Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 13:46:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238268.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_SRR6238268 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238268.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 13:45:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238268.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,912,581
Mapped reads	1,487,545 / 77.78%
Unmapped reads	425,036 / 22.22%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,877 / 0.99%
Read min/max/mean length	30 / 76 / 76.34
Duplicated reads (estimated)	86,796 / 4.54%
Duplication rate	4.78%
Clipped reads	869,361 / 45.45%

2.2. ACGT Content

Number/percentage of A's	26,397,503 / 27.85%
Number/percentage of C's	18,382,241 / 19.4%
Number/percentage of T's	28,997,772 / 30.6%
Number/percentage of G's	20,975,961 / 22.13%
Number/percentage of N's	20,286 / 0.02%
GC Percentage	41.53%

2.3. Coverage

Mean	0.0306

Standard Deviation	0.2903

2.4. Mapping Quality

Mean Mapping Quality	45.1

2.5. Mismatches and indels

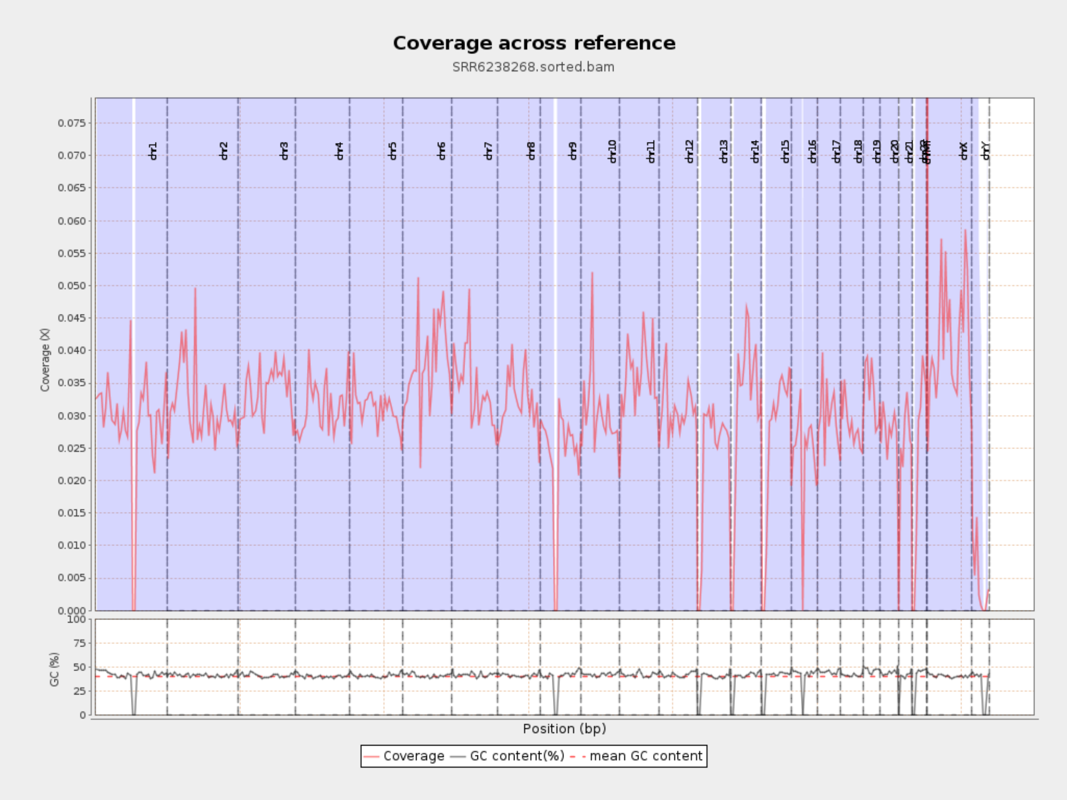
General error rate	0.85%
Mismatches	794,371
Insertions	7,571
Mapped reads with at least one insertion	0.5%
Deletions	21,728
Mapped reads with at least one deletion	1.45%
Homopolymer indels	46.3%

2.6. Chromosome stats

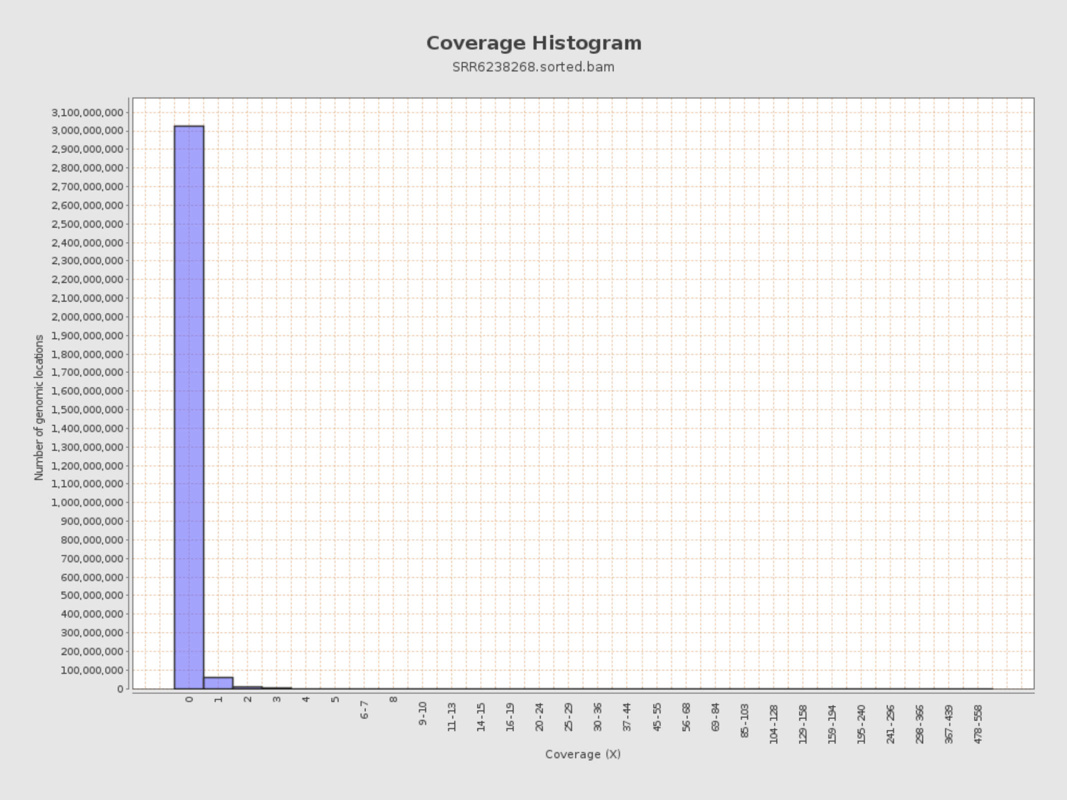
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7188884	0.0288	0.4655
chr2	243199373	7699512	0.0317	0.3518
chr3	198022430	6671747	0.0337	0.232
chr4	191154276	5994201	0.0314	0.2312
chr5	180915260	5632325	0.0311	0.2234
chr6	171115067	6471265	0.0378	0.2782
chr7	159138663	5453864	0.0343	0.345

chr8	146364022	4735442	0.0324	0.3128
chr9	141213431	3348416	0.0237	0.2381
chr10	135534747	4139793	0.0305	0.3018
chr11	135006516	4862679	0.036	0.2776
chr12	133851895	4136078	0.0309	0.2234
chr13	115169878	2709764	0.0235	0.1959
chr14	107349540	3339543	0.0311	0.242
chr15	102531392	2708768	0.0264	0.2209
chr16	90354753	2153316	0.0238	0.2122
chr17	81195210	2430809	0.0299	0.2324
chr18	78077248	2226920	0.0285	0.3678
chr19	59128983	2005564	0.0339	0.3793
chr20	63025520	1738139	0.0276	0.2132
chr21	48129895	1184571	0.0246	0.2028
chr22	51304566	1184549	0.0231	0.19
chrMT	16571	44381	2.6782	2.3735
chrX	155270560	6485458	0.0418	0.2789
chrY	59373566	263053	0.0044	0.1051

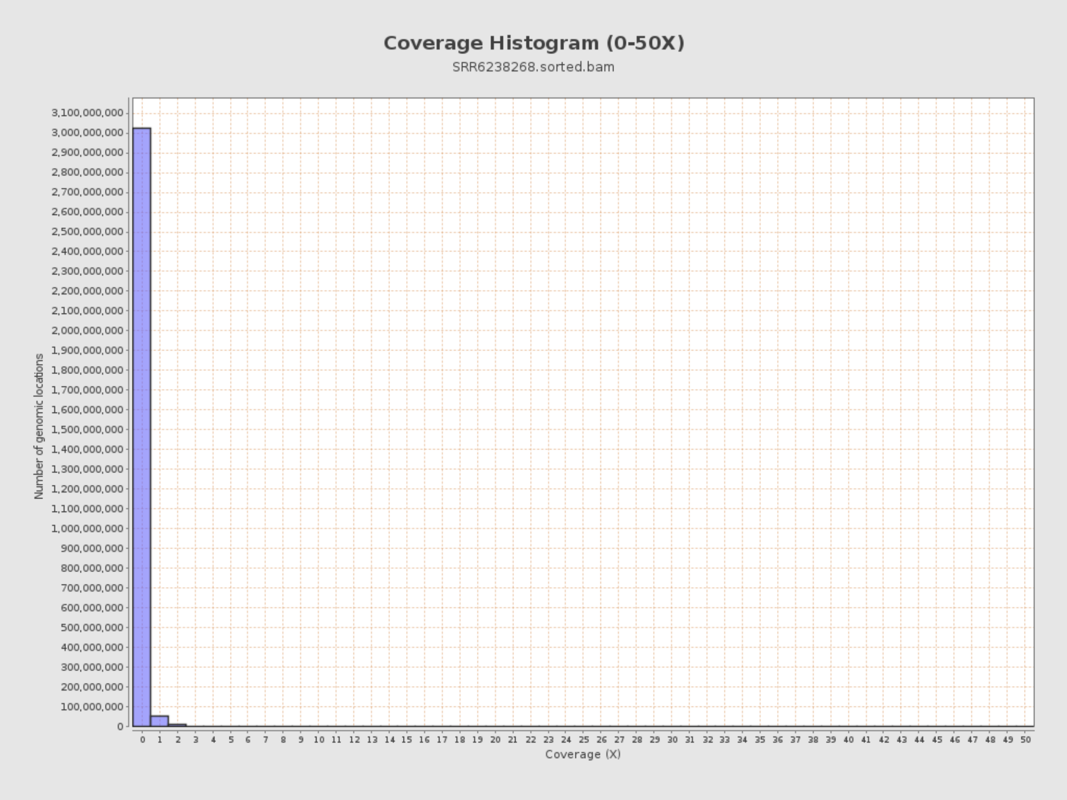
3. Results : Coverage across reference



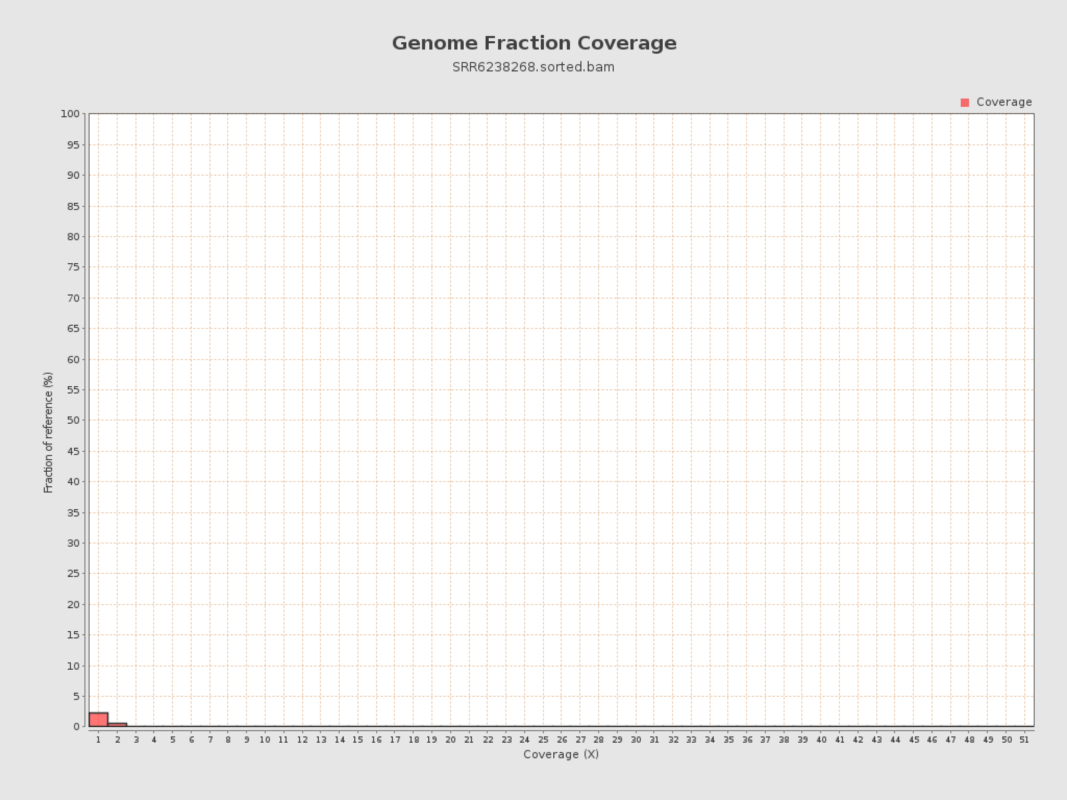
4. Results : Coverage Histogram



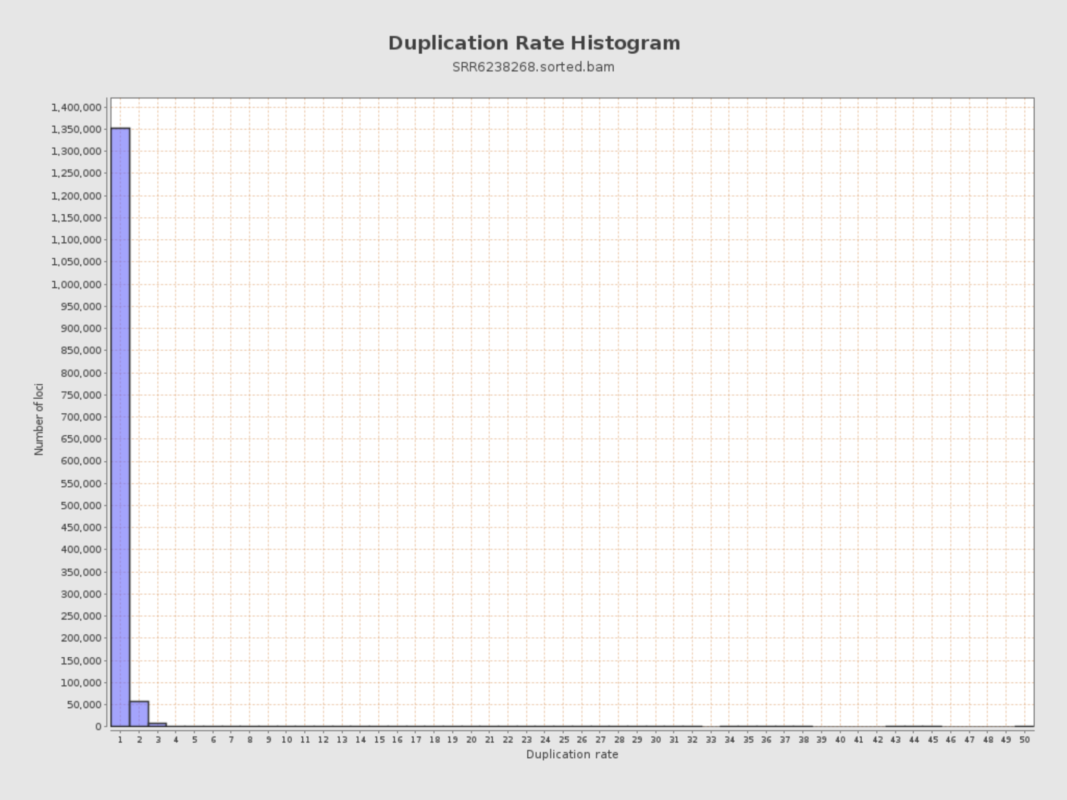
5. Results : Coverage Histogram (0-50X)



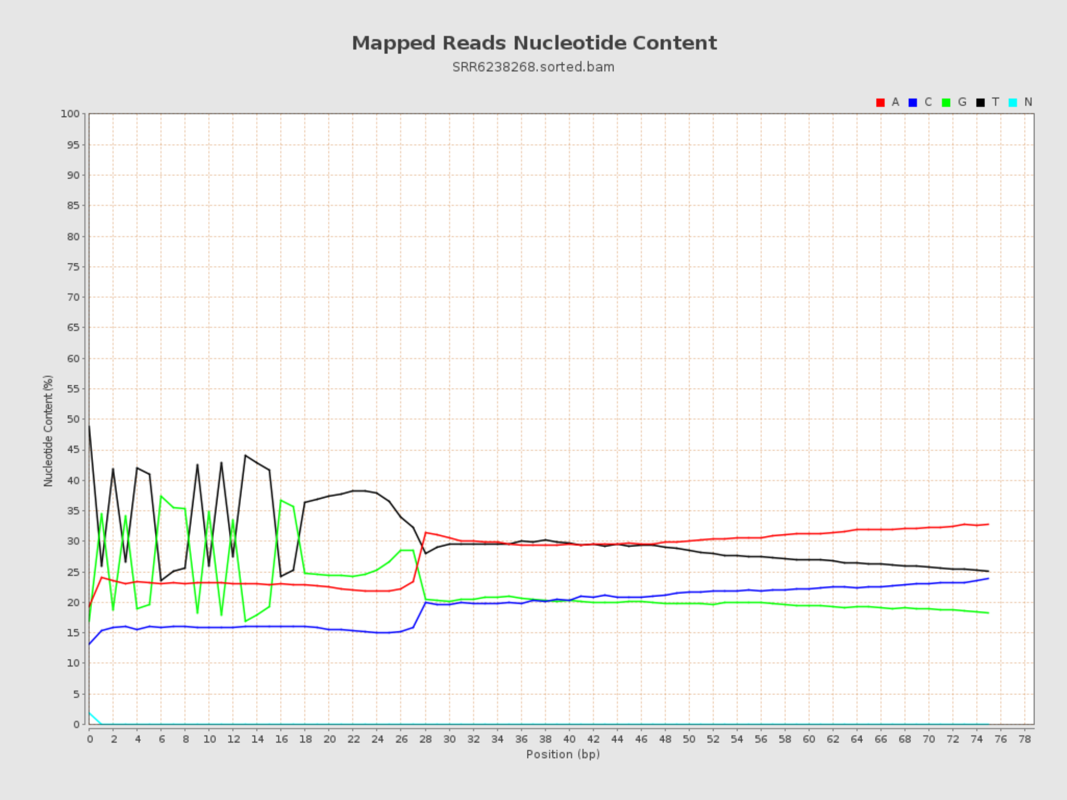
6. Results : Genome Fraction Coverage



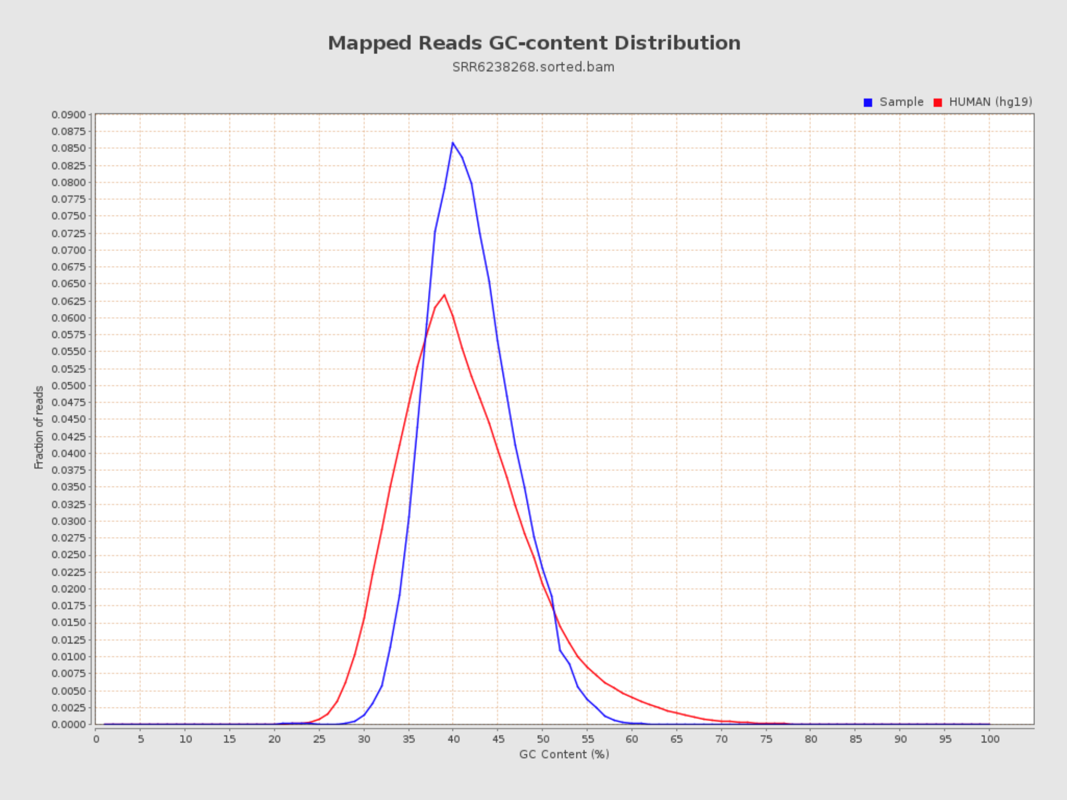
7. Results : Duplication Rate Histogram



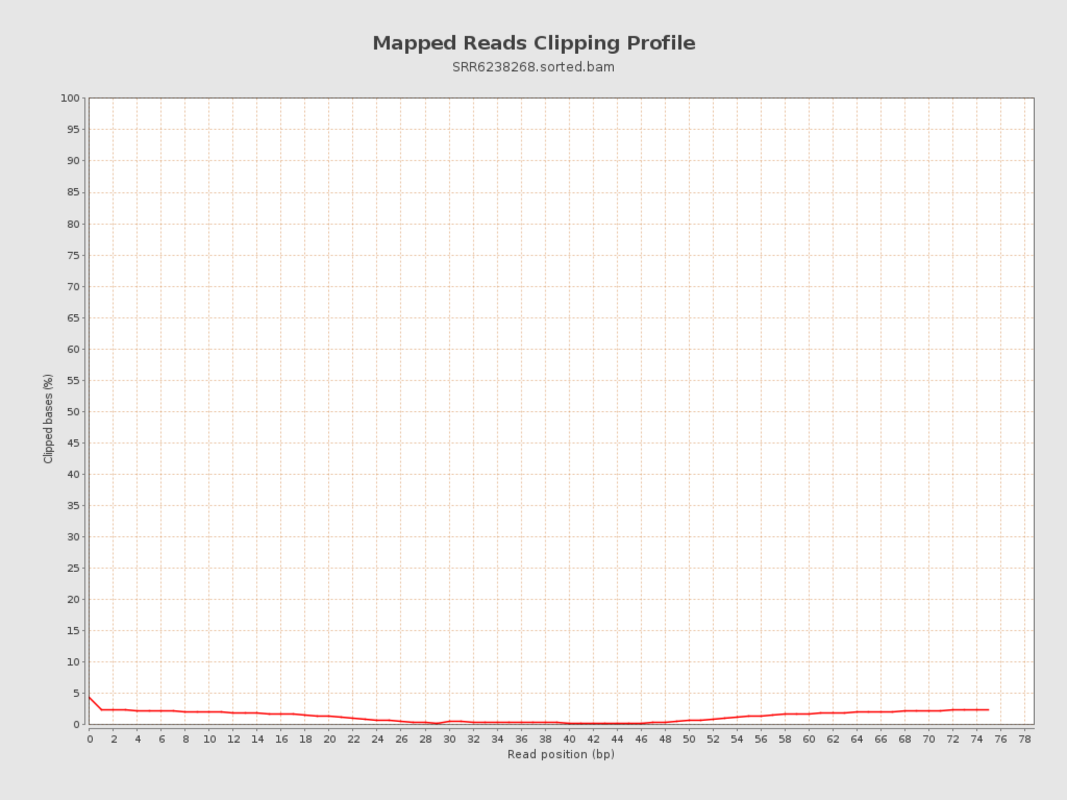
8. Results : Mapped Reads Nucleotide Content



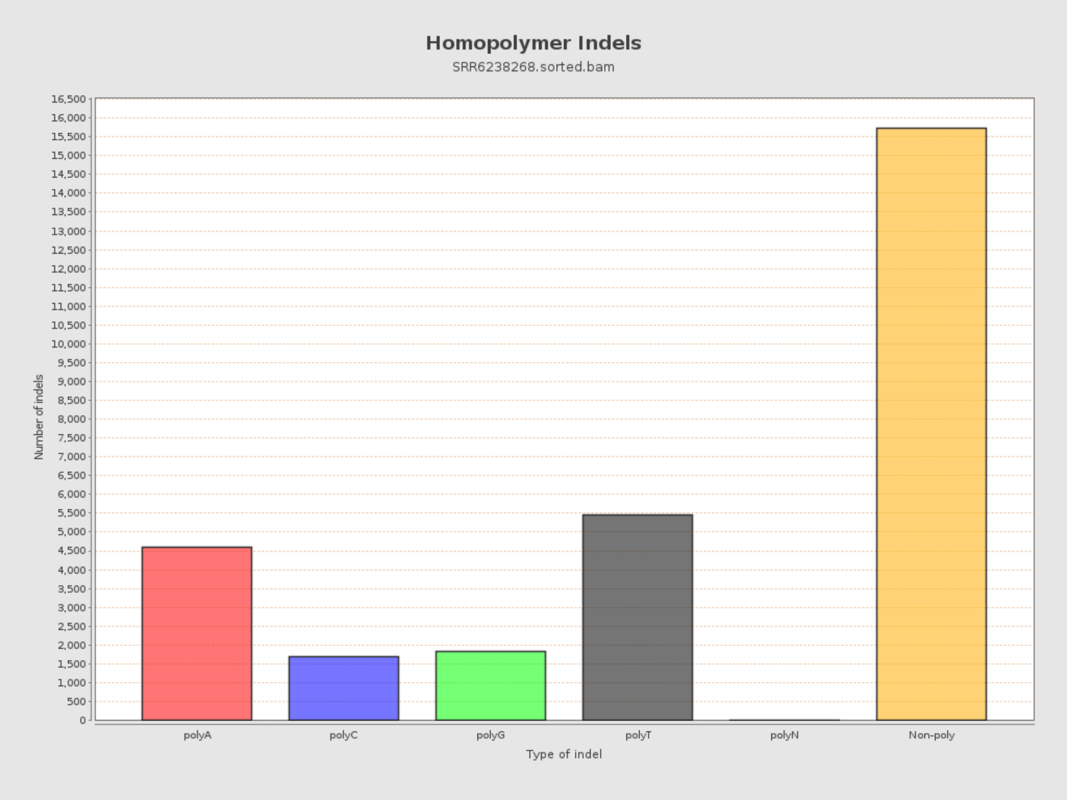
9. Results : Mapped Reads GC-content Distribution



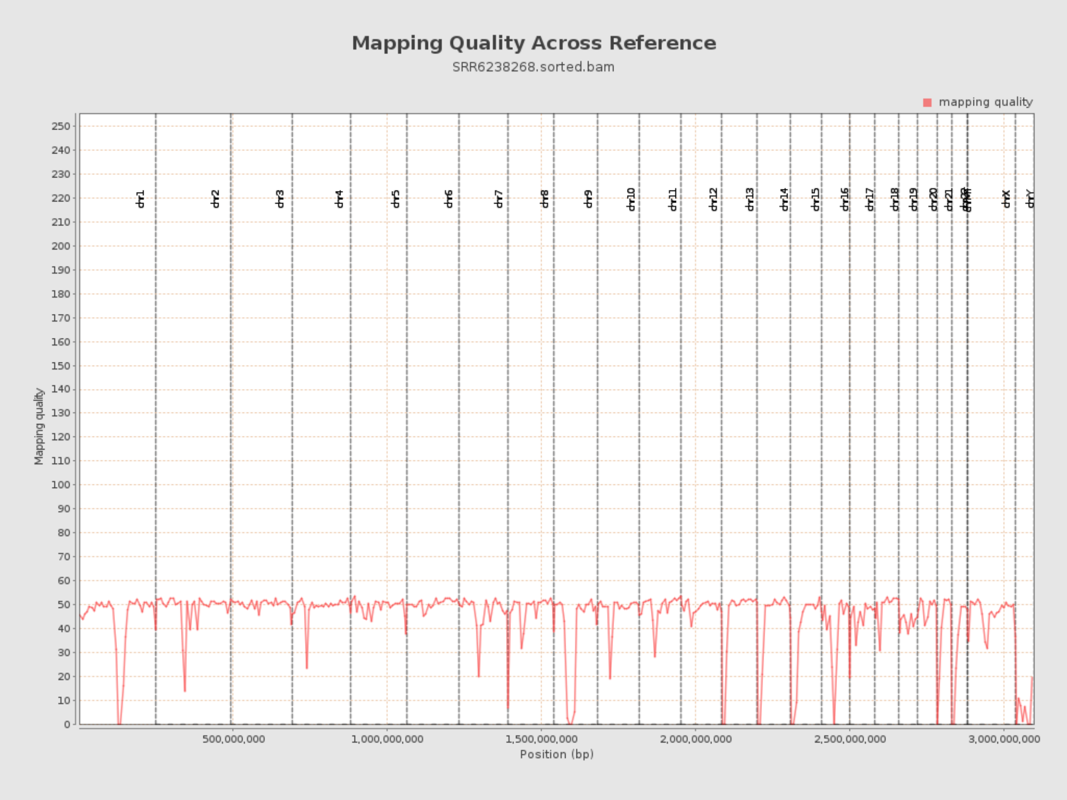
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram