Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 10:14:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238037.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_SRR6238037 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238037.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 10:14:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238037.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,358,933
Mapped reads	1,125,589 / 82.83%
Unmapped reads	233,344 / 17.17%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,551 / 0.63%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	48,881 / 3.6%
Duplication rate	3.49%
Clipped reads	542,696 / 39.94%

2.2. ACGT Content

Number/percentage of A's	19,925,770 / 27.01%
Number/percentage of C's	13,149,076 / 17.83%
Number/percentage of T's	23,865,418 / 32.36%
Number/percentage of G's	16,693,063 / 22.63%
Number/percentage of N's	124,874 / 0.17%
GC Percentage	40.46%

2.3. Coverage

Mean	0.0238

Standard Deviation	0.2643

2.4. Mapping Quality

Mean Mapping Quality	46.49

2.5. Mismatches and indels

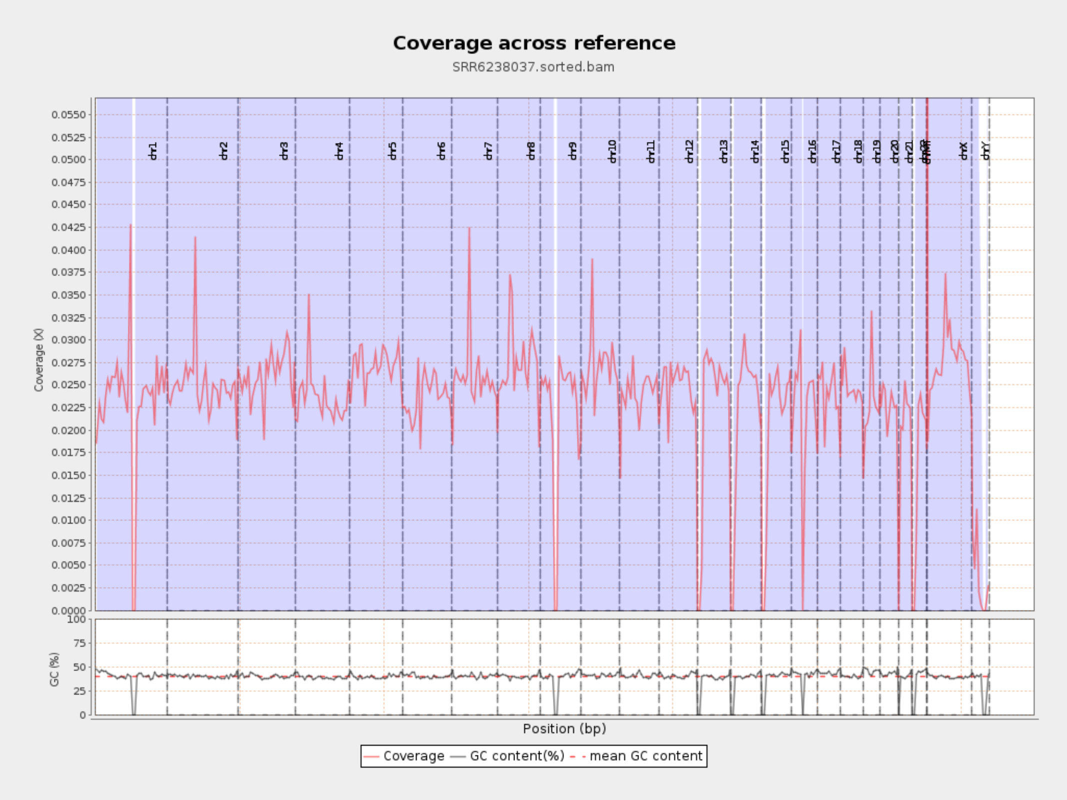
General error rate	0.89%
Mismatches	647,321
Insertions	6,296
Mapped reads with at least one insertion	0.55%
Deletions	25,680
Mapped reads with at least one deletion	2.25%
Homopolymer indels	45%

2.6. Chromosome stats

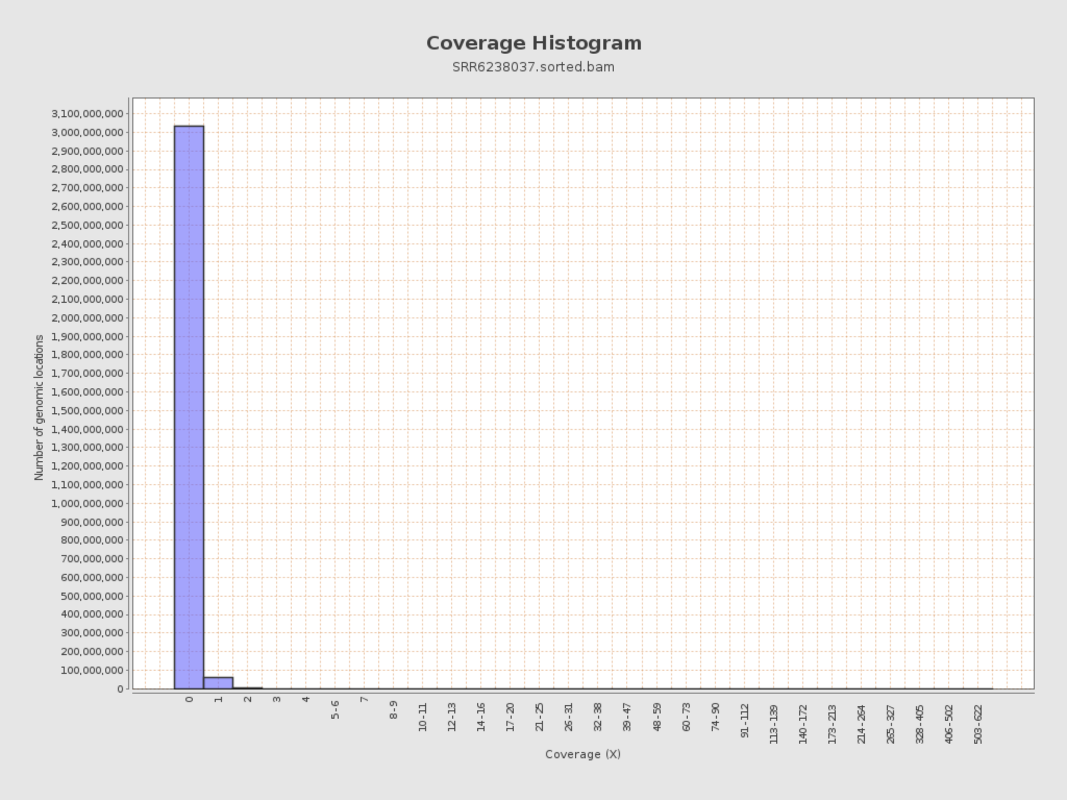
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5773294	0.0232	0.4775
chr2	243199373	6081649	0.025	0.3273
chr3	198022430	5159837	0.0261	0.1791
chr4	191154276	4506937	0.0236	0.1811
chr5	180915260	4928737	0.0272	0.1837
chr6	171115067	4054402	0.0237	0.1955
chr7	159138663	4138678	0.026	0.3193

chr8	146364022	4016942	0.0274	0.4326
chr9	141213431	3092191	0.0219	0.2149
chr10	135534747	3659589	0.027	0.2325
chr11	135006516	3264967	0.0242	0.207
chr12	133851895	3325817	0.0248	0.1773
chr13	115169878	2524537	0.0219	0.1656
chr14	107349540	2317922	0.0216	0.1673
chr15	102531392	2044604	0.0199	0.1559
chr16	90354753	1955629	0.0216	0.1748
chr17	81195210	1950051	0.024	0.1825
chr18	78077248	1936638	0.0248	0.3613
chr19	59128983	1370418	0.0232	0.3114
chr20	63025520	1412879	0.0224	0.1708
chr21	48129895	953546	0.0198	0.1654
chr22	51304566	795962	0.0155	0.1374
chrMT	16571	10956	0.6612	0.8569
chrX	155270560	4314951	0.0278	0.1956
chrY	59373566	210263	0.0035	0.0933

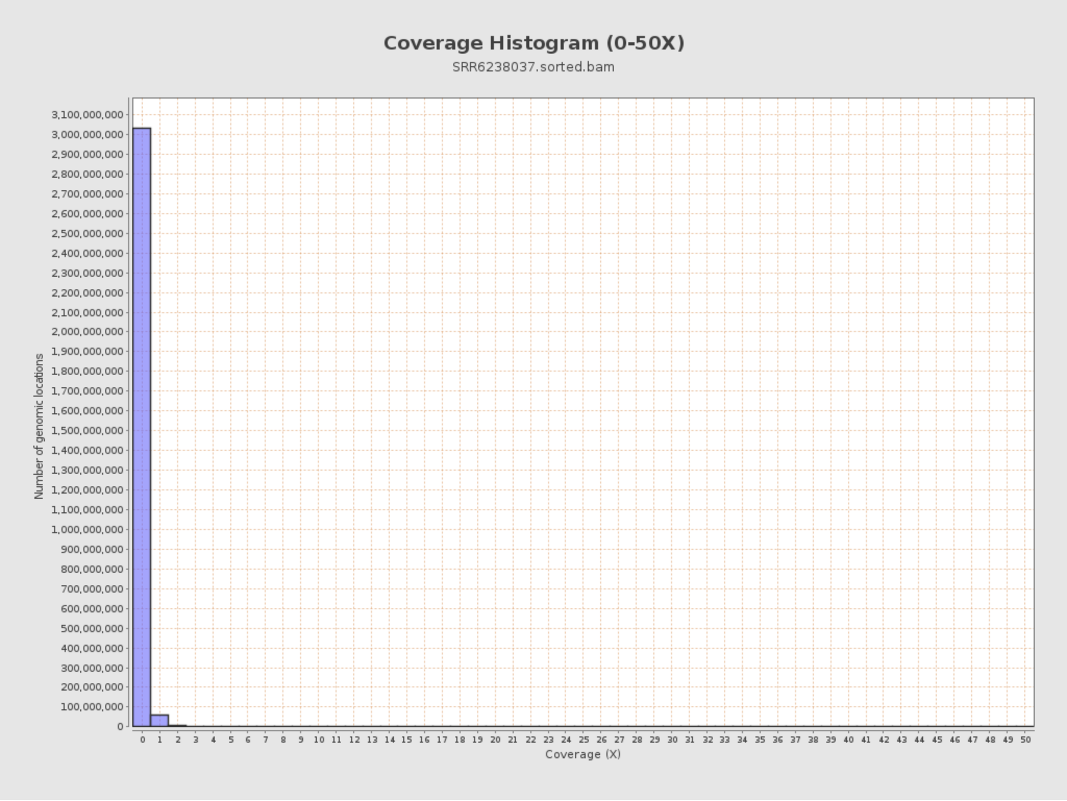
3. Results : Coverage across reference



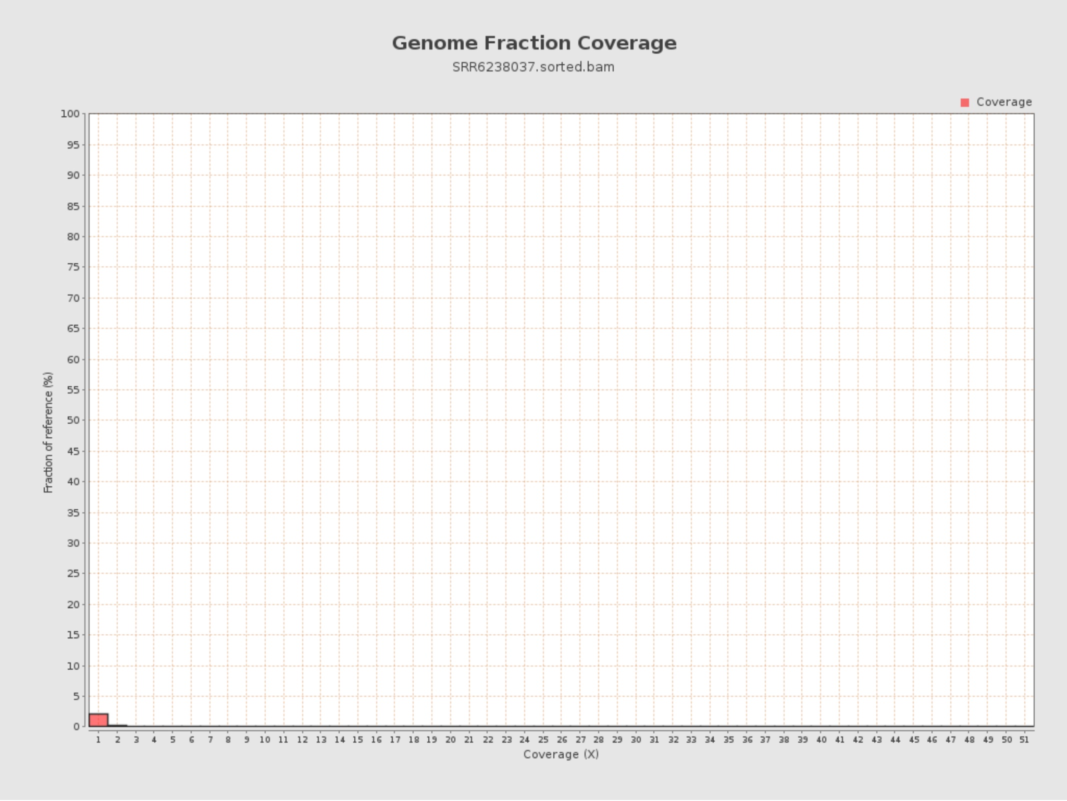
4. Results : Coverage Histogram



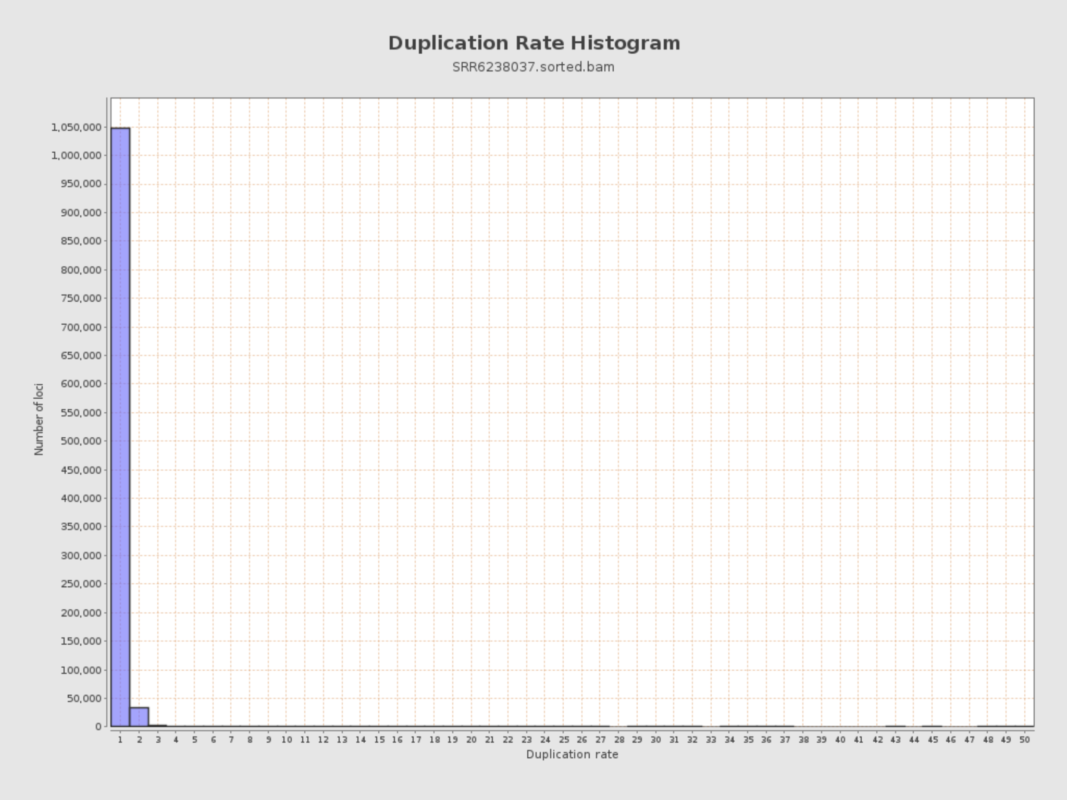
5. Results : Coverage Histogram (0-50X)



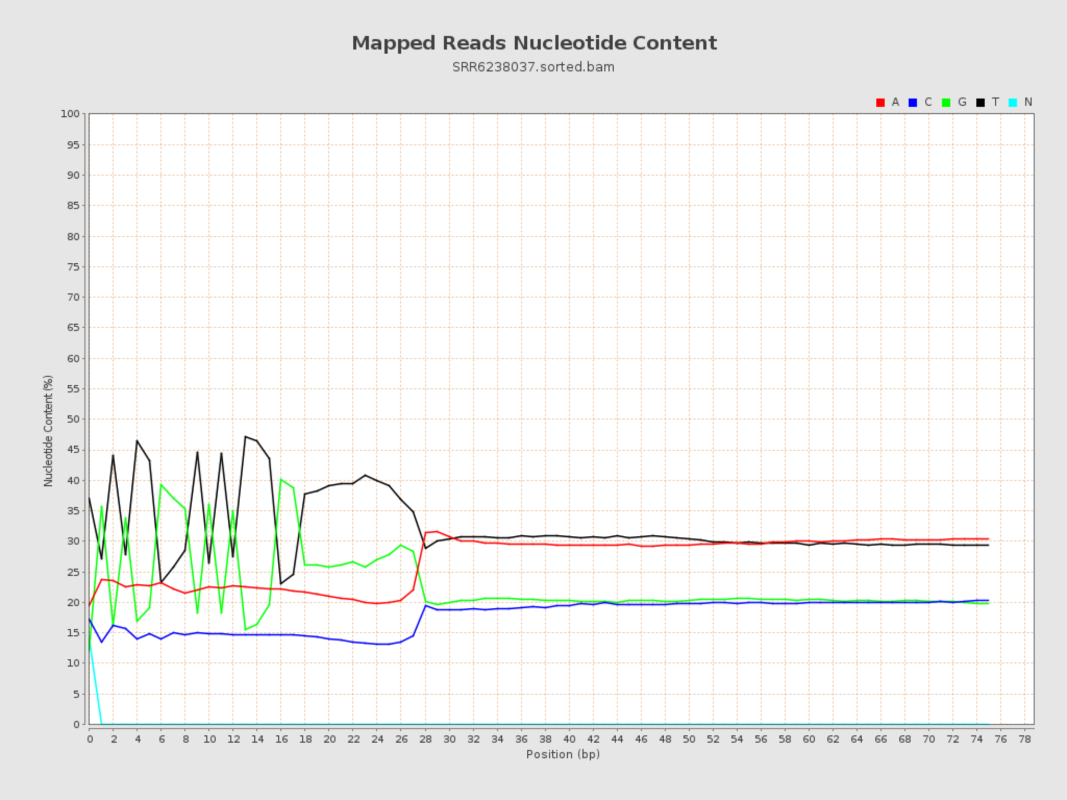
6. Results : Genome Fraction Coverage



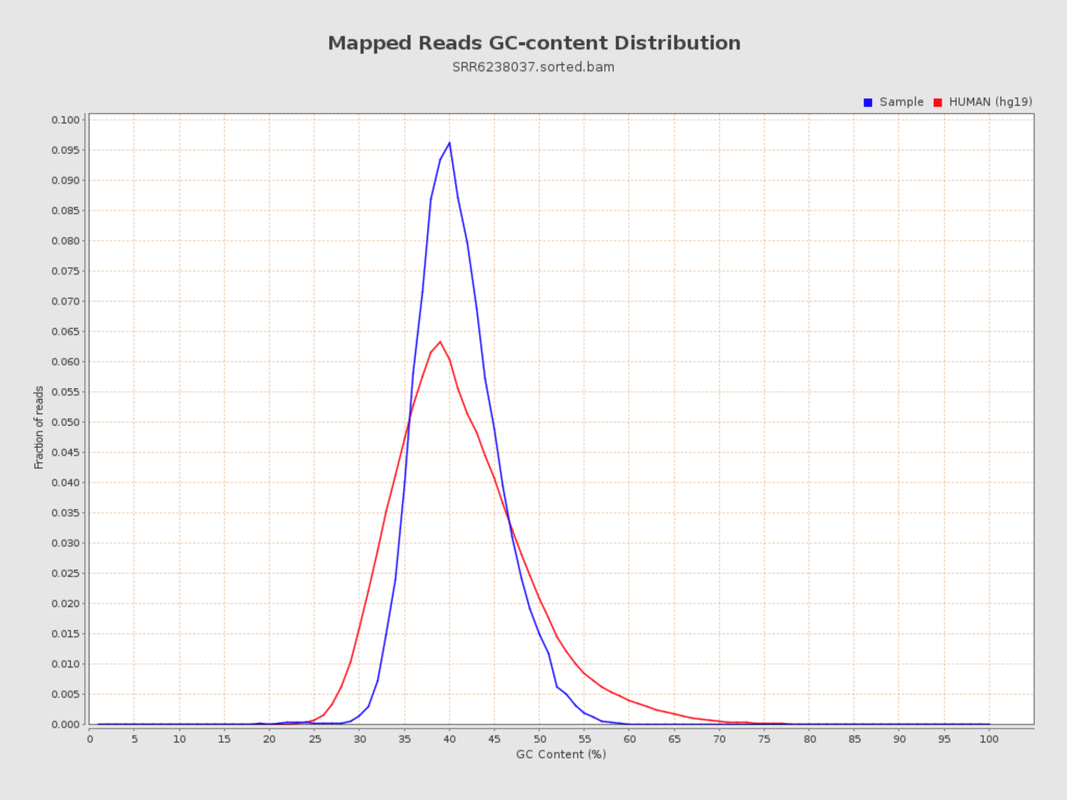
7. Results : Duplication Rate Histogram



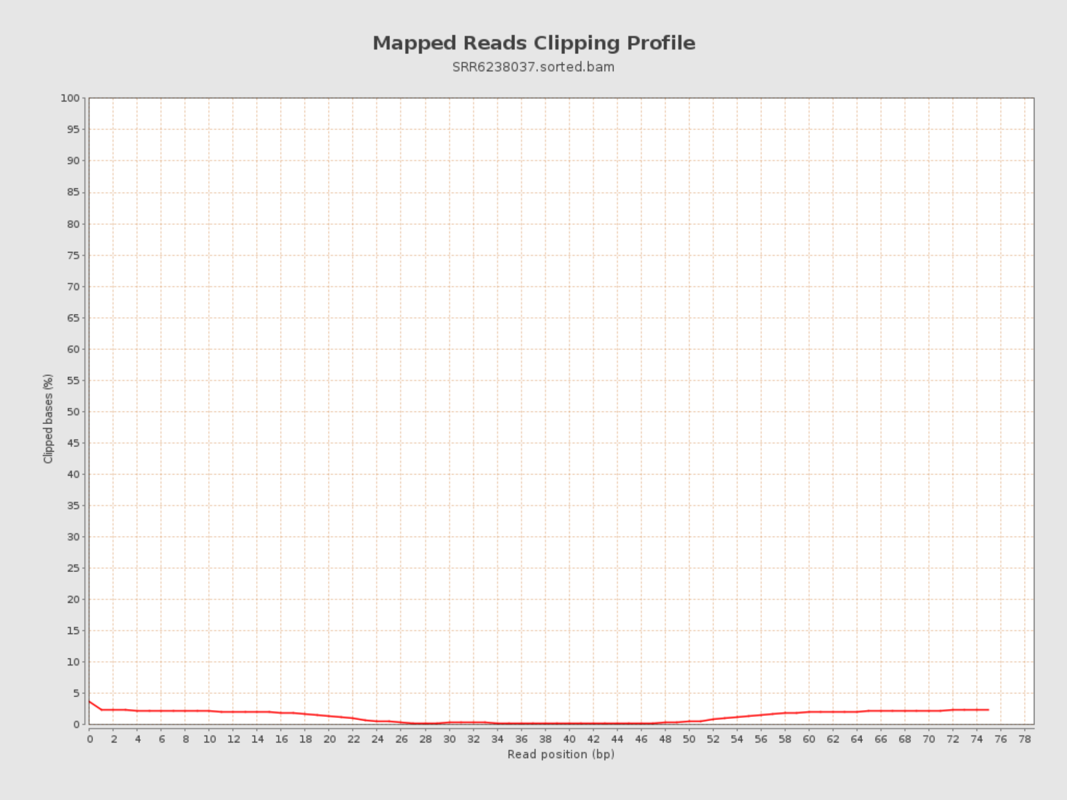
8. Results : Mapped Reads Nucleotide Content



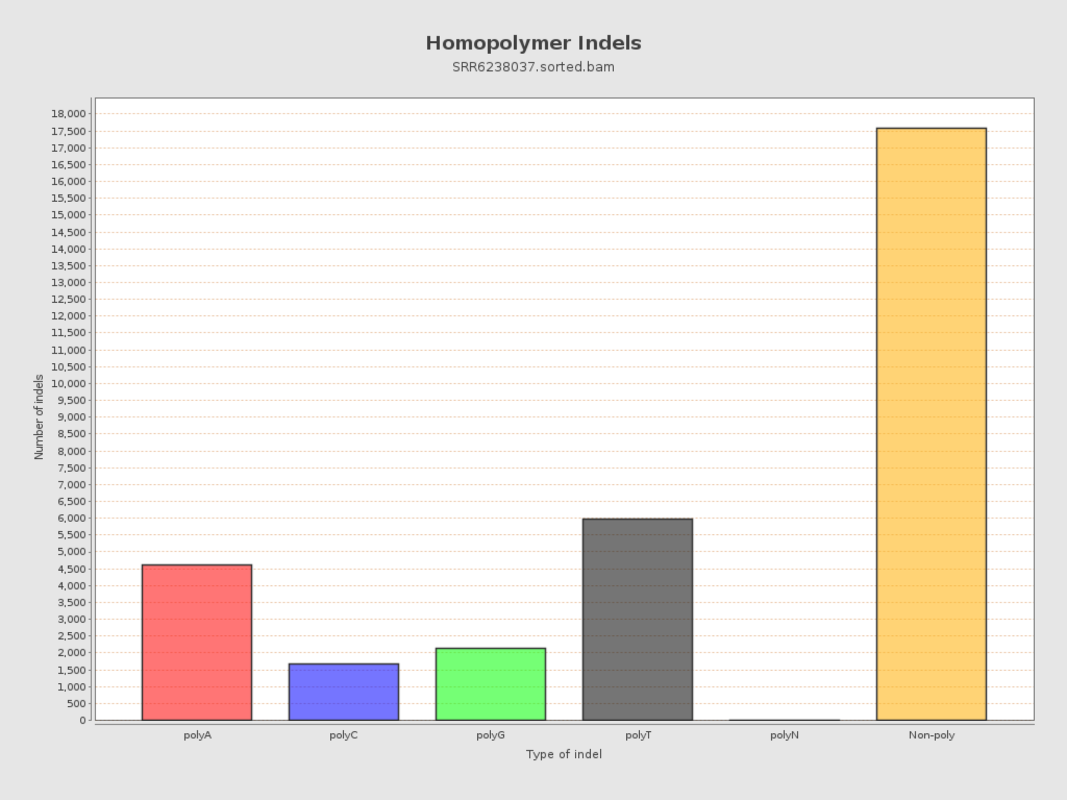
9. Results : Mapped Reads GC-content Distribution



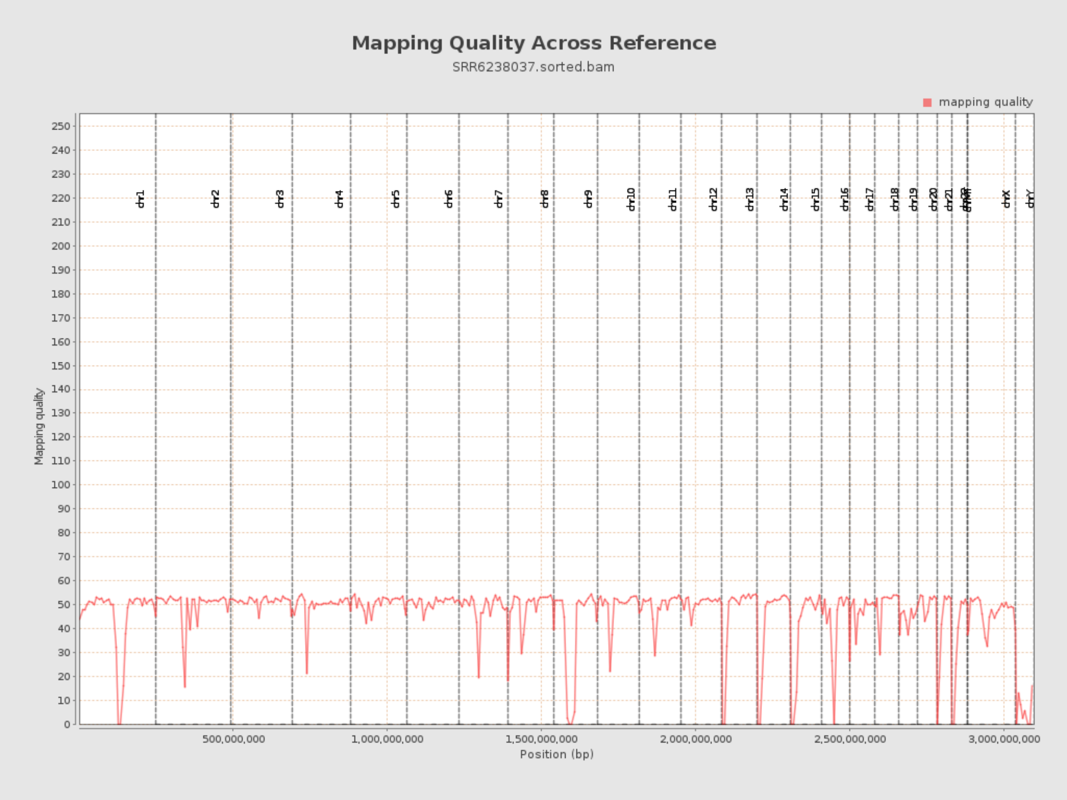
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram