Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 11:01:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238054.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_SRR6238054 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238054.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 11:01:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238054.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,970,622
Mapped reads	1,772,443 / 89.94%
Unmapped reads	198,179 / 10.06%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,743 / 0.95%
Read min/max/mean length	30 / 76 / 76.33
Duplicated reads (estimated)	76,360 / 3.87%
Duplication rate	3.46%
Clipped reads	771,860 / 39.17%

2.2. ACGT Content

Number/percentage of A's	32,169,036 / 27.19%
Number/percentage of C's	22,772,520 / 19.25%
Number/percentage of T's	36,572,795 / 30.91%
Number/percentage of G's	26,771,943 / 22.63%
Number/percentage of N's	15,999 / 0.01%
GC Percentage	41.88%

2.3. Coverage

Mean	0.0382

Standard Deviation	0.3217

2.4. Mapping Quality

Mean Mapping Quality	43.51

2.5. Mismatches and indels

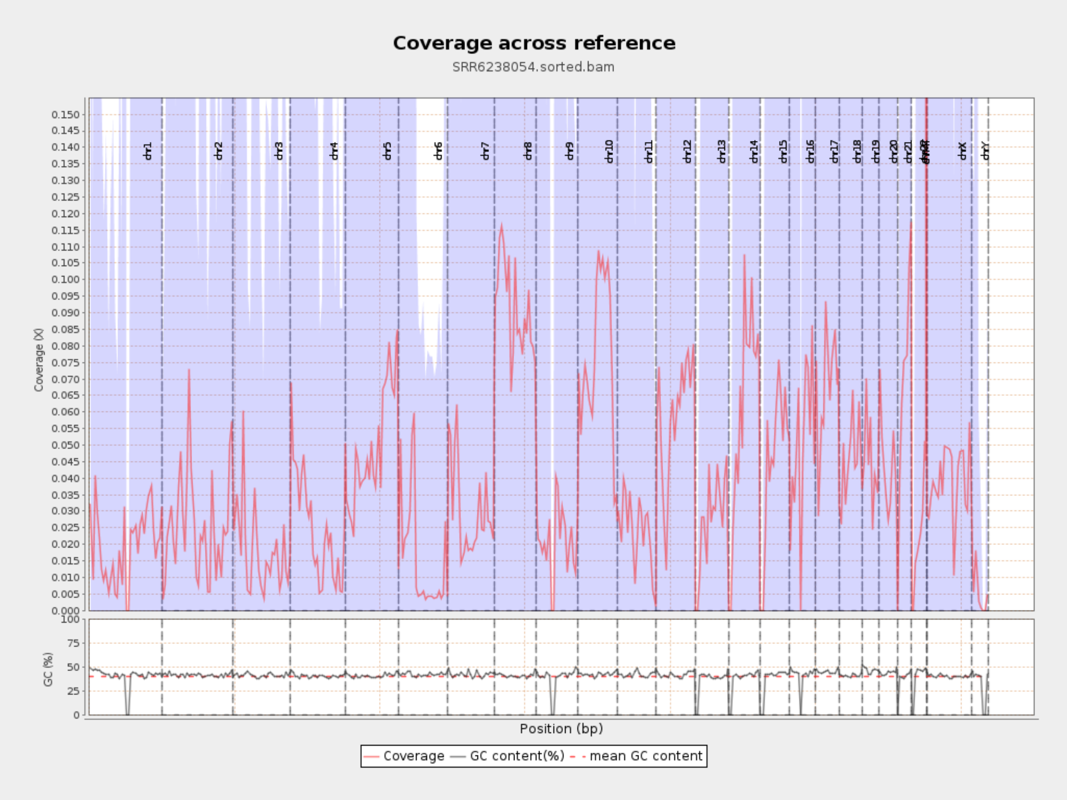
General error rate	0.78%
Mismatches	907,802
Insertions	8,247
Mapped reads with at least one insertion	0.46%
Deletions	33,182
Mapped reads with at least one deletion	1.85%
Homopolymer indels	45.7%

2.6. Chromosome stats

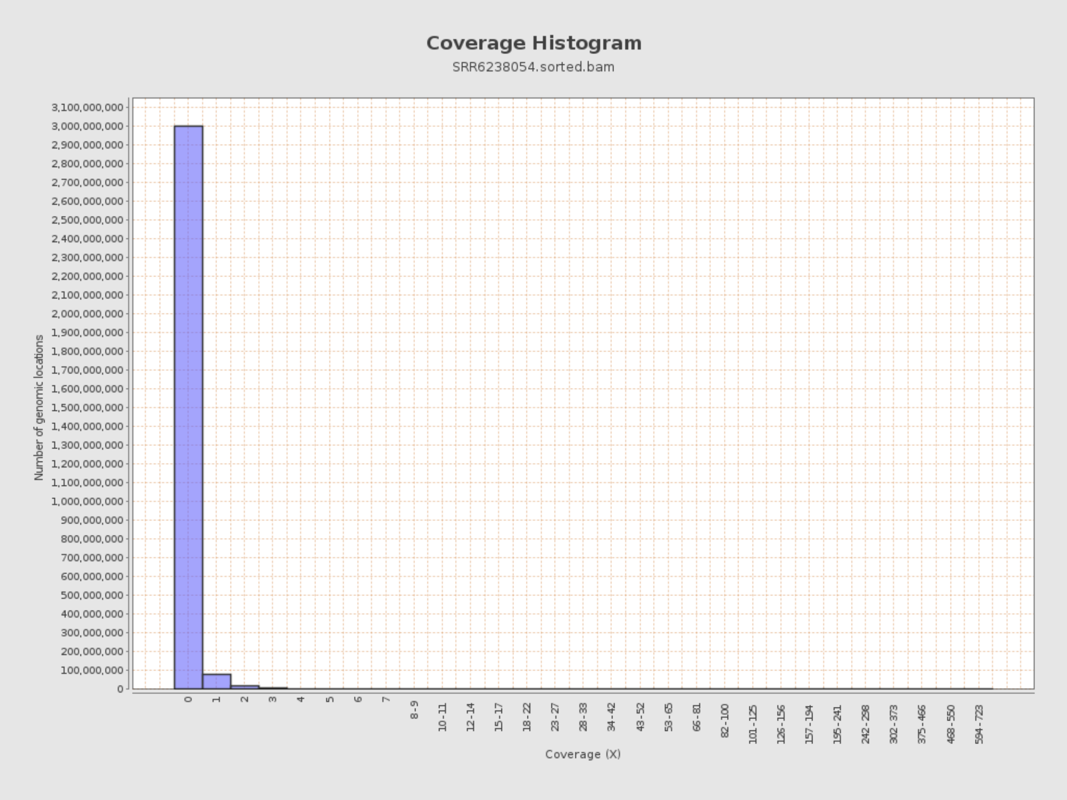
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4826089	0.0194	0.4432
chr2	243199373	6227065	0.0256	0.3449
chr3	198022430	3704445	0.0187	0.16
chr4	191154276	4740016	0.0248	0.1979
chr5	180915260	8998439	0.0497	0.2662
chr6	171115067	2740595	0.016	0.209
chr7	159138663	4805290	0.0302	0.231

chr8	146364022	13400019	0.0916	0.5865
chr9	141213431	2855344	0.0202	0.2428
chr10	135534747	10568620	0.078	0.3772
chr11	135006516	3262567	0.0242	0.2641
chr12	133851895	7906660	0.0591	0.2905
chr13	115169878	3149207	0.0273	0.1941
chr14	107349540	6535889	0.0609	0.3004
chr15	102531392	4657519	0.0454	0.2536
chr16	90354753	4515398	0.05	0.2985
chr17	81195210	5571563	0.0686	0.4116
chr18	78077248	3575928	0.0458	0.5753
chr19	59128983	2690255	0.0455	0.4135
chr20	63025520	2709876	0.043	0.2535
chr21	48129895	3356461	0.0697	0.3259
chr22	51304566	1146842	0.0224	0.1769
chrMT	16571	59891	3.6142	2.9701
chrX	155270560	6042722	0.0389	0.2548
chrY	59373566	314394	0.0053	0.1532

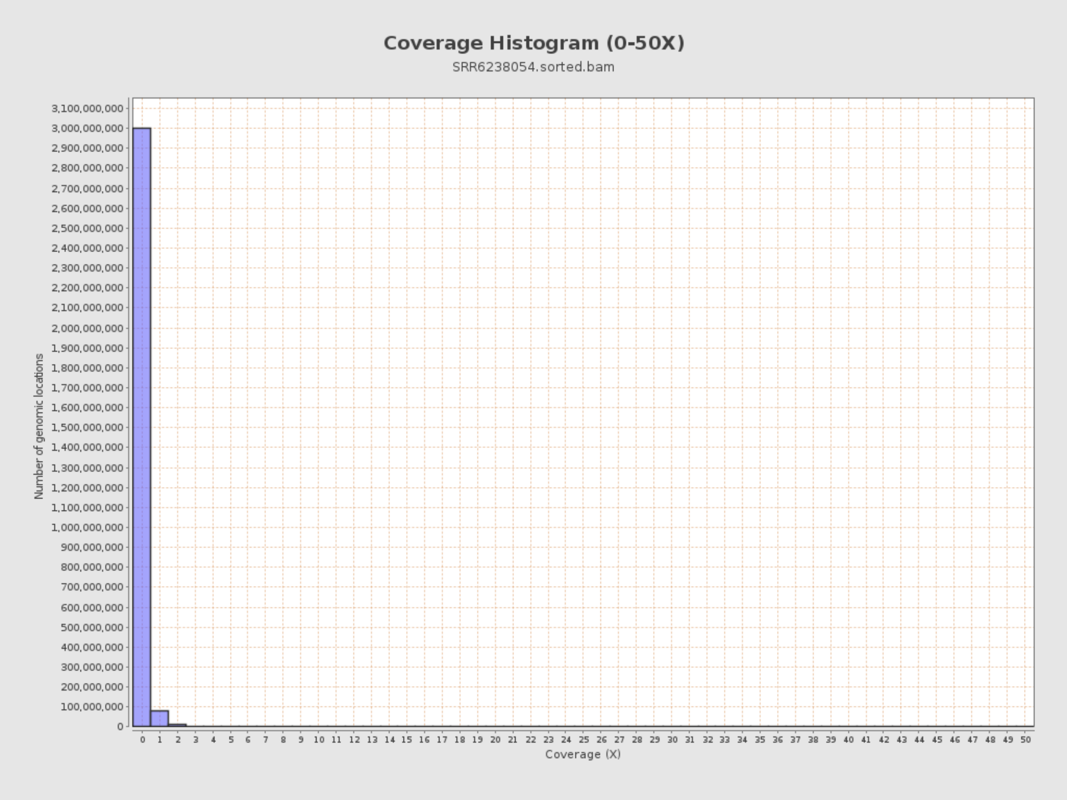
3. Results : Coverage across reference



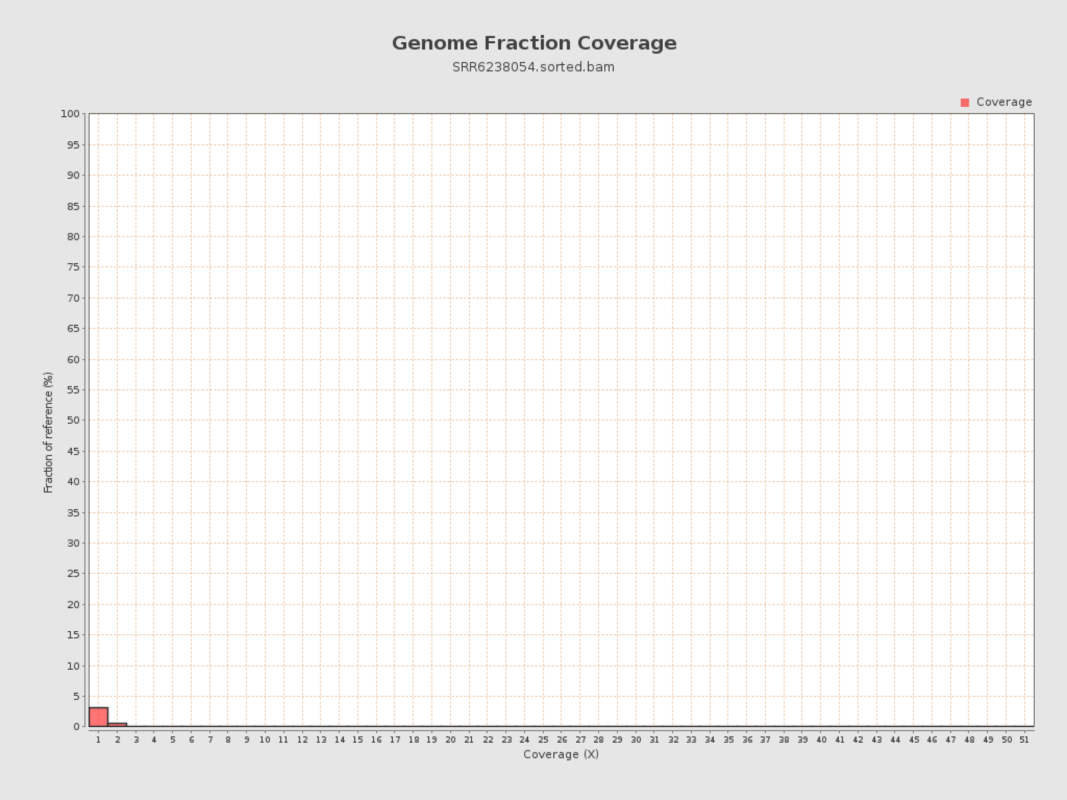
4. Results : Coverage Histogram



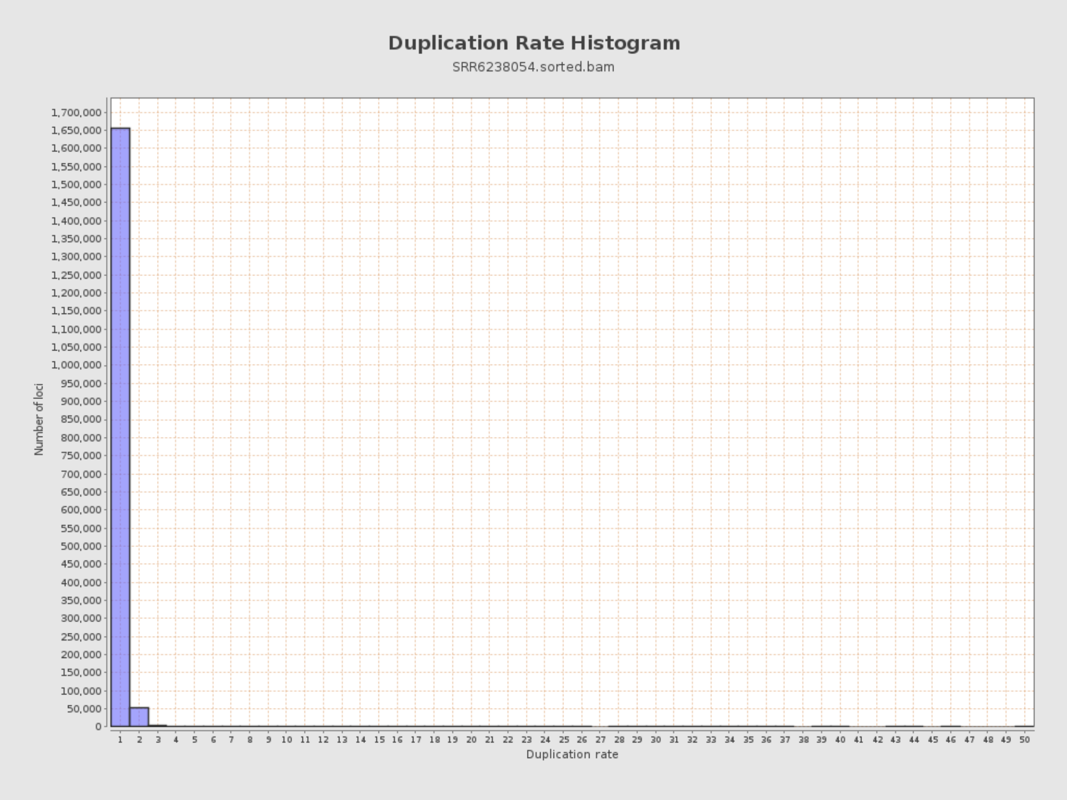
5. Results : Coverage Histogram (0-50X)



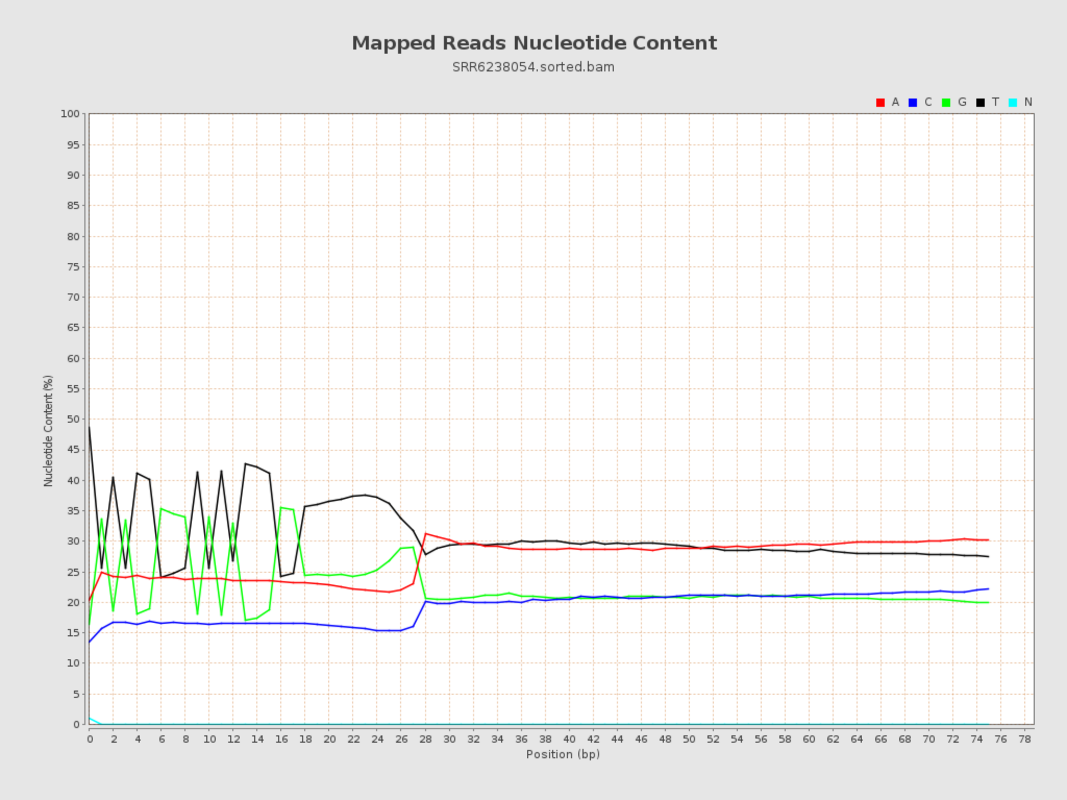
6. Results : Genome Fraction Coverage



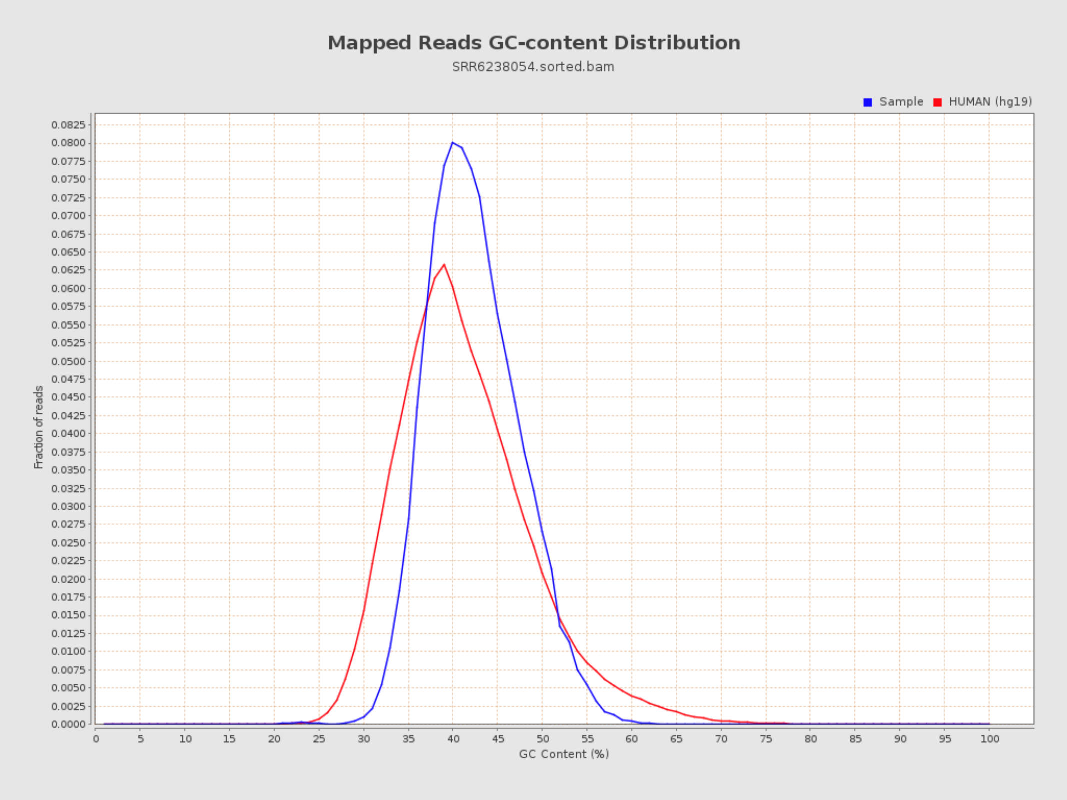
7. Results : Duplication Rate Histogram



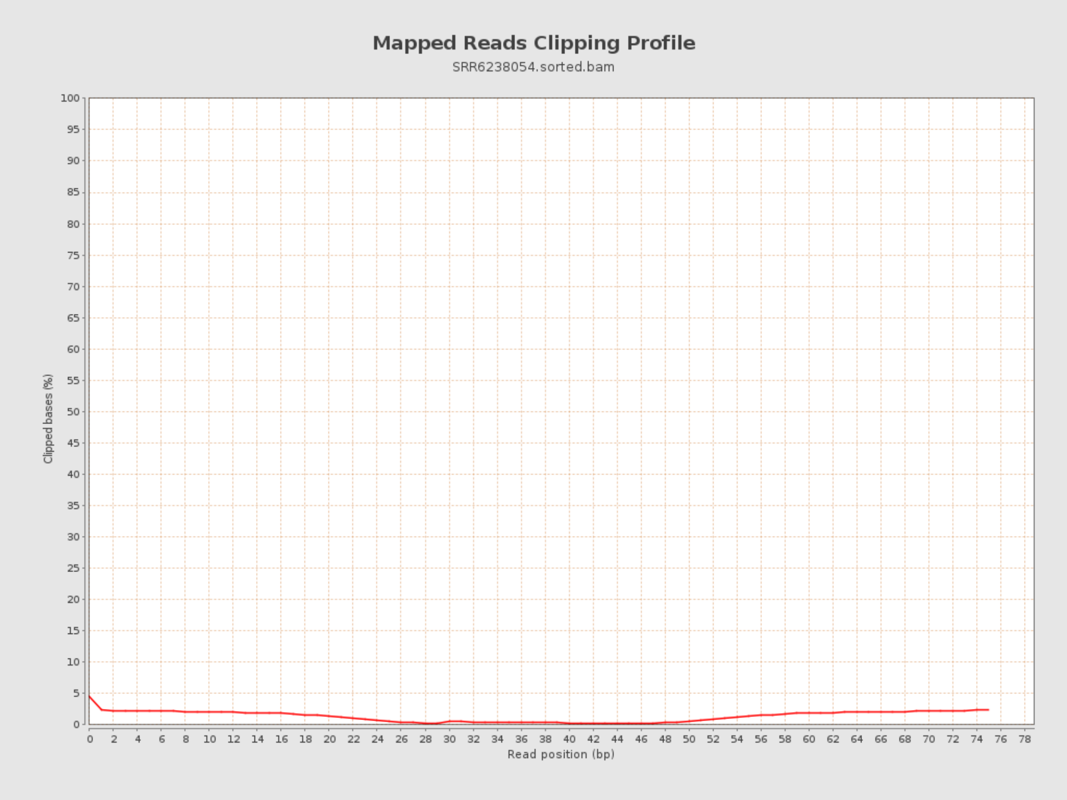
8. Results : Mapped Reads Nucleotide Content



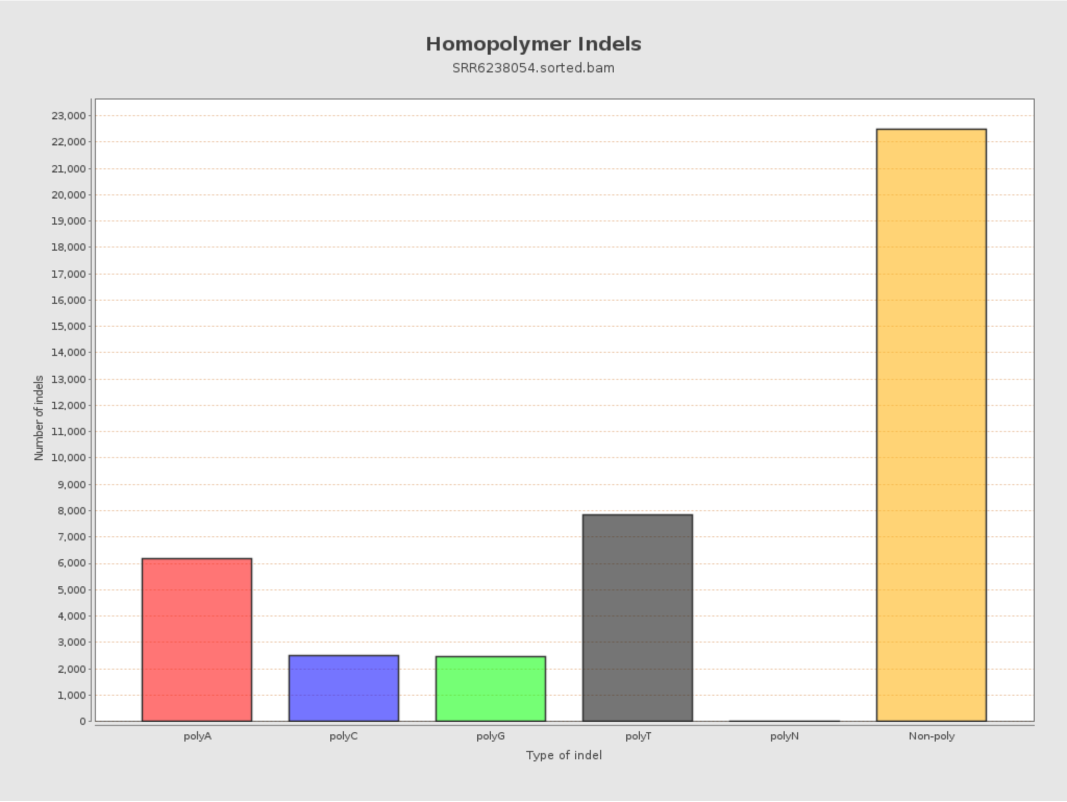
9. Results : Mapped Reads GC-content Distribution



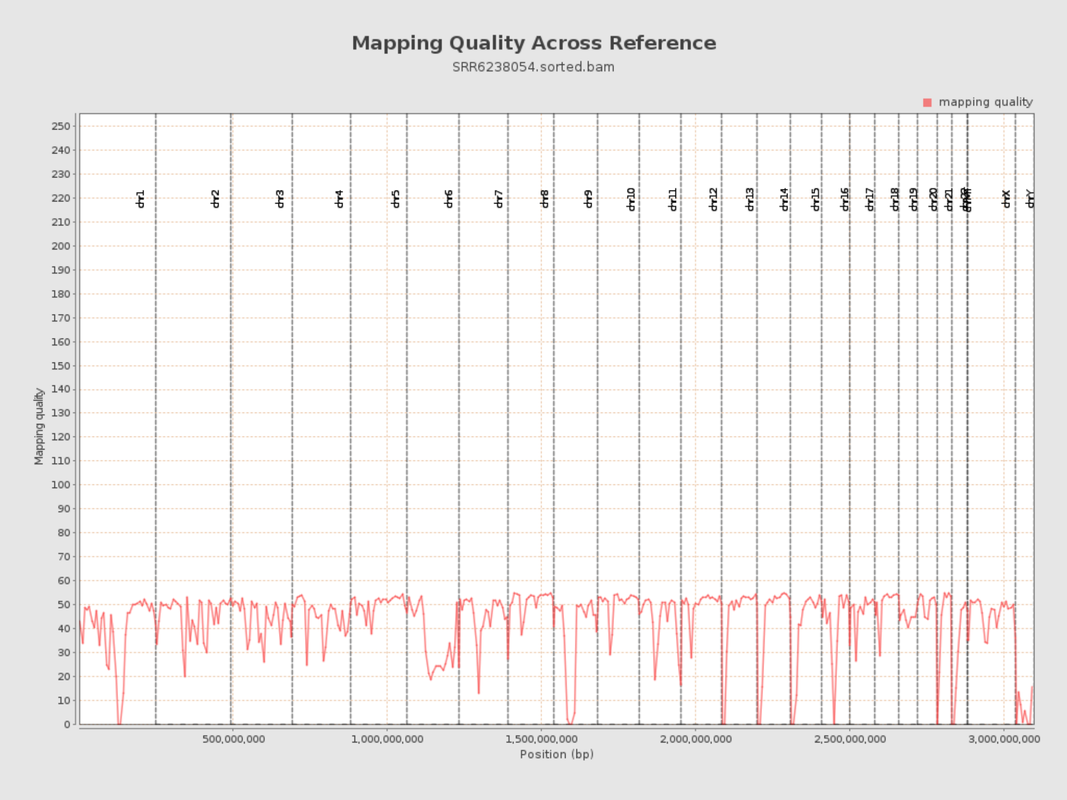
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram