

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 08:41:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240253.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_SRR6240253 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240253.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 08:41:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240253.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	621,888
Mapped reads	450,679 / 72.47%
Unmapped reads	171,209 / 27.53%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,592 / 0.42%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	46,444 / 7.47%
Duplication rate	7.13%
Clipped reads	249,507 / 40.12%

2.2. ACGT Content

Number/percentage of A's	8,306,160 / 28.57%
Number/percentage of C's	5,235,524 / 18.01%
Number/percentage of T's	9,080,576 / 31.24%
Number/percentage of G's	6,431,043 / 22.12%
Number/percentage of N's	15,427 / 0.05%
GC Percentage	40.13%

2.3. Coverage

Mean	0.0094

Standard Deviation	0.2045
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2.4. Mapping Quality

Mean Mapping Quality	43.93
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2.5. Mismatches and indels

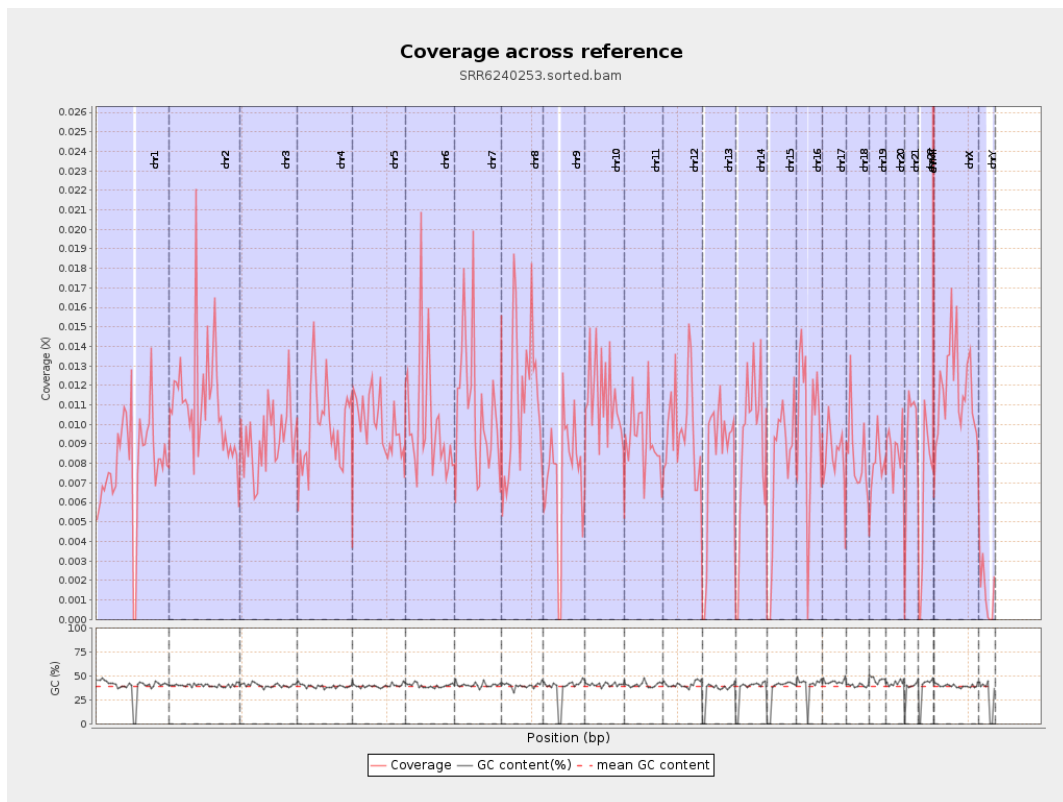
General error rate	1.08%
Mismatches	308,590
Insertions	2,315
Mapped reads with at least one insertion	0.51%
Deletions	9,733
Mapped reads with at least one deletion	2.13%
Homopolymer indels	49%

2.6. Chromosome stats

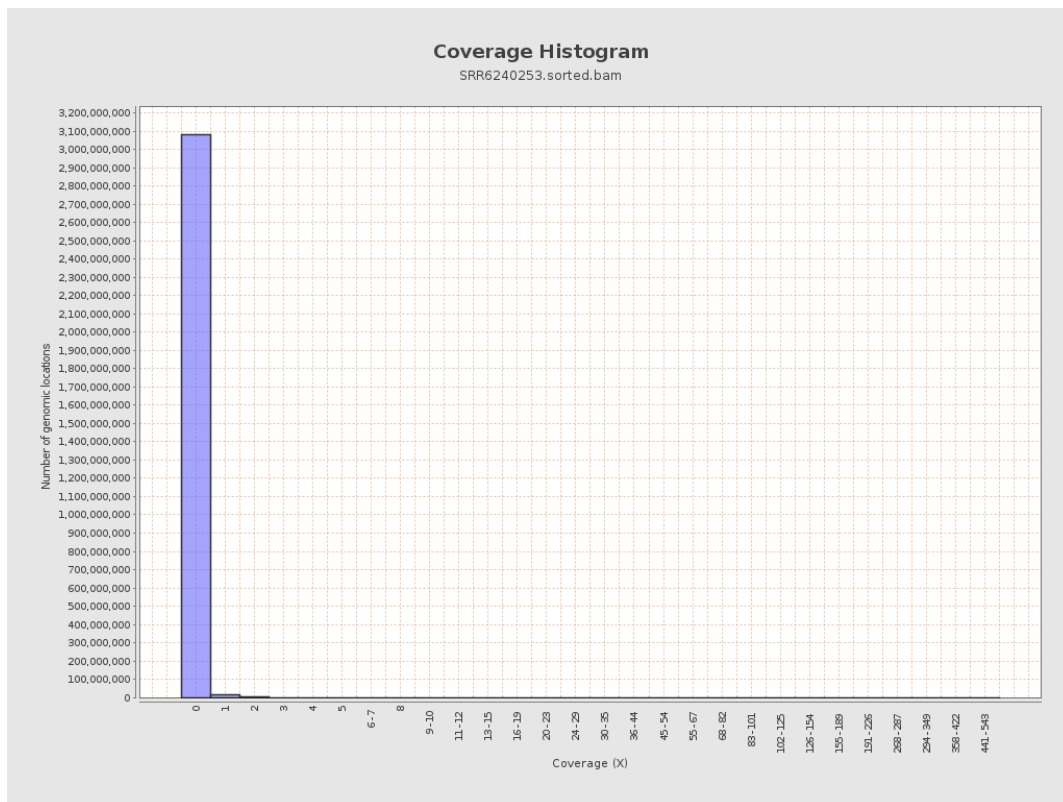
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	2002626	0.008	0.2205
chr2	243199373	2683062	0.011	0.212
chr3	198022430	1834758	0.0093	0.1776
chr4	191154276	1889777	0.0099	0.1841
chr5	180915260	1812460	0.01	0.1914
chr6	171115067	1726155	0.0101	0.193
chr7	159138663	1734852	0.0109	0.2346

chr8	146364022	1635830	0.0112	0.3839
chr9	141213431	1061329	0.0075	0.1679
chr10	135534747	1542573	0.0114	0.2106
chr11	135006516	1236673	0.0092	0.1905
chr12	133851895	1304054	0.0097	0.1817
chr13	115169878	943082	0.0082	0.1787
chr14	107349540	958324	0.0089	0.1766
chr15	102531392	795027	0.0078	0.1642
chr16	90354753	911380	0.0101	0.181
chr17	81195210	672392	0.0083	0.1511
chr18	78077248	660722	0.0085	0.2093
chr19	59128983	471372	0.008	0.1708
chr20	63025520	550388	0.0087	0.1615
chr21	48129895	441025	0.0092	0.1741
chr22	51304566	324876	0.0063	0.1488
chrMT	16571	4611	0.2783	0.6818
chrX	155270560	1805525	0.0116	0.2102
chrY	59373566	83129	0.0014	0.0589

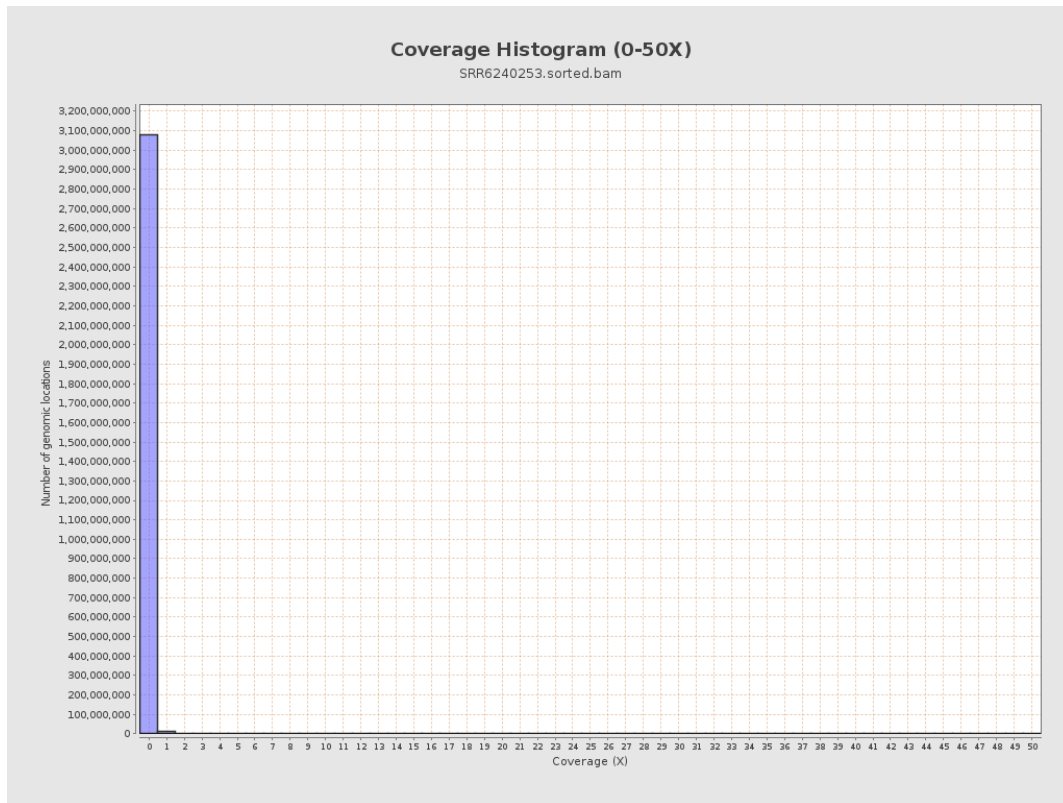
3. Results : Coverage across reference



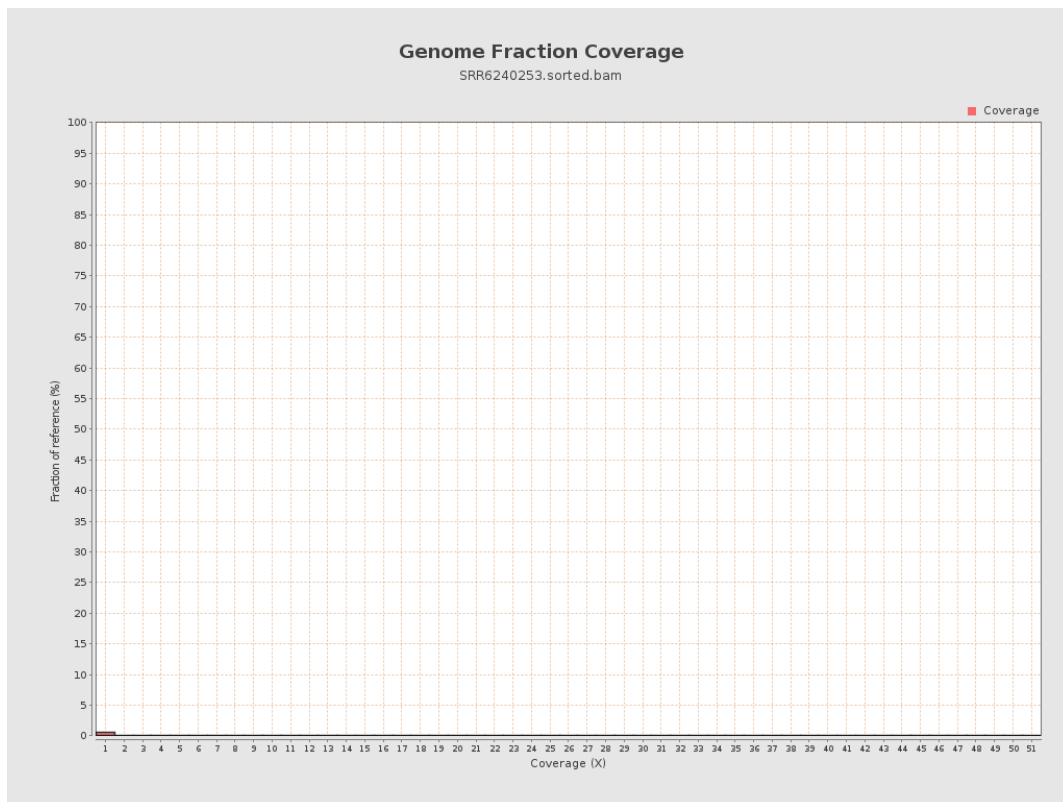
4. Results : Coverage Histogram



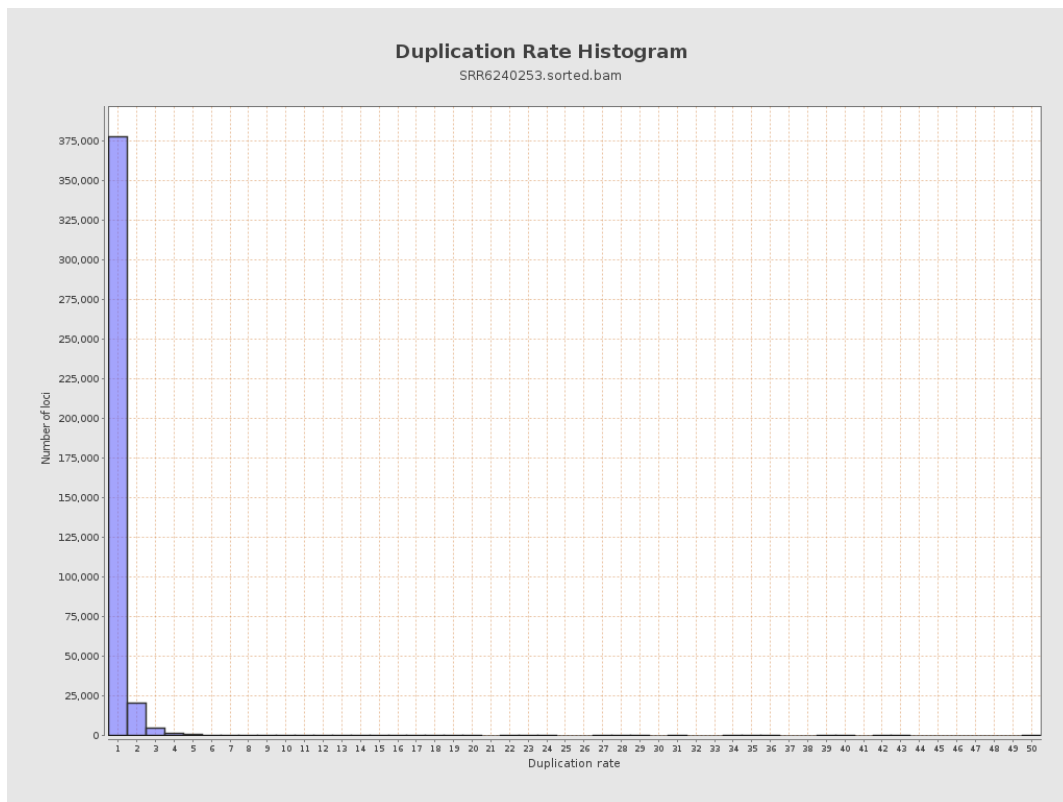
5. Results : Coverage Histogram (0-50X)



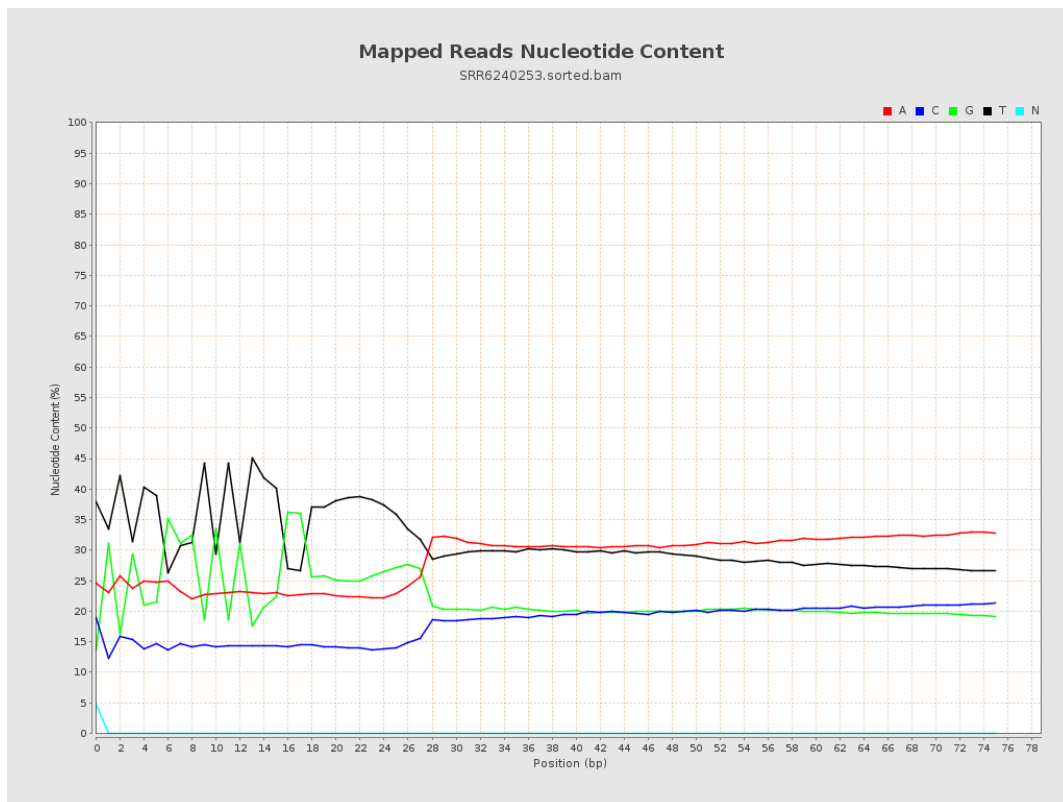
6. Results : Genome Fraction Coverage



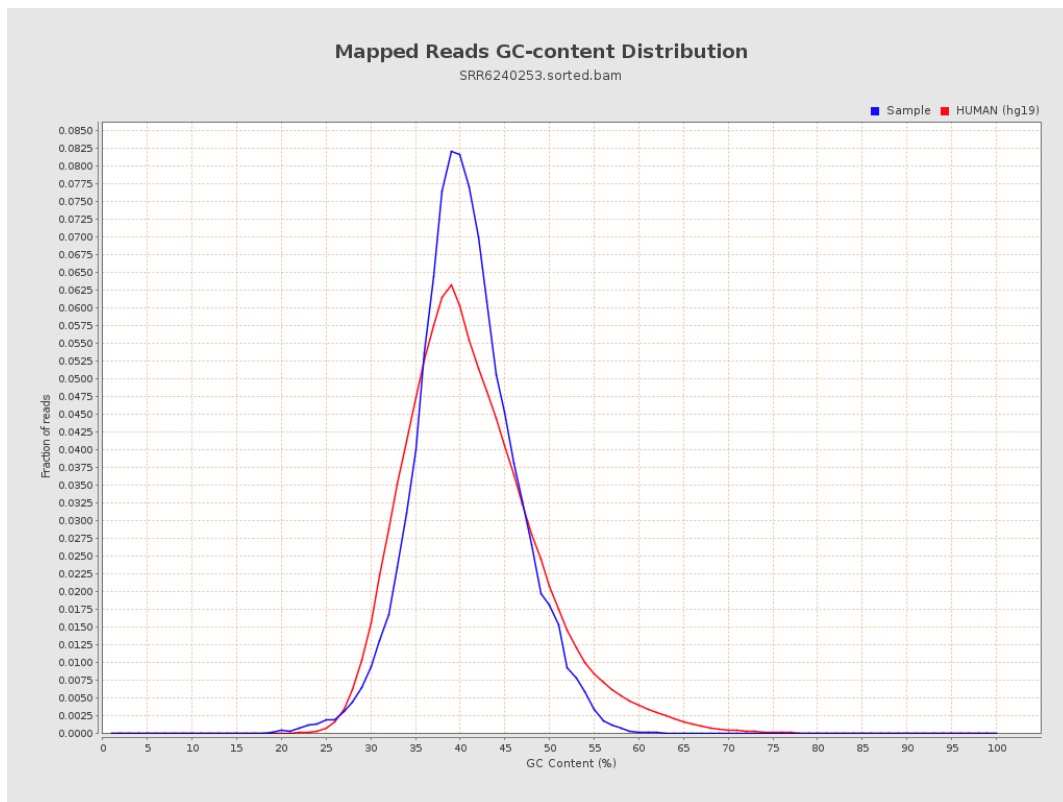
7. Results : Duplication Rate Histogram



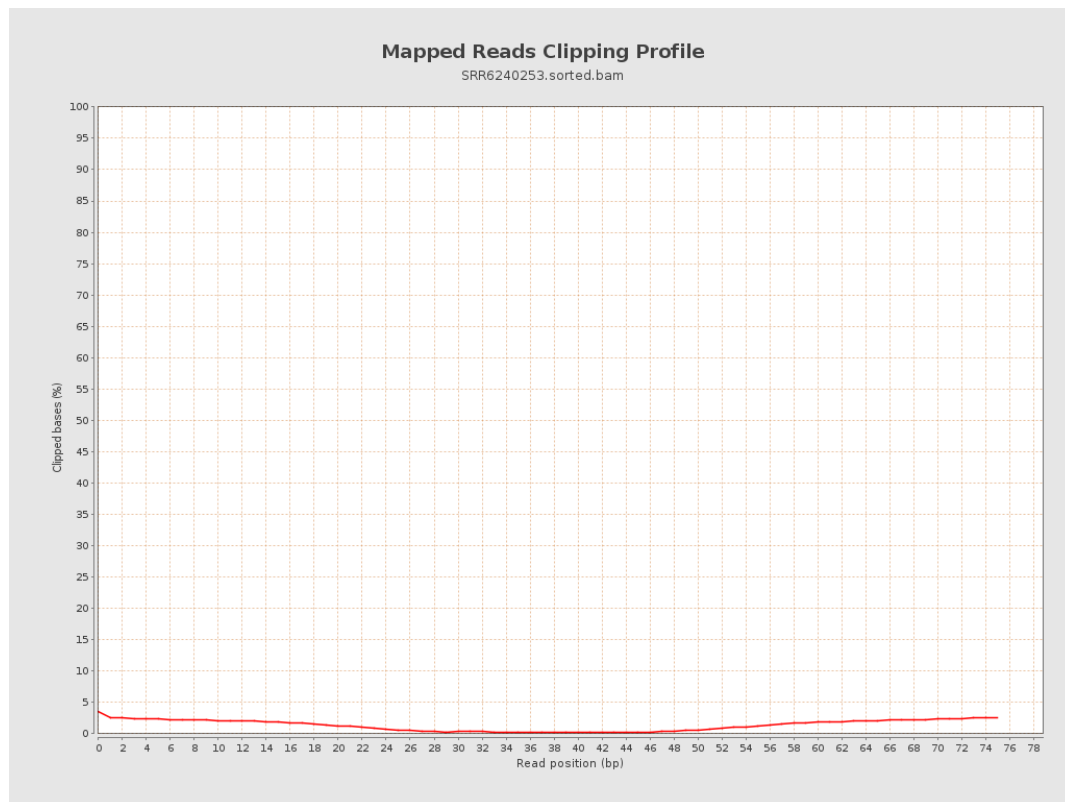
8. Results : Mapped Reads Nucleotide Content



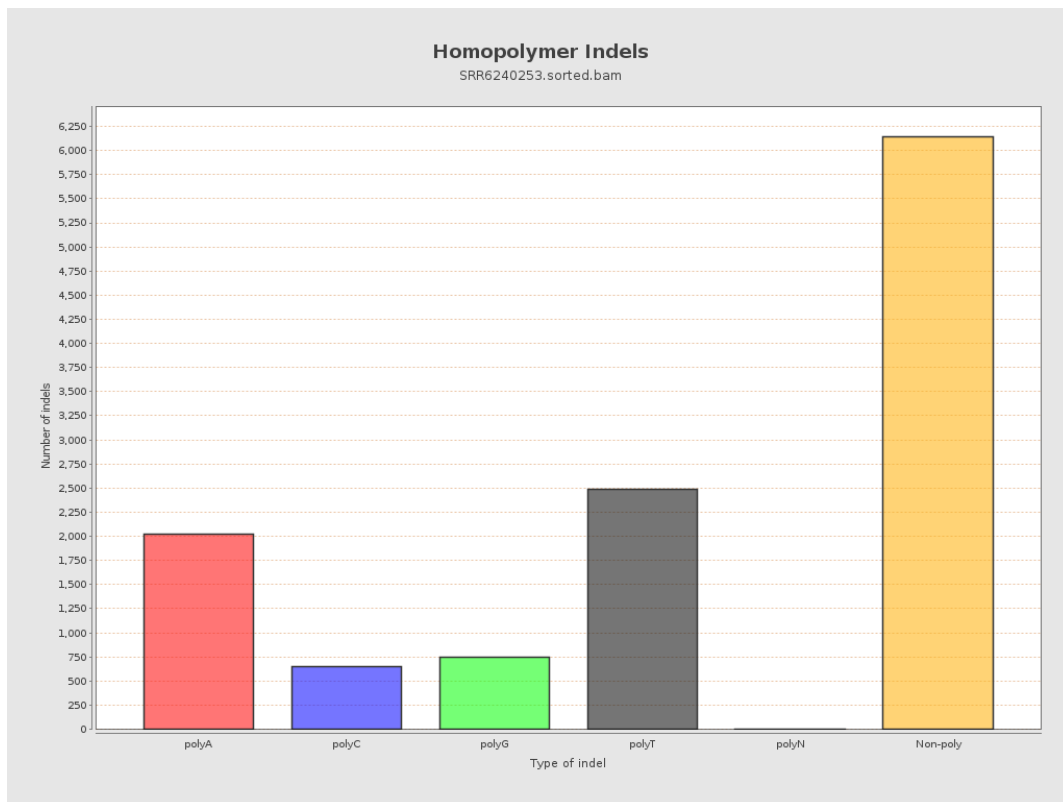
9. Results : Mapped Reads GC-content Distribution



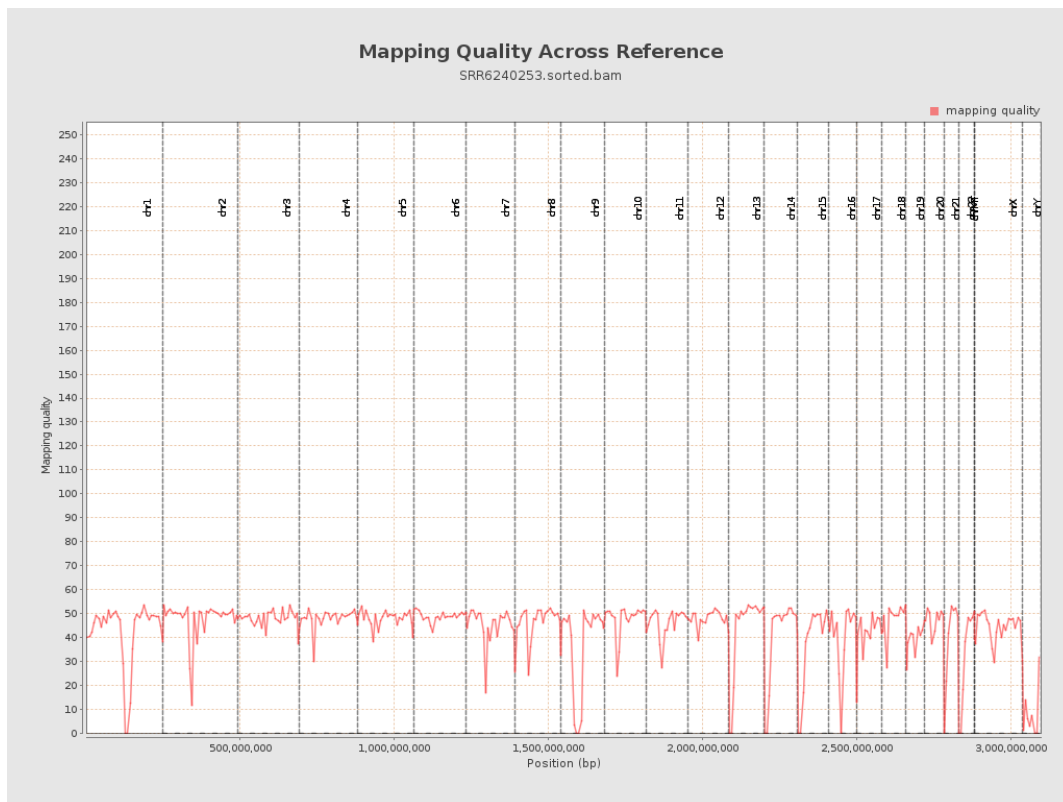
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

