Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 13:46:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818993.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_SRR1818993 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818993.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 13:46:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818993.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,260,033
Mapped reads	2,223,486 / 98.38%
Unmapped reads	36,547 / 1.62%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	33,949 / 1.5%
Read min/max/mean length	30 / 101 / 101.58
Duplicated reads (estimated)	944,635 / 41.8%
Duplication rate	35.26%
Clipped reads	2,241,057 / 99.16%

2.2. ACGT Content

Number/percentage of A's	61,137,813 / 29.73%
Number/percentage of C's	43,385,637 / 21.1%
Number/percentage of T's	57,038,294 / 27.74%
Number/percentage of G's	44,040,500 / 21.42%
Number/percentage of N's	9,917 / 0%
GC Percentage	42.52%

2.3. Coverage

Mean	0.0665

Standard Deviation	0.7432

2.4. Mapping Quality

Mean Mapping Quality	49.26

2.5. Mismatches and indels

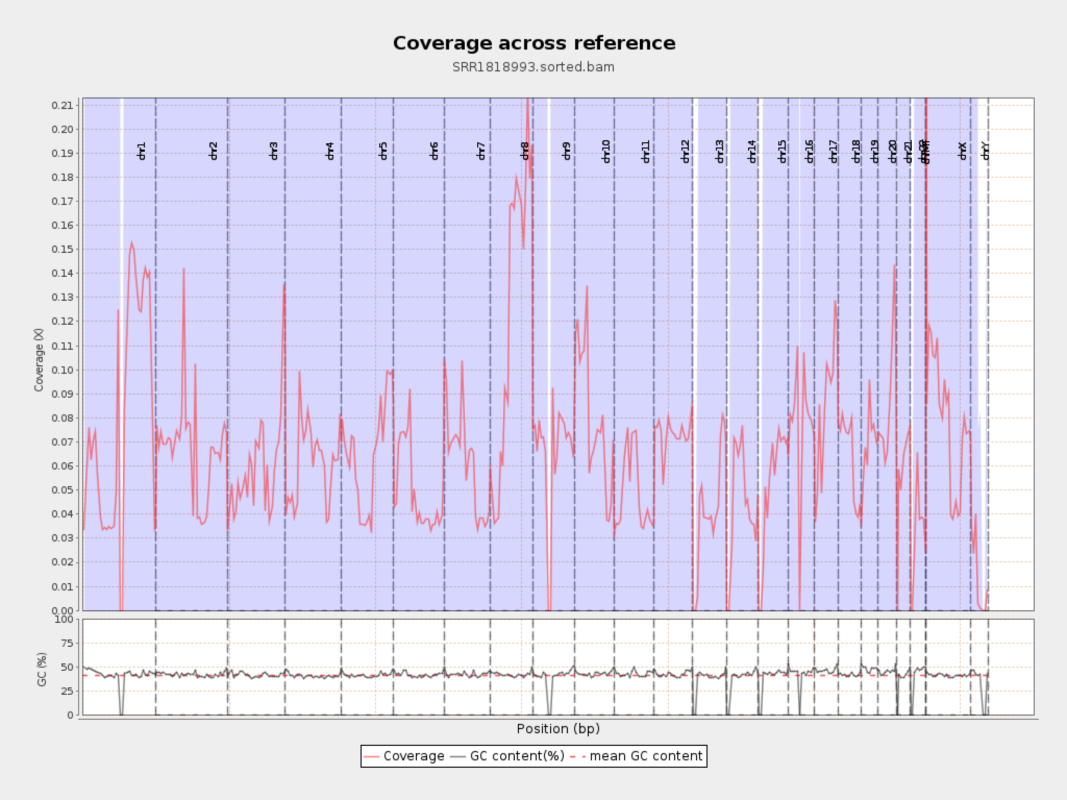
General error rate	0.66%
Mismatches	1,282,281
Insertions	37,156
Mapped reads with at least one insertion	1.62%
Deletions	67,302
Mapped reads with at least one deletion	2.96%
Homopolymer indels	41.74%

2.6. Chromosome stats

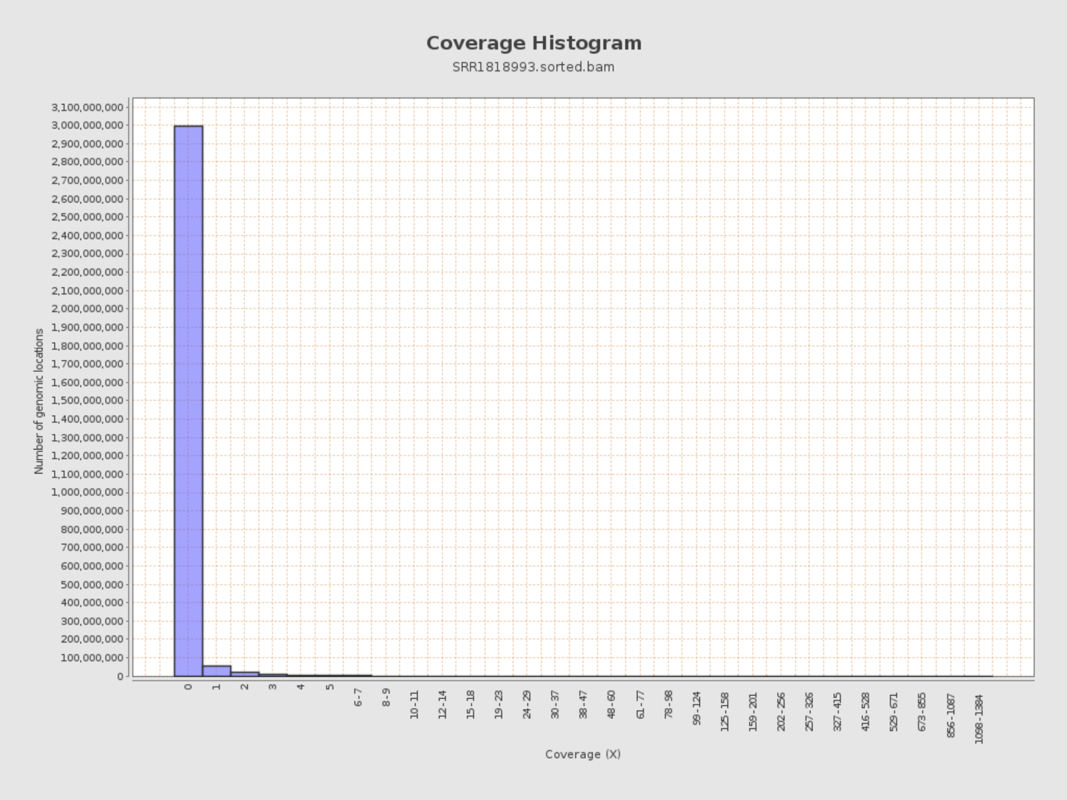
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	19951277	0.08	1.2892
chr2	243199373	16458827	0.0677	1.0818
chr3	198022430	11770340	0.0594	0.436
chr4	191154276	11769780	0.0616	0.5248
chr5	180915260	11780704	0.0651	0.4681
chr6	171115067	8453664	0.0494	0.4873
chr7	159138663	9844165	0.0619	0.8344

chr8	146364022	18514676	0.1265	0.7236
chr9	141213431	9177736	0.065	0.7097
chr10	135534747	10727369	0.0791	0.9019
chr11	135006516	6645527	0.0492	0.4963
chr12	133851895	9856652	0.0736	0.4961
chr13	115169878	4822939	0.0419	0.3622
chr14	107349540	4743337	0.0442	0.4014
chr15	102531392	5169290	0.0504	0.4047
chr16	90354753	6884719	0.0762	0.8276
chr17	81195210	6883302	0.0848	0.6011
chr18	78077248	5018255	0.0643	0.8249
chr19	59128983	4124531	0.0698	1.1734
chr20	63025520	5612430	0.0891	0.5814
chr21	48129895	2825452	0.0587	0.4862
chr22	51304566	1626281	0.0317	0.354
chrMT	16571	28060	1.6933	2.7532
chrX	155270560	12272161	0.079	0.5749
chrY	59373566	774037	0.013	0.8068

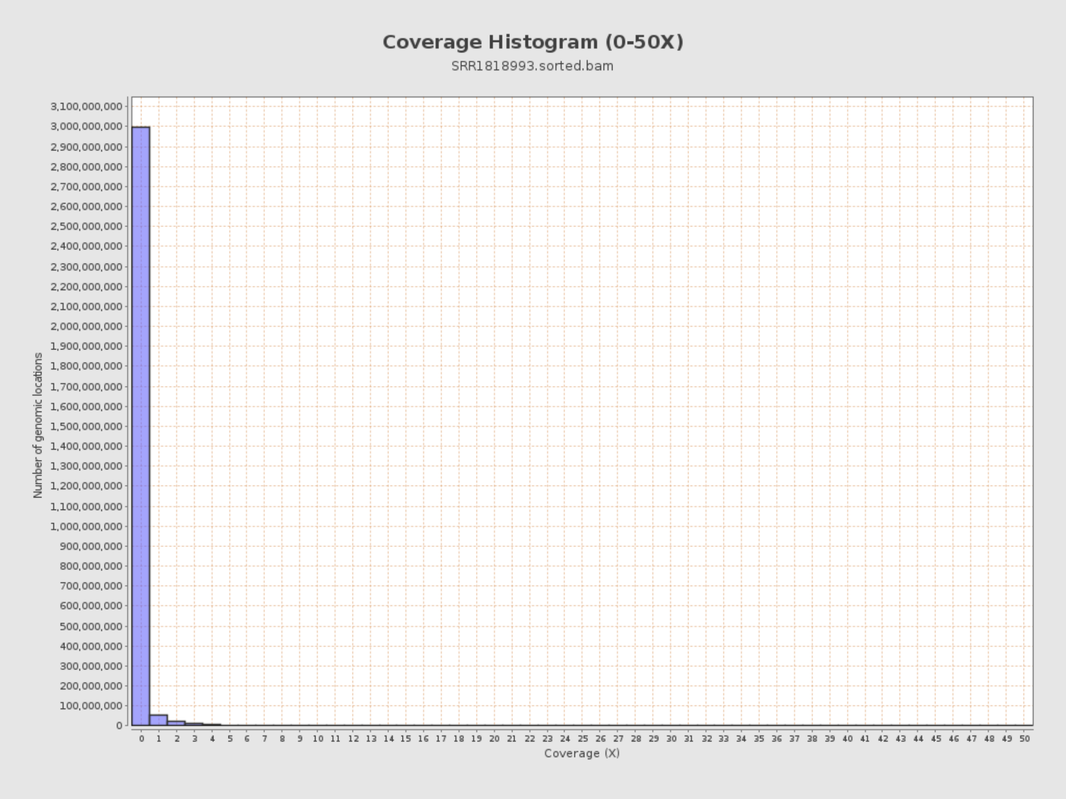
3. Results : Coverage across reference



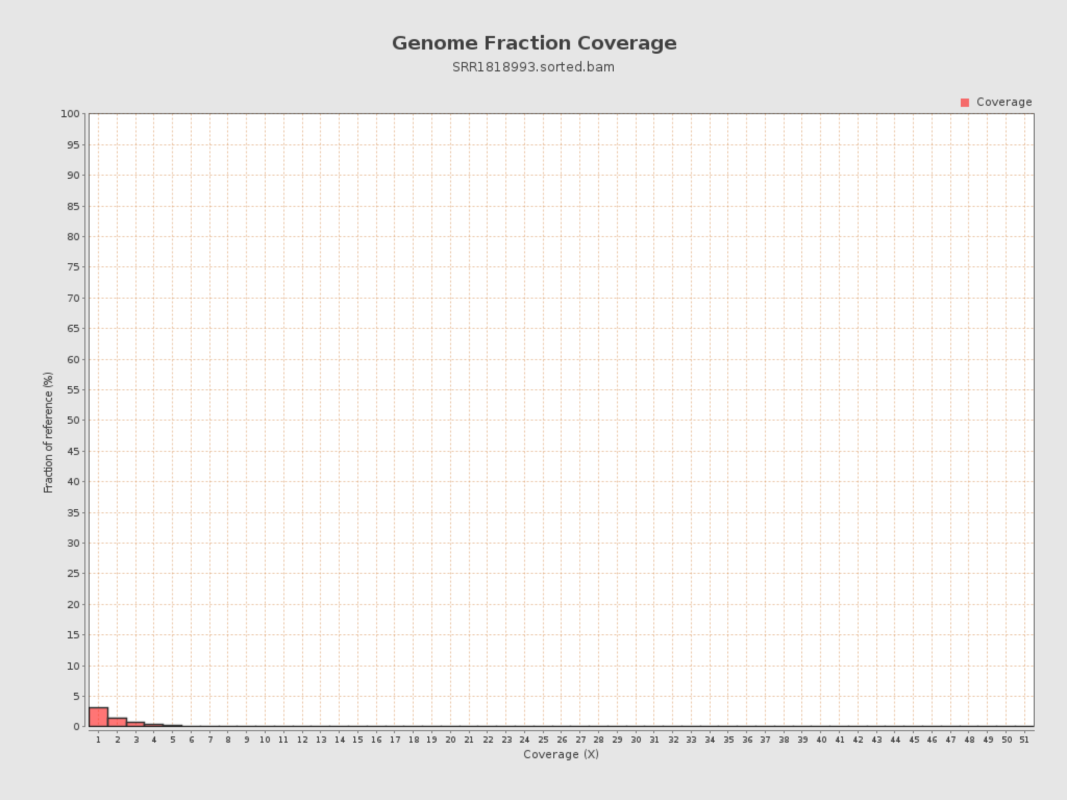
4. Results : Coverage Histogram



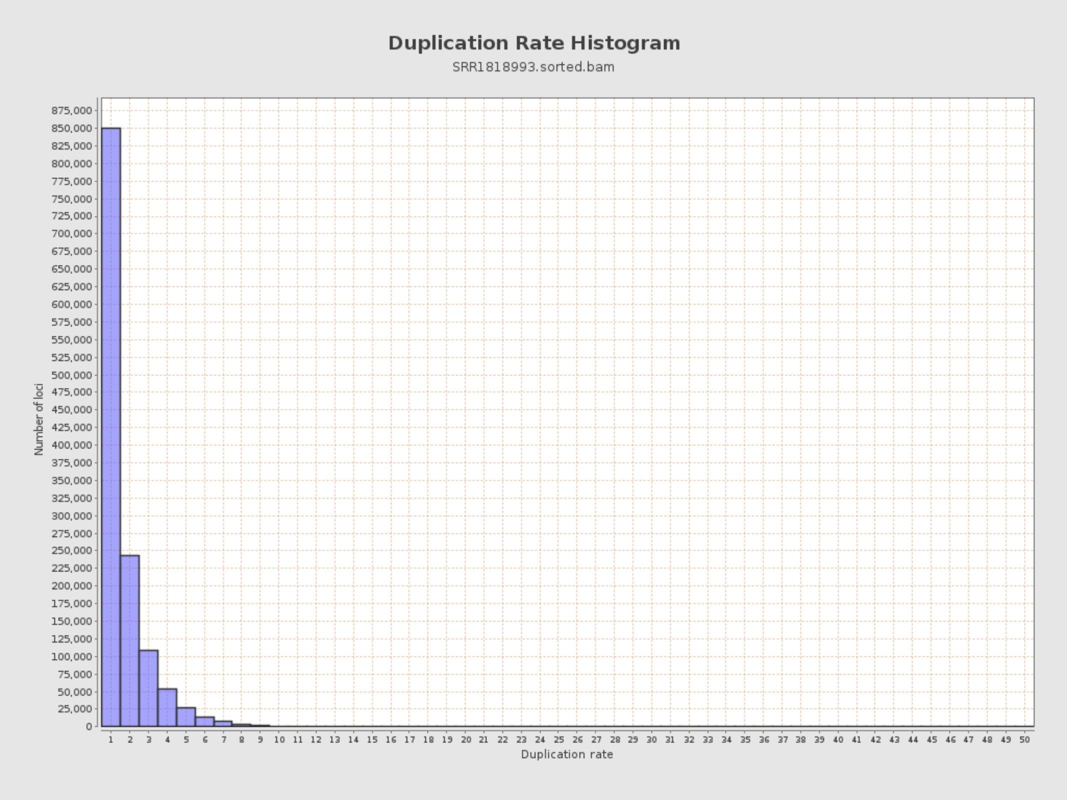
5. Results : Coverage Histogram (0-50X)



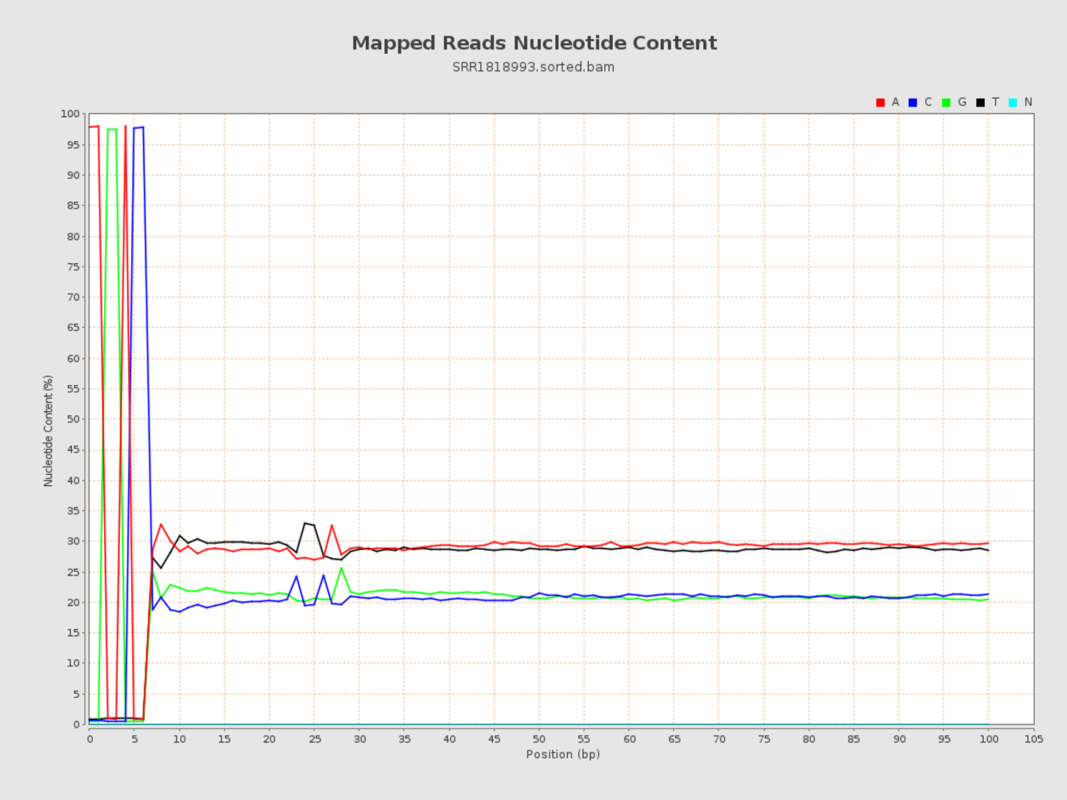
6. Results : Genome Fraction Coverage



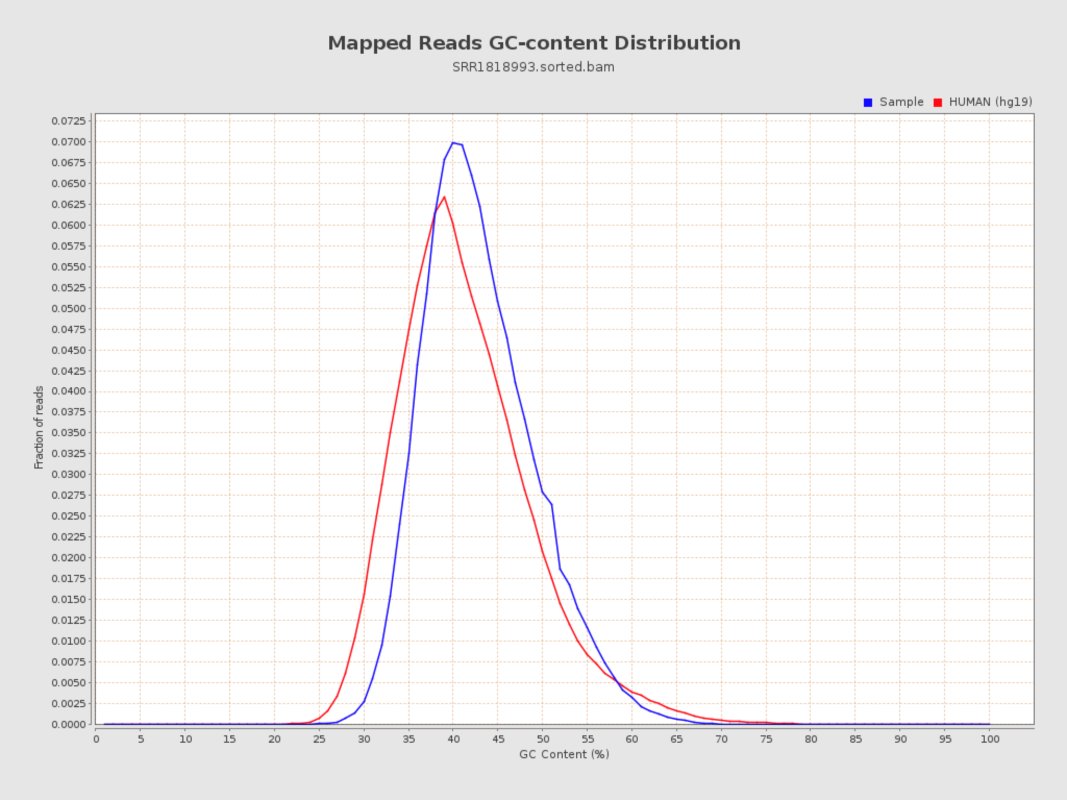
7. Results : Duplication Rate Histogram



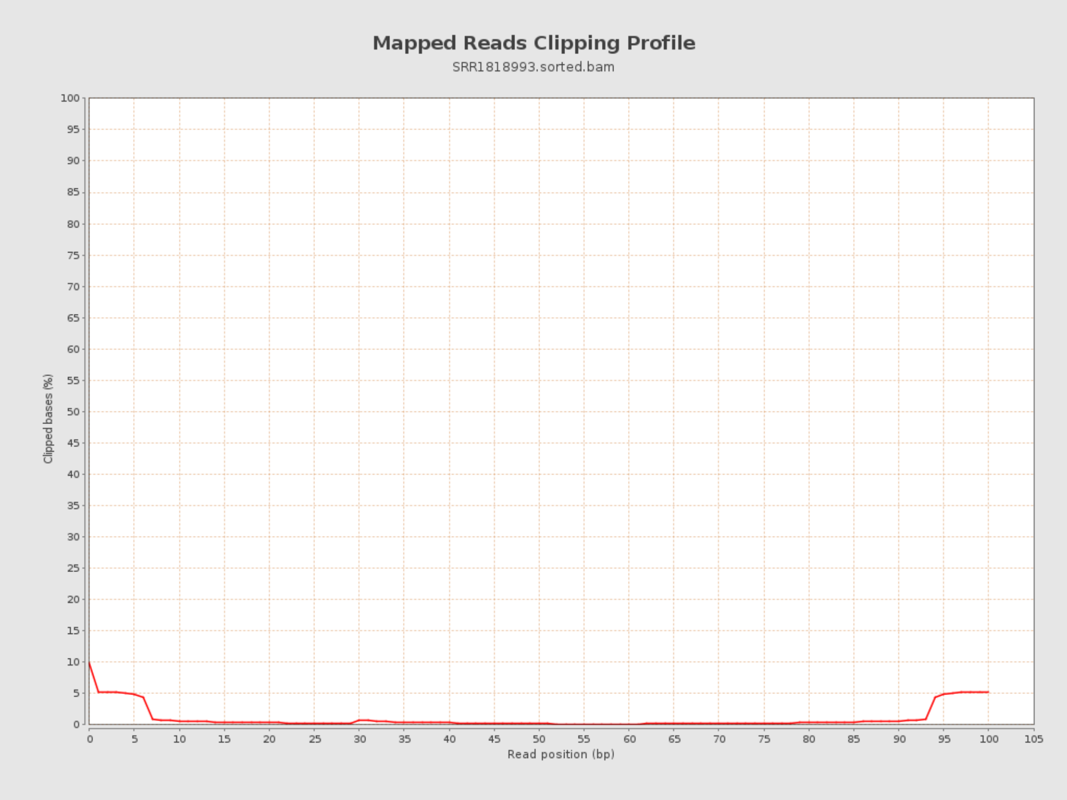
8. Results : Mapped Reads Nucleotide Content



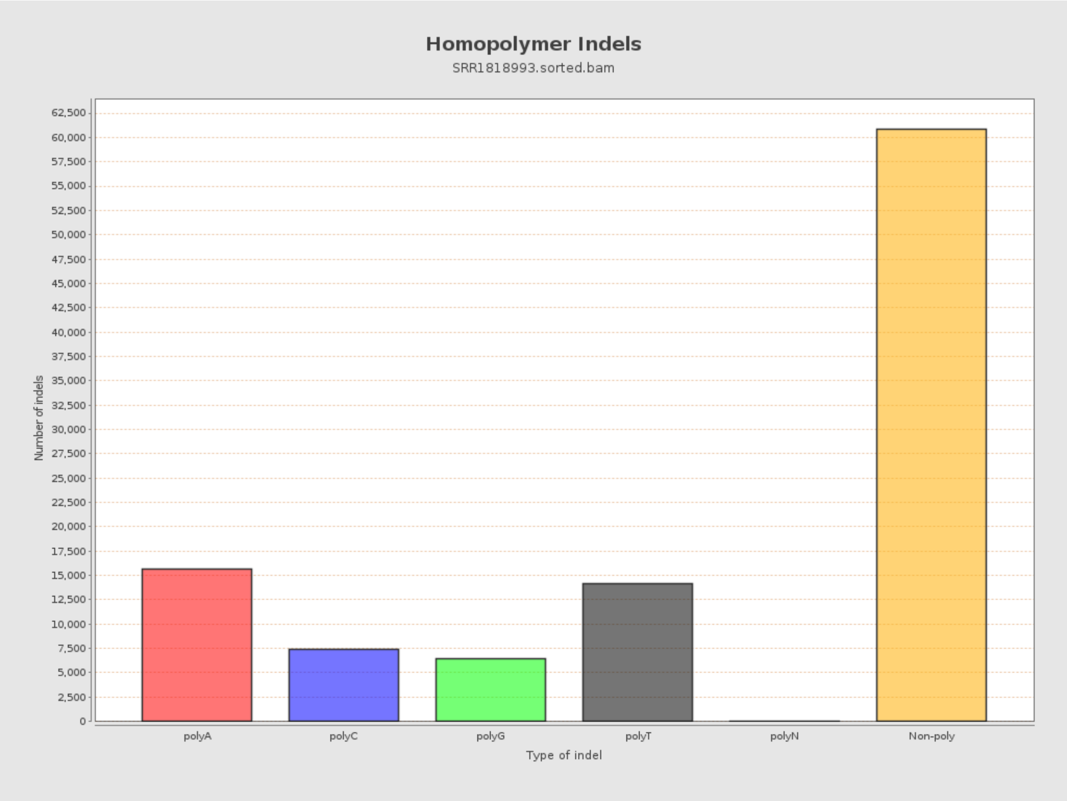
9. Results : Mapped Reads GC-content Distribution



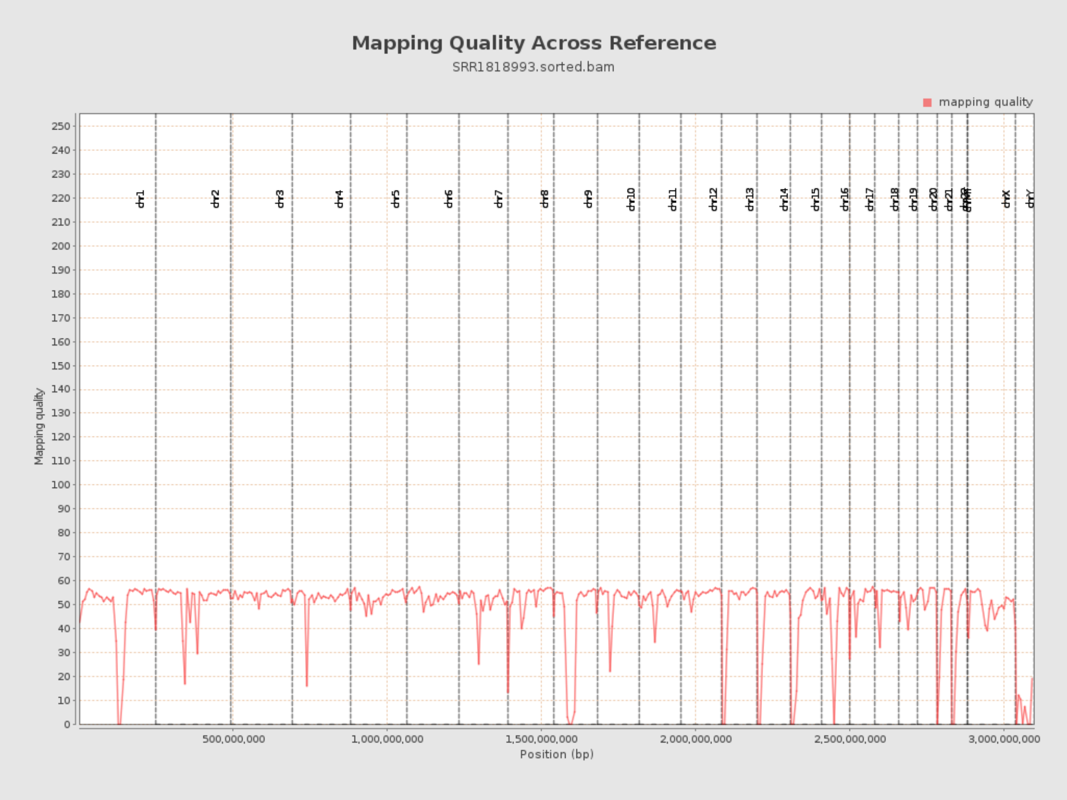
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram