Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/19 23:41:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1506020.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_SRR1506020 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1506020.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Dec 19 23:41:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1506020.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,372,028
Mapped reads	3,562,015 / 66.31%
Unmapped reads	1,810,013 / 33.69%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	143 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	177,344 / 3.3%
Duplication rate	3.82%
Clipped reads	660,215 / 12.29%

2.2. ACGT Content

Number/percentage of A's	48,338,053 / 29.38%
Number/percentage of C's	33,477,884 / 20.35%
Number/percentage of T's	48,058,184 / 29.21%
Number/percentage of G's	34,113,631 / 20.73%
Number/percentage of N's	536,051 / 0.33%
GC Percentage	41.08%

2.3. Coverage

Mean	0.0532

Standard Deviation	0.4682

2.4. Mapping Quality

Mean Mapping Quality	43.25

2.5. Mismatches and indels

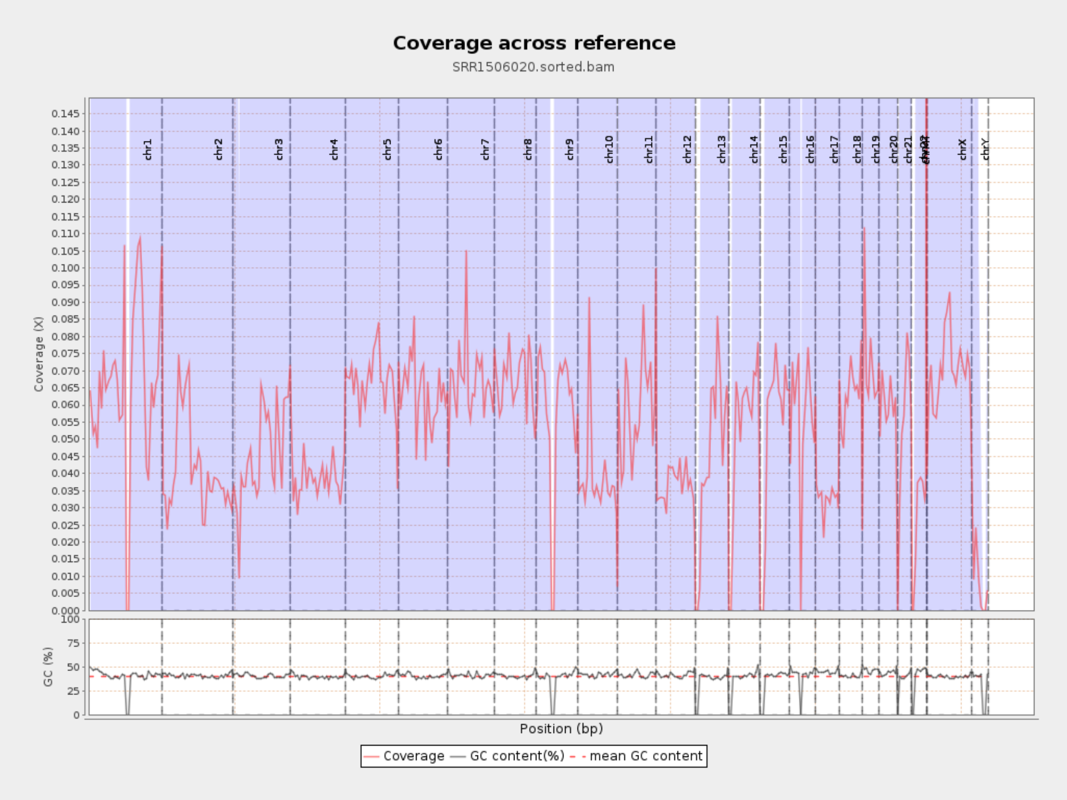
General error rate	0.8%
Mismatches	1,311,257
Insertions	7,339
Mapped reads with at least one insertion	0.21%
Deletions	24,137
Mapped reads with at least one deletion	0.68%
Homopolymer indels	45.36%

2.6. Chromosome stats

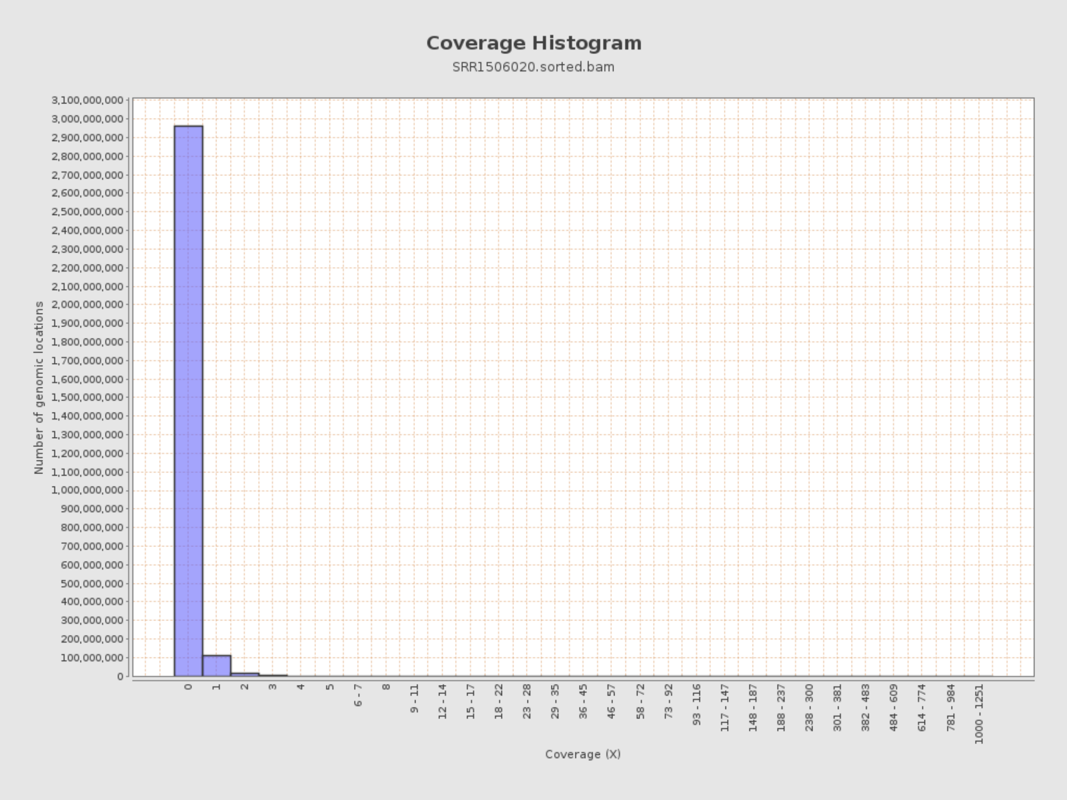
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16426906	0.0659	0.923
chr2	243199373	10082103	0.0415	0.38
chr3	198022430	8899966	0.0449	0.2545
chr4	191154276	7370826	0.0386	0.2446
chr5	180915260	12086583	0.0668	0.3135
chr6	171115067	10878139	0.0636	0.3764
chr7	159138663	10622868	0.0668	0.6618

chr8	146364022	9831972	0.0672	0.5587
chr9	141213431	8125693	0.0575	0.3728
chr10	135534747	5232627	0.0386	0.5094
chr11	135006516	7891227	0.0585	0.3322
chr12	133851895	4933454	0.0369	0.2498
chr13	115169878	5228771	0.0454	0.2533
chr14	107349540	5664102	0.0528	0.7724
chr15	102531392	5372646	0.0524	0.272
chr16	90354753	5134761	0.0568	0.3403
chr17	81195210	2632740	0.0324	0.2331
chr18	78077248	4929273	0.0631	0.4856
chr19	59128983	4220771	0.0714	0.6656
chr20	63025520	3750295	0.0595	0.2997
chr21	48129895	2578444	0.0536	0.2996
chr22	51304566	1305443	0.0254	0.1892
chrMT	16571	11031	0.6657	1.0035
chrX	155270560	10842994	0.0698	0.3527
chrY	59373566	503764	0.0085	0.1471

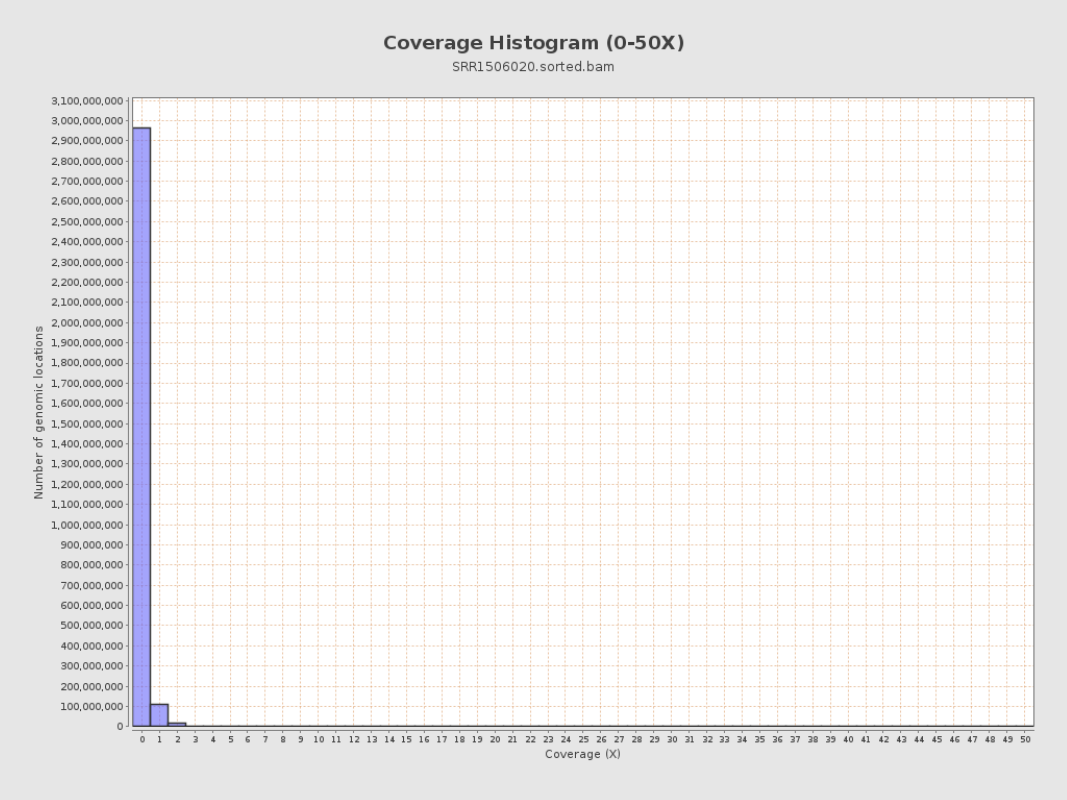
3. Results : Coverage across reference



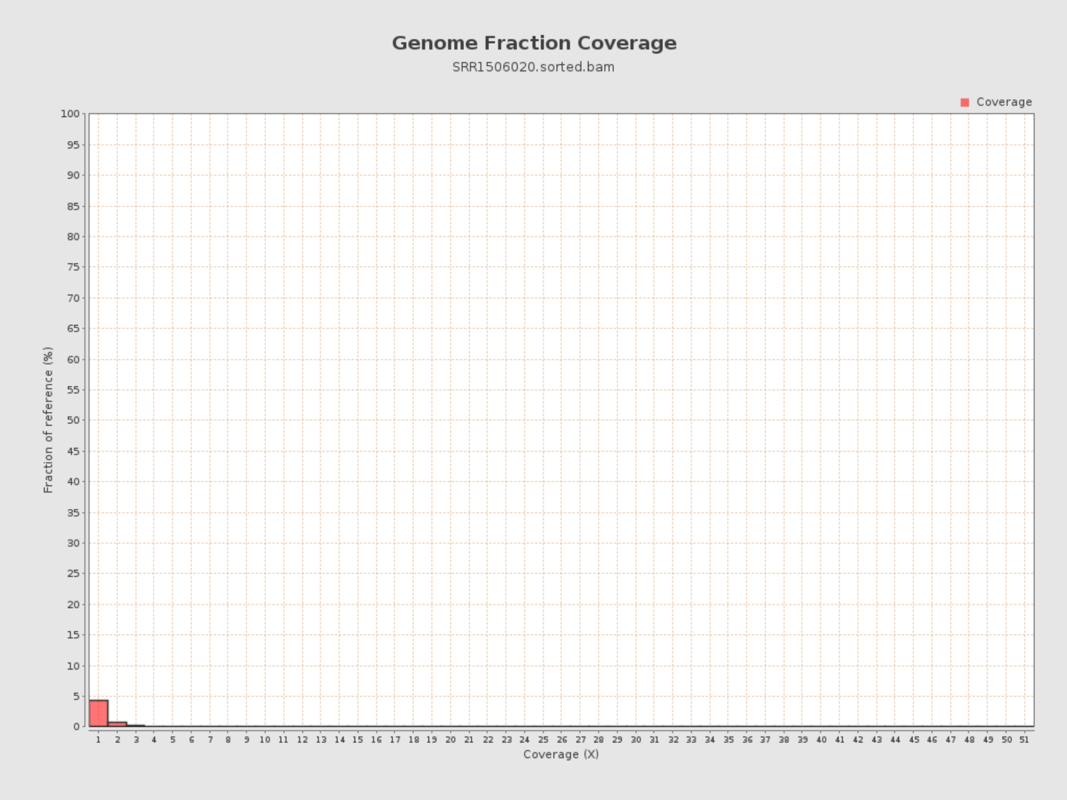
4. Results : Coverage Histogram



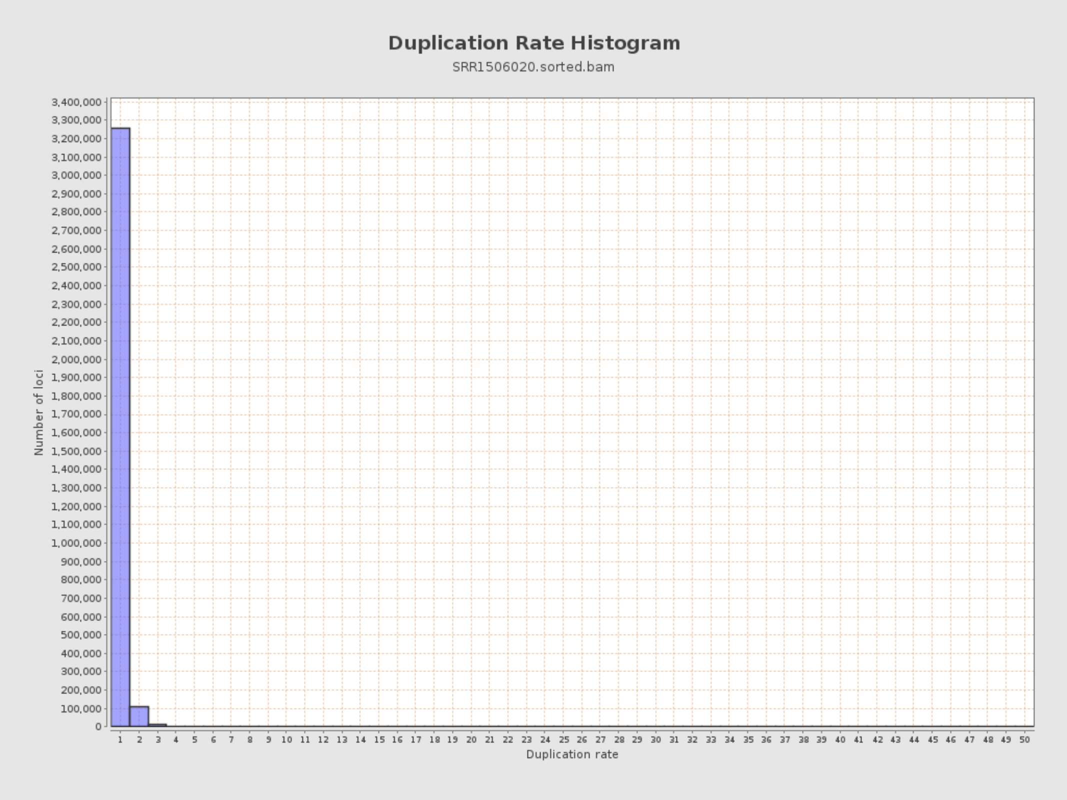
5. Results : Coverage Histogram (0-50X)



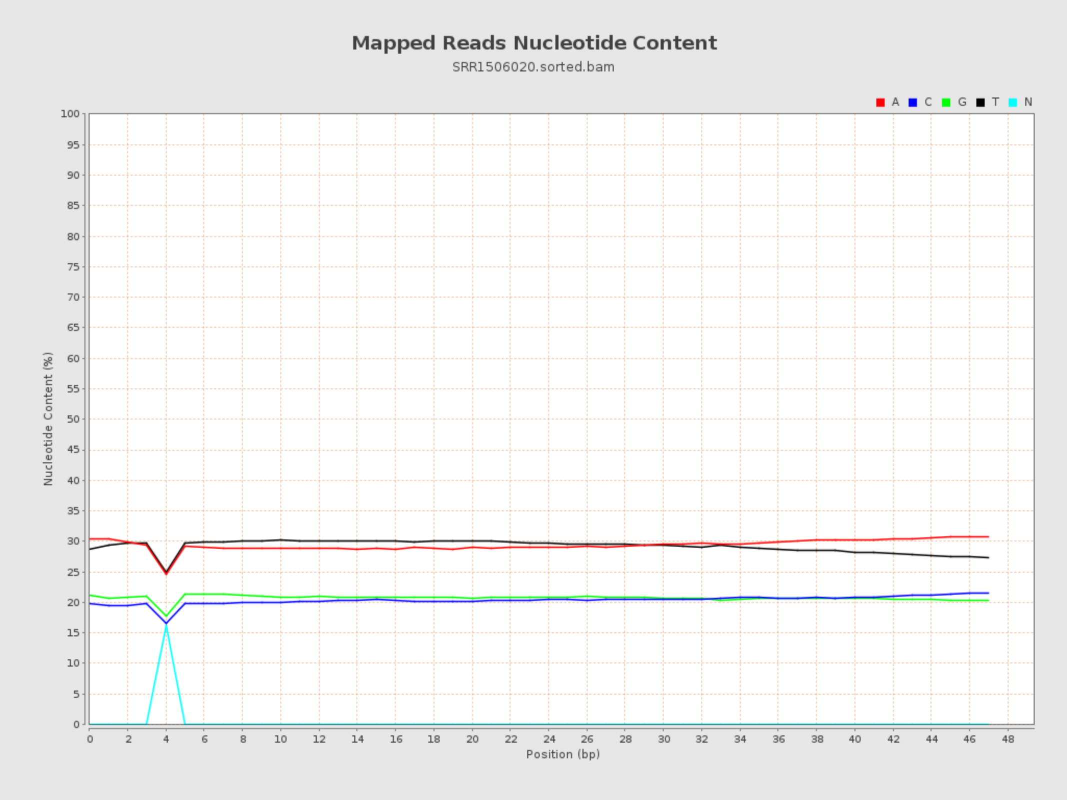
6. Results : Genome Fraction Coverage



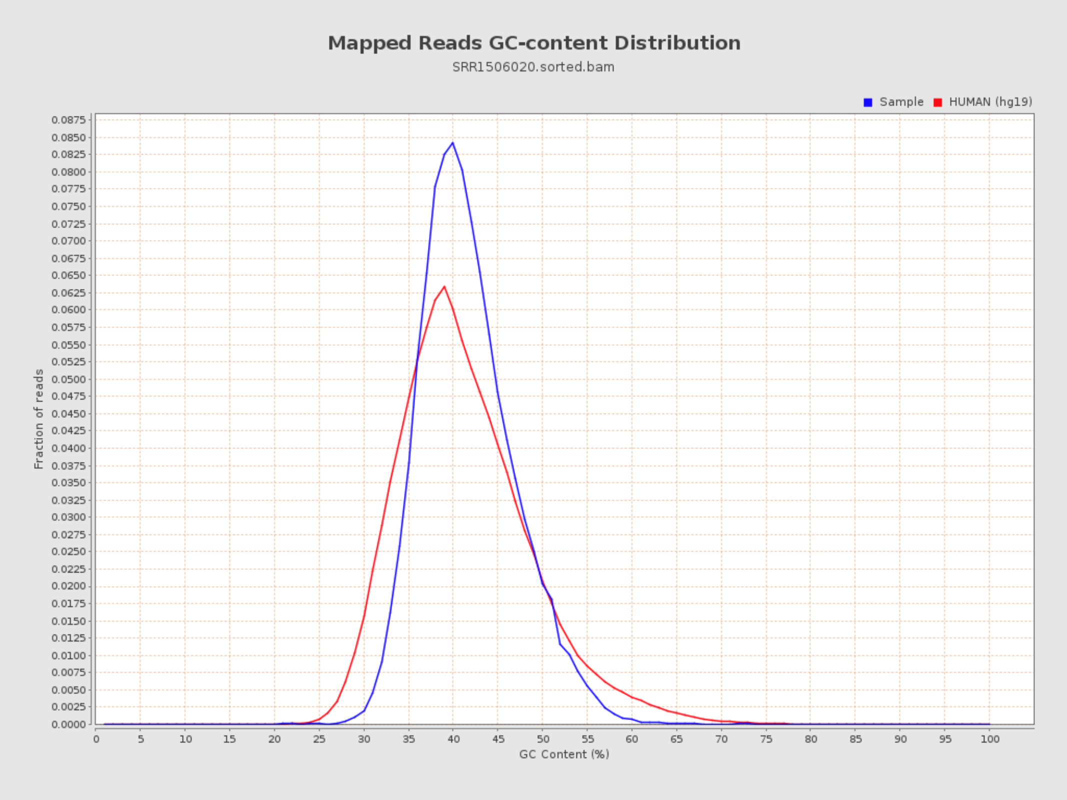
7. Results : Duplication Rate Histogram



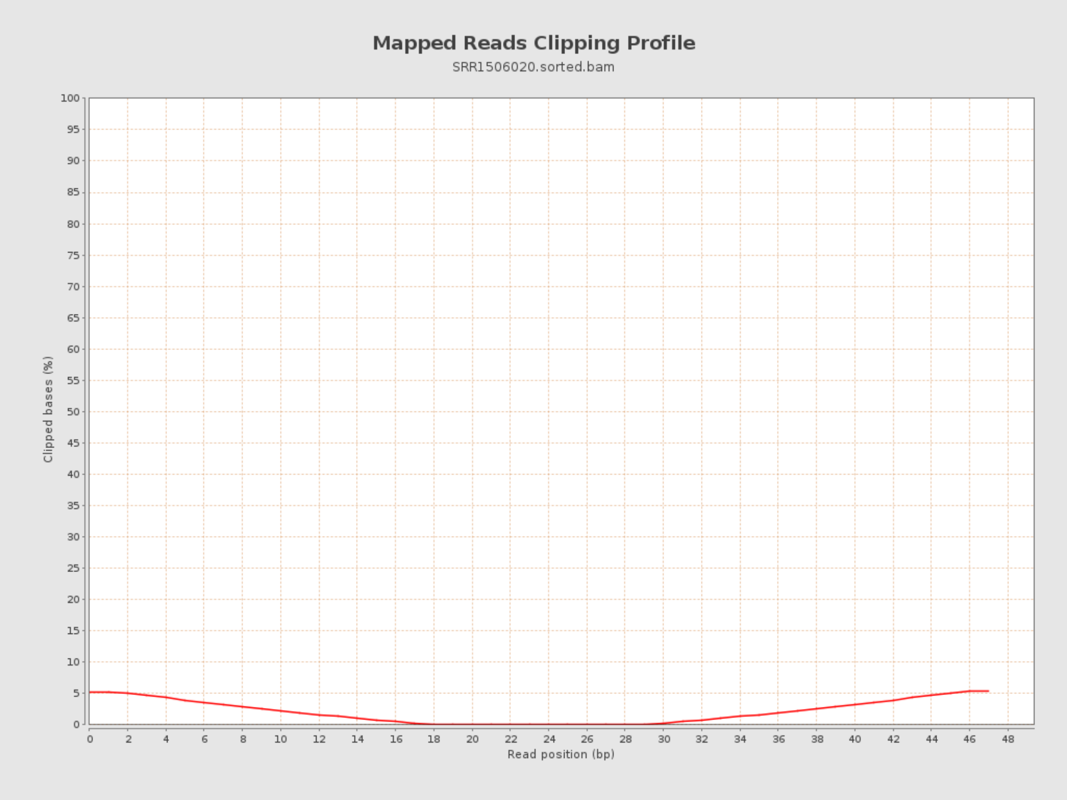
8. Results : Mapped Reads Nucleotide Content



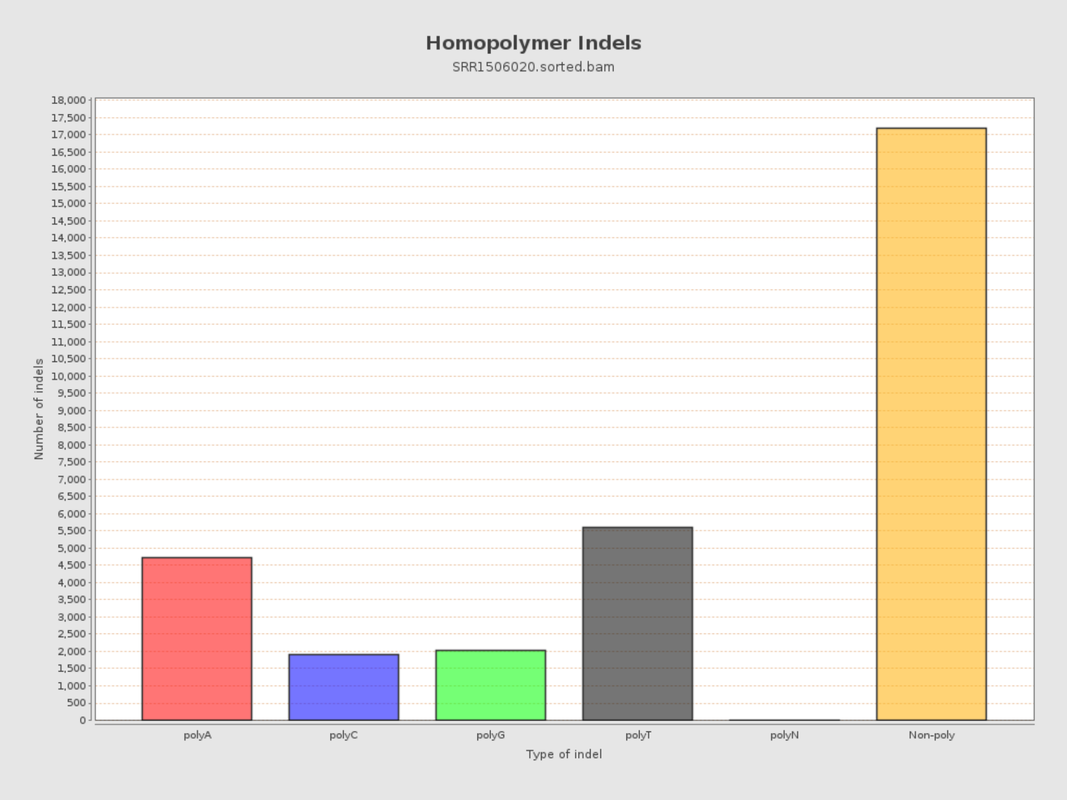
9. Results : Mapped Reads GC-content Distribution



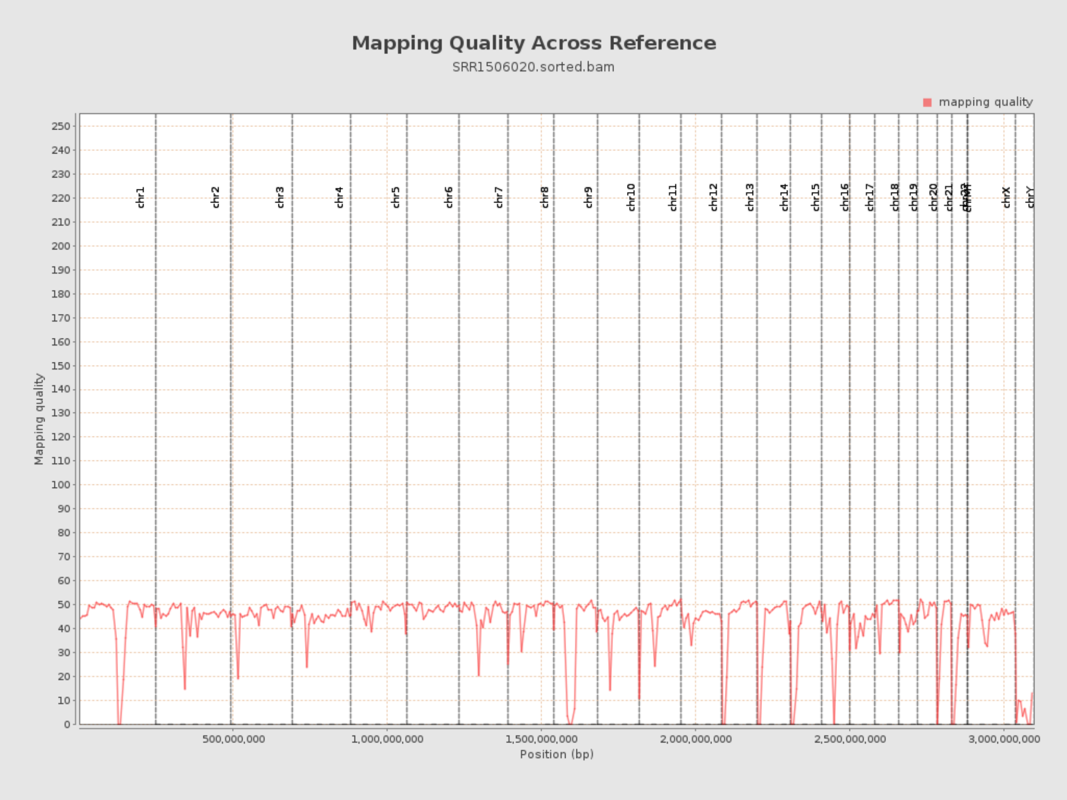
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram