Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 21:24:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6236117.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_SRR6236117 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6236117.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 21:24:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6236117.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,953,122
Mapped reads	5,131,822 / 86.2%
Unmapped reads	821,300 / 13.8%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	49,761 / 0.84%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	650,723 / 10.93%
Duplication rate	9.56%
Clipped reads	2,759,764 / 46.36%

2.2. ACGT Content

Number/percentage of A's	92,341,117 / 27.9%
Number/percentage of C's	60,314,654 / 18.22%
Number/percentage of T's	105,275,911 / 31.81%
Number/percentage of G's	73,007,335 / 22.06%
Number/percentage of N's	54,105 / 0.02%
GC Percentage	40.28%

2.3. Coverage

Mean	0.107

Standard Deviation	0.9283

2.4. Mapping Quality

Mean Mapping Quality	45.2

2.5. Mismatches and indels

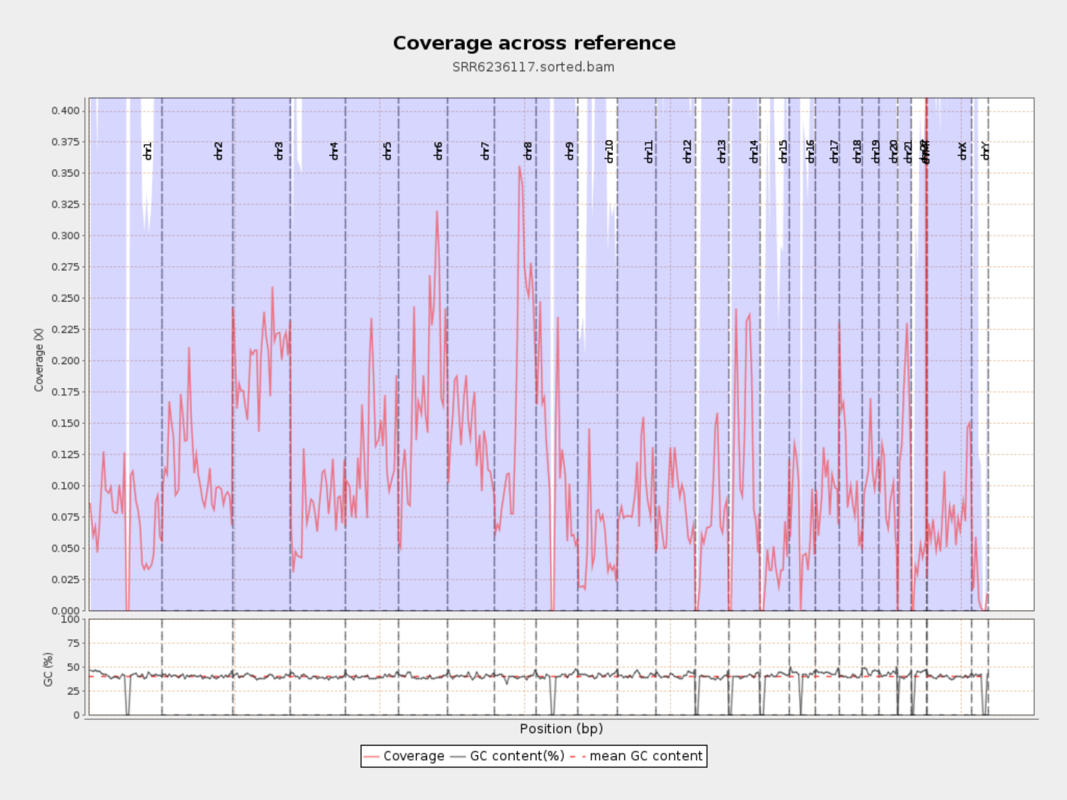
General error rate	0.8%
Mismatches	2,598,491
Insertions	24,721
Mapped reads with at least one insertion	0.48%
Deletions	95,931
Mapped reads with at least one deletion	1.85%
Homopolymer indels	45.37%

2.6. Chromosome stats

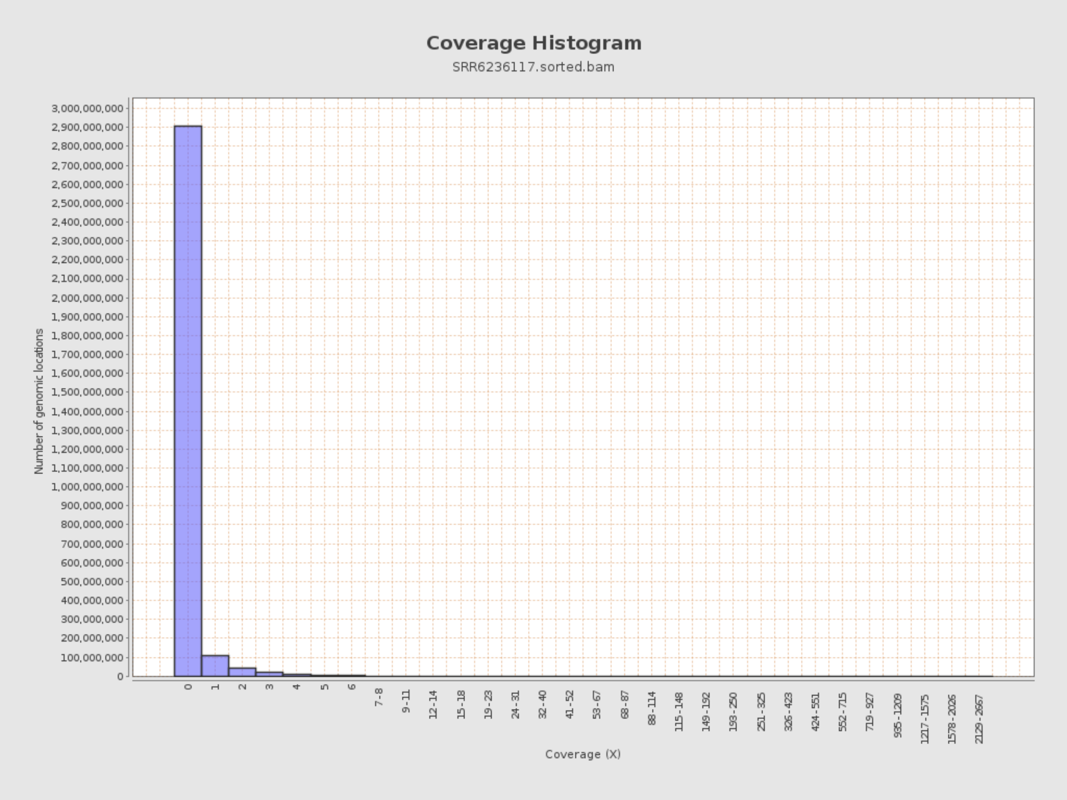
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17920871	0.0719	1.446
chr2	243199373	27951894	0.1149	1.1596
chr3	198022430	39970920	0.2019	0.7074
chr4	191154276	15353448	0.0803	0.6013
chr5	180915260	23342403	0.129	0.5768
chr6	171115067	29795196	0.1741	0.8962
chr7	159138663	22832979	0.1435	0.9809

chr8	146364022	25540810	0.1745	1.7948
chr9	141213431	16259823	0.1151	0.9258
chr10	135534747	6720097	0.0496	0.8362
chr11	135006516	12447985	0.0922	0.6575
chr12	133851895	11028397	0.0824	0.4938
chr13	115169878	8177881	0.071	0.4179
chr14	107349540	12980576	0.1209	0.6169
chr15	102531392	3589913	0.035	0.3156
chr16	90354753	6339493	0.0702	0.5019
chr17	81195210	7878799	0.097	0.5158
chr18	78077248	8617256	0.1104	1.6299
chr19	59128983	6637695	0.1123	1.1026
chr20	63025520	5679385	0.0901	0.5005
chr21	48129895	7000923	0.1455	0.7107
chr22	51304566	1735083	0.0338	0.272
chrMT	16571	521439	31.467	20.1861
chrX	155270560	11951011	0.077	0.5192
chrY	59373566	885091	0.0149	0.4512

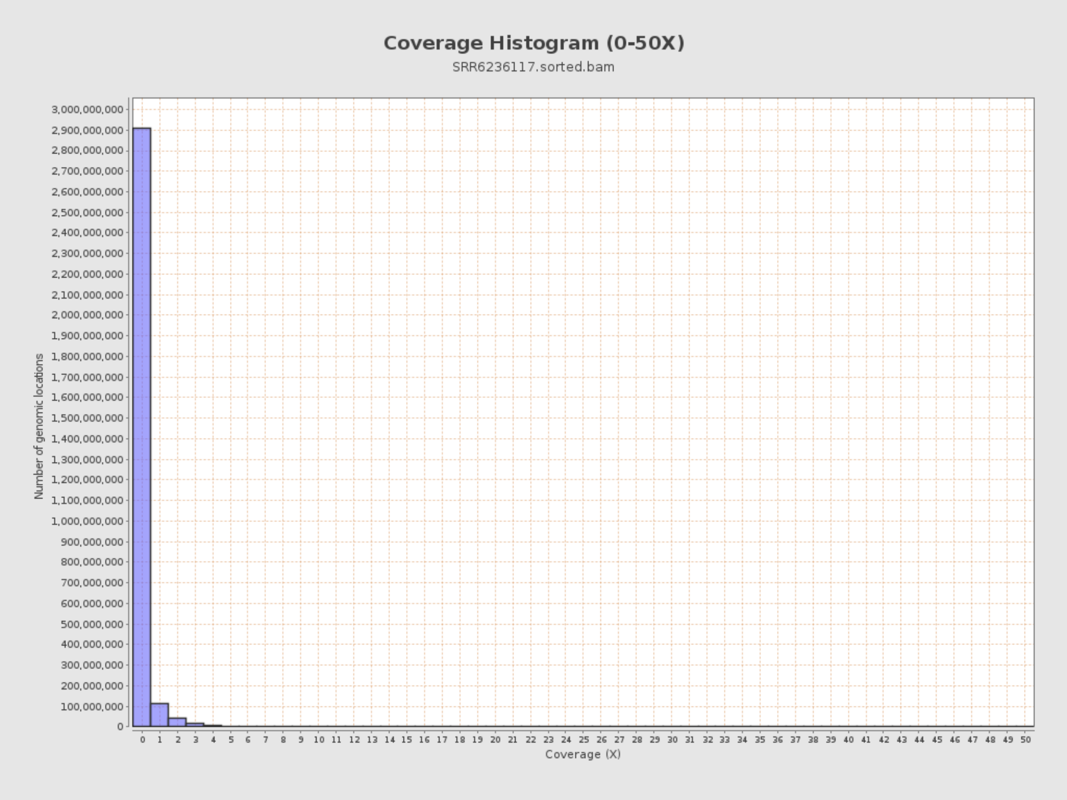
3. Results : Coverage across reference



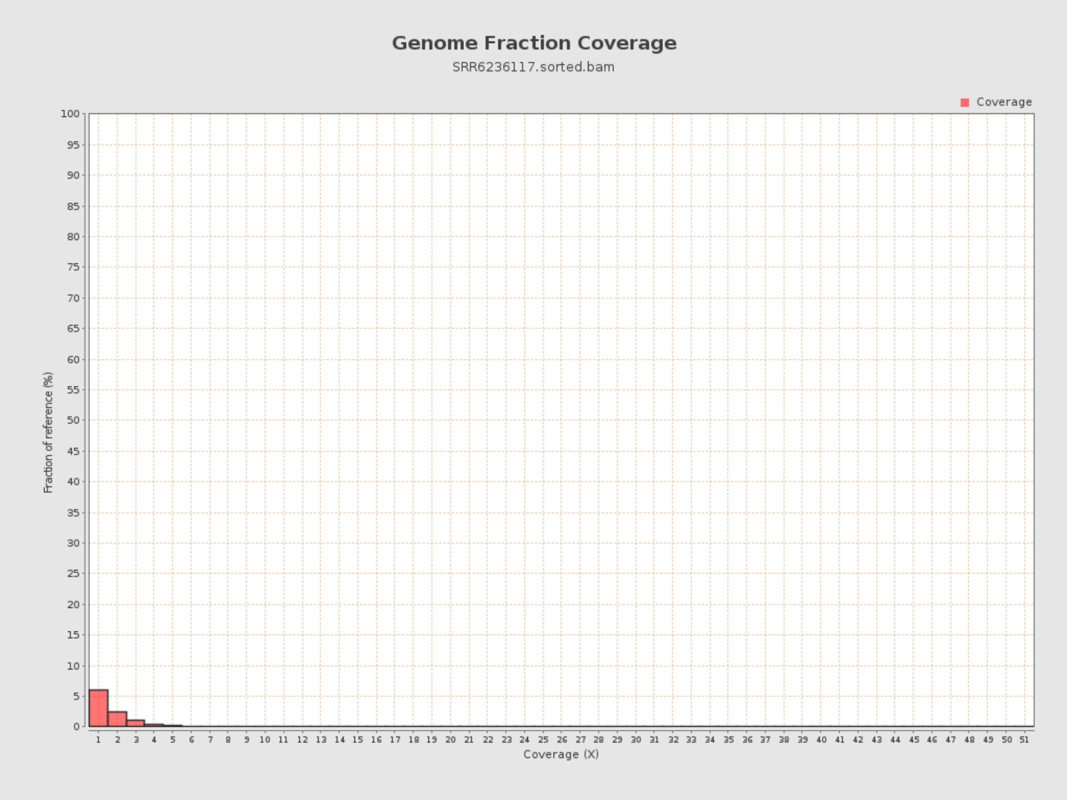
4. Results : Coverage Histogram



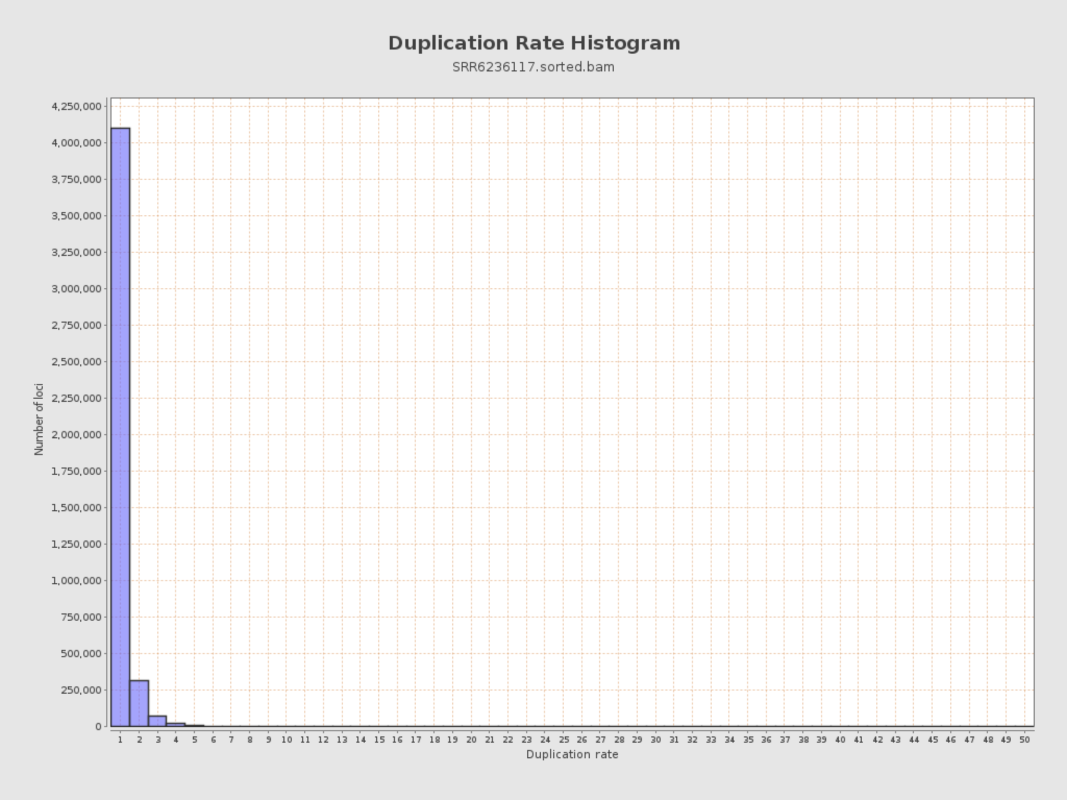
5. Results : Coverage Histogram (0-50X)



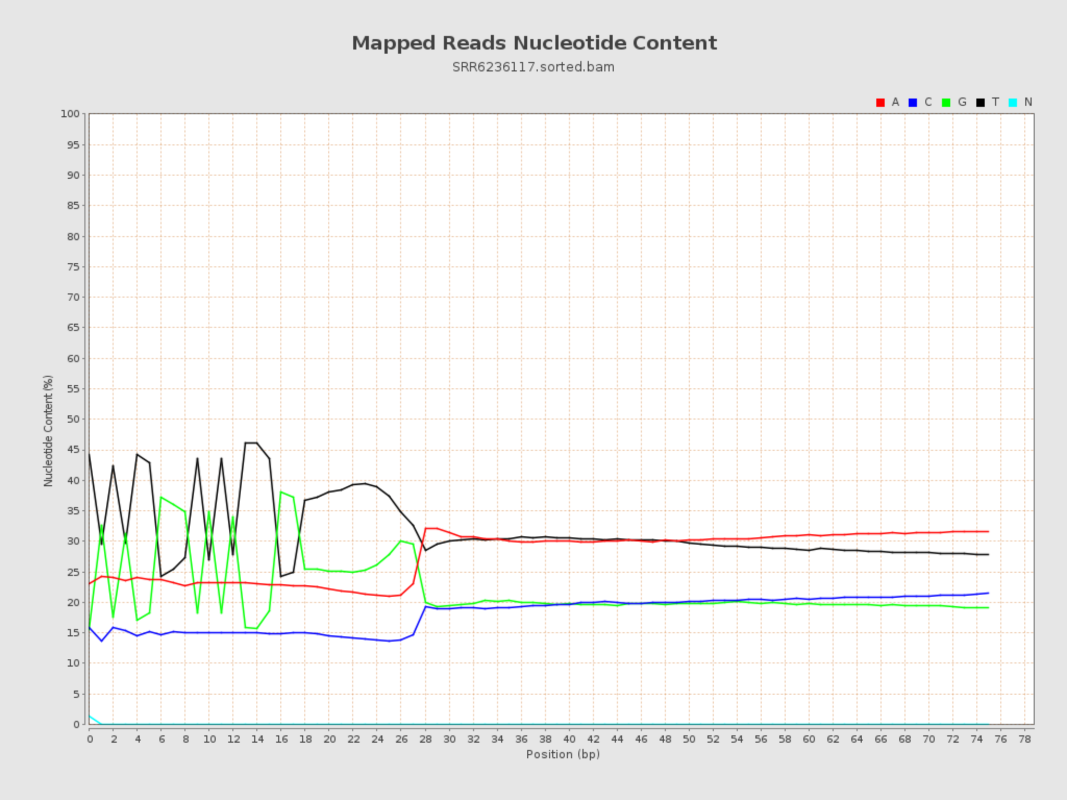
6. Results : Genome Fraction Coverage



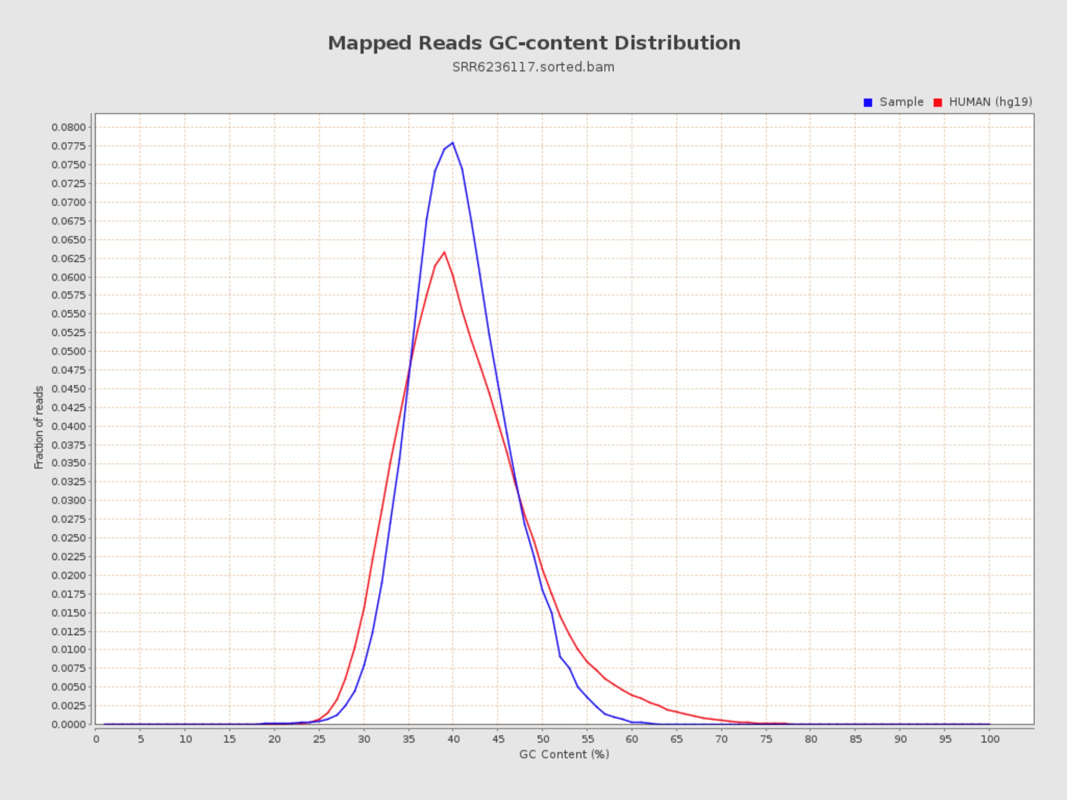
7. Results : Duplication Rate Histogram



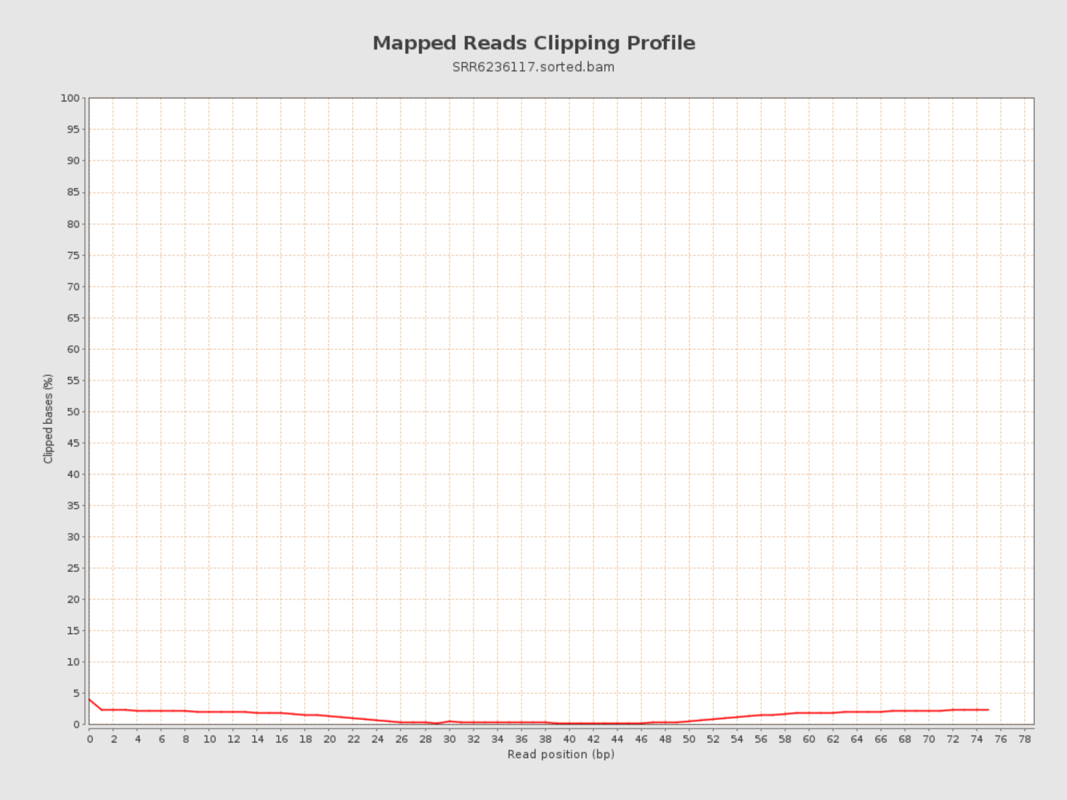
8. Results : Mapped Reads Nucleotide Content



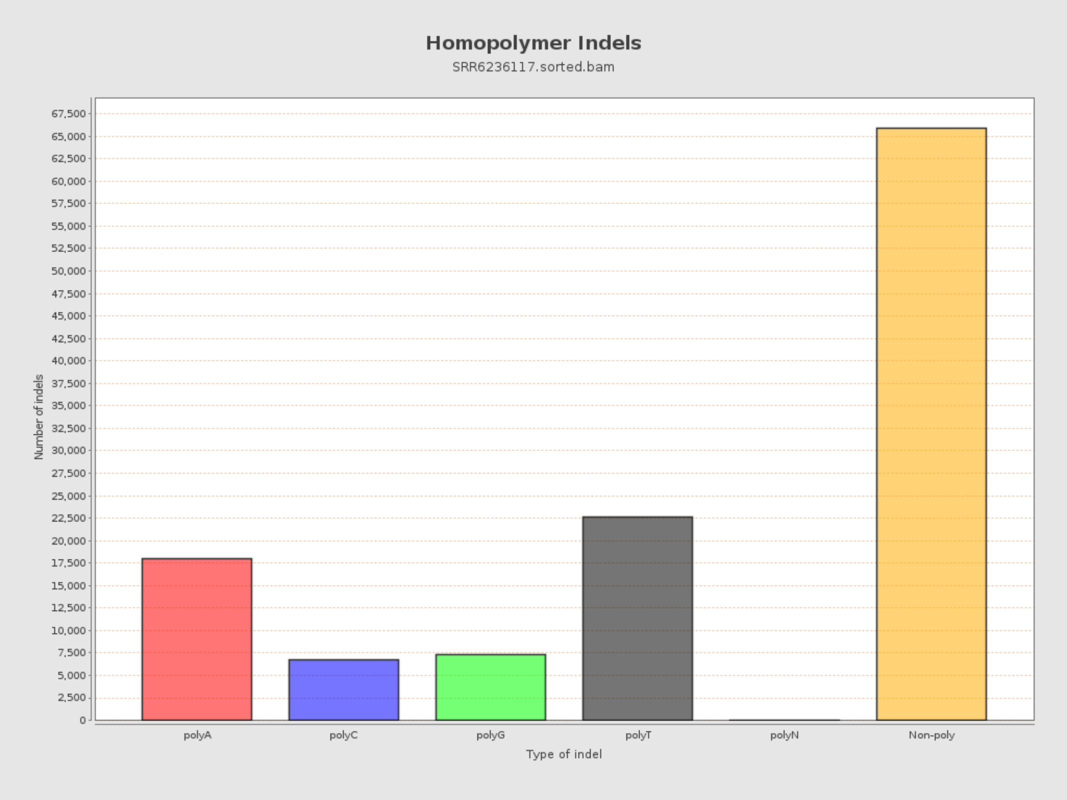
9. Results : Mapped Reads GC-content Distribution



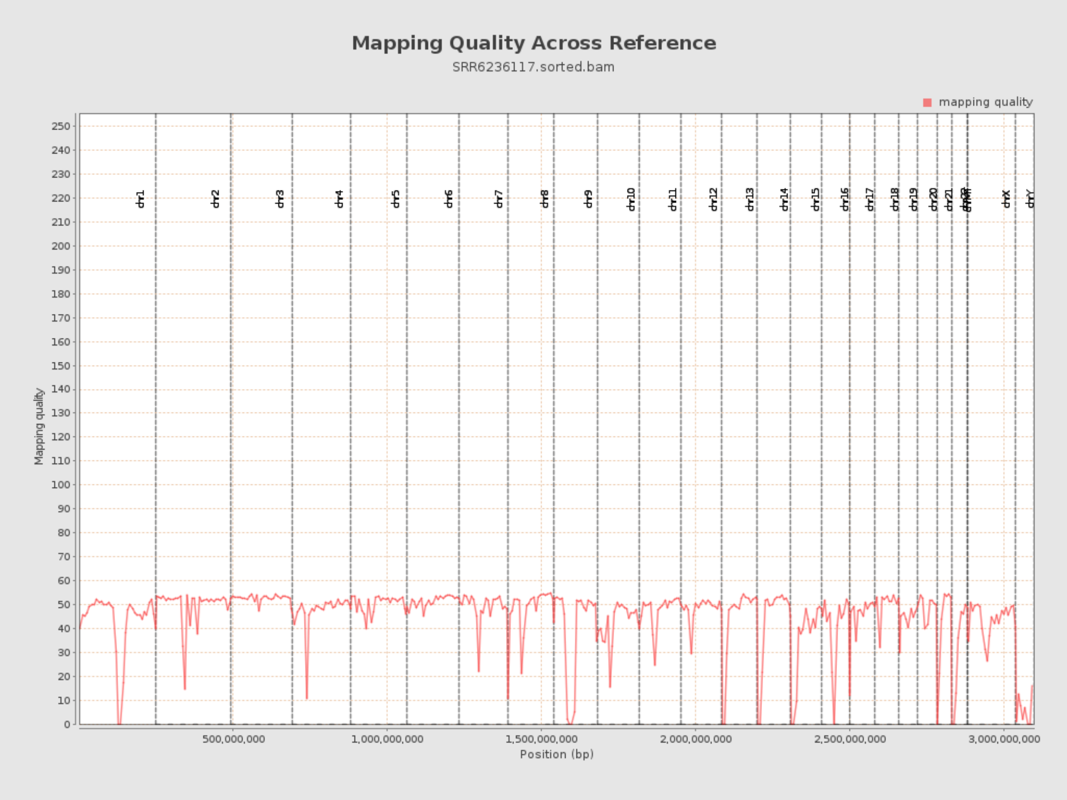
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram