

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 03:09:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240030.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_SRR6240030 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240030.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 03:09:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240030.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,972,037
Mapped reads	1,521,688 / 77.16%
Unmapped reads	450,349 / 22.84%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,256 / 0.62%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	228,824 / 11.6%
Duplication rate	11.33%
Clipped reads	755,351 / 38.3%

2.2. ACGT Content

Number/percentage of A's	27,630,186 / 27.72%
Number/percentage of C's	17,957,610 / 18.02%
Number/percentage of T's	32,418,788 / 32.53%
Number/percentage of G's	21,654,252 / 21.73%
Number/percentage of N's	9,460 / 0.01%
GC Percentage	39.74%

2.3. Coverage

Mean	0.0322

Standard Deviation	0.3894
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2.4. Mapping Quality

Mean Mapping Quality	46.66
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2.5. Mismatches and indels

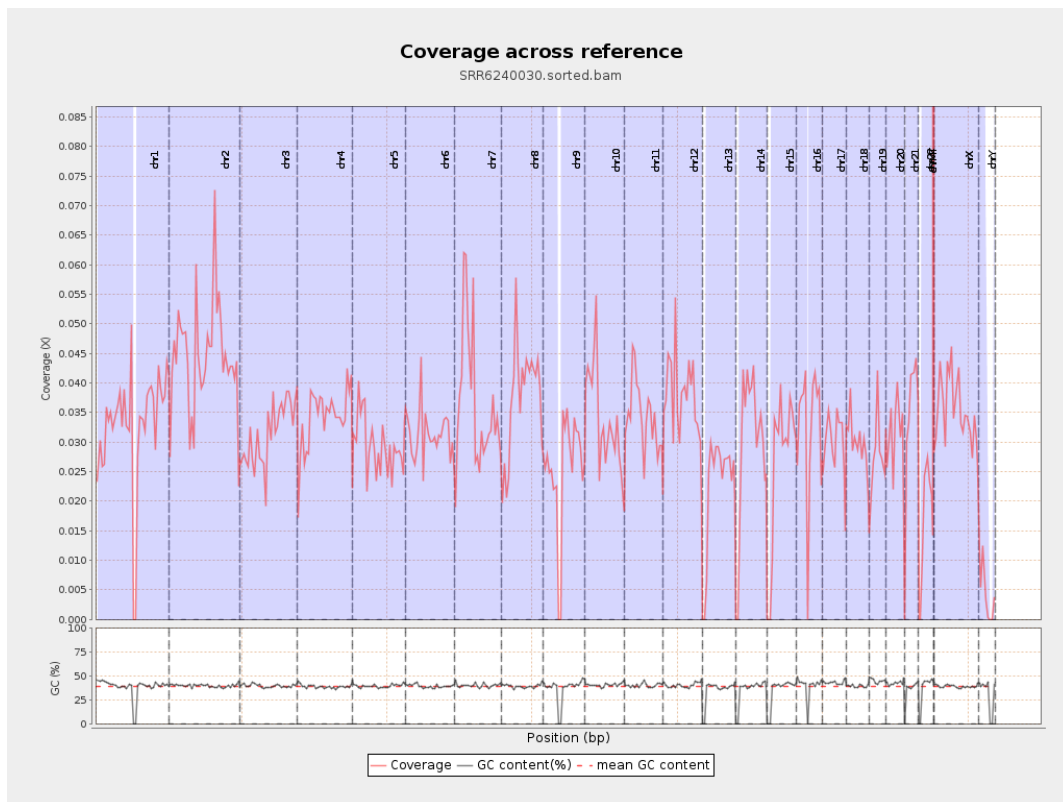
General error rate	0.87%
Mismatches	852,692
Insertions	7,169
Mapped reads with at least one insertion	0.47%
Deletions	28,090
Mapped reads with at least one deletion	1.82%
Homopolymer indels	48.88%

2.6. Chromosome stats

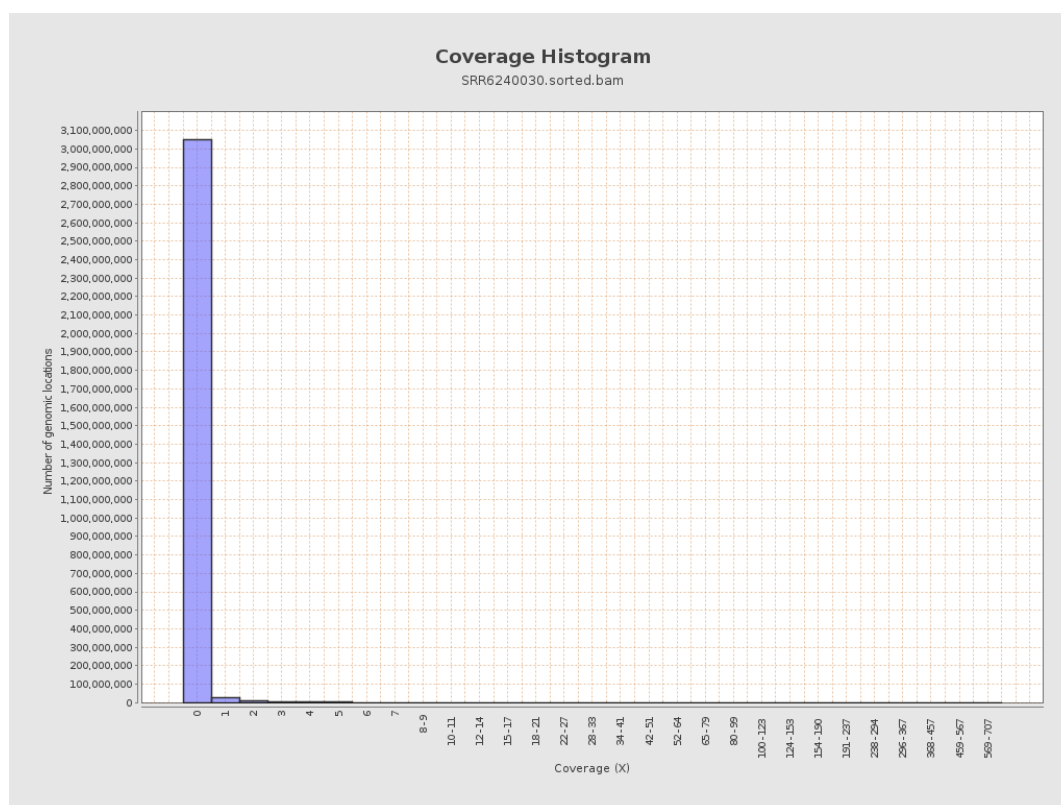
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	8183796	0.0328	0.5639
chr2	243199373	10814415	0.0445	0.4508
chr3	198022430	6190687	0.0313	0.3184
chr4	191154276	6530243	0.0342	0.3385
chr5	180915260	5297436	0.0293	0.3045
chr6	171115067	5358427	0.0313	0.3411
chr7	159138663	5844674	0.0367	0.5226

chr8	146364022	5486559	0.0375	0.5444
chr9	141213431	3591364	0.0254	0.324
chr10	135534747	4611009	0.034	0.3691
chr11	135006516	4596270	0.034	0.3707
chr12	133851895	5055919	0.0378	0.3539
chr13	115169878	2594121	0.0225	0.2716
chr14	107349540	3196364	0.0298	0.3134
chr15	102531392	2747698	0.0268	0.2932
chr16	90354753	2941139	0.0326	0.3187
chr17	81195210	2408428	0.0297	0.317
chr18	78077248	2360720	0.0302	0.4734
chr19	59128983	1652308	0.0279	0.4093
chr20	63025520	1974999	0.0313	0.3159
chr21	48129895	1660135	0.0345	0.3375
chr22	51304566	850748	0.0166	0.2193
chrMT	16571	21153	1.2765	2.1417
chrX	155270560	5497203	0.0354	0.348
chrY	59373566	254003	0.0043	0.1122

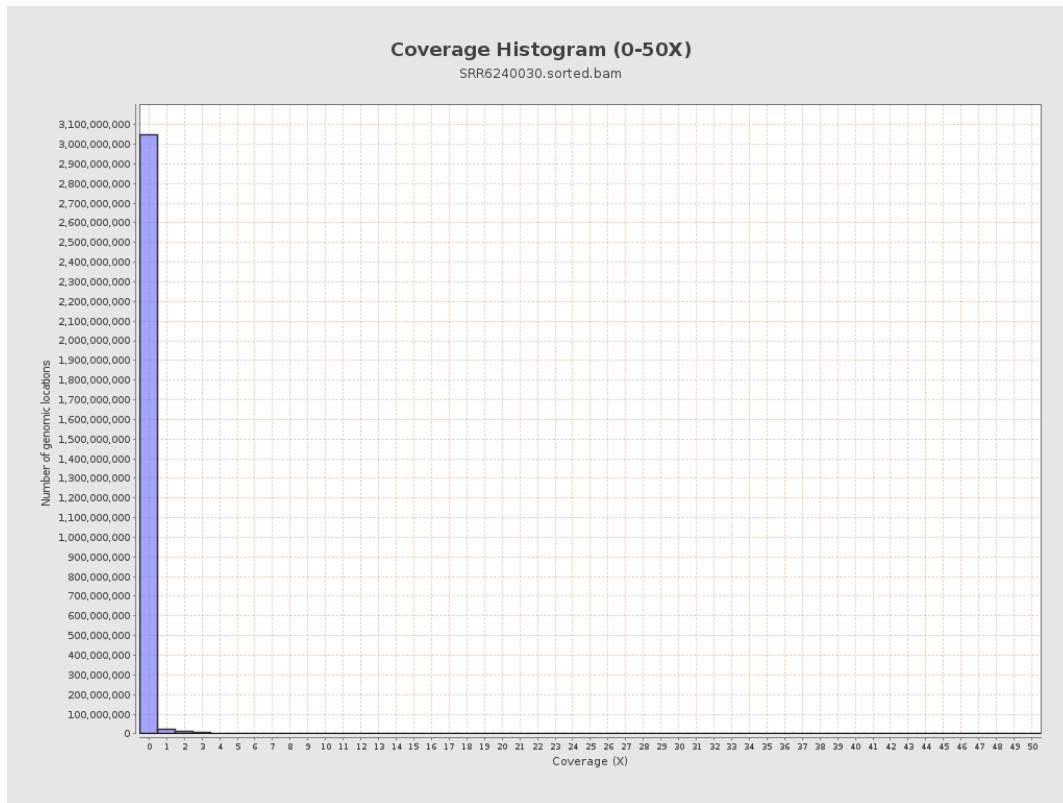
3. Results : Coverage across reference



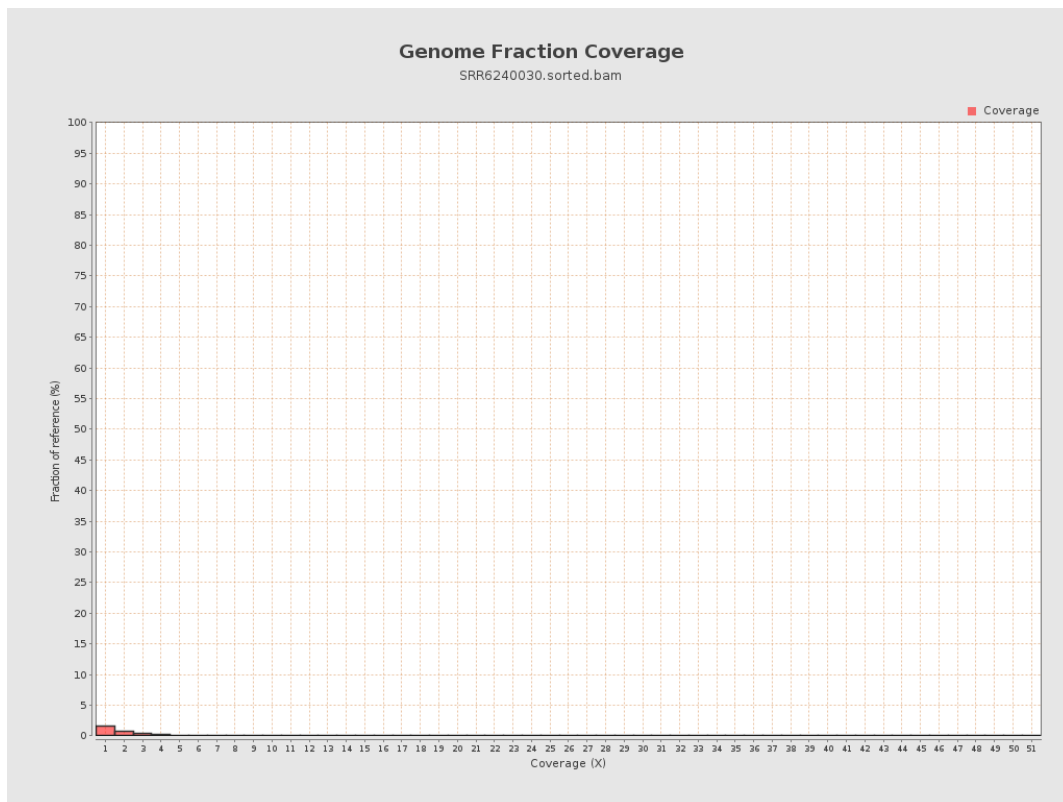
4. Results : Coverage Histogram



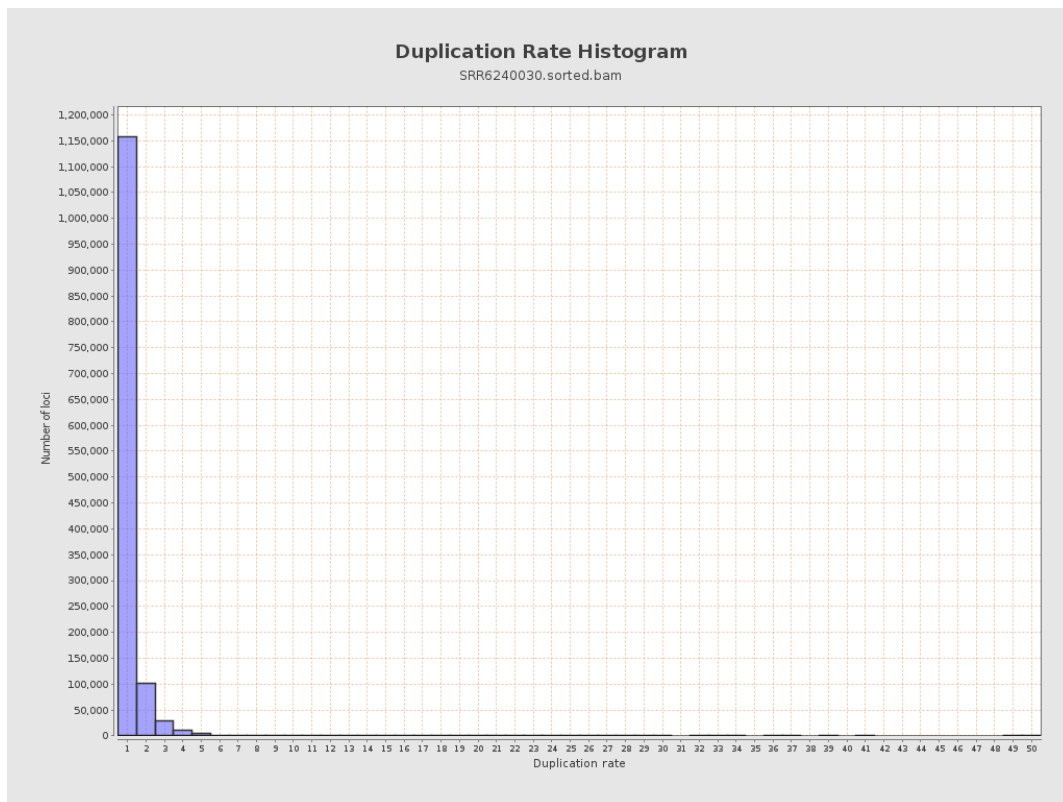
5. Results : Coverage Histogram (0-50X)



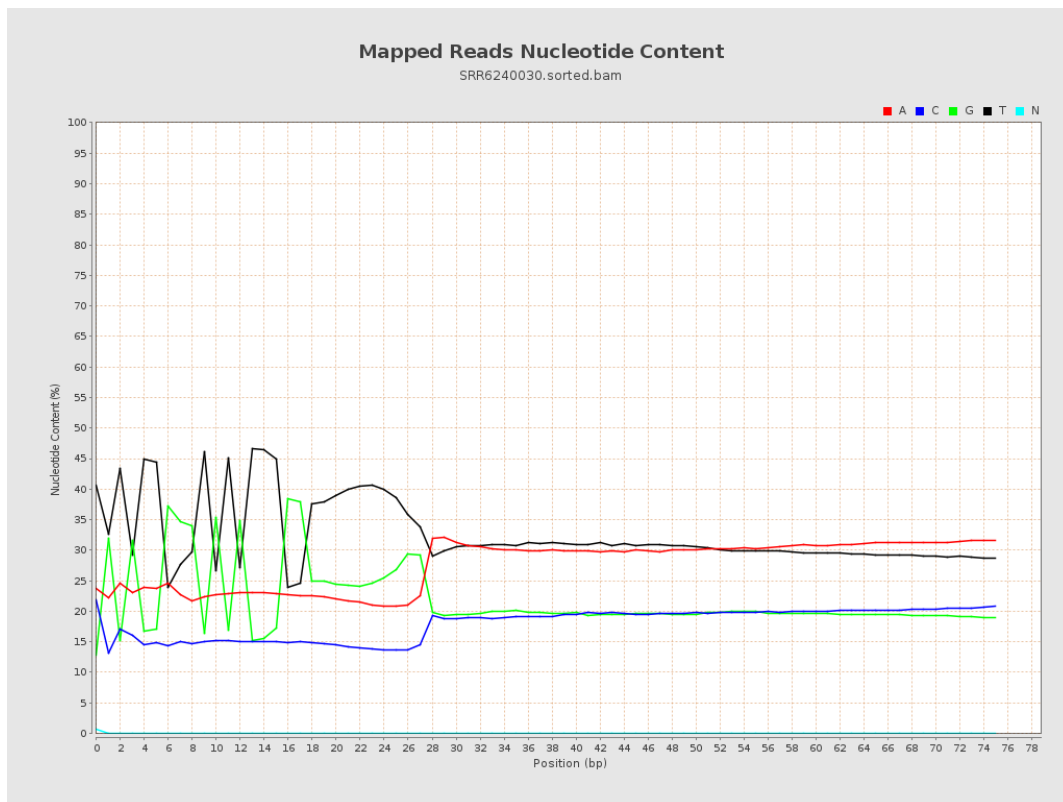
6. Results : Genome Fraction Coverage



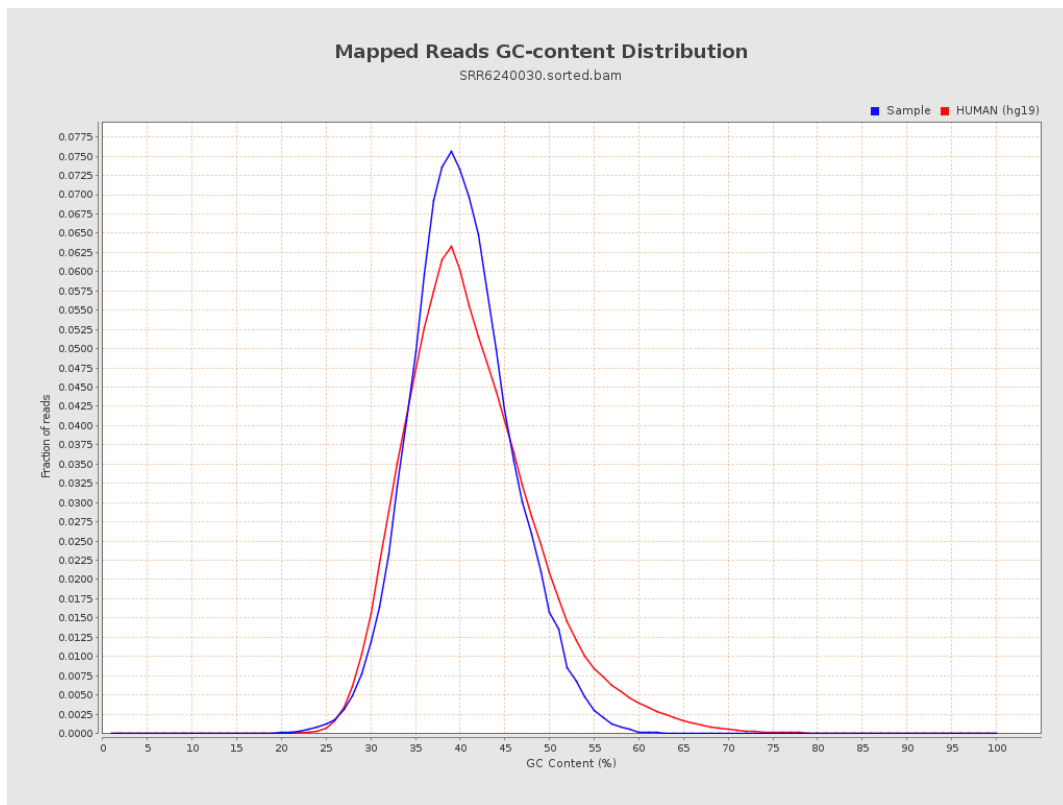
7. Results : Duplication Rate Histogram



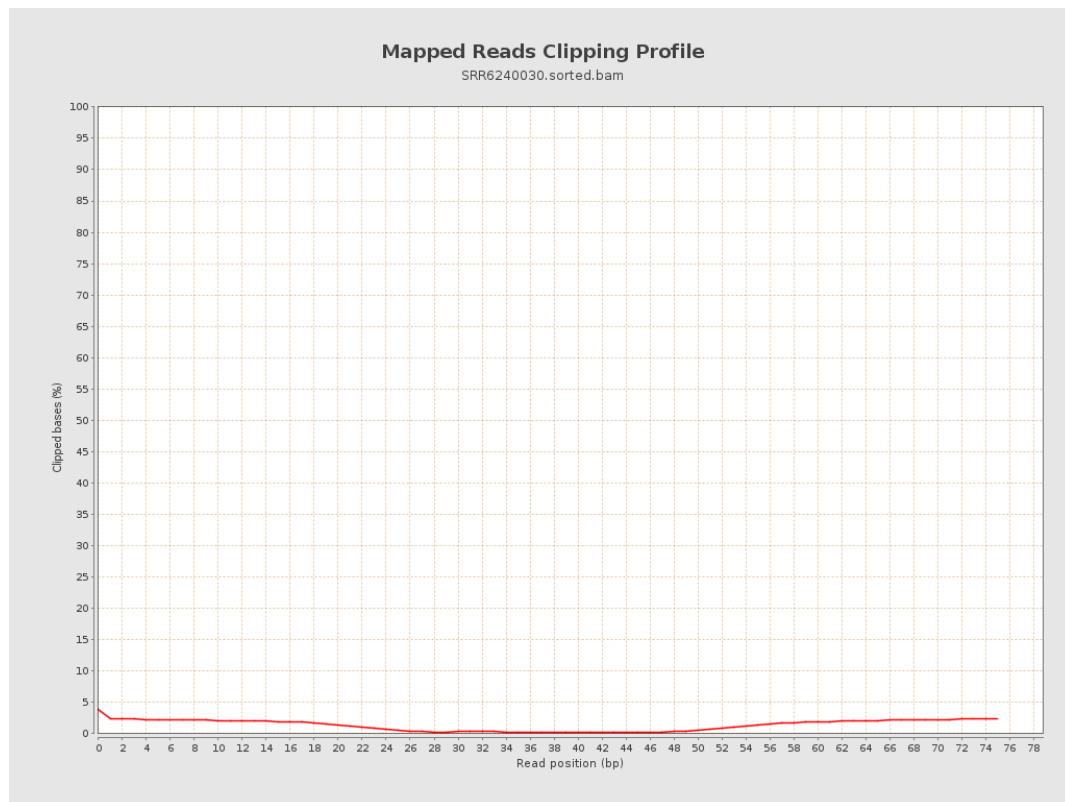
8. Results : Mapped Reads Nucleotide Content



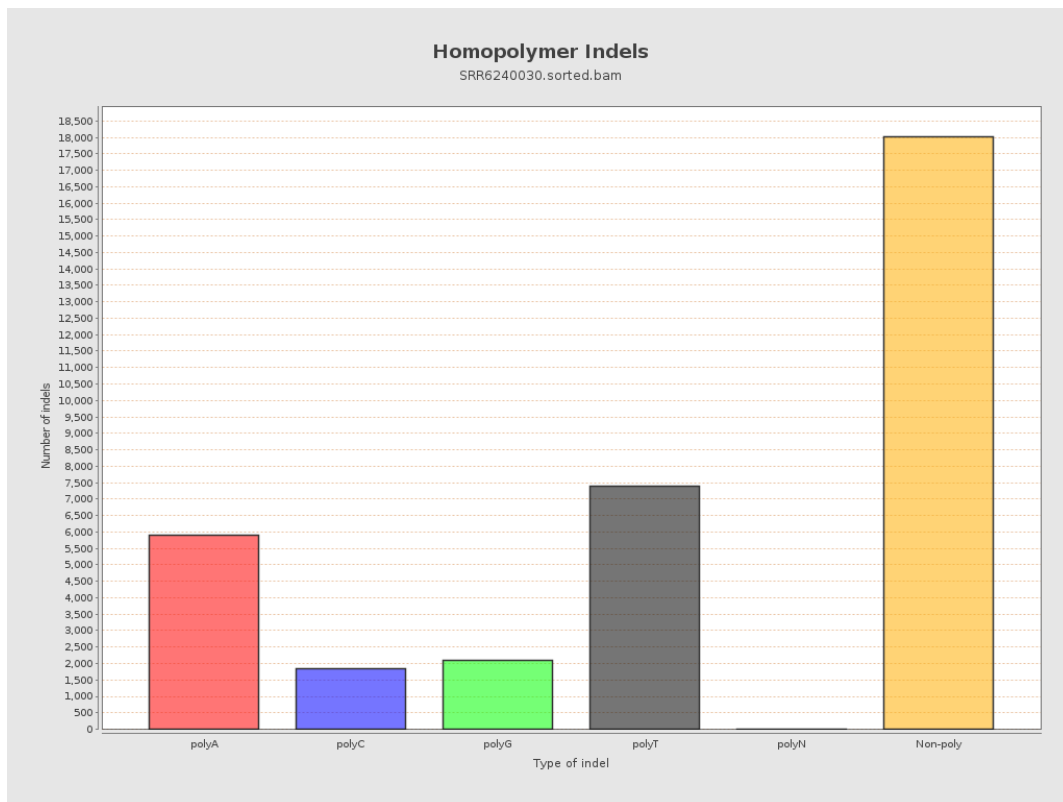
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

