Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 13:05:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238254.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_SRR6238254 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238254.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 13:05:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238254.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,097,748
Mapped reads	2,846,245 / 91.88%
Unmapped reads	251,503 / 8.12%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,722 / 0.73%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	117,060 / 3.78%
Duplication rate	3.03%
Clipped reads	1,305,367 / 42.14%

2.2. ACGT Content

Number/percentage of A's	52,152,968 / 27.49%
Number/percentage of C's	36,685,047 / 19.34%
Number/percentage of T's	57,878,745 / 30.51%
Number/percentage of G's	42,949,331 / 22.64%
Number/percentage of N's	56,497 / 0.03%
GC Percentage	41.97%

2.3. Coverage

Mean	0.0613

Standard Deviation	0.4896

2.4. Mapping Quality

Mean Mapping Quality	44.84

2.5. Mismatches and indels

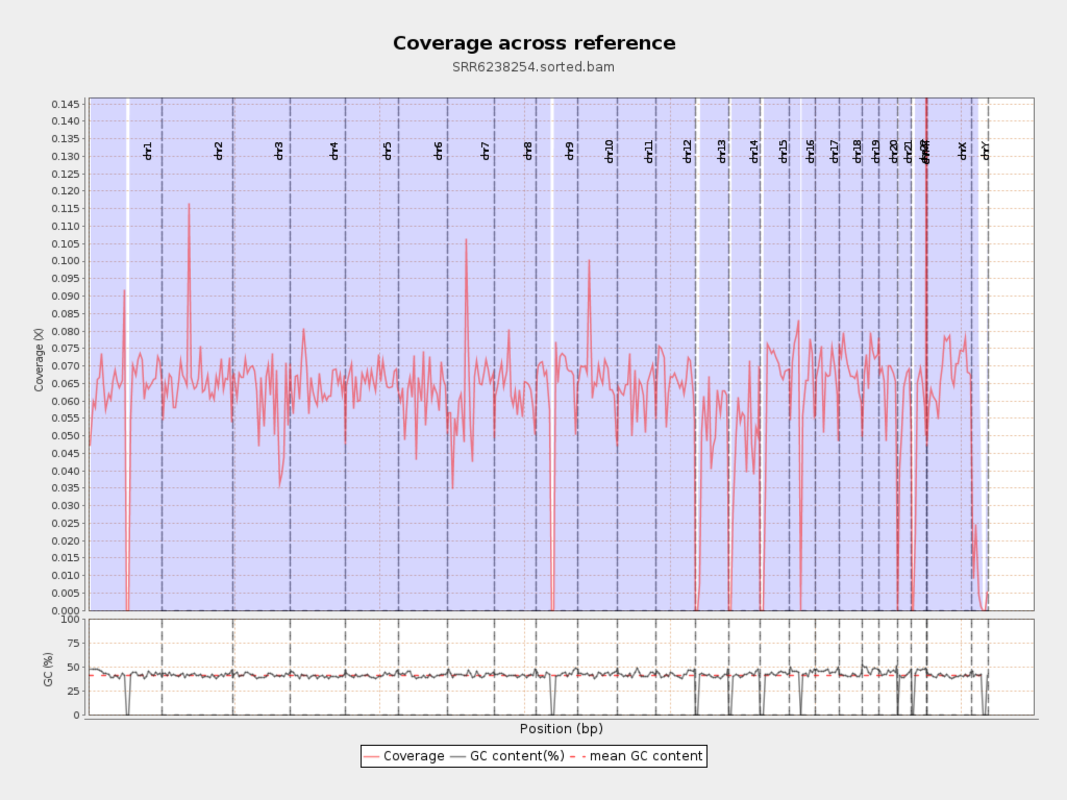
General error rate	0.88%
Mismatches	1,648,766
Insertions	15,409
Mapped reads with at least one insertion	0.54%
Deletions	51,269
Mapped reads with at least one deletion	1.78%
Homopolymer indels	45.67%

2.6. Chromosome stats

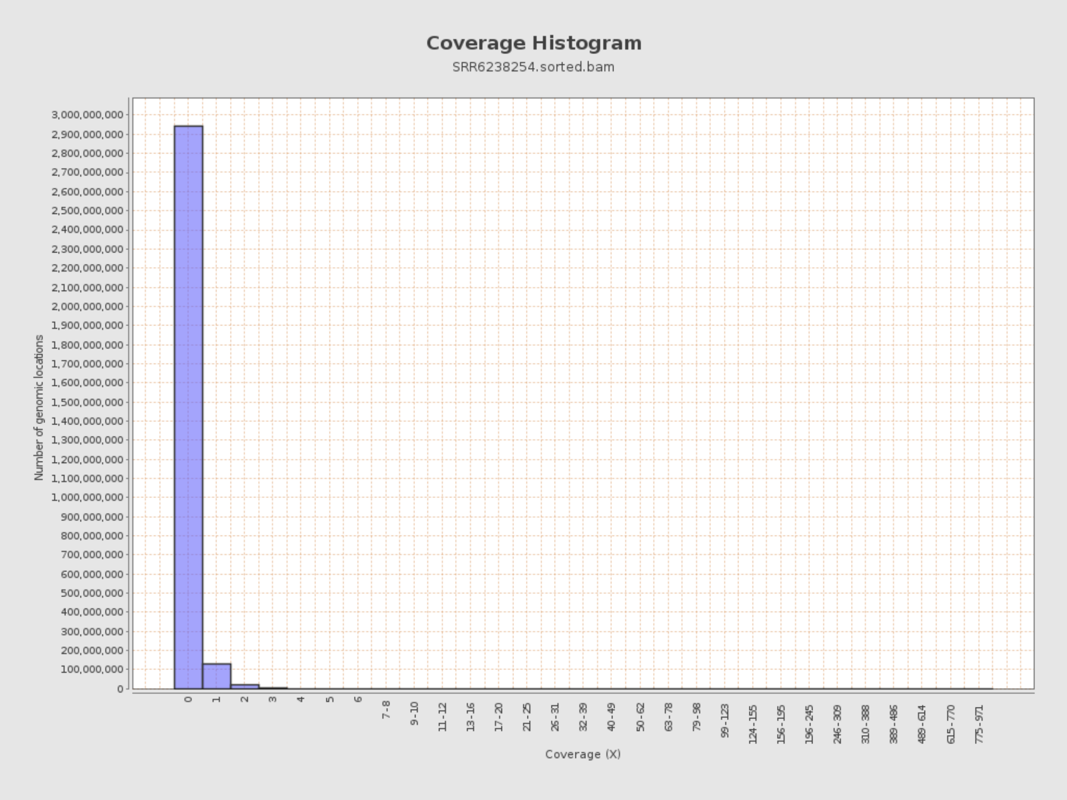
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15409637	0.0618	0.794
chr2	243199373	16177365	0.0665	0.6798
chr3	198022430	12252883	0.0619	0.293
chr4	191154276	12344811	0.0646	0.3328
chr5	180915260	11925959	0.0659	0.3049
chr6	171115067	10684426	0.0624	0.3544
chr7	159138663	9950418	0.0625	0.756

chr8	146364022	9273525	0.0634	0.5386
chr9	141213431	8570471	0.0607	0.4977
chr10	135534747	9204555	0.0679	0.477
chr11	135006516	8484733	0.0628	0.4148
chr12	133851895	8896187	0.0665	0.318
chr13	115169878	5349113	0.0464	0.2535
chr14	107349540	4761639	0.0444	0.3068
chr15	102531392	5968404	0.0582	0.2897
chr16	90354753	5733716	0.0635	0.3414
chr17	81195210	5374102	0.0662	0.3521
chr18	78077248	5415583	0.0694	0.8525
chr19	59128983	4205382	0.0711	0.5842
chr20	63025520	4049990	0.0643	0.3087
chr21	48129895	2523421	0.0524	0.313
chr22	51304566	2268663	0.0442	0.2483
chrMT	16571	8618	0.5201	0.7679
chrX	155270560	10515341	0.0677	0.3566
chrY	59373566	457964	0.0077	0.2017

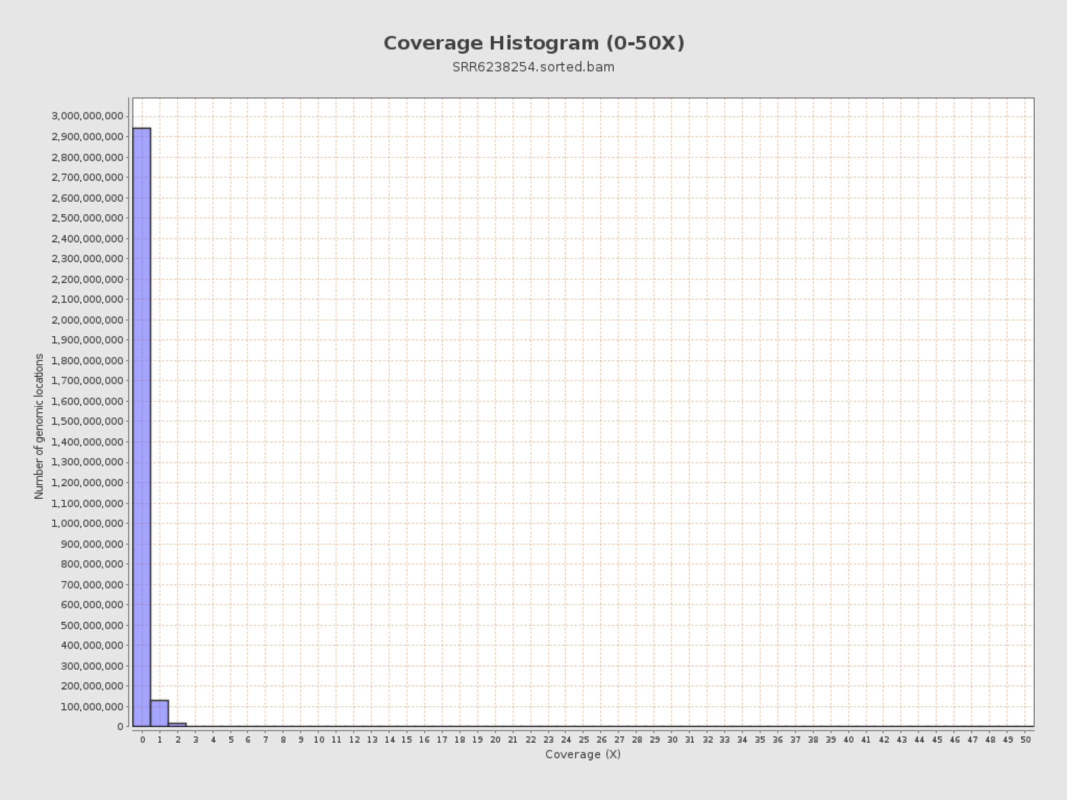
3. Results : Coverage across reference



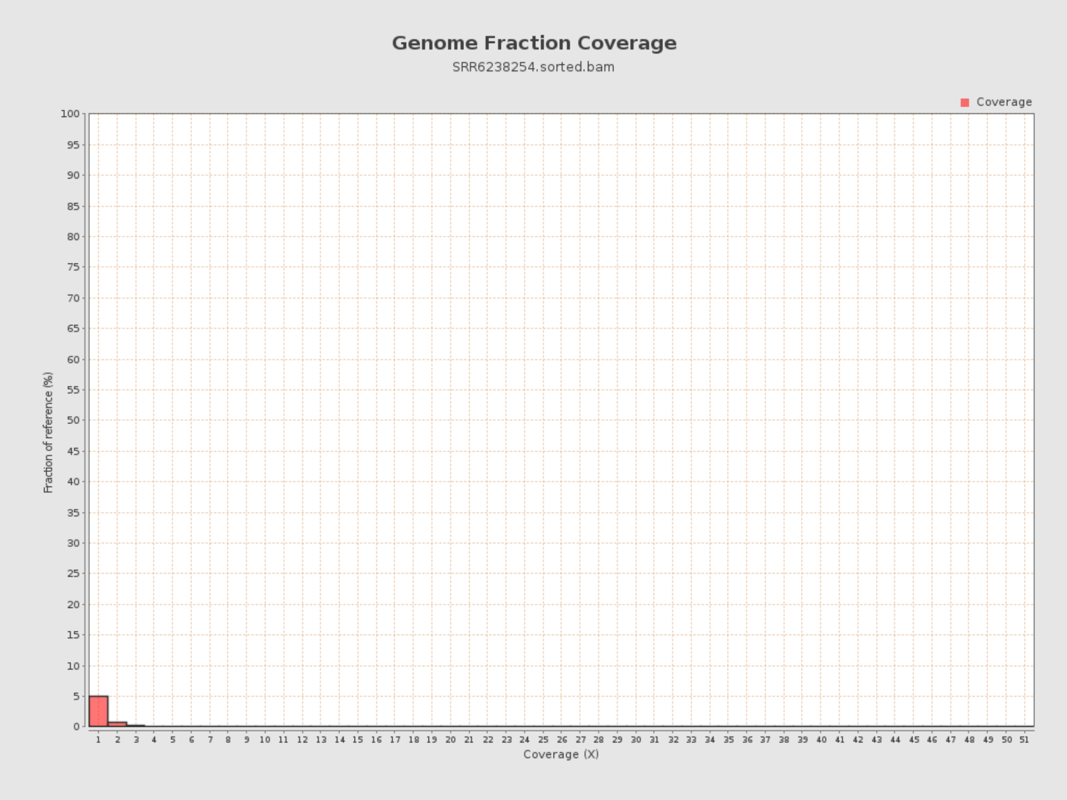
4. Results : Coverage Histogram



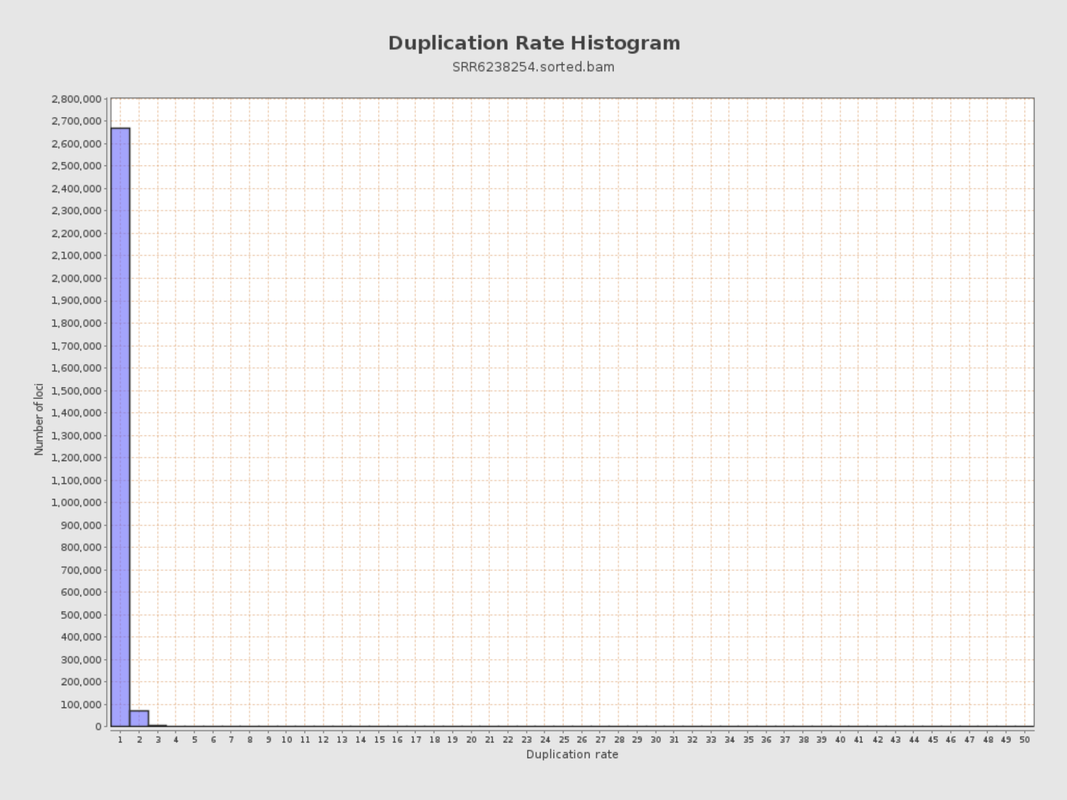
5. Results : Coverage Histogram (0-50X)



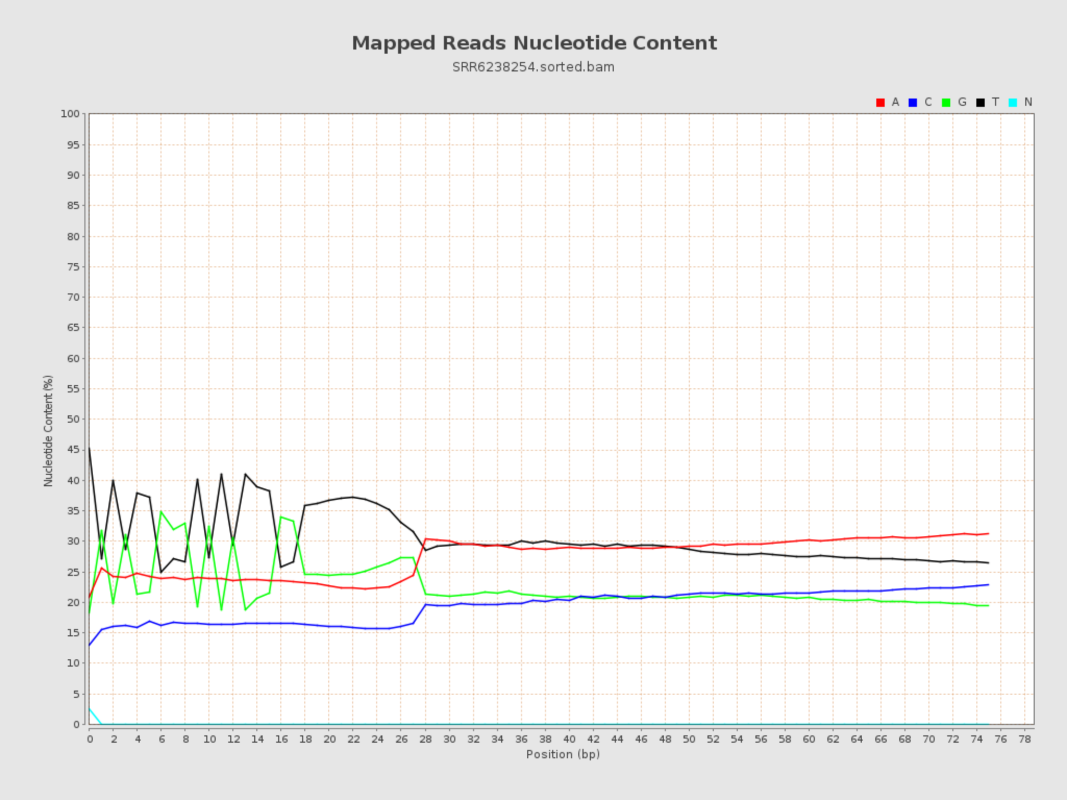
6. Results : Genome Fraction Coverage



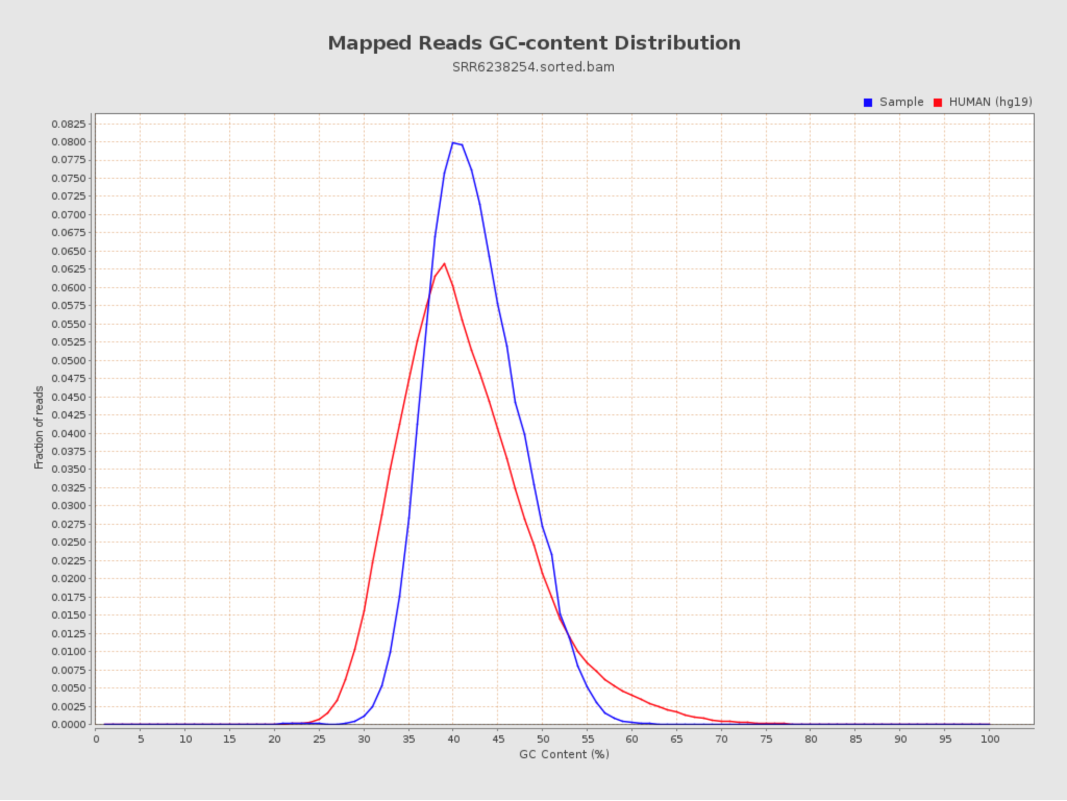
7. Results : Duplication Rate Histogram



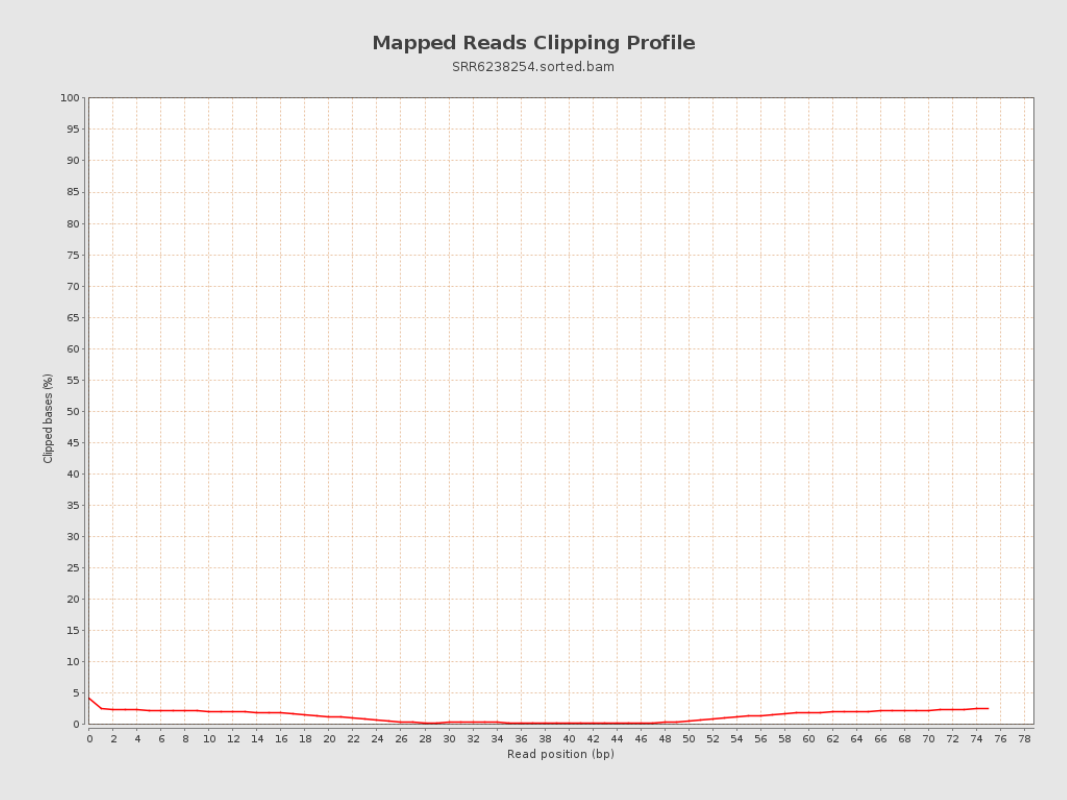
8. Results : Mapped Reads Nucleotide Content



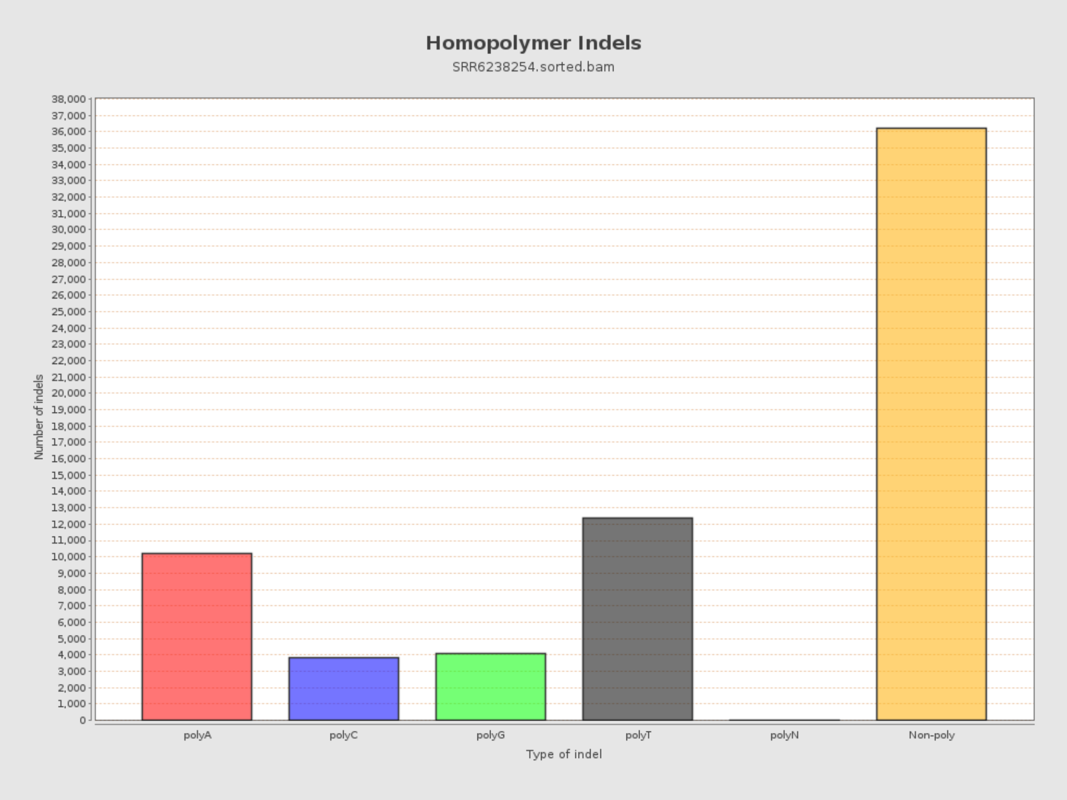
9. Results : Mapped Reads GC-content Distribution



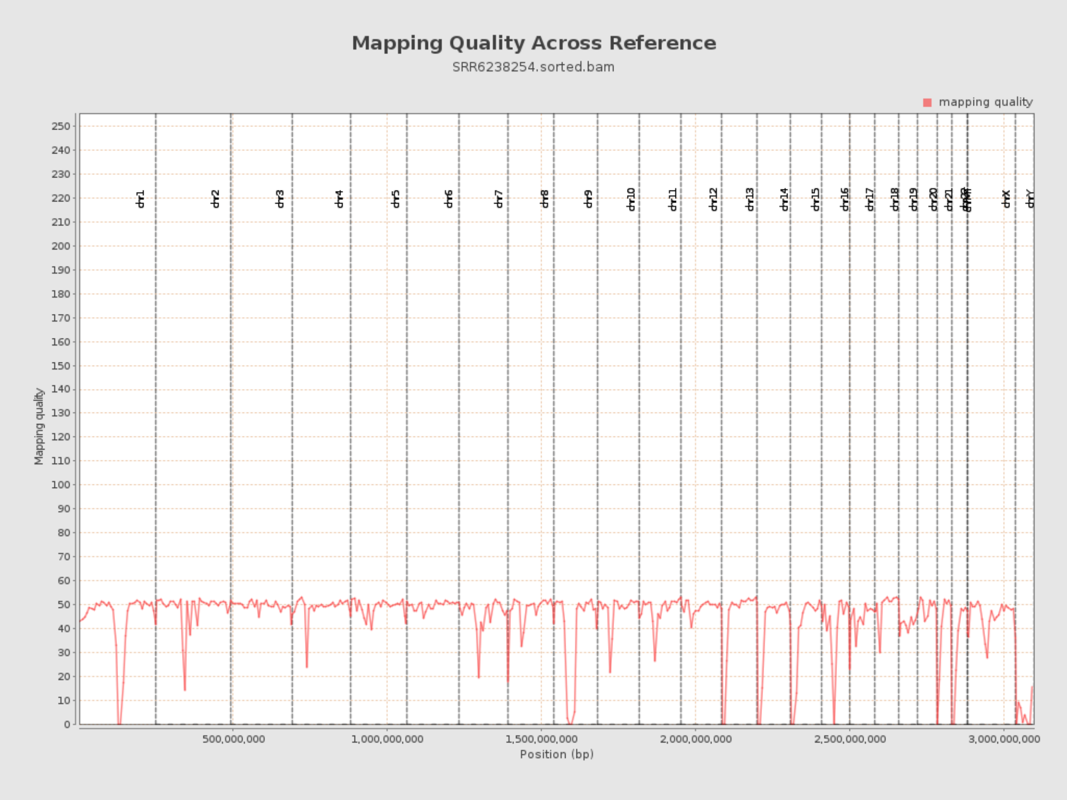
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram