

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 11:13:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234029.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_SRR6234029 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234029.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 11:13:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234029.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,714,189
Mapped reads	1,293,956 / 75.49%
Unmapped reads	420,233 / 24.51%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,893 / 0.34%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	41,790 / 2.44%
Duplication rate	2.53%
Clipped reads	554,927 / 32.37%

2.2. ACGT Content

Number/percentage of A's	24,184,692 / 28.2%
Number/percentage of C's	14,893,218 / 17.36%
Number/percentage of T's	27,571,959 / 32.15%
Number/percentage of G's	19,107,905 / 22.28%
Number/percentage of N's	15,899 / 0.02%
GC Percentage	39.64%

2.3. Coverage

Mean	0.0277

Standard Deviation	0.2553
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2.4. Mapping Quality

Mean Mapping Quality	46.71
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2.5. Mismatches and indels

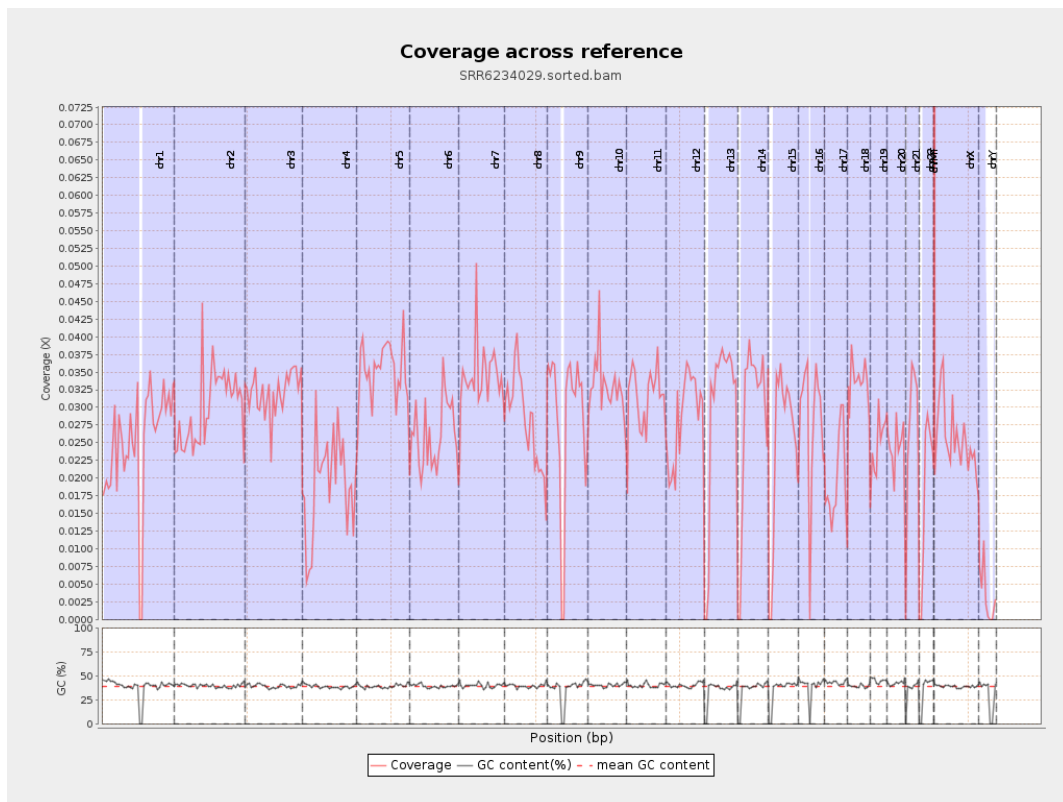
General error rate	0.84%
Mismatches	705,184
Insertions	6,773
Mapped reads with at least one insertion	0.52%
Deletions	23,772
Mapped reads with at least one deletion	1.82%
Homopolymer indels	46.4%

2.6. Chromosome stats

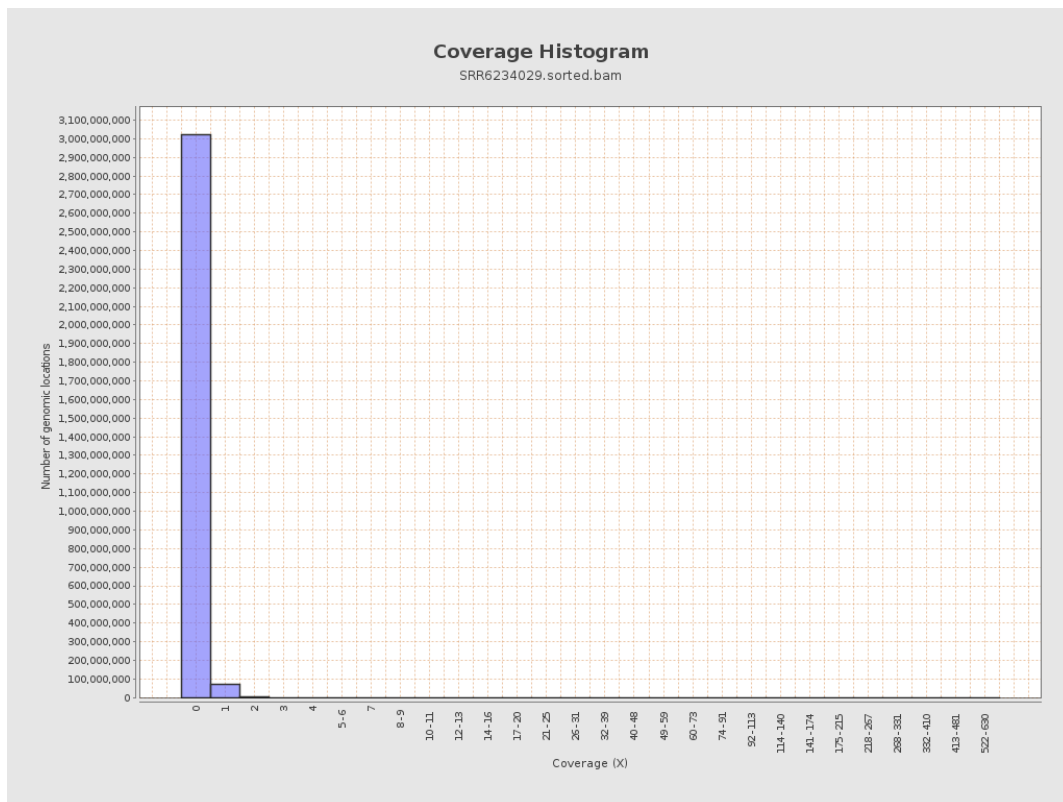
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	6268067	0.0251	0.3619
chr2	243199373	7289056	0.03	0.2881
chr3	198022430	6364180	0.0321	0.1961
chr4	191154276	3658700	0.0191	0.1624
chr5	180915260	6411577	0.0354	0.2065
chr6	171115067	4458493	0.0261	0.1971
chr7	159138663	5480923	0.0344	0.3486

chr8	146364022	4127610	0.0282	0.4231
chr9	141213431	4036093	0.0286	0.2392
chr10	135534747	4452819	0.0329	0.2453
chr11	135006516	4284071	0.0317	0.2309
chr12	133851895	3810966	0.0285	0.1863
chr13	115169878	3373394	0.0293	0.1873
chr14	107349540	3060326	0.0285	0.1952
chr15	102531392	2530682	0.0247	0.1754
chr16	90354753	2496107	0.0276	0.196
chr17	81195210	1583887	0.0195	0.1554
chr18	78077248	2629126	0.0337	0.4549
chr19	59128983	1473335	0.0249	0.2686
chr20	63025520	1528368	0.0242	0.1785
chr21	48129895	1317272	0.0274	0.1907
chr22	51304566	942807	0.0184	0.1473
chrMT	16571	51309	3.0963	2.5692
chrX	155270560	3986098	0.0257	0.188
chrY	59373566	200518	0.0034	0.0913

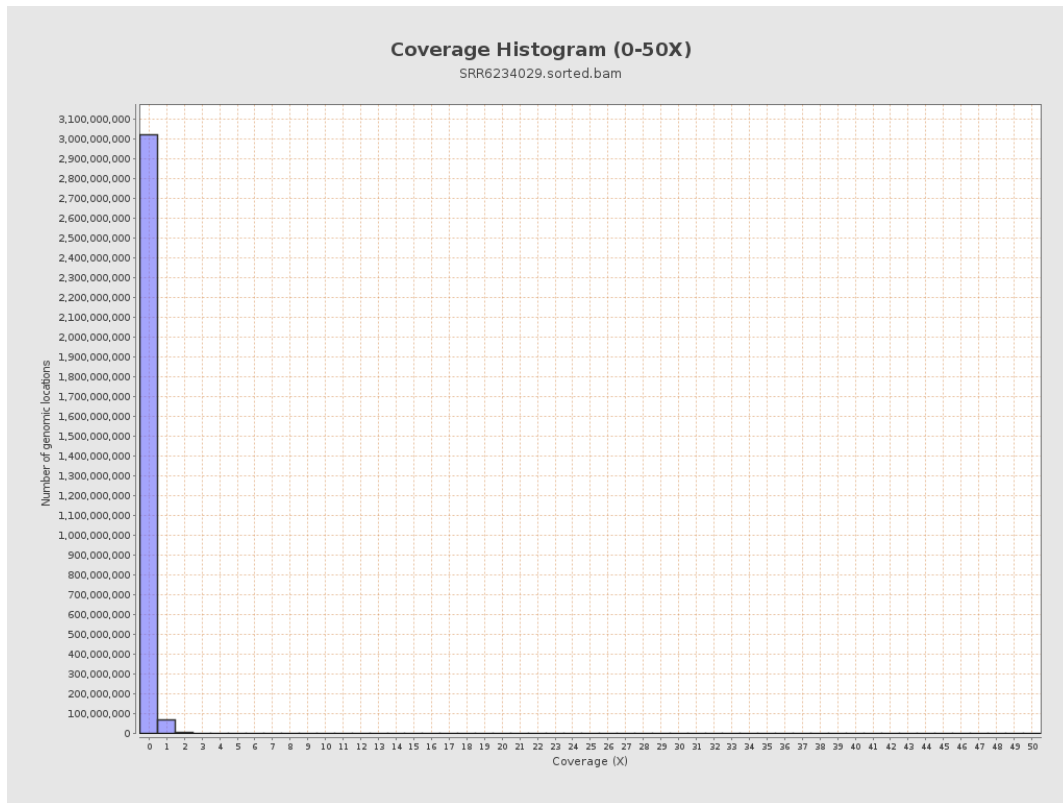
3. Results : Coverage across reference



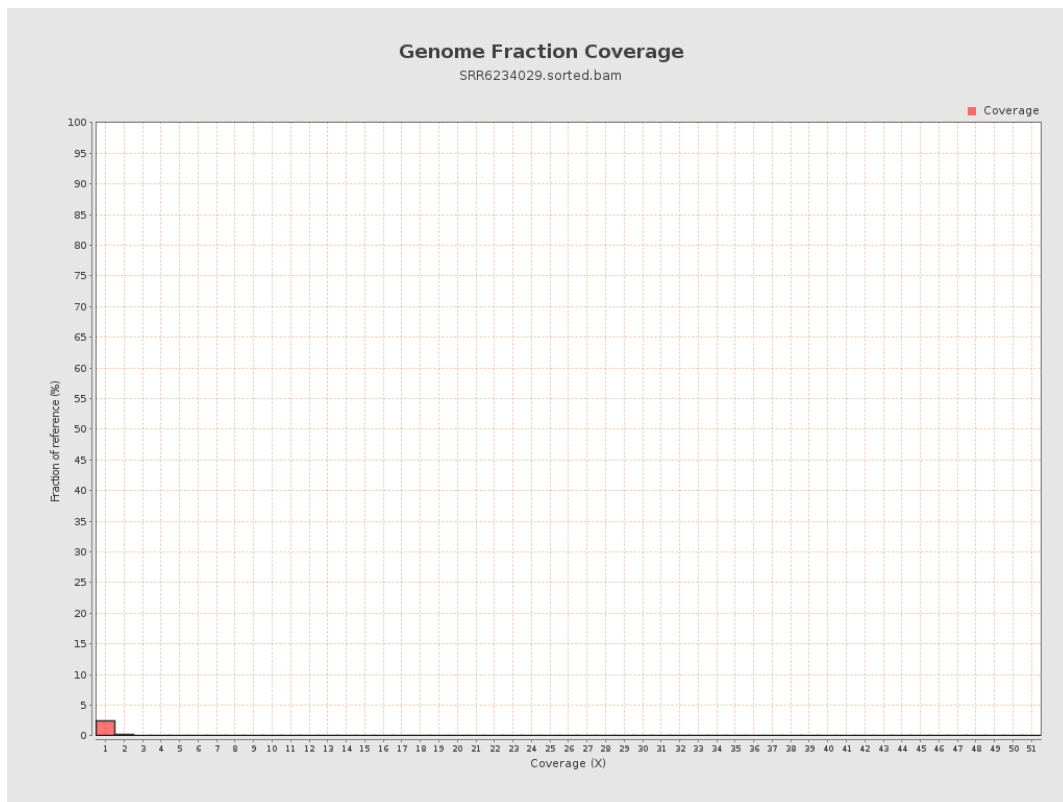
4. Results : Coverage Histogram



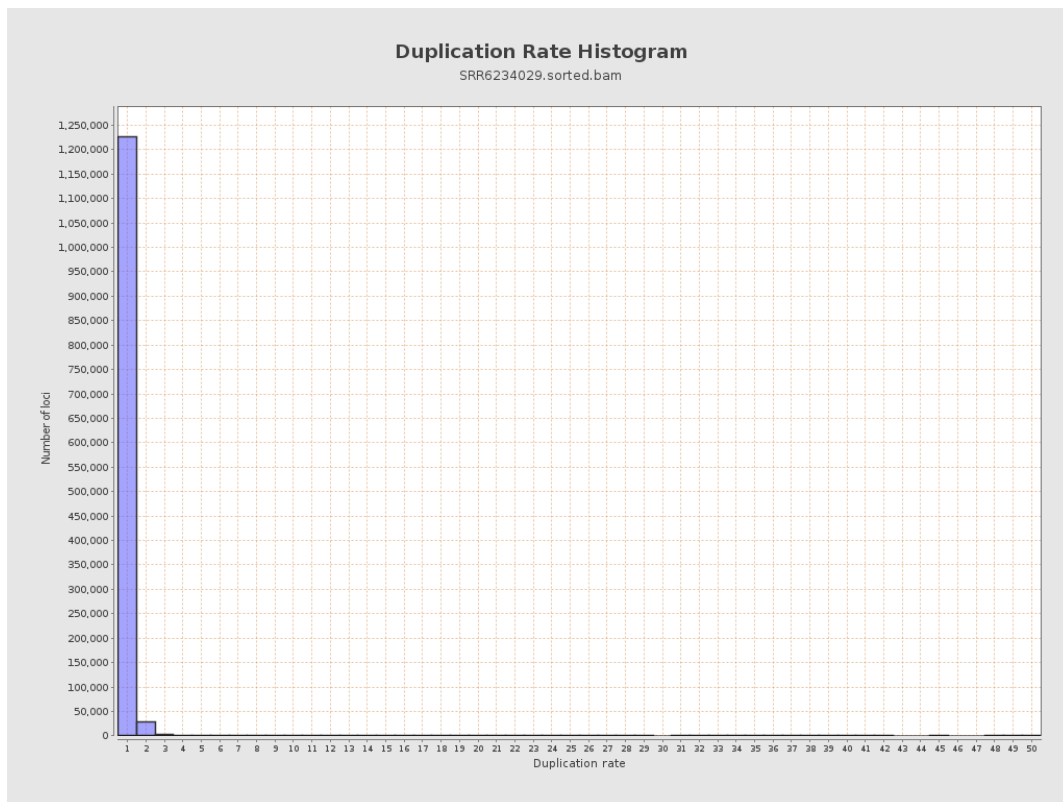
5. Results : Coverage Histogram (0-50X)



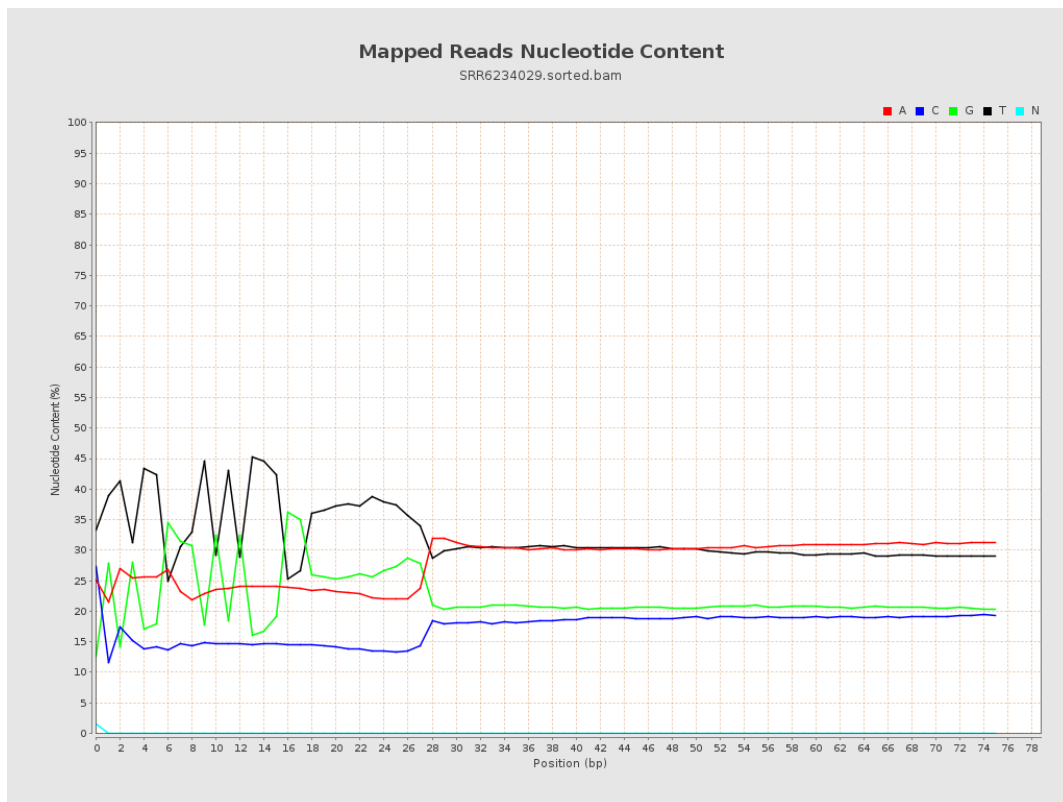
6. Results : Genome Fraction Coverage



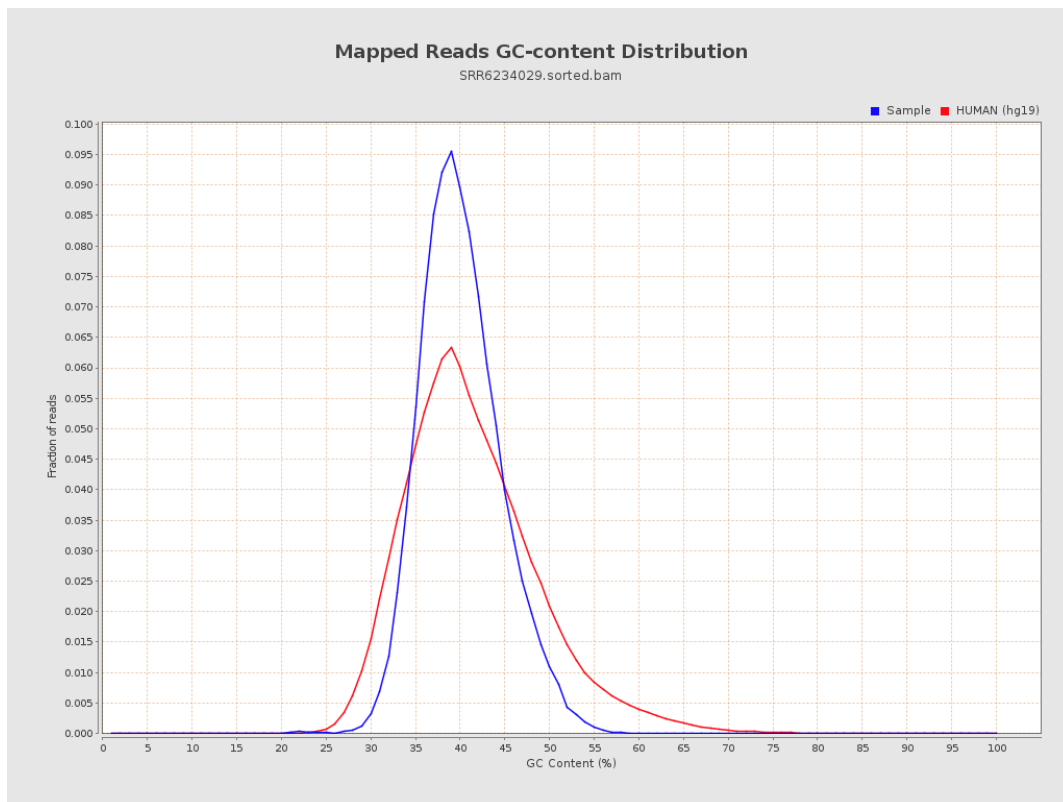
7. Results : Duplication Rate Histogram



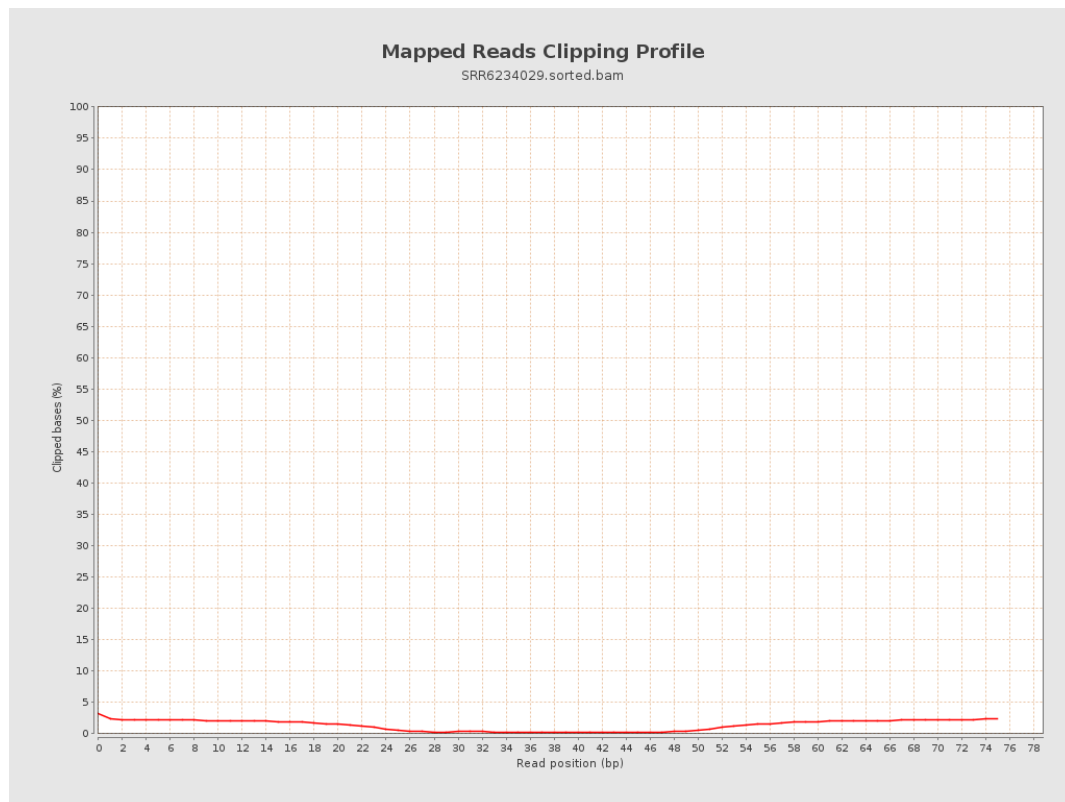
8. Results : Mapped Reads Nucleotide Content



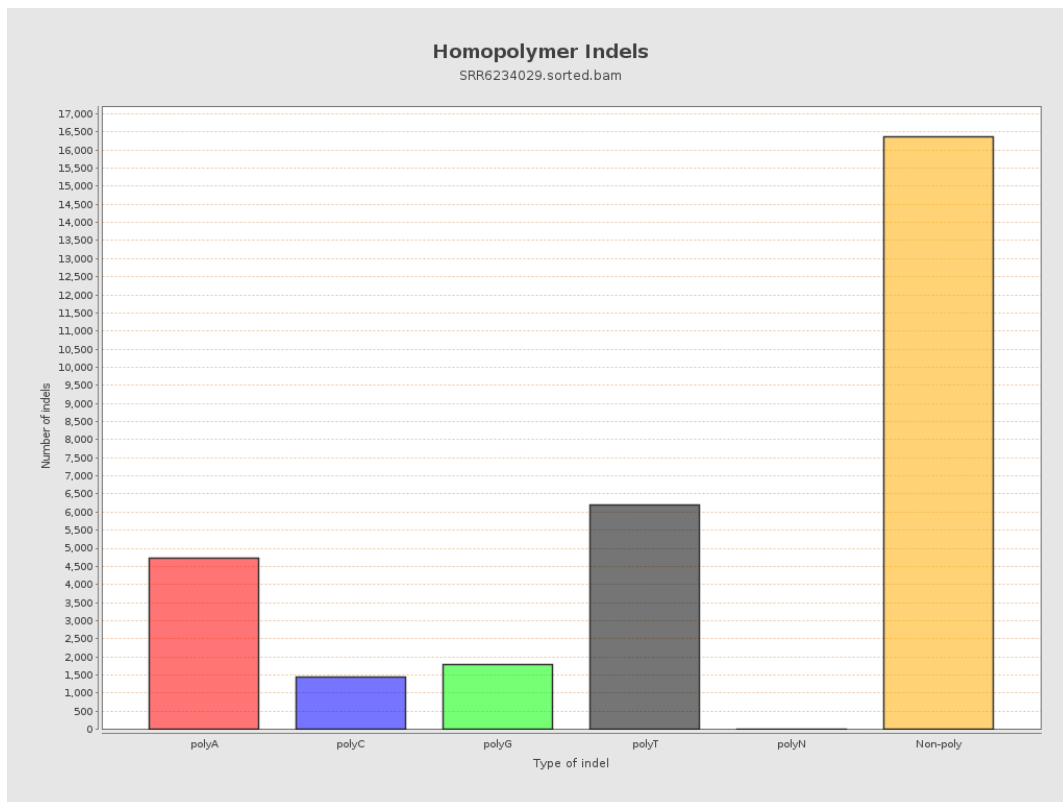
9. Results : Mapped Reads GC-content Distribution



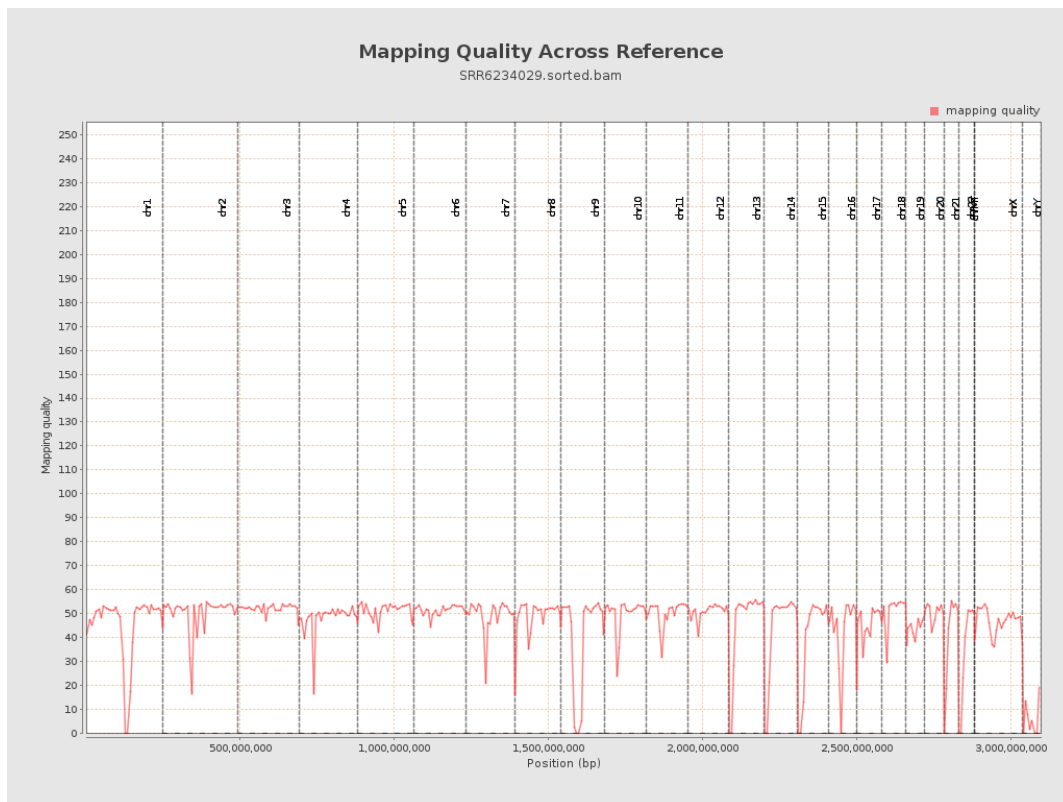
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

