Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 13:22:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238260.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_SRR6238260 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238260.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 13:22:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238260.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,114,247
Mapped reads	1,877,345 / 88.79%
Unmapped reads	236,902 / 11.21%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,801 / 1.13%
Read min/max/mean length	30 / 76 / 76.39
Duplicated reads (estimated)	107,411 / 5.08%
Duplication rate	4.69%
Clipped reads	1,021,285 / 48.3%

2.2. ACGT Content

Number/percentage of A's	34,405,289 / 28.27%
Number/percentage of C's	22,919,536 / 18.83%
Number/percentage of T's	37,862,324 / 31.11%
Number/percentage of G's	26,498,594 / 21.77%
Number/percentage of N's	32,629 / 0.03%
GC Percentage	40.6%

2.3. Coverage

Mean	0.0393

Standard Deviation	0.339

2.4. Mapping Quality

Mean Mapping Quality	45.64

2.5. Mismatches and indels

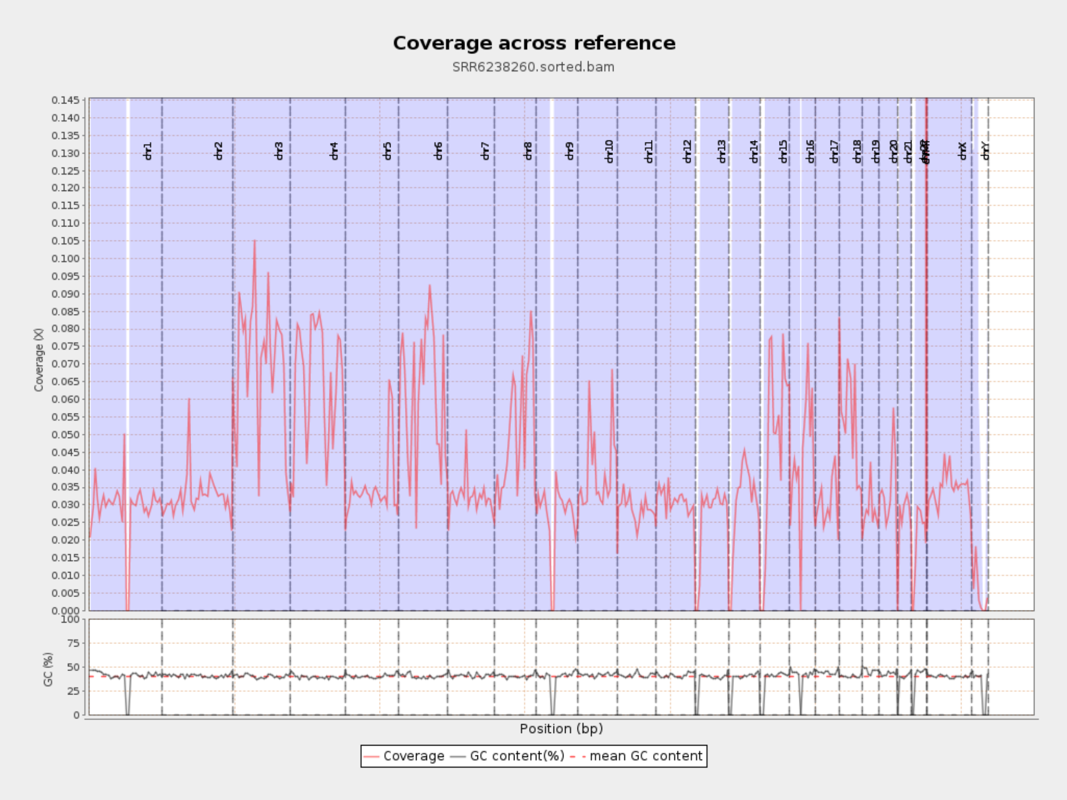
General error rate	0.87%
Mismatches	1,046,610
Insertions	9,605
Mapped reads with at least one insertion	0.51%
Deletions	33,669
Mapped reads with at least one deletion	1.77%
Homopolymer indels	46.8%

2.6. Chromosome stats

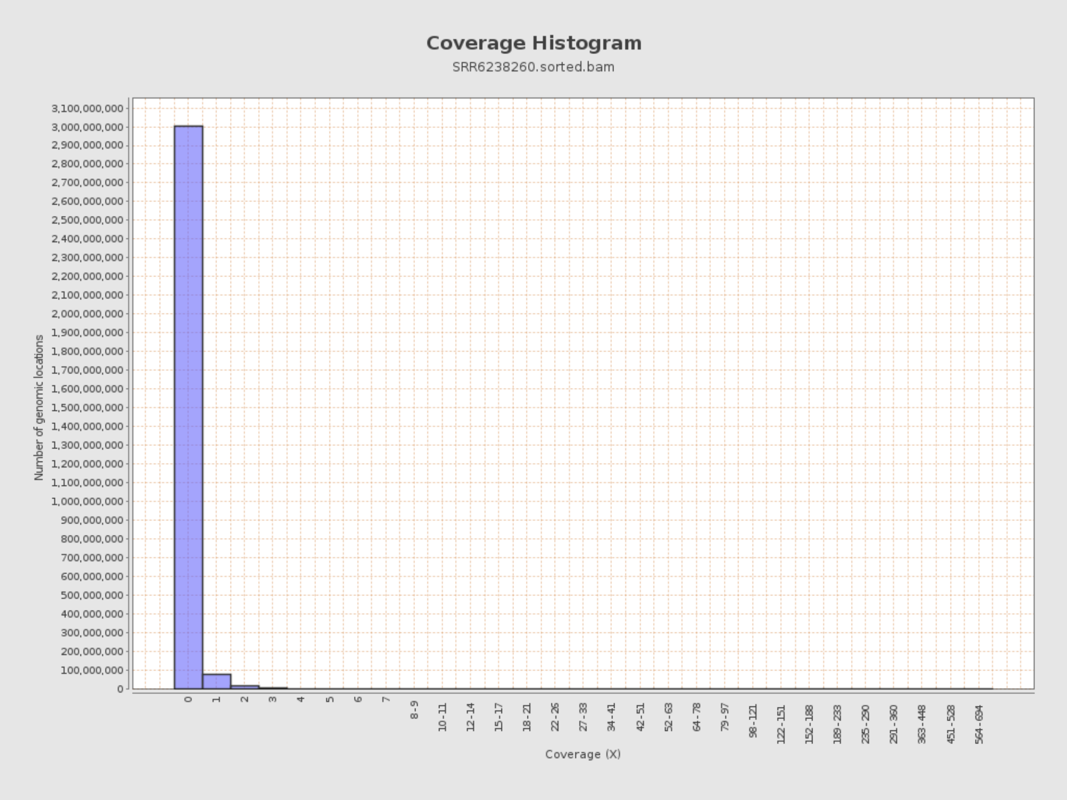
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7309432	0.0293	0.5454
chr2	243199373	7984797	0.0328	0.3763
chr3	198022430	14011195	0.0708	0.3277
chr4	191154276	12402128	0.0649	0.3207
chr5	180915260	6294399	0.0348	0.2306
chr6	171115067	10576661	0.0618	0.3447
chr7	159138663	5186105	0.0326	0.3502

chr8	146364022	7502628	0.0513	0.5
chr9	141213431	3787450	0.0268	0.2834
chr10	135534747	5338903	0.0394	0.3321
chr11	135006516	3879895	0.0287	0.2586
chr12	133851895	4173308	0.0312	0.2211
chr13	115169878	3007928	0.0261	0.2009
chr14	107349540	3218516	0.03	0.2384
chr15	102531392	4853161	0.0473	0.2763
chr16	90354753	3838246	0.0425	0.2802
chr17	81195210	2441957	0.0301	0.2315
chr18	78077248	4184429	0.0536	0.5069
chr19	59128983	1678620	0.0284	0.3916
chr20	63025520	2180762	0.0346	0.2332
chr21	48129895	1259863	0.0262	0.2108
chr22	51304566	968288	0.0189	0.1671
chrMT	16571	23876	1.4408	1.656
chrX	155270560	5367173	0.0346	0.2504
chrY	59373566	303708	0.0051	0.1693

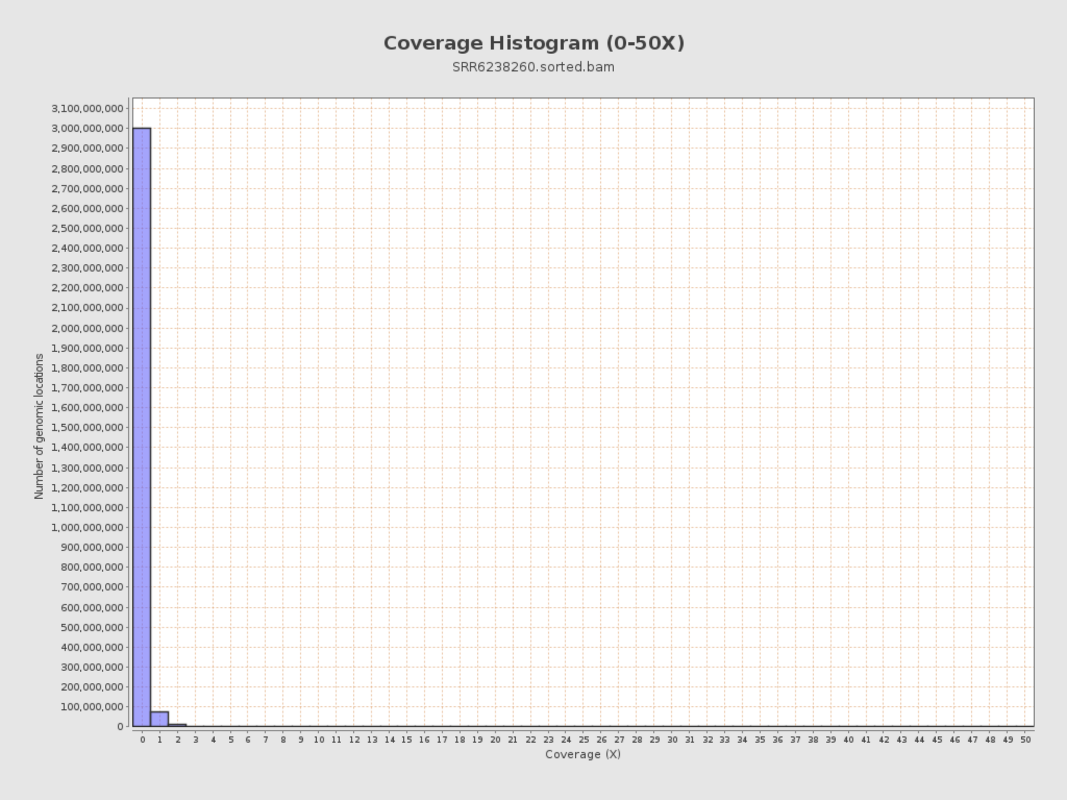
3. Results : Coverage across reference



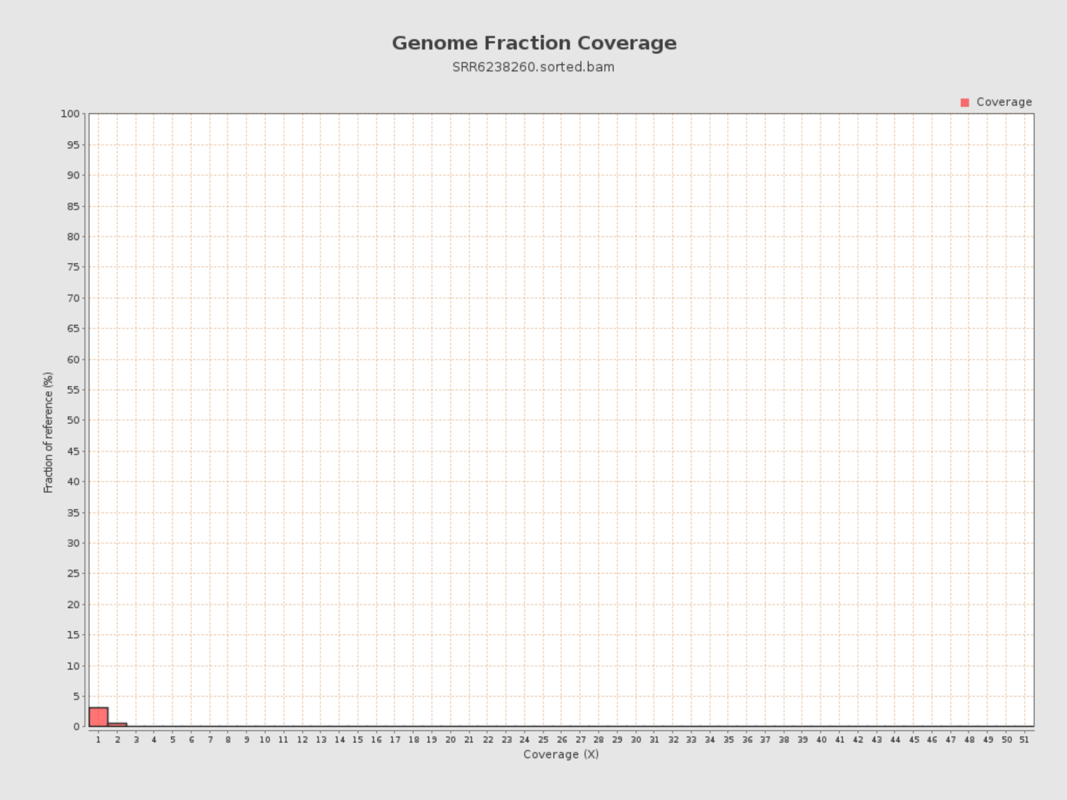
4. Results : Coverage Histogram



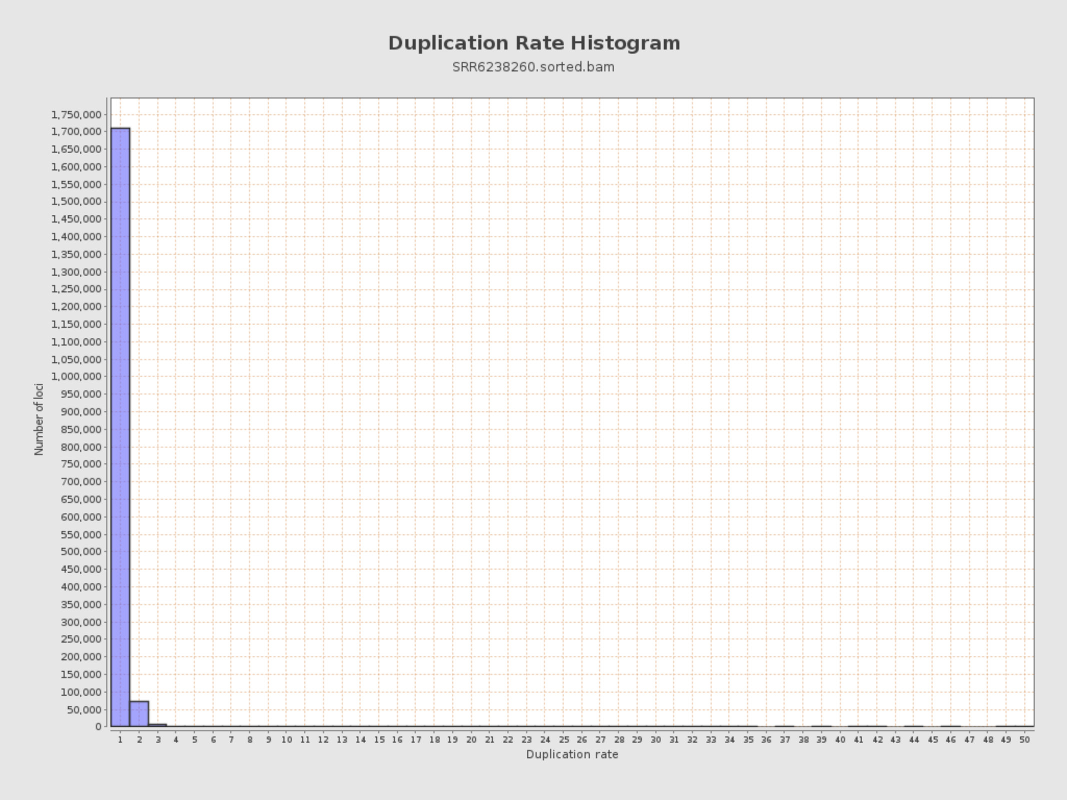
5. Results : Coverage Histogram (0-50X)



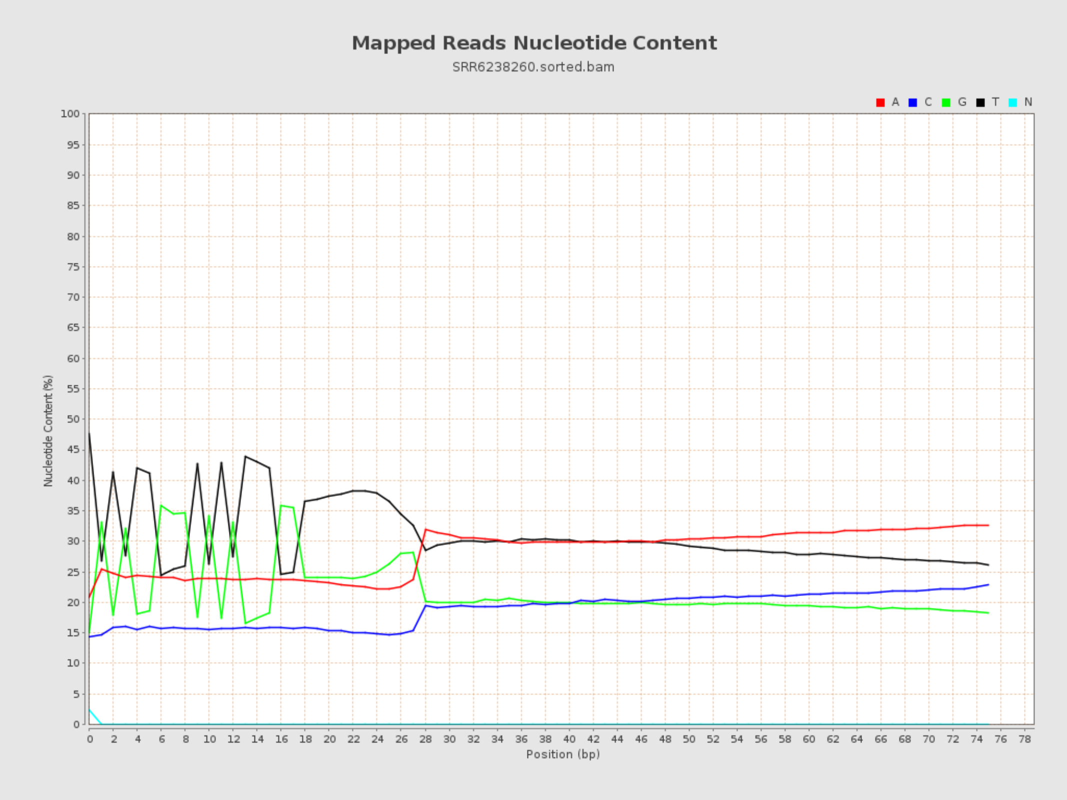
6. Results : Genome Fraction Coverage



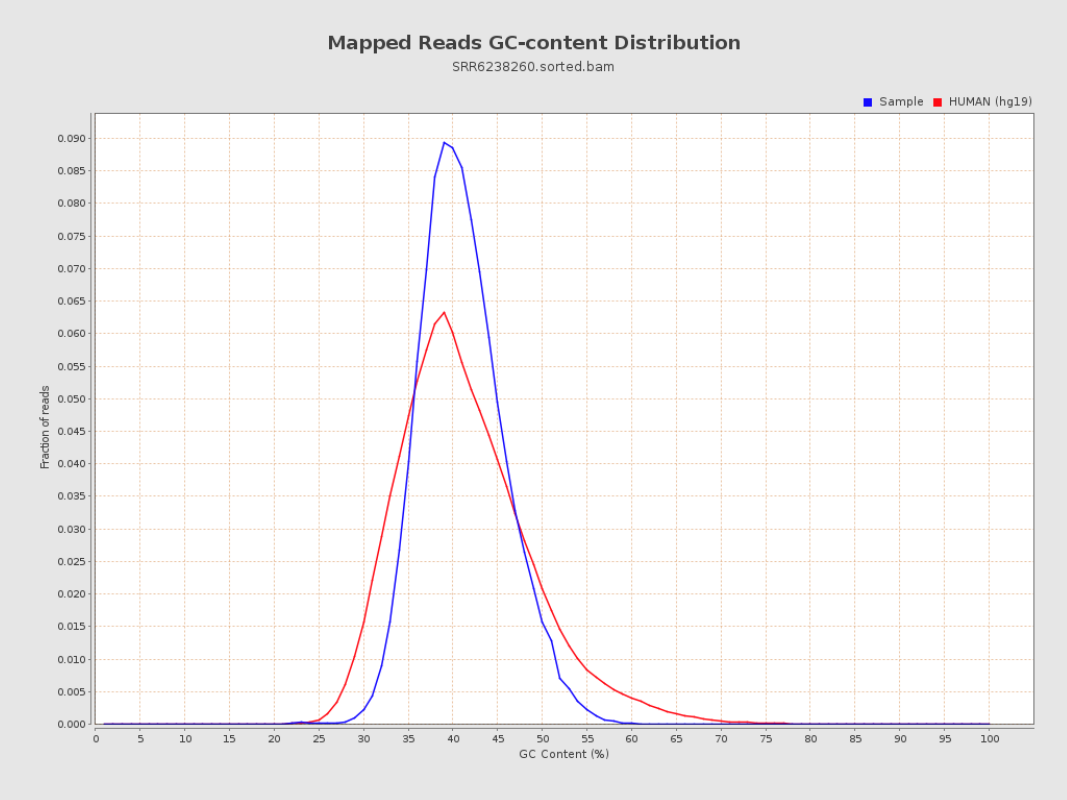
7. Results : Duplication Rate Histogram



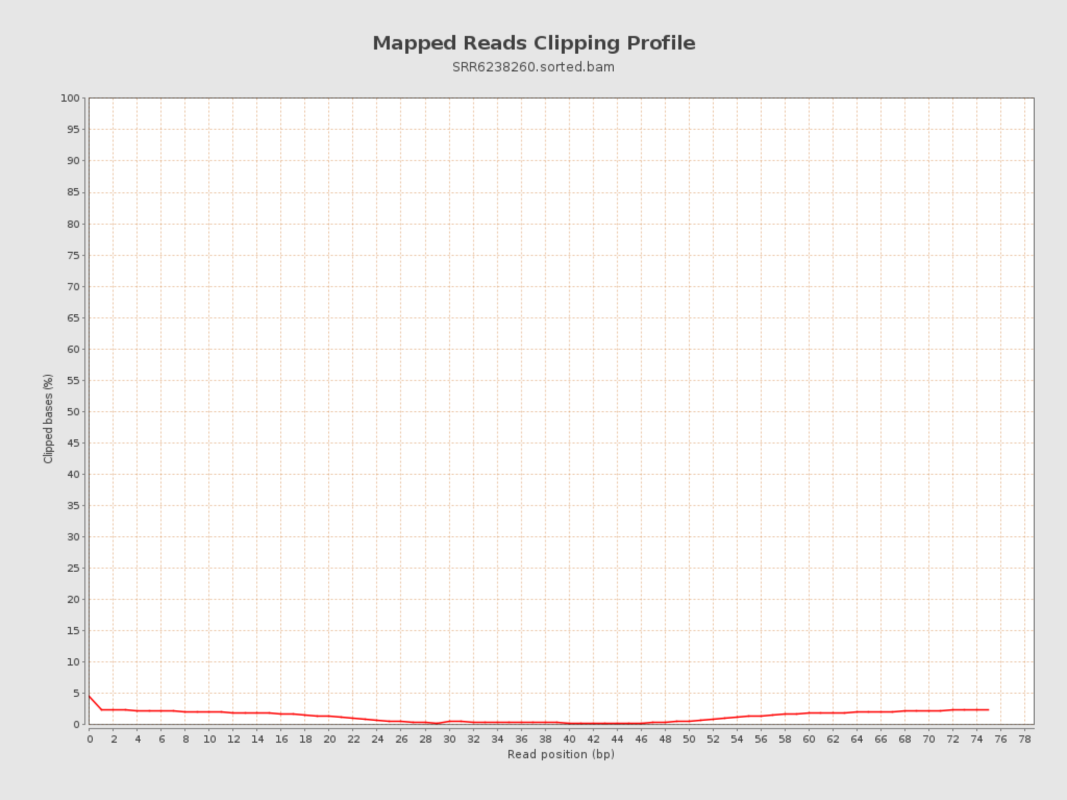
8. Results : Mapped Reads Nucleotide Content



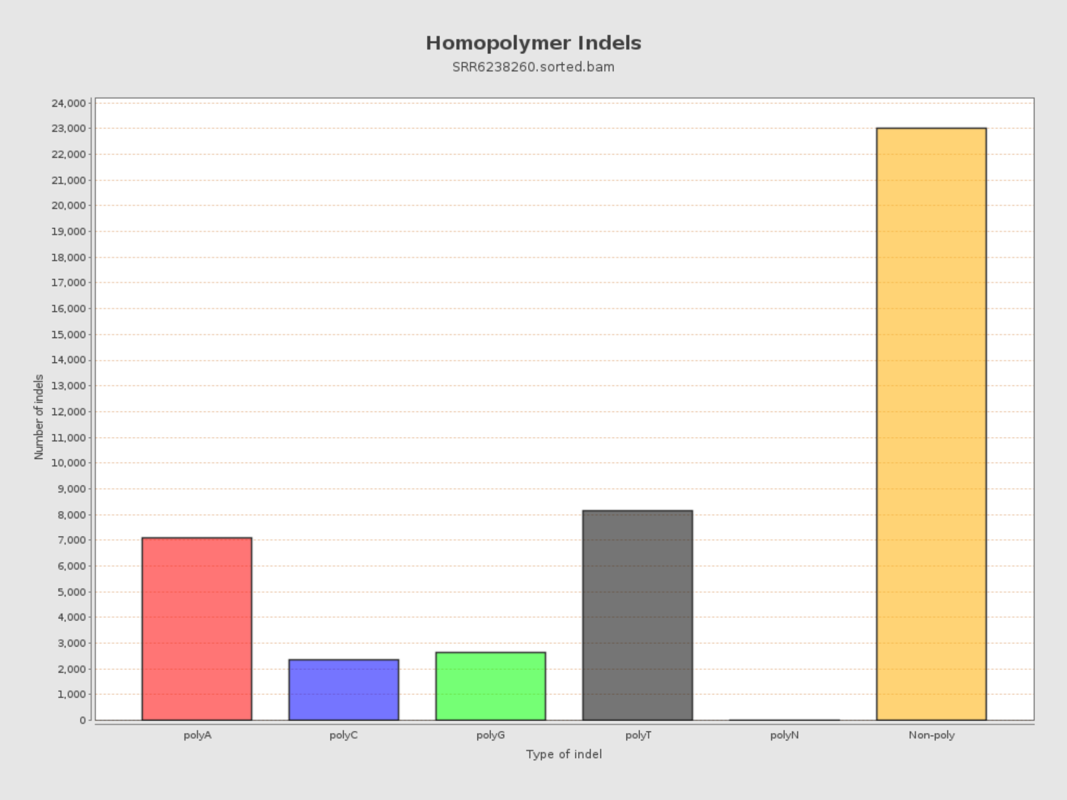
9. Results : Mapped Reads GC-content Distribution



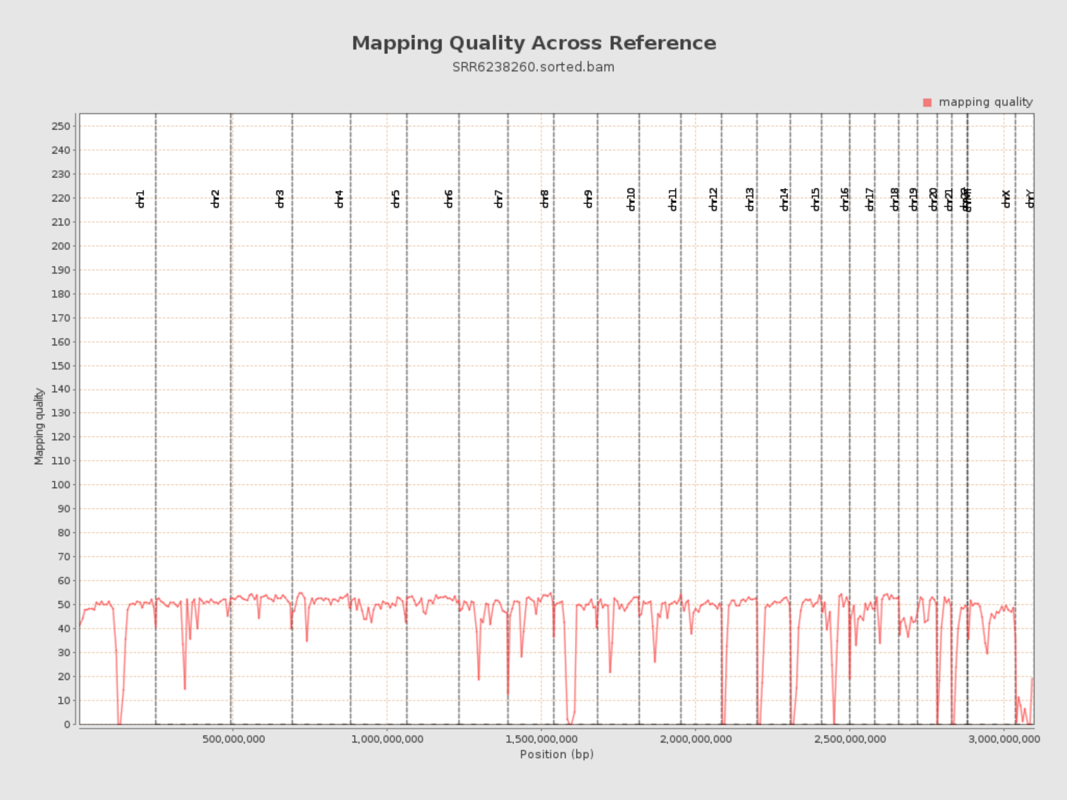
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram