Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 22:04:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238608.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_SRR6238608 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238608.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 22:04:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238608.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,046,978
Mapped reads	1,821,101 / 88.97%
Unmapped reads	225,877 / 11.03%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,285 / 0.8%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	338,191 / 16.52%
Duplication rate	14.84%
Clipped reads	1,198,016 / 58.53%

2.2. ACGT Content

Number/percentage of A's	27,340,950 / 24.56%
Number/percentage of C's	19,880,569 / 17.86%
Number/percentage of T's	37,112,056 / 33.34%
Number/percentage of G's	26,987,063 / 24.24%
Number/percentage of N's	5,455 / 0%
GC Percentage	42.1%

2.3. Coverage

Mean	0.036

Standard Deviation	0.5564

2.4. Mapping Quality

Mean Mapping Quality	44.18

2.5. Mismatches and indels

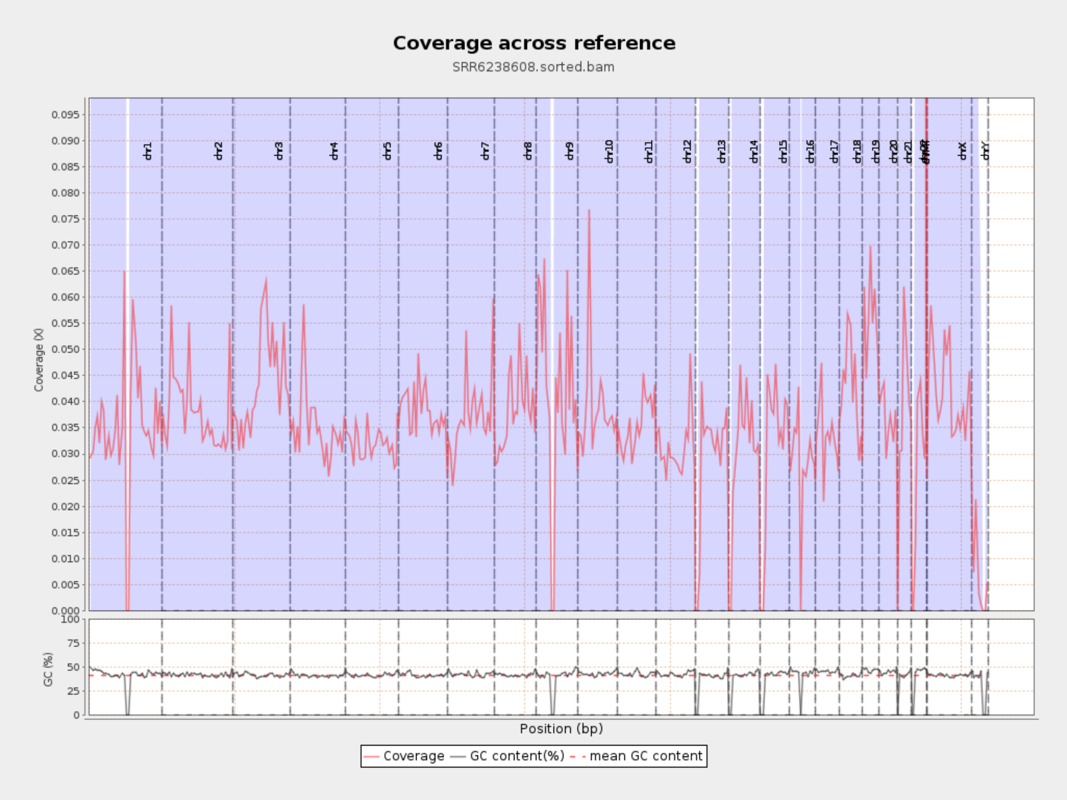
General error rate	0.6%
Mismatches	656,036
Insertions	7,618
Mapped reads with at least one insertion	0.41%
Deletions	28,466
Mapped reads with at least one deletion	1.55%
Homopolymer indels	41.45%

2.6. Chromosome stats

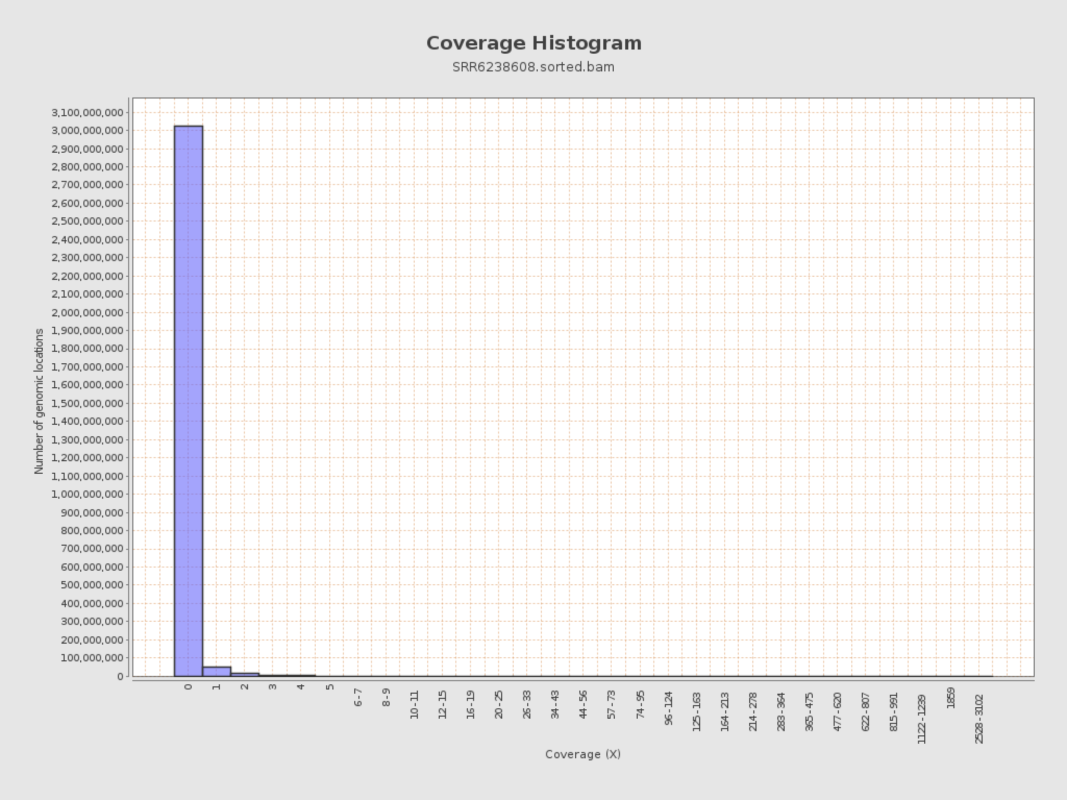
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8762758	0.0352	0.749
chr2	243199373	9300577	0.0382	1.3723
chr3	198022430	8669184	0.0438	0.3149
chr4	191154276	6694325	0.035	0.3007
chr5	180915260	5766421	0.0319	0.2704
chr6	171115067	6541750	0.0382	0.4638
chr7	159138663	5949679	0.0374	0.4082

chr8	146364022	5573570	0.0381	0.3522
chr9	141213431	5962108	0.0422	0.3726
chr10	135534747	5259768	0.0388	0.4231
chr11	135006516	4817832	0.0357	0.3155
chr12	133851895	4171744	0.0312	0.2703
chr13	115169878	3321133	0.0288	0.3359
chr14	107349540	3238232	0.0302	0.2817
chr15	102531392	3188097	0.0311	0.3394
chr16	90354753	2565406	0.0284	0.28
chr17	81195210	2699703	0.0332	0.2785
chr18	78077248	3354418	0.043	0.9313
chr19	59128983	3245984	0.0549	0.5166
chr20	63025520	2330521	0.037	0.2941
chr21	48129895	1814020	0.0377	0.3081
chr22	51304566	1301801	0.0254	0.2325
chrMT	16571	28394	1.7135	2.0811
chrX	155270560	6455638	0.0416	0.3163
chrY	59373566	360723	0.0061	0.2224

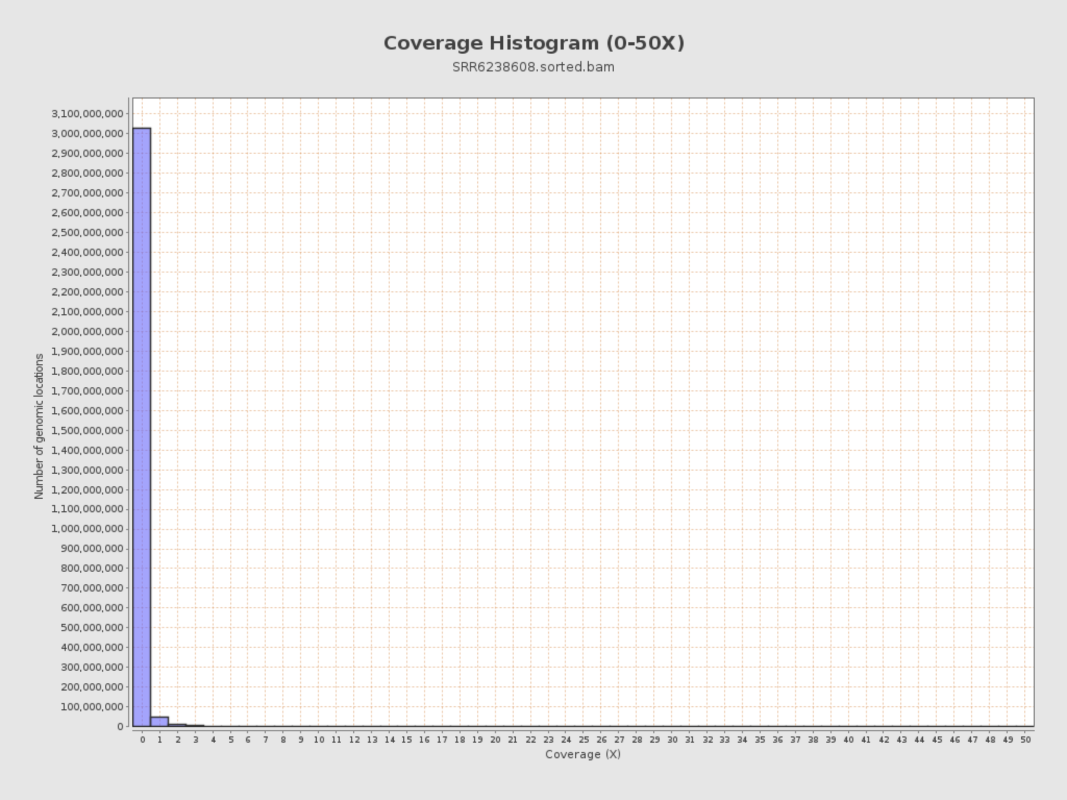
3. Results : Coverage across reference



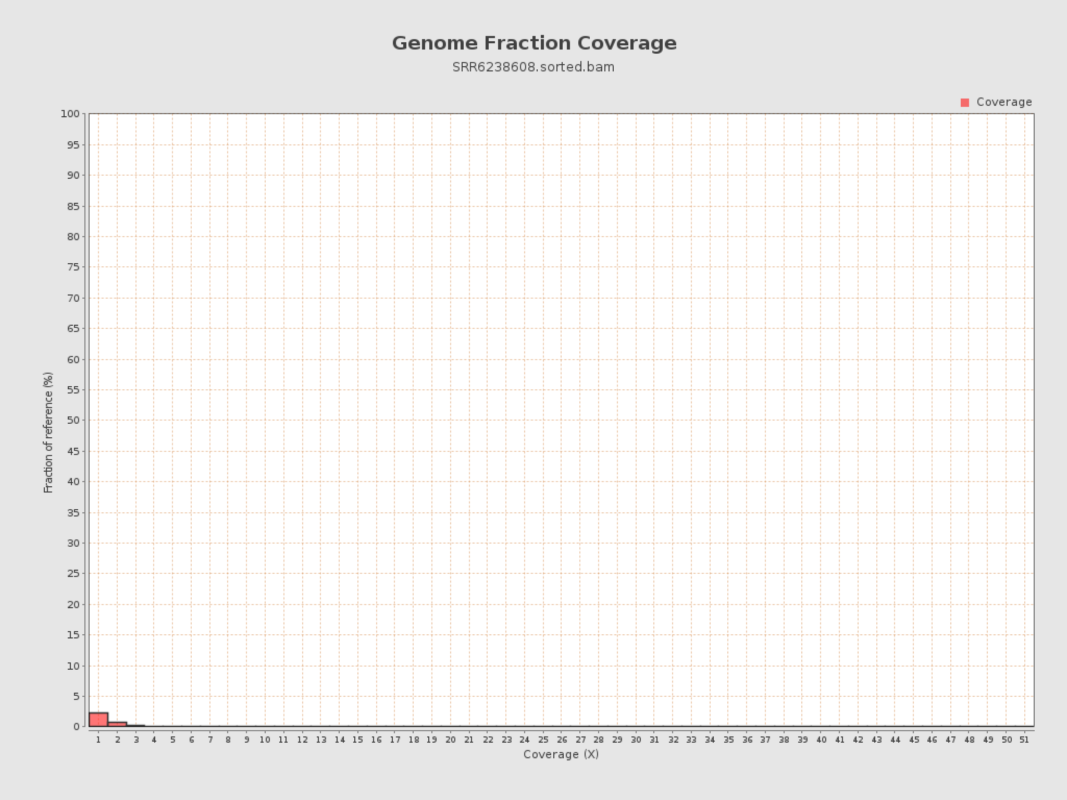
4. Results : Coverage Histogram



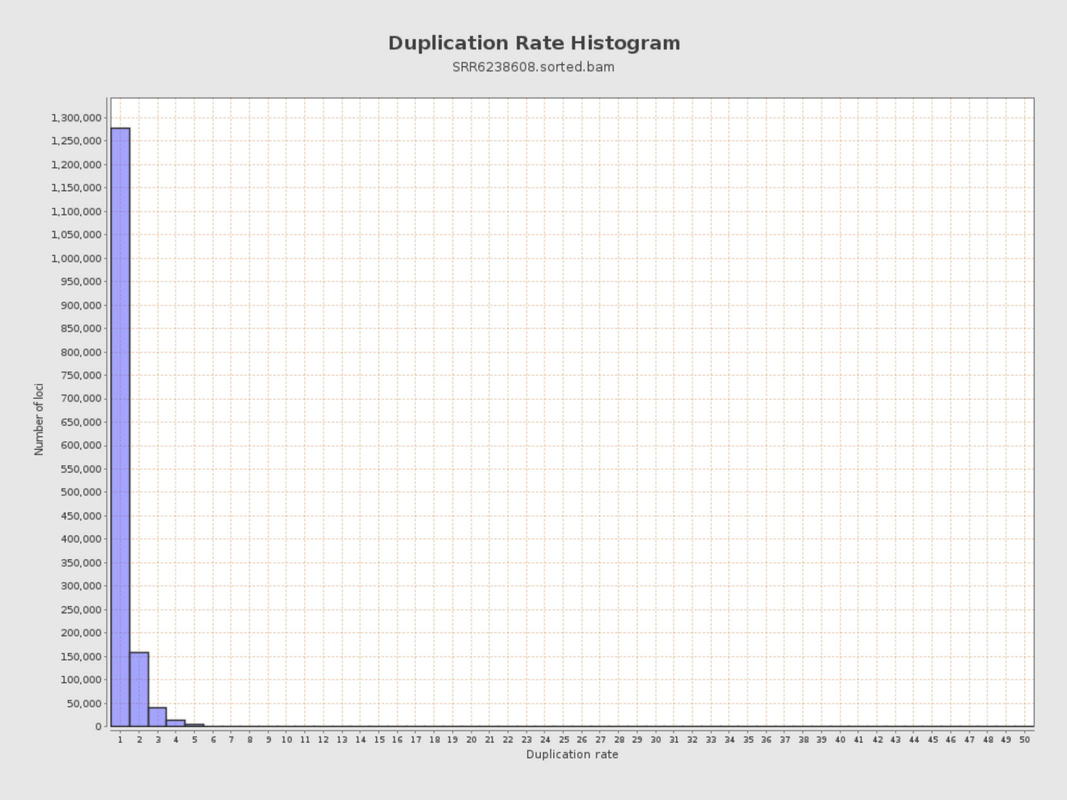
5. Results : Coverage Histogram (0-50X)



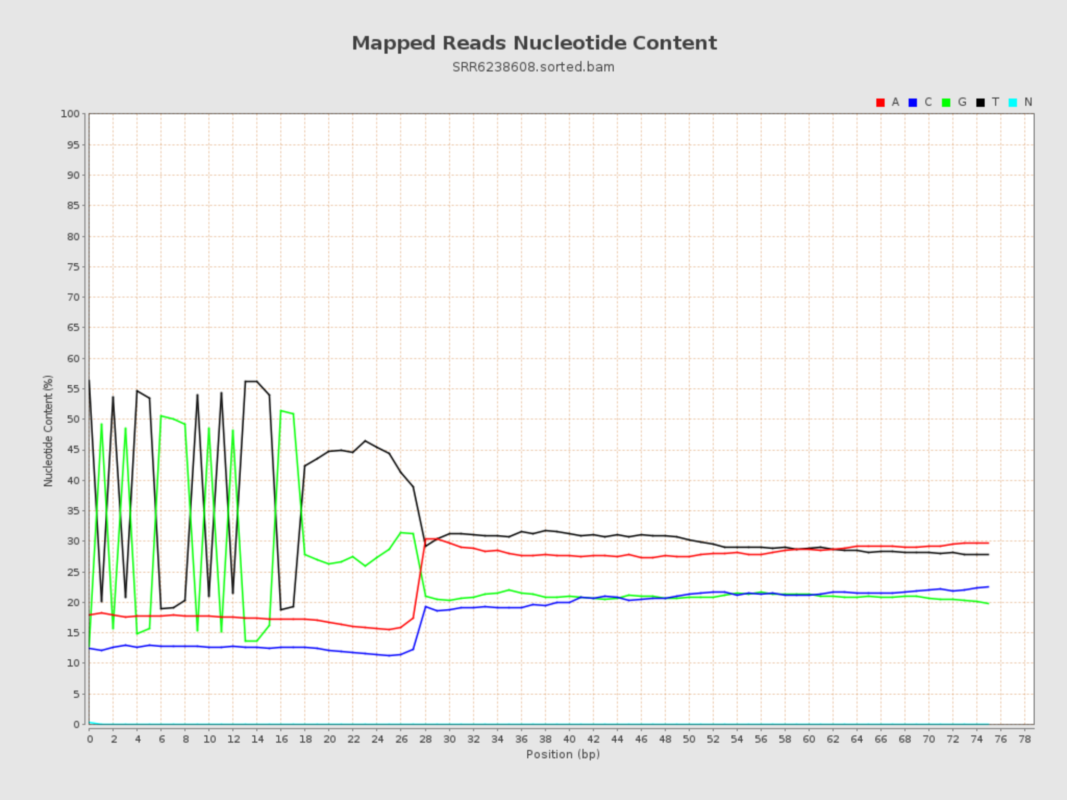
6. Results : Genome Fraction Coverage



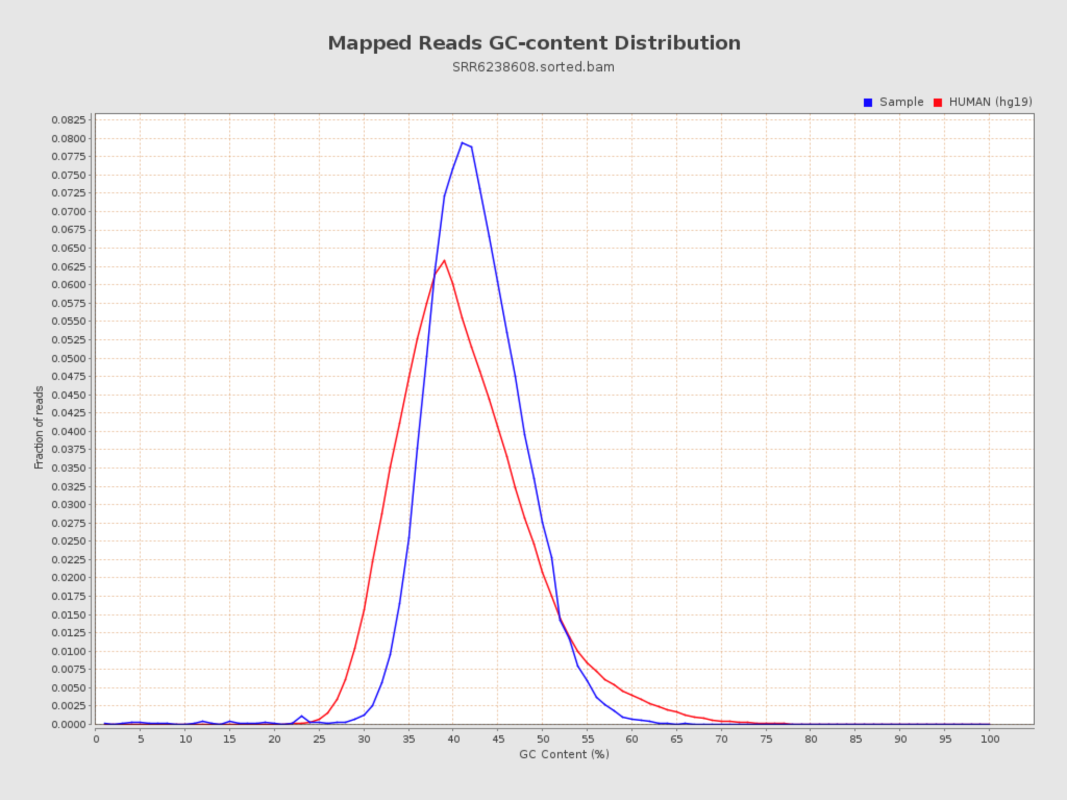
7. Results : Duplication Rate Histogram



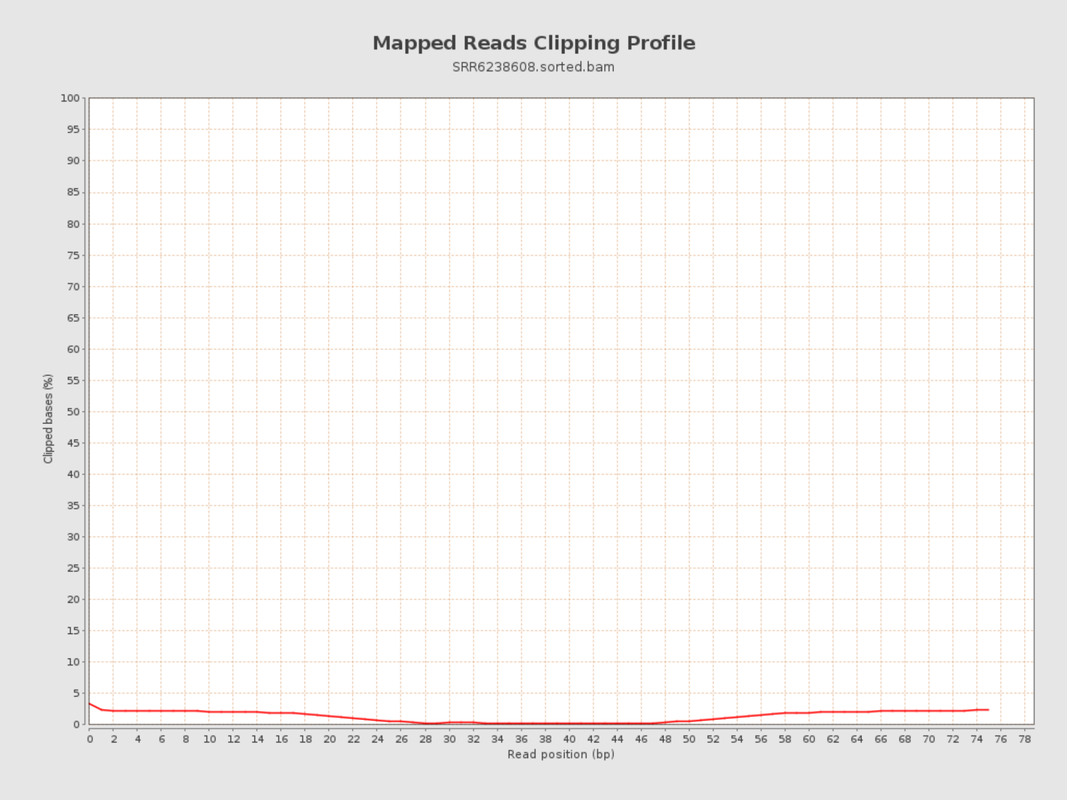
8. Results : Mapped Reads Nucleotide Content



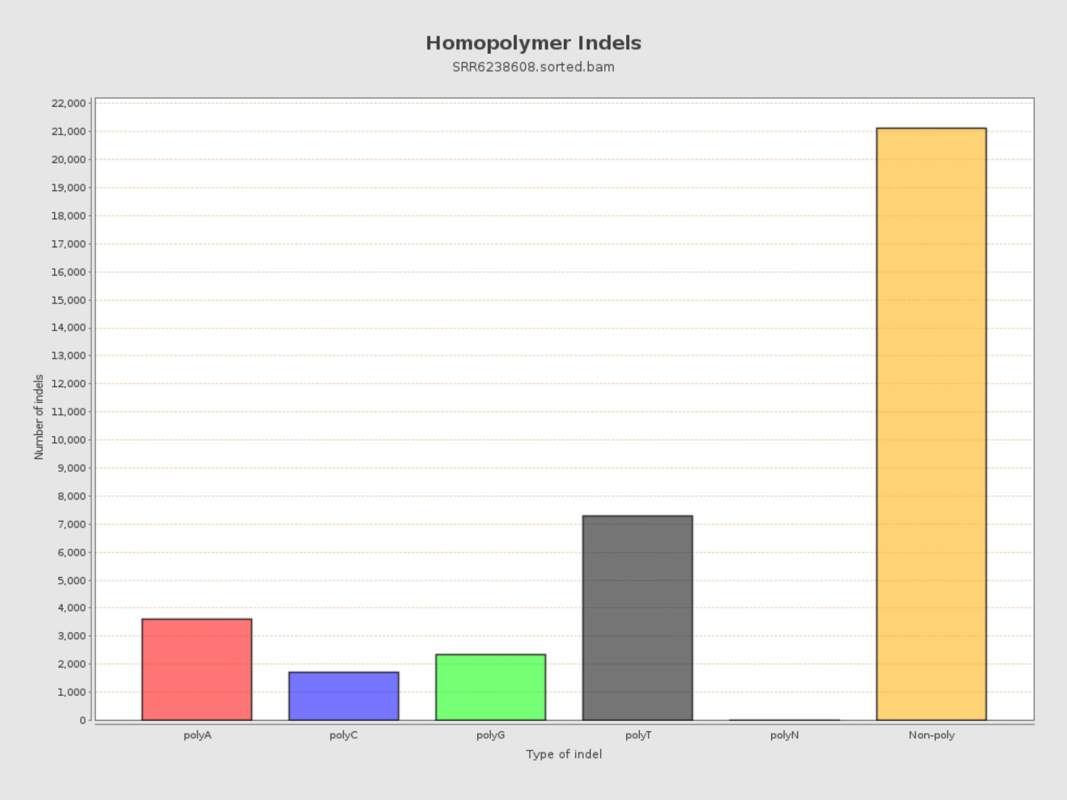
9. Results : Mapped Reads GC-content Distribution



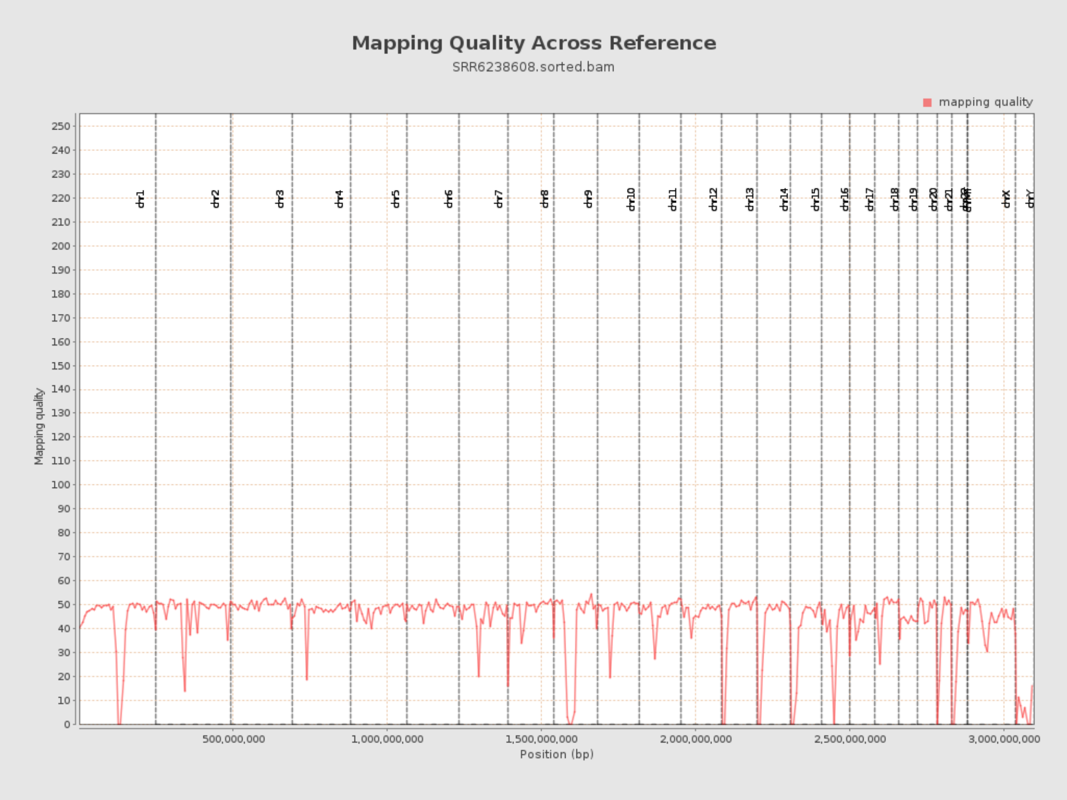
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram