Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 21:49:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238603.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_SRR6238603 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238603.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 21:49:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238603.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,312,239
Mapped reads	3,035,736 / 91.65%
Unmapped reads	276,503 / 8.35%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,475 / 0.68%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	409,750 / 12.37%
Duplication rate	11.25%
Clipped reads	1,822,869 / 55.03%

2.2. ACGT Content

Number/percentage of A's	47,776,437 / 25.27%
Number/percentage of C's	33,631,389 / 17.79%
Number/percentage of T's	62,431,284 / 33.02%
Number/percentage of G's	45,237,442 / 23.92%
Number/percentage of N's	9,719 / 0.01%
GC Percentage	41.71%

2.3. Coverage

Mean	0.0611

Standard Deviation	0.6406

2.4. Mapping Quality

Mean Mapping Quality	43.57

2.5. Mismatches and indels

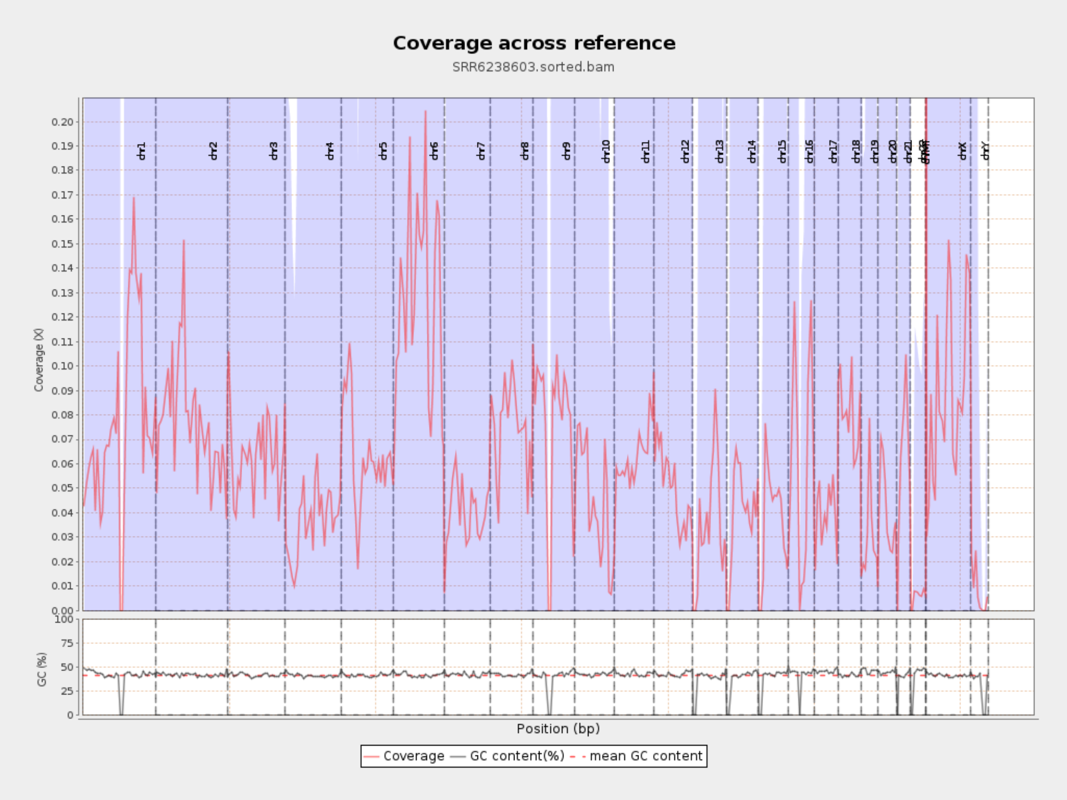
General error rate	0.57%
Mismatches	1,060,562
Insertions	11,962
Mapped reads with at least one insertion	0.39%
Deletions	56,030
Mapped reads with at least one deletion	1.82%
Homopolymer indels	42.13%

2.6. Chromosome stats

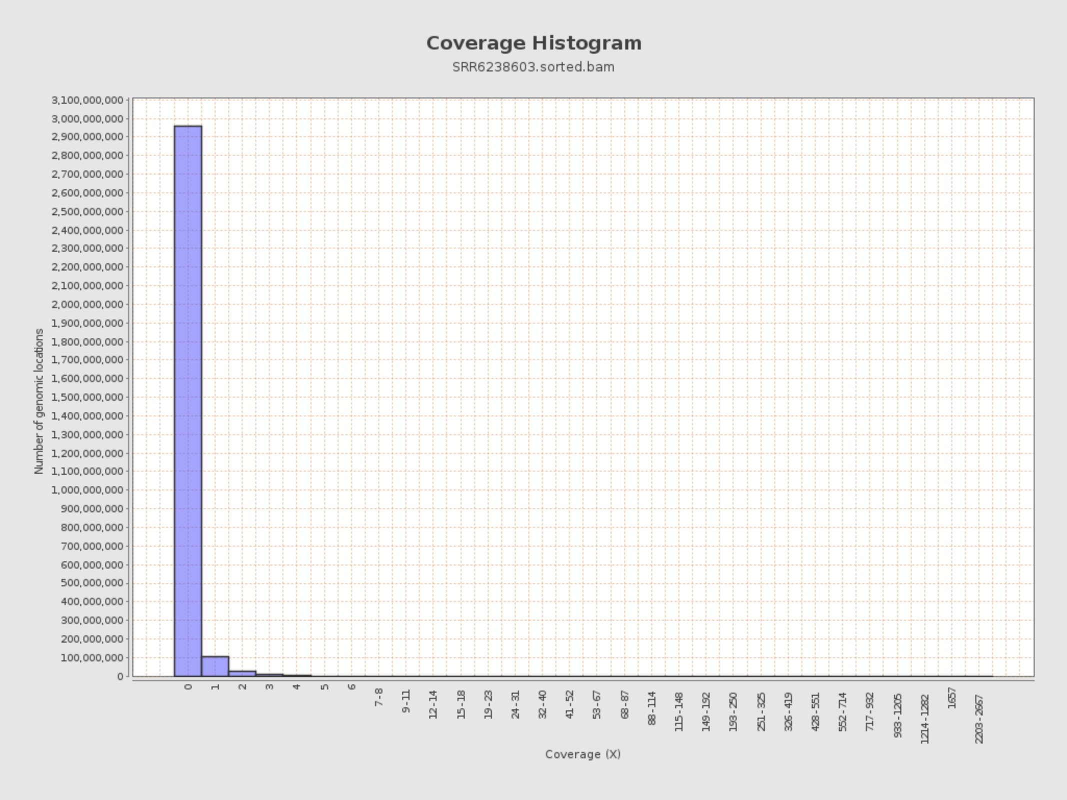
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	19120878	0.0767	1.0549
chr2	243199373	18811495	0.0774	1.2766
chr3	198022430	12454120	0.0629	0.3358
chr4	191154276	6945052	0.0363	0.2771
chr5	180915260	11401571	0.063	0.3385
chr6	171115067	22139990	0.1294	0.8571
chr7	159138663	6440355	0.0405	0.3943

chr8	146364022	10930038	0.0747	0.494
chr9	141213431	10749266	0.0761	0.6173
chr10	135534747	6085785	0.0449	0.3965
chr11	135006516	8351619	0.0619	0.379
chr12	133851895	6708995	0.0501	0.3438
chr13	115169878	4052062	0.0352	0.3387
chr14	107349540	4331878	0.0404	0.3652
chr15	102531392	3826263	0.0373	0.3578
chr16	90354753	5276776	0.0584	0.4042
chr17	81195210	3215064	0.0396	0.2873
chr18	78077248	6225528	0.0797	1.1859
chr19	59128983	1847733	0.0312	0.6173
chr20	63025520	2675061	0.0424	0.3036
chr21	48129895	2981333	0.0619	0.3837
chr22	51304566	295007	0.0058	0.0923
chrMT	16571	21809	1.3161	1.5882
chrX	155270560	13824403	0.089	0.4337
chrY	59373566	471936	0.0079	0.2413

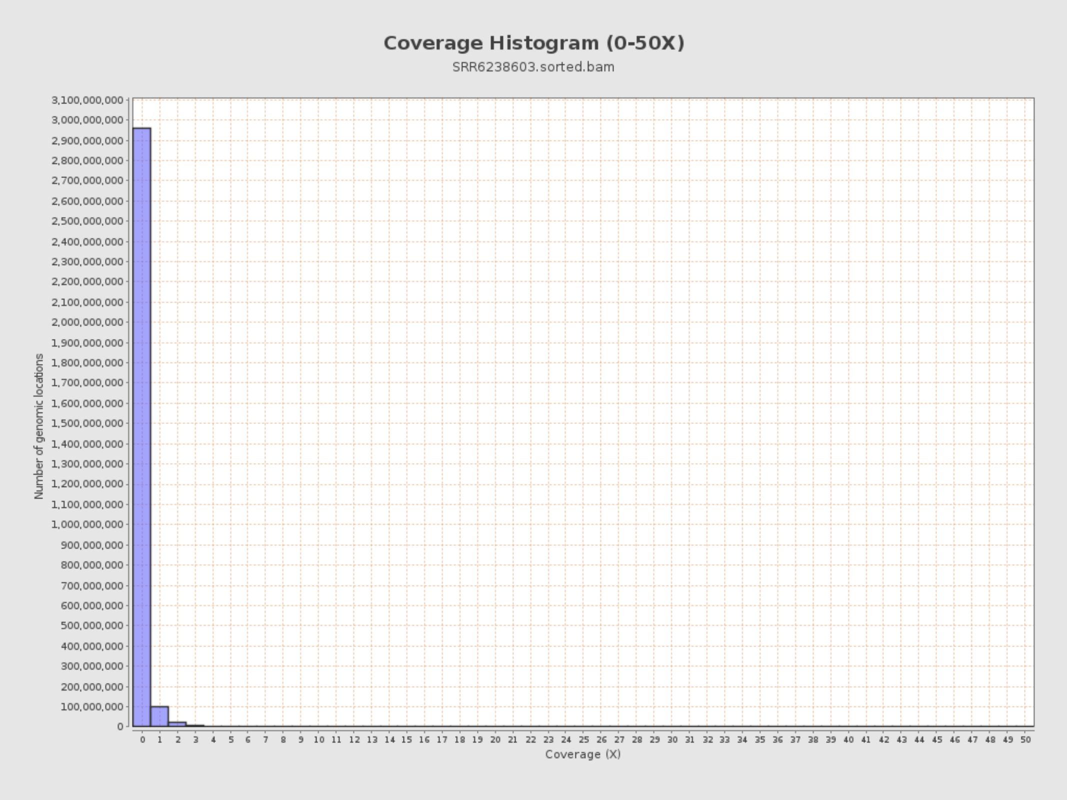
3. Results : Coverage across reference



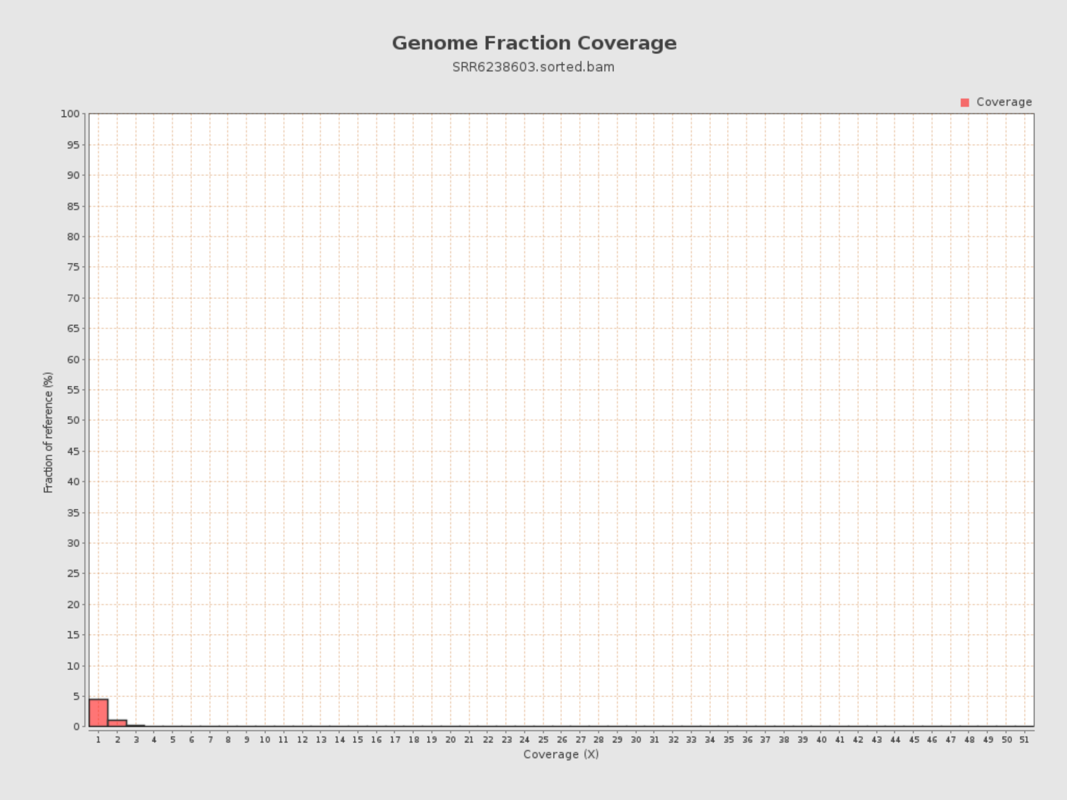
4. Results : Coverage Histogram



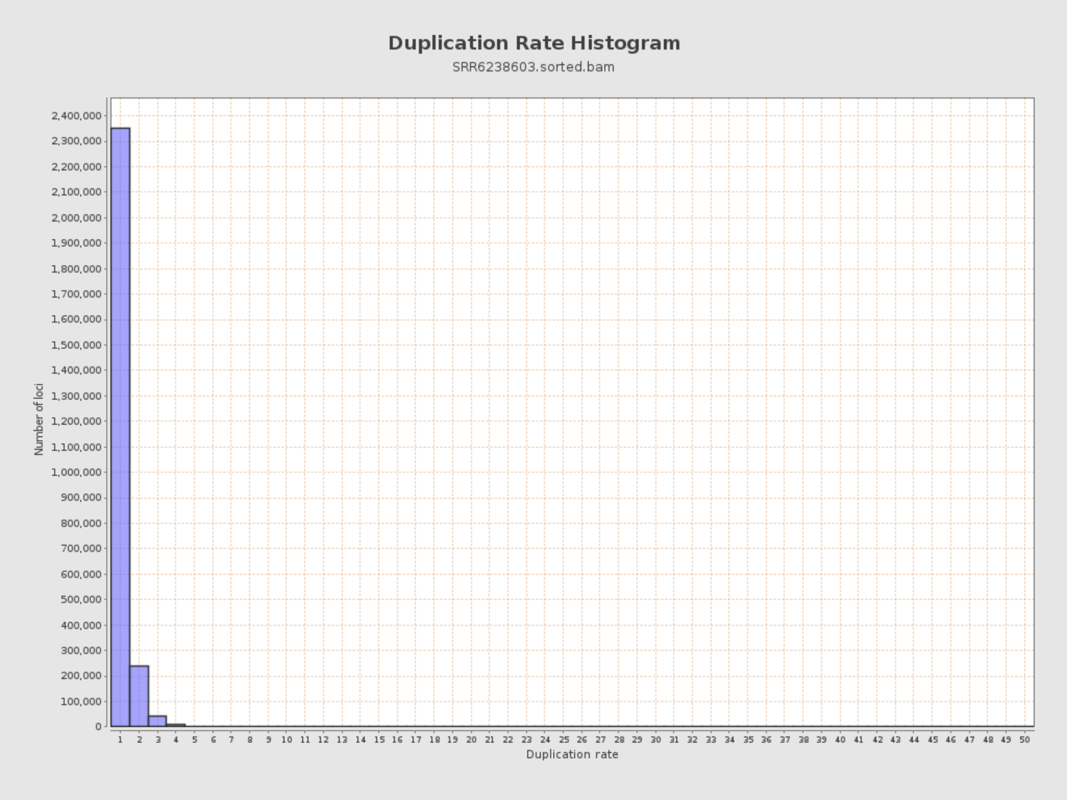
5. Results : Coverage Histogram (0-50X)



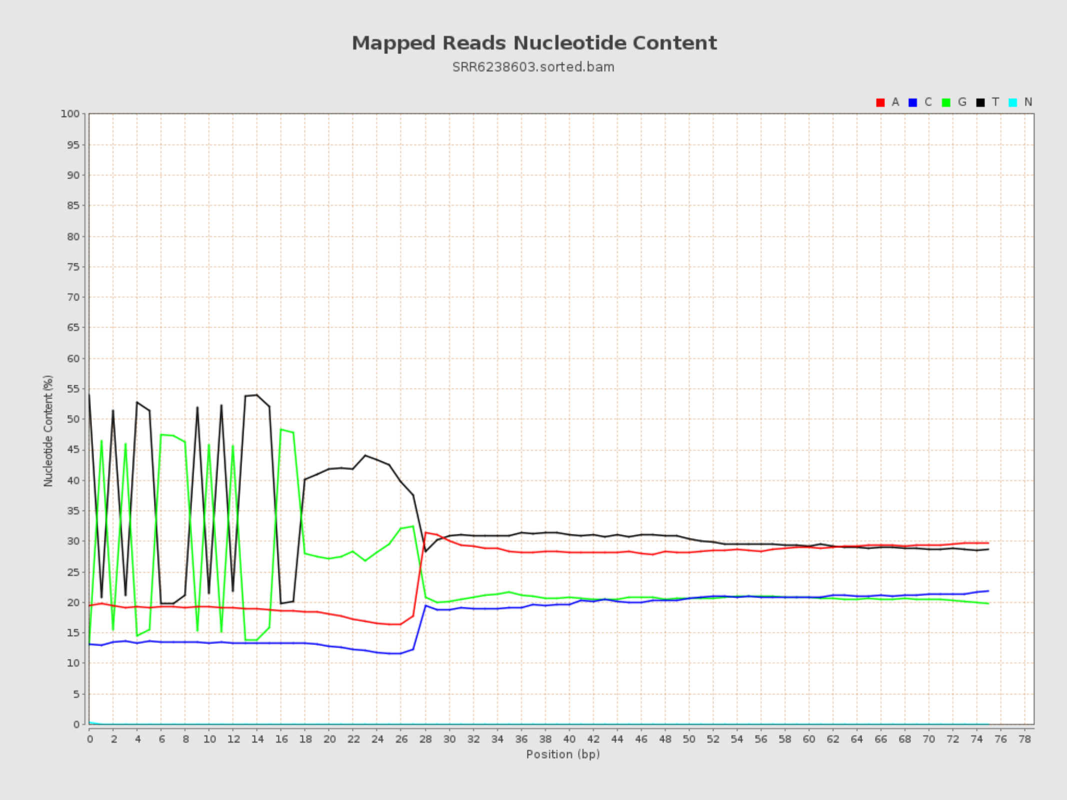
6. Results : Genome Fraction Coverage



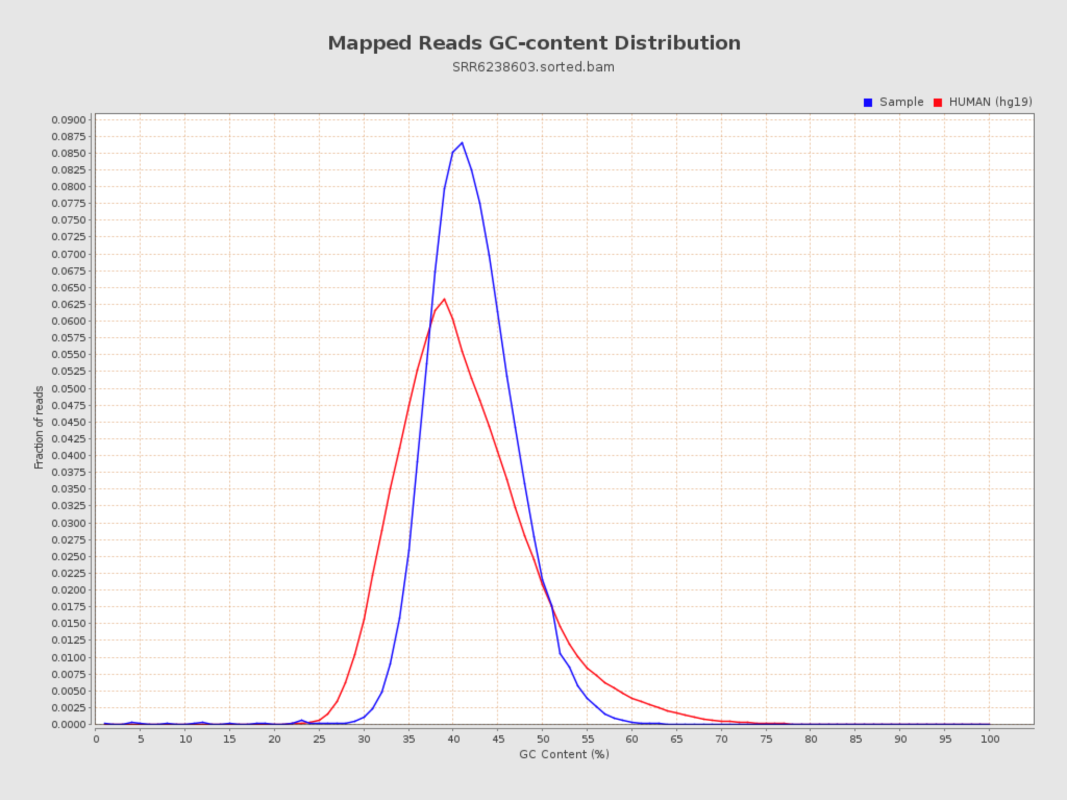
7. Results : Duplication Rate Histogram



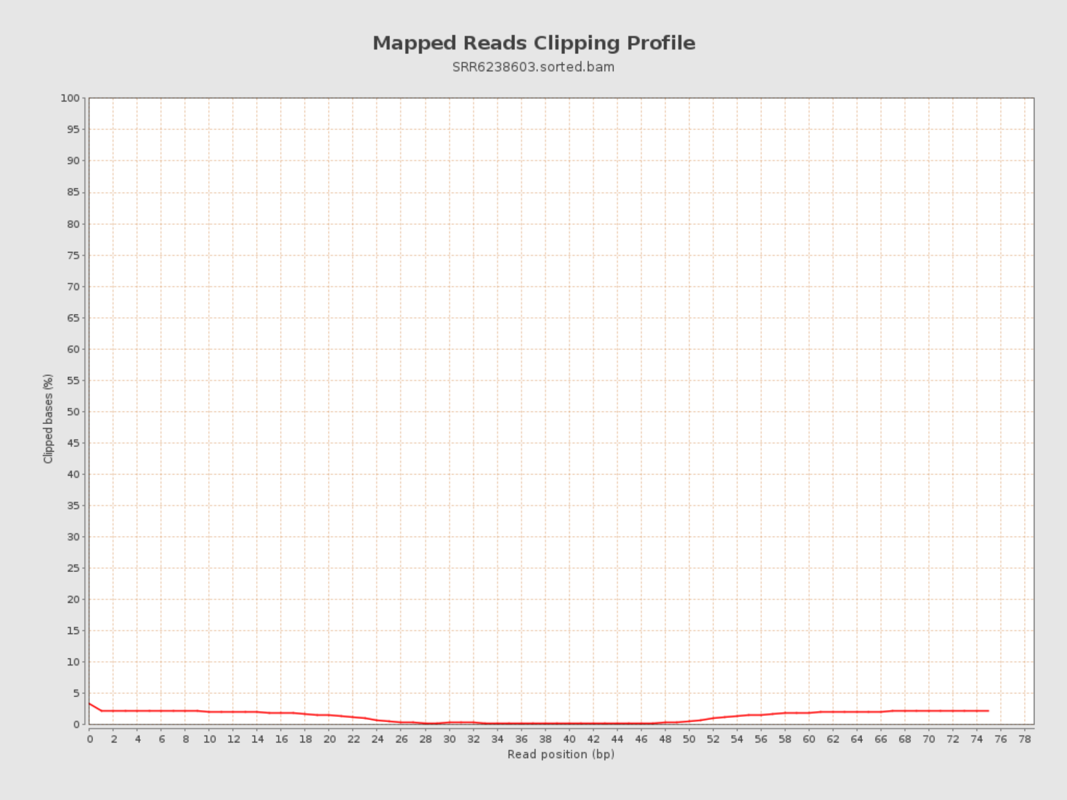
8. Results : Mapped Reads Nucleotide Content



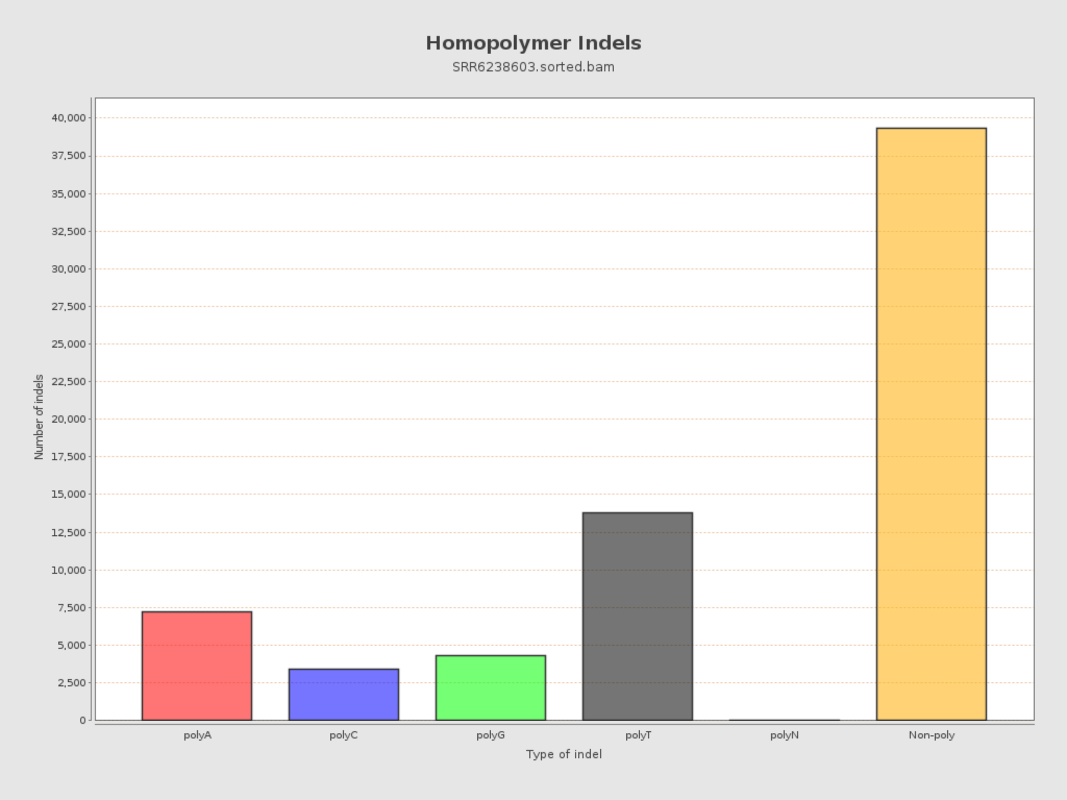
9. Results : Mapped Reads GC-content Distribution



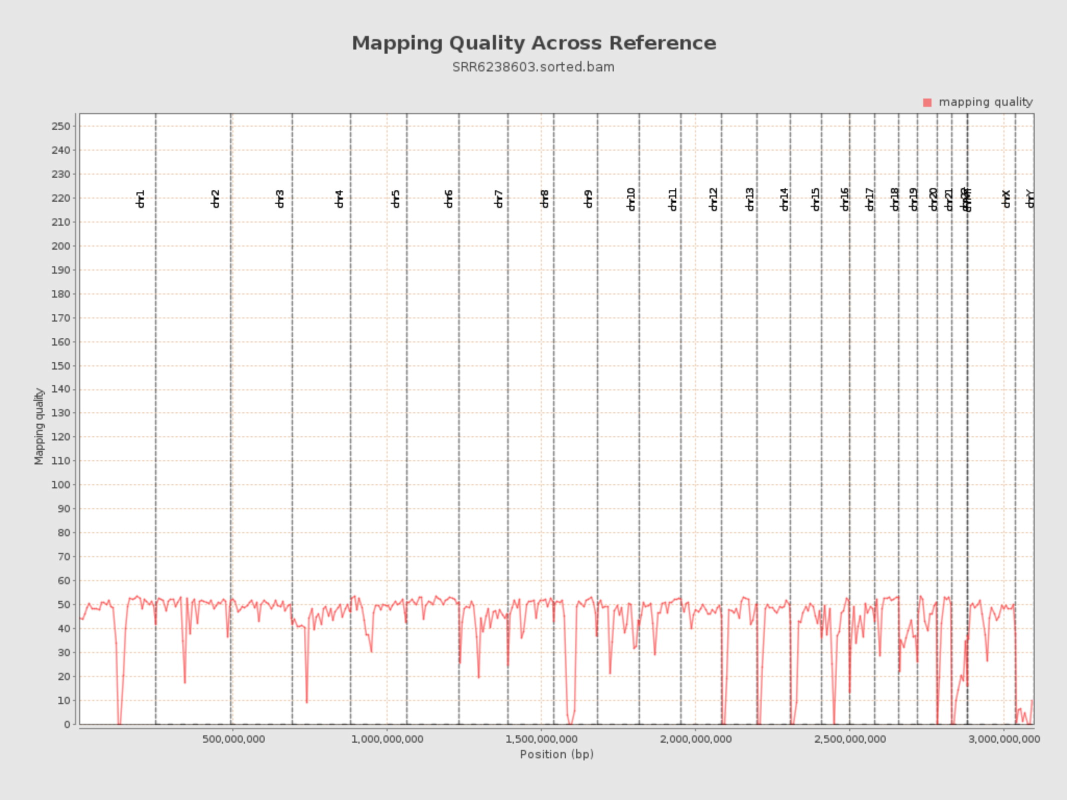
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram