Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 16:46:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818820.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_SRR1818820 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818820.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 16:46:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818820.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,109,803
Mapped reads	1,081,351 / 97.44%
Unmapped reads	28,452 / 2.56%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,532 / 0.68%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	386,115 / 34.79%
Duplication rate	29.47%
Clipped reads	1,077,479 / 97.09%

2.2. ACGT Content

Number/percentage of A's	19,955,318 / 27.19%
Number/percentage of C's	15,184,620 / 20.69%
Number/percentage of T's	21,573,124 / 29.39%
Number/percentage of G's	16,684,330 / 22.73%
Number/percentage of N's	4,219 / 0.01%
GC Percentage	43.42%

2.3. Coverage

Mean	0.0237

Standard Deviation	0.3461

2.4. Mapping Quality

Mean Mapping Quality	47.67

2.5. Mismatches and indels

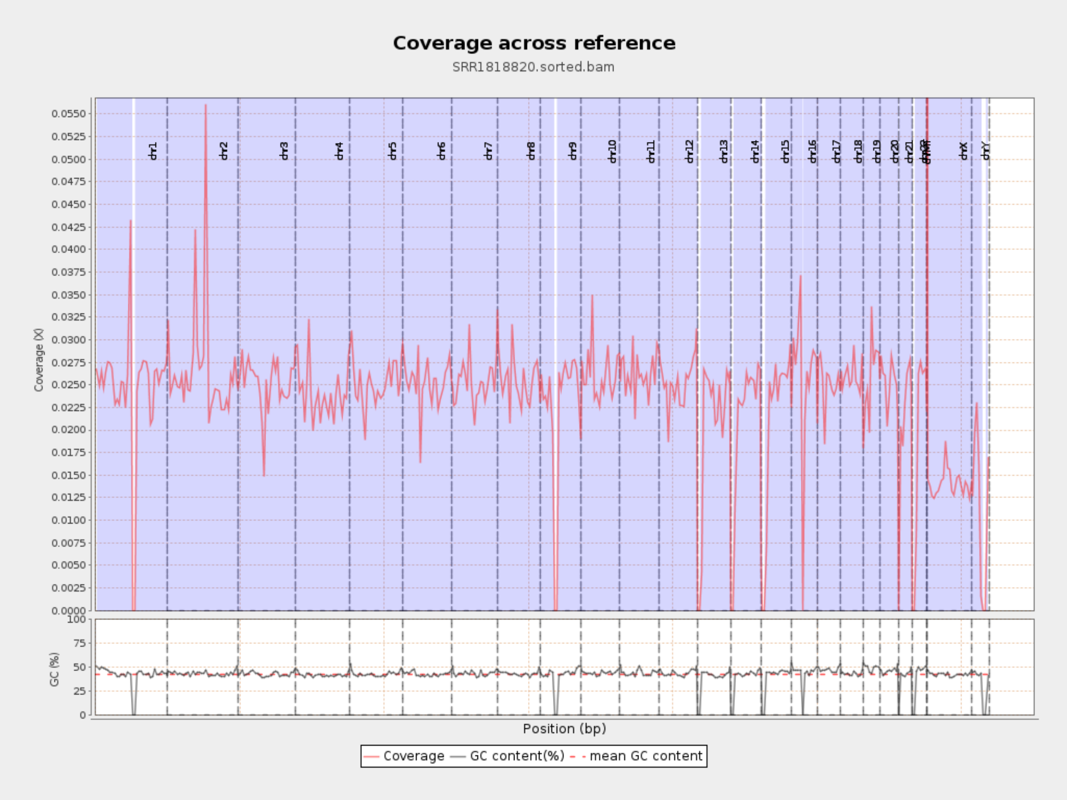
General error rate	0.53%
Mismatches	369,822
Insertions	8,513
Mapped reads with at least one insertion	0.77%
Deletions	18,398
Mapped reads with at least one deletion	1.68%
Homopolymer indels	40.86%

2.6. Chromosome stats

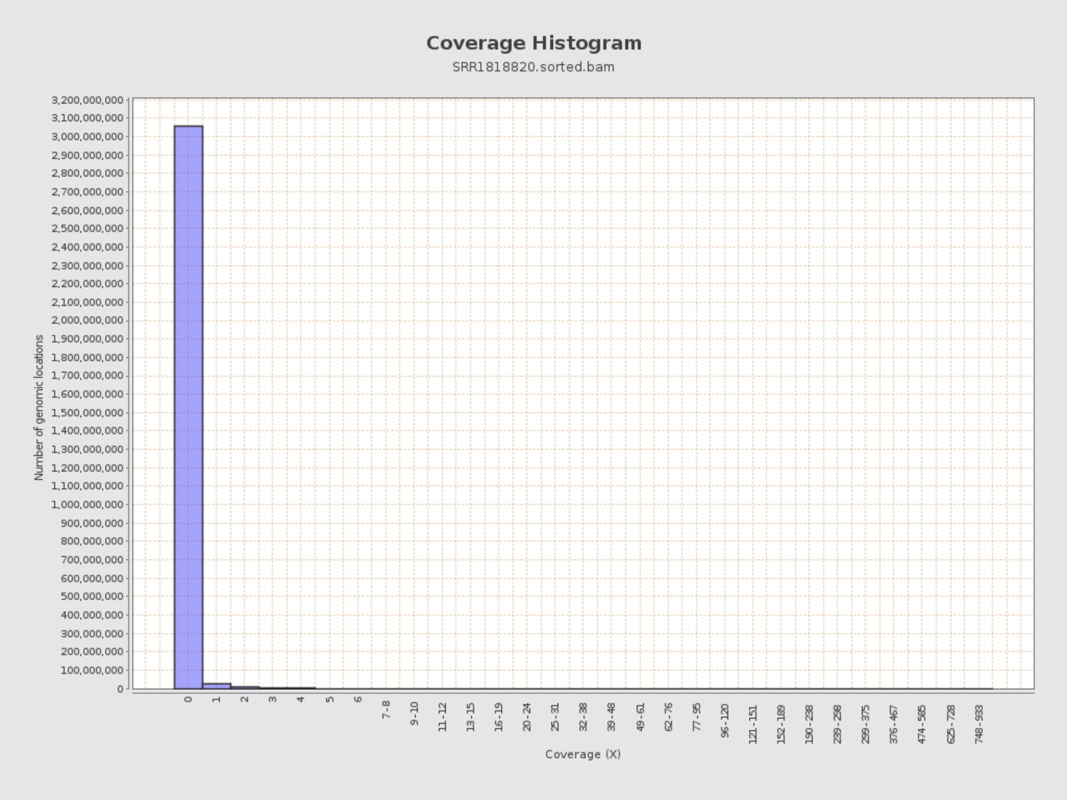
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6100445	0.0245	0.4625
chr2	243199373	6485034	0.0267	0.6132
chr3	198022430	4978011	0.0251	0.2582
chr4	191154276	4611114	0.0241	0.2841
chr5	180915260	4551101	0.0252	0.2714
chr6	171115067	4327182	0.0253	0.2791
chr7	159138663	4021177	0.0253	0.2954

chr8	146364022	3741054	0.0256	0.2775
chr9	141213431	3164839	0.0224	0.2842
chr10	135534747	3560394	0.0263	0.3541
chr11	135006516	3534699	0.0262	0.2911
chr12	133851895	3371213	0.0252	0.2712
chr13	115169878	2311647	0.0201	0.2298
chr14	107349540	2206360	0.0206	0.2579
chr15	102531392	2113629	0.0206	0.2402
chr16	90354753	2291199	0.0254	0.4115
chr17	81195210	2042072	0.0252	0.2807
chr18	78077248	2024112	0.0259	0.341
chr19	59128983	1540301	0.026	0.3925
chr20	63025520	1590620	0.0252	0.2728
chr21	48129895	1017039	0.0211	0.259
chr22	51304566	939601	0.0183	0.2428
chrMT	16571	55822	3.3687	4.8315
chrX	155270560	2187459	0.0141	0.2067
chrY	59373566	665665	0.0112	0.561

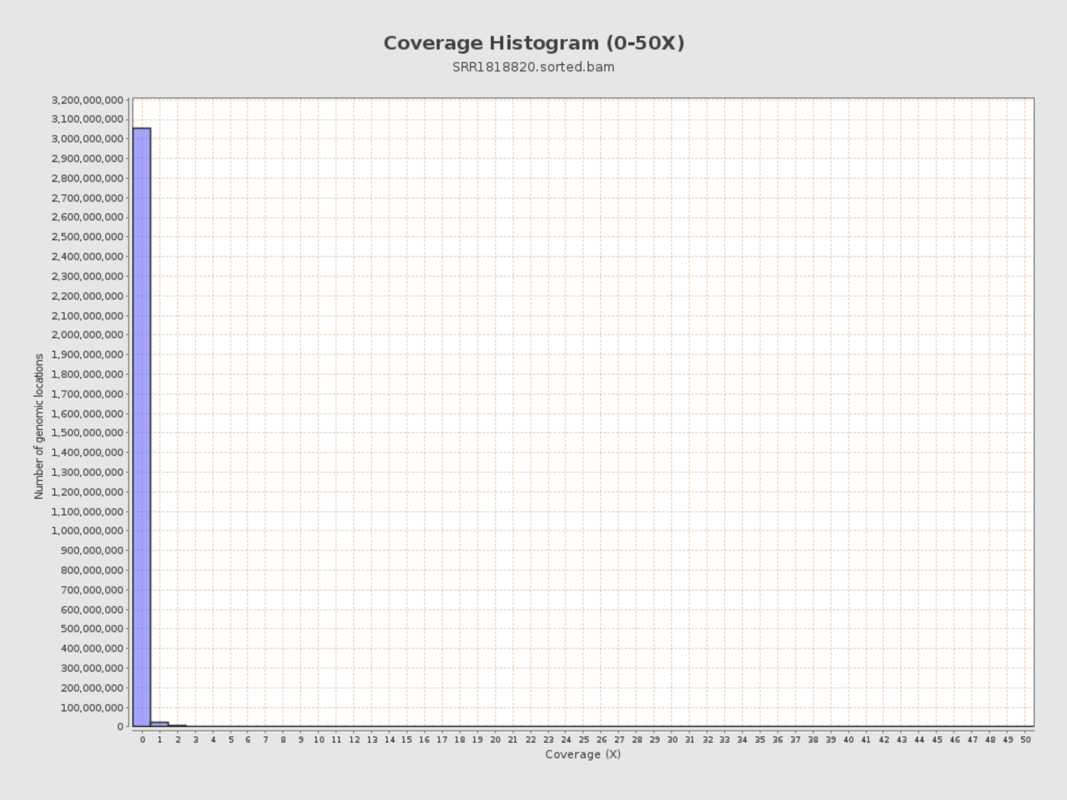
3. Results : Coverage across reference



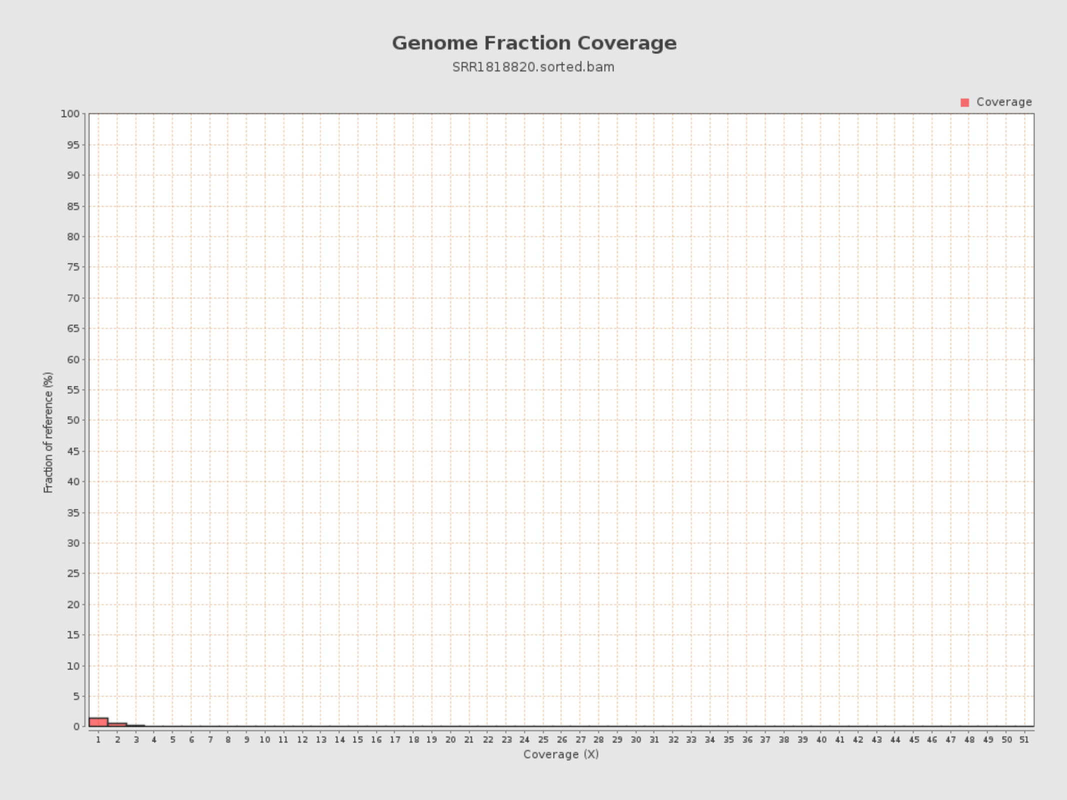
4. Results : Coverage Histogram



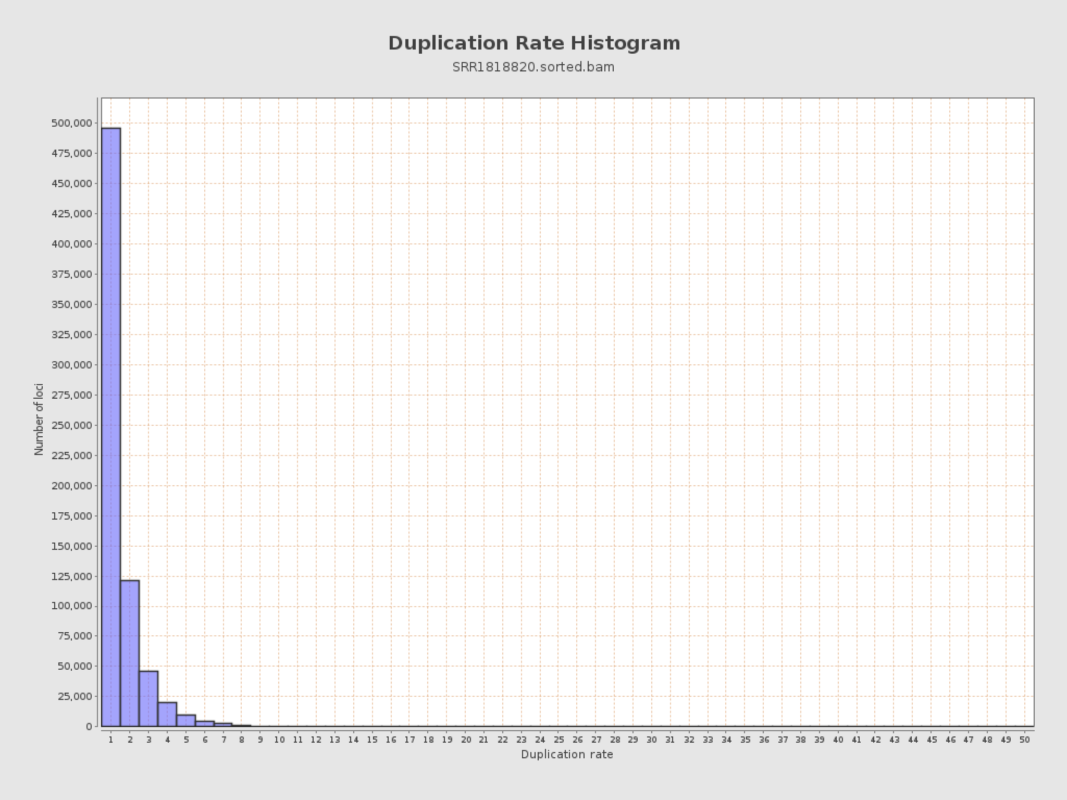
5. Results : Coverage Histogram (0-50X)



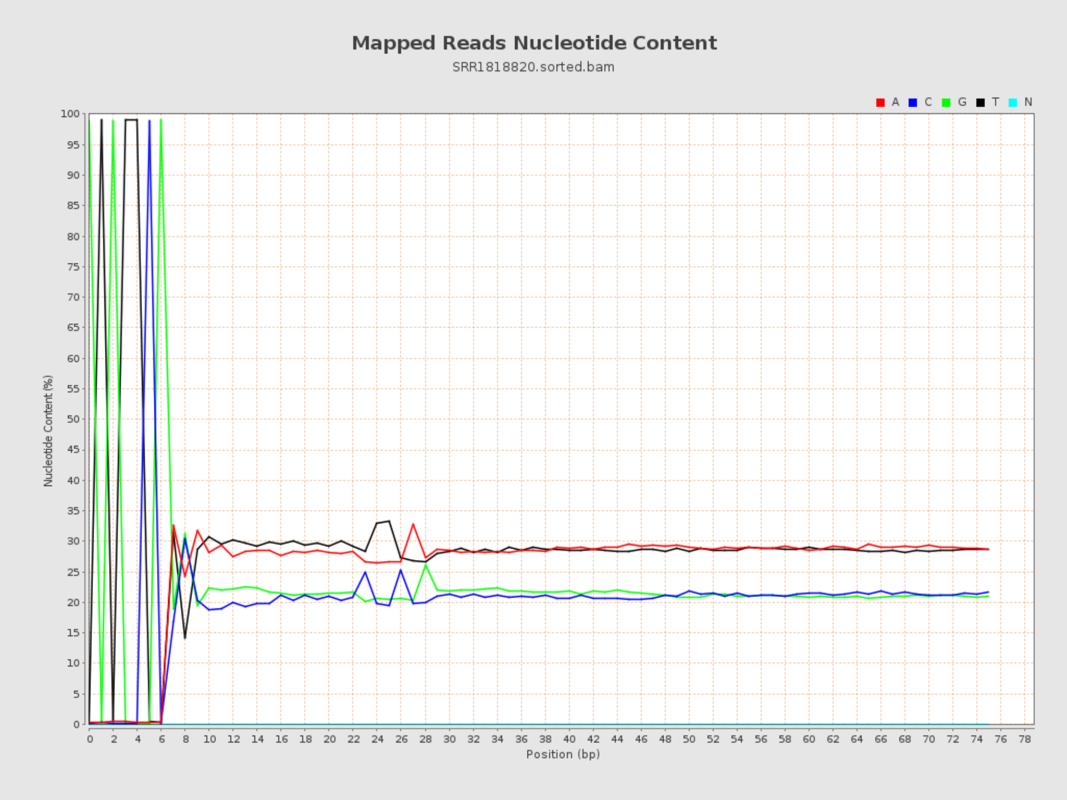
6. Results : Genome Fraction Coverage



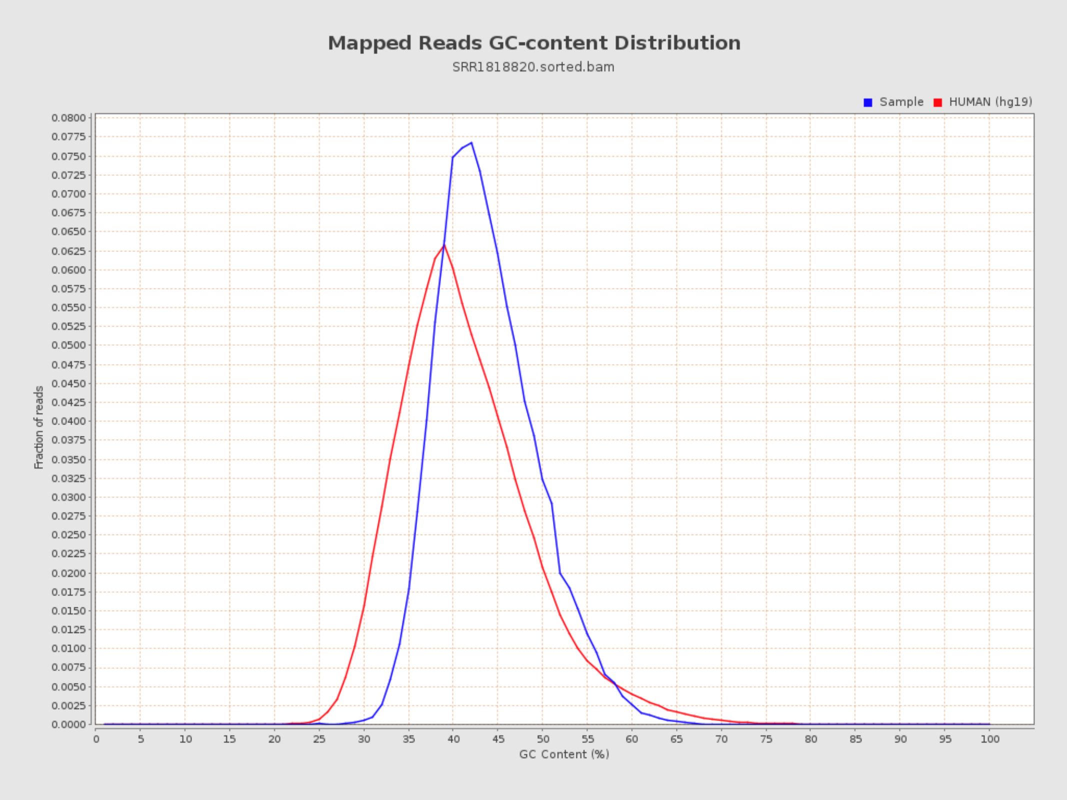
7. Results : Duplication Rate Histogram



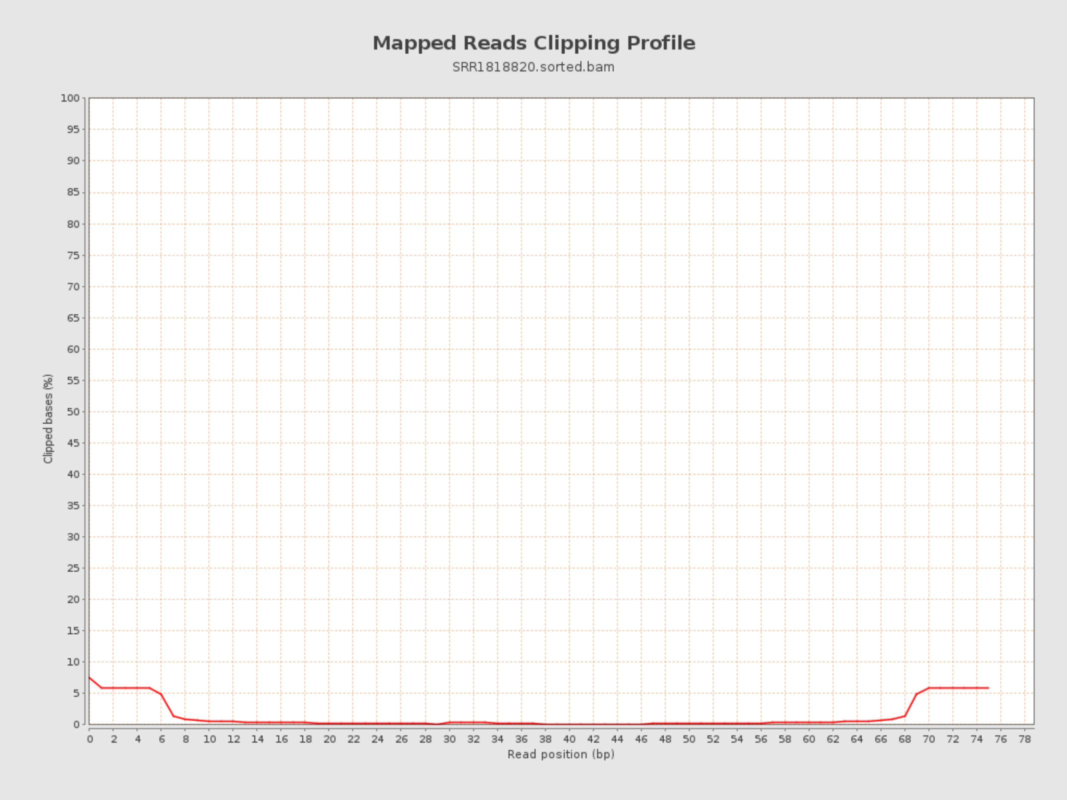
8. Results : Mapped Reads Nucleotide Content



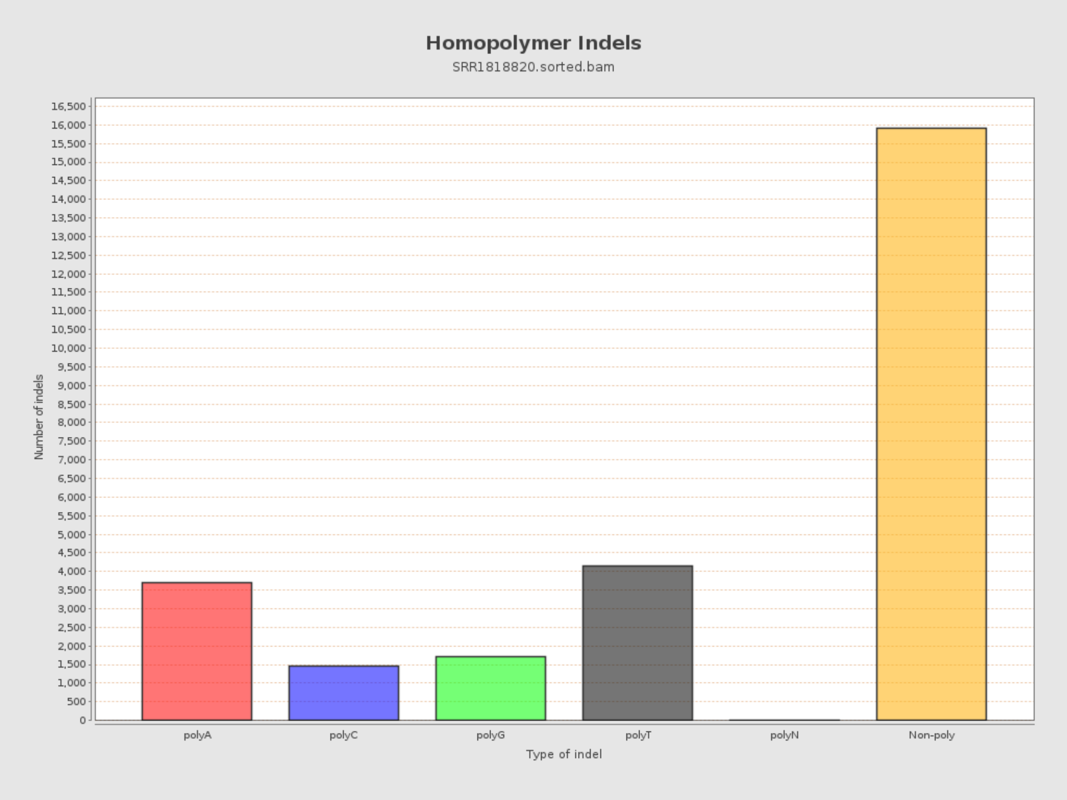
9. Results : Mapped Reads GC-content Distribution



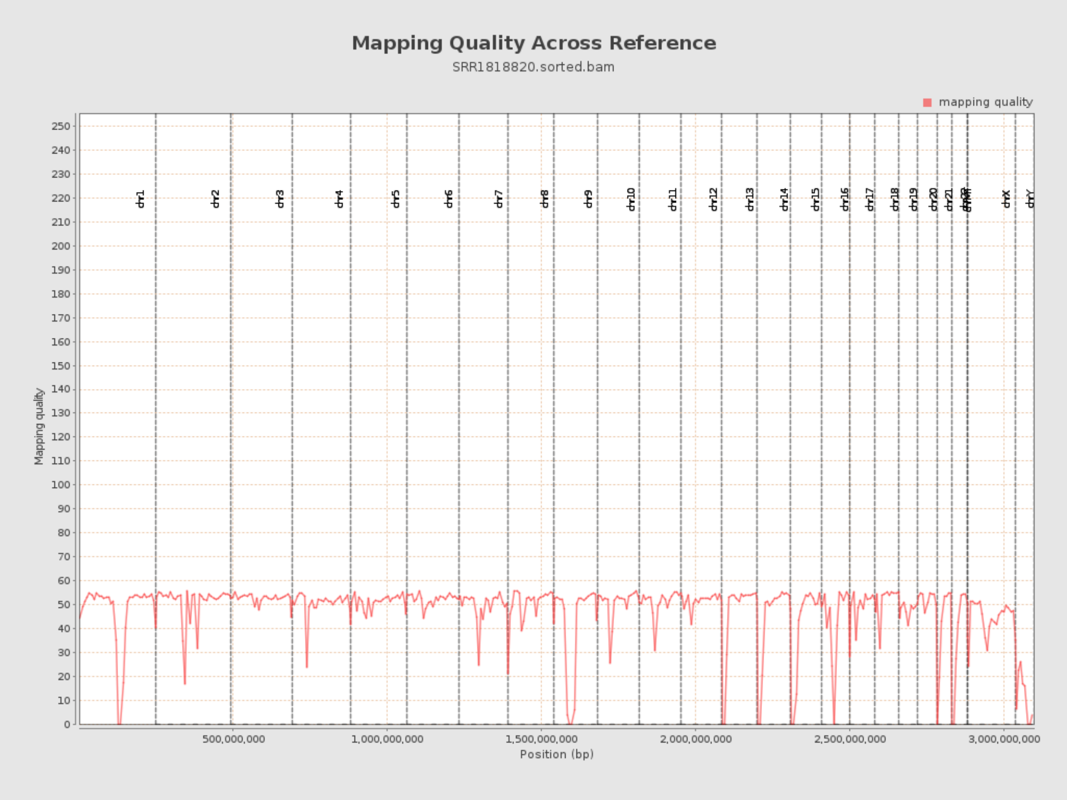
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram