

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 07:42:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240233.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_SRR6240233 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240233.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 07:42:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240233.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,405,683
Mapped reads	1,094,357 / 77.85%
Unmapped reads	311,326 / 22.15%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,330 / 0.59%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	120,848 / 8.6%
Duplication rate	9.06%
Clipped reads	592,604 / 42.16%

2.2. ACGT Content

Number/percentage of A's	19,199,155 / 27.22%
Number/percentage of C's	12,782,339 / 18.12%
Number/percentage of T's	22,753,119 / 32.26%
Number/percentage of G's	15,781,562 / 22.37%
Number/percentage of N's	19,001 / 0.03%
GC Percentage	40.5%

2.3. Coverage

Mean	0.0228

Standard Deviation	0.2665
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2.4. Mapping Quality

Mean Mapping Quality	46.35
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2.5. Mismatches and indels

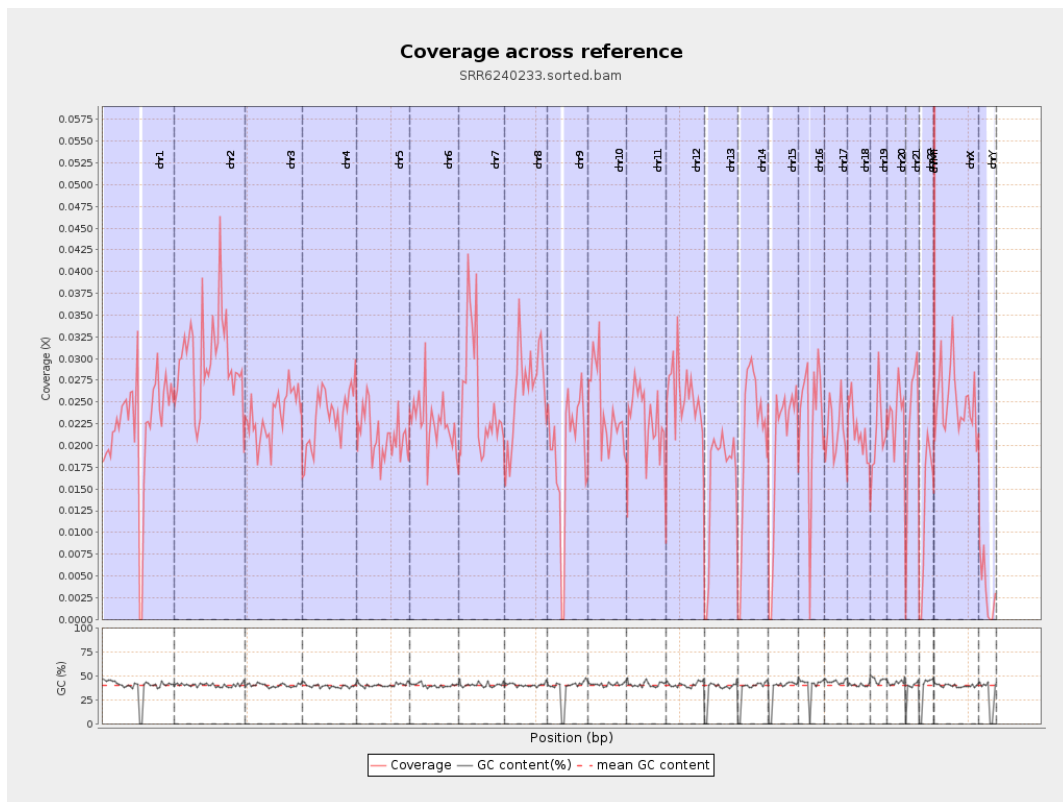
General error rate	0.84%
Mismatches	585,476
Insertions	4,735
Mapped reads with at least one insertion	0.43%
Deletions	19,498
Mapped reads with at least one deletion	1.76%
Homopolymer indels	47.64%

2.6. Chromosome stats

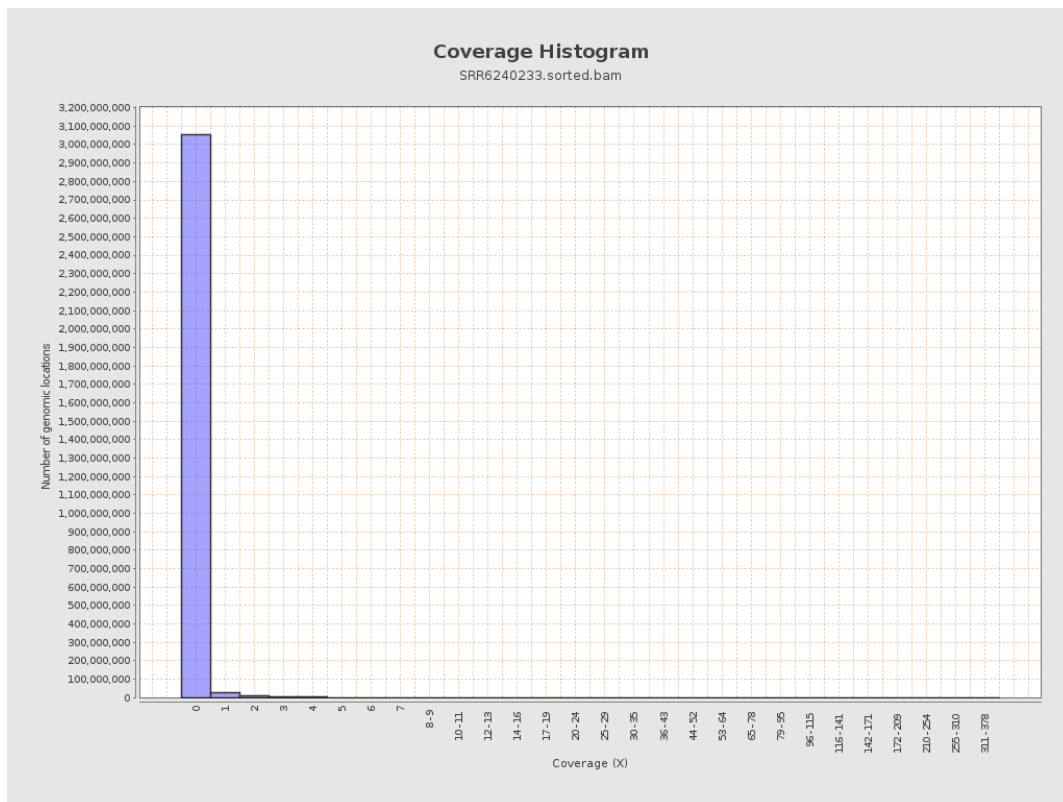
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	5557158	0.0223	0.3681
chr2	243199373	7288403	0.03	0.3297
chr3	198022430	4656253	0.0235	0.2277
chr4	191154276	4475069	0.0234	0.2281
chr5	180915260	3819413	0.0211	0.2161
chr6	171115067	3872505	0.0226	0.2391
chr7	159138663	4057092	0.0255	0.3468

chr8	146364022	3875766	0.0265	0.3176
chr9	141213431	2740965	0.0194	0.242
chr10	135534747	3275216	0.0242	0.2577
chr11	135006516	3125572	0.0232	0.2535
chr12	133851895	3471817	0.0259	0.2414
chr13	115169878	1867296	0.0162	0.189
chr14	107349540	2281077	0.0212	0.22
chr15	102531392	2022320	0.0197	0.2094
chr16	90354753	2081343	0.023	0.2299
chr17	81195210	1754153	0.0216	0.2203
chr18	78077248	1694689	0.0217	0.349
chr19	59128983	1281531	0.0217	0.2778
chr20	63025520	1477644	0.0234	0.2307
chr21	48129895	1098257	0.0228	0.2271
chr22	51304566	664369	0.0129	0.169
chrMT	16571	18128	1.094	1.8684
chrX	155270560	3914068	0.0252	0.2428
chrY	59373566	198919	0.0034	0.0796

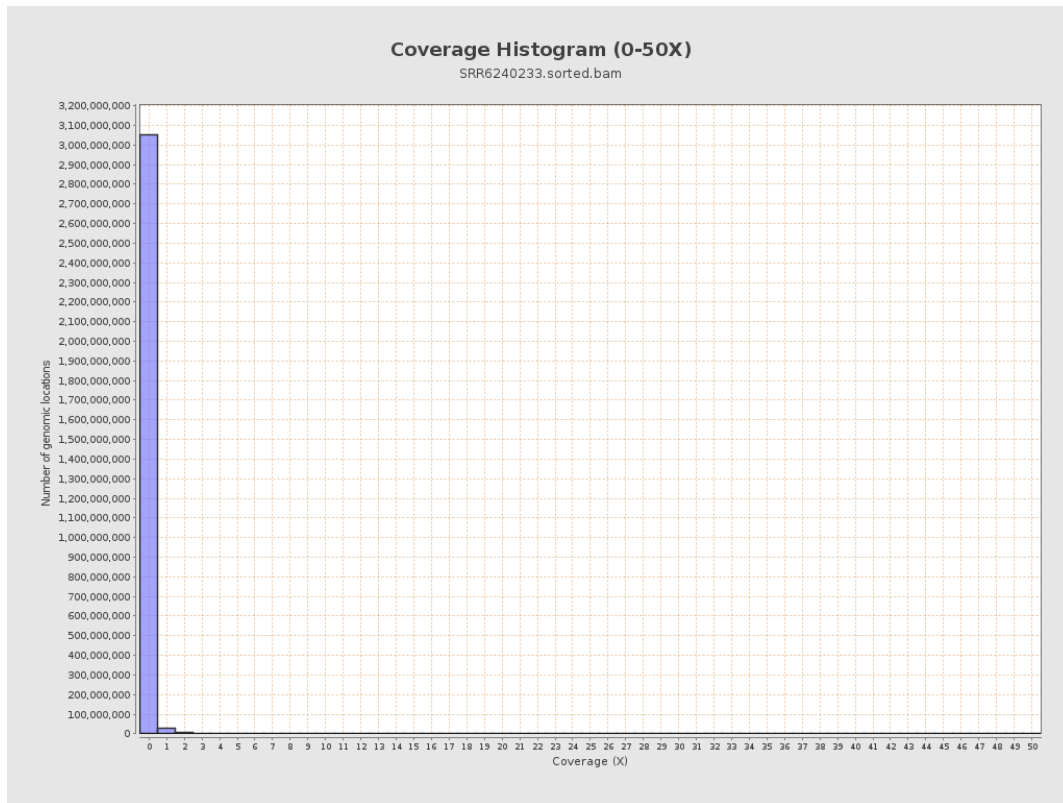
3. Results : Coverage across reference



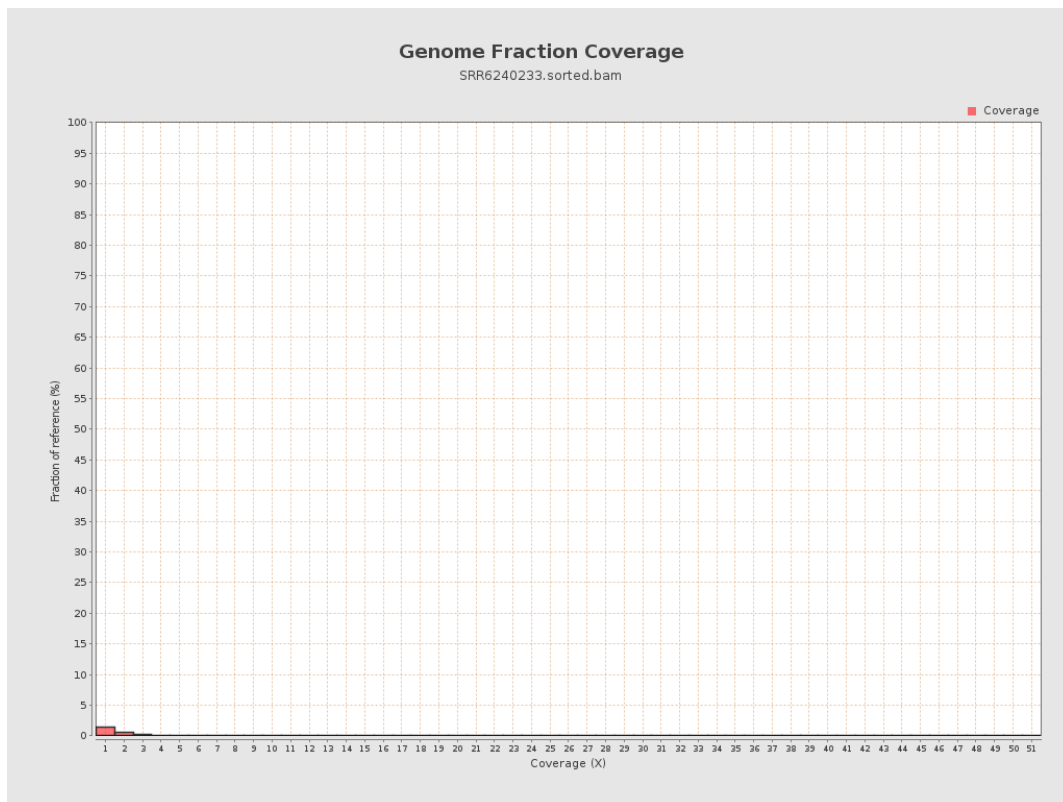
4. Results : Coverage Histogram



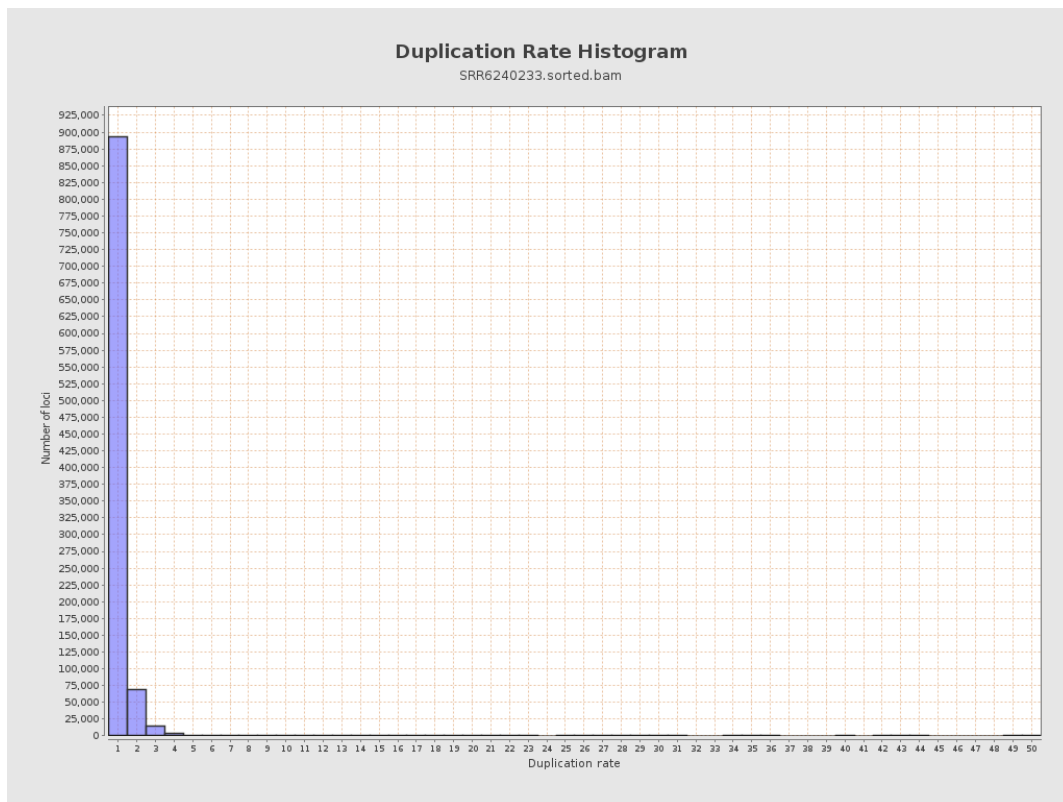
5. Results : Coverage Histogram (0-50X)



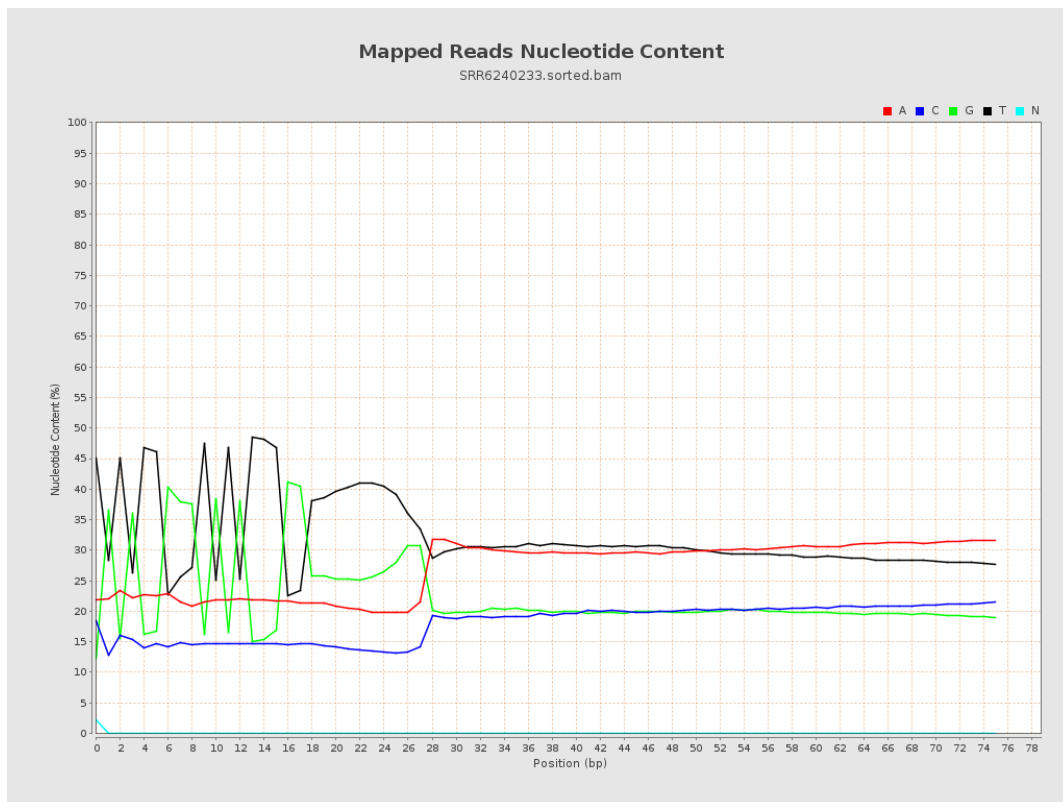
6. Results : Genome Fraction Coverage



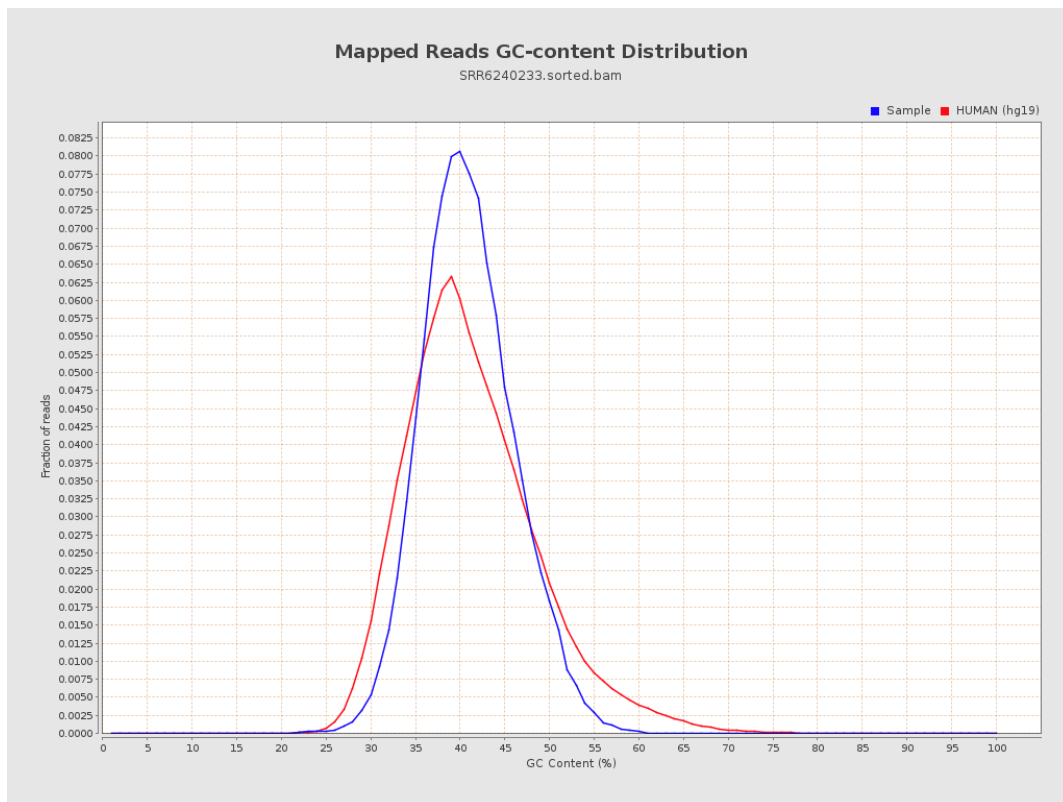
7. Results : Duplication Rate Histogram



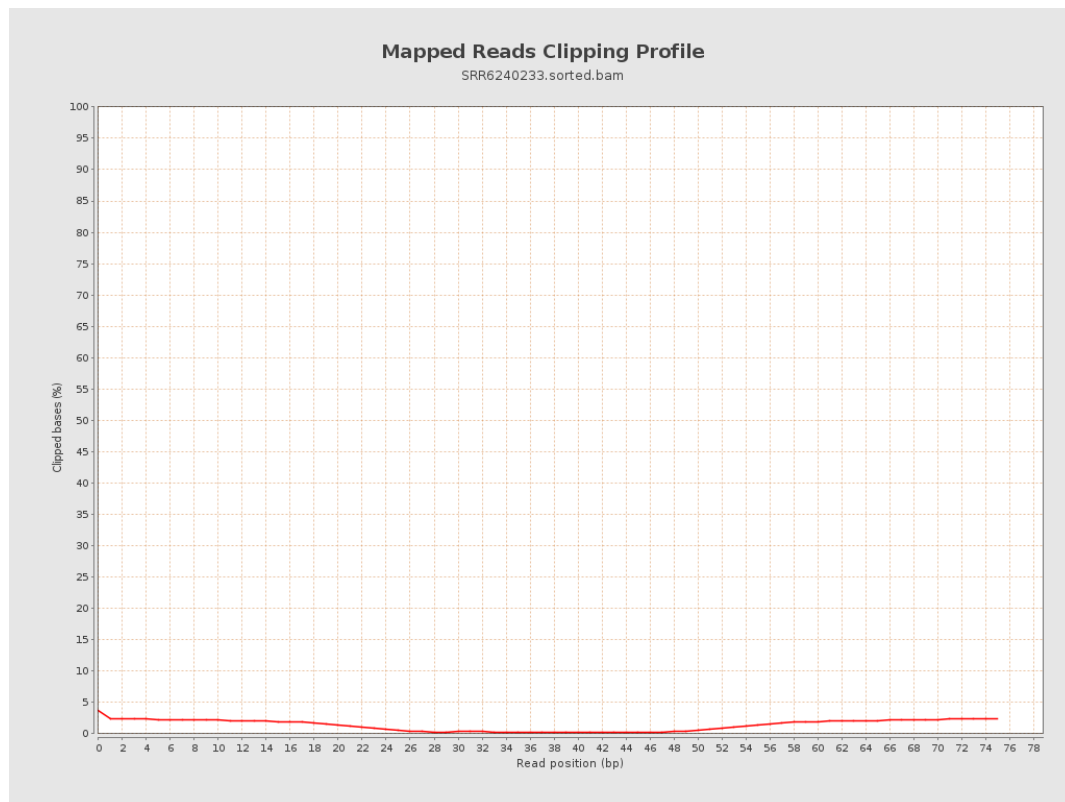
8. Results : Mapped Reads Nucleotide Content



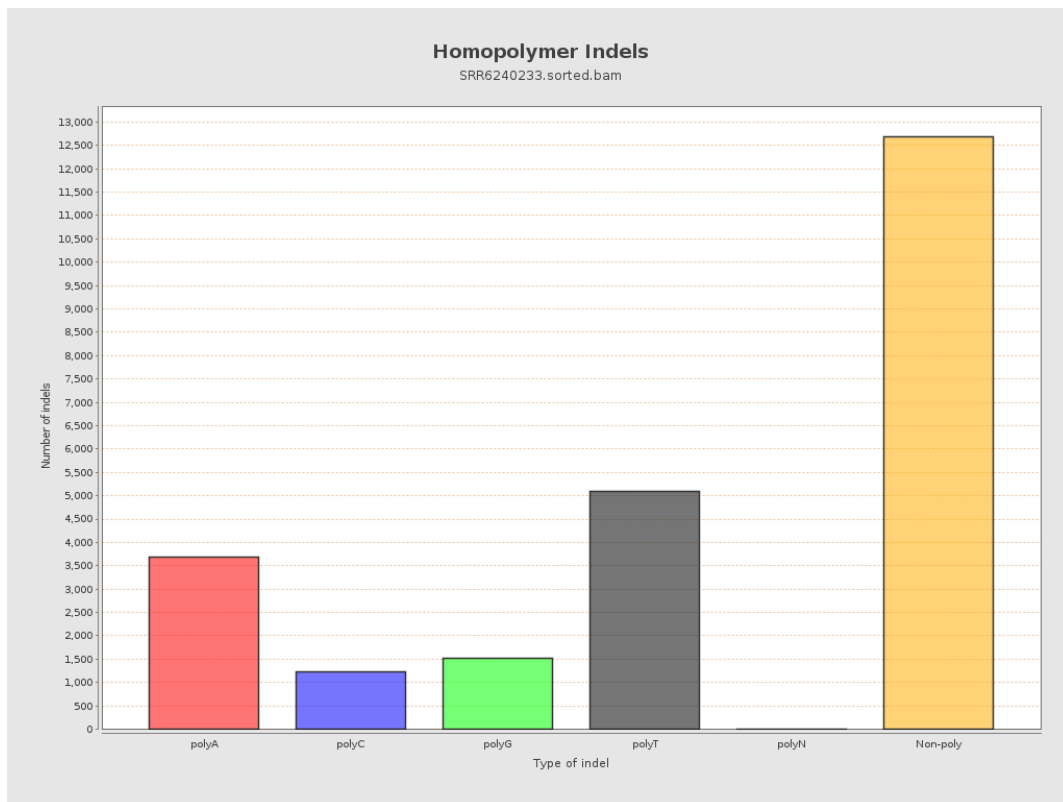
9. Results : Mapped Reads GC-content Distribution



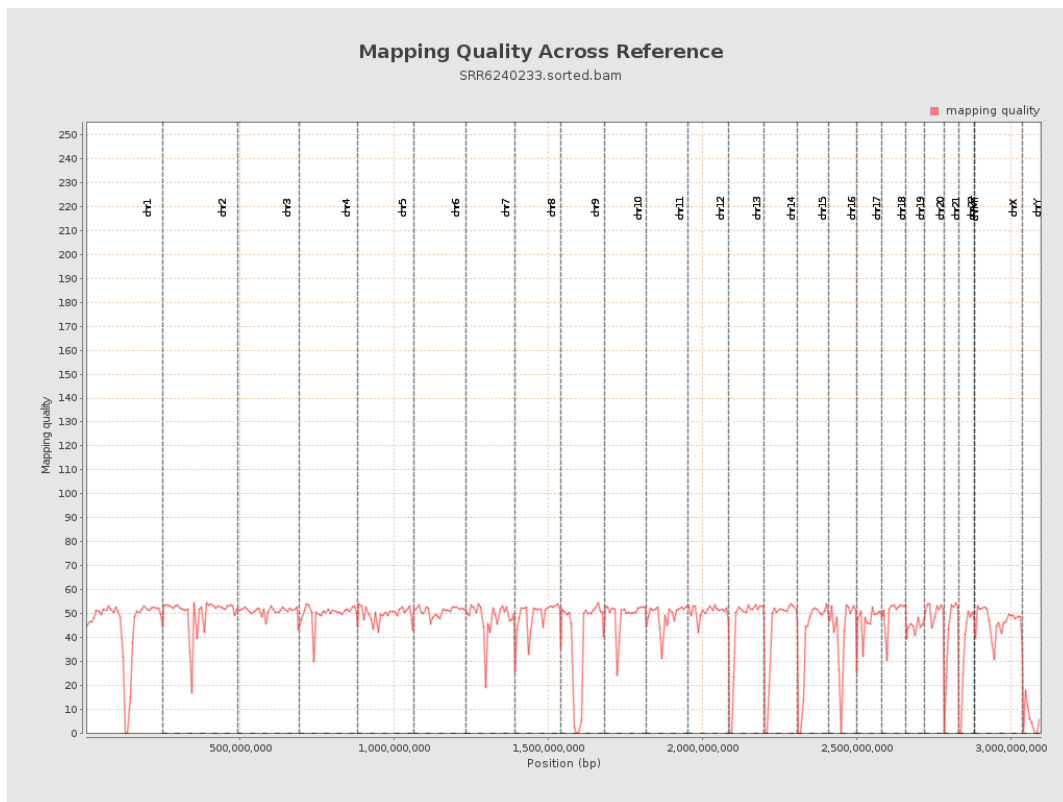
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

