Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 11:18:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238060.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_SRR6238060 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238060.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 11:18:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238060.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,483,226
Mapped reads	1,330,648 / 89.71%
Unmapped reads	152,578 / 10.29%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,479 / 1.04%
Read min/max/mean length	30 / 76 / 76.36
Duplicated reads (estimated)	58,220 / 3.93%
Duplication rate	3.59%
Clipped reads	617,879 / 41.66%

2.2. ACGT Content

Number/percentage of A's	23,991,304 / 27.21%
Number/percentage of C's	17,203,344 / 19.51%
Number/percentage of T's	26,984,411 / 30.61%
Number/percentage of G's	19,976,533 / 22.66%
Number/percentage of N's	11,119 / 0.01%
GC Percentage	42.17%

2.3. Coverage

Mean	0.0285

Standard Deviation	0.265

2.4. Mapping Quality

Mean Mapping Quality	45.5

2.5. Mismatches and indels

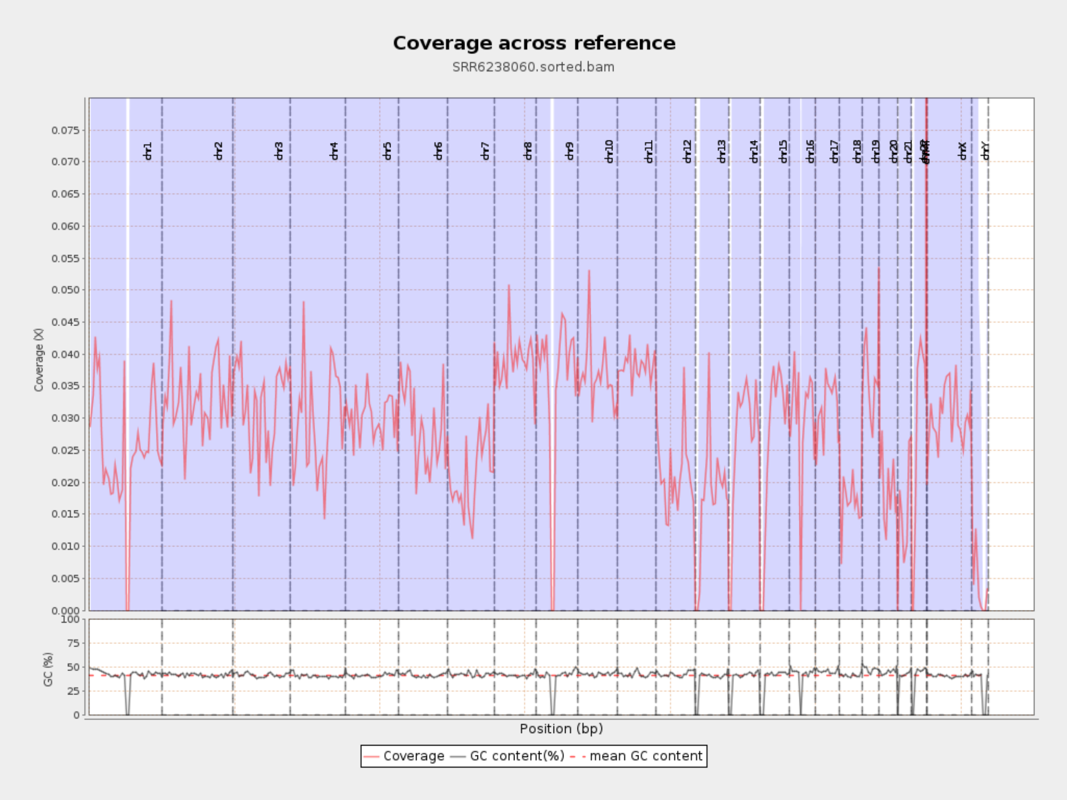
General error rate	0.77%
Mismatches	667,590
Insertions	6,221
Mapped reads with at least one insertion	0.46%
Deletions	25,121
Mapped reads with at least one deletion	1.87%
Homopolymer indels	44.17%

2.6. Chromosome stats

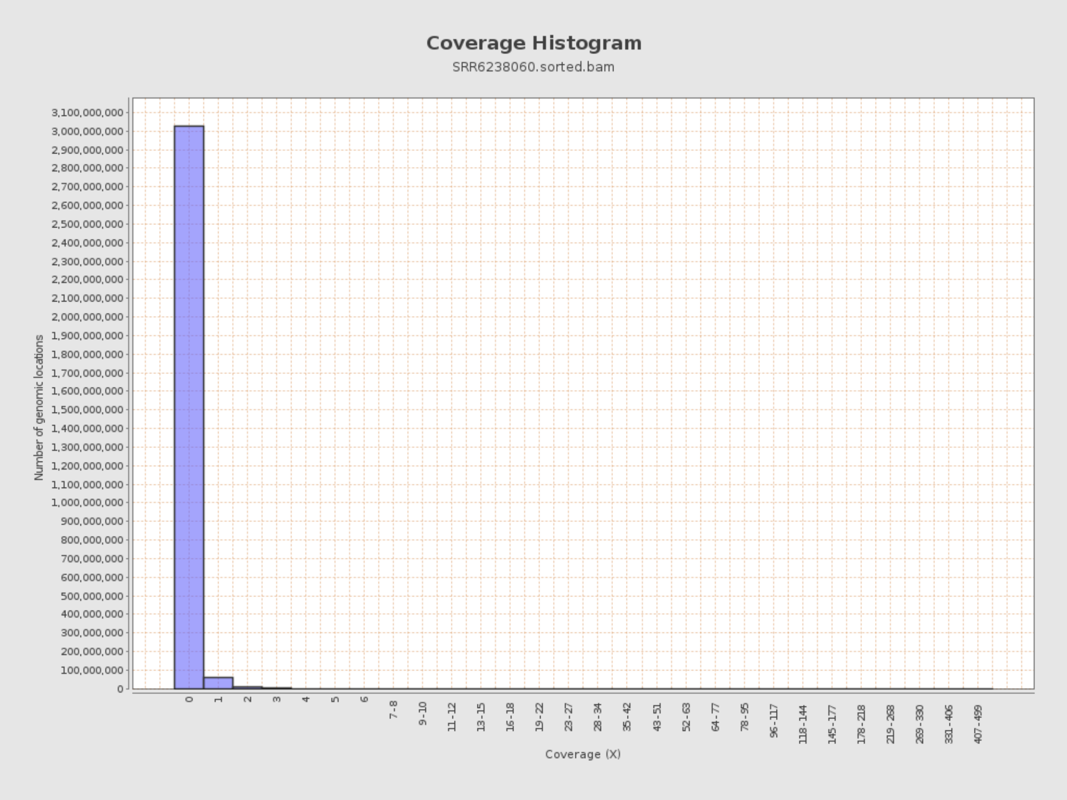
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6254806	0.0251	0.4541
chr2	243199373	8106591	0.0333	0.2864
chr3	198022430	6313001	0.0319	0.2148
chr4	191154276	5594679	0.0293	0.226
chr5	180915260	5485704	0.0303	0.2091
chr6	171115067	4910169	0.0287	0.2199
chr7	159138663	3317505	0.0208	0.209

chr8	146364022	5695320	0.0389	0.2821
chr9	141213431	4970796	0.0352	0.2713
chr10	135534747	4972416	0.0367	0.3138
chr11	135006516	5148359	0.0381	0.2888
chr12	133851895	2836599	0.0212	0.1787
chr13	115169878	2025033	0.0176	0.1588
chr14	107349540	2854565	0.0266	0.2205
chr15	102531392	2742648	0.0267	0.1957
chr16	90354753	2684270	0.0297	0.2265
chr17	81195210	2577610	0.0317	0.2416
chr18	78077248	1335580	0.0171	0.3843
chr19	59128983	2135382	0.0361	0.3227
chr20	63025520	1181639	0.0187	0.1687
chr21	48129895	739048	0.0154	0.1704
chr22	51304566	1409913	0.0275	0.2011
chrMT	16571	5911	0.3567	0.7394
chrX	155270560	4682384	0.0302	0.2206
chrY	59373566	231539	0.0039	0.1279

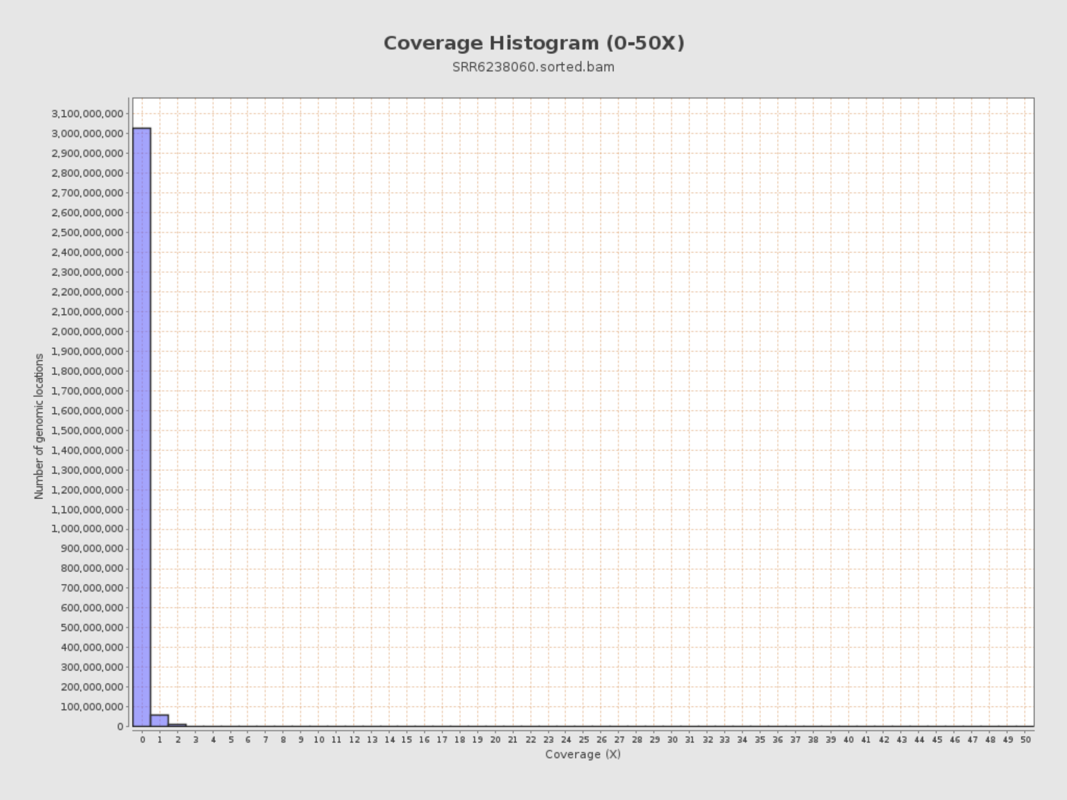
3. Results : Coverage across reference



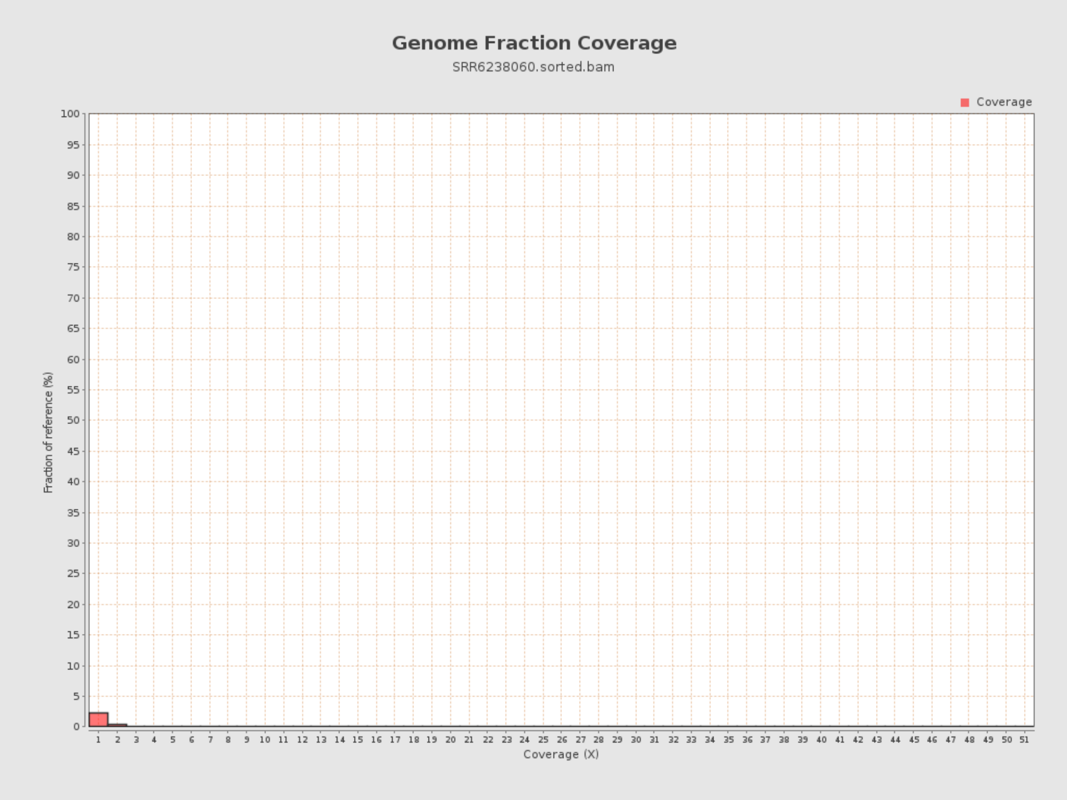
4. Results : Coverage Histogram



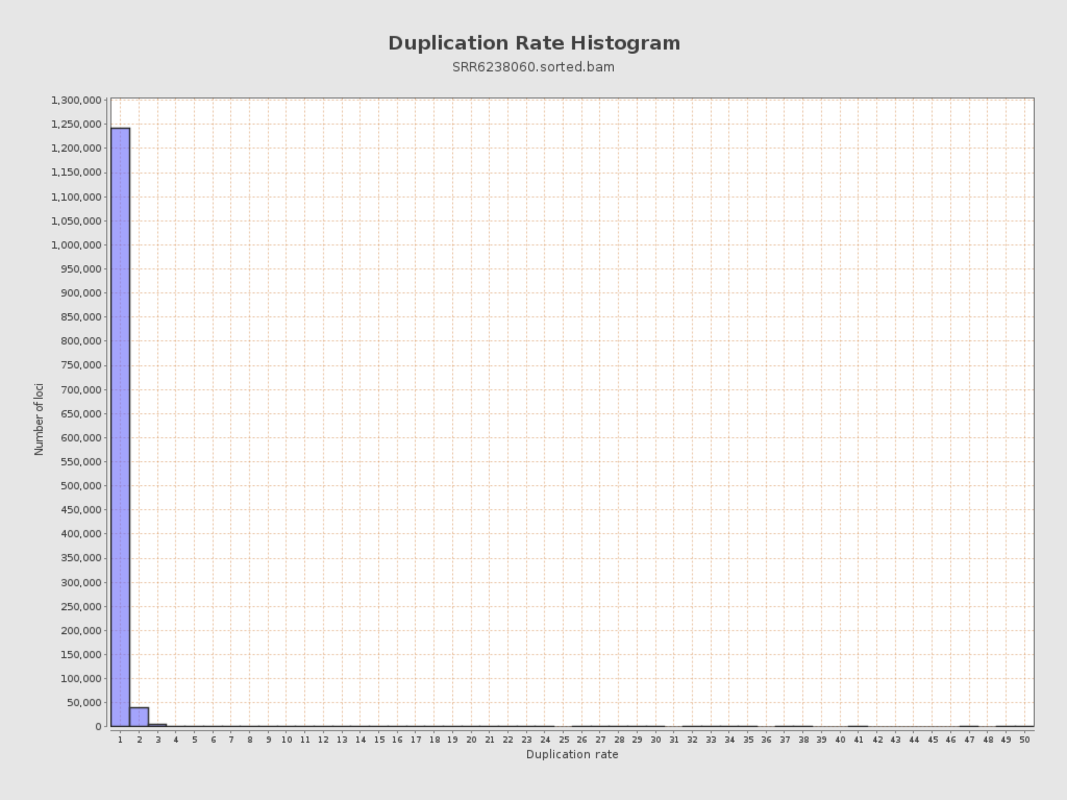
5. Results : Coverage Histogram (0-50X)



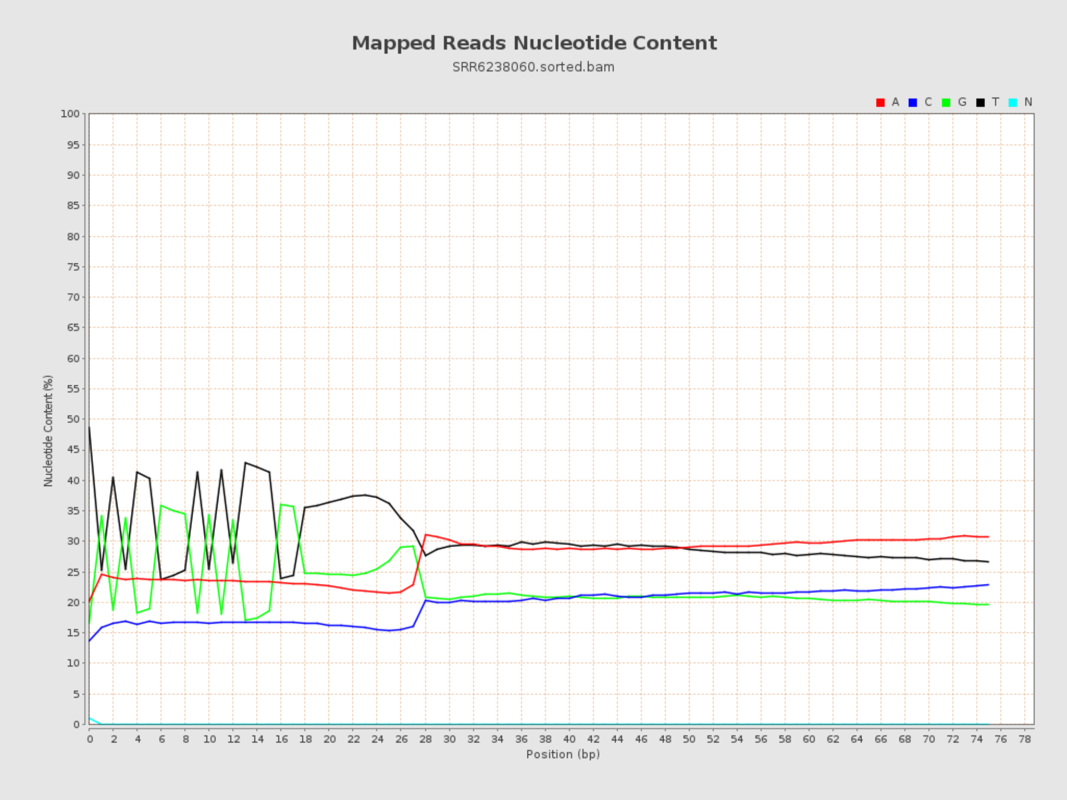
6. Results : Genome Fraction Coverage



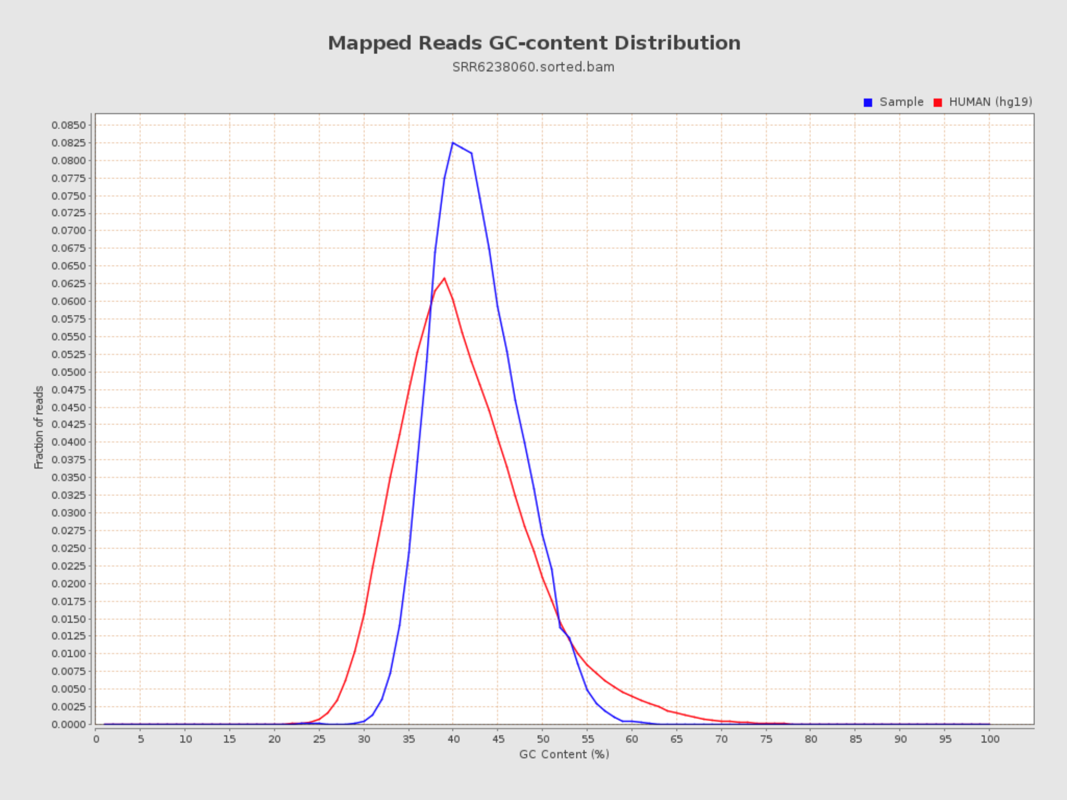
7. Results : Duplication Rate Histogram



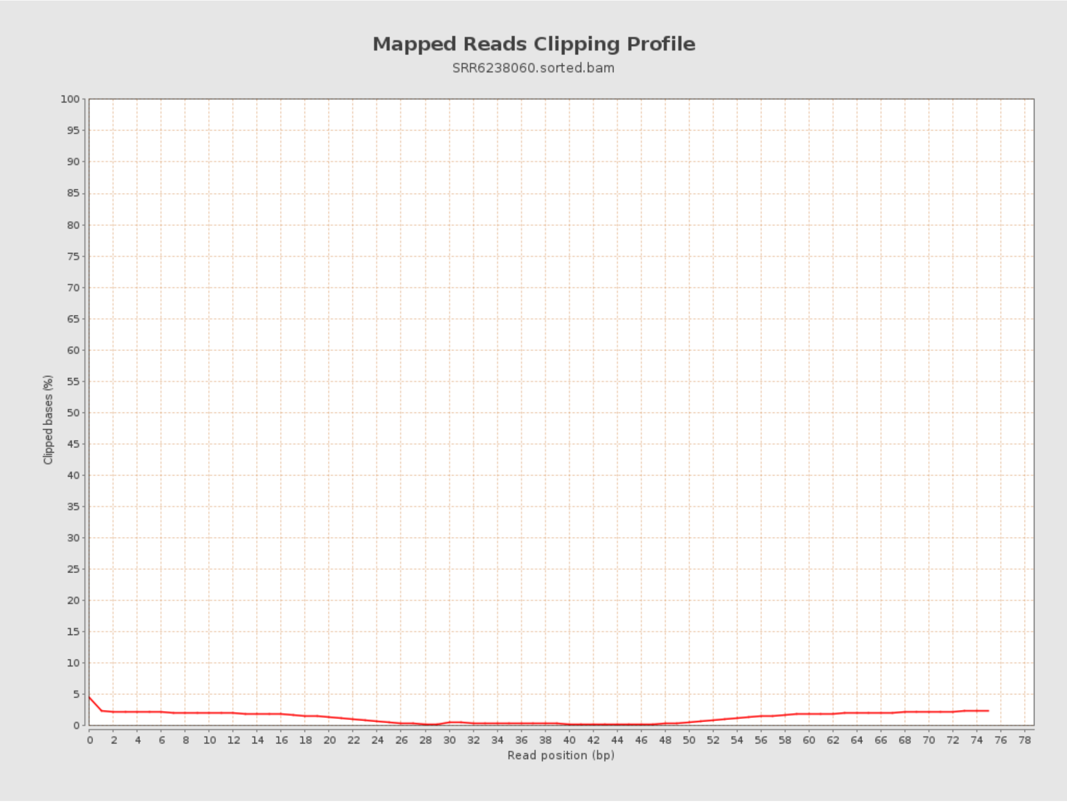
8. Results : Mapped Reads Nucleotide Content



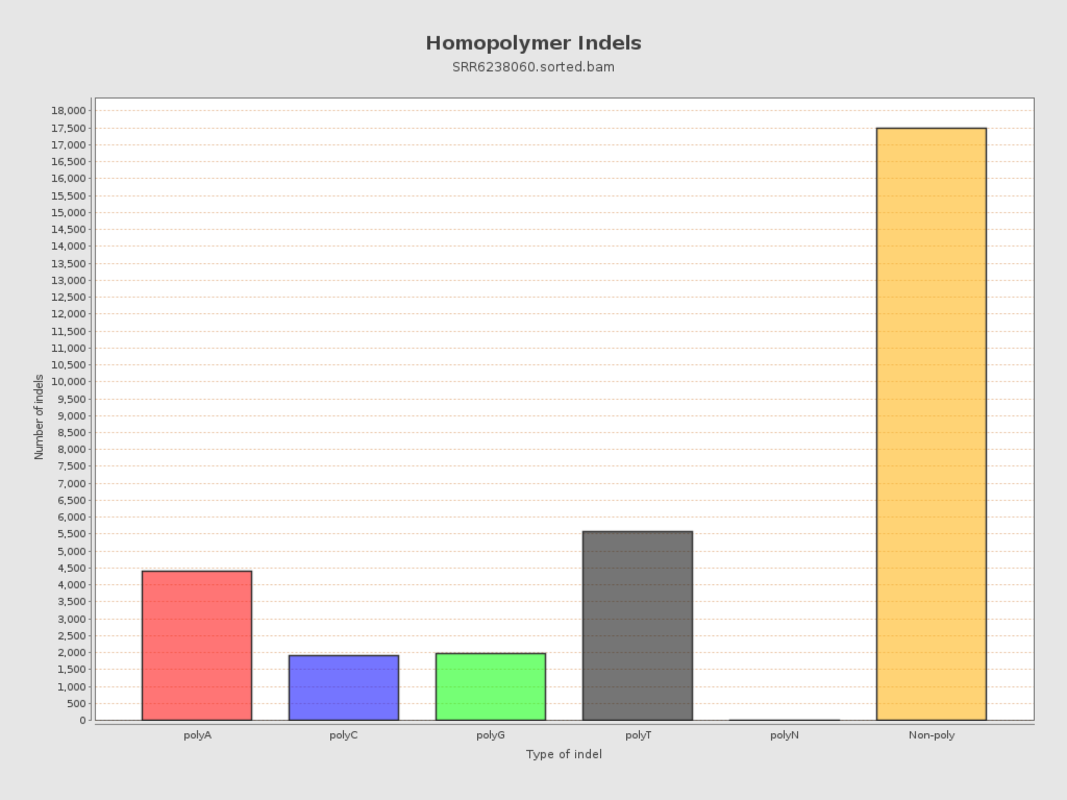
9. Results : Mapped Reads GC-content Distribution



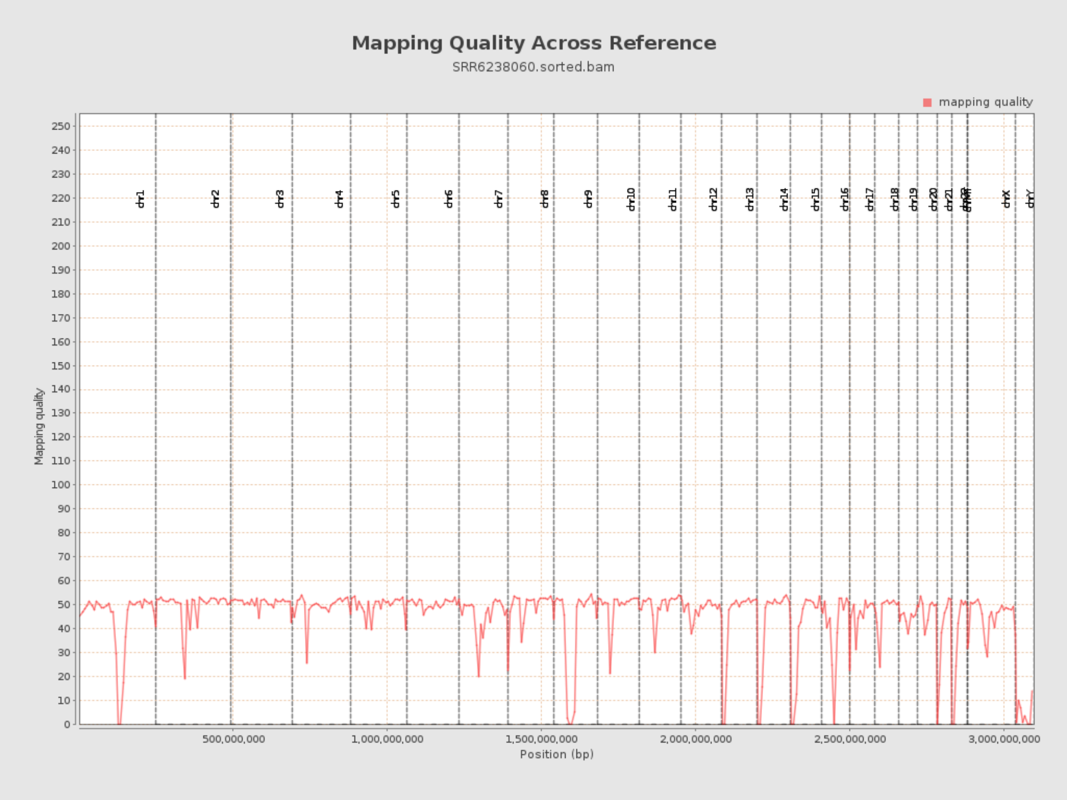
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram