Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 19:47:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6236083.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_SRR6236083 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6236083.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 19:47:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6236083.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,364,136
Mapped reads	2,054,821 / 86.92%
Unmapped reads	309,315 / 13.08%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,553 / 0.49%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	105,462 / 4.46%
Duplication rate	3.8%
Clipped reads	1,004,345 / 42.48%

2.2. ACGT Content

Number/percentage of A's	36,659,013 / 27.28%
Number/percentage of C's	23,999,465 / 17.86%
Number/percentage of T's	43,302,591 / 32.23%
Number/percentage of G's	30,352,954 / 22.59%
Number/percentage of N's	54,224 / 0.04%
GC Percentage	40.45%

2.3. Coverage

Mean	0.0434

Standard Deviation	0.4748

2.4. Mapping Quality

Mean Mapping Quality	44.63

2.5. Mismatches and indels

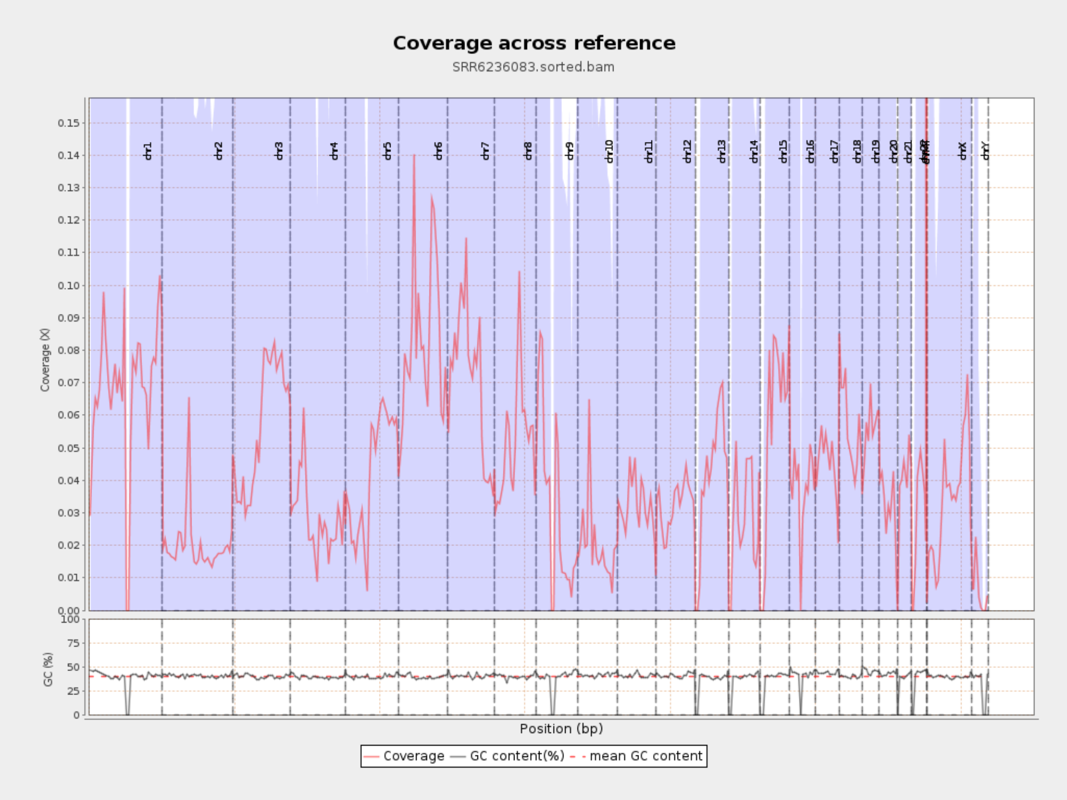
General error rate	0.83%
Mismatches	1,093,638
Insertions	9,953
Mapped reads with at least one insertion	0.48%
Deletions	43,048
Mapped reads with at least one deletion	2.07%
Homopolymer indels	45.78%

2.6. Chromosome stats

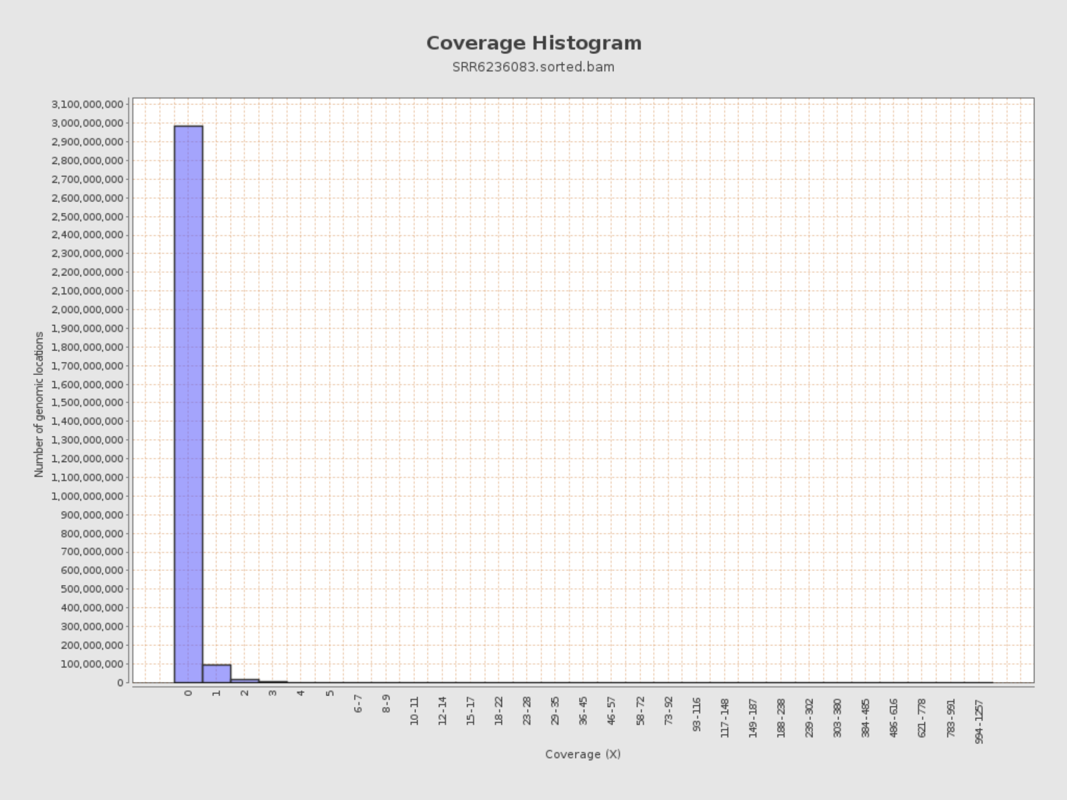
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16930287	0.0679	0.9465
chr2	243199373	4932917	0.0203	0.4061
chr3	198022430	11335737	0.0572	0.2762
chr4	191154276	5420132	0.0284	0.2471
chr5	180915260	7661362	0.0423	0.2418
chr6	171115067	14063239	0.0822	0.5461
chr7	159138663	11324600	0.0712	0.6946

chr8	146364022	7584820	0.0518	0.8386
chr9	141213431	4467701	0.0316	0.3744
chr10	135534747	2723913	0.0201	0.363
chr11	135006516	4346264	0.0322	0.2918
chr12	133851895	4373901	0.0327	0.2185
chr13	115169878	4776327	0.0415	0.2333
chr14	107349540	2863033	0.0267	0.2158
chr15	102531392	5786797	0.0564	0.2792
chr16	90354753	3377516	0.0374	0.2607
chr17	81195210	3620941	0.0446	0.2922
chr18	78077248	4412773	0.0565	0.698
chr19	59128983	3300654	0.0558	0.5685
chr20	63025520	2017042	0.032	0.2176
chr21	48129895	1895061	0.0394	0.2659
chr22	51304566	1462849	0.0285	0.1914
chrMT	16571	74678	4.5065	3.6025
chrX	155270560	5356902	0.0345	0.2456
chrY	59373566	333553	0.0056	0.1915

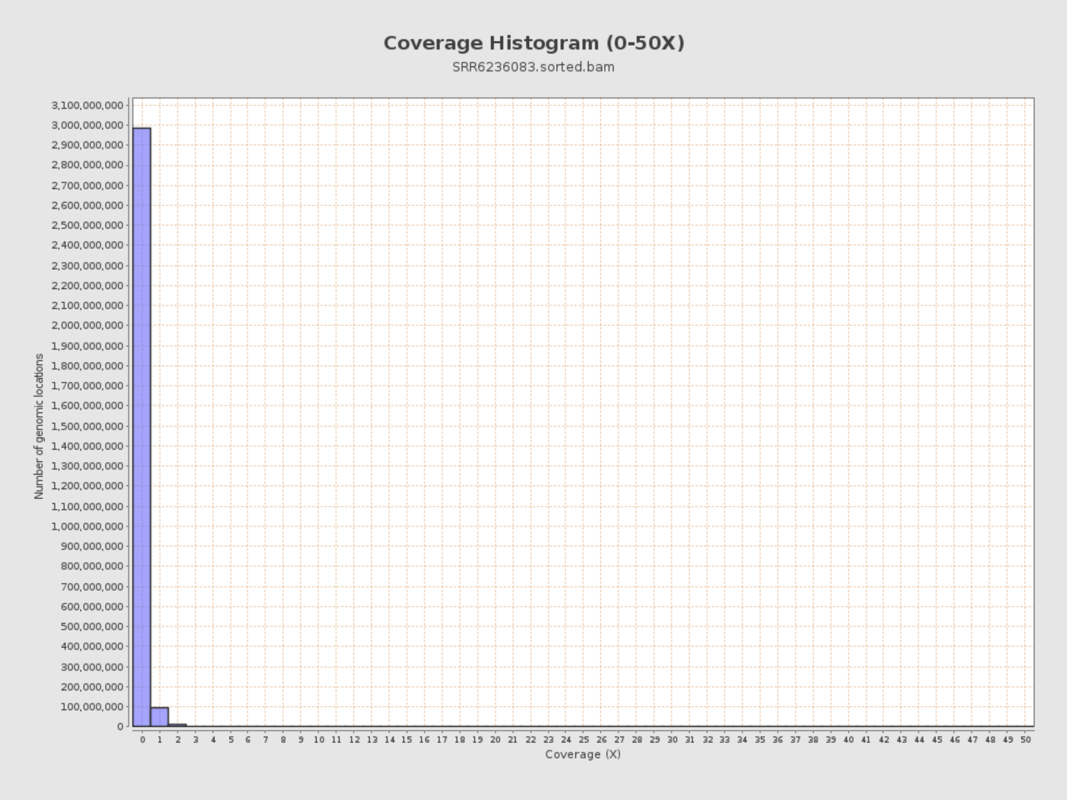
3. Results : Coverage across reference



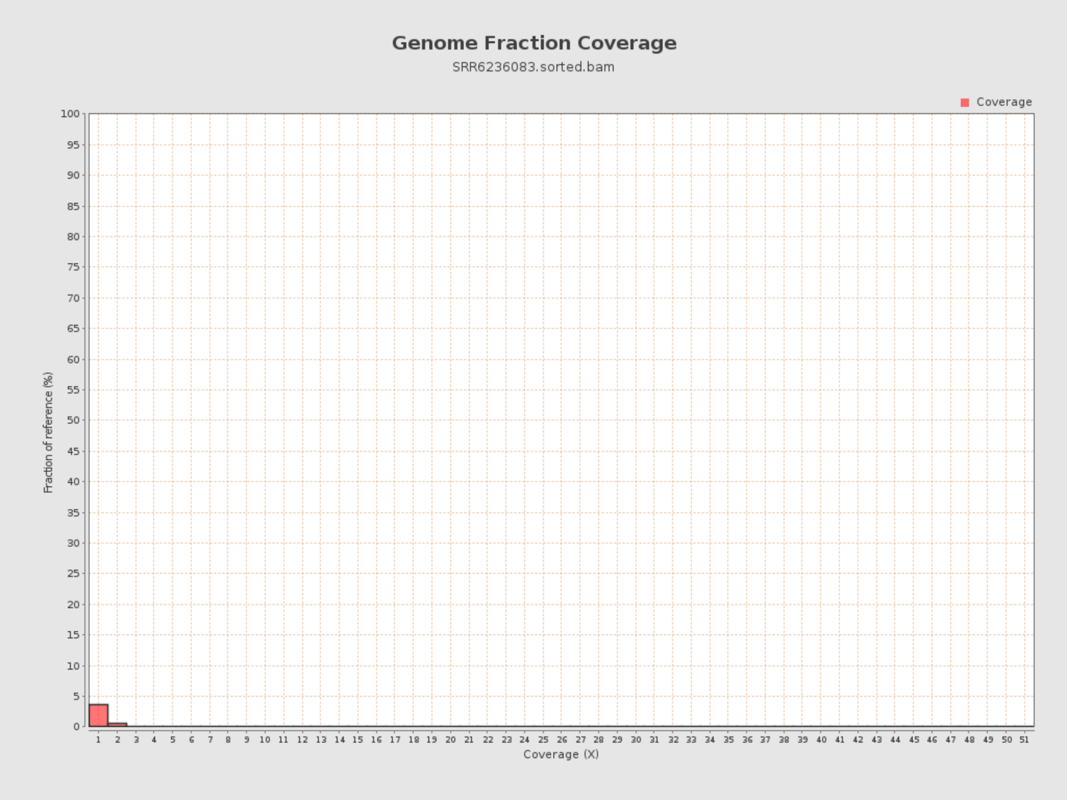
4. Results : Coverage Histogram



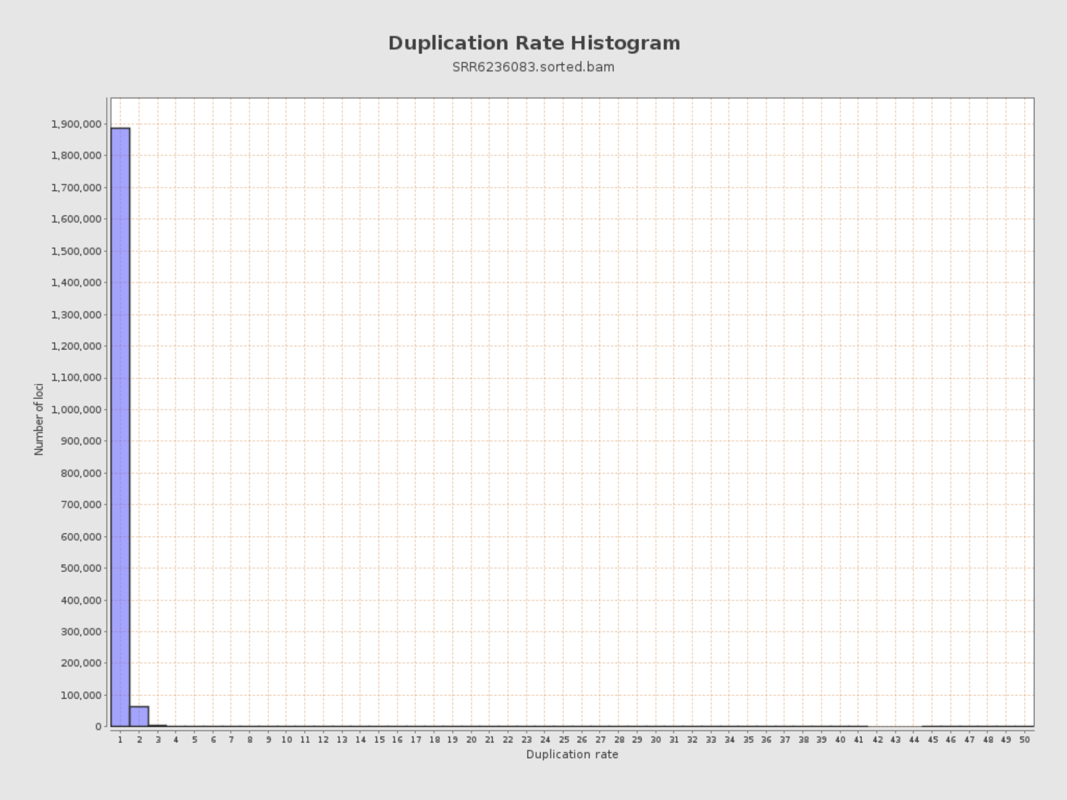
5. Results : Coverage Histogram (0-50X)



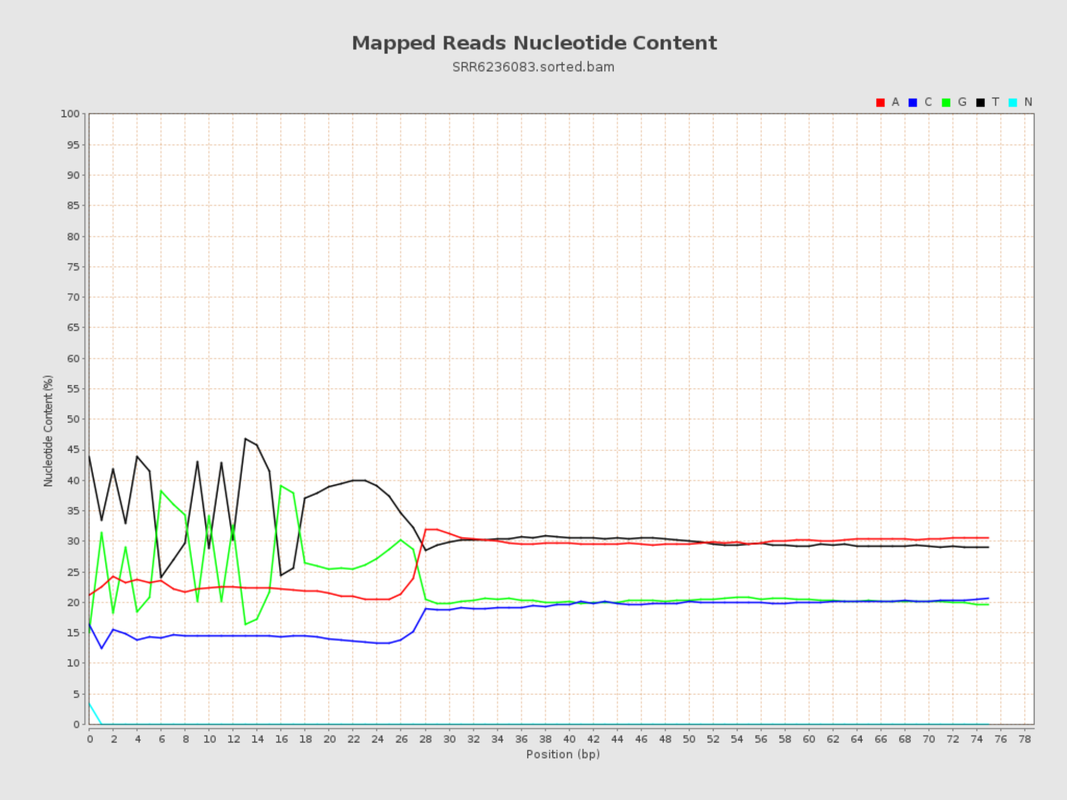
6. Results : Genome Fraction Coverage



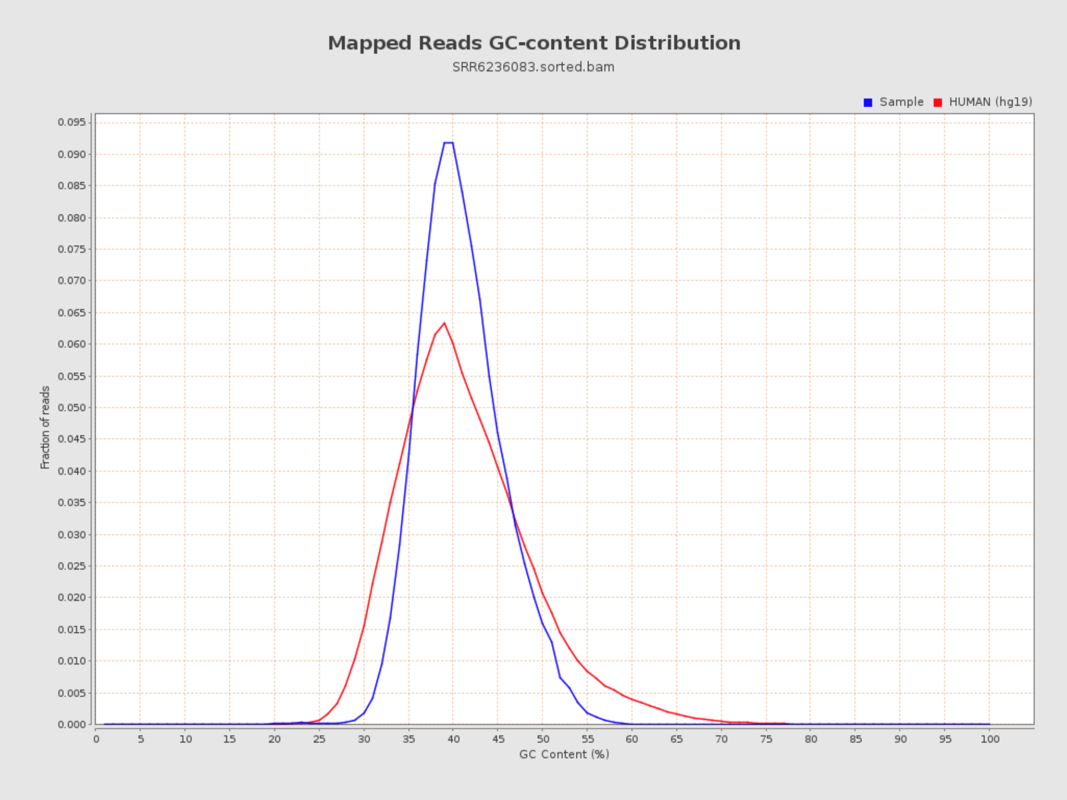
7. Results : Duplication Rate Histogram



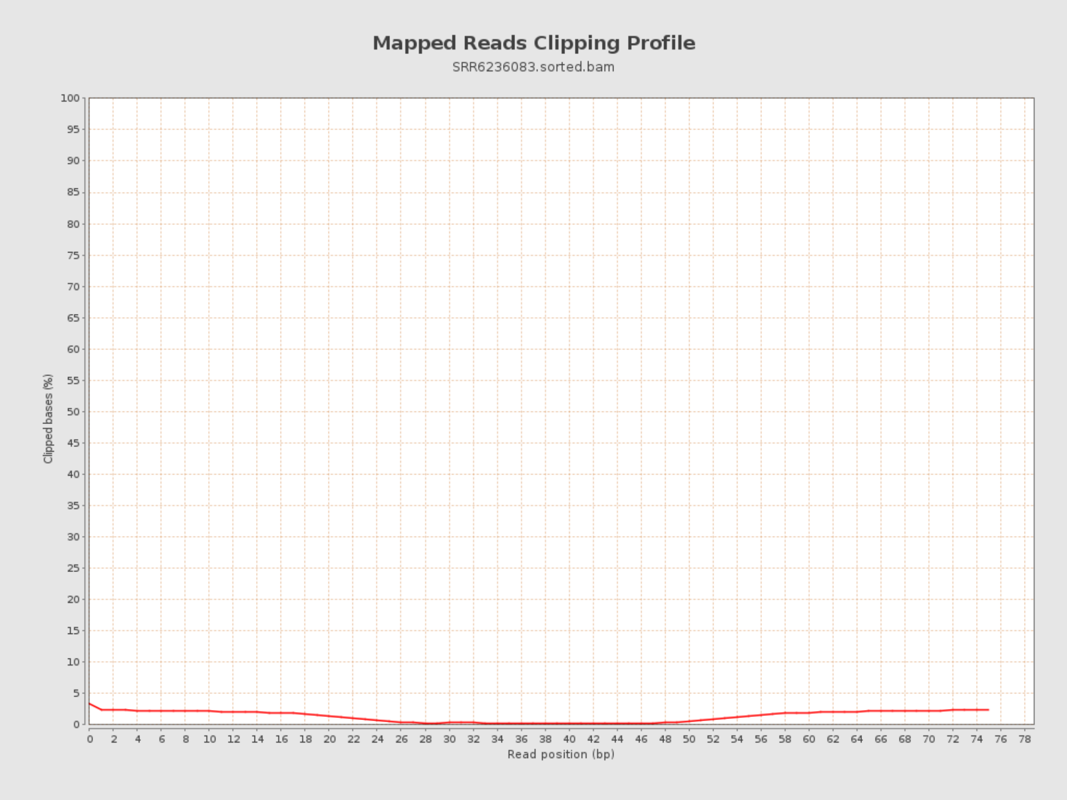
8. Results : Mapped Reads Nucleotide Content



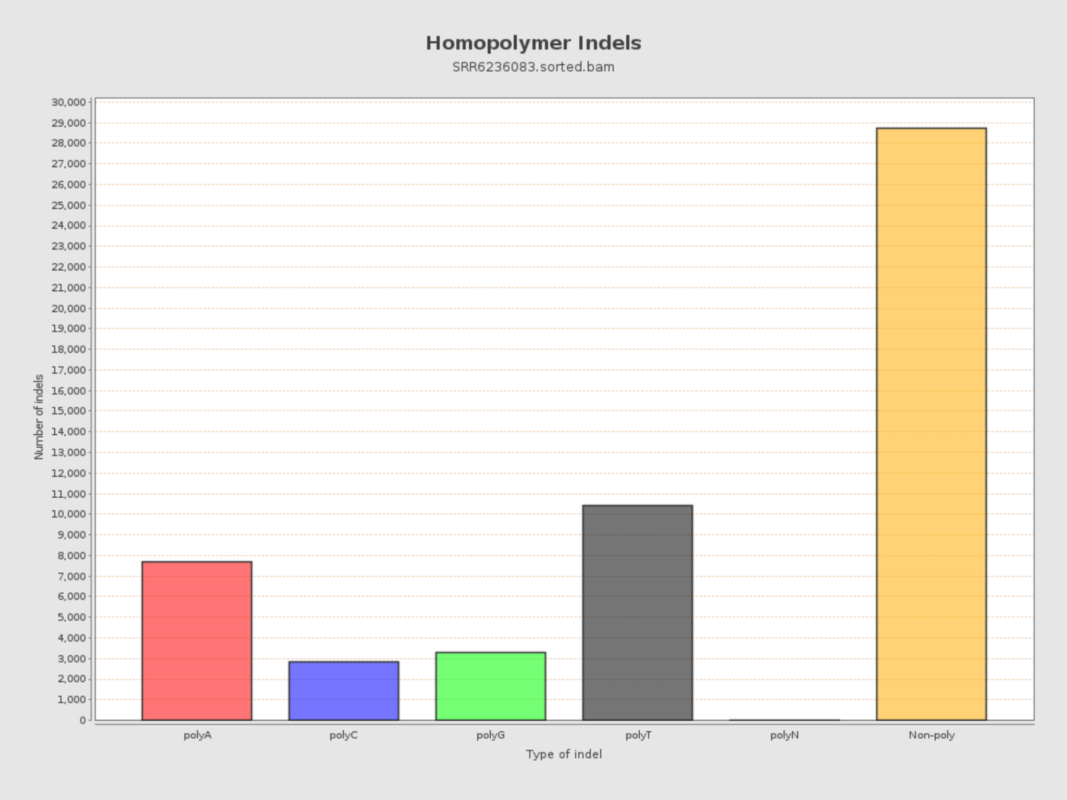
9. Results : Mapped Reads GC-content Distribution



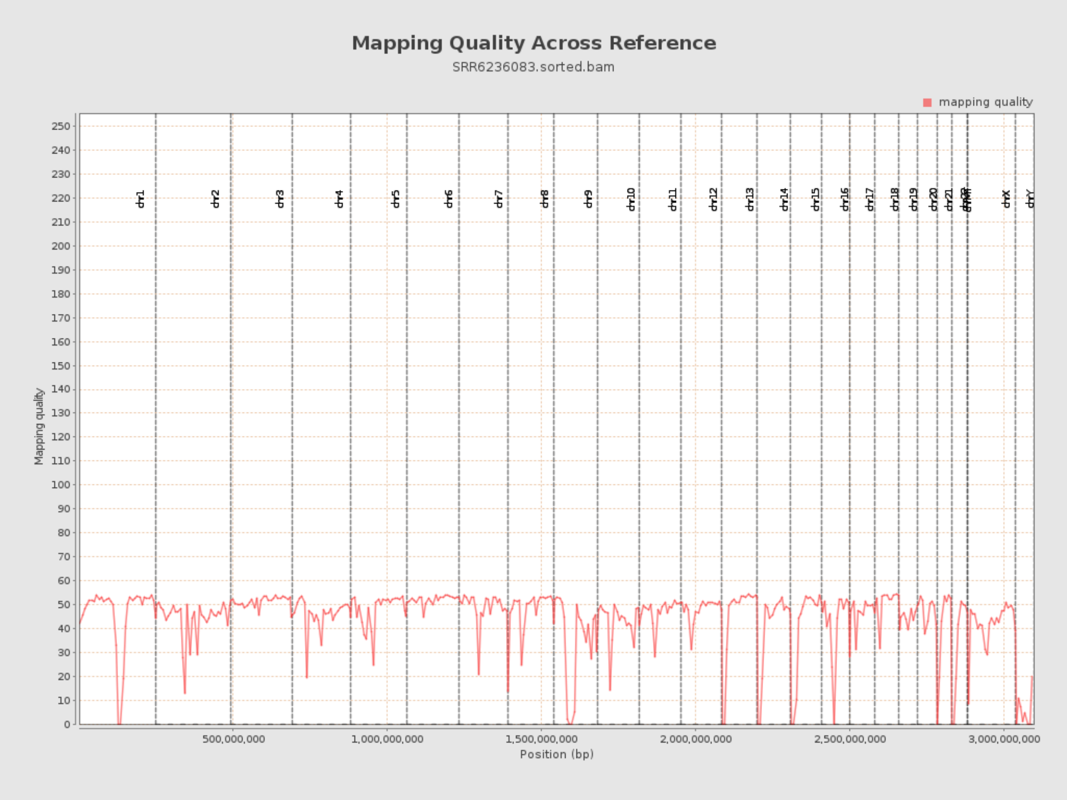
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram