Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 11:30:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238064.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_SRR6238064 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238064.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 11:30:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238064.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,601,886
Mapped reads	1,332,413 / 83.18%
Unmapped reads	269,473 / 16.82%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,287 / 0.77%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	62,281 / 3.89%
Duplication rate	3.67%
Clipped reads	702,554 / 43.86%

2.2. ACGT Content

Number/percentage of A's	22,875,480 / 26.62%
Number/percentage of C's	16,223,878 / 18.88%
Number/percentage of T's	26,908,339 / 31.31%
Number/percentage of G's	19,919,666 / 23.18%
Number/percentage of N's	11,891 / 0.01%
GC Percentage	42.06%

2.3. Coverage

Mean	0.0278

Standard Deviation	0.2947

2.4. Mapping Quality

Mean Mapping Quality	45.09

2.5. Mismatches and indels

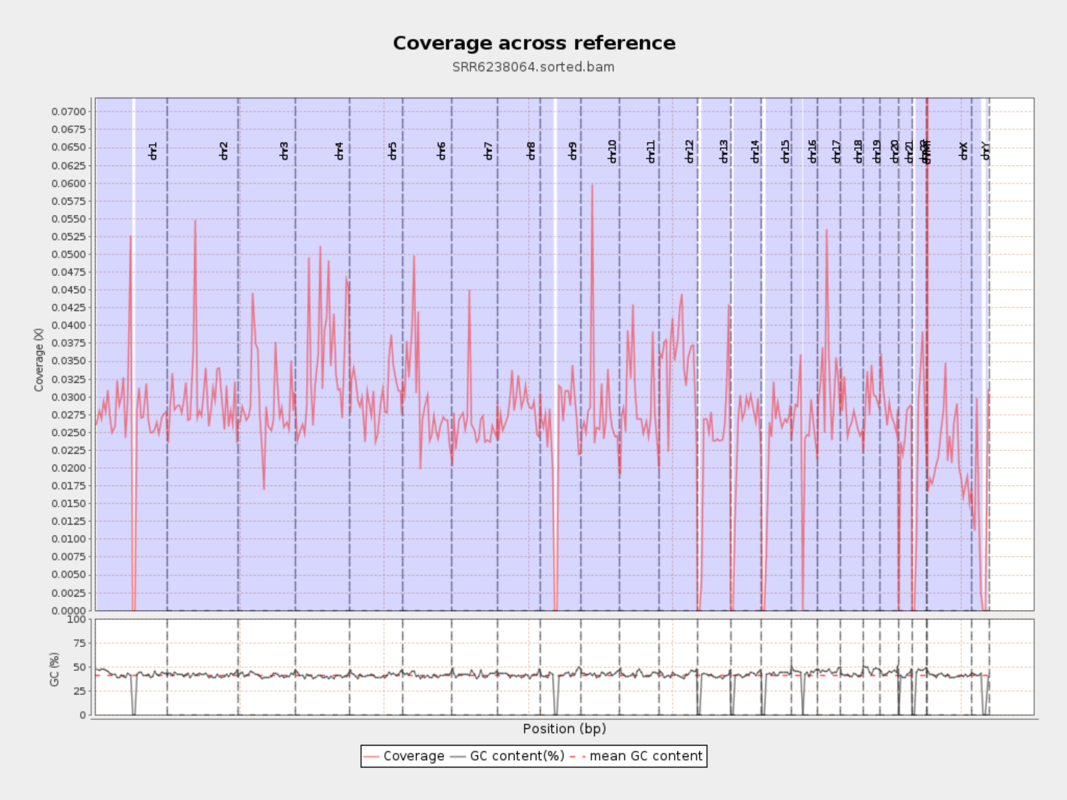
General error rate	0.83%
Mismatches	702,991
Insertions	6,462
Mapped reads with at least one insertion	0.48%
Deletions	23,853
Mapped reads with at least one deletion	1.77%
Homopolymer indels	45.5%

2.6. Chromosome stats

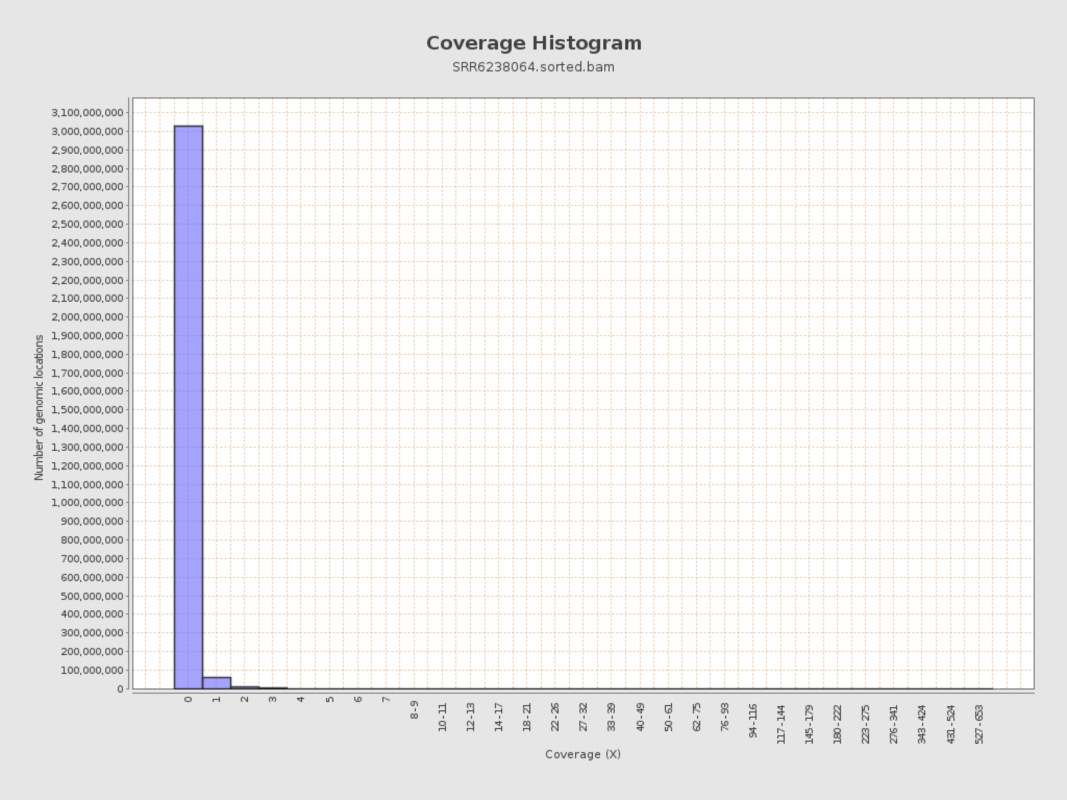
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6686111	0.0268	0.5368
chr2	243199373	7312242	0.0301	0.3488
chr3	198022430	5723251	0.0289	0.2007
chr4	191154276	6657328	0.0348	0.2451
chr5	180915260	5464692	0.0302	0.206
chr6	171115067	5064723	0.0296	0.2495
chr7	159138663	4192891	0.0263	0.3278

chr8	146364022	4157832	0.0284	0.2557
chr9	141213431	3493801	0.0247	0.2397
chr10	135534747	3836246	0.0283	0.3177
chr11	135006516	3946101	0.0292	0.2832
chr12	133851895	4780403	0.0357	0.2246
chr13	115169878	2613133	0.0227	0.1776
chr14	107349540	2515260	0.0234	0.1902
chr15	102531392	2257111	0.022	0.1744
chr16	90354753	2231967	0.0247	0.2059
chr17	81195210	2688372	0.0331	0.2336
chr18	78077248	2119985	0.0272	0.3709
chr19	59128983	1772025	0.03	0.3679
chr20	63025520	1793817	0.0285	0.2074
chr21	48129895	1122088	0.0233	0.205
chr22	51304566	1093564	0.0213	0.1802
chrMT	16571	372458	22.4765	12.7485
chrX	155270560	3336534	0.0215	0.1896
chrY	59373566	750114	0.0126	0.2178

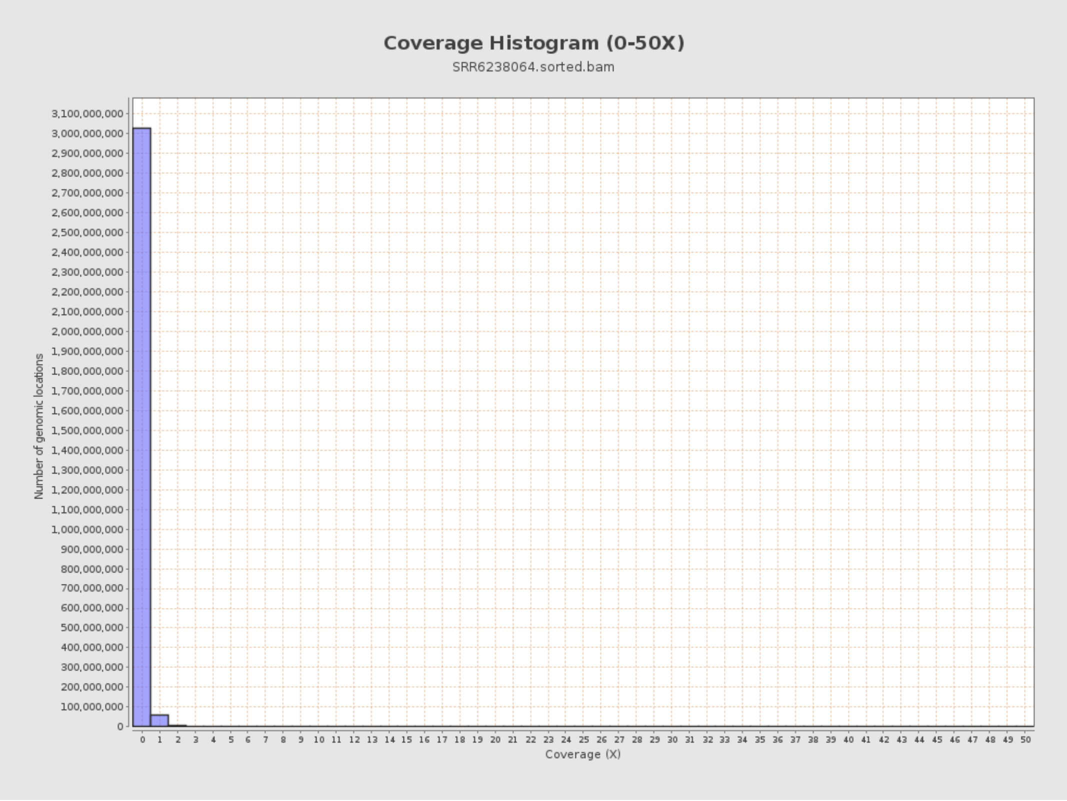
3. Results : Coverage across reference



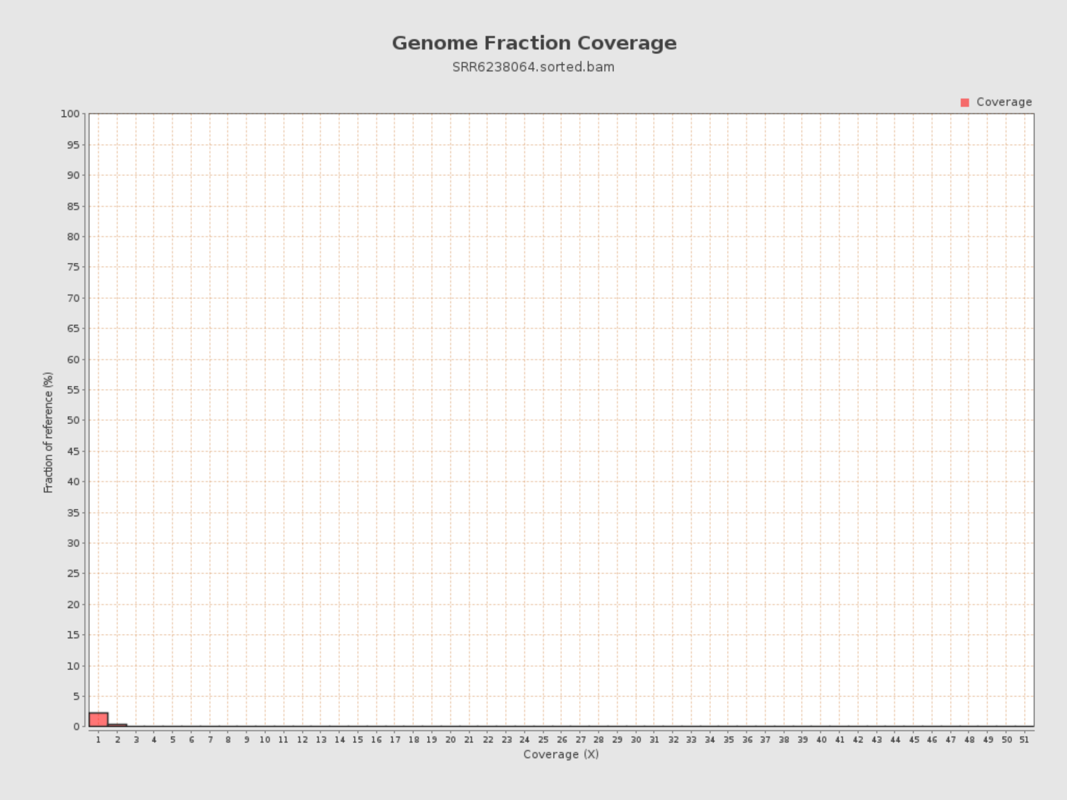
4. Results : Coverage Histogram



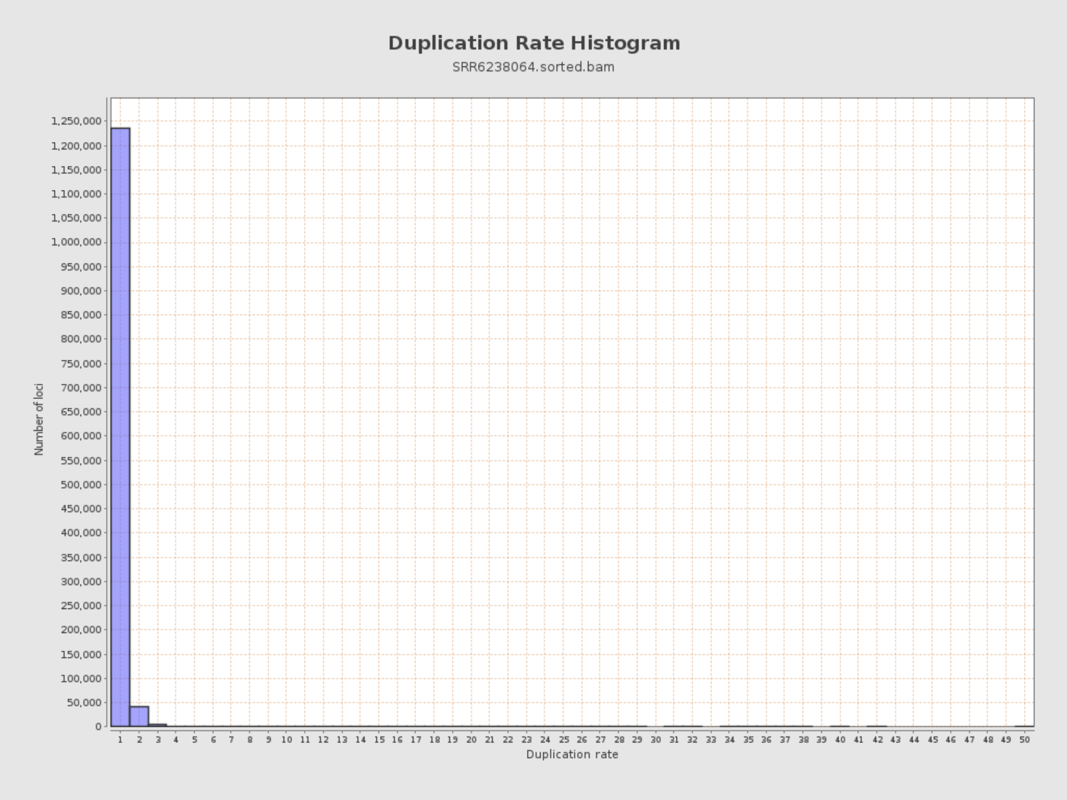
5. Results : Coverage Histogram (0-50X)



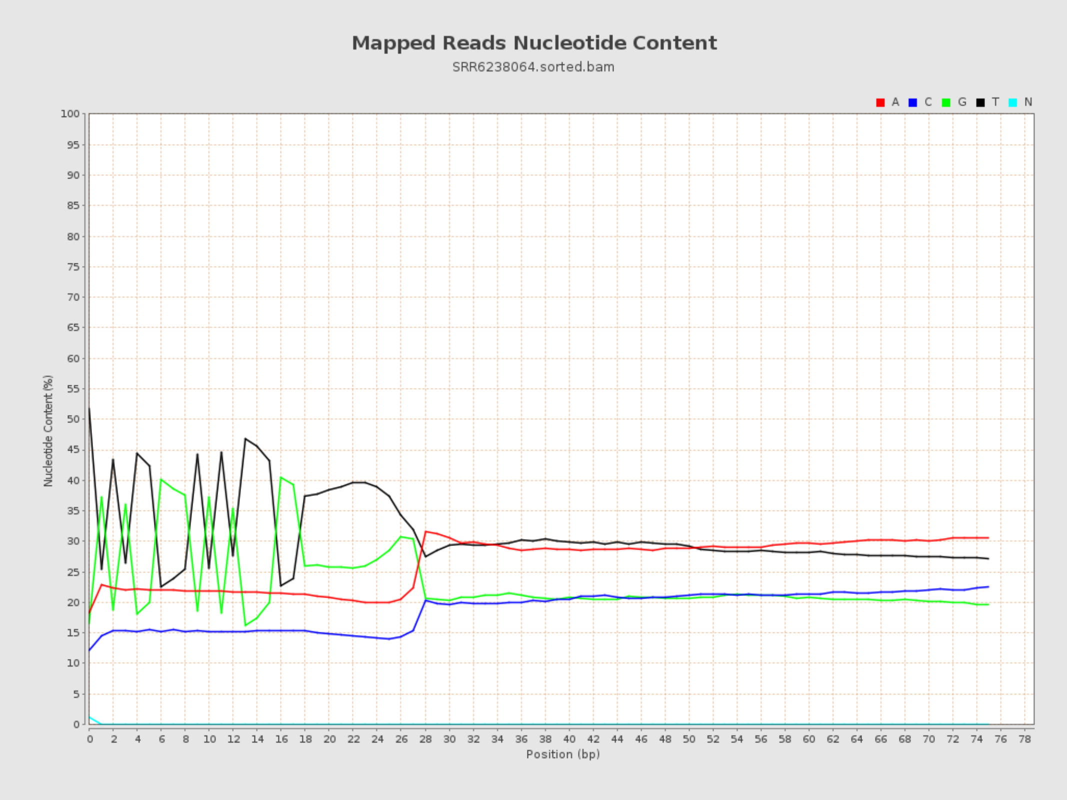
6. Results : Genome Fraction Coverage



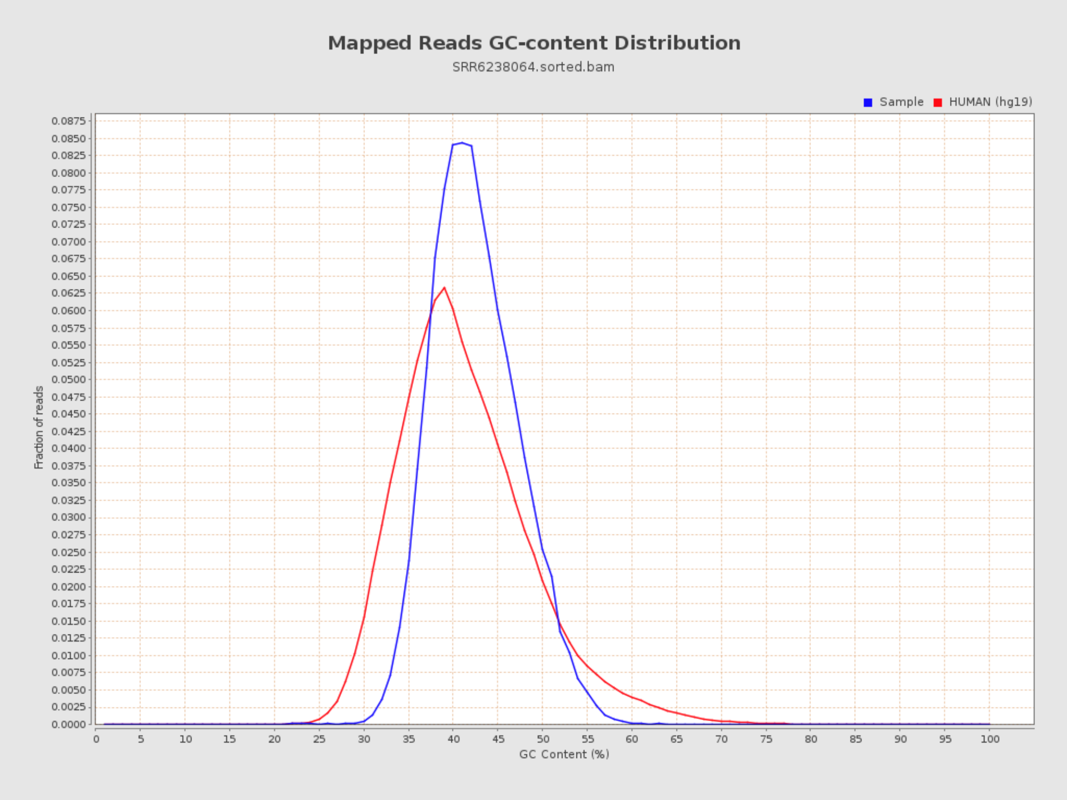
7. Results : Duplication Rate Histogram



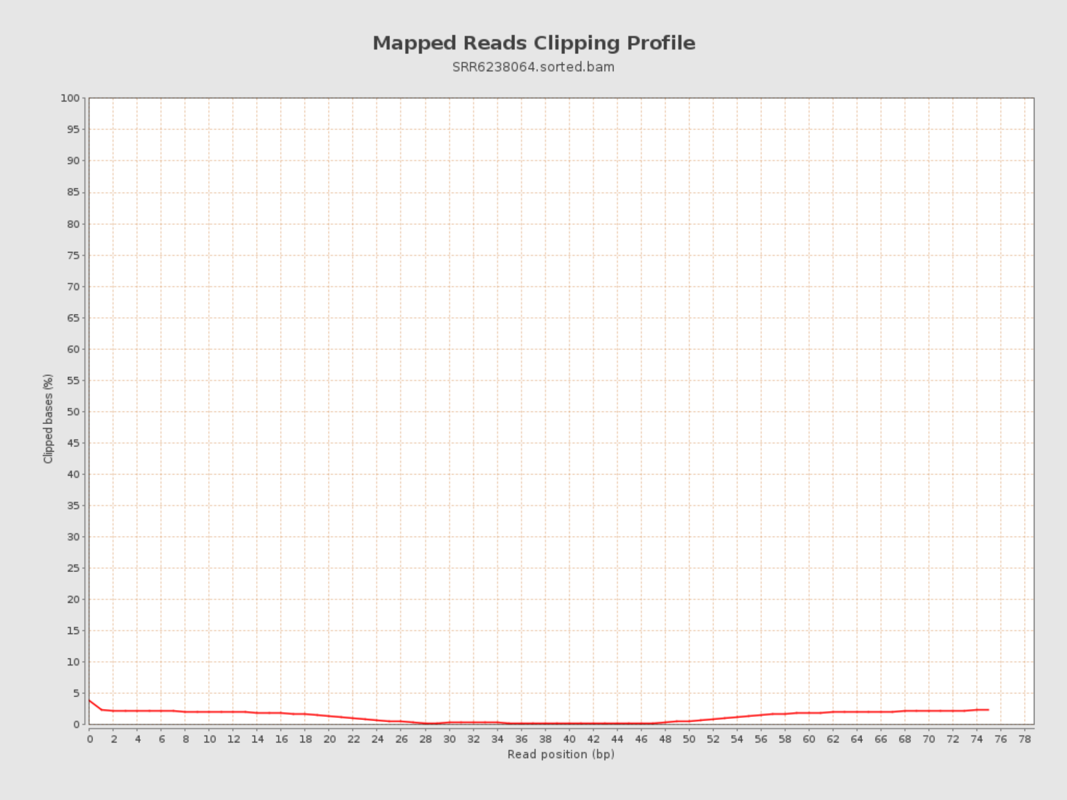
8. Results : Mapped Reads Nucleotide Content



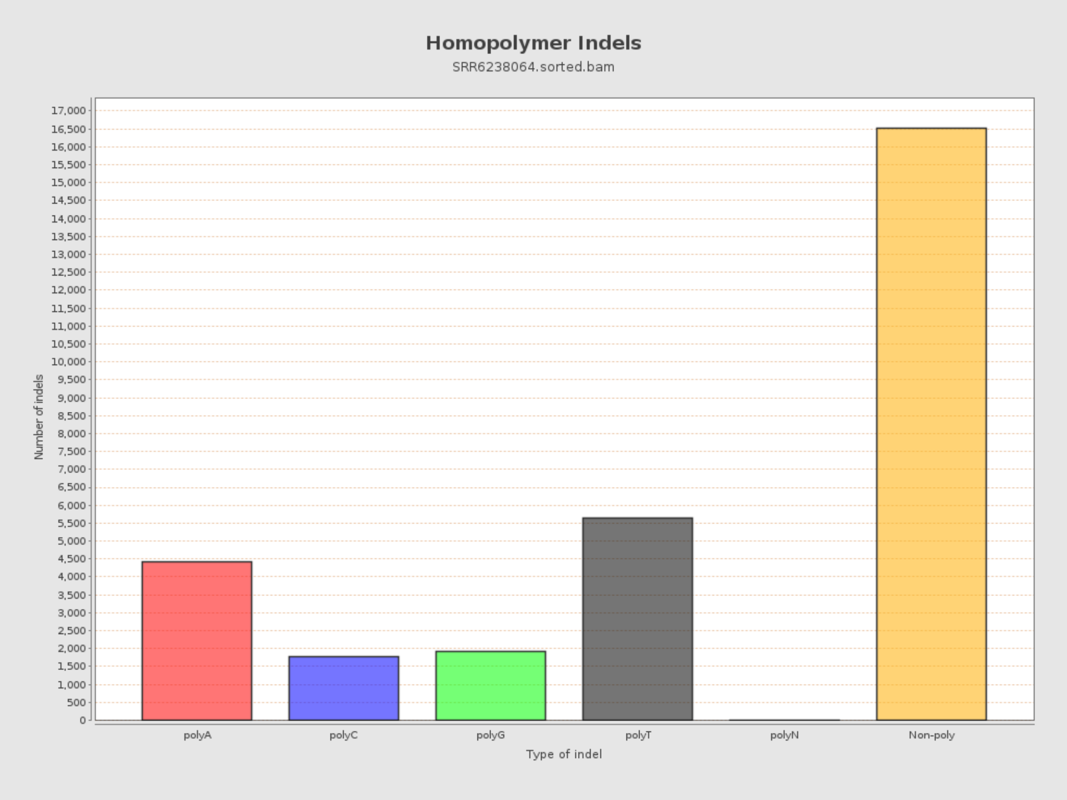
9. Results : Mapped Reads GC-content Distribution



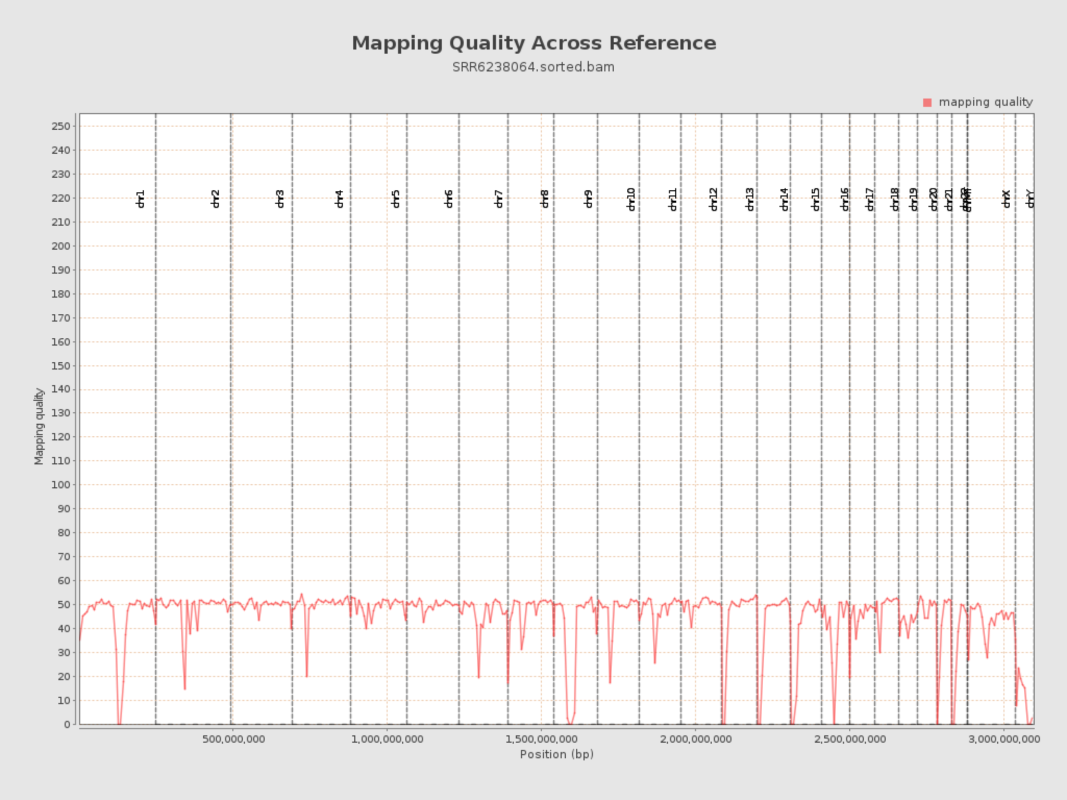
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram