Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 14:40:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068173.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_SRR6068173 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068173.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 14:40:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068173.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,645,710
Mapped reads	3,386,635 / 92.89%
Unmapped reads	259,075 / 7.11%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	30,591 / 0.84%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	396,142 / 10.87%
Duplication rate	9.9%
Clipped reads	1,821,262 / 49.96%

2.2. ACGT Content

Number/percentage of A's	57,894,540 / 26.61%
Number/percentage of C's	38,423,159 / 17.66%
Number/percentage of T's	71,452,942 / 32.84%
Number/percentage of G's	49,758,842 / 22.87%
Number/percentage of N's	24,905 / 0.01%
GC Percentage	40.53%

2.3. Coverage

Mean	0.0703

Standard Deviation	0.7549

2.4. Mapping Quality

Mean Mapping Quality	46.3

2.5. Mismatches and indels

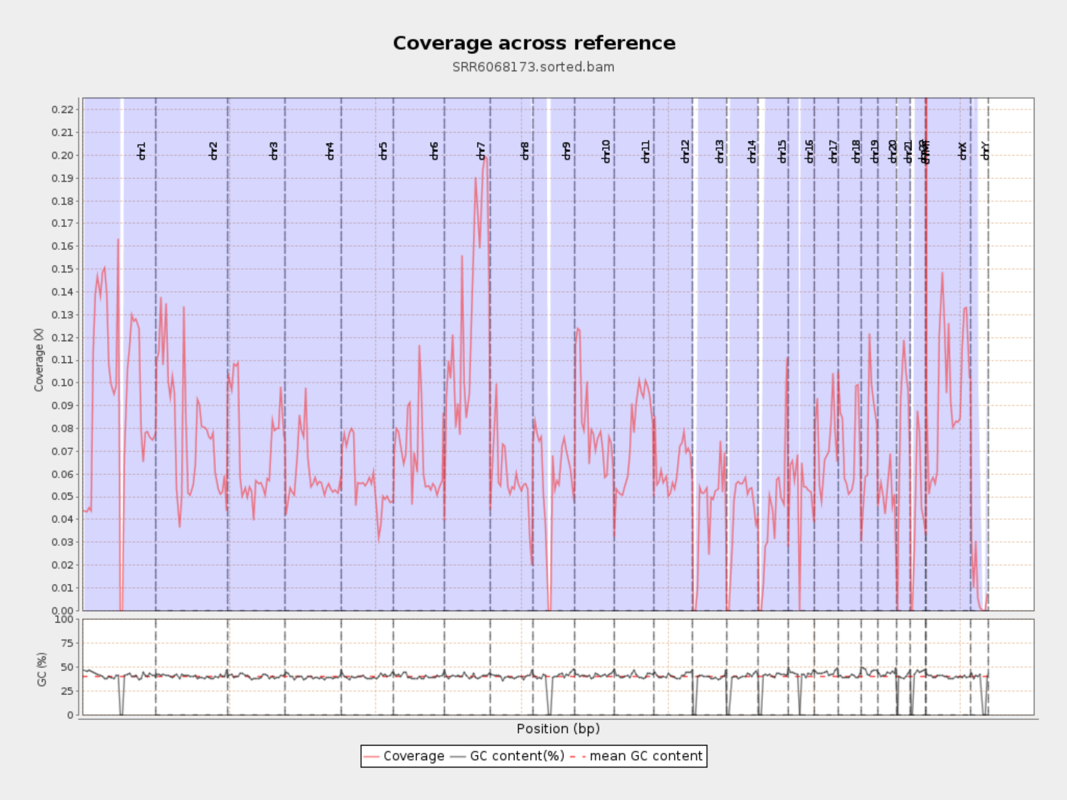
General error rate	0.59%
Mismatches	1,262,705
Insertions	13,978
Mapped reads with at least one insertion	0.41%
Deletions	54,518
Mapped reads with at least one deletion	1.59%
Homopolymer indels	44.56%

2.6. Chromosome stats

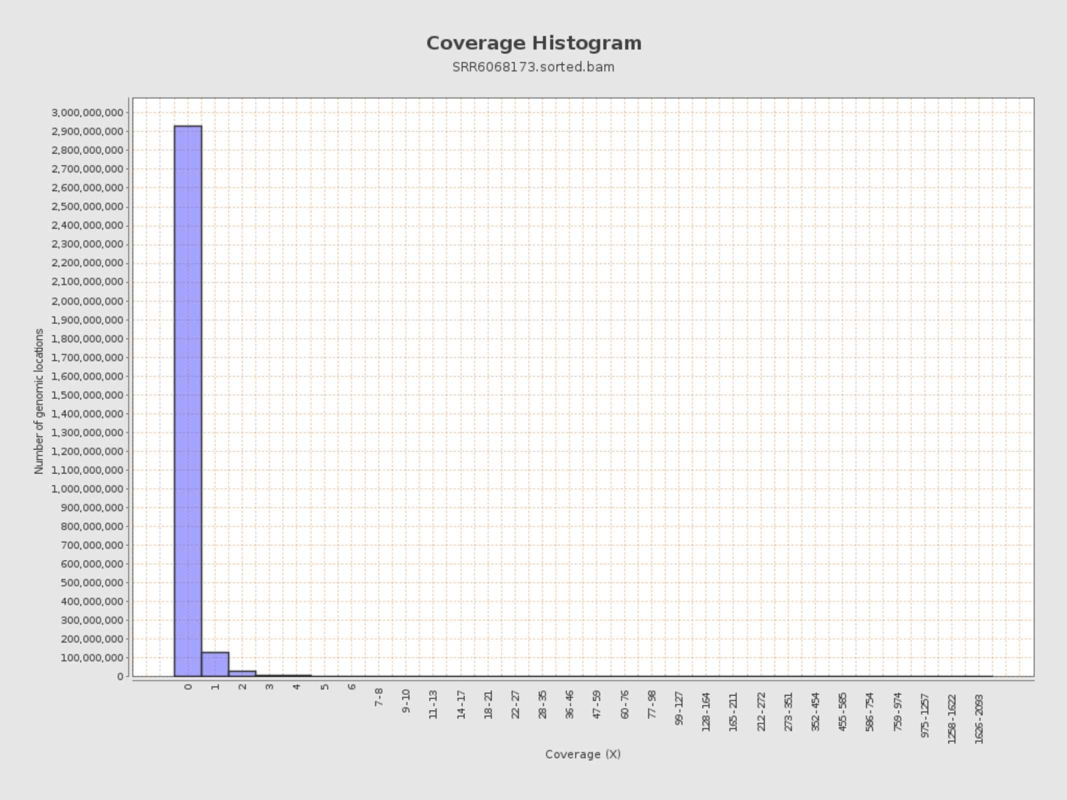
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	23706296	0.0951	1.6986
chr2	243199373	19459643	0.08	1.024
chr3	198022430	14111243	0.0713	0.3377
chr4	191154276	11402363	0.0597	0.3319
chr5	180915260	10347718	0.0572	0.3051
chr6	171115067	11713286	0.0685	0.453
chr7	159138663	20668385	0.1299	1.0399

chr8	146364022	8417272	0.0575	1.0048
chr9	141213431	8113451	0.0575	0.5082
chr10	135534747	11102963	0.0819	0.5079
chr11	135006516	10319982	0.0764	0.4695
chr12	133851895	8460980	0.0632	0.3499
chr13	115169878	5087477	0.0442	0.2954
chr14	107349540	4677549	0.0436	0.3186
chr15	102531392	4253706	0.0415	0.2882
chr16	90354753	4604355	0.051	0.3107
chr17	81195210	6025753	0.0742	0.3669
chr18	78077248	5696416	0.073	0.9688
chr19	59128983	4502450	0.0761	1.0533
chr20	63025520	3220207	0.0511	0.3093
chr21	48129895	3839726	0.0798	0.371
chr22	51304566	2207610	0.043	0.2547
chrMT	16571	375621	22.6674	13.4605
chrX	155270560	14754983	0.095	0.4663
chrY	59373566	579111	0.0098	0.32

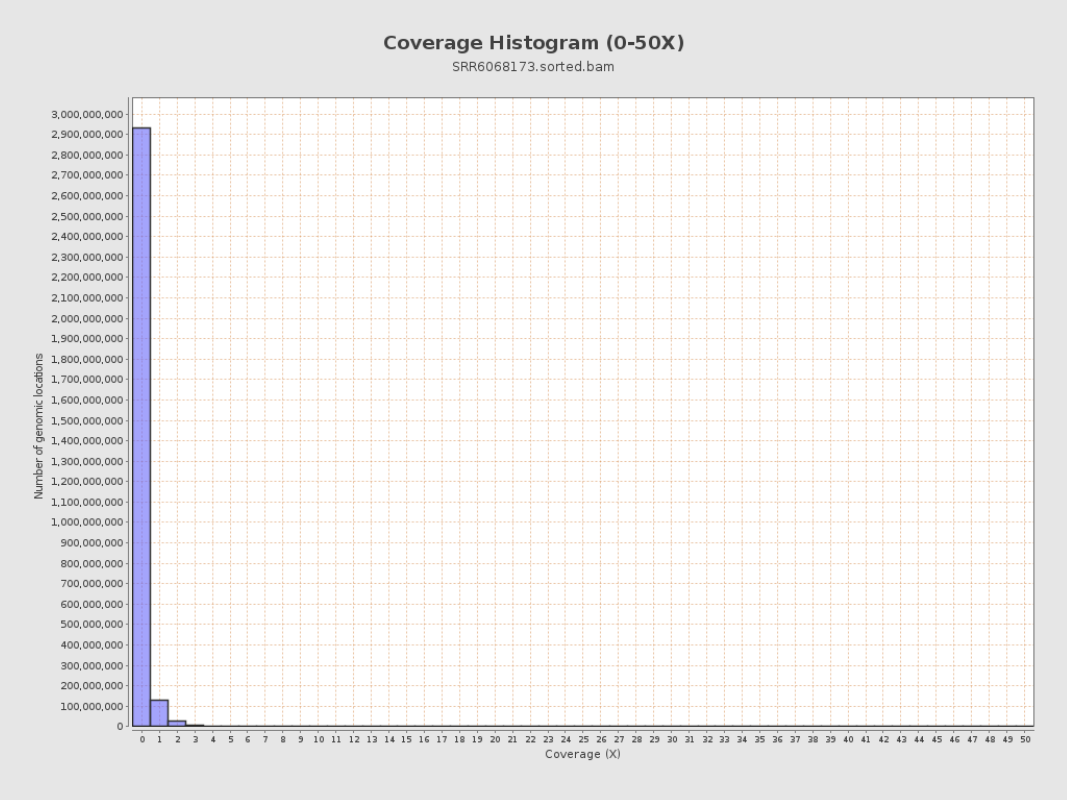
3. Results : Coverage across reference



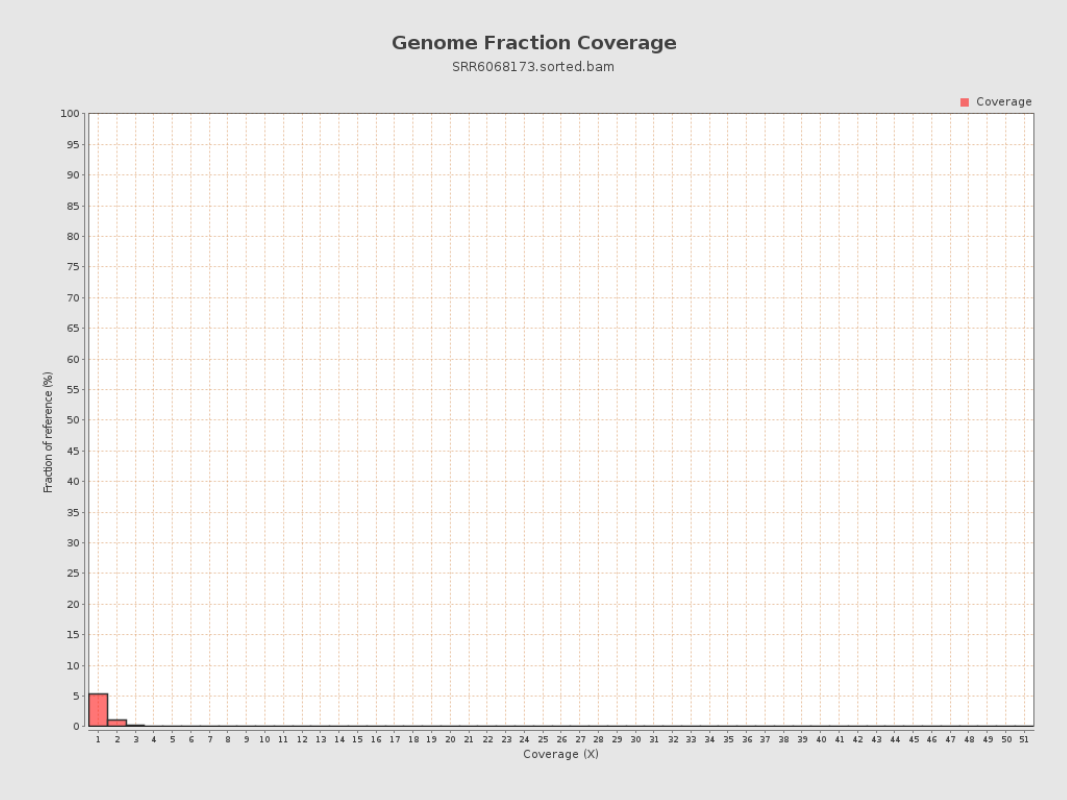
4. Results : Coverage Histogram



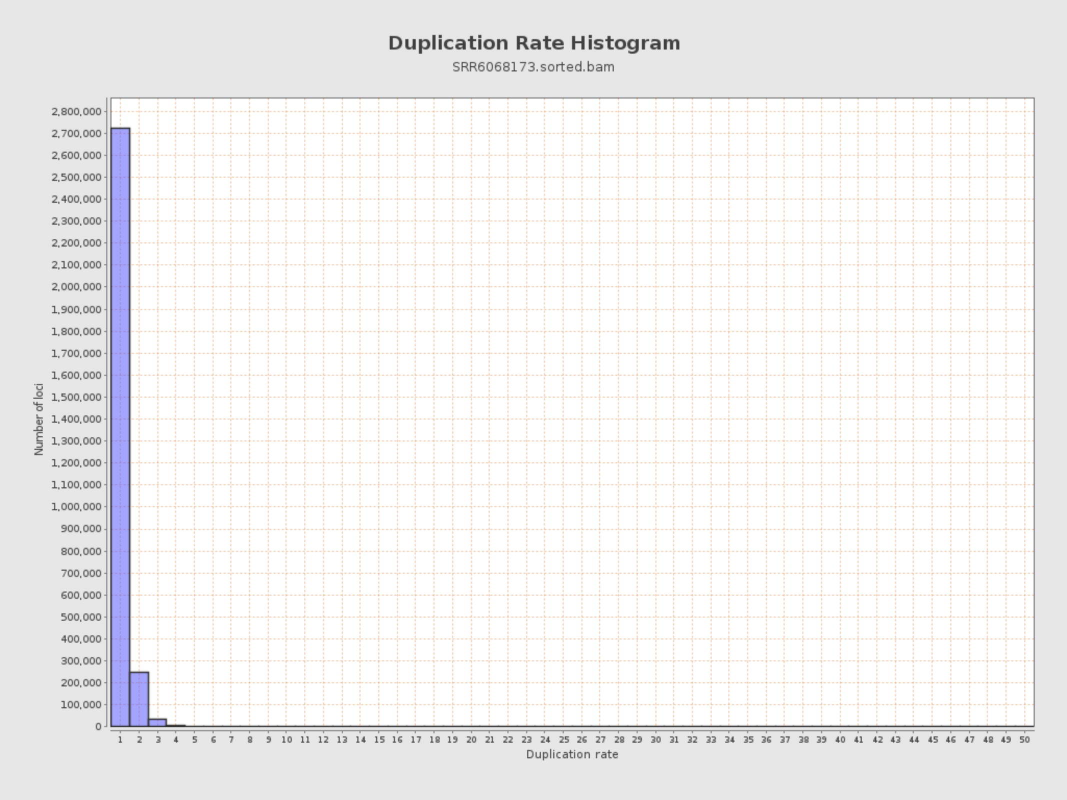
5. Results : Coverage Histogram (0-50X)



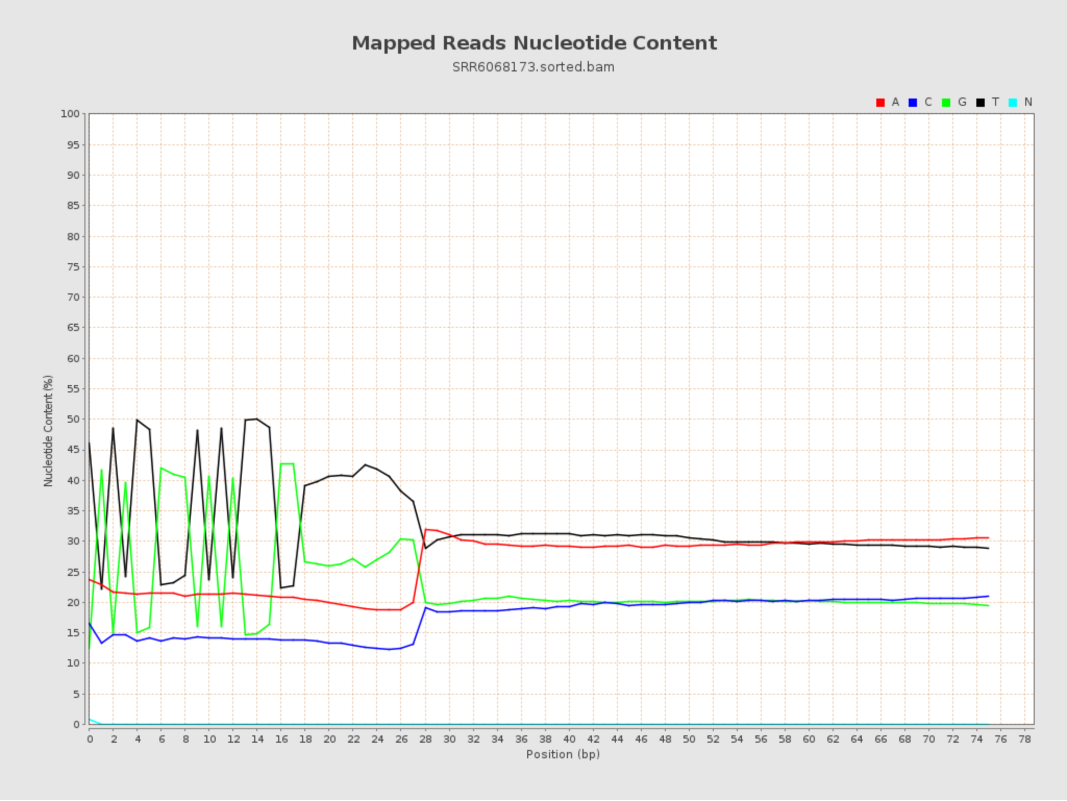
6. Results : Genome Fraction Coverage



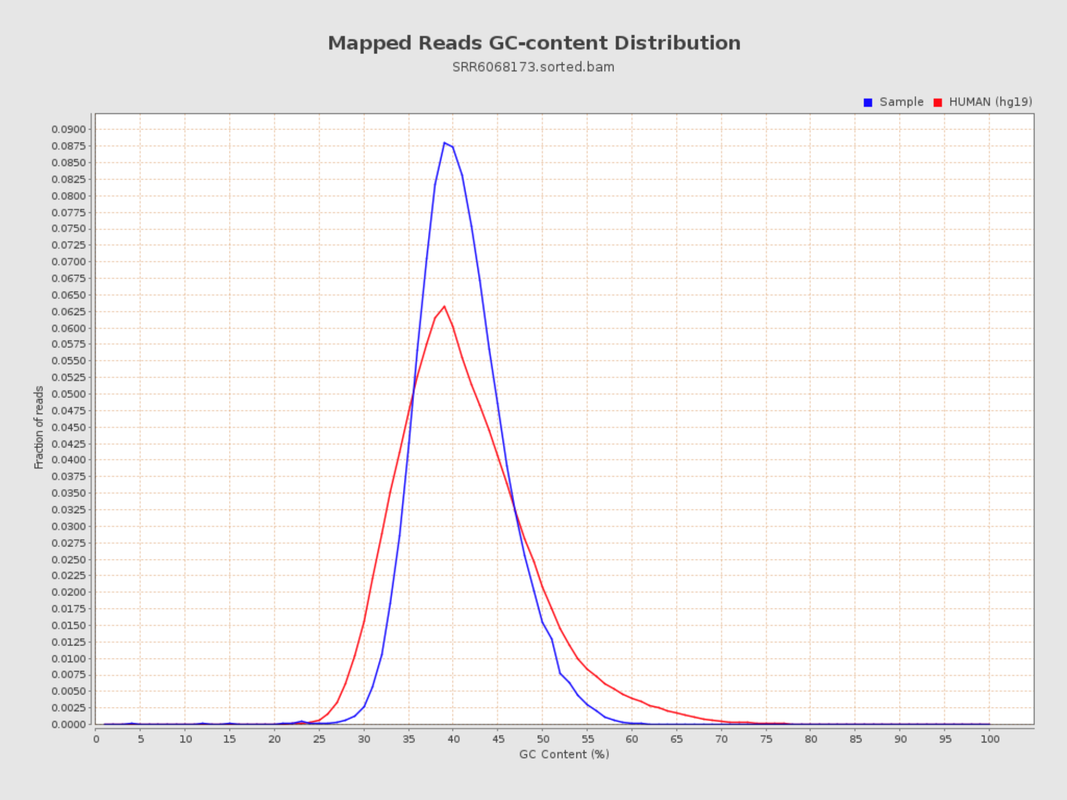
7. Results : Duplication Rate Histogram



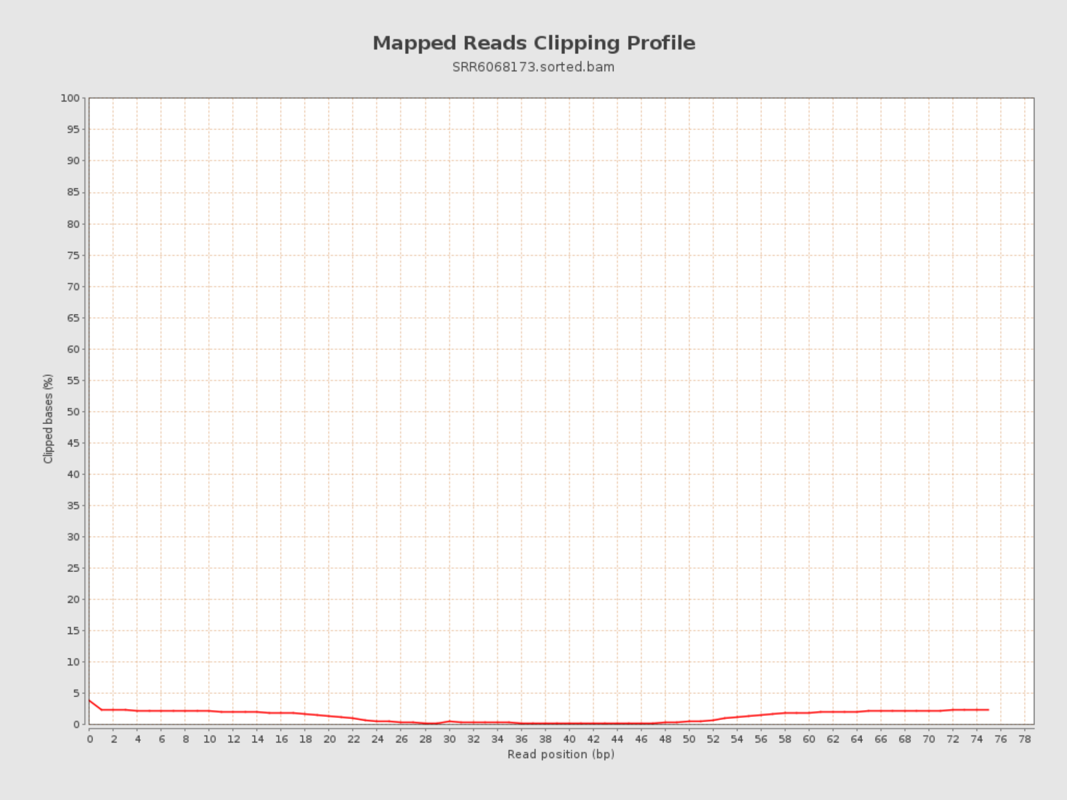
8. Results : Mapped Reads Nucleotide Content



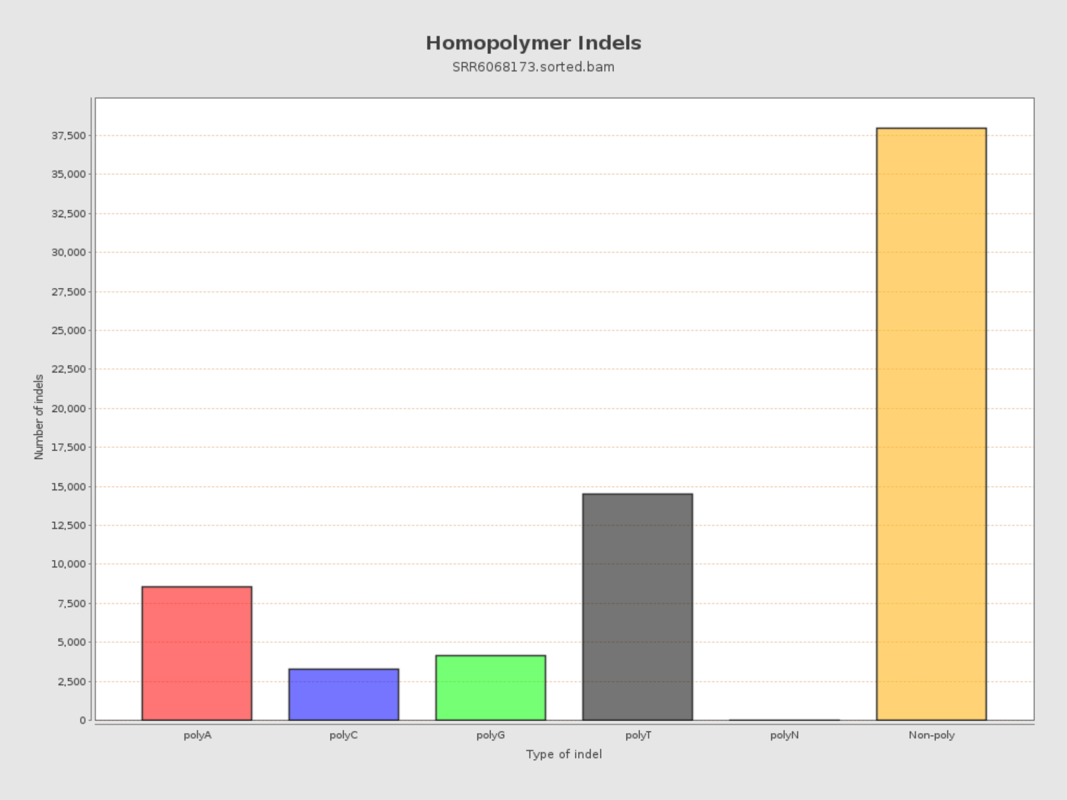
9. Results : Mapped Reads GC-content Distribution



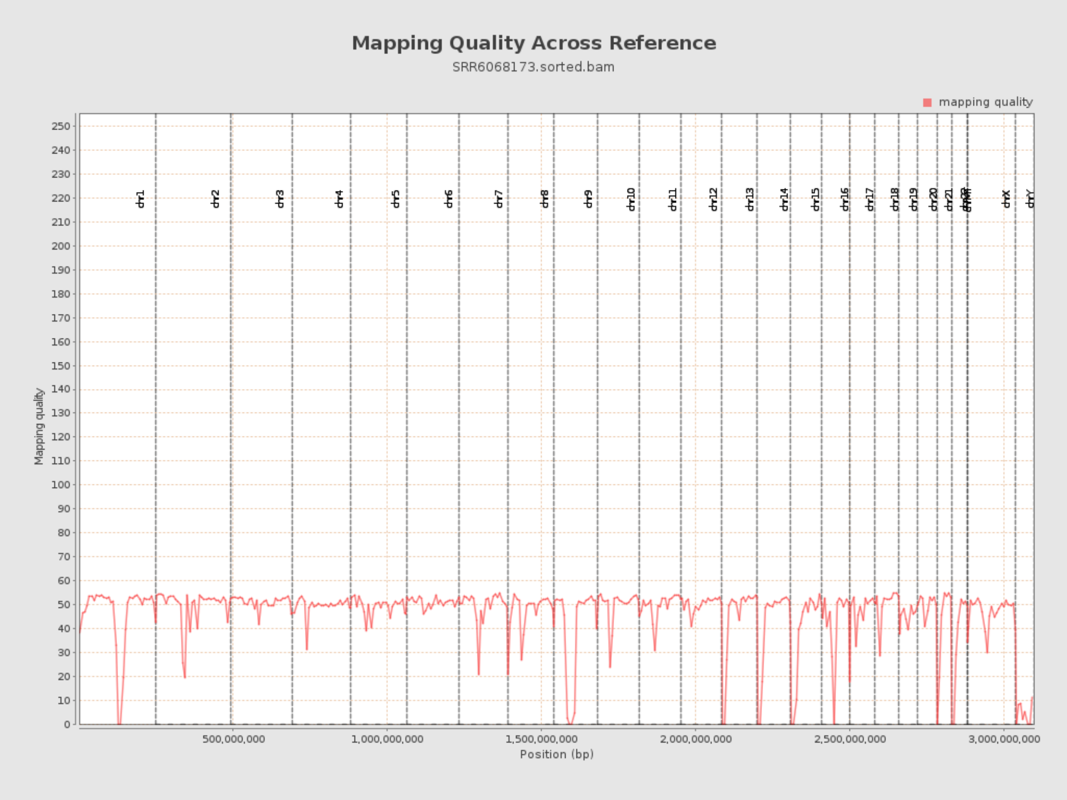
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram