Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 16:35:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238323.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_SRR6238323 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238323.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 16:35:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238323.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,777,068
Mapped reads	1,335,833 / 75.17%
Unmapped reads	441,235 / 24.83%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,037 / 1.07%
Read min/max/mean length	30 / 76 / 76.37
Duplicated reads (estimated)	148,379 / 8.35%
Duplication rate	8.79%
Clipped reads	739,436 / 41.61%

2.2. ACGT Content

Number/percentage of A's	23,802,453 / 27.58%
Number/percentage of C's	16,285,875 / 18.87%
Number/percentage of T's	26,976,424 / 31.26%
Number/percentage of G's	19,210,271 / 22.26%
Number/percentage of N's	20,962 / 0.02%
GC Percentage	41.13%

2.3. Coverage

Mean	0.0279

Standard Deviation	0.3143

2.4. Mapping Quality

Mean Mapping Quality	45.18

2.5. Mismatches and indels

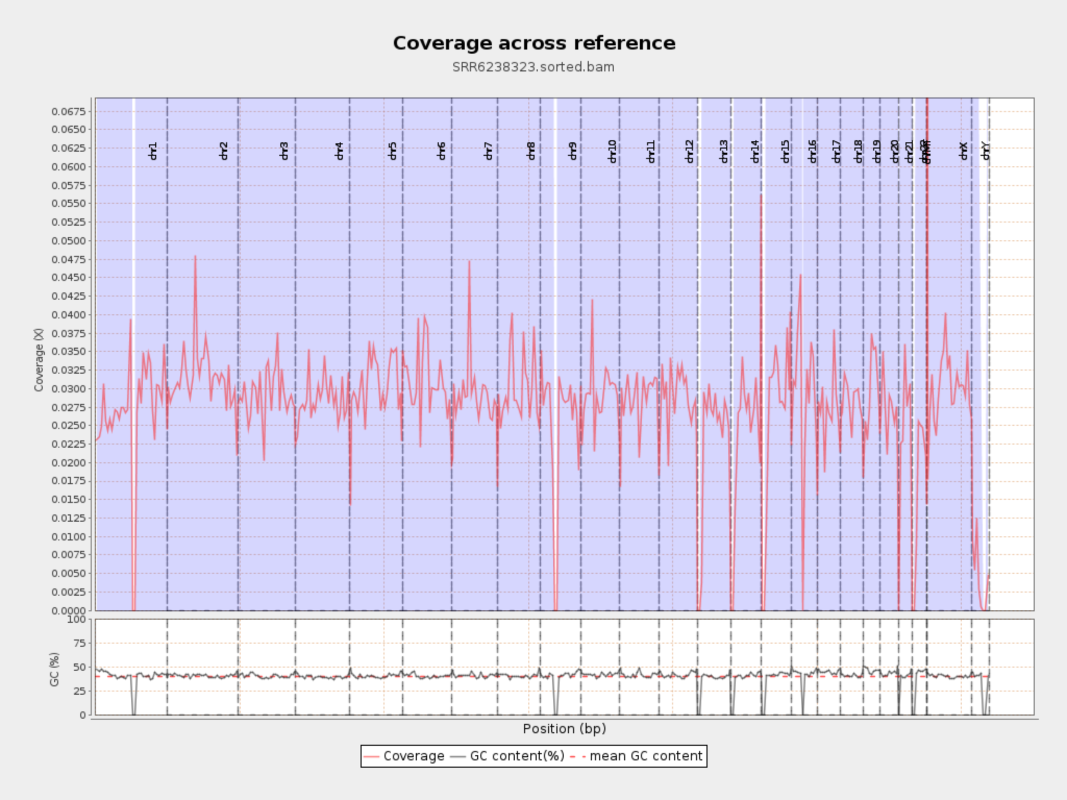
General error rate	0.87%
Mismatches	736,326
Insertions	6,351
Mapped reads with at least one insertion	0.47%
Deletions	23,516
Mapped reads with at least one deletion	1.74%
Homopolymer indels	45.89%

2.6. Chromosome stats

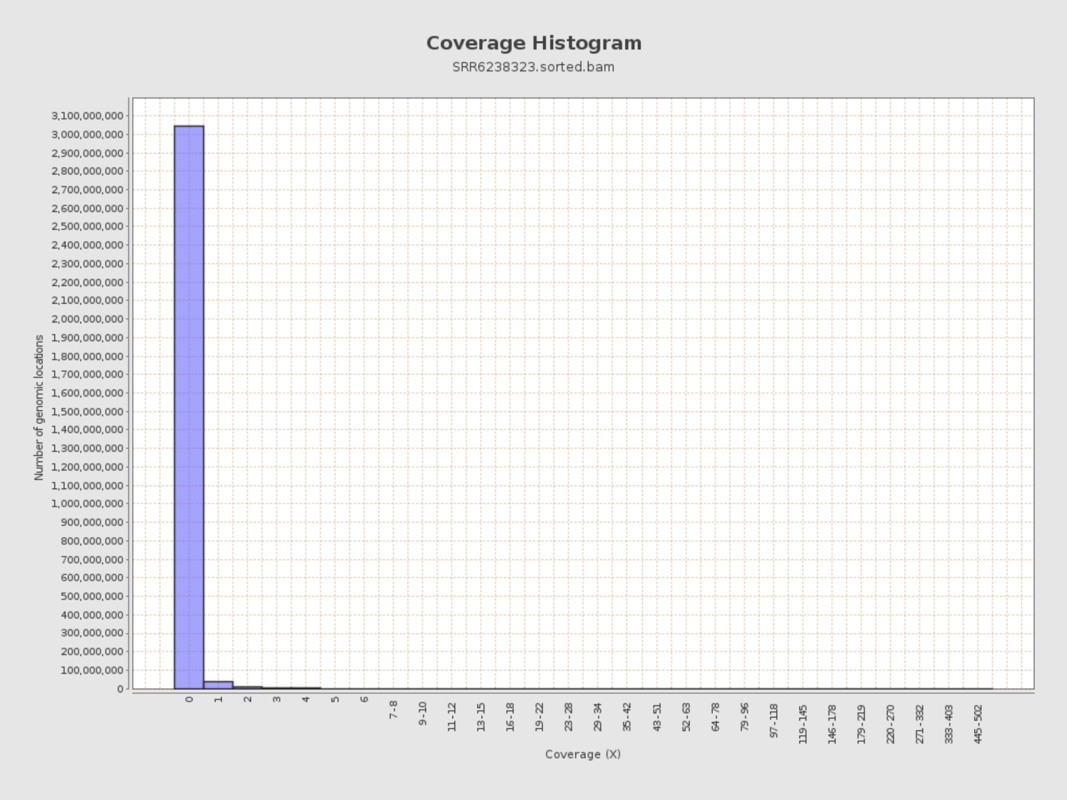
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6667908	0.0268	0.4501
chr2	243199373	7694932	0.0316	0.3695
chr3	198022430	5788036	0.0292	0.258
chr4	191154276	5453028	0.0285	0.2583
chr5	180915260	5570547	0.0308	0.2658
chr6	171115067	5284018	0.0309	0.2954
chr7	159138663	4664461	0.0293	0.3579

chr8	146364022	4401399	0.0301	0.3944
chr9	141213431	3552314	0.0252	0.2847
chr10	135534747	3960249	0.0292	0.2989
chr11	135006516	3894709	0.0288	0.2992
chr12	133851895	3889644	0.0291	0.2593
chr13	115169878	2581278	0.0224	0.2268
chr14	107349540	2505663	0.0233	0.2404
chr15	102531392	2651717	0.0259	0.2475
chr16	90354753	2602046	0.0288	0.2649
chr17	81195210	2229208	0.0275	0.2599
chr18	78077248	2211197	0.0283	0.4171
chr19	59128983	1748402	0.0296	0.3597
chr20	63025520	1721081	0.0273	0.2576
chr21	48129895	1171263	0.0243	0.2376
chr22	51304566	843069	0.0164	0.1874
chrMT	16571	311741	18.8124	13.0731
chrX	155270560	4688129	0.0302	0.2684
chrY	59373566	249888	0.0042	0.1043

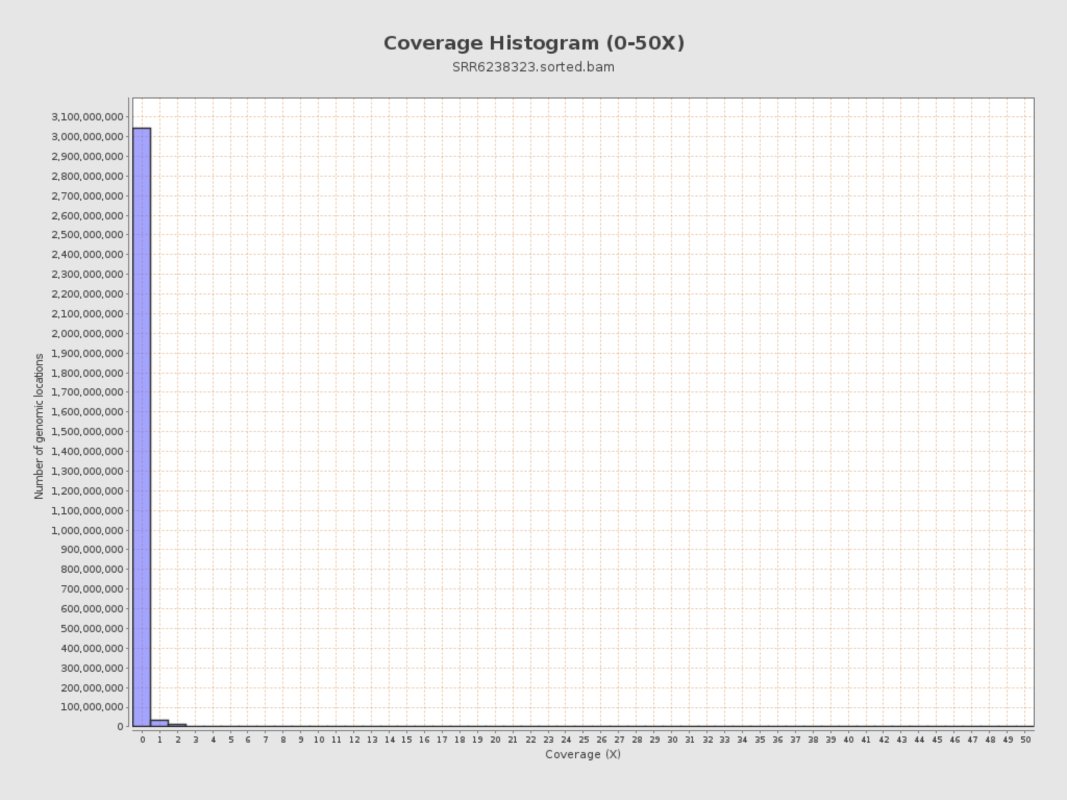
3. Results : Coverage across reference



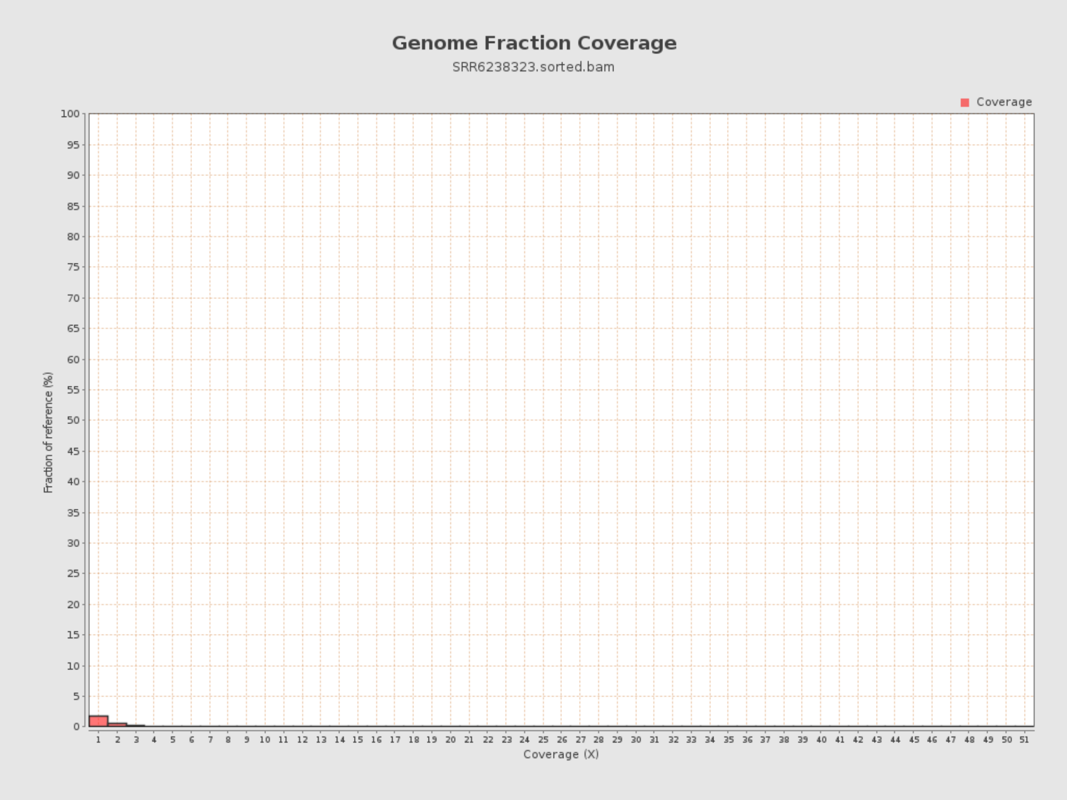
4. Results : Coverage Histogram



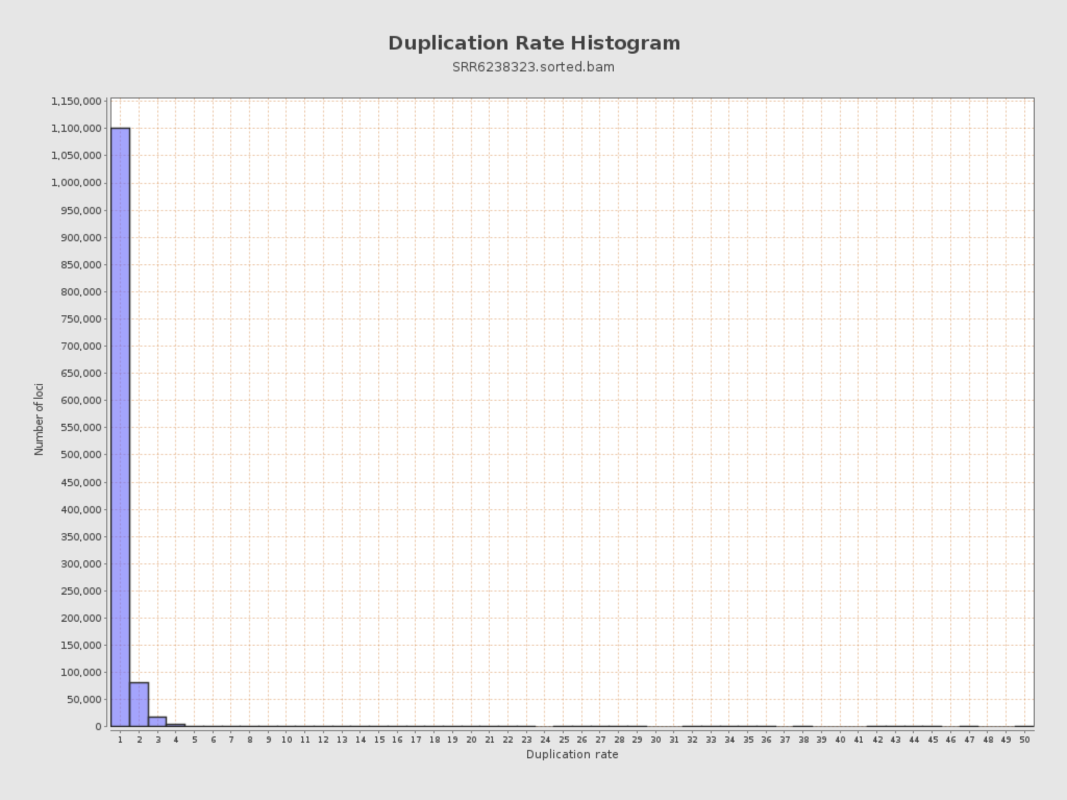
5. Results : Coverage Histogram (0-50X)



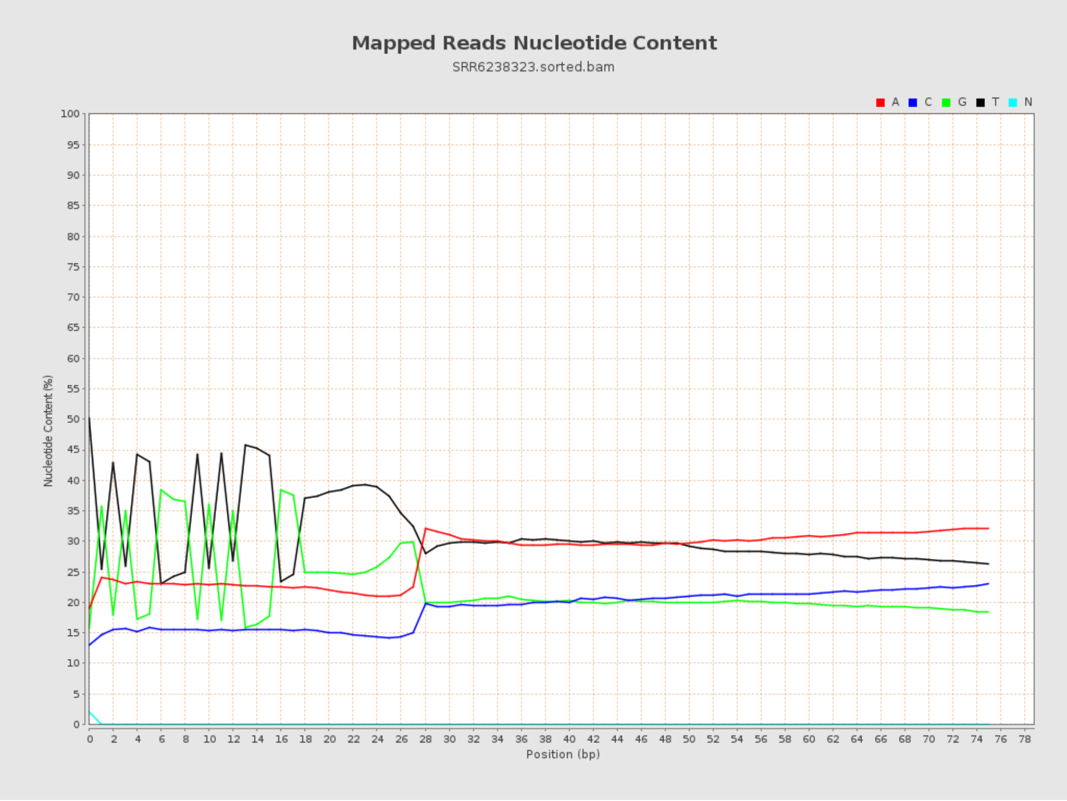
6. Results : Genome Fraction Coverage



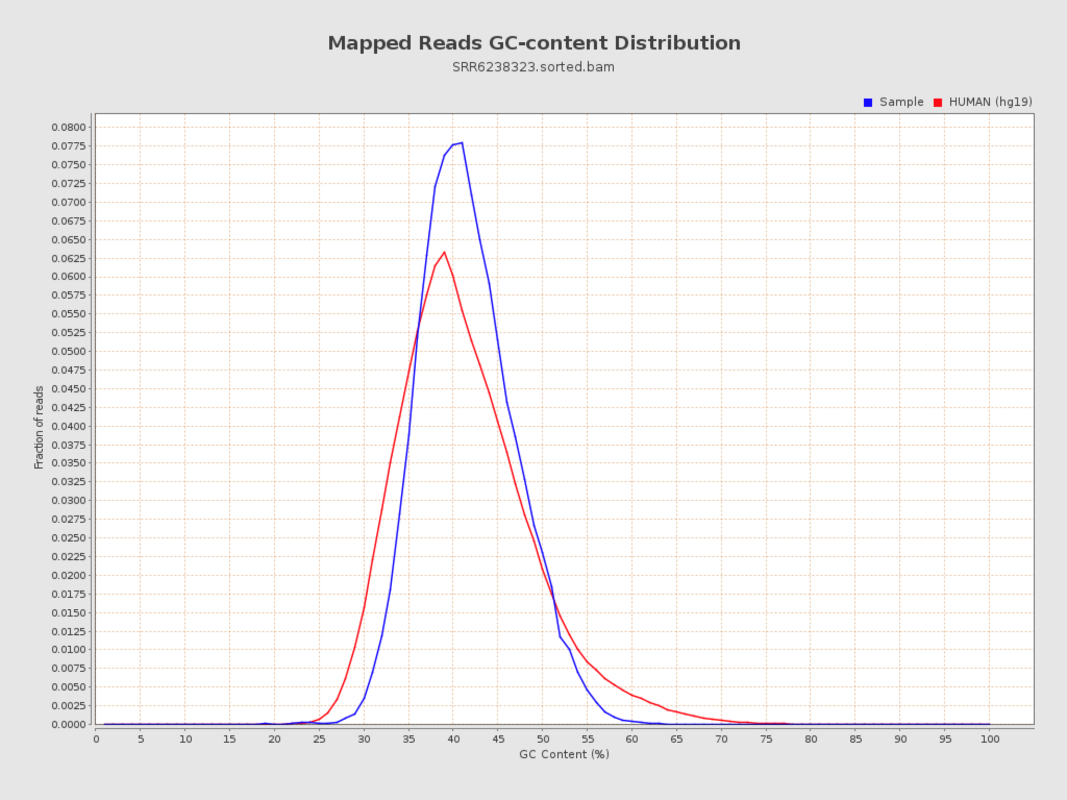
7. Results : Duplication Rate Histogram



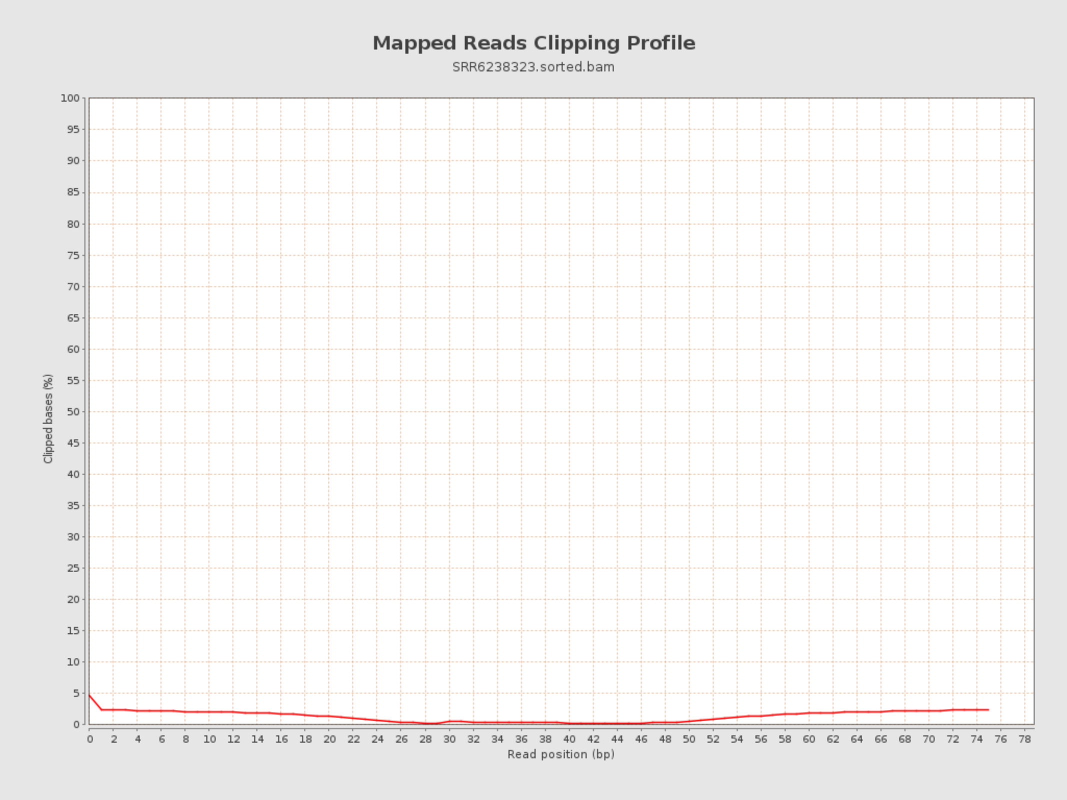
8. Results : Mapped Reads Nucleotide Content



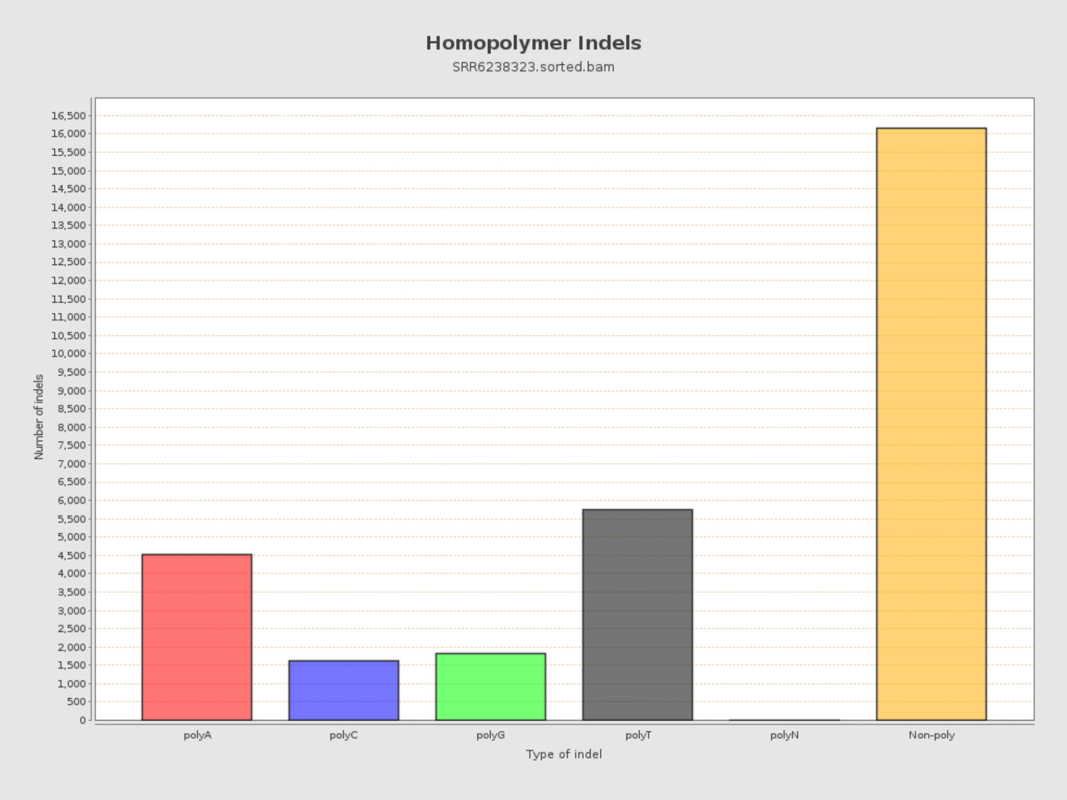
9. Results : Mapped Reads GC-content Distribution



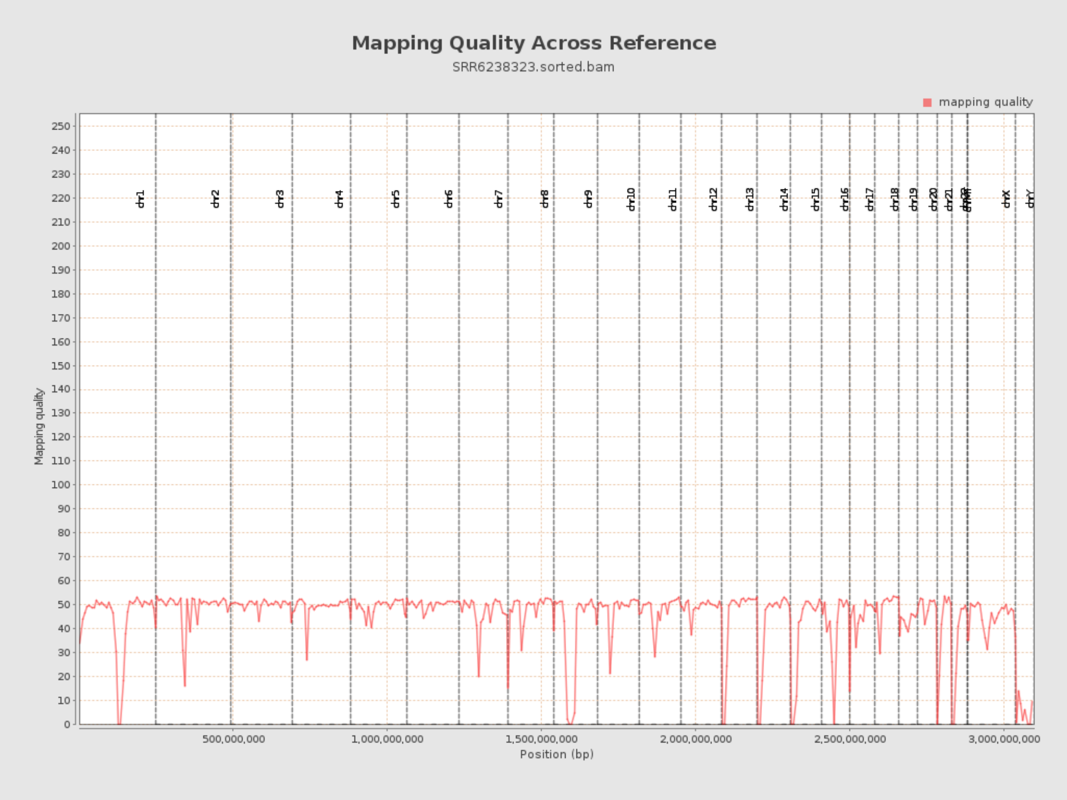
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram