Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 13:57:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238272.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_SRR6238272 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238272.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 13:57:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238272.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,134,048
Mapped reads	2,566,332 / 81.89%
Unmapped reads	567,716 / 18.11%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	26,044 / 0.83%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	231,266 / 7.38%
Duplication rate	7.12%
Clipped reads	1,406,598 / 44.88%

2.2. ACGT Content

Number/percentage of A's	45,439,399 / 27.49%
Number/percentage of C's	31,467,749 / 19.04%
Number/percentage of T's	51,195,889 / 30.97%
Number/percentage of G's	37,140,827 / 22.47%
Number/percentage of N's	40,028 / 0.02%
GC Percentage	41.51%

2.3. Coverage

Mean	0.0534

Standard Deviation	0.4827

2.4. Mapping Quality

Mean Mapping Quality	45.24

2.5. Mismatches and indels

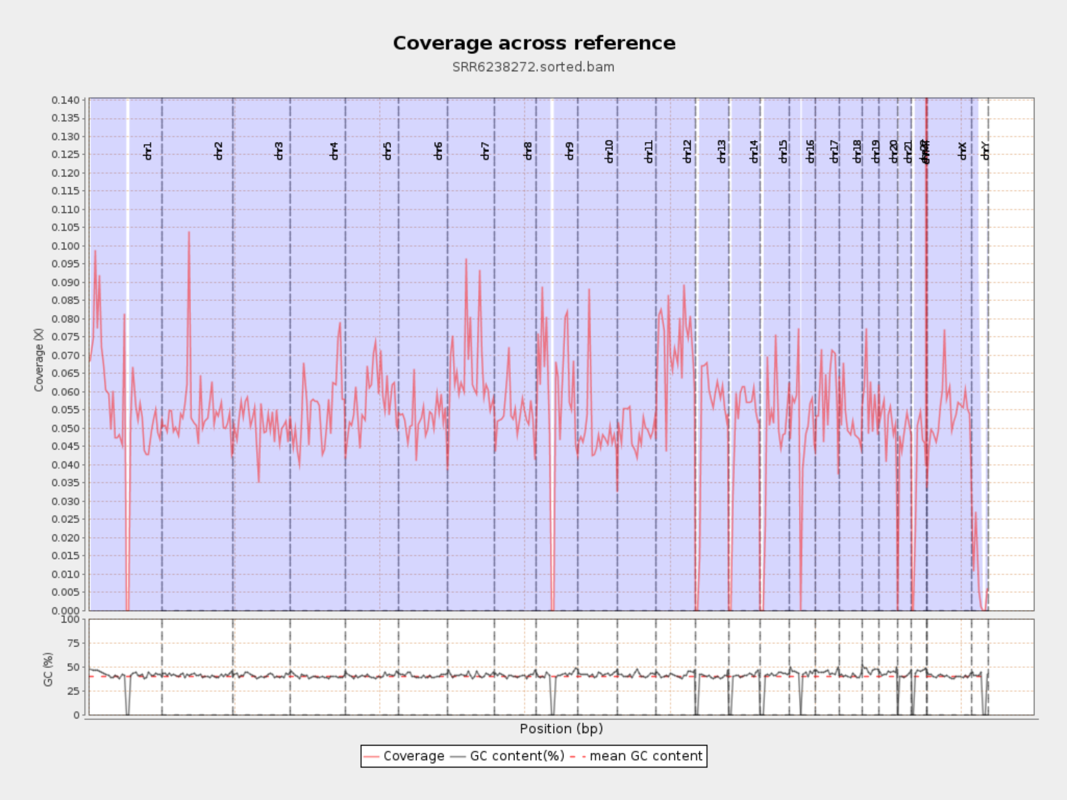
General error rate	1.01%
Mismatches	1,650,185
Insertions	13,732
Mapped reads with at least one insertion	0.53%
Deletions	61,566
Mapped reads with at least one deletion	2.36%
Homopolymer indels	46.7%

2.6. Chromosome stats

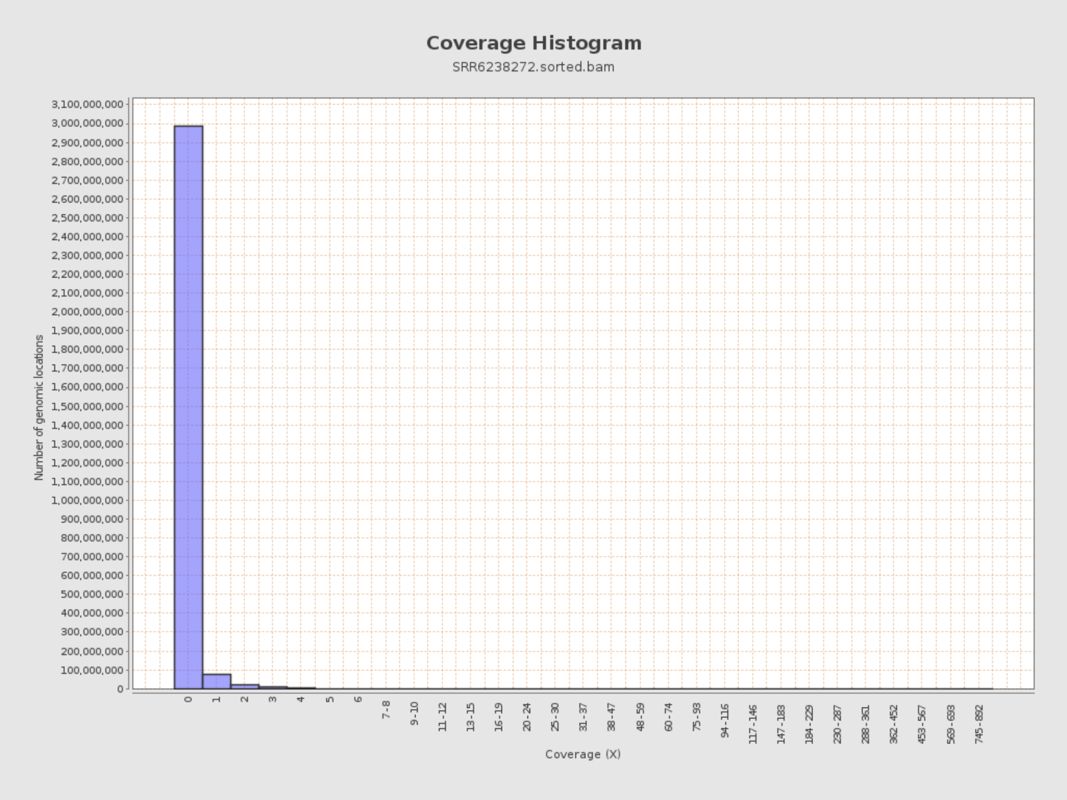
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13780672	0.0553	0.768
chr2	243199373	13273048	0.0546	0.6048
chr3	198022430	10075328	0.0509	0.3141
chr4	191154276	10528833	0.0551	0.35
chr5	180915260	10492008	0.058	0.3353
chr6	171115067	9008980	0.0526	0.3758
chr7	159138663	10568288	0.0664	0.683

chr8	146364022	7859787	0.0537	0.5958
chr9	141213431	8237846	0.0583	0.4903
chr10	135534747	6671183	0.0492	0.4683
chr11	135006516	6677754	0.0495	0.3951
chr12	133851895	9762145	0.0729	0.3846
chr13	115169878	5842912	0.0507	0.3145
chr14	107349540	5197831	0.0484	0.3421
chr15	102531392	4597216	0.0448	0.3163
chr16	90354753	4505434	0.0499	0.3425
chr17	81195210	4793273	0.059	0.3759
chr18	78077248	4050373	0.0519	0.8384
chr19	59128983	3438693	0.0582	0.5716
chr20	63025520	3217081	0.051	0.3255
chr21	48129895	2132590	0.0443	0.3193
chr22	51304566	1780534	0.0347	0.2553
chrMT	16571	11543	0.6966	1.0229
chrX	155270560	8394936	0.0541	0.3519
chrY	59373566	487042	0.0082	0.188

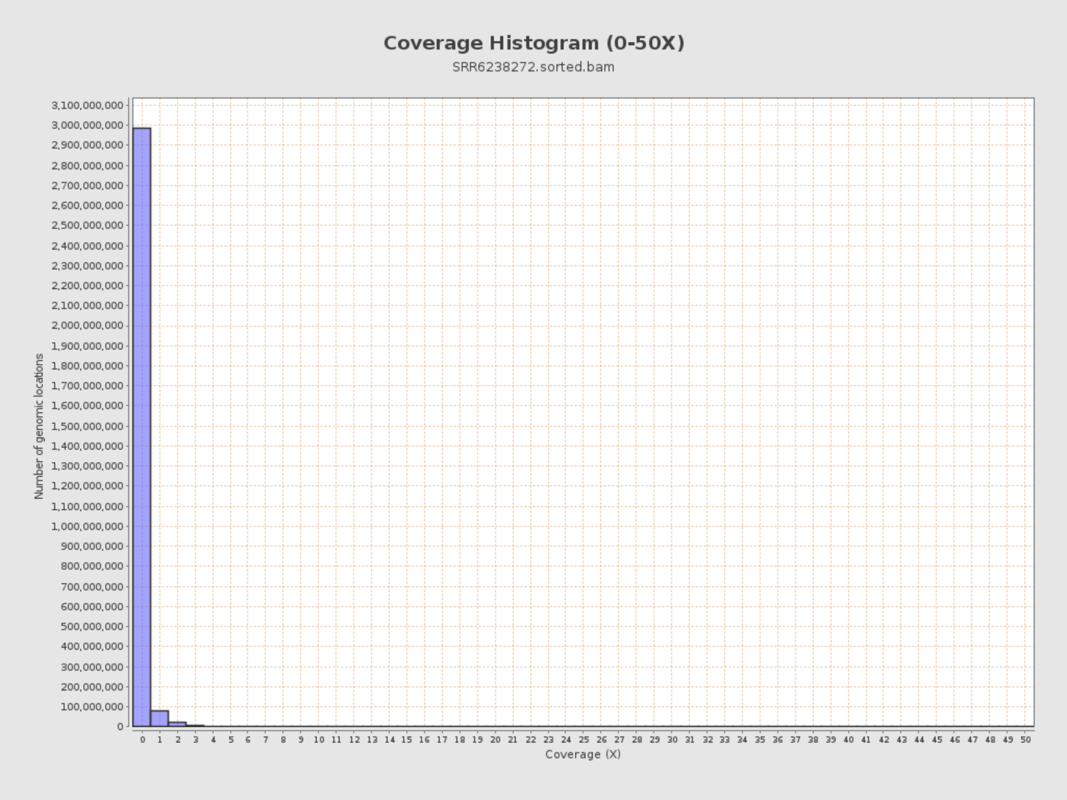
3. Results : Coverage across reference



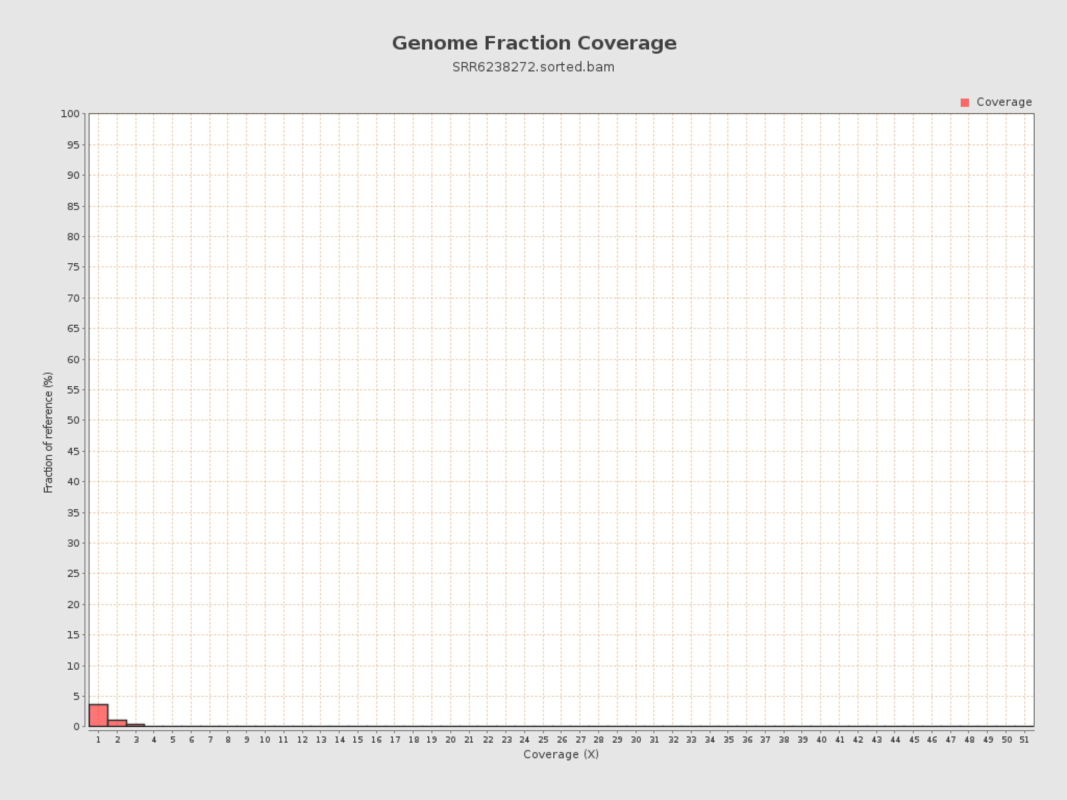
4. Results : Coverage Histogram



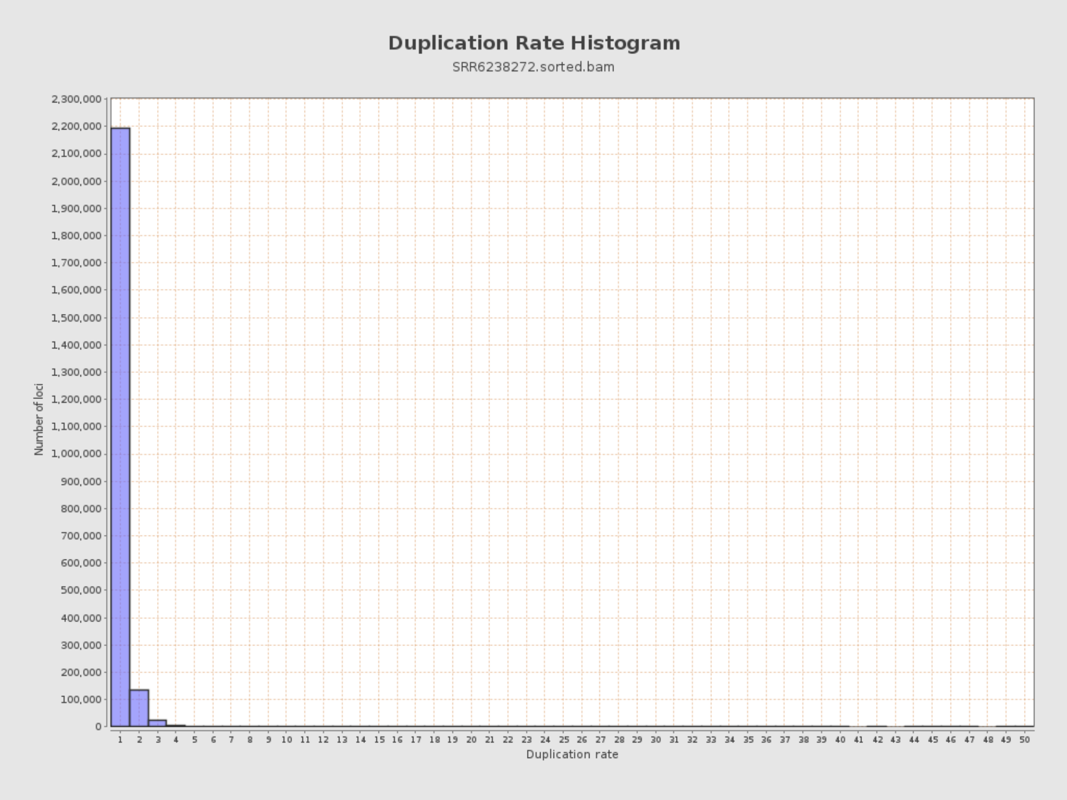
5. Results : Coverage Histogram (0-50X)



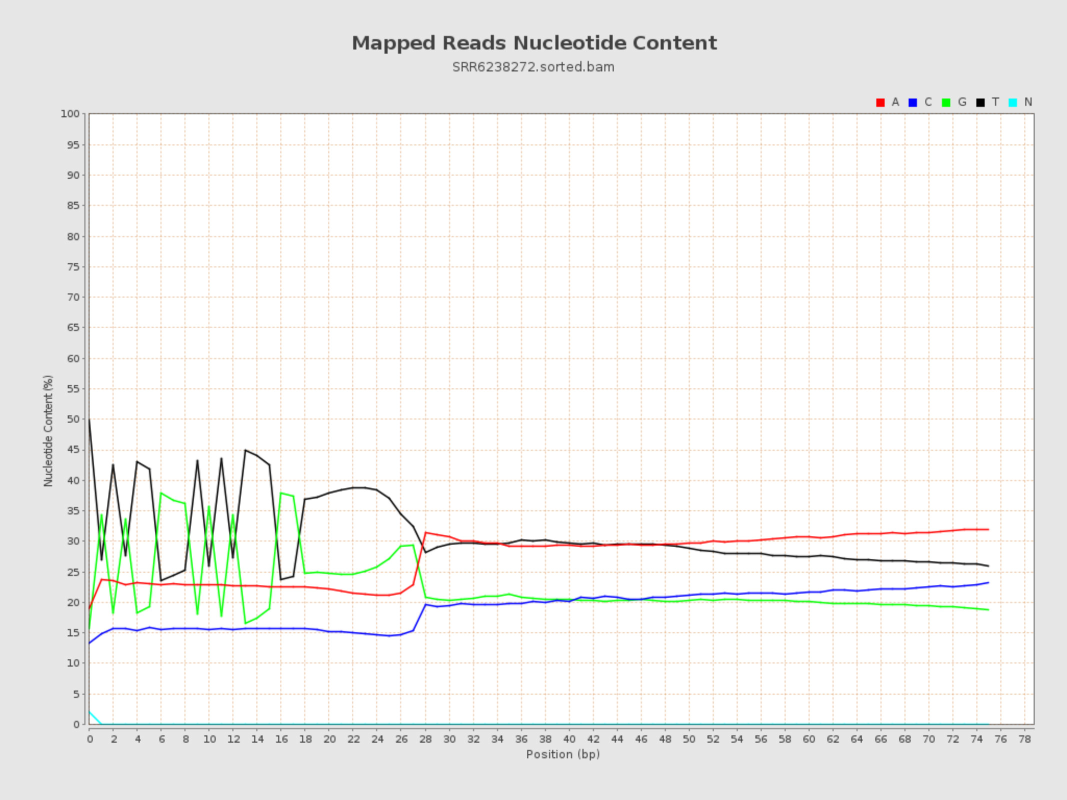
6. Results : Genome Fraction Coverage



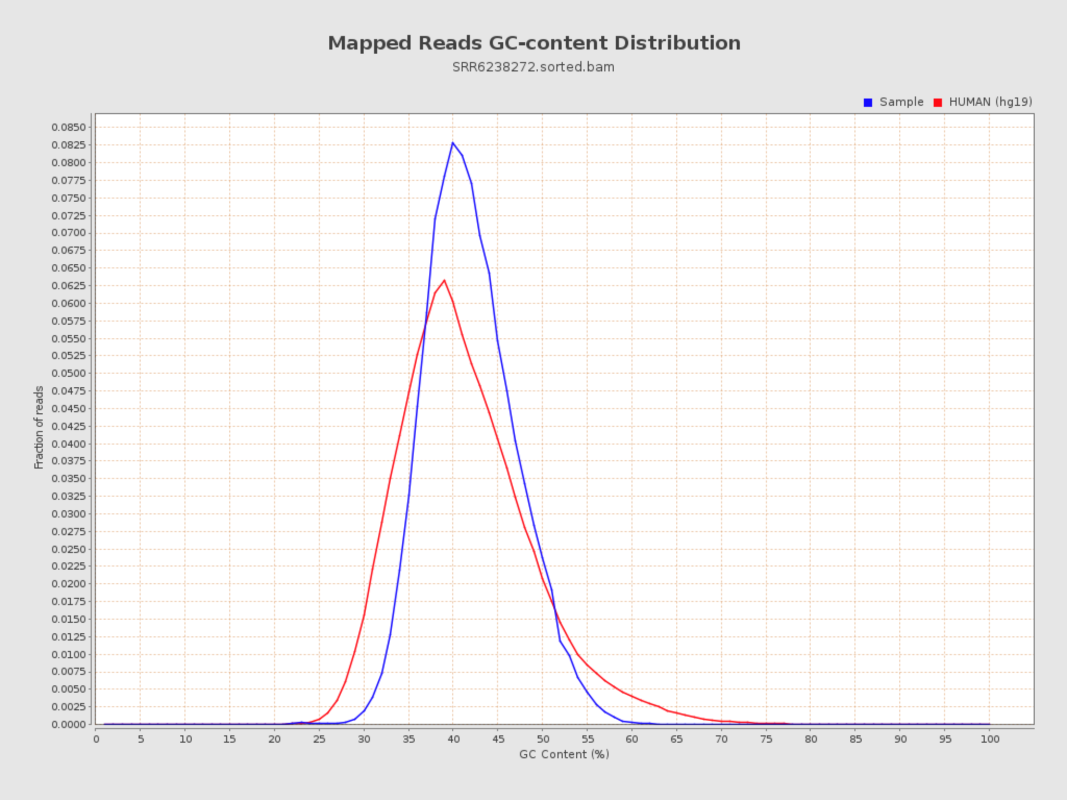
7. Results : Duplication Rate Histogram



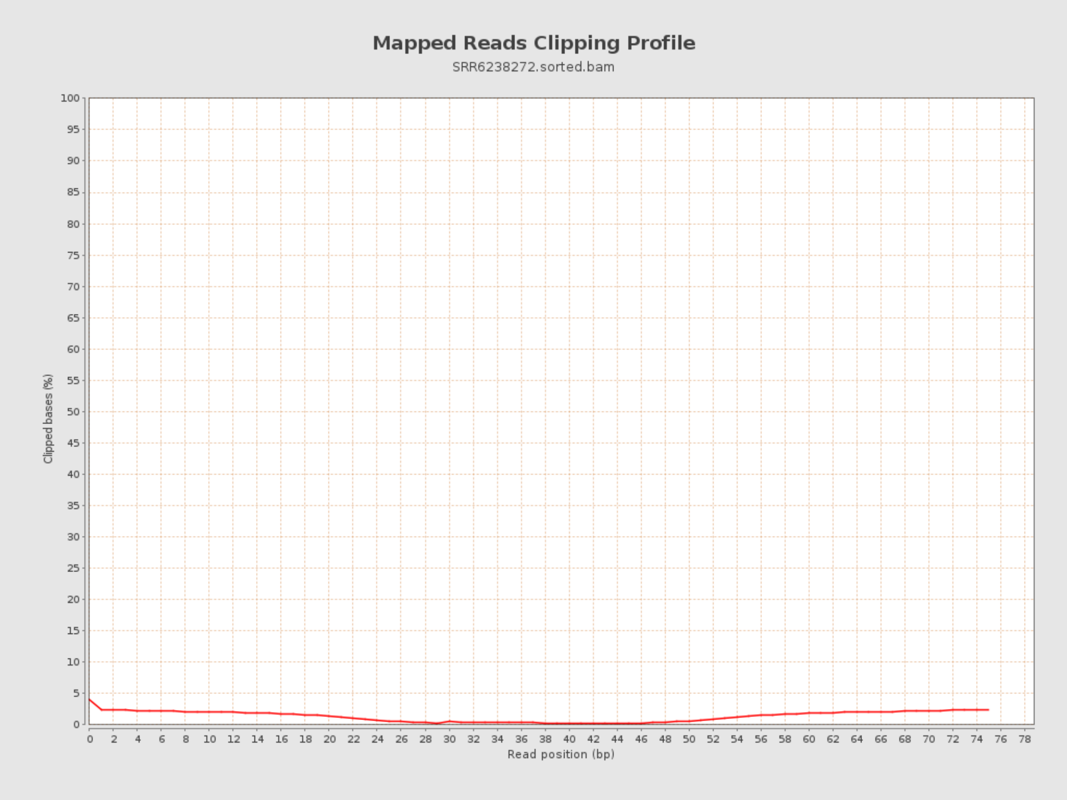
8. Results : Mapped Reads Nucleotide Content



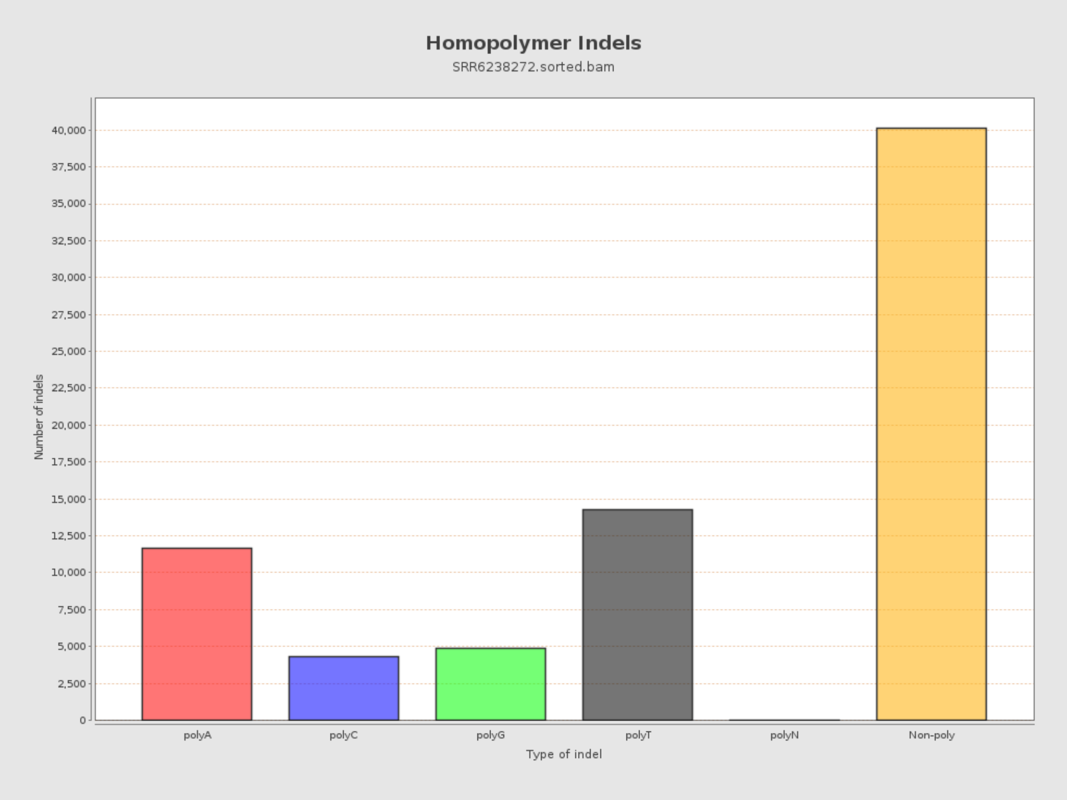
9. Results : Mapped Reads GC-content Distribution



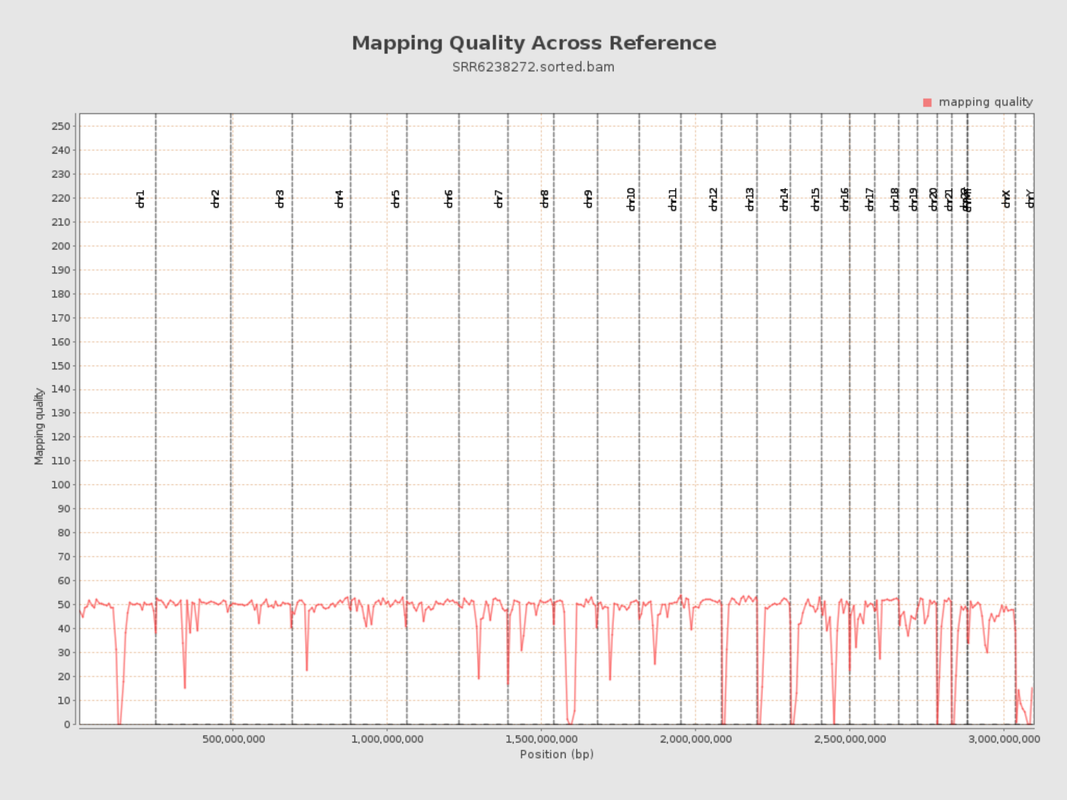
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram