Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 11:04:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238055.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_SRR6238055 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238055.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 11:04:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238055.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,337,472
Mapped reads	991,760 / 74.15%
Unmapped reads	345,712 / 25.85%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,899 / 0.81%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	247,818 / 18.53%
Duplication rate	14.08%
Clipped reads	469,113 / 35.07%

2.2. ACGT Content

Number/percentage of A's	17,603,244 / 27.01%
Number/percentage of C's	12,290,077 / 18.86%
Number/percentage of T's	20,482,789 / 31.42%
Number/percentage of G's	14,796,658 / 22.7%
Number/percentage of N's	8,200 / 0.01%
GC Percentage	41.56%

2.3. Coverage

Mean	0.0211

Standard Deviation	0.7002

2.4. Mapping Quality

Mean Mapping Quality	42.48

2.5. Mismatches and indels

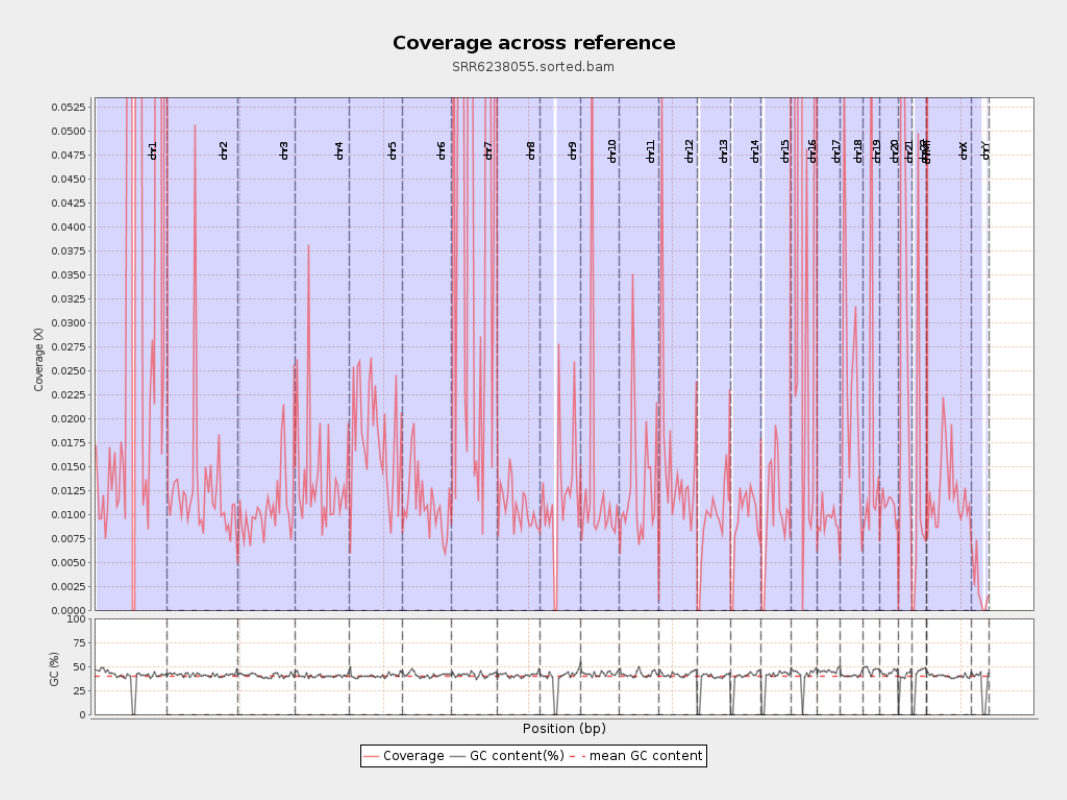
General error rate	0.88%
Mismatches	567,384
Insertions	4,847
Mapped reads with at least one insertion	0.49%
Deletions	15,965
Mapped reads with at least one deletion	1.6%
Homopolymer indels	46.13%

2.6. Chromosome stats

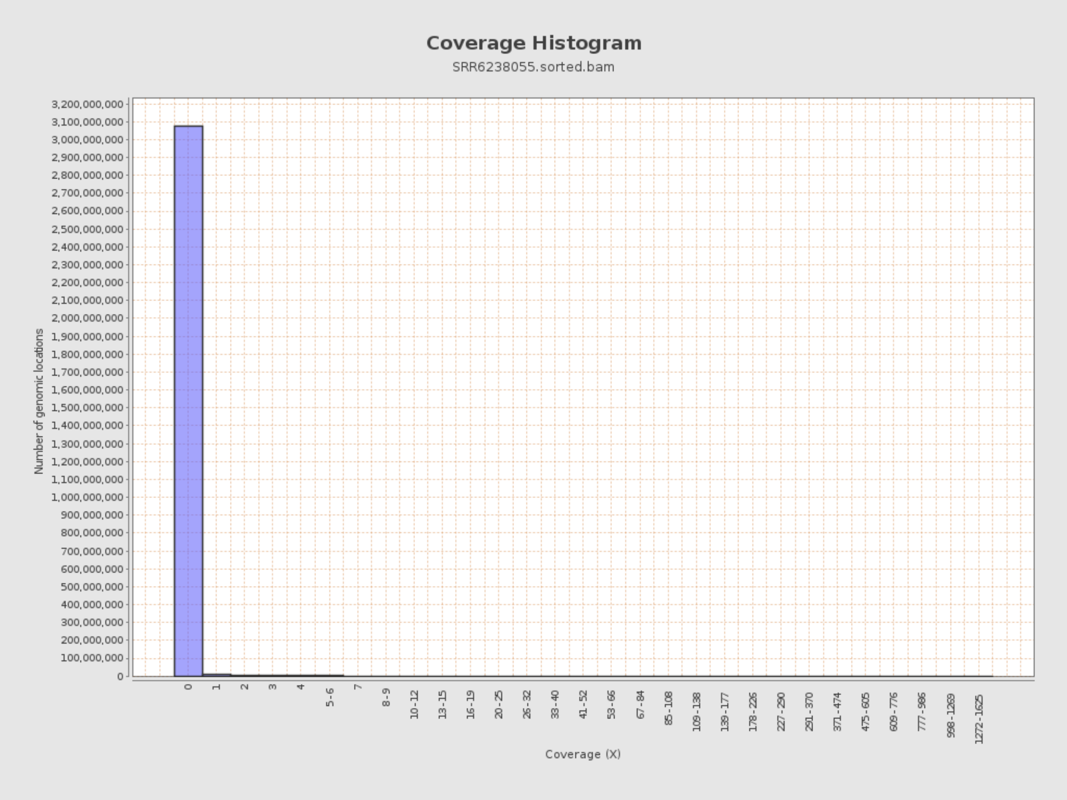
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13335323	0.0535	1.6069
chr2	243199373	3062042	0.0126	0.4232
chr3	198022430	2093552	0.0106	0.2787
chr4	191154276	2706243	0.0142	0.3226
chr5	180915260	3242477	0.0179	0.3508
chr6	171115067	1897157	0.0111	0.2805
chr7	159138663	10187965	0.064	1.3664

chr8	146364022	1567598	0.0107	0.3057
chr9	141213431	1683955	0.0119	0.3335
chr10	135534747	1766082	0.013	0.5684
chr11	135006516	1813582	0.0134	0.3441
chr12	133851895	2063659	0.0154	0.3184
chr13	115169878	1090471	0.0095	0.2607
chr14	107349540	989458	0.0092	0.2938
chr15	102531392	1042597	0.0102	0.3019
chr16	90354753	5708797	0.0632	0.6945
chr17	81195210	757127	0.0093	0.2515
chr18	78077248	1772842	0.0227	0.9342
chr19	59128983	1079878	0.0183	1.4232
chr20	63025520	689695	0.0109	0.2961
chr21	48129895	3226208	0.067	0.6972
chr22	51304566	644753	0.0126	0.3125
chrMT	16571	705040	42.5466	32.3141
chrX	155270560	1942820	0.0125	0.2987
chrY	59373566	140035	0.0024	0.1119

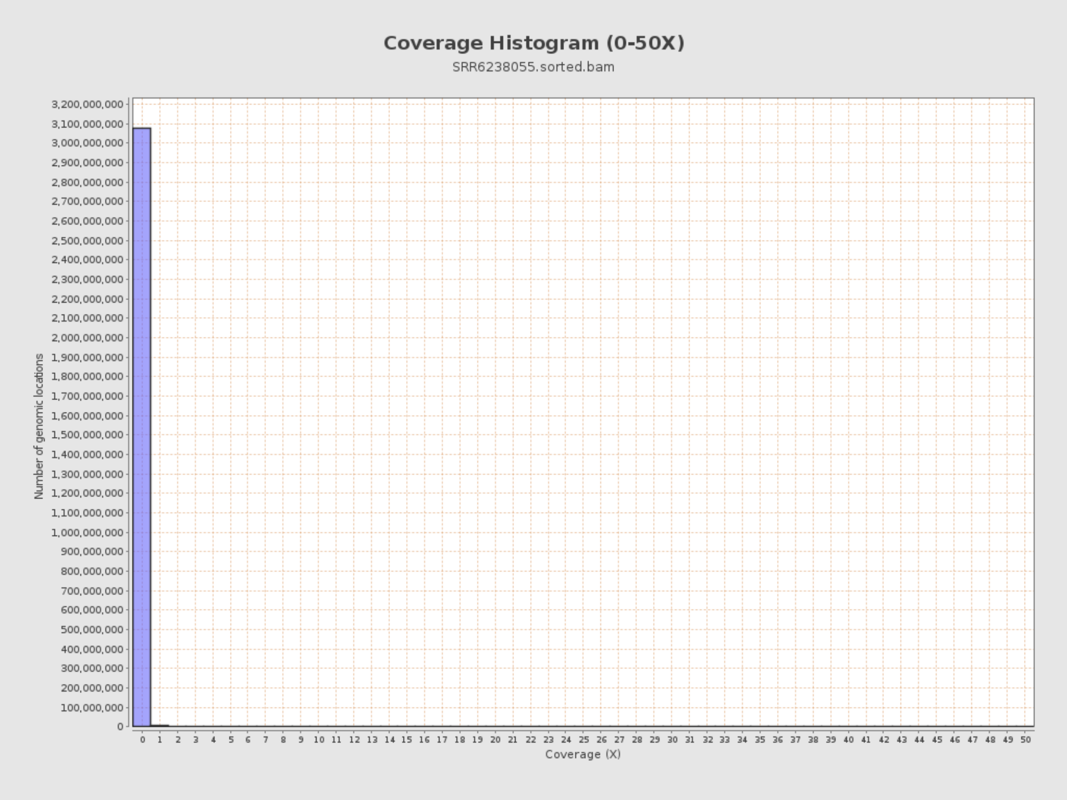
3. Results : Coverage across reference



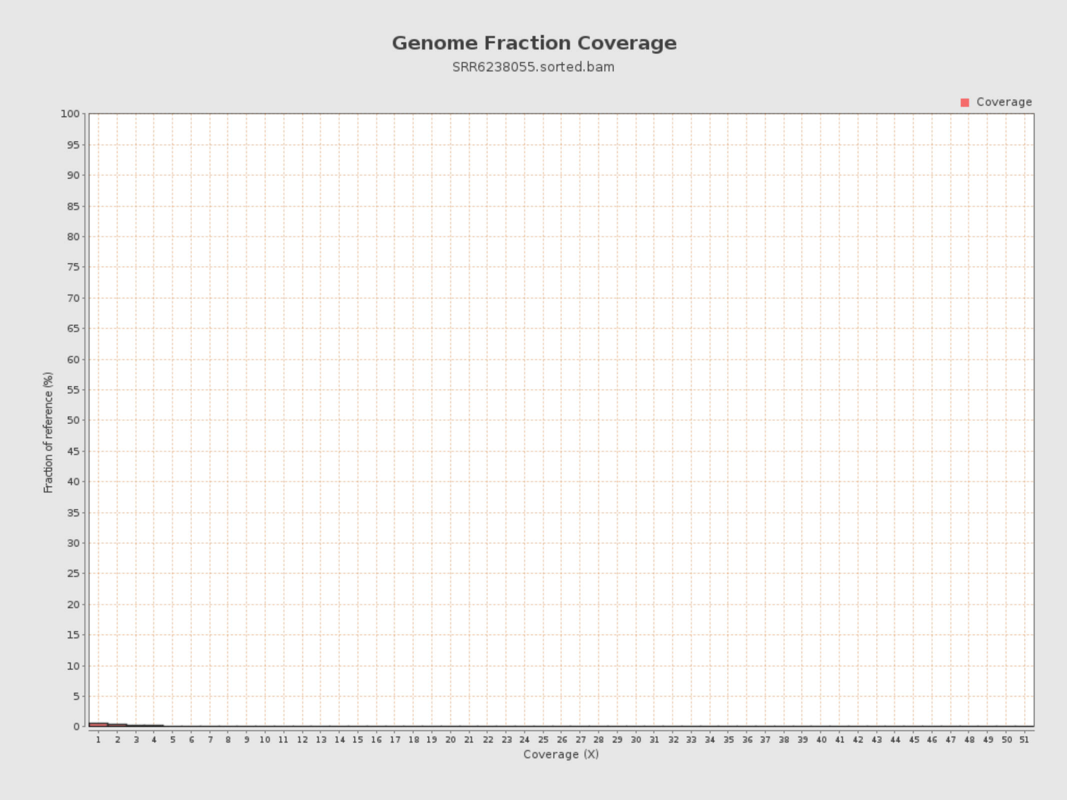
4. Results : Coverage Histogram



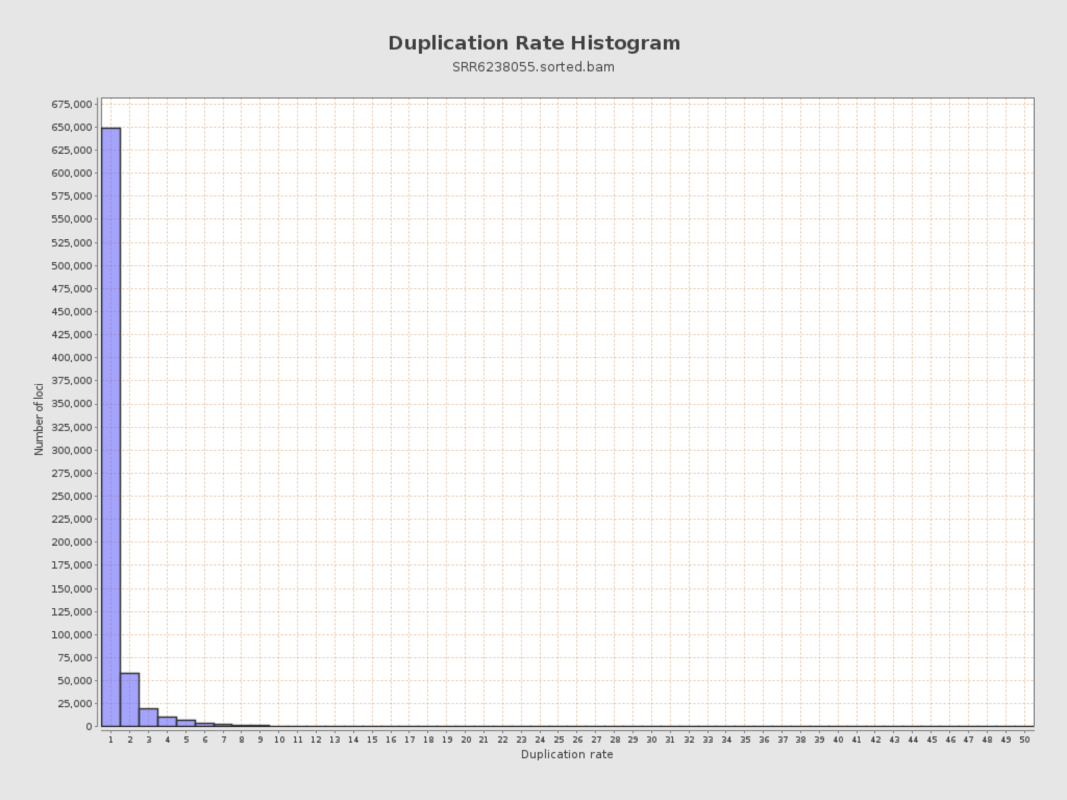
5. Results : Coverage Histogram (0-50X)



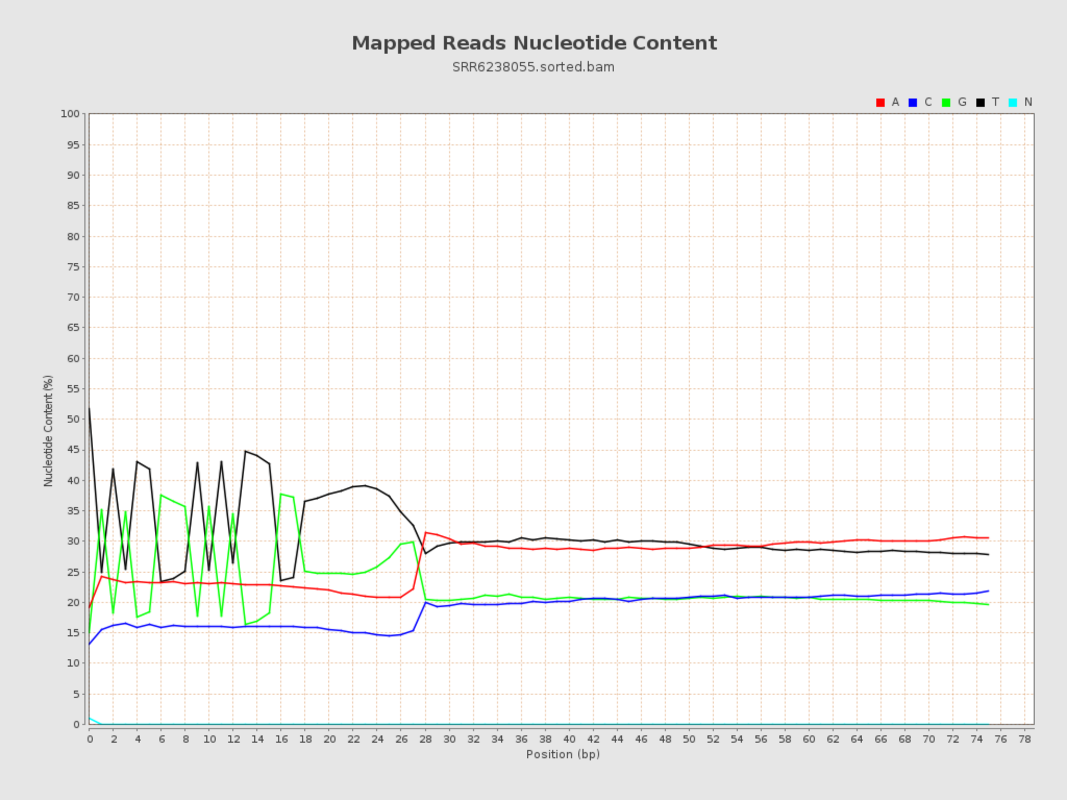
6. Results : Genome Fraction Coverage



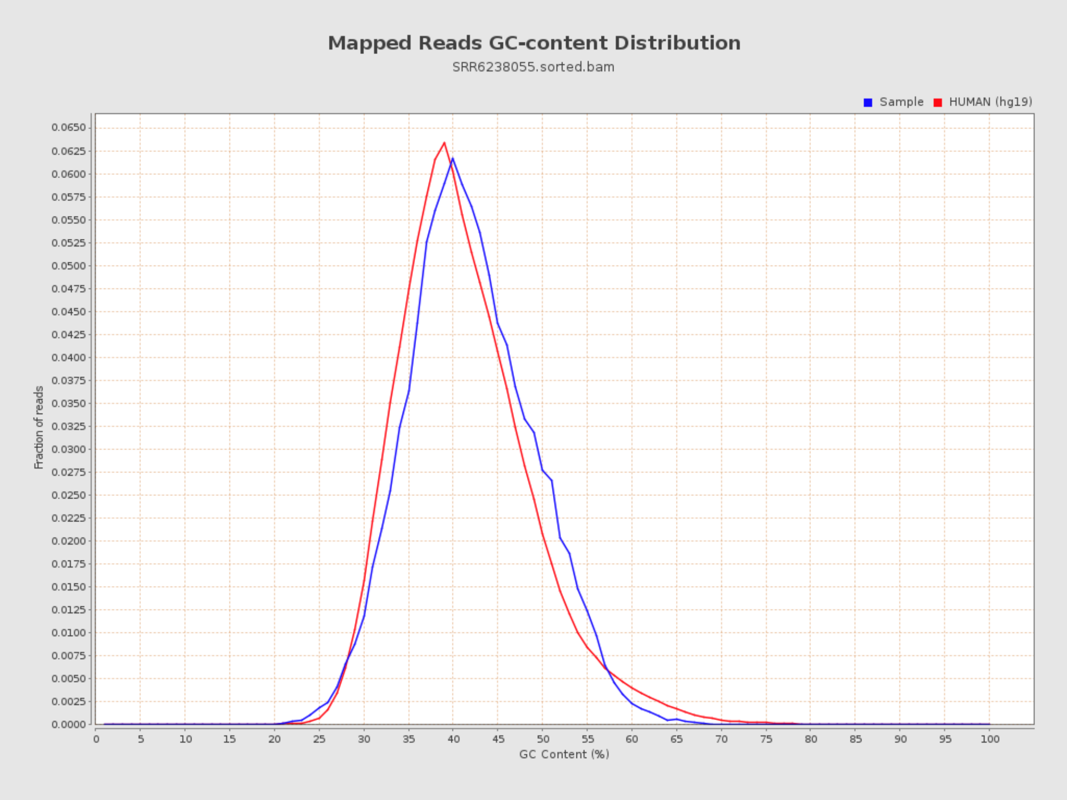
7. Results : Duplication Rate Histogram



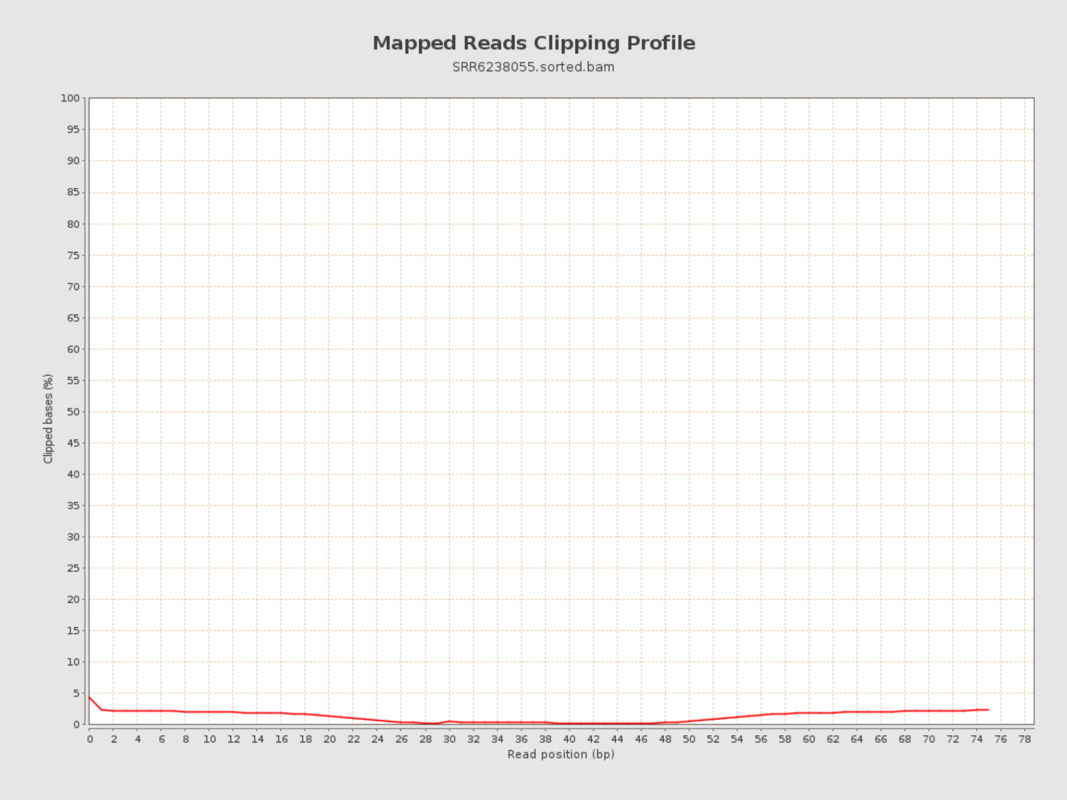
8. Results : Mapped Reads Nucleotide Content



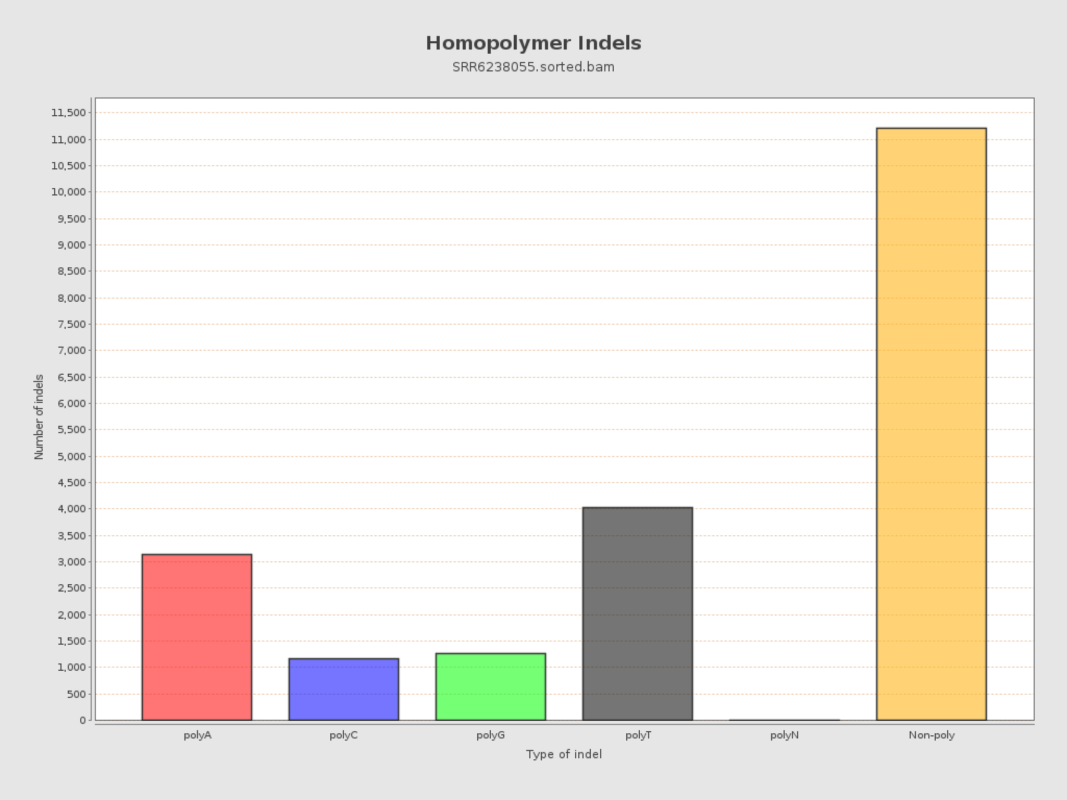
9. Results : Mapped Reads GC-content Distribution



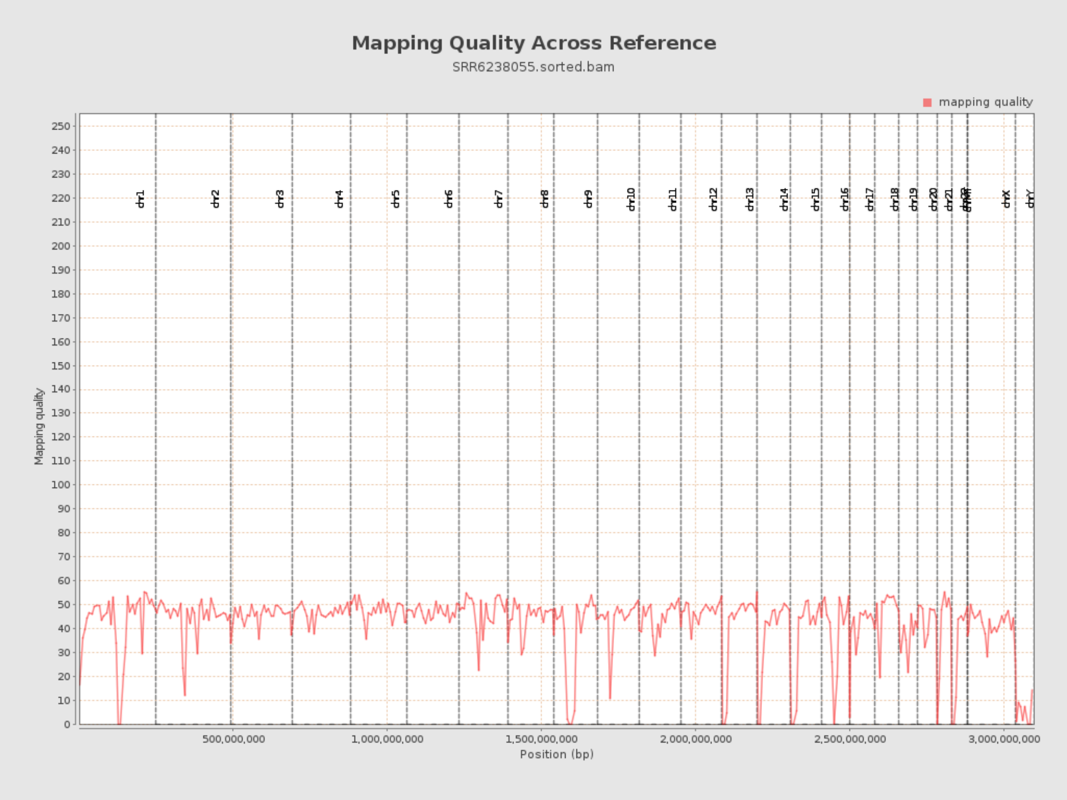
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram