Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 14:22:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238281.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_SRR6238281 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238281.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 14:22:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238281.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,152,324
Mapped reads	912,770 / 79.21%
Unmapped reads	239,554 / 20.79%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,277 / 0.98%
Read min/max/mean length	30 / 76 / 76.34
Duplicated reads (estimated)	80,628 / 7%
Duplication rate	7.15%
Clipped reads	490,312 / 42.55%

2.2. ACGT Content

Number/percentage of A's	16,470,879 / 27.88%
Number/percentage of C's	11,553,188 / 19.56%
Number/percentage of T's	17,946,645 / 30.38%
Number/percentage of G's	13,089,493 / 22.16%
Number/percentage of N's	11,928 / 0.02%
GC Percentage	41.72%

2.3. Coverage

Mean	0.0191

Standard Deviation	0.231

2.4. Mapping Quality

Mean Mapping Quality	45.35

2.5. Mismatches and indels

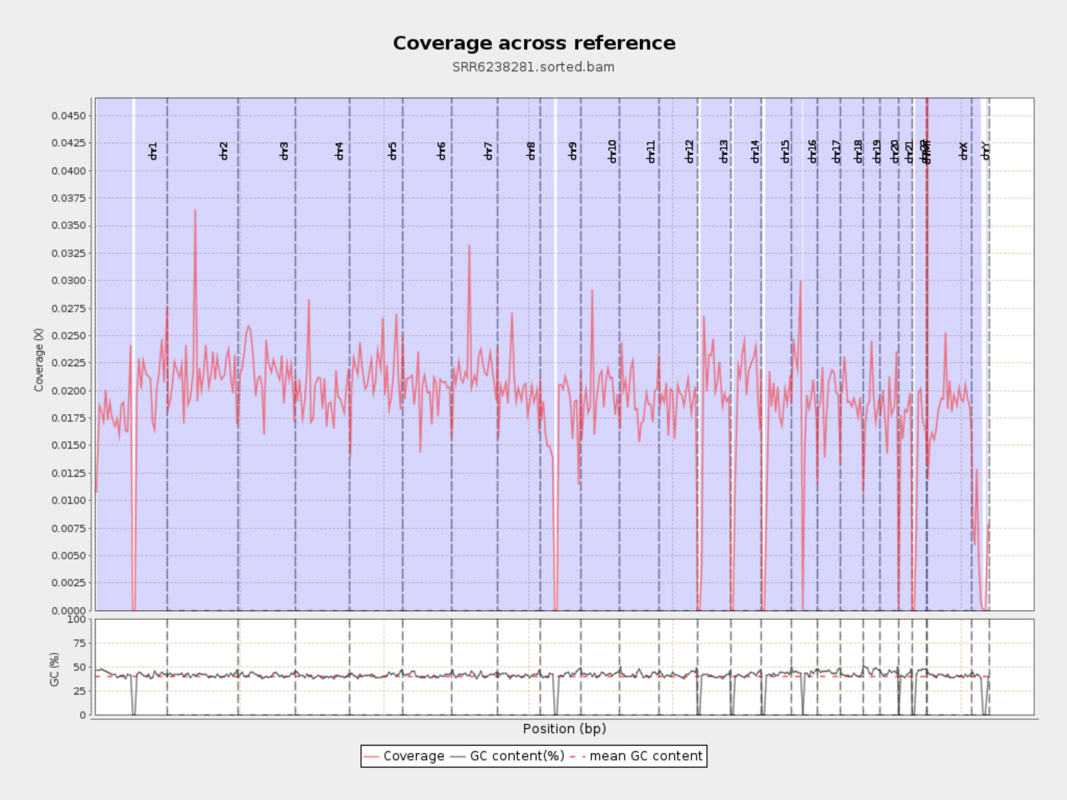
General error rate	0.97%
Mismatches	562,894
Insertions	4,732
Mapped reads with at least one insertion	0.51%
Deletions	21,754
Mapped reads with at least one deletion	2.35%
Homopolymer indels	45.76%

2.6. Chromosome stats

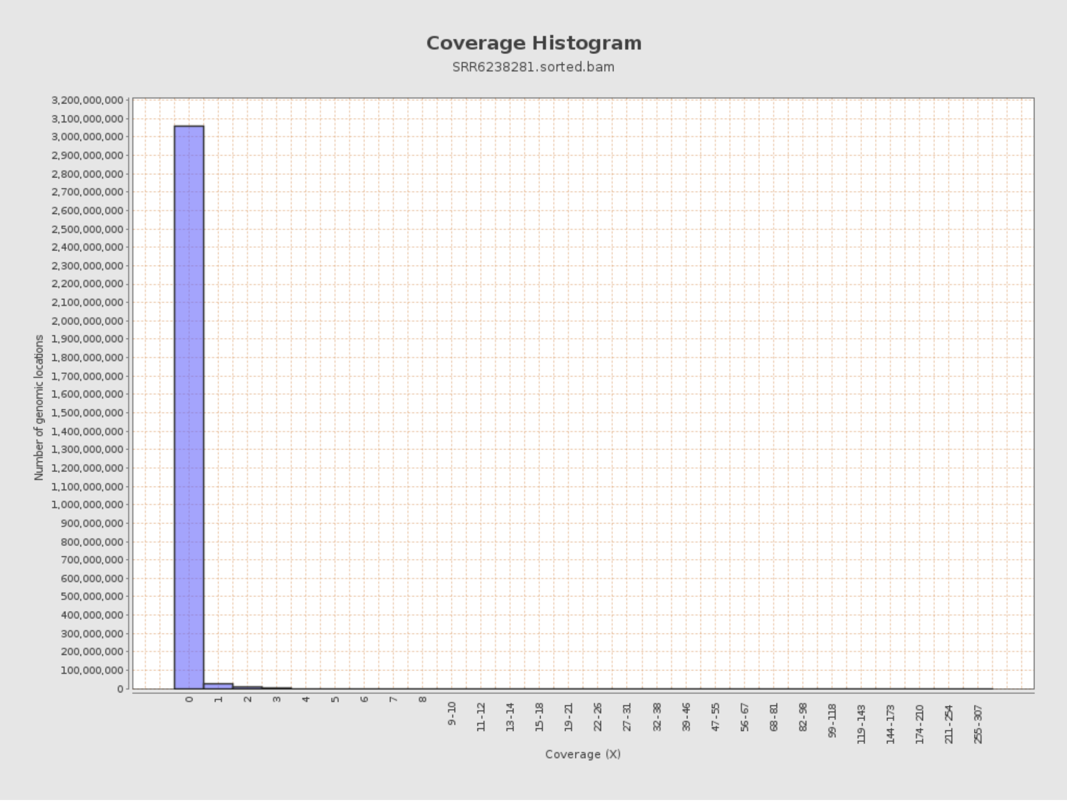
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4524501	0.0182	0.2878
chr2	243199373	5275548	0.0217	0.2693
chr3	198022430	4332765	0.0219	0.2118
chr4	191154276	3782446	0.0198	0.2065
chr5	180915260	3915325	0.0216	0.2087
chr6	171115067	3446902	0.0201	0.2158
chr7	159138663	3505229	0.022	0.2915

chr8	146364022	2916274	0.0199	0.2756
chr9	141213431	2233535	0.0158	0.201
chr10	135534747	2695898	0.0199	0.227
chr11	135006516	2613456	0.0194	0.2166
chr12	133851895	2553978	0.0191	0.1974
chr13	115169878	2054433	0.0178	0.1954
chr14	107349540	1948729	0.0182	0.2325
chr15	102531392	1621522	0.0158	0.2126
chr16	90354753	1727906	0.0191	0.2013
chr17	81195210	1560848	0.0192	0.204
chr18	78077248	1505136	0.0193	0.3024
chr19	59128983	1114163	0.0188	0.2464
chr20	63025520	1176686	0.0187	0.1952
chr21	48129895	768767	0.016	0.1858
chr22	51304566	655873	0.0128	0.1617
chrMT	16571	12431	0.7502	1.4237
chrX	155270560	2879901	0.0185	0.202
chrY	59373566	286168	0.0048	0.1133

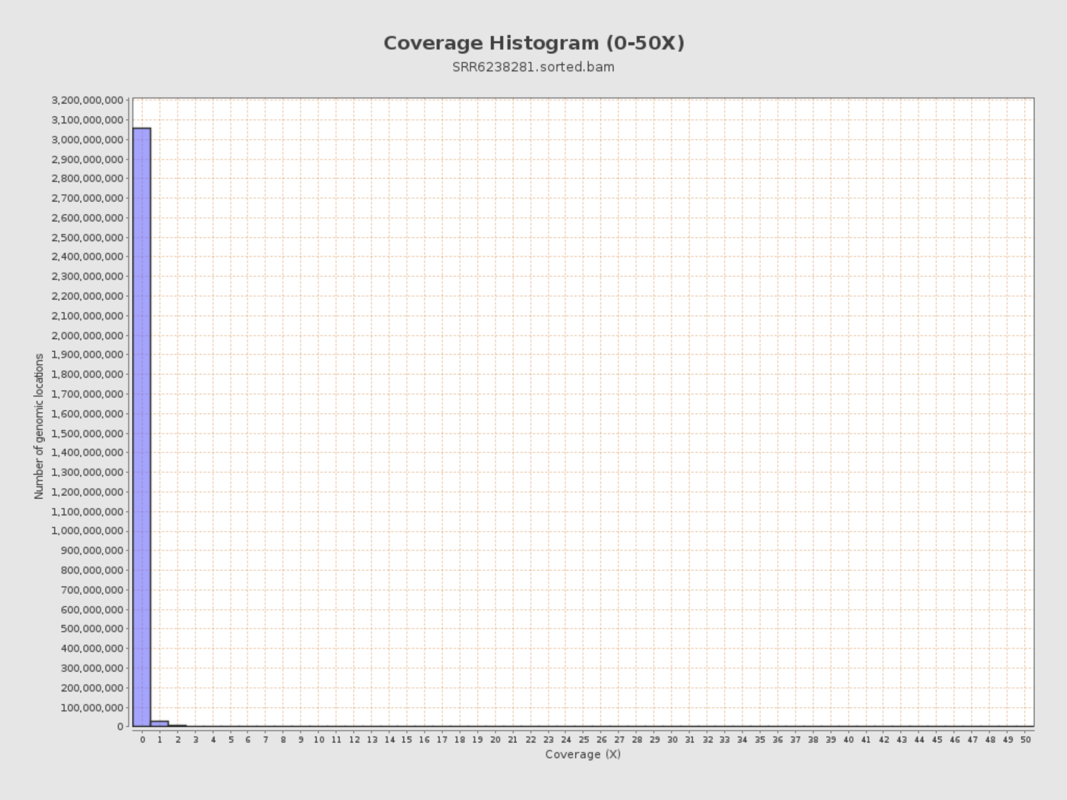
3. Results : Coverage across reference



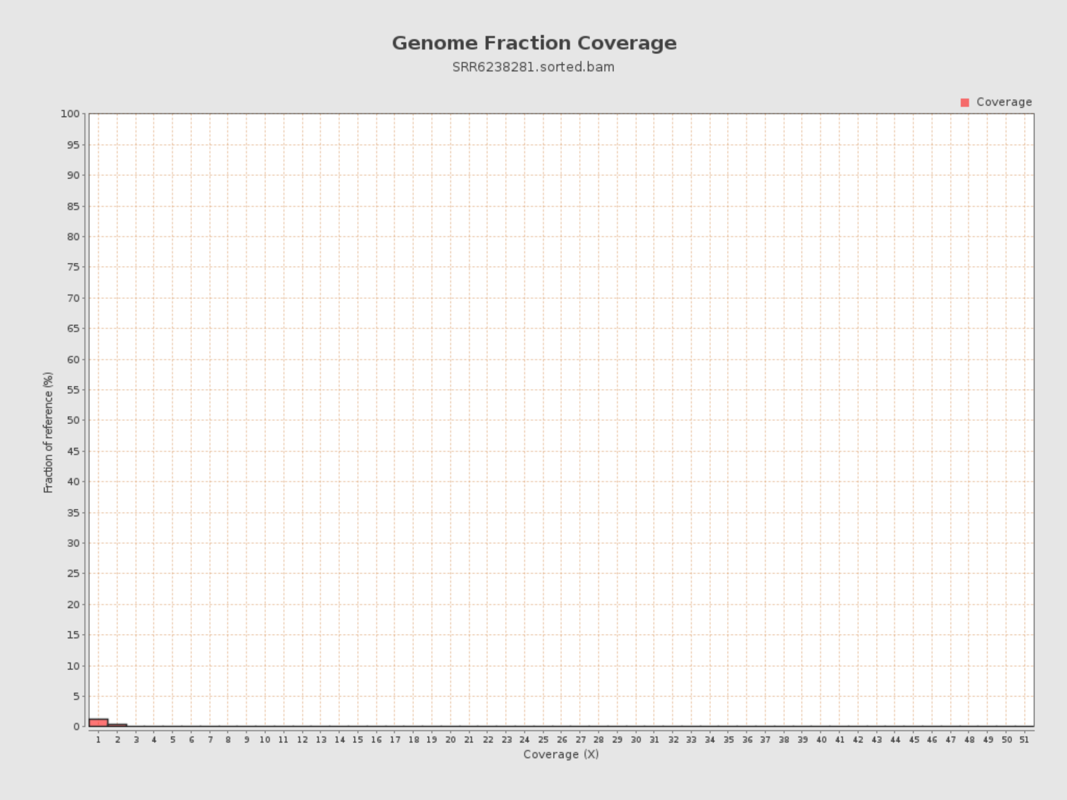
4. Results : Coverage Histogram



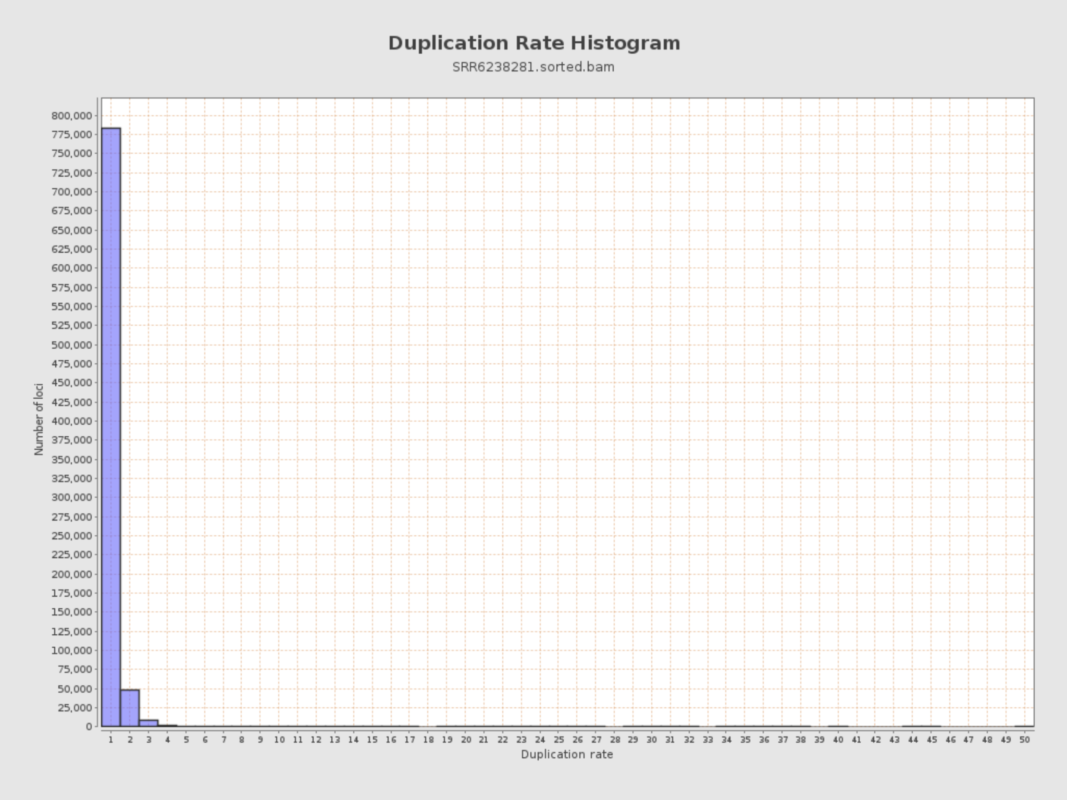
5. Results : Coverage Histogram (0-50X)



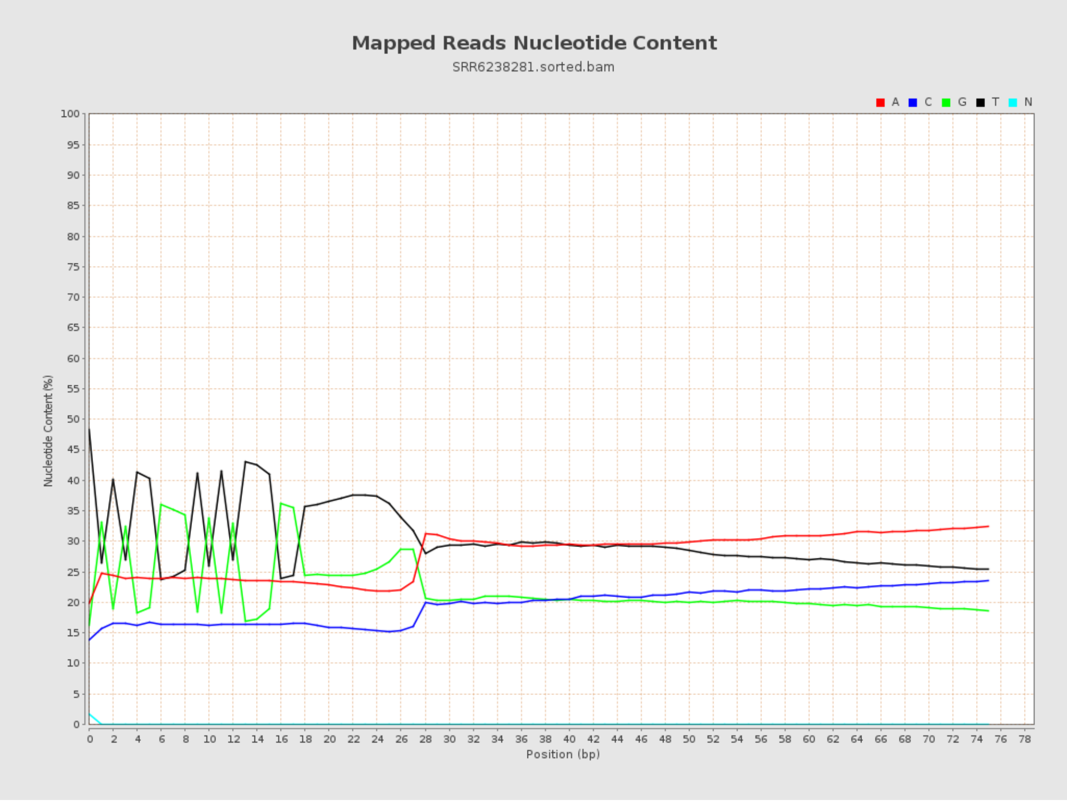
6. Results : Genome Fraction Coverage



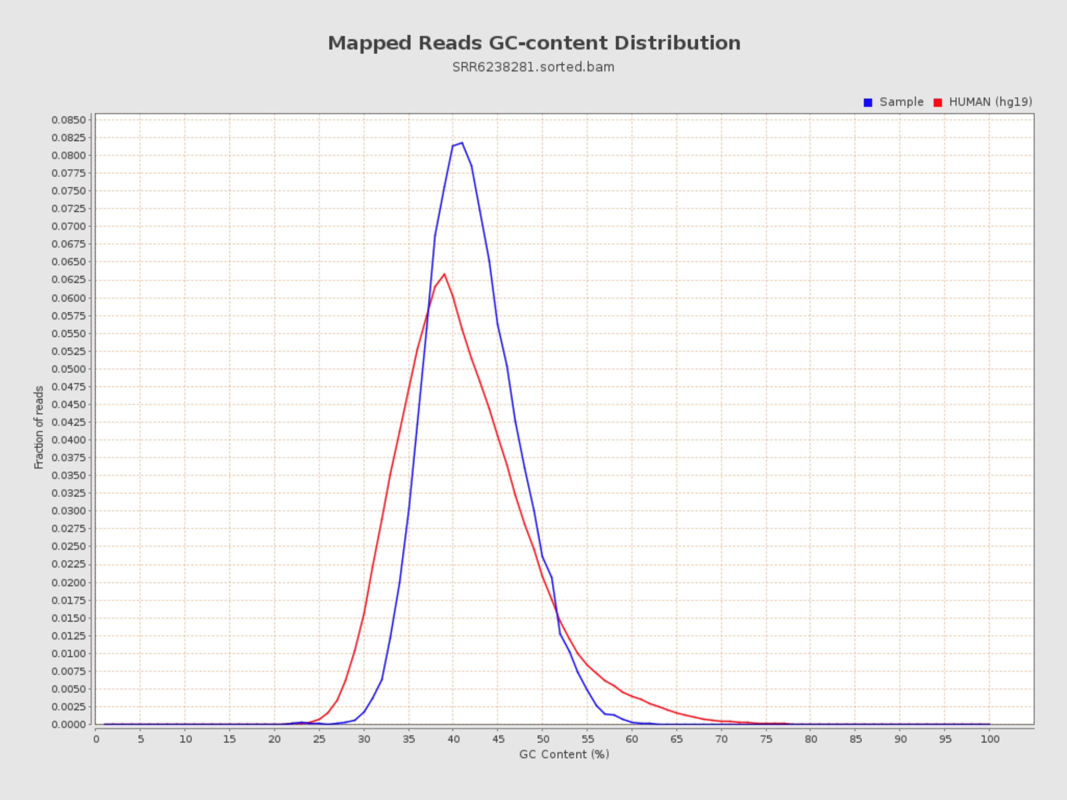
7. Results : Duplication Rate Histogram



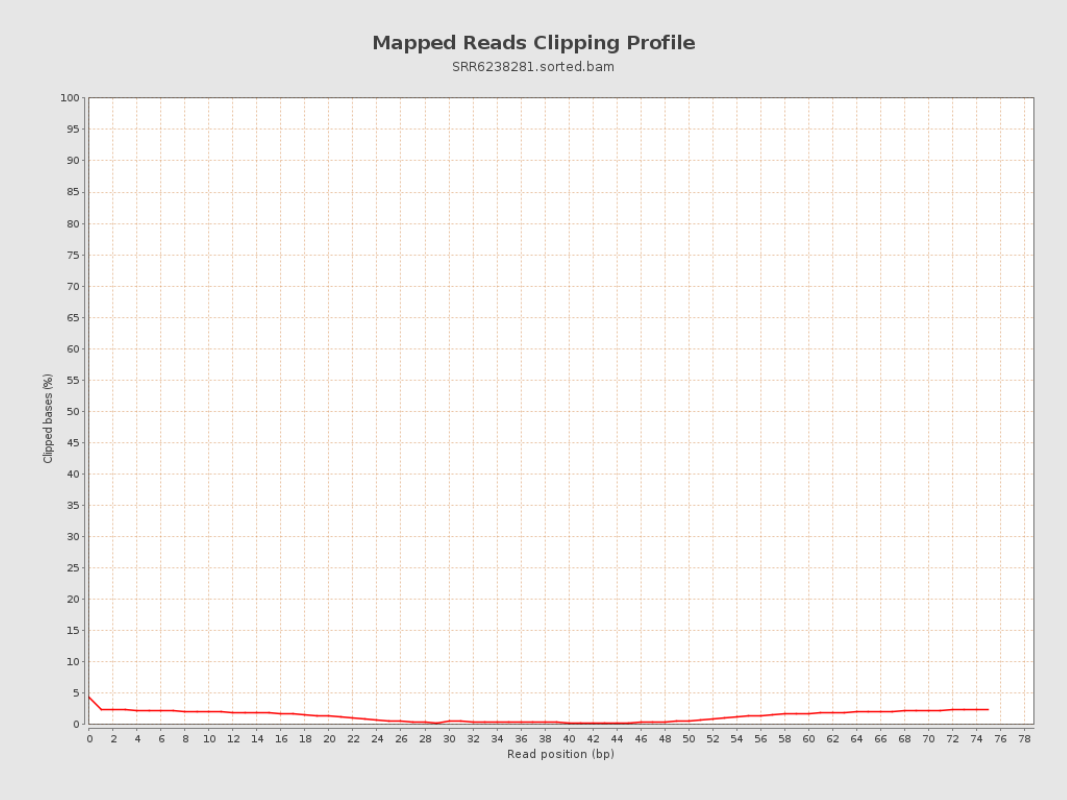
8. Results : Mapped Reads Nucleotide Content



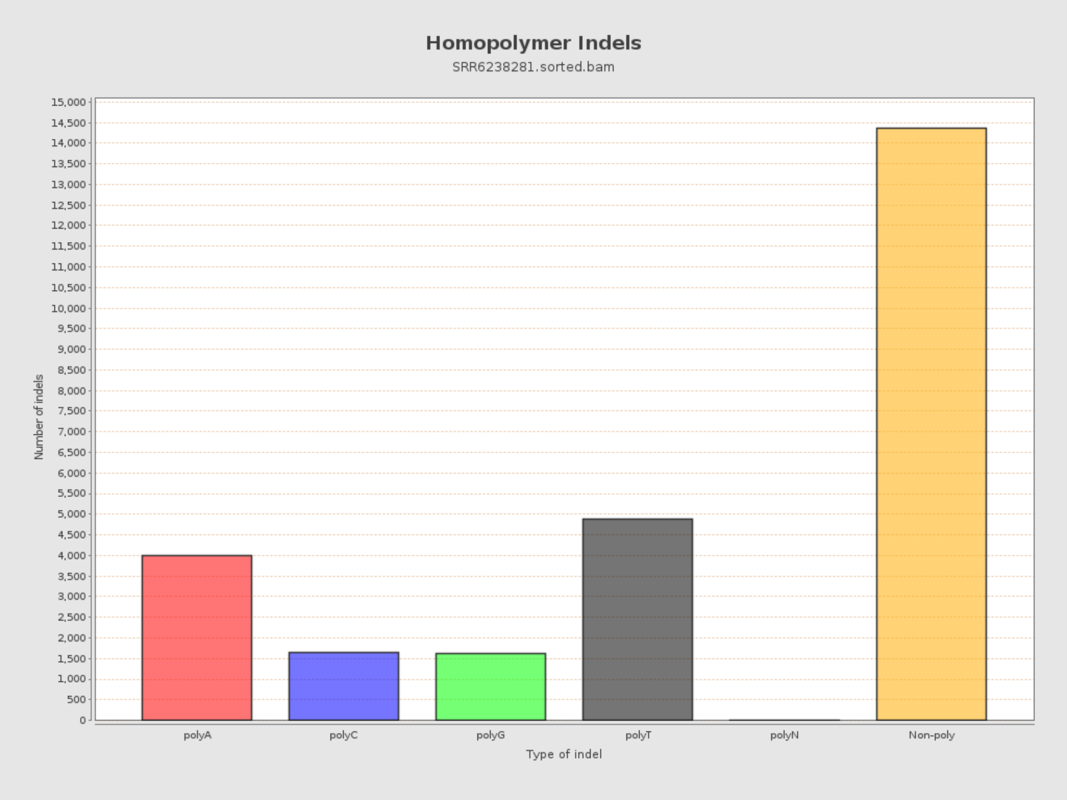
9. Results : Mapped Reads GC-content Distribution



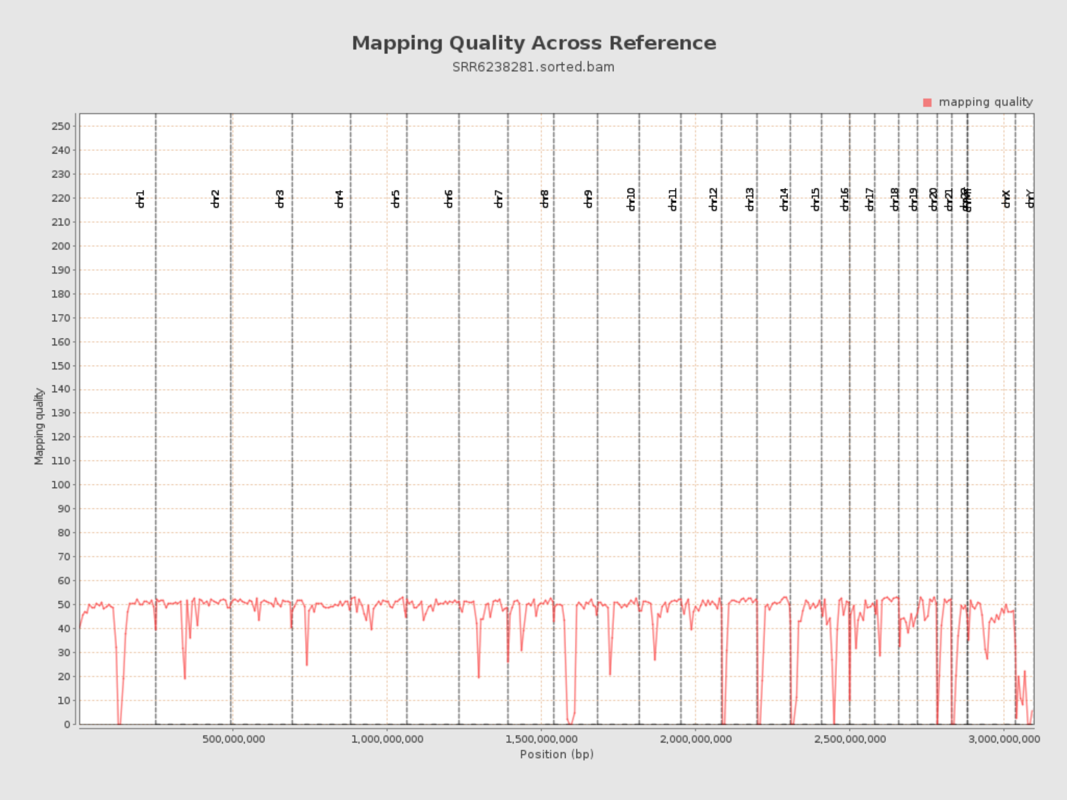
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram