Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 10:40:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238046.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_SRR6238046 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238046.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 10:40:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238046.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,152,594
Mapped reads	176,272 / 4.24%
Unmapped reads	3,976,322 / 95.76%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	802 / 0.02%
Read min/max/mean length	30 / 76 / 76.01
Duplicated reads (estimated)	11,205 / 0.27%
Duplication rate	5.45%
Clipped reads	136,042 / 3.28%

2.2. ACGT Content

Number/percentage of A's	2,593,891 / 25.15%
Number/percentage of C's	1,729,626 / 16.77%
Number/percentage of T's	3,355,760 / 32.54%
Number/percentage of G's	2,633,479 / 25.53%
Number/percentage of N's	459 / 0%
GC Percentage	42.31%

2.3. Coverage

Mean	0.0033

Standard Deviation	0.0693

2.4. Mapping Quality

Mean Mapping Quality	43.43

2.5. Mismatches and indels

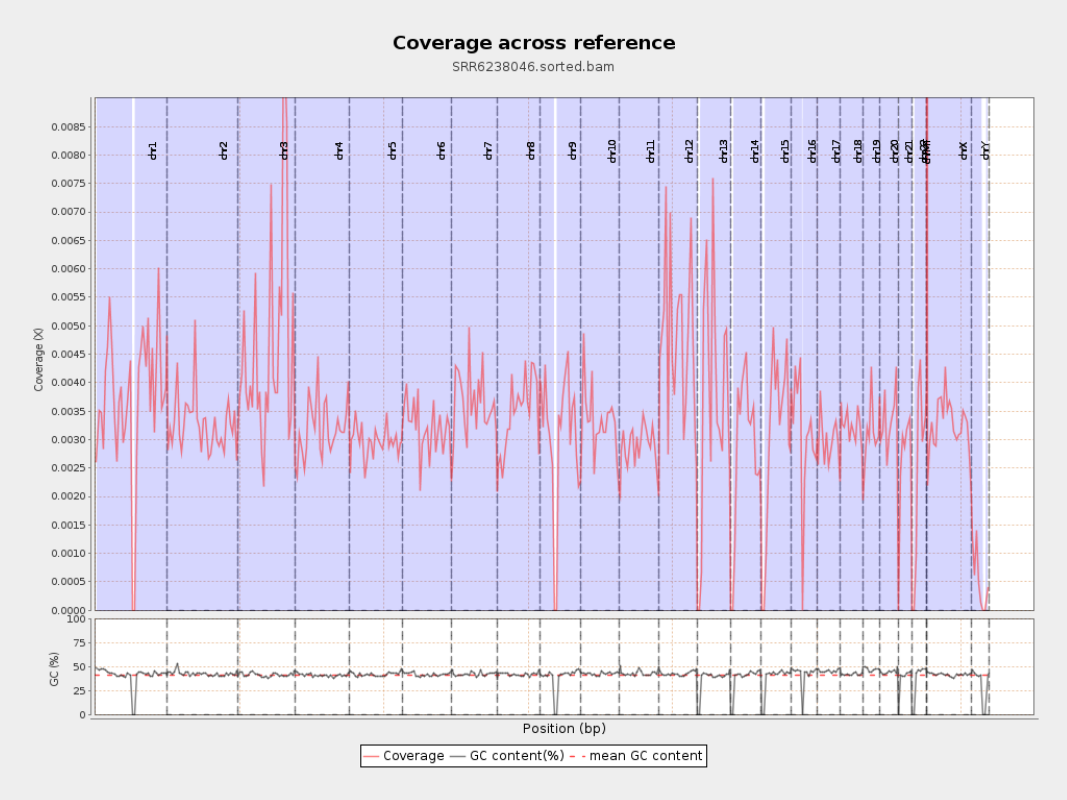
General error rate	0.97%
Mismatches	98,539
Insertions	758
Mapped reads with at least one insertion	0.43%
Deletions	3,910
Mapped reads with at least one deletion	2.19%
Homopolymer indels	48.35%

2.6. Chromosome stats

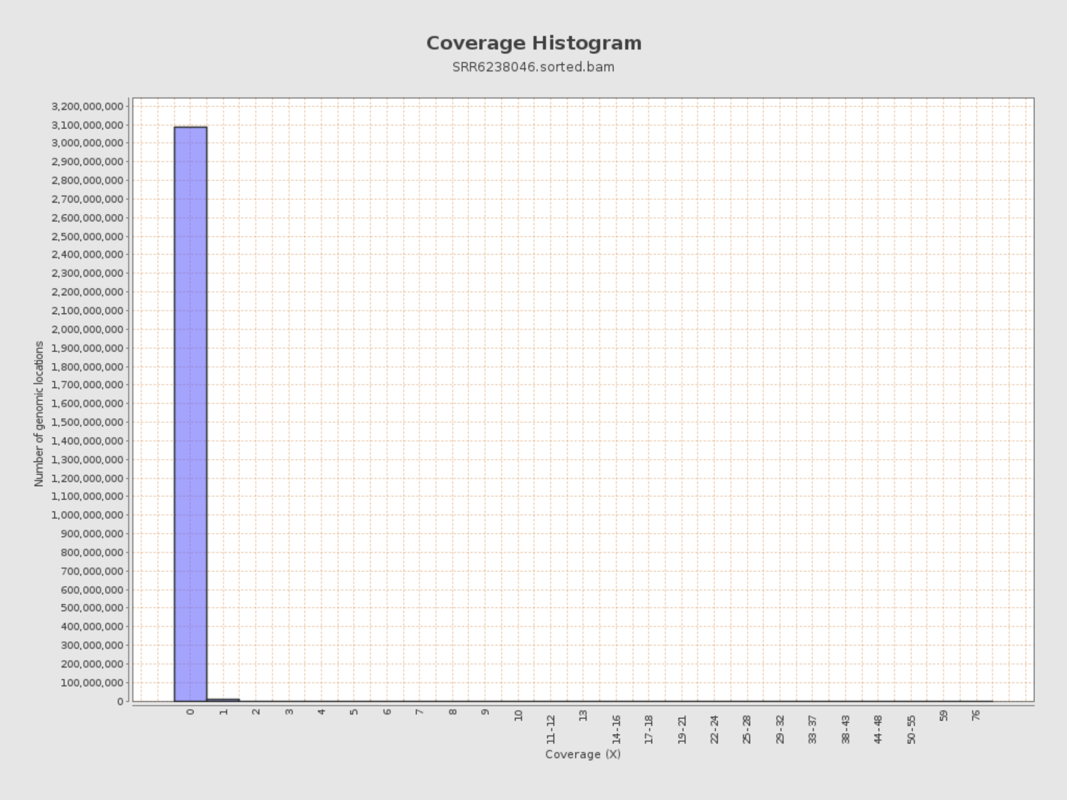
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	921028	0.0037	0.0785
chr2	243199373	794508	0.0033	0.0793
chr3	198022430	902336	0.0046	0.0786
chr4	191154276	609658	0.0032	0.0647
chr5	180915260	539057	0.003	0.0623
chr6	171115067	547866	0.0032	0.0664
chr7	159138663	577944	0.0036	0.0766

chr8	146364022	508560	0.0035	0.0688
chr9	141213431	429710	0.003	0.0651
chr10	135534747	447853	0.0033	0.0676
chr11	135006516	392569	0.0029	0.0623
chr12	133851895	640859	0.0048	0.0808
chr13	115169878	425230	0.0037	0.0702
chr14	107349540	301416	0.0028	0.0608
chr15	102531392	316334	0.0031	0.0641
chr16	90354753	276293	0.0031	0.0637
chr17	81195210	242003	0.003	0.0622
chr18	78077248	253343	0.0032	0.0738
chr19	59128983	185724	0.0031	0.0666
chr20	63025520	208334	0.0033	0.067
chr21	48129895	127991	0.0027	0.0594
chr22	51304566	128656	0.0025	0.0579
chrMT	16571	4823	0.2911	0.6527
chrX	155270560	506793	0.0033	0.0649
chrY	59373566	30363	0.0005	0.0254

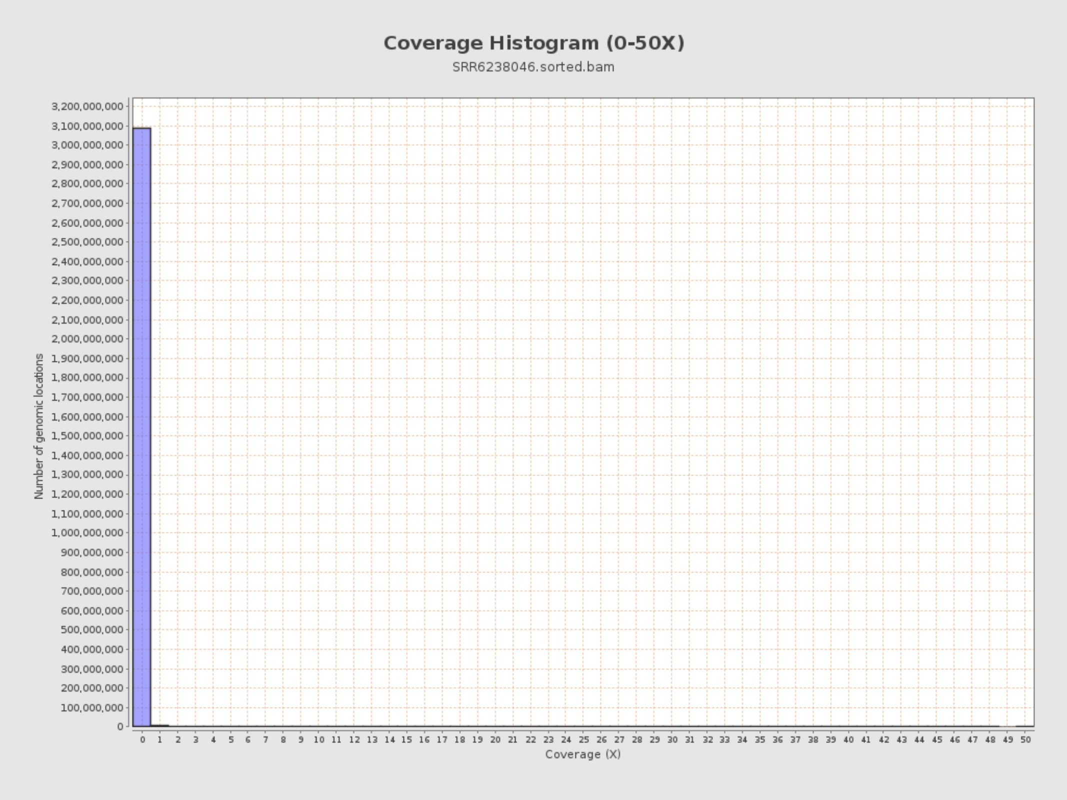
3. Results : Coverage across reference



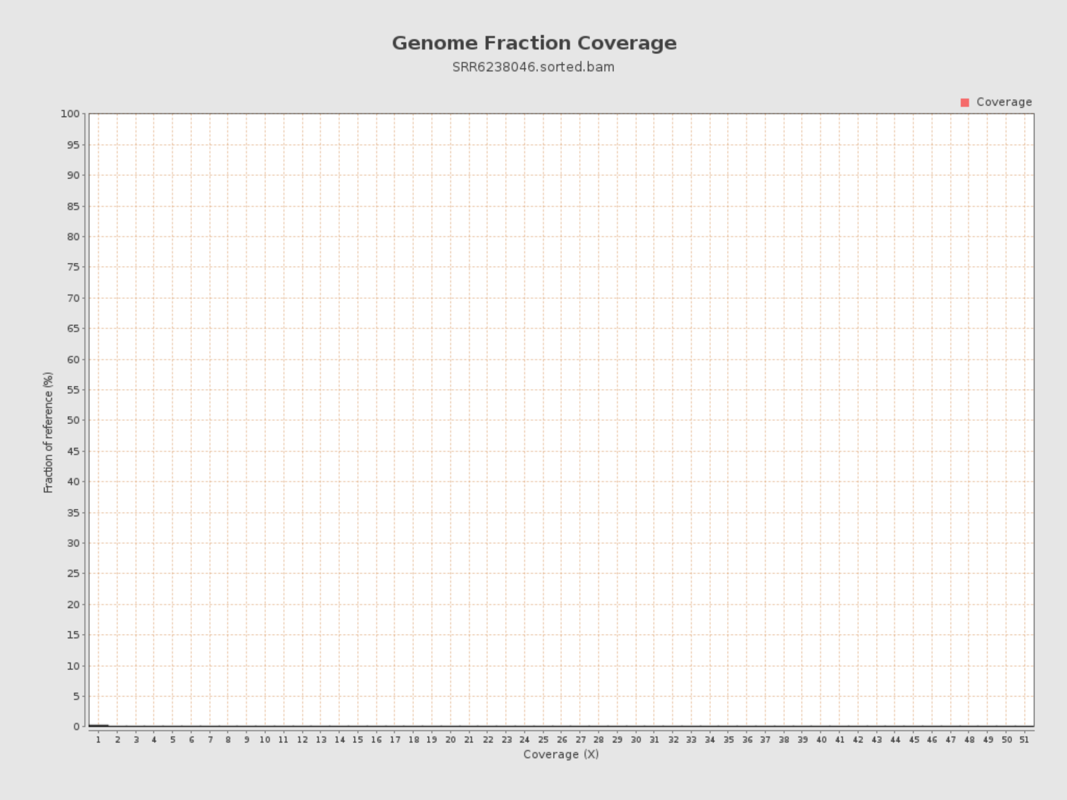
4. Results : Coverage Histogram



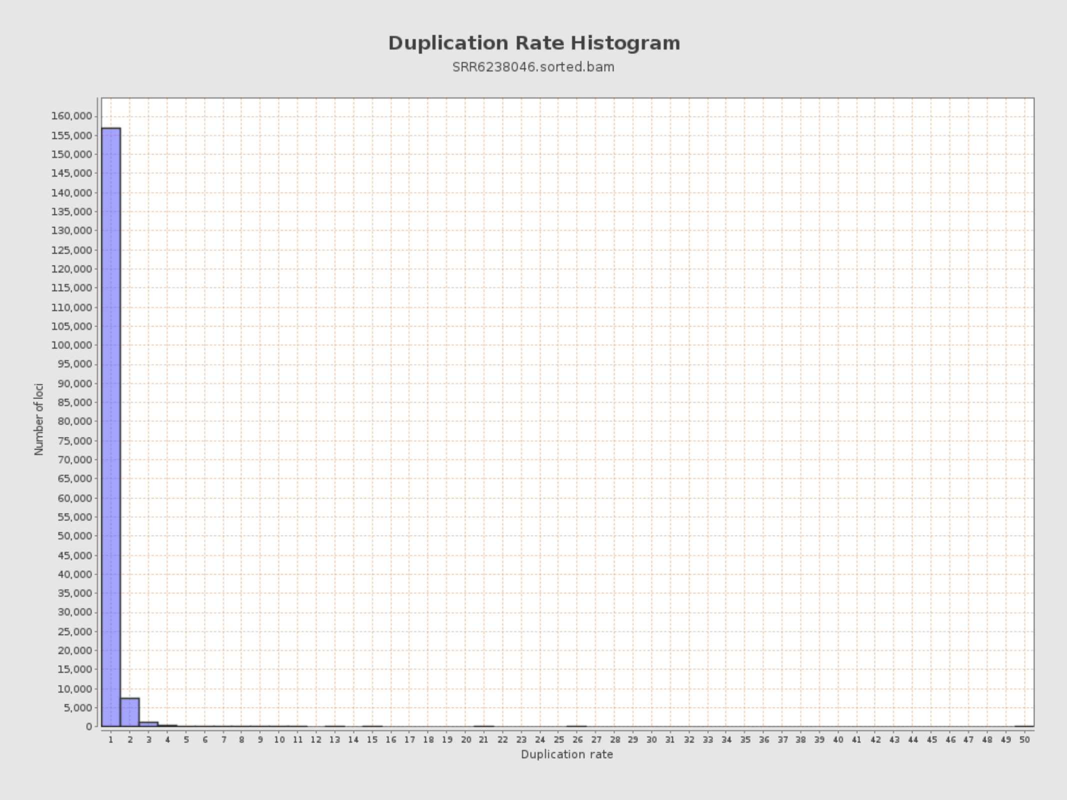
5. Results : Coverage Histogram (0-50X)



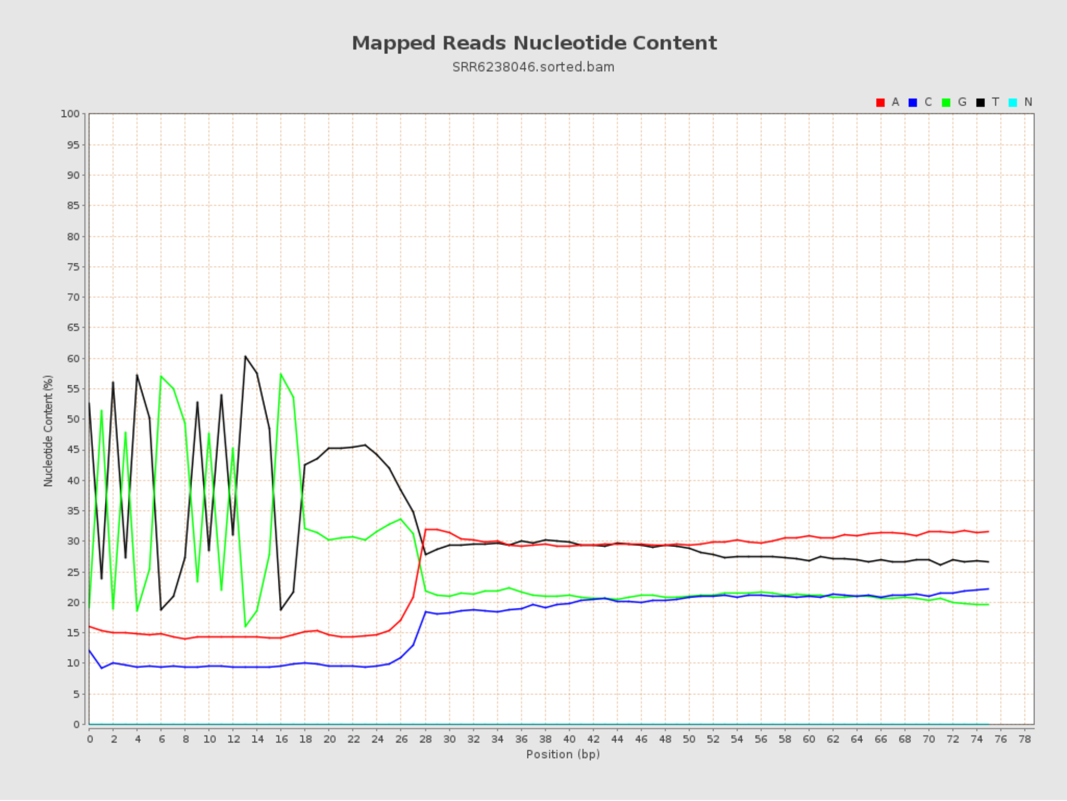
6. Results : Genome Fraction Coverage



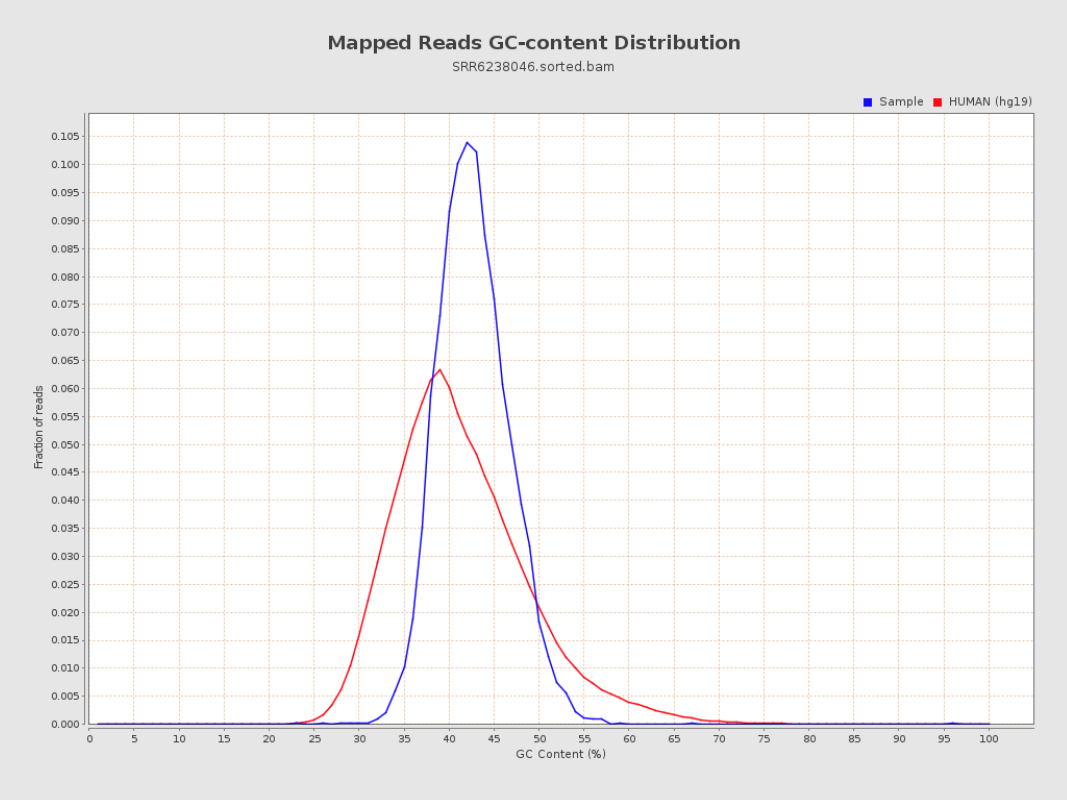
7. Results : Duplication Rate Histogram



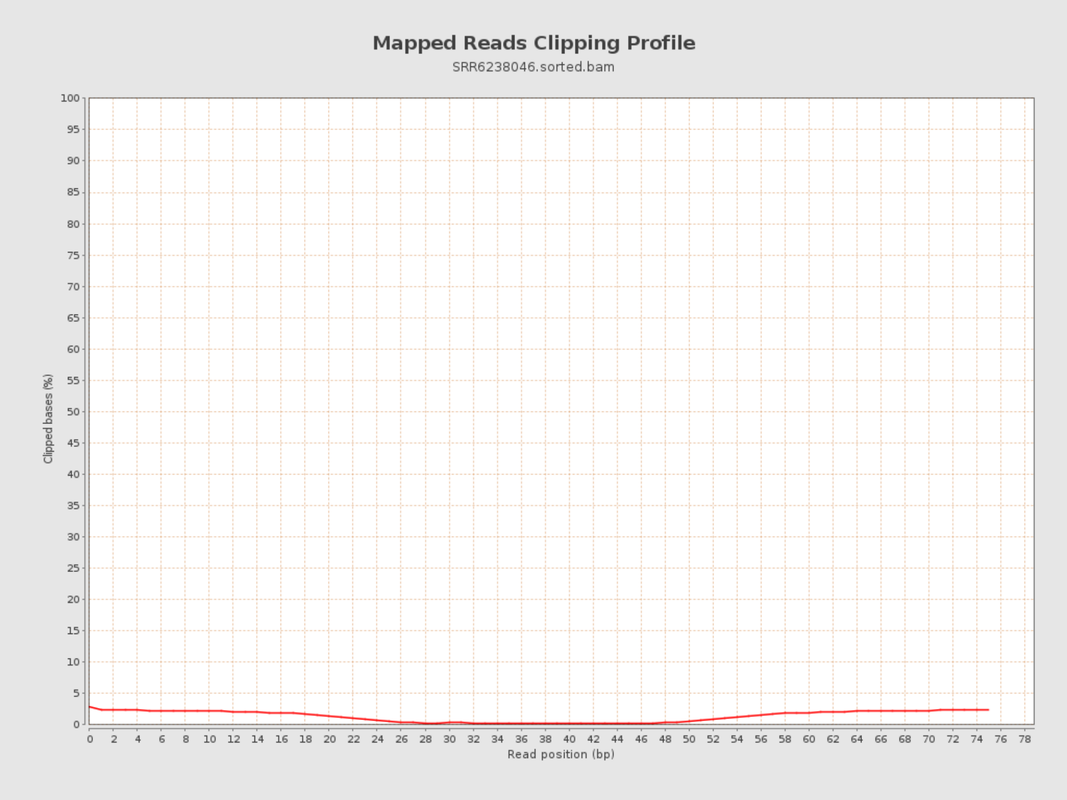
8. Results : Mapped Reads Nucleotide Content



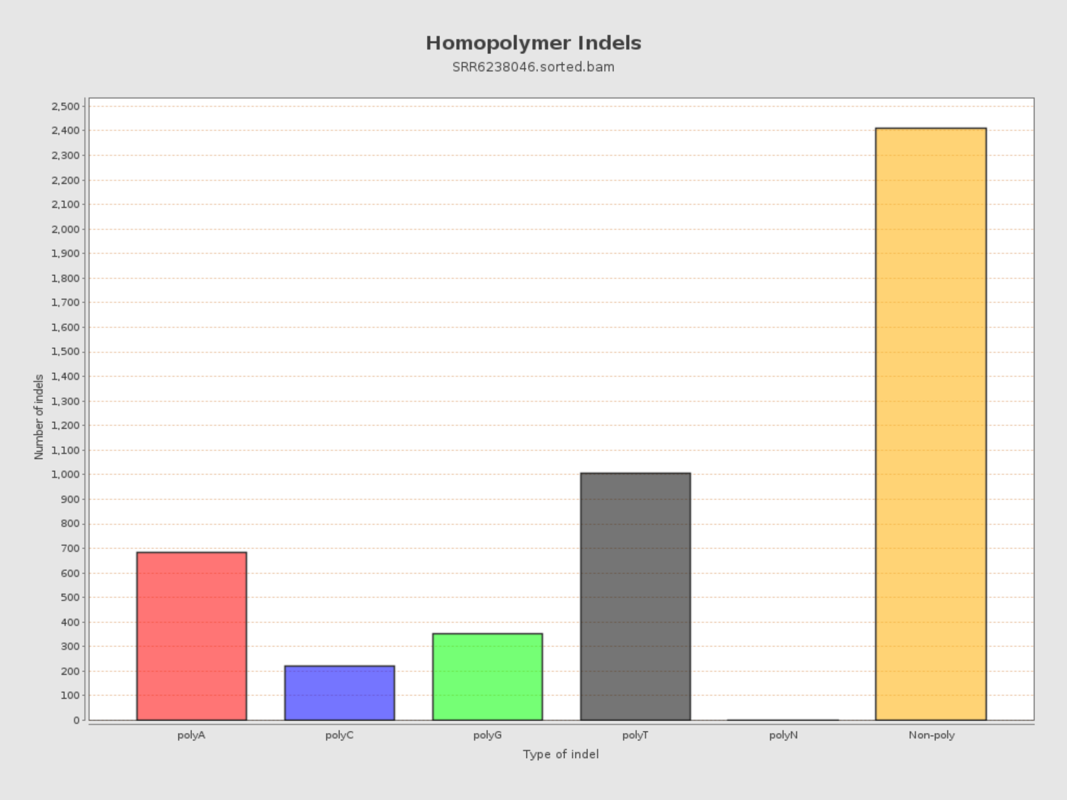
9. Results : Mapped Reads GC-content Distribution



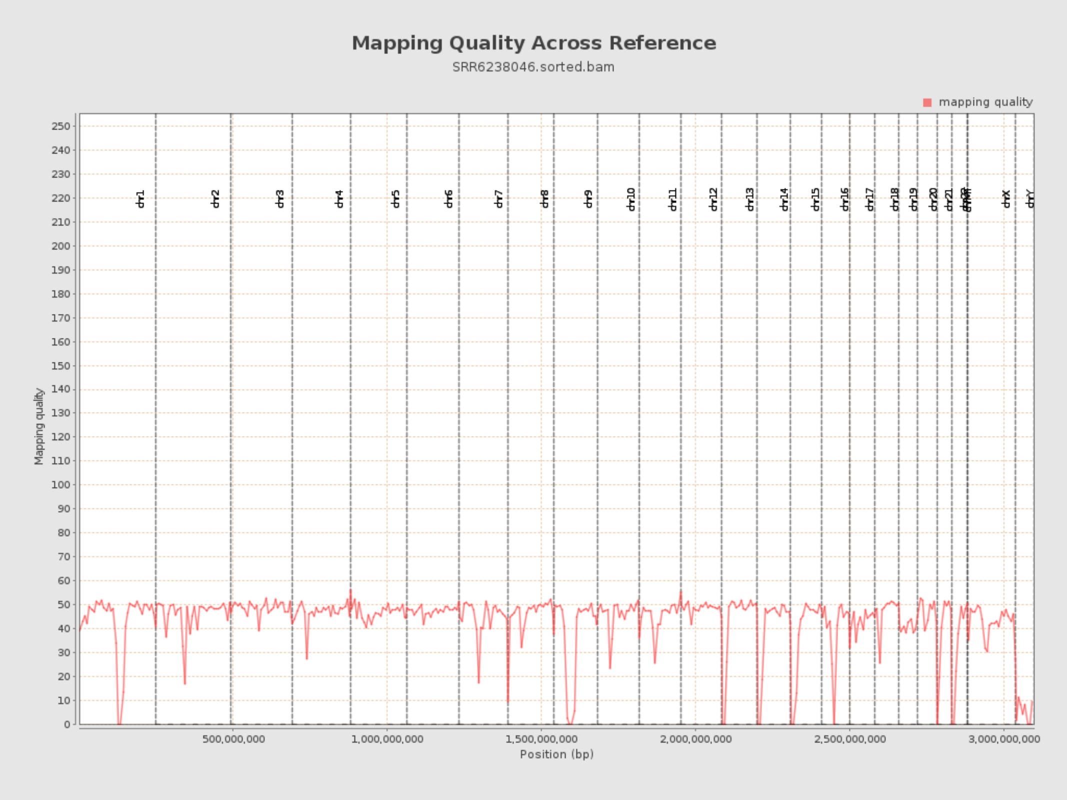
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram