Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 15:54:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013206.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_SRR6013206 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013206.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 15:54:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013206.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,418,627
Mapped reads	2,171,142 / 89.77%
Unmapped reads	247,485 / 10.23%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,745 / 0.69%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	124,188 / 5.13%
Duplication rate	4.16%
Clipped reads	838,882 / 34.68%

2.2. ACGT Content

Number/percentage of A's	42,098,409 / 28.48%
Number/percentage of C's	27,080,167 / 18.32%
Number/percentage of T's	47,351,357 / 32.03%
Number/percentage of G's	31,266,235 / 21.15%
Number/percentage of N's	31,973 / 0.02%
GC Percentage	39.47%

2.3. Coverage

Mean	0.0478

Standard Deviation	0.5413

2.4. Mapping Quality

Mean Mapping Quality	46.73

2.5. Mismatches and indels

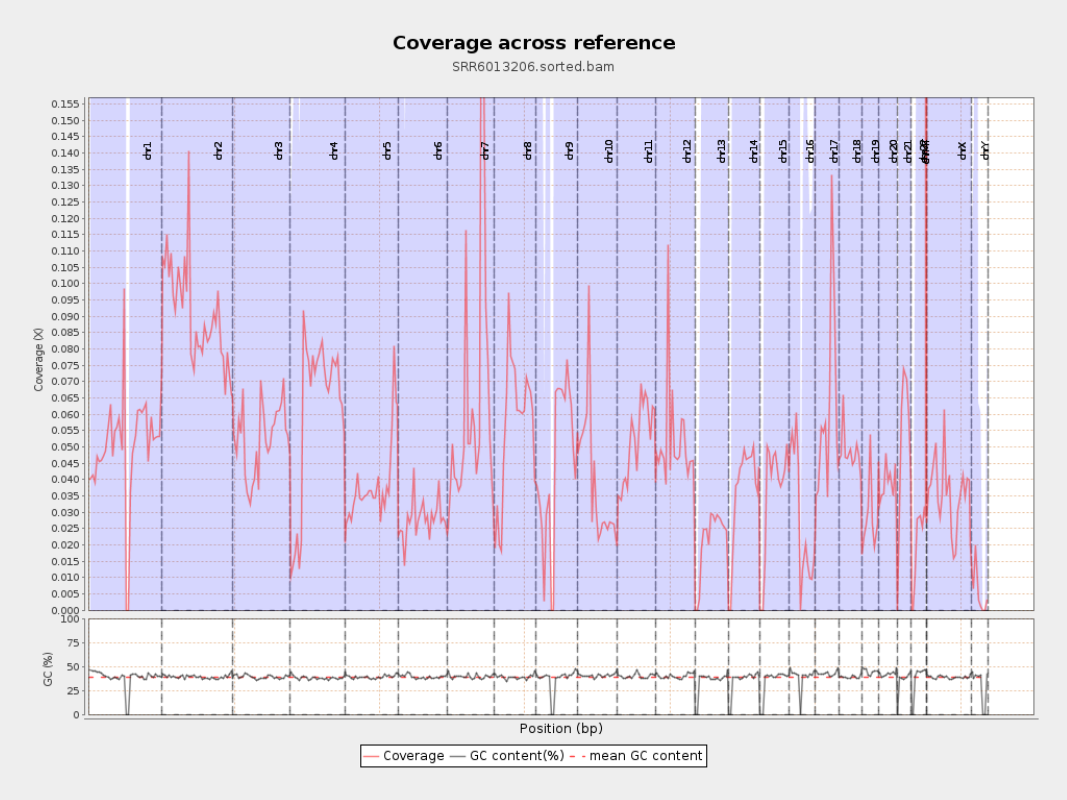
General error rate	0.81%
Mismatches	1,175,478
Insertions	11,294
Mapped reads with at least one insertion	0.52%
Deletions	33,715
Mapped reads with at least one deletion	1.53%
Homopolymer indels	47.3%

2.6. Chromosome stats

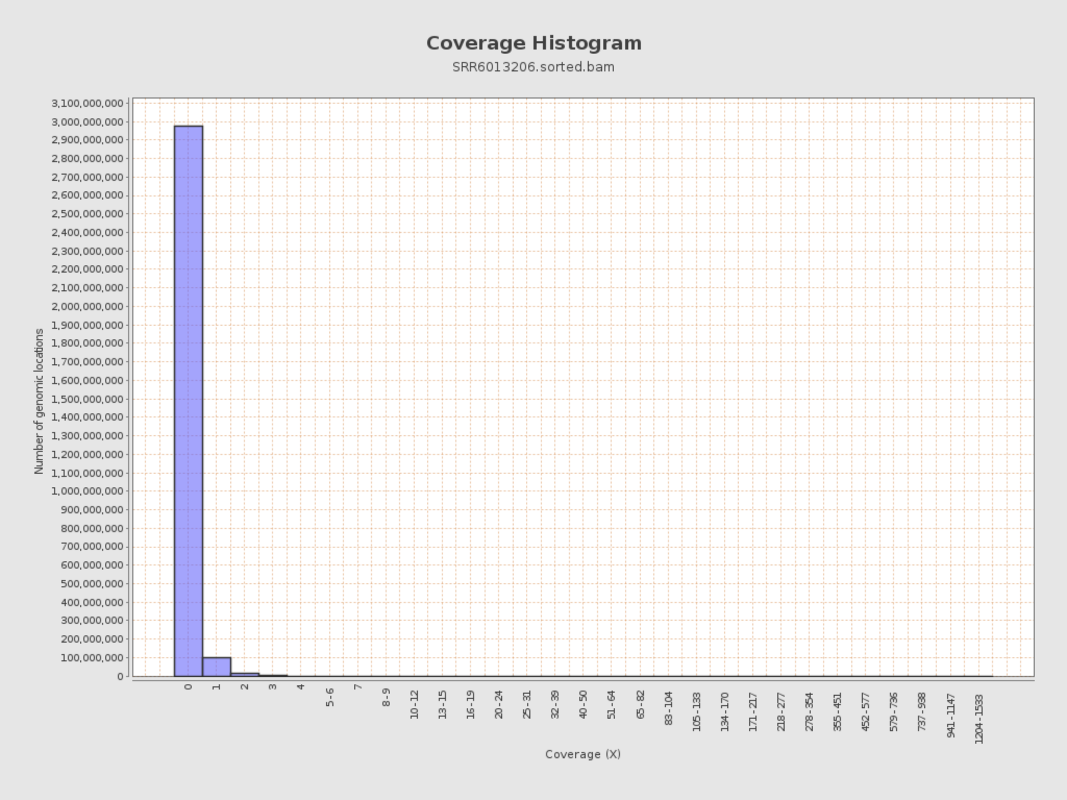
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12518230	0.0502	0.9841
chr2	243199373	22116204	0.0909	0.6256
chr3	198022430	10442995	0.0527	0.2701
chr4	191154276	11527710	0.0603	0.3544
chr5	180915260	6990210	0.0386	0.2346
chr6	171115067	4789105	0.028	0.2255
chr7	159138663	10758115	0.0676	0.9477

chr8	146364022	8302025	0.0567	0.9332
chr9	141213431	6230266	0.0441	0.4572
chr10	135534747	5314144	0.0392	0.5557
chr11	135006516	6922308	0.0513	0.3651
chr12	133851895	6923004	0.0517	0.2804
chr13	115169878	2435236	0.0211	0.1707
chr14	107349540	3894835	0.0363	0.2447
chr15	102531392	3702585	0.0361	0.2204
chr16	90354753	2478180	0.0274	0.2551
chr17	81195210	4909560	0.0605	0.3196
chr18	78077248	3803951	0.0487	0.8477
chr19	59128983	1736290	0.0294	0.6489
chr20	63025520	2443198	0.0388	0.2481
chr21	48129895	2486259	0.0517	0.3147
chr22	51304566	1025767	0.02	0.162
chrMT	16571	347974	20.999	12.0002
chrX	155270560	5477869	0.0353	0.2563
chrY	59373566	311736	0.0053	0.1949

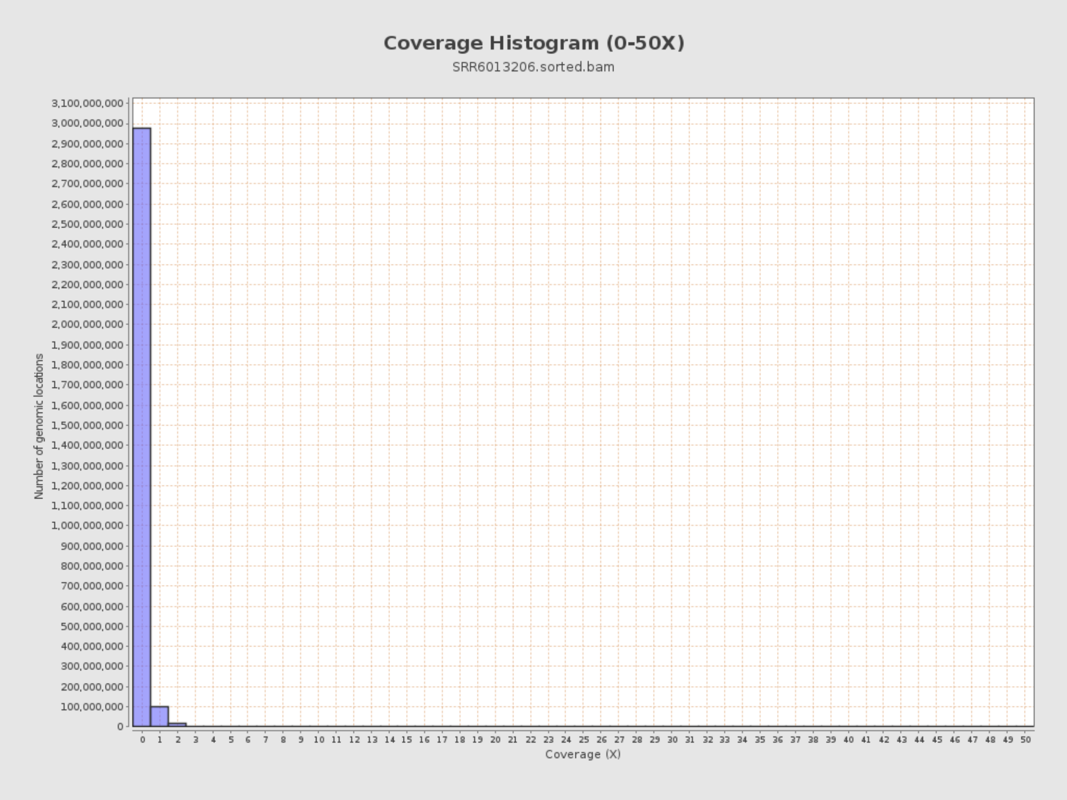
3. Results : Coverage across reference



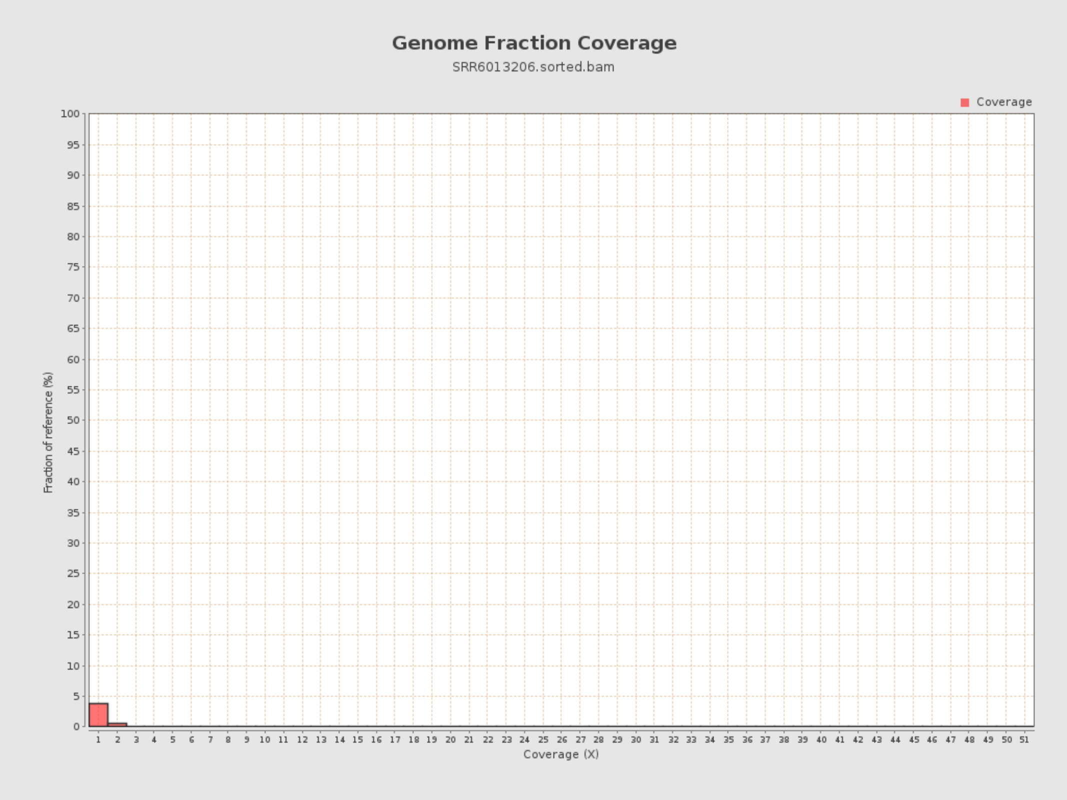
4. Results : Coverage Histogram



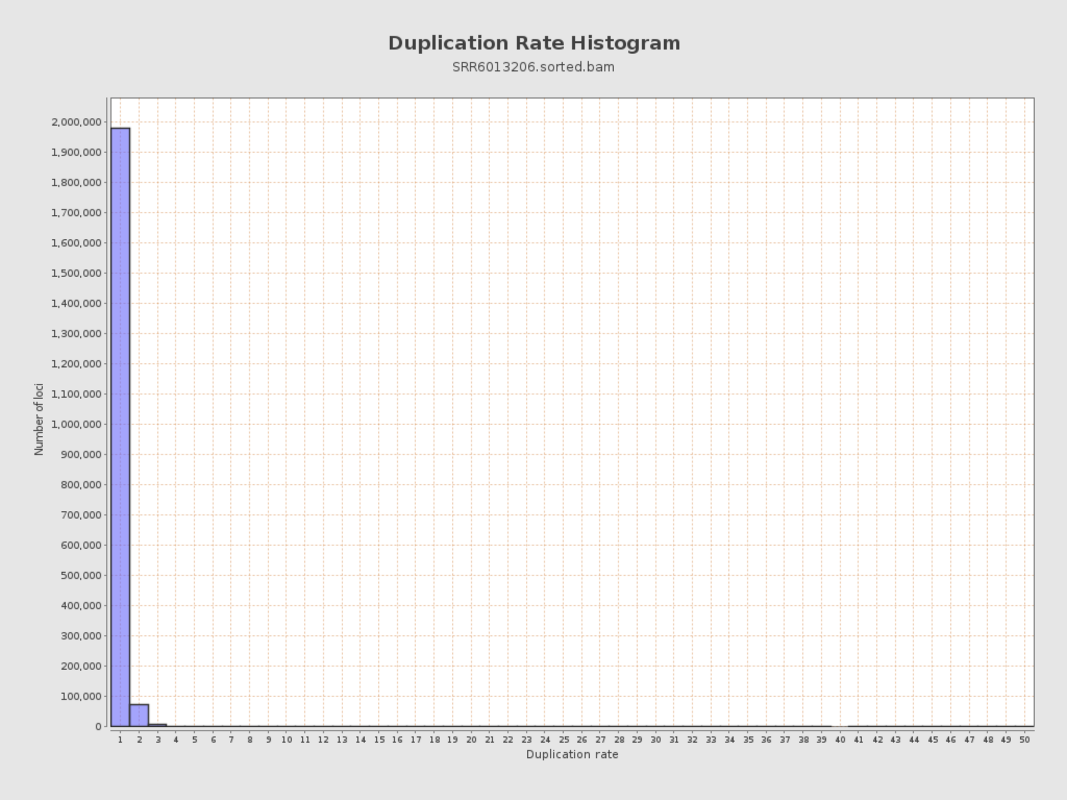
5. Results : Coverage Histogram (0-50X)



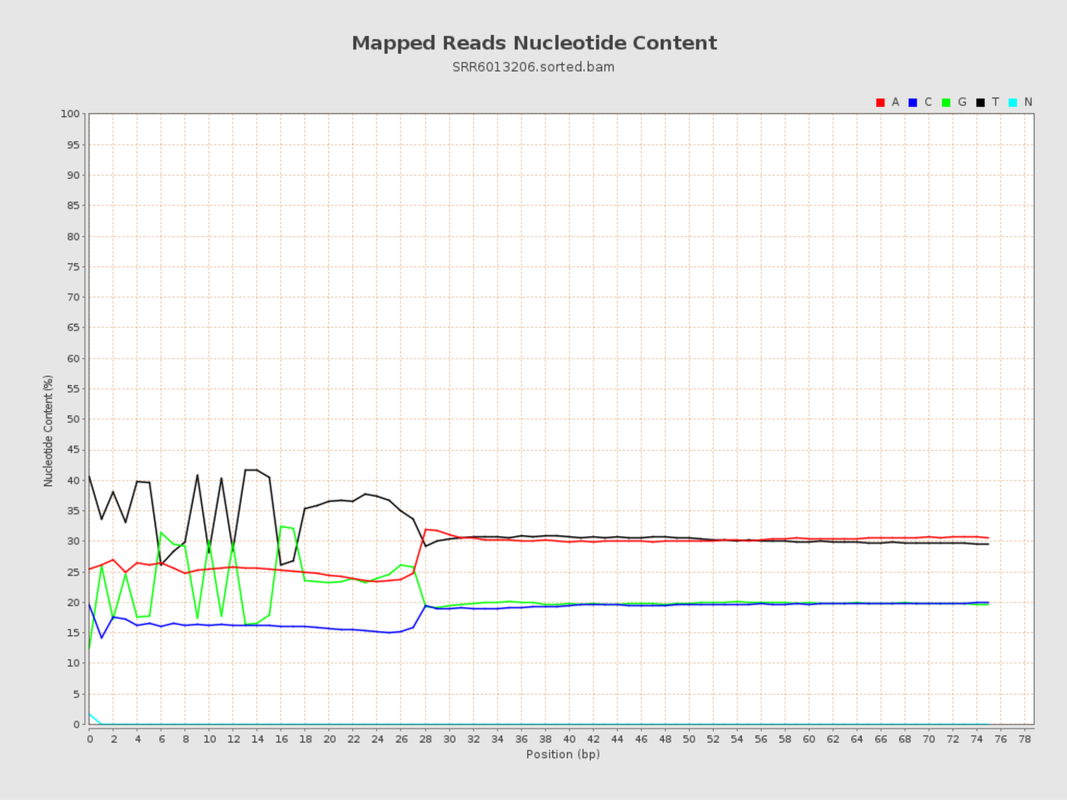
6. Results : Genome Fraction Coverage



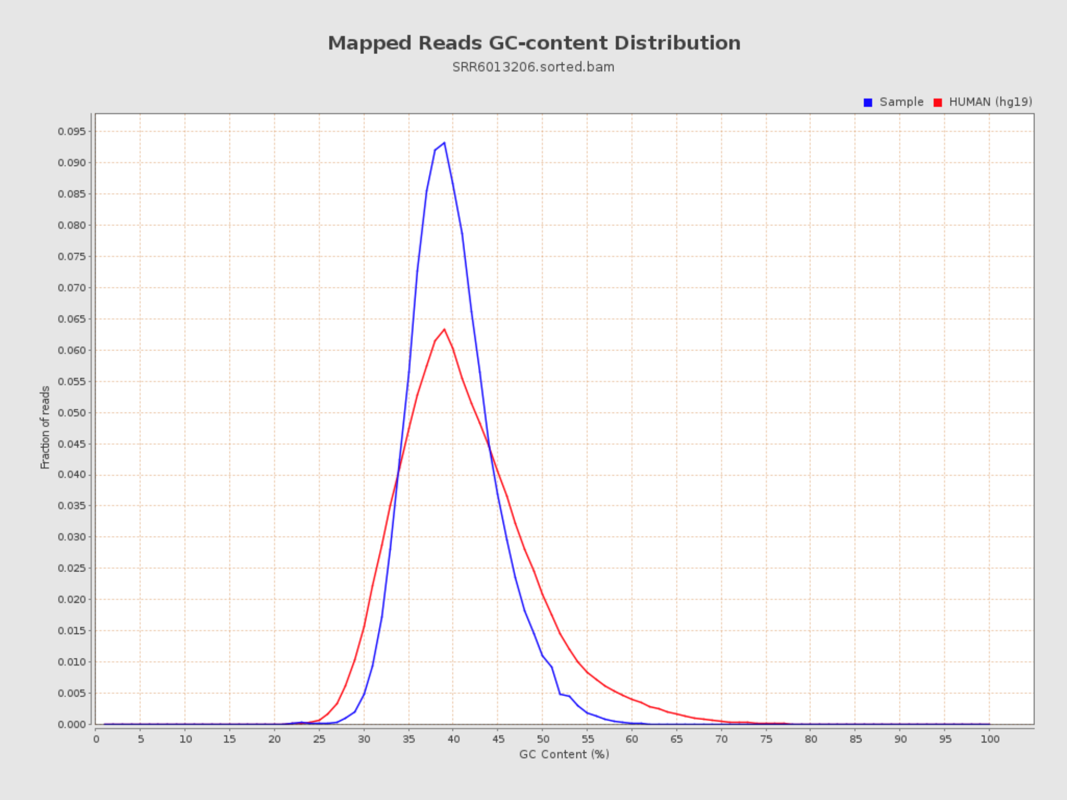
7. Results : Duplication Rate Histogram



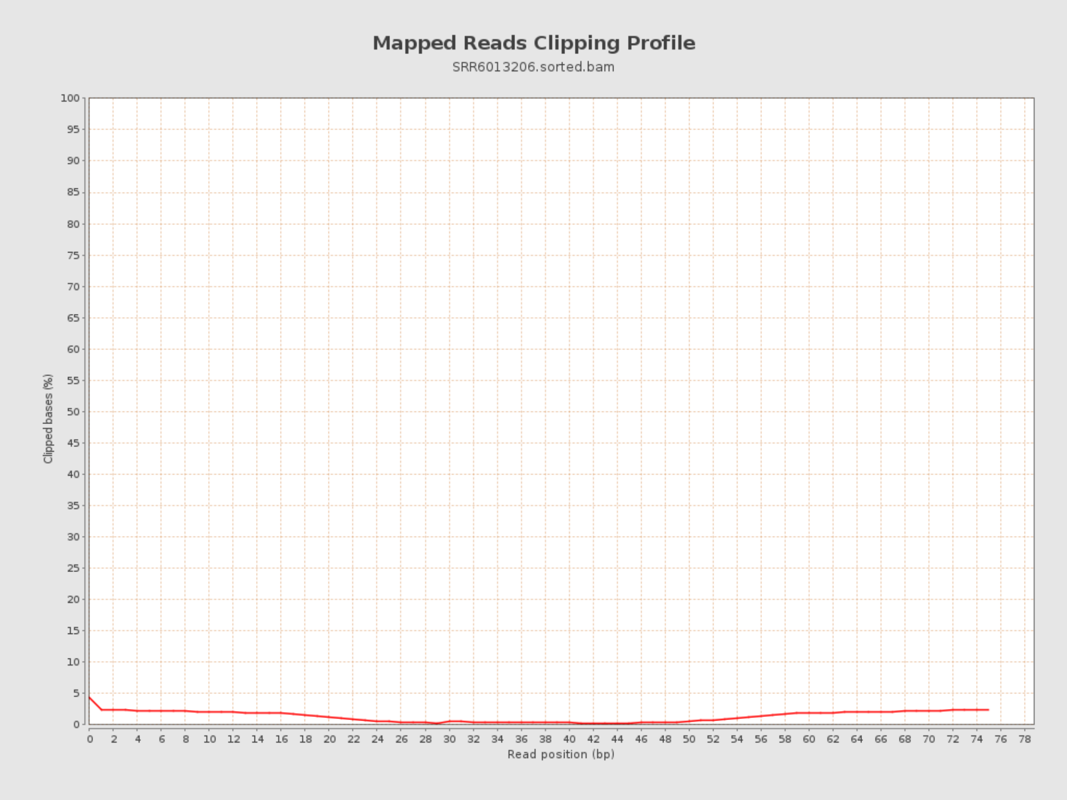
8. Results : Mapped Reads Nucleotide Content



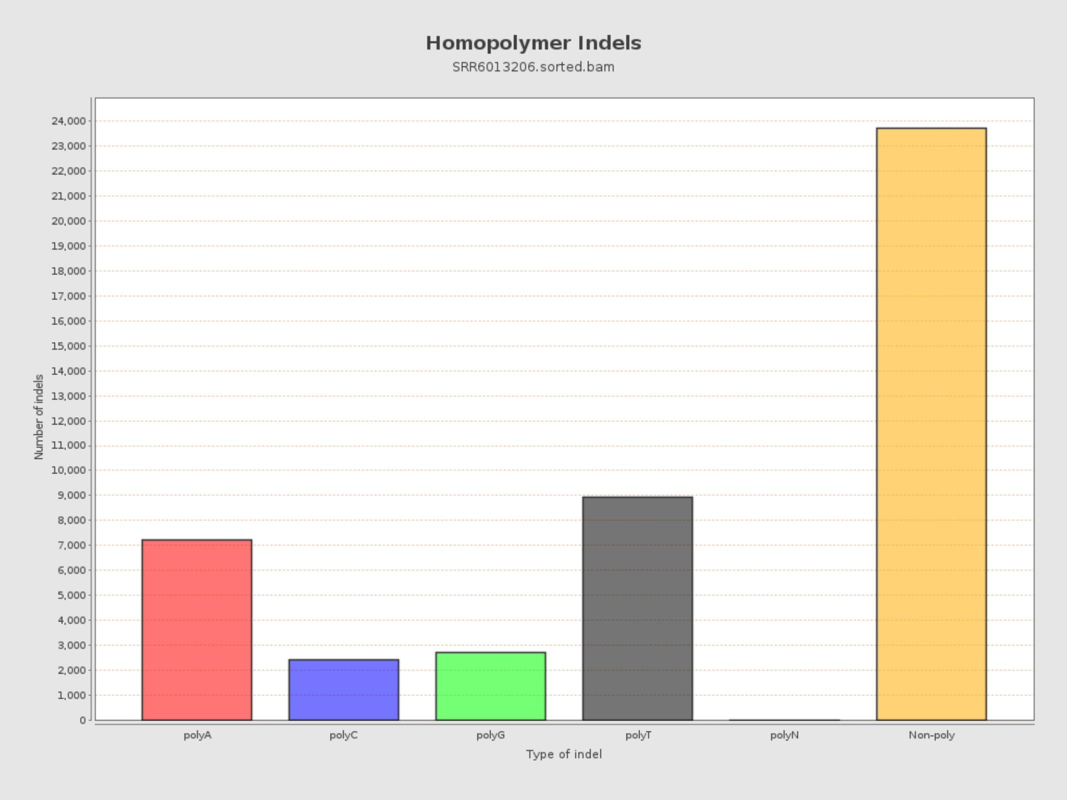
9. Results : Mapped Reads GC-content Distribution



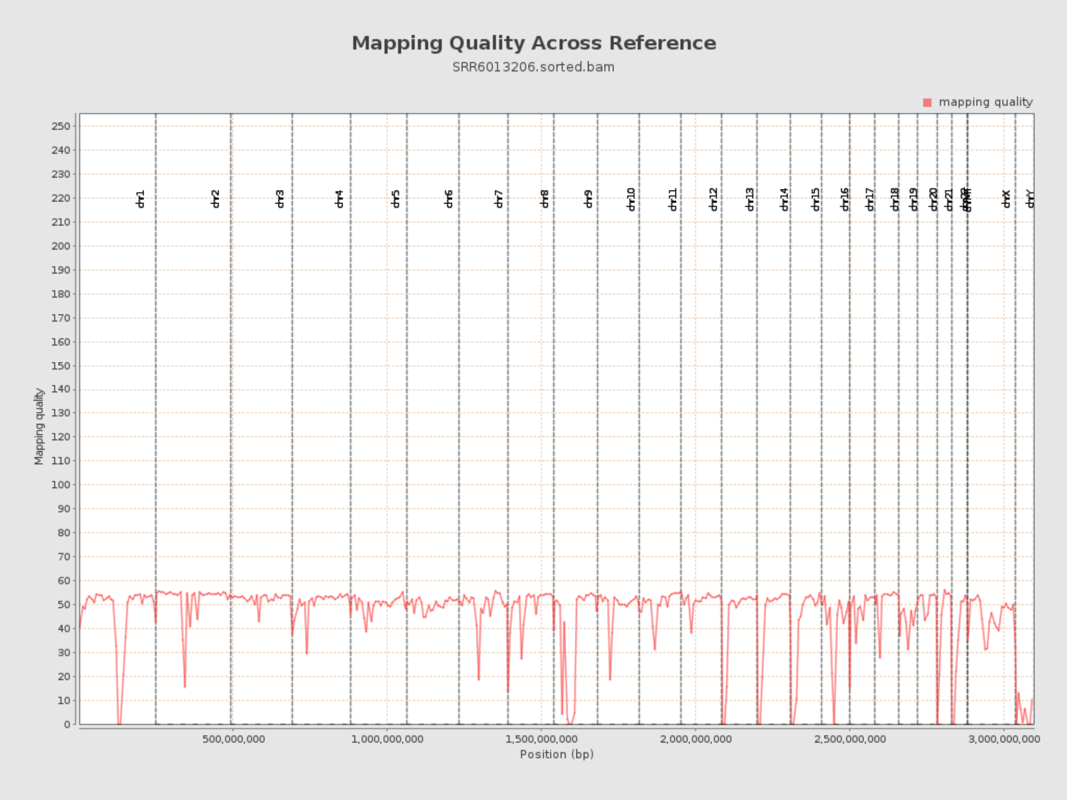
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram