

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 08:43:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240254.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_SRR6240254 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240254.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 08:43:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240254.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,102,864
Mapped reads	1,715,952 / 81.6%
Unmapped reads	386,912 / 18.4%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,657 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	141,698 / 6.74%
Duplication rate	6.84%
Clipped reads	1,142,791 / 54.34%

2.2. ACGT Content

Number/percentage of A's	28,405,838 / 26.99%
Number/percentage of C's	18,127,991 / 17.22%
Number/percentage of T's	34,482,111 / 32.76%
Number/percentage of G's	24,201,811 / 23%
Number/percentage of N's	24,624 / 0.02%
GC Percentage	40.22%

2.3. Coverage

Mean	0.034

Standard Deviation	0.3236
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2.4. Mapping Quality

Mean Mapping Quality	45.35
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2.5. Mismatches and indels

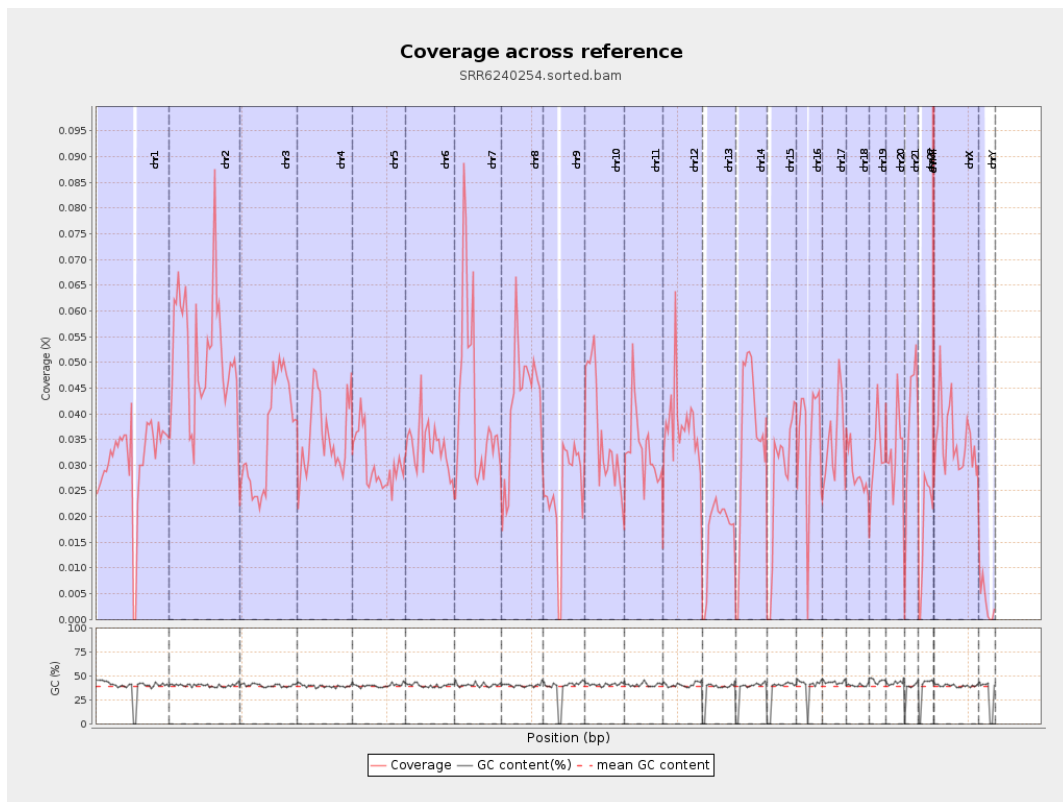
General error rate	0.98%
Mismatches	1,019,139
Insertions	7,231
Mapped reads with at least one insertion	0.42%
Deletions	36,871
Mapped reads with at least one deletion	2.12%
Homopolymer indels	50.42%

2.6. Chromosome stats

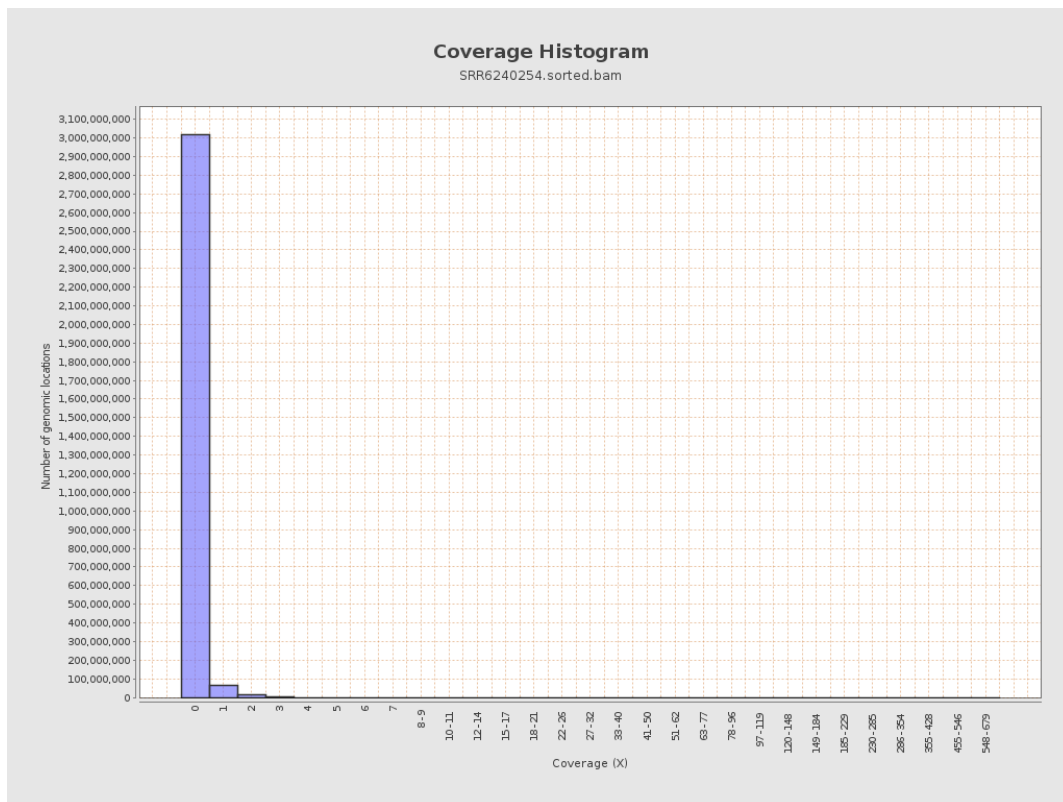
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	7732506	0.031	0.4348
chr2	243199373	12541324	0.0516	0.3852
chr3	198022430	7060018	0.0357	0.2393
chr4	191154276	6811253	0.0356	0.2463
chr5	180915260	5488074	0.0303	0.2214
chr6	171115067	5736710	0.0335	0.2776
chr7	159138663	6692702	0.0421	0.6511

chr8	146364022	6135233	0.0419	0.3946
chr9	141213431	3493368	0.0247	0.2721
chr10	135534747	4933116	0.0364	0.2783
chr11	135006516	4467862	0.0331	0.2921
chr12	133851895	5044252	0.0377	0.2468
chr13	115169878	1944037	0.0169	0.1634
chr14	107349540	3823886	0.0356	0.2496
chr15	102531392	2826555	0.0276	0.2242
chr16	90354753	3171085	0.0351	0.2389
chr17	81195210	2794668	0.0344	0.2517
chr18	78077248	2244785	0.0288	0.4245
chr19	59128983	1941061	0.0328	0.3346
chr20	63025520	2043999	0.0324	0.2332
chr21	48129895	1820974	0.0378	0.2523
chr22	51304566	921633	0.018	0.1645
chrMT	16571	51597	3.1137	3.7611
chrX	155270560	5377134	0.0346	0.2573
chrY	59373566	208840	0.0035	0.0763

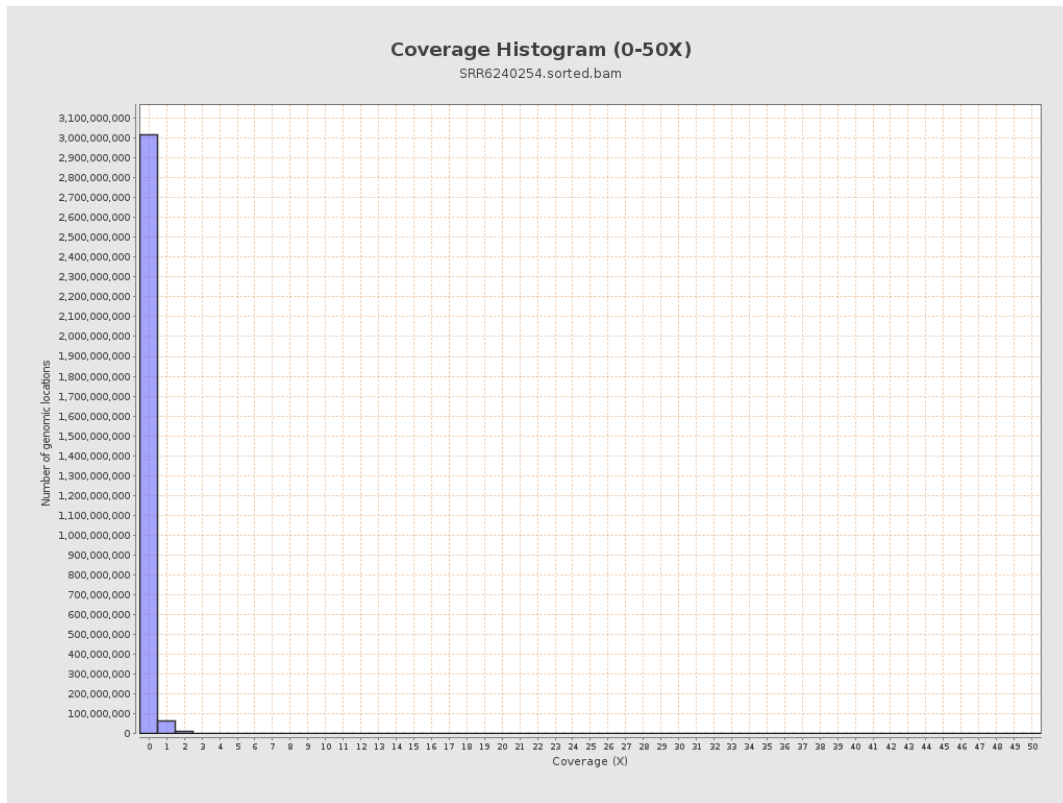
3. Results : Coverage across reference



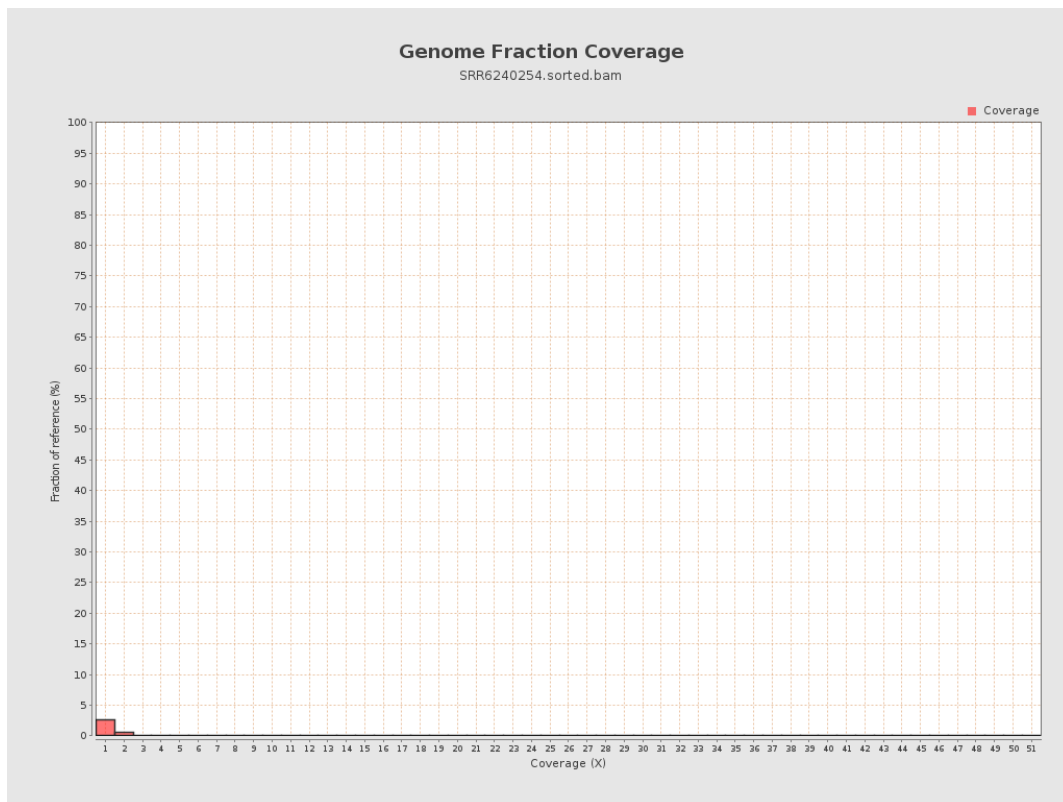
4. Results : Coverage Histogram



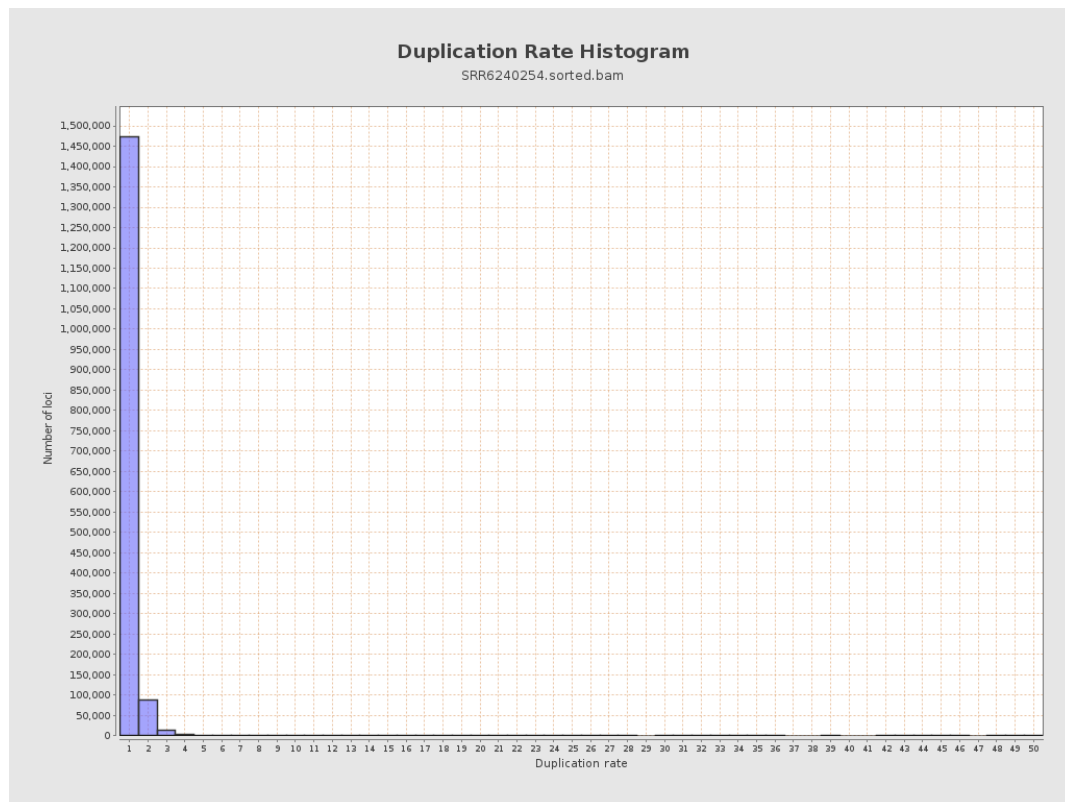
5. Results : Coverage Histogram (0-50X)



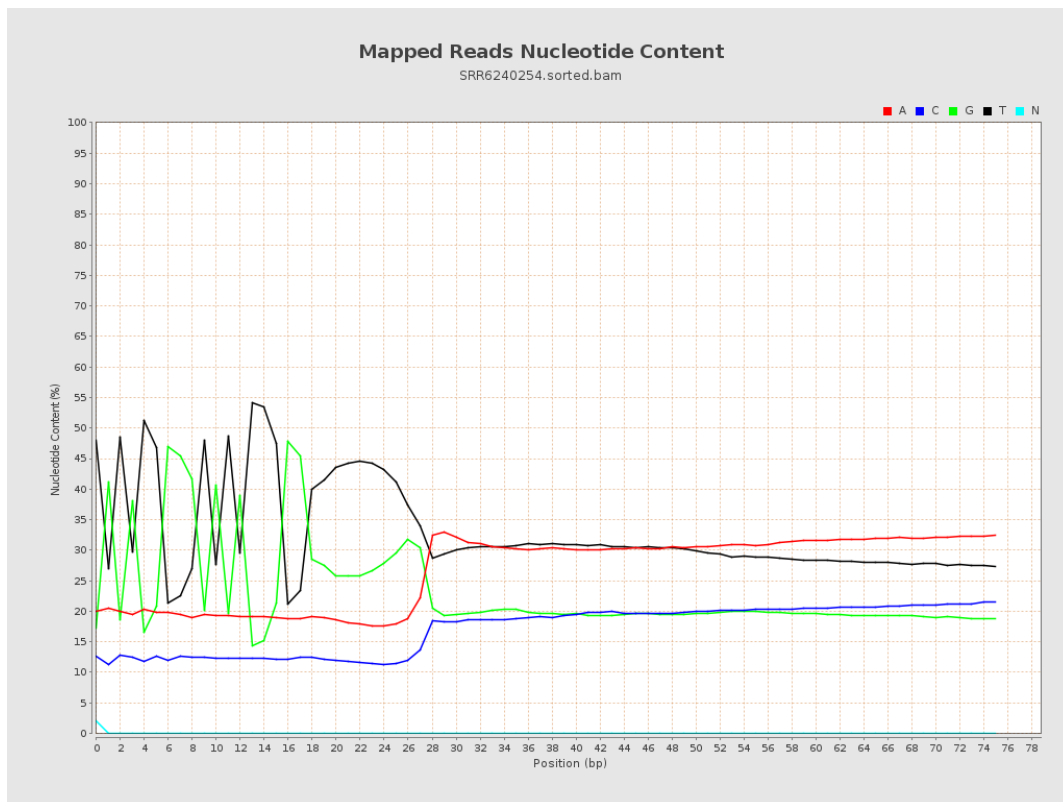
6. Results : Genome Fraction Coverage



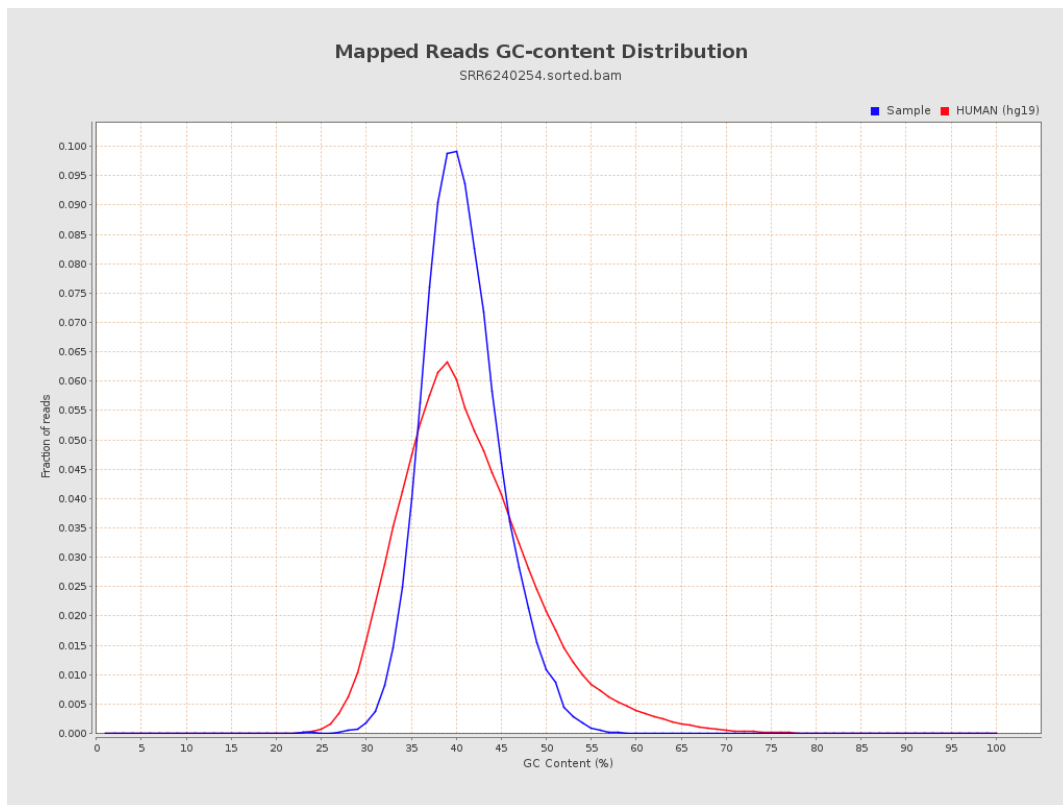
7. Results : Duplication Rate Histogram



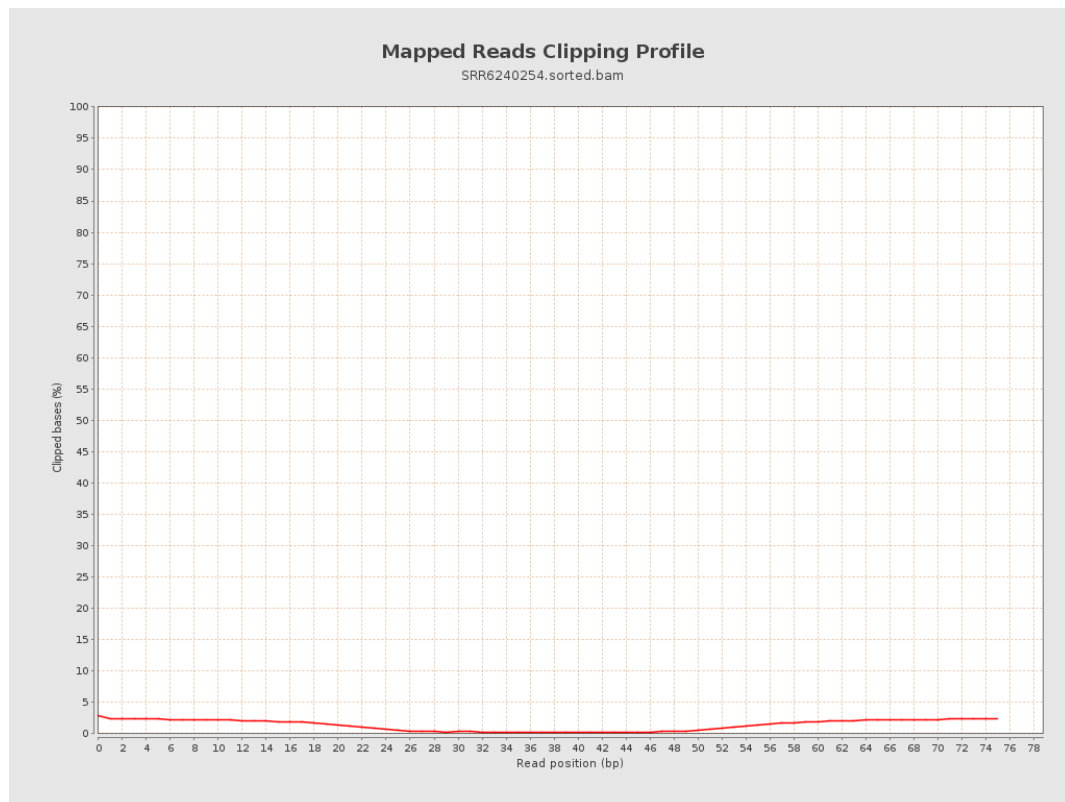
8. Results : Mapped Reads Nucleotide Content



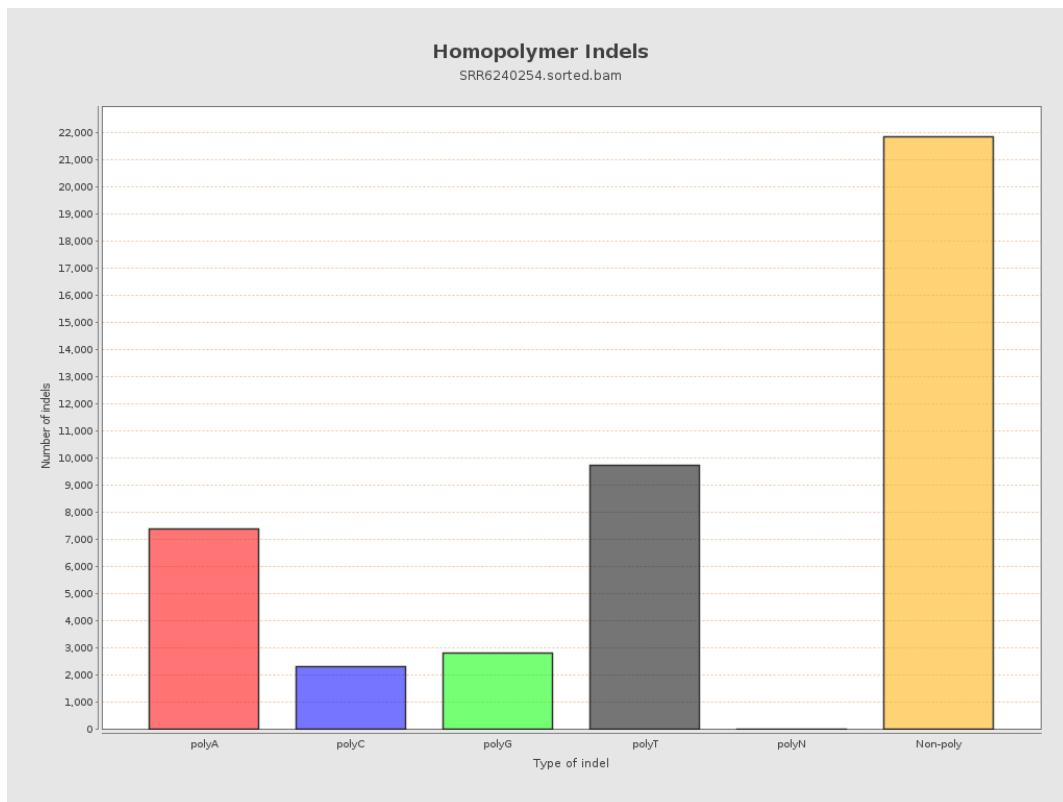
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

