Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 14:04:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238274.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_SRR6238274 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238274.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 14:04:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238274.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,577,600
Mapped reads	1,437,876 / 91.14%
Unmapped reads	139,724 / 8.86%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,935 / 0.76%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	44,927 / 2.85%
Duplication rate	2.05%
Clipped reads	639,231 / 40.52%

2.2. ACGT Content

Number/percentage of A's	26,979,083 / 28.07%
Number/percentage of C's	18,341,530 / 19.08%
Number/percentage of T's	29,402,017 / 30.59%
Number/percentage of G's	21,373,319 / 22.24%
Number/percentage of N's	19,995 / 0.02%
GC Percentage	41.32%

2.3. Coverage

Mean	0.0311

Standard Deviation	0.3445

2.4. Mapping Quality

Mean Mapping Quality	44.4

2.5. Mismatches and indels

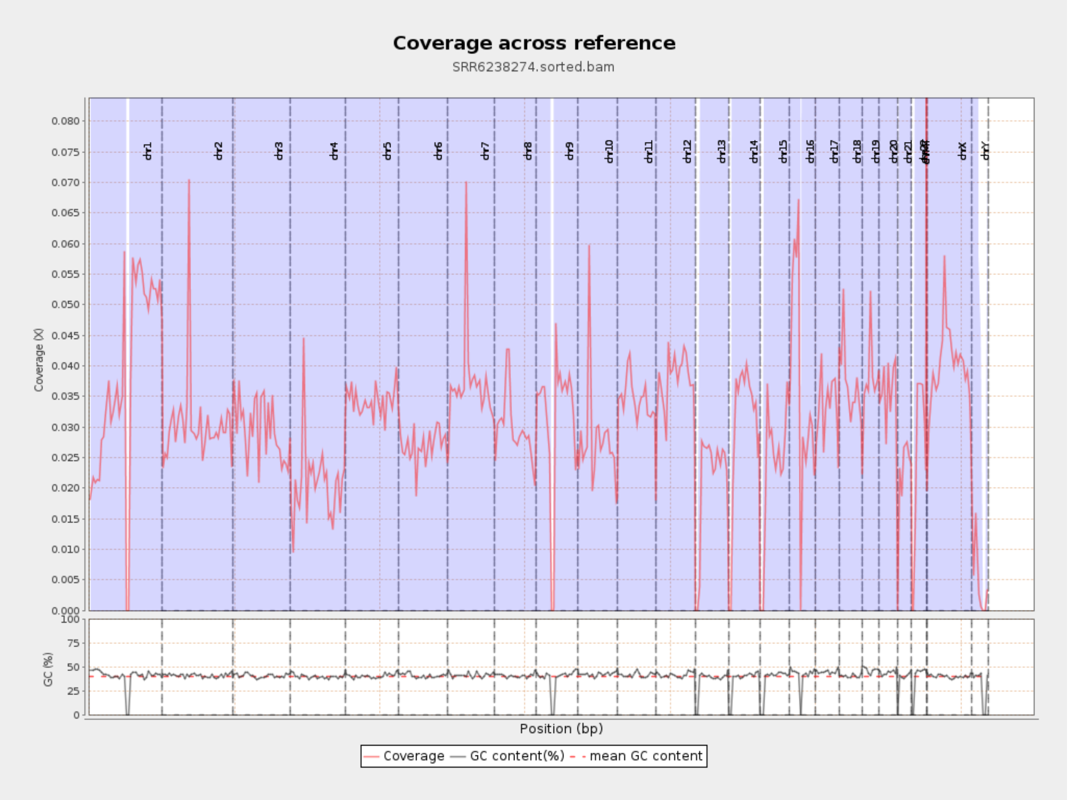
General error rate	0.91%
Mismatches	860,054
Insertions	8,521
Mapped reads with at least one insertion	0.59%
Deletions	30,790
Mapped reads with at least one deletion	2.11%
Homopolymer indels	45.65%

2.6. Chromosome stats

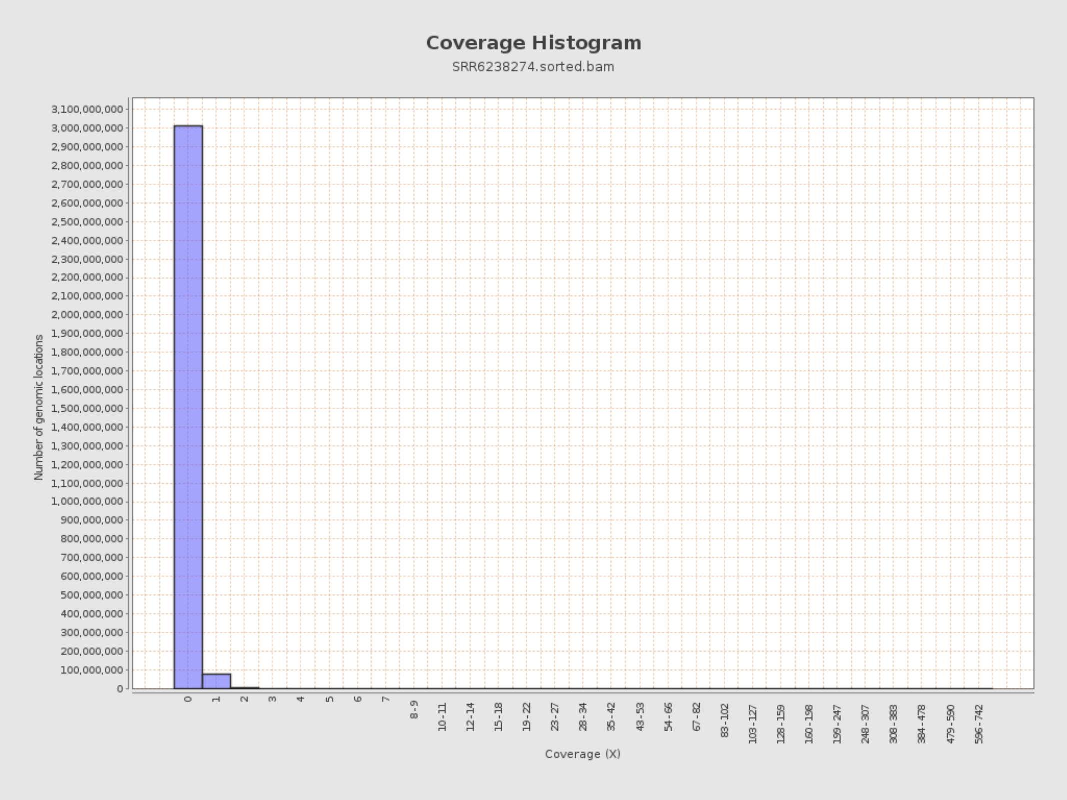
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9558288	0.0383	0.6536
chr2	243199373	7448273	0.0306	0.3778
chr3	198022430	5875178	0.0297	0.1896
chr4	191154276	3956411	0.0207	0.1811
chr5	180915260	6211016	0.0343	0.2045
chr6	171115067	4640619	0.0271	0.2038
chr7	159138663	5959564	0.0374	0.4824

chr8	146364022	4329857	0.0296	0.4144
chr9	141213431	4422367	0.0313	0.3525
chr10	135534747	3788091	0.0279	0.3284
chr11	135006516	4643320	0.0344	0.3034
chr12	133851895	5075255	0.0379	0.218
chr13	115169878	2420250	0.021	0.1552
chr14	107349540	3229486	0.0301	0.2274
chr15	102531392	2406690	0.0235	0.1683
chr16	90354753	3330114	0.0369	0.2478
chr17	81195210	2679203	0.033	0.2353
chr18	78077248	2921955	0.0374	0.68
chr19	59128983	2252425	0.0381	0.4236
chr20	63025520	2256019	0.0358	0.2081
chr21	48129895	1059689	0.022	0.2011
chr22	51304566	1251597	0.0244	0.1697
chrMT	16571	3199	0.193	0.5141
chrX	155270560	6163674	0.0397	0.2466
chrY	59373566	285214	0.0048	0.1439

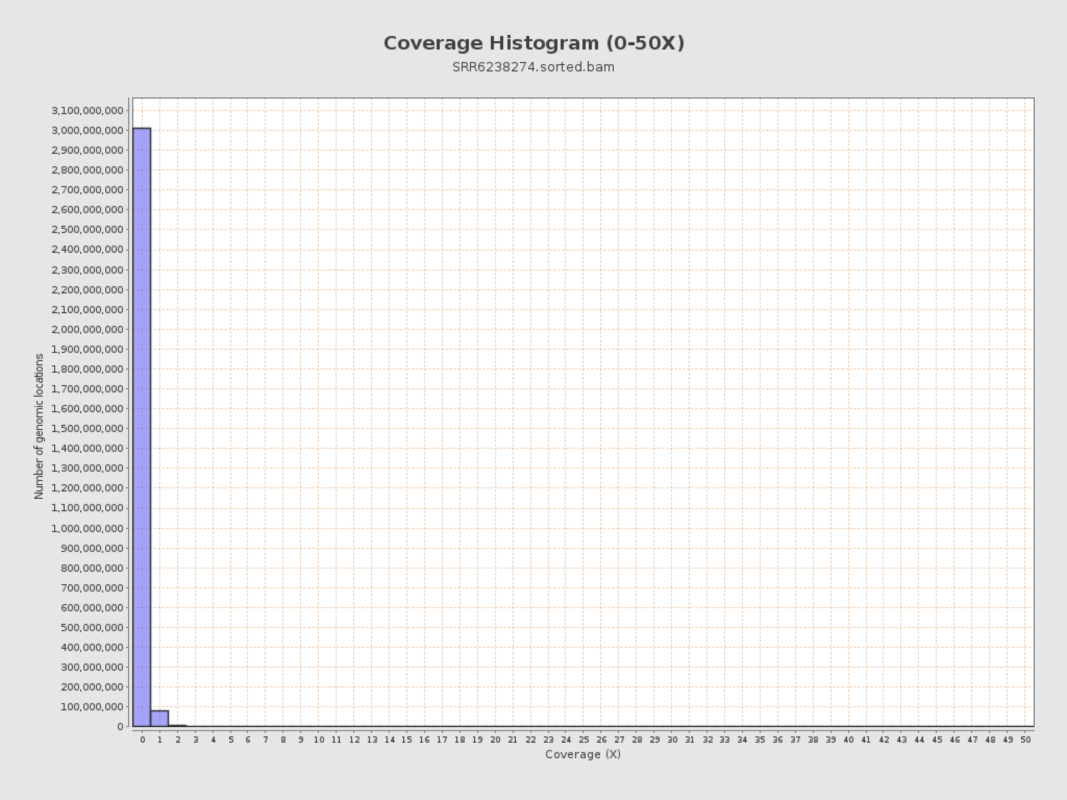
3. Results : Coverage across reference



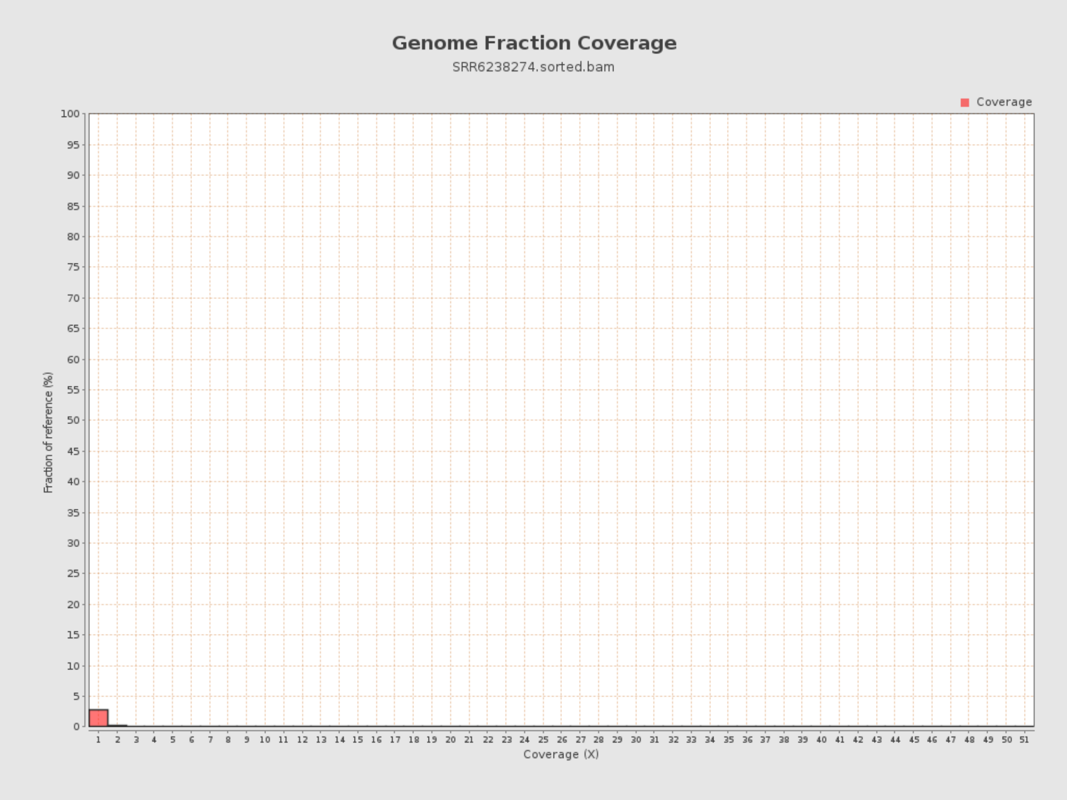
4. Results : Coverage Histogram



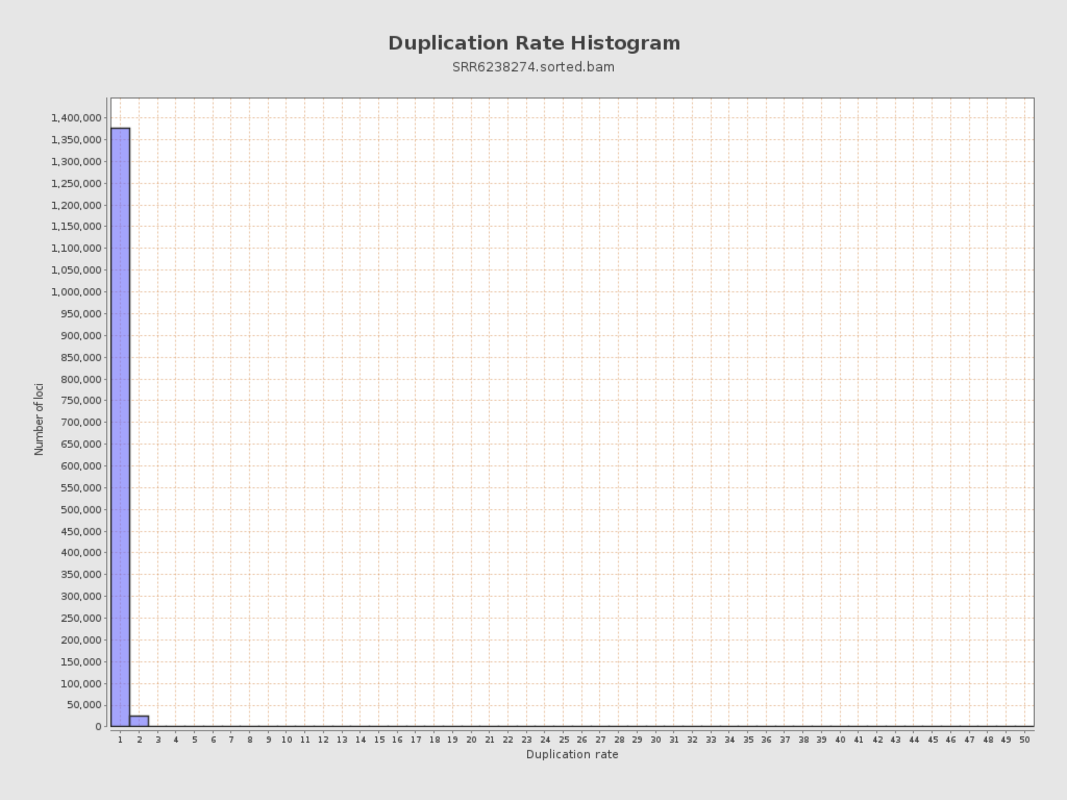
5. Results : Coverage Histogram (0-50X)



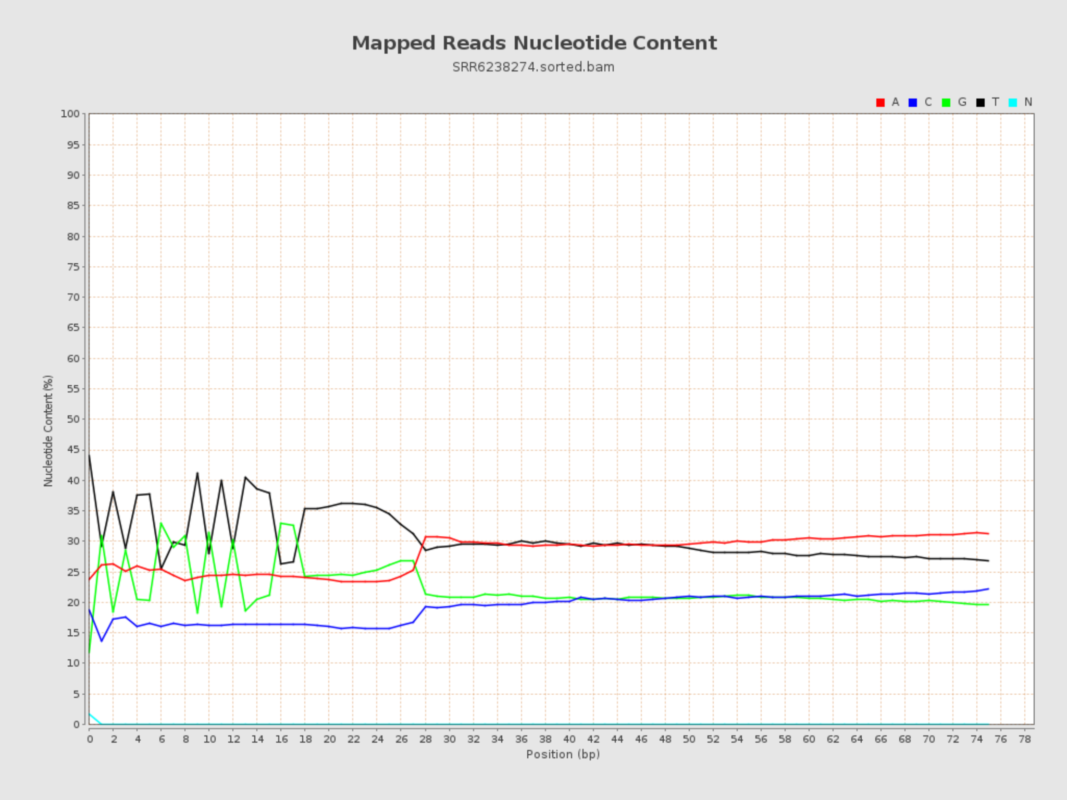
6. Results : Genome Fraction Coverage



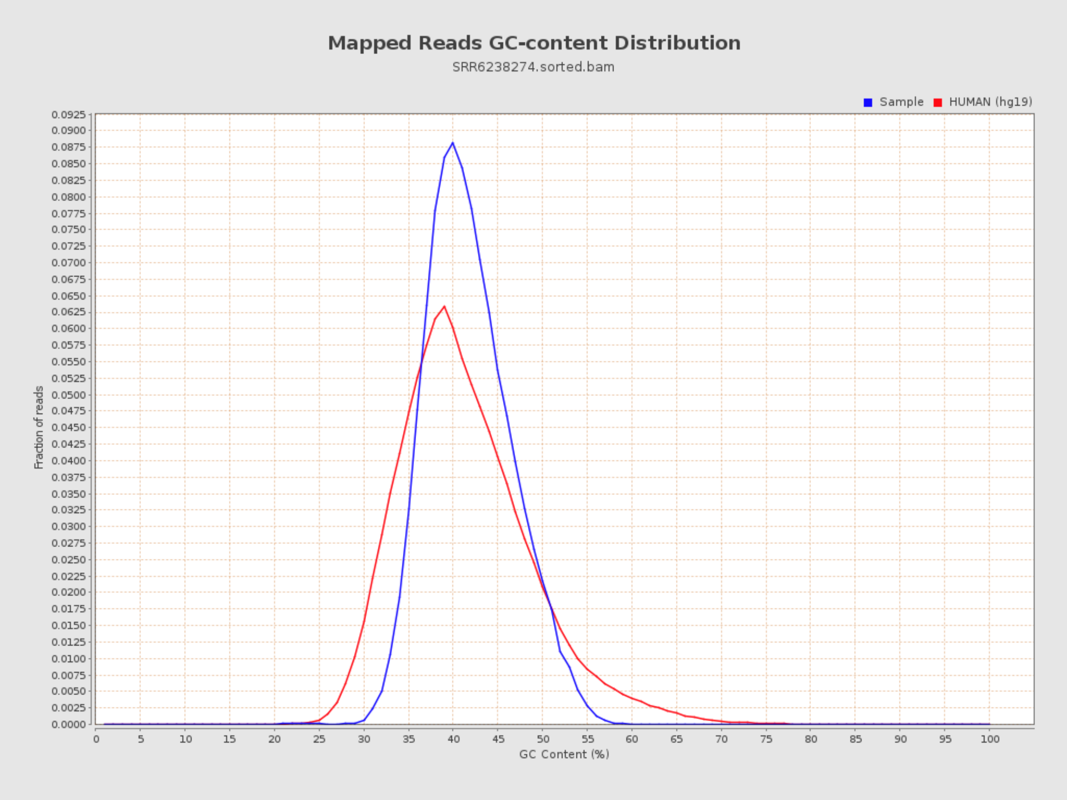
7. Results : Duplication Rate Histogram



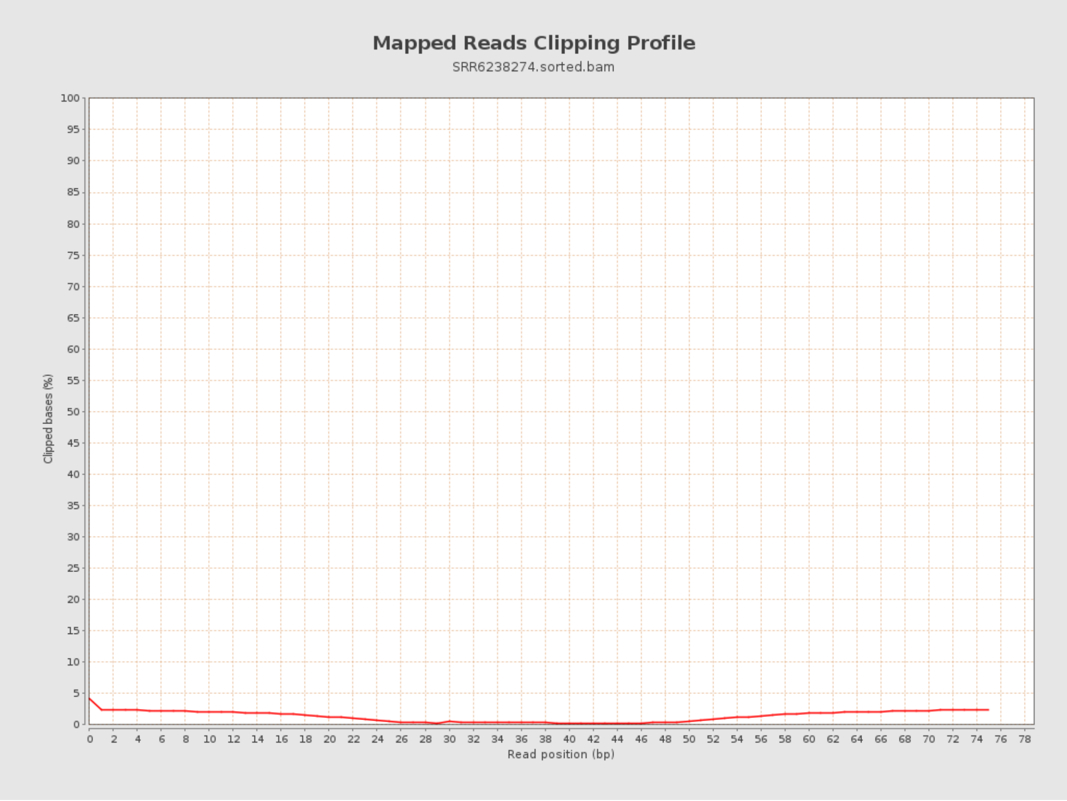
8. Results : Mapped Reads Nucleotide Content



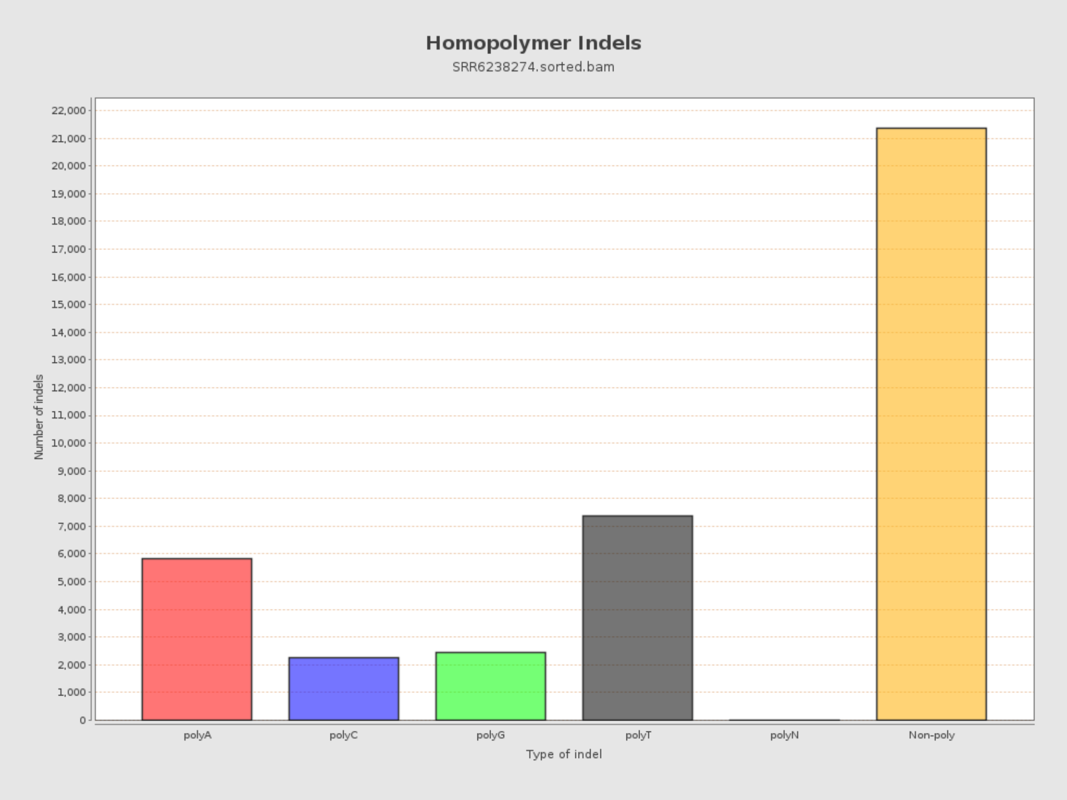
9. Results : Mapped Reads GC-content Distribution



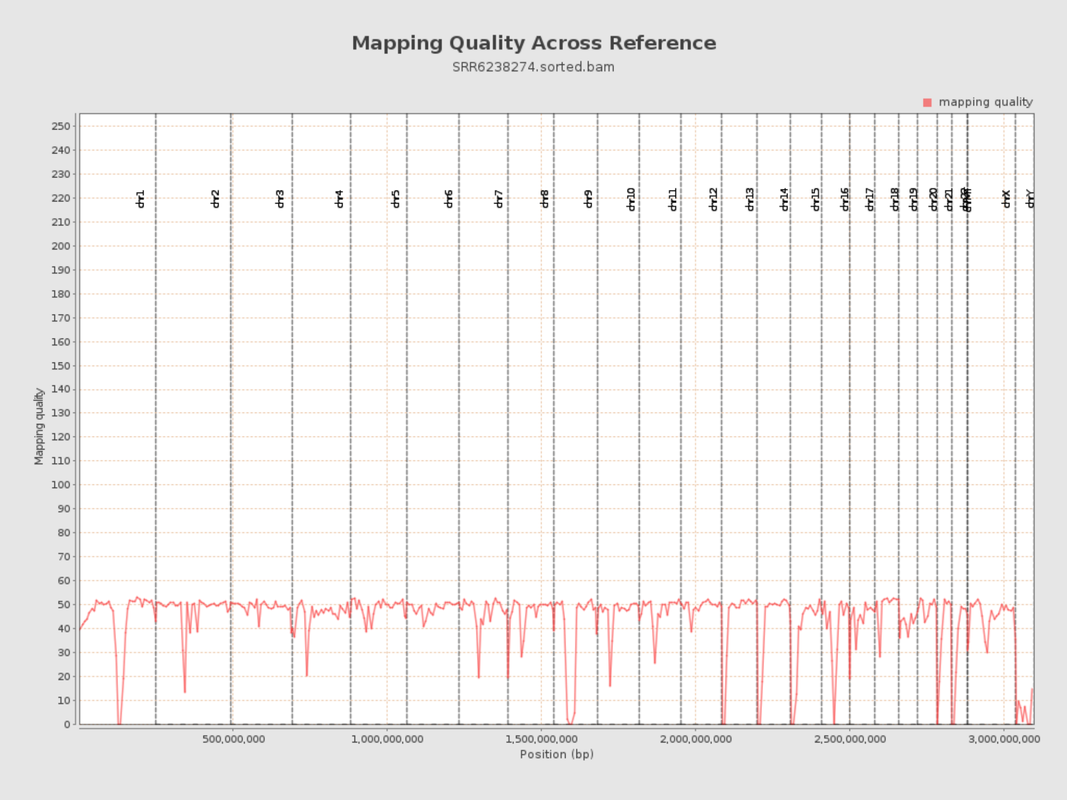
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram