Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 18:59:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013272.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_SRR6013272 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013272.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 18:59:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013272.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,797,533
Mapped reads	1,282,639 / 71.36%
Unmapped reads	514,894 / 28.64%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,719 / 0.93%
Read min/max/mean length	30 / 76 / 76.32
Duplicated reads (estimated)	205,933 / 11.46%
Duplication rate	12.42%
Clipped reads	855,110 / 47.57%

2.2. ACGT Content

Number/percentage of A's	21,910,300 / 27.69%
Number/percentage of C's	14,394,526 / 18.19%
Number/percentage of T's	25,297,777 / 31.97%
Number/percentage of G's	17,509,330 / 22.13%
Number/percentage of N's	15,299 / 0.02%
GC Percentage	40.32%

2.3. Coverage

Mean	0.0256

Standard Deviation	0.3048

2.4. Mapping Quality

Mean Mapping Quality	43.27

2.5. Mismatches and indels

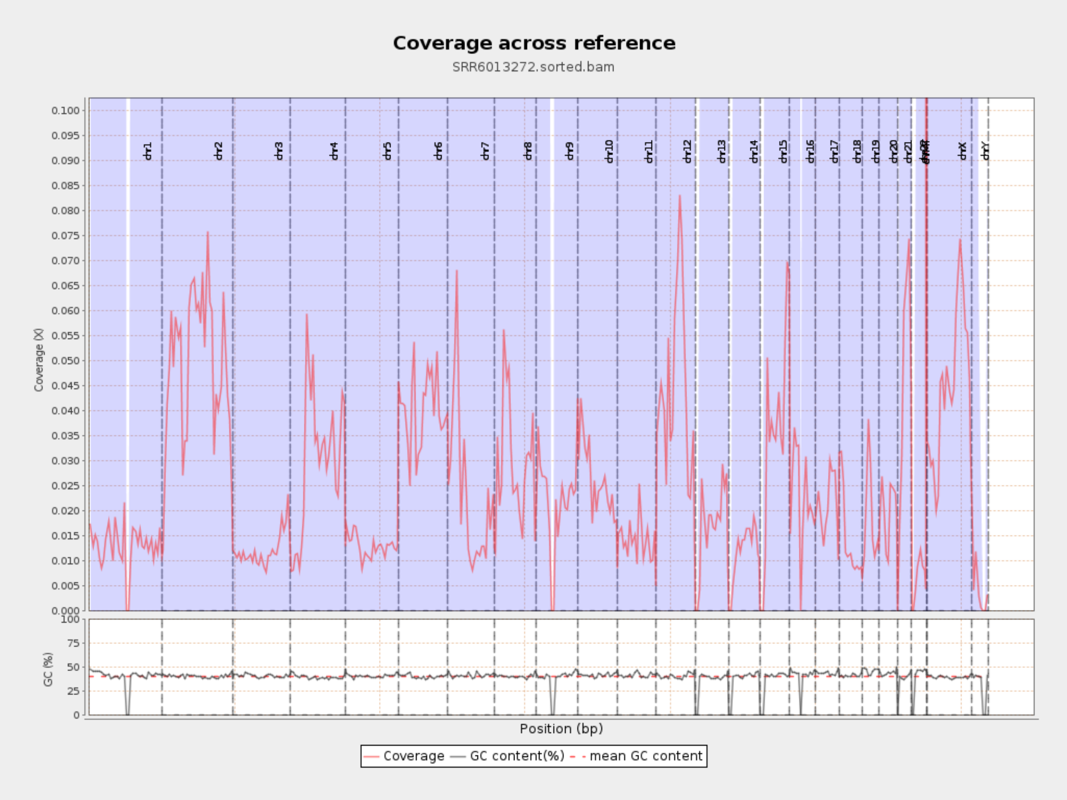
General error rate	1.04%
Mismatches	816,127
Insertions	5,228
Mapped reads with at least one insertion	0.4%
Deletions	38,316
Mapped reads with at least one deletion	2.93%
Homopolymer indels	42.14%

2.6. Chromosome stats

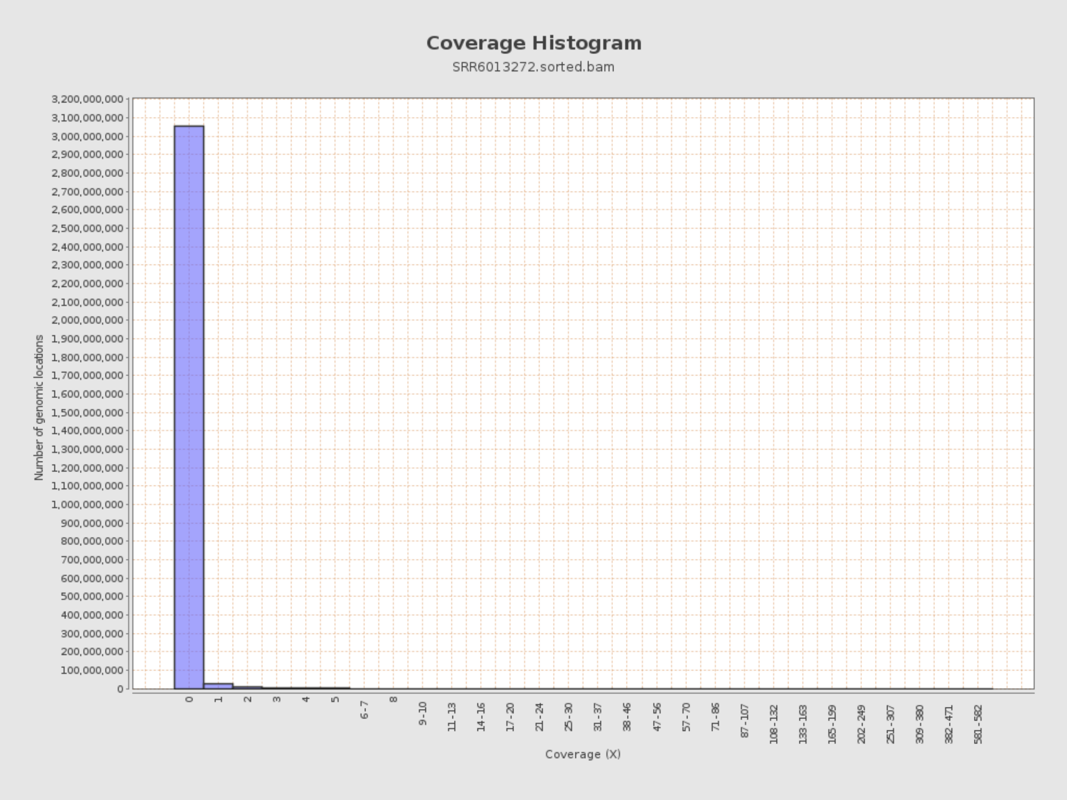
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3205001	0.0129	0.3609
chr2	243199373	12101359	0.0498	0.463
chr3	198022430	2402185	0.0121	0.1794
chr4	191154276	5749814	0.0301	0.2962
chr5	180915260	2331725	0.0129	0.1865
chr6	171115067	6912328	0.0404	0.3907
chr7	159138663	3750722	0.0236	0.2805

chr8	146364022	4289411	0.0293	0.3205
chr9	141213431	3017807	0.0214	0.2599
chr10	135534747	3574691	0.0264	0.2997
chr11	135006516	1918587	0.0142	0.1991
chr12	133851895	6047591	0.0452	0.3679
chr13	115169878	1979329	0.0172	0.2239
chr14	107349540	1278166	0.0119	0.1777
chr15	102531392	3566776	0.0348	0.3166
chr16	90354753	2052291	0.0227	0.2513
chr17	81195210	1699087	0.0209	0.2447
chr18	78077248	1128265	0.0145	0.2802
chr19	59128983	1133492	0.0192	0.2874
chr20	63025520	1266228	0.0201	0.2412
chr21	48129895	2161746	0.0449	0.3701
chr22	51304566	332525	0.0065	0.1296
chrMT	16571	24390	1.4718	1.8479
chrX	155270560	7015120	0.0452	0.3694
chrY	59373566	254722	0.0043	0.1176

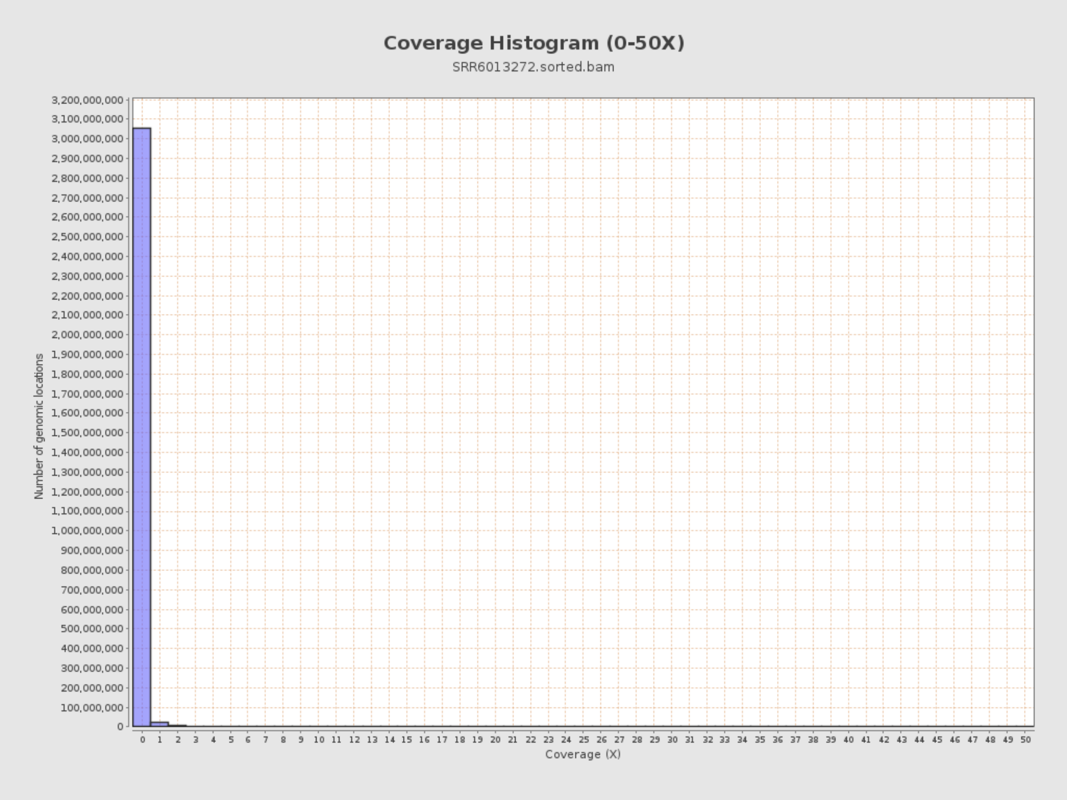
3. Results : Coverage across reference



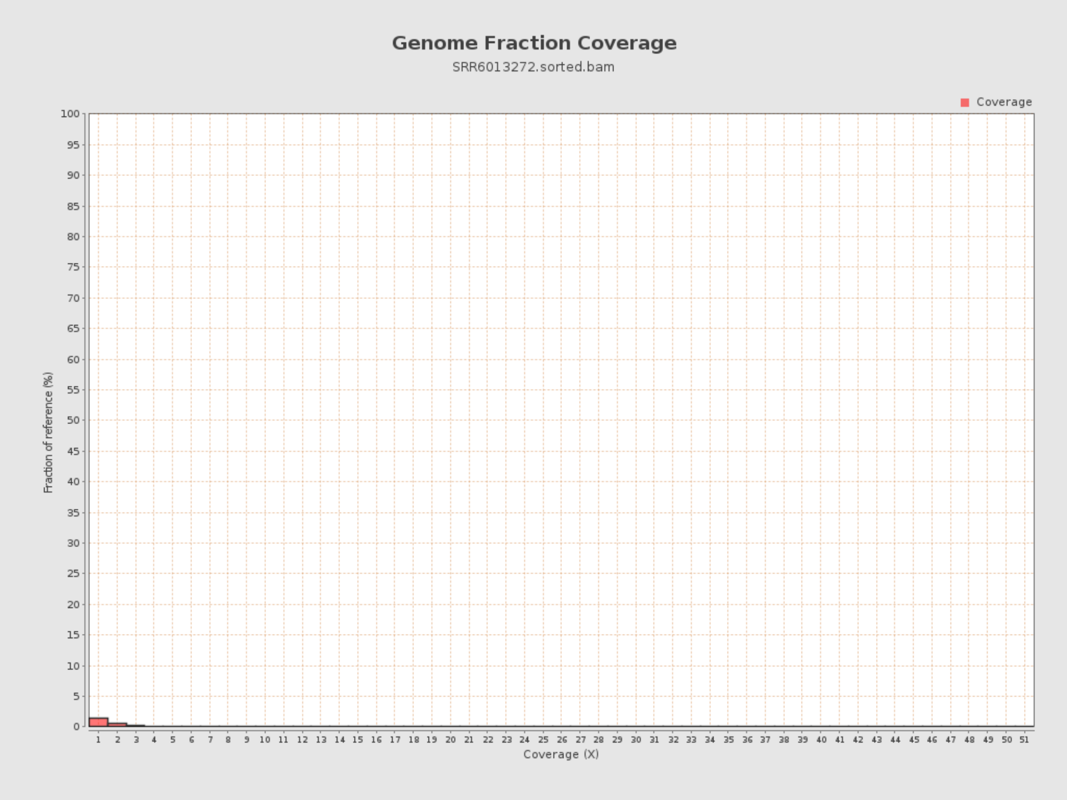
4. Results : Coverage Histogram



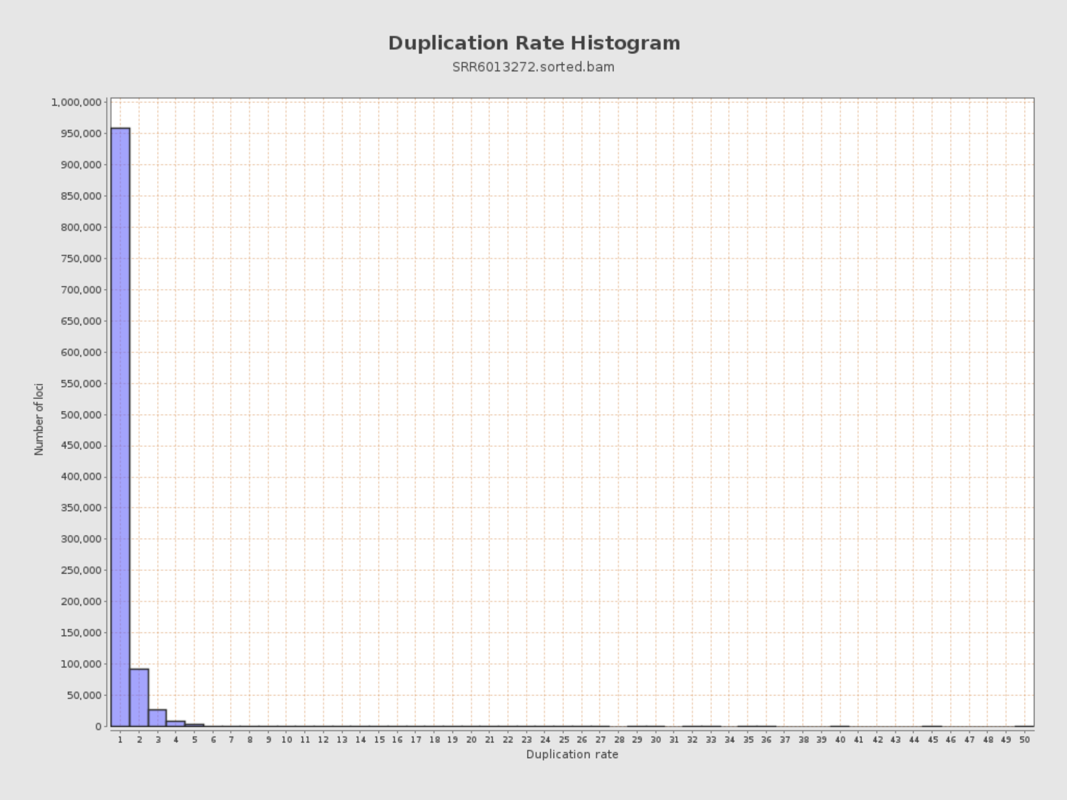
5. Results : Coverage Histogram (0-50X)



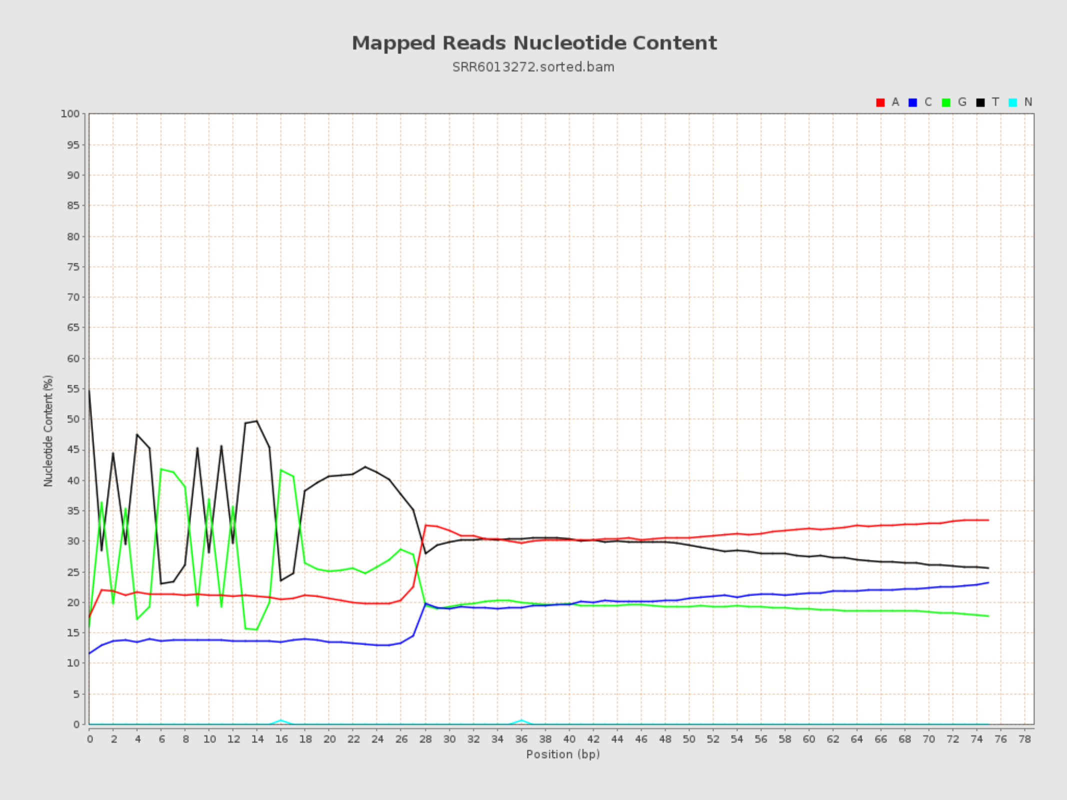
6. Results : Genome Fraction Coverage



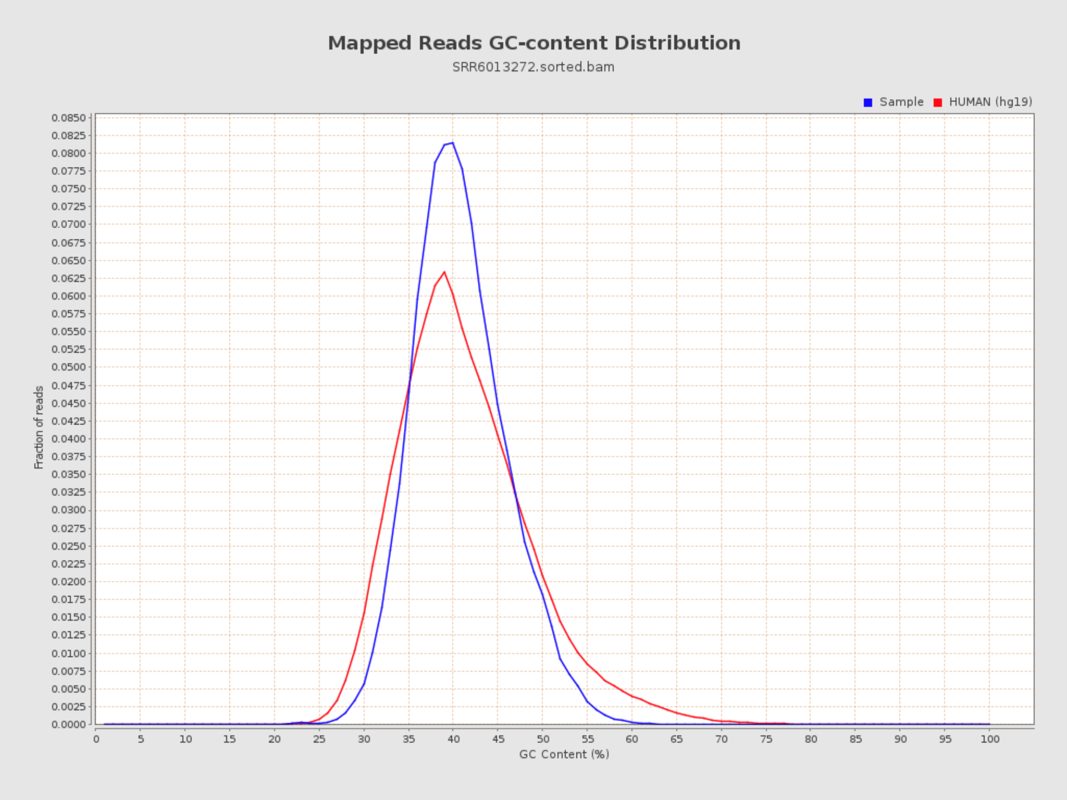
7. Results : Duplication Rate Histogram



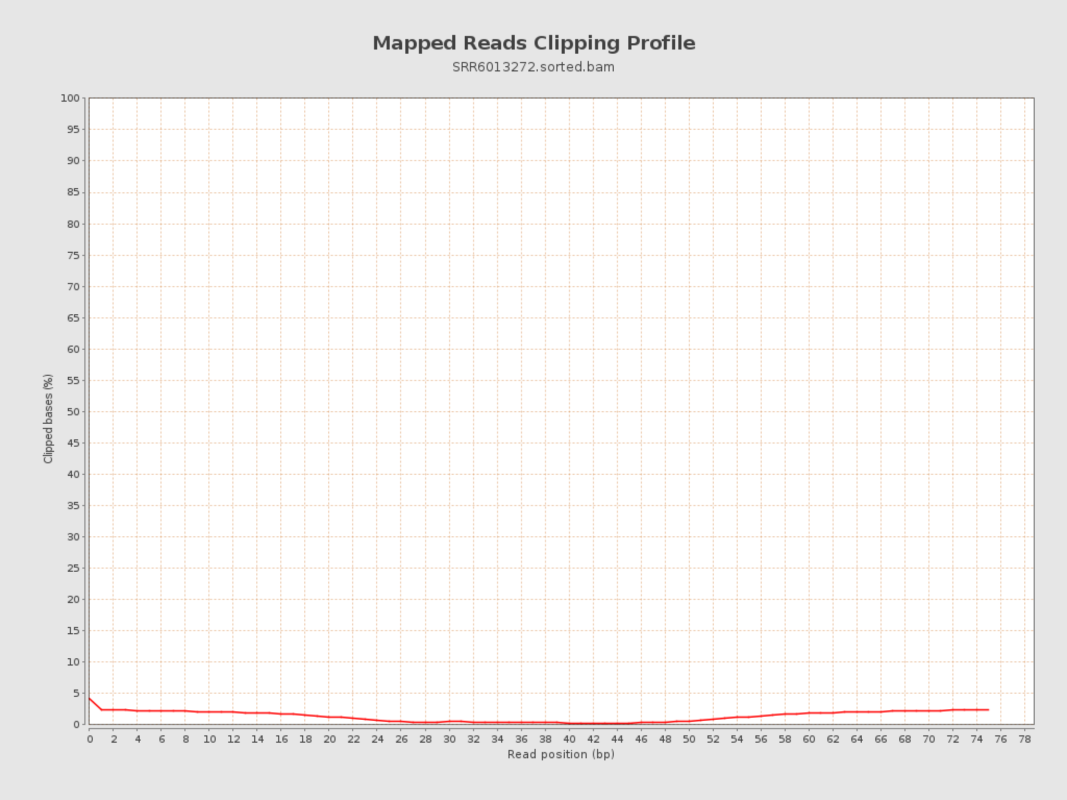
8. Results : Mapped Reads Nucleotide Content



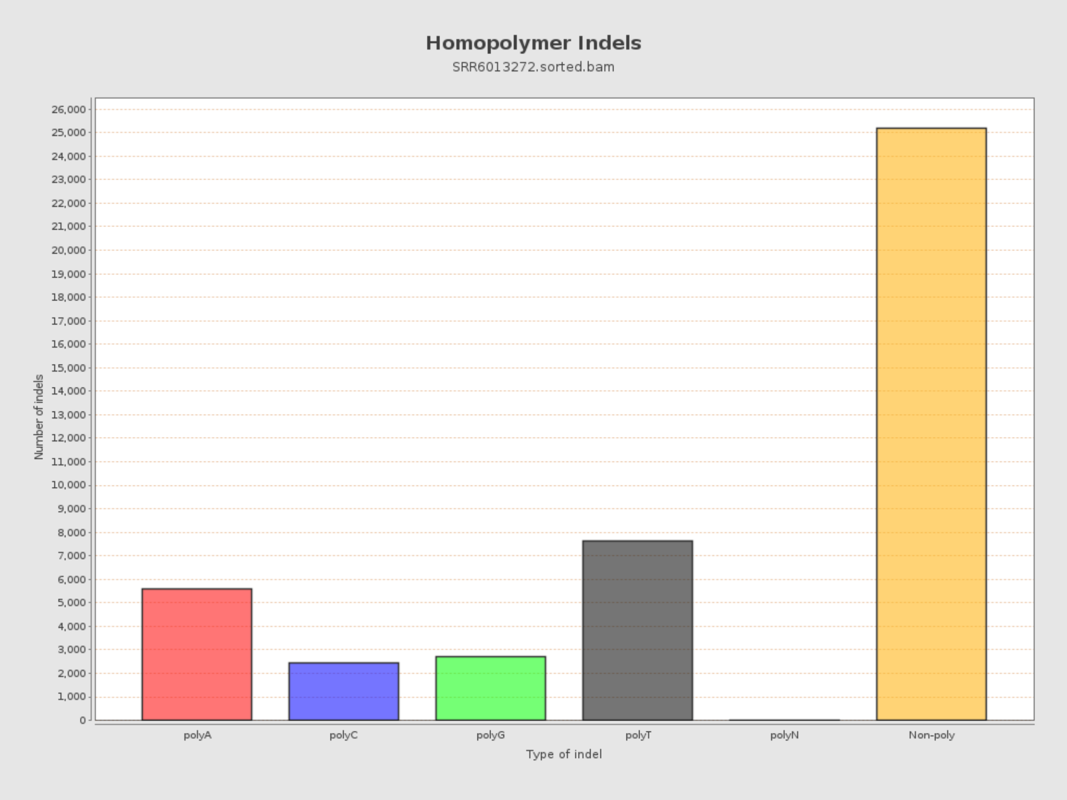
9. Results : Mapped Reads GC-content Distribution



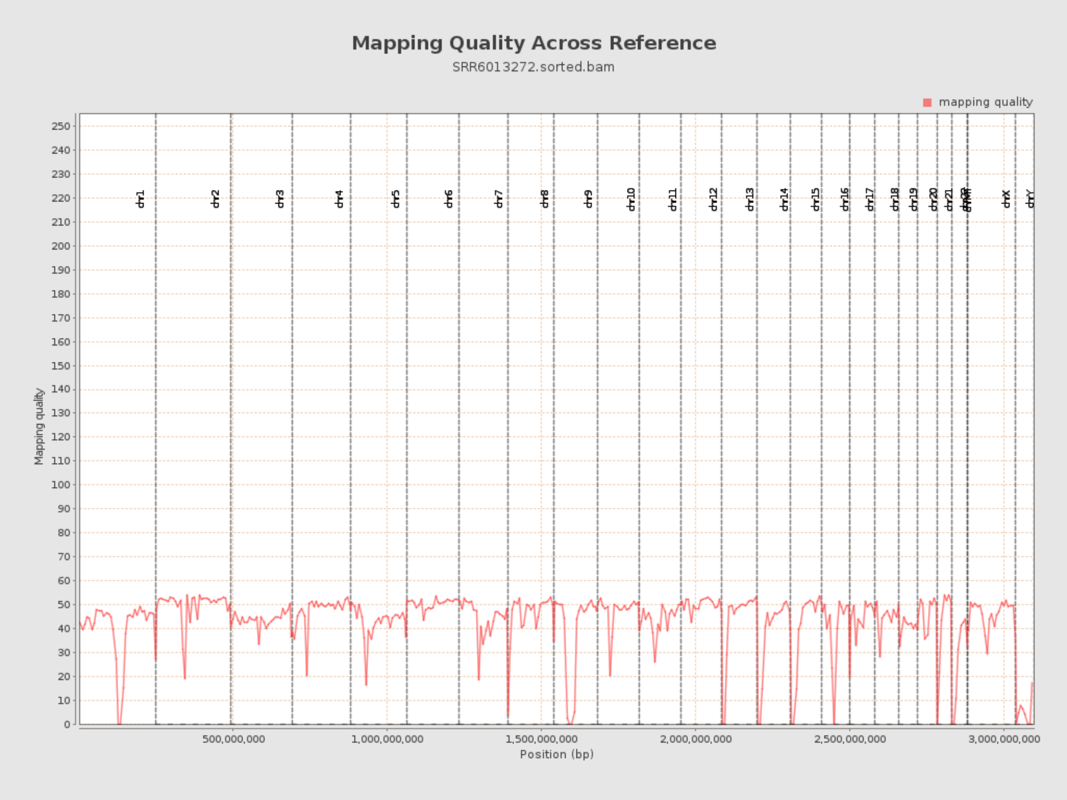
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram