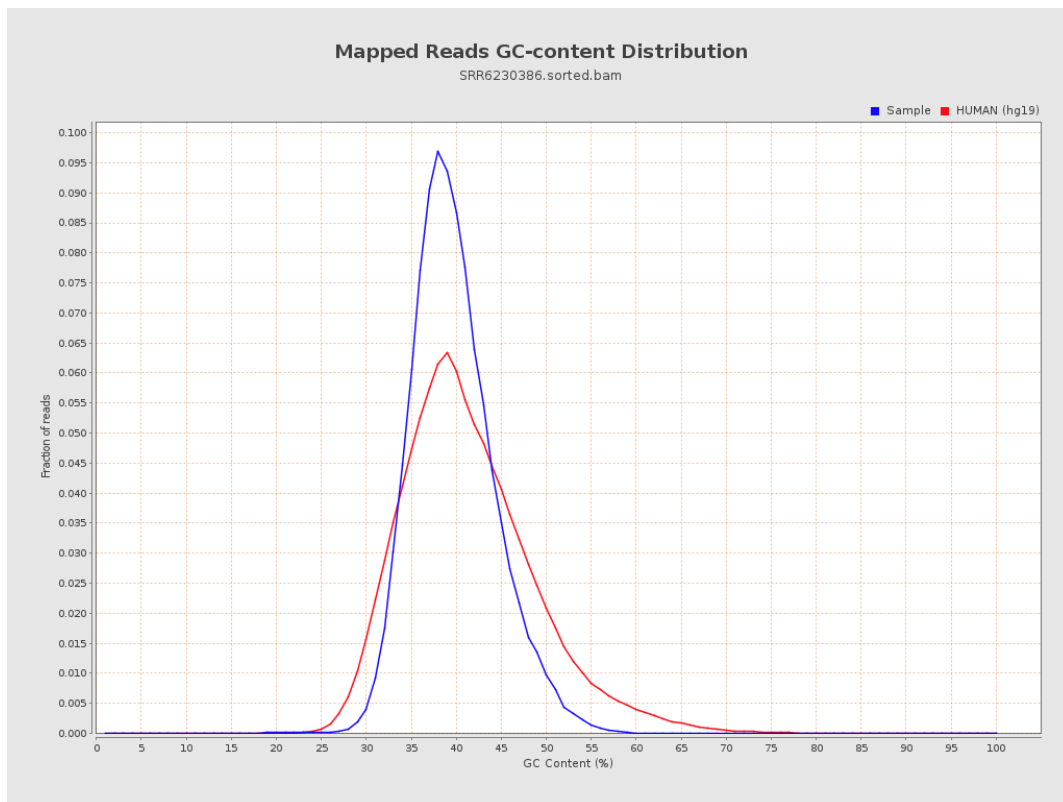
7. Results : Duplication Rate Histogram



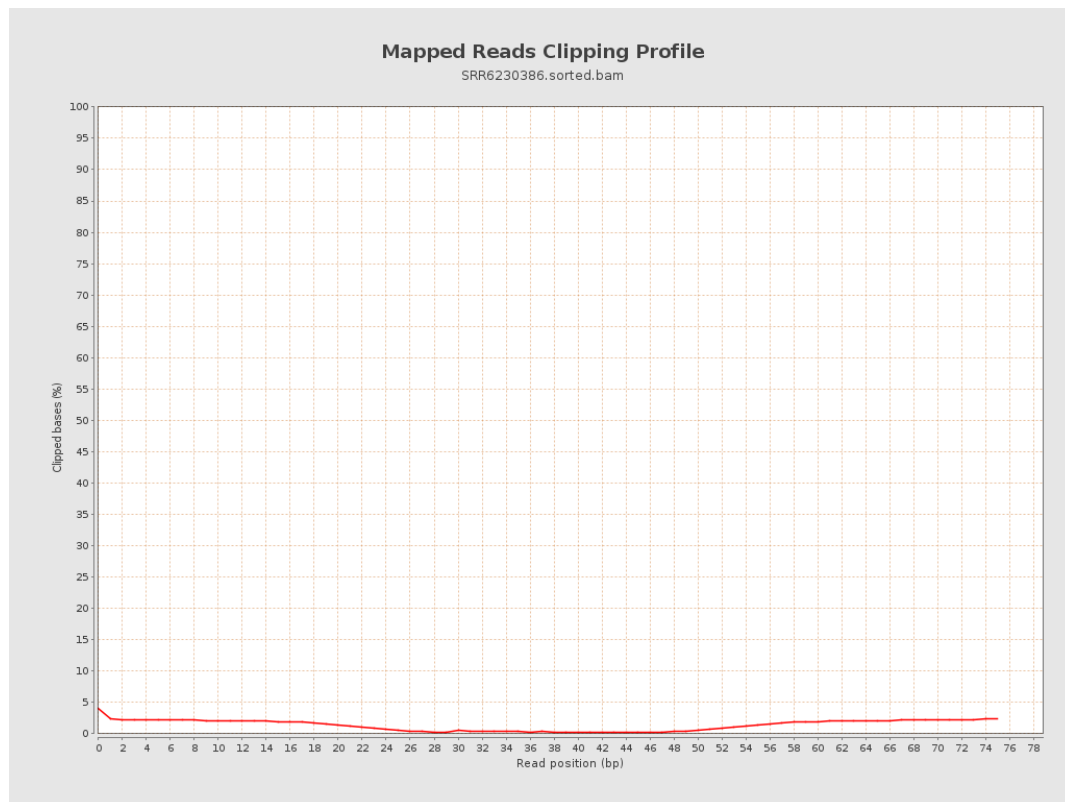
8. Results : Mapped Reads Nucleotide Content



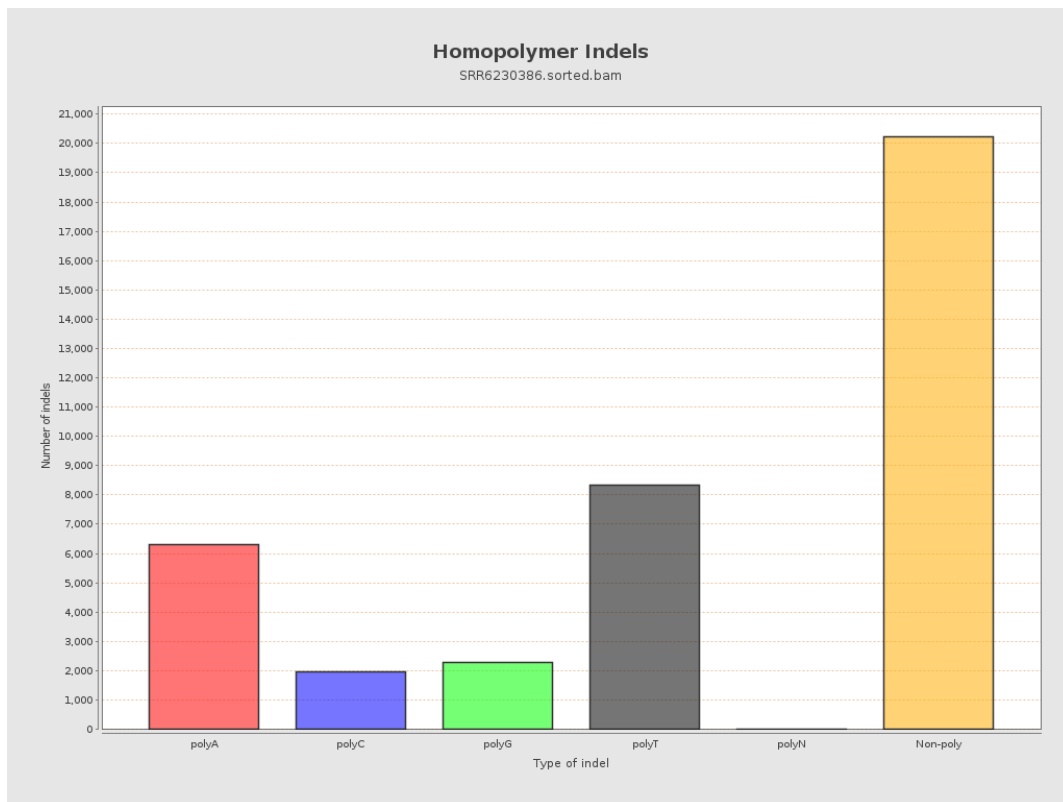
9. Results : Mapped Reads GC-content Distribution



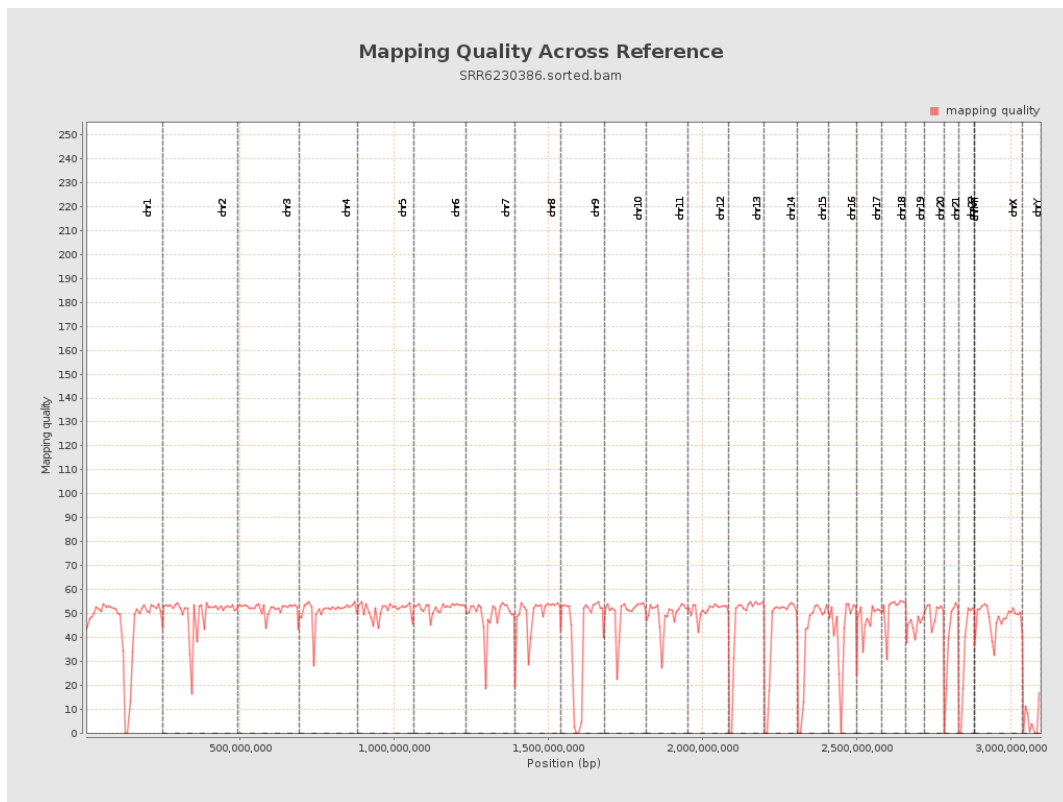
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

