Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 18:46:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238507.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_SRR6238507 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238507.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 18:46:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238507.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,168,013
Mapped reads	2,550,654 / 80.51%
Unmapped reads	617,359 / 19.49%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,457 / 0.61%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	1,295,027 / 40.88%
Duplication rate	23.29%
Clipped reads	1,744,394 / 55.06%

2.2. ACGT Content

Number/percentage of A's	37,997,401 / 24.63%
Number/percentage of C's	25,148,474 / 16.3%
Number/percentage of T's	54,432,913 / 35.28%
Number/percentage of G's	36,699,110 / 23.79%
Number/percentage of N's	3,323 / 0%
GC Percentage	40.09%

2.3. Coverage

Mean	0.0499

Standard Deviation	1.1867

2.4. Mapping Quality

Mean Mapping Quality	42.06

2.5. Mismatches and indels

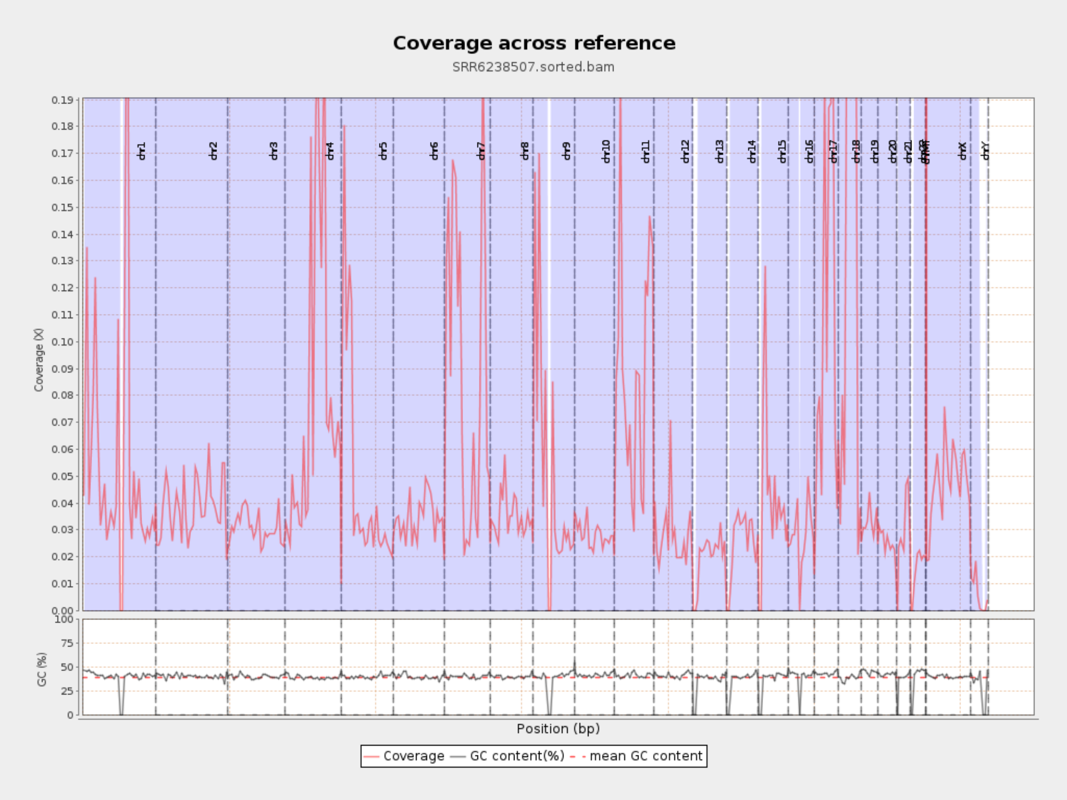
General error rate	0.62%
Mismatches	941,242
Insertions	10,846
Mapped reads with at least one insertion	0.42%
Deletions	48,669
Mapped reads with at least one deletion	1.89%
Homopolymer indels	41.9%

2.6. Chromosome stats

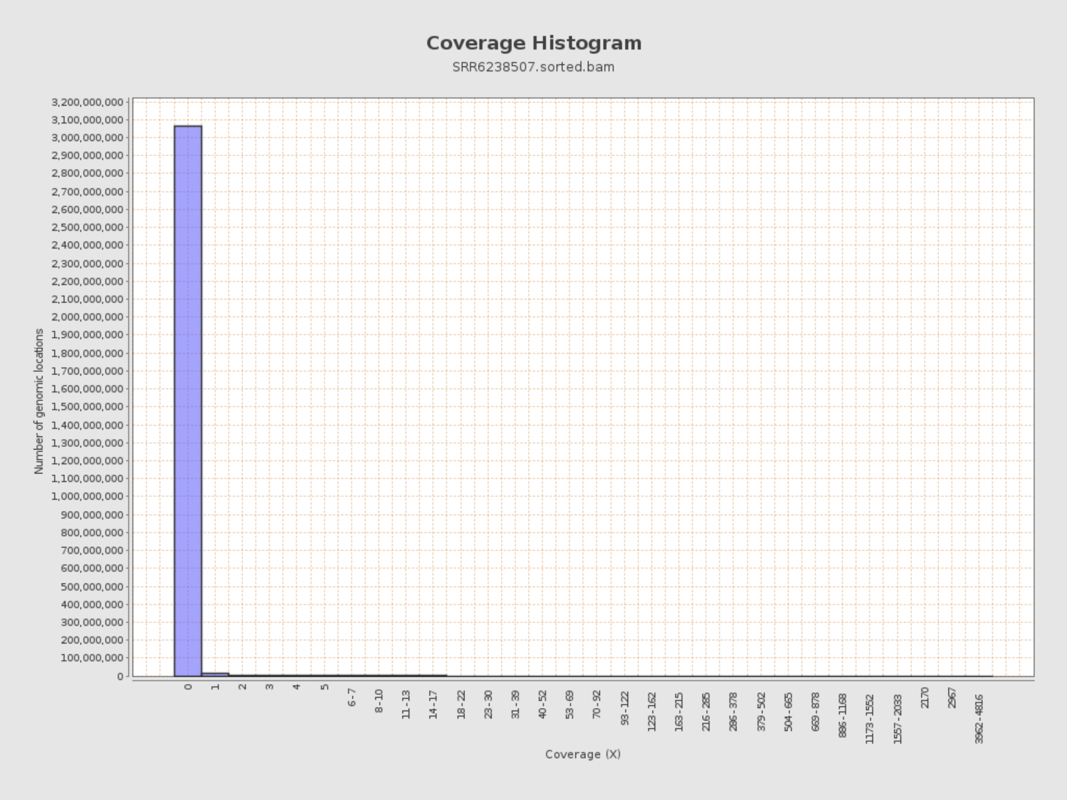
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13596265	0.0545	1.4429
chr2	243199373	9401769	0.0387	2.2168
chr3	198022430	6087633	0.0307	0.6675
chr4	191154276	15484698	0.081	1.0708
chr5	180915260	8773261	0.0485	0.8211
chr6	171115067	5937167	0.0347	0.9908
chr7	159138663	13872596	0.0872	1.1854

chr8	146364022	5172308	0.0353	0.8949
chr9	141213431	7273373	0.0515	0.8622
chr10	135534747	3803444	0.0281	0.6385
chr11	135006516	11861553	0.0879	1.166
chr12	133851895	3780627	0.0282	0.6275
chr13	115169878	2272435	0.0197	0.7139
chr14	107349540	2746589	0.0256	0.6263
chr15	102531392	4378222	0.0427	0.8832
chr16	90354753	2466929	0.0273	0.6406
chr17	81195210	9161380	0.1128	1.2664
chr18	78077248	14670894	0.1879	3.0682
chr19	59128983	1962677	0.0332	0.9564
chr20	63025520	1607936	0.0255	0.609
chr21	48129895	1433103	0.0298	0.6496
chr22	51304566	759967	0.0148	0.415
chrMT	16571	81640	4.9267	9.2059
chrX	155270560	7409590	0.0477	0.8264
chrY	59373566	364982	0.0061	0.4053

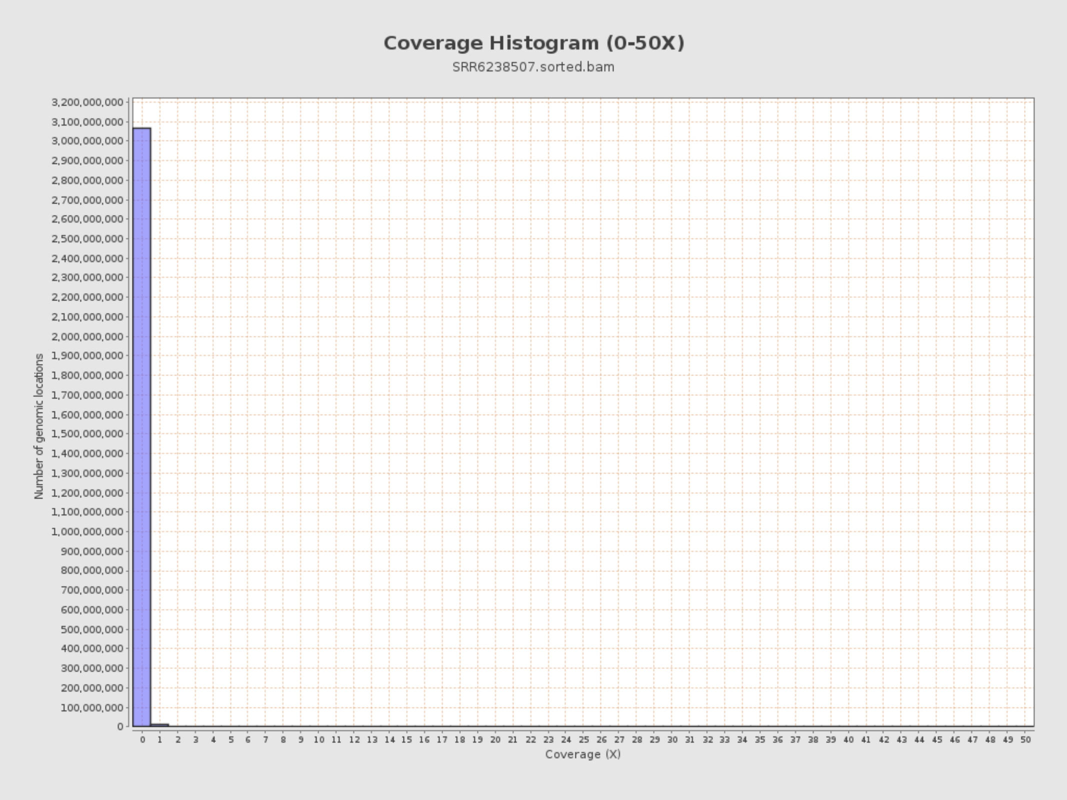
3. Results : Coverage across reference



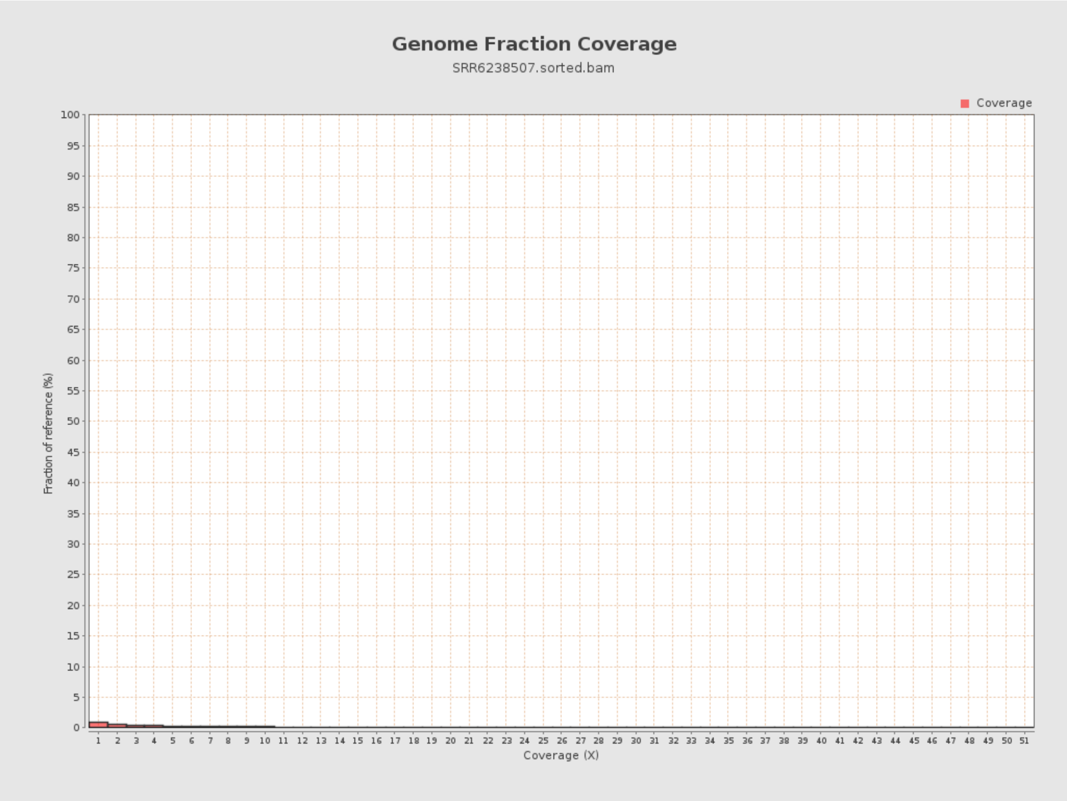
4. Results : Coverage Histogram



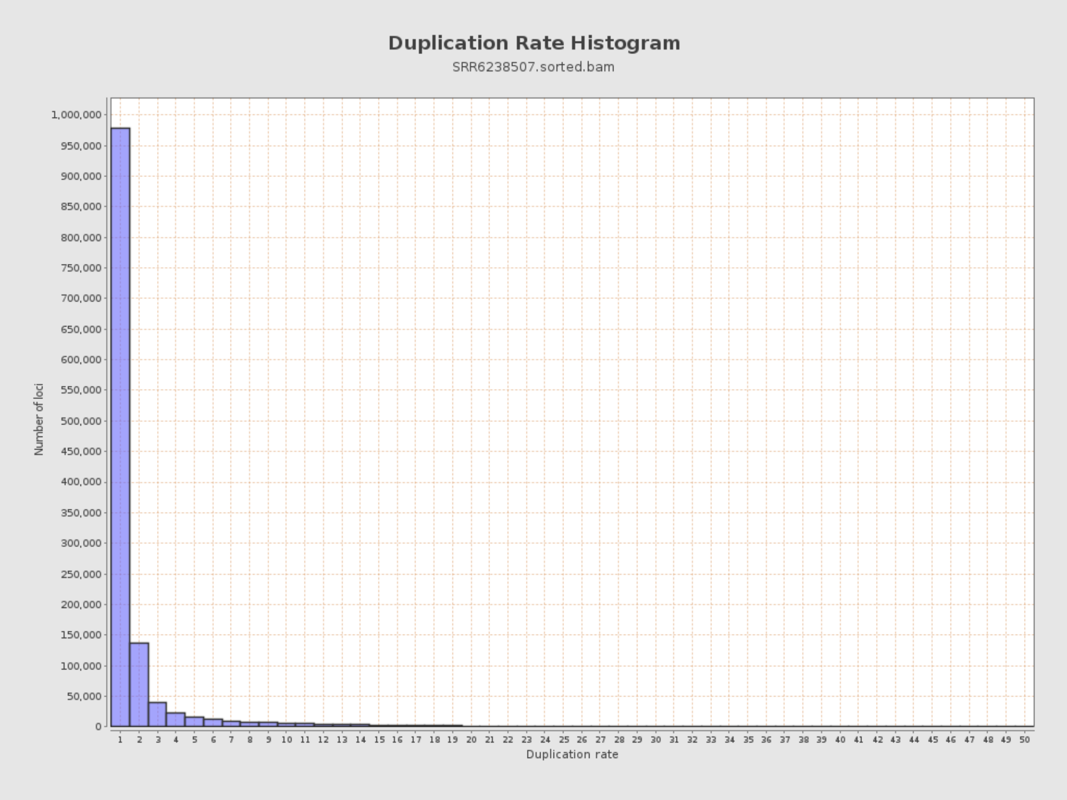
5. Results : Coverage Histogram (0-50X)



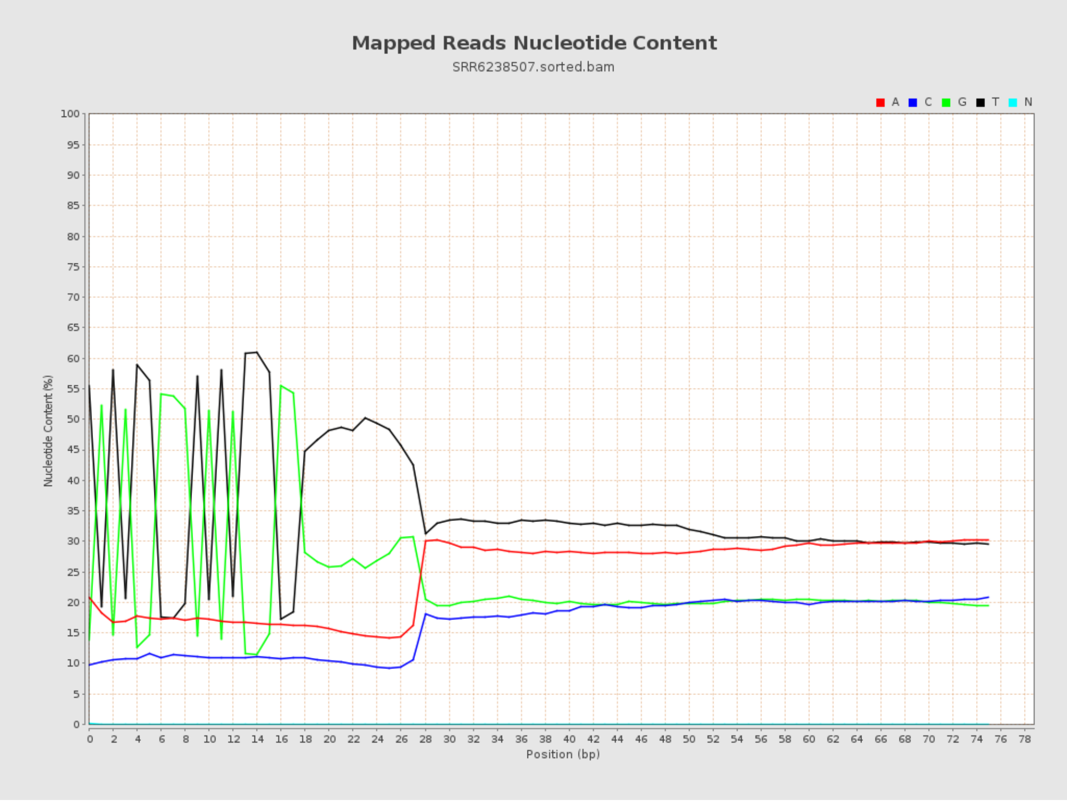
6. Results : Genome Fraction Coverage



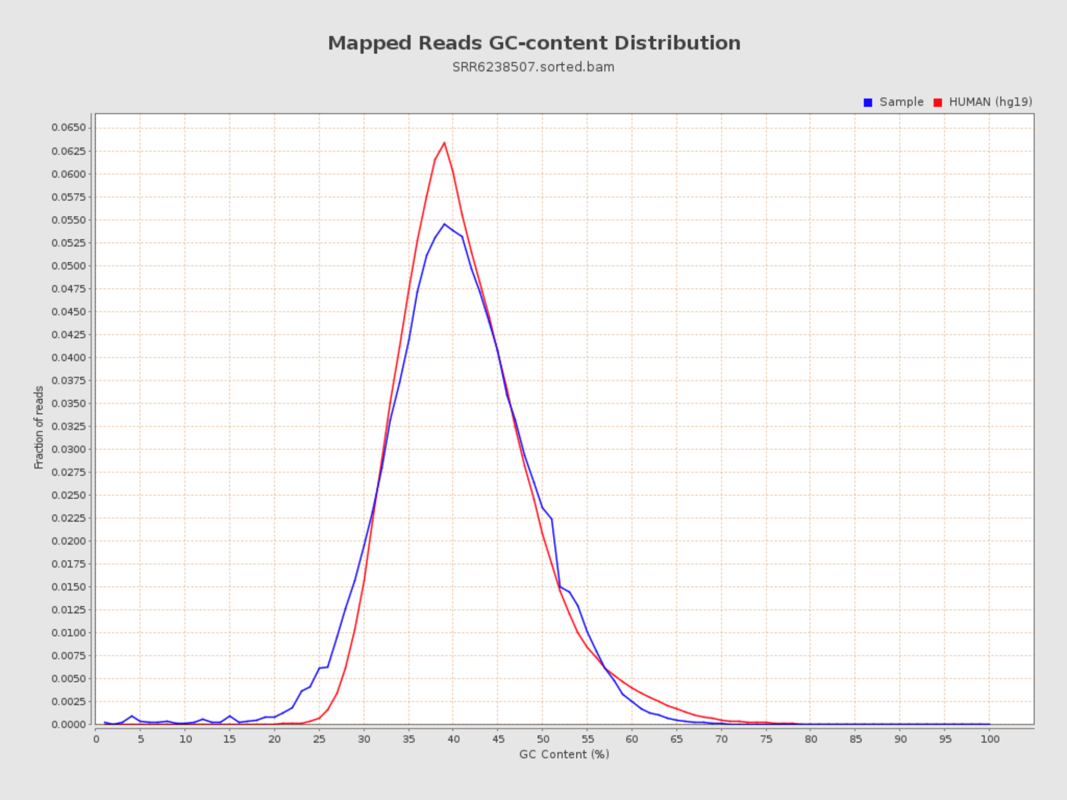
7. Results : Duplication Rate Histogram



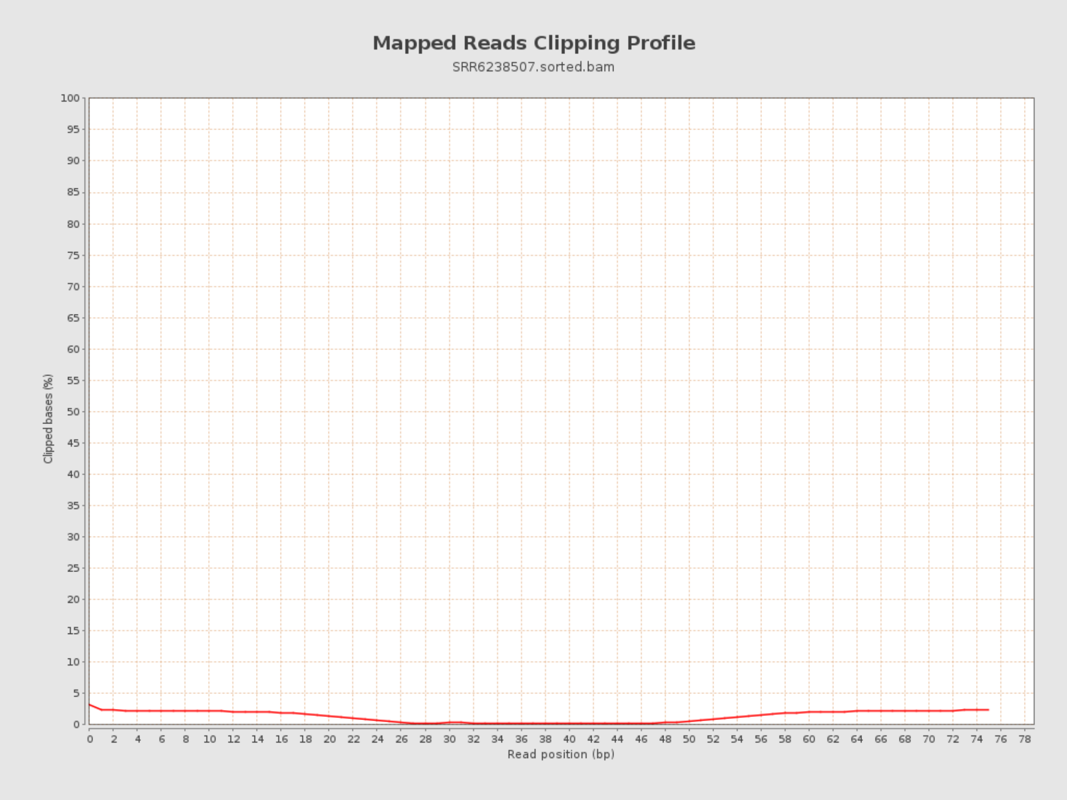
8. Results : Mapped Reads Nucleotide Content



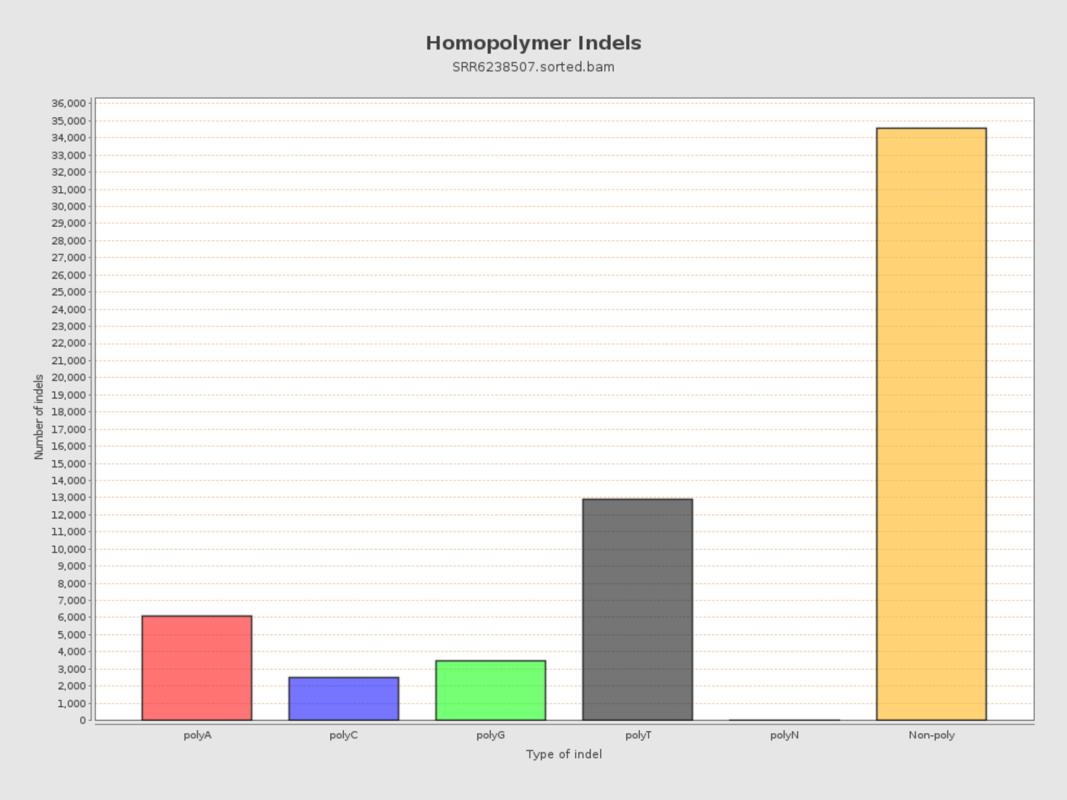
9. Results : Mapped Reads GC-content Distribution



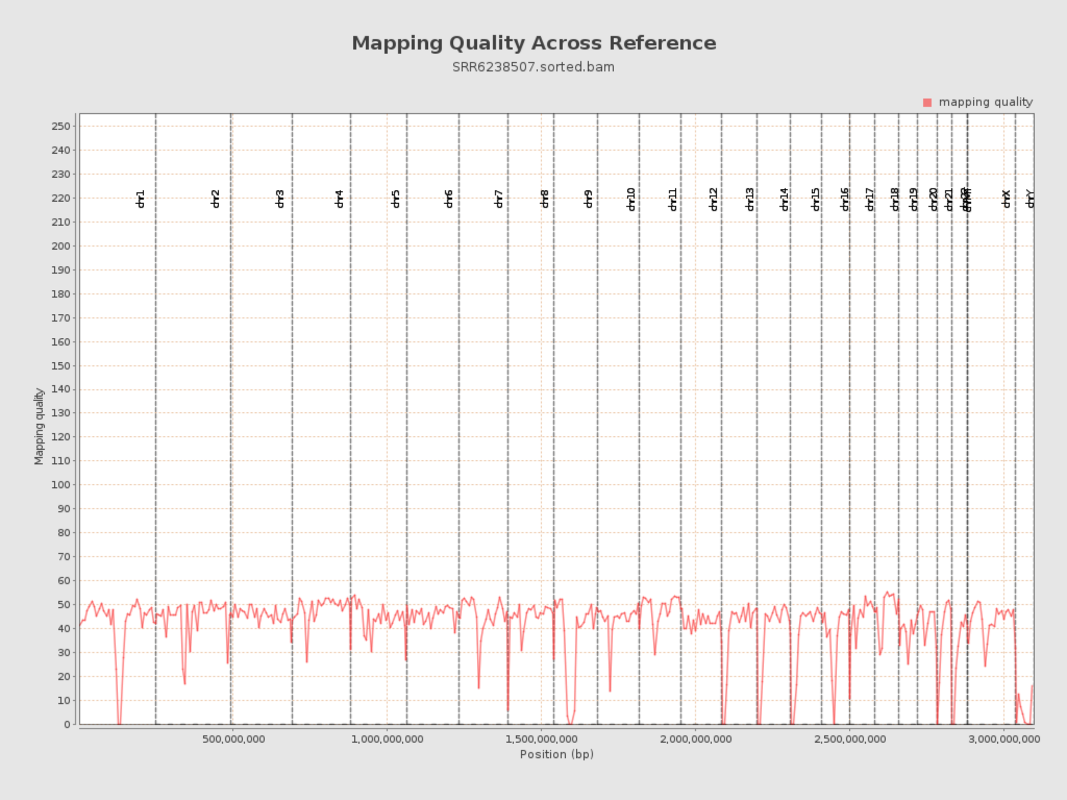
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram