

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 13:51:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234070.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_SRR6234070 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234070.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 13:51:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234070.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,398,467
Mapped reads	6,026,198 / 94.18%
Unmapped reads	372,269 / 5.82%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	43,607 / 0.68%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	800,580 / 12.51%
Duplication rate	11.1%
Clipped reads	3,160,351 / 49.39%

2.2. ACGT Content

Number/percentage of A's	100,903,786 / 25.95%
Number/percentage of C's	70,911,475 / 18.24%
Number/percentage of T's	125,449,500 / 32.27%
Number/percentage of G's	91,498,469 / 23.53%
Number/percentage of N's	39,026 / 0.01%
GC Percentage	41.77%

2.3. Coverage

Mean	0.1256

Standard Deviation	1.2242
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2.4. Mapping Quality

Mean Mapping Quality	44.57
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2.5. Mismatches and indels

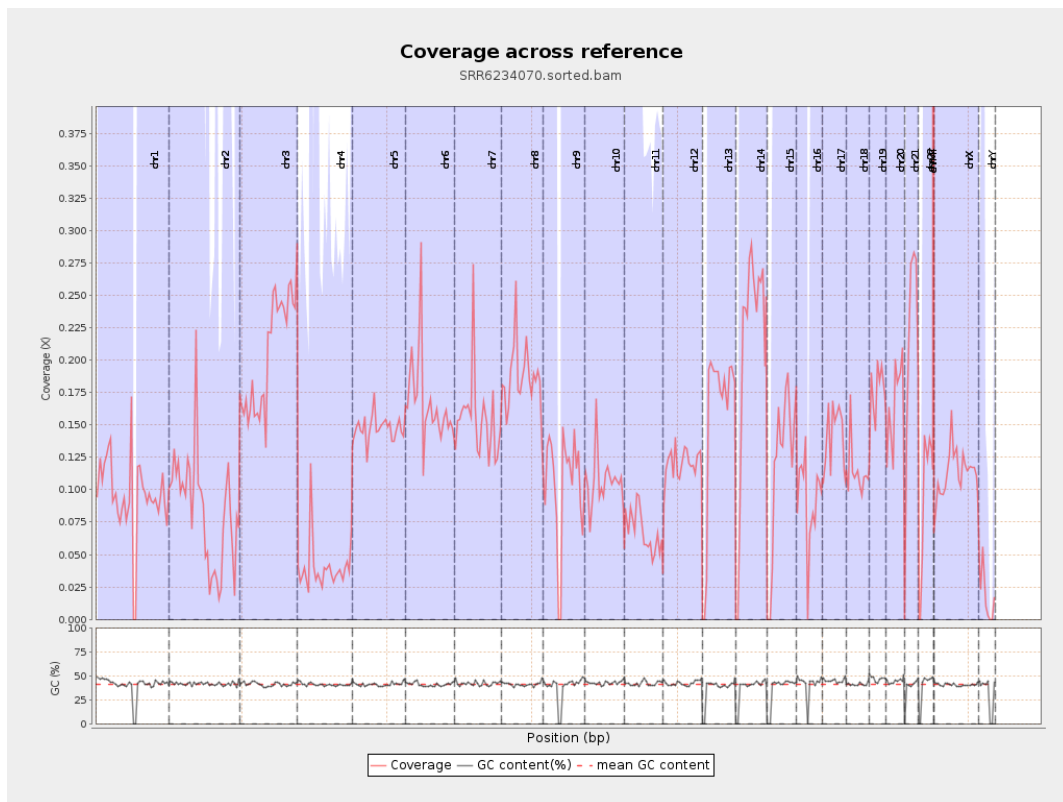
General error rate	0.57%
Mismatches	2,150,310
Insertions	25,407
Mapped reads with at least one insertion	0.42%
Deletions	86,579
Mapped reads with at least one deletion	1.42%
Homopolymer indels	44.38%

2.6. Chromosome stats

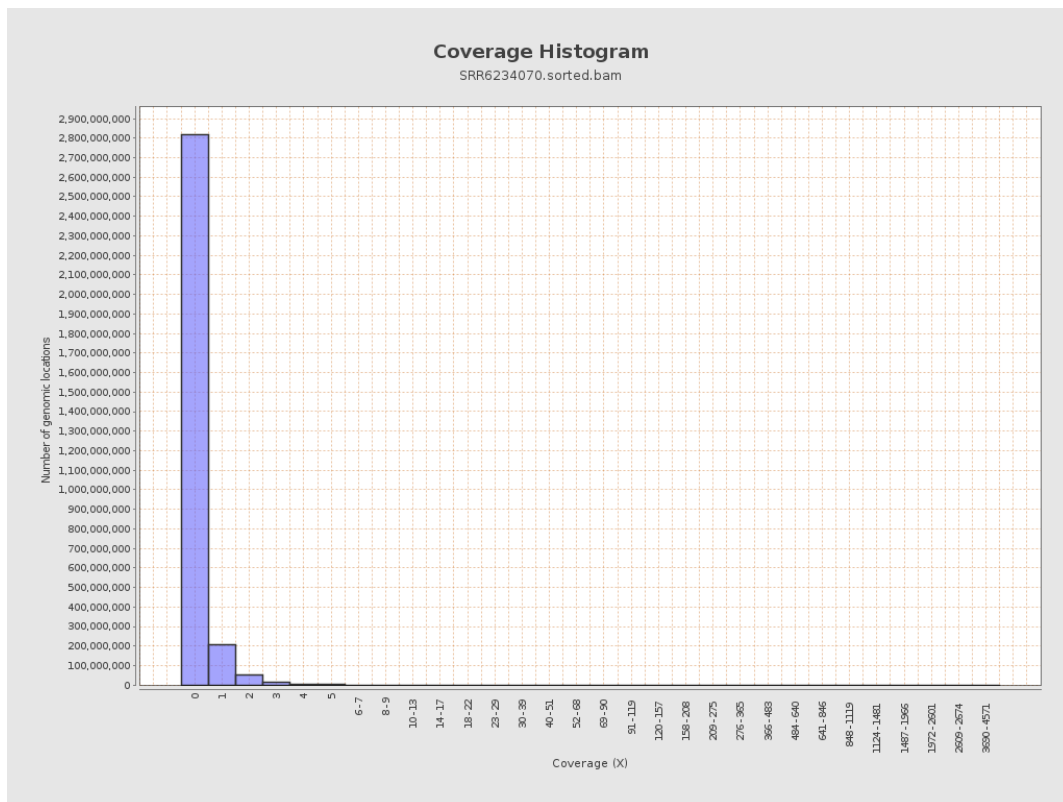
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	23823213	0.0956	2.1517
chr2	243199373	20206404	0.0831	2.1612
chr3	198022430	40363796	0.2038	0.6019
chr4	191154276	7542514	0.0395	0.3992
chr5	180915260	26640569	0.1473	0.527
chr6	171115067	28660515	0.1675	1.0006
chr7	159138663	24622747	0.1547	1.7888

chr8	146364022	27227707	0.186	1.4869
chr9	141213431	14678622	0.1039	0.9437
chr10	135534747	14393977	0.1062	0.9066
chr11	135006516	9094726	0.0674	0.824
chr12	133851895	16048319	0.1199	0.4996
chr13	115169878	17913019	0.1555	0.5786
chr14	107349540	22396493	0.2086	0.6841
chr15	102531392	12222283	0.1192	0.5077
chr16	90354753	8376359	0.0927	0.5986
chr17	81195210	11402658	0.1404	0.6151
chr18	78077248	8907509	0.1141	2.3429
chr19	59128983	10368094	0.1753	1.2528
chr20	63025520	10448705	0.1658	0.6342
chr21	48129895	10181955	0.2116	0.6817
chr22	51304566	4774060	0.0931	0.3929
chrMT	16571	138015	8.3287	5.8488
chrX	155270560	17484049	0.1126	0.6201
chrY	59373566	1037747	0.0175	0.3414

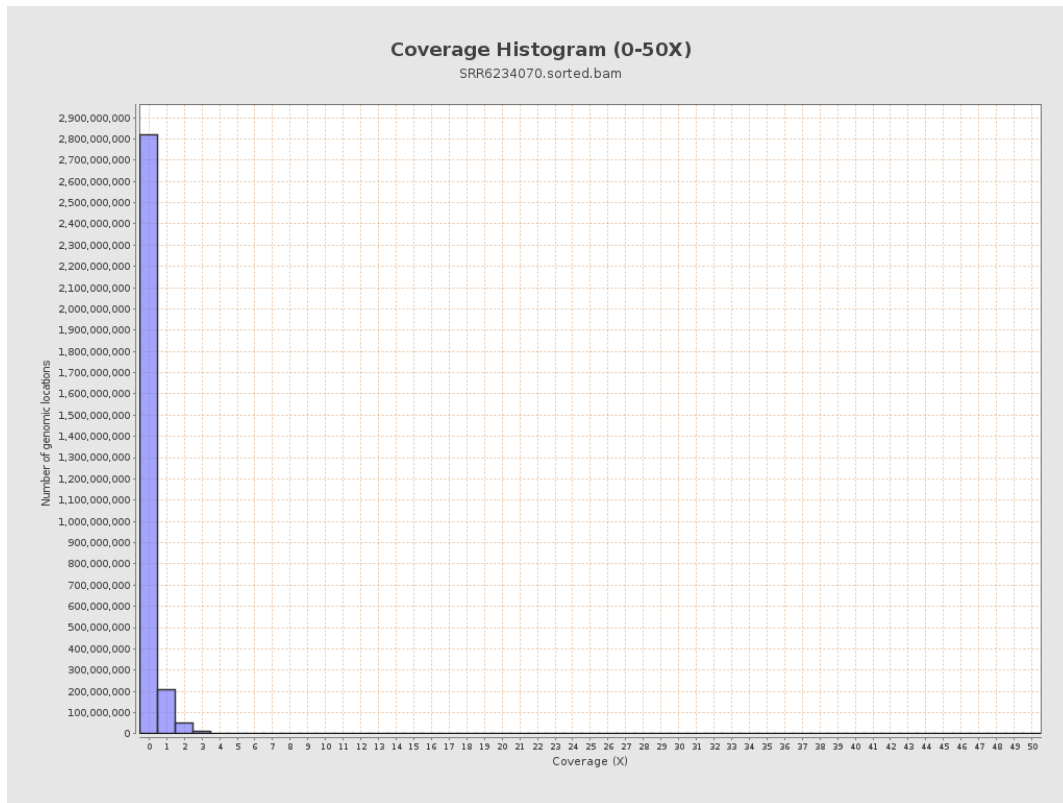
3. Results : Coverage across reference



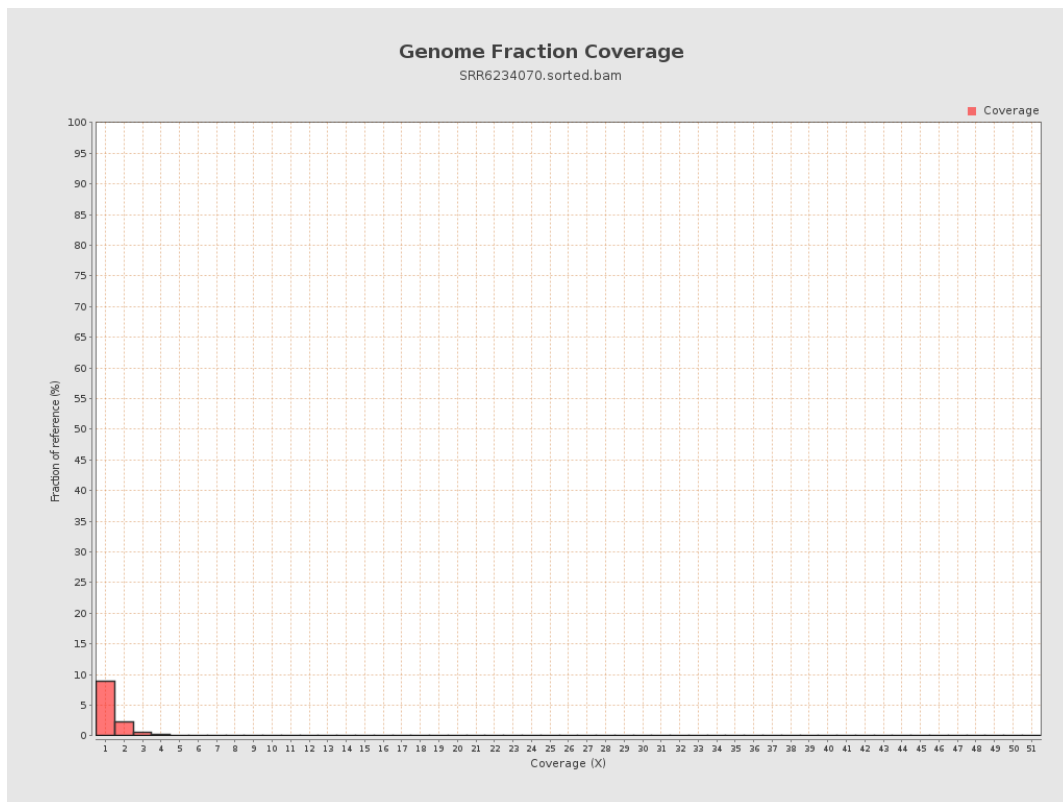
4. Results : Coverage Histogram



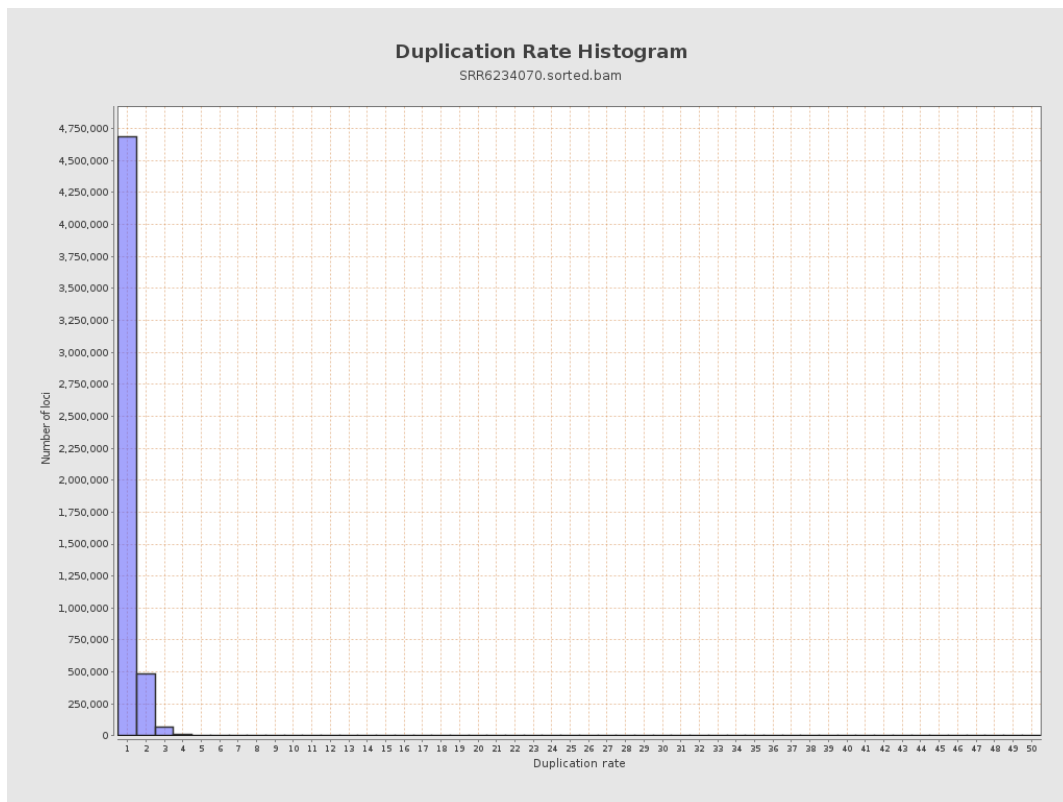
5. Results : Coverage Histogram (0-50X)



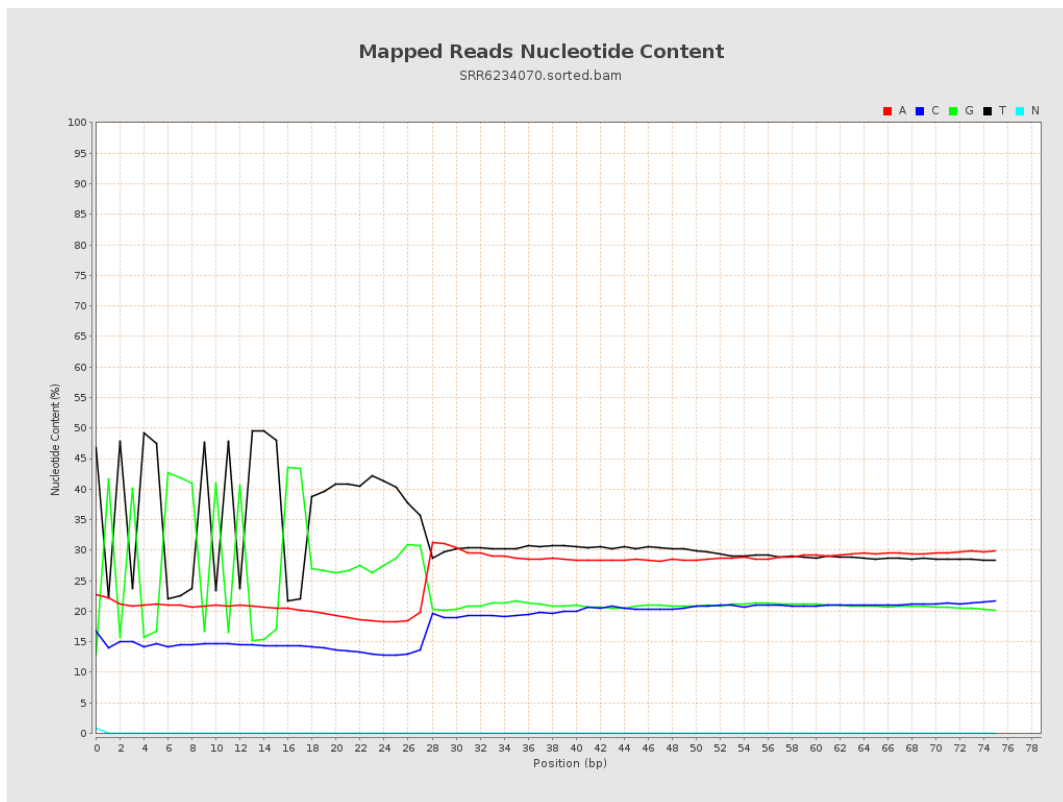
6. Results : Genome Fraction Coverage



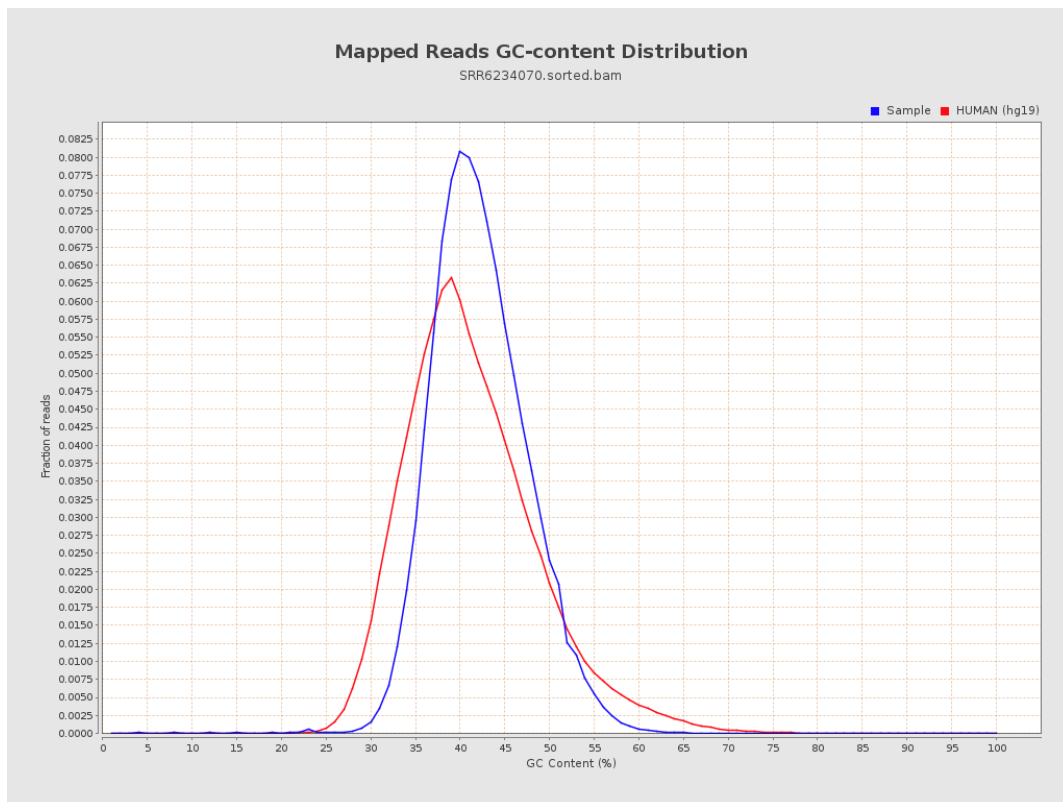
7. Results : Duplication Rate Histogram



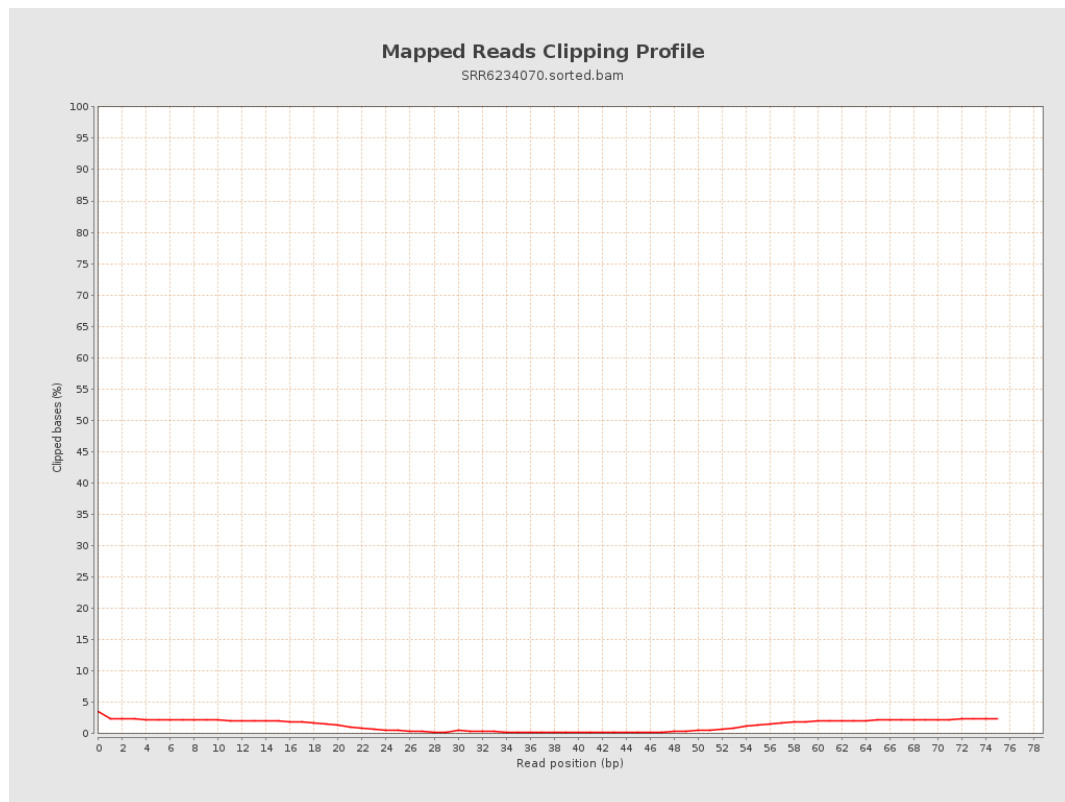
8. Results : Mapped Reads Nucleotide Content



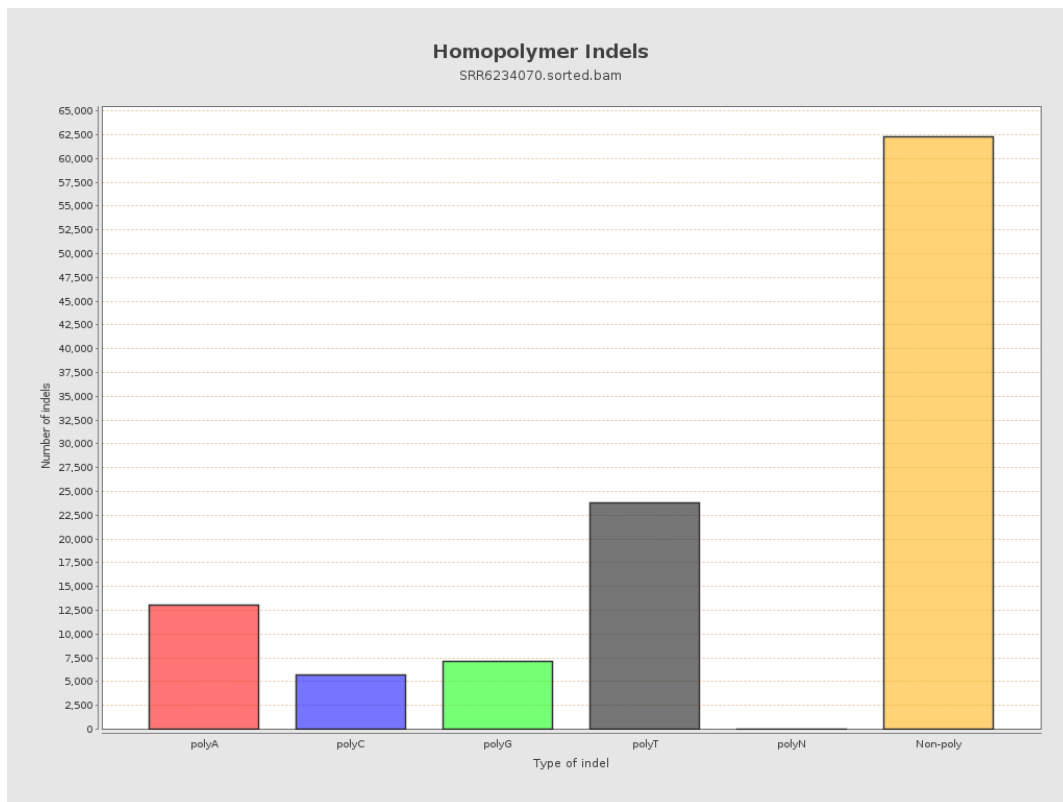
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

