

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 08:17:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240244.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_SRR6240244 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240244.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 08:17:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240244.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,506,183
Mapped reads	2,804,026 / 79.97%
Unmapped reads	702,157 / 20.03%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	30,677 / 0.87%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	470,530 / 13.42%
Duplication rate	11.38%
Clipped reads	1,358,593 / 38.75%

2.2. ACGT Content

Number/percentage of A's	52,513,056 / 28.33%
Number/percentage of C's	34,168,188 / 18.43%
Number/percentage of T's	58,875,263 / 31.76%
Number/percentage of G's	39,778,886 / 21.46%
Number/percentage of N's	17,441 / 0.01%
GC Percentage	39.9%

2.3. Coverage

Mean	0.0599

Standard Deviation	0.748
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2.4. Mapping Quality

Mean Mapping Quality	45.81
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2.5. Mismatches and indels

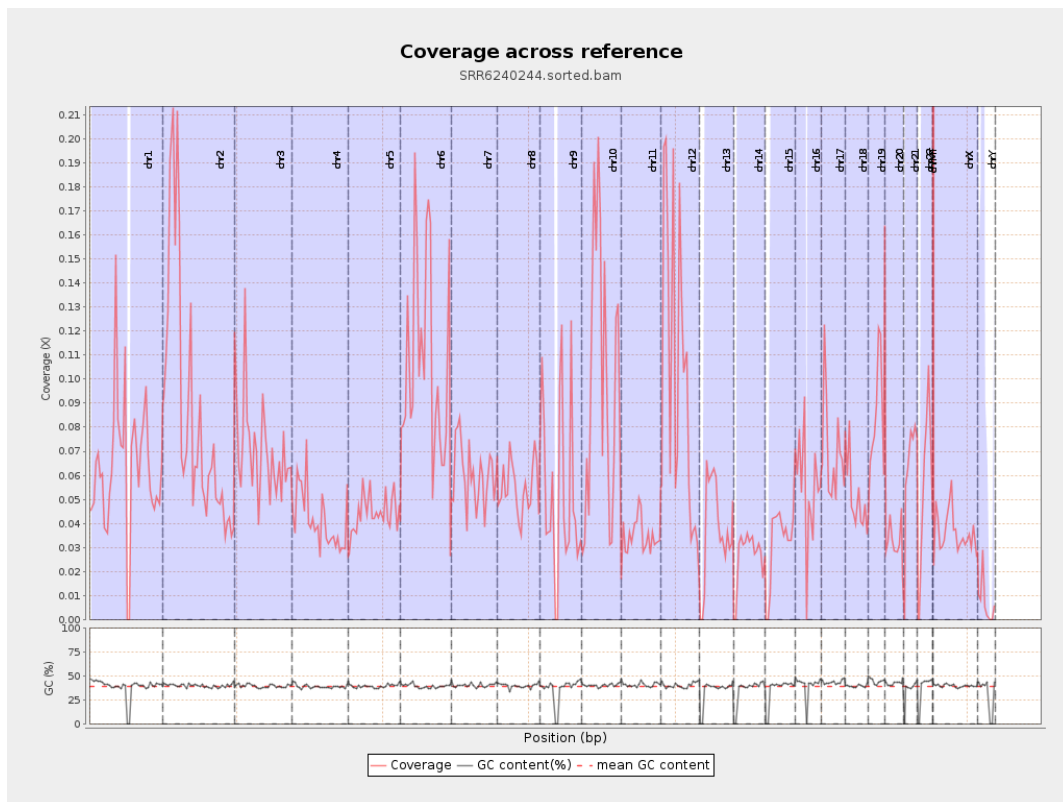
General error rate	0.81%
Mismatches	1,478,679
Insertions	14,029
Mapped reads with at least one insertion	0.5%
Deletions	41,944
Mapped reads with at least one deletion	1.48%
Homopolymer indels	47.64%

2.6. Chromosome stats

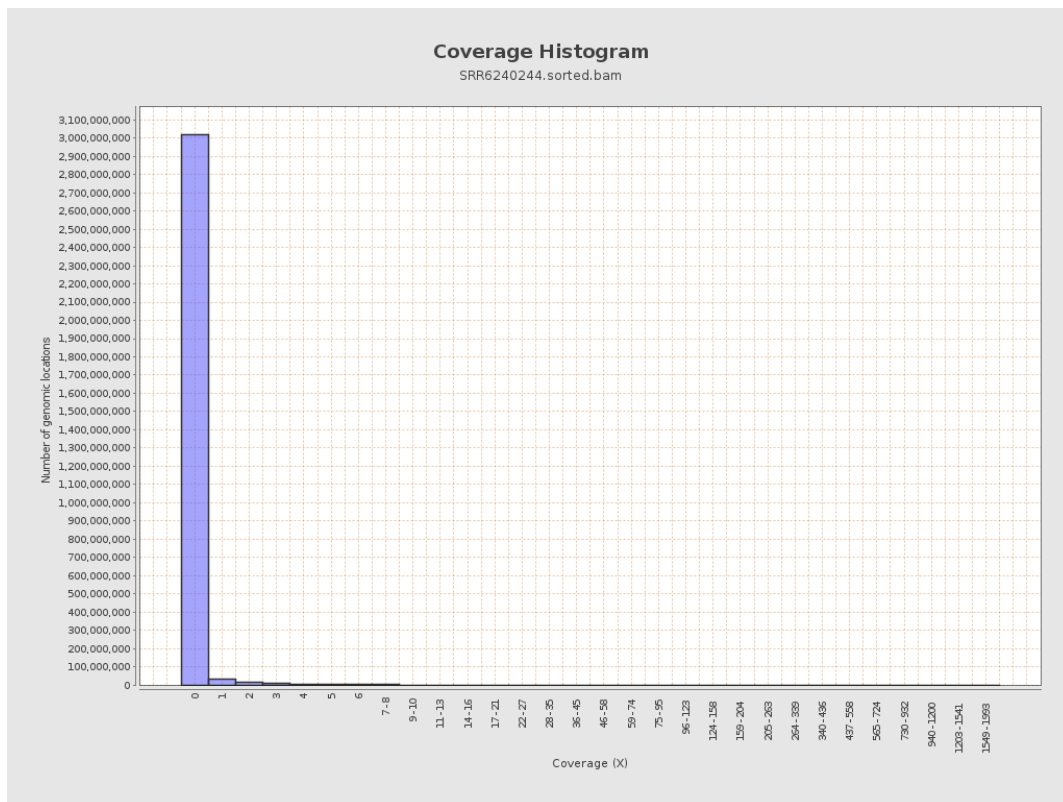
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	15795627	0.0634	1.4388
chr2	243199373	20600418	0.0847	0.7831
chr3	198022430	13938762	0.0704	0.5229
chr4	191154276	7940585	0.0415	0.4235
chr5	180915260	8007593	0.0443	0.4243
chr6	171115067	18530487	0.1083	0.8172
chr7	159138663	9520564	0.0598	0.5876

chr8	146364022	8002142	0.0547	1.2217
chr9	141213431	7474548	0.0529	0.6576
chr10	135534747	13207014	0.0974	0.8378
chr11	135006516	4718948	0.035	0.4356
chr12	133851895	13241071	0.0989	0.6357
chr13	115169878	4330569	0.0376	0.3805
chr14	107349540	2857583	0.0266	0.3921
chr15	102531392	3284866	0.032	0.3514
chr16	90354753	4923233	0.0545	0.4872
chr17	81195210	5770113	0.0711	0.5844
chr18	78077248	3985638	0.051	1.2312
chr19	59128983	5139464	0.0869	0.8721
chr20	63025520	2092262	0.0332	0.3608
chr21	48129895	3103818	0.0645	0.5284
chr22	51304566	2885815	0.0562	0.4449
chrMT	16571	58092	3.5056	3.8133
chrX	155270560	5585063	0.036	0.4216
chrY	59373566	431058	0.0073	0.1956

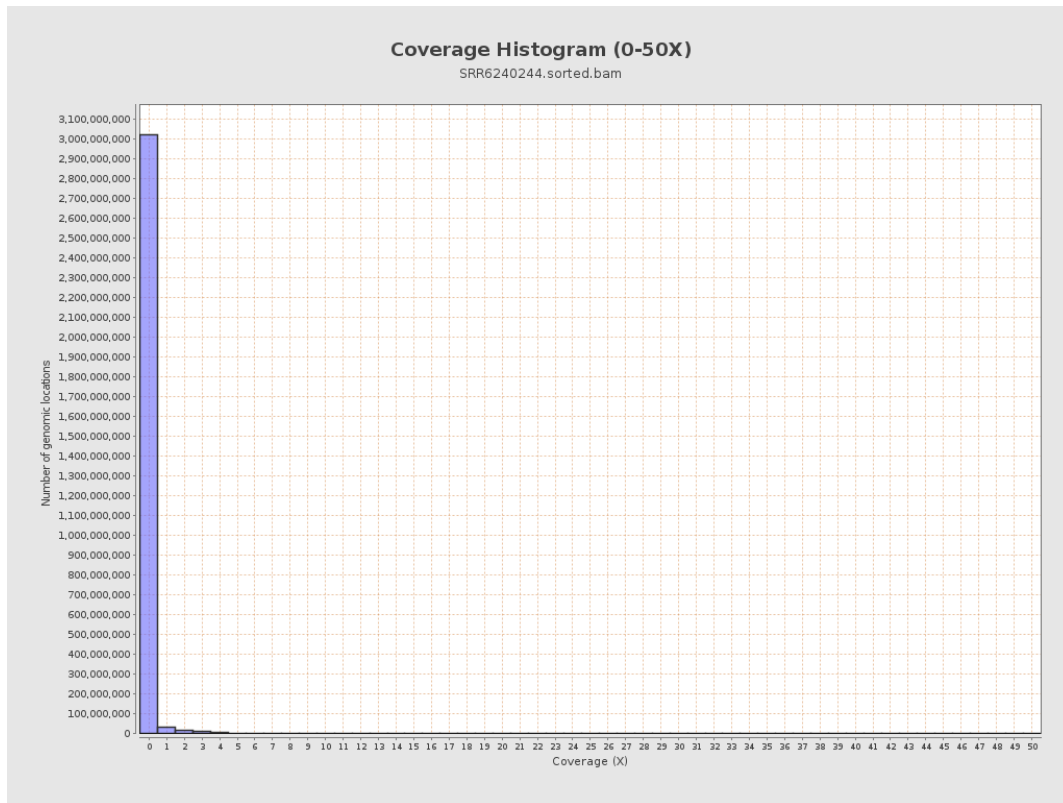
3. Results : Coverage across reference



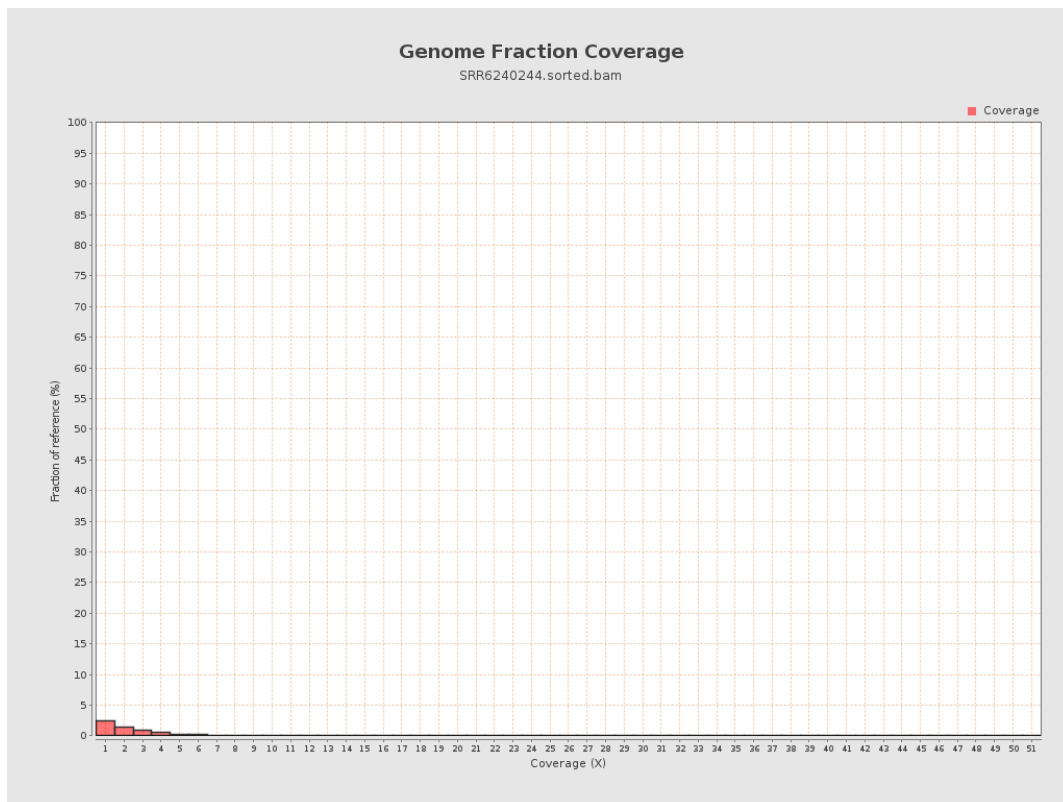
4. Results : Coverage Histogram



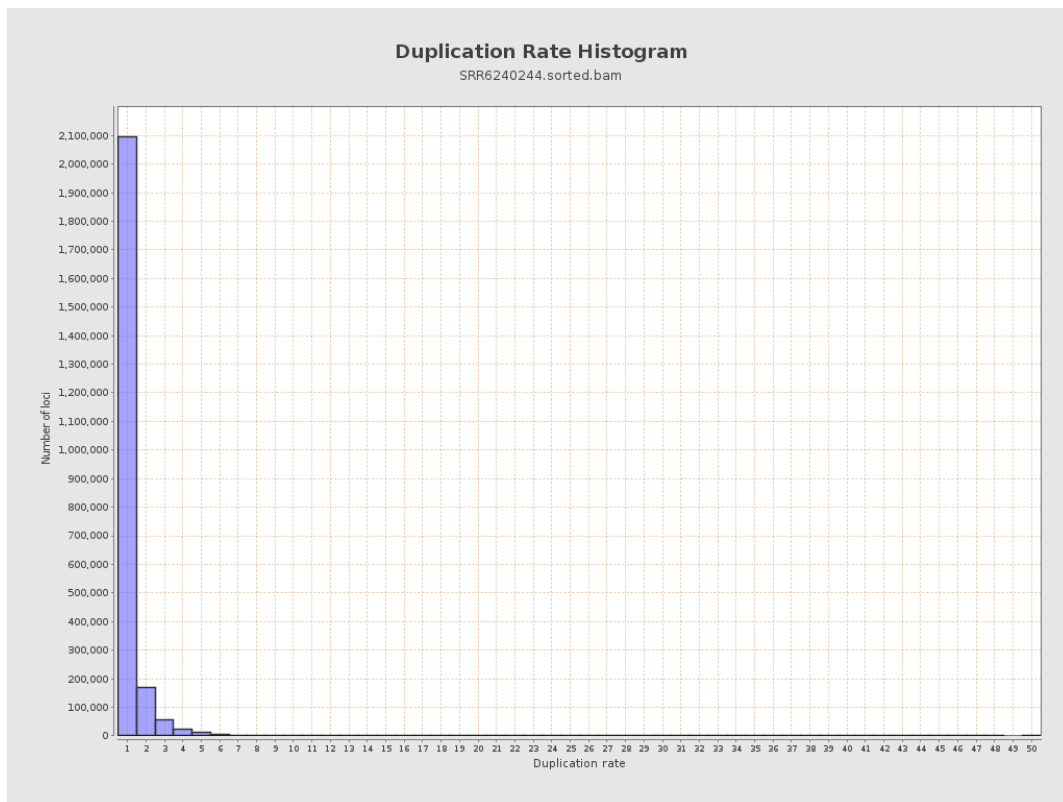
5. Results : Coverage Histogram (0-50X)



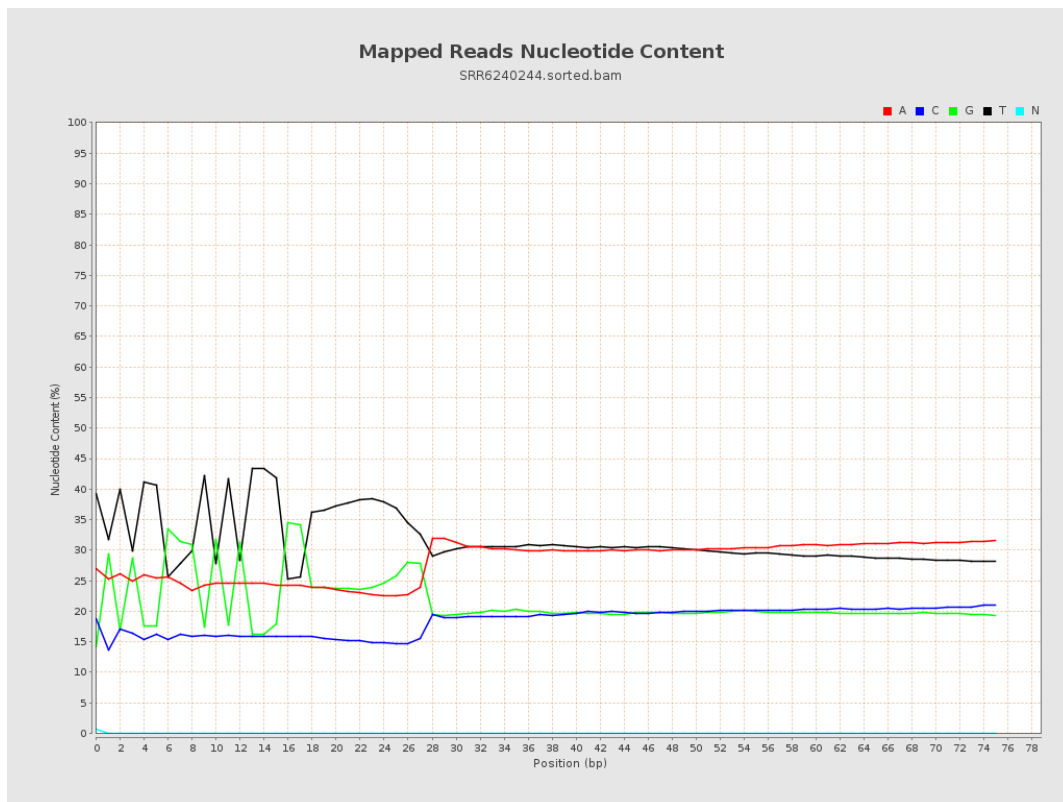
6. Results : Genome Fraction Coverage



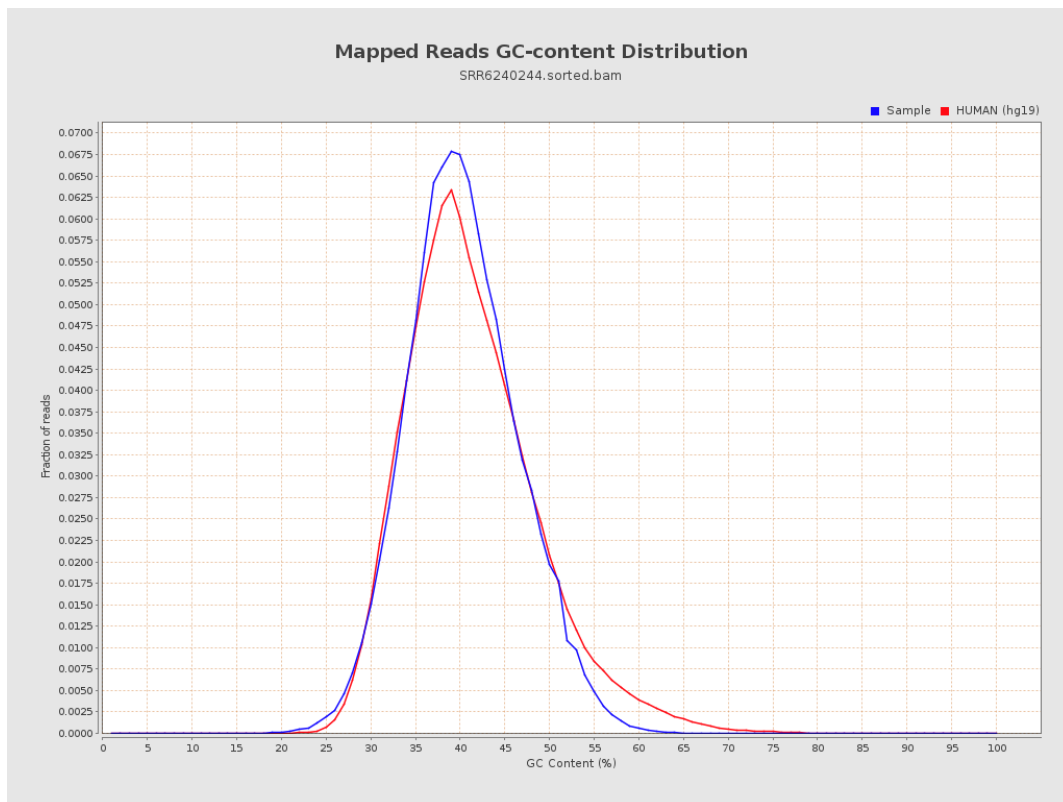
7. Results : Duplication Rate Histogram



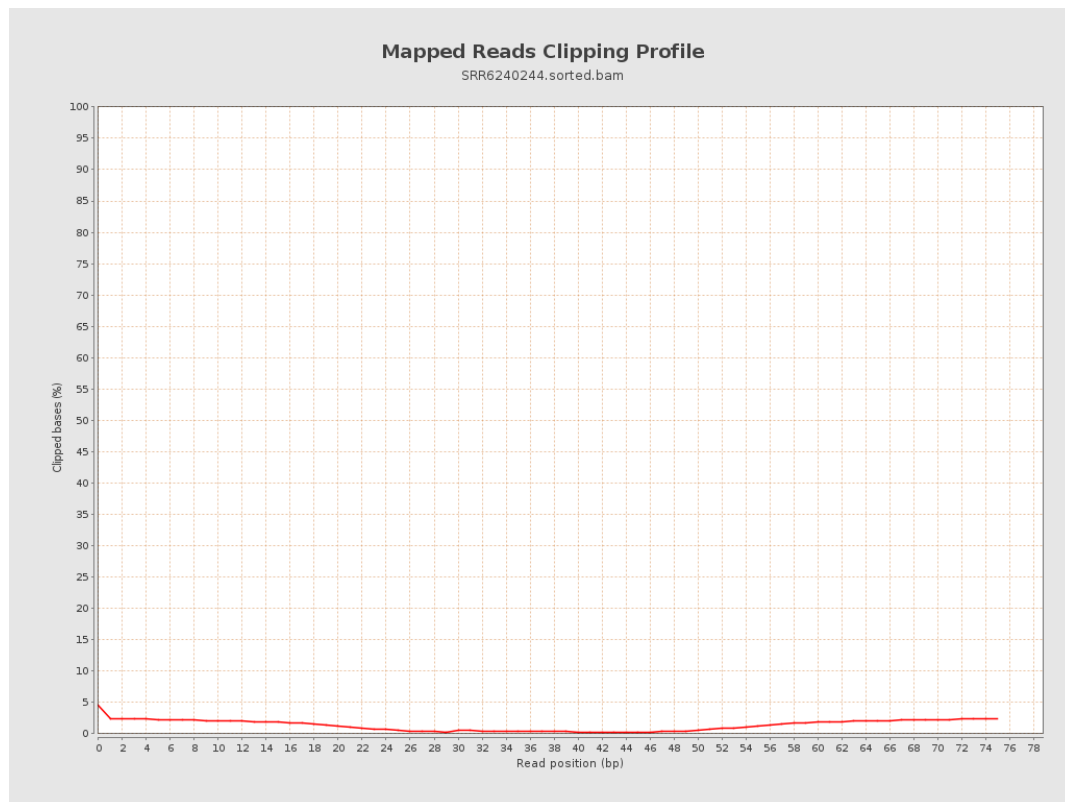
8. Results : Mapped Reads Nucleotide Content



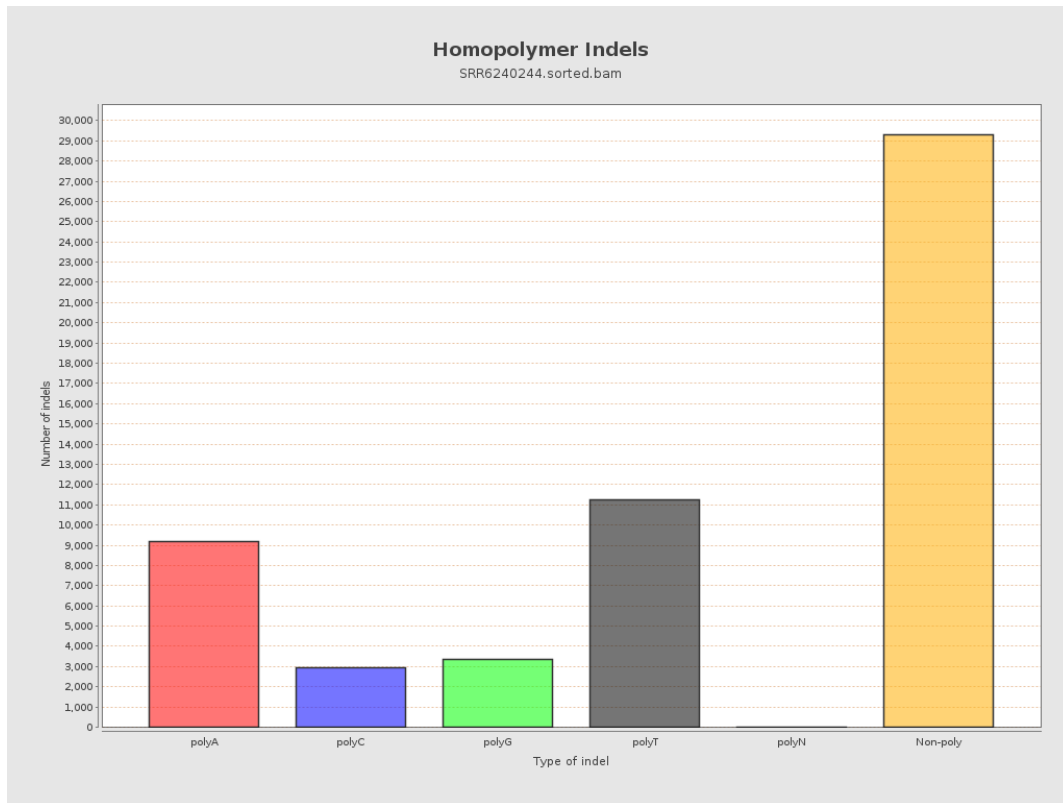
9. Results : Mapped Reads GC-content Distribution



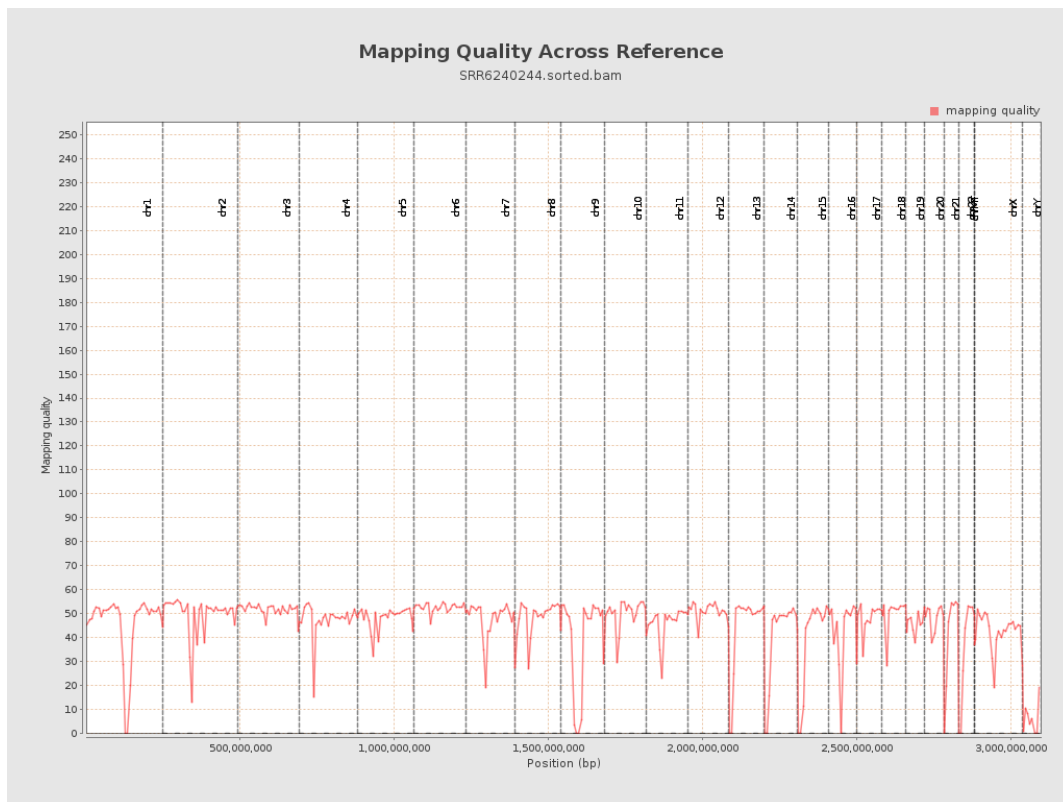
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

