

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 06:56:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240217.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_SRR6240217 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240217.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 06:56:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240217.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,742,302
Mapped reads	1,959,136 / 71.44%
Unmapped reads	783,166 / 28.56%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,710 / 0.65%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	251,221 / 9.16%
Duplication rate	10.21%
Clipped reads	1,209,264 / 44.1%

2.2. ACGT Content

Number/percentage of A's	32,827,286 / 26.79%
Number/percentage of C's	22,784,068 / 18.59%
Number/percentage of T's	38,586,126 / 31.49%
Number/percentage of G's	28,321,805 / 23.11%
Number/percentage of N's	10,386 / 0.01%
GC Percentage	41.71%

2.3. Coverage

Mean	0.0396

Standard Deviation	0.4138
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2.4. Mapping Quality

Mean Mapping Quality	44.99
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2.5. Mismatches and indels

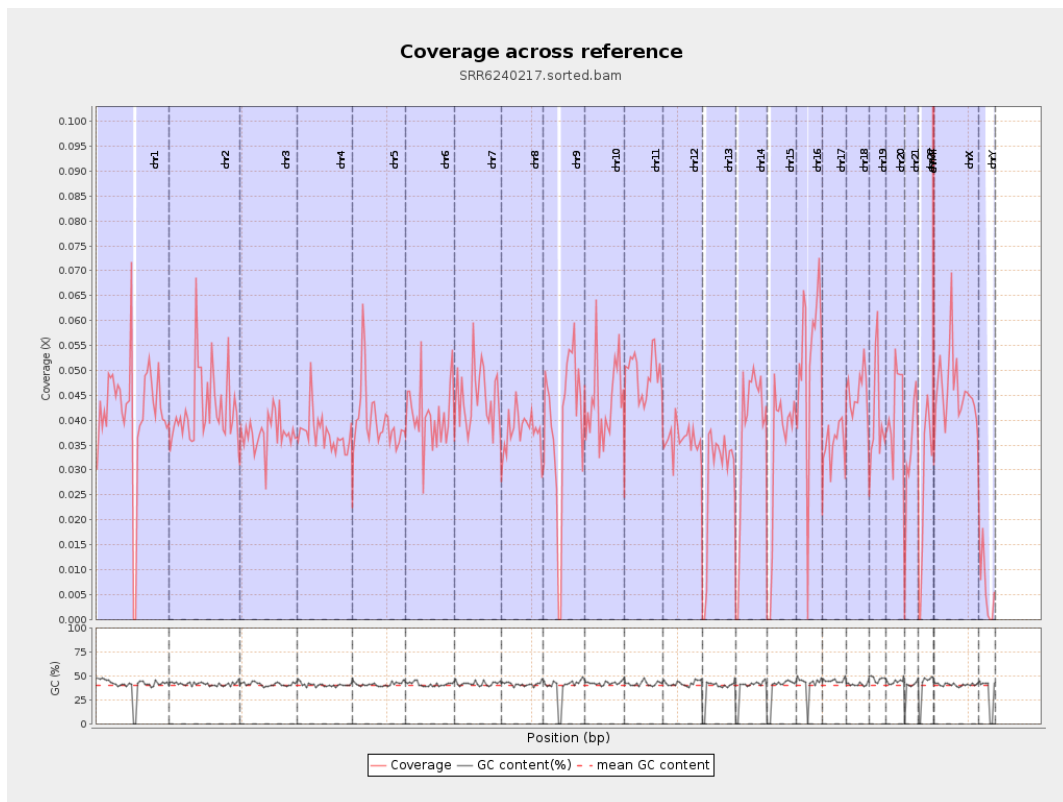
General error rate	0.88%
Mismatches	1,066,603
Insertions	8,462
Mapped reads with at least one insertion	0.43%
Deletions	32,434
Mapped reads with at least one deletion	1.64%
Homopolymer indels	46.22%

2.6. Chromosome stats

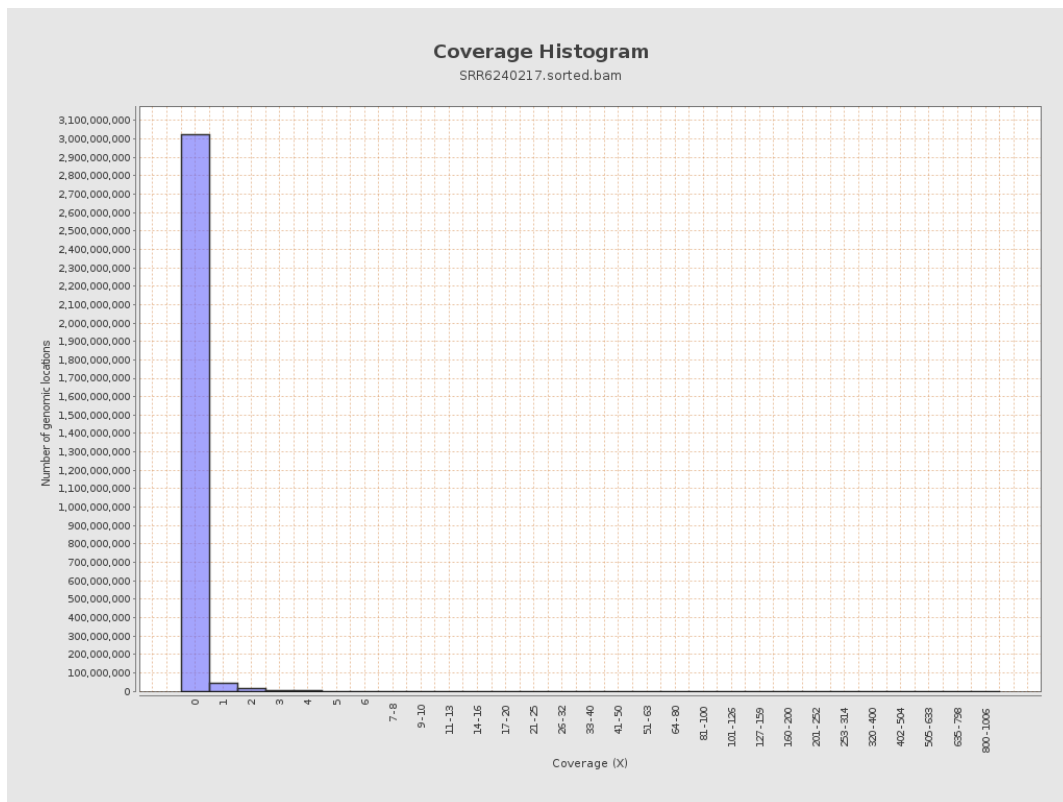
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	10348570	0.0415	0.765
chr2	243199373	10265597	0.0422	0.4741
chr3	198022430	7406101	0.0374	0.2969
chr4	191154276	7119549	0.0372	0.3404
chr5	180915260	7280966	0.0402	0.3093
chr6	171115067	6969389	0.0407	0.3434
chr7	159138663	7111185	0.0447	0.4332

chr8	146364022	5545979	0.0379	0.409
chr9	141213431	5610456	0.0397	0.3594
chr10	135534747	5898942	0.0435	0.403
chr11	135006516	6594182	0.0488	0.3855
chr12	133851895	4841025	0.0362	0.2944
chr13	115169878	3256791	0.0283	0.2555
chr14	107349540	4027197	0.0375	0.3129
chr15	102531392	3437849	0.0335	0.3203
chr16	90354753	4773646	0.0528	0.3687
chr17	81195210	2857786	0.0352	0.306
chr18	78077248	3580061	0.0459	0.5541
chr19	59128983	2436981	0.0412	0.5568
chr20	63025520	2668795	0.0423	0.3198
chr21	48129895	1604461	0.0333	0.2911
chr22	51304566	1379105	0.0269	0.2473
chrMT	16571	100177	6.0453	5.9638
chrX	155270560	7107326	0.0458	0.3521
chrY	59373566	364061	0.0061	0.1462

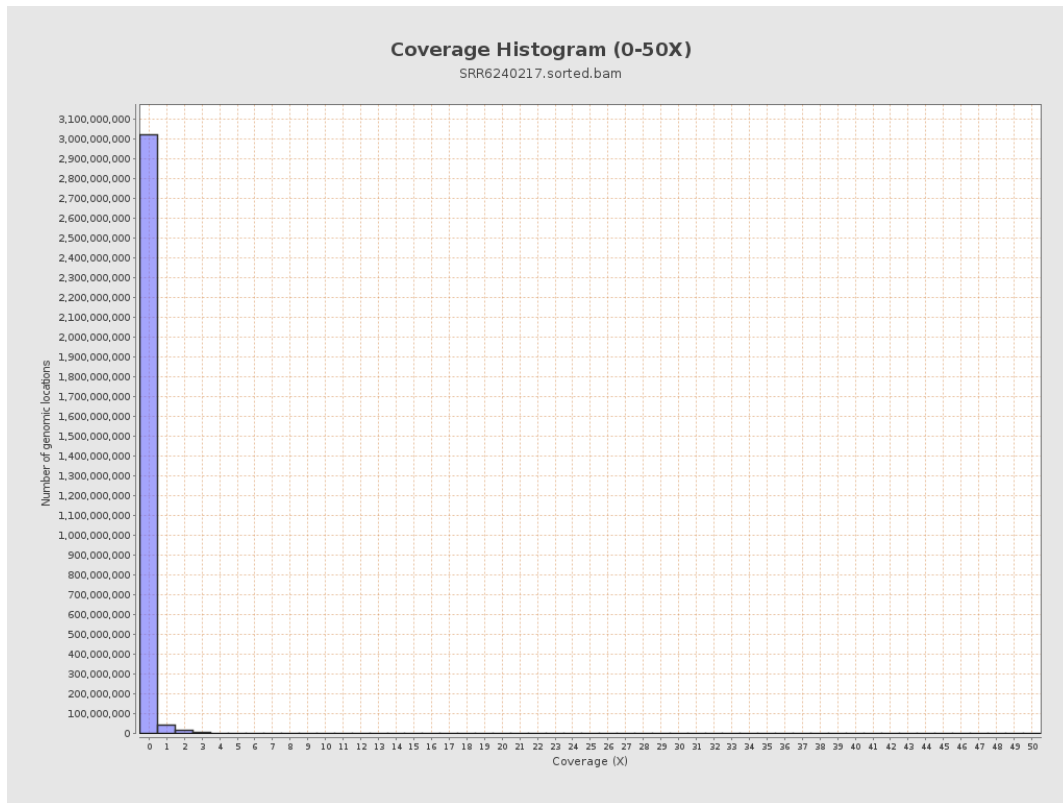
3. Results : Coverage across reference



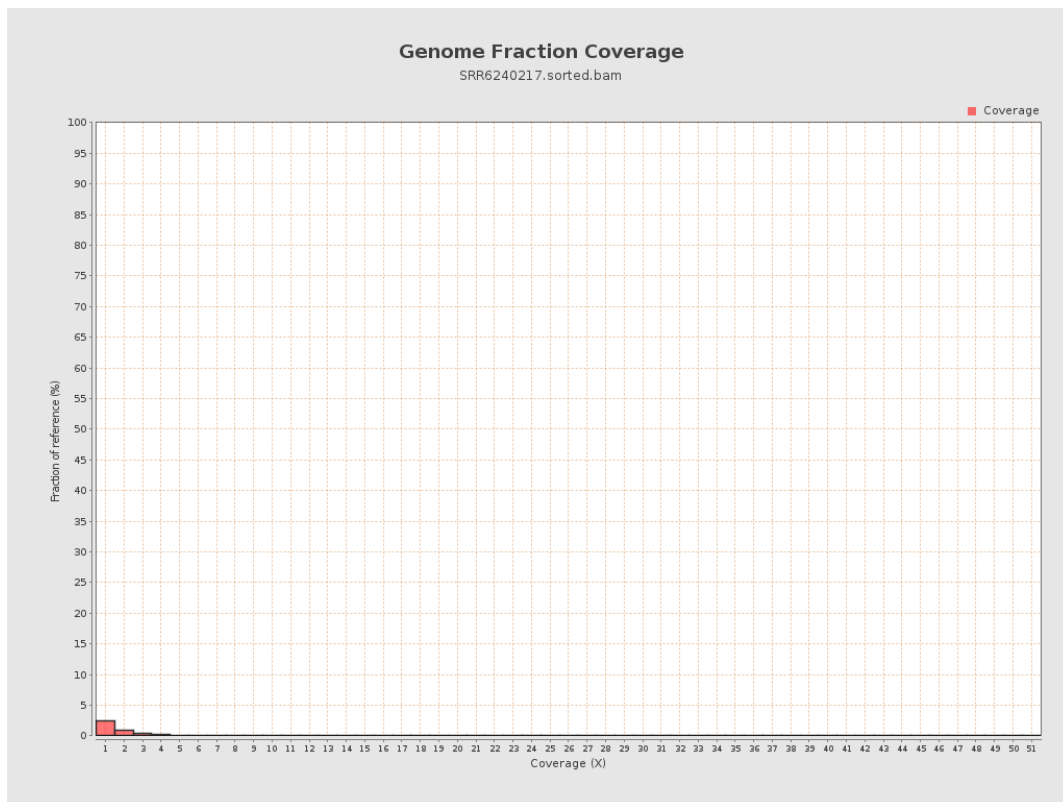
4. Results : Coverage Histogram



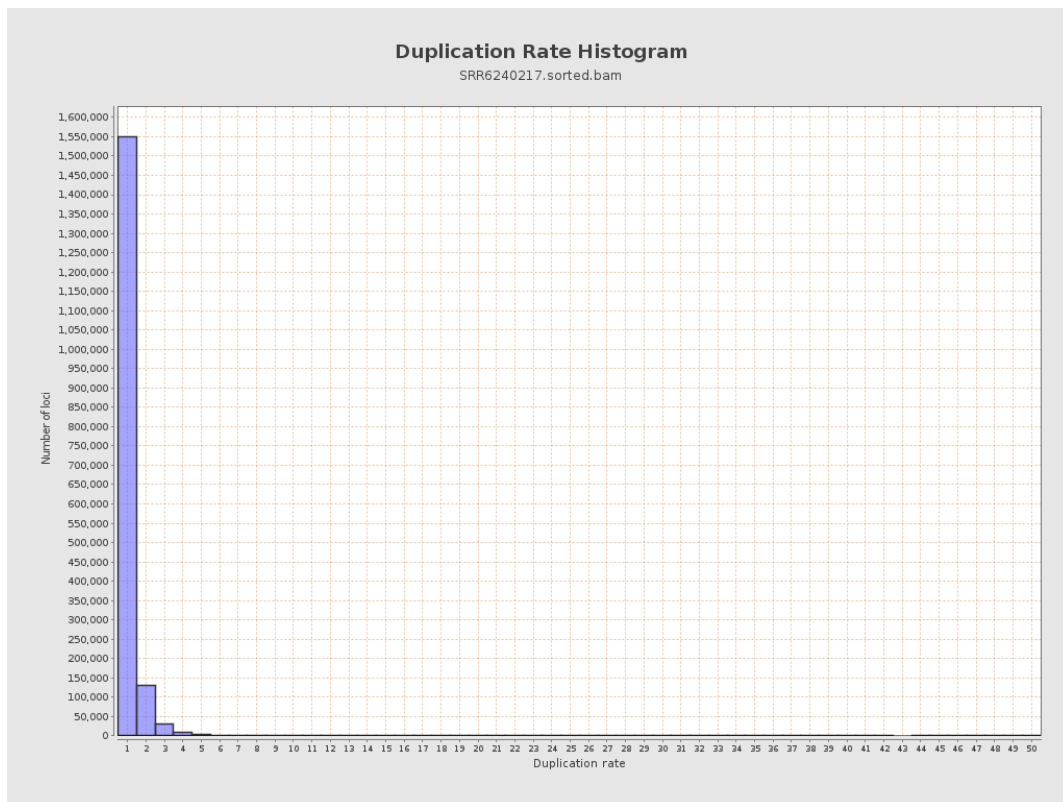
5. Results : Coverage Histogram (0-50X)



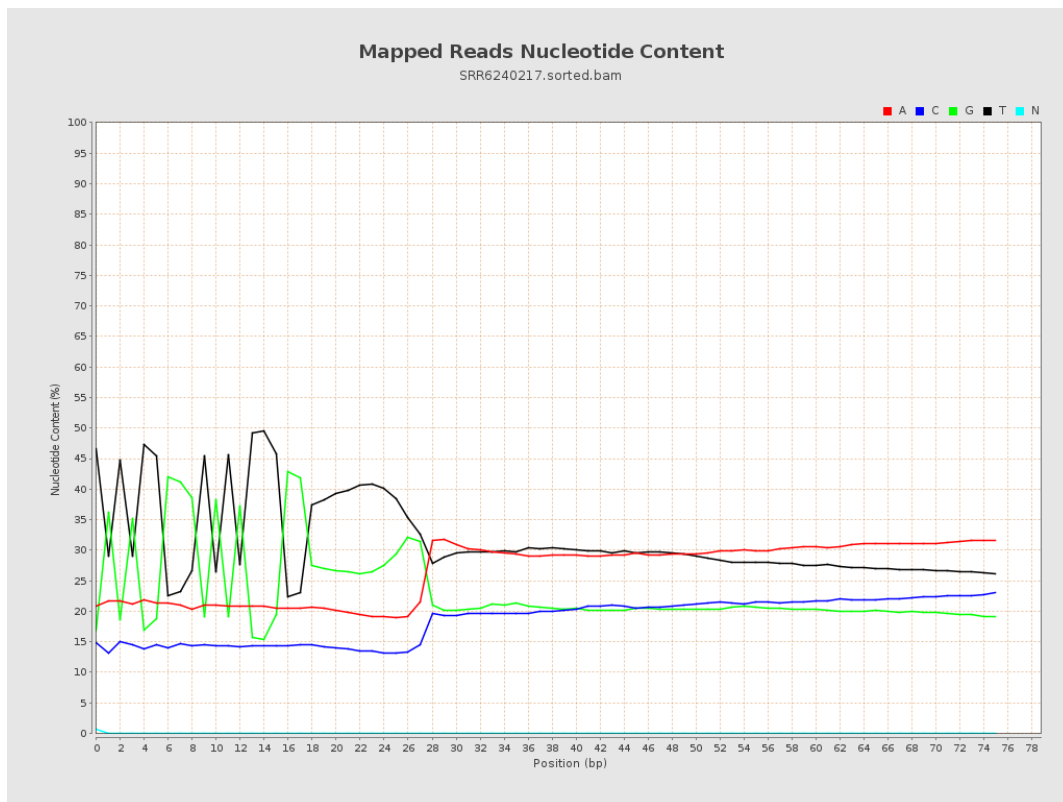
6. Results : Genome Fraction Coverage



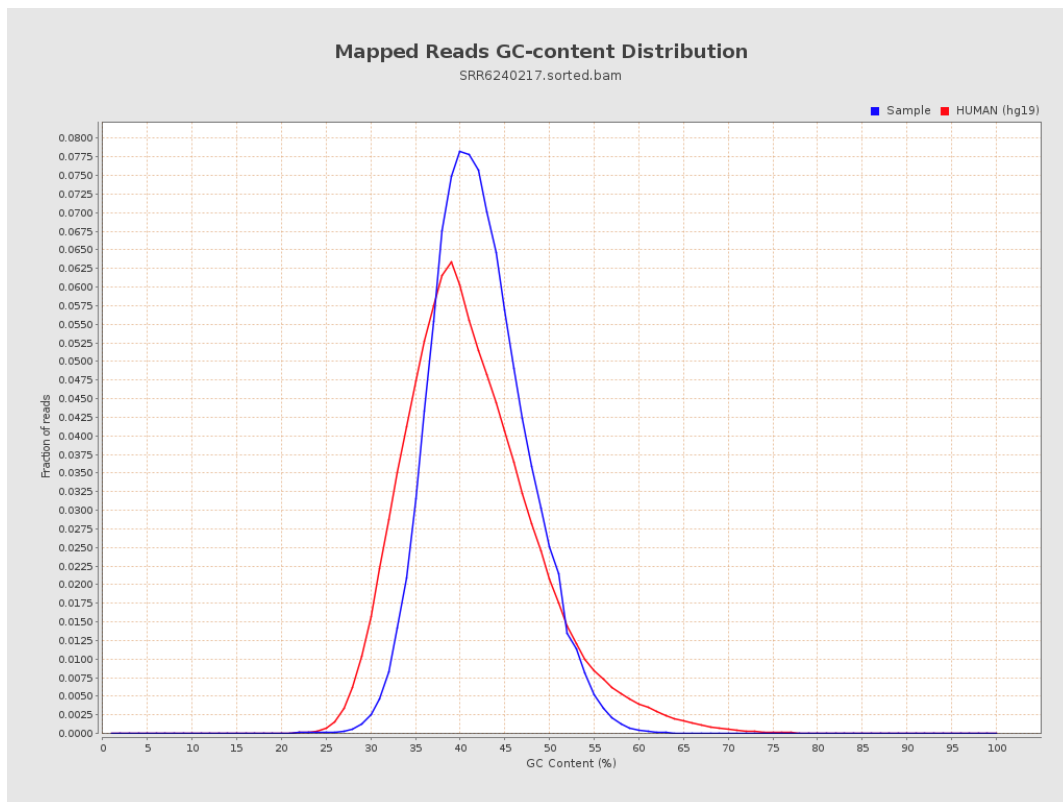
7. Results : Duplication Rate Histogram



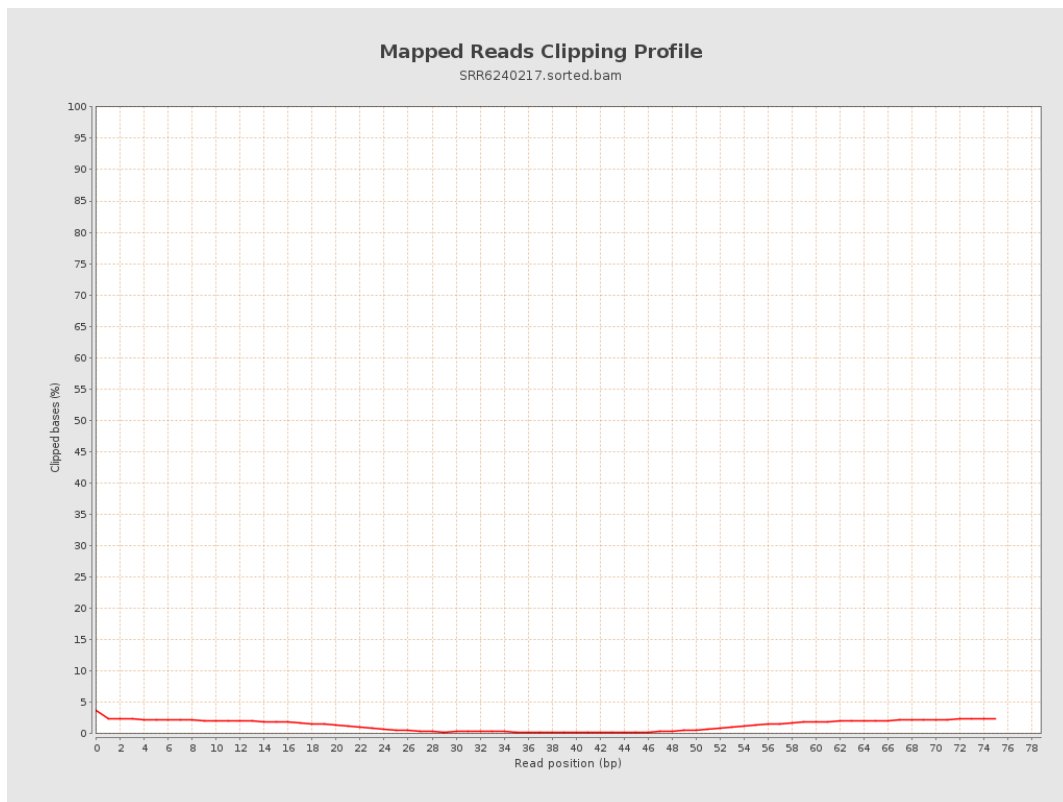
8. Results : Mapped Reads Nucleotide Content



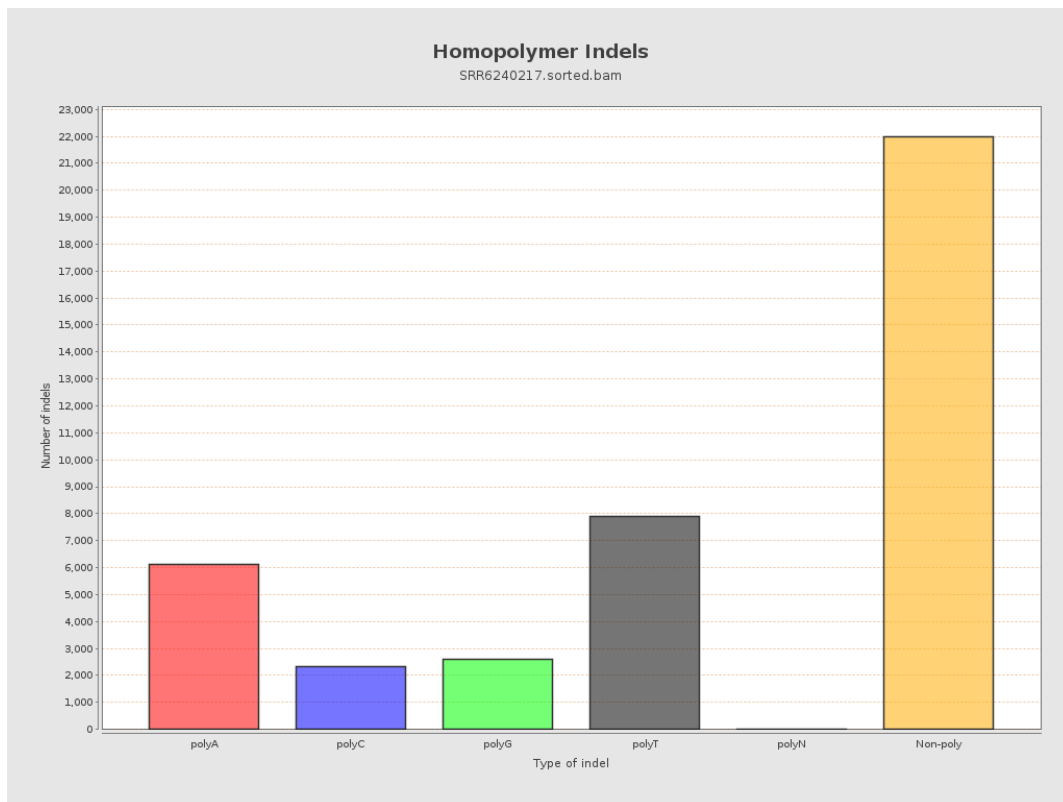
9. Results : Mapped Reads GC-content Distribution



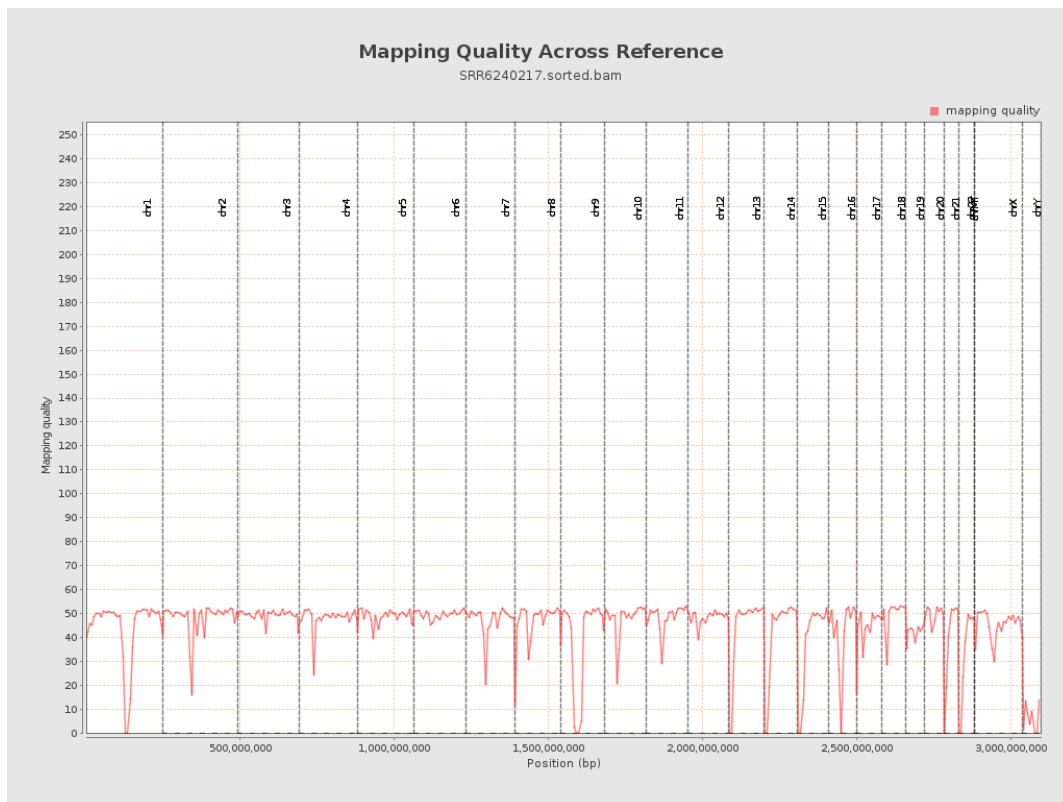
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

