

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 04:33:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240060.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_SRR6240060 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240060.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 04:33:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240060.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,547,820
Mapped reads	2,046,461 / 80.32%
Unmapped reads	501,359 / 19.68%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,223 / 0.72%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	341,150 / 13.39%
Duplication rate	11.91%
Clipped reads	960,162 / 37.69%

2.2. ACGT Content

Number/percentage of A's	38,402,478 / 28.22%
Number/percentage of C's	25,348,402 / 18.63%
Number/percentage of T's	43,330,699 / 31.85%
Number/percentage of G's	28,966,059 / 21.29%
Number/percentage of N's	12,326 / 0.01%
GC Percentage	39.92%

2.3. Coverage

Mean	0.044

Standard Deviation	0.5274
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2.4. Mapping Quality

Mean Mapping Quality	46.92
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2.5. Mismatches and indels

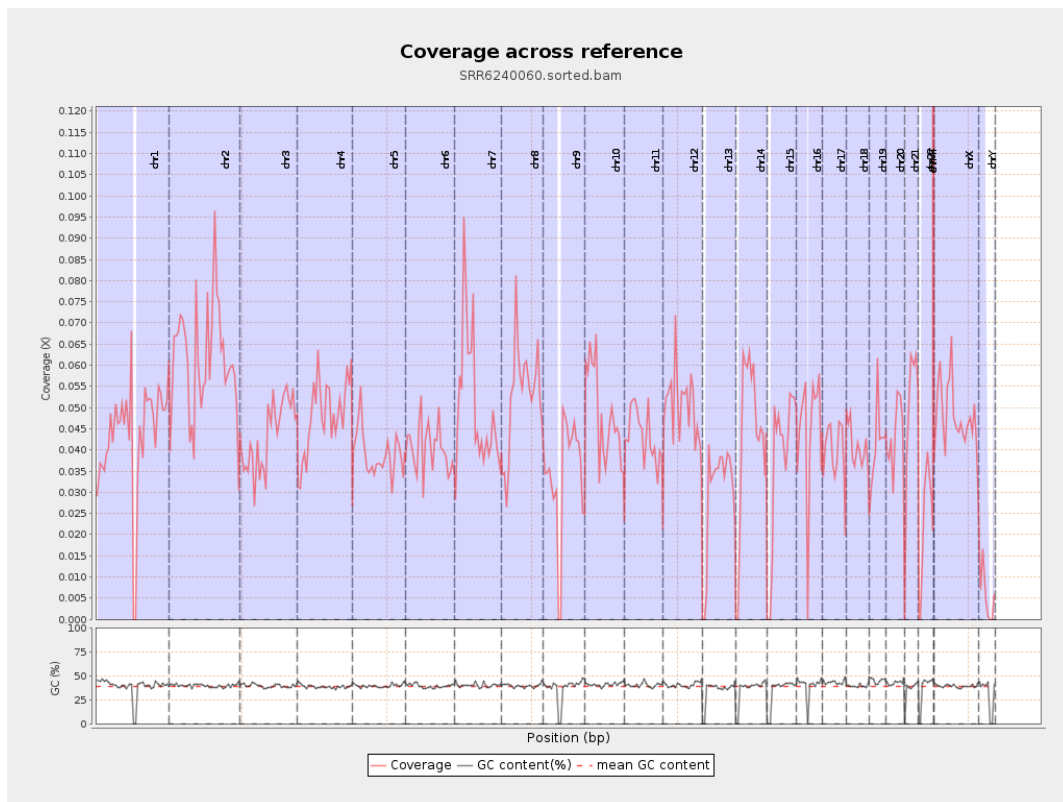
General error rate	0.86%
Mismatches	1,157,565
Insertions	10,109
Mapped reads with at least one insertion	0.49%
Deletions	38,484
Mapped reads with at least one deletion	1.86%
Homopolymer indels	48.8%

2.6. Chromosome stats

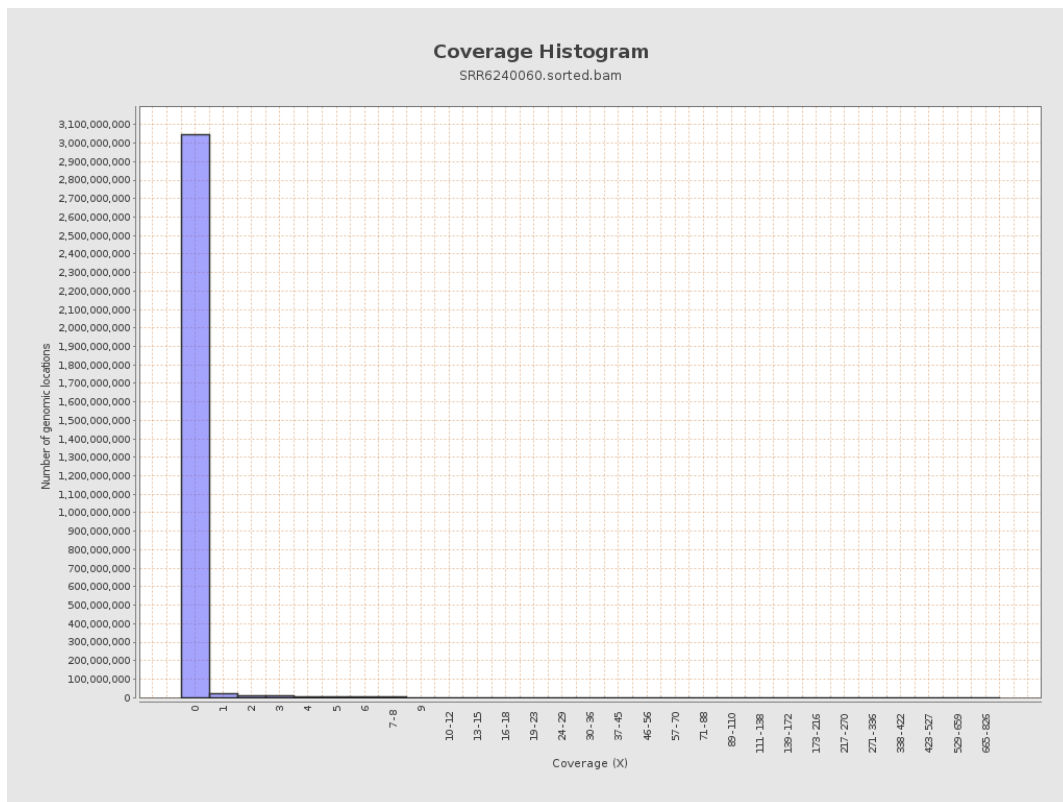
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	10827235	0.0434	0.7803
chr2	243199373	14891014	0.0612	0.6065
chr3	198022430	8618783	0.0435	0.4362
chr4	191154276	9195916	0.0481	0.4688
chr5	180915260	7062151	0.039	0.4076
chr6	171115067	6894440	0.0403	0.4497
chr7	159138663	8102582	0.0509	0.7004

chr8	146364022	7707656	0.0527	0.6916
chr9	141213431	4846319	0.0343	0.4337
chr10	135534747	6566612	0.0484	0.5134
chr11	135006516	5815703	0.0431	0.5052
chr12	133851895	6749267	0.0504	0.4684
chr13	115169878	3429881	0.0298	0.3607
chr14	107349540	4648023	0.0433	0.4439
chr15	102531392	3860422	0.0377	0.4086
chr16	90354753	4027439	0.0446	0.4354
chr17	81195210	3161005	0.0389	0.4146
chr18	78077248	3193335	0.0409	0.6586
chr19	59128983	2455465	0.0415	0.5835
chr20	63025520	2712475	0.043	0.4303
chr21	48129895	2379415	0.0494	0.4759
chr22	51304566	1168557	0.0228	0.2952
chrMT	16571	24119	1.4555	2.6889
chrX	155270560	7446371	0.048	0.4712
chrY	59373566	343641	0.0058	0.1399

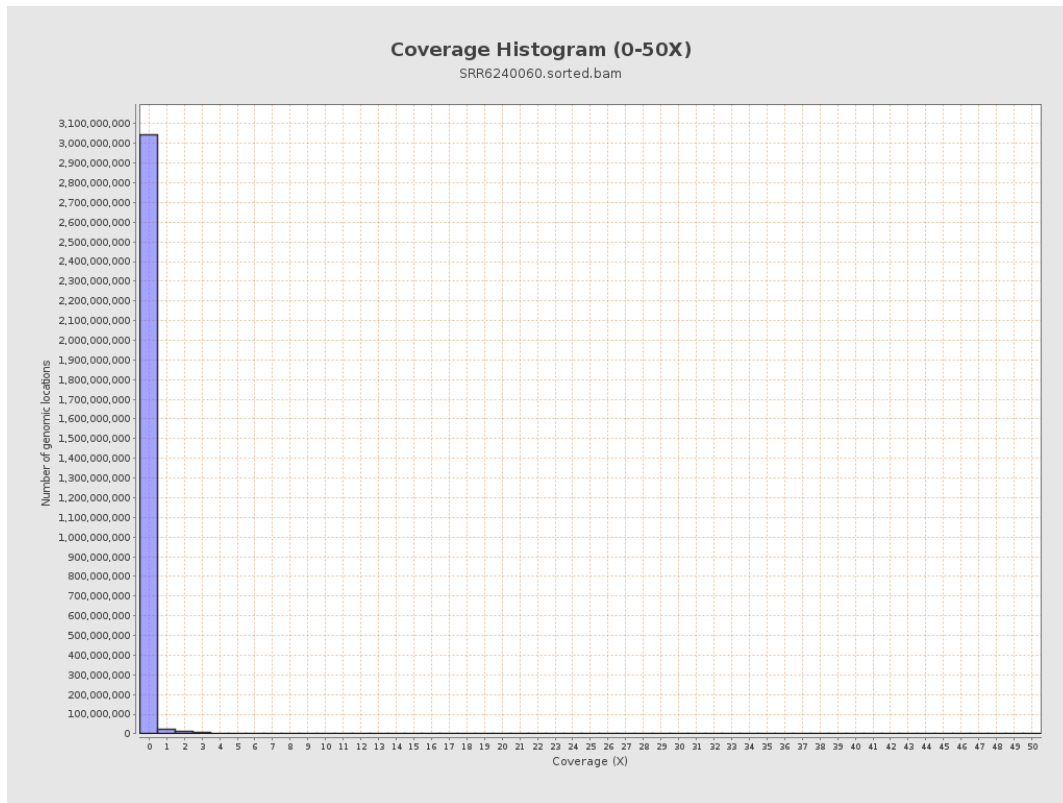
3. Results : Coverage across reference



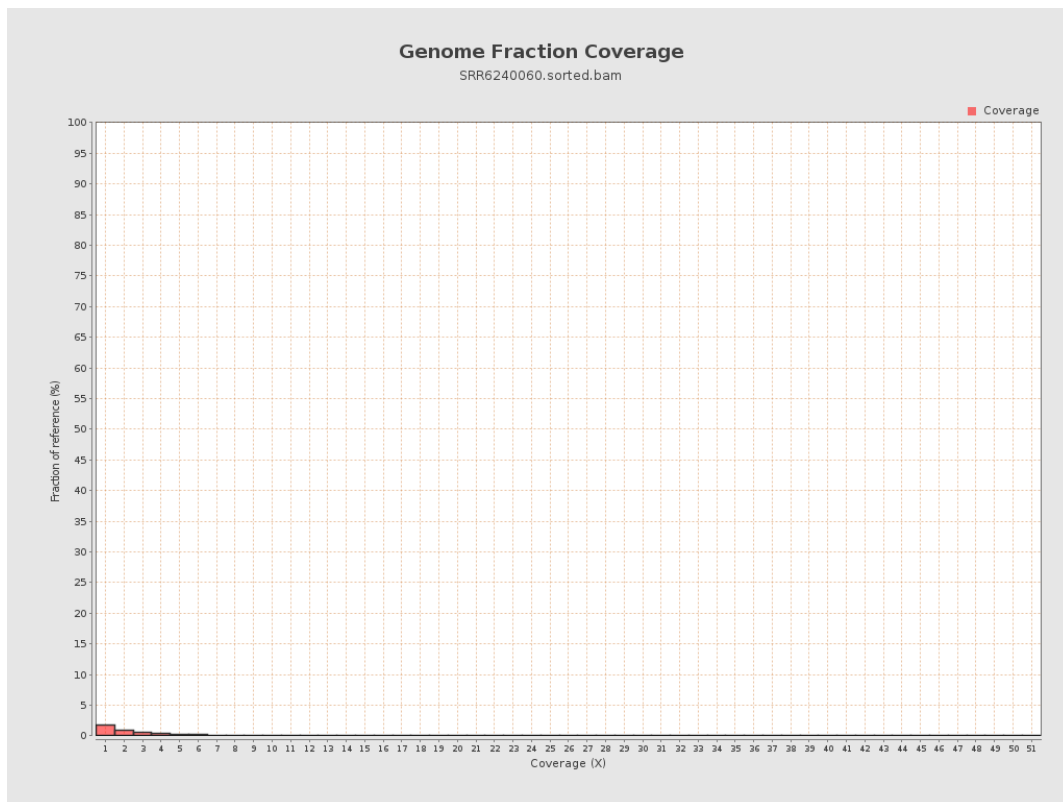
4. Results : Coverage Histogram



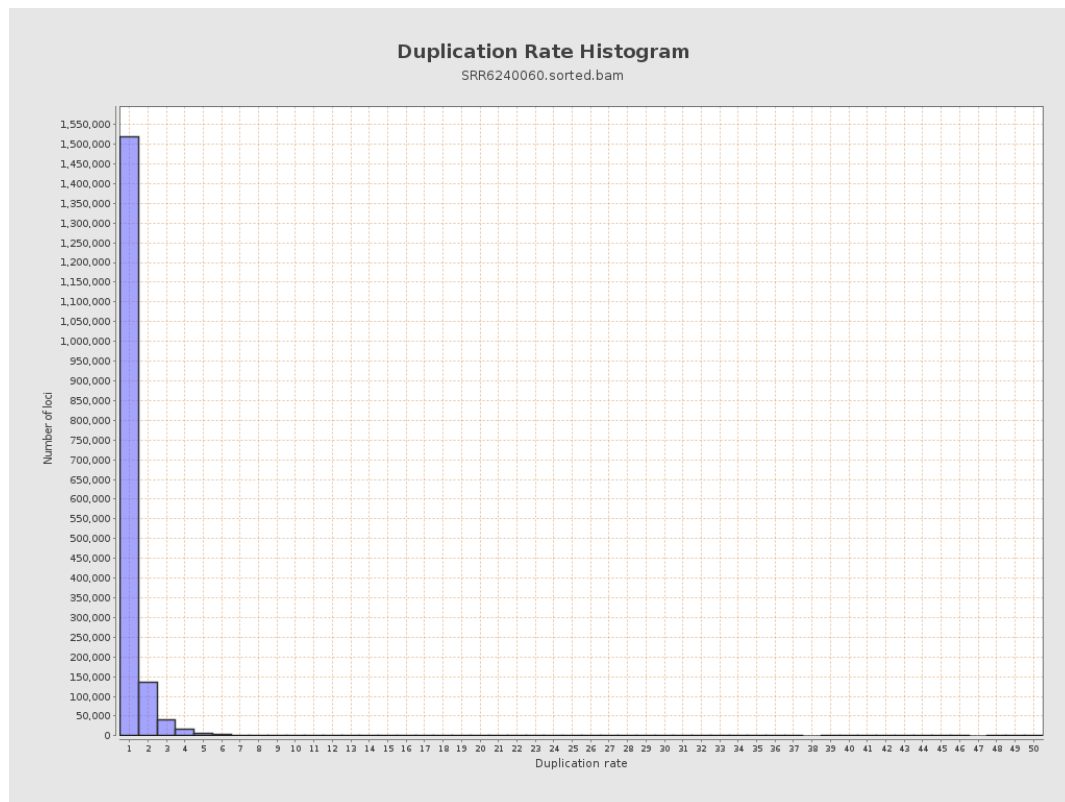
5. Results : Coverage Histogram (0-50X)



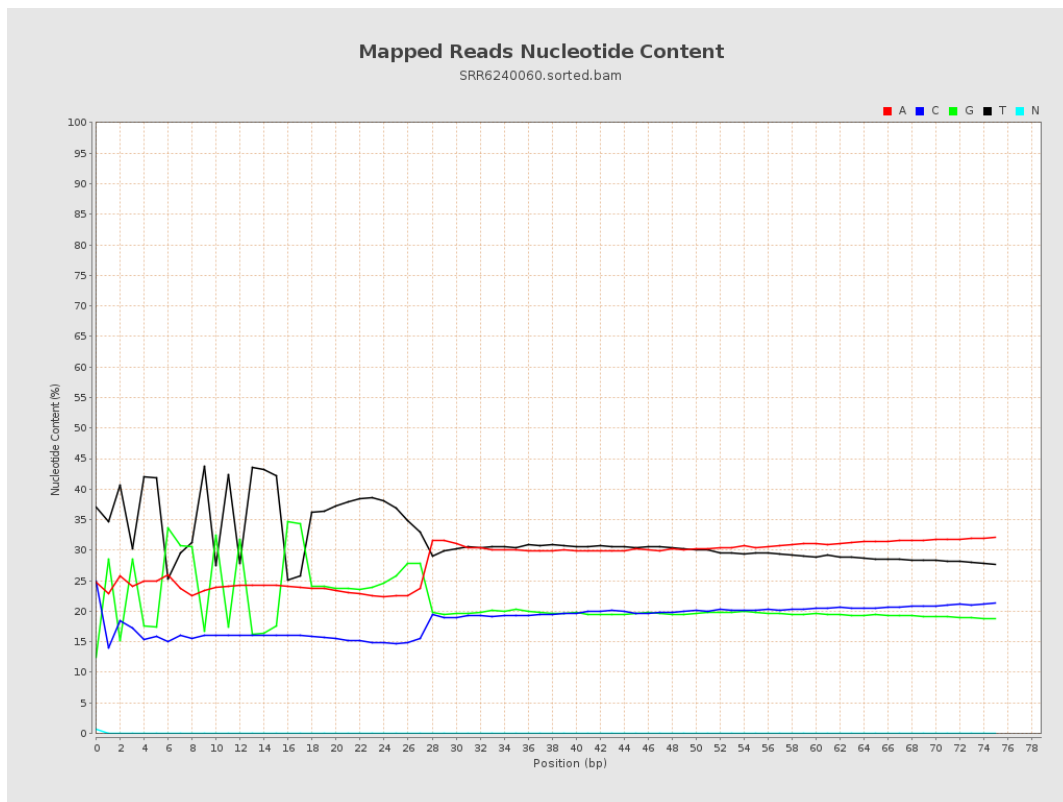
6. Results : Genome Fraction Coverage



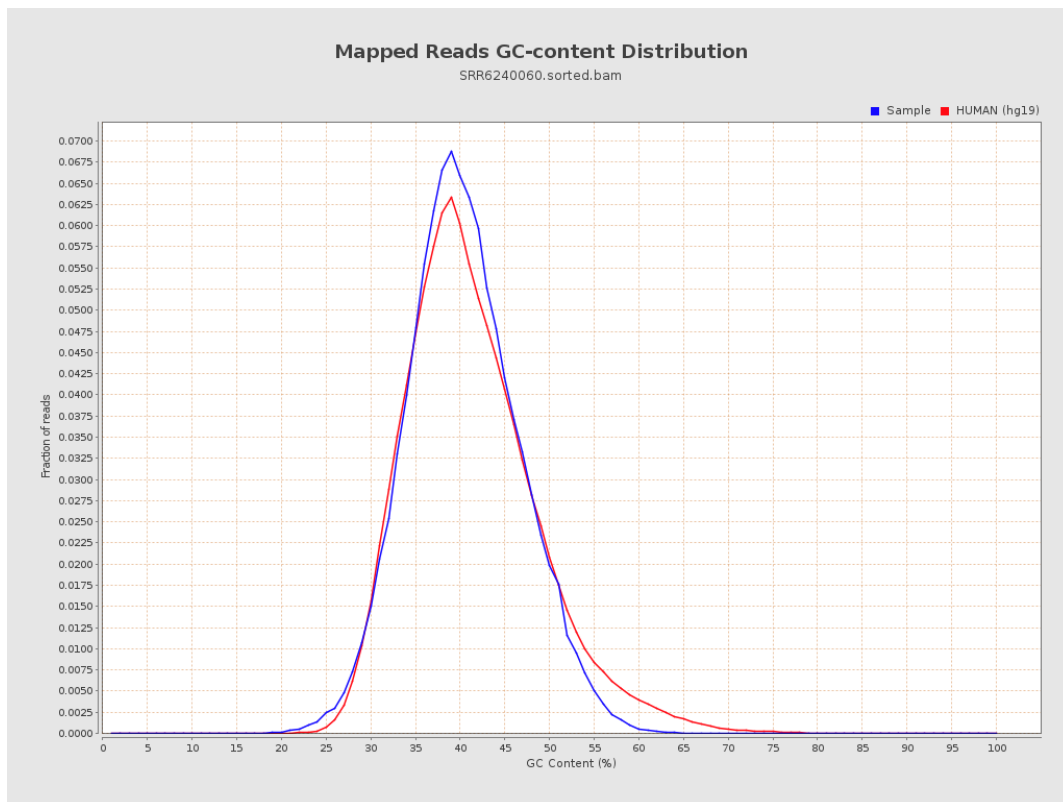
7. Results : Duplication Rate Histogram



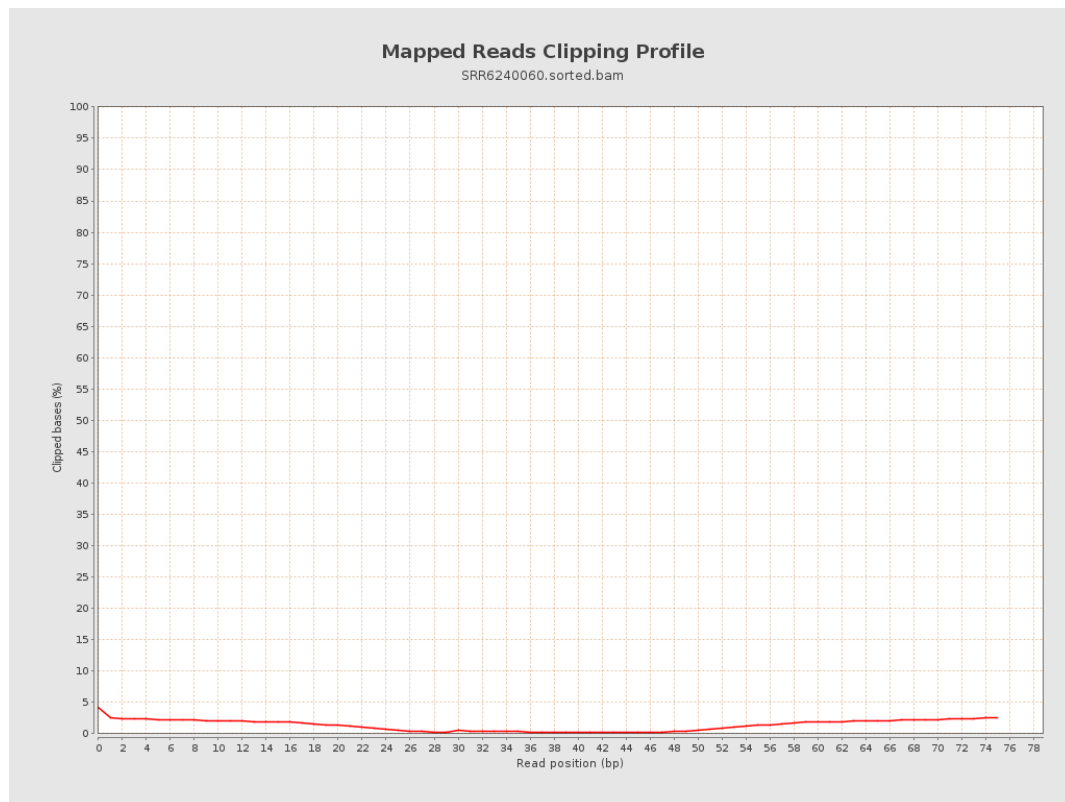
8. Results : Mapped Reads Nucleotide Content



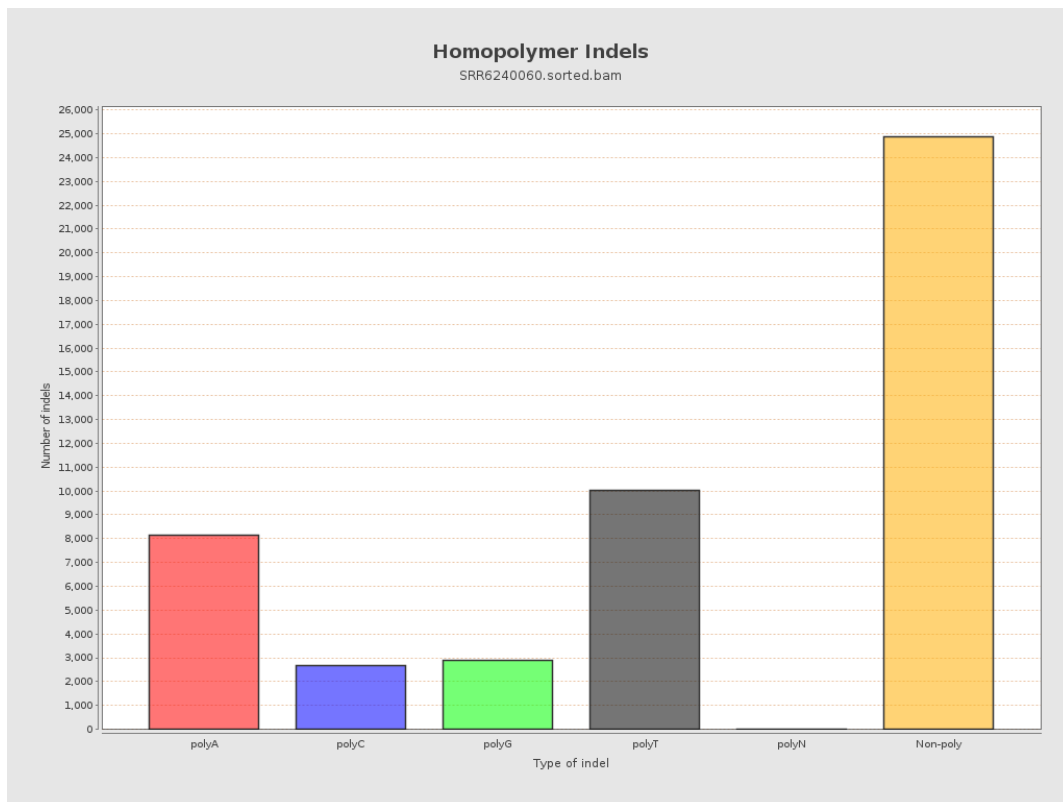
9. Results : Mapped Reads GC-content Distribution



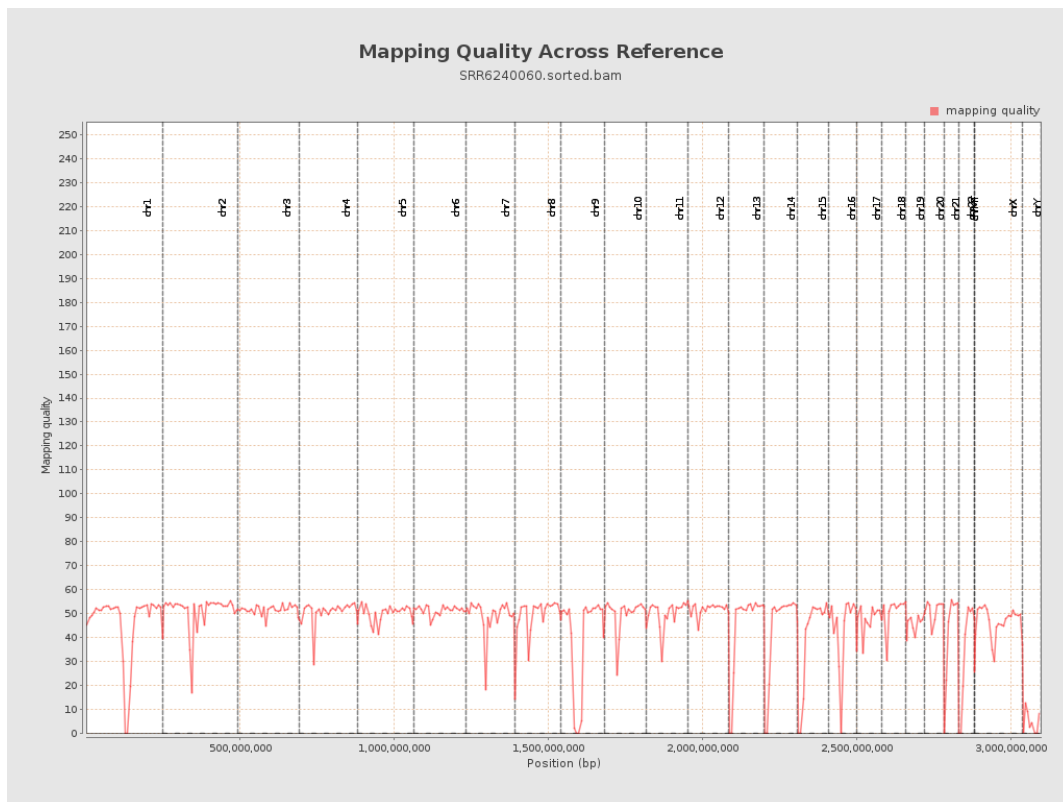
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

