Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/20 10:26:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR090210.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_SRR090210 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR090210.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Apr 20 10:26:37 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR090210.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	26,410,121
Mapped reads	22,824,562 / 86.42%
Unmapped reads	3,585,559 / 13.58%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,230 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	4,536,273 / 17.18%
Duplication rate	12.82%
Clipped reads	2,031,873 / 7.69%

2.2. ACGT Content

Number/percentage of A's	314,475,046 / 29.22%
Number/percentage of C's	219,406,565 / 20.39%
Number/percentage of T's	310,900,714 / 28.89%
Number/percentage of G's	231,102,269 / 21.48%
Number/percentage of N's	169,393 / 0.02%
GC Percentage	41.87%

2.3. Coverage

Mean	0.3477

Standard Deviation	1.882

2.4. Mapping Quality

Mean Mapping Quality	44.36

2.5. Mismatches and indels

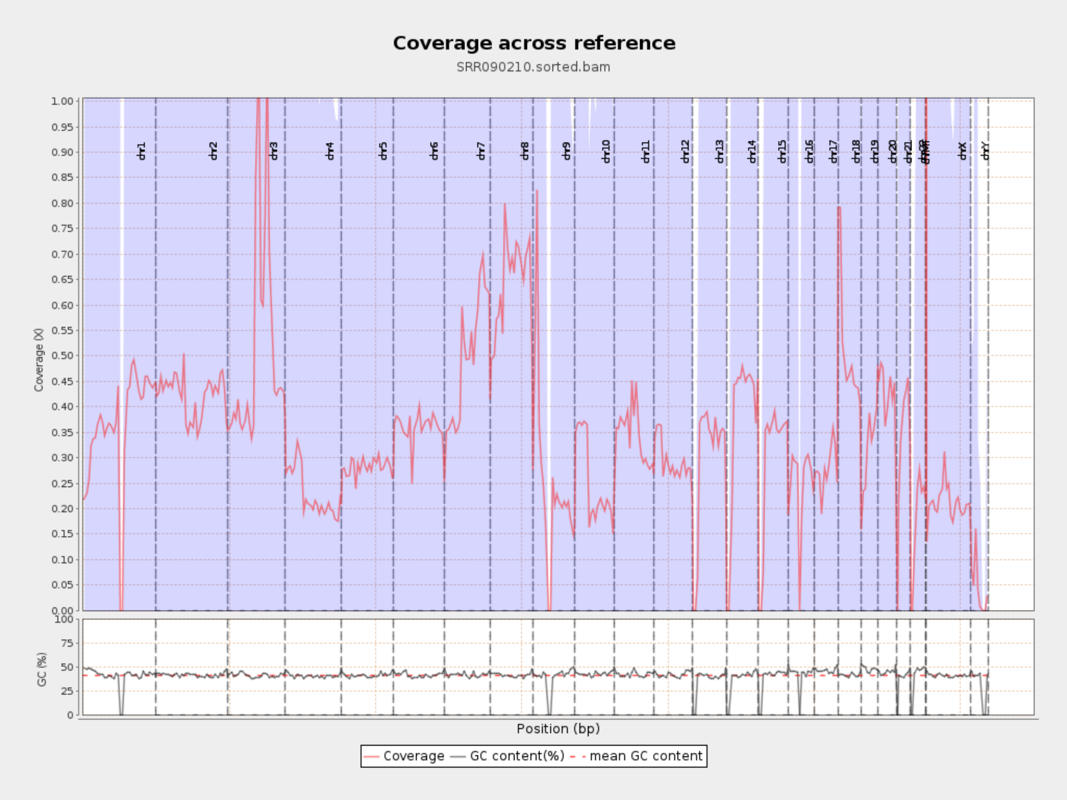
General error rate	0.39%
Mismatches	4,181,646
Insertions	39,291
Mapped reads with at least one insertion	0.17%
Deletions	129,741
Mapped reads with at least one deletion	0.57%
Homopolymer indels	46.94%

2.6. Chromosome stats

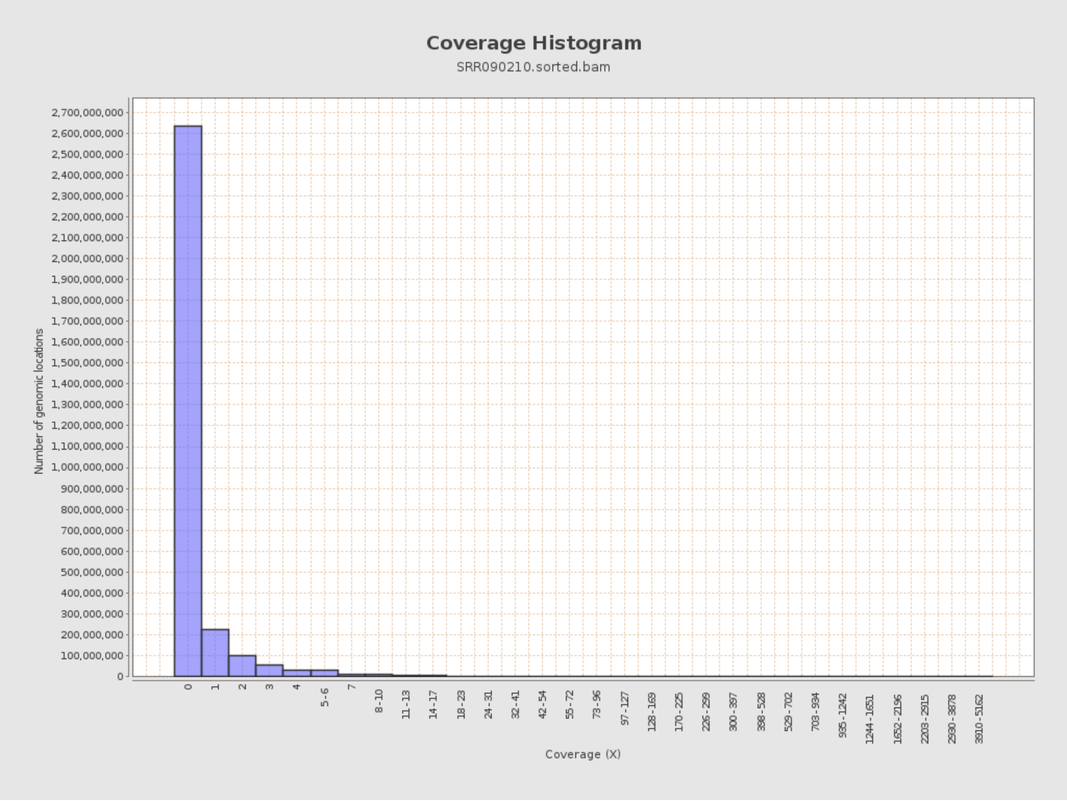
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	90219830	0.362	2.9932
chr2	243199373	102944474	0.4233	2.2299
chr3	198022430	101639500	0.5133	1.4891
chr4	191154276	43897758	0.2296	0.9812
chr5	180915260	50940696	0.2816	1.0535
chr6	171115067	61735177	0.3608	1.3444
chr7	159138663	78934522	0.496	2.9031

chr8	146364022	94537000	0.6459	3.3064
chr9	141213431	35425258	0.2509	1.7803
chr10	135534747	34243860	0.2527	1.4853
chr11	135006516	46593401	0.3451	1.6308
chr12	133851895	39512742	0.2952	1.1192
chr13	115169878	34324784	0.298	1.07
chr14	107349540	40059289	0.3732	1.258
chr15	102531392	29721191	0.2899	1.0657
chr16	90354753	22024398	0.2438	1.0392
chr17	81195210	22878840	0.2818	1.2073
chr18	78077248	39809255	0.5099	2.934
chr19	59128983	19088100	0.3228	2.0419
chr20	63025520	27020973	0.4287	1.3982
chr21	48129895	15955097	0.3315	1.3123
chr22	51304566	8964073	0.1747	0.8261
chrMT	16571	335074	20.2205	14.4935
chrX	155270560	32801468	0.2113	1.1034
chrY	59373566	2644667	0.0445	1.5182

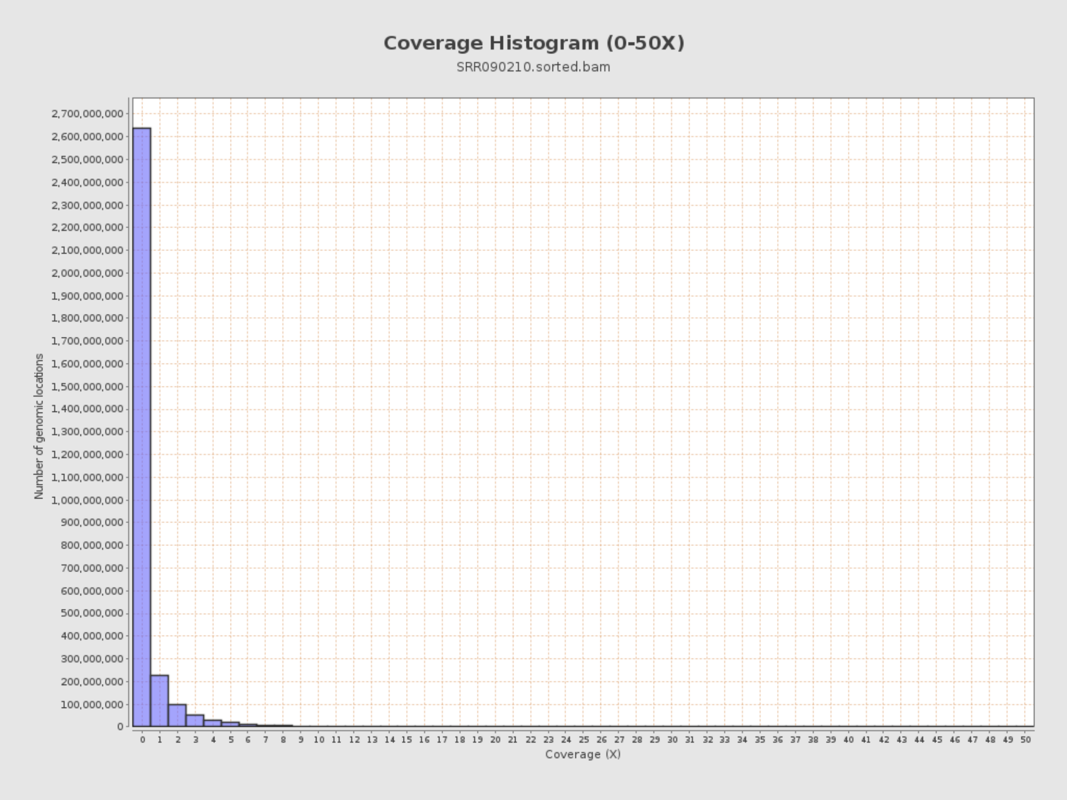
3. Results : Coverage across reference



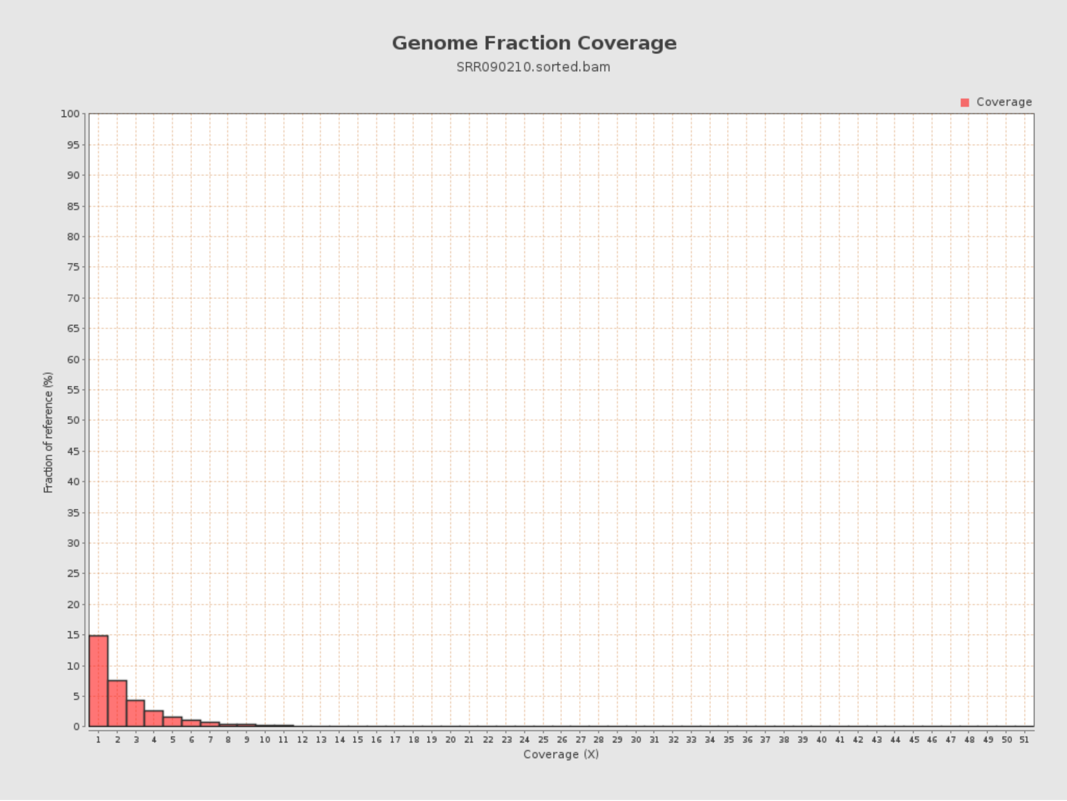
4. Results : Coverage Histogram



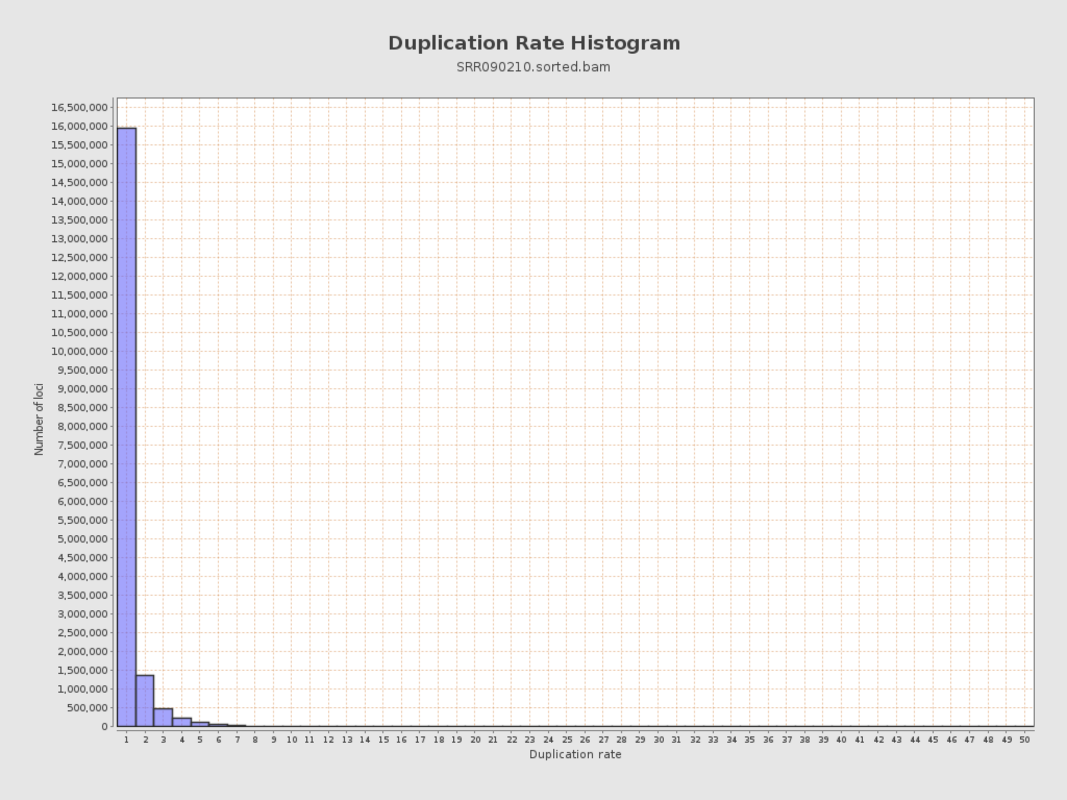
5. Results : Coverage Histogram (0-50X)



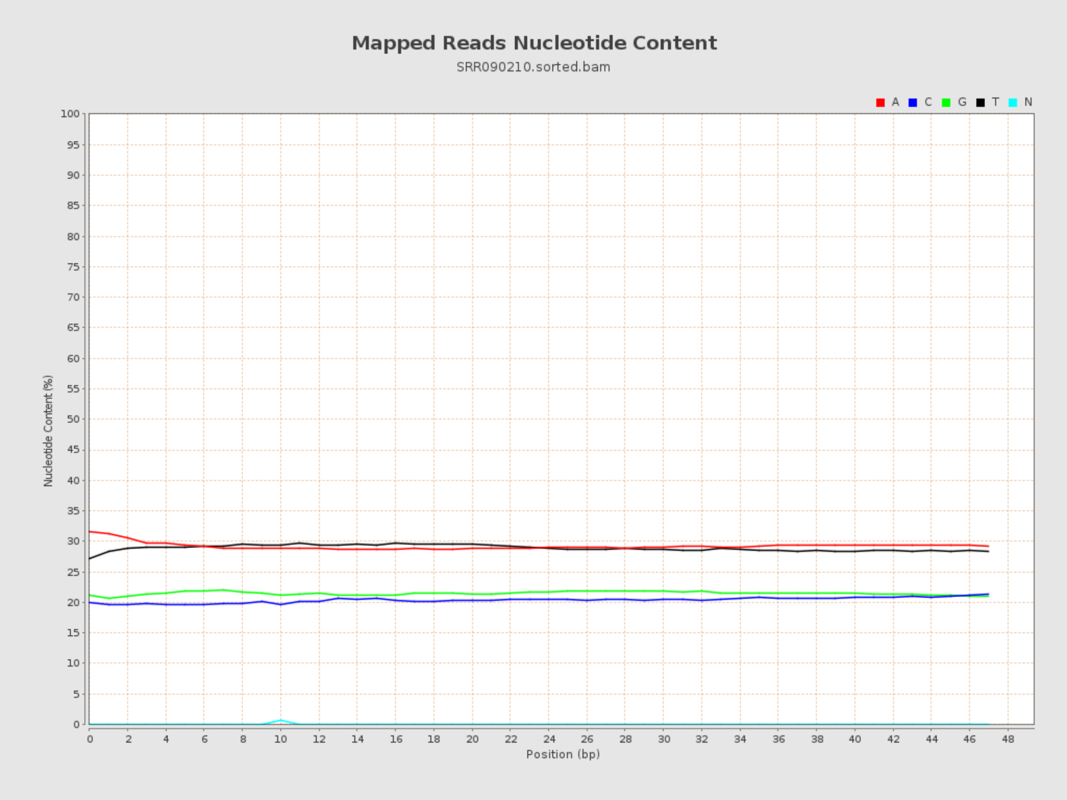
6. Results : Genome Fraction Coverage



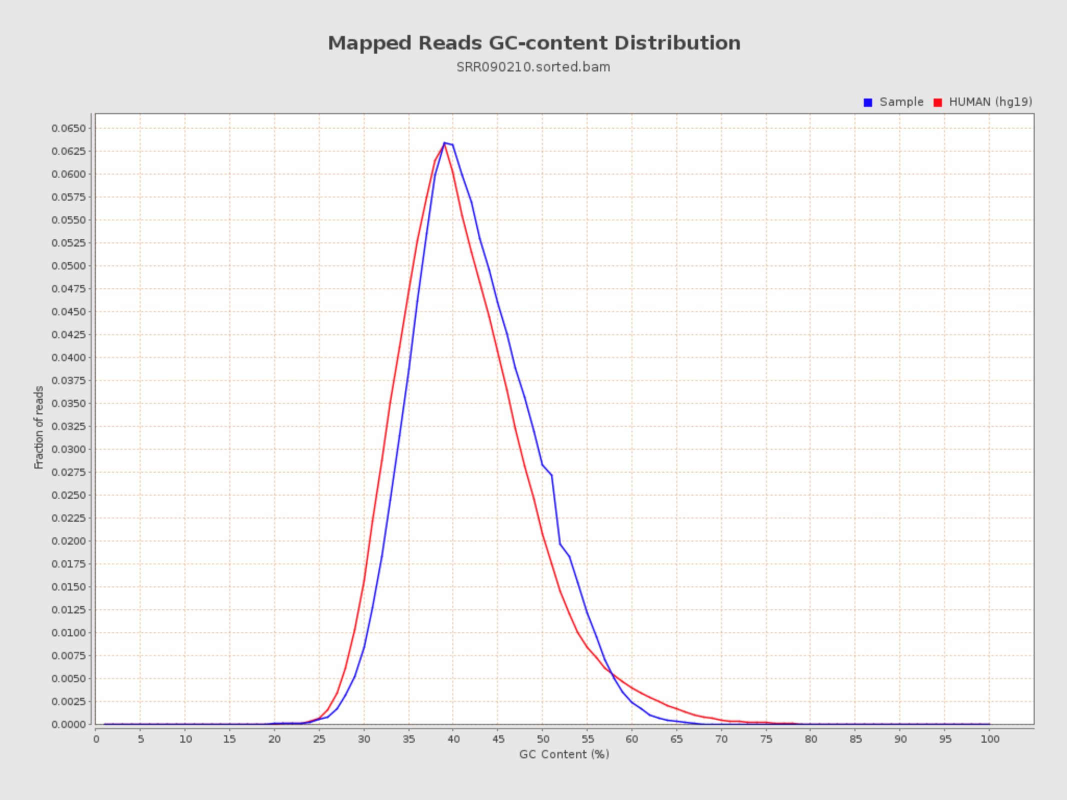
7. Results : Duplication Rate Histogram



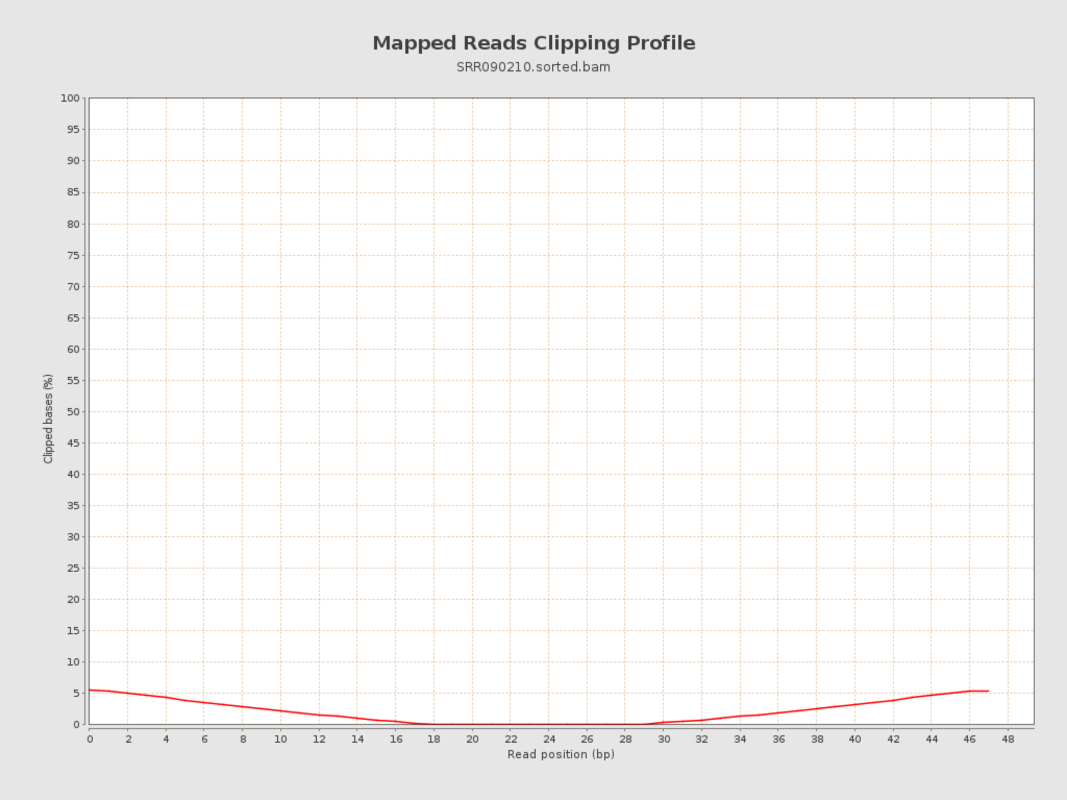
8. Results : Mapped Reads Nucleotide Content



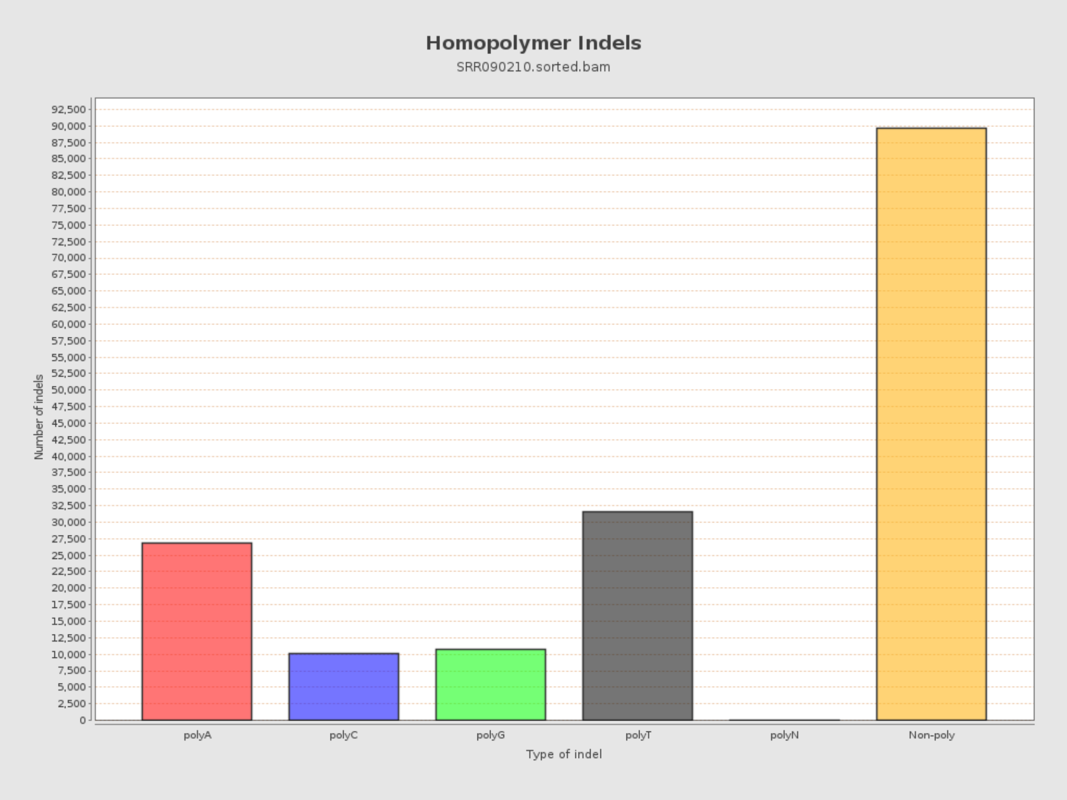
9. Results : Mapped Reads GC-content Distribution



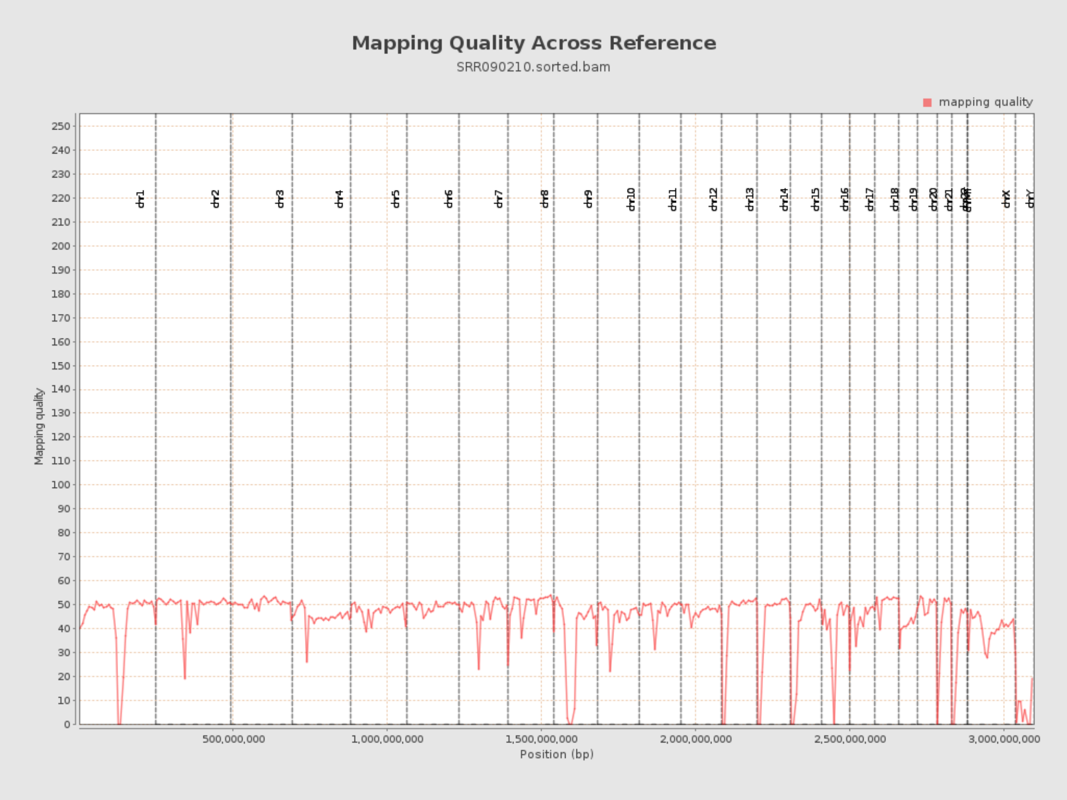
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram