Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/19 23:27:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1506016.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_SRR1506016 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1506016.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Dec 19 23:27:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1506016.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,491,523
Mapped reads	3,239,240 / 72.12%
Unmapped reads	1,252,283 / 27.88%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	160 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	209,076 / 4.65%
Duplication rate	4.82%
Clipped reads	496,089 / 11.05%

2.2. ACGT Content

Number/percentage of A's	44,437,411 / 29.49%
Number/percentage of C's	30,902,946 / 20.51%
Number/percentage of T's	43,637,768 / 28.96%
Number/percentage of G's	31,186,454 / 20.7%
Number/percentage of N's	501,183 / 0.33%
GC Percentage	41.21%

2.3. Coverage

Mean	0.0487

Standard Deviation	0.5371

2.4. Mapping Quality

Mean Mapping Quality	44.39

2.5. Mismatches and indels

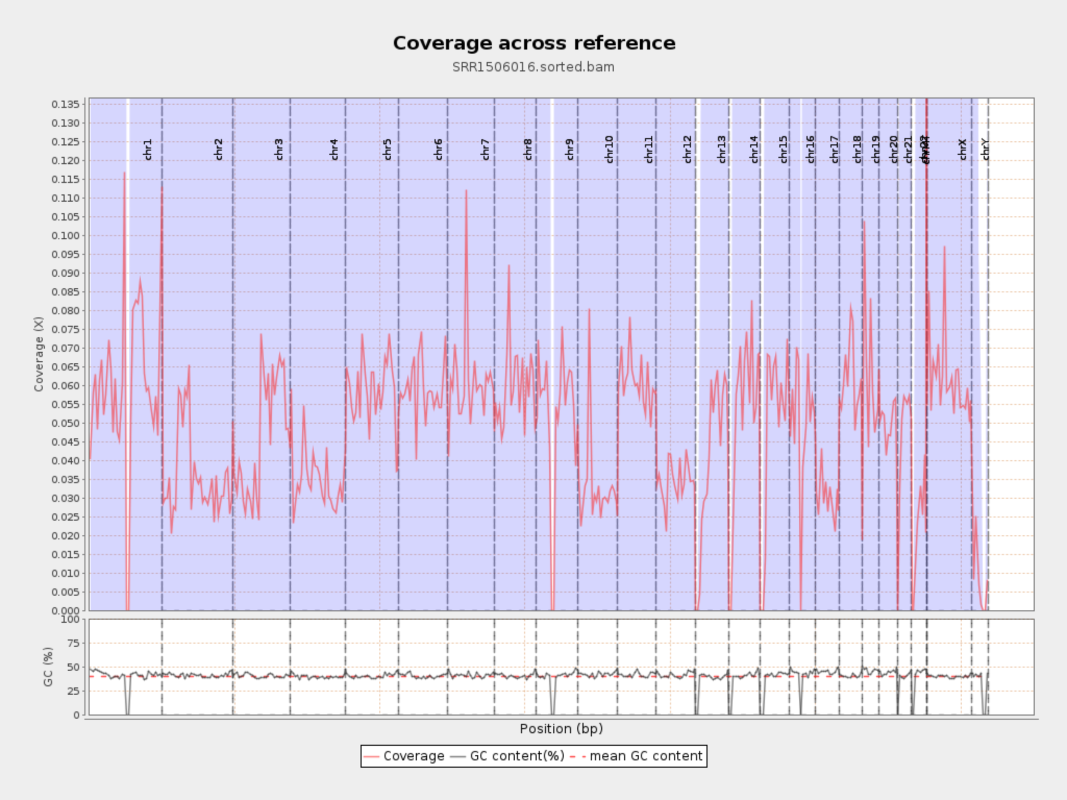
General error rate	0.81%
Mismatches	1,216,809
Insertions	6,662
Mapped reads with at least one insertion	0.21%
Deletions	22,347
Mapped reads with at least one deletion	0.69%
Homopolymer indels	46.34%

2.6. Chromosome stats

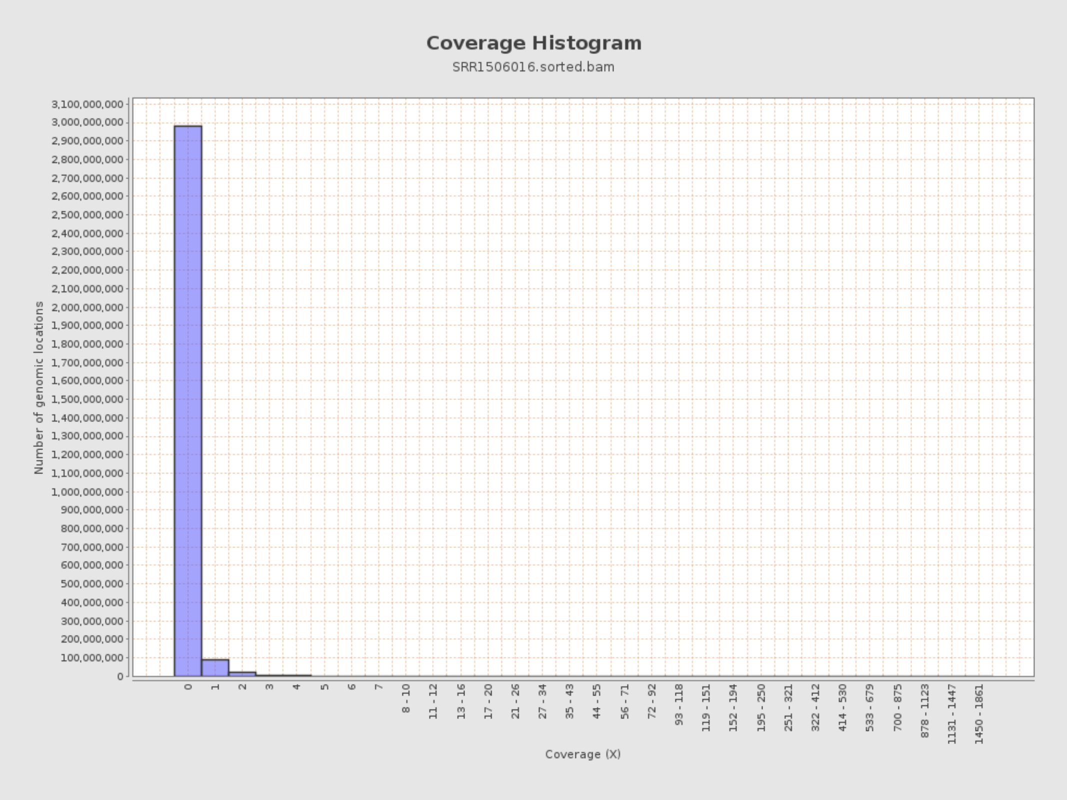
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14874503	0.0597	1.2762
chr2	243199373	8748080	0.036	0.3795
chr3	198022430	9195615	0.0464	0.275
chr4	191154276	6631288	0.0347	0.2457
chr5	180915260	10616474	0.0587	0.3116
chr6	171115067	10083621	0.0589	0.341
chr7	159138663	9797903	0.0616	0.7729

chr8	146364022	8739285	0.0597	0.6184
chr9	141213431	7317312	0.0518	0.379
chr10	135534747	4463347	0.0329	0.4388
chr11	135006516	8155233	0.0604	0.4451
chr12	133851895	4643640	0.0347	0.2472
chr13	115169878	4679628	0.0406	0.2513
chr14	107349540	5579807	0.052	0.4888
chr15	102531392	5004895	0.0488	0.2784
chr16	90354753	4548091	0.0503	0.3124
chr17	81195210	2452612	0.0302	0.2456
chr18	78077248	4830473	0.0619	0.5714
chr19	59128983	3719872	0.0629	0.8398
chr20	63025520	3138875	0.0498	0.2882
chr21	48129895	2213776	0.046	0.2959
chr22	51304566	1092776	0.0213	0.1813
chrMT	16571	5859	0.3536	0.8664
chrX	155270560	9632452	0.062	0.3645
chrY	59373566	531351	0.0089	0.1644

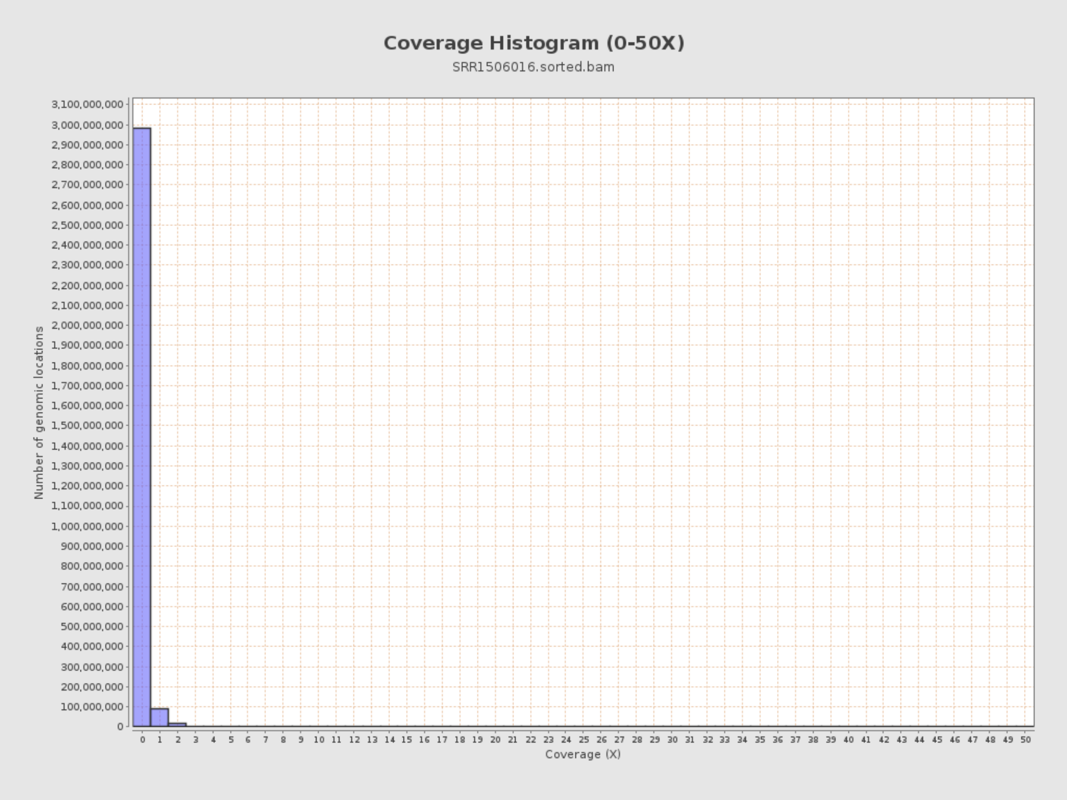
3. Results : Coverage across reference



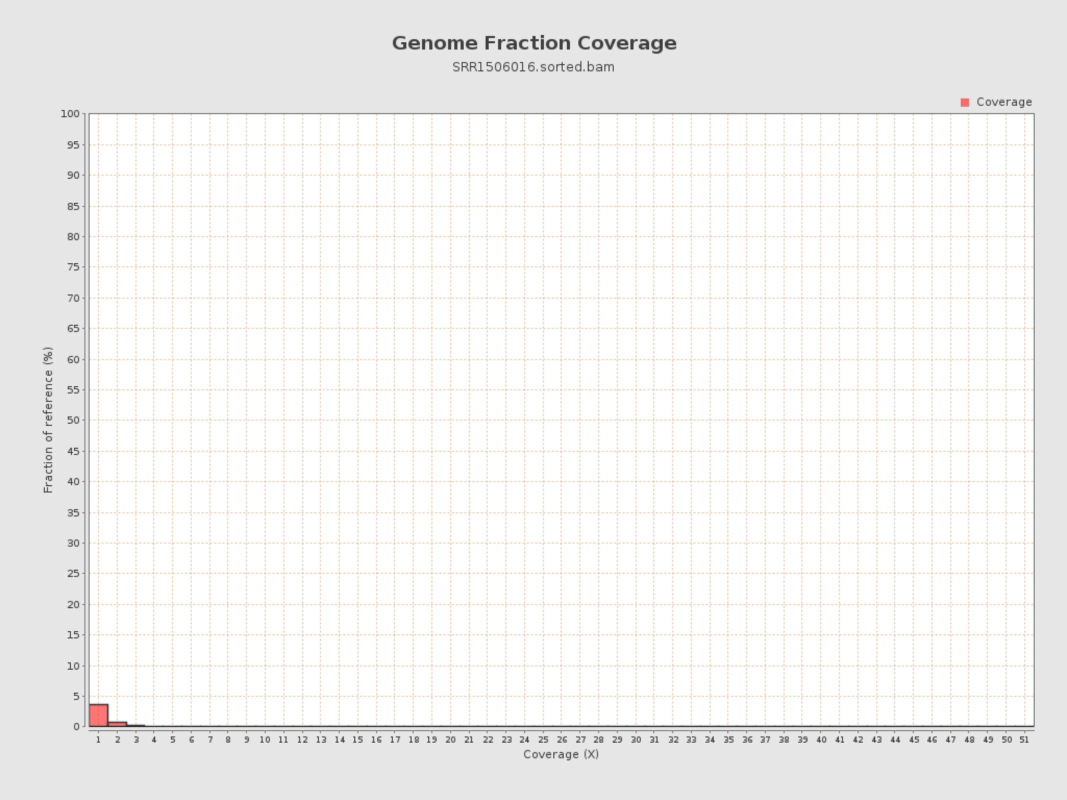
4. Results : Coverage Histogram



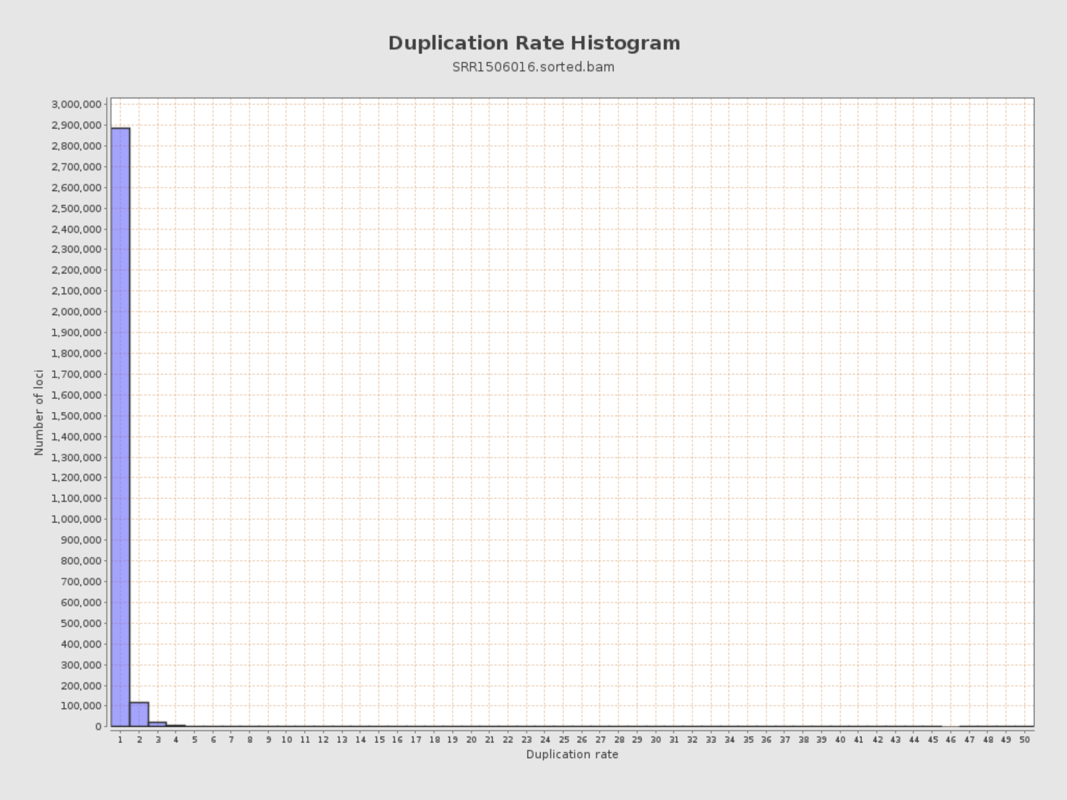
5. Results : Coverage Histogram (0-50X)



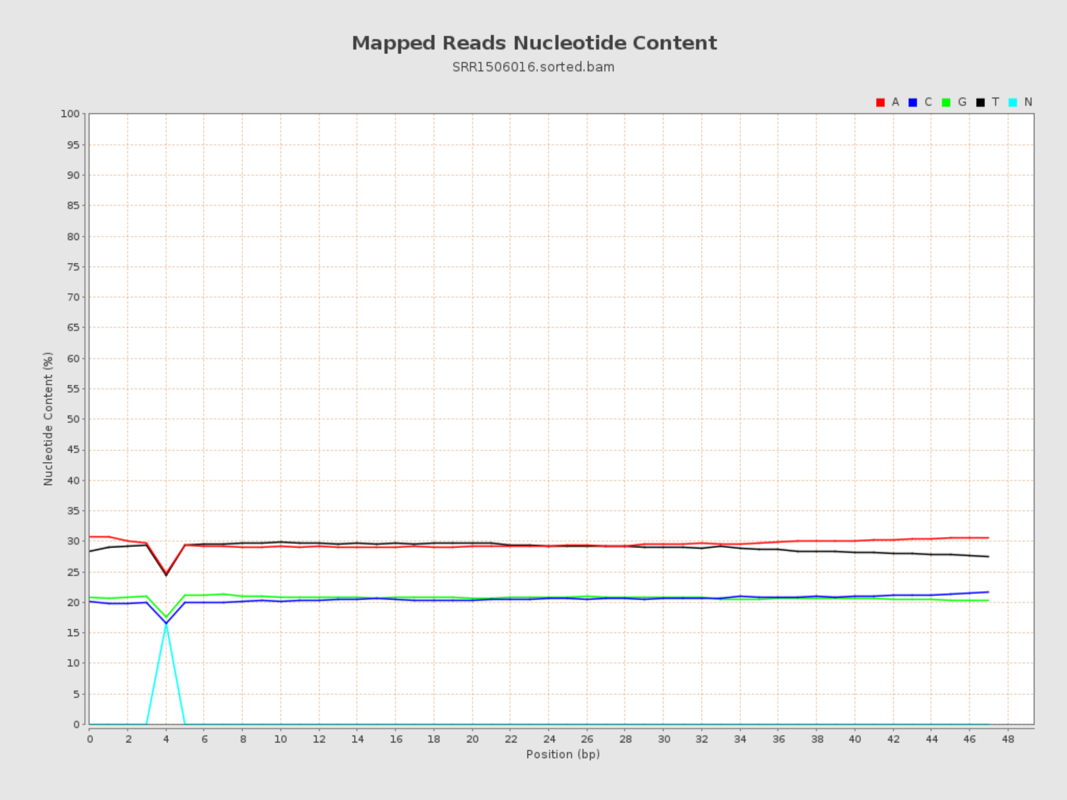
6. Results : Genome Fraction Coverage



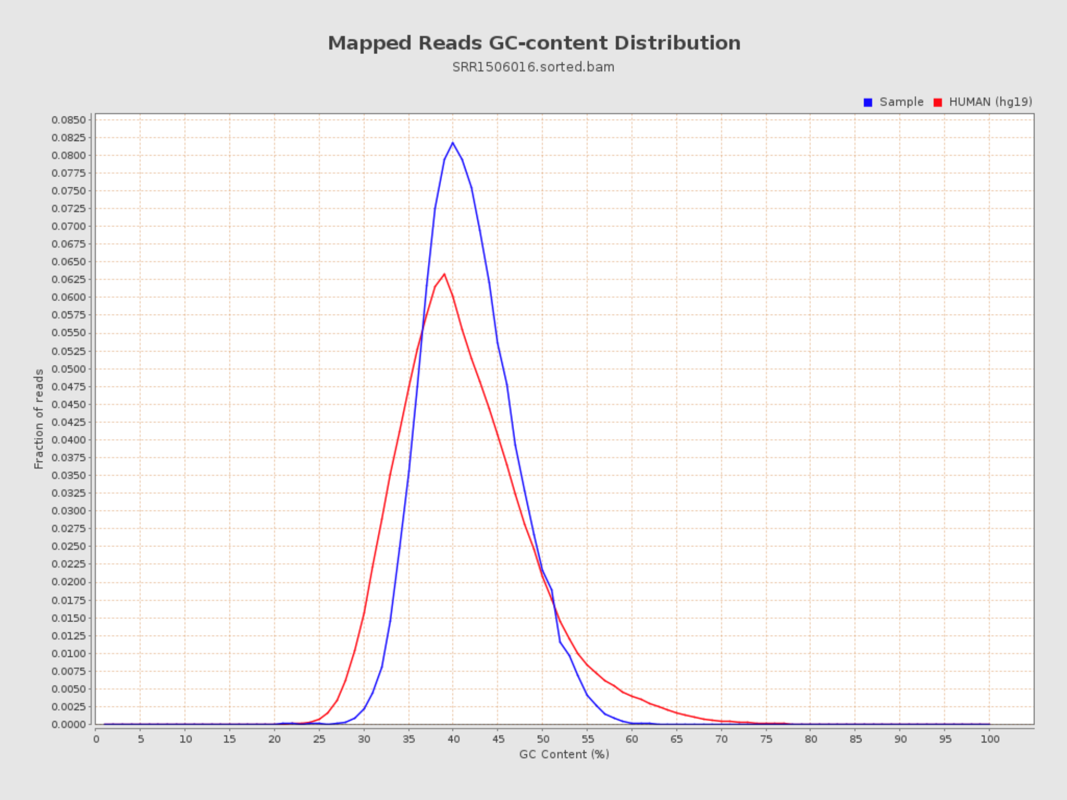
7. Results : Duplication Rate Histogram



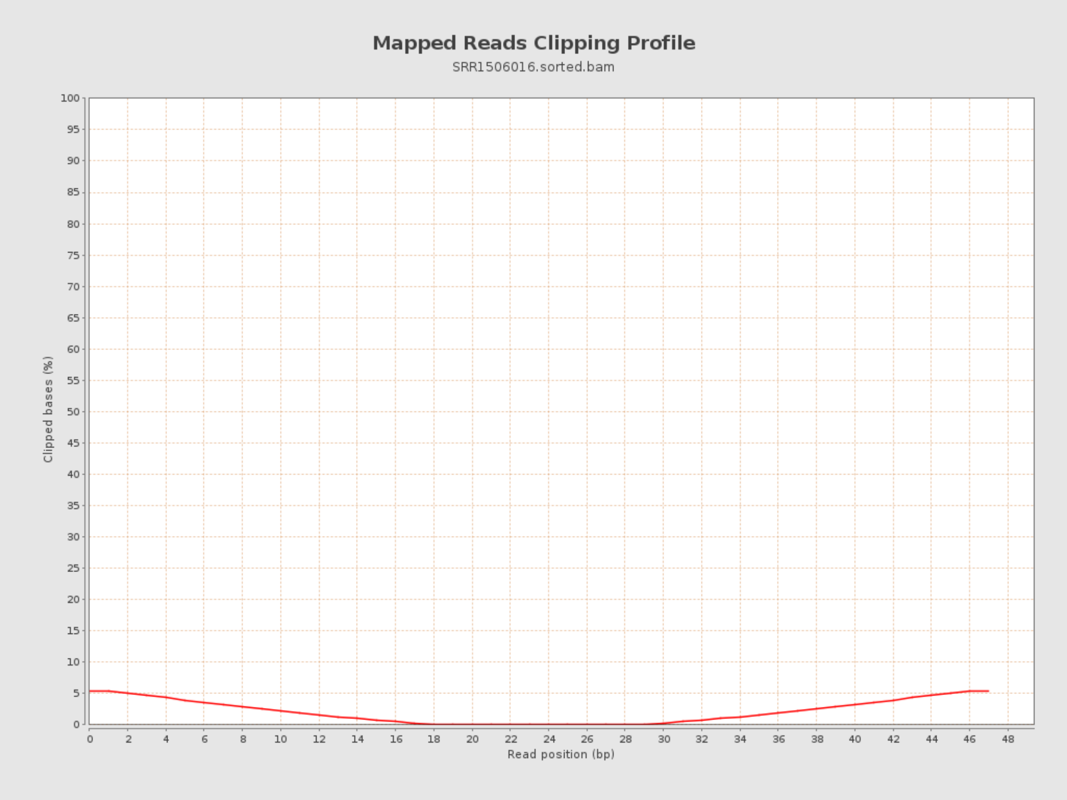
8. Results : Mapped Reads Nucleotide Content



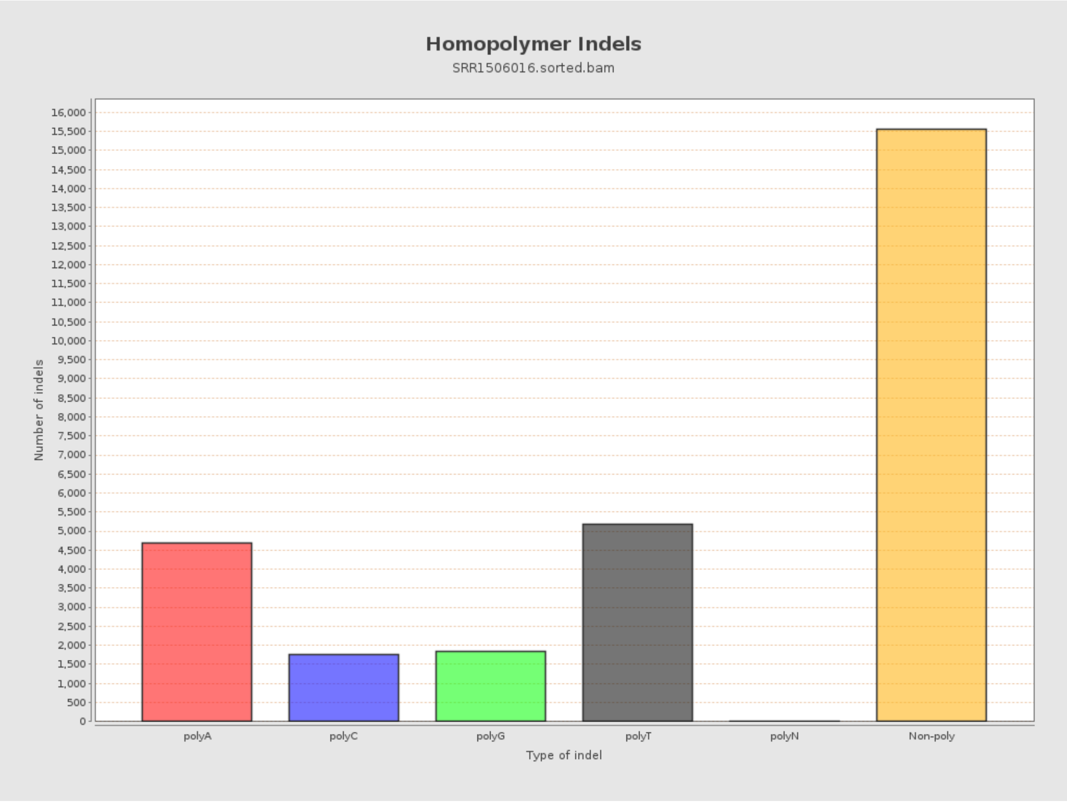
9. Results : Mapped Reads GC-content Distribution



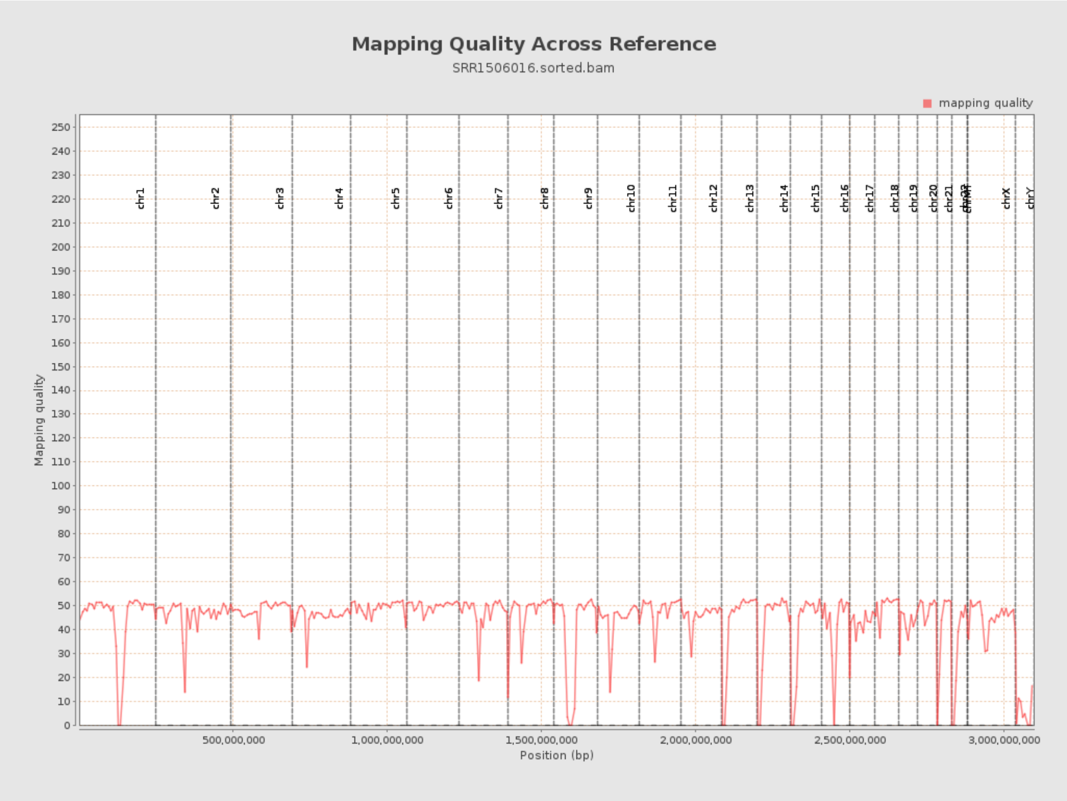
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram