Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 16:29:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238321.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_SRR6238321 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238321.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 16:29:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238321.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,440,545
Mapped reads	2,156,865 / 88.38%
Unmapped reads	283,680 / 11.62%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	32,401 / 1.33%
Read min/max/mean length	30 / 76 / 76.46
Duplicated reads (estimated)	184,130 / 7.54%
Duplication rate	6.79%
Clipped reads	1,194,450 / 48.94%

2.2. ACGT Content

Number/percentage of A's	39,351,777 / 28.21%
Number/percentage of C's	25,870,697 / 18.54%
Number/percentage of T's	44,096,459 / 31.61%
Number/percentage of G's	30,157,447 / 21.62%
Number/percentage of N's	42,537 / 0.03%
GC Percentage	40.16%

2.3. Coverage

Mean	0.0451

Standard Deviation	0.4687

2.4. Mapping Quality

Mean Mapping Quality	45.36

2.5. Mismatches and indels

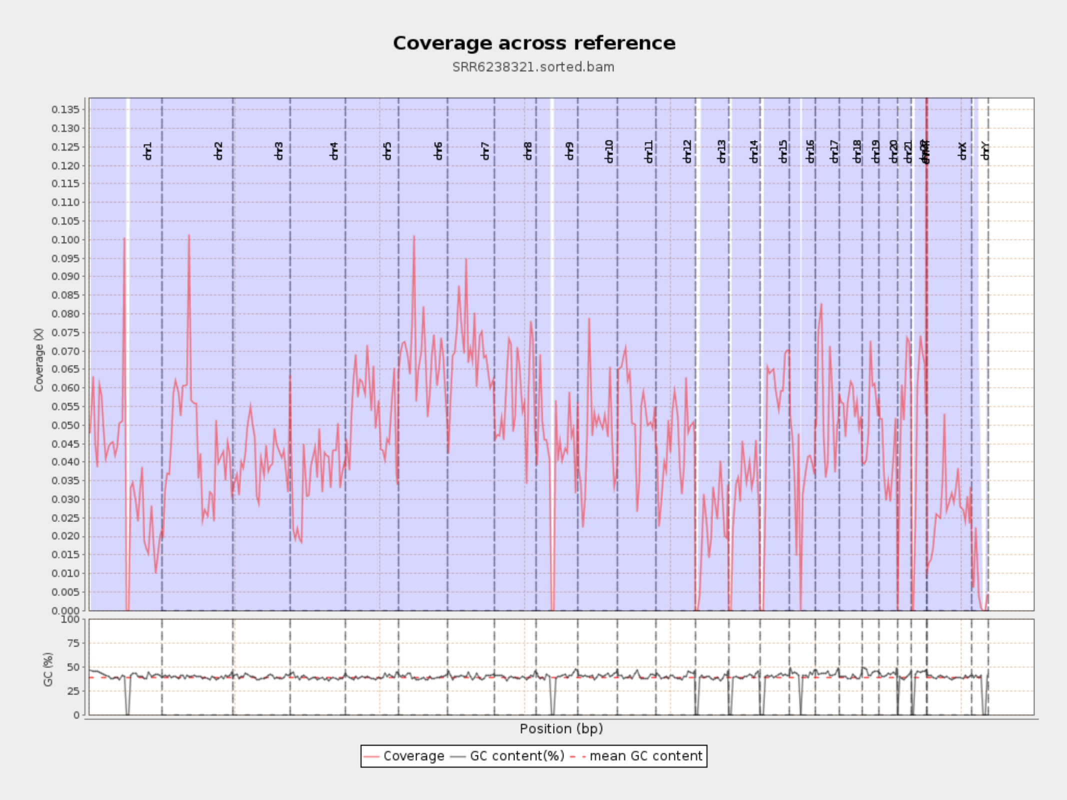
General error rate	0.91%
Mismatches	1,252,021
Insertions	10,809
Mapped reads with at least one insertion	0.5%
Deletions	44,760
Mapped reads with at least one deletion	2.05%
Homopolymer indels	45.21%

2.6. Chromosome stats

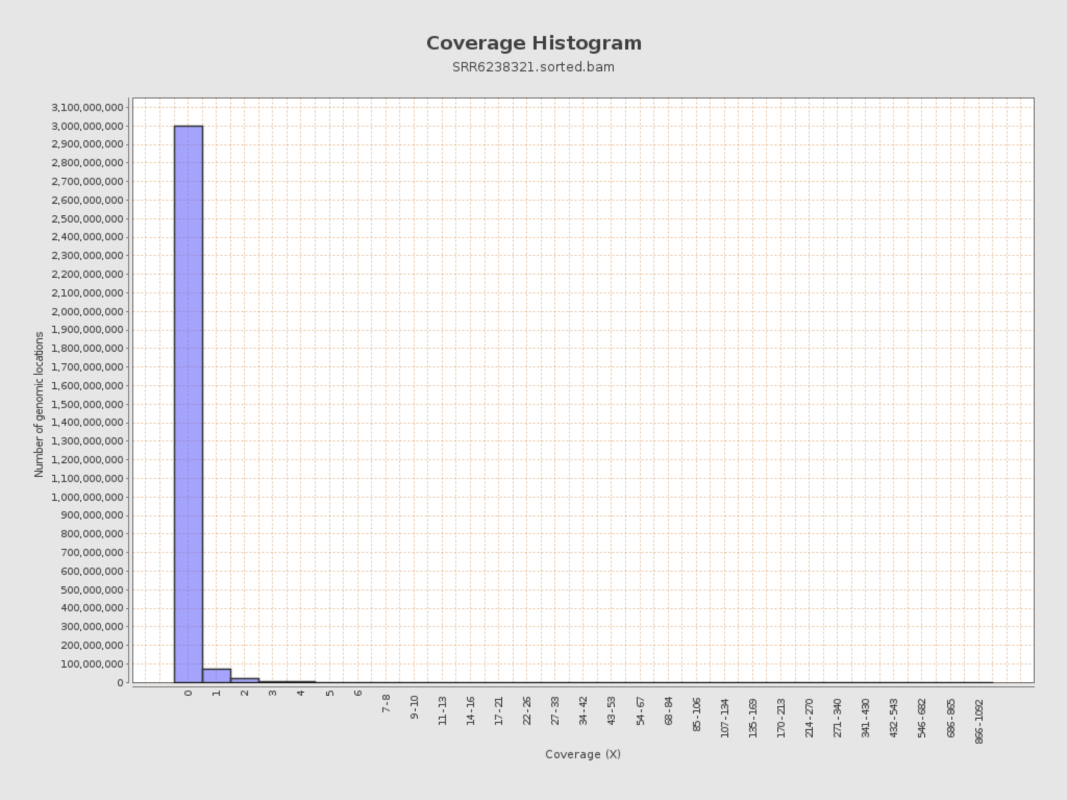
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9005906	0.0361	0.9106
chr2	243199373	10925640	0.0449	0.5083
chr3	198022430	8034031	0.0406	0.2696
chr4	191154276	6861894	0.0359	0.2801
chr5	180915260	9759927	0.0539	0.3156
chr6	171115067	11694279	0.0683	0.4533
chr7	159138663	11169727	0.0702	0.6136

chr8	146364022	8404441	0.0574	0.6881
chr9	141213431	5944596	0.0421	0.3733
chr10	135534747	6318594	0.0466	0.4044
chr11	135006516	7349178	0.0544	0.4039
chr12	133851895	5938565	0.0444	0.2881
chr13	115169878	2429984	0.0211	0.1953
chr14	107349540	3355688	0.0313	0.254
chr15	102531392	5295352	0.0516	0.311
chr16	90354753	3173805	0.0351	0.2699
chr17	81195210	4456768	0.0549	0.3789
chr18	78077248	4288259	0.0549	0.6542
chr19	59128983	3132225	0.053	0.6353
chr20	63025520	2530056	0.0401	0.2729
chr21	48129895	2577270	0.0535	0.3304
chr22	51304566	2377393	0.0463	0.2859
chrMT	16571	4665	0.2815	0.6787
chrX	155270560	4243633	0.0273	0.254
chrY	59373566	324814	0.0055	0.1999

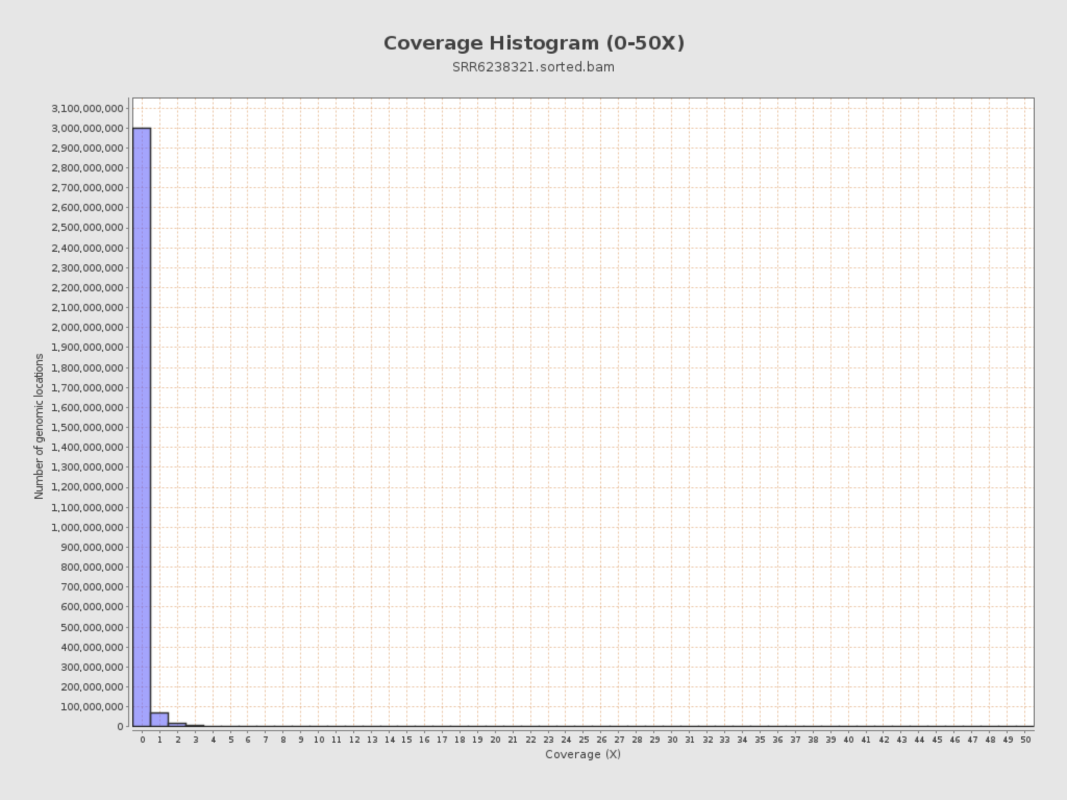
3. Results : Coverage across reference



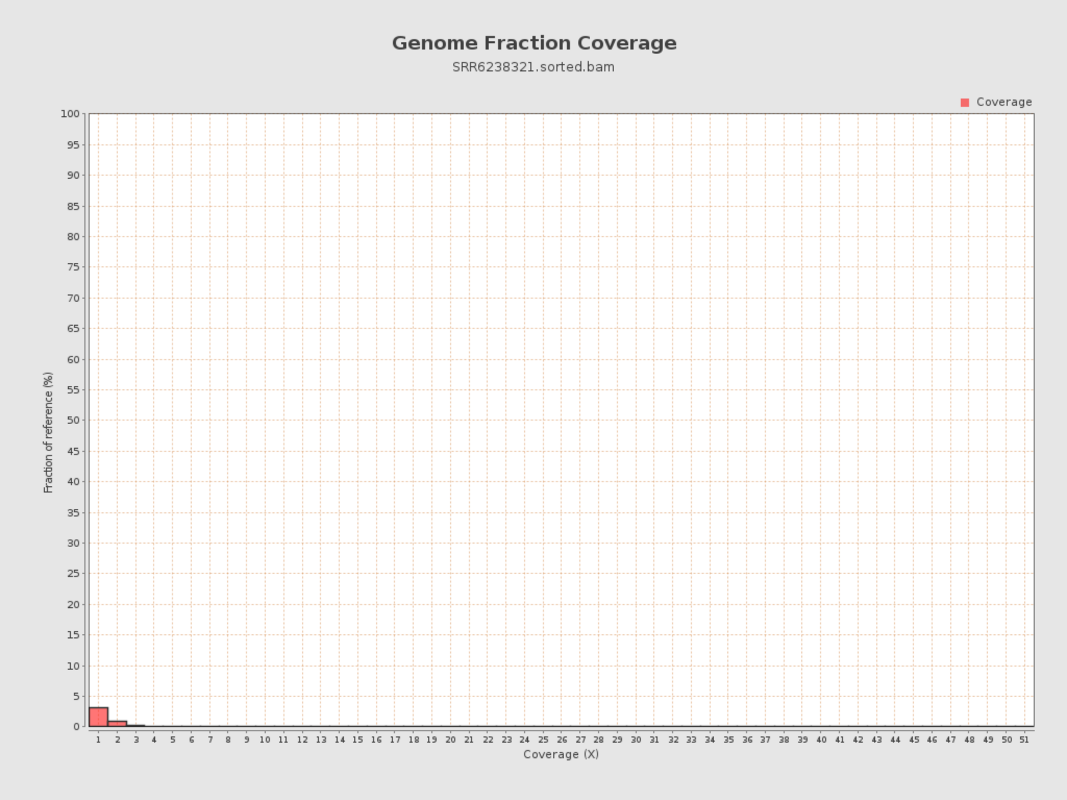
4. Results : Coverage Histogram



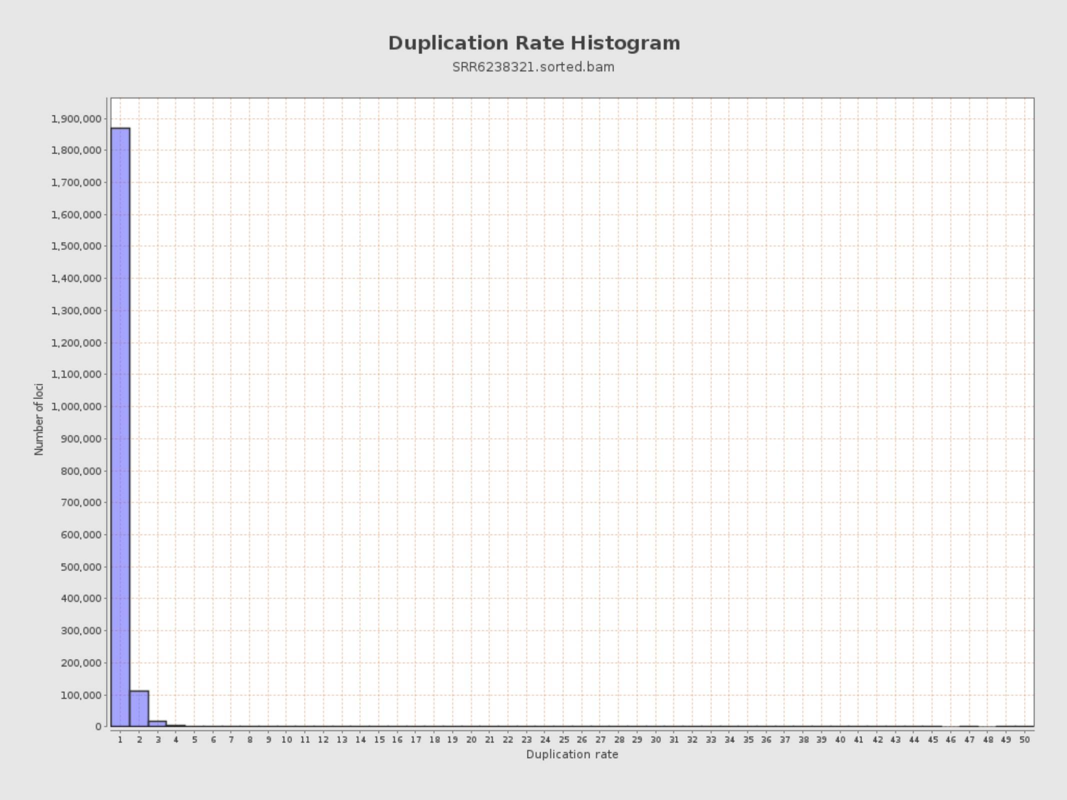
5. Results : Coverage Histogram (0-50X)



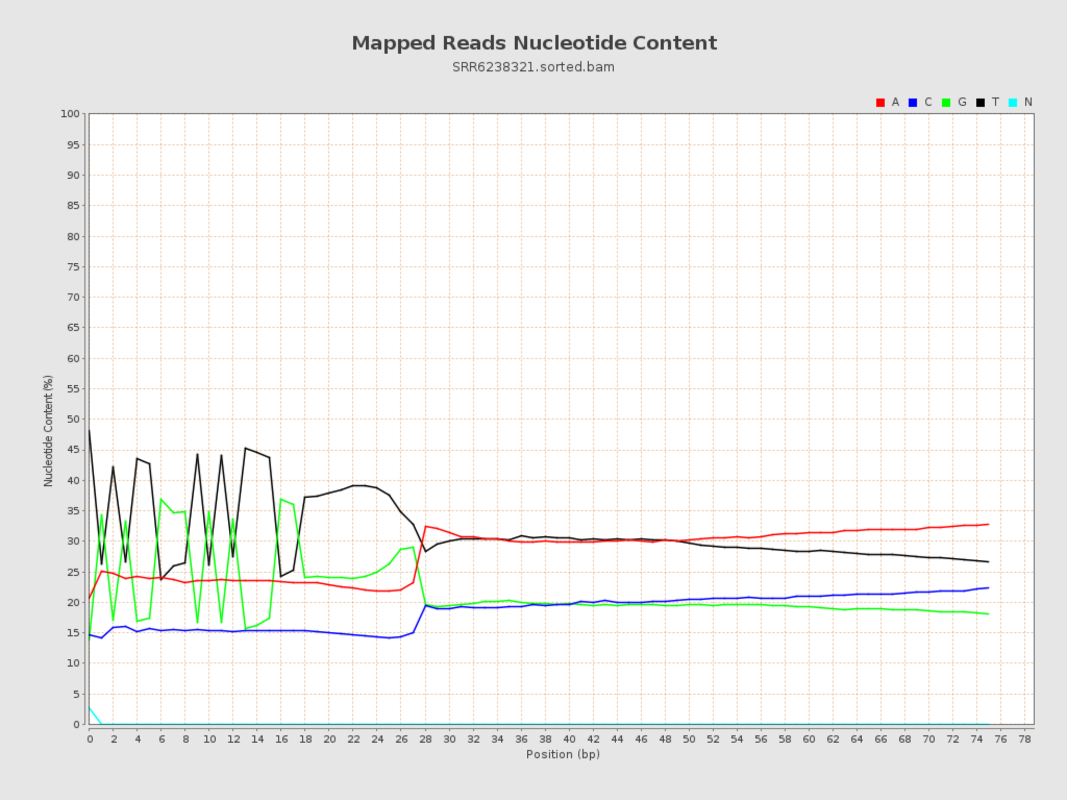
6. Results : Genome Fraction Coverage



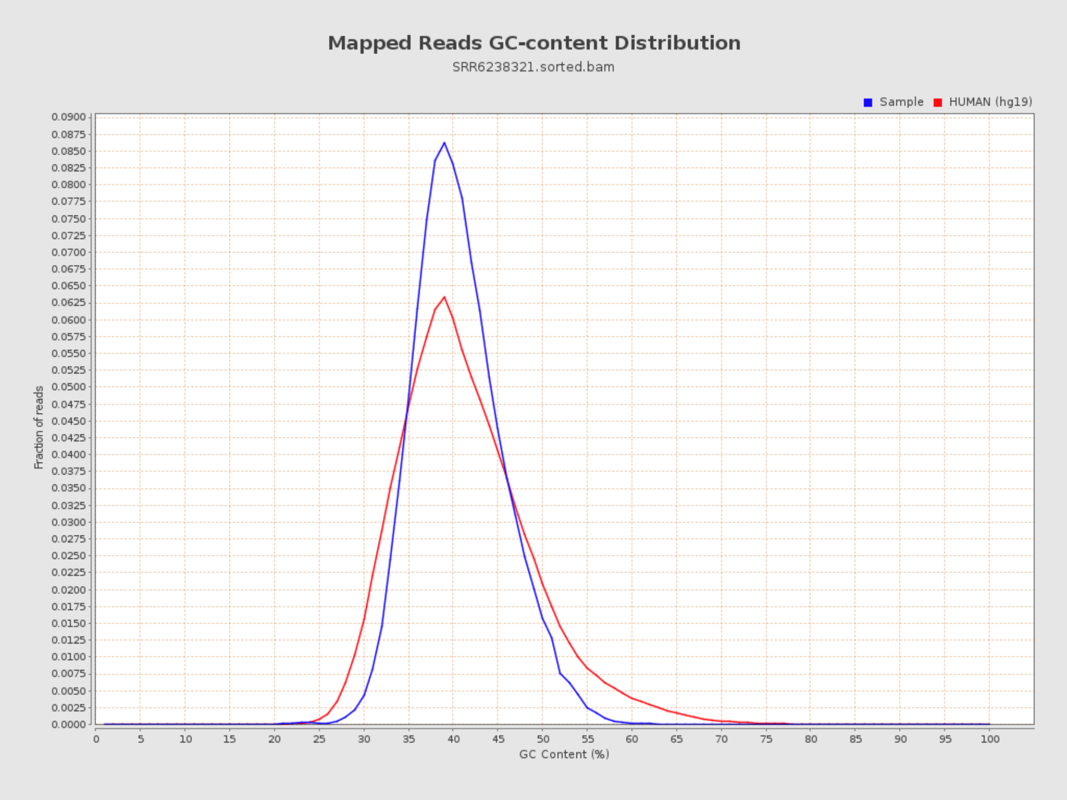
7. Results : Duplication Rate Histogram



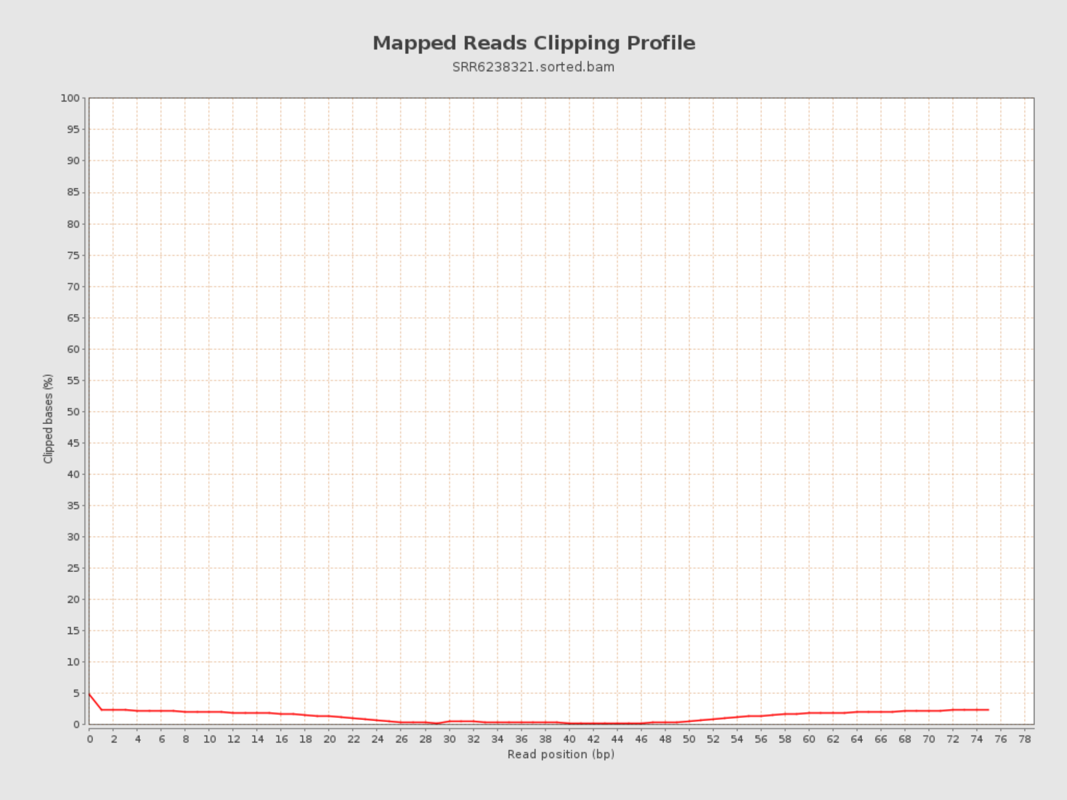
8. Results : Mapped Reads Nucleotide Content



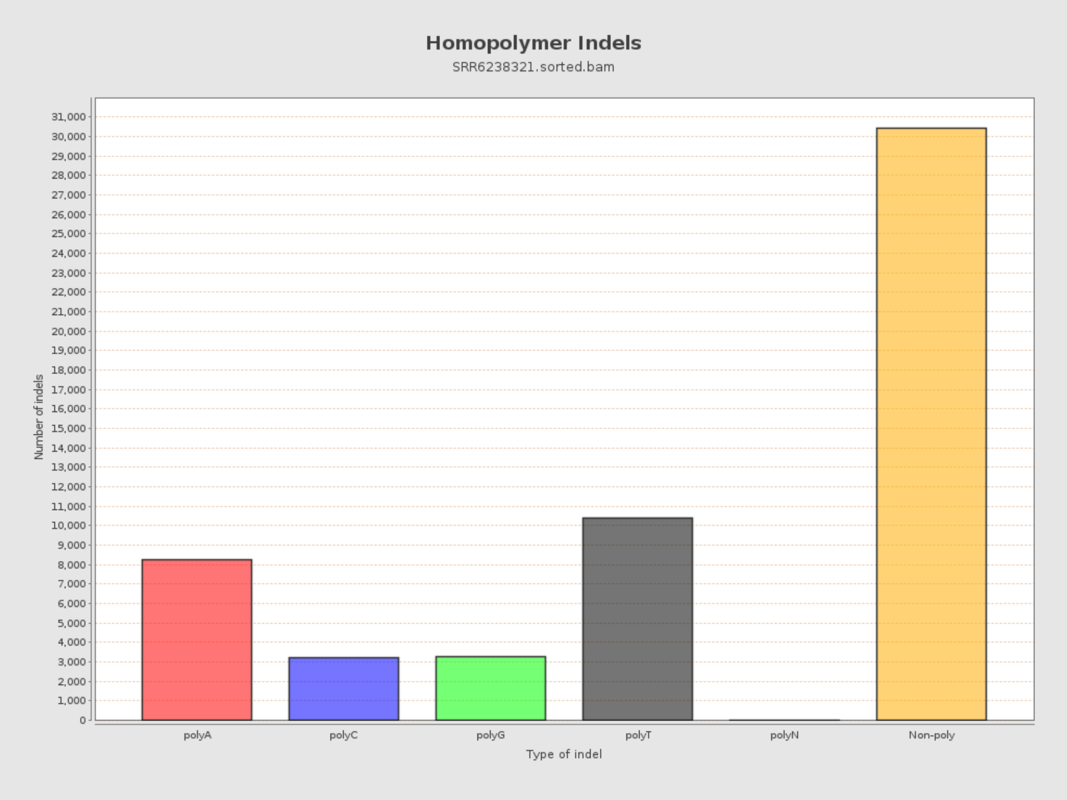
9. Results : Mapped Reads GC-content Distribution



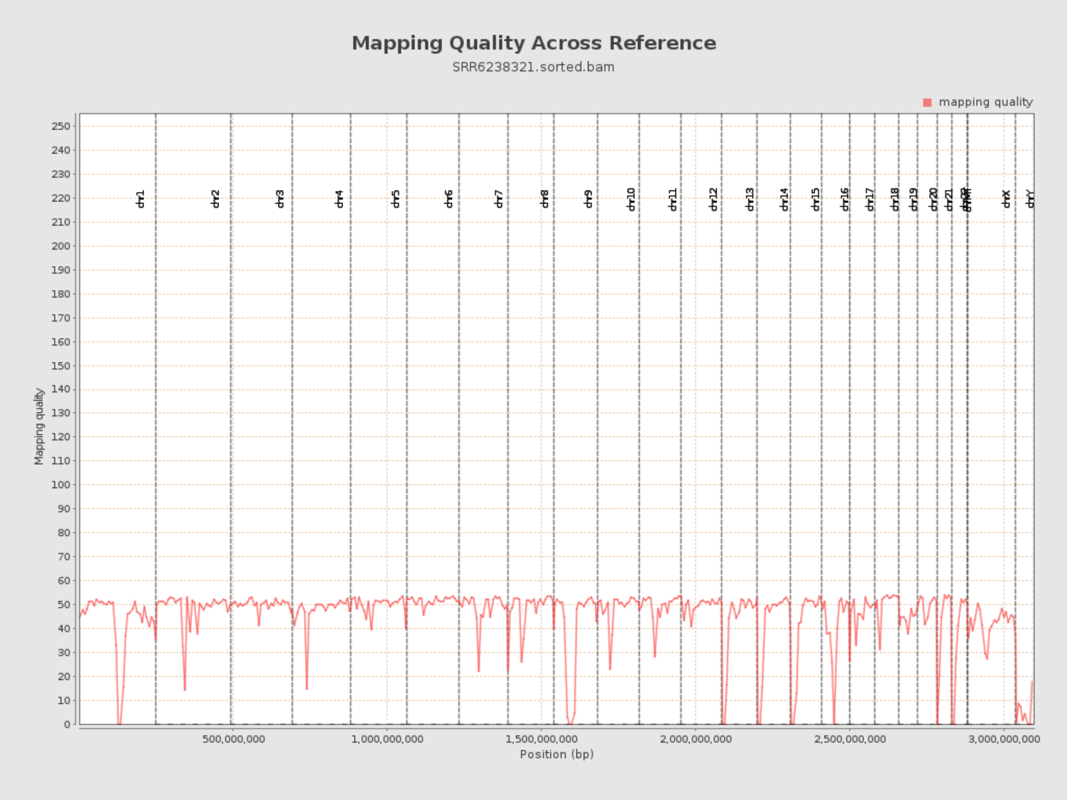
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram