Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 18:30:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238503.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_SRR6238503 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238503.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 18:30:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238503.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,599,984
Mapped reads	3,121,167 / 86.7%
Unmapped reads	478,817 / 13.3%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	29,206 / 0.81%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	1,196,852 / 33.25%
Duplication rate	21.5%
Clipped reads	2,104,364 / 58.45%

2.2. ACGT Content

Number/percentage of A's	45,862,134 / 24.23%
Number/percentage of C's	34,113,341 / 18.02%
Number/percentage of T's	63,041,559 / 33.3%
Number/percentage of G's	46,275,392 / 24.44%
Number/percentage of N's	12,462 / 0.01%
GC Percentage	42.47%

2.3. Coverage

Mean	0.0612

Standard Deviation	1.1953

2.4. Mapping Quality

Mean Mapping Quality	39.94

2.5. Mismatches and indels

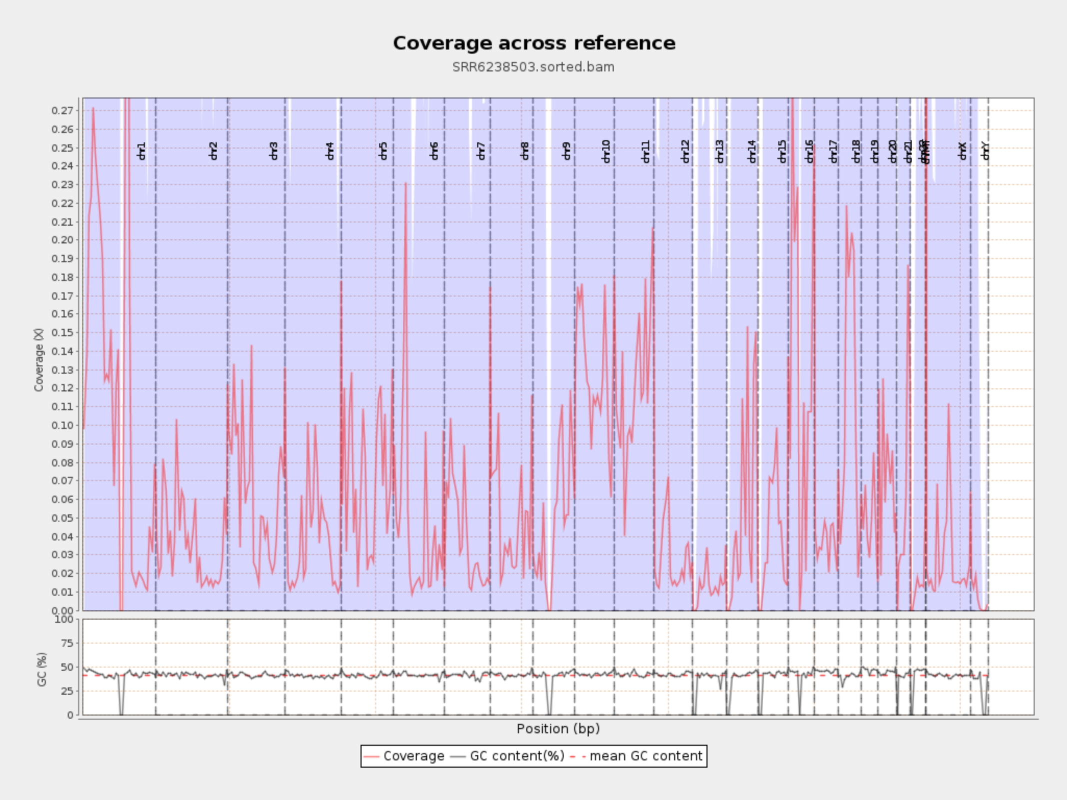
General error rate	0.64%
Mismatches	1,182,054
Insertions	12,986
Mapped reads with at least one insertion	0.41%
Deletions	68,716
Mapped reads with at least one deletion	2.18%
Homopolymer indels	39.57%

2.6. Chromosome stats

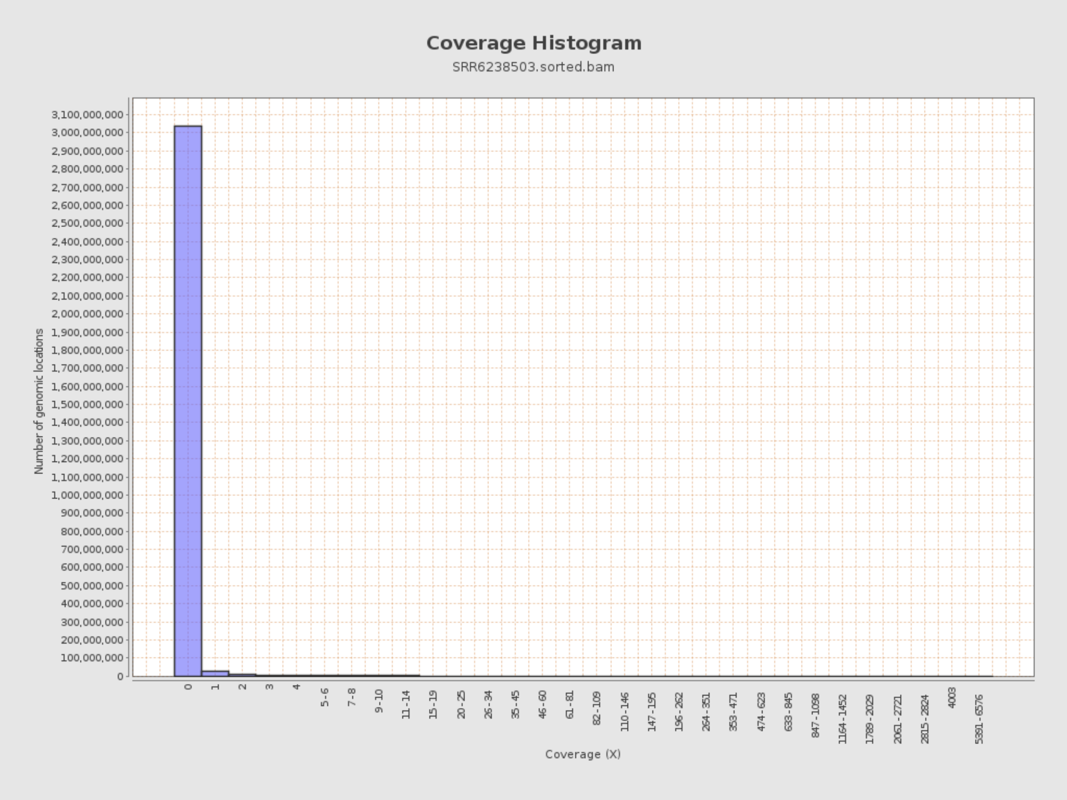
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	29758185	0.1194	1.1207
chr2	243199373	8666883	0.0356	2.9064
chr3	198022430	12990639	0.0656	0.7131
chr4	191154276	7406783	0.0387	0.5192
chr5	180915260	13065118	0.0722	0.7179
chr6	171115067	8120760	0.0475	0.9937
chr7	159138663	6331474	0.0398	0.7014

chr8	146364022	7147159	0.0488	0.7066
chr9	141213431	6622084	0.0469	0.602
chr10	135534747	17212142	0.127	1.0416
chr11	135006516	16400913	0.1215	0.9451
chr12	133851895	3680433	0.0275	0.4337
chr13	115169878	1448249	0.0126	0.7135
chr14	107349540	5899777	0.055	0.6449
chr15	102531392	3984460	0.0389	0.7501
chr16	90354753	11559375	0.1279	1.0512
chr17	81195210	2970289	0.0366	0.5023
chr18	78077248	8793452	0.1126	2.8543
chr19	59128983	2844763	0.0481	0.7191
chr20	63025520	4680212	0.0743	0.7468
chr21	48129895	3178824	0.066	0.7216
chr22	51304566	629415	0.0123	0.2587
chrMT	16571	1022527	61.7058	39.1353
chrX	155270560	4598950	0.0296	0.4416
chrY	59373566	409598	0.0069	0.444

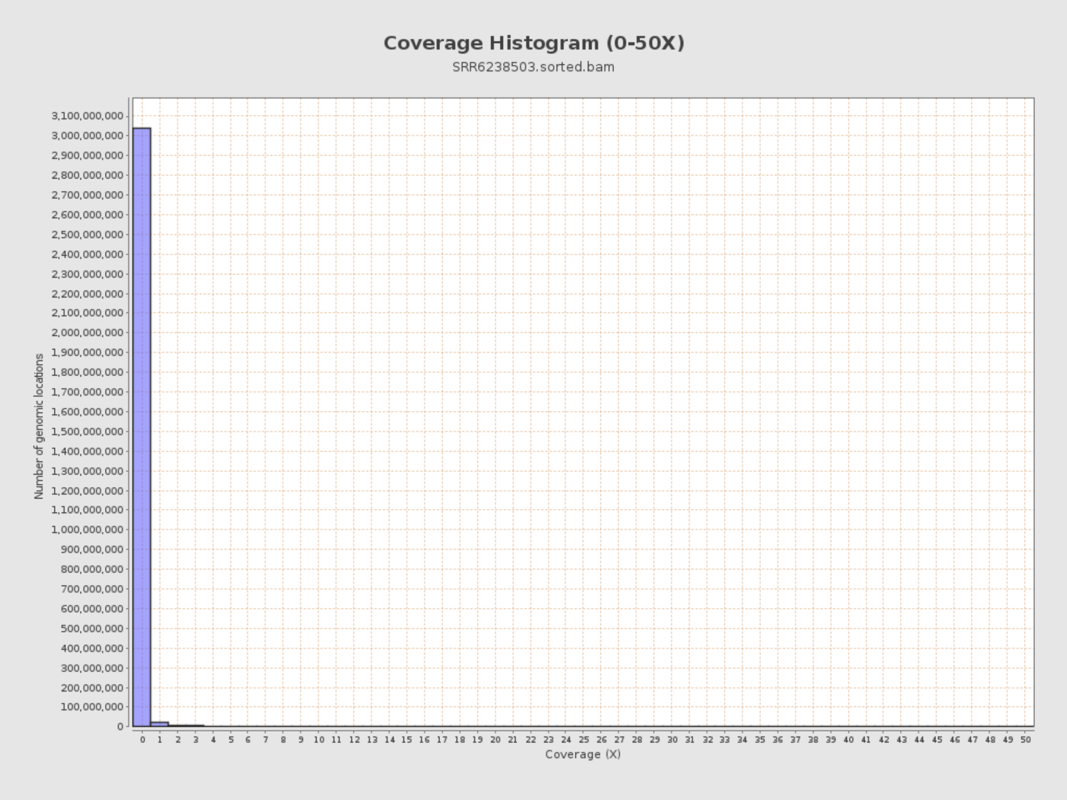
3. Results : Coverage across reference



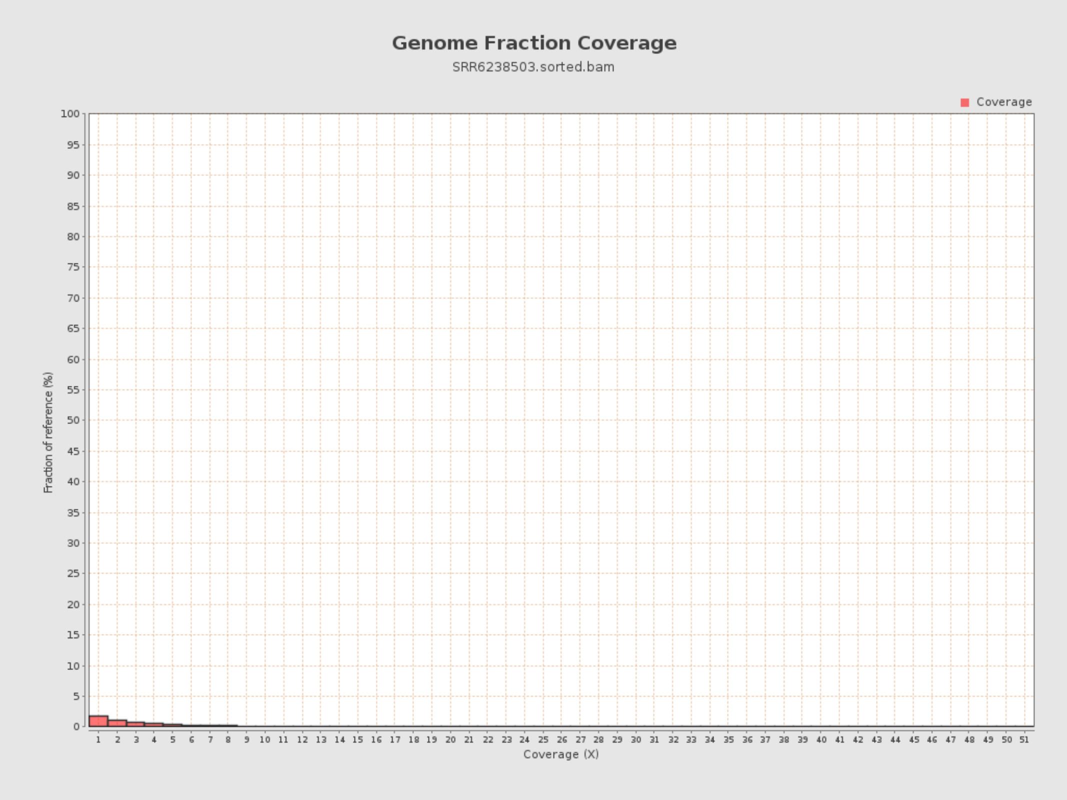
4. Results : Coverage Histogram



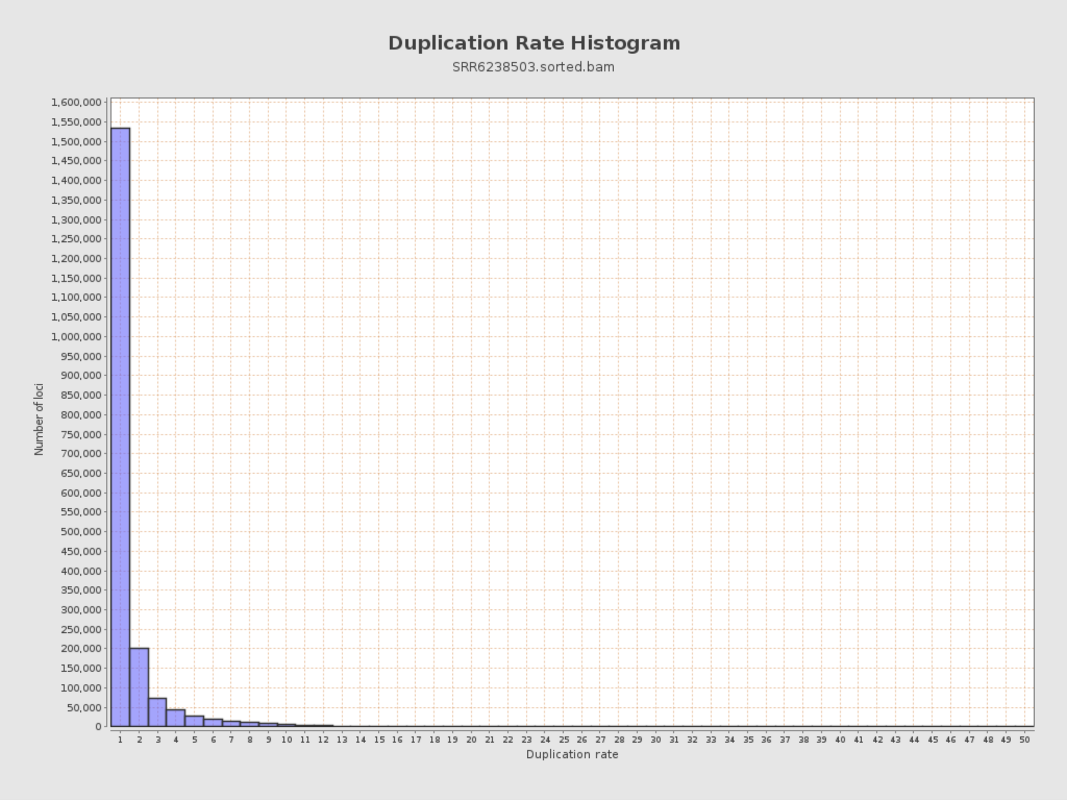
5. Results : Coverage Histogram (0-50X)



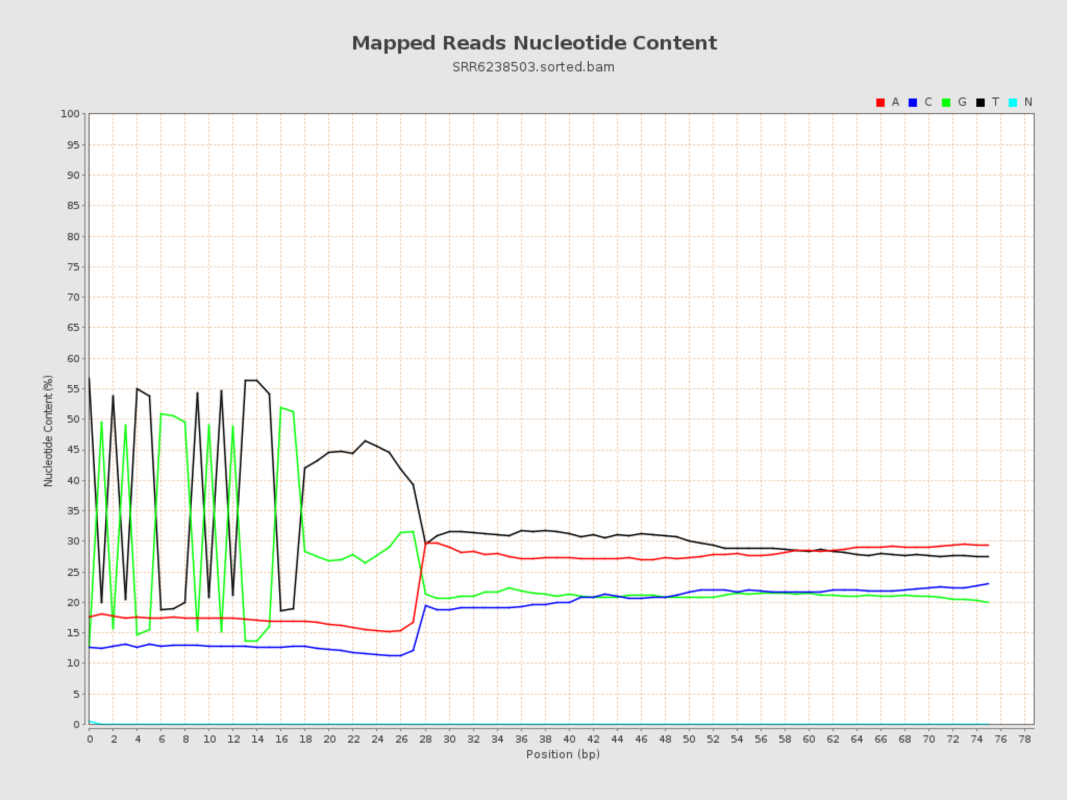
6. Results : Genome Fraction Coverage



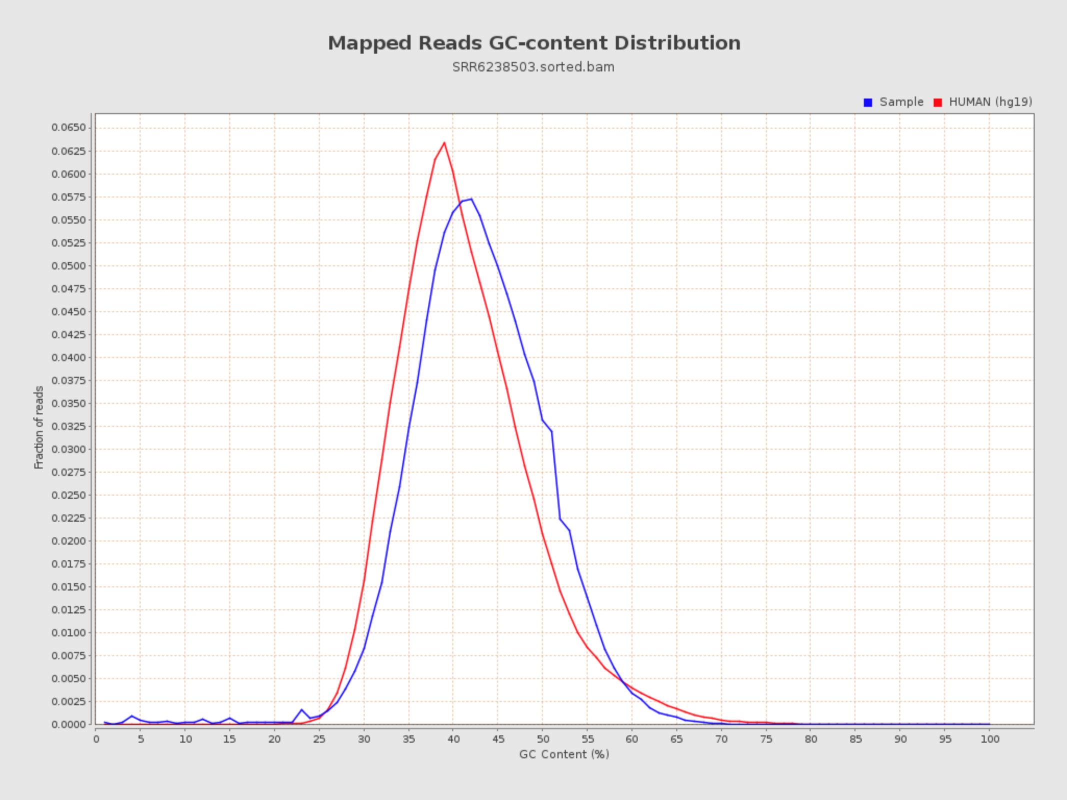
7. Results : Duplication Rate Histogram



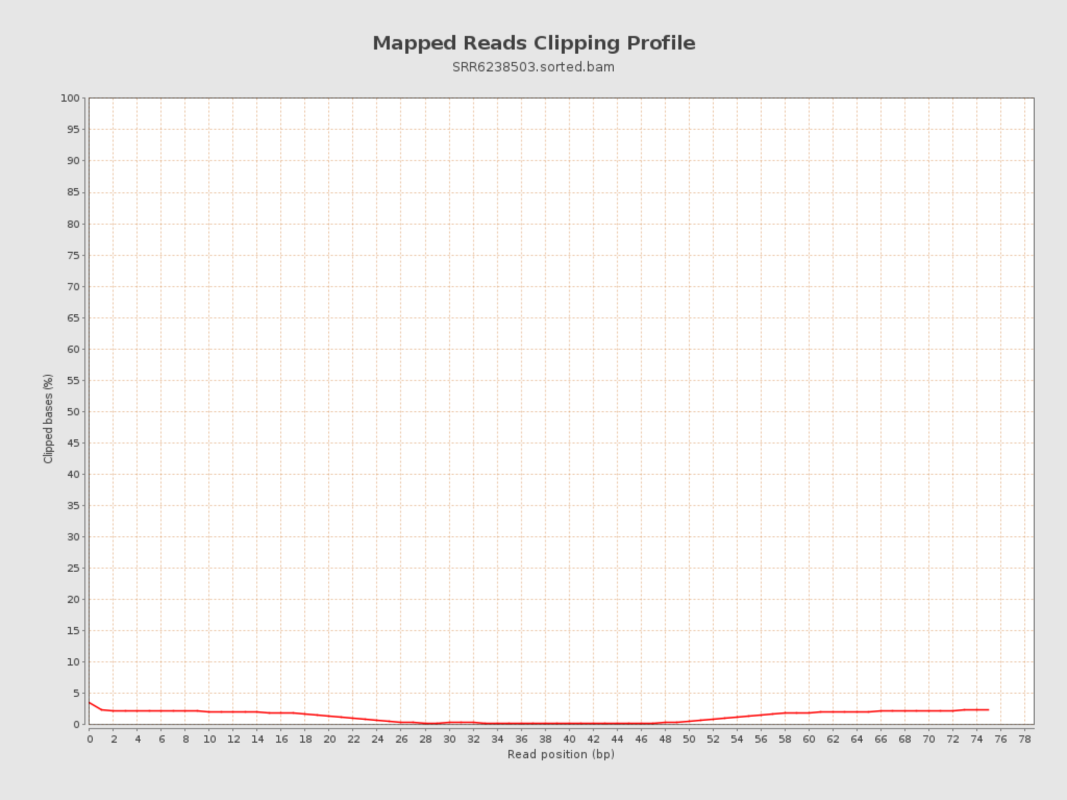
8. Results : Mapped Reads Nucleotide Content



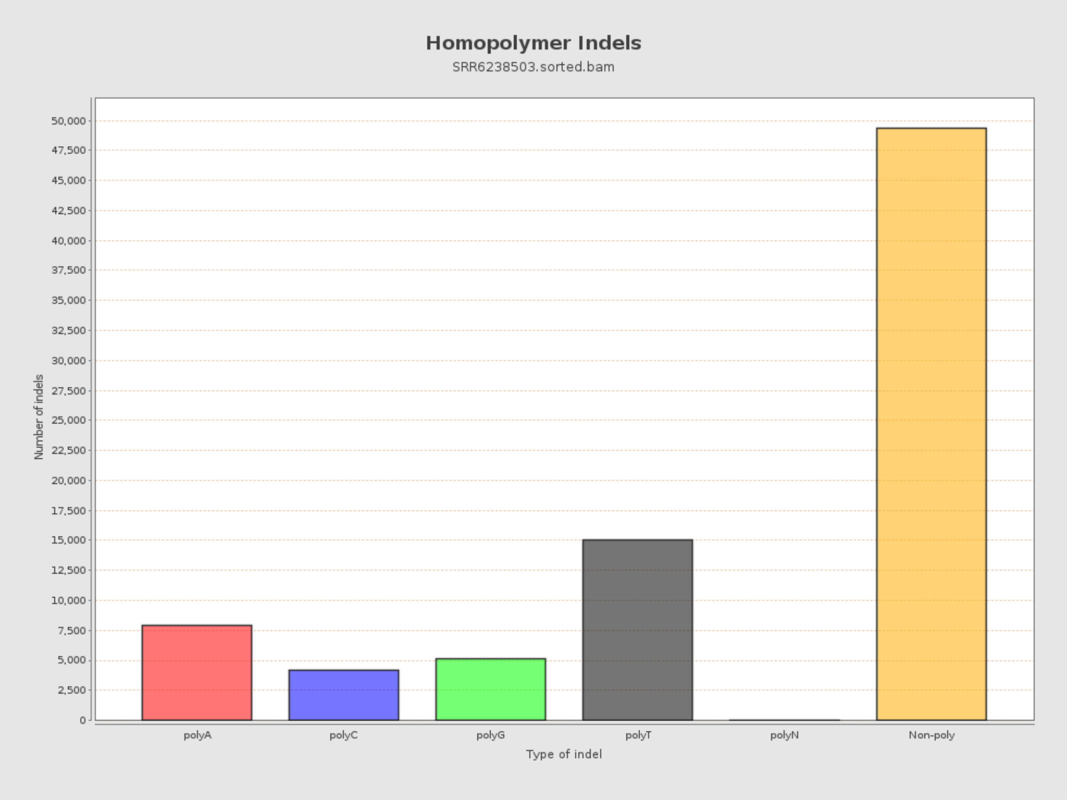
9. Results : Mapped Reads GC-content Distribution



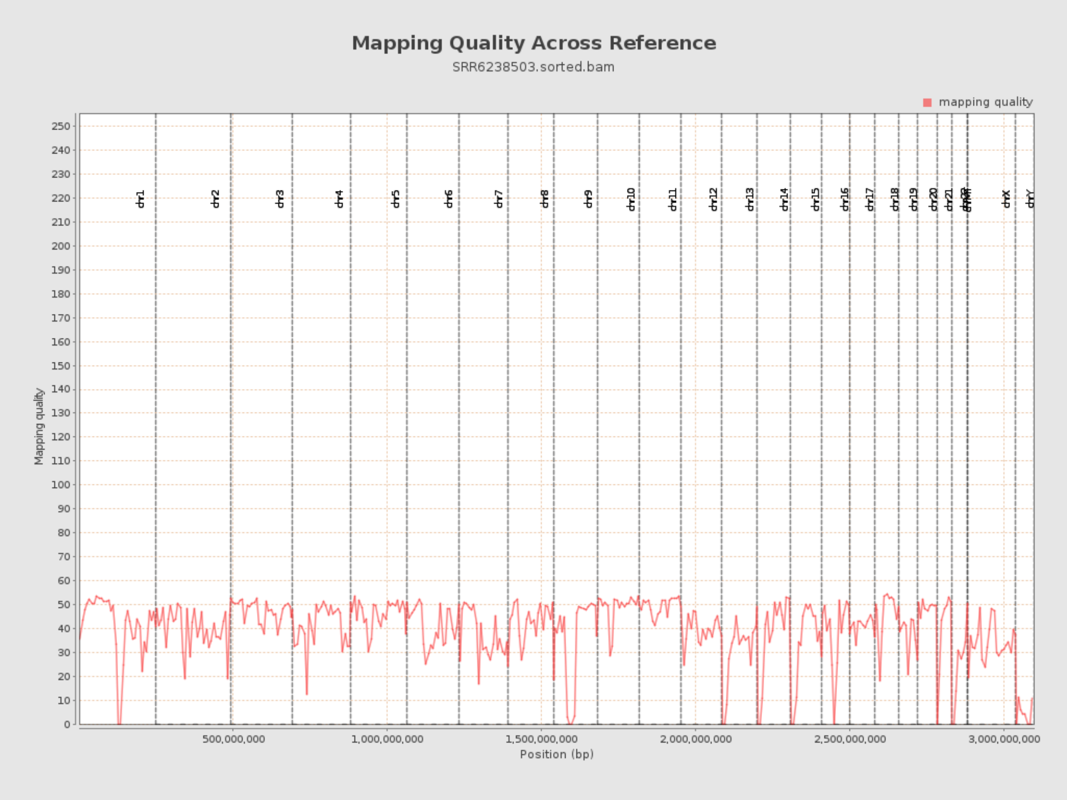
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram