Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 21:04:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238542.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_SRR6238542 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238542.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 21:04:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238542.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,990,975
Mapped reads	3,563,039 / 89.28%
Unmapped reads	427,936 / 10.72%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	28,210 / 0.71%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	658,767 / 16.51%
Duplication rate	15.15%
Clipped reads	2,221,730 / 55.67%

2.2. ACGT Content

Number/percentage of A's	56,271,406 / 25.6%
Number/percentage of C's	38,543,823 / 17.53%
Number/percentage of T's	72,881,588 / 33.15%
Number/percentage of G's	52,132,978 / 23.71%
Number/percentage of N's	15,419 / 0.01%
GC Percentage	41.25%

2.3. Coverage

Mean	0.0711

Standard Deviation	0.7941

2.4. Mapping Quality

Mean Mapping Quality	42.73

2.5. Mismatches and indels

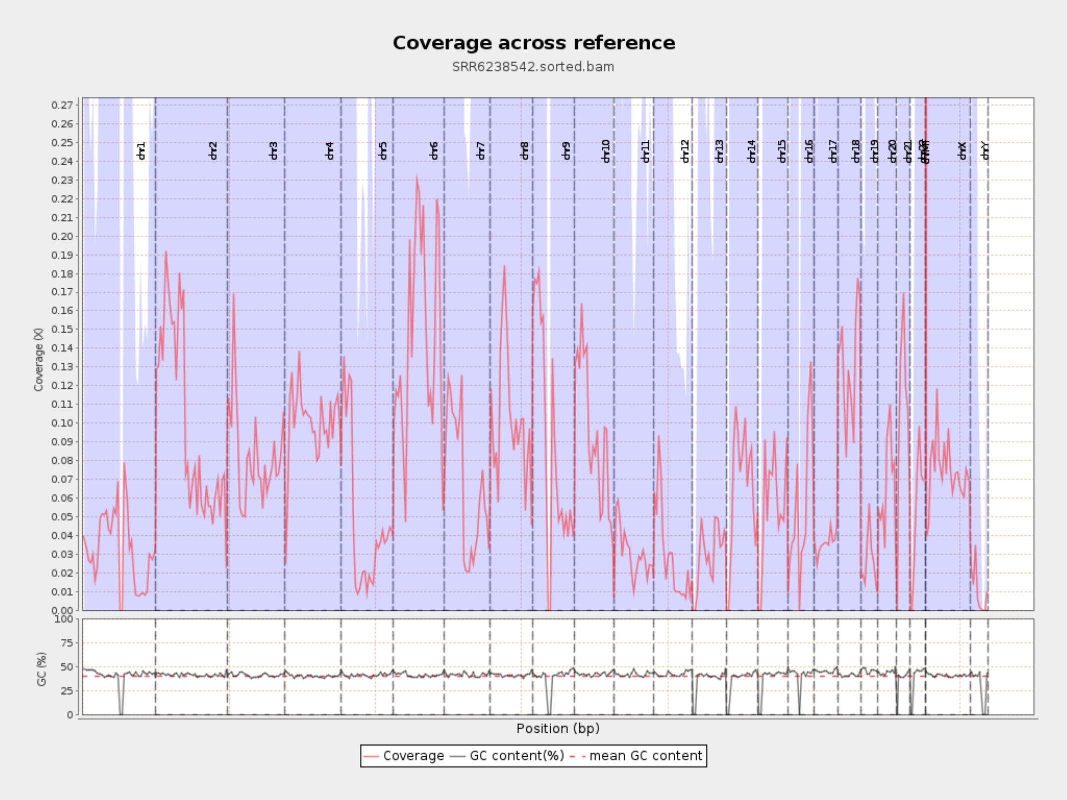
General error rate	0.66%
Mismatches	1,422,991
Insertions	14,371
Mapped reads with at least one insertion	0.4%
Deletions	81,098
Mapped reads with at least one deletion	2.25%
Homopolymer indels	41.11%

2.6. Chromosome stats

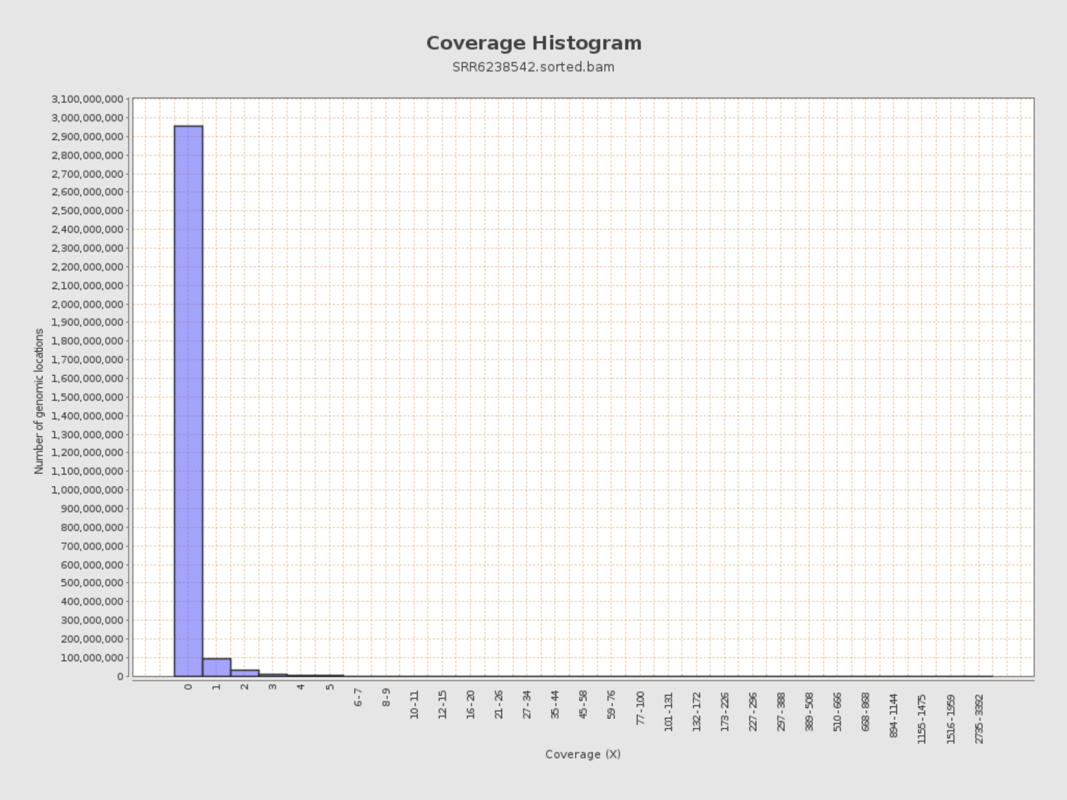
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7983295	0.032	0.601
chr2	243199373	24348681	0.1001	1.6515
chr3	198022430	16491671	0.0833	0.4248
chr4	191154276	19074291	0.0998	0.4818
chr5	180915260	8503521	0.047	0.3341
chr6	171115067	24927117	0.1457	0.9381
chr7	159138663	10629101	0.0668	0.8788

chr8	146364022	14875769	0.1016	1.0805
chr9	141213431	12321776	0.0873	0.86
chr10	135534747	12880244	0.095	0.5925
chr11	135006516	4110754	0.0304	0.3778
chr12	133851895	3975410	0.0297	0.3506
chr13	115169878	3391134	0.0294	0.3606
chr14	107349540	7135149	0.0665	0.5655
chr15	102531392	5732092	0.0559	0.4295
chr16	90354753	4736845	0.0524	0.5156
chr17	81195210	2909633	0.0358	0.2935
chr18	78077248	10185255	0.1305	1.8736
chr19	59128983	1598617	0.027	0.4926
chr20	63025520	4246196	0.0674	0.4437
chr21	48129895	5015028	0.1042	0.5329
chr22	51304566	2765416	0.0539	0.3404
chrMT	16571	62729	3.7855	3.0337
chrX	155270560	11458487	0.0738	0.4919
chrY	59373566	628603	0.0106	0.2986

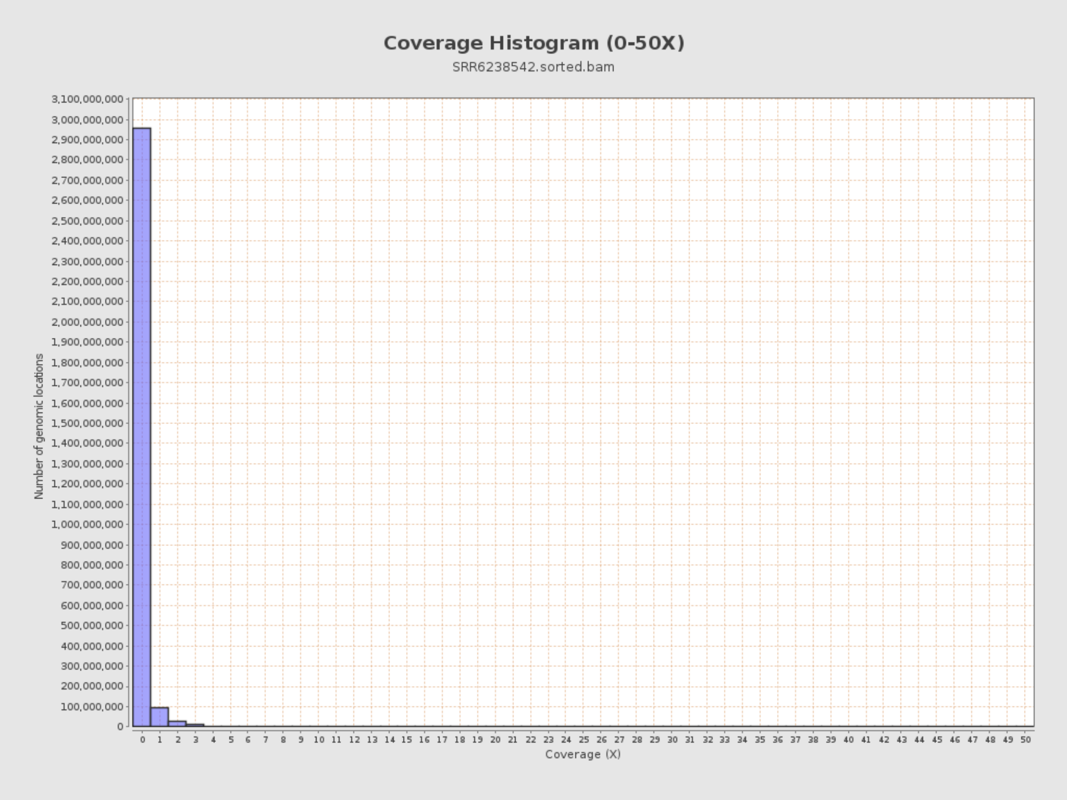
3. Results : Coverage across reference



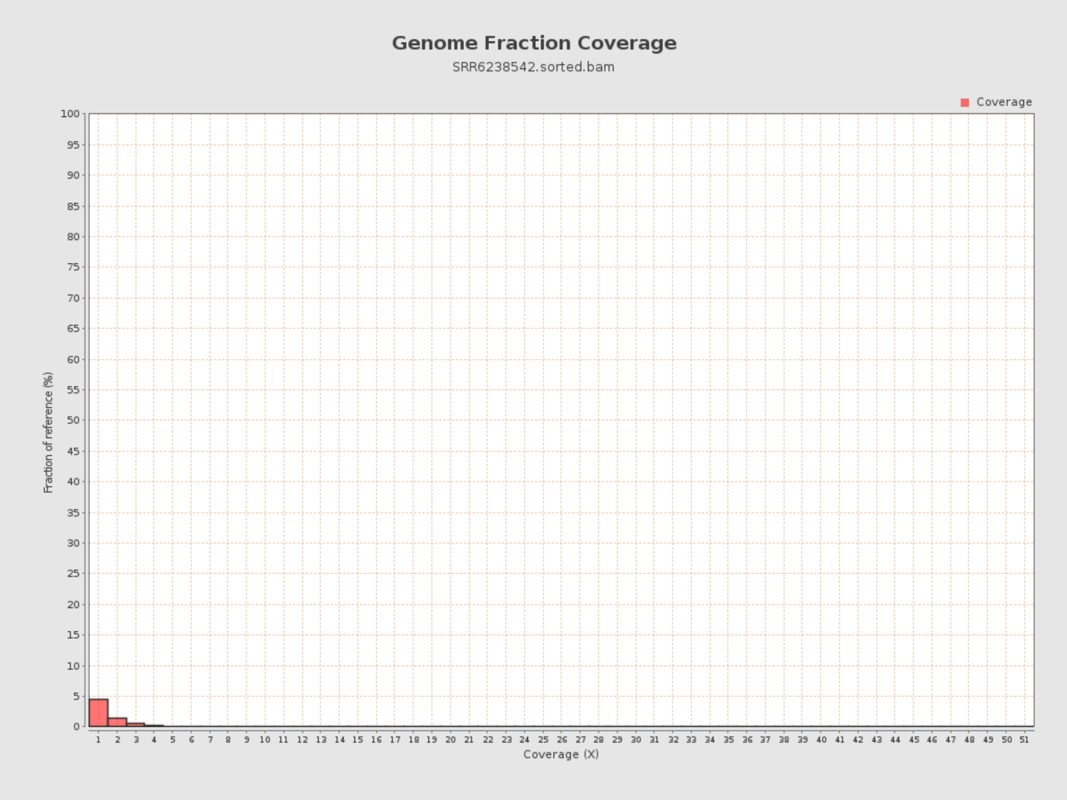
4. Results : Coverage Histogram



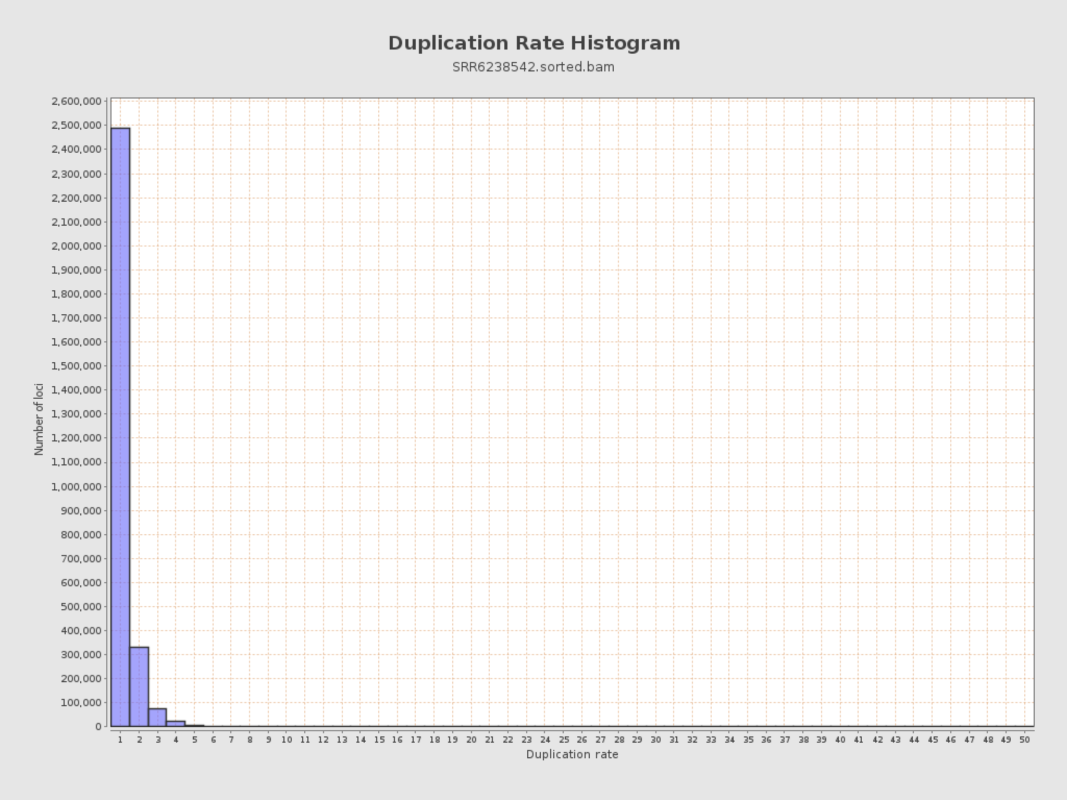
5. Results : Coverage Histogram (0-50X)



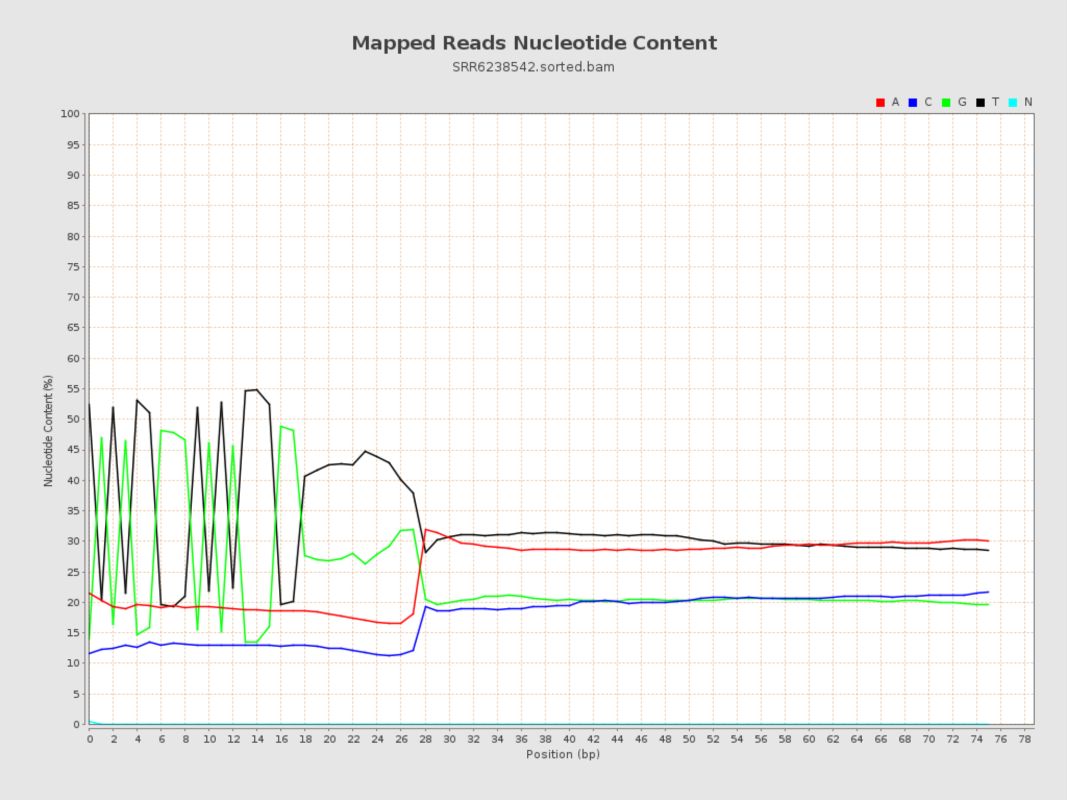
6. Results : Genome Fraction Coverage



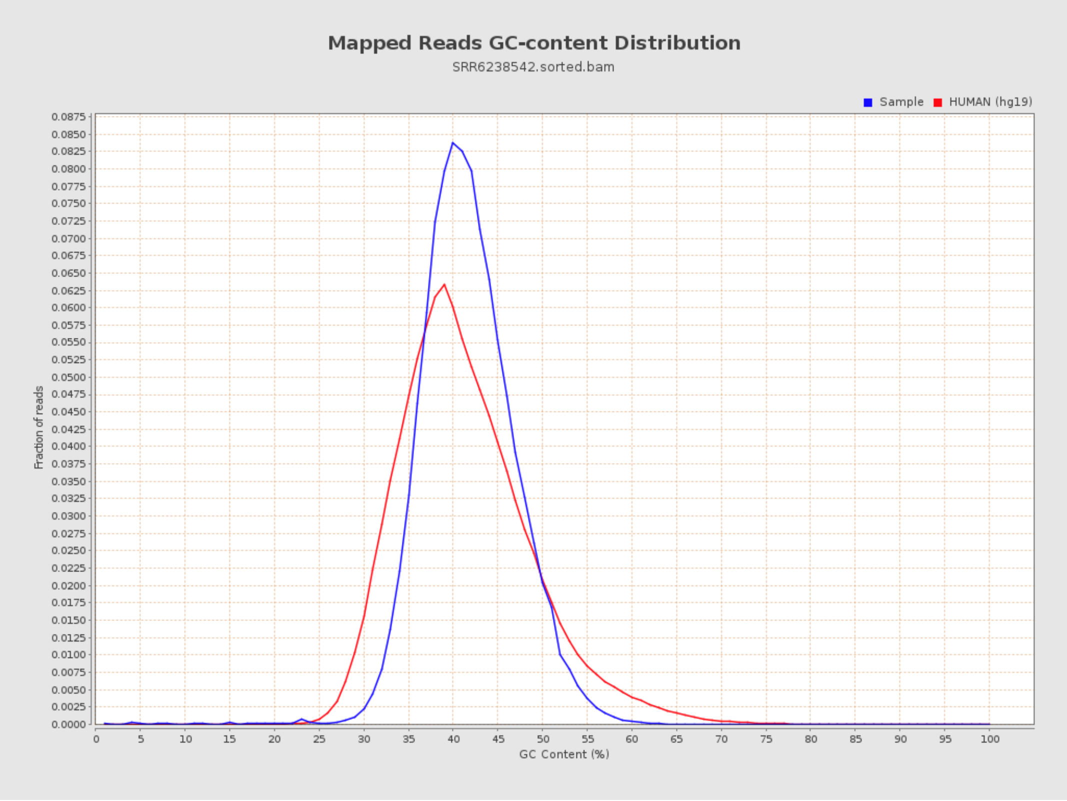
7. Results : Duplication Rate Histogram



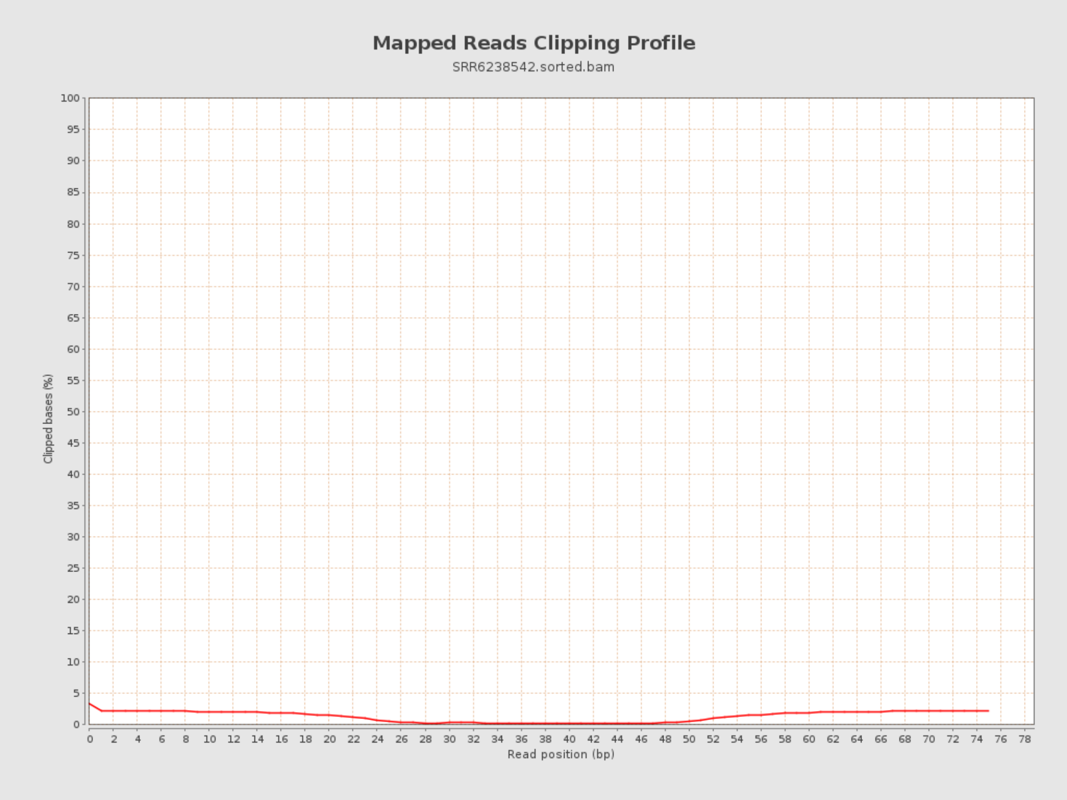
8. Results : Mapped Reads Nucleotide Content



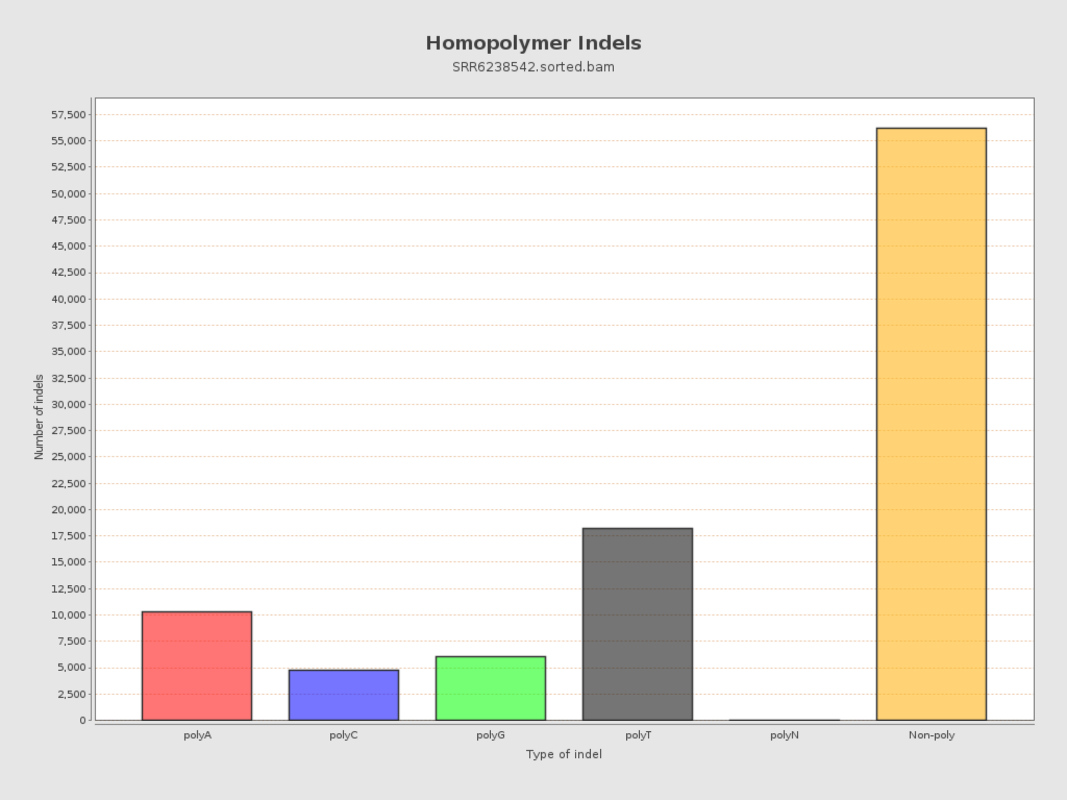
9. Results : Mapped Reads GC-content Distribution



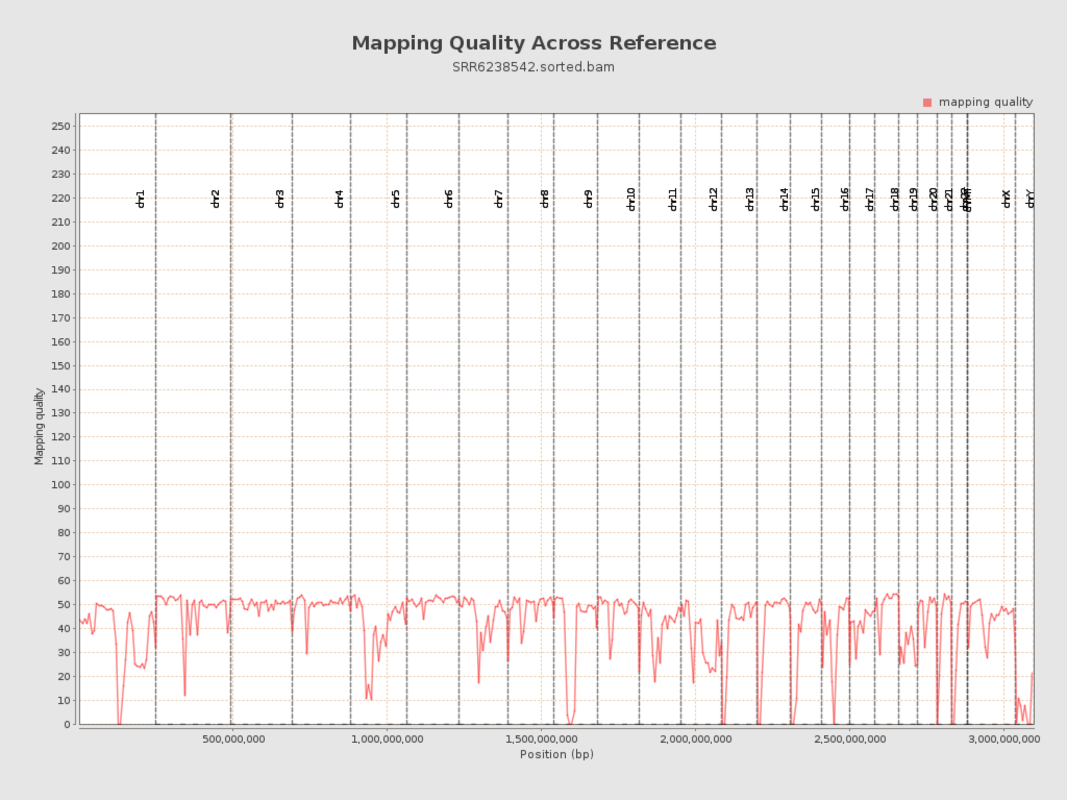
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram