Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 07:39:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818913.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_SRR1818913 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818913.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 07:39:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818913.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,812,740
Mapped reads	1,753,286 / 96.72%
Unmapped reads	59,454 / 3.28%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	25,341 / 1.4%
Read min/max/mean length	30 / 101 / 101.54
Duplicated reads (estimated)	269,912 / 14.89%
Duplication rate	12.24%
Clipped reads	1,754,566 / 96.79%

2.2. ACGT Content

Number/percentage of A's	47,238,467 / 29.08%
Number/percentage of C's	33,751,250 / 20.78%
Number/percentage of T's	45,370,176 / 27.93%
Number/percentage of G's	36,064,828 / 22.2%
Number/percentage of N's	2,270 / 0%
GC Percentage	42.98%

2.3. Coverage

Mean	0.0525

Standard Deviation	0.687

2.4. Mapping Quality

Mean Mapping Quality	49.28

2.5. Mismatches and indels

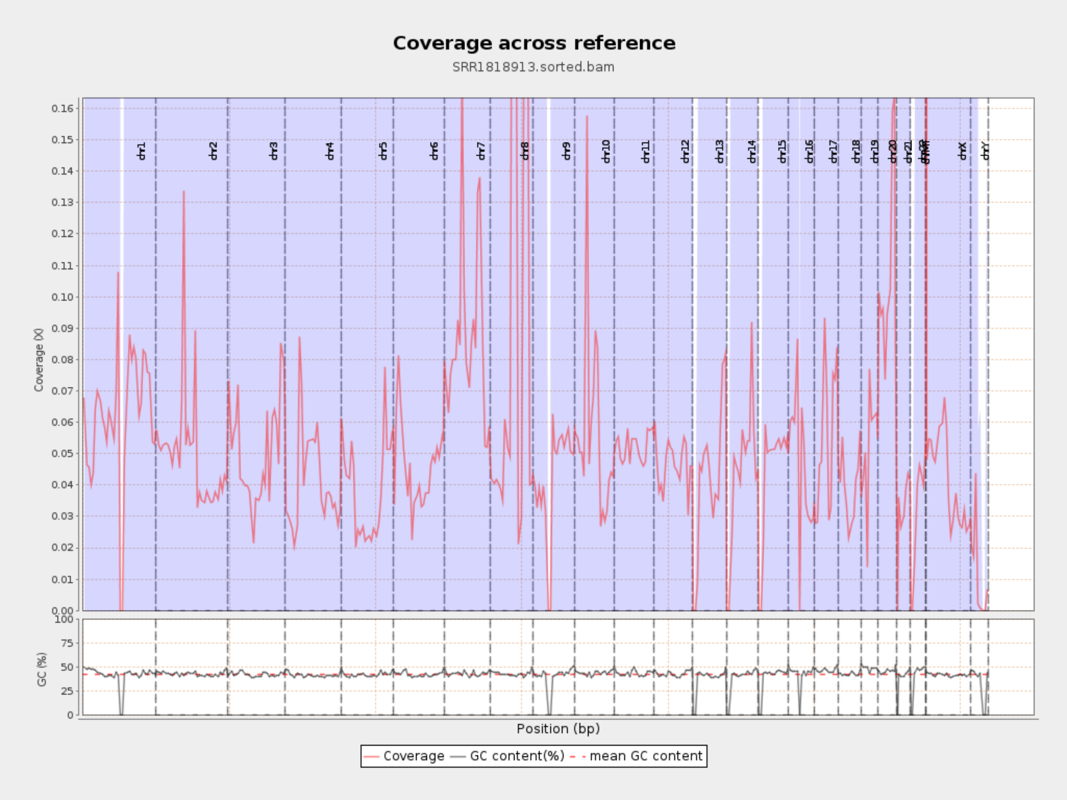
General error rate	0.65%
Mismatches	986,172
Insertions	24,450
Mapped reads with at least one insertion	1.35%
Deletions	48,728
Mapped reads with at least one deletion	2.71%
Homopolymer indels	40.09%

2.6. Chromosome stats

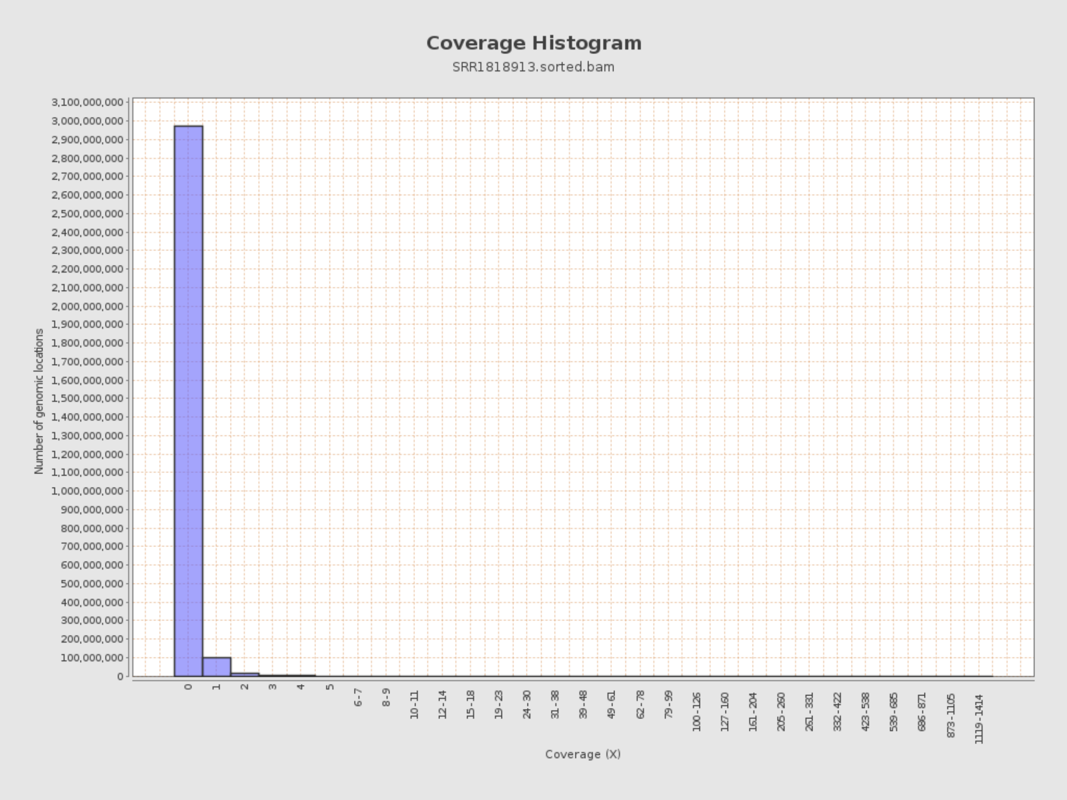
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15418372	0.0619	1.0449
chr2	243199373	12156244	0.05	0.8409
chr3	198022430	9958604	0.0503	0.2844
chr4	191154276	7983861	0.0418	0.3884
chr5	180915260	6984796	0.0386	0.2614
chr6	171115067	7830726	0.0458	0.305
chr7	159138663	13911333	0.0874	1.7024

chr8	146364022	15339715	0.1048	0.5583
chr9	141213431	5957124	0.0422	0.5951
chr10	135534747	7630201	0.0563	0.9393
chr11	135006516	7030487	0.0521	0.3938
chr12	133851895	6258468	0.0468	0.269
chr13	115169878	4858754	0.0422	0.2514
chr14	107349540	4778475	0.0445	0.2869
chr15	102531392	4422868	0.0431	0.2539
chr16	90354753	4193409	0.0464	0.5441
chr17	81195210	4399412	0.0542	0.4789
chr18	78077248	3058423	0.0392	0.686
chr19	59128983	3070632	0.0519	0.9594
chr20	63025520	6912613	0.1097	0.4501
chr21	48129895	1561485	0.0324	0.3094
chr22	51304566	1534895	0.0299	0.2431
chrMT	16571	116696	7.0422	5.429
chrX	155270560	6504592	0.0419	0.3504
chrY	59373566	652248	0.011	0.7745

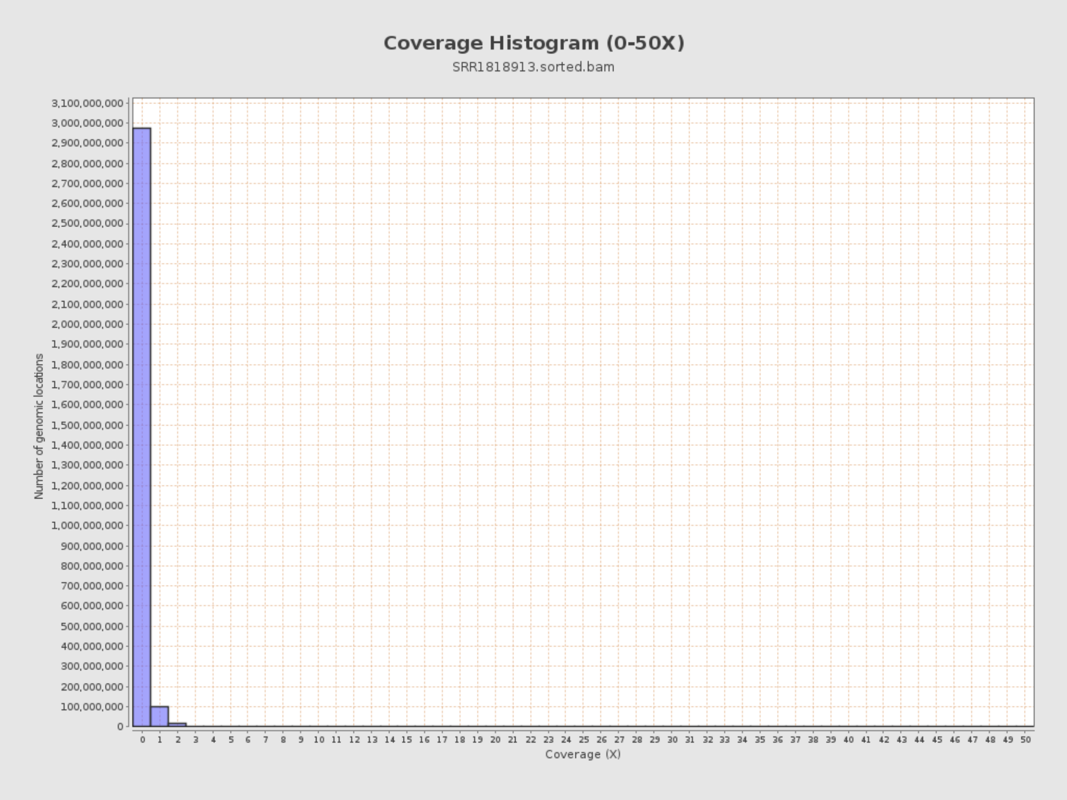
3. Results : Coverage across reference



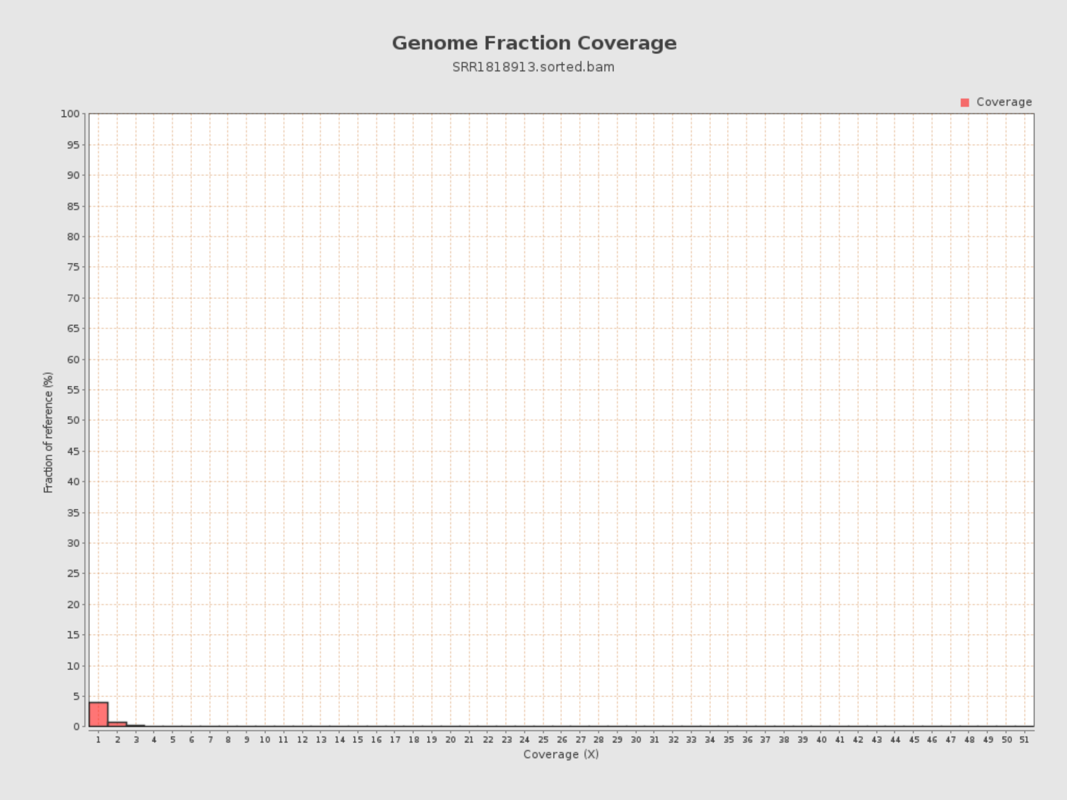
4. Results : Coverage Histogram



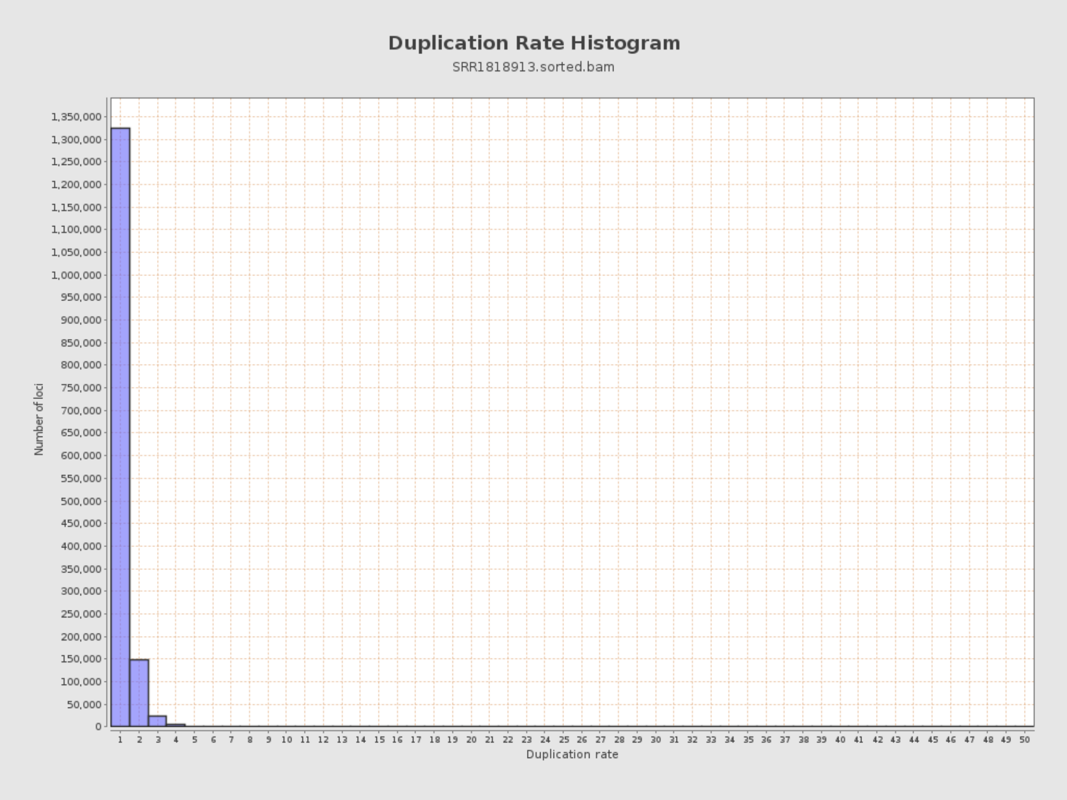
5. Results : Coverage Histogram (0-50X)



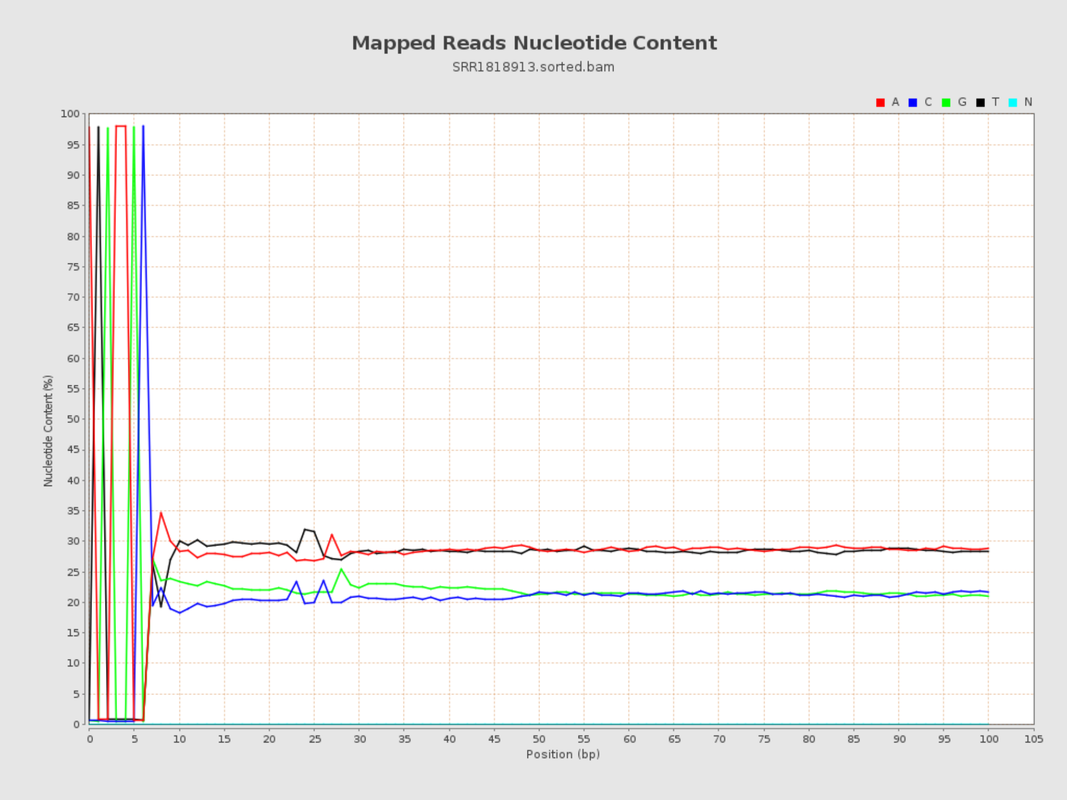
6. Results : Genome Fraction Coverage



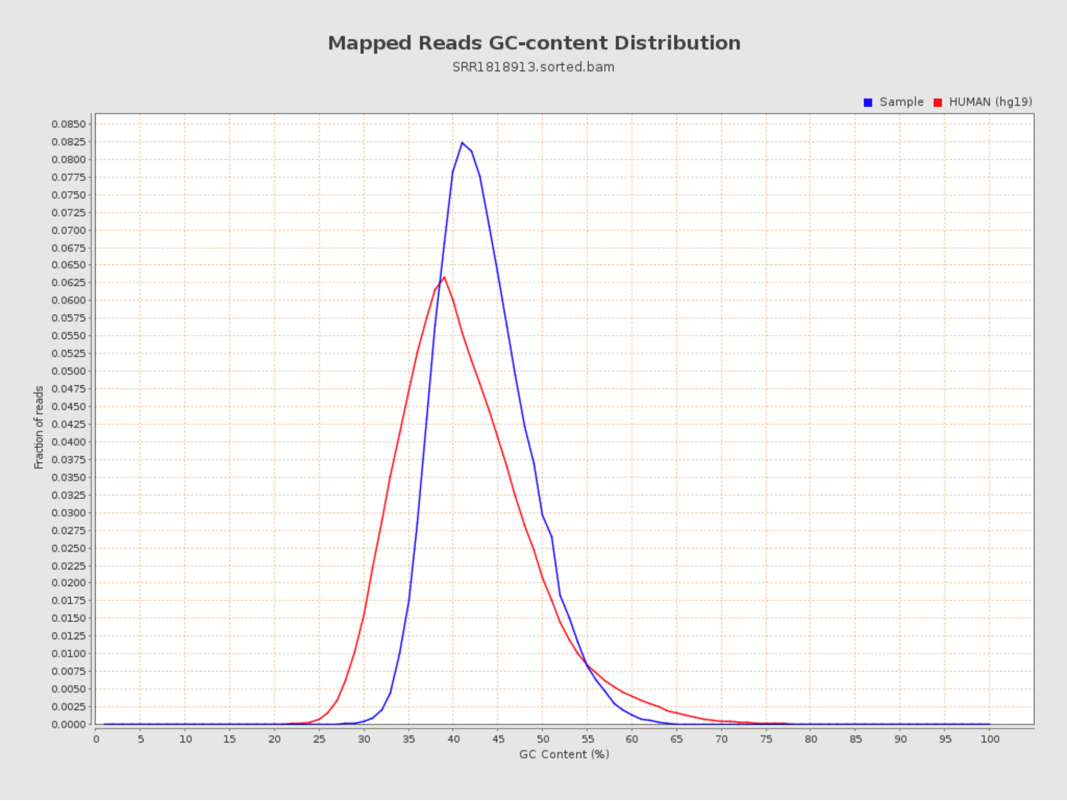
7. Results : Duplication Rate Histogram



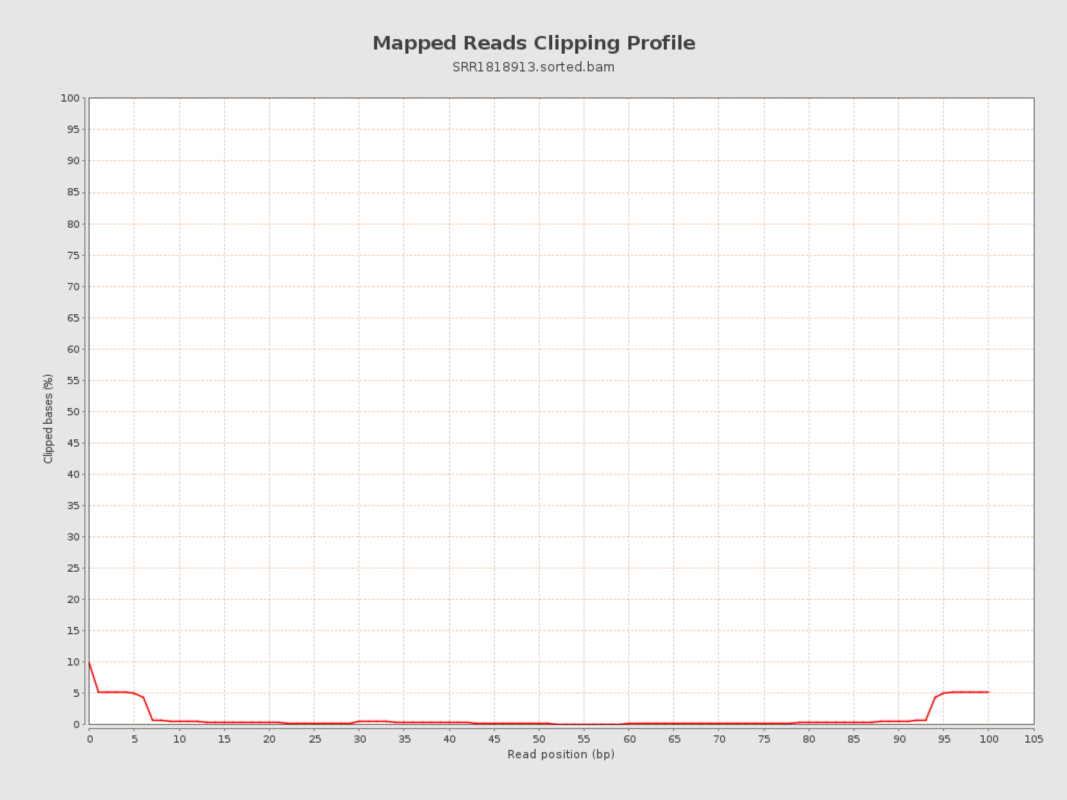
8. Results : Mapped Reads Nucleotide Content



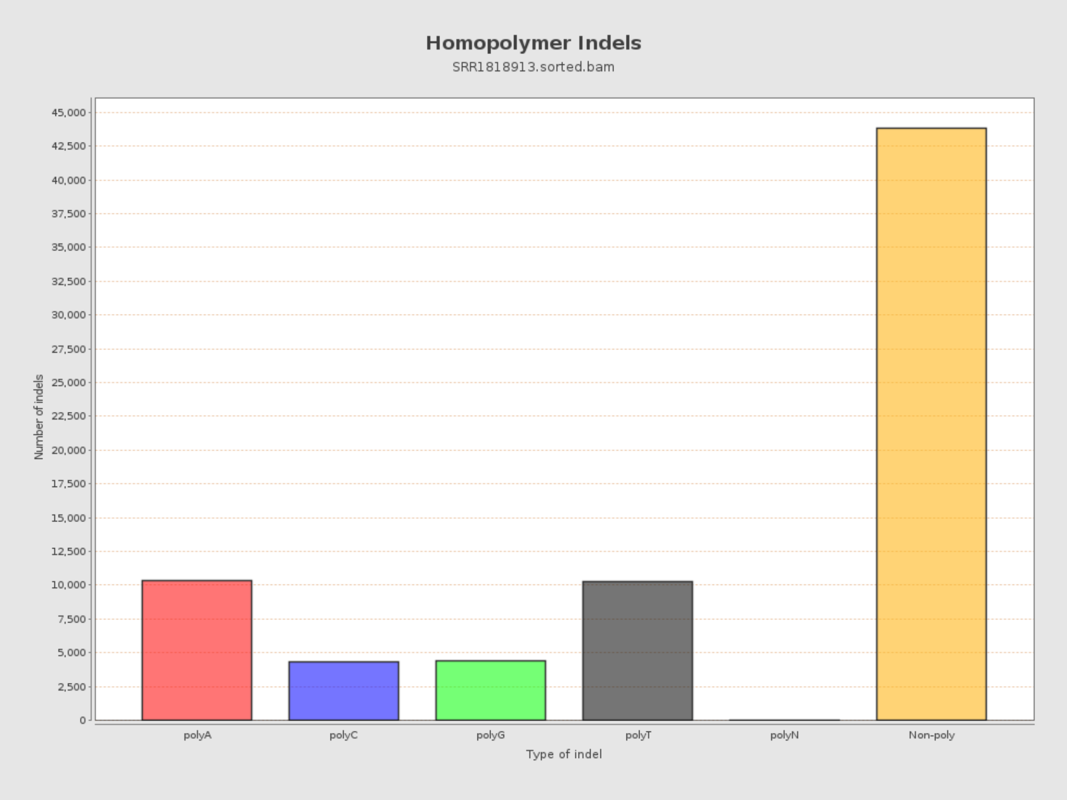
9. Results : Mapped Reads GC-content Distribution



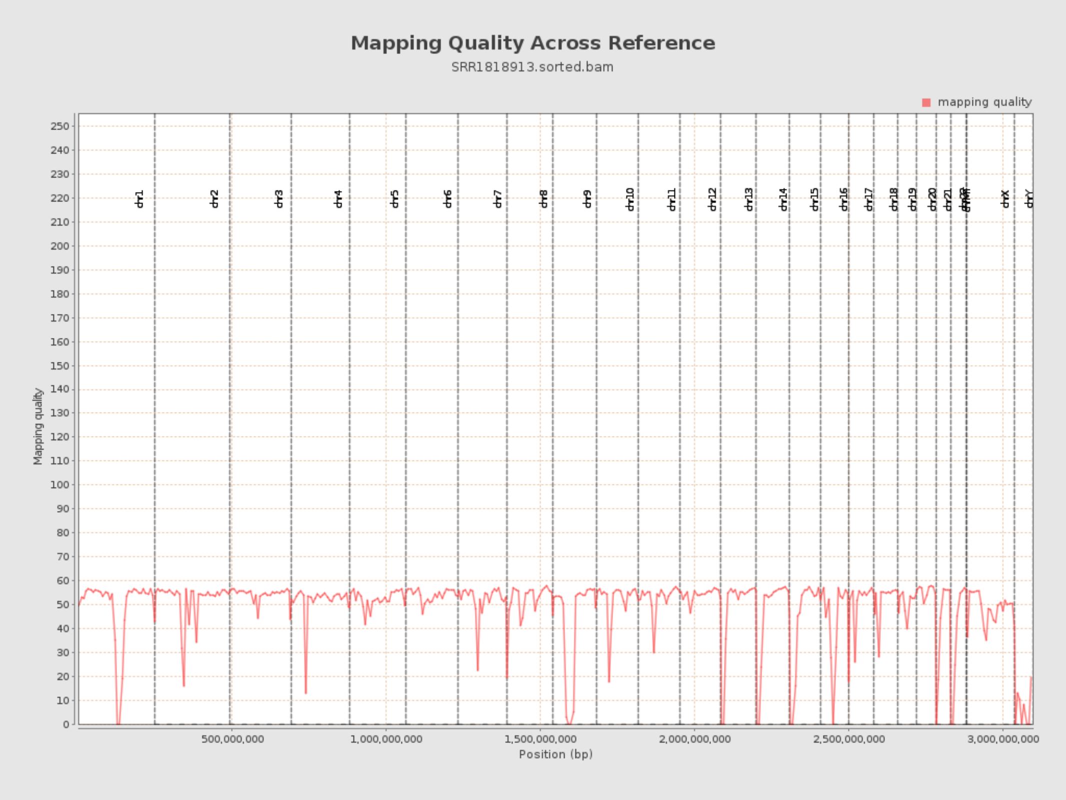
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram