Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/20 10:09:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR090209.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_SRR090209 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR090209.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Apr 20 10:09:18 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR090209.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	22,193,177
Mapped reads	18,485,673 / 83.29%
Unmapped reads	3,707,504 / 16.71%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,083 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	2,713,442 / 12.23%
Duplication rate	10.7%
Clipped reads	2,065,222 / 9.31%

2.2. ACGT Content

Number/percentage of A's	271,812,125 / 31.32%
Number/percentage of C's	170,768,820 / 19.68%
Number/percentage of T's	242,330,179 / 27.92%
Number/percentage of G's	182,948,202 / 21.08%
Number/percentage of N's	30,966 / 0%
GC Percentage	40.76%

2.3. Coverage

Mean	0.2804

Standard Deviation	1.723

2.4. Mapping Quality

Mean Mapping Quality	44.24

2.5. Mismatches and indels

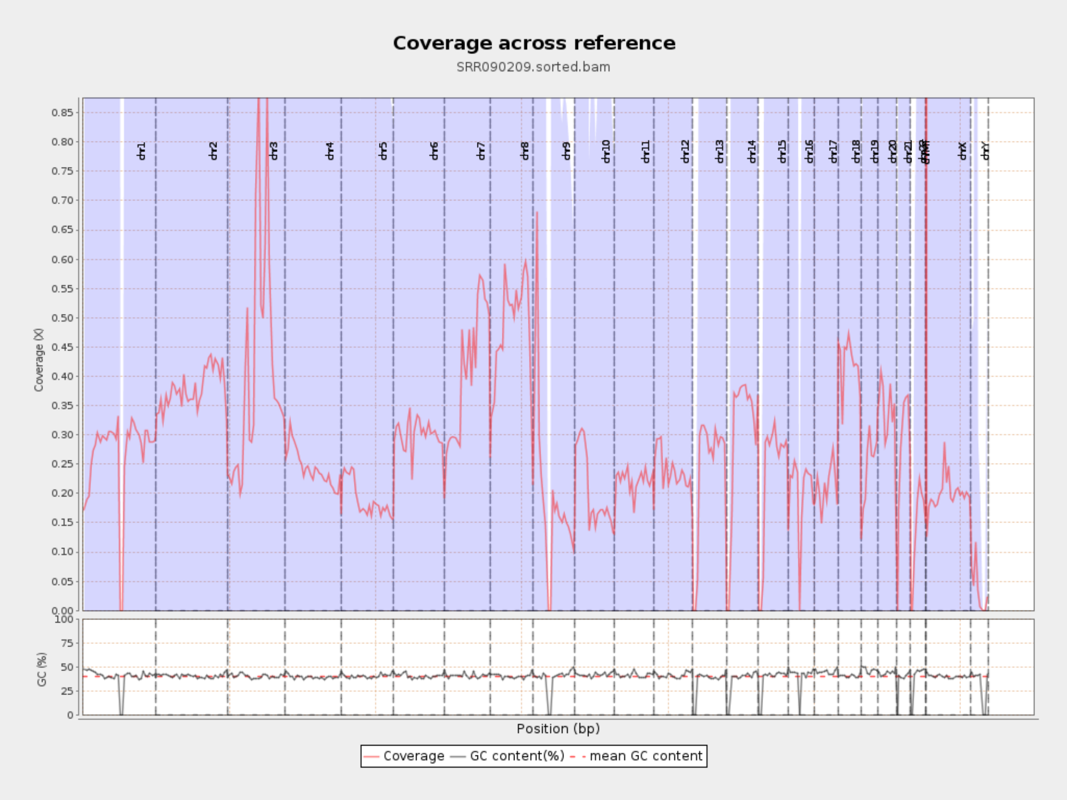
General error rate	0.38%
Mismatches	3,212,202
Insertions	34,987
Mapped reads with at least one insertion	0.19%
Deletions	113,139
Mapped reads with at least one deletion	0.61%
Homopolymer indels	46.66%

2.6. Chromosome stats

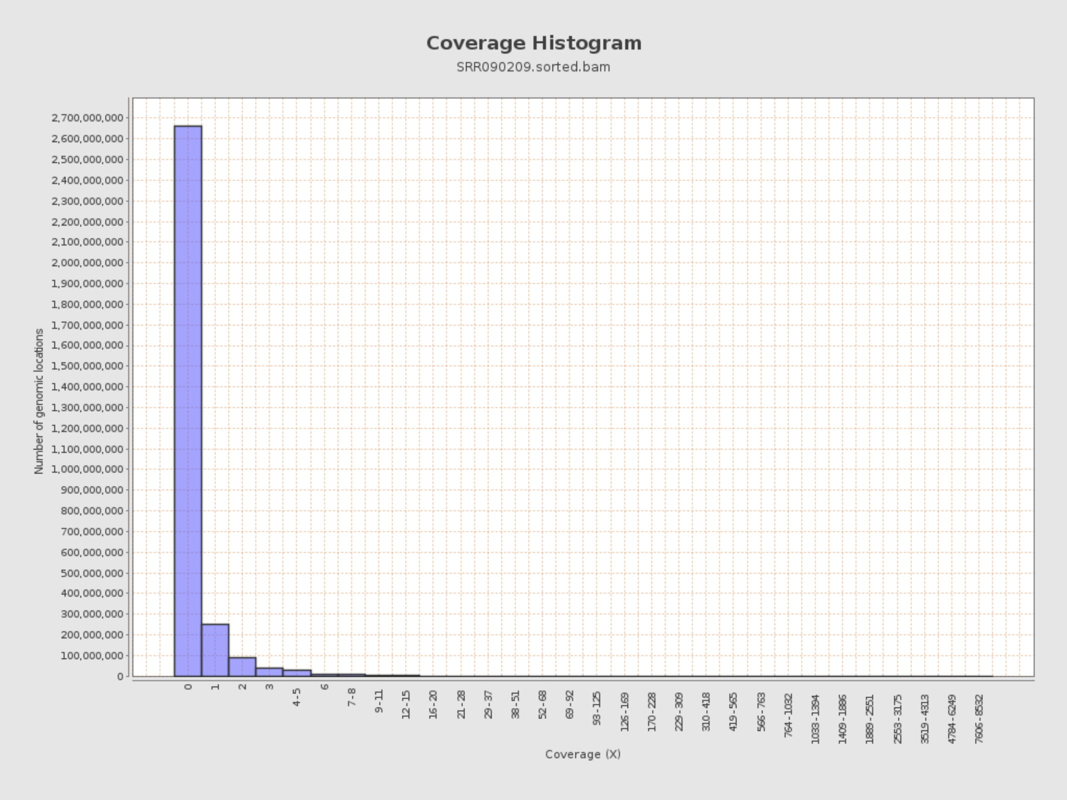
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	66280894	0.2659	2.1118
chr2	243199373	92320807	0.3796	1.7878
chr3	198022430	81174859	0.4099	1.3418
chr4	191154276	46478868	0.2431	0.9545
chr5	180915260	34345564	0.1898	0.8174
chr6	171115067	51529493	0.3011	1.1815
chr7	159138663	65068236	0.4089	2.5564

chr8	146364022	71286913	0.4871	4.7765
chr9	141213431	27776966	0.1967	1.1959
chr10	135534747	27756528	0.2048	1.1113
chr11	135006516	29834231	0.221	1.1982
chr12	133851895	32121665	0.24	0.9454
chr13	115169878	27909210	0.2423	0.9406
chr14	107349540	32222581	0.3002	1.1002
chr15	102531392	23590639	0.2301	0.9153
chr16	90354753	17944416	0.1986	0.8607
chr17	81195210	17423765	0.2146	0.9493
chr18	78077248	33023994	0.423	1.9941
chr19	59128983	14773589	0.2499	1.6731
chr20	63025520	21529279	0.3416	1.1783
chr21	48129895	13224919	0.2748	1.1309
chr22	51304566	7229487	0.1409	0.6841
chrMT	16571	194529	11.7391	10.4088
chrX	155270560	30905867	0.199	0.9734
chrY	59373566	2113528	0.0356	1.0347

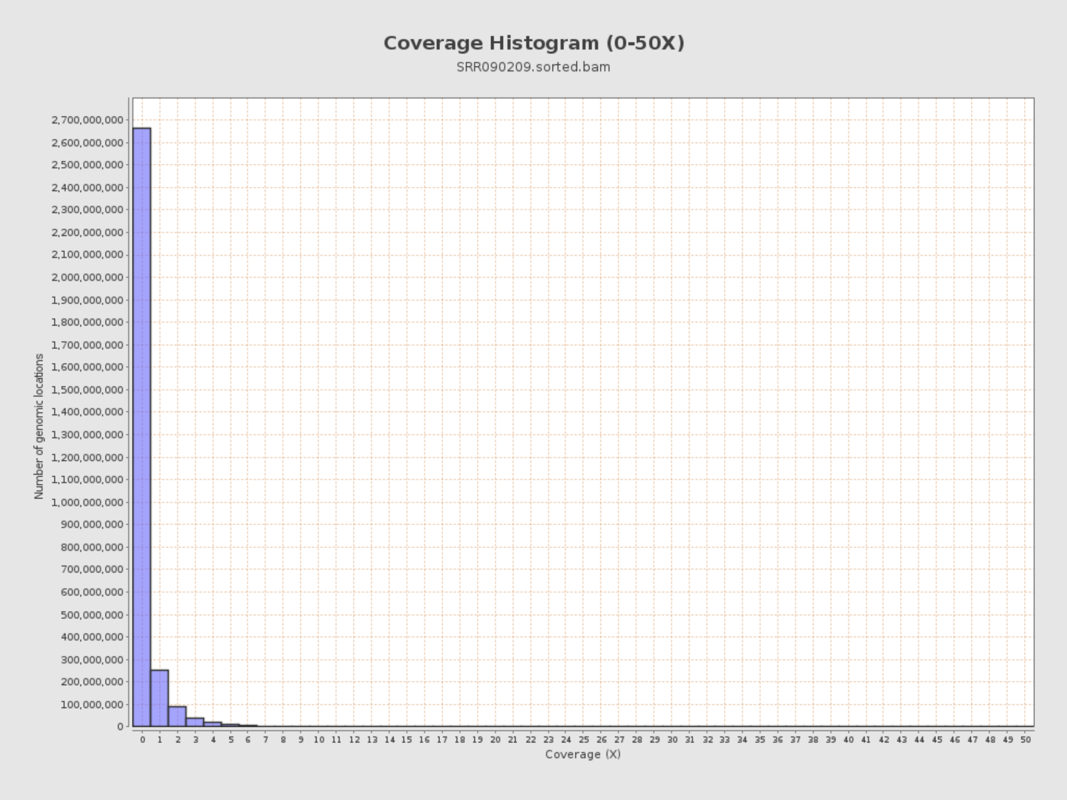
3. Results : Coverage across reference



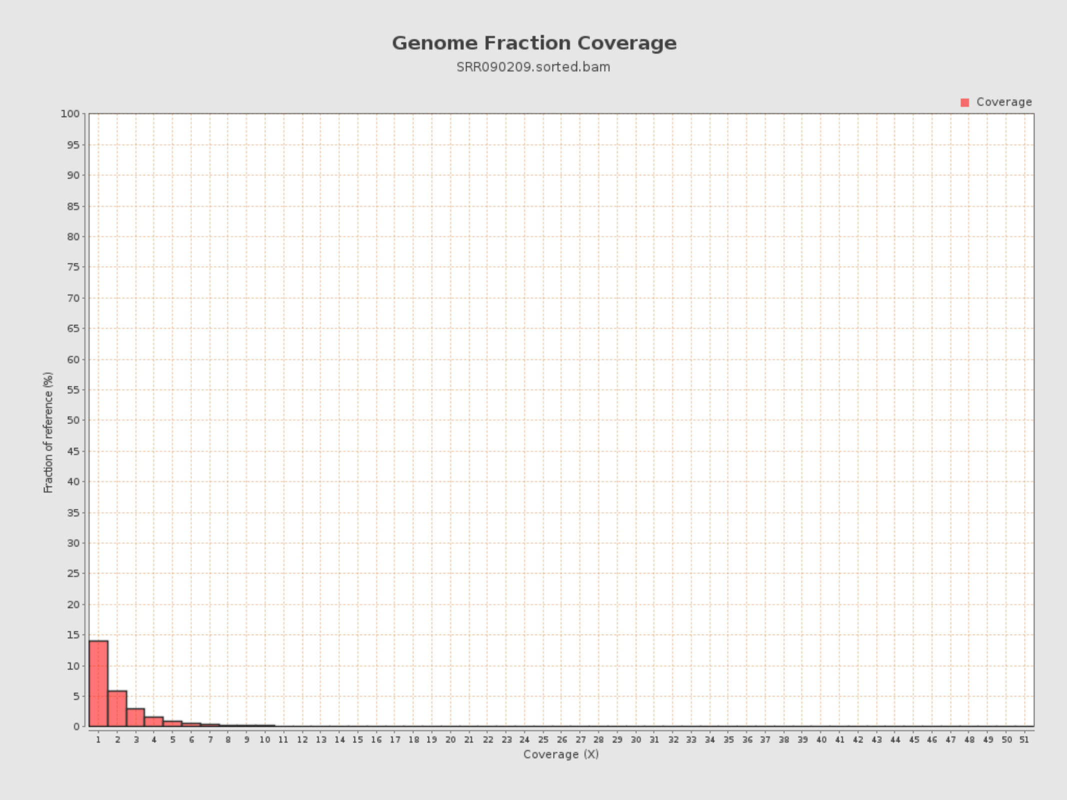
4. Results : Coverage Histogram



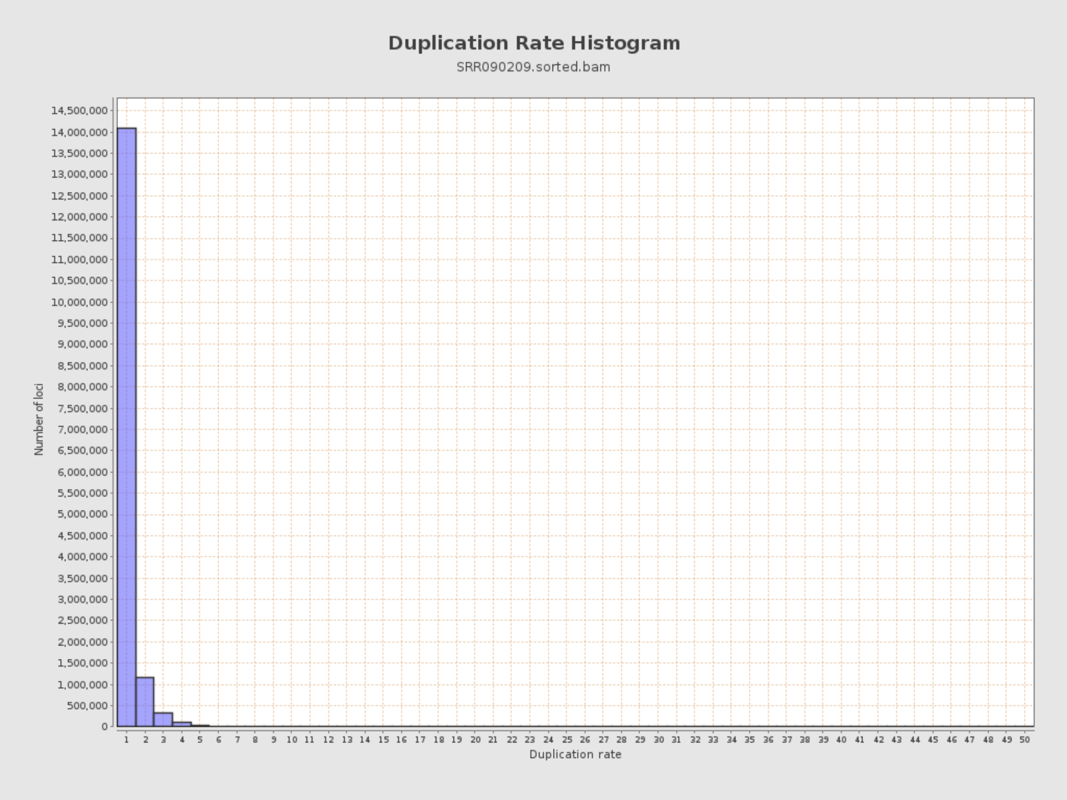
5. Results : Coverage Histogram (0-50X)



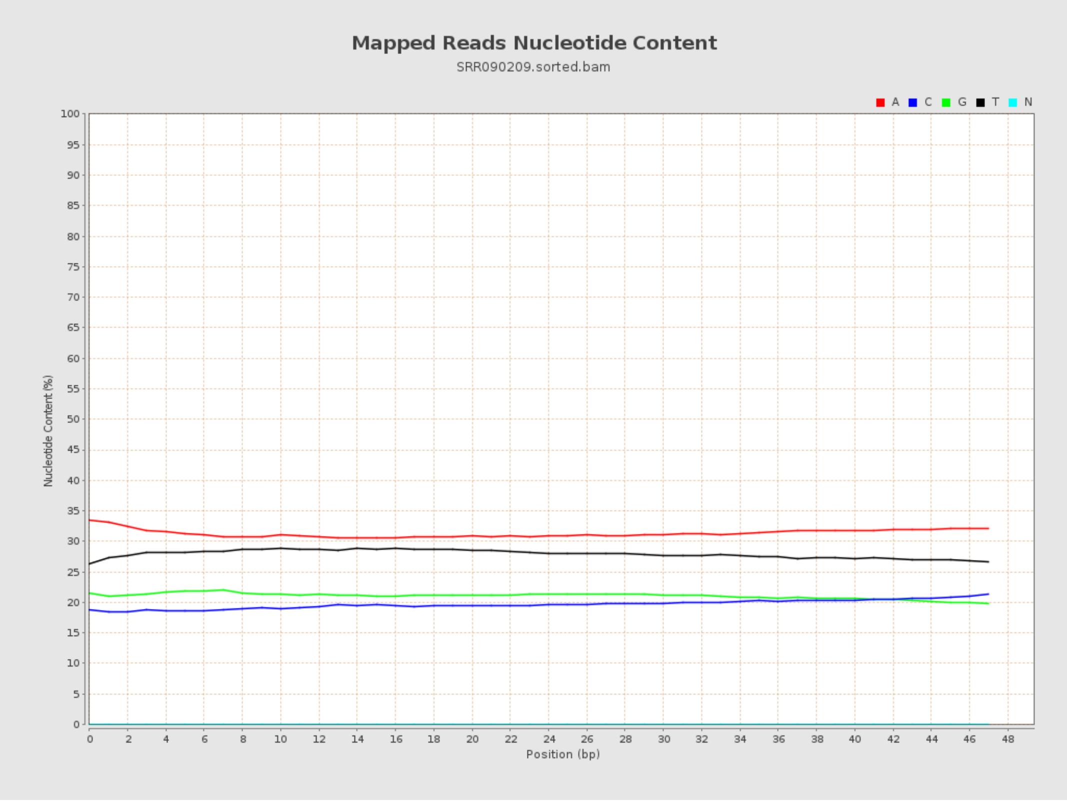
6. Results : Genome Fraction Coverage



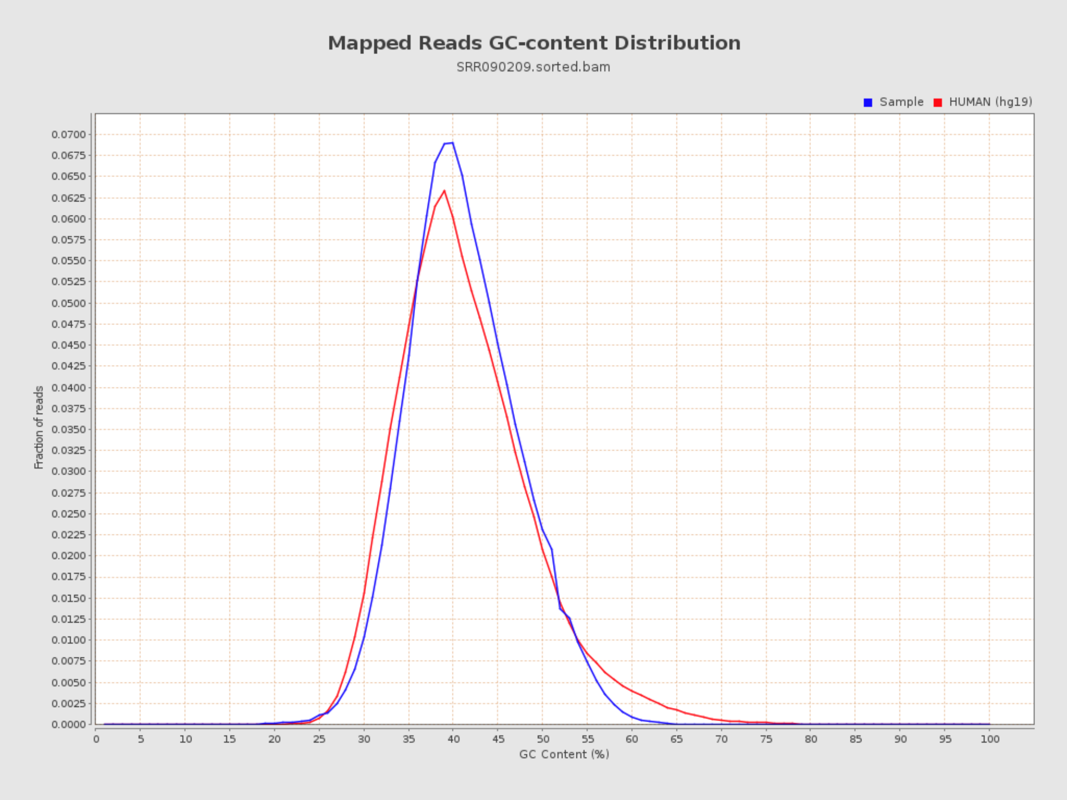
7. Results : Duplication Rate Histogram



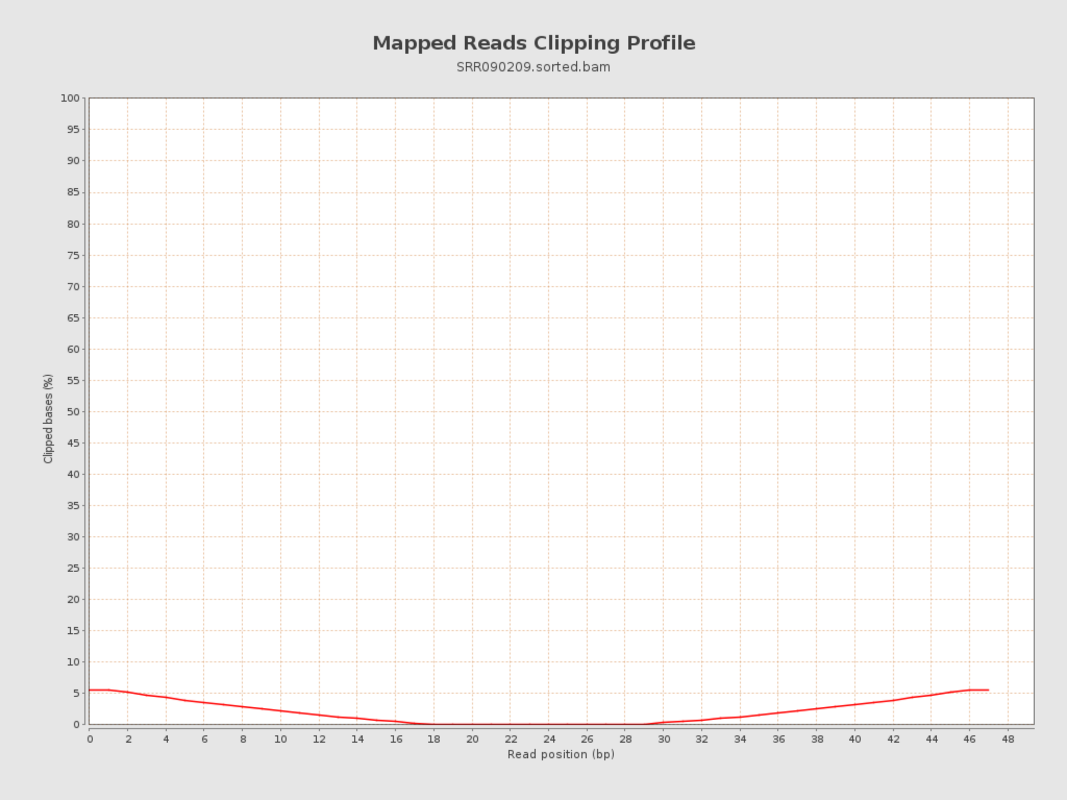
8. Results : Mapped Reads Nucleotide Content



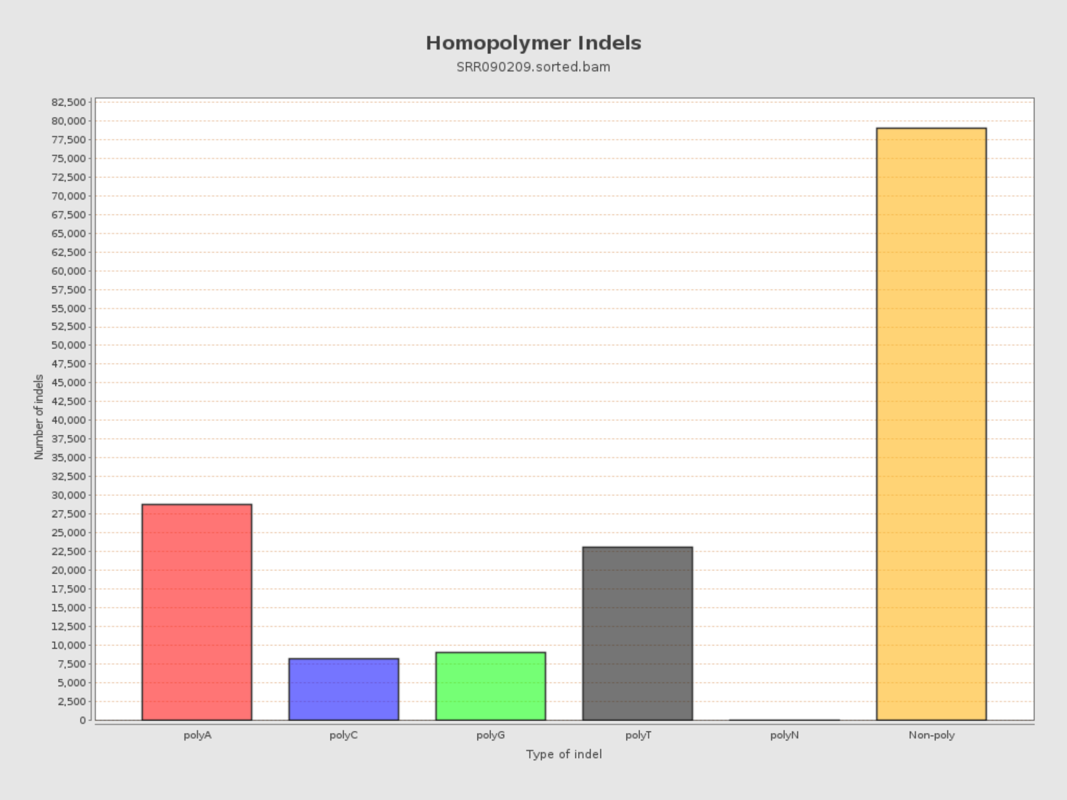
9. Results : Mapped Reads GC-content Distribution



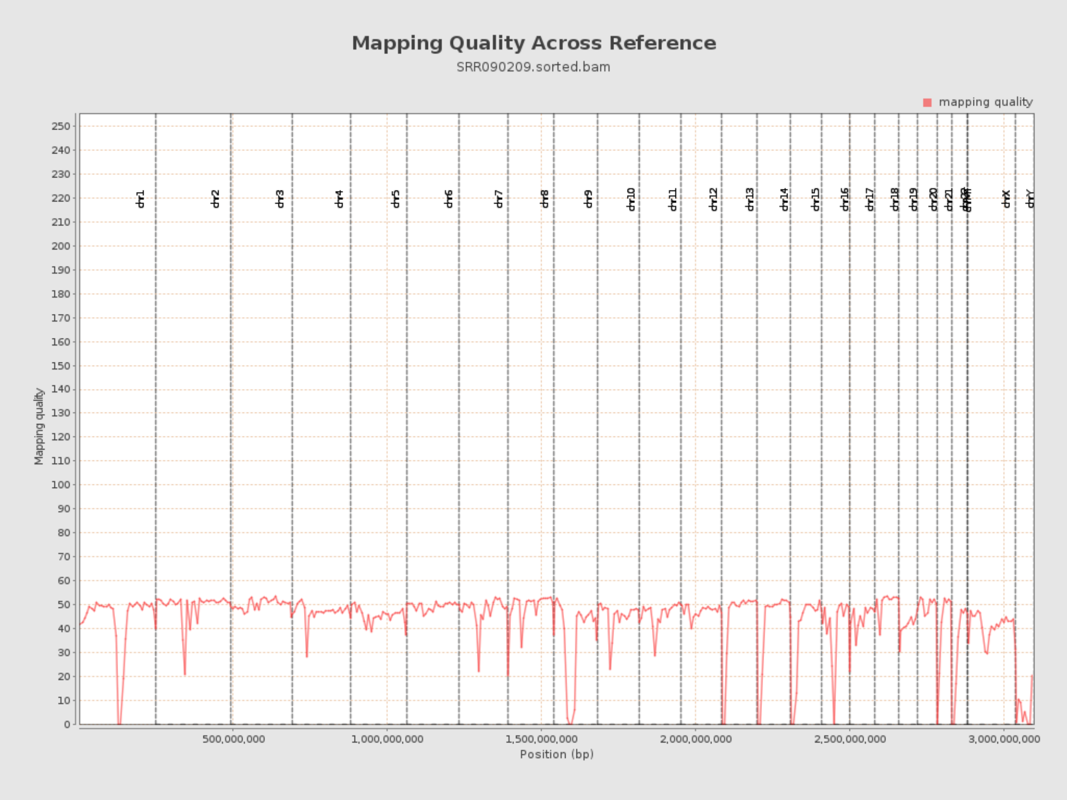
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram