

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 08:28:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240248.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_SRR6240248 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240248.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 08:28:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240248.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,945,352
Mapped reads	1,263,183 / 64.93%
Unmapped reads	682,169 / 35.07%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,099 / 0.62%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	268,121 / 13.78%
Duplication rate	13.96%
Clipped reads	705,406 / 36.26%

2.2. ACGT Content

Number/percentage of A's	22,350,570 / 27.64%
Number/percentage of C's	14,383,885 / 17.79%
Number/percentage of T's	26,349,499 / 32.59%
Number/percentage of G's	17,757,850 / 21.96%
Number/percentage of N's	7,027 / 0.01%
GC Percentage	39.76%

2.3. Coverage

Mean	0.0261

Standard Deviation	0.419
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2.4. Mapping Quality

Mean Mapping Quality	45.91
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2.5. Mismatches and indels

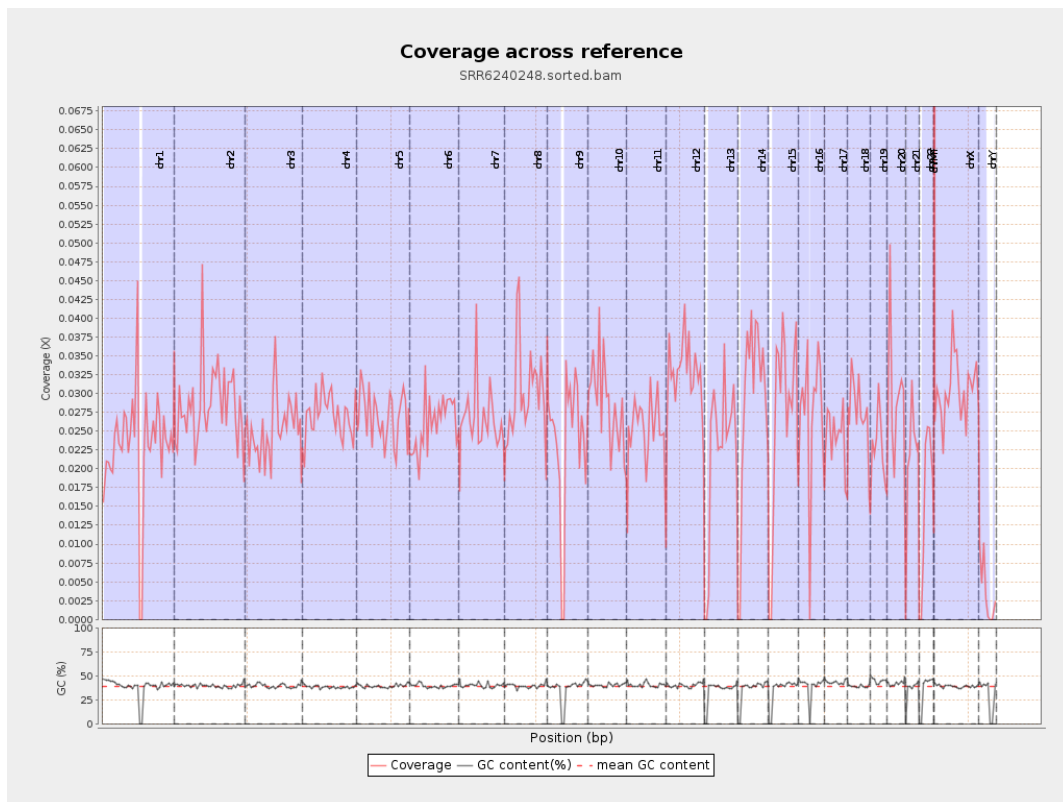
General error rate	0.85%
Mismatches	673,717
Insertions	5,573
Mapped reads with at least one insertion	0.44%
Deletions	21,100
Mapped reads with at least one deletion	1.65%
Homopolymer indels	48.38%

2.6. Chromosome stats

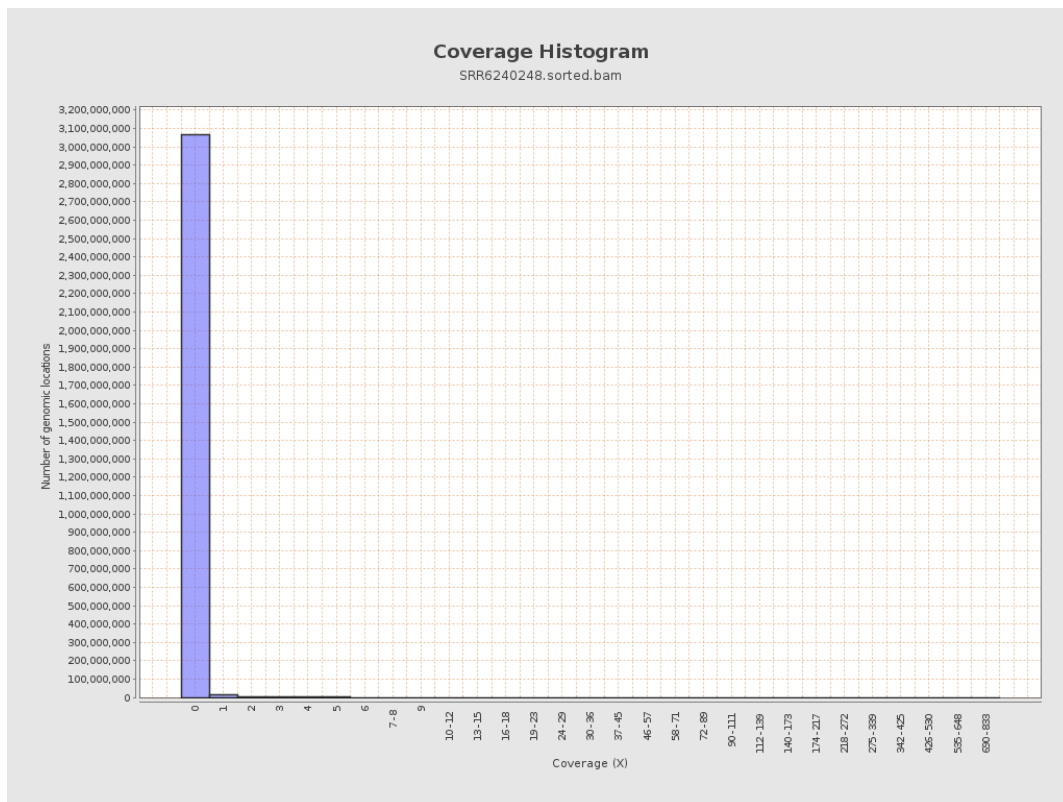
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	5758672	0.0231	0.5924
chr2	243199373	6918187	0.0284	0.4422
chr3	198022430	5007332	0.0253	0.3526
chr4	191154276	5154876	0.027	0.3587
chr5	180915260	4876835	0.027	0.3622
chr6	171115067	4444649	0.026	0.3653
chr7	159138663	4242466	0.0267	0.4288

chr8	146364022	4392469	0.03	0.6163
chr9	141213431	3336075	0.0236	0.3839
chr10	135534747	3855773	0.0284	0.3933
chr11	135006516	3452616	0.0256	0.3837
chr12	133851895	4376046	0.0327	0.4154
chr13	115169878	2552812	0.0222	0.3382
chr14	107349540	3107711	0.0289	0.3969
chr15	102531392	2768511	0.027	0.3789
chr16	90354753	2430142	0.0269	0.3601
chr17	81195210	1959935	0.0241	0.3367
chr18	78077248	2166822	0.0278	0.5504
chr19	59128983	1361089	0.023	0.4191
chr20	63025520	1859444	0.0295	0.4003
chr21	48129895	1054272	0.0219	0.3139
chr22	51304566	812692	0.0158	0.2552
chrMT	16571	32722	1.9747	3.1972
chrX	155270560	4751039	0.0306	0.3935
chrY	59373566	211143	0.0036	0.1145

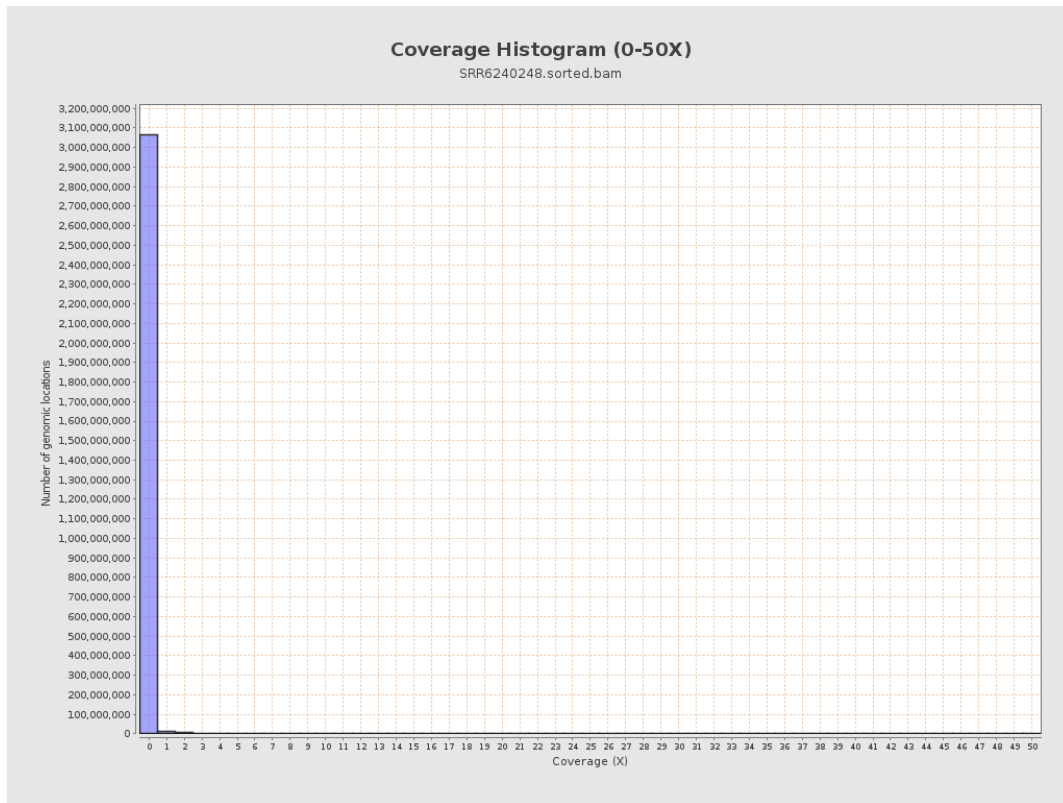
3. Results : Coverage across reference



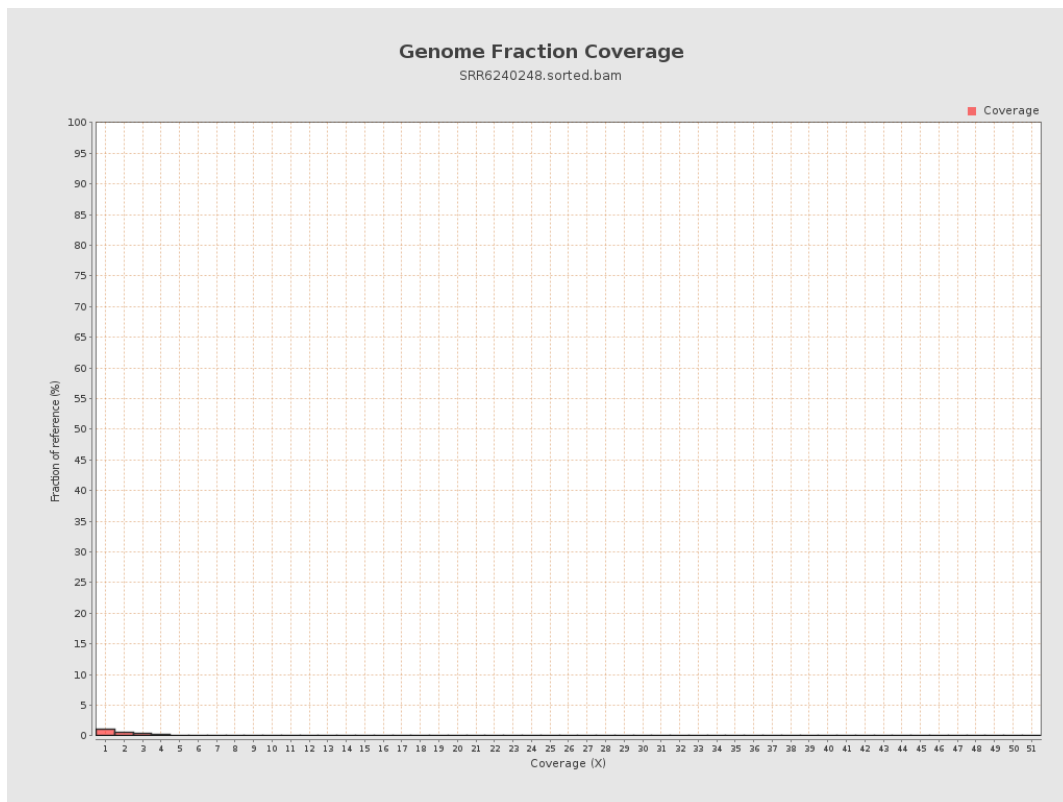
4. Results : Coverage Histogram



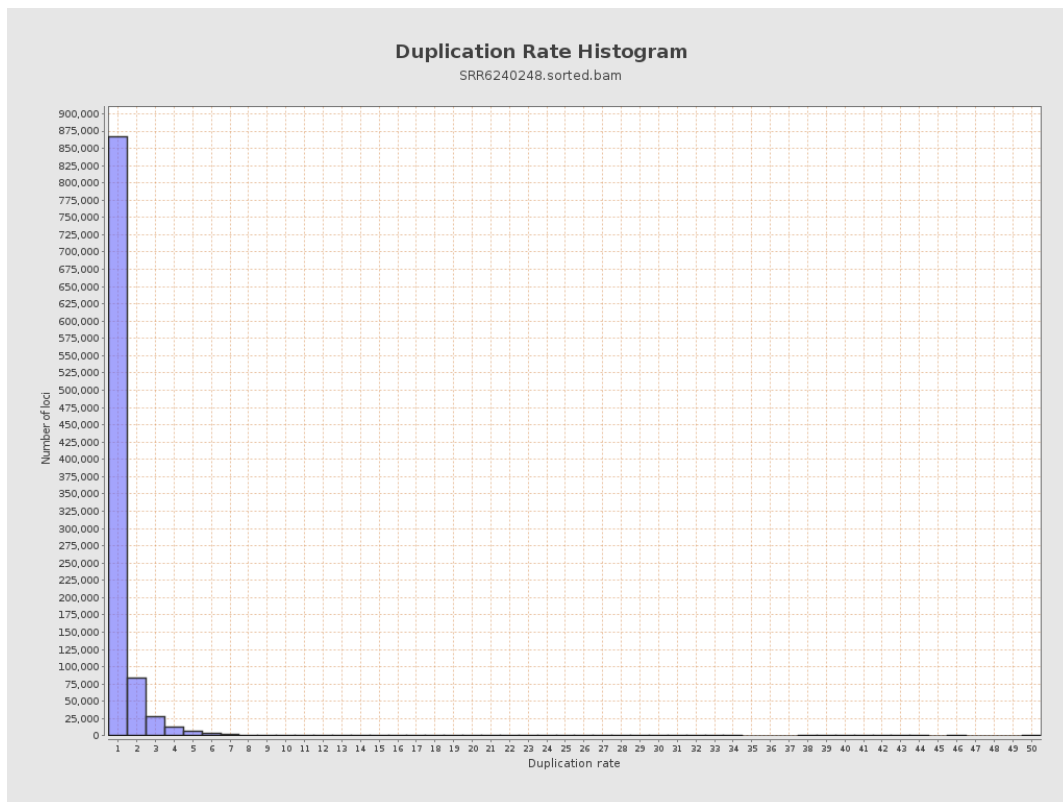
5. Results : Coverage Histogram (0-50X)



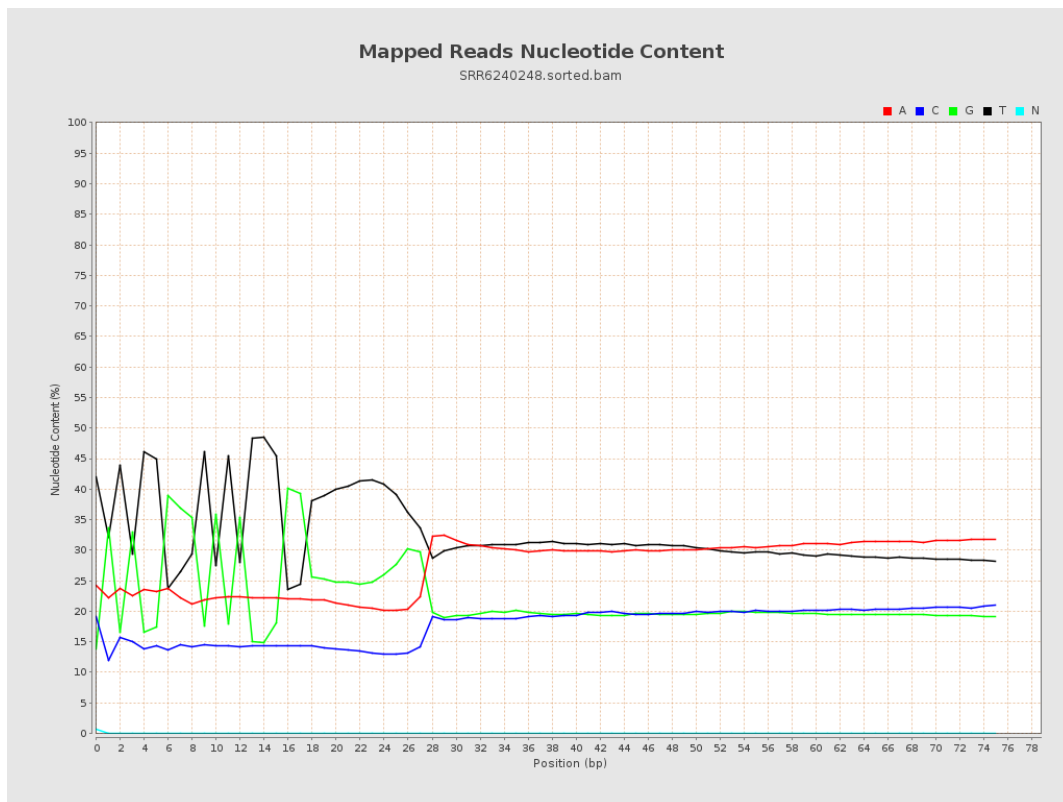
6. Results : Genome Fraction Coverage



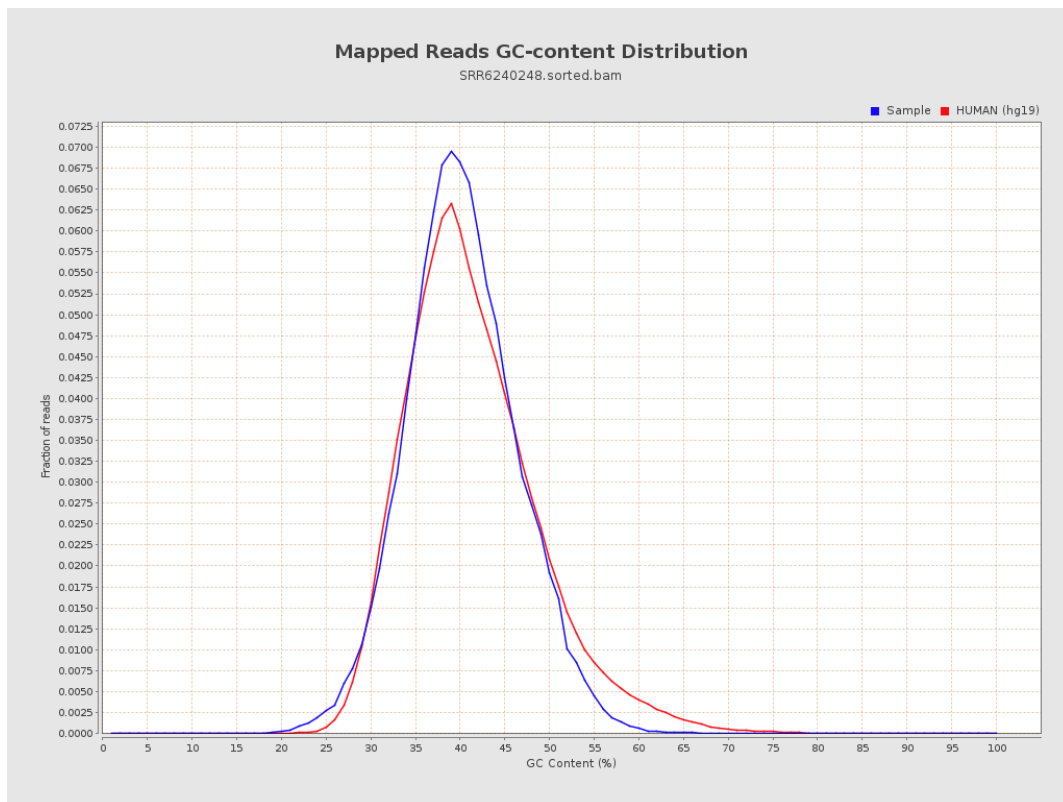
7. Results : Duplication Rate Histogram



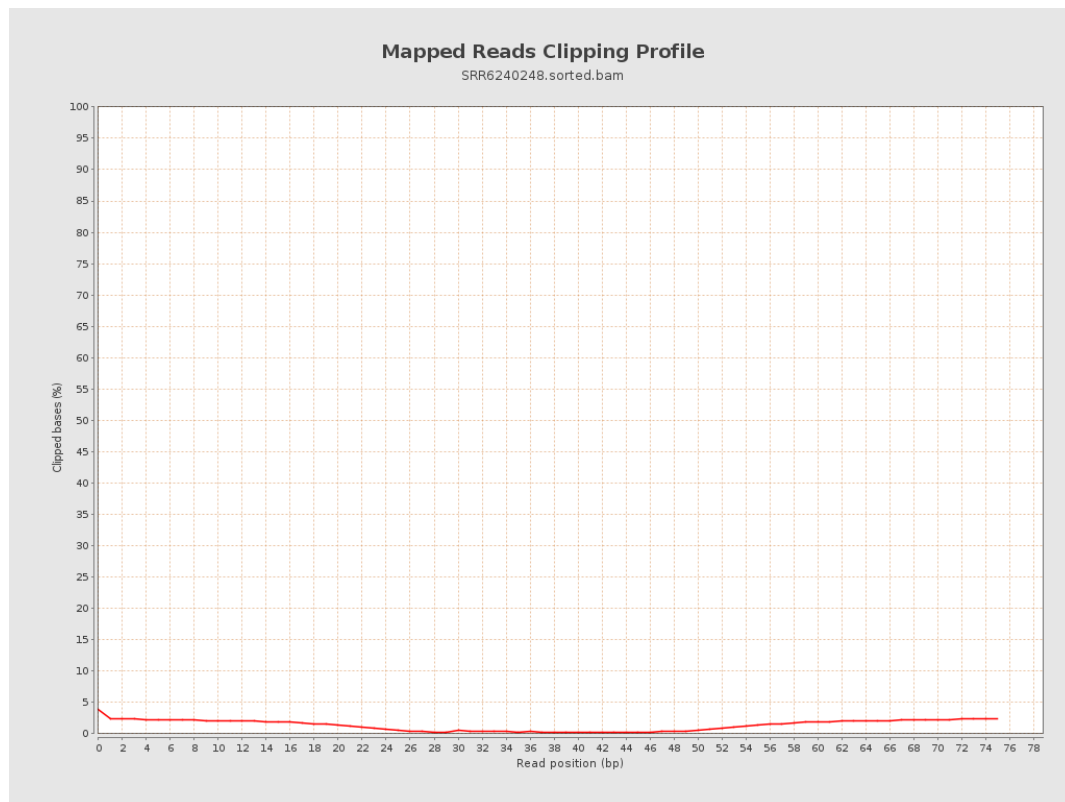
8. Results : Mapped Reads Nucleotide Content



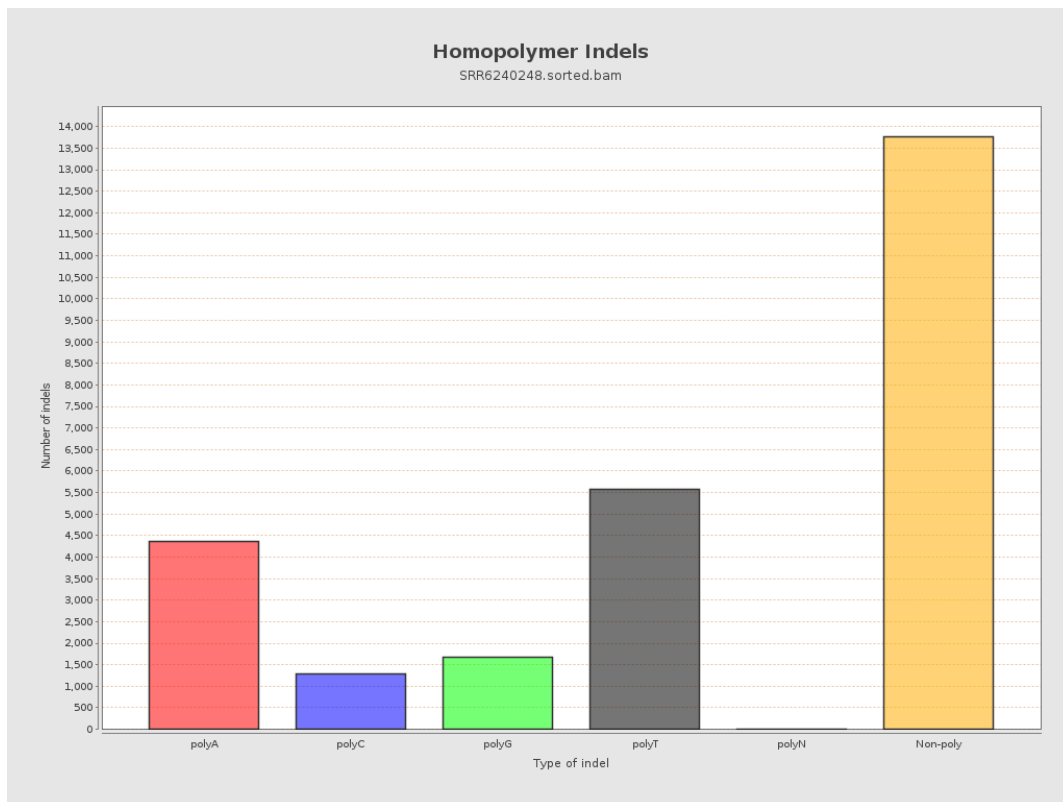
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

