Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 21:54:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6236128.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_SRR6236128 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6236128.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 21:54:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6236128.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,368,860
Mapped reads	2,847,416 / 84.52%
Unmapped reads	521,444 / 15.48%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,859 / 0.53%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	129,987 / 3.86%
Duplication rate	3.49%
Clipped reads	1,377,491 / 40.89%

2.2. ACGT Content

Number/percentage of A's	54,079,505 / 28.79%
Number/percentage of C's	35,370,358 / 18.83%
Number/percentage of T's	58,049,683 / 30.9%
Number/percentage of G's	40,367,922 / 21.49%
Number/percentage of N's	1,868 / 0%
GC Percentage	40.31%

2.3. Coverage

Mean	0.0607

Standard Deviation	0.5063

2.4. Mapping Quality

Mean Mapping Quality	46

2.5. Mismatches and indels

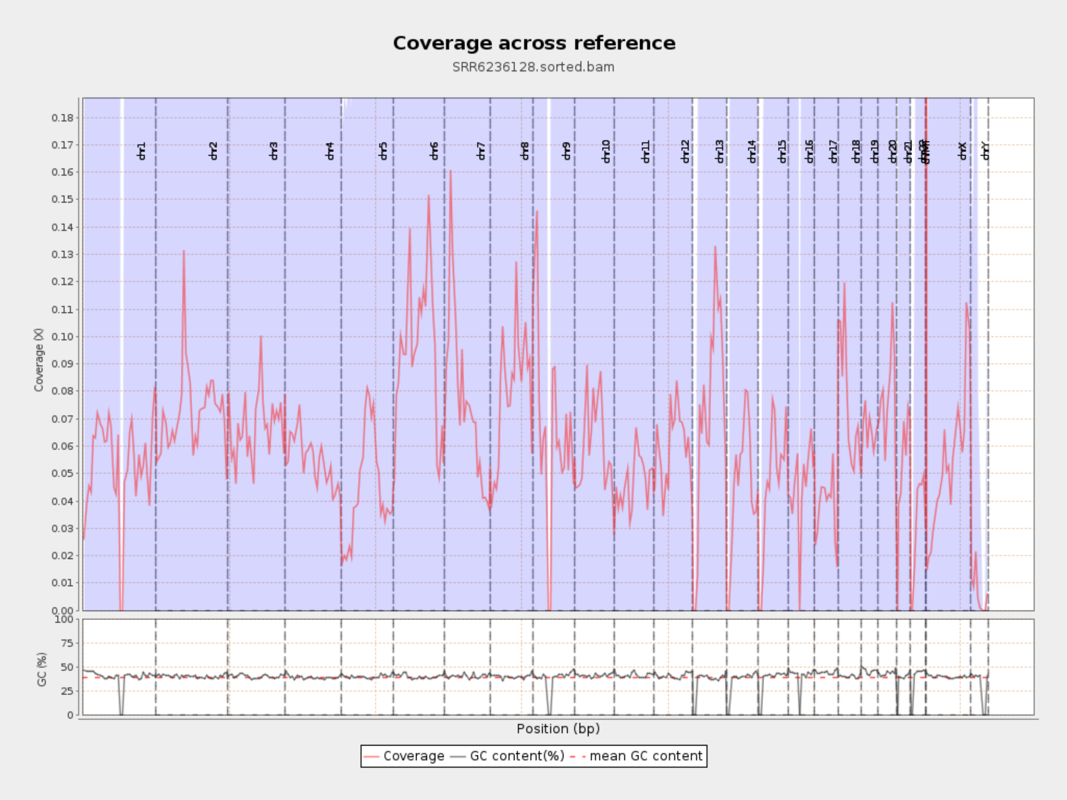
General error rate	0.77%
Mismatches	1,414,008
Insertions	13,830
Mapped reads with at least one insertion	0.48%
Deletions	53,231
Mapped reads with at least one deletion	1.85%
Homopolymer indels	46.17%

2.6. Chromosome stats

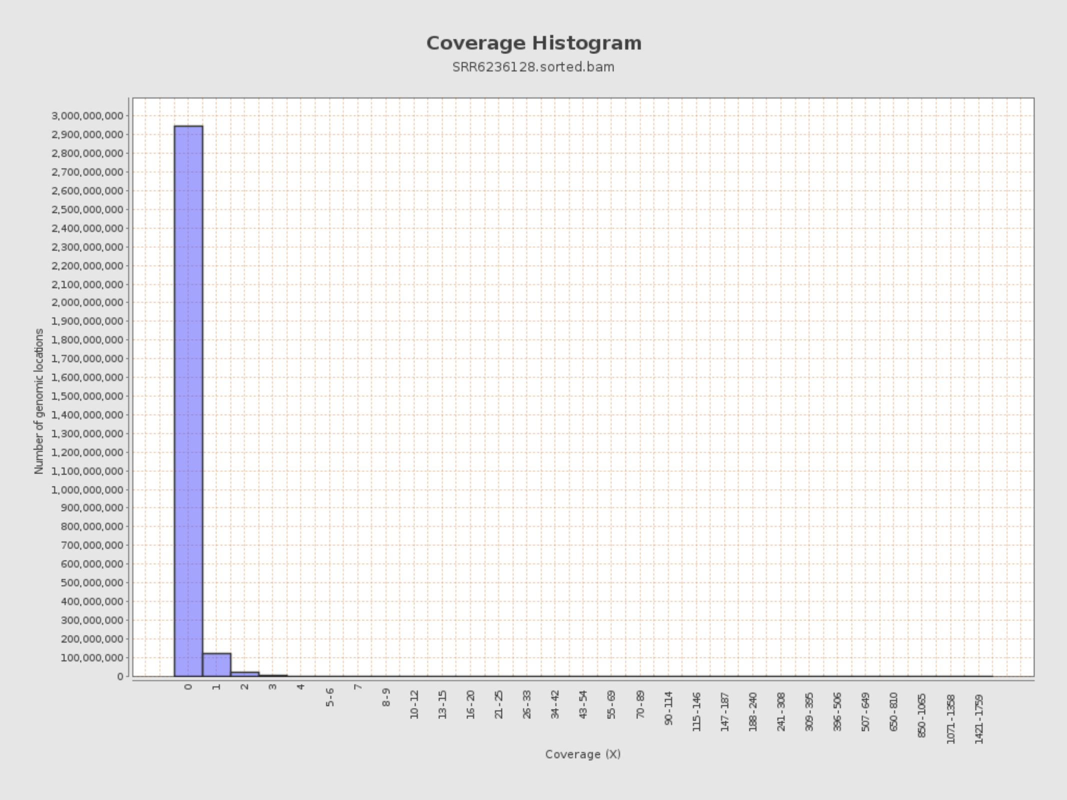
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13244615	0.0531	0.6824
chr2	243199373	17723222	0.0729	0.6077
chr3	198022430	13295294	0.0671	0.313
chr4	191154276	10493026	0.0549	0.3101
chr5	180915260	8020821	0.0443	0.2618
chr6	171115067	16656975	0.0973	0.5549
chr7	159138663	12052906	0.0757	0.5511

chr8	146364022	11768457	0.0804	1.1513
chr9	141213431	9269641	0.0656	0.5337
chr10	135534747	8196082	0.0605	0.4208
chr11	135006516	6296832	0.0466	0.343
chr12	133851895	8035592	0.06	0.3179
chr13	115169878	8390407	0.0729	0.3273
chr14	107349540	4890154	0.0456	0.3287
chr15	102531392	4684233	0.0457	0.266
chr16	90354753	4039447	0.0447	0.3172
chr17	81195210	3055958	0.0376	0.2652
chr18	78077248	6009117	0.077	0.8356
chr19	59128983	3889377	0.0658	0.4803
chr20	63025520	5031951	0.0798	0.3559
chr21	48129895	2526874	0.0525	0.3254
chr22	51304566	1609154	0.0314	0.2104
chrMT	16571	28384	1.7129	1.9543
chrX	155270560	8369927	0.0539	0.3247
chrY	59373566	382834	0.0064	0.1802

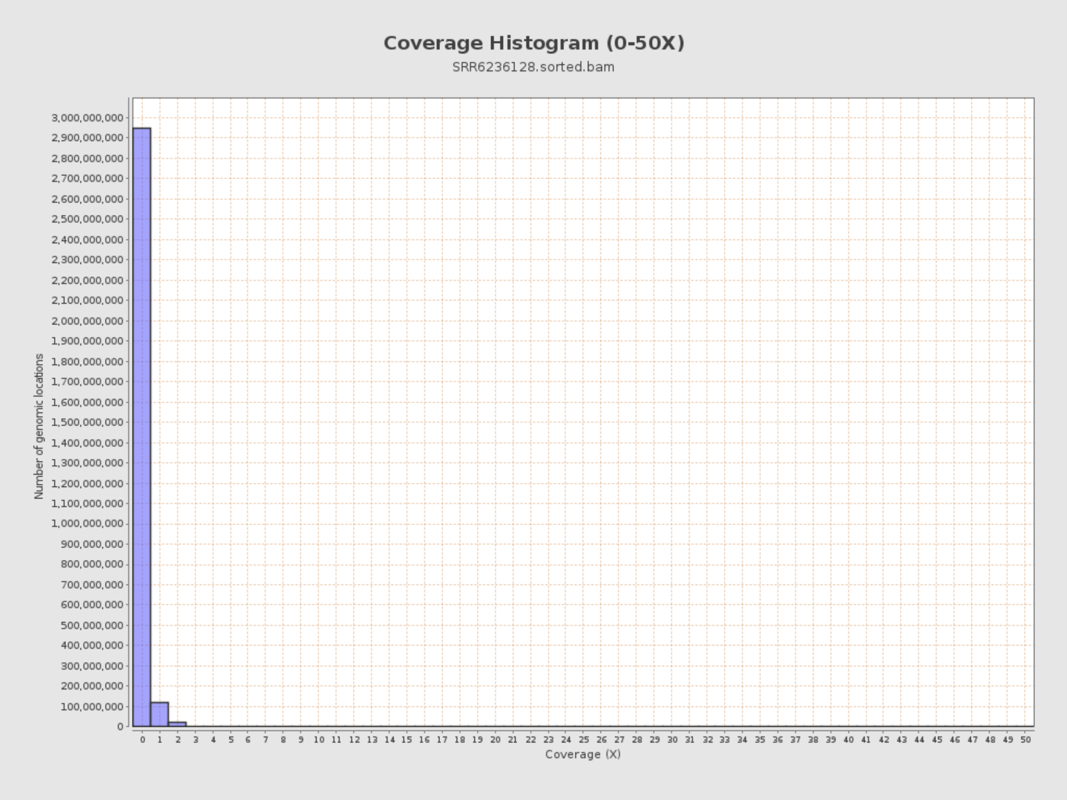
3. Results : Coverage across reference



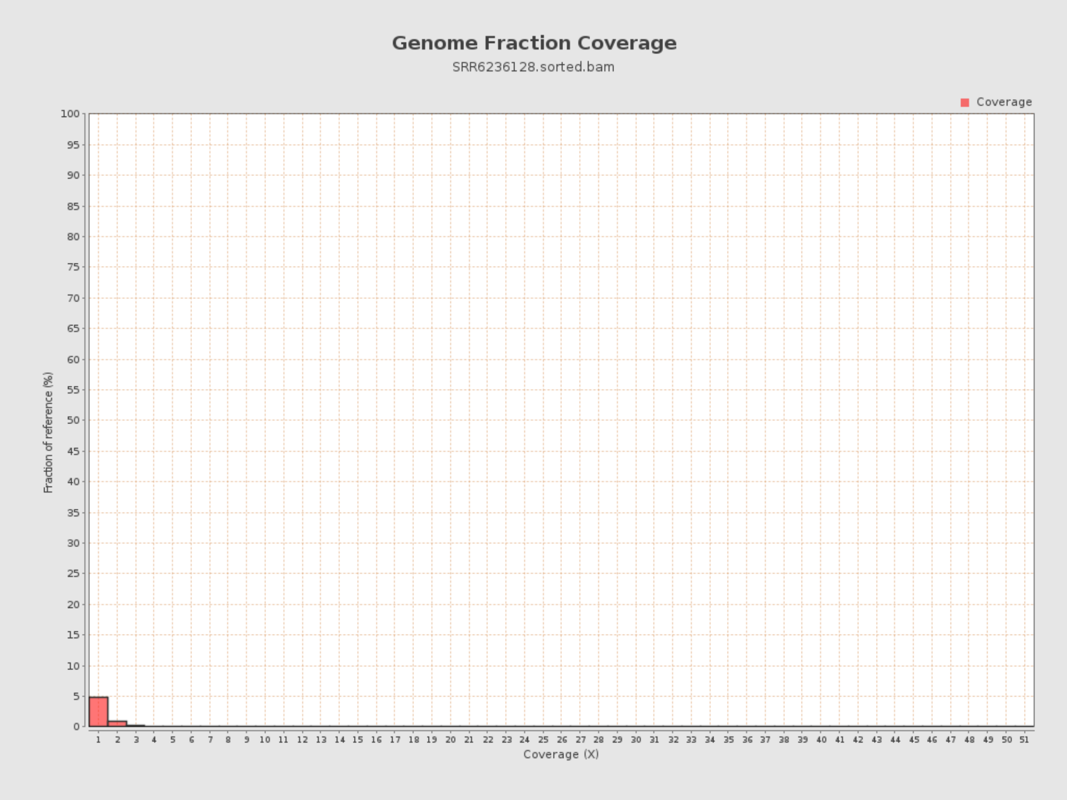
4. Results : Coverage Histogram



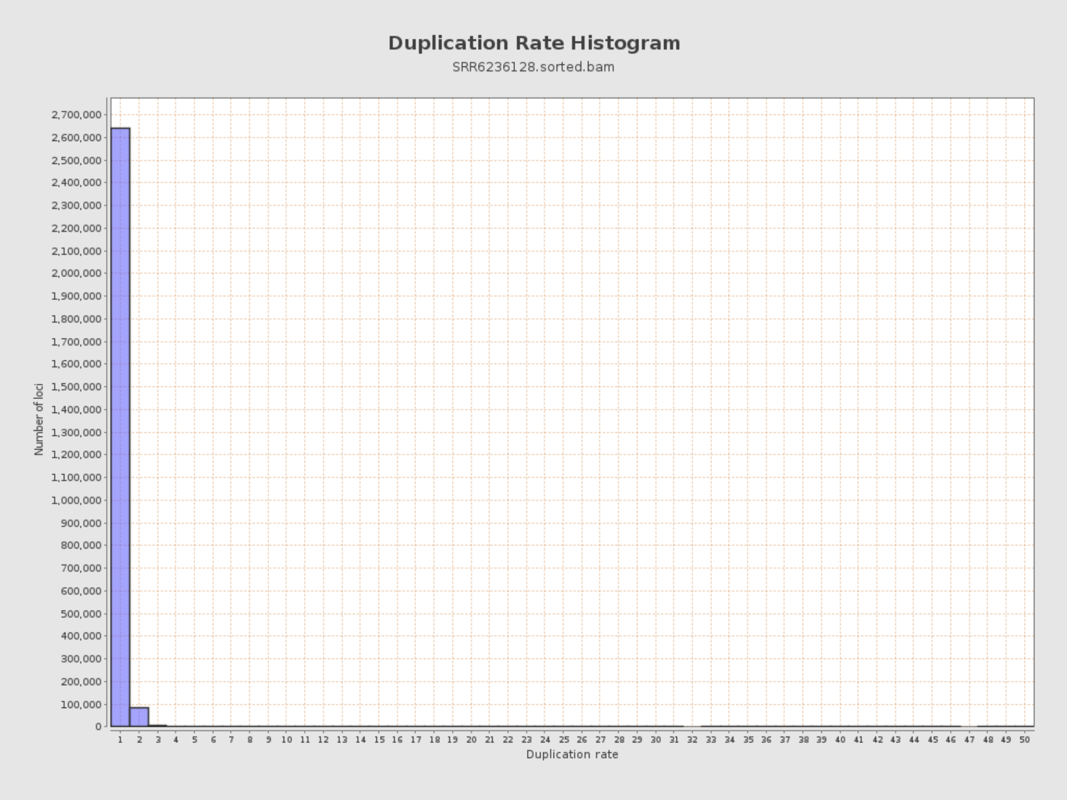
5. Results : Coverage Histogram (0-50X)



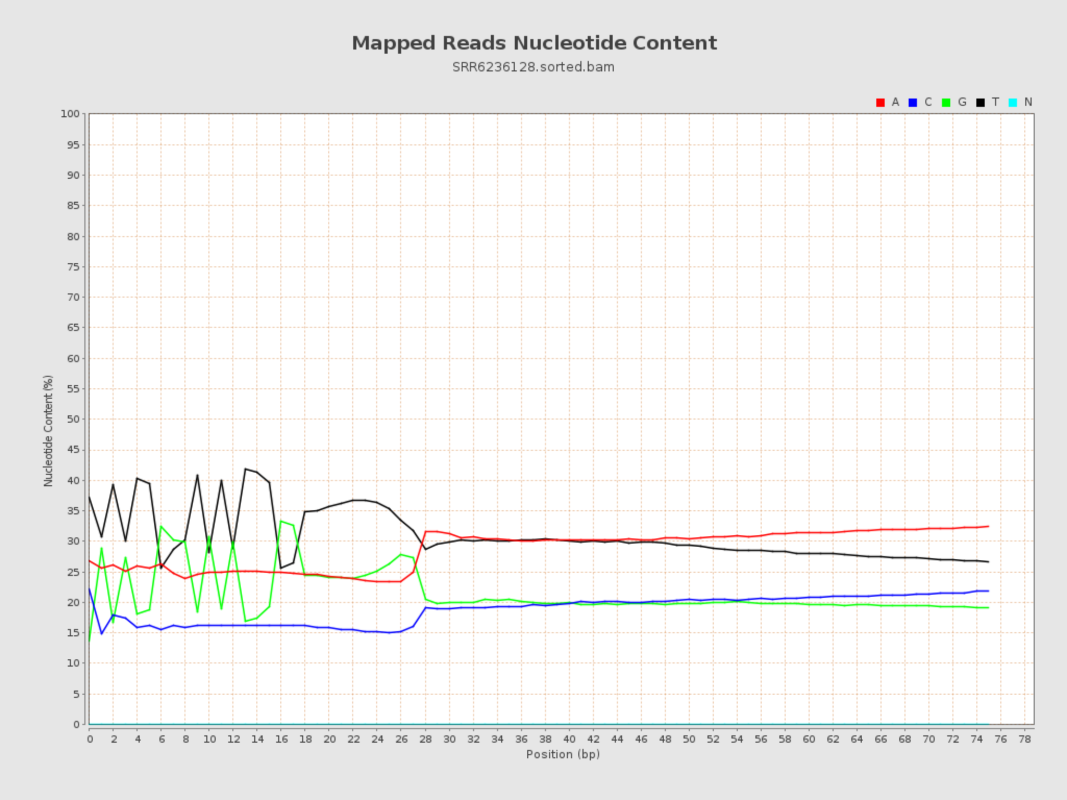
6. Results : Genome Fraction Coverage



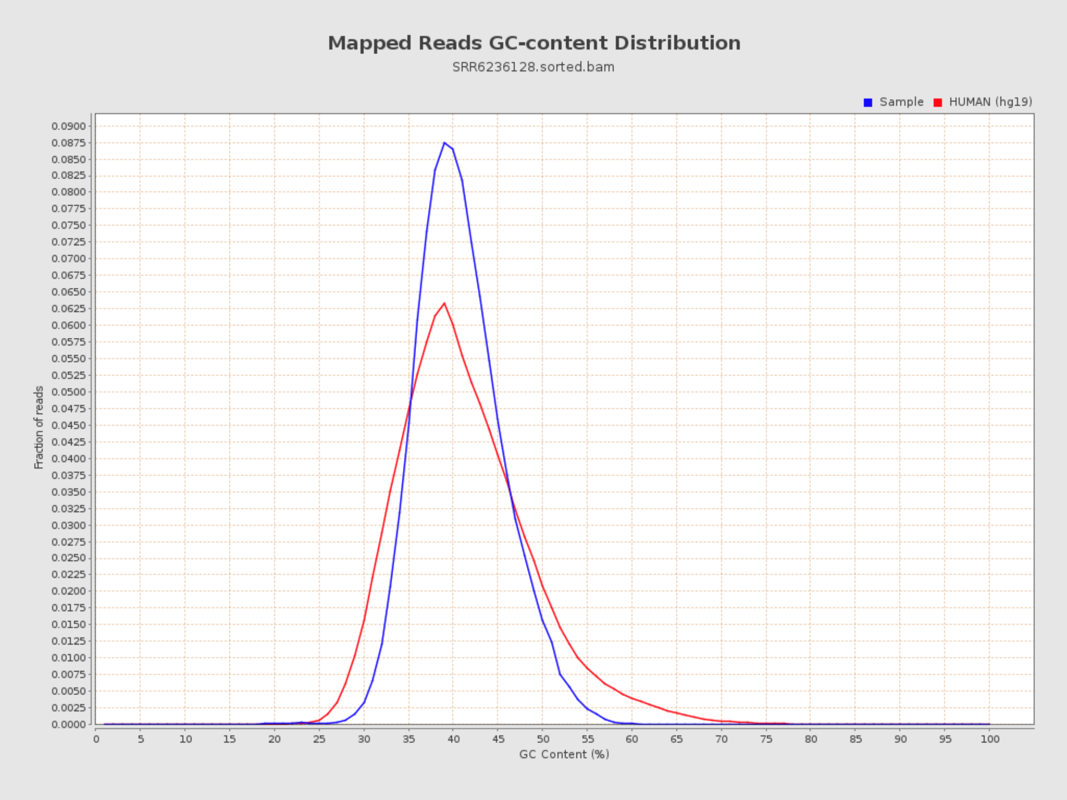
7. Results : Duplication Rate Histogram



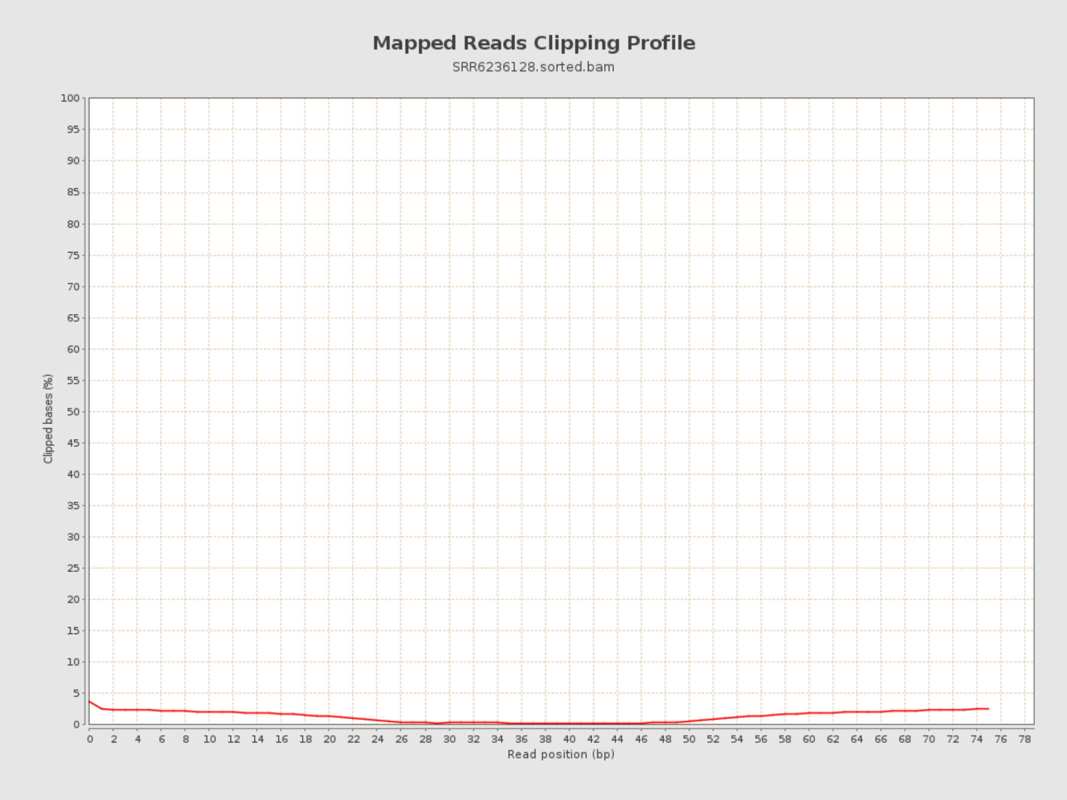
8. Results : Mapped Reads Nucleotide Content



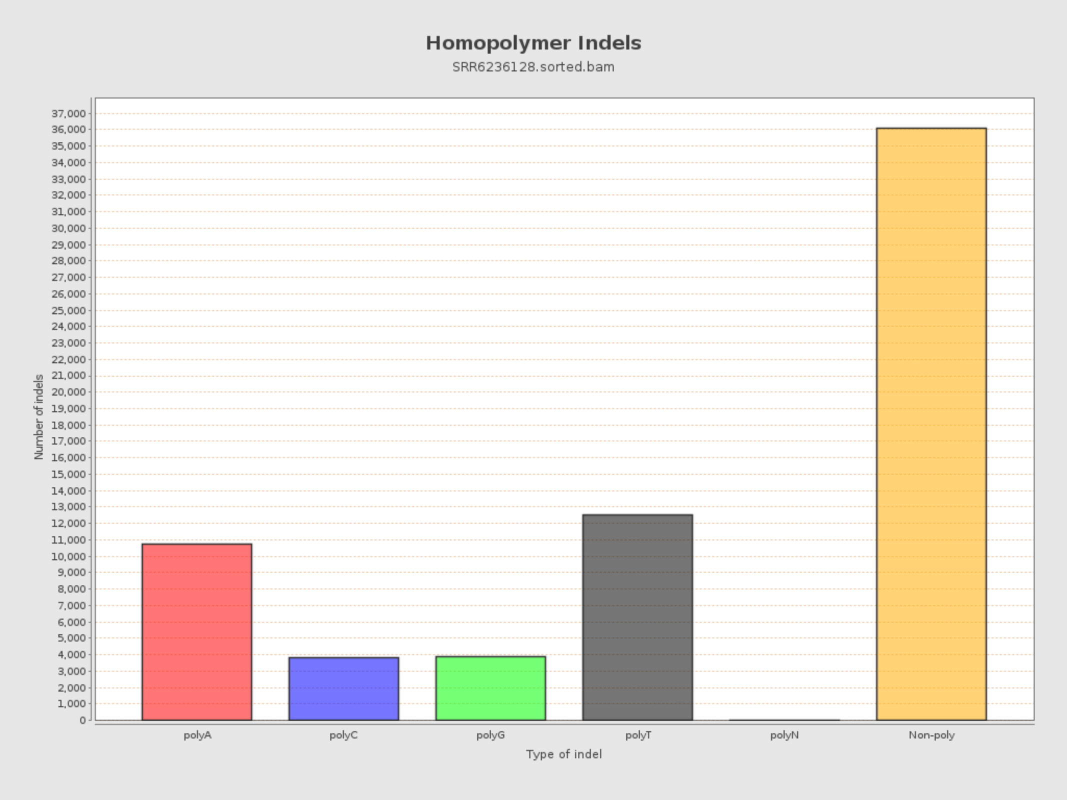
9. Results : Mapped Reads GC-content Distribution



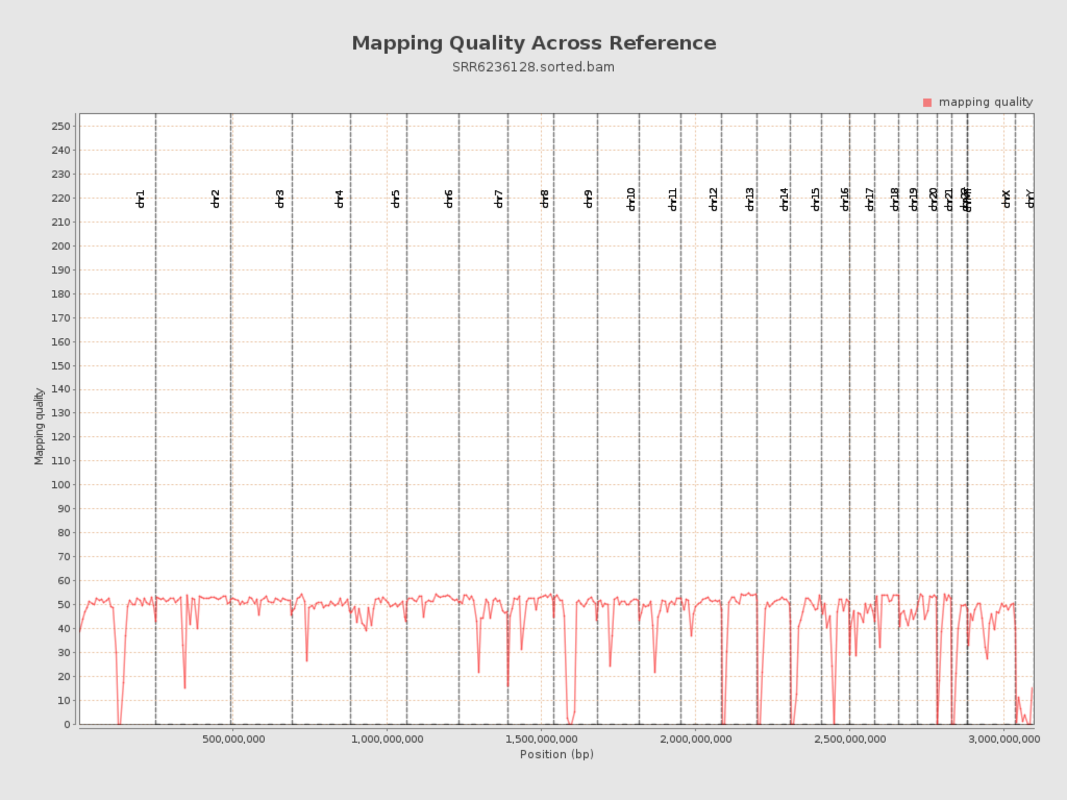
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram