

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 17:58:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013250.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_SRR6013250 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013250.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 17:58:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013250.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,972,919
Mapped reads	1,689,948 / 85.66%
Unmapped reads	282,971 / 14.34%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,420 / 0.53%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	87,676 / 4.44%
Duplication rate	4.1%
Clipped reads	727,237 / 36.86%

2.2. ACGT Content

Number/percentage of A's	30,999,502 / 27.46%
Number/percentage of C's	21,237,915 / 18.81%
Number/percentage of T's	35,431,125 / 31.39%
Number/percentage of G's	25,219,022 / 22.34%
Number/percentage of N's	1,572 / 0%
GC Percentage	41.15%

2.3. Coverage

Mean	0.0365

Standard Deviation	0.3538
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2.4. Mapping Quality

Mean Mapping Quality	46.25
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2.5. Mismatches and indels

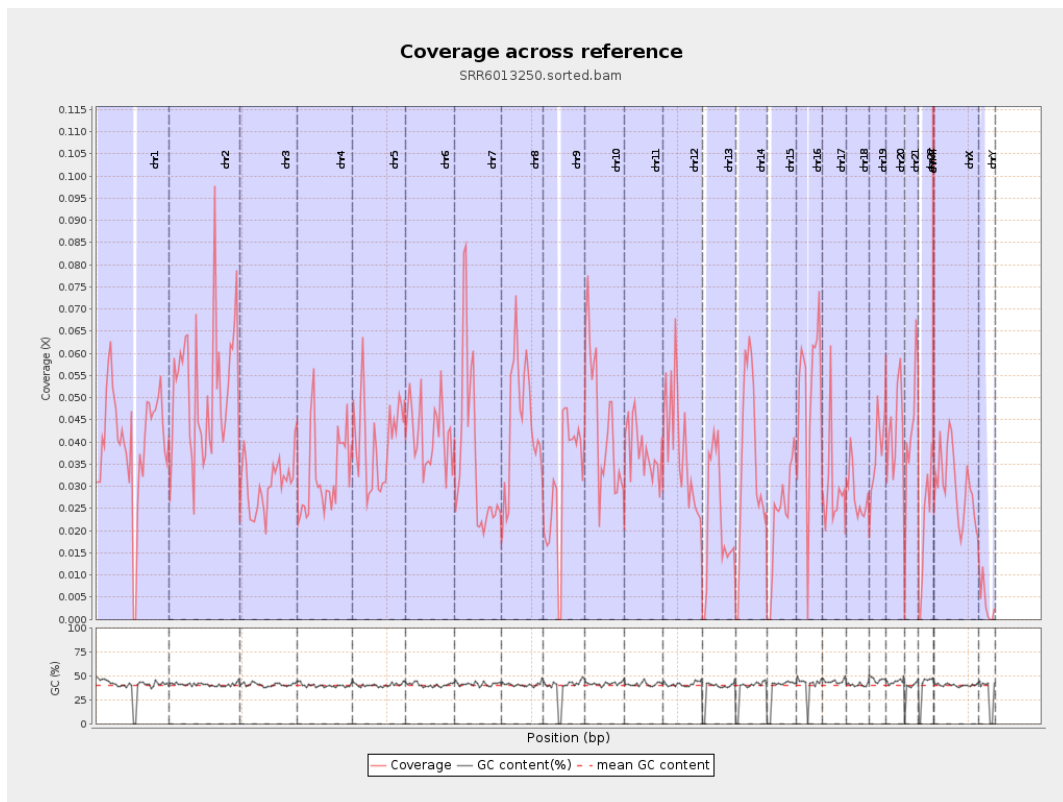
General error rate	0.79%
Mismatches	874,472
Insertions	8,113
Mapped reads with at least one insertion	0.48%
Deletions	34,616
Mapped reads with at least one deletion	2.02%
Homopolymer indels	48.3%

2.6. Chromosome stats

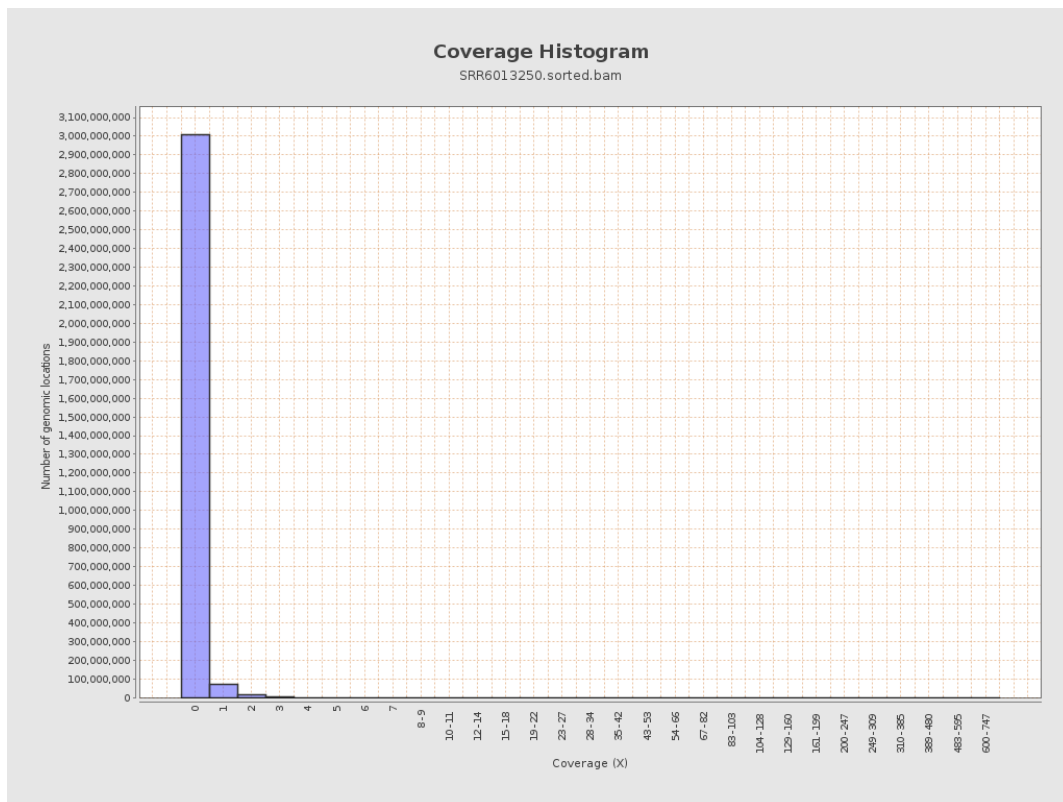
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	10057598	0.0404	0.6644
chr2	243199373	12522726	0.0515	0.4203
chr3	198022430	6015380	0.0304	0.2102
chr4	191154276	6196432	0.0324	0.2326
chr5	180915260	7288479	0.0403	0.242
chr6	171115067	7128680	0.0417	0.3138
chr7	159138663	5716295	0.0359	0.4988

chr8	146364022	6423415	0.0439	0.3971
chr9	141213431	4359067	0.0309	0.3114
chr10	135534747	6008571	0.0443	0.3553
chr11	135006516	5097978	0.0378	0.3119
chr12	133851895	5093445	0.0381	0.2411
chr13	115169878	2511686	0.0218	0.1766
chr14	107349540	3840013	0.0358	0.238
chr15	102531392	2416790	0.0236	0.1888
chr16	90354753	4655647	0.0515	0.286
chr17	81195210	2390784	0.0294	0.2329
chr18	78077248	2221475	0.0285	0.5048
chr19	59128983	2291618	0.0388	0.4154
chr20	63025520	2679677	0.0425	0.2571
chr21	48129895	2063727	0.0429	0.2653
chr22	51304566	1094454	0.0213	0.175
chrMT	16571	16912	1.0206	1.3295
chrX	155270560	4634131	0.0298	0.2314
chrY	59373566	225194	0.0038	0.1027

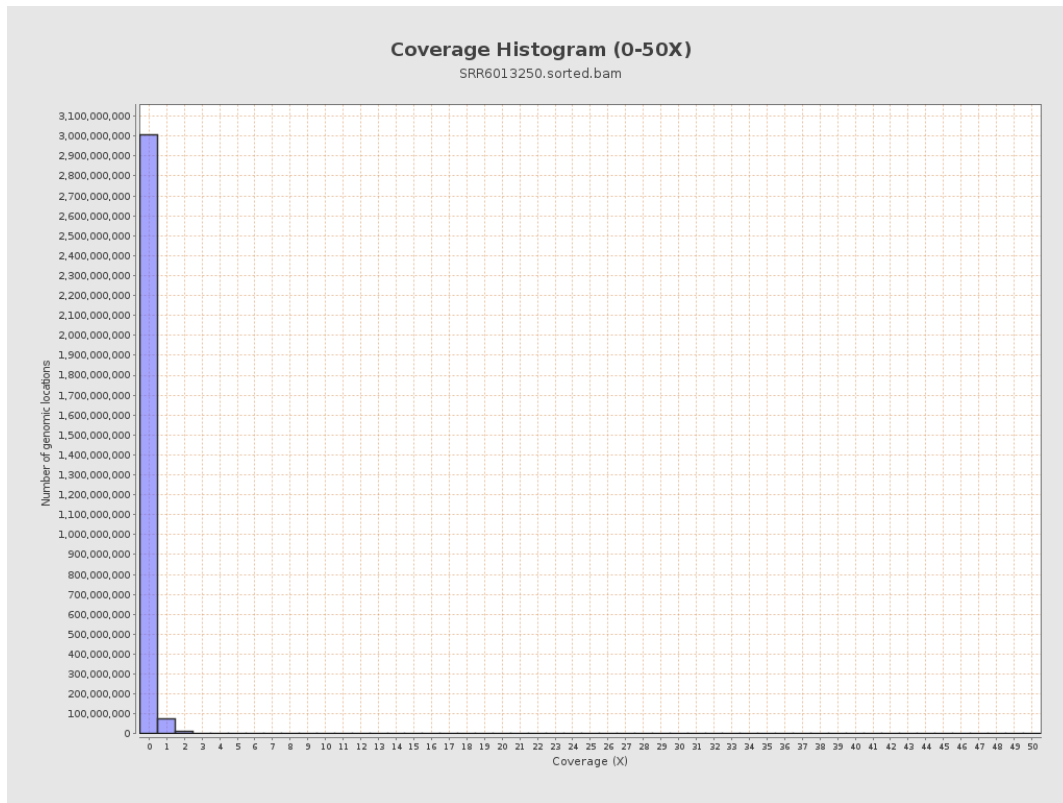
3. Results : Coverage across reference



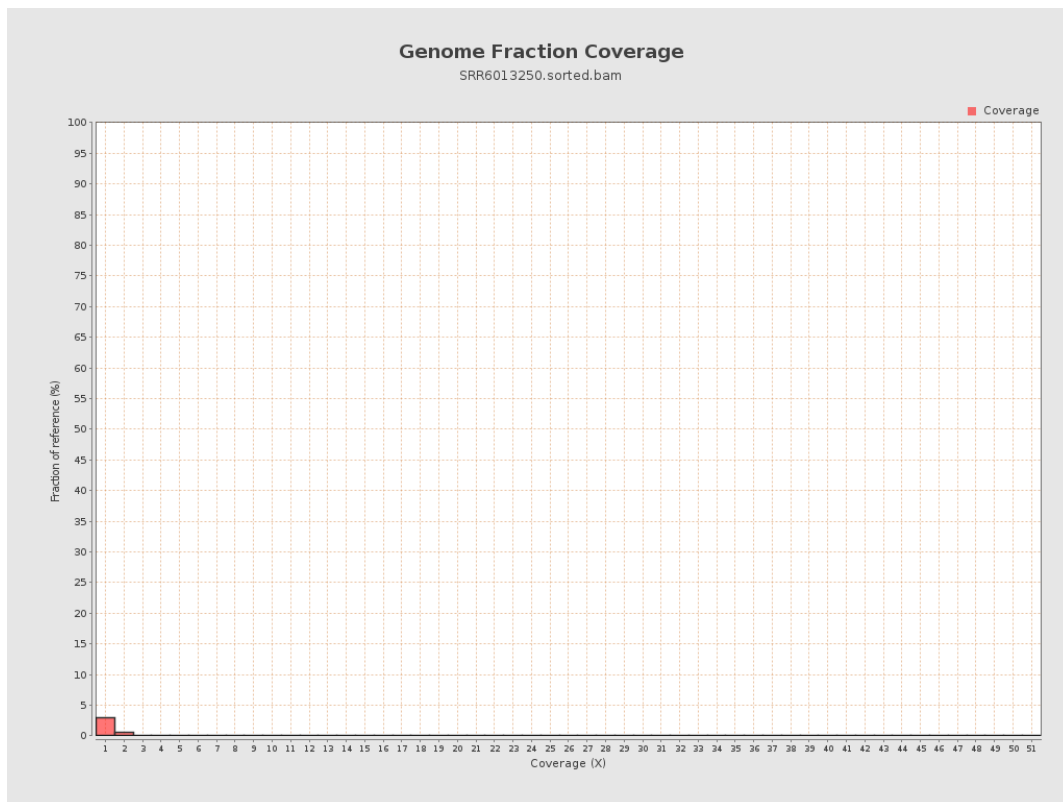
4. Results : Coverage Histogram



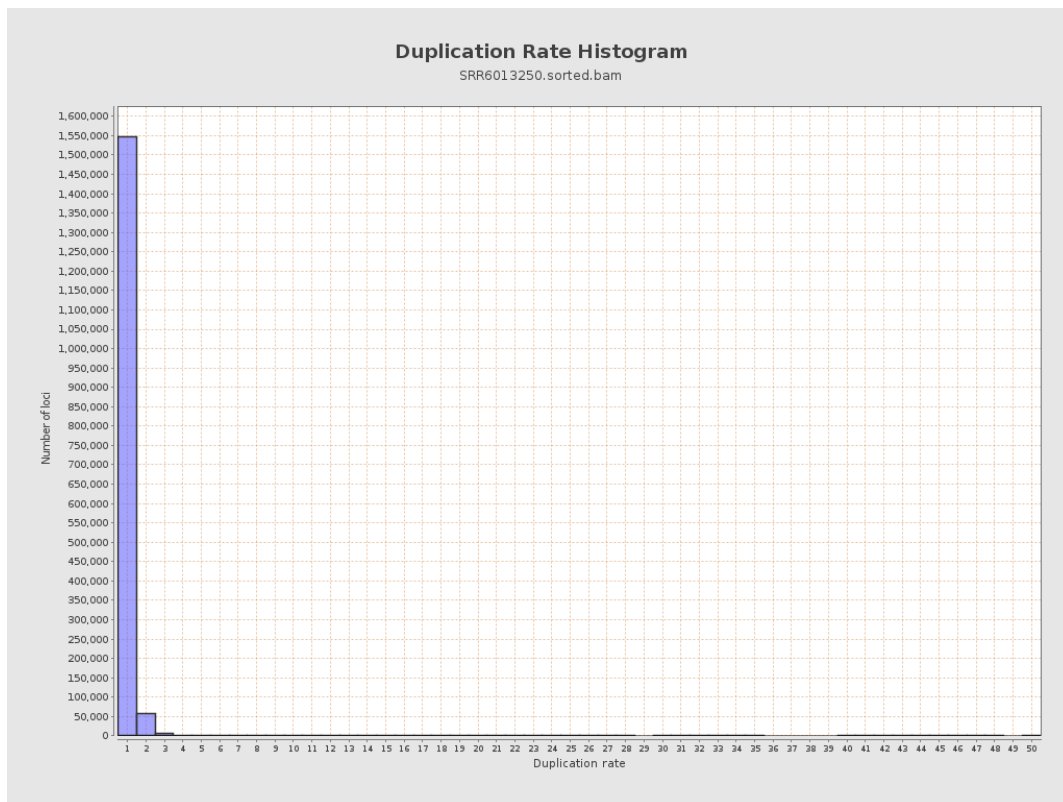
5. Results : Coverage Histogram (0-50X)



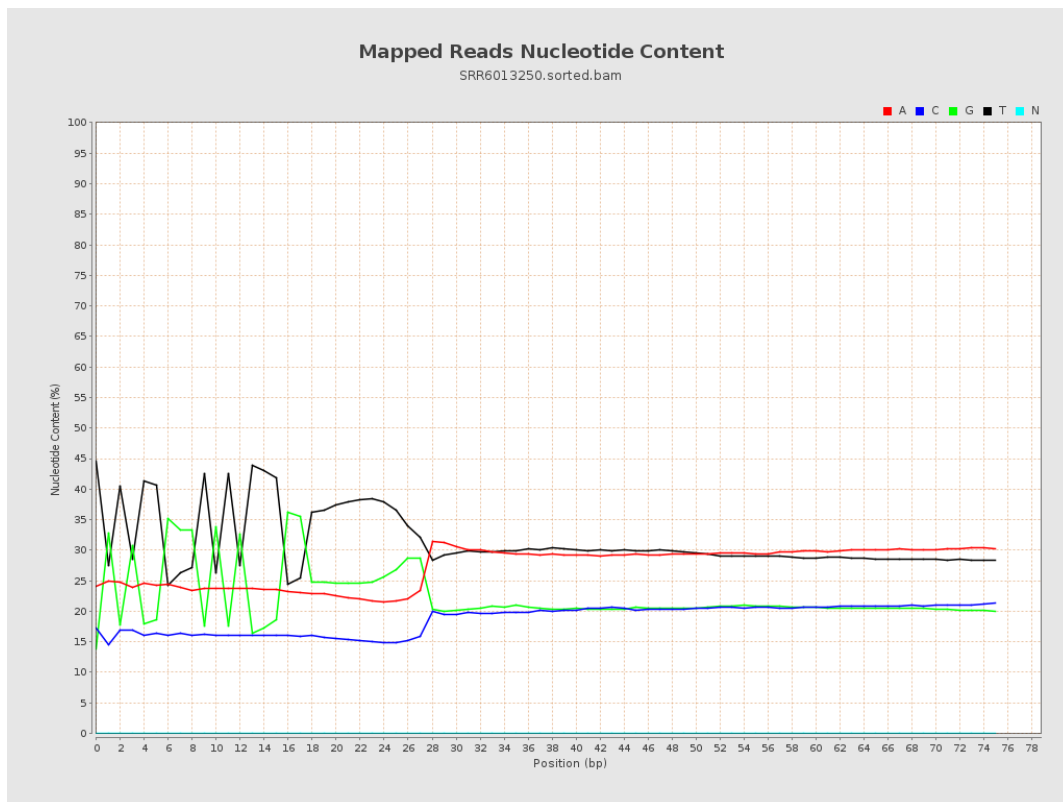
6. Results : Genome Fraction Coverage



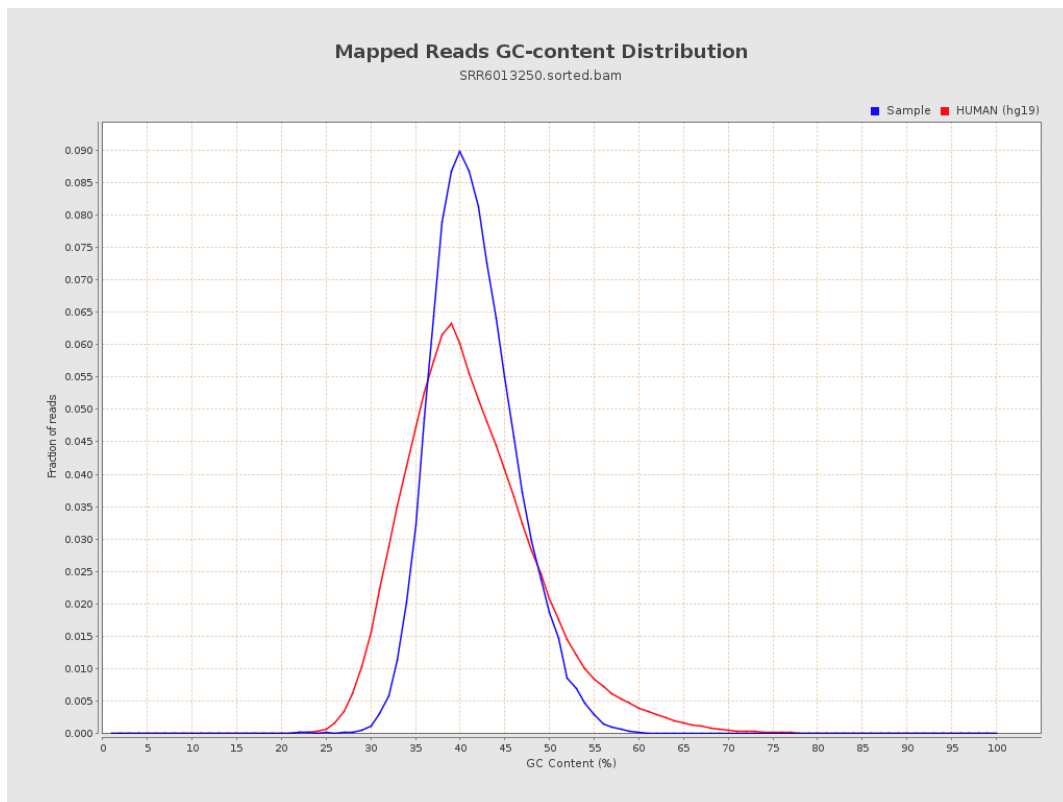
7. Results : Duplication Rate Histogram



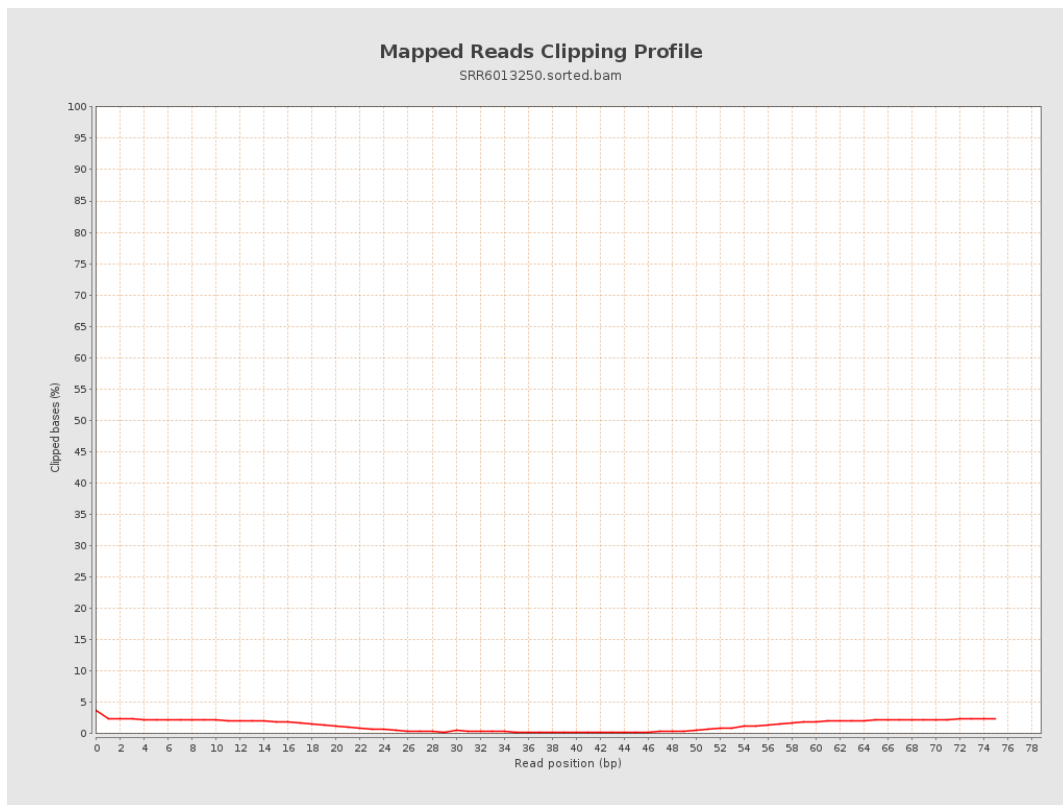
8. Results : Mapped Reads Nucleotide Content



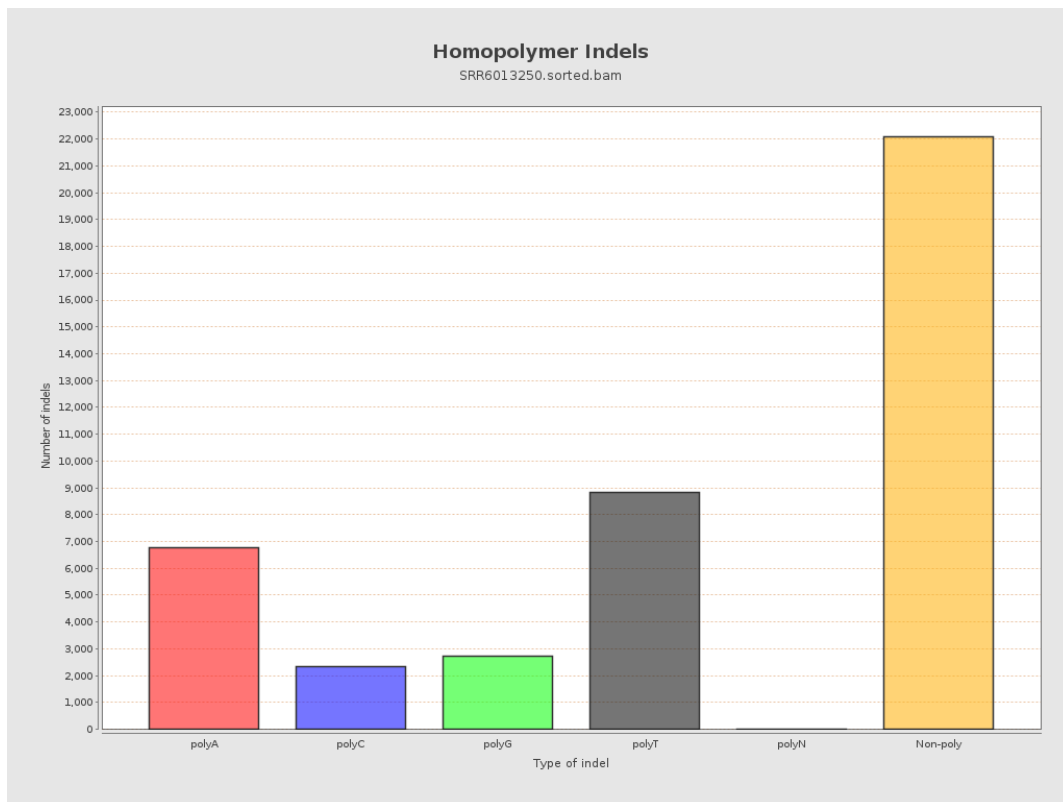
9. Results : Mapped Reads GC-content Distribution



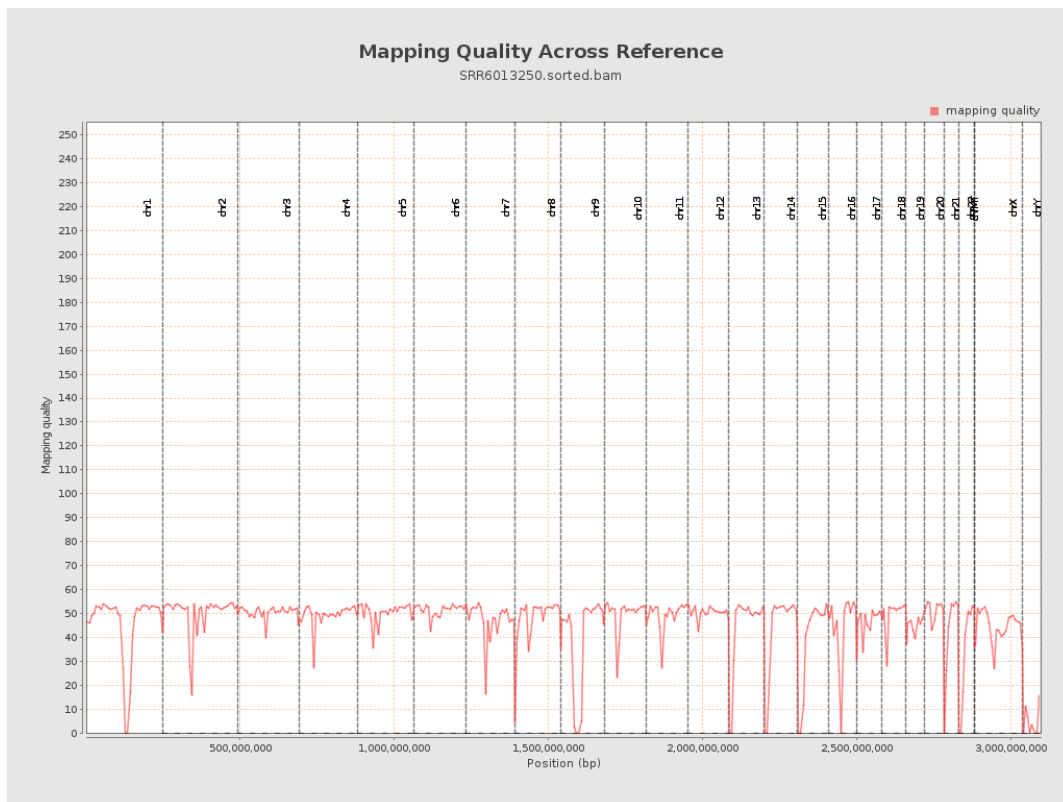
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

