Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 19:48:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6230368.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_SRR6230368 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6230368.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 19:48:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6230368.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,995,092
Mapped reads	2,843,418 / 94.94%
Unmapped reads	151,674 / 5.06%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	24,363 / 0.81%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	161,308 / 5.39%
Duplication rate	4.23%
Clipped reads	718,768 / 24%

2.2. ACGT Content

Number/percentage of A's	61,257,969 / 29.94%
Number/percentage of C's	41,520,900 / 20.29%
Number/percentage of T's	60,166,538 / 29.4%
Number/percentage of G's	41,580,371 / 20.32%
Number/percentage of N's	95,247 / 0.05%
GC Percentage	40.61%

2.3. Coverage

Mean	0.0661

Standard Deviation	0.757

2.4. Mapping Quality

Mean Mapping Quality	48.15

2.5. Mismatches and indels

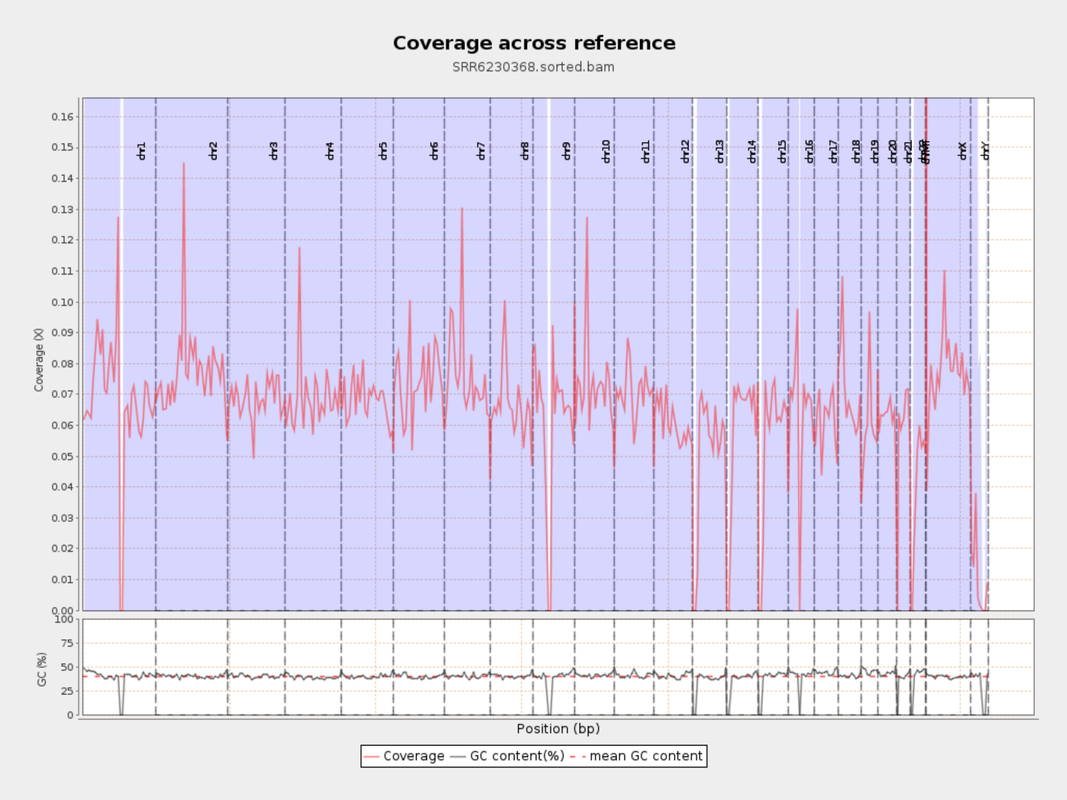
General error rate	0.87%
Mismatches	1,740,794
Insertions	18,406
Mapped reads with at least one insertion	0.64%
Deletions	51,561
Mapped reads with at least one deletion	1.79%
Homopolymer indels	46.98%

2.6. Chromosome stats

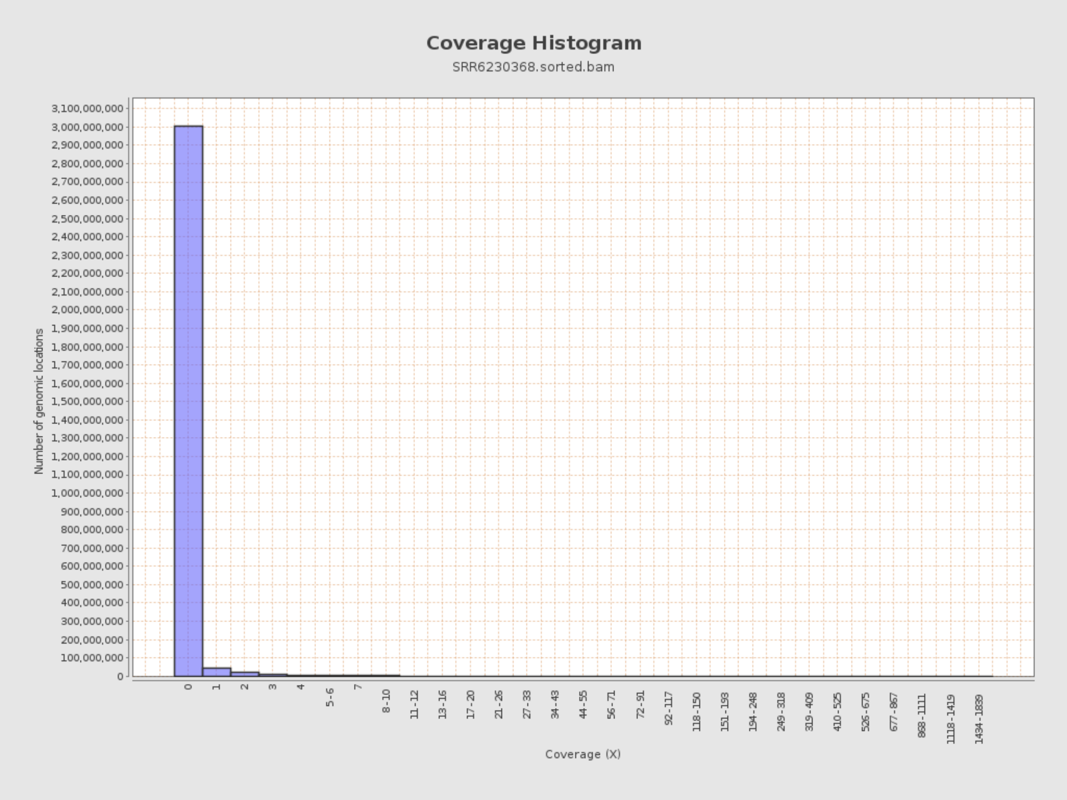
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17089519	0.0686	1.4481
chr2	243199373	19015311	0.0782	0.8048
chr3	198022430	13526008	0.0683	0.5014
chr4	191154276	13263602	0.0694	0.5529
chr5	180915260	12321294	0.0681	0.4976
chr6	171115067	12793311	0.0748	0.5837
chr7	159138663	12113274	0.0761	0.9266

chr8	146364022	9699100	0.0663	0.774
chr9	141213431	8643881	0.0612	0.7238
chr10	135534747	9887081	0.0729	0.733
chr11	135006516	9518497	0.0705	0.7385
chr12	133851895	8133505	0.0608	0.4754
chr13	115169878	5777052	0.0502	0.4239
chr14	107349540	6245615	0.0582	0.4883
chr15	102531392	5494069	0.0536	0.434
chr16	90354753	5611810	0.0621	0.5464
chr17	81195210	5025459	0.0619	0.5306
chr18	78077248	5566011	0.0713	1.3934
chr19	59128983	3610453	0.0611	0.8951
chr20	63025520	3971524	0.063	0.4998
chr21	48129895	2798142	0.0581	0.5061
chr22	51304566	1988246	0.0388	0.3571
chrMT	16571	84373	5.0916	4.605
chrX	155270560	11914475	0.0767	0.5743
chrY	59373566	617113	0.0104	0.3245

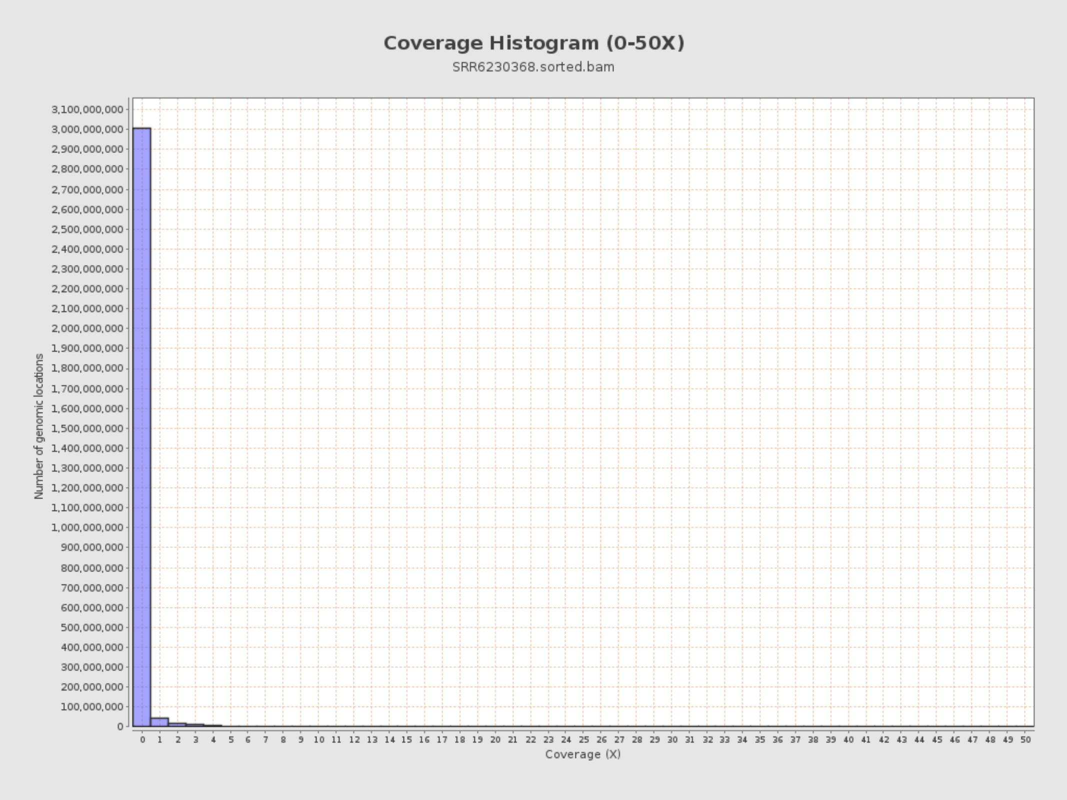
3. Results : Coverage across reference



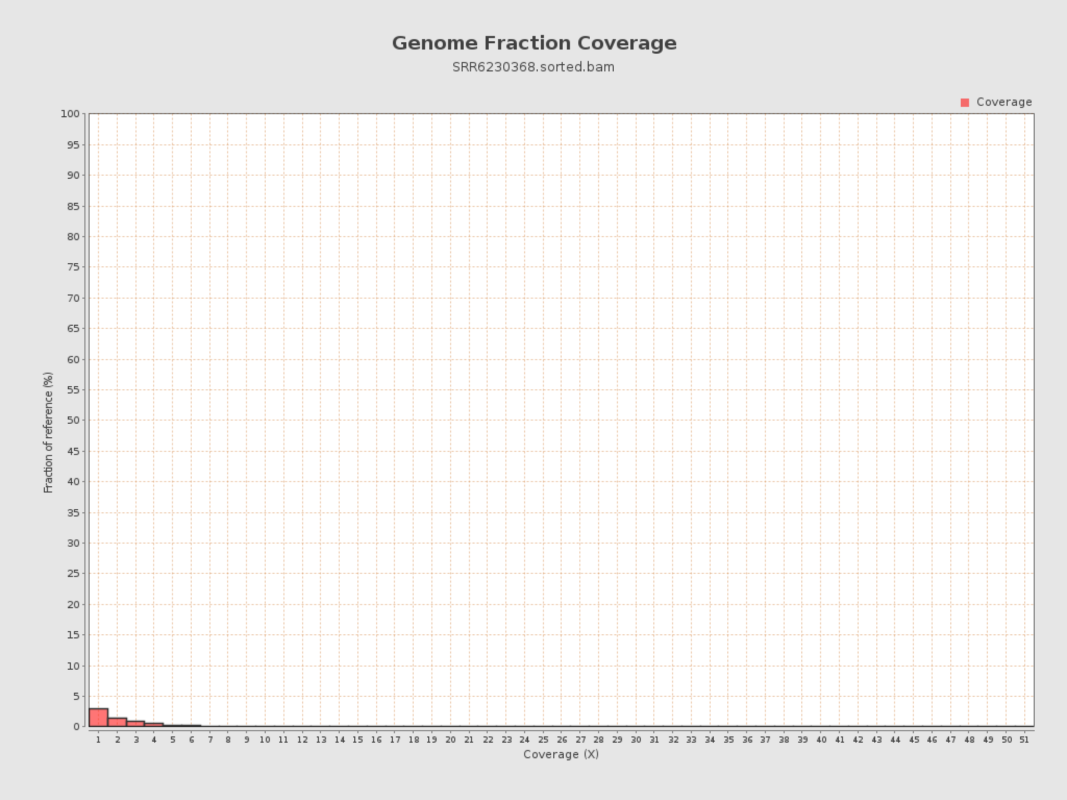
4. Results : Coverage Histogram



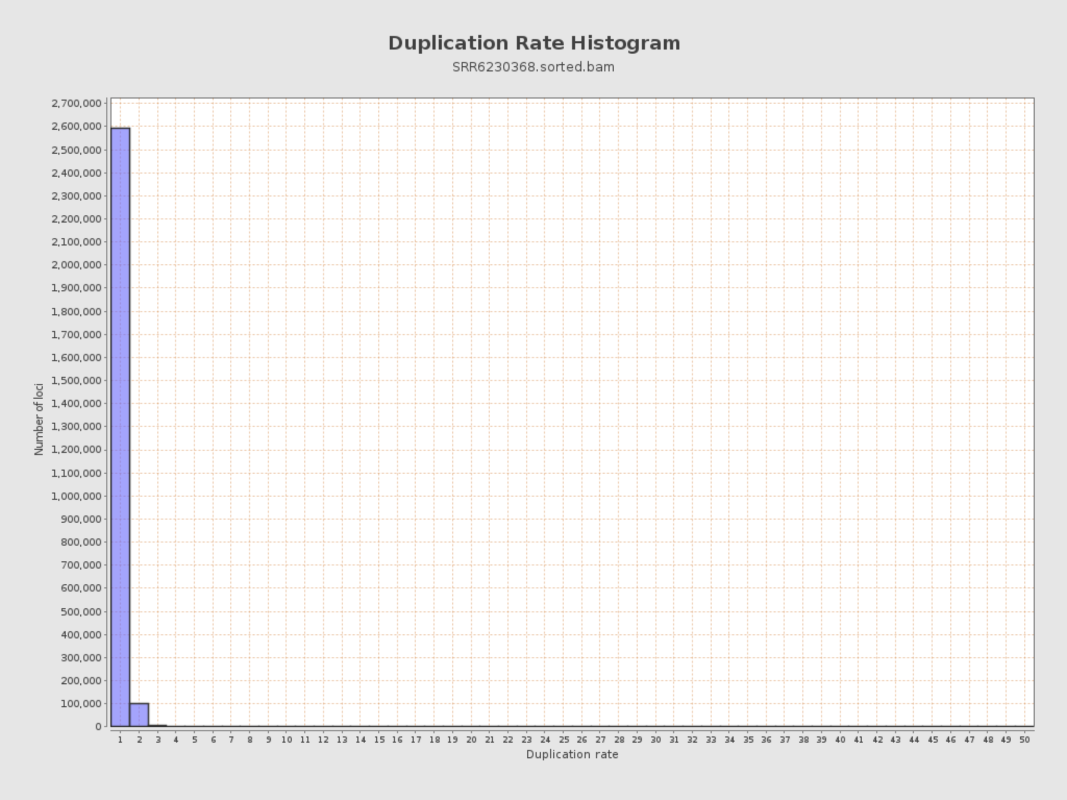
5. Results : Coverage Histogram (0-50X)



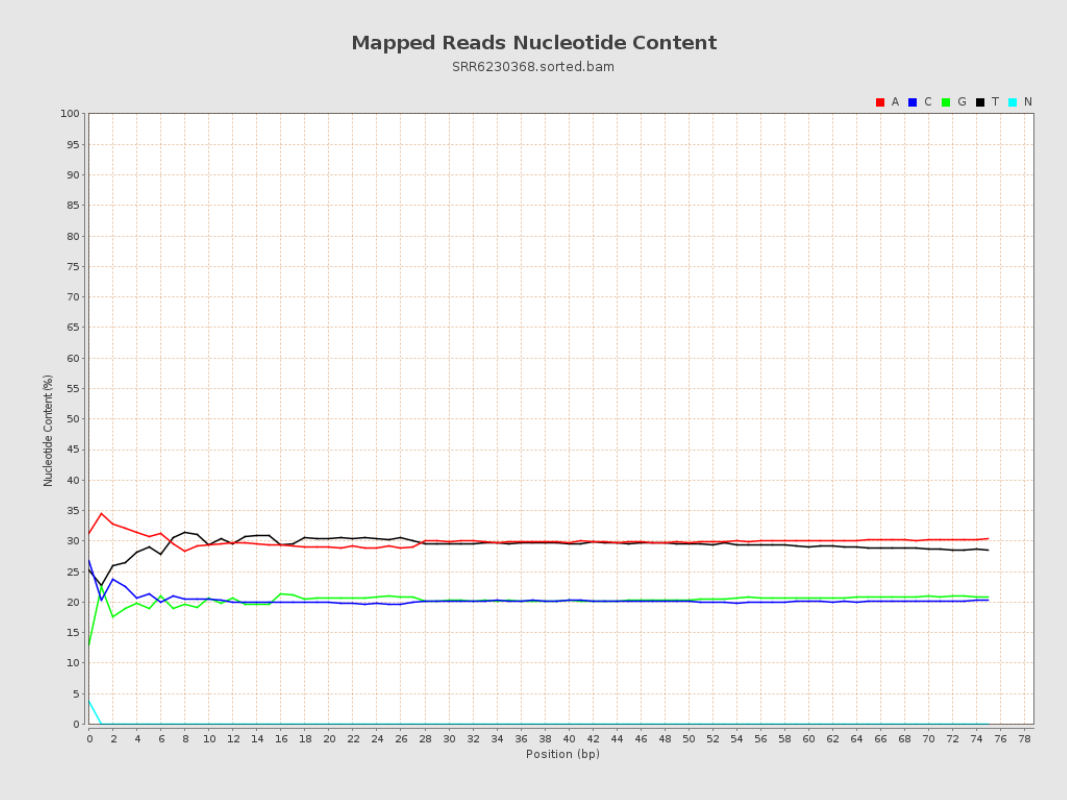
6. Results : Genome Fraction Coverage



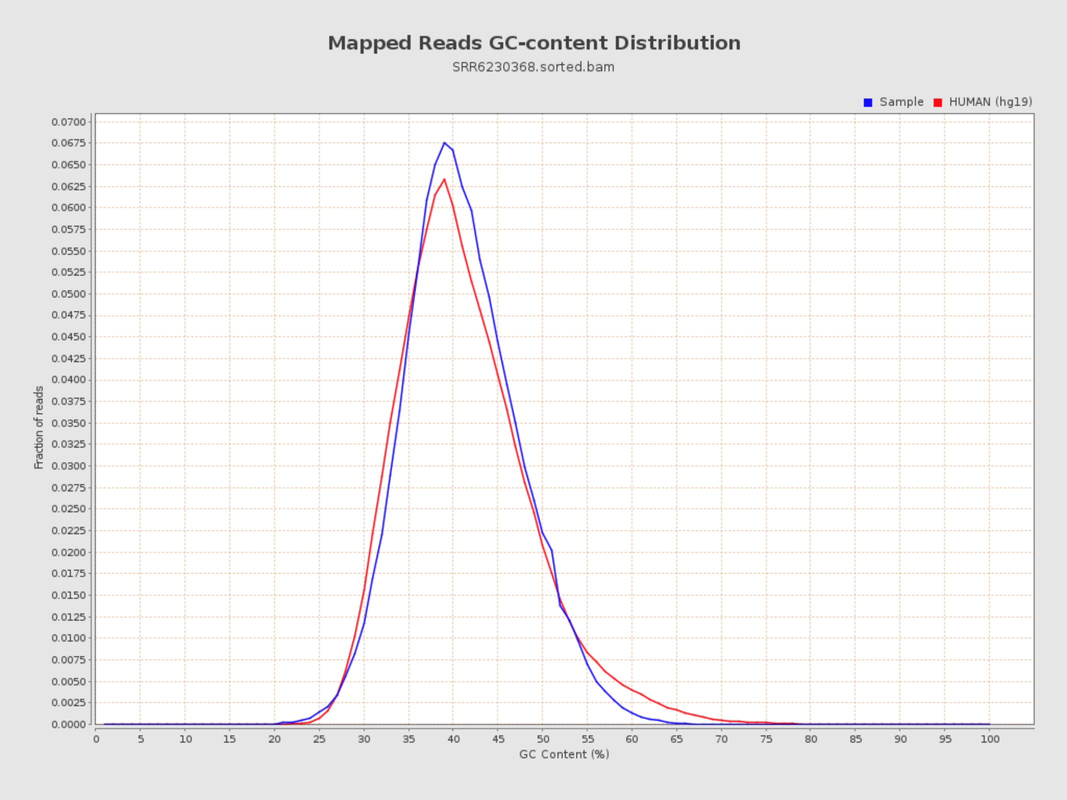
7. Results : Duplication Rate Histogram



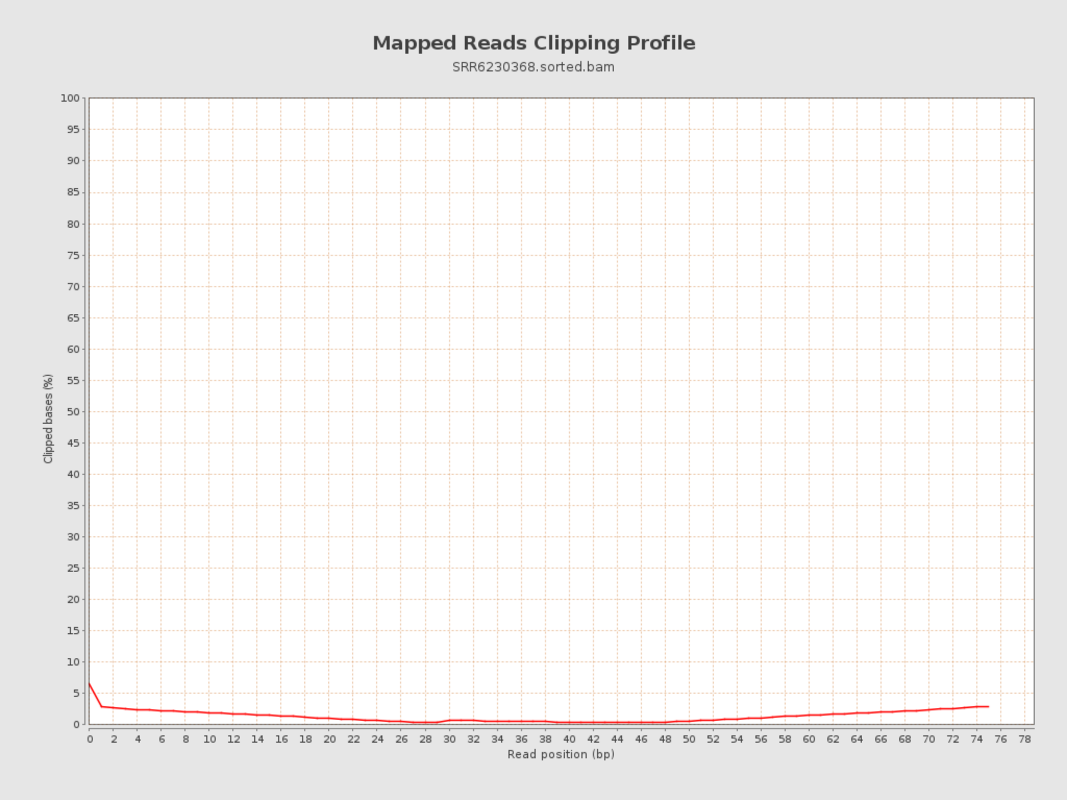
8. Results : Mapped Reads Nucleotide Content



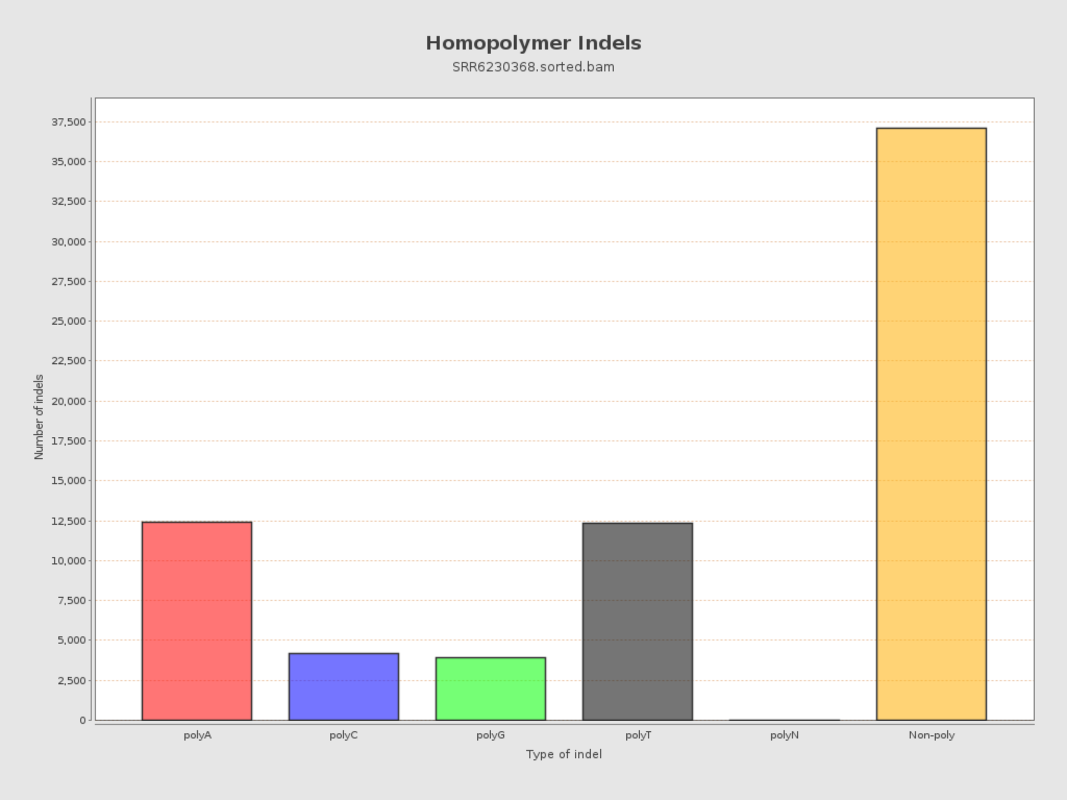
9. Results : Mapped Reads GC-content Distribution



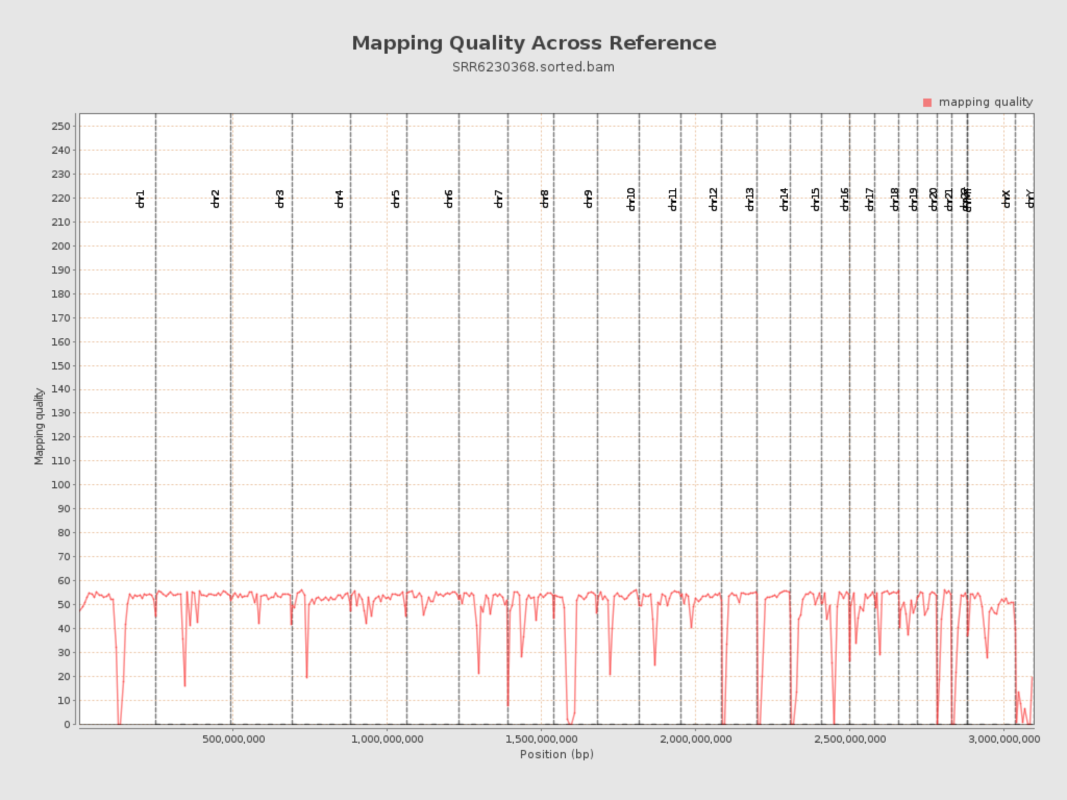
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram