Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 13:36:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238265.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_SRR6238265 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238265.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 13:36:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238265.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,577,063
Mapped reads	2,359,047 / 91.54%
Unmapped reads	218,016 / 8.46%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	27,043 / 1.05%
Read min/max/mean length	30 / 76 / 76.37
Duplicated reads (estimated)	111,020 / 4.31%
Duplication rate	3.44%
Clipped reads	1,193,575 / 46.32%

2.2. ACGT Content

Number/percentage of A's	43,741,041 / 28.21%
Number/percentage of C's	29,387,499 / 18.95%
Number/percentage of T's	47,956,612 / 30.93%
Number/percentage of G's	33,944,521 / 21.89%
Number/percentage of N's	42,192 / 0.03%
GC Percentage	40.84%

2.3. Coverage

Mean	0.0501

Standard Deviation	0.4666

2.4. Mapping Quality

Mean Mapping Quality	45.38

2.5. Mismatches and indels

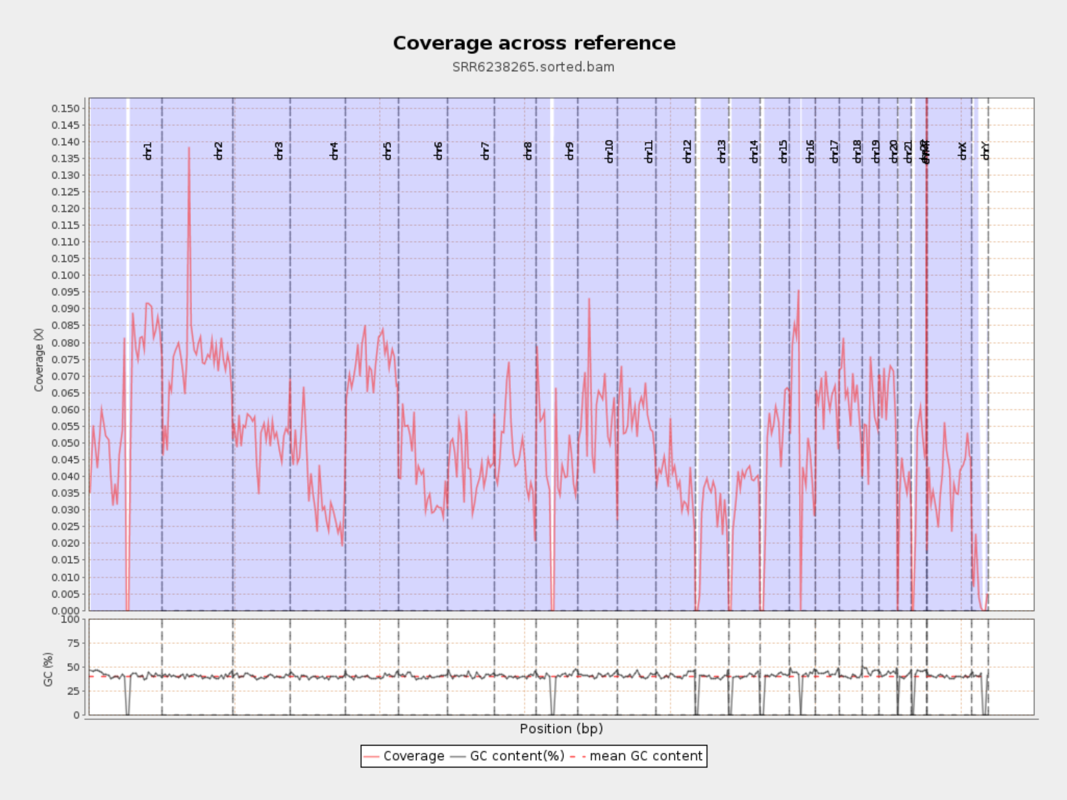
General error rate	0.91%
Mismatches	1,388,692
Insertions	13,134
Mapped reads with at least one insertion	0.55%
Deletions	49,558
Mapped reads with at least one deletion	2.08%
Homopolymer indels	45.36%

2.6. Chromosome stats

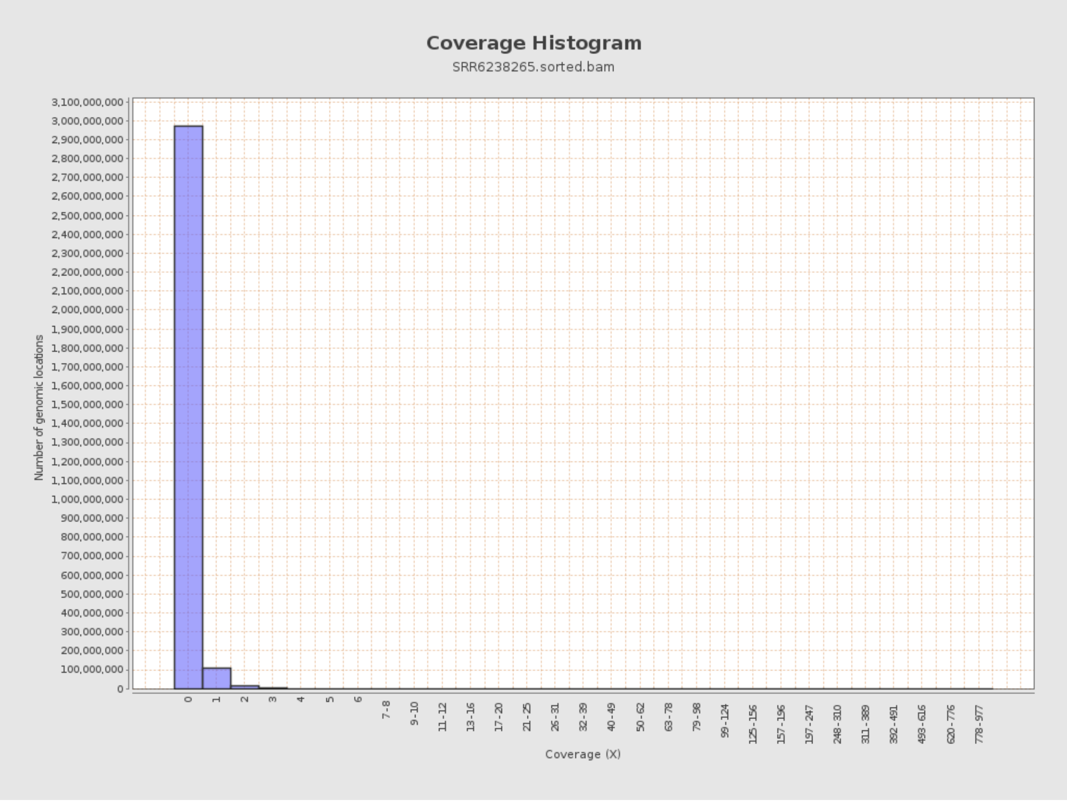
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14981953	0.0601	0.8256
chr2	243199373	18245152	0.075	0.6072
chr3	198022430	10385591	0.0524	0.2675
chr4	191154276	6963371	0.0364	0.2595
chr5	180915260	13367053	0.0739	0.3246
chr6	171115067	6891420	0.0403	0.3018
chr7	159138663	6876203	0.0432	0.3655

chr8	146364022	6727077	0.046	0.641
chr9	141213431	5936978	0.042	0.5018
chr10	135534747	8010220	0.0591	0.4794
chr11	135006516	7810592	0.0579	0.4251
chr12	133851895	5131671	0.0383	0.2518
chr13	115169878	3101275	0.0269	0.1923
chr14	107349540	3594506	0.0335	0.3103
chr15	102531392	4735271	0.0462	0.2531
chr16	90354753	4819722	0.0533	0.3376
chr17	81195210	5074811	0.0625	0.3579
chr18	78077248	5120325	0.0656	0.9841
chr19	59128983	3372641	0.057	0.6632
chr20	63025520	4060173	0.0644	0.3073
chr21	48129895	1675460	0.0348	0.2713
chr22	51304566	1899994	0.037	0.2219
chrMT	16571	2855	0.1723	0.5082
chrX	155270560	6014627	0.0387	0.2923
chrY	59373566	355343	0.006	0.1976

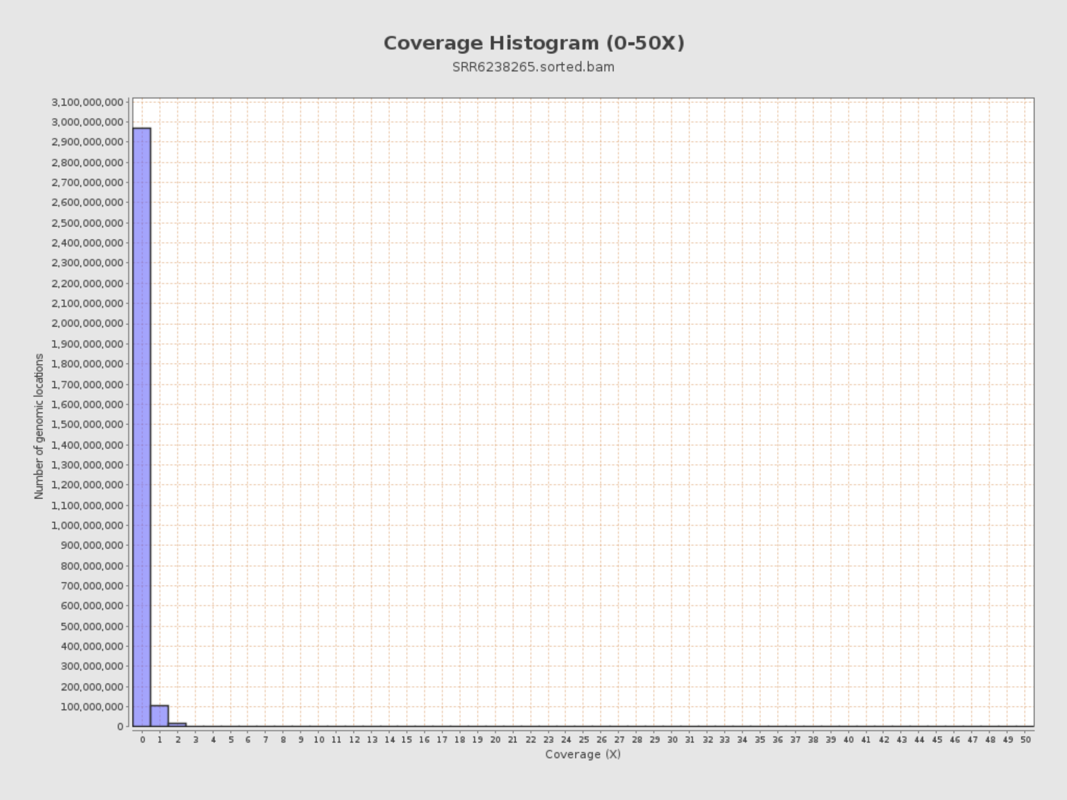
3. Results : Coverage across reference



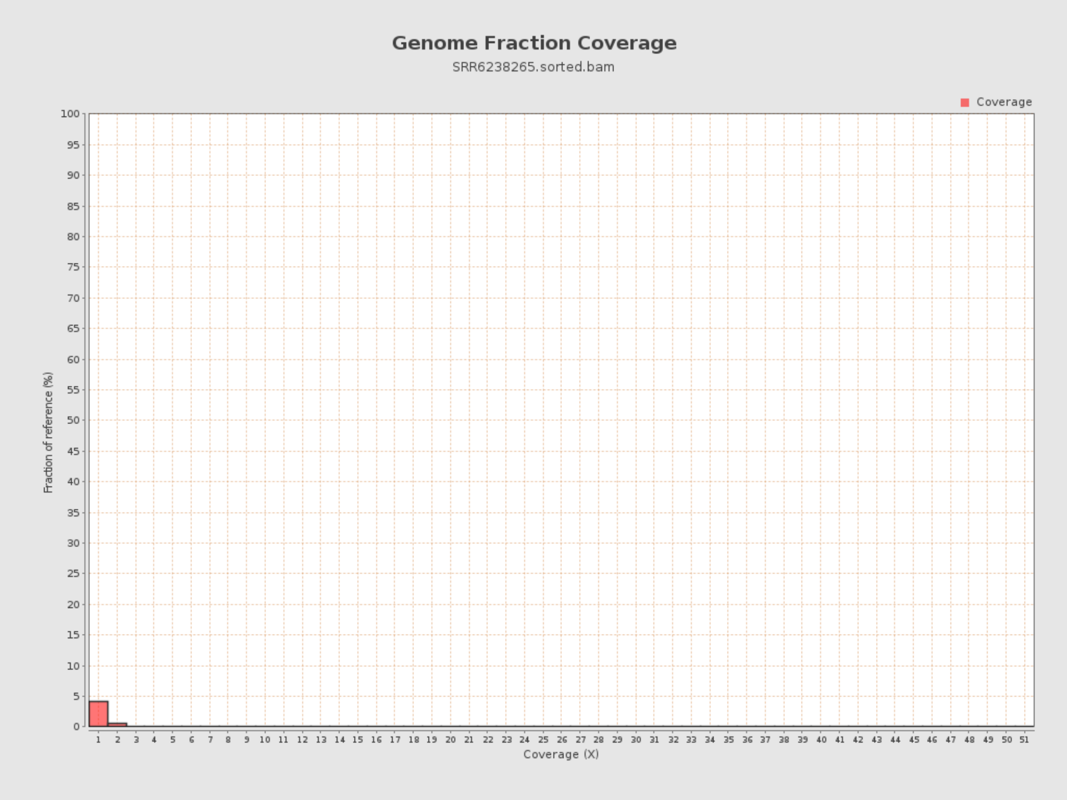
4. Results : Coverage Histogram



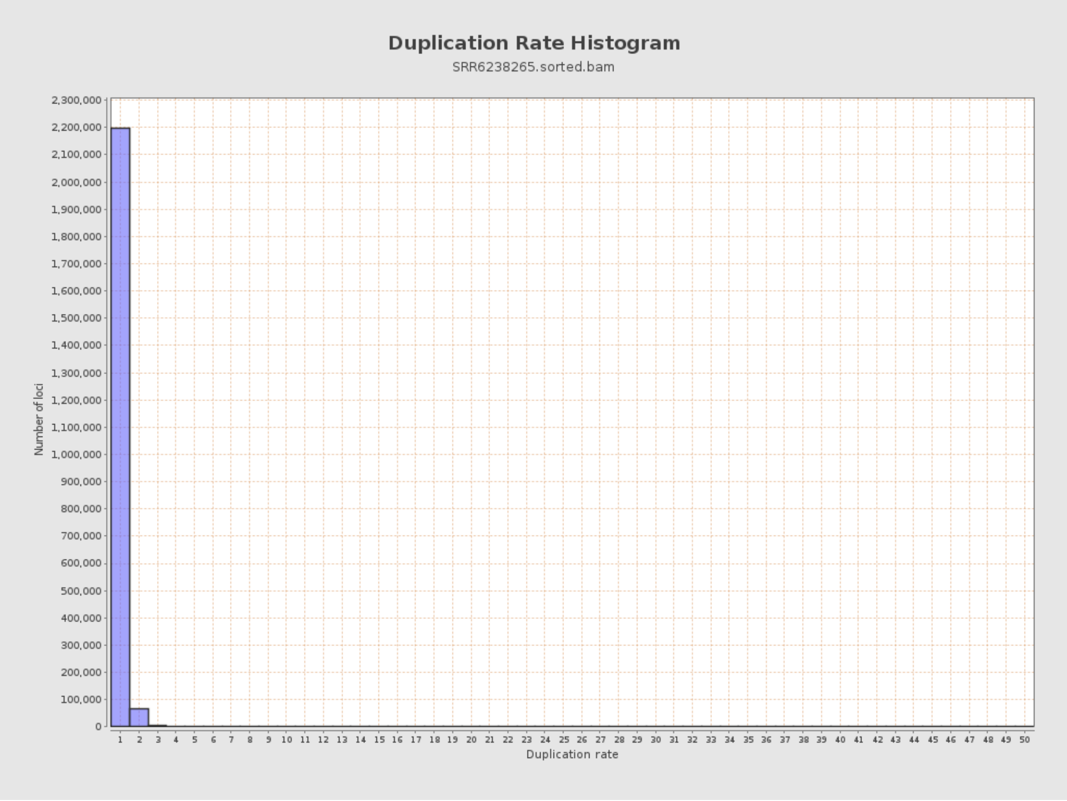
5. Results : Coverage Histogram (0-50X)



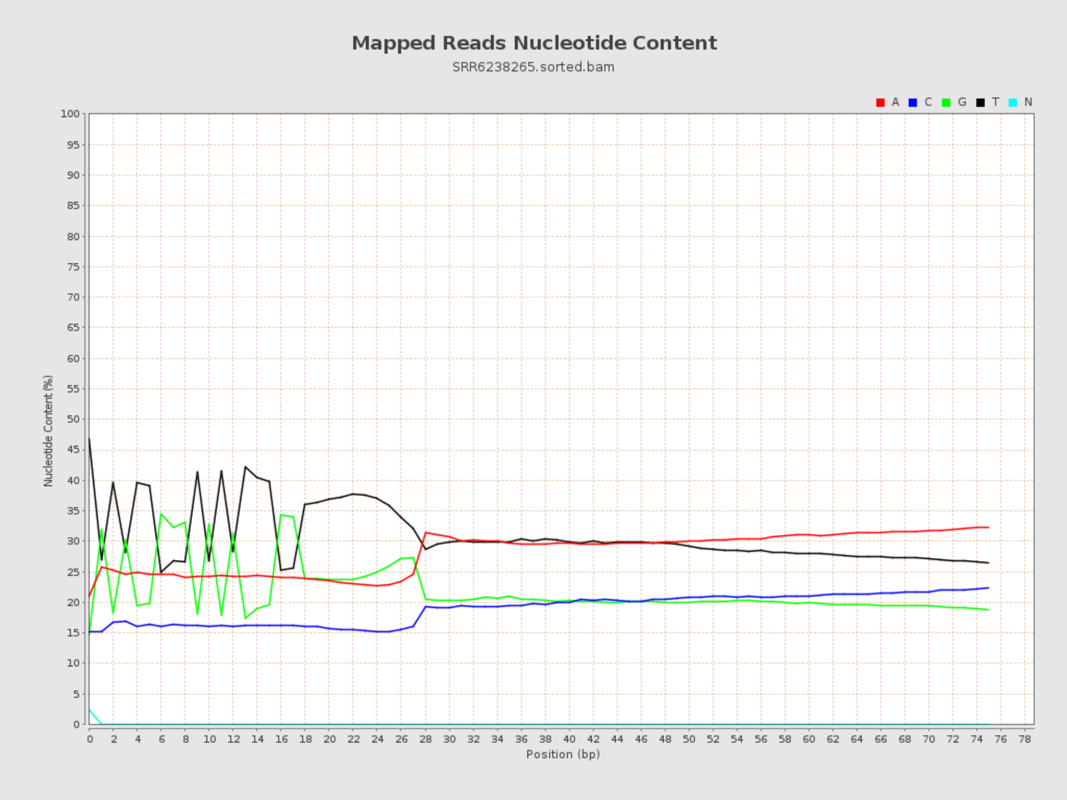
6. Results : Genome Fraction Coverage



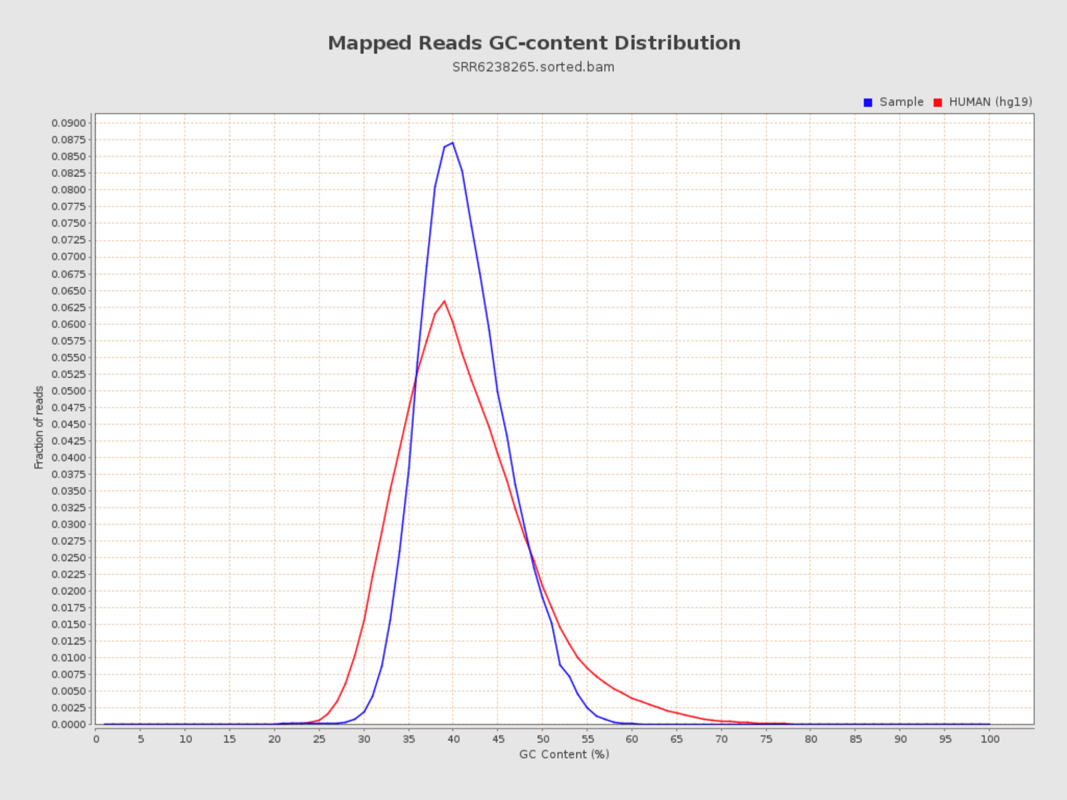
7. Results : Duplication Rate Histogram



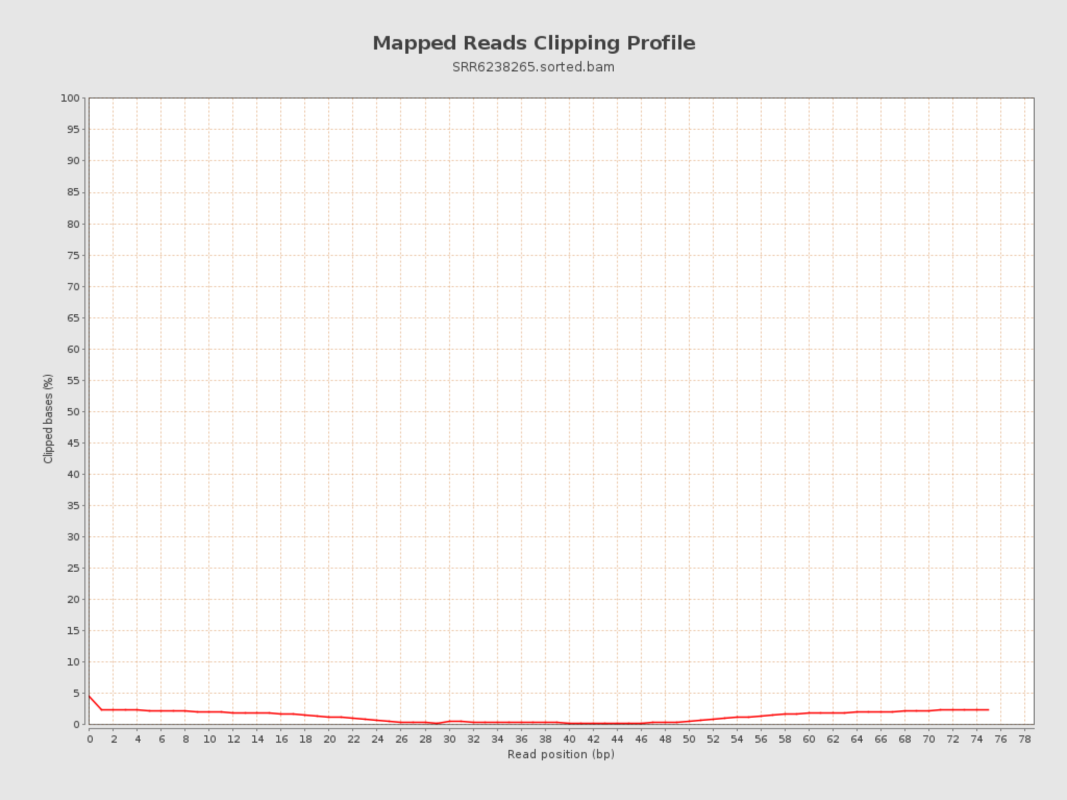
8. Results : Mapped Reads Nucleotide Content



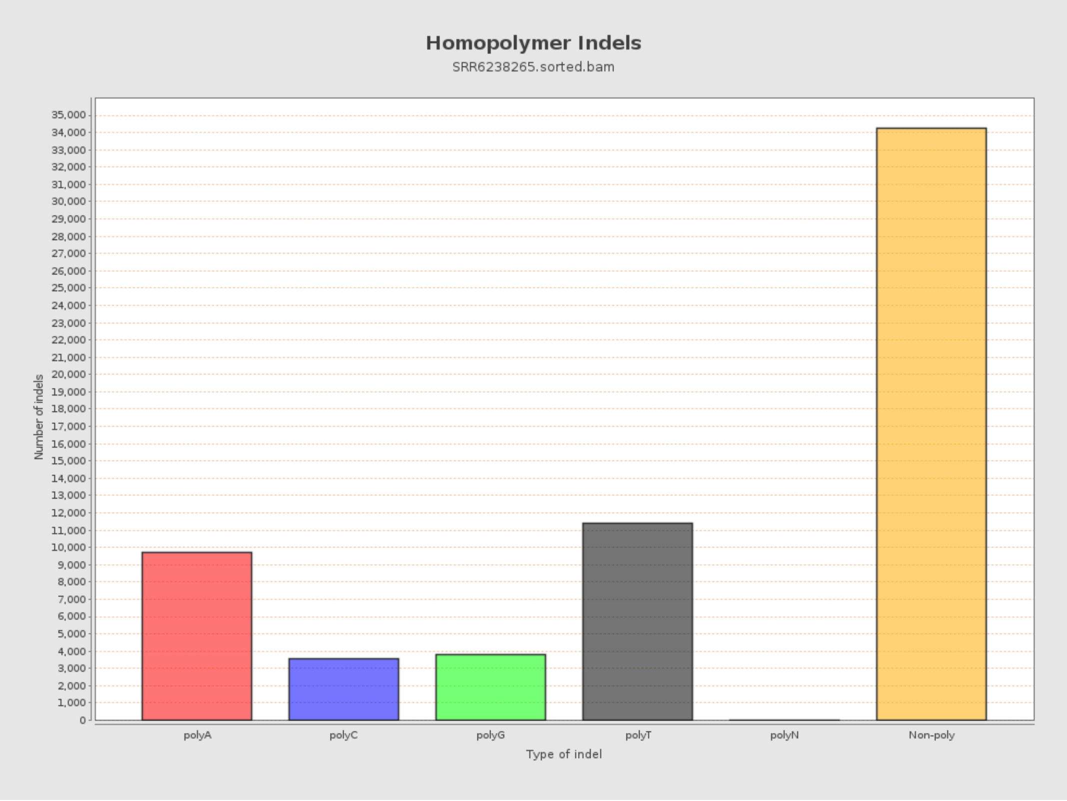
9. Results : Mapped Reads GC-content Distribution



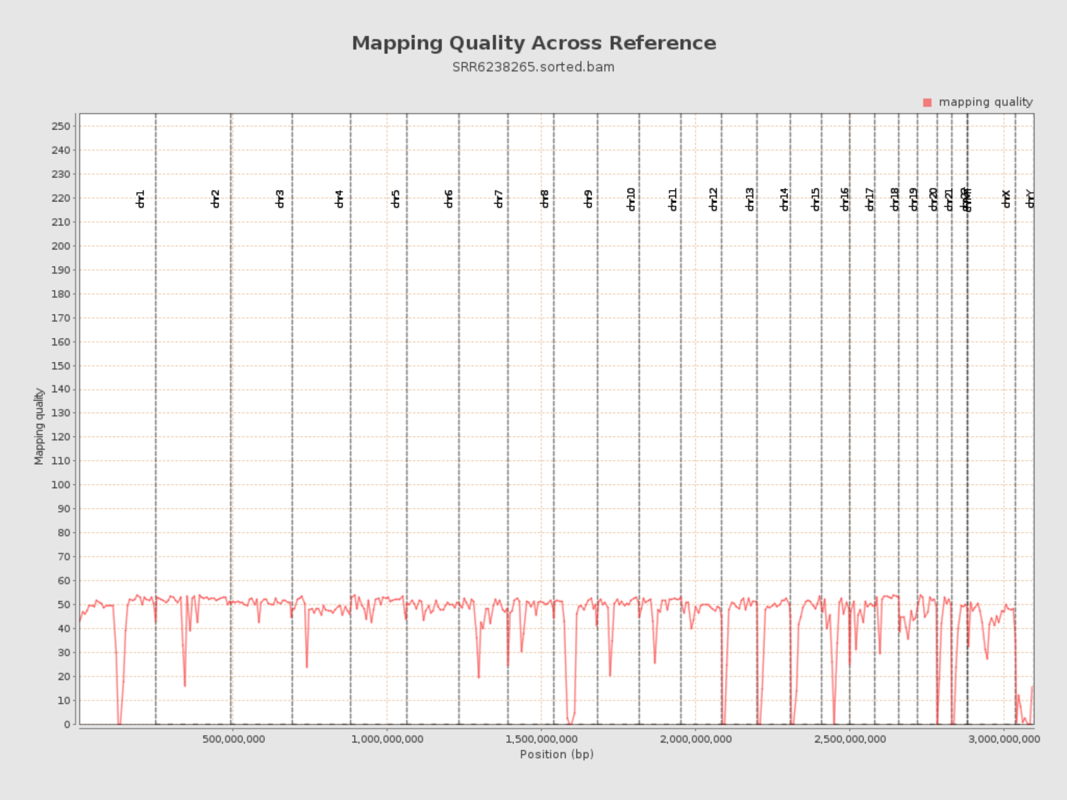
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram