

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 20:35:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6230380.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_SRR6230380 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6230380.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 20:35:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6230380.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,996,728
Mapped reads	3,457,685 / 86.51%
Unmapped reads	539,043 / 13.49%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	43,346 / 1.08%
Read min/max/mean length	30 / 76 / 76.38
Duplicated reads (estimated)	985,069 / 24.65%
Duplication rate	15.66%
Clipped reads	1,942,288 / 48.6%

2.2. ACGT Content

Number/percentage of A's	59,720,427 / 26.87%
Number/percentage of C's	40,873,894 / 18.39%
Number/percentage of T's	70,351,402 / 31.66%
Number/percentage of G's	51,159,714 / 23.02%
Number/percentage of N's	113,646 / 0.05%
GC Percentage	41.42%

2.3. Coverage

Mean	0.0718

Standard Deviation	0.788
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2.4. Mapping Quality

Mean Mapping Quality	44.59
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2.5. Mismatches and indels

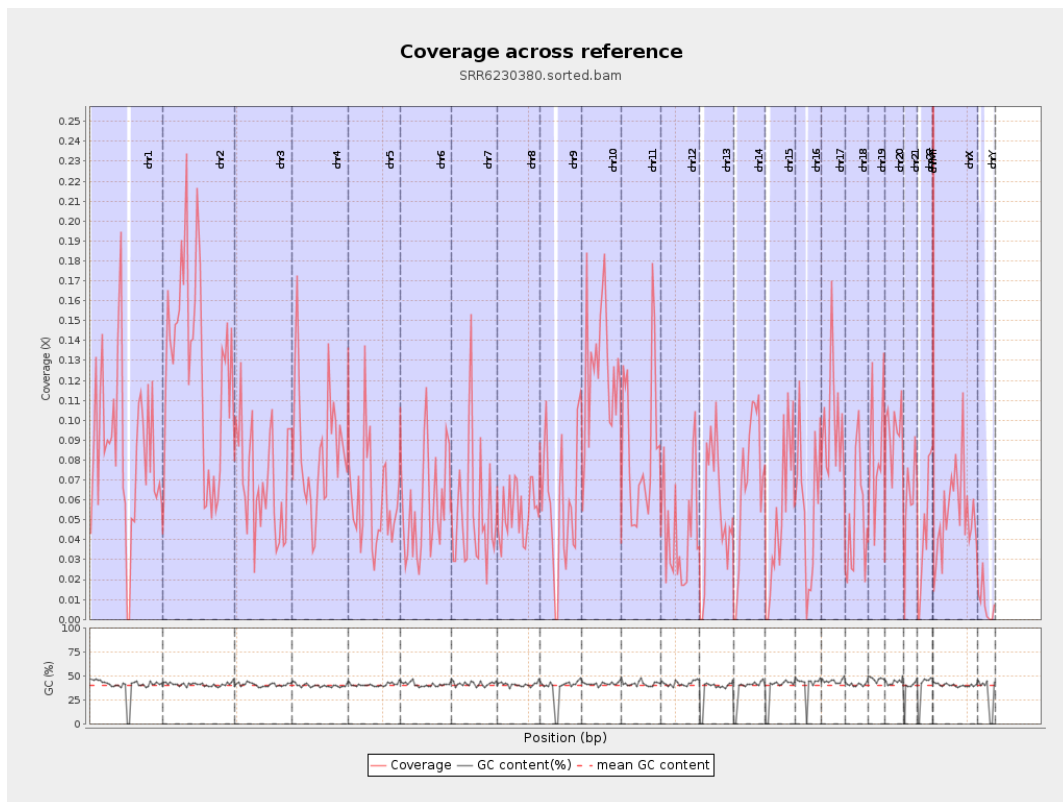
General error rate	0.86%
Mismatches	1,880,255
Insertions	17,387
Mapped reads with at least one insertion	0.5%
Deletions	56,383
Mapped reads with at least one deletion	1.61%
Homopolymer indels	46.75%

2.6. Chromosome stats

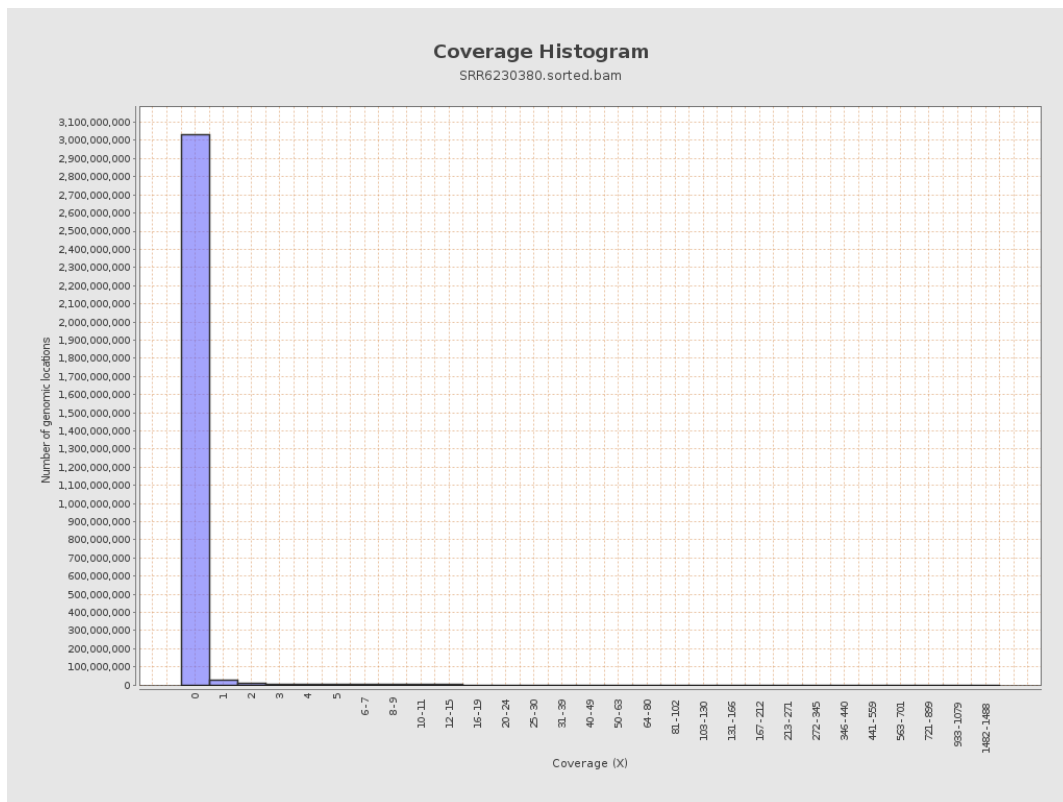
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	21134627	0.0848	0.8967
chr2	243199373	30475107	0.1253	1.139
chr3	198022430	13724464	0.0693	0.6931
chr4	191154276	16223254	0.0849	0.776
chr5	180915260	10827042	0.0598	0.6426
chr6	171115067	9725114	0.0568	0.6391
chr7	159138663	8554288	0.0538	0.9846

chr8	146364022	7960050	0.0544	0.8462
chr9	141213431	8241274	0.0584	0.6973
chr10	135534747	16887615	0.1246	0.9583
chr11	135006516	11597116	0.0859	0.7882
chr12	133851895	6063586	0.0453	0.5531
chr13	115169878	6260926	0.0544	0.6183
chr14	107349540	7524774	0.0701	0.7249
chr15	102531392	5226491	0.051	0.599
chr16	90354753	5148254	0.057	0.6258
chr17	81195210	7990830	0.0984	0.8253
chr18	78077248	3895598	0.0499	0.9325
chr19	59128983	4903266	0.0829	0.7779
chr20	63025520	6012281	0.0954	0.8182
chr21	48129895	2929855	0.0609	0.6551
chr22	51304566	2302514	0.0449	0.5341
chrMT	16571	30798	1.8585	3.9511
chrX	155270560	8198950	0.0528	0.622
chrY	59373566	472887	0.008	0.2251

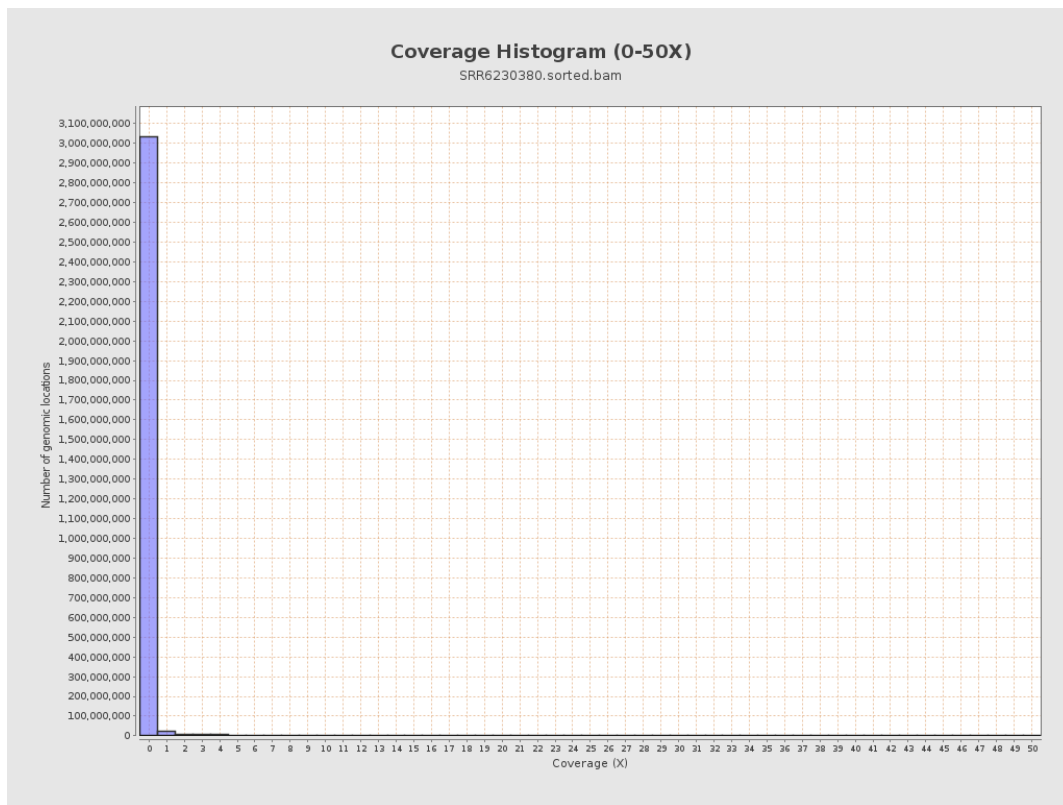
3. Results : Coverage across reference



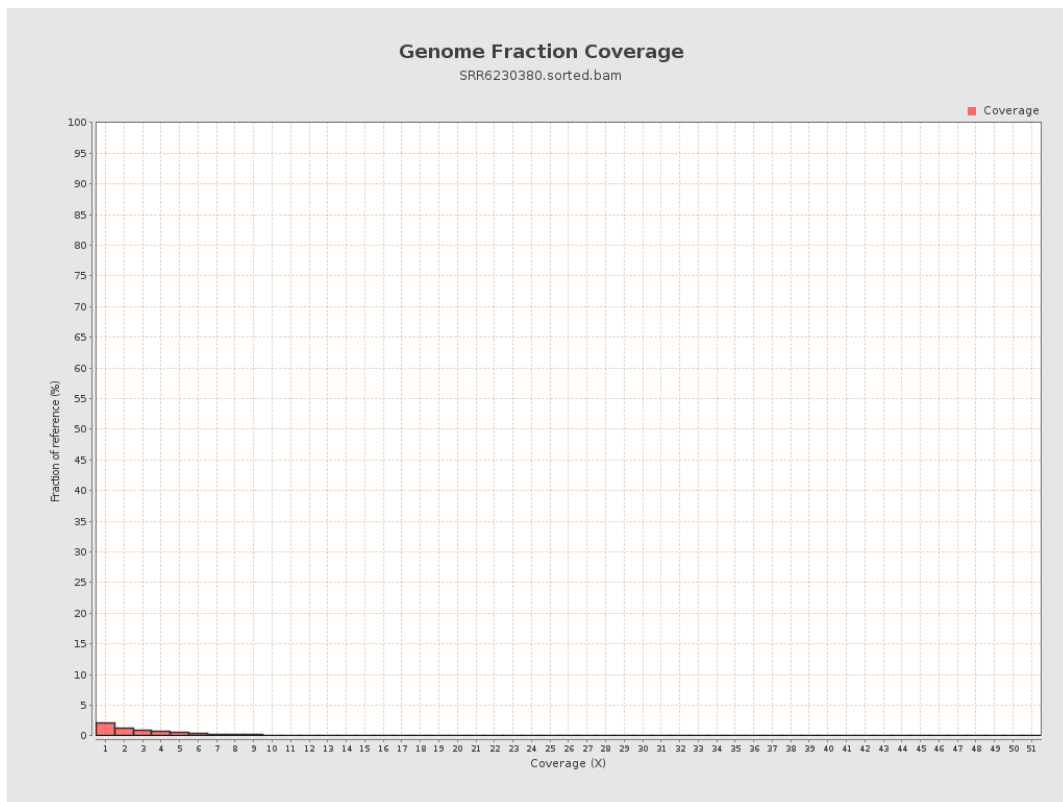
4. Results : Coverage Histogram



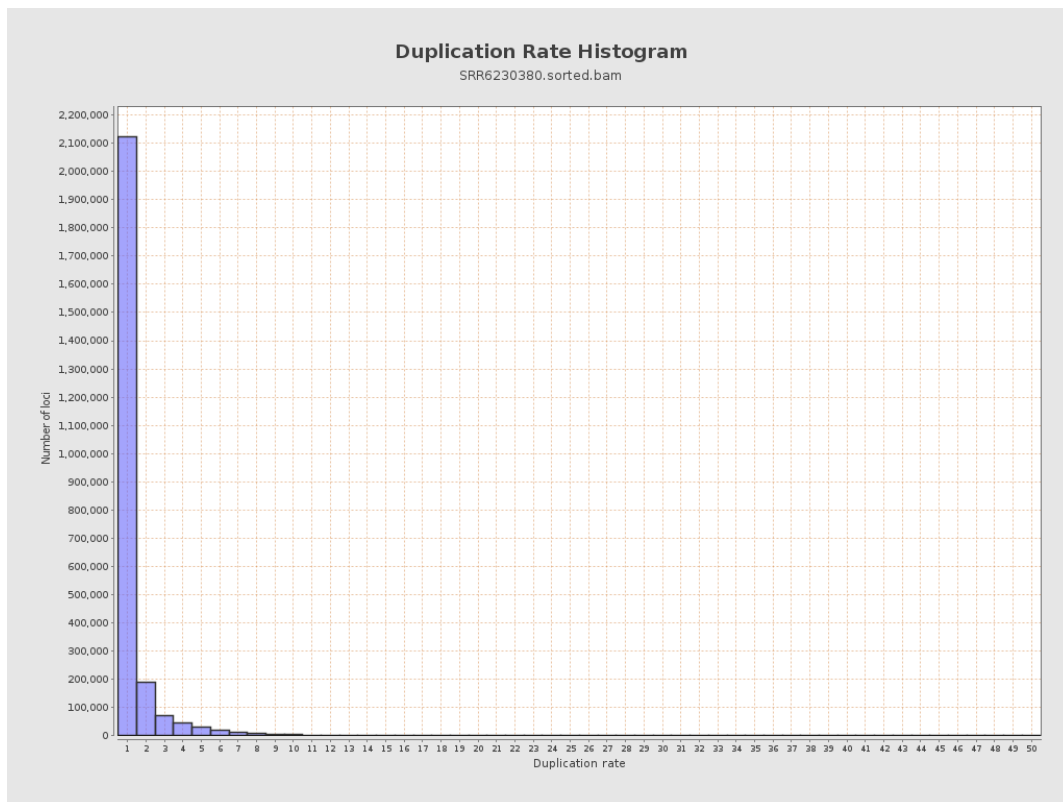
5. Results : Coverage Histogram (0-50X)



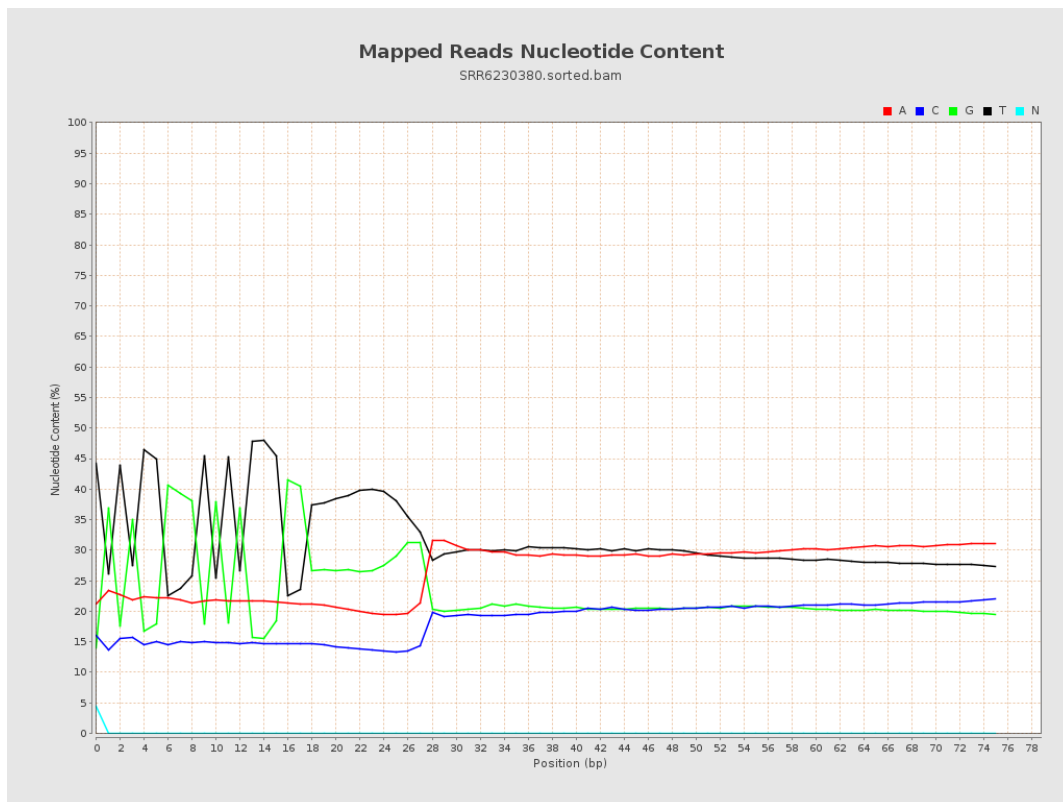
6. Results : Genome Fraction Coverage



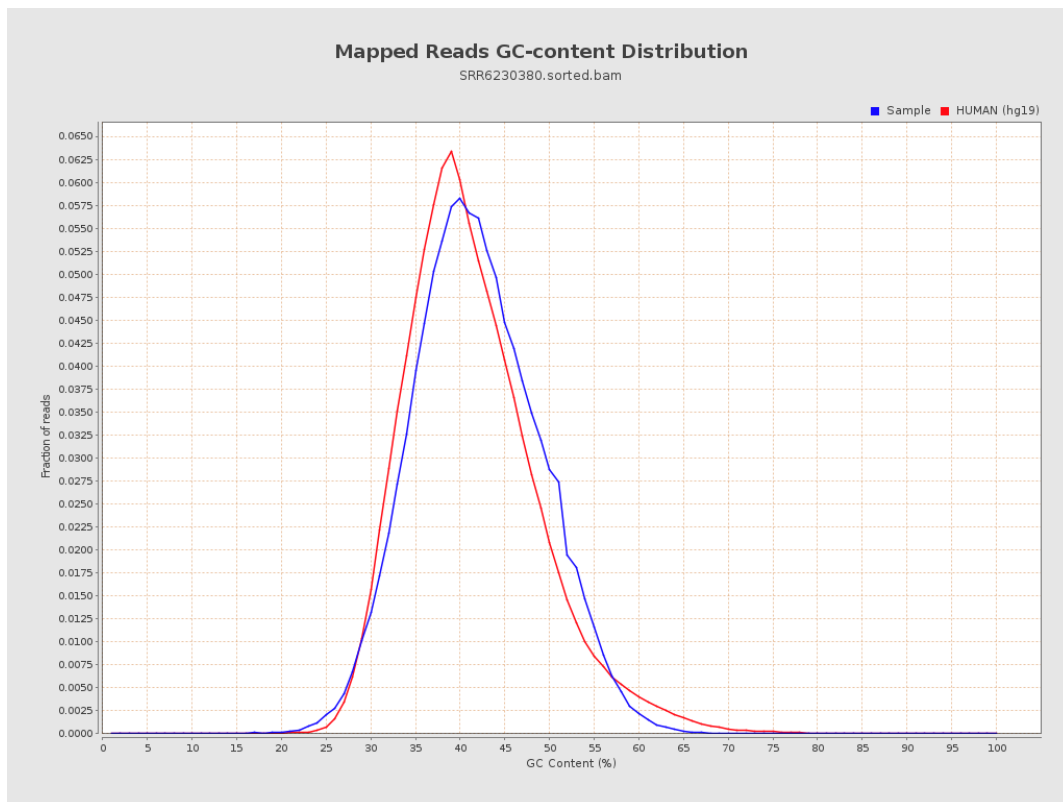
7. Results : Duplication Rate Histogram



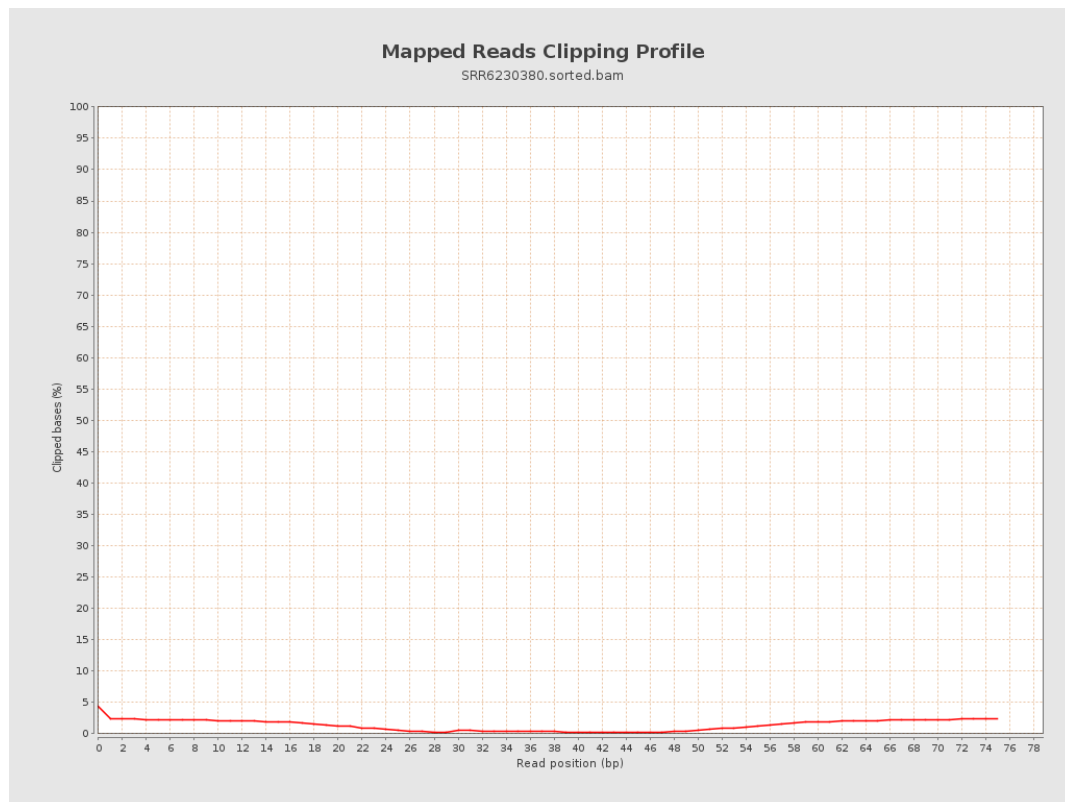
8. Results : Mapped Reads Nucleotide Content



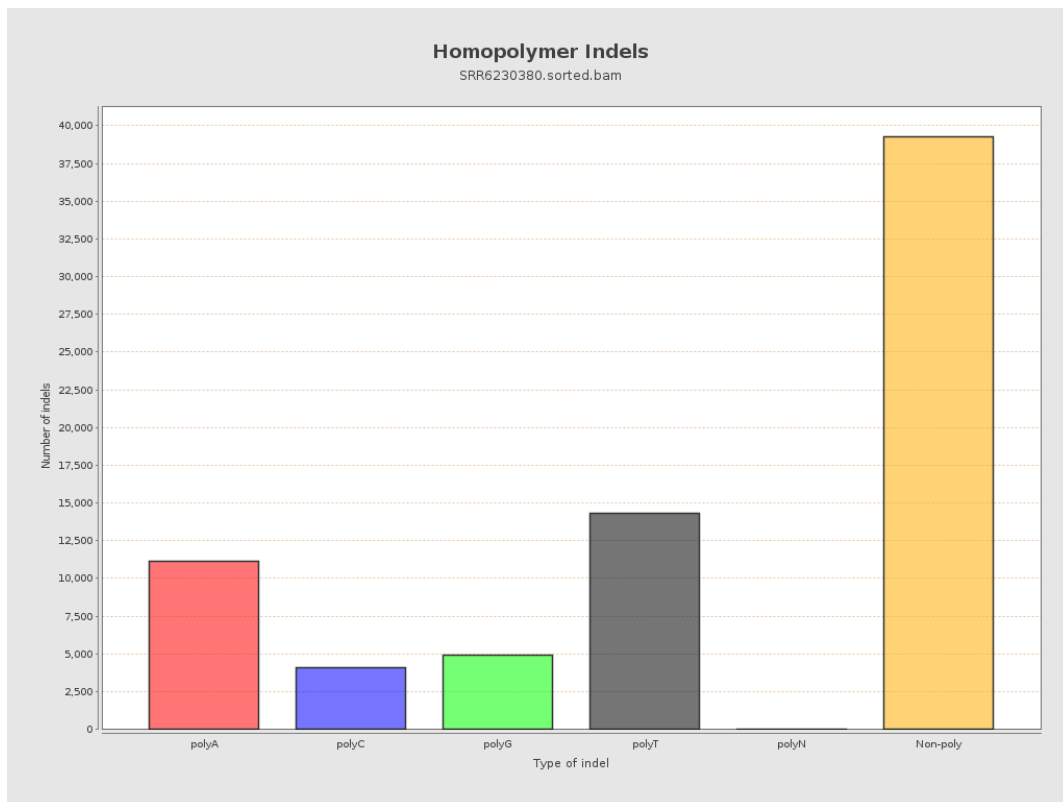
9. Results : Mapped Reads GC-content Distribution



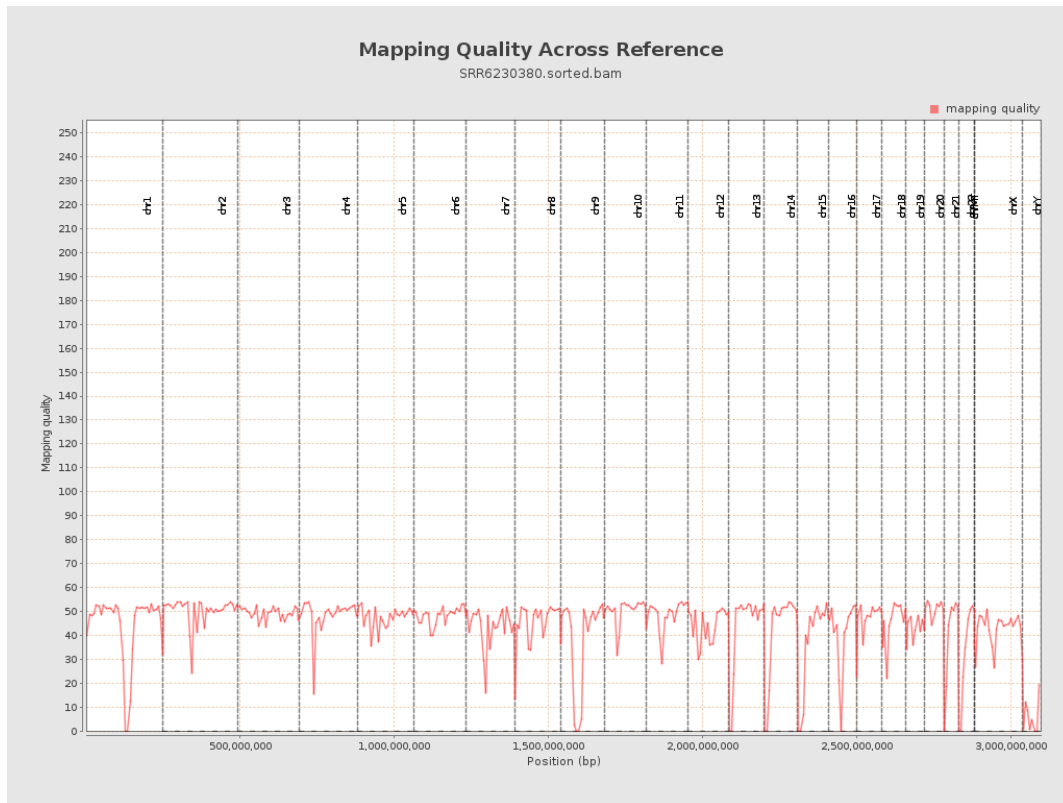
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

