

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 07:09:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240221.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_SRR6240221 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240221.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 07:09:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240221.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,037,820
Mapped reads	1,473,995 / 72.33%
Unmapped reads	563,825 / 27.67%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,107 / 0.74%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	266,946 / 13.1%
Duplication rate	12.71%
Clipped reads	717,679 / 35.22%

2.2. ACGT Content

Number/percentage of A's	27,325,063 / 28.16%
Number/percentage of C's	17,402,807 / 17.93%
Number/percentage of T's	31,598,916 / 32.56%
Number/percentage of G's	20,715,913 / 21.35%
Number/percentage of N's	8,972 / 0.01%
GC Percentage	39.28%

2.3. Coverage

Mean	0.0314

Standard Deviation	0.4901
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2.4. Mapping Quality

Mean Mapping Quality	46.58
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2.5. Mismatches and indels

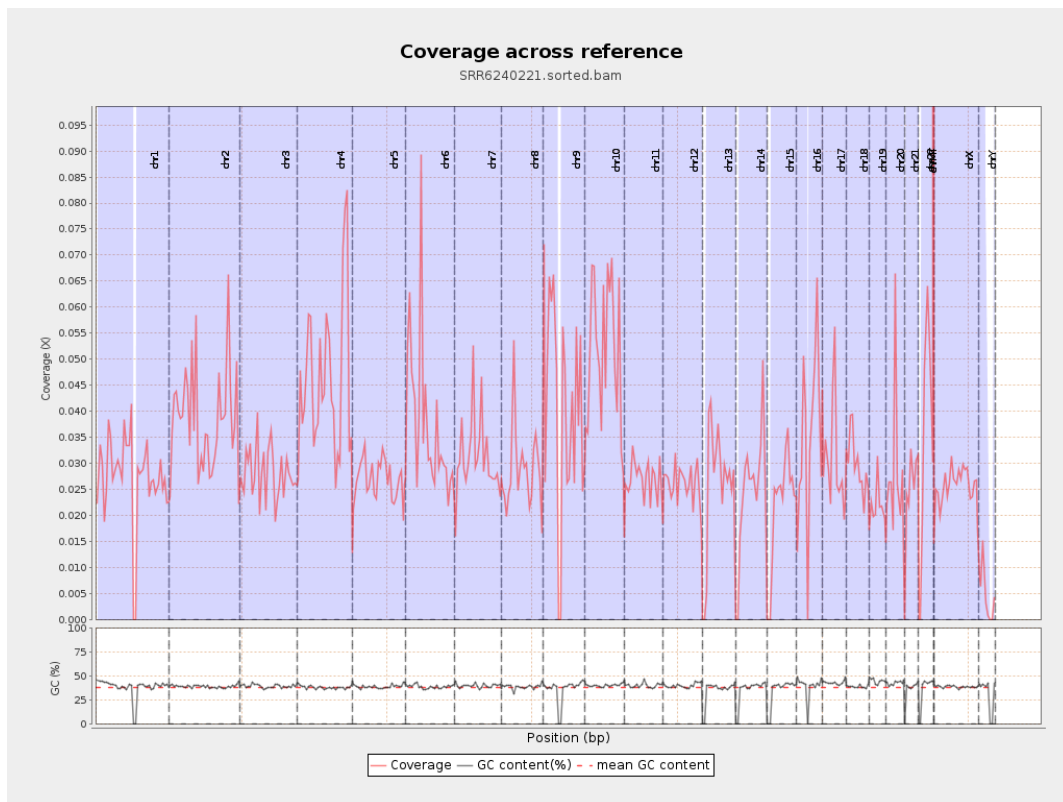
General error rate	0.86%
Mismatches	819,928
Insertions	7,167
Mapped reads with at least one insertion	0.48%
Deletions	28,292
Mapped reads with at least one deletion	1.9%
Homopolymer indels	47.06%

2.6. Chromosome stats

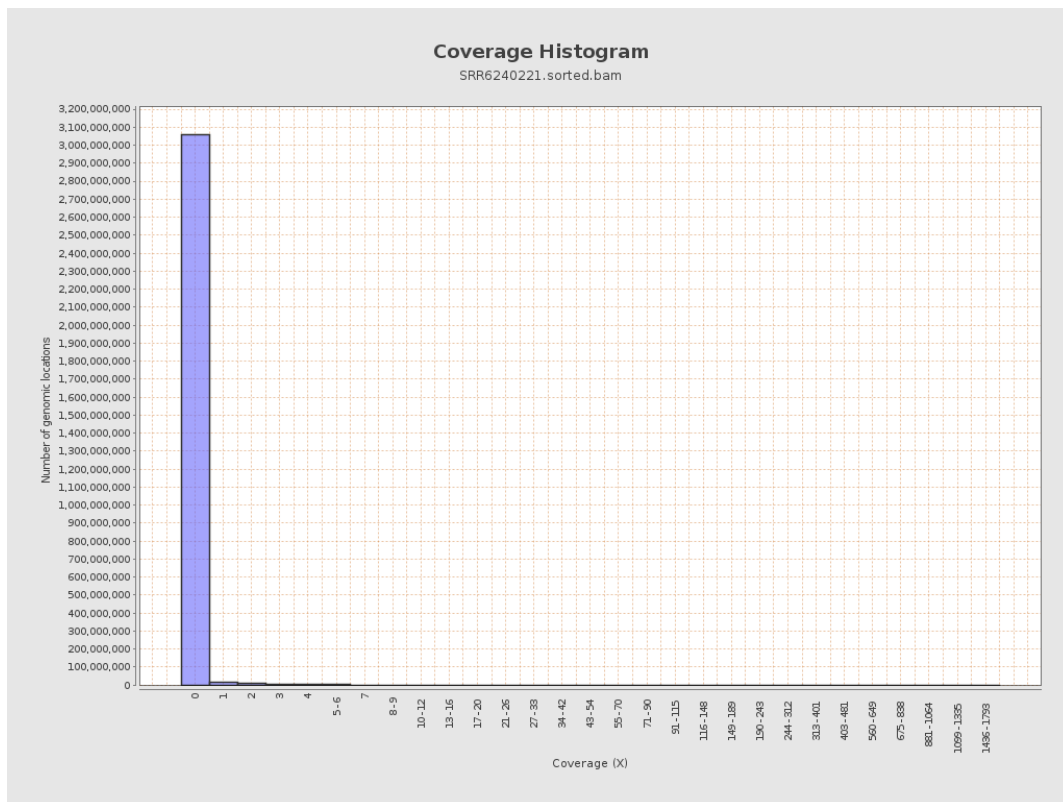
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	6817195	0.0274	0.536
chr2	243199373	9434544	0.0388	0.5071
chr3	198022430	5534170	0.0279	0.3673
chr4	191154276	8811222	0.0461	0.4672
chr5	180915260	4864728	0.0269	0.3654
chr6	171115067	6341852	0.0371	0.544
chr7	159138663	4993738	0.0314	0.4776

chr8	146364022	4182025	0.0286	1.0915
chr9	141213431	5647980	0.04	0.4739
chr10	135534747	7018446	0.0518	0.5099
chr11	135006516	3619675	0.0268	0.4001
chr12	133851895	3498785	0.0261	0.3536
chr13	115169878	2942466	0.0255	0.3466
chr14	107349540	2687508	0.025	0.3566
chr15	102531392	2262045	0.0221	0.3123
chr16	90354753	3211501	0.0355	0.3971
chr17	81195210	2487163	0.0306	0.389
chr18	78077248	2330243	0.0298	0.6639
chr19	59128983	1290910	0.0218	0.3744
chr20	63025520	1800045	0.0286	0.36
chr21	48129895	1194678	0.0248	0.3454
chr22	51304566	1791877	0.0349	0.3751
chrMT	16571	72029	4.3467	5.5204
chrX	155270560	3996220	0.0257	0.3609
chrY	59373566	269808	0.0045	0.1309

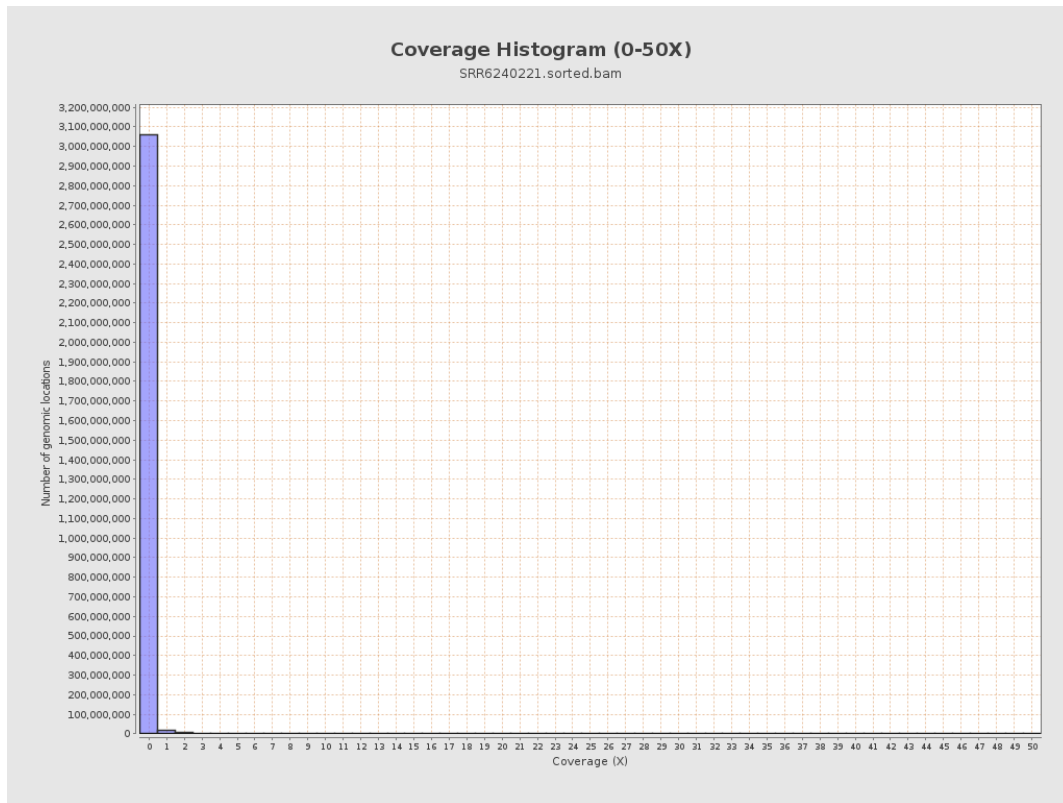
3. Results : Coverage across reference



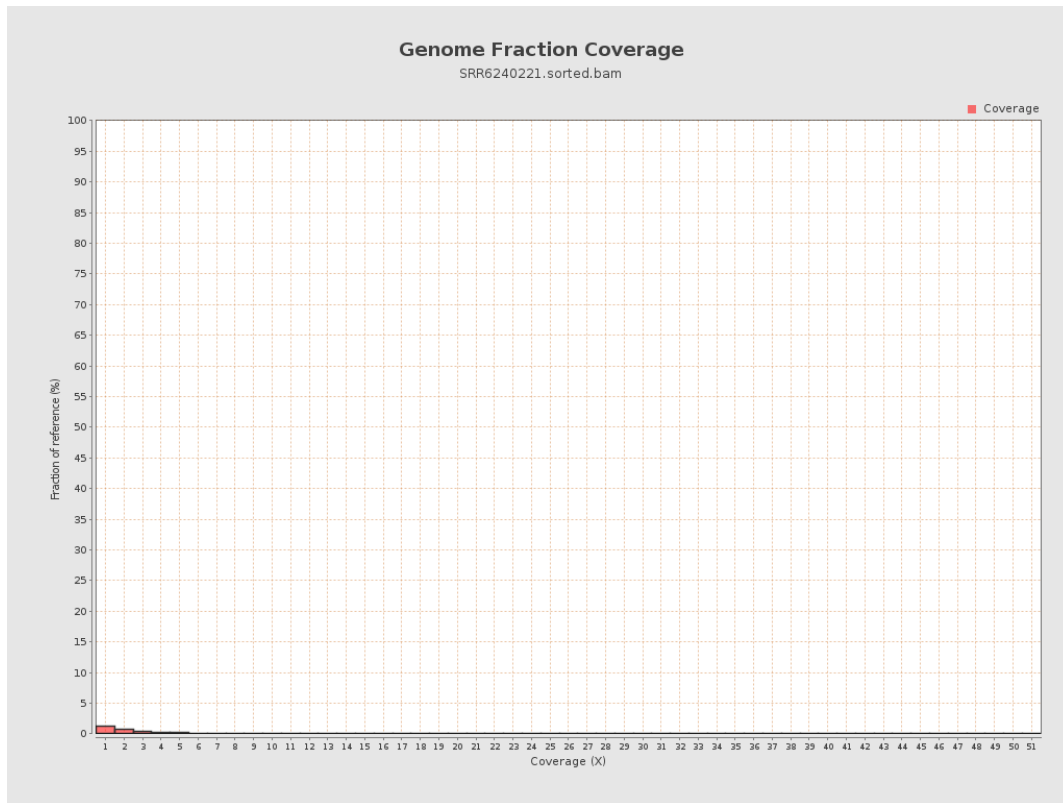
4. Results : Coverage Histogram



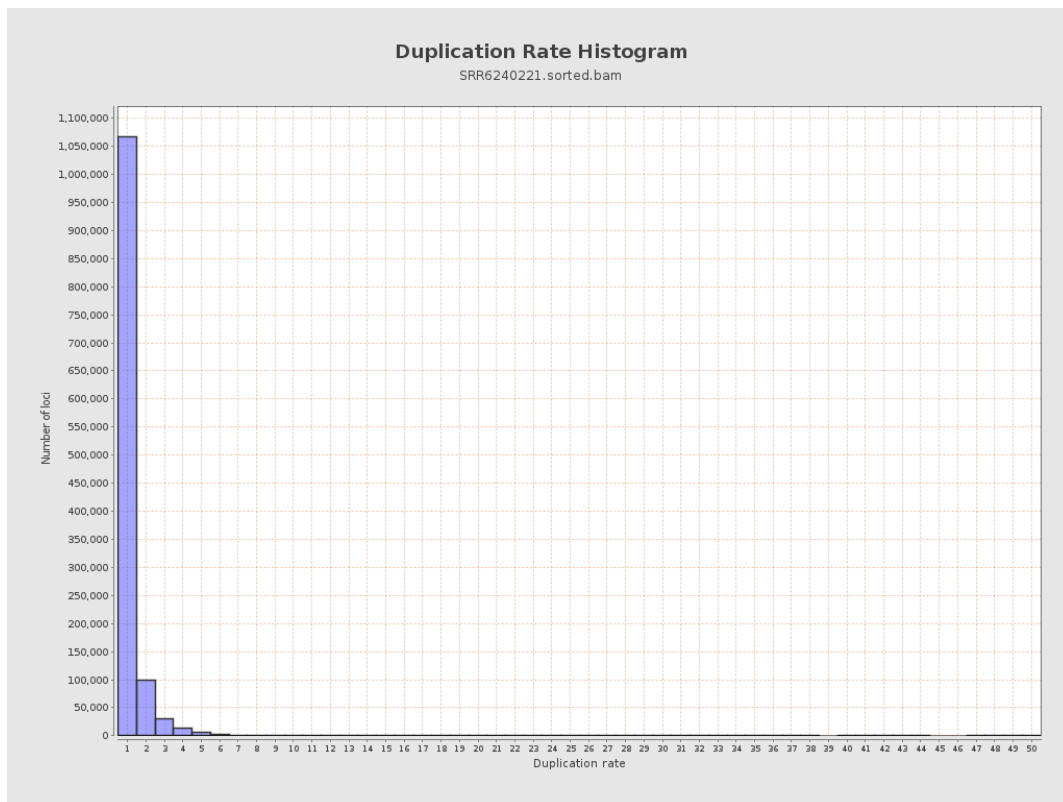
5. Results : Coverage Histogram (0-50X)



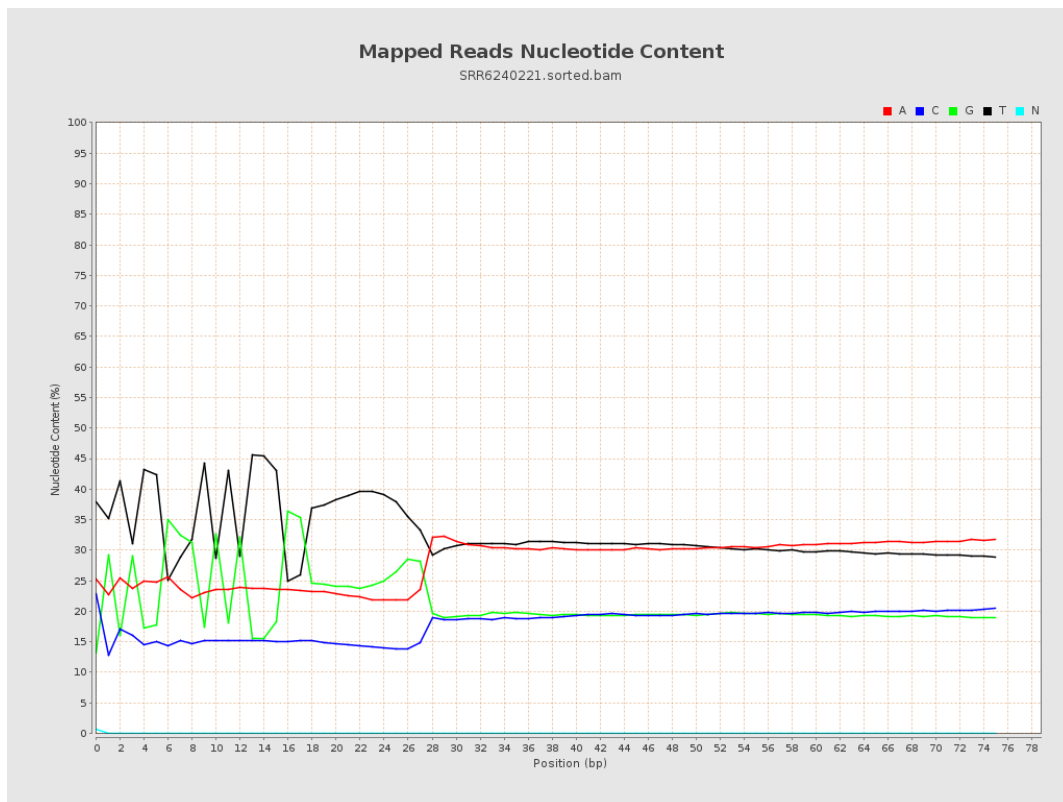
6. Results : Genome Fraction Coverage



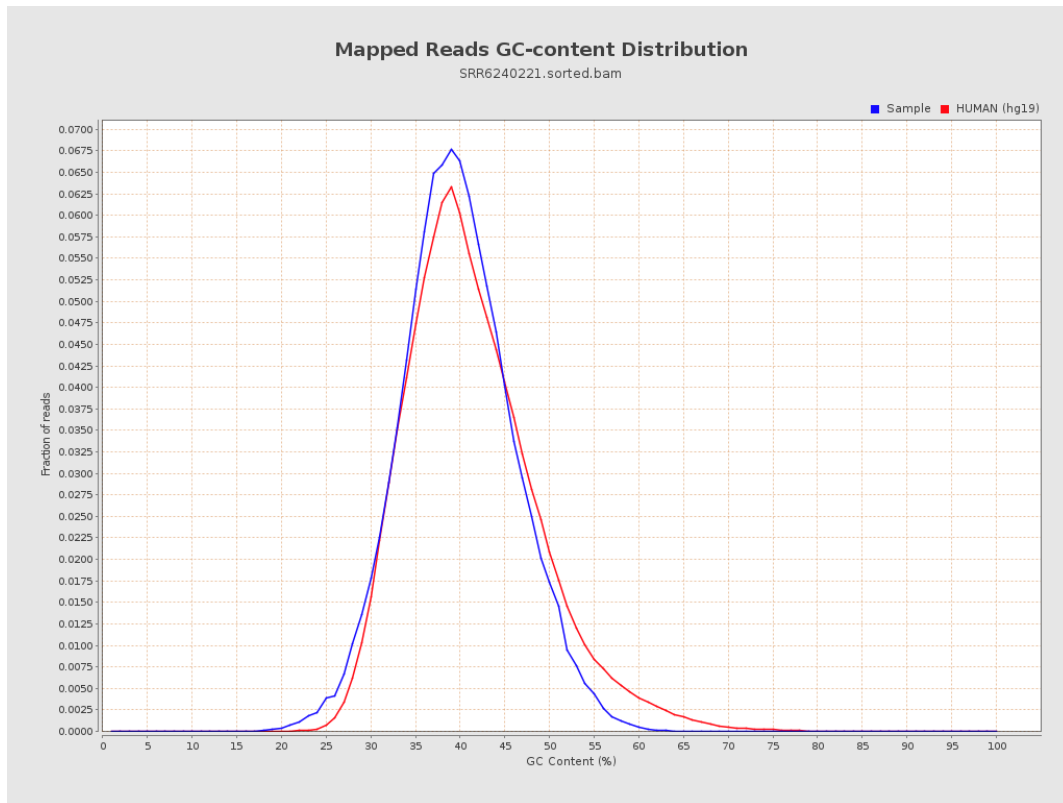
7. Results : Duplication Rate Histogram



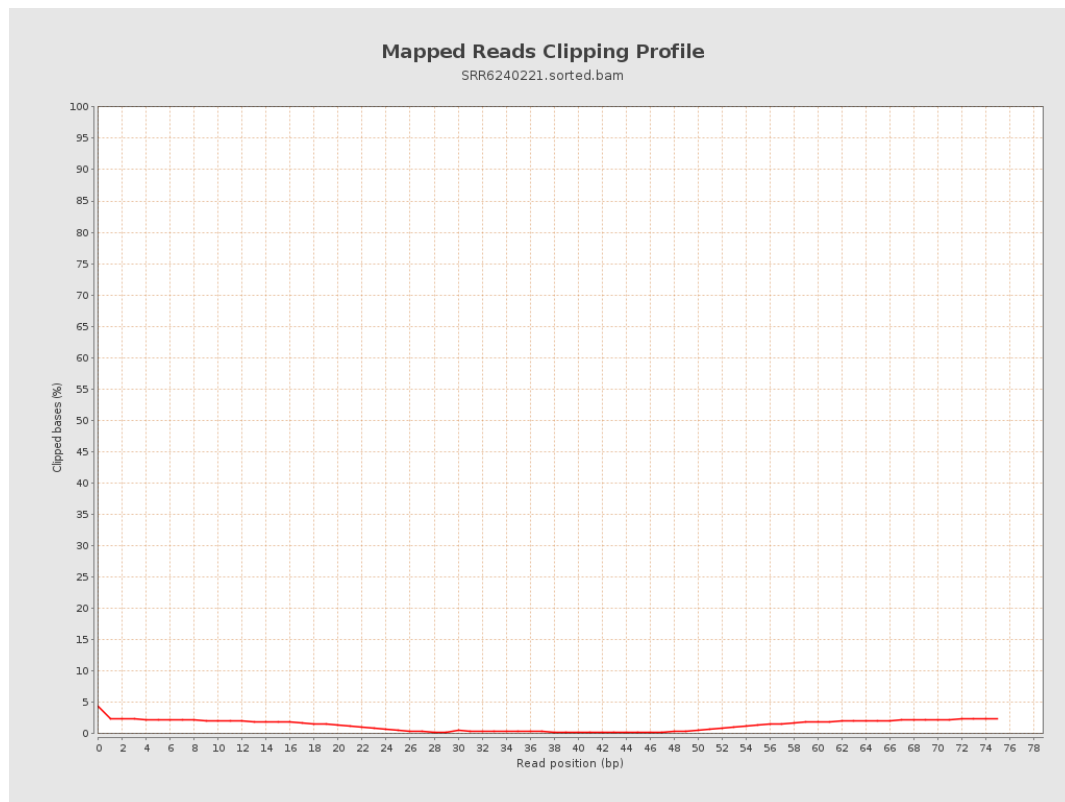
8. Results : Mapped Reads Nucleotide Content



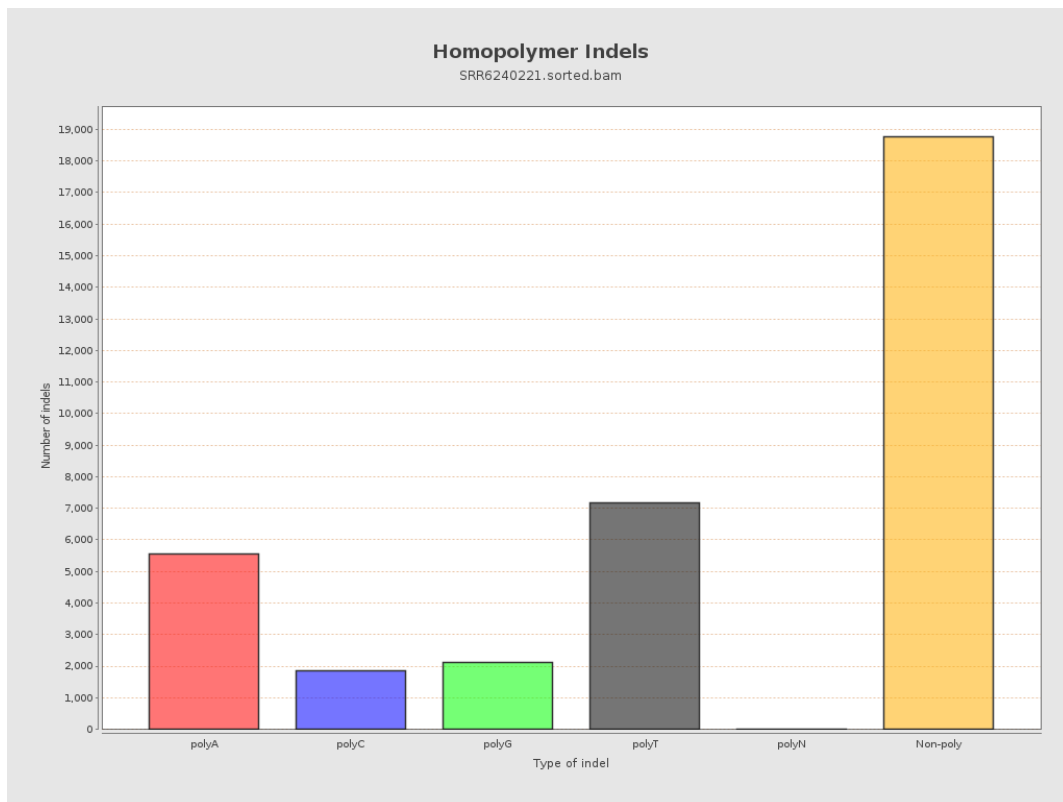
9. Results : Mapped Reads GC-content Distribution



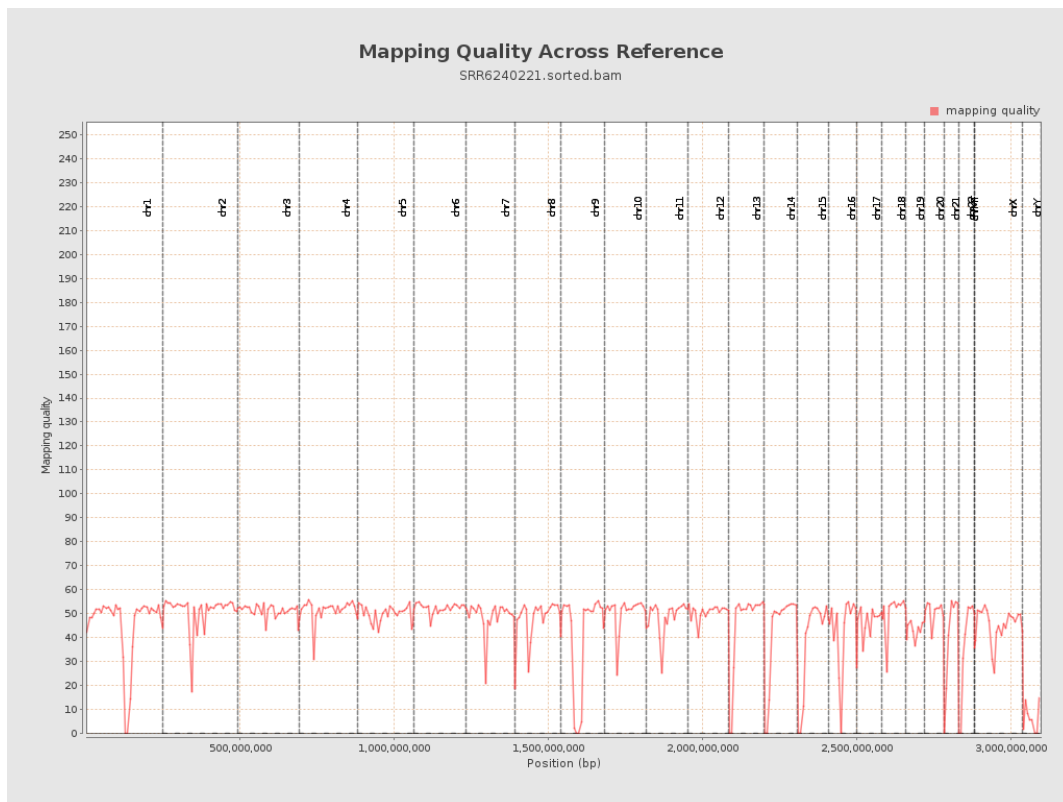
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

