Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 21:25:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238597.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_SRR6238597 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238597.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 21:25:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238597.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,741,213
Mapped reads	2,526,217 / 92.16%
Unmapped reads	214,996 / 7.84%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,871 / 0.8%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	325,437 / 11.87%
Duplication rate	10.89%
Clipped reads	1,423,445 / 51.93%

2.2. ACGT Content

Number/percentage of A's	41,114,918 / 25.73%
Number/percentage of C's	28,831,794 / 18.05%
Number/percentage of T's	52,081,238 / 32.6%
Number/percentage of G's	37,739,936 / 23.62%
Number/percentage of N's	8,510 / 0.01%
GC Percentage	41.67%

2.3. Coverage

Mean	0.0516

Standard Deviation	0.5841

2.4. Mapping Quality

Mean Mapping Quality	45.69

2.5. Mismatches and indels

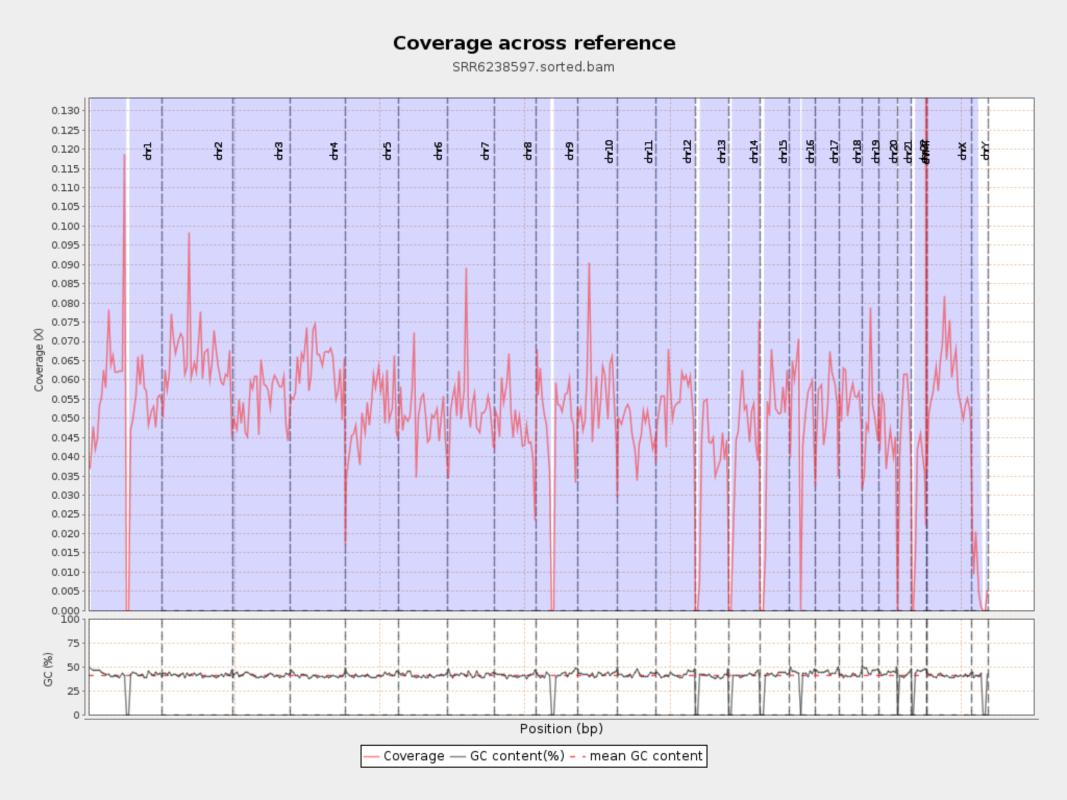
General error rate	0.5%
Mismatches	777,861
Insertions	9,808
Mapped reads with at least one insertion	0.38%
Deletions	29,814
Mapped reads with at least one deletion	1.17%
Homopolymer indels	44.21%

2.6. Chromosome stats

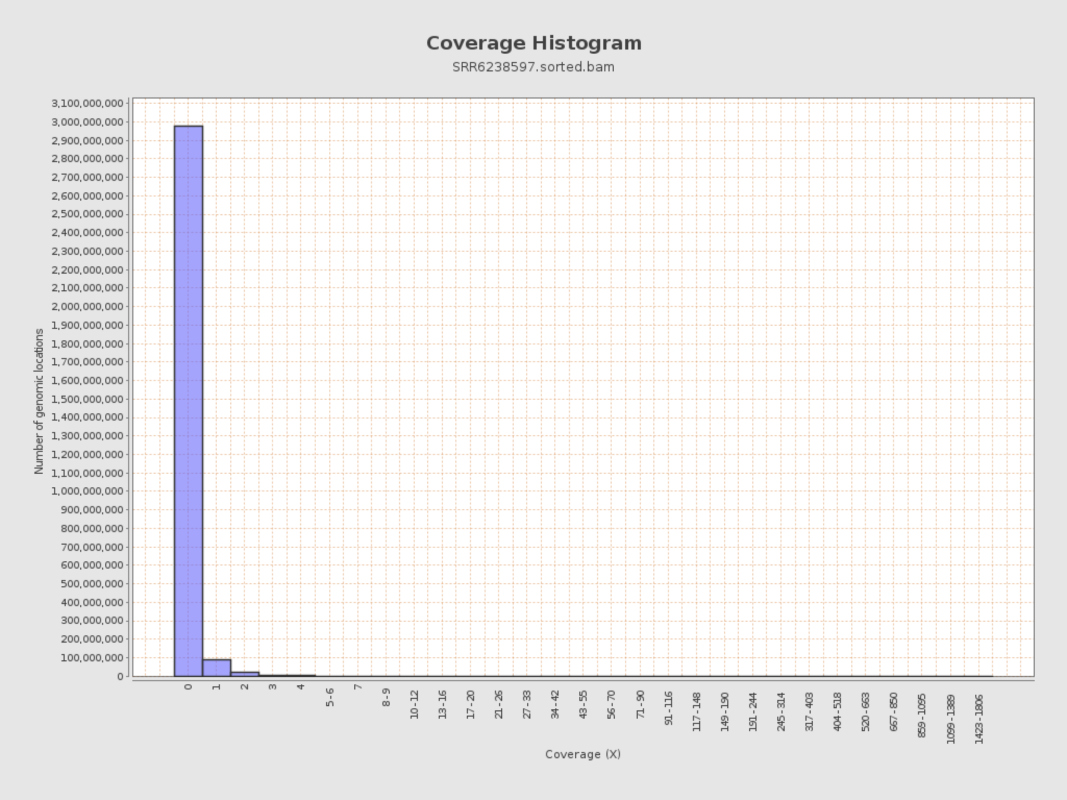
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13614912	0.0546	1.2938
chr2	243199373	16004215	0.0658	0.8876
chr3	198022430	10857057	0.0548	0.3031
chr4	191154276	12143656	0.0635	0.3347
chr5	180915260	9213115	0.0509	0.2939
chr6	171115067	8651812	0.0506	0.4176
chr7	159138663	8552718	0.0537	0.6182

chr8	146364022	7101302	0.0485	0.5474
chr9	141213431	6556285	0.0464	0.4176
chr10	135534747	7675883	0.0566	0.4819
chr11	135006516	6325106	0.0469	0.3547
chr12	133851895	7377715	0.0551	0.3156
chr13	115169878	4203802	0.0365	0.279
chr14	107349540	4434525	0.0413	0.279
chr15	102531392	4597680	0.0448	0.3136
chr16	90354753	4628265	0.0512	0.3273
chr17	81195210	4343338	0.0535	0.3455
chr18	78077248	4380539	0.0561	0.8247
chr19	59128983	2975076	0.0503	0.8101
chr20	63025520	2794105	0.0443	0.2823
chr21	48129895	2264537	0.0471	0.2919
chr22	51304566	1418521	0.0276	0.214
chrMT	16571	33842	2.0422	1.9998
chrX	155270560	9268388	0.0597	0.3481
chrY	59373566	412846	0.007	0.1722

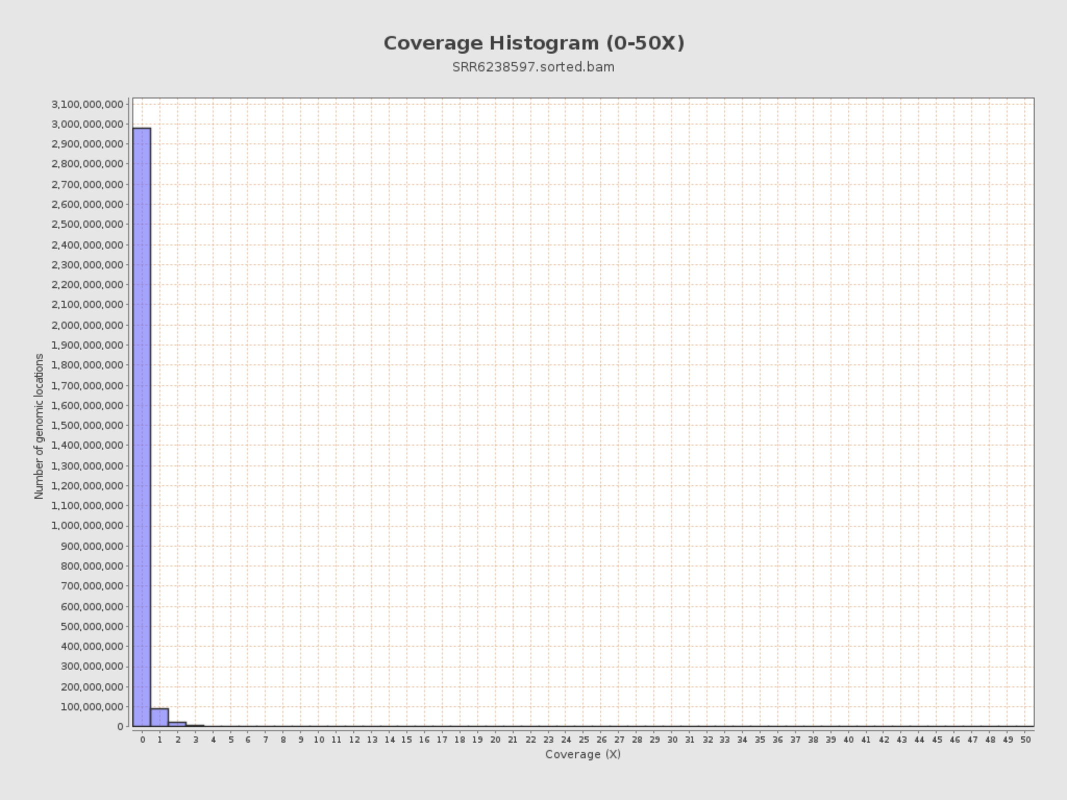
3. Results : Coverage across reference



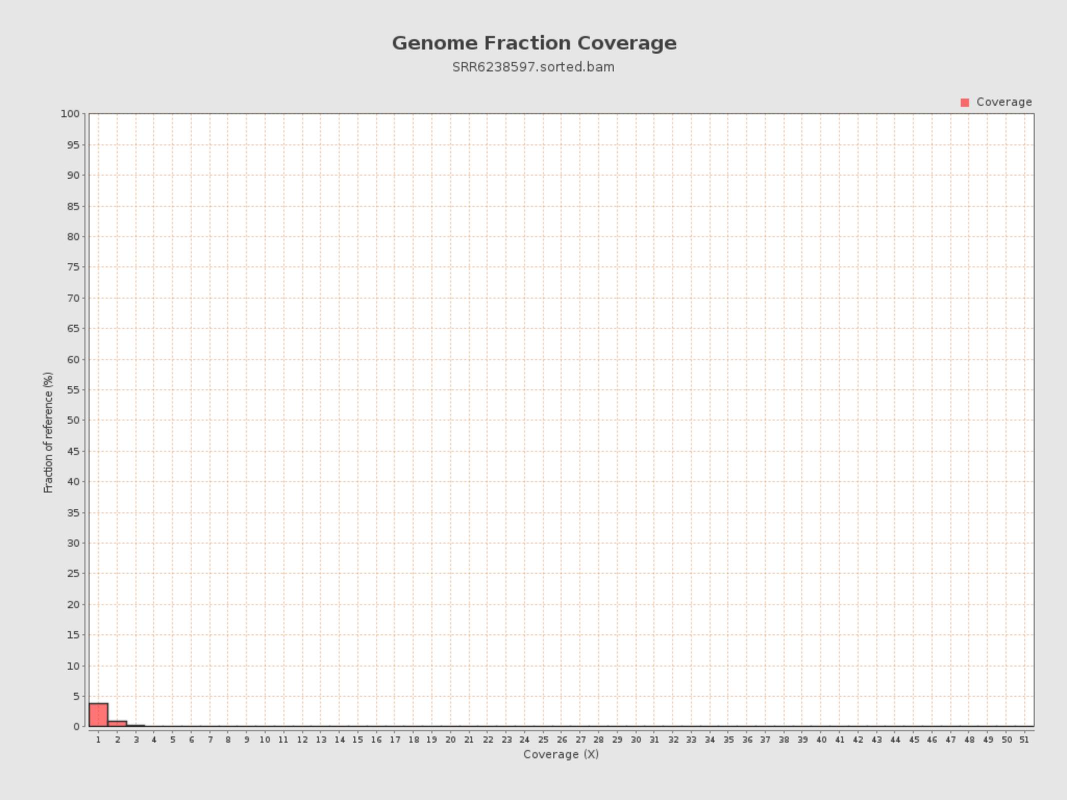
4. Results : Coverage Histogram



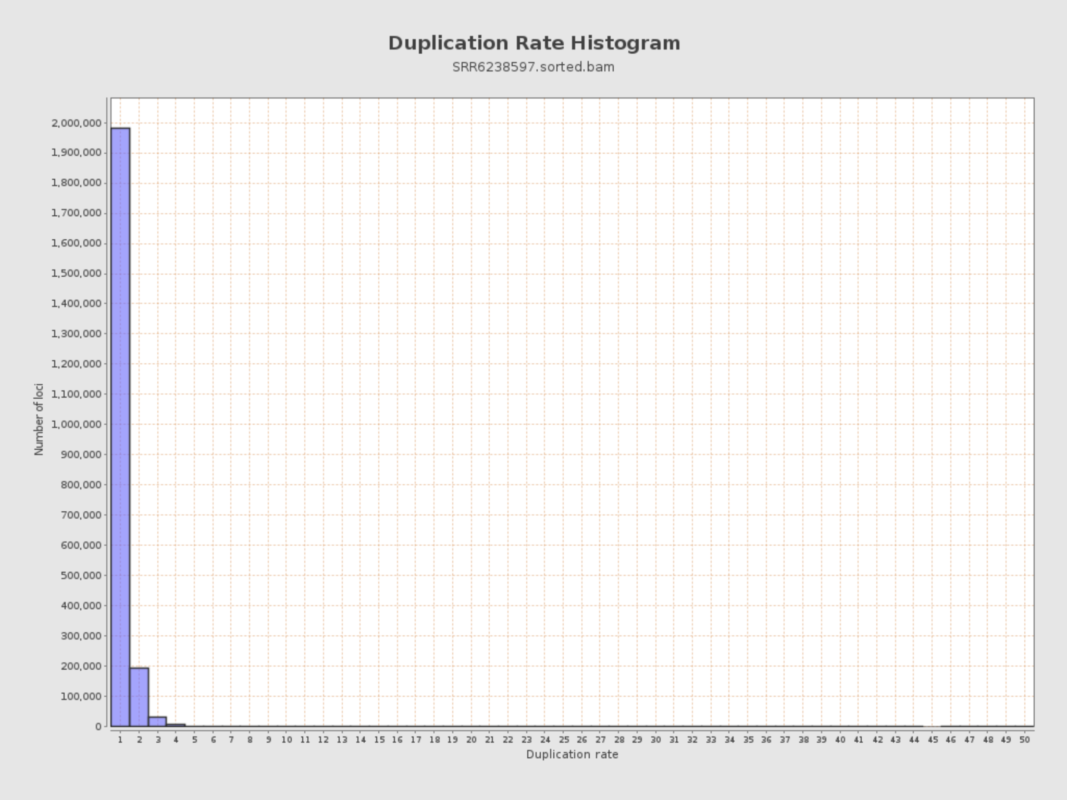
5. Results : Coverage Histogram (0-50X)



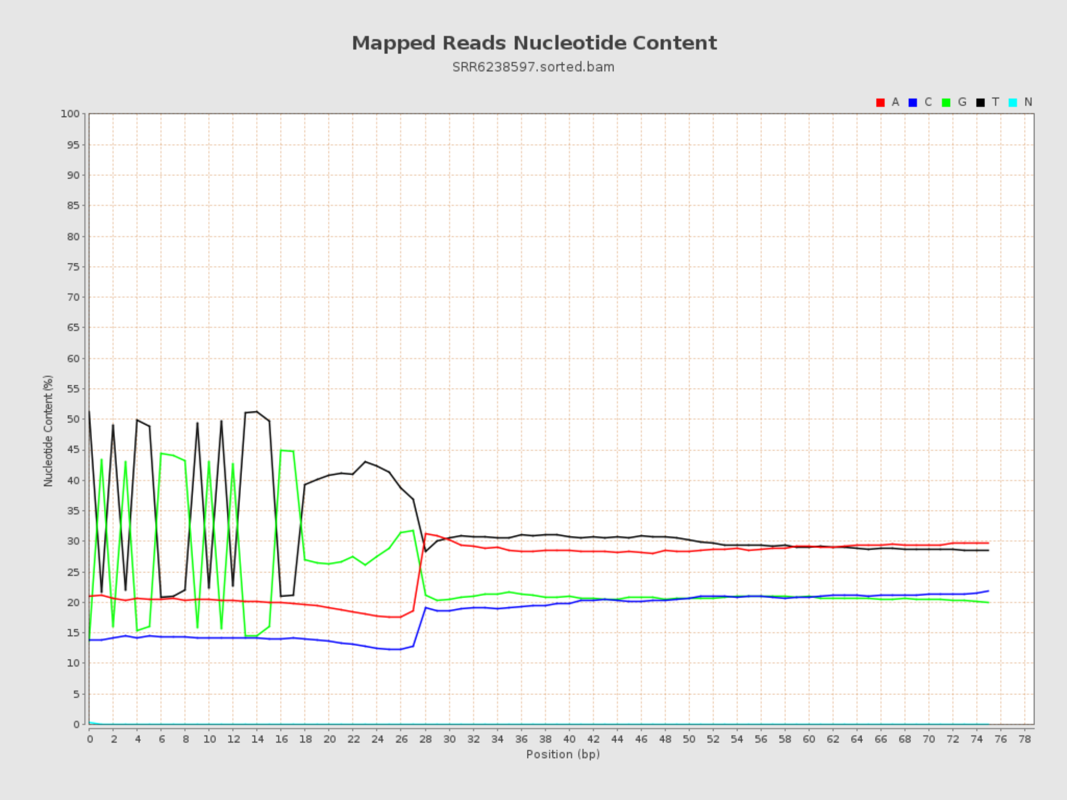
6. Results : Genome Fraction Coverage



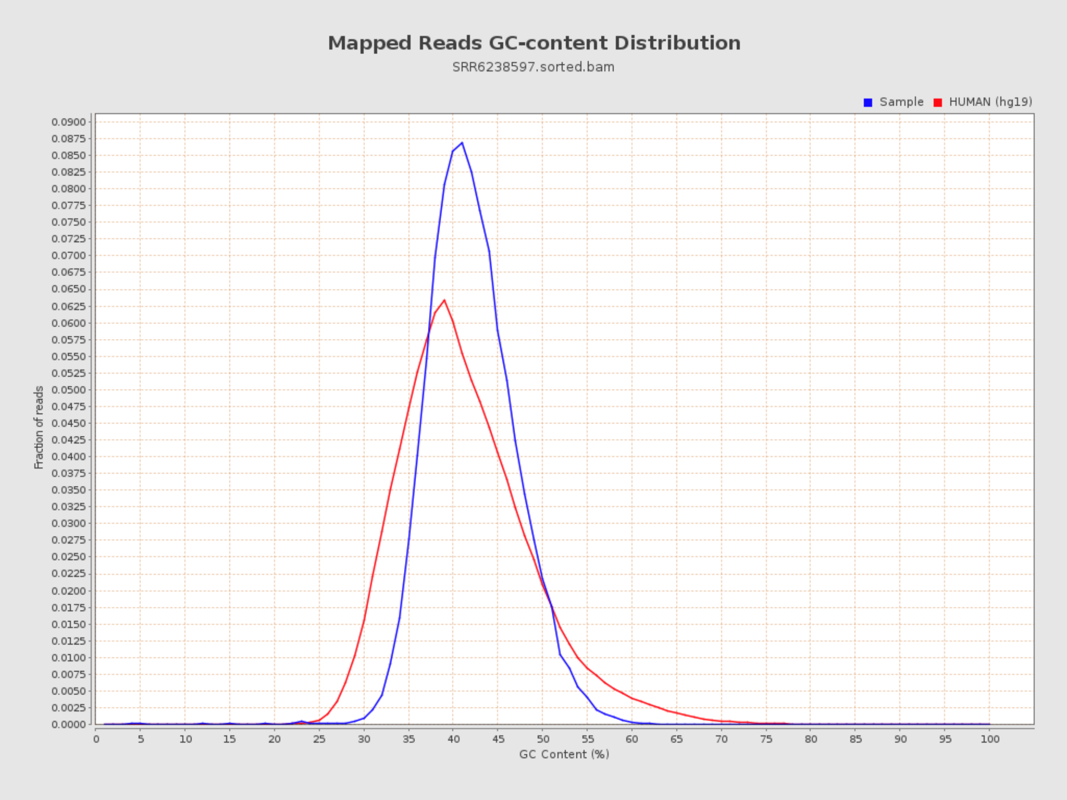
7. Results : Duplication Rate Histogram



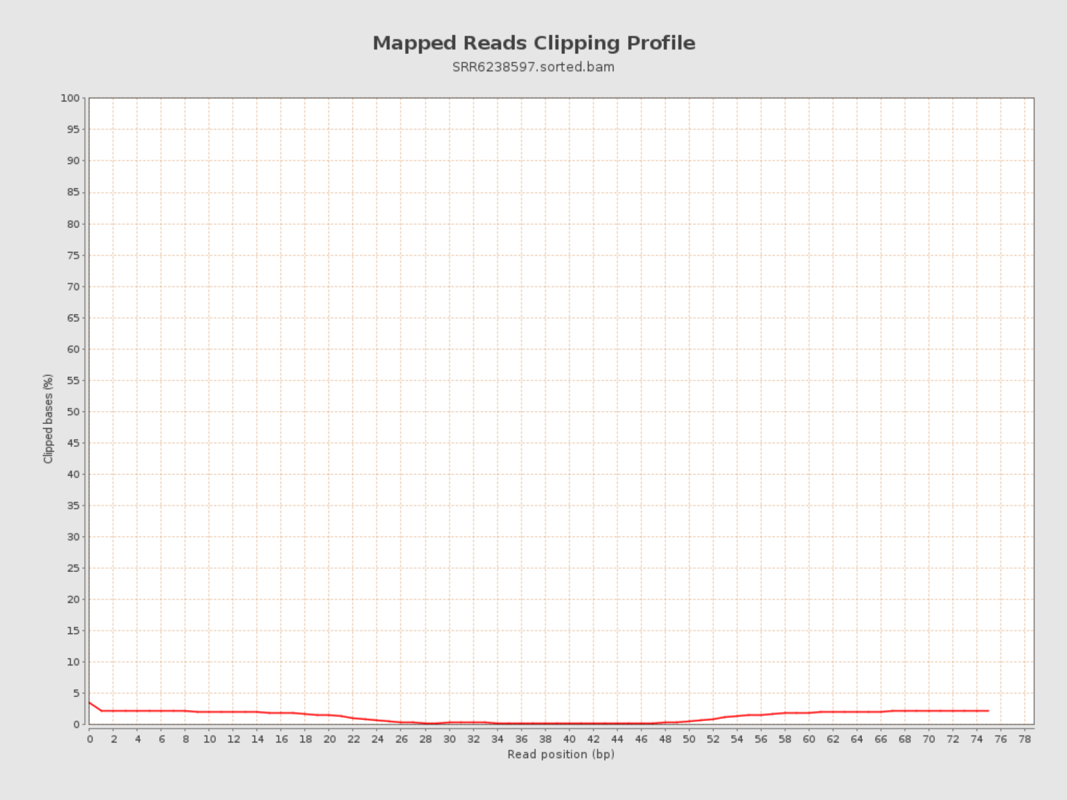
8. Results : Mapped Reads Nucleotide Content



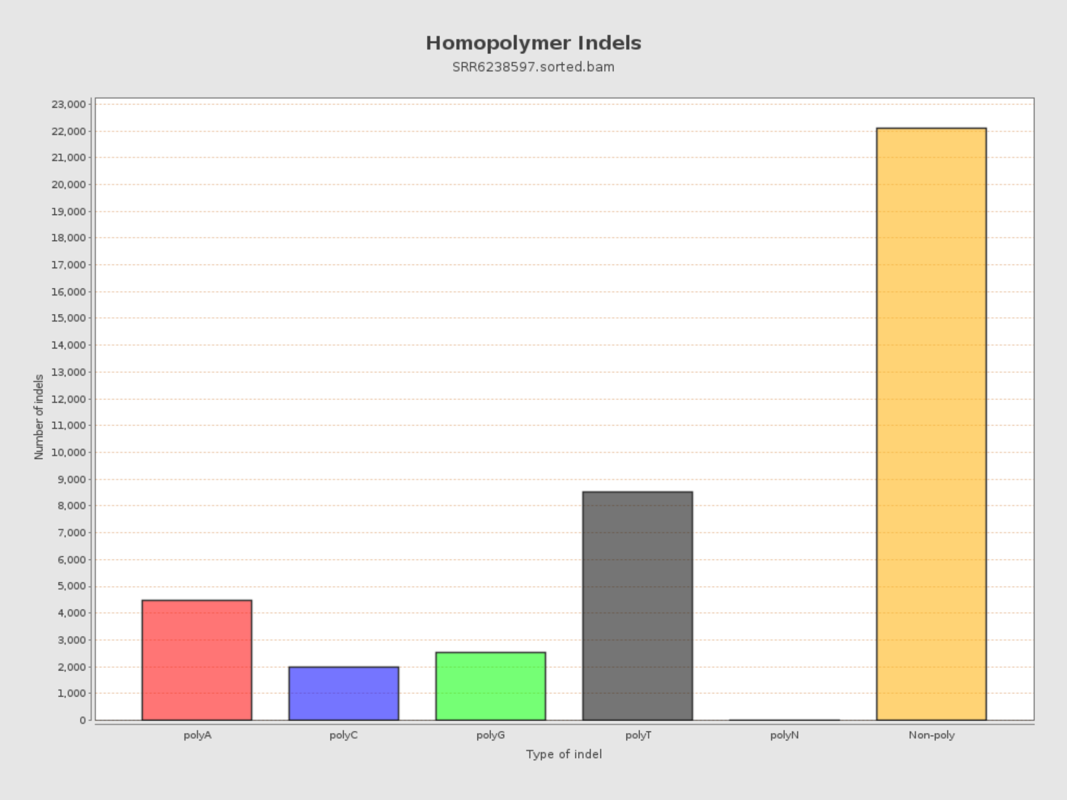
9. Results : Mapped Reads GC-content Distribution



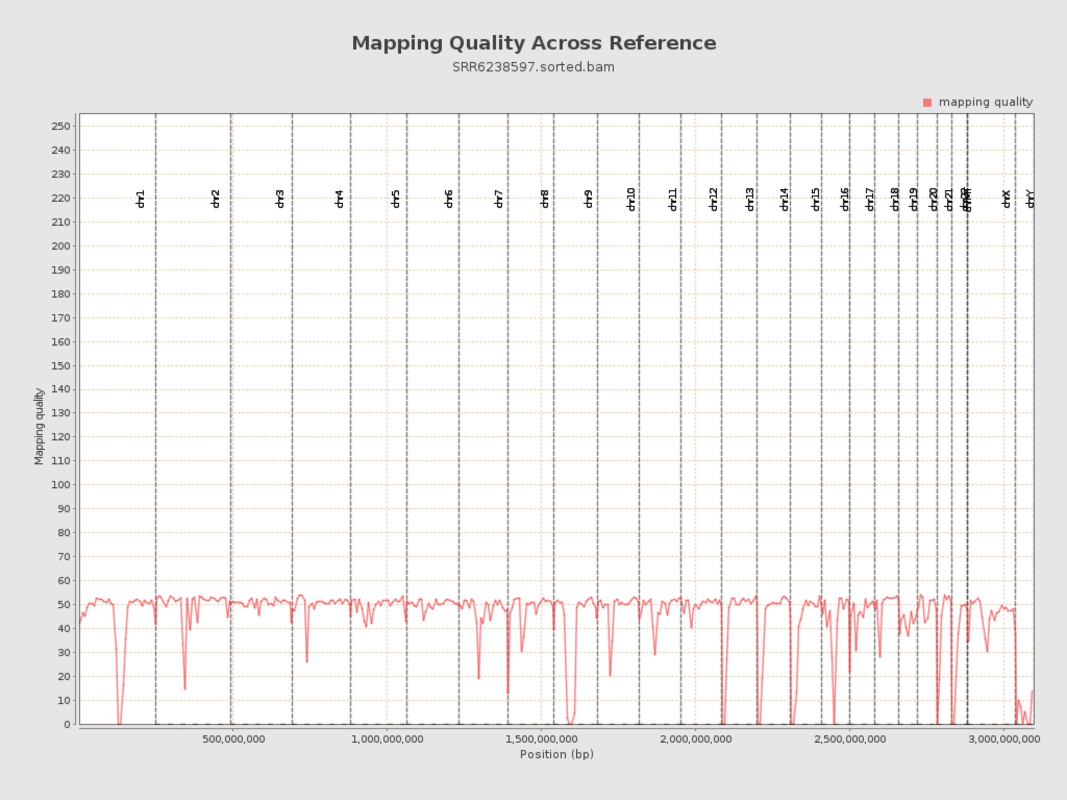
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram