

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 09:04:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240262.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_SRR6240262 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240262.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 09:04:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240262.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,471,727
Mapped reads	1,207,186 / 82.03%
Unmapped reads	264,541 / 17.97%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,059 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	47,090 / 3.2%
Duplication rate	2.94%
Clipped reads	786,764 / 53.46%

2.2. ACGT Content

Number/percentage of A's	20,053,826 / 26.94%
Number/percentage of C's	13,184,563 / 17.71%
Number/percentage of T's	23,067,428 / 30.99%
Number/percentage of G's	18,110,413 / 24.33%
Number/percentage of N's	17,194 / 0.02%
GC Percentage	42.04%

2.3. Coverage

Mean	0.0241

Standard Deviation	0.2556
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2.4. Mapping Quality

Mean Mapping Quality	41.32
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2.5. Mismatches and indels

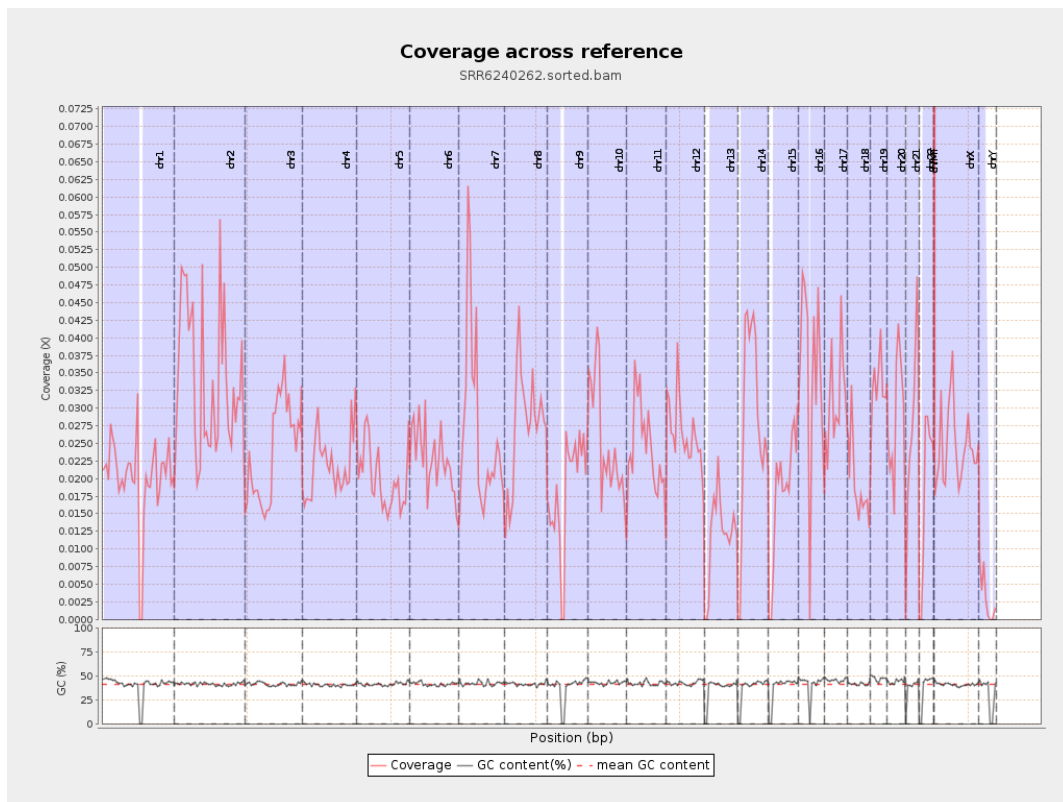
General error rate	1.02%
Mismatches	752,110
Insertions	6,044
Mapped reads with at least one insertion	0.5%
Deletions	24,842
Mapped reads with at least one deletion	2.03%
Homopolymer indels	48.3%

2.6. Chromosome stats

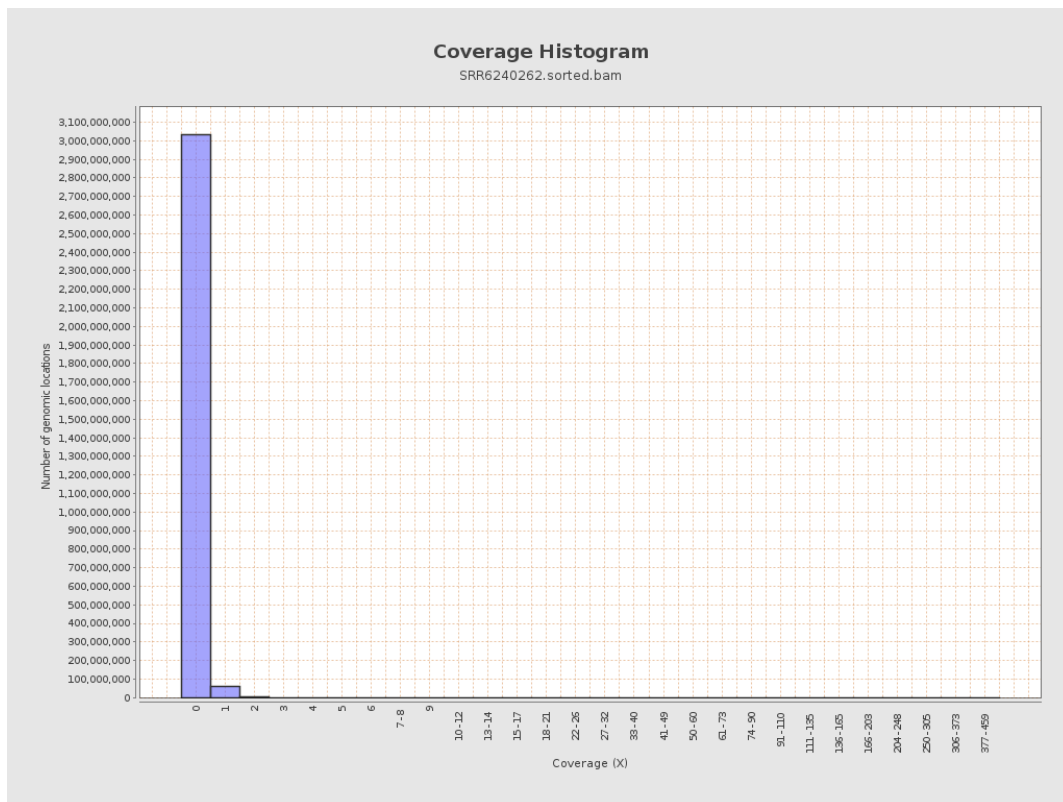
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	5004640	0.0201	0.3633
chr2	243199373	8304885	0.0341	0.3444
chr3	198022430	4740978	0.0239	0.1739
chr4	191154276	4212493	0.022	0.1707
chr5	180915260	3615282	0.02	0.161
chr6	171115067	3870016	0.0226	0.2074
chr7	159138663	4271215	0.0268	0.4131

chr8	146364022	4082833	0.0279	0.3098
chr9	141213431	2571540	0.0182	0.2437
chr10	135534747	3417451	0.0252	0.2264
chr11	135006516	3305760	0.0245	0.2485
chr12	133851895	3559724	0.0266	0.1825
chr13	115169878	1384462	0.012	0.1225
chr14	107349540	3056536	0.0285	0.2025
chr15	102531392	1822494	0.0178	0.1663
chr16	90354753	3143521	0.0348	0.218
chr17	81195210	2547370	0.0314	0.2145
chr18	78077248	1469562	0.0188	0.4082
chr19	59128983	1974011	0.0334	0.3009
chr20	63025520	1786842	0.0284	0.1921
chr21	48129895	1331468	0.0277	0.194
chr22	51304566	962982	0.0188	0.1517
chrMT	16571	30637	1.8488	2.1833
chrX	155270560	3830408	0.0247	0.2006
chrY	59373566	179580	0.003	0.0726

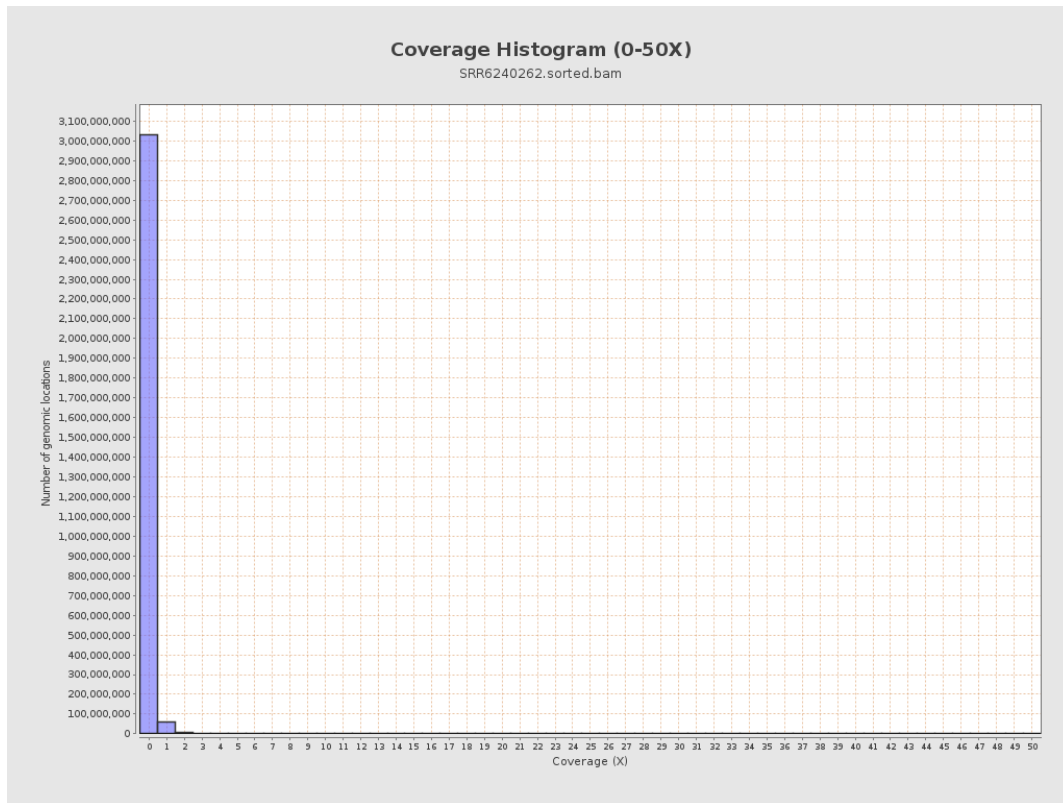
3. Results : Coverage across reference



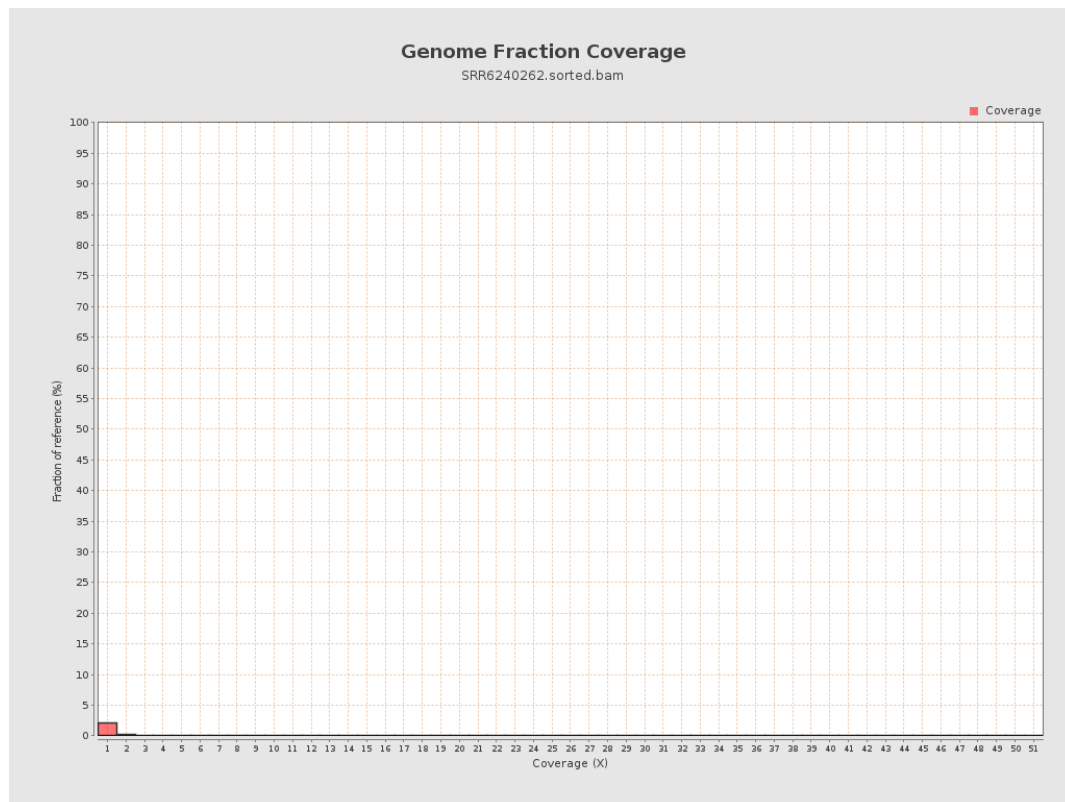
4. Results : Coverage Histogram



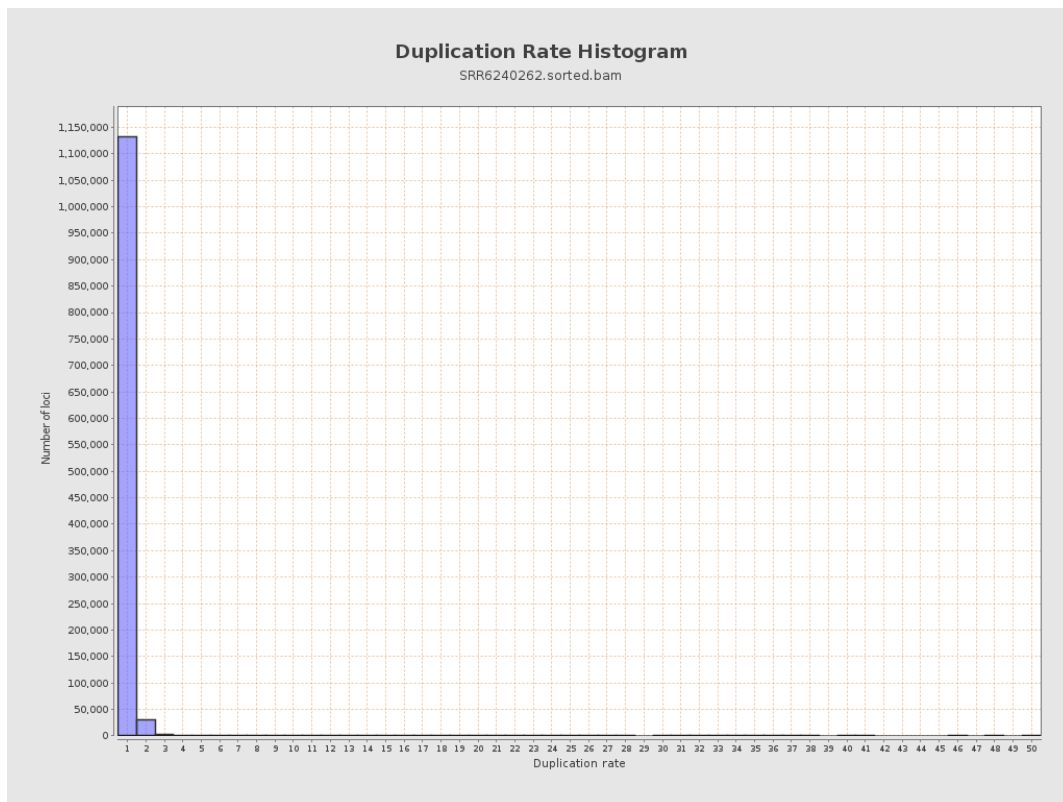
5. Results : Coverage Histogram (0-50X)



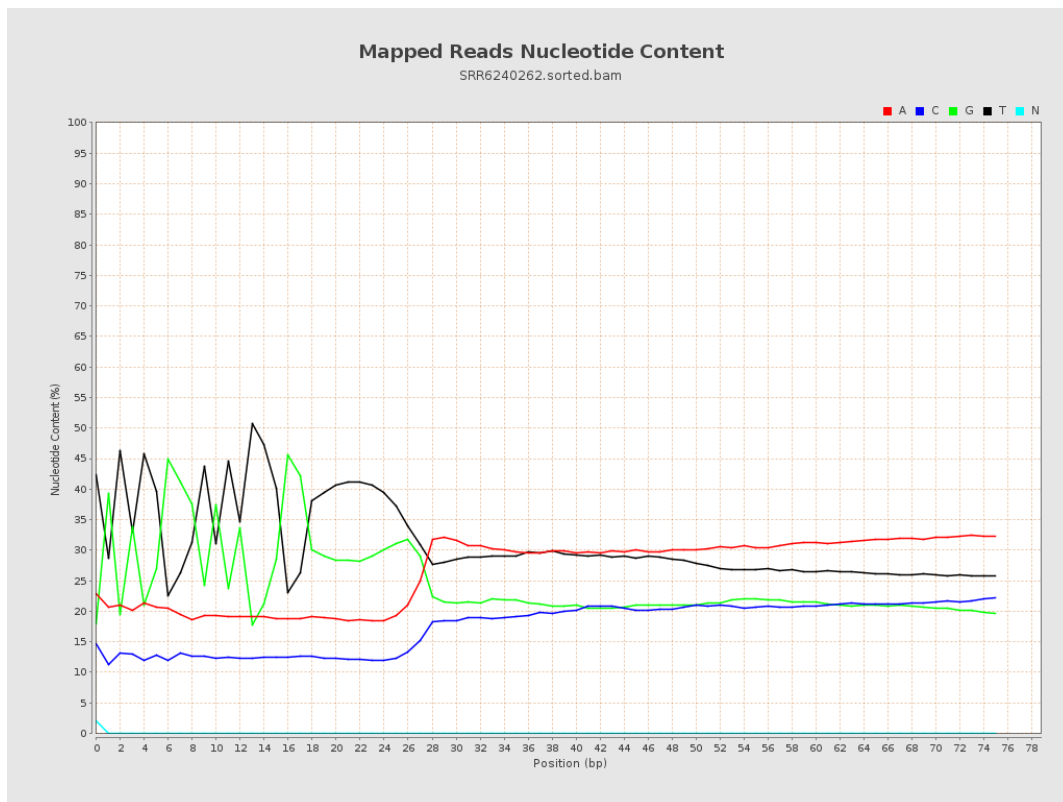
6. Results : Genome Fraction Coverage



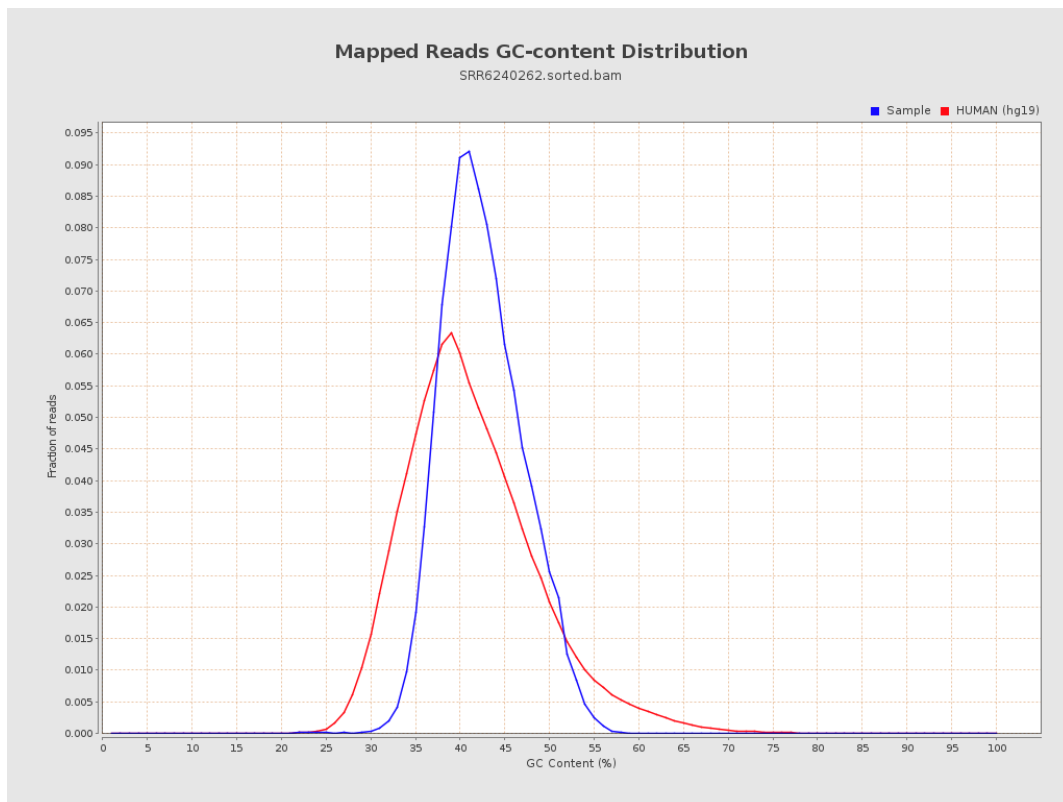
7. Results : Duplication Rate Histogram



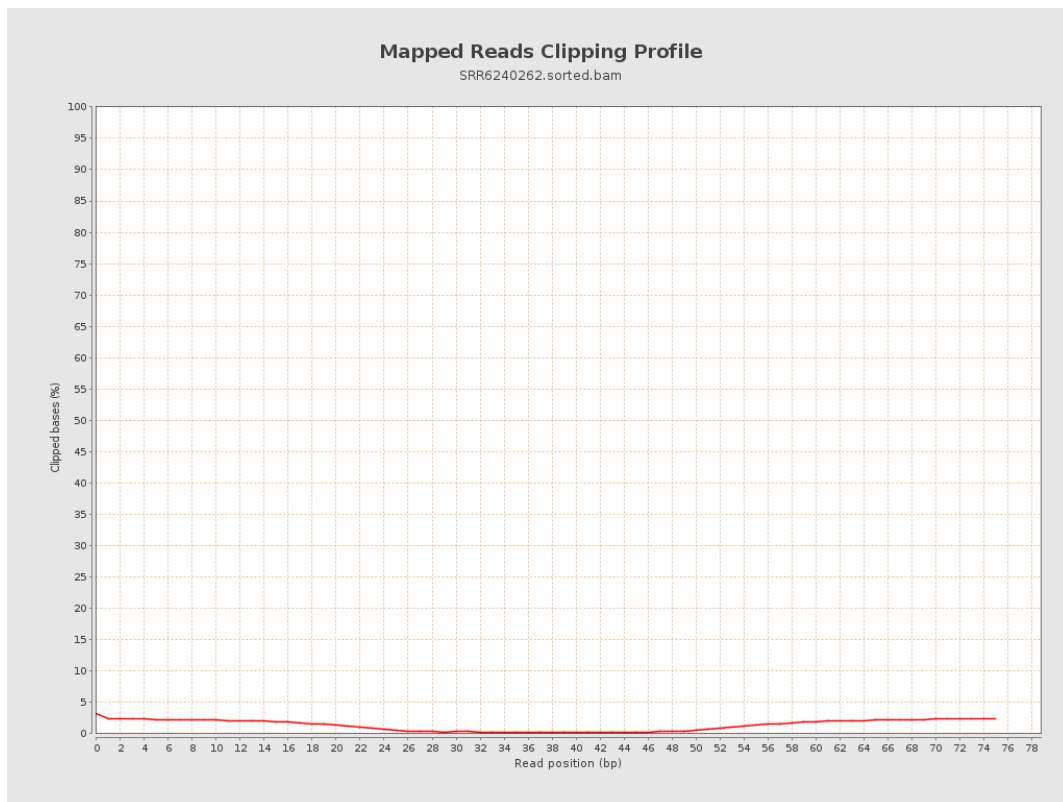
8. Results : Mapped Reads Nucleotide Content



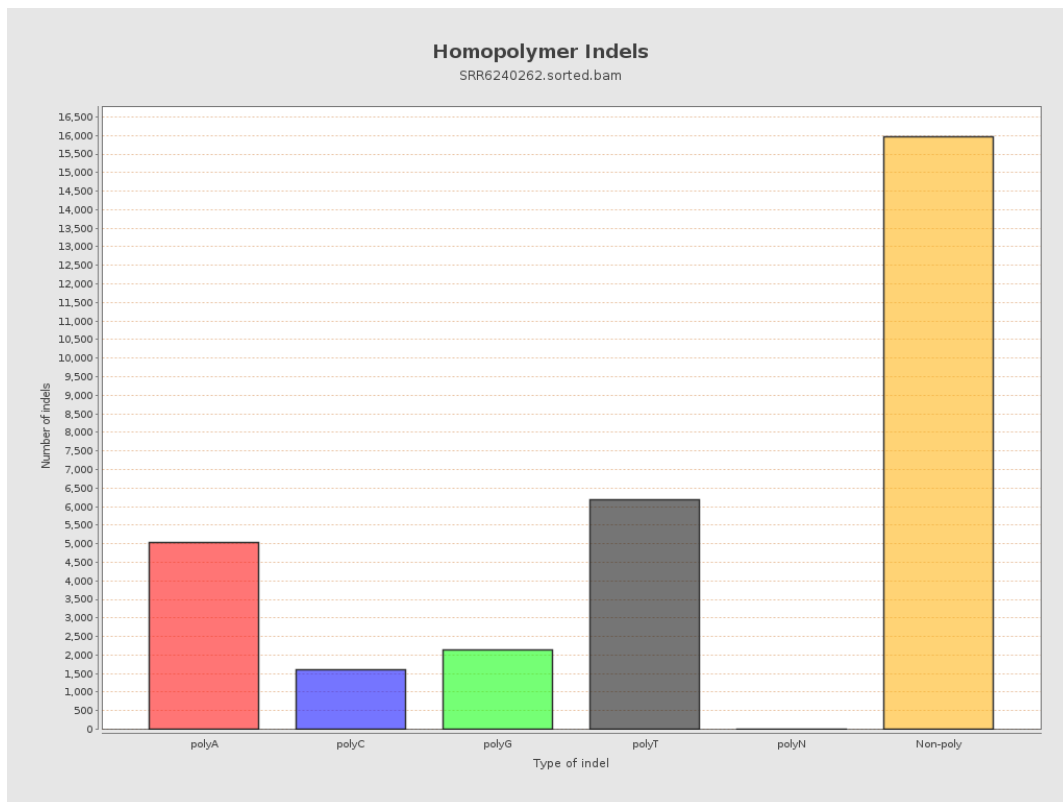
9. Results : Mapped Reads GC-content Distribution



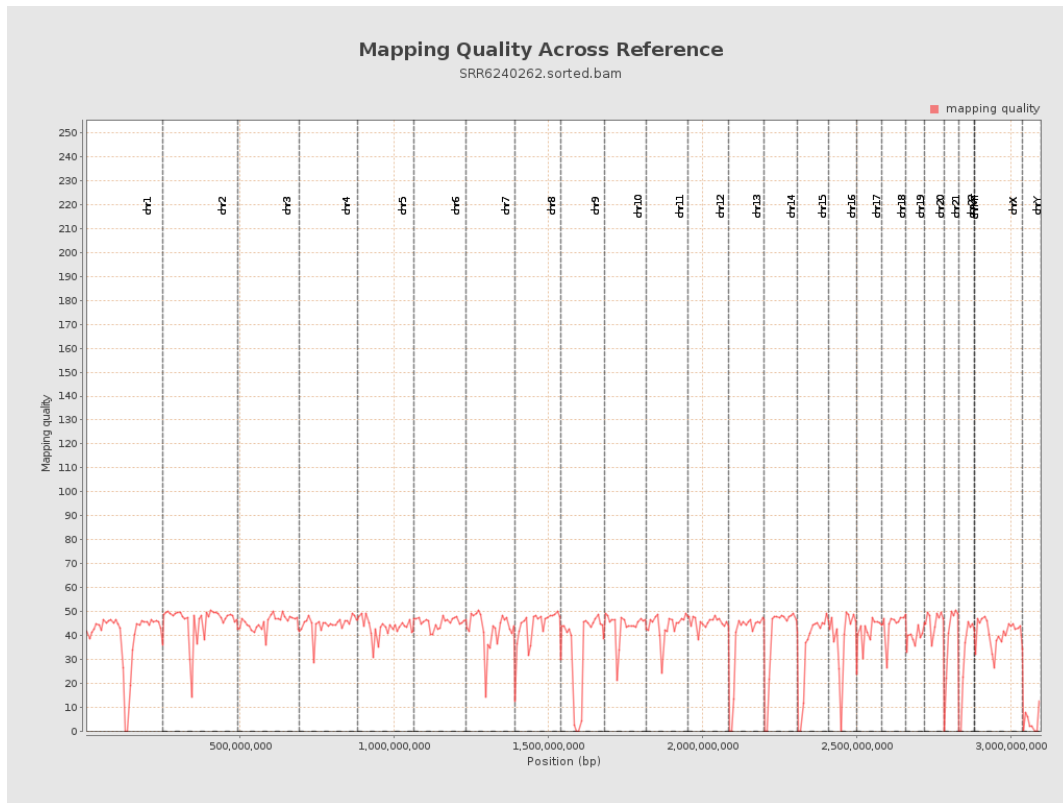
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

