Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 06:24:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818902.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_SRR1818902 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818902.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 06:24:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818902.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,042,128
Mapped reads	2,012,849 / 98.57%
Unmapped reads	29,279 / 1.43%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	25,770 / 1.26%
Read min/max/mean length	30 / 101 / 101.48
Duplicated reads (estimated)	454,687 / 22.27%
Duplication rate	18.74%
Clipped reads	2,032,748 / 99.54%

2.2. ACGT Content

Number/percentage of A's	52,621,907 / 28.23%
Number/percentage of C's	39,452,446 / 21.17%
Number/percentage of T's	53,120,318 / 28.5%
Number/percentage of G's	41,194,565 / 22.1%
Number/percentage of N's	2,799 / 0%
GC Percentage	43.27%

2.3. Coverage

Mean	0.0602

Standard Deviation	0.8008

2.4. Mapping Quality

Mean Mapping Quality	49.27

2.5. Mismatches and indels

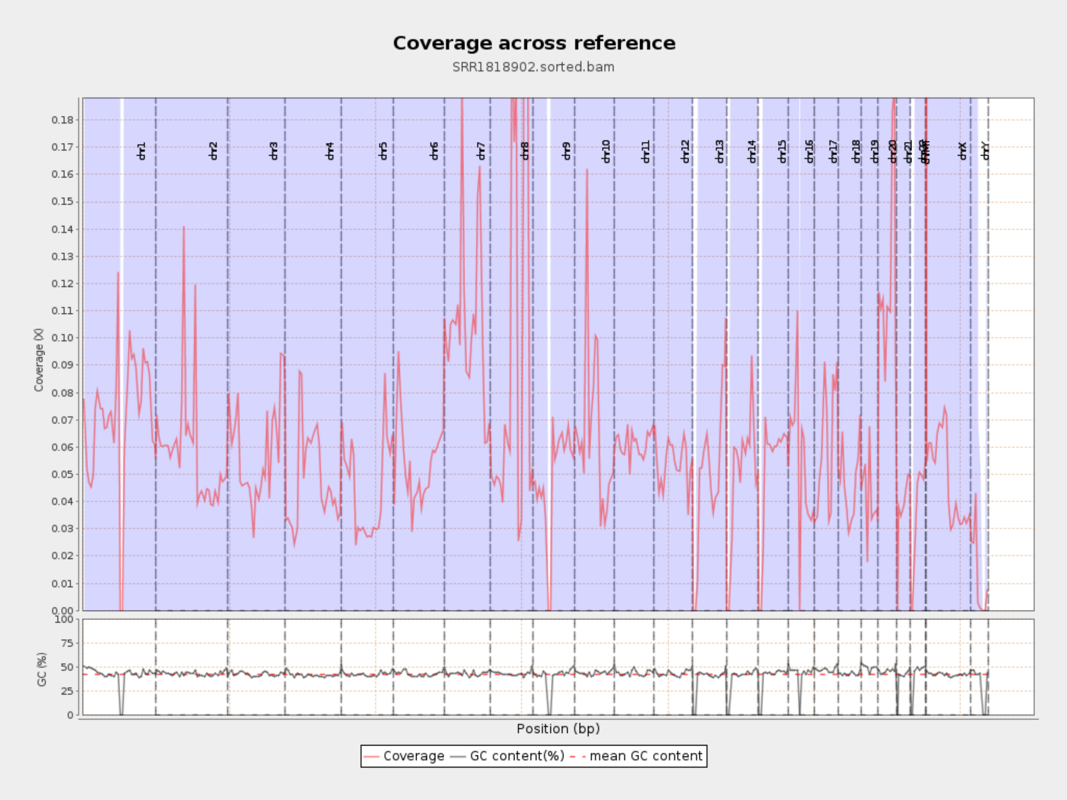
General error rate	0.64%
Mismatches	1,128,496
Insertions	23,764
Mapped reads with at least one insertion	1.13%
Deletions	59,020
Mapped reads with at least one deletion	2.86%
Homopolymer indels	40.94%

2.6. Chromosome stats

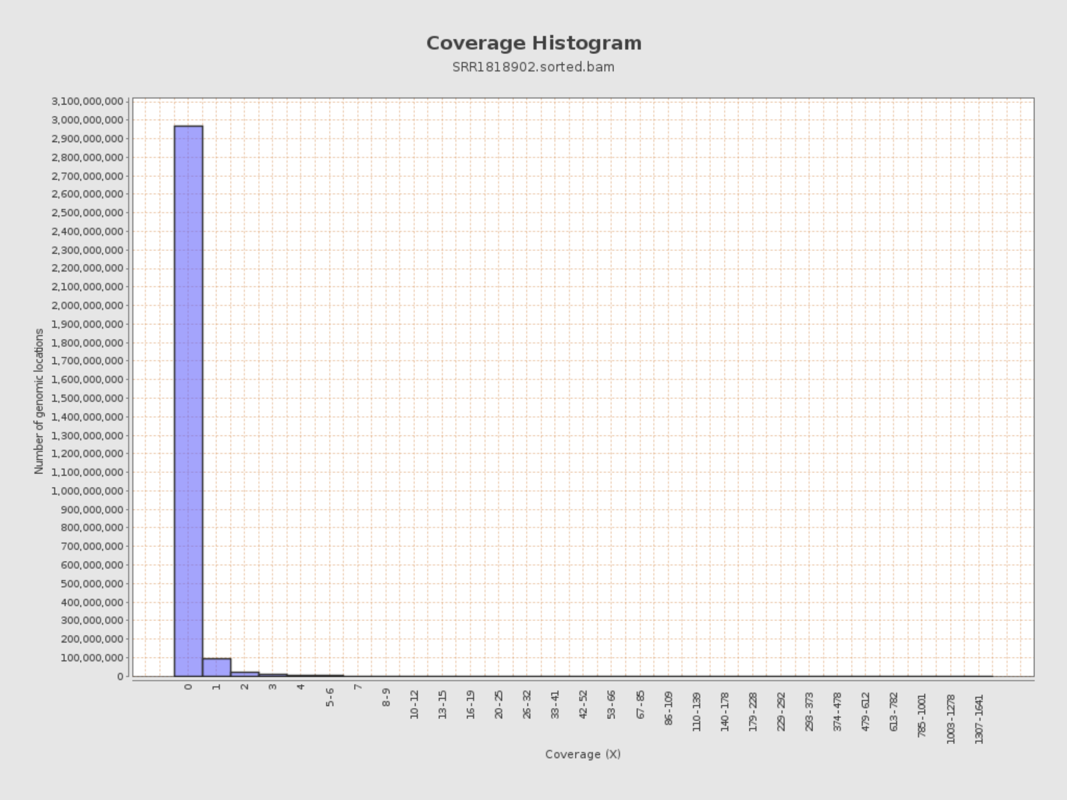
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17733000	0.0711	1.2178
chr2	243199373	14253745	0.0586	1.1415
chr3	198022430	11562113	0.0584	0.3309
chr4	191154276	9258567	0.0484	0.4258
chr5	180915260	8176613	0.0452	0.3063
chr6	171115067	9241926	0.054	0.3612
chr7	159138663	16808371	0.1056	1.8393

chr8	146364022	16044923	0.1096	0.6027
chr9	141213431	6846296	0.0485	0.6526
chr10	135534747	8745312	0.0645	1.0662
chr11	135006516	8233560	0.061	0.4496
chr12	133851895	7283206	0.0544	0.3231
chr13	115169878	5686507	0.0494	0.3002
chr14	107349540	5467153	0.0509	0.3491
chr15	102531392	5205078	0.0508	0.3074
chr16	90354753	4861030	0.0538	0.8473
chr17	81195210	4812678	0.0593	0.4822
chr18	78077248	3636197	0.0466	0.7765
chr19	59128983	2472308	0.0418	1.0958
chr20	63025520	7973579	0.1265	0.5436
chr21	48129895	1836636	0.0382	0.3326
chr22	51304566	1768022	0.0345	0.2912
chrMT	16571	365146	22.0352	14.4291
chrX	155270560	7496190	0.0483	0.3772
chrY	59373566	742076	0.0125	0.9884

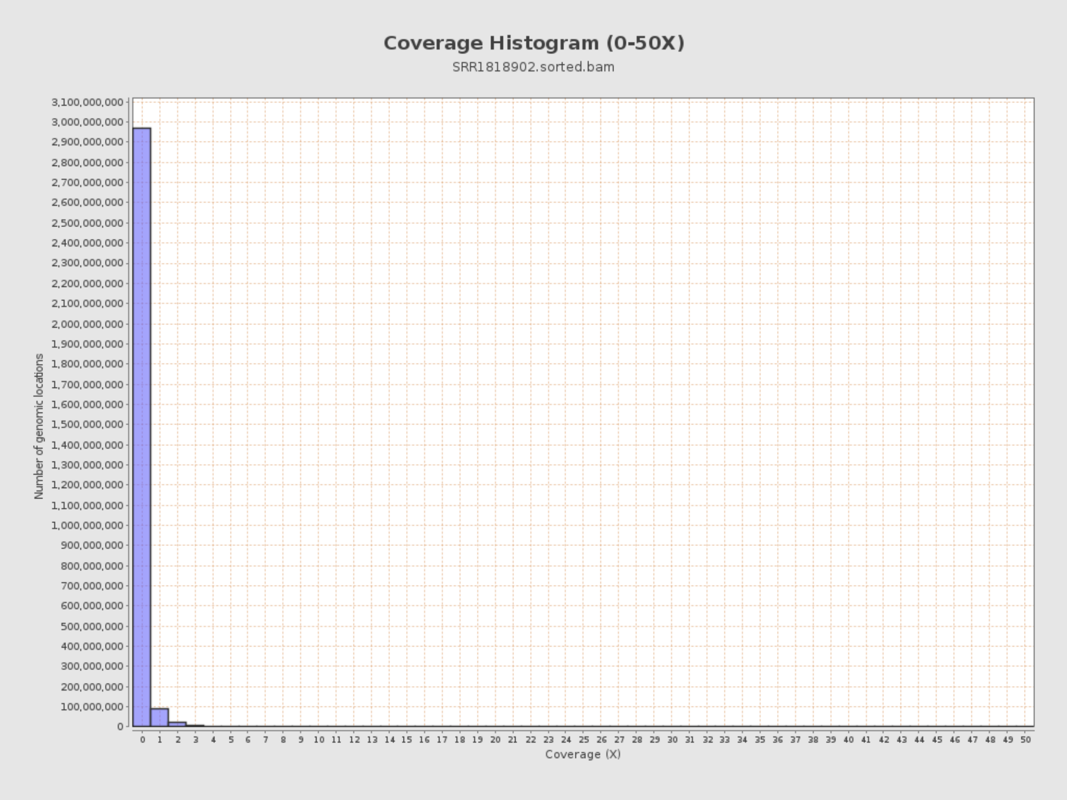
3. Results : Coverage across reference



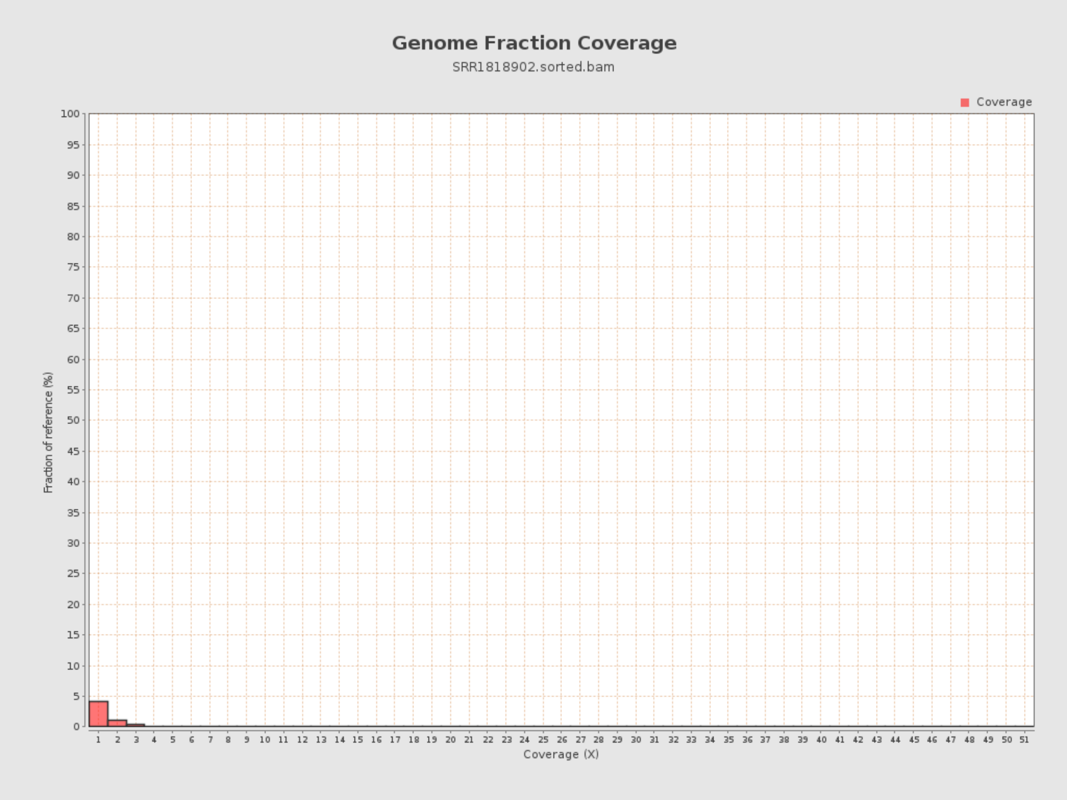
4. Results : Coverage Histogram



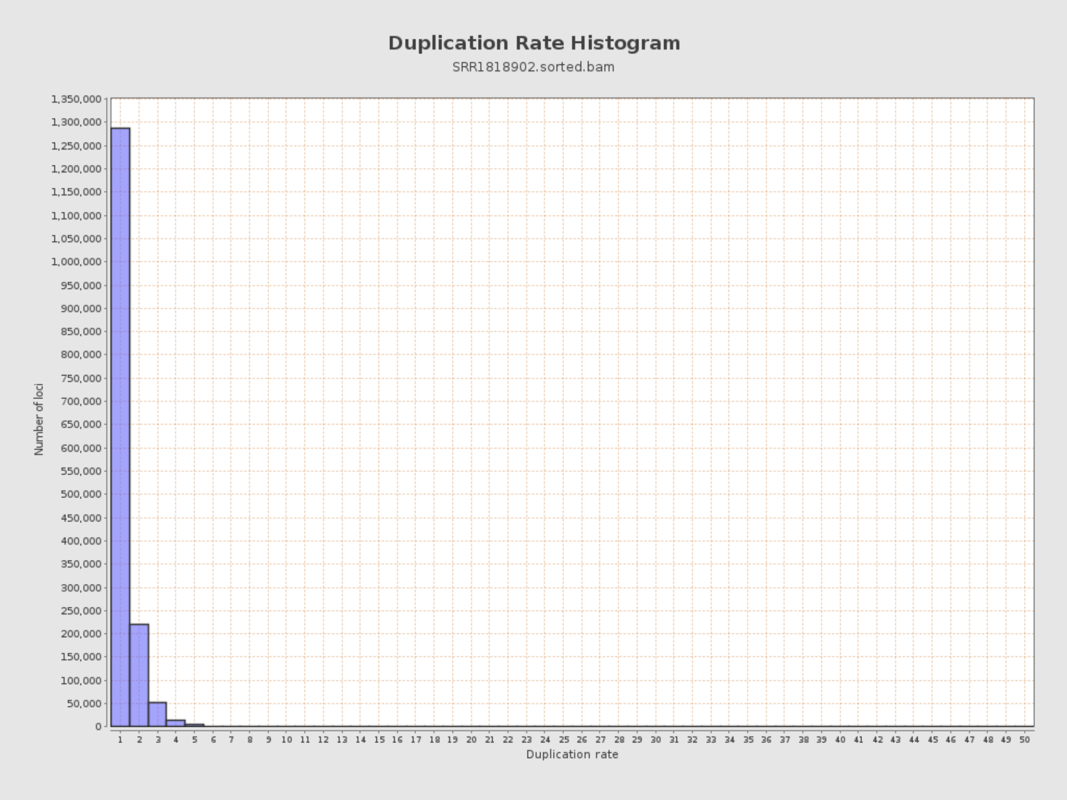
5. Results : Coverage Histogram (0-50X)



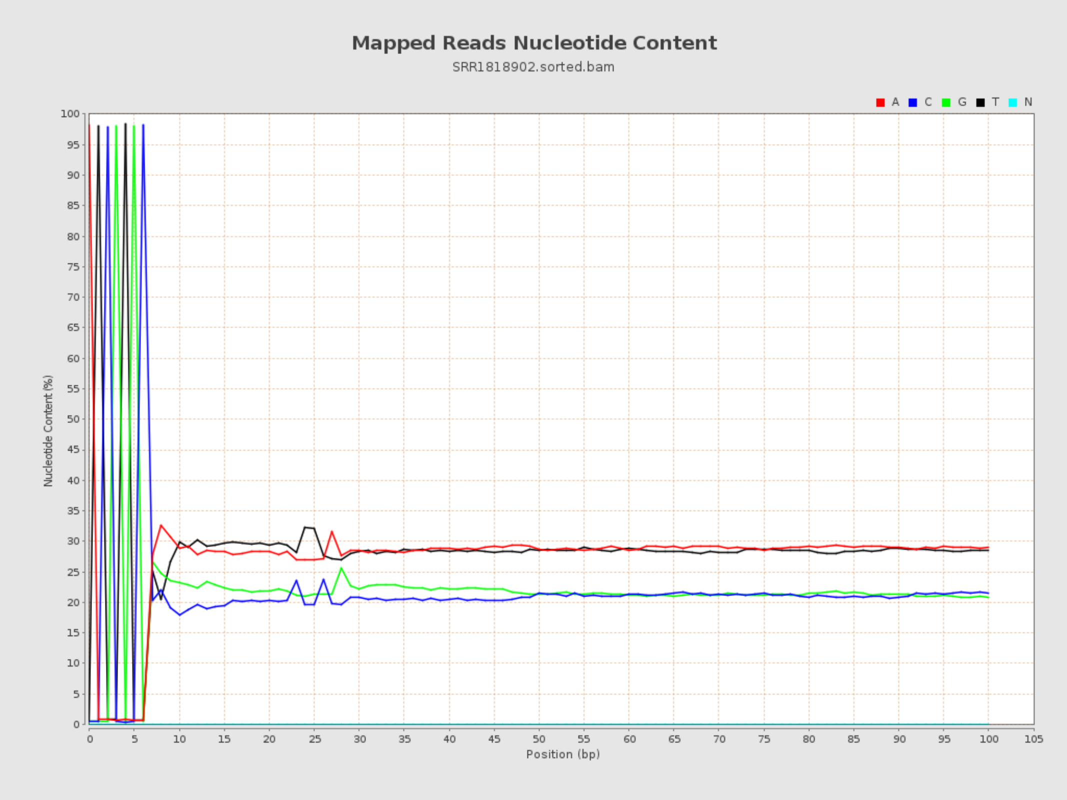
6. Results : Genome Fraction Coverage



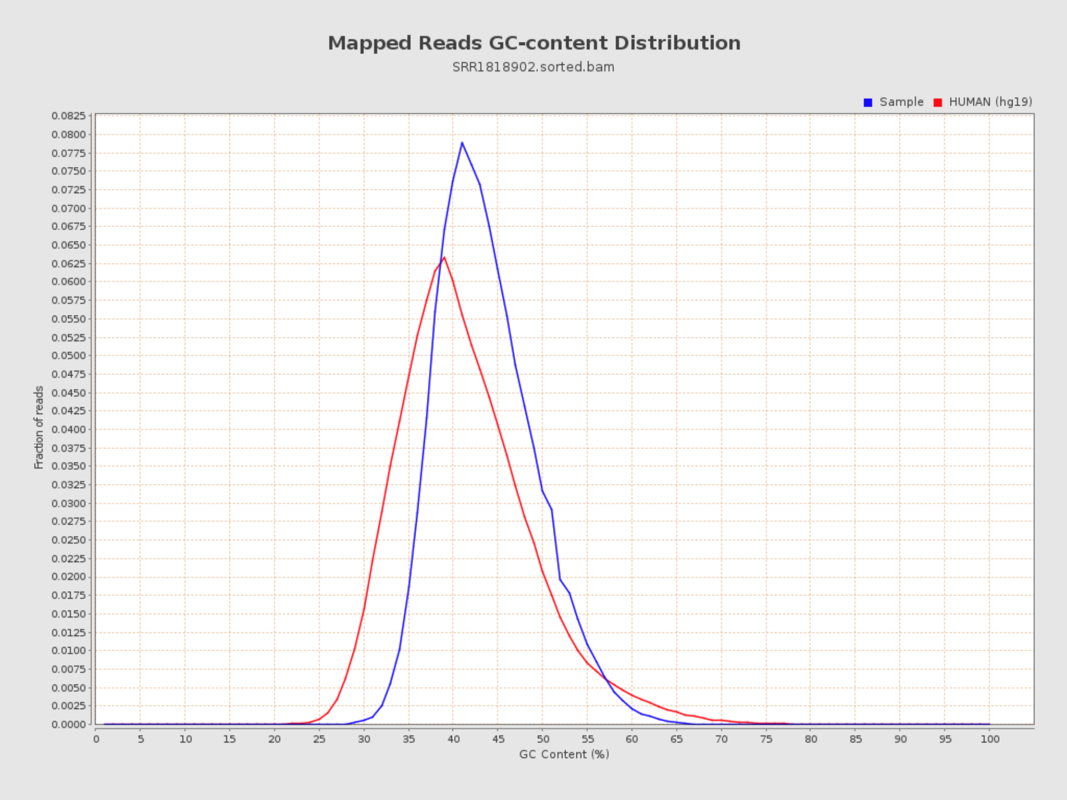
7. Results : Duplication Rate Histogram



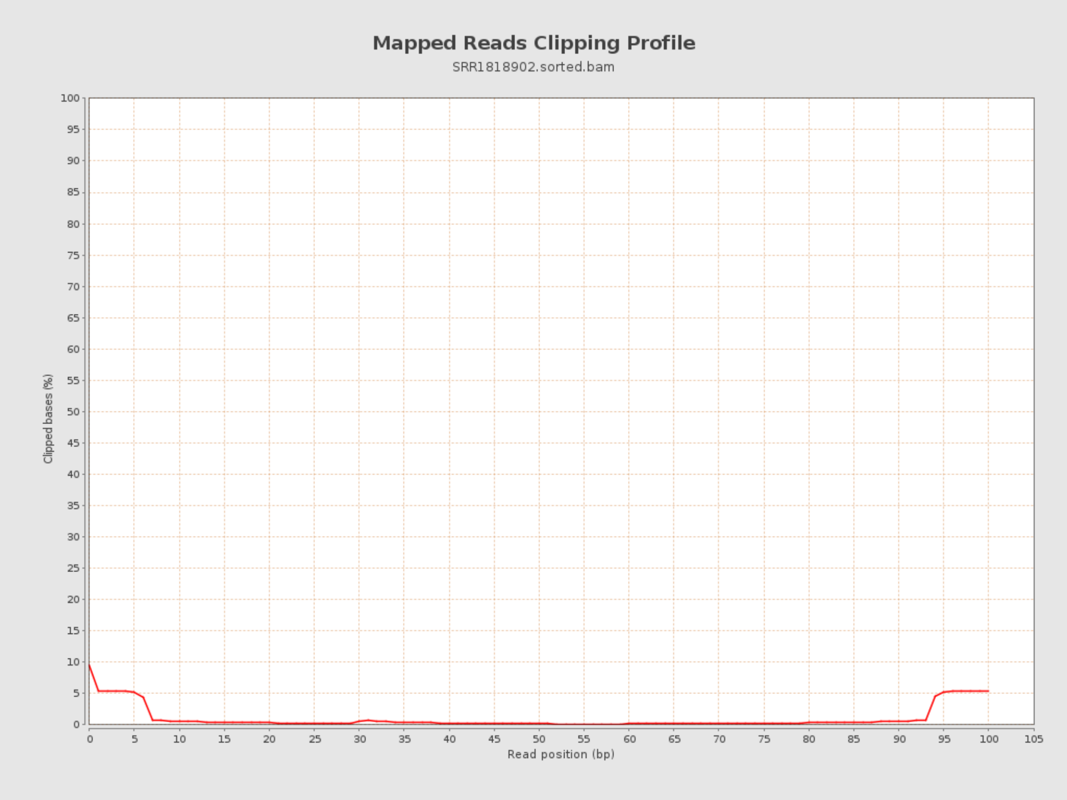
8. Results : Mapped Reads Nucleotide Content



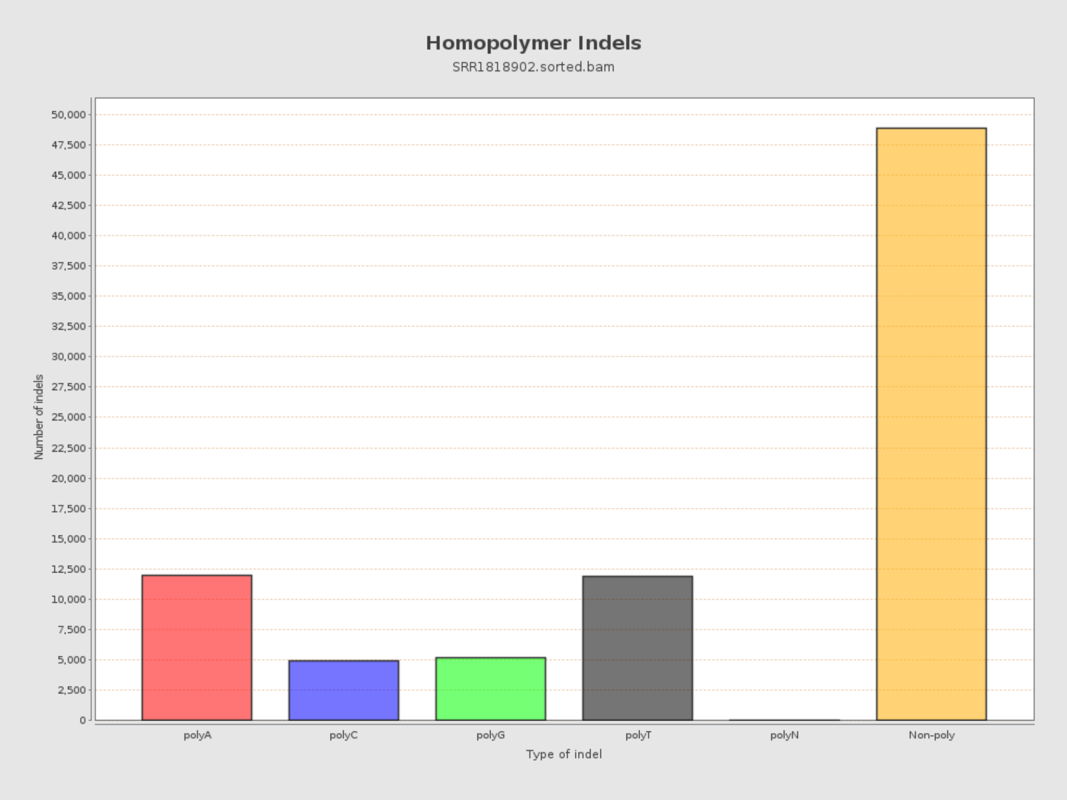
9. Results : Mapped Reads GC-content Distribution



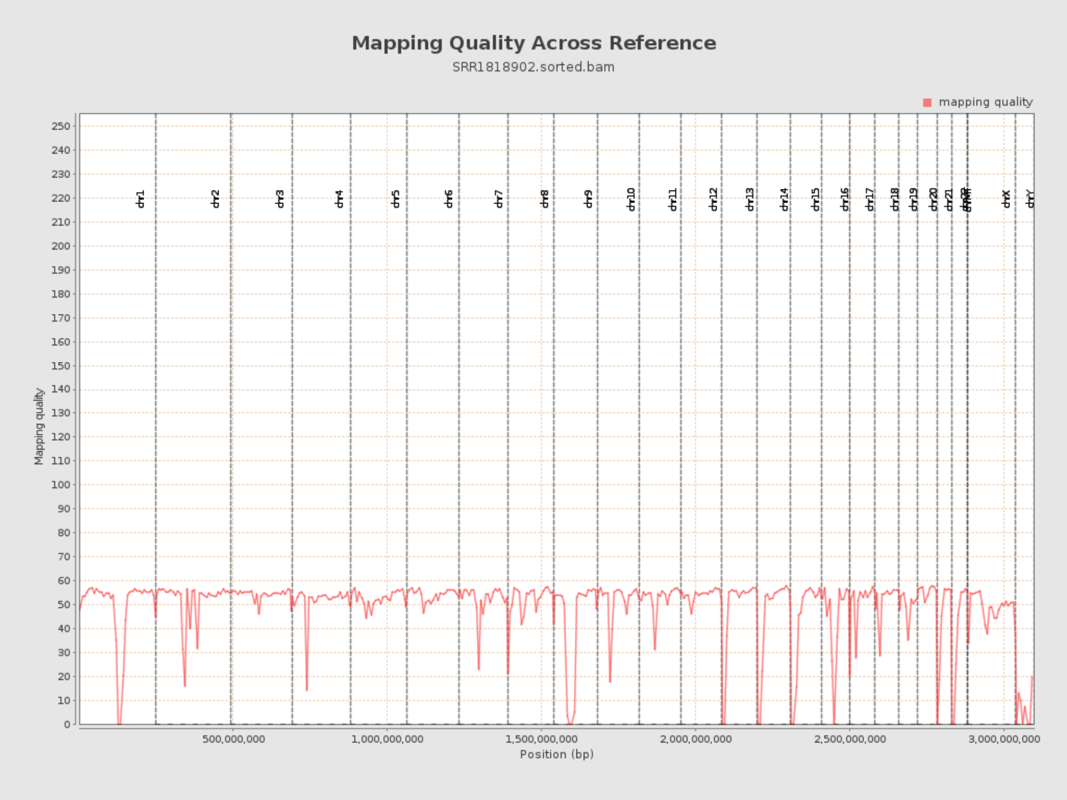
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram