Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 19:48:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2971318.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_SRR2971318 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2971318.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 19:48:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2971318.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,032,940
Mapped reads	13,038,744 / 92.92%
Unmapped reads	994,196 / 7.08%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,547 / 0.02%
Read min/max/mean length	30 / 50 / 50.01
Duplicated reads (estimated)	1,699,891 / 12.11%
Duplication rate	10.57%
Clipped reads	3,104,996 / 22.13%

2.2. ACGT Content

Number/percentage of A's	170,076,836 / 27.3%
Number/percentage of C's	138,256,512 / 22.19%
Number/percentage of T's	173,377,365 / 27.83%
Number/percentage of G's	141,257,635 / 22.67%
Number/percentage of N's	34,919 / 0.01%
GC Percentage	44.87%

2.3. Coverage

Mean	0.2013

Standard Deviation	1.8467

2.4. Mapping Quality

Mean Mapping Quality	32.22

2.5. Mismatches and indels

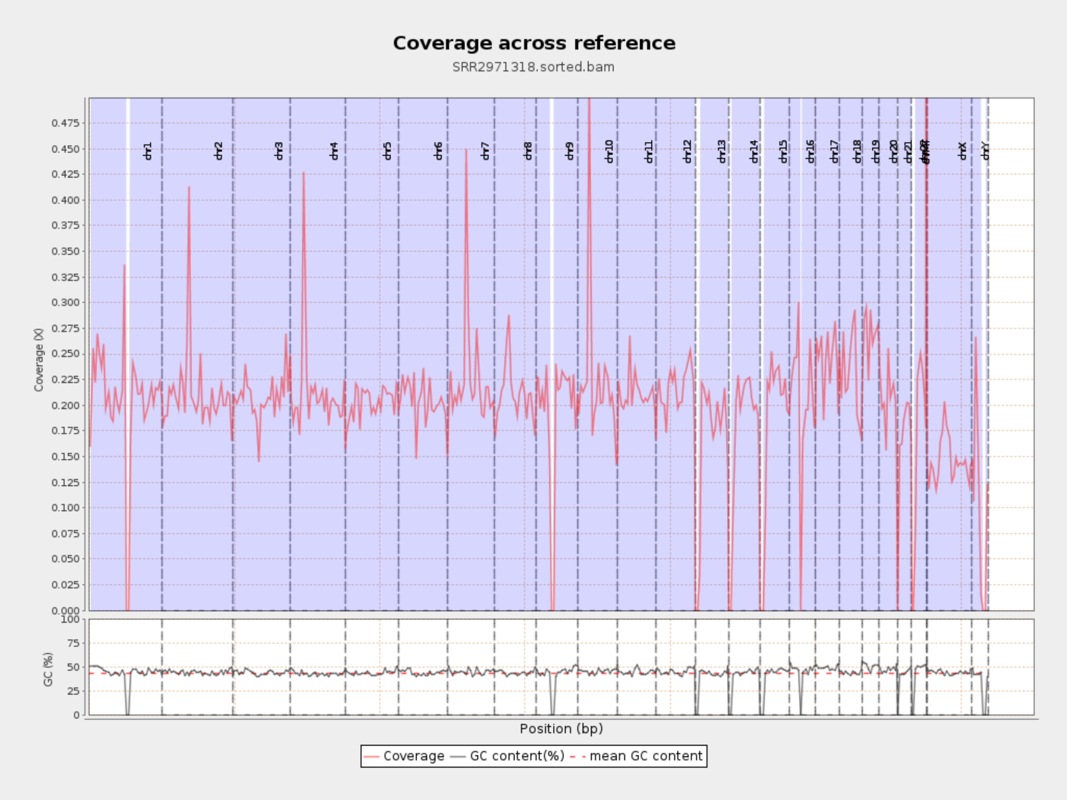
General error rate	0.55%
Mismatches	3,389,430
Insertions	45,403
Mapped reads with at least one insertion	0.35%
Deletions	89,820
Mapped reads with at least one deletion	0.69%
Homopolymer indels	38.44%

2.6. Chromosome stats

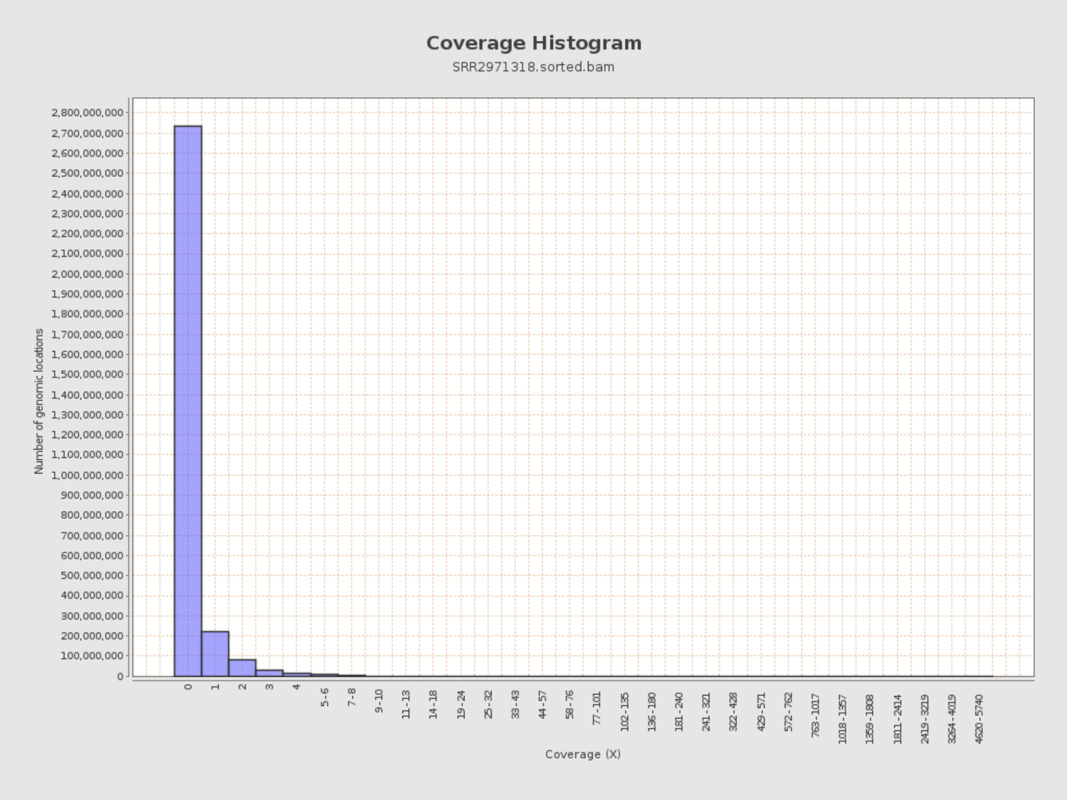
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	50959722	0.2045	3.2608
chr2	243199373	51678739	0.2125	1.8577
chr3	198022430	41158628	0.2078	0.7431
chr4	191154276	40458369	0.2117	1.2953
chr5	180915260	36785380	0.2033	0.733
chr6	171115067	34947161	0.2042	0.7931
chr7	159138663	36148116	0.2271	2.8592

chr8	146364022	30792622	0.2104	3.0547
chr9	141213431	26775108	0.1896	1.8235
chr10	135534747	30443394	0.2246	2.3874
chr11	135006516	28466654	0.2109	1.4267
chr12	133851895	29086203	0.2173	0.8127
chr13	115169878	18754379	0.1628	0.6357
chr14	107349540	18694693	0.1741	0.9933
chr15	102531392	18466374	0.1801	0.6958
chr16	90354753	18460994	0.2043	1.0085
chr17	81195210	19832858	0.2443	1.0259
chr18	78077248	18038261	0.231	3.5441
chr19	59128983	15928527	0.2694	2.7824
chr20	63025520	12936302	0.2053	0.8549
chr21	48129895	7899599	0.1641	1.1794
chr22	51304566	8016565	0.1563	0.8068
chrMT	16571	56924	3.4352	3.1054
chrX	155270560	22689131	0.1461	0.8396
chrY	59373566	5658484	0.0953	1.1944

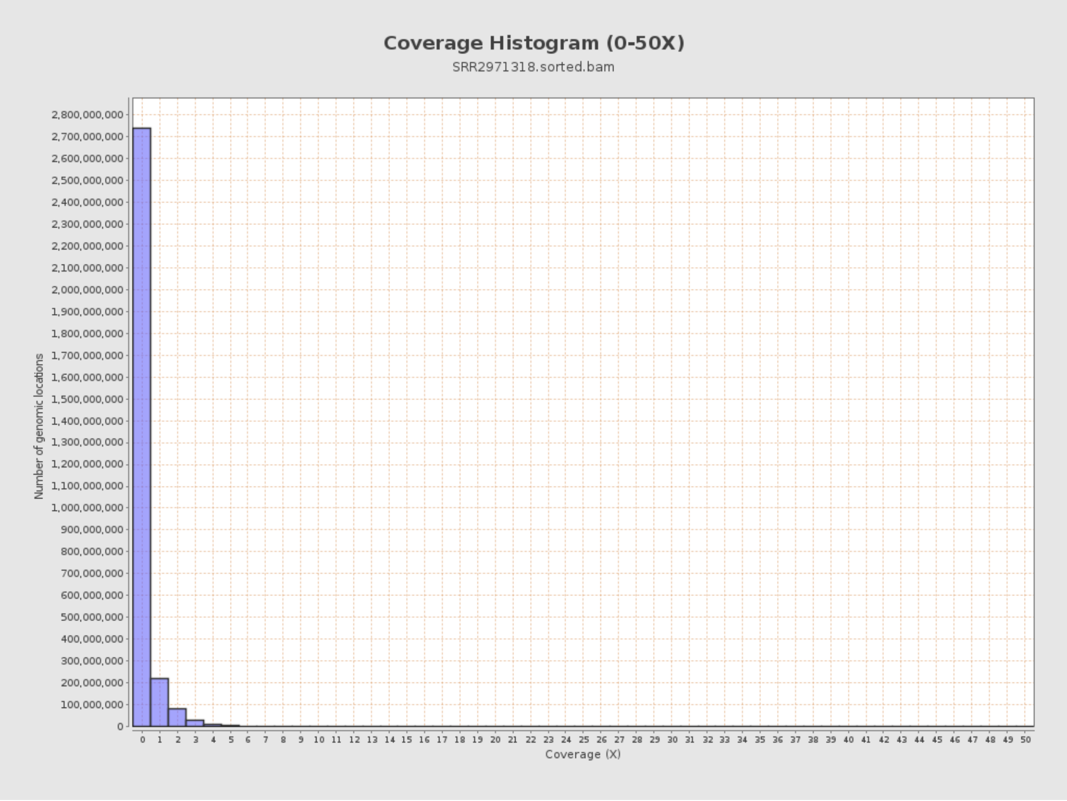
3. Results : Coverage across reference



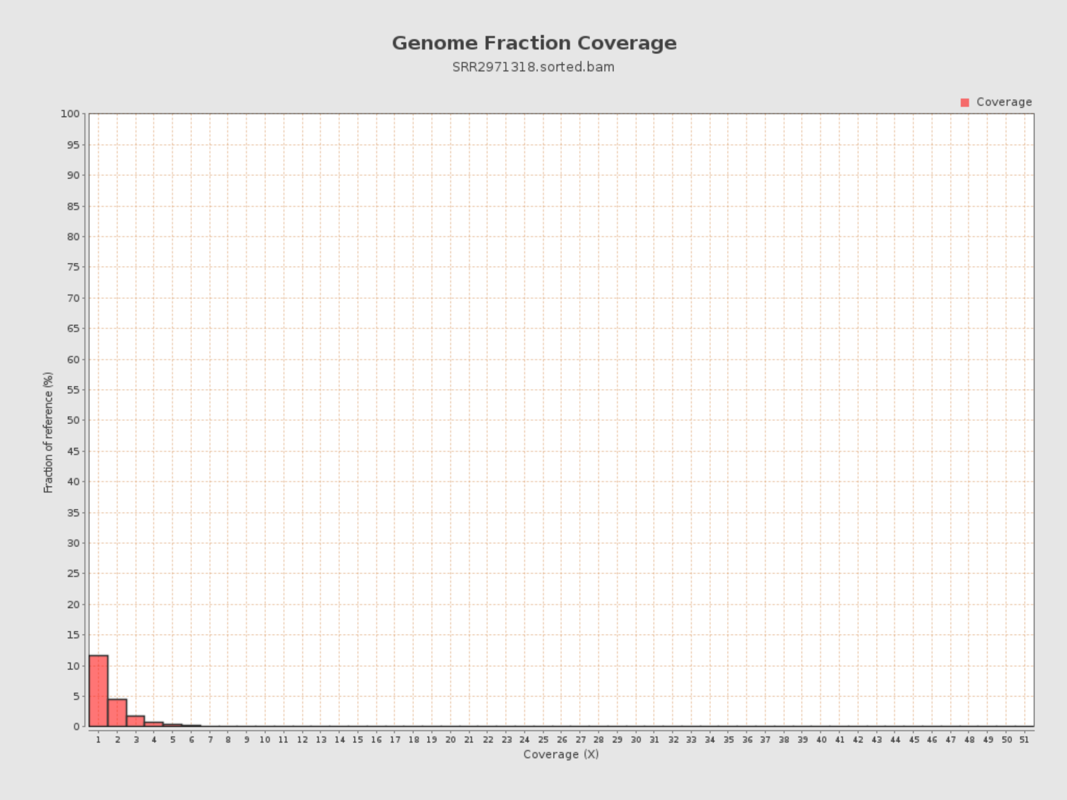
4. Results : Coverage Histogram



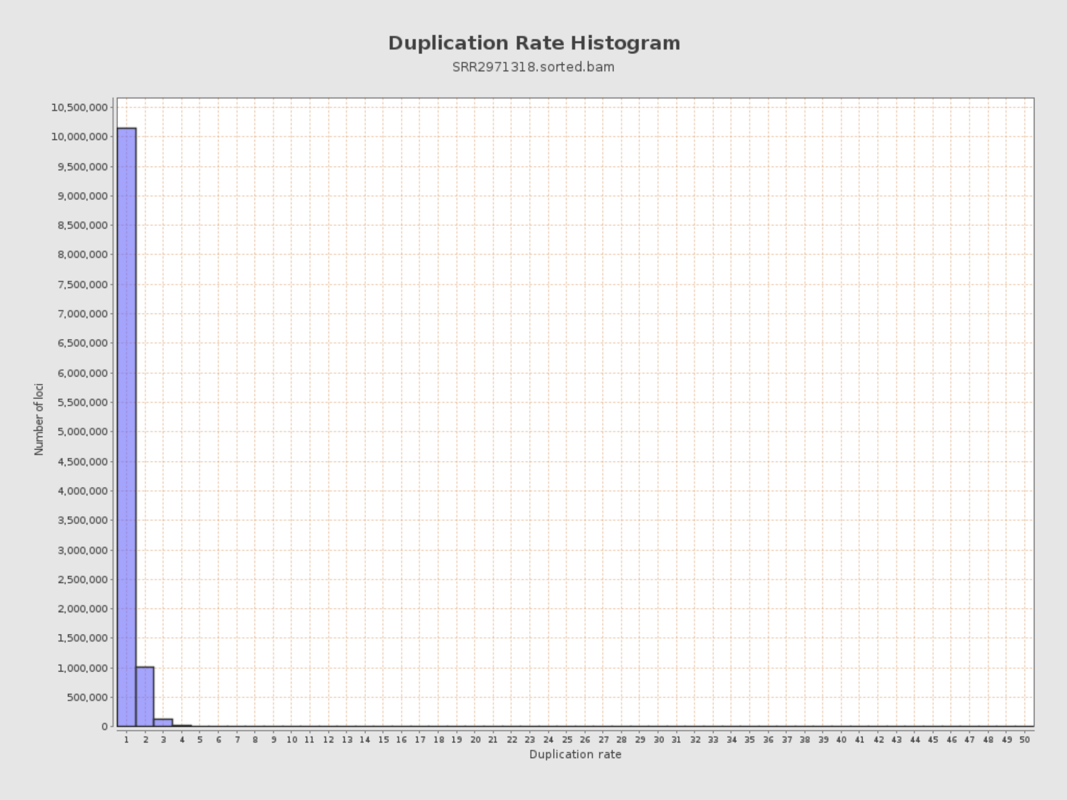
5. Results : Coverage Histogram (0-50X)



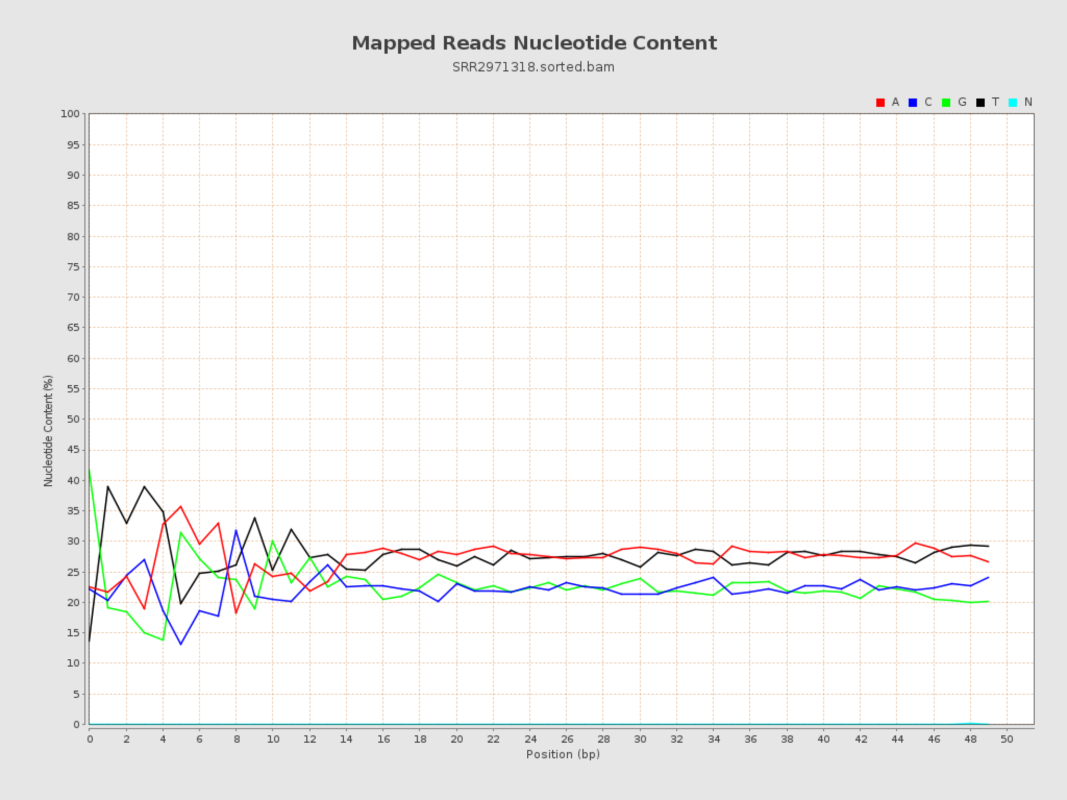
6. Results : Genome Fraction Coverage



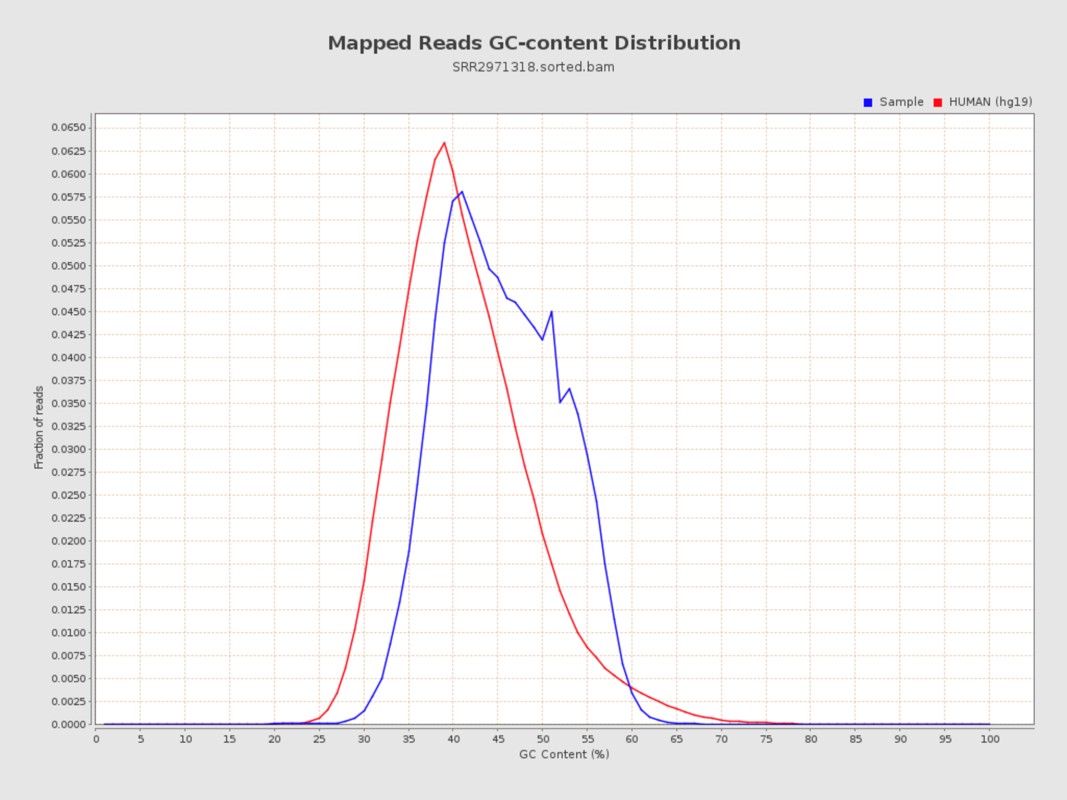
7. Results : Duplication Rate Histogram



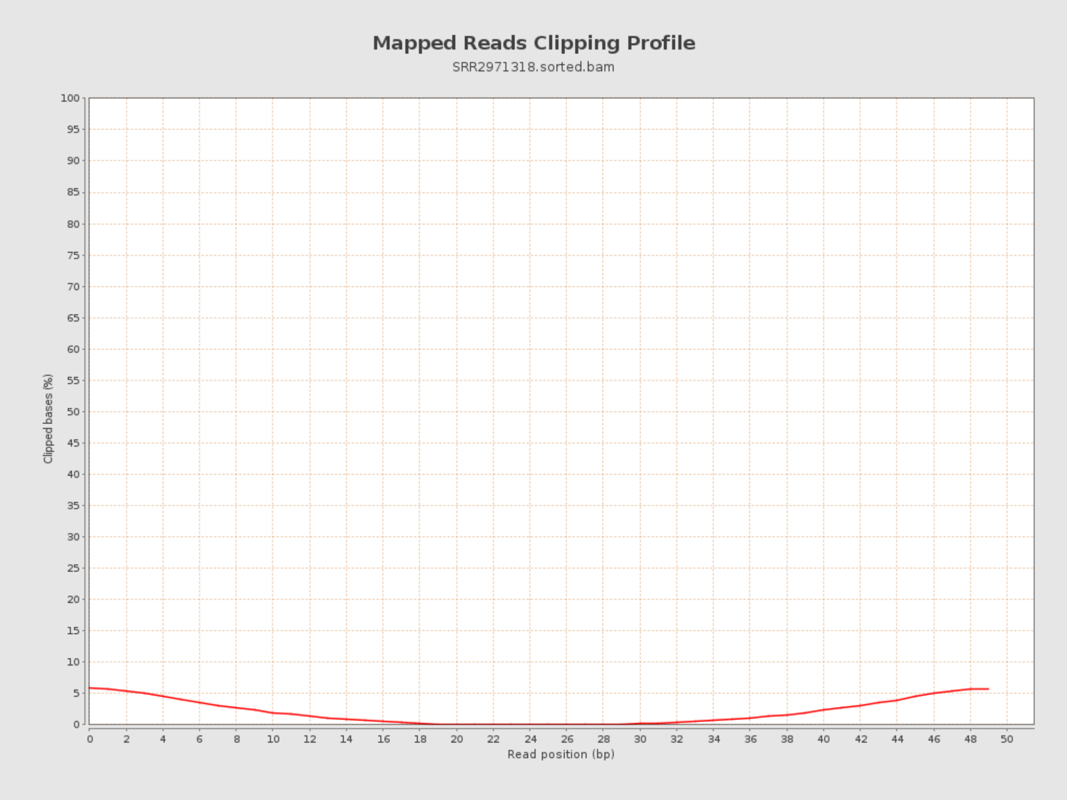
8. Results : Mapped Reads Nucleotide Content



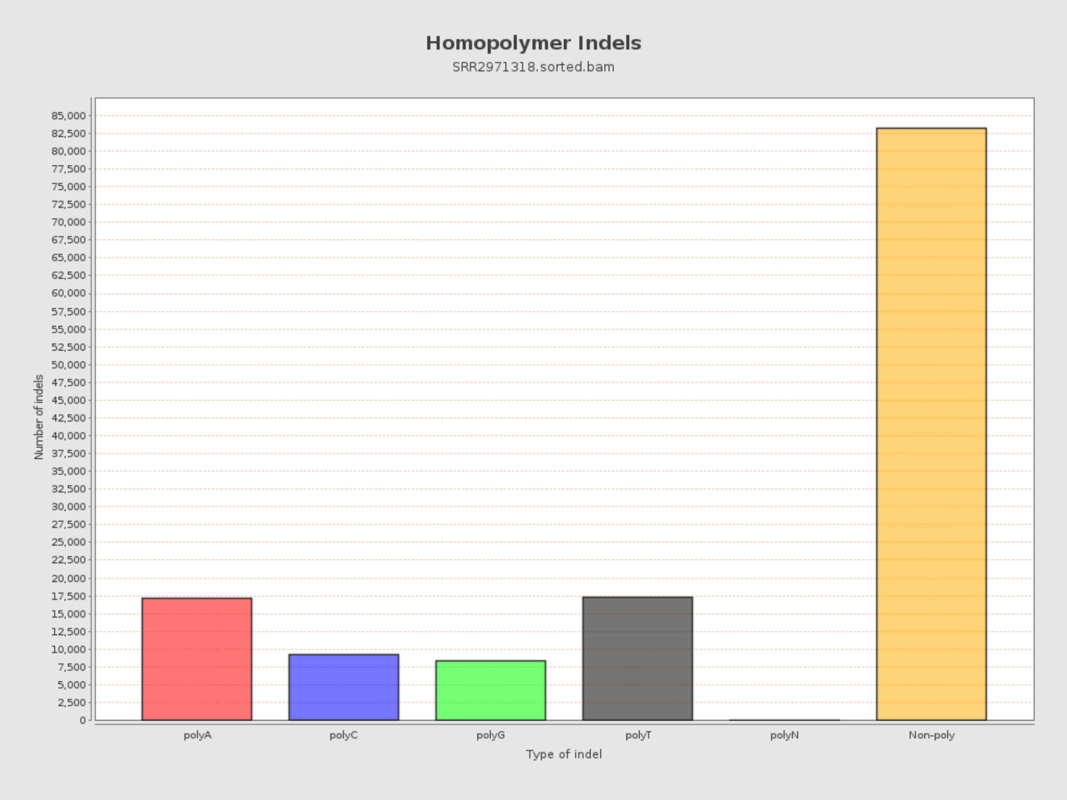
9. Results : Mapped Reads GC-content Distribution



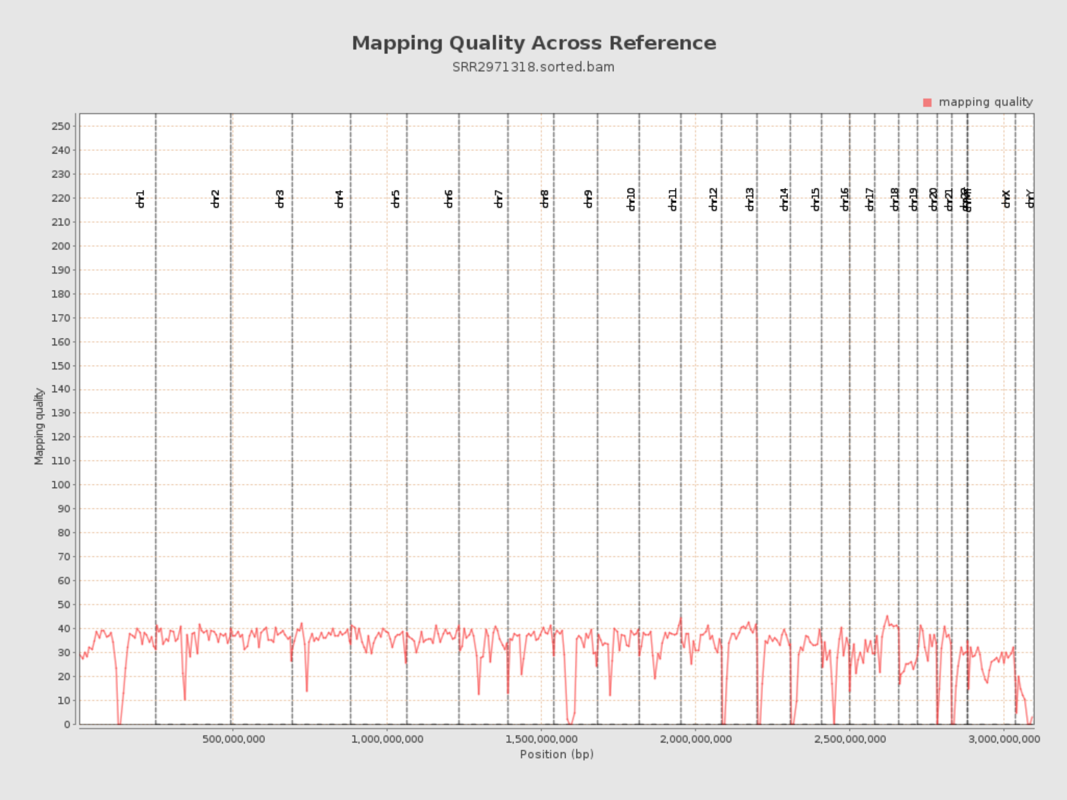
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram