Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 20:58:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6236109.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_SRR6236109 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6236109.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 20:58:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6236109.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	257,336
Mapped reads	217,897 / 84.67%
Unmapped reads	39,439 / 15.33%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,566 / 0.61%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	2,726 / 1.06%
Duplication rate	0.95%
Clipped reads	130,617 / 50.76%

2.2. ACGT Content

Number/percentage of A's	3,908,972 / 28.54%
Number/percentage of C's	2,612,124 / 19.07%
Number/percentage of T's	4,174,955 / 30.48%
Number/percentage of G's	2,995,265 / 21.87%
Number/percentage of N's	5,940 / 0.04%
GC Percentage	40.94%

2.3. Coverage

Mean	0.0044

Standard Deviation	0.0768

2.4. Mapping Quality

Mean Mapping Quality	42.93

2.5. Mismatches and indels

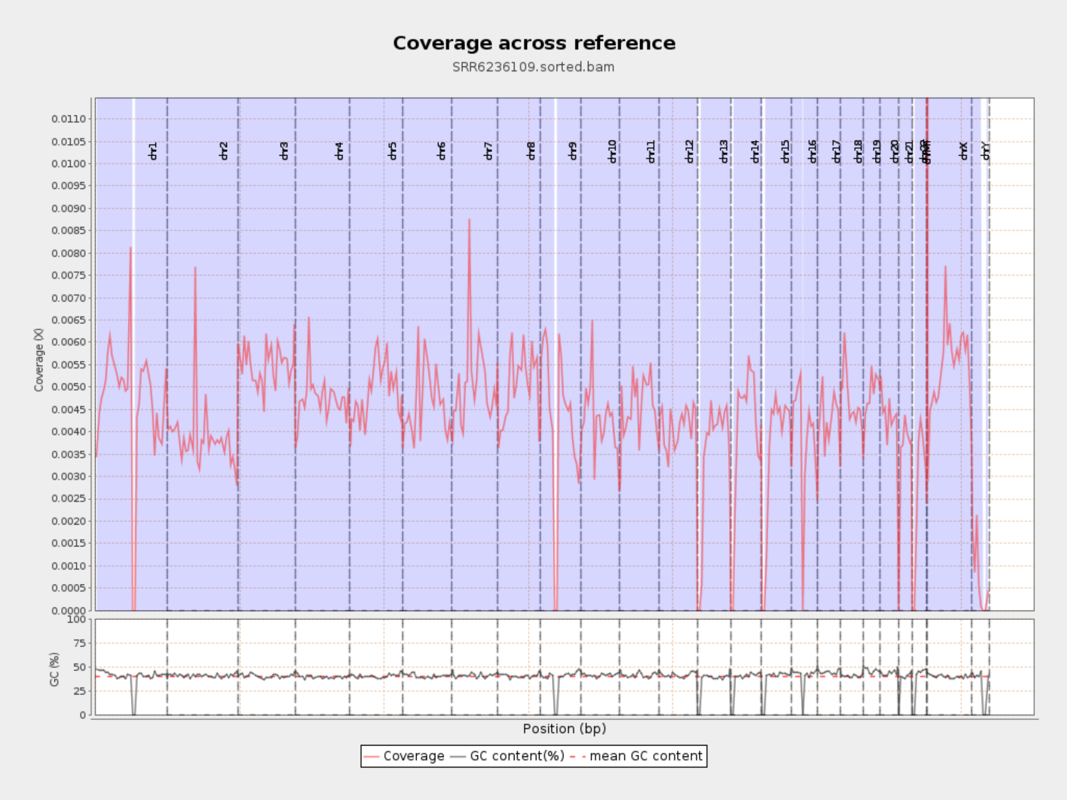
General error rate	1.16%
Mismatches	157,454
Insertions	1,132
Mapped reads with at least one insertion	0.51%
Deletions	3,431
Mapped reads with at least one deletion	1.56%
Homopolymer indels	44.6%

2.6. Chromosome stats

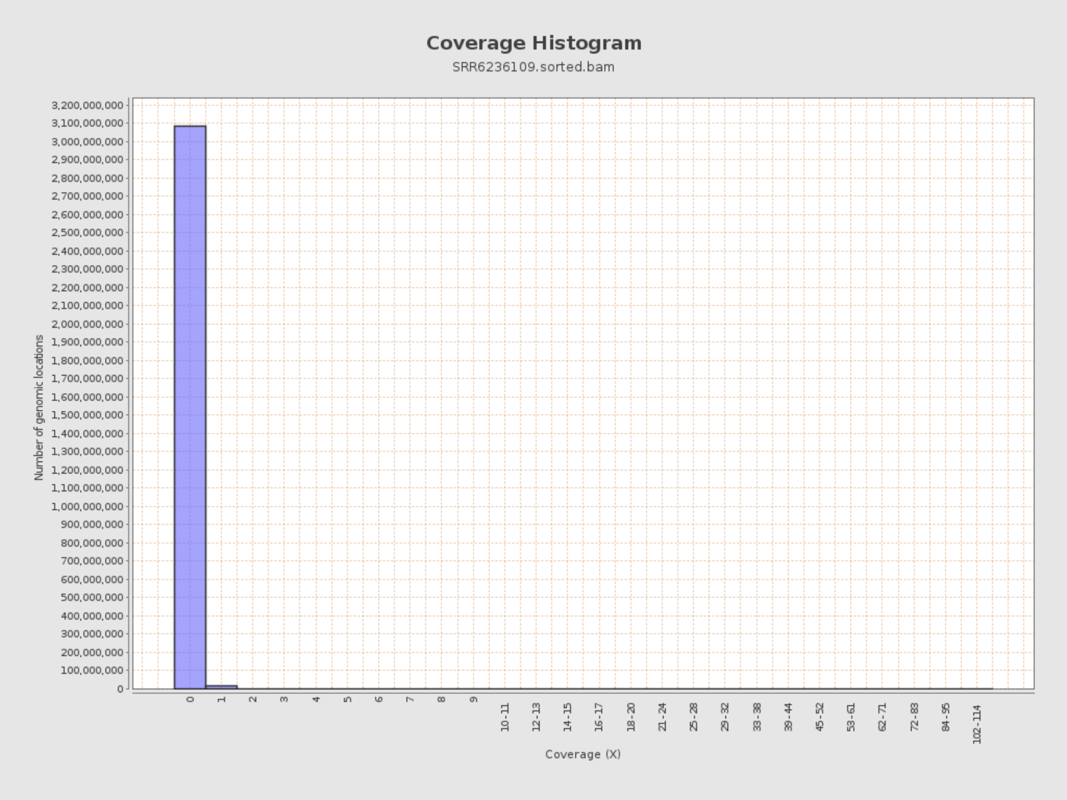
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1169225	0.0047	0.1081
chr2	243199373	939467	0.0039	0.0748
chr3	198022430	1086504	0.0055	0.0756
chr4	191154276	906025	0.0047	0.0708
chr5	180915260	893819	0.0049	0.0715
chr6	171115067	793575	0.0046	0.0715
chr7	159138663	811309	0.0051	0.0918

chr8	146364022	736589	0.005	0.0911
chr9	141213431	599213	0.0042	0.0724
chr10	135534747	580773	0.0043	0.0702
chr11	135006516	623472	0.0046	0.0739
chr12	133851895	551257	0.0041	0.0658
chr13	115169878	395938	0.0034	0.0607
chr14	107349540	419823	0.0039	0.0655
chr15	102531392	361049	0.0035	0.0607
chr16	90354753	344282	0.0038	0.0642
chr17	81195210	349316	0.0043	0.0679
chr18	78077248	367450	0.0047	0.1003
chr19	59128983	286725	0.0048	0.0831
chr20	63025520	271943	0.0043	0.0669
chr21	48129895	169030	0.0035	0.061
chr22	51304566	135998	0.0027	0.0522
chrMT	16571	16164	0.9754	1.2076
chrX	155270560	853454	0.0055	0.0769
chrY	59373566	40632	0.0007	0.0289

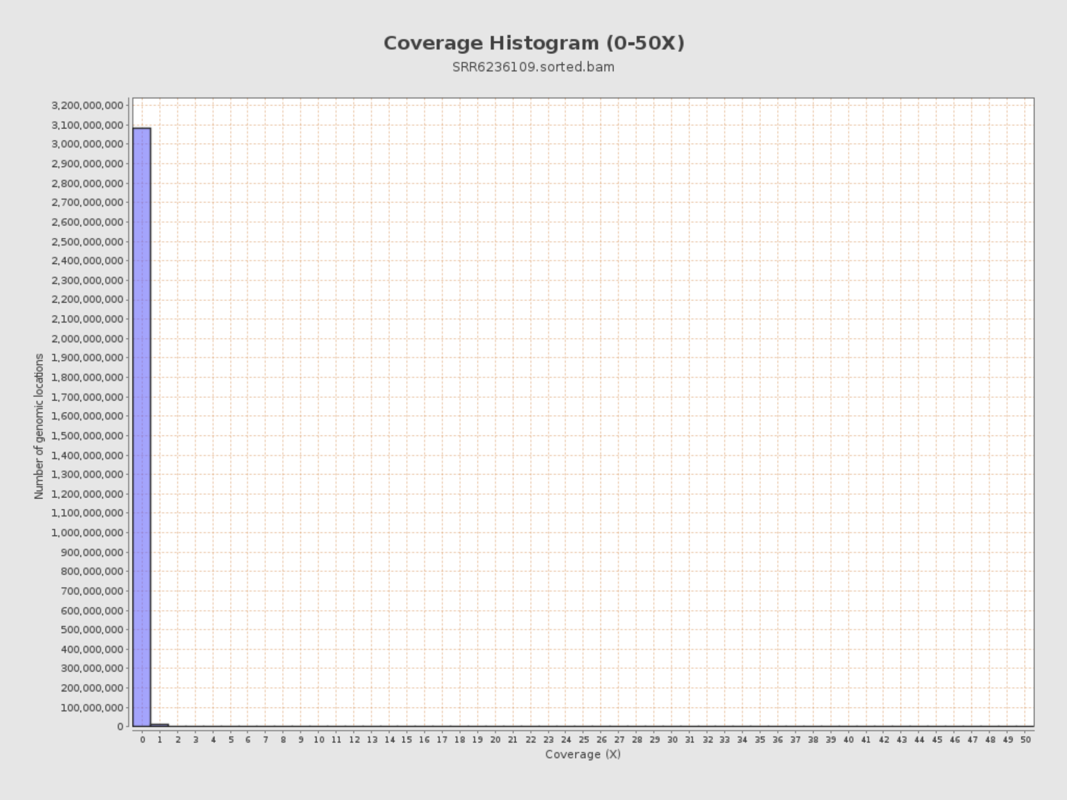
3. Results : Coverage across reference



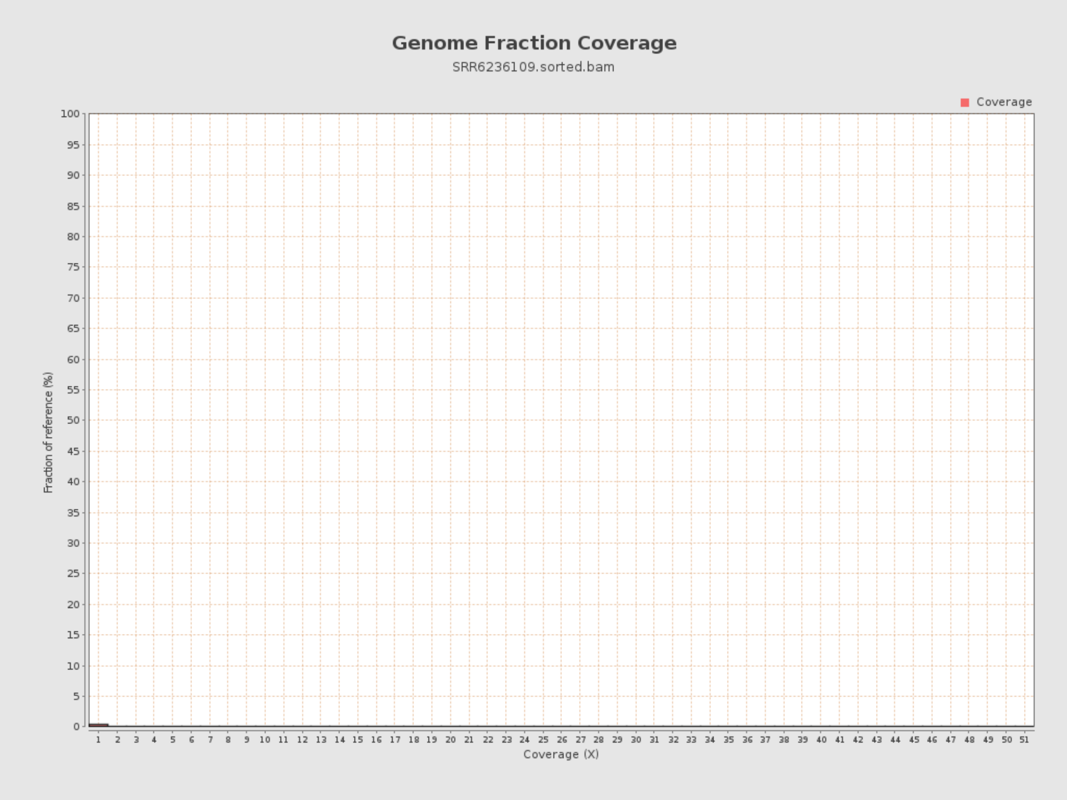
4. Results : Coverage Histogram



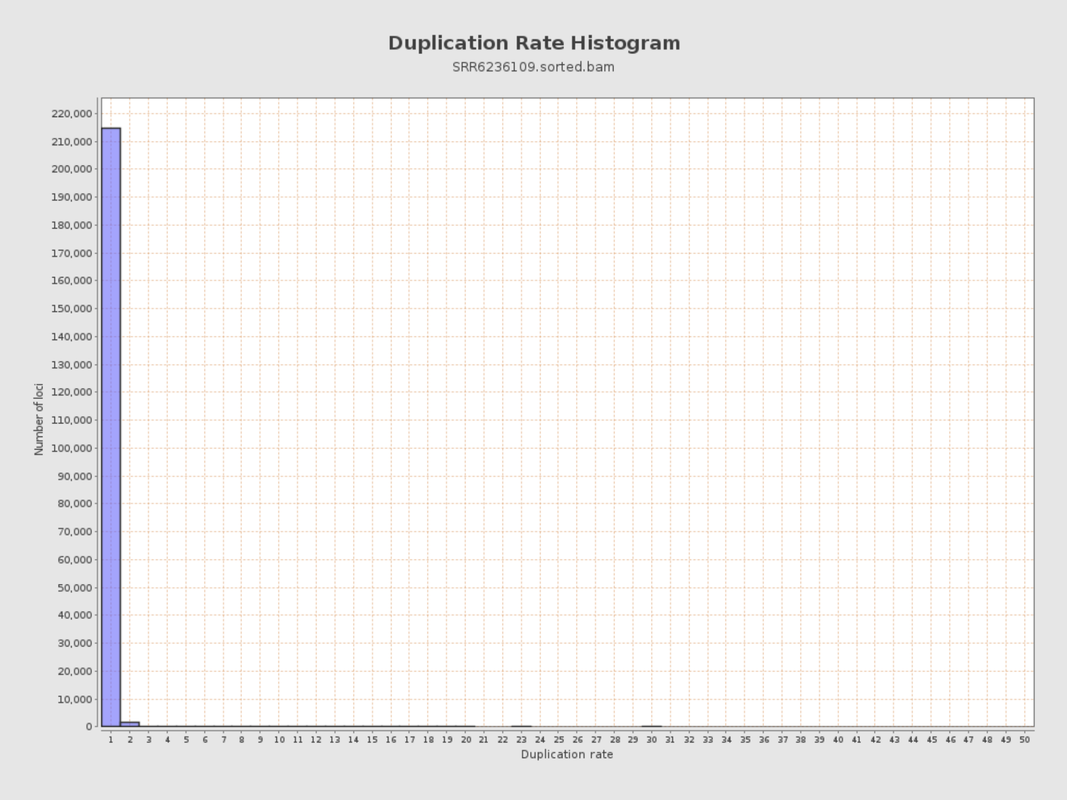
5. Results : Coverage Histogram (0-50X)



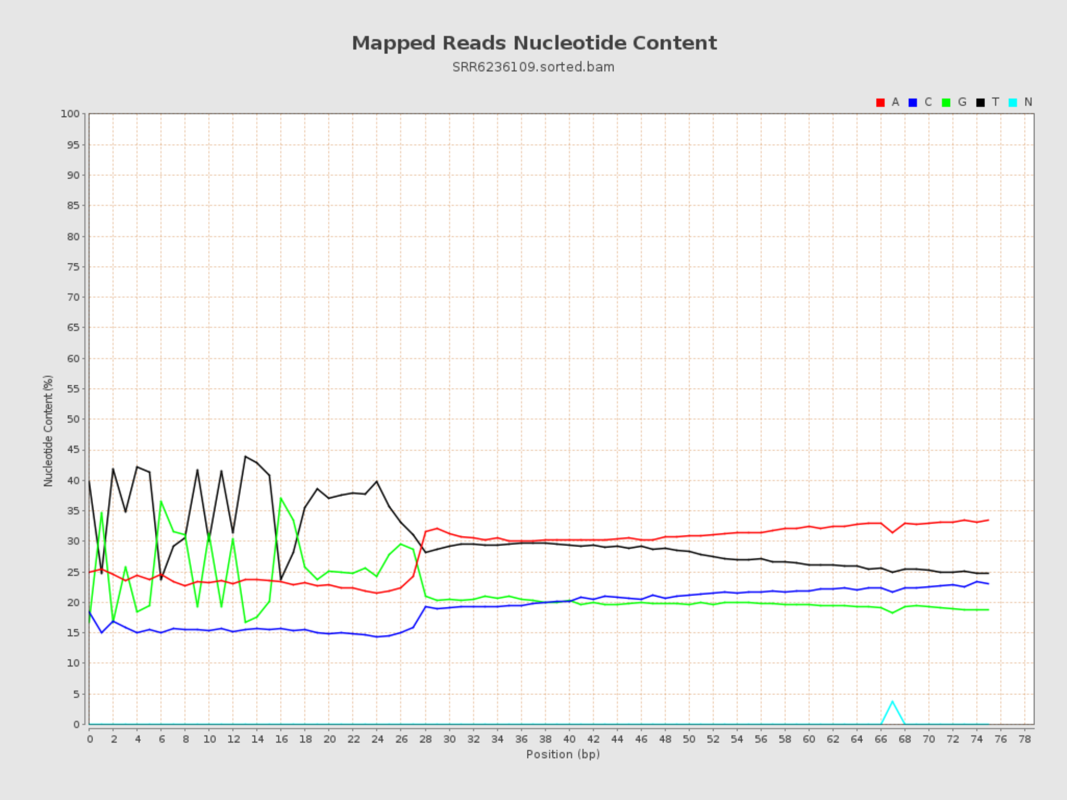
6. Results : Genome Fraction Coverage



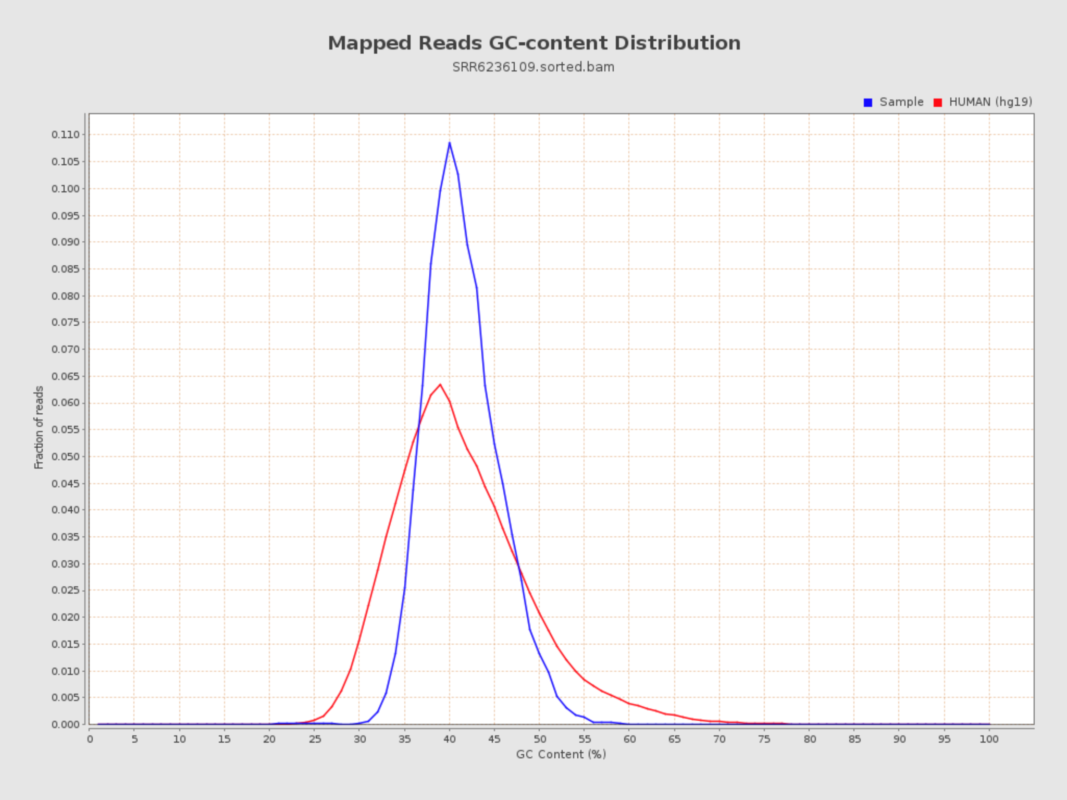
7. Results : Duplication Rate Histogram



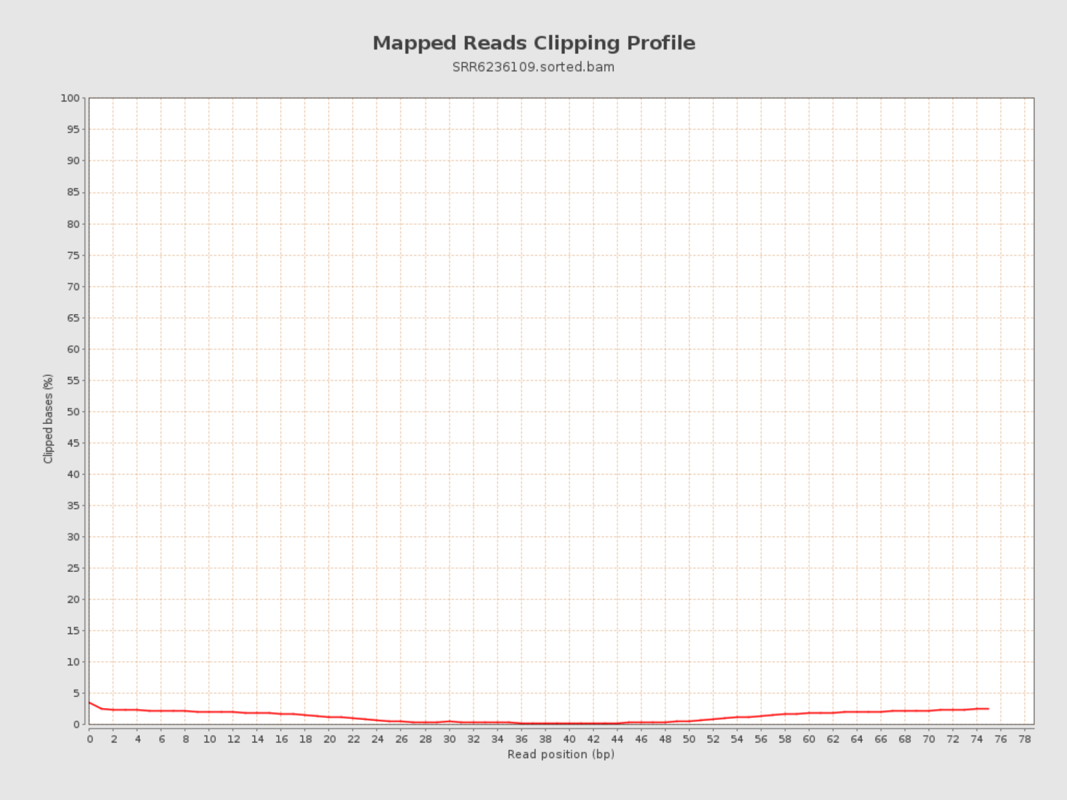
8. Results : Mapped Reads Nucleotide Content



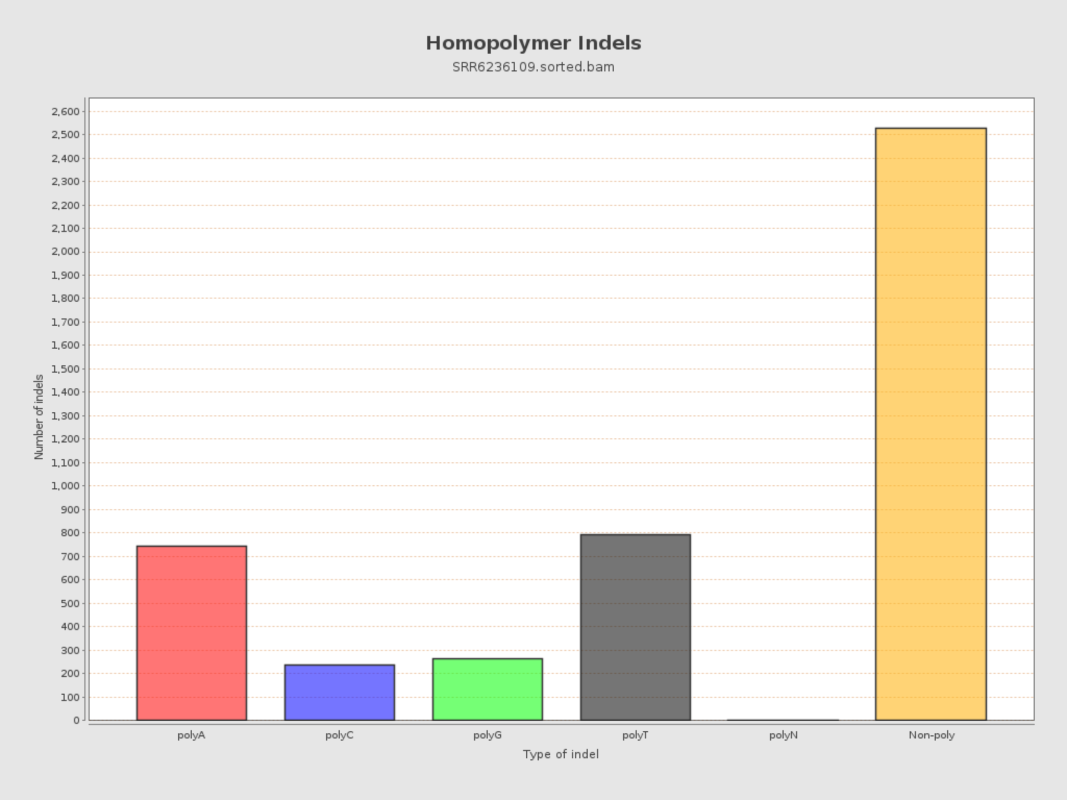
9. Results : Mapped Reads GC-content Distribution



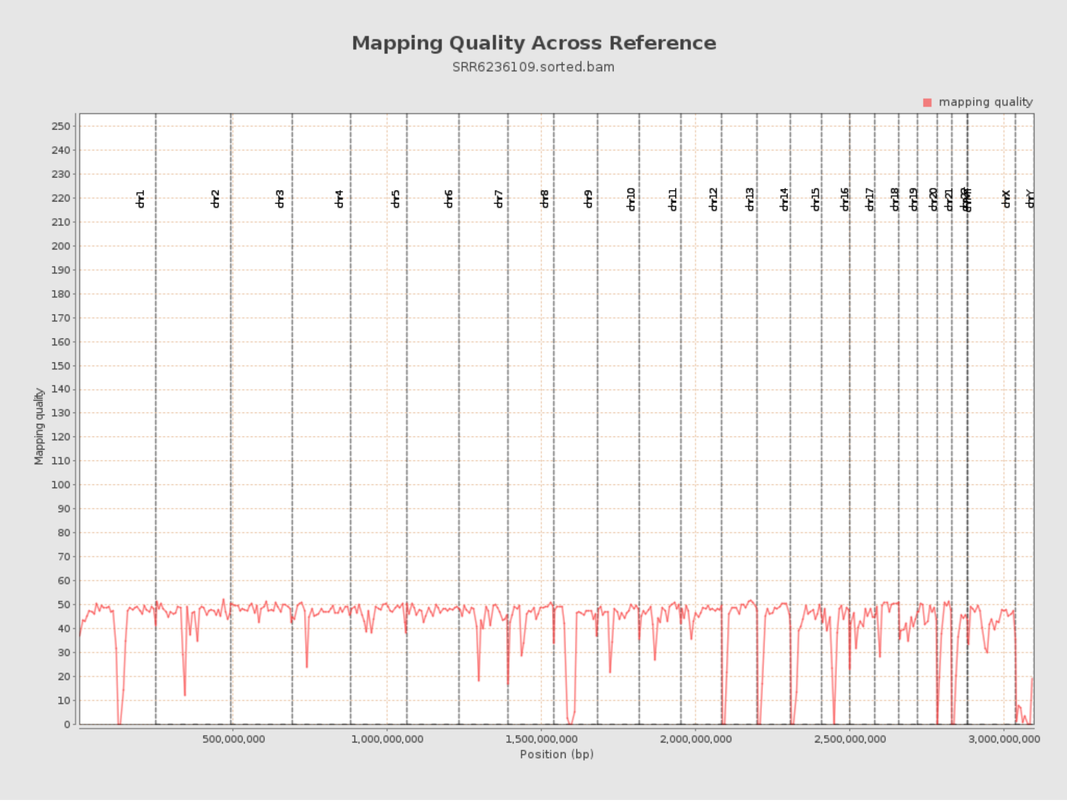
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram