Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 17:23:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238486.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_SRR6238486 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238486.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 17:23:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238486.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,845,091
Mapped reads	2,318,338 / 81.49%
Unmapped reads	526,753 / 18.51%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	24,187 / 0.85%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	991,737 / 34.86%
Duplication rate	23.5%
Clipped reads	1,694,414 / 59.56%

2.2. ACGT Content

Number/percentage of A's	33,462,645 / 24.38%
Number/percentage of C's	23,490,923 / 17.12%
Number/percentage of T's	47,474,477 / 34.59%
Number/percentage of G's	32,814,015 / 23.91%
Number/percentage of N's	2,744 / 0%
GC Percentage	41.03%

2.3. Coverage

Mean	0.0444

Standard Deviation	1.1075

2.4. Mapping Quality

Mean Mapping Quality	40.59

2.5. Mismatches and indels

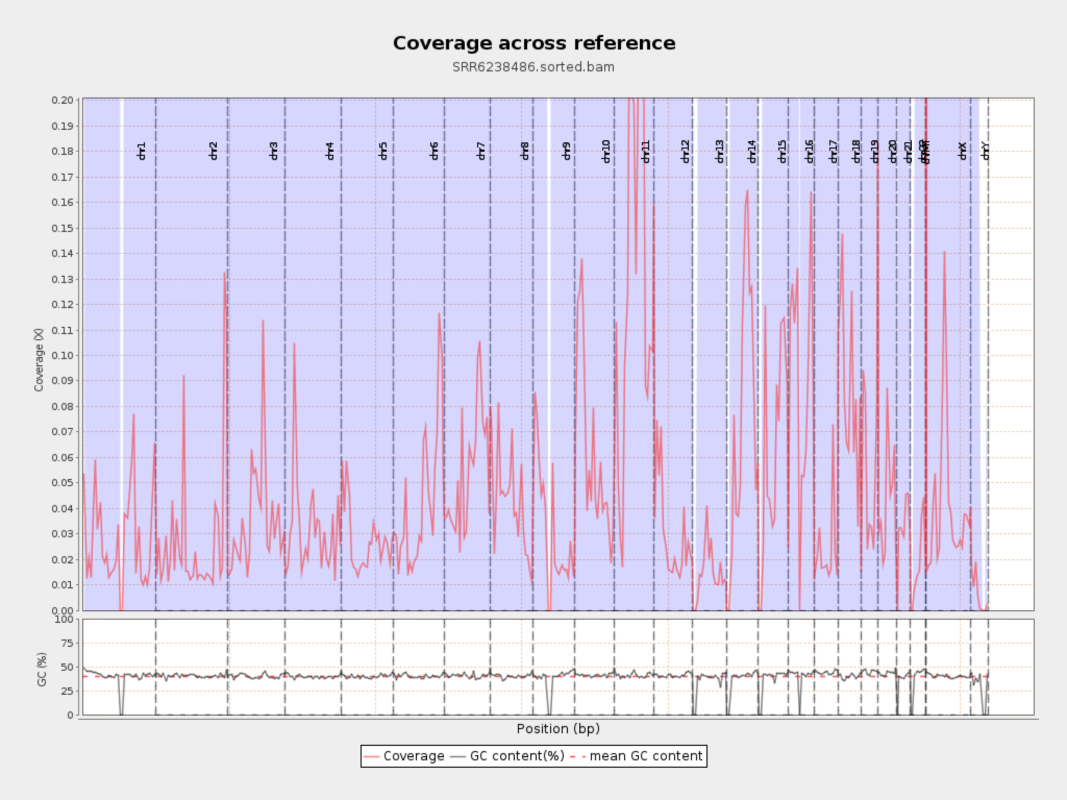
General error rate	0.72%
Mismatches	972,012
Insertions	8,835
Mapped reads with at least one insertion	0.38%
Deletions	52,328
Mapped reads with at least one deletion	2.23%
Homopolymer indels	39.26%

2.6. Chromosome stats

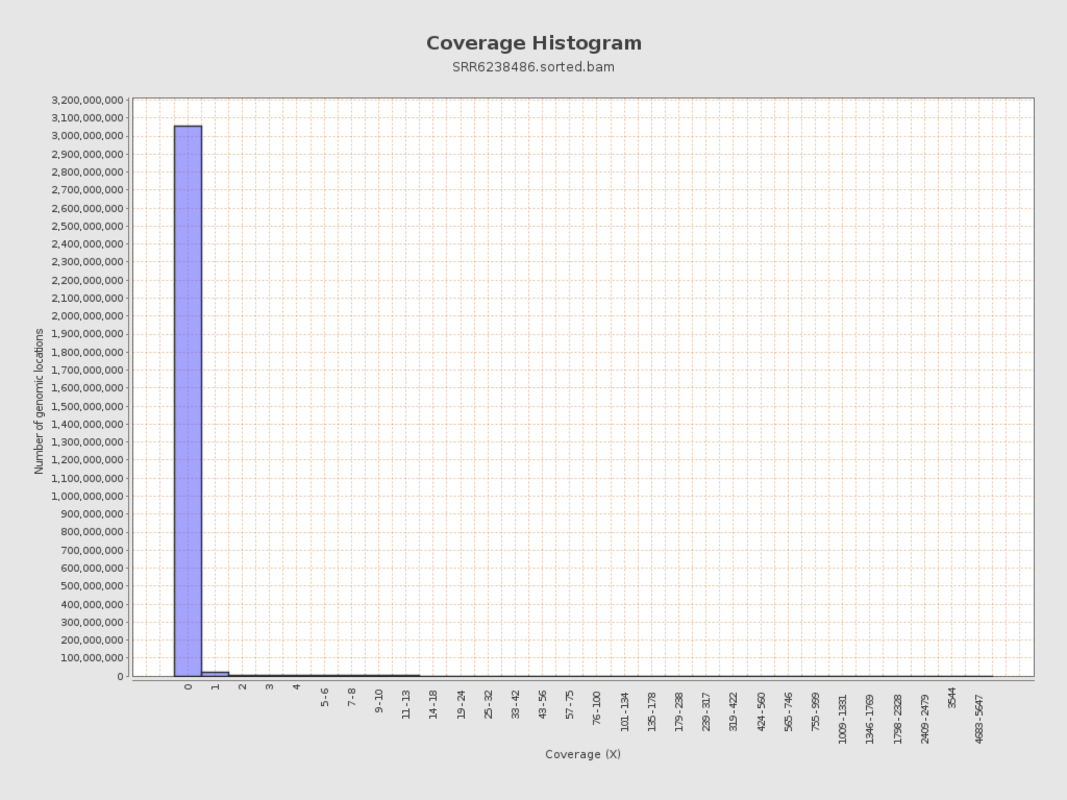
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7094633	0.0285	0.549
chr2	243199373	6592919	0.0271	2.5117
chr3	198022430	7120184	0.036	0.5652
chr4	191154276	6003911	0.0314	0.4876
chr5	180915260	4966008	0.0274	0.4805
chr6	171115067	7189979	0.042	1.0322
chr7	159138663	8657457	0.0544	0.8946

chr8	146364022	6163734	0.0421	0.9085
chr9	141213431	4444101	0.0315	0.5768
chr10	135534747	8499564	0.0627	0.7385
chr11	135006516	18003125	0.1334	1.5744
chr12	133851895	4010875	0.03	0.4984
chr13	115169878	1706958	0.0148	0.7149
chr14	107349540	8128709	0.0757	0.8144
chr15	102531392	6351879	0.062	0.925
chr16	90354753	7893166	0.0874	0.8747
chr17	81195210	1965138	0.0242	0.6267
chr18	78077248	6863882	0.0879	2.8665
chr19	59128983	3331733	0.0563	0.7532
chr20	63025520	2752594	0.0437	0.6
chr21	48129895	1580481	0.0328	0.5065
chr22	51304566	955285	0.0186	0.3716
chrMT	16571	155339	9.3741	10.5095
chrX	155270560	6521131	0.042	0.6469
chrY	59373566	377581	0.0064	0.4394

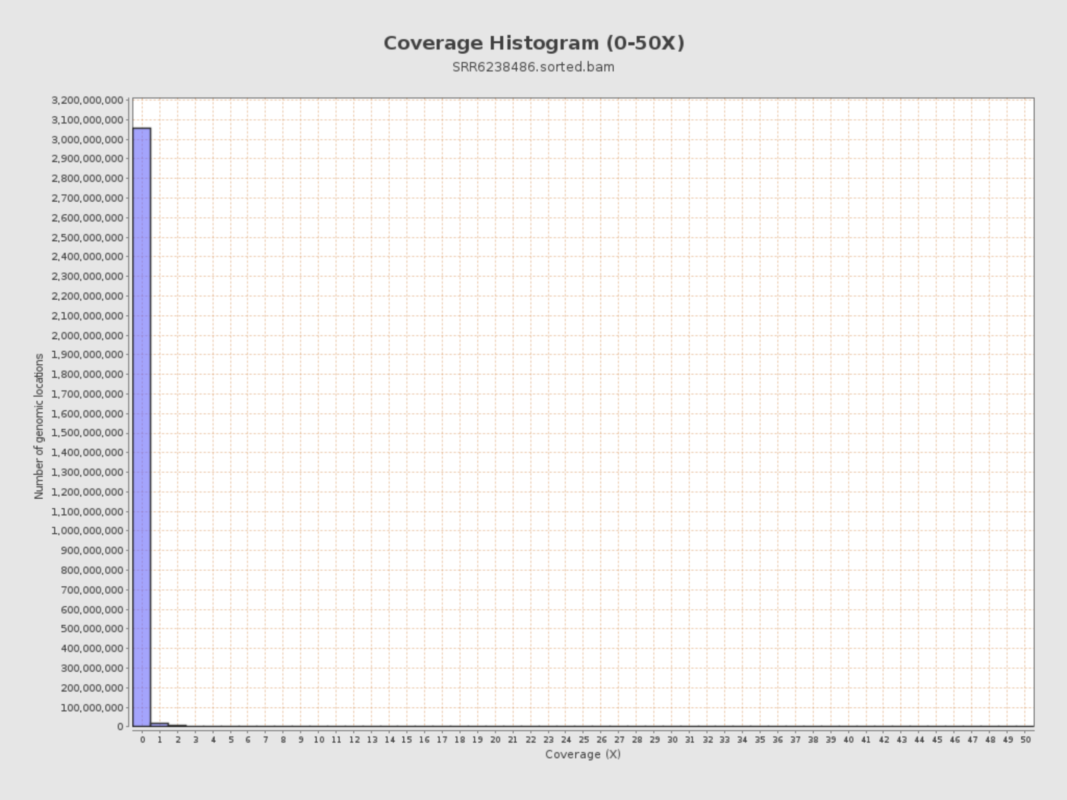
3. Results : Coverage across reference



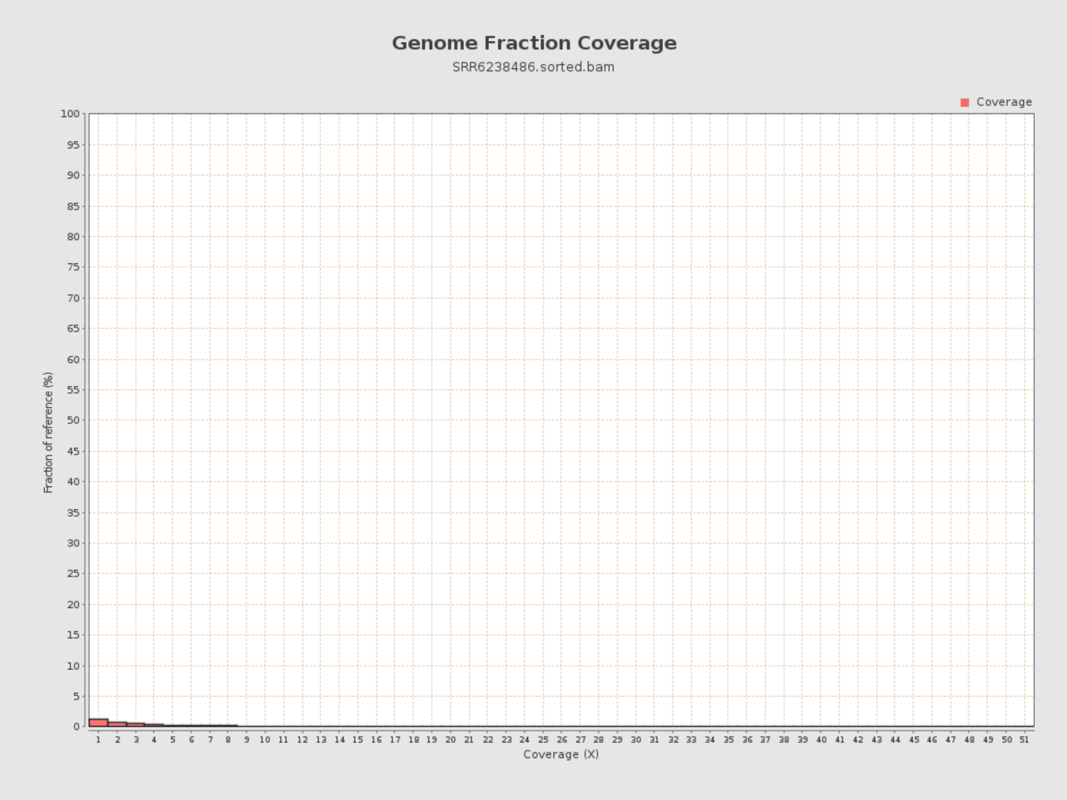
4. Results : Coverage Histogram



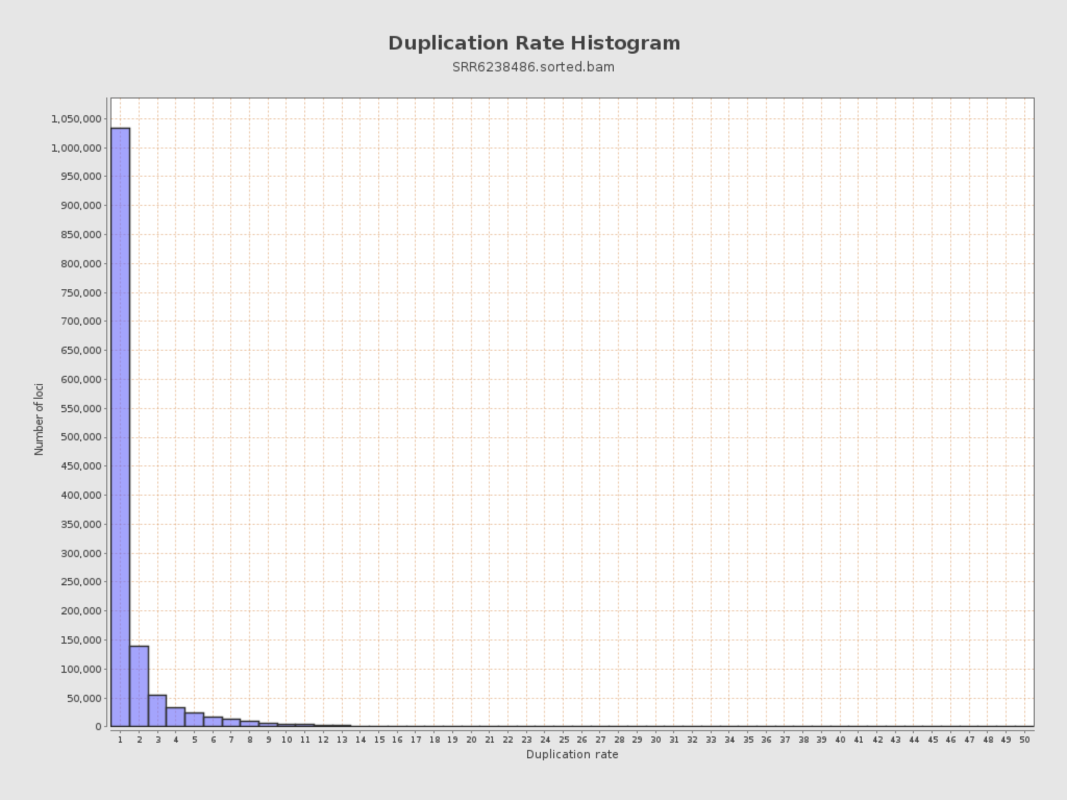
5. Results : Coverage Histogram (0-50X)



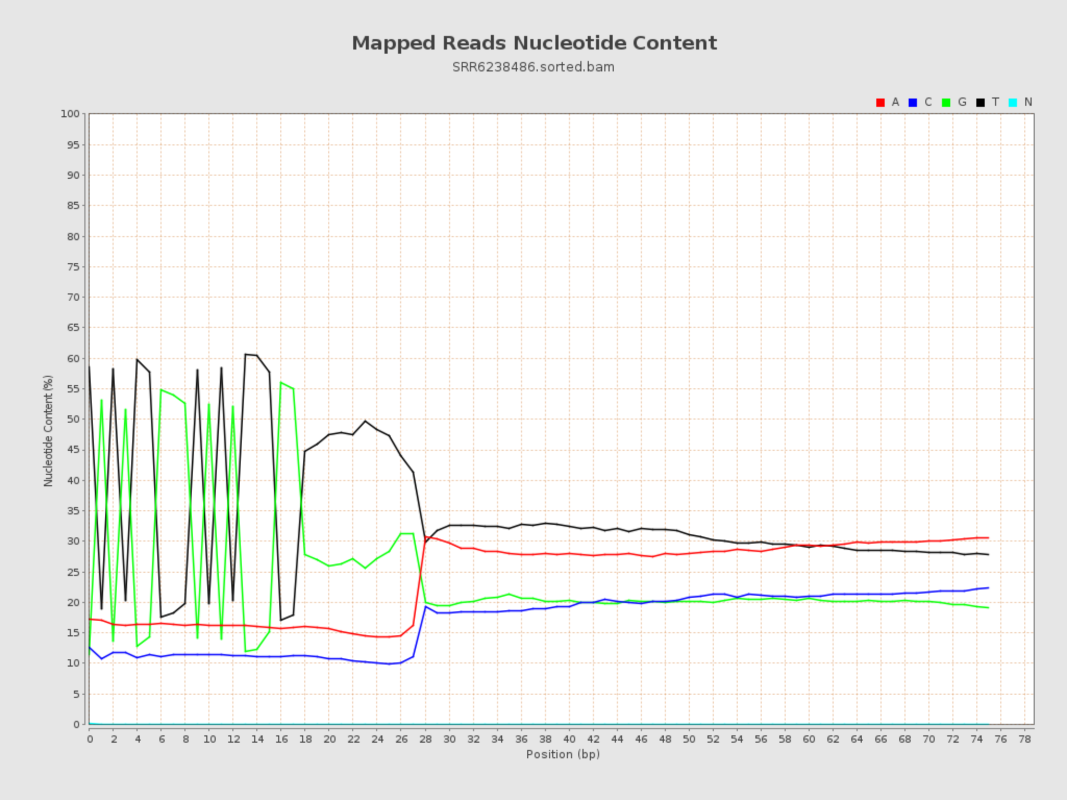
6. Results : Genome Fraction Coverage



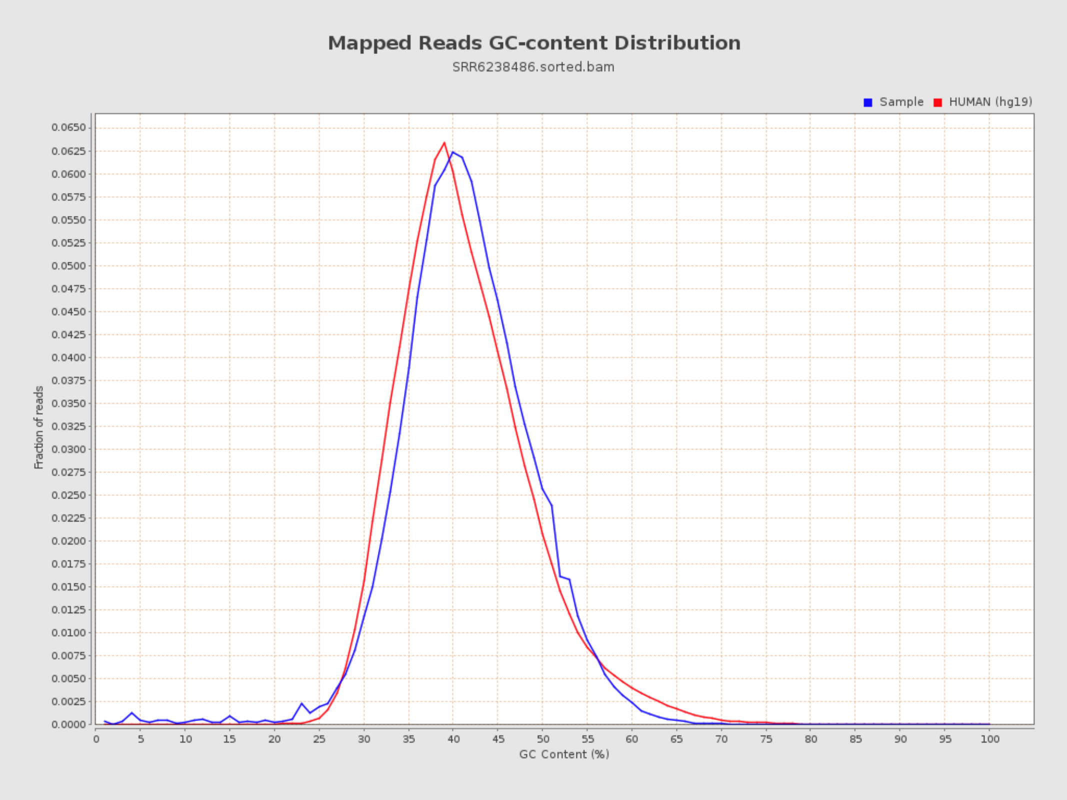
7. Results : Duplication Rate Histogram



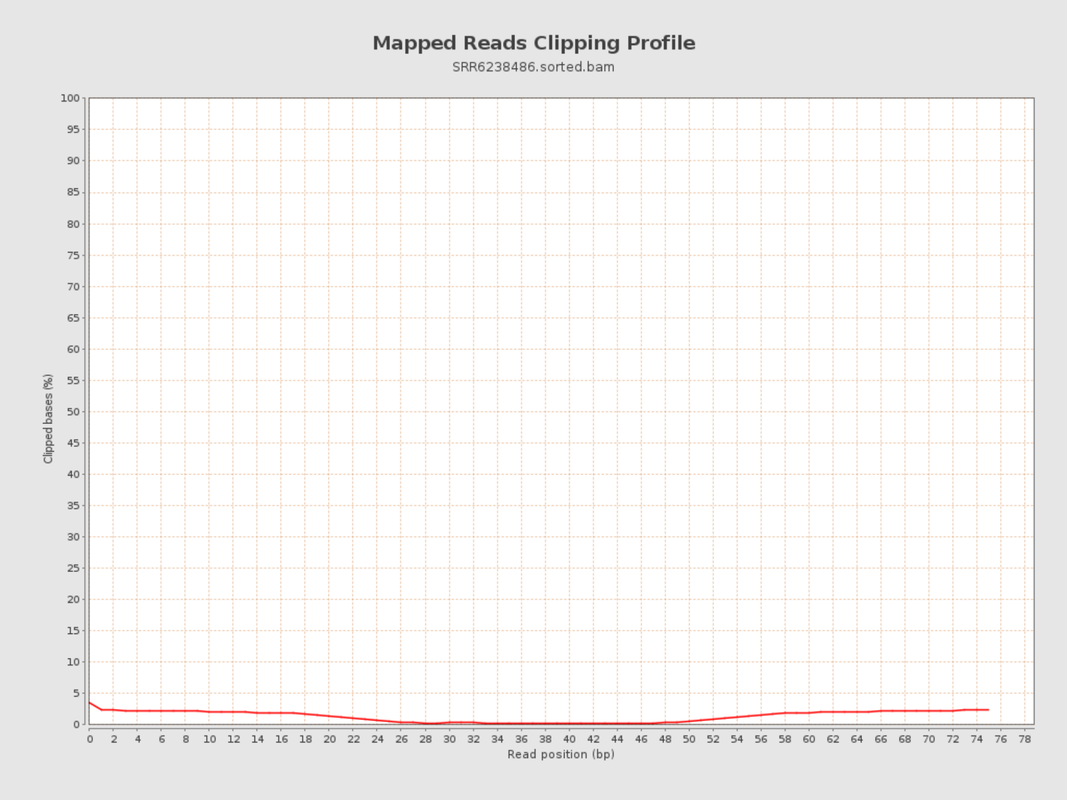
8. Results : Mapped Reads Nucleotide Content



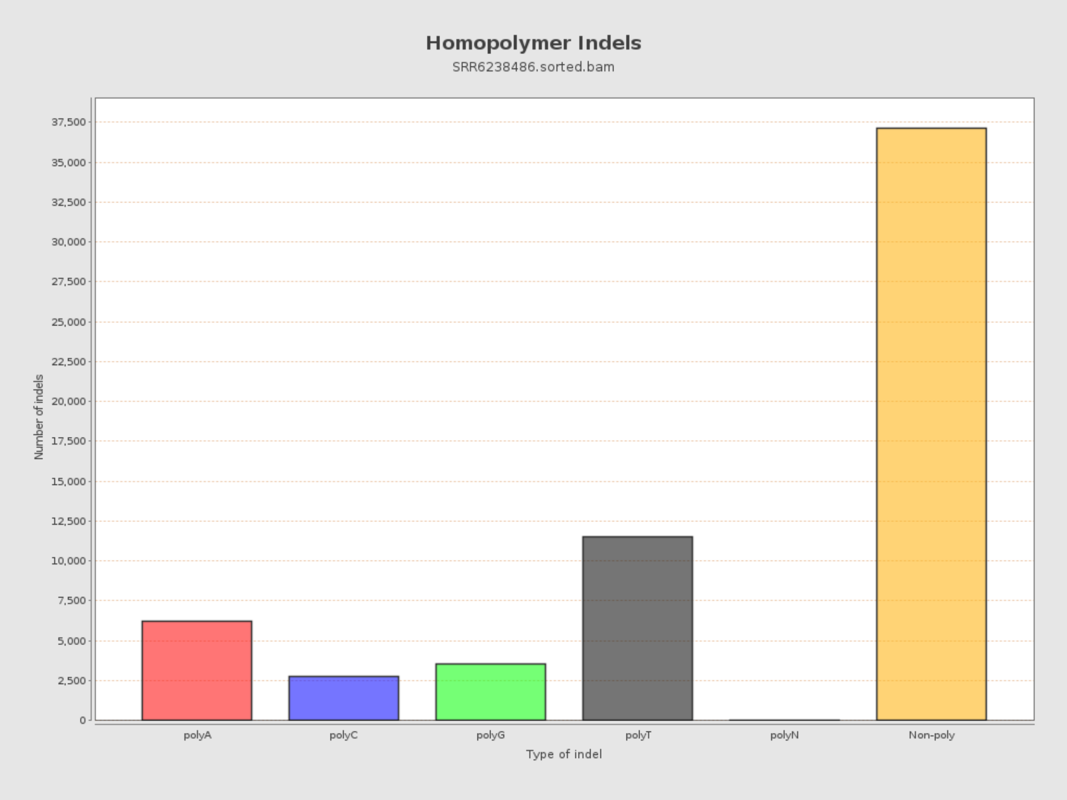
9. Results : Mapped Reads GC-content Distribution



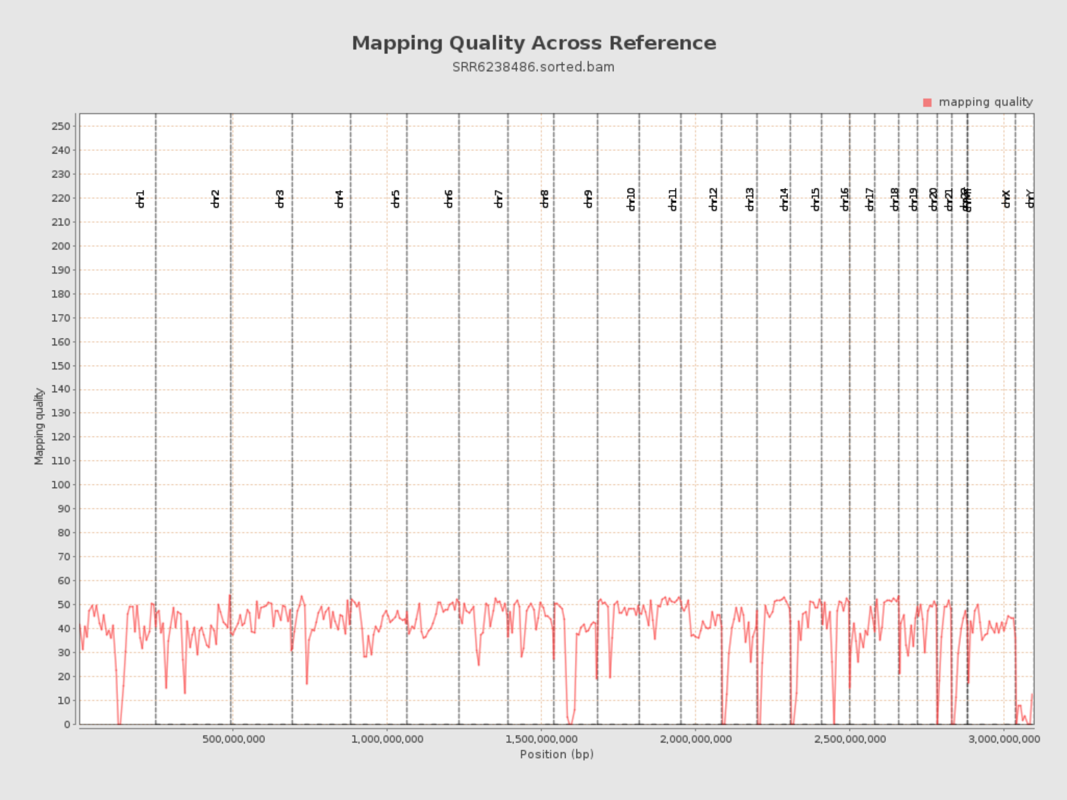
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram