Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 16:13:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068936.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_SRR6068936 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068936.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 16:13:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068936.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,120,337
Mapped reads	1,754,693 / 82.76%
Unmapped reads	365,644 / 17.24%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,893 / 0.42%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	61,833 / 2.92%
Duplication rate	2.12%
Clipped reads	940,358 / 44.35%

2.2. ACGT Content

Number/percentage of A's	29,903,030 / 26.32%
Number/percentage of C's	19,660,432 / 17.31%
Number/percentage of T's	37,386,847 / 32.91%
Number/percentage of G's	26,373,414 / 23.22%
Number/percentage of N's	271,072 / 0.24%
GC Percentage	40.52%

2.3. Coverage

Mean	0.0367

Standard Deviation	0.4147

2.4. Mapping Quality

Mean Mapping Quality	43.89

2.5. Mismatches and indels

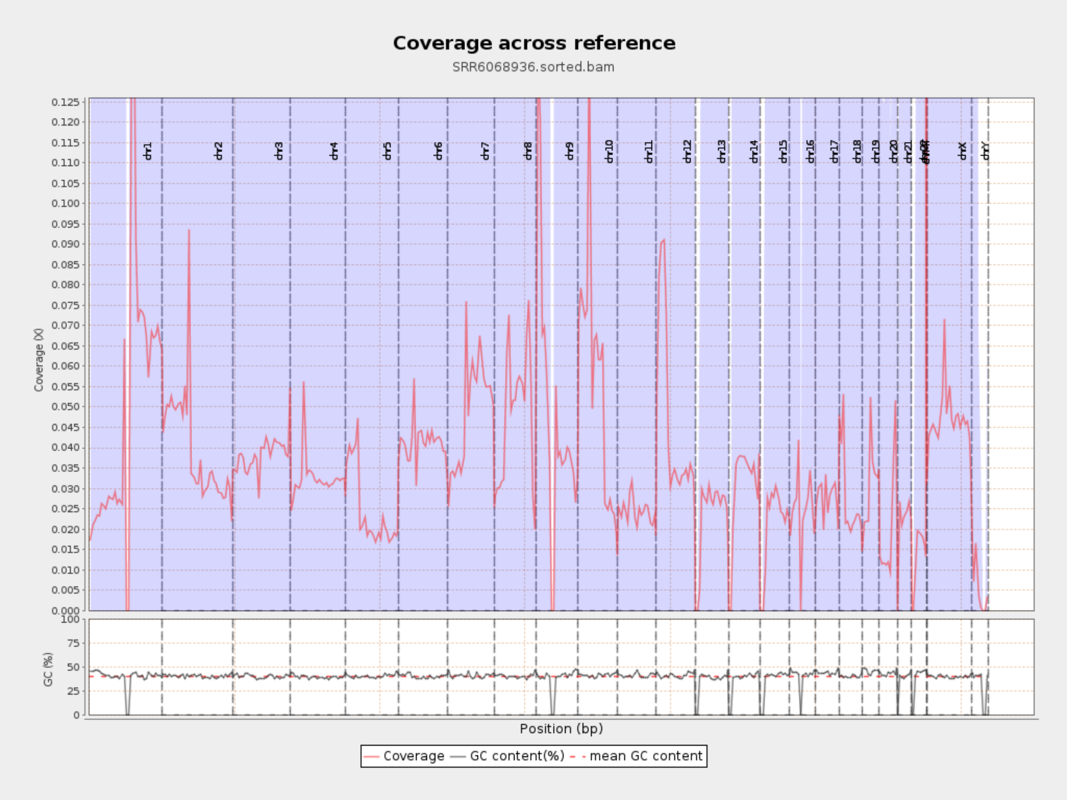
General error rate	0.97%
Mismatches	1,086,258
Insertions	11,020
Mapped reads with at least one insertion	0.62%
Deletions	29,286
Mapped reads with at least one deletion	1.65%
Homopolymer indels	48.07%

2.6. Chromosome stats

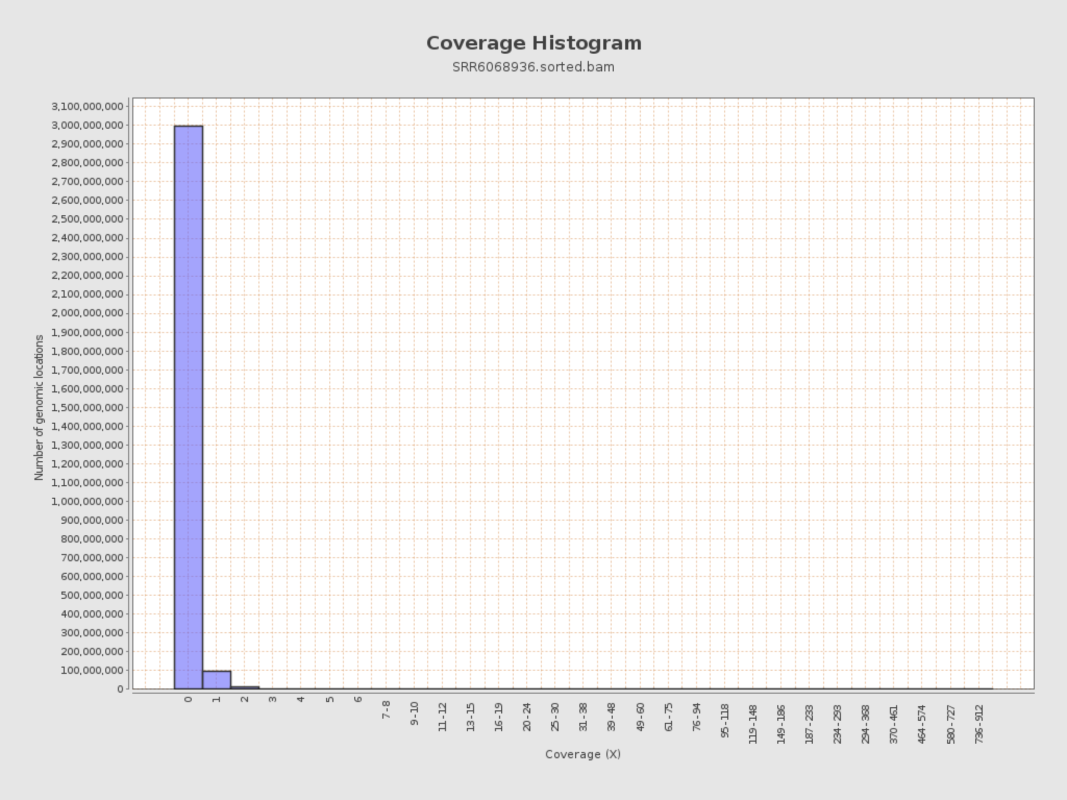
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12308909	0.0494	0.7387
chr2	243199373	9724243	0.04	0.4086
chr3	198022430	7541415	0.0381	0.2751
chr4	191154276	6212284	0.0325	0.2251
chr5	180915260	4483952	0.0248	0.1721
chr6	171115067	7065893	0.0413	0.3019
chr7	159138663	7857582	0.0494	0.5468

chr8	146364022	7047506	0.0482	0.5258
chr9	141213431	6869488	0.0486	0.4349
chr10	135534747	7853862	0.0579	0.7936
chr11	135006516	3267709	0.0242	0.2844
chr12	133851895	6190661	0.0463	0.2487
chr13	115169878	2673743	0.0232	0.1626
chr14	107349540	3192528	0.0297	0.2432
chr15	102531392	2166548	0.0211	0.1573
chr16	90354753	2229722	0.0247	0.2404
chr17	81195210	2233585	0.0275	0.1981
chr18	78077248	2186984	0.028	0.6944
chr19	59128983	1824914	0.0309	0.4634
chr20	63025520	1288640	0.0204	0.1788
chr21	48129895	1053714	0.0219	0.2088
chr22	51304566	660541	0.0129	0.1338
chrMT	16571	83233	5.0228	4.8277
chrX	155270560	7308962	0.0471	0.2858
chrY	59373566	316950	0.0053	0.1379

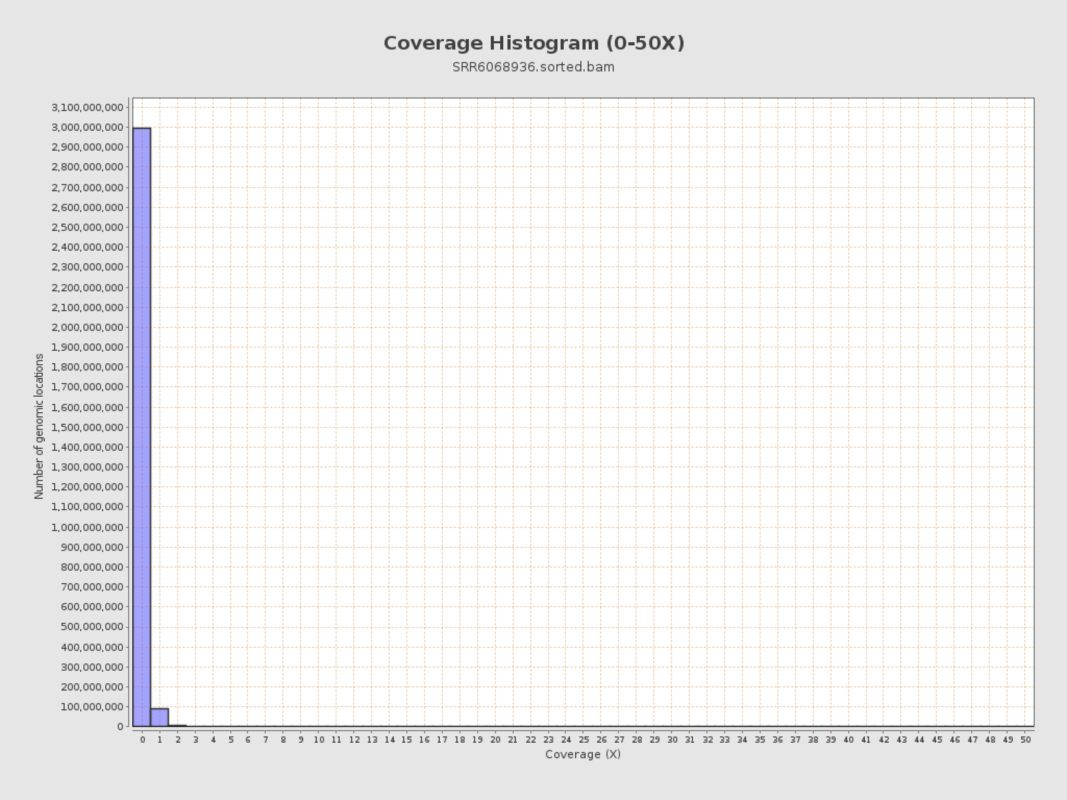
3. Results : Coverage across reference



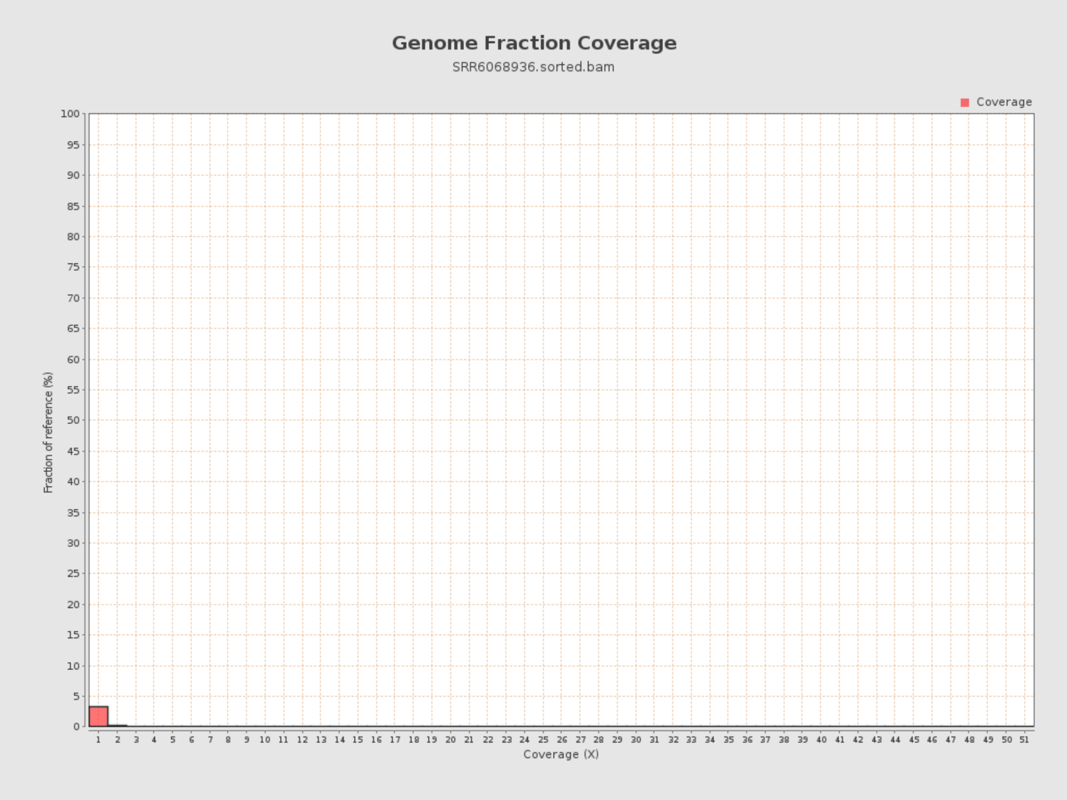
4. Results : Coverage Histogram



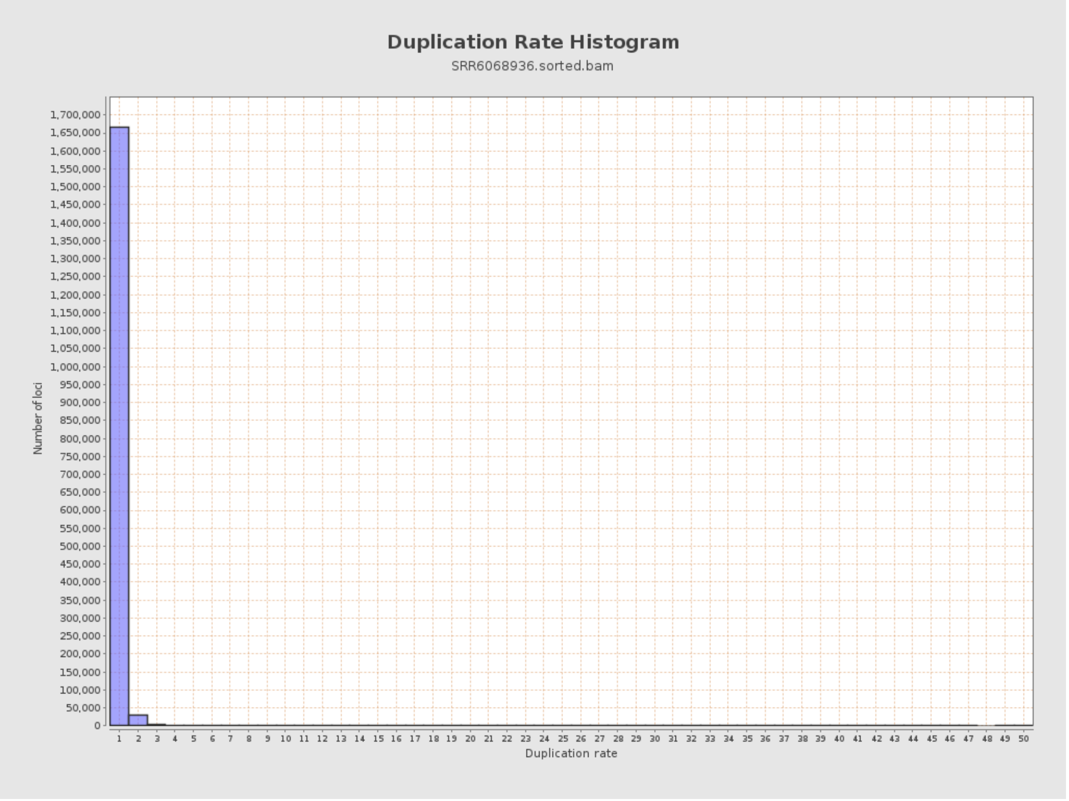
5. Results : Coverage Histogram (0-50X)



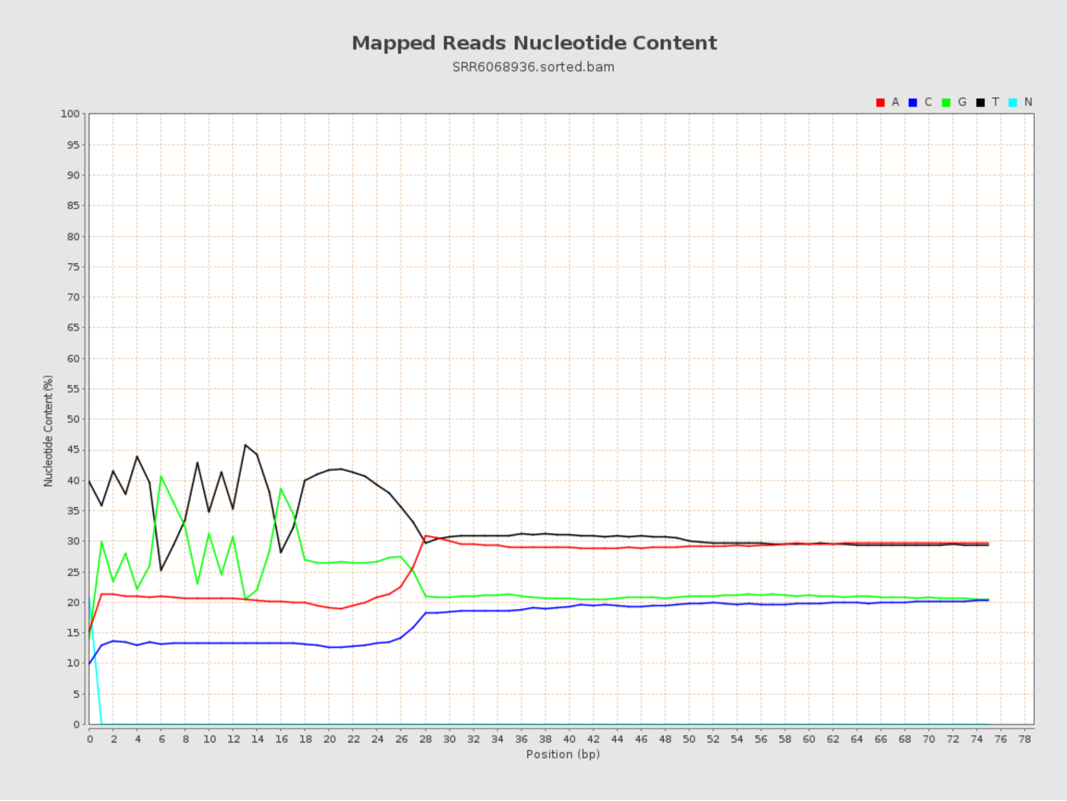
6. Results : Genome Fraction Coverage



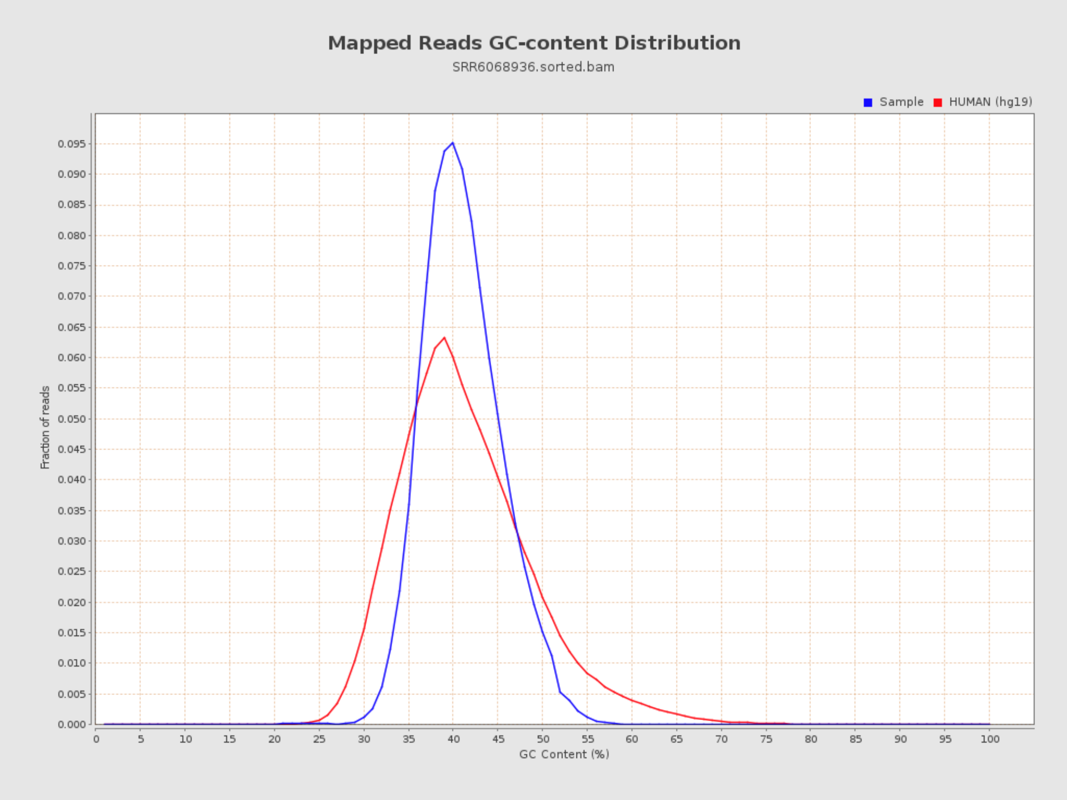
7. Results : Duplication Rate Histogram



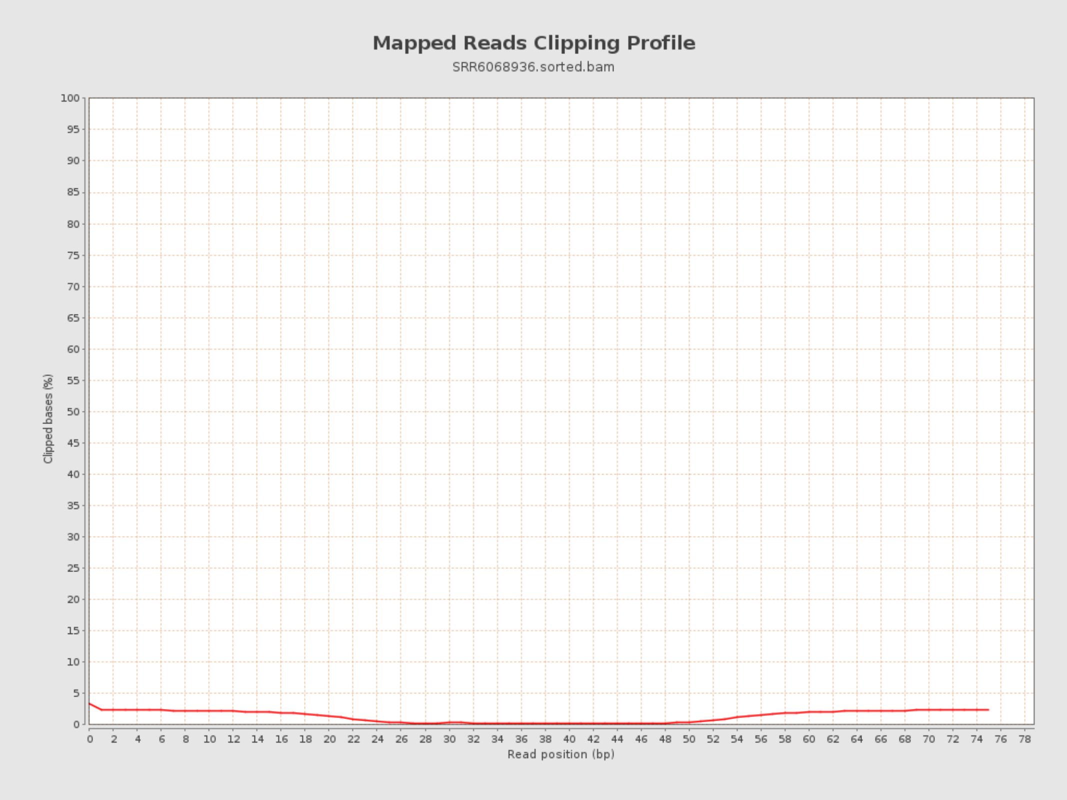
8. Results : Mapped Reads Nucleotide Content



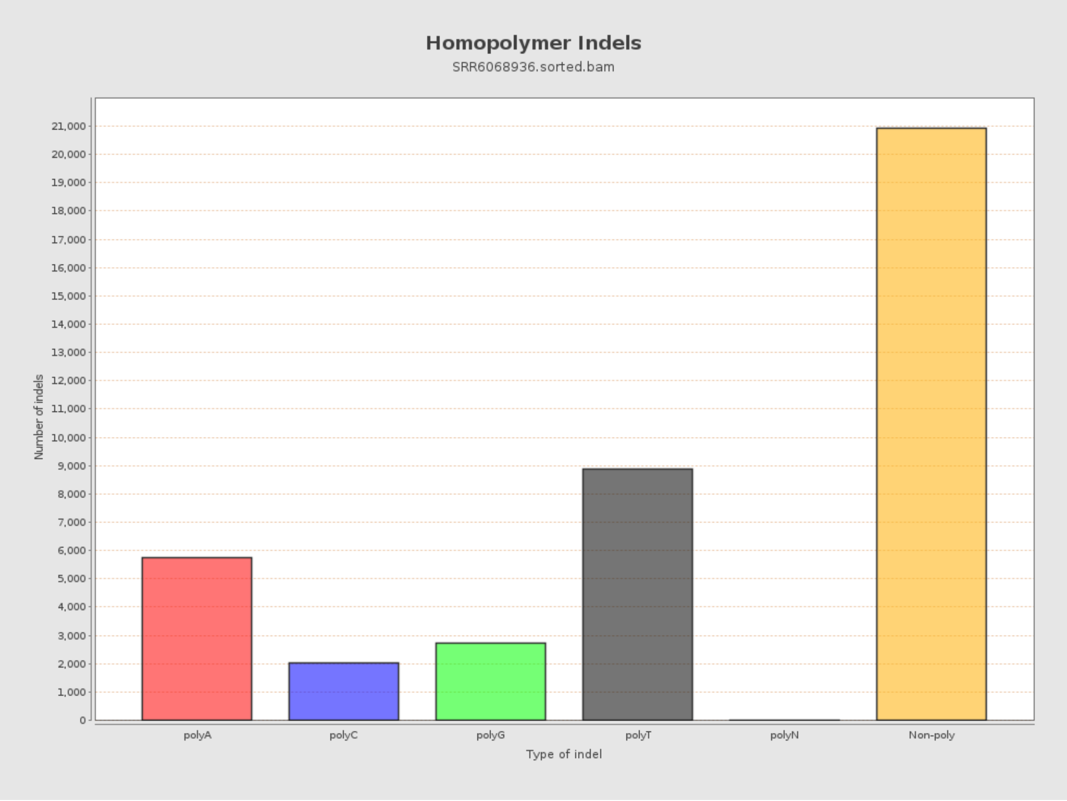
9. Results : Mapped Reads GC-content Distribution



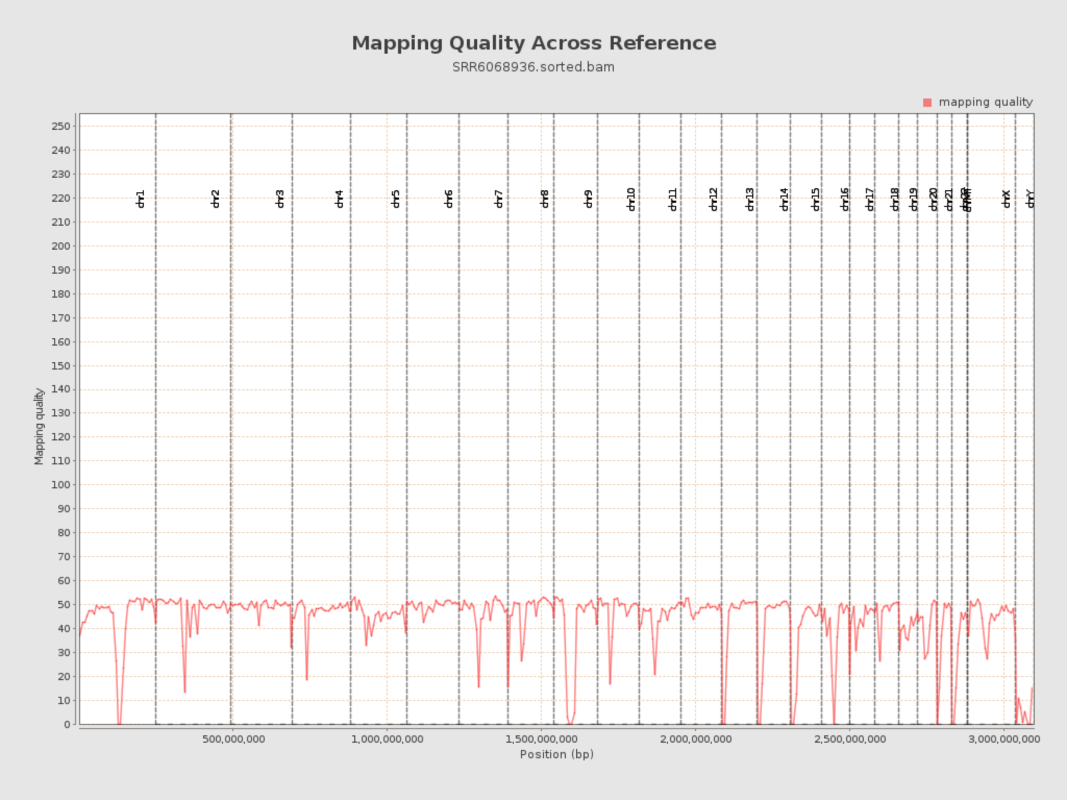
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram