Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 14:53:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819012.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_SRR1819012 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819012.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 14:53:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1819012.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,550,720
Mapped reads	2,486,071 / 97.47%
Unmapped reads	64,649 / 2.53%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	37,142 / 1.46%
Read min/max/mean length	30 / 101 / 101.56
Duplicated reads (estimated)	1,153,325 / 45.22%
Duplication rate	38.55%
Clipped reads	2,496,001 / 97.85%

2.2. ACGT Content

Number/percentage of A's	66,966,802 / 29.11%
Number/percentage of C's	47,487,695 / 20.64%
Number/percentage of T's	64,575,448 / 28.07%
Number/percentage of G's	51,011,749 / 22.17%
Number/percentage of N's	10,662 / 0%
GC Percentage	42.82%

2.3. Coverage

Mean	0.0744

Standard Deviation	0.8806

2.4. Mapping Quality

Mean Mapping Quality	49.16

2.5. Mismatches and indels

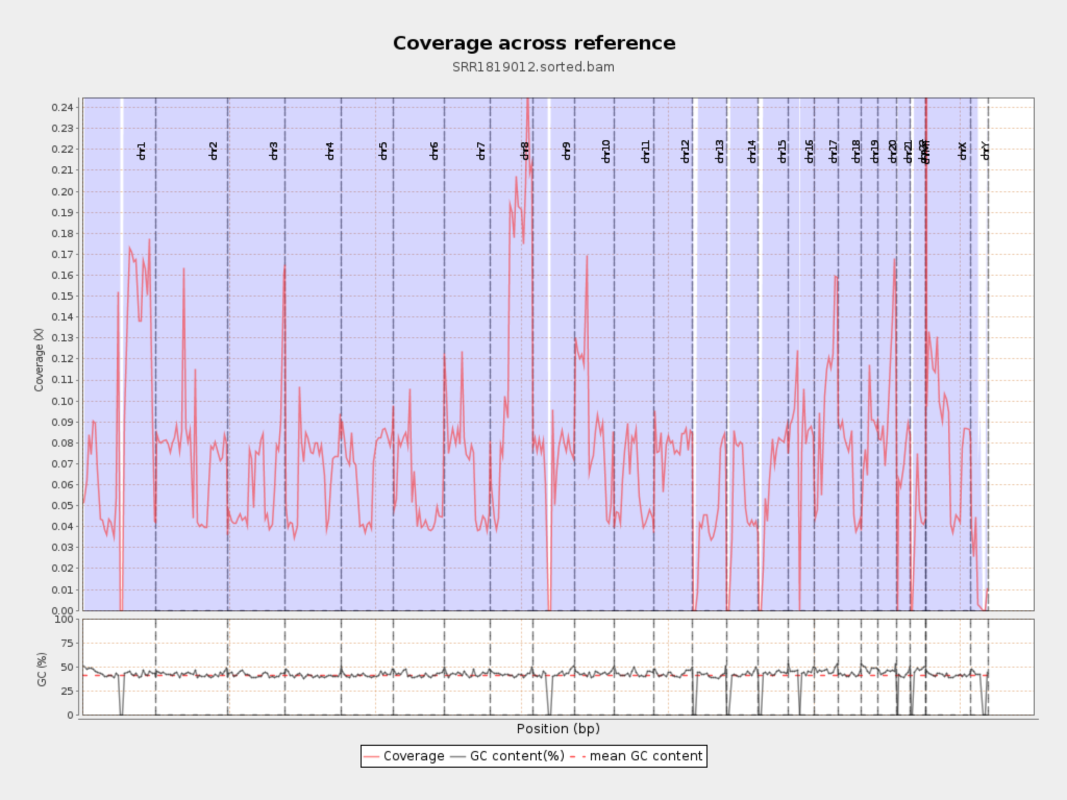
General error rate	0.66%
Mismatches	1,443,263
Insertions	35,814
Mapped reads with at least one insertion	1.4%
Deletions	74,922
Mapped reads with at least one deletion	2.94%
Homopolymer indels	40.39%

2.6. Chromosome stats

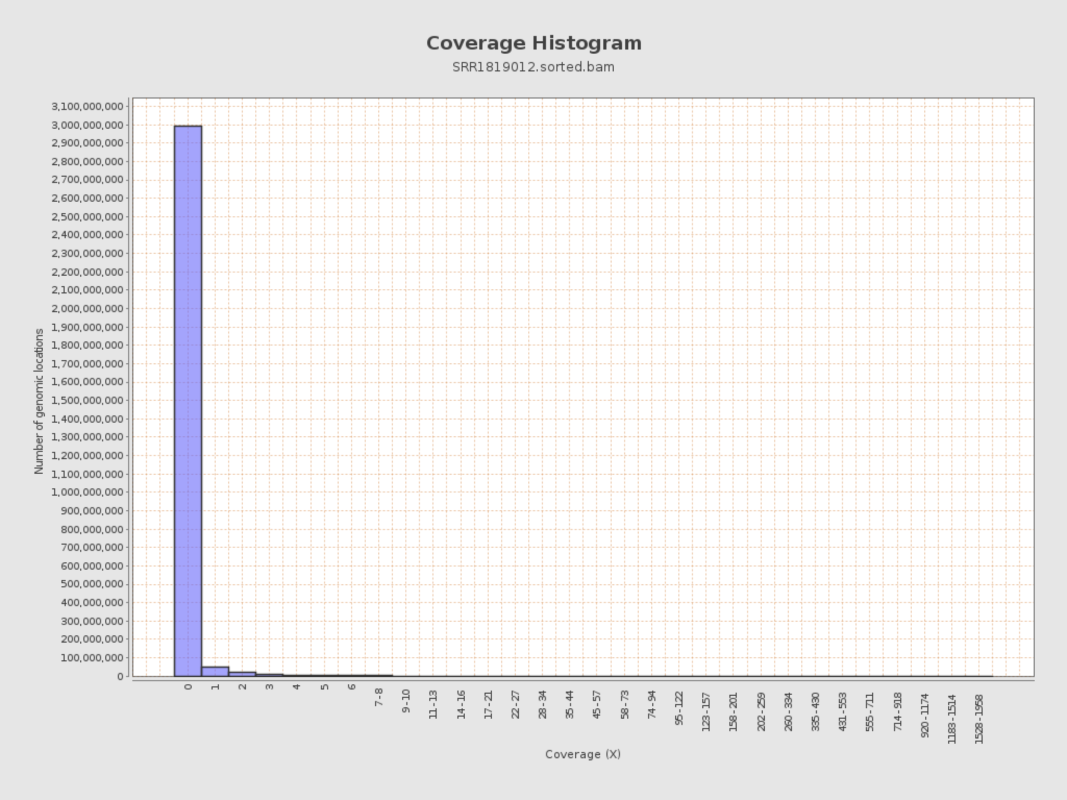
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	23178992	0.093	1.6681
chr2	243199373	18467915	0.0759	1.1985
chr3	198022430	12296988	0.0621	0.4688
chr4	191154276	12684101	0.0664	0.5679
chr5	180915260	12467714	0.0689	0.5207
chr6	171115067	9704075	0.0567	0.5582
chr7	159138663	11330423	0.0712	1.0186

chr8	146364022	21025333	0.1437	0.825
chr9	141213431	9630544	0.0682	0.7806
chr10	135534747	12282153	0.0906	1.092
chr11	135006516	7850159	0.0581	0.5513
chr12	133851895	10673851	0.0797	0.5479
chr13	115169878	4950084	0.043	0.3876
chr14	107349540	5415499	0.0504	0.4579
chr15	102531392	5959480	0.0581	0.4592
chr16	90354753	7496986	0.083	0.9845
chr17	81195210	8216812	0.1012	0.7035
chr18	78077248	5360241	0.0687	0.9301
chr19	59128983	4891668	0.0827	1.5151
chr20	63025520	6735317	0.1069	0.6781
chr21	48129895	3204686	0.0666	0.5577
chr22	51304566	1896049	0.037	0.4028
chrMT	16571	45942	2.7724	3.7984
chrX	155270560	13562054	0.0873	0.6609
chrY	59373566	865429	0.0146	0.8405

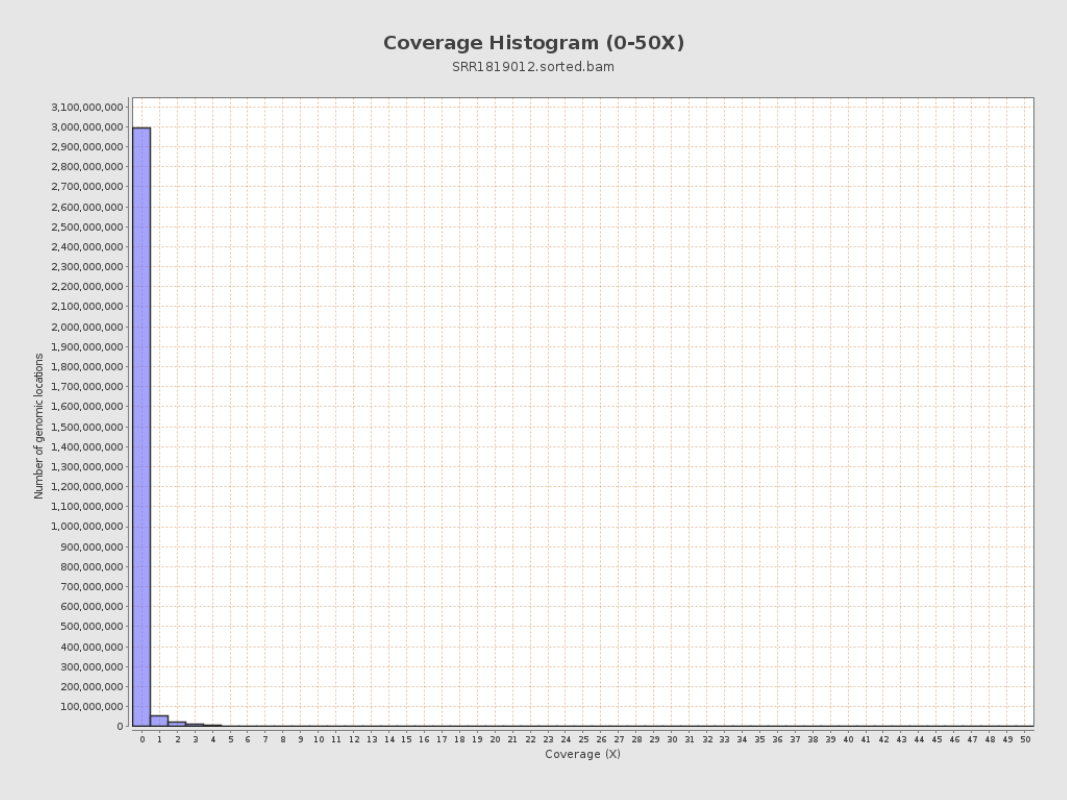
3. Results : Coverage across reference



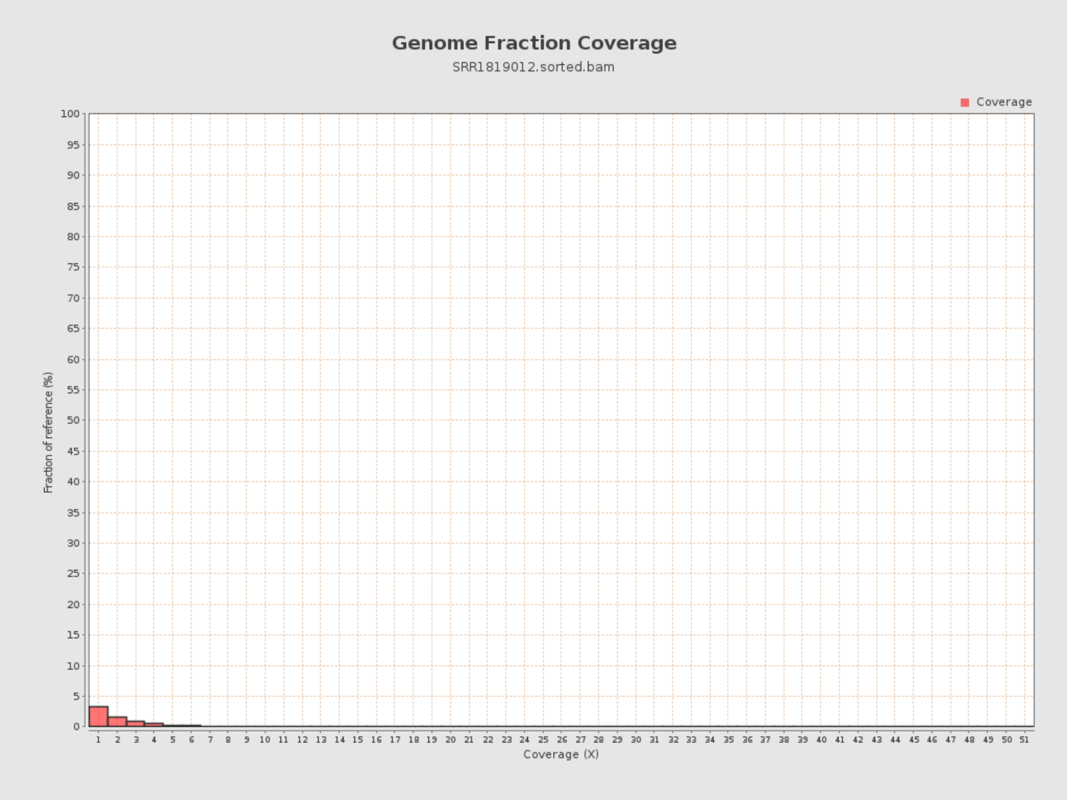
4. Results : Coverage Histogram



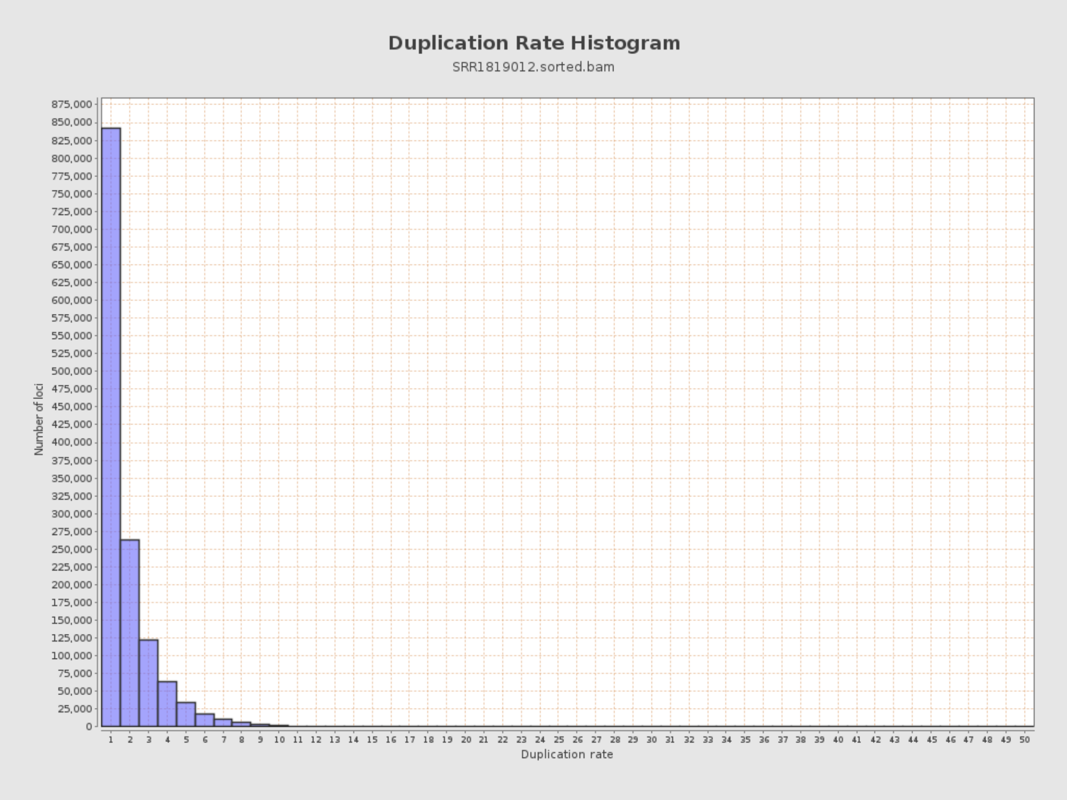
5. Results : Coverage Histogram (0-50X)



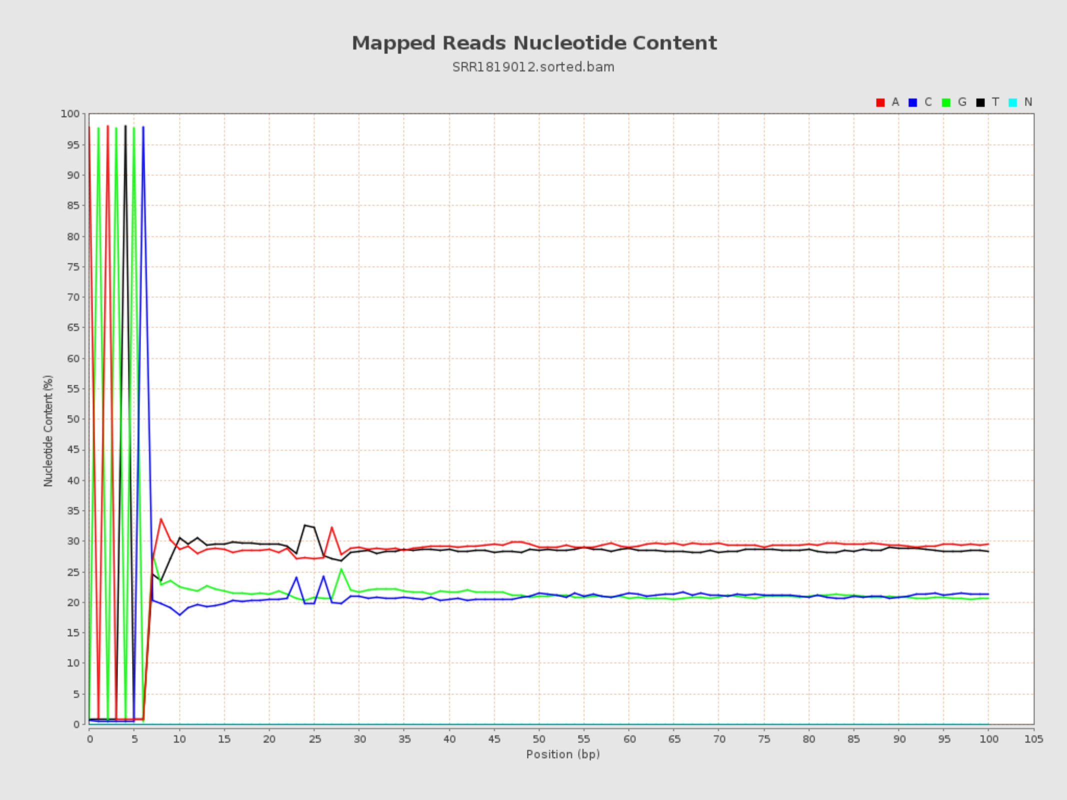
6. Results : Genome Fraction Coverage



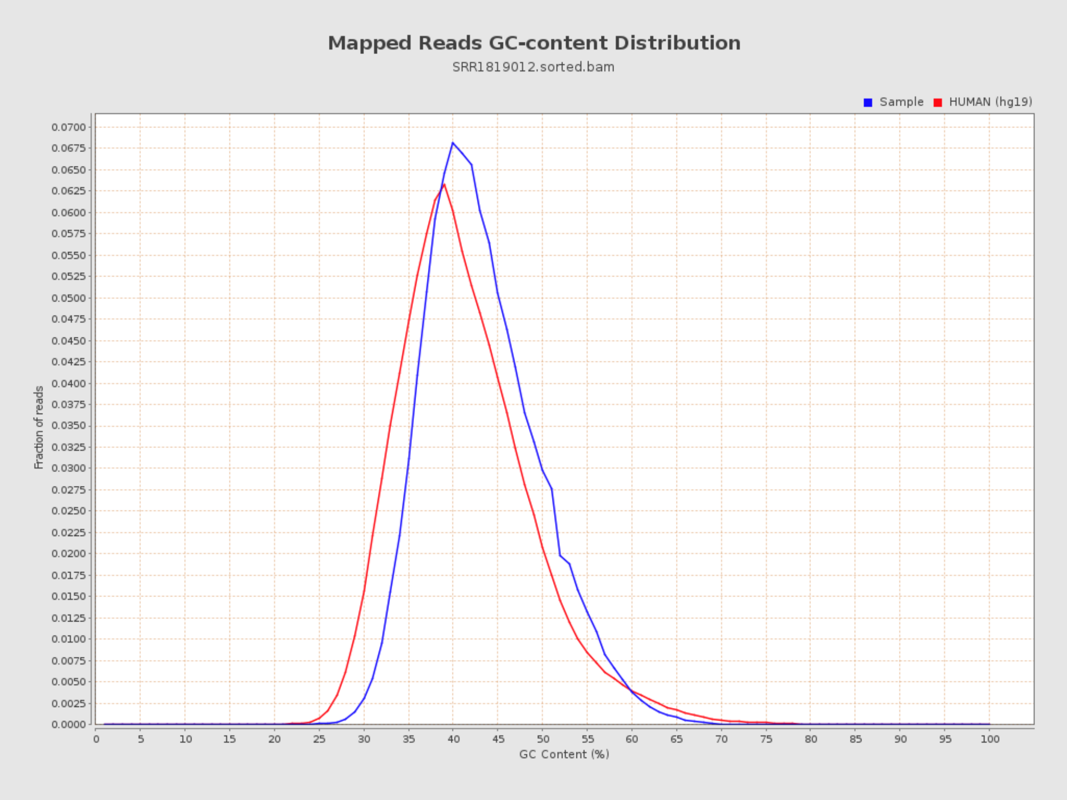
7. Results : Duplication Rate Histogram



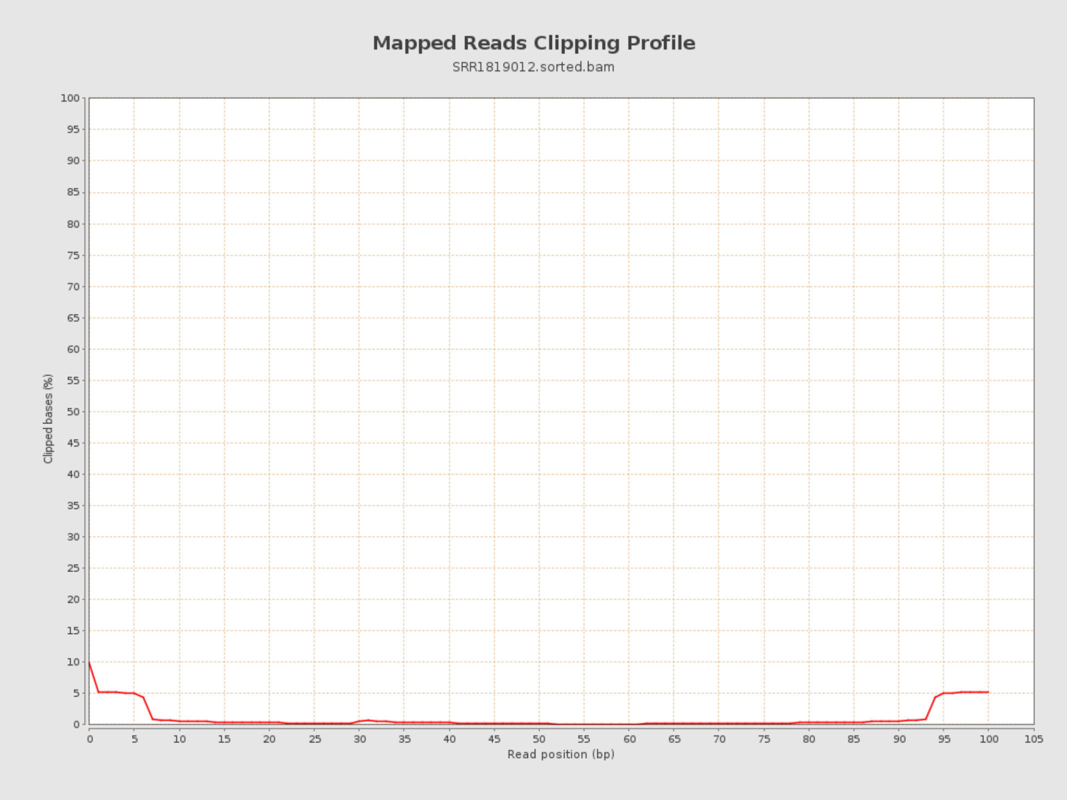
8. Results : Mapped Reads Nucleotide Content



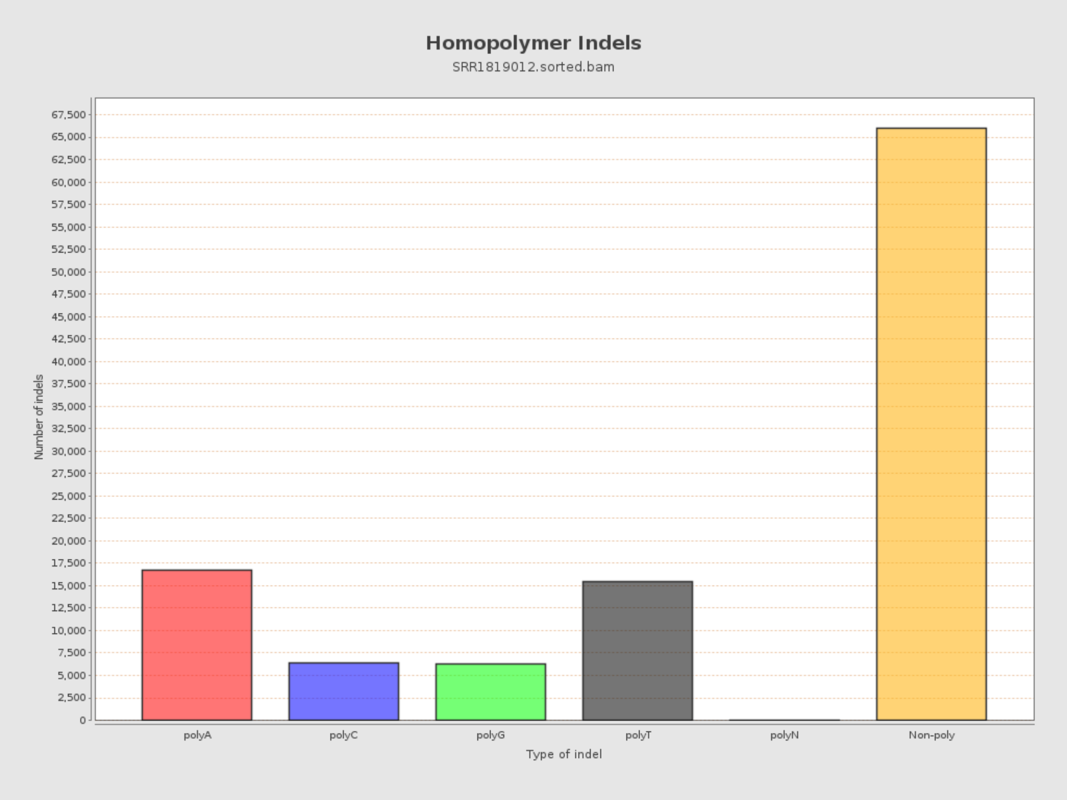
9. Results : Mapped Reads GC-content Distribution



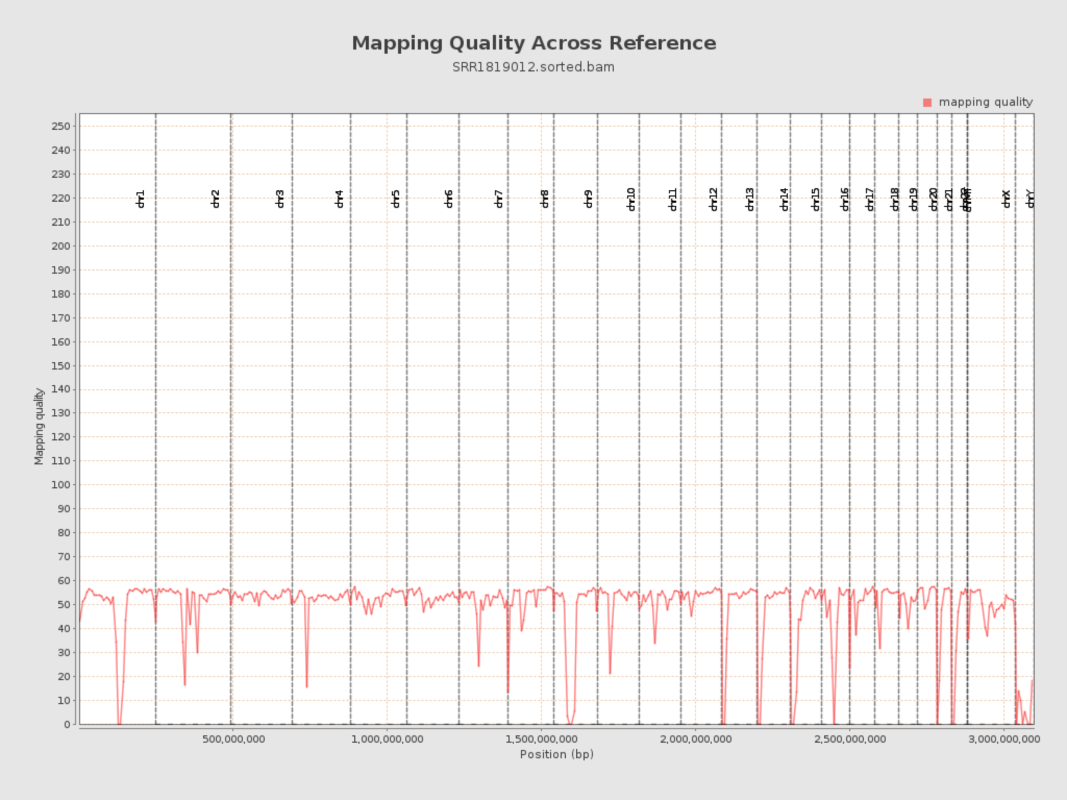
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram