Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/19 23:23:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1506015.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_SRR1506015 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1506015.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Dec 19 23:23:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1506015.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,717,352
Mapped reads	6,798,487 / 69.96%
Unmapped reads	2,918,865 / 30.04%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	332 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	467,202 / 4.81%
Duplication rate	5.19%
Clipped reads	953,700 / 9.81%

2.2. ACGT Content

Number/percentage of A's	93,914,371 / 29.61%
Number/percentage of C's	62,991,940 / 19.86%
Number/percentage of T's	94,407,968 / 29.77%
Number/percentage of G's	64,751,675 / 20.42%
Number/percentage of N's	1,088,231 / 0.34%
GC Percentage	40.28%

2.3. Coverage

Mean	0.1025

Standard Deviation	0.8337

2.4. Mapping Quality

Mean Mapping Quality	44.39

2.5. Mismatches and indels

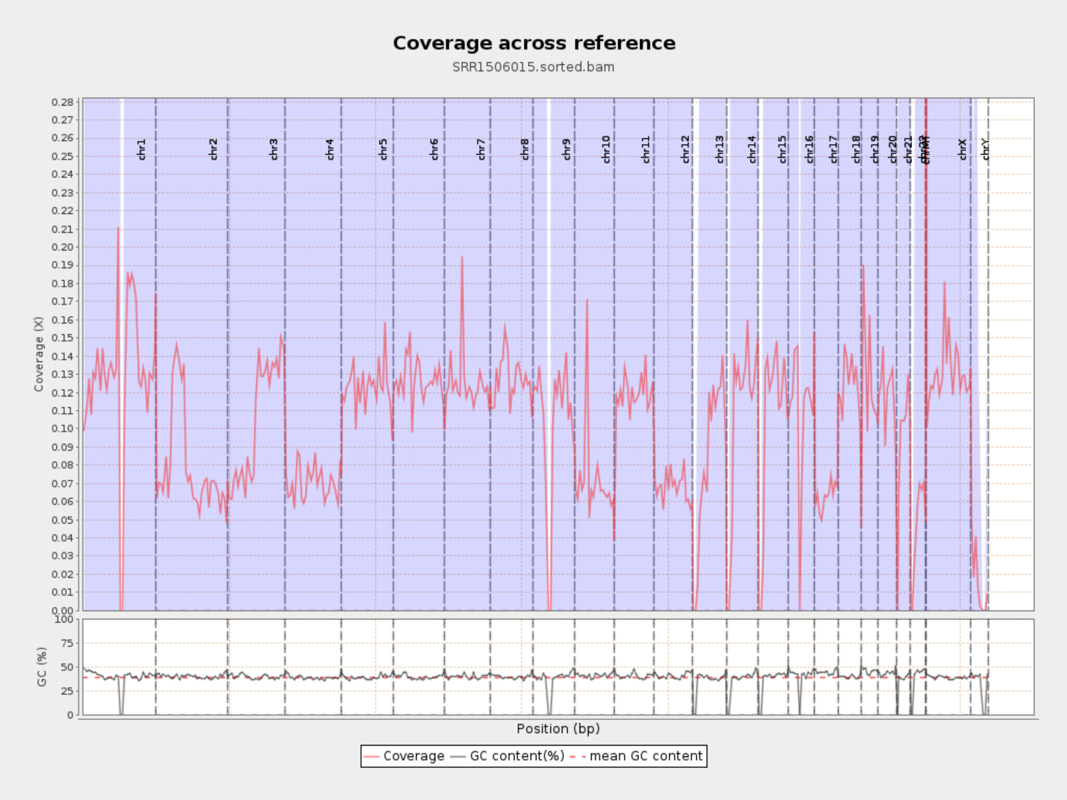
General error rate	0.82%
Mismatches	2,570,223
Insertions	14,681
Mapped reads with at least one insertion	0.22%
Deletions	50,297
Mapped reads with at least one deletion	0.74%
Homopolymer indels	46.83%

2.6. Chromosome stats

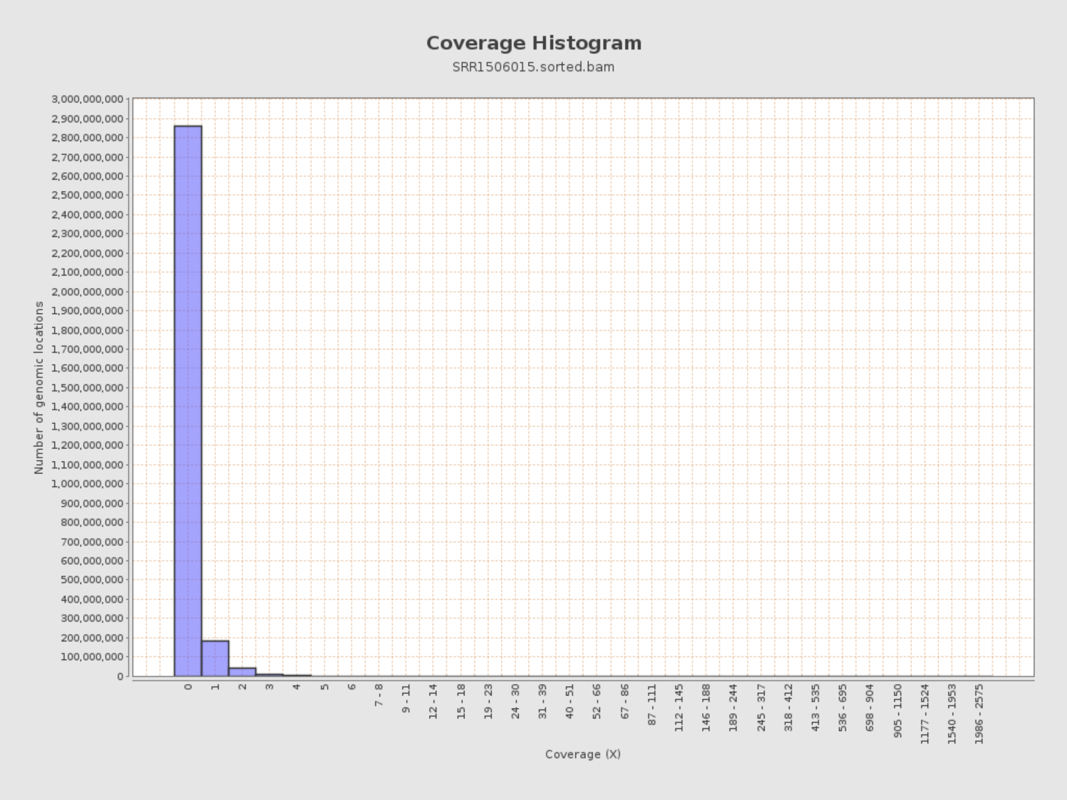
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	32318450	0.1297	1.8244
chr2	243199373	19390975	0.0797	0.6087
chr3	198022430	20563646	0.1038	0.4169
chr4	191154276	13436773	0.0703	0.3541
chr5	180915260	22214222	0.1228	0.4559
chr6	171115067	21737983	0.127	0.6228
chr7	159138663	19879789	0.1249	1.2196

chr8	146364022	18558436	0.1268	1.1002
chr9	141213431	14557025	0.1031	0.5831
chr10	135534747	9713510	0.0717	0.866
chr11	135006516	15986034	0.1184	0.6338
chr12	133851895	9126343	0.0682	0.3645
chr13	115169878	9688363	0.0841	0.3696
chr14	107349540	11644010	0.1085	1.0189
chr15	102531392	10575554	0.1031	0.4086
chr16	90354753	9655942	0.1069	0.5303
chr17	81195210	5102795	0.0628	0.3669
chr18	78077248	9826392	0.1259	1.0048
chr19	59128983	7574169	0.1281	1.2595
chr20	63025520	7531708	0.1195	0.4645
chr21	48129895	4493319	0.0934	0.4418
chr22	51304566	2340671	0.0456	0.2689
chrMT	16571	30297	1.8283	2.0246
chrX	155270560	20372441	0.1312	0.5607
chrY	59373566	905938	0.0153	0.2201

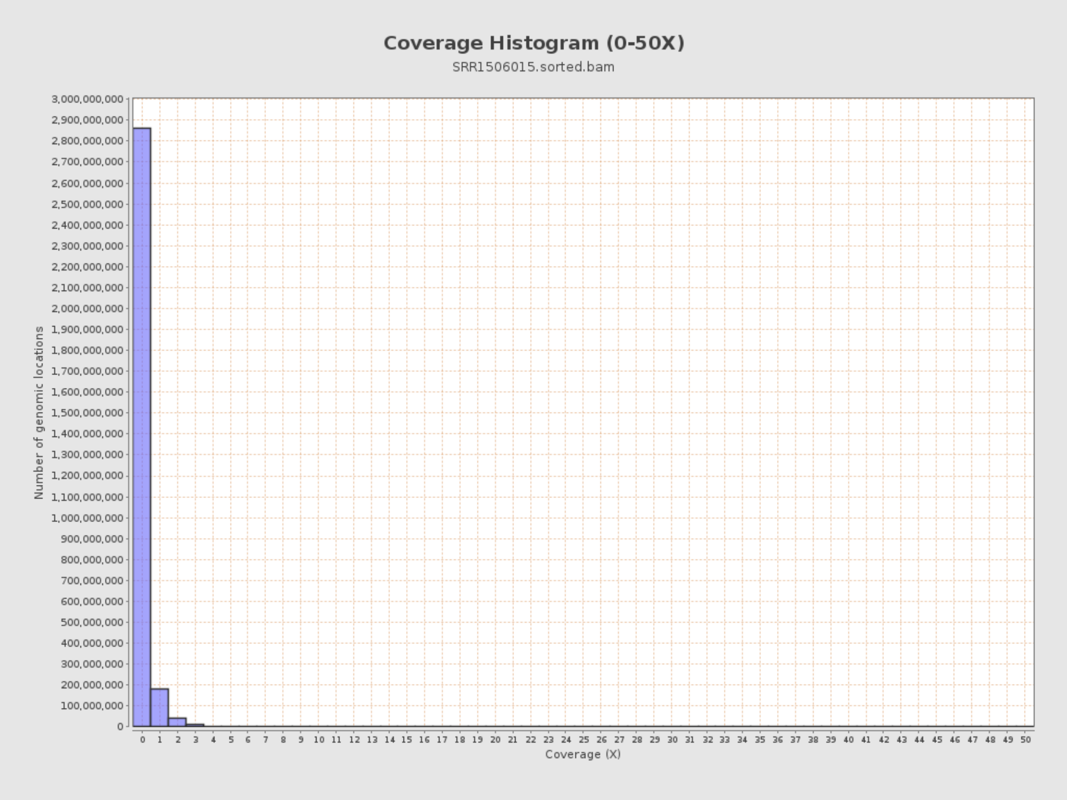
3. Results : Coverage across reference



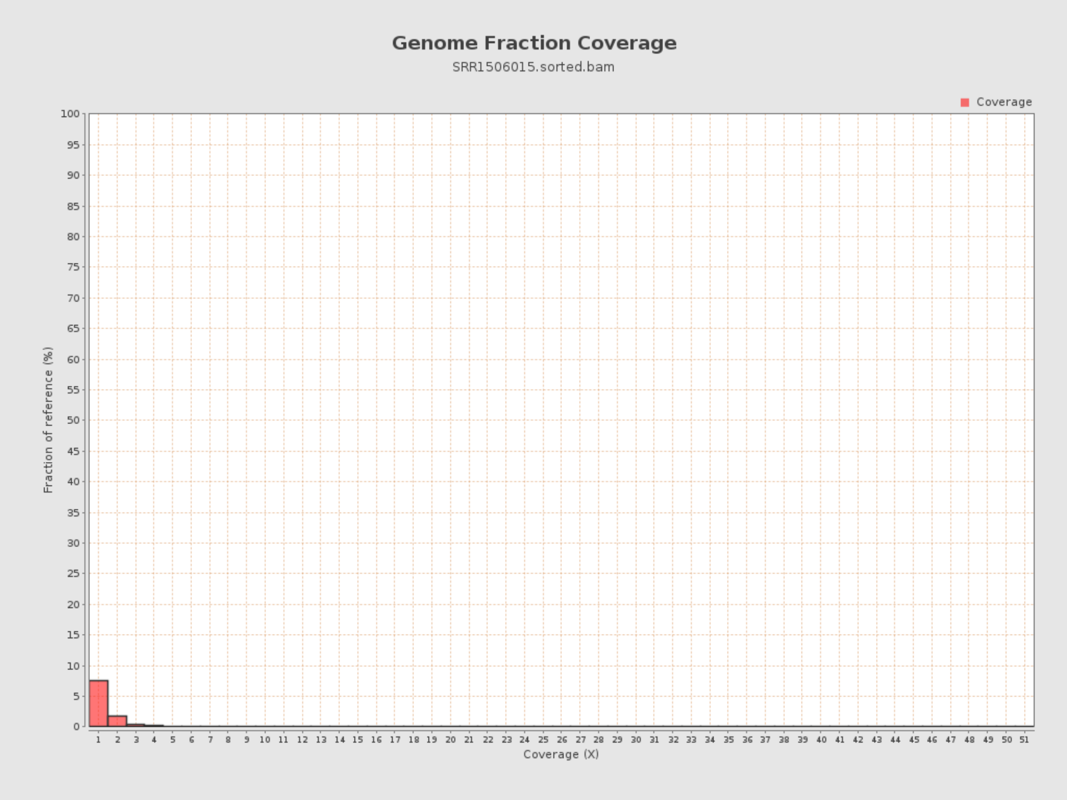
4. Results : Coverage Histogram



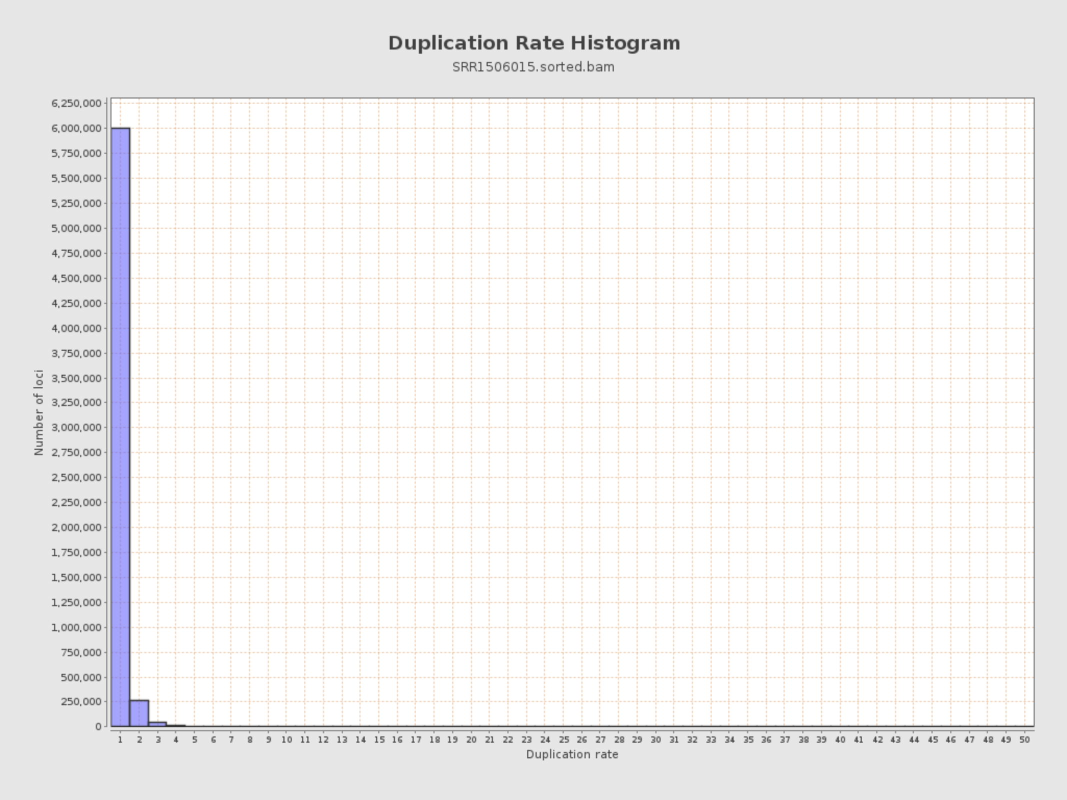
5. Results : Coverage Histogram (0-50X)



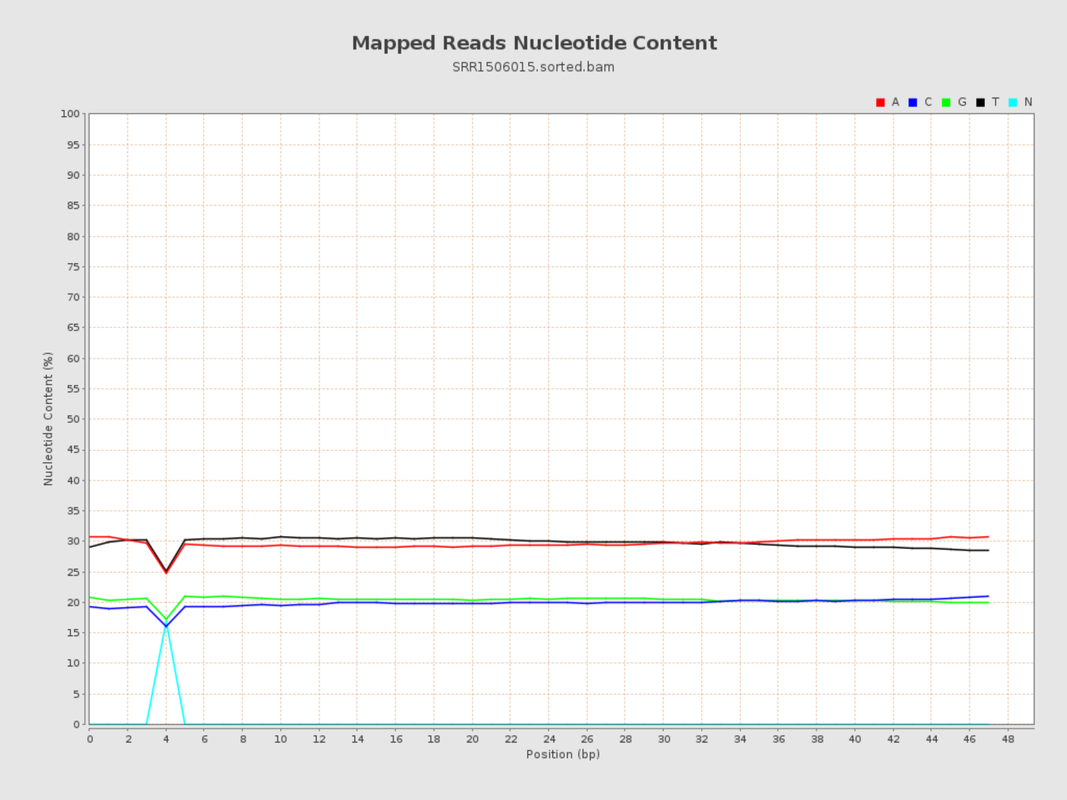
6. Results : Genome Fraction Coverage



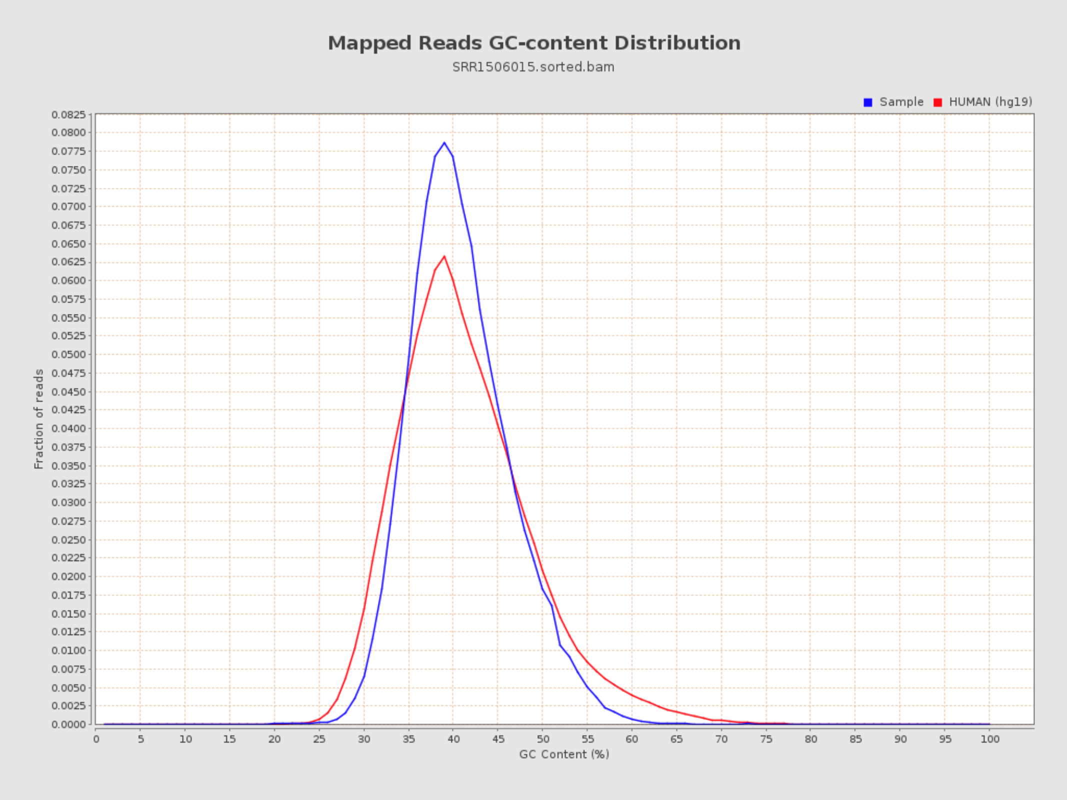
7. Results : Duplication Rate Histogram



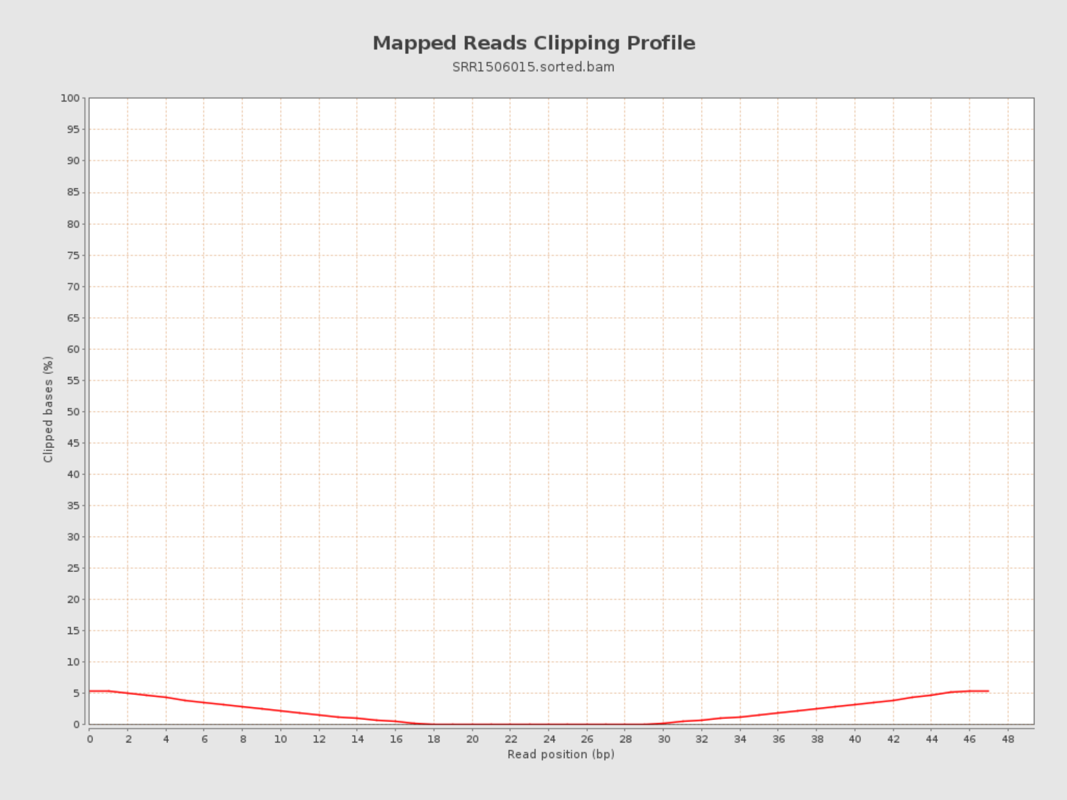
8. Results : Mapped Reads Nucleotide Content



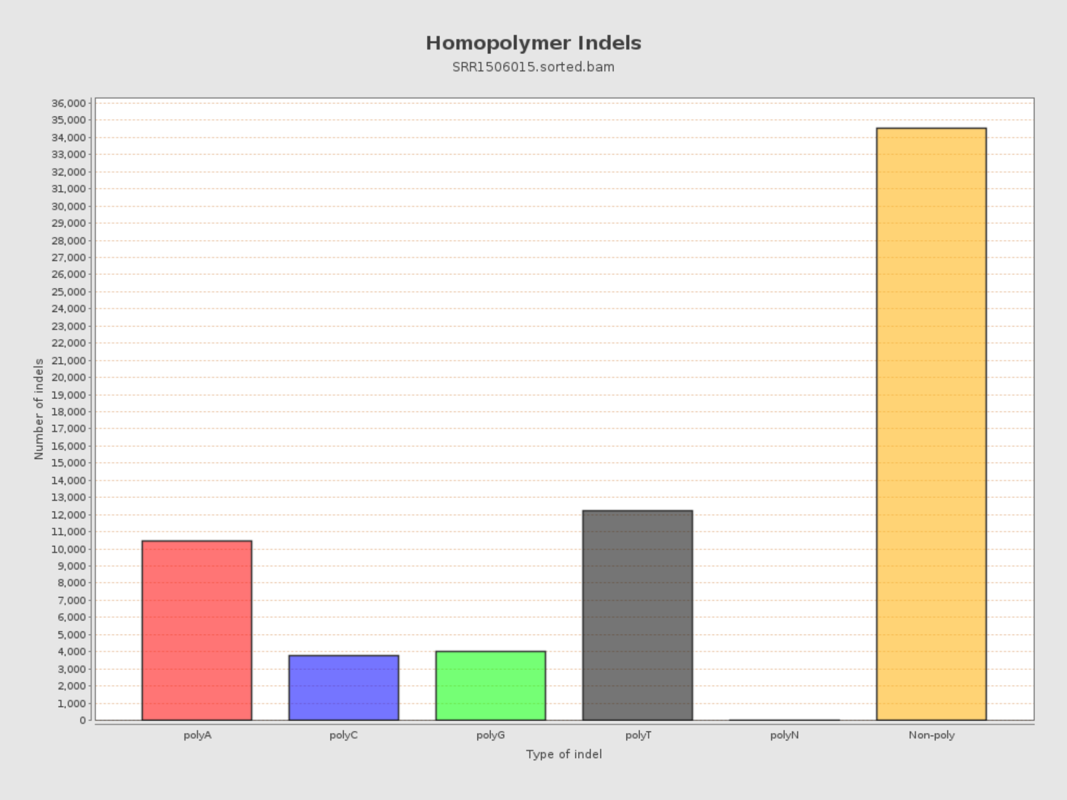
9. Results : Mapped Reads GC-content Distribution



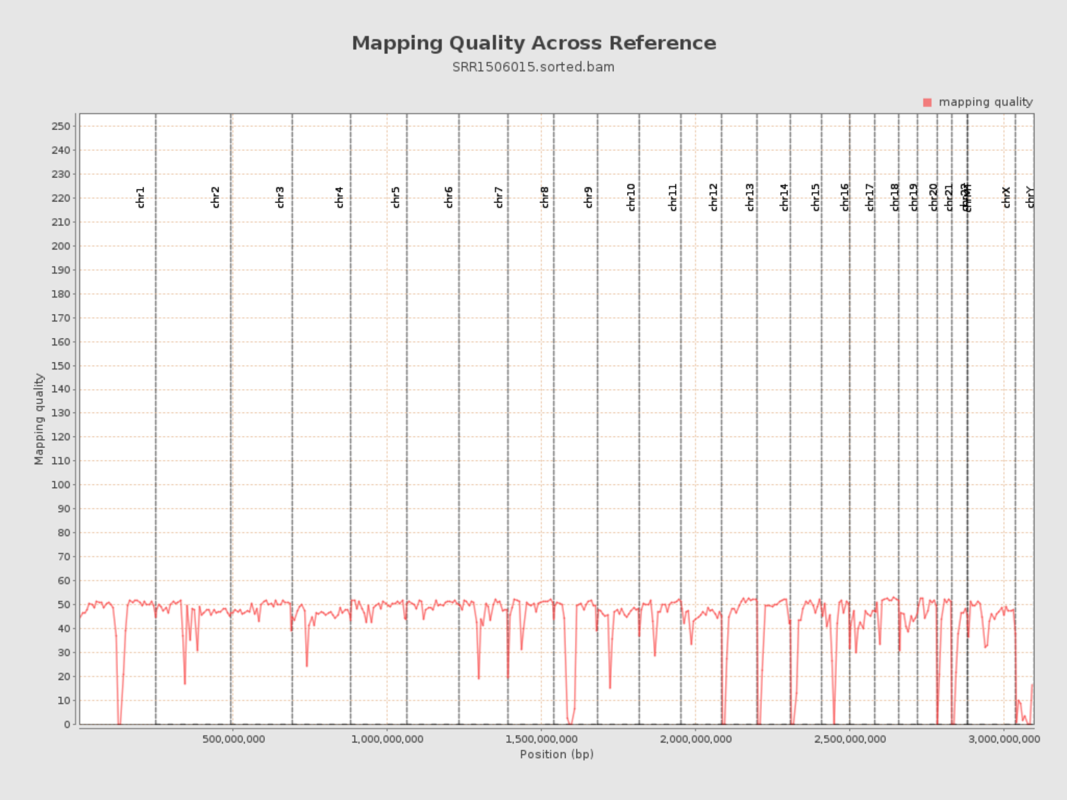
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram