

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 06:12:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240202.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_SRR6240202 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240202.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 06:12:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240202.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,824,139
Mapped reads	1,415,530 / 77.6%
Unmapped reads	408,609 / 22.4%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,281 / 0.29%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	155,927 / 8.55%
Duplication rate	8.91%
Clipped reads	1,027,245 / 56.31%

2.2. ACGT Content

Number/percentage of A's	22,958,239 / 27%
Number/percentage of C's	14,378,035 / 16.91%
Number/percentage of T's	28,219,292 / 33.19%
Number/percentage of G's	19,456,737 / 22.88%
Number/percentage of N's	18,562 / 0.02%
GC Percentage	39.79%

2.3. Coverage

Mean	0.0275

Standard Deviation	0.2828
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2.4. Mapping Quality

Mean Mapping Quality	45.62
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2.5. Mismatches and indels

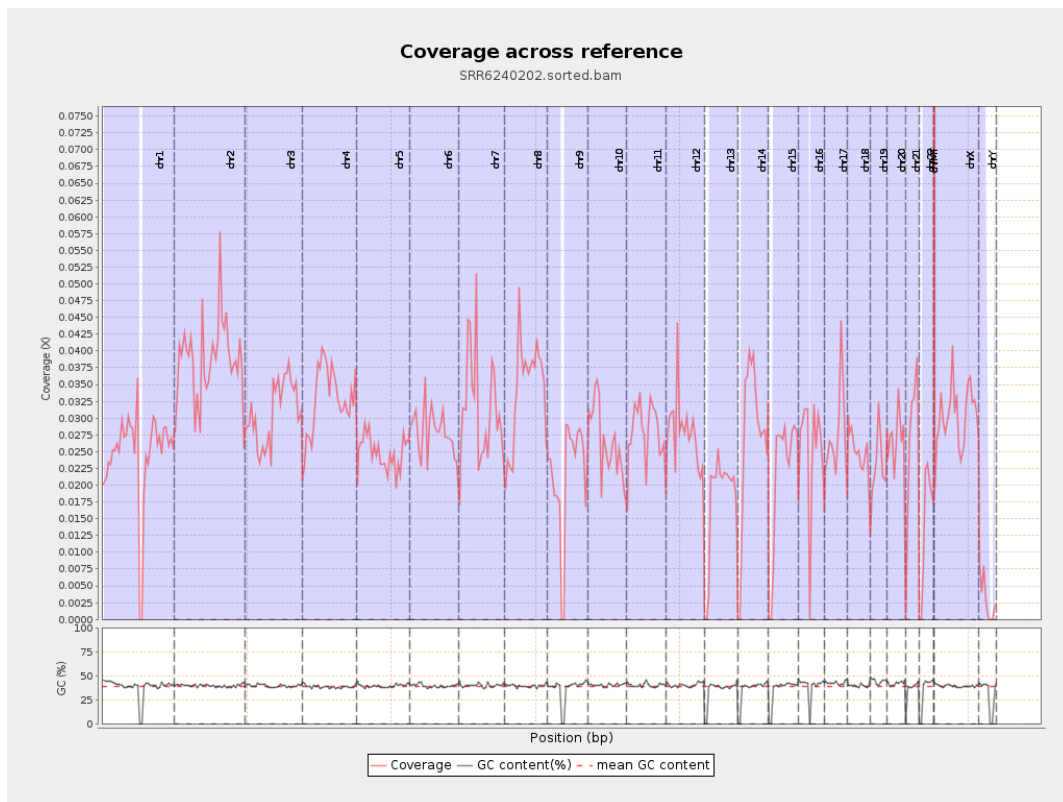
General error rate	1.02%
Mismatches	858,161
Insertions	6,074
Mapped reads with at least one insertion	0.43%
Deletions	29,702
Mapped reads with at least one deletion	2.07%
Homopolymer indels	50.66%

2.6. Chromosome stats

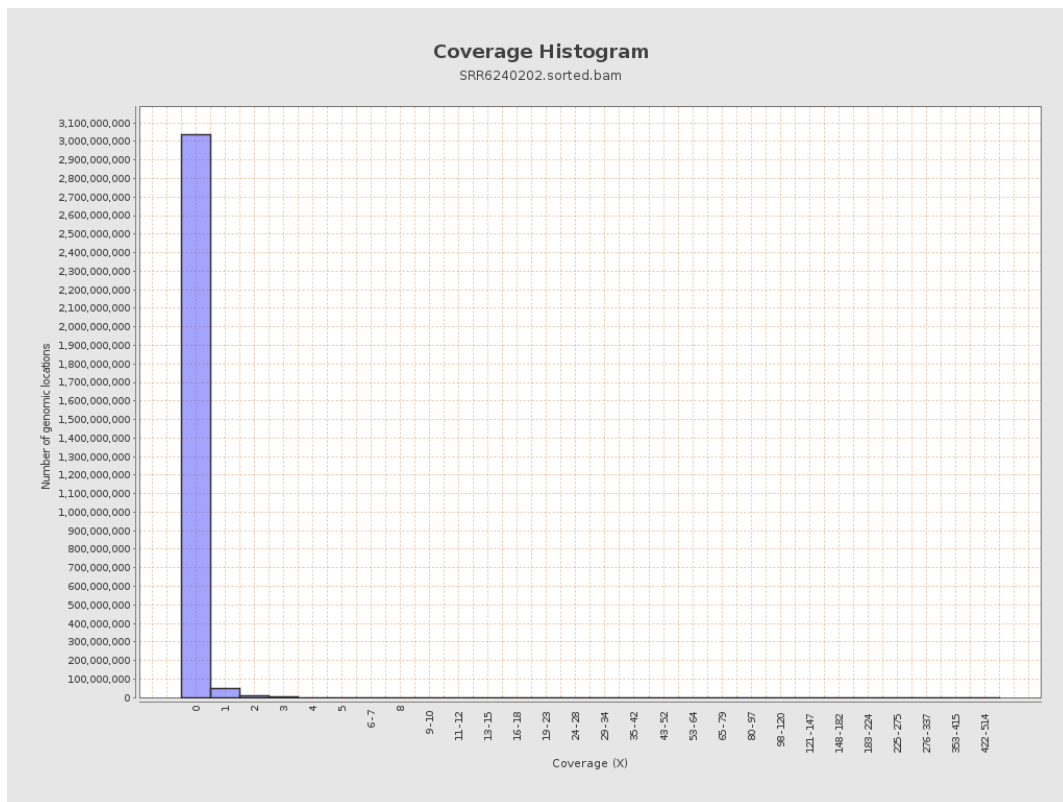
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	6142400	0.0246	0.3668
chr2	243199373	9434576	0.0388	0.3259
chr3	198022430	6112170	0.0309	0.2407
chr4	191154276	6259339	0.0327	0.2533
chr5	180915260	4503450	0.0249	0.214
chr6	171115067	4770345	0.0279	0.2552
chr7	159138663	4995466	0.0314	0.4813

chr8	146364022	5017686	0.0343	0.3965
chr9	141213431	3027088	0.0214	0.2382
chr10	135534747	3575275	0.0264	0.2472
chr11	135006516	3798987	0.0281	0.2574
chr12	133851895	3720456	0.0278	0.223
chr13	115169878	2040475	0.0177	0.1806
chr14	107349540	2933932	0.0273	0.2294
chr15	102531392	2228174	0.0217	0.2076
chr16	90354753	2259322	0.025	0.2123
chr17	81195210	2246321	0.0277	0.2291
chr18	78077248	1955382	0.025	0.3303
chr19	59128983	1380235	0.0233	0.2882
chr20	63025520	1672752	0.0265	0.2211
chr21	48129895	1282662	0.0267	0.2236
chr22	51304566	747632	0.0146	0.1554
chrMT	16571	61034	3.6832	5.2158
chrX	155270560	4739130	0.0305	0.252
chrY	59373566	177159	0.003	0.0721

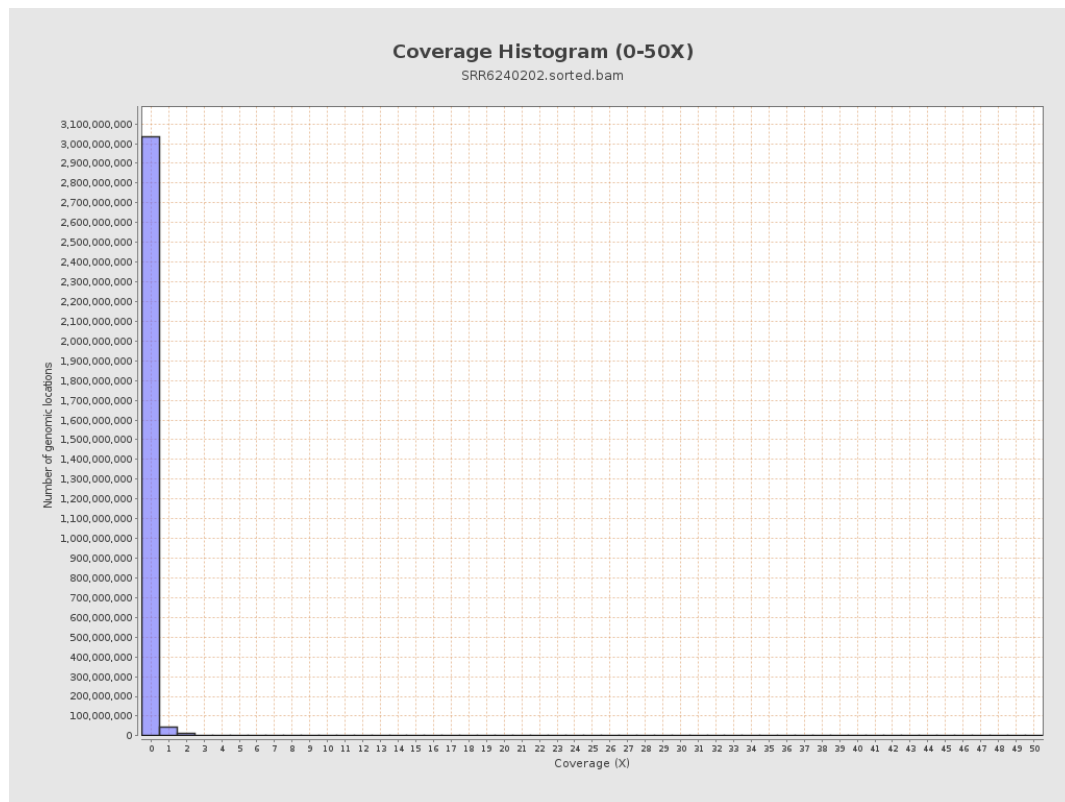
3. Results : Coverage across reference



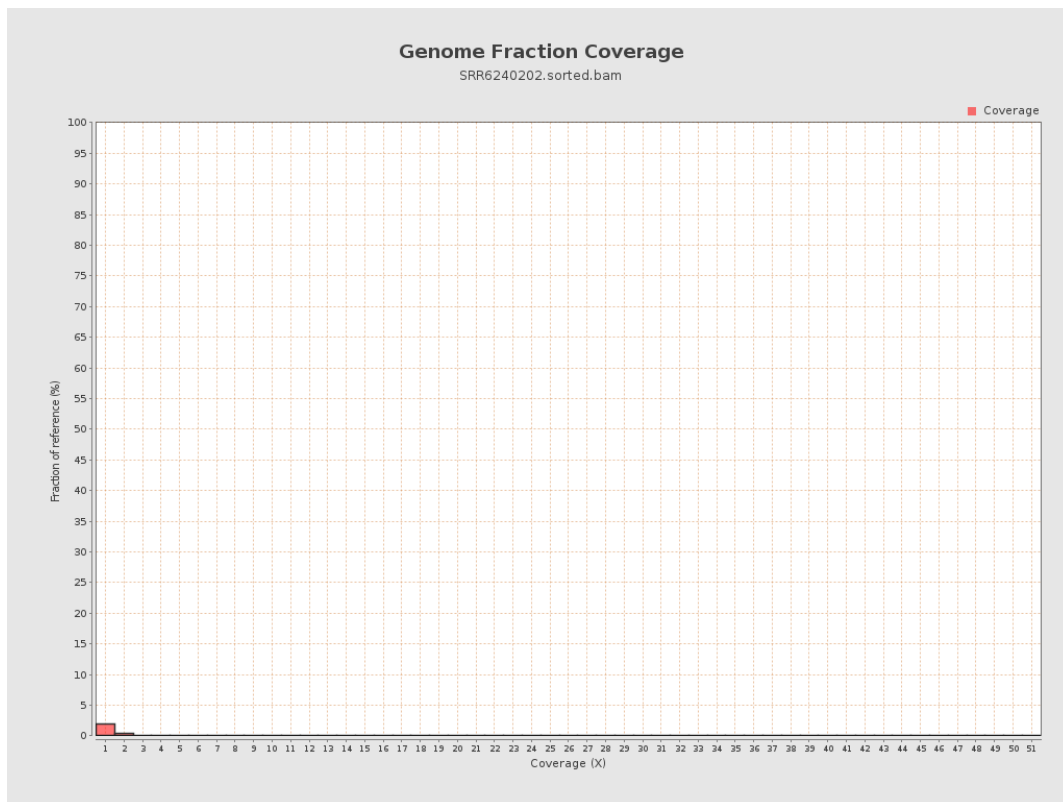
4. Results : Coverage Histogram



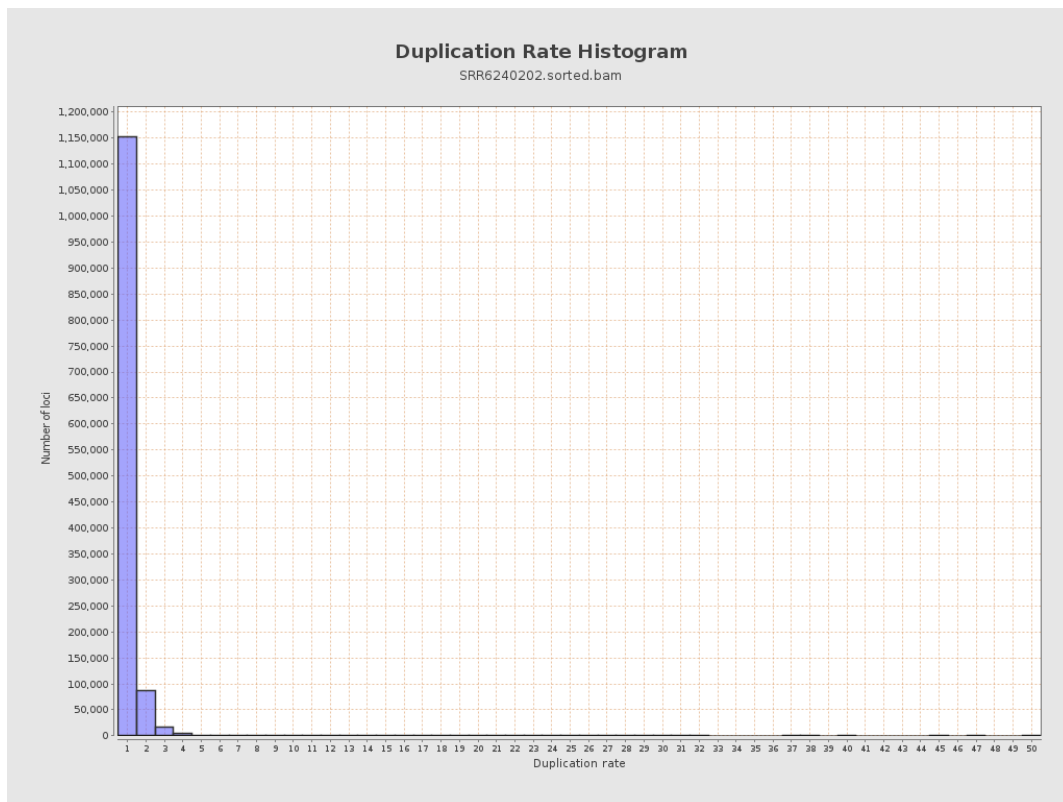
5. Results : Coverage Histogram (0-50X)



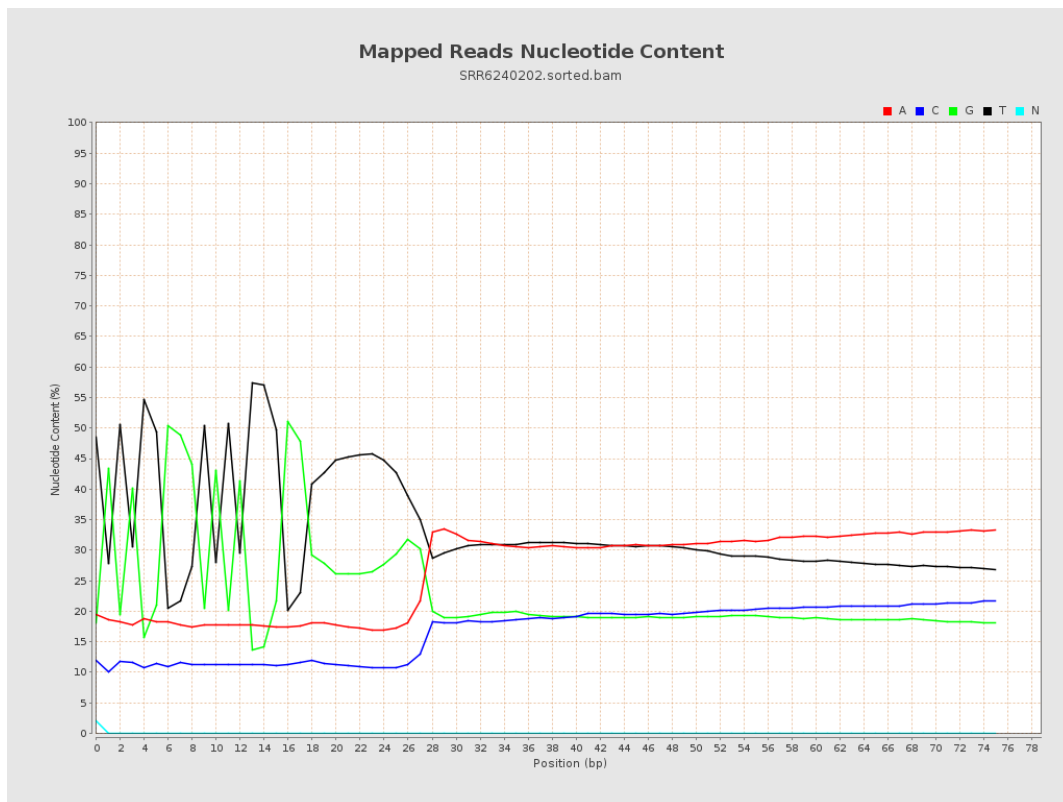
6. Results : Genome Fraction Coverage



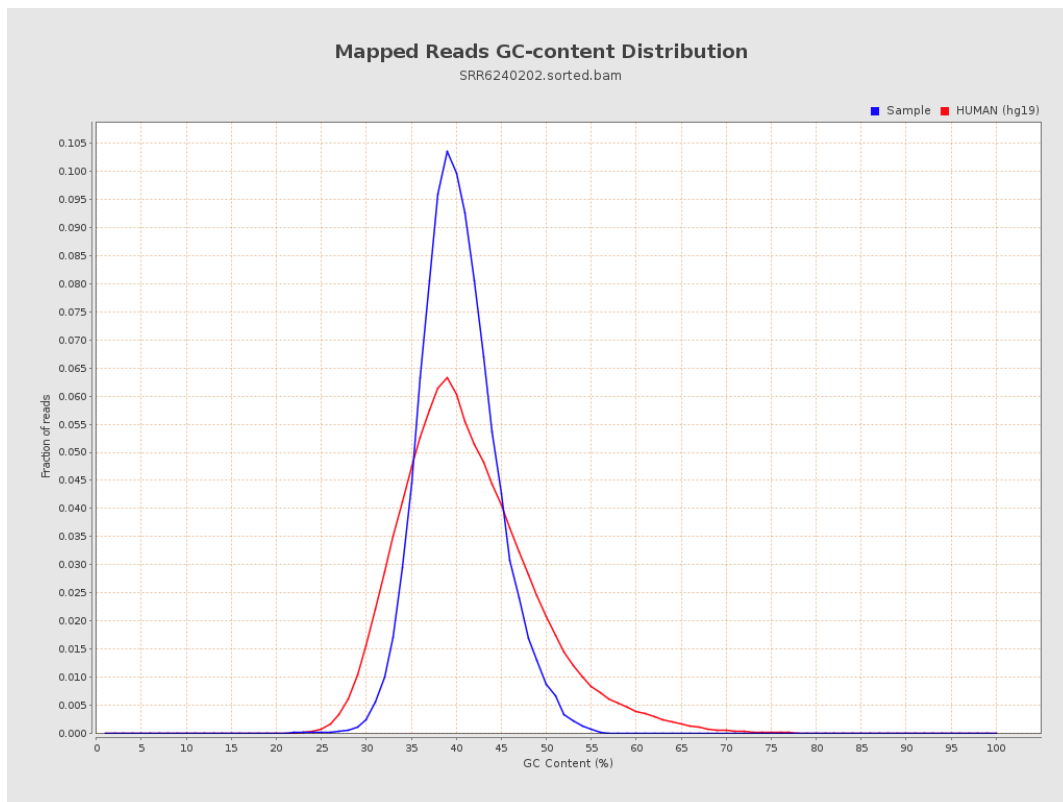
7. Results : Duplication Rate Histogram



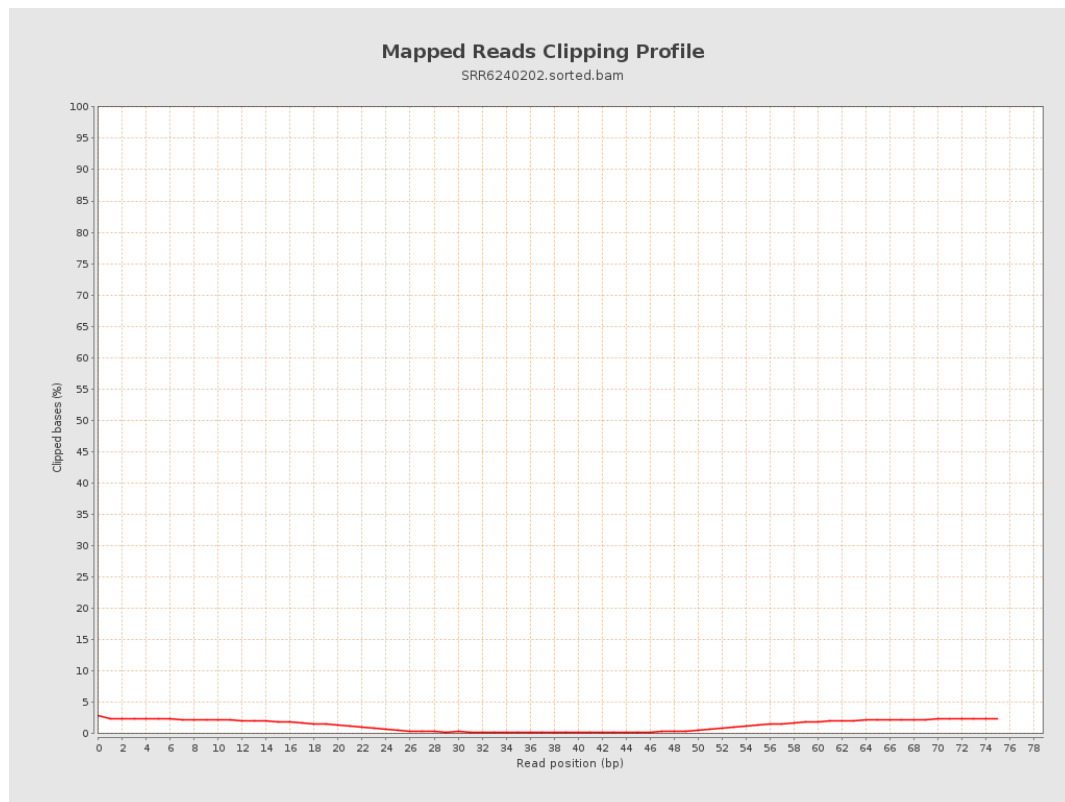
8. Results : Mapped Reads Nucleotide Content



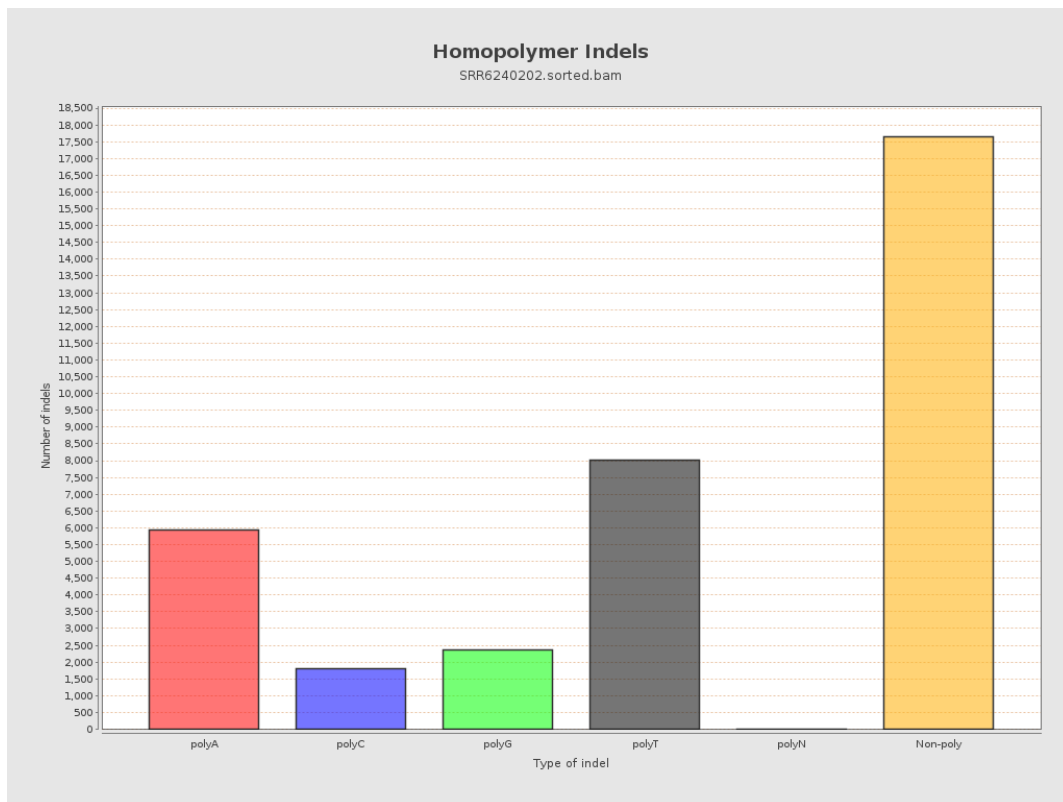
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

