Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 20:54:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6236107.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_SRR6236107 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6236107.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 20:54:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6236107.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,211,033
Mapped reads	1,054,676 / 87.09%
Unmapped reads	156,357 / 12.91%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,467 / 0.53%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	43,495 / 3.59%
Duplication rate	3.31%
Clipped reads	471,412 / 38.93%

2.2. ACGT Content

Number/percentage of A's	19,442,867 / 27.81%
Number/percentage of C's	12,358,327 / 17.68%
Number/percentage of T's	22,781,432 / 32.58%
Number/percentage of G's	15,292,055 / 21.87%
Number/percentage of N's	40,357 / 0.06%
GC Percentage	39.55%

2.3. Coverage

Mean	0.0226

Standard Deviation	0.2446

2.4. Mapping Quality

Mean Mapping Quality	46.37

2.5. Mismatches and indels

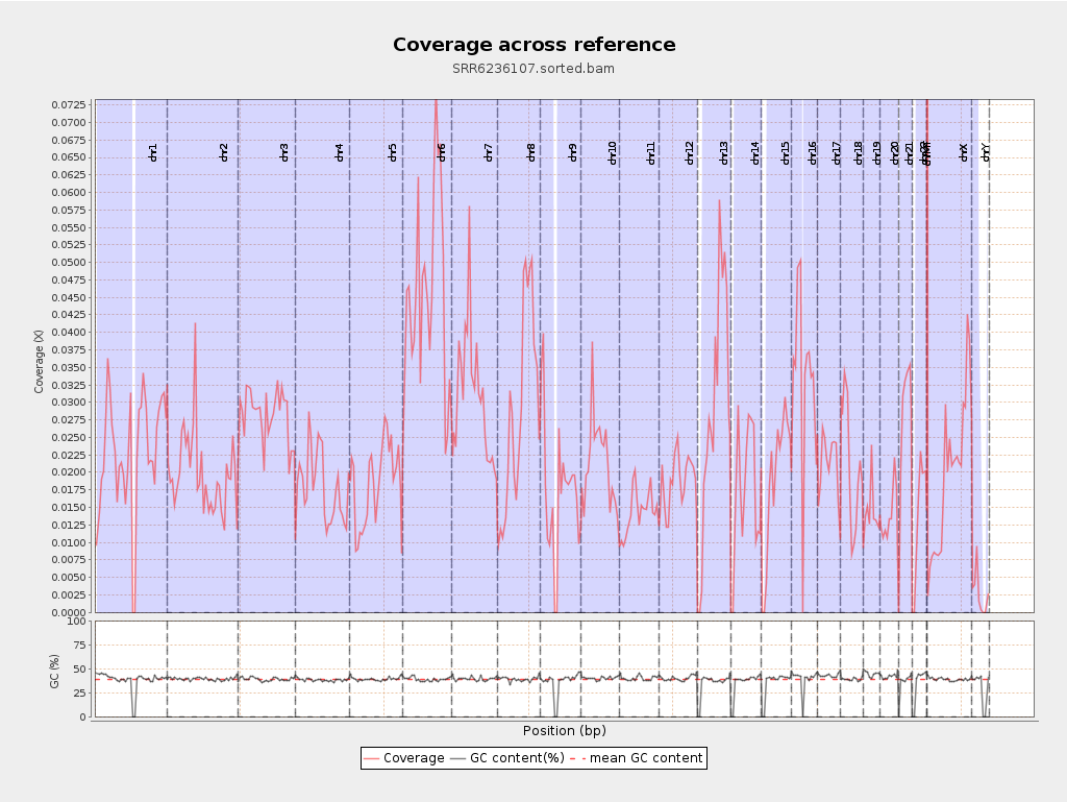
General error rate	0.84%
Mismatches	574,718
Insertions	5,139
Mapped reads with at least one insertion	0.48%
Deletions	20,372
Mapped reads with at least one deletion	1.91%
Homopolymer indels	46.83%

2.6. Chromosome stats

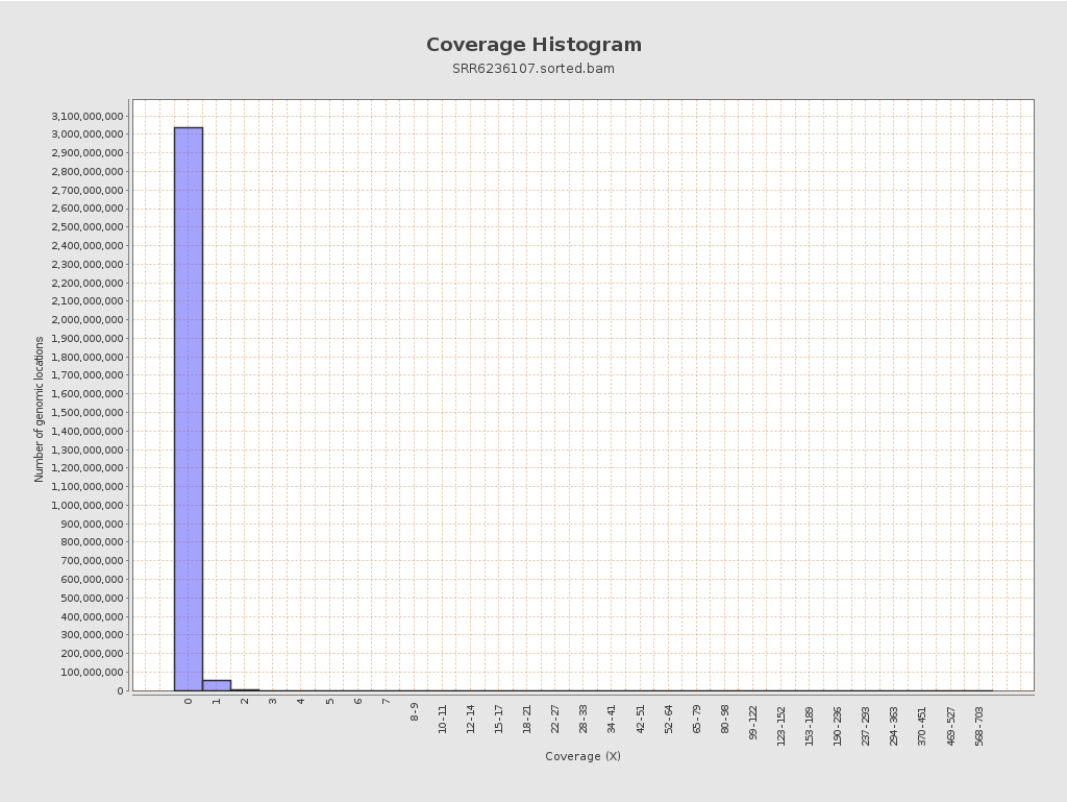
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	5673246	0.0228	0.3117
chr2	243199373	4845417	0.0199	0.2355
chr3	198022430	5584326	0.0282	0.1839
chr4	191154276	3394504	0.0178	0.1547
chr5	180915260	3381728	0.0187	0.1503
chr6	171115067	7722186	0.0451	0.3088
chr7	159138663	4910685	0.0309	0.4112

chr8	146364022	4275967	0.0292	0.4624
chr9	141213431	2468779	0.0175	0.2065
chr10	135534747	2876174	0.0212	0.2166
chr11	135006516	1958849	0.0145	0.1685
chr12	133851895	2489735	0.0186	0.1552
chr13	115169878	3337531	0.029	0.1876
chr14	107349540	1785053	0.0166	0.1491
chr15	102531392	1937315	0.0189	0.1514
chr16	90354753	2957090	0.0327	0.2086
chr17	81195210	1710447	0.0211	0.179
chr18	78077248	1610963	0.0206	0.3689
chr19	59128983	860970	0.0146	0.2435
chr20	63025520	867625	0.0138	0.134
chr21	48129895	1333857	0.0277	0.1892
chr22	51304566	711339	0.0139	0.1278
chrMT	16571	10495	0.6333	0.8783
chrX	155270560	3088380	0.0199	0.1693
chrY	59373566	157788	0.0027	0.0792

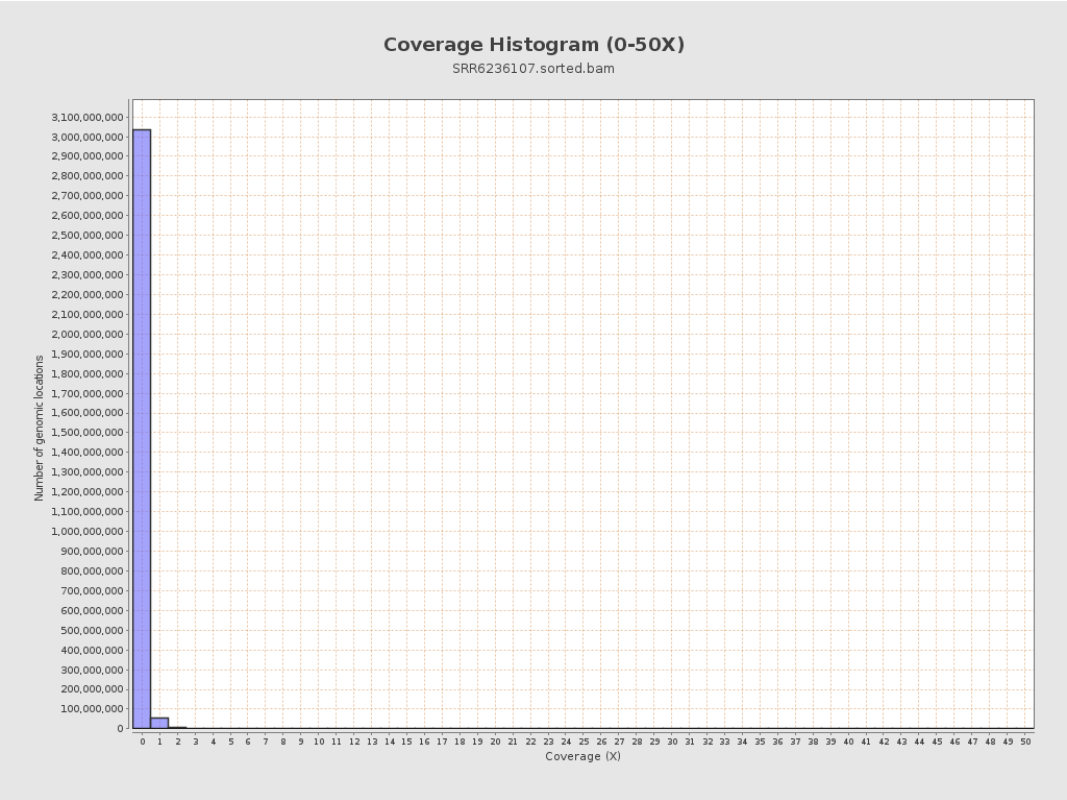
3. Results : Coverage across reference



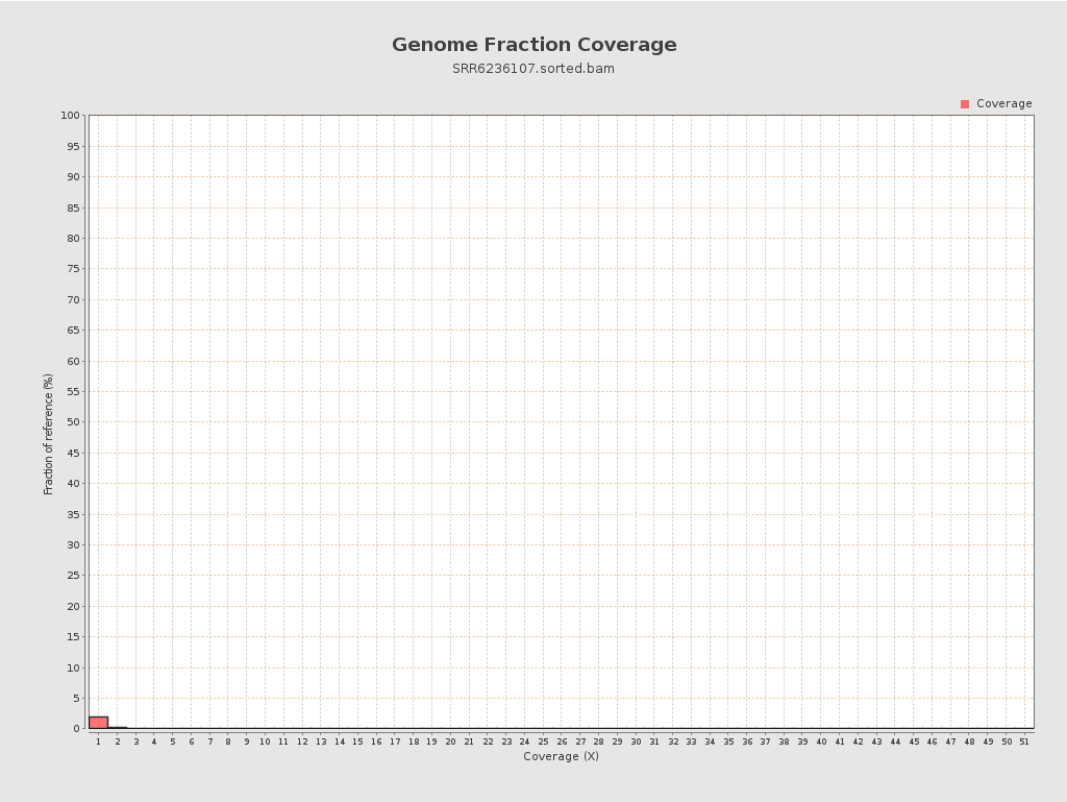
4. Results : Coverage Histogram



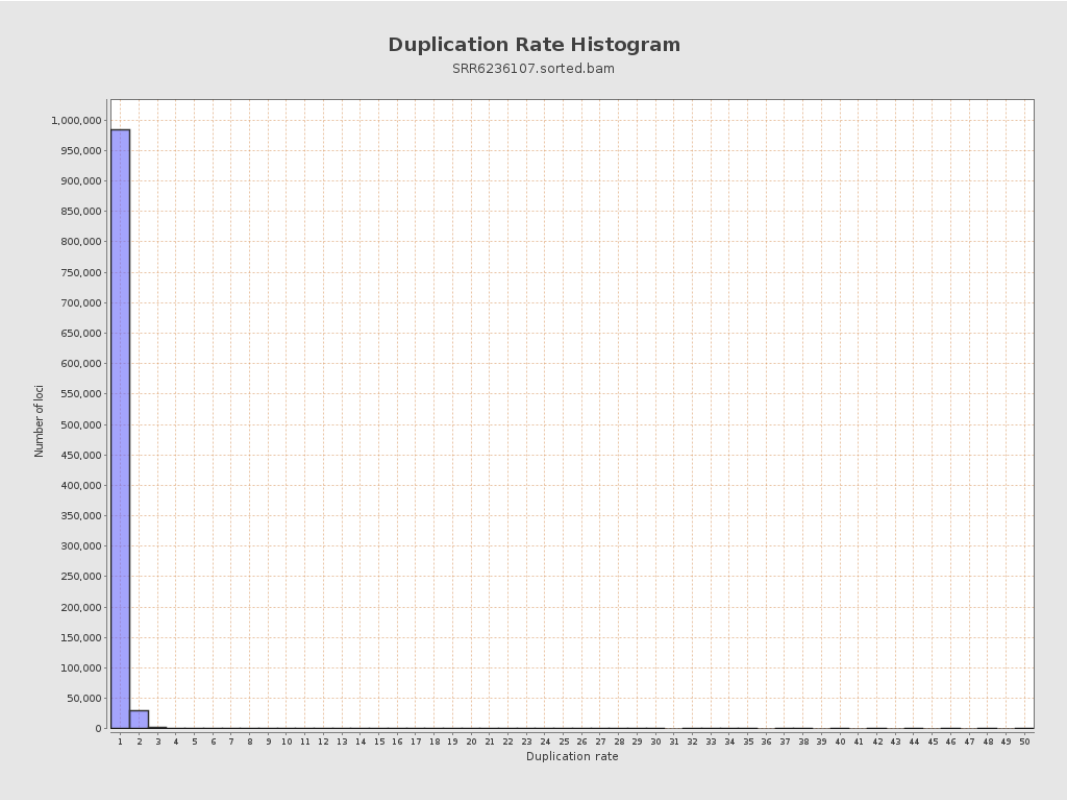
5. Results : Coverage Histogram (0-50X)



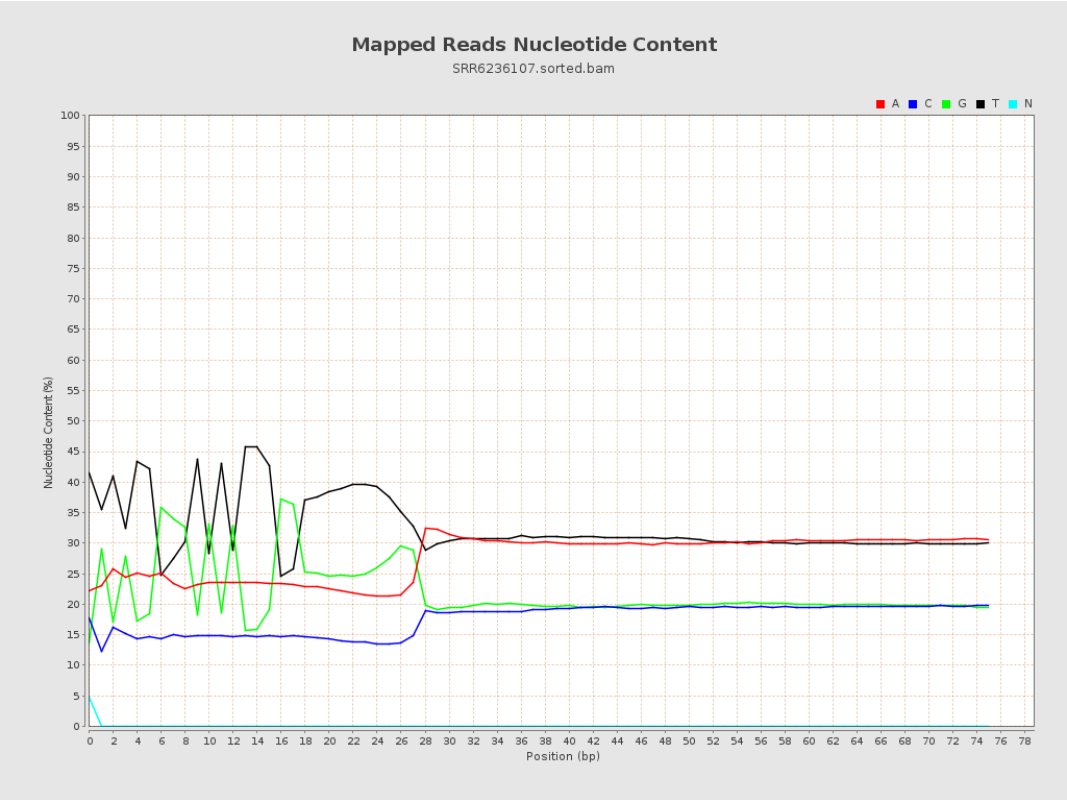
6. Results : Genome Fraction Coverage



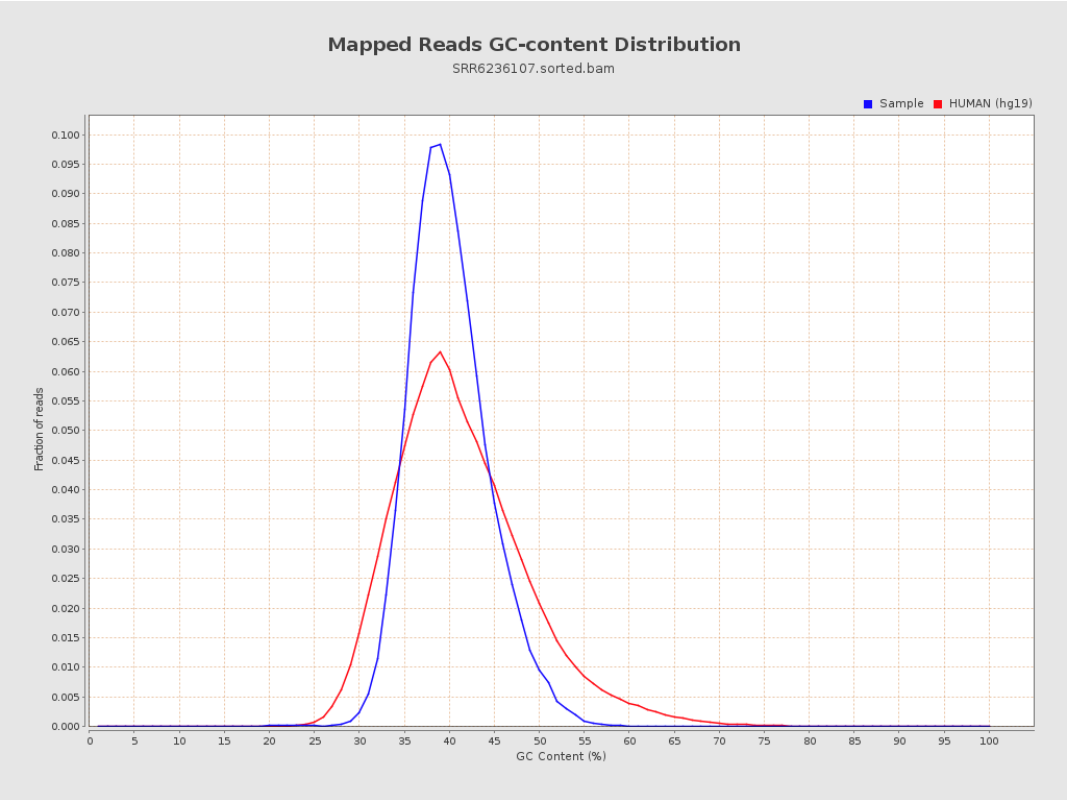
7. Results : Duplication Rate Histogram



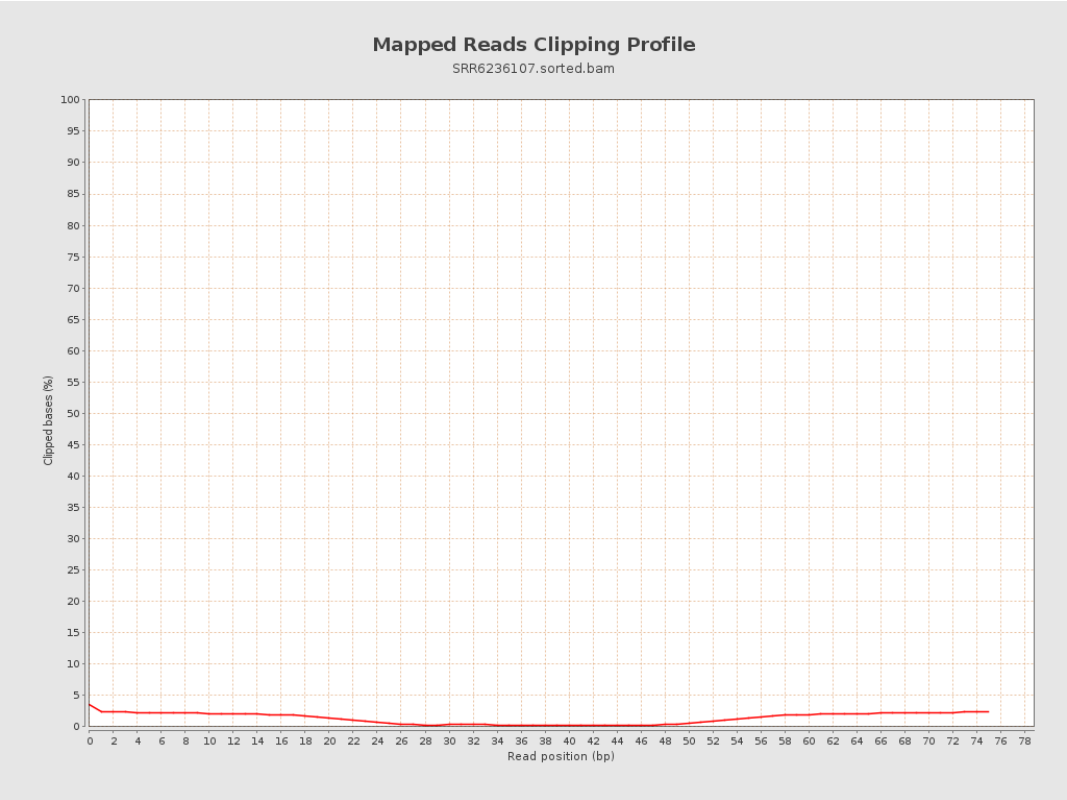
8. Results : Mapped Reads Nucleotide Content



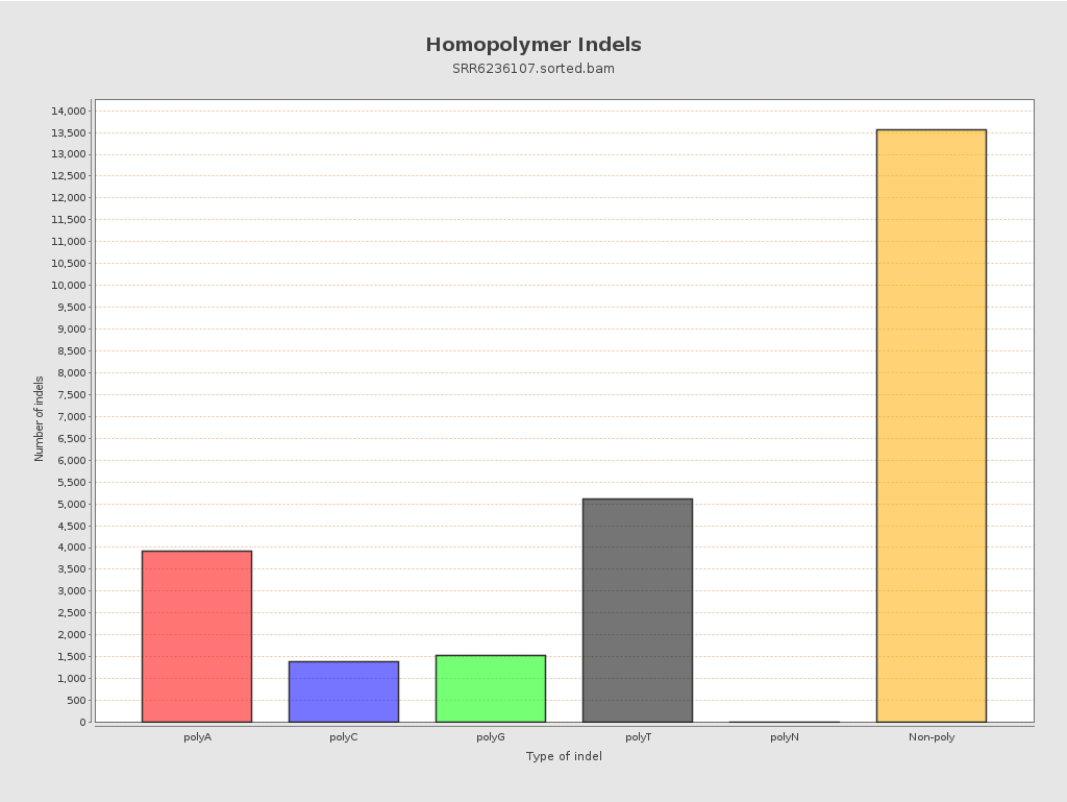
9. Results : Mapped Reads GC-content Distribution



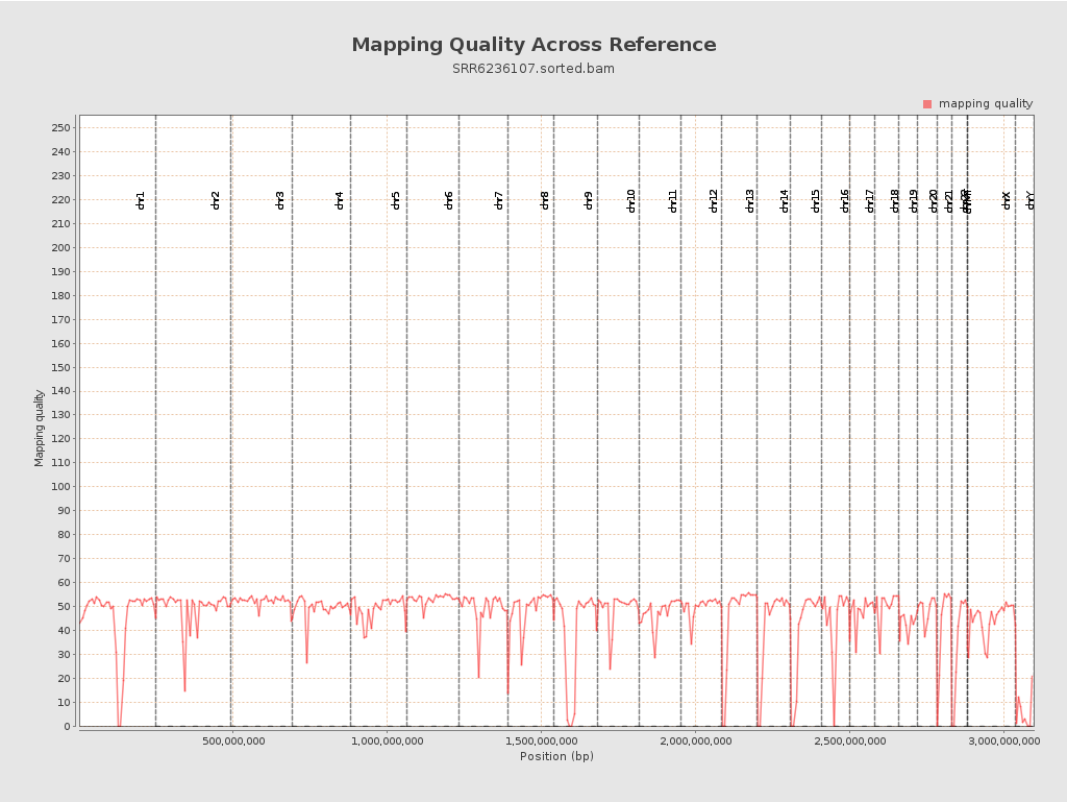
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram