Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 14:52:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238290.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_SRR6238290 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238290.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 14:52:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238290.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,991,894
Mapped reads	1,605,277 / 80.59%
Unmapped reads	386,617 / 19.41%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,027 / 1.16%
Read min/max/mean length	30 / 76 / 76.4
Duplicated reads (estimated)	100,362 / 5.04%
Duplication rate	4.97%
Clipped reads	886,030 / 44.48%

2.2. ACGT Content

Number/percentage of A's	29,011,418 / 28.01%
Number/percentage of C's	19,891,565 / 19.2%
Number/percentage of T's	31,821,103 / 30.72%
Number/percentage of G's	22,841,649 / 22.05%
Number/percentage of N's	25,553 / 0.02%
GC Percentage	41.25%

2.3. Coverage

Mean	0.0335

Standard Deviation	0.3299

2.4. Mapping Quality

Mean Mapping Quality	44.56

2.5. Mismatches and indels

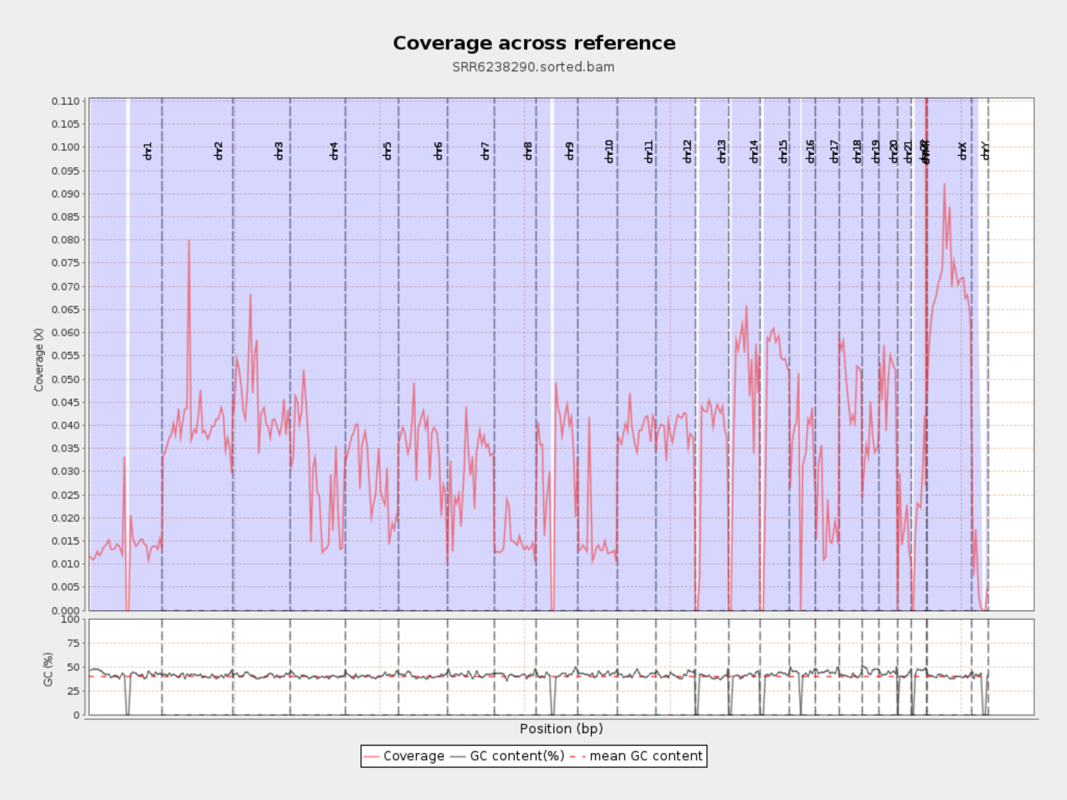
General error rate	0.9%
Mismatches	915,986
Insertions	8,008
Mapped reads with at least one insertion	0.5%
Deletions	30,431
Mapped reads with at least one deletion	1.87%
Homopolymer indels	45%

2.6. Chromosome stats

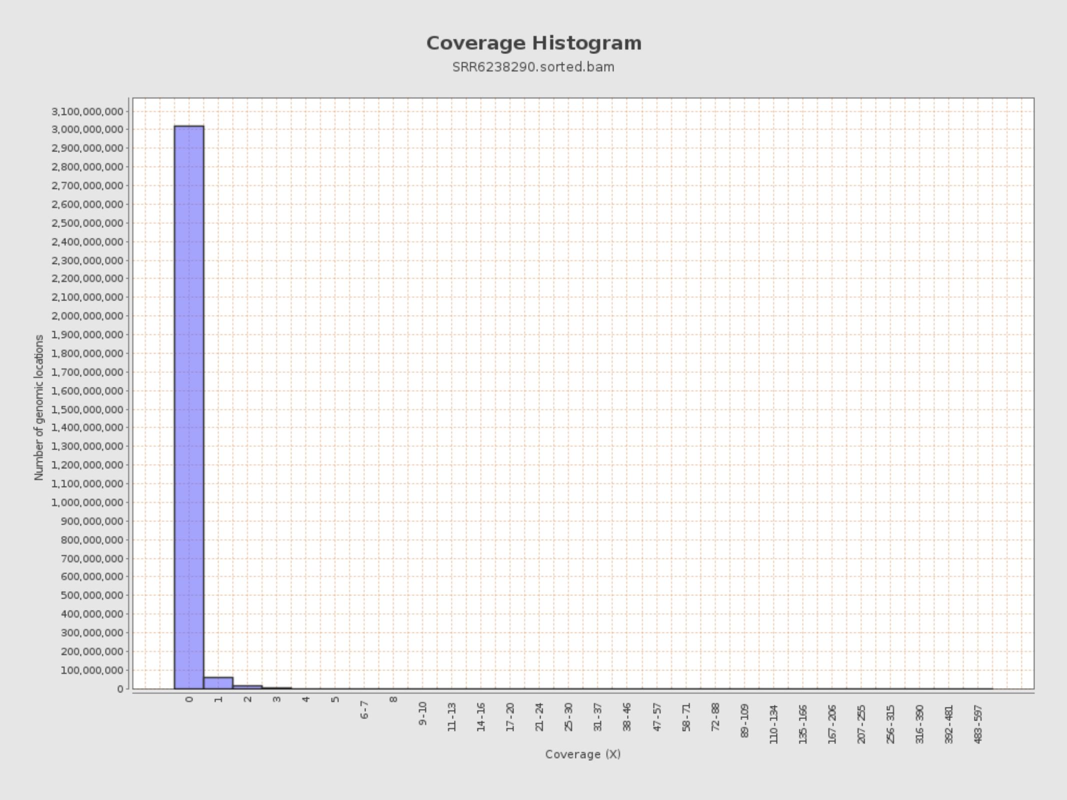
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3367130	0.0135	0.4579
chr2	243199373	9829977	0.0404	0.4504
chr3	198022430	8895603	0.0449	0.2673
chr4	191154276	5427807	0.0284	0.2325
chr5	180915260	5221144	0.0289	0.2172
chr6	171115067	6108672	0.0357	0.2839
chr7	159138663	4844152	0.0304	0.3468

chr8	146364022	2150657	0.0147	0.3685
chr9	141213431	4540301	0.0322	0.3526
chr10	135534747	1975865	0.0146	0.2522
chr11	135006516	5289372	0.0392	0.3192
chr12	133851895	5202950	0.0389	0.2539
chr13	115169878	4056286	0.0352	0.2375
chr14	107349540	4913745	0.0458	0.2987
chr15	102531392	4753822	0.0464	0.2778
chr16	90354753	3141788	0.0348	0.2577
chr17	81195210	1555990	0.0192	0.193
chr18	78077248	3874306	0.0496	0.5908
chr19	59128983	2104305	0.0356	0.3561
chr20	63025520	3127821	0.0496	0.286
chr21	48129895	798898	0.0166	0.1891
chr22	51304566	1091185	0.0213	0.1817
chrMT	16571	71405	4.309	3.4335
chrX	155270560	10937432	0.0704	0.3763
chrY	59373566	360930	0.0061	0.1542

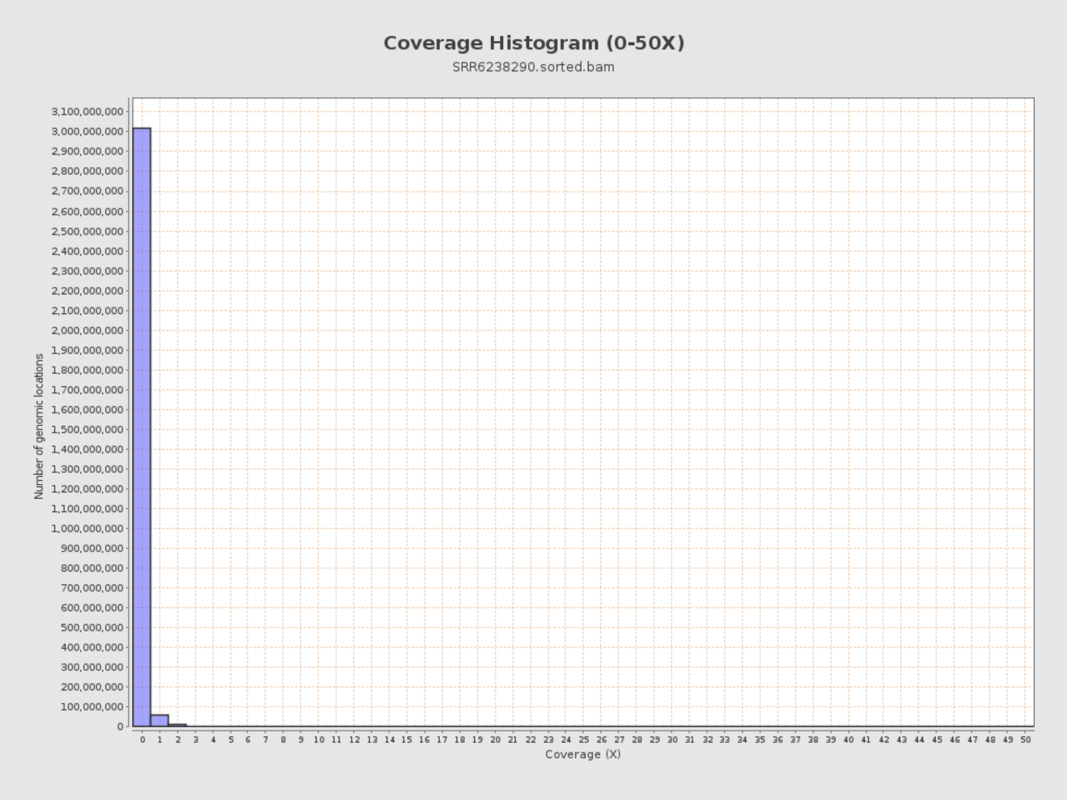
3. Results : Coverage across reference



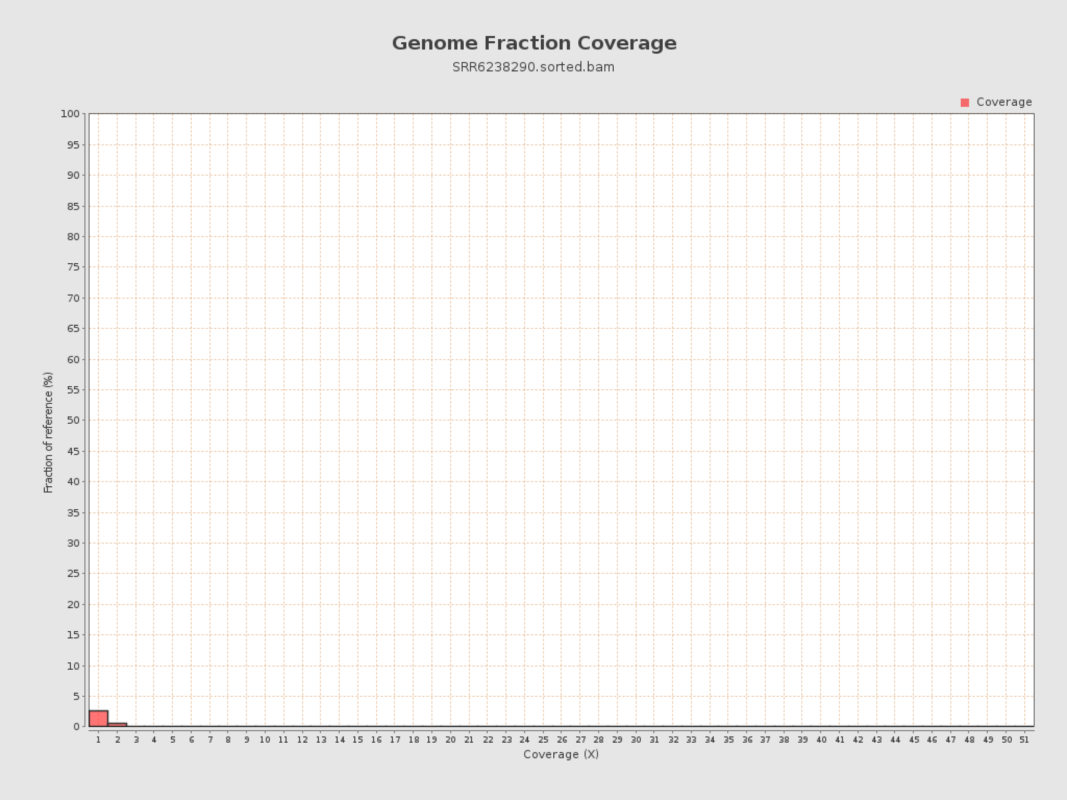
4. Results : Coverage Histogram



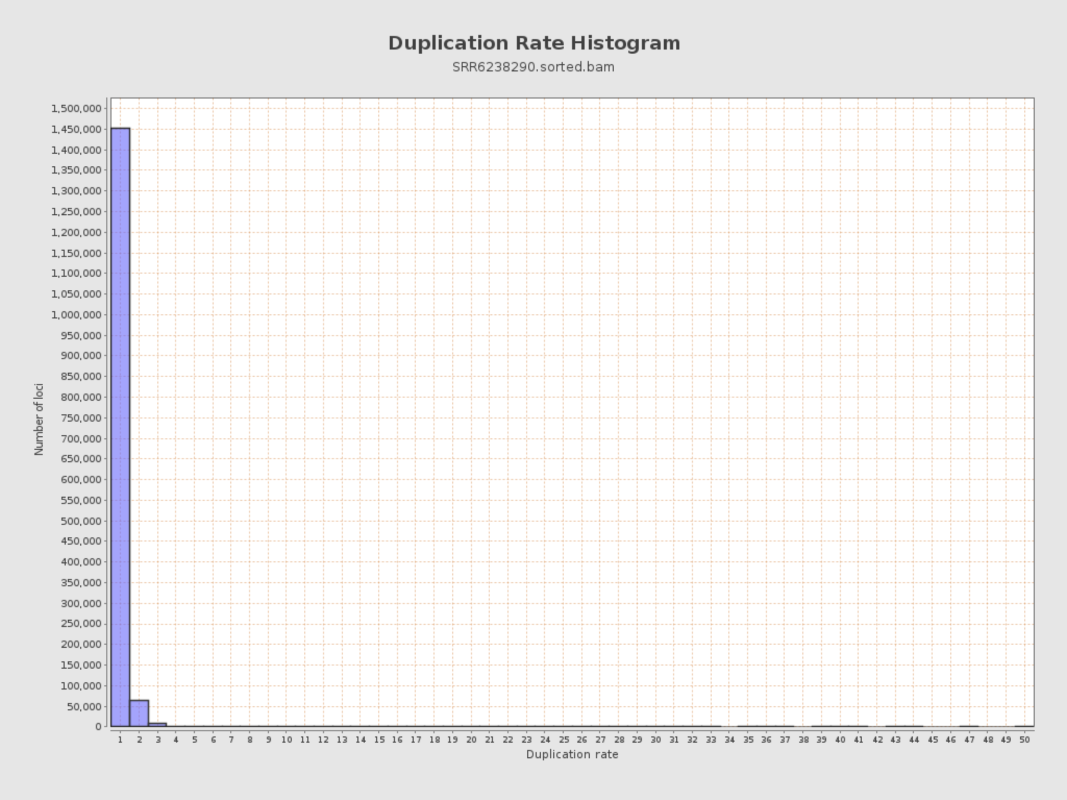
5. Results : Coverage Histogram (0-50X)



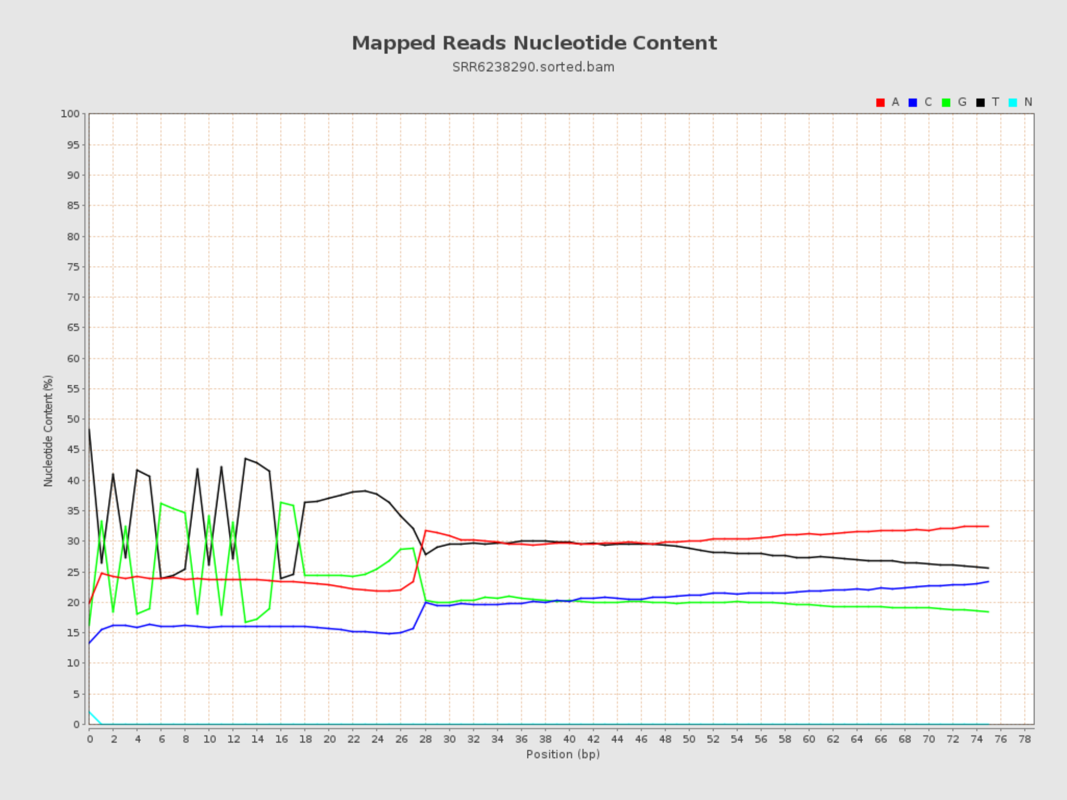
6. Results : Genome Fraction Coverage



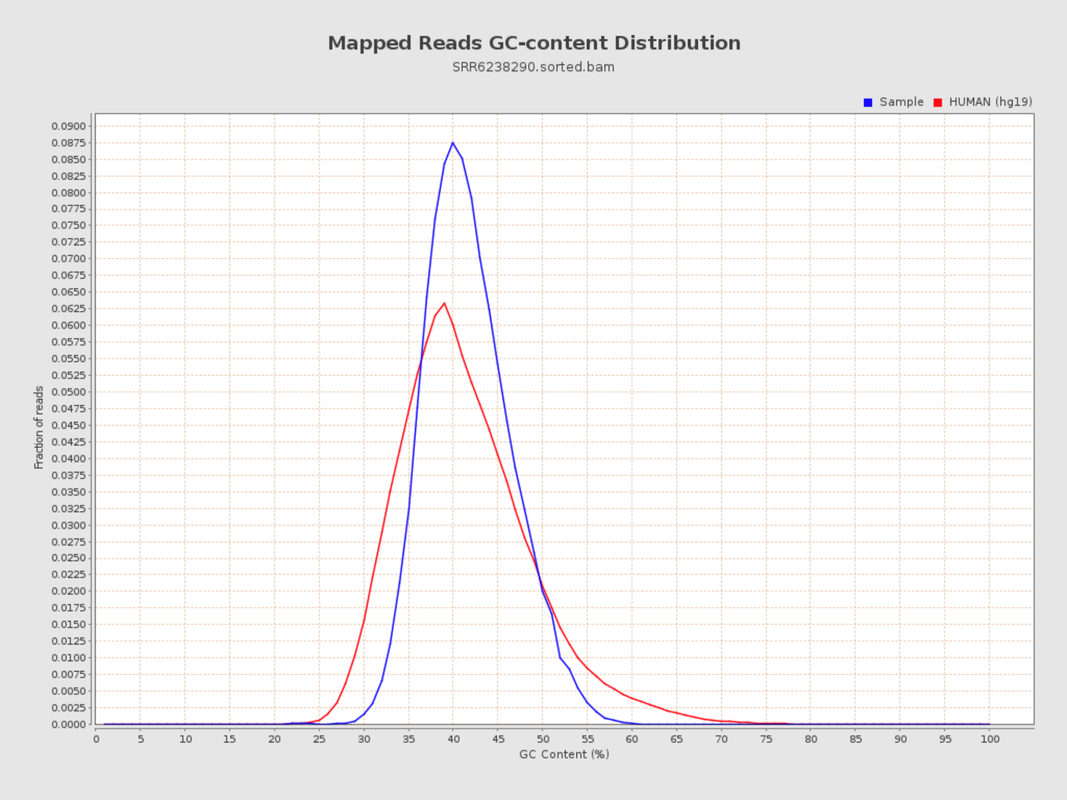
7. Results : Duplication Rate Histogram



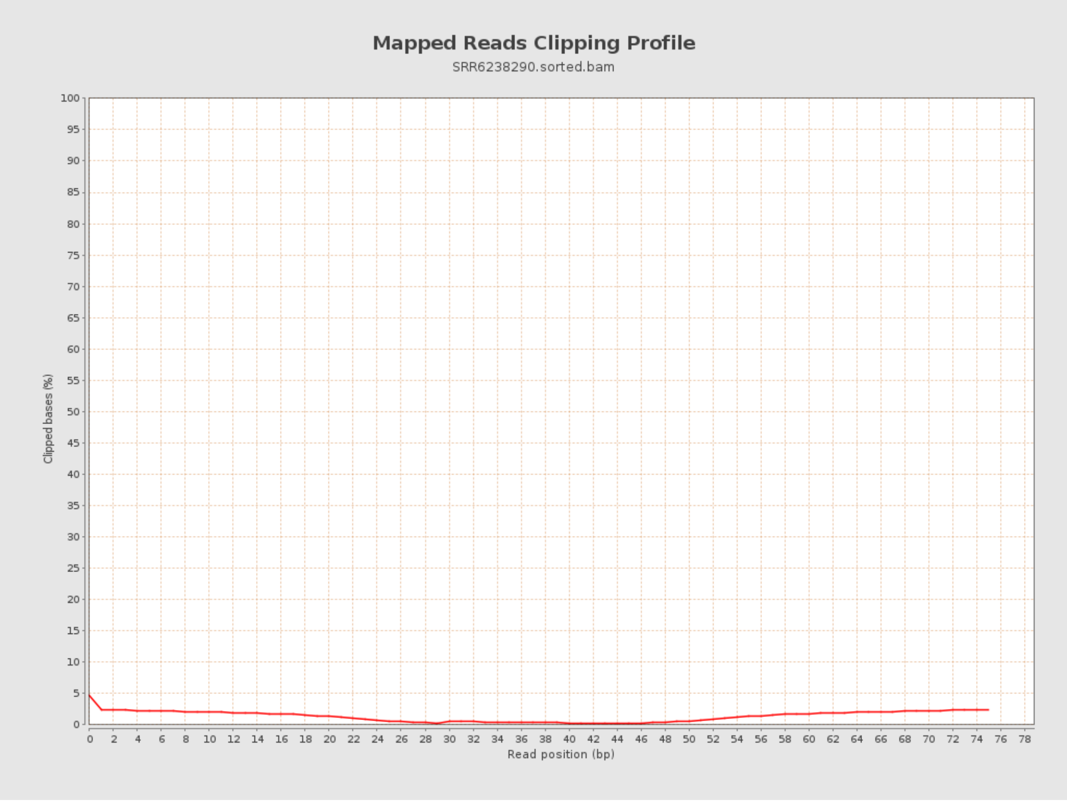
8. Results : Mapped Reads Nucleotide Content



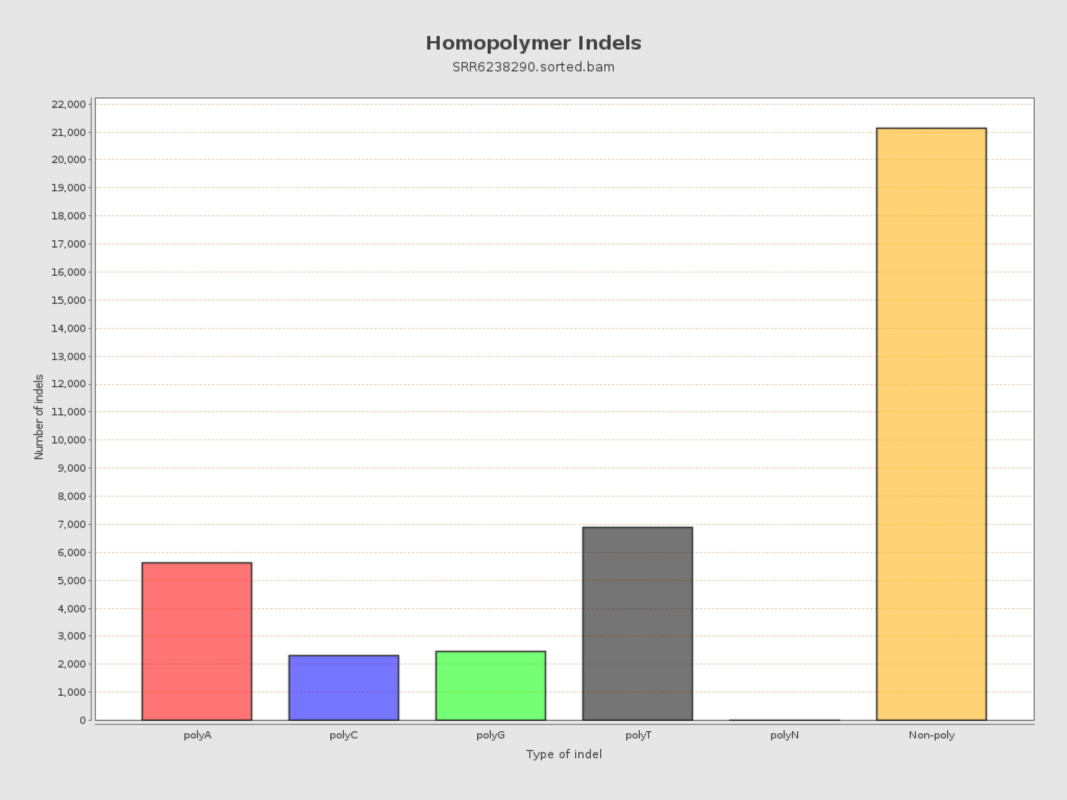
9. Results : Mapped Reads GC-content Distribution



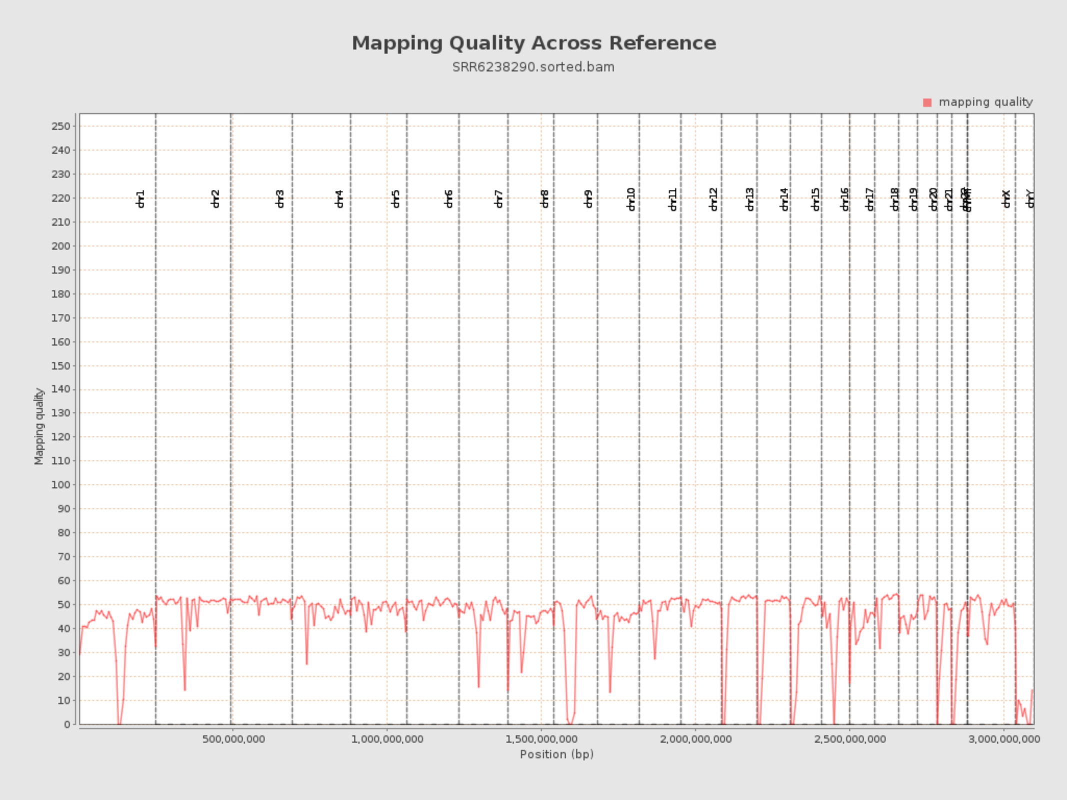
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram